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令和三年度　博士論文

アルツハイマー型認知症に対する介入候補素材としての *Faecalibacterium prausnitzii* 株の同定

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第 1 章 序論

1.1 アルツハイマー型認知症に対する介入の現状

認知症は世界的な健康課題である。世界保健機関（World Health Organization: WHO）の報告によると、認知症患者は 5000 万人であり、2015 年においては 1000 万人近くの方が新たに認知症を発症している [1]。認知症のうちの約 60-70%はアルツハイマー型認知症（Alzheimer's disease: AD）であることが分かっている [1]。AD に対して様々な治療方法が検討されたが、いずれも AD の進行において恐らく誤ったタイミング（遅すぎるタイミング）での検討がなされたため、病態改善を示すには至っていない [2]。近年の研究から AD の臨床症状が発症する約 20 年前からアミロイドβ（amyloid-β: Aβ）プラークやリン酸化タウ（tau）による神経原線維変化に代表される病理的な変化が起こっていることが分かっている [3]。さらに、蓄積した Aβを標的としたヒトモノクローナル抗体を用いた早期介入により、治療の可能性があることが示されつつある [4]。これらの研究から、早期診断および早期介入が必要であり、特に予防という観点では、AD の前段階の軽度認知障害（mild cognitive impairment: MCI）の前あるいはその間における介入が期待されている [5]。

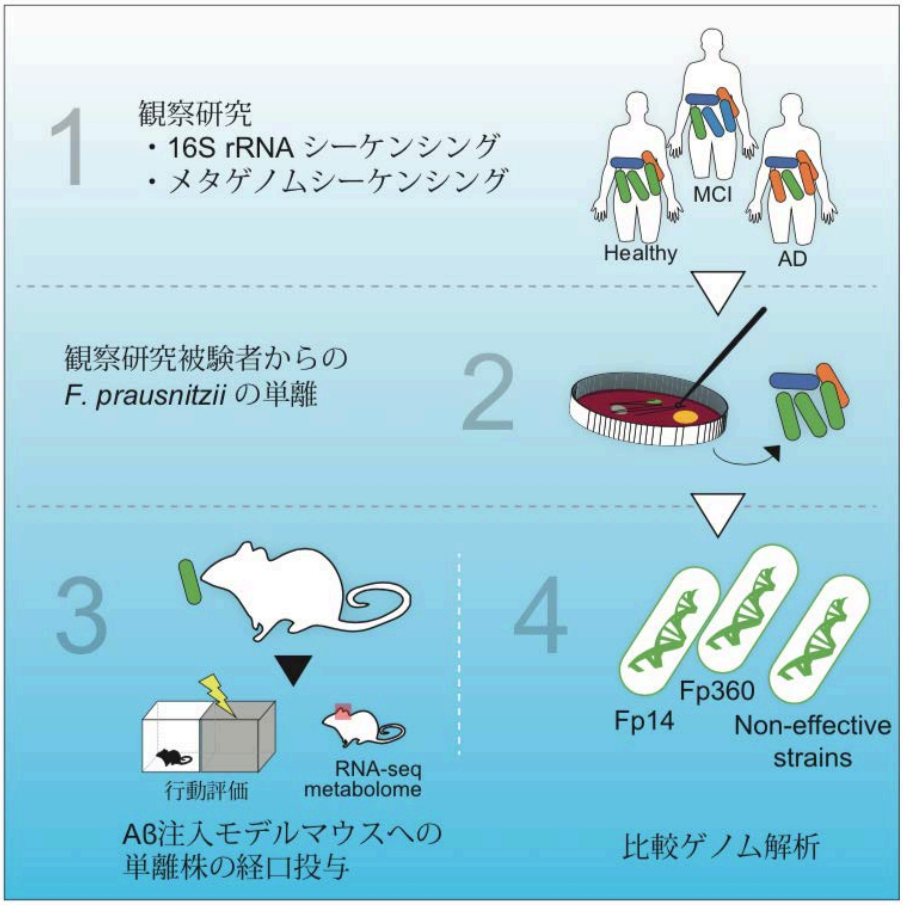
1.2 アルツハイマー型認知症における脳腸相関

腸内細菌と脳は、免疫系、迷走神経や腸管神経系など様々な経路を介して情報伝達を行っている（microbiota-gut-brain-axis、腸内細菌叢–腸–脳軸と呼ばれる）[6]。近年の研究から腸内細菌は microbiota-gut-brain-axis における主要制御因子であると考えられている [6]。特定の腸内細菌を用いて microbiota-gut-brain-axis を介して脳の健康に貢献するサイコバイオティックスと呼ばれる手法は病気に対する介入方法を開発する上で期待されている [6]。脳の病気に関して、自閉症、パーキンソン病、多発性硬化症、そして、AD において脳と腸内細菌の関係性が報告されている。例えば、AD のモデルマウスを用いた報告においては、抗生剤の投与や無菌化が Aβプラークを減少させている [7]。ヒトにおいては、いくつかの観察研究が MCI あるいは AD と腸内細菌との関係性を報告している。例えば、ある観察研究においては、*Bacteroides* の占有率が健常者群と比べ MCI 群で大きかったとの報告がある [8]。別の観察研究においては、*Blautia* や *Ruminococcus* の占有率が健常者群と比べ AD 群で小さかったとの報告がある [9]。このような背景から、特定の腸内細菌は MCI および AD に対する予防介入のための候補素材とな

り得る可能性がある。

1.3 本研究の目的及び構成

これらの背景から本研究においては、腸内細菌を介した MCI に対する介入候補素材を探索し、その候補素材の有効性や特徴を明らかにすることを目的とした。本研究の概要を図 1 に示した。まず、第 2 章では観察研究を実施し、健常者、MCI、および AD の方の糞便を用いた菌叢比較により *Faecalibacterium prausnitzii*（*F. prausnitzii*）を候補素材として選抜した結果を示した。第 3 章では観察研究被験者らから嫌気度要求性の高い *F. prausnitzii* の単離を行い、単離株の系統解析を実施した結果を示した。第 4 章では *F. prausnitzii* 単離株の認知機能に対する有効性を検討するために AD モデルマウスに単離株を投与した結果を示した。第 4 章において *F. prausnitzii* を素材として用いる上で死菌化が実効性のある解決方法となりうることが示されたため、第 5 章では死菌体懸濁液で認知機能に対する有効性を示した単離株 Fp14 の脳内作用メカニズムの検討を実施した結果を示した。第 6 章では認知機能に対する有効性を示した単離株 Fp14 および Fp360 と有効性を示さなかった残りの 10 株との全ゲノムを比較し、有効性を示した Fp14 および Fp360 に特徴的なオーソログを抽出した結果を示した。そして、有効性を示した Fp14 および Fp360 に特徴的なオーソログの観察研究被験者の糞便メタゲノム中の relative abundance を算出し、Fp14 と Fp360 に特徴的なオーソログと MCI や認知機能異常軽減効果との関連性についての考察を示した。第 7 章では上記アルツハイマー型認知症に対する介入候補素材としての *F. prausnitzii* 株の同定の結果を総括し、今後の展望を述べた。



第 2 章

第 3 章

第 4 章

第 5 章

第 6 章

図 1：本研究の概要

（Ueda A et al., *Cell Reports Medicine.* 2021;2(9):100398. https://doi: 10.1016/j.xcrm.2021.100398.より引用し日本語に改変。以下同様。）

第 2 章 ヒト観察研究における菌叢比較

2.1 目的

観察研究を実施し、健常者、MCI、および AD の方の糞便を用いた菌叢比較により、腸内細菌を介した MCI に対する介入候補素材を選抜した。

2.2 材料と方法

2.2.1 被験者選抜

図 2 のフローで被験者選抜を行った。健常者群と MCI 群においては、図 2A のように 2015 年群馬県草津町で 65 歳以上を対象として実施された縦断健康調査（にっこり健診）にて被験者を募集し[10]、説明会および同意取得を実施した。AD 群においては、図 2B のように上記縦断健康調査に参加されている方、草津町の老人ホームにお住まいの方、あるいは、草津町の介護サービスを利用されている方から被験者を募集し、説明会および同意取得を実施した。

被験者に対して 1） 認知機能検査としてミニメンタルステート検査（MMSE*: Mini-Mental State Examination）[11]、Montreal Cognitive Assessment Japanese version（MoCA-J**）[12]、および、臨床認知症尺度（CDR*** : Clinical Dementia Rating）[13] 、2） 日常生活動作能力 basic Activities of Daily Living（ADL）検査として老研式活動能力指標（TMIG-Index of Competence****）[14]、3） 医師の問診（既往歴、薬剤使用等）、4） 血液検査、血圧などその他健診[15]を実施した。説明会、同意取得および検査は東京都健康長寿医療センターの新開省二先生、谷口優先生、北村明彦先生、清野論先生、池内朋子先生、藤原佳典先生、大塚製薬（株）戸羽正道氏と共同で実施した。

*MMSE は時間の見当識、場所の見当識、3 単語の即時再生と遅延再生、計算、物品呼称、文章復唱、3 段階の口頭命令、書字命令、文章書字、図形模写の計 11 項目から構成される 30 点満点の認知機能検査である（日本語標記は日本老年医学会の表記を参考にした）[11]。

**MoCA-J は視空間・遂行機能、命名、記憶、注意力、復唱、語想起、抽象概念、遅延再生、見当識からなり、MCI をスクリーニングする 30 点満点の検査である（日本語標記は日本老年医学会の表記を参考にした）[12]。

***CDR は記憶、見当識、判断力と問題解決、地域社会の活動、家庭および趣味、及び身の回りの世話の 6 項目について遂行検査を被験者に行わせるだけでなく、被験者の情報提供者に 6 項目についてどの程度障害されているか評

価させ、認知症の重症度を測定する検査である[13,16]。

**** TMIG-Index of Competence は手段的 ADL（交通機関を使っての外出、買い物、食事の準備、請求書の支払いなど)、知的能動性（書類を書く、新聞を読む、本・雑誌を読むなど)、社会的役割（友人への訪問、家族や友人からの相談、病人のお見舞いなど）の 13 項目からなる（日本語標記は日本老年医学会の表記を参考にした）[14]。

認知機能検査や採便が実施可能であり、選択基準に合致し、除外基準に抵触しない被験者を選抜した。

>選択基準：

Petersen らは、MCI の概念：(1）本人または家族（介護者）による物忘れの訴えがある、(2）加齢の影響だけでは説明できない記憶障害の存在、(3） 日常生活能力は自立、(4）全般的な認知機能は正常、(5）認知症は認めない、を提唱している[17,18]。今回はこの基準に従い、健常者群および MCI 群を選択した。

-健常者群：1） 半年以内に記憶愁訴がない、2） MMSE 24 点以上、3） MoCA-J 26 点以上、4） CDR = 0、5） ADL に異常がない（TMIG-Index of Competence = 5)、6） 神経的、精神的疾患がない

-MCI 群：1） 半年以内に記憶愁訴がある、2） MMSE 24 点以上、3） MoCA-J 25 点以下、4） CDR = 0.5、5） ADL に異常がない（TMIG-Index of Competence = 5)、6） 神経的、精神的疾患がない

-AD 群 : Diagnostic and Statistical Manual of Mental Disorders （DSM）-IV criteria に従い選抜した[19]: 1）多彩な認知障害（記憶障害および実行機能障害、失行、失認、失語のうち 1 つ以上の障害)、2） 1）の認知障害が、社会的あるいは職業的機能の著しい障害を引き起こし、また、病前の機能水準からの著しい低下を示す、3） 経過は、ゆるやかな発症と持続的な認知機能の低下により特徴づけられる、4） 1）に示した認知機能の障害は、記憶と認知に進行性の障害を引き起こす他の中枢神経疾患、認知症を引き起こすことが知られている全身性疾患、あるいは外因性物質による認知症痴呆のいずれによるもので

もない、5） 上記の障害は、意識障害（せん妄）の期間中だけに出現するものではない、6） 障害は他の主要精神疾患（例：うつ病、精神分裂病など）ではうまく説明されない。なお、当研究では DSM-IV に基づいた診断において、脳画像の取得は行っていない。もし National Institute of Neurological and Communicative Disorders and Stroke & the Alzheimer's Disease and Related Disorders Association （NINCDS-ADRDA）など他の分類に従うと、当試験の AD の方は possible AD あるいは probable AD に分類される。

>除外基準：

（除外基準とはある母集団から研究参加者を対象へと組み入れる過程において、その研究の対象として不適格となるような参加者の特性がある場合や、研究参加に対する参加の許諾が得られない場合など、参加者を対象者から除外する際の基準のこと。日本語標記は日本理学療法学会の標記を参照した）[20]

1）採便日の 2 週間前までに抗生剤の投与を受けた者

2）同意取得の半年以内に開腹手術を受けた者

3）消化器の既往歴（胃切除、IBD（クローン病、潰瘍性大腸炎）、IBS、がん）がある者

4）糖尿病の者

5）アルツハイマー病以外の神経的、精神的疾患の既往歴がある者

>倫理：当試験はヘルシンキ宣言に従い実施した。試験実施前に試験内容を詳細に説明した上で、被験者から文書による同意を取得した。試験計画の倫理委員会の承認取得作業は東京都健康長寿医療センターおよび大塚製薬（株）と共同で実施し、東京都健康長寿医療センターの倫理委員会の承認を得た。

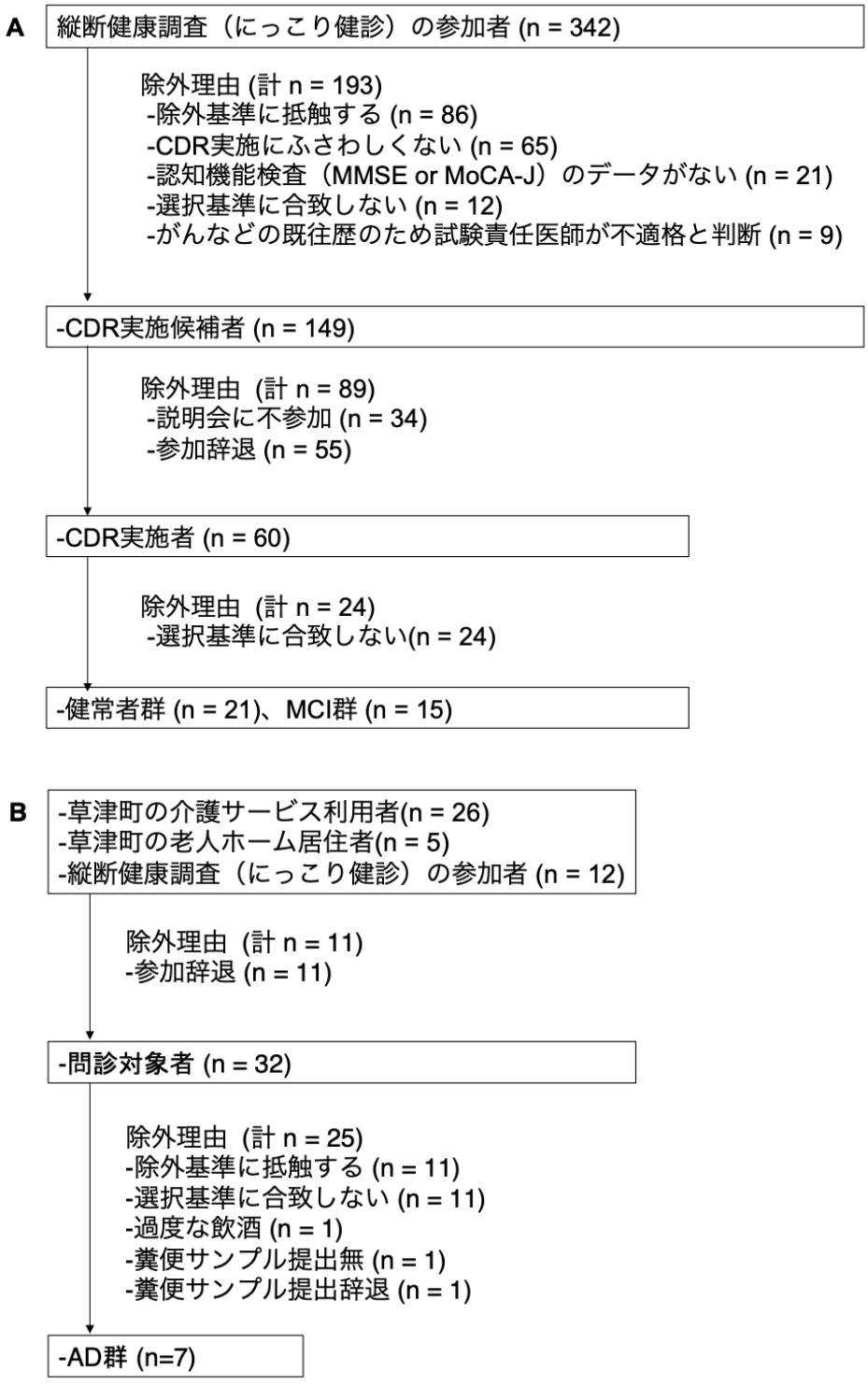


図 2：被験者選抜フロー
（A） 健常者群と MCI 群の被験者選抜フロー、（B） AD 群の被験者選抜フロー

選抜の結果、健常者群（n = 21、%女性= 61.9）、MCI 群 （n = 15、%女性 = 60.0）、AD 群 （n = 7、%女性 = 71.4）を選抜した（表 1、付録 1）。当試験は観察研究であり介入試験であるためサンプルサイズの推定は実施せず、選抜した候補菌株の妥当性に関しては動物モデルで確認することとした。

表 1：選抜した被験者の背景情報
当観察研究における選抜した被験者の背景情報を表 1 に示した。性別以外の値は mean ± S.D. で示した。性別以外の *p* 値はウィルコクソンの順位和検定の結果を示した（vs 健常者群）。性別の *p* 値はフィッシャーの正確確率検定の結果を示した（vs 健常者群）。

	健常者群 （n = 21）	MCI 群 （n = 15）	AD 群 （n = 7）	*p* 値 （HvsM）	*p* 値 （HvsA）
年齢 （歳）	72.7±5.3	79.8±6.1	83.0±9.3	0.0014	0.0092
性別 （n, %女性）	13, 61.9	9, 60.0	5, 71.4	1	1
BMI （kg/m^2）	22.7±3.7	24.4±2.3	22.9±2.7	0.1828	0.8735
MMSE （スコア）	29.5±0.7	26.9±2.3	15.6±4.3	0.0001	<0.0001
MoCA-J （スコア）	27.6±1.5	19.8±2.7	8.4±4.0	<0.0001	<0.0001
学歴 （年）	11.2±1.7	9.8±3.6	8.3±2.0	0.2146	0.0025

2.2.2 糞便 DNA 抽出

糞便サンプルを排便後速やかに 100 mM Tris-HCl （pH 9）、40 mM EDTA、4 M guanidine thiocyanate、0.001% bromothymol 溶液に懸濁し、-80℃に凍結保存した[21]。凍結糞便から GENOME DNA Isolation Kit （MP Biomedicals、USA）を用いて DNA を抽出した[21]。抽出した DNA の品質は Agilent 4200 Tape Station（Agilent Technologies、USA）により確認した。抽出 DNA は TE buffer により懸濁し-80℃に保存した。DNA 抽出および品質確認は（株）日本遺伝子研究所で実施頂いた。

2.2.3 16S rRNA 遺伝子シーケンシング

16S rRNA遺伝子のV3-V4領域をユニバーサルプライマー342F-806R（342F：CTACGGGGGGCAGCAG、806R：GGACTACCGGGGTATCT）を用いてPCR増幅し[22]、Nextera XT Index Kit （Illumina、USA）によりindex付加を行った。目的領域の抽出はE-Gel® SizeSelect™ Gels（Thermo Fisher Scientific、USA）により行い、PCR産物の精製はAMpure XP beads（Beckman Coulter、USA）により行った。濃度測定はQuant-iT dsDNA HS Assay kit （Thermo Fisher Scientific）により行い、

High Sensitivity DNA kit （Agilent Technologies）によりライブラリー溶液の品質を確認した。各サンプルのライブラリー液を等mol混合し、Miseqシーケンシングを実施した（300bp、pair-end)。シーケンシング はタカラバイオ（株）で実施頂いた。サンプル平均で約126488のraw readを得た（付録1)。NCBI Sequence Read Archive (SRA) BioProject PRJNA679347にてリードを登録した。

2.2.4 Relative abundance の解析および Differential abundance analysis

得られたシーケンスリードを QIIME2 （v2019.7.0） の解析パイプラインで解析した[23]。具体的には dada2 plugin によりクオリティーコントロールを実施し、デノイジング、PhiX 配列の削除、3’末端側のクオリティーの低い塩基の削除（quality score の中央値が 25 を下回る時の length で閾値を設定： --p-trunc-len-f 282 --p-trunc-len-r 225)、キメラ配列の削除およびプライマー配列の削除を実施した。サンプル平均で約 63215 の high quality read を得た（付録 1)。続いて、GTDB（Genome Taxonomy Database、GTDB_bac120_arc122_ssu_r89.fa）から 16S rRNA 遺伝子の V3-V4 領域を抽出し、その配列情報と系統情報を用いて細菌系統を推定するナイーブベイズ分類器を作成した。構築した分類器を用いて、各サンプルから得られたシーケンスデータを入力として、細菌属レベルの系統組成を算出した。relative abundance の解析においてはリード数が 10000 を満たないサンプルは除き、1 あるいは 2 サンプルでしか検出されない属および平均 relative abundance が 0.01%に満たない属は除いた。健常者群と MCI 群あるいは健常者群と AD 群の群間比較においては R （v3.6.3）によりウィルコクソンの順位和検定を実施した。加えて、FDR 補正した q 値を算出した。検定の有意水準は $p < 0.05$ とした。

relative abundance の解析では、カウントデータを組成データにして解析を行うため、組成データ特有の制約が乗じる（定数和制約：変数の総和が定数で固定されるため、ある変数が増加すると他の変数は実際に増加していても減少することがある）[24]。この制約を解決する対数比変換を行う Differential abundance analysis の解析を R の ALDEx2 library を用いて実施した。健常者群と MCI 群あるいは健常者群と AD 群の群間比較においては R によりウィルコクソンの順位和検定を実施した。加えて、FDR 補正した q 値を算出した。検定の有意水準は $p < 0.05$ とした。

2.2.5 菌叢の全体像に関する解析および相関解析

QIIME2 および R を用いて α 多様性の指標である Shannon-Wiener 多様度指数* を算出した。また、β 多様性の指標である Bray-Curtis 指数**を算出し、principal coordinates analysis （PCoA） により図示した。健常者群と MCI 群あるいは健常者群と AD 群の群間比較は R を用いてウィルコクソンの順位和検定を実施した。検定の有意水準は $p < 0.05$ とした。

生物群集構造の類似度の群間比較は R を用いて permutational multivariate analysis of variance （PERMANOVA）を実施した[25]。PERMANOVA は距離行列を用いて、グループ間の距離の変動とグループ内の距離を比較して、グループ間の距離が相対的に大きい時にグループに差があると判断する分散分析である（R^2:エフェクトサイズ、$p < 0.05$：グループ間の距離に有意な差あり）[25]。

細菌属の relative abundance と認知機能検査（MoCA-J）スコア（2.2.1 参照）との相関は R を用いて Spearman’s rank-correlation analysis を実施した。検定の有意水準は $p < 0.05$ とした。

* Shannon-Wiener 多様度指数 H’

$$H' = -\sum_{i=1}^{s} pi \ln pi$$

S: 種の数、Pi=ni/N: i 番目の種類の個体数が総個体数 N に占める割合。この指数は種数が多いほど、かつ各種の均等度が高いほど、高い数値になる。

**Bray-Curtis 指数

$$B = \frac{\sum_{i=1}^{n} \left| X_{ij} - X_{ik} \right|}{\sum_{i=1}^{n} \left(X_{ij} + X_{ik} \right)}$$

X ij ：サンプル j で観測された種 i の read 数、X ik ：サンプル k で観測された種 i の read 数、n ：全サンプルで観測された種の数、ただし 0≦B≦1、群集が似ているとき 0 で、まったく異なるときに最大値 1 をとる。

2.3 結果

2.3.1 菌叢の全体像に関する解析

観察研究を実施し、健常者（n=20）、MCI の方（n=15）、および AD の方（n=7）の糞便を用いた菌叢比較を実施した。42 名の被験者から 129 属（平均 67 属/被験者）が検出された。この細菌系統組成を用いた PERMANOVA を実施した結果、健常者群と MCI 群の間で群集構造が異なる傾向が見られた（R^2 = 0.0465、p = 0.0968）が、健常者群と AD 群との間ではその傾向はみられなかった（R^2 = 0.0534、p = 0.1423）。β 多様性の指標である Bray-Curtis 指数を算出した結果、健常者群よりも MCI 群および AD 群で指数が大きく（それぞれ $p = 2.92\times10^{-5}$、p = 0.0203）、この傾向は PCoA で確認された（図 3A、3B）。α 多様性の指標である Shannon-Wiener 多様度指数においては、群間差は見られなかった（図 4）。

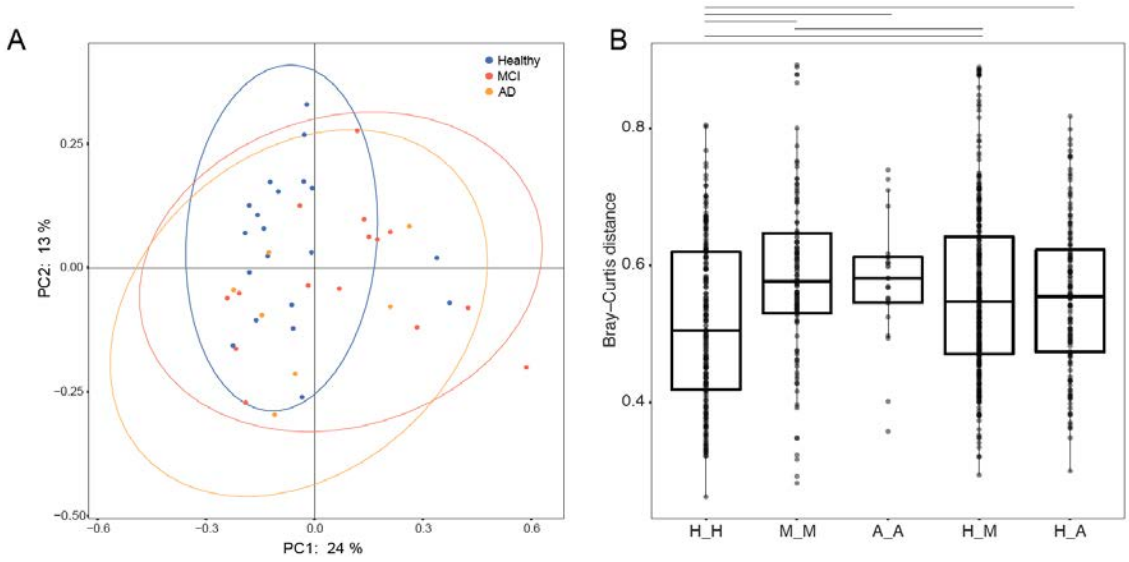


図 3：β 多様性の解析結果

（A）Bray-Curtis 指数を用いた principal coordinates analysis （PCoA）解析、（B）群内の Bray-Curtis 指数（結果は PCoA の傾向を反映）。黒色線は $p < 0.05$ を示す（ウィルコクソンの順位和検定）。健常者（n=20）、MCI の方（n=15）、および AD の方（n=7）。

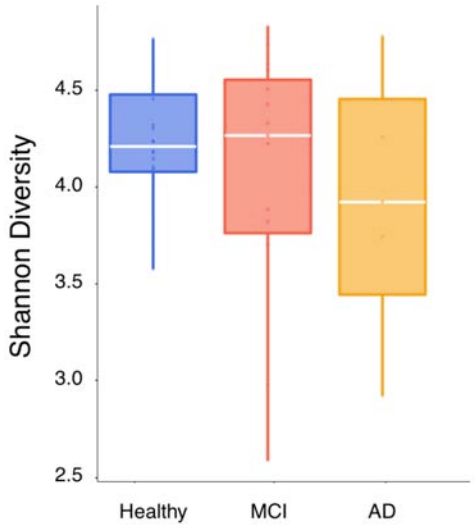


図 4：α多様性の解析結果
各群の Shannon-Wiener 多様度指数（ウィルコクソンの順位和検定、群間差無）。健常者（n=20）、MCI の方（n=15）、および AD の方（n=7）。

2.3.2 Relative abundance の解析

図 5A に属レベルの relative abundance の群間比較結果を示した。129 属が検出され、健常者群と MCI 群の間で 7 つの属で relative abundance に差が見られた（図 5B、付録 2）。*Faecalibacterium*、*Ruminococcaceae genus* unclassified、*Anaerostipes*、*Ruminoccocus_C*、*CAG-41* および *Barnesiella* は MCI 群で減少していた。*Prevotella* は MCI 群で増加していた（図 5B、付録 2）。健常者群と AD 群の間で 5 つの属で relative abundance に差が見られた（図 5C、付録 2）。*Blautia_A*、*Fusicatenibacter*、*Ruminococcus_C*、および *Eubacterium_I* は AD 群で減少していた. *Parabacteroides* は AD 群で増加していた（図 5C、付録 2）。

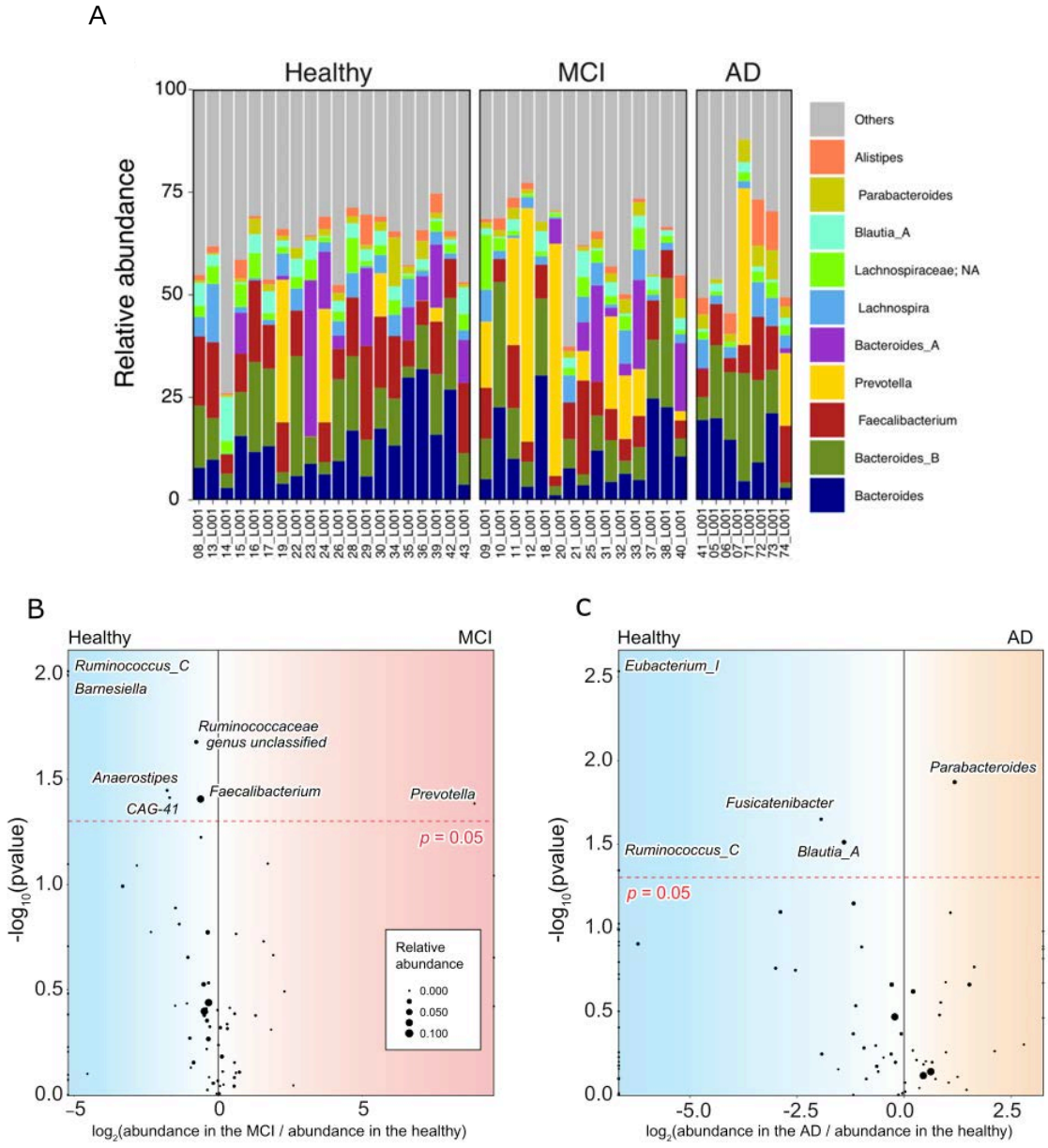


図 5：relative abundance の群間比較結果

（A）被験者それぞれの属レベルの菌叢構造、（B および C）健常者群（n=20）と（B）MCI 群（n=15）あるいは（C）AD 群（n=7）との間で relative abundance に有意な差が見られた属を示す。(B) X 軸: $\log_2$（MCI 群の relative abundance の中央値/健常者群の relative abundance の中央値）。（C）X 軸： $\log_2$ （AD 群の relative abundance の中央値/健常者群の relative abundance の中央値）。Y 軸： $-\log_{10}$ （ウィルコクソンの順位和検定の *p* 値）。赤の水平線： $p = 0.05$。丸の大きさ：それぞれの属の relative abundance。いずれの群の abundance の中央値が 0 の属は示されていない。*Faecalibacterium* 属は一属一種のため *F. prausnitzii* 種と *Faecalibacterium* 属の relative abundance は同じ。

2.3.3 Differential abundance analysis

relative abundance の解析では、特定の生物属にマッピングされた read のカウントデータをその細菌属の組成データにして解析を行うため、組成データ特有の制約（2.2.4 参照）が乗じる。この制約を解決する対数比変換を行う Differential abundance analysis の解析を R の ALDEx2 library を用いて実施した。2.3.2 で群間差の見られた属のうち、健常者群と MCI 群の間で 6 つの属で対数比変換後の relative abundance に差が見られた（図 6A、付録 3）。*Faecalibacterium*、*Ruminococcaceae genus* unclassified、*Anaerostipes*、*Ruminoccocus_C*、および、*CAG-41* は MCI 群で減少していた。*Prevotella* は MCI 群で増加していた（図 6A、付録 3）。健常者群と AD 群の間で 1 つの属で対数比変換後の relative abundance に差が見られた（図 6B、付録 3）。*Eubacterium_I* は AD 群で減少していた（図 6B、付録 3）。これらの relative abundance の群間差を図 7 に示した。

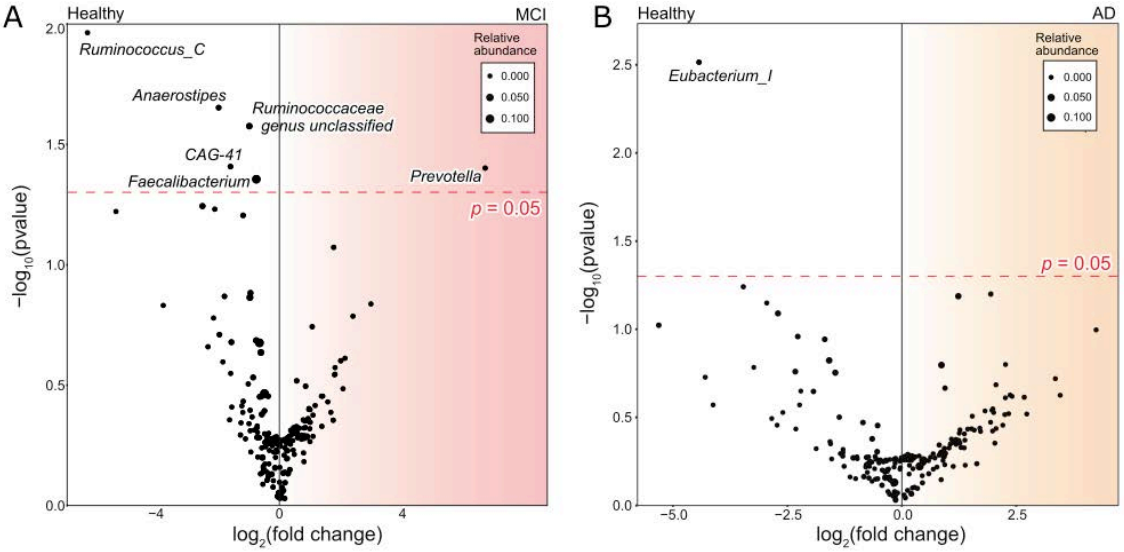


図 6：Differential abundance analysis の群間比較結果
（A および B）Differential abundance analysis （ALDEx2）により健常者群（n=20）と（A）MCI 群（n=15）あるいは（B）AD 群（n=7）との間で対数比変換後の relative abundance に有意な差が見られた属を示す。（A）X 軸： $\log_2$ （健常者群に対する MCI 群の fold change）。（B）X 軸： $\log_2$ （健常者群に対する AD 群の fold change）。Y 軸： $-\log_{10}$ （ウィルコクソンの順位和検定の *p* 値）。赤の水平線： $p = 0.05$。丸の大きさ：それぞれの属の relative abundance。*Faecalibacterium* 属は一属一種のため *F. prausnitzii* 種と *Faecalibacterium* 属の対数比変換後の relative abundance は同じ。

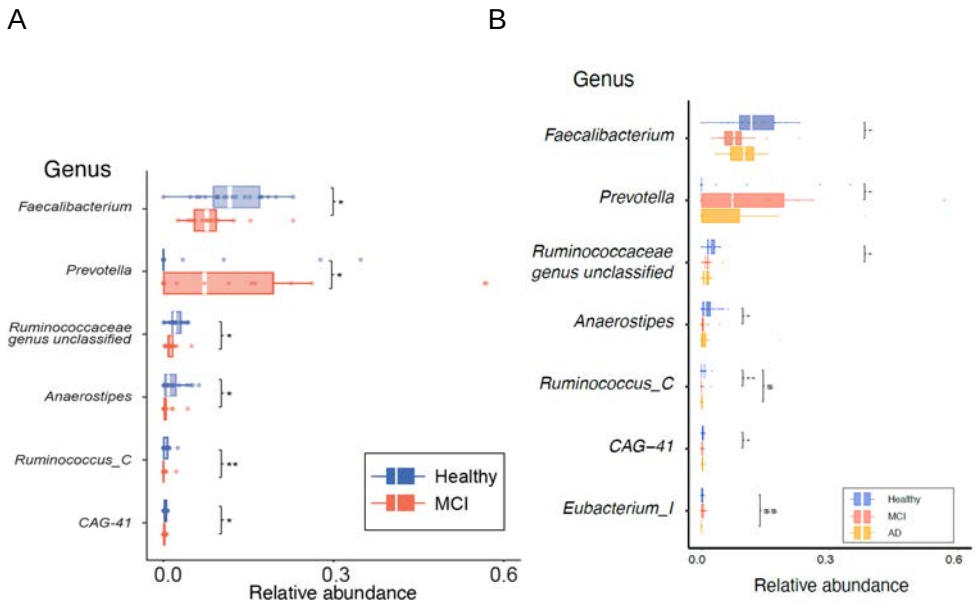


図 7：Differential abundance analysis により差の見られた属の relative abundance
（A）健常者群と MCI 群の間で差の見られた 6 属の relative abundance（ウィルコクソンの順位和検定、$^{**}p < 0.01$、$^{*}p < 0.05$）、（B）健常者群と MCI 群の間あるいは AD 群との間で差の見られた 7 属の relative abundance（ウィルコクソンの順位和検定、健常者群 vs MCI 群：$^{**}p < 0.01$、$^{*}p < 0.05$、健常者群 vs AD 群: $^{\$\$}p < 0.01$、$^{\$}p < 0.05$）、健常者（n=20）、MCI の方（n=15）、および AD の方（n=7）。

2.3.4 *F. prausnitzii* と認知機能の相関解析

認知症の予防という観点では、AD の前段階の軽度認知障害（MCI）の前あるいはその間における介入が期待される。したがって、腸内細菌を介した MCI に対する予防介入候補素材を探索する上で、健常者群と AD 群の間の比較よりも健常者群と MCI 群との比較の方に着目した。健常者群と比べ MCI 群で減少し、属レベルの relative abundance と認知機能検査（MoCA-J）スコアの相関がある属を選抜するため、相関解析を実施した。結果、2.3.3 で健常者群と比べ MCI 群で減少している 6 つの属の relative abundance は認知機能検査（MoCA-J）スコアと相関関係が見られた（付録 4、図 8）。その中で、relative abundance が多く、認知機能検査（MoCA-J）スコアとの相関があり、次世代健康有用菌として着目されている *F. prausnitzii* を候補として選抜した（図 8）。

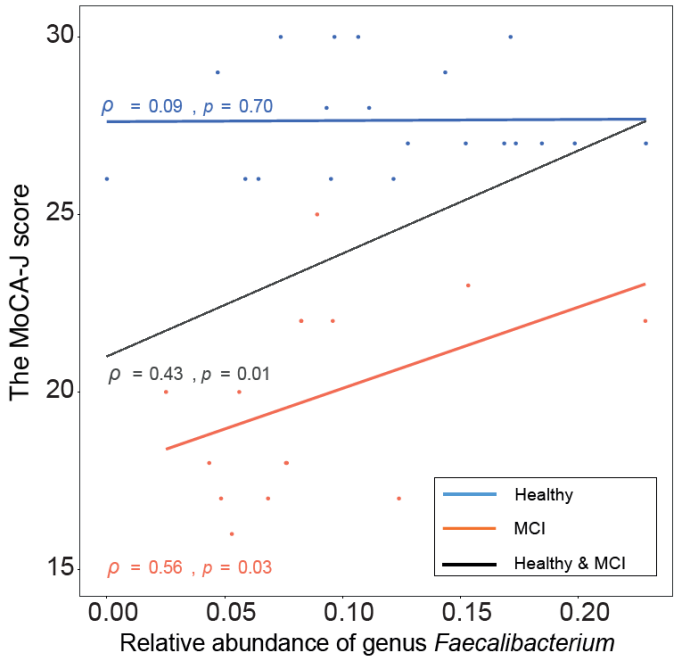


図 8：認知機能検査スコアと *F. prausnitzii* の relative abundance の相関解析結果
認知機能検査（MoCA-J）スコアと *F. prausnitzii* のスピアマンの順位相関係数 ρ および *p* 値（blue : 健常者群、red : MCI 群、black : 健常者群＋MCI 群）、健常者（n=20）、MCI の方（n=15）、および AD の方（n=7）。

2.4 考察

認知症の予防という観点では、AD の前段階の軽度認知障害（MCI）の前あるいはその間における介入が期待される。当研究では、腸内細菌を介した MCI に対する予防介入候補素材を探索した結果、relative abundance が多く、認知機能検査（MoCA-J）スコアとの相関があり、次世代健康有用菌として着目されている *F. prausnitzii* を候補として選抜した（図 6、7、8）。しかしながら、当観察研究においては、表 1 のようにサンプルサイズ、性別、年齢に群間に不均衡が見られた。特に年齢に関しては加齢と共に腸内細菌が変化することが知られているため相関解析を実施したところ [26]、年齢と *F. prausnitzii* の relative abundance との間に相関は見られなかった（図 9A）。この結果から、*F. prausnitzii* が MCI 群で減少していたことは、群の違い（病態の違い）に関係していると推測された。サンプルサイズの不均衡に関しては、MCI および AD 群を認知機能低下群（n=22）としてまとめることで不均衡を軽減し、健常者群（n=20）との *F. prausnitzii* の relative abundance を探索的に比較したところ認知機能低下群での *F. prausnitzii* の減少が依然見られたことを確認している。今後、群間で年齢を調整したよりサ

ンプル数の多い観察研究あるいは縦断研究による検証が期待される。健常者群と MCI 群との比較により得られた我々の結果（=*F. prausnitzii* が MCI 群で減少していた、図 6、7）は、これまで報告されている研究と類似点と相違点が見られた [8,27,28]。本邦において実施された観察研究では、MCI 群と比べ健常者群で *Bacteroides* の存在量が少ないとの報告があり、*F. prausnitzii* については言及されていなかった。この違いは、他の研究においても報告されているように [29,30]、腸内細菌の解析方法の違い（我々の 16S rRNA の次世代シーケンシング解析と T-RFLP 法）によるものと考察された。中国において実施された別の観察研究においては、我々の研究と同様に *F. prausnitzii* が健常者群と比べ MCI 群において減少している事が報告されているが [27]、米国において実施された別の観察研究では結果が異なっていた [28]。これらの結果の類似や相違は、他の研究でも述べられているように地理、文化、そして、食生活など被験者背景の違いによるものであると推測された [31]。健常者群と AD 群との比較に関して、我々の研究では AD 群において *F. prausnitzii* の減少や *Prevotella* の増加は観察されず、健常者群と MCI 群との比較結果と異なっていた（図 6、7、9）。この理由は現在不明であるが、とある米国で実施された観察研究の結果と一致していた [32]。しかしながら、中国や米国で実施された別の観察研究では AD 群において *F. prausnitzii* の減少や *Prevotella denticola* の増加が報告されており我々の結果と異なっていた [33,34]。これらの結果の類似や相違に関しても地理、文化、そして、食生活など被験者背景の違いによるものであると推測された [31]。*F. prausnitzii* の減少が普遍的な現象であるのかについては、複数地域で観察研究を実施し検証する必要があると考える。

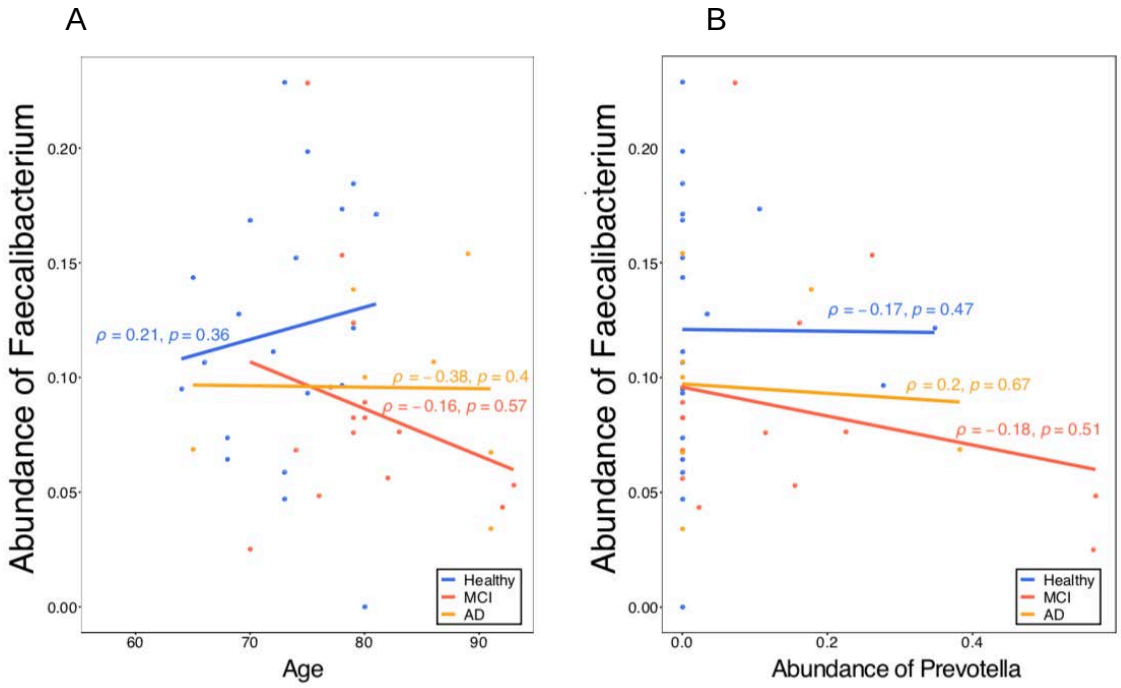


図 9：年齢と relative abundance の相関解析結果
（A）年齢と relative abundance のスピアマンの順位相関係数 ρ および *p* 値を示す（blue：健常者群、red：MCI 群、orange：AD 群）、（B）*Faecalibacterium* の relative abundance と *Prevotella* の relative abundance のスピアマンの順位相関係数 ρ および *p* 値を示す（blue：健常者群、red：MCI 群、orange：AD 群）、 *Faecalibacterium* の relative abundance と年齢や *Prevotella* の relative abundance に相関は見られなかった。

AD の病態は長期において進行し、住居や食事などライフスタイルも変化することも考慮した上で、我々は予防的な介入に着目している背景から、relative abundance が多く、認知機能検査（MoCA-J）スコアとの相関があり、MCI 群で減少していた *F. prausnitzii* に着目した（図 6、7、8）。*F. prausnitzii* は様々な国の観察研究の microbiome においてアバンダントなだけでなく [35–37]、潰瘍性大腸炎、糖尿病、慢性腎臓病など様々な疾患において *F. prausnitzii* が減少しており [38,39]、近年、次世代健康有用菌として着目されている [39,40]。これらの報告と我々の観察研究の結果を考慮し、腸内細菌を介した MCI に対する介入候補素材として *F. prausnitzii* を選択し、単離した（第 3 章）。また、動物に対して単離した *F. prausnitzii* を投与し、認知機能との関連性を検討した（第 4 章）。

第 3 章 観察研究被験者からの *F.prausnitzii* の単離

3.1 目的

腸内細菌を介した軽度認知障害（mild cognitive impairment: MCI）に対する介入候補素材として選抜した*F. prausnitzii* を第 2 章の観察研究被験者らから単離した。

3.2 材料と方法

3.2.1 糞便からの単離

第 2 章の健常者（Fp1、Fp4、Fp14、Fp28、Fp40、Fp45、Fp77、Fp360）および MCI（Fp944）の被験者の糞便から *F. prausnitzii* を単離した。試験実施前に試験内容を詳細に説明した上で、被験者から文書による同意を取得した。並行して、30 代の健常者 2 名の糞便より *F.prausnitzii*（Fp137、Fp1043、Fp1160）を単離した。試験実施前に試験内容を詳細に説明した上で、被験者から文書による同意を取得した。試験計画の倫理委員会の承認取得作業は東京都健康長寿医療センターおよび大塚製薬（株）と共同で実施し、東京都健康長寿医療センターおよび大塚製薬（株）の倫理委員会の承認を得た。以下の単離作業は東京都健康長寿医療センター谷口優先生、大塚製薬（株）小谷吉史様、狩屋貴洋様、戸羽正道様、中部大学牛田一成先生、土田さやか先生と共同で実施した。

採便後速やかに、嫌気チャンバー（N_2 = 90%、CO_2 = 5%、H_2 = 5%）内にて糞便を希釈培地（per 1 L; K_2HPO_4 0.45 g、NaCl 0.9 g、$(NH_4)_2SO_4$ 0.9 g、KH_2PO_4 0.45 g、$MgSO_4{\cdot}7H_2O$ 0.19 g、$CaCl_2{\cdot}2H_2O$ 0.12 g、Na_2CO_3 80 g、resazurin 1 mg、L-cysteine·HCl·H_2O 0.5 g）で 10^{-5} から 10^{-7} に希釈した。希釈糞便溶液を YCFA agar（per 1 L; casitone 10 g、yeast extract 2.5 g、$NaHCO_3$ 4 g、glucose 4.5 g、hemin 10 mg、Tween 80 1 mL、agar 15 g、K_2HPO_4 0.45 g、KH_2PO_4 0.45 g、$(NH_4)_2SO_4$ 0.9 g、NaCl 0.9 g、$MgSO_4{\cdot}7H_2O$ 0.09 g、$CaCl_2{\cdot}2H_2O$ 0.12 g、L-cysteine·HCl·H_2O 1.4 g、acetic acid 53 μL、propionic acid 19 μL、n-valeric acid 3.1 μL、iso-valeric acid 3.1 μL、iso-butyric acid、3.1 μL）あるいは EG agar（per 1 L; Lab-Lemco powder 2.4 g、proteose peptone 10 g、yeast extract 5 g、Na_2HPO_4 4 g、glucose 1.5 g、soluble starch 0.5 g、L-cystine 0.2 g、Tween 80 1 mL、agar 15 g、L-cysteine·HCl·H_2O 0.5 g、horse blood 50 mL）に塗布した。37℃にて 1-2 日間培養後、凡そ 4000 コロニーをピックアップし、新しい YCFA agar あるいは EG agar に塗布した。シングルコロニー化するため、コロニーピックアップおよび新しい培地への塗布を繰り返したのち、20%glycerol ストック溶液に懸濁し、-80℃でストック保存した。

3.2.2 単離株の系統解析

ストック保存前にコロニーを DNA 抽出溶液（5% Triton X-100 およびガラスビーズ）に懸濁してホモジナイズし、16S rRNA 遺伝子をユニバーサルプライマー（27F（5’-AGAGTTTGATCCTGGCTCAG-3’）[41]、1492R（5’-GGTTACCTTGTTACGACTT-3’）[42]）にて PCR 増幅した。27F プライマーを用いて 16S rRNA 遺伝子のシーケンシングを行い、異なる 3 つのデータベース（NCBI、Eztaxon、Living Tree Project、date: Nov 2016）に対して Basic Local Alignment Search Tool （BLAST） を実施し、系統を決定した。シーケンシングは北海道システムサイエンス（株）に実施頂いた。

3.2.3 *F. prausnitzii* 単離株の系統解析

3.2.2 において 27F プライマーによるシーケンシング で *F. prausnitzii* と考えられた菌株に関して、16S rRNA 遺伝子の全長を得るため、27F、1492R、520F（5’-CAGGAGTGCCAGCAGCCGCGG-3’）、520R（5’-ACCGCGGCTGCTGGC-3’）、1100F（5’-CAGGAGCAACGAGCGCAACCC-3’）、1100R（5’-AGGGTTGCGCTCGTTG-3’）[43] プライマーを用いて dye-terminator 法によりシーケンシングした。得られたシーケンスを GeneStudio ™ （Professional Edition version 2.2.0.0）によりアセンブルした [41]。既知の *F. prausnitzii* およびその近縁種の 16S rRNA 遺伝子の配列を NCBI（date: Apr 2020）より入手し（アクセッション番号：図 10 に記載）[44]、MEGA （version 10.1.7）を用いて分子進化・系統学的解析を実施した [45]。系統進化は neighbor-joining method[41] により推定した。系統樹のトポロジーはブートストラップ法により評価した（1000 replicates）。進化的距離は Kimura 2-parameter method[41] により計算した。

3.3 結果・考察

腸内細菌を介したMCIに対する介入候補素材として選抜した*F. prausnitzii*を第2章の観察研究被験者から単離した。結果、約4000の単離株のうち、*F. prausnitzii*を9株単離した。並行して、30代の健常者2名の糞便より *F. prausnitzii* を3株単離し、計12株を第4章以降の試験に用いた。12個の *F. prausnitzii* 単離株と *Ruminococcaceae* の近縁種との系統関係を図 10 に示した。いずれの株も *F. prausnitzii* であることを確認した。

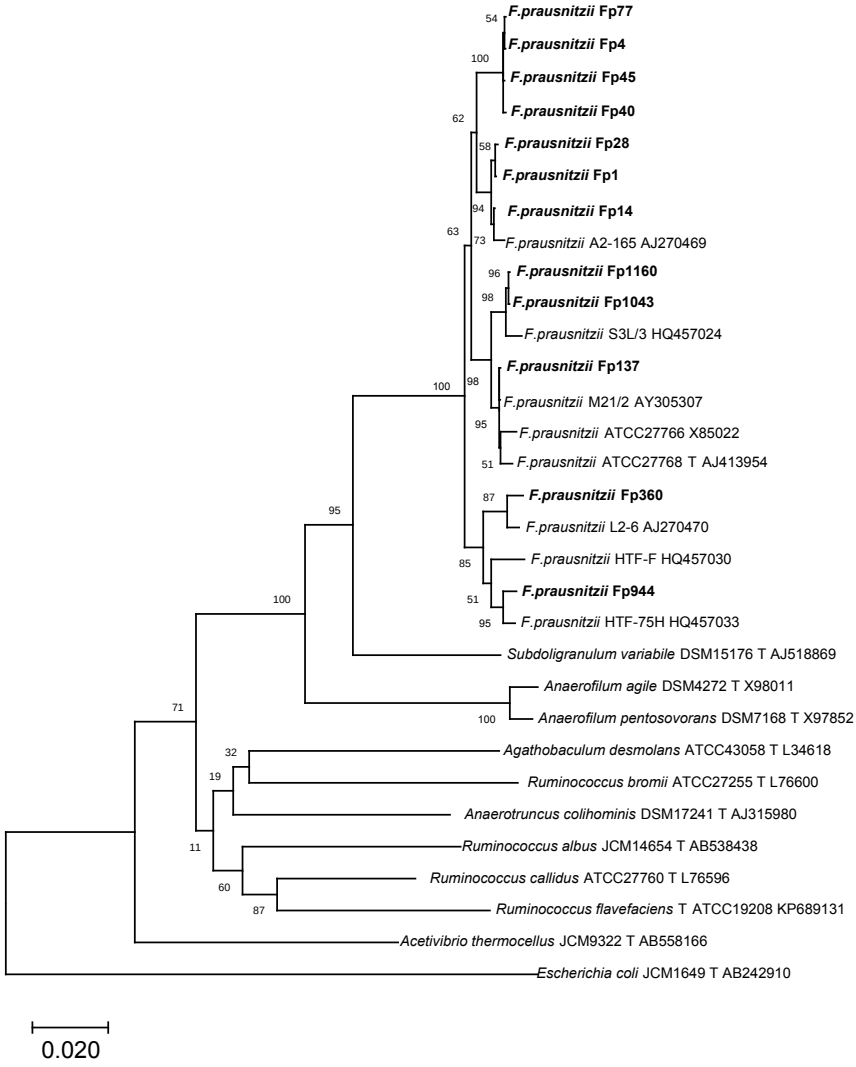


図 10：12 個の *F. prausnitzii* 単離株と *Ruminococcaceae* の近縁種との系統関係の解析結果
16S rRNA 遺伝子の配列を元に 12 個の *F. prausnitzii* 単離株と *Ruminococcaceae* の近縁種との系統関係を示す。系統樹は MEGA を用いて近隣結合法により作成した。ブートストラップ値（1000 回のうちの）は分岐点に示す。スケールバーの長さが 2%異なることを示す。当研究で単離した *F. prausnitzii* 株を太字で示す。参照した近縁種のアクセッション番号を株名の最後に示す。「T」は type strain を意味する。

第 4 章 *F. prausnitzii* 単離株の認知機能に対する有効性の検討

4.1 目的

腸内細菌を介した MCI に対する介入候補素材として単離した *F. prausnitzii* 株の経口投与が Aβ脳室内注入マウスの認知行動へ及ぼす影響を検討した。

4.2 材料と方法

4.2.1 動物

ddY マウス（雄性、7 週齢（評価時）、SPF、日本エスエルシー㈱、RRID: MGI:5558113）を用いた。MF 固形飼料（オリエンタル酵母工業㈱　ガンマ線照射 50kGy）の自由摂取、水道水の自由飲水とした。飼育環境は SPF、明期 12h・暗期 12h のサイクル、温度 23-25℃、4 マウス/ケージ以下とした [46]。作成した動物実験計画は、公益財団法人ヒューマンサイエンス振興財団の第三者認定を受けている日本バイオリサーチセンター（NBR）（株）の動物実験委員会で承認を得て、経口投与、脳室内注入および行動評価を NBR（株）にて実施頂いた。投与する被験物調製は大塚製薬（株）川原知浩氏に協力頂いた。ddY マウスに 4.2.3 に示す Aβ脳室内注入（intracerebroventricular: i.c.v.）を実施し、Aβ脳室内注入マウスに 4.2.2 に示す *F. prausnitzii* 生菌、*F. prausnitzii* 死菌体懸濁液、あるいは、培養上清を 300μL/マウスにて Aβ脳室内注入の 2 日前から 11 日間経口投与（per oral： p.o.）した。陽性対照群（i.c.v.: Aβ）はアリセプト（ドネペジル塩酸塩）を 0.5mg/kg 体重経口投与、sham-operation 群（i.c.v.: distilled water）および vehicle 群（i.c.v.: Aβ）は生理食塩水を 300μL/マウスにて経口投与した。培地対照群（i.c.v.: Aβ）は LYBHI 培地を 300μL/マウスにて経口投与した。期間中、有害事象は観察されなかった。図 11 の試験は n=9、図 12 の試験は n=12、図 13 の試験では n=12 で実施した。

4.2.2 被験物の調製

-*F. prausnitzii* 生菌投与群、培養上清投与群、および、培地対照群の被験物調製方法：

嫌気チャンバー内にて（N_2 = 90%、CO_2 = 5%、H_2 = 5%）、*F. prausnitzii* 株の凍結菌株ストックを YCFA 培地（per 1 L; casitone 10 g、yeast extract 2.5g、$NaHCO_3$ 4g、glucose 4.5g、hemin 10mg、Tween 80 1mL、K_2HPO_4 0.45g、KH_2PO_4 0.45g、$(NH_4)_2SO_4$ 0.9g、NaCl 0.9g、$MgSO_4 \cdot 7H_2O$ 0.09g、$CaCl_2 \cdot 2H_2O$ 0.12g、L-cysteine·HCl·H_2O

1.4g、acetic acid 53μL、propionic acid 19μL、n-valeric acid 3.1μL、iso-valeric acid 3.1μL、iso-butyric acid 3.1μL、resazurin 0.5mg/L）に起こし、37℃で 24 時間培養した。その後、培養液を LYBHI 培地へ継代し（植菌容量：5%、pre 1L; brain heart infusion 37g、yeast extract 5g、hemin 5mg、cellobiose 1g、maltose·H_2O 1.1g、resazurin 0.5mg、L-cysteine·HCl·H_2O 0.7g）、さらに 37℃にて 24 時間又は 48 時間培養した。その培養液を遠心濃縮し（800g、10 minutes）、生菌投与群の被験物とした（20 倍濃縮液マクファーランド濁度が 0.6（1.1×10^9 bacterial cells/ mouse）になるよう培地で懸濁して調整）。菌数は濁度計（DENSIMAT、BioMérieux、France）に基づき試算した。生菌投与群の被験物はマウスへの投与まで 15% glycerol 終濃度にて-80℃で保存した。培地対照群の被験物である LYBHI 培地および培養上清投与群の被験物である培養上清も同様に 15% glycerol 終濃度にて-80℃で保存した。

-*F. prausnitzii* 死菌体懸濁液投与群の被験物調製方法：
生菌被験物の濁度と同様の濃度（20 倍濃縮液マクファーランド濁度:0.6、1.1×10^9 bacterial cells/ mouse 相当分）に調製した 24h 培養濃縮液を生理食塩水にて 2 回遠心洗浄した後（800×g、10 minutes）、生理食塩水にて再懸濁し、70℃、30 分間の加熱処理を行い、これを死菌体懸濁液とした。死菌体懸濁液はマウスへの投与まで-80℃で保存した。

4.2.3 Aβ脳室内注入モデル

我々の用いた Aβ脳室内注入モデルは AD の研究領域において広く用いられており[47–52]、特定の記憶障害を示し、症状的また病態生理学的にヒトの AD を模倣したモデルである。行動評価を通して AD に対する介入候補素材を評価する上で有用なモデルと考えられる。その妥当性は 3 種類の妥当性（face validity、construct validity、predictive validity）に基づき報告されている[53]。face validity に関しては、Aβ脳室内注入モデルが記憶獲得の障害を示すが、過去の記憶の想起には異常を示さないため、ヒト AD の初期の前向性エピソード記憶障害を模倣していることが示されている。construct validity に関しては、海馬の長期増強の減少という生理学的結果が見られることが示されている。predictive validity は AD 治療薬のガランタミンの投与により当モデルで認知機能が改善することが示されている。このような結果から著者は、Aβ脳室内注入モデルは AD に見ら

れる特定の記憶障害を示し、3 種類の妥当性を満たしていると結論している [53]。同様の試験系は他の研究においても用いられている [47–52]。それらの研究においては、Aβの活性領域として考えられている Aβ 25-35 が [54–56]、よく用いられている [47–52]。Aβ 25-35 の脳室内注入量においてはそれら文献と同様の量を選択した。具体的には、Aβ protein 25-35 （PolyPeptide Laboratories、USA） に注射用水を 2 mM となるように加え、37 °C、96h インキュベーションして Aβ注入溶液を調製した。sham-operation（偽手術）群用には注射用水を用意した。動物をペントバルビタールナトリウム 40 mg/kg で腹腔内投与（投与液量：10 mL/kg）し、麻酔した。麻酔後、頭皮にレボブピバカイン塩酸塩を皮下投与（0.1mL）した。動物の頭頂部の毛を刈り、頭部を脳定位固定装置に固定した（Narishige Inc.、Japan）。ドリルを用いて bregma より側方 1 mm（右側）、後方 0.2 mm の頭蓋骨にステンレス製パイプ刺入用の穴を開けた。骨表面から 2.5 mm の深さまでシリコンチューブ及びマイクロシリンジに接続されたステンレス製パイプを垂直に刺入した。脳室内に Aβ注入溶液 3 μL（6 nmol/ 3μL）をマイクロシリンジポンプで 3 分間かけて注入した（1.0μL/minutes）。sham-operation 群は注射用水を 3μL 注入した。注入後は、ステンレス製パイプを挿入したまま 3 分間静置し、ステンレス製パイプをゆっくりと抜去した。頭皮を縫合し、動物を脳定位固定装置から外し、飼育ケージに戻した。

4.2.4 行動評価

脳室内注入 6 日後に Y 迷路による作業記憶の行動評価を実施した（DAY9）[46]。脳室内注入 7 日後に受動回避試験の獲得試行を実施した（DAY10）。脳室内注入 8 日後に受動回避試験の保持試行を実施した（DAY11）[57]。

Y 迷路試験：3 本の arm 間の角度を 120 度とし、arm を全て同じ長さ・大きさとした Y 迷路（arm の走路長 395 mm、壁面高さ 120mm）を用いた。マウスを 1 つのアームの先端に置き自由に 7 分間移動させ、マウスのアームへの進入回数を記録した。すべての arm に侵入した回数と続けて 3 回異なる arm に入った回数（交替行動数）を数え、交替行動数を arm の総侵入回数から 2 を減じた値で除した値を自発的交替行動率として評価した。自発的交替行動率（%） = 交替行動数 ÷（総アーム進入回数－ 2）× 100。SAS software release 9.4（SAS Institute Japan）により vehicle 群あるいは培地投与群との間で対応のないステューデント

の *t* 検定を実施した。検定の有意水準は両側 5%とした。

受動回避試験：獲得試行（学習）では、まず、扉を閉めた明室にマウスを入れ、その 10 秒後にギロチンドアを開けて、マウスが好む暗室内への移動を可能とした。マウスが暗室内に入ると同時にギロチンドアを閉め、電気刺激を与えた（0.2 mA、2 秒）。獲得試行後マウスはホームケージに戻した。獲得試行時に暗室までに移動する時間を反応潜時として記録した。獲得試行の 1 日後に保持試行（テスト）を実施した。具体的には、マウスを再び明室に入れ、暗室への移行時間を反応潜時として測定した。反応潜時（保持試行）が長いほど、嫌悪刺激を記憶していると判定した。反応潜時は 300 秒を最大とし、300 秒経過しても暗室に入らない場合は試験終了とした。SAS software release 9.4（SAS Institute Japan）により vehicle 群あるいは培地投与群との間で対応のないステューデントの *t* 検定を実施した。検定の有意水準は両側 5%とした。

4.3 結果

4.3.1 単離した *F. prausnitzii* 12 株の認知行動へ及ぼす影響

Y 迷路試験では、vehicle 群（i.c.v.: Aβ、p.o.: saline）は、sham-operation 群（i.c.v.: distilled water、p.o.: saline）と比較して、自発的交替行動率（%）が有意に低下し系の成立を確認した（図 11B）。Fp14、Fp28、Fp77、Fp360 投与群 （i.c.v.: Aβ、p.o.:各生菌） は、培地対照群（i.c.v.: Aβ、p.o.: 培地） と比較して、自発的交替行動率（%）が有意に上昇した（図 11B）（Fp14（$p = 0.0070$）、Fp28（$p = 0.0181$）、Fp77（$p = 0.0323$）、Fp360（$p = 0.0001$））。それ以外の菌株投与群は、培地対照群と比較して、自発的交替行動率に有意な差は認められなかった（図 11B）。アーム侵入回数においてはドネペジル投与群と Fp4 投与群以外では差がなく、Fp14、Fp28、Fp77、Fp360 の活性に自発的運動活性は影響がないと考えられた（図 11A）。

受動回避試験では、獲得試行時において群間差は見られず個体差が無いことを確認した（図 11C）。保持試行において vehicle 群（i.c.v.: Aβ、p.o.: saline）は、sham-operation 群（i.c.v.: distilled water、p.o.: saline）と比較して、反応潜時の有意な短縮が認められ、系の成立を確認した（図 11D）。Fp360 生菌投与群（i.c.v.: Aβ、p.o.: Fp360 生菌）は、培地対照群（i.c.v.: Aβ、p.o.: 培地）と比較して、反応潜時の有意な延長が認められた（図 11D）。それ以外の菌株投与群は、培地

対照群と比較して、保持試行時の反応潜時に有意な差は認められなかった（図11D）。両試験において、1番目と3番目に可能性を示したFp360とFp14についてその後の試験に用いた。

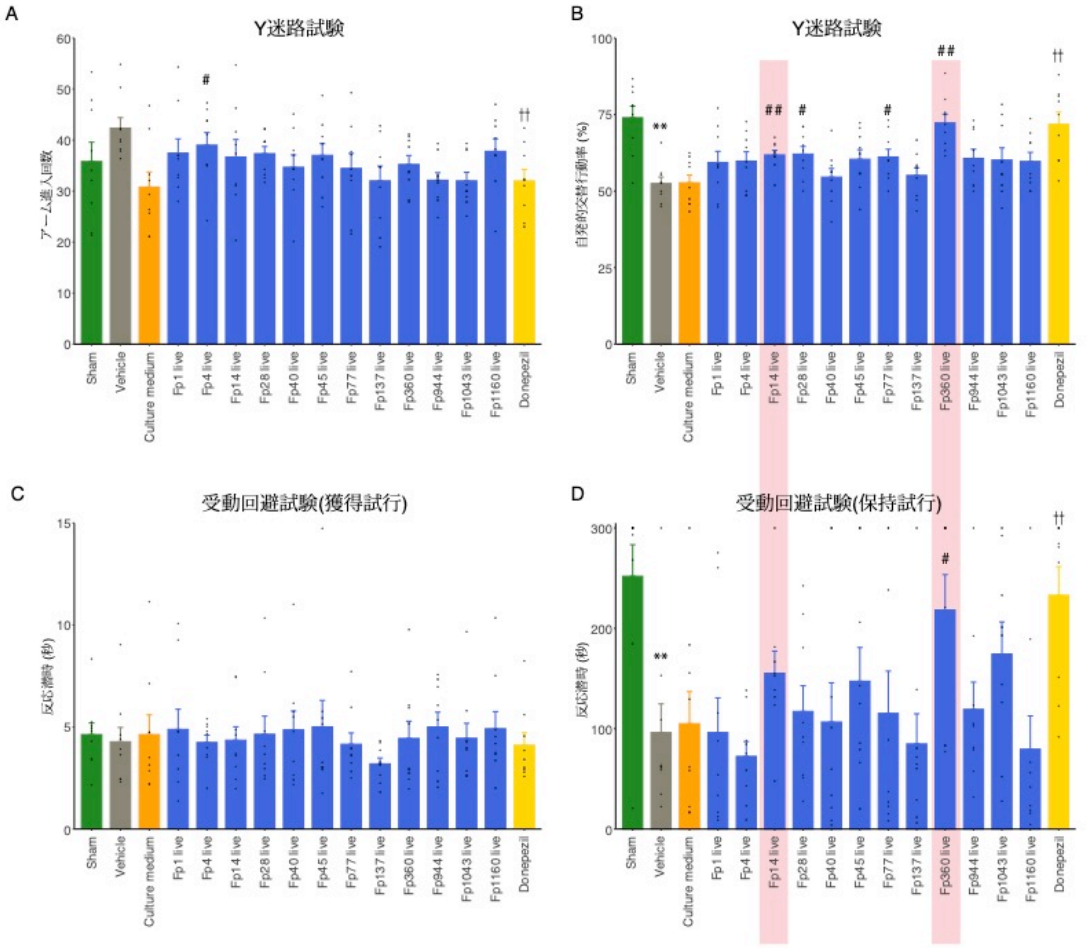


図11：単離した *F. prausnitzii* 12株の認知行動へ及ぼす影響の評価結果
（A）Y迷路試験のアーム侵入回数、（B）Y迷路試験の自発的交替行動率（%）、（C）受動回避試験の獲得試行における反応潜時（秒）、（D）受動回避試験の保持試行における反応潜時（秒）。全ての値はmean + S.E.で示す（n = 9、biological replicates）。$^{**}p < 0.01$（対応の無いステューデントの両側 *t* 検定、sham-operation vs vehicle）、$^{\#}p < 0.05$、$^{\#\#}p < 0.01$（対応の無いステューデントの両側 *t* 検定、vs culture medium）、$^{\dagger\dagger}p < 0.01$（対応の無いステューデントの両側 *t* 検定、vs vehicle）。

4.3.2 選抜したFp14およびFp360の認知行動へ及ぼす影響

選抜したFp14とFp360の有効性が菌体由来なのか培養上清由来なのか検討した。Y迷路試験では、vehicle群（i.c.v.: Aβ、p.o.: saline） は、sham-operation群（i.c.v.: distilled water、p.o.: saline）と比較して、自発的交替行動率（%）が有意

に低下し系の成立を確認した（図 12B）。Fp360 生菌投与群（i.c.v.: Aβ、p.o.: Fp360 生菌）は、培地対照群（i.c.v.: Aβ、p.o.: 培地）と比較して、自発的交替行動率（%）が有意に上昇し図 11B の再現性が確認された（図 12B）（$p = 0.0032$）。Fp14 生菌投与群（i.c.v.: Aβ、p.o.: Fp14 生菌）は、培地対照群（i.c.v.: Aβ、p.o.: 培地）と比較して、自発的交替行動率（%）が上昇する傾向は見られたものの有意な上昇は見られず、図 11B の再現性が得られなかった（図 12B）（$p = 0.0932$）。それ以外の菌体あるいは培養上清投与群は、vehicle 群（i.c.v.: Aβ、p.o.: saline）あるいは培地対照群（i.c.v.: Aβ、p.o.: 培地）と比較して自発的交替行動率に有意な差は認められなかった（図 12B）（Fp14 死菌体懸濁液（$p = 0.5415$）、Fp14 培養上清（$p = 0.1263$）、Fp360 死菌体懸濁液（$p = 0.0717$）、Fp360 培養上清（$p = 0.2319$））。アーム侵入回数においては Fp360 死菌体懸濁液投与群以外では差がなく、Fp360 生菌の活性に自発的運動活性は影響がないと考えられた（図 12A）。

受動回避試験では、獲得試行時において群間差は見られず個体差が無いことを確認した（図 12C）。保持試行において vehicle 群（i.c.v.: Aβ、p.o.: saline）は、sham-operation 群（i.c.v.: distilled water、p.o.: saline）と比較して、反応潜時の有意な短縮が認められ、系の成立を確認した（図 12D）。Fp14 死菌体懸濁液群（i.c.v.: Aβ、p.o.: Fp14 死菌体懸濁液）および Fp360 生菌投与群（i.c.v.: Aβ、p.o.: Fp360 生菌）は、vehicle 群（i.c.v.: Aβ、p.o.: saline）あるいは培地対照群（i.c.v.: Aβ、p.o.: 培地）と比較して、反応潜時の有意な延長が認められた（図 12D）（Fp14 死菌体懸濁液（$p = 0.0003$）、Fp360 生菌（$p = 0.0249$））。それ以外の菌体あるいは培養上清投与群は、vehicle 群（i.c.v.: Aβ、p.o.: saline）あるいは培地対照群（i.c.v.: Aβ、p.o.: 培地）と比較して保持試行時の反応潜時に有意な差は認められなかった（図 12D）（Fp14 生菌（$p = 0.1002$）、Fp14 培養上清（$p = 0.4282$）、Fp360 死菌体懸濁液（$p = 0.1197$）、Fp360 培養上清（$p = 0.6402$））。

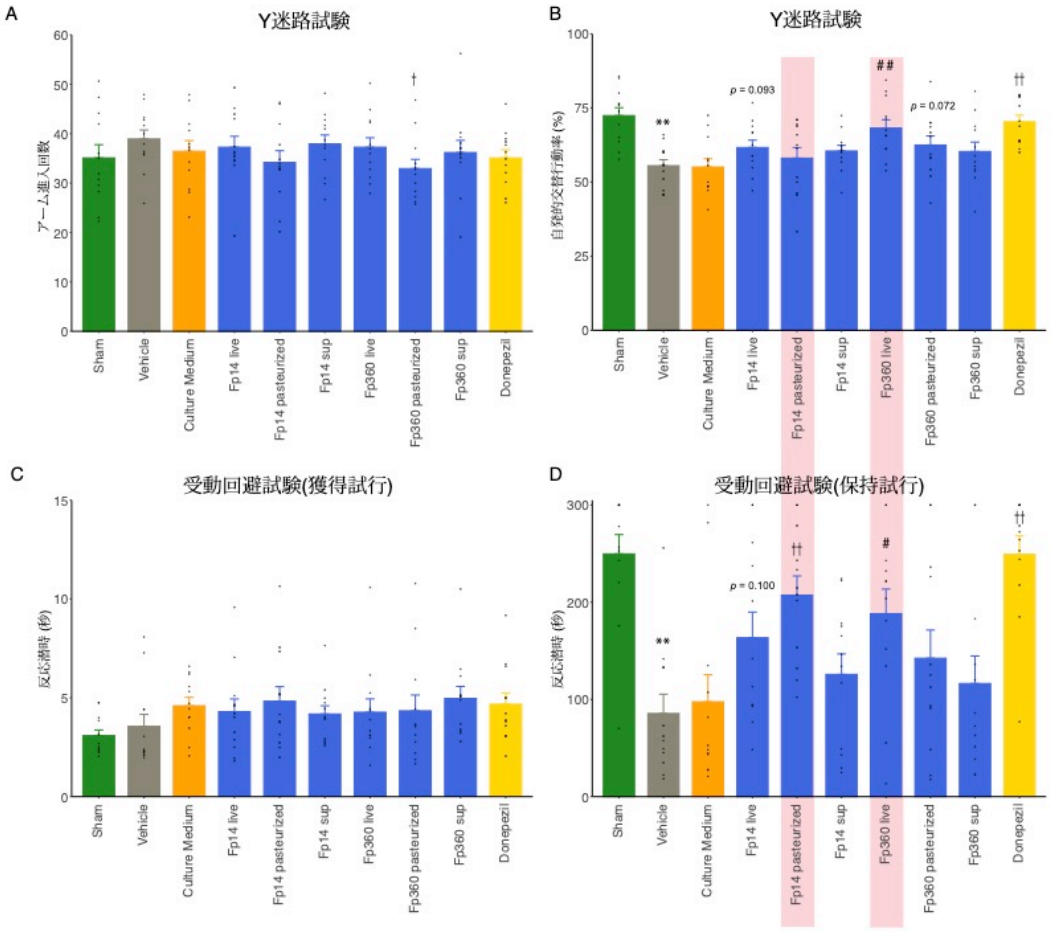


図 12：Fp14 および Fp360 の認知行動へ及ぼす影響の評価結果
（A）Y 迷路試験のアーム侵入回数、（B）Y 迷路試験の自発的交替行動率（%）、（C）受動回避試験の獲得試行における反応潜時（秒）、（D）受動回避試験の保持試行における反応潜時（秒）。全ての値は mean + S.E.で示す（n = 12、biological replicates）。$^{**}p < 0.01$（対応の無いステューデントの両側 *t* 検定、sham-operation vs vehicle）、$^{\#}p < 0.05$、$^{\#\#}p < 0.01$（対応の無いステューデントの両側 *t* 検定、vs culture medium）、$\dagger p < 0.05$、$^{\dagger\dagger}p < 0.01$（対応の無いステューデントの両側 *t* 検定、vs vehicle）。

4.3.3 Fp14 死菌体懸濁液の認知行動へ及ぼす影響の再現性

F. prausnitzii は酸素耐性が低いため、Fp14 にて死菌化で効果が得られたことは *F. prausnitzii* を素材として用いる上で死菌化が実効性のある解決方法となりうることを示したと考える。そこで、Fp14 死菌体懸濁液の効果の再現性を確認した。Y 迷路試験では、vehicle 群（i.c.v.: Aβ、p.o.: saline）は、sham-operation 群（i.c.v.: distilled water、p.o.: saline）と比較して、自発的交替行動率（%）が有意に低下し系の成立を確認した（図 13B）。Fp14 死菌体懸濁液投与群（i.c.v.: Aβ、p.o.: Fp14 死菌体懸濁液）は、vehicle 群（i.c.v.: Aβ、p.o.: saline）と比較して、自発的交替行動率（%）に有意な差は認められなかった（図 13B）。アーム

侵入回数においては差がなく、Fp14 死菌体懸濁液の活性に自発的運動活性は影響がないと考えられた（図 13A）。

受動回避試験では、獲得試行時において群間差は見られず個体差が無いことを確認した（図 13C）。保持試行において vehicle 群（i.c.v.: A β、p.o.: saline）は、sham-operation 群（i.c.v.: distilled water、p.o.: saline）と比較して、反応潜時の有意な短縮が認められ、系の成立を確認した（図 13D）。Fp14 死菌体懸濁液投与群（i.c.v.: A β、p.o.: Fp14 死菌体懸濁液）は、vehicle 群（i.c.v.: A β、p.o.: saline）と比較して、反応潜時の有意な延長が認められ図 12D の再現性を確認した（図 13D）（p = 0.0023）。

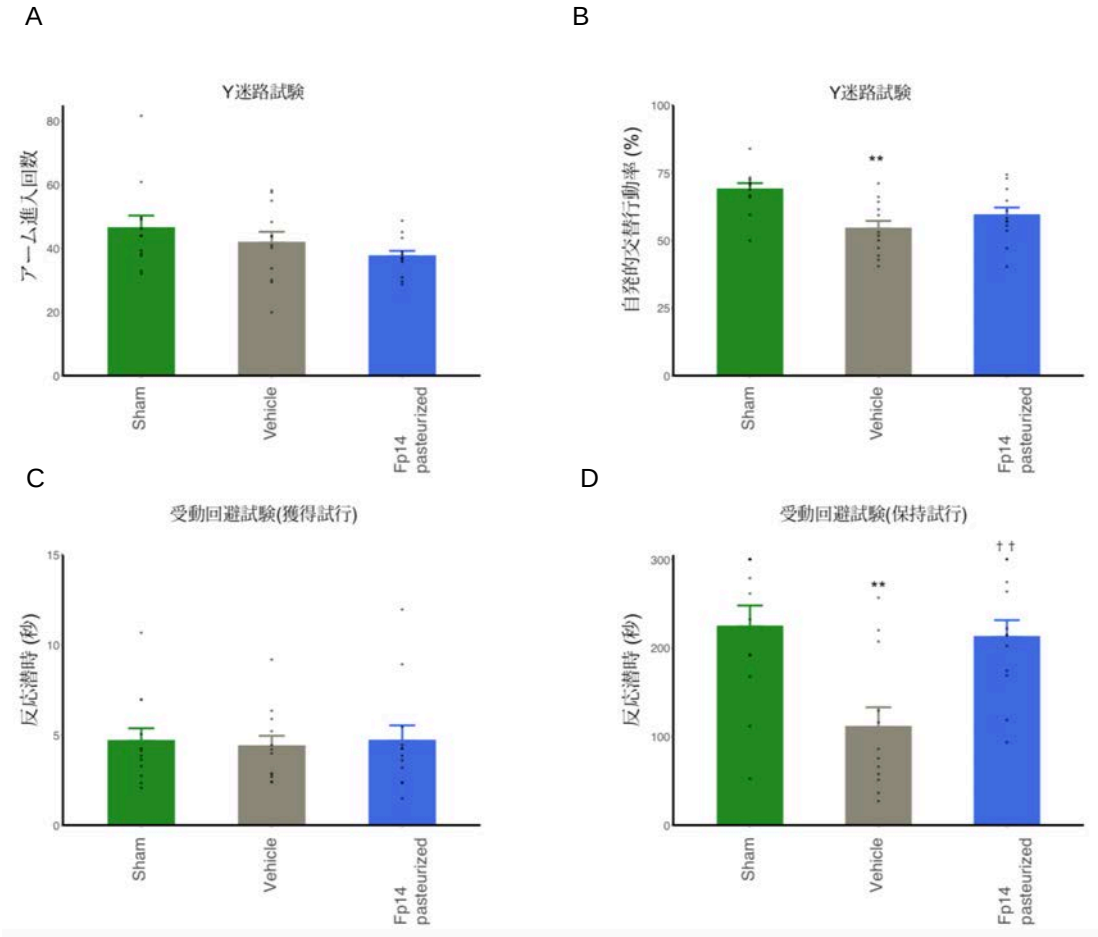


図 13：Fp14 死菌体懸濁液の認知行動へ及ぼす影響の再現性評価結果
（A）Y 迷路試験のアーム侵入回数、（B）Y 迷路試験の自発的交替行動率（%）、（C）受動回避試験の獲得試行における反応潜時（秒）、（D）受動回避試験の保持試行における反応潜時（秒）。全ての値は mean + S.E.で示す（n = 12、biological replicates）。$^{**}p < 0.01$（対応の無いステューデントの両側 t 検定、sham-operation vs vehicle）、$^{††}p < 0.01$（対応の無いステューデントの両側 t 検定、vehicle vs Fp14 死菌体懸濁液）。

4.4 考察

腸内細菌を介した MCI に対する介入候補素材として単離した *F. prausnitzii* 株の経口投与が Aβ脳室内注入マウスへの認知行動へ及ぼす影響を検討した。結果、Y 迷路試験においては Fp360 生菌で、受動回避試験においては Fp14 死菌体懸濁液および Fp360 生菌にて再現性をもって Aβ脳室内注入による認知機能異常を有意に改善する結果が得られた（図 11-13）。

Fp14 死菌体懸濁液が Y 迷路試験（ワーキングメモリーの評価）では有効性を示さず受動回避試験（長期記憶の評価）のみで有効性を示したことに関して（図 12-13）、記憶固定化のプロセスを考えると長期記憶の改善はワーキングメモリーの改善を含むと考えられるため [58]、Fp14 死菌体懸濁液の記憶への作用があると考えられる。Y 迷路試験において改善効果が見られなかったことから Fp14 死菌体懸濁液の記憶以外への作用もある可能性が考えられる。今後、Fp14 死菌体懸濁液の記憶以外への作用を含めメカニズムの詳細な検討が必要であると考える。Fp360 生菌において両試験で有効性を示したことに関しては、後述する第 6 章の *F. prausnitzii* 株の全ゲノム比較解析にて Fp360 に特徴的なオーソログの数が Fp14 よりも多いという結果が得られていることから、Fp360 のみに特徴的なオーソログの組み合わせにより Fp14 とは異なり両試験で効果を示した可能性が 1 つ考えられる。今後、Fp360 の作用メカニズムの詳細な検討が必要であると考える。なお、4.2.3 に記載の通り Aβ脳室内注入モデルは行動評価を通して AD および MCI に対する介入候補素材を評価する上で有用なモデルであるものの、Aβプラークや tau 蓄積など AD の長期的な病理を反映していないため、今後それらを反映したモデルでの評価も期待される。また、将来的にヒト介入試験によるヒトでの認知機能異常軽減効果の検討も期待される。

Fp14 生菌では認知機能異常改善効果は見られなかったが、死菌化することにより認知機能異常の改善効果が見られた点に関して（図 12-13）、*F. prausnitzii* 同様に次世代健康有用菌として注目されているグラム陰性菌の *Akkermansia muciniphila* においても似たような現象（死菌化により有効性が高まる）が報告されている [59]。陰性菌の死菌化により細胞外構成因子が可溶化する、あるいは、膜タンパク質の作用点への近づき易さが増加する等の可能性が考えられる。*F. prausnitzii* は酸素耐性が低いため、Fp14 にて死菌化で効果が得られたことは *F. prausnitzii* を素材として用いる上で死菌化が実効性のある解決方法となりうるこ

とを示したと考え、第 5 章の脳内メカニズムの解析では Fp14 死菌体懸濁液に着目して解析を実施した。

第 5 章 有効株 Fp14 死菌体懸濁液の脳内作用メカニズムの検討

5.1 目的

F. prausnitzii は酸素耐性が低いため、第 4 章で Fp14 にて死菌化で効果が得られたことは *F. prausnitzii* を素材として用いる上で死菌化が実効性のある解決方法となりうることを示した。そこで、脳内作用メカニズムの解析においては Fp14 死菌体懸濁液に着目し、行動試験で得られた海馬サンプルを用いてメタボローム解析および RNA-seq 解析を実施した。

5.2 材料と方法

5.2.1 メタボローム解析

凍結海馬（40-50mg 程度）に対して、zirconia beads （5mmφ、3mmφ）および 50%アセトニトリル水溶液（v/v）（内部標準物質：HMT（ヒューマン・メタボローム・テクノロジーズ）、H3304-1002、濃度 1μM）を加え、冷却下にて破砕機（Shake Master NEO、Bio Medical Science）を用いて破砕（4℃, 1,100 rpm、120 秒×2 回）した。組織破砕後、遠心分離（2,300×g、 4℃、5 分）を行った。遠心分離後、上層を限外ろ過チューブ（UltrafreeMC-PLHCC、HMT、遠心式フィルターユニット 5 kDa）に 400 μL 移し取った。これを遠心（9,100×g、4℃、120 分）し、限外ろ過処理を行った。ろ液を乾固させ、再び 50μL の Milli-Q 水に溶解して測定に用いた。カチオンモード、アニオンモードの測定を以下に示す条件で行った。抽出・測定は HMT（株）にて実施頂いた。

>陽イオン性代謝物質（カチオンモード）

装置

CE: Agilent 7100 CE system

MS: Q Exactive Plus（Thermo Fisher Scientific Inc., USA）

Capillary: Fused silica capillary i.d. 50 μm × 80 cm

Pump: Agilent 1260 isocratic HPLC pump

Adaptor: Agilent G1603A CE-MS adapter kit

Sprayer: Agilent G1607A CE-ESI-MS sprayer kit

Systems: Agilent MassHunter workstation software LC/MS data acquisition for 6200 series TOF/6500 series、Q-TOF version B.08.00（Agilent Technologies）、Xcalibur（Thermo Fisher Scientific）

測定条件

Run buffer: Cation Buffer Solution（p/n : H3301-1001）

Rinse buffer: Cation Buffer Solution（p/n : H3301-1001）

Sample injection: Pressure injection 50 mbar、10 sec

CE voltage: Positive, 30 kV

MS ionization: ESI Positive

MS capillary voltage: 4,000 V

MS scan range: m/z 60-900

Sheath liquid: HMT Sheath Liquid（p/n : I3301-1040）

>陰イオン性代謝物質（アニオンモード）

装置

CE: Agilent 7100 CE system

MS: Q Exactive Plus（Thermo Fisher Scientific Inc.、USA）

Capillary: Fused silica capillary i.d. 50 μm × 80 cm

Pump: Agilent 1260 isocratic HPLC pump

Adaptor: Agilent G1603A CE-MS adapter kit

Sprayer: Agilent G1607A CE-ESI-MS sprayer kit

Systems: Agilent MassHunter workstation software LC/MS data acquisition for 6200 series TOF/6500 series、Q-TOF version B.08.00（Agilent Technologies）、Xcalibur（Thermo Fisher Scientific）

測定条件

Run buffer: Anion Buffer Solution（p/n : H3302-1023）

Rinse buffer: Anion Buffer Solution（p/n : H3302-1023）

Sample injection: Pressure injection 50 mbar, 22 sec

CE voltage: Positive、30 kV

MS ionization: ESI Negative

MS capillary voltage: 3,500 V

MS scan range: m/z 70-1,050

Sheath liquid: HMT Sheath Liquid（p/n : I3301-1040）

CE-FTMS で検出されたピークは、自動積分ソフトウェアの MasterHands ver.2.17.5.19（慶應義塾大学開発）を用いて、シグナル/ノイズ （S/N） 比が 3 以上のピークを自動抽出し、質量電荷比 （m/z）、ピーク面積値、泳動時間（Migration time: MT） を得た[60]。得られたピーク面積値は 相対面積値（relative area） = 目的ピークの面積値 /（内部標準物質の面積値 x 試料量）の計算式により相対面積値に変換した。また、これらのデータには Na+や K+などのアダクトイオン及び、脱水、脱アンモニウムなどのフラグメントイオンが含まれているので、これらの分子量関連イオンを削除した。精査したピークについて、m/z と MT の値をもとに、各試料間のピークの照合・整列化を行った。検出されたピークに対して m/z と MT の値をもとに HMT 代謝物質ライブラリーに登録された全物質との照合、検索を行った。検索のための許容誤差は MT で± 0.5 min、m/z では ± 5ppm とした。恣意性の無いように行動試験の反応潜時の平均値に近い個体を使用して、各群 n=3 にて実施した。代謝物の相対面積値（relative area）に関して R（v3.6.3）により vehicle 群との間で対応のないウェルチの *t* 検定を実施した。検定の有意水準は両側 5%とした（付録 5）。

5.2.2 RNA-seq 解析

凍結脳について、RNeasy Plus Universal Kits（QIAGEN）を用いて RNA をカラム抽出した。RNA 抽出は大塚製薬（株）小林洋大氏と共同で実施した。TruSeq Stranded mRNA Library Prep Kit（Illumina）を用いて、得られた RNA からシークエンスライブラリーを作成した。ライブラリーのクオリティチェックは Agilent 2100 BioAnalyzer により実施した。NovaSeq6000（150bp、paird-end）により RNA-seq を実施した。ライブラリー調製およびシーケンシング はタカラバイオ（株）に実施頂いた。NCBI Sequence Read Archive (SRA) BioProject PRJNA735905 にてリードを登録した。

合計 5,606,129,806 reads（平均 109,924,114 reads/検体）のペアエンドの raw read を得た。raw read に対して以下のクオリティチェックを実施した。研究室の先行研究で城間博紹先生を中心に開発されたものを御指導頂き実施に用いた。1） N（識別されなかった塩基）を含む raw read を除去、2） Bowtie 2 （v2.2.9） [61]

（fast-local オプション）により bacteriophage *PhiX* DNA 配列に read をマッピングすることによって識別し、bacteriophage *PhiX* DNA 配列を含む read を除去、3）Cutadapt （v1.9.1） [62] によりアダプターおよびプライマー配列を除去し、クオリティー17 以下の 3’末端は trim （forward primer オプション：‘-a GATCGGAAGAGCACACGTCTGAACTCCAGTCAC -O 33 -q 17’、reverse primer オプション: ‘-a AGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGT -O 32 -q 17）、4） 50 base pair 以下の長さの read を除去、5） リードの平均クオリティーが 25 以下は除去、6）ペアのないリードは除去した。以上により high quality read を得た。合計 5,546,189,452 reads（平均 108,748,813 reads/検体）のペアエンドリードが、high-quality read として得られ、その後の解析に用いた。

Mus musculus ゲノム GRCm38.p6 を GENCODE よりダウンロードしてインデックスを作成後、HISAT2 にて high quality read をマッピングした [63, 64,65]。SAMtools により出力された sam ファイルを bam ファイルに変換後、StringTie により転写物量を計算した。R の DESeq2 パッケージにより群間差のある変動転写物を抽出した [66]。R（v3.6.3）により vehicle 群との間で Wald test を実施後、FDR 補正を行い、cut-off 値を 0.1 として変動転写物を抽出した。3 回の独立した RNA-seq 試験を行い（恣意性の無いように行動試験の反応潜時の平均値に近い個体を使用して、1 回目:各群 n=6、2 回目:各群 n=6、3 回目：各群 n=5 にて実施した）、2 回以上の試験で変動転写物として抽出されたものを最終的な変動転写物とした（付録 6）。

5.3 結果

5.3.1 メタボローム解析

F. prausnitzii は酸素耐性が低いため、第 4 章で Fp14 にて死菌化で効果が得られたことは *F. prausnitzii* を素材として用いる上で死菌化が実効性のある解決方法となりうることを示した。そこで、脳内作用メカニズムの解析では Fp14 死菌体懸濁液に着目し、行動試験で得られた海馬サンプルを用いてメタボローム解析を実施した（図 14、付録 5）。その結果、いずれの個体でも検出されアノテーションされた代謝物が 355 個検出された（図 14A）。Fp14 死菌体懸濁液は thymine および N^6-Methyl-2'-deoxyadenosine（m6dA、6mA）を有意に低下させ、suberic acid を低下させる傾向が見られた（図 14A、B）。これらは酸化ストレスやミトコン

ドリア機能に関連するとの報告がみられる代謝物であった（図 14A、B）。

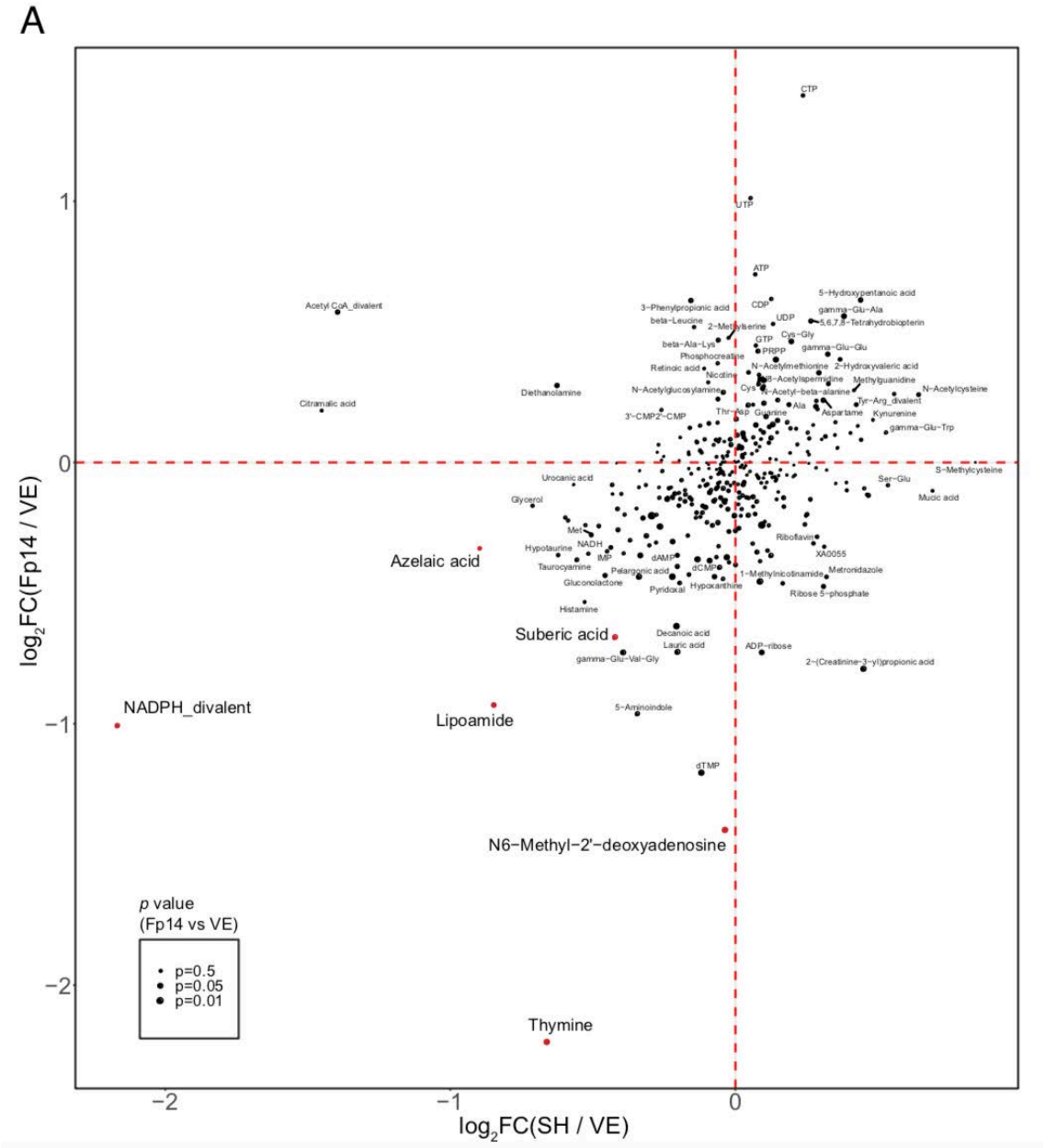


図 14A：海馬サンプルを用いたメタボローム解析の結果
X 軸： $\log_2$（vehicle（VE）群に対する sham-operation（SH）群の fold change）、Y 軸： $\log_2$（vehicle（VE）群に対する Fp14 死菌体懸濁液（Fp14）群の fold change）、n = 3（biological replicates）、丸の大きさ：それぞれの *p* 値（対応の無いウェルチの両側 *t* 検定、vehicle（VE）vs Fp14 死菌体懸濁液（Fp14））

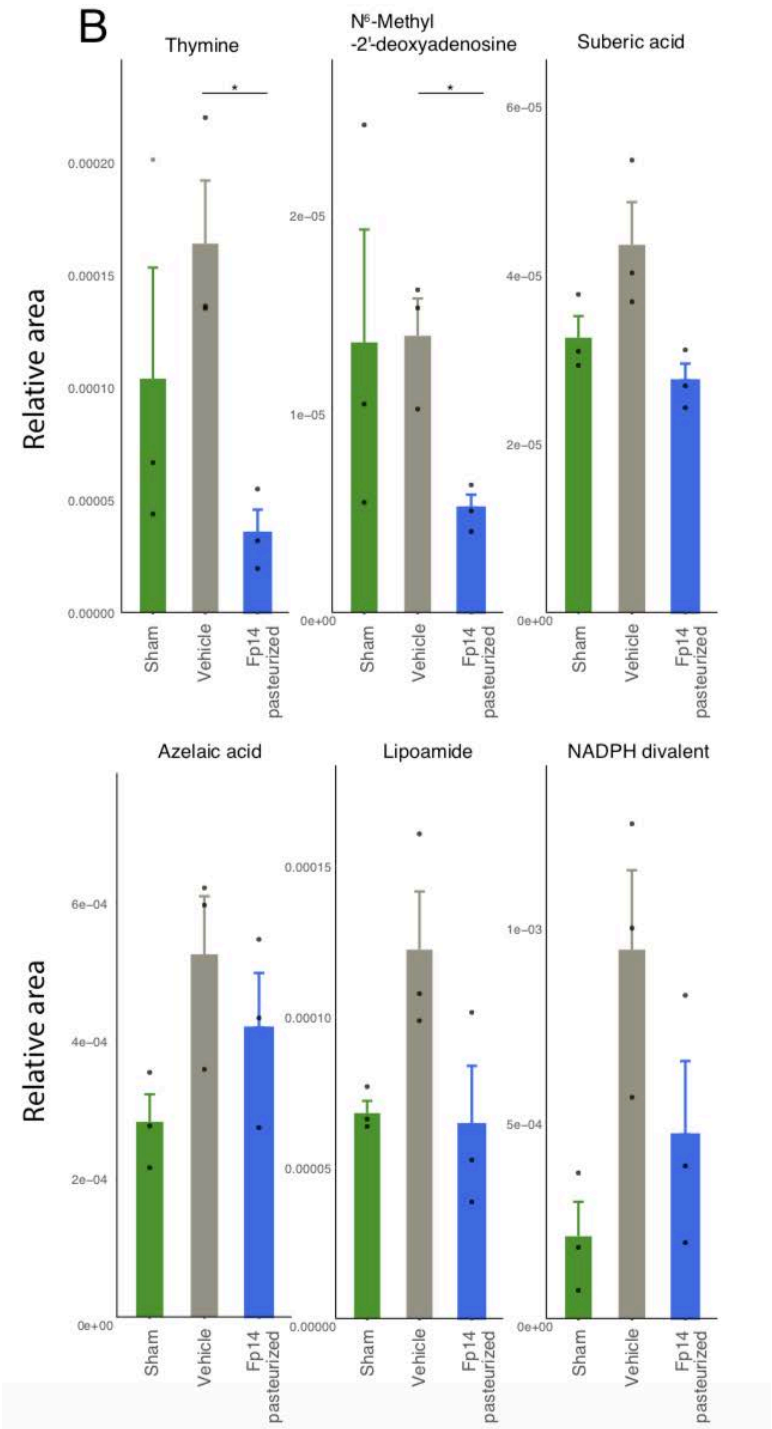


図 14B：海馬サンプルを用いたメタボローム解析の結果
酸化ストレスやミトコンドリア機能に関連する代謝物の relative area を示す。全ての値は mean + S.E. （n = 3、biological replicates）で示す。 $^{*}p < 0.05$（対応の無いウェルチの両側 *t* 検定、vs vehicle）。

5.3.2 RNA-seq 解析

メタボローム解析と同様に、Fp14 死菌体懸濁液に着目し、行動試験にて得られた海馬サンプルを用いて RNA-seq 解析を実施した（表 2、付録 6）。3 回の独立した RNA-seq 試験を行った結果、少なくとも 2 試験以上で変動転写物として検出された転写物が 15 個検出された（表 2）。Fp14 死菌体懸濁液はミトコンドリア機能に関連するとの報告がみられる phosphofurin acidic cluster sorting protein 2（PACS-2）などを有意に変動させた（表 2）。

表 2：海馬サンプルを用いた RNA-seq 解析の結果

vehicle 群との間で Wald test を実施後、FDR 補正を行い、cut-off 値を 0.1 として変動転写物を抽出した。3 回の独立した RNA-seq 試験を行い、2 回以上の試験で変動転写物として抽出されたものを最終的な変動転写物とした。VE：vehicle 群 (i.c.v.: Aβ, p.o.: saline)、Fp14：Fp14 死菌体懸濁液 群 (i.c.v.: Aβ, p.o.: Fp14 死菌体懸濁液)。表は transcript_id 順。.

transcript_id	Ensembl description	experiment1 (n=6, biological replicates)		
		Fp14 vs VE		
		log2(FC)	pvalue	qvalue
ENSMUST00000018803.11	pyridoxine 5'-phosphate oxidase (Pnpo)	-0.376037592	5.45498E-05	0.027092057
ENSMUST00000021407.10	signal recognition particle 54A (Srp54a)	23.29819475	8.72762E-15	2.10354E-11
ENSMUST00000114601.7	myotubularin related protein 1 (Mtmr1)	-4.785889311	1.43011E-05	0.008745774
ENSMUST00000115594.7	FtsJ RNA methyltransferase homolog 1 (E. coli) (Ftsj1)	-23.3175351	8.38653E-15	2.08258E-11
ENSMUST00000130179.1	myotubularin related protein 1 (Mtmr1)	-3.024951393	0.00014104	0.054261916
ENSMUST00000140212.7	homer scaffolding protein 3 (Homer3)	NA	NA	NA
ENSMUST00000141412.7	phospholipase C, delta 4 (Plcd4)	NA	NA	NA
ENSMUST00000149835.1	ADP-ribosylation factor-like 6 interacting protein 4 (Arl6ip4)	NA	NA	NA
ENSMUST00000160107.1	R3H domain and coiled-coil containing 1 like (R3hcc1l)	-6.799291664	1.79675E-07	0.00015832
ENSMUST00000172568.7	L3MBTL2 polycomb repressive complex 1 subunit (L3mbtl2)	NA	NA	NA
ENSMUST00000173216.7	calumenin (Calu)	-22.58353855	5.67369E-14	1.01074E-10
ENSMUST00000198625.4	gamma-aminobutyric acid (GABA) A receptor, subunit alpha 2 (Gabra2)	NA	NA	NA
ENSMUST00000209058.1	MAP/microtubule affinity regulating kinase 4 (Mark4)	5.170021856	1.31494E-07	0.000118412
ENSMUST00000220541.1	phosphofurin acidic cluster sorting protein 2 (Pacs2)	NA	NA	NA
ENSMUST00000234377.1	cDNA sequence BC004004	NA	NA	NA

transcript_id	Ensembl description	experiment2 (n=6, biological replicates)		
		Fp14 vs VE		
		log2(FC)	pvalue	qvalue
ENSMUST00000018803.11	pyridoxine 5'-phosphate oxidase (Pnpo)	0.326418407	3.94174E-06	0.002678518
ENSMUST00000021407.10	signal recognition particle 54A (Srp54a)	-25.75618827	9.83992E-18	5.39099E-14
ENSMUST00000114601.7	myotubularin related protein 1 (Mtmr1)	5.16688647	6.35024E-07	0.000510615
ENSMUST00000115594.7	FtsJ RNA methyltransferase homolog 1 (E. coli) (Ftsj1)	-25.13625502	5.80605E-17	1.95751E-13
ENSMUST00000130179.1	myotubularin related protein 1 (Mtmr1)	3.51119597	4.83791E-05	0.025093891
ENSMUST00000140212.7	homer scaffolding protein 3 (Homer3)	-25.30240508	3.6226E-17	1.38067E-13
ENSMUST00000141412.7	phospholipase C, delta 4 (Plcd4)	-3.648090695	0.000212753	0.079024137
ENSMUST00000149835.1	ADP-ribosylation factor-like 6 interacting protein 4 (Arl6ip4)	-3.401677167	4.11811E-05	0.021738599
ENSMUST00000160107.1	R3H domain and coiled-coil containing 1 like (R3hcc1l)	NA	NA	NA
ENSMUST00000172568.7	L3MBTL2 polycomb repressive complex 1 subunit (L3mbtl2)	5.104049395	0.000246731	0.086860055
ENSMUST00000173216.7	calumenin (Calu)	22.21333237	1.42747E-13	1.62507E-10
ENSMUST00000198625.4	gamma-aminobutyric acid (GABA) A receptor, subunit alpha 2 (Gabra2)	-9.449844535	0.000100474	0.044258463
ENSMUST00000209058.1	MAP/microtubule affinity regulating kinase 4 (Mark4)	-4.904600466	3.35229E-05	0.018028133
ENSMUST00000220541.1	phosphofurin acidic cluster sorting protein 2 (Pacs2)	-27.83765138	1.87388E-20	3.28524E-16
ENSMUST00000234377.1	cDNA sequence BC004004	2.500570501	5.20183E-06	0.003454445

transcript_id	Ensembl description	experiment3 (n=5, biological replicates)		
		Fp14 vs VE		
		log2(FC)	pvalue	qvalue
ENSMUST00000018803.11	pyridoxine 5'-phosphate oxidase (Pnpo)	NA	NA	NA
ENSMUST00000021407.10	signal recognition particle 54A (Srp54a)	NA	NA	NA
ENSMUST00000114601.7	myotubularin related protein 1 (Mtmr1)	NA	NA	NA
ENSMUST00000115594.7	FtsJ RNA methyltransferase homolog 1 (E. coli) (Ftsj1)	NA	NA	NA
ENSMUST00000130179.1	myotubularin related protein 1 (Mtmr1)	NA	NA	NA
ENSMUST00000140212.7	homer scaffolding protein 3 (Homer3)	-24.02847964	2.04432E-15	4.51025E-12
ENSMUST00000141412.7	phospholipase C, delta 4 (Plcd4)	-3.887530867	2.9085E-06	0.001679874
ENSMUST00000149835.1	ADP-ribosylation factor-like 6 interacting protein 4 (Arl6ip4)	-3.246338225	0.000442022	0.088281531
ENSMUST00000160107.1	R3H domain and coiled-coil containing 1 like (R3hcc1l)	5.800031765	1.89104E-09	1.60178E-06
ENSMUST00000172568.7	L3MBTL2 polycomb repressive complex 1 subunit (L3mbtl2)	3.70785139	0.000194726	0.052184353
ENSMUST00000173216.7	calumenin (Calu)	NA	NA	NA
ENSMUST00000198625.4	gamma-aminobutyric acid (GABA) A receptor, subunit alpha 2 (Gabra2)	-23.29373331	1.41713E-14	2.27864E-11
ENSMUST00000209058.1	MAP/microtubule affinity regulating kinase 4 (Mark4)	NA	NA	NA
ENSMUST00000220541.1	phosphofurin acidic cluster sorting protein 2 (Pacs2)	-28.38767261	6.5604E-21	1.55593E-16
ENSMUST00000234377.1	cDNA sequence BC004004	1.748457767	0.000436558	0.087558884

5.4 考察

脳内作用メカニズムの解析においては第 4 章にて死菌体で有効性を示した Fp14 に着目し、行動試験で得られた海馬サンプルを用いてメタボローム解析および RNA-seq 解析を実施した。メタボローム解析において、Fp14 死菌体懸濁液は thymine および N6-Methyl-2'-deoxyadenosine （m6dA、6mA）を有意に低下させ、suberic acid を低下させる傾向が見られた（図 14）。これらは酸化ストレスやミトコンドリア機能に関連するとの報告がみられる代謝物であった[67–71]。例えば thymine の酸化型の thymine glycol は、今回は測定されていないが AD 患者脳で蓄積しているとの報告が見られている[71]。6mA においては慢性的なストレス下にあるマウス脳で蓄積しており[69]、ミトコンドリアにおける ROS 産生を増加させるとの報告がある[67]。Suberic acid や Azeric acid などジカルボン酸は不飽和脂肪酸の酸化分解により作られ、ミトコンドリア機能を調節するとの報告がある[68]。RNA-seq 解析においても、ミトコンドリアのダイナミクスにおいて重要な役割を果たし、AD などの疾患に関わるとの報告がみられる PACS-2 を有意に低下させた（表 2）[72]。これらの結果から、Fp14 死菌体懸濁液の作用と酸化ストレスやミトコンドリア機能との関連性が考えられた。この可能性は、とある化合物が AD モデルマウスである APP/PS1 において Aβ 依存的に起こるミトコンドリア重量の減少や海馬による神経新生の減少を軽減することで認知機能を改善するとの報告と一貫性がある[73]。今後、Fp14 死菌体懸濁液の作用と酸化ストレスやミトコンドリア機能との関連性について更なる検討が必要であると考える。検討方法としては当研究とは別の AD モデルマウス（例えば、前述の APP/PS1 など）を用いた検討が 1 つ考えられる。そして、当研究で使用したモデルにおいても、今回は行動試験実施個体の一部個体におけるメタボローム解析の実施であったため、全個体を実施することで認知機能スコアとの相関解析が実施可能になると考える。さらには、今回は行動試験後の 1 ポイントにおける海馬のサンプリングであったが、Aβ 脳室内注入モデルの行動評価までの期間において継時的に海馬をサンプリングする試験を実施することで、酸化ストレスやミトコンドリア機能への影響をより詳細に検討することが可能になると考えられる。今後、上記のような研究を通して、Fp14 死菌体懸濁液の作用と酸化ストレスやミトコンドリア機能との関連性について更なる検討が必要であると考える。

第 6 章 有効株と非有効株の全ゲノム比較

6.1 目的

Fp14 と Fp360 が認知機能改善効果を示したことから、また、Fp14 と Fp360 の有効性を認めた形態が異なっていたことから（Fp14：死菌体懸濁液、Fp360：生菌）、Fp14 と Fp360 が特徴的な遺伝子配列を共有している、あるいは、Fp14 と Fp360 それぞれに特徴的な遺伝子配列を持つなど、他の非有効株のゲノムとは異なる特徴を持っている可能性がある。仮説検証のため、図 15 に示すパイプラインに沿って、認知機能に対する有効性を示した Fp14 および Fp360 と有効性を示さなかった残りの 10 株との全ゲノムを比較し、特徴的なオーソログの有無を検討した。

次いで、Fp14 と Fp360 に特徴的なオーソログと MCI や認知機能異常軽減効果との関連性を明らかにするため、第 2 章の観察研究から得られたメタゲノムデータを用いて検証した。具体的には糞便メタゲノムにおける Fp14 と Fp360 に特徴的なオーソログの relative abundance を健常者群と MCI 群で比較した。

6.2 材料と方法

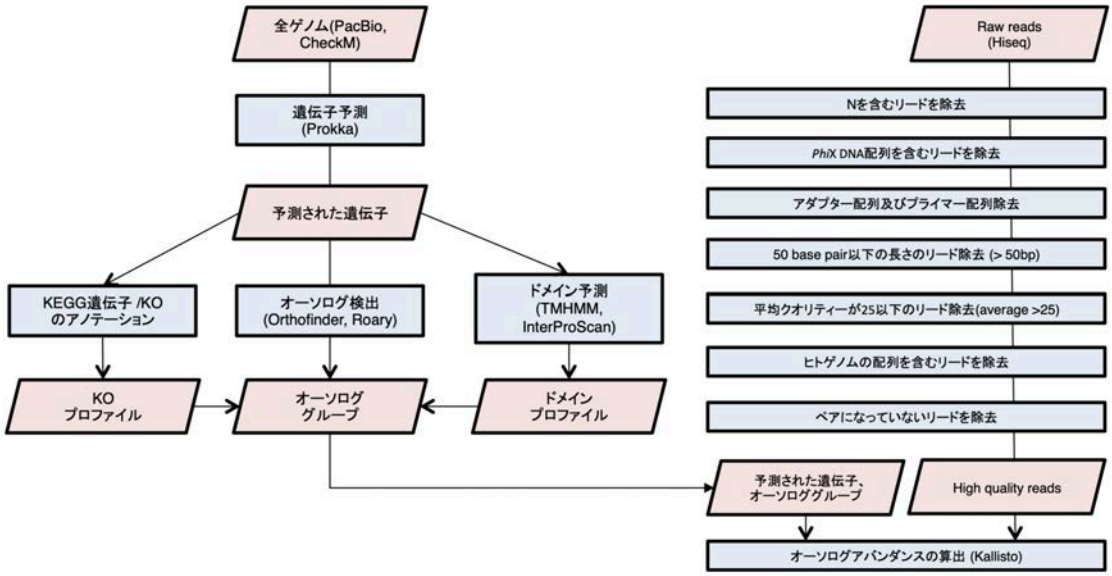


図 15：比較ゲノム解析およびオーソログの relative abundance 解析のパイプライン
比較ゲノム解析のパイプラインに関して、PacBio シーケンスにより得られたゲノム配列を CheckM によりクオリティチェックした。得られたゲノムの配列中の遺伝子予測及びゲノムアノテーションを Prokka を用いて行なった。タンパク質のドメインの予測を InterProScan 及び TMHMM を用いて行なった。DIAMOND を用い、KEGG 遺伝子及び KEGG オーソログ（KO）のアノテーションを行なった。2 つの異なるオーソログ検出ツール Roary および Orthofinder を用いて解析精度を高め、オーソログを推定した。次いで、KO およびドメイン情報それぞれを、Roary 又は Orthofinder によって同定されたオーソログに割り当てた。オーソログの relative abundance 解析のパイプラインに関して、メタゲノムショットガンシーケンスにより得られた raw read のクオリティチェックを実施し、high-quality read を得た。*F. prausnitzii* 単離株のそれぞれの遺伝子のメタゲノム中の relative abundance を Kallisto により算出した。それぞれの遺伝子を Roary 又は Orthofinder により得られたオーソログに分類し、各オーソログの relative abundance を算出した。

6.2.1 ゲノムシーケンスと環状化

Fp14 と Fp360 が認知機能改善効果を示したことから、また、Fp14 と Fp360 の有効性を認めた形態が異なっていたことから（Fp14：死菌体懸濁液、Fp360：生菌）、Fp14 と Fp360 が特徴的な遺伝子配列を共有している、あるいは、Fp14 と Fp360 それぞれに特徴的な遺伝子配列を持つなど、他の非有効株のゲノムとは異なる特徴を持っている可能性がある。仮説検証のため、図 15 に示すパイプラインに沿って、認知機能に対する有効性を示した Fp14 および Fp360 と有効性を示さなかった残りの 10 株との全ゲノムを比較し、特徴的なオーソログの有無を検討した。

ゲノム配列決定を目的としているため、long read のシーケンサーである PacBio にてシーケンスを行った。まず、*F. prausnitzii* 単離株のゲノム DNA を以下の手

順で抽出した。1）嫌気チャンバー内にて、*F. prausnitzii* 単離株を YCFA 培地に播種し、37℃で 24 時間培養した。2）その後、LYBHI 培地へ継代し、24-48 時間培養した。3）培養液を 800×g、10 分、4℃で遠心後、上清を廃棄し、嫌気 PBS （0.5 g L-cysteine·HCl·H2O、1 mg resazurin）により洗浄した。4）その後、遠心及び嫌気 PBS による洗浄を 2 回繰り返し、菌体ペレットを-80℃に凍結保存した。5）菌体ペレットから NucleoBond AXG 20 および NucleoBond Buffer Set III （Macherey-nagel GmbH & Co.、Germany）を用いてゲノム DNA を調製した。得られた当該ゲノム DNA を g-TUBE™ （Covaris, Inc.、USA）によって、物理的に断片化した。断片化した DNA の両末端を平滑化した後、SMRTbell™アダプターを連結し、シーケンスの鋳型となるシーケンスライブラリーを作製した。BluePippin（Sage Science、USA）又は AMPure XP（Beckman Coulter Inc.、USA）を使用してサイズセレクションおよび精製を行った。次いで、シーケンスライブラリー両末端の SMRTbell™アダプターに相補的な配列をもつシーケンスプライマーと DNA ポリメラーゼとを結合させ、シーケンステンプレートとした。このテンプレートを磁気ビーズと結合させ、SMRT Cells 上にアプライし、ウェル内に固定し PacBio RS II （Pacific Biosciences、USA）にてシーケンシングを行なった。シーケンスで得られたリード（表 3）をシーケンサー付属のソフトウェア PacBio SMRT Analysis（v2.3）を用いて de novo アセンブルを行い、PacBio SMRT Analysis に搭載されている Quiver を用いて、高精度コンティグを得るためのポリッシングを行なった [74]。ポリッシングにおいては、コンティグに対してリードのマッピングを行い、その結果を元にコンティグ配列の修正を行った。得られたコンティグについて、Circlator （v1.2.1）[75] により 1）全長が他のコンティグの一部に含まれるものを除去し、2）両末端がオーバーラップするものについて環状化し、3）Circlator に実装されている dnaA 遺伝子配列を使用してゲノム配列開始位置の修正を行った。その後、Quiver を用いて高精度ゲノムを得るための再ポリッシングを行った。再ポリッシングにおいては、環状化処理等を行った後のコンティグ（コンセンサス配列）に対してリードのマッピングを行い、その結果をもとにコンセンサス配列の修正を行った。ゲノム調製以降環状化まで タカラバイオ（株）に実施頂いた。ゲノムの完全性及びコンタミネーションは、CheckM （v1.0.08）により判定した（表 4）[76]。完成したゲノム（表 5）は NCBI Genome BioProject PRJNA679348 にゲノムを登録した。

表 3：PacBio シーケンスの結果

Strain_name	PacBio_id	Read_number	Base_number
Fp1	SD0354_35_b	116,602	1,026,577,518
Fp4	SD0354_49_b	148,327	1,168,961,747
Fp14	SD0354_37_b	141,207	1,069,483,157
Fp28	SD0354_38_b	167,682	1,441,600,715
Fp40	SD0354_39_b	162,028	1,211,993,371
Fp45	SD0354_40_b	156,966	1,255,773,551
Fp77	SD0354_41_b	170,357	1,348,278,659
Fp137	SD0354_55_b	135,858	1,046,754,983
Fp360	SD0354_43_b	175,052	1,485,026,094
Fp944	SD0354_44_b	182,735	1,570,634,794
Fp1043	SD0354_45_b	165,886	1,519,896,416
Fp1160	SD0354_46_b	130,700	978,350,404

表 4：CheckM の結果

単離した *F. prausnitzii* 株 の CheckM の結果を示す。いずれのゲノムも≥95% completeness、≤5% contamination であり全ゲノム解析に適していることを確認した [76]。

Strain_name	Completeness (%)	Contamination (%)	Strain heterogeneity (%)
Fp1	100	0	0
Fp4	100	0	0
Fp14	100	0	0
Fp28	100	0	0
Fp40	100	0	0
Fp45	100	0	0
Fp77	100	0	0
Fp137	100	0	0
Fp360	100	0	0
Fp944	100	0	0
Fp1043	100	0	0
Fp1160	100	0.34	100

表 5：単離した *F. prausnitzii* 株 のドラフトゲノムの情報および次項 Prokka により予測された遺伝子数

Fp4、Fp14、Fp137、Fp1043、Fp1160 の 5 株に関しては短い linear な配列が含まれているが、いずれも長い配列との BLAST の結果、相同性が高いため（98.5%以上）、plasmid ではなくゲノムの一部であると考えられた。

Strain_name	PacBio_id	Contig_Name	Base_number	Circularity	Gene_number
Fp1	SD0354_35_b	unitig_0|quiver|quiver	2,817,361	circular	2634
Fp4	SD0354_49_b	unitig_0|quiver|quiver	2,949,289	circular	2819
		unitig_1|quiver|quiver	20194	linear	
Fp14	SD0354_37_b	unitig_0|quiver|quiver	2,808,710	circular	2682
		unitig_2|quiver|quiver	15,531	linear	
Fp28	SD0354_38_b	unitig_0|quiver|quiver	2,876,607	circular	2698
Fp40	SD0354_39_b	unitig_0|quiver|quiver	2,949,392	circular	2796
Fp45	SD0354_40_b	unitig_0|quiver|quiver	2,948,911	circular	2794
Fp77	SD0354_41_b	unitig_0|quiver|quiver	2,937,510	circular	2784
Fp137	SD0354_55_b	unitig_0|quiver|quiver	3,241,719	circular	3140
		unitig_1|quiver|quiver	20,288	linear	
Fp360	SD0354_43_b	unitig_0|quiver|quiver	3,039,229	circular	2895
Fp944	SD0354_44_b	unitig_0|quiver.unitig_1|quiver|quiver	2,992,243	linear	2895
Fp1043	SD0354_45_b	unitig_0|quiver|quiver	3,098,625	circular	2983
		unitig_1|quiver|quiver	15,352	linear	
Fp1160	SD0354_46_b	unitig_0|quiver|quiver	3,101,195	circular	3005
		unitig_1|quiver|quiver	16,185	linear	
		unitig_4|quiver|quiver	11,912	linear	

6.2.2 遺伝子予測・KEGG およびドメインアノテーション・オーソログ検出

得られたゲノム配列中の遺伝子予測及びゲノムアノテーションを Prokka（v1.12）[77] を用いて行なった（表 5）。また、予測された遺伝子情報に対して、タンパク質のドメインの予測を InterProScan（v5.40-77.0）[78] 及び TMHMM（v2.0）[79] を用いて行なった。なお、TMHMM においては、配列の全体が inside 又は outside と分類された場合には、それは細胞膜貫通ヘリックスドメインを含まないことを意味し、細胞内タンパク質又は細胞外タンパク質であると予測した。一方、配列が少なくとも 1 つ以上の transmembrane helix と分類された場合には、細胞膜

貫通ヘリックスドメインを含むことを意味し、膜貫通型タンパク質であると予測した。また、予測された遺伝子に対して DIAMOND（v0.9.10.111[80]、identity>40、score>70、及び coverage>80）を用い、KEGG 遺伝子及び KEGG オーソログ（KO: date: May 2017）の遺伝子機能アノテーションを行なった。さらに前記予測された遺伝子情報に対して、2 つの異なるオーソログ検出ツール Roary （v3.12.0）[81] および Orthofinder （v2.3.11）[82] を用いて解析精度を高め、オーソログを推定した。Orthofinder では OG で始まる総数 4636 個のオーソロググループ、Roary では group で始まるあるいはアルファベットの総数 7227 個のオーソロググループを得た。各株のオーソログ数を表 6 に示した。次いで、KO およびドメイン情報それぞれを、Roary 又は Orthofinder によって同定されたオーソログに割り当てた（付録 7、8）。特定の単離株にのみに見られるオーソログおよび特定の単離株のみに見られる KO を含むオーソログを“specific ortholog＝特徴的なオーソログ”と定義し（表 7）、各株の specific ortholog の数を表 6 に示した。

表 6：単離した *F. prausnitzii* 株のオーソログ数

specific orthlog の定義は表 7 に記載した。

Strain_name	PacBio_id	Number_of_orthologs		Number_of_specific_orthologs		
		Roary	Orthofinder	Roary	Orthofinder	KO
Fp1	SD0354_35_b_f1	2591	2399	7	6	0
Fp4	SD0354_49_b_f1	2777	2559	19	0	0
Fp14	SD0354_37_b_f1	2636	2427	358	149	7
Fp28	SD0354_38_b_f1	2655	2442	56	23	2
Fp40	SD0354_39_b_f1	2754	2560	2	1	0
Fp45	SD0354_40_b_f1	2752	2558	1	0	0
Fp77	SD0354_41_b_f1	2742	2550	5	0	0
Fp137	SD0354_55_b_f1	3092	2747	503	228	12
Fp360	SD0354_43_b_f1	2854	2479	717	187	36
Fp944	SD0354_44_b_f1	2852	2517	695	231	16
Fp1043	SD0354_45_b_f1	2939	2693	25	3	0
Fp1160	SD0354_46_b_f1	2957	2709	32	9	0

表 7：specific ortholog の定義

特定の単離株にのみ属する ortholog	specific ortholog
特定の単離株にのみ属する KO が割り当てられた ortholog	
上記以外の ortholog	non-specific ortholog

6.2.3 既知の *F. prausnitzii* 株とのゲノム比較

Fp14 と Fp360 に特徴的なオーソログが既知の *F. prausnitzii* 株と共有されているかを調べるために、我々の *F. prausnitzii* 単離株と既知の *F. prausnitzii* 株の全ゲノムを比較した。既知の *F. prausnitzii* 株は図 10 で用いた既知の *F. prausnitzii* 8 株のうち、ゲノムが公開されていないあるいはドラフトゲノムしか公開されていない株を除き、A2-165: GCA_010509575.1、S3L/3: GCA_000209855.1、L2-6: GCA_000210735.1 の 3 株を使用した（https://www.ncbi.nlm.nih.gov/genome/genomes/682、date: Apr 2021）。解析パイプラインは 6.2.1 と同様に実施した。

6.2.4 メタゲノムショットガンシーケンス

Fp14 と Fp360 に特徴的なオーソログと MCI や認知機能異常軽減効果との関連性について、第 2 章の観察研究から得られたメタゲノムデータを用いて検証した。具体的には糞便メタゲノムにおける Fp14 と Fp360 に特徴的なオーソログの relative abundance を健常者群と MCI 群で比較した。メタゲノムショットガンシーケンスに用いるライブラリーは TruSeq Nano DNA Library Prep Kit（Illumina）を用いて調製した。ライブラリーの品質は Agilent 2100 BioAnalyzer を用いて確認した。メタゲノムショットガンシーケンスは HiSeq2500 platform（Illumina）にて行なった。15.0 Gb/sample のターゲットデータサイズにて 150bp のリード長のペアエンドシーケンスを実施した。ライブラリー調製およびシーケンシング はタカラバイオ(株)にて実施頂いた。NCBI Sequence Read Archive (SRA) BioProject PRJNA679346 にてリードを登録した。

6.2.5 メタゲノムショットガンシーケンスリードのクオリティチェック

合計 6,421,909,374 reads/（平均 149,346,730 reads/検体）のペアエンドの raw read を図 15 のパイプラインで処理した。研究室の先行研究で城間博紹先生を中心に開発されたものを御指導頂き実施に用いた。具体的には 1） N（識別されなかった塩基）を含む raw read を除去、2）Bowtie 2 （v2.2.9）[61] （fast-local オプション）により bacteriophage *Phi*X DNA 配列に read をマッピングすることによって識別し、bacteriophage *Phi*X DNA 配列を含む read を除去、3）次いで Cutadapt（v1.9.1）[62] を使用し、アダプター及びプライマー配列を除去し、連続してクオ

リティー17 以下のリードの 3’末端は trim（forward primer オプション:‘-a AGATCGGAAGAGCACACGTCTGAACTCCAGTCA -O 32 -q 17’、reverse primer オプション：‘-a AGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGT -O 32 -q 17’）、4） 50 base pair 以下の長さの read を除去、5） また平均クオリティーが 25 以下のリードを除去、6） Bowtie 2 によりリードをヒトゲノム（24 gi numbers: from 568336000 to 568336023, http://www. ncbi.nlm.nih.gov/nuccore/568336023/、GRCh38）に対してマッピングし、マッピングされたものはヒトゲノムから派生したものと考え、除去、7） 最後にペアになっていないリードを除去。結果、合計 6,229,896,106 reads （平均 144,881,305 reads /検体）のペアエンドリードが、high-quality read として得られ（付録１）、その後のオーソログの relative abundance の算出の解析に用いた。

6.2.6 オーソログの relative abundance の算出

F. prausnitzii 株のそれぞれの遺伝子のメタゲノム中の relative abundance を Kallisto （v0.46.2）[83] により transcripts per million （TPM）を用いて算出した。それぞれの遺伝子を Roary 又は Orthofinder により得られたオーソロググループに分類し、各オーソログの relative abundance を算出した。健常者群と MCI 群あるいは健常者群と AD 群の群間比較においては R によりウィルコクソンの順位和検定を実施した。加えて、FDR 補正した *q* 値を算出した。検定の有意水準は $p < 0.05$ とした（付録 9、10）。

6.3 結果

6.3.1 Fp14 と Fp360 に特徴的なオーソログの抽出

認知機能改善効果を示した Fp14 および Fp360 とそれ以外の *F. prausnitzii* 単離株 10 株のゲノムを比較した結果、4 個の特徴的なオーソログが Fp14 および Fp360 のみに共有されていた（付録 7、8）。4 個のうち 3 個のオーソログは互いに隣接していた（図 16）。

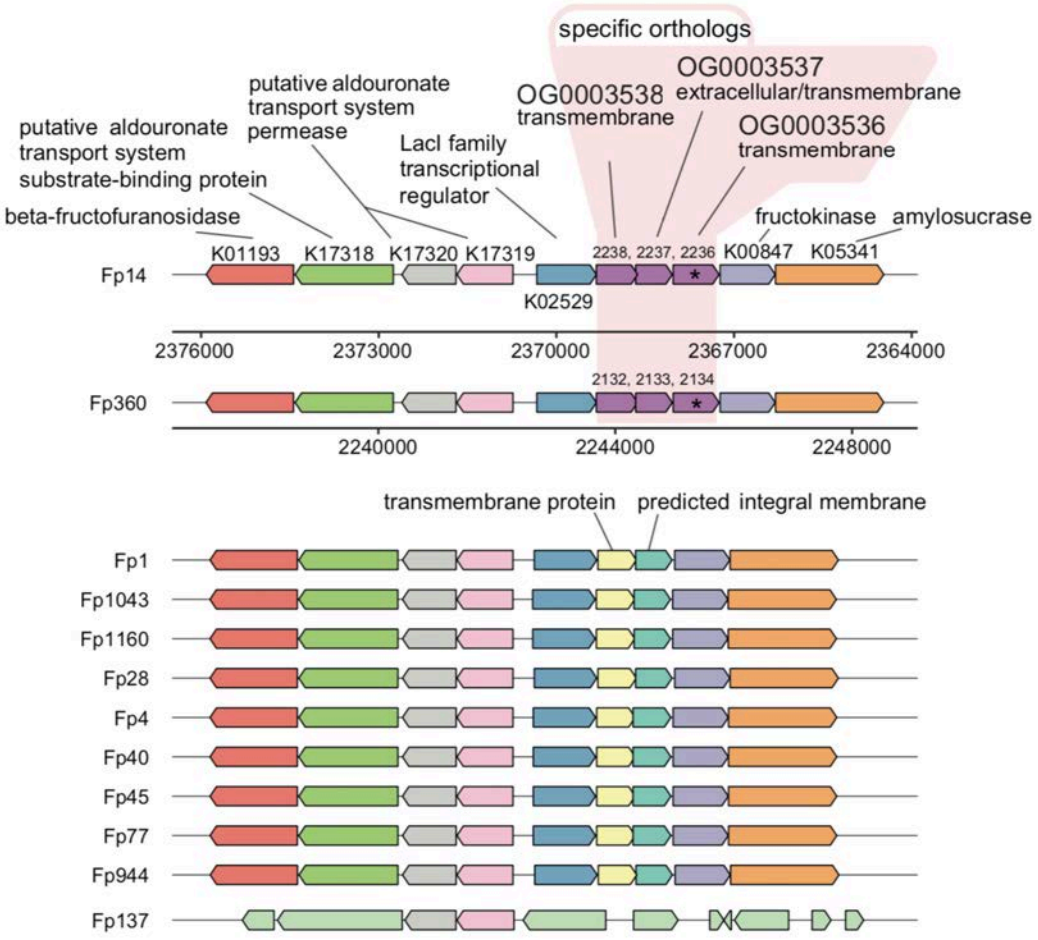
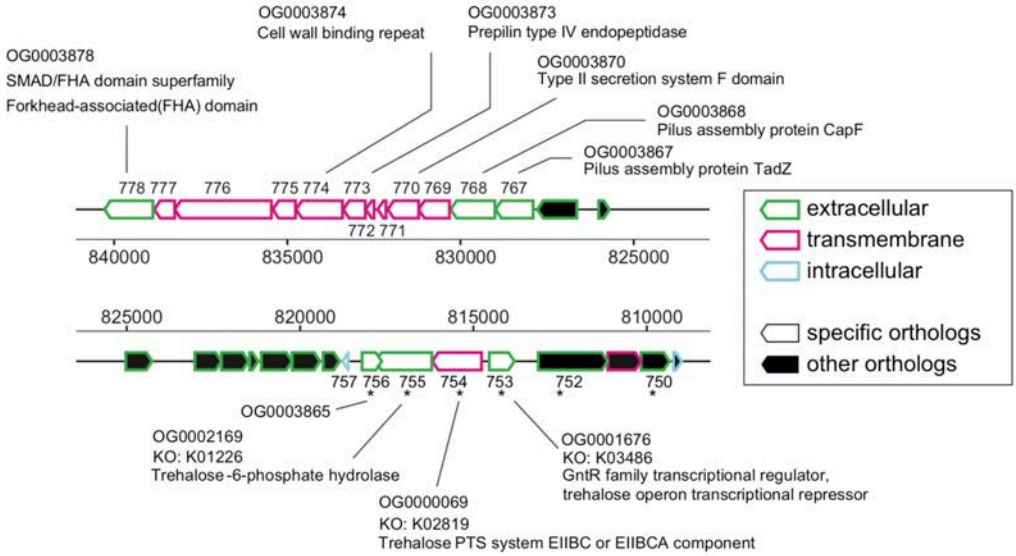


図 16：全ゲノム解析の結果（Fp14 と Fp360 に特徴的なオーソログの抽出）
Fp14 および Fp360 とそれ以外の *F. prausnitzii* 単離株 10 株のゲノムを比較し、Fp14 および Fp360 のみに共有されていた特徴的なオーソログを示す。4 個のうち 3 個のオーソログは互いに隣接していた。Fp14 と Fp360 に特徴的なオーソログの relative abundance を健常者群と MCI 群で比較し、差の見られたオーソログを*で示す（ウィルコクソンの順位和検定、$^{*}p < 0.05$）。DIAMOND、InterProScan、TMHMM により得られた KO およびドメイン情報をオーソログに割り当てた。

続いて、Fp14 とそれ以外の *F. prausnitzii* 単離株 11 株のゲノムを比較した結果、Fp14 においてのみに特徴的なオーソログが 150 個検出された（付録 7、8）。うち、遺伝子 753～757 の 5 個の特徴的なオーソログは互いに隣接しており、そのうち 3 個の特徴的なオーソログはトレハロース代謝に関連していた（図 17）。遺伝子 767~778 の 12 個のオーソログのうち 2 個の特徴的なオーソログは線毛のアセンブリーに関連していた（図 17）。

Fp360 とそれ以外の *F. prausnitzii* 単離株 11 株のゲノムを比較した結果、Fp360 においてのみに特徴的なオーソログが 214 個検出された（付録 7、8）。そのうちのいくつかの特徴的なオーソログは細胞分裂に関連していた（付録 7、8、図 18）。

A



B

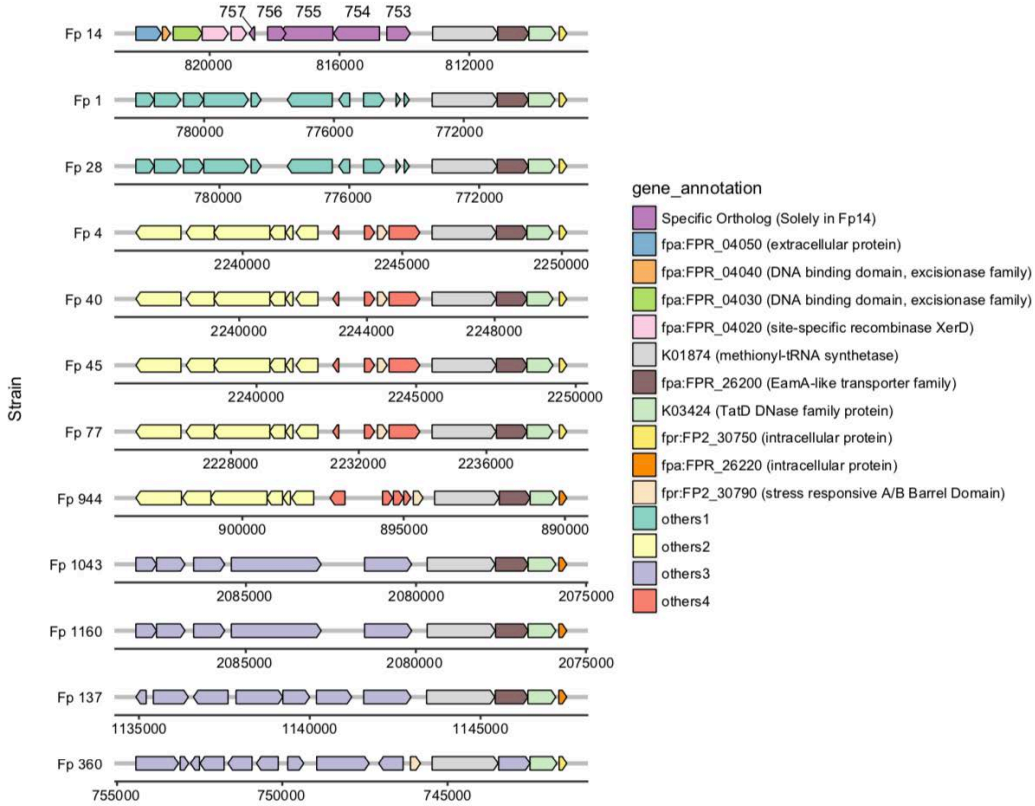


図 17：全ゲノム解析の結果（Fp14 に特徴的なオーソログの抽出）

（A）Fp14 とそれ以外の *F. prausnitzii* 単離株 11 株のゲノムを比較し、Fp14 においてのみに特徴的なオーソログ 150 個のうち、隣接していた 17 個を示す。Fp14 に特徴的なオーソログの relative abundance を健常者群と MCI 群で比較し、差の見られたオーソログを*で示す（ウィルコクソンの順位和検定、$^{*}p < 0.05$）。DIAMOND、InterProScan、TMHMM により得られた KO およびドメイン情報をオーソログに割り当てた。（B）Fp14 においてのみに特徴的なオーソログの隣接していた 17 個のうち 5 個を示す。

6.3.2 特徴的なオーソログのメタゲノム中の relative abundance

上記の Fp14 と Fp360 に特徴的なオーソログが MCI や認知機能異常軽減効果と関連しているのかを第 2 章の観察研究から得られたメタゲノムデータを用いて検証した。図 15 に示すパイプラインに沿って、具体的には糞便メタゲノムにおける Fp14 と Fp360 に特徴的なオーソログの relative abundance を健常者群と MCI 群で比較した。また、特徴的なオーソログの機能を推定するため KO およびドメインプロファイルをそれぞれのオーソログに割り当てた。

Fp14 および Fp360 のみに共有されていた 4 つの特徴的なオーソログのうち、1 つのオーソログ（OG0003536、図 16）の relative abundance が MCI 群に比べて健常者群で多く（$p = 0.0226$）（図 18、付録 9、10）、そのオーソログは TMHMM により膜貫通型タンパク質と推定された（図 16、18、付録 7、8）。

Fp14 においてのみに特徴的だった 150 個のオーソログのうち、4 つのオーソログ（OG0003865、OG0002169、OG0000069 および OG0001676、図 17）の relative abundance が MCI 群に比べて健常者群で多かった（$p = 0.0099$、0.0009、0.0121、0.0024）（図 18、付録 9、10）。それら 4 つのオーソログは互いに隣接しており TMHMM により細胞外タンパク質あるいは膜貫通型タンパク質と推定された（図 17、18、付録 7、8）。また、4 つのうち 3 つのオーソログ（OG0002169、OG0000069、OG0001676）はトレハロース代謝と関連していた（図 17、18、付録 7、8）。

Fp360 においてのみに特徴的だった 214 個のオーソログのうち、3 つのオーソログ（OG0004181、OG0000713、OG0000772）の relative abundance が MCI 群に比べて健常者群で多かった（$p = 0.0416$、 0.0162、0.0195）（図 18、付録 9、10）。それら 3 つのオーソログはそれぞれ、TMHMM により細胞外タンパク質、膜貫通型タンパク質、および、細胞内タンパク質と推定された（図 18、付録 7、8）。3 つのうち 2 つのオーソログ（OG0000713、OG0000772）は細胞分裂に関連していた（図 18、付録 7、8）。

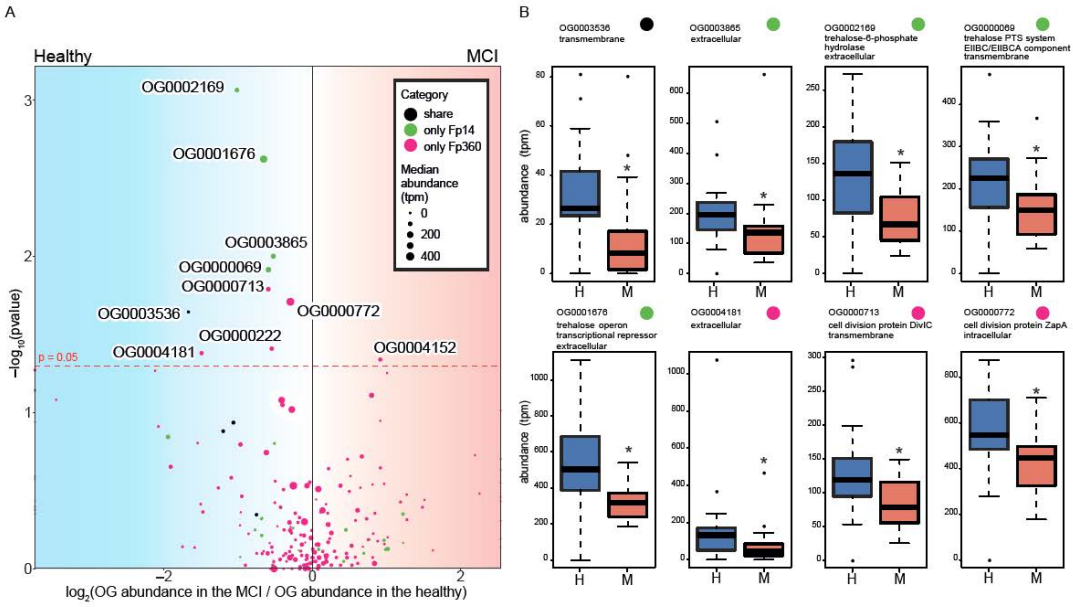


図 18：特徴的なオーソログのメタゲノム中の relative abundance の算出結果
（A）健常者群と MCI 群との間で relative abundance に差が見られたオーソログを示す（ウィルコクソンの順位和検定）。X 軸： $\log_2$ （MCI 群の relative abundance の中央値/健常者群の relative abundance の中央値）、Y 軸：$-\log_{10}$（ウィルコクソンの順位和検定の p 値）、赤の水平線： $p = 0.05$、丸の大きさ：それぞれのオーソログの relative abundance の中央値。黒丸: Fp14 および Fp360 のみに共有、緑丸: Fp14 においてのみ、マゼンタ丸: Fp360 においてのみ、（B）健常者群と MCI 群との間で relative abundance に差が見られた 8 つの特徴的なオーソログの relative abundance を示す（ウィルコクソンの順位和検定、$^{*}p < 0.05$）。黒丸: Fp14 および Fp360 のみに共有、緑丸: Fp14 においてのみ、マゼンタ丸: Fp360 においてのみ。当図では Orthofinder で分類された特徴的なオーソログを示した。Roary においても OG0000222 を除いて同じ結果が観察された（付録 9、10）。Orthofinder により分類された OG0000222 は健常者群において多かったが、OG0000222 に含まれる Fp360 の遺伝子が Roary によって分類されたオーソログの relative abundance は健常者群において多くなかった。

6.4 考察

認知機能に対する有効性を示した Fp14 および Fp360 単離株と有効性を示さなかった残りの 10 株との全ゲノムを比較し、有効性を示した Fp14 と Fp360 に特徴的なオーソログを抽出した。そして、観察研究から得られたメタゲノムデータを用いた検証により、有効性を示した Fp14 と Fp360 に特徴的なオーソログのうちの一部の relative abundance は MCI 群と比較して健常者群において多いことが明らかになった。Fp14 および Fp360 のみに共有されていた 4 つの特徴的なオーソログのうちの 1 つのオーソログ（OG0003536）の relative abundance が MCI 群に比べて健常者群で多く、膜貫通型タンパク質と推定された（図 16、18）。膜貫通型タンパク質が細菌とその周辺環境の相互作用を調節する働きがあることは

広く知られているため[84]、Fp14 および Fp360 の認知機能の改善効果がこの Fp14 および Fp360 のみに共有されていたオーソログと関連している可能性は示唆された。しかしながら、Fp14 と Fp360 の有効性を認めた形態が異なっていたため（Fp14：死菌体懸濁液、Fp360：生菌）、 Fp14 および Fp360 それぞれにおいてのみ検出された特徴的なオーソログと OG0003536 の組み合わせによる作用が、認知機能改善効果をより詳細に説明しうるのではないかと推測される。

Fp14 においてのみに特徴的だったオーソログのうち、4 つのオーソログ（OG0003865、OG0002169、OG0000069 および OG0001676）の relative abundance が MCI 群に比べて健常者群で多く、それらは互いに隣接していた（図 17、18）。この結果から 2 つの可能性が考えられる。1 つ目は、それらのオーソログが細胞外タンパク質あるいは膜貫通型タンパク質と推定されたため（図 17、18）、死菌化によりそれらのタンパク質の作用点への近づき易さが増加した、それらのタンパク質が可溶化した、あるいは、形態が変化したため、死菌体懸濁液においてのみ効果が見られた可能性が考えられた。2 つ目は、4 つのうち 3 つのオーソログ（OG0002169、OG0000069、OG0001676）はトレハロース代謝や細胞外トレハロースの取り込みと関連していたことから、細胞内のトレハロース、トレハロース 6 リン酸あるいはトレハロース代謝に関連する何らかの物質が死菌化により漏出し、関与成分として機能した可能性が推測された。この推測は AD モデルマウスである Tg2576 にトレハロースを投与した報告において認知機能低下が改善した結果と矛盾しない[85]。さらには、トレハロースが酸化ストレスを調節しミトコンドリアの機能不全を軽減するとの報告があることから[86]、第 5 章におけるメタボローム解析と RNA-seq 解析において、Fp14 死菌体懸濁液の作用と酸化ストレスやミトコンドリア機能との関連性が考えられた結果と一貫性がある。Fp14 に特徴的にみられたこれら細胞外タンパク質あるいは膜貫通型タンパク質自身、あるいはこれらのタンパク質とトレハロースに関連する代謝物や OG0003536 との組み合わせによる作用が、Fp14 死菌体懸濁液の作用を説明しうるのか、さらなる研究が必要であると考える。

Fp360 においてのみに特徴的だったのオーソログのうち、3 つのオーソログ（OG0004181、 OG0000713、OG0000772）の relative abundance が MCI 群に比べて健常者群で多く、3 つのうち 2 つのオーソログ（OG0000713：K13052（DivIC）、OG0000772：K09888 （ZapA））は細胞分裂に関連していた（図 18）。DivIC 複

合体は近年、ペリプラズム（細胞膜と細胞外膜の 2 枚の生体膜に囲まれた空間）に大きなドメインを有し、細胞分裂の際に隔壁特異的にペプチドグリカン（PG）合成を導き、隔壁合成のための midcell における PG 合成を開始することが報告されている[87]。これら midcell における DivIC 複合体は細胞分裂時に現れるため、一過性の PG 構造や DivIC 複合体が Fp360 が生菌においてのみ有効性を示すことに必要な可能性が示唆された。これら細胞分裂タンパク質自身、あるいはそれらと OG0003536 との組み合わせによる作用が Fp360 の有効性を説明しうるのか今後の研究が必要であると考える。

本研究では、Fp14 と Fp360 に特徴的なオーソログのうちの一部の relative abundance は MCI 群と比較して健常者群において多いことが明らかとなり、Fp14 と Fp360 に特徴的なオーソログと MCI や認知機能異常軽減効果との関連が示唆された。今後の研究においては、特徴的なオーソログが認知機能改善効果とどの程度関連しているのか検討が必要であると考えられる。検討方法としては、例えば、本研究ではオーソログのアバンダンスを計算する上で Kallisto のみを使用しているが、Bowtie2 などシーケンスリードとの相同性の閾値を設定できる他の解析ツールを用いることで、Fp14 と Fp360 に特徴的なオーソログと相同性の極めて高いリードのみを用いたアバンダンスの算出を行う方法が考えられる。別の検討方法としては例えば、特徴的なオーソログに割り当てられたショットガンシーケンスリードに占める *F. prausnitzii* の寄与率を計算する方法を構築することが考えられる。*F. prausnitzii* のアバンダンスが多いことから、寄与率は高いのではないかと推察している。さらに別の検討方法としては、オーソログを破壊したノックアウト株を作成し、認知機能改善効果が失われるのかを検討する方法が考えられる。今後、上記のような研究を通して、特徴的なオーソログと認知機能改善効果との関連性について検討が必要であると考える。

Fp14 と Fp360 に特徴的なオーソログが既知の *F. prausnitzii* 株と共有されているかを調べるために、我々の *F. prausnitzii* 単離株と既知の *F. prausnitzii* 株の全ゲノムを比較した。既知の *F. prausnitzii* 株は図 10 で用いた既知の *F. prausnitzii* 8 株のうち、ゲノムが公開されていないあるいはドラフトゲノムしか公開されていない株を除き、A2-165、S3L/3、L2-6 の 3 株と比較した。図 18 で示した 8 つのオーソログのうち OG0000713、OG0000772 を除く 6 つのオーソログは A2-165、S3L/3、L2-6 の 3 株に共有されていなかった（付録 7）。しかし、Fp360 において

のみ特徴的なオーソログであった OG0000713、OG0000772 は L2-6 株により共有されていた（付録 7）。図 10 にあるように Fp360 と L2-6 は系統的に近いが、L2-6 株が認知機能へ及ぼす影響は現状明らかになっていない。したがって、L2-6 株および Fp360 が同じ効果を示すのか、そして、それらの株の有効性が Fp360 において特徴的だったオーソログを共有しているからなのかについては今後の研究が必要であると考える。

第 7 章 結論

本研究においては、腸内細菌を介した MCI に対する介入候補素材を探索し、その候補素材の有効性や特徴を明らかにした。まず、第 2 章で示したように、観察研究を実施し、健常者、MCI、および AD の方の糞便を用いて菌叢を比較した。結果、健常者群と MCI 群の比較において、細菌自体の relative abundance が多く、認知機能検査（MoCA-J）スコアとの相関がある *F. prausnitzii* を、腸内細菌を介した MCI に対する介入候補素材として選抜した。第 3 章では観察研究被験者らからの嫌気度要求性の高い *F. prausnitzii* を単離した。第 4 章では *F. prausnitzii* 単離株の認知機能に対する有効性を検討するために AD モデルマウスに単離株 12 株を投与し、12 株のうちの 2 株である Fp14 死菌体懸濁液および Fp360 生菌が再現性をもって Aβ 脳室内注入による認知機能異常を改善することを示した。*F. prausnitzii* を素材として用いる上で死菌化が実効性のある解決方法となりうると考える。第 5 章では Fp14 死菌体懸濁液の脳内メカニズムの検討を RNA-seq およびメタボローム解析にて実施した。結果、酸化ストレスやミトコンドリア機能に関連するとの報告がみられる代謝物や転写物の変動が見られ、Fp14 死菌体懸濁液の作用と酸化ストレスやミトコンドリア機能との関連性が示唆された。第 6 章では認知機能に対する有効性を示した Fp14 および Fp360 と有効性を示さなかった残りの 10 株との全ゲノムを比較し、有効性を示した Fp14 と Fp360 に特徴的なオーソログを見出した。Fp14 と Fp360 のそれぞれに特徴的なオーソログの KO およびドメインプロファイルから、異なる作用形態（死菌体懸濁液あるいは生菌）と特徴的なオーソログとの関係が示唆された。また、有効性を示した Fp14 と Fp360 に特徴的なオーソログの一部は観察研究健常者の糞便メタゲノム中の relative abundance が多く、Fp14 と Fp360 に特徴的なオーソログと MCI や認知機能異常軽減効果との関連が示唆された。以上のように、本研究では腸内細菌を介した MCI に対する介入候補素材として特定のオーソログを有する *F. prausnitzii* 株を見出した。今後、ヒトにおける認知機能異常軽減効果の検討が期待される。また、Fp14 および Fp360 に特徴的なオーソログやメカニズムに関連する可能性のある代謝物あるいは転写物が得られたため、Fp14 あるいは Fp360 の認知機能改善効果にこれらがどのように関連しているのか今後の研究が必要であると考える。

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付録1: 選抜された被験者の情報及びリード数

*1 MMSE: Mini-Mental State Examination

*2 MoCA-J: Montreal Cognitive Assessment Japanese version

Group (1: healthy, 2 MCI, 3: AD)	16S_ID	metagenome_ID	Age (years)	Gender	BMI (kg/m^2)	MMSE*1 (score)	MoCA-J*2 (score)	Education (years)	Number of 16S_raw_reads	Number of 16S_high-quality reads	Number of metagenome_raw_reads	Number of metagenome_high-quality reads
2	AJ8MY_PG0980_01_a_33_L001	HK335BCXX_PG1390_76B0501_H1_L001	93	F	24.4	28	16	6	136,789	56,126	149,142,802	145,430,614
1	AJ8MY_PG0980_01_a_34_L001	HK335BCXX_PG1390_77B0502_H1_L002	74	M	21.0	28	27	12	138,316	79,313	153,062,314	148,456,040
1	AJ8MY_PG0980_01_a_39_L001	HK335BCXX_PG1390_82B0601_H1_L002	69	F	16.8	28	27	9	172,480	95,453	162,375,436	158,673,094
2	AJ8MY_PG0980_01_a_40_L001	HK335BCXX_PG1390_83B0602_H1_L001	74	M	21.3	25	17	9	57,844	26,930	148,619,988	144,829,828
3	AJ8MY_PG0980_01_a_73_L001	HK35KBCXX_PG1390_46B0103_H1_L001	86	F	21.9	24	16	8	230,532	119,164	119,944,770	117,120,838
3	AJ8MY_PG0980_01_a_74_L001	HK35KBCXX_PG1390_47B0104_H1_L002	79	F	25.4	12	6	8	184,688	83,699	129,369,150	126,224,602
2	AJ8MY_PG0980_01_a_11_L001	HK35KBCXX_PG1390_54B0203_H1_L002	78	M	20.6	27	23	9	64,438	34,676	123,584,380	120,741,584
2	AJ8MY_PG0980_01_a_12_L001	HK35KBCXX_PG1390_55B0204_H1_L001	76	F	21.9	25	17	9	86,683	43,814	165,946,338	161,298,346
1	AJ8MY_PG0980_01_a_35_L001	HK3CKBCXX_PG1390_78B0503_H1_L001	68	M	23.2	29	26	12	117,636	52,012	142,823,318	139,303,952
1	AJ8MY_PG0980_01_a_36_L001	HK3CKBCXX_PG1390_79B0504_H1_L002	73	F	22.6	30	26	11	151,240	81,232	139,602,140	136,023,546
2	AJ8MY_PG0980_01_a_41_L001	HK3CKBCXX_PG1390_84B0603_H1_L002	92	F	22.8	22	18	3	187,711	97,757	141,474,502	138,084,694
1	AJ8MY_PG0980_01_a_42_L001	HK3CKBCXX_PG1390_85B0604_H1_L001	64	F	17.6	30	26	12	169,627	85,401	135,995,370	132,720,298
2	AJ8MY_PG0980_01_a_21_L001	HK3CLBCXX_PG1390_64B0305_H1_L001	80	M	23.7	29	25	12	53,879	24,757	159,064,342	154,335,328
1	AJ8MY_PG0980_01_a_22_L001	HK3CLBCXX_PG1390_65B0306_H1_L002	72	F	29.3	30	28	12	105,542	59,659	153,690,704	149,876,970
1	AJ8MY_PG0980_01_a_29_L001	HK3CLBCXX_PG1390_72B0405_H1_L002	73	F	24.9	30	27	12	87,576	48,611	135,231,136	132,235,502
1	AJ8MY_PG0980_01_a_30_L001	HK3CLBCXX_PG1390_73B0406_H1_L001	78	M	24.9	29	27	9	166,201	95,385	157,628,818	153,900,296
3	AJ8MY_PG0980_01_a_05_L001	HK3CWBCXX_PG1390_48B0105_H1_L001	91	M	21.1	14	8	8	52,255	26,087	139,231,488	135,929,930
3	AJ8MY_PG0980_01_a_06_L001	HK3CWBCXX_PG1390_49B0106_H1_L002	80	F	24.2	16	7		91,974	52,298	124,830,434	121,443,216
1	AJ8MY_PG0980_01_a_13_L001	HK3CWBCXX_PG1390_56B0205_H1_L002	79	M	17.8	29	27	9	155,687	78,269	154,523,566	150,229,618
1	AJ8MY_PG0980_01_a_14_L001	HK3CWBCXX_PG1390_57B0206_H1_L001	73	F	22.8	30	29	16	208,123	103,455	144,273,320	139,885,470
3	AJ8MY_PG0980_01_a_71_L001	HK3GVBCXX_PG1390_44B0101_H1_L001	65	F	19.7	11	4	12	186,357	81,478	125,087,790	121,267,490
3	AJ8MY_PG0980_01_a_72_L001	HK3GVBCXX_PG1390_45B0102_H1_L002	89	F	21.2	17	11	6	55,925	24,203	122,718,378	118,158,502
2	AJ8MY_PG0980_01_a_09_L001	HK3GVBCXX_PG1390_52B0201_H1_L002	79	F	25.6	28	17	9	87,310	44,622	124,814,998	120,735,674
2	AJ8MY_PG0980_01_a_10_L001	HK3GVBCXX_PG1390_53B0202_H1_L001	82	F	26.7	30	20	9	84,718	45,267	120,125,334	115,750,898
2	AJ8MY_PG0980_01_a_18_L001	HK5MMBCXX_PG1390_62B0303_H1_L001	79	F	26.3	30	22	14	202,425	107,901	135,244,658	130,946,166
2	AJ8MY_PG0980_01_a_20_L001	HK5MMBCXX_PG1390_63B0304_H1_L002	70	M	24.9	27	20	16	247,274	110,358	142,766,008	138,629,078
1	AJ8MY_PG0980_01_a_27_L001	HK5MMBCXX_PG1390_70B0403_H1_L002	66	M	26.5	29	26	12	56,007	1,286	174,249,934	169,099,890
1	AJ8MY_PG0980_01_a_28_L001	HK5MMBCXX_PG1390_71B0404_H1_L001	65	F	20.8	30	29	12	103,332	53,376	168,652,978	163,968,416
1	AJ8MY_PG0980_01_a_17_L001	HKH3LBCXX_PG1390_60B0301_H1_L001	66	M	17.6	30	30	12	214,377	106,798	145,827,770	140,899,770
1	AJ8MY_PG0980_01_a_19_L001	HKH3LBCXX_PG1390_61B0302_H1_L002	79	F	23.1	29	26	11	175,292	92,370	142,224,336	137,524,666
2	AJ8MY_PG0980_01_a_25_L001	HKH3LBCXX_PG1390_68B0401_H1_L002	75	M	29.0	24	22	12	95,859	22,411	176,940,166	171,911,324
1	AJ8MY_PG0980_01_a_26_L001	HKH3LBCXX_PG1390_69B0402_H1_L001	68	M	27.9	30	30	12	108,025	54,771	161,479,964	156,287,426
1	AJ8MY_PG0980_01_a_23_L001	HKHGKBCXX_PG1390_66B0307_H1_L001	80	M	28.2	28	26	9	108,160	57,595	128,928,972	123,424,664
1	AJ8MY_PG0980_01_a_24_L001	HKHGKBCXX_PG1390_67B0308_H1_L002	78	F	23.8	30	30	12	41,143	17,044	130,518,848	124,795,474
2	AJ8MY_PG0980_01_a_31_L001	HKHGKBCXX_PG1390_74B0407_H1_L002	80	F	24.8	29	22	14	144,285	80,135	159,747,270	152,947,522
2	AJ8MY_PG0980_01_a_32_L001	HKHGKBCXX_PG1390_75B0408_H1_L001	83	F	25.8	26	18	4	52,748	22,561	149,921,820	143,923,264
3	AJ8MY_PG0980_01_a_07_L001	HKHGLBCXX_PG1390_50B0107_H1_L001	91	M	27.0	15	7	8	84,517	45,017	160,934,732	156,912,136
1	AJ8MY_PG0980_01_a_08_L001	HKHGLBCXX_PG1390_51B0108_H1_L002	70	F	18.4	30	27	12	33,757	15,220	173,089,512	167,651,732
1	AJ8MY_PG0980_01_a_15_L001	HKHGLBCXX_PG1390_58B0207_H1_L002	75	F	22.7	30	28	12	208,185	114,733	121,948,652	118,652,900
1	AJ8MY_PG0980_01_a_16_L001	HKHGLBCXX_PG1390_59B0208_H1_L001	75	F	26.0	30	27	9	69,637	31,522	144,512,302	139,941,174
2	AJ8MY_PG0980_01_a_37_L001	HKVMFBCXX_PG1390_80B0505_H1_L002	79	M	26.3	27	18	9	129,419	65,750	317,863,032	306,009,466
2	AJ8MY_PG0980_01_a_38_L001	HKVMFBCXX_PG1390_81B0506_H1_L001	77	F	22.3	26	22	12	197,252	109,471	152,901,214	147,696,206
1	AJ8MY_PG0980_01_a_43_L001	HKVMFBCXX_PG1390_86B0605_H1_L001	81	F	20.8	30	30	9	133,757	70,274	160,996,390	156,018,502

付録2：relative abundanceの群間比較結果

健常者群（H)とMCI群（M)あるいは健常者群とAD群（A)の群間比較においてはウィルコクソンの順位和検定を実施した。加えて、FDR補正したq値を算出した。

＊ frequence:　属が検出されたサンプル数

genus	HvsM (pvalue)	HvsA (pvalue)	HvsM (qvalue)	HvsA (qvalue)	frequence*	max_All	mean_All	median_All	median_groupH	median_groupM	median_groupA
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Bacteroides	0.400198068	0.766248888	0.830777181	0.923795388	42	0.318815245	0.123526849	0.099398796	0.107633752	0.076988327	0.146855632
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Bacteroides_B	0.364026542	0.725252525	0.830777181	0.891024531	42	0.314333457	0.12274886	0.103454436	0.10716643	0.085181257	0.165004332
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Faecalibacterium	0.039220608	0.341094332	0.590833133	0.746807013	41	0.22863138	0.104458669	0.095421393	0.116398806	0.076326404	0.100118551
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Prevotella	0.041220916	0.976591607	0.590833133	1	26	0.569338568	0.082698059	0.00018617	0.000151163	0.07224131	0
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Bacteroides_A	0.794538969	0.094423807	0.960474453	0.642777352	22	0.381213647	0.049269973	0.000123991	0.005102195	0.000219236	0
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnospira	0.542246273	0.240399536	0.889000138	0.721198608	41	0.141959141	0.03733574	0.026761298	0.026976843	0.021307937	0.031230959
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;_	0.297895347	0.21872234	0.830777181	0.697082748	42	0.134238716	0.029219991	0.023936117	0.026824085	0.018903744	0.021944574
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Blautia_A	0.168690172	0.030762474	0.830777181	0.642777352	42	0.106858054	0.025710256	0.023913645	0.030591377	0.023791251	0.011568814
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Tannerellaceae;g_Parabacteroides	0.656775943	0.0134545	0.960474453	0.642777352	41	0.119702949	0.023825317	0.017439499	0.015760269	0.017231096	0.035688274
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Rikenellaceae;g_Alistipes	0.443247795	0.21872234	0.830777181	0.697082748	40	0.11242408	0.022197093	0.0143592	0.0143592	0.010986792	0.041284931
k_Bacteria;_;_;_;_;_	0.419044598	0.081267525	0.830777181	0.642777352	41	0.396850079	0.021780519	0.001669749	0.00094224	0.002319571	0.00199333
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;_	0.020993217	0.071571906	0.590833133	0.642777352	42	0.049319384	0.016959032	0.015546998	0.020186433	0.011908745	0.008924513
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Agathobacter	0.70139299	0.080431648	0.960474453	0.642777352	36	0.073391349	0.016869273	0.012717643	0.017559659	0.009717974	0.002374878
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Acutalibacteraceae;g_Ruminococcus_E	0.101907255	0.12485684	0.761252718	0.642777352	29	0.104995844	0.016183517	0.008252538	0.014547786	0.001460076	0.000196372
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Anaerostipes	0.035715905	0.179475919	0.590833133	0.697082748	40	0.184098818	0.015345365	0.003384451	0.008939203	0.002615132	0.001541237
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Faecalicatena	0.779753518	0.569618144	0.960474453	0.871943564	40	0.08785394	0.013790169	0.006310565	0.005948353	0.009920406	0.001570053
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruminococcus_D	0.221909571	0.523325919	0.830777181	0.871943564	33	0.067564106	0.012834647	0.00628039	0.008549868	0.004121797	0.00446498
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Roseburia	0.478538097	0.431255701	0.831332022	0.84290887	41	0.049518187	0.012674781	0.008163125	0.00805149	0.00847798	0.007684998
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;_	0.483896689	0.293075458	0.831332022	0.746807013	39	0.073047859	0.010491255	0.004962085	0.004610469	0.005756102	0.002107177
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_Sutter	0.880062319	0.674202706	0.960474453	0.871943564	32	0.064082965	0.009563236	0.008176107	0.009284011	0.008254875	0.0059648
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Dorea	0.908355684	0.431255701	0.960474453	0.84290887	42	0.041979605	0.009461785	0.006331237	0.007152427	0.010508726	0.003143328
k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Streptococcus	0.946809866	0.618462179	0.992995713	0.871943564	37	0.110110272	0.009384907	0.001454647	0.001454647	0.001123105	0.001778271
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Acetatifactor	0.537340612	0.638095959	0.889000138	0.871943564	39	0.035858392	0.008861265	0.006922085	0.008690826	0.004392452	0.007552617
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Fusicatenibacter	0.419044598	0.022424918	0.830777181	0.642777352	40	0.031323903	0.008692715	0.006782	0.009595898	0.006870263	0.002504876
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;_	0.216512308	0.547510213	0.830777181	0.871943564	28	0.10228771	0.008155815	0.000654457	0.000267508	0.001009344	0.001158915
k_Bacteria;p_Actinobacteriota;c_Actinobacteria;o_Actinomycetales;f_Bifidobacteriaceae;g_Bifidobac	0.154135737	0.802787647	0.830777181	0.924639343	33	0.040211824	0.007604071	0.002361123	0.003945843	0.00154638	0.002139908
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Eubacterium_E	0.293379826	0.174584985	0.830777181	0.697082748	36	0.039176454	0.006839133	0.005364035	0.006502637	0.00516153	0.000814004
k_Bacteria;p_Firmicutes_C;c_Negativicutes;o_Selenomonadales;f_Selenomonadaceae;g_Megamonas	0.031753069	0.059523494	0.590833133	0.642777352	9	0.075569188	0.006744911	0	0	0	0
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Clostridium_Q	0.986880315	0.569618144	1	0.871943564	41	0.017840304	0.006624567	0.006086753	0.006112924	0.006251795	0.004958243
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_ER4	0.827031245	0.79975302	0.960474453	0.924639343	29	0.032391613	0.006367658	0.004259896	0.004259896	0.006295977	0
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Christensenellales;f_CAG-74;g_OEMS01	0.77436884	1	0.960474453	1	29	0.043047772	0.005966495	0.001060146	0.001144665	0.00127813	0.000503508
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Coprococcus	0.984985244	0.632034554	1	0.871943564	16	0.072060316	0.005848967	0	0	0	0
k_Bacteria;p_Firmicutes_A;c_Clostridia;_;_;_	0.489777005	0.702869634	0.831332022	0.888923361	22	0.055008242	0.005587354	0.000114218	9.74E−05	0.00034941	3.36E−05
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_CAG−110	0.385639123	1	0.830777181	1	26	0.075363208	0.005574865	0.00044079	0.000414529	0.00054777	0
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Eisenbergiella	0.70139299	0.332626277	0.960474453	0.746807013	37	0.025528133	0.004934784	0.002417199	0.001631898	0.002420732	0.002892203
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Eubacterium_G	0.129243538	0.725252525	0.830777181	0.891024531	39	0.021622165	0.004661731	0.001834581	0.002889734	0.001033389	0.001900591
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Acutalibacteraceae;g_Eubacterium_R	0.411353897	0.102546878	0.830777181	0.642777352	29	0.022503447	0.004557549	0.003229398	0.003158601	0.00469962	0
k_Bacteria;p_Firmicutes_C;c_Negativicutes;o_Acidaminococcales;f_Acidaminococcaceae;g_Phascola	0.442554448	0.495251513	0.830777181	0.871461805	13	0.029900672	0.004469254	0	0	0	0
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Butyricicoccaceae;g_Agathobaculum	0.856440412	0.130364965	0.960474453	0.642777352	41	0.010917193	0.003623649	0.003488275	0.003634986	0.003606414	0.001828714
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Blautia	1	0.698346693	1	0.888923361	20	0.0533372	0.003613085	0	0.00011241	0	0
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_RF32;f_CAG−239;g_CAG−495	0.450809323	0.310742434	0.830777181	0.746807013	4	0.094466193	0.003574449	0	0	0	0
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_Oscillibacter	0.473548821	0.637941971	0.831332022	0.871943564	39	0.010260135	0.003513216	0.003359486	0.003359486	0.002749587	0.005292775
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Coprococcus_B	0.785488641	0.667457955	0.960474453	0.871943564	26	0.022840849	0.003487176	0.001022042	0.000896147	0.001373932	0
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_CAG−81	0.059583766	1	0.748238929	1	38	0.010199072	0.003408212	0.002400997	0.002634417	0.001740217	0.002401462
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruminococcus_C	0.009685786	0.045376352	0.590833133	0.642777352	23	0.025044705	0.003340142	0.000922028	0.004050053	0	0
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruminiclostridium_E	0.761398205	0.450988833	0.960474453	0.868321783	12	0.042166344	0.003184492	0	0	0	0
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Er	0.080084427	0.189615102	0.748238929	0.697082748	16	0.085280032	0.003068461	0	0.000230518	0	0
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Eubacterium_Q	0.72066737	0.222563239	0.960474453	0.697082748	15	0.03132494	0.00306606	0	0	0	0
k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Lactobacillus_B	0.245367552	0.040964455	0.830777181	0.642777352	12	0.093832048	0.003054955	0	0	0	0
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Clostridiales;f_Clostridiaceae;g_Clostridium	0.322369583	0.211633757	0.830777181	0.697082748	26	0.029931559	0.002972265	0.000403695	0.000261313	0.001292564	0.0005119
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Monoglobales;f_UBA1381;g_CAG−41	0.03862917	0.50666384	0.590833133	0.871461805	37	0.008585414	0.002645713	0.002151929	0.003454809	0.001072716	0.002184996
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Marinifilaceae;g_Odoribacter	0.460705587	0.171537338	0.831332022	0.697082748	32	0.012113313	0.002499842	0.001994332	0.001780865	0.002208773	0.005536504
k_Bacteria;p_Firmicutes_C;c_Negativicutes;o_Acidaminococcales;f_Acidaminococcaceae;g_Phascola	0.684394564	0.213113581	0.960474453	0.697082748	16	0.018459346	0.002388111	0	0	0	0
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Paraprevotella	0.761398205	0.817499915	0.960474453	0.933252115	14	0.020717746	0.002225938	0	0	0	0
k_Bacteria;p_Verrucomicrobiota;c_Verrucomicrobiae;o_Verrucomicrobiales;f_Akkermansiaceae;g_Akk	0.090769725	0.129409593	0.761252718	0.642777352	17	0.036498665	0.002133303	0	0	0.000156873	0.000266566
k_Bacteria;p_Firmicutes_C;c_Negativicutes;o_Veillonellales;f_Dialisteraceae;g_Dialister	0.882493803	0.104890433	0.960474453	0.642777352	21	0.015284347	0.002109696	2.10E−05	0	0.000105274	0.001859274
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_Lawsonibacter	0.171699798	0.955870161	0.830777181	1	39	0.008442057	0.002045692	0.001402031	0.001353362	0.002085245	0.001377257
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Eubacterium_I	0.605287785	0.002920291	0.940748485	0.376717601	35	0.010872073	0.002014831	0.000973049	0.001511961	0.00114874	0
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Barnesiellaceae;g_Barnesiella	0.010144552	0.127817167	0.590833133	0.642777352	12	0.014280087	0.00184602	0	0.000309313	0	0
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_GCA−900066575	0.98662363	0.977862342	1	1	33	0.01684162	0.001835773	0.000626491	0.00064696	0.000623597	0.000629385
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Acutalibacteraceae;g_CAG−180	0.803195452	0.675925243	0.960474453	0.871943564	10	0.022635893	0.001795833	0	0	0	0
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Eubacterium_F	0.757260538	0.648577884	0.960474453	0.871943564	19	0.016026292	0.001792907	0	0	0	0
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Christensenellales;f_CAG−138;g_UBA3857	0.308366893	0.33906573	0.830777181	0.746807013	16	0.020656655	0.001725756	0	0	0	0
k_Bacteria;p_Fusobacteriota;c_Fusobacteriia;o_Fusobacteriales;f_Fusobacteriaceae;g_Fusobacteriur	0.253488005	0.303368518	0.830777181	0.746807013	8	0.033137974	0.00159296	0	0	0	0
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_KLE1615	0.39519267	0.279896017	0.830777181	0.746807013	37	0.008548319	0.00158269	0.001176303	0.001152411	0.001135469	0.00208421
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_CAG−56	0.741500667	0.394810396	0.960474453	0.821460341	23	0.009091931	0.001550937	0.000378921	0.000554697	0.000287185	0
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Coprococcus_A	0.579112918	0.843595624	0.931462516	0.946294222	30	0.006161074	0.001550777	0.001292392	0.001284211	0.001294007	0.001303331
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Clostridium_M	0.823994649	0.556168612	0.960474453	0.871943564	27	0.020001736	0.001484147	0.000367151	0.000332192	0.000267256	0.00065456
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Acutalibacteraceae;g_GCA−900066995	0.100383947	0.502922622	0.761252718	0.871461805	6	0.022864652	0.001399476	0	0	0	0
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_Parasu	0.901342788	0.499756814	0.960474453	0.871461805	22	0.009860361	0.001305167	0.000144151	3.78E−05	0.000231622	0.000262847
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Peptostreptococcales;f_Peptostreptococcaceae;g_Romboi	0.168215123	0.932614711	0.830777181	1	26	0.013821012	0.001255298	0.000202272	0.000320058	6.34E−05	0.000879575
k_Bacteria;p_Firmicutes_C;c_Negativicutes;o_Veillonellales;f_Veillonellaceae;g_Veillonella	0.414508079	0.843595624	0.830777181	0.946294222	25	0.007075364	0.001252786	0.000327553	0.000353363	0	0.000726605
k_Bacteria;p_Desulfobacterota_A;c_Desulfovibrionia;o_Desulfovibrionales;f_Desulfovibrionaceae;g_Bi	0.403501897	0.542164782	0.830777181	0.871943564	35	0.004725936	0.001152639	0.000847568	0.000899087	0.000685113	0.001034998
k_Bacteria;p_Firmicutes_C;c_Negativicutes;o_Acidaminococcales;f_Acidaminococcaceae;g_Acidamin	0.644599431	0.084907121	0.960474453	0.642777352	13	0.01595674	0.001098803	0	0	0	0
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Christensenellales;f_GCA−900066905;g_GCA−900066905	0.117993846	0.327301699	0.801116113	0.746807013	10	0.01760325	0.001034663	0	0	0	0
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Acutalibacteraceae;g_Acutalibacter	0.186214562	0.594386459	0.830777181	0.871943564	31	0.004211163	0.000975089	0.000466174	0.000262519	0.00078395	0
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Peptostreptococcales;f_Peptostreptococcaceae;_	0.847161752	0.629378881	0.960474453	0.871943564	24	0.006664782	0.000974928	0.000267942	0.000312565	0	0.000444765
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Acutalibacteraceae;_	0.893304019	0.656312352	0.960474453	0.871943564	33	0.006795395	0.00092578	0.000542573	0.000497177	0.000565497	0.000681012
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Muribaculaceae;g_Muribaculum	0.293943167	0.310742434	0.830777181	0.746807013	7	0.015601569	0.000887846	0	0	0	0
k_Bacteria;p_Firmicutes_C;c_Negativicutes;o_Veillonellales;f_Megasphaeraceae;g_Megasphaera	0.810152982	0.722752245	0.960474453	0.891024531	4	0.029774093	0.000866063	0	0	0	0
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Marinifilaceae;g_Butyricimonas	0.079479304	1	0.748238929	1	28	0.003750464	0.000833762	0.000301176	0.000271589	0.000898484	0
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Anaerotignaceae;g_Anaerotignum	0.906896767	0.802341235	0.960474453	0.924639343	34	0.004012446	0.000824602	0.000518991	0.000488969	0.000511472	0.000812435
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Acutalibacteraceae;g_Clostridium_A	0.387914367	0.556168612	0.830777181	0.871943564	27	0.013119986	0.000788487	0.000225553	0.000231819	0.000174705	0
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_TF01−11	0.278845149	0.876518342	0.830777181	0.974748846	15	0.00777503	0.000782312	0	0	0	0
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_4C28d−15;f_CAG−917;g_CAG−475	0.410143469	0.61208988	0.830777181	0.871943564	3	0.015949809	0.00078222	0	0	0	0
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;_;_	0.266941318	1	0.830777181	1	9	0.012603731	0.00077312	0	0	0	0
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Coprobacteraceae;g_Coprobacter	0.623502804	0.202609747	0.957522163	0.697082748	17	0.012184007	0.000712671	0	5.23E−05	0	0
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Rikenellaceae;g_Alistipes_A	0.801825549	0.633370255	0.960474453	0.871943564	19	0.014351913	0.000648698	0	0.000103553	0	0
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_Flavonifractor	0.376391953	0.779279531	0.830777181	0.924639343	27	0.004431751	0.000610579	0.000293522	0.000305754	0.000108737	0.000726605
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Kl	0.905067336	0.653455794	0.960474453	0.871943564	8	0.012489755	0.000580175	0	0	0	0
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Ci	0.310974043	0.909231325	0.830777181	0.985637319	7	0.008758255	0.000547523	0	0	0	0
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;_;_	0.300639772	0.21384035	0.830777181	0.697082748	18	0.005644263	0.000469205	0	0	0	6.66E−05
k_Bacteria;p_Proteobacteria;_;_;_;_	0.592092452	0.316041753	0.931462516	0.746807013	17	0.005683115	0.000420515	0	0.000105385	0	0
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Ra	0.901107414	0.502922622	0.960474453	0.871461805	3	0.01648674	0.000410221	0	0	0	0
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_CAG−95	0.144979237	0.621281209	0.830777181	0.871943564	12	0.0085608	0.000357573	0	0	0	0
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_UBA1191	0.081204225	0.597187275	0.748238929	0.871943564	29	0.002600164	0.000346521	0.000182801	0.000320398	4.53E−05	0.000229454
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Butyricicoccaceae;g_Butyricicoccus_A	0.181323235	0.757822791	0.830777181	0.922256038	10	0.006787717	0.000334709	0	0	0	0
k_Bacteria;p_Firmicutes;c_Bacilli;o_Acholeplasmatales;f_Acholeplasmataceae;_	0.070716356	0.61208988	0.748238929	0.871943564	5	0.006188815	0.00033319	0	0	0	0
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Anaerotignaceae;g_An114	0.367282881	0.160471135	0.830777181	0.697082748	25	0.001142934	0.000330601	0.000191586	0.000396946	0.000187184	0
k_Bacteria;p_Actinobacteriota;c_Coriobacteriia;o_Coriobacteriales;f_Coriobacteriaceae;g_Collinsella	0.196779613	0.121090429	0.830777181	0.642777352	19	0.003818085	0.000290246	0	0.000192472	0	0
k_Bacteria;p_Firmicutes;c_Bacilli;o_Haloplasmatales;f_Turicibateraceae;g_Turicibacter	0.341390371	0.276649535	0.830777181	0.746807013	12	0.004927757	0.00028336	0	0	0	0
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Monoglobales;f_Monoglobaceae;g_Monoglobus	0.267965348	1	0.830777181	1	12	0.003489886	0.000279863	0	0	0	0
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Rikenellaceae;g_Tidjanibacter	0.487844566	0.310742434	0.831332022	0.746807013	4	0.009747751	0.000266364	0	0	0	0
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_GCA−900066135	0.954976994	0.46279034	0.993484131	0.871461805	16	0.0016674	0.000232457	0	0	0	0
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;_	0.379700531	0.346264324	0.830777181	0.746807013	21	0.001974283	0.000230728	3.80E−05	0	0.000111213	0.000159444
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_CAG−45	0.544426441	0.16522392	0.889000138	0.697082748	10	0.005711481	0.000230707	0	0	0	0
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Es	0.705800423	0.347352099	0.960474453	0.746807013	5	0.004341704	0.000228729	0	0	0	0
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Clostridiales;f_Clostridiaceae;g_Clostridium_P	0.427128895	0.066256957	0.830777181	0.642777352	8	0.003569676	0.00022837	0	0	0	0
k_Bacteria;p_Firmicutes_C;c_Negativicutes;o_Veillonellales;f_Megasphaeraceae;g_Anaeroglobus	0.450246332	0.428536792	0.830777181	0.84290887	4	0.008836741	0.000226518	0	0	0	0
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Cellulosilyticaceae;g_Niameybacter	0.272656469	0.017544482	0.830777181	0.642777352	3	0.008547172	0.000222627	0	0	0	0
k_Bacteria;p_Firmicutes_C;c_Negativicutes;o_Selenomonadales;f_Selenomonadaceae;g_Mitsuokella	0.757423884	0.428536792	0.960474453	0.84290887	3	0.006629338	0.000219391	0	0	0	0

k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Tyzzerella	0.418923441	0.084846724	0.830777181	0.642777352	3	0.005328324	0.000216349	0	0	0	0
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruthenibacterium	0.222817251	0.134534795	0.830777181	0.642777352	22	0.001534919	0.000212615	7.97E-05	0	0.000139016	0.000377635
k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Lactobacillus_H	0.442014393	0.47185595	0.830777181	0.871461805	14	0.002665913	0.000188053	0	0	0	0
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Negativibacillus	0.808070341	0.1528503	0.960474453	0.697082748	15	0.00103293	0.000179948	0	0	0	0.000498333
k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Lactobacillus_C	0.835928468	0.104832331	0.960474453	0.642777352	4	0.00632153	0.000166718	0	0	0	0
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_Papillibacter	0.027264593	0.104832331	0.590833133	0.642777352	8	0.004061629	0.000166308	0	0	0	0
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_UBA9475	0.905067336	0.902546269	0.960474453	0.985637319	8	0.001964054	0.00016485	0	0	0	0
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruminococcus_F	0.450809323	0.310742434	0.830777181	0.746807013	4	0.004571343	0.000155251	0	0	0	0
k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Weissella	0.666183848	0.790224546	0.960474453	0.924639343	8	0.003545942	0.000136942	0	0	0	0
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Acetivibrionales;f_Acetivibrionaceae;g_Ruminiclostridium	0.106221309	0.108319381	0.761252718	0.642777352	3	0.004178326	0.000121883	0	0	0	0
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Fournierella	0.826598625	0.310742434	0.960474453	0.746807013	5	0.001847768	0.000121408	0	0	0	0
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Christensenellales;f_Christensenellaceae;g_Christensenella	0.330050239	0.907788779	0.830777181	0.985637319	22	0.000714518	0.00012012	7.54E-05	0.000102711	0	0.000131423
k_Bacteria;p_Actinobacteriota;c_Coriobacteriia;o_Coriobacteriales;f_Eggerthellaceae;g_Raoultibacte	1	0.354546815	1	0.749779331	17	0.001445466	0.000119766	0	0	0	0
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_4C28d-15;f_CAG-727;g_UBA1259	0.740048412	0.263253034	0.960474453	0.746807013	6	0.002986998	0.000118869	0	0	0	0
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_Dakar	0.194633151	0.128385832	0.830777181	0.642777352	6	0.002171336	0.000118536	0	0	0	0
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Ethanoligenenaceae;g_Ethanoligenens	0.587612311	0.495251513	0.931462516	0.871461805	10	0.001558948	0.00010601	0	0	0	0
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_Intestinimonas	0.896446296	0.518249412	0.960474453	0.871943564	10	0.001050208	0.000105924	0	0	0	0
k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Bacillaceae;g_Bacillus	0.310974043	0.226957174	0.830777181	0.697082748	5	0.001846213	0.000102127	0	0	0	0

付録3: Differential abundance analysisの群間比較結果

Differential abundance analysisの解析をRのALDEx2 libraryを用いて実施した。健常者群(H)とMCI群(M)あるいは健常者群(H)とAD群(A)の群間比較においてはウィルコクソンの順位和検定を実施した。加えて、FDR補正したq値を算出した。

HvsM

genus	log2(FC)	pvalue	qvalue
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruminococcus_C	−6.217624825	0.01084799	0.558885434
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Anaerostipes	−1.958706351	0.022208577	0.643943826
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;_	−0.9583233846	0.02646713	0.651537023
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Monoglobales;f_UBA1381;g_CAG-41	−1.576695819	0.039013707	0.680547445
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Prevotella	6.686606648	0.039588971	0.678278153
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Faecalibacterium	−0.71691272	0.043846279	0.681802475
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Oscillospirales;f_Acutalibacteraceae;g_Ruminococcus_E	−2.481324253	0.056879269	0.715010879
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_UBA1191	−2.086819664	0.058670269	0.710790417
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Barnesiellaceae;g_Barnesiella	−5.296975129	0.060015287	0.641706125
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_CAG-81	−1.167639132	0.062215279	0.724802877
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Marinifilaceae;g_Butyricimonas	1.770671999	0.084510866	0.761026514
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Lachnospirales;f_Fusicatenibacter	−0.924430349	0.130541613	0.819994952
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Eubacterium_G	−1.771465014	0.135005341	0.825237213
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Blautia_A	−0.9375506034	0.136201566	0.821973898
k_Bacteria;p_Verrucomicrobiota;c_Verrucomicrobiae;o_Verrucomicrobiales;f_Akkermansiaceae;g_Akkermansia	2.976088052	0.14524548	0.7784264
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Enterobacter	−3.761097819	0.147349603	0.782284537
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_Papillibacter	2.394607959	0.163304067	0.739272367
k_Bacteria;p_Firmicutes;C;c_Negativicutes;o_Selenomonadales;f_Selenomonadaceae;g_Megamonas	−2.129532357	0.166179519	0.762166236
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Oscillospirales;f_Acutalibacteraceae;g_Acutalibacter	1.073861399	0.180507127	0.842818618
k_Bacteria;p_Actinobacteriota;c_Actinobacteria;o_Actinomycetales;f_Bifidobacteriaceae;g_Bifidobacterium	−1.934436056	0.194670236	0.851611081
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Rikenellaceae;g_Alistipes	−0.736759357	0.205612842	0.853354292
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruminococcus_D	−1.544060838	0.209134266	0.857130721
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Bacteroides	−0.613489064	0.209718236	0.85475517
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Peptostreptococcales;f_Peptostreptococcaceae;g_Romboutsia	−2.308135715	0.218731693	0.853617028
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;_	−0.580806233	0.23049135	0.863127761
k_Bacteria;p_Firmicutes;A;c_Christensenellales;f_GCA-900066905;g_GCA-900066905	2.138728039	0.24410003	0.811675613
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;_	2.001997297	0.249949391	0.869502199
k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Lactobacillus	−1.827743758	0.25284493	0.812650026
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Oscillospirales;f_Acutalibacteraceae;g_GCA-900066995	1.813706466	0.266903736	0.805406357
k_Bacteria;p_Actinobacteriota;c_Coriobacteriia;o_Coriobacteriales;f_Coriobacteriaceae;g_Collinsella	−1.574190218	0.282340027	0.868896892
k_Bacteria;p_Firmicutes;c_Bacilli;o_Acholeplasmatales;f_Acholeplasmataceae;_	1.812661461	0.28451584	0.819554281
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_CAG-95	1.79552707	0.285731715	0.851674442
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Eubacterium_E	−0.837472598	0.293005742	0.884360346
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_Lawsonibacter	0.572183262	0.302853829	0.888509721
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Lachnospirales;f_Anaerotignaceae;g_An114	−1.001685684	0.312197477	0.887228093
k_Bacteria;_;_;_;_;_	0.861611197	0.318823241	0.893475727
k_Bacteria;p_Firmicutes;A;c_Christensenellales;f_CAG-138;g_UBA3857	2.071899498	0.3268773	0.857566939
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Bacteroides_B	−0.452929974	0.340301201	0.8965029
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_Oscillibacter	−0.352125668	0.350663702	0.897949767
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lactonifactor	1.411956719	0.350799346	0.845886859
k_Bacteria;p_Firmicutes;B;_;_;_;_	1.371593196	0.350852573	0.844982457
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Acetatifactor	−0.621530712	0.35239766	0.900946271
k_Bacteria;p_Desulfobacterota_A;c_Desulfovibrionia;o_Desulfovibrionales;f_Desulfovibrionaceae;g_Bilophila	−0.574763714	0.352975187	0.899633748
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Oscillospirales;f_Acutalibacteraceae;g_Clostridium_A	−1.165365346	0.368408755	0.904495032
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Oscillospirales;_;_	1.578057739	0.370548066	0.886347887
k_Archaea;p_Euryarchaeota;c_Methanobacteria;o_Methanobacteriales;f_Methanobacteriaceae;g_Methanobrevibacter_A	1.167603512	0.383720349	0.866675769
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_SS-A14a	−1.211286064	0.385039474	0.873642671
k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Lactobacillus_B	−1.53789241	0.389385573	0.889548959
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Monoglobales;f_Monoglobaceae;g_Monoglobus	0.966263698	0.394952599	0.867745273
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Acetivibrionales;f_Acetivibrionaceae;g_Ruminiclostridium	0.96224889	0.398719866	0.869824014
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_UC5-1-2E3	1.003201898	0.39900573	0.863058324
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_Flavonifractor	−0.940834203	0.401410454	0.912492853
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Oscillospirales;f_Butyricicoccaceae;g_Agathobaculum	−0.471893129	0.403669304	0.911638918
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;_;_	1.676508694	0.409643542	0.888350924
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Oscillospirales;f_Butyricicoccaceae;g_Butyricicoccus_A	−1.179682574	0.409917415	0.890377267
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Roseburia	−0.555435683	0.417031346	0.919239275
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_Dakarella	1.097873655	0.42051718	0.882443225
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Christensenellales;f_Christensenellaceae;g_Christensenella	−0.877778309	0.428092794	0.911791773
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Prevotellamassilia	0.93867674	0.434624396	0.878823229
k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Enterococcaceae;g_Enterococcus	0.780157004	0.43992412	0.883907929
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_TF01-11	−1.609776715	0.440212091	0.907116016
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Clostridiales;f_Clostridiaceae;g_Clostridium	1.75461099	0.441563002	0.922796257
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_Duodenibacillus	0.804979353	0.442578597	0.88984588
k_Bacteria;p_Firmicutes;B;c_Dehalobacteriia;o_Dehalobacteriales;f_Dehalobacteriaceae;g_Dehalobacterium	0.869582741	0.44316293	0.887727573
k_Bacteria;p_Fusobacteriota;c_Fusobacteriia;o_Fusobacteriales;f_Fusobacteriaceae;g_Cetobacterium_A	0.838436655	0.44511365	0.883645994
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruthenibacterium	0.96695148	0.446169772	0.919941601
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;_	1.008152621	0.450418224	0.920473863
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Monoglobaceae;g_Monoglobus	−1.238832896	0.452804662	0.90596243
k_Bacteria;p_Actinobacteriota;c_Coriobacteriia;o_Coriobacteriales;f_Eggerthellaceae;g_Eggerthella	−0.979529153	0.456645456	0.893605263
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Peptostreptococcales;f_Peptostreptococcaceae;g_Terrisporobacter	−0.710894429	0.466542017	0.894823187
k_Bacteria;p_Firmicutes;A;c_Clostridia;_;_;_	1.385148137	0.468312043	0.92577762
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_UBA1394	0.572722486	0.469622461	0.898635121
k_Bacteria;p_Proteobacteria;o_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiaceae;g_Leaf454	0.54789883	0.470245447	0.899117008
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Flavobacteriales;f_UBA1820;g_UBA1820	0.575241421	0.472753964	0.901965949
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Clostridiales;f_Clostridiaceae;g_Clostridium_P	0.85162187	0.47318044	0.906658177
k_Bacteria;p_Actinobacteriota;c_Coriobacteriia;o_Coriobacteriales;f_Eggerthellaceae;g_Gordonibacter	0.581771205	0.473383775	0.899479582
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Oscillospirales;f_Acutalibacteraceae;g_DTU053	0.466638845	0.474314215	0.900552174
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Lachnospirales;f_Cellulosilyticaceae;g_Niameybacter	0.565230002	0.475163628	0.897473972
k_Bacteria;p_Actinobacteriota;c_Coriobacteriia;o_Coriobacteriales;f_Eggerthellaceae;_	−0.722904656	0.475236455	0.901611056
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacterales;f_Succinivibrionaceae;g_Succinivibrio	0.620573747	0.475715323	0.897771802
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_D5	0.806354694	0.475946515	0.90529505
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Angelakisella	0.541844661	0.476095874	0.901943487
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Monoglobales;_;_	0.552792662	0.476567115	0.895211877
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Pseudobutyrivibrio	0.656913482	0.476813909	0.904619478
k_Bacteria;p_Fusobacteriota;c_Fusobacteriia;o_Fusobacteriales;f_Fusobacteriaceae;g_Fusobacterium_A	0.993845697	0.479196103	0.910053855
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Provencibacterium	0.49532837	0.480285419	0.904707387
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Muribaculaceae;g_Duncaniella	0.52706702	0.482703815	0.900568174
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Plesiomonas	0.52903856	0.483771297	0.901675208
k_Bacteria;p_Firmicutes;C;c_Negativicutes;o_Acidaminococcales;f_Acidaminococcaceae;_	0.507446906	0.485166872	0.907349669
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Phocea	−0.809256396	0.485448254	0.907944665
k_Bacteria;p_Fusobacteriota;c_Fusobacteriia;o_Fusobacteriales;f_Leptotrichiaceae;_	0.520530692	0.486003874	0.904796894
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Acetivibrionales;f_Acetivibrionaceae;_	0.372293754	0.486282709	0.903720479
k_Bacteria;p_Actinobacteriota;c_Actinobacteria;o_Actinomycetales;f_Micrococcaceae;g_Rothia	0.514455423	0.486986329	0.905740425
k_Bacteria;p_Actinobacteriota;c_Coriobacteriia;o_Coriobacteriales;f_Eggerthellaceae;g_Slackia_A	−0.939901992	0.48849524	0.90438625
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;_	0.502201028	0.490134311	0.90473744
k_Bacteria;p_Firmicutes;A;c_Clostridia;f_Caloramatoraceae;_	0.507379167	0.494914479	0.907068258
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Hafnia	0.577773512	0.495347893	0.902710232
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Pygmaiobacter	0.476403409	0.495983182	0.903366349
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_4C28d-15;f_UBA1242;g_UBA7862	0.514988922	0.496020797	0.909429179
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Oscillospirales;f_Acutalibacteraceae;g_An200	−0.702551101	0.496548628	0.914177761
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Neobitarella	−0.339817565	0.500478683	0.913637427
k_Bacteria;p_Synergistota;c_Synergistia;o_Synergistales;f_Synergistaceae;g_Cloacibacillus	0.563355898	0.500546734	0.910180409
k_Bacteria;p_Firmicutes;c_Bacilli;o_Erysipelotrichales;f_Erysipelotrichaceae;g_Holdemanella	−0.474095231	0.502705348	0.910937515
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;_	0.462845548	0.502732268	0.908907058
k_Bacteria;p_Spirochaetota;c_Brachyspirae;o_Brachyspirales;f_Brachyspiraceae;g_Brachyspira	0.400400347	0.505896319	0.911487589
k_Bacteria;p_Firmicutes;C;c_Negativicutes;o_Veillonellales;f_Veillonellaceae;g_Veillonella	−1.254766808	0.508618461	0.937872331
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Hungatella_A	0.715433299	0.508898631	0.912075495
k_Bacteria;p_Firmicutes;C;c_Negativicutes;o_Veillonellales;f_Megasphaeraceae;g_Anaeroglobus	0.602120289	0.510985365	0.914118231
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_Sporobacter	0.823222527	0.511158596	0.917525056
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_CAG-521	−0.40837203	0.51141031	0.915169963
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_CAG-45	0.915439809	0.513634338	0.924676451
k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Lactococcus	0.338574733	0.514099429	0.909934637
k_Bacteria;p_Firmicutes;C;c_Negativicutes;o_Acidaminococcales;f_Acidaminococcaceae;g_Phascolarctobacterium_A	1.09785981	0.515401081	0.926329756
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_CAG-353	−0.087066868	0.516925982	0.918167012
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_Pseudoflavonifractor	0.318869362	0.517087149	0.919137152
k_Bacteria;p_Verrucomicrobiota;c_Lentisphaeria;o_Victivallales;f_Victivallaceae;g_Victivallis	−0.125958885	0.519064139	0.916412101
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_CAG-110	0.910301175	0.519982217	0.944291694
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Citrobacter	−0.733253396	0.52097911	0.920571334
k_Bacteria;p_Actinobacteriota;c_Actinobacteria;o_Actinomycetales;f_Actinomycetaceae;g_Varibaculum;_	0.271439431	0.521308117	0.919724293
k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Aerococcaceae;g_Granulicatella	−0.632363279	0.521642443	0.917822139
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Raoultella	0.332805778	0.521938559	0.91959946
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Neisseriaceae;g_Neisseria	−0.133424027	0.521967533	0.915551937
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_4C28d-15;f_CAG-917;g_CAG-475	0.594732899	0.522187874	0.920003694
k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Bacillaceae;g_Bacillus	−0.67909948	0.523500299	0.918167463
k_Bacteria;p_Campylobacterota;c_Campylobacteria;o_Campylobacterales;f_Campylobacteraceae;g_Campylobacter_A	−0.080053752	0.523921444	0.917454094
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Bacteroides_F	−0.149235249	0.525239734	0.918516022
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_Marseille-P3106	−0.216020339	0.52532012	0.918975003
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_UBA6382	−0.119506038	0.525846745	0.918569648
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Muribaculaceae;g_Muribaculum	0.80542271	0.526117813	0.925282051
k_Bacteria;p_Actinobacteriota;c_Actinobacteria;o_Actinomycetales;f_Actinomycetaceae;g_Paujensenia	−0.111143019	0.527462	0.921314552
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Eubacteriales;f_Eubacteriaceae;g_Eubacterium	−0.048462383	0.527503988	0.920954874
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Soleaferrea	−0.064963846	0.527701572	0.91766904
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Hungatella	−0.272347689	0.527728686	0.922325622
k_Bacteria;p_Firmicutes;c_Bacilli;o_Haloplasmatales;f_Turicibacteraceae;g_Turicibacter	−1.093307732	0.527791037	0.926530821
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Oscillospirales;f_Butyricicoccaceae;_	−0.330087608	0.527882204	0.920596991
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Oscillospirales;f_Ethanoligenenaceae;_	−0.062186583	0.528218452	0.918249625
k_Bacteria;p_Actinobacteriota;c_Coriobacteriia;o_Coriobacteriales;f_Atopobiaceae;g_Lancefieldella	−0.15251277	0.528659338	0.920112908
k_Bacteria;p_Cyanobacteria;c_Vampirovibrionia;o_Gastranaerophilales;f_Gastranaerophilaceae;g_Zag111	−0.17978515	0.528799264	0.91557028
k_Bacteria;p_Actinobacteriota;c_Coriobacteriia;o_Coriobacteriales;f_Eggerthellaceae;g_Senegalimassilia	−0.114551851	0.529161563	0.922127576

HvsA

genus	log2(FC)	pvalue	qvalue
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Eubacterium_I	−4.422933205	0.003048573	0.393842772
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruminococcus_C	−3.454623418	0.057268199	0.737663345
k_Bacteria;_;_;_;_;_	1.955529546	0.063007026	0.753321591
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Tannerellaceae;g_Parabacteroides	1.254093282	0.064673805	0.755887254
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Lachnospirales;f_Anaerotignaceae;g_An114	−2.943478277	0.070808854	0.739058213
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Agathobacter	−2.690606483	0.080972004	0.768854415
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Oscillospirales;f_Acutalibacteraceae;g_Eubacterium_R	−5.300880348	0.094659026	0.767055744
k_Bacteria;p_Firmicutes;C;c_Negativicutes;o_Veillonellales;f_Dialisteraceae;g_Dialister	4.254709309	0.100695445	0.778654259
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Eubacterium_E	−2.260612772	0.109648211	0.785659938
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Fusicatenibacter	−1.670434097	0.113699972	0.788761761
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Blautia_A	−1.567560985	0.149563645	0.811874066
k_Bacteria;p_Firmicutes;B;c_Dehalobacteriia;o_Dehalobacteriales;f_Dehalobacteriaceae;g_Dehalobacterium	2.273846096	0.158236609	0.72589867
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnospira	0.887473624	0.15884838	0.816893196
k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Lactobacillus_B	−3.228026769	0.164237189	0.765917714
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Oscillospirales;f_Acutalibacteraceae;g_Ruminococcus_E	−2.314091618	0.17326706	0.824613202
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;_	−1.436614334	0.17571694	0.828492238
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Bacteroides_A	−4.28918504	0.186823496	0.82339437
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Clostridiales;f_Clostridiaceae;g_Clostridium_P	3.363574327	0.190311411	0.774941586
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruthenibacterium	2.065363231	0.206207576	0.831698762
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Marinifilaceae;g_Odoribacter	0.955381565	0.215191548	0.844410378
k_Bacteria;p_Actinobacteriota;c_Coriobacteriia;o_Coriobacteriales;f_Coriobacteriaceae;g_Collinsella	−2.201108516	0.223862974	0.835584707
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Anaerostipes	−1.91971684	0.224642423	0.860142999
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Oscillospirales;_;_	2.373624849	0.235816485	0.830962233
k_Bacteria;p_Verrucomicrobiota;c_Verrucomicrobiae;o_Verrucomicrobiales;f_Akkermansiaceae;g_Akkermansia	3.469217189	0.236464646	0.836673041
k_Bacteria;p_Firmicutes;B;_;_;_;_	2.417845434	0.239787677	0.780998666
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Clostridiales;f_Clostridiaceae;g_Clostridium	2.684404375	0.242582722	0.861613448
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Negativibacillus	2.270487136	0.244461494	0.844334707
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Barnesiellaceae;g_Barnesiella	−4.117167207	0.268311395	0.847502268
k_Bacteria;p_Firmicutes;C;c_Negativicutes;o_Selenomonadales;f_Selenomonadaceae;g_Megamonas	−2.227658218	0.268365998	0.822234192
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_Papillibacter	1.99701956	0.282393912	0.809376284
k_Bacteria;p_Firmicutes;A;c_Christensenellales;_;_;_	1.977518879	0.287343034	0.818805866
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Lachnospirales;f_Cellulosilyticaceae;g_Niameybacter	1.825972381	0.290169046	0.8037851
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Enterobacter	−2.594196699	0.296176482	0.867871546
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Oscillospirales;f_Acutalibacteraceae;g_UBA1033	2.015681904	0.296414777	0.82127776
k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Enterococcaceae;_	2.341643842	0.300881248	0.826067125
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Christensenellales;f_CAG-138;g_UBA3857	2.738349068	0.302187426	0.856631124
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_Dakarella	2.257295612	0.304578782	0.829704577
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;_	1.547486517	0.310789279	0.87084561
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Eisenbergiella	−1.355776767	0.314541466	0.902678773
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Coprobacteraceae;g_Coprobacter	−2.836629535	0.320405741	0.86758378
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Tyzzerella	1.947955347	0.336352754	0.844918504
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;_	−0.836204284	0.337214559	0.907378394
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Acidaminococcales;f_Acidaminococcaceae;g_Phascolarctobacterium	−2.718609923	0.349511432	0.875784344
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Escherichia	2.214397412	0.349652861	0.853688818
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Clostridium_Q	−0.515094987	0.35062808	0.90969488
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Christensenellales;f_Christensenellaceae;_	1.711669705	0.365319017	0.863116916
k_Bacteria;p_Firmicutes;A;c_Clostridia;o_Christensenellales;f_GCA-900066905;g_GCA-900066905	2.066791106	0.365355524	0.860059281
k_Bacteria;p_Firmicutes;C;c_Negativicutes;o_Veillonellales;f_Megasphaeraceae;g_Cetobacter	1.531196845	0.366437242	0.84271158
k_Bacteria;p_Firmicutes;C;c_Negativicutes;o_Acidaminococcales;f_Acidaminococcaceae;g_Acidaminococcus	−2.310054216	0.367268658	0.870138688
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Flavobacteriales;f_UBA1820;g_UBA1820	1.446959221	0.367970144	0.84861325
k_Bacteria;p_Firmicutes;A;c_

k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_Mogibacterium	−0.1218068	0.529228148	0.919781687
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_Emergencia	0.720451922	0.529851396	0.922172819
k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Lactobacillus_F	−0.111762013	0.529891768	0.924129533
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnoclostridium_A	−0.398013365	0.530470437	0.92267908
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Porphyromonadaceae;g_Porphyromonas	−0.171298397	0.530509289	0.919078198
k_Bacteria;p_Fusobacteriota;c_Fusobacteriia;o_Fusobacteriales;f_Fusobacteriaceae;g_Fusobacterium	0.278107001	0.530578661	0.919897828
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruminococcus	0.160809655	0.530658858	0.920988144
k_Bacteria;p_Firmicutes;c_Bacilli;o_Erysipelotrichales;f_Erysipelatoclostridiaceae;g_Erysipelatoclostridium	−0.033455502	0.531333631	0.915599042
k_Bacteria;p_Patescibacteria;c_Saccharimonadia;o_Saccharimonadales;f_Saccharimonadaceae;g_TM7x	0.311868252	0.531451638	0.922634443
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_4C28d-15;_;_	0.287736932	0.531773475	0.920659621
k_Bacteria;p_Firmicutes;c_Bacilli;o_Acholeplasmatales;_;_	−0.152828246	0.532104216	0.920943695
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Christensenellales;_;_	−0.250474799	0.532392164	0.915125314
k_Bacteria;p_Fusobacteriota;c_Fusobacteriia;o_Fusobacteriales;f_Leptotrichiaceae;g_Leptotrichia	0.201020037	0.532500481	0.922265449
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Muribaculaceae;g_CAG-873	−0.120081509	0.532726956	0.921372846
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Acutalibacteraceae;g_MS4	−0.088801613	0.532801971	0.917188738
k_Bacteria;p_Synergistota;c_Synergistia;o_Synergistales;f_Dethiosulfovibrionaceae;g_Pyramidobacter	−0.255762373	0.532839566	0.919428687
k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Lactobacillus_D	0.01578565	0.533353466	0.92149692
k_Bacteria;p_Actinobacteriota;c_Coriobacteriia;o_Coriobacteriales;f_Eggerthellaceae;g_Adlercreutzia	−0.039284647	0.533584401	0.920991373
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Pseudomonadaceae;g_Pseudomonas_E	−0.209036512	0.53396334	0.924603337
k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Enterococcaceae;_	−0.102767166	0.534229016	0.925863839
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Klebsiella_A	−0.104549877	0.53469981	0.91890076
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Tissierellales;f_Helcococcaceae;g_Parvimonas	0.289308025	0.535685009	0.921493365
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_Comamonas	0.195376153	0.536089576	0.922479937
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_4C28d-15;f_CAG-727;g_UBA1259	0.440395889	0.536749344	0.927216535
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Marvinbryantia	0.262085396	0.536989817	0.924215404
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Butyrivibrio_A	−0.249844328	0.537031273	0.922177751
k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Lactobacillus_C	0.116092309	0.537063726	0.923460744
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Tyzzerella	0.009534531	0.537623138	0.922849308
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Providencia	−0.175301747	0.539296778	0.922325584
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Acutalibacteraceae;g_Marseille-P4683	0.233602633	0.53998692	0.923739923
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_CAG-462	−0.18846495	0.540572704	0.924124203
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacterales;f_Succinivibrionaceae;g_Succinatimonas	−0.190285527	0.541662781	0.922809974
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_RF32;f_CAG-239;g_CAG-495	−0.158074496	0.541815529	0.927232408
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Bittarella	−0.357922743	0.542113669	0.926305486
k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Lactobacillus_H	0.99894211	0.542160344	0.934390173
k_Bacteria;p_Firmicutes_C;c_Negativicutes;o_Veillonellales;f_Veillonellaceae;g_Veillonella_A	−0.035689079	0.542196254	0.924725051
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacterales;f_Pasteurellaceae;g_Haemophilus_D	−0.444520681	0.542676872	0.926337814
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Acutalibacteraceae;g_UBA1033	−0.021603811	0.543694385	0.927785416
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruminococcus_F	−0.467241113	0.546752274	0.929252257
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Rikenellaceae;g_Tidjanibacter	−0.362439206	0.547110176	0.929992812
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Sellimonas	0.234346505	0.550412054	0.931175043
k_Bacteria;p_Firmicutes;c_Bacilli;o_Staphylococcales;f_Gemellaceae;g_Gemella	−0.077745544	0.552610374	0.932191163
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;_;_	0.340989934	0.553193297	0.930787953
k_Bacteria;p_Firmicutes_C;c_Negativicutes;o_Veillonellales;f_Dialisteraceae;g_Allisonella	−0.33933271	0.554336388	0.931772408
k_Bacteria;p_Desulfobacterota_A;c_Desulfovibrionia;o_Desulfovibrioniales;f_Desulfovibrionaceae;g_Desulfovibrio	0.36641278	0.555662026	0.932403077
k_Bacteria;p_Firmicutes_C;c_Negativicutes;o_Veillonellales;f_Megasphaeraceae;g_Megasphaera	0.000891388	0.557913755	0.930907124
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Escherichia	−0.021946325	0.55854976	0.930505469
k_Bacteria;p_Firmicutes_C;c_Negativicutes;o_Selenomonadales;f_Selenomonadaceae;g_Mitsuokella	0.030010344	0.560111999	0.934350362
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Christensenellales;f_Christensenellaceae;_	−0.215314401	0.563979787	0.930505581
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_Oxalobacter	0.03648814	0.566990264	0.935308103
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Eubacteriales;f_Anaerofustaceae;g_Anaerofustis	−0.439672625	0.56890406	0.933594277
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Anaerotignaceae;_	0.185309429	0.575296941	0.933312692
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Ethanoligenenaceae;g_Ethanoligenens	−0.565558862	0.575560762	0.940091572
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Fournierella	−0.090958953	0.586306136	0.942359687
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Klebsiella	0.455231033	0.587756237	0.940930719
k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Weissella	−0.31714518	0.589795845	0.941270209
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Kineothrix	0.278652788	0.590852515	0.944283268
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_KLE1615	0.253659814	0.591525966	0.959353011
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Massilimaliae	−0.068156376	0.597420448	0.942706019
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Coprobacteraceae;g_Coprobacter	−0.919456784	0.598560607	0.950135292
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Massilioclostridium	−0.174913923	0.599238474	0.944019398
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruminiclostridium_E	0.790893389	0.603930529	0.946566196
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Acutalibacteraceae;g_CAG-180	0.48986275	0.612542749	0.948747147
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_UBA9475	0.159115533	0.617348558	0.946874541
k_Bacteria;p_Proteobacteria;_;_;_;_	−0.695056412	0.628288537	0.952943365
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Agathobacter	−0.53538217	0.629731573	0.971512059
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Acutalibacteraceae;g_Anaeromassilibacillus	−0.119308681	0.629912824	0.951890036
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_Intestinimonas	0.268983115	0.636564693	0.953698564
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Peptostreptococcales;_;_	0.242149566	0.639841122	0.955371003
k_Bacteria;p_Firmicutes_C;c_Negativicutes;o_Acidaminococcales;f_Acidaminococcaceae;g_Acidaminococcus	0.804338526	0.656734025	0.958820946
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Negativibacillus	−0.334600804	0.670650992	0.960939656
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Paraprevotella	−0.461032009	0.671895025	0.961877867
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Rikenellaceae;g_Alistipes_A	−0.520265574	0.687149076	0.965946784
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Anaerotruncus	0.019427887	0.693364924	0.965795495
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Eubacterium_G	−0.515163067	0.695707818	0.966673563
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Clostridium_Q	−0.127418788	0.695854759	0.973710245
k_Bacteria;p_Firmicutes_C;c_Negativicutes;o_Acidaminococcales;f_Acidaminococcaceae;g_Phascolarctobacterium	−0.507784922	0.705724559	0.96965107
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Eisenbergiella	0.349623867	0.708605356	0.979970171
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Eubacterium_F	−0.425142167	0.72008942	0.970655288
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_GCA-900066135	0.184833228	0.725725495	0.9712481
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_CAG-56	−0.539928047	0.729170302	0.975535283
k_Bacteria;p_Actinobacteriota;c_Coriobacteriia;o_Coriobacteriales;f_Eggerthellaceae;g_Raoultibacter	0.12443162	0.72934775	0.97223451
k_Bacteria;p_Firmicutes_C;c_Negativicutes;o_Veillonellales;f_Dialisteraceae;g_Dialister	−0.36218487	0.732692393	0.97228232
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Acutalibacteraceae;g_Eubacterium_R	0.294199894	0.735533654	0.979919918
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Coprococcus	0.13347045	0.735657295	0.973691232
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Clostridium_M	−0.604096458	0.737723694	0.978084547
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Dorea	−0.234830761	0.739373535	0.981856615
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Peptostreptococcales;f_Peptostreptococcaceae;_	−0.355845011	0.759023984	0.977651218
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Coprococcus_B	−0.390956641	0.783952509	0.983607102
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Blautia	−0.1884323	0.787697636	0.981270318
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_Parasutterella	0.015923079	0.799457359	0.983636898
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Coprococcus_A	0.1955906	0.802336541	0.985550207
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Bacteroides_A	−0.527456893	0.814676442	0.985354624
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Anaerotignaceae;g_Anaerotignum	−0.197376272	0.83743409	0.987848646
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Marinifilaceae;g_Odoribacter	0.095660948	0.839604758	0.987648946
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Faecalicatena	0.138835102	0.864300586	0.989515422
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_ER4	0.010464736	0.882236508	0.990281777
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Acutalibacteraceae;_	−0.023665925	0.883957155	0.990531589
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_Sutterella	0.071252099	0.887930992	0.991112853
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;_	0.055042696	0.89018251	0.990900493
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Christensenellales;f_CAG-74;g_OEMS01	−0.013808989	0.891075254	0.991029207
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_GCA-900066575	−0.040711515	0.91179403	0.992452217
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Tannerellaceae;g_Parabacteroides	−0.024190059	0.912906008	0.992200295
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnospira	0.047610883	0.922206804	0.99267741
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Eubacterium_I	0.023222353	0.925745602	0.993155611
k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Streptococcus	0.179262937	0.932200568	0.993571052
k_Bacteria;p_Firmicutes;c_Bacilli;o_Staphylococcales;f_Gemellaceae;g_Gemella	−0.255651757	0.547296918	0.923260096
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacterales;f_Succinivibrionaceae;g_Succinatimonas	0.165546779	0.547667542	0.920008431
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Butyricicoccaceae;_	−0.110298083	0.548099968	0.920456356
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Porphyromonadaceae;g_Porphyromonas	0.137336221	0.549375808	0.92240815
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Butyrivibrio_A	0.000475616	0.549597819	0.922608141
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Fournierella	−0.470967802	0.54991343	0.921177077
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Bittarella	−0.343292378	0.549960807	0.921543743
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_UBA6382	0.142008487	0.549996142	0.921255476
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Bacteroides_B	0.505297152	0.550151399	0.948296477
k_Bacteria;p_Actinobacteriota;c_Coriobacteriia;o_Coriobacteriales;f_Eggerthellaceae;g_Senegalimassilia	0.143973717	0.551028545	0.925917494
k_Bacteria;p_Cyanobacteria;c_Vampirovibrionia;o_Gastranaerophilales;f_Gastranaerophilaceae;g_Zag111	0.064464165	0.551571865	0.924457672
k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Lactobacillus_D	0.217661228	0.553513276	0.920494935
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Neobittarella	−0.134747648	0.554230398	0.927067731
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Citrobacter	0.906894303	0.555211226	0.928521767
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacterales;f_Pasteurellaceae;g_Haemophilus_D	−0.486946216	0.555422695	0.922593738
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruminococcus_F	−0.44457855	0.555682265	0.921518785
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Sellimonas	0.592140146	0.555693565	0.923838343
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_RF32;f_CAG-239;g_CAG-495	−0.329132502	0.558207671	0.92268195
k_Bacteria;p_Actinobacteriota;c_Coriobacteriia;o_Coriobacteriales;f_Eggerthellaceae;g_Eggerthella	−0.692632632	0.558531721	0.92490671
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnoclostridium_A	−0.432659359	0.559397403	0.923036639
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Hungatella	−0.0324392	0.559780269	0.922243861
k_Bacteria;p_Firmicutes_C;c_Negativicutes;o_Veillonellales;f_Dialisteraceae;g_Allisonella	−0.391719976	0.564547215	0.923957501
k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Lactobacillus_H	−0.644505001	0.566027939	0.930652718
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Faecalicatena	−0.696552188	0.567451528	0.951677772
k_Bacteria;p_Actinobacteriota;c_Coriobacteriia;o_Coriobacteriales;f_Eggerthellaceae;_	−0.493331101	0.572077863	0.928896535
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Anaerotignaceae;_	0.48376512	0.573507702	0.932524866
k_Bacteria;p_Firmicutes;c_Bacilli;o_Erysipelotrichales;f_Erysipelotrichaceae;g_Holdemanella	−0.1400546	0.575511739	0.931887991
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;_	1.648545251	0.578097497	0.946810035
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Coprococcus_A	−0.7548789	0.582884427	0.94915342
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Acutalibacteraceae;g_CAG-180	0.945718084	0.588063323	0.934993864
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Paraprevotella	1.3923044	0.589863501	0.94031165
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Ethanoligenenaceae;g_Ethanoligenens	−0.773483083	0.589912765	0.935126627
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Kineothrix	0.173560148	0.590245768	0.936824867
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Bacteroides	0.422751051	0.59486947	0.952705047
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Acutalibacteraceae;g_Acutalibacter	−1.252331946	0.597960413	0.953191865
k_Bacteria;p_Firmicutes_A;c_Clostridia;_;_;_	1.131483907	0.598810803	0.949427613
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruminiclostridium_E	−0.701169774	0.599009584	0.938391563
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_Intestinimonas	−0.781678648	0.603967576	0.937974779
k_Bacteria;p_Actinobacteriota;c_Coriobacteriia;o_Coriobacteriales;f_Eggerthellaceae;g_Slackia_A	−0.163154932	0.604289193	0.941269139
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_UBA9475	−0.0254486	0.608727812	0.942826944
k_Bacteria;p_Firmicutes_C;c_Negativicutes;o_Acidaminococcales;f_Acidaminococcaceae;g_Phascolarctobacterium_A	−0.588351308	0.617474457	0.941658992
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Klebsiella	0.250477964	0.617502455	0.943660278
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_CAG-95	−0.282016187	0.620097408	0.942822005
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Peptostreptococcales;f_Anaerovoraceae;g_S5-A14a	0.695133112	0.620898763	0.943230343
k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Aerococcaceae;g_Granulicatella	−0.034198504	0.621317661	0.940090824
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Massilioclostridium	−0.3127785	0.624597397	0.944361604
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Peptostreptococcales;f_Anaerovoraceae;g_UBA1191	−0.420191637	0.627949174	0.953455296
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Anaerotruncus	−0.308914487	0.63903071	0.949369235
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Butyricicoccaceae;g_Agathobaculum	−0.35675621	0.64311574	0.958372263
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_GCA-900066135	−0.745876596	0.647344392	0.949054959
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Clostridium_M	0.597690397	0.658794862	0.959705853
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Butyricicoccaceae;g_Butyricicoccus_A	0.166637851	0.661682407	0.950407002
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Monoglobales;f_Monoglobaceae;g_Monoglobus	0.453032359	0.676562122	0.956414331
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_ER4	−0.816532623	0.683679124	0.961927673
k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Lactobacillus	−0.263489593	0.686369315	0.957638933
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Eubacterium_F	−1.124079743	0.687607616	0.958850432
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;_	−0.340451364	0.69151867	0.962681237
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Coprococcus_B	−0.709372233	0.696199932	0.962684493
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Acetatifactor	−0.270400422	0.69983282	0.963628848
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Rikenellaceae;g_Alistipes_A	−1.002746045	0.702859747	0.961851861
k_Bacteria;p_Desulfobacterota_A;c_Desulfovibrionia;o_Desulfovibrioniales;f_Desulfovibrionaceae;g_Bilophila	−0.518252651	0.703910798	0.964352885
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Coprococcus	−0.56951612	0.707633584	0.960617998
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_Flavonifractor	0.868394106	0.712287042	0.965131869
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_Lawsonibacter	−0.239872111	0.71599249	0.965678822
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Blautia	−0.642654728	0.727105263	0.964682333
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Faecalibacterium	−0.129898584	0.733949682	0.966893986
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Acutalibacteraceae;_	0.460388028	0.74166262	0.969125766
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_TF01-11	−0.179621381	0.756761932	0.967906391
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_CAG-81	−0.422494273	0.765238554	0.970556222
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Prevotella	0.283700789	0.786774221	0.973932857
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Christensenellales;f_Christensenellaceae;g_Christensenella	0.239059752	0.793768235	0.974157698
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Peptostreptococcales;f_Peptostreptococcaceae;_	0.349393849	0.798011623	0.974997539
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_CAG-110	0.135587033	0.819527214	0.97653895
k_Bacteria;p_Firmicutes_C;c_Negativicutes;o_Veillonellales;f_Veillonellaceae;g_Veillonella	−0.293332431	0.832493157	0.978308754
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_Oscillibacter	−0.144724142	0.833916467	0.977068782
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Marinifilaceae;g_Butyricimonas	−0.083800806	0.846516453	0.980097333
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_Sutterella	0.223265228	0.855058667	0.981108278
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Anaerotignaceae;g_Anaerotignum	−0.257137481	0.861426988	0.980738041
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Peptostreptococcales;f_Peptostreptococcaceae;g_Romboutsia	0.056493886	0.870630393	0.982816932
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Christensenellales;f_CAG-74;g_OEMS01	−0.134463611	0.878501654	0.983414673
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Monoglobales;f_UBA1381;g_CAG-41	−0.17485344	0.881748932	0.983191767
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_GCA-900066575	0.087180364	0.902545491	0.986530824
k_Bacteria;p_Actinobacteriota;c_Actinobacteriia;o_Actinomycetales;f_Bifidobacteriaceae;g_Bifidobacterium	−0.12531743	0.921969046	0.988116135
k_Bacteria;p_Fir

付録4：認知機能検査（MoCA-J）スコアとF. prausnitziiのrelative abundanceの相関解析結果

＊ MoCA-J:　Montreal Cognitive Assessment Japanese version　**健常者群: H、MCI群: M、健常者群+MCI群: H_M

genus_name	spearman_H_MoCA_cor	spearman_H_MoCA_cor.p.val	spearman_M_MoCA_cor	spearman_M_MoCA_cor.p.val	spearman_H_M_MoCA_cor	spearman_H_M_MoCA_cor.p.val
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Faecalibacterium	0.092589202	0.697834398	0.555941098	0.031402617	0.430690324	0.00980115
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Anaerostipes	0.23730846	0.313729744	0.385161806	0.156274555	0.430861615	0.009768799
k_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Prevotella	0.111755031	0.639014589	−0.333668387	0.224215362	−0.33724988	0.047567855
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Monoglobales;f_UBA1381;g_CAG-41	0.173507497	0.464435225	−0.025526543	0.928048237	0.367303679	0.02996215
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;_	0.07391575	0.756788758	0.014534408	0.958998735	0.419259814	0.012175863
k_Bacteria;p_Firmicutes_A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruminococcus_C	−0.087021494	0.715255746	0.005408077	0.984738837	0.343097534	0.043613226

付録5：海馬サンプルを用いたメタボローム解析の結果

Group
SH: sham-operation 群 (i.c.v.: distilled water, p.o.: saline)
VE: vehicle 群 (i.c.v.: Aβ, p.o.: saline)
Fp14: Fp14死菌体懸濁液 群 (i.c.v.: Aβ, p.o.: Fp14死菌体懸濁液)

代謝物の相対面積値（relative area）に関してVehicle群との間で対応のないウェルチのt検定を実施した。

			relative area												
Compound_name	m.z	MT.RT	SH_1	SH_2	SH_3	VE_1	VE_2	VE_2	Fp14_3	Fp14_3	Fp14_3	log2FC(SH/VE)	SH_VE_pvalue	log2FC(Fp14/VE)	Fp14_VE_pvalue
Thymine	127.0501867	22.03966925	6.61E−05	4.38E−05	0.000201712	0.000220013	0.000135155	0.000136466	3.19E−05	1.93E−05	5.47E−05	−0.657831466	0.364257606	−2.214764989	0.03232759
N6−Methyl−2′−deoxyadenosine	266.12363	9.607479167	1.06E−05	5.61E−06	2.46E−05	1.62E−05	1.02E−05	1.54E−05	5.25E−06	4.15E−06	6.42E−06	−0.032621889	0.960246017	−1.403119636	0.032873958
dTMP	321.0493582	9.653170545	2.60E−05	4.17E−05	1.38E−05	3.66E−05	2.97E−05	2.21E−05	8.37E−06	1.87E−05	1.18E−05	−0.1155781	0.816703677	−1.184247461	0.037762014
NADPH_divalent	371.53815	11.3937765	0.000180301	7.58E−05	0.000377248	0.001002985	0.000568594	0.001268483	0.000830837	0.000190866	0.000394182	−2.164794151	0.052221725	−1.004218109	0.163256023
5−Aminoindole	133.0761725	7.427708567	2.63E−05	2.55E−05	8.01E−05	6.08E−05	7.83E−05	2.78E−05	3.49E−05	2.86E−05	2.24E−05	−0.340732816	0.644644049	−0.958859569	0.204936612
Lipoamide	206.0659	22.26328175	6.29E−05	7.61E−05	6.54E−05	0.000160638	0.000107351	9.90E−05	5.20E−05	0.000102441	3.87E−05	−0.844300607	0.101176199	−0.925948758	0.101734032
2−(Creatinine−3−yl)propionic acid	186.0874242	10.75963604	4.50E−05	5.84E−05	0.000174961	7.44E−05	6.46E−05	6.43E−05	2.41E−05	4.64E−05	4.74E−05	0.452962723	0.606361613	−0.786567326	0.047794627
gamma−Glu−Val−Gly	304.15057	12.955355	3.55E−05	4.61E−05	5.75E−05	5.36E−05	5.31E−05	7.56E−05	2.84E−05	3.51E−05	4.68E−05	−0.389982336	0.216001975	−0.724274291	0.064625238
ADP−ribose	558.06555	8.61132525	0.003358109	0.003583607	0.002808753	0.003700999	0.003123149	0.002300798	0.001992984	0.001900696	0.001629873	0.095655468	0.683986851	−0.724219588	0.089195443
Lauric acid	199.170415	7.753870025	0.002015488	0.002248021	0.002751552	0.003164281	0.002822001	0.002068546	0.001796299	0.001562081	0.001524519	−0.199398195	0.430818959	−0.722115669	0.073822209
Suberic acid	173.081884	12.90462135	3.10E−05	2.93E−05	3.77E−05	5.37E−05	3.70E−05	4.04E−05	2.44E−05	2.70E−05	3.13E−05	−0.418611479	0.150042855	−0.665445297	0.071579046
Decanoic acid	171.1391283	8.05224075	0.000346915	0.000336379	0.000354501	0.000424588	0.000343395	0.000426411	0.000233493	0.000265019	0.000276874	−0.202757393	0.193204442	−0.623292388	0.021398508
Histamine	112.0869607	4.511980083	0.000213773	0.000201284	0.00025192	9.71E−05	0.000200067	0.000663827	0.000292738	0.000184404	0.000187315	−0.526869368	0.631006409	−0.532329928	0.630519147
Ribose 5−phosphate	229.01195	10.67205888	0.000498818	0.000490642	0.000513065	0.000434904	0.000384803	0.00039072	0.000305301	0.00039292	0.000174342	0.311874797	0.014685533	−0.472183484	0.213502168
1−Methylnicotinamide	137.07101	7.015283383	0.000922339	0.000545184	0.001280842	0.001225747	0.000718308	0.000501525	0.00047398	0.000729874	0.000573189	0.168396459	0.75496665	−0.460698586	0.412527762
Pyridoxal	168.065475	8.365746292	0.000336159	0.000216409	0.000336183	0.000459678	0.000306907	0.000249216	0.000240298	0.000337541	0.000161056	−0.1927664	0.604785331	−0.459176425	0.320087594
Fructose 1,6−diphosphate	338.98867	14.63812367	0.03009045	0.01780234	0.04940808	0.027239056	0.031296829	0.032864606	0.023513125	0.022353679	0.020943976	0.090250788	0.851797643	−0.452121024	0.024887612
Hypoxanthine	137.04584	10.72785208	0.037082781	0.013161641	0.035643009	0.035972581	0.027638884	0.024738826	0.025710102	0.032697642	0.006577044	−0.040787843	0.92924946	−0.443132823	0.433469687
Metronidazole	172.0716617	9.091539833	2.71E−05	2.35E−05	4.90E−05	2.56E−05	1.78E−05	3.63E−05	1.95E−05	1.16E−05	2.78E−05	0.322033916	0.532789838	−0.43587147	0.385974185
dCMP	306.0497467	9.843308917	0.000117019	8.34E−05	0.000116356	0.00012154	9.47E−05	0.000116313	9.76E−05	9.11E−05	5.73E−05	−0.07021512	0.724198124	−0.434837647	0.136944121
Pelargonic acid	157.1233883	8.229229833	0.001029938	0.000851403	0.001063654	0.001054928	0.001286336	0.001371944	0.000976542	0.000790658	0.000980739	−0.334400955	0.098758127	−0.434316379	0.055661162
N2−Acetylaminoadipic acid	202.0720433	12.31161163	0.000145033	0.000221827	0.000147313	0.000216192	0.000184558	0.000197001	0.000160497	0.000156058	0.000125922	−0.217289953	0.388559025	−0.433942183	0.0230737
Gluconolactone	179.0550867	22.87572817	0.000315138	0.000256081	0.000322708	0.00032622	0.000450859	0.000450241	0.000244348	0.000259519	0.000405073	−0.454222617	0.103833916	−0.430196129	0.190850932
2′−Deoxyguanosine	268.1041833	11.1048135	5.67E−05	1.38E−05	9.72E−05	5.72E−05	4.81E−05	8.20E−05	6.51E−05	4.87E−05	2.56E−05	−0.160472183	0.820393771	−0.426864371	0.35622933
Myristoleic acid	225.18615	7.578295925	5.59E−05	3.77E−05	8.28E−05	5.04E−05	6.83E−05	6.43E−05	5.73E−05	4.99E−05	3.16E−05	−0.052274488	0.887677877	−0.398781942	0.198492495
dAMP	330.0611283	9.496015125	3.16E−05	2.43E−05	2.93E−05	3.63E−05	2.87E−05	3.29E−05	2.87E−05	2.95E−05	1.63E−05	−0.200878431	0.241055296	−0.395379906	0.203316461
N−Acetylputrescine	131.1180042	8.089504667	2.32E−05	3.31E−05	4.11E−05	3.17E−05	4.11E−05	2.42E−05	2.62E−05	2.50E−05	2.29E−05	0.003237204	0.985959956	−0.389687352	0.256492819
Citraconic acid	129.01938	16.91252633	0.00062732	0.000544163	0.000567093	0.000583164	0.000622938	0.000557023	0.000120203	0.000626416	0.000607824	−0.020229743	0.80767442	−0.380436624	0.498031613
trans−Glutaconic acid	131.0339667	22.92901617	0.006781838	0.006166153	0.006683835	0.006682975	0.006105988	0.005668646	0.001317466	0.006407423	0.006498827	0.088978663	0.335939647	−0.375917122	0.497734181
Thiamine phosphate	345.0781	10.29812558	0.000262981	0.000204454	0.000197615	0.000255374	0.00024863	0.000202376	0.000206352	0.000179925	0.000159118	−0.086982218	0.633076892	−0.373139672	0.069822526
Taurocyamine	168.04372	22.03904475	0.000257346	0.00025394	0.000332138	0.000335412	0.000551611	0.000350618	0.000341571	0.000326981	0.00028901	−0.553262309	0.191579721	−0.370152771	0.310895839
Ethanolamine	62.0601285	6.03450635	0.006147394	0.004882437	0.00659614	0.006552978	0.006940257	0.005780734	0.005027482	0.005202613	0.004705873	−0.128950868	0.429870541	−0.367862864	0.035929717
Uracil	113.0345383	22.072221	0.013610558	0.005980746	0.016588002	0.015196121	0.01166676	0.010964515	0.012211256	0.013138226	0.004119691	−0.064266782	0.883737554	−0.360224934	0.445669667
Myristic acid	227.20179	7.532063925	0.000787646	0.000884705	0.001367719	0.001145558	0.000946451	0.001004269	0.000856804	0.00081252	0.00074332	−0.026430527	0.928579549	−0.359991145	0.04074747
N−AcetylgalactosamineN−AcetylmannosamineN−Acetylglucosamine	222.0971867	22.04180583	0.001238906	0.000865167	0.001777128	0.001798122	0.00147264	0.001190066	0.001262645	0.001367773	0.00086181	−0.20080827	0.580533588	−0.353163313	0.240425495
Serotonin	177.1021525	8.364292958	0.000921206	0.000683514	0.000999448	0.000750875	0.000673442	0.000958467	0.000644546	0.000576869	0.000644006	0.128174473	0.594207151	−0.353147235	0.173366453
Hexanoic acid	115.07648	9.028054417	0.000536716	0.000439491	0.000561276	0.000585354	0.000729416	0.000618074	0.000495282	0.000485012	0.000532935	−0.330155311	0.084610212	−0.353094966	0.072657726
Hypotaurine	110.0270863	17.90759633	0.015595583	0.016582441	0.015770239	0.019476939	0.035040108	0.019141559	0.019064477	0.021645564	0.016983876	−0.619375549	0.243572084	−0.352434895	0.418852226
NADH	664.11736	8.278340792	0.00070782	0.000748406	0.001408583	0.001225105	0.000951419	0.001912664	0.001497278	0.001128903	0.000587673	−0.513375316	0.329266631	−0.347510077	0.495452065
Saccharopine	277.1394492	10.33856392	0.002865948	0.001399567	0.001732762	0.004173496	0.00179041	0.00189427	0.002250325	0.00184429	0.002088227	−0.389646636	0.535886311	−0.345924432	0.548483357
Nicotinamide	123.0552833	7.057983942	0.087248692	0.071551486	0.059179255	0.075170881	0.078793123	0.052460866	0.057911163	0.059008866	0.046089966	0.078575218	0.755940504	−0.340656379	0.21611738
IMP	347.0399375	9.670024667	0.021722629	0.01946495	0.021100517	0.023786351	0.028258049	0.03290217	0.032230395	0.024353175	0.010620733	−0.447599224	0.094891153	−0.338002101	0.45783053
Acetoacetamide	102.0549687	11.19495342	0.000188397	0.000371683	0.000212749	0.000302463	0.000266887	0.000144124	0.000177746	0.000194616	0.000193139	0.115289952	0.804992212	−0.335329254	0.412022132
Azelaic acid	187.09762	12.21202996	0.000216325	0.000354114	0.00027799	0.000595736	0.000357966	0.000623038	0.000548471	0.000274455	0.000434263	−0.894078076	0.08413043	−0.326743962	0.40972625
Triethanolamine	150.112585	7.88844905	0.00019048	0.000102434	0.000174442	0.000241809	0.000236673	0.00015304	0.000143384	0.000151001	0.000210363	−0.434308882	0.238507398	−0.323268112	0.307659669
XA0055	368.9993533	14.3987725	0.003008605	0.000966335	0.00380326	0.002375948	0.002043121	0.001838556	0.001609619	0.002546114	0.000855056	0.31382087	0.611670584	−0.320577542	0.490623307
Uridine	245.0768167	22.07590742	0.015510894	0.007142942	0.016066905	0.016125207	0.012345698	0.011803035	0.013057221	0.014175213	0.005064988	−0.056740666	0.881923606	−0.318427576	0.466568964
Cystathionine	223.0746675	9.529515333	0.01229666	0.011667884	0.01539998	0.014407653	0.023079943	0.010960043	0.015762857	0.012726719	0.010446036	−0.299530333	0.49517975	−0.315336104	0.483658182
Ribulose 5−phosphate	229.01195	11.08634958	0.006123886	0.003276922	0.005850494	0.005688687	0.004450557	0.004457817	0.004689826	0.005045676	0.002049646	0.0632544	0.841689504	−0.308708101	0.436093445
Riboflavin	377.1455667	21.91455933	8.73E−05	3.15E−05	8.61E−05	6.77E−05	3.52E−05	6.64E−05	4.41E−05	4.51E−05	4.76E−05	0.276169599	0.613252163	−0.307696445	0.415229547
Anserine_divalent	121.0684183	6.5187875	0.001930072	0.00191523	0.001734582	0.00116448	0.003131425	0.002460625	0.001798127	0.001862498	0.00180951	−0.276047645	0.567627938	−0.304706025	0.535070525
myo−Inositol 1−phosphatemyo−Inositol 3−phosphate	259.0226233	10.36959729	0.013465172	0.012828636	0.017233148	0.016273246	0.017926698	0.016389146	0.014629345	0.015070358	0.011388642	−0.216917171	0.222663499	−0.300097092	0.095125745
Octanoic acid	143.1077933	8.4480955	0.000357776	0.000289282	0.000405651	0.000311626	0.000571505	0.000474367	0.000362651	0.000337801	0.000405594	−0.366845354	0.314931453	−0.295540106	0.385113818
Dihydroxyacetone phosphate	168.9907333	12.75527713	0.007718961	0.008576091	0.003848154	0.004579844	0.004905267	0.00700043	0.004519646	0.005695405	0.003338553	0.289092151	0.510990222	−0.282524666	0.392377704
Gluconic acid	195.0510633	8.239333417	0.001486625	0.000945808	0.00121279	0.001738395	0.001404897	0.001372957	0.001194108	0.001113673	0.00141635	−0.309118152	0.21623231	−0.278220961	0.1530463
Imidazole−4−acetic acid	127.050272	7.67438633	1.53E−05	2.34E−05	2.24E−05	2.13E−05	2.99E−05	1.71E−05	2.18E−05	1.98E−05	1.48E−05	−0.164530766	0.629301028	−0.277945325	0.422367431
Met	150.0581	10.31332192	0.01682096	0.013472954	0.018369996	0.028238909	0.01899373	0.021717439	0.02113117	0.018813372	0.017038458	−0.502699953	0.116312408	−0.275020602	0.282544585
3−Methylguanine	166.0724325	8.207413083	7.38E−05	5.06E−05	7.62E−05	5.99E−05	7.62E−05	6.74E−05	7.08E−05	4.72E−05	5.17E−05	−0.020118103	0.924398938	−0.262236485	0.272345717
Allantoic acid	175.0469217	8.596879917	0.000140886	0.000141387	0.000173466	0.000178317	0.00012126	0.000155361	0.000137634	0.000125223	0.000117266	0.002536556	0.989972283	−0.259204604	0.268243115
allo−Threonine	120.0655757	10.36608692	0.001259202	0.000982074	0.001356038	0.00149239	0.0014271	0.00185699	0.001432906	0.001479219	0.001089339	−0.409028213	0.089444253	−0.255420048	0.228599292
Choline	104.1069475	6.533999533	0.132531752	0.083157142	0.120506934	0.108243944	0.120104563	0.104344696	0.093442112	0.112912243	0.073469438	0.015109427	0.946126685	−0.249673762	0.258780925
Thiaproline	134.0270817	13.60355442	0.000787941	0.000816475	0.001027232	0.001093099	0.001001219	0.001058141	0.000910153	0.000938071	0.000816733	−0.260511496	0.136648166	−0.242365721	0.026940542
Heptanoic acid	129.0922	8.704693727	0.000184966	0.000170646	0.00020822	0.000217996	0.000323446	0.000243129	0.000195658	0.000212203	0.000256013	−0.47663858	0.135649348	−0.24099339	0.347578761
Adenine	136.0618555	7.264894392	0.004942372	0.002243034	0.00533427	0.004355822	0.003309603	0.003380214	0.003752506	0.004095032	0.001920958	0.119350461	0.771135582	−0.238638415	0.490490153
S−Adenosylhomocysteine	385.1288733	8.346935875	0.000397772	0.000286911	0.000456769	0.0003915	0.000413752	0.000399498	0.000317464	0.000417122	0.000286501	−0.077863996	0.71398881	−0.238627712	0.258779741
Isovalerylcarnitine	246.17003	9.418200708	0.000711778	0.001111243	0.000830118	0.001019668	0.001327108	0.001467264	0.000914129	0.001532025	0.000787396	−0.523619391	0.095546315	−0.238200849	0.51564829
N6−Methyllysine	161.12833	6.7655923	0.00102164	0.000464338	0.000759097	0.000720502	0.000701125	0.000677519	0.000600798	0.000614212	0.000567147	0.096961961	0.791333601	−0.236176682	0.005057604
N−Acetylornithine	175.1078267	9.159508417	0.000160567	0.000150742	0.000173509	0.000146797	0.000160665	0.000101241	0.000131132	0.000103128	0.000113034	0.246390176	0.291590826	−0.234894318	0.380735416
Glucuronic acid−1Galacturonic acid−1	193.03525	8.198891083	6.41E−05	6.11E−05	6.85E−05	6.67E−05	6.01E−05	7.49E−05	5.20E−05	6.38E−05	5.66E−05	−0.058348458	0.617175397	−0.227600873	0.153098343
GMP	362.0507	9.270711583	0.044497137	0.033796422	0.041357192	0.045909663	0.038438195	0.043645698	0.042668372	0.042384454	0.024309617	−0.097241714	0.516594671	−0.2269538	0.419443313
Inosine	269.08825	19.35399183	0.09778048	0.050842969	0.092463208	0.087280439	0.073776795	0.06310498	0.06680218	0.092772974	0.03223666	0.105008703	0.754752451	−0.224851526	0.613103886
Dodecanedioic acid	229.1444633	10.83082646	1.87E−05	1.97E−05	1.44E−05	3.04E−05	3.01E−05	1.89E−05	1.81E−05	3.00E−05	1.99E−05	−0.584581852	0.129844259	−0.220166694	0.512654946
Isovaleric acid−1DL−2−Methylbutyric acid−1Valeric acid−1	101.0607995	9.36022825	0.00026474	0.000259461	0.000312246	0.000303486	0.000369385	0.000372154	0.000288998	0.000305427	0.000308788	−0.321192495	0.07315388	−0.210398307	0.162530088
O−Acetylhomoserine2−Aminoadipic acid	162.07594	10.519891	0.006540332	0.006444509	0.005886625	0.007792125	0.004484817	0.008463021	0.006578117	0.006990296	0.004370131	−0.136206741	0.66454994	−0.209350507	0.565805055
8−Hydroxyoctanoic acid−12−Hydroxyoctanoic acid−1	159.10269	8.15264575	2.20E−05	2.57E−05	3.36E−05	3.26E−05	4.01E−05	5.02E−05	0.000034116	2.66E−05	4.57E−05	−0.594420328	0.096461873	−0.208702206	0.506849499
3′−Dephospho CoA	686.1408958	8.107859083	0.000362947	0.000236583	0.000320396	0.000367307	0.000302374	0.000330331	0.00030588	0.000392663	0.000168258	−0.120427771	0.567351097	−0.206244673	0.5722728
Cytidine	244.0928067	9.296096833	0.018345553	0.008997083	0.016130429	0.014914045	0.013326249	0.014601758	0.015839228	0.016289213	0.005108662	0.021094236	0.947767209	−0.202286771	0.661111654
Gulonolactone	179.0549233	22.35020283	8.80E−05	0.000177174	0.000173997	0.000136524	0.000162934	7.00E−05	8.97E−05	0.000124861	0.000106593	0.249378361	0.594473643	−0.202176012	0.629065678
Gln	147.07644	10.34366292	1.294685908	1.295890336	1.386987443	1.295505035	1.242277996	1.440398736	1.252688069	1.161895633	1.046644193	−0.000224165	0.997727052	−0.200825261	0.109570646
His−Glu	285.11937	7.221475983	0.000113902	0.000146735	0.000105275	0.000146189	0.000152592	0.000148173	0.000133694	0.000125819	0.000129595	−0.288631099	0.163188451	−0.199958781	0.003200509
Pipecolic acid	130.0863658	9.895851083	0.003405985	0.004207255	0.004029638	0.003456764	0.004059154	0.003743525	0.003263976	0.002871319	0.003670078	0.048312287	0.693027629	−0.199491035	0.174011624
S−Lactoylglutathione	380.1125958	13.40096217	0.006222409	0.003591138	0.005960758	0.005783818	0.006666092	0.006630519	0.005415807	0.007514656	0.00370027	−0.274517115	0.318274067	−0.198241912	0.540293064
N−Acetylglutamine	187.0724742	8.206821417	0.000191819	0.000258367	0.00022503	0.00034607	0.000328911	0.000207532	0.000281083	0.000206183	0.000282392	−0.386270455	0.250745427	−0.197401688	0.506104362
Pyridoxamine	169.0972308	5.641325008	6.18E−05	4.87E−05	5.21E−05	5.27E−05	4.58E−05	3.80E−05	3.86E−05	4.14E−05	3.91E−05	0.253945699	0.207294553	−0.196307506	0.303937101
Gly−Gly	133.060885	8.018666042	0.000728808	0.000542386	0.000727726	0.000716245	0.000626059	0.000559842	0.000544835	0.000660022	0.000456565	0.071592895	0.69780411	−0.195209277	0.344749178
1−Methyladenosine	282.119775	9.571412	0.001791041	0.001369758	0.001544824	0.001604408	0.002016067	0.001541952	0.001744989	0.00152466	0.001255659	−0.133664364	0.474723997	−0.190033765	0.359451168
2−Deoxystreptamine	163.10775	8.304311333	9.91E−05	0.000117855	0.000129173	0.000102817	0.000145862	0.000125582	0.00010801	0.00010748	0.000112619	−0.112911459	0.574519063	−0.189914189	0.34108577
2′−Deoxycytidine	228.0979483	9.044575625	0.000230387	0.00014875	0.000232361	0.000170948	0.000225262	0.000204987	0.000199907	0.00020604	0.000125964	0.024509346	0.920394824	−0.176655059	0.495283697
Phe	166.086335	10.89683008	0.060787403	0.064616187	0.066107715	0.064074614	0.066040546	0.064537431	0.06608172	0.054410275	0.05177878	−0.023471995	0.586822265	−0.176223573	0.230177546
Morpholine	88.07569333	6.309614625	0.000377706	0.000375456	0.000360916	0.000556549	0.000498728	0.00042572	0.000476592	0.000455343	0.000379329	−0.410718014	0.081200161	−0.175610936	0.307453059
Allantoin	159.051255	22.02116875	0.000394132	0.000483908	0.000665892	0.000656922	0.000882767	0.000420852	0.000617558	0.000475436	0.000643991	−0.344641851	0.432544004	−0.174666028	0.643908899
gamma−Glu−Phe	295.12885	12.65105167	8.79E−05	8.80E−05	6.73E−05	9.14E−05	8.20E−05	8.74E−05	7.56E−05	7.11E−05	8.52E−05	−0.101361988	0.493709676	−0.169450618	0.135926784
Glucose 1−phosphate	259.0226642	10.20647454	0.003153935	0.002281135	0.003348055	0.002564683	0.002624462	0.002604595	0.002148013	0.00280808	0.001985781	0.172418181	0.420710664	−0.16699086	0.375992916
Guanosine	284.09915	12.13610583	0.024212097	0.014307575	0.019153108	0.019601505	0.018108259	0.017444499	0.019574123	0.019576399	0.009984939	0.064418166	0.799233055	−0.166707795	0.596872625
3−Amino−2−piperidone	115.0866575	7.255478192	2.12E−05	2.36E−05	2.40E−05	2.00E−05	2.10E−05	3.01E−05	1.18E−05	2.44E−05	2.73E−05	−0.048598371	0.836835323	−0.164725729	0.684806653
XC0132	325.1606833	8.306473667	0.001308556	0.001315347	0.001537727	0.001355838	0.001686107	0.001455847	0.001505694	0.001307794	0.001200295	−0.112067851	0.418343011	−0.164254124	0.290819212
Glycerol	93.05459833	22.02730442	0.124442405	0.108607682	0.184437866	0.249997336	0.198474793	0.234066642	0.253656582	0.173535414	0.182102471	−0.709176429	0.040561773	−0.163771359	0.46551513
5′−Deoxy−5′−methylthioadenosine	298.0970058	9.699340667	0.00046919	0.000410727	0.000542787	0.000542272	0.000562338	0.000524971	0.000564485	0.000404486	0.000486303	−0.195866533	0.207063667	−0.16321013	0.334748942
Adenosine	268.1041375	9.481096792	0.373659828	0.220529623	0.30210477	0.330535851	0.290371095	0.26761872	0.336632182	0.299152282	0.160306743	0.012558944	0.96067665	−0.158479723	0.632056811
Glyceric acid	105.01935	10.4800415	0.000270975	0.000215041	0.000291502	0.000359328	0.000250956	0.00025272	0.000264278	0.000233852	0.00027515	−0.150489467	0.545341015	−0.158374155	0.498787232
AMP	346.05582	9.433180875	0.242158124	0.251258171	0.237085873	0.260087211	0.24548723	0.24256442	0.232903073	0.249893425	0.149021576	−0.034417517	0.440621576	−0.150516685	0.289923215
GABA	104.0705318	7.306119892	0.490761437	0.482378265	0.535031366	0.488570855	0.469312812	0.471090967	0.471418183	0.461372878	0.357560933	0.077819772	0.242678631	−0.147215637	0.331316826
Nw−Methylarginine	189.1346958	7.109357175	4.76E−05	3.97E−05	5.13E−05	5.34E−05	5.36E−05	4.93E−05	4.10E−05	5.40E−05	4.64E−05	−0.174388434	0.220400256	−0.146391399	0.318813564
Thiamine diphosphate	423.02975	8.066687917	0.000455686	0.000416426	0.000485334	0.000473655	0.000448581	0.000505388	0.000471177	0.000429593	0.000390126	−0.072721536	0.41848378	−0.145244733	0.194279744
XC0089Nicotinamide riboside	255.0976883	9.134956167	0.000426487	0.000388071	0.000361188	0.000412856	0.000415625	0.000377391	0.000376969	0.00038249	0.000331582	−0.036500108	0.683281594	−0.144370808	0.137218674
4−Methylpyrazole	83.06035292	6.573814708	9.27E−05	0.000100262	8.36E−05	7.15E−05	0.000126333	8.48E−05	0.000102166	8.92E−05	6.49E−05	−0.031225058	0.915697251	−0.14172442	0.683363447
Citrulline	176.102925	10.65707392	0.009362433	0.009412047	0.010972156	0.00912282	0.0121385	0.00993944	0.010694997	0.008338519	0.009269848	−0.06885463	0.671997909	−0.140607581	0.444661194
Carnitine	162.1124667	8.152434333	0.11039256	0.110559863	0.129160416	0.110850542	0.152457471	0.125570479	0.114424535	0.131360091	0.107229405	−0.151499479	0.4150304	−0.139593919	0.455434976
Xanthine	153.0407242	19.305471	0.005907344	0.003243281	0.006014848	0.005317557	0.004282198	0.004101286	0.004574493	0.005056705	0.002807357	0.146504943	0.657175192	−0.139466625	0.626353264
N,N−Dimethylglycine	104.070585	10.53931125	0.000579394	0.000486479	0.000617421	0.000471276	0.000450008	0.000479137	0.000453553	0.000464491	0.000353817	0.265426989	0.130164902	−0.138919342	0.34745697
CDP−choline	487.1009642	6.912792533	0.002090194	0.001337405	0.001655275	0.00207469	0.001781338	0.001949303	0.002047993	0.001970519	0.001257416	−0.19173363	0.389946859	−0.137953032	0.563488375
Taurine	126.0219242	22.00639808	0.839480052	0.801735612	0.966566852	1.018942636	1.075584242	0.976405428	0.962230351	0.950445701	0.879401993	−0.235853154	0.069937377	−0.137337442	0.074699331
Betaine	118.0862358	10.88670175	0.026753089	0.025952079	0.031837105	0.025343942	0.044482424	0.028411809	0.031358767	0.02427247	0.033833005	−0.21661085	0.528099345	−0.134972583	0.688358496
His	156.0767942	6.96027395	0.049560825	0.047297667	0.062692447	0.049636124	0.055788837	0.048814726	0.050926768	0.051292551	0.038340079	0.048843063	0.760867279	−0.133994108	0.411635072
Methionine sulfoxide	166.053275	11.39558771	0.000362263	0.000483904	0.000450628	0.000568165	0.000382666	0.000575391	0.000377871	0.000426656	0.000586942	−0.235014326	0.366220104	−0.133356862	0.641226613
N−Acetylserine	148.0604933	23.09213333	0.002950341	0.003121419	0.003622542	0.003048801	0.0026797	0.002876748	0.002370671	0.002628805	0.002847796	0.171919924	0.208709256	−0.133025858	0.225111219
Octanoylcarnitine	288.21715	10.05336425	0.00012921	0.00010712	0.000165423	0.000165891	0.000171311	0.00014536	0.000155198	0.0001697	0.000115185	−0.264403406	0.251486188	−0.132937058	0.49341818
UMP	323.0288058	9.893

SDMA	203.15031	7.446506725	0.000533756	0.000462462	0.000671766	0.000471103	0.000628404	0.000521749	0.000546791	0.000459258	0.000473766	0.04099394	0.850199795	−0.131694262	0.440432961
Thr	120.0655362	10.12983754	0.116790864	0.114313027	0.1126794	0.119629264	0.141074488	0.139408203	0.131881757	0.132376379	0.101362452	−0.218904311	0.108277293	−0.130056429	0.411695565
Arg−Glu	304.1619	7.160721967	0.000118685	0.000140004	0.000114704	0.000128686	0.000118417	0.000109859	0.000112032	0.00010956	0.000104789	0.064921514	0.600761745	−0.129214601	0.193439612
2−Aminoisobutyric acid2−Aminobutyric acid	104.070627	9.266490083	0.001524128	0.001765635	0.001585028	0.001501942	0.001739208	0.001540794	0.001367687	0.00170892	0.00130976	0.02774284	0.779267028	−0.124570955	0.424434141
Glutathione (GSSG)_divalent	307.08332	11.78753008	0.323041562	0.420798434	0.522026817	0.331994497	0.288882628	0.293358243	0.279162597	0.260239637	0.299680156	0.469488083	0.172466381	−0.123753154	0.234397667
5−Methyltetrahydrofolic acid	460.1943683	11.46416979	5.12E−05	5.86E−05	7.31E−05	5.33E−05	4.28E−05	3.66E−05	2.71E−05	5.01E−05	4.48E−05	0.463483388	0.111885221	−0.121095491	0.698418106
gamma−Glu−Arg_divalent	152.5844458	8.325989	9.60E−05	0.000110962	8.47E−05	0.000101918	0.000118524	0.000108324	0.000107201	0.000108115	8.72E−05	−0.172424757	0.253745008	−0.120089849	0.360507466
cAMP	328.0454117	7.618038025	0.002016744	0.003105001	0.003726893	0.002178022	0.004009038	0.005727864	0.004822929	0.003059289	0.003086185	−0.429242533	0.438172149	−0.119416351	0.805520251
IsovalerylalanineN−Acetylleucine	172.0979783	8.149033458	4.79E−05	0.000151569	0.000186714	0.000138142	0.000188461	0.000182313	0.000136506	0.000144839	0.000187484	−0.397961827	0.436644723	−0.118368018	0.582459094
myo−Inositol 2−phosphate	259.0227458	10.5587375	0.006883023	0.006152446	0.006631479	0.007691553	0.007424485	0.007628454	0.007506991	0.007081718	0.006381686	−0.209744139	0.028900287	−0.117163195	0.208464257
Stachydrine	144.1019233	11.12710213	0.001055959	0.001245601	0.001356945	0.001162663	0.001607092	0.001419982	0.001272262	0.001060551	0.001536934	−0.195605521	0.327315389	−0.114620451	0.602123281
N−Formylmethionine	176.038755	8.706676167	4.09E−05	2.85E−05	5.59E−05	4.57E−05	3.52E−05	4.30E−05	4.19E−05	3.78E−05	3.50E−05	0.015426281	0.960246251	−0.112811645	0.464988794
3−Hydroxy−2−methyl−4−pyrone	127.038938	22.07531233	0.006567903	0.006751355	0.00776446	0.007589829	0.007819246	0.006985301	0.007071293	0.006834088	0.006806789	−0.087007134	0.391682649	−0.112657701	0.142344648
Adenylosuccinic acid	462.06702	13.86592492	0.008794702	0.004780749	0.005809431	0.006756734	0.00543257	0.0052578	0.006366806	0.007364457	0.00241736	0.151944264	0.656595615	−0.111576556	0.806384769
Mucic acid	209.03026	14.1824565	0.000280469	0.000332082	0.000587321	0.000255492	0.000231919	0.000254644	0.000219315	0.000172001	0.000297741	0.693283264	0.24842282	−0.106901513	0.680373917
Pro	116.0706613	10.41878717	0.061890028	0.06570258	0.066040998	0.066013132	0.062402315	0.068177937	0.061724297	0.067699578	0.053186132	−0.021885426	0.670914126	−0.106448952	0.389380156
5−Oxoproline	128.03537	9.59492275	0.001947947	0.002648711	0.001879567	0.001849948	0.001345474	0.00173685	0.001635217	0.001504391	0.001446827	0.39290082	0.163865103	−0.104879332	0.538375324
6,8−Thioctic acid	205.03542	8.59540275	5.72E−05	8.09E−05	9.95E−05	8.34E−05	8.26E−05	0.000102176	6.17E−05	9.09E−05	9.69E−05	−0.174522878	0.513751948	−0.104063485	0.653211234
S−Adenosylmethionine	399.1447333	6.780078983	0.005588539	0.004907626	0.005005369	0.005989158	0.004968965	0.005401329	0.005774966	0.004560985	0.00494973	−0.082994927	0.451399	−0.103225034	0.462246708
Trp	205.0971667	10.59860717	0.009609477	0.009840689	0.012133924	0.01116784	0.010237087	0.011652017	0.012180172	0.009525071	0.009145452	−0.065755361	0.625788952	−0.099650359	0.535396868
Decarboxylated S−Adenosylmethionine	355.1547467	5.340041158	0.000121465	7.17E−05	0.000133655	8.34E−05	7.42E−05	8.09E−05	7.66E−05	8.48E−05	6.15E−05	0.454359783	0.259119745	−0.09745448	0.537034018
5−Hydroxylysine	163.10777	6.812648408	4.85E−05	4.60E−05	4.45E−05	5.91E−05	4.78E−05	5.62E−05	5.03E−05	5.26E−05	4.96E−05	−0.230696926	0.129806775	−0.096837367	0.408304195
UDP−glucuronic acid	579.02734	11.11593613	0.00183717	0.001906113	0.001836147	0.001858176	0.00186748	0.002009119	0.001824422	0.001890378	0.00164858	−0.039619102	0.411924022	−0.09659459	0.237715112
XC0016	129.06589	8.365025792	0.039899845	0.038780455	0.040204081	0.039750087	0.039645475	0.044746156	0.039716827	0.040330334	0.036146602	−0.062428833	0.408672943	−0.095455384	0.285255236
Betaine aldehyde_+H2O	120.1020348	7.116579758	8.85E−05	7.00E−05	0.000101856	8.64E−05	7.99E−05	7.56E−05	5.75E−05	8.38E−05	8.53E−05	0.105856898	0.581975985	−0.094136836	0.637699639
PropionylcarnitineXC0061	218.13867	8.940486083	0.007015587	0.00388781	0.004435015	0.006276684	0.006136349	0.005494872	0.006095463	0.007290714	0.003394413	−0.223447469	0.470895909	−0.093803117	0.777673741
Ectoine	143.08168	9.062676917	0.00013833	0.000171306	0.000219011	0.000162244	0.00028989	0.000183642	0.000184377	0.000173878	0.000237514	−0.266213747	0.489181664	−0.09376391	0.782540268
XC0040	174.087345	11.77742658	0.000401218	0.000428861	0.000407014	0.000463176	0.000562682	0.00053619	0.000633191	0.000442766	0.000388097	−0.336483905	0.058551308	−0.093470002	0.714085171
Xanthopterin	180.0519583	12.84215613	7.02E−05	8.04E−05	8.59E−05	8.17E−05	8.13E−05	8.33E−05	9.14E−05	7.91E−05	6.07E−05	−0.058781468	0.552159328	−0.091206918	0.629708815
6−Aminopenicillanic acid	217.0638833	10.21004225	0.000121881	0.000119309	0.000146542	0.000142092	0.000149356	0.000130735	0.000163529	0.000113946	0.000119118	−0.122804817	0.335647981	−0.090209417	0.650558973
XA0019	191.0197667	8.399692333	0.003070601	0.003180765	0.005078354	0.003928646	0.003544419	0.003978111	0.003181039	0.002803474	0.004803264	−0.015383625	0.956649064	−0.086098113	0.755866018
dTDP−glucose	563.0681825	8.561502958	0.001272289	0.001174397	0.001151002	0.001358071	0.001138115	0.001363697	0.001181805	0.001224674	0.001230924	−0.101487035	0.371275309	−0.085647903	0.424287576
Ser−Glu	235.092695	10.00923563	0.000571002	0.000504759	0.000581677	0.00041928	0.000378371	0.000344307	0.000397225	0.000340575	0.000338542	0.537445748	0.006246065	−0.085373334	0.492900038
11−Aminoundecanoic acid	202.180245	9.303288917	0.000483224	0.000420049	0.00061383	0.000664408	0.000570532	0.000648383	0.000628058	0.000493894	0.000654235	−0.311962875	0.153504258	−0.084497602	0.57577839
Sebacic acid	201.1131092	11.67233225	6.09E−05	5.97E−05	7.51E−05	8.80E−05	9.04E−05	8.53E−05	7.82E−05	9.19E−05	7.86E−05	−0.429723085	0.035554342	−0.083529338	0.384854816
Urocanic acid	139.0503036	7.930387009	0.000104235	0.000106422	0.000116999	0.000205578	0.000108562	0.000170777	0.000255653	0.000124556	7.75E−05	−0.565556524	0.204063752	−0.083296449	0.889998234
Creatinine	114.066245	6.965339083	0.011103865	0.008632047	0.011456584	0.010012125	0.010500166	0.010026042	0.009731387	0.010076956	0.009035504	0.030577713	0.83044739	−0.082357694	0.200203559
dTDP	401.0154025	11.4125435	7.28E−05	8.09E−05	5.89E−05	5.84E−05	5.85E−05	9.41E−05	7.24E−05	6.01E−05	6.69E−05	0.01126607	0.970929508	−0.08178275	0.780731204
S−Methylglutathione	322.1068133	12.97196083	0.000893689	0.000760223	0.000879575	0.00092195	0.000887401	0.000898009	0.000950068	0.000840625	0.000767929	−0.095761876	0.302853212	−0.081518932	0.44900912
Cytosine	112.0505525	6.919031975	3.19E−05	2.60E−05	3.00E−05	2.60E−05	1.57E−05	2.70E−05	1.47E−05	1.73E−05	3.31E−05	0.353711649	0.212354266	−0.078764819	0.869819701
7−Methylguanine	166.0724525	7.87329795	9.66E−05	8.01E−05	8.93E−05	9.53E−05	9.30E−05	8.89E−05	0.000101842	8.05E−05	8.01E−05	−0.058898666	0.526539186	−0.078180868	0.568391649
Uric acid	167.02095	9.023017583	0.000372434	0.000372768	0.000364085	0.000319708	0.000395901	0.00032472	0.000381156	0.000340648	0.000264741	0.092593582	0.449167945	−0.076581705	0.693969519
N−Acetylglucosamine 6−phosphate	300.0490967	9.274327667	0.000386069	0.000286961	0.000360462	0.000369863	0.000347627	0.000317508	0.000325418	0.000367141	0.000289336	−0.002099091	0.988943071	−0.075987257	0.554222392
NMN	335.0641192	20.58550842	0.000802021	0.000886847	0.000878006	0.000904537	0.000804911	0.000905946	0.00077737	0.000840218	0.000864426	−0.027015242	0.726363468	−0.075516127	0.356206108
OctopamineDopamine	154.0863225	8.3340335	8.48E−05	8.40E−05	8.58E−05	7.12E−05	5.73E−05	6.57E−05	4.60E−05	6.25E−05	7.58E−05	0.391160359	0.036135048	−0.075230332	0.752941102
gamma−Glu−His	285.1194183	8.323077833	2.67E−05	3.63E−05	2.57E−05	1.88E−05	3.29E−05	3.04E−05	2.71E−05	2.25E−05	2.84E−05	0.111852452	0.710925767	−0.074782198	0.792303069
Glycerol 3−phosphate	171.00636	12.22791388	0.033974106	0.027146657	0.033921428	0.032022871	0.028216941	0.038372167	0.035930057	0.036846952	0.020922226	−0.05319481	0.766713912	−0.073725629	0.800080795
Glycerophosphocholine	258.11047	21.60286225	0.537095788	0.526926389	0.533503795	0.499680251	0.548007755	0.513486458	0.491599424	0.465338163	0.526719389	0.033207617	0.489854428	−0.073474193	0.324139752
2−Deoxyglucose 6−phosphate	243.02777	10.26997658	0.000710898	0.001384266	0.000697332	0.000727679	0.000778587	0.001022916	0.000855019	0.000830177	0.000726205	0.142884023	0.746336555	−0.068798689	0.721453391
4−Guanidinobutyric acid	146.092495	7.929692592	0.002457724	0.002484386	0.002488756	0.002403159	0.003128391	0.002492937	0.002823789	0.002525117	0.002317621	−0.110678945	0.477447716	−0.06583	0.686607774
Ser	106.0498683	9.604667917	0.187085023	0.167443631	0.179037847	0.217048839	0.189457026	0.200657893	0.203053086	0.184604467	0.192465854	−0.186417588	0.073848712	−0.065725847	0.409529405
Ribulose 1,5−diphosphate	308.9783	15.800039	0.000353599	0.000250983	0.000298194	0.000304537	0.000243287	0.000268238	0.00026994	0.000279147	0.000233083	0.145691099	0.4598204	−0.062191877	0.640256517
Carnosine	227.1138	6.436296675	0.015900281	0.019140077	0.013290545	0.01012705	0.02048447	0.014479374	0.017865465	0.013759718	0.011686659	0.100109815	0.773592714	−0.058074592	0.875655598
Val	118.0862488	9.643622583	0.063427639	0.061368612	0.058650846	0.06028036	0.057317116	0.05553152	0.058639981	0.05808252	0.049640697	0.083516706	0.15373186	−0.057511037	0.536807809
Homoserine	120.0655628	9.700025833	0.002129017	0.002309142	0.002453967	0.002471047	0.002363247	0.00247287	0.002799803	0.002419583	0.001810365	−0.084362232	0.276725361	−0.055838058	0.77954151
FAD_divalent	391.571425	7.982880433	0.000833704	0.000726072	0.000801652	0.000807299	0.000630038	0.000717863	0.000695411	0.00066307	0.000716589	0.131837472	0.329185849	−0.054661954	0.660130957
ADMA	203.1502517	7.289511317	0.000465111	0.000415961	0.000547173	0.000464014	0.000368506	0.000463165	0.000387021	0.000461021	0.000400271	0.140529784	0.425768829	−0.05373539	0.708495173
Leu	132.101955	9.941321625	0.083977409	0.082319186	0.070039944	0.079540882	0.076634896	0.067350288	0.066299012	0.083707717	0.065460808	0.080399622	0.498770231	−0.052972547	0.724060128
Sedoheptulose 7−phosphate	289.0331	9.71045875	0.001813815	0.001065472	0.001879722	0.001723692	0.001297945	0.001106064	0.001108535	0.001518426	0.001354299	0.205323003	0.548995049	−0.052113407	0.835419006
N1−Acetylspermidine	188.175845	6.020747142	0.000490822	0.000499532	0.000787957	0.00045707	0.000736475	0.000745685	0.000636626	0.000497381	0.000412442	0.153130762	0.695368442	−0.048418194	0.893308169
1−Methyl−4−imidazoleacetic acid	141.0659367	7.884125367	0.000103163	0.0011457	0.001388718	0.001053333	0.000893048	0.001180336	0.001271536	0.000833231	0.000921941	0.182187277	0.370316718	−0.046898735	0.844636425
Succinic acid	117.0193675	21.11614142	0.061220169	0.040941157	0.056973411	0.060826744	0.044854012	0.048859846	0.052775182	0.060033262	0.036818121	0.042262872	0.854838969	−0.04661958	0.855419622
Fructose 6−phosphate	259.022705	10.05123838	0.002865834	0.002941081	0.003214427	0.002632718	0.002550352	0.002609956	0.001951161	0.002440682	0.003153664	0.211158557	0.054347529	−0.046566652	0.835384288
N−Acetyllysine	189.12344	9.404505292	0.003008595	0.002846152	0.003585397	0.003451103	0.003095234	0.002405829	0.003270453	0.002510617	0.002889361	0.076572033	0.692617732	−0.046133111	0.81684945
Glycolic acid	75.00871875	12.75884642	0.000298536	0.000351292	0.000328882	0.000347202	0.000324534	0.000319256	0.000377174	0.000285842	0.000296846	−0.017991302	0.829687105	−0.046043892	0.758236748
beta−Hydroxyisovaleric acid	117.0557857	9.234598417	0.000180767	0.000157914	0.000154438	0.000175849	0.000186987	0.000143581	0.000149149	0.000136617	0.000204789	−0.038396322	0.790400213	−0.045911991	0.842675043
1−Aminocyclopropane−1−carboxylic acidHomoserinelactone	102.0549377	6.777928642	0.00181969	0.001661658	0.001693898	0.001832545	0.001709181	0.001848097	0.002048574	0.001602008	0.001579952	−0.058610402	0.334940924	−0.043279693	0.765952904
GDP−mannoseGDP−galactoseGDP−glucose	604.0693	8.386700125	0.002483831	0.002371775	0.002240659	0.002964924	0.002432886	0.002492395	0.00263966	0.002588537	0.00243751	−0.153002787	0.253031905	−0.041643634	0.708883824
N−Acetylglucosamine 1−phosphate	300.0490967	9.651249125	0.00130057	0.001249562	0.001293499	0.001164101	0.001099312	0.00131154	0.001069512	0.001175068	0.001230155	0.104545634	0.287753705	−0.041021706	0.693992794
Homocarnosine	241.12949	6.57599225	0.029551184	0.035336712	0.029483715	0.024162241	0.037027252	0.025082604	0.033482251	0.028075843	0.022362734	0.129458904	0.598806277	−0.039865116	0.888802999
beta−Ala	90.05497667	7.003687875	0.00890658	0.00865775	0.010400648	0.009002177	0.00889389	0.00776537	0.008807031	0.008090034	0.008092834	0.124019212	0.323006578	−0.038256938	0.658393607
UDP−N−acetylgalactosamine−2UDP−N−acetylglucosamine−2	606.074	8.560771292	0.012752326	0.01211503	0.011878502	0.013523675	0.011797983	0.012518617	0.012768891	0.012178608	0.011974221	−0.042340968	0.563883904	−0.035452804	0.62083905
N−Acetylaspartic acid	174.04071	14.61793358	0.535988656	0.528225582	0.574910352	0.578406863	0.556005337	0.561425618	0.555911002	0.54035098	0.558500001	−0.049072687	0.325526632	−0.035374486	0.197298004
XC0137	350.1016	13.11979333	0.003169455	0.002641349	0.004661645	0.003291224	0.003349364	0.003897692	0.003715592	0.003512638	0.003058628	−0.009040482	0.975095947	−0.034837013	0.774916375
Carboxymethyllysine	205.1183192	8.843642833	0.000796286	0.000805134	0.000798787	0.000700064	0.00087245	0.000741066	0.000755829	0.000714061	0.000791946	0.053031864	0.634624817	−0.032632839	0.782545673
Sulfotyrosine	260.0236333	8.466866833	6.67E−05	6.81E−05	4.93E−05	7.20E−05	7.04E−05	7.72E−05	7.07E−05	7.23E−05	7.19E−05	−0.253949375	0.18099705	−0.03073172	0.528110726
Adenosine 5''−phosphosulfate	426.0128767	10.24036792	1.89E−05	3.18E−05	2.22E−05	1.87E−05	2.92E−05	4.40E−05	3.37E−05	2.49E−05	3.14E−05	−0.334456003	0.500221711	−0.030229894	0.941298586
Arg	175.118975	6.780078983	0.087717007	0.083520754	0.096708603	0.0967134	0.098045323	0.082236561	0.112589887	0.083726251	0.075062582	−0.047917167	0.662760485	−0.029553818	0.890514955
N2−Succinylornithine	233.1133308	9.896549583	0.000852049	0.000909553	0.0007205	0.000658635	0.000642362	0.000684992	0.000812134	0.000565941	0.000570156	0.321704646	0.091557514	−0.027692393	0.891951094
Thiamine	265.11197	6.271232192	0.001342394	0.001025381	0.001384038	0.001271296	0.001074624	0.001012703	0.001170739	0.001179484	0.000946644	0.159718203	0.400708863	−0.026773865	0.859416698
Glutaric acid−1Methylsuccinic acid−1	131.034925	16.89306917	5.24E−05	3.53E−05	3.24E−05	3.75E−05	3.31E−05	5.51E−05	5.37E−05	4.12E−05	2.85E−05	−0.064940684	0.848700726	−0.025834161	0.94203861
UDP−glucose−2UDP−galactose−2	565.0487	8.742064833	0.01867722	0.018769152	0.017749337	0.019935997	0.019122754	0.021225309	0.02052778	0.018984164	0.019845236	−0.127220436	0.296636724	−0.022354026	0.706172994
N−Acetylglycine	116.0352598	9.659921917	3.35E−05	3.18E−05	2.44E−05	4.15E−05	2.95E−05	2.47E−05	3.24E−05	3.00E−05	3.19E−05	−0.091336656	0.748915522	−0.022137891	0.934477655
gamma−Glu−Cys	251.0698267	12.42676458	0.002219291	0.001880742	0.001633218	0.002002014	0.002182759	0.00223012	0.002351571	0.002142411	0.001823633	−0.162071849	0.314041155	−0.022045187	0.860552272
Isethionic acid	124.9914092	11.74305342	0.000545167	0.004830849	0.004572461	0.004889236	0.004990695	0.005102402	0.000515609	0.005177919	0.004568726	−0.052344863	0.326606953	−0.021349272	0.733394928
2,3−Diphosphoglyceric acid	264.95223	18.60068667	0.003942634	0.004070382	0.006590027	0.005085848	0.00455559	0.006642826	0.00485883	0.004248179	0.004986268	0.031842322	0.914013424	−0.019419544	0.832791812
Ophthalmic acid	290.1351208	12.83491371	0.00053148	0.000471039	0.000482492	0.000395274	0.000416405	0.000407303	0.000356834	0.000411906	0.000434223	0.284796889	0.030955872	−0.019085096	0.840986295
gamma−Glu−Asp	263.08755	12.56016608	0.001523211	0.001428677	0.001422595	0.001513236	0.001439924	0.001363904	0.001380651	0.00140946	0.001478207	0.019062416	0.742316192	−0.016382512	0.772076867
gamma−Glu−Ornitine	262.14005	8.051195375	0.000257365	0.00025488	0.00028317	0.00025528	0.000242527	0.000276968	0.000269218	0.000263752	0.000235974	0.037931319	0.637972967	−0.010899237	0.899064161
1−Methylhistamine	126.1026677	4.650372225	0.000688381	0.000663258	0.001164037	0.000872983	0.000551444	0.000755517	0.000740211	0.000633085	0.000793292	0.206655049	0.591259619	−0.008865764	0.968915657
CMP	322.0449508	9.693140708	0.005744547	0.007654242	0.005505066	0.006018031	0.00598331	0.006582053	0.005928419	0.00573281	0.00681846	0.024666463	0.892048892	−0.008073495	0.933997589
FMN	455.0974	8.440867458	4.01E−05	5.04E−05	4.43E−05	5.66E−05	4.57E−05	4.14E−05	5.14E−05	4.31E−05	4.86E−05	−0.092783634	0.617588059	−0.006577007	0.971346349
Ethanolamine phosphate	140.0118833	8.131694833	0.055717187	0.054860994	0.047172939	0.056071751	0.0533855	0.053843107	0.05291155	0.055951434	0.053750346	−0.049885946	0.572359475	−0.006082427	0.861299119
Glucose 6−phosphate	259.0226642	9.936456417	0.010881266	0.011213207	0.012641094	0.009472314	0.009967022	0.009589214	0.007279449	0.010115773	0.011579299	0.258941169	0.062882254	−0.002687684	0.989949658
XA0017	186.1133833	7.966265658	0.000413234	0.00226381	0.002390778	0.002007546	0.00238486	0.002364515	0.002086825	0.002010745	0.002654594	−0.414999928	0.472674001	−0.001015757	0.995052153
gamma−Butyrobetaine	146.11767	7.742377167	0.020353659	0.018923849	0.020236866	0.020260201	0.022550772	0.020976323	0.022693489	0.020887901	0.020179173	−0.100030955	0.166069599	−0.000604749	0.993380047
ADP−glucoseGDP−fucose	588.0742	8.414323917	0.001056719	0.000936285	0.000812123	0.000965905	0.00083407	0.000997388	0.000908889	0.000968034	0.000922721	0.003998894	0.977723155	0.001175398	0.989641878
S−Methylcysteine	136.0426983	11.17257413	0.000135877	6.29E−05	0.000121507	3.55E−05	9.73E−05	4.58E−05	7.04E−05	7.29E−05	3.56E−05	0.842717632	0.184978064	0.00133743	0.996717317
Homoarginine	189.1348275	6.855348608	0.00033649	0.000200197	0.000369689	0.000272262	0.000317081	0.000345782	0.000321848	0.000387876	0.000227217	−0.045050815	0.876501542	0.002796304	0.991372778
cis−Aconitic acid	173.0092	28.26558267	0.000840324	0.001032237	0.000795943	0.000904981	0.000870983	0.000969577	0.00097287	0.000833075	0.000945061	−0.041059527	0.766687542	0.002868672	0.973744314
gamma−Glu−Ilegamma−Glu−Leu	261.144875	12.53351879	0.000642967	0.000604856	0.000469172	0.000558581	0.000565083	0.000532389	0.000504726	0.000574221	0.000580454	0.052137966	0.739327787	0.002914208	0.969071856
Urea	61.039715	21.06175925	0.191048557	0.210866568	0.213444682	0.210502763	0.216096721	0.203238557	0.198271075	0.211081268	0.221772124	−0.03355068	0.588276514	0.002943658	0.959228354
Gly−Asp	191.0662033	9.4991255	0.001288437	0.00124975	0.001233835	0.001296884	0.001286896	0.00119309	0.001291547	0.001302231	0.001195116	−0.001852932	0.967830987	0.004585317	0.936771581
gamma−Glu−Taurine	253.0501008	8.236448083	0.000120503	0.000132909	9.56E−05	0.000114305	0.000112877	0.000118994	0.000107637	0.000123377	0.000116306	0.011970129	0.939648065	0.004759355	0.943620466
Butyrylcarnitine	232.1542733	9.200706917	0.005706426	0.006298711	0.00814169	0.007621832	0.00779442	0.007659519	0.008178704	0.008152229	0.006872306	−0.195826258	0.314306097	0.007947334	0.930757178
gamma−Glu−Lys_divalent	138.5814217	8.21098925	7.81E−05	6.61E−05	7.22E−05	8.45E−05	8.60E−05	8.83E−05	7.87E−05	8.86E−05	9.33E−05	−0.257718089	0.044502941	0.009940588	0.903639621
DaminozideAla−Ala	161.0922275	8.884108792	0.000596178	0.000585513	0.000562467	0.000543808	0.00050045	0.000533795	0.000531593	0.000566314	0.000493843	0.144384752	0.031350861	0.012467594	0.863914371
Lactic acid	89.024454	10.93766413	0.460472083	0.414052534	0.412451831	0.417529062	0.36919966	0.394869287	0.399558859	0.416792577	0.3781416	0.123246354	0.171431828	0.015659145	0.822422729
4−Oxopyrrolidine−2−carboxylic acid	130.0499275	10.51407979	0.404418719	0.326516388	0.395039614	0.40424966	0.368355817	0.385800286	0.44343326	0.395855821	0.333363982	−0.040966246	0.715087772	0.017635561	0.898263188
Asp	134.04478	11.16900854	0.597839926	0.65550452	0.508133535	0.582258795	0.609970029	0.534772671	0.58493919	0.576490629	0.590317261	0.02851711	0.826895883	0.02052516	0.745208327
Ascorbic acid	175.0246525	8.602655583	0.197837885	0.196114494	0.197708387	0.212400649	0.173605979	0.195868944	0.19701703	0.203192797	0.191005041	0.024059549	0.799105341	0.022971869	0.812637728
Citric acid	191.01982	26.6121725	0.042301354	0.048940364	0.035446662	0.043957076	0.043340952	0.045149524	0.045238475	0.042151271	0.04720799	−0.064136977	0.672099219	0.02323296	0.683509678
Guanidinosuccinic acid	176.0667708	9.730360333	4.52E−05	4.72E−05	3.83E−05	4.02E−05	7.22E−05	4.30E−05	4.80E−05	5.24E−05	5.76E−05	−0.249971004	0.509221168	0.0242902	0.941434878
Creatine	132.076735	8.402571333	4.46284769	4.483606706	4.420415789	4.942292061	4.600851945	4.235187265	4.856121775	5.002921458	4.16334933	−0.043739468	0.571388293	0.025331336	0.81787359
CMP−N−acetyleuraminate	613.14075	8.266068	0.002081056	0.002065694	0.001954464	0.002141176	0.001976227	0.002098347	0.002080856	0.002060702	0.002194997	−0.027064028	0.578746109	0.027538035	0.571939256
Gly	76.039295	7.953568167	0.068565181	0.065465496	0.070470139	0.069755358	0.062780266	0.068292153	0.070774968	0.067638862	0.066751948	0.026147777	0.662392145	0.030831281	0.594153308
Pyridoxamine 5''−phosphate	249.0636158	10.08439092	0.003115233	0.002585192	0.003898896	0.002786798	0.002757728	0.002470581	0.002939525	0.002331082	0.002921573	0.260210804	0.298793631	0.031525829	0.809386781
O−Acetylcarnitine	204.1229975	8.647722542	0.116884373	0.120488532	0.135267401	0.132261078	0.145963196	0.138477102	0.153407175	0.143666315	0.129189408	−0.161230133	0.107435647	0.032729621	0.718232746
N−Acetyleuraminic acid	308.0990267	7.305903242	0.008614465	0.008703707	0.008246759	0.008957702	0.007355103

XA0065	445.0537267	7.060942467	0.010929407	0.012223406	0.011005304	0.010919145	0.011161313	0.0118181	0.01049002	0.012461948	0.012271263	0.011004552	0.871873511	0.055303334	0.568512526
6-Phosphogluconic acid	275.01752	14.78737475	0.002097297	0.001889375	0.002579627	0.001878625	0.001685856	0.001556292	0.001375881	0.001804768	0.002143194	0.358719022	0.127821211	0.05610678	0.7989699
O-Succinylhomoserine	218.067	12.30513288	0.000293603	0.000150638	0.000228466	0.00023321	0.000128717	0.000162066	0.000199109	0.000242994	0.000103528	0.360429833	0.394791604	0.058374662	0.895750543
N6,N6,N6-Trimethyllysine	189.15983	6.845224017	0.008079453	0.006957148	0.00794274	0.007681718	0.007527568	0.007390029	0.007880871	0.007672323	0.007999575	0.024058309	0.757660838	0.059617599	0.068229964
Putrescine	89.10731333	4.448204025	0.00029329	0.000485305	0.000467098	0.000336044	0.000507459	0.000329677	0.000493491	0.000379321	0.000352032	0.086523905	0.789011391	0.062173214	0.825010789
Hydroxyproline	132.0655958	11.64973863	0.014122127	0.011289377	0.015916422	0.013172963	0.013107712	0.014632548	0.017013273	0.011685032	0.014165714	0.014549778	0.93039414	0.067199953	0.720592726
Orotidine	287.0520667	8.054405917	0.000237703	0.000267027	0.000192633	0.000239226	0.000234933	0.000259968	0.000301821	0.000215682	0.000252631	−0.074120295	0.637425753	0.069079523	0.684485425
UDP-N-acetylgalactosamine-1UDP-N-acetylglucosamine-1	606.074145	8.387413292	0.00010503	8.33E−05	7.66E−05	0.000130841	9.94E−05	8.89E−05	0.000110168	0.000111351	0.000113341	−0.267985993	0.309554889	0.069470097	0.71822046
CoA_divalent	382.5505117	10.72691392	0.01072567	0.009799277	0.009666383	0.010313853	0.009872401	0.010270629	0.010869062	0.01010384	0.011008448	−0.012633987	0.82407144	0.070462595	0.206234765
Noradrenaline6-Hydroxydopamine	170.0811783	8.633278583	0.000244075	0.000202535	0.000268334	0.000190909	0.000236835	0.00018634	0.000218697	0.000225951	0.000200351	0.219394851	0.253150703	0.07086328	0.605831642
GDP	442.01727	10.77888383	0.026079799	0.033828859	0.024556328	0.025929235	0.02623168	0.028106444	0.027308532	0.026062523	0.031136357	0.073539989	0.677857629	0.074264449	0.464679178
Sorbitol 6-phosphate	261.03819	10.05556646	0.000226389	0.000237593	0.000193209	0.00022169	0.000194218	0.000188916	0.000222294	0.0002154	0.000200375	0.119796969	0.360146359	0.077198933	0.41811561
Ornithine	133.0972292	6.492741242	0.002213996	0.002621254	0.002399195	0.002958083	0.002370367	0.00259819	0.002924124	0.002887345	0.002561574	−0.131827401	0.336133276	0.07904246	0.515812275
3-Hydroxybutyric acid	103.0400367	9.640418125	0.000915351	0.000979097	0.0008094	0.001119546	0.000803753	0.000850715	0.001192956	0.001109444	0.00063249	−0.036960749	0.845625638	0.081331469	0.805553977
1-MethylhydantoinGlycine anhydride	115.0502792	21.99839725	0.001046739	0.000938993	0.001321422	0.001280922	0.001260697	0.001090089	0.001592908	0.001305887	0.000946915	−0.135058382	0.462170658	0.082601385	0.745868434
Phosphorylcholine	184.073345	20.45385542	0.286783909	0.296414627	0.303367962	0.304005343	0.316793646	0.301747586	0.314012572	0.300850024	0.362625048	−0.057392901	0.148587258	0.083456719	0.434451532
Cadaverine	103.12302	4.713399958	1.35E−05	3.73E−06	1.17E−05	9.58E−06	1.06E−05	8.02E−06	1.04E−05	8.22E−06	1.13E−05	0.038520344	0.943767366	0.086616104	0.654113431
Lys	147.11279	6.55139785	0.105150123	0.075217275	0.11293906	0.108337411	0.101807947	0.096791322	0.11192078	0.117922435	0.096462055	−0.06553222	0.736132991	0.088281223	0.436384626
1-Methylhistidine3-Methylhistidine	170.0924017	7.141895375	0.006359099	0.006415828	0.006329051	0.004626704	0.00464377	0.004779843	0.005097274	0.005493437	0.004349608	0.44327041	7.07E−05	0.088608245	0.47040334
dADP	410.0269833	11.09573004	3.26E−05	4.23E−05	2.58E−05	2.95E−05	1.69E−05	3.52E−05	3.99E−05	2.69E−05	2.01E−05	0.304332888	0.428454615	0.089796481	0.834778251
Glu	148.06042	10.51044175	2.761197461	2.476306061	2.693437041	2.894689774	2.663903373	2.973753683	3.396473729	3.042084365	2.64667065	−0.10545064	0.188870991	0.090580228	0.496710781
XA0012	166.0179	9.534272667	0.001555677	0.001545376	0.001666261	0.001723188	0.001460117	0.001634938	0.001662157	0.001751646	0.001717324	−0.015330059	0.85708428	0.090768769	0.308800383
Orotic acid	155.00989	10.04256442	0.000102593	9.18E−05	8.57E−05	9.61E−05	7.66E−05	9.00E−05	9.89E−05	0.000109174	7.18E−05	0.092034499	0.488282386	0.091041147	0.679247068
Trigonelline	138.05502	10.07347192	0.002814337	0.002178634	0.004040196	0.002538448	0.003928237	0.002904376	0.003063861	0.002419061	0.004503501	−0.052980613	0.87819011	0.091755642	0.79807184
Ile	132.101955	9.836582917	0.038181786	0.039034368	0.034519781	0.032535843	0.032275569	0.028416065	0.031695146	0.038118393	0.029687684	0.26126612	0.032632146	0.093959052	0.518653468
Asn	133.06081	10.09884263	0.025288517	0.021961974	0.023489581	0.022723925	0.020539384	0.02146012	0.024249561	0.022522041	0.022437655	0.12823962	0.167501318	0.096676965	0.159565411
Phosphoenolpyruvic acid	166.97498	21.216917	8.10E−05	0.000189596	4.57E−05	0.000112174	0.000116956	0.000132206	0.000112622	9.88E−05	0.000175118	−0.191826715	0.762935806	0.097136719	0.758527209
NAD+	662.1018667	6.677917458	0.028536454	0.029288785	0.027471458	0.026042737	0.027045422	0.030327208	0.029628409	0.029849129	0.029806247	0.032176673	0.687701876	0.098084997	0.269512366
Glu-Glu	277.10312	10.46426292	0.000417925	0.000455937	0.000386971	0.00039584	0.0004604	0.000348949	0.00046949	0.000417863	0.000402754	0.065116871	0.655556819	0.098231067	0.506158593
N-Glycolylneuraminic acid	324.093595	7.281328075	0.000365058	0.000393391	0.000525467	0.000356327	0.000362877	0.000310509	0.000361164	0.000346011	0.000397612	0.318308814	0.222698169	0.1015251	0.328525264
Ascorbate 2-glucoside	337.0776067	7.227854517	0.000116042	8.86E−05	9.55E−05	9.42E−05	5.10E−05	9.02E−05	7.81E−05	7.96E−05	9.58E−05	0.35106889	0.264664751	0.106602853	0.715910684
gamma-Glu-Val	247.12901	12.31919979	0.000216253	0.00021875	0.000200545	0.000197108	0.000228281	0.000206246	0.000229729	0.000220497	0.000230012	0.008910536	0.911341591	0.10695036	0.215638608
N-Acetylasparagine	173.0567433	8.510928	2.27E−05	2.56E−05	3.69E−05	3.62E−05	1.49E−05	3.26E−05	2.50E−05	2.94E−05	3.58E−05	0.025930493	0.952899949	0.107409045	0.786587713
Muscimol	115.050315	7.201240983	0.000148236	0.000154135	0.000130854	0.000140593	0.000137277	0.000146523	0.000160052	0.000144315	0.000154969	0.029713171	0.724491396	0.114146758	0.112322189
Homocitrulline	190.11868	10.7769745	0.000995328	0.001385758	0.001211372	0.000999174	0.00068899	0.001023922	0.000733946	0.001006788	0.001195379	0.405568288	0.133420717	0.114504505	0.687378943
5-Hydroxyindoleacetic acid	190.0510117	8.329615542	0.000122353	9.27E−05	0.00012402	0.000104041	6.89E−05	0.000133116	0.000130668	0.000122945	7.81E−05	0.148071604	0.637993212	0.116294798	0.747483198
5-Aminoimidazole-4-carboxamide ribotide	337.0556067	9.553051917	9.46E−05	0.00011321	9.31E−05	8.62E−05	7.75E−05	8.82E−05	0.000106049	9.56E−05	7.15E−05	0.255932409	0.110706842	0.116438809	0.567225313
gamma-Glu-Trp	334.140015	12.73259008	3.37E−05	5.24E−05	2.68E−05	3.00E−05	2.19E−05	2.62E−05	2.55E−05	2.72E−05	3.20E−05	0.530663503	0.265196842	0.116836036	0.511005664
N-Acetylglutamic acid	188.056535	13.30847333	0.003355055	0.003241204	0.002861072	0.003149643	0.002789152	0.002877379	0.003458176	0.003127635	0.002976626	0.101280269	0.317038965	0.117225564	0.241324802
Imidazolelactic acid	157.060565	8.3780415	0.000260231	0.0001812	0.000316943	0.000326108	0.000226853	0.000159921	0.000344836	0.000221184	0.000211892	0.089247409	0.820095093	0.125944799	0.754112283
3-Methoxytyrosine	212.0918909	11.39348373	1.75E−05	1.37E−05	2.62E−05	2.10E−05	1.41E−05	1.44E−05	2.11E−05	1.55E−05	1.77E−05	0.215015489	0.582459917	0.131125715	0.598473755
gamma-Glu-Gln	276.1191883	12.61562567	0.015683412	0.022301019	0.009948766	0.013793901	0.014711937	0.013348935	0.013339371	0.014488118	0.018054866	0.195632991	0.628228983	0.132547278	0.447321801
gamma-Glu-Thr	249.1082083	12.3322245	0.000553533	0.00063133	0.000485875	0.000551955	0.000594437	0.000716858	0.000718906	0.000728247	0.000597987	−0.157335424	0.379973918	0.134378575	0.403949256
Threonic acid	135.02997	9.37686075	0.006104929	0.005777986	0.005808184	0.005484073	0.005342641	0.005435538	0.006673462	0.005763251	0.005465533	0.12149652	0.031317084	0.138613437	0.270539223
XA0004	144.030205	9.454120333	2.50E−05	2.28E−05	4.67E−05	2.31E−05	1.33E−05	3.37E−05	2.42E−05	2.46E−05	2.85E−05	0.431235125	0.449004714	0.14162908	0.726491776
3-Phosphoglyceric acid	184.98561	19.83456008	0.000354198	0.000527255	0.000193005	0.000381843	0.00037183	0.000415138	0.000364561	0.000406085	0.000519913	−0.12143191	0.776420469	0.142954029	0.478171044
Cysteine glutathione disulfide	427.0951125	11.25557433	0.000268319	0.000451451	0.000123279	0.000301372	0.000201875	0.00019356	0.000171671	0.00023679	0.000362029	0.274855728	0.668260467	0.14501729	0.731109328
N-Acetylalanine	130.0510158	8.996286917	0.000181756	0.000186429	0.000166666	0.000173645	0.000168965	0.000165202	0.00018625	0.000200796	0.000174736	0.074842144	0.267393577	0.14571767	0.129178726
NADP+	742.0676417	9.492402	0.002185958	0.002294779	0.002339617	0.002007875	0.00197846	0.002226742	0.002221672	0.002306368	0.002356764	0.134538822	0.105632427	0.148107619	0.085022511
Acetylcholine	146.1176533	7.254794767	0.016472507	0.02435243	0.03559513	0.02556021	0.028500157	0.027298251	0.031322704	0.025945305	0.033105747	−0.090343639	0.795858904	0.151608727	0.296958063
Arginininosuccinic acid	291.1300975	9.048899125	0.002633377	0.002993394	0.002090916	0.002422581	0.003180393	0.002443973	0.003660428	0.002903934	0.002391158	−0.060273129	0.776745737	0.154335716	0.538281088
3-Hydroxykynurenine	225.0870925	9.365519	2.66E−05	1.69E−05	3.61E−05	1.97E−05	1.97E−05	2.29E−05	2.80E−05	1.58E−05	2.56E−05	0.353308154	0.408010634	0.155747576	0.596307191
gamma-Glu-Asn	262.1036467	12.34600967	6.21E−05	6.89E−05	4.46E−05	4.88E−05	5.33E−05	5.23E−05	4.92E−05	5.52E−05	6.78E−05	0.18430699	0.432773374	0.156076234	0.393188339
XC0126	310.11344	14.61322767	0.0006246	0.000532734	0.0006389	0.000583841	0.000511111	0.0005204	0.000565595	0.00057767	0.000668446	0.150770458	0.222632358	0.163147733	0.186137383
Kynurenine	209.0921467	9.507131167	5.46E−05	8.83E−05	7.98E−05	5.47E−05	6.48E−05	3.96E−05	7.39E−05	2.91E−05	7.54E−05	0.484298104	0.171813942	0.164741547	0.729197115
gamma-Glu-Ser	235.09252	12.21397738	0.000816471	0.000844488	0.000553967	0.000775808	0.000711127	0.000719248	0.000733863	0.000847464	0.000898298	0.00570611	0.978032148	0.168569798	0.192926789
gamma-Glu-Gly	205.0820217	11.650499	0.000556352	0.000656135	0.000443156	0.000532735	0.000486396	0.000514225	0.000547207	0.000539555	0.000647492	0.110698939	0.578725487	0.177623077	0.184880187
Citramalic acid	147.029855	17.51393275	0.000100865	0.000106786	1.44E−05	0.000280387	0.00022266	0.000103461	0.000213847	0.000282952	0.000199981	−1.449324059	0.117213582	0.200177031	0.64106167
3'-CMP2'-CMP	322.0447267	9.893837583	9.77E−05	0.00016876	3.46E−05	7.06E−05	0.000159385	0.000129767	0.000149119	0.000110719	0.000154251	−0.257032178	0.699768899	0.202982407	0.582179188
2-Hydroxy-4-methylvaleric acid	131.07141	8.989767417	0.00011731	8.76E−05	8.19E−05	7.82E−05	7.45E−05	8.18E−05	9.17E−05	6.45E−05	0.000114325	0.290322106	0.250758892	0.205845232	0.493048721
Spermidine	146.1652625	4.2713741	0.005025359	0.005166228	0.00510653	0.003932774	0.004758536	0.003861929	0.004869529	0.004506319	0.005210067	0.285294518	0.083504005	0.216516379	0.134721489
Thr-Asp	235.092555	10.22165917	9.32E−05	0.000104549	9.09E−05	9.03E−05	0.000108805	8.01E−05	0.000104089	0.0001037	0.000117848	0.047957163	0.760137585	0.222107885	0.201912172
Guanine	152.0567317	7.94705065	0.000186614	0.000250478	0.000186837	0.000215387	0.000146171	0.000235179	0.000189564	0.000171582	0.000335285	0.064284924	0.805572614	0.222885568	0.60922807
Ala	90.054935	8.653506333	0.184171624	0.147352916	0.161718056	0.172223678	0.133991692	0.125969182	0.173654347	0.174592608	0.156309134	0.190649892	0.322272005	0.223367153	0.227315132
2-Hydroxyisobutyric acid	103.040109	9.980487583	0.000383597	0.000646375	0.00032716	0.000309399	0.000399892	0.000300448	0.000428339	0.000419838	0.000330711	0.426578686	0.36161543	0.223444759	0.274258192
Malic acid	133.014195	21.52329667	0.113336658	0.150222638	0.0829159	0.109715465	0.1023201	0.110544528	0.125229231	0.1109708	0.14197327	0.103094668	0.723056885	0.229390105	0.166723796
Pantothenic acid	218.10365	7.772650658	0.003166773	0.003897029	0.002795331	0.003215706	0.002891514	0.001976806	0.002558164	0.003906473	0.003066547	0.286386753	0.296775655	0.237581335	0.422733194
Aspartame	295.1288492	10.46426292	4.91E−05	6.08E−05	3.95E−05	4.59E−05	3.51E−05	3.94E−05	4.72E−05	4.96E−05	4.54E−05	0.311550653	0.25719528	0.240715183	0.133997199
N-Acetylhistidine	198.0873267	9.430520292	5.33E−05	4.46E−05	6.72E−05	4.98E−05	5.07E−05	4.82E−05	6.35E−05	6.62E−05	4.59E−05	0.151308055	0.494047784	0.240777046	0.293598374
gamma-Glu-Met	279.1010592	12.56673821	0.000106565	0.000127492	6.88E−05	0.000129927	9.99E−05	8.56E−05	0.000129546	0.000116247	0.000127897	−0.058542771	0.856128263	0.244581685	0.27238531
N-Acetylcysteine	162.02301	9.008009773	2.38E−05	3.66E−05	3.67E−05	1.84E−05	2.69E−05	1.68E−05	2.42E−05	2.51E−05	2.52E−05	0.645412827	0.099061179	0.26193959	0.317630079
Tyr-Arg_divalent	169.5948136	7.370938655	1.93E−05	2.36E−05	1.13E−05	9.21E−06	1.16E−05	1.60E−05	2.02E−05	1.10E−05	1.30E−05	0.559092823	0.250625287	0.263949981	0.516231877
N-Acetylglucosylamine	221.1131775	9.550477333	2.97E−05	1.63E−05	3.82E−05	3.03E−05	3.06E−05	2.56E−05	3.09E−05	4.14E−05	3.21E−05	−0.039372834	0.916761178	0.271055445	0.207556924
Methylguanidine	74.07130875	5.875929525	4.48E−05	6.14E−05	5.90E−05	5.59E−05	2.68E−05	4.09E−05	2.81E−05	4.39E−05	7.79E−05	0.41851448	0.246167557	0.27825972	0.63835958
Spermine	203.2230808	4.21341435	0.001930515	0.002533841	0.001691711	0.002147374	0.001747134	0.001854145	0.002478121	0.001952024	0.002580315	0.09878483	0.659745931	0.28628523	0.153893126
2-Oxoglutaric acid	145.0142083	21.67866958	0.000700927	0.000923426	0.000406898	0.000665551	0.000614591	0.000612668	0.000613294	0.000566529	0.001140693	0.101838623	0.787548304	0.293915624	0.520092325
Diethanolamine	106.0862467	7.280809775	0.000934185	0.001084489	0.002184108	0.002312769	0.002167135	0.001991476	0.002902075	0.002847777	0.00220101	−0.62272882	0.189878835	0.297037712	0.147587265
ADP	426.0221	10.99684333	0.074916982	0.100258962	0.07425059	0.064868249	0.083510496	0.086836482	0.085489404	0.076904872	0.127633922	0.08463349	0.688768664	0.302211706	0.37049156
N-Acetyl-beta-alanine	130.05103	9.058373375	3.30E−05	4.50E−05	6.98E−05	2.74E−05	4.90E−05	4.12E−05	5.56E−05	5.03E−05	3.92E−05	0.328676708	0.4772055	0.303045818	0.317237247
Nicotine	163.1230545	5.050940336	3.49E−06	5.13E−06	1.06E−05	5.12E−06	9.06E−06	6.31E−06	6.53E−06	5.38E−06	1.35E−05	−0.09336577	0.873316396	0.308124336	0.600814174
Fumaric acid	115.0037367	25.60145092	0.004290456	0.005104353	0.002954321	0.003913001	0.003756777	0.003831394	0.004667637	0.004316481	0.005348249	0.102628675	0.696487992	0.317496229	0.086305582
Ascorbate 2-phosphate	254.99136	13.43828675	0.000143259	0.000128758	0.000115612	0.000120598	0.000113351	0.000129966	0.00018326	0.000138926	0.000132513	0.091074237	0.453778406	0.321138344	0.191166434
Cys	122.0270896	10.91480796	0.000135503	0.0001685	0.000158392	0.000155736	0.000168763	0.000111375	0.000161005	0.000125976	0.00026372	0.085213892	0.685999286	0.337355293	0.462632293
N8-Acetylspermidine	188.175795	6.097496975	7.68E−05	8.78E−05	7.89E−05	6.21E−05	7.75E−05	5.87E−05	9.12E−05	9.16E−05	6.92E−05	0.295895642	0.10385242	0.345493102	0.133537579
3,4-Dihydroxyhydrocinnamic acidHomovanillic acidHydroxyphenyllactic	181.05063	8.372250083	0.000397057	0.000345213	0.00047752	0.000515122	0.00027688	0.000387364	0.000655069	0.000409608	0.000434836	0.048621152	0.874759726	0.346481496	0.363650404
Retinoic acid	299.2016	7.297222817	2.17E−05	2.63E−05	4.88E−05	3.78E−05	4.35E−05	2.29E−05	2.79E−05	2.12E−05	8.48E−05	−0.107728749	0.824891817	0.360995789	0.67852393
Phosphocreatine	210.02853	12.34841592	0.000263809	0.000378424	0.000431492	0.000270392	0.000407444	0.000441231	0.000387872	0.000304632	0.000765463	−0.059672385	0.843912353	0.381661775	0.51795939
N-Acetylmethionine	190.0543267	8.221281667	0.000130346	0.000121337	8.69E−05	8.44E−05	0.000110352	0.000111319	0.000141813	0.000139295	0.000121698	0.145689835	0.53823014	0.396275384	0.046451824
2-Hydroxyvaleric acid	117.0557127	9.352296292	0.000628245	0.00070088	0.000490642	0.000653396	0.000342344	0.000412671	0.00058402	0.000481827	0.000788083	0.369684993	0.299892589	0.396518402	0.318079753
gamma-Glu-Glu	277.1033033	12.70804021	0.007376572	0.009584922	0.004063948	0.005960704	0.005763306	0.005036395	0.006073358	0.007245697	0.00905283	0.32707913	0.47016759	0.416629901	0.154056061
PRPP	388.94443	16.845519	0.000610474	0.001143356	0.00034081	0.000501602	0.000727446	0.000749523	0.000702688	0.000823795	0.001136327	0.08224366	0.888314213	0.428490913	0.220831603
GTP	521.98334	11.57708396	0.008229751	0.013774547	0.008532372	0.008646303	0.009596061	0.010767593	0.010589478	0.008246118	0.020776994	0.073994548	0.809825558	0.449410899	0.455972008
Cys-Gly	179.0486017	8.824183208	2.37E−05	2.91E−05	1.98E−05	1.69E−05	2.38E−05	2.26E−05	3.14E−05	3.27E−05	2.33E−05	0.199364205	0.420407562	0.465988992	0.09792449
beta-Ala-Lys	218.1499017	6.409512175	0.000138296	0.000114631	0.000125923	0.000115969	0.000140113	0.000138102	0.000239475	0.000170637	0.000136116	−0.057248191	0.646782852	0.470629716	0.233089975
2-Methylserine	120.0656013	9.988982167	0.004873803	0.000631994	0.000684536	0.003197312	0.000844135	0.002242103	0.000562834	0.004667121	0.003526525	−0.021562731	0.985425247	0.478771247	0.595981836
beta-Leucine	132.101525	8.41345325	7.73E−05	0.000146735	0.00027683	0.000145781	0.000216992	0.00019004	0.000147953	0.000189184	0.000455455	−0.142471916	0.80168648	0.519786204	0.49630552
UDP	402.9952208	11.7574885	0.003462959	0.008796474	0.003921589	0.003210691	0.00562978	0.005900807	0.005465468	0.003991757	0.011857098	0.134441138	0.818008963	0.531961702	0.466517128
5,6,7,8-Tetrahydrobiopterin	242.124795	9.271508417	9.66E−05	6.58E−05	2.40E−05	5.85E−05	5.57E−05	4.07E−05	8.62E−05	8.97E−05	4.98E−05	0.267406661	0.671809446	0.543703945	0.197276626
gamma-Glu-Ala	219.0976867	11.91739167	0.000582633	0.000634466	0.000310768	0.000469188	0.000346875	0.000354446	0.00047091	0.000578127	0.000679636	0.38438201	0.360983115	0.56252899	0.070899049
Acetyl CoA_divalent	403.5559	10.35588813	0.000290317	0.000141266	0.000378406	0.00054158	0.00065111	0.000933283	0.001321116	0.000795638	0.001057674	−1.392149949	0.042879946	0.578373696	0.14655434
3-Phenylpropionic acid	149.0608083	8.903143125	6.70E−05	7.78E−05	5.33E−05	3.74E−05	9.88E−05	8.41E−05	0.00012434	0.000116964	9.78E−05	−0.152891461	0.73746767	0.622316704	0.153672271
5-Hydroxypentanoic acid	117.0556883	9.122708583	4.75E−05	3.46E−05	4.41E−05	2.56E−05	3.85E−05	2.88E−05	5.78E−05	5.20E−05	3.33E−05	0.442375658	0.112402412	0.624360401	0.138003405
CDP	402.0106542	11.56482175	0.000771911	0.002050322	0.000914679	0.000738163	0.001211379	0.001469229	0.001272459	0.000900864	0.003109622	0.12836891	0.831467563	0.627864445	0.463558844
ATP	505.9894	11.87724996	0.026440891	0.049666315	0.030017429	0.02445096	0.037483382	0.039031278	0.038199676	0.027708392	0.1006017	0.071895454	0.852426418	0.721742683	0.439452403
UTP	482.9615792	12.68311008	0.000987731	0.003155705	0.001209395	0.000989639	0.0019675	0.002193078	0.002058177	0.001170663	0.007170485	0.05566901	0.93647131	1.013784849	0.449403467
CTP	481.97731	12.46237533	0.000222206	0.000751741	0.000225617	0.000185399	0.000433317	0.000397315	0.000430166	0.000259544	0.002004101	0.239567804	0.772907121	1.406705099	0.420217973

付録6: 海馬サンプルを用いたRNA-seq解析の結果

Group

SH: sham-operation 群 (i.c.v.: distilled water, p.o.: saline)

VE: vehicle 群 (i.c.v.: Aβ , p.o.: saline)

Fp14: Fp14死菌体懸濁液 群 (i.c.v.: Aβ , p.o.: Fp14死菌体懸濁液)

vehicle群との間でWald testを実施後、FDR補正を行い、cut-off値を0.1としてある変動転写物を抽出した。3回の独立したRNA-seq試験を行い、2回以上の試験で変動転写物として抽出されたものを最終的な変動転写物とした。

transcript_id	Ensembl description	experiment1 (n=6, biological replicates)						experiment2 (n=6, biological replicates)						experiment3 (n=5, biological replicates)					
		SH vs VE			Fp14 vs VE			SH vs VE			Fp14 vs VE			SH vs VE			Fp14 vs VE		
		log2(FC)	pvalue	qvalue	log2(FC)	pvalue	qvalue	log2(FC)	pvalue	qvalue	log2(FC)	pvalue	qvalue	log2(FC)	pvalue	qvalue	log2(FC)	pvalue	qvalue
ENSMUST00000018803.11	pyridoxine 5'-phosphate oxidase (Pnpo)	−0.099848341	0.308693716	0.999960388	−0.376037592	5.45498E−05	0.02709205 7	0.23707641	0.014778344	0.741360493	0.326418407	3.94174E−06	0.002678518	NA	NA	NA	NA	NA	NA
ENSMUST00000021407.10	signal recognition particle 54A (Srp54a)	25.07383408	6.9045E−17	3.18227E−13	23.29819475	8.72762E−15	2.10354E−11	−1.874431337	0.516047755	0.999937028	−25.75618827	9.83992E−18	5.39099E−14	NA	NA	NA	NA	NA	NA
ENSMUST00000114601.7	myotubularin related protein 1 (Mtmr1)	−0.775508665	0.611502026	0.999960388	−4.785889311	1.43011E−05	0.008745774	−0.364906657	0.438252495	0.999937028	5.16688647	6.35024E−07	0.000510615	NA	NA	NA	NA	NA	NA
ENSMUST00000115594.7	FtsJ RNA methyltransferase homolog 1 (E. coli) (Ftsj1)	0.160138709	0.955772871	0.999960388	−23.3175351	8.38653E−15	2.08258E−11	−0.71973701	0.803066804	0.999937028	−25.13625502	5.80605E−17	1.95751E−13	NA	NA	NA	NA	NA	NA
ENSMUST00000130179.1	myotubularin related protein 1 (Mtmr1)	−0.781033925	0.480963354	0.999960388	−3.024951393	0.00014104	0.054261916	−0.111923772	0.536657347	0.999937028	3.51119597	4.83791E−05	0.025093891	NA	NA	NA	NA	NA	NA
ENSMUST00000140212.7	homer scaffolding protein 3 (Homer3)	NA	NA	NA	NA	NA	NA	−25.29031347	3.74928E−17	3.3876E−13	−25.30240508	3.6226E−17	1.38067E−13	−24.04340449	1.96466E−15	5.3335E−12	−24.02847964	2.04432E−15	4.51025E−12
ENSMUST00000141412.7	phospholipase C, delta 4 (Plcd4)	NA	NA	NA	NA	NA	NA	0.533526804	0.693884443	0.999937028	−3.640890695	0.000212753	0.079024137	−0.770486138	0.468954467	0.999997185	−3.887530867	2.9085E−06	0.001679874
ENSMUST00000149835.1	ADP-ribosylation factor-like 6 interacting protein 4 (Arl6ip4)	NA	NA	NA	NA	NA	NA	−3.586774831	2.06444E−05	0.01157768	−3.401677167	4.11811E−05	0.021738599	0.467445414	0.68279793	0.999997185	−3.246338225	0.000442022	0.088281531
ENSMUST00000160107.1	R3H domain and coiled-coil containing 1 like (R3hcc1l)	−2.286540976	0.149649482	0.999960388	−6.799291664	1.79675E−07	0.00015832	NA	NA	NA	NA	NA	NA	4.295716598	0.121309557	0.999997185	5.800031765	1.89104E−09	1.60178E−06
ENSMUST00000172568.7	L3MBTL2 polycomb repressive complex 1 subunit (L3mbtl2)	NA	NA	NA	NA	NA	NA	0.201640347	0.839923617	0.999937028	5.104049395	0.000246731	0.086860055	−1.020603618	0.012678552	0.655941223	3.70785139	0.000194726	0.052184353
ENSMUST00000173216.7	calumenin (Calu)	−22.3699572	9.74424E−14	1.34625E−10	−22.58353855	5.67369E−14	1.01074E−10	22.41851809	8.49528E−14	1.0628E−10	22.21333237	1.42747E−13	1.62507E−10	NA	NA	NA	NA	NA	NA
ENSMUST00000198625.4	gamma-aminobutyric acid (GABA) A receptor, subunit alpha 2 (Gabra2)	NA	NA	NA	NA	NA	NA	−3.30793676	0.243434657	0.999937028	−9.449844535	0.000100474	0.044258463	−1.414901787	0.624329778	0.999997185	−23.29373331	1.41713E−14	2.27864E−11
ENSMUST00000209058.1	MAP/microtubule affinity regulating kinase 4 (Mark4)	4.136617284	0.001662204	0.273176196	5.170021856	1.31494E−07	0.000118412	1.089616643	0.476539031	0.999937028	−4.904600466	3.35229E−05	0.018028133	NA	NA	NA	NA	NA	NA
ENSMUST00000220541.1	phosphofurin acidic cluster sorting protein 2 (Pacs2)	NA	NA	NA	NA	NA	NA	−0.540767289	0.851337735	0.999937028	−27.83765138	1.87388E−20	3.28524E−16	−0.992995422	0.730740573	0.999997185	−28.38767261	6.56044E−21	1.55593E−16
ENSMUST00000234377.1	cDNA sequence BC004004	NA	NA	NA	NA	NA	NA	2.445681814	1.58895E−05	0.009295691	2.500570501	5.20183E−06	0.003454445	0.594800139	0.355917612	0.999997185	1.748457767	0.000436558	0.087558884

付録7: オーソロググループ、TMHMMおよびKOのアサインメント結果 (Fp14、Fp360)

異なるオーソログ検出ツールを用いて、特定の単離株にのみに見られるオーソログおよび特定の単離株のみに見られるKOを含むオーソログを"specific ortholog"と定義した

category	
shared:	Fp14およびFp360のみに共有されていた特徴的なオーソログ
specific_fp14:	Fp14においてのみに特徴的なオーソログ
specific_fp360:	Fp360においてのみに特徴的なオーソログ
NA	特徴的なオーソログではない

gene_ID	ortholog_orthofinder	ortholog_roary	TMHMM_outside (number of hit)	TMHMM_inside (number of hit)	TMHMM_Tmhelix (number of hit)	KEGG_gene	KO	category	not shared by 3 reference strains
ICBIDGAJ_00001	OG0000137	group_548	1	0	0	fpr:FP2_03070	NA	NA	
ICBIDGAJ_00002	OG0000137	group_4002	1	0	0	fpr:FP2_03070	NA	NA	
ICBIDGAJ_00003	OG0000168	group_641	1	0	0	fpr:FP2_03080	NA	NA	
ICBIDGAJ_00004	OG0000168	group_642	1	0	0	fpa:FPR_28060	NA	NA	
ICBIDGAJ_00005	OG0000236	group_546	1	0	0	fpr:FP2_03090	ko:K02334	NA	
ICBIDGAJ_00006	OG0000136	pta_1	1	0	0	fpr:FP2_03100;fpa:FPR_28080	ko:K00625	NA	
ICBIDGAJ_00007	OG0000136	pta_2	0	1	0	fpr:FP2_03100	ko:K00625	NA	
ICBIDGAJ_00008	OG0000136	pta_3	1	0	0	fpr:FP2_03100	ko:K00625	NA	
ICBIDGAJ_00009	OG0000235	group_639	1	0	0	fpa:FPR_28100	ko:K02343	NA	
ICBIDGAJ_00010	OG0000234	recR_1	1	0	0	NA	NA	NA	
ICBIDGAJ_00014	OG0002291	group_2170	1	0	0	fpr:FP2_23410	NA	NA	
ICBIDGAJ_00015	OG0001921	group_2167	1	0	0	NA	NA	NA	
ICBIDGAJ_00016	OG0000276	dnaA	1	0	0	fpr:FP2_20100	ko:K02313	NA	
ICBIDGAJ_00017	OG0000277	dnaN	1	0	0	ruk:A4V00_08915	ko:K02338	NA	
ICBIDGAJ_00018	OG0000278	group_940	1	0	0	fpa:FPR_09140	ko:K14761	NA	
ICBIDGAJ_00019	OG0000279	recF_1	1	0	0	fpr:FP2_20070	ko:K03629	NA	
ICBIDGAJ_00020	OG0000280	group_942	1	0	0	fpr:FP2_20060	NA	NA	
ICBIDGAJ_00021	OG0000281	gyrB_1	1	0	0	fpa:FPR_09170	ko:K02470	NA	
ICBIDGAJ_00022	OG0000282	gyrA_1	1	0	0	fpr:FP2_20040	ko:K02469	NA	
ICBIDGAJ_00023	OG0000283	mntP	4	3	6	fpr:FP2_20030	NA	NA	
ICBIDGAJ_00024	OG0000284	rspR_1	1	0	0	fpa:FPR_09200	NA	NA	
ICBIDGAJ_00025	OG0002562	group_2760	1	0	0	NA	NA	NA	
ICBIDGAJ_00026	OG0000285	group_945	1	0	0	cpy:Cphy_1041	ko:K06180	NA	
ICBIDGAJ_00027	OG0000286	nudF	1	0	0	fpa:FPR_09220	ko:K01515	NA	
ICBIDGAJ_00028	OG0000287	por_1	1	0	0	fpr:FP2_19990	ko:K03737	NA	
ICBIDGAJ_00029	OG0000085	higA1	1	0	0	fpa:FPR_09240	NA	NA	
ICBIDGAJ_00030	OG0001979	group_3597	1	0	0	fpa:FPR_09250	NA	NA	
ICBIDGAJ_00031	OG0000187	group_947	2	2	3	fpa:FPR_09260	ko:K06213	NA	
ICBIDGAJ_00032	OG0000288	group_680	3	4	6	fpr:FP2_19930	NA	NA	
ICBIDGAJ_00033	OG0000289	dnaX_1	1	0	0	fpa:FPR_09290	ko:K02341	NA	
ICBIDGAJ_00034	OG0000290	dacB_1	1	2	2	fpr:FP2_19950	ko:K07258	NA	
ICBIDGAJ_00035	OG0000291	dapH	1	0	0	fpa:FPR_09300	NA	NA	
ICBIDGAJ_00036	OG0000292	birA_1	1	0	0	fpa:FPR_09320	ko:K03524	NA	
ICBIDGAJ_00037	OG0000293	yfcE_1	1	0	0	NA	NA	NA	
ICBIDGAJ_00038	OG0000294	rsmI	1	0	0	fpr:FP2_19900	ko:K07056	NA	
ICBIDGAJ_00039	OG0000295	yfiC	1	0	0	fpr:FP2_19890	NA	NA	
ICBIDGAJ_00040	OG0000296	group_1954	0	1	0	fpa:FPR_09360	NA	NA	
ICBIDGAJ_00041	OG0000297	group_952	1	0	0	fpr:FP2_19870	NA	NA	
ICBIDGAJ_00042	OG0000298	swrC	6	7	12	fpr:FP2_19860	NA	NA	
ICBIDGAJ_00043	OG0001788	group_4003	1	0	0	NA	NA	NA	
ICBIDGAJ_00044	OG0000299	mro	1	0	0	fpr:FP2_19850	ko:K01785	NA	
ICBIDGAJ_00045	OG0000300	lnpD	1	0	0	fpr:FP2_19840	ko:K01784	NA	
ICBIDGAJ_00046	OG0000301	feoB_1	5	5	9	fpr:FP2_19830	ko:K04759	NA	
ICBIDGAJ_00047	OG0000302	slyA_1	1	0	0	rix:RO1_08090;rim:ROI_19660	NA	NA	
ICBIDGAJ_00048	OG0000303	group_957	4	5	8	fpa:FPR_09430	ko:K07090	NA	
ICBIDGAJ_00049	OG0000304	tig_1	1	0	0	fpr:FP2_19800	ko:K03545	NA	
ICBIDGAJ_00050	OG0000305	sdhB	1	0	0	fpa:FPR_09450	ko:K01752	NA	
ICBIDGAJ_00051	OG0000306	sdhA	1	0	0	fpla:A4U99_02185	ko:K01752	NA	
ICBIDGAJ_00053	OG0000025	xerC_1	1	0	0	fpa:FPR_09480	NA	NA	
ICBIDGAJ_00054	OG0000026	group_326	0	1	0	fpr:FP2_28450	NA	NA	
ICBIDGAJ_00055	OG0000307	pre	1	0	0	fpa:FPR_09500	NA	NA	
ICBIDGAJ_00056	OG0000053	group_7225	1	0	0	fpa:FPR_09510	ko:K06919	NA	
ICBIDGAJ_00057	OG0000054	dnaG_1	1	0	0	fpa:FPR_20450	NA	NA	
ICBIDGAJ_00058	OG0000068	group_959	1	0	0	fpa:FPR_09530	NA	NA	
ICBIDGAJ_00059	OG0001676	yvoA	1	0	0	fpr:FP2_19700	ko:K03710	NA	
ICBIDGAJ_00060	OG0001879	sorF	1	0	0	fpr:FP2_19690	ko:K19506	NA	
ICBIDGAJ_00061	OG0001880	sorB	1	0	0	fpr:FP2_19680	ko:K02794	NA	
ICBIDGAJ_00062	OG0001677	sorA	4	4	7	fpr:FP2_19670	ko:K02795	NA	
ICBIDGAJ_00063	OG0001881	manZ_1	3	2	4	fpr:FP2_19660	ko:K02796	NA	
ICBIDGAJ_00064	OG0001882	frlB	1	0	0	fpr:FP2_19650	NA	NA	
ICBIDGAJ_00065	OG0001678	group_3603	1	0	0	fpr:FP2_19640	NA	NA	
ICBIDGAJ_00066	OG0000120	group_3605	3	3	5	fpr:FP2_19630	NA	NA	
ICBIDGAJ_00067	OG0000014	group_139	0	1	0	fpr:FP2_19620	NA	NA	
ICBIDGAJ_00068	OG0001891	group_2809	1	0	0	fpla:A4U99_12610	NA	NA	
ICBIDGAJ_00069	OG0002112	group_2353	0	1	0	NA	NA	NA	
ICBIDGAJ_00070	OG0000200	group_3684	0	1	0	rbr:RBR_01110;esr:ES1_15140;cso:CLS_30000;ibu:IB211_03279	NA	NA	
ICBIDGAJ_00071	OG0002113	fliA_1	1	0	0	cso:CLS_29990;cdl:CDR20291_1773;rbr:RBR_01100;esr:ES1_15130	NA	NA	
ICBIDGAJ_00072	OG0002572	rlmN_1	1	0	0	cdl:CDR20291_1774;ibu:IB211_02811c;rbr:RBR_01090	ko:K06941	NA	
ICBIDGAJ_00073	OG0001892	group_1985	1	0	0	rbr:RBR_01070;esr:ES1_15100	NA	NA	
ICBIDGAJ_00074	OG0000201	group_2812	0	1	0	fpa:FPR_01200	NA	NA	
ICBIDGAJ_00075	OG0000155	group_718	1	0	0	fpa:FPR_01190	NA	NA	
ICBIDGAJ_00076	OG0002114	group_2356	1	0	0	ibu:IB211_02846c	NA	NA	
ICBIDGAJ_00077	OG0001803	group_720	1	0	0	fpa:FPR_01130	NA	NA	
ICBIDGAJ_00078	OG0002115	group_2357	1	0	0	efau:EFAU085_00722;efc:EFAU004_02788	NA	NA	
ICBIDGAJ_00079	OG0000071	group_726	1	0	0	fpa:FPR_01110	NA	NA	
ICBIDGAJ_00080	OG0000056	group_727	1	0	0	efc:EFAU004_02790;efau:EFAU085_00720	ko:K03169	NA	
ICBIDGAJ_00081	OG0000477	group_1088	1	2	2	fpa:FPR_13260	NA	NA	
ICBIDGAJ_00082	OG0000072	group_2815	0	1	0	fpa:FPR_13250	NA	NA	
ICBIDGAJ_00083	OG0000110	group_1092	1	1	1	efau:EFAU085_00717;efc:EFAU004_02793	NA	NA	
ICBIDGAJ_00084	OG0001893	group_1986	1	0	0	fpa:FPR_13230	ko:K00558	NA	
ICBIDGAJ_00085	OG0001693	group_3686	1	0	0	efau:EFAU085_00716	NA	NA	
ICBIDGAJ_00086	OG0001694	group_3690	3	3	5	efc:EFAU004_02796;efau:EFAU085_00714	NA	NA	
ICBIDGAJ_00087	OG0001804	group_223	1	2	2	fpa:FPR_13190	NA	NA	
ICBIDGAJ_00088	OG0000202	group_450	1	0	0	fpa:FPR_13180	ko:K03205	NA	
ICBIDGAJ_00089	OG0003846	group_4004	1	0	0	NA	NA	specific_fp14	○
ICBIDGAJ_00090	OG0001864	agrB	3	3	5	fpa:FPR_08600	ko:K07813	NA	
ICBIDGAJ_00091	OG0002292	group_4005	1	2	2	fpa:FPR_08610	NA	NA	
ICBIDGAJ_00092	OG0003156	group_4006	1	1	1	fpa:FPR_08620	NA	NA	
ICBIDGAJ_00093	OG0002162	group_3085	1	1	1	NA	NA	NA	
ICBIDGAJ_00094	OG0002163	group_4007	1	0	0	NA	NA	NA	
ICBIDGAJ_00095	OG0002407	group_4008	1	1	1	fpa:FPR_08630	NA	NA	
ICBIDGAJ_00096	OG0002293	group_3086	1	0	0	fpa:FPR_08640	NA	NA	
ICBIDGAJ_00097	OG0000055	group_1	1	0	0	fpr:FP2_27630	NA	NA	
ICBIDGAJ_00098	OG0000308	gltR_2	1	0	0	fpr:FP2_29070	NA	NA	
ICBIDGAJ_00099	OG0002101	group_2772	1	0	0	bprm:CL3_05260	NA	NA	
ICBIDGAJ_00100	OG0000309	yqaB	1	0	0	fpa:FPR_18440	NA	NA	
ICBIDGAJ_00101	OG0000310	ilvK	1	0	0	fpr:FP2_28020	ko:K00826	NA	
ICBIDGAJ_00102	OG0000311	xynZ	1	0	0	fpa:FPR_18420	NA	NA	
ICBIDGAJ_00103	OG0000312	group_969	1	0	0	fpr:FP2_28040	NA	NA	
ICBIDGAJ_00104	OG0000313	purD_1	1	0	0	fpr:FP2_28050	NA	NA	
ICBIDGAJ_00105	OG0000107	group_3613	1	0	0	fpa:FPR_15300	ko:K03488	NA	
ICBIDGAJ_00106	OG0000069	bglF_1	5	5	9	fro:AALO17_21280	ko:K02755;ko:K02756;ko:K02757	NA	
ICBIDGAJ_00107	OG0000015	bglH_1	1	0	0	csr:Cspa_c38060	ko:K01223	NA	
ICBIDGAJ_00108	OG0000314	group_971	1	0	0	fpr:FP2_28070	NA	NA	

ICBIDGAJ_00109	OG0000315	bar	1	0	0	nmg:Nmag_1813	ko:K03823	NA	
ICBIDGAJ_00110	OG0000316	argG_1	1	0	0	fpa:FPR_18280	ko:K01940	NA	
ICBIDGAJ_00111	OG0000317	argH	1	0	0	fpr:FP2_28110	ko:K01755	NA	
ICBIDGAJ_00112	OG0000318	argC	1	0	0	fpa:FPR_18300	ko:K00145	NA	
ICBIDGAJ_00113	OG0000319	argJ	1	0	0	fpa:FPR_18310	ko:K00620	NA	
ICBIDGAJ_00114	OG0000320	argB	1	0	0	fpr:FP2_28140	ko:K00930	NA	
ICBIDGAJ_00115	OG0000321	argD	1	0	0	fpa:FPR_18330	ko:K00821	NA	
ICBIDGAJ_00116	OG0000322	argF_1	1	0	0	fpr:FP2_28170	ko:K00611	NA	
ICBIDGAJ_00117	OG0000323	mepA_1	6	7	12	fpa:FPR_18390	NA	NA	
ICBIDGAJ_00118	OG0002102	group_2773	1	0	0	lacy:A4V08_11070	ko:K05349	NA	
ICBIDGAJ_00119	OG0001680	group_3616	6	6	11	brm:Bmur_2040	NA	NA	
ICBIDGAJ_00120	OG0003049	group_3617	1	1	1	NA	NA	NA	
ICBIDGAJ_00121	OG0001680	uidB	5	6	10	bpw:WESB_1777	NA	NA	
ICBIDGAJ_00122	OG0002103	group_2322	1	1	1	NA	NA	NA	
ICBIDGAJ_00123	OG0002104	group_2775	1	1	1	NA	NA	NA	
ICBIDGAJ_00124	OG0002563	group_4009	1	0	0	bprm:CL3_06100	NA	NA	
ICBIDGAJ_00125	OG0000085	group_4010	0	1	0	cso:CLS_31480;bprm:CL3_06110	NA	NA	
ICBIDGAJ_00126	OG0000121	group_2776	1	0	0	fpr:FP2_04120	ko:K01190	NA	
ICBIDGAJ_00128	OG0000273	group_2545	1	0	0	ibu:IB211_01075c	NA	NA	
ICBIDGAJ_00129	OG0002620	group_2546	0	1	0	NA	NA	NA	
ICBIDGAJ_00130	OG0003847	group_4011	1	0	0	cst:CLOST_0307	NA	specific_fp14	○
ICBIDGAJ_00131	OG0000027	group_2143	1	0	0	dru:Desru_2296;dru:Desru_0118;dru:Desru_2710	ko:K07497	NA	
ICBIDGAJ_00132	OG0000149	group_513	1	0	0	fpa:FPR_00900	ko:K09768	NA	
ICBIDGAJ_00133	OG0000122	group_409	1	0	0	fpa:FPR_00910	NA	NA	
ICBIDGAJ_00134	OG0002164	group_2549	1	0	0	fpv:IA03_10715;fpk:IA06_10645;fpw:IA04_10595;fps:FP2169;fpq:IB65_10930	ko:K07316	NA	
ICBIDGAJ_00135	OG0003516	group_4012	1	0	0	fpr:FP2_12710	ko:K01156	NA	
ICBIDGAJ_00136	OG0003848	group_4013	1	0	0	NA	NA	specific_fp14	○
ICBIDGAJ_00137	OG0003849	group_4014	0	1	0	nin:NADRNF5_1546	NA	specific_fp14	○
ICBIDGAJ_00138	OG0003850	group_4015	1	0	0	NA	NA	specific_fp14	○
ICBIDGAJ_00139	OG0002621	group_2550	1	0	0	NA	NA	NA	
ICBIDGAJ_00140	OG0002622	group_3087	1	0	0	sri:SELR_pSRC600280	NA	NA	
ICBIDGAJ_00141	OG0002408	group_1901	0	1	0	fpa:FPR_19140	NA	NA	
ICBIDGAJ_00142	OG0002623	group_1905	1	0	0	fpla:A4U99_01590	NA	NA	
ICBIDGAJ_00143	OG0003851	group_4016	1	0	0	NA	NA	specific_fp14	○
ICBIDGAJ_00144	OG0001773	group_1906	0	1	0	NA	NA	NA	
ICBIDGAJ_00145	OG0000021	group_404	1	0	0	fpa:FPR_24000	NA	NA	
ICBIDGAJ_00146	OG0000100	group_505	1	0	0	fpa:FPR_15970	NA	NA	
ICBIDGAJ_00147	OG0000101	group_507	1	0	0	fpr:FP2_13880	NA	NA	
ICBIDGAJ_00148	OG0002624	group_4017	1	0	0	fpa:FPR_20470	NA	NA	
ICBIDGAJ_00149	OG0000064	group_2464	1	0	0	fpr:FP2_30030	NA	NA	
ICBIDGAJ_00150	OG0000140	group_2102	0	1	0	fpr:FP2_30020;fpa:FPR_20500	NA	NA	
ICBIDGAJ_00151	OG0000048	group_19	1	0	0	fpa:FPR_20510	NA	NA	
ICBIDGAJ_00152	OG0003852	group_4018	1	0	0	ccl:Clocl_0235	NA	specific_fp14	○
ICBIDGAJ_00153	OG0003853	group_4019	1	0	0	spj:MGAS2096_Spy1119	NA	specific_fp14	○
ICBIDGAJ_00154	OG0000122	group_411	1	0	0	fpa:FPR_00910	NA	NA	
ICBIDGAJ_00155	OG0003854	group_412	0	1	0	fpr:FP2_28180	NA	specific_fp14	○
ICBIDGAJ_00156	OG0002165	mutT	1	0	0	fpr:FP2_04080	ko:K03574	NA	
ICBIDGAJ_00157	OG0002166	radD_1	1	0	0	esu:EUS_17830	NA	NA	
ICBIDGAJ_00158	OG0002409	gloC_1	1	0	0	hsd:SD1D_1282	NA	NA	
ICBIDGAJ_00159	OG0000125	group_4021	3	4	6	csh:Closa_3336	NA	NA	
ICBIDGAJ_00160	OG0000229	group_4022	4	4	7	csh:Closa_3337	NA	NA	
ICBIDGAJ_00161	OG0001865	group_4023	1	0	0	NA	NA	NA	
ICBIDGAJ_00162	OG0001866	yehU	1	1	1	cle:Clole_0505	ko:K07718	NA	
ICBIDGAJ_00163	OG0002117	group_4025	1	0	0	pod:PODO_09280	ko:K02027	NA	
ICBIDGAJ_00164	OG0003855	cesA	1	0	0	sgp:SpiGrapes_1542	NA	specific_fp14	
ICBIDGAJ_00165	OG0000190	group_4027	3	4	6	NA	NA	NA	
ICBIDGAJ_00166	OG0003050	group_2778	4	4	7	NA	NA	NA	
ICBIDGAJ_00167	OG0000324	group_979	1	0	0	fpa:FPR_17590	NA	NA	
ICBIDGAJ_00168	OG0000325	mleN	6	7	12	fpa:FPR_17600	NA	NA	
ICBIDGAJ_00169	OG0001884	group_2779	1	0	0	NA	NA	NA	
ICBIDGAJ_00170	OG0000326	flK	1	0	0	fpr:FP2_32500	NA	NA	
ICBIDGAJ_00171	OG0000327	ziaR	1	0	0	fpa:FPR_17630	NA	NA	
ICBIDGAJ_00172	OG0000328	group_983	0	1	0	fpa:FPR_17640	NA	NA	
ICBIDGAJ_00173	OG0000329	cadA	3	4	6	fpa:FPR_17650	ko:K01534	NA	
ICBIDGAJ_00174	OG0000330	ypdF	1	0	0	fpr:FP2_32360	ko:K01262	NA	
ICBIDGAJ_00175	OG0000331	epsJ_1	1	0	0	fpr:FP2_32350	NA	NA	
ICBIDGAJ_00176	OG0000332	group_986	1	0	0	fpr:FP2_32340	NA	NA	
ICBIDGAJ_00177	OG0000188	yniC	1	0	0	fpa:FPR_10480	NA	NA	
ICBIDGAJ_00178	OG0000333	group_686	1	0	0	fpr:FP2_32320	ko:K07001	NA	
ICBIDGAJ_00179	OG0000334	ptsI_1	1	0	0	fpa:FPR_10460	ko:K08483	NA	
ICBIDGAJ_00180	OG0000335	rsmE	1	0	0	fpr:FP2_32280	ko:K09761	NA	
ICBIDGAJ_00181	OG0000336	prmA	1	0	0	fpa:FPR_10440	ko:K02687	NA	
ICBIDGAJ_00182	OG0001681	nagE	5	6	10	fpa:FPR_18550	ko:K02803;ko:K02804	NA	
ICBIDGAJ_00183	OG0000123	nagB	1	0	0	fpr:FP2_30850	ko:K02564	NA	
ICBIDGAJ_00184	OG0000189	nagA	1	0	0	fpa:FPR_18560	ko:K01443	NA	
ICBIDGAJ_00185	OG0000337	group_687	1	0	0	fpr:FP2_32250	NA	NA	
ICBIDGAJ_00186	OG0002105	group_3621	1	0	0	NA	NA	NA	
ICBIDGAJ_00187	OG0000338	pstS1_1	1	0	0	fpr:FP2_32240	ko:K02040	NA	
ICBIDGAJ_00188	OG0000339	pstC	3	4	6	fpa:FPR_09930	ko:K02037	NA	
ICBIDGAJ_00189	OG0000340	pstA	3	4	6	fpr:FP2_32220	ko:K02038	NA	
ICBIDGAJ_00190	OG0000341	pstB3	1	0	0	fpa:FPR_09950	ko:K02036	NA	
ICBIDGAJ_00191	OG0000342	phoU	1	0	0	fpa:FPR_09960	ko:K02039	NA	
ICBIDGAJ_00192	OG0000343	btr_1	1	0	0	fpr:FP2_32190	NA	NA	
ICBIDGAJ_00193	OG0000344	group_995	1	0	0	fpr:FP2_32180	NA	NA	
ICBIDGAJ_00194	OG0002221	group_2780	1	2	2	NA	NA	NA	
ICBIDGAJ_00195	OG0002352	relJ	0	1	0	fpa:FPR_21210	NA	NA	
ICBIDGAJ_00196	OG0002106	pepV_1	1	0	0	ain:Acin_0145	ko:K01439	NA	
ICBIDGAJ_00197	OG0001885	group_1964	1	0	0	fpr:FP2_32170	ko:K19802	NA	
ICBIDGAJ_00198	OG0000027	group_2139	1	0	0	dru:Desru_0118;dru:Desru_2710;dru:Desru_2296	ko:K07497	NA	
ICBIDGAJ_00199	OG0000345	sstT	4	5	8	fpa:FPR_09800	ko:K07862	NA	
ICBIDGAJ_00200	OG0003051	group_3622	0	1	0	NA	NA	NA	
ICBIDGAJ_00201	OG0000346	group_691	3	3	5	fpr:FP2_32140	NA	NA	
ICBIDGAJ_00202	OG0003856	group_4028	5	5	9	rob:CK5_23910	NA	specific_fp14	
ICBIDGAJ_00203	OG0000347	tkt	1	0	0	fpr:FP2_32130	ko:K00615	NA	
ICBIDGAJ_00204	OG0000348	dxs_1	1	1	1	fpa:FPR_10200	ko:K00615	NA	
ICBIDGAJ_00205	OG0001797	patB	1	0	0	bii:BINDI_0998	ko:K14155	NA	
ICBIDGAJ_00206	OG0001982	murR	1	0	0	fpr:FP2_12040	NA	NA	
ICBIDGAJ_00207	OG0000349	group_999	1	0	0	fpr:FP2_12030	ko:K07137	NA	
ICBIDGAJ_00208	OG0000350	group_692	3	4	6	fpa:FPR_10730	NA	NA	
ICBIDGAJ_00209	OG0000351	mepA_2	6	7	12	elm:ELI_0476	NA	NA	
ICBIDGAJ_00210	OG0000352	cmk_1	1	0	0	fpa:FPR_10710	NA	NA	
ICBIDGAJ_00211	OG0000353	group_1000	1	0	0	fpr:FP2_11990	NA	NA	
ICBIDGAJ_00212	OG0000190	group_1001	3	4	6	fpr:FP2_11980	NA	NA	
ICBIDGAJ_00213	OG0000354	plsC_1	1	1	1	fpa:FPR_10680	ko:K00655	NA	
ICBIDGAJ_00214	OG0000191	group_2327	1	1	1	fpr:FP2_11960	NA	NA	
ICBIDGAJ_00215	OG0000355	group_3623	0	1	0	NA	NA	NA	
ICBIDGAJ_00216	OG0000356	pheA	1	0	0	fpr:FP2_11940	ko:K14170	NA	
ICBIDGAJ_00217	OG0000357	aroB	1	0	0	fpr:FP2_11930	ko:K01735	NA	
ICBIDGAJ_00218	OG0000358	aroC	1	0	0	fpa:FPR_10630	ko:K01736	NA	
ICBIDGAJ_00219	OG0000359	aroE	1	0	0	fpr:FP2_11910	ko:K00014	NA	
ICBIDGAJ_00220	OG0000360	yqhS	1	0	0	fpr:FP2_11900	ko:K03786	NA	
ICBIDGAJ_00221	OG0000361	aroF_1	1	0	0	fpr:FP2_11890	ko:K03856	NA	
ICBIDGAJ_00222	OG0000362	aroA	1	0	0	fpr:FP2_11880	ko:K00800	NA	
ICBIDGAJ_00223	OG0000363	tyrA	1	0	0	fpa:FPR_10580	ko:K04517	NA	

ICBIDGAJ_00224	OG0000364	group_694	1	0	0	fpr:FP2_11860	NA	NA	
ICBIDGAJ_00225	OG0000192	spoVK	1	0	0	fpr:FP2_12050	NA	NA	
ICBIDGAJ_00226	OG0000365	pulA	1	0	0	fpr:FP2_12060	ko:K01200	NA	
ICBIDGAJ_00227	OG0000366	htrA	1	1	1	fpr:FP2_12070	ko:K04771	NA	
ICBIDGAJ_00228	OG0000367	rsmH_1	1	0	0	fpr:FP2_12090	NA	NA	
ICBIDGAJ_00229	OG0000368	prfC	1	0	0	fpr:FP2_12100	ko:K02837	NA	
ICBIDGAJ_00230	OG0000369	yhdN	1	0	0	fpa:FPR_10110	ko:K18471	NA	
ICBIDGAJ_00231	OG0000108	group_516	0	1	0	fpr:FP2_14360	NA	NA	
ICBIDGAJ_00232	OG0001983	acm_1	1	0	0	fpr:FP2_04890	NA	NA	
ICBIDGAJ_00233	OG0001682	group_3625	1	0	0	fpa:FPR_13530	NA	NA	
ICBIDGAJ_00234	OG0000370	group_1013	1	1	1	NA	NA	NA	
ICBIDGAJ_00235	OG0000371	glgB_2	1	0	0	fpa:FPR_13510	ko:K00700	NA	
ICBIDGAJ_00236	OG0000193	glgC	1	0	0	fpr:FP2_14410	ko:K00975	NA	
ICBIDGAJ_00237	OG0000372	glgD	1	0	0	fpa:FPR_13480	ko:K00975	NA	
ICBIDGAJ_00238	OG0000373	glgA	1	0	0	fpr:FP2_14430	ko:K00703	NA	
ICBIDGAJ_00239	OG0003052	group_2784	1	0	0	rto:RTO_05750	NA	NA	
ICBIDGAJ_00240	OG0000374	group_1018	1	2	2	NA	NA	NA	
ICBIDGAJ_00241	OG0000375	group_1019	2	2	3	fpr:FP2_14450	NA	NA	
ICBIDGAJ_00242	OG0000376	atpB_2	3	3	5	fpa:FPR_13440	ko:K02108	NA	
ICBIDGAJ_00243	OG0000377	atpE_2	1	2	2	fpa:FPR_13430	ko:K02110	NA	
ICBIDGAJ_00244	OG0000378	atpF_2	1	1	1	fpa:FPR_13420	ko:K02109	NA	
ICBIDGAJ_00245	OG0000379	atpH	1	0	0	fpa:FPR_13410	ko:K02113	NA	
ICBIDGAJ_00246	OG0000194	atpA_2	1	0	0	fpa:FPR_13400	ko:K02111	NA	
ICBIDGAJ_00247	OG0000195	atpG_2	1	0	0	fpr:FP2_14510	ko:K02115	NA	
ICBIDGAJ_00248	OG0000196	atpD_2	1	0	0	fpr:FP2_14520	ko:K02112	NA	
ICBIDGAJ_00249	OG0000150	atpC_2	1	0	0	fpa:FPR_13370	ko:K02114	NA	
ICBIDGAJ_00250	OG0003053	group_3626	5	6	10	NA	NA	NA	
ICBIDGAJ_00251	OG0000380	aroD	1	0	0	fpa:FPR_01000	ko:K03785	NA	
ICBIDGAJ_00255	OG0000070	group_575	1	1	1	NA	NA	NA	
ICBIDGAJ_00256	OG0000070	group_576	1	1	1	NA	NA	NA	
ICBIDGAJ_00257	OG0000197	rapA_2	1	0	0	fpr:FP2_23420	NA	NA	
ICBIDGAJ_00258	OG0001984	group_2332	1	0	0	fpr:FP2_23430	NA	NA	
ICBIDGAJ_00259	OG0000381	group_1026	1	0	0	fpr:FP2_23440	ko:K01273	NA	
ICBIDGAJ_00260	OG0001886	blaZ	1	0	0	fpr:FP2_23450	ko:K17836	NA	
ICBIDGAJ_00261	OG0000382	group_1027	4	4	7	fpa:FPR_11950	ko:K07090	NA	
ICBIDGAJ_00262	OG0000383	group_1028	1	0	0	fpr:FP2_23470	NA	NA	
ICBIDGAJ_00263	OG0000384	group_2785	1	1	1	fpa:FPR_11970	ko:K07052	NA	
ICBIDGAJ_00264	OG0000385	tadA	1	0	0	fpa:FPR_11980	ko:K11991	NA	
ICBIDGAJ_00265	OG0000386	fabG_1	1	0	0	eha:Ethha_0424	ko:K00059	NA	
ICBIDGAJ_00266	OG0000387	sigA_1	1	0	0	fpr:FP2_23510	ko:K03086	NA	
ICBIDGAJ_00267	OG0000388	group_1032	1	1	1	fpr:FP2_11320	NA	NA	
ICBIDGAJ_00268	OG0000198	ptsH_2	0	1	0	fpr:FP2_11310	ko:K11189	NA	
ICBIDGAJ_00269	OG0000389	ptsI_2	1	0	0	fpr:FP2_11300	ko:K08483	NA	
ICBIDGAJ_00270	OG0000390	fieF	3	3	5	fpr:FP2_11290	NA	NA	
ICBIDGAJ_00271	OG0000391	aspC	1	0	0	fpr:FP2_11280	ko:K11358	NA	
ICBIDGAJ_00272	OG0001683	icd	1	0	0	fpa:FPR_00980	ko:K00031	NA	
ICBIDGAJ_00273	OG0000392	lacL	1	0	0	fpa:FPR_14990	NA	NA	
ICBIDGAJ_00274	OG0000393	group_3627	1	0	0	fpr:FP2_11250	NA	NA	
ICBIDGAJ_00275	OG0000394	mfd	1	0	0	fpa:FPR_15030	ko:K03723	NA	
ICBIDGAJ_00276	OG0000395	pth	1	0	0	fpa:FPR_15040	ko:K01056	NA	
ICBIDGAJ_00277	OG0000396	glmU	1	0	0	fpa:FPR_15060	ko:K04042	NA	
ICBIDGAJ_00278	OG0000397	ppdK	1	0	0	fpa:FPR_15080	ko:K01006	NA	
ICBIDGAJ_00279	OG0002107	pepD_2	1	1	1	fpr:FP2_10900	NA	NA	
ICBIDGAJ_00280	OG0001684	group_2790	1	0	0	fpa:FPR_15480	ko:K07012	NA	
ICBIDGAJ_00281	OG0001685	group_2791	1	0	0	fpa:FPR_15490	ko:K19123	NA	
ICBIDGAJ_00282	OG0001686	group_3631	1	0	0	fpa:FPR_15500	ko:K19046	NA	
ICBIDGAJ_00283	OG0001687	casC	1	0	0	fpa:FPR_15510	ko:K19124	NA	
ICBIDGAJ_00284	OG0001688	group_2792	1	0	0	fpa:FPR_15520	ko:K19125	NA	
ICBIDGAJ_00285	OG0001689	group_3632	1	0	0	fpa:FPR_15530	ko:K19126	NA	
ICBIDGAJ_00286	OG0000398	ltaE	1	0	0	fpr:FP2_25470	ko:K01620	NA	
ICBIDGAJ_00287	OG0000399	crr	1	0	0	fpr:FP2_25460	ko:K02777	NA	
ICBIDGAJ_00288	OG0001887	gltT	4	5	8	bprs:CK3_11880	NA	NA	
ICBIDGAJ_00289	OG0003857	group_4029	1	2	2	NA	NA	specific_fp14	O
ICBIDGAJ_00290	OG0003055	group_3635	6	6	11	cst:CLOST_1866	NA	NA	
ICBIDGAJ_00291	OG0000151	group_2794	1	2	2	fpr:FP2_26300	ko:K06872	NA	
ICBIDGAJ_00292	OG0000152	group_2340	1	1	1	fpr:FP2_26290	NA	NA	
ICBIDGAJ_00293	OG0000153	group_2341	1	0	0	fpr:FP2_26280	NA	NA	
ICBIDGAJ_00294	OG0000401	group_1044	3	3	5	fpa:FPR_05890	NA	NA	
ICBIDGAJ_00295	OG0000402	thiM	1	0	0	fpa:FPR_05880	ko:K00878	NA	
ICBIDGAJ_00296	OG0000199	thiE	1	0	0	fpr:FP2_26250	ko:K00788	NA	
ICBIDGAJ_00297	OG0000403	thiC	1	0	0	fpa:FPR_05860	ko:K03147	NA	
ICBIDGAJ_00298	OG0000404	yidA	1	0	0	fpa:FPR_12240	NA	NA	
ICBIDGAJ_00299	OG0000405	polC_1	1	0	0	fpa:FPR_12250	NA	NA	
ICBIDGAJ_00300	OG0000406	ydjZ	3	3	5	fpr:FP2_25260	NA	NA	
ICBIDGAJ_00301	OG0000407	cysS	1	0	0	fpr:FP2_15130	ko:K01883	NA	
ICBIDGAJ_00302	OG0000408	group_2342	1	1	1	fpr:FP2_25050	NA	NA	
ICBIDGAJ_00303	OG0000409	dnaJ_1	1	0	0	fpr:FP2_25060	ko:K03686	NA	
ICBIDGAJ_00304	OG0000410	group_1049	1	0	0	fpr:FP2_25070	NA	NA	
ICBIDGAJ_00305	OG0000411	group_707	1	2	2	fpa:FPR_14650	NA	NA	
ICBIDGAJ_00306	OG0000412	lacZ_1	1	0	0	fpa:FPR_14660	ko:K01190	NA	
ICBIDGAJ_00307	OG0003056	group_2795	1	1	1	NA	NA	NA	
ICBIDGAJ_00308	OG0003057	group_3636	1	0	0	NA	NA	NA	
ICBIDGAJ_00309	OG0000413	sgcG	1	0	0	fpr:FP2_25100	NA	NA	
ICBIDGAJ_00310	OG0000414	rsmD	1	0	0	fpr:FP2_25110	ko:K08316	NA	
ICBIDGAJ_00311	OG0000415	group_1053	1	0	0	fpr:FP2_25120	NA	NA	
ICBIDGAJ_00312	OG0000416	rsmH_2	1	0	0	fpr:FP2_25130	ko:K03438	NA	
ICBIDGAJ_00313	OG0000417	ftsL_1	1	0	0	fpr:FP2_25140	NA	NA	
ICBIDGAJ_00314	OG0000418	spoVD_1	1	1	1	fpa:FPR_14740	ko:K08384	NA	
ICBIDGAJ_00315	OG0000419	murF	1	0	0	fpa:FPR_14750	ko:K01929	NA	
ICBIDGAJ_00316	OG0000420	mraY_1	6	5	10	fpr:FP2_25170	ko:K01000	NA	
ICBIDGAJ_00317	OG0000421	ftsW_1	4	5	8	fpr:FP2_25180	ko:K03588	NA	
ICBIDGAJ_00318	OG0000422	murG	1	0	0	fpa:FPR_14790	ko:K02563	NA	
ICBIDGAJ_00319	OG0000423	group_2796	1	1	1	fpr:FP2_25200	ko:K03589	NA	
ICBIDGAJ_00320	OG0000424	murE	1	0	0	fpa:FPR_14810	ko:K01928	NA	
ICBIDGAJ_00321	OG0001888	group_1974	7	6	12	fpr:FP2_25500	NA	NA	
ICBIDGAJ_00322	OG0001889	kdpE_1	1	0	0	fpr:FP2_25490	ko:K07667	NA	
ICBIDGAJ_00323	OG0001890	kdpD_1	2	3	4	fpr:FP2_25480	ko:K07646	NA	
ICBIDGAJ_00324	OG0000029	group_388	1	0	0	fpa:FPR_02700	ko:K03431	NA	
ICBIDGAJ_00325	OG0000425	group_2797	1	2	2	NA	NA	NA	
ICBIDGAJ_00326	OG0002109	group_2798	1	0	0	NA	NA	NA	
ICBIDGAJ_00327	OG0001867	group_4030	0	1	0	fpr:FP2_12630	NA	NA	
ICBIDGAJ_00328	OG0003157	group_4031	1	0	0	fpr:FP2_12590	NA	NA	
ICBIDGAJ_00329	OG0003858	group_4032	1	0	0	fpr:FP2_12580	NA	specific_fp14	
ICBIDGAJ_00330	OG0000426	lepA	1	0	0	fpa:FPR_13830	ko:K03596	NA	
ICBIDGAJ_00331	OG0000427	alr1	1	0	0	fpa:FPR_13840	ko:K01775	NA	
ICBIDGAJ_00332	OG0001985	group_1976	1	0	0	fpr:FP2_10310	NA	NA	
ICBIDGAJ_00333	OG0000428	group_2345	1	1	1	fpr:FP2_10300	NA	NA	
ICBIDGAJ_00334	OG0000429	rplM	1	0	0	fpa:FPR_13870	ko:K02871	NA	
ICBIDGAJ_00335	OG0000430	rpsI	1	0	0	fpa:FPR_13880	ko:K02996	NA	
ICBIDGAJ_00336	OG0002057	group_2201	1	0	0	csh:Closa_3728	NA	NA	
ICBIDGAJ_00337	OG0002151	group_4033	1	0	0	tpi:TREPR_3038	NA	NA	
ICBIDGAJ_00338	OG0000189	nagA_2	1	0	0	gfe:Gferi_07175	ko:K01443	NA	
ICBIDGAJ_00339	OG0003859	group_4035	1	0	0	NA	NA	specific_fp14	
ICBIDGAJ_00340	OG0002294	group_4036	3	3	5	rum:CK1_13620	ko:K02796	NA	

ICBIDGAJ_00341	OG0001677	group_4037	4	5	8	NA	NA	NA	
ICBIDGAJ_00342	OG0002295	group_4038	1	0	0	acg:AWM71_06015	ko:K02794	NA	
ICBIDGAJ_00343	OG0002410	manX	1	0	0	NA	NA	NA	
ICBIDGAJ_00344	OG0002411	group_4039	1	0	0	NA	NA	NA	
ICBIDGAJ_00345	OG0002127	group_2884	1	0	0	ibu:IB211_01831c	ko:K12267	NA	
ICBIDGAJ_00346	OG0000781	resA	1	1	1	bprs:CK3_14300	NA	NA	
ICBIDGAJ_00347	OG0000782	yccM_2	2	2	3	ibu:IB211_01833c	NA	NA	
ICBIDGAJ_00348	OG0000783	group_2038	1	1	1	ibu:IB211_01834c	NA	NA	
ICBIDGAJ_00349	OG0000165	ctrA	1	0	0	ruk:A4V00_13775	NA	NA	
ICBIDGAJ_00350	OG0000784	arlS	2	1	2	ruk:A4V00_13770	NA	NA	
ICBIDGAJ_00351	OG0000431	ylaC	1	0	0	fpa:FPR_18220	ko:K03088	NA	
ICBIDGAJ_00352	OG0001801	group_3638	1	1	1	fpa:FPR_18210	NA	NA	
ICBIDGAJ_00353	OG0000432	group_1063	1	1	1	fpr:FP2_12140	NA	NA	
ICBIDGAJ_00354	OG0000433	group_1064	1	1	1	NA	NA	NA	
ICBIDGAJ_00355	OG0000434	mutY	1	0	0	cls:CXIVA_05380	ko:K03575	NA	
ICBIDGAJ_00356	OG0000435	asnS	1	0	0	fpr:FP2_12170	ko:K01893	NA	
ICBIDGAJ_00357	OG0001986	group_3639	2	1	2	NA	NA	NA	
ICBIDGAJ_00358	OG0000436	group_709	1	1	1	fpr:FP2_12180	ko:K06385	NA	
ICBIDGAJ_00359	OG0000437	gpr	1	0	0	fpr:FP2_12190	ko:K06012	NA	
ICBIDGAJ_00360	OG0000438	rpsT	0	1	0	fpa:FPR_18100;fpr:FP2_12200	ko:K02968	NA	
ICBIDGAJ_00361	OG0002110	group_3640	1	2	2	fpa:FPR_18090	NA	NA	
ICBIDGAJ_00362	OG0000439	group_1066	2	2	3	fpr:FP2_12220	ko:K06407	NA	
ICBIDGAJ_00363	OG0000440	spoVAD	1	0	0	fpa:FPR_18070	ko:K06406	NA	
ICBIDGAJ_00364	OG0000441	group_711	2	3	4	fpr:FP2_12240	ko:K06405	NA	
ICBIDGAJ_00365	OG0000442	vanYB	1	1	1	fpr:FP2_12250	ko:K07260	NA	
ICBIDGAJ_00366	OG0000443	group_1977	1	0	0	fpa:FPR_18040	NA	NA	
ICBIDGAJ_00367	OG0000444	patA_3	6	6	11	cpf:CPF_1766	ko:K19294	NA	
ICBIDGAJ_00368	OG0000445	group_712	1	1	1	fpa:FPR_18020	NA	NA	
ICBIDGAJ_00369	OG0001690	group_3641	1	2	2	fpr:FP2_12290	NA	NA	
ICBIDGAJ_00370	OG0000154	group_3642	2	1	2	NA	NA	NA	
ICBIDGAJ_00371	OG0000446	group_1069	1	0	0	fpa:FPR_10390	ko:K03671	NA	
ICBIDGAJ_00372	OG0002563	group_3643	1	0	0	ere:EUBREC_3011	NA	NA	
ICBIDGAJ_00373	OG0000085	group_3644	1	0	0	era:ERE_12040;ere:EUBREC_3010	NA	NA	
ICBIDGAJ_00374	OG0000447	hisG	1	0	0	fpa:FPR_17570	NA	NA	
ICBIDGAJ_00375	OG0000448	hisD	1	0	0	fpa:FPR_17560	ko:K00013	NA	
ICBIDGAJ_00376	OG0000449	hisC	1	0	0	fpa:FPR_17550	ko:K00817	NA	
ICBIDGAJ_00377	OG0000450	hisB	1	0	0	fpa:FPR_17540	ko:K01693	NA	
ICBIDGAJ_00378	OG0000451	hisH	1	0	0	fpa:FPR_17530	ko:K02501	NA	
ICBIDGAJ_00379	OG0000452	hisA	1	0	0	fpa:FPR_17520	ko:K01814	NA	
ICBIDGAJ_00380	OG0000453	hisF	1	0	0	fpa:FPR_17510	ko:K02500	NA	
ICBIDGAJ_00381	OG0000454	hisI	1	0	0	fpa:FPR_17500	ko:K11755	NA	
ICBIDGAJ_00382	OG0000455	hisK	1	0	0	fpr:FP2_32050	ko:K04486	NA	
ICBIDGAJ_00383	OG0000456	mepA_3	6	7	12	fpa:FPR_17480	NA	NA	
ICBIDGAJ_00384	OG0000457	pyrE_1	1	0	0	fpr:FP2_32010	ko:K00762	NA	
ICBIDGAJ_00385	OG0000124	group_4040	1	0	0	NA	NA	NA	
ICBIDGAJ_00386	OG0000458	group_3646	1	0	0	fpr:FP2_31990	NA	NA	
ICBIDGAJ_00387	OG0000459	immR_3	1	0	0	fpa:FPR_18630	NA	NA	
ICBIDGAJ_00388	OG0000460	cobC	1	0	0	fpr:FP2_31970	ko:K02226	NA	
ICBIDGAJ_00389	OG0000461	group_1081	1	1	1	fpa:FPR_18600	NA	NA	
ICBIDGAJ_00390	OG0000462	yerB_2	1	0	0	fpr:FP2_31950	NA	NA	
ICBIDGAJ_00391	OG0000463	yerB_1	1	1	1	fpr:FP2_31940	NA	NA	
ICBIDGAJ_00393	OG0000025	group_317	1	0	0	fpr:FP2_13920	NA	NA	
ICBIDGAJ_00394	OG0000026	group_327	1	0	0	fpa:FPR_09490	NA	NA	
ICBIDGAJ_00395	OG0002412	group_2204	1	0	0	elm:ELI_1142	ko:K06919	NA	
ICBIDGAJ_00396	OG0002413	group_2551	1	0	0	fpa:FPR_23820	NA	NA	
ICBIDGAJ_00397	OG0002604	group_4041	1	0	0	det:DET1114	ko:K01156	NA	
ICBIDGAJ_00398	OG0002387	group_4042	1	0	0	scd:Spica_0102	ko:K07316	NA	
ICBIDGAJ_00399	OG0003860	group_4043	1	0	0	mox:DAMO_2836	ko:K07316	specific_fp14	○
ICBIDGAJ_00400	OG0002387	group_4044	1	0	0	det:DET1112	ko:K07316	NA	
ICBIDGAJ_00401	OG0002384	group_4045	1	0	0	osp:Odosp_1818	NA	NA	
ICBIDGAJ_00402	OG0002605	group_4046	1	0	0	det:DET1110	NA	NA	
ICBIDGAJ_00403	OG0002606	group_4047	1	0	0	det:DET1109	NA	NA	
ICBIDGAJ_00404	OG0002566	group_2803	1	0	0	med:MELS_0834	NA	NA	
ICBIDGAJ_00405	OG0000025	group_318	1	0	0	fpr:FP2_13920	NA	NA	
ICBIDGAJ_00406	OG0000026	group_328	1	0	0	fpr:FP2_28450;fpa:FPR_09490;fpr:FP2_19750	NA	NA	
ICBIDGAJ_00407	OG0000465	group_2802	1	0	0	med:MELS_0988	NA	NA	
ICBIDGAJ_00408	OG0003058	group_3659	1	0	0	NA	NA	NA	
ICBIDGAJ_00409	OG0003059	group_2349	1	0	0	NA	NA	NA	
ICBIDGAJ_00410	OG0002354	hsdR_1	1	0	0	fpr:FP2_18260	ko:K01153	NA	
ICBIDGAJ_00411	OG0002414	lacI	1	0	0	rho:RHOM_01140	ko:K02529	NA	
ICBIDGAJ_00412	OG0001361	group_4049	1	2	2	rho:RHOM_01145	NA	NA	
ICBIDGAJ_00413	OG0001705	group_2883	1	0	0	fpa:FPR_03330	NA	NA	
ICBIDGAJ_00414	OG0002253	group_2882	1	0	0	rim:ROI_39990;rix:RO1_00280	NA	NA	
ICBIDGAJ_00415	OG0000130	ypdB_2	1	0	0	fpa:FPR_03350	NA	NA	
ICBIDGAJ_00416	OG0002252	group_2400	4	4	7	rim:ROI_39970;rix:RO1_00260	NA	NA	
ICBIDGAJ_00417	OG0003062	rhaS_1	1	1	1	NA	NA	NA	
ICBIDGAJ_00418	OG0003063	group_3677	1	0	0	pjd:Pjdr2_1762	NA	NA	
ICBIDGAJ_00419	OG0000125	group_3678	3	4	6	pow:IJ21_09600	ko:K17320	NA	
ICBIDGAJ_00420	OG0003064	group_3679	3	3	5	mas:Mahau_0139	ko:K17319	NA	
ICBIDGAJ_00421	OG0003065	group_3680	1	0	0	NA	NA	NA	
ICBIDGAJ_00422	OG0003066	yteT	1	0	0	NA	NA	NA	
ICBIDGAJ_00423	OG0000467	group_3682	1	0	0	fpa:FPR_14920	ko:K01126	NA	
ICBIDGAJ_00424	OG0000015	bglH	1	0	0	fpa:FPR_14930	ko:K01223	NA	
ICBIDGAJ_00425	OG0000468	purC	1	0	0	fpr:FP2_25330	ko:K01923	NA	
ICBIDGAJ_00426	OG0000469	serA	1	0	0	fpa:FPR_01890	ko:K00058	NA	
ICBIDGAJ_00427	OG0000470	serC	1	0	0	fpa:FPR_01900	ko:K00831	NA	
ICBIDGAJ_00428	OG0000471	blaI	1	0	0	fpa:FPR_01910	NA	NA	
ICBIDGAJ_00429	OG0000472	rlmCD_1	1	0	0	fpr:FP2_24980	ko:K03215	NA	
ICBIDGAJ_00430	OG0003067	group_3683	1	0	0	byl:A4V09_22410	NA	NA	
ICBIDGAJ_00431	OG0001692	yeaJ_1	4	4	7	fpa:FPR_01310	NA	NA	
ICBIDGAJ_00432	OG0000473	group_1085	3	2	4	rho:RHOM_04715	NA	NA	
ICBIDGAJ_00433	OG0000474	group_1086	3	3	5	fpr:FP2_26090	ko:K06147	NA	
ICBIDGAJ_00434	OG0000475	tig_3	1	0	0	fpr:FP2_26070	NA	NA	
ICBIDGAJ_00435	OG0000476	group_1087	2	1	2	fpr:FP2_26060	NA	NA	
ICBIDGAJ_00437	OG0001891	group_2810	1	0	0	fpla:A4U99_12610	NA	NA	
ICBIDGAJ_00438	OG0002112	group_2354	0	1	0	NA	NA	NA	
ICBIDGAJ_00439	OG0000200	group_3837	0	1	0	fpa:FPR_01280	NA	NA	
ICBIDGAJ_00440	OG0002137	fliA_2	1	0	0	fpa:FPR_01270	NA	NA	
ICBIDGAJ_00441	OG0003158	group_3089	2	2	3	NA	NA	NA	
ICBIDGAJ_00442	OG0002058	group_4050	6	7	12	rto:RTO_12820	ko:K01992	NA	
ICBIDGAJ_00443	OG0001927	group_4051	1	0	0	rto:RTO_12810	ko:K01990	NA	
ICBIDGAJ_00444	OG0003861	group_4052	2	2	3	rto:RTO_12800	NA	specific_fp14	○
ICBIDGAJ_00445	OG0003862	group_4053	3	4	6	rto:RTO_12790	NA	specific_fp14	○
ICBIDGAJ_00446	OG0001723	group_2077	1	0	0	fpa:FPR_01210	NA	NA	
ICBIDGAJ_00447	OG0000201	group_2814	0	1	0	fpa:FPR_01200	NA	NA	
ICBIDGAJ_00448	OG0000155	group_717	1	0	0	fpa:FPR_01190	NA	NA	
ICBIDGAJ_00449	OG0002378	group_2941	1	0	0	fpa:FPR_01180	NA	NA	
ICBIDGAJ_00450	OG0003863	group_4054	1	0	0	bacc:BRDCF_p387	NA	specific_fp14	○
ICBIDGAJ_00451	OG0001803	group_722	1	0	0	fpa:FPR_01130	NA	NA	
ICBIDGAJ_00452	OG0002115	group_2358	1	0	0	efau:EFAU085_00722;efc:EFAU004_02788	NA	NA	
ICBIDGAJ_00453	OG0000071	group_724	1	0	0	fpa:FPR_01110	NA	NA	
ICBIDGAJ_00454	OG0000056	group_728	1	0	0	efau:EFAU085_00720;efc:EFAU004_02790	ko:K03169	NA	
ICBIDGAJ_00455	OG0000477	group_1089	1	2	2	fpa:FPR_13260	NA	NA	
ICBIDGAJ_00456	OG0000072	group_2818	0	1	0	fpa:FPR_13250	NA	NA	

ICBIDGAJ_00457	OG0000110	iap_6	1	1	1	efau:EFAU085_00717;efc:EFAU004_02793	NA	NA	
ICBIDGAJ_00458	OG0001893	group_1987	1	0	0	fpa:FPR_13230	ko:K00558	NA	
ICBIDGAJ_00459	OG0001693	group_3688	1	0	0	efau:EFAU085_00716	NA	NA	
ICBIDGAJ_00460	OG0001694	group_3692	3	3	5	efc:EFAU004_02796;efau:EFAU085_00714	NA	NA	
ICBIDGAJ_00461	OG0001804	group_227	1	2	2	fpa:FPR_13190	NA	NA	
ICBIDGAJ_00462	OG0000202	traG	1	0	0	fpa:FPR_13180	ko:K03205	NA	
ICBIDGAJ_00463	OG0000156	group_1991	1	0	0	efc:EFAU004_02799;efau:EFAU085_00687	NA	NA	
ICBIDGAJ_00464	OG0000057	group_2820	1	0	0	fpa:FPR_13160	NA	NA	
ICBIDGAJ_00465	OG0000478	alsT_1	5	5	9	rob:CK5_16720	ko:K03310	NA	
ICBIDGAJ_00467	OG0002116	group_3694	1	1	1	NA	NA	NA	
ICBIDGAJ_00468	OG0001990	rbn	1	0	0	fpr:FP2_24410	ko:K00784	NA	
ICBIDGAJ_00469	OG0000479	group_3695	1	0	0	fpa:FPR_15750	ko:K00974	NA	
ICBIDGAJ_00470	OG0000480	mnmA_1	1	0	0	fpr:FP2_24430	ko:K00566	NA	
ICBIDGAJ_00471	OG0000481	tcdA	1	0	0	fpr:FP2_24440	NA	NA	
ICBIDGAJ_00472	OG0000482	tdcB	1	0	0	fpr:FP2_26200	ko:K01754	NA	
ICBIDGAJ_00473	OG0000483	ruvB_1	1	0	0	fpa:FPR_15880	ko:K06923	NA	
ICBIDGAJ_00474	OG0000126	ilvB	1	0	0	fpa:FPR_15890	ko:K01652	NA	
ICBIDGAJ_00475	OG0000484	ilvH	1	0	0	fpa:FPR_15900	ko:K01653	NA	
ICBIDGAJ_00476	OG0000485	ilvC	1	0	0	fpa:FPR_15910	ko:K00053	NA	
ICBIDGAJ_00477	OG0000486	ilvD_2	1	0	0	fpa:FPR_15920	ko:K01687	NA	
ICBIDGAJ_00479	OG0000487	group_3696	1	2	2	NA	NA	NA	
ICBIDGAJ_00480	OG0000488	sigR	1	0	0	fpr:FP2_23830	ko:K03088	NA	
ICBIDGAJ_00481	OG0000489	group_1106	1	0	0	fpr:FP2_23840	NA	NA	
ICBIDGAJ_00482	OG0000490	argF_2	1	0	0	fpa:FPR_16420	ko:K00611	NA	
ICBIDGAJ_00483	OG0000491	ribD_1	0	1	0	fpr:FP2_23870	ko:K01493	NA	
ICBIDGAJ_00484	OG0000492	fusA_1	1	0	0	fpa:FPR_16450	ko:K02355	NA	
ICBIDGAJ_00485	OG0000493	flr	0	1	0	fpr:FP2_30430	NA	NA	
ICBIDGAJ_00486	OG0000494	ykoT	1	2	2	fpa:FPR_05500	NA	NA	
ICBIDGAJ_00487	OG0000495	fixK	1	0	0	fpr:FP2_30450	NA	NA	
ICBIDGAJ_00488	OG0000496	mqnD	1	1	1	fpr:FP2_30460	ko:K02051	NA	
ICBIDGAJ_00489	OG0000497	ssuC	3	3	5	fpr:FP2_30480	ko:K02050	NA	
ICBIDGAJ_00490	OG0000498	artM	1	0	0	fpr:FP2_30490	NA	NA	
ICBIDGAJ_00491	OG0000499	hemN	1	0	0	fpr:FP2_30510	NA	NA	
ICBIDGAJ_00492	OG0000500	ybhL	3	4	6	fpr:FP2_30520	ko:K06890	NA	
ICBIDGAJ_00493	OG0000501	spoIIQ	1	1	1	fpr:FP2_30550	NA	NA	
ICBIDGAJ_00494	OG0000502	group_1116	1	0	0	fpa:FPR_02090	ko:K07007	NA	
ICBIDGAJ_00495	OG0000503	cmk_2	1	0	0	fpr:FP2_30570	ko:K00945	NA	
ICBIDGAJ_00496	OG0000504	plsC_2	1	1	1	fpa:FPR_02110	ko:K00655	NA	
ICBIDGAJ_00497	OG0000505	rpsA_1	1	0	0	fpa:FPR_02120	ko:K02945;ko:K03527	NA	
ICBIDGAJ_00498	OG0000506	group_732	2	3	4	fpr:FP2_30610	NA	NA	
ICBIDGAJ_00499	OG0000507	group_1994	1	1	1	fpa:FPR_02140	NA	NA	
ICBIDGAJ_00500	OG0000508	deoC	1	0	0	fpa:FPR_02150	ko:K01619	NA	
ICBIDGAJ_00501	OG0000157	metK	1	0	0	fpa:FPR_02170	ko:K00789	NA	
ICBIDGAJ_00502	OG0000509	yeeO_1	5	6	10	fpa:FPR_03450	NA	NA	
ICBIDGAJ_00503	OG0000510	exoA	1	0	0	fpr:FP2_15310	ko:K01142	NA	
ICBIDGAJ_00504	OG0000511	group_1123	2	3	4	fpa:FPR_03470	NA	NA	
ICBIDGAJ_00505	OG0000512	pepV_2	1	0	0	fpa:FPR_03480	ko:K01439	NA	
ICBIDGAJ_00506	OG0000513	group_733	1	0	0	fpa:FPR_03490	NA	NA	
ICBIDGAJ_00507	OG0000514	cysE	1	0	0	fpr:FP2_15350	ko:K00640	NA	
ICBIDGAJ_00508	OG0000515	pyrC	1	0	0	fpr:FP2_15380	ko:K01465	NA	
ICBIDGAJ_00509	OG0000516	pyrF	1	0	0	fpr:FP2_15390	ko:K01591	NA	
ICBIDGAJ_00510	OG0000517	pyrK	1	0	0	fpa:FPR_16790	ko:K02823	NA	
ICBIDGAJ_00511	OG0000518	pyrDB	1	0	0	fpa:FPR_16800	ko:K17828	NA	
ICBIDGAJ_00512	OG0000519	pyrE_2	1	0	0	fpr:FP2_15420	ko:K00762	NA	
ICBIDGAJ_00513	OG0000520	carA	1	0	0	fpr:FP2_15430	ko:K01956	NA	
ICBIDGAJ_00514	OG0000521	carB	1	0	0	fpr:FP2_15440	ko:K01955	NA	
ICBIDGAJ_00515	OG0000522	hup_1	1	0	0	fpr:FP2_15450	ko:K03530	NA	
ICBIDGAJ_00516	OG0000523	cshA	1	0	0	fpa:FPR_16850	ko:K05592	NA	
ICBIDGAJ_00517	OG0001695	nolA	1	2	2	fpa:FPR_16860	NA	NA	
ICBIDGAJ_00518	OG0001696	group_1999	1	0	0	fpa:FPR_16870	NA	NA	
ICBIDGAJ_00519	OG0001697	group_2000	4	5	8	fpa:FPR_16880	NA	NA	
ICBIDGAJ_00523	OG0000073	group_2001	1	0	0	fpa:FPR_31730	ko:K10947	NA	
ICBIDGAJ_00524	OG0001698	group_2002	2	3	4	fpa:FPR_31720	NA	NA	
ICBIDGAJ_00525	OG0000524	group_1132	1	0	0	fpa:FPR_12380	NA	NA	
ICBIDGAJ_00526	OG0003864	group_581	1	0	0	NA	NA	specific_fp14	O
ICBIDGAJ_00527	OG0000525	group_580	1	0	0	rho:RHOM_09380	NA	NA	
ICBIDGAJ_00528	OG0000526	group_582	1	0	0	fpr:FP2_23790	NA	NA	
ICBIDGAJ_00529	OG0000527	group_3697	1	1	1	NA	NA	NA	
ICBIDGAJ_00530	OG0000528	glnS	1	0	0	fpr:FP2_23770	ko:K01886	NA	
ICBIDGAJ_00532	OG0000000	group_37	0	1	0	fpa:FPR_08500	NA	NA	
ICBIDGAJ_00533	OG0002059	group_915	1	0	0	fpa:FPR_03190	NA	NA	
ICBIDGAJ_00534	OG0000018	group_171	1	0	0	fpr:FP2_29840	NA	NA	
ICBIDGAJ_00535	OG0000065	group_177	0	1	0	fpa:FPR_03220	NA	NA	
ICBIDGAJ_00536	OG0002625	group_4055	4	3	6	lsa:LCA_1347	ko:K07150	NA	
ICBIDGAJ_00537	OG0002296	group_4056	1	0	0	fpr:FP2_08870	ko:K01684	shared	
ICBIDGAJ_00538	OG0000141	nlhH	1	0	0	NA	NA	NA	
ICBIDGAJ_00539	OG0002626	group_4058	5	6	10	fpr:FP2_08890	NA	NA	
ICBIDGAJ_00540	OG0000169	tetD	1	0	0	fpr:FP2_08900	NA	NA	
ICBIDGAJ_00541	OG0000048	group_35	1	0	0	fpr:FP2_17170	NA	NA	
ICBIDGAJ_00542	OG0002355	group_3698	0	1	0	NA	NA	NA	
ICBIDGAJ_00543	OG0002573	group_2824	1	0	0	fpr:FP2_01650	NA	NA	
ICBIDGAJ_00544	OG0000529	cymR_1	1	0	0	fpa:FPR_12060	NA	NA	
ICBIDGAJ_00545	OG0000530	cysK1	1	0	0	fpr:FP2_22970	ko:K01738	NA	
ICBIDGAJ_00546	OG0000531	dusC	1	0	0	fpr:FP2_22860	NA	NA	
ICBIDGAJ_00547	OG0000532	group_1137	1	0	0	ccel:CCDG5_0595	NA	NA	
ICBIDGAJ_00548	OG0000533	acpS	1	0	0	fpr:FP2_22880	ko:K00997	NA	
ICBIDGAJ_00549	OG0000203	ndoA_1	1	0	0	fpr:FP2_22890	ko:K07171	NA	
ICBIDGAJ_00550	OG0000534	mntR	1	0	0	fpr:FP2_22900	NA	NA	
ICBIDGAJ_00551	OG0000535	prs	1	0	0	fpa:FPR_02180	ko:K00948	NA	
ICBIDGAJ_00552	OG0000536	fumA	1	0	0	fpa:FPR_11900	ko:K01678	NA	
ICBIDGAJ_00553	OG0000537	ttdA	1	0	0	fpa:FPR_11890	ko:K01677	NA	
ICBIDGAJ_00554	OG0000538	group_2003	1	0	0	fpa:FPR_11880	ko:K00027	NA	
ICBIDGAJ_00555	OG0000539	tig_5	1	0	0	cct:CC1_00890	ko:K03545	NA	
ICBIDGAJ_00556	OG0000540	clpB1	1	0	0	fpr:FP2_22980	ko:K03695	NA	
ICBIDGAJ_00557	OG0000541	tlyC	3	2	4	fpa:FPR_14520	NA	NA	
ICBIDGAJ_00558	OG0000542	group_1145	1	1	1	fpr:FP2_26520	ko:K06381	NA	
ICBIDGAJ_00559	OG0000543	epsE	1	0	0	fpr:FP2_26530	ko:K20444	NA	
ICBIDGAJ_00560	OG0000544	wbbL_2	1	0	0	fpa:FPR_02840	NA	NA	
ICBIDGAJ_00561	OG0000545	rfbA	1	0	0	fpa:FPR_02850	ko:K00973	NA	
ICBIDGAJ_00562	OG0000546	rmlD_2	1	0	0	fpr:FP2_26560	ko:K00067	NA	
ICBIDGAJ_00563	OG0000204	rffG	1	0	0	fpr:FP2_26570	ko:K01710	NA	
ICBIDGAJ_00564	OG0000547	pfp_4	1	0	0	fpr:FP2_26310	ko:K21071	NA	
ICBIDGAJ_00567	OG0000548	group_2364	4	5	8	fpr:FP2_26320	ko:K07052	NA	
ICBIDGAJ_00568	OG0001699	pepD_1	1	0	0	fpr:FP2_26700	ko:K08659	NA	
ICBIDGAJ_00569	OG0000549	group_2826	1	1	1	fpr:FP2_26750	NA	NA	
ICBIDGAJ_00570	OG0000550	lrpC	1	0	0	fpr:FP2_26740	ko:K03719	NA	
ICBIDGAJ_00571	OG0000551	hflX	1	0	0	fpa:FPR_04870	ko:K03665	NA	
ICBIDGAJ_00572	OG0000552	group_2365	1	0	0	fpr:FP2_27000	NA	NA	
ICBIDGAJ_00573	OG0000553	yitJ	1	0	0	fpr:FP2_27030	ko:K00547;ko:K00297	NA	
ICBIDGAJ_00574	OG0000158	valS	1	0	0	fpr:FP2_27060	ko:K01873	NA	
ICBIDGAJ_00575	OG0000159	group_2366	1	2	2	fpr:FP2_27070	NA	NA	
ICBIDGAJ_00576	OG0000127	fpgS_2	1	0	0	fpr:FP2_27080	ko:K11754	NA	
ICBIDGAJ_00577	OG0000205	spoIIAA	1	0	0	fpr:FP2_27090	ko:K06378	NA	
ICBIDGAJ_00578	OG0000206	spoIIAB	0	1	0	fpr:FP2_27100	ko:K06379	NA	

ICBIDGAJ_00579	OG0000128	sigF	1	0	0	fpr:FP2_27110	ko:K03091	NA
ICBIDGAJ_00587	OG0000000	group_46	0	1	0	fpa:FPR_24750	NA	NA
ICBIDGAJ_00588	OG0002403	crp_2	1	0	0	rho:RHOM_00095	NA	NA
ICBIDGAJ_00589	OG0002612	hadI_1	1	0	0	fpr:FP2_27770	NA	NA
ICBIDGAJ_00590	OG0002404	group_2148	1	0	0	rho:RHOM_00075	NA	NA
ICBIDGAJ_00591	OG0002613	group_3041	1	0	0	fpr:FP2_27790	ko:K02013	NA
ICBIDGAJ_00592	OG0002614	group_2510	4	5	8	fpr:FP2_27800	ko:K02015	NA
ICBIDGAJ_00593	OG0002289	yfmC	1	0	0	fpr:FP2_27810	ko:K02016	NA
ICBIDGAJ_00594	OG0001774	group_1909	1	0	0	fpr:FP2_29830	NA	NA
ICBIDGAJ_00595	OG0001851	group_2552	1	2	2	cct:CC1_32160	NA	NA
ICBIDGAJ_00596	OG0001852	group_3042	1	0	0	cct:CC1_32170	NA	NA
ICBIDGAJ_00597	OG0002041	group_180	0	1	0	NA	NA	NA
ICBIDGAJ_00598	OG0002152	ctpC	1	1	1	fpa:FPR_03390	NA	NA
ICBIDGAJ_00599	OG0001748	yccM_3	3	4	6	fpa:FPR_03400	NA	NA
ICBIDGAJ_00600	OG0001749	group_2150	1	1	1	fpa:FPR_03410	NA	NA
ICBIDGAJ_00601	OG0001394	rsxG_2	1	1	1	fpa:FPR_03420	NA	NA
ICBIDGAJ_00602	OG0001853	group_2151	1	1	1	fpa:FPR_03430	NA	NA
ICBIDGAJ_00603	OG0002615	group_3043	1	0	0	rim:ROI_15360	NA	NA
ICBIDGAJ_00604	OG0001750	baeB	1	0	0	fpa:FPR_07060	NA	NA
ICBIDGAJ_00605	OG0001751	group_883	1	0	0	fpr:FP2_27870	NA	NA
ICBIDGAJ_00606	OG0002153	group_1723	3	2	4	fpa:FPR_07090	NA	NA
ICBIDGAJ_00607	OG0002154	group_2512	1	0	0	esr:ES1_24850	NA	NA
ICBIDGAJ_00608	OG0001395	group_479	1	0	0	fpa:FPR_07130	NA	NA
ICBIDGAJ_00609	OG0001752	group_884	0	1	0	fpa:FPR_07140	NA	NA
ICBIDGAJ_00610	OG0001854	group_3960	2	2	3	fpa:FPR_07150	NA	NA
ICBIDGAJ_00611	OG0003143	group_3961	1	2	2	fpa:FPR_07440	ko:K07238	NA
ICBIDGAJ_00612	OG0001920	rob	1	0	0	NA	NA	NA
ICBIDGAJ_00613	OG0002042	group_3963	1	0	0	shi:Shel_21750	NA	NA
ICBIDGAJ_00614	OG0001753	irtA	3	3	5	ibu:IB211_02463c	ko:K06147	NA
ICBIDGAJ_00615	OG0001754	group_1725	1	2	2	fpr:FP2_27920	ko:K06147	NA
ICBIDGAJ_00616	OG0000036	group_2527	1	0	0	tsu:Tresu_1912	NA	NA
ICBIDGAJ_00617	OG0001923	group_2182	0	1	0	fpa:FPR_04630	NA	NA
ICBIDGAJ_00618	OG0000024	dnaI	1	0	0	fpa:FPR_04640	ko:K02315	NA
ICBIDGAJ_00619	OG0001537	group_918	1	0	0	fpa:FPR_04650	NA	NA
ICBIDGAJ_00620	OG0000102	group_3090	0	1	0	bprm:CL3_04980	NA	NA
ICBIDGAJ_00621	OG0002122	group_4060	1	0	0	lacy:A4V08_07830	NA	NA
ICBIDGAJ_00622	OG0001763	group_894	1	0	0	rho:RHOM_10395	NA	NA
ICBIDGAJ_00623	OG0001860	group_2181	0	1	0	rho:RHOM_01690	NA	NA
ICBIDGAJ_00624	OG0001762	group_2553	1	0	0	rto:RTO_05140	NA	NA
ICBIDGAJ_00625	OG0001859	group_3091	1	0	0	cct:CC1_32150;rto:RTO_05150	NA	NA
ICBIDGAJ_00626	OG0002167	group_4061	1	1	1	fpa:FPR_08200	NA	NA
ICBIDGAJ_00627	OG0001754	group_1724	2	1	2	fpr:FP2_27920	ko:K06147	NA
ICBIDGAJ_00628	OG0002155	group_15	1	0	0	fpa:FPR_25010	NA	NA
ICBIDGAJ_00629	OG0000178	group_14	1	0	0	fpr:FP2_29980	NA	NA
ICBIDGAJ_00630	OG0002297	group_16	1	0	0	fpr:FP2_27630	NA	NA
ICBIDGAJ_00631	OG0003076	group_2830	1	0	0	elm:ELI_2135	ko:K03088	NA
ICBIDGAJ_00632	OG0003077	group_2831	3	4	6	NA	NA	NA
ICBIDGAJ_00633	OG0003078	group_3717	1	0	0	byl:A4V09_22590	NA	NA
ICBIDGAJ_00634	OG0003079	group_3718	3	4	6	NA	NA	NA
ICBIDGAJ_00635	OG0000554	ntpJ	5	6	10	fpa:FPR_27430	ko:K03498	NA
ICBIDGAJ_00636	OG0000555	ktrA	1	0	0	fpr:FP2_19510	ko:K03499	NA
ICBIDGAJ_00637	OG0000556	kdpD_2	2	1	2	fpr:FP2_19500	ko:K07646	NA
ICBIDGAJ_00638	OG0000557	kdpE_2	1	0	0	fpa:FPR_27460	ko:K07667	NA
ICBIDGAJ_00639	OG0000558	group_1154	1	0	0	fpa:FPR_03380	NA	NA
ICBIDGAJ_00640	OG0000559	group_532	1	0	0	fpa:FPR_03390	NA	NA
ICBIDGAJ_00641	OG0000207	malP_1	1	0	0	fpa:FPR_12120	ko:K00688	NA
ICBIDGAJ_00642	OG0000208	rclR	1	0	0	fpa:FPR_12110	NA	NA
ICBIDGAJ_00643	OG0002119	malR	1	0	0	rto:RTO_00190	NA	NA
ICBIDGAJ_00644	OG0002168	glcB	5	5	9	cso:CLS_10310	ko:K20107;ko:K20108	NA
ICBIDGAJ_00645	OG0002415	mapP	1	0	0	fro:AALO17_01780	ko:K06896	NA
ICBIDGAJ_00646	OG0001928	malQ_2	1	0	0	rum:CK1_29460	ko:K00705	NA
ICBIDGAJ_00647	OG0003080	nfrA1	1	0	0	ruk:A4V00_16525	NA	NA
ICBIDGAJ_00648	OG0000209	group_1159	1	0	0	fpa:FPR_16660	NA	NA
ICBIDGAJ_00649	OG0000560	xpt	1	0	0	fpa:FPR_16670	ko:K03816	NA
ICBIDGAJ_00650	OG0000561	spoVD_2	1	1	1	fpr:FP2_01820	ko:K08384	NA
ICBIDGAJ_00651	OG0000562	ftsW_2	5	5	9	fpr:FP2_01830	ko:K03588	NA
ICBIDGAJ_00652	OG0000563	murAA	1	0	0	fpr:FP2_01840	ko:K00790	NA
ICBIDGAJ_00653	OG0000564	ftsZ	1	0	0	fpr:FP2_01850	ko:K03531	NA
ICBIDGAJ_00654	OG0000565	group_3719	1	0	0	NA	NA	NA
ICBIDGAJ_00655	OG0000566	group_1163	1	0	0	fpr:FP2_01870	NA	NA
ICBIDGAJ_00656	OG0000567	group_1164	1	0	0	fpa:FPR_03510	NA	NA
ICBIDGAJ_00657	OG0000568	group_3720	1	0	0	fpr:FP2_01890	NA	NA
ICBIDGAJ_00658	OG0000569	sbcC	1	0	0	rim:ROI_19580	ko:K03546	NA
ICBIDGAJ_00659	OG0000570	sbcD	1	0	0	fpr:FP2_01950	ko:K03547	NA
ICBIDGAJ_00660	OG0000571	lyc_2	1	0	0	fpa:FPR_03560	NA	NA
ICBIDGAJ_00661	OG0000572	group_3721	1	0	0	fpr:FP2_01970	ko:K06387	NA
ICBIDGAJ_00662	OG0000573	group_2373	1	0	0	fpr:FP2_01980	ko:K09157	NA
ICBIDGAJ_00663	OG0000574	purU	1	0	0	fpr:FP2_01990	ko:K07166	NA
ICBIDGAJ_00664	OG0000575	group_2011	1	0	0	fpa:FPR_03600	NA	NA
ICBIDGAJ_00665	OG0000161	patA_2	1	0	0	fpa:FPR_03610	ko:K10907	NA
ICBIDGAJ_00666	OG0000576	ispE	1	0	0	fpa:FPR_03620	ko:K00919	NA
ICBIDGAJ_00667	OG0000577	group_1171	1	2	2	lao:AOX59_15010	ko:K09779	NA
ICBIDGAJ_00668	OG0001700	group_2012	1	0	0	fpa:FPR_03640	NA	NA
ICBIDGAJ_00669	OG0000578	group_1172	1	0	0	fpa:FPR_03650	NA	NA
ICBIDGAJ_00670	OG0000579	group_1173	1	0	0	fpa:FPR_03660	ko:K03768	NA
ICBIDGAJ_00671	OG0000580	yrrK	1	0	0	fpr:FP2_02090	ko:K07447	NA
ICBIDGAJ_00672	OG0000581	addB	1	0	0	fpa:FPR_03680	ko:K16899	NA
ICBIDGAJ_00673	OG0000582	addA	1	0	0	fpr:FP2_02130	ko:K16898	NA
ICBIDGAJ_00674	OG0000583	infC	1	0	0	ruk:A4V00_13445	ko:K02520	NA
ICBIDGAJ_00675	OG0000584	rpmI	0	1	0	fpa:FPR_03710;fpr:FP2_02150	ko:K02916	NA
ICBIDGAJ_00676	OG0000585	rplT	0	1	0	fpa:FPR_03720	ko:K02887	NA
ICBIDGAJ_00677	OG0000586	group_1177	1	0	0	fpr:FP2_02170	ko:K03437	NA
ICBIDGAJ_00678	OG0000587	dprA	1	0	0	NA	NA	NA
ICBIDGAJ_00679	OG0000588	topA	1	0	0	fpr:FP2_02190	ko:K03168	NA
ICBIDGAJ_00680	OG0000589	trmFO	1	0	0	fpr:FP2_02200	ko:K04094	NA
ICBIDGAJ_00681	OG0000590	plsX	1	0	0	fpa:FPR_03770	ko:K03621	NA
ICBIDGAJ_00682	OG0000591	rnc	1	0	0	fpr:FP2_02210	ko:K03685	NA
ICBIDGAJ_00683	OG0000592	smc_1	1	0	0	fpa:FPR_03790	ko:K03529	NA
ICBIDGAJ_00684	OG0000593	ftsY	1	0	0	fpr:FP2_02230	ko:K03110	NA
ICBIDGAJ_00685	OG0000594	rdgB	1	0	0	fpr:FP2_02240	ko:K02428	NA
ICBIDGAJ_00686	OG0000595	yhbY	1	0	0	fpr:FP2_02250	ko:K07574	NA
ICBIDGAJ_00687	OG0000596	nadD	1	0	0	fpr:FP2_02260	ko:K00969	NA
ICBIDGAJ_00688	OG0000597	rny_1	1	0	0	fpr:FP2_02270	NA	NA
ICBIDGAJ_00689	OG0000598	yvhJ	1	1	1	fpa:FPR_03860	NA	NA
ICBIDGAJ_00690	OG0000599	rsfS	1	0	0	fpr:FP2_02290	ko:K09710	NA
ICBIDGAJ_00691	OG0000600	leuS	1	0	0	fpr:FP2_02300	ko:K01869	NA
ICBIDGAJ_00692	OG0000601	rpsU	0	1	0	fpa:FPR_03890;fpr:FP2_02310	ko:K02970	NA
ICBIDGAJ_00693	OG0000602	gph_1	1	0	0	fpr:FP2_02320	ko:K07015	NA
ICBIDGAJ_00694	OG0000603	nfo	1	0	0	eha:Ethha_0220	ko:K01151	NA
ICBIDGAJ_00695	OG0000604	efp	1	0	0	fpr:FP2_02350	ko:K02356	NA
ICBIDGAJ_00696	OG0000605	group_1189	1	0	0	fpa:FPR_03930	NA	NA
ICBIDGAJ_00697	OG0000606	group_1190	1	0	0	fpr:FP2_15500	NA	NA
ICBIDGAJ_00698	OG0000607	fhs	1	0	0	fpa:FPR_03960	ko:K01938	NA
ICBIDGAJ_00699	OG0003081	group_3722	1	0	0	NA	NA	NA

ICBIDGAJ_00700	OG0000608	group_2375	1	1	1	fpr:FP2_15490	NA	NA	
ICBIDGAJ_00701	OG0000609	group_1192	1	0	0	fpa:FPR_03970	ko:K04487	NA	
ICBIDGAJ_00702	OG0000610	thiI	1	0	0	fpr:FP2_15530	ko:K03151	NA	
ICBIDGAJ_00703	OG0000611	cinA_2	1	0	0	fpr:FP2_15540	ko:K03742	NA	
ICBIDGAJ_00704	OG0000612	group_3723	1	0	0	fpa:FPR_04000	NA	NA	
ICBIDGAJ_00705	OG0000613	secA	1	0	0	fpa:FPR_05210	ko:K03070	NA	
ICBIDGAJ_00706	OG0000210	yxeP	1	0	0	fpa:FPR_05220	NA	NA	
ICBIDGAJ_00707	OG0000211	queT	2	3	4	fpr:FP2_17990	NA	NA	
ICBIDGAJ_00708	OG0000614	group_1198	1	0	0	fpr:FP2_17980	NA	NA	
ICBIDGAJ_00709	OG0000615	trmL	1	0	0	fpa:FPR_06450	ko:K03216	NA	
ICBIDGAJ_00710	OG0000616	pdxK	1	0	0	ccel:CCDG5_1749	ko:K00868	NA	
ICBIDGAJ_00711	OG0000617	group_3724	1	1	1	fpr:FP2_17950	NA	NA	
ICBIDGAJ_00712	OG0000618	group_2014	1	1	1	fpa:FPR_06480	NA	NA	
ICBIDGAJ_00713	OG0000212	ydhY_2	1	0	0	fpa:FPR_06490	NA	NA	
ICBIDGAJ_00714	OG0000619	mtaB	1	0	0	fpr:FP2_02600	ko:K18707	NA	
ICBIDGAJ_00715	OG0000620	dacF_1	1	1	1	fpr:FP2_02610	ko:K07258	NA	
ICBIDGAJ_00716	OG0000621	pgiB	1	0	0	fpr:FP2_02620	ko:K01810	NA	
ICBIDGAJ_00717	OG0000622	group_1202	1	0	0	fpa:FPR_06530	NA	NA	
ICBIDGAJ_00718	OG0000623	group_1203	1	0	0	fpr:FP2_02640	ko:K07040	NA	
ICBIDGAJ_00719	OG0000624	rpmF	0	1	0	fpa:FPR_06550	ko:K02911	NA	
ICBIDGAJ_00720	OG0000625	group_1204	1	0	0	fpr:FP2_02660	NA	NA	
ICBIDGAJ_00721	OG0000626	der	1	0	0	fpa:FPR_06570	ko:K03977	NA	
ICBIDGAJ_00722	OG0000627	plsY	3	4	6	fpr:FP2_02680	ko:K08591	NA	
ICBIDGAJ_00724	OG0000628	nahK	1	0	0	fpa:FPR_27470	NA	NA	
ICBIDGAJ_00725	OG0000213	adaA_2	1	0	0	fpr:FP2_19470	NA	NA	
ICBIDGAJ_00726	OG0000629	msmE	1	0	0	fpa:FPR_27490	ko:K10200	NA	
ICBIDGAJ_00727	OG0000630	ugpA_2	3	4	6	fpa:FPR_27500	ko:K10201	NA	
ICBIDGAJ_00728	OG0000631	sugB_1	3	4	6	fpr:FP2_19440	ko:K10202	NA	
ICBIDGAJ_00729	OG0000632	group_2017	1	2	2	fpa:FPR_27520	NA	NA	
ICBIDGAJ_00730	OG0000633	group_2378	1	0	0	fpa:FPR_27530	ko:K15533	NA	
ICBIDGAJ_00731	OG0000634	nspC	1	0	0	fpr:FP2_18070	ko:K13747	NA	
ICBIDGAJ_00732	OG0000635	group_2018	1	0	0	fpa:FPR_20600	ko:K00290	NA	
ICBIDGAJ_00733	OG0000636	speB	1	0	0	fpa:FPR_20590	ko:K01480	NA	
ICBIDGAJ_00734	OG0000637	speE	1	0	0	fpa:FPR_20580	ko:K00797	NA	
ICBIDGAJ_00735	OG0000638	speA_1	1	0	0	fpr:FP2_18110	NA	NA	
ICBIDGAJ_00737	OG0002120	mepA_11	5	6	10	NA	NA	NA	
ICBIDGAJ_00738	OG0001992	group_2379	1	0	0	fpr:FP2_26210	NA	NA	
ICBIDGAJ_00739	OG0000639	group_1211	6	7	12	fpr:FP2_09560	NA	NA	
ICBIDGAJ_00740	OG0000640	dus	1	0	0	fpa:FPR_16540	NA	NA	
ICBIDGAJ_00741	OG0001894	yhdN_2	1	0	0	fpr:FP2_09520	ko:K07079	NA	
ICBIDGAJ_00742	OG0000075	group_3729	1	0	0	fpr:FP2_02720	NA	NA	
ICBIDGAJ_00743	OG0000641	group_1213	1	0	0	fpr:FP2_26420	ko:K01989	NA	
ICBIDGAJ_00744	OG0000642	group_1214	4	5	8	fpr:FP2_26430	ko:K05832	NA	
ICBIDGAJ_00745	OG0000643	metN2	1	0	0	fpr:FP2_26440	ko:K05833	NA	
ICBIDGAJ_00746	OG0001806	mshD_2	1	0	0	NA	NA	NA	
ICBIDGAJ_00747	OG0002237	group_2845	1	0	0	fpr:FP2_15210	NA	NA	
ICBIDGAJ_00748	OG0002238	group_2846	0	1	0	fpr:FP2_15200	NA	NA	
ICBIDGAJ_00749	OG0000644	group_2020	0	1	0	fpr:FP2_30750	NA	NA	
ICBIDGAJ_00750	OG0000645	dtd3	1	0	0	fpr:FP2_30760	ko:K03424	NA	
ICBIDGAJ_00751	OG0000646	eamA	5	6	10	fpa:FPR_26200	NA	NA	
ICBIDGAJ_00752	OG0000647	metG	1	0	0	fpa:FPR_26190	ko:K01874	NA	
ICBIDGAJ_00753	OG0001676	treR	1	0	0	bfi:CIY_23030	ko:K03486	specific_fp14	○
ICBIDGAJ_00754	OG0000069	treB	5	6	10	cle:Clole_3451	ko:K02818;ko:K02819	specific_fp14	○
ICBIDGAJ_00755	OG0002169	treA	1	0	0	cle:Clole_3450	ko:K01226	specific_fp14	○
ICBIDGAJ_00756	OG0003865	group_4065	1	0	0	NA	NA	specific_fp14	○
ICBIDGAJ_00757	OG0003866	group_4066	0	1	0	NA	NA	specific_fp14	
ICBIDGAJ_00758	OG0003082	group_2022	1	0	0	fpa:FPR_04020	NA	NA	
ICBIDGAJ_00759	OG0002239	group_2023	1	0	0	fpa:FPR_04020	NA	NA	
ICBIDGAJ_00760	OG0002240	group_3093	1	0	0	fpa:FPR_04030	NA	NA	
ICBIDGAJ_00761	OG0002241	group_4067	1	0	0	fpa:FPR_04040	NA	NA	
ICBIDGAJ_00762	OG0000184	group_4068	1	0	0	fpa:FPR_04050	NA	NA	
ICBIDGAJ_00763	OG0003159	group_4069	1	0	0	cls:CXIVA_10320	ko:K07171	NA	
ICBIDGAJ_00764	OG0001999	group_4070	1	0	0	fpr:FP2_21390	NA	NA	
ICBIDGAJ_00765	OG0000720	group_2865	1	0	0	fpr:FP2_27370	NA	NA	
ICBIDGAJ_00766	OG0002249	group_4071	1	0	0	rto:RTO_27050	NA	NA	
ICBIDGAJ_00767	OG0003867	group_4072	1	0	0	NA	NA	specific_fp14	○
ICBIDGAJ_00768	OG0003868	group_4073	1	0	0	rbr:RBR_05250	ko:K02283	specific_fp14	○
ICBIDGAJ_00769	OG0003869	group_4074	2	2	3	NA	NA	specific_fp14	○
ICBIDGAJ_00770	OG0003870	group_4075	3	2	4	NA	NA	specific_fp14	○
ICBIDGAJ_00771	OG0003871	group_4076	1	1	1	NA	NA	specific_fp14	○
ICBIDGAJ_00772	OG0003872	group_4077	1	1	1	NA	NA	specific_fp14	○
ICBIDGAJ_00773	OG0003873	group_4078	4	4	7	NA	NA	specific_fp14	○
ICBIDGAJ_00774	OG0003874	group_4079	1	1	1	NA	NA	specific_fp14	○
ICBIDGAJ_00775	OG0003875	group_4080	1	1	1	NA	NA	specific_fp14	○
ICBIDGAJ_00776	OG0003876	group_4081	1	1	1	NA	NA	specific_fp14	○
ICBIDGAJ_00777	OG0003877	group_4082	1	1	1	NA	NA	specific_fp14	○
ICBIDGAJ_00778	OG0003878	group_4083	1	0	0	NA	NA	specific_fp14	○
ICBIDGAJ_00779	OG0002248	group_4084	1	0	0	NA	NA	NA	
ICBIDGAJ_00780	OG0002627	group_4085	1	0	0	fpa:FPR_20030	NA	NA	
ICBIDGAJ_00781	OG0002628	group_3094	1	0	0	NA	NA	NA	
ICBIDGAJ_00782	OG0002629	patA_1	5	5	9	fpa:FPR_20070	ko:K19294	NA	
ICBIDGAJ_00783	OG0002630	algJ	1	1	1	NA	NA	NA	
ICBIDGAJ_00784	OG0002631	group_2555	1	0	0	fpa:FPR_20090	NA	NA	
ICBIDGAJ_00785	OG0002632	toxA	1	1	1	NA	NA	NA	
ICBIDGAJ_00786	OG0002633	ddpX	1	0	0	fpa:FPR_20110	NA	NA	
ICBIDGAJ_00787	OG0002416	group_2205	1	1	1	NA	NA	NA	
ICBIDGAJ_00788	OG0002416	group_2206	1	1	1	NA	NA	NA	
ICBIDGAJ_00789	OG0002416	group_4086	1	1	1	bfi:CIY_34320	NA	NA	
ICBIDGAJ_00790	OG0002247	group_4087	1	0	0	NA	NA	NA	
ICBIDGAJ_00791	OG0002416	group_2207	1	0	0	NA	NA	NA	
ICBIDGAJ_00792	OG0000089	group_763	1	0	0	fpr:FP2_09570	NA	NA	
ICBIDGAJ_00793	OG0000010	group_187	1	0	0	fpa:FPR_18840	NA	NA	
ICBIDGAJ_00794	OG0000088	group_761	2	2	3	fpa:FPR_18850	NA	NA	
ICBIDGAJ_00795	OG0000023	group_262	1	0	0	fpa:FPR_18860	NA	NA	
ICBIDGAJ_00796	OG0001915	group_99	1	0	0	fpr:FP2_27160	NA	NA	
ICBIDGAJ_00797	OG0000067	group_1669	1	0	0	ere:EUBREC_0807;ere:EUBREC_2688	ko:K00986	NA	
ICBIDGAJ_00798	OG0000035	group_391	0	1	0	fpa:FPR_05610	NA	NA	
ICBIDGAJ_00799	OG0000002	group_217	1	0	0	fpr:FP2_21840	ko:K03497	NA	
ICBIDGAJ_00800	OG0000004	group_159	1	0	0	fpa:FPR_07940	ko:K03496	NA	
ICBIDGAJ_00801	OG0000008	group_135	1	0	0	fpr:FP2_09070	NA	NA	
ICBIDGAJ_00802	OG0002170	group_4088	0	1	0	NA	NA	NA	
ICBIDGAJ_00803	OG0002298	group_3098	0	1	0	fpr:FP2_09090;fpa:FPR_05570	NA	NA	
ICBIDGAJ_00805	OG0000648	ktrB	5	6	10	fpr:FP2_09510	ko:K03498	NA	
ICBIDGAJ_00806	OG0000649	pepT	1	0	0	fpr:FP2_26900	ko:K01258	NA	
ICBIDGAJ_00807	OG0000650	atpC_1	1	0	0	fpr:FP2_01360	ko:K02114	NA	
ICBIDGAJ_00808	OG0000651	atpD_1	1	0	0	fpr:FP2_01350	ko:K02112	NA	
ICBIDGAJ_00809	OG0000652	atpG_1	1	0	0	fpa:FPR_26330	ko:K02115	NA	
ICBIDGAJ_00810	OG0000653	atpA_1	1	0	0	fpr:FP2_01330	ko:K02111	NA	
ICBIDGAJ_00811	OG0000654	atpF_1	1	1	1	fpr:FP2_01320	ko:K02109	NA	
ICBIDGAJ_00812	OG0000655	atpE_1	2	1	2	fpr:FP2_01310	ko:K02110	NA	
ICBIDGAJ_00813	OG0000656	atpB_1	2	3	4	fpr:FP2_01300	ko:K02108	NA	
ICBIDGAJ_00814	OG0001701	group_3767	2	2	3	NA	NA	NA	
ICBIDGAJ_00815	OG0000657	group_750	1	0	0	fpr:FP2_30790	NA	NA	
ICBIDGAJ_00816	OG0001898	sarA_3	1	0	0	fpr:FP2_26820	ko:K15580	NA	

ICBIDGAJ_00817	OG0000658	group_601	1	0	0	fpr:FP2_26830	NA	NA	
ICBIDGAJ_00818	OG0000659	tig_4	1	0	0	fpr:FP2_26840	ko:K03545	NA	
ICBIDGAJ_00819	OG0000660	group_2851	8	7	14	fpa:FPR_03000	NA	NA	
ICBIDGAJ_00820	OG0000661	glgB_1	1	0	0	fpr:FP2_26860	ko:K00700	NA	
ICBIDGAJ_00821	OG0000662	tvaII	1	0	0	fpa:FPR_03020	NA	NA	
ICBIDGAJ_00822	OG0000663	niaR	0	1	0	fpr:FP2_26880	ko:K07105	NA	
ICBIDGAJ_00823	OG0000664	group_2381	1	0	0	rob:CK5_34480	NA	NA	
ICBIDGAJ_00824	OG0000665	recG	1	0	0	fpr:FP2_30150	ko:K03655	NA	
ICBIDGAJ_00825	OG0002378	group_4089	1	0	0	ere:EUBREC_0175	NA	NA	
ICBIDGAJ_00831	OG0000666	gyrB_2	1	0	0	fpr:FP2_30180	ko:K02470	NA	
ICBIDGAJ_00832	OG0000667	gyrA_2	1	0	0	fpr:FP2_30190	ko:K02469	NA	
ICBIDGAJ_00833	OG0000668	rlmH	1	0	0	fpa:FPR_19870	ko:K00783	NA	
ICBIDGAJ_00834	OG0000669	glyQS	1	0	0	fpa:FPR_19900	ko:K01880	NA	
ICBIDGAJ_00835	OG0000670	group_751	1	0	0	gwc:GWCH70_2065	ko:K19689	NA	
ICBIDGAJ_00836	OG0003090	group_3768	1	1	1	NA	NA	NA	
ICBIDGAJ_00837	OG0000671	rimP	1	0	0	fpa:FPR_25770	ko:K09748	NA	
ICBIDGAJ_00838	OG0000672	nusA	1	0	0	fpr:FP2_30250	ko:K02600	NA	
ICBIDGAJ_00839	OG0000673	group_1235	0	1	0	fpr:FP2_30260	ko:K07742	NA	
ICBIDGAJ_00840	OG0000674	group_1236	1	0	0	fpa:FPR_25800	NA	NA	
ICBIDGAJ_00841	OG0000675	infB	1	0	0	fpa:FPR_25810	ko:K02519	NA	
ICBIDGAJ_00842	OG0000676	rbfA	1	0	0	fpr:FP2_30290	ko:K02834	NA	
ICBIDGAJ_00843	OG0000677	nrnA	1	0	0	fpa:FPR_25830	ko:K06881	NA	
ICBIDGAJ_00844	OG0000678	truB	1	0	0	fpr:FP2_30310	ko:K03177	NA	
ICBIDGAJ_00845	OG0000679	ribF	1	0	0	fpr:FP2_30320	ko:K11753	NA	
ICBIDGAJ_00846	OG0000680	rpsO	0	1	0	fpr:FP2_30350	ko:K02956	NA	
ICBIDGAJ_00847	OG0000681	pnp	1	0	0	fpr:FP2_30360	ko:K00962	NA	
ICBIDGAJ_00848	OG0001899	ytrA	1	0	0	fpr:FP2_26390	NA	NA	
ICBIDGAJ_00849	OG0001900	ytrB_2	1	0	0	fpr:FP2_26400	ko:K01990	NA	
ICBIDGAJ_00850	OG0001901	group_2852	4	4	7	NA	NA	NA	
ICBIDGAJ_00851	OG0000027	group_2140	1	0	0	dru:Desru_2296;dru:Desru_2710;dru:Desru_0118	ko:K07497	NA	
ICBIDGAJ_00852	OG0000682	asnB	1	0	0	fpr:FP2_30810	ko:K01953	NA	
ICBIDGAJ_00853	OG0000683	perR_1	1	0	0	fpr:FP2_30820	ko:K03711	NA	
ICBIDGAJ_00854	OG0000214	rspR_3	1	0	0	fpa:FPR_16480	NA	NA	
ICBIDGAJ_00855	OG0000215	fucO	1	0	0	fpr:FP2_03020	ko:K00048	NA	
ICBIDGAJ_00856	OG0000684	group_752	6	5	10	fpr:FP2_16130	NA	NA	
ICBIDGAJ_00857	OG0000162	yrbG	6	5	10	fpa:FPR_25630	ko:K07301	NA	
ICBIDGAJ_00858	OG0001995	group_2853	1	1	1	NA	NA	NA	
ICBIDGAJ_00859	OG0000685	group_2854	1	1	1	fpr:FP2_21210	NA	NA	
ICBIDGAJ_00860	OG0001996	group_2385	1	0	0	fpr:FP2_21180	ko:K07010	NA	
ICBIDGAJ_00862	OG0000686	lldD	1	0	0	fpr:FP2_21160	NA	NA	
ICBIDGAJ_00863	OG0002246	group_3769	1	1	1	fpr:FP2_21150	NA	NA	
ICBIDGAJ_00864	OG0000687	rluC_1	1	0	0	esr:ES1_10950	ko:K06179	NA	
ICBIDGAJ_00865	OG0000688	group_3770	1	0	0	fpa:FPR_06670	NA	NA	
ICBIDGAJ_00866	OG0000689	alaS_1	1	0	0	fpa:FPR_06680	ko:K01872	NA	
ICBIDGAJ_00867	OG0000690	group_1245	1	0	0	fpa:FPR_06690	ko:K02503	NA	
ICBIDGAJ_00868	OG0000691	purR_2	1	0	0	fpr:FP2_21100;fpa:FPR_06700	ko:K00759	NA	
ICBIDGAJ_00869	OG0000692	group_3099	6	5	10	fpa:FPR_06710	ko:K02238	NA	
ICBIDGAJ_00870	OG0000693	psuK	1	0	0	fpa:FPR_25710	ko:K16328	NA	
ICBIDGAJ_00871	OG0000694	comM	1	0	0	fpr:FP2_09920	ko:K07391	NA	
ICBIDGAJ_00872	OG0000695	pgcA	1	0	0	fpa:FPR_27610	ko:K01835	NA	
ICBIDGAJ_00873	OG0000696	ispF	1	0	0	fpa:FPR_27620	ko:K12506	NA	
ICBIDGAJ_00874	OG0000697	cdaA	2	1	2	fpr:FP2_09960	ko:K18672	NA	
ICBIDGAJ_00875	OG0000698	group_1251	1	1	1	fpr:FP2_09970	NA	NA	
ICBIDGAJ_00876	OG0000699	group_1252	1	0	0	fpr:FP2_09980	ko:K07137	NA	
ICBIDGAJ_00877	OG0000700	group_2029	2	2	3	fpa:FPR_27660	NA	NA	
ICBIDGAJ_00878	OG0000701	recJ	1	0	0	fpr:FP2_10000	ko:K07462	NA	
ICBIDGAJ_00879	OG0000702	relA	1	0	0	fpr:FP2_10010	ko:K00951	NA	
ICBIDGAJ_00880	OG0000703	dtd	1	0	0	fpr:FP2_10020	ko:K07560	NA	
ICBIDGAJ_00881	OG0000704	gloC	1	0	0	fpr:FP2_10030	NA	NA	
ICBIDGAJ_00882	OG0000705	hemZ	1	0	0	fpr:FP2_10040	NA	NA	
ICBIDGAJ_00883	OG0000706	udk_3	1	0	0	fpa:FPR_27720	ko:K00876	NA	
ICBIDGAJ_00884	OG0000707	group_1259	1	0	0	fpa:FPR_27730	NA	NA	
ICBIDGAJ_00885	OG0000708	mazG	1	0	0	fpr:FP2_10070	ko:K02499	NA	
ICBIDGAJ_00886	OG0000709	hup_2	1	0	0	fpr:FP2_10080	ko:K03530	NA	
ICBIDGAJ_00887	OG0000710	group_1262	1	0	0	fpr:FP2_10090	NA	NA	
ICBIDGAJ_00888	OG0000711	yabP	1	0	0	fpr:FP2_10100	NA	NA	
ICBIDGAJ_00889	OG0000712	group_3772	2	1	2	fpr:FP2_10110	NA	NA	
ICBIDGAJ_00890	OG0000713	ftsL_2	1	1	1	fpa:FPR_27790	NA	NA	
ICBIDGAJ_00891	OG0000714	yugI	1	0	0	ble:BleG1_4086	ko:K07571	NA	
ICBIDGAJ_00892	OG0000715	rlmL	1	0	0	fpr:FP2_10140	ko:K07444	NA	
ICBIDGAJ_00893	OG0000716	group_1266	1	0	0	fpr:FP2_10150	NA	NA	
ICBIDGAJ_00894	OG0000717	group_1913	2	3	4	fpr:FP2_10160	NA	NA	
ICBIDGAJ_00895	OG0000718	glmS	1	0	0	fpa:FPR_27850	ko:K00820	NA	
ICBIDGAJ_00898	OG0000000	group_41	0	1	0	fpa:FPR_08500	NA	NA	
ICBIDGAJ_00899	OG0001987	melR	1	0	0	fpa:FPR_08510	NA	NA	
ICBIDGAJ_00900	OG0000109	group_3649	6	7	12	fpa:FPR_08520	ko:K03292	NA	
ICBIDGAJ_00901	OG0001988	group_2801	1	0	0	fpa:FPR_08530	NA	NA	
ICBIDGAJ_00902	OG0001775	group_563	0	1	0	NA	NA	NA	
ICBIDGAJ_00903	OG0000044	group_443	1	0	0	fpr:FP2_22730	NA	NA	
ICBIDGAJ_00904	OG0000018	group_164	1	0	0	fpr:FP2_29840	NA	NA	
ICBIDGAJ_00905	OG0000065	group_182	1	0	0	fpa:FPR_03220	NA	NA	
ICBIDGAJ_00906	OG0002299	group_4090	1	0	0	NA	NA	NA	
ICBIDGAJ_00907	OG0002417	group_4091	1	0	0	msj:MSSAC_2117	ko:K03427	NA	
ICBIDGAJ_00908	OG0003879	group_4092	1	0	0	bvs:BARVI_02630	NA	specific_fp14	○
ICBIDGAJ_00909	OG0003880	group_4093	1	0	0	NA	NA	specific_fp14	○
ICBIDGAJ_00910	OG0002418	group_4094	1	1	1	mdh:AYM39_02170	ko:K01154	NA	
ICBIDGAJ_00911	OG0003881	group_4095	1	0	0	NA	NA	specific_fp14	○
ICBIDGAJ_00912	OG0002419	hsdR	1	0	0	ols:Olsu_1674	ko:K01153	NA	
ICBIDGAJ_00913	OG0000048	group_36	1	0	0	fpa:FPR_20510	NA	NA	
ICBIDGAJ_00914	OG0000027	group_2141	1	0	0	dru:Desru_2710;dru:Desru_0118;dru:Desru_2296	ko:K07497	NA	
ICBIDGAJ_00915	OG0002577	group_3773	1	0	0	NA	NA	NA	
ICBIDGAJ_00916	OG0002578	group_2855	0	1	0	NA	NA	NA	
ICBIDGAJ_00917	OG0002579	group_2856	1	0	0	NA	NA	NA	
ICBIDGAJ_00919	OG0000721	thiT	2	3	4	fpr:FP2_27460	ko:K16789	NA	
ICBIDGAJ_00920	OG0000722	spoIIID	0	1	0	fpr:FP2_27470	ko:K06283	NA	
ICBIDGAJ_00921	OG0000723	sigG	1	0	0	fpr:FP2_27480	ko:K03091	NA	
ICBIDGAJ_00922	OG0000724	sigE_2	1	0	0	fpa:FPR_20660	ko:K03091	NA	
ICBIDGAJ_00923	OG0000725	group_3785	2	3	4	NA	NA	NA	
ICBIDGAJ_00925	OG0000726	lagD	4	3	6	fpa:FPR_27890	ko:K20344	NA	
ICBIDGAJ_00926	OG0000217	group_3786	1	0	0	NA	NA	NA	
ICBIDGAJ_00927	OG0000727	group_2871	1	0	0	fpr:FP2_10210	NA	NA	
ICBIDGAJ_00928	OG0000728	hlyD	1	1	1	fpr:FP2_10200	ko:K20345	NA	
ICBIDGAJ_00929	OG0000729	group_2872	1	2	2	fpr:FP2_10190	NA	NA	
ICBIDGAJ_00930	OG0000730	group_767	2	1	2	fpa:FPR_20130	NA	NA	
ICBIDGAJ_00931	OG0000731	group_2034	1	0	0	fpa:FPR_20140	NA	NA	
ICBIDGAJ_00932	OG0000732	apbE	1	0	0	fpr:FP2_01400	ko:K03734	NA	
ICBIDGAJ_00933	OG0000733	group_769	0	1	0	fpr:FP2_01410	NA	NA	
ICBIDGAJ_00934	OG0000734	aroF_2	1	0	0	fpa:FPR_25910	ko:K03856	NA	
ICBIDGAJ_00935	OG0000735	ybaK	1	0	0	fpr:FP2_01450	ko:K03976	NA	
ICBIDGAJ_00936	OG0000736	purE	1	1	1	fpa:FPR_25940	ko:K01588	NA	
ICBIDGAJ_00937	OG0000737	purF	1	0	0	fpr:FP2_01470	ko:K00764	NA	
ICBIDGAJ_00938	OG0000738	purM	1	0	0	fpr:FP2_01480	ko:K01933	NA	
ICBIDGAJ_00939	OG0000739	purN	1	0	0	rbr:RBR_16740	ko:K11175	NA	
ICBIDGAJ_00940	OG0000740	group_1286	1	0	0	fpa:FPR_25980	NA	NA	

ICBIDGAJ_00941	OG0000741	purH	1	0	0	fpr:FP2_01510	ko:K00602	NA	
ICBIDGAJ_00942	OG0000742	purD_2	1	0	0	fpa:FPR_26000	ko:K01945	NA	
ICBIDGAJ_00943	OG0000743	purL	1	0	0	fpa:FPR_26010	ko:K01952	NA	
ICBIDGAJ_00944	OG0000744	purB	1	0	0	fpr:FP2_01550	ko:K01756	NA	
ICBIDGAJ_00945	OG0000745	rsuA	1	0	0	fpr:FP2_01560	ko:K06183	NA	
ICBIDGAJ_00946	OG0000746	cdaR	1	0	0	fpa:FPR_26040	ko:K02647	NA	
ICBIDGAJ_00947	OG0000747	ftsE	1	0	0	fpr:FP2_01580	ko:K09812	NA	
ICBIDGAJ_00948	OG0000748	ftsX	3	3	5	fpr:FP2_01590	ko:K09811	NA	
ICBIDGAJ_00949	OG0000749	mepM_2	1	1	1	fpa:FPR_26070	ko:K21471	NA	
ICBIDGAJ_00950	OG0000750	group_1295	1	1	1	NA	NA	NA	
ICBIDGAJ_00951	OG0000751	ctpA	1	1	1	fpr:FP2_01620	ko:K03797	NA	
ICBIDGAJ_00952	OG0000752	rsmA	1	0	0	fpa:FPR_26100	ko:K02528	NA	
ICBIDGAJ_00953	OG0000091	group_772	1	0	0	fpr:FP2_15620	ko:K15580	NA	
ICBIDGAJ_00954	OG0000092	dppB_1	3	3	5	fpr:FP2_15590	ko:K15581	NA	
ICBIDGAJ_00955	OG0002000	oppC	3	3	5	fpr:FP2_15580	ko:K15582	NA	
ICBIDGAJ_00956	OG0000033	oppD_2	1	0	0	fpr:FP2_15570	ko:K15583	NA	
ICBIDGAJ_00957	OG0000093	oppF_2	1	0	0	fpr:FP2_15560	ko:K10823	NA	
ICBIDGAJ_00958	OG0000091	sarA_1	1	0	0	fpr:FP2_15620	ko:K15580	NA	
ICBIDGAJ_00959	OG0002001	group_2035	2	2	3	fpr:FP2_15630	NA	NA	
ICBIDGAJ_00960	OG0000753	group_1298	1	0	0	fpr:FP2_15640	NA	NA	
ICBIDGAJ_00961	OG0000754	nnr	1	0	0	fpa:FPR_04970	ko:K17758;ko:K17759	NA	
ICBIDGAJ_00962	OG0000755	cobB	1	0	0	fpr:FP2_15660	ko:K12410	NA	
ICBIDGAJ_00963	OG0000756	hprA	1	0	0	fpa:FPR_20200	ko:K00018	NA	
ICBIDGAJ_00964	OG0000757	galM_1	1	0	0	fpa:FPR_20290	NA	NA	
ICBIDGAJ_00965	OG0000758	gcdB_2	6	5	10	fpr:FP2_04240	ko:K01572	NA	
ICBIDGAJ_00966	OG0000759	group_774	1	1	1	NA	NA	NA	
ICBIDGAJ_00967	OG0000760	dapL	1	0	0	fpa:FPR_20330	ko:K10206	NA	
ICBIDGAJ_00968	OG0000761	dapF	1	0	0	fpr:FP2_15800	ko:K01778	NA	
ICBIDGAJ_00969	OG0000762	acpP_2	1	0	0	fpr:FP2_15810	ko:K02078	NA	
ICBIDGAJ_00970	OG0000763	proS	1	0	0	fpr:FP2_15820	ko:K01881	NA	
ICBIDGAJ_00971	OG0000764	gabR_1	1	0	0	fpa:FPR_20340	ko:K07979	NA	
ICBIDGAJ_00972	OG0000765	ytrB	1	0	0	fpa:FPR_20350	ko:K01990	NA	
ICBIDGAJ_00973	OG0001703	group_2876	3	4	6	NA	NA	NA	
ICBIDGAJ_00974	OG0000766	mgtE	3	3	5	fpr:FP2_15830	ko:K06213	NA	
ICBIDGAJ_00975	OG0002002	dfx_4	1	0	0	fpr:FP2_15840	NA	NA	
ICBIDGAJ_00976	OG0000767	group_1306	1	0	0	fpr:FP2_15850	NA	NA	
ICBIDGAJ_00977	OG0000768	hflC	1	1	1	fpa:FPR_21450	NA	NA	
ICBIDGAJ_00978	OG0000769	group_1308	1	2	2	fpr:FP2_15870	NA	NA	
ICBIDGAJ_00979	OG0000770	apu	1	0	0	fpr:FP2_15880	NA	NA	
ICBIDGAJ_00980	OG0000771	malP_2	1	0	0	fpr:FP2_15900	ko:K00688	NA	
ICBIDGAJ_00981	OG0000772	zapA	0	1	0	fpa:FPR_21490	NA	NA	
ICBIDGAJ_00982	OG0000773	ydcP_1	1	0	0	fpr:FP2_15920	ko:K08303	NA	
ICBIDGAJ_00983	OG0000774	dut	1	0	0	fpa:FPR_21510	ko:K01520	NA	
ICBIDGAJ_00984	OG0000775	maf	1	0	0	fpr:FP2_15940	ko:K06287	NA	
ICBIDGAJ_00985	OG0000776	mreB_1	1	0	0	fpr:FP2_15950	ko:K03569	NA	
ICBIDGAJ_00986	OG0000777	mreC	1	1	1	fpa:FPR_21540	ko:K03570	NA	
ICBIDGAJ_00987	OG0000778	group_2395	3	3	5	fpr:FP2_15970	ko:K03571	NA	
ICBIDGAJ_00988	OG0000779	mrdA	1	1	1	fpa:FPR_21560	ko:K05515	NA	
ICBIDGAJ_00989	OG0000780	mgsA_1	1	0	0	fpa:FPR_21570	ko:K01734	NA	
ICBIDGAJ_00990	OG0002581	albA	1	0	0	fpr:FP2_19170	NA	NA	
ICBIDGAJ_00991	OG0002003	group_1318	1	0	0	fpr:FP2_04220	NA	NA	
ICBIDGAJ_00992	OG0000218	group_2878	3	3	5	fpr:FP2_29400	NA	NA	
ICBIDGAJ_00993	OG0000164	btr_2	1	0	0	rho:RHOM_14145	NA	NA	
ICBIDGAJ_00994	OG0000046	yjmB_2	5	6	10	fpa:FPR_25670	ko:K03292	NA	
ICBIDGAJ_00995	OG0001808	menH	1	0	0	fpa:FPR_25660	ko:K06889	NA	
ICBIDGAJ_00996	OG0001809	group_2881	1	0	0	fpa:FPR_25650	NA	NA	
ICBIDGAJ_00997	OG0002250	group_2398	1	1	1	fpa:FPR_19720	NA	NA	
ICBIDGAJ_00998	OG0000076	group_608	1	1	1	fpr:FP2_10240	NA	NA	
ICBIDGAJ_00999	OG0000050	group_756	1	0	0	fpr:FP2_21660	NA	NA	
ICBIDGAJ_01000	OG0000041	group_377	1	0	0	rus:RBI_II00371	ko:K03091	NA	
ICBIDGAJ_01001	OG0000094	group_616	1	1	1	NA	NA	NA	
ICBIDGAJ_01002	OG0000785	sttH	1	0	0	fpa:FPR_06820	NA	NA	
ICBIDGAJ_01003	OG0000219	ymdB_1	1	0	0	fpa:FPR_06830	NA	NA	
ICBIDGAJ_01004	OG0001706	group_464	1	0	0	fpr:FP2_03770	NA	NA	
ICBIDGAJ_01005	OG0000080	sfsA	1	0	0	era:ERE_03180	ko:K06206	NA	
ICBIDGAJ_01006	OG0000786	group_2404	1	0	0	fpr:FP2_03810;fpa:FPR_06870	NA	NA	
ICBIDGAJ_01007	OG0000787	ybiV	1	0	0	fpr:FP2_03820	NA	NA	
ICBIDGAJ_01008	OG0000060	group_468	1	0	0	fpa:FPR_06890	NA	NA	
ICBIDGAJ_01009	OG0000788	group_7227	1	0	0	fpr:FP2_03850	ko:K04794	NA	
ICBIDGAJ_01010	OG0000789	group_7202	1	0	0	sbu:SpiBuddy_1502	NA	NA	
ICBIDGAJ_01011	OG0000790	ymdB_2	1	0	0	fpa:FPR_07340	NA	NA	
ICBIDGAJ_01012	OG0000061	group_460	1	0	0	ssg:Selsp_2007	NA	NA	
ICBIDGAJ_01013	OG0000220	punA	1	0	0	fpr:FP2_03890	ko:K03783	NA	
ICBIDGAJ_01014	OG0003882	group_4097	1	0	0	NA	NA	specific_fp14	O
ICBIDGAJ_01015	OG0000043	group_398	1	0	0	fpr:FP2_17680;fpa:FPR_06960	NA	NA	
ICBIDGAJ_01016	OG0000131	group_2406	1	0	0	NA	NA	NA	
ICBIDGAJ_01017	OG0000132	group_2046	3	4	6	fpa:FPR_19630	NA	NA	
ICBIDGAJ_01018	OG0000222	group_2408	1	0	0	fpa:FPR_06970	ko:K18369	NA	
ICBIDGAJ_01019	OG0000222	adh	1	0	0	fpa:FPR_06970	ko:K18369	NA	
ICBIDGAJ_01020	OG0000791	adeC	1	0	0	fpr:FP2_03930	ko:K01486	NA	
ICBIDGAJ_01021	OG0000792	group_2888	1	0	0	fpa:FPR_07010;fpr:FP2_04060	NA	NA	
ICBIDGAJ_01022	OG0000793	fic_2	1	0	0	fpr:FP2_04070	NA	NA	
ICBIDGAJ_01023	OG0000794	group_7185	1	0	0	fpr:FP2_04140;fpa:FPR_07210	NA	NA	
ICBIDGAJ_01024	OG0000795	group_2889	1	0	0	fpa:FPR_07230	NA	NA	
ICBIDGAJ_01025	OG0002255	group_2050	1	0	0	fpa:FPR_07240	NA	NA	
ICBIDGAJ_01026	OG0000041	sigE_1	0	1	0	ova:OBV_12200	ko:K03091	NA	
ICBIDGAJ_01027	OG0002128	group_2051	1	0	0	fpa:FPR_07650	NA	NA	
ICBIDGAJ_01028	OG0003093	group_465	1	1	1	NA	NA	NA	
ICBIDGAJ_01029	OG0001710	group_2890	1	0	0	fpa:FPR_07280	ko:K01187	NA	
ICBIDGAJ_01030	OG0000042	dinB_1	1	0	0	fpr:FP2_17610	ko:K03502	NA	
ICBIDGAJ_01031	OG0000051	group_473	1	0	0	fpa:FPR_07310	NA	NA	
ICBIDGAJ_01032	OG0000094	group_615	1	1	1	NA	NA	NA	
ICBIDGAJ_01033	OG0000796	mta	1	0	0	fpr:FP2_03790	NA	NA	
ICBIDGAJ_01034	OG0000219	draG_2	0	1	0	fpa:FPR_06830	NA	NA	
ICBIDGAJ_01035	OG0002584	group_3795	1	0	0	fpr:FP2_12120	NA	NA	
ICBIDGAJ_01036	OG0000043	group_399	1	0	0	fpr:FP2_17680;fpa:FPR_06960	NA	NA	
ICBIDGAJ_01037	OG0002300	group_4098	0	1	0	NA	NA	NA	
ICBIDGAJ_01038	OG0000027	group_4100	1	0	0	cad:Curi_c00320	NA	NA	
ICBIDGAJ_01039	OG0002005	nnr_2	1	0	0	fpa:FPR_07370	ko:K17758;ko:K17759	NA	
ICBIDGAJ_01040	OG0001711	group_1323	1	0	0	fpa:FPR_07380	NA	NA	
ICBIDGAJ_01041	OG0002375	group_2895	2	1	2	bprs:CK3_12710	NA	NA	
ICBIDGAJ_01042	OG0001712	group_784	1	0	0	fpa:FPR_07400	NA	NA	
ICBIDGAJ_01043	OG0002006	pip	1	0	0	fpr:FP2_17710	NA	NA	
ICBIDGAJ_01044	OG0001713	group_2897	1	0	0	fpr:FP2_17720	NA	NA	
ICBIDGAJ_01045	OG0002420	sttH_2	1	0	0	fpr:FP2_17730	NA	NA	
ICBIDGAJ_01046	OG0000797	group_789	1	1	1	fpa:FPR_07430	NA	NA	
ICBIDGAJ_01047	OG0000798	zupT_2	4	4	7	fpa:FPR_07440	ko:K07238	NA	
ICBIDGAJ_01048	OG0000062	rebM_1	1	0	0	fpr:FP2_27850	NA	NA	
ICBIDGAJ_01049	OG0000133	group_476	1	0	0	fpa:FPR_07450	NA	NA	
ICBIDGAJ_01050	OG0003094	group_478	1	0	0	fpa:FPR_07130	NA	NA	
ICBIDGAJ_01051	OG0002007	ybiR	6	6	11	fpa:FPR_07470	NA	NA	
ICBIDGAJ_01052	OG0002130	group_2410	3	3	5	fpa:FPR_07480	ko:K07088	NA	
ICBIDGAJ_01053	OG0002258	group_2898	6	6	11	fpa:FPR_07500	ko:K03308	NA	
ICBIDGAJ_01054	OG0002259	cmpR	1	0	0	fpa:FPR_07510	NA	NA	

ICBIDGAJ_01055	OG0002421	group_4102	1	0	0	ral:Rumal_1887	NA	NA	
ICBIDGAJ_01056	OG0000095	group_3798	1	0	0	fpa:FPR_07580	NA	NA	
ICBIDGAJ_01057	OG0000799	rsxB_1	1	0	0	fpa:FPR_07590	NA	NA	
ICBIDGAJ_01058	OG0001714	pyk_1	1	0	0	fpa:FPR_25720	ko:K00873	NA	
ICBIDGAJ_01059	OG0000043	group_400	1	0	0	fpa:FPR_06960	NA	NA	
ICBIDGAJ_01060	OG0003095	group_470	0	1	0	NA	NA	NA	
ICBIDGAJ_01061	OG0000800	yodJ	1	1	1	fpa:FPR_21090	ko:K07260	NA	
ICBIDGAJ_01062	OG0000801	group_1324	1	0	0	NA	NA	NA	
ICBIDGAJ_01063	OG0000802	group_1325	1	0	0	fpr:FP2_05740	NA	NA	
ICBIDGAJ_01064	OG0000803	lgt	4	4	7	fpa:FPR_21120	ko:K13292	NA	
ICBIDGAJ_01065	OG0000804	group_3799	1	0	0	fpr:FP2_05760	NA	NA	
ICBIDGAJ_01066	OG0003096	group_3800	1	0	0	fpr:FP2_05770	NA	NA	
ICBIDGAJ_01067	OG0000805	rplU	1	0	0	fpa:FPR_21130	ko:K02888	NA	
ICBIDGAJ_01068	OG0000806	rpmA	1	0	0	fpa:FPR_21140	ko:K02899	NA	
ICBIDGAJ_01069	OG0000807	obg	1	0	0	fpa:FPR_21150	ko:K03979	NA	
ICBIDGAJ_01070	OG0002008	group_2412	0	1	0	NA	NA	NA	
ICBIDGAJ_01071	OG0000808	rsmF	1	0	0	fpr:FP2_05830	NA	NA	
ICBIDGAJ_01072	OG0000809	group_2413	1	0	0	fpr:FP2_05840	NA	NA	
ICBIDGAJ_01073	OG0003883	group_4103	1	0	0	NA	NA	specific_fp14	○
ICBIDGAJ_01074	OG0003884	group_4104	1	1	1	NA	NA	specific_fp14	○
ICBIDGAJ_01075	OG0003160	group_4105	1	0	0	NA	NA	NA	
ICBIDGAJ_01076	OG0000045	group_3100	0	1	0	rim:ROI_23630	NA	NA	
ICBIDGAJ_01077	OG0002052	group_3101	1	0	0	bprl:CL2_12660	NA	NA	
ICBIDGAJ_01078	OG0002053	group_3102	1	0	0	fpa:FPR_11180	NA	NA	
ICBIDGAJ_01079	OG0000810	prkC_2	1	1	1	fpa:FPR_21340	ko:K12132	NA	
ICBIDGAJ_01080	OG0000811	gltB_1	1	0	0	fpr:FP2_19270	ko:K00266	NA	
ICBIDGAJ_01081	OG0000812	gltB_2	1	0	0	fpr:FP2_19280	NA	NA	
ICBIDGAJ_01082	OG0002585	group_4106	1	1	1	NA	NA	NA	
ICBIDGAJ_01083	OG0000813	hcp	1	0	0	fpa:FPR_21380	ko:K05601	NA	
ICBIDGAJ_01084	OG0000814	gdh	1	0	0	fpa:FPR_21390	ko:K00262	NA	
ICBIDGAJ_01085	OG0000815	group_3803	1	0	0	btp:D805_0114	NA	NA	
ICBIDGAJ_01086	OG0000816	apbC	1	0	0	fpa:FPR_21400	NA	NA	
ICBIDGAJ_01087	OG0000817	spoVB	6	6	11	fpr:FP2_19320	ko:K06409	NA	
ICBIDGAJ_01088	OG0000818	pglF	2	2	3	cno:NT01CX_1779	NA	NA	
ICBIDGAJ_01089	OG0000819	lysA	1	0	0	fpr:FP2_19340	ko:K01586	NA	
ICBIDGAJ_01090	OG0000820	group_1336	2	2	3	fpr:FP2_19350	NA	NA	
ICBIDGAJ_01091	OG0002131	group_3804	2	1	2	NA	NA	NA	
ICBIDGAJ_01093	OG0000821	pyrH	1	0	0	fpr:FP2_05500	ko:K09903	NA	
ICBIDGAJ_01094	OG0000822	frr	1	0	0	fpr:FP2_05510	ko:K02838	NA	
ICBIDGAJ_01095	OG0000823	uppS	1	0	0	fpa:FPR_24380	ko:K00806	NA	
ICBIDGAJ_01096	OG0000824	cdsA	4	5	8	fpr:FP2_05530	ko:K00981	NA	
ICBIDGAJ_01097	OG0000825	dxr	1	0	0	fpa:FPR_24400	ko:K00099	NA	
ICBIDGAJ_01098	OG0003885	rasP	1	1	1	fpa:FPR_24410	ko:K11749	NA	
ICBIDGAJ_01099	OG0000826	group_543	1	2	2	fpa:FPR_24410	ko:K11749	NA	
ICBIDGAJ_01100	OG0000827	ispG	1	0	0	fpa:FPR_24420	ko:K03526	NA	
ICBIDGAJ_01101	OG0001810	group_3805	1	0	0	rch:RUM_23380	ko:K04095	NA	
ICBIDGAJ_01102	OG0000828	polC_3	1	0	0	fpr:FP2_05580	ko:K03763	NA	
ICBIDGAJ_01103	OG0000829	phoU_2	5	5	9	fpa:FPR_21020	ko:K03324	NA	
ICBIDGAJ_01104	OG0002009	group_1342	1	0	0	NA	NA	NA	
ICBIDGAJ_01105	OG0002616	group_4107	1	0	0	fpr:FP2_15180	NA	NA	
ICBIDGAJ_01106	OG0001798	group_4108	1	0	0	NA	NA	NA	
ICBIDGAJ_01107	OG0002010	group_2903	1	0	0	eha:Ethha_1796	NA	NA	
ICBIDGAJ_01108	OG0000830	group_1343	1	0	0	fpa:FPR_24460	NA	NA	
ICBIDGAJ_01109	OG0000831	group_1344	1	0	0	fpr:FP2_05600	NA	NA	
ICBIDGAJ_01110	OG0000832	group_1345	1	0	0	fpa:FPR_24440	ko:K07030	NA	
ICBIDGAJ_01111	OG0000833	group_2904	1	1	1	fpr:FP2_05650	NA	NA	
ICBIDGAJ_01112	OG0000834	pbpF	1	1	1	fpa:FPR_21040	ko:K05366	NA	
ICBIDGAJ_01113	OG0000835	group_2055	1	0	0	ccel:CCDG5_0140	ko:K06209	NA	
ICBIDGAJ_01114	OG0000836	hom	1	0	0	fpr:FP2_05690	ko:K00003	NA	
ICBIDGAJ_01115	OG0000837	thrB	1	0	0	fpr:FP2_05700	ko:K00872	NA	
ICBIDGAJ_01116	OG0000838	group_1349	1	0	0	fpa:FPR_21080	ko:K00928	NA	
ICBIDGAJ_01117	OG0001716	dmdA_2	1	0	0	med:MELS_0490	ko:K01681	NA	
ICBIDGAJ_01118	OG0000839	phnPP	1	0	0	fpr:FP2_18910	NA	NA	
ICBIDGAJ_01119	OG0000840	group_1351	1	0	0	fpr:FP2_18900	NA	NA	
ICBIDGAJ_01120	OG0000841	clpC_1	1	0	0	fpr:FP2_04930	ko:K03696	NA	
ICBIDGAJ_01121	OG0000842	bmrU	1	0	0	fpa:FPR_21840	NA	NA	
ICBIDGAJ_01122	OG0000843	groS	1	0	0	fpr:FP2_04980	ko:K04078	NA	
ICBIDGAJ_01123	OG0000844	groL	1	0	0	fpa:FPR_23720	ko:K04077	NA	
ICBIDGAJ_01124	OG0000845	group_2415	1	1	1	fpr:FP2_05000	ko:K05515	NA	
ICBIDGAJ_01125	OG0000846	secG	1	2	2	fpa:FPR_23880	ko:K03075	NA	
ICBIDGAJ_01126	OG0000847	rnr	1	0	0	fpr:FP2_05020	ko:K12573	NA	
ICBIDGAJ_01127	OG0000848	group_618	1	0	0	fpa:FPR_28270	ko:K10254	NA	
ICBIDGAJ_01128	OG0000849	mggB	1	0	0	ibu:1B211_02952c	NA	NA	
ICBIDGAJ_01129	OG0002132	group_2906	1	0	0	NA	NA	NA	
ICBIDGAJ_01131	OG0000850	group_1359	0	1	0	fpa:FPR_28290	NA	NA	
ICBIDGAJ_01132	OG0000851	group_2907	0	1	0	fpr:FP2_04270	NA	NA	
ICBIDGAJ_01133	OG0000852	group_1360	1	0	0	fpa:FPR_28310	ko:K06871	NA	
ICBIDGAJ_01134	OG0000853	speA_2	1	0	0	fpa:FPR_28320	NA	NA	
ICBIDGAJ_01135	OG0003098	group_3808	1	0	0	bfa:Bfae_12220	ko:K19002	NA	
ICBIDGAJ_01136	OG0000854	copA	4	5	8	fpr:FP2_19250	ko:K01533	NA	
ICBIDGAJ_01137	OG0000855	group_3809	1	0	0	fpr:FP2_19260	ko:K21600	NA	
ICBIDGAJ_01138	OG0000856	group_2057	1	0	0	fpr:FP2_05880	NA	NA	
ICBIDGAJ_01139	OG0000857	group_620	1	0	0	fpa:FPR_29800	NA	NA	
ICBIDGAJ_01140	OG0000858	group_794	1	0	0	fpr:FP2_05900	NA	NA	
ICBIDGAJ_01141	OG0000859	rpmB	0	1	0	fpr:FP2_05910	ko:K02902	NA	
ICBIDGAJ_01142	OG0000860	group_1363	3	3	5	fpa:FPR_29820	NA	NA	
ICBIDGAJ_01143	OG0000861	scpA	1	0	0	fpr:FP2_05930	ko:K05896	NA	
ICBIDGAJ_01144	OG0000862	scpB	1	0	0	fpa:FPR_29840	ko:K06024	NA	
ICBIDGAJ_01145	OG0000863	group_2416	1	1	1	fpr:FP2_05950	NA	NA	
ICBIDGAJ_01146	OG0000864	ytfJ	1	0	0	fpr:FP2_05980	NA	NA	
ICBIDGAJ_01147	OG0000865	rluB	1	0	0	fpr:FP2_05990	ko:K06178	NA	
ICBIDGAJ_01148	OG0000866	group_1367	1	0	0	fpa:FPR_30100	NA	NA	
ICBIDGAJ_01149	OG0000867	gcdC	1	0	0	fpa:FPR_30110	NA	NA	
ICBIDGAJ_01150	OG0000868	group_2418	1	0	0	fpa:FPR_30120	ko:K01571	NA	
ICBIDGAJ_01151	OG0001717	group_1368	4	4	7	rto:RTO_29700	NA	NA	
ICBIDGAJ_01152	OG0001718	betI	1	0	0	fpa:FPR_14610	NA	NA	
ICBIDGAJ_01153	OG0000869	group_1369	1	0	0	fpa:FPR_30140	NA	NA	
ICBIDGAJ_01154	OG0000870	group_1370	1	0	0	fpa:FPR_30150	ko:K09777	NA	
ICBIDGAJ_01155	OG0000871	gmk	1	0	0	fpr:FP2_06050	ko:K00942	NA	
ICBIDGAJ_01156	OG0000872	priA	1	0	0	fpa:FPR_30170	ko:K04066	NA	
ICBIDGAJ_01157	OG0000873	def1	1	0	0	fpa:FPR_30180	ko:K01462	NA	
ICBIDGAJ_01158	OG0000874	fmt	1	0	0	fpr:FP2_06080	ko:K00604	NA	
ICBIDGAJ_01159	OG0000875	rsmB	1	0	0	fpa:FPR_30200	ko:K03500	NA	
ICBIDGAJ_01160	OG0000876	rlmN	1	0	0	fpr:FP2_06100	ko:K06941	NA	
ICBIDGAJ_01161	OG0000877	stp	1	0	0	fpa:FPR_30220	ko:K20074	NA	
ICBIDGAJ_01162	OG0000878	prkC_1	1	1	1	fpa:FPR_30230	ko:K12132	NA	
ICBIDGAJ_01163	OG0000879	rsgA	1	0	0	fpa:FPR_30240	ko:K06949	NA	
ICBIDGAJ_01164	OG0000880	thiN	1	0	0	fpr:FP2_06140	ko:K00949	NA	
ICBIDGAJ_01165	OG0000881	dppE	1	1	1	NA	NA	NA	
ICBIDGAJ_01166	OG0000882	murD	1	0	0	fpa:FPR_29440	ko:K01925	NA	
ICBIDGAJ_01167	OG0000883	group_2420	1	0	0	NA	NA	NA	
ICBIDGAJ_01168	OG0000884	group_1382	1	0	0	fpr:FP2_20740	NA	NA	
ICBIDGAJ_01169	OG0002133	pepE	1	0	0	afn:Acfer_1040	ko:K01372	NA	
ICBIDGAJ_01170	OG0002011	group_2909	4	4	7	fpr:FP2_20720	NA	NA	

ICBIDGAJ_01171	OG0002012	regX3_2	1	0	0	fpr:FP2_20710	NA	NA	
ICBIDGAJ_01172	OG0000885	urdA	1	0	0	fpr:FP2_20700	NA	NA	
ICBIDGAJ_01173	OG0000886	mgsA_2	1	0	0	fpr:FP2_20690	ko:K01734	NA	
ICBIDGAJ_01174	OG0000223	proA	1	0	0	fpr:FP2_20680	ko:K00147	NA	
ICBIDGAJ_01175	OG0000887	proB	1	0	0	fpr:FP2_20670	ko:K00931	NA	
ICBIDGAJ_01176	OG0000888	proC	1	0	0	fpr:FP2_20660	ko:K00286	NA	
ICBIDGAJ_01177	OG0000889	dhaS	1	0	0	fpr:FP2_20650	NA	NA	
ICBIDGAJ_01178	OG0002134	group_619	1	0	0	fpla:A4U99_16770	ko:K10254	NA	
ICBIDGAJ_01179	OG0000890	mftC	1	0	0	fpa:FPR_29530	NA	NA	
ICBIDGAJ_01180	OG0000077	group_4109	1	2	2	NA	NA	NA	
ICBIDGAJ_01181	OG0003161	group_3103	1	1	1	NA	NA	NA	
ICBIDGAJ_01182	OG0000891	group_1386	4	5	8	fpr:FP2_20630	NA	NA	
ICBIDGAJ_01183	OG0000892	cat1	1	0	0	fpa:FPR_29560	NA	NA	
ICBIDGAJ_01184	OG0000893	coaD	1	0	0	fpa:FPR_29570	ko:K00954	NA	
ICBIDGAJ_01185	OG0000894	thlA	1	0	0	fpa:FPR_29580	ko:K00626	NA	
ICBIDGAJ_01186	OG0000895	crt	1	0	0	fpa:FPR_29590	ko:K01715	NA	
ICBIDGAJ_01187	OG0000896	hbd	1	0	0	fpa:FPR_29600	ko:K00074	NA	
ICBIDGAJ_01188	OG0000897	bcd_1	1	0	0	fpa:FPR_29610	NA	NA	
ICBIDGAJ_01189	OG0000898	acrB	1	0	0	fpr:FP2_20560	ko:K03521	NA	
ICBIDGAJ_01190	OG0000899	acrA	1	0	0	fpa:FPR_29630	ko:K03522	NA	
ICBIDGAJ_01191	OG0000900	group_2423	1	0	0	fpr:FP2_06170	NA	NA	
ICBIDGAJ_01192	OG0000901	xanP	7	7	13	fpr:FP2_06200	NA	NA	
ICBIDGAJ_01193	OG0000902	mobA_5	1	0	0	fpa:FPR_30830	ko:K07141	NA	
ICBIDGAJ_01194	OG0000903	coxM	1	0	0	fpr:FP2_06960	NA	NA	
ICBIDGAJ_01195	OG0000904	hcrC	1	0	0	fpr:FP2_06970	ko:K03518	NA	
ICBIDGAJ_01196	OG0000905	xdhA	1	0	0	fpr:FP2_06980	NA	NA	
ICBIDGAJ_01197	OG0000906	group_2062	1	0	0	fpr:FP2_06990	NA	NA	
ICBIDGAJ_01198	OG0000907	selD	1	0	0	fpr:FP2_07000	ko:K01008	NA	
ICBIDGAJ_01199	OG0000908	group_622	1	0	0	fpr:FP2_07010	NA	NA	
ICBIDGAJ_01200	OG0000909	csdA	1	0	0	cct:CC1_06390	NA	NA	
ICBIDGAJ_01201	OG0000910	group_2063	1	0	0	fpa:FPR_30750	NA	NA	
ICBIDGAJ_01202	OG0000911	group_3810	1	0	0	fpr:FP2_07040	ko:K07402	NA	
ICBIDGAJ_01203	OG0000912	group_800	1	0	0	fpa:FPR_30730	ko:K07402	NA	
ICBIDGAJ_01204	OG0000913	group_1394	1	0	0	fpr:FP2_08280	NA	NA	
ICBIDGAJ_01205	OG0000914	rpsA_2	1	0	0	fpr:FP2_08270	NA	NA	
ICBIDGAJ_01206	OG0000915	group_801	1	0	0	fpa:FPR_28890	NA	NA	
ICBIDGAJ_01207	OG0000916	prfA	1	0	0	fpr:FP2_08250	ko:K02835	NA	
ICBIDGAJ_01208	OG0000917	ywlC	1	0	0	fpr:FP2_08240	ko:K07566	NA	
ICBIDGAJ_01209	OG0000918	coaE	1	0	0	fpa:FPR_28920	ko:K00859	NA	
ICBIDGAJ_01210	OG0000919	slt	1	1	1	fpr:FP2_08220	ko:K08309	NA	
ICBIDGAJ_01211	OG0000920	apeA	1	0	0	fpr:FP2_08210	NA	NA	
ICBIDGAJ_01212	OG0001811	hmrR	1	2	2	fpa:FPR_28950	NA	NA	
ICBIDGAJ_01213	OG0000921	group_1400	1	1	1	fpa:FPR_28960	NA	NA	
ICBIDGAJ_01216	OG0000922	spoIVB	1	1	1	fpr:FP2_08190	ko:K06399	NA	
ICBIDGAJ_01217	OG0000923	spo0A	1	0	0	fpa:FPR_24320	ko:K07699	NA	
ICBIDGAJ_01218	OG0001719	group_3812	4	5	8	cbut:ATN24_18215	NA	NA	
ICBIDGAJ_01219	OG0001812	group_2064	4	5	8	fpa:FPR_19750	NA	NA	
ICBIDGAJ_01220	OG0000924	rpmE	0	1	0	fpa:FPR_28670	ko:K02909	NA	
ICBIDGAJ_01221	OG0000925	yxlF_2	1	0	0	ova:OBV_00490	ko:K01990	NA	
ICBIDGAJ_01222	OG0000926	group_1401	4	5	8	fpr:FP2_08120	ko:K01992	NA	
ICBIDGAJ_01223	OG0000927	group_2426	1	2	2	fpr:FP2_08110	ko:K01992	NA	
ICBIDGAJ_01224	OG0000928	group_2912	1	1	1	fpa:FPR_28710	NA	NA	
ICBIDGAJ_01225	OG0000224	potA_1	1	0	0	fpa:FPR_28720	ko:K11072	NA	
ICBIDGAJ_01226	OG0000225	potH	3	4	6	fpa:FPR_28730	ko:K11071	NA	
ICBIDGAJ_01227	OG0000929	ydcV	3	4	6	fpr:FP2_08070	ko:K11070	NA	
ICBIDGAJ_01228	OG0000930	potD	1	2	2	fpa:FPR_28750	ko:K11069	NA	
ICBIDGAJ_01229	OG0000931	group_2427	1	0	0	fpr:FP2_08050	NA	NA	
ICBIDGAJ_01230	OG0000166	guaB	1	0	0	fpr:FP2_08030	ko:K00088	NA	
ICBIDGAJ_01231	OG0000167	pncB2	1	0	0	fpa:FPR_28390	ko:K00763	NA	
ICBIDGAJ_01233	OG0002013	ttcA	1	0	0	fpr:FP2_06910	NA	NA	
ICBIDGAJ_01234	OG0000932	iscS_2	1	0	0	fpr:FP2_06920	ko:K04487	NA	
ICBIDGAJ_01235	OG0000933	pyrP	6	7	12	fpr:FP2_06930	ko:K02824	NA	
ICBIDGAJ_01236	OG0000934	rbr3B	1	0	0	fpr:FP2_06940	NA	NA	
ICBIDGAJ_01237	OG0000226	group_1408	4	5	8	fpr:FP2_06210	NA	NA	
ICBIDGAJ_01238	OG0000935	group_2065	1	0	0	fpa:FPR_30020	NA	NA	
ICBIDGAJ_01239	OG0002014	group_2066	1	0	0	rim:ROI_20080	NA	NA	
ICBIDGAJ_01240	OG0000936	group_1409	0	1	0	fpa:FPR_30030	NA	NA	
ICBIDGAJ_01241	OG0000937	hdl IVa	1	0	0	fpa:FPR_30040	NA	NA	
ICBIDGAJ_01242	OG0000938	group_2916	1	0	0	fpr:FP2_06250	NA	NA	
ICBIDGAJ_01243	OG0000939	ltaS1	3	3	5	fpr:FP2_06260	NA	NA	
ICBIDGAJ_01244	OG0000940	rpsB	1	0	0	fpa:FPR_30070	ko:K02967	NA	
ICBIDGAJ_01245	OG0000941	tsf	1	0	0	fpa:FPR_30080	ko:K02357	NA	
ICBIDGAJ_01246	OG0000942	group_2917	1	0	0	fpa:FPR_24550	ko:K06889	NA	
ICBIDGAJ_01247	OG0000943	mshD_1	1	0	0	fpr:FP2_06290	NA	NA	
ICBIDGAJ_01248	OG0000944	cstA_1	8	8	15	fpa:FPR_24560	ko:K06200	NA	
ICBIDGAJ_01249	OG0000945	group_1414	0	1	0	fpa:FPR_24570	NA	NA	
ICBIDGAJ_01250	OG0000946	group_1415	1	0	0	fpr:FP2_06320	NA	NA	
ICBIDGAJ_01251	OG0000947	group_1416	1	0	0	fpa:FPR_24590	ko:K01091	NA	
ICBIDGAJ_01252	OG0000948	group_2067	1	1	1	fpr:FP2_06340	NA	NA	
ICBIDGAJ_01253	OG0000949	group_3813	1	0	0	fpr:FP2_06350	NA	NA	
ICBIDGAJ_01254	OG0000950	yfnB	1	0	0	fpr:FP2_06360	ko:K01560	NA	
ICBIDGAJ_01255	OG0000951	yheS	1	0	0	fpa:FPR_24630	ko:K06158	NA	
ICBIDGAJ_01256	OG0000952	group_1419	3	3	5	fpa:FPR_24640	ko:K00805	NA	
ICBIDGAJ_01257	OG0000953	lon1	1	0	0	fpr:FP2_06390	ko:K01338	NA	
ICBIDGAJ_01258	OG0000954	engB	1	0	0	fpa:FPR_24660	ko:K03978	NA	
ICBIDGAJ_01259	OG0000955	group_1422	1	0	0	fpr:FP2_06410	NA	NA	
ICBIDGAJ_01260	OG0000956	hslO	1	0	0	fpr:FP2_06420	ko:K04083	NA	
ICBIDGAJ_01261	OG0002422	esiB_1	1	0	0	NA	NA	NA	
ICBIDGAJ_01262	OG0000957	group_2918	1	0	0	fpr:FP2_06430	ko:K06438	NA	
ICBIDGAJ_01263	OG0000958	group_2068	0	1	0	fpa:FPR_24710	NA	NA	
ICBIDGAJ_01264	OG0000959	group_2919	3	4	6	fpr:FP2_06450	NA	NA	
ICBIDGAJ_01265	OG0000960	group_805	1	0	0	fpr:FP2_07700	NA	NA	
ICBIDGAJ_01266	OG0000961	nusB	1	0	0	fpr:FP2_07710	ko:K03625	NA	
ICBIDGAJ_01267	OG0000962	tsaD_1	1	0	0	rus:RBI_I01341	ko:K01409	NA	
ICBIDGAJ_01268	OG0000963	xseA	1	0	0	eha:Ethha_1210	ko:K03601	NA	
ICBIDGAJ_01269	OG0000964	xseB	1	0	0	fpr:FP2_07740	ko:K03602	NA	
ICBIDGAJ_01270	OG0000965	group_1425	1	0	0	fpr:FP2_07750	ko:K13789	NA	
ICBIDGAJ_01271	OG0000966	group_1426	2	2	3	fpr:FP2_07760	ko:K09775	NA	
ICBIDGAJ_01272	OG0000967	dxs_2	1	0	0	fpr:FP2_07770	ko:K01662	NA	
ICBIDGAJ_01274	OG0000968	nadK	1	0	0	fpa:FPR_30460	ko:K00858	NA	
ICBIDGAJ_01275	OG0000969	argR	1	0	0	fpr:FP2_07800	ko:K03402	NA	
ICBIDGAJ_01276	OG0000970	recN	1	0	0	fpr:FP2_07810	ko:K03631	NA	
ICBIDGAJ_01277	OG0000971	tyrS	1	0	0	fpr:FP2_07820	ko:K01866	NA	
ICBIDGAJ_01278	OG0000972	lysC	1	0	0	fpr:FP2_07830	ko:K00928	NA	
ICBIDGAJ_01279	OG0002015	capA	1	1	1	fpr:FP2_07840	ko:K07282	NA	
ICBIDGAJ_01280	OG0000973	dapB	1	0	0	fpr:FP2_07850	ko:K00215	NA	
ICBIDGAJ_01281	OG0000974	dapA	1	0	0	fpr:FP2_07860	ko:K01714	NA	
ICBIDGAJ_01282	OG0000975	asd	1	0	0	fpa:FPR_30550	ko:K00133	NA	
ICBIDGAJ_01283	OG0000976	queA	1	0	0	fpa:FPR_30560	ko:K07568	NA	
ICBIDGAJ_01284	OG0001704	hin_1	1	0	0	cct:CC1_19830	NA	NA	
ICBIDGAJ_01285	OG0003886	group_4112	1	0	0	scz:ABE83_20045	NA	specific_fp14	O
ICBIDGAJ_01286	OG0002423	group_4113	1	0	0	NA	NA	NA	
ICBIDGAJ_01287	OG0003887	group_4114	1	0	0	NA	NA	specific_fp14	
ICBIDGAJ_01288	OG0002634	group_4115	1	0	0	bprl:CL2_18310	NA	NA	

ICBIDGAJ_01289	OG0003888	group_4116	1	0	0	NA	NA	specific_fp14	○
ICBIDGAJ_01290	OG0002635	group_4117	1	0	0	NA	NA	NA	
ICBIDGAJ_01291	OG0003889	group_4118	1	0	0	NA	NA	specific_fp14	○
ICBIDGAJ_01292	OG0003890	group_4119	1	0	0	NA	NA	specific_fp14	○
ICBIDGAJ_01293	OG0003891	group_4120	1	0	0	NA	NA	specific_fp14	○
ICBIDGAJ_01294	OG0003517	group_4121	1	0	0	NA	NA	NA	
ICBIDGAJ_01295	OG0003892	group_4122	1	0	0	bprl:CL2_18350	NA	specific_fp14	○
ICBIDGAJ_01296	OG0000024	group_4123	1	0	0	ere:EUBREC_2129	ko:K02315	NA	
ICBIDGAJ_01297	OG0003518	group_4124	1	0	0	NA	NA	NA	
ICBIDGAJ_01298	OG0003519	group_4125	1	0	0	ere:EUBREC_2127	NA	NA	
ICBIDGAJ_01299	OG0003520	group_4126	1	0	0	NA	NA	NA	
ICBIDGAJ_01300	OG0000134	ssbA_1	1	0	0	cth:Cthe_2186;ctx:Clo1313_2850	ko:K03111	NA	
ICBIDGAJ_01301	OG0003893	group_4128	1	0	0	NA	NA	specific_fp14	○
ICBIDGAJ_01302	OG0000157	group_4129	1	0	0	afl:Aflv_0414	ko:K00789	NA	
ICBIDGAJ_01303	OG0003162	group_4130	1	0	0	NA	NA	NA	
ICBIDGAJ_01304	OG0003894	group_4131	0	1	0	NA	NA	specific_fp14	○
ICBIDGAJ_01305	OG0003895	group_4132	1	0	0	ere:EUBREC_2118	NA	specific_fp14	○
ICBIDGAJ_01307	OG0003896	group_4134	1	0	0	bprl:CL2_18550	NA	specific_fp14	○
ICBIDGAJ_01308	OG0003897	group_4135	1	0	0	bprl:CL2_18560	NA	specific_fp14	○
ICBIDGAJ_01309	OG0003898	group_4136	1	0	0	ere:EUBREC_2115	NA	specific_fp14	○
ICBIDGAJ_01310	OG0003899	group_4137	1	0	0	gtn:GTNG_2829	NA	specific_fp14	○
ICBIDGAJ_01311	OG0003900	group_4138	1	0	0	NA	NA	specific_fp14	○
ICBIDGAJ_01312	OG0003901	group_4139	1	0	0	NA	NA	specific_fp14	○
ICBIDGAJ_01313	OG0003902	group_4140	0	1	0	NA	NA	specific_fp14	○
ICBIDGAJ_01314	OG0003903	group_4141	1	0	0	NA	NA	specific_fp14	○
ICBIDGAJ_01315	OG0002301	group_4142	1	0	0	NA	NA	NA	
ICBIDGAJ_01316	OG0003163	group_4143	1	0	0	NA	NA	NA	
ICBIDGAJ_01317	OG0002636	group_4144	0	1	0	NA	NA	NA	
ICBIDGAJ_01318	OG0002577	group_4145	1	0	0	NA	NA	NA	
ICBIDGAJ_01319	OG0003904	group_4146	1	0	0	stz:SPYALAB49_001010;spy:SPy_0980	NA	specific_fp14	
ICBIDGAJ_01320	OG0003905	group_4147	1	0	0	NA	NA	specific_fp14	○
ICBIDGAJ_01321	OG0003164	group_4148	1	0	0	bge:BC1002_6544	NA	NA	
ICBIDGAJ_01322	OG0003165	group_4149	1	0	0	bpt:Bpet0979	ko:K09960	NA	
ICBIDGAJ_01323	OG0003166	group_4150	1	0	0	NA	NA	NA	
ICBIDGAJ_01324	OG0003167	group_4151	1	0	0	NA	NA	NA	
ICBIDGAJ_01325	OG0003168	group_4152	0	1	0	NA	NA	NA	
ICBIDGAJ_01326	OG0003169	group_4153	1	0	0	NA	NA	NA	
ICBIDGAJ_01327	OG0003170	group_4154	1	0	0	aacn:AANUM_1176	NA	NA	
ICBIDGAJ_01328	OG0003906	group_4155	1	0	0	NA	NA	specific_fp14	○
ICBIDGAJ_01329	OG0003907	group_4156	1	0	0	NA	NA	specific_fp14	○
ICBIDGAJ_01330	OG0003171	group_4157	1	0	0	NA	NA	NA	
ICBIDGAJ_01331	OG0003172	group_4158	1	0	0	hit:NTHI1539	NA	NA	
ICBIDGAJ_01332	OG0003173	group_4159	1	0	0	NA	NA	NA	
ICBIDGAJ_01333	OG0003174	group_4160	1	0	0	NA	NA	NA	
ICBIDGAJ_01334	OG0002637	group_4161	3	3	5	eha:Ethha_1597	NA	NA	
ICBIDGAJ_01335	OG0003175	group_4162	1	0	0	NA	NA	NA	
ICBIDGAJ_01336	OG0003176	group_4163	1	0	0	NA	NA	NA	
ICBIDGAJ_01337	OG0003521	group_4164	1	0	0	NA	NA	NA	
ICBIDGAJ_01338	OG0003908	group_4165	1	0	0	NA	NA	specific_fp14	○
ICBIDGAJ_01339	OG0003177	group_4166	1	0	0	NA	NA	NA	
ICBIDGAJ_01340	OG0003178	group_4167	1	0	0	NA	NA	NA	
ICBIDGAJ_01341	OG0003179	group_4168	1	0	0	NA	NA	NA	
ICBIDGAJ_01342	OG0003180	group_4169	1	0	0	NA	NA	NA	
ICBIDGAJ_01343	OG0003181	group_4170	1	0	0	NA	NA	NA	
ICBIDGAJ_01344	OG0002301	group_4171	1	0	0	NA	NA	NA	
ICBIDGAJ_01345	OG0003909	group_4172	1	0	0	NA	NA	specific_fp14	○
ICBIDGAJ_01346	OG0003182	group_4173	1	0	0	fpr:FP2_16940	NA	NA	
ICBIDGAJ_01347	OG0002424	group_4174	1	0	0	spor:SporoP33_04460	NA	NA	
ICBIDGAJ_01348	OG0002638	group_4175	1	0	0	NA	NA	NA	
ICBIDGAJ_01349	OG0003910	group_4176	1	0	0	NA	NA	specific_fp14	
ICBIDGAJ_01350	OG0003522	group_4177	0	1	0	NA	NA	NA	
ICBIDGAJ_01351	OG0003911	group_4178	1	0	0	NA	NA	specific_fp14	
ICBIDGAJ_01352	OG0003912	group_4179	1	1	1	bprl:CL2_00100	NA	specific_fp14	○
ICBIDGAJ_01353	OG0001776	group_3104	1	1	1	amt:Amet_0863	NA	NA	
ICBIDGAJ_01354	OG0000108	group_4180	0	1	0	fpr:FP2_14360	NA	NA	
ICBIDGAJ_01355	OG0003523	group_4181	1	1	1	NA	NA	NA	
ICBIDGAJ_01356	OG0003913	group_4182	1	0	0	NA	NA	specific_fp14	○
ICBIDGAJ_01357	OG0003914	group_4183	1	0	0	NA	NA	specific_fp14	○
ICBIDGAJ_01358	OG0003915	group_4184	0	1	0	NA	NA	specific_fp14	○
ICBIDGAJ_01359	OG0003916	group_4185	0	1	0	NA	NA	specific_fp14	○
ICBIDGAJ_01360	OG0003917	group_4186	1	0	0	NA	NA	specific_fp14	○
ICBIDGAJ_01361	OG0003524	group_4187	0	1	0	NA	NA	NA	
ICBIDGAJ_01362	OG0003918	group_4188	1	1	1	NA	NA	specific_fp14	○
ICBIDGAJ_01363	OG0003919	group_4189	1	0	0	ssw:SSGZ1_0493	NA	specific_fp14	○
ICBIDGAJ_01364	OG0003920	group_4190	1	0	0	NA	NA	specific_fp14	○
ICBIDGAJ_01365	OG0003921	group_4191	1	0	0	NA	NA	specific_fp14	○
ICBIDGAJ_01366	OG0003922	group_4192	1	0	0	NA	NA	specific_fp14	○
ICBIDGAJ_01367	OG0003923	group_4193	1	0	0	NA	NA	specific_fp14	○
ICBIDGAJ_01368	OG0003924	group_4194	1	0	0	ruk:A4V00_11500	NA	specific_fp14	○
ICBIDGAJ_01369	OG0003925	group_4195	1	0	0	NA	NA	specific_fp14	○
ICBIDGAJ_01370	OG0003926	group_4196	1	0	0	bprs:CK3_26660	ko:K07171	specific_fp14	
ICBIDGAJ_01371	OG0003927	group_4197	1	0	0	NA	NA	specific_fp14	○
ICBIDGAJ_01372	OG0003928	group_4198	0	1	0	NA	NA	specific_fp14	○
ICBIDGAJ_01373	OG0003929	group_4199	0	1	0	NA	NA	specific_fp14	○
ICBIDGAJ_01374	OG0003930	group_4200	0	1	0	NA	NA	specific_fp14	○
ICBIDGAJ_01375	OG0003931	group_4201	1	0	0	NA	NA	specific_fp14	○
ICBIDGAJ_01376	OG0003932	group_4202	1	0	0	fpa:FPR_22590	NA	specific_fp14	
ICBIDGAJ_01377	OG0003933	group_4203	1	0	0	NA	NA	specific_fp14	○
ICBIDGAJ_01378	OG0003183	group_4204	1	0	0	NA	NA	NA	
ICBIDGAJ_01379	OG0003934	group_4205	1	0	0	NA	NA	specific_fp14	○
ICBIDGAJ_01380	OG0003935	group_4206	1	0	0	NA	NA	specific_fp14	○
ICBIDGAJ_01381	OG0003936	group_4207	1	0	0	NA	NA	specific_fp14	○
ICBIDGAJ_01382	OG0003937	group_4208	1	0	0	NA	NA	specific_fp14	○
ICBIDGAJ_01383	OG0003184	group_4209	1	0	0	fpr:FP2_00860	NA	NA	
ICBIDGAJ_01384	OG0002302	group_4210	1	0	0	NA	NA	NA	
ICBIDGAJ_01385	OG0003938	group_4211	0	1	0	NA	NA	specific_fp14	○
ICBIDGAJ_01386	OG0003939	group_4212	1	1	1	NA	NA	specific_fp14	
ICBIDGAJ_01387	OG0002425	group_4213	0	1	0	NA	NA	NA	
ICBIDGAJ_01388	OG0003940	group_4214	1	0	0	NA	NA	specific_fp14	○
ICBIDGAJ_01389	OG0003525	group_4215	1	0	0	NA	NA	NA	
ICBIDGAJ_01390	OG0000977	tgt	1	0	0	fpr:FP2_07890	ko:K00773	NA	
ICBIDGAJ_01391	OG0000978	group_2070	1	1	1	fpa:FPR_30580	ko:K03210	NA	
ICBIDGAJ_01392	OG0000979	group_2920	2	3	4	fpr:FP2_07910	NA	NA	
ICBIDGAJ_01393	OG0000980	group_3814	3	3	5	fpr:FP2_07920	NA	NA	
ICBIDGAJ_01395	OG0003099	group_2922	1	0	0	NA	NA	NA	
ICBIDGAJ_01396	OG0003941	group_4217	0	1	0	NA	NA	specific_fp14	○
ICBIDGAJ_01397	OG0003100	asbF	1	0	0	paej:H70737_15730	NA	NA	
ICBIDGAJ_01398	OG0002265	pht4	1	0	0	paej:H70737_15725	NA	NA	
ICBIDGAJ_01399	OG0002586	rifL	1	0	0	pmar:B0X71_16965	NA	NA	
ICBIDGAJ_01400	OG0003101	group_3820	1	0	0	pjd:Pjdr2_4072	NA	NA	
ICBIDGAJ_01401	OG0000981	group_1437	1	0	0	fpr:FP2_08010	ko:K06217	NA	
ICBIDGAJ_01402	OG0000982	ybeY	1	0	0	fpr:FP2_08000	ko:K07042	NA	
ICBIDGAJ_01403	OG0000983	era	1	0	0	rus:RBI_I00964	ko:K03595	NA	
ICBIDGAJ_01404	OG0000984	recO	1	0	0	fpr:FP2_07980	ko:K03584	NA	

ICBIDGAJ_01405	OG0000985	mutS2	1	0	0	fpa:FPR_30640	ko:K07456	NA
ICBIDGAJ_01406	OG0000986	amiB	1	1	1	cpro:CPRO_01620	ko:K01448	NA
ICBIDGAJ_01407	OG0002135	group_3821	1	0	0	csh:Closa_3311	NA	NA
ICBIDGAJ_01408	OG0000987	xerC_6	1	0	0	fpa:FPR_30620	NA	NA
ICBIDGAJ_01409	OG0000988	radA	1	0	0	fpr:FP2_07930	ko:K04485	NA
ICBIDGAJ_01410	OG0000989	group_1442	1	1	1	fpr:FP2_07690	ko:K06397	NA
ICBIDGAJ_01411	OG0000990	group_2923	1	1	1	fpr:FP2_07680	ko:K06396	NA
ICBIDGAJ_01412	OG0000991	group_2924	1	0	0	fpr:FP2_07670	NA	NA
ICBIDGAJ_01413	OG0000992	spoIIIAE	4	4	7	fpr:FP2_07660	ko:K06394	NA
ICBIDGAJ_01414	OG0000993	group_2925	1	2	2	fpr:FP2_07650	ko:K06393	NA
ICBIDGAJ_01415	OG0000994	group_2072	2	1	2	fpr:FP2_07640	ko:K06392	NA
ICBIDGAJ_01416	OG0000995	group_3823	1	0	0	fpa:FPR_30300	NA	NA
ICBIDGAJ_01417	OG0000996	group_2431	1	0	0	fpr:FP2_07620	ko:K06390	NA
ICBIDGAJ_01418	OG0000997	ligA	1	0	0	ruk:A4V00_16770	ko:K01972	NA
ICBIDGAJ_01419	OG0001813	panE	1	1	1	rto:RTO_24400	ko:K00077	NA
ICBIDGAJ_01420	OG0000998	pfkA	1	0	0	fpr:FP2_07600	ko:K00850	NA
ICBIDGAJ_01421	OG0000999	dnaE	1	0	0	fpr:FP2_07590	ko:K02337	NA
ICBIDGAJ_01422	OG0001000	whiA	1	0	0	fpr:FP2_07580	ko:K09762	NA
ICBIDGAJ_01423	OG0001001	yvcJ	1	0	0	fpr:FP2_07570	ko:K06958	NA
ICBIDGAJ_01424	OG0001002	murB	1	0	0	fpr:FP2_07560	ko:K00075	NA
ICBIDGAJ_01425	OG0001003	hprK	1	0	0	fpa:FPR_31130	ko:K06023	NA
ICBIDGAJ_01426	OG0001004	group_1447	5	5	9	fpa:FPR_31140	ko:K03324	NA
ICBIDGAJ_01427	OG0001005	phoB	1	0	0	fpa:FPR_31150	ko:K07658	NA
ICBIDGAJ_01428	OG0001006	senX3	2	1	2	fpr:FP2_07520	ko:K07636	NA
ICBIDGAJ_01429	OG0001007	group_2926	1	1	1	fpr:FP2_07510	NA	NA
ICBIDGAJ_01430	OG0001008	group_2927	3	4	6	fpr:FP2_07500	NA	NA
ICBIDGAJ_01431	OG0001009	gerBA	3	3	5	fpa:FPR_31190	ko:K06295	NA
ICBIDGAJ_01432	OG0001010	group_1450	1	2	2	fpa:FPR_31200	NA	NA
ICBIDGAJ_01433	OG0001011	group_1451	1	1	1	fpr:FP2_07460	NA	NA
ICBIDGAJ_01434	OG0001012	nrdR	1	0	0	fpr:FP2_07450	ko:K07738	NA
ICBIDGAJ_01435	OG0001013	group_1453	6	7	12	fpr:FP2_07440	ko:K12257	NA
ICBIDGAJ_01436	OG0001014	group_1454	1	0	0	fpr:FP2_07430	NA	NA
ICBIDGAJ_01437	OG0001015	clpX	1	0	0	fpa:FPR_31250	ko:K03544	NA
ICBIDGAJ_01438	OG0001016	clpP	1	0	0	fpa:FPR_31260	ko:K01358	NA
ICBIDGAJ_01439	OG0001017	tig_2	1	0	0	fpr:FP2_07400	ko:K03545	NA
ICBIDGAJ_01440	OG0001018	cpdA_2	1	0	0	fpr:FP2_07390	ko:K07099	NA
ICBIDGAJ_01441	OG0001019	thrC	1	0	0	fpa:FPR_31290	ko:K01733	NA
ICBIDGAJ_01442	OG0001020	group_1459	1	0	0	fpa:FPR_31300	ko:K07460	NA
ICBIDGAJ_01443	OG0001021	rnhB	1	0	0	fpr:FP2_07360	ko:K03470	NA
ICBIDGAJ_01444	OG0001022	rbgA	1	0	0	fpa:FPR_31320	ko:K14540	NA
ICBIDGAJ_01445	OG0000227	sipT	1	1	1	fpr:FP2_07340	ko:K03100	NA
ICBIDGAJ_01446	OG0001023	rplS	1	0	0	fpr:FP2_07330	ko:K02884	NA
ICBIDGAJ_01447	OG0001024	group_1463	1	0	0	fpr:FP2_07320	NA	NA
ICBIDGAJ_01448	OG0001025	group_1464	1	0	0	fpr:FP2_07310	NA	NA
ICBIDGAJ_01449	OG0001026	group_635	2	3	4	fpr:FP2_07300	NA	NA
ICBIDGAJ_01450	OG0001027	mepM_1	1	1	1	fpa:FPR_31380	NA	NA
ICBIDGAJ_01451	OG0000228	ppk	1	0	0	fpr:FP2_07280	ko:K00937	NA
ICBIDGAJ_01452	OG0001028	group_3824	1	1	1	fpa:FPR_31400	ko:K02237	NA
ICBIDGAJ_01453	OG0001029	group_2929	1	0	0	fpr:FP2_07260	NA	NA
ICBIDGAJ_01454	OG0001030	rluD_1	1	0	0	fpr:FP2_07250	ko:K06180	NA
ICBIDGAJ_01455	OG0001031	lspA	2	3	4	fpa:FPR_31430	ko:K03101	NA
ICBIDGAJ_01456	OG0001032	ileS	1	0	0	ccel:CCDG5_1587	ko:K01870	NA
ICBIDGAJ_01457	OG0001033	gpsB	1	0	0	fpr:FP2_07220	ko:K04074	NA
ICBIDGAJ_01458	OG0001034	group_1471	1	0	0	fpr:FP2_07210	NA	NA
ICBIDGAJ_01459	OG0001035	sepF	1	0	0	fpa:FPR_31470	ko:K09772	NA
ICBIDGAJ_01460	OG0001036	group_1473	1	1	1	fpa:FPR_31480	NA	NA
ICBIDGAJ_01461	OG0001037	miaA	1	0	0	rch:RUM_08860	ko:K00791	NA
ICBIDGAJ_01462	OG0001038	mutL	1	0	0	fpr:FP2_07170	ko:K03572	NA
ICBIDGAJ_01463	OG0001039	mutS_2	1	0	0	fpa:FPR_31510	ko:K03555	NA
ICBIDGAJ_01464	OG0001040	group_1475	1	0	0	fpr:FP2_07140	NA	NA
ICBIDGAJ_01465	OG0001041	miaB	1	0	0	ruk:A4V00_02495	ko:K06168	NA
ICBIDGAJ_01466	OG0001042	perR_2	1	0	0	fpr:FP2_07120	ko:K09825	NA
ICBIDGAJ_01467	OG0001043	group_1478	1	0	0	fpa:FPR_31550	ko:K07478	NA
ICBIDGAJ_01468	OG0001044	pdg	1	0	0	fpr:FP2_07100	ko:K10773	NA
ICBIDGAJ_01469	OG0001045	group_2557	2	3	4	NA	NA	NA
ICBIDGAJ_01470	OG0002060	group_2558	1	0	0	fpa:FPR_30700	NA	NA
ICBIDGAJ_01471	OG0002061	group_3105	1	1	1	fpa:FPR_30710	NA	NA
ICBIDGAJ_01472	OG0001720	slyA_3	1	0	0	NA	NA	NA
ICBIDGAJ_01473	OG0001721	group_2073	3	3	5	fpa:FPR_20960	ko:K06147	NA
ICBIDGAJ_01474	OG0001722	group_2074	3	3	5	fpa:FPR_20950	ko:K06147	NA
ICBIDGAJ_01475	OG0001046	ygaZ	3	3	5	fpr:FP2_07080	NA	NA
ICBIDGAJ_01476	OG0001047	group_814	2	2	3	fpr:FP2_07070	NA	NA
ICBIDGAJ_01477	OG0001048	group_2931	1	0	0	fpa:FPR_30860	ko:K00067	NA
ICBIDGAJ_01478	OG0001049	spoIVA	1	0	0	rch:RUM_03970	ko:K06398	NA
ICBIDGAJ_01479	OG0001050	group_3825	1	0	0	NA	NA	NA
ICBIDGAJ_01480	OG0001051	hexR	1	0	0	fpr:FP2_10600	NA	NA
ICBIDGAJ_01481	OG0001052	group_1482	1	0	0	fpa:FPR_16150	ko:K02027	NA
ICBIDGAJ_01482	OG0000229	lacF_3	3	4	6	fpa:FPR_16160	ko:K02025	NA
ICBIDGAJ_01483	OG0001053	araQ_3	3	4	6	fpr:FP2_10560	ko:K02026	NA
ICBIDGAJ_01484	OG0001054	nanA	1	0	0	fpr:FP2_10550	ko:K01639	NA
ICBIDGAJ_01485	OG0001055	tabA	1	0	0	fpr:FP2_10540	NA	NA
ICBIDGAJ_01486	OG0001056	nanE	1	0	0	fpa:FPR_16200	ko:K01788	NA
ICBIDGAJ_01487	OG0001057	glcK_1	1	0	0	fpa:FPR_16210	ko:K00845	NA
ICBIDGAJ_01488	OG0001058	group_1487	1	0	0	fpr:FP2_10510	NA	NA
ICBIDGAJ_01489	OG0002136	group_2933	1	0	0	ckr:CKR_2086;ckl:CKL_2367	NA	NA
ICBIDGAJ_01490	OG0001059	aspS2	1	0	0	fpa:FPR_28850	ko:K01876	NA
ICBIDGAJ_01491	OG0001060	pglC	1	1	1	fpr:FP2_19210	ko:K13012	NA
ICBIDGAJ_01492	OG0001908	group_2076	1	0	0	cle:Clole_0482	ko:K01187	NA
ICBIDGAJ_01493	OG0001061	mepA_10	6	7	12	fpr:FP2_05400	NA	NA
ICBIDGAJ_01494	OG0001062	group_816	1	0	0	fpr:FP2_05380	NA	NA
ICBIDGAJ_01495	OG0001063	yurK	1	0	0	fpr:FP2_05370	ko:K03710	NA
ICBIDGAJ_01496	OG0001064	pyrB_2	1	0	0	fpr:FP2_05360	ko:K00609	NA
ICBIDGAJ_01497	OG0001065	pyrI	1	0	0	fpr:FP2_05350	ko:K00610	NA
ICBIDGAJ_01498	OG0003942	group_1919	0	1	0	NA	NA	NA
ICBIDGAJ_01499	OG0001066	group_2934	4	3	6	fpa:FPR_29900	NA	NA
ICBIDGAJ_01500	OG0001067	lytR_1	1	0	0	fpa:FPR_29890	NA	NA
ICBIDGAJ_01501	OG0001068	group_1494	6	6	11	fpr:FP2_21060	ko:K03308	NA
ICBIDGAJ_01502	OG0003102	sigE_3	1	0	0	bprs:CK3_22120	ko:K03088	NA
ICBIDGAJ_01503	OG0003103	group_3827	1	2	2	NA	NA	NA
ICBIDGAJ_01504	OG0003104	group_2935	4	3	6	NA	NA	NA
ICBIDGAJ_01505	OG0003105	group_3828	3	4	6	bprs:CK3_22150	NA	NA
ICBIDGAJ_01506	OG0003106	group_3829	1	2	2	NA	NA	NA
ICBIDGAJ_01507	OG0000230	group_1495	1	0	0	fpr:FP2_05450	ko:K07576	NA
ICBIDGAJ_01508	OG0001069	typA	1	0	0	fpa:FPR_27910	ko:K06207	NA
ICBIDGAJ_01509	OG0001070	group_817	1	1	1	fpr:FP2_05430	NA	NA
ICBIDGAJ_01510	OG0001071	group_1496	1	0	0	fpr:FP2_05420	ko:K21071	NA
ICBIDGAJ_01511	OG0001072	pfp_2	1	0	0	fpa:FPR_20400	ko:K21071	NA
ICBIDGAJ_01512	OG0001073	group_1498	1	0	0	fpr:FP2_18530	NA	NA
ICBIDGAJ_01513	OG0001074	group_2436	2	3	4	fpr:FP2_18520	NA	NA
ICBIDGAJ_01514	OG0002587	sigL	1	0	0	fpr:FP2_14680	ko:K03088	NA
ICBIDGAJ_01515	OG0002588	group_2937	1	0	0	fpr:FP2_14690	NA	NA
ICBIDGAJ_01516	OG0001075	group_1499	1	0	0	fpr:FP2_18510	NA	NA
ICBIDGAJ_01517	OG0001076	group_1500	1	0	0	fpr:FP2_01750	NA	NA
ICBIDGAJ_01518	OG0001077	rlmI	1	0	0	fpa:FPR_29020	ko:K06969	NA

ICBIDGAJ_01519	OG0001078	glnA_1	1	0	0	fpa:FPR_29010	ko:K01915	NA	
ICBIDGAJ_01520	OG0001079	glnA_2	1	0	0	fpa:FPR_29000	ko:K01915	NA	
ICBIDGAJ_01521	OG0001080	pdtaR	1	0	0	fpr:FP2_01710	ko:K07183	NA	
ICBIDGAJ_01522	OG0001081	pyrG	1	0	0	fpa:FPR_28980	ko:K01937	NA	
ICBIDGAJ_01523	OG0001082	xlnA_1	1	0	0	fpr:FP2_01690	NA	NA	
ICBIDGAJ_01524	OG0001083	gerN	6	5	10	fpa:FPR_24270	NA	NA	
ICBIDGAJ_01525	OG0001084	rpsF	1	0	0	fpa:FPR_24260	ko:K02990	NA	
ICBIDGAJ_01526	OG0000134	ssb	1	0	0	fpr:FP2_05080	ko:K03111	NA	
ICBIDGAJ_01527	OG0001085	rpsR	1	0	0	fpa:FPR_24240	ko:K02963	NA	
ICBIDGAJ_01528	OG0001086	ccpA_3	1	0	0	fpr:FP2_18430	ko:K02529	NA	
ICBIDGAJ_01529	OG0001087	group_818	1	0	0	fpr:FP2_18420	ko:K10117	NA	
ICBIDGAJ_01530	OG0001088	ugpA	3	4	6	fpa:FPR_24200	ko:K10118	NA	
ICBIDGAJ_01531	OG0001089	araQ_4	3	4	6	fpr:FP2_18400	ko:K10119	NA	
ICBIDGAJ_01532	OG0001090	malQ_1	1	0	0	fpr:FP2_18390	ko:K00705	NA	
ICBIDGAJ_01533	OG0001091	group_3830	1	1	1	NA	NA	NA	
ICBIDGAJ_01534	OG0001092	group_2938	1	0	0	NA	NA	NA	
ICBIDGAJ_01535	OG0001093	galK_1	1	0	0	fpr:FP2_18360	ko:K00849	NA	
ICBIDGAJ_01536	OG0001094	araC_2	1	0	0	fpa:FPR_24140	NA	NA	
ICBIDGAJ_01537	OG0001095	group_636	1	0	0	fpr:FP2_18340	ko:K03215	NA	
ICBIDGAJ_01538	OG0000165	desR	1	0	0	apr:Apre_1519	NA	NA	
ICBIDGAJ_01539	OG0003943	group_4219	3	4	6	rto:RTO_29030	NA	specific_fp14	○
ICBIDGAJ_01540	OG0003944	group_4220	3	4	6	NA	NA	specific_fp14	○
ICBIDGAJ_01541	OG0003945	group_4221	3	4	6	rto:RTO_28990	NA	specific_fp14	○
ICBIDGAJ_01542	OG0001927	group_4222	1	0	0	rto:RTO_28980	ko:K01990	NA	
ICBIDGAJ_01543	OG0003185	group_3106	1	0	0	rho:RHOM_06470	NA	NA	
ICBIDGAJ_01544	OG0000177	group_4223	0	1	0	cct:CC1_08280;coo:CCU_02570;fpa:FPR_10820	NA	NA	
ICBIDGAJ_01545	OG0000102	group_922	0	1	0	rho:RHOM_06480;rob:CK5_03870;cct:CC1_08290	NA	NA	
ICBIDGAJ_01546	OG0003186	group_4224	1	0	0	coo:CCU_02560;cct:CC1_08300;fpa:FPR_10840;rho:RHOM_06485	NA	NA	
ICBIDGAJ_01547	OG0000103	group_4225	1	0	0	rho:RHOM_06490	NA	NA	
ICBIDGAJ_01548	OG0000059	group_276	1	0	0	rho:RHOM_06500	NA	NA	
ICBIDGAJ_01549	OG0003187	group_4226	0	1	0	fpa:FPR_10880;rho:RHOM_06505;coo:CCU_02520;cct:CC1_08340	NA	NA	
ICBIDGAJ_01550	OG0001868	group_4227	1	0	0	rho:RHOM_06510	NA	NA	
ICBIDGAJ_01551	OG0003526	group_4228	1	0	0	NA	NA	NA	
ICBIDGAJ_01552	OG0001929	bin3_1	1	0	0	ibu:IB211_00448c	NA	NA	
ICBIDGAJ_01553	OG0002426	rapA_3	1	0	0	dhd:Dhaf_0637	NA	NA	
ICBIDGAJ_01554	OG0003946	group_4230	1	0	0	sdr:SCD_n00858	NA	specific_fp14	○
ICBIDGAJ_01555	OG0003947	group_4231	1	0	0	dhd:Dhaf_0638	ko:K07445	specific_fp14	○
ICBIDGAJ_01556	OG0003948	group_4232	1	0	0	dhd:Dhaf_0639	NA	specific_fp14	○
ICBIDGAJ_01557	OG0000096	group_291	1	0	0	fpa:FPR_18710	NA	NA	
ICBIDGAJ_01558	OG0000086	group_2007	1	0	0	ibu:IB211_02791	NA	NA	
ICBIDGAJ_01559	OG0000024	dnaI_2	1	0	0	fpla:A4U99_10850	ko:K02315	NA	
ICBIDGAJ_01560	OG0002593	group_4233	1	0	0	coo:CCU_17040	NA	NA	
ICBIDGAJ_01561	OG0001909	group_2443	1	0	0	coo:CCU_17030	ko:K06400	NA	
ICBIDGAJ_01563	OG0001096	ydcP_2	1	0	0	fpr:FP2_05340	ko:K08303	NA	
ICBIDGAJ_01564	OG0001097	mltG	1	1	1	fpa:FPR_29990	ko:K07082	NA	
ICBIDGAJ_01565	OG0001098	group_1522	1	0	0	fpr:FP2_05320	NA	NA	
ICBIDGAJ_01566	OG0001099	tmk	1	0	0	fpr:FP2_05310	ko:K00943	NA	
ICBIDGAJ_01567	OG0000232	thyX	1	0	0	fpr:FP2_05300	ko:K03465	NA	
ICBIDGAJ_01568	OG0001100	pcrA	1	0	0	fpr:FP2_05290	ko:K03657	NA	
ICBIDGAJ_01569	OG0001101	gcdB_1	5	5	9	fpr:FP2_05280	ko:K01572	NA	
ICBIDGAJ_01570	OG0001102	group_1526	1	1	1	fpa:FPR_24530	NA	NA	
ICBIDGAJ_01571	OG0001103	mreB_2	1	0	0	fpr:FP2_05260	ko:K03569	NA	
ICBIDGAJ_01572	OG0001104	recD2	1	0	0	fpr:FP2_05250	ko:K03581	NA	
ICBIDGAJ_01573	OG0001105	mepA_8	5	6	10	fpa:FPR_28220	NA	NA	
ICBIDGAJ_01574	OG0003949	group_4234	1	0	0	NA	NA	specific_fp14	○
ICBIDGAJ_01575	OG0001810	group_4235	1	0	0	ova:OBV_28520	ko:K04095	NA	
ICBIDGAJ_01576	OG0003527	group_4236	0	1	0	NA	NA	NA	
ICBIDGAJ_01577	OG0001106	tcyC	1	0	0	fpr:FP2_05210	ko:K02028	NA	
ICBIDGAJ_01578	OG0001107	tcyB_2	3	2	4	cth:Cthe_1457;ctx:Clo1313_0794	ko:K02029	NA	
ICBIDGAJ_01579	OG0001108	fliY_2	1	0	0	fpa:FPR_28190	ko:K02030	NA	
ICBIDGAJ_01580	OG0001109	group_2446	1	0	0	fpa:FPR_28170	NA	NA	
ICBIDGAJ_01581	OG0001110	ywiE_1	2	2	3	fpr:FP2_05150	ko:K06131	NA	
ICBIDGAJ_01582	OG0001111	group_821	1	0	0	fpr:FP2_05140	NA	NA	
ICBIDGAJ_01583	OG0001112	group_822	1	0	0	fpr:FP2_05130	NA	NA	
ICBIDGAJ_01584	OG0001113	yycJ	1	0	0	fpa:FPR_31620	NA	NA	
ICBIDGAJ_01585	OG0001114	murAB	1	0	0	ccel:CCDG5_1556	ko:K00790	NA	
ICBIDGAJ_01586	OG0001115	fbp	1	0	0	fpr:FP2_18140	ko:K04041	NA	
ICBIDGAJ_01587	OG0001116	group_1537	1	0	0	fpr:FP2_18130	ko:K04070	NA	
ICBIDGAJ_01588	OG0000233	kdgK_2	1	0	0	fpa:FPR_31660	ko:K00874	NA	
ICBIDGAJ_01589	OG0003108	nagZ	1	1	1	pru:PRU_0656	ko:K01207	NA	
ICBIDGAJ_01590	OG0001117	opuBA	1	0	0	fpr:FP2_18050	ko:K05833	NA	
ICBIDGAJ_01591	OG0001118	group_1539	4	5	8	fpr:FP2_18040	ko:K05832	NA	
ICBIDGAJ_01592	OG0001119	group_1540	1	0	0	fpa:FPR_31690	ko:K01989	NA	
ICBIDGAJ_01593	OG0001120	group_1541	1	0	0	fpr:FP2_18020	ko:K06940	NA	
ICBIDGAJ_01594	OG0001814	dacB_3	1	1	1	fpa:FPR_31710	ko:K07258	NA	
ICBIDGAJ_01595	OG0003109	group_2948	1	0	0	NA	NA	NA	
ICBIDGAJ_01599	OG0000234	recR	1	0	0	fpr:FP2_03170	ko:K06187	NA	
ICBIDGAJ_01600	OG0001121	group_1542	1	0	0	fpr:FP2_03180	ko:K09747	NA	
ICBIDGAJ_01601	OG0000235	dnaX_2	1	0	0	fpr:FP2_03190	ko:K02343	NA	
ICBIDGAJ_01602	OG0000136	pta	1	0	0	fpr:FP2_03100	ko:K00625	NA	
ICBIDGAJ_01603	OG0000236	group_545	1	0	0	fpr:FP2_03090	ko:K02334	NA	
ICBIDGAJ_01604	OG0000168	group_640	1	0	0	fpr:FP2_03080	NA	NA	
ICBIDGAJ_01605	OG0000137	dinG	1	0	0	fpr:FP2_03070	NA	NA	
ICBIDGAJ_01606	OG0002016	group_3845	1	0	0	fpr:FP2_03060	ko:K00077	NA	
ICBIDGAJ_01607	OG0001122	merA	1	0	0	fpr:FP2_03050	NA	NA	
ICBIDGAJ_01608	OG0001724	yfcE_2	1	0	0	fpa:FPR_25730	ko:K07095	NA	
ICBIDGAJ_01609	OG0001123	mepA_9	6	7	12	fpr:FP2_03040	NA	NA	
ICBIDGAJ_01610	OG0001725	yitU_2	1	0	0	fpa:FPR_21720	NA	NA	
ICBIDGAJ_01611	OG0001124	group_2084	1	1	1	fpa:FPR_21700	NA	NA	
ICBIDGAJ_01612	OG0001125	group_2085	1	1	1	NA	NA	NA	
ICBIDGAJ_01613	OG0001126	ftsH	2	1	2	ruk:A4V00_10730	ko:K03798	NA	
ICBIDGAJ_01614	OG0001127	hpt	1	0	0	fpa:FPR_21670	ko:K00760	NA	
ICBIDGAJ_01615	OG0001128	tilS	1	0	0	fpa:FPR_21660	ko:K04075	NA	
ICBIDGAJ_01616	OG0001129	dnaC_2	1	0	0	fpr:FP2_16060	ko:K02314	NA	
ICBIDGAJ_01617	OG0001130	rplI	1	0	0	fpr:FP2_16050	ko:K02939	NA	
ICBIDGAJ_01618	OG0001131	glf	1	0	0	fpr:FP2_16040	ko:K01854	NA	
ICBIDGAJ_01619	OG0001132	gdpP	1	2	2	fpr:FP2_16030	NA	NA	
ICBIDGAJ_01620	OG0001133	rnjA	1	0	0	fpa:FPR_21610	ko:K12574	NA	
ICBIDGAJ_01621	OG0001134	rnhA	1	0	0	fpr:FP2_16010	ko:K03469	NA	
ICBIDGAJ_01622	OG0001135	mnmA_2	1	0	0	fpa:FPR_21580	ko:K00566	NA	
ICBIDGAJ_01623	OG0002138	group_3846	1	0	0	fpa:FPR_29640	NA	NA	
ICBIDGAJ_01624	OG0001136	group_1550	1	0	0	fpr:FP2_04950	NA	NA	
ICBIDGAJ_01625	OG0002017	group_2450	1	0	0	fpr:FP2_04960	NA	NA	
ICBIDGAJ_01626	OG0002018	group_3847	1	0	0	fpr:FP2_04970	NA	NA	
ICBIDGAJ_01627	OG0001137	potA_2	1	0	0	fpa:FPR_05270	ko:K02017	NA	
ICBIDGAJ_01628	OG0001138	modB	3	3	5	fpr:FP2_25930	ko:K02018	NA	
ICBIDGAJ_01629	OG0001139	modA	1	0	0	fpr:FP2_25940	ko:K02020	NA	
ICBIDGAJ_01630	OG0001140	mog	1	0	0	fpr:FP2_25950	NA	NA	
ICBIDGAJ_01631	OG0001141	moaA	1	0	0	fpr:FP2_25960	ko:K03639	NA	
ICBIDGAJ_01632	OG0001142	moaC	1	0	0	fpa:FPR_05320	ko:K03637	NA	
ICBIDGAJ_01633	OG0001143	cinA_1	1	0	0	fpr:FP2_25980	NA	NA	
ICBIDGAJ_01634	OG0001144	mobB	1	0	0	cbei:LF65_03646	ko:K03753	NA	
ICBIDGAJ_01635	OG0001726	moeA	1	0	0	fpa:FPR_05350	ko:K03750	NA	
ICBIDGAJ_01636	OG0001727	group_2088	1	0	0	fpa:FPR_05360	NA	NA	

ICBIDGAJ_01637	OG0001728	ydhV	1	0	0	fpa:FPR_05370	NA	NA	
ICBIDGAJ_01638	OG0001729	ydhY	1	0	0	fpr:FP2_26030	NA	NA	
ICBIDGAJ_01639	OG0001730	rsxG_1	1	1	1	fpr:FP2_26040	NA	NA	
ICBIDGAJ_01640	OG0001731	fdhD	1	0	0	fpr:FP2_26050	ko:K02379	NA	
ICBIDGAJ_01641	OG0001732	group_2951	3	4	6	NA	NA	NA	
ICBIDGAJ_01642	OG0002139	ecfT_1	3	2	4	rob:CK5_16700	ko:K16785	NA	
ICBIDGAJ_01643	OG0001691	ykoD	1	0	0	rob:CK5_16690	ko:K16786;ko:K16787	NA	
ICBIDGAJ_01644	OG0002140	group_2954	3	3	5	rob:CK5_16680	ko:K16924	NA	
ICBIDGAJ_01645	OG0000237	group_2955	1	0	0	fpa:FPR_05100	NA	NA	
ICBIDGAJ_01646	OG0001145	nirQ	1	0	0	fpr:FP2_02980	NA	NA	
ICBIDGAJ_01647	OG0001146	group_1555	1	0	0	fpr:FP2_02970	NA	NA	
ICBIDGAJ_01648	OG0001147	group_2956	1	0	0	fpr:FP2_02960	NA	NA	
ICBIDGAJ_01649	OG0001148	folD	1	0	0	fpr:FP2_09690	ko:K01491	NA	
ICBIDGAJ_01650	OG0001149	fchA	1	0	0	fpa:FPR_28010	NA	NA	
ICBIDGAJ_01651	OG0001150	ygfA	1	0	0	fpr:FP2_09710	ko:K01934	NA	
ICBIDGAJ_01652	OG0002019	pspB_1	1	0	0	fpr:FP2_02890	ko:K02226	NA	
ICBIDGAJ_01653	OG0001151	btuR	1	0	0	fpr:FP2_02930	ko:K19221	NA	
ICBIDGAJ_01654	OG0002020	group_3848	6	7	12	ruk:A4V00_06795	NA	NA	
ICBIDGAJ_01655	OG0001152	mraY_2	5	5	9	fpr:FP2_09640	ko:K01000	NA	
ICBIDGAJ_01656	OG0001153	yeeO_2	5	5	9	fpr:FP2_09630	NA	NA	
ICBIDGAJ_01657	OG0001154	ribU	3	3	5	fpa:FPR_27970	NA	NA	
ICBIDGAJ_01658	OG0001155	ynaI	2	1	2	fpa:FPR_27960	ko:K16052	NA	
ICBIDGAJ_01659	OG0002380	group_2454	3	3	5	fpr:FP2_04210	ko:K06147	NA	
ICBIDGAJ_01660	OG0003950	msbA	1	0	0	fpr:FP2_04200	NA	specific_fp14	○
ICBIDGAJ_01661	OG0002381	msbA_3	2	2	3	fpr:FP2_04200	NA	NA	
ICBIDGAJ_01662	OG0002269	group_2455	4	5	8	fpa:FPR_05020	NA	NA	
ICBIDGAJ_01663	OG0002270	group_2092	1	0	0	fpa:FPR_05040	NA	NA	
ICBIDGAJ_01665	OG0001156	group_1563	1	0	0	fpa:FPR_31590	NA	NA	
ICBIDGAJ_01666	OG0001157	group_1564	1	0	0	fpr:FP2_18880	NA	NA	
ICBIDGAJ_01667	OG0001158	dnaC_1	1	0	0	fpr:FP2_18870	ko:K02315	NA	
ICBIDGAJ_01668	OG0002382	pnbA_1	1	0	0	ruk:A4V00_05520	ko:K03929	NA	
ICBIDGAJ_01669	OG0002596	group_2093	6	7	12	lacy:A4V08_14040	NA	NA	
ICBIDGAJ_01670	OG0000169	rhaS	1	0	0	fpr:FP2_20910	NA	NA	
ICBIDGAJ_01671	OG0001733	group_1567	1	0	0	fpr:FP2_20920	NA	NA	
ICBIDGAJ_01672	OG0001159	group_1568	1	0	0	fpr:FP2_20930	NA	NA	
ICBIDGAJ_01673	OG0001160	group_1569	1	0	0	fpa:FPR_24500	NA	NA	
ICBIDGAJ_01674	OG0003111	ycdT	1	0	0	bprl:CL2_13100	NA	NA	
ICBIDGAJ_01675	OG0002021	group_2456	4	3	6	fpr:FP2_20970	ko:K18890	NA	
ICBIDGAJ_01676	OG0002022	yheI	3	3	5	ruk:A4V00_03995	ko:K18889	NA	
ICBIDGAJ_01682	OG0001161	group_1570	1	0	0	fpa:FPR_24480	ko:K00528	NA	
ICBIDGAJ_01683	OG0001162	gltD_2	1	0	0	fpr:FP2_21000	ko:K00266	NA	
ICBIDGAJ_01684	OG0001163	yitU_1	1	0	0	bprl:CL2_09020	NA	NA	
ICBIDGAJ_01685	OG0000238	srlR	1	0	0	fpa:FPR_05460	ko:K03436	NA	
ICBIDGAJ_01686	OG0001164	lacC	1	0	0	fpr:FP2_26720	ko:K00882	NA	
ICBIDGAJ_01687	OG0001165	fruA	5	5	9	fpa:FPR_05440	ko:K02768;ko:K02769;ko:K02770	NA	
ICBIDGAJ_01688	OG0002597	group_2962	1	0	0	rob:CK5_36530	NA	NA	
ICBIDGAJ_01689	OG0000170	group_3850	1	0	0	fpr:FP2_15140	ko:K02027	NA	
ICBIDGAJ_01690	OG0001166	group_3851	2	1	2	fpa:FPR_03060	NA	NA	
ICBIDGAJ_01691	OG0002271	uvrA_1	1	0	0	abao:BEQ56_04990	ko:K03701	NA	
ICBIDGAJ_01692	OG0001167	prfB	1	0	0	fpr:FP2_05120	ko:K02836	NA	
ICBIDGAJ_01693	OG0001168	group_2459	2	2	3	fpr:FP2_05110	NA	NA	
ICBIDGAJ_01694	OG0001169	gtaB	1	0	0	fpa:FPR_24280	ko:K00963	NA	
ICBIDGAJ_01695	OG0001910	group_2096	5	6	10	fpa:FPR_06620	NA	NA	
ICBIDGAJ_01696	OG0001170	group_2963	1	0	0	NA	NA	NA	
ICBIDGAJ_01697	OG0001171	pstS1_2	1	0	0	fpa:FPR_06600	ko:K02040	NA	
ICBIDGAJ_01698	OG0001172	group_1920	1	1	1	fpr:FP2_02690	NA	NA	
ICBIDGAJ_01699	OG0001911	yoeB_1	1	0	0	fsu:Fisuc_0032;fsc:FSU_0425	ko:K19158	NA	
ICBIDGAJ_01700	OG0001815	group_3853	1	0	0	fne:FSDG_00116;fus:HMPREF0409_01044	ko:K07473	NA	
ICBIDGAJ_01701	OG0002598	glnH	1	0	0	lacy:A4V08_29780	ko:K02030	NA	
ICBIDGAJ_01702	OG0002383	yhdY	1	0	0	cpro:CPRO_10120	ko:K02029	NA	
ICBIDGAJ_01703	OG0002599	yxeN	1	1	1	cpro:CPRO_10110	ko:K02029	NA	
ICBIDGAJ_01704	OG0003113	group_4237	1	0	0	NA	NA	NA	
ICBIDGAJ_01705	OG0003114	lexA_1	1	0	0	fpr:FP2_06870	ko:K01356	NA	
ICBIDGAJ_01706	OG0000138	group_2964	1	0	0	fpa:FPR_13540	NA	NA	
ICBIDGAJ_01707	OG0003115	group_3856	1	0	0	eyy:EGYY_28350	NA	NA	
ICBIDGAJ_01708	OG0001173	group_1577	1	0	0	fpr:FP2_18500	NA	NA	
ICBIDGAJ_01709	OG0001174	hadI	1	0	0	ova:OBV_20290	NA	NA	
ICBIDGAJ_01710	OG0001175	gchK	1	0	0	fpa:FPR_19610	NA	NA	
ICBIDGAJ_01711	OG0001176	group_3858	1	0	0	NA	NA	NA	
ICBIDGAJ_01712	OG0001177	yknY	2	3	4	fpa:FPR_19580	ko:K02003;ko:K02004	NA	
ICBIDGAJ_01713	OG0001178	group_1579	1	0	0	fpa:FPR_29360	ko:K06950	NA	
ICBIDGAJ_01714	OG0001179	group_1580	1	0	0	fpr:FP2_18580	NA	NA	
ICBIDGAJ_01715	OG0001180	htpG	1	0	0	fpr:FP2_18560	ko:K04079	NA	
ICBIDGAJ_01716	OG0001734	group_2966	2	2	3	fpa:FPR_29310	NA	NA	
ICBIDGAJ_01717	OG0000239	galK_2	1	0	0	fpa:FPR_29300	ko:K00849	NA	
ICBIDGAJ_01718	OG0001181	galT	1	0	0	fpr:FP2_18540	ko:K00965	NA	
ICBIDGAJ_01719	OG0001735	cutC	1	0	0	fpa:FPR_29280	ko:K06201	NA	
ICBIDGAJ_01720	OG0001182	glpG	2	3	4	cth:Cthe_0259;ctx:Clo1313_1970	NA	NA	
ICBIDGAJ_01721	OG0002141	hutI	1	0	0	fpa:FPR_27580	NA	NA	
ICBIDGAJ_01722	OG0001183	group_1585	1	0	0	fpa:FPR_06720	ko:K02340	NA	
ICBIDGAJ_01723	OG0001184	rnmV	1	0	0	fpr:FP2_21070	ko:K05985	NA	
ICBIDGAJ_01724	OG0001185	zupT_1	4	3	6	fpla:A4U99_01735	ko:K07238	NA	
ICBIDGAJ_01725	OG0001186	yvdD	1	0	0	fpr:FP2_18840	ko:K06966	NA	
ICBIDGAJ_01726	OG0000240	thiD	1	0	0	fpa:FPR_28350	ko:K00941	NA	
ICBIDGAJ_01727	OG0001187	chrA	3	3	5	fpa:FPR_28780	ko:K07240	NA	
ICBIDGAJ_01728	OG0001188	srpC_3	2	3	4	fpa:FPR_28770	ko:K07240	NA	
ICBIDGAJ_01729	OG0002023	group_2967	1	0	0	eel:EUBELI_01762	NA	NA	
ICBIDGAJ_01730	OG0001189	guaA	1	0	0	fpr:FP2_21030	ko:K01951	NA	
ICBIDGAJ_01731	OG0001190	group_1591	1	0	0	fpa:FPR_31050	NA	NA	
ICBIDGAJ_01732	OG0003528	group_3107	1	0	0	fpr:FP2_32020	NA	NA	
ICBIDGAJ_01733	OG0003951	group_4238	1	0	0	fpr:FP2_32030	ko:K06218	specific_fp14	
ICBIDGAJ_01734	OG0001191	tufA	1	0	0	fpr:FP2_18790	ko:K02358	NA	
ICBIDGAJ_01735	OG0000241	fusA_2	1	0	0	fpa:FPR_29730	ko:K02355	NA	
ICBIDGAJ_01736	OG0001192	rpsG	0	1	0	fpr:FP2_18770	ko:K02992	NA	
ICBIDGAJ_01737	OG0001193	rpsL	1	0	0	fpa:FPR_29710	ko:K02950	NA	
ICBIDGAJ_01738	OG0001194	rpoC	1	0	0	fpr:FP2_18750	ko:K03046	NA	
ICBIDGAJ_01739	OG0001195	rpoB	1	0	0	fpr:FP2_18740	ko:K03043	NA	
ICBIDGAJ_01740	OG0001196	sigA_2	1	0	0	fpr:FP2_18720	ko:K03086	NA	
ICBIDGAJ_01741	OG0001197	dnaG_3	1	0	0	fpr:FP2_18710	ko:K02316	NA	
ICBIDGAJ_01742	OG0001198	dgt	1	0	0	fpr:FP2_18700	ko:K01129	NA	
ICBIDGAJ_01743	OG0001199	yigZ	1	0	0	ele:Elen_2997	NA	NA	
ICBIDGAJ_01744	OG0002603	icaR	1	0	0	rch:RUM_04540	NA	NA	
ICBIDGAJ_01745	OG0002025	group_2463	0	1	0	fpa:FPR_07620	NA	NA	
ICBIDGAJ_01746	OG0002026	group_1597	1	0	0	fpa:FPR_07630	NA	NA	
ICBIDGAJ_01747	OG0002027	group_2974	1	0	0	ibu:IB211_01254	NA	NA	
ICBIDGAJ_01748	OG0002143	cbgA	1	0	0	fpa:FPR_27540	ko:K01190	NA	
ICBIDGAJ_01749	OG0003188	group_3108	1	2	2	ruk:A4V00_13095	NA	NA	
ICBIDGAJ_01750	OG0001983	lyc_3	1	0	0	fpr:FP2_04890	NA	NA	
ICBIDGAJ_01751	OG0003952	group_4239	0	1	0	NA	NA	specific_fp14	○
ICBIDGAJ_01752	OG0003529	group_4240	1	0	0	NA	NA	NA	
ICBIDGAJ_01753	OG0001682	group_4241	1	0	0	fpa:FPR_13530	NA	NA	
ICBIDGAJ_01754	OG0003530	group_4242	1	0	0	NA	NA	NA	
ICBIDGAJ_01755	OG0003953	group_4243	1	0	0	NA	NA	specific_fp14	○
ICBIDGAJ_01756	OG0003954	group_4244	1	0	0	NA	NA	specific_fp14	

ICBIDGAJ_01757	OG0003955	group_4245	1	0	0	NA	NA	specific_fp14	○
ICBIDGAJ_01758	OG0000244	group_4246	1	0	0	fpa:FPR_02360	NA	NA	
ICBIDGAJ_01759	OG0003956	group_4247	1	0	0	fpa:FPR_02350	NA	specific_fp14	○
ICBIDGAJ_01760	OG0003957	group_4248	0	1	0	fpr:FP2_29230	NA	specific_fp14	○
ICBIDGAJ_01761	OG0000245	group_848	1	0	0	fpr:FP2_29220	NA	NA	
ICBIDGAJ_01762	OG0000246	group_4249	1	0	0	fpr:FP2_29210	NA	NA	
ICBIDGAJ_01763	OG0000247	group_850	1	0	0	fpr:FP2_29200	NA	NA	
ICBIDGAJ_01764	OG0000248	group_852	1	0	0	fpa:FPR_02290	NA	NA	
ICBIDGAJ_01765	OG0003958	group_4250	1	0	0	NA	NA	specific_fp14	○
ICBIDGAJ_01766	OG0000261	group_4251	0	1	0	NA	NA	NA	
ICBIDGAJ_01767	OG0003959	group_4252	1	0	0	fpa:FPR_26690	NA	specific_fp14	
ICBIDGAJ_01768	OG0003960	group_4253	1	0	0	NA	NA	specific_fp14	
ICBIDGAJ_01769	OG0003961	group_4254	0	1	0	NA	NA	specific_fp14	○
ICBIDGAJ_01770	OG0003962	group_4255	1	0	0	NA	NA	specific_fp14	
ICBIDGAJ_01771	OG0003963	group_4256	1	0	0	NA	NA	specific_fp14	○
ICBIDGAJ_01772	OG0003964	group_4257	1	0	0	NA	NA	specific_fp14	○
ICBIDGAJ_01773	OG0003965	group_4258	0	1	0	NA	NA	specific_fp14	○
ICBIDGAJ_01774	OG0003966	group_4259	1	2	2	NA	NA	specific_fp14	○
ICBIDGAJ_01775	OG0003967	group_4260	1	0	0	NA	NA	specific_fp14	○
ICBIDGAJ_01776	OG0003968	group_4261	1	0	0	NA	NA	specific_fp14	
ICBIDGAJ_01777	OG0003969	group_4262	1	0	0	NA	NA	specific_fp14	○
ICBIDGAJ_01778	OG0002171	group_4263	1	0	0	fpr:FP2_04820	NA	NA	
ICBIDGAJ_01779	OG0003970	group_4264	1	1	1	rfe:RF_0823	NA	specific_fp14	○
ICBIDGAJ_01780	OG0003971	group_4265	1	1	1	plz:S4054249_10850	NA	specific_fp14	○
ICBIDGAJ_01781	OG0003972	group_4266	1	0	0	cth:Cthe_2457	NA	specific_fp14	○
ICBIDGAJ_01782	OG0000085	group_4267	1	0	0	NA	NA	NA	
ICBIDGAJ_01783	OG0003531	group_4268	1	0	0	NA	NA	NA	
ICBIDGAJ_01784	OG0000048	group_4269	1	0	0	bprs:CK3_02050	NA	NA	
ICBIDGAJ_01785	OG0000048	group_32	1	0	0	fpr:FP2_17170	NA	NA	
ICBIDGAJ_01786	OG0002639	group_2563	1	0	0	NA	NA	NA	
ICBIDGAJ_01787	OG0002640	group_3109	1	0	0	fpr:FP2_17140	NA	NA	
ICBIDGAJ_01788	OG0002379	group_4270	1	0	0	fpr:FP2_17130	ko:K01153	NA	
ICBIDGAJ_01789	OG0003532	group_4271	1	0	0	fpr:FP2_17120	NA	NA	
ICBIDGAJ_01790	OG0002111	group_4272	1	0	0	fty:CH70_1798	ko:K01154	NA	
ICBIDGAJ_01791	OG0002641	group_2208	1	0	0	fpr:FP2_13070	NA	NA	
ICBIDGAJ_01792	OG0002268	group_4273	1	0	0	fpr:FP2_13060	ko:K01154	NA	
ICBIDGAJ_01793	OG0002062	group_3111	1	0	0	fpr:FP2_17100	ko:K03427	NA	
ICBIDGAJ_01794	OG0000065	group_175	1	0	0	fpr:FP2_29850	NA	NA	
ICBIDGAJ_01795	OG0000018	group_168	1	0	0	fpr:FP2_29840	NA	NA	
ICBIDGAJ_01796	OG0002607	group_2468	1	0	0	fpr:FP2_17060	NA	NA	
ICBIDGAJ_01797	OG0003533	group_4274	1	0	0	sele:ADJ74_03545	NA	NA	
ICBIDGAJ_01798	OG0003534	group_4275	1	0	0	fpr:FP2_17040	NA	NA	
ICBIDGAJ_01800	OG0001200	uvrA	1	0	0	ccel:CCDG5_1092	ko:K03701	NA	
ICBIDGAJ_01801	OG0001201	uvrB	1	0	0	fpa:FPR_26430	ko:K03702	NA	
ICBIDGAJ_01802	OG0001202	group_2981	1	0	0	fpr:FP2_19380	ko:K03630	NA	
ICBIDGAJ_01803	OG0001203	rluC_2	1	0	0	fpr:FP2_19370	ko:K06179	NA	
ICBIDGAJ_01804	OG0002144	group_2982	1	0	0	rto:RTO_20700	NA	NA	
ICBIDGAJ_01805	OG0001204	fprA1_1	1	0	0	fpa:FPR_29420	NA	NA	
ICBIDGAJ_01806	OG0001205	group_1602	1	1	1	fpa:FPR_29410	ko:K09760	NA	
ICBIDGAJ_01807	OG0001736	group_2105	1	0	0	fpr:FP2_18630	NA	NA	
ICBIDGAJ_01808	OG0000141	group_2983	1	1	1	fpr:FP2_18620	NA	NA	
ICBIDGAJ_01809	OG0001206	pitA	1	0	0	fpr:FP2_18600	ko:K03823	NA	
ICBIDGAJ_01810	OG0001207	smpB	1	0	0	fpr:FP2_03160	ko:K03664	NA	
ICBIDGAJ_01812	OG0001208	ogt	1	0	0	cct:CC1_29370	ko:K00567	NA	
ICBIDGAJ_01813	OG0001209	pheT	1	0	0	fpa:FPR_24740	ko:K01890	NA	
ICBIDGAJ_01814	OG0001210	pheS	1	0	0	fpr:FP2_18670	ko:K01889	NA	
ICBIDGAJ_01815	OG0002145	mdtH	2	3	4	fpr:FP2_18660	NA	NA	
ICBIDGAJ_01816	OG0001211	trkH	5	6	10	fpa:FPR_21780	ko:K03498	NA	
ICBIDGAJ_01817	OG0001212	trkA_1	1	0	0	fpr:FP2_09900	ko:K03499	NA	
ICBIDGAJ_01818	OG0001213	pdp	1	0	0	fpa:FPR_21760	ko:K00756	NA	
ICBIDGAJ_01819	OG0001214	group_1608	5	5	9	fpa:FPR_20800	ko:K02057	NA	
ICBIDGAJ_01820	OG0001215	mglC_2	5	4	8	fpr:FP2_09870	ko:K02057	NA	
ICBIDGAJ_01821	OG0001216	mglA_2	1	0	0	cpy:Cphy_3268	ko:K02056	NA	
ICBIDGAJ_01822	OG0001217	tmpC	1	0	0	fpr:FP2_09850	ko:K07335	NA	
ICBIDGAJ_01823	OG0001218	cdd	1	0	0	fpr:FP2_09840	ko:K01489	NA	
ICBIDGAJ_01824	OG0001219	deoD	1	0	0	fpr:FP2_09830	ko:K03784	NA	
ICBIDGAJ_01825	OG0001220	nlpD	2	2	3	NA	NA	NA	
ICBIDGAJ_01826	OG0001221	rluD_2	1	0	0	fpr:FP2_09810	ko:K06180	NA	
ICBIDGAJ_01827	OG0001222	nadE	1	0	0	fpr:FP2_09800	ko:K01950	NA	
ICBIDGAJ_01828	OG0001223	group_846	1	1	1	fpa:FPR_20710	NA	NA	
ICBIDGAJ_01829	OG0001224	lytR_2	2	2	3	fpr:FP2_09780	NA	NA	
ICBIDGAJ_01830	OG0002146	group_2989	1	0	0	NA	NA	NA	
ICBIDGAJ_01831	OG0001225	deoB	1	0	0	fpa:FPR_21750	ko:K01839	NA	
ICBIDGAJ_01832	OG0001226	pyk_2	1	0	0	fpr:FP2_09760	ko:K00873	NA	
ICBIDGAJ_01833	OG0001227	luxS	1	0	0	fpr:FP2_09750	ko:K07173	NA	
ICBIDGAJ_01834	OG0001228	gpmI	1	0	0	fpa:FPR_25880	ko:K15633	NA	
ICBIDGAJ_01835	OG0001229	tpiA	1	0	0	fpr:FP2_02560	ko:K01803	NA	
ICBIDGAJ_01836	OG0001230	pgk	1	0	0	fpa:FPR_25860	ko:K00927	NA	
ICBIDGAJ_01837	OG0000242	group_3873	7	8	14	lhe:lhv_1796	NA	NA	
ICBIDGAJ_01838	OG0003116	epsH_1	1	0	0	dmi:Desmer_4142	NA	NA	
ICBIDGAJ_01839	OG0000066	group_3875	1	0	0	csr:Cspa_c53580	NA	NA	
ICBIDGAJ_01840	OG0003117	group_3876	4	4	7	NA	NA	NA	
ICBIDGAJ_01841	OG0002388	group_3877	1	0	0	bfs:BF9343_0185	NA	NA	
ICBIDGAJ_01842	OG0000066	epsJ_5	1	0	0	bbrn:B2258_0404	NA	NA	
ICBIDGAJ_01843	OG0001737	epsF	1	0	0	bbrv:B689b_0427	NA	NA	
ICBIDGAJ_01844	OG0003118	gnu	1	0	0	dmi:Desmer_4163	ko:K19997	NA	
ICBIDGAJ_01845	OG0003119	group_3880	3	3	5	rho:RHOM_12340	NA	NA	
ICBIDGAJ_01846	OG0000032	group_672	1	0	0	fpa:FPR_19190	NA	NA	
ICBIDGAJ_01847	OG0003973	group_4276	1	0	0	NA	NA	specific_fp14	
ICBIDGAJ_01848	OG0000029	group_382	1	0	0	fpa:FPR_02700	ko:K03431	NA	
ICBIDGAJ_01849	OG0002427	betL	6	7	12	eel:EUBELI_20482	ko:K03451	NA	
ICBIDGAJ_01850	OG0002428	glmU_1	1	0	0	eel:EUBELI_20483	NA	NA	
ICBIDGAJ_01851	OG0002429	gtaB_2	1	0	0	eel:EUBELI_20484	NA	NA	
ICBIDGAJ_01852	OG0003535	group_4277	1	0	0	NA	NA	NA	
ICBIDGAJ_01853	OG0002303	group_4278	6	7	12	sgt:SGGB_0941	NA	NA	
ICBIDGAJ_01854	OG0003974	group_4279	1	0	0	lga:LGAS_1147	NA	specific_fp14	○
ICBIDGAJ_01855	OG0003975	group_4280	6	6	11	NA	NA	specific_fp14	○
ICBIDGAJ_01856	OG0002304	epsE_2	1	0	0	sans:DK43_00820	ko:K12997	specific_fp14	○
ICBIDGAJ_01857	OG0002304	wfgD	1	0	0	NA	NA	NA	
ICBIDGAJ_01858	OG0003976	group_4283	1	0	0	paeh:H70357_14535	NA	specific_fp14	
ICBIDGAJ_01859	OG0003060	tuaG	1	0	0	paee:R70331_24890	NA	NA	
ICBIDGAJ_01860	OG0002567	wecA	3	3	5	fpa:FPR_02490	NA	NA	
ICBIDGAJ_01861	OG0000075	radD_2	1	0	0	fpa:FPR_02480	NA	NA	
ICBIDGAJ_01862	OG0000466	Int-Tn_1	1	0	0	fpa:FPR_19200	NA	NA	
ICBIDGAJ_01863	OG0001670	group_2211	0	1	0	fpa:FPR_28500	NA	NA	
ICBIDGAJ_01864	OG0000118	group_2212	1	0	0	fpa:FPR_28490	NA	NA	
ICBIDGAJ_01865	OG0000104	group_2218	1	0	0	fpa:FPR_28480	NA	NA	
ICBIDGAJ_01866	OG0002423	group_4284	1	0	0	NA	NA	NA	
ICBIDGAJ_01867	OG0001929	group_2565	0	1	0	NA	NA	NA	
ICBIDGAJ_01868	OG0001929	hin_2	1	0	0	cpro:CPRO_13190	NA	NA	
ICBIDGAJ_01869	OG0002305	group_4285	1	1	1	fpa:FPR_28450	NA	NA	
ICBIDGAJ_01870	OG0003977	group_4286	1	0	0	NA	NA	specific_fp14	○
ICBIDGAJ_01871	OG0003189	group_3115	0	1	0	NA	NA	NA	
ICBIDGAJ_01872	OG0001777	group_3116	1	0	0	NA	NA	NA	

ICBIDGAJ_01873	OG0000119	group_3119	1	0	0	NA	NA	NA	
ICBIDGAJ_01874	OG0001671	group_2222	1	0	0	NA	NA	NA	
ICBIDGAJ_01875	OG0003190	group_3120	0	1	0	NA	NA	NA	
ICBIDGAJ_01876	OG0003191	group_3121	1	0	0	NA	NA	NA	
ICBIDGAJ_01877	OG0003978	group_4287	1	0	0	NA	NA	specific_fp14	O
ICBIDGAJ_01878	OG0002172	group_2567	1	0	0	NA	NA	NA	
ICBIDGAJ_01879	OG0002173	group_2568	1	0	0	NA	NA	NA	
ICBIDGAJ_01880	OG0002430	group_3122	1	0	0	NA	NA	NA	
ICBIDGAJ_01881	OG0002174	xerD_1	1	0	0	cpro:CPRO_21370	ko:K04763	NA	
ICBIDGAJ_01882	OG0001231	gap	1	0	0	fpr:FP2_02530	ko:K00134	NA	
ICBIDGAJ_01883	OG0001232	group_3881	4	5	8	fpa:FPR_26160	NA	NA	
ICBIDGAJ_01884	OG0001738	gltA	1	0	0	fpa:FPR_26140	ko:K01647	NA	
ICBIDGAJ_01885	OG0001233	lytB	1	1	1	fpr:FP2_02500	ko:K06381	NA	
ICBIDGAJ_01886	OG0001234	group_1621	1	1	1	fpr:FP2_02490	NA	NA	
ICBIDGAJ_01887	OG0001235	wbbL_1	1	1	1	fpr:FP2_26380	NA	NA	
ICBIDGAJ_01888	OG0001236	group_1623	1	1	1	fpr:FP2_26370	NA	NA	
ICBIDGAJ_01889	OG0001237	spxA	1	0	0	fpa:FPR_04920	NA	NA	
ICBIDGAJ_01890	OG0001238	fdx	1	0	0	fpr:FP2_26350	ko:K05337	NA	
ICBIDGAJ_01891	OG0000243	polA	1	0	0	fpa:FPR_04940	ko:K02335	NA	
ICBIDGAJ_01892	OG0001239	tsaD_2	1	0	0	fpa:FPR_04950	ko:K01409	NA	
ICBIDGAJ_01893	OG0001240	rplL	1	0	0	fpa:FPR_16650	ko:K02935	NA	
ICBIDGAJ_01894	OG0001241	rplJ	1	0	0	fpr:FP2_02460	ko:K02864	NA	
ICBIDGAJ_01895	OG0001242	rplA	1	0	0	fpr:FP2_02450	ko:K02863	NA	
ICBIDGAJ_01896	OG0001243	rplK	1	0	0	fpa:FPR_16620	ko:K02867	NA	
ICBIDGAJ_01897	OG0001244	nusG	1	0	0	fpr:FP2_02430	ko:K02601	NA	
ICBIDGAJ_01898	OG0001245	secE	1	1	1	fpr:FP2_02420	ko:K03073	NA	
ICBIDGAJ_01899	OG0001246	rpmG2	0	1	0	fpr:FP2_02410;fpa:FPR_16590	ko:K02913	NA	
ICBIDGAJ_01900	OG0001247	ddlA	1	0	0	fpr:FP2_02400	ko:K01921	NA	
ICBIDGAJ_01901	OG0001248	murI	1	0	0	fpa:FPR_16570	ko:K01776	NA	
ICBIDGAJ_01902	OG0001249	group_2472	1	0	0	ttm:Tthe_0220;tto:Thethe_00208	NA	NA	
ICBIDGAJ_01903	OG0001250	argS	1	0	0	fpa:FPR_16550	ko:K01887	NA	
ICBIDGAJ_01904	OG0003120	group_3882	1	1	1	NA	NA	NA	
ICBIDGAJ_01905	OG0001251	group_1632	1	0	0	fpr:FP2_30140	NA	NA	
ICBIDGAJ_01906	OG0001252	group_1633	1	2	2	fpr:FP2_30130	ko:K07258	NA	
ICBIDGAJ_01907	OG0001253	cwlM_2	1	0	0	fpr:FP2_15670	NA	NA	
ICBIDGAJ_01908	OG0001254	cwlM_3	1	0	0	fpa:FPR_20230	NA	NA	
ICBIDGAJ_01909	OG0000089	group_766	1	0	0	fpr:FP2_09570	NA	NA	
ICBIDGAJ_01910	OG0003121	group_3883	5	4	8	cpas:Clopa_1747	ko:K07088	NA	
ICBIDGAJ_01911	OG0001816	group_2473	1	2	2	fpa:FPR_26400	NA	NA	
ICBIDGAJ_01912	OG0001817	walR_1	1	0	0	fpa:FPR_26390	NA	NA	
ICBIDGAJ_01913	OG0001818	yxlF_1	1	0	0	fpa:FPR_26380	ko:K20459	NA	
ICBIDGAJ_01914	OG0001819	group_2995	3	4	6	fpa:FPR_26370	ko:K20460	NA	
ICBIDGAJ_01915	OG0001820	group_2475	3	4	6	fpa:FPR_26360	ko:K20461	NA	
ICBIDGAJ_01916	OG0001255	group_3884	1	0	0	fpa:FPR_02380	NA	NA	
ICBIDGAJ_01917	OG0001256	group_1636	1	0	0	fpr:FP2_29260	NA	NA	
ICBIDGAJ_01918	OG0000244	group_2112	1	0	0	fpr:FP2_29250	NA	NA	
ICBIDGAJ_01919	OG0001257	group_2113	1	0	0	fpr:FP2_29240	NA	NA	
ICBIDGAJ_01920	OG0001258	group_1637	0	1	0	fpr:FP2_29230	NA	NA	
ICBIDGAJ_01921	OG0000245	group_847	1	0	0	fpa:FPR_02330	NA	NA	
ICBIDGAJ_01922	OG0000246	group_2996	1	0	0	fpr:FP2_29210	NA	NA	
ICBIDGAJ_01923	OG0000247	group_849	1	0	0	fpr:FP2_29200	NA	NA	
ICBIDGAJ_01924	OG0000248	group_851	1	0	0	fpr:FP2_29190	NA	NA	
ICBIDGAJ_01925	OG0001259	group_853	1	0	0	fpr:FP2_29180	NA	NA	
ICBIDGAJ_01926	OG0001260	group_1638	1	0	0	fpr:FP2_29170	ko:K06972	NA	
ICBIDGAJ_01927	OG0001261	group_1639	6	7	12	fpr:FP2_29150	ko:K06902	NA	
ICBIDGAJ_01928	OG0001262	group_2476	1	0	0	fpr:FP2_29140	NA	NA	
ICBIDGAJ_01929	OG0000027	group_2142	1	0	0	dru:Desru_2710;dru:Desru_0118;dru:Desru_2296	ko:K07497	NA	
ICBIDGAJ_01930	OG0001263	murC	1	0	0	fpr:FP2_23390	ko:K01924	NA	
ICBIDGAJ_01931	OG0001914	group_2114	1	0	0	slp:Slip_1123	NA	NA	
ICBIDGAJ_01932	OG0002028	group_2477	3	3	5	elm:ELI_2761	NA	NA	
ICBIDGAJ_01933	OG0002029	cydD	3	4	6	trm:JO41_10970	NA	NA	
ICBIDGAJ_01934	OG0001264	group_649	1	0	0	fpr:FP2_26970	NA	NA	
ICBIDGAJ_01935	OG0001739	group_2115	1	1	1	NA	NA	NA	
ICBIDGAJ_01936	OG0001265	feoB_2	6	7	12	fpr:FP2_26950	ko:K04759	NA	
ICBIDGAJ_01937	OG0001266	feoA	0	1	0	fpr:FP2_26940	ko:K04758	NA	
ICBIDGAJ_01938	OG0001267	group_1642	1	0	0	fpr:FP2_26930	ko:K04758	NA	
ICBIDGAJ_01939	OG0001268	group_854	1	0	0	fpr:FP2_26920	NA	NA	
ICBIDGAJ_01940	OG0002030	group_2480	1	0	0	NA	NA	NA	
ICBIDGAJ_01941	OG0002175	group_2226	1	1	1	NA	NA	NA	
ICBIDGAJ_01942	OG0001269	group_2997	1	0	0	fpr:FP2_26910	NA	NA	
ICBIDGAJ_01943	OG0001740	group_2116	1	0	0	fpa:FPR_02200	ko:K02003	NA	
ICBIDGAJ_01944	OG0001741	group_2117	4	5	8	tur:AT726_08205	ko:K02004	NA	
ICBIDGAJ_01945	OG0001270	livF	1	0	0	fpr:FP2_24820	ko:K01996	NA	
ICBIDGAJ_01946	OG0000171	lptB	1	0	0	fpr:FP2_24810	ko:K01995	NA	
ICBIDGAJ_01947	OG0000172	livH_2	4	4	7	fpr:FP2_24800	ko:K01998	NA	
ICBIDGAJ_01948	OG0000173	livH	4	4	7	fpr:FP2_24790	ko:K01997	NA	
ICBIDGAJ_01949	OG0000174	group_1921	1	0	0	fpr:FP2_24780	ko:K01999	NA	
ICBIDGAJ_01950	OG0000142	group_3885	6	7	12	fpa:FPR_12670	NA	NA	
ICBIDGAJ_01951	OG0001271	eno	1	0	0	fpr:FP2_24770	ko:K01689	NA	
ICBIDGAJ_01952	OG0003979	group_4288	1	1	1	ele:Elen_0844	NA	specific_fp14	
ICBIDGAJ_01953	OG0001821	group_2119	2	3	4	ruk:A4V00_05010	NA	NA	
ICBIDGAJ_01954	OG0001822	group_2481	1	1	1	fpa:FPR_13010	NA	NA	
ICBIDGAJ_01955	OG0001742	bglK	1	0	0	fpa:FPR_13020	NA	NA	
ICBIDGAJ_01956	OG0001272	por_2	1	0	0	fpa:FPR_21250	ko:K00040	NA	
ICBIDGAJ_01957	OG0001273	uxuA	1	0	0	fpr:FP2_24760	ko:K01686	NA	
ICBIDGAJ_01958	OG0001274	rspR_2	1	0	0	fpr:FP2_23320	NA	NA	
ICBIDGAJ_01959	OG0001275	group_650	2	3	4	fpr:FP2_23310	NA	NA	
ICBIDGAJ_01960	OG0001276	ywpJ	1	0	0	fpr:FP2_23300	NA	NA	
ICBIDGAJ_01961	OG0001277	eda	1	0	0	fpa:FPR_14560	ko:K01625	NA	
ICBIDGAJ_01962	OG0001278	kdgK_1	1	0	0	fpa:FPR_14550	ko:K00874	NA	
ICBIDGAJ_01963	OG0001279	kduI	1	0	0	fpa:FPR_14540	ko:K01815	NA	
ICBIDGAJ_01964	OG0001280	gno_1	1	0	0	fpr:FP2_23260	ko:K00046	NA	
ICBIDGAJ_01965	OG0001281	group_855	1	1	1	fpr:FP2_24450	NA	NA	
ICBIDGAJ_01966	OG0001282	galM	1	0	0	fpr:FP2_23330	NA	NA	
ICBIDGAJ_01967	OG0001283	uxaA	1	0	0	fpr:FP2_23350	ko:K01685	NA	
ICBIDGAJ_01968	OG0001284	uxaB	1	0	0	fpa:FPR_15630	ko:K00041	NA	
ICBIDGAJ_01969	OG0001285	uxaC	1	0	0	fpr:FP2_23370	ko:K01812	NA	
ICBIDGAJ_01970	OG0002031	group_3890	1	1	1	eyy:EGYY_06210	NA	NA	
ICBIDGAJ_01971	OG0002032	norM	6	7	12	lho:LOOC260_120870	NA	NA	
ICBIDGAJ_01972	OG0001286	yohK	4	3	6	fpa:FPR_12090	NA	NA	
ICBIDGAJ_01973	OG0001287	lrgA	2	2	3	cah:CAETHG_1207;cle:Clole_2690;clj:CLJU_c33090	ko:K06518	NA	
ICBIDGAJ_01974	OG0001288	yjiA	1	0	0	fpr:FP2_25440	NA	NA	
ICBIDGAJ_01975	OG0002033	group_2485	2	3	4	fpr:FP2_25340	NA	NA	
ICBIDGAJ_01976	OG0002147	inlA	1	1	1	NA	NA	NA	
ICBIDGAJ_01977	OG0001289	rodA	4	5	8	fpa:FPR_05990	ko:K05837	NA	
ICBIDGAJ_01978	OG0001290	group_3891	1	1	1	fpa:FPR_06000	NA	NA	
ICBIDGAJ_01979	OG0001291	tsaE	1	0	0	fpa:FPR_06010	ko:K06925	NA	
ICBIDGAJ_01980	OG0001292	tsaB	1	0	0	fpa:FPR_06020	NA	NA	
ICBIDGAJ_01981	OG0001293	ywlF	1	0	0	fpr:FP2_25820	ko:K01808	NA	
ICBIDGAJ_01982	OG0000249	upp	1	0	0	fpr:FP2_25830	ko:K00761	NA	
ICBIDGAJ_01983	OG0001294	group_857	2	2	3	NA	NA	NA	
ICBIDGAJ_01984	OG0001295	group_858	1	1	1	fpa:FPR_15830	NA	NA	
ICBIDGAJ_01985	OG0001296	group_1659	1	0	0	fpa:FPR_15820	NA	NA	
ICBIDGAJ_01986	OG0001297	group_1660	1	1	1	fpa:FPR_15810	NA	NA	

ICBIDGAJ_01987	OG0001298	group_1661	1	0	0	fpr:FP2_24340	NA	NA
ICBIDGAJ_01988	OG0001299	group_1662	1	0	0	fpr:FP2_24350	NA	NA
ICBIDGAJ_01989	OG0001300	group_1663	4	4	7	fpr:FP2_24360	ko:K07089	NA
ICBIDGAJ_01990	OG0001301	leuB	1	0	0	fpr:FP2_26190	ko:K00052	NA
ICBIDGAJ_01991	OG0001302	DmdB	1	0	0	fpr:FP2_26180	ko:K01704	NA
ICBIDGAJ_01992	OG0001303	dmdA_1	1	0	0	fpa:FPR_06290	ko:K01703	NA
ICBIDGAJ_01993	OG0001304	leuA	1	0	0	fpr:FP2_26160	ko:K01649	NA
ICBIDGAJ_01994	OG0001305	ftsH4	2	1	2	fpa:FPR_06260	ko:K03798	NA
ICBIDGAJ_01995	OG0001306	group_3892	1	0	0	fpr:FP2_26130	NA	NA
ICBIDGAJ_01996	OG0000070	group_577	1	1	1	NA	NA	NA
ICBIDGAJ_01997	OG0003122	group_3893	1	0	0	sxl:SXYLSMQ121_1370	NA	NA
ICBIDGAJ_01998	OG0001307	mglC	5	5	9	csh:Closa_2372	ko:K10541	NA
ICBIDGAJ_01999	OG0001308	mglA_1	1	0	0	fpa:FPR_02260	ko:K10542	NA
ICBIDGAJ_02000	OG0001309	mglB	1	0	0	fpr:FP2_30680	ko:K10540	NA
ICBIDGAJ_02001	OG0002148	adaA_1	1	0	0	fpr:FP2_04110	NA	NA
ICBIDGAJ_02002	OG0000046	yjmB_1	6	6	11	fpr:FP2_04100	ko:K03292	NA
ICBIDGAJ_02003	OG0000143	uidA_1	1	0	0	byl:A4V09_20285	ko:K01195	NA
ICBIDGAJ_02004	OG0001310	comEC_1	1	0	0	ibu:IB211_01356	NA	NA
ICBIDGAJ_02005	OG0001311	group_651	1	0	0	fpr:FP2_24280	NA	NA
ICBIDGAJ_02006	OG0001312	spoIIIE	3	3	5	fpr:FP2_24270	ko:K03466	NA
ICBIDGAJ_02007	OG0003123	pnbA_2	1	0	0	paej:H70737_03190	ko:K03929	NA
ICBIDGAJ_02008	OG0000015	bglA_1	1	0	0	fpr:FP2_28840	ko:K01223	NA
ICBIDGAJ_02009	OG0003124	group_3895	1	0	0	fpr:FP2_28830	NA	NA
ICBIDGAJ_02010	OG0001743	group_3896	5	5	9	fpr:FP2_28820	ko:K07088	NA
ICBIDGAJ_02011	OG0003125	neuA	1	0	0	fpr:FP2_28810	NA	NA
ICBIDGAJ_02012	OG0003126	cocE	1	0	0	fpr:FP2_28800	ko:K06978	NA
ICBIDGAJ_02013	OG0002276	group_3899	1	0	0	fpr:FP2_28790	ko:K10823	NA
ICBIDGAJ_02014	OG0003127	group_3900	1	0	0	fpr:FP2_28780	ko:K02031	NA
ICBIDGAJ_02015	OG0003128	gsiD	3	4	6	tco:Theco_0419	ko:K02034	NA
ICBIDGAJ_02016	OG0003129	dppB_2	3	4	6	fpr:FP2_28760	ko:K02033	NA
ICBIDGAJ_02017	OG0003130	gsiB	1	0	0	fpr:FP2_28750	ko:K02035	NA
ICBIDGAJ_02018	OG0003131	group_3904	1	0	0	fpr:FP2_28730	NA	NA
ICBIDGAJ_02019	OG0003132	group_3905	1	0	0	fpr:FP2_28720	ko:K07720	NA
ICBIDGAJ_02020	OG0003133	ypdA	2	1	2	fpr:FP2_28710	ko:K07718	NA
ICBIDGAJ_02021	OG0003134	group_3906	1	0	0	fpr:FP2_28700	NA	NA
ICBIDGAJ_02022	OG0003135	group_3907	1	0	0	fpr:FP2_28690	NA	NA
ICBIDGAJ_02023	OG0003136	group_3908	1	0	0	fpr:FP2_28680	NA	NA
ICBIDGAJ_02024	OG0003137	group_3909	1	0	0	fpr:FP2_28670	NA	NA
ICBIDGAJ_02025	OG0003138	uctC	1	0	0	fpr:FP2_28660	NA	NA
ICBIDGAJ_02026	OG0002608	citN	6	7	12	fpr:FP2_28650	ko:K03300	NA
ICBIDGAJ_02027	OG0003139	group_3912	1	0	0	fpr:FP2_28640	NA	NA
ICBIDGAJ_02028	OG0003140	group_3913	1	0	0	fpr:FP2_28630	NA	NA
ICBIDGAJ_02029	OG0003141	group_3005	1	0	0	fpr:FP2_28620	NA	NA
ICBIDGAJ_02030	OG0001744	lacZ_3	1	0	0	fpr:FP2_29970	ko:K01190	NA
ICBIDGAJ_02031	OG0001823	group_2489	0	1	0	fpr:FP2_21880	NA	NA
ICBIDGAJ_02032	OG0000008	group_134	1	0	0	fpa:FPR_07930	NA	NA
ICBIDGAJ_02033	OG0000004	group_157	1	0	0	fpr:FP2_21850	ko:K03496	NA
ICBIDGAJ_02034	OG0000002	parB	1	0	0	fpa:FPR_07950	ko:K03497	NA
ICBIDGAJ_02035	OG0000035	group_392	0	1	0	fpa:FPR_05610	NA	NA
ICBIDGAJ_02036	OG0000067	ltrA_1	1	0	0	ere:EUBREC_2688;ere:EUBREC_0807	ko:K00986	NA
ICBIDGAJ_02037	OG0001915	group_100	1	0	0	fpr:FP2_27160	NA	NA
ICBIDGAJ_02038	OG0000023	mbeC	1	0	0	fpa:FPR_18860	NA	NA
ICBIDGAJ_02039	OG0000088	group_760	2	2	3	fpa:FPR_18850	NA	NA
ICBIDGAJ_02040	OG0003142	group_1673	0	1	0	NA	NA	NA
ICBIDGAJ_02041	OG0000010	group_188	1	0	0	fpa:FPR_04440	NA	NA
ICBIDGAJ_02042	OG0000010	group_189	1	0	0	fpr:FP2_08910	NA	NA
ICBIDGAJ_02043	OG0000250	group_765	1	0	0	fpr:FP2_09570	NA	NA
ICBIDGAJ_02044	OG0001824	sinR	1	0	0	ckl:CKL_2928;ckr:CKR_2595	NA	NA
ICBIDGAJ_02045	OG0002277	group_654	1	0	0	NA	NA	NA
ICBIDGAJ_02046	OG0002034	nqrC	1	0	0	fpa:FPR_04350	NA	NA
ICBIDGAJ_02047	OG0002035	gmr	1	0	0	byl:A4V09_13705	NA	NA
ICBIDGAJ_02048	OG0002036	menG	1	0	0	ibu:IB211_01262	NA	NA
ICBIDGAJ_02049	OG0001825	ftn	1	0	0	fpr:FP2_23560	ko:K02217	NA
ICBIDGAJ_02050	OG0002389	group_657	1	0	0	fpr:FP2_23550	ko:K09825	NA
ICBIDGAJ_02051	OG0002390	pspE_1	1	0	0	ibu:IB211_01259c	NA	NA
ICBIDGAJ_02052	OG0001313	ribD_2	1	0	0	fpa:FPR_16330	ko:K11752	NA
ICBIDGAJ_02053	OG0001314	ribE	1	0	0	ere:EUBREC_3131;ert:EUR_06260;era:ERE_13220	ko:K00793	NA
ICBIDGAJ_02054	OG0001315	ribBA	1	0	0	fpr:FP2_23950	ko:K14652	NA
ICBIDGAJ_02055	OG0001316	ribH	1	0	0	fpa:FPR_16300	ko:K00794	NA
ICBIDGAJ_02056	OG0001317	cpxR	1	0	0	fpr:FP2_23930	NA	NA
ICBIDGAJ_02057	OG0001318	yfkJ_2	1	0	0	fpr:FP2_23920	ko:K01104	NA
ICBIDGAJ_02058	OG0002267	rlmCD_2	1	0	0	fpa:FPR_24120	NA	NA
ICBIDGAJ_02059	OG0002391	ywnA	1	0	0	ibu:IB211_01258c	NA	NA
ICBIDGAJ_02060	OG0001826	fprA1_2	1	0	0	fpa:FPR_04300	NA	NA
ICBIDGAJ_02061	OG0002392	group_3915	1	0	0	ibu:IB211_01252	NA	NA
ICBIDGAJ_02062	OG0002393	group_3916	0	1	0	ibu:IB211_01251	NA	NA
ICBIDGAJ_02063	OG0000095	group_3917	1	0	0	ibu:IB211_01248c	NA	NA
ICBIDGAJ_02064	OG0000027	group_2146	1	0	0	dru:Desru_0118;dru:Desru_2296;dru:Desru_2710	ko:K07497	NA
ICBIDGAJ_02065	OG0001827	trxB_2	1	0	0	fpa:FPR_04320	ko:K00384	NA
ICBIDGAJ_02066	OG0001828	trxA	0	1	0	fpa:FPR_04310	ko:K03671	NA
ICBIDGAJ_02067	OG0001829	group_3918	1	0	0	fpa:FPR_04290	NA	NA
ICBIDGAJ_02068	OG0001830	nrdB	1	0	0	fpa:FPR_04280	ko:K00526	NA
ICBIDGAJ_02069	OG0001831	nrdE1	1	0	0	fpa:FPR_04270	ko:K00525	NA
ICBIDGAJ_02070	OG0001832	fprA	1	0	0	bprs:CK3_14540	NA	NA
ICBIDGAJ_02071	OG0001833	bcd_2	1	0	0	fpa:FPR_04250	NA	NA
ICBIDGAJ_02072	OG0001834	group_2494	1	0	0	fpa:FPR_04240	NA	NA
ICBIDGAJ_02073	OG0002278	ywaC	1	0	0	bprs:CK3_14500	ko:K07816	NA
ICBIDGAJ_02074	OG0002149	cdr	1	0	0	bprs:CK3_14490	NA	NA
ICBIDGAJ_02075	OG0002279	group_2495	1	0	0	tsu:Tresu_0819	ko:K03671	NA
ICBIDGAJ_02076	OG0002280	group_3013	2	3	4	byl:A4V09_12060	NA	NA
ICBIDGAJ_02077	OG0002281	group_3014	1	0	0	NA	NA	NA
ICBIDGAJ_02078	OG0001835	dfx_1	1	0	0	bprs:CK3_14460	ko:K05919	NA
ICBIDGAJ_02079	OG0001836	rbr1	1	0	0	bprs:CK3_14450	NA	NA
ICBIDGAJ_02080	OG0001837	crp	1	0	0	bprs:CK3_14440	ko:K01420	NA
ICBIDGAJ_02081	OG0001838	group_2125	1	0	0	bprs:CK3_14430	NA	NA
ICBIDGAJ_02082	OG0001839	group_3928	1	1	1	rum:CK1_03440	NA	NA
ICBIDGAJ_02083	OG0001930	group_553	1	0	0	fpr:FP2_25440	NA	NA
ICBIDGAJ_02084	OG0000129	group_7171	3	3	5	fpa:FPR_06810	NA	NA
ICBIDGAJ_02085	OG0001319	lexA_3	1	0	0	NA	NA	NA
ICBIDGAJ_02086	OG0001320	group_2127	1	0	0	fpr:FP2_28430	NA	NA
ICBIDGAJ_02087	OG0000251	group_1677	1	0	0	fpa:FPR_19500	NA	NA
ICBIDGAJ_02088	OG0000028	group_2496	1	0	0	fpr:FP2_29380	NA	NA
ICBIDGAJ_02089	OG0000090	group_1274	1	0	0	fpa:FPR_19520	NA	NA
ICBIDGAJ_02090	OG0000175	mazF_2	1	0	0	fpr:FP2_04130	ko:K07171	NA
ICBIDGAJ_02091	OG0001840	group_419	1	0	0	fpa:FPR_19540	NA	NA
ICBIDGAJ_02092	OG0001745	group_3015	1	0	0	fpr:FP2_29360	NA	NA
ICBIDGAJ_02093	OG0001321	xerC_3	1	0	0	fpr:FP2_29350	NA	NA
ICBIDGAJ_02095	OG0001916	group_2128	1	0	0	fpr:FP2_29340	NA	NA
ICBIDGAJ_02096	OG0001322	group_864	1	0	0	fpa:FPR_02430	NA	NA
ICBIDGAJ_02097	OG0001323	group_1679	3	3	5	fpr:FP2_25890	NA	NA
ICBIDGAJ_02098	OG0000252	afr	1	0	0	fpa:FPR_13610	NA	NA
ICBIDGAJ_02099	OG0001324	coaX_1	1	0	0	fpr:FP2_25870	ko:K03525	NA
ICBIDGAJ_02100	OG0001325	coaBC	1	0	0	fpa:FPR_13630	ko:K13038	NA
ICBIDGAJ_02101	OG0000092	oppB	3	3	5	fpr:FP2_26810	ko:K15581	NA

ICBIDGAJ_02102	OG0001917	dppC	3	3	5	fpr:FP2_26800	ko:K15582	NA	
ICBIDGAJ_02103	OG0000033	oppD_3	1	0	0	fpr:FP2_26790	ko:K15583	NA	
ICBIDGAJ_02104	OG0000093	oppF_3	1	0	0	fpr:FP2_26780	ko:K10823	NA	
ICBIDGAJ_02105	OG0001326	lcfB	1	0	0	fpr:FP2_26770	ko:K01897	NA	
ICBIDGAJ_02106	OG0001327	group_3016	1	1	1	fpr:FP2_26760	NA	NA	
ICBIDGAJ_02107	OG0001328	gpsA	1	0	0	fpr:FP2_29130	ko:K00057	NA	
ICBIDGAJ_02108	OG0000176	tcyB_1	3	2	4	fpa:FPR_06190	ko:K10009	NA	
ICBIDGAJ_02109	OG0001329	tcyN	1	0	0	fpa:FPR_06180	ko:K10010	NA	
ICBIDGAJ_02110	OG0001330	tcyA	1	0	0	fpa:FPR_06170	ko:K02424	NA	
ICBIDGAJ_02111	OG0000073	group_4289	1	0	0	fpa:FPR_06160	ko:K10947	NA	
ICBIDGAJ_02112	OG0002642	group_4290	1	0	0	fpa:FPR_06150	NA	NA	
ICBIDGAJ_02113	OG0001331	uvrC	1	0	0	fpa:FPR_06140	ko:K03703	NA	
ICBIDGAJ_02114	OG0001332	crh	1	1	1	fpr:FP2_26660;fpa:FPR_06130	ko:K11189	NA	
ICBIDGAJ_02115	OG0001333	trmD	1	0	0	fpr:FP2_26650	ko:K00554	NA	
ICBIDGAJ_02116	OG0001334	rimM	1	0	0	fpa:FPR_06110	ko:K02860	NA	
ICBIDGAJ_02117	OG0001335	group_3017	1	0	0	fpa:FPR_06100	ko:K06960	NA	
ICBIDGAJ_02118	OG0001336	rpsP	0	1	0	fpa:FPR_06090	ko:K02959	NA	
ICBIDGAJ_02119	OG0001337	ffh	1	0	0	fpa:FPR_06080	ko:K03106	NA	
ICBIDGAJ_02120	OG0001338	group_1687	1	0	0	fpr:FP2_26600	ko:K09787	NA	
ICBIDGAJ_02121	OG0001339	cysK	1	0	0	NA	NA	NA	
ICBIDGAJ_02122	OG0001340	mepA_6	6	6	11	fpa:FPR_06050	NA	NA	
ICBIDGAJ_02123	OG0001341	tepA	1	0	0	fpr:FP2_24260	NA	NA	
ICBIDGAJ_02124	OG0001342	rex	1	0	0	fpr:FP2_24250	ko:K01926	NA	
ICBIDGAJ_02125	OG0001343	tdk	1	0	0	fpa:FPR_01990	ko:K00857	NA	
ICBIDGAJ_02126	OG0001344	yesO	1	0	0	fpr:FP2_24230	ko:K10192	NA	
ICBIDGAJ_02127	OG0001345	lacF_1	3	4	6	fpr:FP2_24220	ko:K10193	NA	
ICBIDGAJ_02128	OG0000253	araQ_1	3	4	6	fpr:FP2_24210	ko:K10194	NA	
ICBIDGAJ_02129	OG0001346	group_2501	1	0	0	fpr:FP2_24200	NA	NA	
ICBIDGAJ_02130	OG0000254	pgl	1	0	0	fpa:FPR_02040	NA	NA	
ICBIDGAJ_02131	OG0001347	yteR	1	0	0	fpr:FP2_24180	ko:K15532	NA	
ICBIDGAJ_02132	OG0001348	group_2502	2	2	3	fpa:FPR_12950	NA	NA	
ICBIDGAJ_02133	OG0001349	group_3018	2	3	4	fpr:FP2_24560	NA	NA	
ICBIDGAJ_02134	OG0001350	group_3019	1	0	0	fpr:FP2_24570	NA	NA	
ICBIDGAJ_02135	OG0001351	sigW	1	0	0	fpa:FPR_12920	ko:K03088	NA	
ICBIDGAJ_02136	OG0001352	birA_2	1	0	0	fpr:FP2_24590	ko:K03524	NA	
ICBIDGAJ_02137	OG0003980	group_4291	1	1	1	NA	NA	specific_fp14	
ICBIDGAJ_02138	OG0002221	group_4292	1	1	1	NA	NA	NA	
ICBIDGAJ_02139	OG0001353	group_3020	1	0	0	fpr:FP2_24530	NA	NA	
ICBIDGAJ_02140	OG0001354	acpP_1	1	0	0	fpr:FP2_24520	ko:K02078	NA	
ICBIDGAJ_02141	OG0000097	lcfB_2	1	0	0	fpr:FP2_24510	ko:K01897	NA	
ICBIDGAJ_02142	OG0000097	fadD	1	1	1	fpr:FP2_24500	ko:K01897	NA	
ICBIDGAJ_02143	OG0001355	group_3022	5	6	10	fpr:FP2_24490	NA	NA	
ICBIDGAJ_02144	OG0001356	group_3023	1	0	0	fpr:FP2_24480	NA	NA	
ICBIDGAJ_02145	OG0001357	cotSA	1	0	0	fpr:FP2_24470	NA	NA	
ICBIDGAJ_02146	OG0001358	group_870	5	5	9	fpa:FPR_12490	ko:K07027	NA	
ICBIDGAJ_02147	OG0002150	group_3931	1	1	1	fpa:FPR_12480	NA	NA	
ICBIDGAJ_02148	OG0001359	pflB	1	0	0	fpr:FP2_24860	ko:K00656	NA	
ICBIDGAJ_02149	OG0001360	pflA	1	0	0	fpa:FPR_12460	ko:K04069	NA	
ICBIDGAJ_02150	OG0002037	group_3024	1	0	0	fpr:FP2_09580	NA	NA	
ICBIDGAJ_02151	OG0000031	group_36	1	0	0	fpa:FPR_11000	NA	NA	
ICBIDGAJ_02152	OG0002306	macB_1	4	5	8	fpr:FP2_27620	ko:K02004	NA	
ICBIDGAJ_02153	OG0000047	lolD	1	0	0	fpr:FP2_27610	ko:K02003	NA	
ICBIDGAJ_02154	OG0000063	resE_2	1	2	2	fpr:FP2_27600	NA	NA	
ICBIDGAJ_02155	OG0000135	regX3_3	1	0	0	fpr:FP2_27590	NA	NA	
ICBIDGAJ_02156	OG0000065	group_176	1	0	0	fpa:FPR_03220	NA	NA	
ICBIDGAJ_02157	OG0000018	group_166	1	0	0	fpr:FP2_29840	NA	NA	
ICBIDGAJ_02158	OG0002059	group_917	1	0	0	fpa:FPR_03190	NA	NA	
ICBIDGAJ_02159	OG0000036	group_961	1	0	0	fpa:FPR_24760	NA	NA	
ICBIDGAJ_02160	OG0001679	group_1957	1	0	0	NA	NA	NA	
ICBIDGAJ_02161	OG0001980	group_2768	1	0	0	fpr:FP2_19480	NA	NA	
ICBIDGAJ_02162	OG0003981	group_4294	1	0	0	bon:A361_27665	NA	specific_fp14	○
ICBIDGAJ_02163	OG0003982	group_4295	1	0	0	pen:PSEEN0279	NA	specific_fp14	○
ICBIDGAJ_02164	OG0001361	mepA_5	6	7	12	fpr:FP2_24620	NA	NA	
ICBIDGAJ_02165	OG0001362	cbiC	1	0	0	fpa:FPR_29060	ko:K06042	NA	
ICBIDGAJ_02166	OG0001363	cobQ	1	0	0	fpa:FPR_29070	ko:K02232	NA	
ICBIDGAJ_02167	OG0001364	cobD_2	1	0	0	fpa:FPR_29080	ko:K04720	NA	
ICBIDGAJ_02168	OG0001365	cobD_1	1	0	0	fpr:FP2_02900	ko:K02227	NA	
ICBIDGAJ_02169	OG0001746	pspB_2	1	0	0	fpa:FPR_29100	ko:K02226	NA	
ICBIDGAJ_02170	OG0001366	group_1704	1	0	0	fpa:FPR_29110	ko:K02231	NA	
ICBIDGAJ_02171	OG0001367	cobS	2	2	3	fpa:FPR_29120	ko:K02233	NA	
ICBIDGAJ_02172	OG0001368	cobU	1	0	0	fpa:FPR_29130	ko:K02231	NA	
ICBIDGAJ_02173	OG0001369	cobT	1	0	0	fpa:FPR_29140	ko:K00768	NA	
ICBIDGAJ_02174	OG0001370	cbiA	1	0	0	fpa:FPR_29150	ko:K02224	NA	
ICBIDGAJ_02175	OG0001371	cbiET	1	0	0	fpa:FPR_29160	ko:K00595	NA	
ICBIDGAJ_02176	OG0001372	cbiJ	1	0	0	fpa:FPR_29170	ko:K05895	NA	
ICBIDGAJ_02177	OG0001373	cbiH	1	0	0	fpr:FP2_02810	NA	NA	
ICBIDGAJ_02178	OG0001374	cbiG	1	0	0	fpa:FPR_29190	ko:K02189	NA	
ICBIDGAJ_02179	OG0001375	cbiF	1	0	0	fpa:FPR_29200	ko:K05936	NA	
ICBIDGAJ_02180	OG0001376	cbiD	1	0	0	fpa:FPR_29210	ko:K02188	NA	
ICBIDGAJ_02181	OG0001377	hmuU	5	5	9	fpa:FPR_29220	ko:K02015	NA	
ICBIDGAJ_02182	OG0001378	group_1712	1	0	0	fpa:FPR_29230	ko:K02016	NA	
ICBIDGAJ_02183	OG0001379	group_1923	1	0	0	fpa:FPR_29240	NA	NA	
ICBIDGAJ_02184	OG0001380	cbiK	1	1	1	fpa:FPR_29250	NA	NA	
ICBIDGAJ_02185	OG0001381	group_874	1	0	0	fpr:FP2_29060	ko:K11529	NA	
ICBIDGAJ_02187	OG0001383	group_3031	1	0	0	fpr:FP2_16240	NA	NA	
ICBIDGAJ_02188	OG0000255	group_1714	1	1	1	fpr:FP2_16230	NA	NA	
ICBIDGAJ_02189	OG0000256	group_1715	2	3	4	fpr:FP2_16220	ko:K02004	NA	
ICBIDGAJ_02190	OG0000257	macB_2	1	0	0	fpa:FPR_19980	ko:K02003	NA	
ICBIDGAJ_02191	OG0000258	czcB	1	0	0	fpa:FPR_19970	ko:K02005	NA	
ICBIDGAJ_02192	OG0001384	group_3032	3	3	5	fpr:FP2_21040	ko:K03523	NA	
ICBIDGAJ_02193	OG0002611	group_3033	1	0	0	fpr:FP2_21050	ko:K09706	NA	
ICBIDGAJ_02194	OG0000027	group_2144	1	0	0	dru:Desru_0118;dru:Desru_2710;dru:Desru_2296	ko:K07497	NA	
ICBIDGAJ_02195	OG0003983	group_4297	1	0	0	tbe:Trebr_0407	NA	specific_fp14	
ICBIDGAJ_02196	OG0003984	group_4298	0	1	0	NA	NA	specific_fp14	○
ICBIDGAJ_02197	OG0002431	group_3124	0	1	0	NA	NA	NA	
ICBIDGAJ_02198	OG0002643	group_3125	1	0	0	lacy:A4V08_03905	NA	NA	
ICBIDGAJ_02199	OG0002359	group_270	1	0	0	fpa:FPR_00210	NA	NA	
ICBIDGAJ_02200	OG0000059	group_269	1	0	0	rho:RHOM_06500	NA	NA	
ICBIDGAJ_02201	OG0001672	group_930	1	0	0	fpa:FPR_23850	NA	NA	
ICBIDGAJ_02202	OG0000083	group_4299	0	1	0	ral:Rumal_1101	NA	NA	
ICBIDGAJ_02203	OG0000083	group_4300	1	0	0	erb:A4V01_00060	NA	NA	
ICBIDGAJ_02204	OG0002378	group_4301	1	0	0	lacy:A4V08_16095	NA	NA	
ICBIDGAJ_02205	OG0001849	group_1721	1	1	1	NA	NA	NA	
ICBIDGAJ_02209	OG0001393	lpxT	2	3	4	fpr:FP2_29280	NA	NA	
ICBIDGAJ_02210	OG0001392	group_2135	1	0	0	fpa:FPR_02400	NA	NA	
ICBIDGAJ_02211	OG0001391	group_1720	1	0	0	fpr:FP2_29300	NA	NA	
ICBIDGAJ_02212	OG0001390	group_663	1	0	0	eel:EUBELI_01251	NA	NA	
ICBIDGAJ_02213	OG0002040	ypwA	1	0	0	fpr:FP2_29320	ko:K01299	NA	
ICBIDGAJ_02214	OG0001389	hisS	1	0	0	fpr:FP2_16140	ko:K01892	NA	
ICBIDGAJ_02215	OG0001388	yhjX	6	7	12	fpa:FPR_19920	ko:K08177	NA	
ICBIDGAJ_02216	OG0001387	group_3034	1	0	0	fpa:FPR_19930	NA	NA	
ICBIDGAJ_02217	OG0001386	group_7140	1	0	0	fpa:FPR_19940;fpr:FP2_16170	NA	NA	
ICBIDGAJ_02218	OG0001385	fccA	1	0	0	fpr:FP2_16180	ko:K00244	NA	
ICBIDGAJ_02219	OG0002039	group_1716	1	1	1	fpa:FPR_19960	NA	NA	

ICBIDGAJ_02220	OG0000027	group_2145	1	0	0	dru:Desru_0118;dru:Desru_2710;dru:Desru_2296	ko:K07497	NA	
ICBIDGAJ_02221	OG0002271	uvrA_3	1	0	0	fhw:RN87_04025	ko:K03701	NA	
ICBIDGAJ_02222	OG0003985	albA_2	1	0	0	NA	NA	specific_fp14	○
ICBIDGAJ_02223	OG0000083	group_3126	1	0	0	erb:A4V01_00060	NA	NA	
ICBIDGAJ_02224	OG0001672	group_928	1	0	0	erb:A4V01_00065	NA	NA	
ICBIDGAJ_02225	OG0000040	group_295	1	0	0	fpr:FP2_24000	NA	NA	
ICBIDGAJ_02226	OG0000231	group_486	1	0	0	fpr:FP2_14000	ko:K06919	NA	
ICBIDGAJ_02227	OG0003986	group_4304	1	0	0	NA	NA	specific_fp14	○
ICBIDGAJ_02228	OG0000192	spoVK_2	1	0	0	meye:TL18_04690	NA	NA	
ICBIDGAJ_02229	OG0000083	Int-Tn_3	1	0	0	esu:EUS_03540	NA	NA	
ICBIDGAJ_02230	OG0001672	group_929	1	0	0	fpla:A4U99_10845	NA	NA	
ICBIDGAJ_02231	OG0000059	group_272	1	0	0	rho:RHOM_06500	NA	NA	
ICBIDGAJ_02232	OG0000040	group_296	1	0	0	fpr:FP2_24000	NA	NA	
ICBIDGAJ_02233	OG0001805	group_1152	0	1	0	fpa:FPR_23810	NA	NA	
ICBIDGAJ_02234	OG0000087	ams_2	1	0	0	fpr:FP2_08630	ko:K05341	NA	
ICBIDGAJ_02235	OG0000037	scrK_2	1	0	0	fpr:FP2_08640	ko:K00847	NA	
ICBIDGAJ_02236	OG0003536	group_4307	4	3	6	NA	NA	shared	○
ICBIDGAJ_02237	OG0003537	group_3127	1	0	0	NA	NA	shared	
ICBIDGAJ_02238	OG0003538	group_3128	1	1	1	NA	NA	shared	○
ICBIDGAJ_02239	OG0002644	group_4308	1	0	0	abao:BEQ56_06495	ko:K02529	NA	
ICBIDGAJ_02240	OG0001770	group_4309	3	3	5	abao:BEQ56_06490	ko:K17319	NA	
ICBIDGAJ_02241	OG0000125	group_4310	3	4	6	abao:BEQ56_06485	ko:K17320	NA	
ICBIDGAJ_02242	OG0001769	group_4311	1	0	0	abao:BEQ56_06480	ko:K17318	NA	
ICBIDGAJ_02243	OG0001768	sacA	1	0	0	fpr:FP2_08710	ko:K01193	NA	
ICBIDGAJ_02244	OG0000014	group_145	1	0	0	fpr:FP2_13830	NA	NA	
ICBIDGAJ_02245	OG0001396	lysS	1	0	0	fpr:FP2_23910	ko:K04567	NA	
ICBIDGAJ_02246	OG0001397	greA	1	0	0	fpa:FPR_16260	ko:K03624	NA	
ICBIDGAJ_02247	OG0000070	group_3044	1	0	0	NA	NA	NA	
ICBIDGAJ_02248	OG0001398	mepA_13	6	6	11	fpa:FPR_01350	NA	NA	
ICBIDGAJ_02249	OG0001399	rhaR	1	0	0	paea:R70723_24145	NA	NA	
ICBIDGAJ_02250	OG0001400	group_2153	1	0	0	fpr:FP2_24740	ko:K10112	NA	
ICBIDGAJ_02251	OG0001401	araQ_2	3	4	6	fpa:FPR_05940	ko:K02026	NA	
ICBIDGAJ_02252	OG0001402	lacF_2	3	4	6	fpa:FPR_05930	ko:K02025	NA	
ICBIDGAJ_02253	OG0001403	group_1731	1	0	0	fpa:FPR_05920	NA	NA	
ICBIDGAJ_02254	OG0001404	group_1732	1	0	0	fpa:FPR_05910	ko:K02529	NA	
ICBIDGAJ_02255	OG0000179	cbpA	1	0	0	fpa:FPR_05900	ko:K00702	NA	
ICBIDGAJ_02256	OG0001405	glnQ	1	0	0	rim:ROI_10800	ko:K02028	NA	
ICBIDGAJ_02257	OG0001406	artQ	3	3	5	fpa:FPR_06330	ko:K02029	NA	
ICBIDGAJ_02258	OG0001407	fliY_1	1	0	0	fpa:FPR_06340	ko:K02030	NA	
ICBIDGAJ_02259	OG0002156	group_3964	1	0	0	NA	NA	NA	
ICBIDGAJ_02260	OG0001408	group_1735	3	3	5	fpr:FP2_26500	NA	NA	
ICBIDGAJ_02261	OG0001409	group_1736	3	3	5	fpr:FP2_26510;fpa:FPR_06380	NA	NA	
ICBIDGAJ_02262	OG0000259	group_2154	1	1	1	fpa:FPR_13650	ko:K01421	NA	
ICBIDGAJ_02263	OG0000260	ydfJ	6	6	11	fpa:FPR_13660	ko:K07003	NA	
ICBIDGAJ_02264	OG0001410	bepR	1	0	0	fpa:FPR_13670	NA	NA	
ICBIDGAJ_02266	OG0001411	fabZ	1	0	0	fpr:FP2_20800	ko:K02372	NA	
ICBIDGAJ_02267	OG0001412	fabF	1	0	0	fpa:FPR_14900	ko:K09458	NA	
ICBIDGAJ_02268	OG0001413	fabG_3	1	0	0	fpr:FP2_20820	ko:K00059	NA	
ICBIDGAJ_02269	OG0001414	fabD	1	0	0	fpa:FPR_14880	ko:K00645	NA	
ICBIDGAJ_02270	OG0001415	group_1744	1	0	0	fpa:FPR_14870	NA	NA	
ICBIDGAJ_02271	OG0001416	group_1745	1	0	0	fpr:FP2_20850	ko:K02371	NA	
ICBIDGAJ_02272	OG0001417	fabH	1	0	0	fpa:FPR_14850	ko:K00648	NA	
ICBIDGAJ_02273	OG0001418	accA	1	0	0	fpr:FP2_20870	ko:K01962	NA	
ICBIDGAJ_02274	OG0001419	accD	1	0	0	fpr:FP2_20880	ko:K01963	NA	
ICBIDGAJ_02275	OG0001420	acpP_3	1	0	0	fpa:FPR_14820	ko:K02078	NA	
ICBIDGAJ_02276	OG0001421	pepF1	1	0	0	fpa:FPR_12970	NA	NA	
ICBIDGAJ_02277	OG0001422	pbuG	6	5	10	fpr:FP2_30730	ko:K06901	NA	
ICBIDGAJ_02278	OG0001423	group_1750	1	1	1	fpr:FP2_30720	NA	NA	
ICBIDGAJ_02279	OG0002043	panS	5	5	9	fpa:FPR_01880	ko:K03453	NA	
ICBIDGAJ_02280	OG0000400	yvbK	0	1	0	bprs:CK3_14360	NA	NA	
ICBIDGAJ_02281	OG0001755	group_2158	1	0	0	esu:EUS_17460	NA	NA	
ICBIDGAJ_02282	OG0001756	group_2159	1	0	0	tpk:JO40_10610	NA	NA	
ICBIDGAJ_02283	OG0001757	mgrA	1	0	0	rob:CK5_13830	NA	NA	
ICBIDGAJ_02284	OG0000139	yybR	1	0	0	bprl:CL2_21260	NA	NA	
ICBIDGAJ_02285	OG0002405	group_3966	1	0	0	rto:RTO_32390	NA	NA	
ICBIDGAJ_02287	OG0001424	group_2161	1	1	1	fpr:FP2_25610	NA	NA	
ICBIDGAJ_02288	OG0000261	group_3045	0	1	0	fpr:FP2_25600	NA	NA	
ICBIDGAJ_02289	OG0001425	group_3967	0	1	0	fpr:FP2_25590	NA	NA	
ICBIDGAJ_02290	OG0002044	lexA_2	1	0	0	fpr:FP2_25580	ko:K01356	NA	
ICBIDGAJ_02291	OG0001426	trmO	1	0	0	fpr:FP2_25570	NA	NA	
ICBIDGAJ_02292	OG0000262	group_1751	1	0	0	fpr:FP2_25560	NA	NA	
ICBIDGAJ_02293	OG0003987	group_888	0	1	0	fpr:FP2_30420	ko:K01266	specific_fp14	○
ICBIDGAJ_02294	OG0001758	group_887	1	0	0	fpa:FPR_19780	ko:K01266	NA	
ICBIDGAJ_02295	OG0001427	metA	1	0	0	fpr:FP2_30410	ko:K00651	NA	
ICBIDGAJ_02296	OG0001428	mgl_2	1	0	0	fpa:FPR_06420	ko:K01740	NA	
ICBIDGAJ_02297	OG0001429	metI	3	3	5	fpr:FP2_30390	ko:K02072	NA	
ICBIDGAJ_02298	OG0001430	metN	1	0	0	fpla:A4U99_16580	ko:K02071	NA	
ICBIDGAJ_02299	OG0001431	group_1755	1	0	0	fpr:FP2_30370	ko:K02073	NA	
ICBIDGAJ_02300	OG0001432	dnaK_1	1	0	0	fpa:FPR_12190	ko:K04043	NA	
ICBIDGAJ_02301	OG0001433	group_3046	1	0	0	fpr:FP2_26110	ko:K07126	NA	
ICBIDGAJ_02302	OG0003144	group_3968	1	0	0	NA	NA	NA	
ICBIDGAJ_02303	OG0001856	group_2513	1	1	1	fpr:FP2_25550	NA	NA	
ICBIDGAJ_02304	OG0002176	rbr	1	0	0	fpr:FP2_25540	NA	NA	
ICBIDGAJ_02305	OG0001434	group_3969	4	4	7	fpr:FP2_25530	NA	NA	
ICBIDGAJ_02306	OG0001435	group_1757	1	0	0	fpr:FP2_25520	ko:K03218	NA	
ICBIDGAJ_02307	OG0000263	fba	1	0	0	fpr:FP2_25510	ko:K01624	NA	
ICBIDGAJ_02308	OG0001436	fpgS_1	1	0	0	fpr:FP2_15280	ko:K11754	NA	
ICBIDGAJ_02309	OG0001437	folT	3	3	5	fpa:FPR_12980	NA	NA	
ICBIDGAJ_02310	OG0002045	iolC	1	0	0	fpr:FP2_24710	ko:K00847	NA	
ICBIDGAJ_02311	OG0001438	group_1760	2	2	3	fpr:FP2_25270	ko:K06147	NA	
ICBIDGAJ_02312	OG0001439	group_1761	3	3	5	fpr:FP2_25280	ko:K06147	NA	
ICBIDGAJ_02313	OG0001440	slyA_2	1	0	0	fpa:FPR_14950	NA	NA	
ICBIDGAJ_02314	OG0001441	group_1763	6	7	12	fpa:FPR_12560	NA	NA	
ICBIDGAJ_02315	OG0001442	group_1764	1	0	0	fpa:FPR_12570	ko:K09765	NA	
ICBIDGAJ_02316	OG0001443	group_1765	0	1	0	fpr:FP2_23020	NA	NA	
ICBIDGAJ_02317	OG0001444	purA_1	1	0	0	fpr:FP2_23010	ko:K01939	NA	
ICBIDGAJ_02318	OG0001445	group_1767	1	1	1	fpa:FPR_12600	NA	NA	
ICBIDGAJ_02319	OG0002046	group_3970	1	1	1	fpr:FP2_31410	ko:K07284	NA	
ICBIDGAJ_02320	OG0001446	rsxB_2	1	1	1	fpa:FPR_12890	ko:K03616	NA	
ICBIDGAJ_02321	OG0001447	rsxA	4	3	6	fpr:FP2_23070	ko:K03617	NA	
ICBIDGAJ_02322	OG0001448	rnfE	3	4	6	fpr:FP2_23080	ko:K03613	NA	
ICBIDGAJ_02323	OG0001449	rnfG	1	1	1	fpr:FP2_23090	ko:K03612	NA	
ICBIDGAJ_02324	OG0001450	rsxD_1	5	5	9	fpa:FPR_12850	ko:K03614	NA	
ICBIDGAJ_02325	OG0001451	rnfC	1	0	0	fpr:FP2_23110	ko:K03615	NA	
ICBIDGAJ_02326	OG0001452	group_2164	1	1	1	NA	NA	NA	
ICBIDGAJ_02327	OG0003145	group_3972	1	1	1	NA	NA	NA	
ICBIDGAJ_02328	OG0001453	group_1773	1	0	0	fpa:FPR_12810	NA	NA	
ICBIDGAJ_02329	OG0001454	hyaD	1	0	0	fpa:FPR_12800	ko:K20444	NA	
ICBIDGAJ_02330	OG0001455	tagH	1	0	0	fpr:FP2_23150	ko:K01990	NA	
ICBIDGAJ_02331	OG0001456	tagG	3	4	6	fpa:FPR_12780	ko:K01992	NA	
ICBIDGAJ_02332	OG0001457	rfbC	1	0	0	fpa:FPR_12770	ko:K01790	NA	
ICBIDGAJ_02333	OG0001458	dacF_3	1	2	2	fpr:FP2_23180	ko:K07258	NA	
ICBIDGAJ_02334	OG0001459	dpaB	1	1	1	fpa:FPR_12750	ko:K06411	NA	
ICBIDGAJ_02335	OG0001460	dpaA	1	0	0	fpa:FPR_12740	ko:K06410	NA	

ICBIDGAJ_02336	OG0003146	group_3973	1	0	0	ruk:A4V00_04415	NA	NA	
ICBIDGAJ_02337	OG0001759	creC	1	2	2	fpa:FPR_00450	ko:K20487	NA	
ICBIDGAJ_02338	OG0001760	arlR	1	0	0	fpla:A4U99_00925	ko:K20488	NA	
ICBIDGAJ_02339	OG0001761	group_891	5	4	8	fpa:FPR_00430	NA	NA	
ICBIDGAJ_02340	OG0001921	group_2166	1	0	0	NA	NA	NA	
ICBIDGAJ_02341	OG0002291	group_2169	1	0	0	fpr:FP2_23410	NA	NA	
ICBIDGAJ_02347	OG0001461	nrdD	1	0	0	fpa:FPR_00520	ko:K21636	NA	
ICBIDGAJ_02348	OG0001462	nrdG	1	0	0	fpa:FPR_00510	ko:K04068	NA	
ICBIDGAJ_02349	OG0000070	group_4312	1	1	1	NA	NA	NA	
ICBIDGAJ_02350	OG0001463	recQ	1	0	0	fpa:FPR_00500	ko:K03654	NA	
ICBIDGAJ_02351	OG0001464	epsH	1	0	0	fpr:FP2_22560	NA	NA	
ICBIDGAJ_02352	OG0001465	kefB	5	5	9	fpr:FP2_22570	NA	NA	
ICBIDGAJ_02353	OG0001466	clpC_2	1	0	0	fpr:FP2_22590	NA	NA	
ICBIDGAJ_02354	OG0001467	group_1785	3	3	5	fpr:FP2_22600	NA	NA	
ICBIDGAJ_02355	OG0001468	group_3048	1	1	1	fpr:FP2_22610	ko:K03641	NA	
ICBIDGAJ_02356	OG0001469	truA	1	0	0	fpa:FPR_11100	ko:K06173	NA	
ICBIDGAJ_02357	OG0001470	ecfT_2	3	2	4	fpa:FPR_11090	ko:K16785	NA	
ICBIDGAJ_02358	OG0001471	ecfA2	1	0	0	fpr:FP2_22640	ko:K16787	NA	
ICBIDGAJ_02359	OG0001472	ecfA1	1	0	0	fpr:FP2_22650	ko:K16786	NA	
ICBIDGAJ_02360	OG0001473	rlmK	1	0	0	fpa:FPR_11060	ko:K06969	NA	
ICBIDGAJ_02361	OG0001474	ruvB_2	1	0	0	fpr:FP2_22680	ko:K03551	NA	
ICBIDGAJ_02362	OG0001475	ruvA	1	0	0	fpa:FPR_11040	ko:K03550	NA	
ICBIDGAJ_02363	OG0001476	ruvC	1	0	0	ruk:A4V00_10760	ko:K01159	NA	
ICBIDGAJ_02365	OG0003147	group_3976	5	6	10	rim:ROI_08600	NA	NA	
ICBIDGAJ_02366	OG0001477	group_1794	1	0	0	fpa:FPR_19840	NA	NA	
ICBIDGAJ_02367	OG0002047	oppF_1	1	0	0	fpa:FPR_10240	ko:K10823	NA	
ICBIDGAJ_02368	OG0000033	oppD_1	1	0	0	fpa:FPR_10230	ko:K15583	NA	
ICBIDGAJ_02369	OG0002048	oppC_1	3	4	6	fpr:FP2_31120	ko:K15582	NA	
ICBIDGAJ_02370	OG0002049	oppB_1	3	4	6	bhu:bhn_I2685	ko:K15581	NA	
ICBIDGAJ_02371	OG0002050	dppE_1	1	0	0	fpr:FP2_31140	ko:K15580	NA	
ICBIDGAJ_02372	OG0001478	rny	1	1	1	fpr:FP2_31170	ko:K18682	NA	
ICBIDGAJ_02373	OG0001479	gltC_2	1	0	0	fpr:FP2_31180	ko:K01104	NA	
ICBIDGAJ_02374	OG0000082	ridA	1	0	0	fpr:FP2_02700	NA	NA	
ICBIDGAJ_02375	OG0001480	asnA	1	0	0	fpa:FPR_12610	ko:K01914	NA	
ICBIDGAJ_02376	OG0001922	group_3053	3	4	6	NA	NA	NA	
ICBIDGAJ_02377	OG0001481	pgsA	2	3	4	fpr:FP2_15090	ko:K00995	NA	
ICBIDGAJ_02378	OG0001482	rimO	1	0	0	fpa:FPR_11850	ko:K14441	NA	
ICBIDGAJ_02379	OG0001483	recX	1	0	0	fpr:FP2_15070	ko:K03565	NA	
ICBIDGAJ_02380	OG0001484	recA	1	0	0	fpa:FPR_11830	ko:K03553	NA	
ICBIDGAJ_02381	OG0001485	prmC	1	0	0	fpr:FP2_15050	ko:K02493	NA	
ICBIDGAJ_02382	OG0001486	group_1803	2	3	4	fpa:FPR_11810	NA	NA	
ICBIDGAJ_02383	OG0001487	phoR_2	2	1	2	fpr:FP2_15030	NA	NA	
ICBIDGAJ_02384	OG0001488	regX3_1	1	0	0	fpr:FP2_15020	NA	NA	
ICBIDGAJ_02385	OG0001489	group_1806	1	0	0	fpa:FPR_11780	NA	NA	
ICBIDGAJ_02386	OG0001490	rplQ	1	0	0	fpr:FP2_15000	ko:K02879	NA	
ICBIDGAJ_02387	OG0001491	rpoA	1	0	0	fpr:FP2_14990	ko:K03040	NA	
ICBIDGAJ_02388	OG0001492	rpsD	1	0	0	fpa:FPR_11750	ko:K02986	NA	
ICBIDGAJ_02389	OG0001493	rpsK	0	1	0	fpr:FP2_14970	ko:K02948	NA	
ICBIDGAJ_02390	OG0001494	rpsM	1	0	0	fpa:FPR_11730	ko:K02952	NA	
ICBIDGAJ_02391	OG0001495	rpmJ	0	1	0	fpr:FP2_14950;fpa:FPR_11720	ko:K02919	NA	
ICBIDGAJ_02392	OG0001496	infA	1	0	0	eha:Ethha_0391	ko:K02518	NA	
ICBIDGAJ_02393	OG0001497	map	1	0	0	esu:EUS_27830;esr:ES1_24550	ko:K01265	NA	
ICBIDGAJ_02394	OG0001498	adk	1	0	0	fpa:FPR_11690	ko:K00939	NA	
ICBIDGAJ_02395	OG0001499	secY	5	6	10	eha:Ethha_0387	ko:K03076	NA	
ICBIDGAJ_02396	OG0001500	rplO	1	0	0	fpr:FP2_14900	ko:K02876	NA	
ICBIDGAJ_02397	OG0001501	rpmD	1	0	0	fpa:FPR_11660;fpr:FP2_14890	ko:K02907	NA	
ICBIDGAJ_02398	OG0001502	rpsE	1	0	0	fpa:FPR_11650	ko:K02988	NA	
ICBIDGAJ_02399	OG0001503	rplR	0	1	0	fpr:FP2_14870	ko:K02881	NA	
ICBIDGAJ_02400	OG0001504	rplF	1	0	0	fpa:FPR_11630	ko:K02933	NA	
ICBIDGAJ_02401	OG0001505	rpsH	1	0	0	fpr:FP2_14850	ko:K02994	NA	
ICBIDGAJ_02402	OG0001506	rpsZ	0	1	0	fpr:FP2_14840;fpa:FPR_11610	ko:K02954	NA	
ICBIDGAJ_02403	OG0001507	rplE	1	0	0	fpr:FP2_14830	ko:K02931	NA	
ICBIDGAJ_02404	OG0001508	rplX	1	0	0	fpr:FP2_14820	ko:K02895	NA	
ICBIDGAJ_02405	OG0001509	rplN	1	0	0	fpa:FPR_11580	ko:K02874	NA	
ICBIDGAJ_02406	OG0001510	rpsQ	0	1	0	fpa:FPR_11570	ko:K02961	NA	
ICBIDGAJ_02407	OG0001511	rpmC	0	1	0	fpr:FP2_14790;fpa:FPR_11560	ko:K02904	NA	
ICBIDGAJ_02408	OG0001512	rplP	1	0	0	fpr:FP2_14780	ko:K02878	NA	
ICBIDGAJ_02409	OG0001513	rpsC	1	0	0	fpr:FP2_14770	ko:K02982	NA	
ICBIDGAJ_02410	OG0001514	rplV	1	0	0	fpa:FPR_11530;fpr:FP2_14760	ko:K02890	NA	
ICBIDGAJ_02411	OG0001515	rpsS	1	0	0	fpr:FP2_14750	ko:K02965	NA	
ICBIDGAJ_02412	OG0001516	rplB	1	0	0	fpa:FPR_11510	ko:K02886	NA	
ICBIDGAJ_02413	OG0001517	rplW	1	0	0	fpa:FPR_11500	ko:K02892	NA	
ICBIDGAJ_02414	OG0001518	rplD	1	0	0	fpa:FPR_11490	ko:K02926	NA	
ICBIDGAJ_02415	OG0001519	rplC	1	0	0	fpa:FPR_11480	ko:K02906	NA	
ICBIDGAJ_02416	OG0001520	rpsJ	0	1	0	fpr:FP2_14700	ko:K02946	NA	
ICBIDGAJ_02417	OG0001521	group_1810	1	0	0	fpa:FPR_11460	NA	NA	
ICBIDGAJ_02418	OG0001522	group_892	1	0	0	fpr:FP2_14660	NA	NA	
ICBIDGAJ_02419	OG0001523	trmK	1	0	0	tco:Theco_2355	ko:K06967	NA	
ICBIDGAJ_02420	OG0001524	group_1812	1	0	0	fpr:FP2_14640	NA	NA	
ICBIDGAJ_02421	OG0001525	group_3061	1	0	0	fpr:FP2_14630	NA	NA	
ICBIDGAJ_02422	OG0001526	ackA	1	0	0	fpr:FP2_14620	ko:K00925	NA	
ICBIDGAJ_02423	OG0001527	group_1814	1	0	0	fpr:FP2_14610	NA	NA	
ICBIDGAJ_02424	OG0003988	gltD_1	1	0	0	fpa:FPR_13720	ko:K00266	NA	
ICBIDGAJ_02425	OG0001528	gltD_3	1	1	1	fpa:FPR_13720	ko:K00266	NA	
ICBIDGAJ_02426	OG0001529	group_893	7	8	14	eel:EUBELI_01841	NA	NA	
ICBIDGAJ_02427	OG0001530	group_1815	1	0	0	fpa:FPR_11410	NA	NA	
ICBIDGAJ_02428	OG0001531	group_1816	4	3	6	fpr:FP2_14570	NA	NA	
ICBIDGAJ_02429	OG0000115	group_3977	1	0	0	bag:Bcoa_0587	NA	NA	
ICBIDGAJ_02430	OG0003148	rihA	1	0	0	pec:W5S_2717	NA	NA	
ICBIDGAJ_02431	OG0000180	ywiE_2	2	2	3	fpr:FP2_14560	ko:K06131	NA	
ICBIDGAJ_02432	OG0002051	group_2522	1	0	0	fpr:FP2_14550	NA	NA	
ICBIDGAJ_02433	OG0000144	udk_1	1	0	0	fpa:FPR_13360	ko:K00876	NA	
ICBIDGAJ_02434	OG0000144	group_489	0	1	0	fpr:FP2_14540	ko:K00876	NA	
ICBIDGAJ_02435	OG0001532	iscU	1	0	0	fpr:FP2_23210	ko:K04488	NA	
ICBIDGAJ_02436	OG0001533	iscS_3	1	0	0	fpr:FP2_23220	ko:K04487	NA	
ICBIDGAJ_02437	OG0001534	group_1817	1	0	0	fpa:FPR_12410	NA	NA	
ICBIDGAJ_02438	OG0001535	pspE	1	0	0	fpa:FPR_12420	NA	NA	
ICBIDGAJ_02439	OG0001536	cymR_2	1	0	0	fpr:FP2_23250	NA	NA	
ICBIDGAJ_02443	OG0001858	adhE	1	0	0	fpa:FPR_12440	NA	NA	
ICBIDGAJ_02445	OG0000008	group_126	1	0	0	fpr:FP2_28240	NA	NA	
ICBIDGAJ_02446	OG0000004	soj_3	1	0	0	fpr:FP2_21910	ko:K03496	NA	
ICBIDGAJ_02447	OG0000002	spo0C_4	1	0	0	fpa:FPR_00840	ko:K03497	NA	
ICBIDGAJ_02448	OG0000145	group_1822	1	0	0	fpa:FPR_00820	NA	NA	
ICBIDGAJ_02449	OG0000039	group_305	1	0	0	fpr:FP2_09020	NA	NA	
ICBIDGAJ_02450	OG0000017	group_429	1	0	0	fpr:FP2_09010	NA	NA	
ICBIDGAJ_02451	OG0000185	group_76	1	2	2	fpr:FP2_21800	ko:K03205	NA	
ICBIDGAJ_02452	OG0003192	group_4313	1	0	0	fpa:FPR_08010	NA	NA	
ICBIDGAJ_02453	OG0000049	group_2850	1	0	0	fpa:FPR_05670	NA	NA	
ICBIDGAJ_02454	OG0002307	group_4314	1	0	0	fpa:FPR_05690	NA	NA	
ICBIDGAJ_02455	OG0000105	group_4315	1	0	0	fpa:FPR_05700	NA	NA	
ICBIDGAJ_02456	OG0001929	bin3	1	0	0	ibu:IB211_00448c	NA	NA	
ICBIDGAJ_02457	OG0003989	group_4316	0	1	0	NA	NA	specific_fp14	○
ICBIDGAJ_02458	OG0002432	group_4317	1	0	0	NA	NA	NA	
ICBIDGAJ_02459	OG0003990	group_4318	1	0	0	NA	NA	specific_fp14	○

ICBIDGAJ_02460	OG0003991	group_4319	1	0	0	NA	NA	specific_fp14	O
ICBIDGAJ_02461	OG0002422	esiB_2	1	0	0	NA	NA	NA	
ICBIDGAJ_02462	OG0000034	group_534	1	0	0	fpa:FPR_00420	NA	NA	
ICBIDGAJ_02463	OG0002230	group_2367	1	0	0	rto:RTO_16330	NA	NA	
ICBIDGAJ_02464	OG0000030	mobA_1	1	0	0	fpr:FP2_22490	NA	NA	
ICBIDGAJ_02465	OG0001869	group_4321	1	0	0	NA	NA	NA	
ICBIDGAJ_02466	OG0000001	group_60	1	0	0	fpr:FP2_19610	ko:K03205	NA	
ICBIDGAJ_02467	OG0000006	group_7117	1	2	2	ova:OBV_30190	NA	NA	
ICBIDGAJ_02468	OG0000011	group_7183	3	3	5	fpr:FP2_22330	NA	NA	
ICBIDGAJ_02469	OG0000016	group_363	1	2	2	csh:Closa_3716	NA	NA	
ICBIDGAJ_02470	OG0000009	group_198	1	0	0	fpr:FP2_22350	NA	NA	
ICBIDGAJ_02471	OG0000012	iap_1	1	1	1	fpr:FP2_00570	NA	NA	
ICBIDGAJ_02472	OG0000013	group_338	1	0	0	fpr:FP2_22380	NA	NA	
ICBIDGAJ_02473	OG0000007	mapZ	1	2	2	fpr:FP2_22390	NA	NA	
ICBIDGAJ_02474	OG0000003	topB_1	1	0	0	fpr:FP2_00540	ko:K03169	NA	
ICBIDGAJ_02475	OG0000019	group_374	1	0	0	fpa:FPR_19070	NA	NA	
ICBIDGAJ_02476	OG0000022	group_344	1	0	0	fpr:FP2_10260	NA	NA	
ICBIDGAJ_02477	OG0000020	group_308	1	0	0	fpa:FPR_04570	NA	NA	
ICBIDGAJ_02478	OG0002038	yccM_1	4	4	7	cls:CXIVA_04360	NA	NA	
ICBIDGAJ_02479	OG0001382	arsC	1	0	0	eel:EUBELI_20104	ko:K03741	NA	
ICBIDGAJ_02480	OG0000005	group_88	1	0	0	fpr:FP2_27160	NA	NA	
ICBIDGAJ_02481	OG0000023	group_267	1	0	0	fpr:FP2_21550	NA	NA	
ICBIDGAJ_02482	OG0000038	group_435	2	2	3	fpr:FP2_08920	NA	NA	
ICBIDGAJ_02483	OG0000264	group_1674	1	0	0	NA	NA	NA	
ICBIDGAJ_02484	OG0000010	group_193	1	0	0	fpa:FPR_04440	NA	NA	
ICBIDGAJ_02485	OG0000098	immR_2	1	0	0	NA	NA	NA	
ICBIDGAJ_02486	OG0000099	group_655	1	0	0	NA	NA	NA	
ICBIDGAJ_02487	OG0001538	group_7215	0	1	0	NA	NA	NA	
ICBIDGAJ_02488	OG0001539	group_7115	1	0	0	csh:Closa_0107	NA	NA	
ICBIDGAJ_02489	OG0001540	group_7119	1	0	0	csh:Closa_0106	NA	NA	
ICBIDGAJ_02490	OG0001541	group_7127	1	0	0	csh:Closa_0105	NA	NA	
ICBIDGAJ_02491	OG0001542	group_3064	1	0	0	csh:Closa_0104	NA	NA	
ICBIDGAJ_02492	OG0001543	group_3065	2	3	4	csh:Closa_0103	NA	NA	
ICBIDGAJ_02493	OG0001544	group_7180	2	3	4	csh:Closa_0102	NA	NA	
ICBIDGAJ_02494	OG0001545	sugC_1	1	0	0	csh:Closa_0101	ko:K10112	NA	
ICBIDGAJ_02495	OG0001546	group_2530	2	3	4	csh:Closa_0100	NA	NA	
ICBIDGAJ_02496	OG0001547	group_7128	2	3	4	csh:Closa_0099	NA	NA	
ICBIDGAJ_02497	OG0001548	group_7204	1	0	0	csh:Closa_0098	NA	NA	
ICBIDGAJ_02498	OG0001549	ycjP_1	3	4	6	csh:Closa_0097	ko:K17320	NA	
ICBIDGAJ_02499	OG0001550	yteP_1	4	4	7	csh:Closa_0096	ko:K17319	NA	
ICBIDGAJ_02500	OG0001551	group_7186	5	6	10	cle:Clole_2247	NA	NA	
ICBIDGAJ_02501	OG0000265	kdgR	1	0	0	csh:Closa_0094	NA	NA	
ICBIDGAJ_02502	OG0001552	pfp_1	1	0	0	fpr:FP2_05410	ko:K21071	NA	
ICBIDGAJ_02503	OG0001553	group_7107	0	1	0	NA	NA	NA	
ICBIDGAJ_02504	OG0001554	spo0C_1	1	0	0	fpr:FP2_21840	ko:K03497	NA	
ICBIDGAJ_02505	OG0001555	group_7106	1	0	0	fpla:A4U99_07135	NA	NA	
ICBIDGAJ_02506	OG0001556	group_7114	1	0	0	fpa:FPR_18730	NA	NA	
ICBIDGAJ_02507	OG0000266	group_2185	0	1	0	fpa:FPR_18720	NA	NA	
ICBIDGAJ_02508	OG0000096	group_286	1	0	0	fpa:FPR_18710	NA	NA	
ICBIDGAJ_02509	OG0000116	group_2531	1	0	0	fpa:FPR_18700	NA	NA	
ICBIDGAJ_02510	OG0001557	ndoA_6	1	0	0	fpa:FPR_18690	ko:K07171	NA	
ICBIDGAJ_02511	OG0001861	group_3981	1	0	0	NA	NA	NA	
ICBIDGAJ_02512	OG0003992	group_4322	1	0	0	fpr:FP2_11490	NA	specific_fp14	
ICBIDGAJ_02514	OG0001558	group_1823	1	1	1	fpr:FP2_11480	NA	NA	
ICBIDGAJ_02515	OG0001559	group_1824	2	3	4	fpr:FP2_11470	NA	NA	
ICBIDGAJ_02516	OG0001560	group_668	1	1	1	fpr:FP2_11460	NA	NA	
ICBIDGAJ_02517	OG0001561	group_3066	1	1	1	fpa:FPR_11350	NA	NA	
ICBIDGAJ_02518	OG0001562	group_1825	5	6	10	fpr:FP2_11440	NA	NA	
ICBIDGAJ_02519	OG0001563	group_1826	1	0	0	fpr:FP2_11430	ko:K07043	NA	
ICBIDGAJ_02520	OG0001564	group_1827	6	7	12	NA	NA	NA	
ICBIDGAJ_02521	OG0001565	metH	1	0	0	eel:EUBELI_01382	ko:K00548	NA	
ICBIDGAJ_02522	OG0001566	group_1829	1	0	0	fpa:FPR_15560	NA	NA	
ICBIDGAJ_02523	OG0000064	dinJ	0	1	0	elm:ELI_1789	NA	NA	
ICBIDGAJ_02524	OG0000140	group_4324	0	1	0	gva:HMPREF0424_0746	NA	NA	
ICBIDGAJ_02525	OG0002617	group_3067	1	0	0	NA	NA	NA	
ICBIDGAJ_02526	OG0001567	mgl_1	1	0	0	fpr:FP2_24380	ko:K01740	NA	
ICBIDGAJ_02527	OG0001568	group_1830	1	0	0	fpr:FP2_11410	NA	NA	
ICBIDGAJ_02528	OG0001569	abrB	0	1	0	fpa:FPR_00470	ko:K06284	NA	
ICBIDGAJ_02529	OG0001570	gltX_1	1	0	0	fpa:FPR_11160	ko:K01885	NA	
ICBIDGAJ_02530	OG0001571	spoIIE	4	4	7	fpr:FP2_11350	ko:K06382	NA	
ICBIDGAJ_02531	OG0001572	pemA	1	0	0	fpr:FP2_11340	ko:K01051	NA	
ICBIDGAJ_02532	OG0001573	group_1833	1	1	1	fpr:FP2_11330	NA	NA	
ICBIDGAJ_02533	OG0001574	phoR_1	1	1	1	fpr:FP2_31400	NA	NA	
ICBIDGAJ_02534	OG0001575	srrA_1	1	0	0	fpr:FP2_31390	ko:K07775	NA	
ICBIDGAJ_02535	OG0001576	group_3983	2	1	2	fpr:FP2_31380	NA	NA	
ICBIDGAJ_02536	OG0001577	group_1836	1	0	0	fpr:FP2_31370	NA	NA	
ICBIDGAJ_02537	OG0001578	group_1837	1	0	0	fpa:FPR_11290	ko:K06997	NA	
ICBIDGAJ_02538	OG0001579	group_1838	3	2	4	fpr:FP2_31350	ko:K06147	NA	
ICBIDGAJ_02539	OG0000182	group_2187	1	2	2	fpa:FPR_11150	NA	NA	
ICBIDGAJ_02540	OG0000182	group_2188	1	1	1	fpa:FPR_11150	NA	NA	
ICBIDGAJ_02541	OG0000267	group_3068	1	0	0	fpa:FPR_11140	ko:K07729	NA	
ICBIDGAJ_02542	OG0003150	group_3984	1	0	0	fpr:FP2_15180	NA	NA	
ICBIDGAJ_02543	OG0001798	group_3985	1	0	0	NA	NA	NA	
ICBIDGAJ_02544	OG0003151	group_3986	1	0	0	erb:A4V01_02580	NA	NA	
ICBIDGAJ_02545	OG0001580	glcK_2	1	0	0	fpr:FP2_31340	ko:K00845	NA	
ICBIDGAJ_02546	OG0001581	tatC	3	4	6	ova:OBV_43450	ko:K03118	NA	
ICBIDGAJ_02547	OG0001582	tatAy	1	0	0	fpr:FP2_31320	ko:K03116	NA	
ICBIDGAJ_02548	OG0001583	tatB	1	0	0	fpa:FPR_12150	ko:K03117	NA	
ICBIDGAJ_02549	OG0001584	group_1843	1	0	0	fpr:FP2_31300	NA	NA	
ICBIDGAJ_02550	OG0001585	yraA	1	0	0	fpr:FP2_31290	ko:K03152	NA	
ICBIDGAJ_02551	OG0001586	group_1844	1	0	0	fpr:FP2_31280	NA	NA	
ICBIDGAJ_02552	OG0001587	group_1845	1	0	0	fpa:FPR_18510	NA	NA	
ICBIDGAJ_02553	OG0001765	frp	1	0	0	fpa:FPR_18520	NA	NA	
ICBIDGAJ_02554	OG0002054	group_2537	1	1	1	fpr:FP2_31260	NA	NA	
ICBIDGAJ_02555	OG0002159	group_3987	3	4	6	NA	NA	NA	
ICBIDGAJ_02556	OG0001588	xlnA	1	0	0	fpr:FP2_31250	NA	NA	
ICBIDGAJ_02557	OG0001589	mutX	1	0	0	fpr:FP2_31240	ko:K03574	NA	
ICBIDGAJ_02558	OG0001590	group_1848	4	5	8	fpa:FPR_18270	ko:K07035	NA	
ICBIDGAJ_02559	OG0001591	acm	1	1	1	fpr:FP2_31220	NA	NA	
ICBIDGAJ_02560	OG0002406	group_3069	1	0	0	fpr:FP2_31210	NA	NA	
ICBIDGAJ_02561	OG0001592	dnaJ_2	1	0	0	fpa:FPR_17970	ko:K03686	NA	
ICBIDGAJ_02562	OG0000268	dnaK_2	1	0	0	fpr:FP2_12320	ko:K04043	NA	
ICBIDGAJ_02563	OG0001593	grpE	1	0	0	fpr:FP2_12330	ko:K03687	NA	
ICBIDGAJ_02564	OG0001594	hrcA	1	0	0	fpa:FPR_17940	ko:K03705	NA	
ICBIDGAJ_02565	OG0001595	spoVT	1	0	0	fpr:FP2_12360	ko:K04769	NA	
ICBIDGAJ_02566	OG0001673	group_4325	1	0	0	clo:HMPREF0868_0124	NA	NA	
ICBIDGAJ_02567	OG0001766	group_4326	1	2	2	rhd:R2APBS1_2472	NA	NA	
ICBIDGAJ_02568	OG0001596	group_900	1	0	0	fpa:FPR_17900	ko:K07007	NA	
ICBIDGAJ_02569	OG0001597	alsT_2	6	6	11	fpa:FPR_17840	ko:K03310	NA	
ICBIDGAJ_02570	OG0001598	group_2538	1	1	1	NA	NA	NA	
ICBIDGAJ_02571	OG0001599	gabR_2	1	0	0	fpr:FP2_12420	ko:K00375	NA	
ICBIDGAJ_02572	OG0001600	group_902	3	4	6	fpr:FP2_12430	NA	NA	
ICBIDGAJ_02573	OG0001601	ppiB	1	0	0	fpa:FPR_10750	ko:K03768	NA	
ICBIDGAJ_02574	OG0001602	group_903	1	0	0	fpa:FPR_10910	NA	NA	

ICBIDGAJ_02575	OG0001603	group_1854	1	0	0	fpa:FPR_10920	NA	NA	
ICBIDGAJ_02576	OG0001604	lexA	1	0	0	fpa:FPR_10930	ko:K01356	NA	
ICBIDGAJ_02579	OG0001605	group_2189	2	3	4	fpa:FPR_10940	NA	NA	
ICBIDGAJ_02580	OG0000269	gltC_1	1	0	0	fpr:FP2_31480	NA	NA	
ICBIDGAJ_02581	OG0001606	group_3989	1	0	0	fpr:FP2_31470	NA	NA	
ICBIDGAJ_02582	OG0001607	group_1857	6	6	11	fpa:FPR_05420	ko:K03308	NA	
ICBIDGAJ_02583	OG0001608	rlmA	1	0	0	fpa:FPR_17810	ko:K00563	NA	
ICBIDGAJ_02584	OG0001609	rhlE	1	0	0	fpr:FP2_12470	ko:K11927	NA	
ICBIDGAJ_02585	OG0001610	group_1859	1	0	0	fpr:FP2_12480	NA	NA	
ICBIDGAJ_02586	OG0001611	group_3070	1	1	1	fpr:FP2_12490	NA	NA	
ICBIDGAJ_02587	OG0001612	nqrE	4	3	6	fpr:FP2_12500	ko:K03617	NA	
ICBIDGAJ_02588	OG0001613	rsxE	2	3	4	fpr:FP2_12510	ko:K03613	NA	
ICBIDGAJ_02589	OG0001614	rsxD_2	3	4	6	fpr:FP2_12520	ko:K03614	NA	
ICBIDGAJ_02590	OG0001615	rpe	1	0	0	fpa:FPR_17740	ko:K01783	NA	
ICBIDGAJ_02591	OG0001616	phoR_4	2	1	2	fpr:FP2_12540	NA	NA	
ICBIDGAJ_02592	OG0000270	srrA_2	1	0	0	fpr:FP2_12550	NA	NA	
ICBIDGAJ_02593	OG0001617	group_3071	1	0	0	lacy:A4V08_06930	NA	NA	
ICBIDGAJ_02594	OG0001618	ychF	1	0	0	fpr:FP2_13440	ko:K06942	NA	
ICBIDGAJ_02595	OG0001619	mtnN	1	0	0	fpr:FP2_13450	ko:K01243	NA	
ICBIDGAJ_02596	OG0001620	group_1866	1	0	0	fpr:FP2_13460	NA	NA	
ICBIDGAJ_02597	OG0000027	group_4101	1	0	0	cad:Curi_c00320	NA	NA	
ICBIDGAJ_02598	OG0002300	group_4099	0	1	0	NA	NA	NA	
ICBIDGAJ_02599	OG0001621	group_2539	1	0	0	fpr:FP2_13470	NA	NA	
ICBIDGAJ_02600	OG0001622	malQ_3	1	0	0	fpr:FP2_13480	ko:K00705	NA	
ICBIDGAJ_02601	OG0001623	alaS_2	1	0	0	fpr:FP2_13490	ko:K01872	NA	
ICBIDGAJ_02602	OG0001624	trmB	1	0	0	fpr:FP2_13500	ko:K03439	NA	
ICBIDGAJ_02603	OG0001625	group_906	3	3	5	fpa:FPR_10060	NA	NA	
ICBIDGAJ_02604	OG0000070	group_578	1	1	1	ova:OBV_p-00390	NA	NA	
ICBIDGAJ_02605	OG0000183	group_3072	1	1	1	NA	NA	NA	
ICBIDGAJ_02606	OG0000117	group_907	1	0	0	fpr:FP2_13530	NA	NA	
ICBIDGAJ_02607	OG0001626	bdhA	1	0	0	fpr:FP2_13560	ko:K07124	NA	
ICBIDGAJ_02608	OG0001627	group_1870	1	0	0	fpa:FPR_09850	NA	NA	
ICBIDGAJ_02609	OG0003993	group_4327	1	0	0	rix:RO1_16140;rim:ROI_30260	NA	specific_fp14	
ICBIDGAJ_02610	OG0003994	group_4328	1	0	0	NA	NA	specific_fp14	○
ICBIDGAJ_02611	OG0001628	group_909	1	1	1	fpa:FPR_09840	NA	NA	
ICBIDGAJ_02612	OG0001629	nrgA	6	6	11	erb:A4V01_11425	ko:K03320	NA	
ICBIDGAJ_02613	OG0001630	eriC	5	6	10	fpa:FPR_08910	NA	NA	
ICBIDGAJ_02614	OG0001631	thrS	1	0	0	fpr:FP2_13630	ko:K01868	NA	
ICBIDGAJ_02615	OG0002433	immR_9	3	4	6	rim:ROI_17680;rix:RO1_06130	NA	NA	
ICBIDGAJ_02616	OG0001632	trpS2	1	0	0	fpr:FP2_13660	ko:K01867	NA	
ICBIDGAJ_02619	OG0001633	pckA	1	0	0	fpr:FP2_13680	ko:K01610	NA	
ICBIDGAJ_02620	OG0000271	group_3074	2	2	3	ova:OBV_13610	NA	NA	
ICBIDGAJ_02621	OG0000046	yjmB_3	6	5	10	NA	NA	NA	
ICBIDGAJ_02622	OG0001924	opuE	6	7	12	ova:OBV_05240	ko:K11928	NA	
ICBIDGAJ_02623	OG0001767	ansA	1	0	0	fpr:FP2_32430	ko:K01424	NA	
ICBIDGAJ_02624	OG0001634	trxB_1	1	0	0	fpr:FP2_32410	ko:K00384	NA	
ICBIDGAJ_02625	OG0001635	group_3075	1	1	1	fpa:FPR_10550	NA	NA	
ICBIDGAJ_02626	OG0001636	group_1876	1	0	0	fpr:FP2_32380	NA	NA	
ICBIDGAJ_02627	OG0001637	yeiR	1	0	0	fpr:FP2_32370	NA	NA	
ICBIDGAJ_02628	OG0000000	group_47	1	0	0	fpa:FPR_24750	NA	NA	
ICBIDGAJ_02633	OG0001638	coaX_2	1	0	0	fpr:FP2_20540	ko:K03525	NA	
ICBIDGAJ_02634	OG0003152	group_3993	1	0	0	NA	NA	NA	
ICBIDGAJ_02636	OG0001639	mepA_14	6	7	12	fpr:FP2_20530	NA	NA	
ICBIDGAJ_02637	OG0002618	dkgB	1	0	0	rho:RHOM_14175	NA	NA	
ICBIDGAJ_02638	OG0001640	group_1880	2	2	3	fpa:FPR_08690	NA	NA	
ICBIDGAJ_02639	OG0000052	cstA_2	6	7	12	fpa:FPR_08700	NA	NA	
ICBIDGAJ_02640	OG0000052	cstA_3	6	7	12	fpr:FP2_20400	NA	NA	
ICBIDGAJ_02641	OG0001641	tfdR	1	0	0	fpa:FPR_08710	NA	NA	
ICBIDGAJ_02642	OG0000272	pspA	1	0	0	fpa:FPR_08730	ko:K15634	NA	
ICBIDGAJ_02643	OG0003153	group_3994	1	1	1	NA	NA	NA	
ICBIDGAJ_02644	OG0001642	mepA_15	6	7	12	fpa:FPR_08740	NA	NA	
ICBIDGAJ_02645	OG0002056	group_2541	1	0	0	NA	NA	NA	
ICBIDGAJ_02646	OG0001643	smc_2	1	0	0	fpa:FPR_08750	NA	NA	
ICBIDGAJ_02647	OG0001644	group_1883	1	0	0	fpr:FP2_20480	NA	NA	
ICBIDGAJ_02648	OG0001645	group_1884	1	0	0	fpr:FP2_20490	NA	NA	
ICBIDGAJ_02649	OG0001926	group_4330	1	1	1	NA	NA	NA	
ICBIDGAJ_02650	OG0002160	group_2196	1	1	1	fpa:FPR_08800	NA	NA	
ICBIDGAJ_02651	OG0001646	group_1885	1	0	0	fpr:FP2_20500	ko:K15986	NA	
ICBIDGAJ_02652	OG0002619	group_3998	1	0	0	NA	NA	NA	
ICBIDGAJ_02653	OG0001647	yeeO_4	5	5	9	fpa:FPR_08830	NA	NA	
ICBIDGAJ_02654	OG0001648	group_911	2	2	3	fpa:FPR_08840	NA	NA	
ICBIDGAJ_02655	OG0003154	group_3999	1	1	1	NA	NA	NA	
ICBIDGAJ_02656	OG0003155	group_4000	1	1	1	NA	NA	NA	
ICBIDGAJ_02657	OG0001649	gltX_2	1	0	0	fpa:FPR_08850	ko:K01885	NA	
ICBIDGAJ_02658	OG0001650	apeB	1	0	0	fpr:FP2_20360	ko:K01267	NA	
ICBIDGAJ_02659	OG0001771	malP_3	5	6	10	fpa:FPR_08870	ko:K02790;ko:K02791	NA	
ICBIDGAJ_02660	OG0001651	group_3080	1	1	1	fpa:FPR_08890	NA	NA	
ICBIDGAJ_02661	OG0001652	rsxB_3	1	0	0	fpr:FP2_20340	ko:K07138	NA	
ICBIDGAJ_02662	OG0001653	uppP	4	3	6	fpr:FP2_20330	ko:K06153	NA	
ICBIDGAJ_02663	OG0001654	trkA_2	1	0	0	fpa:FPR_08930	ko:K03499	NA	
ICBIDGAJ_02664	OG0001655	trkA_3	1	0	0	fpr:FP2_20310	ko:K03499	NA	
ICBIDGAJ_02665	OG0001656	group_4001	1	2	2	fpa:FPR_08950	NA	NA	
ICBIDGAJ_02666	OG0001657	group_2543	3	4	6	fpr:FP2_20290	NA	NA	
ICBIDGAJ_02667	OG0001658	gph_2	1	0	0	fpa:FPR_08970	ko:K01091	NA	
ICBIDGAJ_02668	OG0002161	group_3081	1	0	0	euu:ADJ67_01005	NA	NA	
ICBIDGAJ_02671	OG0001659	serS	1	0	0	fpr:FP2_20240	ko:K01875	NA	
ICBIDGAJ_02672	OG0001660	spo0C_6	1	0	0	fpa:FPR_08990	ko:K03497	NA	
ICBIDGAJ_02673	OG0001661	soj_6	1	0	0	ccel:CCDG5_2082	ko:K03496	NA	
ICBIDGAJ_02674	OG0001662	noc	1	0	0	fpr:FP2_20200	ko:K03497	NA	
ICBIDGAJ_02675	OG0001663	rsmG	1	0	0	fpr:FP2_20190	ko:K03501	NA	
ICBIDGAJ_02676	OG0001664	mnmG	1	0	0	fpr:FP2_20180	ko:K03495	NA	
ICBIDGAJ_02677	OG0001665	mnmE	1	0	0	fpa:FPR_09050	ko:K03650	NA	
ICBIDGAJ_02678	OG0001666	group_913	1	0	0	fpa:FPR_09070	ko:K06346	NA	
ICBIDGAJ_02679	OG0001667	yidC	2	2	3	fpr:FP2_20140	ko:K03217	NA	
ICBIDGAJ_02680	OG0001772	yidD	0	1	0	aos:AXE84_05030	ko:K08998	NA	
ICBIDGAJ_02681	OG0001668	rnpA	0	1	0	fpa:FPR_09100	ko:K03536	NA	
ICBIDGAJ_02682	OG0001669	rpmH	0	1	0	fpr:FP2_20110;fpa:FPR_09110	ko:K02914	NA	
BLCPAMOF_00001	OG0000276	dnaA	1	0	0	fpr:FP2_20100	ko:K02313	NA	
BLCPAMOF_00002	OG0000277	dnaN	1	0	0	ruk:A4V00_08915	ko:K02338	NA	
BLCPAMOF_00003	OG0000278	group_940	1	0	0	fpr:FP2_20080	ko:K14761	NA	
BLCPAMOF_00004	OG0000279	recF_1	1	0	0	fpr:FP2_20070	ko:K03629	NA	
BLCPAMOF_00005	OG0000280	group_942	1	0	0	fpr:FP2_20060	NA	NA	
BLCPAMOF_00006	OG0000281	gyrB_1	1	0	0	fpr:FP2_20050	ko:K02470	NA	
BLCPAMOF_00007	OG0000282	gyrA_1	1	0	0	fpr:FP2_20040	ko:K02469	NA	
BLCPAMOF_00008	OG0000283	mntP	3	3	5	fpr:FP2_20030	NA	NA	
BLCPAMOF_00009	OG0000284	rspR_1	1	0	0	fpr:FP2_20020	NA	NA	
BLCPAMOF_00010	OG0000285	group_945	1	0	0	cpy:Cphy_1041	ko:K06180	NA	
BLCPAMOF_00011	OG0000286	nudF	1	0	0	fpr:FP2_20000	ko:K01515	NA	
BLCPAMOF_00012	OG0000287	por_1	1	0	0	fpr:FP2_19990	ko:K03737	NA	
BLCPAMOF_00013	OG0000187	group_947	2	2	3	fpa:FPR_09260	ko:K06213	NA	
BLCPAMOF_00014	OG0000291	dapH	1	0	0	fpr:FP2_19970	NA	NA	
BLCPAMOF_00015	OG0002436	dacB_2	1	1	1	fpr:FP2_19960	ko:K07258	NA	
BLCPAMOF_00016	OG0000290	dacB_1	1	2	2	fpr:FP2_19950	ko:K07258	NA	
BLCPAMOF_00017	OG0000289	dnaX_1	1	0	0	fpr:FP2_19940	ko:K02341	NA	

BLCPAMOF_00018	OG0000288	group_680	3	4	6	fpr:FP2_19930	NA	NA	
BLCPAMOF_00019	OG0000292	birA_1	1	0	0	fpr:FP2_19920	ko:K03524	NA	
BLCPAMOF_00020	OG0000293	yfcE_1	1	0	0	geo:Geob_2907	ko:K07095	NA	
BLCPAMOF_00021	OG0000294	rsmI	1	0	0	fpr:FP2_19900	ko:K07056	NA	
BLCPAMOF_00022	OG0000295	yfiC	1	0	0	fpr:FP2_19890	NA	NA	
BLCPAMOF_00023	OG0000296	group_1954	0	1	0	fpr:FP2_19880	NA	NA	
BLCPAMOF_00024	OG0000297	group_952	1	0	0	fpr:FP2_19870	NA	NA	
BLCPAMOF_00025	OG0000298	swrC	6	7	12	fpr:FP2_19860	NA	NA	
BLCPAMOF_00026	OG0000299	mro	1	0	0	fpr:FP2_19850	ko:K01785	NA	
BLCPAMOF_00027	OG0000300	lnpD	1	0	0	fpr:FP2_19840	ko:K01784	NA	
BLCPAMOF_00028	OG0000301	feoB_1	6	5	10	fpr:FP2_19830	ko:K04759	NA	
BLCPAMOF_00029	OG0000302	group_4906	1	0	0	fpr:FP2_19820	NA	NA	
BLCPAMOF_00030	OG0000303	group_957	4	5	8	fpa:FPR_09430	ko:K07090	NA	
BLCPAMOF_00031	OG0004018	group_4907	1	1	1	fpr:FP2_19810	NA	specific_fp360	
BLCPAMOF_00032	OG0000304	tig_1	1	0	0	fpr:FP2_19800	ko:K03545	NA	
BLCPAMOF_00033	OG0000305	sdhB	1	0	0	fpr:FP2_19790	ko:K01752	NA	
BLCPAMOF_00034	OG0000306	sdhA	1	0	0	fpla:A4U99_02185	ko:K01752	NA	
BLCPAMOF_00036	OG0000058	group_359	1	0	0	fpr:FP2_14030	NA	NA	
BLCPAMOF_00037	OG0002947	group_459	0	1	0	fpa:FPR_10350	NA	NA	
BLCPAMOF_00038	OG0003543	group_3256	1	0	0	fpa:FPR_10340	ko:K06919	NA	
BLCPAMOF_00039	OG0003544	group_4908	1	0	0	fpa:FPR_10330	NA	specific_fp360	
BLCPAMOF_00040	OG0003545	group_3258	0	1	0	NA	NA	specific_fp360	
BLCPAMOF_00041	OG0002227	group_1978	1	0	0	fpa:FPR_10320	NA	NA	
BLCPAMOF_00042	OG0002228	group_1980	1	0	0	fpa:FPR_10310	NA	NA	
BLCPAMOF_00043	OG0001676	yvoA	1	0	0	fpr:FP2_19700	ko:K03710	NA	
BLCPAMOF_00044	OG0001879	sorF	1	0	0	fpr:FP2_19690	ko:K19506	NA	
BLCPAMOF_00045	OG0001880	sorB	1	0	0	fpr:FP2_19680	ko:K02794	NA	
BLCPAMOF_00046	OG0001677	sorA	4	4	7	fpr:FP2_19670	ko:K02795	NA	
BLCPAMOF_00047	OG0001881	manZ_1	3	2	4	fpr:FP2_19660	ko:K02796	NA	
BLCPAMOF_00048	OG0001882	frlB	1	0	0	fpr:FP2_19650	NA	NA	
BLCPAMOF_00049	OG0001678	group_3603	1	0	0	fpr:FP2_19640	NA	NA	
BLCPAMOF_00050	OG0000120	group_3605	3	3	5	fpr:FP2_19630	NA	NA	
BLCPAMOF_00051	OG0000014	group_139	0	1	0	fpa:FPR_09610	NA	NA	
BLCPAMOF_00052	OG0000055	group_1	1	0	0	fpr:FP2_27630	NA	NA	
BLCPAMOF_00053	OG0001796	srpC_2	3	3	5	fpa:FPR_03310	ko:K07240	NA	
BLCPAMOF_00054	OG0001795	srpC_1	2	3	4	fpa:FPR_03300	ko:K07240	NA	
BLCPAMOF_00055	OG0001794	group_2321	1	0	0	fpa:FPR_03290	ko:K06871	NA	
BLCPAMOF_00056	OG0001793	araR	1	0	0	fpr:FP2_17560	ko:K02103	NA	
BLCPAMOF_00057	OG0001792	betC	1	0	0	fpr:FP2_17570	NA	NA	
BLCPAMOF_00058	OG0001791	group_2769	5	5	9	fpr:FP2_17580	ko:K07793	NA	
BLCPAMOF_00059	OG0001790	group_1961	3	3	5	lacy:A4V08_20790	NA	NA	
BLCPAMOF_00060	OG0001789	group_3610	1	0	0	fpa:FPR_03230	NA	NA	
BLCPAMOF_00061	OG0000065	group_181	1	0	0	fpa:FPR_03220	NA	NA	
BLCPAMOF_00062	OG0000018	group_171	1	0	0	fpr:FP2_29840	NA	NA	
BLCPAMOF_00063	OG0002059	group_915	1	0	0	fpa:FPR_03190	NA	NA	
BLCPAMOF_00064	OG0000000	group_37	0	1	0	fpr:FP2_29810	NA	NA	
BLCPAMOF_00065	OG0001855	group_322	1	0	0	fpa:FPR_09480	NA	NA	
BLCPAMOF_00066	OG0004019	group_4910	3	2	4	NA	NA	specific_fp360	○
BLCPAMOF_00067	OG0004020	group_4911	1	0	0	NA	NA	specific_fp360	○
BLCPAMOF_00068	OG0003202	group_3260	1	1	1	fpr:FP2_27720	NA	NA	
BLCPAMOF_00069	OG0004021	group_4912	1	0	0	fpr:FP2_27730	NA	specific_fp360	
BLCPAMOF_00070	OG0003203	group_3261	1	0	0	NA	NA	NA	
BLCPAMOF_00071	OG0000014	group_144	0	1	0	fpa:FPR_09610	NA	NA	
BLCPAMOF_00072	OG0002101	group_2772	1	0	0	rix:RO1_41590	NA	NA	
BLCPAMOF_00073	OG0001873	group_4913	2	1	2	fpr:FP2_27990	NA	NA	
BLCPAMOF_00074	OG0000309	group_4914	1	0	0	fpr:FP2_28010	NA	NA	
BLCPAMOF_00075	OG0000310	ilvK	1	0	0	fpr:FP2_28020	ko:K00826	NA	
BLCPAMOF_00076	OG0000311	xynZ	1	0	0	fpr:FP2_28030	NA	NA	
BLCPAMOF_00077	OG0000312	group_969	1	0	0	fpr:FP2_28040	NA	NA	
BLCPAMOF_00078	OG0000313	purD_1	1	0	0	fpr:FP2_28050	NA	NA	
BLCPAMOF_00079	OG0004022	group_4915	1	1	1	fpr:FP2_28060	NA	specific_fp360	
BLCPAMOF_00080	OG0000314	group_971	1	0	0	fpr:FP2_28070	NA	NA	
BLCPAMOF_00081	OG0000315	bar	1	0	0	fpr:FP2_28080	ko:K07461	NA	
BLCPAMOF_00082	OG0000316	argG_1	1	0	0	fpr:FP2_28090	ko:K01940	NA	
BLCPAMOF_00083	OG0000317	argH	1	0	0	fpr:FP2_28110	ko:K01755	NA	
BLCPAMOF_00084	OG0000318	argC	1	0	0	fpr:FP2_28120	ko:K00145	NA	
BLCPAMOF_00085	OG0000319	argJ	1	0	0	fpr:FP2_28130	ko:K00620	NA	
BLCPAMOF_00086	OG0000320	argB	1	0	0	fpr:FP2_28140	ko:K00930	NA	
BLCPAMOF_00087	OG0000321	argD	1	0	0	fpr:FP2_28160	ko:K00821	NA	
BLCPAMOF_00088	OG0000322	argF_1	1	0	0	fpr:FP2_28170	ko:K00611	NA	
BLCPAMOF_00089	OG0001934	group_3148	1	0	0	fpa:FPR_00890	NA	NA	
BLCPAMOF_00090	OG0004023	group_4916	1	0	0	NA	NA	specific_fp360	
BLCPAMOF_00091	OG0002384	group_4917	1	0	0	era:ERE_10780	NA	NA	
BLCPAMOF_00092	OG0003192	group_3262	1	0	0	fpa:FPR_08010	NA	NA	
BLCPAMOF_00093	OG0002307	group_4918	0	1	0	rob:CK5_05450	NA	NA	
BLCPAMOF_00094	OG0000105	group_4919	0	1	0	rob:CK5_05460	NA	NA	
BLCPAMOF_00095	OG0000249	upp_1	1	0	0	NA	NA	NA	
BLCPAMOF_00096	OG0003546	group_4921	1	0	0	cst:CLOST_0499	ko:K07023	NA	
BLCPAMOF_00097	OG0003547	group_4922	1	0	0	rho:RHOM_01750	NA	NA	
BLCPAMOF_00098	OG0000030	group_4923	1	0	0	fpa:FPR_08380	NA	NA	
BLCPAMOF_00099	OG0003548	group_4924	1	0	0	rob:CK5_05610	NA	NA	
BLCPAMOF_00100	OG0001915	group_96	1	0	0	fpr:FP2_27160	NA	NA	
BLCPAMOF_00101	OG0000010	group_186	1	0	0	fpa:FPR_18840	NA	NA	
BLCPAMOF_00102	OG0000047	group_4925	4	4	7	ppm:PPSC2_19590;ppo:PPM_3924	NA	NA	
BLCPAMOF_00103	OG0004024	group_4926	1	0	0	NA	NA	specific_fp360	○
BLCPAMOF_00104	OG0004025	group_4927	1	1	1	NA	NA	specific_fp360	○
BLCPAMOF_00105	OG0001991	group_4928	1	0	0	ppq:PPSQR21_039530	ko:K06871	NA	
BLCPAMOF_00106	OG0004026	group_4929	0	1	0	rum:CK1_30440	NA	specific_fp360	
BLCPAMOF_00107	OG0001067	natR_1	0	1	0	NA	NA	NA	
BLCPAMOF_00108	OG0001066	group_4931	3	4	6	NA	NA	NA	
BLCPAMOF_00109	OG0004027	agrB_1	2	3	4	NA	NA	specific_fp360	
BLCPAMOF_00110	OG0004028	group_4933	1	0	0	NA	NA	specific_fp360	○
BLCPAMOF_00111	OG0004029	group_4934	1	0	0	NA	NA	specific_fp360	○
BLCPAMOF_00112	OG0002423	group_4935	1	0	0	cls:CXIVA_10280	NA	NA	
BLCPAMOF_00113	OG0000266	group_2186	1	0	0	fpa:FPR_18720	NA	NA	
BLCPAMOF_00114	OG0001870	group_293	1	0	0	fpa:FPR_18710	NA	NA	
BLCPAMOF_00115	OG0000184	group_2647	1	0	0	fpa:FPR_18700	NA	NA	
BLCPAMOF_00116	OG0002351	group_2324	1	0	0	fpa:FPR_18680	NA	NA	
BLCPAMOF_00117	OG0000273	group_2234	1	0	0	fpa:FPR_18670	NA	NA	
BLCPAMOF_00118	OG0002623	group_1904	1	0	0	eac:EAL2_c06560	NA	NA	
BLCPAMOF_00119	OG0002408	group_1903	0	1	0	fpa:FPR_18980	NA	NA	
BLCPAMOF_00120	OG0003204	group_3263	1	0	0	NA	NA	NA	
BLCPAMOF_00121	OG0003205	hyuC	1	0	0	NA	NA	NA	
BLCPAMOF_00122	OG0003206	triA	1	0	0	bco:Bcell_0730	ko:K12960	NA	
BLCPAMOF_00123	OG0003207	allB	1	0	0	NA	NA	NA	
BLCPAMOF_00124	OG0002644	group_4939	1	0	0	NA	NA	NA	
BLCPAMOF_00125	OG0002180	bacC	1	0	0	cyc:PCC7424_5536	NA	NA	
BLCPAMOF_00126	OG0003208	steT	6	7	12	efu:HMPREF0351_12788	ko:K19540	NA	
BLCPAMOF_00127	OG0003209	yabJ	1	0	0	cld:CLSPO_c30720	ko:K09022	NA	
BLCPAMOF_00128	OG0003210	group_1905	1	0	0	NA	NA	NA	
BLCPAMOF_00129	OG0002408	group_1901	0	1	0	fpa:FPR_18980	NA	NA	
BLCPAMOF_00130	OG0002622	group_3087	1	0	0	sri:SELR_pSRC600280	NA	NA	
BLCPAMOF_00131	OG0002621	group_2550	0	1	0	NA	NA	NA	
BLCPAMOF_00132	OG0000148	group_3266	1	0	0	ccl:Clocl_2850	NA	NA	

BLCPAMOF_00133	OG0000122	group_409	1	0	0	fpr:FP2_28180	NA	NA	
BLCPAMOF_00134	OG0000149	group_513	1	0	0	fpr:FP2_28190	ko:K09768	NA	
BLCPAMOF_00135	OG0002620	group_2546	1	0	0	NA	NA	NA	
BLCPAMOF_00136	OG0000273	group_2545	1	0	0	ibu:IB211_01075c	NA	NA	
BLCPAMOF_00137	OG0001934	group_3147	1	0	0	fpa:FPR_00890	NA	NA	
BLCPAMOF_00138	OG0000008	group_124	1	0	0	fpr:FP2_28240	NA	NA	
BLCPAMOF_00139	OG0000004	soj_1	1	0	0	fpa:FPR_07940	ko:K03496	NA	
BLCPAMOF_00140	OG0000002	spo0C_2	1	0	0	fpa:FPR_00840	ko:K03497	NA	
BLCPAMOF_00141	OG0001933	group_4425	1	0	0	fpr:FP2_09040	NA	NA	
BLCPAMOF_00142	OG0000039	group_306	1	0	0	fpa:FPR_00810	NA	NA	
BLCPAMOF_00143	OG0000017	group_428	1	0	0	fpa:FPR_00800	NA	NA	
BLCPAMOF_00144	OG0000001	group_60	1	1	1	fpr:FP2_21800	ko:K03205	NA	
BLCPAMOF_00145	OG0000006	group_7116	1	2	2	ova:OBV_30190	NA	NA	
BLCPAMOF_00146	OG0001673	fic_1	1	0	0	fpa:FPR_01760	NA	NA	
BLCPAMOF_00147	OG0000011	group_7183	3	3	5	fpr:FP2_22330	NA	NA	
BLCPAMOF_00148	OG0000016	group_367	1	2	2	cso:CLS_04930	NA	NA	
BLCPAMOF_00149	OG0001843	group_203	1	0	0	fpr:FP2_22350	NA	NA	
BLCPAMOF_00150	OG0000067	group_3932	1	0	0	sequ:Q426_01745;sezo:SeseC_01909	ko:K00986	NA	
BLCPAMOF_00151	OG0001918	group_198	1	0	0	fpr:FP2_22350	NA	NA	
BLCPAMOF_00152	OG0000012	iap_1	1	1	1	fpa:FPR_16900	NA	NA	
BLCPAMOF_00153	OG0002518	ltrA_2	1	0	0	erb:A4V01_21510	NA	NA	
BLCPAMOF_00154	OG0000013	group_339	1	0	0	fpr:FP2_22380	NA	NA	
BLCPAMOF_00155	OG0000007	mapZ	1	2	2	fpr:FP2_22390	NA	NA	
BLCPAMOF_00156	OG0000003	group_119	1	0	0	fpr:FP2_00540	ko:K03169	NA	
BLCPAMOF_00157	OG0000019	group_374	1	0	0	fpa:FPR_04590	NA	NA	
BLCPAMOF_00158	OG0000022	group_344	1	0	0	fpr:FP2_21680	NA	NA	
BLCPAMOF_00159	OG0000020	group_7181	1	0	0	fpa:FPR_04570	NA	NA	
BLCPAMOF_00160	OG0002948	flr_2	1	0	0	rob:CK5_11400	NA	NA	
BLCPAMOF_00161	OG0000139	ytcD	1	0	0	rob:CK5_11410	NA	NA	
BLCPAMOF_00162	OG0001382	arsC	1	0	0	eel:EUBELI_20104	ko:K03741	NA	
BLCPAMOF_00163	OG0000181	group_494	1	0	0	fpa:FPR_19000	NA	NA	
BLCPAMOF_00164	OG0000005	group_88	1	0	0	fpr:FP2_27160	NA	NA	
BLCPAMOF_00165	OG0000023	group_267	1	0	0	fpa:FPR_18860	NA	NA	
BLCPAMOF_00166	OG0000038	group_435	2	2	3	fpr:FP2_08920	NA	NA	
BLCPAMOF_00167	OG0000264	group_1674	0	1	0	NA	NA	NA	
BLCPAMOF_00168	OG0000010	group_193	1	0	0	fpa:FPR_04440	NA	NA	
BLCPAMOF_00169	OG0000098	immR_2	1	0	0	NA	NA	NA	
BLCPAMOF_00170	OG0000099	group_655	1	0	0	NA	NA	NA	
BLCPAMOF_00171	OG0001538	group_7215	0	1	0	NA	NA	NA	
BLCPAMOF_00172	OG0001539	group_7115	1	0	0	csh:Closa_0107	NA	NA	
BLCPAMOF_00173	OG0001540	group_7119	1	0	0	csh:Closa_0106	NA	NA	
BLCPAMOF_00174	OG0001541	group_7127	1	0	0	csh:Closa_0105	NA	NA	
BLCPAMOF_00175	OG0001542	group_3064	1	0	0	csh:Closa_0104	NA	NA	
BLCPAMOF_00176	OG0001543	group_3065	2	3	4	csh:Closa_0103	NA	NA	
BLCPAMOF_00177	OG0001544	group_7180	2	3	4	csh:Closa_0102	NA	NA	
BLCPAMOF_00178	OG0001545	sugC_1	1	0	0	csh:Closa_0101	ko:K10112	NA	
BLCPAMOF_00179	OG0001546	group_2530	2	3	4	csh:Closa_0100	NA	NA	
BLCPAMOF_00180	OG0001547	group_7128	2	3	4	csh:Closa_0099	NA	NA	
BLCPAMOF_00181	OG0001548	group_7204	1	0	0	csh:Closa_0098	NA	NA	
BLCPAMOF_00182	OG0001549	ycjP_1	3	4	6	csh:Closa_0097	ko:K17320	NA	
BLCPAMOF_00183	OG0001550	yteP_1	4	4	7	csh:Closa_0096	ko:K17319	NA	
BLCPAMOF_00184	OG0001551	group_7186	5	6	10	cle:Clole_2247	NA	NA	
BLCPAMOF_00185	OG0000265	kdgR	1	0	0	csh:Closa_0094	NA	NA	
BLCPAMOF_00186	OG0001552	pfp_1	1	0	0	fpr:FP2_05410	ko:K21071	NA	
BLCPAMOF_00187	OG0001553	group_7107	0	1	0	NA	NA	NA	
BLCPAMOF_00188	OG0001554	spo0C_1	1	0	0	fpr:FP2_21840	ko:K03497	NA	
BLCPAMOF_00189	OG0001555	group_7106	1	0	0	fpla:A4U99_07135	NA	NA	
BLCPAMOF_00190	OG0001556	group_7114	1	0	0	fpa:FPR_18730	NA	NA	
BLCPAMOF_00191	OG0000266	group_2185	0	1	0	fpa:FPR_18720	NA	NA	
BLCPAMOF_00192	OG0001870	group_4424	1	0	0	bprm:CL3_18290	NA	NA	
BLCPAMOF_00193	OG0000184	group_4423	1	0	0	cso:CLS_04470	NA	NA	
BLCPAMOF_00194	OG0001747	mazF_1	1	0	0	fpa:FPR_07200	ko:K07171	NA	
BLCPAMOF_00195	OG0002351	group_2323	1	0	0	fpa:FPR_18680	NA	NA	
BLCPAMOF_00196	OG0000273	group_2233	1	0	0	fpa:FPR_18670	NA	NA	
BLCPAMOF_00198	OG0000323	mepA_1	6	6	11	fpr:FP2_32550	NA	NA	
BLCPAMOF_00199	OG0004030	group_4949	1	0	0	NA	NA	specific_fp360	○
BLCPAMOF_00200	OG0002477	group_4950	2	3	4	rho:RHOM_05905	NA	NA	
BLCPAMOF_00201	OG0002478	group_4951	3	3	5	rho:RHOM_05900	NA	NA	
BLCPAMOF_00202	OG0002949	group_4952	1	0	0	hyl:LPB072_01260	NA	specific_fp360	○
BLCPAMOF_00203	OG0004031	group_4953	3	3	5	NA	NA	specific_fp360	○
BLCPAMOF_00204	OG0003549	group_4954	6	7	12	hyl:LPB072_01270	ko:K07793	specific_fp360	
BLCPAMOF_00205	OG0000324	group_979	1	0	0	fpr:FP2_32530	NA	NA	
BLCPAMOF_00206	OG0000325	mleN	7	7	13	fpa:FPR_17600	NA	NA	
BLCPAMOF_00207	OG0000326	flK	1	0	0	fpr:FP2_32500	NA	NA	
BLCPAMOF_00208	OG0003550	group_4955	4	4	7	fpr:FP2_32490	NA	NA	
BLCPAMOF_00209	OG0000327	ziaR	1	0	0	fpr:FP2_32480	NA	NA	
BLCPAMOF_00210	OG0000328	group_983	0	1	0	fpr:FP2_32470	NA	NA	
BLCPAMOF_00211	OG0000329	cadA	3	4	6	fpa:FPR_17650	ko:K01534	NA	
BLCPAMOF_00212	OG0002519	ygaZ_2	2	3	4	olo:ADJ70_11575	NA	NA	
BLCPAMOF_00213	OG0002520	group_2650	2	2	3	cls:CXIVA_18760	NA	NA	
BLCPAMOF_00214	OG0001767	ansA	1	0	0	fpr:FP2_32430	ko:K01424	NA	
BLCPAMOF_00215	OG0001634	trxB_1	1	0	0	fpr:FP2_32410	ko:K00384	NA	
BLCPAMOF_00216	OG0001935	vfr	1	0	0	fpr:FP2_32400	ko:K01420	NA	
BLCPAMOF_00217	OG0001635	group_4956	1	1	1	fpr:FP2_32390	NA	NA	
BLCPAMOF_00218	OG0001636	group_1876	1	0	0	fpr:FP2_32380	NA	NA	
BLCPAMOF_00219	OG0001637	yeiR	1	0	0	fpr:FP2_32370	NA	NA	
BLCPAMOF_00220	OG0000330	ypdF	1	0	0	fpr:FP2_32360	ko:K01262	NA	
BLCPAMOF_00221	OG0000331	epsJ_1	1	0	0	fpr:FP2_32350	NA	NA	
BLCPAMOF_00222	OG0000332	group_986	1	0	0	fpr:FP2_32340	NA	NA	
BLCPAMOF_00223	OG0000188	group_4957	1	0	0	fpr:FP2_32330	NA	NA	
BLCPAMOF_00224	OG0000333	group_686	1	0	0	fpr:FP2_32320	ko:K07001	NA	
BLCPAMOF_00225	OG0000334	ptsI_1	1	0	0	fpr:FP2_32310	ko:K08483	NA	
BLCPAMOF_00226	OG0000335	rsmE	1	0	0	fpr:FP2_32280	ko:K09761	NA	
BLCPAMOF_00227	OG0000336	prmA	1	0	0	fpr:FP2_32270	ko:K02687	NA	
BLCPAMOF_00228	OG0003551	group_4958	1	1	1	fpr:FP2_32260	ko:K02803;ko:K02804	NA	
BLCPAMOF_00229	OG0000337	group_687	1	0	0	fpr:FP2_32250	NA	NA	
BLCPAMOF_00230	OG0000338	pstS1_1	1	0	0	fpr:FP2_32240	ko:K02040	NA	
BLCPAMOF_00231	OG0000339	pstC	3	4	6	fpr:FP2_32230	ko:K02037	NA	
BLCPAMOF_00232	OG0000340	pstA	3	4	6	fpr:FP2_32220	ko:K02038	NA	
BLCPAMOF_00233	OG0000341	pstB3	1	0	0	fpr:FP2_32210	ko:K02036	NA	
BLCPAMOF_00234	OG0000342	phoU	1	0	0	fpr:FP2_32200	ko:K02039	NA	
BLCPAMOF_00235	OG0002339	group_4959	1	1	1	NA	NA	NA	
BLCPAMOF_00236	OG0000343	btr_1	1	0	0	fpr:FP2_32190	NA	NA	
BLCPAMOF_00237	OG0000344	group_995	1	0	0	fpr:FP2_32180	NA	NA	
BLCPAMOF_00238	OG0001885	group_1964	1	0	0	fpr:FP2_32170	ko:K19802	NA	
BLCPAMOF_00239	OG0000345	sstT	4	5	8	fpr:FP2_32160	ko:K07862	NA	
BLCPAMOF_00240	OG0000346	group_691	3	3	5	fpr:FP2_32140	NA	NA	
BLCPAMOF_00241	OG0000347	tkt	1	0	0	fpr:FP2_32130	ko:K00615	NA	
BLCPAMOF_00242	OG0000348	dxs_1	1	1	1	fpr:FP2_32120	ko:K00615	NA	
BLCPAMOF_00243	OG0002950	gcvA	1	0	0	fpr:FP2_32090	NA	NA	
BLCPAMOF_00244	OG0002521	ksdD	1	0	0	cbac:JI75_00605	NA	NA	
BLCPAMOF_00245	OG0000446	group_1069	1	0	0	fpr:FP2_32070	ko:K03671	NA	
BLCPAMOF_00246	OG0000447	hisG	1	0	0	fpa:FPR_17570	NA	NA	
BLCPAMOF_00247	OG0000448	hisD	1	0	0	fpa:FPR_17560	ko:K00013	NA	

BLCPAMOF_00248	OG0000449	hisC	1	0	0	fpa:FPR_17550	ko:K00817	NA	
BLCPAMOF_00249	OG0000450	hisB	1	0	0	fpa:FPR_17540	ko:K01693	NA	
BLCPAMOF_00250	OG0000451	hisH	1	0	0	fpa:FPR_17530	ko:K02501	NA	
BLCPAMOF_00251	OG0000452	hisA	1	0	0	fpa:FPR_17520	ko:K01814	NA	
BLCPAMOF_00252	OG0000453	hisF	1	0	0	fpa:FPR_17510	ko:K02500	NA	
BLCPAMOF_00253	OG0000454	hisI	1	0	0	fpr:FP2_32060	ko:K11755	NA	
BLCPAMOF_00254	OG0000455	hisK	1	0	0	fpr:FP2_32050	ko:K04486	NA	
BLCPAMOF_00255	OG0000456	mepA_3	5	6	10	fpr:FP2_32040	NA	NA	
BLCPAMOF_00256	OG0000457	pyrE_1	1	0	0	fpr:FP2_32010	ko:K00762	NA	
BLCPAMOF_00257	OG0000124	group_2280	1	0	0	fpr:FP2_32000	NA	NA	
BLCPAMOF_00258	OG0000458	group_4961	1	0	0	fpr:FP2_31990	NA	NA	
BLCPAMOF_00259	OG0000459	immR_3	1	0	0	fpr:FP2_31980	NA	NA	
BLCPAMOF_00260	OG0000460	cobC	1	0	0	fpr:FP2_31970	ko:K02226	NA	
BLCPAMOF_00261	OG0000461	group_1081	1	2	2	fpr:FP2_31960	NA	NA	
BLCPAMOF_00262	OG0000462	group_4962	1	1	1	fpr:FP2_31950	NA	NA	
BLCPAMOF_00263	OG0000463	group_4963	1	1	1	fpr:FP2_31940	NA	NA	
BLCPAMOF_00265	OG0000025	group_317	1	0	0	fpr:FP2_13920	NA	NA	
BLCPAMOF_00266	OG0000026	group_327	0	1	0	fpa:FPR_09490	NA	NA	
BLCPAMOF_00267	OG0002412	group_2204	1	0	0	elm:ELI_1142	ko:K06919	NA	
BLCPAMOF_00268	OG0002413	group_2551	1	0	0	fpa:FPR_23820	NA	NA	
BLCPAMOF_00269	OG0002353	group_2348	1	0	0	fpr:FP2_18320	ko:K03427	NA	
BLCPAMOF_00270	OG0002111	group_4964	1	0	0	pste:PSTEL_07960	ko:K01154	NA	
BLCPAMOF_00271	OG0000465	group_2802	1	0	0	med:MELS_0988	NA	NA	
BLCPAMOF_00272	OG0004032	group_4965	1	0	0	NA	NA	specific_fp360	○
BLCPAMOF_00273	OG0004033	group_4966	1	0	0	NA	NA	specific_fp360	
BLCPAMOF_00274	OG0002354	hsdR_1	1	0	0	fpr:FP2_18260	ko:K01153	NA	
BLCPAMOF_00275	OG0002566	group_2803	1	0	0	med:MELS_0834	NA	NA	
BLCPAMOF_00276	OG0004034	group_4967	0	1	0	NA	NA	specific_fp360	○
BLCPAMOF_00277	OG0002340	bcrC_1	3	2	4	fpr:FP2_21870	ko:K19302	NA	
BLCPAMOF_00278	OG0003552	cckA_1	2	1	2	NA	NA	specific_fp360	
BLCPAMOF_00279	OG0004035	group_4969	1	1	1	NA	NA	specific_fp360	○
BLCPAMOF_00280	OG0003549	group_4970	7	6	12	sbr:SY1_17620	ko:K07793	specific_fp360	○
BLCPAMOF_00281	OG0004036	group_4971	3	3	5	NA	NA	specific_fp360	○
BLCPAMOF_00282	OG0002949	group_819	1	0	0	gfe:Gferi_08420	NA	specific_fp360	○
BLCPAMOF_00283	OG0003553	phoP_1	1	0	0	pta:HPL003_27855	NA	specific_fp360	
BLCPAMOF_00284	OG0000104	group_2218	1	0	0	fpa:FPR_28480	NA	NA	
BLCPAMOF_00285	OG0000118	group_2212	1	0	0	fpa:FPR_28490	NA	NA	
BLCPAMOF_00286	OG0001670	group_2211	0	1	0	fpa:FPR_28500	NA	NA	
BLCPAMOF_00287	OG0003211	group_360	1	0	0	fpa:FPR_10360	NA	NA	
BLCPAMOF_00288	OG0002947	group_458	0	1	0	fpa:FPR_10350	NA	NA	
BLCPAMOF_00289	OG0003543	group_3257	1	0	0	fpa:FPR_10340	ko:K06919	specific_fp360	
BLCPAMOF_00290	OG0003544	group_4909	1	0	0	fpa:FPR_10330	NA	specific_fp360	
BLCPAMOF_00291	OG0003545	group_3259	0	1	0	NA	NA	specific_fp360	
BLCPAMOF_00292	OG0002227	group_1979	1	0	0	fpa:FPR_10320	NA	NA	
BLCPAMOF_00293	OG0002228	group_1981	1	0	0	fpa:FPR_10310	NA	NA	
BLCPAMOF_00294	OG0000135	regX3_3	1	0	0	fpr:FP2_27590	NA	NA	
BLCPAMOF_00295	OG0000063	resE_2	1	2	2	fpr:FP2_27600	NA	NA	
BLCPAMOF_00296	OG0000047	lolD	1	0	0	fpr:FP2_27610	ko:K02003	NA	
BLCPAMOF_00297	OG0002306	macB_1	4	5	8	fpr:FP2_27620	ko:K02004	NA	
BLCPAMOF_00298	OG0000014	group_148	0	1	0	fpa:FPR_09610	NA	NA	
BLCPAMOF_00299	OG0002951	group_2652	1	0	0	NA	NA	NA	
BLCPAMOF_00300	OG0000014	group_147	1	0	0	fpr:FP2_08720	NA	NA	
BLCPAMOF_00301	OG0002404	group_2149	0	1	0	fpr:FP2_31490	NA	NA	
BLCPAMOF_00302	OG0000269	gltC_1	1	0	0	fpr:FP2_31480	NA	NA	
BLCPAMOF_00303	OG0001606	group_4973	1	0	0	fpr:FP2_31470	NA	NA	
BLCPAMOF_00304	OG0004037	group_4974	1	1	1	fpr:FP2_31460	NA	specific_fp360	
BLCPAMOF_00305	OG0000227	group_4975	1	1	1	rum:CK1_26420	ko:K03100	NA	
BLCPAMOF_00306	OG0002585	group_4976	1	1	1	fpr:FP2_31440	NA	NA	
BLCPAMOF_00307	OG0003212	group_4977	1	1	1	fpr:FP2_31430	ko:K08600	specific_fp360	
BLCPAMOF_00308	OG0002522	group_4978	1	2	2	fpr:FP2_31420	NA	NA	
BLCPAMOF_00309	OG0002046	group_4979	1	0	0	fpr:FP2_31410	ko:K07284	NA	
BLCPAMOF_00310	OG0004038	group_4980	1	1	1	NA	NA	specific_fp360	○
BLCPAMOF_00311	OG0001574	phoR_1	1	1	1	fpr:FP2_31400	NA	NA	
BLCPAMOF_00312	OG0001575	srrA_1	1	0	0	fpr:FP2_31390	ko:K07775	NA	
BLCPAMOF_00313	OG0001576	group_2653	2	1	2	fpr:FP2_31380	NA	NA	
BLCPAMOF_00314	OG0001577	group_1836	1	0	0	fpr:FP2_31370	NA	NA	
BLCPAMOF_00315	OG0001578	group_1837	1	0	0	fpr:FP2_31360	ko:K06997	NA	
BLCPAMOF_00316	OG0001579	group_1838	3	3	5	fpr:FP2_31350	ko:K06147	NA	
BLCPAMOF_00317	OG0001580	glcK_2	1	0	0	fpr:FP2_31340	ko:K00845	NA	
BLCPAMOF_00318	OG0001581	tatC	3	4	6	ova:OBV_43450	ko:K03118	NA	
BLCPAMOF_00319	OG0001582	tatAy	1	0	0	fpr:FP2_31320	ko:K03116	NA	
BLCPAMOF_00320	OG0001583	tatB	1	1	1	fpr:FP2_31310	ko:K03117	NA	
BLCPAMOF_00321	OG0001584	group_1843	1	0	0	fpr:FP2_31300	NA	NA	
BLCPAMOF_00322	OG0001585	yraA	1	0	0	fpr:FP2_31290	ko:K03152	NA	
BLCPAMOF_00323	OG0001586	group_1844	1	0	0	fpr:FP2_31280	NA	NA	
BLCPAMOF_00324	OG0001587	group_1845	1	0	0	fpr:FP2_31270	NA	NA	
BLCPAMOF_00325	OG0002054	group_2537	1	1	1	fpr:FP2_31260	NA	NA	
BLCPAMOF_00326	OG0001588	xlnA	1	0	0	fpr:FP2_31250	NA	NA	
BLCPAMOF_00327	OG0001589	mutX	1	0	0	fpr:FP2_31240	ko:K03574	NA	
BLCPAMOF_00328	OG0001810	group_4981	1	0	0	ruk:A4V00_17495	ko:K04095	NA	
BLCPAMOF_00329	OG0003527	group_4982	0	1	0	NA	NA	NA	
BLCPAMOF_00330	OG0001590	group_1848	4	5	8	fpr:FP2_31230	ko:K07035	NA	
BLCPAMOF_00331	OG0001591	group_4983	1	1	1	fpr:FP2_31220	NA	NA	
BLCPAMOF_00332	OG0002406	group_4984	1	0	0	fpr:FP2_31210	NA	NA	
BLCPAMOF_00333	OG0001187	group_4985	3	3	5	fpr:FP2_31200	ko:K07240	NA	
BLCPAMOF_00334	OG0001188	chrA1	3	3	5	fpr:FP2_31190	ko:K07240	NA	
BLCPAMOF_00335	OG0001479	gltC_2	1	0	0	fpr:FP2_31180	ko:K01104	NA	
BLCPAMOF_00336	OG0001478	rny	1	1	1	fpr:FP2_31170	ko:K18682	NA	
BLCPAMOF_00337	OG0004039	group_4987	1	1	1	fpr:FP2_31150	ko:K06956	specific_fp360	
BLCPAMOF_00338	OG0002050	dppE_1	1	1	1	fpr:FP2_31140	ko:K15580	NA	
BLCPAMOF_00339	OG0002049	oppB_1	3	4	6	bhu:bhn_l2685	ko:K15581	NA	
BLCPAMOF_00340	OG0002048	oppC_1	3	4	6	fpr:FP2_31120	ko:K15582	NA	
BLCPAMOF_00341	OG0000033	oppD_1	1	0	0	fpr:FP2_31110	ko:K15583	NA	
BLCPAMOF_00342	OG0002047	oppF_1	1	0	0	fpr:FP2_31100	ko:K10823	NA	
BLCPAMOF_00343	OG0000162	group_607	5	5	9	fpr:FP2_31080	ko:K07301	NA	
BLCPAMOF_00344	OG0004040	group_4988	1	1	1	fpr:FP2_31070	NA	specific_fp360	
BLCPAMOF_00345	OG0000380	aroD	1	0	0	fpr:FP2_31060	ko:K03785	NA	
BLCPAMOF_00346	OG0000126	budB	1	0	0	fpr:FP2_31050	ko:K01652	NA	
BLCPAMOF_00350	OG0002291	group_2171	1	0	0	fpr:FP2_23410	NA	NA	
BLCPAMOF_00351	OG0001914	group_2114	1	0	0	slp:Slip_1123	NA	NA	
BLCPAMOF_00352	OG0001263	murC	1	0	0	fpr:FP2_23390	ko:K01924	NA	
BLCPAMOF_00353	OG0001285	uxaC	1	0	0	fpr:FP2_23370	ko:K01812	NA	
BLCPAMOF_00354	OG0001284	uxaB	1	0	0	fpr:FP2_23360	ko:K00041	NA	
BLCPAMOF_00355	OG0001283	uxaA	1	0	0	fpr:FP2_23350	ko:K01685	NA	
BLCPAMOF_00356	OG0001936	group_2654	1	1	1	fpr:FP2_23340	NA	NA	
BLCPAMOF_00357	OG0001282	galM	1	0	0	fpr:FP2_23330	NA	NA	
BLCPAMOF_00358	OG0001274	rspR_2	1	0	0	fpr:FP2_23320	NA	NA	
BLCPAMOF_00359	OG0001275	group_650	2	3	4	fpr:FP2_23310	NA	NA	
BLCPAMOF_00360	OG0001276	group_4990	1	0	0	fpr:FP2_23300	NA	NA	
BLCPAMOF_00361	OG0001277	eda	1	0	0	fpr:FP2_23290	ko:K01625	NA	
BLCPAMOF_00362	OG0001278	kdgK_1	1	0	0	fpr:FP2_23280	ko:K00874	NA	
BLCPAMOF_00363	OG0001279	kduI	1	0	0	fpr:FP2_23270	ko:K01815	NA	
BLCPAMOF_00364	OG0001280	gno_1	1	0	0	fpr:FP2_23260	ko:K00046	NA	
BLCPAMOF_00365	OG0001995	group_4991	1	1	1	NA	NA	NA	

BLCPAMOF_00366	OG0002952	def	1	0	0	fpa:FPR_05950	ko:K01462	NA	
BLCPAMOF_00367	OG0000032	group_4992	1	0	0	NA	NA	NA	
BLCPAMOF_00368	OG0001989	intQ	1	0	0	fpr:FP2_31820	NA	NA	
BLCPAMOF_00369	OG0004041	group_4994	1	0	0	NA	NA	specific_fp360	○
BLCPAMOF_00370	OG0001861	group_4995	1	0	0	fpr:FP2_31850	NA	NA	
BLCPAMOF_00371	OG0004042	group_4996	0	1	0	NA	NA	specific_fp360	○
BLCPAMOF_00372	OG0002312	group_4997	1	0	0	NA	NA	NA	
BLCPAMOF_00373	OG0004043	group_4998	1	0	0	NA	NA	specific_fp360	○
BLCPAMOF_00374	OG0002636	group_4999	1	0	0	ypy:YPK_0953;ypb:YPTS_3238;ypu:BZ21_2433;ypo:BZ17_3502	NA	NA	
BLCPAMOF_00375	OG0004044	group_5000	1	0	0	NA	NA	specific_fp360	○
BLCPAMOF_00376	OG0002355	group_5001	0	1	0	NA	NA	NA	
BLCPAMOF_00377	OG0002311	group_2573	1	0	0	lacy:A4V08_01775	NA	NA	
BLCPAMOF_00378	OG0003521	group_5002	1	0	0	NA	NA	NA	
BLCPAMOF_00380	OG0001536	cymR_2	1	0	0	fpr:FP2_23250	NA	NA	
BLCPAMOF_00381	OG0001535	pspE	1	0	0	fpr:FP2_23240	NA	NA	
BLCPAMOF_00382	OG0001534	group_1817	1	0	0	fpr:FP2_23230	NA	NA	
BLCPAMOF_00383	OG0001533	iscS_3	1	0	0	fpr:FP2_23220	ko:K04487	NA	
BLCPAMOF_00384	OG0001532	iscU	1	0	0	fpr:FP2_23210	ko:K04488	NA	
BLCPAMOF_00385	OG0001460	dpaA	1	0	0	fpa:FPR_12740	ko:K06410	NA	
BLCPAMOF_00386	OG0001459	dpaB	1	0	0	fpr:FP2_23190	ko:K06411	NA	
BLCPAMOF_00387	OG0001458	dacF_3	1	2	2	fpr:FP2_23180	ko:K07258	NA	
BLCPAMOF_00388	OG0001457	rfbC	1	0	0	fpr:FP2_23170	ko:K01790	NA	
BLCPAMOF_00389	OG0001456	tagG	3	4	6	fpa:FPR_12780	ko:K01992	NA	
BLCPAMOF_00390	OG0001455	tagH	1	0	0	fpr:FP2_23150	ko:K01990	NA	
BLCPAMOF_00391	OG0001454	hyaD	1	0	0	fpr:FP2_23140	ko:K20444	NA	
BLCPAMOF_00392	OG0001453	group_1773	1	0	0	fpr:FP2_23130	NA	NA	
BLCPAMOF_00393	OG0001452	group_5003	1	1	1	fpr:FP2_23120	NA	NA	
BLCPAMOF_00394	OG0001451	rnfC	1	0	0	fpr:FP2_23110	ko:K03615	NA	
BLCPAMOF_00395	OG0001450	rsxD_1	5	5	9	fpr:FP2_23100	ko:K03614	NA	
BLCPAMOF_00396	OG0001449	rnfG	1	1	1	fpr:FP2_23090	ko:K03612	NA	
BLCPAMOF_00397	OG0001448	rnfE	3	4	6	fpr:FP2_23080	ko:K03613	NA	
BLCPAMOF_00398	OG0001447	rsxA	4	3	6	fpr:FP2_23070	ko:K03617	NA	
BLCPAMOF_00399	OG0001446	rsxB_2	1	1	1	fpa:FPR_12890	ko:K03616	NA	
BLCPAMOF_00400	OG0001441	group_1763	6	6	11	fpr:FP2_23050	NA	NA	
BLCPAMOF_00401	OG0001442	group_1764	1	0	0	fpa:FPR_12570	ko:K09765	NA	
BLCPAMOF_00402	OG0001443	group_1765	0	1	0	fpr:FP2_23020	NA	NA	
BLCPAMOF_00403	OG0001444	purA_1	1	0	0	fpr:FP2_23010	ko:K01939	NA	
BLCPAMOF_00404	OG0001445	group_1767	1	0	0	fpr:FP2_23000	NA	NA	
BLCPAMOF_00405	OG0000541	tlyC	3	2	4	fpa:FPR_14520	NA	NA	
BLCPAMOF_00406	OG0000540	clpB1	1	0	0	fpr:FP2_22980	ko:K03695	NA	
BLCPAMOF_00407	OG0000530	cysK1	1	0	0	fpr:FP2_22970	ko:K01738	NA	
BLCPAMOF_00408	OG0000529	cymR_1	1	0	0	fpr:FP2_22960	NA	NA	
BLCPAMOF_00409	OG0000539	group_5004	1	0	0	NA	NA	NA	
BLCPAMOF_00410	OG0000538	group_2003	1	0	0	fpr:FP2_22940	ko:K00027	NA	
BLCPAMOF_00411	OG0000537	ttdA	1	0	0	fpa:FPR_11890	ko:K01677	NA	
BLCPAMOF_00412	OG0000536	fumA	1	0	0	fpr:FP2_22910	ko:K01678	NA	
BLCPAMOF_00413	OG0000534	mntR	1	0	0	fpr:FP2_22900	NA	NA	
BLCPAMOF_00414	OG0000203	ndoA_1	1	0	0	fpr:FP2_22890	ko:K07171	NA	
BLCPAMOF_00415	OG0000533	acpS	1	0	0	fpr:FP2_22880	ko:K00997	NA	
BLCPAMOF_00416	OG0000532	group_1137	1	0	0	ccel:CCDG5_0595	NA	NA	
BLCPAMOF_00417	OG0000531	dusC	1	0	0	fpr:FP2_22860	NA	NA	
BLCPAMOF_00418	OG0002030	group_5005	1	0	0	NA	NA	NA	
BLCPAMOF_00419	OG0000139	yybR	1	0	0	bprl:CL2_21260	NA	NA	
BLCPAMOF_00420	OG0002405	group_3966	1	0	0	rto:RTO_32390	NA	NA	
BLCPAMOF_00421	OG0000031	group_24	1	0	0	fpa:FPR_11000	NA	NA	
BLCPAMOF_00422	OG0002181	group_4454	1	0	0	fpr:FP2_25620	NA	NA	
BLCPAMOF_00424	OG0001476	ruvC	1	0	0	ruk:A4V00_10760	ko:K01159	NA	
BLCPAMOF_00425	OG0001475	ruvA	1	0	0	fpr:FP2_22690	ko:K03550	NA	
BLCPAMOF_00426	OG0001474	ruvB_2	1	0	0	fpr:FP2_22680	ko:K03551	NA	
BLCPAMOF_00427	OG0000029	group_3271	1	0	0	fpr:FP2_22670	ko:K03431	NA	
BLCPAMOF_00428	OG0001473	rlmK	1	0	0	fpr:FP2_22660	ko:K06969	NA	
BLCPAMOF_00429	OG0001472	ecfA1	1	0	0	fpr:FP2_22650	ko:K16786	NA	
BLCPAMOF_00430	OG0001471	ecfA2	1	0	0	fpr:FP2_22640	ko:K16787	NA	
BLCPAMOF_00431	OG0001470	ecfT_2	3	2	4	fpr:FP2_22630	ko:K16785	NA	
BLCPAMOF_00432	OG0001469	truA	1	0	0	fpr:FP2_22620	ko:K06173	NA	
BLCPAMOF_00433	OG0001468	group_5006	1	1	1	fpr:FP2_22610	ko:K03641	NA	
BLCPAMOF_00434	OG0001467	group_1785	3	2	4	fpr:FP2_22600	NA	NA	
BLCPAMOF_00435	OG0001466	clpC_2	1	0	0	fpr:FP2_22590	NA	NA	
BLCPAMOF_00436	OG0000183	group_5007	1	0	0	fpr:FP2_22580	NA	NA	
BLCPAMOF_00437	OG0001465	kefB	4	4	7	fpr:FP2_22570	NA	NA	
BLCPAMOF_00438	OG0001464	epsH	1	0	0	fpr:FP2_22560	NA	NA	
BLCPAMOF_00439	OG0001463	recQ	1	0	0	fpr:FP2_22550	ko:K03654	NA	
BLCPAMOF_00440	OG0001462	nrdG	1	0	0	fpr:FP2_22540	ko:K04068	NA	
BLCPAMOF_00441	OG0001461	nrdD	1	0	0	fpr:FP2_22530	ko:K21636	NA	
BLCPAMOF_00447	OG0000197	rapA_2	1	0	0	fpr:FP2_23420	NA	NA	
BLCPAMOF_00448	OG0001984	group_2332	1	0	0	fpr:FP2_23430	NA	NA	
BLCPAMOF_00449	OG0000381	group_1026	1	0	0	fpr:FP2_23440	ko:K01273	NA	
BLCPAMOF_00450	OG0001886	blaZ	1	0	0	fpr:FP2_23450	ko:K17836	NA	
BLCPAMOF_00451	OG0000382	group_1027	4	3	6	fpr:FP2_23460	ko:K07090	NA	
BLCPAMOF_00452	OG0000383	group_1028	1	0	0	fpr:FP2_23470	NA	NA	
BLCPAMOF_00453	OG0000384	group_5008	1	2	2	fpa:FPR_11970	ko:K07052	NA	
BLCPAMOF_00454	OG0000385	tadA	1	0	0	fpr:FP2_23490	ko:K11991	NA	
BLCPAMOF_00455	OG0000386	fabG_1	1	0	0	eha:Ethha_0424	ko:K00059	NA	
BLCPAMOF_00456	OG0000387	sigA_1	1	0	0	fpr:FP2_23510	ko:K03086	NA	
BLCPAMOF_00461	OG0000528	glnS	1	0	0	fpr:FP2_23770	ko:K01886	NA	
BLCPAMOF_00462	OG0000527	group_2236	1	1	1	fpr:FP2_23780	NA	NA	
BLCPAMOF_00463	OG0000526	group_582	1	0	0	fpr:FP2_23790	NA	NA	
BLCPAMOF_00464	OG0000525	group_580	1	0	0	rho:RHOM_09380	NA	NA	
BLCPAMOF_00465	OG0000524	group_1132	1	0	0	fpr:FP2_23810	NA	NA	
BLCPAMOF_00467	OG0000487	group_5009	1	2	2	fpr:FP2_23820	NA	NA	
BLCPAMOF_00468	OG0000488	sigR	1	0	0	fpr:FP2_23830	ko:K03088	NA	
BLCPAMOF_00469	OG0000489	group_1106	1	0	0	fpr:FP2_23840	NA	NA	
BLCPAMOF_00470	OG0000490	argF_2	1	0	0	fpr:FP2_23850	ko:K00611	NA	
BLCPAMOF_00471	OG0000491	ribD_1	0	1	0	fpr:FP2_23870	ko:K01493	NA	
BLCPAMOF_00472	OG0000492	fusA_1	1	0	0	fpr:FP2_23890	ko:K02355	NA	
BLCPAMOF_00473	OG0001397	greA	1	0	0	fpr:FP2_23900	ko:K03624	NA	
BLCPAMOF_00474	OG0001396	lysS	1	0	0	fpr:FP2_23910	ko:K04567	NA	
BLCPAMOF_00475	OG0001318	yfkJ_2	1	0	0	fpr:FP2_23920	ko:K01104	NA	
BLCPAMOF_00476	OG0001317	cpxR	1	0	0	fpr:FP2_23930	NA	NA	
BLCPAMOF_00477	OG0001316	ribH	1	0	0	fpa:FPR_16300	ko:K00794	NA	
BLCPAMOF_00478	OG0001315	ribBA	1	0	0	fpr:FP2_23950	ko:K14652	NA	
BLCPAMOF_00479	OG0001314	ribE	1	0	0	era:ERE_13220;ere:EUBREC_3131;ert:EUR_06260	ko:K00793	NA	
BLCPAMOF_00480	OG0001313	ribD_2	1	0	0	fpa:FPR_16330	ko:K11752	NA	
BLCPAMOF_00481	OG0000231	group_481	1	0	0	fpr:FP2_14000	ko:K06919	NA	
BLCPAMOF_00482	OG0000040	group_295	1	0	0	fpr:FP2_24000	NA	NA	
BLCPAMOF_00483	OG0001672	group_928	1	0	0	erb:A4V01_00065	NA	NA	
BLCPAMOF_00484	OG0000083	group_3126	1	0	0	erb:A4V01_00060	NA	NA	
BLCPAMOF_00485	OG0001347	yteR	1	0	0	fpr:FP2_24180	ko:K15532	NA	
BLCPAMOF_00486	OG0000254	pgl	1	0	0	fpr:FP2_24190	NA	NA	
BLCPAMOF_00487	OG0001346	group_5010	1	0	0	fpr:FP2_24200	NA	NA	
BLCPAMOF_00488	OG0000253	araQ_1	3	4	6	fpr:FP2_24210	ko:K10194	NA	
BLCPAMOF_00489	OG0001345	lacF_1	4	4	7	fpr:FP2_24220	ko:K10193	NA	
BLCPAMOF_00490	OG0001344	yesO	1	0	0	fpr:FP2_24230	ko:K10192	NA	
BLCPAMOF_00491	OG0001343	tdk	1	0	0	fpr:FP2_24240	ko:K00857	NA	

BLCPAMOF_00492	OG0001342	rex	1	0	0	fpr:FP2_24250	ko:K01926	NA	
BLCPAMOF_00493	OG0001341	tepA	1	0	0	fpr:FP2_24260	NA	NA	
BLCPAMOF_00494	OG0001312	spoIIIE	3	3	5	fpr:FP2_24270	ko:K03466	NA	
BLCPAMOF_00495	OG0001311	group_651	1	0	0	fpr:FP2_24280	NA	NA	
BLCPAMOF_00496	OG0001310	comEC_1	1	1	1	ibu:IB211_01356	NA	NA	
BLCPAMOF_00497	OG0000254	pehX	1	0	0	bgy:BGLY_3901	NA	NA	
BLCPAMOF_00498	OG0001294	group_857	1	2	2	NA	NA	NA	
BLCPAMOF_00499	OG0001295	group_858	1	1	1	fpr:FP2_24310	NA	NA	
BLCPAMOF_00500	OG0001296	group_1659	1	0	0	fpr:FP2_24320	NA	NA	
BLCPAMOF_00501	OG0001297	group_1660	1	2	2	fpr:FP2_24330	NA	NA	
BLCPAMOF_00502	OG0001298	group_1661	1	0	0	fpr:FP2_24340	NA	NA	
BLCPAMOF_00503	OG0001299	group_1662	1	0	0	fpr:FP2_24350	NA	NA	
BLCPAMOF_00504	OG0001300	group_1663	4	4	7	fpr:FP2_24360	ko:K07089	NA	
BLCPAMOF_00505	OG0002617	group_5012	1	0	0	NA	NA	NA	
BLCPAMOF_00506	OG0001567	mgl_1	1	0	0	fpr:FP2_24380	ko:K01740	NA	
BLCPAMOF_00507	OG0004045	group_5013	1	0	0	fpr:FP2_24400	NA	specific_fp360	○
BLCPAMOF_00508	OG0001990	rbn	1	0	0	fpr:FP2_24410	ko:K00784	NA	
BLCPAMOF_00509	OG0000479	cca	1	0	0	fpr:FP2_24420	ko:K00974	NA	
BLCPAMOF_00510	OG0000480	mnmA_1	1	0	0	fpr:FP2_24430	ko:K00566	NA	
BLCPAMOF_00511	OG0000481	tcdA	1	0	0	fpr:FP2_24440	NA	NA	
BLCPAMOF_00512	OG0001281	group_855	1	1	1	fpr:FP2_24450	NA	NA	
BLCPAMOF_00513	OG0001358	group_5014	4	4	7	fpr:FP2_24460	ko:K07027	NA	
BLCPAMOF_00514	OG0001357	cotSA	1	0	0	fpr:FP2_24470	NA	NA	
BLCPAMOF_00515	OG0001356	group_5015	1	0	0	fpr:FP2_24480	NA	NA	
BLCPAMOF_00516	OG0001355	group_5016	5	6	10	fpr:FP2_24490	NA	NA	
BLCPAMOF_00517	OG0000097	fadD_1	1	0	0	fpr:FP2_24500	ko:K01897	NA	
BLCPAMOF_00518	OG0000097	lcfB_2	1	1	1	fpr:FP2_24510	ko:K01897	NA	
BLCPAMOF_00519	OG0001354	acpP_1	1	0	0	fpr:FP2_24520	ko:K02078	NA	
BLCPAMOF_00520	OG0001353	group_5018	1	0	0	fpr:FP2_24530	NA	NA	
BLCPAMOF_00521	OG0001887	gltT	4	5	8	bprs:CK3_11880	NA	NA	
BLCPAMOF_00522	OG0001348	group_5019	2	2	3	fpr:FP2_24550	NA	NA	
BLCPAMOF_00523	OG0001349	group_5020	2	3	4	fpr:FP2_24560	NA	NA	
BLCPAMOF_00524	OG0001350	group_5021	1	0	0	fpr:FP2_24570	NA	NA	
BLCPAMOF_00525	OG0001351	sigW	1	0	0	fpa:FPR_12920	ko:K03088	NA	
BLCPAMOF_00526	OG0001352	birA_2	1	0	0	fpr:FP2_24590	ko:K03524	NA	
BLCPAMOF_00527	OG0002448	group_3156	3	3	5	fpr:FP2_24600	ko:K07240	NA	
BLCPAMOF_00528	OG0002447	srpC_4	3	3	5	fpr:FP2_24610	ko:K07240	NA	
BLCPAMOF_00529	OG0001361	mepA_5	6	6	11	fpr:FP2_24620	NA	NA	
BLCPAMOF_00530	OG0001972	group_5023	1	2	2	fpr:FP2_24640	NA	NA	
BLCPAMOF_00531	OG0000275	ypdA_2	2	1	2	fpr:FP2_24650	NA	NA	
BLCPAMOF_00532	OG0001971	group_2272	1	0	0	fpr:FP2_24660	NA	NA	
BLCPAMOF_00533	OG0001970	dctP_2	1	0	0	fpr:FP2_24670	NA	NA	
BLCPAMOF_00534	OG0001969	group_347	1	0	0	fpr:FP2_24680	NA	NA	
BLCPAMOF_00535	OG0001968	siaQ_2	2	3	4	fpr:FP2_24690	NA	NA	
BLCPAMOF_00536	OG0001785	dctM	6	6	11	fpr:FP2_24700	NA	NA	
BLCPAMOF_00537	OG0002045	iolC_1	1	0	0	fpr:FP2_24710	ko:K00847	NA	
BLCPAMOF_00538	OG0001398	mepA_13	5	6	10	fpr:FP2_24720	NA	NA	
BLCPAMOF_00539	OG0001399	rhaR	1	0	0	paea:R70723_24145	NA	NA	
BLCPAMOF_00540	OG0001400	group_2153	1	0	0	fpr:FP2_24740	ko:K10112	NA	
BLCPAMOF_00541	OG0001272	por_2	1	0	0	fpr:FP2_24750	ko:K00040	NA	
BLCPAMOF_00542	OG0001273	uxuA	1	0	0	fpr:FP2_24760	ko:K01686	NA	
BLCPAMOF_00543	OG0001271	eno	1	0	0	fpr:FP2_24770	ko:K01689	NA	
BLCPAMOF_00544	OG0000174	group_1921	1	0	0	fpr:FP2_24780	ko:K01999	NA	
BLCPAMOF_00545	OG0000173	livH	4	4	7	fpr:FP2_24790	ko:K01997	NA	
BLCPAMOF_00546	OG0000172	livH_2	4	4	7	fpr:FP2_24800	ko:K01998	NA	
BLCPAMOF_00547	OG0000171	lptB	1	0	0	fpr:FP2_24810	ko:K01995	NA	
BLCPAMOF_00548	OG0001270	livF	1	0	0	fpr:FP2_24820	ko:K01996	NA	
BLCPAMOF_00549	OG0001360	pflA	1	0	0	fpr:FP2_24850	ko:K04069	NA	
BLCPAMOF_00550	OG0001359	pflB	1	0	0	fpr:FP2_24860	ko:K00656	NA	
BLCPAMOF_00551	OG0000260	ydfJ	6	7	12	fpr:FP2_24870	ko:K07003	NA	
BLCPAMOF_00552	OG0000259	group_5025	1	0	0	fpr:FP2_24880	ko:K01421	NA	
BLCPAMOF_00553	OG0001964	group_5026	1	0	0	fpr:FP2_24910	ko:K01687	NA	
BLCPAMOF_00554	OG0001963	gntP	7	7	13	amo:Anamo_1330	ko:K03299	specific_fp360	
BLCPAMOF_00555	OG0004046	iolI	1	0	0	fpr:FP2_24950	ko:K06606	specific_fp360	
BLCPAMOF_00556	OG0002586	iolX	1	0	0	fpr:FP2_24960	NA	NA	
BLCPAMOF_00557	OG0001784	lldR_1	1	0	0	fpr:FP2_24970	ko:K05799	NA	
BLCPAMOF_00558	OG0000472	rlmCD_1	1	0	0	fpr:FP2_24980	ko:K03215	NA	
BLCPAMOF_00559	OG0000471	blaI	1	0	0	fpr:FP2_24990	NA	NA	
BLCPAMOF_00560	OG0000470	serC	1	0	0	fpr:FP2_25000	ko:K00831	NA	
BLCPAMOF_00561	OG0000469	serA	1	0	0	fpr:FP2_25010	ko:K00058	NA	
BLCPAMOF_00562	OG0000408	group_2342	1	1	1	fpr:FP2_25050	NA	NA	
BLCPAMOF_00563	OG0000409	dnaJ_1	1	0	0	fpr:FP2_25060	ko:K03686	NA	
BLCPAMOF_00564	OG0000410	group_1049	1	0	0	fpr:FP2_25070	NA	NA	
BLCPAMOF_00565	OG0000411	group_707	1	2	2	fpr:FP2_25080	NA	NA	
BLCPAMOF_00566	OG0000412	lacZ_1	1	0	0	fpr:FP2_25090	ko:K01190	NA	
BLCPAMOF_00567	OG0000413	sgcG	1	0	0	fpr:FP2_25100	NA	NA	
BLCPAMOF_00568	OG0000414	rsmD	1	0	0	fpr:FP2_25110	ko:K08316	NA	
BLCPAMOF_00569	OG0000415	group_1053	1	0	0	fpr:FP2_25120	NA	NA	
BLCPAMOF_00570	OG0000416	rsmH_2	1	0	0	fpr:FP2_25130	ko:K03438	NA	
BLCPAMOF_00571	OG0000417	ftsL_1	1	0	0	fpr:FP2_25140	NA	NA	
BLCPAMOF_00572	OG0000418	spoVD_1	1	1	1	fpa:FPR_14740	ko:K08384	NA	
BLCPAMOF_00573	OG0000419	murF	1	0	0	fpr:FP2_25160	ko:K01929	NA	
BLCPAMOF_00574	OG0000420	group_5031	6	5	10	fpr:FP2_25170	ko:K01000	NA	
BLCPAMOF_00575	OG0000421	ftsW_1	4	5	8	fpr:FP2_25180	ko:K03588	NA	
BLCPAMOF_00576	OG0000422	murG	1	0	0	fpr:FP2_25190	ko:K02563	NA	
BLCPAMOF_00577	OG0000423	group_5032	1	1	1	fpr:FP2_25200	ko:K03589	NA	
BLCPAMOF_00578	OG0000424	murE	1	0	0	fpr:FP2_25210	ko:K01928	NA	
BLCPAMOF_00579	OG0000559	group_532	1	0	0	fpr:FP2_25220	NA	NA	
BLCPAMOF_00580	OG0000558	group_1154	1	0	0	fpr:FP2_25230	NA	NA	
BLCPAMOF_00581	OG0000404	yidA	1	0	0	fpr:FP2_25240	NA	NA	
BLCPAMOF_00582	OG0000405	polC_1	1	0	0	fpr:FP2_25250	NA	NA	
BLCPAMOF_00583	OG0000406	ydjZ	3	3	5	fpr:FP2_25260	NA	NA	
BLCPAMOF_00584	OG0001438	group_1760	3	3	5	fpr:FP2_25270	ko:K06147	NA	
BLCPAMOF_00585	OG0001439	group_1761	3	4	6	fpr:FP2_25280	ko:K06147	NA	
BLCPAMOF_00586	OG0001440	slyA_2	1	0	0	fpr:FP2_25300	NA	NA	
BLCPAMOF_00587	OG0000467	group_5033	1	0	0	fpr:FP2_25310	ko:K01126	NA	
BLCPAMOF_00588	OG0000468	purC	1	0	0	fpr:FP2_25330	ko:K01923	NA	
BLCPAMOF_00589	OG0002033	group_2485	3	3	5	fpr:FP2_25340	NA	NA	
BLCPAMOF_00590	OG0002446	gltC_3	1	0	0	bprs:CK3_31820	NA	NA	
BLCPAMOF_00591	OG0000210	abgB	1	0	0	bprs:CK3_31810	NA	NA	
BLCPAMOF_00592	OG0004047	group_5036	7	7	13	cso:CLS_17250	NA	specific_fp360	○
BLCPAMOF_00593	OG0000120	group_5037	3	3	5	lacy:A4V08_19825	NA	NA	
BLCPAMOF_00594	OG0004048	citD	1	0	0	fpr:FP2_25350	ko:K01646	specific_fp360	
BLCPAMOF_00595	OG0004049	citE	1	0	0	fpr:FP2_25360	ko:K01644	specific_fp360	
BLCPAMOF_00596	OG0004050	citF	1	0	0	fpr:FP2_25370	ko:K01643	specific_fp360	
BLCPAMOF_00597	OG0003553	phoP_2	1	0	0	fpr:FP2_25390	NA	specific_fp360	
BLCPAMOF_00598	OG0003552	cckA_2	2	1	2	fpr:FP2_25400	NA	specific_fp360	
BLCPAMOF_00599	OG0002608	group_5043	7	7	13	fpr:FP2_25420	ko:K03300	NA	
BLCPAMOF_00600	OG0004051	cynT	1	0	0	fpr:FP2_25430	ko:K01673	specific_fp360	
BLCPAMOF_00601	OG0001288	group_554	1	0	0	fpr:FP2_25440	NA	NA	
BLCPAMOF_00602	OG0000129	group_5045	3	3	5	fpr:FP2_25450	NA	NA	
BLCPAMOF_00603	OG0000399	ptsG_1	1	0	0	fpr:FP2_25460	ko:K02777	NA	
BLCPAMOF_00604	OG0000398	ltaE	1	0	0	fpr:FP2_25470	ko:K01620	NA	
BLCPAMOF_00605	OG0001890	kdpD_1	2	2	3	fpr:FP2_25480	ko:K07646	NA	

BLCPAMOF_00606	OG0001889	kdpE_1	1	0	0	fpr:FP2_25490	ko:K07667	NA	
BLCPAMOF_00607	OG0001888	group_1974	7	6	12	fpr:FP2_25500	NA	NA	
BLCPAMOF_00609	OG0000000	group_46	0	1	0	fpr:FP2_29810	NA	NA	
BLCPAMOF_00610	OG0002403	crp_2	1	0	0	fpr:FP2_27750	NA	NA	
BLCPAMOF_00611	OG0002612	hadI_1	1	0	0	fpr:FP2_27770	NA	NA	
BLCPAMOF_00612	OG0002404	group_2148	1	0	0	rho:RHOM_00075	NA	NA	
BLCPAMOF_00613	OG0002613	group_3041	1	0	0	fpr:FP2_27790	ko:K02013	NA	
BLCPAMOF_00614	OG0002614	group_2510	4	5	8	fpr:FP2_27800	ko:K02015	NA	
BLCPAMOF_00615	OG0002289	yfmC	1	0	0	fpr:FP2_27810	ko:K02016	NA	
BLCPAMOF_00616	OG0000044	group_441	1	0	0	fpr:FP2_22730	NA	NA	
BLCPAMOF_00617	OG0000018	group_165	1	0	0	fpr:FP2_29840	NA	NA	
BLCPAMOF_00618	OG0000018	group_164	1	0	0	fpr:FP2_29840	NA	NA	
BLCPAMOF_00619	OG0000065	group_182	1	0	0	fpa:FPR_03220	NA	NA	
BLCPAMOF_00620	OG0004052	group_5047	1	0	0	NA	NA	specific_fp360	O
BLCPAMOF_00621	OG0002953	mtlA	2	3	4	fpa:FPR_09640	ko:K02798;ko:K02799;ko:K02800	NA	
BLCPAMOF_00622	OG0001784	lldR_2	1	0	0	cbe:Cbei_4096;cbz:Cbs_4096	NA	NA	
BLCPAMOF_00623	OG0002296	group_5049	1	0	0	cace:CACET_c06540	ko:K01684	shared	
BLCPAMOF_00624	OG0003554	dgoA	1	0	0	pms:KNP414_01528	ko:K01625	NA	
BLCPAMOF_00625	OG0000037	group_5051	1	0	0	sbu:SpiBuddy_1716	ko:K00874	NA	
BLCPAMOF_00626	OG0000265	kdgR_2	1	0	0	cace:CACET_c14840	NA	NA	
BLCPAMOF_00627	OG0001702	group_2386	2	3	4	rob:CK5_13970	NA	NA	
BLCPAMOF_00628	OG0000048	group_19	1	0	0	fpa:FPR_20510	NA	NA	
BLCPAMOF_00629	OG0000140	group_2102	0	1	0	fpa:FPR_20500;fpr:FP2_30020	NA	NA	
BLCPAMOF_00630	OG0000064	group_2464	1	0	0	fpr:FP2_30030	NA	NA	
BLCPAMOF_00631	OG0000101	sigA_3	1	0	0	fpr:FP2_13880	NA	NA	
BLCPAMOF_00632	OG0000100	group_505	1	0	0	fpr:FP2_13890	NA	NA	
BLCPAMOF_00633	OG0000054	dnaG_4	1	0	0	fpa:FPR_20450	NA	NA	
BLCPAMOF_00634	OG0000053	group_7224	1	0	0	fpa:FPR_09510	ko:K06919	NA	
BLCPAMOF_00635	OG0000021	group_403	1	0	0	fpa:FPR_24000	NA	NA	
BLCPAMOF_00636	OG0001773	group_1907	0	1	0	NA	NA	NA	
BLCPAMOF_00637	OG0000000	group_44	0	1	0	fpa:FPR_24750	NA	NA	
BLCPAMOF_00639	OG0001252	group_1633	1	2	2	fpr:FP2_30130	ko:K07258	NA	
BLCPAMOF_00640	OG0001251	group_1632	1	0	0	fpr:FP2_30140	NA	NA	
BLCPAMOF_00641	OG0000665	recG	1	0	0	fpr:FP2_30150	ko:K03655	NA	
BLCPAMOF_00642	OG0004053	group_5053	2	3	4	fpla:A4U99_02145	NA	specific_fp360	
BLCPAMOF_00648	OG0000666	gyrB_2	1	0	0	fpr:FP2_30180	ko:K02470	NA	
BLCPAMOF_00649	OG0000667	gyrA_2	1	0	0	fpr:FP2_30190	ko:K02469	NA	
BLCPAMOF_00650	OG0000668	rlmH	1	0	0	fpr:FP2_30200	ko:K00783	NA	
BLCPAMOF_00651	OG0000669	glyQS	1	0	0	fpr:FP2_30220	ko:K01880	NA	
BLCPAMOF_00652	OG0000670	group_751	1	0	0	gtk:GT3570_10160;gka:GK2140;gte:GTCCBUS3UF5_24210	ko:K19689	NA	
BLCPAMOF_00653	OG0000671	rimP	1	0	0	fpr:FP2_30240	ko:K09748	NA	
BLCPAMOF_00654	OG0000672	nusA	1	0	0	fpr:FP2_30250	ko:K02600	NA	
BLCPAMOF_00655	OG0000673	group_1235	0	1	0	fpr:FP2_30260	ko:K07742	NA	
BLCPAMOF_00656	OG0000674	group_1236	0	1	0	fpr:FP2_30270	NA	NA	
BLCPAMOF_00657	OG0000675	infB	1	0	0	fpr:FP2_30280	ko:K02519	NA	
BLCPAMOF_00658	OG0000676	rbfA	1	0	0	fpr:FP2_30290	ko:K02834	NA	
BLCPAMOF_00659	OG0000677	nrnA	1	0	0	fpr:FP2_30300	ko:K06881	NA	
BLCPAMOF_00660	OG0000678	truB	1	0	0	fpr:FP2_30310	ko:K03177	NA	
BLCPAMOF_00661	OG0000679	ribF	1	0	0	fpr:FP2_30320	ko:K11753	NA	
BLCPAMOF_00662	OG0004054	group_5054	1	1	1	NA	NA	specific_fp360	
BLCPAMOF_00663	OG0001692	group_5055	4	4	7	fsu:Fisuc_0653;fsc:FSU_1084	NA	NA	
BLCPAMOF_00664	OG0002382	pnbA	1	0	0	fpr:FP2_30340	ko:K03929	NA	
BLCPAMOF_00665	OG0000680	rpsO	0	1	0	fpr:FP2_30350	ko:K02956	NA	
BLCPAMOF_00666	OG0000681	pnp	1	0	0	fpr:FP2_30360	ko:K00962	NA	
BLCPAMOF_00667	OG0001431	group_1755	1	0	0	fpr:FP2_30370	ko:K02073	NA	
BLCPAMOF_00668	OG0001430	metN	1	0	0	ibu:IB211_00817c	ko:K02071	NA	
BLCPAMOF_00669	OG0001429	metI	3	3	5	fpr:FP2_30390	ko:K02072	NA	
BLCPAMOF_00670	OG0001428	mgl_2	1	0	0	fpr:FP2_30400	ko:K01740	NA	
BLCPAMOF_00671	OG0001427	metA	1	0	0	fpr:FP2_30410	ko:K00651	NA	
BLCPAMOF_00672	OG0001758	group_887	1	0	0	fpr:FP2_30420	ko:K01266	NA	
BLCPAMOF_00673	OG0000493	flr	0	1	0	fpr:FP2_30430	NA	NA	
BLCPAMOF_00674	OG0000494	ykoT	1	2	2	fpr:FP2_30440	NA	NA	
BLCPAMOF_00675	OG0000495	fixK	1	0	0	fpr:FP2_30450	NA	NA	
BLCPAMOF_00676	OG0000496	mqnD	1	0	0	fpr:FP2_30460	ko:K02051	NA	
BLCPAMOF_00677	OG0001944	brnQ	6	7	12	fpr:FP2_30470	ko:K03311	NA	
BLCPAMOF_00678	OG0000497	ssuC	2	2	3	fpr:FP2_30480	ko:K02050	NA	
BLCPAMOF_00679	OG0000498	artM	1	0	0	fpr:FP2_30490	NA	NA	
BLCPAMOF_00680	OG0004055	group_5057	2	2	3	fpr:FP2_30500	NA	specific_fp360	
BLCPAMOF_00681	OG0000499	hemN	1	0	0	fpr:FP2_30510	NA	NA	
BLCPAMOF_00682	OG0000500	ybhL	3	4	6	fpr:FP2_30520	ko:K06890	NA	
BLCPAMOF_00683	OG0002954	group_5058	1	0	0	NA	NA	NA	
BLCPAMOF_00684	OG0000501	group_5059	1	1	1	fpr:FP2_30550	NA	NA	
BLCPAMOF_00685	OG0000502	group_1116	1	0	0	fpr:FP2_30560	ko:K07007	NA	
BLCPAMOF_00686	OG0000503	cmk_2	1	0	0	fpr:FP2_30570	ko:K00945	NA	
BLCPAMOF_00687	OG0000504	plsC_2	1	0	0	fpr:FP2_30580	ko:K00655	NA	
BLCPAMOF_00688	OG0000505	rpsA_1	1	0	0	fpa:FPR_02120	ko:K02945;ko:K03527	NA	
BLCPAMOF_00689	OG0000506	group_732	2	3	4	fpr:FP2_30610	NA	NA	
BLCPAMOF_00690	OG0000507	group_1994	1	1	1	fpr:FP2_30620	NA	NA	
BLCPAMOF_00691	OG0000508	deoC	1	0	0	fpr:FP2_30630	ko:K01619	NA	
BLCPAMOF_00692	OG0000157	metK	1	0	0	fpr:FP2_30640	ko:K00789	NA	
BLCPAMOF_00693	OG0000535	prs	1	0	0	fpr:FP2_30650	ko:K00948	NA	
BLCPAMOF_00695	OG0004056	group_5060	0	1	0	fpr:FP2_30740	NA	specific_fp360	
BLCPAMOF_00696	OG0001422	pbuG	6	5	10	fpr:FP2_30730	ko:K06901	NA	
BLCPAMOF_00697	OG0001423	group_1750	1	1	1	fpr:FP2_30720	NA	NA	
BLCPAMOF_00698	OG0001307	mglC	5	5	9	csh:Closa_2372	ko:K10541	NA	
BLCPAMOF_00699	OG0001308	mglA_1	1	0	0	fpr:FP2_30690	ko:K10542	NA	
BLCPAMOF_00700	OG0001309	mglB	1	0	0	fpr:FP2_30680	ko:K10540	NA	
BLCPAMOF_00701	OG0000186	group_5061	1	0	0	fpr:FP2_30670	ko:K07814	NA	
BLCPAMOF_00702	OG0001954	group_5062	1	0	0	fpr:FP2_30660	NA	NA	
BLCPAMOF_00703	OG0000644	group_2020	0	1	0	fpr:FP2_30750	NA	NA	
BLCPAMOF_00704	OG0000645	dtd3	1	0	0	fpr:FP2_30760	ko:K03424	NA	
BLCPAMOF_00705	OG0000646	eamA	5	6	10	fpr:FP2_30770	NA	NA	
BLCPAMOF_00706	OG0000647	metG	1	0	0	fpr:FP2_30780	ko:K01874	NA	
BLCPAMOF_00707	OG0000657	group_750	1	0	0	fpr:FP2_30790	NA	NA	
BLCPAMOF_00708	OG0001856	group_5063	2	1	2	fpr:FP2_30800	NA	NA	
BLCPAMOF_00709	OG0000682	asnB	1	0	0	fpr:FP2_30810	ko:K01953	NA	
BLCPAMOF_00710	OG0000683	perR_1	1	0	0	fpr:FP2_30820	ko:K03711	NA	
BLCPAMOF_00711	OG0000214	rspR_3	1	0	0	fpr:FP2_30830	NA	NA	
BLCPAMOF_00712	OG0001605	group_5064	2	3	4	fpr:FP2_30840	NA	NA	
BLCPAMOF_00713	OG0000123	nagB	1	0	0	fpr:FP2_30850	ko:K02564	NA	
BLCPAMOF_00714	OG0004057	group_5065	1	1	1	fpr:FP2_30860	NA	specific_fp360	
BLCPAMOF_00715	OG0000198	group_5066	0	1	0	fpr:FP2_30870	ko:K11189	NA	
BLCPAMOF_00716	OG0004058	kbaZ	1	0	0	fpr:FP2_30880	ko:K16371	specific_fp360	
BLCPAMOF_00717	OG0000189	group_3273	1	0	0	fpr:FP2_30890	ko:K01443	NA	
BLCPAMOF_00718	OG0004059	agaS	1	0	0	fpr:FP2_30900	ko:K02082	specific_fp360	
BLCPAMOF_00719	OG0004060	group_5069	1	0	0	fpr:FP2_30910	ko:K02744	specific_fp360	
BLCPAMOF_00720	OG0004061	group_5070	1	1	1	fpr:FP2_30920	ko:K03210	specific_fp360	
BLCPAMOF_00721	OG0000263	kbaY	1	0	0	fpr:FP2_30930	ko:K08302	specific_fp360	
BLCPAMOF_00722	OG0000252	group_5072	1	0	0	fpr:FP2_30940	NA	NA	
BLCPAMOF_00723	OG0000213	rhaR_1	1	0	0	fpr:FP2_30950	NA	NA	
BLCPAMOF_00724	OG0002295	levE	1	0	0	fpr:FP2_30960	ko:K02745	specific_fp360	
BLCPAMOF_00725	OG0001677	agaC	4	5	8	fpr:FP2_30970	ko:K02746	specific_fp360	
BLCPAMOF_00726	OG0002294	group_5076	4	3	6	fpr:FP2_30980	ko:K02747	specific_fp360	
BLCPAMOF_00727	OG0001678	group_5077	1	0	0	fpr:FP2_30990	NA	NA	

BLCPAMOF_00729	OG0000648	ktrB	5	6	10	fpr:FP2_09510	ko:K03498	NA	
BLCPAMOF_00730	OG0001894	yhdN_2	1	0	0	fpr:FP2_09520	ko:K07079	NA	
BLCPAMOF_00731	OG0001959	group_3220	1	1	1	NA	NA	NA	
BLCPAMOF_00732	OG0000640	dus	1	0	0	fpr:FP2_09540	NA	NA	
BLCPAMOF_00733	OG0002523	yfbR	1	0	0	fpr:FP2_09550	ko:K08722	NA	
BLCPAMOF_00734	OG0000639	group_1211	6	7	12	fpr:FP2_09560	NA	NA	
BLCPAMOF_00735	OG0000089	group_766	1	0	0	fpr:FP2_09570	NA	NA	
BLCPAMOF_00736	OG0002037	group_5078	1	0	0	fpr:FP2_09580	NA	NA	
BLCPAMOF_00737	OG0000095	group_5079	1	0	0	eel:EUBELI_01507	NA	NA	
BLCPAMOF_00738	OG0001185	zupT_1	3	3	5	fpla:A4U99_01735	ko:K07238	NA	
BLCPAMOF_00739	OG0001155	group_5080	3	2	4	fpr:FP2_09610	ko:K16052	NA	
BLCPAMOF_00740	OG0001154	ribU	3	3	5	fpr:FP2_09620	NA	NA	
BLCPAMOF_00741	OG0001153	yeeO_2	4	4	7	fpr:FP2_09630	NA	NA	
BLCPAMOF_00742	OG0001152	mraY_2	5	5	9	fpr:FP2_09640	ko:K01000	NA	
BLCPAMOF_00743	OG0002383	glnQ_1	1	0	0	afn:Acfer_0777	ko:K10041	specific_fp360	
BLCPAMOF_00744	OG0002949	peb1A	1	0	0	fpr:FP2_09660	ko:K10039	specific_fp360	
BLCPAMOF_00745	OG0000176	glnM	3	3	5	fpr:FP2_09670	ko:K10040	specific_fp360	
BLCPAMOF_00746	OG0000176	gltK	2	3	4	fpr:FP2_09680	ko:K10040	specific_fp360	
BLCPAMOF_00747	OG0001148	folD	1	0	0	fpr:FP2_09690	ko:K01491	NA	
BLCPAMOF_00748	OG0001149	fchA	1	1	1	fpa:FPR_28010	NA	NA	
BLCPAMOF_00749	OG0001150	group_2254	1	0	0	fpr:FP2_09710	ko:K01934	NA	
BLCPAMOF_00750	OG0001947	glyA	1	0	0	fpa:FPR_28030	ko:K00600	NA	
BLCPAMOF_00751	OG0000237	group_5085	1	0	0	fpr:FP2_09740	NA	NA	
BLCPAMOF_00752	OG0001227	luxS	1	0	0	fpr:FP2_09750	ko:K07173	NA	
BLCPAMOF_00753	OG0001226	pyk_2	1	0	0	fpr:FP2_09760	ko:K00873	NA	
BLCPAMOF_00754	OG0001225	deoB	1	0	0	fpr:FP2_09770	ko:K01839	NA	
BLCPAMOF_00755	OG0001224	lytR_2	2	2	3	fpr:FP2_09780	NA	NA	
BLCPAMOF_00756	OG0001223	group_846	1	1	1	fpr:FP2_09790	NA	NA	
BLCPAMOF_00757	OG0001222	nadE	1	0	0	fpr:FP2_09800	ko:K01950	NA	
BLCPAMOF_00758	OG0001221	group_645	1	0	0	fpr:FP2_09810	ko:K06180	NA	
BLCPAMOF_00759	OG0004062	rluD_2	1	0	0	fpr:FP2_09810	ko:K06180	NA	
BLCPAMOF_00760	OG0001220	group_5086	2	2	3	NA	NA	NA	
BLCPAMOF_00761	OG0001219	deoD	1	0	0	fpr:FP2_09830	ko:K03784	NA	
BLCPAMOF_00762	OG0001911	yoeB_2	1	0	0	bpb:bpr_IV095	ko:K19158	NA	
BLCPAMOF_00763	OG0001815	group_2987	1	0	0	abao:BEQ56_03355	ko:K07473	NA	
BLCPAMOF_00764	OG0001218	cdd	1	0	0	fpr:FP2_09840	ko:K01489	NA	
BLCPAMOF_00765	OG0001217	tmpC	1	0	0	fpr:FP2_09850	ko:K07335	NA	
BLCPAMOF_00766	OG0001216	mglA_2	1	0	0	cpy:Cphy_3268	ko:K02056	NA	
BLCPAMOF_00767	OG0001215	mglC_2	4	5	8	fpr:FP2_09870	ko:K02057	NA	
BLCPAMOF_00768	OG0001214	group_1608	5	5	9	fpr:FP2_09880	ko:K02057	NA	
BLCPAMOF_00769	OG0001213	pdp	1	0	0	fpr:FP2_09890	ko:K00756	NA	
BLCPAMOF_00770	OG0002339	group_5087	1	1	1	NA	NA	NA	
BLCPAMOF_00771	OG0000237	group_5088	1	0	0	NA	NA	NA	
BLCPAMOF_00772	OG0000425	group_5089	1	2	2	fpa:FPR_05090	NA	NA	
BLCPAMOF_00773	OG0004063	group_5090	1	0	0	csh:Closa_2512	NA	specific_fp360	O
BLCPAMOF_00774	OG0001212	trkA_1	1	0	0	fpr:FP2_09900	ko:K03499	NA	
BLCPAMOF_00775	OG0001211	trkH	5	6	10	fpr:FP2_09910	ko:K03498	NA	
BLCPAMOF_00776	OG0000694	comM	1	0	0	fpr:FP2_09920	ko:K07391	NA	
BLCPAMOF_00777	OG0001958	group_5091	0	1	0	fpr:FP2_09930	NA	NA	
BLCPAMOF_00778	OG0000695	pgcA	1	0	0	fpr:FP2_09940	ko:K01835	NA	
BLCPAMOF_00779	OG0000696	ispF	1	0	0	fpa:FPR_27620	ko:K12506	NA	
BLCPAMOF_00780	OG0000697	cdaA	2	1	2	fpr:FP2_09960	ko:K18672	NA	
BLCPAMOF_00781	OG0000698	group_1251	1	1	1	fpr:FP2_09970	NA	NA	
BLCPAMOF_00782	OG0000699	group_1252	1	0	0	fpr:FP2_09980	ko:K07137	NA	
BLCPAMOF_00783	OG0000700	group_5092	1	2	2	fpr:FP2_09990	NA	NA	
BLCPAMOF_00784	OG0000701	recJ	1	0	0	fpr:FP2_10000	ko:K07462	NA	
BLCPAMOF_00785	OG0000702	relA	1	0	0	fpr:FP2_10010	ko:K00951	NA	
BLCPAMOF_00786	OG0000703	dtd	1	0	0	fpr:FP2_10020	ko:K07560	NA	
BLCPAMOF_00787	OG0000704	gloC	1	0	0	fpr:FP2_10030	NA	NA	
BLCPAMOF_00788	OG0000705	hemZ	1	0	0	fpr:FP2_10040	NA	NA	
BLCPAMOF_00789	OG0000706	udk_3	1	0	0	fpr:FP2_10050	ko:K00876	NA	
BLCPAMOF_00790	OG0000707	group_1259	1	0	0	fpr:FP2_10060	NA	NA	
BLCPAMOF_00791	OG0000708	mazG	1	0	0	fpr:FP2_10070	ko:K02499	NA	
BLCPAMOF_00792	OG0000709	hup_2	1	0	0	fpr:FP2_10080	ko:K03530	NA	
BLCPAMOF_00793	OG0000710	group_1262	1	0	0	fpr:FP2_10090	NA	NA	
BLCPAMOF_00794	OG0000711	yabP	0	1	0	fpr:FP2_10100	NA	NA	
BLCPAMOF_00795	OG0000712	group_5093	2	2	3	fpr:FP2_10110	NA	NA	
BLCPAMOF_00796	OG0000713	ftsL_2	1	1	1	fpr:FP2_10120	ko:K13052	specific_fp360	
BLCPAMOF_00797	OG0000714	yugI	1	0	0	ruk:A4V00_16910	ko:K07571	NA	
BLCPAMOF_00798	OG0000715	rlmL	1	0	0	fpr:FP2_10140	ko:K07444	NA	
BLCPAMOF_00799	OG0000716	group_1266	1	0	0	fpr:FP2_10150	NA	NA	
BLCPAMOF_00800	OG0000717	group_1913	2	3	4	fpr:FP2_10160	NA	NA	
BLCPAMOF_00801	OG0000718	glmS	1	0	0	fpr:FP2_10180	ko:K00820	NA	
BLCPAMOF_00802	OG0000729	group_5094	1	2	2	fpr:FP2_10190	NA	NA	
BLCPAMOF_00803	OG0000728	hlyD	1	1	1	fpr:FP2_10200	ko:K20345	NA	
BLCPAMOF_00804	OG0000727	group_5095	0	1	0	fpr:FP2_10210	NA	NA	
BLCPAMOF_00805	OG0000217	group_5096	1	0	0	fpr:FP2_27550	NA	NA	
BLCPAMOF_00806	OG0000726	lagD	4	3	6	fpr:FP2_27540	ko:K20344	NA	
BLCPAMOF_00807	OG0000217	group_5097	1	0	0	fpr:FP2_27530	NA	NA	
BLCPAMOF_00809	OG0000725	group_5098	2	3	4	NA	NA	NA	
BLCPAMOF_00810	OG0000724	sigE_2	1	0	0	fpa:FPR_20660	ko:K03091	NA	
BLCPAMOF_00811	OG0000723	sigG	1	0	0	fpr:FP2_27480	ko:K03091	NA	
BLCPAMOF_00812	OG0000722	spoIIID	1	0	0	fpr:FP2_27470	ko:K06283	NA	
BLCPAMOF_00813	OG0000721	thiT	3	3	5	fpr:FP2_27460	ko:K16789	NA	
BLCPAMOF_00815	OG0000112	group_685	1	0	0	fpr:FP2_21330	NA	NA	
BLCPAMOF_00816	OG0001763	group_895	1	0	0	lacy:A4V08_07835	NA	NA	
BLCPAMOF_00817	OG0001860	group_2181	0	1	0	fpa:FPR_04680	NA	NA	
BLCPAMOF_00818	OG0002470	group_3196	1	0	0	rto:RTO_05130	NA	NA	
BLCPAMOF_00819	OG0001762	group_2553	1	0	0	rto:RTO_05140	NA	NA	
BLCPAMOF_00820	OG0001859	group_3091	1	0	0	rto:RTO_05150;cct:CC1_32150	NA	NA	
BLCPAMOF_00821	OG0002167	group_4061	1	1	1	fpr:FP2_08590	NA	NA	
BLCPAMOF_00822	OG0000431	group_5099	1	0	0	rto:RTO_05170	ko:K03088	NA	
BLCPAMOF_00823	OG0000079	group_241	1	1	1	fpa:FPR_08180	NA	NA	
BLCPAMOF_00824	OG0002373	group_80	1	0	0	fpa:FPR_05790	ko:K03205	NA	
BLCPAMOF_00825	OG0003213	group_5100	1	1	1	ppq:PPSQR21_024920	NA	NA	
BLCPAMOF_00826	OG0003214	group_5101	1	0	0	NA	NA	NA	
BLCPAMOF_00827	OG0003215	group_3274	1	0	0	rim:ROI_09510	NA	NA	
BLCPAMOF_00828	OG0003216	group_3275	0	1	0	rim:ROI_09500	NA	NA	
BLCPAMOF_00829	OG0003217	group_3276	1	0	0	cdl:CDR20291_1770	NA	NA	
BLCPAMOF_00830	OG0003218	group_3277	1	0	0	bprm:CL3_25310	NA	NA	
BLCPAMOF_00831	OG0003219	group_3278	1	0	0	cls:CXIVA_09870	NA	NA	
BLCPAMOF_00832	OG0000105	group_3279	0	1	0	rim:ROI_09450	NA	NA	
BLCPAMOF_00833	OG0002307	group_3280	1	0	0	rim:ROI_09440	NA	NA	
BLCPAMOF_00834	OG0000068	group_3281	1	0	0	elm:ELI_0210	NA	NA	
BLCPAMOF_00835	OG0004064	group_5102	1	0	0	rim:ROI_09410	NA	specific_fp360	O
BLCPAMOF_00836	OG0004065	group_5103	0	1	0	rim:ROI_09400	NA	specific_fp360	O
BLCPAMOF_00837	OG0000049	group_3282	1	0	0	rim:ROI_09390	NA	NA	
BLCPAMOF_00838	OG0000001	group_79	1	0	0	fpr:FP2_21800;fpa:FPR_05790	ko:K03205	NA	
BLCPAMOF_00839	OG0001869	group_3283	0	1	0	rto:RTO_05200	NA	NA	
BLCPAMOF_00840	OG0000111	group_3284	1	0	0	bprs:CK3_12740	NA	NA	
BLCPAMOF_00841	OG0003555	group_3285	1	0	0	rum:CK1_03630	NA	NA	
BLCPAMOF_00842	OG0003556	group_3286	1	0	0	rho:RHOM_01640	NA	NA	
BLCPAMOF_00843	OG0003054	group_2793	1	1	1	cso:CLS_32990;ert:EUR_10880	NA	NA	
BLCPAMOF_00844	OG0000226	group_5104	4	4	7	aso:SFBmNL_00743	NA	NA	

BLCPAMOF_00845	OG0001786	group_5105	0	1	0	rho:RHOM_01625	NA	NA	
BLCPAMOF_00846	OG0002341	group_71	1	1	1	rto:RTO_05270	NA	NA	
BLCPAMOF_00847	OG0000719	group_1268	1	0	0	fpa:FPR_07990	NA	NA	
BLCPAMOF_00848	OG0002098	group_300	1	0	0	fpa:FPR_07980	NA	NA	
BLCPAMOF_00849	OG0003220	group_2657	1	0	0	fpr:FP2_09030	NA	NA	
BLCPAMOF_00850	OG0000035	group_390	0	1	0	fpa:FPR_05610	NA	NA	
BLCPAMOF_00851	OG0000002	group_216	1	0	0	fpa:FPR_07950	ko:K03497	NA	
BLCPAMOF_00852	OG0000004	soj_2	1	0	0	fpa:FPR_07940	ko:K03496	NA	
BLCPAMOF_00853	OG0000084	group_130	1	0	0	fpr:FP2_21860	NA	NA	
BLCPAMOF_00854	OG0000014	group_140	0	1	0	fpr:FP2_13930	NA	NA	
BLCPAMOF_00855	OG0000120	group_3606	3	3	5	fpr:FP2_19630	NA	NA	
BLCPAMOF_00856	OG0001678	group_3604	1	0	0	fpr:FP2_19640	NA	NA	
BLCPAMOF_00857	OG0000112	frlB_2	1	0	0	fpr:FP2_21330	NA	NA	
BLCPAMOF_00858	OG0002126	group_2388	1	0	0	fpr:FP2_27440	NA	NA	
BLCPAMOF_00859	OG0003557	group_420	1	0	0	fpr:FP2_21350	NA	NA	
BLCPAMOF_00860	OG0001918	group_211	1	0	0	fpr:FP2_21750	NA	NA	
BLCPAMOF_00861	OG0000067	ltrA_3	1	0	0	sequ:Q426_01745;sezo:SeseC_01909	ko:K00986	NA	
BLCPAMOF_00862	OG0001843	group_210	1	0	0	fpr:FP2_21750	NA	NA	
BLCPAMOF_00863	OG0002200	yjcS	1	0	0	pmic:NW74_05755	NA	NA	
BLCPAMOF_00864	OG0002084	group_2263	1	0	0	rim:ROI_40040	NA	NA	
BLCPAMOF_00865	OG0002955	group_5106	1	0	0	fpr:FP2_01230	NA	NA	
BLCPAMOF_00866	OG0002084	group_2264	1	0	0	rim:ROI_40040	NA	NA	
BLCPAMOF_00867	OG0001705	group_3189	1	0	0	fpr:FP2_01240	NA	NA	
BLCPAMOF_00868	OG0001946	dcuS	4	4	7	fpa:FPR_20540	NA	NA	
BLCPAMOF_00869	OG0000130	group_2617	1	0	0	fpr:FP2_01270	NA	NA	
BLCPAMOF_00870	OG0002282	bdhA_1	1	0	0	fpr:FP2_01290	ko:K19955	NA	
BLCPAMOF_00871	OG0002198	group_2262	2	3	4	fpa:FPR_26270	NA	NA	
BLCPAMOF_00872	OG0004066	group_5108	1	0	0	NA	NA	specific_fp360	○
BLCPAMOF_00873	OG0000656	atpB_1	3	3	5	fpr:FP2_01300	ko:K02108	NA	
BLCPAMOF_00874	OG0000655	atpE_1	2	1	2	fpr:FP2_01310	ko:K02110	NA	
BLCPAMOF_00875	OG0000654	atpF_1	1	1	1	fpr:FP2_01320	ko:K02109	NA	
BLCPAMOF_00876	OG0000653	atpA_1	1	0	0	fpr:FP2_01330	ko:K02111	NA	
BLCPAMOF_00877	OG0000652	atpG_1	1	0	0	fpr:FP2_01340	ko:K02115	NA	
BLCPAMOF_00878	OG0000651	atpD_1	1	0	0	fpr:FP2_01350	ko:K02112	NA	
BLCPAMOF_00879	OG0000650	atpC_1	1	0	0	fpr:FP2_01360	ko:K02114	NA	
BLCPAMOF_00880	OG0000730	group_767	2	1	2	fpr:FP2_01370	NA	NA	
BLCPAMOF_00881	OG0000731	group_2034	1	0	0	fpr:FP2_01380	NA	NA	
BLCPAMOF_00882	OG0004067	group_5109	4	3	6	fpr:FP2_01390	NA	specific_fp360	
BLCPAMOF_00883	OG0000732	apbE	1	0	0	fpr:FP2_01400	ko:K03734	NA	
BLCPAMOF_00884	OG0000733	group_769	0	1	0	fpr:FP2_01410	NA	NA	
BLCPAMOF_00885	OG0000734	aroF_2	1	0	0	fpr:FP2_01430	ko:K03856	NA	
BLCPAMOF_00886	OG0000735	ybaK	1	0	0	fpr:FP2_01450	ko:K03976	NA	
BLCPAMOF_00887	OG0000736	purE	1	1	1	fpr:FP2_01460	ko:K01588	NA	
BLCPAMOF_00888	OG0000737	purF	1	0	0	fpr:FP2_01470	ko:K00764	NA	
BLCPAMOF_00889	OG0000738	purM	1	0	0	fpr:FP2_01480	ko:K01933	NA	
BLCPAMOF_00890	OG0000739	purN	1	0	0	rbr:RBR_16740	ko:K11175	NA	
BLCPAMOF_00891	OG0000740	group_1286	1	0	0	fpr:FP2_01500	NA	NA	
BLCPAMOF_00892	OG0000741	purH	1	0	0	fpr:FP2_01510	ko:K00602	NA	
BLCPAMOF_00893	OG0000742	purD_2	1	0	0	fpr:FP2_01520	ko:K01945	NA	
BLCPAMOF_00894	OG0000743	purL	1	0	0	fpr:FP2_01540	ko:K01952	NA	
BLCPAMOF_00895	OG0000744	purB	1	0	0	fpr:FP2_01550	ko:K01756	NA	
BLCPAMOF_00896	OG0000745	rsuA	1	0	0	fpr:FP2_01560	ko:K06183	NA	
BLCPAMOF_00897	OG0000746	cdaR	1	0	0	fpa:FPR_26040	ko:K02647	NA	
BLCPAMOF_00898	OG0000747	ftsE	1	0	0	fpr:FP2_01580	ko:K09812	NA	
BLCPAMOF_00899	OG0000748	ftsX	2	3	4	fpr:FP2_01590	ko:K09811	NA	
BLCPAMOF_00900	OG0000749	mepM_2	1	1	1	fpa:FPR_26070	ko:K21471	NA	
BLCPAMOF_00901	OG0000750	group_1295	1	1	1	NA	NA	NA	
BLCPAMOF_00902	OG0000751	ctpA	1	1	1	fpr:FP2_01620	ko:K03797	NA	
BLCPAMOF_00903	OG0000752	rsmA	1	0	0	fpr:FP2_01630	ko:K02528	NA	
BLCPAMOF_00904	OG0002956	group_5110	1	0	0	fpr:FP2_01640	NA	NA	
BLCPAMOF_00905	OG0000464	group_5111	1	0	0	NA	NA	NA	
BLCPAMOF_00906	OG0000119	group_2611	1	0	0	NA	NA	NA	
BLCPAMOF_00907	OG0002052	group_3101	1	0	0	bprl:CL2_12660	NA	NA	
BLCPAMOF_00908	OG0002053	group_3102	1	0	0	fpa:FPR_11180	NA	NA	
BLCPAMOF_00909	OG0001874	group_5112	1	1	1	NA	NA	NA	
BLCPAMOF_00910	OG0001929	group_2565	1	0	0	cpro:CPRO_13190	NA	NA	
BLCPAMOF_00911	OG0004068	group_5113	0	1	0	NA	NA	specific_fp360	○
BLCPAMOF_00912	OG0002342	group_5114	1	0	0	fpa:FPR_28470	NA	NA	
BLCPAMOF_00913	OG0000104	group_2219	1	0	0	fpa:FPR_28480	NA	NA	
BLCPAMOF_00914	OG0001932	group_5115	1	0	0	NA	NA	NA	
BLCPAMOF_00915	OG0004069	group_5116	1	1	1	NA	NA	specific_fp360	○
BLCPAMOF_00916	OG0003160	group_5117	1	1	1	NA	NA	NA	
BLCPAMOF_00917	OG0003160	group_5118	1	1	1	NA	NA	NA	
BLCPAMOF_00918	OG0000045	group_3100	0	1	0	rim:ROI_23630	NA	NA	
BLCPAMOF_00920	OG0002573	group_5119	1	0	0	fpr:FP2_01650	NA	NA	
BLCPAMOF_00921	OG0001171	pstS1_2	1	0	0	fpr:FP2_01660	ko:K02040	NA	
BLCPAMOF_00922	OG0001170	group_5120	1	0	0	fpr:FP2_01670	NA	NA	
BLCPAMOF_00923	OG0001910	group_2096	4	4	7	fpr:FP2_01680	NA	NA	
BLCPAMOF_00924	OG0001082	xlnA_1	1	0	0	fpr:FP2_01690	NA	NA	
BLCPAMOF_00925	OG0001081	pyrG	1	0	0	fpr:FP2_01700	ko:K01937	NA	
BLCPAMOF_00926	OG0001080	pdtaR	1	0	0	fpr:FP2_01710	ko:K07183	NA	
BLCPAMOF_00927	OG0001079	glnA_2	1	0	0	fpr:FP2_01720	ko:K01915	NA	
BLCPAMOF_00928	OG0001078	glnA_1	1	0	0	fpr:FP2_01730	ko:K01915	NA	
BLCPAMOF_00929	OG0001077	rlmI	1	0	0	fpr:FP2_01740	ko:K06969	NA	
BLCPAMOF_00930	OG0001076	group_1500	1	0	0	fpr:FP2_01750	NA	NA	
BLCPAMOF_00931	OG0001182	glpG	2	3	4	cth:Cthe_0259;ctx:Clo1313_1970	NA	NA	
BLCPAMOF_00932	OG0004070	group_5121	6	6	11	bpb:bpr_I1194	NA	specific_fp360	
BLCPAMOF_00933	OG0004071	group_5122	1	2	2	fpr:FP2_01780	NA	specific_fp360	
BLCPAMOF_00934	OG0000209	group_1159	1	0	0	fpr:FP2_01790	NA	NA	
BLCPAMOF_00935	OG0000560	xpt	1	0	0	fpr:FP2_01800	ko:K03816	NA	
BLCPAMOF_00936	OG0000561	spoVD_2	1	1	1	fpr:FP2_01820	ko:K08384	NA	
BLCPAMOF_00937	OG0000562	ftsW_2	5	5	9	fpr:FP2_01830	ko:K03588	NA	
BLCPAMOF_00938	OG0000563	murAA	1	0	0	fpr:FP2_01840	ko:K00790	NA	
BLCPAMOF_00939	OG0000564	ftsZ	1	0	0	fpr:FP2_01850	ko:K03531	NA	
BLCPAMOF_00940	OG0000565	group_5123	1	0	0	NA	NA	NA	
BLCPAMOF_00941	OG0000566	group_1163	1	0	0	fpr:FP2_01870	NA	NA	
BLCPAMOF_00942	OG0000567	group_1164	1	0	0	fpr:FP2_01880	NA	NA	
BLCPAMOF_00943	OG0000568	group_5124	1	0	0	fpr:FP2_01890	NA	NA	
BLCPAMOF_00944	OG0000569	sbcC	1	0	0	cls:CXIVA_09350	ko:K03546	NA	
BLCPAMOF_00945	OG0000570	sbcD	1	0	0	fpr:FP2_01950	ko:K03547	NA	
BLCPAMOF_00946	OG0000571	lyc_2	1	0	0	fpr:FP2_01960	NA	NA	
BLCPAMOF_00947	OG0000572	group_5125	1	1	1	fpr:FP2_01970	ko:K06387	NA	
BLCPAMOF_00948	OG0000573	group_2373	1	0	0	fpr:FP2_01980	ko:K09157	NA	
BLCPAMOF_00949	OG0000574	purU	1	0	0	fpr:FP2_01990	ko:K07166	NA	
BLCPAMOF_00950	OG0000575	group_2011	1	0	0	fpr:FP2_02010	NA	NA	
BLCPAMOF_00951	OG0000161	patA_2	1	0	0	fpr:FP2_02020	ko:K10907	NA	
BLCPAMOF_00952	OG0000576	ispE	1	0	0	fpr:FP2_02030	ko:K00919	NA	
BLCPAMOF_00953	OG0000577	group_1171	1	2	2	fpla:A4U99_06005	ko:K09779	NA	
BLCPAMOF_00954	OG0000578	group_1172	1	0	0	fpr:FP2_02050	NA	NA	
BLCPAMOF_00955	OG0000579	group_1173	1	0	0	fpr:FP2_02060	ko:K03768	NA	
BLCPAMOF_00956	OG0001926	group_5126	1	1	1	fpr:FP2_02080	NA	NA	
BLCPAMOF_00957	OG0000580	yrrK	1	0	0	fpr:FP2_02090	ko:K07447	NA	
BLCPAMOF_00958	OG0000581	addB	1	0	0	fpa:FPR_03680	ko:K16899	NA	
BLCPAMOF_00959	OG0000582	addA	1	0	0	fpr:FP2_02130	ko:K16898	NA	

BLCPAMOF_00960	OG0000583	infC	1	0	0	ruk:A4V00_13445	ko:K02520	NA	
BLCPAMOF_00961	OG0000584	rpmI	0	1	0	fpa:FPR_03710;fpr:FP2_02150	ko:K02916	NA	
BLCPAMOF_00962	OG0000585	rplT	0	1	0	fpr:FP2_02160	ko:K02887	NA	
BLCPAMOF_00963	OG0000586	group_1177	1	0	0	fpr:FP2_02170	ko:K03437	NA	
BLCPAMOF_00964	OG0000587	dprA	1	0	0	adn:Alide_4268	ko:K04096	NA	
BLCPAMOF_00965	OG0000588	topA	1	0	0	fpr:FP2_02190	ko:K03168	NA	
BLCPAMOF_00966	OG0000589	trmFO	1	0	0	fpr:FP2_02200	ko:K04094	NA	
BLCPAMOF_00967	OG0000590	plsX	1	0	0	fpa:FPR_03770	ko:K03621	NA	
BLCPAMOF_00968	OG0000591	rnc	1	0	0	fpr:FP2_02210	ko:K03685	NA	
BLCPAMOF_00969	OG0000592	smc_1	1	0	0	fpr:FP2_02220	ko:K03529	NA	
BLCPAMOF_00970	OG0000593	ftsY	1	0	0	fpr:FP2_02230	ko:K03110	NA	
BLCPAMOF_00971	OG0000594	rdgB	1	0	0	fpr:FP2_02240	ko:K02428	NA	
BLCPAMOF_00972	OG0000595	yhbY	1	0	0	fpr:FP2_02250	ko:K07574	NA	
BLCPAMOF_00973	OG0000596	nadD	1	0	0	fpr:FP2_02260	ko:K00969	NA	
BLCPAMOF_00974	OG0000597	rny_1	1	0	0	fpr:FP2_02270	NA	NA	
BLCPAMOF_00975	OG0000598	yvhJ	1	1	1	fpa:FPR_03860	NA	NA	
BLCPAMOF_00976	OG0000599	rsfS	1	0	0	fpr:FP2_02290	ko:K09710	NA	
BLCPAMOF_00977	OG0000600	leuS	1	0	0	fpr:FP2_02300	ko:K01869	NA	
BLCPAMOF_00978	OG0000601	rpsU	0	1	0	fpr:FP2_02310;fpa:FPR_03890	ko:K02970	NA	
BLCPAMOF_00979	OG0000602	gph_1	1	0	0	fpr:FP2_02320	ko:K07015	NA	
BLCPAMOF_00980	OG0000603	nfo	1	0	0	eha:Ethha_0220	ko:K01151	NA	
BLCPAMOF_00981	OG0000604	efp	1	0	0	fpr:FP2_02350	ko:K02356	NA	
BLCPAMOF_00982	OG0000605	group_1189	1	0	0	fpr:FP2_02360	NA	NA	
BLCPAMOF_00983	OG0001250	argS	1	0	0	fpr:FP2_02370	ko:K01887	NA	
BLCPAMOF_00984	OG0001249	group_2472	1	0	0	ccel:CCDG5_1955	NA	NA	
BLCPAMOF_00985	OG0001248	murI	1	0	0	fpr:FP2_02390	ko:K01776	NA	
BLCPAMOF_00986	OG0001247	ddlA	1	0	0	fpr:FP2_02400	ko:K01921	NA	
BLCPAMOF_00987	OG0001246	rpmG2	0	1	0	fpr:FP2_02410;fpa:FPR_16590	ko:K02913	NA	
BLCPAMOF_00988	OG0001245	secE	1	1	1	fpr:FP2_02420	ko:K03073	NA	
BLCPAMOF_00989	OG0001244	nusG	1	0	0	fpr:FP2_02430	ko:K02601	NA	
BLCPAMOF_00990	OG0001243	rplK	1	0	0	fpr:FP2_02440	ko:K02867	NA	
BLCPAMOF_00991	OG0001242	rplA	1	0	0	fpr:FP2_02450	ko:K02863	NA	
BLCPAMOF_00992	OG0001241	rplJ	1	0	0	fpr:FP2_02460	ko:K02864	NA	
BLCPAMOF_00993	OG0001240	rplL	1	0	0	fpr:FP2_02470	ko:K02935	NA	
BLCPAMOF_00994	OG0000607	fhs	1	0	0	fpr:FP2_02480	ko:K01938	NA	
BLCPAMOF_00995	OG0001234	group_1621	1	0	0	fpr:FP2_02490	NA	NA	
BLCPAMOF_00996	OG0001233	group_5127	1	1	1	fpr:FP2_02500	ko:K06381	NA	
BLCPAMOF_00997	OG0001232	group_5128	4	5	8	fpa:FPR_26160	NA	NA	
BLCPAMOF_00998	OG0001231	gap	1	0	0	fpr:FP2_02530	ko:K00134	NA	
BLCPAMOF_00999	OG0002343	group_1939	1	0	0	NA	NA	NA	
BLCPAMOF_01000	OG0002343	group_1941	1	0	0	fro:AALO17_22620	NA	NA	
BLCPAMOF_01001	OG0002334	group_3210	0	1	0	ste:STER_1065	NA	NA	
BLCPAMOF_01002	OG0002196	group_2621	1	0	0	ste:STER_1064	NA	NA	
BLCPAMOF_01003	OG0004072	group_5129	5	5	9	NA	NA	specific_fp360	○
BLCPAMOF_01004	OG0004073	group_5130	1	0	0	NA	NA	specific_fp360	○
BLCPAMOF_01005	OG0002344	group_5131	1	0	0	NA	NA	NA	
BLCPAMOF_01006	OG0002524	group_5132	1	0	0	NA	NA	NA	
BLCPAMOF_01007	OG0000242	group_5133	7	8	14	NA	NA	NA	
BLCPAMOF_01008	OG0001737	group_5134	1	0	0	NA	NA	NA	
BLCPAMOF_01009	OG0003535	tarL	1	0	0	NA	NA	NA	
BLCPAMOF_01010	OG0003221	rmlB	1	0	0	bvu:BVU_2952	NA	NA	
BLCPAMOF_01011	OG0003222	tarI	1	0	0	tbe:Trebr_1637	ko:K00991	NA	
BLCPAMOF_01012	OG0000126	ilvG	1	0	0	era:ERE_05900	ko:K01652	NA	
BLCPAMOF_01013	OG0000126	ilvB_1	1	0	0	era:ERE_05910	ko:K01652	NA	
BLCPAMOF_01014	OG0004074	group_5140	4	5	8	NA	NA	specific_fp360	
BLCPAMOF_01015	OG0000029	group_381	1	0	0	fpa:FPR_02700	ko:K03431	NA	
BLCPAMOF_01016	OG0000032	group_671	0	1	0	NA	NA	NA	
BLCPAMOF_01017	OG0001895	group_2658	1	0	0	NA	NA	NA	
BLCPAMOF_01018	OG0003558	group_5141	1	0	0	syu:M744_12375;syf:Synpcc7942_0873;syc:syc0667_d	NA	specific_fp360	
BLCPAMOF_01019	OG0002431	group_3124	0	1	0	NA	NA	NA	
BLCPAMOF_01020	OG0002643	group_3125	1	0	0	lacy:A4V08_03905	NA	NA	
BLCPAMOF_01021	OG0000086	group_5142	1	0	0	ibu:IB211_02791	NA	NA	
BLCPAMOF_01022	OG0000024	group_739	1	0	0	bprs:CK3_12830;rob:CK5_35320;rho:RHOM_10380	ko:K02315	NA	
BLCPAMOF_01023	OG0002178	group_5143	1	0	0	NA	NA	NA	
BLCPAMOF_01024	OG0001779	group_5144	1	0	0	cpro:CPRO_18420	NA	NA	
BLCPAMOF_01025	OG0002435	group_5145	1	0	0	NA	NA	NA	
BLCPAMOF_01026	OG0000049	group_5146	0	1	0	rum:CK1_30230	NA	NA	
BLCPAMOF_01027	OG0002179	group_3287	1	0	0	NA	NA	NA	
BLCPAMOF_01028	OG0003223	group_2660	1	0	0	NA	NA	NA	
BLCPAMOF_01029	OG0002525	radA_3	1	0	0	eha:Ethha_1275	NA	NA	
BLCPAMOF_01030	OG0003224	group_2285	1	0	0	NA	NA	NA	
BLCPAMOF_01031	OG0000113	group_2662	1	0	0	avu:BK816_07010	NA	NA	
BLCPAMOF_01032	OG0002957	group_2287	1	0	0	NA	NA	NA	
BLCPAMOF_01033	OG0003225	group_2290	1	0	0	NA	NA	NA	
BLCPAMOF_01034	OG0004075	group_5147	1	0	0	cso:CLS_37400	ko:K07816	specific_fp360	○
BLCPAMOF_01035	OG0004076	group_5148	0	1	0	fpr:FP2_25380	NA	specific_fp360	
BLCPAMOF_01036	OG0002958	ugd_1	1	0	0	rto:RTO_19030	ko:K00012	NA	
BLCPAMOF_01037	OG0004077	group_5149	1	0	0	ldb:Ldb1945	NA	specific_fp360	○
BLCPAMOF_01038	OG0004078	epsG	4	5	8	NA	NA	specific_fp360	○
BLCPAMOF_01039	OG0000242	group_5151	7	7	13	cls:CXIVA_01120	NA	NA	
BLCPAMOF_01040	OG0004079	group_5152	4	4	7	NA	NA	specific_fp360	○
BLCPAMOF_01041	OG0000029	glmM_1	1	0	0	fpa:FPR_19400	ko:K03431	NA	
BLCPAMOF_01042	OG0002332	group_670	0	1	0	NA	NA	NA	
BLCPAMOF_01043	OG0001895	group_2659	1	0	0	NA	NA	NA	
BLCPAMOF_01044	OG0001994	group_3288	1	0	0	rch:RUM_18080	NA	NA	
BLCPAMOF_01045	OG0003559	group_3289	1	0	0	NA	NA	NA	
BLCPAMOF_01046	OG0002959	group_5153	1	0	0	NA	NA	NA	
BLCPAMOF_01047	OG0003226	group_5154	1	0	0	NA	NA	NA	
BLCPAMOF_01048	OG0002435	group_3290	1	0	0	NA	NA	NA	
BLCPAMOF_01049	OG0002179	group_3292	1	0	0	NA	NA	NA	
BLCPAMOF_01050	OG0001919	group_2229	1	0	0	fpr:FP2_13220	NA	NA	
BLCPAMOF_01051	OG0003560	group_5155	1	0	0	ral:Rumal_0718	NA	NA	
BLCPAMOF_01052	OG0003561	group_5156	1	0	0	ral:Rumal_0717	NA	NA	
BLCPAMOF_01053	OG0002958	ugd_2	1	0	0	fpr:FP2_02540	ko:K00012	NA	
BLCPAMOF_01054	OG0001230	pgk	1	0	0	fpr:FP2_02550	ko:K00927	NA	
BLCPAMOF_01055	OG0001229	tpiA	1	0	0	fpr:FP2_02560	ko:K01803	NA	
BLCPAMOF_01056	OG0001228	gpmI	1	0	0	fpr:FP2_02570	ko:K15633	NA	
BLCPAMOF_01057	OG0000618	group_5157	1	1	1	fpr:FP2_02580	NA	NA	
BLCPAMOF_01058	OG0000212	ydhY_2	1	0	0	fpr:FP2_02590	NA	NA	
BLCPAMOF_01059	OG0000619	mtaB	1	0	0	fpr:FP2_02600	ko:K18707	NA	
BLCPAMOF_01060	OG0000620	dacF_1	1	1	1	fpr:FP2_02610	ko:K07258	NA	
BLCPAMOF_01061	OG0000621	pgiB	1	0	0	fpr:FP2_02620	ko:K01810	NA	
BLCPAMOF_01062	OG0000622	group_1202	1	0	0	fpr:FP2_02630	NA	NA	
BLCPAMOF_01063	OG0000623	group_1203	1	0	0	fpr:FP2_02640	ko:K07040	NA	
BLCPAMOF_01064	OG0000624	rpmF	1	0	0	fpr:FP2_02650	ko:K02911	NA	
BLCPAMOF_01065	OG0000625	group_1204	1	0	0	fpr:FP2_02660	NA	NA	
BLCPAMOF_01066	OG0000626	der	1	0	0	fpr:FP2_02670	ko:K03977	NA	
BLCPAMOF_01067	OG0000627	plsY	3	4	6	fpr:FP2_02680	ko:K08591	NA	
BLCPAMOF_01068	OG0001172	group_1920	1	1	1	fpr:FP2_02690	NA	NA	
BLCPAMOF_01069	OG0000082	ridA	1	0	0	fpr:FP2_02700	NA	NA	
BLCPAMOF_01070	OG0000075	group_5158	1	0	0	fpr:FP2_02720	NA	NA	
BLCPAMOF_01071	OG0001380	cbiK	1	1	1	fpr:FP2_02730	NA	NA	
BLCPAMOF_01072	OG0001379	group_1923	1	0	0	fpr:FP2_02740	NA	NA	
BLCPAMOF_01073	OG0001378	group_5159	1	0	0	fpr:FP2_02750	ko:K02016	NA	

BLCPAMOF_01074	OG0001377	hmuU	5	5	9	fpr:FP2_02760	ko:K02015	NA	
BLCPAMOF_01075	OG0001376	cbiD	1	0	0	fpr:FP2_02770	ko:K02188	NA	
BLCPAMOF_01076	OG0003562	group_5160	1	0	0	fpr:FP2_02780	ko:K03394	NA	
BLCPAMOF_01077	OG0001375	cbiF	1	0	0	fpr:FP2_02790	ko:K05936	NA	
BLCPAMOF_01078	OG0001374	cbiG	1	0	0	fpa:FPR_29190	ko:K02189	NA	
BLCPAMOF_01079	OG0001373	cbiH	1	0	0	fpr:FP2_02810	NA	NA	
BLCPAMOF_01080	OG0001372	cbiJ	1	0	0	fpr:FP2_02820	ko:K05895	NA	
BLCPAMOF_01081	OG0001371	group_5161	1	0	0	fpr:FP2_02830	ko:K00595	NA	
BLCPAMOF_01082	OG0001370	cbiA	1	0	0	fpr:FP2_02840	ko:K02224	NA	
BLCPAMOF_01083	OG0001369	cobT	1	0	0	fpr:FP2_02850	ko:K00768	NA	
BLCPAMOF_01084	OG0001368	cobU	1	0	0	fpr:FP2_02860	ko:K02231	NA	
BLCPAMOF_01085	OG0001367	cobS	3	4	6	fpa:FPR_29120	ko:K02233	NA	
BLCPAMOF_01086	OG0001366	group_1704	1	0	0	fpr:FP2_02880	ko:K02231	NA	
BLCPAMOF_01087	OG0001746	pspB_2	1	0	0	fpr:FP2_02890	ko:K02226	NA	
BLCPAMOF_01088	OG0001365	cobD_1	2	2	3	fpr:FP2_02900	ko:K02227	NA	
BLCPAMOF_01089	OG0001364	cobD_2	1	0	0	fpr:FP2_02910	ko:K04720	NA	
BLCPAMOF_01090	OG0001363	cobQ	1	0	0	fpr:FP2_02920	ko:K02232	NA	
BLCPAMOF_01091	OG0001151	btuR	1	0	0	fpr:FP2_02930	ko:K19221	NA	
BLCPAMOF_01092	OG0001362	cbiC	1	0	0	fpa:FPR_29060	ko:K06042	NA	
BLCPAMOF_01093	OG0004080	group_5162	1	0	0	fpr:FP2_02950	NA	specific_fp360	
BLCPAMOF_01094	OG0001147	group_5163	1	0	0	fpr:FP2_02960	NA	NA	
BLCPAMOF_01095	OG0001146	group_1555	1	0	0	fpr:FP2_02970	NA	NA	
BLCPAMOF_01096	OG0001145	nirQ	1	0	0	fpr:FP2_02980	NA	NA	
BLCPAMOF_01097	OG0002526	group_2664	6	6	11	fpr:FP2_02990	ko:K03310	NA	
BLCPAMOF_01098	OG0000215	fucO	1	0	0	fpr:FP2_03020	ko:K00048	NA	
BLCPAMOF_01099	OG0000684	group_752	5	5	9	fpr:FP2_16130	NA	NA	
BLCPAMOF_01100	OG0001389	hisS	1	0	0	fpr:FP2_16140	ko:K01892	NA	
BLCPAMOF_01101	OG0001388	yhjX	6	7	12	fpa:FPR_19920	ko:K08177	NA	
BLCPAMOF_01102	OG0001387	group_3034	1	0	0	fpr:FP2_16160	NA	NA	
BLCPAMOF_01103	OG0001386	group_7140	1	0	0	fpa:FPR_19940;fpr:FP2_16170	NA	NA	
BLCPAMOF_01104	OG0001385	fccA	1	1	1	fpr:FP2_16180	ko:K00244	NA	
BLCPAMOF_01105	OG0002039	group_1716	1	1	1	fpr:FP2_16190	NA	NA	
BLCPAMOF_01106	OG0000258	czcB	1	1	1	fpr:FP2_16200	ko:K02005	NA	
BLCPAMOF_01107	OG0000257	macB_2	1	0	0	fpr:FP2_16210	ko:K02003	NA	
BLCPAMOF_01108	OG0000256	group_1715	2	3	4	fpr:FP2_16220	ko:K02004	NA	
BLCPAMOF_01109	OG0000255	group_1714	1	1	1	fpr:FP2_16230	NA	NA	
BLCPAMOF_01110	OG0001383	group_5164	1	0	0	fpr:FP2_16240	NA	NA	
BLCPAMOF_01112	OG0000114	group_877	1	0	0	fpa:FPR_27230	NA	NA	
BLCPAMOF_01113	OG0001873	group_5165	1	0	0	cct:CC1_31830	NA	NA	
BLCPAMOF_01114	OG0000181	group_495	0	1	0	NA	NA	NA	
BLCPAMOF_01115	OG0001382	arsC_2	1	0	0	eel:EUBELI_20104	ko:K03741	NA	
BLCPAMOF_01116	OG0002038	yccM_1	4	5	8	cls:CXIVA_04360	NA	NA	
BLCPAMOF_01117	OG0002960	group_2665	1	1	1	fpr:FP2_15190	NA	NA	
BLCPAMOF_01118	OG0000020	group_315	1	0	0	fpa:FPR_19020	NA	NA	
BLCPAMOF_01119	OG0000064	group_2466	1	0	0	fpr:FP2_30030	NA	NA	
BLCPAMOF_01120	OG0000140	group_2103	0	1	0	fpa:FPR_20500;fpr:FP2_30020	NA	NA	
BLCPAMOF_01121	OG0002498	group_18	0	1	0	fpr:FP2_17170	NA	NA	
BLCPAMOF_01122	OG0000617	group_5166	1	1	1	fpr:FP2_17950	NA	NA	
BLCPAMOF_01123	OG0000616	pdxK	1	0	0	ccel:CCDG5_1749	ko:K00868	NA	
BLCPAMOF_01124	OG0000615	trmL	1	0	0	fpr:FP2_17970	ko:K03216	NA	
BLCPAMOF_01125	OG0000614	group_1198	1	0	0	fpr:FP2_17980	NA	NA	
BLCPAMOF_01126	OG0000211	queT	3	3	5	fpr:FP2_17990	NA	NA	
BLCPAMOF_01127	OG0000271	group_5167	1	0	0	fpr:FP2_18000	NA	NA	
BLCPAMOF_01128	OG0000135	sphR_2	1	0	0	rob:CK5_03780	NA	NA	
BLCPAMOF_01129	OG0000063	group_2444	2	1	2	rob:CK5_03790	NA	NA	
BLCPAMOF_01130	OG0002337	group_2644	1	0	0	bpsc:BBPC_0521	NA	NA	
BLCPAMOF_01131	OG0000047	yknY_2	1	0	0	fpa:FPR_10790	ko:K02003	NA	
BLCPAMOF_01132	OG0002266	group_2944	4	5	8	rob:CK5_03810	ko:K02004	NA	
BLCPAMOF_01133	OG0003185	group_3106	1	0	0	coo:CCU_02590;fpa:FPR_10810;cct:CC1_08260	NA	NA	
BLCPAMOF_01134	OG0000177	group_4223	0	1	0	fpa:FPR_10820;cct:CC1_08280;coo:CCU_02570	NA	NA	
BLCPAMOF_01135	OG0000102	group_922	0	1	0	rho:RHOM_06480;rob:CK5_03870;cct:CC1_08290	NA	NA	
BLCPAMOF_01136	OG0003186	group_4224	1	0	0	coo:CCU_02560;cct:CC1_08300;fpa:FPR_10840;rho:RHOM_06485	NA	NA	
BLCPAMOF_01137	OG0000103	group_4225	1	0	0	rho:RHOM_06490	NA	NA	
BLCPAMOF_01138	OG0000059	group_276	1	0	0	rho:RHOM_06500	NA	NA	
BLCPAMOF_01139	OG0003187	group_4226	0	1	0	rho:RHOM_06505;fpa:FPR_10880;cct:CC1_08340;coo:CCU_02520	NA	NA	
BLCPAMOF_01140	OG0001868	group_4227	1	0	0	rho:RHOM_06510	NA	NA	
BLCPAMOF_01141	OG0004081	group_5168	2	3	4	fpr:FP2_18000	NA	specific_fp360	
BLCPAMOF_01142	OG0001120	group_1541	1	0	0	fpr:FP2_18020	ko:K06940	NA	
BLCPAMOF_01143	OG0001119	group_1540	1	0	0	fpr:FP2_18030	ko:K01989	NA	
BLCPAMOF_01144	OG0001118	group_1539	4	5	8	fpr:FP2_18040	ko:K05832	NA	
BLCPAMOF_01145	OG0001117	opuBA	1	0	0	fpr:FP2_18050	ko:K05833	NA	
BLCPAMOF_01146	OG0000478	alsT_1	5	6	10	rob:CK5_16720	ko:K03310	NA	
BLCPAMOF_01147	OG0000634	nspC	1	0	0	fpr:FP2_18070	ko:K13747	NA	
BLCPAMOF_01148	OG0000635	group_2018	1	0	0	fpa:FPR_20600	ko:K00290	NA	
BLCPAMOF_01149	OG0000636	speB	1	0	0	fpr:FP2_18090	ko:K01480	NA	
BLCPAMOF_01150	OG0000637	speE	1	0	0	fpr:FP2_18100	ko:K00797	NA	
BLCPAMOF_01151	OG0000638	speA_1	1	0	0	fpr:FP2_18110	NA	NA	
BLCPAMOF_01152	OG0000233	kdgK_2	1	0	0	fpr:FP2_18120	ko:K00874	NA	
BLCPAMOF_01153	OG0001116	group_1537	1	0	0	fpr:FP2_18130	ko:K04070	NA	
BLCPAMOF_01154	OG0001115	fbp	1	0	0	fpr:FP2_18140	ko:K04041	NA	
BLCPAMOF_01155	OG0001114	murAB	1	0	0	ccel:CCDG5_1556	ko:K00790	NA	
BLCPAMOF_01156	OG0001113	yycJ	1	0	0	fpr:FP2_18160	NA	NA	
BLCPAMOF_01157	OG0001939	glpK	1	0	0	fpr:FP2_18170	ko:K00864	NA	
BLCPAMOF_01158	OG0001095	group_636	1	0	0	fpr:FP2_18340	ko:K03215	NA	
BLCPAMOF_01159	OG0001094	araC_2	1	0	0	fpr:FP2_18350	NA	NA	
BLCPAMOF_01160	OG0001093	galK_1	1	0	0	fpr:FP2_18360	ko:K00849	NA	
BLCPAMOF_01161	OG0001092	group_5169	1	0	0	fpr:FP2_18370	NA	NA	
BLCPAMOF_01162	OG0001091	group_5170	1	0	0	fpr:FP2_18380	NA	NA	
BLCPAMOF_01163	OG0001090	malQ_1	1	0	0	fpr:FP2_18390	ko:K00705	NA	
BLCPAMOF_01164	OG0001089	araQ_4	3	3	5	fpr:FP2_18400	ko:K10119	NA	
BLCPAMOF_01165	OG0001088	ugpA	3	4	6	fpr:FP2_18410	ko:K10118	NA	
BLCPAMOF_01166	OG0001087	group_818	1	0	0	fpr:FP2_18420	ko:K10117	NA	
BLCPAMOF_01167	OG0001086	ccpA_3	1	0	0	fpr:FP2_18430	ko:K02529	NA	
BLCPAMOF_01168	OG0004082	group_5171	1	0	0	NA	NA	specific_fp360	○
BLCPAMOF_01169	OG0001177	group_5172	2	3	4	fpr:FP2_18450	ko:K02003;ko:K02004	NA	
BLCPAMOF_01170	OG0001950	group_5173	1	0	0	fpr:FP2_18460	NA	NA	
BLCPAMOF_01171	OG0001176	group_5174	1	0	0	NA	NA	NA	
BLCPAMOF_01172	OG0001175	group_5175	1	0	0	fpa:FPR_19610	NA	NA	
BLCPAMOF_01173	OG0001174	hadI	1	0	0	ova:OBV_20290	NA	NA	
BLCPAMOF_01174	OG0001173	group_1577	1	0	0	fpr:FP2_18500	NA	NA	
BLCPAMOF_01175	OG0001075	group_1499	1	0	0	fpr:FP2_18510	NA	NA	
BLCPAMOF_01176	OG0001074	group_2436	3	2	4	fpr:FP2_18520	NA	NA	
BLCPAMOF_01177	OG0001073	group_1498	1	0	0	fpr:FP2_18530	NA	NA	
BLCPAMOF_01178	OG0001181	galT	1	0	0	fpr:FP2_18540	ko:K00965	NA	
BLCPAMOF_01179	OG0000239	galK_2	1	0	0	fpr:FP2_18550	ko:K00849	NA	
BLCPAMOF_01180	OG0001180	htpG	1	0	0	fpr:FP2_18560	ko:K04079	NA	
BLCPAMOF_01181	OG0000115	axeA1_2	1	0	0	fpr:FP2_18570	NA	NA	
BLCPAMOF_01182	OG0001179	group_1580	1	0	0	fpr:FP2_18580	NA	NA	
BLCPAMOF_01183	OG0001178	group_1579	1	0	0	fpr:FP2_18590	ko:K06950	NA	
BLCPAMOF_01184	OG0001206	pitA	1	0	0	fpr:FP2_18600	ko:K03823	NA	
BLCPAMOF_01185	OG0004083	ycdX	1	0	0	fpr:FP2_18610	ko:K04486	specific_fp360	
BLCPAMOF_01186	OG0000141	group_5177	1	1	1	fpr:FP2_18620	NA	NA	
BLCPAMOF_01187	OG0001736	group_2105	1	0	0	fpr:FP2_18630	NA	NA	
BLCPAMOF_01188	OG0001205	group_1602	1	1	1	fpr:FP2_18640	ko:K09760	NA	

BLCPAMOF_01189	OG0001204	fprA1_1	1	0	0	fpr:FP2_18650	NA	NA	
BLCPAMOF_01190	OG0001867	immR_1	0	1	0	ruk:A4V00_04200	NA	NA	
BLCPAMOF_01191	OG0004084	group_5178	0	1	0	NA	NA	specific_fp360	○
BLCPAMOF_01192	OG0003563	group_5179	1	1	1	NA	NA	NA	
BLCPAMOF_01193	OG0001210	pheS	1	0	0	fpr:FP2_18670	ko:K01889	NA	
BLCPAMOF_01194	OG0001209	pheT	1	0	0	fpr:FP2_18680	ko:K01890	NA	
BLCPAMOF_01195	OG0001199	yigZ	1	0	0	ele:Elen_2997	NA	NA	
BLCPAMOF_01196	OG0001198	dgt	1	0	0	fpr:FP2_18700	ko:K01129	NA	
BLCPAMOF_01197	OG0001197	dnaG_3	1	0	0	fpr:FP2_18710	ko:K02316	NA	
BLCPAMOF_01198	OG0001196	sigA_2	1	0	0	fpr:FP2_18720	ko:K03086	NA	
BLCPAMOF_01199	OG0001195	rpoB	1	0	0	fpr:FP2_18740	ko:K03043	NA	
BLCPAMOF_01200	OG0001194	rpoC	1	0	0	fpr:FP2_18750	ko:K03046	NA	
BLCPAMOF_01201	OG0001193	rpsL	1	0	0	fpr:FP2_18760	ko:K02950	NA	
BLCPAMOF_01202	OG0001192	rpsG	0	1	0	fpr:FP2_18770	ko:K02992	NA	
BLCPAMOF_01203	OG0000241	fusA_2	1	0	0	fpa:FPR_29730	ko:K02355	NA	
BLCPAMOF_01204	OG0001191	tufA	1	0	0	fpr:FP2_18790	ko:K02358	NA	
BLCPAMOF_01205	OG0001190	group_1591	1	0	0	fpa:FPR_31050	NA	NA	
BLCPAMOF_01206	OG0001957	group_1919	1	0	0	fpr:FP2_18810	NA	NA	
BLCPAMOF_01207	OG0004085	group_5180	0	1	0	NA	NA	specific_fp360	
BLCPAMOF_01208	OG0001813	panE	1	1	1	fpr:FP2_18830	ko:K00077	NA	
BLCPAMOF_01209	OG0001186	yvdD	1	0	0	fpr:FP2_18840	ko:K06966	NA	
BLCPAMOF_01210	OG0001607	group_1857	6	6	11	fpr:FP2_18850	ko:K03308	NA	
BLCPAMOF_01211	OG0000693	psuK	1	0	0	fpr:FP2_18860	ko:K16328	NA	
BLCPAMOF_01212	OG0001158	dnaC_1	1	0	0	fpr:FP2_18870	ko:K02315	NA	
BLCPAMOF_01213	OG0001157	group_1564	1	0	0	fpr:FP2_18880	NA	NA	
BLCPAMOF_01214	OG0001156	group_1563	1	0	0	fpr:FP2_18890	NA	NA	
BLCPAMOF_01216	OG0000840	group_1351	1	0	0	fpr:FP2_18900	NA	NA	
BLCPAMOF_01217	OG0000839	phnPP	1	0	0	fpr:FP2_18910	NA	NA	
BLCPAMOF_01218	OG0002080	group_5181	1	0	0	fpr:FP2_18920	NA	NA	
BLCPAMOF_01219	OG0002527	nadX	1	0	0	fpa:FPR_28370	ko:K06989	NA	
BLCPAMOF_01220	OG0002528	group_2296	1	0	0	fpa:FPR_28360	NA	NA	
BLCPAMOF_01221	OG0002025	group_2463	1	0	0	fpa:FPR_07620	NA	NA	
BLCPAMOF_01222	OG0002026	group_1597	1	0	0	fpr:FP2_18940	NA	NA	
BLCPAMOF_01223	OG0000942	group_5182	1	0	0	fpr:FP2_18950	ko:K06889	NA	
BLCPAMOF_01224	OG0002468	group_5183	1	0	0	selo:AXE86_00220	NA	NA	
BLCPAMOF_01225	OG0004086	group_5184	1	0	0	ded:DHBDCA_p182;dec:DCF50_p243	NA	specific_fp360	○
BLCPAMOF_01226	OG0002469	group_5185	1	0	0	NA	NA	NA	
BLCPAMOF_01227	OG0000008	group_128	1	0	0	fpr:FP2_28240	NA	NA	
BLCPAMOF_01228	OG0000004	group_156	1	0	0	fpa:FPR_07940	ko:K03496	NA	
BLCPAMOF_01230	OG0002581	albA	1	0	0	fpr:FP2_19170	NA	NA	
BLCPAMOF_01231	OG0001908	group_2076	1	0	0	fpa:FPR_07280	ko:K01187	NA	
BLCPAMOF_01232	OG0001060	pglC	1	1	1	fpr:FP2_19210	ko:K13012	NA	
BLCPAMOF_01233	OG0001059	aspS2	1	0	0	fpr:FP2_19240	ko:K01876	NA	
BLCPAMOF_01234	OG0000854	copA	4	5	8	fpr:FP2_19250	ko:K01533	NA	
BLCPAMOF_01235	OG0000855	csoR	0	1	0	fpr:FP2_19260	ko:K21600	NA	
BLCPAMOF_01236	OG0000811	gltB_1	1	0	0	fpr:FP2_19270	ko:K00266	NA	
BLCPAMOF_01237	OG0000812	gltB_2	1	0	0	fpr:FP2_19280	NA	NA	
BLCPAMOF_01238	OG0000813	hcp	1	0	0	fpr:FP2_19290	ko:K05601	NA	
BLCPAMOF_01239	OG0000814	gdh	1	0	0	fpr:FP2_19300	ko:K00262	NA	
BLCPAMOF_01240	OG0000816	apbC	1	0	0	fpa:FPR_21400	NA	NA	
BLCPAMOF_01241	OG0000817	spoVB	5	6	10	fpr:FP2_19320	ko:K06409	NA	
BLCPAMOF_01242	OG0000818	pglF	2	2	3	mas:Mahau_0321	NA	NA	
BLCPAMOF_01243	OG0000819	lysA	1	0	0	fpr:FP2_19340	ko:K01586	NA	
BLCPAMOF_01244	OG0000820	group_1336	1	2	2	fpr:FP2_19350	NA	NA	
BLCPAMOF_01245	OG0001163	group_5186	1	0	0	fpr:FP2_19360	NA	NA	
BLCPAMOF_01246	OG0002467	cmlA	1	0	0	fpla:A4U99_03485	ko:K19271	NA	
BLCPAMOF_01247	OG0001203	rluC_2	1	0	0	fpr:FP2_19370	ko:K06179	NA	
BLCPAMOF_01248	OG0001202	group_5187	1	0	0	fpr:FP2_19380	ko:K03630	NA	
BLCPAMOF_01249	OG0001201	uvrB	1	0	0	fpa:FPR_26430	ko:K03702	NA	
BLCPAMOF_01250	OG0001200	uvrA	1	0	0	ccel:CCDG5_1092	ko:K03701	NA	
BLCPAMOF_01251	OG0000633	group_2378	1	0	0	fpr:FP2_19420	ko:K15533	NA	
BLCPAMOF_01252	OG0000632	group_2017	1	2	2	fpr:FP2_19430	NA	NA	
BLCPAMOF_01253	OG0000631	sugB_1	3	4	6	fpr:FP2_19440	ko:K10202	NA	
BLCPAMOF_01254	OG0000630	ugpA_2	3	4	6	fpa:FPR_27500	ko:K10201	NA	
BLCPAMOF_01255	OG0000629	msmE	1	0	0	fpr:FP2_19460	ko:K10200	NA	
BLCPAMOF_01256	OG0000213	adaA_2	1	0	0	fpr:FP2_19470	NA	NA	
BLCPAMOF_01257	OG0000628	nahK	1	0	0	fpa:FPR_27470	NA	NA	
BLCPAMOF_01258	OG0000175	ndoA_2	1	0	0	NA	NA	NA	
BLCPAMOF_01259	OG0004087	group_421	1	0	0	fpr:FP2_08320	NA	NA	
BLCPAMOF_01260	OG0000177	group_3030	0	1	0	fpa:FPR_27240;fpr:FP2_08310	NA	NA	
BLCPAMOF_01261	OG0000114	xerD	1	0	0	fpa:FPR_27230	NA	NA	
BLCPAMOF_01263	OG0001049	spoIVA	1	0	0	esu:EUS_12530	ko:K06398	NA	
BLCPAMOF_01264	OG0000913	group_1394	1	0	0	fpr:FP2_08280	NA	NA	
BLCPAMOF_01265	OG0000914	rpsA_2	1	0	0	fpr:FP2_08270	NA	NA	
BLCPAMOF_01266	OG0000915	group_801	1	0	0	fpr:FP2_08260	NA	NA	
BLCPAMOF_01267	OG0000916	prfA	1	0	0	fpr:FP2_08250	ko:K02835	NA	
BLCPAMOF_01268	OG0000917	ywlC	1	0	0	fpr:FP2_08240	ko:K07566	NA	
BLCPAMOF_01269	OG0000918	coaE	1	0	0	fpr:FP2_08230	ko:K00859	NA	
BLCPAMOF_01270	OG0000919	slt	1	1	1	fpr:FP2_08220	ko:K08309	NA	
BLCPAMOF_01271	OG0000920	apeA	1	0	0	fpr:FP2_08210	NA	NA	
BLCPAMOF_01272	OG0000921	group_1400	1	1	1	fpa:FPR_28960	NA	NA	
BLCPAMOF_01274	OG0001891	group_2809	1	0	0	fpla:A4U99_12610	NA	NA	
BLCPAMOF_01275	OG0002112	group_2353	0	1	0	NA	NA	NA	
BLCPAMOF_01276	OG0000200	group_5188	0	1	0	efc:EFAU004_02772;efau:EFAU085_00740	NA	NA	
BLCPAMOF_01277	OG0002137	group_5189	1	0	0	efau:EFAU085_00739;efc:EFAU004_02773	NA	NA	
BLCPAMOF_01278	OG0002330	group_3200	3	3	5	cdl:CDR20291_1752	ko:K01992	NA	
BLCPAMOF_01279	OG0002328	walR_2	1	0	0	rum:CK1_03940	NA	NA	
BLCPAMOF_01280	OG0001953	group_933	1	0	0	rum:CK1_03930	NA	NA	
BLCPAMOF_01281	OG0001723	group_2078	1	0	0	fpla:A4U99_01480	NA	NA	
BLCPAMOF_01282	OG0000201	group_5190	0	1	0	ibu:IB211_02850c	NA	NA	
BLCPAMOF_01283	OG0000155	group_5191	1	0	0	ibu:IB211_02849c	NA	NA	
BLCPAMOF_01284	OG0002574	bspRIM	1	0	0	sdq:SDSE167_1675	ko:K00558	NA	
BLCPAMOF_01285	OG0004088	prrB	1	0	0	rim:ROI_02070	NA	specific_fp360	○
BLCPAMOF_01286	OG0004089	group_5194	1	0	0	NA	NA	specific_fp360	○
BLCPAMOF_01287	OG0000102	group_5195	0	1	0	ibu:IB211_02845	NA	NA	
BLCPAMOF_01288	OG0004090	group_5196	1	0	0	fpla:A4U99_01500	NA	specific_fp360	○
BLCPAMOF_01289	OG0002098	group_3294	1	0	0	fpla:A4U99_01500	NA	NA	
BLCPAMOF_01290	OG0002529	group_5197	1	0	0	fpla:A4U99_01500	NA	NA	
BLCPAMOF_01291	OG0004091	group_5198	1	0	0	bprm:CL3_18970	NA	specific_fp360	○
BLCPAMOF_01292	OG0000057	group_5199	1	0	0	fpla:A4U99_01515	ko:K03169	NA	
BLCPAMOF_01294	OG0000922	spoIVB	1	1	1	fpr:FP2_08190	ko:K06399	NA	
BLCPAMOF_01295	OG0000923	spo0A	1	0	0	fpr:FP2_08180	ko:K07699	NA	
BLCPAMOF_01296	OG0002314	natR_2	1	0	0	fpr:FP2_08170	NA	NA	
BLCPAMOF_01297	OG0003227	group_5201	4	4	7	rix:RO1_25930;rim:ROI_37330	NA	NA	
BLCPAMOF_01298	OG0004092	group_5202	1	1	1	rix:RO1_25940	NA	specific_fp360	
BLCPAMOF_01299	OG0000924	rpmE	0	1	0	fpa:FPR_28670	ko:K02909	NA	
BLCPAMOF_01300	OG0000925	yxlF_2	1	0	0	ova:OBV_00490	ko:K01990	NA	
BLCPAMOF_01301	OG0000926	group_1401	4	5	8	fpr:FP2_08120	ko:K01992	NA	
BLCPAMOF_01302	OG0000927	group_2426	1	2	2	fpr:FP2_08110	ko:K01992	NA	
BLCPAMOF_01303	OG0000928	group_5203	1	1	1	fpr:FP2_08100	NA	NA	
BLCPAMOF_01304	OG0000224	potA_1	1	0	0	fpr:FP2_08090	ko:K11072	NA	
BLCPAMOF_01305	OG0000225	potH	3	4	6	fpr:FP2_08080	ko:K11071	NA	
BLCPAMOF_01306	OG0000929	ydcV	3	4	6	fpr:FP2_08070	ko:K11070	NA	
BLCPAMOF_01307	OG0000930	potD	1	2	2	fpr:FP2_08060	ko:K11069	NA	

BLCPAMOF_01308	OG0000931	group_5204	1	0	0	fpr:FP2_08050	NA	NA	
BLCPAMOF_01309	OG0000166	guaB	1	0	0	fpr:FP2_08030	ko:K00088	NA	
BLCPAMOF_01310	OG0000167	pncB2	1	0	0	fpr:FP2_08020	ko:K00763	NA	
BLCPAMOF_01312	OG0002013	ttcA	1	0	0	fpr:FP2_06910	NA	NA	
BLCPAMOF_01313	OG0000932	iscS_2	1	0	0	fpr:FP2_06920	ko:K04487	NA	
BLCPAMOF_01314	OG0000933	pyrP	6	7	12	fpr:FP2_06930	ko:K02824	NA	
BLCPAMOF_01315	OG0000934	rbr3B	1	0	0	fpr:FP2_06940	NA	NA	
BLCPAMOF_01316	OG0000902	group_5205	1	0	0	fpr:FP2_06950	ko:K07141	NA	
BLCPAMOF_01317	OG0000903	coxM	1	0	0	fpr:FP2_06960	NA	NA	
BLCPAMOF_01318	OG0000904	hcrC	1	0	0	fpr:FP2_06970	ko:K03518	NA	
BLCPAMOF_01319	OG0000905	xdhA	1	0	0	fpr:FP2_06980	NA	NA	
BLCPAMOF_01320	OG0000906	group_2062	1	0	0	fpr:FP2_06990	NA	NA	
BLCPAMOF_01321	OG0000907	selD	1	0	0	fpr:FP2_07000	ko:K01008	NA	
BLCPAMOF_01322	OG0000908	group_622	1	0	0	fpr:FP2_07010	NA	NA	
BLCPAMOF_01323	OG0000909	csdA	1	0	0	cct:CC1_06390	NA	NA	
BLCPAMOF_01324	OG0000910	group_5206	0	1	0	fpr:FP2_07030	NA	NA	
BLCPAMOF_01325	OG0000911	group_5207	1	0	0	fpr:FP2_07040	ko:K07402	NA	
BLCPAMOF_01326	OG0000912	group_800	1	0	0	fpr:FP2_07050	ko:K07402	NA	
BLCPAMOF_01327	OG0001048	group_5208	1	0	0	fpr:FP2_07060	ko:K00067	NA	
BLCPAMOF_01328	OG0001047	group_814	2	2	3	fpr:FP2_07070	NA	NA	
BLCPAMOF_01329	OG0001046	ygaZ	3	4	6	fpr:FP2_07080	NA	NA	
BLCPAMOF_01330	OG0001045	group_3295	2	2	3	NA	NA	NA	
BLCPAMOF_01331	OG0001044	pdg	1	0	0	fpr:FP2_07100	ko:K10773	NA	
BLCPAMOF_01332	OG0001043	group_1478	1	0	0	fpr:FP2_07110	ko:K07478	NA	
BLCPAMOF_01333	OG0001042	perR_2	1	0	0	fpr:FP2_07120	ko:K09825	NA	
BLCPAMOF_01334	OG0001041	miaB	1	0	0	ruk:A4V00_02495	ko:K06168	NA	
BLCPAMOF_01335	OG0001040	group_1475	1	0	0	fpr:FP2_07140	NA	NA	
BLCPAMOF_01336	OG0001039	mutS_2	1	0	0	fpa:FPR_31510	ko:K03555	NA	
BLCPAMOF_01337	OG0001038	mutL	1	0	0	fpr:FP2_07170	ko:K03572	NA	
BLCPAMOF_01338	OG0001037	miaA	1	0	0	rch:RUM_08860	ko:K00791	NA	
BLCPAMOF_01339	OG0001036	group_1473	1	1	1	fpa:FPR_31480	NA	NA	
BLCPAMOF_01340	OG0001035	sepF	1	0	0	fpr:FP2_07200	ko:K09772	NA	
BLCPAMOF_01341	OG0001034	group_1471	1	0	0	fpr:FP2_07210	NA	NA	
BLCPAMOF_01342	OG0001033	gpsB	1	0	0	fpr:FP2_07220	ko:K04074	NA	
BLCPAMOF_01343	OG0001032	ileS	1	0	0	eha:Ethha_0701	ko:K01870	NA	
BLCPAMOF_01344	OG0001031	lspA	2	3	4	fpr:FP2_07240	ko:K03101	NA	
BLCPAMOF_01345	OG0001030	rluD_1	1	0	0	fpr:FP2_07250	ko:K06180	NA	
BLCPAMOF_01346	OG0001029	group_5209	1	0	0	fpr:FP2_07260	NA	NA	
BLCPAMOF_01347	OG0001028	group_5210	1	1	1	fpr:FP2_07270	ko:K02237	NA	
BLCPAMOF_01348	OG0000228	ppk	1	0	0	fpr:FP2_07280	ko:K00937	NA	
BLCPAMOF_01349	OG0001027	mepM_1	1	1	1	fpa:FPR_31380	NA	NA	
BLCPAMOF_01350	OG0001026	group_635	2	2	3	fpr:FP2_07300	NA	NA	
BLCPAMOF_01351	OG0001025	group_1464	1	0	0	fpr:FP2_07310	NA	NA	
BLCPAMOF_01352	OG0001024	group_1463	1	0	0	fpr:FP2_07320	NA	NA	
BLCPAMOF_01353	OG0001023	rplS	1	0	0	fpr:FP2_07330	ko:K02884	NA	
BLCPAMOF_01354	OG0000227	sipT	1	1	1	fpr:FP2_07340	ko:K03100	NA	
BLCPAMOF_01355	OG0001022	rbgA	1	0	0	fpr:FP2_07350	ko:K14540	NA	
BLCPAMOF_01356	OG0001021	rnhB	1	0	0	fpr:FP2_07360	ko:K03470	NA	
BLCPAMOF_01357	OG0001020	group_1459	0	1	0	fpr:FP2_07370	ko:K07460	NA	
BLCPAMOF_01358	OG0001019	thrC	1	0	0	fpr:FP2_07380	ko:K01733	NA	
BLCPAMOF_01359	OG0001018	cpdA_2	1	0	0	fpr:FP2_07390	ko:K07099	NA	
BLCPAMOF_01360	OG0001017	tig_2	1	0	0	fpr:FP2_07400	ko:K03545	NA	
BLCPAMOF_01361	OG0001016	clpP	1	0	0	fpr:FP2_07410	ko:K01358	NA	
BLCPAMOF_01362	OG0001015	clpX	1	0	0	fpr:FP2_07420	ko:K03544	NA	
BLCPAMOF_01363	OG0001014	group_1454	1	0	0	fpr:FP2_07430	NA	NA	
BLCPAMOF_01364	OG0001013	group_1453	6	7	12	fpr:FP2_07440	ko:K12257	NA	
BLCPAMOF_01365	OG0001012	nrdR	1	0	0	fpr:FP2_07450	ko:K07738	NA	
BLCPAMOF_01366	OG0001011	group_1451	1	1	1	fpr:FP2_07460	NA	NA	
BLCPAMOF_01367	OG0001010	group_1450	1	2	2	fpa:FPR_31200	NA	NA	
BLCPAMOF_01368	OG0001009	gerBA	2	3	4	fpa:FPR_31190	ko:K06295	NA	
BLCPAMOF_01369	OG0001008	group_5211	3	4	6	fpr:FP2_07500	NA	NA	
BLCPAMOF_01370	OG0001007	group_5212	1	1	1	fpr:FP2_07510	NA	NA	
BLCPAMOF_01371	OG0001006	senX3	2	1	2	fpr:FP2_07520	ko:K07636	NA	
BLCPAMOF_01372	OG0001005	phoB	1	0	0	fpr:FP2_07530	ko:K07658	NA	
BLCPAMOF_01373	OG0001004	group_1447	5	5	9	fpr:FP2_07540	ko:K03324	NA	
BLCPAMOF_01374	OG0001003	hprK	1	0	0	fpr:FP2_07550	ko:K06023	NA	
BLCPAMOF_01375	OG0001002	murB	1	0	0	fpr:FP2_07560	ko:K00075	NA	
BLCPAMOF_01376	OG0001001	yvcJ	1	0	0	fpr:FP2_07570	ko:K06958	NA	
BLCPAMOF_01377	OG0001000	whiA	1	0	0	fpr:FP2_07580	ko:K09762	NA	
BLCPAMOF_01378	OG0000999	dnaE	1	0	0	fpr:FP2_07590	ko:K02337	NA	
BLCPAMOF_01379	OG0000998	pfkA	1	0	0	fpr:FP2_07600	ko:K00850	NA	
BLCPAMOF_01380	OG0000997	ligA	1	0	0	ruk:A4V00_16770	ko:K01972	NA	
BLCPAMOF_01381	OG0000996	group_5213	1	0	0	fpr:FP2_07620	ko:K06390	NA	
BLCPAMOF_01382	OG0000995	group_5214	1	0	0	fpa:FPR_30300	NA	NA	
BLCPAMOF_01383	OG0000994	group_2072	2	1	2	fpr:FP2_07640	ko:K06392	NA	
BLCPAMOF_01384	OG0000993	group_5215	1	1	1	fpr:FP2_07650	ko:K06393	NA	
BLCPAMOF_01385	OG0000992	group_5216	4	4	7	fpr:FP2_07660	ko:K06394	NA	
BLCPAMOF_01386	OG0000991	group_5217	1	0	0	fpr:FP2_07670	NA	NA	
BLCPAMOF_01387	OG0000990	group_5218	1	1	1	fpr:FP2_07680	ko:K06396	NA	
BLCPAMOF_01388	OG0000989	group_1442	1	1	1	fpr:FP2_07690	ko:K06397	NA	
BLCPAMOF_01389	OG0000960	group_805	1	0	0	fpr:FP2_07700	NA	NA	
BLCPAMOF_01390	OG0000961	nusB	1	0	0	fpr:FP2_07710	ko:K03625	NA	
BLCPAMOF_01391	OG0000962	tsaD_1	1	0	0	rus:RBI_I01341	ko:K01409	NA	
BLCPAMOF_01392	OG0000963	xseA	1	0	0	eha:Ethha_1210	ko:K03601	NA	
BLCPAMOF_01393	OG0000964	xseB	1	0	0	fpr:FP2_07740	ko:K03602	NA	
BLCPAMOF_01394	OG0000965	group_1425	1	0	0	fpr:FP2_07750	ko:K13789	NA	
BLCPAMOF_01395	OG0000966	group_1426	2	2	3	fpr:FP2_07760	ko:K09775	NA	
BLCPAMOF_01396	OG0000967	dxs_2	1	0	0	fpr:FP2_07770	ko:K01662	NA	
BLCPAMOF_01397	OG0001955	tlyA	1	0	0	eha:Ethha_1215	ko:K06442	NA	
BLCPAMOF_01398	OG0000968	nadK	1	0	0	fpr:FP2_07790	ko:K00858	NA	
BLCPAMOF_01399	OG0000969	argR	1	0	0	fpr:FP2_07800	ko:K03402	NA	
BLCPAMOF_01400	OG0000970	recN	1	0	0	fpr:FP2_07810	ko:K03631	NA	
BLCPAMOF_01401	OG0000971	tyrS	1	0	0	fpr:FP2_07820	ko:K01866	NA	
BLCPAMOF_01402	OG0000972	lysC	1	0	0	fpr:FP2_07830	ko:K00928	NA	
BLCPAMOF_01403	OG0002015	capA	1	1	1	fpr:FP2_07840	ko:K07282	NA	
BLCPAMOF_01404	OG0000973	dapB	1	0	0	fpr:FP2_07850	ko:K00215	NA	
BLCPAMOF_01405	OG0000974	dapA	1	0	0	fpr:FP2_07860	ko:K01714	NA	
BLCPAMOF_01406	OG0000975	asd	1	0	0	fpr:FP2_07870	ko:K00133	NA	
BLCPAMOF_01407	OG0000976	queA	1	0	0	fpr:FP2_07880	ko:K07568	NA	
BLCPAMOF_01408	OG0000977	tgt	1	0	0	fpr:FP2_07890	ko:K00773	NA	
BLCPAMOF_01409	OG0000978	group_2070	1	1	1	fpr:FP2_07900	ko:K03210	NA	
BLCPAMOF_01410	OG0000979	group_5219	2	3	4	fpr:FP2_07910	NA	NA	
BLCPAMOF_01411	OG0000980	group_5220	3	3	5	fpr:FP2_07920	NA	NA	
BLCPAMOF_01412	OG0000988	radA	1	0	0	fpr:FP2_07930	ko:K04485	NA	
BLCPAMOF_01413	OG0000987	xerC_6	1	0	0	fpa:FPR_30620	NA	NA	
BLCPAMOF_01414	OG0004093	group_5221	1	0	0	NA	NA	specific_fp360	O
BLCPAMOF_01415	OG0000986	amiB	1	0	0	cpro:CPRO_01620	ko:K01448	NA	
BLCPAMOF_01416	OG0000985	mutS2	1	0	0	fpa:FPR_30640	ko:K07456	NA	
BLCPAMOF_01417	OG0000984	recO	1	0	0	fpr:FP2_07980	ko:K03584	NA	
BLCPAMOF_01418	OG0002961	group_5222	1	0	0	NA	NA	NA	
BLCPAMOF_01419	OG0000983	era	1	0	0	rus:RBI_I00964	ko:K03595	NA	
BLCPAMOF_01420	OG0000982	ybeY	1	0	0	fpr:FP2_08000	ko:K07042	NA	
BLCPAMOF_01421	OG0000981	group_1437	1	0	0	fpr:FP2_08010	ko:K06217	NA	
BLCPAMOF_01422	OG0002171	group_5223	0	1	0	NA	NA	NA	

BLCPAMOF_01423	OG0000108	group_517	0	1	0	fpr:FP2_06470	NA	NA	
BLCPAMOF_01424	OG0003188	group_3108	1	2	2	ruk:A4V00_13095	NA	NA	
BLCPAMOF_01425	OG0001776	group_3296	0	1	0	fpr:FP2_05470	NA	NA	
BLCPAMOF_01426	OG0003564	group_3298	0	1	0	NA	NA	specific_fp360	○
BLCPAMOF_01427	OG0003565	group_3300	1	1	1	NA	NA	specific_fp360	○
BLCPAMOF_01428	OG0004094	group_5224	1	0	0	NA	NA	specific_fp360	○
BLCPAMOF_01429	OG0001682	group_5225	1	0	0	NA	NA	NA	
BLCPAMOF_01430	OG0003530	group_5226	1	0	0	NA	NA	NA	
BLCPAMOF_01431	OG0000267	group_5227	0	1	0	NA	NA	NA	
BLCPAMOF_01432	OG0002171	group_5228	1	0	0	fpr:FP2_04820	NA	NA	
BLCPAMOF_01433	OG0004095	group_5229	1	0	0	NA	NA	specific_fp360	○
BLCPAMOF_01434	OG0004096	group_5230	1	0	0	bca:BCE_0423	NA	specific_fp360	○
BLCPAMOF_01435	OG0003566	group_3302	1	0	0	med:MELS_1429	NA	NA	
BLCPAMOF_01436	OG0001919	group_2230	1	1	1	fpr:FP2_13220	NA	NA	
BLCPAMOF_01437	OG0004097	group_5231	1	0	0	NA	NA	specific_fp360	○
BLCPAMOF_01438	OG0003567	cetB	1	0	0	rto:RTO_19310	ko:K08234	specific_fp360	○
BLCPAMOF_01439	OG0003568	group_3303	2	2	3	NA	NA	NA	
BLCPAMOF_01440	OG0000071	traC	1	0	0	rob:CK5_08830	NA	NA	
BLCPAMOF_01441	OG0001915	mutS_3	1	0	0	NA	NA	NA	
BLCPAMOF_01442	OG0002171	group_5233	1	0	0	NA	NA	NA	
BLCPAMOF_01443	OG0002962	group_5235	1	0	0	NA	NA	NA	
BLCPAMOF_01444	OG0002171	group_5234	1	0	0	NA	NA	NA	
BLCPAMOF_01445	OG0002530	group_5236	1	0	0	NA	NA	NA	
BLCPAMOF_01447	OG0000959	group_5237	3	3	5	fpr:FP2_06450	NA	NA	
BLCPAMOF_01448	OG0000958	group_2068	0	1	0	fpa:FPR_24710	NA	NA	
BLCPAMOF_01449	OG0000957	group_5238	1	1	1	fpr:FP2_06430	ko:K06438	NA	
BLCPAMOF_01450	OG0000956	hslO	1	0	0	fpr:FP2_06420	ko:K04083	NA	
BLCPAMOF_01451	OG0000955	group_1422	1	0	0	fpr:FP2_06410	NA	NA	
BLCPAMOF_01452	OG0000954	engB	1	0	0	fpr:FP2_06400	ko:K03978	NA	
BLCPAMOF_01453	OG0000953	lon1	1	0	0	fpr:FP2_06390	ko:K01338	NA	
BLCPAMOF_01454	OG0000952	group_1419	3	3	5	fpr:FP2_06380	ko:K00805	NA	
BLCPAMOF_01455	OG0000951	yheS	1	0	0	fpr:FP2_06370	ko:K06158	NA	
BLCPAMOF_01456	OG0000950	yfnB	1	0	0	fpr:FP2_06360	ko:K01560	NA	
BLCPAMOF_01457	OG0000949	group_5239	1	0	0	fpr:FP2_06350	NA	NA	
BLCPAMOF_01458	OG0000948	group_2067	1	1	1	fpr:FP2_06340	NA	NA	
BLCPAMOF_01459	OG0000947	group_1416	1	0	0	fpa:FPR_24590	ko:K01091	NA	
BLCPAMOF_01460	OG0000946	group_1415	0	1	0	fpr:FP2_06320	NA	NA	
BLCPAMOF_01461	OG0000945	group_1414	0	1	0	fpr:FP2_06310	NA	NA	
BLCPAMOF_01462	OG0000944	cstA_1	8	8	15	fpr:FP2_06300	ko:K06200	NA	
BLCPAMOF_01463	OG0000943	mshD_1	1	0	0	fpr:FP2_06290	NA	NA	
BLCPAMOF_01464	OG0000941	tsf	1	0	0	fpr:FP2_06280	ko:K02357	NA	
BLCPAMOF_01465	OG0000940	rpsB	1	0	0	fpr:FP2_06270	ko:K02967	NA	
BLCPAMOF_01466	OG0000939	ltaS1	3	3	5	fpr:FP2_06260	NA	NA	
BLCPAMOF_01467	OG0000938	group_5240	1	0	0	fpr:FP2_06250	NA	NA	
BLCPAMOF_01468	OG0000937	hdl IVa	1	0	0	fpr:FP2_06240	NA	NA	
BLCPAMOF_01469	OG0000936	group_1409	0	1	0	fpr:FP2_06230	NA	NA	
BLCPAMOF_01470	OG0000935	group_2065	1	0	0	fpr:FP2_06220	NA	NA	
BLCPAMOF_01471	OG0000226	group_1408	4	4	7	fpr:FP2_06210	NA	NA	
BLCPAMOF_01472	OG0000901	xanP	7	7	13	fpr:FP2_06200	NA	NA	
BLCPAMOF_01473	OG0002531	group_5241	1	1	1	fpr:FP2_06180	NA	NA	
BLCPAMOF_01474	OG0000900	group_2423	1	0	0	fpr:FP2_06170	NA	NA	
BLCPAMOF_01475	OG0004098	group_5242	1	1	1	NA	NA	specific_fp360	○
BLCPAMOF_01476	OG0001926	group_5243	1	1	1	NA	NA	NA	
BLCPAMOF_01477	OG0001956	group_5244	1	0	0	fpr:FP2_06160	NA	NA	
BLCPAMOF_01478	OG0004099	group_5245	1	0	0	NA	NA	specific_fp360	○
BLCPAMOF_01479	OG0000880	thiN	1	0	0	fpr:FP2_06140	ko:K00949	NA	
BLCPAMOF_01480	OG0004100	group_5246	1	0	0	NA	NA	specific_fp360	
BLCPAMOF_01481	OG0000879	rsgA	1	0	0	fpr:FP2_06130	ko:K06949	NA	
BLCPAMOF_01482	OG0000878	prkC_1	1	1	1	fpr:FP2_06120	ko:K12132	NA	
BLCPAMOF_01483	OG0000877	stp	1	0	0	fpr:FP2_06110	ko:K20074	NA	
BLCPAMOF_01484	OG0000876	rlmN	1	0	0	fpr:FP2_06100	ko:K06941	NA	
BLCPAMOF_01485	OG0000875	rsmB	1	0	0	fpa:FPR_30200	ko:K03500	NA	
BLCPAMOF_01486	OG0000874	fmt	1	0	0	fpr:FP2_06080	ko:K00604	NA	
BLCPAMOF_01487	OG0000873	def1	1	0	0	fpr:FP2_06070	ko:K01462	NA	
BLCPAMOF_01488	OG0000872	priA	1	0	0	fpr:FP2_06060	ko:K04066	NA	
BLCPAMOF_01489	OG0000871	gmk	1	0	0	fpr:FP2_06050	ko:K00942	NA	
BLCPAMOF_01490	OG0000870	group_1370	1	0	0	fpr:FP2_06040	ko:K09777	NA	
BLCPAMOF_01491	OG0000869	group_1369	1	0	0	fpr:FP2_06030	NA	NA	
BLCPAMOF_01492	OG0000868	group_2418	1	0	0	fpr:FP2_06020	ko:K01571	NA	
BLCPAMOF_01493	OG0000867	gcdC	1	0	0	fpr:FP2_06010	NA	NA	
BLCPAMOF_01494	OG0000866	group_1367	1	0	0	fpr:FP2_06000	NA	NA	
BLCPAMOF_01495	OG0000865	rluB	1	0	0	fpr:FP2_05990	ko:K06178	NA	
BLCPAMOF_01496	OG0000864	ytfJ	1	0	0	fpr:FP2_05980	NA	NA	
BLCPAMOF_01497	OG0000863	group_5247	1	1	1	fpr:FP2_05950	NA	NA	
BLCPAMOF_01498	OG0000862	scpB	1	0	0	fpr:FP2_05940	ko:K06024	NA	
BLCPAMOF_01499	OG0000861	scpA	1	0	0	fpr:FP2_05930	ko:K05896	NA	
BLCPAMOF_01500	OG0000860	group_1363	3	3	5	fpr:FP2_05920	NA	NA	
BLCPAMOF_01501	OG0000859	rpmB	0	1	0	fpr:FP2_05910	ko:K02902	NA	
BLCPAMOF_01502	OG0000858	group_794	1	0	0	fpr:FP2_05900	NA	NA	
BLCPAMOF_01503	OG0000857	group_620	1	0	0	fpr:FP2_05890	NA	NA	
BLCPAMOF_01504	OG0000856	group_2057	1	0	0	fpr:FP2_05880	NA	NA	
BLCPAMOF_01505	OG0000810	prkC_2	1	1	1	fpr:FP2_05860	ko:K12132	NA	
BLCPAMOF_01506	OG0002595	group_2959	1	0	0	tde:TDE1635	ko:K09803	NA	
BLCPAMOF_01507	OG0003225	group_2291	1	0	0	NA	NA	NA	
BLCPAMOF_01508	OG0002957	group_2289	1	0	0	NA	NA	NA	
BLCPAMOF_01509	OG0000113	group_2663	1	0	0	avu:BK816_07010	NA	NA	
BLCPAMOF_01510	OG0003224	group_2286	1	0	0	NA	NA	NA	
BLCPAMOF_01511	OG0002525	group_2283	1	0	0	byl:A4V09_22095	NA	NA	
BLCPAMOF_01512	OG0003223	group_2661	1	0	0	NA	NA	NA	
BLCPAMOF_01513	OG0000029	group_388	1	0	0	fpa:FPR_02700;fpa:FPR_19400	ko:K03431	NA	
BLCPAMOF_01514	OG0002343	group_1942	1	0	0	fro:AALO17_22620	NA	NA	
BLCPAMOF_01515	OG0002343	group_1940	0	1	0	NA	NA	NA	
BLCPAMOF_01516	OG0000274	group_2251	1	1	1	fpr:FP2_05850	NA	NA	
BLCPAMOF_01517	OG0000809	group_2413	1	0	0	fpr:FP2_05840	NA	NA	
BLCPAMOF_01518	OG0000808	rsmF	1	0	0	fpr:FP2_05830	NA	NA	
BLCPAMOF_01519	OG0002008	group_3215	0	1	0	NA	NA	NA	
BLCPAMOF_01520	OG0001715	mrnC	1	0	0	fpr:FP2_05810	ko:K11145	NA	
BLCPAMOF_01521	OG0000807	obg	1	0	0	fpr:FP2_05800	ko:K03979	NA	
BLCPAMOF_01522	OG0000806	rpmA	1	0	0	fpr:FP2_05790	ko:K02899	NA	
BLCPAMOF_01523	OG0000805	rplU	1	0	0	fpr:FP2_05780	ko:K02888	NA	
BLCPAMOF_01524	OG0000803	lgt	4	4	7	fpr:FP2_05750	ko:K13292	NA	
BLCPAMOF_01525	OG0000802	group_1325	1	0	0	fpr:FP2_05740	NA	NA	
BLCPAMOF_01526	OG0000801	group_1324	1	0	0	NA	NA	NA	
BLCPAMOF_01527	OG0000800	vanYB_1	1	1	1	fpa:FPR_21090	ko:K07260	NA	
BLCPAMOF_01528	OG0000838	group_1349	1	0	0	fpr:FP2_05710	ko:K00928	NA	
BLCPAMOF_01529	OG0000837	thrB	1	0	0	fpr:FP2_05700	ko:K00872	NA	
BLCPAMOF_01530	OG0000836	hom	1	0	0	fpr:FP2_05690	ko:K00003	NA	
BLCPAMOF_01531	OG0000835	group_2055	1	0	0	ccel:CCDG5_0140	ko:K06209	NA	
BLCPAMOF_01532	OG0000834	pbpF	1	0	0	fpa:FPR_21040	ko:K05366	NA	
BLCPAMOF_01533	OG0000833	group_5249	1	1	1	fpr:FP2_05650	NA	NA	
BLCPAMOF_01534	OG0000829	phoU_2	5	5	9	fpr:FP2_05640	ko:K03324	NA	
BLCPAMOF_01535	OG0002009	group_1342	1	0	0	fpr:FP2_05630	NA	NA	
BLCPAMOF_01536	OG0002080	group_5250	1	0	0	fpr:FP2_05620	NA	NA	
BLCPAMOF_01537	OG0000830	group_1343	1	0	0	fpr:FP2_05610	NA	NA	

BLCPAMOF_01538	OG0000831	group_1344	1	0	0	fpr:FP2_05600	NA	NA	
BLCPAMOF_01539	OG0000832	group_1345	1	0	0	fpr:FP2_05590	ko:K07030	NA	
BLCPAMOF_01540	OG0000828	polC_2	1	0	0	fpr:FP2_05580	ko:K03763	NA	
BLCPAMOF_01541	OG0000827	ispG	1	0	0	fpr:FP2_05560	ko:K03526	NA	
BLCPAMOF_01542	OG0000826	rasP	2	3	4	fpr:FP2_05550	ko:K11749	NA	
BLCPAMOF_01543	OG0000825	dxr	1	0	0	fpr:FP2_05540	ko:K00099	NA	
BLCPAMOF_01544	OG0000824	cdsA	5	5	9	fpr:FP2_05530	ko:K00981	NA	
BLCPAMOF_01545	OG0000823	uppS	1	0	0	fpr:FP2_05520	ko:K00806	NA	
BLCPAMOF_01546	OG0000822	frr	1	0	0	fpr:FP2_05510	ko:K02838	NA	
BLCPAMOF_01547	OG0000821	pyrH	1	0	0	fpr:FP2_05500	ko:K09903	NA	
BLCPAMOF_01549	OG0000108	group_514	0	1	0	fpr:FP2_14360	NA	NA	
BLCPAMOF_01550	OG0002345	group_2670	1	1	1	fpa:FPR_13580	NA	NA	
BLCPAMOF_01551	OG0001776	group_3297	0	1	0	fpr:FP2_05470	NA	NA	
BLCPAMOF_01552	OG0003564	group_3299	0	1	0	NA	NA	specific_fp360	○
BLCPAMOF_01553	OG0003565	group_3301	0	1	0	NA	NA	specific_fp360	○
BLCPAMOF_01554	OG0004101	group_5251	1	0	0	NA	NA	specific_fp360	○
BLCPAMOF_01555	OG0000138	group_5252	1	0	0	fpa:FPR_13540	NA	NA	
BLCPAMOF_01556	OG0000230	group_1495	1	0	0	fpr:FP2_05450	ko:K07576	NA	
BLCPAMOF_01557	OG0001069	typA	1	0	0	fpr:FP2_05440	ko:K06207	NA	
BLCPAMOF_01558	OG0004102	group_5253	1	0	0	NA	NA	specific_fp360	○
BLCPAMOF_01559	OG0001070	group_817	1	1	1	fpr:FP2_05430	NA	NA	
BLCPAMOF_01560	OG0001071	group_1496	1	0	0	fpr:FP2_05420	ko:K21071	NA	
BLCPAMOF_01561	OG0001072	pfp_2	1	0	0	fpr:FP2_05410	ko:K21071	NA	
BLCPAMOF_01562	OG0001061	mepA_10	5	6	10	fpr:FP2_05400	NA	NA	
BLCPAMOF_01563	OG0001062	group_816	1	0	0	fpr:FP2_05380	NA	NA	
BLCPAMOF_01564	OG0001063	yurK	1	0	0	fpr:FP2_05370	ko:K03710	NA	
BLCPAMOF_01565	OG0001064	pyrB_2	1	0	0	fpr:FP2_05360	ko:K00609	NA	
BLCPAMOF_01566	OG0001065	pyrI	1	0	0	fpr:FP2_05350	ko:K00610	NA	
BLCPAMOF_01567	OG0001096	ydcP_2	1	0	0	fpr:FP2_05340	ko:K08303	NA	
BLCPAMOF_01568	OG0001097	mltG	1	1	1	fpr:FP2_05330	ko:K07082	NA	
BLCPAMOF_01569	OG0001098	group_1522	1	0	0	fpr:FP2_05320	NA	NA	
BLCPAMOF_01570	OG0001099	tmk	1	0	0	fpr:FP2_05310	ko:K00943	NA	
BLCPAMOF_01571	OG0000232	thyX	1	0	0	fpr:FP2_05300	ko:K03465	NA	
BLCPAMOF_01572	OG0001100	pcrA	1	0	0	fpr:FP2_05290	ko:K03657	NA	
BLCPAMOF_01573	OG0001101	gcdB_1	5	5	9	fpr:FP2_05280	ko:K01572	NA	
BLCPAMOF_01574	OG0001102	group_1526	1	1	1	fpr:FP2_05270	NA	NA	
BLCPAMOF_01575	OG0001103	mreB_2	1	0	0	fpr:FP2_05260	ko:K03569	NA	
BLCPAMOF_01576	OG0001104	recD2	1	0	0	fpr:FP2_05250	ko:K03581	NA	
BLCPAMOF_01577	OG0001105	mepA_8	5	6	10	fpr:FP2_05240	NA	NA	
BLCPAMOF_01578	OG0002080	group_5254	1	1	1	fpr:FP2_05230	NA	NA	
BLCPAMOF_01579	OG0004103	group_5255	1	0	0	fpr:FP2_05230	NA	specific_fp360	
BLCPAMOF_01580	OG0002080	group_5256	1	1	1	fpr:FP2_05230	NA	NA	
BLCPAMOF_01581	OG0001106	tcyC	1	0	0	fpr:FP2_05210	ko:K02028	NA	
BLCPAMOF_01582	OG0001107	tcyB_2	3	2	4	ctx:Clo1313_0794;cth:Cthe_1457	ko:K02029	NA	
BLCPAMOF_01583	OG0001108	fliY_2	1	0	0	fpr:FP2_05190	ko:K02030	NA	
BLCPAMOF_01584	OG0001109	group_5257	1	0	0	fpr:FP2_05170	NA	NA	
BLCPAMOF_01585	OG0001110	ywiE_1	2	2	3	fpr:FP2_05150	ko:K06131	NA	
BLCPAMOF_01586	OG0001111	group_821	1	0	0	fpr:FP2_05140	NA	NA	
BLCPAMOF_01587	OG0001112	group_822	1	0	0	fpr:FP2_05130	NA	NA	
BLCPAMOF_01588	OG0001167	prfB	1	0	0	fpr:FP2_05120	ko:K02836	NA	
BLCPAMOF_01589	OG0001168	group_2459	3	2	4	fpr:FP2_05110	NA	NA	
BLCPAMOF_01590	OG0001169	gtaB	1	0	0	fpr:FP2_05100	ko:K00963	NA	
BLCPAMOF_01591	OG0001085	rpsR	1	0	0	fpr:FP2_05090	ko:K02963	NA	
BLCPAMOF_01592	OG0000134	ssb	1	0	0	fpr:FP2_05080	ko:K03111	NA	
BLCPAMOF_01593	OG0001084	rpsF	1	0	0	fpr:FP2_05070	ko:K02990	NA	
BLCPAMOF_01594	OG0001083	gerN	6	5	10	fpr:FP2_05060	NA	NA	
BLCPAMOF_01595	OG0000849	mggB	1	0	0	ibu:IB211_02952c	NA	NA	
BLCPAMOF_01596	OG0000848	group_618	1	0	0	fpr:FP2_05040	ko:K10254	NA	
BLCPAMOF_01597	OG0001477	group_5258	1	0	0	fpr:FP2_05030	NA	NA	
BLCPAMOF_01598	OG0000847	rnr	1	0	0	fpr:FP2_05020	ko:K12573	NA	
BLCPAMOF_01599	OG0000846	secG	1	2	2	fpr:FP2_05010	ko:K03075	NA	
BLCPAMOF_01600	OG0000845	spoVD_3	1	1	1	fpr:FP2_05000	ko:K05515	NA	
BLCPAMOF_01601	OG0000844	groL	1	0	0	fpr:FP2_04990	ko:K04077	NA	
BLCPAMOF_01602	OG0000843	groS	1	0	0	fpr:FP2_04980	ko:K04078	NA	
BLCPAMOF_01603	OG0002018	group_3206	1	0	0	fpr:FP2_04970	NA	NA	
BLCPAMOF_01604	OG0002017	group_2450	1	0	0	fpr:FP2_04960	NA	NA	
BLCPAMOF_01605	OG0001136	group_1550	1	0	0	fpr:FP2_04950	NA	NA	
BLCPAMOF_01606	OG0000842	bmrU	1	0	0	fpa:FPR_21840	NA	NA	
BLCPAMOF_01607	OG0000841	clpC_1	1	0	0	fpr:FP2_04930	ko:K03696	NA	
BLCPAMOF_01609	OG0000850	group_1359	1	0	0	fpr:FP2_04320	NA	NA	
BLCPAMOF_01610	OG0000851	group_2907	0	1	0	fpr:FP2_04270	NA	NA	
BLCPAMOF_01611	OG0000852	group_1360	1	0	0	fpr:FP2_04260	ko:K06871	NA	
BLCPAMOF_01612	OG0000853	group_5260	1	0	0	fpr:FP2_04250	NA	NA	
BLCPAMOF_01613	OG0000758	gcdB_2	6	5	10	fpr:FP2_04240	ko:K01572	NA	
BLCPAMOF_01614	OG0000759	group_774	1	1	1	NA	NA	NA	
BLCPAMOF_01615	OG0004104	group_5261	1	0	0	NA	NA	specific_fp360	○
BLCPAMOF_01616	OG0000272	cobC_2	1	0	0	sub:SUB0839	ko:K15634	NA	
BLCPAMOF_01617	OG0004105	group_5263	0	1	0	NA	NA	specific_fp360	○
BLCPAMOF_01618	OG0002094	group_2643	1	0	0	fpa:FPR_15280;fpr:FP2_10980	NA	NA	
BLCPAMOF_01619	OG0002095	group_3249	1	0	0	fpr:FP2_10990	NA	NA	
BLCPAMOF_01620	OG0004106	group_5264	0	1	0	NA	NA	specific_fp360	○
BLCPAMOF_01621	OG0002532	group_5265	1	0	0	fpr:FP2_11010	NA	NA	
BLCPAMOF_01622	OG0004107	group_5266	1	0	0	NA	NA	specific_fp360	○
BLCPAMOF_01623	OG0004108	group_5267	0	1	0	NA	NA	specific_fp360	○
BLCPAMOF_01624	OG0001782	group_2585	0	1	0	fpr:FP2_11100	NA	NA	
BLCPAMOF_01625	OG0002963	group_5268	1	0	0	rbr:RBR_20410	ko:K00661	specific_fp360	
BLCPAMOF_01626	OG0002003	group_1318	1	0	0	fpr:FP2_04220	NA	NA	
BLCPAMOF_01627	OG0002380	group_2454	3	3	5	fpr:FP2_04210	ko:K06147	NA	
BLCPAMOF_01628	OG0002381	msbA_3	2	2	3	fpr:FP2_04200	NA	NA	
BLCPAMOF_01629	OG0003569	mexR	0	1	0	bprs:CK3_34360	NA	NA	
BLCPAMOF_01630	OG0002583	group_401	1	0	0	fpr:FP2_04190	NA	NA	
BLCPAMOF_01631	OG0000041	sigE_1	1	0	0	rus:RBI_II00371	ko:K03091	NA	
BLCPAMOF_01632	OG0000795	group_2889	1	0	0	fpa:FPR_07230	NA	NA	
BLCPAMOF_01633	OG0001993	group_5269	0	1	0	NA	NA	NA	
BLCPAMOF_01634	OG0001993	group_3192	1	0	0	cls:CXIVA_10510	ko:K07726	NA	
BLCPAMOF_01635	OG0000794	group_7185	1	0	0	fpr:FP2_04140;fpa:FPR_07210	NA	NA	
BLCPAMOF_01636	OG0000096	ndoA_5	1	0	0	fpa:FPR_18710	NA	NA	
BLCPAMOF_01637	OG0002077	group_2618	0	1	0	fpa:FPR_07180	NA	NA	
BLCPAMOF_01638	OG0002007	group_1916	6	6	11	fpa:FPR_07470	NA	NA	
BLCPAMOF_01639	OG0002005	group_1322	1	0	0	fpa:FPR_07370	ko:K17758;ko:K17759	NA	
BLCPAMOF_01640	OG0000098	group_2183	1	0	0	ere:EUBREC_3535	NA	NA	
BLCPAMOF_01641	OG0000099	group_653	1	0	0	NA	NA	NA	
BLCPAMOF_01642	OG0002165	mutT	0	1	0	fpr:FP2_04080	ko:K03574	NA	
BLCPAMOF_01643	OG0000793	fic_2	1	0	0	fpr:FP2_04070	NA	NA	
BLCPAMOF_01644	OG0001709	nudC	1	0	0	fpa:FPR_07020	ko:K03426	NA	
BLCPAMOF_01645	OG0000792	group_2888	1	0	0	fpa:FPR_07010	NA	NA	
BLCPAMOF_01646	OG0002584	group_3795	1	0	0	fpr:FP2_12120	NA	NA	
BLCPAMOF_01647	OG0000943	ypeA	1	0	0	fpr:FP2_12130	NA	NA	
BLCPAMOF_01648	OG0000791	adeC	1	0	0	fpr:FP2_03930	ko:K01486	NA	
BLCPAMOF_01649	OG0000043	group_398	1	0	0	fpr:FP2_03920	NA	NA	
BLCPAMOF_01650	OG0002254	cysK1_2	1	0	0	fpr:FP2_03910	ko:K01738	NA	
BLCPAMOF_01651	OG0002582	rbsK	1	0	0	ssm:Spirs_1177	ko:K00852	NA	
BLCPAMOF_01652	OG0000220	punA	1	0	0	fpr:FP2_03890	ko:K03783	NA	
BLCPAMOF_01653	OG0000061	group_460	1	0	0	ssg:Selsp_0971	NA	NA	

BLCPAMOF_01654	OG0001778	group_677	1	0	0	fpa:FPR_07350	NA	NA	
BLCPAMOF_01655	OG0000790	ymdB_2	1	0	0	fpa:FPR_07340	NA	NA	
BLCPAMOF_01656	OG0000789	group_7202	1	0	0	sbu:SpiBuddy_1502	NA	NA	
BLCPAMOF_01657	OG0003570	group_3307	1	1	1	fpr:FP2_03860	NA	NA	
BLCPAMOF_01658	OG0000788	group_7227	1	0	0	fpr:FP2_03850	ko:K04794	NA	
BLCPAMOF_01659	OG0000060	group_468	1	0	0	fpr:FP2_03840	NA	NA	
BLCPAMOF_01660	OG0001949	ybiV	1	0	0	fpr:FP2_03830	ko:K01104	NA	
BLCPAMOF_01661	OG0000083	group_5271	1	0	0	byl:A4V09_08940	NA	NA	
BLCPAMOF_01662	OG0001672	group_930	1	0	0	fpla:A4U99_10845	NA	NA	
BLCPAMOF_01663	OG0000059	group_269	1	0	0	rho:RHOM_06500	NA	NA	
BLCPAMOF_01664	OG0002359	group_271	1	0	0	rho:RHOM_06500	NA	NA	
BLCPAMOF_01665	OG0000040	group_298	1	0	0	fpa:FPR_23820	NA	NA	
BLCPAMOF_01666	OG0000164	cdhR	1	0	0	NA	NA	NA	
BLCPAMOF_01667	OG0004109	group_5272	1	1	1	NA	NA	specific_fp360	○
BLCPAMOF_01668	OG0002533	group_5273	1	0	0	lacy:A4V08_22760	NA	NA	
BLCPAMOF_01669	OG0002964	group_5274	2	2	3	lacy:A4V08_22765	NA	NA	
BLCPAMOF_01670	OG0002099	dctM_2	6	6	11	lacy:A4V08_22770	NA	NA	
BLCPAMOF_01671	OG0002534	yicI	1	0	0	lacy:A4V08_18450	ko:K01187	NA	
BLCPAMOF_01672	OG0002534	group_5276	1	0	0	lacy:A4V08_22780	ko:K01187	NA	
BLCPAMOF_01673	OG0002032	norM	6	7	12	lho:LOOC260_120870	NA	NA	
BLCPAMOF_01674	OG0000787	ybjI	1	0	0	fpr:FP2_03820	NA	NA	
BLCPAMOF_01675	OG0000786	group_2404	1	0	0	fpa:FPR_06870	NA	NA	
BLCPAMOF_01676	OG0002465	immR_5	1	0	0	bprs:CK3_14420	NA	NA	
BLCPAMOF_01677	OG0000106	dfx_2	1	0	0	fpr:FP2_03800	ko:K05919	NA	
BLCPAMOF_01678	OG0000080	sfsA	1	0	0	era:ERE_03180	ko:K06206	NA	
BLCPAMOF_01679	OG0001706	group_464	1	1	1	fpa:FPR_07270	NA	NA	
BLCPAMOF_01680	OG0000219	ymdB_1	1	0	0	fpa:FPR_06830	NA	NA	
BLCPAMOF_01681	OG0000785	sttH	1	0	0	fpa:FPR_06820	NA	NA	
BLCPAMOF_01682	OG0000094	group_616	1	1	1	NA	NA	NA	
BLCPAMOF_01683	OG0002043	panS	4	5	8	fpa:FPR_01880	ko:K03453	NA	
BLCPAMOF_01684	OG0004110	group_5277	1	0	0	NA	NA	specific_fp360	○
BLCPAMOF_01685	OG0002466	ptsG	7	7	13	fpr:FP2_17520	ko:K20116;ko:K20117;ko:K20118	NA	
BLCPAMOF_01686	OG0000107	licT	1	0	0	rus:RBI_I00378	ko:K03488	NA	
BLCPAMOF_01687	OG0002081	barA	1	0	0	fpa:FPR_07660	NA	NA	
BLCPAMOF_01688	OG0001704	hin	1	0	0	fpr:FP2_03230	NA	NA	
BLCPAMOF_01689	OG0000041	sigK_2	1	0	0	rus:RBI_I00371	ko:K03091	NA	
BLCPAMOF_01690	OG0000235	dnaX_2	1	0	0	fpr:FP2_03190	ko:K02343	NA	
BLCPAMOF_01691	OG0001121	group_1542	1	0	0	fpr:FP2_03180	ko:K09747	NA	
BLCPAMOF_01692	OG0000234	recR	1	0	0	fpr:FP2_03170	ko:K06187	NA	
BLCPAMOF_01693	OG0001207	smpB	1	0	0	fpr:FP2_03160	ko:K03664	NA	
BLCPAMOF_01695	OG0001909	group_2443	1	0	0	esr:ES1_00510	NA	NA	
BLCPAMOF_01696	OG0002593	group_3833	0	1	0	rob:CK5_03740	NA	NA	
BLCPAMOF_01697	OG0003107	group_2940	0	1	0	NA	NA	NA	
BLCPAMOF_01698	OG0000021	pre_2	1	0	0	esr:ES1_00480	NA	NA	
BLCPAMOF_01699	OG0000231	group_486	1	0	0	bprs:CK3_15400	ko:K06919	NA	
BLCPAMOF_01700	OG0002592	group_2441	1	0	0	bprs:CK3_15410	NA	NA	
BLCPAMOF_01701	OG0002591	group_2440	1	0	0	rob:CK5_03690	NA	NA	
BLCPAMOF_01702	OG0000400	group_1043	1	0	0	cct:CC1_26470	NA	NA	
BLCPAMOF_01703	OG0002590	group_2439	1	0	0	rob:CK5_03670	NA	NA	
BLCPAMOF_01704	OG0002377	group_3831	1	0	0	rum:CK1_09170	NA	NA	
BLCPAMOF_01705	OG0000063	group_2438	1	0	0	rob:CK5_03650	NA	NA	
BLCPAMOF_01706	OG0000047	yknY_1	1	0	0	rob:CK5_03640	ko:K02003	NA	
BLCPAMOF_01707	OG0002376	group_2939	4	5	8	rum:CK1_09200	ko:K02004	NA	
BLCPAMOF_01708	OG0002589	group_50	1	0	0	bprs:CK3_15470	NA	NA	
BLCPAMOF_01709	OG0002267	group_637	1	1	1	esr:ES1_00380	ko:K03215	NA	
BLCPAMOF_01710	OG0004111	group_5279	1	0	0	NA	NA	specific_fp360	
BLCPAMOF_01711	OG0000136	pta	1	0	0	fpr:FP2_03100	ko:K00625	NA	
BLCPAMOF_01712	OG0000236	group_545	1	0	0	fpr:FP2_03090	ko:K02334	NA	
BLCPAMOF_01713	OG0000168	group_640	1	0	0	fpr:FP2_03080	NA	NA	
BLCPAMOF_01714	OG0000137	dinG	1	0	0	fpr:FP2_03070	NA	NA	
BLCPAMOF_01715	OG0002016	group_5280	1	0	0	fpr:FP2_03060	ko:K00077	NA	
BLCPAMOF_01716	OG0001122	merA	1	0	0	fpr:FP2_03050	NA	NA	
BLCPAMOF_01717	OG0002083	group_5281	2	1	2	fpa:FPR_20810	NA	NA	
BLCPAMOF_01718	OG0001961	yveL	1	0	0	fpa:FPR_20820	NA	NA	
BLCPAMOF_01719	OG0001960	ywqE	1	0	0	fpa:FPR_20830	ko:K01104	NA	
BLCPAMOF_01720	OG0001123	mepA_9	6	7	12	fpr:FP2_03040	NA	NA	
BLCPAMOF_01721	OG0001948	group_5282	4	4	7	fpr:FP2_03030	ko:K03324	NA	
BLCPAMOF_01722	OG0001124	group_5283	1	1	1	fpr:FP2_16120	NA	NA	
BLCPAMOF_01723	OG0001125	group_5284	1	1	1	NA	NA	NA	
BLCPAMOF_01724	OG0001126	ftsH	2	1	2	ruk:A4V00_10730	ko:K03798	NA	
BLCPAMOF_01725	OG0001127	hpt	1	0	0	fpr:FP2_16080	ko:K00760	NA	
BLCPAMOF_01726	OG0001128	group_5285	1	0	0	fpr:FP2_16070	ko:K04075	NA	
BLCPAMOF_01727	OG0001129	dnaC_2	1	0	0	fpr:FP2_16060	ko:K02314	NA	
BLCPAMOF_01728	OG0001130	rplI	1	0	0	fpr:FP2_16050	ko:K02939	NA	
BLCPAMOF_01729	OG0001131	glf	1	0	0	fpr:FP2_16040	ko:K01854	NA	
BLCPAMOF_01730	OG0001132	gdpP	1	2	2	fpr:FP2_16030	NA	NA	
BLCPAMOF_01731	OG0001133	rnjA	1	0	0	fpr:FP2_16020	ko:K12574	NA	
BLCPAMOF_01732	OG0001134	rnhA	1	0	0	fpr:FP2_16010	ko:K03469	NA	
BLCPAMOF_01733	OG0001135	group_5286	1	0	0	fpr:FP2_16000	ko:K00566	NA	
BLCPAMOF_01734	OG0000780	mgsA_1	1	0	0	fpr:FP2_15990	ko:K01734	NA	
BLCPAMOF_01735	OG0000779	mrdA	1	1	1	fpr:FP2_15980	ko:K05515	NA	
BLCPAMOF_01736	OG0000778	group_2395	2	3	4	fpr:FP2_15970	ko:K03571	NA	
BLCPAMOF_01737	OG0000777	mreC	1	1	1	fpa:FPR_21540	ko:K03570	NA	
BLCPAMOF_01738	OG0000776	mreB_1	1	0	0	fpr:FP2_15950	ko:K03569	NA	
BLCPAMOF_01739	OG0000775	maf	1	0	0	fpr:FP2_15940	ko:K06287	NA	
BLCPAMOF_01740	OG0000774	dut	1	0	0	fpr:FP2_15930	ko:K01520	NA	
BLCPAMOF_01741	OG0000773	ydcP_1	1	0	0	fpr:FP2_15920	ko:K08303	NA	
BLCPAMOF_01742	OG0000772	zapA	0	1	0	fpr:FP2_15910	ko:K09888	specific_fp360	
BLCPAMOF_01743	OG0000771	malP_2	1	0	0	fpr:FP2_15900	ko:K00688	NA	
BLCPAMOF_01744	OG0000770	apu	1	0	0	fpr:FP2_15880	NA	NA	
BLCPAMOF_01745	OG0000769	group_1308	1	2	2	fpr:FP2_15870	NA	NA	
BLCPAMOF_01746	OG0000768	hflC	1	1	1	fpr:FP2_15860	NA	NA	
BLCPAMOF_01747	OG0000767	group_1306	1	0	0	fpr:FP2_15850	NA	NA	
BLCPAMOF_01748	OG0002535	group_5287	1	2	2	NA	NA	NA	
BLCPAMOF_01749	OG0002002	dfx_4	1	0	0	fpr:FP2_15840	NA	NA	
BLCPAMOF_01750	OG0000766	mgtE	3	3	5	fpr:FP2_15830	ko:K06213	NA	
BLCPAMOF_01751	OG0000763	proS	1	0	0	fpr:FP2_15820	ko:K01881	NA	
BLCPAMOF_01752	OG0000762	acpP_2	1	0	0	fpr:FP2_15810	ko:K02078	NA	
BLCPAMOF_01753	OG0000761	dapF	1	0	0	fpr:FP2_15800	ko:K01778	NA	
BLCPAMOF_01754	OG0000760	dapL	1	0	0	fpr:FP2_15790	ko:K10206	NA	
BLCPAMOF_01755	OG0000757	galM_1	1	0	0	fpr:FP2_15780	NA	NA	
BLCPAMOF_01756	OG0000784	group_2673	2	1	2	fpa:FPR_20280	NA	NA	
BLCPAMOF_01757	OG0000165	ctrA	1	0	0	fpa:FPR_20270	NA	NA	
BLCPAMOF_01758	OG0000783	group_2038	1	1	1	fpa:FPR_20260	NA	NA	
BLCPAMOF_01759	OG0000782	yccM_2	2	2	3	ibu:1B211_01833c	NA	NA	
BLCPAMOF_01760	OG0000781	group_2297	1	0	0	fpa:FPR_20240	NA	NA	
BLCPAMOF_01761	OG0004112	group_5288	1	0	0	NA	NA	specific_fp360	○
BLCPAMOF_01762	OG0001779	group_5289	1	0	0	fpr:FP2_15760	NA	NA	
BLCPAMOF_01763	OG0001783	group_3246	1	0	0	NA	NA	NA	
BLCPAMOF_01764	OG0001965	arcB	1	2	2	rob:CK5_07740	NA	NA	
BLCPAMOF_01765	OG0000186	rpfG_3	1	0	0	fpa:FPR_12710	ko:K07814	NA	
BLCPAMOF_01766	OG0001966	fliY_3	1	0	0	fpr:FP2_15720	ko:K02030	NA	
BLCPAMOF_01767	OG0001967	luxQ_2	1	1	1	ddt:AAY81_09860	NA	NA	
BLCPAMOF_01768	OG0002336	rcsC	2	1	2	fpr:FP2_15700	NA	NA	

BLCPAMOF_01769	OG0001783	group_2624	1	0	0	rob:CK5_03310	ko:K10117	NA	
BLCPAMOF_01770	OG0002075	evgS	1	1	1	fpa:FPR_07600	NA	NA	
BLCPAMOF_01771	OG0001254	cwlM_3	1	0	0	fpr:FP2_15680	NA	NA	
BLCPAMOF_01772	OG0001253	cwlM_2	1	0	0	fpr:FP2_15670	NA	NA	
BLCPAMOF_01773	OG0000755	cobB	1	0	0	fpr:FP2_15660	ko:K12410	NA	
BLCPAMOF_01774	OG0000754	nnr	1	0	0	fpr:FP2_15650	ko:K17758;ko:K17759	NA	
BLCPAMOF_01775	OG0000753	group_1298	1	0	0	fpr:FP2_15640	NA	NA	
BLCPAMOF_01776	OG0002001	group_2035	2	2	3	fpr:FP2_15630	NA	NA	
BLCPAMOF_01777	OG0000091	sarA_2	1	0	0	fpr:FP2_15620	ko:K15580	NA	
BLCPAMOF_01778	OG0000091	group_5290	1	0	0	fpr:FP2_15610	ko:K15580	NA	
BLCPAMOF_01779	OG0000091	group_772	1	0	0	fpr:FP2_15600	ko:K15580	NA	
BLCPAMOF_01780	OG0000092	dppB_1	3	3	5	fpr:FP2_15590	ko:K15581	NA	
BLCPAMOF_01781	OG0002000	oppC	3	3	5	fpr:FP2_15580	ko:K15582	NA	
BLCPAMOF_01782	OG0000033	oppD_2	1	0	0	fpr:FP2_15570	ko:K15583	NA	
BLCPAMOF_01783	OG0000093	oppF_2	1	0	0	fpr:FP2_15560	ko:K10823	NA	
BLCPAMOF_01784	OG0000612	group_5291	1	1	1	fpa:FPR_04000	NA	NA	
BLCPAMOF_01785	OG0000611	cinA_2	1	0	0	fpr:FP2_15540	ko:K03742	NA	
BLCPAMOF_01786	OG0000610	thiI	1	0	0	fpr:FP2_15530	ko:K03151	NA	
BLCPAMOF_01787	OG0000609	group_1192	1	0	0	fpa:FPR_03970	ko:K04487	NA	
BLCPAMOF_01788	OG0000606	group_1190	1	0	0	fpr:FP2_15500	NA	NA	
BLCPAMOF_01789	OG0000608	group_2375	1	1	1	fpr:FP2_15490	NA	NA	
BLCPAMOF_01790	OG0000210	yxeP	1	0	0	fpr:FP2_15480	NA	NA	
BLCPAMOF_01791	OG0000613	secA	1	0	0	fpr:FP2_15470	ko:K03070	NA	
BLCPAMOF_01792	OG0001921	group_2168	1	0	0	NA	NA	NA	
BLCPAMOF_01796	OG0004113	group_5292	0	1	0	NA	NA	specific_fp360	
BLCPAMOF_01797	OG0000899	acrA	1	0	0	fpr:FP2_20550	ko:K03522	NA	
BLCPAMOF_01798	OG0000898	acrB	1	0	0	fpr:FP2_20560	ko:K03521	NA	
BLCPAMOF_01799	OG0000897	bcd_1	1	0	0	fpr:FP2_20570	NA	NA	
BLCPAMOF_01800	OG0000896	hbd	1	0	0	fpr:FP2_20580	ko:K00074	NA	
BLCPAMOF_01801	OG0000895	crt	1	0	0	fpr:FP2_20590	ko:K01715	NA	
BLCPAMOF_01802	OG0000894	thlA	1	0	0	fpr:FP2_20600	ko:K00626	NA	
BLCPAMOF_01803	OG0000893	coaD	1	0	0	fpr:FP2_20610	ko:K00954	NA	
BLCPAMOF_01804	OG0000892	cat1	1	0	0	fpr:FP2_20620	NA	NA	
BLCPAMOF_01805	OG0000891	group_1386	4	5	8	fpr:FP2_20630	NA	NA	
BLCPAMOF_01806	OG0000890	mftC	1	0	0	fpr:FP2_20640	NA	NA	
BLCPAMOF_01807	OG0000889	dhaS	1	0	0	fpr:FP2_20650	NA	NA	
BLCPAMOF_01808	OG0000888	proC	1	0	0	fpr:FP2_20660	ko:K00286	NA	
BLCPAMOF_01809	OG0000887	proB	1	0	0	fpr:FP2_20670	ko:K00931	NA	
BLCPAMOF_01810	OG0000223	proA	1	0	0	fpr:FP2_20680	ko:K00147	NA	
BLCPAMOF_01811	OG0000886	mgsA_2	1	0	0	fpr:FP2_20690	ko:K01734	NA	
BLCPAMOF_01812	OG0000885	urdA	1	0	0	fpr:FP2_20700	NA	NA	
BLCPAMOF_01813	OG0002012	regX3_2	1	0	0	fpr:FP2_20710	NA	NA	
BLCPAMOF_01814	OG0002011	group_5293	4	4	7	fpr:FP2_20720	NA	NA	
BLCPAMOF_01815	OG0004114	ybdL	0	1	0	NA	NA	NA	
BLCPAMOF_01816	OG0000884	group_1382	1	0	0	fpr:FP2_20740	NA	NA	
BLCPAMOF_01817	OG0000883	group_2420	1	0	0	NA	NA	NA	
BLCPAMOF_01818	OG0000882	murD	1	0	0	fpr:FP2_20780	ko:K01925	NA	
BLCPAMOF_01819	OG0000881	dppE	1	1	1	NA	NA	NA	
BLCPAMOF_01820	OG0001411	fabZ	1	0	0	fpr:FP2_20800	ko:K02372	NA	
BLCPAMOF_01821	OG0001412	fabF	1	0	0	fpr:FP2_20810	ko:K09458	NA	
BLCPAMOF_01822	OG0001413	fabG_3	1	0	0	fpr:FP2_20820	ko:K00059	NA	
BLCPAMOF_01823	OG0001414	fabD	1	0	0	fpr:FP2_20830	ko:K00645	NA	
BLCPAMOF_01824	OG0001415	group_1744	1	0	0	fpr:FP2_20840	NA	NA	
BLCPAMOF_01825	OG0001416	group_1745	1	0	0	fpr:FP2_20850	ko:K02371	NA	
BLCPAMOF_01826	OG0001417	fabH	1	0	0	fpr:FP2_20860	ko:K00648	NA	
BLCPAMOF_01827	OG0001418	accA	1	0	0	fpr:FP2_20870	ko:K01962	NA	
BLCPAMOF_01828	OG0001419	accD	1	0	0	fpr:FP2_20880	ko:K01963	NA	
BLCPAMOF_01829	OG0001420	acpP_3	1	0	0	fpr:FP2_20890	ko:K02078	NA	
BLCPAMOF_01830	OG0003567	group_5294	1	0	0	fpr:FP2_20900	ko:K01759	specific_fp360	
BLCPAMOF_01831	OG0002596	group_2093	5	6	10	lacy:A4V08_14040	NA	NA	
BLCPAMOF_01832	OG0000169	rhaS	1	0	0	fpr:FP2_20910	NA	NA	
BLCPAMOF_01833	OG0001733	group_1567	1	0	0	fpr:FP2_20920	NA	NA	
BLCPAMOF_01834	OG0001159	group_1568	1	0	0	fpr:FP2_20930	NA	NA	
BLCPAMOF_01835	OG0001160	group_1569	1	0	0	fpr:FP2_20940	NA	NA	
BLCPAMOF_01836	OG0001743	group_2619	6	5	10	fpr:FP2_20950	ko:K07088	NA	
BLCPAMOF_01837	OG0004115	pat	1	0	0	fpr:FP2_20960	ko:K03823	specific_fp360	
BLCPAMOF_01838	OG0002021	group_2456	4	4	7	fpr:FP2_20970	ko:K18890	NA	
BLCPAMOF_01839	OG0002022	yheI	3	3	5	ruk:A4V00_03995	ko:K18889	NA	
BLCPAMOF_01845	OG0001161	group_1570	1	0	0	fpr:FP2_20990	ko:K00528	NA	
BLCPAMOF_01846	OG0001162	gltD_2	1	0	0	fpr:FP2_21000	ko:K00266	NA	
BLCPAMOF_01847	OG0001208	group_5296	1	0	0	bbay:A4V04_11570	ko:K00567	NA	
BLCPAMOF_01848	OG0004116	alkA	1	1	1	fpr:FP2_21020	ko:K01247	specific_fp360	
BLCPAMOF_01849	OG0003571	group_5298	3	3	5	NA	NA	NA	
BLCPAMOF_01850	OG0003572	group_5299	3	2	4	cls:CXIVA_05470	NA	NA	
BLCPAMOF_01851	OG0002272	hsdR_2	1	0	0	fpa:FPR_30900	ko:K01153	NA	
BLCPAMOF_01852	OG0003573	group_3310	1	0	0	NA	NA	NA	
BLCPAMOF_01853	OG0001912	group_2099	1	0	0	blk:BLNIAS_02570	ko:K01154	NA	
BLCPAMOF_01854	OG0001912	group_1944	1	0	0	asb:RATSFB_1265	ko:K01154	NA	
BLCPAMOF_01855	OG0002965	group_3311	1	0	0	NA	NA	NA	
BLCPAMOF_01856	OG0002142	group_2969	1	0	0	fpa:FPR_30940	NA	NA	
BLCPAMOF_01857	OG0002273	group_3864	1	0	0	fpa:FPR_30950	ko:K03427	NA	
BLCPAMOF_01858	OG0001913	group_843	1	0	0	fpa:FPR_30970	NA	NA	
BLCPAMOF_01859	OG0001913	group_844	1	0	0	fpa:FPR_30970	NA	NA	
BLCPAMOF_01860	OG0002024	group_3312	1	0	0	bpsc:BBPC_0780	NA	NA	
BLCPAMOF_01861	OG0002179	group_5300	1	0	0	ova:OBV_30560	NA	NA	
BLCPAMOF_01862	OG0001779	group_5301	1	0	0	fpla:A4U99_15995	NA	NA	
BLCPAMOF_01863	OG0001779	group_5302	1	0	0	fpla:A4U99_16000	NA	NA	
BLCPAMOF_01864	OG0001779	group_5303	1	0	0	fpla:A4U99_16000	NA	NA	
BLCPAMOF_01865	OG0002178	group_5304	1	0	0	fpla:A4U99_16005	NA	NA	
BLCPAMOF_01866	OG0001878	group_5305	0	1	0	rob:CK5_29090	ko:K03088	NA	
BLCPAMOF_01867	OG0002331	regX3_4	1	0	0	rob:CK5_29100	NA	NA	
BLCPAMOF_01868	OG0004117	group_5307	1	0	0	esr:ES1_14680;fpr:FP2_10830	NA	specific_fp360	
BLCPAMOF_01869	OG0004118	group_5308	4	3	6	fpr:FP2_10820;rob:CK5_29160	NA	specific_fp360	
BLCPAMOF_01870	OG0004119	group_5309	1	1	1	rob:CK5_29170	NA	specific_fp360	
BLCPAMOF_01871	OG0004120	group_5310	3	4	6	rob:CK5_29180;fpr:FP2_10810	NA	specific_fp360	
BLCPAMOF_01872	OG0000765	ytrB_1	1	0	0	fpr:FP2_10800	ko:K01990	NA	
BLCPAMOF_01873	OG0000764	ytrA_1	1	0	0	rob:CK5_29200;esr:ES1_14750	ko:K07979	NA	
BLCPAMOF_01874	OG0002377	luxO	1	0	0	bbrv:B689b_1160	NA	NA	
BLCPAMOF_01875	OG0002266	group_2945	4	5	8	ruk:A4V00_15705	ko:K02004	NA	
BLCPAMOF_01876	OG0000047	yknY_4	1	0	0	fpa:FPR_01240	ko:K02003	NA	
BLCPAMOF_01877	OG0003228	group_3313	1	2	2	NA	NA	NA	
BLCPAMOF_01878	OG0004121	group_5314	2	3	4	NA	NA	specific_fp360	
BLCPAMOF_01879	OG0000063	group_2445	2	1	2	rho:RHOM_06455	NA	NA	
BLCPAMOF_01880	OG0000135	group_2943	1	0	0	rho:RHOM_06450	NA	NA	
BLCPAMOF_01881	OG0002266	group_5315	4	5	8	NA	NA	NA	
BLCPAMOF_01882	OG0004122	idi	1	0	0	cso:CLS_07260	NA	specific_fp360	O
BLCPAMOF_01883	OG0000188	group_5317	1	0	0	cso:CLS_07250	NA	NA	
BLCPAMOF_01884	OG0000199	thiE_1	1	0	0	cso:CLS_07240	ko:K00788	NA	
BLCPAMOF_01885	OG0000240	thiD_1	1	0	0	cso:CLS_07230	ko:K00941	NA	
BLCPAMOF_01886	OG0002536	group_5320	1	0	0	cso:CLS_07220	ko:K03707	NA	
BLCPAMOF_01887	OG0003574	group_5321	1	0	0	lacy:A4V08_29605	NA	NA	
BLCPAMOF_01888	OG0003575	group_5322	2	2	3	rob:CK5_29220	NA	NA	
BLCPAMOF_01889	OG0004123	group_5323	0	1	0	rob:CK5_29280	NA	specific_fp360	
BLCPAMOF_01890	OG0002115	group_5324	1	0	0	rob:CK5_29290	NA	NA	

BLCPAMOF_01891	OG0004124	group_5325	1	0	0	rob:CK5_29300	NA	specific_fp360	○
BLCPAMOF_01892	OG0004125	group_5326	1	0	0	fpla:A4U99_16035	NA	specific_fp360	○
BLCPAMOF_01893	OG0002966	group_5327	0	1	0	rob:CK5_29320	NA	NA	
BLCPAMOF_01894	OG0004126	group_5328	1	0	0	rob:CK5_29330	NA	specific_fp360	○
BLCPAMOF_01895	OG0000056	group_122	1	0	0	rob:CK5_29340	ko:K03169	NA	
BLCPAMOF_01896	OG0004127	group_5329	1	1	1	rob:CK5_29350	NA	specific_fp360	○
BLCPAMOF_01897	OG0003195	group_5330	1	0	0	rob:CK5_29360	NA	NA	
BLCPAMOF_01898	OG0000720	group_5331	1	0	0	rob:CK5_29370	NA	NA	
BLCPAMOF_01899	OG0004128	dut_2	1	0	0	rob:CK5_29380	ko:K01520	specific_fp360	○
BLCPAMOF_01900	OG0000232	group_5333	1	0	0	fpla:A4U99_16090	ko:K03465	NA	
BLCPAMOF_01901	OG0004129	group_5334	1	0	0	fpla:A4U99_16095	NA	specific_fp360	○
BLCPAMOF_01902	OG0003229	group_5335	1	0	0	rob:CK5_29410	NA	NA	
BLCPAMOF_01903	OG0004130	group_5336	1	0	0	fpla:A4U99_16105	NA	specific_fp360	○
BLCPAMOF_01904	OG0004131	group_5337	1	0	0	rob:CK5_29430	NA	specific_fp360	○
BLCPAMOF_01905	OG0003212	group_5338	2	2	3	rob:CK5_29440	NA	NA	
BLCPAMOF_01906	OG0000477	group_5339	1	2	2	rob:CK5_29450	NA	NA	
BLCPAMOF_01907	OG0000072	group_5340	1	0	0	lacy:A4V08_29440	NA	NA	
BLCPAMOF_01908	OG0002518	ltrA_4	1	0	0	erb:A4V01_21510	NA	NA	
BLCPAMOF_01909	OG0001807	mepM_4	1	1	1	rob:CK5_29470	NA	NA	
BLCPAMOF_01910	OG0000009	group_5341	1	0	0	gfe:Gferi_03805	NA	NA	
BLCPAMOF_01911	OG0004132	group_5342	1	0	0	efa:EF2331	NA	specific_fp360	○
BLCPAMOF_01912	OG0001931	group_2676	1	0	0	rob:CK5_29510	NA	NA	
BLCPAMOF_01913	OG0004133	group_5343	0	1	0	rob:CK5_29520	ko:K06412	specific_fp360	○
BLCPAMOF_01914	OG0002308	group_5344	3	3	5	rob:CK5_29530	NA	NA	
BLCPAMOF_01915	OG0000006	group_240	1	2	2	rob:CK5_29540	NA	NA	
BLCPAMOF_01916	OG0000001	group_81	2	2	3	rob:CK5_29550	ko:K03205	NA	
BLCPAMOF_01917	OG0001897	group_5345	1	0	0	fpla:A4U99_16190	NA	NA	
BLCPAMOF_01918	OG0004134	group_5346	1	0	0	rob:CK5_29570	NA	specific_fp360	
BLCPAMOF_01919	OG0002098	group_5347	1	0	0	rob:CK5_29580	NA	NA	
BLCPAMOF_01920	OG0004135	group_5348	1	0	0	fpla:A4U99_16205	NA	specific_fp360	○
BLCPAMOF_01921	OG0004136	group_5349	1	0	0	lacy:A4V08_29180	NA	specific_fp360	○
BLCPAMOF_01922	OG0004137	group_5350	1	0	0	lacy:A4V08_29175	NA	specific_fp360	○
BLCPAMOF_01923	OG0004138	group_5351	1	0	0	rob:CK5_29620	NA	specific_fp360	○
BLCPAMOF_01924	OG0004139	group_5352	0	1	0	rob:CK5_29630	ko:K07726	specific_fp360	○
BLCPAMOF_01925	OG0004140	group_5353	1	0	0	rob:CK5_29640	NA	specific_fp360	○
BLCPAMOF_01926	OG0000111	group_5354	1	0	0	rob:CK5_29650	NA	NA	
BLCPAMOF_01927	OG0000057	group_5355	1	0	0	rob:CK5_29660	NA	NA	
BLCPAMOF_01928	OG0002122	group_5356	1	0	0	rob:CK5_29670	NA	NA	
BLCPAMOF_01929	OG0001189	guaA	1	0	0	fpr:FP2_21030	ko:K01951	NA	
BLCPAMOF_01930	OG0001384	group_3032	3	3	5	fpr:FP2_21040	ko:K03523	NA	
BLCPAMOF_01931	OG0002611	group_3033	1	0	0	fpr:FP2_21050	ko:K09706	NA	
BLCPAMOF_01932	OG0001068	group_1494	6	6	11	fpr:FP2_21060	ko:K03308	NA	
BLCPAMOF_01933	OG0001184	rnmV	1	0	0	fpr:FP2_21070	ko:K05985	NA	
BLCPAMOF_01934	OG0001183	group_1585	1	0	0	fpa:FPR_06720	ko:K02340	NA	
BLCPAMOF_01935	OG0000692	group_5357	5	5	9	fpa:FPR_06710	ko:K02238	NA	
BLCPAMOF_01936	OG0000691	purR_2	1	0	0	fpr:FP2_21100	ko:K00759	NA	
BLCPAMOF_01937	OG0000690	group_1245	1	0	0	fpr:FP2_21110	ko:K02503	NA	
BLCPAMOF_01938	OG0000689	alaS_1	1	0	0	fpr:FP2_21120	ko:K01872	NA	
BLCPAMOF_01939	OG0000688	group_5358	1	1	1	fpr:FP2_21130	NA	NA	
BLCPAMOF_01940	OG0000687	rluC_1	1	0	0	esr:ES1_10950	ko:K06179	NA	
BLCPAMOF_01941	OG0000686	lldD	1	0	0	fpr:FP2_21160	NA	NA	
BLCPAMOF_01943	OG0001996	group_2385	1	0	0	fpr:FP2_21180	ko:K07010	NA	
BLCPAMOF_01944	OG0004141	coaE_2	1	0	0	fpr:FP2_21200	NA	specific_fp360	
BLCPAMOF_01945	OG0000685	group_5360	1	1	1	fpr:FP2_21210	NA	NA	
BLCPAMOF_01946	OG0000799	rsxB_1	1	0	0	fpr:FP2_21220	NA	NA	
BLCPAMOF_01947	OG0004142	citC	1	0	0	fpr:FP2_21230	ko:K01910	specific_fp360	
BLCPAMOF_01948	OG0004143	citG	1	0	0	fpr:FP2_21240	ko:K13927	specific_fp360	
BLCPAMOF_01949	OG0000269	group_5363	1	0	0	fpr:FP2_21250	NA	NA	
BLCPAMOF_01950	OG0002492	group_5364	1	0	0	fpr:FP2_21260	ko:K07012	NA	
BLCPAMOF_01951	OG0004144	group_5365	1	0	0	fpr:FP2_21270	ko:K19119	specific_fp360	
BLCPAMOF_01952	OG0004145	group_5366	1	0	0	fpr:FP2_21280	ko:K19117	specific_fp360	
BLCPAMOF_01953	OG0002493	group_5367	1	0	0	fpr:FP2_21290	ko:K19118	NA	
BLCPAMOF_01954	OG0002494	group_3226	1	0	0	fpla:A4U99_08325	ko:K07464	NA	
BLCPAMOF_01955	OG0002495	cas1	1	0	0	fpr:FP2_21300	ko:K15342	NA	
BLCPAMOF_01956	OG0002496	cas2	1	0	0	fpr:FP2_21310	ko:K09951	NA	
BLCPAMOF_01957	OG0002497	group_5368	1	0	0	NA	NA	NA	
BLCPAMOF_01958	OG0003576	group_5369	1	0	0	fpr:FP2_21320	ko:K03660	NA	
BLCPAMOF_01960	OG0000112	group_684	1	0	0	fpr:FP2_21330	NA	NA	
BLCPAMOF_01961	OG0002126	group_2389	1	0	0	fpr:FP2_27440	NA	NA	
BLCPAMOF_01962	OG0000078	group_417	1	0	0	fpr:FP2_27430	NA	NA	
BLCPAMOF_01963	OG0000175	ndoA_3	1	0	0	fpr:FP2_28260	ko:K03497	NA	
BLCPAMOF_01964	OG0002076	group_91	1	0	0	fpr:FP2_17350	NA	NA	
BLCPAMOF_01965	OG0002486	group_4802	1	0	0	ibu:IB211_01242	NA	NA	
BLCPAMOF_01966	OG0002485	group_4801	1	0	0	mac:MA_0533	NA	NA	
BLCPAMOF_01967	OG0000022	group_343	0	1	0	fpr:FP2_10260	NA	NA	
BLCPAMOF_01968	OG0000019	group_373	1	0	0	fpa:FPR_04590	NA	NA	
BLCPAMOF_01969	OG0000003	topB_7	1	0	0	fpa:FPR_19060	ko:K03169	NA	
BLCPAMOF_01970	OG0004146	group_5370	0	1	0	NA	NA	specific_fp360	
BLCPAMOF_01971	OG0003577	group_5371	1	0	0	amr:AM1_A0346	NA	NA	
BLCPAMOF_01972	OG0001928	malQ_2	1	0	0	rum:CK1_29460	ko:K00705	NA	
BLCPAMOF_01973	OG0002340	bcrC_2	2	2	3	fpr:FP2_21870	ko:K19302	NA	
BLCPAMOF_01974	OG0000148	group_3267	1	0	0	ccl:Clocl_2850	NA	NA	
BLCPAMOF_01975	OG0000233	iolC_2	1	0	0	fpa:FPR_04360	ko:K00874	NA	
BLCPAMOF_01976	OG0002034	nqrC	1	0	0	fpa:FPR_04350	NA	NA	
BLCPAMOF_01977	OG0002035	gmr	1	0	0	rum:CK1_25500	NA	NA	
BLCPAMOF_01978	OG0001825	ftn	1	0	0	fpa:FPR_04340	ko:K02217	NA	
BLCPAMOF_01979	OG0001827	trxB_2	1	0	0	fpa:FPR_04320	ko:K00384	NA	
BLCPAMOF_01980	OG0001828	trxA	1	0	0	bprs:CK3_14580	ko:K03671	NA	
BLCPAMOF_01981	OG0001826	fprA1_2	1	0	0	fpa:FPR_04300	NA	NA	
BLCPAMOF_01982	OG0001829	group_3918	1	0	0	fpa:FPR_04290	NA	NA	
BLCPAMOF_01983	OG0001830	nrdB	1	0	0	fpa:FPR_04280	ko:K00526	NA	
BLCPAMOF_01984	OG0001831	nrdE1	1	0	0	fpa:FPR_04270	ko:K00525	NA	
BLCPAMOF_01985	OG0001832	fprA	1	0	0	fpa:FPR_04260	NA	NA	
BLCPAMOF_01986	OG0001833	bcd_2	1	0	0	fpa:FPR_04250	NA	NA	
BLCPAMOF_01987	OG0001834	group_2494	1	0	0	bprs:CK3_14520	NA	NA	
BLCPAMOF_01988	OG0002278	ywaC	1	0	0	bprs:CK3_14500	ko:K07816	NA	
BLCPAMOF_01989	OG0002149	cdr	1	0	0	bprs:CK3_14490	NA	NA	
BLCPAMOF_01990	OG0002279	group_2495	1	0	0	tsu:Tresu_0819	ko:K03671	NA	
BLCPAMOF_01991	OG0002280	group_3013	2	3	4	byl:A4V09_12060	NA	NA	
BLCPAMOF_01992	OG0002281	group_3014	1	0	0	NA	NA	NA	
BLCPAMOF_01993	OG0001835	dfx_1	1	0	0	bprs:CK3_14460	ko:K05919	NA	
BLCPAMOF_01994	OG0001836	rbr1	1	0	0	bprs:CK3_14450	NA	NA	
BLCPAMOF_01995	OG0001837	crp	1	0	0	bprs:CK3_14440	ko:K01420	NA	
BLCPAMOF_01996	OG0001838	group_2125	1	0	0	bprs:CK3_14430	NA	NA	
BLCPAMOF_01997	OG0001839	group_3928	1	2	2	rum:CK1_03440	NA	NA	
BLCPAMOF_01998	OG0000002	group_5372	1	0	0	esr:ES1_15340	NA	NA	
BLCPAMOF_01999	OG0002346	group_3314	1	0	0	ckr:CKR_0246;ckl:CKL_0294	NA	NA	
BLCPAMOF_02000	OG0002529	group_5373	1	0	0	cso:CLS_25100	NA	NA	
BLCPAMOF_02001	OG0001321	xerC_4	1	0	0	fpr:FP2_29350	NA	NA	
BLCPAMOF_02002	OG0001823	group_2489	0	1	0	fpr:FP2_21880	NA	NA	
BLCPAMOF_02003	OG0000008	group_132	1	0	0	fpa:FPR_07930	NA	NA	
BLCPAMOF_02004	OG0000004	soj_4	1	0	0	fpr:FP2_21850	ko:K03496	NA	
BLCPAMOF_02005	OG0000002	spo0C_3	1	0	0	fpa:FPR_07950	ko:K03497	NA	
BLCPAMOF_02006	OG0000035	group_394	1	0	0	fpa:FPR_05610	NA	NA	

BLCPAMOF_02007	OG0000039	group_304	1	0	0	fpa:FPR_00810	NA	NA	
BLCPAMOF_02008	OG0000017	group_430	1	0	0	fpr:FP2_09010	NA	NA	
BLCPAMOF_02009	OG0000001	group_67	1	1	1	fpr:FP2_21800	ko:K03205	NA	
BLCPAMOF_02010	OG0000006	group_7118	1	2	2	ova:OBV_30190	NA	NA	
BLCPAMOF_02011	OG0001841	group_3025	1	0	0	fpr:FP2_22290	NA	NA	
BLCPAMOF_02012	OG0001842	group_2505	1	0	0	fpr:FP2_22300	NA	NA	
BLCPAMOF_02013	OG0000011	group_7198	3	3	5	fpa:FPR_16940	NA	NA	
BLCPAMOF_02014	OG0000016	group_363	1	2	2	csh:Closa_3716	NA	NA	
BLCPAMOF_02015	OG0001843	group_209	1	0	0	fpr:FP2_22350	NA	NA	
BLCPAMOF_02016	OG0000067	ltrA	1	0	0	sequ:Q426_01745;sezo:SeseC_01909	ko:K00986	NA	
BLCPAMOF_02017	OG0001918	group_204	1	0	0	fpr:FP2_22350	NA	NA	
BLCPAMOF_02018	OG0000012	group_255	1	1	1	fpa:FPR_16900	NA	NA	
BLCPAMOF_02019	OG0000013	group_334	1	0	0	fpr:FP2_22380	NA	NA	
BLCPAMOF_02020	OG0000007	group_247	1	2	2	fpr:FP2_22390	NA	NA	
BLCPAMOF_02021	OG0000003	topB_1	1	0	0	fpa:FPR_19060	ko:K03169	NA	
BLCPAMOF_02022	OG0000019	group_369	1	0	0	fpa:FPR_04590	NA	NA	
BLCPAMOF_02023	OG0000022	group_340	1	0	0	fpr:FP2_10260	NA	NA	
BLCPAMOF_02024	OG0000020	group_7182	1	0	0	fpa:FPR_04570	NA	NA	
BLCPAMOF_02025	OG0000050	group_753	1	0	0	fpa:FPR_04560	NA	NA	
BLCPAMOF_02026	OG0000076	group_608	1	1	1	fpr:FP2_17370	NA	NA	
BLCPAMOF_02027	OG0000216	recF_2	1	0	0	fpr:FP2_21640;fpa:FPR_04540	NA	NA	
BLCPAMOF_02028	OG0000163	group_2031	1	0	0	fpr:FP2_21630	NA	NA	
BLCPAMOF_02029	OG0001997	group_2859	1	1	1	NA	NA	NA	
BLCPAMOF_02030	OG0000077	group_7217	1	2	2	fpr:FP2_27120	NA	NA	
BLCPAMOF_02031	OG0000005	group_95	1	0	0	csh:Closa_3704	NA	NA	
BLCPAMOF_02032	OG0000023	group_261	1	0	0	fpr:FP2_21550	NA	NA	
BLCPAMOF_02033	OG0000038	group_432	2	2	3	fpr:FP2_08920	NA	NA	
BLCPAMOF_02034	OG0000010	group_187	1	0	0	fpr:FP2_08910	NA	NA	
BLCPAMOF_02035	OG0000250	group_763	1	0	0	fpr:FP2_09570	NA	NA	
BLCPAMOF_02036	OG0003578	group_3315	1	0	0	fpr:FP2_00430	NA	NA	
BLCPAMOF_02037	OG0003579	group_3316	1	2	2	fpr:FP2_00420	NA	NA	
BLCPAMOF_02038	OG0003580	group_5374	1	0	0	fpr:FP2_00410	NA	NA	
BLCPAMOF_02039	OG0002323	group_2601	1	0	0	NA	NA	NA	
BLCPAMOF_02040	OG0002322	group_2600	1	0	0	fpr:FP2_00390	NA	NA	
BLCPAMOF_02041	OG0002321	group_4532	1	0	0	fpr:FP2_29600	NA	NA	
BLCPAMOF_02042	OG0004147	group_5375	1	0	0	bprm:CL3_15290	NA	specific_fp360	○
BLCPAMOF_02043	OG0004148	group_5376	1	0	0	NA	NA	specific_fp360	○
BLCPAMOF_02044	OG0004149	group_5377	1	0	0	NA	NA	specific_fp360	○
BLCPAMOF_02045	OG0002320	group_2599	1	0	0	fpla:A4U99_12295	NA	NA	
BLCPAMOF_02046	OG0002319	group_3317	1	0	0	fpr:FP2_00360	NA	NA	
BLCPAMOF_02047	OG0003581	group_3318	1	0	0	fpr:FP2_00350	NA	NA	
BLCPAMOF_02048	OG0002967	group_2298	1	0	0	fpr:FP2_00330	NA	NA	
BLCPAMOF_02049	OG0004150	group_5378	0	1	0	coc:Coch_1637	NA	specific_fp360	○
BLCPAMOF_02050	OG0002967	group_2299	1	0	0	fpr:FP2_00310	NA	NA	
BLCPAMOF_02051	OG0003582	group_3319	1	0	0	fpr:FP2_00300	NA	NA	
BLCPAMOF_02052	OG0003583	group_3320	1	0	0	fpr:FP2_00280	NA	NA	
BLCPAMOF_02053	OG0003584	group_3321	1	0	0	fpr:FP2_00270	NA	NA	
BLCPAMOF_02054	OG0003585	group_5379	1	0	0	bprm:CL3_15030	NA	specific_fp360	
BLCPAMOF_02055	OG0002453	group_3170	1	0	0	bprm:CL3_15000	NA	NA	
BLCPAMOF_02056	OG0004151	group_5380	1	0	0	bprm:CL3_14990	NA	specific_fp360	○
BLCPAMOF_02057	OG0004152	group_5381	1	0	0	fpla:A4U99_12425	NA	specific_fp360	○
BLCPAMOF_02058	OG0002318	group_3169	2	1	2	fpr:FP2_00260	NA	NA	
BLCPAMOF_02059	OG0002317	group_2598	1	0	0	fpr:FP2_00250	NA	NA	
BLCPAMOF_02060	OG0002316	group_3168	0	1	0	fpr:FP2_00240	NA	NA	
BLCPAMOF_02061	OG0004153	group_5382	1	0	0	fpla:A4U99_12445	NA	specific_fp360	
BLCPAMOF_02062	OG0002315	group_3167	1	0	0	fpla:A4U99_12450	NA	NA	
BLCPAMOF_02063	OG0000218	group_2243	3	3	5	fpr:FP2_29400	NA	NA	
BLCPAMOF_02064	OG0000032	group_592	1	0	0	NA	NA	NA	
BLCPAMOF_02065	OG0001945	group_2597	0	1	0	NA	NA	NA	
BLCPAMOF_02066	OG0001319	lexA_3	1	0	0	NA	NA	NA	
BLCPAMOF_02067	OG0003230	group_2677	0	1	0	NA	NA	NA	
BLCPAMOF_02068	OG0001320	group_2127	1	0	0	fpr:FP2_28430	NA	NA	
BLCPAMOF_02069	OG0000251	group_1677	1	0	0	fpa:FPR_19500	NA	NA	
BLCPAMOF_02070	OG0000028	group_2496	1	0	0	fpr:FP2_29380	NA	NA	
BLCPAMOF_02071	OG0000090	group_1274	1	0	0	fpa:FPR_19520	NA	NA	
BLCPAMOF_02072	OG0000175	mazF_2	1	0	0	fpr:FP2_04130	ko:K07171	NA	
BLCPAMOF_02073	OG0001840	group_419	1	0	0	fpa:FPR_19540	NA	NA	
BLCPAMOF_02074	OG0001745	group_3015	1	0	0	fpr:FP2_29360	NA	NA	
BLCPAMOF_02075	OG0001321	xerC_3	1	0	0	fpr:FP2_29350	NA	NA	
BLCPAMOF_02077	OG0001916	group_2128	1	0	0	fpr:FP2_29340	NA	NA	
BLCPAMOF_02078	OG0001322	group_864	1	0	0	fpr:FP2_29330	NA	NA	
BLCPAMOF_02079	OG0002040	ypwA	1	0	0	fpr:FP2_29320	ko:K01299	NA	
BLCPAMOF_02080	OG0001390	group_663	1	0	0	eel:EUBELI_01251	NA	NA	
BLCPAMOF_02081	OG0001391	group_1720	1	0	0	fpr:FP2_29300	NA	NA	
BLCPAMOF_02082	OG0001392	group_2135	1	0	0	fpr:FP2_29290	NA	NA	
BLCPAMOF_02083	OG0001393	group_5383	2	3	4	fpr:FP2_29280	NA	NA	
BLCPAMOF_02086	OG0001255	group_5384	1	0	0	fpr:FP2_29270	NA	NA	
BLCPAMOF_02087	OG0001256	group_1636	1	0	0	fpr:FP2_29260	NA	NA	
BLCPAMOF_02088	OG0000244	group_2112	1	0	0	fpr:FP2_29250	NA	NA	
BLCPAMOF_02089	OG0001257	group_2113	1	0	0	fpr:FP2_29240	NA	NA	
BLCPAMOF_02090	OG0001258	group_1637	0	1	0	fpr:FP2_29230	NA	NA	
BLCPAMOF_02091	OG0000245	group_847	1	0	0	fpr:FP2_29220	NA	NA	
BLCPAMOF_02092	OG0000246	group_5385	1	0	0	fpr:FP2_29210	NA	NA	
BLCPAMOF_02093	OG0000247	group_849	1	0	0	fpr:FP2_29200	NA	NA	
BLCPAMOF_02094	OG0000248	group_851	1	0	0	fpr:FP2_29190	NA	NA	
BLCPAMOF_02095	OG0001259	group_853	0	1	0	fpr:FP2_29180	NA	NA	
BLCPAMOF_02096	OG0001260	group_1638	1	0	0	fpr:FP2_29170	ko:K06972	NA	
BLCPAMOF_02097	OG0001261	group_1639	6	7	12	fpr:FP2_29150	ko:K06902	NA	
BLCPAMOF_02098	OG0001262	group_2476	1	0	0	fpr:FP2_29140	NA	NA	
BLCPAMOF_02099	OG0001328	gpsA	1	0	0	fpr:FP2_29130	ko:K00057	NA	
BLCPAMOF_02100	OG0000176	tcyB_1	3	2	4	fpr:FP2_29120	ko:K10009	NA	
BLCPAMOF_02101	OG0001329	tcyN	1	0	0	fpr:FP2_29110	ko:K10010	NA	
BLCPAMOF_02102	OG0001330	tcyA	1	0	0	fpr:FP2_29100	ko:K02424	NA	
BLCPAMOF_02103	OG0002271	uvrA_1	1	0	0	fpr:FP2_29080	ko:K03701	NA	
BLCPAMOF_02104	OG0000015	group_5386	1	0	0	rob:CK5_16390	ko:K05350	NA	
BLCPAMOF_02105	OG0000308	gltR_2	1	0	0	fpr:FP2_29070	NA	NA	
BLCPAMOF_02106	OG0001381	group_874	1	0	0	fpr:FP2_29060	ko:K11529	NA	
BLCPAMOF_02107	OG0004154	group_5387	1	0	0	cbut:ATN24_03050	ko:K06987	specific_fp360	○
BLCPAMOF_02108	OG0000557	kdpE_2	1	0	0	fpr:FP2_19490	ko:K07667	NA	
BLCPAMOF_02109	OG0000556	kdpD_2	2	2	3	fpr:FP2_19500	ko:K07646	NA	
BLCPAMOF_02110	OG0000555	ktrA	1	0	0	fpr:FP2_19510	ko:K03499	NA	
BLCPAMOF_02111	OG0000554	ntpJ	5	6	10	fpa:FPR_27430	ko:K03498	NA	
BLCPAMOF_02112	OG0000000	group_48	0	1	0	fpa:FPR_24750	NA	NA	
BLCPAMOF_02113	OG0002501	group_4834	1	1	1	fpr:FP2_28550	NA	NA	
BLCPAMOF_02114	OG0002502	group_3241	1	0	0	fpr:FP2_28540	ko:K20391	NA	
BLCPAMOF_02115	OG0002503	group_4835	0	1	0	NA	NA	NA	
BLCPAMOF_02116	OG0002504	queE	1	0	0	ssd:SPSINT_1650	ko:K06871	NA	
BLCPAMOF_02117	OG0002505	group_4837	5	6	10	NA	NA	NA	
BLCPAMOF_02118	OG0001991	chuR	1	0	0	fpr:FP2_28510	ko:K06871	NA	
BLCPAMOF_02119	OG0001802	msbA_2	3	3	5	fpr:FP2_28500	NA	NA	
BLCPAMOF_02120	OG0000068	group_960	1	0	0	fpr:FP2_27640	NA	NA	
BLCPAMOF_02121	OG0000054	dnaG_5	1	0	0	fpa:FPR_25070	NA	NA	
BLCPAMOF_02122	OG0000053	group_7225	1	0	0	fpa:FPR_09510	ko:K06919	NA	
BLCPAMOF_02123	OG0000307	pre	1	0	0	fpr:FP2_19740	NA	NA	

BLCPAMOF_02124	OG0000026	group_329	0	1	0	fpa:FPR_09490	NA	NA	
BLCPAMOF_02125	OG0000025	xerC_8	1	0	0	fpr:FP2_13920	NA	NA	
BLCPAMOF_02126	OG0000014	group_145	1	0	0	fpr:FP2_13830	NA	NA	
BLCPAMOF_02127	OG0001768	sacA	1	0	0	fpr:FP2_08710	ko:K01193	NA	
BLCPAMOF_02128	OG0001769	group_4311	1	0	0	abao:BEQ56_06480	ko:K17318	NA	
BLCPAMOF_02129	OG0000125	group_4310	3	4	6	abao:BEQ56_06485	ko:K17320	NA	
BLCPAMOF_02130	OG0001770	group_4309	3	3	5	abao:BEQ56_06490	ko:K17319	NA	
BLCPAMOF_02131	OG0002537	group_4308	1	0	0	abao:BEQ56_06495	ko:K02529	NA	
BLCPAMOF_02132	OG0003538	group_3128	1	1	1	NA	NA	shared	○
BLCPAMOF_02133	OG0003537	group_3127	1	1	1	NA	NA	shared	
BLCPAMOF_02134	OG0003536	group_4307	3	3	5	NA	NA	shared	○
BLCPAMOF_02135	OG0000037	scrK_2	1	0	0	fpr:FP2_08640	ko:K00847	NA	
BLCPAMOF_02136	OG0000087	ams_2	1	0	0	fpr:FP2_08630	ko:K05341	NA	
BLCPAMOF_02137	OG0001805	group_1152	0	1	0	fpa:FPR_23810	NA	NA	
BLCPAMOF_02138	OG0000040	group_297	1	0	0	fpa:FPR_23820	NA	NA	
BLCPAMOF_02139	OG0000059	group_273	1	0	0	rho:RHOM_06500	NA	NA	
BLCPAMOF_02140	OG0000160	group_457	1	0	0	fpr:FP2_14020	NA	NA	
BLCPAMOF_02141	OG0000058	xerC_10	1	0	0	fpr:FP2_14030	NA	NA	
BLCPAMOF_02149	OG0000128	sigF	1	0	0	fpr:FP2_27110	ko:K03091	NA	
BLCPAMOF_02150	OG0000206	spoIIAB	1	0	0	fpr:FP2_27100	ko:K06379	NA	
BLCPAMOF_02151	OG0000205	spoIIAA	1	0	0	fpr:FP2_27090	ko:K06378	NA	
BLCPAMOF_02153	OG0000159	group_2366	2	2	3	fpr:FP2_27070	NA	NA	
BLCPAMOF_02154	OG0000158	valS	1	0	0	fpr:FP2_27060	ko:K01873	NA	
BLCPAMOF_02155	OG0000066	group_5389	1	0	0	sui:SSUJS14_0536	NA	NA	
BLCPAMOF_02156	OG0002968	group_5390	5	6	10	fpr:FP2_27040	NA	NA	
BLCPAMOF_02157	OG0000553	yitJ	1	0	0	fpr:FP2_27030	ko:K00547;ko:K00297	NA	
BLCPAMOF_02158	OG0000067	ltrA_6	1	0	0	sequ:Q426_01745;sezo:SeseC_01909	ko:K00986	NA	
BLCPAMOF_02159	OG0004155	group_584	0	1	0	fpr:FP2_27030	ko:K00547;ko:K00297	NA	
BLCPAMOF_02160	OG0000804	group_3242	1	0	0	fpr:FP2_27020	NA	NA	
BLCPAMOF_02161	OG0002506	group_5391	1	0	0	fpr:FP2_27010	NA	NA	
BLCPAMOF_02162	OG0000552	group_2365	1	0	0	fpr:FP2_27000	NA	NA	
BLCPAMOF_02163	OG0000551	hflX	1	0	0	fpr:FP2_26980	ko:K03665	NA	
BLCPAMOF_02164	OG0001264	group_649	1	0	0	fpr:FP2_26970	NA	NA	
BLCPAMOF_02165	OG0001739	group_2115	1	1	1	fpr:FP2_26960	NA	NA	
BLCPAMOF_02166	OG0001265	feoB_2	6	7	12	fpr:FP2_26950	ko:K04759	NA	
BLCPAMOF_02167	OG0001266	feoA	0	1	0	fpr:FP2_26940	ko:K04758	NA	
BLCPAMOF_02168	OG0001267	group_1642	1	0	0	fpr:FP2_26930	ko:K04758	NA	
BLCPAMOF_02169	OG0001268	group_854	1	0	0	fpr:FP2_26920	NA	NA	
BLCPAMOF_02170	OG0001269	group_5392	1	0	0	fpr:FP2_26910	NA	NA	
BLCPAMOF_02171	OG0000649	pepT	1	0	0	fpr:FP2_26900	ko:K01258	NA	
BLCPAMOF_02172	OG0000664	group_2381	1	0	0	rob:CK5_34480	NA	NA	
BLCPAMOF_02173	OG0000663	niaR	0	1	0	fpr:FP2_26880	ko:K07105	NA	
BLCPAMOF_02174	OG0000662	tvaII	1	0	0	fpr:FP2_26870	NA	NA	
BLCPAMOF_02175	OG0000661	glgB_1	1	0	0	fpr:FP2_26860	ko:K00700	NA	
BLCPAMOF_02176	OG0000660	group_2679	7	7	13	fpr:FP2_26850	NA	NA	
BLCPAMOF_02177	OG0000659	tig_4	1	0	0	fpr:FP2_26840	ko:K03545	NA	
BLCPAMOF_02178	OG0000658	group_601	1	0	0	fpr:FP2_26830	NA	NA	
BLCPAMOF_02179	OG0001898	sarA_3	1	0	0	fpr:FP2_26820	ko:K15580	NA	
BLCPAMOF_02180	OG0000092	oppB	3	3	5	fpr:FP2_26810	ko:K15581	NA	
BLCPAMOF_02181	OG0001917	dppC	3	3	5	fpr:FP2_26800	ko:K15582	NA	
BLCPAMOF_02182	OG0000033	oppD_3	1	0	0	fpr:FP2_26790	ko:K15583	NA	
BLCPAMOF_02183	OG0000093	oppF_3	1	0	0	fpr:FP2_26780	ko:K10823	NA	
BLCPAMOF_02184	OG0001326	lcfB	1	1	1	fpr:FP2_26770	ko:K01897	NA	
BLCPAMOF_02185	OG0001327	group_5393	1	0	0	fpr:FP2_26760	NA	NA	
BLCPAMOF_02186	OG0000549	group_2680	1	2	2	fpr:FP2_26750	NA	NA	
BLCPAMOF_02187	OG0000550	lrpC	1	0	0	fpr:FP2_26740	ko:K03719	NA	
BLCPAMOF_02188	OG0001165	fruA	5	6	10	fpr:FP2_26730	ko:K02768;ko:K02769;ko:K02770	NA	
BLCPAMOF_02189	OG0001164	lacC	1	0	0	fpr:FP2_26720	ko:K00882	NA	
BLCPAMOF_02190	OG0000238	srlR	1	0	0	fpr:FP2_26710	ko:K03436	NA	
BLCPAMOF_02191	OG0001699	pepD_1	1	0	0	fpr:FP2_26700	ko:K08659	NA	
BLCPAMOF_02192	OG0000815	group_2259	1	0	0	fpr:FP2_26690	NA	NA	
BLCPAMOF_02193	OG0001331	uvrC	1	0	0	fpr:FP2_26680	ko:K03703	NA	
BLCPAMOF_02194	OG0004156	group_5394	1	2	2	fpr:FP2_26670	NA	specific_fp360	
BLCPAMOF_02195	OG0001332	crh	1	1	1	fpa:FPR_06130;fpr:FP2_26660	ko:K11189	NA	
BLCPAMOF_02196	OG0001333	trmD	1	0	0	fpr:FP2_26650	ko:K00554	NA	
BLCPAMOF_02197	OG0001334	rimM	1	0	0	fpr:FP2_26640	ko:K02860	NA	
BLCPAMOF_02198	OG0001335	group_3017	1	0	0	fpr:FP2_26630	ko:K06960	NA	
BLCPAMOF_02199	OG0001336	rpsP	0	1	0	fpr:FP2_26620	ko:K02959	NA	
BLCPAMOF_02200	OG0001337	ffh	1	0	0	fpr:FP2_26610	ko:K03106	NA	
BLCPAMOF_02201	OG0001338	group_1687	1	0	0	fpr:FP2_26600	ko:K09787	NA	
BLCPAMOF_02202	OG0001339	cysK	1	0	0	dpr:Despr_2989	ko:K01738	NA	
BLCPAMOF_02203	OG0001340	mepA_6	5	6	10	fpr:FP2_26580	NA	NA	
BLCPAMOF_02204	OG0000204	rffG	1	0	0	fpr:FP2_26570	ko:K01710	NA	
BLCPAMOF_02205	OG0000546	rmlD_2	1	0	0	fpr:FP2_26560	ko:K00067	NA	
BLCPAMOF_02206	OG0000545	rfbA	1	0	0	fpr:FP2_26550	ko:K00973	NA	
BLCPAMOF_02207	OG0000544	wbbL_2	1	0	0	fpa:FPR_02840	NA	NA	
BLCPAMOF_02208	OG0000543	epsE	1	0	0	fpr:FP2_26530	ko:K20444	NA	
BLCPAMOF_02209	OG0000542	group_1145	1	1	1	fpr:FP2_26520	ko:K06381	NA	
BLCPAMOF_02210	OG0001409	group_1736	2	3	4	fpr:FP2_26510	NA	NA	
BLCPAMOF_02211	OG0001408	group_1735	3	3	5	fpr:FP2_26500	NA	NA	
BLCPAMOF_02212	OG0001943	nfrA2	1	0	0	fpr:FP2_26480	NA	NA	
BLCPAMOF_02213	OG0001407	fliY_1	1	1	1	fpr:FP2_26470	ko:K02030	NA	
BLCPAMOF_02214	OG0001406	artQ	3	3	5	fpr:FP2_26460	ko:K02029	NA	
BLCPAMOF_02215	OG0001405	glnQ	1	0	0	byl:A4V09_03965	ko:K02028	NA	
BLCPAMOF_02216	OG0000643	metN2	1	0	0	fpr:FP2_26440	ko:K05833	NA	
BLCPAMOF_02217	OG0000642	group_1214	4	5	8	fpr:FP2_26430	ko:K05832	NA	
BLCPAMOF_02218	OG0000641	group_1213	1	0	0	fpr:FP2_26420	ko:K01989	NA	
BLCPAMOF_02219	OG0001901	group_5395	3	4	6	fpr:FP2_26410	NA	NA	
BLCPAMOF_02220	OG0001900	ytrB_2	1	0	0	fpr:FP2_26400	ko:K01990	NA	
BLCPAMOF_02221	OG0001899	ytrA	1	0	0	fpr:FP2_26390	NA	NA	
BLCPAMOF_02222	OG0001235	wbbL_1	2	1	2	fpr:FP2_26380	NA	NA	
BLCPAMOF_02223	OG0001236	group_1623	1	1	1	fpr:FP2_26370	NA	NA	
BLCPAMOF_02224	OG0001237	spxA	1	0	0	fpr:FP2_26360	NA	NA	
BLCPAMOF_02225	OG0001238	fdx	1	0	0	fpr:FP2_26350	ko:K05337	NA	
BLCPAMOF_02226	OG0000243	polA	1	0	0	fpr:FP2_26340	ko:K02335	NA	
BLCPAMOF_02227	OG0001239	tsaD_2	1	0	0	fpr:FP2_26330	ko:K01409	NA	
BLCPAMOF_02228	OG0000548	group_5396	4	5	8	fpr:FP2_26320	ko:K07052	NA	
BLCPAMOF_02231	OG0000547	pfp_4	1	0	0	fpr:FP2_26310	ko:K21071	NA	
BLCPAMOF_02232	OG0000151	group_5397	1	2	2	fpr:FP2_26300	ko:K06872	NA	
BLCPAMOF_02233	OG0000152	group_2340	1	1	1	fpr:FP2_26290	NA	NA	
BLCPAMOF_02234	OG0000153	group_2341	1	0	0	fpr:FP2_26280	NA	NA	
BLCPAMOF_02235	OG0000401	group_1044	3	3	5	fpr:FP2_26270	NA	NA	
BLCPAMOF_02236	OG0000402	thiM	1	0	0	fpr:FP2_26260	ko:K00878	NA	
BLCPAMOF_02237	OG0000199	thiE	1	0	0	fpr:FP2_26250	ko:K00788	NA	
BLCPAMOF_02238	OG0000240	thiD	1	0	0	fpr:FP2_26240	ko:K00941	NA	
BLCPAMOF_02239	OG0000403	thiC	1	0	0	fpr:FP2_26230	ko:K03147	NA	
BLCPAMOF_02241	OG0004157	group_5398	2	2	3	fpr:FP2_26220	NA	specific_fp360	
BLCPAMOF_02242	OG0001992	group_2379	1	0	0	fpr:FP2_26210	NA	NA	
BLCPAMOF_02243	OG0000482	tdcB	1	0	0	fpr:FP2_26200	ko:K01754	NA	
BLCPAMOF_02244	OG0001301	leuB	1	0	0	fpr:FP2_26190	ko:K00052	NA	
BLCPAMOF_02245	OG0001302	DmdB	1	0	0	fpr:FP2_26180	ko:K01704	NA	
BLCPAMOF_02246	OG0001303	dmdA_1	1	0	0	fpr:FP2_26170	ko:K01703	NA	
BLCPAMOF_02247	OG0001304	leuA	1	0	0	fpr:FP2_26160	ko:K01649	NA	
BLCPAMOF_02248	OG0001305	ftsH4	2	1	2	fpr:FP2_26140	ko:K03798	NA	

BLCPAMOF_02249	OG0001306	group_3157	1	1	1	fpr:FP2_26130	NA	NA	
BLCPAMOF_02250	OG0001432	dnaK_1	1	0	0	fpr:FP2_26120	ko:K04043	NA	
BLCPAMOF_02251	OG0001433	group_5399	1	0	0	fpr:FP2_26110	ko:K07126	NA	
BLCPAMOF_02252	OG0000473	group_1085	3	2	4	rho:RHOM_04715	NA	NA	
BLCPAMOF_02253	OG0000474	group_1086	3	3	5	fpr:FP2_26090	ko:K06147	NA	
BLCPAMOF_02254	OG0000475	tig_3	1	0	0	fpr:FP2_26070	NA	NA	
BLCPAMOF_02255	OG0000476	group_1087	2	1	2	fpr:FP2_26060	NA	NA	
BLCPAMOF_02257	OG0001731	fdhD	1	0	0	fpr:FP2_26050	ko:K02379	NA	
BLCPAMOF_02258	OG0001730	rsxG_1	1	1	1	fpr:FP2_26040	NA	NA	
BLCPAMOF_02259	OG0001729	ydhY	1	0	0	fpr:FP2_26030	NA	NA	
BLCPAMOF_02260	OG0001728	ydhV	1	0	0	fpr:FP2_26020	NA	NA	
BLCPAMOF_02261	OG0001727	group_2088	1	0	0	fpr:FP2_26010	NA	NA	
BLCPAMOF_02262	OG0001726	moeA	1	0	0	fpr:FP2_26000	ko:K03750	NA	
BLCPAMOF_02263	OG0001144	mobB	1	0	0	csr:Cspa_c30200	ko:K03753	NA	
BLCPAMOF_02264	OG0001143	cinA_1	1	0	0	fpr:FP2_25980	NA	NA	
BLCPAMOF_02265	OG0001142	moaC	1	0	0	fpr:FP2_25970	ko:K03637	NA	
BLCPAMOF_02266	OG0001141	moaA	1	0	0	fpr:FP2_25960	ko:K03639	NA	
BLCPAMOF_02267	OG0001140	mog	1	0	0	fpr:FP2_25950	NA	NA	
BLCPAMOF_02268	OG0004158	mog_2	1	0	0	fpr:FP2_25950	NA	specific_fp360	
BLCPAMOF_02269	OG0001139	modA	1	1	1	fpr:FP2_25940	ko:K02020	NA	
BLCPAMOF_02270	OG0001138	modB	3	3	5	fpr:FP2_25930	ko:K02018	NA	
BLCPAMOF_02271	OG0001137	potA_2	1	0	0	fpr:FP2_25920	ko:K02017	NA	
BLCPAMOF_02272	OG0001565	metH	1	0	0	rus:RBI_I01351	ko:K00548	NA	
BLCPAMOF_02273	OG0001566	group_1829	1	0	0	fpr:FP2_25900	NA	NA	
BLCPAMOF_02274	OG0001323	group_1679	3	3	5	fpr:FP2_25890	NA	NA	
BLCPAMOF_02275	OG0000252	afr	1	0	0	fpr:FP2_25880	NA	NA	
BLCPAMOF_02276	OG0001324	coaX_1	1	0	0	fpr:FP2_25870	ko:K03525	NA	
BLCPAMOF_02277	OG0001325	coaBC	1	0	0	fpr:FP2_25850	ko:K13038	NA	
BLCPAMOF_02278	OG0000183	group_5400	1	1	1	fpr:FP2_25840	NA	NA	
BLCPAMOF_02279	OG0000249	upp	1	0	0	fpr:FP2_25830	ko:K00761	NA	
BLCPAMOF_02280	OG0001293	ywlF	1	0	0	fpr:FP2_25820	ko:K01808	NA	
BLCPAMOF_02281	OG0001292	tsaB	1	0	0	fpr:FP2_25810	ko:K14742	NA	
BLCPAMOF_02282	OG0001291	tsaE	1	0	0	fpr:FP2_25800	ko:K06925	NA	
BLCPAMOF_02283	OG0001290	group_5401	1	1	1	fpa:FPR_06000	NA	NA	
BLCPAMOF_02284	OG0001289	rodA	4	5	8	fpr:FP2_25780	ko:K05837	NA	
BLCPAMOF_02285	OG0004159	group_5402	1	1	1	NA	NA	specific_fp360	O
BLCPAMOF_02286	OG0000486	ilvD_2	1	0	0	fpr:FP2_25760	ko:K01687	NA	
BLCPAMOF_02287	OG0000485	ilvC	1	0	0	fpr:FP2_25750	ko:K00053	NA	
BLCPAMOF_02288	OG0000484	ilvH	1	0	0	fpr:FP2_25740	ko:K01653	NA	
BLCPAMOF_02289	OG0000126	ilvB	1	0	0	fpr:FP2_25730	ko:K01652	NA	
BLCPAMOF_02290	OG0000483	ruvB_1	1	0	0	fpr:FP2_25720	ko:K06923	NA	
BLCPAMOF_02291	OG0004160	group_5403	1	0	0	fpr:FP2_25710	ko:K09124	specific_fp360	
BLCPAMOF_02292	OG0004161	group_5404	1	0	0	rix:RO1_06020	NA	specific_fp360	O
BLCPAMOF_02293	OG0002166	radD_1	1	0	0	esu:EUS_17830	NA	NA	
BLCPAMOF_02294	OG0001780	group_2237	1	0	0	fpa:FPR_01720	NA	NA	
BLCPAMOF_02295	OG0001896	group_4466	1	0	0	cso:CLS_06550	ko:K07133	NA	
BLCPAMOF_02296	OG0001781	group_2580	1	0	0	fpa:FPR_01710	NA	NA	
BLCPAMOF_02297	OG0001850	group_3159	1	0	0	fpr:FP2_25650	NA	NA	
BLCPAMOF_02298	OG0002065	group_2582	1	0	0	fpa:FPR_01690	NA	NA	
BLCPAMOF_02299	OG0000146	tnpR_1	1	0	0	fpa:FPR_01670	NA	NA	
BLCPAMOF_02300	OG0002066	group_2586	1	0	0	fpa:FPR_01660	NA	NA	
BLCPAMOF_02301	OG0001937	group_2591	1	0	0	fpa:FPR_01490	NA	NA	
BLCPAMOF_02302	OG0001938	group_2593	1	0	0	fpa:FPR_01480	NA	NA	
BLCPAMOF_02303	OG0001872	group_1927	1	0	0	fpa:FPR_01470	NA	NA	
BLCPAMOF_02304	OG0000031	group_30	1	0	0	fpa:FPR_01460	NA	NA	
BLCPAMOF_02305	OG0001163	cof	1	0	0	eel:EUBELI_00334	NA	NA	
BLCPAMOF_02306	OG0002023	group_5405	1	0	0	ere:EUBREC_3620	NA	NA	
BLCPAMOF_02307	OG0000169	rhaS_2	1	0	0	eel:EUBELI_20101	NA	NA	
BLCPAMOF_02309	OG0001424	group_2161	1	1	1	fpr:FP2_25610	NA	NA	
BLCPAMOF_02310	OG0000261	group_5407	0	1	0	fpr:FP2_25600	NA	NA	
BLCPAMOF_02311	OG0001425	group_5408	0	1	0	fpr:FP2_25590	NA	NA	
BLCPAMOF_02312	OG0002044	lexA_2	1	0	0	fpr:FP2_25580	ko:K01356	NA	
BLCPAMOF_02313	OG0001426	trmO	1	0	0	fpr:FP2_25570	NA	NA	
BLCPAMOF_02314	OG0000262	group_1751	1	0	0	fpr:FP2_25560	NA	NA	
BLCPAMOF_02315	OG0001856	group_2513	1	1	1	fpr:FP2_25550	NA	NA	
BLCPAMOF_02316	OG0002176	rbr	1	0	0	fpr:FP2_25540	NA	NA	
BLCPAMOF_02317	OG0001434	group_5409	4	5	8	fpr:FP2_25530	NA	NA	
BLCPAMOF_02318	OG0001435	group_1757	1	0	0	fpr:FP2_25520	ko:K03218	NA	
BLCPAMOF_02319	OG0000263	fba	1	0	0	fpr:FP2_25510	ko:K01624	NA	
BLCPAMOF_02320	OG0002969	group_3323	1	1	1	fpa:FPR_05810	ko:K09974	NA	
BLCPAMOF_02324	OG0000523	cshA	1	0	0	fpr:FP2_15460	ko:K05592	NA	
BLCPAMOF_02325	OG0000522	hup_1	1	0	0	fpr:FP2_15450	ko:K03530	NA	
BLCPAMOF_02326	OG0000521	carB	1	0	0	fpr:FP2_15440	ko:K01955	NA	
BLCPAMOF_02327	OG0000520	carA	1	0	0	fpr:FP2_15430	ko:K01956	NA	
BLCPAMOF_02328	OG0000519	pyrE_2	1	0	0	fpr:FP2_15420	ko:K00762	NA	
BLCPAMOF_02329	OG0000518	pyrDB	1	0	0	fpr:FP2_15410	ko:K17828	NA	
BLCPAMOF_02330	OG0000517	pyrK	1	0	0	fpr:FP2_15400	ko:K02823	NA	
BLCPAMOF_02331	OG0000516	pyrF	1	0	0	fpr:FP2_15390	ko:K01591	NA	
BLCPAMOF_02332	OG0000515	pyrC	1	0	0	fpr:FP2_15380	ko:K01465	NA	
BLCPAMOF_02333	OG0001940	group_5410	0	1	0	NA	NA	NA	
BLCPAMOF_02334	OG0000514	cysE	1	0	0	fpr:FP2_15350	ko:K00640	NA	
BLCPAMOF_02335	OG0000513	group_733	1	0	0	fpa:FPR_03490	NA	NA	
BLCPAMOF_02336	OG0000512	pepV_2	1	0	0	fpr:FP2_15330	ko:K01439	NA	
BLCPAMOF_02337	OG0000511	group_1123	2	3	4	fpr:FP2_15320	NA	NA	
BLCPAMOF_02338	OG0000510	exoA	1	0	0	fpr:FP2_15310	ko:K01142	NA	
BLCPAMOF_02339	OG0000509	yeeO_1	4	5	8	fpr:FP2_15300	NA	NA	
BLCPAMOF_02340	OG0001436	fpgS_1	1	0	0	fpr:FP2_15280	ko:K11754	NA	
BLCPAMOF_02341	OG0001437	folT	3	3	5	fpr:FP2_15270	NA	NA	
BLCPAMOF_02342	OG0001421	pepF1	1	0	0	fpr:FP2_15260	NA	NA	
BLCPAMOF_02343	OG0002538	mscL	1	2	2	fpa:FPR_12220	ko:K03282	NA	
BLCPAMOF_02345	OG0001857	group_2518	1	0	0	rob:CK5_36400	ko:K05995	NA	
BLCPAMOF_02346	OG0002616	group_3052	1	0	0	NA	NA	NA	
BLCPAMOF_02347	OG0001757	mgrA	1	0	0	rob:CK5_13830	NA	NA	
BLCPAMOF_02348	OG0001756	group_2159	1	0	0	tpk:JO40_10610	NA	NA	
BLCPAMOF_02349	OG0001755	group_2158	1	0	0	esu:EUS_17460	NA	NA	
BLCPAMOF_02350	OG0001287	lrgA	2	3	4	cah:CAETHG_1207;clj:CLJU_c33090	ko:K06518	NA	
BLCPAMOF_02351	OG0001286	yohK	3	4	6	fpr:FP2_15160	NA	NA	
BLCPAMOF_02352	OG0001166	group_5411	2	1	2	fpr:FP2_15150	NA	NA	
BLCPAMOF_02353	OG0000170	group_5412	1	1	1	fpr:FP2_15140	ko:K02027	NA	
BLCPAMOF_02354	OG0000407	cysS	1	0	0	fpr:FP2_15130	ko:K01883	NA	
BLCPAMOF_02355	OG0002443	group_3154	1	0	0	fpr:FP2_15120	NA	NA	
BLCPAMOF_02356	OG0001480	asnA	1	0	0	fpr:FP2_15110	ko:K01914	NA	
BLCPAMOF_02357	OG0001922	group_5413	3	4	6	NA	NA	NA	
BLCPAMOF_02358	OG0001481	pgsA	2	3	4	fpr:FP2_15090	ko:K00995	NA	
BLCPAMOF_02359	OG0001482	rimO	1	0	0	fpr:FP2_15080	ko:K14441	NA	
BLCPAMOF_02360	OG0001483	recX	1	0	0	fpr:FP2_15070	ko:K03565	NA	
BLCPAMOF_02361	OG0001484	recA	1	0	0	fpr:FP2_15060	ko:K03553	NA	
BLCPAMOF_02362	OG0001485	prmC	1	0	0	fpr:FP2_15050	ko:K02493	NA	
BLCPAMOF_02363	OG0001486	group_1803	2	2	3	fpr:FP2_15040	NA	NA	
BLCPAMOF_02364	OG0001487	phoR_2	2	1	2	fpr:FP2_15030	NA	NA	
BLCPAMOF_02365	OG0001488	regX3_1	1	0	0	fpr:FP2_15020	NA	NA	
BLCPAMOF_02366	OG0001489	group_1806	1	1	1	fpa:FPR_11780	NA	NA	
BLCPAMOF_02367	OG0001490	rplQ	1	0	0	fpr:FP2_15000	ko:K02879	NA	
BLCPAMOF_02368	OG0001491	rpoA	1	0	0	fpr:FP2_14990	ko:K03040	NA	

BLCPAMOF_02369	OG0001492	rpsD	1	0	0	fpr:FP2_14980	ko:K02986	NA		
BLCPAMOF_02370	OG0001493	rpsK	0	1	0	fpr:FP2_14970	ko:K02948	NA		
BLCPAMOF_02371	OG0001494	rpsM	1	0	0	fpr:FP2_14960	ko:K02952	NA		
BLCPAMOF_02372	OG0001495	rpmJ	0	1	0	fpr:FP2_14950;fpa:FPR_11720	ko:K02919	NA		
BLCPAMOF_02373	OG0001496	infA	1	0	0	eha:Ethha_0391	ko:K02518	NA		
BLCPAMOF_02374	OG0001497	map	1	0	0	esu:EUS_27830;esr:ES1_24550	ko:K01265	NA		
BLCPAMOF_02375	OG0001498	adk	1	0	0	fpr:FP2_14920	ko:K00939	NA		
BLCPAMOF_02376	OG0001499	secY	5	6	10	eha:Ethha_0387	ko:K03076	NA		
BLCPAMOF_02377	OG0001500	rplO	1	0	0	fpr:FP2_14900	ko:K02876	NA		
BLCPAMOF_02378	OG0001501	rpmD	1	0	0	fpr:FP2_14890;fpa:FPR_11660	ko:K02907	NA		
BLCPAMOF_02379	OG0001502	rpsE	1	0	0	fpr:FP2_14880	ko:K02988	NA		
BLCPAMOF_02380	OG0001503	rplR	0	1	0	fpr:FP2_14870	ko:K02881	NA		
BLCPAMOF_02381	OG0001504	rplF	1	0	0	fpr:FP2_14860	ko:K02933	NA		
BLCPAMOF_02382	OG0001505	rpsH	1	0	0	fpr:FP2_14850	ko:K02994	NA		
BLCPAMOF_02383	OG0001506	rpsZ	0	1	0	fpr:FP2_14840;fpa:FPR_11610	ko:K02954	NA		
BLCPAMOF_02384	OG0001507	rplE	1	0	0	fpr:FP2_14830	ko:K02931	NA		
BLCPAMOF_02385	OG0001508	rplX	1	0	0	fpr:FP2_14820	ko:K02895	NA		
BLCPAMOF_02386	OG0001509	rplN	1	0	0	fpr:FP2_14810	ko:K02874	NA		
BLCPAMOF_02387	OG0001510	rpsQ	0	1	0	fpr:FP2_14800	ko:K02961	NA		
BLCPAMOF_02388	OG0001511	rpmC	0	1	0	fpa:FPR_11560;fpr:FP2_14790	ko:K02904	NA		
BLCPAMOF_02389	OG0001512	rplP	1	0	0	fpr:FP2_14780	ko:K02878	NA		
BLCPAMOF_02390	OG0001513	rpsC	1	0	0	fpr:FP2_14770	ko:K02982	NA		
BLCPAMOF_02391	OG0001514	rplV	1	0	0	fpa:FPR_11530;fpr:FP2_14760	ko:K02890	NA		
BLCPAMOF_02392	OG0001515	rpsS	1	0	0	fpr:FP2_14750	ko:K02965	NA		
BLCPAMOF_02393	OG0001516	rplB	1	0	0	fpr:FP2_14740	ko:K02886	NA		
BLCPAMOF_02394	OG0001517	rplW	1	0	0	fpr:FP2_14730	ko:K02892	NA		
BLCPAMOF_02395	OG0001518	rplD	1	0	0	fpr:FP2_14720	ko:K02926	NA		
BLCPAMOF_02396	OG0001519	rplC	1	0	0	fpr:FP2_14710	ko:K02906	NA		
BLCPAMOF_02397	OG0001520	rpsJ	0	1	0	fpr:FP2_14700	ko:K02946	NA		
BLCPAMOF_02398	OG0002588	group_5414	1	0	0	fpr:FP2_14690	NA	NA		
BLCPAMOF_02399	OG0002587	group_5415	1	0	0	fpr:FP2_14680	ko:K03088	NA		
BLCPAMOF_02400	OG0001521	group_1810	1	0	0	fpr:FP2_14670	NA	NA		
BLCPAMOF_02401	OG0001522	group_892	1	0	0	fpr:FP2_14660	NA	NA		
BLCPAMOF_02402	OG0001523	trmK	1	0	0	sth:STH597	ko:K06967	NA		
BLCPAMOF_02403	OG0001524	group_1812	1	0	0	fpr:FP2_14640	NA	NA		
BLCPAMOF_02404	OG0001525	group_3061	1	0	0	fpr:FP2_14630	NA	NA		
BLCPAMOF_02405	OG0001526	ackA	1	0	0	fpr:FP2_14620	ko:K00925	NA		
BLCPAMOF_02406	OG0001527	group_1814	1	0	0	fpr:FP2_14610	NA	NA		
BLCPAMOF_02407	OG0001528	gltD_1	1	0	0	fpr:FP2_14600	ko:K00266	NA		
BLCPAMOF_02408	OG0001529	group_893	7	8	14	eel:EUBELI_01841	NA	NA		
BLCPAMOF_02409	OG0001530	group_1815	1	0	0	fpa:FPR_11410	NA	NA		
BLCPAMOF_02410	OG0001531	group_1816	3	3	5	fpr:FP2_14570	NA	NA		
BLCPAMOF_02411	OG0000180	ywiE_2	2	2	3	fpr:FP2_14560	ko:K06131	NA		
BLCPAMOF_02412	OG0002051	group_2522	1	0	0	fpr:FP2_14550	NA	NA		
BLCPAMOF_02413	OG0000144	udk_1	1	0	0	fpr:FP2_14540	ko:K00876	NA		
BLCPAMOF_02414	OG0000150	atpC_2	1	0	0	fpr:FP2_14530	ko:K02114	NA		
BLCPAMOF_02415	OG0000196	atpD_2	1	0	0	fpr:FP2_14520	ko:K02112	NA		
BLCPAMOF_02416	OG0000195	atpG_2	1	0	0	fpr:FP2_14510	ko:K02115	NA		
BLCPAMOF_02417	OG0000194	atpA_2	1	0	0	fpr:FP2_14500	ko:K02111	NA		
BLCPAMOF_02418	OG0000379	atpH	1	0	0	fpr:FP2_14490	ko:K02113	NA		
BLCPAMOF_02419	OG0000378	atpF_2	1	1	1	fpa:FPR_13420	ko:K02109	NA		
BLCPAMOF_02420	OG0000377	atpE_2	1	2	2	fpr:FP2_14470	ko:K02110	NA		
BLCPAMOF_02421	OG0000376	atpB_2	3	3	5	fpr:FP2_14460	ko:K02108	NA		
BLCPAMOF_02422	OG0000375	group_1019	2	2	3	fpr:FP2_14450	NA	NA		
BLCPAMOF_02423	OG0000374	group_1018	1	2	2	NA	NA	NA		
BLCPAMOF_02424	OG0000373	glgA	1	0	0	fpr:FP2_14430	ko:K00703	NA		
BLCPAMOF_02425	OG0000372	glgD	1	0	0	fpr:FP2_14420	ko:K00975	NA		
BLCPAMOF_02426	OG0000193	glgC	1	0	0	fpr:FP2_14410	ko:K00975	NA		
BLCPAMOF_02427	OG0000371	glgB_2	1	0	0	fpr:FP2_14400	ko:K00700	NA		
BLCPAMOF_02428	OG0000370	group_1013	1	1	1	NA	NA	NA		
BLCPAMOF_02429	OG0001682	group_5416	1	0	0	fpr:FP2_14370	NA	NA		
BLCPAMOF_02430	OG0000108	group_516	0	1	0	fpr:FP2_14360	NA	NA		
BLCPAMOF_02431	OG0004162	group_5417	1	1	1	fpr:FP2_14350	NA	specific_fp360		
BLCPAMOF_02432	OG0002530	Int-Tn_5	1	0	0	csh:Closa_3672	NA	NA		
BLCPAMOF_02433	OG0002970	group_5421	1	0	0	csh:Closa_3673	NA	NA		
BLCPAMOF_02434	OG0002539	group_5423	0	1	0	csh:Closa_3675	ko:K07171	NA		
BLCPAMOF_02435	OG0002971	group_2681	1	0	0	csh:Closa_3676	NA	NA		
BLCPAMOF_02436	OG0002647	group_5424	1	0	0	csh:Closa_3677	NA	NA		
BLCPAMOF_02437	OG0002646	group_5425	1	0	0	csh:Closa_3678	NA	NA		
BLCPAMOF_02438	OG0002645	group_5426	0	1	0	csh:Closa_3679	NA	NA		
BLCPAMOF_02439	OG0003231	group_5427	1	0	0	ssw:SSGZ1_0472	ko:K02346	NA		
BLCPAMOF_02440	OG0001994	group_5428	1	0	0	csh:Closa_3681	NA	NA		
BLCPAMOF_02441	OG0001895	group_5429	1	0	0	csh:Closa_3682	NA	NA		
BLCPAMOF_02442	OG0003232	cbh	1	1	1	rho:RHOM_15180	ko:K01442	NA		
BLCPAMOF_02443	OG0002540	group_5431	4	4	7	fpa:FPR_04180	NA	NA		
BLCPAMOF_02444	OG0002347	baeS	1	2	2	fpa:FPR_04170	NA	NA		
BLCPAMOF_02445	OG0002541	hssR	1	0	0	rix:RO1_33830;ere:EUBREC_3485	NA	NA		
BLCPAMOF_02446	OG0002542	clsC	1	1	1	eel:EUBELI_20657	NA	NA		
BLCPAMOF_02447	OG0002543	ywiE_3	2	2	3	fpa:FPR_04140	ko:K06131	NA		
BLCPAMOF_02448	OG0003233	ywaC_1	1	0	0	rum:CK1_27710	ko:K07816	NA		
BLCPAMOF_02449	OG0004163	group_5435	0	1	0	NA	NA	specific_fp360		
BLCPAMOF_02450	OG0004164	group_5436	1	0	0	csh:Closa_3686	NA	specific_fp360	○	
BLCPAMOF_02451	OG0004165	group_5437	1	2	2	csh:Closa_3687	NA	specific_fp360	○	
BLCPAMOF_02452	OG0002348	lon_1	1	0	0	csh:Closa_3688	ko:K01338	NA		
BLCPAMOF_02453	OG0003234	group_5438	1	0	0	csh:Closa_3689	NA	NA		
BLCPAMOF_02454	OG0003235	group_5439	1	0	0	csh:Closa_3690	NA	NA		
BLCPAMOF_02455	OG0003236	group_5440	1	0	0	csh:Closa_3691	NA	NA		
BLCPAMOF_02456	OG0003237	group_5441	1	0	0	csh:Closa_3692	NA	NA		
BLCPAMOF_02457	OG0003238	group_3328	1	0	0	csh:Closa_3693	NA	NA		
BLCPAMOF_02458	OG0003239	group_5442	1	0	0	csh:Closa_3694	NA	NA		
BLCPAMOF_02459	OG0003240	group_5443	1	0	0	csh:Closa_3695	NA	NA		
BLCPAMOF_02460	OG0003241	group_5444	1	0	0	csh:Closa_3696	NA	NA		
BLCPAMOF_02461	OG0003242	group_5445	1	0	0	csh:Closa_3697	NA	NA		
BLCPAMOF_02462	OG0003243	group_3329	1	0	0	csh:Closa_3700	NA	NA		
BLCPAMOF_02463	OG0003244	group_3330	0	1	0	csh:Closa_3701	NA	NA		
BLCPAMOF_02464	OG0003245	group_3331	2	2	3	csh:Closa_3702	NA	NA		
BLCPAMOF_02465	OG0002360	group_5446	1	0	0	csh:Closa_3703	NA	NA		
BLCPAMOF_02466	OG0001915	group_104	1	0	0	csh:Closa_3704	NA	NA		
BLCPAMOF_02467	OG0002958	ugd_3	1	0	0	rto:RTO_19030	ko:K00012	NA		
BLCPAMOF_02468	OG0002334	murG_2	1	0	0	tur:AT726_03370	NA	NA		
BLCPAMOF_02469	OG0002196	group_5448	1	0	0	tur:AT726_03365	NA	NA		
BLCPAMOF_02470	OG0003246	group_5449	1	0	0	bca:BCE_5388;bcef:BcrFT9_04217	NA	NA		
BLCPAMOF_02471	OG0004166	group_5450	1	0	0	bpj:B2904_orf1282	NA	specific_fp360		
BLCPAMOF_02472	OG0002524	group_5451	1	0	0	rbr:RBR_07430	NA	NA		
BLCPAMOF_02473	OG0002963	group_5452	1	0	0	cls:CXIVA_02150	NA	NA		
BLCPAMOF_02474	OG0004167	group_5453	6	6	11	NA	NA	specific_fp360	○	
BLCPAMOF_02475	OG0000242	rfbX_3	7	7	13	bmeg:BG04_3429	NA	NA		
BLCPAMOF_02476	OG0002344	group_5455	1	0	0	NA	NA	NA		
BLCPAMOF_02477	OG0002479	group_3209	1	0	0	rto:RTO_19160	NA	NA		
BLCPAMOF_02478	OG0003586	group_5456	1	0	0	NA	NA	NA		
BLCPAMOF_02479	OG0004168	group_5457	0	1	0	rob:CK5_28080	NA	specific_fp360	○	
BLCPAMOF_02480	OG0004169	group_5458	1	0	0	NA	NA	specific_fp360	○	
BLCPAMOF_02481	OG0000071	gmk_2	1	0	0	esu:EUS_14300;fpa:FPR_14310	NA	NA		
BLCPAMOF_02482	OG0003587	group_5460	1	0	0	NA	NA	NA		

BLCPAMOF_02483	OG0003588	group_5461	1	0	0	NA	NA	NA	
BLCPAMOF_02484	OG0003589	group_3332	1	0	0	sri:SELR_pSRC600250	NA	NA	
BLCPAMOF_02485	OG0003229	group_3333	1	0	0	ere:EUBREC_3450	NA	NA	
BLCPAMOF_02486	OG0002643	group_5462	1	0	0	lacy:A4V08_03905	NA	NA	
BLCPAMOF_02487	OG0002431	group_5463	0	1	0	NA	NA	NA	
BLCPAMOF_02488	OG0002178	group_5464	0	1	0	NA	NA	NA	
BLCPAMOF_02489	OG0001779	group_5465	1	0	0	csh:Closa_3493	NA	NA	
BLCPAMOF_02490	OG0003226	group_5466	1	0	0	NA	NA	NA	
BLCPAMOF_02491	OG0002435	group_3291	1	0	0	NA	NA	NA	
BLCPAMOF_02492	OG0002179	group_3293	1	0	0	NA	NA	NA	
BLCPAMOF_02493	OG0004170	group_5467	1	0	0	NA	NA	specific_fp360	○
BLCPAMOF_02494	OG0001919	group_2231	1	0	0	fpr:FP2_13220	NA	NA	
BLCPAMOF_02495	OG0003590	group_5468	1	0	0	rto:RTO_19270	NA	NA	
BLCPAMOF_02496	OG0004171	group_5469	1	0	0	rto:RTO_19280	NA	specific_fp360	○
BLCPAMOF_02497	OG0003558	group_5470	1	0	0	afa:UZ73_15885	NA	specific_fp360	
BLCPAMOF_02498	OG0000005	group_103	1	0	0	csh:Closa_3704	NA	NA	
BLCPAMOF_02499	OG0001786	group_5471	1	0	0	csh:Closa_3704	NA	NA	
BLCPAMOF_02500	OG0002243	group_5472	1	0	0	csh:Closa_3705	NA	NA	
BLCPAMOF_02501	OG0002361	group_3334	1	0	0	csh:Closa_3706	NA	NA	
BLCPAMOF_02502	OG0003247	group_3335	0	1	0	csh:Closa_3707	NA	NA	
BLCPAMOF_02503	OG0003248	group_3336	1	0	0	csh:Closa_3708	NA	NA	
BLCPAMOF_02504	OG0000056	group_123	1	0	0	csh:Closa_3709	ko:K03169	NA	
BLCPAMOF_02505	OG0002972	epsJ_4	1	0	0	fpa:FPR_00330	NA	NA	
BLCPAMOF_02506	OG0003249	group_5474	1	1	1	csh:Closa_3712	NA	NA	
BLCPAMOF_02507	OG0002244	group_5475	1	0	0	csh:Closa_3713	NA	NA	
BLCPAMOF_02508	OG0002518	ltrA_7	1	0	0	erb:A4V01_21510	NA	NA	
BLCPAMOF_02509	OG0001807	iap_2	1	0	0	csh:Closa_3714	NA	NA	
BLCPAMOF_02510	OG0000009	group_205	1	0	0	csh:Closa_3715	NA	NA	
BLCPAMOF_02511	OG0002121	group_5476	1	2	2	csh:Closa_3716	NA	NA	
BLCPAMOF_02512	OG0002245	group_597	3	4	6	csh:Closa_3717	NA	NA	
BLCPAMOF_02513	OG0003250	group_5477	1	0	0	NA	NA	NA	
BLCPAMOF_02514	OG0000006	group_230	1	2	2	fpr:FP2_09380;csh:Closa_3718;csh:Closa_3719	NA	NA	
BLCPAMOF_02515	OG0000006	group_231	1	2	2	fpr:FP2_09380;csh:Closa_3719;csh:Closa_3718	NA	NA	
BLCPAMOF_02516	OG0000001	group_73	1	0	0	csh:Closa_3720	ko:K03205	NA	
BLCPAMOF_02517	OG0001897	group_3338	1	0	0	csh:Closa_3721	NA	NA	
BLCPAMOF_02518	OG0002123	group_5479	1	0	0	csh:Closa_3722	NA	NA	
BLCPAMOF_02519	OG0002973	group_3339	1	0	0	csh:Closa_3723	NA	NA	
BLCPAMOF_02520	OG0002124	group_221	1	0	0	csh:Closa_3724	ko:K03497	NA	
BLCPAMOF_02521	OG0003251	group_3341	0	1	0	NA	NA	NA	
BLCPAMOF_02522	OG0000024	group_2684	1	0	0	csh:Closa_3725	ko:K02315	NA	
BLCPAMOF_02523	OG0000057	group_5481	1	0	0	csh:Closa_3726	NA	NA	
BLCPAMOF_02524	OG0002057	group_2201	1	0	0	csh:Closa_3728	NA	NA	
BLCPAMOF_02525	OG0000430	rpsI	1	0	0	fpr:FP2_10280	ko:K02996	NA	
BLCPAMOF_02526	OG0000429	rplM	1	0	0	fpr:FP2_10290	ko:K02871	NA	
BLCPAMOF_02527	OG0000428	group_2345	1	1	1	fpr:FP2_10300	NA	NA	
BLCPAMOF_02528	OG0001985	group_1976	1	0	0	fpr:FP2_10310	NA	NA	
BLCPAMOF_02529	OG0000427	alr1	1	0	0	fpr:FP2_10320	ko:K01775	NA	
BLCPAMOF_02530	OG0000426	lepA	1	0	0	fpr:FP2_10330	ko:K03596	NA	
BLCPAMOF_02531	OG0000147	pglA	1	1	1	bpb:bpr_I0344	NA	NA	
BLCPAMOF_02532	OG0002518	ltrA_8	1	0	0	erb:A4V01_21510	NA	NA	
BLCPAMOF_02533	OG0000147	group_5482	1	0	0	fro:AALO17_22620	NA	NA	
BLCPAMOF_02534	OG0002974	group_5483	1	0	0	NA	NA	NA	
BLCPAMOF_02535	OG0002463	group_5484	1	0	0	fpr:FP2_10360	NA	NA	
BLCPAMOF_02536	OG0004172	group_5485	1	0	0	fpr:FP2_10370	NA	specific_fp360	
BLCPAMOF_02537	OG0002450	group_5486	1	0	0	fpr:FP2_10380	NA	NA	
BLCPAMOF_02538	OG0002071	group_5487	6	6	11	fpr:FP2_10400	ko:K19168	specific_fp360	
BLCPAMOF_02539	OG0002068	group_5488	1	1	1	fpr:FP2_10410	ko:K07098	NA	
BLCPAMOF_02540	OG0002069	group_5489	1	2	2	fpr:FP2_10420	NA	NA	
BLCPAMOF_02541	OG0002070	group_5490	1	2	2	fpr:FP2_10430	NA	NA	
BLCPAMOF_02542	OG0004173	group_5491	9	10	18	amt:Amet_0231	NA	specific_fp360	○
BLCPAMOF_02543	OG0004174	group_5492	1	0	0	NA	NA	specific_fp360	○
BLCPAMOF_02544	OG0002975	pdxA2	1	0	0	fpa:FPR_17400	ko:K00097	NA	
BLCPAMOF_02545	OG0002093	dapA_2	1	0	0	fpa:FPR_17390	ko:K01714	NA	
BLCPAMOF_02546	OG0002976	adh1	1	0	0	fpa:FPR_17380	NA	NA	
BLCPAMOF_02547	OG0002977	group_3346	1	0	0	fpa:FPR_17360	NA	NA	
BLCPAMOF_02548	OG0002978	zraR	1	0	0	fpa:FPR_17350	NA	NA	
BLCPAMOF_02549	OG0004175	group_5493	1	0	0	NA	NA	specific_fp360	○
BLCPAMOF_02550	OG0004176	group_5494	1	2	2	NA	NA	specific_fp360	○
BLCPAMOF_02551	OG0002064	group_2574	1	0	0	fpr:FP2_10450	NA	NA	
BLCPAMOF_02552	OG0001680	group_5495	6	7	12	fpr:FP2_10460	NA	NA	
BLCPAMOF_02553	OG0001975	group_5496	1	2	2	ibu:IB211_00778c	ko:K05349	NA	
BLCPAMOF_02554	OG0000121	uidA	1	0	0	fpr:FP2_10480	NA	NA	
BLCPAMOF_02555	OG0001976	group_5498	3	4	6	NA	NA	NA	
BLCPAMOF_02556	OG0001977	group_5499	1	0	0	fpr:FP2_10500	NA	NA	
BLCPAMOF_02557	OG0000179	cbpA	1	0	0	fpa:FPR_05900	ko:K00702	NA	
BLCPAMOF_02558	OG0001404	group_1732	1	0	0	fpa:FPR_05910	ko:K02529	NA	
BLCPAMOF_02559	OG0001403	group_1731	1	0	0	fpa:FPR_05920	NA	NA	
BLCPAMOF_02560	OG0001402	lacF_2	3	4	6	fpa:FPR_05930	ko:K02025	NA	
BLCPAMOF_02561	OG0001401	araQ_2	3	4	6	fpa:FPR_05940	ko:K02026	NA	
BLCPAMOF_02562	OG0001058	group_1487	1	0	0	fpr:FP2_10510	NA	NA	
BLCPAMOF_02563	OG0001057	glcK_1	1	0	0	fpr:FP2_10520	ko:K00845	NA	
BLCPAMOF_02564	OG0001056	nanE	1	0	0	fpr:FP2_10530	ko:K01788	NA	
BLCPAMOF_02565	OG0001055	group_5500	1	0	0	fpr:FP2_10540	NA	NA	
BLCPAMOF_02566	OG0001054	nanA	1	0	0	fpr:FP2_10550	ko:K01639	NA	
BLCPAMOF_02567	OG0001053	araQ_3	3	4	6	fpr:FP2_10560	ko:K02026	NA	
BLCPAMOF_02568	OG0000229	lacF_3	3	4	6	fpa:FPR_16160	ko:K02025	NA	
BLCPAMOF_02569	OG0001052	group_1482	1	0	0	fpr:FP2_10580	ko:K02027	NA	
BLCPAMOF_02570	OG0001051	hexR	1	0	0	fpr:FP2_10600	NA	NA	
BLCPAMOF_02571	OG0000218	group_2244	3	3	5	fpa:FPR_04200	NA	NA	
BLCPAMOF_02572	OG0001866	group_5501	2	1	2	fpr:FP2_10610	NA	NA	
BLCPAMOF_02573	OG0001865	group_5502	1	0	0	fpr:FP2_10620	ko:K07720	NA	
BLCPAMOF_02574	OG0002949	futA1	1	0	0	fpr:FP2_10630	ko:K02012	specific_fp360	
BLCPAMOF_02575	OG0000224	potA_3	1	0	0	fpr:FP2_10640	ko:K02010	specific_fp360	
BLCPAMOF_02576	OG0000225	potH_2	6	7	12	fpr:FP2_10650	ko:K02011	NA	
BLCPAMOF_02577	OG0004177	group_5506	1	0	0	NA	NA	specific_fp360	○
BLCPAMOF_02578	OG0002517	group_5507	1	0	0	fpr:FP2_11110	NA	NA	
BLCPAMOF_02579	OG0004178	group_5508	1	0	0	fpr:FP2_11120	NA	specific_fp360	○
BLCPAMOF_02580	OG0002483	group_3217	1	0	0	fpr:FP2_11120	NA	NA	
BLCPAMOF_02581	OG0004179	group_5509	1	0	0	NA	NA	specific_fp360	○
BLCPAMOF_02582	OG0000008	group_138	1	0	0	fpr:FP2_28240	NA	NA	
BLCPAMOF_02583	OG0000021	group_5510	0	1	0	rbr:RBR_00680	NA	NA	
BLCPAMOF_02584	OG0000038	group_431	2	2	3	fpr:FP2_29680	NA	NA	
BLCPAMOF_02585	OG0001896	group_5511	1	0	0	fpla:A4U99_02525	ko:K07133	NA	
BLCPAMOF_02586	OG0000010	group_196	1	0	0	fpa:FPR_18840	NA	NA	
BLCPAMOF_02587	OG0000148	group_3264	1	0	0	fpr:FP2_11690	NA	NA	
BLCPAMOF_02588	OG0001877	tnpR_7	1	0	0	NA	NA	NA	
BLCPAMOF_02589	OG0001800	group_5512	1	0	0	fpr:FP2_10730	NA	NA	
BLCPAMOF_02590	OG0001799	group_5513	1	0	0	fpr:FP2_10740	NA	NA	
BLCPAMOF_02591	OG0004180	group_5514	1	0	0	tpk:JO40_06670	NA	specific_fp360	
BLCPAMOF_02592	OG0000397	ppdK	1	0	0	fpr:FP2_11200	ko:K01006	NA	
BLCPAMOF_02593	OG0000396	glmU	1	0	0	fpr:FP2_11220	ko:K04042	NA	
BLCPAMOF_02594	OG0000395	pth	1	0	0	fpr:FP2_11230	ko:K01056	NA	
BLCPAMOF_02595	OG0000394	mfd	1	0	0	fpr:FP2_11240	ko:K03723	NA	
BLCPAMOF_02596	OG0000393	group_5515	1	1	1	fpr:FP2_11250	NA	NA	

BLCPAMOF_02597	OG0003591	group_5516	1	1	1	fpr:FP2_11260	NA	specific_fp360	
BLCPAMOF_02598	OG0003591	group_5517	1	1	1	fpr:FP2_11260	NA	specific_fp360	
BLCPAMOF_02599	OG0002516	group_5518	1	1	1	NA	NA	NA	
BLCPAMOF_02600	OG0000392	lacL	1	0	0	fpr:FP2_11270	NA	NA	
BLCPAMOF_02601	OG0000391	aspC	1	0	0	fpr:FP2_11280	ko:K11358	NA	
BLCPAMOF_02602	OG0000390	fieF	2	2	3	fpr:FP2_11290	NA	NA	
BLCPAMOF_02603	OG0000389	ptsI_2	1	0	0	fpr:FP2_11300	ko:K08483	NA	
BLCPAMOF_02604	OG0000198	ptsH_2	0	1	0	fpr:FP2_11310	ko:K11189	NA	
BLCPAMOF_02605	OG0000388	group_1032	1	1	1	fpr:FP2_11320	NA	NA	
BLCPAMOF_02606	OG0001570	gltX_1	1	0	0	fpr:FP2_11380	ko:K01885	NA	
BLCPAMOF_02607	OG0002052	group_2534	1	0	0	fpr:FP2_11370	NA	NA	
BLCPAMOF_02608	OG0002053	group_2535	1	0	0	fpr:FP2_11360	NA	NA	
BLCPAMOF_02609	OG0001571	spoIIE	5	5	9	fpr:FP2_11350	ko:K06382	NA	
BLCPAMOF_02610	OG0001572	pemA	1	0	0	fpr:FP2_11340	ko:K01051	NA	
BLCPAMOF_02611	OG0001573	group_1833	1	1	1	fpr:FP2_11330	NA	NA	
BLCPAMOF_02612	OG0001569	abrB	1	0	0	fpr:FP2_11400	ko:K06284	NA	
BLCPAMOF_02613	OG0001568	group_1830	1	0	0	fpr:FP2_11410	NA	NA	
BLCPAMOF_02614	OG0001564	group_1827	6	7	12	NA	NA	NA	
BLCPAMOF_02615	OG0001563	group_1826	1	0	0	fpr:FP2_11430	ko:K07043	NA	
BLCPAMOF_02616	OG0001562	group_1825	4	5	8	fpr:FP2_11440	NA	NA	
BLCPAMOF_02617	OG0001561	group_5519	1	1	1	fpr:FP2_11450	NA	NA	
BLCPAMOF_02618	OG0001560	group_668	1	1	1	fpr:FP2_11460	NA	NA	
BLCPAMOF_02619	OG0001559	group_1824	2	3	4	fpr:FP2_11470	NA	NA	
BLCPAMOF_02620	OG0001558	group_1823	1	1	1	fpr:FP2_11480	NA	NA	
BLCPAMOF_02622	OG0003592	group_5520	1	1	1	bprs:CK3_04760	NA	NA	
BLCPAMOF_02623	OG0000031	group_26	1	0	0	fpa:FPR_01460	NA	NA	
BLCPAMOF_02624	OG0001861	group_3981	1	0	0	NA	NA	NA	
BLCPAMOF_02625	OG0001557	group_292	1	0	0	fpa:FPR_18690	ko:K07171	NA	
BLCPAMOF_02626	OG0000184	group_2648	1	0	0	fpa:FPR_18700	NA	NA	
BLCPAMOF_02627	OG0000038	group_433	2	2	3	fpr:FP2_08920	NA	NA	
BLCPAMOF_02628	OG0000023	group_264	1	0	0	fpa:FPR_18860	NA	NA	
BLCPAMOF_02629	OG0000005	group_87	1	0	0	fpr:FP2_27160	NA	NA	
BLCPAMOF_02630	OG0000077	group_7218	1	2	2	fpa:FPR_19120	NA	NA	
BLCPAMOF_02631	OG0000181	group_498	1	0	0	fpa:FPR_19110	NA	NA	
BLCPAMOF_02632	OG0002158	group_2532	1	1	1	fpa:FPR_01450	NA	NA	
BLCPAMOF_02633	OG0002544	group_310	1	0	0	fpa:FPR_04570	NA	NA	
BLCPAMOF_02634	OG0000022	group_342	1	0	0	fpr:FP2_21680	NA	NA	
BLCPAMOF_02635	OG0000019	group_370	1	0	0	fpa:FPR_04590	NA	NA	
BLCPAMOF_02636	OG0000003	group_115	1	0	0	fpa:FPR_19060	ko:K03169	NA	
BLCPAMOF_02637	OG0000221	group_2043	1	0	0	fpr:FP2_22510	NA	NA	
BLCPAMOF_02638	OG0002004	group_2886	0	1	0	NA	NA	NA	
BLCPAMOF_02639	OG0000030	mobA_1	1	0	0	fpr:FP2_22490	NA	NA	
BLCPAMOF_02640	OG0000034	group_535	1	0	0	fpa:FPR_00420	NA	NA	
BLCPAMOF_02641	OG0002188	sigX	1	0	0	fpr:FP2_30070	ko:K03088	NA	
BLCPAMOF_02642	OG0003593	group_3348	1	0	0	NA	NA	NA	
BLCPAMOF_02643	OG0002190	group_4535	1	1	1	fpa:FPR_01050;fpr:FP2_22430	NA	NA	
BLCPAMOF_02644	OG0001843	group_199	1	0	0	fpr:FP2_22350	NA	NA	
BLCPAMOF_02645	OG0000016	group_365	1	2	2	csh:Closa_3716	NA	NA	
BLCPAMOF_02646	OG0000011	group_600	3	3	5	fpr:FP2_22330	NA	NA	
BLCPAMOF_02647	OG0003594	group_3349	0	1	0	NA	NA	NA	
BLCPAMOF_02648	OG0001868	group_5521	1	0	0	cso:CLS_22150	NA	NA	
BLCPAMOF_02649	OG0002214	group_2302	0	1	0	rho:RHOM_01845	NA	NA	
BLCPAMOF_02650	OG0002215	group_2559	1	0	0	cso:CLS_22170	NA	NA	
BLCPAMOF_02651	OG0002216	group_2687	1	0	0	ere:EUBREC_0790;ere:EUBREC_2705	NA	NA	
BLCPAMOF_02652	OG0000030	mobA_6	1	0	0	rbr:RBR_21030	NA	NA	
BLCPAMOF_02653	OG0003585	group_5523	1	0	0	cle:Clole_1953	NA	specific_fp360	O
BLCPAMOF_02654	OG0000034	group_2690	1	0	0	ere:EUBREC_0795;ere:EUBREC_2700	NA	NA	
BLCPAMOF_02655	OG0000086	group_2308	1	0	0	cdl:CDR20291_1781	NA	NA	
BLCPAMOF_02656	OG0000102	group_924	0	1	0	rbr:RBR_20990;fpa:FPR_17080;fpa:FPR_08340;fpr:FP2_22180	NA	NA	
BLCPAMOF_02657	OG0002100	group_2692	1	0	0	cdl:CDR20291_1780	NA	NA	
BLCPAMOF_02658	OG0002349	group_3350	1	0	0	rho:RHOM_01735	NA	NA	
BLCPAMOF_02659	OG0000049	group_785	1	0	0	rho:RHOM_01730	NA	NA	
BLCPAMOF_02660	OG0000081	group_5525	1	0	0	esu:EUS_10510;cso:CLS_22290;rho:RHOM_01725;rob:CK5_08570;bprs:CK3_12860	NA	NA	
BLCPAMOF_02661	OG0000036	group_2527	1	0	0	tsu:Tresu_1912	NA	NA	
BLCPAMOF_02662	OG0001923	group_2182	0	1	0	cso:CLS_18770	NA	NA	
BLCPAMOF_02663	OG0000024	dnaI	1	0	0	ibu:IB211_02774;cso:CLS_06780;cls:CXIVA_10090;fpr:FP2_04660	ko:K02315	NA	
BLCPAMOF_02664	OG0001537	group_918	1	0	0	fpla:A4U99_10855	NA	NA	
BLCPAMOF_02665	OG0001764	group_2525	1	0	0	cls:CXIVA_10070;ibu:IB211_02772;fpr:FP2_04680	NA	NA	
BLCPAMOF_02666	OG0001763	group_894	1	0	0	cso:CLS_18820	NA	NA	
BLCPAMOF_02667	OG0001860	group_2180	0	1	0	cls:CXIVA_10050	NA	NA	
BLCPAMOF_02668	OG0001762	group_2524	1	0	0	cso:CLS_29660	NA	NA	
BLCPAMOF_02669	OG0001859	group_3063	1	0	0	cso:CLS_29650	NA	NA	
BLCPAMOF_02670	OG0003149	group_3980	1	0	0	fpa:FPR_13040;coo:CCU_17140	NA	NA	
BLCPAMOF_02671	OG0000073	yqjI	0	1	0	fpa:FPR_13060;coo:CCU_17120	ko:K10947	NA	
BLCPAMOF_02672	OG0000079	group_235	1	1	1	cls:CXIVA_10000	NA	NA	
BLCPAMOF_02673	OG0000001	group_76	1	1	1	fpr:FP2_21800	ko:K03205	NA	
BLCPAMOF_02674	OG0000017	group_429	1	0	0	fpa:FPR_00800	NA	NA	
BLCPAMOF_02675	OG0000145	group_1822	1	0	0	fpa:FPR_00820	NA	NA	
BLCPAMOF_02676	OG0000002	spo0C_4	1	0	0	fpa:FPR_00840	ko:K03497	NA	
BLCPAMOF_02677	OG0000004	soj_3	1	0	0	fpa:FPR_07940	ko:K03496	NA	
BLCPAMOF_02678	OG0000008	group_126	1	0	0	fpr:FP2_28240	NA	NA	
BLCPAMOF_02679	OG0001873	luxQ_5	2	1	2	rob:CK5_16060	NA	NA	
BLCPAMOF_02682	OG0001604	lexA	1	0	0	fpr:FP2_11820	ko:K01356	NA	
BLCPAMOF_02683	OG0001603	group_1854	1	0	0	fpr:FP2_11830	NA	NA	
BLCPAMOF_02684	OG0001602	group_903	1	0	0	fpr:FP2_11840	NA	NA	
BLCPAMOF_02685	OG0001601	ppiB	1	0	0	fpr:FP2_11850	ko:K03768	NA	
BLCPAMOF_02686	OG0001797	group_1967	1	0	0	bii:BINDI_0998	ko:K14155	NA	
BLCPAMOF_02687	OG0000364	group_694	1	0	0	fpr:FP2_11860	NA	NA	
BLCPAMOF_02688	OG0000363	tyrA	1	0	0	fpr:FP2_11870	ko:K04517	NA	
BLCPAMOF_02689	OG0000362	aroA	1	0	0	fpr:FP2_11880	ko:K00800	NA	
BLCPAMOF_02690	OG0000361	aroF_1	1	0	0	fpr:FP2_11890	ko:K03856	NA	
BLCPAMOF_02691	OG0000360	yqhS	1	0	0	fpr:FP2_11900	ko:K03786	NA	
BLCPAMOF_02692	OG0000359	aroE	1	0	0	fpr:FP2_11910	ko:K00014	NA	
BLCPAMOF_02693	OG0000358	aroC	1	0	0	fpr:FP2_11920	ko:K01736	NA	
BLCPAMOF_02694	OG0000357	aroB	1	0	0	fpr:FP2_11930	ko:K01735	NA	
BLCPAMOF_02695	OG0000356	pheA	1	0	0	fpr:FP2_11940	ko:K14170	NA	
BLCPAMOF_02696	OG0000355	group_5527	0	1	0	fpr:FP2_11950	NA	NA	
BLCPAMOF_02697	OG0000191	group_2327	1	1	1	fpr:FP2_11960	NA	NA	
BLCPAMOF_02698	OG0000354	plsC_1	1	1	1	fpa:FPR_10680	ko:K00655	NA	
BLCPAMOF_02699	OG0000190	group_1001	3	3	5	fpr:FP2_11980	NA	NA	
BLCPAMOF_02700	OG0000353	group_1000	1	0	0	fpr:FP2_11990	NA	NA	
BLCPAMOF_02701	OG0000352	cmk_1	1	0	0	fpr:FP2_12000	NA	NA	
BLCPAMOF_02702	OG0000351	mepA_2	6	7	12	rho:RHOM_13945	NA	NA	
BLCPAMOF_02703	OG0000350	group_692	3	4	6	fpr:FP2_12020	NA	NA	
BLCPAMOF_02704	OG0000349	group_999	1	0	0	fpr:FP2_12030	ko:K07137	NA	
BLCPAMOF_02705	OG0001982	group_5528	1	0	0	fpr:FP2_12040	NA	NA	
BLCPAMOF_02706	OG0002954	group_5529	1	1	1	NA	NA	NA	
BLCPAMOF_02707	OG0000192	spoVK	1	0	0	fpr:FP2_12050	NA	NA	
BLCPAMOF_02708	OG0000365	pulA	1	0	0	fpr:FP2_12060	ko:K01200	NA	
BLCPAMOF_02709	OG0000366	htrA	1	1	1	fpr:FP2_12070	ko:K04771	NA	
BLCPAMOF_02710	OG0000367	rsmH_1	1	0	0	fpr:FP2_12090	NA	NA	
BLCPAMOF_02711	OG0000368	prfC	1	0	0	fpr:FP2_12100	ko:K02837	NA	
BLCPAMOF_02712	OG0000369	yhdN	1	0	0	fpr:FP2_12110	ko:K18471	NA	
BLCPAMOF_02713	OG0004181	group_5530	1	0	0	NA	NA	specific_fp360	O

BLCPAMOF_02714	OG0000432	group_1063	1	1	1	fpr:FP2_12140	NA	NA	
BLCPAMOF_02715	OG0000433	group_1064	1	1	1	NA	NA	NA	
BLCPAMOF_02716	OG0000434	mutY	1	0	0	fpla:A4U99_05095	ko:K03575	NA	
BLCPAMOF_02717	OG0000435	asnS	1	0	0	fpr:FP2_12170	ko:K01893	NA	
BLCPAMOF_02718	OG0000436	group_709	1	1	1	fpr:FP2_12180	ko:K06385	NA	
BLCPAMOF_02719	OG0000437	gpr	1	0	0	fpr:FP2_12190	ko:K06012	NA	
BLCPAMOF_02720	OG0000438	rpsT	0	1	0	fpr:FP2_12200;fpa:FPR_18100	ko:K02968	NA	
BLCPAMOF_02721	OG0004182	group_5531	1	2	2	fpr:FP2_12210	NA	specific_fp360	
BLCPAMOF_02722	OG0000439	group_1066	2	2	3	fpr:FP2_12220	ko:K06407	NA	
BLCPAMOF_02723	OG0000440	spoVAD	1	0	0	fpa:FPR_18070	ko:K06406	NA	
BLCPAMOF_02724	OG0000441	group_711	2	3	4	fpr:FP2_12240	ko:K06405	NA	
BLCPAMOF_02725	OG0000442	vanYB	1	1	1	fpr:FP2_12250	ko:K07260	NA	
BLCPAMOF_02726	OG0000443	group_3151	1	1	1	fpr:FP2_12260	NA	NA	
BLCPAMOF_02727	OG0000444	patA_3	6	6	11	cpf:CPF_1766	ko:K19294	NA	
BLCPAMOF_02728	OG0000445	group_712	1	1	1	fpr:FP2_12280	NA	NA	
BLCPAMOF_02729	OG0001690	group_5532	1	2	2	fpr:FP2_12290	NA	NA	
BLCPAMOF_02730	OG0000154	group_5533	1	2	2	fpr:FP2_12300	NA	NA	
BLCPAMOF_02731	OG0001592	dnaJ_2	1	0	0	fpr:FP2_12310	ko:K03686	NA	
BLCPAMOF_02732	OG0000268	dnaK_2	1	0	0	fpr:FP2_12320	ko:K04043	NA	
BLCPAMOF_02733	OG0001593	grpE	1	0	0	fpr:FP2_12330	ko:K03687	NA	
BLCPAMOF_02734	OG0001594	hrcA	1	0	0	fpr:FP2_12340	ko:K03705	NA	
BLCPAMOF_02735	OG0001595	spoVT	1	0	0	fpr:FP2_12360	ko:K04769	NA	
BLCPAMOF_02736	OG0001596	group_900	1	0	0	fpr:FP2_12370	ko:K07007	NA	
BLCPAMOF_02737	OG0001597	alsT_2	6	6	11	fpr:FP2_12380	ko:K03310	NA	
BLCPAMOF_02738	OG0003595	group_5534	1	0	0	fpr:FP2_12390	NA	NA	
BLCPAMOF_02739	OG0001598	group_5535	1	1	1	NA	NA	NA	
BLCPAMOF_02740	OG0001599	gabR_2	1	0	0	fpr:FP2_12420	ko:K00375	NA	
BLCPAMOF_02741	OG0001600	group_902	3	4	6	fpr:FP2_12430	NA	NA	
BLCPAMOF_02742	OG0001608	rlmA	1	0	0	fpr:FP2_12460	ko:K00563	NA	
BLCPAMOF_02743	OG0001609	rhlE	1	0	0	fpr:FP2_12470	ko:K11927	NA	
BLCPAMOF_02744	OG0001610	group_1859	1	0	0	fpr:FP2_12480	NA	NA	
BLCPAMOF_02745	OG0001611	group_5536	1	1	1	fpr:FP2_12490	NA	NA	
BLCPAMOF_02746	OG0001612	nqrE	4	3	6	fpr:FP2_12500	ko:K03617	NA	
BLCPAMOF_02747	OG0001613	rsxE	3	4	6	fpr:FP2_12510	ko:K03613	NA	
BLCPAMOF_02748	OG0001614	rsxD_2	3	4	6	fpr:FP2_12520	ko:K03614	NA	
BLCPAMOF_02749	OG0001615	rpe	1	0	0	fpr:FP2_12530	ko:K01783	NA	
BLCPAMOF_02750	OG0001616	phoR_4	2	1	2	fpr:FP2_12540	NA	NA	
BLCPAMOF_02751	OG0000270	srrA_2	1	0	0	fpr:FP2_12550	NA	NA	
BLCPAMOF_02752	OG0004183	group_5537	1	0	0	fpr:FP2_12560	NA	specific_fp360	
BLCPAMOF_02753	OG0003157	group_5538	1	1	1	fpr:FP2_12570	NA	NA	
BLCPAMOF_02754	OG0003157	group_5539	1	0	0	fpr:FP2_12590	NA	NA	
BLCPAMOF_02755	OG0004184	group_5540	1	1	1	fpr:FP2_12600	NA	specific_fp360	
BLCPAMOF_02756	OG0004185	group_5541	0	1	0	fpr:FP2_12610	NA	specific_fp360	
BLCPAMOF_02757	OG0004186	group_5542	1	0	0	esr:ES1_15780	NA	specific_fp360	○
BLCPAMOF_02758	OG0001867	group_5543	1	0	0	fpr:FP2_12620	NA	NA	
BLCPAMOF_02759	OG0002545	group_3351	5	6	10	fpr:FP2_12640	NA	NA	
BLCPAMOF_02760	OG0001617	group_3352	1	0	0	fpr:FP2_12650	NA	NA	
BLCPAMOF_02761	OG0000082	ridA_2	1	0	0	fpr:FP2_12660	ko:K09022	NA	
BLCPAMOF_02762	OG0002275	dauR	1	0	0	fpr:FP2_12670	NA	NA	
BLCPAMOF_02763	OG0001986	group_5544	2	1	2	NA	NA	NA	
BLCPAMOF_02764	OG0002079	group_5545	1	0	0	fpa:FPR_20840	NA	NA	
BLCPAMOF_02765	OG0004187	group_5546	1	1	1	NA	NA	specific_fp360	○
BLCPAMOF_02766	OG0001618	ychF	1	0	0	fpr:FP2_13440	ko:K06942	NA	
BLCPAMOF_02767	OG0001619	mtnN	1	0	0	fpr:FP2_13450	ko:K01243	NA	
BLCPAMOF_02768	OG0001620	group_1866	1	0	0	fpr:FP2_13460	NA	NA	
BLCPAMOF_02769	OG0001621	group_2539	1	0	0	fpr:FP2_13470	NA	NA	
BLCPAMOF_02770	OG0001622	malQ_3	1	0	0	fpr:FP2_13480	ko:K00705	NA	
BLCPAMOF_02771	OG0001623	alaS_2	1	0	0	fpr:FP2_13490	ko:K01872	NA	
BLCPAMOF_02772	OG0001624	trmB	1	0	0	fpr:FP2_13500	ko:K03439	NA	
BLCPAMOF_02773	OG0001973	group_2278	1	0	0	fpr:FP2_13510	NA	NA	
BLCPAMOF_02774	OG0001625	group_906	3	3	5	fpa:FPR_10060	NA	NA	
BLCPAMOF_02775	OG0000117	group_907	1	0	0	fpr:FP2_13530	NA	NA	
BLCPAMOF_02776	OG0002546	group_2695	2	3	4	fpa:FPR_09810	NA	NA	
BLCPAMOF_02777	OG0002283	gpr_2	1	0	0	rob:CK5_32280	ko:K19265	specific_fp360	○
BLCPAMOF_02778	OG0001626	bdhA	1	0	0	fpr:FP2_13560	ko:K07124	NA	
BLCPAMOF_02779	OG0002547	group_550	1	0	0	fpr:FP2_13570	ko:K00046	NA	
BLCPAMOF_02780	OG0001627	group_1870	1	0	0	fpr:FP2_13580	NA	NA	
BLCPAMOF_02781	OG0001628	group_909	1	1	1	fpa:FPR_09840	NA	NA	
BLCPAMOF_02782	OG0001629	nrgA	6	6	11	erb:A4V01_11425	ko:K03320	NA	
BLCPAMOF_02783	OG0001630	eriC	6	6	11	fpr:FP2_13610	NA	NA	
BLCPAMOF_02784	OG0001631	thrS	1	0	0	fpr:FP2_13630	ko:K01868	NA	
BLCPAMOF_02785	OG0001632	trpS2	1	0	0	fpr:FP2_13660	ko:K01867	NA	
BLCPAMOF_02788	OG0001974	group_2279	1	0	0	fpr:FP2_13670	NA	NA	
BLCPAMOF_02789	OG0001633	pckA	1	0	0	fpr:FP2_13680	ko:K01610	NA	
BLCPAMOF_02790	OG0001802	group_5548	3	3	5	fpr:FP2_13700	NA	NA	
BLCPAMOF_02791	OG0001924	opuE	6	7	12	rob:CK5_23380	ko:K11928	NA	
BLCPAMOF_02792	OG0002096	group_2645	2	3	4	fpr:FP2_13730	NA	NA	
BLCPAMOF_02793	OG0002097	bglB_1	1	0	0	fpr:FP2_13740	ko:K05349	NA	
BLCPAMOF_02794	OG0001975	group_3355	1	2	2	fpa:FPR_09740	ko:K05349	NA	
BLCPAMOF_02795	OG0001976	group_5549	3	3	5	fpr:FP2_13760	NA	NA	
BLCPAMOF_02796	OG0001977	ypdB_4	1	0	0	fpr:FP2_13770	NA	NA	
BLCPAMOF_02797	OG0000255	group_5550	1	1	1	fpr:FP2_13780	NA	NA	
BLCPAMOF_02798	OG0000256	macB_4	2	3	4	fpr:FP2_13790	ko:K02004	NA	
BLCPAMOF_02799	OG0000257	macB_5	1	0	0	fpr:FP2_13800	ko:K02003	NA	
BLCPAMOF_02800	OG0000258	yknX	1	1	1	fpr:FP2_13810	ko:K02005	NA	
BLCPAMOF_02801	OG0002507	group_5553	1	0	0	fpr:FP2_29050	NA	NA	
BLCPAMOF_02802	OG0002508	group_5554	2	2	3	fpr:FP2_29040	NA	NA	
BLCPAMOF_02803	OG0002509	group_5555	1	0	0	fpr:FP2_29030	NA	NA	
BLCPAMOF_02804	OG0002510	group_5556	1	1	1	fpr:FP2_29020	ko:K06330	NA	
BLCPAMOF_02805	OG0002511	group_3244	6	6	11	bbrj:B7017_0053	ko:K21012	NA	
BLCPAMOF_02806	OG0002512	wbnH	1	0	0	fpr:FP2_29000	ko:K21011	NA	
BLCPAMOF_02807	OG0002513	group_5557	1	1	1	fpr:FP2_28990	NA	NA	
BLCPAMOF_02808	OG0002514	group_5558	1	2	2	fpr:FP2_28980	NA	NA	
BLCPAMOF_02809	OG0002515	group_5559	2	1	2	fpr:FP2_28970	ko:K01784	NA	
BLCPAMOF_02810	OG0000024	dnaI_1	1	0	0	sans:DK43_04030;fpa:FPR_08270	ko:K02315	NA	
BLCPAMOF_02811	OG0001855	xerC_11	1	0	0	fpr:FP2_13920	NA	NA	
BLCPAMOF_02812	OG0002297	group_14	1	0	0	fpr:FP2_29980	NA	NA	
BLCPAMOF_02813	OG0001754	group_1724	1	0	0	fpr:FP2_27920	ko:K06147	NA	
BLCPAMOF_02814	OG0004188	group_5560	1	0	0	NA	NA	specific_fp360	○
BLCPAMOF_02815	OG0001395	group_478	1	0	0	fpa:FPR_07130	NA	NA	
BLCPAMOF_02816	OG0000133	group_476	1	0	0	fpa:FPR_07450	NA	NA	
BLCPAMOF_02817	OG0000062	rebM_1	1	0	0	fpr:FP2_27850	NA	NA	
BLCPAMOF_02818	OG0000798	zupT_2	4	4	7	fpa:FPR_07440	ko:K07238	NA	
BLCPAMOF_02819	OG0000797	group_789	1	1	1	fpa:FPR_07430	NA	NA	
BLCPAMOF_02820	OG0001394	rsxG_2	1	1	1	fpa:FPR_03420	NA	NA	
BLCPAMOF_02821	OG0001855	group_324	1	0	0	fpr:FP2_13920	NA	NA	
BLCPAMOF_02822	OG0000014	group_152	1	0	0	fpr:FP2_13830	NA	NA	
BLCPAMOF_02823	OG0004189	nagC	1	0	0	fpr:FP2_13940	NA	specific_fp360	
BLCPAMOF_02824	OG0000222	group_5562	1	0	0	fpr:FP2_13950	ko:K00008	specific_fp360	
BLCPAMOF_02825	OG0004190	group_5563	1	0	0	fpr:FP2_13960	NA	specific_fp360	
BLCPAMOF_02826	OG0000046	group_5564	6	6	11	fpr:FP2_13970	ko:K16248	specific_fp360	
BLCPAMOF_02827	OG0000037	group_5565	1	0	0	fpr:FP2_13980	ko:K00847	NA	
BLCPAMOF_02828	OG0004191	group_5566	0	1	0	fpr:FP2_13990	NA	specific_fp360	
BLCPAMOF_02829	OG0000231	group_480	1	0	0	fpr:FP2_14000	ko:K06919	NA	

BLCPAMOF_02830	OG0000040	group_294	1	0	0	fpr:FP2_24000	NA	NA
BLCPAMOF_02831	OG0000160	group_456	1	0	0	fpr:FP2_14020	NA	NA
BLCPAMOF_02832	OG0000058	group_355	1	0	0	fpr:FP2_14030	NA	NA
BLCPAMOF_02837	OG0001638	coaX_2	1	0	0	fpr:FP2_20540	ko:K03525	NA
BLCPAMOF_02839	OG0000000	group_39	0	1	0	fpa:FPR_08500	NA	NA
BLCPAMOF_02840	OG0001774	group_1910	1	0	0	fpa:FPR_08550	NA	NA
BLCPAMOF_02841	OG0000018	group_172	1	0	0	fpr:FP2_22740	NA	NA
BLCPAMOF_02842	OG0001883	group_173	0	1	0	fpr:FP2_22750	NA	NA
BLCPAMOF_02843	OG0001707	group_2042	4	4	7	fpa:FPR_08580	NA	NA
BLCPAMOF_02844	OG0001708	ypdB_3	1	0	0	fpa:FPR_08590	NA	NA
BLCPAMOF_02845	OG0001864	agrB	3	3	5	fpa:FPR_08600	ko:K07813	NA
BLCPAMOF_02846	OG0002292	group_4005	1	2	2	fpa:FPR_08610	NA	NA
BLCPAMOF_02847	OG0003156	group_4006	1	1	1	fpa:FPR_08620	NA	NA
BLCPAMOF_02848	OG0002162	group_3085	1	1	1	NA	NA	NA
BLCPAMOF_02849	OG0002407	group_4008	1	1	1	fpa:FPR_08630	NA	NA
BLCPAMOF_02850	OG0002293	group_3086	1	0	0	fpa:FPR_08640	NA	NA
BLCPAMOF_02851	OG0000055	group_29	1	0	0	fpr:FP2_27630	NA	NA
BLCPAMOF_02852	OG0001639	mepA_14	6	7	12	fpr:FP2_20530	NA	NA
BLCPAMOF_02853	OG0001640	group_1880	1	2	2	fpr:FP2_20520	NA	NA
BLCPAMOF_02854	OG0001647	yeeO_4	6	6	11	fpr:FP2_20510	NA	NA
BLCPAMOF_02855	OG0001646	group_1885	1	0	0	fpr:FP2_20500	ko:K15986	NA
BLCPAMOF_02856	OG0002548	yccX	1	0	0	rim:ROI_41120	ko:K01512	NA
BLCPAMOF_02857	OG0001788	group_5568	1	1	1	NA	NA	NA
BLCPAMOF_02858	OG0001645	group_1884	1	0	0	fpr:FP2_20490	NA	NA
BLCPAMOF_02859	OG0001644	group_1883	1	0	0	fpr:FP2_20480	NA	NA
BLCPAMOF_02860	OG0001643	smc_2	1	0	0	fpr:FP2_20470	NA	NA
BLCPAMOF_02861	OG0002056	group_2541	1	0	0	NA	NA	NA
BLCPAMOF_02862	OG0001642	mepA_15	6	6	11	fpr:FP2_20450	NA	NA
BLCPAMOF_02863	OG0001652	rsxB_3	1	0	0	fpr:FP2_20340	ko:K07138	NA
BLCPAMOF_02864	OG0001651	group_5569	1	0	0	fpr:FP2_20350	NA	NA
BLCPAMOF_02865	OG0001650	apeB	1	0	0	fpr:FP2_20360	ko:K01267	NA
BLCPAMOF_02866	OG0001649	gltX_2	1	0	0	fpa:FPR_08850	ko:K01885	NA
BLCPAMOF_02867	OG0001648	group_911	2	2	3	fpr:FP2_20390	NA	NA
BLCPAMOF_02868	OG0000052	cstA_2	6	7	12	fpr:FP2_20400	NA	NA
BLCPAMOF_02869	OG0001641	tfdR	1	0	0	fpa:FPR_08710	NA	NA
BLCPAMOF_02870	OG0001978	group_5570	0	1	0	fpr:FP2_20420	NA	NA
BLCPAMOF_02871	OG0001813	group_3357	1	0	0	bag:Bcoa_2555	ko:K00077	NA
BLCPAMOF_02872	OG0000272	group_558	1	0	0	fpr:FP2_20440	ko:K15634	NA
BLCPAMOF_02873	OG0001653	uppP	4	4	7	fpr:FP2_20330	ko:K06153	NA
BLCPAMOF_02874	OG0001654	trkA_2	1	0	0	fpr:FP2_20320	ko:K03499	NA
BLCPAMOF_02875	OG0001655	trkA_3	1	0	0	fpr:FP2_20310	ko:K03499	NA
BLCPAMOF_02876	OG0001656	group_5571	2	2	3	fpa:FPR_08950	NA	NA
BLCPAMOF_02877	OG0001657	group_5572	3	4	6	fpr:FP2_20290	NA	NA
BLCPAMOF_02878	OG0001658	gph_2	1	0	0	fpr:FP2_20280	ko:K01091	NA
BLCPAMOF_02879	OG0003596	fabG_5	1	0	0	fpr:FP2_20270	NA	NA
BLCPAMOF_02882	OG0001659	serS	1	0	0	fpr:FP2_20240	ko:K01875	NA
BLCPAMOF_02883	OG0001660	spo0C_6	1	0	0	fpr:FP2_20230	ko:K03497	NA
BLCPAMOF_02884	OG0001661	soj_6	1	0	0	ctx:Clo1313_0007;cth:Cthe_2377	ko:K03496	NA
BLCPAMOF_02885	OG0001662	noc	1	0	0	fpr:FP2_20200	ko:K03497	NA
BLCPAMOF_02886	OG0001663	rsmG	1	0	0	fpr:FP2_20190	ko:K03501	NA
BLCPAMOF_02887	OG0001664	mnmG	1	0	0	fpr:FP2_20180	ko:K03495	NA
BLCPAMOF_02888	OG0001665	mnmE	1	0	0	fpr:FP2_20170	ko:K03650	NA
BLCPAMOF_02889	OG0002445	group_5573	3	4	6	bpb:bpr_I0327	NA	NA
BLCPAMOF_02890	OG0002979	yfkN	1	1	1	fpr:FP2_20160	ko:K01119	NA
BLCPAMOF_02891	OG0001666	group_913	1	0	0	fpr:FP2_20150	ko:K06346	NA
BLCPAMOF_02892	OG0001667	yidC	3	4	6	fpr:FP2_20140	ko:K03217	NA
BLCPAMOF_02893	OG0001772	yidD	1	0	0	dva:DAD186_21380	ko:K08998	NA
BLCPAMOF_02894	OG0001668	rnpA	0	1	0	fpr:FP2_20120	ko:K03536	NA
BLCPAMOF_02895	OG0001669	rpmH	0	1	0	fpr:FP2_20110;fpa:FPR_09110	ko:K02914	NA

付録8: InterProScanのアサインメント結果 (Fp14、Fp360に特徴的なオーソログに関して)

異なるオーソログ検出ツールを用いて、特定の単離株にのみに見られるオーソログおよび特定の単離株のみに見られるKOを含むオーソログを"specific ortholog"と定義した

category	
shared:	Fp14およびFp360のみに共有されていた特徴的なオーソログ
specific_fp14:	Fp14においてのみに特徴的なオーソログ
specific_fp360:	Fp360においてのみに特徴的なオーソログ

gene_ID	database	database_ID	annotation	Interproscan_ID	Interproscan_annotation	category
ICBIDGAJ_02238	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	shared
ICBIDGAJ_02238	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	shared
ICBIDGAJ_02238	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	shared
ICBIDGAJ_02238	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	shared
ICBIDGAJ_02237	Phobius	SIGNAL_PEPTIDE_C_REGION	C-terminal region of a signal peptide.	NA	NA	shared
ICBIDGAJ_02237	SignalP_GRAM_POSITIVE	SignalP-TM	NA	NA	NA	shared
ICBIDGAJ_02237	SignalP_EUK	SignalP-noTM	NA	NA	NA	shared
ICBIDGAJ_02237	Phobius	SIGNAL_PEPTIDE_N_REGION	N-terminal region of a signal peptide.	NA	NA	shared
ICBIDGAJ_02237	Phobius	SIGNAL_PEPTIDE	Signal peptide region	NA	NA	shared
ICBIDGAJ_02237	Phobius	SIGNAL_PEPTIDE_H_REGION	Hydrophobic region of a signal peptide.	NA	NA	shared
ICBIDGAJ_02237	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	shared
ICBIDGAJ_02236	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	shared
ICBIDGAJ_02236	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	shared
ICBIDGAJ_02236	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	shared
ICBIDGAJ_02236	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	shared
ICBIDGAJ_02236	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	shared
ICBIDGAJ_02236	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	shared
ICBIDGAJ_02236	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	shared
ICBIDGAJ_02236	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	shared
ICBIDGAJ_02236	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	shared
ICBIDGAJ_02236	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	shared
ICBIDGAJ_02236	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	shared
ICBIDGAJ_02236	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	shared
ICBIDGAJ_02236	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	shared
ICBIDGAJ_02236	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	shared
ICBIDGAJ_02236	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	shared
ICBIDGAJ_02236	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	shared
ICBIDGAJ_02236	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	shared
ICBIDGAJ_02236	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	shared
ICBIDGAJ_02236	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	shared
ICBIDGAJ_00537	Coils	Coil				shared
ICBIDGAJ_00537	Pfam	PF13378	Enolase C-terminal domain-like	IPR029065	Enolase C-terminal domain-like	shared
ICBIDGAJ_00537	SMART	SM00922		IPR013342	Mandelate racemase/muconate lactonizing enzyme, C-terminal	shared
ICBIDGAJ_00537	SFLD	SFLDS00001	Enolase			shared
ICBIDGAJ_00537	Pfam	PF02746	Mandelate racemase / muconate lactonizing enzyme, N-terminal domain	IPR013341	Mandelate racemase/muconate lactonizing enzyme, N-terminal domain	shared
ICBIDGAJ_00537	SUPERFAMILY	SSF54826		IPR029017	Enolase-like, N-terminal	shared
ICBIDGAJ_00537	CDD	cd03316	MR_like			shared
ICBIDGAJ_00537	Gene3D	G3DSA:3.20.20.120		IPR036849	Enolase-like, C-terminal domain superfamily	shared
ICBIDGAJ_00537	ProSitePatterns	PS00908	Mandelate racemase / muconate lactonizing enzyme family signature 1.	IPR018110	Mandelate racemase/muconate lactonizing enzyme, conserved site	shared
ICBIDGAJ_00537	SUPERFAMILY	SSF51604		IPR036849	Enolase-like, C-terminal domain superfamily	shared
ICBIDGAJ_00537	SFLD	SFLDG00179	mandelate racemase			shared
ICBIDGAJ_00537	Gene3D	G3DSA:3.30.390.10		IPR029017	Enolase-like, N-terminal	shared
ICBIDGAJ_00089	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_00769	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp14
ICBIDGAJ_00769	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp14
ICBIDGAJ_00769	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00769	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_00769	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00769	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00769	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00769	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00769	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_00769	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00769	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp14
ICBIDGAJ_00769	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp14
ICBIDGAJ_00769	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00769	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp14
ICBIDGAJ_00769	PANTHER	PTHR35007	NA	NA	NA	specific_fp14
ICBIDGAJ_00768	Pfam	PF00437	Type II/IV secretion system protein	IPR001482	Type II/IV secretion system protein	specific_fp14
ICBIDGAJ_00768	Gene3D	G3DSA:3.40.50.300	NA	NA	NA	specific_fp14
ICBIDGAJ_00768	Gene3D	G3DSA:3.30.450.380	NA	NA	NA	specific_fp14
ICBIDGAJ_00768	PANTHER	PTHR30258	NA	NA	NA	specific_fp14
ICBIDGAJ_00768	PANTHER	PTHR30258:SF3	NA	NA	NA	specific_fp14
ICBIDGAJ_00768	CDD	cd01130	VirB11-like_ATPase	NA	NA	specific_fp14
ICBIDGAJ_00768	SUPERFAMILY	SSF52540	NA	IPR027417	P-loop containing nucleoside triphosphate hydrolase	specific_fp14
ICBIDGAJ_00767	SUPERFAMILY	SSF52540	NA	IPR027417	P-loop containing nucleoside triphosphate hydrolase	specific_fp14
ICBIDGAJ_00767	Gene3D	G3DSA:3.40.50.300	NA	NA	NA	specific_fp14
ICBIDGAJ_00767	CDD	cd17869	TadZ-like	NA	NA	specific_fp14
ICBIDGAJ_00767	Gene3D	G3DSA:3.40.50.10850	NA	NA	NA	specific_fp14
ICBIDGAJ_01574	Phobius	SIGNAL_PEPTIDE_N_REGION	N-terminal region of a signal peptide.	NA	NA	specific_fp14
ICBIDGAJ_01574	Phobius	SIGNAL_PEPTIDE_C_REGION	C-terminal region of a signal peptide.	NA	NA	specific_fp14
ICBIDGAJ_01574	Phobius	SIGNAL_PEPTIDE	Signal peptide region	NA	NA	specific_fp14
ICBIDGAJ_01574	Phobius	SIGNAL_PEPTIDE_H_REGION	Hydrophobic region of a signal peptide.	NA	NA	specific_fp14
ICBIDGAJ_01574	SignalP_GRAM_NEGATIVE	SignalP-noTM	NA	NA	NA	specific_fp14
ICBIDGAJ_01574	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_01574	SignalP_GRAM_POSITIVE	SignalP-TM	NA	NA	NA	specific_fp14
ICBIDGAJ_01364	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_01365	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_01366	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_01367	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_01360	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_01362	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01362	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp14
ICBIDGAJ_01362	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_01362	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01363	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_01074	Phobius	SIGNAL_PEPTIDE_N_REGION	N-terminal region of a signal peptide.	NA	NA	specific_fp14
ICBIDGAJ_01074	SignalP_EUK	SignalP-noTM	NA	NA	NA	specific_fp14
ICBIDGAJ_01074	Phobius	SIGNAL_PEPTIDE_C_REGION	C-terminal region of a signal peptide.	NA	NA	specific_fp14
ICBIDGAJ_01074	Phobius	SIGNAL_PEPTIDE_H_REGION	Hydrophobic region of a signal peptide.	NA	NA	specific_fp14
ICBIDGAJ_01074	SignalP_GRAM_NEGATIVE	SignalP-noTM	NA	NA	NA	specific_fp14
ICBIDGAJ_01074	Phobius	SIGNAL_PEPTIDE	Signal peptide region	NA	NA	specific_fp14
ICBIDGAJ_01074	SignalP_GRAM_POSITIVE	SignalP-TM	NA	NA	NA	specific_fp14
ICBIDGAJ_01074	ProSiteProfiles	PS51257	Prokaryotic membrane lipoprotein lipid attachment site profile.	NA	NA	specific_fp14
ICBIDGAJ_01074	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_01074	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01368	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_01369	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_01073	SignalP_GRAM_NEGATIVE	SignalP-noTM	NA	NA	NA	specific_fp14
ICBIDGAJ_01073	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp14
ICBIDGAJ_01073	Phobius	SIGNAL_PEPTIDE_C_REGION	C-terminal region of a signal peptide.	NA	NA	specific_fp14
ICBIDGAJ_01073	Phobius	SIGNAL_PEPTIDE_N_REGION	N-terminal region of a signal peptide.	NA	NA	specific_fp14
ICBIDGAJ_01073	Phobius	SIGNAL_PEPTIDE_H_REGION	Hydrophobic region of a signal peptide.	NA	NA	specific_fp14
ICBIDGAJ_01073	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp14
ICBIDGAJ_01073	ProSiteProfiles	PS51257	Prokaryotic membrane lipoprotein lipid attachment site profile.	NA	NA	specific_fp14
ICBIDGAJ_01073	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_01073	SignalP_EUK	SignalP-noTM	NA	NA	NA	specific_fp14
ICBIDGAJ_01073	SignalP_GRAM_POSITIVE	SignalP-TM	NA	NA	NA	specific_fp14
ICBIDGAJ_01073	Phobius	SIGNAL_PEPTIDE	Signal peptide region	NA	NA	specific_fp14
ICBIDGAJ_01777	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_01776	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_01775	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_01774	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01774	Phobius	SIGNAL_PEPTIDE	Signal peptide region	NA	NA	specific_fp14
ICBIDGAJ_01774	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01774	ProSiteProfiles	PS51257	Prokaryotic membrane lipoprotein lipid attachment site profile.	NA	NA	specific_fp14
ICBIDGAJ_01774	Phobius	SIGNAL_PEPTIDE_C_REGION	C-terminal region of a signal peptide.	NA	NA	specific_fp14
ICBIDGAJ_01774	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_01774	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01774	Phobius	SIGNAL_PEPTIDE_H_REGION	Hydrophobic region of a signal peptide.	NA	NA	specific_fp14
ICBIDGAJ_01774	Phobius	SIGNAL_PEPTIDE_N_REGION	N-terminal region of a signal peptide.	NA	NA	specific_fp14
ICBIDGAJ_01774	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp14
ICBIDGAJ_01773	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_01772	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_01771	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_01770	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp14
ICBIDGAJ_01770	Coils	Coil	NA	NA	NA	specific_fp14
ICBIDGAJ_01770	Coils	Coil	NA	NA	NA	specific_fp14

ICBIDGAJ_01770	Coils	Coil	NA	NA	NA	specific_fp14
ICBIDGAJ_01770	Coils	Coil	NA	NA	NA	specific_fp14
ICBIDGAJ_01770	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp14
ICBIDGAJ_01779	Phobius	SIGNAL_PEPTIDE_N_REGION	N-terminal region of a signal peptide.	NA	NA	specific_fp14
ICBIDGAJ_01779	Phobius	SIGNAL_PEPTIDE_C_REGION	C-terminal region of a signal peptide.	NA	NA	specific_fp14
ICBIDGAJ_01779	Coils	Coil	NA	NA	NA	specific_fp14
ICBIDGAJ_01779	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01779	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_01779	Phobius	SIGNAL_PEPTIDE	Signal peptide region	NA	NA	specific_fp14
ICBIDGAJ_01779	Coils	Coil	NA	NA	NA	specific_fp14
ICBIDGAJ_01779	Gene3D	G3DSA:3.40.1350.10	NA	IPR011856	tRNA endonuclease-like domain superfamily	specific_fp14
ICBIDGAJ_01779	SUPERFAMILY	SSF52980	NA	IPR011335	Restriction endonuclease type II-like	specific_fp14
ICBIDGAJ_01779	Pfam	PF04471	Restriction endonuclease	IPR007560	Restriction endonuclease type IV, Mrr	specific_fp14
ICBIDGAJ_01779	Phobius	SIGNAL_PEPTIDE_H_REGION	Hydrophobic region of a signal peptide.	NA	NA	specific_fp14
ICBIDGAJ_01855	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01855	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01855	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01855	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01855	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01855	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp14
ICBIDGAJ_01855	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp14
ICBIDGAJ_01855	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01855	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_01855	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01855	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01855	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01855	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01855	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01855	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01855	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01855	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01855	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01855	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01855	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp14
ICBIDGAJ_01855	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_01855	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_01855	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01855	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01855	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01855	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp14
ICBIDGAJ_01855	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_01855	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01855	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01855	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01855	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_01855	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_01855	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp14
ICBIDGAJ_01388	Coils	Coil	NA	NA	NA	specific_fp14
ICBIDGAJ_01386	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01386	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_01386	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp14
ICBIDGAJ_01386	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01385	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_01382	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_01380	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_01381	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_01540	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp14
ICBIDGAJ_01540	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01540	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp14
ICBIDGAJ_01540	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01540	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_01540	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01540	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01540	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01540	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01540	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp14
ICBIDGAJ_01540	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01540	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01540	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_01540	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_01540	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01540	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01540	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp14
ICBIDGAJ_01540	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01540	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01541	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01541	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01541	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01541	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp14
ICBIDGAJ_01541	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01541	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01541	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01541	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01541	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_01541	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_01541	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01541	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp14
ICBIDGAJ_01541	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_01541	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp14
ICBIDGAJ_01541	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp14
ICBIDGAJ_01541	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01541	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01541	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01541	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01780	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp14
ICBIDGAJ_01780	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01780	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01780	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01780	Pfam	PF14015	Protein of unknown function (DUF4231)	IPR025325	Protein of unknown function DUF4231	specific_fp14
ICBIDGAJ_01780	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp14
ICBIDGAJ_01780	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_01780	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp14
ICBIDGAJ_01781	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_01373	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_01372	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_01371	Gene3D	G3DSA:1.10.260.40	NA	IPR010982	Lambda repressor-like, DNA-binding domain superfamily	specific_fp14
ICBIDGAJ_01371	SUPERFAMILY	SSF47413	NA	IPR010982	Lambda repressor-like, DNA-binding domain superfamily	specific_fp14
ICBIDGAJ_01371	CDD	cd00093	HTH_XRE	IPR001387	Cro/C1-type helix-turn-helix domain	specific_fp14
ICBIDGAJ_01370	Pfam	PF02452	PemK-like, MazF-like toxin of type II toxin-antitoxin system	IPR003477	mRNA interferase PemK-like	specific_fp14
ICBIDGAJ_01370	Coils	Coil	NA	NA	NA	specific_fp14
ICBIDGAJ_01370	SUPERFAMILY	SSF50118	NA	NA	NA	specific_fp14
ICBIDGAJ_01370	Gene3D	G3DSA:2.30.30.110	NA	IPR011067	Plasmid maintenance toxin/Cell growth inhibitor	specific_fp14
ICBIDGAJ_01370	PANTHER	PTHR33988	NA	IPR003477	mRNA interferase PemK-like	specific_fp14
ICBIDGAJ_01377	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_01376	Coils	Coil	NA	NA	NA	specific_fp14
ICBIDGAJ_01375	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_01374	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_01379	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_00164	SUPERFAMILY	SSF53474	NA	IPR029058	Alpha/Beta hydrolase fold	specific_fp14
ICBIDGAJ_00399	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_00399	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00399	SignalP_EUK	SignalP-noTM	NA	NA	NA	specific_fp14
ICBIDGAJ_00399	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp14
ICBIDGAJ_02460	Phobius	SIGNAL_PEPTIDE	Signal peptide region	NA	NA	specific_fp14
ICBIDGAJ_02460	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_02460	Phobius	SIGNAL_PEPTIDE_N_REGION	N-terminal region of a signal peptide.	NA	NA	specific_fp14
ICBIDGAJ_02460	Phobius	SIGNAL_PEPTIDE_C_REGION	C-terminal region of a signal peptide.	NA	NA	specific_fp14
ICBIDGAJ_02460	Phobius	SIGNAL_PEPTIDE_H_REGION	Hydrophobic region of a signal peptide.	NA	NA	specific_fp14
ICBIDGAJ_01660	PANTHER	PTHR24222	NA	NA	NA	specific_fp14
ICBIDGAJ_01660	Pfam	PF00005	ABC transporter	IPR003439	ABC transporter-like	specific_fp14
ICBIDGAJ_01660	SUPERFAMILY	SSF52540	NA	IPR027417	P-loop containing nucleoside triphosphate hydrolase	specific_fp14
ICBIDGAJ_01660	Gene3D	G3DSA:3.40.50.300	NA	NA	NA	specific_fp14
ICBIDGAJ_01660	PANTHER	PTHR24222:SF22	NA	NA	NA	specific_fp14
ICBIDGAJ_01847	SUPERFAMILY	SSF52467	NA	IPR029035	DHS-like NAD/FAD-binding domain superfamily	specific_fp14
ICBIDGAJ_01847	Pfam	PF13289	SIR2-like domain	IPR039444	SIR2-like domain	specific_fp14
ICBIDGAJ_01396	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp14

ICBIDGAJ_01556	Pfam	PF04465	Protein of unknown function (DUF499)	IPR007555	Protein of unknown function DUF499	specific_fp14
ICBIDGAJ_01556	Pfam	PF18731	Swt1-like HEPN	IPR041650	Swt1-like HEPN	specific_fp14
ICBIDGAJ_01555	Pfam	PF06634	Protein of unknown function (DUF1156)	IPR009537	Domain of unknown function DUF1156	specific_fp14
ICBIDGAJ_01555	SUPERFAMILY	SSF53335	NA	IPR029063	S-adenosyl-L-methionine-dependent methyltransferase	specific_fp14
ICBIDGAJ_01554	Gene3D	G3DSA:3.40.50.300	NA	NA	NA	specific_fp14
ICBIDGAJ_01554	SUPERFAMILY	SSF52540	NA	IPR027417	P-loop containing nucleoside triphosphate hydrolase	specific_fp14
ICBIDGAJ_02163	Pfam	PF14487	ssDNA thymidine ADP-ribosyltransferase, DarT	IPR029494	ssDNA thymidine ADP-ribosyltransferase, DarT	specific_fp14
ICBIDGAJ_02162	Gene3D	G3DSA:3.40.220.10	NA	NA	NA	specific_fp14
ICBIDGAJ_02162	CDD	cd02901	Macro_Poa1p_like	NA	NA	specific_fp14
ICBIDGAJ_02162	PANTHER	PTHR12521	NA	NA	NA	specific_fp14
ICBIDGAJ_02162	SUPERFAMILY	SSF52949	NA	NA	NA	specific_fp14
ICBIDGAJ_02162	SMART	SM00506	NA	IPR002589	Macro domain	specific_fp14
ICBIDGAJ_02162	ProSiteProfiles	PS51154	Macro domain profile.	IPR002589	Macro domain	specific_fp14
ICBIDGAJ_02162	Pfam	PF01661	Macro domain	IPR002589	Macro domain	specific_fp14
ICBIDGAJ_00155	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_00152	Gene3D	G3DSA:3.30.460.10	NA	NA	NA	specific_fp14
ICBIDGAJ_00152	Pfam	PF01909	Nucleotidyltransferase domain	IPR002934	Polymerase, nucleotidyl transferase domain	specific_fp14
ICBIDGAJ_00152	CDD	cd05403	NT_KNTase_like	NA	NA	specific_fp14
ICBIDGAJ_00152	Coils	Coil	NA	NA	NA	specific_fp14
ICBIDGAJ_00152	SUPERFAMILY	SSF81301	NA	NA	NA	specific_fp14
ICBIDGAJ_00153	PANTHER	PTHR37812	NA	NA	NA	specific_fp14
ICBIDGAJ_00153	SUPERFAMILY	SSF46689	NA	IPR009057	Homeobox-like domain superfamily	specific_fp14
ICBIDGAJ_01307	Coils	Coil	NA	NA	NA	specific_fp14
ICBIDGAJ_01307	Coils	Coil	NA	NA	NA	specific_fp14
ICBIDGAJ_01304	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_01305	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp14
ICBIDGAJ_01870	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_01877	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_01301	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_01014	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_01308	Pfam	PF02195	ParB-like nuclease domain	IPR003115	ParB/Sulfiredoxin	specific_fp14
ICBIDGAJ_01308	SUPERFAMILY	SSF110849	NA	IPR036086	ParB/Sulfiredoxin superfamily	specific_fp14
ICBIDGAJ_01309	Pfam	PF13384	Homeodomain-like domain	NA	NA	specific_fp14
ICBIDGAJ_01952	CDD	cd00085	HNHc	IPR003615	HNH nuclease	specific_fp14
ICBIDGAJ_01952	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01952	Coils	Coil	NA	NA	NA	specific_fp14
ICBIDGAJ_01952	Pfam	PF01844	HNH endonuclease	IPR002711	HNH endonuclease	specific_fp14
ICBIDGAJ_01952	PANTHER	PTHR33877	NA	NA	NA	specific_fp14
ICBIDGAJ_01952	Coils	Coil	NA	NA	NA	specific_fp14
ICBIDGAJ_01952	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01952	Gene3D	G3DSA:3.30.40.60	NA	NA	NA	specific_fp14
ICBIDGAJ_01952	SMART	SM00507	NA	IPR003615	HNH nuclease	specific_fp14
ICBIDGAJ_01952	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp14
ICBIDGAJ_01952	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_02293	Gene3D	G3DSA:3.60.70.12	NA	NA	NA	specific_fp14
ICBIDGAJ_02293	SUPERFAMILY	SSF56266	NA	IPR016117	ArgJ-like domain superfamily	specific_fp14
ICBIDGAJ_02293	Pfam	PF03576	Peptidase family S58	IPR005321	Peptidase S58, DmpA	specific_fp14
ICBIDGAJ_01854	Pfam	PF00534	Glycosyl transferases group 1	IPR001296	Glycosyl transferase, family 1	specific_fp14
ICBIDGAJ_01854	PANTHER	PTHR46401:SF5	NA	NA	NA	specific_fp14
ICBIDGAJ_01854	Gene3D	G3DSA:3.40.50.11090	NA	NA	NA	specific_fp14
ICBIDGAJ_01854	PANTHER	PTHR46401	NA	NA	NA	specific_fp14
ICBIDGAJ_01854	SUPERFAMILY	SSF53756	NA	NA	NA	specific_fp14
ICBIDGAJ_01854	CDD	cd03801	GT4_PimA-like	NA	NA	specific_fp14
ICBIDGAJ_01854	Gene3D	G3DSA:3.40.50.2000	NA	NA	NA	specific_fp14
ICBIDGAJ_00143	Gene3D	G3DSA:3.40.50.300	NA	NA	NA	specific_fp14
ICBIDGAJ_00143	PANTHER	PTHR34301	NA	NA	NA	specific_fp14
ICBIDGAJ_00143	SUPERFAMILY	SSF52540	NA	IPR027417	P-loop containing nucleoside triphosphate hydrolase	specific_fp14
ICBIDGAJ_01314	Coils	Coil	NA	NA	NA	specific_fp14
ICBIDGAJ_01314	Coils	Coil	NA	NA	NA	specific_fp14
ICBIDGAJ_01311	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp14
ICBIDGAJ_01310	Gene3D	G3DSA:3.40.50.300	NA	NA	NA	specific_fp14
ICBIDGAJ_01310	TIGRFAM	TIGR01630	psiM2_ORF9: phage uncharacterized protein, C-terminal domain	IPR006517	Archaeophage PsiM2, terminase large subunit	specific_fp14
ICBIDGAJ_01310	Pfam	PF03237	Terminase-like family	IPR004921	Terminase large subunit, T4likevirus-type	specific_fp14
ICBIDGAJ_01310	Pfam	PF17289	Terminase RNaseH-like domain	IPR035421	Terminase, large subunit gp17-like	specific_fp14
ICBIDGAJ_01313	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_01312	Coils	Coil	NA	NA	NA	specific_fp14
ICBIDGAJ_01312	Phobius	SIGNAL_PEPTIDE_C_REGION	C-terminal region of a signal peptide.	NA	NA	specific_fp14
ICBIDGAJ_01312	Phobius	SIGNAL_PEPTIDE_N_REGION	N-terminal region of a signal peptide.	NA	NA	specific_fp14
ICBIDGAJ_01312	Phobius	SIGNAL_PEPTIDE	Signal peptide region	NA	NA	specific_fp14
ICBIDGAJ_01312	Phobius	SIGNAL_PEPTIDE_H_REGION	Hydrophobic region of a signal peptide.	NA	NA	specific_fp14
ICBIDGAJ_01312	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_01319	ProSiteProfiles	PS51750	Bro-N domain profile.	IPR003497	BRO N-terminal domain	specific_fp14
ICBIDGAJ_01319	PANTHER	PTHR36180:SF2	NA	NA	NA	specific_fp14
ICBIDGAJ_01319	Pfam	PF03374	Phage antirepressor protein KilAC domain	IPR005039	Antirepressor protein, C-terminal	specific_fp14
ICBIDGAJ_01319	Pfam	PF02498	BRO family, N-terminal domain	IPR003497	BRO N-terminal domain	specific_fp14
ICBIDGAJ_01319	SMART	SM01040	NA	IPR003497	BRO N-terminal domain	specific_fp14
ICBIDGAJ_01319	PANTHER	PTHR36180	NA	NA	NA	specific_fp14
ICBIDGAJ_02609	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_02609	Phobius	SIGNAL_PEPTIDE_H_REGION	Hydrophobic region of a signal peptide.	NA	NA	specific_fp14
ICBIDGAJ_02609	Phobius	SIGNAL_PEPTIDE_C_REGION	C-terminal region of a signal peptide.	NA	NA	specific_fp14
ICBIDGAJ_02609	Pfam	PF05128	Domain of unknown function (DUF697)	IPR021147	Protein of unknown function DUF697	specific_fp14
ICBIDGAJ_02609	Phobius	SIGNAL_PEPTIDE_N_REGION	N-terminal region of a signal peptide.	NA	NA	specific_fp14
ICBIDGAJ_02609	Phobius	SIGNAL_PEPTIDE	Signal peptide region	NA	NA	specific_fp14
ICBIDGAJ_00289	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00289	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00289	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_00289	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00289	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp14
ICBIDGAJ_01320	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_02459	Coils	Coil	NA	NA	NA	specific_fp14
ICBIDGAJ_02459	Coils	Coil	NA	NA	NA	specific_fp14
ICBIDGAJ_01733	Gene3D	G3DSA:3.30.2310.20	NA	IPR035093	Toxin-antitoxin system, RelE/ParE toxin domain superfamily	specific_fp14
ICBIDGAJ_01733	Pfam	PF05016	ParE toxin of type II toxin-antitoxin system, parDE	IPR007712	Toxin-antitoxin system, RelE/ParE toxin family	specific_fp14
ICBIDGAJ_01733	SUPERFAMILY	SSF143011	NA	IPR035093	Toxin-antitoxin system, RelE/ParE toxin domain superfamily	specific_fp14
ICBIDGAJ_02227	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_01539	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01539	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp14
ICBIDGAJ_01539	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01539	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_01539	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp14
ICBIDGAJ_01539	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01539	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01539	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01539	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01539	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01539	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01539	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01539	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01539	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_01539	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_01539	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp14
ICBIDGAJ_01539	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp14
ICBIDGAJ_01539	Gene3D	G3DSA:3.30.565.10	NA	IPR036890	Histidine kinase/HSP90-like ATPase superfamily	specific_fp14
ICBIDGAJ_01539	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01539	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_01539	CDD	cd16917	HATPase_UhpB-NarQ-NarX-like	NA	NA	specific_fp14
ICBIDGAJ_01539	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01539	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01858	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_02222	SFLD	SFLDS00029	Radical SAM	IPR007197	Radical SAM	specific_fp14
ICBIDGAJ_02222	PANTHER	PTHR11228	NA	NA	NA	specific_fp14
ICBIDGAJ_02222	CDD	cd01335	Radical_SAM	NA	NA	specific_fp14
ICBIDGAJ_02222	Gene3D	G3DSA:3.20.20.70	NA	IPR013785	Aldolase-type TIM barrel	specific_fp14
ICBIDGAJ_02222	ProSitePatterns	PS01305	moaA / nifB / pqqE family signature.	IPR000385	MoaA/NifB/PqqE, iron-sulphur binding, conserved site	specific_fp14
ICBIDGAJ_02222	Pfam	PF13353	4Fe-4S single cluster domain	NA	NA	specific_fp14
ICBIDGAJ_02222	SFLD	SFLDG01067	SPASM/twitch domain containing	NA	NA	specific_fp14
ICBIDGAJ_02222	Pfam	PF04055	Radical SAM superfamily	IPR007197	Radical SAM	specific_fp14
ICBIDGAJ_02222	SUPERFAMILY	SSF102114	NA	NA	NA	specific_fp14
ICBIDGAJ_00136	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_00137	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00137	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp14
ICBIDGAJ_00137	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_00137	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp14
ICBIDGAJ_00137	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_02610	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_00130	Pfam	PF03235	Protein of unknown function DUF262	IPR004919	Domain of unknown function DUF262	specific_fp14
ICBIDGAJ_00526	NA	NA	NA	NA	NA	specific_fp14

ICBIDGAJ_01328	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_01329	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp14
ICBIDGAJ_01329	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp14
ICBIDGAJ_00444	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00444	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00444	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00444	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00444	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp14
ICBIDGAJ_00444	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_00444	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp14
ICBIDGAJ_00444	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_00444	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00444	Pfam	PF07853	Protein of unknown function (DUF1648)	IPR012867	Domain of unknown function DUF1648	specific_fp14
ICBIDGAJ_00444	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00445	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00445	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00445	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00445	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_00445	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00445	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_00445	Phobius	SIGNAL_PEPTIDE_H_REGION	Hydrophobic region of a signal peptide.	NA	NA	specific_fp14
ICBIDGAJ_00445	Phobius	SIGNAL_PEPTIDE_N_REGION	N-terminal region of a signal peptide.	NA	NA	specific_fp14
ICBIDGAJ_00445	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00445	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp14
ICBIDGAJ_00445	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00445	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00445	Phobius	SIGNAL_PEPTIDE	Signal peptide region	NA	NA	specific_fp14
ICBIDGAJ_00445	Pfam	PF13630	SdpI/YhfL protein family	IPR025962	SdpI/YhfL protein family	specific_fp14
ICBIDGAJ_00445	Phobius	SIGNAL_PEPTIDE_C_REGION	C-terminal region of a signal peptide.	NA	NA	specific_fp14
ICBIDGAJ_00445	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00445	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00445	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00445	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp14
ICBIDGAJ_00445	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00445	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_00445	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp14
ICBIDGAJ_00138	Coils	Coil	NA	NA	NA	specific_fp14
ICBIDGAJ_00138	Coils	Coil	NA	NA	NA	specific_fp14
ICBIDGAJ_00138	Coils	Coil	NA	NA	NA	specific_fp14
ICBIDGAJ_00138	Gene3D	G3DSA:3.40.50.300	NA	NA	NA	specific_fp14
ICBIDGAJ_00138	Pfam	PF12532	Protein of unknown function (DUF3732)	IPR022205	Protein of unknown function DUF3732	specific_fp14
ICBIDGAJ_01359	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_01358	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_02137	Phobius	SIGNAL_PEPTIDE_N_REGION	N-terminal region of a signal peptide.	NA	NA	specific_fp14
ICBIDGAJ_02137	Phobius	SIGNAL_PEPTIDE	Signal peptide region	NA	NA	specific_fp14
ICBIDGAJ_02137	SignalP_GRAM_POSITIVE	SignalP-TM	NA	NA	NA	specific_fp14
ICBIDGAJ_02137	Phobius	SIGNAL_PEPTIDE_C_REGION	C-terminal region of a signal peptide.	NA	NA	specific_fp14
ICBIDGAJ_02137	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_02137	Phobius	SIGNAL_PEPTIDE_H_REGION	Hydrophobic region of a signal peptide.	NA	NA	specific_fp14
ICBIDGAJ_02137	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00756	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_00757	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_00202	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00202	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp14
ICBIDGAJ_00202	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00202	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_00202	Pfam	PF13231	Dolichyl-phosphate-mannose-protein mannosyltransferase	IPR038731	Glycosyltransferase RgtA/B/C/D-like	specific_fp14
ICBIDGAJ_00202	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00202	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00202	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00202	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00202	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_00202	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00202	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00202	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp14
ICBIDGAJ_00202	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00202	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00202	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp14
ICBIDGAJ_00202	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00202	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_00202	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00202	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00202	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00202	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00202	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00202	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp14
ICBIDGAJ_00202	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp14
ICBIDGAJ_00202	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00202	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp14
ICBIDGAJ_00202	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00202	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_00202	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_00202	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01338	SMART	SM01040	NA	IPR003497	BRO N-terminal domain	specific_fp14
ICBIDGAJ_00778	SUPERFAMILY	SSF49879	NA	IPR008984	SMAD/FHA domain superfamily	specific_fp14
ICBIDGAJ_00778	CDD	cd00060	FHA	IPR000253	Forkhead-associated (FHA) domain	specific_fp14
ICBIDGAJ_00778	ProSiteProfiles	PS50006	Forkhead-associated (FHA) domain profile.	IPR000253	Forkhead-associated (FHA) domain	specific_fp14
ICBIDGAJ_00778	Coils	Coil	NA	NA	NA	specific_fp14
ICBIDGAJ_00778	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp14
ICBIDGAJ_00778	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp14
ICBIDGAJ_00778	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp14
ICBIDGAJ_00778	Pfam	PF00498	FHA domain	IPR000253	Forkhead-associated (FHA) domain	specific_fp14
ICBIDGAJ_00778	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp14
ICBIDGAJ_00778	Gene3D	G3DSA:2.60.200.20	NA	NA	NA	specific_fp14
ICBIDGAJ_00778	PANTHER	PTHR23308	NA	NA	NA	specific_fp14
ICBIDGAJ_00329	ProSiteProfiles	PS51257	Prokaryotic membrane lipoprotein lipid attachment site profile.	NA	NA	specific_fp14
ICBIDGAJ_00329	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_00329	SignalP_GRAM_POSITIVE	SignalP-TM	NA	NA	NA	specific_fp14
ICBIDGAJ_00329	Phobius	SIGNAL_PEPTIDE_H_REGION	Hydrophobic region of a signal peptide.	NA	NA	specific_fp14
ICBIDGAJ_00329	Phobius	SIGNAL_PEPTIDE	Signal peptide region	NA	NA	specific_fp14
ICBIDGAJ_00329	Phobius	SIGNAL_PEPTIDE_C_REGION	C-terminal region of a signal peptide.	NA	NA	specific_fp14
ICBIDGAJ_00329	Phobius	SIGNAL_PEPTIDE_N_REGION	N-terminal region of a signal peptide.	NA	NA	specific_fp14
ICBIDGAJ_00329	SignalP_EUK	SignalP-noTM	NA	NA	NA	specific_fp14
ICBIDGAJ_00450	Pfam	PF12358	Protein of unknown function (DUF3644)	IPR022104	Domain of unknown function DUF3644	specific_fp14
ICBIDGAJ_01291	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp14
ICBIDGAJ_01292	SUPERFAMILY	SSF52980	NA	IPR011335	Restriction endonuclease type II-like	specific_fp14
ICBIDGAJ_01292	PANTHER	PTHR31340:SF5	NA	NA	NA	specific_fp14
ICBIDGAJ_01292	PANTHER	PTHR31340	NA	NA	NA	specific_fp14
ICBIDGAJ_01293	Coils	Coil	NA	NA	NA	specific_fp14
ICBIDGAJ_01295	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp14
ICBIDGAJ_01295	Coils	Coil	NA	NA	NA	specific_fp14
ICBIDGAJ_01295	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp14
ICBIDGAJ_01295	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp14
ICBIDGAJ_01295	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp14
ICBIDGAJ_01295	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp14
ICBIDGAJ_00911	Coils	Coil	NA	NA	NA	specific_fp14
ICBIDGAJ_01349	Coils	Coil	NA	NA	NA	specific_fp14
ICBIDGAJ_00339	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp14
ICBIDGAJ_00339	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00339	Coils	Coil	NA	NA	NA	specific_fp14
ICBIDGAJ_00339	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00339	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_00339	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp14
ICBIDGAJ_01345	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_01759	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_01755	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp14
ICBIDGAJ_01755	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp14
ICBIDGAJ_02196	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_01757	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_01756	Coils	Coil	NA	NA	NA	specific_fp14
ICBIDGAJ_01751	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_01287	Gene3D	G3DSA:1.10.260.40	NA	IPR010982	Lambda repressor-like, DNA-binding domain superfamily	specific_fp14
ICBIDGAJ_01287	SMART	SM00530	NA	IPR001387	Cro/C1-type helix-turn-helix domain	specific_fp14
ICBIDGAJ_01287	ProSiteProfiles	PS50943	Cro/C1-type HTH domain profile.	IPR001387	Cro/C1-type helix-turn-helix domain	specific_fp14
ICBIDGAJ_01287	CDD	cd00093	HTH_XRE	IPR001387	Cro/C1-type helix-turn-helix domain	specific_fp14
ICBIDGAJ_01287	SUPERFAMILY	SSF47413	NA	IPR010982	Lambda repressor-like, DNA-binding domain superfamily	specific_fp14
ICBIDGAJ_01287	Pfam	PF01381	Helix-turn-helix	IPR001387	Cro/C1-type helix-turn-helix domain	specific_fp14

ICBIDGAJ_02195	Pfam	PF04055	Radical SAM superfamily	IPR007197	Radical SAM	specific_fp14
ICBIDGAJ_02195	Pfam	PF05402	Coenzyme PQQ synthesis protein D (PqqD)	IPR008792	Coenzyme PQQ synthesis protein D	specific_fp14
ICBIDGAJ_02195	CDD	cd01335	Radical_SAM	NA	NA	specific_fp14
ICBIDGAJ_02195	Gene3D	G3DSA:3.20.20.70	NA	IPR013785	Aldolase-type TIM barrel	specific_fp14
ICBIDGAJ_02195	PANTHER	PTHR11228	NA	NA	NA	specific_fp14
ICBIDGAJ_02195	SFLD	SFLDG01067	SPASM/twitch domain containing	NA	NA	specific_fp14
ICBIDGAJ_02195	SUPERFAMILY	SSF102114	NA	NA	NA	specific_fp14
ICBIDGAJ_02195	Pfam	PF13353	4Fe-4S single cluster domain	NA	NA	specific_fp14
ICBIDGAJ_02195	SFLD	SFLDS00029	Radical SAM	IPR007197	Radical SAM	specific_fp14
ICBIDGAJ_01289	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_00909	Coils	Coil	NA	NA	NA	specific_fp14
ICBIDGAJ_00908	Gene3D	G3DSA:3.60.20.10	NA	IPR029055	Nucleophile aminohydrolases, N-terminal	specific_fp14
ICBIDGAJ_00908	SUPERFAMILY	SSF56235	NA	IPR029055	Nucleophile aminohydrolases, N-terminal	specific_fp14
ICBIDGAJ_00770	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_00770	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00770	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_00770	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00770	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00770	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00770	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp14
ICBIDGAJ_00770	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_00770	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00770	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00770	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00770	Pfam	PF00482	Type II secretion system (T2SS), protein F	IPR018076	Type II secretion system F domain	specific_fp14
ICBIDGAJ_00770	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp14
ICBIDGAJ_00770	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00770	PANTHER	PTHR35007	NA	NA	NA	specific_fp14
ICBIDGAJ_00770	PANTHER	PTHR35007:SF2	NA	NA	NA	specific_fp14
ICBIDGAJ_00771	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00771	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_00771	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00771	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp14
ICBIDGAJ_00772	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00772	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp14
ICBIDGAJ_00772	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00772	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_00773	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00773	Pfam	PF01478	Type IV leader peptidase family	IPR000045	Prepilin type IV endopeptidase, peptidase domain	specific_fp14
ICBIDGAJ_00773	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp14
ICBIDGAJ_00773	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00773	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00773	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00773	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00773	PANTHER	PTHR30487	NA	NA	NA	specific_fp14
ICBIDGAJ_00773	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00773	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp14
ICBIDGAJ_00773	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00773	Phobius	SIGNAL_PEPTIDE_H_REGION	Hydrophobic region of a signal peptide.	NA	NA	specific_fp14
ICBIDGAJ_00773	Phobius	SIGNAL_PEPTIDE_N_REGION	N-terminal region of a signal peptide.	NA	NA	specific_fp14
ICBIDGAJ_00773	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00773	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00773	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp14
ICBIDGAJ_00773	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_00773	Phobius	SIGNAL_PEPTIDE_C_REGION	C-terminal region of a signal peptide.	NA	NA	specific_fp14
ICBIDGAJ_00773	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_00773	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_00773	Phobius	SIGNAL_PEPTIDE	Signal peptide region	NA	NA	specific_fp14
ICBIDGAJ_00773	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00773	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00773	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00773	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00773	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_00774	Phobius	SIGNAL_PEPTIDE_N_REGION	N-terminal region of a signal peptide.	NA	NA	specific_fp14
ICBIDGAJ_00774	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_00774	PANTHER	PTHR37841	NA	NA	NA	specific_fp14
ICBIDGAJ_00774	PANTHER	PTHR37841	NA	NA	NA	specific_fp14
ICBIDGAJ_00774	Phobius	SIGNAL_PEPTIDE_C_REGION	C-terminal region of a signal peptide.	NA	NA	specific_fp14
ICBIDGAJ_00774	Phobius	SIGNAL_PEPTIDE	Signal peptide region	NA	NA	specific_fp14
ICBIDGAJ_00774	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00774	SUPERFAMILY	SSF69360	NA	NA	NA	specific_fp14
ICBIDGAJ_00774	Pfam	PF14903	WG containing repeat	IPR032774	WG containing repeat	specific_fp14
ICBIDGAJ_00774	Pfam	PF14903	WG containing repeat	IPR032774	WG containing repeat	specific_fp14
ICBIDGAJ_00774	Phobius	SIGNAL_PEPTIDE_H_REGION	Hydrophobic region of a signal peptide.	NA	NA	specific_fp14
ICBIDGAJ_00774	SignalP_GRAM_POSITIVE	SignalP-TM	NA	NA	NA	specific_fp14
ICBIDGAJ_00775	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_00775	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp14
ICBIDGAJ_00775	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00775	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00776	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_00776	Coils	Coil	NA	NA	NA	specific_fp14
ICBIDGAJ_00776	Phobius	SIGNAL_PEPTIDE_N_REGION	N-terminal region of a signal peptide.	NA	NA	specific_fp14
ICBIDGAJ_00776	Phobius	SIGNAL_PEPTIDE_C_REGION	C-terminal region of a signal peptide.	NA	NA	specific_fp14
ICBIDGAJ_00776	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00776	Coils	Coil	NA	NA	NA	specific_fp14
ICBIDGAJ_00776	Phobius	SIGNAL_PEPTIDE_H_REGION	Hydrophobic region of a signal peptide.	NA	NA	specific_fp14
ICBIDGAJ_00776	Phobius	SIGNAL_PEPTIDE	Signal peptide region	NA	NA	specific_fp14
ICBIDGAJ_00777	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_00777	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp14
ICBIDGAJ_00777	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_00777	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01351	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_02512	CDD	cd01189	INT_ICEBs1_C_like	NA	NA	specific_fp14
ICBIDGAJ_02512	Pfam	PF00589	Phage integrase family	IPR002104	Integrase, catalytic domain	specific_fp14
ICBIDGAJ_02512	PANTHER	PTHR30349	NA	NA	NA	specific_fp14
ICBIDGAJ_02512	SUPERFAMILY	SSF56349	NA	IPR011010	DNA breaking-rejoining enzyme, catalytic core	specific_fp14
ICBIDGAJ_02512	Gene3D	G3DSA:1.10.443.10	NA	IPR013762	Integrase-like, catalytic domain superfamily	specific_fp14
ICBIDGAJ_02512	Gene3D	G3DSA:1.10.150.130	NA	IPR010998	Integrase/recombinase, N-terminal	specific_fp14
ICBIDGAJ_02512	Coils	Coil	NA	NA	NA	specific_fp14
ICBIDGAJ_01352	Coils	Coil	NA	NA	NA	specific_fp14
ICBIDGAJ_01352	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01352	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp14
ICBIDGAJ_01352	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp14
ICBIDGAJ_01352	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp14
ICBIDGAJ_01352	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp14
ICBIDGAJ_01352	Coils	Coil	NA	NA	NA	specific_fp14
ICBIDGAJ_01357	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_01356	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_01768	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_01769	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_02457	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_01760	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp14
ICBIDGAJ_01765	Coils	Coil	NA	NA	NA	specific_fp14
ICBIDGAJ_01765	Gene3D	G3DSA:1.10.10.10	NA	IPR036388	Winged helix-like DNA-binding domain superfamily	specific_fp14
ICBIDGAJ_01765	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp14
ICBIDGAJ_01767	Coils	Coil	NA	NA	NA	specific_fp14
ICBIDGAJ_01767	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp14
ICBIDGAJ_01285	NA	NA	NA	NA	NA	specific_fp14
ICBIDGAJ_00753	SUPERFAMILY	SSF64288		IPR028978	Chorismate pyruvate-lyase/UbiC transcription regulator-associated domain superfamily	specific_fp14
ICBIDGAJ_00753	CDD	cd07377	WHTH_GntR	IPR000524	Transcription regulator HTH, GntR	specific_fp14
ICBIDGAJ_00753	Pfam	PF07702	UTRA domain	IPR011663	UbiC transcription regulator-associated	specific_fp14
ICBIDGAJ_00753	SUPERFAMILY	SSF46785		IPR036390	Winged helix DNA-binding domain superfamily	specific_fp14
ICBIDGAJ_00753	SMART	SM00345		IPR000524	Transcription regulator HTH, GntR	specific_fp14
ICBIDGAJ_00753	PRINTS	PR00035	GntR bacterial regulatory protein HTH signature	IPR000524	Transcription regulator HTH, GntR	specific_fp14
ICBIDGAJ_00753	PRINTS	PR00035	GntR bacterial regulatory protein HTH signature	IPR000524	Transcription regulator HTH, GntR	specific_fp14
ICBIDGAJ_00753	Gene3D	G3DSA:3.40.1410.10		IPR028978	Chorismate pyruvate-lyase/UbiC transcription regulator-associated domain superfamily	specific_fp14
ICBIDGAJ_00753	TIGRFAM	TIGR02404	trehalos_R_Bsub: trehalose operon repressor	IPR012770	Trehalose operon transcriptional repressor	specific_fp14
ICBIDGAJ_00753	Pfam	PF00392	Bacterial regulatory proteins, gntR family	IPR000524	Transcription regulator HTH, GntR	specific_fp14
ICBIDGAJ_00753	Gene3D	G3DSA:1.10.10.10		IPR036388	Winged helix-like DNA-binding domain superfamily	specific_fp14
ICBIDGAJ_00753	ProSiteProfiles	PS50949	GntR-type HTH domain profile.	IPR000524	Transcription regulator HTH, GntR	specific_fp14
ICBIDGAJ_00753	SMART	SM00866		IPR011663	UbiC transcription regulator-associated	specific_fp14
ICBIDGAJ_00754	Gene3D	G3DSA:3.30.1360.60		IPR036678	Glucose permease domain IIB	specific_fp14
ICBIDGAJ_00754	ProSiteProfiles	PS51098	PTS_EIIB type-1 domain profile.	IPR001996	Phosphotransferase system, IIB component, type 1	specific_fp14
ICBIDGAJ_00754	TIGRFAM	TIGR00826	EIIB_glc: PTS system, glucose-like IIB component	IPR001996	Phosphotransferase system, IIB component, type 1	specific_fp14
ICBIDGAJ_00754	ProSiteProfiles	PS51103	PTS_EIIC type-1 domain profile.	IPR013013	Phosphotransferase system, EIIC component, type 1	specific_fp14
ICBIDGAJ_00754	CDD	cd00212	PTS_IIB_glc	IPR018113	Phosphotransferase system EIIB, cysteine phosphorylation site	specific_fp14
ICBIDGAJ_00754	Pfam	PF00367	phosphotransferase system, EIIB	IPR018113	Phosphotransferase system EIIB, cysteine phosphorylation site	specific_fp14

ICBIDGAJ_00754	SUPERFAMILY	SSF55604		IPR036878	Glucose permease domain IIB	specific_fp14
ICBIDGAJ_00754	TIGRFAM	TIGR01992	PTS-IIBC-Tre: PTS system, trehalose-specific IIBC component	IPR011296	Phosphotransferase system, trehalose-specific IIBC component	specific_fp14
ICBIDGAJ_00754	Pfam	PF02378	Phosphotransferase system, EIIC	IPR003352	Phosphotransferase system, EIIC	specific_fp14
ICBIDGAJ_00755	SUPERFAMILY	SSF51011				specific_fp14
ICBIDGAJ_00755	SUPERFAMILY	SSF51445		IPR017853	Glycoside hydrolase superfamily	specific_fp14
ICBIDGAJ_00755	Gene3D	G3DSA:3.20.20.80				specific_fp14
ICBIDGAJ_00755	Gene3D	G3DSA:2.60.40.1180		IPR013780	Glycosyl hydrolase, all-beta	specific_fp14
ICBIDGAJ_00755	Gene3D	G3DSA:3.90.400.10				specific_fp14
ICBIDGAJ_00755	SMART	SM00642		IPR006047	Glycosyl hydrolase, family 13, catalytic domain	specific_fp14
ICBIDGAJ_00755	CDD	cd11333	AmyAc_SI_OligoGlu_DGase			specific_fp14
ICBIDGAJ_00755	Pfam	PF00128	Alpha amylase, catalytic domain	IPR006047	Glycosyl hydrolase, family 13, catalytic domain	specific_fp14
ICBIDGAJ_00755	Pfam	PF11941	Domain of unknown function (DUF3459)	IPR022567	Glycosyl hydrolase, C-terminal (DUF3459)	specific_fp14
ICBIDGAJ_00755	TIGRFAM	TIGR02403	trehalose_treC: alpha,alpha-phosphotrehalase	IPR012769	Trehalose-6-phosphate hydrolase	specific_fp14
ICBIDGAJ_01856	SUPERFAMILY	SSF53448		IPR029044	Nucleotide-diphospho-sugar transferases	specific_fp14
ICBIDGAJ_01856	CDD	cd04196	GT_2_like_d			specific_fp14
ICBIDGAJ_01856	Pfam	PF00535	Glycosyl transferase family 2	IPR001173	Glycosyltransferase 2-like	specific_fp14
ICBIDGAJ_01856	Gene3D	G3DSA:3.90.550.10		IPR029044	Nucleotide-diphospho-sugar transferases	specific_fp14
BLCPAMOF_02134	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	shared
BLCPAMOF_02134	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	shared
BLCPAMOF_02134	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	shared
BLCPAMOF_02134	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	shared
BLCPAMOF_02134	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	shared
BLCPAMOF_02134	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	shared
BLCPAMOF_02134	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	shared
BLCPAMOF_02134	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	shared
BLCPAMOF_02134	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	shared
BLCPAMOF_02134	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	shared
BLCPAMOF_02134	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	shared
BLCPAMOF_02134	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	shared
BLCPAMOF_02134	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	shared
BLCPAMOF_02134	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	shared
BLCPAMOF_02134	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	shared
BLCPAMOF_02134	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	shared
BLCPAMOF_02134	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	shared
BLCPAMOF_02134	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	shared
BLCPAMOF_02133	Phobius	SIGNAL_PEPTIDE_C_REGION	C-terminal region of a signal peptide.	NA	NA	shared
BLCPAMOF_02133	Phobius	SIGNAL_PEPTIDE_N_REGION	N-terminal region of a signal peptide.	NA	NA	shared
BLCPAMOF_02133	Phobius	SIGNAL_PEPTIDE	Signal peptide region	NA	NA	shared
BLCPAMOF_02133	SignalP_EUK	SignalP-noTM	NA	NA	NA	shared
BLCPAMOF_02133	Phobius	SIGNAL_PEPTIDE_H_REGION	Hydrophobic region of a signal peptide.	NA	NA	shared
BLCPAMOF_02133	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	shared
BLCPAMOF_02133	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	shared
BLCPAMOF_02132	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	shared
BLCPAMOF_02132	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	shared
BLCPAMOF_02132	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	shared
BLCPAMOF_02132	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	shared
BLCPAMOF_00623	CDD	cd03325	D-galactonate_dehydratase	IPR023592	D-galactonate dehydratase	shared
BLCPAMOF_00623	Gene3D	G3DSA:3.20.20.120		IPR036849	Enolase-like, C-terminal domain superfamily	shared
BLCPAMOF_00623	SMART	SM00922		IPR013342	Mandelate racemase/muconate lactonizing enzyme, C-terminal	shared
BLCPAMOF_00623	SFLD	SFLDF00003	D-galactonate dehydratase	IPR023592	D-galactonate dehydratase	shared
BLCPAMOF_00623	ProSitePatterns	PS00909	Mandelate racemase / muconate lactonizing enzyme family signature 2.	IPR018110	Mandelate racemase/muconate lactonizing enzyme, conserved site	shared
BLCPAMOF_00623	SUPERFAMILY	SSF54826		IPR029017	Enolase-like, N-terminal	shared
BLCPAMOF_00623	ProSitePatterns	PS00908	Mandelate racemase / muconate lactonizing enzyme family signature 1.	IPR018110	Mandelate racemase/muconate lactonizing enzyme, conserved site	shared
BLCPAMOF_00623	Gene3D	G3DSA:3.30.390.10		IPR029017	Enolase-like, N-terminal	shared
BLCPAMOF_00623	Pfam	PF13378	Enolase C-terminal domain-like	IPR029065	Enolase C-terminal domain-like	shared
BLCPAMOF_00623	Pfam	PF02746	Mandelate racemase / muconate lactonizing enzyme, N-terminal domain	IPR013341	Mandelate racemase/muconate lactonizing enzyme, N-terminal domain	shared
BLCPAMOF_00623	SUPERFAMILY	SSF51604		IPR036849	Enolase-like, C-terminal domain superfamily	shared
BLCPAMOF_00623	SFLD	SFLDG00179	mandelate racemase			shared
BLCPAMOF_00067	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_00066	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00066	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00066	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00066	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00066	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00066	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00066	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00066	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00066	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00066	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_00066	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00066	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00066	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_00069	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_01414	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_00555	PANTHER	PTHR12110:SF27	NA	NA	NA	specific_fp360
BLCPAMOF_00555	Gene3D	G3DSA:3.20.20.150	NA	NA	NA	specific_fp360
BLCPAMOF_00555	SUPERFAMILY	SSF51658	NA	IPR036237	Xylose isomerase-like superfamily	specific_fp360
BLCPAMOF_00555	PANTHER	PTHR12110	NA	NA	NA	specific_fp360
BLCPAMOF_00555	Pfam	PF01261	Xylose isomerase-like TIM barrel	IPR013022	Xylose isomerase-like, TIM barrel domain	specific_fp360
BLCPAMOF_01552	Pfam	PF09693	Phage uncharacterised protein (Phage_XkdX)	IPR010022	Protein of unknown function XkdX	specific_fp360
BLCPAMOF_01553	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_01554	Gene3D	G3DSA:2.120.10.80	NA	IPR015915	Kelch-type beta propeller	specific_fp360
BLCPAMOF_01554	Gene3D	G3DSA:2.120.10.80	NA	IPR015915	Kelch-type beta propeller	specific_fp360
BLCPAMOF_01554	SUPERFAMILY	SSF117281	NA	IPR015915	Kelch-type beta propeller	specific_fp360
BLCPAMOF_01093	Pfam	PF13673	Acetyltransferase (GNAT) domain	IPR000182	GNAT domain	specific_fp360
BLCPAMOF_01093	CDD	cd04301	NAT_SF	NA	NA	specific_fp360
BLCPAMOF_01093	Gene3D	G3DSA:3.40.630.30	NA	NA	NA	specific_fp360
BLCPAMOF_01093	SUPERFAMILY	SSF55729	NA	IPR016181	Acyl-CoA N-acyltransferase	specific_fp360
BLCPAMOF_01093	ProSiteProfiles	PS51186	Gcn5-related N-acetyltransferase (GNAT) domain profile.	IPR000182	GNAT domain	specific_fp360
BLCPAMOF_00662	Phobius	SIGNAL_PEPTIDE_H_REGION	Hydrophobic region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_00662	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00662	SignalP_EUK	SignalP-noTM	NA	NA	NA	specific_fp360
BLCPAMOF_00662	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00662	Phobius	SIGNAL_PEPTIDE_N_REGION	N-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_00662	Phobius	SIGNAL_PEPTIDE	Signal peptide region	NA	NA	specific_fp360
BLCPAMOF_00662	Phobius	SIGNAL_PEPTIDE_C_REGION	C-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_01558	Phobius	SIGNAL_PEPTIDE	Signal peptide region	NA	NA	specific_fp360
BLCPAMOF_01558	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp360
BLCPAMOF_01558	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_01558	Phobius	SIGNAL_PEPTIDE_C_REGION	C-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_01558	Phobius	SIGNAL_PEPTIDE_N_REGION	N-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_01558	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp360
BLCPAMOF_01558	Phobius	SIGNAL_PEPTIDE_H_REGION	Hydrophobic region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_01622	Phobius	SIGNAL_PEPTIDE_N_REGION	N-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_01622	Phobius	SIGNAL_PEPTIDE_C_REGION	C-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_01622	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_01622	Phobius	SIGNAL_PEPTIDE_H_REGION	Hydrophobic region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_01622	SignalP_EUK	SignalP-noTM	NA	NA	NA	specific_fp360
BLCPAMOF_01622	Phobius	SIGNAL_PEPTIDE	Signal peptide region	NA	NA	specific_fp360
BLCPAMOF_01623	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_01620	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_01018	Coils	Coil	NA	NA	NA	specific_fp360
BLCPAMOF_01018	Pfam	PF13271	Domain of unknown function (DUF4062)	IPR025139	Domain of unknown function DUF4062	specific_fp360
BLCPAMOF_01014	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01014	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01014	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01014	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01014	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01014	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01014	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_01014	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_01014	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01014	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01014	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_01014	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01014	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01014	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01014	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01014	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01014	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01014	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_01014	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_01014	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_01014	Pfam	PF01757	Acyltransferase family	IPR002656	Acyltransferase 3	specific_fp360
BLCPAMOF_01014	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01014	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_01014	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360

BLCPAMOF_01014	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_01014	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00304	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp360
BLCPAMOF_00304	SignalP_GRAM_POSITIVE	SignalP-TM	NA	NA	NA	specific_fp360
BLCPAMOF_00304	Phobius	SIGNAL_PEPTIDE_C_REGION	C-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_00304	Phobius	SIGNAL_PEPTIDE_N_REGION	N-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_00304	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00304	SignalP_GRAM_NEGATIVE	SignalP-TM	NA	NA	NA	specific_fp360
BLCPAMOF_00304	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp360
BLCPAMOF_00304	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp360
BLCPAMOF_00304	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp360
BLCPAMOF_00304	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp360
BLCPAMOF_00304	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp360
BLCPAMOF_00304	SignalP_EUK	SignalP-noTM	NA	NA	NA	specific_fp360
BLCPAMOF_00304	Phobius	SIGNAL_PEPTIDE	Signal peptide region	NA	NA	specific_fp360
BLCPAMOF_00304	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00304	Phobius	SIGNAL_PEPTIDE_H_REGION	Hydrophobic region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_00304	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp360
BLCPAMOF_01951	PIRSF	PIRSF029950	NA	IPR010155	CRISPR pre-crRNA endoribonuclease Cas5d	specific_fp360
BLCPAMOF_01951	PIRSF	PIRSF029950	NA	IPR010155	CRISPR pre-crRNA endoribonuclease Cas5d	specific_fp360
BLCPAMOF_01951	TIGRFAM	TIGR01876	cas_Cas5d: CRISPR-associated protein Cas5, subtype I-C/DVULG	IPR010155	CRISPR pre-crRNA endoribonuclease Cas5d	specific_fp360
BLCPAMOF_01951	Gene3D	G3DSA:3.30.70.2660	NA	NA	NA	specific_fp360
BLCPAMOF_01951	TIGRFAM	TIGR02593	CRISPR_cas5: CRISPR-associated protein Cas5	IPR013422	CRISPR-associated protein Cas5, N-terminal	specific_fp360
BLCPAMOF_01951	Pfam	PF09704	CRISPR-associated protein (Cas_Cas5)	IPR021124	CRISPR-associated protein, Cas5	specific_fp360
BLCPAMOF_01951	CDD	cd09752	Cas5_I-C	NA	NA	specific_fp360
BLCPAMOF_01952	CDD	cd09757	Cas8c_I-C	NA	NA	specific_fp360
BLCPAMOF_01952	Pfam	PF09709	CRISPR-associated protein (Cas_Csd1)	IPR010144	CRISPR-associated protein, Csd1-type	specific_fp360
BLCPAMOF_01952	TIGRFAM	TIGR01863	cas_Csd1: CRISPR-associated protein Cas8c/Csd1, subtype I-C/DVULG	IPR010144	CRISPR-associated protein, Csd1-type	specific_fp360
BLCPAMOF_01796	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_00719	Gene3D	G3DSA:3.40.50.510	NA	IPR036662	Phosphotransferase system, mannose-type IIA component superfamily	specific_fp360
BLCPAMOF_00719	PANTHER	PTHR33799	NA	NA	NA	specific_fp360
BLCPAMOF_00719	Pfam	PF03610	PTS system fructose IIA component	IPR004701	Phosphotransferase system, mannose-type IIA component	specific_fp360
BLCPAMOF_00719	PANTHER	PTHR33799:SF1	NA	NA	NA	specific_fp360
BLCPAMOF_00719	CDD	cd00006	PTS_IIA_man	IPR033887	PTS system mannose/sorbose specific IIA subunit	specific_fp360
BLCPAMOF_00719	ProSiteProfiles	PS51096	PTS_EIIA type-4 domain profile.	IPR004701	Phosphotransferase system, mannose-type IIA component	specific_fp360
BLCPAMOF_00719	SUPERFAMILY	SSF53062	NA	IPR036662	Phosphotransferase system, mannose-type IIA component superfamily	specific_fp360
BLCPAMOF_00718	Gene3D	G3DSA:3.40.50.10490	NA	NA	NA	specific_fp360
BLCPAMOF_00718	PANTHER	PTHR32502	NA	NA	NA	specific_fp360
BLCPAMOF_00718	Pfam	PF01380	SIS domain	IPR001347	Sugar isomerase (SIS)	specific_fp360
BLCPAMOF_00718	PANTHER	PTHR32502:SF3	NA	NA	NA	specific_fp360
BLCPAMOF_00718	SUPERFAMILY	SSF53697	NA	NA	NA	specific_fp360
BLCPAMOF_00718	CDD	cd05008	SIS_GlmS_GlmD_1	IPR035466	GlmS/AgaS, SIS domain 1	specific_fp360
BLCPAMOF_00718	CDD	cd05010	SIS_AgaS_like	IPR035464	AgaS, SIS domain	specific_fp360
BLCPAMOF_00718	Gene3D	G3DSA:3.40.50.10490	NA	NA	NA	specific_fp360
BLCPAMOF_00718	ProSiteProfiles	PS51464	SIS domain profile.	IPR001347	Sugar isomerase (SIS)	specific_fp360
BLCPAMOF_00718	ProSiteProfiles	PS51464	SIS domain profile.	IPR001347	Sugar isomerase (SIS)	specific_fp360
BLCPAMOF_01426	Pfam	PF09693	Phage uncharacterised protein (Phage_XkdX)	IPR010022	Protein of unknown function XkdX	specific_fp360
BLCPAMOF_01427	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01869	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01869	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01869	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_01869	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_01869	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01869	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01869	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01869	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01869	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_01869	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01869	Pfam	PF04892	VanZ like family	IPR006976	VanZ-like	specific_fp360
BLCPAMOF_01869	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01869	PANTHER	PTHR36834	NA	NA	NA	specific_fp360
BLCPAMOF_01869	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_01869	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01869	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_01869	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01869	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_01869	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01869	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01869	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_02450	Gene3D	G3DSA:3.30.460.10	NA	NA	NA	specific_fp360
BLCPAMOF_02450	CDD	cd05400	NT_2-5OAS_ClassI-CCAase	NA	NA	specific_fp360
BLCPAMOF_02450	SUPERFAMILY	SSF81301	NA	NA	NA	specific_fp360
BLCPAMOF_02450	Pfam	PF18144	Second Messenger Oligonucleotide or Dinucleotide Synthetase domain	NA	NA	specific_fp360
BLCPAMOF_02451	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02451	Pfam	PF18186	SMODS and SLOG-associating 2TM effector domain family 4	IPR040811	SMODS and SLOG-associating 2TM effector domain	specific_fp360
BLCPAMOF_02451	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02451	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02451	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02451	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_02451	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_02451	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_01428	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp360
BLCPAMOF_00835	Coils	Coil	NA	NA	NA	specific_fp360
BLCPAMOF_00836	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_00716	Pfam	PF08013	Tagatose 6 phosphate kinase	IPR012062	D-tagatose-1,6-bisphosphate aldolase subunit GatZ/KbaZ-like	specific_fp360
BLCPAMOF_00716	PANTHER	PTHR32502:SF2	NA	NA	NA	specific_fp360
BLCPAMOF_00716	Gene3D	G3DSA:1.10.400.20	NA	NA	NA	specific_fp360
BLCPAMOF_00716	Gene3D	G3DSA:3.20.20.70	NA	IPR013785	Aldolase-type TIM barrel	specific_fp360
BLCPAMOF_00716	SUPERFAMILY	SSF51569	NA	NA	NA	specific_fp360
BLCPAMOF_00716	PIRSF	PIRSF009264	NA	IPR012062	D-tagatose-1,6-bisphosphate aldolase subunit GatZ/KbaZ-like	specific_fp360
BLCPAMOF_00716	PANTHER	PTHR32502	NA	NA	NA	specific_fp360
BLCPAMOF_02061	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_01141	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01141	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_01141	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_01141	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01141	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01141	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01141	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01141	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01141	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01141	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_01141	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_01141	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01141	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_01970	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_01225	Gene3D	G3DSA:3.40.50.200	NA	IPR036852	Peptidase S8/S53 domain superfamily	specific_fp360
BLCPAMOF_01225	PANTHER	PTHR43806	NA	NA	NA	specific_fp360
BLCPAMOF_01225	SUPERFAMILY	SSF52743	NA	IPR036852	Peptidase S8/S53 domain superfamily	specific_fp360
BLCPAMOF_01225	PANTHER	PTHR43806:SF37	NA	NA	NA	specific_fp360
BLCPAMOF_01225	Pfam	PF00082	Subtilase family	IPR000209	Peptidase S8/S53 domain	specific_fp360
BLCPAMOF_01225	PRINTS	PR00723	Subtilisin serine protease family (S8) signature	IPR015500	Peptidase S8, subtilisin-related	specific_fp360
BLCPAMOF_01225	PRINTS	PR00723	Subtilisin serine protease family (S8) signature	IPR015500	Peptidase S8, subtilisin-related	specific_fp360
BLCPAMOF_01225	PRINTS	PR00723	Subtilisin serine protease family (S8) signature	IPR015500	Peptidase S8, subtilisin-related	specific_fp360
BLCPAMOF_01225	CDD	cd04847	Peptidases_S8_Subtilisin_like_2	IPR034074	Y4bN, peptidase domain	specific_fp360
BLCPAMOF_01225	ProSitePatterns	PS00136	Serine proteases, subtilase family, aspartic acid active site.	IPR023827	Peptidase S8, subtilisin, Asp-active site	specific_fp360
BLCPAMOF_02581	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_00310	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00310	SignalP_EUK	SignalP-noTM	NA	NA	NA	specific_fp360
BLCPAMOF_00310	Phobius	SIGNAL_PEPTIDE_N_REGION	N-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_00310	SignalP_GRAM_POSITIVE	SignalP-TM	NA	NA	NA	specific_fp360
BLCPAMOF_00310	Phobius	SIGNAL_PEPTIDE	Signal peptide region	NA	NA	specific_fp360
BLCPAMOF_00310	Phobius	SIGNAL_PEPTIDE_H_REGION	Hydrophobic region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_00310	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00310	SignalP_GRAM_NEGATIVE	SignalP-noTM	NA	NA	NA	specific_fp360
BLCPAMOF_00310	Phobius	SIGNAL_PEPTIDE_C_REGION	C-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_00090	TIGRFAM	TIGR02646	TIGR02646: TIGR02646 family protein	IPR013467	Conserved hypothetical protein CHP02646	specific_fp360
BLCPAMOF_02268	PANTHER	PTHR43764	NA	NA	NA	specific_fp360
BLCPAMOF_02268	SUPERFAMILY	SSF53218	NA	IPR036425	MoaB/Mog-like domain superfamily	specific_fp360
BLCPAMOF_02268	Gene3D	G3DSA:3.40.980.10	NA	IPR036425	MoaB/Mog-like domain superfamily	specific_fp360
BLCPAMOF_01947	PIRSF	PIRSF005751	NA	IPR005216	Citrate lyase ligase	specific_fp360
BLCPAMOF_01947	SMART	SM00764	NA	IPR013166	Citrate lyase ligase, C-terminal	specific_fp360
BLCPAMOF_01947	ProSiteProfiles	PS51186	Gcn5-related N-acetyltransferase (GNAT) domain profile.	IPR000182	GNAT domain	specific_fp360
BLCPAMOF_01947	CDD	cd02169	Citrate_lyase_ligase	IPR005216	Citrate lyase ligase	specific_fp360
BLCPAMOF_01947	SUPERFAMILY	SSF52374	NA	NA	NA	specific_fp360
BLCPAMOF_01947	TIGRFAM	TIGR00124	cit_ly_ligase: [citrate (pro-3S)-lyase] ligase	IPR005216	Citrate lyase ligase	specific_fp360
BLCPAMOF_01947	TIGRFAM	TIGR00125	cyt_tran_rel: cytidyltransferase-like domain	IPR004821	Cytidyltransferase-like domain	specific_fp360

BLCPAMOF_01947	Gene3D	G3DSA:3.40.50.620	NA	IPR014729	Rossmann-like alpha/beta/alpha sandwich fold	specific_fp360
BLCPAMOF_01947	PANTHER	PTHR40599	NA	IPR005216	Citrate lyase ligase	specific_fp360
BLCPAMOF_01947	Pfam	PF08218	Citrate lyase ligase C-terminal domain	IPR013166	Citrate lyase ligase, C-terminal	specific_fp360
BLCPAMOF_01947	Gene3D	G3DSA:3.40.630.30	NA	NA	NA	specific_fp360
BLCPAMOF_01947	SUPERFAMILY	SSF55729	NA	IPR016181	Acyl-CoA N-acyltransferase	specific_fp360
BLCPAMOF_00882	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00882	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_00882	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_00882	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00882	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00882	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00882	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00882	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00882	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00882	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00882	Pfam	PF10086	YhfC intramembrane metalloprotease	IPR011397	Intramembrane metalloprotease YhfC	specific_fp360
BLCPAMOF_00882	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_00882	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00882	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00882	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00882	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00882	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00882	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00882	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00882	PIRSF	PIRSF033101	NA	IPR011397	Intramembrane metalloprotease YhfC	specific_fp360
BLCPAMOF_00882	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_00882	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00882	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01948	PANTHER	PTHR30201	NA	IPR002736	Triphosphoribosyl-dephospho-CoA protein	specific_fp360
BLCPAMOF_01948	Pfam	PF03802	Apo-citrate lyase phosphoribosyl-dephospho-CoA transferase	IPR005551	Apo-citrate lyase phosphoribosyl-dephospho-CoA transferase	specific_fp360
BLCPAMOF_01948	Pfam	PF01874	ATP:dephospho-CoA triphosphoribosyl transferase	IPR002736	Triphosphoribosyl-dephospho-CoA protein	specific_fp360
BLCPAMOF_01948	Hamap	MF_00397	2-(5''-triphosphoribosyl)-3'-dephosphocoenzyme-A synthase [citG].	IPR017551	Triphosphoribosyl-dephospho-CoA synthase CitG	specific_fp360
BLCPAMOF_01948	Gene3D	G3DSA:1.10.4200.10	NA	NA	NA	specific_fp360
BLCPAMOF_01948	TIGRFAM	TIGR03125	citrate_citG: triphosphoribosyl-dephospho-CoA synthase CitG	IPR017551	Triphosphoribosyl-dephospho-CoA synthase CitG	specific_fp360
BLCPAMOF_01948	TIGRFAM	TIGR03124	citrate_citX: holo-ACP synthase CitX	IPR005551	Apo-citrate lyase phosphoribosyl-dephospho-CoA transferase	specific_fp360
BLCPAMOF_01667	Pfam	PF14317	YcxB-like protein	IPR025588	YcxB-like protein	specific_fp360
BLCPAMOF_01667	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01667	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_01667	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_01667	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01433	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp360
BLCPAMOF_01924	Gene3D	G3DSA:1.10.260.40	NA	IPR010982	Lambda repressor-like, DNA-binding domain superfamily	specific_fp360
BLCPAMOF_00720	TIGRFAM	TIGR00739	yajC: preprotein translocase, YajC subunit	IPR003849	Preprotein translocase YajC	specific_fp360
BLCPAMOF_00720	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00720	SMART	SM01323	NA	IPR003849	Preprotein translocase YajC	specific_fp360
BLCPAMOF_00720	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00720	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_00720	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00720	PANTHER	PTHR33909	NA	IPR003849	Preprotein translocase YajC	specific_fp360
BLCPAMOF_00720	Pfam	PF02699	Preprotein translocase subunit	IPR003849	Preprotein translocase YajC	specific_fp360
BLCPAMOF_01920	Pfam	PF18852	Large polyvalent protein associated domain 34	IPR040672	Large polyvalent protein associated domain 34	specific_fp360
BLCPAMOF_01920	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp360
BLCPAMOF_01923	Coils	Coil	NA	NA	NA	specific_fp360
BLCPAMOF_01923	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp360
BLCPAMOF_01434	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_01438	PANTHER	PTHR36113	NA	NA	NA	specific_fp360
BLCPAMOF_01438	PANTHER	PTHR36113:SF1	NA	NA	NA	specific_fp360
BLCPAMOF_01438	Pfam	PF00903	Glyoxalase/Bleomycin resistance protein/Dioxygenase superfamily	IPR004360	Glyoxalase/fosfomycin resistance/dioxygenase domain	specific_fp360
BLCPAMOF_01438	SUPERFAMILY	SSF54593	NA	IPR029068	Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase	specific_fp360
BLCPAMOF_01438	Gene3D	G3DSA:3.10.180.10	NA	IPR029068	Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase	specific_fp360
BLCPAMOF_01438	ProSiteProfiles	PS51819	Vicinal oxygen chelate (VOC) domain profile.	IPR037523	Vicinal oxygen chelate (VOC) domain	specific_fp360
BLCPAMOF_01438	ProSitePatterns	PS00934	Glyoxalase I signature 1.	IPR018146	Glyoxalase I, conserved site	specific_fp360
BLCPAMOF_01438	CDD	cd08352	VOC_Bs_YwkD_like	IPR037478	YwkD-like domain	specific_fp360
BLCPAMOF_00642	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00642	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00642	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00642	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00642	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00642	Pfam	PF06081	Aromatic acid exporter family member 1	IPR010343	Aromatic acid exporter family member 1	specific_fp360
BLCPAMOF_00642	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00642	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00642	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00642	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00642	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00642	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00642	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_00642	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_00642	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00642	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_02449	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_02431	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02431	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_02431	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_02431	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02194	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02194	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02194	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02194	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02194	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_02194	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_02194	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_01037	SUPERFAMILY	SSF53448	NA	IPR029044	Nucleotide-diphospho-sugar transferases	specific_fp360
BLCPAMOF_01037	Gene3D	G3DSA:3.90.550.10	NA	IPR029044	Nucleotide-diphospho-sugar transferases	specific_fp360
BLCPAMOF_01037	Pfam	PF00535	Glycosyl transferase family 2	IPR001173	Glycosyltransferase 2-like	specific_fp360
BLCPAMOF_01037	PANTHER	PTHR43179:SF1	NA	NA	NA	specific_fp360
BLCPAMOF_01037	PANTHER	PTHR43179	NA	NA	NA	specific_fp360
BLCPAMOF_02598	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_02598	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02598	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02598	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_01035	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_01034	SUPERFAMILY	SSF81301	NA	NA	NA	specific_fp360
BLCPAMOF_01034	CDD	cd05399	NT_Rel-Spo_like	IPR007685	RelA/SpoT	specific_fp360
BLCPAMOF_01034	Pfam	PF04607	Region found in RelA / SpoT proteins	IPR007685	RelA/SpoT	specific_fp360
BLCPAMOF_01034	Gene3D	G3DSA:3.30.460.10	NA	NA	NA	specific_fp360
BLCPAMOF_01034	SMART	SM00954	NA	IPR007685	RelA/SpoT	specific_fp360
BLCPAMOF_02757	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_02756	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_02755	Phobius	SIGNAL_PEPTIDE	Signal peptide region	NA	NA	specific_fp360
BLCPAMOF_02755	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_02755	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02755	Phobius	SIGNAL_PEPTIDE_C_REGION	C-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_02755	Phobius	SIGNAL_PEPTIDE_N_REGION	N-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_02755	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_02755	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02755	Phobius	SIGNAL_PEPTIDE_H_REGION	Hydrophobic region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_02591	Pfam	PF12710	haloacid dehalogenase-like hydrolase	NA	NA	specific_fp360
BLCPAMOF_02591	CDD	cd01427	HAD_like	NA	NA	specific_fp360
BLCPAMOF_02591	Gene3D	G3DSA:3.40.50.1000	NA	IPR023214	HAD superfamily	specific_fp360
BLCPAMOF_02591	SUPERFAMILY	SSF56784	NA	IPR036412	HAD-like superfamily	specific_fp360
BLCPAMOF_01911	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_02597	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_02597	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02597	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02597	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_01038	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01038	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_01038	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01038	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01038	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_01038	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01038	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01038	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01038	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_01038	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01038	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_01038	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360

BLCPAMOF_01038	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_01038	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01038	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01038	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01038	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_01038	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_01038	Pfam	PF14897	EpsG family	NA	NA	specific_fp360
BLCPAMOF_01038	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01038	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01038	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_01038	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01038	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_01038	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01038	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_01038	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01038	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02292	Pfam	PF01987	Mitochondrial biogenesis AIM24	IPR002838	Mitochondrial biogenesis protein AIM24	specific_fp360
BLCPAMOF_02292	PANTHER	PTHR31801	NA	NA	NA	specific_fp360
BLCPAMOF_02292	SUPERFAMILY	SSF51219	NA	IPR016031	Tryptophan RNA-binding attenuator protein-like domain superfamily	specific_fp360
BLCPAMOF_02292	Gene3D	G3DSA:3.60.160.10	NA	IPR036983	Mitochondrial biogenesis AIM24 superfamily	specific_fp360
BLCPAMOF_02292	PANTHER	PTHR31801:SF0	NA	NA	NA	specific_fp360
BLCPAMOF_02291	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_01837	Gene3D	G3DSA:3.40.630.30	NA	NA	NA	specific_fp360
BLCPAMOF_01837	PANTHER	PTHR43420:SF9	NA	NA	NA	specific_fp360
BLCPAMOF_01837	Pfam	PF13420	Acetyltransferase (GNAT) domain	NA	NA	specific_fp360
BLCPAMOF_01837	PANTHER	PTHR43420	NA	NA	NA	specific_fp360
BLCPAMOF_01837	ProSiteProfiles	PS51186	Gcn5-related N-acetyltransferase (GNAT) domain profile.	IPR000182	GNAT domain	specific_fp360
BLCPAMOF_01837	CDD	cd04301	NAT_SF	NA	NA	specific_fp360
BLCPAMOF_01837	SUPERFAMILY	SSF55729	NA	IPR016181	Acyl-CoA N-acyltransferase	specific_fp360
BLCPAMOF_01830	CDD	cd07241	VOC_BsYyaH	NA	NA	specific_fp360
BLCPAMOF_01830	PANTHER	PTHR36113	NA	NA	NA	specific_fp360
BLCPAMOF_01830	SUPERFAMILY	SSF54593	NA	IPR029068	Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase	specific_fp360
BLCPAMOF_01830	ProSiteProfiles	PS51819	Vicinal oxygen chelate (VOC) domain profile.	IPR037523	Vicinal oxygen chelate (VOC) domain	specific_fp360
BLCPAMOF_01830	PANTHER	PTHR36113:SF5	NA	NA	NA	specific_fp360
BLCPAMOF_01830	Gene3D	G3DSA:3.10.180.10	NA	IPR029068	Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase	specific_fp360
BLCPAMOF_01830	Pfam	PF13669	Glyoxalase/Bleomycin resistance protein/Dioxygenase superfamily	NA	NA	specific_fp360
BLCPAMOF_01285	Coils	Coil	NA	NA	NA	specific_fp360
BLCPAMOF_01285	SUPERFAMILY	SSF55874	NA	IPR036890	Histidine kinase/HSP90-like ATPase superfamily	specific_fp360
BLCPAMOF_01285	PANTHER	PTHR43065	NA	NA	NA	specific_fp360
BLCPAMOF_01285	SMART	SM00387	NA	IPR003594	Histidine kinase/HSP90-like ATPase	specific_fp360
BLCPAMOF_01285	Gene3D	G3DSA:3.30.565.10	NA	IPR036890	Histidine kinase/HSP90-like ATPase superfamily	specific_fp360
BLCPAMOF_01285	Pfam	PF13589	Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase	NA	NA	specific_fp360
BLCPAMOF_01285	Gene3D	G3DSA:3.30.565.10	NA	IPR036890	Histidine kinase/HSP90-like ATPase superfamily	specific_fp360
BLCPAMOF_01285	CDD	cd16926	HATPase_MutL-MLH-PMS-like	NA	NA	specific_fp360
BLCPAMOF_01285	Coils	Coil	NA	NA	NA	specific_fp360
BLCPAMOF_01285	SUPERFAMILY	SSF55874	NA	IPR036890	Histidine kinase/HSP90-like ATPase superfamily	specific_fp360
BLCPAMOF_01285	Pfam	PF02518	Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase	IPR003594	Histidine kinase/HSP90-like ATPase	specific_fp360
BLCPAMOF_01285	CDD	cd00075	HATPase	NA	NA	specific_fp360
BLCPAMOF_01285	ProSiteProfiles	PS50109	Histidine kinase domain profile.	IPR005467	Histidine kinase domain	specific_fp360
BLCPAMOF_01286	Coils	Coil	NA	NA	NA	specific_fp360
BLCPAMOF_01286	Gene3D	G3DSA:3.40.50.2300	NA	NA	NA	specific_fp360
BLCPAMOF_01286	CDD	cd05667	M20_Acy1-like	NA	NA	specific_fp360
BLCPAMOF_01913	Pfam	PF04026	SpoVG	IPR007170	Stage V sporulation protein G	specific_fp360
BLCPAMOF_01913	Gene3D	G3DSA:3.30.1120.40	NA	IPR036751	Stage V sporulation protein G superfamily	specific_fp360
BLCPAMOF_01913	PANTHER	PTHR38429	NA	IPR007170	Stage V sporulation protein G	specific_fp360
BLCPAMOF_01913	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp360
BLCPAMOF_01913	SUPERFAMILY	SSF160537	NA	IPR036751	Stage V sporulation protein G superfamily	specific_fp360
BLCPAMOF_01913	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp360
BLCPAMOF_01918	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_01944	SUPERFAMILY	SSF52540	NA	IPR027417	P-loop containing nucleoside triphosphate hydrolase	specific_fp360
BLCPAMOF_01944	Pfam	PF13238	AAA domain	NA	NA	specific_fp360
BLCPAMOF_01944	PANTHER	PTHR37816	NA	NA	NA	specific_fp360
BLCPAMOF_01944	Gene3D	G3DSA:3.40.50.300	NA	NA	NA	specific_fp360
BLCPAMOF_01944	PANTHER	PTHR37816:SF1	NA	NA	NA	specific_fp360
BLCPAMOF_01288	Pfam	PF14195	Domain of unknown function (DUF4316)	IPR025465	Domain of unknown function DUF4316	specific_fp360
BLCPAMOF_01288	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp360
BLCPAMOF_01288	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp360
BLCPAMOF_01617	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_00031	SignalP_GRAM_NEGATIVE	SignalP-noTM	NA	NA	NA	specific_fp360
BLCPAMOF_00031	Phobius	SIGNAL_PEPTIDE_N_REGION	N-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_00031	Phobius	SIGNAL_PEPTIDE_C_REGION	C-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_00031	SignalP_GRAM_POSITIVE	SignalP-TM	NA	NA	NA	specific_fp360
BLCPAMOF_00031	SignalP_EUK	SignalP-noTM	NA	NA	NA	specific_fp360
BLCPAMOF_00031	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00031	Phobius	SIGNAL_PEPTIDE	Signal peptide region	NA	NA	specific_fp360
BLCPAMOF_00031	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00031	Pfam	PF13349	Putative adhesin	IPR025164	Putative adhesin	specific_fp360
BLCPAMOF_00031	Phobius	SIGNAL_PEPTIDE_H_REGION	Hydrophobic region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_01615	Gene3D	G3DSA:3.40.50.1240	NA	IPR029033	Histidine phosphatase superfamily	specific_fp360
BLCPAMOF_01615	Pfam	PF00300	Histidine phosphatase superfamily (branch 1)	IPR013078	Histidine phosphatase superfamily, clade-1	specific_fp360
BLCPAMOF_01615	SUPERFAMILY	SSF53254	NA	IPR029033	Histidine phosphatase superfamily	specific_fp360
BLCPAMOF_02579	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_00039	PANTHER	PTHR30313	NA	NA	NA	specific_fp360
BLCPAMOF_00039	SUPERFAMILY	SSF57783	NA	NA	NA	specific_fp360
BLCPAMOF_00039	Pfam	PF01807	CHC2 zinc finger	IPR002694	Zinc finger, CHC2-type	specific_fp360
BLCPAMOF_00039	Gene3D	G3DSA:3.90.580.10	NA	IPR036977	DNA Primase, CHC2-type zinc finger	specific_fp360
BLCPAMOF_00039	SMART	SM00400	NA	IPR002694	Zinc finger, CHC2-type	specific_fp360
BLCPAMOF_01207	Phobius	SIGNAL_PEPTIDE	Signal peptide region	NA	NA	specific_fp360
BLCPAMOF_01207	Phobius	SIGNAL_PEPTIDE_C_REGION	C-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_01207	Phobius	SIGNAL_PEPTIDE_H_REGION	Hydrophobic region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_01207	SignalP_EUK	SignalP-noTM	NA	NA	NA	specific_fp360
BLCPAMOF_01207	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp360
BLCPAMOF_01207	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_01207	SignalP_GRAM_POSITIVE	SignalP-TM	NA	NA	NA	specific_fp360
BLCPAMOF_01207	Phobius	SIGNAL_PEPTIDE_N_REGION	N-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_01207	SignalP_GRAM_NEGATIVE	SignalP-noTM	NA	NA	NA	specific_fp360
BLCPAMOF_01207	ProSiteProfiles	PS51257	Prokaryotic membrane lipoprotein lipid attachment site profile.	NA	NA	specific_fp360
BLCPAMOF_00507	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_00337	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00337	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00337	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_00337	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01040	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01040	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01040	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01040	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01040	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_01040	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01040	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_01040	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_01040	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01040	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01040	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_01040	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_01040	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_01040	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01040	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_01040	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_01040	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01040	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_01040	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01040	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_01040	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01040	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01040	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01040	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01040	Pfam	PF01757	Acyltransferase family	IPR002656	Acyltransferase 3	specific_fp360
BLCPAMOF_01040	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01040	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01904	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_01903	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_00592	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00592	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00592	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00592	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00592	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00592	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360

BLCPAMOF_00592	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00592	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_00592	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00592	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_00592	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00592	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00592	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00592	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00592	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00592	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00592	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00592	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00592	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00592	PANTHER	PTHR43652	NA	NA	NA	specific_fp360
BLCPAMOF_00592	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_00592	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00592	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00592	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00592	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00592	PANTHER	PTHR43652	NA	NA	NA	specific_fp360
BLCPAMOF_00592	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_00592	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00592	PANTHER	PTHR43652:SF4	NA	NA	NA	specific_fp360
BLCPAMOF_00592	PANTHER	PTHR43652:SF4	NA	NA	NA	specific_fp360
BLCPAMOF_00592	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_00592	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00592	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00592	Pfam	PF03606	C4-dicarboxylate anaerobic carrier	IPR018385	C4-dicarboxylate anaerobic carrier-like	specific_fp360
BLCPAMOF_00592	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00592	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00592	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00592	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_00592	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00592	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_00592	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00592	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00592	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00592	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00592	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02054	Pfam	PF10020	Uncharacterized protein conserved in bacteria (DUF2262)	IPR019260	Domain of unknown function DUF2262	specific_fp360
BLCPAMOF_01848	CDD	cd00056	ENDO3c	IPR003265	HhH-GPD domain	specific_fp360
BLCPAMOF_01848	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01848	SMART	SM00478	NA	IPR003265	HhH-GPD domain	specific_fp360
BLCPAMOF_01848	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_01848	Gene3D	G3DSA:1.10.1670.40	NA	NA	NA	specific_fp360
BLCPAMOF_01848	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_01848	SUPERFAMILY	SSF48150	NA	IPR011257	DNA glycosylase	specific_fp360
BLCPAMOF_01848	Pfam	PF00730	HhH-GPD superfamily base excision DNA repair protein	IPR003265	HhH-GPD domain	specific_fp360
BLCPAMOF_01848	ProSitePatterns	PS00516	Alkylbase DNA glycosidases alkA family signature.	IPR000035	Alkylbase DNA glycosidase, conserved site	specific_fp360
BLCPAMOF_01848	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01848	Gene3D	G3DSA:1.10.340.30	NA	NA	NA	specific_fp360
BLCPAMOF_01848	PANTHER	PTHR43003	NA	NA	NA	specific_fp360
BLCPAMOF_02057	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_02721	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_02721	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_02721	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02721	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02721	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_02721	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02721	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00933	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_00933	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00933	Phobius	SIGNAL_PEPTIDE	Signal peptide region	NA	NA	specific_fp360
BLCPAMOF_00933	Phobius	SIGNAL_PEPTIDE_N_REGION	N-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_00933	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00933	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00933	SignalP_EUK	SignalP-noTM	NA	NA	NA	specific_fp360
BLCPAMOF_00933	Gene3D	G3DSA:2.160.20.110	NA	NA	NA	specific_fp360
BLCPAMOF_00933	Gene3D	G3DSA:2.160.20.110	NA	NA	NA	specific_fp360
BLCPAMOF_00933	Coils	Coil	NA	NA	NA	specific_fp360
BLCPAMOF_00933	SignalP_GRAM_NEGATIVE	SignalP-noTM	NA	NA	NA	specific_fp360
BLCPAMOF_00933	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00933	SignalP_GRAM_POSITIVE	SignalP-TM	NA	NA	NA	specific_fp360
BLCPAMOF_00933	Phobius	SIGNAL_PEPTIDE_H_REGION	Hydrophobic region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_00933	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp360
BLCPAMOF_00933	Phobius	SIGNAL_PEPTIDE_C_REGION	C-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_00932	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00932	Pfam	PF03176	MMPL family	IPR004869	Membrane transport protein MMPL domain	specific_fp360
BLCPAMOF_00932	Pfam	PF03176	MMPL family	IPR004869	Membrane transport protein MMPL domain	specific_fp360
BLCPAMOF_00932	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00932	Coils	Coil	NA	NA	NA	specific_fp360
BLCPAMOF_00932	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00932	SUPERFAMILY	SSF82866	NA	NA	NA	specific_fp360
BLCPAMOF_00932	PANTHER	PTHR33406:SF2	NA	NA	NA	specific_fp360
BLCPAMOF_00932	PANTHER	PTHR33406	NA	NA	NA	specific_fp360
BLCPAMOF_00932	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_00932	PANTHER	PTHR33406	NA	NA	NA	specific_fp360
BLCPAMOF_00932	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00932	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00932	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_00932	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00932	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00932	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00932	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00932	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_00932	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00932	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00932	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00932	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00932	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_00932	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00932	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00932	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_00932	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00932	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00932	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00932	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00932	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00932	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00932	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00932	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_00932	SUPERFAMILY	SSF82866	NA	NA	NA	specific_fp360
BLCPAMOF_00932	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00932	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00932	PANTHER	PTHR33406:SF2	NA	NA	NA	specific_fp360
BLCPAMOF_00932	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00932	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00932	Gene3D	G3DSA:1.20.1640.10	NA	NA	NA	specific_fp360
BLCPAMOF_00932	Gene3D	G3DSA:1.20.1640.10	NA	NA	NA	specific_fp360
BLCPAMOF_00932	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_00932	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00932	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00932	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01925	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_01291	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp360
BLCPAMOF_01291	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp360
BLCPAMOF_02549	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_00620	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_01298	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01298	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_01298	Phobius	SIGNAL_PEPTIDE	Signal peptide region	NA	NA	specific_fp360
BLCPAMOF_01298	SignalP_EUK	SignalP-noTM	NA	NA	NA	specific_fp360
BLCPAMOF_01298	Phobius	SIGNAL_PEPTIDE_C_REGION	C-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_01298	Phobius	SIGNAL_PEPTIDE_N_REGION	N-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_01298	Phobius	SIGNAL_PEPTIDE_H_REGION	Hydrophobic region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_01298	SignalP_GRAM_POSITIVE	SignalP-TM	NA	NA	NA	specific_fp360
BLCPAMOF_01298	SignalP_GRAM_NEGATIVE	SignalP-noTM	NA	NA	NA	specific_fp360

BLCPAMOF_02542	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02542	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02542	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_02542	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02542	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02542	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02542	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02542	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02542	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02542	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02542	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02542	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_02542	PANTHER	PTHR43849	NA	NA	NA	specific_fp360
BLCPAMOF_02542	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_02542	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_02542	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02542	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02542	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02542	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02542	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_02542	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_02542	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02542	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02542	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02542	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02542	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_02542	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_02542	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02542	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02542	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02542	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02542	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02542	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02542	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_02542	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_02542	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02542	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_02542	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_02542	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02542	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_02542	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_02542	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02542	Pfam	PF06808	Tripartite ATP-independent periplasmic transporter, DctM component	IPR010656	TRAP C4-dicarboxylate transport system permease DctM subunit	specific_fp360
BLCPAMOF_02542	TIGRFAM	TIGR02123	TRAP_fused: TRAP transporter, 4TM/12TM fusion protein	IPR011853	TRAP C4-dicarboxylate transport system permease, fused DctM-DctQ	specific_fp360
BLCPAMOF_02542	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02542	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02542	Coils	Coil	NA	NA	NA	specific_fp360
BLCPAMOF_02542	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02542	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02542	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02542	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_02542	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_02542	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_02542	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02542	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02542	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02542	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_02543	Phobius	SIGNAL_PEPTIDE_C_REGION	C-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_02543	Pfam	PF16868	NMT1-like family	IPR011852	TRAP transporter solute receptor, TAXI family	specific_fp360
BLCPAMOF_02543	SignalP_GRAM_POSITIVE	SignalP-TM	NA	NA	NA	specific_fp360
BLCPAMOF_02543	Gene3D	G3DSA:3.40.190.10	NA	NA	NA	specific_fp360
BLCPAMOF_02543	Gene3D	G3DSA:3.40.190.10	NA	NA	NA	specific_fp360
BLCPAMOF_02543	Phobius	SIGNAL_PEPTIDE_N_REGION	N-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_02543	SignalP_GRAM_NEGATIVE	SignalP-noTM	NA	NA	NA	specific_fp360
BLCPAMOF_02543	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_02543	PANTHER	PTHR42941	NA	IPR011852	TRAP transporter solute receptor, TAXI family	specific_fp360
BLCPAMOF_02543	TIGRFAM	TIGR02122	TRAP_TAXI: TRAP transporter solute receptor, TAXI family	IPR011852	TRAP transporter solute receptor, TAXI family	specific_fp360
BLCPAMOF_02543	Phobius	SIGNAL_PEPTIDE_H_REGION	Hydrophobic region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_02543	ProSiteProfiles	PS51318	Twin arginine translocation (Tat) signal profile.	IPR006311	Twin-arginine translocation pathway, signal sequence	specific_fp360
BLCPAMOF_02543	Pfam	PF10518	TAT (twin-arginine translocation) pathway signal sequence	IPR019546	Twin-arginine translocation pathway, signal sequence, bacterial/archaeal	specific_fp360
BLCPAMOF_02543	TIGRFAM	TIGR01409	TAT_signal_seq: Tat (twin-arginine translocation) pathway signal sequence	IPR019546	Twin-arginine translocation pathway, signal sequence, bacterial/archaeal	specific_fp360
BLCPAMOF_02543	SUPERFAMILY	SSF53850	NA	NA	NA	specific_fp360
BLCPAMOF_02543	Phobius	SIGNAL_PEPTIDE	Signal peptide region	NA	NA	specific_fp360
BLCPAMOF_01191	Pfam	PF01402	Ribbon-helix-helix protein, copG family	IPR002145	Ribbon-helix-helix protein, CopG	specific_fp360
BLCPAMOF_00744	Phobius	SIGNAL_PEPTIDE	Signal peptide region	NA	NA	specific_fp360
BLCPAMOF_00744	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00744	Pfam	PF10518	TAT (twin-arginine translocation) pathway signal sequence	IPR019546	Twin-arginine translocation pathway, signal sequence, bacterial/archaeal	specific_fp360
BLCPAMOF_00744	Gene3D	G3DSA:3.40.190.10	NA	NA	NA	specific_fp360
BLCPAMOF_00744	SignalP_GRAM_NEGATIVE	SignalP-noTM	NA	NA	NA	specific_fp360
BLCPAMOF_00744	CDD	cd13691	PBP2_Peb1a_like	NA	NA	specific_fp360
BLCPAMOF_00744	SUPERFAMILY	SSF53850	NA	NA	NA	specific_fp360
BLCPAMOF_00744	ProSiteProfiles	PS51318	Twin arginine translocation (Tat) signal profile.	IPR006311	Twin-arginine translocation pathway, signal sequence	specific_fp360
BLCPAMOF_00744	Phobius	SIGNAL_PEPTIDE_N_REGION	N-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_00744	SignalP_EUK	SignalP-noTM	NA	NA	NA	specific_fp360
BLCPAMOF_00744	PANTHER	PTHR35936:SF9	NA	NA	NA	specific_fp360
BLCPAMOF_00744	Phobius	SIGNAL_PEPTIDE_H_REGION	Hydrophobic region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_00744	Gene3D	G3DSA:3.40.190.10	NA	NA	NA	specific_fp360
BLCPAMOF_00744	SMART	SM00062	NA	IPR001638	Solute-binding protein family 3/N-terminal domain of MltF	specific_fp360
BLCPAMOF_00744	SignalP_GRAM_POSITIVE	SignalP-TM	NA	NA	NA	specific_fp360
BLCPAMOF_00744	TIGRFAM	TIGR01409	TAT_signal_seq: Tat (twin-arginine translocation) pathway signal sequence	IPR019546	Twin-arginine translocation pathway, signal sequence, bacterial/archaeal	specific_fp360
BLCPAMOF_00744	Pfam	PF00497	Bacterial extracellular solute-binding proteins, family 3	IPR001638	Solute-binding protein family 3/N-terminal domain of MltF	specific_fp360
BLCPAMOF_00744	Phobius	SIGNAL_PEPTIDE_C_REGION	C-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_00744	PANTHER	PTHR35936	NA	NA	NA	specific_fp360
BLCPAMOF_00109	SMART	SM00793	NA	IPR006741	Accessory gene regulator B	specific_fp360
BLCPAMOF_00109	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00109	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00109	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_00109	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00109	Pfam	PF04647	Accessory gene regulator B	IPR006741	Accessory gene regulator B	specific_fp360
BLCPAMOF_00109	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_00109	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00109	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00109	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00109	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00109	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00109	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00109	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_00109	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00109	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00109	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00104	Phobius	SIGNAL_PEPTIDE_N_REGION	N-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_00104	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00104	Phobius	SIGNAL_PEPTIDE_H_REGION	Hydrophobic region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_00104	Phobius	SIGNAL_PEPTIDE	Signal peptide region	NA	NA	specific_fp360
BLCPAMOF_00104	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00104	Phobius	SIGNAL_PEPTIDE_C_REGION	C-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_00104	Pfam	PF13349	Putative adhesin	IPR025164	Putative adhesin	specific_fp360
BLCPAMOF_00104	SignalP_EUK	SignalP-noTM	NA	NA	NA	specific_fp360
BLCPAMOF_01437	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_00106	CDD	cd00093	HTH_XRE	IPR001387	Cro/C1-type helix-turn-helix domain	specific_fp360
BLCPAMOF_00106	Gene3D	G3DSA:1.10.260.40	NA	IPR010982	Lambda repressor-like, DNA-binding domain superfamily	specific_fp360
BLCPAMOF_00106	ProSiteProfiles	PS50943	Cro/C1-type HTH domain profile.	IPR001387	Cro/C1-type helix-turn-helix domain	specific_fp360
BLCPAMOF_00106	SUPERFAMILY	SSF47413	NA	IPR010982	Lambda repressor-like, DNA-binding domain superfamily	specific_fp360
BLCPAMOF_00106	SMART	SM00530	NA	IPR001387	Cro/C1-type helix-turn-helix domain	specific_fp360
BLCPAMOF_00103	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_00344	SignalP_GRAM_NEGATIVE	SignalP-noTM	NA	NA	NA	specific_fp360
BLCPAMOF_00344	Phobius	SIGNAL_PEPTIDE_H_REGION	Hydrophobic region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_00344	Phobius	SIGNAL_PEPTIDE	Signal peptide region	NA	NA	specific_fp360
BLCPAMOF_00344	Phobius	SIGNAL_PEPTIDE_C_REGION	C-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_00344	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00344	Phobius	SIGNAL_PEPTIDE_N_REGION	N-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_00344	SignalP_EUK	SignalP-noTM	NA	NA	NA	specific_fp360
BLCPAMOF_00344	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00344	ProSiteProfiles	PS51257	Prokaryotic membrane lipoprotein lipid attachment site profile.	NA	NA	specific_fp360
BLCPAMOF_00344	SignalP_GRAM_POSITIVE	SignalP-TM	NA	NA	NA	specific_fp360
BLCPAMOF_01922	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_02043	NA	NA	NA	NA	NA	specific_fp360

BLCPAMOF_02042	SUPERFAMILY	SSF160631	NA	NA	NA	specific_fp360
BLCPAMOF_02044	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_02049	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_02536	CDD	cd01335	Radical_SAM	NA	NA	specific_fp360
BLCPAMOF_02536	Pfam	PF04055	Radical SAM superfamily	IPR007197	Radical SAM	specific_fp360
BLCPAMOF_02536	PANTHER	PTHR11228	NA	NA	NA	specific_fp360
BLCPAMOF_02536	Pfam	PF13186	Iron-sulfur cluster-binding domain	IPR023885	4Fe4S-binding SPASM domain	specific_fp360
BLCPAMOF_02536	Pfam	PF13394	4Fe-4S single cluster domain	NA	NA	specific_fp360
BLCPAMOF_02536	Gene3D	G3DSA:3.20.20.70	NA	IPR013785	Aldolase-type TIM barrel	specific_fp360
BLCPAMOF_02536	PANTHER	PTHR11228:SF7	NA	NA	NA	specific_fp360
BLCPAMOF_02536	SFLD	SFLDS00029	Radical SAM	IPR007197	Radical SAM	specific_fp360
BLCPAMOF_02536	SFLD	SFLDG01067	SPASM/twitch domain containing	NA	NA	specific_fp360
BLCPAMOF_02536	SUPERFAMILY	SSF102114	NA	NA	NA	specific_fp360
BLCPAMOF_01185	CDD	cd12110	PHP_HisPPase_Hisj_like	NA	NA	specific_fp360
BLCPAMOF_01185	PANTHER	PTHR21039	NA	IPR010140	Histidinol phosphate phosphatase, HisJ	specific_fp360
BLCPAMOF_01185	Gene3D	G3DSA:3.20.20.140	NA	NA	NA	specific_fp360
BLCPAMOF_01185	SUPERFAMILY	SSF89550	NA	IPR016195	Polymerase/histidinol phosphatase-like	specific_fp360
BLCPAMOF_01185	Pfam	PF02811	PHP domain	IPR004013	PHP domain	specific_fp360
BLCPAMOF_02550	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02550	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_02550	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02550	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_02550	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_02550	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02550	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00290	PANTHER	PTHR30313	NA	NA	NA	specific_fp360
BLCPAMOF_00290	SUPERFAMILY	SSF57783	NA	NA	NA	specific_fp360
BLCPAMOF_00290	Pfam	PF01807	CHC2 zinc finger	IPR002694	Zinc finger, CHC2-type	specific_fp360
BLCPAMOF_00290	Gene3D	G3DSA:3.90.580.10	NA	IPR036977	DNA Primase, CHC2-type zinc finger	specific_fp360
BLCPAMOF_00290	SMART	SM00400	NA	IPR002694	Zinc finger, CHC2-type	specific_fp360
BLCPAMOF_00291	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_00695	Pfam	PF01627	Hpt domain	IPR008207	Signal transduction histidine kinase, phosphotransfer (Hpt) domain	specific_fp360
BLCPAMOF_00695	Gene3D	G3DSA:1.20.120.160	NA	IPR036641	HPT domain superfamily	specific_fp360
BLCPAMOF_00695	SUPERFAMILY	SSF47226	NA	IPR036641	HPT domain superfamily	specific_fp360
BLCPAMOF_00111	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_00110	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_02828	SUPERFAMILY	SSF55594	NA	IPR035895	HPr-like superfamily	specific_fp360
BLCPAMOF_01684	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_01684	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_01684	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00911	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_00915	Phobius	SIGNAL_PEPTIDE_N_REGION	N-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_00915	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00915	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00915	Phobius	SIGNAL_PEPTIDE_C_REGION	C-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_00915	SignalP_GRAM_NEGATIVE	SignalP-TM	NA	NA	NA	specific_fp360
BLCPAMOF_00915	SignalP_EUK	SignalP-noTM	NA	NA	NA	specific_fp360
BLCPAMOF_00915	Phobius	SIGNAL_PEPTIDE	Signal peptide region	NA	NA	specific_fp360
BLCPAMOF_00915	Phobius	SIGNAL_PEPTIDE_H_REGION	Hydrophobic region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_00915	SignalP_GRAM_POSITIVE	SignalP-TM	NA	NA	NA	specific_fp360
BLCPAMOF_00915	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp360
BLCPAMOF_00598	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00598	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00598	CDD	cd16919	HATPase_CckA-like	NA	NA	specific_fp360
BLCPAMOF_00598	PANTHER	PTHR43065	NA	NA	NA	specific_fp360
BLCPAMOF_00598	CDD	cd00082	HisKA	IPR003661	Signal transduction histidine kinase, dimerisation/phosphoacceptor domain	specific_fp360
BLCPAMOF_00598	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00598	CDD	cd12912	PDC2_MCP_like	NA	NA	specific_fp360
BLCPAMOF_00598	SUPERFAMILY	SSF52172	NA	IPR011006	CheY-like superfamily	specific_fp360
BLCPAMOF_00598	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00598	Gene3D	G3DSA:1.10.287.130	NA	NA	NA	specific_fp360
BLCPAMOF_00598	Gene3D	G3DSA:3.40.50.2300	NA	NA	NA	specific_fp360
BLCPAMOF_00598	SMART	SM00387	NA	IPR003594	Histidine kinase/HSP90-like ATPase	specific_fp360
BLCPAMOF_00598	PANTHER	PTHR43065:SF35	NA	NA	NA	specific_fp360
BLCPAMOF_00598	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00598	PRINTS	PR00344	Bacterial sensor protein C-terminal signature	IPR004358	Signal transduction histidine kinase-related protein, C-terminal	specific_fp360
BLCPAMOF_00598	PRINTS	PR00344	Bacterial sensor protein C-terminal signature	IPR004358	Signal transduction histidine kinase-related protein, C-terminal	specific_fp360
BLCPAMOF_00598	PRINTS	PR00344	Bacterial sensor protein C-terminal signature	IPR004358	Signal transduction histidine kinase-related protein, C-terminal	specific_fp360
BLCPAMOF_00598	PRINTS	PR00344	Bacterial sensor protein C-terminal signature	IPR004358	Signal transduction histidine kinase-related protein, C-terminal	specific_fp360
BLCPAMOF_00598	ProSiteProfiles	PS50109	Histidine kinase domain profile.	IPR005467	Histidine kinase domain	specific_fp360
BLCPAMOF_00598	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00598	CDD	cd00156	REC	IPR001789	Signal transduction response regulator, receiver domain	specific_fp360
BLCPAMOF_00598	SUPERFAMILY	SSF55874	NA	IPR036890	Histidine kinase/HSP90-like ATPase superfamily	specific_fp360
BLCPAMOF_00598	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_00598	Gene3D	G3DSA:3.30.450.20	NA	NA	NA	specific_fp360
BLCPAMOF_00598	Gene3D	G3DSA:3.30.565.10	NA	IPR036890	Histidine kinase/HSP90-like ATPase superfamily	specific_fp360
BLCPAMOF_00598	ProSiteProfiles	PS50110	Response regulatory domain profile.	IPR001789	Signal transduction response regulator, receiver domain	specific_fp360
BLCPAMOF_00598	SMART	SM00448	NA	IPR001789	Signal transduction response regulator, receiver domain	specific_fp360
BLCPAMOF_00598	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_00598	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00598	SMART	SM00388	NA	IPR003661	Signal transduction histidine kinase, dimerisation/phosphoacceptor domain	specific_fp360
BLCPAMOF_00598	Pfam	PF00072	Response regulator receiver domain	IPR001789	Signal transduction response regulator, receiver domain	specific_fp360
BLCPAMOF_00598	SUPERFAMILY	SSF47384	NA	IPR036097	Signal transduction histidine kinase, dimerisation/phosphoacceptor domain superfamily	specific_fp360
BLCPAMOF_00598	Pfam	PF02518	Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase	IPR003594	Histidine kinase/HSP90-like ATPase	specific_fp360
BLCPAMOF_00597	Gene3D	G3DSA:3.40.50.2300	NA	NA	NA	specific_fp360
BLCPAMOF_00597	ProSiteProfiles	PS50110	Response regulatory domain profile.	IPR001789	Signal transduction response regulator, receiver domain	specific_fp360
BLCPAMOF_00597	PANTHER	PTHR26402:SF725	NA	NA	NA	specific_fp360
BLCPAMOF_00597	Pfam	PF00072	Response regulator receiver domain	IPR001789	Signal transduction response regulator, receiver domain	specific_fp360
BLCPAMOF_00597	SUPERFAMILY	SSF52172	NA	IPR011006	CheY-like superfamily	specific_fp360
BLCPAMOF_00597	SMART	SM00448	NA	IPR001789	Signal transduction response regulator, receiver domain	specific_fp360
BLCPAMOF_00597	Gene3D	G3DSA:1.10.10.10	NA	IPR036388	Winged helix-like DNA-binding domain superfamily	specific_fp360
BLCPAMOF_00597	CDD	cd00383	trans_reg_C	IPR001867	OmpR/PhoB-type DNA-binding domain	specific_fp360
BLCPAMOF_00597	SMART	SM00862	NA	IPR001867	OmpR/PhoB-type DNA-binding domain	specific_fp360
BLCPAMOF_00597	PANTHER	PTHR26402	NA	IPR039420	Transcriptional regulatory protein WalR-like	specific_fp360
BLCPAMOF_00597	ProSiteProfiles	PS51755	OmpR/PhoB-type DNA-binding domain profile.	IPR001867	OmpR/PhoB-type DNA-binding domain	specific_fp360
BLCPAMOF_00597	CDD	cd00156	REC	IPR001789	Signal transduction response regulator, receiver domain	specific_fp360
BLCPAMOF_00597	Pfam	PF00486	Transcriptional regulatory protein, C terminal	IPR001867	OmpR/PhoB-type DNA-binding domain	specific_fp360
BLCPAMOF_00596	Gene3D	G3DSA:3.40.1080.10	NA	NA	NA	specific_fp360
BLCPAMOF_00596	PANTHER	PTHR40596	NA	IPR006472	Citrate lyase, alpha subunit	specific_fp360
BLCPAMOF_00596	PIRSF	PIRSF009451	NA	IPR006472	Citrate lyase, alpha subunit	specific_fp360
BLCPAMOF_00596	Pfam	PF04223	Citrate lyase, alpha subunit (CitF)	IPR006472	Citrate lyase, alpha subunit	specific_fp360
BLCPAMOF_00596	SUPERFAMILY	SSF100950	NA	IPR037171	NagB/RpiA transferase-like	specific_fp360
BLCPAMOF_00596	TIGRFAM	TIGR01584	citF: citrate lyase, alpha subunit	IPR006472	Citrate lyase, alpha subunit	specific_fp360
BLCPAMOF_00596	SUPERFAMILY	SSF100950	NA	IPR037171	NagB/RpiA transferase-like	specific_fp360
BLCPAMOF_00596	Gene3D	G3DSA:3.40.1080.10	NA	NA	NA	specific_fp360
BLCPAMOF_00595	PANTHER	PTHR32308:SF10	NA	NA	NA	specific_fp360
BLCPAMOF_00595	Gene3D	G3DSA:3.20.20.60	NA	IPR040442	Pyruvate kinase-like domain superfamily	specific_fp360
BLCPAMOF_00595	Pfam	PF03328	HpcH/HpaI aldolase/citrate lyase family	IPR005000	HpcH/HpaI aldolase/citrate lyase domain	specific_fp360
BLCPAMOF_00595	PANTHER	PTHR32308	NA	NA	NA	specific_fp360
BLCPAMOF_00595	SUPERFAMILY	SSF51621	NA	IPR015813	Pyruvate/Phosphoenolpyruvate kinase-like domain superfamily	specific_fp360
BLCPAMOF_00595	PIRSF	PIRSF015582	NA	IPR011206	Citrate lyase beta subunit-like	specific_fp360
BLCPAMOF_00594	TIGRFAM	TIGR01608	citD: citrate lyase acyl carrier protein	IPR006495	Citrate lyase acyl carrier protein CitD	specific_fp360
BLCPAMOF_00594	Pfam	PF06857	Malonate decarboxylase delta subunit (MdcD)	IPR023439	Malonate decarboxylase/citrate lyase acyl carrier protein	specific_fp360
BLCPAMOF_00594	Hamap	MF_00805	Citrate lyase acyl carrier protein [citD].	IPR006495	Citrate lyase acyl carrier protein CitD	specific_fp360
BLCPAMOF_00594	PIRSF	PIRSF002736	NA	IPR006495	Citrate lyase acyl carrier protein CitD	specific_fp360
BLCPAMOF_01868	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_00278	Pfam	PF00072	Response regulator receiver domain	IPR001789	Signal transduction response regulator, receiver domain	specific_fp360
BLCPAMOF_00278	CDD	cd00082	HisKA	IPR003661	Signal transduction histidine kinase, dimerisation/phosphoacceptor domain	specific_fp360
BLCPAMOF_00278	Phobius	SIGNAL_PEPTIDE	Signal peptide region	NA	NA	specific_fp360
BLCPAMOF_00278	Phobius	SIGNAL_PEPTIDE_N_REGION	N-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_00278	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00278	SUPERFAMILY	SSF52172	NA	IPR011006	CheY-like superfamily	specific_fp360
BLCPAMOF_00278	SUPERFAMILY	SSF55874	NA	IPR036890	Histidine kinase/HSP90-like ATPase superfamily	specific_fp360
BLCPAMOF_00278	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00278	ProSiteProfiles	PS50109	Histidine kinase domain profile.	IPR005467	Histidine kinase domain	specific_fp360
BLCPAMOF_00278	SMART	SM00448	NA	IPR001789	Signal transduction response regulator, receiver domain	specific_fp360
BLCPAMOF_00278	ProSiteProfiles	PS50110	Response regulatory domain profile.	IPR001789	Signal transduction response regulator, receiver domain	specific_fp360
BLCPAMOF_00278	Gene3D	G3DSA:3.30.565.10	NA	IPR036890	Histidine kinase/HSP90-like ATPase superfamily	specific_fp360
BLCPAMOF_00278	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00278	Phobius	SIGNAL_PEPTIDE_H_REGION	Hydrophobic region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_00278	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00278	Pfam	PF00512	His Kinase A (phospho-acceptor) domain	IPR003661	Signal transduction histidine kinase, dimerisation/phosphoacceptor domain	specific_fp360
BLCPAMOF_00278	CDD	cd12912	PDC2_MCP_like	NA	NA	specific_fp360
BLCPAMOF_00278	SMART	SM00388	NA	IPR003661	Signal transduction histidine kinase, dimerisation/phosphoacceptor domain	specific_fp360
BLCPAMOF_00278	SMART	SM00387	NA	IPR003594	Histidine kinase/HSP90-like ATPase	specific_fp360
BLCPAMOF_00278	Gene3D	G3DSA:3.30.450.20	NA	NA	NA	specific_fp360
BLCPAMOF_00278	PANTHER	PTHR43065:SF35	NA	NA	NA	specific_fp360

BLCPAMOF_00278	CDD	cd00156	REC	IPR001789	Signal transduction response regulator, receiver domain	specific_fp360
BLCPAMOF_00278	Gene3D	G3DSA:1.10.287.130	NA	NA	NA	specific_fp360
BLCPAMOF_00278	SUPERFAMILY	SSF47384	NA	IPR036097	Signal transduction histidine kinase, dimerisation/phosphoacceptor domain superfamily	specific_fp360
BLCPAMOF_00278	Pfam	PF02518	Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase	IPR003594	Histidine kinase/HSP90-like ATPase	specific_fp360
BLCPAMOF_00278	Gene3D	G3DSA:3.40.50.2300	NA	NA	NA	specific_fp360
BLCPAMOF_00278	PANTHER	PTHR43065	NA	NA	NA	specific_fp360
BLCPAMOF_00278	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_00278	PRINTS	PR00344	Bacterial sensor protein C-terminal signature	IPR004358	Signal transduction histidine kinase-related protein, C-terminal	specific_fp360
BLCPAMOF_00278	PRINTS	PR00344	Bacterial sensor protein C-terminal signature	IPR004358	Signal transduction histidine kinase-related protein, C-terminal	specific_fp360
BLCPAMOF_00278	PRINTS	PR00344	Bacterial sensor protein C-terminal signature	IPR004358	Signal transduction histidine kinase-related protein, C-terminal	specific_fp360
BLCPAMOF_00278	PRINTS	PR00344	Bacterial sensor protein C-terminal signature	IPR004358	Signal transduction histidine kinase-related protein, C-terminal	specific_fp360
BLCPAMOF_00278	CDD	cd16919	HATPase_CckA-like	NA	NA	specific_fp360
BLCPAMOF_00278	Pfam	PF02743	Cache domain	IPR033479	Double Cache domain 1	specific_fp360
BLCPAMOF_00278	Phobius	SIGNAL_PEPTIDE_C_REGION	C-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_01901	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_02241	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02241	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_02241	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02241	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02241	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_02241	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_02241	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02241	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02241	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02241	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00600	Pfam	PF00484	Carbonic anhydrase	IPR001765	Carbonic anhydrase	specific_fp360
BLCPAMOF_00600	ProSitePatterns	PS00704	Prokaryotic-type carbonic anhydrases signature 1.	IPR015892	Carbonic anhydrase, prokaryotic-like, conserved site	specific_fp360
BLCPAMOF_00600	Gene3D	G3DSA:3.40.1050.10	NA	IPR036874	Carbonic anhydrase superfamily	specific_fp360
BLCPAMOF_00600	PANTHER	PTHR11002:SF17	NA	NA	NA	specific_fp360
BLCPAMOF_00600	SMART	SM00947	NA	IPR001765	Carbonic anhydrase	specific_fp360
BLCPAMOF_00600	PANTHER	PTHR11002	NA	NA	NA	specific_fp360
BLCPAMOF_00600	SUPERFAMILY	SSF53056	NA	IPR036874	Carbonic anhydrase superfamily	specific_fp360
BLCPAMOF_00289	PANTHER	PTHR35372	NA	NA	NA	specific_fp360
BLCPAMOF_00289	TIGRFAM	TIGR01613	primase_Cterm: phage/plasmid primase, P4 family, C-terminal domain	IPR006500	DNA primase, phage/plasmid	specific_fp360
BLCPAMOF_00289	SUPERFAMILY	SSF52540	NA	IPR027417	P-loop containing nucleoside triphosphate hydrolase	specific_fp360
BLCPAMOF_00289	ProSiteProfiles	PS51206	Superfamily 3 helicase of DNA viruses domain profile.	IPR014015	Helicase, superfamily 3, DNA virus	specific_fp360
BLCPAMOF_01478	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_00040	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_01475	Phobius	SIGNAL_PEPTIDE_C_REGION	C-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_01475	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_01475	SignalP_EUK	SignalP-noTM	NA	NA	NA	specific_fp360
BLCPAMOF_01475	SignalP_GRAM_NEGATIVE	SignalP-noTM	NA	NA	NA	specific_fp360
BLCPAMOF_01475	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01475	SignalP_GRAM_POSITIVE	SignalP-TM	NA	NA	NA	specific_fp360
BLCPAMOF_01475	Phobius	SIGNAL_PEPTIDE_N_REGION	N-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_01475	ProSiteProfiles	PS51257	Prokaryotic membrane lipoprotein lipid attachment site profile.	NA	NA	specific_fp360
BLCPAMOF_01475	Phobius	SIGNAL_PEPTIDE_H_REGION	Hydrophobic region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_01475	Phobius	SIGNAL_PEPTIDE	Signal peptide region	NA	NA	specific_fp360
BLCPAMOF_00283	PANTHER	PTHR26402	NA	IPR039420	Transcriptional regulatory protein WalR-like	specific_fp360
BLCPAMOF_00283	PANTHER	PTHR26402:SF502	NA	NA	NA	specific_fp360
BLCPAMOF_00283	ProSiteProfiles	PS51755	OmpR/PhoB-type DNA-binding domain profile.	IPR001867	OmpR/PhoB-type DNA-binding domain	specific_fp360
BLCPAMOF_00283	Pfam	PF00486	Transcriptional regulatory protein, C terminal	IPR001867	OmpR/PhoB-type DNA-binding domain	specific_fp360
BLCPAMOF_00283	SMART	SM00862	NA	IPR001867	OmpR/PhoB-type DNA-binding domain	specific_fp360
BLCPAMOF_00283	SUPERFAMILY	SSF52172	NA	IPR011006	CheY-like superfamily	specific_fp360
BLCPAMOF_00283	SMART	SM00448	NA	IPR001789	Signal transduction response regulator, receiver domain	specific_fp360
BLCPAMOF_00283	ProSiteProfiles	PS50110	Response regulatory domain profile.	IPR001789	Signal transduction response regulator, receiver domain	specific_fp360
BLCPAMOF_00283	CDD	cd00156	REC	IPR001789	Signal transduction response regulator, receiver domain	specific_fp360
BLCPAMOF_00283	Gene3D	G3DSA:1.10.10.10	NA	IPR036388	Winged helix-like DNA-binding domain superfamily	specific_fp360
BLCPAMOF_00283	CDD	cd00383	trans_reg_C	IPR001867	OmpR/PhoB-type DNA-binding domain	specific_fp360
BLCPAMOF_00283	Pfam	PF00072	Response regulator receiver domain	IPR001789	Signal transduction response regulator, receiver domain	specific_fp360
BLCPAMOF_00283	SUPERFAMILY	SSF46894	NA	IPR016032	Signal transduction response regulator, C-terminal effector	specific_fp360
BLCPAMOF_00283	Gene3D	G3DSA:3.40.50.12740	NA	NA	NA	specific_fp360
BLCPAMOF_00282	Pfam	PF03401	Tripartite tricarboxylate transporter family receptor	IPR005064	Bordetella uptake gene	specific_fp360
BLCPAMOF_00282	SignalP_GRAM_POSITIVE	SignalP-TM	NA	NA	NA	specific_fp360
BLCPAMOF_00282	Phobius	SIGNAL_PEPTIDE_C_REGION	C-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_00282	ProSiteProfiles	PS51318	Twin arginine translocation (Tat) signal profile.	IPR006311	Twin-arginine translocation pathway, signal sequence	specific_fp360
BLCPAMOF_00282	PANTHER	PTHR42928	NA	IPR005064	Bordetella uptake gene	specific_fp360
BLCPAMOF_00282	CDD	cd07012	PBP2_Bug_TTT	NA	NA	specific_fp360
BLCPAMOF_00282	Phobius	SIGNAL_PEPTIDE_H_REGION	Hydrophobic region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_00282	SignalP_GRAM_NEGATIVE	SignalP-noTM	NA	NA	NA	specific_fp360
BLCPAMOF_00282	Gene3D	G3DSA:3.40.190.150	NA	IPR042100	Bordetella uptake gene, domain 1	specific_fp360
BLCPAMOF_00282	Phobius	SIGNAL_PEPTIDE_N_REGION	N-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_00282	PIRSF	PIRSF017082	NA	IPR005064	Bordetella uptake gene	specific_fp360
BLCPAMOF_00282	Gene3D	G3DSA:3.40.190.10	NA	NA	NA	specific_fp360
BLCPAMOF_00282	Phobius	SIGNAL_PEPTIDE	Signal peptide region	NA	NA	specific_fp360
BLCPAMOF_00282	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00282	SignalP_EUK	SignalP-noTM	NA	NA	NA	specific_fp360
BLCPAMOF_00282	Pfam	PF10518	TAT (twin-arginine translocation) pathway signal sequence	IPR019546	Twin-arginine translocation pathway, signal sequence, bacterial/archaeal	specific_fp360
BLCPAMOF_00281	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_00281	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_00281	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00281	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00281	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00281	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00281	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00281	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00281	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_00281	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00281	Pfam	PF07331	Tripartite tricarboxylate transporter TctB family	IPR009936	Protein of unknown function DUF1468	specific_fp360
BLCPAMOF_00281	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00281	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00281	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00281	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00280	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00280	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00280	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00280	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00280	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00280	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00280	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00280	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00280	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00280	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_00280	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00280	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00280	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00280	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_00280	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_00280	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00280	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00280	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00280	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00280	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00280	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_00280	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00280	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_00280	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00280	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00280	PANTHER	PTHR35342	NA	NA	NA	specific_fp360
BLCPAMOF_00280	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00280	Pfam	PF01970	Tripartite tricarboxylate transporter TctA family	IPR002823	Protein of unknown function DUF112, transmembrane	specific_fp360
BLCPAMOF_00280	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_00280	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00280	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00280	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00280	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_00280	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00280	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00280	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00280	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00280	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00280	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00280	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00280	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00369	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_01761	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp360
BLCPAMOF_01889	Pfam	PF05713	Bacterial mobilisation protein (MobC)	IPR008687	Bacterial mobilisation	specific_fp360

BLCPAMOF_00680	Phobius	SIGNAL_PEPTIDE_N_REGION	N-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_00680	Phobius	SIGNAL_PEPTIDE	Signal peptide region	NA	NA	specific_fp360
BLCPAMOF_00680	SignalP_GRAM_POSITIVE	SignalP-TM	NA	NA	NA	specific_fp360
BLCPAMOF_00680	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00680	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00680	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00680	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00680	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00680	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_00680	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00680	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00680	Phobius	SIGNAL_PEPTIDE_H_REGION	Hydrophobic region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_00680	Phobius	SIGNAL_PEPTIDE_C_REGION	C-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_01882	Pfam	PF00293	NUDIX domain	IPR000086	NUDIX hydrolase domain	specific_fp360
BLCPAMOF_01882	Gene3D	G3DSA:3.90.79.10	NA	NA	NA	specific_fp360
BLCPAMOF_01882	SUPERFAMILY	SSF55811	NA	IPR015797	NUDIX hydrolase-like domain superfamily	specific_fp360
BLCPAMOF_01882	ProSiteProfiles	PS51462	Nudix hydrolase domain profile.	IPR000086	NUDIX hydrolase domain	specific_fp360
BLCPAMOF_01882	PANTHER	PTHR10885:SF7	NA	NA	NA	specific_fp360
BLCPAMOF_01882	ProSitePatterns	PS00893	Nudix box signature.	IPR020084	NUDIX hydrolase, conserved site	specific_fp360
BLCPAMOF_01882	PANTHER	PTHR10885	NA	NA	NA	specific_fp360
BLCPAMOF_01579	Coils	Coil	NA	NA	NA	specific_fp360
BLCPAMOF_02285	Pfam	PF03417	Acyl-coenzyme A:6-aminopenicillanic acid acyl-transferase	IPR005079	Peptidase C45	specific_fp360
BLCPAMOF_02285	Phobius	SIGNAL_PEPTIDE_C_REGION	C-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_02285	Phobius	SIGNAL_PEPTIDE	Signal peptide region	NA	NA	specific_fp360
BLCPAMOF_02285	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02285	SignalP_GRAM_POSITIVE	SignalP-TM	NA	NA	NA	specific_fp360
BLCPAMOF_02285	SUPERFAMILY	SSF56235	NA	IPR029055	Nucleophile aminohydrolases, N-terminal	specific_fp360
BLCPAMOF_02285	Gene3D	G3DSA:3.60.60.10	NA	NA	NA	specific_fp360
BLCPAMOF_02285	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_02285	Phobius	SIGNAL_PEPTIDE_H_REGION	Hydrophobic region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_02285	Phobius	SIGNAL_PEPTIDE_N_REGION	N-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_02285	PANTHER	PTHR35527	NA	NA	NA	specific_fp360
BLCPAMOF_02496	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_00204	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00204	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00204	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00204	Pfam	PF01970	Tripartite tricarboxylate transporter TctA family	IPR002823	Protein of unknown function DUF112, transmembrane	specific_fp360
BLCPAMOF_00204	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00204	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_00204	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00204	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00204	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00204	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_00204	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00204	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_00204	PANTHER	PTHR35342	NA	NA	NA	specific_fp360
BLCPAMOF_00204	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00204	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00204	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_00204	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00204	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00204	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00204	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00204	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00204	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00204	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00204	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00204	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00204	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00204	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_00204	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00204	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00204	PANTHER	PTHR35342:SF5	NA	NA	NA	specific_fp360
BLCPAMOF_00204	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00204	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00204	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00204	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00204	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00204	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00204	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00204	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00204	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_00204	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00203	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00203	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00203	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00203	Pfam	PF07331	Tripartite tricarboxylate transporter TctB family	IPR009936	Protein of unknown function DUF1468	specific_fp360
BLCPAMOF_00203	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00203	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_00203	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00203	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_00203	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00203	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00203	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00203	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00203	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00203	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00203	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_00203	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00203	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00202	Gene3D	G3DSA:3.40.190.150	NA	IPR042100	Bordetella uptake gene, domain 1	specific_fp360
BLCPAMOF_00202	PIRSF	PIRSF017082	NA	IPR005064	Bordetella uptake gene	specific_fp360
BLCPAMOF_00202	Pfam	PF03401	Tripartite tricarboxylate transporter family receptor	IPR005064	Bordetella uptake gene	specific_fp360
BLCPAMOF_00202	Phobius	SIGNAL_PEPTIDE	Signal peptide region	NA	NA	specific_fp360
BLCPAMOF_00202	ProSiteProfiles	PS51318	Twin arginine translocation (Tat) signal profile.	IPR006311	Twin-arginine translocation pathway, signal sequence	specific_fp360
BLCPAMOF_00202	PANTHER	PTHR42928:SF5	NA	NA	NA	specific_fp360
BLCPAMOF_00202	SignalP_GRAM_NEGATIVE	SignalP-noTM	NA	NA	NA	specific_fp360
BLCPAMOF_00202	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00202	CDD	cd07012	PBP2_Bug_TTT	NA	NA	specific_fp360
BLCPAMOF_00202	Gene3D	G3DSA:3.40.190.10	NA	NA	NA	specific_fp360
BLCPAMOF_00202	Pfam	PF10518	TAT (twin-arginine translocation) pathway signal sequence	IPR019546	Twin-arginine translocation pathway, signal sequence, bacterial/archaeal	specific_fp360
BLCPAMOF_00202	PANTHER	PTHR42928	NA	IPR005064	Bordetella uptake gene	specific_fp360
BLCPAMOF_00202	Phobius	SIGNAL_PEPTIDE_N_REGION	N-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_00202	SignalP_GRAM_POSITIVE	SignalP-TM	NA	NA	NA	specific_fp360
BLCPAMOF_00202	Phobius	SIGNAL_PEPTIDE_C_REGION	C-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_00202	Phobius	SIGNAL_PEPTIDE_H_REGION	Hydrophobic region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_02493	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_02825	CDD	cd06587	VOC	NA	NA	specific_fp360
BLCPAMOF_02825	PANTHER	PTHR43048	NA	NA	NA	specific_fp360
BLCPAMOF_02825	Pfam	PF13669	Glyoxalase/Bleomycin resistance protein/Dioxygenase superfamily	NA	NA	specific_fp360
BLCPAMOF_02825	ProSiteProfiles	PS51819	Vicinal oxygen chelate (VOC) domain profile.	IPR037523	Vicinal oxygen chelate (VOC) domain	specific_fp360
BLCPAMOF_02825	SUPERFAMILY	SSF54593	NA	IPR029068	Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase	specific_fp360
BLCPAMOF_02825	Gene3D	G3DSA:3.10.180.10	NA	IPR029068	Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase	specific_fp360
BLCPAMOF_02752	SignalP_EUK	SignalP-noTM	NA	NA	NA	specific_fp360
BLCPAMOF_02752	Phobius	SIGNAL_PEPTIDE_N_REGION	N-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_02752	SignalP_GRAM_NEGATIVE	SignalP-noTM	NA	NA	NA	specific_fp360
BLCPAMOF_02752	Phobius	SIGNAL_PEPTIDE_H_REGION	Hydrophobic region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_02752	SignalP_GRAM_POSITIVE	SignalP-TM	NA	NA	NA	specific_fp360
BLCPAMOF_02752	ProSiteProfiles	PS51318	Twin arginine translocation (Tat) signal profile.	IPR006311	Twin-arginine translocation pathway, signal sequence	specific_fp360
BLCPAMOF_02752	Phobius	SIGNAL_PEPTIDE_C_REGION	C-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_02752	Phobius	SIGNAL_PEPTIDE	Signal peptide region	NA	NA	specific_fp360
BLCPAMOF_02752	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_02713	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_02056	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_02823	PANTHER	PTHR18964	NA	IPR000600	ROK family	specific_fp360
BLCPAMOF_02823	SUPERFAMILY	SSF53067	NA	IPR043129	ATPase, nucleotide binding domain	specific_fp360
BLCPAMOF_02823	Pfam	PF00480	ROK family	IPR000600	ROK family	specific_fp360
BLCPAMOF_02823	SUPERFAMILY	SSF46785	NA	IPR036390	Winged helix DNA-binding domain superfamily	specific_fp360
BLCPAMOF_02823	PANTHER	PTHR18964:SF166	NA	NA	NA	specific_fp360
BLCPAMOF_02823	Pfam	PF13412	Winged helix-turn-helix DNA-binding	NA	NA	specific_fp360
BLCPAMOF_02823	Gene3D	G3DSA:3.30.420.40	NA	NA	NA	specific_fp360
BLCPAMOF_02823	Gene3D	G3DSA:3.30.420.40	NA	NA	NA	specific_fp360
BLCPAMOF_02823	Gene3D	G3DSA:1.10.10.10	NA	IPR036388	Winged helix-like DNA-binding domain superfamily	specific_fp360
BLCPAMOF_02823	CDD	cd00012	NBD_sugar-kinase_HSP70_actin	NA	NA	specific_fp360
BLCPAMOF_01871	Phobius	SIGNAL_PEPTIDE_H_REGION	Hydrophobic region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_01871	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_01871	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360

BLCPAMOF_01871	Phobius	SIGNAL_PEPTIDE	Signal peptide region	NA	NA	specific_fp360
BLCPAMOF_01871	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_01871	Phobius	SIGNAL_PEPTIDE_N_REGION	N-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_01871	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01871	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_01871	Phobius	SIGNAL_PEPTIDE_C_REGION	C-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_01871	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01871	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_01871	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01871	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01871	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_01871	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01871	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_01871	Pfam	PF13346	ABC-2 family transporter protein	IPR025699	ABC-2 membrane transporter-like	specific_fp360
BLCPAMOF_01871	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01871	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01871	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01871	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01871	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01871	PANTHER	PTHR41309	NA	NA	NA	specific_fp360
BLCPAMOF_01870	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_01870	Phobius	SIGNAL_PEPTIDE_H_REGION	Hydrophobic region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_01870	Phobius	SIGNAL_PEPTIDE_C_REGION	C-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_01870	Phobius	SIGNAL_PEPTIDE_N_REGION	N-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_01870	Phobius	SIGNAL_PEPTIDE	Signal peptide region	NA	NA	specific_fp360
BLCPAMOF_01870	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02653	Pfam	PF10020	Uncharacterized protein conserved in bacteria (DUF2262)	IPR019260	Domain of unknown function DUF2262	specific_fp360
BLCPAMOF_02107	Pfam	PF04952	Succinylglutamate desuccinylase / Aspartoacylase family	IPR007036	Succinylglutamate desuccinylase/aspartoacylase	specific_fp360
BLCPAMOF_02107	Gene3D	G3DSA:3.40.630.10	NA	NA	NA	specific_fp360
BLCPAMOF_02107	PANTHER	PTHR37326	NA	NA	NA	specific_fp360
BLCPAMOF_02107	SUPERFAMILY	SSF53187	NA	NA	NA	specific_fp360
BLCPAMOF_02107	CDD	cd06253	M14_ASTE_ASPA-like	NA	NA	specific_fp360
BLCPAMOF_01921	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp360
BLCPAMOF_01921	Pfam	PF18796	Large polyvalent protein-associated domain 1	IPR041047	Large polyvalent protein-associated domain 1	specific_fp360
BLCPAMOF_01878	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_01878	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01878	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01878	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01878	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01878	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_01878	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01878	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_01878	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_01878	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01878	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01878	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_01878	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00199	Coils	Coil	NA	NA	NA	specific_fp360
BLCPAMOF_00199	Pfam	PF11185	Protein of unknown function (DUF2971)	IPR021352	Protein of unknown function DUF2971	specific_fp360
BLCPAMOF_00872	Phobius	SIGNAL_PEPTIDE_C_REGION	C-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_00872	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00872	Phobius	SIGNAL_PEPTIDE_H_REGION	Hydrophobic region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_00872	Phobius	SIGNAL_PEPTIDE_N_REGION	N-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_00872	Phobius	SIGNAL_PEPTIDE	Signal peptide region	NA	NA	specific_fp360
BLCPAMOF_02574	Phobius	SIGNAL_PEPTIDE_C_REGION	C-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_02574	SignalP_GRAM_NEGATIVE	SignalP-noTM	NA	NA	NA	specific_fp360
BLCPAMOF_02574	PANTHER	PTHR30006:SF2	NA	NA	NA	specific_fp360
BLCPAMOF_02574	PIRSF	PIRSF002825	NA	IPR026045	Ferric binding protein	specific_fp360
BLCPAMOF_02574	ProSiteProfiles	PS51318	Twin arginine translocation (Tat) signal profile.	IPR006311	Twin-arginine translocation pathway, signal sequence	specific_fp360
BLCPAMOF_02574	PANTHER	PTHR30006	NA	NA	NA	specific_fp360
BLCPAMOF_02574	Phobius	SIGNAL_PEPTIDE_H_REGION	Hydrophobic region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_02574	SignalP_EUK	SignalP-noTM	NA	NA	NA	specific_fp360
BLCPAMOF_02574	CDD	cd13546	PBP2_BitB	NA	NA	specific_fp360
BLCPAMOF_02574	SUPERFAMILY	SSF53850	NA	NA	NA	specific_fp360
BLCPAMOF_02574	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_02574	Pfam	PF13343	Bacterial extracellular solute-binding protein	NA	NA	specific_fp360
BLCPAMOF_02574	Gene3D	G3DSA:3.40.190.10	NA	NA	NA	specific_fp360
BLCPAMOF_02574	SignalP_GRAM_POSITIVE	SignalP-TM	NA	NA	NA	specific_fp360
BLCPAMOF_02574	Phobius	SIGNAL_PEPTIDE_N_REGION	N-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_02574	Phobius	SIGNAL_PEPTIDE	Signal peptide region	NA	NA	specific_fp360
BLCPAMOF_02574	Gene3D	G3DSA:3.40.190.10	NA	NA	NA	specific_fp360
BLCPAMOF_02479	Pfam	PF13443	Cro/C1-type HTH DNA-binding domain	IPR001387	Cro/C1-type helix-turn-helix domain	specific_fp360
BLCPAMOF_02479	SUPERFAMILY	SSF47413	NA	IPR010982	Lambda repressor-like, DNA-binding domain superfamily	specific_fp360
BLCPAMOF_02479	SMART	SM00530	NA	IPR001387	Cro/C1-type helix-turn-helix domain	specific_fp360
BLCPAMOF_02479	Gene3D	G3DSA:1.10.260.40	NA	IPR010982	Lambda repressor-like, DNA-binding domain superfamily	specific_fp360
BLCPAMOF_02479	ProSiteProfiles	PS50943	Cro/C1-type HTH domain profile.	IPR001387	Cro/C1-type helix-turn-helix domain	specific_fp360
BLCPAMOF_02474	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_02474	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02474	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02474	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02474	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02474	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02474	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02474	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_02474	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02474	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02474	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02474	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_02474	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02474	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02474	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02474	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_02474	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02474	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_02474	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02474	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02474	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02474	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_02474	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02474	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_02474	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_02474	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02474	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_02474	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02474	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02474	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_02474	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_02474	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_02474	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_02474	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02474	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02474	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00773	Gene3D	G3DSA:1.10.260.40	NA	IPR010982	Lambda repressor-like, DNA-binding domain superfamily	specific_fp360
BLCPAMOF_00773	SUPERFAMILY	SSF47413	NA	IPR010982	Lambda repressor-like, DNA-binding domain superfamily	specific_fp360
BLCPAMOF_00773	Pfam	PF13443	Cro/C1-type HTH DNA-binding domain	IPR001387	Cro/C1-type helix-turn-helix domain	specific_fp360
BLCPAMOF_00079	SignalP_EUK	SignalP-noTM	NA	NA	NA	specific_fp360
BLCPAMOF_00079	Phobius	SIGNAL_PEPTIDE_H_REGION	Hydrophobic region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_00079	Phobius	SIGNAL_PEPTIDE_N_REGION	N-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_00079	Phobius	SIGNAL_PEPTIDE_C_REGION	C-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_00079	Phobius	SIGNAL_PEPTIDE	Signal peptide region	NA	NA	specific_fp360
BLCPAMOF_00079	SignalP_GRAM_POSITIVE	SignalP-TM	NA	NA	NA	specific_fp360
BLCPAMOF_00079	SignalP_GRAM_NEGATIVE	SignalP-noTM	NA	NA	NA	specific_fp360
BLCPAMOF_00079	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00079	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_02471	SUPERFAMILY	SSF53448	NA	IPR029044	Nucleotide-diphospho-sugar transferases	specific_fp360
BLCPAMOF_00714	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_00714	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00714	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp360
BLCPAMOF_00714	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00714	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_00714	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp360
BLCPAMOF_01710	SignalP_GRAM_POSITIVE	SignalP-TM	NA	NA	NA	specific_fp360
BLCPAMOF_01710	Pfam	PF12708	Pectate lyase superfamily protein	IPR024535	Pectate lyase superfamily protein	specific_fp360
BLCPAMOF_01710	SUPERFAMILY	SSF51126	NA	IPR011050	Pectin lyase fold/virulence factor	specific_fp360
BLCPAMOF_01710	Gene3D	G3DSA:2.160.20.10	NA	IPR012334	Pectin lyase fold	specific_fp360
BLCPAMOF_01710	Phobius	SIGNAL_PEPTIDE	Signal peptide region	NA	NA	specific_fp360
BLCPAMOF_01710	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360

BLCPAMOF_01710	Phobius	SIGNAL_PEPTIDE_H_REGION	Hydrophobic region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_01710	Phobius	SIGNAL_PEPTIDE_N_REGION	N-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_01710	SignalP_EUK	SignalP-noTM	NA	NA	NA	specific_fp360
BLCPAMOF_01710	SignalP_GRAM_NEGATIVE	SignalP-noTM	NA	NA	NA	specific_fp360
BLCPAMOF_01710	Phobius	SIGNAL_PEPTIDE_C_REGION	C-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_01710	ProSiteProfiles	PS51257	Prokaryotic membrane lipoprotein lipid attachment site profile.	NA	NA	specific_fp360
BLCPAMOF_02497	Coils	Coil	NA	NA	NA	specific_fp360
BLCPAMOF_02497	Pfam	PF13271	Domain of unknown function (DUF4062)	IPR025139	Domain of unknown function DUF4062	specific_fp360
BLCPAMOF_01899	SUPERFAMILY	SSF51283	NA	IPR036157	dUTPase-like superfamily	specific_fp360
BLCPAMOF_01899	PANTHER	PTHR11241	NA	IPR008181	Deoxyuridine triphosphate nucleotidohydrolase	specific_fp360
BLCPAMOF_01899	PANTHER	PTHR11241:SF0	NA	NA	NA	specific_fp360
BLCPAMOF_01899	Pfam	PF00692	dUTPase	IPR029054	dUTPase-like	specific_fp360
BLCPAMOF_01899	CDD	cd07557	trimeric_dUTPase	IPR033704	dUTPase, trimeric	specific_fp360
BLCPAMOF_01899	Gene3D	G3DSA:2.70.40.10	NA	IPR036157	dUTPase-like superfamily	specific_fp360
BLCPAMOF_00373	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_01894	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_00371	Pfam	PF03592	Terminase small subunit	IPR005335	Terminase small subunit	specific_fp360
BLCPAMOF_00371	PANTHER	PTHR41328:SF2	NA	NA	NA	specific_fp360
BLCPAMOF_00371	PANTHER	PTHR41328	NA	NA	NA	specific_fp360
BLCPAMOF_00371	Gene3D	G3DSA:1.10.10.1400	NA	IPR038713	Terminase small subunit, N-terminal domain superfamily	specific_fp360
BLCPAMOF_01896	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01896	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_01896	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01896	Pfam	PF12664	Protein of unknown function (DUF3789)	IPR024522	Protein of unknown function DUF3789	specific_fp360
BLCPAMOF_01896	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_01891	Pfam	PF14195	Domain of unknown function (DUF4316)	IPR025465	Domain of unknown function DUF4316	specific_fp360
BLCPAMOF_01891	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp360
BLCPAMOF_01891	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp360
BLCPAMOF_01891	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp360
BLCPAMOF_00375	Pfam	PF18812	phage-Barnase-EndoU-ColicinE5/D-RelE like nuclease3	IPR041301	Phage-Barnase-EndoU-ColicinE5/D-RelE like nuclease 3	specific_fp360
BLCPAMOF_01892	MobiDBLite	mobidb-lite	consensus disorder prediction	NA	NA	specific_fp360
BLCPAMOF_00272	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_00273	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_01480	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_02480	Pfam	PF17338	Gene product 88	IPR020290	Gene product 88	specific_fp360
BLCPAMOF_00276	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_01168	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_01004	CDD	cd08996	GH32_FFase	NA	NA	specific_fp360
BLCPAMOF_01004	Gene3D	G3DSA:2.115.10.20	NA	IPR023296	Glycosyl hydrolase, five-bladed beta-propellor domain superfamily	specific_fp360
BLCPAMOF_01004	SUPERFAMILY	SSF75005	NA	IPR023296	Glycosyl hydrolase, five-bladed beta-propellor domain superfamily	specific_fp360
BLCPAMOF_00279	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00279	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_00279	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_00279	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_02814	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_01003	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01003	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01003	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_01003	Phobius	SIGNAL_PEPTIDE	Signal peptide region	NA	NA	specific_fp360
BLCPAMOF_01003	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_01003	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_01003	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01003	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_01003	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01003	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01003	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01003	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01003	Phobius	SIGNAL_PEPTIDE_C_REGION	C-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_01003	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01003	Phobius	SIGNAL_PEPTIDE_N_REGION	N-terminal region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_01003	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01003	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01003	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_01003	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01003	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01003	Phobius	SIGNAL_PEPTIDE_H_REGION	Hydrophobic region of a signal peptide.	NA	NA	specific_fp360
BLCPAMOF_01003	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_01003	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_01003	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_01003	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01003	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01003	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_01003	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01003	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01003	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01003	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01003	Phobius	TRANSMEMBRANE	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01003	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_01003	Phobius	CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the cytoplasm.	NA	NA	specific_fp360
BLCPAMOF_01003	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_01003	Phobius	NON_CYTOPLASMIC_DOMAIN	Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region.	NA	NA	specific_fp360
BLCPAMOF_02765	TMHMM	TMhelix	Region of a membrane-bound protein predicted to be embedded in the membrane.	NA	NA	specific_fp360
BLCPAMOF_02577	NA	NA	NA	NA	NA	specific_fp360
BLCPAMOF_00724	ProSiteProfiles	PS51101	PTS_EIIB type-4 domain profile.	IPR004720	Phosphotransferase system, sorbose subfamily IIB component	specific_fp360
BLCPAMOF_00724	Gene3D	G3DSA:3.40.35.10		IPR036667	Phosphotransferase system, sorbose subfamily IIB component superfamily	specific_fp360
BLCPAMOF_00724	SUPERFAMILY	SSF52728		IPR036667	Phosphotransferase system, sorbose subfamily IIB component superfamily	specific_fp360
BLCPAMOF_00724	TIGRFAM	TIGR00854	pts-sorbose: PTS system, mannose/fructose/sorbose family, IIB component	IPR018455	Phosphotransferase system, sorbose subfamily IIB component, subgroup	specific_fp360
BLCPAMOF_00724	CDD	cd00001	PTS_IIB_man	IPR004720	Phosphotransferase system, sorbose subfamily IIB component	specific_fp360
BLCPAMOF_00724	Pfam	PF03830	PTS system sorbose subfamily IIB component	IPR004720	Phosphotransferase system, sorbose subfamily IIB component	specific_fp360
BLCPAMOF_00725	ProSiteProfiles	PS51106	PTS_EIIC type-4 domain profile.	IPR004700	Phosphotransferase system, mannose/fructose/sorbose family, IIC subunit	specific_fp360
BLCPAMOF_00725	Pfam	PF03609	PTS system sorbose-specific iic component	IPR004700	Phosphotransferase system, mannose/fructose/sorbose family, IIC subunit	specific_fp360
BLCPAMOF_00726	ProSiteProfiles	PS51108	PTS_EIID domain profile.	IPR004704	Phosphotransferase system, mannose/fructose/sorbose family IID component	specific_fp360
BLCPAMOF_00726	Pfam	PF03613	PTS system mannose/fructose/sorbose family IID component	IPR004704	Phosphotransferase system, mannose/fructose/sorbose family IID component	specific_fp360
BLCPAMOF_00721	PIRSF	PIRSF001359		IPR000771	Fructose-bisphosphate aldolase, class-II	specific_fp360
BLCPAMOF_00721	Gene3D	G3DSA:3.20.20.70		IPR013785	Aldolase-type TIM barrel	specific_fp360
BLCPAMOF_00721	Pfam	PF01116	Fructose-bisphosphate aldolase class-II	IPR000771	Fructose-bisphosphate aldolase, class-II	specific_fp360
BLCPAMOF_00721	SUPERFAMILY	SSF51569				specific_fp360
BLCPAMOF_00721	TIGRFAM	TIGR00167	cbbA: ketose-bisphosphate aldolase	IPR000771	Fructose-bisphosphate aldolase, class-II	specific_fp360
BLCPAMOF_00721	ProSitePatterns	PS00806	Fructose-bisphosphate aldolase class-II signature 2.	IPR000771	Fructose-bisphosphate aldolase, class-II	specific_fp360
BLCPAMOF_00721	CDD	cd00947	TBP_aldolase_IIB	IPR000771	Fructose-bisphosphate aldolase, class-II	specific_fp360
BLCPAMOF_00721	TIGRFAM	TIGR01859	fruc_bis_ald_: fructose-1,6-bisphosphate aldolase, class II	IPR011289	Fructose-1,6-bisphosphate aldolase, class 2	specific_fp360
BLCPAMOF_00554	Pfam	PF02447	GntP family permease	IPR003474	Gluconate transporter	specific_fp360
BLCPAMOF_00746	TIGRFAM	TIGR01726	HEQRo_perm_3TM: amino ABC transporter, permease protein, 3-TM region, His/Glu/Gln/Arg/opine family	IPR010065	Amino acid ABC transporter, permease protein, 3-TM domain	specific_fp360
BLCPAMOF_00746	Pfam	PF00528	Binding-protein-dependent transport system inner membrane component	IPR000515	ABC transporter type 1, transmembrane domain MetI-like	specific_fp360
BLCPAMOF_00746	Gene3D	G3DSA:1.10.3720.10		IPR035906	MetI-like superfamily	specific_fp360
BLCPAMOF_00746	ProSiteProfiles	PS50928	ABC transporter integral membrane type-1 domain profile.	IPR000515	ABC transporter type 1, transmembrane domain MetI-like	specific_fp360
BLCPAMOF_00746	CDD	cd06261	TM_PBP2	IPR000515	ABC transporter type 1, transmembrane domain MetI-like	specific_fp360
BLCPAMOF_00746	SUPERFAMILY	SSF161098		IPR035906	MetI-like superfamily	specific_fp360
BLCPAMOF_00745	Gene3D	G3DSA:1.10.3720.10		IPR035906	MetI-like superfamily	specific_fp360
BLCPAMOF_00745	ProSiteProfiles	PS50928	ABC transporter integral membrane type-1 domain profile.	IPR000515	ABC transporter type 1, transmembrane domain MetI-like	specific_fp360
BLCPAMOF_00745	CDD	cd06261	TM_PBP2	IPR000515	ABC transporter type 1, transmembrane domain MetI-like	specific_fp360
BLCPAMOF_00745	Pfam	PF00528	Binding-protein-dependent transport system inner membrane component	IPR000515	ABC transporter type 1, transmembrane domain MetI-like	specific_fp360
BLCPAMOF_00745	SUPERFAMILY	SSF161098		IPR035906	MetI-like superfamily	specific_fp360
BLCPAMOF_00745	TIGRFAM	TIGR01726	HEQRo_perm_3TM: amino ABC transporter, permease protein, 3-TM region, His/Glu/Gln/Arg/opine family	IPR010065	Amino acid ABC transporter, permease protein, 3-TM domain	specific_fp360
BLCPAMOF_00743	SUPERFAMILY	SSF52540		IPR027417	P-loop containing nucleoside triphosphate hydrolase	specific_fp360
BLCPAMOF_00743	CDD	cd03262	ABC_HisP_GlnQ			specific_fp360
BLCPAMOF_00743	PIRSF	PIRSF039085		IPR030679	ABC-type amino acid transport system, ATPase component, HisP-type	specific_fp360
BLCPAMOF_00743	ProSitePatterns	PS00211	ABC transporters family signature.	IPR017871	ABC transporter, conserved site	specific_fp360
BLCPAMOF_00743	SMART	SM00382		IPR003593	AAA+ ATPase domain	specific_fp360
BLCPAMOF_00743	ProSiteProfiles	PS50893	ATP-binding cassette, ABC transporter-type domain profile.	IPR003439	ABC transporter-like	specific_fp360
BLCPAMOF_00743	Pfam	PF00005	ABC transporter	IPR003439	ABC transporter-like	specific_fp360
BLCPAMOF_00743	Gene3D	G3DSA:3.40.50.300				specific_fp360
BLCPAMOF_01625	CDD	cd03357	LbH_MAT_GAT			specific_fp360
BLCPAMOF_01625	SMART	SM01266		IPR024688	Maltose/galactoside acetyltransferase	specific_fp360
BLCPAMOF_01625	ProSitePatterns	PS00101	Hexapeptide-repeat containing-transferases signature.	IPR018357	Hexapeptide transferase, conserved site	specific_fp360
BLCPAMOF_01625	Gene3D	G3DSA:2.160.10.10				specific_fp360
BLCPAMOF_01625	SUPERFAMILY	SSF51161		IPR011004	Trimeric LpxA-like superfamily	specific_fp360
BLCPAMOF_01625	Pfam	PF12464	Maltose acetyltransferase	IPR024688	Maltose/galactoside acetyltransferase	specific_fp360
BLCPAMOF_01625	Pfam	PF00132	Bacterial transferase hexapeptide (six repeats)	IPR001451	Hexapeptide repeat	specific_fp360
BLCPAMOF_01742	SUPERFAMILY	SSF102829		IPR036192	Cell division protein ZapA-like superfamily	specific_fp360
BLCPAMOF_01742	Pfam	PF05164	Cell division protein ZapA	IPR007838	Cell division protein ZapA-like	specific_fp360
BLCPAMOF_01742	Coils	Coil				specific_fp360
BLCPAMOF_00307	SUPERFAMILY	SSF63817		IPR023365	Sortase domain superfamily	specific_fp360
BLCPAMOF_00307	CDD	cd05826	Sortase_B	IPR009835	Sortase B family	specific_fp360
BLCPAMOF_00307	Gene3D	G3DSA:2.40.260.10		IPR023365	Sortase domain superfamily	specific_fp360
BLCPAMOF_00307	TIGRFAM	TIGR03064	sortase_srtB: sortase, SrtB family	IPR009835	Sortase B family	specific_fp360
BLCPAMOF_00307	Pfam	PF04203	Sortase domain	IPR005754	Sortase family	specific_fp360

BLCPAMOF_02826	Gene3D	G3DSA:1.20.1250.20				specific_fp360
BLCPAMOF_02826	SUPERFAMILY	SSF103473		IPR036259	MFS transporter superfamily	specific_fp360
BLCPAMOF_02826	Gene3D	G3DSA:1.20.1250.20				specific_fp360
BLCPAMOF_02826	CDD	cd17332	MFS_MelB_like			specific_fp360
BLCPAMOF_02826	TIGRFAM	TIGR00792	gph: sugar (Glycoside-Pentoside-Hexuronide) transporter	IPR001927	Sodium:galactoside symporter	specific_fp360
BLCPAMOF_02826	Pfam	PF13347	MFS/sugar transport protein			specific_fp360
BLCPAMOF_02777	Pfam	PF00248	Aldo/keto reductase family	IPR023210	NADP-dependent oxidoreductase domain	specific_fp360
BLCPAMOF_02777	Gene3D	G3DSA:3.20.20.100		IPR036812	NADP-dependent oxidoreductase domain superfamily	specific_fp360
BLCPAMOF_02777	CDD	cd06660	Aldo_ket_red	IPR023210	NADP-dependent oxidoreductase domain	specific_fp360
BLCPAMOF_02777	SUPERFAMILY	SSF51430		IPR036812	NADP-dependent oxidoreductase domain superfamily	specific_fp360
BLCPAMOF_02538	MobiDBLite	mobidb-lite	consensus disorder prediction			specific_fp360
BLCPAMOF_02538	Coils	Coil				specific_fp360
BLCPAMOF_02575	Gene3D	G3DSA:2.40.50.140				specific_fp360
BLCPAMOF_02575	Gene3D	G3DSA:3.40.50.300				specific_fp360
BLCPAMOF_02575	SUPERFAMILY	SSF50331		IPR008995	Molybdate/tungstate binding, C-terminal	specific_fp360
BLCPAMOF_02575	ProSitePatterns	PS00211	ABC transporters family signature.	IPR017871	ABC transporter, conserved site	specific_fp360
BLCPAMOF_02575	Pfam	PF00005	ABC transporter	IPR003439	ABC transporter-like	specific_fp360
BLCPAMOF_02575	ProSiteProfiles	PS50893	ATP-binding cassette, ABC transporter-type domain profile.	IPR003439	ABC transporter-like	specific_fp360
BLCPAMOF_02575	Pfam	PF08402	TOBE domain	IPR013611	Transport-associated OB, type 2	specific_fp360
BLCPAMOF_02575	SMART	SM00382		IPR003593	AAA+ ATPase domain	specific_fp360
BLCPAMOF_02575	Gene3D	G3DSA:2.40.50.100				specific_fp360
BLCPAMOF_02575	SUPERFAMILY	SSF52540		IPR027417	P-loop containing nucleoside triphosphate hydrolase	specific_fp360
BLCPAMOF_00796	Coils	Coil				specific_fp360
BLCPAMOF_00796	Pfam	PF04977	Septum formation initiator	IPR007060	Septum formation initiator FtsL/DivIC	specific_fp360
BLCPAMOF_02824	SUPERFAMILY	SSF51735		IPR036291	NAD(P)-binding domain superfamily	specific_fp360
BLCPAMOF_02824	ProSitePatterns	PS00059	Zinc-containing alcohol dehydrogenases signature.	IPR002328	Alcohol dehydrogenase, zinc-type, conserved site	specific_fp360
BLCPAMOF_02824	SUPERFAMILY	SSF50129		IPR011032	GroES-like superfamily	specific_fp360
BLCPAMOF_02824	Pfam	PF00107	Zinc-binding dehydrogenase	IPR013149	Alcohol dehydrogenase, C-terminal	specific_fp360
BLCPAMOF_02824	CDD	cd05285	sorbitol_DH			specific_fp360
BLCPAMOF_02824	Pfam	PF08240	Alcohol dehydrogenase GroES-like domain	IPR013154	Alcohol dehydrogenase, N-terminal	specific_fp360
BLCPAMOF_02824	SMART	SM00829		IPR020843	Polyketide synthase, enoylreductase domain	specific_fp360
BLCPAMOF_02824	Gene3D	G3DSA:3.40.50.720				specific_fp360
BLCPAMOF_02824	Gene3D	G3DSA:3.90.180.10				specific_fp360

付録9：Fp14とFp360に特徴的なオーソログのrelative abundanceの群間比較結果（Orthofinder）

異なるオーソログ検出ツールを用いて、特定の単離株にのみに見られるオーソログおよび特定の単離株のみに見られるKOを含むオーソログを"specific ortholog"と定義した

category

shared: Fp14およびFp360のみに共有されていた特徴的なオーソログ

specific_fp14: Fp14においてのみに特徴的なオーソログ

specific_fp360: Fp360においてのみに特徴的なオーソログ

健常者群（H）とMCI群（M）あるいは健常者群とAD群（A）の群間比較においてはウィルコクソンの順位和検定を実施した。FDR補正したq値を算出した。

ortholog_orthofinder (specific orthologs)	median	mean	H.mean	M.mean	A.mean	H.median	M.median	A.median	log2_mean_M_H	log2_mean_A_H	log2_median_M_H	log2_median_A_H	HvsM (pvalue)	HvsA (pvalue)	HvsM (qvalue)	HvsA (qvalue)	category
OG0002296	32.3144	37.33347542	41.71452098	33.52147273	32.35891591	38.41774	22.785	30.0974064	−0.315464145	−0.366386403	−0.753688282	−0.352133482	0.450787766	0.65196352	0.678455391	0.951961856	shared
OG0003536	20.33668	25.47321802	32.30191471	16.59289633	24.01638871	26.4836	8.31721	9.63531	−0.96105395	−0.427600451	−1.670927682	−1.458696257	0.022627113	0.222294081	0.213177836	0.793831443	shared
OG0003537	56.2488	64.83361814	78.31486376	48.3986034	59.60777	66.2789	31.6982	52.6856	−0.694320732	−0.393785748	−1.064148741	−0.33114096	0.115791241	0.499119962	0.325315857	0.895160802	shared
OG0003538	44.08165	55.12061172	70.28790543	40.72103133	40.47497429	55.9763	24.32677	24.9265	−0.787502363	−0.796246299	−1.20227135	−1.167135805	0.131427634	0.296035607	0.347992434	0.825398011	shared
OG0001676	397.5774	439.9105997	534.1079854	324.1145621	405.4528086	503.45974	319.375438	429.986394	−0.720627613	−0.397597448	−0.656623051	−0.227585406	0.002374388	0.296035607	0.212118871	0.825398011	specific_fp14
OG0000069	178.29698	190.0758441	229.322227	156.5351267	144.2096614	224.9339	149.22624	163.9052682	−0.550889758	−0.669208373	−0.591999865	−0.456638882	0.012135407	0.031465153	0.212118871	0.586871465	specific_fp14
OG0003846	0	0.008132256	0	0.023312467	0	0	0	0	Inf	NA	NA	NA	0.25979646	NA	0.501276023	NA	specific_fp14
OG0003847	0.21099	15.83133549	20.09447505	7.828101333	20.19170429	0.544456	0	7.57376	−1.360064552	0.006963798	#NAME?	3.798122337	0.444744002	0.407139063	0.67383504	0.881848321	specific_fp14
OG0003848	0	3.263139814	3.098028571	2.86972	4.601516	0	0	0	−0.11044047	0.570758796	NA	NA	0.429867808	0.474649843	0.665047154	0.895160802	specific_fp14
OG0003849	0	4.033396744	6.058376667	1.926683333	2.472842857	0	0	0	−1.652811805	−1.292760714	NA	NA	0.486087467	1	0.707189221	1	specific_fp14
OG0003850	0	4.075700326	4.747497619	2.676752267	5.058054286	0	0	0	−0.826683653	0.091415244	NA	NA	0.429867808	0.474649843	0.665047154	0.895160802	specific_fp14
OG0003851	0	0.995811512	1.276842857	1.067079667	0	0	0	0	−0.258913092	#NAME?	NA	NA	0.791324196	0.44006229	0.912626558	0.888199117	specific_fp14
OG0003852	0	8.005661372	5.990635048	12.3492186	4.743117714	0	0	0	1.043638906	−0.336873273	NA	NA	0.800151502	0.464291219	0.912626558	0.892687029	specific_fp14
OG0003853	0	22.30535744	15.81075429	36.190918	12.03439429	0	0	2.60827	1.194721507	−0.393742666	NA	Inf	1	0.256764922	1	0.811609317	specific_fp14
OG0003854	7.26064	15.66225628	21.21216333	10.21743333	10.68001286	8.9125	5.57387	2.49719	−1.053858932	−0.989978379	−0.677150817	−1.835524578	0.473908708	0.431112111	0.698256698	0.888199117	specific_fp14
OG0003855	0	4.809997279	4.068858762	7.2714	1.758978429	0	0	0	0.837608958	−1.209886412	NA	NA	0.597324185	0.950647639	0.788870461	1	specific_fp14
OG0003856	15.4398	34.40585072	38.11249714	37.1932274	17.31296143	20.271	12.5849	8.36363	−0.035224195	−1.138411614	−0.687723508	−1.277216116	0.479670259	0.287314122	0.703860076	0.825398011	specific_fp14
OG0003857	36.3997	48.53545	54.26384095	45.78026267	37.25425	36.7792	39.0074	18.0728	−0.245265429	−0.54258615	0.084857741	−1.025070061	0.751396543	0.189265565	0.885854961	0.766351369	specific_fp14
OG0003858	3.21417	18.67145726	21.10840619	18.91187613	10.84542714	6.69675	3.41448	0	−0.158525159	−0.960730777	−0.971795228	#NAME?	0.842715172	0.347492606	0.937013432	0.847858149	specific_fp14
OG0003859	0.942443	7.198435093	7.60765619	6.152801267	8.211415714	1.75946	1.55062	0.525167	−0.306208654	0.110178927	−0.182287538	−1.744284547	0.762409457	0.910960048	0.894506275	0.996172645	specific_fp14
OG0003860	0	2.854104651	5.763247619	0.11322	0	0	0	0	−5.669681273	#NAME?	NA	NA	0.444643599	0.323219522	0.67383504	0.834697703	specific_fp14
OG0003861	16.3737	34.44422679	23.50182476	50.07322213	33.78072857	16.3838	9.58867	25.0361	1.091266517	0.523427667	−0.772867385	0.611739835	0.563451914	0.750197895	0.76696918	0.973934811	specific_fp14
OG0003862	34.9536	93.76567791	71.64403333	125.6522053	91.80233857	43.0555	26.815	84.9907	0.810517528	0.357684347	−0.683157289	0.981107443	0.611998112	0.811273213	0.794841852	0.987043838	specific_fp14
OG0003863	0	9.961170419	8.199017524	13.56993333	7.514565714	0	0	2.27286	0.726890684	−0.125761315	NA	Inf	0.970235302	0.46226794	0.994521172	0.892687029	specific_fp14
OG0003864	0	1.034174884	0.717704762	1.959848	0	0	0	0	1.44927937	#NAME?	NA	NA	0.58667146	0.323219522	0.781948365	0.834697703	specific_fp14
OG0002169	101.53562	103.7250452	135.0656135	73.48007337	74.51399391	135.827474	67.133328	92.912392	−0.878235452	−0.858077127	−1.016674257	−0.547832394	0.000857284	0.027125773	0.212118871	0.569641228	specific_fp14
OG0003865	146.052	172.8509454	204.0414883	151.16134	125.7570429	195.618	135.838	86.8726	−0.432773316	−0.69822333	−0.526152005	−1.171066006	0.009949752	0.05474984	0.212118871	0.657803345	specific_fp14
OG0003866	92.9177	132.3228623	163.6219619	93.829812	120.9106714	130.793	33.9297	102.848	−0.802248125	−0.436424824	−1.946664751	−0.346771591	0.142970245	0.70820366	0.361331903	0.958503833	specific_fp14
OG0003867	0	0.354956302	0.700438095	0.036928067	0	0	0	0	−4.245467912	#NAME?	NA	NA	0.871601636	0.620690717	0.948638299	0.942642691	specific_fp14
OG0003868	0	0.388739	0.762373333	0.047062467	0	0	0	0	−4.017848814	#NAME?	NA	NA	0.674408456	0.239341328	0.843922919	0.793831443	specific_fp14
OG0003869	0	0.467763791	0.848452	0.110729667	0.090772286	0	0	0	−2.937791243	−3.224509252	NA	NA	0.280087211	0.485469317	0.521919158	0.895160802	specific_fp14
OG0003870	0	0.501004814	0.960091429	0.064036933	0.060104714	0	0	0	−3.906195673	−3.997621741	NA	NA	0.377619692	0.554342983	0.621969757	0.923650038	specific_fp14
OG0003871	0	0.200573256	0.410697619	0	0	0	0	0	#NAME?	#NAME?	NA	NA	0.430222691	0.620690717	0.665047154	0.942642691	specific_fp14
OG0003872	0	0.025071628	0.051337143	0	0	0	0	0	#NAME?	#NAME?	NA	NA	0.430222691	0.620690717	0.665047154	0.942642691	specific_fp14
OG0003873	0	0.362511628	0.742285714	0	0	0	0	0	#NAME?	#NAME?	NA	NA	0.430222691	0.620690717	0.665047154	0.942642691	specific_fp14
OG0003874	0	0.270220256	0.50717781	0.043791333	0.044552429	0	0	0	−3.533774343	−3.508915644	NA	NA	0.830992978	0.930545821	0.929690983	1	specific_fp14
OG0003875	0	0.272790698	0.558571429	0	0	0	0	0	#NAME?	#NAME?	NA	NA	0.430222691	0.620690717	0.665047154	0.942642691	specific_fp14
OG0003876	0	0.21763293	0.438298571	0.010263067	0	0	0	0	−5.41638019	#NAME?	NA	NA	0.871601636	0.620690717	0.948638299	0.942642691	specific_fp14
OG0003877	0	0.449700233	0.86382381	0.079787333	0	0	0	0	−3.436505448	#NAME?	NA	NA	0.871601636	0.620690717	0.948638299	0.942642691	specific_fp14
OG0003878	0	0.255899116	0.506109762	0.0250238	0	0	0	0	−4.338077509	#NAME?	NA	NA	0.788922711	0.44006229	0.91242816	0.888199117	specific_fp14
OG0003879	0	0.526285093	1.033473333	0	0.132474143	0	0	0	#NAME?	−2.963718466	NA	NA	0.241286619	0.843379402	0.478332881	0.998085231	specific_fp14
OG0003880	0	0.402052558	0.823250476	0	0	0	0	0	#NAME?	#NAME?	NA	NA	0.241286619	0.44006229	0.478332881	0.888199117	specific_fp14
OG0003881	0	2.119355163	4.339632	0	0	0	0	0	#NAME?	#NAME?	NA	NA	0.027851244	0.129742991	0.21634025	0.735188	specific_fp14
OG0003882	18.5708	38.80000537	47.33216667	39.9746554	10.68641429	31.0235	21.6054	0	−0.243735367	−2.147043111	−0.521969516	#NAME?	0.907853874	0.182685108	0.969481451	0.766351369	specific_fp14
OG0003883	0	2.77165	0.666804762	7.01187	0	0	0	0	3.394462936	#NAME?	NA	NA	0.069656206	0.620690717	0.261777809	0.942642691	specific_fp14
OG0003884	0	2.095234651	0.518166667	5.280906	0	0	0	0	3.349297346	#NAME?	NA	NA	0.15819907	0.620690717	0.382374682	0.942642691	specific_fp14
OG0003886	0	10.50999423	8.238336762	15.41046	6.823968571	0	0	0	0.903484921	−0.271742099	NA	NA	0.745131852	0.733544565	0.885854961	0.973934811	specific_fp14
OG0003887	0	8.721809535	6.379852857	13.01246667	6.553414286	0	0	0	1.028299412	0.038723587	NA	NA	0.919084503	0.576826376	0.9733491	0.932231154	specific_fp14
OG0003888	0	0.310289302	0.166657143	0.656176	0	0	0	0	1.977199675	#NAME?	NA	NA	0.746400229	0.44006229	0.885854961	0.888199117	specific_fp14
OG0003889	0	5.738225093	4.133977095	8.354810667	4.944	0	0	0	1.01507674	0.258148348	NA	NA	0.919084503	0.576826376	0.9733491	0.932231154	specific_fp14
OG0003890	0	11.15734081	7.549667905	16.9050486	9.663842857	0	0	0	1.162969074	0.356183811	NA	NA	0.852001032	0.37052313	0.938700433	0.863672559	specific_fp14
OG0003891	0	9.148163628	5.926362714	14.68566	6.947502714	0	0	0	1.309189272	0.229347566	NA	NA	0.968621817	0.847827158	0.994521172	0.998085231	specific_fp14
OG0003892	0	8.996896419	7.00730981	12.81695133	6.779824286	0	0	0	0.871120553	−0.047612799	NA	NA	0.501814744	0.673452718	0.72143331	0.951961856	specific_fp14
OG0003893	0	6.30326093	5.492211429	6.563758667	8.1782	0	0	0	0.257135031	0.57439618	NA	NA	0.542178517	0.948999012	0.752799652	1	specific_fp14
OG0003894	0	12.06199953	8.40644	18.83948333	8.505498571	0	0	0	1.164192525	0.016900835	NA	NA	0.908660058	0.898206191	0.969698335	0.996172645	specific_fp14
OG0003895	0	11.13642488	8.47883619	15.865334	8.975814286	0	0	0	0.903939735	0.082176573	NA	NA	0.634977689	0.717940902	0.811038887	0.959192298	specific_fp14
OG0003896	0	7.537232977	5.386281714	11.43202613	5.644101429	0	0	0	1.085719526	0.067454227	NA	NA	0.770177257	0.630078669	0.900355814	0.942642691	specific_fp14
OG0003897	0	7.390831302	5.505036619	10.9820498	5.352747143	0	0	0	0.996323293	−0.040472657	NA	NA	0.518913942	0.536905841	0.736867357	0.915901312	specific_fp14
OG0003898	0	6.30279393	5.188847095	8.84359	4.200071429	0	0	0	0.769218118	−0.03500016	NA	NA	0.660086409	0.37052313	0.830043404	0.863672559	specific_fp14
OG0003899	0	6.653470326	4.888676286	9.742453467	5.328602857	0	0	0	0.994841258	0.124313435	NA	NA	0.661230751	0.587943793	0.831030495	0.939271229	specific_fp14
OG0003900	0	15.578892	10.37305381	23.5525884	14.10991429	0	0	0	1.183044935	0.44386854	NA	NA	1	0.898206191	1	0.996172645	specific_fp14
OG0003901	0	6.637453535	4.788887476	9.500443	6.048174286	0	0	0	0.98830425	0.336809176	NA	NA	0.714977939	0.630078669	0.869288372	0.942642691	specific_fp14
OG0003902	0	7.12909493	5.250541048	11.92883	2.47961	0	0	0	1.183914548	−1.082352867	NA	NA	0.464518769	0.834245362	0.6892569	0.987043838	specific_fp14
OG0003903	0	8.485488326	5.963471952	13.19060067	5.969153857	0	0	0	1.145285841	0.001373923	NA	NA	0.688014554	0.687457524	0.851959119	0.957796671	specific_fp14
OG0003904	0	13.45026674	9.923951429	19.07550667	11.97512714	0	0	0	0.942734798	0.271054394	NA	NA	0.716374834	0.642503534	0.870300396	0.944136873	specific_fp14
OG0003905	0	20.19123023	16.98315238	34.10511333	0	0	0	0	1.005883783	#NAME?	NA	NA	1	0.323219522	1	0.834697703	specific_fp14
OG0003906	0	5.225278767	3.97986319	7.816437333	3.409042857	0	0	0	0.973792351	−0.223352102	NA	NA	0.431435689	0.37052313	0.665622479	0.863672559	specific_fp14
OG0003907	0	8.092778767	5.875980095	11.72159433	6.967141429	0	0	0	0.9962674	0.245737341	NA	NA	0.927258428	0.733544565	0.974675052	0.973934811	specific_fp14
OG0003908	0	10.50411728	7.395538714	15.85499333	8.36369	0	0	0	1.100210124	0.177484348	NA	NA	0.291518641	0.898206191	0.536071185	0.996172645	specific_fp14
OG0003909	0	0.390912558	0.562339048	0.333341333	0	0	0	0	−0.75444001	#NAME?	NA	NA	0.517774898	0.323219522	0.735717726	0.834697703	specific_fp14
OG0003910	0	2.249292791	1.547574286	2.743255333	3.295957143	0	0	0	0.825880247	1.090688821	NA	NA	0.899276375	0.767510812	0.961653927	0.980589573	specific_fp14
OG0003911	0	2.208784419	1.431854762	0.946485333	7.2445	0	0	0	−0.597233107	2.339000959	NA	NA	0.429867808	0.767510812	0.665047154	0.980589573	specific_fp14
OG0003912	0	8.412495977	2.073915095	11.010126	21.86188857	0	0	0	2.408402242	3.397898298	NA	NA	0.503669852	0.867906725	0.72143331	0.998085231	specific_fp14
OG0003913	0	64.36487395	50.22887524	98.2644	34.13102857	0	0	0	0.968151871	−0.557433077	NA	NA	0.625820746	0.847827158	0.808271698	0.998085231	specific_fp14
OG0003914	0	13.64022605	12.99210476	15.51173333	11.57421714	0	0	0	0.255724736	−0.166720555	NA	NA	0.556545025	0.474649843	0.763253857	0.895160802	specific_fp14
OG0003915	0	3.108592093	0.613293333	7.033266667	2.184471429	0	0	0	3.519545745	1.832635063	NA	NA	0.556545025	0.930545821	0.763253857	1	specific_fp14
OG0003916	0	4.485182093	1.964425238	9.396131333	1.52399	0	0	0	2.257959616	−0.366253827	NA	NA	0.621135528	0.474649843	0.803342231	0.895160802	specific_fp14
OG0003917	0	5.052892093	1.55018381	10.28918667	4.340385714	0	0	0	2.73061775	1.485383965	NA	NA	1	0.930545821	1	1	specific_fp14
OG0003918	0	30.8917107	19.43862905	48.20240333	28.15661429	0	0	0	1.310178607	0.534547393	NA	NA	0.455508279	0.673452718	0.684256882	0.951961856	specific_fp14
OG0003919	0	5.318610465	8.099633333	3.907196667	0	0	0	0	−1.051722725	#NAME?	NA	NA	0.962962468	0.239341328	0.992357712	0.793831443	specific_fp14
OG0003920	0	12.34076884	8.523637143	19.09610933	9.316434286	0	0	0	1.163737649	0.128308714	NA	NA	0.970235302	0.687457524	0.994521172	0.957796671	specific_fp14
OG0003921	0	5.349103488	1.979062857	10.21553533	5.031157143	0	0	0	2.367875469	1.346072817	NA	NA	0.791379234	0.767510812	0.912626558	0.980589573	specific_fp14
OG0003922	0	18.66852512	12.73611048	27.88535333	16.71542286	0	0	0	1.130582796	0.392255097	NA	NA	0.478905805	0.780612619	0.703860076	0.980589573	specific_fp14
OG0003923	0	9.929005349	18.59317762	2.23723	0.418864286	0	0	0	−3.054987865	−5.472146663	NA	NA	0.275746652	0.200799534	0.518636952	0.782207757	specific_fp14
OG0003924	0	18.7909673	11.98115714	29.77402627	15.68527143	0	0	0	1.313287076	0.388643244	NA	NA	0.940512011	0.828498832	0.982645549	0.987043838	specific_fp14
OG0003925	0	4.504675814	2.849051429	7.368505333	3.334771429	0	0	0	1.370890341	0.227106216	NA	NA	0.64256877	0.576826376	0.818023827	0.932231154	specific_fp14
OG0003926	0	12.85148788	9.030865238	19.45423327	10.16461571	0	0	0	1.107147999	0.170619551	NA	NA	1	0.687457524	1	0.957796671	specific_fp14
OG0003927	0	20.05006256	18.58710762	26.18693933	11.28847714	0	0	0	0.494545164	−0.719451412	NA	NA	0.910871362	0.687457524	0.970463038	0.957796671	specific_fp14
OG0003928	0	1.054193256	0.271787143	2.200898667	0.944185714	0	0	0	3.017543608	1.796593445	NA	NA	0.659223296	0.692735596	0.829743238	0.958503833	specific_fp14
OG0003929	0	1.57690186	0.171777619	3.619033333	1.416278571	0	0	0	4.396990411	3.043491076	NA	NA	0.659223296	0.692735596	0.829743238	0.958503833	specific_fp14
OG0003930	0	2.16630186	0.520753333	4.923157333	1.1954	0	0	0	3.240911772	1.198821374	NA	NA	0.659223296	0.692735596	0.829743238	0.958503833	specific_fp14
OG0003931	0	0.853161651	0.095076714	1.772586667	1.15722	0	0	0	4.22062031	3.605427305	NA	NA	0.840868769	0.692735596	0.937013432	0.958503833	specific_fp14
OG0003932	0	0.768781628	0.1266	1.712147333	0.673828571	0	0	0	3.757457544	2.412104198	NA	NA	0.659223296	0.692735596	0.829743238	0.958503833	specific_fp14
OG0003933	0	5.404645884	2.211102048	10.14220867	4.833357143	0	0	0	2.197534346	1.128259991	NA	NA	0.767731966	0.711724872	0.898699151	0.958503833	specific_fp14
OG0003934	0	11.72858316	8.914632381	14.55758907	14.10828	0	0	0	0.707524235	0.662294903	NA	NA	0.822851427	0.687457524	0.924484186	0.957796671	specific_fp14
OG0003935	0	4.594925349	1.583856667	10.95472	0	0	0	0	2.790038922	#NAME?	NA	NA	0.748015584	0.239341328	0.885854961	0.793831443	specific_fp14
OG0003936	0	6.157873953	0.968855238	16.08687933	0.44849	0	0	0	4.053459556	−1.111205303	NA	NA	0.957447423	1	0.989319556	1	specific_fp14
OG0003937	0	2.466562791	3.4361	2.260273333	0	0	0	0	−0.604274776	#NAME?	NA	NA	0.336840379	0.239341328	0.586892051	0.793831443	specific_fp14
OG0003938	0	0.910329767	0.985539048	0.560762	1.433775714	0	0	0	−0.813524444	0.540834423	NA	NA	0.915015792	0.474649843	0.9733491	0.895160802	specific_fp14
OG0003939	0	2.761329535	5.005081905	0.45984	0.961835714	0	0	0	−3.444189806	−2.379531276	NA	NA	0.480451083	1	0.703860076	1	specific_fp14
OG0003940	0	3.924432116	3.25319719	5.782802667	1.955914286	0	0	0	0.829910599	−0.734015125	NA	NA	0.688014554	0.337328199	0.851959119	0.847858149	specific_fp14
OG0003941	7.87709	30.29243163	34.91463571	20.34814733	37.735	8.33045	6.95891	0	−0.778934475	0.112071354	−0.259533081	#NAME?	0.548783668	0.82505324	0.756745518	0.987043838	specific_fp14
OG0003943	38.7573	93.3091984	99.44280433	85.51446333	91.61138429	20.5655	47.9558	51.5783	−0.217698533	−0.118340093	1.221479164	1.326538075	0.44611522	0.466438634	0.67383504	0.892687029	specific_fp14
OG0003944	35.058	107.7728251	117.7558952	93.90452533	107.5414	26.629	52.0257	73.251	−0.326532698	−0.130907129	0.966226219	1.459850203	0.657256698	0.404628222	0.828964338	0.879709358	specific_fp14
OG0003945	31.0716	88.85988326	98.49359619	78.66195867	81.81144	21.3314	42.3172	51.7702	−0.324363818	−0.267727332	0.988265518	1.279143237	0.751396543	0.499119962	0.885854961	0.895160802	specific_fp14
OG0003946	0	6.677528814	6.19830819	5.7536238	10.09498714	0	0	2.77933	−0.107403596	0.703692678	NA	Inf	0.898297293	0.184797844	0.961653927	0.766351369	specific_fp14
OG0003947	0.462371	5.366360379	6.427132852	3.296076927	6.620364643	1.27119	0	1.79732	−0.96342538	0.042735387	#NAME?	0.499667613	0.114659637	0.769358107	0.325315857	0.980589573	specific_fp14
OG0003948	0.642424	6.465601551	7.670636795	3.862011333	8.429617714	0.712757	0	2.39721	−0.989993953	0.136120855	#NAME?	1.749874089	0.257404488	0.829146551	0.49811538	0.987043838	specific_fp14
OG0003949	0	5.640707512	7.685872857	5.4098062	0	1.2771	0	0	−0.506632199	#NAME?	#NAME?	#NAME?	0.364430704	0.009470242	0.61135002	0.551400211	specific_fp14
OG0003950	0	0.919301837	1.138569952	0.851044667	0.407762857	0	0	0	−0.419916174	−1.481420659	NA	NA	0.813416237	0.387119234	0.924336633	0.879709358	specific_fp14
OG0003951	0	14.74865674	14.45526857	15.49362667	14.03245714	0	0	0	0.100079469	−0.04282776	NA	NA	0.747066198	0.856676809	0.885854961	0.989805231	specific_fp14
OG0003952	0	14.10916698	23.34585714	4.852425333	6.234971429	0	0	0	−2.266388639	−1.904711704	NA	NA	0.555155156	0.657441267	0.762575763	0.951961856	specific_fp14
OG0003953	0	7.166601442	10.26989	4.54104	3.482938857	0	0	0	−1.177326079	−1.560043677	NA	NA	0.559027851	0.859957553	0.766075203	0.989805231	specific_fp14
OG0003954	0	9.383341628	13.00592429	6.12099	5.506347143	0	0	0	−1.087332014	−1.240001459	NA	NA	0.634977689	0.54716072	0.811038887	0.923650038	specific_fp14
OG0003955	0	4.385008605	7.33293	2.304256	0	0	0	0	−1.67008876	#NAME?	NA	NA	0.939032539	0.094115052	0.982645549	0.726019928	specific_fp14
OG0003956	0	16.45540977	27.04629095	6.692620667	5.603028571	0	0	0	−2.01478761	−2.271152006	NA	NA	0.465171623	0.47003372	0.6892569	0.895160802	specific_fp14
OG0003957	0	14.20363279	19.65609048	8.42152	10.23650143	0	0	0	−1.22282385	−0.94125368	NA	NA	0.848357367	0.852695307	0.937013432	0.989805231	specific_fp14
OG0003958	0	9.092676977	12.27999905	5.94744	6.270504286	0	0	0	−1.045969731	−0.969657072	NA	NA	0.737007695	0.904163098	0.88117266	0.996172645	specific_fp14
OG0003959	0	7.123663488	11.87052524	1.840666667	4.203785714	0	0	0	−2.689083479	−1.497622736	NA	NA	0.486087467	0.711724872	0.707189221	0.958503833	specific_fp14
OG0003960	0	17.86083302	24.03935048	13.31254	9.071622857	0	0	0	−0.852612056	−1.405965348	NA	NA	0.910871362	1	0.970463038	1	specific_fp14
OG0003961	0	15.44919651	23.5325481	10.569876	1.654828571	0	0	0	−1.154699092	−3.829903867	NA	NA	0.752993315	0.815881646	0.887059114	0.987043838	specific_fp14
OG0003962	5.12623	13.44531367	11.62482785	13.19530333	19.44250759	5.24933	4.86247	3.83875	0.182815164	0.74200495	−0.110443947	−0.451496688	0.974369358	0.710308715	0.994521172	0.958503833	specific_fp14
OG0003963	0	33.24450395	45.47490667	27.00381333	9.926204286	0	0	0	−0.751907526	−2.195756626	NA	NA	0.848357367	0.756965909	0.937013432	0.974688545	specific_fp14
OG0003964	0	30.25993721	43.28286667	19.12821333	15.04484286	0	0	0	−1.178093928	−1.524527016	NA	NA	1	0.856676809	1	0.989805231	specific_fp14

OG0003965	0	0.669917907	1.371736667	0	0	0	0	0	#NAME?	#NAME?	NA	NA	0.140911852	0.323219522	0.358192386	0.834697703	specific_fp14
OG0003966	0	25.57118209	36.08717714	16.49036667	13.48208714	0	0	0	−1.129862818	−1.42044244	NA	NA	0.765317467	0.95199474	0.896553517	1	specific_fp14
OG0003967	3.5588	45.81957512	56.11836905	38.545232	30.51107143	3.5588	8.31168	0	−0.541920669	−0.879140238	1.223749254	#NAME?	0.683998017	1	0.848575865	1	specific_fp14
OG0003968	11.3476	38.07173047	35.37853571	41.63106067	38.52417857	6.65927	11.3476	22.6672	0.234785978	0.122889858	0.768951261	1.767170251	0.648590233	0.705695457	0.824328065	0.958503833	specific_fp14
OG0003969	0	0.463367442	0.9488	0	0	0	0	0	#NAME?	#NAME?	NA	NA	0.430222691	0.620690717	0.665047154	0.942642691	specific_fp14
OG0003970	0	0.274937209	0.562966667	0	0	0	0	0	#NAME?	#NAME?	NA	NA	0.430222691	0.620690717	0.665047154	0.942642691	specific_fp14
OG0003971	0	5.40464186	8.704138095	3.307513333	0	0	0	0	−1.395554473	#NAME?	NA	NA	0.791324196	0.44006229	0.912626558	0.888199117	specific_fp14
OG0003972	0	4.328590698	6.40937619	3.4355	0	0	0	0	−0.899663867	#NAME?	NA	NA	0.836952327	0.44006229	0.93500109	0.888199117	specific_fp14
OG0003973	0	5.281232558	5.52897619	7.398966667	0	0	0	0	0.42031144	#NAME?	NA	NA	1	0.323219522	1	0.834697703	specific_fp14
OG0003974	0	0.277274419	0.567752381	0	0	0	0	0	#NAME?	#NAME?	NA	NA	0.430222691	0.620690717	0.665047154	0.942642691	specific_fp14
OG0003975	0	0.297972093	0.610133333	0	0	0	0	0	#NAME?	#NAME?	NA	NA	0.430222691	0.620690717	0.665047154	0.942642691	specific_fp14
OG0002304	0	9.394132084	19.1243732	0.069488053	0.1847888	0	0	0	−8.104431784	−6.693391336	NA	NA	0.040803928	0.680584397	0.230808539	0.954264011	specific_fp14
OG0003976	0	28.45798279	32.54599524	33.12623467	6.190548571	0	1.02056	0	0.025494195	−2.394340868	Inf	NA	0.728315819	0.517694468	0.874813882	0.910532643	specific_fp14
OG0003977	0	2.761002326	1.796867143	3.133919333	4.8543	0	0	0	0.802484303	1.433779529	NA	NA	0.546061402	0.767510812	0.754420397	0.980589573	specific_fp14
OG0003978	14.8902	29.64460581	41.24354286	12.06739	32.51325714	25.7074	0	0	−1.773054591	−0.343140176	#NAME?	#NAME?	0.07205803	0.44355419	0.261777809	0.892517578	specific_fp14
OG0003979	0	0.980204651	0.812138095	1.672926667	0	0	0	0	1.042577238	#NAME?	NA	NA	0.808441869	0.620690717	0.920040267	0.942642691	specific_fp14
OG0003980	0	20.73706535	19.35428095	25.31056	15.08507286	0	0	0	0.387086718	−0.359531045	NA	NA	0.962962468	0.739446455	0.992357712	0.973934811	specific_fp14
OG0003981	0	10.13165521	12.25675367	6.271323933	12.02849829	0	0	0.32498	−0.96673497	−0.027120378	NA	Inf	0.221197909	0.576067305	0.466715479	0.932231154	specific_fp14
OG0003982	0	18.104388	22.75281	9.460744933	22.68121429	0	0	0	−1.266019041	−0.004546851	NA	NA	0.371340323	0.948999012	0.618244672	1	specific_fp14
OG0003983	49.8668	91.71247165	86.95037386	109.8955587	67.03500714	48.3533	66.1443	29.5709	0.337868946	−0.375277531	0.452002484	−0.709436201	0.563451914	0.558941703	0.76696918	0.923650038	specific_fp14
OG0003984	3.2556	140.4175416	110.8260476	196.6320593	108.7323429	0	3.62318	12.4904	0.827201561	−0.027515861	Inf	Inf	0.197441085	0.41954703	0.435255014	0.888199117	specific_fp14
OG0003985	1.00961	50.13607084	36.94479605	73.6918674	39.23318829	0	1.07618	6.89961	0.996134249	0.086703417	Inf	Inf	0.23307403	0.263448836	0.478332881	0.811609317	specific_fp14
OG0003986	0	1.797382977	1.502233333	3.0493712	0	0	0	0	1.021402864	#NAME?	NA	NA	0.38426935	0.620690717	0.631124199	0.942642691	specific_fp14
OG0003987	0	5.378511163	10.15290381	1.204333333	0	0	0	0	−3.075585749	#NAME?	NA	NA	0.033797161	0.032734395	0.222954936	0.599096931	specific_fp14
OG0003989	83.4123	112.4453551	112.20699	101.57668	136.4504686	46.822	94.7813	102.328	−0.143593326	0.282214797	1.017415888	1.127942498	0.746406843	0.872070479	0.885854961	0.989805231	specific_fp14
OG0003990	22.994	29.89689419	31.80174971	26.4149744	31.64358429	17.2844	23.1543	24.6455	−0.267750132	−0.00719312	0.421809619	0.511853727	0.897078863	0.914509149	0.961653927	0.996172645	specific_fp14
OG0003991	20.8746	28.23655326	28.85964619	25.98585133	31.19020714	13.0541	21.1118	20.8746	−0.151327288	0.112039521	0.693546593	0.677245557	0.795863119	0.957193011	0.912626558	1	specific_fp14
OG0003992	19.5054	40.71297137	57.15403619	17.1139686	41.95906857	27.7946	19.5054	12.0256	−1.739681036	−0.445872732	−0.510931036	−1.208695743	0.157459987	0.632818278	0.382374682	0.942642691	specific_fp14
OG0003993	0	22.05268498	26.82627333	23.71657427	4.166442857	0	0	0	−0.177751016	−2.686758553	NA	NA	0.583352808	0.815881646	0.781948365	0.987043838	specific_fp14
OG0003994	0	12.71437553	23.14120952	4.0501832	0	0	0	0	−2.514405201	#NAME?	NA	NA	0.455064321	0.44006229	0.684256882	0.888199117	specific_fp14
OG0001677	111.442698	123.2708955	133.9909607	94.21270872	153.3782433	121.5052	91.92631	131.29069	−0.508142088	0.194958175	−0.402468322	0.111746559	0.089167183	0.404628222	0.283825342	0.879709358	specific_fp360
OG0000713	108.05752	111.9417142	132.4272127	85.29910267	107.5765291	119.06099	78.9124	94.4941	−0.634597145	−0.299836267	−0.593414545	−0.333442309	0.01618207	0.249489882	0.212118871	0.793831443	specific_fp360
OG0000772	503.703879	509.4407548	558.2949468	427.879055	537.6532497	547.55316	446.017084	524.7799	−0.383824438	−0.054351467	−0.295900066	−0.061286574	0.019476603	0.835782575	0.212118871	0.987043838	specific_fp360
OG0000046	103.032818	118.1580778	147.3296271	104.7225514	59.43384363	148.626734	75.92148	58.0895416	−0.492475426	−1.309690988	−0.96911362	−1.355343291	0.159894624	0.006998074	0.382374682	0.551400211	specific_fp360
OG0000222	95.93462	112.637159	134.8235195	90.39458641	93.74073291	122.45492	83.79136	70.58773	−0.576763912	−0.524324212	−0.547377344	−0.794761408	0.038886485	0.15527516	0.225988841	0.750388324	specific_fp360
OG0000224	190.64541	192.2221509	183.7120196	170.9570455	263.3206277	191.3484	182.052964	243.964944	−0.103812139	0.519374523	−0.071843608	0.35047202	0.293709056	0.031465153	0.536071185	0.586871465	specific_fp360
OG0002383	135.0247	141.5017934	123.0365246	129.803204	221.9660057	118.361554	135.0247	216.63437	0.077239337	0.851252086	0.1900228	0.872061608	0.82453995	0.010122969	0.924484186	0.551400211	specific_fp360
OG0000176	325.164932	305.7417852	313.5730948	253.612554	393.9533516	325.164932	244.01753	359.340378	−0.306175617	0.32922303	−0.414186882	0.14417938	0.083138871	0.171669876	0.273483129	0.766351369	specific_fp360
OG0002283	93.3793	105.8047667	110.2962838	96.828164	111.5657929	81.8909	93.3793	105.7386	−0.187885539	0.016510568	0.18939963	0.368727082	0.899199214	0.567784872	0.961653927	0.923650038	specific_fp360
OG0002063	339.424048	319.1383703	331.4812997	274.6986794	377.3374914	349.288802	288.28656	411.20767	−0.271077509	0.186927967	−0.276916812	0.235446783	0.095532467	0.189265565	0.293775041	0.766351369	specific_fp360
OG0002294	52.4155	58.46093246	59.25758048	42.84211037	89.53989286	43.3331	42.303012	89.9459	−0.467970173	0.595530871	−0.034709061	1.053588072	0.279179577	0.05474984	0.521346141	0.657803345	specific_fp360
OG0002295	124.353	154.8102996	141.6629916	120.6238801	267.5088371	105.465	112.252	234.67423	−0.231947366	0.917123638	0.089976849	1.153895125	0.849288715	0.003846154	0.937013432	0.551400211	specific_fp360
OG0002071	41.8632	44.6276622	48.332123	50.51927073	20.8894044	48.50562	43.89596	14.3719	0.063851446	−1.210211008	−0.144063745	−1.75490111	0.822168743	0.167697552	0.924484186	0.766351369	specific_fp360
OG0001963	55.08391	60.24297129	66.45647628	60.54921852	40.94621229	56.3070728	55.08391	52.431798	−0.134301459	−0.698679797	−0.031685183	−0.102874133	0.924313351	0.189265565	0.9733941	0.766351369	specific_fp360
OG0004018	45.4565	63.13714816	49.88763719	47.56297267	136.2589143	46.7181	38.7321	141.368	−0.068834455	1.44959637	−0.270451877	1.597402082	0.822270056	0.012632521	0.924484186	0.551400211	specific_fp360
OG0003543	34.921	41.08431202	43.91636746	36.86377667	41.63215	37.01322	32.3583	30.2576	−0.252554845	−0.077060662	−0.193904834	−0.290743091	0.505237295	0.835782575	0.72143331	0.987043838	specific_fp360
OG0003544	109.72501	112.7476333	122.605341	97.46756867	115.9175057	116.96233	94.4539	101.683	−0.331027665	−0.080923371	−0.308361685	−0.201965456	0.505237295	0.958683828	0.72143331	1	specific_fp360
OG0003545	22.05181	32.52882721	37.43118333	23.908128	36.29468571	22.7182	20.3875	42.4267	−0.646739486	−0.044482334	−0.156163655	0.901123936	0.606861521	0.524112796	0.794841852	0.910532643	specific_fp360
OG0004019	9.92805	67.34538023	76.65691095	41.088388	95.67577143	7.84757	8.47053	21.7403	−0.899685132	0.319737765	0.110206249	1.470053951	0.434663163	0.70820366	0.668545769	0.958503833	specific_fp360
OG0004020	3.06736	17.70935942	12.71428214	20.29559933	27.14407714	0.993825	3.06736	9.81104	0.675001243	1.094187427	1.625933759	3.303342336	0.762409457	0.538520259	0.894506275	0.917052561	specific_fp360
OG0004021	16.6993	78.20649163	91.47824571	71.77910467	52.16420143	15.4072	27.0645	16.6993	−0.349864771	−0.810368627	0.812797035	0.116182929	0.847137033	0.749567537	0.937013432	0.973934811	specific_fp360
OG0004022	62.1798	89.11964451	72.22685019	65.50307067	190.4049714	61.4316	54.8052	218.251	−0.140972717	1.398463987	−0.164668174	1.8289354	0.974400707	0.012632521	0.994521172	0.551400211	specific_fp360
OG0004023	9.87634	45.19792435	29.57497043	67.82722467	43.57542829	8.34735	20.1716	35.2678	1.197487736	0.559138118	1.272935354	2.078961415	0.335114519	0.506621831	0.585739457	0.903067463	specific_fp360
OG0004024	0	3.296242093	2.613841905	0.473789333	11.39155571	0	0	2.19417	−2.46385426	2.123720996	NA	Inf	0.084171452	0.427237991	0.276682989	0.888199117	specific_fp360
OG0004025	2.15364	11.68452347	5.771697429	13.8304502	24.82458714	1.28906	0.86762	13.4803	1.260780543	2.104702148	−0.571184201	3.386461282	1	0.038777504	1	0.629437975	specific_fp360
OG0004026	4.89783	21.81549512	12.72992286	19.87186133	53.23714143	4.89783	2.49065	9.7629	0.642503335	2.064209431	−0.9756204	0.995167054	0.527089257	0.363381407	0.73872358	0.863672559	specific_fp360
OG0004027	2.31186	11.98902102	6.481307143	10.7176776	31.23647	1.97049	1.42131	12.2439	0.725635615	2.268874717	−0.471333175	2.635436834	0.534467797	0.042178982	0.746264283	0.632684734	specific_fp360
OG0004028	0	6.855822093	3.490152381	6.74641	17.18728571	0	0	9.79507	0.950829972	2.299979795	NA	Inf	0.770177257	0.053865069	0.900355834	0.657803345	specific_fp360
OG0004029	9.37053	30.63046884	18.10576333	26.83134867	76.34555714	9.37053	5.16281	58.6431	0.567470571	2.076095202	−0.859974144	2.645758815	0.596719138	0.023459901	0.788870461	0.569641228	specific_fp360
OG0004030	5.45086	11.10382177	7.159393333	14.80861307	14.99826857	4.65766	8.16873	7.24094	1.04852728	1.066886715	0.810506469	0.636571667	0.289031101	0.352500644	0.534921505	0.856231849	specific_fp360
OG0002949	125.24186	162.9870592	134.4739735	127.1187527	325.3869729	118.1087	100.7792	387.6931	−0.081150103	1.274829516	−0.22891733	1.71479982	0.874183012	0.014333975	0.948638299	0.551400211	specific_fp360
OG0004031	30.3583	43.49716465	34.73484762	32.77741867	92.755	29.7049	24.3886	98.6922	−0.083681527	1.417041285	−0.284493988	1.732235136	0.724049268	0.0125961	0.8743474	0.551400211	specific_fp360
OG0003549	42.9449	51.33022525	43.69153246	38.141169	102.508567	42.9449	29.4009	115.219	−0.196004647	1.230318872	−0.546626493	1.423819925	0.727457037	0.006998074	0.8743474	0.551400211	specific_fp360
OG0004032	0	2.099502093	3.655880476	0.538791333	0.774747143	0	0	0	−2.762420355	−2.23842147	NA	NA	0.603793006	0.750675769	0.794841852	0.973934811	specific_fp360
OG0004033	0	0.300509767	0.497383333	0.165124667	0	0	0	0	−1.590802516	#NAME?	NA	NA	0.737898749	0.44006229	0.88117266	0.888199117	specific_fp360
OG0004034	18.4753	67.47091023	51.50839619	70.153148	109.6108	21.1288	14.5356	72.7413	0.445700224	1.08951043	−0.539620208	1.783563877	0.782789446	0.505157462	0.908051464	0.903067463	specific_fp360
OG0003552	36.83286	47.41273319	39.19736271	36.892056	94.60315286	36.83286	28.71002	115.712	−0.087446397	1.271131675	−0.359439088	1.651473159	0.799959914	0.014333975	0.912626558	0.551400211	specific_fp360
OG0004035	4.68852	9.215138837	9.206010952	8.384729333	11.02197143	6.77303	3.47005	5.17247	−0.134811946	0.259734228	−0.964844935	−0.388948013	0.434663163	0.893972439	0.668545769	0.996172645	specific_fp360
OG0004036	4.20377	12.63609993	12.11929576	11.9822224	15.58767857	4.48828	3.01174	6.02565	−0.016410351	0.36310022	−0.575565452	0.424954196	0.685168656	0.539820057	0.849662131	0.91892729	specific_fp360
OG0003553	91.7971	116.1360855	103.1995904	88.0676224	215.0922771	91.7971	74.60967	255.552	−0.228753623	1.059518481	−0.29908595	1.477096399	0.568137602	0.019899666	0.76696918	0.56402733	specific_fp360
OG0004037	30.2604	41.08634568	33.09588543	30.32714467	88.11315714	25.8741	24.579	94.3027	−0.126042196	1.412705591	−0.07408246	1.865790397	0.974400707	0.010864488	0.994521172	0.551400211	specific_fp360
OG0003212	85.8776	132.9904823	127.0156528	103.1470693	214.8651414	80.2348	104.33288	215.7839	−0.300303467	0.758425148	0.378893875	1.427287214	0.293709056	0.272117496	0.536071185	0.811609317	specific_fp360
OG0004038	19.7378	38.25736558	23.55794667	24.643676	111.5278143	18.4875	12.8874	89.5404	0.065003675	2.24311785	−0.520588914	2.275988616	0.897504334	0.020391723	0.961653927	0.569641228	specific_fp360
OG0004039	118.391	153.0858174	122.2335652	142.6147587	268.0805571	90.1362	137.559	292.284	0.222482786	1.133026088	0.609871998	1.697192322	0.422326539	0.022451016	0.684063444	0.569641228	specific_fp360
OG0004040	57.6295	78.98258984	57.38893014	65.208082	173.2803714	45.7902	53.0951	168.245	0.184278306	1.594263856	0.213539858	1.877452859	0.676559184	0.010864488	0.844102031	0.551400211	specific_fp360
OG0004041	0	2.820000698	4.693138571	0.910152667	1.293118571	0	0	0	−2.366372594	−1.859698491	NA	NA	0.457492859	0.657441267	0.686090944	0.951961856	specific_fp360
OG0004042	0	7.492632698	7.233745714	4.255125067	15.20681	0	0	0	−0.765541348	1.071902755	NA	NA	0.724318329	0.727264628	0.8743474	0.970526454	specific_fp360
OG0004043	0	9.619668605	6.711792857	5.671438	26.80379	0	0	0	−0.242983613	1.997666913	NA	NA	1	0.630941086	1	0.942642691	specific_fp360
OG0004044	0	2.945936047	4.98284381	0.916328	1.184372857	0	0	0	−2.443033343	−2.072846019	NA	NA	0.377619692	0.505939882	0.621969757	0.903067463	specific_fp360
OG0004045	116.291	140.9418256	118.4671714	114.20864	265.6511857	104.082	115.325	326.415	−0.052815531	1.165045825	0.147984703	1.648986766	0.923292653	0.17548821	0.9733491	0.766351369	specific_fp360
OG0004046	7.01962	12.47351233	8.385708571	12.39611067	24.90278429	7.01962	5.36356	14.8842	0.563882942	1.570302455	−0.388202043	1.084316842	1	0.150876199	1	0.750388324	specific_fp360
OG0004047	19.6014	30.74048043	26.40445803	17.999256	71.05117143	20.37	14.4016	50.9474	−0.552844256	1.428076906	−0.500216878	1.322562543	0.274976326	0.007974357	0.517921977	0.551400211	specific_fp360
OG0004048	91.8664	123.5572547	107.9016381	96.78653667	227.8899286	91.8664	83.2951	216.413	−0.156838484	1.0786204	−0.141305666	1.236177965	0.70018293	0.016947799	0.859961416	0.551400211	specific_fp360
OG0004049	34.8024	42.42252023	36.08937286	30.81110933	86.30355714	36.0553	27.6887	94.6685	−0.228123446	1.257845951	−0.380914026	1.392673117	0.563527243	0.012632521	0.76696918	0.551400211	specific_fp360
OG0004050	36.653	46.27845651	40.18313952	34.62808	89.5295	40.5545	33.3595	95.9602	−0.214647889	1.155772842	−0.281764342	1.242574157	0.589884939	0.012075606	0.781948365	0.551400211	specific_fp360
OG0004051	68.8808	87.98869023	71.64002476	68.097024	179.6596857	66.2177	62.9246	171.536	−0.073174086	1.326428974	−0.073592761	1.373222578	0.82453995	0.006998074	0.924484186	0.551400211	specific_fp360
OG0004052	21.0866	64.06837442	43.23612381	87.81917333	75.67055714	16.9828	15.2571	50.357	1.022298765	0.807494879	−0.154593572	1.568117998	0.771018624	0.350842883	0.900355834	0.854001116	specific_fp360
OG0004053	23.7547	43.11002509	24.4318809	34.34976533	117.9164429	17.1265	30.7336	94.6892	0.491535308	2.270928069	0.843586418	2.466969535	0.44094788	0.004918205	0.67383504	0.551400211	specific_fp360
OG0004054	0	1.534894186	1.288475714	1.634646667	2.060394286	0	0	0	0.343313482	0.677255099	NA	NA	0.52909389	0.405674265	0.741308465	0.879975196	specific_fp360
OG0004055	27.7314	37.27777233	28.87809571	29.68521333	78.74657143	24.8358	24.9674	88.7723	0.03976887	1.4472415	0.007624374	1.837688358	0.897846171	0.014610022	0.961653927	0.551400211	specific_fp360
OG0004056	40.7587	71.83103372	48.21801762	89.474132	104.8634429	28.2616	46.9722	85.9189	0.891898304	1.120867574	0.732964021	1.604132378	0.478646962	0.312097529	0.703860076	0.834697703	specific_fp360
OG0004057	8.52525	12.32723581	10.21107	10.347968	22.91702143	8.21892	5.21613	16.0573	0.019213446	1.166285495	−0.655969004	0.966208592	0.772459737	0.038423313	0.900355834	0.629437975	specific_fp360
OG0004058	29.2555	38.2499034	33.91000267	27.518166	74.26618571	26.4303	26.2632	78.4065	−0.301326576	1.130994586	−0.009150091	1.56878046	0.568137602	0.008438904	0.76696918	0.551400211	specific_fp360
OG0004059	35.8275	46.72061186	39.39506333	34.66823867	94.52377143	33.0354	33.3294	93.8126	−0.184400313	1.262662339	0.012782533	1.505768891	0.775571382	0.008438904	0.900355834	0.551400211	specific_fp360
OG0004060	47.0687	58.65674744	50.78122381	43.523156	114.7124429	37.9453	45.3132	103.65	−0.222511989	1.17565482	0.256010176	1.449727	0.948827759	0.003517549	0.982645549	0.551400211	specific_fp360
OG0004061	32.627	39.36009209	31.81666571	30.872032	80.17907143	28.805	27.4262	83.1927	−0.043482209	1.333443056	−0.070764512	1.530137682	0.936022389	0.007948639	0.980805306	0.551400211	specific_fp360
OG0004063	3.15209	8.208521628	4.202465714	16.06257733	3.39657	3.15209	2.57216	3.54134	1.934395446	−0.307157462	−0.29332834	0.167986634	0.540670011	0.849281295	0.752512429	0.989805231	specific_fp360
OG0004064	76.5155	87.49229326	104.1581719	92.10986	27.59987143	90.9575	84.2039	28.3864	−0.177348528	−1.916042581	−0.111305547	−1.679992706	0.611998112	0.003109692	0.794841852	0.551400211	specific_fp360
OG0004065	28.5734	36.28867256	41.12769619	40.59477667	12.54423571	38.5271	24.0951	8.45856	−0.018816152	−1.713085686	−0.677133807	−2.187389614	0.799959914	0.006998074	0.912626558	0.551400211	specific_fp360
OG0004066	98.229	126.1551721	108.2537	89.64814	258.0889429	92.7475	61.1	198.953	−0.27207078	1.253451999	−0.602136015	1.101047354	0.797359979	0.014610022	0.912626558	0.551400211	specific_fp360
OG0004067	40.6228	54.17814814	47.71930952	38.12719133	107.9495714	44.7748	33.2934	111.384	−0.32375291	1.177712443	−0.427450779	1.314783115	0.404097301	0.010864488	0.648828314	0.551400211	specific_fp360
OG0004068	0	3.684263721	2.046472381	3.244316	9.540382857	0	0	0	0.66477515	2.220907967	NA	NA	1	0.382222719	1	0.874192556	specific_fp360
OG0004069	0	2.453482023	1.358347952	2.049716667	6.604095714	0	0	0	0.593571414	2.281507944	NA	NA	0.825533669	0.675567129	0.924701676	0.951961856	specific_fp360
OG0004070	27.1646	36.10834972	30.51967943	26.401438	73.67488571	28.212	22.8082	71.8219	−0.209123298	1.271433109	−0.30675635	1.348114874	0.775571382	0.016926793	0.900355834	0.551400211	specific_fp360
OG0004071	24.5667	33.56265844	27.30650205	24.53874467	71.66808571	23.7512	22.4124	73.4761	−0.154183071	1.392086303	−0.08370326	1.629274647	0.874183012	0.012075606	0.948638299	0.551400211	specific_fp360
OG0004072	0	0.398058886	0.513355386	0.3783588	0.094383857	0	0	0	−0.440202921	−2.443345885	NA	NA	0.852644436	0.873767975	0.938700433	0.989805231	specific_fp360
OG0004073	0	0.50057186	0.594131619	0.5614944	0.089344286	0	0	0	−0.081510935	−2.733335204	NA	NA	0.423504686	0.766955903	0.665047154	0.980589573	specific_fp360
OG0004074	0.183937	7.119376977	3.194568714	10.08400847	12.54102	0	1.5454	0	1.658376158	1.972961615	Inf	NA	0.096518368	0.680584397	0.296609601	0.954264011	specific_fp360
OG0003558	0.46934	7.277474419	8.910527571	6.535740067	3.967745714	0.877062	0	0	−0.447160246	−1.167191284	#NAME?	#NAME?	0.401035699	0.47250231	0.646719006	0.895160802	specific_fp360
OG0004075	38.4158	48.91811558	44.60321286	51.70274	55.89577143	32.1205	39.5058	51.1649	0.213093105	0.325591512	0.298570126	0.671660085	0.772687801	0.404628222	0.900355834	0.879709358	specific_fp360
OG0004076	39.776	47.86120302	47.45988333	33.56487933	79.70014143	42.9871	32.831	63.1647	−0.499756098	0.74787373	−0.388845093	0.555214738	0.311042398	0.457367719	0.557153793	0.892687029	specific_fp360
OG0004077	0	5.383706186	8.837999095	3.060092333	0	0	0	0	−1.530144599	#NAME?	NA	NA	0.969493981	0.094115052	0.994521172	0.726019928	specific_fp360
OG0004078	0	2.999756977	5.644912286	0.696426133	0	0	0	0	−3.018908918	#NAME?	NA	NA	0.937292144	0.129742991	0.981874557	0.735188	specific_fp360
OG0004079	0	4.026523721	7.111481429	1.586627333	0	0	0	0	−2.164186818	#NAME?	NA	NA	0.854910545	0.129742991	0.940747387	0.735188	specific_fp360
OG0004080	21.0905	29.50996988	22.1628531	24.914646	61.39844286	15.665	22.1348	50.922	0.16885046	1.470058451	0.498771568	1.700744314	0.319753075	0.049513817	0.56917668	0.657803345	specific_fp360
OG0004081	53.8283	78.2201993	59.64008571	55.77169133	182.0644857	52.5418	50.0195	141.568	−0.096749308	1.610095295	−0.07097499	1.429957665	0.974395765	0.009290942	0.994521172	0.551400211	specific_fp360
OG0004082	37.5935	60.47693023	38.83965714	58.54206	129.5349	27.8775	32.4288	124.875	0.591943047	1.737738479	0.21817445	2.163311584	0.228569312	0.009290942	0.470883327	0.551400211	specific_fp360
OG0004083	38.5367	49.96549279	40.80184286	35.73035267	107.9603143	38.0358	35.3891	111.859	−0.191484161	1.403794862	−0.104052877	1.556251484	0.94881789	0.016902611	0.982645549	0.551400211	specific_fp360
OG0004084	0	15.81287302	5.90453619	26.25295333	23.16628286	0	0	5.78568	2.152584085	1.972130932	NA	Inf	0.370326622	0.303402384	0.617879014	0.834697703	specific_fp360
OG0004085	101.145	136.9430953	102.8291952	106.95986	303.5345857	94.7525	96.9536	264.026	0.05681955	1.561610979	0.03313046	1.478444092	0.784915825	0.01083195	0.909518511	0.551400211	specific_fp360
OG0004086	0.0351709	3.412814233	4.440225467	3.329614813	0.508865	0.069833	0	0	−0.415277647	−3.125278065	#NAME?	#NAME?	0.420137894	0.19843671	0.66273457	0.782207757	specific_fp360
OG0004088	0	0.586289426	0.991921014

OG0004101	4.2475	11.61417886	6.176100952	17.2246594	15.90595429	2.52639	5.10515	9.01691	1.479707216	1.36479869	1.014875985	1.835555756	0.6290568	0.221089193	0.809726376	0.793831443	specific_fp360
OG0004102	5.66256	10.11618216	7.017496667	13.50975933	12.14028757	5.24526	8.21546	6.58518	0.944973596	0.790774217	0.64732707	0.328208589	0.302767383	0.558401346	0.549999664	0.923650038	specific_fp360
OG0004103	38.0064	52.20808047	45.79831429	30.111896	118.7863457	38.0064	33.6825	136.659	−0.604960947	1.375002608	−0.174243155	1.846266192	0.47002925	0.022451016	0.694310214	0.569641228	specific_fp360
OG0004104	3.55541	11.64302116	9.618850952	10.196472	20.81528	1.48785	4.24314	7.45517	0.084133595	1.113706497	1.511903194	2.325012164	0.362061967	0.154903273	0.608922399	0.750388324	specific_fp360
OG0004105	0	13.10635581	8.720524762	20.05998	11.36322571	0	0	0	1.20183331	0.381885578	NA	NA	0.414726992	0.564835117	0.655764902	0.923650038	specific_fp360
OG0004106	22.7504	181.2105235	257.2653776	89.314372	149.9662857	93.2274	0	57.7967	−1.526293064	−0.778619113	#NAME?	−0.689766911	0.053360476	0.914841177	0.239582744	0.996172645	specific_fp360
OG0004107	39.6596	136.7713628	152.5567052	52.46319133	270.0757029	43.5572	15.6636	105.938	−1.539668117	0.824018264	−1.475495387	1.282237056	0.432644642	0.200727376	0.666327496	0.782207757	specific_fp360
OG0004108	0	8.957680233	7.531031429	8.553982667	14.10269286	0	7.57671	0	0.183748818	0.905051295	Inf	NA	0.492748482	1	0.713513378	1	specific_fp360
OG0002963	16.48899	33.32697588	22.62248219	33.7467358	64.54097143	15.81686	23.68699	30.3734	0.576990728	1.512458059	0.582632208	0.941345192	0.490242342	0.232509604	0.710551812	0.793831443	specific_fp360
OG0004109	5.54586	27.15125405	29.00706	34.2607916	6.349112857	9.86817	0.900244	3.90069	0.240154406	−2.191777152	−3.454394585	−1.339053222	0.08270565	0.144005728	0.273483129	0.750063654	specific_fp360
OG0004110	24.5662	31.20307209	26.3279581	36.810512	33.81247143	19.4438	27.0103	31.7196	0.483522181	0.360959835	0.474199464	0.706064378	0.199029103	0.312097529	0.437110372	0.834697703	specific_fp360
OG0004111	7.35093	12.47810209	9.391711905	13.965428	18.55014571	6.46784	7.35093	14.6262	0.57239973	0.981970461	0.184642793	1.1771991	0.385680777	0.20165923	0.631871623	0.782207757	specific_fp360
OG0004112	50.1373	67.54416558	55.78551429	49.78028133	140.8855857	41.847	43.1507	137.731	−0.164316165	1.33656156	0.044259763	1.718657207	0.897865788	0.010864488	0.961653927	0.551400211	specific_fp360
OG0004113	272.153	364.3151442	281.6593	339.3825267	665.7097143	242.466	266.647	526.918	0.268961181	1.240942113	0.137148638	1.119796006	0.422416141	0.010864488	0.664063444	0.551400211	specific_fp360
OG0004115	44.7255	58.67681721	48.49708048	44.107192	120.4366529	44.4127	41.055	107.221	−0.136883983	1.312304714	−0.113414345	1.27154331	0.949501181	0.012075606	0.982645549	0.551400211	specific_fp360
OG0004116	50.9464	67.94712553	53.45380514	53.18105267	143.0686714	43.1664	45.4352	146.074	−0.007380317	1.420343236	0.07390165	1.758718728	1	0.007974357	1	0.551400211	specific_fp360
OG0004117	381.548	651.9595093	558.8044714	627.7522	983.2974286	381.548	266.739	425.993	0.167851615	0.815284305	−0.516435787	0.15896516	1	0.434931252	1	0.888199117	specific_fp360
OG0004118	135.104	314.7313721	255.8712174	278.2851067	569.4108143	135.104	133.462	184.166	0.121145526	1.154051719	−0.01764136	0.446936352	0.634461044	0.466438634	0.810826839	0.892687029	specific_fp360
OG0004119	287.534	470.5049186	376.4124762	527.29632	631.0863857	271.964	287.534	377.835	0.486299481	0.745523054	0.080316866	0.474340655	0.308723468	0.755748117	0.554072968	0.973934811	specific_fp360
OG0004120	164.473	245.456293	212.1624095	226.55584	385.8389143	105.787	189.123	165.153	0.094697615	0.86282959	0.838162478	0.642640829	0.924313351	0.603656971	0.9733491	0.939271229	specific_fp360
OG0004121	186.896	346.8590953	432.0192143	249.1267933	300.8051	277.11	180.325	152.481	−0.794215288	−0.522266451	−0.61985935	−0.861829288	0.180087982	0.296035607	0.41110904	0.825398011	specific_fp360
OG0004122	121.054	333.2232163	358.3083905	224.92476	490.0358143	116.765	139.492	70.1294	−0.671759344	0.451685365	0.256574489	−0.735516605	0.589884939	0.375566704	0.781948365	0.863672559	specific_fp360
OG0004123	18.3595	59.18367651	54.04697381	44.596538	105.8519386	18.3595	15.6794	21.736	−0.277282122	0.969761945	−0.227656416	0.243559702	0.652852621	0.288373038	0.827215143	0.825398011	specific_fp360
OG0004124	17.1598	55.16347079	40.89180281	47.091913	115.27467	16.3939	13.5455	31.1805	0.203667661	1.495191962	−0.275345455	0.92748496	1	0.375566704	1	0.863672559	specific_fp360
OG0004125	24.1863	95.63358542	70.21463586	85.189778	194.2700214	23.8303	24.0093	55.9944	0.278908547	1.468219601	0.010796228	1.232485437	0.849288715	0.228151076	0.937013432	0.793831443	specific_fp360
OG0004126	13.6551	43.07010186	31.60493429	33.30409133	98.39277	7.41232	13.6551	25.2869	0.075549605	1.638402494	0.881442808	1.770393112	0.664681435	0.137179565	0.834913536	0.735188	specific_fp360
OG0004127	11.8206	34.43096256	20.56741333	27.411564	91.06317857	10.2801	3.42246	35.0926	0.414424281	2.146507453	−1.586748713	1.771312542	0.731376587	0.142628368	0.877007185	0.744689036	specific_fp360
OG0004128	42.3627	111.7923786	73.10052619	104.6062147	243.2668586	36.5391	50.2794	72.9523	0.517014869	1.734586092	0.460526335	0.997512364	0.797359979	0.099979041	0.912626558	0.726019928	specific_fp360
OG0004129	40.249	99.15082116	74.96224	84.10145133	203.9652143	30.1357	43.6229	51.6662	0.165966633	1.444087156	0.533612105	0.777747202	0.949501181	0.347768656	0.982645549	0.847858149	specific_fp360
OG0004130	42.8252	112.2657988	95.45276571	89.898284	210.6352871	37.6799	42.8252	50.8749	−0.086493422	1.141888242	0.184664848	0.433158917	0.849288715	0.603656971	0.937013432	0.939271229	specific_fp360
OG0004131	76.2972	213.4800614	147.6331114	183.5805667	475.0912571	58.366	84.2272	108.016	0.314397019	1.68618833	0.529158007	0.888044925	0.71210625	0.14003581	0.866708265	0.735188	specific_fp360
OG0004132	33.6891	100.3365848	78.14362171	81.94779933	206.3200143	31.1489	16.6621	45.9801	0.068577085	1.400683752	−0.902610975	0.561828387	0.949501181	0.347768656	0.982645549	0.847858149	specific_fp360
OG0004133	19.375	56.55725465	45.14734286	48.188826	108.7193371	17.7268	10.5349	30.4517	0.094057573	1.26789558	−0.750755508	0.780590643	0.797359979	0.296035607	0.912626558	0.825398011	specific_fp360
OG0004134	22.3373	72.81012837	52.65877286	63.89785133	152.3619314	21.9474	15.1633	33.3028	0.279093517	1.532756675	−0.533466278	0.601593439	0.949501181	0.375566704	0.982645549	0.863672559	specific_fp360
OG0004135	17.6827	57.62223558	38.77682048	58.434804	112.4172629	14.8979	41.6833	27.5699	0.591633386	1.535597175	1.484360514	0.887985051	0.404006531	0.288571101	0.648828314	0.825398011	specific_fp360
OG0004136	17.3712	50.57364184	34.24891695	50.03681355	100.6981629	13.5654	32.8304	19.7865	0.546931552	1.555907091	1.275100739	0.54458485	0.485094963	0.466438634	0.706411902	0.892687029	specific_fp360
OG0004137	20.934	56.45691967	37.78214743	56.27911133	112.8622543	15.6322	35.624	21.5014	0.574894845	1.578786463	1.188328686	0.459909769	0.373620294	0.466438634	0.618244672	0.892687029	specific_fp360
OG0004138	1.60434	19.20140351	12.97586562	26.12532827	23.04103557	1.48763	6.79439	3.1103	1.009618381	0.828374776	2.191328285	1.064037993	0.187317478	0.872932081	0.423549556	0.998805231	specific_fp360
OG0004139	9.46162	29.41350279	17.90544333	27.940208	67.09474143	10.898	8.55628	9.46162	0.641944521	1.905801459	−0.349007796	−0.203904271	0.897504334	0.670389959	0.961653927	0.951961856	specific_fp360
OG0004140	2.21386	11.14906488	6.857734286	9.796371333	26.92168571	2.21386	2.07494	4.5063	0.514515455	1.972964837	−0.093494373	1.02537937	0.960885718	0.687262553	0.991405037	0.957796671	specific_fp360
OG0004141	115.711	162.0835405	120.7844019	122.03896	371.7907714	97.8378	103.319	356.689	0.014907634	1.622056803	0.078641717	1.866202856	0.70018293	0.004918205	0.859961416	0.551400211	specific_fp360
OG0004142	27.1913	38.27610488	30.39757143	28.59136133	82.66472714	24.8483	24.5928	85.5876	−0.088376753	1.4433158	−0.014911151	1.78425464	0.923292653	0.0125961	0.9733491	0.551400211	specific_fp360
OG0004143	23.9396	32.75346013	26.05680218	25.76313467	67.82270286	22.0964	21.9716	74.2726	−0.0163519	1.380108239	−0.008171409	1.749018741	0.847321768	0.016947799	0.937013432	0.551400211	specific_fp360
OG0004144	39.0127	56.87750733	42.88329976	39.41060133	136.2892143	29.4686	36.8944	139.784	−0.121832159	1.668183567	0.324223332	2.245948809	0.847321768	0.012632521	0.937013432	0.551400211	specific_fp360
OG0004145	22.5999	29.8933164	23.85583905	22.823975	63.15433714	17.8107	20.0507	70.7489	−0.063792357	1.404539386	0.170908386	1.989963499	0.822236304	0.014610022	0.924484186	0.551400211	specific_fp360
OG0004146	0	9.611983023	11.34566524	2.293473333	20.09345714	0	0	0	−2.306535164	0.824584604	NA	NA	0.31068583	0.630941086	0.556946497	0.942642691	specific_fp360
OG0004147	58.5538	88.30718558	92.01195619	89.46958667	74.70201429	54.1468	74.8976	91.4877	−0.040423988	−0.300674195	0.468043411	0.756701715	0.849288715	0.835782575	0.937013432	0.987043838	specific_fp360
OG0004148	154.953	212.1134791	195.1518429	256.9688133	166.8798143	111.999	194.753	165.75	0.396996193	−0.225787629	0.798159701	0.565523019	0.077436237	0.640466538	0.268964281	0.942642691	specific_fp360
OG0004149	7.20806	35.61705247	53.33061238	10.4729264	36.35664286	12.2972	2.82832	18.7545	−2.34829927	−0.552744906	−2.120312597	0.608906941	0.053889168	0.710308715	0.24150911	0.958503833	specific_fp360
OG0004150	31.9622	45.34962186	46.83453143	44.887532	41.88508571	28.6359	37.2738	37.3713	−0.061257855	−0.161136005	0.38033696	0.384105804	0.949501181	0.640466538	0.982645549	0.942642691	specific_fp360
OG0003585	217.2951	225.4870409	222.0079689	222.1273533	243.1235877	216.958	175.77595	268.5884	0.000775599	0.131078407	−0.303678093	0.307981214	0.849288715	0.532917807	0.937013432	0.910532643	specific_fp360
OG0004151	28.532	39.98047256	38.24219143	41.879478	41.12601857	22.4795	34.3541	28.532	0.131078262	0.104886213	0.611872341	0.343970932	0.924313351	0.87647039	0.9733491	0.989805231	specific_fp360
OG0004152	76.1781	115.6332256	85.33280476	166.0396867	98.52064286	49.3079	93.0207	80.3795	0.960355741	0.207325574	0.915732986	0.705008793	0.04567655	0.755748117	0.232658637	0.973934811	specific_fp360
OG0004153	86.0487	96.62195116	90.42900476	113.1675467	79.74594286	67.8259	107.689	83.4283	0.323602801	−0.181374463	0.666962701	0.298700562	0.190849141	0.640466538	0.423549556	0.942642691	specific_fp360
OG0004154	60.2377	84.73807023	80.40937143	73.37337467	122.0770857	60.2377	62.6337	38.7073	−0.132107012	0.60235687	0.056272421	−0.638061009	0.700127833	0.690288043	0.859961416	0.958503833	specific_fp360
OG0004156	16.3521	23.70535023	19.97794286	18.28816933	46.49581714	15.4138	14.7058	49.1927	−0.127497369	1.218692899	−0.067837307	1.674221665	0.859827027	0.033720767	0.944677098	0.610940957	specific_fp360
OG0004157	52.8736	69.3579693	52.1616181	46.84790667	169.1828714	49.3197	36.4693	98.3815	−0.155004039	1.697522984	−0.435481516	0.996223027	0.872528725	0.005792892	0.948638299	0.551400211	specific_fp360
OG0004158	8.34243	10.93786767	9.776260952	12.261648	11.58601571	7.1871	14.048	6.92501	0.326798194	0.245029827	0.966883085	−0.053593605	0.285901059	0.935089021	0.53041523	1	specific_fp360
OG0004159	37.1223	51.37205444	41.61618767	37.51975333	110.3231571	36.3044	32.2465	116.898	−0.149494467	1.406518933	−0.171001829	1.687033932	1	0.005766697	1	0.551400211	specific_fp360
OG0004160	42.4989	69.95964105	55.57225214	47.70927133	160.8011714	38.9892	39.1412	149.07	−0.220095057	1.532841303	0.005613434	1.93484349	0.748290253	0.007974357	0.885854961	0.551400211	specific_fp360
OG0004161	23.1403	41.9924993	28.23380095	65.19058133	33.55841857	18.8481	21.7637	24.6599	1.207240177	0.249251367	0.207504748	0.387747851	0.440653258	0.490129184	0.67383504	0.895160802	specific_fp360
OG0004162	92.8146	110.9261349	118.0216381	94.78536667	124.2269857	87.7717	93.028	156.608	−0.316315135	0.073927215	0.08390916	0.835330156	0.961587057	0.613754585	0.991405037	0.942642691	specific_fp360
OG0004163	468.822	480.7659767	533.6361905	435.8329333	418.4404286	527.186	441.482	346.047	−0.292081295	−0.350834264	−0.255957441	−0.607344061	0.293709056	0.404628222	0.536071185	0.879709358	specific_fp360
OG0004164	18.6732	51.76906135	54.6608581	39.25500933	69.90949686	22.8691	16.1069	9.00236	−0.47763134	0.354980344	−0.505720737	−1.345024427	0.377527994	0.466438634	0.621969757	0.892687029	specific_fp360
OG0004165	17.9077	54.43358456	57.5332729	41.54974667	72.74274357	18.1325	13.8387	9.44203	−0.469556863	0.338406796	−0.389869426	−0.941408877	0.82453995	0.466438634	0.924484186	0.892687029	specific_fp360
OG0004166	0	3.763515279	3.933070333	3.045914667	4.792565714	0	0.73869	0	−0.368780461	0.285142228	Inf	NA	0.368782159	0.926030467	0.615593933	1	specific_fp360
OG0004167	0	3.297362186	2.811121048	2.606702533	6.236070571	0	0.856906	0	−0.10891962	1.149491677	Inf	NA	0.281553144	0.717940902	0.524228377	0.959192298	specific_fp360
OG0004168	0	13.69482186	23.41240476	4.798769333	3.605042857	0	0	0	−2.286536753	−2.69918481	NA	NA	0.932751383	0.604907155	0.979336016	0.939701095	specific_fp360
OG0004169	0	3.765646767	6.03913	1.861670733	1.025145714	0	0	0	−1.697742798	−2.55851174	NA	NA	1	0.604907155	1	0.939701095	specific_fp360
OG0004170	0	2.145667674	2.519366667	2.498826667	0.267801429	0	0	0	−0.011810275	−3.233825544	NA	NA	0.939032539	0.31832406	0.982645549	0.834697703	specific_fp360
OG0004171	2.09295	13.6375743	7.503263571	8.282946	43.51471	1.94387	1.81724	5.62735	0.142625746	2.535913039	−0.097182773	1.533523957	0.679329355	0.359072335	0.844751243	0.863672559	specific_fp360
OG0004172	6.52904	10.36156744	8.587976667	15.08476533	5.561201429	6.43449	9.17967	2.53346	0.812702077	−0.626921678	0.512616487	−1.344716754	0.254629798	0.264943694	0.492952205	0.811609317	specific_fp360
OG0004173	33.5453	41.16959784	34.18829033	32.33476067	81.04531429	29.9097	32.975	59.0374	−0.080416347	1.245226498	0.140759219	0.981015747	0.775571382	0.019899666	0.900355834	0.56402733	specific_fp360
OG0004174	45.4858	58.48463581	51.13975571	43.029318	113.6378143	45.6766	38.9492	89.2203	−0.249125295	1.151925814	−0.229861569	0.965916733	0.44121265	0.007974357	0.67383504	0.551400211	specific_fp360
OG0004175	1.84602	6.847776977	3.52519619	11.66908067	6.484154286	1.78164	1.84602	2.66068	1.726915448	0.879214868	0.05121233	0.578589154	0.359782008	0.580519645	0.606367826	0.93645278	specific_fp360
OG0004176	2.62959	24.01637884	11.59914	37.87417067	31.57282714	1.11145	5.30046	17.924	1.707196455	1.444665608	2.253674521	4.011377678	0.329988705	0.224069942	0.579642141	0.793831443	specific_fp360
OG0004177	26.3404	51.87981328	34.51217814	68.13537733	69.14936714	19.3597	36.5536	26.6063	0.981298542	1.002610519	0.916956901	0.4587113	0.225875574	0.507145862	0.467206856	0.903067463	specific_fp360
OG0004178	6.22076	16.35845907	9.02602381	28.4552	12.43417714	4.25705	8.55304	6.18916	1.65652983	0.462148548	1.006583252	0.539889583	0.055673407	0.625080465	0.246666991	0.942642691	specific_fp360
OG0004179	16.5398	40.00614928	41.653419	38.93102667	37.36817429	20.5719	6.11393	19.1904	−0.097514529	−0.156624841	−1.750503106	−0.100290263	0.723158869	0.873192376	0.8743474	0.998805231	specific_fp360
OG0004180	0	5.401482093	9.452021429	0.448438667	3.863528571	0	0	0	−4.397640315	−1.290703833	NA	NA	0.040803928	0.239604223	0.230808539	0.793831443	specific_fp360
OG0003591	366.708	610.5012609	396.3744295	472.45824	1548.688229	320.07	297.522	1164.01	0.253322921	1.966110939	−0.105391109	1.862644087	0.499863693	0.007897331	0.720964648	0.551400211	specific_fp360
OG0004181	84.5512	152.3488219	167.7851048	83.82448933	252.8778286	133.142	47.2975	151.521	−1.001170951	0.591825907	−1.493129911	0.186552012	0.041581863	0.249489882	0.230808539	0.793831443	specific_fp360
OG0004182	131.857	165.4804695	132.6182333	135.1874527	328.9807857	108.749	126.075	310.552	0.027682114	1.310724184	0.213280091	1.513832724	0.520929553	0.009290942	0.737579258	0.551400211	specific_fp360
OG0004183	56.4004	109.7473274	96.38922857	51.34613467	274.9670371	69.9861	32.8096	248.566	−0.908616261	1.512314839	−1.09295041	1.828488651	0.261289694	0.24305388	0.502239632	0.793831443	specific_fp360
OG0004184	16.4607	80.36369279	76.80903667	15.935902	229.0872129	30.4354	7.22549	113.522	−2.268995375	1.576548972	−2.074582994	1.89914968	0.122666912	0.202279003	0.336375047	0.782207757	specific_fp360
OG0004185	10.6123	29.19739698	27.38488524	10.03308533	75.70131429	8.81038	6.52222	70.4241	−1.448614509	1.466938513	−0.43384114	2.998793071	0.40242674	0.043211371	0.648509991	0.64383533	specific_fp360
OG0004186	44.6155	94.76600814	89.26595238	54.20241067	198.18817	51.0812	26.4248	173.025	−0.719752994	1.150688934	−0.950899865	1.760116182	0.343543032	0.288373038	0.590925304	0.825398011	specific_fp360
OG0004187	19.8378	39.95971349	27.07951333	50.29755333	56.4478	17.5733	29.6035	41.2181	0.893286412	1.059715543	0.752382622	1.22989287	0.651505539	0.221089193	0.827210915	0.793831443	specific_fp360
OG0004188	3.14572	8.739993721	7.589374762	12.60073733	3.918828571	2.96762	5.59785	0	0.731455214	−0.953558573	0.91556646	#NAME?	0.11280836	0.349474915	0.322858084	0.851568621	specific_fp360
OG0004189	14.2278	37.71220837	45.76412714	30.47294133	29.06916714	31.4474	11.0747	5.02528	−0.586688405	−0.654727427	−1.505673125	−2.645664855	0.385680777	0.287314122	0.631871623	0.825398011	specific_fp360
OG0004190	9.35305	20.38768581	27.29245048	14.21179333	12.90744714	18.0712	6.18533	0	−0.94141332	−1.080298244	−1.546769837	#NAME?	0.156494372	0.132854956	0.381542685	0.735188	specific_fp360
OG0004191	33.5889	70.68104767	84.48775333	54.81180867	63.26644286	51.262	21.2955	16.8883	−0.624255494	−0.417301752	−1.267341163	−1.601865655	0.303424631	0.36477722	0.550977197	0.863672559	specific_fp360

付録10：Fp14とFp360に特徴的なオーソログのrelative abundanceの群間比較結果（Roary）

異なるオーソログ検出ツールを用いて、特定の単離株にのみに見られるオーソログおよび特定の単離株のみに見られるKOを含むオーソログを“specific ortholog”と定義した

category	
shared:	Fp14およびFp360のみに共有されていた特徴的なオーソログ
specific_fp14:	Fp14においてのみに特徴的なオーソログ
specific_fp360:	Fp360においてのみに特徴的なオーソログ

健常者群（H）とMCI群（M）あるいは健常者群とAD群（A）の群間比較においてはウィルコクソンの順位和検定を実施した。FDR補正したq値を算出した。

ortholog_roary (specific orthologs)	median	mean	H.mean	M.mean	A.mean	H.median	M.median	A.median	log2_mean_M_H	log2_mean_A_H	log2_median_M_H	log2_median_A_H	HvsM (pvalue)	HvsA (pvalue)	HvsM (qvalue)	HvsA (qvalue)	category
group_4056	0	3.846451488	3.606374952	4.830769533	2.457428143	1.02252	0	0	0.421703626	−0.553400169	#NAME?	#NAME?	0.587346863	0.268848222	0.83261548	0.702872455	shared
group_4307	20.33668	25.47321802	32.30191471	16.59289633	24.01638871	26.4836	8.31721	9.63531	−0.96105395	−0.427600451	−1.670927682	−1.458696257	0.022627113	0.222294081	0.292042112	0.676550263	shared
group_3127	56.2488	64.83361814	78.31486376	48.3986034	59.60777	66.2789	31.6982	52.6856	−0.694320732	−0.393785748	−1.064148741	−0.33114096	0.115791241	0.499119962	0.422031382	0.822638471	shared
group_3128	44.08165	55.12061172	70.28790543	40.72103133	40.47497429	55.9763	24.32677	24.9265	−0.787502363	−0.796246299	−1.20227135	−1.167135805	0.131427634	0.296035607	0.443698536	0.71412011	shared
group_5049	22.785	28.93695709	31.04021881	25.579316	29.82211714	27.413	13.6769	17.9884	−0.279161041	−0.057756046	−1.003118955	−0.607793351	0.241492133	0.894464113	0.574981269	0.989877233	shared
group_4004	0	0.008132256	0	0.023312467	0	0	0	0	Inf	NA	NA	NA	0.25979646	NA	0.597805852	NA	specific_fp14
group_4011	0.21099	15.83133549	20.09447505	7.828101333	20.19170429	0.544456	0	7.57376	−1.360064552	0.006963798	#NAME?	3.798122337	0.444744002	0.407139063	0.73975808	0.779690279	specific_fp14
group_4013	0	3.263139814	3.098028571	2.86972	4.601516	0	0	0	−0.11044047	0.570758796	NA	NA	0.429867808	0.474649843	0.733861396	0.813055507	specific_fp14
group_4014	0	4.033396744	6.058376667	1.926683333	2.472842857	0	0	0	−1.652811805	−1.292760714	NA	NA	0.486087467	1	0.770209015	1	specific_fp14
group_4015	0	4.075700326	4.747497619	2.676752267	5.058054286	0	0	0	−0.826683653	0.091415244	NA	NA	0.429867808	0.474649843	0.733861396	0.813055507	specific_fp14
group_4016	0	0.995811512	1.276842857	1.067079667	0	0	0	0	−0.258913092	#NAME?	NA	NA	0.791324196	0.44006229	0.941662441	0.795297293	specific_fp14
group_4018	0	8.005661372	5.990635048	12.3492186	4.743117714	0	0	0	1.043638906	−0.336873273	NA	NA	0.800151502	0.464291219	0.941662441	0.805513981	specific_fp14
group_4019	0	22.30535744	15.81075429	36.190918	12.03439429	0	0	2.60827	1.194721507	−0.393742666	NA	Inf	1	0.256764922	1	0.694644283	specific_fp14
group_412	7.26064	15.66225628	21.21216333	10.21743333	10.68001286	8.9125	5.57387	2.49719	−1.053858932	−0.989978379	−0.677150817	−1.835524578	0.473908708	0.431112111	0.762830918	0.795297293	specific_fp14
cesA	0	4.809997279	4.068858762	7.2714	1.758978429	0	0	0	0.837608958	−1.209886412	NA	NA	0.597324185	0.950647639	0.839331407	0.998970498	specific_fp14
group_4028	15.4398	34.40585072	38.11249714	37.1932274	17.31296143	20.271	12.5849	8.36363	−0.035224195	−1.138411614	−0.687723508	−1.277216116	0.479670259	0.287314122	0.767698136	0.71412011	specific_fp14
group_4029	36.3997	48.53545	54.26384095	45.78026267	37.25425	36.7792	39.0074	18.0728	−0.245265429	−0.54258615	0.084857741	−1.025070061	0.751396543	0.189265565	0.922587843	0.638072518	specific_fp14
group_4032	3.21417	18.67145726	21.10840619	18.91187613	10.84542714	6.69675	3.41448	0	−0.158525159	−0.960730777	−0.971795228	#NAME?	0.842715172	0.347492606	0.962518298	0.743402024	specific_fp14
group_4035	0.942443	7.198435093	7.60765619	6.152801267	8.211415714	1.75946	1.55062	0.525167	−0.306208654	0.110178927	−0.182287538	−1.744284547	0.762409457	0.910960048	0.930713477	0.989877233	specific_fp14
group_4043	0	2.854104651	5.763247619	0.11322	0	0	0	0	−5.669681273	#NAME?	NA	NA	0.444643599	0.323219522	0.73975808	0.729068877	specific_fp14
group_4052	16.3737	34.44422679	23.50182476	50.07322213	33.78072857	16.3838	9.58867	25.0361	1.09126517	0.523427667	−0.772867385	0.611739835	0.563451914	0.750197895	0.822000841	0.944159956	specific_fp14
group_4053	34.9536	93.76567791	71.64403333	125.6522053	91.80233857	43.0555	26.815	84.9907	0.810517528	0.357684347	−0.683157289	0.981107443	0.611998112	0.811273213	0.847276289	0.972982434	specific_fp14
group_4054	0	9.961170419	8.199017524	13.56993333	7.514565714	0	0	2.27286	0.726890684	−0.125761315	NA	Inf	0.970235302	0.46226794	0.998451488	0.805513981	specific_fp14
group_581	0	1.034174884	0.717704762	1.959848	0	0	0	0	1.44927937	#NAME?	NA	NA	0.58667146	0.323219522	0.83261548	0.729068877	specific_fp14
treR	188.633	195.7937	255.0216667	134.72904	148.9626429	240.31	121.1	137.426	−0.920558976	−0.77566925	−0.988697819	−0.806241707	0.000979908	0.014333975	0.291922302	0.291280954	specific_fp14
treB	94.4714	98.62596163	126.6016381	65.48007667	85.72582857	133.835	57.4414	74.789	−0.951168156	−0.562494223	−1.220292636	−0.839557455	0.000979908	0.062296882	0.291922302	0.538244542	specific_fp14
treA	64.8237	80.24112528	106.2669418	53.17664067	60.159	116.7	42.1023	48.1518	−0.998828318	−0.820840372	−1.470833608	−1.277142926	0.002103351	0.027125773	0.291922302	0.374398142	specific_fp14
group_4065	146.052	172.8509454	204.0414883	151.16134	125.7570429	195.618	135.838	86.8726	−0.432773316	−0.69822333	−0.526152005	−1.171066006	0.009949752	0.05474984	0.291922302	0.512638146	specific_fp14
group_4066	92.9177	132.3228623	163.6219619	93.829812	120.9106714	130.793	33.9297	102.848	−0.802248125	−0.436424824	−1.946664751	−0.346771591	0.142970245	0.70820366	0.457504784	0.923318374	specific_fp14
group_4072	0	0.354956302	0.700438095	0.036928067	0	0	0	0	−4.245467912	#NAME?	NA	NA	0.871601636	0.620690717	0.969519052	0.891693103	specific_fp14
group_4073	0	0.388739	0.762373333	0.047062467	0	0	0	0	−4.017848814	#NAME?	NA	NA	0.674408456	0.239341328	0.887757152	0.680607651	specific_fp14
group_4074	0	0.467763791	0.848452	0.110729667	0.090772286	0	0	0	−2.937791243	−3.224509252	NA	NA	0.280087211	0.485469317	0.612956814	0.822638471	specific_fp14
group_4075	0	0.501004814	0.960091429	0.064036933	0.060104714	0	0	0	−3.906195673	−3.997621741	NA	NA	0.377619692	0.554342983	0.699835723	0.864297421	specific_fp14
group_4076	0	0.200573256	0.410697619	0	0	0	0	0	#NAME?	#NAME?	NA	NA	0.430222691	0.620690717	0.733861396	0.891693103	specific_fp14
group_4077	0	0.025071628	0.0513373143	0	0	0	0	0	#NAME?	#NAME?	NA	NA	0.430222691	0.620690717	0.733861396	0.891693103	specific_fp14
group_4078	0	0.362511628	0.742285714	0	0	0	0	0	#NAME?	#NAME?	NA	NA	0.430222691	0.620690717	0.733861396	0.891693103	specific_fp14
group_4079	0	0.270220256	0.50717781	0.043791333	0.044552429	0	0	0	−3.533774343	−3.508915644	NA	NA	0.830992978	0.930545821	0.958684416	0.998970498	specific_fp14
group_4080	0	0.272790698	0.558571429	0	0	0	0	0	#NAME?	#NAME?	NA	NA	0.430222691	0.620690717	0.733861396	0.891693103	specific_fp14
group_4081	0	0.21763293	0.438298571	0.010263067	0	0	0	0	−5.41638019	#NAME?	NA	NA	0.871601636	0.620690717	0.969519052	0.891693103	specific_fp14
group_4082	0	0.449700233	0.86382381	0.079787333	0	0	0	0	−3.436505448	#NAME?	NA	NA	0.871601636	0.620690717	0.969519052	0.891693103	specific_fp14
group_4083	0	0.255899116	0.506109762	0.0250238	0	0	0	0	−4.338077509	#NAME?	NA	NA	0.788922711	0.44006229	0.941662441	0.795297293	specific_fp14
group_4092	0	0.526285093	1.033473333	0	0.132474143	0	0	0	#NAME?	−2.963718466	NA	NA	0.241286619	0.843379402	0.574981269	0.977920647	specific_fp14
group_4093	0	0.402052558	0.823250476	0	0	0	0	0	#NAME?	#NAME?	NA	NA	0.241286619	0.44006229	0.574981269	0.795297293	specific_fp14
group_4095	0	2.119355163	4.339632	0	0	0	0	0	#NAME?	#NAME?	NA	NA	0.027851244	0.129742991	0.297372342	0.609562655	specific_fp14
group_4097	18.5708	38.80000537	47.33216667	39.9746554	10.68641429	31.0235	21.6054	0	−0.243735367	−2.147043111	−0.521969516	#NAME?	0.907853874	0.182685108	0.981611036	0.638072518	specific_fp14
group_4103	0	2.77165	0.666804762	7.01187	0	0	0	0	3.394462936	#NAME?	NA	NA	0.069656206	0.620690717	0.351865196	0.891693103	specific_fp14
group_4104	0	2.095234651	0.518166667	5.280906	0	0	0	0	3.349297346	#NAME?	NA	NA	0.15819907	0.620690717	0.481288165	0.891693103	specific_fp14
group_4112	0	10.50999423	8.238336762	15.41046	6.823968571	0	0	0	0.903484921	−0.271742099	NA	NA	0.745131852	0.733544565	0.922587843	0.938597681	specific_fp14
group_4114	0	8.721809535	6.379852857	13.01246667	6.553414286	0	0	0	1.028299412	0.038723587	NA	NA	0.919084503	0.576826376	0.982441117	0.872802773	specific_fp14
group_4116	0	0.310289302	0.166657143	0.656176	0	0	0	0	1.977199675	#NAME?	NA	NA	0.746400229	0.44006229	0.922587843	0.795297293	specific_fp14
group_4118	0	5.738225093	4.133977095	8.354810667	4.944	0	0	0	1.01507674	0.258148348	NA	NA	0.919084503	0.576826376	0.982441117	0.872802773	specific_fp14
group_4119	0	11.15734081	7.549667905	16.9050486	9.663842857	0	0	0	1.162969074	0.356183811	NA	NA	0.852001032	0.37052313	0.96434809	0.756970046	specific_fp14
group_4120	0	9.148163628	5.926362714	14.68566	6.947502714	0	0	0	1.309189272	0.229347566	NA	NA	0.968621817	0.847827158	0.998451488	0.977920647	specific_fp14
group_4122	0	8.996896419	7.00730981	12.81695133	6.779824286	0	0	0	0.871120553	−0.047612799	NA	NA	0.501814744	0.673452718	0.782706606	0.911169378	specific_fp14
group_4128	0	6.30326093	5.492211429	6.563758667	8.1782	0	0	0	0.257135031	0.57439618	NA	NA	0.542178517	0.948999012	0.809386217	0.998970498	specific_fp14
group_4131	0	12.06199953	8.40644	18.83948333	8.505498571	0	0	0	1.164192525	0.016900835	NA	NA	0.908660058	0.898206191	0.981705449	0.989877233	specific_fp14
group_4132	0	11.13642488	8.478883619	15.865334	8.975814286	0	0	0	0.903939735	0.082176573	NA	NA	0.634977689	0.717940902	0.863099747	0.923727505	specific_fp14
group_4134	0	7.537232977	5.386281714	11.43202613	5.644101429	0	0	0	1.085719526	0.067454227	NA	NA	0.770177257	0.630078669	0.932862337	0.891693103	specific_fp14
group_4135	0	7.390831302	5.505036619	10.9820498	5.352747143	0	0	0	0.996323293	−0.040472657	NA	NA	0.518913942	0.536905841	0.795265685	0.845432432	specific_fp14
group_4136	0	6.30279393	5.188847095	8.84359	4.200071429	0	0	0	0.769218118	−0.30500016	NA	NA	0.660086409	0.37052313	0.8767058	0.756970046	specific_fp14
group_4137	0	6.653470326	4.888676286	9.742453467	5.328602857	0	0	0	0.994841258	0.124313435	NA	NA	0.661230751	0.587943793	0.87790179	0.884498706	specific_fp14
group_4138	0	15.578892	10.37305381	23.5525884	14.10991429	0	0	0	1.183044935	0.44386854	NA	NA	1	0.898206191	1	0.989877233	specific_fp14
group_4139	0	6.637453535	4.788887476	9.500443	6.048174286	0	0	0	0.98830425	0.336809176	NA	NA	0.714977939	0.630078669	0.910477743	0.891693103	specific_fp14
group_4140	0	7.12909493	5.250541048	11.92883	2.47961	0	0	0	1.183914548	−1.082352867	NA	NA	0.464518769	0.834245362	0.753514984	0.972982434	specific_fp14
group_4141	0	8.485488326	5.963471952	13.19060067	5.969153857	0	0	0	1.145285841	0.001373923	NA	NA	0.688014554	0.687457524	0.894584468	0.918014309	specific_fp14
group_4146	0	13.45026674	9.923951429	19.07550667	11.97512714	0	0	0	0.942734798	0.271054394	NA	NA	0.716374834	0.642503534	0.911772813	0.892111009	specific_fp14
group_4147	0	20.19123023	16.98315238	34.10511333	0	0	0	0	1.005883783	#NAME?	NA	NA	1	0.323219522	1	0.729068877	specific_fp14
group_4155	0	5.225278767	3.97986319	7.816437333	3.409042857	0	0	0	0.973792351	−0.223352102	NA	NA	0.431435689	0.37052313	0.733861396	0.756970046	specific_fp14
group_4156	0	8.092778767	5.875980095	11.72159433	6.967141429	0	0	0	0.9962674	0.245737341	NA	NA	0.927258428	0.733544565	0.984263701	0.938597681	specific_fp14
group_4165	0	10.50411728	7.395538714	15.85499333	8.36369	0	0	0	1.100210124	0.177484348	NA	NA	0.291518641	0.898206191	0.623806844	0.989877233	specific_fp14
group_4172	0	0.390912558	0.562339048	0.333341333	0	0	0	0	−0.75444001	#NAME?	NA	NA	0.517774898	0.323219522	0.795265685	0.729068877	specific_fp14
group_4176	0	2.249292791	1.547574286	2.743255333	3.295957143	0	0	0	0.825880247	1.090688821	NA	NA	0.899276375	0.767510812	0.973799052	0.954543453	specific_fp14
group_4178	0	2.208784419	1.431854762	0.946485333	7.2445	0	0	0	−0.597233107	2.339000959	NA	NA	0.429867808	0.767510812	0.733861396	0.954543453	specific_fp14
group_4179	0	8.412495977	2.073915095	11.010126	21.86188857	0	0	0	2.408402242	3.397989298	NA	NA	0.503669852	0.867906725	0.782706606	0.977920647	specific_fp14
group_4182	0	64.36487395	50.22887524	98.2644	34.13102857	0	0	0	0.968151871	−0.557433077	NA	NA	0.625820746	0.847827158	0.860563287	0.977920647	specific_fp14
group_4183	0	13.64022605	12.99210476	15.51173333	11.57421714	0	0	0	0.255724736	−0.166720555	NA	NA	0.556545025	0.474649843	0.817751605	0.813055507	specific_fp14
group_4184	0	3.108592093	0.613293333	7.033266667	2.184471429	0	0	0	3.519545745	1.832635063	NA	NA	0.556545025	0.930545821	0.817751605	0.998970498	specific_fp14
group_4185	0	4.485182093	1.964425238	9.396131333	1.52399	0	0	0	2.257959616	−0.366253827	NA	NA	0.621135528	0.474649843	0.855100536	0.813055507	specific_fp14
group_4186	0	5.052892093	1.55018381	10.28918667	4.340385714	0	0	0	2.73061775	1.485383965	NA	NA	1	0.930545821	1	0.998970498	specific_fp14
group_4188	0	30.8917107	19.43862905	48.20240333	28.15661429	0	0	0	1.310178607	0.534547393	NA	NA	0.455508279	0.673452718	0.749474198	0.911169378	specific_fp14
group_4189	0	5.318610465	8.099633333	3.907196667	0	0	0	0	−1.051722725	#NAME?	NA	NA	0.962962468	0.239341328	0.998451488	0.680607651	specific_fp14
group_4190	0	12.34076884	8.523637143	19.09610933	9.316434286	0	0	0	1.163737649	0.128308714	NA	NA	0.970235302	0.687457524	0.998451488	0.918014309	specific_fp14
group_4191	0	5.349103488	1.979062857	10.21553533	5.031157143	0	0	0	2.367875469	1.346072817	NA	NA	0.791379234	0.767510812	0.941662441	0.954543453	specific_fp14
group_4192	0	18.66852512	12.73611048	27.88535333	16.71542286	0	0	0	1.130582796	0.392255097	NA	NA	0.478905805	0.780612619	0.767698136	0.960944453	specific_fp14
group_4193	0	9.929005349	18.59317762	2.23723	0.418864286	0	0	0	−3.054987865	−5.472146663	NA	NA	0.275746652	0.200799534	0.6117942	0.654553408	specific_fp14
group_4194	0	18.7909673	11.98115714	29.77402627	15.68527143	0	0	0	1.313287076	0.388643244	NA	NA	0.940512011	0.828498832	0.99049674	0.972982434	specific_fp14
group_4195	0	4.504675814	2.849051429	7.368505333	3.334771429	0	0	0	1.370890341	0.227106216	NA	NA	0.64256877	0.576826376	0.870460046	0.872802773	specific_fp14
group_4196	0	12.85148788	9.030865238	19.45423327	10.16461571	0	0	0	1.107147999	0.170619551	NA	NA	1	0.687457524	1	0.918014309	specific_fp14
group_4197	0	20.05006256	18.58710762	26.18693933	11.28847714	0	0	0	0.494545164	−0.719451412	NA	NA	0.910871362	0.687457524	0.98192451	0.918014309	specific_fp14
group_4198	0	1.054193256	0.271787143	2.200898667	0.944185714	0	0	0	3.017543608	1.796593445	NA	NA	0.659223296	0.692735596	0.8767058	0.919767665	specific_fp14
group_4199	0	1.57690186	0.171777619	3.619033333	1.416278571	0	0	0	4.396990411	3.043491076	NA	NA	0.659223296	0.692735596	0.8767058	0.919767665	specific_fp14
group_4200	0	2.16630186	0.520753333	4.923157333	1.1954	0	0	0	3.240911772	1.198821374	NA	NA	0.659223296	0.692735596	0.8767058	0.919767665	specific_fp14
group_4201	0	0.853161651	0.095076714	1.772586667	1.15722	0	0	0	4.22062031	3.605427305	NA	NA	0.840868769	0.692735596	0.962518298	0.919767665	specific_fp14
group_4202	0	0.768781628	0.1266	1.712147333	0.673828571	0	0	0	3.757457544	2.412104198	NA	NA	0.659223296	0.692735596	0.8767058	0.919767665	specific_fp14
group_4203	0	5.404645884	2.211102048	10.14220867	4.833357143	0	0	0	2.197534346	1.128259991	NA	NA	0.767731966	0.711724872	0.932862337	0.923318374	specific_fp14
group_4205	0	11.72858316	8.914632381	14.55758907	14.10828	0	0	0	0.707524235	0.662294903	NA	NA	0.822851427	0.687457524	0.953072345	0.918014309	specific_fp14
group_4206	0	4.594925349	1.583856667	10.95472	0	0	0	0	2.790038922	#NAME?	NA	NA	0.748015584	0.239341328	0.922587843	0.680607651	specific_fp14
group_4207	0	6.157873953	0.968855238	16.08687933	0.44849	0	0	0	4.053459556	−1.111205303	NA	NA	0.957447423	1	0.997052567	1	specific_fp14
group_4208	0	2.466562791	3.4361	2.260273333	0	0	0	0	−0.604274776	#NAME?	NA	NA	0.336840379	0.239341328	0.668164411	0.680607651	specific_fp14
group_4211	0	0.910329767	0.985539048	0.560762	1.433775714	0	0	0	−0.813524444	0.540834423	NA	NA	0.915015792	0.474649843	0.982441117	0.813055507	specific_fp14
group_4212	0	2.761329535	5.005081905	0.45984	0.961835714	0	0	0	−3.444189806	−2.379531276	NA	NA	0.480451083	1	0.767698136	1	specific_fp14
group_4214	0	3.924432116	3.25319719	5.782802667	1.955914286	0	0	0	0.829910599	−0.734015125	NA	NA	0.688014554	0.337328199	0.894584468	0.743402024	specific_fp14
group_4217	7.87709	30.29243163	34.91463571	20.34814733	37.735	8.33045	6.95891	0	−0.778934475	0.112071354	−0.259533081	#NAME?	0.548783668	0.82505324	0.81201036	0.972982434	specific_fp14
group_4219	38.7573	93.3091984	99.44280433	85.51446333	91.61138429	20.5655	47.9558	51.5783	−0.217698533	−0.118340093	1.221479164	1.326538075	0.44611522	0.466438634	0.73975808	0.805513981	specific_fp14
group_4220	35.058	107.7728251	117.7558952	93.90452533	107.5414	26.629	52.0257	73.251	−0.326532698	−0.130907129	0.966226219	1.459850203	0.657256698	0.404628222	0.875855678	0.777353902	specific_fp14
group_4221	31.0716	88.85988326	98.49359619	78.66195867	81.81144	21.3314	42.3172	51.7702	−0.324363818	−0.267727332	0.988265518	1.279143237	0.751396543	0.499119962	0.922587843	0.822638471	specific_fp14
group_4230	0	6.677528814	6.19830819	5.7536238	10.09498714	0	0	2.77933	−0.107403596	0.703692678	NA	Inf	0.898297293	0.184797844	0.973799052	0.638072518	specific_fp14
group_4231	0.462371	5.366360379	6.427132852	3.296076927	6.620364643	1.27119	0	1.79732	−0.96342538	0.042735387	#NAME?	0.499667613	0.114659637	0.769358107	0.422031382	0.955683909	specific_fp14
group_4232	0.642424	6.465601551	7.670636795	3.862011333	8.429617714	0.712757	0	2.39721	−0.989993953	0.136120855	#NAME?	1.749874089	0.257404488	0.829146551	0.594772886	0.972982434	specific_fp14
group_4234	0	5.640707512	7.685872857	5.4098062	0	1.2771	0	0	−0.506632199	#NAME?	#NAME?	#NAME?	0.364430704	0.009470242	0.689230646	0.291280954	specific_fp14
msbA	0	0.919301837	1.138569952	0.851044667	0.407762857	0	0	0	−0.419916174	−1.481420659	NA	NA	0.813416237	0.387119234	0.952601969	0.771342314	specific_fp14
group_4238	0	14.74865674	14.45526857	15.49362667	14.03245714	0	0	0	0.100079469	−0.04282776	NA	NA	0.747066198	0.856676809	0.922587843	0.977920647	specific_fp14
group_4239	0	14.10916698	23.34585714	4.852425333	6.234971429	0	0	0	−2.266388639	−1.904711704	NA	NA	0.555155156	0.657441267	0.816738275	0.907768846	specific_fp14
group_4243	0	7.166601442	10.26989	4.54104	3.482938857	0	0	0	−1.177326079	−1.560043677	NA	NA	0.559027851	0.859957553	0.820424078	0.977920647	specific_fp14
group_4244	0	9.383341628	13.00592429	6.12099	5.506347143	0	0	0	−1.087332014	−1.240001459	NA	NA	0.634977689	0.54716072	0.863099747	0.856101203	specific_fp14
group_4245	0	4.385008605	7.33293	2.304256	0	0	0	0	−1.67008876	#NAME?	NA	NA	0.939032539	0.094115052	0.99049674	0.597602212	specific_fp14
group_4247	0	16.45540977	27.04629095	6.692620667	5.603028571	0	0	0	−2.01478761	−2.271152006	NA	NA	0.465171623	0.47003372	0.753514984	0.810360221	specific_fp14
group_4248	0	14.20363279	19.65609048	8.42152	10.23650143	0	0	0	−1.22282385	−0.94125368	NA	NA	0.848357367	0.852695307	0.962518298	0.977920647	specific_fp14
group_4250	0	9.092676977	12.27999905	5.94744	6.270504286	0	0	0	−1.045969731	−0.969657072	NA	NA	0.737007695	0.904163098	0.92045582	0.989877233	specific_fp14
group_4252	0	7.123663488	11.87052524	1.840666667	4.203785714	0	0	0	−2.689083479	−1.497622736	NA	NA	0.486087467	0.711724872	0.770209015	0.923318374	specific_fp14

group_4253	0	17.86083302	24.03935048	13.31254	9.071622857	0	0	0	−0.852612056	−1.405965348	NA	NA	0.910871362	1	0.98192451	1	specific_fp14
group_4254	0	15.44919651	23.5325481	10.569876	1.654828571	0	0	0	−1.154699092	−3.829903867	NA	NA	0.752993315	0.815881646	0.923918177	0.972982434	specific_fp14
group_4255	5.12623	13.44531367	11.62482785	13.19530333	19.44250759	5.24933	4.86247	3.83875	0.182815164	0.74200495	−0.110443947	−0.451496688	0.974369358	0.710308715	0.998451488	0.923318374	specific_fp14
group_4256	0	33.24450395	45.47490667	27.00381333	9.926204286	0	0	0	−0.751907526	−2.195756626	NA	NA	0.848357367	0.756965909	0.962518298	0.945024627	specific_fp14
group_4257	0	30.25993721	43.28286667	19.12821333	15.04484286	0	0	0	−1.178093928	−1.524527016	NA	NA	1	0.856676809	1	0.977920647	specific_fp14
group_4258	0	0.669917907	1.371736667	0	0	0	0	0	#NAME?	#NAME?	NA	NA	0.140911852	0.323219522	0.453881617	0.729068877	specific_fp14
group_4259	0	25.57118209	36.08717714	16.49036667	13.48208714	0	0	0	−1.129862818	−1.42044244	NA	NA	0.765317467	0.95199474	0.932862337	0.998970498	specific_fp14
group_4260	3.5588	45.81957512	56.11836905	38.545232	30.51107143	3.5588	8.31168	0	−0.541920669	−0.879140238	1.223749254	#NAME?	0.683998017	1	0.891848192	1	specific_fp14
group_4261	11.3476	38.07173047	35.37853571	41.63106067	38.52417857	6.65927	11.3476	22.6672	0.234785978	0.122889858	0.768951261	1.767170251	0.648590233	0.705695457	0.875855678	0.923318374	specific_fp14
group_4262	0	0.463367442	0.9488	0	0	0	0	0	#NAME?	#NAME?	NA	NA	0.430222691	0.620690717	0.733861396	0.891693103	specific_fp14
group_4264	0	0.274937209	0.562966667	0	0	0	0	0	#NAME?	#NAME?	NA	NA	0.430222691	0.620690717	0.733861396	0.891693103	specific_fp14
group_4265	0	5.40464186	8.704138095	3.307513333	0	0	0	0	−1.395954473	#NAME?	NA	NA	0.791324196	0.44006229	0.941662441	0.795297293	specific_fp14
group_4266	0	4.328590698	6.40937619	3.4355	0	0	0	0	−0.899663867	#NAME?	NA	NA	0.836952327	0.44006229	0.962518298	0.795297293	specific_fp14
group_4276	0	5.281232558	5.52897619	7.398966667	0	0	0	0	0.42031144	#NAME?	NA	NA	1	0.323219522	1	0.729068877	specific_fp14
group_4279	0	0.277274419	0.567752381	0	0	0	0	0	#NAME?	#NAME?	NA	NA	0.430222691	0.620690717	0.733861396	0.891693103	specific_fp14
group_4280	0	0.297972093	0.610133333	0	0	0	0	0	#NAME?	#NAME?	NA	NA	0.430222691	0.620690717	0.733861396	0.891693103	specific_fp14
epsE_2	0	0.2922	0.598314286	0	0	0	0	0	#NAME?	#NAME?	NA	NA	0.430222691	0.620690717	0.733861396	0.891693103	specific_fp14
group_4283	0	28.45798279	32.54599524	33.12623467	6.190548571	0	1.02056	0	0.025494195	−2.394340868	Inf	NA	0.728315819	0.517694468	0.914803889	0.840581695	specific_fp14
group_4286	0	2.761002326	1.796867143	3.133919333	4.8543	0	0	0	0.802484303	1.433779529	NA	NA	0.546061402	0.767510812	0.809864888	0.954543453	specific_fp14
group_4287	14.8902	29.64460581	41.24354286	12.06739	32.51325714	25.7074	0	0	−1.773054591	−0.343140176	#NAME?	#NAME?	0.07205803	0.44355419	0.351865196	0.797998044	specific_fp14
group_4288	0	0.980204651	0.812138095	1.672926667	0	0	0	0	1.042577238	#NAME?	NA	NA	0.808441869	0.620690717	0.948473433	0.891693103	specific_fp14
group_4291	0	20.73706535	19.35428095	25.31056	15.08507286	0	0	0	0.387086718	−0.359531045	NA	NA	0.962962468	0.739446455	0.998451488	0.944159956	specific_fp14
group_4294	0	10.13165521	12.25675367	6.271323933	12.02849829	0	0	0.32498	−0.96673497	−0.027120378	NA	Inf	0.221197909	0.576067305	0.56449293	0.872802773	specific_fp14
group_4295	0	18.104388	22.75281	9.460744933	22.68121429	0	0	0	−1.266019041	−0.004546851	NA	NA	0.371340323	0.948999012	0.695900657	0.998970498	specific_fp14
group_4297	49.8668	91.71247165	86.95037386	109.8955587	67.03500714	48.3533	66.1443	29.5709	0.337868946	−0.375277531	0.452002484	−0.709436201	0.563451914	0.558941703	0.822000841	0.864297421	specific_fp14
group_4298	3.2556	140.4175416	110.8260476	196.6320593	108.7323429	0	3.62318	12.4904	0.827201561	−0.027515861	Inf	Inf	0.197441085	0.41954703	0.535635198	0.795297293	specific_fp14
albA_2	1.00961	50.13607084	36.94479605	73.6918674	39.23318829	0	1.07618	6.89961	0.996134249	0.086703417	Inf	Inf	0.23307403	0.263448836	0.574981269	0.701218295	specific_fp14
group_4304	0	1.797382977	1.502233333	3.0493712	0	0	0	0	1.021402864	#NAME?	NA	NA	0.38426935	0.620690717	0.708482658	0.891693103	specific_fp14
group_888	0	5.378511163	10.15290381	1.204333333	0	0	0	0	−3.075585749	#NAME?	NA	NA	0.033797161	0.032734395	0.308106745	0.409379185	specific_fp14
group_4316	83.4123	112.4453551	112.20699	101.57668	136.4504686	46.822	94.7813	102.328	−0.143593326	0.282214797	1.017415888	1.127942498	0.746406843	0.872070479	0.922587843	0.977920647	specific_fp14
group_4318	22.994	29.89689419	31.80174971	26.4149744	31.64358429	17.2844	23.1543	24.6455	−0.267750132	−0.00719312	0.421809619	0.511853727	0.897078863	0.914509149	0.973799052	0.989877233	specific_fp14
group_4319	20.8746	28.23655326	28.85964619	25.98585133	31.19020714	13.0541	21.1118	20.8746	−0.151327288	0.112039521	0.693546593	0.677245557	0.795863119	0.957193011	0.941662441	0.998970498	specific_fp14
group_4322	19.5054	40.71297137	57.15403619	17.1139686	41.95906857	27.7946	19.5054	12.0256	−1.739681036	−0.445872732	−0.510931036	−1.208695743	0.157459987	0.632818278	0.481288165	0.891693103	specific_fp14
group_4327	0	22.05268498	26.82627333	23.71657427	4.166442857	0	0	0	−0.177751016	−2.686758553	NA	NA	0.583352808	0.815881646	0.83261548	0.972982434	specific_fp14
group_4328	0	12.71437553	23.14120952	4.0501832	0	0	0	0	−2.514405201	#NAME?	NA	NA	0.455064321	0.44006229	0.749474198	0.795297293	specific_fp14
ftsL_2	108.05752	111.9417142	132.4272127	85.29910267	107.5765291	119.064099	78.9124	94.4941	−0.634597145	−0.299836267	−0.593414545	−0.333442309	0.01618207	0.249489882	0.291922302	0.681911623	specific_fp360
zapA	503.703879	509.4407548	558.2949468	427.879055	537.6532497	547.55316	446.017084	524.7799	−0.383824438	−0.054351467	−0.295900066	−0.061286574	0.019476603	0.835782575	0.291922302	0.972982434	specific_fp360
group_4907	45.4565	63.13714816	49.88763719	47.56297267	136.2589143	46.7181	38.7321	141.368	−0.068843455	1.44959637	−0.270451877	1.597402082	0.822270056	0.012632521	0.953072345	0.291280954	specific_fp360
group_4908	28.6991	48.50809186	54.00788429	44.72410933	40.11724857	26.7809	27.6981	41.4373	−0.272117281	−0.42894737	0.048582571	0.629725557	0.849288715	1	0.962518298	1	specific_fp360
group_3258	0	7.57621186	9.86166	3.15443	10.19511429	0	0	0	−1.644451178	0.047975529	NA	NA	0.380796788	0.587943793	0.704092674	0.884498706	specific_fp360
group_4910	9.92805	67.34538023	76.65691095	41.088388	95.67577143	7.84757	8.47053	21.7403	−0.899685132	0.319737765	0.110206249	1.470053951	0.434663163	0.70820366	0.736370534	0.923318374	specific_fp360
group_4911	3.06736	17.70935942	12.71428214	20.29959933	27.14407714	0.993825	3.06736	9.81104	0.675001243	1.094187427	1.625933759	3.303342336	0.762409457	0.538520259	0.930713477	0.847003321	specific_fp360
group_4912	16.6993	78.20649163	91.47824571	71.77910467	52.16420143	15.4072	27.0645	16.6993	−0.349864771	−0.810368627	0.812797035	0.116182929	0.847137033	0.749567537	0.962518298	0.944159956	specific_fp360
group_4915	62.1798	89.11964451	72.22685019	65.50307067	190.4049714	61.4316	54.8052	218.251	−0.140972717	1.398463987	−0.164668174	1.8289354	0.974400707	0.012632521	0.998451488	0.291280954	specific_fp360
group_4916	9.87634	45.19792435	29.57497043	67.82722467	43.57542829	8.34735	20.1716	35.2678	1.197487736	0.559138118	1.272935354	2.078961415	0.335114519	0.506621831	0.667517327	0.829765334	specific_fp360
group_4926	0	3.296242093	2.613841905	0.473789333	11.39155571	0	0	2.19417	−2.46385426	2.123720996	NA	Inf	0.084171452	0.427237991	0.373864562	0.795297293	specific_fp360
group_4927	2.15364	11.68452347	5.771697429	13.8304502	24.82458714	1.28906	0.86762	13.4803	1.260780543	2.104702148	−0.571184201	3.386461282	1	0.038777504	1	0.444735302	specific_fp360
group_4929	4.89783	21.81549512	12.72992286	19.87186133	53.23714143	4.89783	2.49065	9.7629	0.642503335	2.064209431	−0.9756204	0.995167054	0.527089257	0.363381407	0.796107122	0.756970046	specific_fp360
agrB_1	2.31186	11.98902102	6.481307143	10.7176776	31.23647	1.97049	1.42131	12.2439	0.725635615	2.268874717	−0.471333175	2.635436834	0.534467797	0.042178982	0.804887709	0.466629325	specific_fp360
group_4933	0	6.855822093	3.490152381	6.74641	17.18728571	0	0	9.79507	0.950829972	2.299979795	NA	Inf	0.770177257	0.053865069	0.932862337	0.512638146	specific_fp360
group_4934	9.37053	30.63046884	18.10576333	26.83134867	76.34555714	9.37053	5.16281	58.6431	0.567470571	2.076095202	−0.859974144	2.645758815	0.596719138	0.023459901	0.839300213	0.341597731	specific_fp360
group_4949	5.45086	11.10382177	7.159393333	14.80861307	14.99826857	4.65766	8.16873	7.24094	1.04852728	1.066886715	0.810506469	0.636571667	0.289031101	0.352500644	0.623806844	0.749950335	specific_fp360
group_4952	46.3212	62.9637384	49.99943719	48.78880467	132.2315	37.0069	36.5232	150.737	−0.035361718	1.403082134	−0.018981115	2.026167391	0.974400707	0.012632521	0.998451488	0.291280954	specific_fp360
group_4953	30.3583	43.49716465	34.74848762	32.77741867	92.755	29.7049	24.3886	98.6922	−0.083681527	1.417041285	−0.284493988	1.732235136	0.724049268	0.0125961	0.91408214	0.291280954	specific_fp360
group_4954	30.1137	43.222104	35.32319057	31.30221133	92.46147143	30.1137	25.9358	91.7979	−0.174351081	1.388236661	−0.215475109	1.608041171	0.849288715	0.005766697	0.962518298	0.291280954	specific_fp360
group_4965	0	2.099502093	3.655880476	0.538791333	0.774747143	0	0	0	−2.762420355	−2.23842147	NA	NA	0.603793006	0.750675769	0.84627402	0.944159956	specific_fp360
group_4966	0	0.300509767	0.497383333	0.165124667	0	0	0	0	−1.590802516	#NAME?	NA	NA	0.737898749	0.44006229	0.92045582	0.795297293	specific_fp360
group_4967	18.4753	67.47091023	51.50839619	70.153148	109.6108	21.1288	14.5356	72.7413	0.445700224	1.08951043	−0.539620208	1.783563877	0.782789446	0.505157462	0.940746951	0.829765334	specific_fp360
cckA_1	3.03825	7.615988186	7.651431048	6.707631333	9.456138571	3.01606	3.03825	5.02835	−0.189926203	0.305521577	0.010575457	0.737419943	0.550606308	0.729842056	0.813536922	0.93560145	specific_fp360
group_4969	4.68852	9.215138837	9.206010952	8.384729333	11.02197143	6.77303	3.47005	5.17247	−0.134811946	0.259734228	−0.964844935	−0.388948013	0.434663163	0.893972439	0.736370534	0.989877233	specific_fp360
group_4970	2.79288	8.108121249	8.36834189	6.838957667	10.04709557	2.92435	2.22916	5.30866	−0.291165335	0.263764806	−0.391615819	0.860231755	0.351473793	0.936559683	0.679404074	0.998970498	specific_fp360
group_4971	4.20377	12.63609993	12.11929576	11.9822224	15.58767857	4.48828	3.01174	6.02565	−0.016410351	0.36310022	−0.575565452	0.424954196	0.685168656	0.539820057	0.892983782	0.848490936	specific_fp360
group_819	3.37013	10.60451849	10.33056262	9.383758	14.04230143	3.37013	3.06319	8.11765	−0.138681115	0.442860574	−0.137769388	1.268257895	0.448353325	0.613754585	0.742827765	0.891693103	specific_fp360
phoP_1	8.5256	22.10111874	22.83124905	18.6720224	27.25879143	9.96597	4.07792	18.968	−0.290131592	0.25571181	−1.289176758	0.928485432	0.20913679	0.750098681	0.550359975	0.944159956	specific_fp360
group_3257	21.6489	24.39832969	25.26092889	25.638092	19.15389857	24.3677	21.7344	18.601	0.021381209	−0.399269623	−0.164989816	−0.389589902	0.657256698	0.375566704	0.875855678	0.756970046	specific_fp360
group_4909	60.351	64.2395414	68.59745667	52.74345933	75.80025714	77.0985	36.6582	70.78	−0.37916289	0.144047655	−1.072566844	−0.12336103	0.574412037	0.640466538	0.827484326	0.891693103	specific_fp360
group_3259	16.3112	24.95261535	27.56952333	20.753698	26.09957143	15.9641	14.7012	30.266	−0.409705898	−0.079048207	−0.1188973	0.922866798	0.699167965	0.313160454	0.901149756	0.729068877	specific_fp360
group_4974	30.2604	41.08634568	33.09588543	30.32714467	88.11315714	25.8741	24.579	94.3027	−0.126042196	1.412705591	−0.07408246	1.865790397	0.974400707	0.010864488	0.998451488	0.291280954	specific_fp360
group_4977	29.4066	39.45429172	32.29879448	30.14503067	80.8692	27.8849	25.0994	88.9305	−0.099560122	1.324110021	−0.15183122	1.6731942	0.948827759	0.010864488	0.99049674	0.291280954	specific_fp360
group_4980	19.7378	38.25736558	23.55794667	24.643676	111.5278143	18.4875	12.8874	89.5404	0.065003675	2.24311785	−0.520588914	2.275988616	0.897504334	0.020391723	0.973799052	0.321572104	specific_fp360
group_4987	118.391	153.0858174	122.2335652	142.6147587	268.0805571	90.1362	137.559	292.284	0.222482786	1.133026088	0.609871998	1.697192322	0.422326539	0.022451016	0.733861396	0.338583911	specific_fp360
group_4988	57.6295	78.98258984	57.38893014	65.208082	173.2803714	45.7902	53.0951	168.245	0.184278306	1.594263856	0.213539858	1.877452859	0.676559184	0.010864488	0.887757152	0.291280954	specific_fp360
group_4994	0	2.820000698	4.693138571	0.910152667	1.293118571	0	0	0	−2.366372594	−1.859698491	NA	NA	0.457492859	0.657441267	0.751356885	0.907768846	specific_fp360
group_4996	0	7.492632698	7.233745714	4.255125067	15.20681	0	0	0	−0.765541348	1.071902755	NA	NA	0.724318329	0.727264628	0.91408214	0.933552293	specific_fp360
group_4998	0	9.619668605	6.711792857	5.671438	26.80379	0	0	0	−0.242983613	1.997666913	NA	NA	1	0.630941086	1	0.891693103	specific_fp360
group_5000	0	2.945936047	4.98284381	0.916328	1.184372857	0	0	0	−2.443033343	−2.072846019	NA	NA	0.377619692	0.505939882	0.699835723	0.829765334	specific_fp360
group_5013	116.291	140.9418256	118.4671714	114.20864	265.6511857	104.082	115.325	326.415	−0.052815531	1.165045825	0.147984703	1.648986766	0.923292653	0.17548821	0.982441117	0.637558112	specific_fp360
gntP	4.79051	8.606175767	6.007090143	10.915053	11.45583857	4.79051	4.04765	7.5945	0.861580917	0.93134485	−0.243094708	0.664775731	0.699556711	0.394643965	0.901149756	0.777353902	specific_fp360
iolI	7.01962	12.47351233	8.385708571	12.39611067	24.90278429	7.01962	5.36356	14.8842	0.563882942	1.570302455	−0.388202043	1.084316842	1	0.150876199	1	0.62344147	specific_fp360
group_5036	19.6014	30.74048043	26.40445803	17.999256	71.05117143	20.37	14.4016	50.9474	−0.552844256	1.428076906	−0.500216878	1.322562543	0.274976326	0.007974357	0.611093516	0.291280954	specific_fp360
citD	91.8664	123.5572547	107.9016381	96.78653667	227.8899286	91.8664	83.2951	216.413	−0.156838484	1.0786204	−0.141305666	1.236177965	0.70018293	0.016947799	0.901149756	0.297974622	specific_fp360
citE	34.8024	42.42252023	36.08937286	30.81110933	86.30355714	36.0553	27.6887	94.6685	−0.228123446	1.257845951	−0.380914026	1.392673117	0.563527243	0.012632521	0.822000841	0.291280954	specific_fp360
citF	36.653	46.27845651	40.18313952	34.62808	89.5295	40.5545	33.3595	95.9602	−0.214647889	1.155772842	−0.281764342	1.242574157	0.589884939	0.012075606	0.83261548	0.291280954	specific_fp360
phoP_2	70.5821	94.03496672	80.36834138	69.3956	187.8334857	70.5821	64.6891	188.205	−0.211783116	1.224755067	−0.125779714	1.414930697	0.657256998	0.012075606	0.875855678	0.291280954	specific_fp360
cckA_2	28.0751	39.796745	31.54593167	30.18442467	85.14701429	28.0751	25.4975	86.8868	−0.063649657	1.432501983	−0.138935362	1.629845856	0.897865788	0.012632521	0.973799052	0.291280954	specific_fp360
cynT	68.8808	87.98869023	71.64002476	68.097024	179.6596857	66.2177	62.9246	171.536	−0.073174086	1.326428974	−0.073592761	1.373222578	0.82453995	0.006998074	0.953072345	0.291280954	specific_fp360
group_5047	21.0866	64.06837442	43.23612381	87.81917333	75.67055714	16.9828	15.2571	50.357	1.022298765	0.807494879	−0.154593572	1.568117998	0.771018624	0.350842883	0.932862337	0.748638329	specific_fp360
group_5053	23.7547	43.11002509	24.4318809	34.34976533	117.9164429	17.1265	30.7336	94.6892	0.491535308	2.270928069	0.843586418	2.466969535	0.44094788	0.004918205	0.73975808	0.291280954	specific_fp360
group_5054	0	1.534894186	1.288475714	1.634646667	2.060394286	0	0	0	0.343313482	0.677255099	NA	NA	0.52909389	0.405674265	0.798967284	0.777353902	specific_fp360
group_5057	27.7314	37.27777233	28.87809571	29.68521333	78.74657143	24.8358	24.9674	88.7723	0.03976887	1.4472415	0.007624374	1.837688358	0.897846171	0.014610022	0.973799052	0.291280954	specific_fp360
group_5060	40.7587	71.83103372	48.21801762	89.474132	104.8634429	28.2616	46.9722	85.9189	0.891898304	1.120867574	0.732964021	1.604132378	0.478646962	0.312097529	0.767698136	0.729068877	specific_fp360
group_5065	8.52525	12.32723581	10.21107	10.347968	22.91702143	8.21892	5.21613	16.0573	0.019213446	1.166285495	−0.655969004	0.966208592	0.772459737	0.038423313	0.932862337	0.442291965	specific_fp360
kbaZ	29.2555	38.2499034	33.91000267	27.518166	74.26618571	26.4303	26.2632	78.4065	−0.301326576	1.130994586	−0.009150091	1.56878046	0.568137602	0.008438904	0.822890915	0.291280954	specific_fp360
agaS	35.8275	46.72061186	39.39506333	34.66823867	94.52377143	33.0354	33.3294	93.8126	−0.184400313	1.262662339	0.012782533	1.505768891	0.775571382	0.008438904	0.932862337	0.291280954	specific_fp360
group_5069	47.0687	58.65674744	50.78122381	43.523156	114.7124429	37.9453	45.3132	103.65	−0.222511989	1.17565482	0.256010176	1.44972701	0.948827759	0.003517549	0.99049674	0.291280954	specific_fp360
group_5070	32.627	39.36009209	31.81666571	30.872032	80.17907143	28.805	27.4262	83.1927	−0.043482209	1.333443056	−0.070764512	1.530137682	0.936022389	0.007948639	0.989957038	0.291280954	specific_fp360
kbaY	47.0658	64.27028349	52.25329048	48.88819933	133.2828714	46.2681	43.8587	143.877	−0.09603562	1.350897593	−0.077154806	1.636746222	0.974738265	0.012075606	0.998451488	0.291280954	specific_fp360
levE	95.874	124.3800823	107.2109958	93.27625533	242.5384	84.4985	92.3233	233.534	−0.200871103	1.177760302	0.127769061	1.46663497	1	0.014333975	1	0.291280954	specific_fp360
agaC	35.2103	46.88647263	44.66802205	32.951344	83.40281429	35.2103	27.3136	100.72	−0.438905062	0.900853694	−0.366378042	1.516280764	0.485094963	0.016926793	0.769313597	0.297974622	specific_fp360
group_5076	35.9732	43.81239953	43.55994095	30.07175467	74.01401429	33.9596	30.4606	62.0626	−0.534592948	0.764796467	−0.156875106	0.869904671	0.391043067	0.019899666	0.708482658	0.316589591	specific_fp360
glnQ_1	71.8843	90.84898947	75.70868795	66.70047333	188.0167143	71.8843	55.1041	211.073	−0.182761867	1.312330149	−0.383517045	1.553993428	0.680367217	0.008438904	0.887757152	0.291280954	specific_fp360
peb1A	37.5497	47.27014116	39.89788095	36.68688467	92.06532857	36.0842	32.2203	93.247	−0.121047724	1.206345821	−0.163397343	1.369690041	0.872528725	0.043758505	0.969519052	0.473896702	specific_fp360
glnM	39.5031	44.01991628	39.10312381	31.13191333	86.38744286	39.8577	28.6118	80.8175	−0.328889618	1.143537756	−0.478248199	1.019809263	0.304485084	0.007974357	0.637850627	0.291280954	specific_fp360
gltK	55.4818	67.31122772	60.35399819	50.09536867	125.0740429	55.2327	41.5252	131.711	−0.268772114	1.05126116	−0.411535537	1.25378128	0.634461044	0.012075606	0.862886195	0.291280954	specific_fp360
group_5090	3.15209	8.208521628	4.202465714	16.06257733	3.39657	3.15209	2.57216	3.54134	1.934395446	−0.307157462	−0.29332834	0.167986634	0.540670011	0.849281295	0.809381392	0.977920647	specific_fp360
group_5102	76.5155	87.49229326	104.1581719	92.10986	27.59987143	90.9575	84.2039	28.3864	−0.177348528	−1.916042581	−0.111305547	−1.679992706	0.611998112	0.003109692	0.847276289	0.291280954	specific_fp360
group_5103	28.5734	36.28867256	41.12769619	40.59477667	12.54423571	38.5271	24.0951	8.45856	−0.018816152	−1.713085686	−0.677133807	−2.187389614	0.799959914	0.006998074	0.941662441	0.291280954	specific_fp360
group_5108	98.229	126.1551721	108.2537	89.64814	258.0889429	92.7475	61.1	198.953	−0.27207078	1.253451999	−0.602136015	1.101047354	0.797359979	0.014610022	0.941662441	0.291280954	specific_fp360
group_5109	40.6228	54.17814814	47.71930952	38.12719133	107.9495714	44.7748	33.2934	111.384	−0.32375291	1.177712443	−0.427450779	1.314783115	0.404097301	0.010864488	0.721244563	0.291280954	specific_fp360
group_5113	0	3.684263721	2.046472381	3.244316	9.540382857	0	0	0	0.66477515	2.220907967	NA	NA	1	0.382222719	1	0.764339147	specific_fp360
group_5116	0	2.453482023	1.358347952	2.049716667	6.604095714	0	0	0	0.593571414	2.281507944	NA	NA	0.825533669	0.675567129	0.953149842	0.911169378	specific_fp360
group_5121	27.1646	36.10834972	30.51967943	26.401438	73.67488571	28.212	22.8082	71.8219	−0.209123298	1.271433109	−0.30675635	1.348114874	0.775571382	0.016926793	0.932862337	0.297974622	specific_fp360
group_5122	24.5667	33.56265844	27.30650205	24.53874467	71.66808571	23.7512	22.4124	73.4761	−0.154183071	1.392086303	−0.08370326	1.629274647	0.874183012	0.012075606	0.969519052	0.291280954	specific_fp360
group_5129	0	0.398058886	0.513355386	0.3783588	0.094383857	0	0	0	−0.440202921	−2.443345885	NA	NA	0.852644436	0.873767975	0.96434809	0.977920647	specific_fp360
group_5130	0	0.50057186	0.594131619	0.5614944	0.089344286	0	0	0	−0.081510935	−2.733335204	NA	NA	0.423504686	0.766955903	0.733861396	0.954543453	specific_fp360
group_5140	0.183937	7.119376977	3.194568714	10.08400847	12.54102	0	1.5454	0	1.658376158	1.972961615	Inf	NA	0.096518368	0.680584397	0.394175977	0.91358641	specific_fp360
group_5141	0	0.413741581	0.628894667	0.305606667	0	0	0	0	−1.041142385	#NAME?	NA	NA	0.788922711	0.44006229	0.941662441	0.795297293	specific_fp360
group_5147	38.4158	48.91811558	44.60321286	51.70274	55.89577143	32.1205	39.5058	51.1649	0.213093105	0.325591512	0.298570126	0.671660085	0.772687801	0.404628222	0.932862337	0.777353902	specific_fp360
group_5148	39.776	47.86120302	47.45988333	33.56487933	79.70014143	42.9871	32.831	63.1647	−0.499756098	0.74787373	−0.388845093	0.555214738	0.311042398	0.457367719	0.642617203	0.805513981	specific_fp360
group_5149	0	5.383706186	8.837999095	3.060092333	0	0	0	0	−1.530144599	#NAME?	NA	NA	0.969493981	0.094115052	0.998451488	0.597602212	specific_fp360
epsG	0	2.999756977	5.644912286	0.696426133	0	0	0	0	−3.018908918	#NAME?	NA	NA	0.937292144	0.129742991	0.99049674	0.609562655	specific_fp360
group_5152	0	4.026523721	7.111481429	1.586627333	0	0	0	0	−2.164186818	#NAME?	NA	NA	0.854910545	0.129742991	0.966303912	0.609562655	specific_fp360
group_5162	21.0905	29.50996988	22.1628531	24.914646	61.39844286	15.665	22.1348	50.922	0.16885046	1.470058451	0.498771568	1.700744314	0.319753075	0.049513817	0.652748016	0.487745008	specific_fp360
group_5168	53.8283	78.2201993

group_5202	90.6375	125.6681042	97.67653905	93.91347733	277.6884286	85.472	82.8197	276.551	−0.056679872	1.507383073	−0.045477904	1.694021773	1	0.007974357	1	0.291280954	specific_fp360
group_5221	19.1941	25.23232721	20.9160681	29.38350333	29.28572714	19.0215	22.357	13.0583	0.490394743	0.485586044	0.233095593	−0.542663928	0.640987391	0.770128299	0.868971798	0.956145131	specific_fp360
group_3298	0	20.1760207	18.35453714	23.16928067	19.22634286	0	2.589	0	0.33607652	0.066947633	Inf	NA	0.618970932	1	0.853736359	1	specific_fp360
group_3300	0	2.558362047	1.15199081	1.852106067	8.290881429	0	0	2.82249	0.685037514	2.84739628	NA	Inf	0.333182313	0.011921903	0.665809784	0.291280954	specific_fp360
group_5224	0	11.12813558	2.808034286	15.56203933	26.58721714	0	0	0	2.470398675	3.243100324	NA	NA	0.914389623	0.596608039	0.982441117	0.885590377	specific_fp360
group_5229	81.8831	131.0728047	161.7602333	98.67768667	108.4286286	109.595	29.1711	63.7391	−0.713061184	−0.577111259	−1.909570286	−0.781931427	0.222126391	0.690288043	0.56449293	0.919767665	specific_fp360
group_5230	0	4.202975581	1.64964281	1.4363054	17.79155286	0	0	1.47315	−0.199791137	3.430966853	NA	Inf	0.886023345	0.133847855	0.973799052	0.609562655	specific_fp360
group_5231	0	11.31535093	15.42935524	10.81743273	0.040305571	0	0	0	−0.512319626	−8.580482785	NA	NA	0.854910545	0.364516349	0.966303912	0.756970046	specific_fp360
cetB	17.4238	24.93562674	24.99193238	21.1113 38	32.96161429	17.4238	4.13407	23.8369	−0.243444438	0.399324445	−2.075424577	0.452137326	0.922206555	0.320703715	0.982441117	0.729068877	specific_fp360
group_5242	11.9014	27.52049316	29.311386	22.827344	32.20456286	9.61669	16.9812	17.8444	−0.360698179	0.135803921	0.820326094	0.891859074	0.595669292	0.576946899	0.838970834	0.872802773	specific_fp360
group_5245	22.1868	100.1234653	81.37562905	103.1832867	149.8102143	22.1868	33.1573	0	0.34254061	0.880467297	0.57962493	#NAME?	0.842715172	0.82505324	0.962518298	0.972982434	specific_fp360
group_5246	0	52.62784558	39.69228143	17.683144	166.3160414	6.84591	0	9.14729	−1.166483684	2.066996933	#NAME?	0.418102064	0.266321546	0.46729956	0.600281297	0.806806996	specific_fp360
group_3299	0	2.190511163	2.75779	1.961213333	0.980027143	0	0	0	−0.491766128	−1.492618991	NA	NA	0.788922711	0.766955903	0.941662441	0.954543453	specific_fp360
group_3301	7.48395	19.09240233	12.59183429	21.063918	34.36943	7.48339	17.1797	8.16897	0.742285351	1.448637466	1.198940975	0.126462221	0.67081347	0.554895669	0.886537626	0.864297421	specific_fp360
group_5251	4.2475	11.61417886	6.176100952	17.2246594	15.90595429	2.52639	5.10515	9.01691	1.479707216	1.36479869	1.014875985	1.835555756	0.6290568	0.221089193	0.862403882	0.676550263	specific_fp360
group_5253	5.66256	10.11618216	7.017496667	13.50975933	12.14028757	5.24526	8.21546	6.58518	0.944973596	0.790774217	0.64732707	0.328208589	0.302767383	0.558401346	0.636474498	0.864297421	specific_fp360
group_5255	38.0064	52.20808047	45.79831429	30.1118 96	118.7863457	38.0064	33.6825	136.659	−0.604960947	1.375002608	−0.174243155	1.846266192	0.47002925	0.022451016	0.758791614	0.338583911	specific_fp360
group_5261	3.55541	11.64302116	9.618850952	10.196472	20.81528	1.48785	4.24314	7.45517	0.084133595	1.113706497	1.511903194	2.325012164	0.362061967	0.154903273	0.686192725	0.62344147	specific_fp360
group_5263	0	13.10635581	8.720524762	20.05998	11.36322571	0	0	0	1.20183331	0.381885578	NA	NA	0.414726992	0.564835117	0.727945964	0.864297421	specific_fp360
group_5264	22.7504	181.2105235	257.2653776	89.314372	149.9662857	93.2274	0	57.7967	−1.526293064	−0.778619113	#NAME?	−0.689766911	0.053360476	0.914841177	0.322851313	0.989877233	specific_fp360
group_5266	39.6596	136.7713628	152.5567052	52.46319133	270.0757029	43.5572	15.6636	105.938	−1.539968117	0.824018264	−1.475495387	1.282237056	0.432644642	0.200727376	0.734504224	0.654553408	specific_fp360
group_5267	0	8.957680233	7.531031429	8.553982667	14.10269286	0	7.57671	0	0.183748818	0.905051295	Inf	NA	0.492748482	1	0.77649137	1	specific_fp360
group_5268	12.3732	25.4369716	18.28990429	31.34626127	34.21541	9.82569	23.2628	13.0709	0.777245855	0.90359871	1.24394128	0.411727854	0.40382487	0.524112796	0.721244563	0.840581695	specific_fp360
group_5272	5.54586	27.15125405	29.00706	34.2607916	6.349112857	9.86817	0.900244	3.90069	0.240154406	−2.191777152	−3.454394585	−1.339053222	0.08270565	0.144005728	0.369734325	0.619620551	specific_fp360
group_5277	24.5662	31.20307209	26.3279581	36.810512	33.81247143	19.4438	27.0103	31.7196	0.483522181	0.360959835	0.474199464	0.706064378	0.199029103	0.312097529	0.536253054	0.729068877	specific_fp360
group_5279	7.35093	12.47810209	9.391711905	13.965428	18.55014571	6.46784	7.35093	14.6262	0.57239973	0.981970461	0.184642793	1.1771991	0.385680777	0.20165923	0.708482658	0.654553408	specific_fp360
group_5288	50.1373	67.54416558	55.78551429	49.78028133	140.8855857	41.847	43.1507	137.731	−0.164316165	1.33656156	0.044259763	1.718657207	0.897865788	0.010864488	0.973799052	0.291280954	specific_fp360
group_5292	272.153	364.3151442	281.6593	339.3825267	665.7097143	242.466	266.647	526.918	0.268961181	1.240942113	0.137148638	1.119796006	0.422416141	0.010864488	0.733861396	0.291280954	specific_fp360
group_5294	103.858	155.4018465	123.0144238	117.4420933	333.9064429	98.7365	103.339	340.756	−0.066877897	1.440616445	0.065729418	1.787083649	0.923292653	0.01950584	0.982441117	0.316589591	specific_fp360
pat	44.7255	58.67681721	48.49708048	44.107192	120.4366529	44.4127	41.055	107.221	−0.136883983	1.312304714	−0.113414345	1.27154331	0.949501181	0.012075606	0.99049674	0.291280954	specific_fp360
alkA	50.9464	67.94712553	53.45380514	53.18105267	143.0686714	43.1664	45.4352	146.074	−0.007380317	1.420343236	0.07390165	1.758718728	1	0.007974357	1	0.291280954	specific_fp360
group_5307	381.548	651.9595093	558.8044714	627.7522	983.2974286	381.548	266.739	425.993	0.167851615	0.815284305	−0.516435787	0.15896516	1	0.434931252	1	0.795297293	specific_fp360
group_5308	135.104	314.7313721	255.8712714	278.2851067	569.4108143	135.104	133.462	184.166	0.121145526	1.154051719	−0.01764136	0.446936352	0.634461044	0.466438634	0.862886195	0.805513981	specific_fp360
group_5309	287.534	470.5049186	376.4124762	527.29632	631.0863857	271.964	287.534	377.835	0.486299481	0.745523054	0.080316866	0.474340655	0.308723468	0.755748117	0.639286104	0.944159956	specific_fp360
group_5310	164.473	245.456293	212.1624095	226.55584	385.8389143	105.787	189.123	165.153	0.094697615	0.86282959	0.838162478	0.642640829	0.924313351	0.603656971	0.982441117	0.885590377	specific_fp360
group_5314	186.896	346.8590953	432.0192143	249.1267933	300.8051	277.11	180.325	152.481	−0.794215288	−0.522266451	−0.61985935	−0.861829288	0.180087982	0.296035607	0.510284718	0.71412011	specific_fp360
idi	121.054	333.2232163	358.3083905	224.92476	490.0358143	116.765	139.492	70.1294	−0.671759344	0.451685365	0.256574489	−0.735516605	0.589884939	0.375566704	0.83261548	0.756970046	specific_fp360
group_5323	18.3595	59.18367651	54.04697381	44.596538	105.8519386	18.3595	15.6794	21.736	−0.277282122	0.969761945	−0.227656416	0.243559702	0.652852621	0.288373038	0.875855678	0.71412011	specific_fp360
group_5325	17.1598	55.16347079	40.89180281	47.091913	115.27467	16.3939	13.5455	31.1805	0.203667661	1.495191962	−0.275345455	0.92748496	1	0.375566704	1	0.756970046	specific_fp360
group_5326	24.1863	95.63358542	70.21463586	85.189778	194.2700214	23.8303	24.0093	55.9944	0.278908547	1.468219601	0.010796228	1.232485437	0.849288715	0.228151076	0.962518298	0.676550263	specific_fp360
group_5328	13.6551	43.07010186	31.60493429	33.30409133	98.39277	7.41232	13.6551	25.2869	0.075549605	1.638402494	0.881442808	1.770393112	0.664681435	0.137197565	0.880372762	0.609562655	specific_fp360
group_5329	11.8206	34.43096256	20.56741333	27.411564	91.06317857	10.2801	3.42246	35.0926	0.414424281	2.146507453	−1.586748713	1.771312542	0.731376587	0.142628368	0.916767309	0.617583823	specific_fp360
dut_2	42.3627	111.7923786	73.10052619	104.6062147	243.2668586	36.5391	50.2794	72.9523	0.517014869	1.734586092	0.460526335	0.997512364	0.797359979	0.099979041	0.941662441	0.597602212	specific_fp360
group_5334	40.249	99.15082116	74.96224	84.10145133	203.9652143	30.1357	43.6229	51.6662	0.165966633	1.444087156	0.533612105	0.777747202	0.949501181	0.347768656	0.99049674	0.743402024	specific_fp360
group_5336	42.8252	112.2657988	95.45276571	89.898284	210.6352871	37.6799	42.8252	50.8749	−0.086493422	1.141888242	0.184664848	0.433158917	0.849288715	0.603656971	0.962518298	0.885590377	specific_fp360
group_5337	76.2972	213.4800614	147.6331114	183.5805667	475.0912571	58.366	84.2272	108.016	0.314397019	1.68618833	0.529158007	0.888044925	0.71210625	0.14003581	0.907784172	0.609562655	specific_fp360
group_5342	33.6891	100.3365848	78.14362171	81.94779933	206.3200143	31.1489	16.6621	45.9801	0.068577085	1.400683752	−0.902610975	0.561828387	0.949501181	0.347768656	0.99049674	0.743402024	specific_fp360
group_5343	19.375	56.55725465	45.14734286	48.188826	108.7193371	17.7268	10.5349	30.4517	0.094057573	1.26789558	−0.750755508	0.780590643	0.797359979	0.296035607	0.941662441	0.71412011	specific_fp360
group_5346	22.3373	72.81012837	52.65877286	63.89785133	152.3619314	21.9474	15.1633	33.3028	0.279093517	1.532756675	−0.533466278	0.601593439	0.949501181	0.375566704	0.99049674	0.756970046	specific_fp360
group_5348	17.6827	57.62223558	38.77682048	58.434804	112.4172629	14.8979	41.6833	27.5699	0.591633386	1.535597175	1.484360514	0.887985051	0.404006531	0.288571101	0.721244563	0.71412011	specific_fp360
group_5349	17.3712	50.57364184	34.24891695	50.03681355	100.6981629	13.5654	32.8304	19.7865	0.546931552	1.555907091	1.275100739	0.54458485	0.485094963	0.466438634	0.769313597	0.805513981	specific_fp360
group_5350	20.934	56.45691967	37.78214743	56.27911133	112.8622543	15.6322	35.624	21.5014	0.574894845	1.578786463	1.188328686	0.459909769	0.373620294	0.466438634	0.696006757	0.805513981	specific_fp360
group_5351	1.60434	19.20140351	12.97586562	26.12532827	23.04103557	1.48763	6.79439	3.1103	1.009618381	0.828374776	2.191328285	1.064037993	0.187317478	0.872932081	0.523733381	0.977920647	specific_fp360
group_5352	9.46162	29.41350279	17.90544333	27.940208	67.09474143	10.898	8.55628	9.46162	0.641944521	1.905801459	−0.349007796	−0.203904271	0.897504334	0.670389959	0.973799052	0.911169378	specific_fp360
group_5353	2.21386	11.14906488	6.857734286	9.796371333	26.92168571	2.21386	2.07494	4.5063	0.514515455	1.972964837	−0.093494373	1.02537937	0.960885718	0.687262553	0.998451488	0.918014309	specific_fp360
coaE_2	115.711	162.0835405	120.7844019	122.03896	371.7907714	97.8378	103.319	356.689	0.014907634	1.622056803	0.078641717	1.866202856	0.70018293	0.004918205	0.901149756	0.291280954	specific_fp360
citC	27.1913	38.27610488	30.39757143	28.59136133	82.66472714	24.8483	24.5928	85.5876	−0.088376753	1.4433158	−0.014911151	1.78425464	0.923292653	0.0125961	0.982441117	0.291280954	specific_fp360
citG	23.9396	32.75346013	26.05680218	25.76313467	67.82270286	22.0964	21.9716	74.2726	−0.0163519	1.380108239	−0.008171409	1.749018741	0.847321768	0.016947799	0.962518298	0.297974622	specific_fp360
group_5365	39.0127	56.87750733	42.88329976	39.41060133	136.2892143	29.4686	36.8944	139.784	−0.121832159	1.668183567	0.324223332	2.245948809	0.847321768	0.012632521	0.962518298	0.291280954	specific_fp360
group_5366	22.5999	29.8933164	23.85583905	22.823975	63.15433714	17.8107	20.0507	70.7489	−0.063792357	1.404539386	0.170908386	1.989963499	0.822236304	0.014610022	0.953072345	0.291280954	specific_fp360
group_5370	0	9.611983023	11.34566524	2.293473333	20.09345714	0	0	0	−2.306535164	0.824584604	NA	NA	0.31068583	0.630941086	0.642612703	0.891693103	specific_fp360
group_5375	58.5538	88.30718558	92.01195619	89.46958667	74.70201429	54.1468	74.8976	91.4877	−0.040423988	−0.300674195	0.468043411	0.756701715	0.849288715	0.853782575	0.962518298	0.972982434	specific_fp360
group_5376	154.953	212.1134791	195.1518429	256.9688133	166.8798143	111.999	194.753	165.75	0.396996193	−0.225787629	0.798159701	0.565523019	0.077436237	0.640466538	0.363642868	0.891693103	specific_fp360
group_5377	7.20806	35.61705247	53.33061238	10.4729264	36.35664286	12.2972	2.82832	18.7545	−2.34829927	−0.552744906	−2.120312597	0.608906941	0.053889168	0.710308715	0.325232195	0.923318374	specific_fp360
group_5378	31.9622	45.34962186	46.83453143	44.887532	41.88508571	28.6359	37.2738	37.3713	−0.061257855	−0.161136005	0.38033696	0.384105804	0.949501181	0.640466538	0.99049674	0.891693103	specific_fp360
group_5379	180.752	192.8857884	175.9323714	204.9696	217.8521571	141.989	174.456	231.186	0.220388991	0.308328437	0.297084049	0.703274867	0.44611522	0.466438634	0.73975808	0.805513981	specific_fp360
group_5380	28.532	39.98047256	38.24219143	41.879478	41.12601857	22.4795	34.3541	28.532	0.131078262	0.104886213	0.611872341	0.343970932	0.924313351	0.87647039	0.982441117	0.977920647	specific_fp360
group_5381	76.1781	115.6332256	85.33280476	166.0396867	98.52064286	49.3079	93.0207	80.3795	0.960355741	0.207325574	0.915732986	0.705008793	0.04567655	0.755748117	0.317137086	0.944159956	specific_fp360
group_5382	86.0487	96.62195116	90.42900476	113.1675467	79.74594286	67.8259	107.689	83.4283	0.323602801	−0.181374463	0.666962701	0.298700562	0.190849141	0.640466538	0.523733381	0.891693103	specific_fp360
group_5387	60.2377	84.73807023	80.40937143	73.37337467	122.0770857	60.2377	62.6337	38.7073	−0.132107012	0.60235687	0.056272421	−0.638061009	0.700127833	0.690288043	0.901149756	0.919767665	specific_fp360
group_5394	16.3521	23.70535023	19.97794286	18.28816933	46.49581714	15.4138	14.7058	49.1927	−0.127497369	1.218692899	−0.067837307	1.674221665	0.859827027	0.033720767	0.969519052	0.413285019	specific_fp360
group_5398	52.8736	69.3579693	52.1616181	46.84790667	169.1828714	49.3197	36.4693	98.3815	−0.155004039	1.697522984	−0.435481516	0.996223027	0.872528725	0.005792892	0.969519052	0.291280954	specific_fp360
mog_2	8.34243	10.93786767	9.776260952	12.261648	11.58601571	7.1871	14.048	6.92501	0.326798194	0.245029827	0.966883085	−0.053593605	0.285901059	0.935089021	0.620228575	0.998970498	specific_fp360
group_5402	37.1223	51.37205444	41.61618767	37.51975333	110.3231571	36.3044	32.2465	116.898	−0.149494467	1.406518933	−0.171001829	1.687033932	1	0.005766697	1	0.291280954	specific_fp360
group_5403	42.4989	69.95964105	55.57225214	47.70927133	160.8011714	38.9892	39.1412	149.07	−0.220095057	1.532841303	0.005613434	1.93484349	0.748290253	0.007974357	0.922587843	0.291280954	specific_fp360
group_5404	23.1403	41.9924993	28.23380095	65.19058133	33.55841857	18.8481	21.7637	24.6599	1.207240177	0.249251367	0.207504748	0.387747851	0.440653258	0.490129184	0.73975808	0.822638471	specific_fp360
group_5417	92.8146	110.9261349	118.0216381	94.78536667	124.2269857	87.7717	93.028	156.608	−0.316315135	0.073927215	0.08390916	0.835330156	0.961587057	0.613754585	0.998451488	0.891693103	specific_fp360
group_5435	468.822	480.7659767	533.6361905	435.8329333	418.4404286	527.186	441.482	346.047	−0.292081295	−0.350834264	−0.255957441	−0.607344061	0.293709056	0.404628222	0.623806844	0.777353902	specific_fp360
group_5436	18.6732	51.76906135	54.6608581	39.25500933	69.90949686	22.8691	16.1069	9.00236	−0.47763134	0.354980344	−0.505720737	−1.345024427	0.377527994	0.466438634	0.699835723	0.805513981	specific_fp360
group_5437	17.9077	54.43358456	57.5332729	41.54974667	72.74274357	18.1325	13.8387	9.44203	−0.469556863	0.338406796	−0.389869426	−0.941408877	0.82453995	0.466438634	0.953072345	0.805513981	specific_fp360
group_5450	0	3.763515279	3.933070333	3.045914667	4.792565714	0	0.73869	0	−0.368780461	0.285142228	Inf	NA	0.368782159	0.926030467	0.691905282	0.998213924	specific_fp360
group_5453	0	3.297362186	2.811121048	2.606702533	6.236070571	0	0.856906	0	−0.10891962	1.149491677	Inf	NA	0.281553144	0.717940902	0.614059326	0.923727505	specific_fp360
group_5457	0	13.69482186	23.41240476	4.798769333	3.605042857	0	0	0	−2.286536753	−2.69918481	NA	NA	0.932751383	0.604907155	0.988927987	0.886285116	specific_fp360
group_5458	0	3.765646767	6.03913	1.861670733	1.025145714	0	0	0	−1.697742798	−2.55851174	NA	NA	1	0.604907155	1	0.886285116	specific_fp360
group_5467	0	2.145667674	2.519366667	2.498826667	0.267801429	0	0	0	−0.011810275	−3.233825544	NA	NA	0.939032539	0.31832406	0.99049674	0.729068877	specific_fp360
group_5469	2.09295	13.6375743	7.503263571	8.282946	43.51471	1.94387	1.81724	5.62735	0.142625746	2.535913039	−0.097182773	1.533523957	0.679329355	0.359072335	0.887757152	0.756970046	specific_fp360
group_5470	0.377394	6.863732837	8.281632905	6.2301334	3.967745714	0.877062	0	0	−0.4106522	−1.061595686	#NAME?	#NAME?	0.313585277	0.543261479	0.643703081	0.851666295	specific_fp360
group_5485	6.52904	10.36156744	8.587976667	15.08476533	5.561201429	6.43449	9.17967	2.53346	0.812702077	−0.626921678	0.512616487	−1.344716754	0.254629798	0.264943694	0.588739418	0.701218295	specific_fp360
group_5487	2.2577	7.386355335	5.317536876	11.6943114	4.361476286	2.2577	2.43282	1.7755	1.136976875	−0.285941588	0.107775786	−0.346628435	0.540624129	0.873192376	0.809381392	0.977920647	specific_fp360
group_5491	33.5453	41.16959784	34.18829033	32.33476067	81.04531429	29.9097	32.975	59.0374	−0.080416347	1.245226498	0.140759219	0.981015747	0.775571382	0.019899666	0.932862337	0.316589591	specific_fp360
group_5492	45.4858	58.48463581	51.13975571	43.029318	113.6378143	45.6766	38.9492	89.2203	−0.249125295	1.151925814	−0.229861569	0.965916733	0.44121265	0.007974357	0.73975808	0.291280954	specific_fp360
group_5493	1.84602	6.847776977	3.525196119	11.66908067	6.484154286	1.78164	1.84602	2.66068	1.726915448	0.879214868	0.05121233	0.578589154	0.359782008	0.580519645	0.683636009	0.87571151	specific_fp360
group_5494	2.62959	24.01637884	11.59914	37.87417067	31.57282714	1.11145	5.30046	17.924	1.707196455	1.444665608	2.253674521	4.011377678	0.329988705	0.224069942	0.662554008	0.676550263	specific_fp360
futA1	30.7559	42.14866112	34.24609276	32.25930533	87.04784286	27.4769	29.786	90.7436	−0.086224024	1.345869151	0.11641515	1.72357665	0.899199214	0.010122969	0.973799052	0.291280954	specific_fp360
potA_3	35.7009	44.98199395	38.21985476	35.42471933	85.74828571	34.8354	31.4922	88.2966	−0.109565873	1.165785533	−0.145559584	1.341803756	0.849288715	0.006998074	0.962518298	0.291280954	specific_fp360
group_5506	26.3404	51.87981328	34.51217814	68.13537733	69.14936714	19.3597	36.5536	26.6063	0.981298542	1.002610519	0.916956901	0.4587113	0.225875574	0.507145862	0.56449293	0.829765334	specific_fp360
group_5508	6.22076	16.35845907	9.026023 81	28.4552	12.43417714	4.25705	8.55304	6.18916	1.65652983	0.462148548	1.006583252	0.539889583	0.055673407	0.625080465	0.332349516	0.891693103	specific_fp360
group_5509	16.5398	40.00614928	41.653419	38.93102667	37.36817429	20.5719	6.11393	19.1904	−0.097514529	−0.156624841	−1.750503106	−0.100290263	0.723158869	0.873192376	0.91408214	0.977920647	specific_fp360
group_5514	0	5.401482093	9.452021429	0.448438667	3.863528571	0	0	0	−4.397640315	−1.290703833	NA	NA	0.040803928	0.239604223	0.315612553	0.680607651	specific_fp360
group_5516	183.354	305.2506305	198.1872148	236.22912	774.3441143	160.035	148.761	582.005	0.253322921	1.966110939	−0.105391109	1.862644087	0.499863693	0.007897331	0.782706606	0.291280954	specific_fp360
group_5517	183.354	305.2506305	198.1872148	236.22912	774.3441143	160.035	148.761	582.005	0.253322921	1.966110939	−0.105391109	1.862644087	0.499863693	0.007897331	0.782706606	0.291280954	specific_fp360
group_5523	8.73908	32.60125256	46.07559743	17.15775333	25.27143057	7.32584	9.25596	22.3739	−1.425142216	−0.866495537	0.337388438	1.610750658	0.987198706	0.936559683	1	0.998970498	specific_fp360
group_5530	84.5512	152.3488219	167.7851048	83.82448933	252.8778286	133.142	47.2975	151.521	−1.001170951	0.591825907	−1.493129911	0.186552012	0.041581863	0.249489882	0.315612553	0.681911623	specific_fp360
group_5531	131.857	165.4804695	132.6182333	135.1874527	328.9807857	108.749	126.075	310.552	0.027682114	1.310724184	0.213280091	1.513832724	0.520929553	0.009290942	0.795265685	0.291280954	specific_fp360
group_5537	56.4004	109.7473274	96.38922857	51.34613467	274.9670371	69.9861	32.8696	248.566	−0.908616261	1.512314839	−1.09295041	1.828488651	0.261289694	0.24305388	0.598046521	0.680607651	specific_fp360
group_5540	16.4607	80.36369279	76.80903667	15.935902	229.0872129	30.4354	7.22549	113.522	−2.268995375	1.576548972	−2.074582994	1.89914968	0.122666912	0.202279003	0.433342763	0.654553408	specific_fp360
group_5541	10.6123	29.19739698	27.38488524	10.03308533	75.70131429	8.81038	6.52222	70.4241	−1.448614509	1.466938513	−0.43384114	2.998793071	0.40242674	0.043211371	0.721244563	0.473896702	specific_fp360
group_5542	44.6155	94.76600814	89.26595238	54.20241067	198.18817	51.0812	26.4248	173.025	−0.719752994	1.150688934	−0.950899865	1.760116182	0.343543032	0.288373038	0.671966192	0.71412011	specific_fp360
group_5546	19.8378	39.95971349	27.07951333	50.29755333	56.4478	17.5733	29.6035	41.2181	0.893286412	1.059715543	0.752382622	1.22989287	0.651505539	0.221089193	0.875855678	0.676550263	specific_fp360
gpr_2	75.1753	89.98256767	91.39780048	86.36521333	93.48834286	73.7894	77.127	85.2687	−0.081709114	0.032627039	0.063822411	0.208602677	0.949501181	0.795508598	0.99049674	0.960944453	specific_fp360
group_5560	3.14572	8.739993721	7.589374762	12.60073733	3.918828571	2.96762	5.59785	0	0.731455214	−0.953558573	0.91556646	#NAME?	0.11280836	0.349474915	0.421057642	0.746605499	specific_fp360
nagC	14.2278	37.71220837	45.76412714	30.47294133	29.06916714	31.4474	11.0747	5.02528	−0.586688405	−0.654727427	−1.505673125	−2.645664855	0.385680777	0.287314122	0.708482658	0.71412011	specific_fp360
group_5562	12.143	31.42175674	38.52879048	24.79958267	24.29102857	26.4232	10.4839	6.82362	−0.635621054	−0.665513316	−1.333629698	−1.953195984	0.335612878	0.151774517	0.667517327	0.62344147	specific_fp360
group_5563	9.35305	20.38768581	27.29245048	14.21179333	12.90744714	18.0712	6.18533	0	−0.94141332	−1.080298244	−1.546769837	#NAME?	0.156494372	0.132854956	0.481288165	0.609562655	specific_fp360
group_5564	8.82289	25.39701716	31.45876181	19.58785467	19.65998857	21.3972	8.60664	3.69066	−0.683502492	−0.678199406	−1.313899991	−2.535471279	0.403521741	0.263894377	0.721244563	0.70128295	specific_fp360
group_5566	33.5889	70.68104767	84.48775333	54.81180867	63.26644286	51.262	21.2955	16.8883	−0.624255494	−0.417301752	−1.267341163	−1.601865655	0.303424631	0.36477722	0.63692634	0.756970046	specific_fp360