UNIVERSIDADE FEDERAL DE MATO GROSSO

INSETOS E MICRORGANISMOS: INTERAÇÕES POSITIVAS E NEGATIVAS COMO ABORDAGEM PARA A PROSPECÇÃO DE PRODUTOS BIOTECNOLÓGICOS

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Doctor Scientiae

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Tese apresentada à Universidade Federal de Mato Grosso, como parte das exigências do Programa de Pós-Graduação em Biotecnologia e Biodiversidade, para obtenção do título de *Doctor Scientiae*.

Orientador: Prof. Dr. Marcos Antônio Soares

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RESUMO

FALQUETO, Silvia Altoé. Universidade Federal de Mato Grosso – UFMT. Junho/2021. **Insetos e Microrganismos: interações positivas e negativas como abordagem para a prospecção de produtos biotecnológicos.** Orientador: Prof. Dr. Marcos Antônio Soares, Co-orientador: Prof. Dr. Wolf Christian Luz

Insetos, bactérias e fungos são grupos megadiversos que interagem em praticamente todos os ambientes terrestres, trazendo implicações à vida humana, animal e ao ambiente. Partimos de interações positivas e negativas entre os insetos para a prospecção de microrganismos com aplicações biotecnológicas. Em uma abordagem às interações negativas, prospectamos bactérias do gênero *Bacillus* capazes de matar larvas do mosquito *Aedes aegypti*. Obtivemos quatro isolados (*Bacillus safensis* BacI67, *Bacillus paranthracis* C21, *Bacillus velezensis* B15 e B64a) capazes de produzir sobrenadantes e lipopeptídeos tóxicos à larva, mas inócuos a organismos modelo como *Caenorhabditis elegans*, *Galleria mellonella*, *Tetrahymena pyriformis* e *Chlorella vulgaris*. Montamos os genomas dos quatro isolados e encontramos, por meio de *genome mining*, *clusters* para lipopeptídeos, terpenos, e outras moléculas que podem ser responsáveis pela ação larvicida. Na abordagem às interações positivas, estudamos a microbiota intestinal de uma larva de besouro da subfamília Rutelinae – *Pelidnota luridipes* – que vive em madeira em decomposição, usando métodos dependentes e independentes de cultivo. Isolamos 272 isolados bacterianos e e 29 de leveduras; identificadas em 57 e 7 espécies, respectivamente, enquanto detectamos por *metabarcoding* 1.481 e 267 OTUs de bactérias e fungos, respectivamente. A microbiota de suas câmaras intestinais se distingue pela composição e abundância de bactérias e fungos, com uma tendência a maior riqueza e diversidade de leveduras na câmara anterior, e de bactérias na posterior. Isolamos microrganismos capazes de produzir diversas enzimas – que podem ajudar o inseto a sobreviver com uma dieta nutricionalmente fraca. Entre os isolados, *Apiotrichum siamense* L29A e *Bacillus* sp. BL17B tiveram atividade antibacteriana *in vitro* e protegeram a larva da mariposa *Galleria mellonella* contra infecção pelas bactérias patogênicas *Listeria monocytogenes* ATCC19111 e *Pseudomonas aeruginosa* ATCC 9027. Este é o primeiro trabalho com a microbiota de larvas tribo Rutelini, demonstrando sua diversidade e potencial na prospecção de produtos microbianos como probióticos. O trabalho mostra que as interações entre microrganismos e insetos são um ponto de partida importante para a busca e desenvolvimento de produtos biotecnológicos.

Palavras-chave: microbioma, insetos vetores, *Bacillus*, probióticos, diversidade microbiana

ABSTRACT

FALQUETO, Silvia Altoé. Universidade Federal de Mato Grosso. 2021, June. **Insects and Microbes: Positive and negative interactions as starting points for prospection of biotechnological and natural product discovery.** Advisor: Prof. Dr. Marcos Antônio Soares, Co-Advisor: Prof. Dr. Wolf Christian Luz

Insects, bacteria and fungi are megadiverse groups that interact in practically all terrestrial environments, with implications to human life. We start from positive and negative interactions between insects and microbes to prospect for microorganisms with biotechnological applications. Approaching negative interactions, we prospect *Bacillus* bacteria able to kill *Aedes aegypti* mosquito larvae. We obtained four isolates (*Bacillus safensis* BacI67, *Bacillus paranthracis* C21, *Bacillus velezensis* B15 and B64a) producing supernatants and lipopeptides toxic to the larva but safe to model organisms such as *Caenorhabditis elegans*, *Galleria mellonella*, *Tetrahymena pyriformis* and *Chlorella vulgaris*. We assembled and mined the genomes of the four bacteria and found clusters for lipopeptides, terpenes, and other molecules that may be accountable for the larvicidal action. Approaching positive interactions, we studied the intestinal microbiota of the larva of a Rutelinae beetle - *Pelidnota luridipes* - that lives in decomposing wood by dependent and independent cultivation methods. We isolated 272 and 29 bacterial isolates and yeasts identified in 57 and 7 species, respectively. Using metabarcoding, we found 1,481 and 267 OTUs of bacteria and fungi, respectively. Microbiota of midgut and hindgut is distinguished by the composition and abundance of bacteria and fungi, with a tendency for greater richness and diversity of yeasts in the anterior chamber, and the opposite for bacterial communities. We isolated microbes able to produce several enzymes - which can help the insect to survive on a nutritionally weak diet. Among the isolates, *Apiotrichum siamense* L29A and *Bacillus sp.* BL17B hadprobiotic and antibacterial activity in vitro and protected *Galleria mellonella* moth larvae against infection by the pathogens *Listeria monocytogenes* ATCC19111 and *Pseudomonas aeruginosa* ATCC 9027. This is the first work with the larval microbiota Rutelini, demonstrating its diversity and potential for prospection of microbial products like probiotics. This work shows that the interactions between microorganisms and insects are an important starting point for the search and development of biotechnological products.

Keywords: microbiome, vector insects, *Bacillus*, probiotics, microbial diversity

SUMÁRIO

Introdução Geral.....1
Justificativa.....2
Revisão bibliográfica.....3
Interações entre Insetos e Microrganismos.....3
As doenças transmitidas pelo *Aedes aegypti* e o combate às larvas.....4
Microbiomas de insetos e a busca de novos probióticos.....8
Objetivo Geral.....12
Objetivos Específicos - Capítulo 1.....12
Objetivos Específicos - Capítulo 2.....12
Bibliografia (referente à Introdução Geral e Revisão Bibliográfica).....13
Capítulo 1 - Bacillus spp. metabolites are effective in eradicating Aedes aegypti (Diptera: Culicidae) larvae with low toxicity to non-target species.....25
Abstract.....26
1. Introduction.....26
2. Materials and methods.....27
2.1 Bacterial strains.....27
2.2. Aedes aegypti larvae rearing.....27
2.3. Screening for larvicidal activity.....27
2.4 Lipopeptide production and larvicidal activity.....28
2.5 Larvicidal activity of bacterial cells and culture supernatants.....28
2.6 Determination of lethal concentrations of supernatants and CLEs.....28
2.7 Toxicity of supernatants and lipopeptide extracts.....28
2.8 Persistence of larvicidal activity.....28
2.9 Genome assembly and mining.....28
3. Results.....29
4. Discussion.....31
5. Conclusion.....32
Funding.....33
Bibliography.....33
Anexo 1 - Material Suplementar para o Capítulo 1.....36
Table S1. Larvicidal activity of 254 bacterial strains against *Aedes aegypti* larvae L3, after 48 hours of treatment.....37

Table S2: Assembly parameters for each strain....43
Table S3. Putative assignments of m/z peaks from peptide spectrograms of *B. velezensis* B64a and *B. velezensis* B15 crude lipopeptide extracts....45
Table S4. Larvicidal activity of supernatants (SN) treated with denaturing agents....47
Table S5. Partial QUAST report for assemblies performed using different assemblers....48
Table S6. GO annotation for *B. safensis* BacI67, *B. paranthracis* C21, *B. velezensis* B64a, and *B. velezensis* B15....50
Table S7. Secondary metabolite gene clusters of *B. safensis* BacI67 detected by AntiSMASH....53
Table S8. Secondary metabolite gene clusters of *B. paranthracis* C21 detected by AntiSMASH....54
Table S9. Secondary metabolite gene clusters of *B. velezensis* B64a detected by AntiSMASH....55
Table S10. Secondary metabolite gene clusters of *B. velezensis* B15 detected by AntiSMASH....57
Capítulo 2 - Larval gut microbiome of *Pelidnota luridipes* (Coleoptera: Scarabaeidae): high bacterial diversity, different metabolic profiles on gut chambers and species with probiotic potential....59
Abstract....61
Introduction....62
Material and Methods....64
Insect collection and processing....64
Isolation and identification of cultivable microorganisms from larval guts....65
Sequencing and metabarcoding of gut samples....65
Evaluation of probiotic functional traits of isolates....66
Evaluation of antagonistic activity *in vivo* in *Galleria mellonella* larvae....67
Statistical analyses....69
Results....70
Gut microbial community of *Pelidnota luridipes* analysed by culture-dependent method....70
Analysis of the non-cultivable microbial community of mid and hindgut of *P. luridipes*....72
Functional profile of microbial community on gut chambers....86
Evaluation of functional traits and antibiosis *in vivo* in *Galleria mellonella* larvae....86
Discussion....88
References....94
Anexo 2 - Material Suplementar do Capítulo 2....124
Fig. S1. Third instar larvae of *Pelidnota luridipes*....125
Fig. S2. NMDS ordinations of cultivable (first row) and uncultivable (second and third row) microbial communities from *P. luridipes* using Bray-Curtis distances....126

Fig. S3. NMDS ordinations of cultivable (first row) and uncultivable (second and third row) microbial communities from *P. luridipes* using Jaccard distances.....127
Fig. S4. Hierarchical clustering of KO descriptors predicted for the bacterial community of *P. luridipes* using Bray-Curtis distance and Ward algorithm.....128
Fig. S5. Seven day plates of *Galleria mellonella* on confrontation tests with *Bacillus* sp. BL17B (BL17B) and *S. flexneri* ATCC 12022 (SF).....129
Fig. S6. Seven day plates of *G. mellonella* on confrontation tests with *A. siamense* L29A (L29A) and *P.* aeruginosa ATCC 9027 (PA).....130
Fig. S7. Seven day plates of *G. mellonella* on confrontation tests with *A. siamense* L29A (L29A) and *L. monocytogenes* ATCC 1911 (LM).....131
Table S1. Functional traits of microbial isolates from *Pelidnota luridipes*.....132
Table S2. Relative Frequency (%) of cultivable bacteria on gut compartiments of *Pelidnota luridipes*.....140
Tabela S3. Relative Frequency (%) of cultivable yeasts on gut compartiments of *Pelidnota luridipes*.....142
Tabela S4. Absolute and Relative abundance of bacterial OTUs on gut compartiments of *P. luridipes*.....143
Table S5. Absolute and Relative abundance of fungal OTUs in *Pelidnota luridipes* gut.....183
Tabela S6. Metabolic pathways identified by KO descriptors of *Pelidnota luridipes* gut microbiome.....197
Tabela S7. KEGG pathway map predicted by PICRUST differentially represented in bacterial communities found in midgut and hindgut of *Pelidnota luridipes*. 198
Table S8. Proportion (%) of isolates presenting funtional traits according to gut source.....199
Tabela S9. Comparison of predicted KO identifiers using PICRUSt between midgut and hindgut of *Pelidnota luridipes*. 200
Tabela S10. KEGG pathway map predicted by PICRUST differentially represented in bacterial communities found in mid and hindgut of *Pelidnota luridipes*.....247
Conclusão Geral.....252
Anexo 3 – Normas para publicação no Journal of Invertebrate Pathology.....253
Anexo 4 - Normas para publicação na Revista Applied Microbiology and Biotechnology.....272

Introdução Geral

A interação entre microrganismos e insetos é muito importante ambientalmente, já que ambos os grupos têm funções ecológicas muito diversas e participam de inúmeros processos em praticamente todos os ambientes. Microrganismos são a base de diversas cadeias alimentares, e sua interação com insetos permite que estes ocupem nichos diferentes[1]. Por sua vez, os insetos facilitam a sobrevivência e dispersão de microrganismos, agindo como vetores e sobre materiais (triturando, abrindo túneis) usados pelos microrganismos [2].

Microrganismos interagem com animais e plantas no ambiente influenciando sua sobrevivência e performance. O estudo destas interações é uma abordagem para a descoberta de novas aplicações biotecnológicas. Falando de microrganismos e insetos, a alta diversidade metabólica e de habitats dos dois grupos, e a influência de ambos nos ecossistemas e na vida humana, animal e no ambiente são um tema de estudo quase inesgotável O estudo destas interações pode ajudar a desenhar aplicações biotecnológicas mais alinhadas ao conceito do One Health, que aponta a necessidade de considerar a conexão entre a saúde ambiental, animal e humana nas atividades humanas[3,4]. As aplicações biotecnológicas das interações entre insetos e microrganismos podem ser exploradas no controle biológico e manejo de pragas[5], no estudo da decomposição e detoxificação de materiais[6], na produção de probióticos[7], fármacos e suplementos[8] e na produção de energia .

Os insetos sofrem efeitos negativos de microrganismos quando estes são patogênicos, ou seja, causam infecções e esta é, provavelmente, a interação microrganismo-inseto mais estudada. No entanto, há outros exemplos de interações negativas entre os dois: alguns microrganismos produzem compostos tóxicos que podem matar o inseto ou reduzir seu crescimento[10]. Há ainda microrganismos associados a insetos, como a bactéria *Wolbachia*, que apesar de trazer alguns benefícios ao hospedeiro podem causar problemas reprodutivos como incompatibilidade citoplasmática, morte ou feminilização em embriões machos[11]. O estudo deste tipo de interação para o manejo de pragas e vetores é uma abordagem promissora em estudo.

No entanto, há interações em que insetos têm sua performance e sobrevivência aumentadas pelos microrganismos. O estudo dos microbiomas de insetos (e de outros animais) têm mostrado que os microrganismos associados ao intestino e cutícula de vários insetos têm papel na defesa contra patógenos, no enriquecimento da dieta[12], na detoxificação de compostos inibitórios[13] e na digestão de materiais recalcitrantes[14]. Entender este tipo de interação permite a busca de microrganismos que produzam enzimas e compostos de interesse biotecnológico ou que possam ser usados como probióticos.

Justificativa

A diversidade de interações entre microrganismos e insetos é um ponto de partida para a busca de aplicações biotecnológicas para resolver problemas médicos e ambientais. A existência de insetos vetores de agentes causadores de doenças e a necessidade de controlá-los causando menos impacto ambiental justifica a procura por microrganismos patogênicos e/ou produtores de moléculas para o controle. Ao mesmo tempo, a diversidade de microrganismos associados a intestinos de insetos que vivem em ambientes nutricionalmente desafiadores como a madeira em decomposição pode ser acessada para a busca de probióticos com aplicação humana ou animal.

Assim, neste trabalho, focamos em duas abordagens biotecnológicas envolvendo interações entre microrganismos e insetos:

1. a busca de bactérias patogênicas ou produtoras de moléculas larvicidas para o controle de *Aedes aegypti* e

2. o estudo da microbiota intestinal de uma larva de besouro que vive em madeira (*Pelidnota luridipes*, um besouro da família Scarabaeidae, subfamília Rutelinae) e o isolamento de microrganismos intestinais da mesma para uso como probióticos.

O trabalho justifica-se pela necessidade de novas alternativas de larvicidas e probióticos, que abordamos pela perspectiva da interação entre microrganismos e insetos como um caminho para encontrar produtos biotecnológicos seguros, efetivos e menos impactantes ambientalmente.

Revisão bibliográfica

Interações entre Insetos e Microrganismos

O estudo de grupos megadiversos e de suas interações abriga inúmeras possibilidades biotecnológicas e os insetos e microrganismos são dois destes grupos. As estimativas do número de espécies de bactérias e fungos mais atuais giram na casa dos milhões para bactérias, arquéias e fungos[1,15,16]. Alguns autores propoem números ainda maiores: entre 10^{11}–10^{12} espécies microbianas no planeta [17]. Outras estimativas, mais recentes e que tomam em conta novas metodologias de amostragem, estimam que haja cerca de 5,5 bilhões de espécies de insetos[18]. Tanto insetos quanto microrganismos estão espalhados por todos os ambientes do planeta (exceto, para os insetos, o alto-mar) e se associam de várias maneiras. A diversidade de espécies, de habitats e modos de vida de ambos os grupos, torna a interação microrganismo-inseto um objeto de estudo bastante profícuo, assim como suas possíveis aplicações biotecnológicas.

Interações biológicas costumam ser analisadas quanto aos benefícios e desvantagens que trazem para os organismos envolvidos. No entanto, as interações também costumam ter uma certa flexibilidade, que pode levar uma espécie a cooperar em determinadas situações e não cooperar em outras[19]. Há ainda as interações neutras, em que as espécies estão associadas por interações que não trazem prejuízo nem benefício para nenhuma delas. Em todos os casos, o estudo das interações biológicas tem o potencial de encontrar funções e processos que podem ser aplicados na biotecnologia.

Os avanços metodológicos das últimas décadas, especialmente o surgimento das ciências "Ômicas" e da Bioinformática, representaram uma imensa revolução no conhecimento das interações entre microrganismos e hospedeiros, sejam eles humanos, animais ou plantas[20,21]. Até a década de 1990, o conhecimento das comunidades microbianas era severamente limitado pelas técnicas existentes: cerca de 1% das espécies de uma comunidade conseguem crescer em meio de cultura, os outros 99% dependem de condições praticamente impossíveis de simular em laboratório. O surgimento de técnicas independentes de cultivo, baseadas em extração de ácidos nucleicos totais das amostras, permitiu a detecção de uma imensa diversidade microbiana não cultivável. No momento, é possível não só saber que espécies estão presentes em uma amostra, mas ter uma noção também de que funções elas desempenham neste sistema, que genes abrigam, que enzimas e metabólitos produzem. O relativo barateamento das técnicas de sequenciamento de DNA e os avanços da bioinformática também tornaram acessível o sequenciamento de genomas[22] e a identificação de *clusters* gênicos de metabólitos de interess[23].

Nos últimos anos, inúmeros estudos relacionam a microbiota associada a um organismo à sua saúde e desempenho. Acredita-se que os microrganismos podem ter tido um papel importante na imensa diversificação

dos insetos, melhorando dietas pobres[14]; ajudando a digerir compostos tóxicos ou recalcitrantes[13,24,25]; protegendo de predadores, parasitas e patógenos[26]; contribuindo com a comunicação intra e interespecífica; afetando sua eficiência como vetores de doenças[27] e interferindo em sistemas de acasalamento e reprodução[28]. Para os microrganismos, a associação com os insetos traz os benefícios do acesso a fontes de açúcares (e à dispersão quando estas acabam)[1]; ao aumento da superfície acessível às enzimas pela trituração ou abertura de túneis[29] e o acesso à microambientes mais favoráveis dentro e fora do inseto[14]. O estudo das interações benéficas entre insetos e microrganismos inicialmente se concentrava em simbioses obrigatórias (por exemplo, entre pulgões e seus endossimbiontes ou entre cupins e protozoários). No entanto, nem todas as interações entre insetos e microrganismos são positivas ou neutras. Entre estas, a patogênese – definida aqui como a capacidade de um organismo de produzir uma infecção[30]– e a capacidade de produzir compostos que causem dano a um organismo[31–33] são as mais comuns e de maior potencial biotecnológico.

Patógenos microbianos são alternativas ao controle químico de pragas e vetores, tendo menor risco do desenvolvimento de resistência pelas pragas, maior seletividade e podendo ser biodegradados ao final do período de ação[34]. O mercado de inseticidas tem uma longa história de ingredientes ativos derivados ou inspirados por produtos naturais: calcula-se que 60% dos modos de ação conhecidos de produtos para proteção de plantas são de produtos naturais e 70% das vendas globais de inseticidas são de produtos naturais ou baseados neles (NPSEs – *Natural Product Synthetic Equivalents*)[35]. A crescente preocupação com os impactos de pesticidas no ambiente e na saúde humana e animal torna ainda mais urgente a busca por novas alternativas de controle de pragas e vetores que sejam mais específicas (menos tóxicas para espécies não alvo), seguras para a saúde humana, economicamente viáveis e ambientalmente amigáveis. Produtos biotecnológicos também são usados para proteger animais e humanos de infecções e promover seu crescimento[36], pela produção de compostos antimicrobianos, exclusão competitiva de patógenos. Microrganismos benéficos aos insetos podem ser explorados para esse tipo de aplicação.

As doenças transmitidas pelo *Aedes aegypti* e o combate às larvas

O mosquito *Aedes aegypti* é o transmissor de três arboviroses importantes no Brasil atualmente, a dengue, a chikungunya e a zika. Reportada no Brasil desde 1846, a dengue ganhou importância epidemiológica a partir da década de 80 do século XX[37]. Desde então, o número de casos, de estados e localidades atingidas pela doença tem aumentado ano a ano, tendo atingido 1.527.119 casos prováveis em 2019[38]. A entrada da febre chikungunya no ano de 2014 e da zika, em 2015, causam ainda agora grande sofrimento e preocupação à população e entidades governamentais. Há ainda a preocupação quanto à expansão global destas doenças, principalmente em países em desenvolvimento, já que o mosquito transmissor tem ampla distribuição[39,40]. O número de casos reportados anualmente à Organização Mundial de Saúde aumentou de 0,5 milhões em 2010

para 3,34 milhões em 2016[41]. Em 2019, através da Organização Panamericana da Saúde, foram reportados à OMS mais de 2,7 milhões de casos, com 1.206 mortes de janeiro a outubro. Destes casos, 2 milhões foram reportados pelo Brasil[42].

A dengue manifesta-se, clinicamente, sob duas formas principais: a dengue clássica (também chamada febre de dengue); e a forma hemorrágica, ou febre hemorrágica de dengue (FHD), às vezes com síndrome de choque de dengue (FHD/SCD)[37]. Os sintomas podem variar de leves a fatais, geralmente sendo eles: febre alta repentina (39 a 40°C), dores de cabeça, pelo corpo e nas juntas, fraqueza, dor atrás dos olhos, coceira e vermelhidão pelo corpo. Podem ocorrer perda de peso, náuseas e vômitos. Em casos mais severos, o paciente pode apresentar dor abdominal severa, sangramento de mucosas e outros sintomas, que podem ser fatais[43]. A febre chikungunya tem sintomas parecidos, porém, o paciente apresenta fortes dores nas juntas, pés, mãos, tornozelos e punhos. Cerca de 30% dos casos são assintomáticos[44]. Quanto à zika, aproximadamente 80% das pessoas infectadas não desenvolve nenhum sintoma, porém, nos casos sintomáticos, os sintomas costumam ser mais leves que os da dengue e incluem dor de cabeça, febre baixa, dores moderadas nas juntas e vermelhidão na pele e olhos. Geralmente, a evolução da zika é benigna e os sintomas desaparecem espontaneamente depois de 3 a 7 dias da infecção, no entanto, as dores nas juntas ainda podem persistir por cerca de um mês[45]. A maior preocupação é a associação da infecção pelo vírus da zika em gestantes ao nascimento de bebês com microcefalia[46].

Até o momento, só há uma vacina para a dengue, mas ela só é recomendada para pacientes que já tiveram a doença pelo menos uma vez, sob o risco de provocar sintomas ainda mais fortes quando da infecção[47]. Assim, a estratégia para prevenir ou reduzir a transmissão do vírus depende inteiramente do controle do vetor[41]. Desde o início do século XX, o Brasil leva a cabo campanhas para erradicar o *Ae. aegypti*, inicialmente por causa dos surtos de febre amarela, e, mais para o fim do século XX, pelos surtos de dengue. O principal meio de controle tem sido a aplicação de inseticidas químicos, como em fumigações para controle dos adultos, uso de larvicidas em recipientes d'água e uso caseiro de inseticidas e repelentes pela população[37]. O principal produto larvicida em uso é o organofosforado Temefós: ele é um inibidor de acetilcolinesterase, considerado seguro para aplicação em água potável. No entanto, há vários estudos mostrando desenvolvimento de resistência pelas larvas[48–51].

O desenvolvimento de resistência aumenta os custos e diminui a segurança do controle populacional do *A. aegypti*, já que uma maior quantidade de aplicações é necessária para garantir um controle satisfatório. Outras moléculas têm sido usadas, como o inibidor de crescimento piriproxifeno, um inseticida de amplo espectro, da classe dos reguladores de crescimento, análogo ao hormônio juvenil dos insetos e considerado seguro para uso em água potável [52]. Novas formas de aplicação têm sido testadas com este inseticida, com bons resultados, como a dispersão por adultos para criadouros de difícil acesso[53]. No entanto, a aplicação deste larvicida em corpos d'água e suas proximidades não é recomendada[54] pela sua longa persistência e por ter efeitos

deletérios a vertebrados aquáticos. Por exemplo, o piriproxifeno reduz a performance natatória[55] e a eclosão de ovos[56] de peixes, provoca anormalidade severa no desenvolvimento de embriões em altas concentrações[57] e provoca disrupção hormonal, limitação da função cardíaca, alterações enzimáticas e comportamentais em girinos[58]. O efeito deletério pode ser potencializado se houver presença de toxinas produzidas por algas, como a microcistina, comum em corpos d'água com florescimento de cianobactérias[56].

Há ainda na literatura estudos com o spinosad e outros inseticidas. O spinosad é a combinação de dois macrolídeos tetracíclicos, as espinosinas A e D, produzidas pela actinobacteria *Saccharopolyspora spinosa*, o que o classifica como um produto natural[59]. Foi inclusive reconhecido, em 2008, como um inseticida essencial para o manejo de pragas-chave, contribuindo para a sustentabilidade da agricultura e recebendo autorização para uso em cultivos orgânicos pela *European Union Council Regulation*[33]. No entanto, os mesmos autores citam vários estudos em que o spinosad foi tóxico contra mamíferos, embora em doses bem maiores que as usadas para o controle do mosquito. Testes da eficácia deste inseticida no controle de larvas de *Aedes* em pneus, ao lado da lambda-cialotrina e do piriproxifeno, em uma área onde já havia sido detectada resistência ao temefós pelos mosquitos, mostraram que os pneus com spinosad e lambda-cialotrina tiveram menos larvas e pupas de *Aedes aegypti*, mas o spinosad foi menos tóxico que a lambda-cialotrina para larvas do mosquito *Toxorhynchites* spp., predador de outras larvas de mosquito[60]. No entanto, os pneus com lambda-cialotrina tiveram menos ovos de *Aedes*.

No Brasil, além do piriproxifeno, usa-se o diflubenzuron, um inibidor da síntese de quitina. No entanto, já há relatos de resistência a este inseticida: em testes de inibição da emergência de adultos pelo diflubenzuron e pelo temefós em 16 localidades do estado de Pernambuco, todas as populações apresentaram graus variados de resistência ao temefós e Doses de Inibição de Emergência muito maiores que a população suscetível de referência[51]. O quadro é ainda mais preocupante: 100% das populações testadas pelos autores quanto à eficácia da cipermetrina (um piretróide usado para controle de adultos) se mostraram resistentes.

Para o controle de adultos, os piretróides, como a deltametrina e a cipermetrina, são os principais inseticidas encontrados no mercado. São seguros para humanos, mas tem alto custo e são tóxicos para peixes[61], e por isso, não podem ser usados como larvicidas. Apesar disso, mesmo as larvas de *Ae. aegypti* tem desenvolvido resistência à piretróides, provavelmente um reflexo da resistência desenvolvida pelos adultos[62]. De acordo com a *Arthropod Pesticide Resistance Database* (http://www.pesticideresistance.org), que compila relatos de resistência a inseticidas, há relatos de resistência do *Ae. aegypti* a moléculas de diversas classes e até a agentes de controle biológico, intensificando a necessidade de pesquisa e métodos alternativos de controle.

Dentre as alternativas existentes para o controle dos vetores está o controle biológico por microrganismos patogênicos, antagônicos ou que produzem substâncias tóxicas para o organismo a ser controlado (embora o controle biológico microbiano não seja livre de problemas e sua aplicação também precise ser racionalizada e minimizada[63]. O mercado global de agentes de biocontrole foi avaliado em US $ 1,3 bilhões

em 2011, e esperava-se que chegasse a US $ 3,2 bilhões em 2017[64]. Na prática, a Markets and Markets Research Private Ltd. estimava que o mercado de Biopesticidas em 2018 havia atingido a marca de US$ 3 bilhões, e previa um aumento significativo do seu valor, chegando a US$ 6,4 bilhões em 2023[65]. Especificamente quanto a larvicidas, o mercado mundial atingiu o valor de USD 719,7 milhões em 2017, e a projeção é de que atinja os 952,7 milhões em 2023[66]. Quanto aos ativos disponíveis, nos EUA há cerca de 356 ingredientes ativos biopesticidas registrados, entre estas 57 espécies ou linhagens microbianas usadas contra ácaros, insetos e nematóides[67]. O aumento da demanda por biopesticidas se deve, segundo o mesmo trabalho, à preocupação crescente com o uso excessivo de pesticidas químicos, a mudanças nos padrões de segurança de resíduos e à demanda por alimentos orgânicos.

Especificamente para o *Ae. aegypti*, há várias frentes de estudo, como predação por outros artrópodes [68], novos metabólitos microbianos [33,69], microrganismos associados que produzem efeitos reprodutivos deletérios, como *Wolbachia* spp.[70], outros microrganismos patogênicos[71] e, mais recentemente, até o uso de RNA-i[72]. O organismo mais bem-sucedido até o momento é o *Bacillus thuringiensis* var. *israelensis* (Bti)[73]. Os produtos à base de Bti são formulações granuladas ou líquidas contendo esporos e células vegetativas. Os esporos contêm duas proteínas, que, dentro do tubo digestivo do inseto, são ativadas e se ligam à membrana das células epiteliais, formando poros e desorganizando o epitélio[74]. O inseto morre por sepse e por não conseguir se alimentar. Além de altamente efetivo, é um produto para o qual quase não houve desenvolvimento de resistência, provavelmente pela dificuldade de desenvolver resistência a todas as suas várias proteínas tóxicas[48,75]. No entanto, é um produto de alto custo, o que limita sua implementação em países em desenvolvimento. Além disso, há problemas com a inativação das pró-toxinas pela luz UV, embora novas linhagens e alterações nas formulações tentem aumentar a persistência da sua atividade[76].

A diversidade metabólica microbiana faz com que os microrganismos sejam objeto permanente de pesquisa em produtos naturais. Além de abrigar patógenos para controle biológico, o gênero *Bacillus* é especialmente diverso metabolicamente: várias espécies são produtoras de lipopeptídeos com várias aplicações de interesse, embora estes tenham sido pouco explorados como inseticidas. Lipopeptídeos são compostos sintetizados por vários microrganismos como metabólitos secundários, constituído por cadeias de ácidos graxos hidrofóbicas e por uma cadeia peptídica hidrofílica cíclica curta[77]. Entre as aplicações já estudadas estão a ação fungicida, surfactante, antitumoral, antiinflamatória, antiviral e antibiótica, além do uso como aditivo em alimentos para aumentar sua vida de prateleira[77]. Como inseticidas, há alguns trabalhos citando seu uso[32,78], mas há bastante campo para pesquisa.

O gênero *Bacillus* é um excelente candidato para a prospecção de inseticidas, já que além de abrigar várias espécies que produzem proteínas inseticidas, também são conhecidos produtores de lipopeptídeos[79–81]. Além da prospecção tradicional, podemos explorar compostos pelo *genome mining*, que consiste em identificar *clusters* gênicos em genomas sequenciados, mesmo sem extrair uma estrutura química da cultura. Mesmo

linhagens bem estudadas podem conter o potencial genético para sintetizar muitos outros compostos que não foram analiticamente detectados a partir de seu cultivo, e esta capacidade é revelada pelo *genome mining*[82]. Com a popularização das técnicas de sequenciamento e o *boom* da bioinformática, a montagem de genomas e a exploração de *clusters* gênicos para metabólitos de interesse se tornaram mais acessíveis, assim como a análise das sequências das enzimas codificadas por estes *clusters* gênicos e identificação experimental dos produtos dos *clusters* gênicos encontrados. Além disso, a montagem e análise do genoma permitem conhecer os mecanismos de regulação dos genes envolvidos na síntese dos produtos de interesse.

Microbiomas de insetos e a busca de novos probióticos

A decomposição da madeira envolve processos de degradação e mineralização da celulose, hemicelulose e lignina em unidades menos complexas. É um processo lento que pode se estender por décadas nos ecossistemas florestais, onde a madeira em decomposição pode representar de 10 a 25% da biomassa acima do solo[29]. Os processos de decomposição são efetuados pela microbiota e o acesso dos microrganismos à madeira é facilitado por invertebrados saproxílicos. Organismos saproxílicos são os que dependem direta ou indiretamente da madeira em decomposição[83]. Estes animais facilitam a ação e acesso dos microrganismos à madeira por meio de abertura de túneis, trituração mecânica e ação enzimática, além de interações simbióticas com microrganismos decompositores[29].

A interação entre cupins e protozoários decompositores de celulose é um exemplo clássico deste processo[84]. Cupins da família Termitidae abrigam em seus intestinos uma diversa comunidade bacteriana capaz de degradar celulose e fixar nitrogênio[85,86]. No caso da subfamília Macrotermitinae, existe ainda uma associação com fungos Basidiomicetos[87]. Os cupins coletam resíduos vegetais e os digerem parcialmente, misturando-os com esporos do fungo durante uma primeira passagem pelo seu intestino. As fezes são depositadas no jardim de fungos, e a ingestão do fungo pelos cupins fornece biomassa fúngica e material vegetal um pouco mais digerido. A digestão da celulose é finalizada nesta segunda passagem pelo intestino[87]. Em geral, não apenas os cupins, mas outros insetos da madeira, por sua vez, tem o potencial de acelerar a liberação de nitrogênio imobilizado em tecidos fúngicos e de promover a atividade de procariotos fixadores de nitrogênio, aumentando a quantidade deste elemento no ambiente[88]. Segundo o mesmo autor, os procariotos fixadores de nitrogênio já foram reportados nas ordens Blattodea, Coleoptera e Hymenoptera, em 13 famílias, 33 gêneros e pelo menos 60 espécies. A associação entre microrganismos e insetos parece promover uma transformação benéfica à madeira, aumentando seu valor nutricional, como no caso da larva do besouro de madeira *Cetonia aurataeformis* Curtis, 1913[89].

Os besouros são o grupo mais diverso de animais, abrigando várias famílias com espécies saproxílicas, como Anobiidae, Bostrichidae, Brentidae, Buprestidae, Cerambycidae, Lymexylidae, Zopheridae e

várias famílias de Scarabaeoidea[29]. O intestino dos insetos possui ampla variação morfológica, tendo comprimentos e compartimentalização que variam com a espécie, o estágio de desenvolvimento e tipo de dieta[28,90]. A composição microbiana costuma ser diferente em cada compartimento, e o perfil funcional da microbiota também mostra compartimentalização de funções[91,92].

Por ser um material pobre em nitrogênio e constituído por moléculas recalcitrantes, muitas vezes impregnado com compostos tóxicos[25], a digestão da madeira é um processo lento e difícil[1,29]. Há evidências de que os microrganismos intestinais dos insetos saproxílicos são os responsáveis por contornar estes problemas. Os microrganismos forneceriam aos insetos moléculas que não estão presentes na madeira e que ele não consegue sintetizar, como esteróis e aminoácidos[93,94]. A análise paralela do transcriptoma do besouro saproxílico *Anoplophora glabripennis* (Motschulsky, 1854) (Cerambycidae) e do seu metatranscriptoma intestinal mostra que sua microbiota possui genes responsáveis por vias metabólicas para a produção de celulases, aminoácidos essenciais, esteróis e vitaminas, sem as quais a sua sobrevivência não seria possível[95]. Experimentos com administração de antibióticos a insetos de madeira ou a autoclavagem do substrato e isolamento de larvas com o intuito de impedir a colonização normal do intestino das larvas resultam em atrasos ou cessamento do desenvolvimento das mesmas[96].

Microrganismos são responsáveis por detoxificar compostos presentes na madeira ou material vegetal: a madeira rica em resinas terpenóides ingerida pela broca do pinus *Hylobius abietis* W. Roelofs, 1873 tem uma grande redução nos níveis de diterpenos após a passagem pelo tubo digestivo do inseto, e a administração de antibióticos reduz significativamente esta detoxificação[25]. No mesmo trabalho, os autores ainda encontraram, através de metagenômica, *clusters* de genes para a degradação de diterpenos, além de isolados bacterianos, provenientes do intestino do inseto, capazes de degradar um ácido diterpênico proveniente de uma conífera. Outros trabalhos relatam a diminuição de toxinas presentes em materiais vegetais pela microbiota de besouros (como a redução dos níveis de cafeína em grãos de café pela microbiota da broca *Hypothenemus hampei* Ferrari, 1867[13] ou a detoxificação de diversas toxinas pela levedura *Symbiotaphrina kochii,* isolada do besouro do fumo *Lasioderma serricorne* (Fabricius, 1792)[24].

O comportamento e anatomia do hospedeiro indicam a importância da microbiota associada: estruturas contendo leveduras, comportamentos de trofalaxia (regurgitação para alimentar outro indivíduo) e coprofagia são estratégias frequentes em besouros de madeira. Os besouros da família Passalidae tem comportamento subsocial, vivendo em pequenos grupos familiares compostos por um casal de adultos, larvas e às vezes, adultos juvenis que ajudam no cuidado das larvas[96]. As larvas são alimentadas pelos adultos, e acredita-se que estes inoculem microrganismos que colonizam o tubo digestivo das larvas. Os adultos do passalídeo *Odontotaenius disjunctus* (Illiger, 1800), recém-saídos da pupa, readquirem leveduras das paredes da galeria onde vivem, ingerindo uma massa composta por uma mistura de fezes com esporos e madeira[91]. Em várias famílias de besouros saproxílicos, os adultos, especialmente as fêmeas, possuem micângios: invaginações da

cutícula que abrigam leveduras[93,97–99]. Algumas das leveduras isoladas de micângios conseguem degradar xilose[97], o principal monossacarídeo liberado pela decomposição da hemicelulose, uma característica desejável biotecnologicamente[100]. Em algumas famílias, como Lucanidae, o micângio só está presente nas fêmeas e a abertura do mesmo se encontra logo acima do ovipositor, evidenciando sua função inoculatória[97]. Nesta família, as fêmeas morrem após a oviposição; assim, a inoculação de microrganismos e a escolha do local de oviposição são as únicas contribuições maternas possíveis[101]. A maioria dos micângios estudados abriga leveduras, como *Pichia* e *Saccharomyces*. No entanto, 1.546 filotipos de bactérias foram encontrados em micângios de exemplares de besouros que cultivam fungos (família Curculionidae, subfamílias Scolytidae e Platypodidae) de nove localidades ao redor do mundo, usando técnicas de metagenômica[98]. Alguns dos filotipos encontrados neste trabalho se repetem consistentemente em várias espécies ao longo do mundo.

A possibilidade de encontrar aplicações biotecnológicas em interações simbióticas é quase ilimitada, visto que as interações envolvem serviços mútuos que podem ter utilidade para o homem[102]. Nesse sentido, a associação de microrganismos com insetos saproxílicos pode fornecer desde enzimas a compostos de defesa[103], e conhecer os sistemas e as espécies nele envolvidas é o primeiro passo para a elucidação de suas aplicações.

Uma das possíveis aplicações de microrganismos associados aos besouros saproxílicos é a sua utilização como probióticos. Probióticos são organismos vivos que quando administrados em quantidades adequadas conferem um benefício à saúde do hospedeiro, segundo a definição do Consenso da *International Scientific Association for Probiotics and Prebiotics*[104]. Entre os possíveis benefícios estão o favorecimento de co-habitantes benéficos à saúde do hospedeiro, em detrimento de patógenos ou parasitas, a produção de moléculas de defesa e a disponibilização de vitaminas e enzimas ao hospedeiro. Os efeitos mais comuns produzidos pela maioria das cepas probióticas são a resistência à colonização e exclusão competitiva de patógenos, regulação da microbiota, produção de ácidos e aumento da renovação dos enterócitos, além de regularização do trânsito intestinal. Efeitos mais específicos dependem da capacidade enzimática de cada espécie ou linhagem probiótica, como produção de vitaminas e enzimas, antagonismo direto a patógenos, reforço da barreira intestinal, neutralização de carcinógenos e, dependendo da cepa, até efeitos neurológicos, imunológicos e endócrinos[104].

As principais espécies estudadas e comercialmente disponíveis de probióticos são as bactérias do ácido lático *Lactobacillus* spp., *Bifidobacterium* spp. e *Enterococcus* spp., e a levedura *Saccharomyces boulardii*, que podem ser administrados em pílulas, alimentos e bebidas[104] ou encontradas em alimentos fermentados[105]. Probióticos e alimentos contendo células microbianas vivas e ativas têm sido relacionados em várias metanálises a benefícios na saúde humana e animal, como redução da necessidade de prescrição de antibióticos em crianças[106], a melhora de enfermidades gastrointestinais em adultos[107] ou a prevenção e redução da duração de quadros de diarreia[108–111]. Em ratos, a administração de *Lactobacillus plantarum* provocou aumento da diversidade alfa da microbiota intestinal, redução de peso corporal, melhora em inflamações de baixo grau e do perfil lipídico, além de reversão de quadros de síndrome metabólica induzida por monolaurato de glicerol[112].

Lactobacillus brevis isolado de alimentos fermentados mostrou ser capaz de inibir o crescimento *in vitro* do patógeno intestinal *Listeria monocytogenes*, além de apresentar capacidade antifúngica e anti-aflatoxigênica[113]. Os microrganismos probióticos têm sido estudados como uma alternativa para a urgente substituição dos antibióticos em alimentação animal[36,114], com bons resultados em suínos[115], aves[116,117], gado bovino[118], cães[119] e até em moscas da fruta estéreis criadas para controle biológico[120].

Da mesma forma, como auxiliam os insetos saproxílicos a sobreviver em uma dieta nutricionalmente pobre como a madeira, digerindo material vegetal, detoxificando compostos e produzindo vitaminas e aminoácidos, os microrganismos associados ao intestino destes insetos podem ter interesse probiótico para humanos e animais, especialmente, no caso destes últimos, para a introdução e aproveitamento de material vegetal de difícil digestão. O interesse em estudar a microbiota de intestinos de besouros saproxílicos tem aumentado nos últimos anos pelo seu potencial de fornecer degradadores de material vegetal que permitam a sua utilização como fontes renováveis de energia [121]. Além disso, a alta diversidade microbiana do sistema[28] e a diversidade de interações já relatadas na literatura [25,99,122] indicam que este seja um sistema onde podem ser encontrados isolados com capacidades probióticas úteis tanto para uso humano como produção e tratamento animal.

Pelidnota luridipes Blanchard, 1850 é uma das espécies mais comuns do gênero *Pelidnota* na região de Cuiabá. Sabe-se muito pouco a respeito de sua biologia, mas suas larvas são encontradas em troncos em decomposição em fragmentos florestais (observação pessoal). Assim como outras espécies do gênero *Pelidnota*, os adultos são capturados no início da estação chuvosa. O gênero comporta 195 espécies e subespécies segundo a última sinopse taxonômica da tribo[123]. O gênero pertence à subfamília de escarabeídeos herbívoros Rutelinae, próxima filogeneticamente às subfamílias Melolonthinae e Dynastinae, que abrigam várias espécies cujas larvas são rizófagas (corós)[124,125]. Os adultos de *Pelidnota* são frequentemente capturados em armadilhas de luz ou frutas[126,127], mas há relatos de adultos de várias espécies se alimentando de material vegetal vivo, como brotos, flores e folhas[123,127–129]. As larvas do gênero já descritas são saproxílicas (como as da espécie *Pelidnota virescens* Burmeister, 1844, encontradas em troncos de mangueira apodrecidos no México[127]) ou rizófagas[125]. As espécies cujo ciclo de vida já foi descrito são uni ou bivoltinas, o ciclo pode se estender mais em climas mais frios e os indivíduos passam a maior parte do ciclo como larvas de terceiro ínstar[127,130]. Estudos da microbiota intestinal de besouros das subfamílias Melolonthinae e Dynastinae encontraram uma alta diversidade microbiana, com espécies capazes de degradar celulose e xilose[121,124,131]. Os hábitos e dieta das espécies destas subfamílias são similares aos de espécies de Rutelinae, assim como a morfologia intestinal de larvas e adultos. O estudo da microbiota de *P. luridipes* e sua caracterização funcional são importantes para entender a participação destes insetos na degradação da madeira e seu potencial como fonte de novos probióticos e enzimas.

Objetivo Geral

Prospectar microrganismos com potencial biotecnológico (larvicida ou probiótico) usando insetos como fonte de microrganismos ou visando o controle de insetos vetores.

Objetivos Específicos - Capítulo 1

- Prospectar bactérias capazes de matar larvas de *Aedes aegypti*.
- Determinar o efeito larvicida das células e de metabólitos das bactérias selecionadas;
- Sequenciar e avaliar os genomas das linhagens larvicidas.

Objetivos Específicos - Capítulo 2

- Avaliar a estrutura da comunidade da microbiota associada ao intestino da larva *Pelidnota luridipes* por métodos dependentes e independentes de cultivo.
- Detectar se há diferenças de diversidade, composição e abundância entre a câmara anterior e posterior do tubo digestivo de *P. luridipes*.
- Selecionar bactérias e leveduras probióticas do intestino da larva com traços funcionais importantes para uso humano ou veterinário.

O documento está organizado em uma Introdução Geral, uma Revisão Bibliográfica e dois capítulos em forma de artigo. O primeiro capítulo, intitulado "***Bacillus* spp. metabolites are effective in eradicating *Aedes aegypti* (Diptera:Culicidae) larvae with low toxicity to non-target species**" foi publicado no periódico *Journal of Invertebrate Pathology* em janeiro de 2021. O segundo, intitulado "**Microbiota associada ao intestino de *Pelidnota luridipes* Blanchard (Coleoptera: Scarabaeidae) com potencial probiótico**" será submetido à revista *Applied Microbiology and Biotechnology*. O primeiro capítulo trata da prospecção de bactérias do gênero *Bacillus* com atividade contra larvas de *Aedes aegypti*, identificando alguns dos compostos produzidos por estas e sequenciando o seu genoma. O segundo capítulo explora a diversidade microbiana associada ao trato gastrointestinal de *Pelidnota luridipes* – um besouro cujas larvas vivem em madeira em decomposição – por métodos dependentes e independentes de cultivo. O segundo capítulo também trata do isolamento e prospecção de bactérias e leveduras com características interessantes para uso como probiótico. O documento de tese termina com a Conclusão Geral.

Bibliografia

(referente à Introdução Geral e Revisão Bibliográfica)

1. Blackwell M. Made for Each Other: Ascomycete Yeasts and Insects. In: *The Fungal Kingdom*. American Society of Microbiology; 2017:945-962. doi:10.1128/microbiolspec.FUNK-0081-2016

2. Stefanini I. Yeast-insect associations: It takes guts. *Yeast*. 2018;35(4):315-330. doi:10.1002/yea.3309

3. van Bruggen AHC, Goss EM, Havelaar A, van Diepeningen AD, Finckh MR, Morris JG. One Health - Cycling of diverse microbial communities as a connecting force for soil, plant, animal, human and ecosystem health. *Science of the Total Environment*. 2019;664:927-937. doi:10.1016/j.scitotenv.2019.02.091

4. World Health Organization W. One Health. Published 2017. Accessed June 20, 2021. https://www.who.int/news-room/q-a-detail/one-health

5. Ye YH, Carrasco AM, Frentiu FD, et al. Wolbachia reduces the transmission potential of dengue-infected Aedes aegypti. *PLoS Neglected Tropical Diseases*. 2015;9(6):1-19. doi:10.1371/journal.pntd.0003894

6. Jang S, Kikuchi Y. Impact of the insect gut microbiota on ecology, evolution, and industry. *Current Opinion in Insect Science*. 2020;41:33-39. doi:10.1016/j.cois.2020.06.004

7. Praet J, Meeus I, Cnockaert M, Aerts M, Smagghe G, Vandamme P. Bifidobacterium commune sp. nov. isolated from the bumble bee gut. *Antonie van Leuwenhook*. 2015;107:1307-1313.

8. Shao Y, Chen B, Sun C, et al. Symbiont-Derived Antimicrobials Contribute to the Control of the Lepidopteran Gut Microbiota Article Symbiont-Derived Antimicrobials Contribute to the Control of the Lepidopteran Gut Microbiota. *Cell Chemical Biology*. 2017;24(1):66-75. doi:10.1016/j.chembiol.2016.11.015

9. Selim KA, Easa SM, El-Diwany AI. The xylose metabolizing yeast Spathaspora passalidarum is a promising genetic treasure for improving bioethanol production. *Fermentation*. 2020;6(1):1-12. doi:10.3390/FERMENTATION6010033

10. Pérez CM, Marina CF, Bond JG, Rojas JC, Valle J, Williams T. Spinosad, a naturally derived insecticide, for control of Aedes aegypti (Diptera: Culicidae): efficacy, persistence, and elicited oviposition response. *Journal of medical entomology*. 2007;44(4):631-638. doi:10.1603/0022-2585(2007)44[631:SANDIF]2.0.CO;2

11. Xie S, Lan Y, Sun C, Shao Y. Insect microbial symbionts as a novel source for biotechnology. *World Journal of Microbiology and Biotechnology*. 2019;35(2):0. doi:10.1007/s11274-019-2599-8

12. Vigneron A, Masson F, Vallier A, et al. Insects recycle endosymbionts when the benefit is over. *Current Biology*. 2014;24(19):2267-2273. doi:10.1016/j.cub.2014.07.065

13. Ceja-Navarro JA, Vega FE, Karaoz U, et al. Gut microbiota mediate caffeine detoxification in the primary insect pest of coffee. *Nature Communications*. 2015;6(May):1-9. doi:10.1038/ncomms8618

14. Ceja-Navarro JA, Karaoz U, Bill M, et al. Gut anatomical properties and microbial functional assembly promote lignocellulose deconstruction and colony subsistence of a wood-feeding beetle. *Nature Microbiology*. 2019;4(5):864-875. doi:10.1038/s41564-019-0384-y

15. Schloss PD, Girard RA, Martin T, Edwards J, Thrash JC. Status of the archaeal and bacterial census: An update. *mBio*. 2016;7(3):1-10. doi:10.1128/mBio.00201-16

16. Tedersoo L, Bahram M, Põlme S, et al. Ecology. Disentangling global soil fungal diversity. *Science (New York, NY)*. 2014;346(6213):1052-1053. doi:10.1126/science.aaa1185

17. Locey KJ, Lennon JT. Scaling laws predict global microbial diversity. *Proceedings of the National Academy of Sciences of the United States of America*. 2016;113(21):5970-5975. doi:10.1073/pnas.1521291113

18. Stork NE. How Many Species of Insects and Other Terrestrial Arthropods Are There on Earth? *Annual Review of Entomology*. 2018;63(1):31-45. doi:10.1146/annurev-ento-020117-043348

19. Hammer TJ, Sanders JG, Fierer N. Not all animals need a microbiome. *FEMS microbiology letters*. 2019;366(10):1-11. doi:10.1093/femsle/fnz117

20. Oulas A, Pavloudi C, Polymenakou P, et al. Metagenomics: Tools and insights for analyzing next-generation sequencing data derived from biodiversity studies. *Bioinformatics and Biology Insights*. 2015;9:75-88. doi:10.4137/BBI.S12462

21. Bashiardes S, Zilberman-schapira G, Elinav E. Bashiardes, 2016 - Use of metatranscriptomics in Microbiome research.pdf. Published online 2016:19-25. doi:10.4137/BBI.S34610.TYPE

22. Baker M. De novo genome assembly: What every biologist should know. *Nature Methods*. 2012;9(4):333-337. doi:10.1038/nmeth.1935

23. Bachmann BO, Van Lanen SG, Baltz RH. Microbial genome mining for accelerated natural products. 2015;41(2):175-184. doi:10.1007/s10295-013-1389-9.Microbial

24. Shen SK, Dowd PF. Detoxification spectrum of the cigarette beetle symbiont Symbiotaphrina kochii in culture. *Entomologia Experimentalis et Applicata*. 1991;60(1):51-59. doi:10.1111/j.1570-7458.1991.tb01522.x

25. Berasategui A, Salem H, Paetz C, et al. Gut microbiota of the pine weevil degrades conifer diterpenes and increases insect fitness. *Molecular Ecology*. 2017;26(15):4099-4110. doi:10.1111/mec.14186

26. Raymann K, Moran NA. The role of the gut microbiome in health and disease of adult honey bee workers. *Current Opinion in Insect Science*. 2018;26:97-104. doi:10.1016/j.cois.2018.02.012

27. Johnson KN. Bacteria and antiviral immunity in insects. *Current Opinion in Insect Science*. 2015;8:97-103. doi:10.1016/j.cois.2015.01.008

28. Engel P, Moran NA. The gut microbiota of insects - diversity in structure and function. *FEMS Microbiology Reviews*. 2013;37(5):699-735. doi:10.1111/1574-6976.12025

29. Ulyshen MD. Wood decomposition as influenced by invertebrates. *Biological Reviews*. 2016;91(1):70-85. doi:10.1111/brv.12158

30. Yoshinori Tanada, Harry K Kaya. *Insect Pathology*. 1st ed. Academic Press, Inc. ; 1993.

31. Abinaya M, Vaseeharan B, Divya M, et al. Structural characterization of Bacillus licheniformis Dahb1 exopolysaccharide—antimicrobial potential and larvicidal activity on malaria and Zika virus mosquito vectors. *Environmental Science and Pollution Research*. 2018;25(19):18604-18619. doi:10.1007/s11356-018-2002-6

32. Parthipan P, Sarankumar RK, Jaganathan A, et al. Biosurfactants produced by Bacillus subtilis A1 and Pseudomonas stutzeri NA3 reduce longevity and fecundity of Anopheles stephensi and show high toxicity against young instars. *Environmental Science and Pollution Research*. 2018;25(11):10471-10481. doi:10.1007/s11356-017-0105-0

33. Santos VSV, Pereira BB. Properties, toxicity and current applications of the biolarvicide spinosad. *Journal of Toxicology and Environmental Health - Part B: Critical Reviews*. 2019;00(00):1-14. doi:10.1080/10937404.2019.1689878

34. Lacey LA, Grzywacz D, Shapiro-Ilan DI, Frutos R, Brownbridge M, Goettel MS. Insect pathogens as biological control agents: Back to the future. *Journal of Invertebrate Pathology*. 2015;132:1-41. doi:10.1016/j.jip.2015.07.009

35. Lorsbach BA, Sparks TC, Cicchillo RM, Garizi N V., Hahn DR, Meyer KG. Natural products: a strategic lead generation approach in crop protection discovery. *Pest Management Science*. 2019;75(9):2301-2309. doi:10.1002/ps.5350

36. Liao SF, Nyachoti M. Using probiotics to improve swine gut health and nutrient utilization. *Animal Nutrition*. 2017;3(4):331-343. doi:10.1016/j.aninu.2017.06.007

37. Braga IA, Valle D. Aedes aegypti: inseticidas, mecanismos de ação e resistência. *Epidemiologia e Serviços de Saúde*. 2007;16(4):279-293. doi:10.5123/S1679-49742007000400006

38. Arboviroses C-G de V de. Monitoramento dos casos de arboviroses urbanas transmitidas pelo Aedes (dengue, chikungunya e Zika), Semanas Epidemiológicas 1 a 49. *Boletim Epidemiológico*. 2019;50(38):1-9.

39. Staples JE, Breiman RF, Powers AM. Chikungunya Fever: An Epidemiological Review of a Re-Emerging Infectious Disease. *Clinical Infectious Diseases*. 2009;49(6):942-948. doi:10.1086/605496

40. Akiner MM, Demirci B, Babuadze G, Robert V, Schaffner F. Spread of the Invasive Mosquitoes Aedes aegypti and Aedes albopictus in the Black Sea Region Increases Risk of Chikungunya, Dengue, and Zika Outbreaks in Europe. *PLoS Neglected Tropical Diseases*. 2016;10(4):1-5. doi:10.1371/journal.pntd.0004664

41. World Health Organization W. Dengue and severe dengue. Published 2019. Accessed January 10, 2020. https://www.who.int/news-room/fact-sheets/detail/dengue-and-severe-dengue

42. World Health Organization W. WHO Region of the Americas records highest number of dengue cases in history; cases spike in other regions. Published 2019. Accessed January 9, 2020. https://www.who.int/news-room/detail/21-11-2019-who-region-of-the-americas-records-highest-number-of-dengue-cases-in-history-cases-spike-in-other-regions

43. Brasil M da S. Dengue: causas, sintomas, tratamento e prevenção. Published 2019. Accessed February 25, 2020. https://saude.gov.br/saude-de-a-z/dengue

44. Brasil M da S. Chikungunya: causas, sintomas, tratamento e prevenção. Published 2019. Accessed February 25, 2020. https://saude.gov.br/saude-de-a-z/chikungunya

45. Brasil M da S. Zika Vírus: causas, sintomas, tratamento e prevenção. Published 2019. Accessed February 25, 2020. https://saude.gov.br/saude-de-a-z/zika-virus

46. Martinez ME. Preventing Zika Virus Infection during Pregnancy Using a Seasonal Window of Opportunity for Conception. *PLoS Biology*. 2016;14(7):1-11. doi:10.1371/journal.pbio.1002520

47. CDC. Dengue Vaccine . Published 2019. Accessed January 10, 2020. https://www.cdc.gov/dengue/prevention/dengue-vaccine.html

48. Araújo AP, Araujo Diniz DF, Helvecio E, et al. The susceptibility of Aedes aegypti populations displaying temephos resistance to Bacillus thuringiensis israelensis: A basis for management. *Parasites and Vectors*. 2013;6(1):297. doi:10.1186/1756-3305-6-297

49. Dos Santos Dias L, MacOris MDLDG, Andrighetti MTMO, et al. Toxicity of spinosad to temephos-resistant Aedes aegypti populations in Brazil. *PLoS ONE*. 2017;12(3):1-15. doi:10.1371/journal.pone.0173689

50. Garcia G de A, David MR, Martins A de J, et al. The impact of insecticide applications on the dynamics of resistance: The case of four Aedes aegypti populations from different Brazilian regions. *PLoS Neglected Tropical Diseases*. 2018;12(2):1-20. doi:10.1371/journal.pntd.0006227

51. Araújo AP de, Paiva MHS, Cabral AM, et al. Screening Aedes aegypti (Diptera: Culicidae) Populations from Pernambuco, Brazil for Resistance to Temephos, Diflubenzuron, and Cypermethrin and Characterization of Potential Resistance Mechanisms. *Journal of Insect Science*. 2019;19(3). doi:10.1093/jisesa/iez054

52. Fawell J, Cotruvo J, Giddings M, et al. Pyriproxyfen in Drinking-water: Use for Vector Control in Drinking-water Sources and Containers. *Background document for development of WHO Guidelines for Drinking-water Quality*. 2008;(WHO/HSE/AMR/08.03/9).

53. Abad-Franch F, Zamora-Perea E, Ferraz G, Padilla-Torres SD, Luz SLB. Mosquito-Disseminated Pyriproxyfen Yields High Breeding-Site Coverage and Boosts Juvenile Mosquito Mortality at the Neighborhood Scale. *PLoS Neglected Tropical Diseases*. 2015;9(4):0-3. doi:10.1371/journal.pntd.0003702

54. Sullivan JJ, Goh KS. Environmental fate and properties of pyriproxyfen. *Journal of Pesticide Science*. 2008;33(4):339-350. doi:10.1584/jpestics.R08-02

55. Caixeta ES, Silva CF, Santos VSV, Olegário de Campos Júnior E, Pereira BB. Ecotoxicological assessment of pyriproxyfen under environmentally realistic exposure conditions of integrated vector management for Aedes aegypti control in Brazil. *Journal of Toxicology and Environmental Health - Part A: Current Issues*. 2016;79(18):799-803. doi:10.1080/15287394.2016.1191400

56. Azevedo-Linhares M, Souza ATC, Lenz CA, et al. Microcystin and pyriproxyfen are toxic to early stages of development in Rhamdia quelen: An experimental and modelling study. *Ecotoxicology and Environmental Safety*. 2018;166(August):311-319. doi:10.1016/j.ecoenv.2018.09.064

57. Maharajan K, Muthulakshmi S, Nataraj B, Ramesh M, Kadirvelu K. Toxicity assessment of pyriproxyfen in vertebrate model zebrafish embryos (Danio rerio): A multi biomarker study. *Aquatic Toxicology*. 2018;196(January):132-145. doi:10.1016/j.aquatox.2018.01.010

58. Lajmanovich RC, Peltzer PM, Martinuzzi CS, Attademo AM, Bassó A, Colussi CL. Insecticide pyriproxyfen (Dragón®) damage biotransformation, thyroid hormones, heart rate, and swimming performance of Odontophrynus americanus tadpoles. *Chemosphere*. 2019;220:714-722. doi:10.1016/j.chemosphere.2018.12.181

59. Kirst HA. The spinosyn family of insecticides: Realizing the potential of natural products research. *Journal of Antibiotics*. 2010;63(3):101-111. doi:10.1038/ja.2010.5

60. Williams T, Farfán JL, Mercado G, Valle J, Abella A, Marina CF. Efficacy of spinosad granules and lambda-cyhalothrin contrasts with reduced performance of temephos for control of aedes spp. In vehicle tires in veracruz, Mexico. *Insects*. 2019;10(8). doi:10.3390/insects10080242

61. Haya K. Toxicity of pyrethroid insecticides to fish. *Environmental Toxicology and Chemistry*. 1989;8(5):381-391. doi:10.1002/etc.5620080504

62. Smith LB, Kasai S, Scott JG. Pyrethroid resistance in Aedes aegypti and Aedes albopictus: Important mosquito vectors of human diseases. *Pesticide Biochemistry and Physiology*. 2016;133:1-12. doi:10.1016/j.pestbp.2016.03.005

63. Togni PHB, Venzon M, Lagôa ACG, Sujii ER. Brazilian Legislation Leaning Towards Fast Registration of Biological Control Agents to Benefit Organic Agriculture. *Neotropical Entomology*. 2019;48(2):175-185. doi:10.1007/s13744-019-00675-8

64. Kumar S. Biopesticides: A need for food and environmental safety. *Journal of Biofertilizers and Biopesticides*. 2012;3(4). doi:10.4172/2155

65. Markets and Markets Research Private Ltd. Biopesticides Market worth $6.4 billion by 2023. Published 2019. Accessed January 20, 2020. https://www.marketsandmarkets.com/PressReleases/biopesticide.asp

66. Markets and Markets Research Private Ltd. Larvicides Market by End-use Sector - Global Forecast 2023. Published 2018. Accessed January 20, 2020. https://www.marketsandmarkets.com/Market-Reports/larvicide-market-193619828.html

67. Arthurs S, Dara SK. Microbial biopesticides for invertebrate pests and their markets in the United States. *Journal of Invertebrate Pathology*. 2018;(January):0-1. doi:10.1016/j.jip.2018.01.008

68. Digma JR, Sumalde AC, Salibay CC. Laboratory evaluation of predation of Toxorhynchites amboinensis (Diptera:Culicidae) on three mosquito vectors of arboviruses in the Philippines. *Biological Control*. 2019;137(March):104009. doi:10.1016/j.biocontrol.2019.104009

69. Bücker A, Bücker NCF, de Souza AQL, et al. Larvicidal effects of endophytic and basidiomycete fungus extracts on Aedes and Anopheles larvae (Diptera, Culicidae). *Revista da Sociedade Brasileira de Medicina Tropical*. 2013;46(4):411-419. doi:10.1590/0037-8682-0063-2013

70. Werren JH. Biology of Wolbachia. *Annu Rev Entomol*. 1997;124(42):587-609. doi:doi:10.1146/annurev.ento.42.1.587

71. Park Y. Entomopathogenic bacterium, Xenorhabdus nematophila and Photorhabdus luminescens, enhances Bacillus thuringiensis Cry4Ba toxicity against yellow fever mosquito, Aedes aegypti (Diptera: Culicidae). *Journal of Asia-Pacific Entomology*. 2015;18(3):459-463. doi:10.1016/j.aspen.2015.05.002

72. Lopez SBG, Guimarães-Ribeiro V, Rodriguez JVG, et al. RNAi-based bioinsecticide for Aedes mosquito control. *Scientific Reports*. 2019;9(1):1-13. doi:10.1038/s41598-019-39666-5

73. Polanczyk RA, Garcia Mde O, Alves SB. Potential of Bacillus thuringiensis israelensis Berliner for controlling Aedes aegypti. *Rev Saude Publica*. 2003;37(6):813-816. doi:S0034-89102003000600020 [pii]

74. Bravo A, Gill SS, Soberón M. Mode of action of Bacillus thuringiensis Cry and Cyt toxins and their potential for insect control. *Toxicon*. 2007;49(4):423-435. doi:10.1016/j.toxicon.2006.11.022

75. Carvalho KDS, Crespo MM, Araújo AP, et al. Long-term exposure of Aedes aegypti to Bacillus thuringiensis svar. Israelensis did not involve altered susceptibility to this microbial larvicide or to other control agents. *Parasites and Vectors*. 2018;11(1):1-11. doi:10.1186/s13071-018-3246-1

76. Zhang L, Zhang X, Zhang Y, et al. A new formulation of Bacillus thuringiensis: UV protection and sustained release mosquito larvae studies. *Scientific Reports*. 2016;6(1):39425. doi:10.1038/srep39425

77. Zhao H, Shao D, Jiang C, et al. Biological activity of lipopeptides from Bacillus. *Applied Microbiology and Biotechnology*. 2017;101(15):5951-5960. doi:10.1007/s00253-017-8396-0

78. Ghribi D, Abdelkefi-Mesrati L, Boukedi H, Elleuch M, Ellouze-Chaabouni S, Tounsi S. The impact of the Bacillus subtilis SPB1 biosurfactant on the midgut histology of Spodoptera littoralis (Lepidoptera: Noctuidae) and determination of its putative receptor. *Journal of Invertebrate Pathology*. 2012;109(2):183-186. doi:10.1016/j.jip.2011.10.014

79. Hamdache A, Lamarti A, Aleu J, Collado IG. Non-peptide metabolites from the genus bacillus. *Journal of Natural Products*. 2011;74(4):893-899. doi:10.1021/np100853e

80. Pueyo MT, Bloch C, Carmona-Ribeiro AM, Di Mascio P. Lipopeptides produced by a soil bacillus megaterium strain. *Microbial Ecology*. 2009;57(2):367-378. doi:10.1007/s00248-008-9464-x

81. Liu X, Ruan L, Peng D, Li L, Sun M, Yu Z. Thuringiensin: A thermostable secondary metabolite from Bacillus thuringiensis with insecticidal activity against a wide range of insects. *Toxins*. 2014;6(8):2229-2238. doi:10.3390/toxins6082229

82. Ziemert N, Alanjary M, Weber T. The evolution of genome mining in microbes-a review. *Natural Product Reports*. 2016;33(8):988-1005. doi:10.1039/c6np00025h

83. Seibold S, Bässler C, Brandl R, et al. Microclimate and habitat heterogeneity as the major drivers of beetle diversity in dead wood. *Journal of Applied Ecology*. Published online 2016. doi:10.1111/1365-2664.12607

84. Brune A, Ohkuma M. Role of the termite gut microbiota in symbiotic digestion. In: Bignell DE, Roisin Y, Lo N, eds. *In Biology OfTermites: A Modern Synthesis*. Springer; 2011:439–475.

85. Brune A. Symbiotic digestion of lignocellulose in termite guts. *Nature Reviews Microbiology*. 2014;12(3):168-180. doi:10.1038/nrmicro3182

86. Tokuda G, Watanabe H. Hidden cellulases in termites: Revision of an old hypothesis. *Biology Letters*. 2007;3(3):336-339. doi:10.1098/rsbl.2007.0073

87. Brune A, Dietrich C. The Gut Microbiota of Termites: Digesting the Diversity in the Light of Ecology and Evolution. *Annual Review of Microbiology*. 2015;69(1):145-166. doi:10.1146/annurev-micro-092412-155715

88. Ulyshen MD. Insect-mediated nitrogen dynamics in decomposing wood. *Ecological Entomology*. 2015;40(S1):97-112. doi:10.1111/een.12176

89. Micó E, Juárez M, Sánchez A, Galante E. Action of the saproxylic scarab larva cetonia aurataeformis (Coleoptera: Scarabaeoidea: Cetoniidae) on woody substrates. *Journal of Natural History*. 2011;45(41-42):2527-2542. doi:10.1080/00222933.2011.596953

90. Nardi JB, Bee CM, Miller LA, Nguyen NH, Suh SO, Blackwell M. Communities of microbes that inhabit the changing hindgut landscape of a subsocial beetle. *Arthropod Structure and Development*. 2006;35(1):57-68. doi:10.1016/j.asd.2005.06.003

91. Blackwell M. Yeasts in insects and other invertebrates. In: Buzzini P, Lachance MA, Yurkov A, eds. *Yeasts in Natural Ecosystems: Diversity*. ; 2017:1-499. doi:10.1007/978-3-319-62683-3

92. Ceja-Navarro JA, Nguyen NH, Karaoz U, et al. Compartmentalized microbial composition, oxygen gradients and nitrogen fixation in the gut of Odontotaenius disjunctus. *ISME Journal*. 2014;8(1):6-18. doi:10.1038/ismej.2013.134

93. Davis TS. The Ecology of Yeasts in the Bark Beetle Holobiont: A Century of Research Revisited. *Microbial Ecology*. 2015;69(4):723-732. doi:10.1007/s00248-014-0479-1

94. Ayayee PA, Larsen T, Rosa C, Felton GW, Ferry JG, Hoover K. Essential amino acid supplementation by gut microbes of a wood-feeding cerambycid. *Environmental Entomology*. 2016;45(1):66-73. doi:10.1093/ee/nvv153

95. Scully ED, Geib SM, Carlson JE, Tien M, McKenna D, Hoover K. Functional genomics and microbiome profiling of the Asian longhorned beetle (Anoplophora glabripennis) reveal insights into the digestive physiology and nutritional ecology of wood feeding beetles. *BMC Genomics*. 2014;15(1):1-21. doi:10.1186/1471-2164-15-1096

96. Pearse A, Patterson M, Rankin J, Wharton G. The Ecology of Passalus cornutus Fabricius, a Beetle wich lives in rotting logs. *Ecological Monographs*. 1936;6(4):455-490.

97. Tanahashi M, Kubota K, Matsushita N, Togashi K. Discovery of mycangia and the associated xylose-fermenting yeasts in stag beetles (Coleoptera: Lucanidae). *Naturwissenschaften*. 2010;97(3):311-317. doi:10.1007/s00114-009-0643-5

98. Hulcr J, Rountree NR, Diamond SE, et al. Mycangia of Ambrosia Beetles Host Communities of Bacteria. *Microbial Ecology*. 2012;64(3):784-793. doi:10.1007/s00248-012-0055-5

99. Toki W, Tanahashi M, Togashi K, Fukatsu T. Fungal farming in a non-social beetle. *PLoS ONE*. 2012;7(7). doi:10.1371/journal.pone.0041893

100. Gírio FM, Fonseca C, Carvalheiro F, Duarte LC, Marques S, Bogel-Łukasik R. Hemicelluloses for fuel ethanol: A review. *Bioresource Technology*. 2010;101(13):4775-4800. doi:10.1016/j.biortech.2010.01.088

101. Songvorawit N, Butcher BA, Chaisuekul C. Decaying Wood Preference of Stag Beetles (Coleoptera: Lucanidae) in a Tropical Dry-Evergreen Forest. *Environmental Entomology*. 2017;46(6):1322-1328. doi:10.1093/ee/nvx143

102. Adnani N, Rajski SR, Bugni TS. Symbiosis-inspired approaches to antibiotic discovery. *Natural Product Reports*. 2017;34(7):784-814. doi:10.1039/C7NP00009J

103. Rosengaus RB, Mead K, Du Comb WS, Benson RW, Godoy VG. Nest sanitation through defecation: Antifungal properties of wood cockroach feces. *Naturwissenschaften*. 2013;100(11):1051-1059. doi:10.1007/s00114-013-1110-x

104. Hill C, Guarner F, Reid G, et al. The International Scientific Association for Probiotics and Prebiotics consensus statement on the scope and appropriate use of the term probiotic. *Nature Reviews Gastroenterology and Hepatology*. 2014;11:506. https://doi.org/10.1038/nrgastro.2014.66

105. Rezac S, Kok CR, Heermann M, Hutkins R. Fermented foods as a dietary source of live organisms. *Frontiers in Microbiology*. 2018;9(AUG). doi:10.3389/fmicb.2018.01785

106. King S, Tancredi D, Lenoir-Wijnkoop I, et al. Does probiotic consumption reduce antibiotic utilization for common acute infections? A systematic review and meta-analysis. *European Journal of Public Health*. Published online 2018:1-6. doi:10.1093/eurpub/cky185

107. Ritchie ML, Romanuk TN. A meta-analysis of probiotic efficacy for gastrointestinal diseases. *PLoS ONE*. 2012;7(4). doi:10.1371/journal.pone.0034938

108. Bernaola Aponte G, Bada Mancilla CA, Carreazo Pariasca NY, Rojas Galarza RA. Cochrane Review: Probiotics for treating persistent diarrhoea in children. *Evidence-Based Child Health: A Cochrane Review Journal*. 2011;6(6):1867-1889. doi:10.1002/ebch.867

109. Goldenberg J, Lytvyn L, Steurich J, Parkin P, S M, Johnston B. Probiotics for the prevention of pediatric antibiotic-associated diarrhea. *Cochrane Database of Systematic Reviews*. 2015;12(6):463-466. doi:10.1002/14651858.CD004827.pub4.Hayes

110. Goldenberg J, Ma S, Saxton J, Al. E. Probiotics for the prevention of *Clostridium difficile*- associated diarrhea in adults and children (Review) SUMMARY OF FINDINGS FOR THE MAIN COMPARISON. *The Cochrane database of systematic reviews*. 2013;(12). doi:10.1002/14651858.CD006095.pub4.www.cochranelibrary.com

111. Bustos SP, Chamorro JFV. Probiotics in acute, antibiotic-associated and nosocomial diarrhea: Evidence in pediatrics | Probióticos en diarrea aguda, asociada a antibióticos y nosocomial: Evidencia en pediatría. *Revista Colombiana de Gastroenterologia*. 2018;33(1):41-48. doi:10.22516/25007440.230

112. Zhang H, Zhao M, Liu T, Feng F, Li Y, Zhang X. *Lactobacillus plantarum* helps to suppress body weight gain, improve serum lipid profile and ameliorate low-grade inflammation in mice administered with

glycerol monolaurate. *Journal of Functional Foods*. 2019;53(September 2018):54-61. doi:10.1016/j.jff.2018.12.015

113. Sadeghi A, Ebrahimi M, Raeisi M, Nematollahi Z. Biological control of foodborne pathogens and aflatoxins by selected probiotic LAB isolated from rice bran sourdough. *Biological Control*. 2019;130(October 2018):70-79. doi:10.1016/j.biocontrol.2018.09.017

114. Okocha RC, Olatoye IO, Adedeji OB. Food safety impacts of antimicrobial use and their residues in aquaculture. *Public Health Reviews*. 2018;39(1):1-22. doi:10.1186/s40985-018-0099-2

115. Veljovic K, Dinic M, Lukic J, et al. Promotion of early gut colonization by probiotic intervention on microbiota diversity in pregnant sows. *Frontiers in Microbiology*. 2017;8(OCT):1-12. doi:10.3389/fmicb.2017.02028

116. de Lemos MJ, Calixto LFL, Souza DS, Reis TL, Nascimento AA, Oliveira CA. Comparative effect of the inclusion of zootechnical additives in the feed of Japanese quails in two productive phases. *Anais da Academia Brasileira de Ciencias*. 2018;90(4):3313-3325. doi:10.1590/0001-3765201820170801

117. Mehdi Y, Létourneau-Montminy M, Gaucher M, et al. Use of Antibiotics in broiler production: Global impacts and alternatives. *Animal Nutrition*. 2018;4(170):178. doi:1037//0033-2909.I26.1.78

118. Maldonado NC, Chiaraviglio J, Bru E, de Chazal L, Santos V, Nader-Macías MEF. Effect of Milk Fermented with Lactic Acid Bacteria on Diarrheal Incidence, Growth Performance and Microbiological and Blood Profiles of Newborn Dairy Calves. *Probiotics and Antimicrobial Proteins*. Published online 2017:1-9. doi:10.1007/s12602-017-9308-4

119. Rose L, Rose J, Gosling S, Holmes M. Efficacy of a Probiotic-Prebiotic Supplement on Incidence of Diarrhea in a Dog Shelter: A Randomized, Double-Blind, Placebo-Controlled Trial. *Journal of Veterinary Internal Medicine*. 2017;31(2):377-382. doi:10.1111/jvim.14666

120. Bourtzis K, Bai S, Zhao Z, et al. Intestinal probiotics restore the ecological fitness decline of *Bactrocera dorsalis* by irradiation. *Evolutionary Applications*. 2018;11(10):1946-1963. doi:10.1111/eva.12698

121. Gales A, Chatellard L, Abadie M, et al. Screening of phytophagous and xylophagous insects guts microbiota abilities to degrade lignocellulose in bioreactor. *Frontiers in Microbiology*. 2018;9(OCT):1-14. doi:10.3389/fmicb.2018.02222

122. Lichtwardt RW, White MM, Cafaro MJ, Misra JK. Fungi Associated with Passalid Beetles and Their Mites. *Mycologia*. 1999;91(4):694-702. doi:10.2307/3761257

123. Moore MRM, Jameson MML, Garner BBH, Audibert C, Smith AABT, Seidel M. Synopsis of the pelidnotine scarabs (Coleoptera, Scarabaeidae, Rutelinae, Rutelini) and annotated catalog of the species and subspecies. *ZooKeys*. 2017;666(666Special Issue):1-349. doi:10.3897/zookeys.666.9191

124. Handique G, Phukan A, Bhattacharyya B, Baruah AALH, Rahman SW, Baruah R. Characterization of cellulose degrading bacteria from the larval gut of the white grub beetle *Lepidiota mansueta* (Coleoptera: Scarabaeidae). *Archives of Insect Biochemistry and Physiology*. 2017;94(2):1-8. doi:10.1002/arch.21370

125. Barnett K, Riegler M, Frew A, et al. Belowground Ecology of Scarabs Feeding on Grass Roots: Current Knowledge and Future Directions for Management in Australasia. *Frontiers in Plant Science*. 2016;7(March):1-15. doi:10.3389/fpls.2016.00321

126. Rodrigues SR, Morón MA, Nogueira GA de L. Description of the Third Instar of *Pelidnota fulva* Blanchard, 1850 (Coleoptera: Scarabaeidae: Rutelinae). *The Coleopterists Bulletin*. 2012;66(3):266-270. doi:10.1649/072.066.0314

127. Morón MAÁ, Deloya C. Observaciones sobre el ciclo de vida de *Pelidnota (Pelidnota) virescens* Burmeister, 1844 (Coleoptera: Melolonthidae; Rutelinae). *Acta Zoológica Mexicana (n.s)*. 2002;85:109-118.

128. Lunz AM, Vaz-De-Mello FZ, Monteiro OMO, Mello FZV de, Monteiro OMO. *Pelidnota filippiniae* Soula, 2009 (Coleoptera: Melolonthidae: Rutelinae): um novo desfolhador de acácia-australiana, *Racosperma mangium* (Willd.) Pedley (Fabaceae), na Amazônia Oriental, Brasil. *Acta Amazonica*. 2011;41(3):439-442. doi:10.1590/s0044-59672011000300017

129. Ritcher PO. *White Grubs and Their Allies. A Study of North American Scarabaeoid Larvae*. Oregon State University Press.; 1966.

130. Rodrigues R, Falco S. Aspectos biológicos de *Pelidnota fulva* Blanchard, 1850 (Coleoptera, Scarabaeidae, Rutelinae). *Biota neotropica*. 2011;11(1):157-160.

131. Egert M, Stingl U, Bruun LD, Pommerenke B, Brune A, Friedrich MW. Structure and topology of microbial communities in the major gut compartments of *Melolontha melolontha* larvae (Coleoptera: Scarabaeidae). *Applied and Environmental Microbiology*. 2005;71(8):4556-4566. doi:10.1128/AEM.71.8.4556-4566.2005

Capítulo 1- Bacillus spp. metabolites are effective in eradicating Aedes aegypti (Diptera: Culicidae) larvae with low toxicity to non-target species

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Bacillus spp. metabolites are effective in eradicating *Aedes aegypti* (Diptera: Culicidae) larvae with low toxicity to non-target species

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ABSTRACT

The growing spread of dengue, chikungunya and Zika viruses demand the development of new and environmentally safe control methods for their vector, the mosquito *Aedes aegypti.* This study aims to find novel larvicidal agents from mutualistic (endophytic and rhizospheric) or edaphic bacteria that have no action against non-target organisms. Eleven out of the 254 bacterial strains tested were able to kill *Ae. aegypti* larvae. Larvicidal activity did not depend on presence of cells, since culture supernatants or crude lipopeptide extracts (CLEs) killed the larvae. *Bacillus safensis* BacI67 and *Bacillus paranthracis* C21 supernatants were the best performing supernatants, displaying the lowest lethal concentrations (LC50 = 31.11 μL/mL and 45.84 μL/mL, respectively). *Bacillus velezensis* B64a and *Bacillus velezensis* B15 produced the best performing CLEs (LC50 = 0.11 mg/mL and 0.12 mg/mL, respectively). Mass spectrometry analysis of CLEs detected a mixture of surfactins, iturins, and fengycins. The samples tested were weakly- or non-toxic to mammalian cells (RAW 264.7 macrophages and VERO cells) and non-target organisms (*Caenorhabditis elegans*, *Galleria mellonella*, *Scenedesmus obliquus*, and *Tetrahymena pyriformis*) – especially *B. velezensis* B15 CLE. The biosynthetic gene clusters related to secondary metabolism identified by whole genome sequencing of the four best performing bacteria strains revealed clusters for bacteriocin, beta-lactone, lanthipeptide, non-ribosomal peptide synthetases, polyketide synthases (PKS), siderophores, T3PKS, type 1 PKS-like, terpenes, thiopeptides, and *trans*-AT-PKS. Purification of lipopeptides may clarify the mechanisms by which these extracts kill *Ae. aegypti* larvae.

1. Introduction

Illnesses transmitted by the mosquito *Aedes aegypti* have rapidly grown in the last century. Dengue fever has had an immense geographical spread since 1943, with the appearance of four new serotypes of dengue virus (Messina et al., 2014), and now represents a major threat to about half of the world's population (World Health Organization, 2018). The 2005 chikungunya epidemic in the Indian Ocean islands (Leparc-Goffart et al., 2014; Ng and Ojcius, 2009) and the emergence of this illness in the Americas in 2016 have shifted the disease paradigm from minor to major concern, with forecast of worldwide spreading in the next few years (Charrel et al., 2014). In Brazil, the need to effectively control this vector after the last Zika epidemic in 2016 and its possible association with microcephaly and Guillain-Barré syndrome are even more clear (Khaiboullina et al., 2018). In addition, the recent reemergence of yellow fever has signaled the return of a dangerous lethal disease transmitted by *Ae. aegypti* in urban areas as well (Wilder-Smith et al., 2017).

Larval source management (LSM) is a quintessential mosquito control measure (World Health Organization-WHO, 2013). Standing water containers and improperly disposed trash are breeding grounds for *Ae. aegypti* larvae, whose development is traditionally controlled with

Abbreviations: CLE, Crude Lipopeptide Extract; NRPS, Non-Ribosomal Peptide Synthetases; PKS, Polyketide Synthases; ESI-IT-MS, Electrospray Ionization - Ion Trap - Mass Spectrometry.

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chemical and biological larvicides. However, the vector's increasing resistance to several chemicals and the low persistence of biological agents make the search for novel alternatives necessary (Araújo et al., 2013, 2019). In Brazil, LSM is performed mainly using the chemical larvicides temephos and pyriproxyfen, but *Ae. aegypti* larvae from most localities are resistant to the former (Araújo et al., 2013, 2019; Dos Santos Dias et al., 2017; Garcia et al., 2018).

Resistance to larvicides increases the costs of larvae population control and the risk of toxicity to non-target organisms due to the need of higher doses. Pyriproxifen is a wide-range insect growth regulator that is safe for potable water (Fawell et al., 2008) but is not recommended for natural water bodies (Sullivan and Goh, 2008) due to deleterious effects on fish and tadpoles (Azevedo-Linhares et al., 2018; Caixeta et al., 2016; Lajmanovich et al., 2019; Maharajan et al., 2018). Methoprene is a juvenile hormone analogue that is considered more rational and safe than pyriproxyfen (Lawler, 2017), but its effects can accumulate in the presence of other toxins, such as microcystin in algal blooms (Azevedo-Linhares et al., 2018). Other molecules used as larvicides are diflubenzuron and spinosad: the former is toxic and harmful to fish in doses much smaller than the LC50 (Abe et al., 2019), while the latter is toxic to some mammals in doses much higher than the toxic doses to mosquitoes (Santos and Pereira, 2019). Spinosad is a natural product synthesized by the actinobacteria *Saccharopolispora spinosa* whose use for pest management in organic crops is authorized by the European Union Council Regulation. Despite being a good alternative for LSM when resistance to other molecules is present, spinosad is not as target-specific as bacterial larvicides (World Health Organization-WHO, 2013).

Bacteria and their metabolites are highly diverse and have a wide variety of applications (Sansinenea and Ortiz, 2011). *Bacillus thuringiensis* has dominated the insect pest-control agents market because it is efficient and specific, does not affect natural enemies, and is less prone to resistance development in target species when compared with chemical insecticides (Chattopadhyay et al., 2004). Other bacteria strains are currently being investigated and used to control pests and vectors, such as the nematode symbionts *Xenorhabdus* and *Photorhabdus* (Cardoso et al., 2015; Park et al., 2016) that produce promising microbial metabolites to control mosquito larvae growth (Kim et al., 2017).]

Microbial toxins and metabolites are used to control *Culex*, *Aedes* and *Anopheles* mosquitoes. *Bacillus thuringiensis* var. *israelensis* (Bti) and *Lysinibacillus sphaericus* (Ls, formerly *Bacillus sphaericus*/Bs) produce effective toxins against these mosquito larvae; when used together, Bti and Ls toxins act synergistically to kill *Aedes* and *Culex* larvae and may delay the development of resistance (Asha et al., 2011; Lawler, 2017). Bti is the main microbial product used to control *Aedes* larvae (Lacey et al., 2015) with high efficacy. However, its toxins have low resistance to UV light (Porter, 1996; Zhang et al., 2016) and must be ingested to kill the insect, which means that they must be available where the insects feed. This can be a drawback for mosquito control because toxins in water bodies can be taken away from the larval feeding zone and be adsorbed by clay particles on the bottom (Porter, 1996; World Health Organization-WHO, 1999). Bti treatment may have lackluster results in organically enriched waters, where bacteria communities are already concentrated, since larvae do not need to filter much water to develop and thereby may not ingest an amount of crystals sufficient to cause death (Lawler, 2017). In addition, its high final costs can also be prohibitive in developing countries (Chattopadhyay et al., 2004).

Lipopeptides are a structurally diverse group of molecules with a wide range of biotechnological applications, from oil displacement to antibiotics (Gond et al., 2015; Raaijmakers et al., 2010; Zhang et al., 2017), and these molecules show thermal, pH and UV resistance (Chen et al., 2017). *Bacillus subtilis* (Das and Mukherjee, 2006; Geetha et al., 2010; Ghribi et al., 2012; Parthipan et al., 2018; Revathi et al., 2013), *Bacillus amyloliquefaciens* (Ben Khedher et al., 2015; Geetha et al., 2011), and *Bacillus tequilensis* (Pradhan et al., 2018) produce lipopeptide larvicides and insecticides with desirable characteristics, such as low lethal doses, shortening of oviposition periods, and decreased longevity of adulthood. To date, few studies have explored the chemical composition of extracts from these bacteria strains and their toxicity to non-target organisms.

The search for new alternative molecules and biocontrol agents for LSM is still extremely important, as we face the ever-increasing spread of *Aedes* diseases and the complexity of their control. *Bacillus* species and related genera are good candidates for finding novel pathogenic strains and larvicidal metabolites, due to their known metabolic diversity, which may harbor undiscovered larvicidal molecules. This study aims to identify bacteria strains from different niches that are capable of controlling *Ae. aegypti* larvae development and can be used in LSM in tropical areas without impacting non-target organisms.

2. Materials and methods

2.1 Bacterial strains

We screened a set of 76 bacterial strains (Table S1) previously isolated and preserved in 20% glycerol at −20 ℃, composed of endophytic or rhizospheric bacterial strains associated with the host plants *Aeschynomene fluminensis* Vell., *Polygonum acuminatum* Kunth., *Paullinia cupana* Mart., and *Phaseolus vulgaris L.* (Liotti et al., 2018; Mariano et al., 2020; Mello et al., 2019). In addition, we isolated and identified sediment lineages from samples collected in lakes from the Brazilian Pantanal, an extensive repository of Brazilian biodiversity (16°23′18″S, 56°26′50″W) (Junk et al., 2014). The collected sediments were diluted tenfold in 225 mL of sterile saline and incubated for 30 min, at 80 ℃ (Wendisch et al., 2001). The suspension was then serially diluted and plated on Nutrient Agar, Trypticase Soy Agar, and T3 Agar. The plates were incubated at 28 ± 3 ℃ and analyzed daily for the appearance of colonies. Colonies with different morphologies were purified and preserved in 20% glycerol at −20 ℃.

The sediment lineages that killed at least 75% of larvae were identified by amplifying and sequencing 16S rRNA (Miller et al., 2013). The amplicons were enzymatically purified (ExoSAP-IT, Applied Biosystems) and Sanger sequenced using BigDye Terminator Cycle Sequencing. The reads were then edited using BioEdit version 7.2.5, and then compared with existing sequences from GenBank, using the BLASTN tool (http://www.ncbi.nlm.nih.gov/). Finally, the sequences that shared 97% of similarity with a bank entry were identified at the species level (Tindall et al., 2010) and deposited in GenBank (http://www.ncbi.nlm.nih.gov) under accession numbers MT269006 to MT269009.

2.2. *Aedes aegypti larvae rearing*

Ae. aegypti eggs in filter paper strips were obtained from the insectary facility of the Institute of Biomedical Sciences at the University of São Paulo. The eggs were allowed to hatch for 3 to 4 days in plastic boxes filled with 10 mL water per larvae and placed in BOD chambers, at 28 ± 1 °C with a 12/12 h (light/dark) photoperiod. Larvae were fed ground fish food (Tetramin®, Tetra) and kept until they reached the third instar (L3). The L3 larvae were used in the assays.

2.3. *Screening for larvicidal activity*

Bacterial isolates were grown in liquid T3 broth for 72 h, at 28 °C, on a rotary shaker (150 rpm). For the initial screening, 10 L3 larvae in 20 mL of water were treated with 3 mL of bacterial cultures or sterile T3 broth (control), in plastic cups, at 28 ± 1 °C with a 12/12 h (light/dark) photoperiod. Live and dead larvae were counted after 24 h (first screening 1° SC – Table S1). The bacterial strains that killed more than 50% of larvae were assayed again (second screening 2° SC – Table S1), using 20 L3 larvae and 3 cups per strain, and following a standard procedure recommended by the WHO (WHO, 2005). Negative control cups received T3 broth just as before, and positive control cups received a spray of a Bti-based commercial product (Biovech® - Neovech - Campo

Bom/RS, Brazil), according to the manufacturer's instructions.

2.4 Lipopeptide production and larvicidal activity

Production of lipopeptides by the strains selected in the first screening (Table S1) was analyzed as reported by Zhao et al. (2013). Crude lipopeptide extracts (CLEs) were obtained by acid precipitation; after determining their weight, they were suspended in water and stored at −20 °C. The larvicidal activity of CLEs was determined at the concentration of 0.5 mg/mL (WHO, 2005), after 24 h of treatment. The CLEs selected were analyzed by mass spectrometry (ESI-IT-MS and MS/MS) on an ESI-Qq-TOF-MS Bruker Maxis Impact High-Resolution Mass Spectrometer, using the acquisition range *m/z* 0 – 3200 (Kim et al., 2010).

2.5 Larvicidal activity of bacterial cells and culture supernatants

The bacterial strains that killed more than 75% of larvae in the second screening were grown in T3 broth for 72 h, at 28 ± 3 °C, under shaking at 150 rpm, and then centrifuged (500 rpm/10 min). Supernatants were filter-sterilized with a 0.22 μM PES membrane filter, while pellets were washed twice with 10 mL of 0.85% saline and suspended in 0.85% saline to adjust the optical density to 0.8 at 600 nm. Larvicidal assays were performed as described before, using 3 mL of cell suspension or sterile supernatant. Control cups were treated with 3 mL of 0.85% saline or sterile T3 broth. Cups were incubated as described in Section 2.3, and dead larvae were counted 24 h later. All treatments were performed in triplicate.

The protein nature of supernatants was investigated using different denaturing agents: (1) thermal treatment, where supernatants were autoclaved for 2 min at 121 °C; (2) pH variations, where the samples were alkalized to pH 10 for 2 h and acidified to reach the original pH. The larvicidal activity of treated and untreated supernatants was determined as described above.

2.6 Determination of lethal concentrations of supernatants and CLEs

The concentration that killed 50% (CL50), 90% (CL90), and 99% (CL99) of *Ae. aegypti* larvae L3 was determined using different concentrations of supernatant or CLE. Larvicidal activity of supernatants was assessed as described above (WHO, 2005), while the concentration-dependent effect of CLEs was assayed on a smaller scale, using five L3 larvae in 5 mL of water. All the supernatant and CLE concentrations were tested in quadruplicate. Dead and live larvae were counted after 24 h, to calculate the mean mortality rate. LC50, LC90, and LC99 were calculated with the aid of the R software (R Core Team, 2018), using the *calcula.lc* function (Pacheco et al., 2013).

2.7 Toxicity of supernatants and lipopeptide extracts

The toxicity of bacterial supernatants and CLEs was tested in different models. First, cytotoxicity to RAW 264.7 macrophages and VERO cells was assessed in triplicate using the tetrazolium colorimetric assay (MTT) to analyze the cell metabolic viability, according to the procedure reported by Sousa et al. (2019). The percentages of cell viability of treated cells and the positive control (10% DMSO) were compared with the negative control (RPMI medium) using T tests on SPSS software (SPSS, 2007).

Second, toxicity of supernatants and CLEs to the model organisms *Caenorhabditis elegans* N2 (nematode) and *Galleria mellonella* (moth) was determined. Adult (stage L4) *C. elegans* N2 were synchronized in M9 medium (Porta-De-La-Riva et al., 2012) and used in the toxicity bioassay (Sousa et al., 2019), performed in triplicate. Supernatants and CLEs were diluted to their LC90 concentration in K medium. Untreated K medium was used as the control. The nematode survival was determined visually and confirmed with contact stimuli after 24 h of treatment at 25 ± 1 °C. Ten last-stage *Galleria mellonella* larvae weighing 0.2 to 0.3 g were injected with 10 μL of supernatants or CLE (Kavanagh and Fallon, 2010; Megaw et al., 2015). Dead larvae were counted daily for seven days. Positive control treatments were performed with autoclaved and non-autoclaved *Bacillus thuringiensis* var. *israelensis* cells in saline (OD = 0.2), while negative control treatments were performed with sterile T3 broth and sterile saline. All treatments were carried out in triplicate. The survival curves were compared using a Log-rank (Mantel-Cox) Test for trends on the GraphPad Prism software (GraphPad Software, La Jolla California USA).

Third, toxicity of supernatants and CLEs at the LC90 concentration to the ciliated protozoa *Tetrahymena pyriformis* was assessed according to Maurya et al. (2019). Sterile T3 broth, Proteose Peptone Yeast Extract Medium (PPY) (used to grow *T. pyriforms* cells), and saline buffer were used as negative controls. Autoclaved and non-autoclaved Bti were used as positive controls. Cells were counted after 48 h of growth at 25 ± 1 °C. The number of living cells from each treatment was compared with the control treated with PPY medium, using a T test on the SPSS software (SPSS, 2007).

Last, toxicity of supernatants and CLEs at the LC90 concentration to the algae *Scenedesmus obliquus* BR003 was assessed using the protocol reported by Sousa et al. (2019). Supernatants and CLEs were added to flasks containing 20 mL of algae cell suspension (1×10^3 cells/mL) in BG11 medium, and the mixture was incubated for 14 days, at 28 ± 1 °C, under fluorescent lamps and constant stirring. Aliquots were taken at days 7 and 14 to count cells in a Neubauer Chamber and assess algae growth. Results were analyzed as described for *T. pyriformis*.

2.8 Persistence of larvicidal activity

To assess the persistence of larvicidal activity of selected supernatants and CLEs over time, they were diluted to the concentrations corresponding to their LC99 and stored in plastic bottles for up to 30 days, at 28 ± 3 °C, protected from direct sunlight. At t = 0, 10, 20 and 30 days after dilution, 20 mL of supernatants and CLEs were used to treat 20 L3 larvae. The mortality rate was determined 24 h later and each treatment was performed in triplicate.

2.9. Genome assembly and mining

Total DNA from *B. safensis* BacI67, *B. paranthracis* C21, *B. velezensis* B64a, and *B. velezensis* B15 was extracted using the DNEasy PowerSoil Kit (Qiagen), according to the manufacturer's instructions. DNA was quantified using the NanoDrop One/OneC Microvolume UV–Vis spectrophotometer and libraries were prepared following the Nextera XT DNA Library Prep (Illumina Inc., San Diego, CA). Libraries were normalized by qPCR with the KAPA Library Quantification Kit Illumina® Platforms (Roche Sequencing, Pleasanton, CA) and sequenced using the Illumina HiSeq 2500 Platform (Illumina Inc., San Diego, CA). Raw data was processed with Trimmomatic (Bolger et al., 2014) to trim and filter adapters, primer sites, and low quality ends of reads (parameters on Table S2). The trimmed reads were assembled using Spades v3.13.0 without error correction (Bankevich et al., 2012) and Newbler (Roche) with default settings, then combined these assemblies using MegaMerge (Scholz et al., 2014) with default settings. Assemblies were compared and analyzed using QUAST (Gurevich et al., 2013) and COMPASS (Fass, 2020), and the best ones were chosen for gene prediction on Prokka (Seemann, 2014). BUSCO (Seppey et al., 2019) and BLASTp were used to evaluate completeness. Functional annotation of predicted proteins was carried out using BLAST2GO (Conesa et al., 2005). Assemblies were annotated using Prokka (Seemann, 2014) and PGAP (Tatusova et al., 2016). The strain identity was confirmed using the Type (Strain) Genome Server - TYGS (Meier-Kolthoff and Göker, 2019), which compares query genomes with reference species strains' genomes. A plasmid search was performed on PlasmidFinder (Carattoli et al., 2014). Secondary metabolism genes were searched on AntiSMASH

5.0 (Blin et al., 2019).

3 Results

We examined the larvicidal activity of 254 bacterial strains, from which 178 strains were isolated in this study and 76 strains were previously isolated by other authors. About one quarter (24%) of the strains exerted larvicidal activity ranging from 4% to 100% in the first screening (Table S1).

After the second screening, eight bacterial strains killed more than 75% of *Aedes aegypti* larvae L3 (Fig. 1 and Table S1): three strains were isolated from Pantanal sediments and identified as *Bacillus pumilus* B08 (Genebank: MT269006), *Bacillus safensis* B138 (Genebank: MT269007), and *Bacillus safensis* B145 (Genebank: MT269008); three strains were isolated from *Polygonum acuminatum* rhizospheric soil (*Bacillus subtilis* C10, *Bacillus paranthracis* C21, *Bacillus aerophilus* C57) (Mariano et al., 2020); one endophytic strain was isolated from *Aeschynomene fluminensis* (*Bacillus safensis* BacI67) (Mello et al., 2019); and one endophytic strain was isolated from *Paullinia cupana* (*Bacillus subtilis* R236b) (Liotti et al., 2018).

Four out of the 23 strains selected in the first screening produced CLE after acid precipitation at pH 2.0: *B. velezensis* B15 (from *Phaseolus vulgaris* rhizospheric soil, Genebank: MH279754), *B. subtilis* C10, *B. velezensis* B64a (from Pantanal sediment, GeneBank: MT269009), and *Bacillus sp*. C101 (from *Polygonum acuminatum* rhizospheric soil) (Table S1). The supernatants from three out of the four strains (*B. velezensis* B15, *B. velezensis* B64a, and *Bacillus* sp. C101) did not achieve the minimum threshold of 75% of dead larvae on the second screening (Table S1); thus, only their CLEs were tested in the subsequent experiments.

Supernatants were mostly responsible for larval deaths, killing 100% of L3 larvae after 24 h (Fig. 1). Bacterial cells had very low larvicidal activity and killed from 0% (*B. paranthracis* C21) to 3.33 ± 2.89% of larvae (*B. safensis* BacI67). The commercial biological control agent Biovech® (*Bacillus thuringiensis* var. *israelensis* – Bti) exhibited inverse results: the cell fraction was essential for its larvicidal activity and killed 100% of L3 larvae after 24 h (Fig. 1).

The supernatants produced by *B. safensis* BacI67 and *B. paranthracis* C21 killed larvae but did not yield lipopeptide precipitates at pH 2.0. We examined the protein nature of these supernatants with denaturing agents and tested their efficacy. Heat or alkalization did not affect their larvicidal activity (Table S4, binomial GLMM tests: $p > 0.05$).

The lethal concentrations were determined in order to rank the most efficient supernatants and CLEs (Fig. 2). Supernatants from *B. safensis* BacI67 and *B. paranthracis* C21 had the lowest values of LC50 (31.11 μL/mL and 45.84 μL/mL, respectively) and LC90 (61.22 μL/mL and 85.52 μL/mL, respectively). CLEs from *B. velezensis* B64a and *B. velezensis* B15 were the most efficient larvicides, since their LC50 (0.11 mg/mL and 0.12 mg/mL, respectively) and LC90 (0.17 mg/mL and 0.34 mg/mL, respectively) values were the lowest ones.

Three peptide clusters around the *m/z* 1080, *m/z* 1460, and *m/z* 1270 regions were detected in the ESI-IT mass spectra of *B. velezensis* B64a and B15. The ions found after expansion of these clusters and their putative identification are reported in Supplementary Material (Table S3). *B. velezensis* B64a CLE had a more diverse profile, with 21 peaks identified on the spectrograms that corresponded mainly to fengycins, surfactins and iturins; it also contained a lipo-chitin-oligosaccharide, a monosialoganglioside, an O-deacylated lipopolysaccharide glycoform, mepartricin A, and diacetylmepartricin.

Only the CLE from *B. velezensis* B15 reduced viability of VERO cells at the LC50 and LC90 concentrations (Table 1); the other agents were not toxic to this cell line. The *B. safensis* BacI67 supernatant reduced viability of RAW 264.7 macrophages at the LC50 and LC90 concentrations (Table 1).

The *B. safensis* BacI67 and *B. paranthracis* C21 supernatants, as well as *B. velezensis* B64a and B15 CLEs were not toxic to *T. pyriformis*, *C. elegans*, and *G. mellonella* larvae (Table 2). Non-autoclaved Bti was highly toxic to both model organisms: it killed 100% of *C. elegans* individuals in 24 h and 90% of *G. mellonella* larvae in 7 days. Autoclaved Bti cells, saline and T3 broth did not kill *G. mellonella* larvae. Compared with the sterile T3 broth control, the *B. velezensis* B64a CLE was weakly toxic to *Scenedesmus obliquus* after 7 and 14 days of treatment (T test: $p = 0.00129$) (Table 2). The *B. safensis* BacI67 culture supernatant was weakly toxic and reduced algae growth only after 14 days of treatment (T test: $p < 0.01$ for 7 days, $p = 0.0048$ for 14 days) (Table 2).

Next, we assessed the persistence of supernatants from *B. safensis* BacI67 and *B. paranthracis* C21 and of CLEs from B. *velezensis* B64a and *B. velezensis* B15 (Fig. 3). CLE fractions were more persistent than supernatants and killed 100% larvae until the 20th day after dilution.

We assembled the genomes of the strains with the lowest LC50s for supernatants or CLEs. The genome assemblies performed using Spades, Newbler and MegaMerge were analyzed on QUAST (Table S5). To select the best assembly for each strain, we took into account the lowest number of scaffolds, the highest N50 and L50 values, the highest fraction assembled, and the lowest number of misassemblies. The MegaMerge assembly was chosen for the four strains.

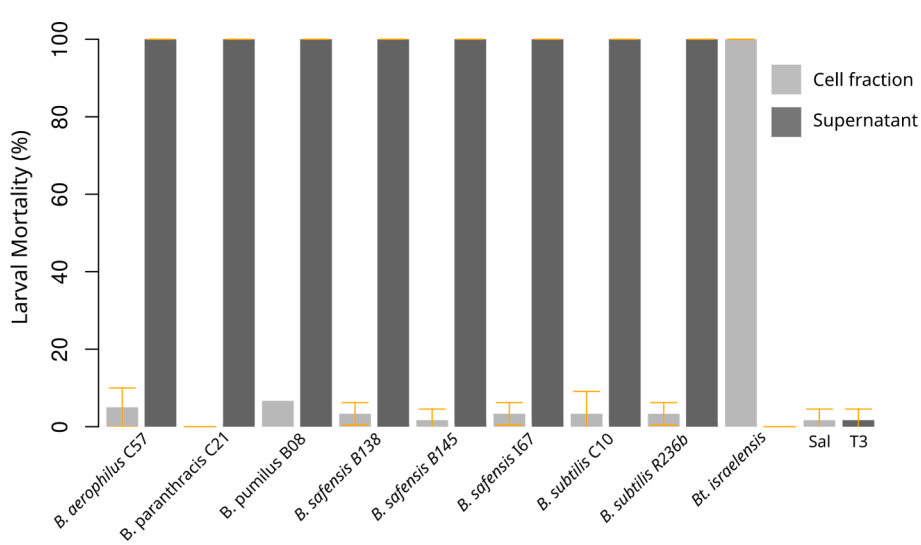

Fig. 1. Larvicidal activity of cell and supernatant fractions of bacterial cultures. Bars are mean and standard deviation of percentage larval mortality. Sal: Saline buffer; T3: T3 broth.

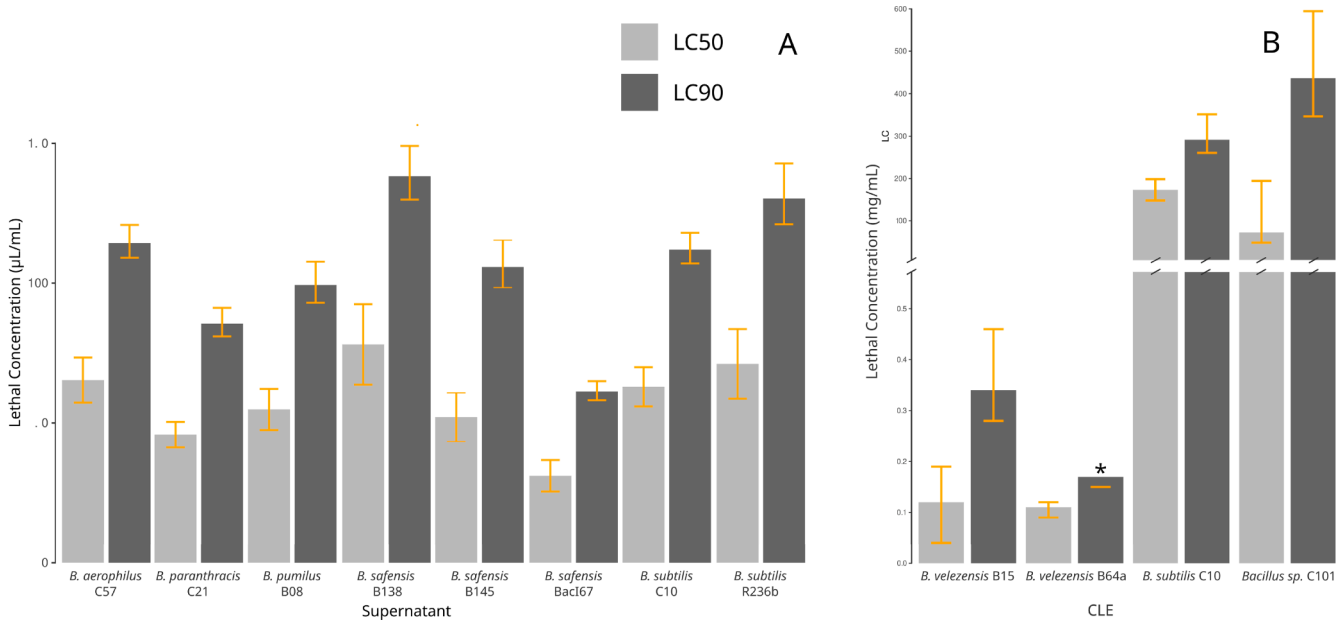

Fig. 2. Lethal concentrations of supernatants (A) and CLEs (B). Bars are calculated LC50 and LC90 with a 95% confidence interval. *Upper limit for LC90 of *B. velezensis* 64a CLE is a NaN (not a number).

Table 1
Cytotoxicity of larvicidal supernatants and crude lipopeptide extract (CLE).

Sample	RAW 264.7 macrophages (% viability)		Vero cells (% viability)	
	LC50	LC90	LC50	LC90
Supernatant				
B. paranthracis C21	86.12 ± 11.34	63.16 ± 4.51*	112.14 ± 7.96	102.91 ± 6.85
B. safensis BacI67	84.32 ± 5.98*	81.32 ± 2.25*	91.46 ± 6.36	88.90 ± 7.94
RMPI medium	100 ± 0.52	100 ± 0.52	100 ± 2.96	100 ± 2.96
DMSO 10%	6.78 ± 1.17**	6.78 ± 1.17**	0.01 ± 0.00**	0.01 ± 0.00**
CLE				
B. velezensis B15	99.72 ± 1.52	91.25 ± 3.51	10.29 ± 1.39**	5.43 ± 2.89**
B. velezensis B64a	90.90 ± 5.80	83.57 ± 2.12	107.14 ± 9.19	96.15 ± 4.87
RMPI medium	100 ± 10.93	100 ± 10.93	100 ± 18.87	100 ± 18.87
DMSO 10%	8.99 ± 0.58**	8.99 ± 0.58**	12.20 ± 0.22**	12.20 ± 0.22**

Data are expressed as mean ± standard deviation (n = 3). *$p < 0.05$ and **$p < 0.01$ when compared with the respective RMPI medium treatment (*t*-test).

Table 2
Toxicity of larvicidal supernatants (SN) and crude lipopeptide extract (CLE) at their DL90 to non-target algae and animal models.

Sample	*C. elegans* survival (%)	*G. mellonella* survival (%)[1]	*T. pyriformis* survival (log cell/mL)[2]	*S. obliquus* survival (log cell/mL)[3]	
				7 days	14 days
B. paranthracis C21 – SN	100	100	5.02 ± 0.10	6.17 ± 0.05	6.76 ± 0.00
B. safensis BacI67 – SN	100	100	5.03 ± 0.05	6.49 ± 0.03	6.46 ± 0.07*
B. velezensis B15 - CLE	100	100	4.97 ± 0.06	6.57 ± 0.11	6.58 ± 0.09
B. velezensis B64a – CLE	100	100	5.10 ± 0.18	5.84 ± 0.22*	6.37 ± 0.03*
Bti - Autoclaved	100	100	4.86 ± 0.31	–	–
Bti – Not Autoclaved	0	10**	5.06 ± 0.25	–	–
PPY medium	–	–	5.04 ± 0.09	–	–
K medium	100	–	–	–	–
Saline	–	100	5.14 ± 0.06	–	–
T3 Broth	–	100	5.30 ± 0.04	6.37 ± 0.12	6.73 ± 0.12

[1] Survival curves significantly differed from the control T3 Broth, in Log-rank (Mantel-Cox) tests (**$p \leq 0.001$); [2]Means in the column did not differ from the PPY medium treatment (*t*-test; $p > 0.05$); [3]Survival means significantly differed from the T3 Broth treatment (*$p < 0.05$, *t*-test).

Assemblies varied from 3.88 Mbp (*B. safensis* BacI67) to 5.7 Mpb (*B. paranthracis* C21) (Table 3). The GC content of the *B. safensis* BacI67, *B. paranthracis* C21, *B. velezensis* B64a, and *B. velezensis* B15 genomes was 41.23%, 35.25%, 46.16%, and 46.42%, respectively. The number of genes predicted by Prokka varied from 3.943 (*B. safensis* I67) to 5.857 (*B. paranthracis* C21). The strain identity was confirmed using the TYGS (Type (Strain) Genome Server) platform; this analysis confirmed the identity of *B. velezensis* B64a but corrected prior identities of the other three strains determined using 16S rDNA sequencing – *B. safensis* BacI67, *B. paranthracis* C21, and *B. velezensis* B15 were previously identified as *B. pumilus*, *B. safensis*, and *Lysinibacillus xylanilyticus*, respectively. Plasmid search on PlasmidFinder did not find any plasmid in the four assemblies.

The *B. velezensis* B64a and *B. velezensis* B15 genomes had similar profiles and percentage of annotated proteins, as detected by functional annotation on Blast2GO (Table S6). Both *B. velezensis* strains differed with respect to the composition of (i) proteins related to carboxylic acid metabolic process and cation and drug binding, which were present in the B64a genome; and (ii) proteins involved in cellular amino acid metabolic process (biological process) detected in the B15 genome (Table S6). Genome profiles of *B. safensis* BacI67 and *B. paranthracis* C21 displayed similar proportion of proteins involved in molecular functions (Table S6).

Genome mining on AntiSMASH detected 13 classes of biosynthetic gene clusters (BGCs) in the four genomes analyzed (Tables S7-S10), such

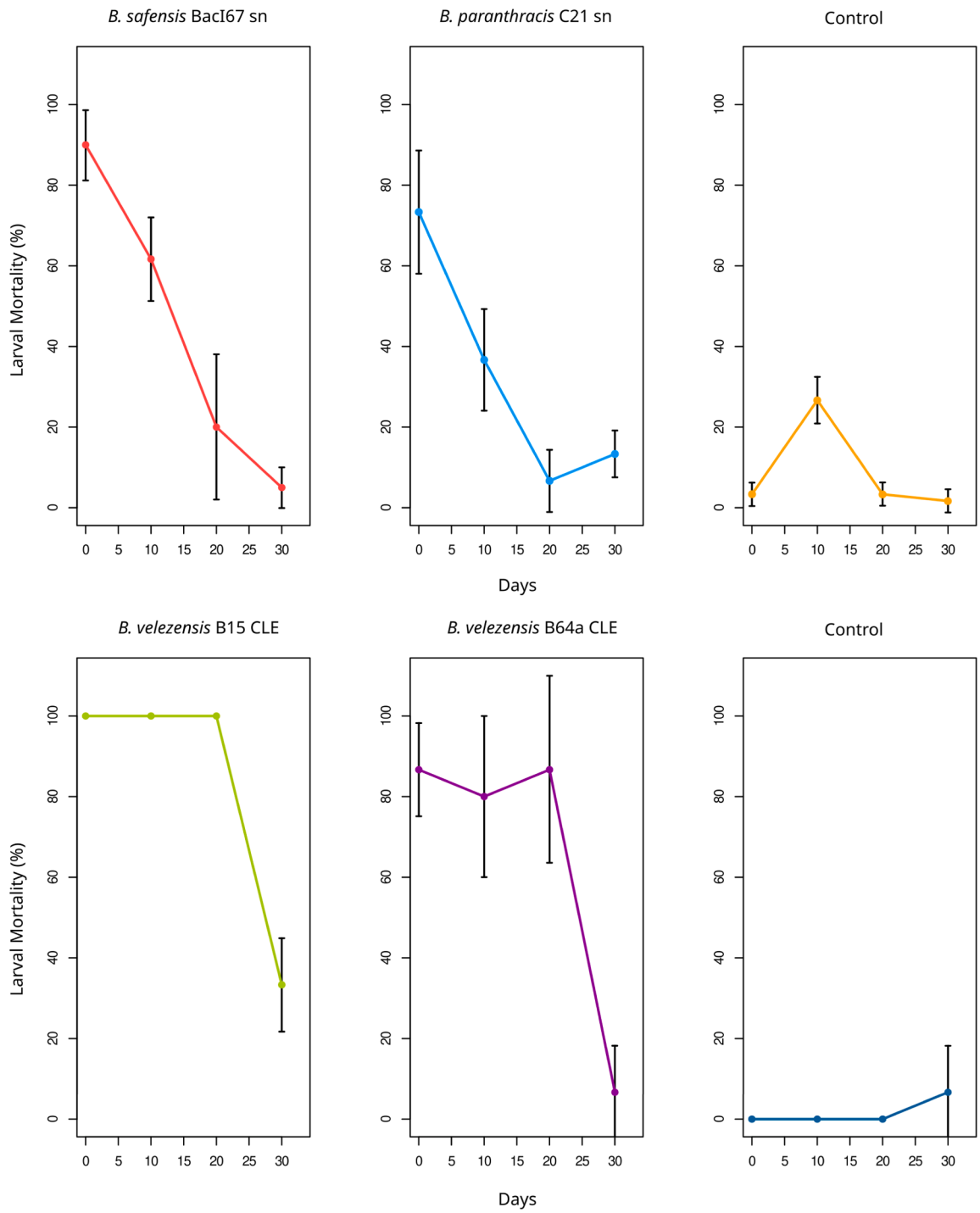

Fig. 3. Persistence of supernatants (SN) and crude lipopeptide extracts (CLE) for up to 30 days. Data expressed as means and standard deviation of the percentage of larvae mortality. Concentrations used: *B. safensis* BacI67 supernatant = 85.9 μL/mL; *B. paranthracis* C21 supernatant = 117.25 μL/mL; *B. velezensis* B64a CLE = 244 μg/mL; *B. velezensis* B15 CLE = 520 μg/mL.

as bacteriocin, beta-lactone, lanthipeptide, NRPS (non-ribosomal peptide synthetases), PKS (type 1 polyketide synthases)-like, siderophore, T3PKS, terpene, thiopeptide, *trans*-AT-PKS, and fengycin. Specifically, the software detected seven classes (nine clusters) of BGCs in *B. safensis* BacI67 genome, five classes (seven clusters) in *B. paranthracis* C21 genome, nine classes (fourteen clusters) in *B. velezensis* B64a genome, and ten classes (fifteen clusters) in *B. velezensis* B15 genome (Tables S7-S10). *B. velezensis* B64a had a plipastatin gene cluster and three other unknown metabolic gene clusters that were absent in *B. velezensis* B15.

4 Discussion

In the present study, we identified four bacterial strains – *B. safensis* BacI67, *B. paranthracis* C21, *B. velezensis* 64a, and *B. velezensis* B15 – that produced larvicidal compounds against *Ae. aegypti*. Their mechanism of action was independent from the presence of bacterial cells and spores, in contrast to the Bti-derived larvicidal products (Ben-Dov, 2014; Khawaled et al., 1992). It is an advantageous feature that makes our agents less prone to the common problems of biological larvicides, like susceptibility to UV radiation and maintenance of cell viability (Zhang

Table 3
Genome assembly and annotation statistics.

Parameter	*B. safensis* BacI67	*B. paranthracis* C21	*B. velezensis* B64a	*B. velezensis* B15
Assembly statistics				
Paired end reads used	13,474,416	15,588,021	8,978,117	13,547,724
Assembly size (bp)	3,876,779	5,666,621	3,995,905	4,163,934
Number of contigs	61	171	44	67
Scaffold N50 (bp)	399,846	225,045	673,669	337,314
Scaffold L50 (Kbp)	4	8	3	5
Maximum scaffold length (bp)	713,688	640,754	915,485	558,274
Total aligned length	326,822	902,102	3,664,547	3,805,198
GC content	41.23	35.25	46.16	46.42
Genome reference species	*B. pumilus*	*B. cereus*	*B. velezensis*	*B. velezensis*
Gene statistics				
Number of genes (predicted by Prokka)	3,943	5,857	3,955	4,057
rRNA genes	1	2	3	3
tRNA genes	47	36	43	54

et al., 2016). Bti is a widely used larvicide that is usually considered very safe and specific (Raymond et al., 2017), but it was toxic to *G. mellonella* and *C. elegans* under the conditions assessed in our study. Other authors have reported the Bti toxicity to non-target invertebrates (Allgeier et al., 2019; Iatsenko et al., 2014; Olmo et al., 2016) and tadpoles (Lajmanovich et al., 2015), with both direct and indirect effects on food chains (Allgeier et al., 2018).

B. safensis BacI67 and *B. paranthracis* C21 are endophytic and rhizospheric bacteria, respectively, originated from the Brazilian wetlands known as the Pantanal (Mariano et al., 2020; Mello et al., 2019). The culture supernatants from these strains exhibited similar larvicidal activity against *Ae. aegypti* larvae, which was not affected by temperature and pH variation. *B. safensis* and *B. velezensis* belong to the endospore-forming endophytic bacteria from the *B. subtilis* group (Rabbee et al., 2019), while *B. paranthracis* C21 belongs to the *B. cereus* taxonomic group (Carroll et al., 2019). These species are known producers of a range of special metabolites that promote plant growth and protect the host against phytopathogens and pests, and are important to pesticide development (Fan et al., 2018; Grady et al., 2019; Rabbee et al., 2019; Zhang et al., 2018).

B. safensis BacI67, *B. paranthracis* C21, *B. velezensis* 64a, and *B. velezensis* B15 genomes have size, number of genes, CDSs, and RNA genes similar to other strains from the same species (Coil et al., 2015; Domingos et al., 2015; Ficarra et al., 2016; Gan et al., 2015). Genomic annotation has detected clusters for several NRPS, PKS and terpenes in *Bacillus* (Chen et al., 2019; Domingos et al., 2015; Gan et al., 2015; Ma and Hu, 2019), as well as a range of other secondary metabolites (Ficarra et al., 2016; Yi et al., 2018) identified on the genomes of strains selected in this study.

Insecticidal activity of *Bacillus* species is usually mediated by crystal proteins (Bravo et al., 2007; Debro et al., 1986; Elleuch et al., 2015; Mnif and Ghribi, 2015; Park et al., 2010; Vachon et al., 2012) or lipopeptides (Hathout et al., 2000; Mnif and Ghribi, 2015; Pradhan et al., 2018). *B. safensis* Bac I67 and *B. paranthracis* C21 did not produce precipitates at pH 2.0, indicating low or no presence of lipopeptides in the extracts able to precipitate under acidic conditions. However, AntiSMASH analysis detected *B. safensis* BacI67 gene clusters for fengycin, lichenysin, and bacillibactin. Type III-PKS gene clusters may also be responsible for at least part of this activity, since chalcone-like compounds have larvicidal and insecticidal activity against *Drosophila melanogaster* and *Ae. aegypti* (Gross et al., 2018; Targanski et al., 2020). Future studies are required to investigate the presence of chalcones or terpenes in culture supernatants that are toxic to insects (Cheng et al., 2003; Smith et al., 2018).

Several lipopeptides produced by *Bacillus* exhibit a wide range of applications (Aleti et al., 2015; Chen et al., 2017; Cochrane and Vederas, 2016; Das and Mukherjee, 2006; Hertlein et al., 2016; Jha et al., 2016; Jin et al., 2017; Ongena and Jacques, 2008; Pradhan et al., 2018; Raaijmakers et al., 2010; Soares et al., 2016). *B. velezensis* produced CLEs that killed larvae at low concentrations and that were not toxic to non-target animal species. The low toxicity of these CLEs to *C. elegans, G. mellonella, T. pyriformis* protozoa cells, and *S. obliquus* algae cells is a good indicator of their environmental safety. The *B. velezensis* strains B64a and B15 were isolated from the Pantanal sediment and *Phaseolus vulgaris* rhizosphere, respectively.

B. subtilis produces lipopeptide extracts that inhibit the development of *Anopheles stephensi* pupae (Geetha et al., 2010) and *Culex quinquefasciatus* larvae (Das and Mukherjee, 2006); however, there are no reports on their action on non-target organisms. Surfactins, fengycins and iturins usually account for the larvicidal activity (Assié et al., 2002; Geetha et al., 2011, 2010; Pradhan et al., 2018). Surfactins decrease water surface tension and hinder larvae permanence on surfaces, which elevates the energetic expenditure and kill larvae by exhaustion and asphyxia (Pradhan et al., 2018).

B. velezensis genome has gene clusters for NRPSs that encode several lipopeptides (Domingos et al., 2015; Grady et al., 2019; Vater et al., 2018; Xu et al., 2018) and produce mixtures that may have distinct lipopeptide signatures under different conditions (Farias et al., 2018). We detected other gene clusters in *B. velezensis* B64a and B15 related to *trans*-AT-PKS and *trans*-AT-PKS-like, T3-PKS, terpenes, lanthipeptides, and thiopeptides (Chen et al., 2019; Fan et al., 2018; Ma and Hu, 2019; Yi et al., 2018; Zhang et al., 2018). Future work to explore different culture conditions may render a diversity of mixtures with improved efficacy.

5 Conclusion

B. paranthracis C21 (LC50 = 45.84 μL/mL) and *B. safensis* BacI67 (LC50 = 31.11 μL/mL) culture supernatants and *B. velezensis* B15 (LC50 = 0.11 mg/mL) and B64a (LC50 = 0.12 mg/mL) CLEs are effective larvicidal agents against *Ae. aegypti*, whose action do not depend on the presence of bacterial cells. The genomes of these bacteria strains bear a series of gene clusters for NRPSs, *trans*-AT-PKSs and *trans*-AT-PKSs-like, T3-PKSs, terpenes, lanthipeptides, and thiopeptides that may account for larvicidal activity.

CLEs from *B. velezensis* strains contain fengycin, iturin and surfactin lipopeptides. The CLE from *B. velezensis* B15 is especially promising due to its low larvicidal dose, persistence of its activity for 20 days, and lack of toxicity to the non-target organisms tested (*C. elegans*, *G. mellonella*, *S. obliquus*, and *T. pyriformis*). Future purification of lipopeptides may demonstrate and improve their action against *Ae. aegypti* larvae.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.jip.2020.107525.

Bibliography

Abe, F.R., Machado, A.A., Coleone, A.C., da Cruz, C., Machado-Neto, J.G., 2019. Toxicity of diflubenzuron and temephos on freshwater fishes: Ecotoxicological assays with *Oreochromis niloticus* and *Hyphessobrycon eques*. Water Air Soil Pollut. 230 https://doi.org/10.1007/s11270-019-4128-7.

Aleti, G., Sessitsch, A., Brader, G., 2015. Genome mining: Prediction of lipopeptides and polyketides from *Bacillus* and related Firmicutes. Comput. Struct. Biotechnol. J. 13, 192–203. https://doi.org/10.1016/j.csbj.2015.03.003.

Allgeier, S., Frombold, B., Mingo, V., Brühl, C.A., 2018. European common frog *Rana temporaria* (Anura: Ranidae) larvae show subcellular responses under field-relevant *Bacillus thuringiensis* var. *israelensis* (Bti) exposure levels. Environ. Res. 162, 271–279. https://doi.org/10.1016/j.envres.2018.01.010.

Allgeier, S., Kästel, A., Brühl, C.A., 2019. Adverse effects of mosquito control using *Bacillus thuringiensis* var. *israelensis*: Reduced chironomid abundances in mesocosm, semi-field and field studies. Ecotoxicol. Environ. Saf. 169, 786–796. https://doi.org/10.1016/j.ecoenv.2018.11.050.

Araújo, A.P., Araujo Diniz, D.F., Helvecio, E., De Barros, R.A., De Oliveira, C.M.F., Ayres, C.F.J., De Melo-Santos, M.A.V., Regis, L.N., Silva-Filha, M.H.N.L., 2013. The susceptibility of *Aedes aegypti* populations displaying temephos resistance to *Bacillus thuringiensis israelensis*: A basis for management. Parasites Vectors 6, 297. https://doi.org/10.1186/1756-3305-6-297.

de Araújo, A.P., Paiva, M.H.S., Cabral, A.M., Cavalcanti, A.E.H.D., Pessoa, L.F.F., Diniz, D.F.A., Helvecio, E., Da Silva, E.V.G., Silva, N.M., Anastácio, D.B., Pontes, C., Nunes, V., De Souza, M.D.F.M., Magalhães, F.J.R., De Melo Santos, M.A.V., Ayres, C. F.J., 2019. Screening *Aedes aegypti* (Diptera: Culicidae) populations from Pernambuco, Brazil for resistance to temephos, diflubenzuron, and cypermethrin and characterization of potential resistance mechanisms. J. Insect Sci. 19 https://doi.org/10.1093/jisesa/iez054.

Asha, M., Sreshty, L., Kumar, K.P., Murty, U.S.N., 2011. Synergism between wild-type *Bacillus thuringiensis* subsp. *israelensis* and *B. sphaericus* strains: A study based on isobolographic analysis and histopathology. Acta Trop. 118, 14–20. https://doi.org/10.1016/j.actatropica.2010.12.012.

Assié, L., Deleu, M., Arnaud, L., Paquot, M., Thonart, P., Gaspar, C., Haubruge, E., 2002. Insecticide activity of surfactins and iturins from a biopesticide *Bacillus subtilis* Cohn (S499 strain). Meded Rijksuniv Gent Fak Landbouwkd Toegep Biol Wet. 67, 647–655.

Azevedo-Linhares, M., Souza, A.T.C., Lenz, C.A., Leite, N.F., Brito, I.A., Folle, N.M.T., Garcia, J.E., Filipak Neto, F., Oliveira Ribeiro, C.A., 2018. Microcystin and pyriproxyfen are toxic to early stages of development in *Rhamdia quelen*: An experimental and modelling study. Ecotoxicol. Environ. Saf. 166, 311–319. https://doi.org/10.1016/j.ecoenv.2018.09.064.

Bankevich, A., Nurk, S., Antipov, D., Gurevich, A.A., Dvorkin, M., Kulikov, A.S., Lesin, V. M., Nikolenko, S.I., Pham, S., Prjibelski, A.D., Pyshkin, A.V., Sirotkin, A.V., Vyahhi, N., Tesler, G., Alekseyev, M.A., Pevzner, P.A., 2012. SPAdes: A new genome assembly algorithm and its applications to single-cell sequencing. J. Comput. Biol. 19, 455–477. https://doi.org/10.1089/cmb.2012.0021.

Ben-Dov, E., 2014. *Bacillus thuringiensis* subsp. *israelensis* and its dipteran-specific toxins. Toxins (Basel). 6, 1222–1243. https://doi.org/10.3390/toxins6041222.

Ben Khedher, S., Boukedi, H., Kilani-Feki, O., Chaib, I., Laarif, A., Abdelkefi-Mesrati, L., Tounsi, S., 2015. *Bacillus amyloliquefaciens* AG1 biosurfactant: Putative receptor diversity and histopathological effects on *Tuta absoluta* midgut. J. Invertebr. Pathol. 132, 42–47. https://doi.org/10.1016/j.jip.2015.08.010.

Blin, K., Shaw, S., Steinke, K., Villebro, R., Ziemert, N., Lee, S.Y., Medema, M.H., Weber, T., 2019. antiSMASH 5.0: updates to the secondary metabolite genome mining pipeline. Nucleic Acids Res. 47, W81–W87. https://doi.org/10.1093/nar/gkz310.

Bolger AM, Lohse M, U.B., 2014. Trimmomatic: a flexible trimmer for Illumina sequence data. Bioinformatics 30, 2114–20.

Bravo, A., Gill, S.S., Soberón, M., 2007. Mode of action of *Bacillus thuringiensis* Cry and Cyt toxins and their potential for insect control. Toxicon 49, 423–435. https://doi.org/10.1016/j.toxicon.2006.11.022.

Caixeta, E.S., Silva, C.F., Santos, V.S.V., de Campos, Olegário, Júnior, E., Pereira, B.B., 2016. Ecotoxicological assessment of pyriproxyfen under environmentally realistic exposure conditions of integrated vector management for *Aedes aegypti* control in Brazil. J. Toxicol. Environ. Heal. - Part A Curr. Issues 79, 799–803. https://doi.org/10.1080/15287394.2016.1191400.

Carattoli, A., Zankari, E., Garciá-Fernández, A., Larsen, M.V., Lund, O., Villa, L., Aarestrup, F.M., Hasman, H., 2014. In silico detection and typing of plasmids using plasmidfinder and plasmid multilocus sequence typing. Antimicrob. Agents Chemother. 58, 3895–3903. https://doi.org/10.1128/AAC.02412-14.

Cardoso, D., Gomes, V., Dolinski, C., Souza, R., 2015. Potential of entomopathogenic nematodes as biocontrol agents of immature stages of *Aedes aegypti*. Nematoda 2, e092015. https://doi.org/10.4322/nematoda.09015.

Carroll, L.M., Wiedmann, M., Mukherjee, M., Nicholas, D.C., Mingle, L.A., Dumas, N.B., Cole, J.A., Kovac, J., 2019. Characterization of emetic and diarrheal *Bacillus cereus* strains from a 2016 foodborne outbreak using whole-genome sequencing: Addressing the microbiological, epidemiological, and bioinformatic challenges. Front. Microbiol. 10 https://doi.org/10.3389/fmicb.2019.00144.

Charrel, R.N., Leparc-Goffart, I., Gallian, P., de Lamballerie, X., 2014. Globalization of Chikungunya: 10 years to invade the world. Clin. Microbiol. Infect. 20, 662–663. https://doi.org/10.1111/1469-0691.12694.

Chattopadhyay, A., Bhatnagar, N.B., Bhatnagar, R., 2004. Bacterial insecticidal toxins. Crit. Rev. Microbiol. 30, 33–54. https://doi.org/10.1080/10408410490270712.

Chen, L., Shi, H., Heng, J., Wang, D., Bian, K., 2019. Antimicrobial, plant growth-promoting and genomic properties of the peanut endophyte *Bacillus velezensis* LDO2. Microbiol. Res. 218, 41–48. https://doi.org/10.1016/j.micres.2018.10.002.

Chen, Y., Liu, S.A., Mou, H., Ma, Y., Li, M., Hu, X., 2017. Characterization of lipopeptide biosurfactants produced by *Bacillus licheniformis* MB01 from marine sediments. Front. Microbiol. 8, 1–11. https://doi.org/10.3389/fmicb.2017.00871.

Cheng, S.S., Chang, H.T., Chang, S.T., Tsai, K.H., Chen, W.J., 2003. Bioactivity of selected plant essential oils against the yellow fever mosquito *Aedes aegypti* larvae. Bioresour. Technol. 89, 99–102. https://doi.org/10.1016/S0960-8524(03)00008-7.

Cochrane, S.A., Vederas, J.C., 2016. Lipopeptides from *Bacillus* and *Paenibacillus* spp.: A gold mine of antibiotic candidates. Med. Res. Rev. 36, 4–31. https://doi.org/10.1002/med.21321.

Coil, D.A., Benardini, J.N., Eisen, J.A., 2015. Draft genome sequence of *Bacillus safensis* JPL-MERTA-8-2, isolated from a Mars-Bound Spacecraft. Genome Announc. 3, 2164. https://doi.org/10.1128/genomeA.01360-15.

Conesa, A., Götz, S., García-Gómez, J.M., Terol, J., Talón, M., Robles, M., 2005. Blast2GO: A universal tool for annotation, visualization and analysis in functional genomics research. Bioinformatics 21, 3674–3676. https://doi.org/10.1093/bioinformatics/bti610.

Das, K., Mukherjee, A.K., 2006. Assessment of mosquito larvicidal potency of cyclic lipopeptides produced by *Bacillus subtilis* strains. Acta Trop. 97, 168–173. https://doi.org/10.1016/j.actatropica.2005.10.002.

Debro, L., Fitz-James, P., Aronson, A., 1986. Different parasporal inclusions are produced by *Bacillus thuringiensis* subsp. finitimus 165, 258–268.

Domingos, D.F., de Faria, A.F., de Souza Galaverna, R., Eberlin, M.N., Greenfield, P., Zucchi, T.D., Melo, I.S., Tran-Dinh, N., Midgley, D., de Oliveira, V.M., 2015. Genomic and chemical insights into biosurfactant production by the mangrove-derived strain *Bacillus safensis* CCMA-560. Appl. Microbiol. Biotechnol. 99, 3155–3167. https://doi.org/10.1007/s00253-015-6377-8.

Dos Santos Dias, L., MacOris, M.D.L.D.G., Andrighetti, M.T.M.O., Otrera, V.C.G., Dias, A. D.S., Bauzer, L.G.S.D.R., Rodovalho, C.D.M., Martins, A.J., Lima, J.B.P., 2017. Toxicity of spinosad to temephos-resistant *Aedes aegypti* populations in Brazil. PLoS ONE 12, 1–15. https://doi.org/10.1371/journal.pone.0173689.

Elleuch, J., Zribi Zghal, R., Lacoix, M.N., Chandre, F., Tounsi, S., Jaoua, S., 2015. Evidence of two mechanisms involved in *Bacillus thuringiensis israelensis* decreased toxicity against mosquito larvae: Genome dynamic and toxins stability. Microbiol. Res. 176, 48–54. https://doi.org/10.1016/j.micres.2015.04.007.

Fan, B., Wang, C., Song, X., Ding, X., Wu, L., Wu, H., Gao, X., Borriss, R., 2018. *Bacillus velezensis* FZB42 in 2018: The gram-positive model strain for plant growth promotion and biocontrol. Front. Microbiol. 9, 1–14. https://doi.org/10.3389/fmicb.2018.02491.

Farias, B.C.S., Hissa, D.C., do Nascimento, C.T.M., Oliveira, S.A., Zampieri, D., Eberlin, M.N., Migueleti, D.L.S., Martins, L.F., Sousa, M.P., Moyses, D.N., Melo, V.M.M., 2018. Cyclic lipopeptide signature as fingerprinting for the screening of halotolerant Bacillus strains towards microbial enhanced oil recovery. Appl. Microbiol. Biotechnol. 102, 1179–1190. Doi: 10.1007/s00253-017-8675-9.

Fass, J.N., 2020. Compass: Perl / R scripts to COMpare a DNA sequence ASSembly to a trusted reference sequence.

Fawell, J., Cotruvo, J., Giddings, M., Jackson, P., Magara, Y., Festo Ngowi, A., Ohanian, E., 2008. Pyriproxyfen in drinking-water: Use for vector control in drinking-water sources and containers. Backgr. Doc. Dev. WHO Guidel. Drink. Qual.

Ficarra, F.A., Santecchia, I., Lagorio, S.H., Alarcón, S., Magni, C., Espariz, M., 2016. Genome mining of lipolytic exoenzymes from *Bacillus safensis* S9 and *Pseudomonas alcaliphila* ED1 isolated from a dairy wastewater lagoon. Arch. Microbiol. 198, 893–904. https://doi.org/10.1007/s00203-016-1250-4.

Gan, H.Y., Gan, H.M., Savka, M.A., Triassi, A.J., Wheatley, M.S., Naqvi, K.F., Foxhall, T. E., Anauo, M.J., Baldwin, M.L., Burkhardt, R.N., O'Bryon, I.G., Dailey, L.K., Busairi, N.I., Keith, R.C., Khair, M.H.M.M., Rasul, M.Z.M., Rosdi, N.A.M., Mountzouros, J.R., Rhoads, A.C., Selochan, M.A., Tautanov, T.B., Polter, S.J., Marks, K.D., Caraball, A.A., Hudson, A.O., 2015. Whole-genome sequencing and annotation of *Bacillus safensis* RIT372 and *Pseudomonas oryzihabitans* RIT370 from *Capsicum annuum* (Bird's Eye Chili) and *Capsicum chinense* (Yellow Lantern Chili), respectively. Genome Announc. 3, 2–3. https://doi.org/10.1128/genomeA.00288-15.Copyright.

Geetha, I., Manonmani, A.M., Paily, K.P., 2010. Identification and characterization of a mosquito pupicidal metabolite of a *Bacillus subtilis* subsp. *subtilis* strain. Appl. Microbiol. Biotechnol. 86, 1737–1744. https://doi.org/10.1007/s00253-010-2449-y.

Geetha, I., Manonmani, A.M., Prabakaran, G., 2011. *Bacillus amyloliquefaciens*: A mosquitocidal bacterium from mangrove forests of Andaman & Nicobar islands. India. Acta Trop. 120, 155–159. https://doi.org/10.1016/j.actatropica.2011.07.006.

Ghribi, D., Abdelkefi-Mesrati, L., Boukedi, H., Elleuch, M., Ellouze-Chaabouni, S., Tounsi, S., 2012. The impact of the *Bacillus subtilis* SPB1 biosurfactant on the midgut histology of *Spodoptera littoralis* (Lepidoptera: Noctuidae) and determination of its putative receptor. J. Invertebr. Pathol. 109, 183–186. https://doi.org/10.1016/j.jip.2011.10.014.

Gond, S.K., Bergen, M.S., Torres, M.S., White, J.F., 2015. Endophytic *Bacillus spp*. produce antifungal lipopeptides and induce host defence gene expression in maize. Microbiol. Res. 172, 79–87. https://doi.org/10.1016/j.micres.2014.11.004.

Grady, E.N., MacDonald, J., Ho, M.T., Weselowski, B., McDowell, T., Solomon, O., Renaud, J., Yuan, Z.C., 2019. Characterization and complete genome analysis of the surfactin-producing, plant-protecting bacterium *Bacillus velezensis* 9D–6. BMC Microbiol. 19, 1–14. https://doi.org/10.1186/s12866-018-1380-8.

Gross, A.D., Tabanca, N., Islam, R., Ali, A., Khan, I.A., Kaplancikli, Z.A., Altintop, M.D., Ozdemir, A., Bloomquist, J.R., Bartholomay, L., 2018. Toxicity and synergistic activities of chalcones against *Aedes aegypti* (Diptera: Culicidae) and *Drosophila melanogaster* (Diptera: Drosophilidae). J. Med. Entomol. 54, 382–386. https://doi.org/10.1093/jme/tjw183.

Gurevich, A., Saveliev, V., Vyahhi, N., Tesler, G., 2013. QUAST: Quality assessment tool for genome assemblies. Bioinformatics 29, 1072–1075. https://doi.org/10.1093/bioinformatics/btt086.

Hathout, Y., Ho, Y.P., Ryzhov, V., Demirev, P., Fenselau, C., 2000. Kurstakins: A new class of lipopeptides isolated from *Bacillus thuringiensis*. J. Nat. Prod. 63, 1492–1496. https://doi.org/10.1021/np000169q.

Hertlein, G., Seiffert, M., Gensel, S., Garcia-Gonzalez, E., Ebeling, J., Skobalj, R., Kuthning, A., Süssmuth, R.D., Genersch, E., 2016. Biological role of paenilarvins, iturin-like lipopeptide secondary metabolites produced by the honey bee pathogen *Paenibacillus larvae*. PLoS ONE 11, 1–14. https://doi.org/10.1371/journal.pone.0164656.

Iatsenko, I., Boichenko, I., Sommer, R.J., 2014. *Bacillus thuringiensis* DB27 produces two novel protoxins, Cry21Fa1 and Cry21Ha1, which act synergistically against nematodes. Appl. Environ. Microbiol. 80, 3266–3275. https://doi.org/10.1128/AEM.00464-14.

Jha, S.S., Joshi, S.J., Geetha, S.J., 2016. Lipopeptide production by *Bacillus subtilis* R1 and its possible applications. Brazilian J. Microbiol. 47, 955–964. https://doi.org/10.1016/j.bjm.2016.07.006.

Jin, Q., Jiang, Q., Zhao, L., Su, C., Li, Songshuo, Si, F., Li, Shanshan, Zhou, C., Mu, Y., Xiao, M., 2017. Complete genome sequence of *Bacillus velezensis* S3–1, a potential biological pesticide with plant pathogen inhibiting and plant promoting capabilities. J. Biotechnol. 259, 199–203. https://doi.org/10.1016/j.jbiotec.2017.07.011.

Junk, W., Piedade, M., Lourival, R., Wittmann, F., Kandus, P., Lacerda, L., Bozelli, R., Esteves, F., Nunes da Cunha, C., Maltchik, L., Schöngart, J., Schaeffer-Novelli, Y., Agostinho, A., 2014. Brazilian wetlands: their definition, delineation, and classification for research, sustain- able management, and protection. Aquat Conserv Mar Freshw Ecosyst 24, 5–22. https://doi.org/10.1002/aqc2386.

Kavanagh, K., Fallon, J.P., 2010. *Galleria mellonella* larvae as models for studying fungal virulence. Fungal Biol. Rev. 24, 79–83. https://doi.org/10.1016/j.fbr.2010.04.001.

Khaiboullina, S., Uppal, T., Martynova, E., Rizvanov, A., Baranwal, M., Verma, S.C., 2018. History of ZIKV infections in India and management of disease outbreaks. Front. Microbiol. 9, 1–8. https://doi.org/10.3389/fmicb.2018.02126.

Khawaled, K., Cohen, T., Zaritsky, A., 1992. Digestion of *Bacillus thuringiensis* var. *israelensis* spores by larvae of *Aedes aegypti*. J. Invertebr. Pathol. 59, 186–189. https://doi.org/10.1016/0022-2011(92)90031-X.

Kim, I., Aryal, S.K., Aghai, D.T., Casanova-torres, Á.M., Hillman, K., Kozuch, M.P., Mans, E.J., Mauer, T.J., Ogier, J., Ensign, J.C., Gaudriault, S., Goodman, W.G., Goodrich-blair, H., Dillman, A.R., 2017. The insect pathogenic bacterium Xenorhabdus innexi has attenuated virulence in multiple insect model hosts yet encodes a potent mosquitocidal toxin 1–25. Doi: 10.1186/s12864-017-4311-4.

Kim PI, Ryu J, Kim YH, C.Y., 2010. Production of biosurfactant lipopeptides Iturin A, fengycin and surfactin A from Bacillus subtilis CMB32 for control of Colletotrichum gloeosporioides. J Microbiol Biotechnol 20, 138–145. Doi: 10.4014/jmb.0905.05007.

Lacey, L.A., Grzywacz, D., Shapiro-Ilan, D.I., Frutos, R., Brownbridge, M., Goettel, M.S., 2015. Insect pathogens as biological control agents: Back to the future. J. Invertebr. Pathol. 132, 1–41. https://doi.org/10.1016/j.jip.2015.07.009.

Lajmanovich, R.C., Junges, C.M., Cabagna-Zenklusen, M.C., Attademo, A.M., Peltzer, P. M., Maglianese, M., Márquez, V.E., Beccaria, A.J., 2015. Toxicity of *Bacillus thuringiensis* var. *israelensis* in aqueous suspension on the South American common frog *Leptodactylus latrans* (Anura: Leptodactylidae) tadpoles. Environ. Res. 136, 205–212. https://doi.org/10.1016/j.envres.2014.10.022.

Lajmanovich, R.C., Peltzer, P.M., Martinuzzi, C.S., Attademo, A.M., Bassó, A., Colussi, C. L., 2019. Insecticide pyriproxyfen (Dragón®) damage biotransformation, thyroid hormones, heart rate, and swimming performance of *Odontophrynus americanus* tadpoles. Chemosphere 220, 714–722. https://doi.org/10.1016/j.chemosphere.2018.12.181.

Lawler, S.P., 2017. Environmental safety review of methoprene and bacterially-derived pesticides commonly used for sustained mosquito control. Ecotoxicol. Environ. Saf. 139, 335–343. https://doi.org/10.1016/j.ecoenv.2016.12.038.

Leparc-Goffart, I., Nougairede, A., Cassadou, S., Prat, C., de Lamballerie, X., 2014. Chikungunya in the Americas. Lancet. https://doi.org/10.1016/S0140-6736(14)60185-9.

Liotti, R.G., Figueiredo, M.I. da S., Silva, G.F. da, Mendonça, E.A.F. de, Soares, M.A., 2018. Diversity of cultivable bacterial endophytes in Paullinia cupana and their potential for plant growth promotion and phytopathogen control. Microbiol. Res. 207, 8–18. Doi: 10.1016/j.micres.2017.10.011.

Ma, Z., Hu, J., 2019. Complete genome sequence of a marine-sediment-derived bacterial strain *Bacillus velezensis* SH-B74, a cyclic lipopeptides producer and a biopesticide. 3. Biotech 9, 1–7. https://doi.org/10.1007/s13205-019-1694-8.

Maharajan, K., Muthulakshmi, S., Nataraj, B., Ramesh, M., Kadirvelu, K., 2018. Toxicity assessment of pyriproxyfen in vertebrate model zebrafish embryos (*Danio rerio*): A multi biomarker study. Aquat. Toxicol. 196, 132–145. https://doi.org/10.1016/j.aquatox.2018.01.010.

Mariano, C., Mello, I.S., Barros, B.M., da Silva, G.F., Terezo, A.J., Soares, M.A., 2020. Mercury alters the rhizobacterial community in Brazilian wetlands and it can be bioremediated by the plant-bacteria association. Environ. Sci. Pollut. Res. Doi: 10.1007/s11356-020-07913-2.

Maurya, R., Dubey, K., Singh, D., Jain, A.K., Pandey, A.K., 2019. Effect of difenoconazole fungicide on physiological responses and ultrastructural modifications in model organism *Tetrahymena pyriformis*. Ecotoxicol. Environ. Saf. 182, 109375 https://doi.org/10.1016/j.ecoenv.2019.109375.

Megaw, J., Thompson, T.P., Lafferty, R.A., Gilmore, B.F., 2015. *Galleria mellonella* as a novel in vivo model for assessment of the toxicity of 1-alkyl-3-methylimidazolium chloride ionic liquids. Chemosphere 139, 197–201. https://doi.org/10.1016/J.CHEMOSPHERE.2015.06.026.

Meier-Kolthoff, J.P., Göker, M., 2019. TYGS is an automated high-throughput platform for state-of-the-art genome-based taxonomy. Nat. Commun. 10 https://doi.org/10.1038/s41467-019-10210-3.

Mello, I.S., Pietro-Souza, W., Barros, B.M., da Silva, G.F., Campos, M.L., Soares, M.A., 2019. Endophytic bacteria mitigate mercury toxicity to host plants. Symbiosis 79, 251–262. https://doi.org/10.1007/s13199-019-00644-0.

Messina, J.P., Brady, O.J., Scott, T.W., Zou, C., Pigott, D.M., Duda, K.A., Bhatt, S., Katzelnick, L., Howes, R.E., Battle, K.E., Simmons, C.P., Hay, S.I., 2014. Global spread of dengue virus types: Mapping the 70 year history. Trends Microbiol. 22, 138–146. https://doi.org/10.1016/j.tim.2013.12.011.

Miller, C.S., Handley, K.M., Wrighton, K.C., Frischkorn, K.R., Thomas, B.C., Banfield, J. F., 2013. Short-read assembly of full-length 16S amplicons reveals bacterial diversity in subsurface sediments. PLoS ONE 8, 1–11. https://doi.org/10.1371/journal.pone.0056018.

Mnif, I., Ghribi, D., 2015. Review lipopeptides biosurfactants: Mean classes and new insights for industrial, biomedical, and environmental applications. Biopolymers 104, 129–147. https://doi.org/10.1002/bip.22630.

Ng, L.F.P., Ojcius, D.M., 2009. Chikungunya fever - Re-emergence of an old disease. Microbes Infect. 11, 1163–1164. https://doi.org/10.1016/j.micinf.2009.09.001.

Olmo, C., Marco, A., Armengol, X., Ortells, R., 2016. Effects of Bacillus thuringiensis var. israelensis on nonstandard microcrustacean species isolated from fi eld zooplankton communities 1730–1738. Doi: 10.1007/s10646-016-1708-9.

Ongena, M., Jacques, P., 2008. *Bacillus* lipopeptides: versatile weapons for plant disease biocontrol. Trends Microbiol. 16, 115–125. https://doi.org/10.1016/j.tim.2007.12.009.

Pacheco, A.G., Rebelo, M.de.F., 2013. A simple R-based function to estimate lethal concentrations. Mar. Environ. Res. 91, 41–44. https://doi.org/10.1016/j.marenvres.2013.08.003.

Park, H.W., Bideshi, D.K., Federici, B.A., 2010. Properties and applied use of the mosquitocidal bacterium, *Bacillus sphaericus*. J. Asia. Pac. Entomol. 13, 159–168. https://doi.org/10.1016/j.aspen.2010.03.002.

Park, Y., Kyo Jung, J., Kim, Y., 2016. A mixture of *Bacillus thuringiensis* subsp. *israelensis* with *Xenorhabdus nematophila*-cultured broth enhances toxicity against mosquitoes *Aedes albopictus* and *Culex pipiens pallens* (Diptera: Culicidae). J. Econ. Entomol. 109, 1086–1093. https://doi.org/10.1093/jee/tow063.

Parthipan, P., Sarankumar, R.K., Jaganathan, A., Amuthavalli, P., Babujanarthanam, R., Rahman, P.K.S.M., Murugan, K., Higuchi, A., Benelli, G., Rajasekar, A., 2018. Biosurfactants produced by *Bacillus subtilis* A1 and *Pseudomonas stutzeri* NA3 reduce longevity and fecundity of *Anopheles stephensi* and show high toxicity against young instars. Environ. Sci. Pollut. Res. 25, 10471–10481. https://doi.org/10.1007/s11356-017-0105-0.

Porta-De-La-Riva, M., Fontrodona, L., Villanueva, A., Cerón, J., 2012. Basic *Caenorhabditis elegans* Methods: Synchronization and observation. J. Vis. Exp. https://doi.org/10.3791/4019.

Porter, A.G., 1996. Mosquitocidal toxins, genes and bacteria: The hit squad. Parasitol. Today 12, 175–179. https://doi.org/10.1016/0169-4758(96)10013-2.

Pradhan, A.K., Rath, A., Pradhan, N., Hazra, R.K., Nayak, R.R., Kanjilal, S., 2018. Cyclic lipopeptide biosurfactant from *Bacillus tequilensis* exhibits multifarious activity. 3. Biotech 8. https://doi.org/10.1007/s13205-018-1288-x.

R Core Team, 2018. R: a Language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria.

Raaijmakers, J.M., de Bruijn, I., Nybroe, O., Ongena, M., 2010. Natural functions of lipopeptides from *Bacillus* and *Pseudomonas*: More than surfactants and antibiotics. FEMS Microbiol. Rev. 34, 1037–1062. https://doi.org/10.1111/j.1574-6976.2010.00221.x.

Rabbee, M.F., Sarafat Ali, M., Choi, J., Hwang, B.S., Jeong, S.C., Baek, K.hyun., 2019. *Bacillus velezensis*: A valuable member of bioactive molecules within plant microbiomes. Molecules 24, 1–13. https://doi.org/10.3390/molecules24061046.

Raymond, B., Federici, B.A., Raymond, B., 2017. In defence of Bacillus thuringiensis, the safest and most successful microbial insecticide available to humanity — a response to EFSA 1–8. Doi: 10.1093/femsec/fix084.

Revathi, K., Chandrasekaran, R., Thanigaivel, A., Kirubakaran, S.A., Sathish-Narayanan, S., Senthil-Nathan, S., 2013. Effects of *Bacillus subtilis* metabolites on larval *Aedes aegypti* L. Pestic. Biochem. Physiol. 107, 369–376. https://doi.org/10.1016/J.PESTBP.2013.10.005.

Sansinenea, E., Ortiz, A., 2011. Secondary metabolites of soil *Bacillus* spp. Biotechnol. Lett. 33, 1523–1538. https://doi.org/10.1007/s10529-011-0617-5.

Santos, V.S.V., Pereira, B.B., 2019. Properties, toxicity and current applications of the biolarvicide spinosad. J. Toxicol Environ. Heal. - Part B Crit. Rev. 00, 1–14. https://doi.org/10.1080/10937404.2019.1689878.

Scholz, M., Lo, C.C., Chain, P.S.G., 2014. Improved assemblies using a source-agnostic pipeline for metagenomic assembly by merging (MeGAMerge) of contigs. Sci. Rep. 4, 1–9. https://doi.org/10.1038/srep06480.

Seemann, T., 2014. Prokka: Rapid prokaryotic genome annotation. Bioinformatics 30, 2068–2069. https://doi.org/10.1093/bioinformatics/btu153.

Seppey M., Manni M., Z.E.M., 2019. BUSCO: Assessing genome assembly and annotation completeness, in: Kollmar, M. (Ed.), Gene Prediction. Methods in Molecular Biology. Humana, New York. Doi: https://link.springer.com/protocol/10.1007/978-1-4939-9173-0_14.

Smith, G.H., Roberts, J.M., Pope, T.W., 2018. Terpene based biopesticides as potential alternatives to synthetic insecticides for control of aphid pests on protected ornamentals. Crop Prot. 110, 125–130. https://doi.org/10.1016/j.cropro.2018.04.011.

Soares, M.A., Li, H.Y., Bergen, M., da Silva, J.M., Kowalski, K.P., White, J.F., 2016. Functional role of an endophytic *Bacillus amyloliquefaciens* in enhancing growth and disease protection of invasive English ivy (Hedera helix L.). Plant Soil 405, 107–123. https://doi.org/10.1007/s11104-015-2638-7.

Sousa, J.R., Silva, F.A., Targanski, S.K., Fazolo, B.R., Souza, J.M., Campos, M.G., Vieira, L.C.C., de Oliveira Mendes, T.A., Soares, M.A., 2019. Synthesis and larvicidal activity of indole derivatives against *Aedes aegypti* (Diptera: Culicidae). J. Appl. Entomol. https://doi.org/10.1111/jen.12685.

SPSS, I., 2007. SPSS for Windows.

Sullivan, J.J., Goh, K.S., 2008. Environmental fate and properties of pyriproxyfen. J. Pestic. Sci. 33, 339–350. https://doi.org/10.1584/jpestics.R08-02.

Targanski, S.K., Sousa, J.R., Pádua, G.M., Sousa, J.M., Vieira, L.C., Soares, M.A., 2020. Larvicidal activity of substituted chalcones against Aedes aegypti (Diptera: Culicidae) and non-target organisms. Pest Manag. Sci. Doi: 10.1002/ps.6021.

Tatusova, T., Dicuccio, M., Badretdin, A., Chetvernin, V., Nawrocki, E.P., Zaslavsky, L., Lomsadze, A., Pruitt, K.D., Borodovsky, M., Ostell, J., 2016. NCBI prokaryotic genome annotation pipeline. Nucleic Acids Res. 44, 6614–6624. https://doi.org/10.1093/nar/gkw569.

Tindall, B.J., Rosselló-Móra, R., Busse, H.J., Ludwig, W., Kämpfer, P., 2010. Notes on the characterization of prokaryote strains for taxonomic purposes. Int. J. Syst. Evol. Microbiol. 60, 249–266. https://doi.org/10.1099/ijs.0.016949-0.

Vachon, V., Laprade, R., Schwartz, J., 2012. Current models of the mode of action of *Bacillus thuringiensis* insecticidal crystal proteins: A critical review. J. Invertebr. Pathol. 111, 1–12. https://doi.org/10.1016/j.jip.2012.05.001.

Vater, J., Herfort, S., Doellinger, J., Weydmann, M., Borriss, R., Lasch, P., 2018. Genome mining of the lipopeptide biosynthesis of *Paenibacillus polymyxa* E681 in combination with mass spectrometry: Discovery of the lipoheptapeptide paenilipoheptin. ChemBioChem 19, 744–753. https://doi.org/10.1002/cbic.201700615.

Wendisch, V.F., Zimmer, D.P., Khodursky, A., Cozzarelli, N., Kustu, S., 2001. Isolation of *Bacillus thuringiensis* from the state of Amazonas, in Brazil, and screening against *Aedes aegypti* (Diptera, Culicidae). Anal. Biochem. 213, 205–213.

WHO, 2005. Guidelines for laboratory and field testing of mosquito larvicides. World Heal. Organ. 1–41. Doi: Ref: WHO/CDS/WHOPES/GCDPP/2005.11.

Wilder-Smith, A., Gubler, D.J., Weaver, S.C., Monath, T.P., Heymann, D.L., Scott, T.W., 2017. Epidemic arboviral diseases: priorities for research and public health. Lancet Infect. Dis. 17, e101–e106. https://doi.org/10.1016/S1473-3099(16)30518-7.

World Health Organization-WHO, 2013. Larval source management: a supplementary measure for malaria vector control: an operational manual. Doi: 10.1564/v25.

World Health Organization-WHO, 1999. Microbial pest control agent: Bacillus thuringiensis 1–109.

World Health Organization, W., 2018. Dengue control [WWW Document]. Doi: 10.1564/v25.

Xu, B.H., Lu, Y.Q., Ye, Z.W., Zheng, Q.W., Wei, T., Lin, J.F., Guo, L.Q., 2018. Genomics-guided discovery and structure identification of cyclic lipopeptides from the *Bacillus siamensis* JFL15. PLoS ONE 13, 1–18. https://doi.org/10.1371/journal.pone.0202893.

Yi, Y., Zhang, Z., Zhao, F., Liu, H., Yu, L., Zha, J., Wang, G., 2018. Probiotic potential of *Bacillus velezensis* JW: Antimicrobial activity against fish pathogenic bacteria and immune enhancement effects on *Carassius auratus*. Fish Shellfish Immunol. 78, 322–330. https://doi.org/10.1016/j.fsi.2018.04.055.

Zhang, L., Zhang, X., Zhang, Y., Wu, S., Gelbič, I., Xu, L., Guan, X., 2016. A new formulation of *Bacillus thuringiensis*: UV protection and sustained release mosquito larvae studies. Sci. Rep. 6, 39425. https://doi.org/10.1038/srep39425.

Zhang, Q.X., Zhang, Y., He, L.L., Ji, Z.L., Tong, Y.H., 2018. Identification of a small antimycotic peptide produced by *Bacillus amyloliquefaciens* 6256. Pestic. Biochem. Physiol. 150, 78–82. https://doi.org/10.1016/j.pestbp.2018.07.006.

Zhang, Q.X., Zhang, Y., Shan, H.H., Tong, Y.H., Chen, X.J., Liu, F.Q., 2017. Isolation and identification of antifungal peptides from *Bacillus amyloliquefaciens* W10. Environ. Sci. Pollut. Res. 24, 25000–25009. https://doi.org/10.1007/s11356-017-0179-8.

Zhao, P., Quan, C., Jin, L., Wang, L., Wang, J., Fan, S., 2013. Effects of critical medium components on the production of antifungal lipopeptides from *Bacillus amyloliquefaciens* Q-426 exhibiting excellent biosurfact properties. World J. Microbiol. Biotechnol. 29, 401–409. https://doi.org/10.1007/s11274-012-1180-5.

Anexo 1 - Material Suplementar para o Capítulo 1

Supplementary data

Table S1. Larvicidal activity of 254 bacterial strains against *Aedes aegypti* larvae L3, after 48 hours of treatment.

Source	Strain	Larvae mortality (%)		Lipopeptide
		1º SC*	2º SC**	***
Sediment from Pantanal lagoons	*Bacillus safensis* B138 (MT269007)	100	97.50 ± 2.5	-
	Bacillus safensis B145 (MT269008)	100	95.83 ± 4.49	-
	Bacillus pumilus B08 (MT269006)	100	78.73 ± 23.39	-
	B77	100	48.33 ± 48.45	-
	B95	100	5.83 ± 5.34	-
	B61	90	55.00 ± 17.56	-
	B23	90	30.83 ± 19.24	-
	B108	80	1.67 ± 2.36	-
	Bacillus velezensis B64a (MT269009)	70	31.67 ± 31.31	+
	B07	70	0.83 ± 1.86	-
	B155	60	0.00 ± 0.00	-
	B119	40	-	NS
	B123	40	-	NS
	B53	30	-	NS
	B88	20	-	NS

B92	20	-	NS
B132	20	-	NS
B174	20	-	NS
B116	15	-	NS
B151	10	-	NS
B182	10	-	NS
B52	10	-	NS
B122	10	-	NS
B173	10	-	NS
B92	10	-	NS
B180	10	-	NS
B41	10	-	NS
B46	10	-	NS
B98	10	-	NS
B99	10	-	NS
B1, B2, B3, B4, B5, B6, B9, B11, B12, B13, B14, B15, B16, B17, B18, B19, B20, B21, B22, B24, B25, B26, B27, B28, B29, B30, B31, B32, B33, B34, B35, B36,	0	-	NS

	B37, B38, B39, B40, B42, B43, B44, B45, B47, B48, B49, B50, B51, B54, B55, B56, B57, B58, B59, B60, B62, B63, B65, B66, B67, B68, B69, B70, B71, B72, B73, B74, B76, B78, B79, B80, B82, B83, B84, B85, B87, B90, B91, B93, B94, B96, B97, B100, B101, B102, B103, B104, B105, B106, B107, B109A, B109C, B110, B111, B112, B113, B114, B115, B116, B117, B118, B120, B121, B125, B126, B127, B128, B129, B130, B133, B134, B135, B136, B137, B139, B140, B142, B143, B144, B146, B147, B148, B149, B149B, B150, B151, B152, B153, B154, B156, B157, B158, B159, B160A, B160B, B162, B163, B164, B165, B166, B168, B169, B170, B171, B172, B174, B175, B177, B178, B179, B184			
Rhizosphere of *Phaseolus vulgaris* (unpublished)	*Bacillus amyloliquefaciens* N05 (MH279750)	70	9.17 ± 9.75	-
	Bacillus velezensis B15 (MH279754)	60	68.33 ± 12.47	+
	Paenibacillus alvei N52 (MH279770)	60	5 ± 7.64	-
	Paenibacillus illinoisensis N12 (MH279755)	40	-	NS
	Paenibacillus lautus N46 (MH279757)	40	-	NS

	Bacillus megaterium N09 (MH279752)	30	-	NS
	Lysinibacillus sphaericus N44 (MH279753)	10	-	NS
	Brevibacillus brevis N16 (MH279759), *Bacillus cereus* N13 (MH279756), *Bacillus cereus* N56 (MH279756), *Bacillus cereus* N62 (MH279756), *Bacillus megaterium* N39 (MH279752), *Bacillus niacini* N03 (MH279776), *Bacillus pumilus* N29 (MH279766), *Bacillus pumilus* N61 (MH279766), *Bacillus subtilis* N25 (MH279764), *Lysinibacillus sphaericus* N10 (MH279753), *Paenibacillus lautus* N14 (MH279757), *Paenibacillus polymyxa* N21 (MH279762), *Paenibacillus illinoisensis* N49 (MH279755)	0	-	NS
Rhizosphere of *A. fluminensis* or *P. accuminatum* (Mariano et al., 2020)	*Bacillus safensis* C55	100	56.67 ± 43.56	-
	Bacillus sp. C101	100	36.67 ± 35.32	+
	Bacillus safensis C21	90	97.50 ± 3.82	-
	Bacillus aerophilus C57	80	90.00 ± 10.41	-
	Bacillus subtilis C10	50	86.67 ± 15.46	+
	Bacillus cereus C27	20	-	NS

	Bacillus cereus C29	10	-	NS
	Bacillus cereus C94	10	-	NS
	Bacillus megaterium C100	10	-	NS
	Bacillus subtilis C89	10	-	NS
	Bacillus amyloliquefaciens C13, *Bacillus aryabhattai* C84, *Bacillus cereus* C88, *Bacillus megaterium* C28, *Bacillus megaterium* C46, *Bacillus megaterium* C58, *Bacillus megaterium* C61, *Bacillus megaterium* C71, *Bacillus methylotrophicus* C4, *Bacillus shandongensis* C37	0	-	NS
Endophyte from *A. fluminensis* or *P. accuminatum* (Mello et al., 2019)	*Bacillus pumilus* BacI67 (KX641551)	96	99.17 ± 1.86	-
	Bacillus subtilis BacI75 (KX641559)	68	0.00 ± 0.00	-
	Bacillus sp. BacI19 (KX641508)	48	-	NS
	Bacillus velezensis BacI82 (KX641565)	8	-	NS
	Bacillus megaterium BacI64 (KX641548)	8	-	NS
	Bacillus sp. BacI95 (KX641578)	8	-	NS
	Bacillus cereus BacI87 (KX641570)	4	-	NS
	Bacillus cereus BacI96 (KX641579)	4	-	NS

	Bacillus amyloliquefaciens BacI76 (KX641560), *Bacillus cereus* BacI42 (KX641526), *Bacillus cereus* BacI61 (KX641545), *Bacillus cereus* BacI86 (KX641569), *Bacillus sp.* BacI30 (KX641585), *Bacillus sp.* BacI34 (KX641519)	0	-	NS
Endophyte from *Paulinia cupana* (Liotti et al., 2018)	*Bacillus subtilis* R236B (KX618358)	100	94.17 ± 6.07	-
	Bacillus altitudinis R409 (KX618335)	80	68.33 ± 28.38	-
	Bacillus stratosphericus R212 (KX618327)	40	-	NS
	Bacillus pumilus R15 (KX618264)	20	-	NS
	Bacillus safensis R7 (KX618337)	20	-	NS
	Bacillus aquimaris R51 (KX618263)	10	-	NS
	Bacillus anthracis R13(KX618295), *Bacillus anthracis* R66 (KX618295), *Bacillus aquimaris* R50 (KX618265), *Bacillus cereus* R8 (KX618250), *Bacillus cereus R31 (KX618339), Bacillus cereus R123 (KX618250), Bacillus marisflavi* R56 (KX618339), *Bacillus megaterium* R202 (KX618350), *Bacillus pumilus* R16 (KX618294), *Bacillus sp.* R128	0	-	NS

	(KX618346), *Bacillus thuringiensis* R125 (KX618303), *Bacillus thuringiensis* R256 (KX618266), *Bacillus thuringiensis* R302 (KX618266), *Paenibacillus dendritiformis* R105 (KX618387), *Paenibacillus sp.* R190 (KX618292), *Paenibacillus sp2* R201B (KX618276)			
Control	*B. thuringiensis* var. *israelensis* (Bti)	100	100	NS
Control	T3 broth	0	0	NS
Control	*Water*	0	0	NS

The strain codes in parenthesis are GenBank Accession Numbers. *1st SC – First screening (n = 1 cup): selection of strains that cause larval mortality ≥ 50%; **2nd SC – Second screening (n = 3): mean ± standard deviation of the percentage of dead *A. aegypti* larvae L3; ***Lipopeptide – presence (+) or absence (-) of precipitate under acidic conditions. NS: Not screened.

Table S2: Assembly parameters for each strain.

Assembly	*B. safensis* BacI67	*B. paranthracis* C21	*B. velezensis* 64a	*B. velezensis* B15
Trimmomatic Slinding Window	4:18	4:17	4:17	4:18
Trimmomatic Min Lenght	70	65	100	70

Assembly chosen	Mega Merge	Mega Merge	Mega Merge	Mega Merge

Table S3. Putative assignments of m/z peaks from peptide spectrograms of *B. velezensis* B64a and *B. velezensis* B15 crude lipopeptide extracts.

Peak mass (m/z)	*B. velezensis* B64a	*B. velezensis* B15	Putative assignments	Reference
1016.6	X	-	C13 surfactin [M+Na+]	
1022.6	-	X	C14 surfactin [M+H]+	
1030.6	X	X	C13 surfactin [M+Na+]	
1043.5	X	-	C14 iturin [M+H+]	
1044.6	-	X	C14 surfactin, [M+Na and K]+	
1057.5	X	X	C15 iturin [M+H+]	
1065.5	X	X	C14 iturin [M+Na+]	
1072.6	-	X	C16 surfactin [M+Na]+	
1079.5	X	X	C15 iturin A [M+Na+]	
1093.5	X	X	C16 iturin A	
1107.5	X	X	C17 iturin [M+Na+]	
1117.4	X	X	Lipo-chitin oligossacharide [M+Na]+	
1240.1	X	-	mepartricin A [M+Na]+	
1247.1	X	-	NN'-diacetylmepartricin A [M+Na]+	
1261.1	X	-	monosialoganglioside GM2	
1301.1	X	-	O-deacylated lipopolysaccharide	

1435.7	X	X	fengycin A [M+H]+	
1449.7	X	X	C15 fengycin	
1463.8	X	X	fengycin A [M+H]+	
1471.3	X	X	C15 fengycin [M+Na]+	
1477.8	-	X	fengycin B2	
1478.8	X	-	fengycin A	
1485.3	X	X	C16 fengycin [M+Na]+	
1492.8	X	X	C16 fengycinB	
1499.8	-	X	C17 fengycin [M+Na]+	
1505.8	X	X	fengycin A [M+H]+	
1513.3	-	X	C16 fengycin [M+Na]+	
1519.8	-	X	C17 fengycin B1 [M+H]+	

Table S4. Larvicidal activity of supernatants (SN) treated with denaturing agents.

Strain	Larvae mortality (%)		
	Untreated SN	Autoclaved SN	Alkalized SN
B. safensis BacI67	98.33 ± 2.88[a]	96.67 ± 2.88[a]	98.33 ± 2.88[a]
B. paranthracis C21	100.00 ± 0[a]	100.00 ± 0[a]	100.00 ± 0[a]

Data expressed as the mean ± standard deviation (n = 3) of the percentage of larvae mortality after 24 hours of treatment. Means on the same line followed by the same letter are statistically similar, according to the binomial GLMM test ($p < .05$).

Table S5. Partial QUAST report for assemblies performed using different assemblers.

Parameter	*B. safensis* BacI67			*B. paranthracis* C21			*B. velezensis* B64a		*B. velezensis* B15		
	Newbler	Spades	MMerge	Newbler	Spades	MMerge	Spades	MMerge	Newbler	Spades	MMerge
N50	60.984	399.846	399.846	141.075	225.045	225.045	673.669	673.669	107.975	330.779	337.314
L50	20	4	4	13	8	8	3	3	11	5	5
# Contigs	93	198	61	128	484	171	134	44	62	185	67
Largest contig	253.555	713.688	713.688	640.673	640.754	640.754	915.485	915.485	358.624	558.274	558.274
Genome fraction (%)	8.199	8.491	8.414	16.582	16.732	16.596	93.35	93.239	93.337	94.095	93.984
Duplication ratio	1.001	1.007	1.003	1.001	1.007	1.004	1.001	1.001	1.001	1.002	1.031
Largest alignment	55.749	55.898	55.898	55.121	55.368	55.368	453.157	453.157	326.814	326.814	326.814
Total aligned length	318.242	331.045	326.822	900.832	912.463	902.012	3.671.283	3.664.547	3.669.211	3.702.262	3.805.198
# Misassemblies	0	0	0	0	0	0	55	55	40	42	45
# Unaligned mis. contigs	58	21	21	53	36	36	0	0	0	0	0
# Fully unaligned contigs	17	128	29	58	332	108	56	19	3	84	27
Fully unaligned length	194.100	34.037	25.472	384.103	390.668	369.819	19.154	16.023	76.079	30.003	25.534

# Partially unaligned contigs	76	23	23	68	48	48	9	9	32	13	13
Partially unaligned length	3.312.975	3.524.148	3.523.915	4.239.706	4.392.432	4.392.693	313.831	313.831	240.740	326.335	331.193
# Mismatches	12.144	12.252	12.230	34.239	34.031	33.950	75.744	75.684	55.283	55.911	57.442
# Mismatches per 100 kbp	3818.52	3719.89	3747.44	3.804.79	3.747.68	3.769.34	2064.73	2065.56	1507.2	1512.03	1555.27
# N's	0	96	116	0	1850	1755	781	781	0	774	779
# N's per 100 kbp	0	2.47	2.99	0	32.47	30.97	19.5	19.55	0	19.06	18.71

Table S6. GO annotation for *B. safensis* BacI67, *B. paranthracis* C21, *B. velezensis* B64a, and *B. velezensis* B15.

GO-term	*B. safensis* BacI67	*B. paranthacis* C21	*B. velezensis* B64a	*B. velezensis* B15
BIOLOGICAL PROCESS (BP)	**3,159***	**3,262**	**3,669**	**3,566**
Aromatic compound biosynthetic process	6.49**	-	-	-
Carboxylic acid metabolic process	-	8.52	7.96	-
Cellular amino acid metabolic process	6.08	-	-	5.78
Cellular component organization or biogenesis	5.95	-	5.67	5.97
Cellular macromolecule biosynthetic process	6.84	0	7.88	8.1
Cellular macromolecule metabolic process	-	13.27	-	-
Cellular nitrogen compound biosynthetic process	9.91	9.2	-	-
Cellular protein metabolic process	6.46	-	6.16	6.17
Cellular response to stimulus	-	6.71	5.72	5.8
Gene expression	8.17	8.06	8.67	8.95
Heterocycle biosynthetic process	6.93	6.62	-	-
Nucleic acid metabolic process	-	10.58	-	-
Nucleobase-containing compound biosynthetic process	-	-	6.6	6.7
Organic cyclic compound biosynthetic process	7.09	6.77	-	-
Organic cyclic compound biosynthetic process	-	-	-	-
Organonitrogen compound biosynthetic process	8.96	8.95	10.22	10.66
Oxidation-reduction process	-	-	6.76	6.79

Phosphate-containing compound metabolic process	-	-	7.09	6.87
Protein metabolic process	-	6.62	-	-
Regulation of cellular process	6.39	6.93	7.11	7.23
Response to stimulus	8.26	-	-	-
RNA metabolic process	6.11	-	6.68	7.04
Small molecule biosynthetic process	-	-	6.16	6.48
Transmembrane transport	-	-	7.33	7.46
Transport	6.36	7.76	-	-
CELLULAR COMPONENT (CC)	**3,068**	**1,687**	**2,223**	**2,252**
Cytosol	-	18.44	13.99	14.34
Plasma membrane	-	23.12	22.31	22.25
Protein-containing complex	-	12.63	8.73	8.97
Cell	-	45.82	37.97	38.54
DNA binding	14.6	-	-	-
Hydrolase activity	19.65	-	-	-
Integral component of membrane	-	-	17	15.9
Ion binding	22.78	-	-	-
Oxidoreductase activity	11.8	-	-	-
Transferase activity	19.36	-	-	-
Transmembrane transporter activity	11.8	-	-	-

MOLECULAR FUNCTION (MF)	2,374	3,068	3,210	2,739
Anion binding	-	-	10.44	11.39
Cation binding	-	-	7.82	0
DNA binding	13.06	14.6	10.56	13.58
Drug binding	-	-	7.98	0
Hydrolase activity	18.07	19.65	16.7	19.97
Ion binding	27.38	22.78	-	-
Nucleotide binding	-	-	9.72	10.7
Oxidoreductase activity	12.05	11.8	10.47	13.11
Transferase activity	18.7	19.36	17.23	20.41
Transmembrane transporter activity	10.74	11.8	9.1	10.84

* Total number of proteins identified in the category; ** Percentage of proteins identified in each category.

Table S7. Secondary metabolite gene clusters of *B. safensis* BacI67 detected by AntiSMASH.

Type	From	To	Size (nt)	Metabolite/MSKC
Bacteriocin	77,829	88,146	10,318	Unknown
Beta-lactone	451,990	478,368	26,379	Unknown
Siderophore	376,986	405,622	28,637	Unknown
Terpene	67,095	88,696	21,875	Unknown
LAP	240,543	226,723	22,181	Plantazolicin (91%)
NRPS	194,741	229,869	35,129	Bacillibactin (53%)
NRPS	75,803	159,509	83,707	Lichenysin (92%)
Beta-lactone	137,221	165,633	28,413	Fengycin (53%)
T3PKS	1	28,888	28,888	Unknown
Terpene	67,095	88,969	21,875	Unknown

MSKC: Most similar known cluster in the MiBig database, where the numbers in parenthesis are the percentage of similarity.

Table S8. Secondary metabolite gene clusters of *B. paranthracis* C21 detected by AntiSMASH.

Type	From	To	Size (nt)	Metabolite/MSKC
NRPS	17,433	67,160	49,718	Bacillibactin (46%)
Beta-lactone	200,565	225,803	25,239	Fengycin (40%)
Bacteriocin	327,225	337,491	10,267	Unknown
LAP, Bacteriocin	162,585	186,091	23,507	Unknown
Terpene	1	13,499	13,499	Unknown
Bacteriocin	1	6,639	6,639	Unknown
Bacteriocin	1	5,870	5,870	Unknown

MSKC: Most similar known cluster in the MiBig database, where the numbers in parenthesis are the percentage of similarity.

Table S9. Secondary metabolite gene clusters of *B. velezensis* B64a detected by AntiSMASH.

Type	From	To	Size (nt)	Metabolite/MSKC
Other	228,781	270,199	41,419	Bacylisin (100%)
Bacteriocin, NRPS	786,361	838,154	51,794	Bacillibactin (100%)
Trans-AT-PKS, *trans*-AT-PKS-like	542,296	648,462	106,167	Difficidin (100%)
Trans-AT-PKS-like, *trans*-AT-PKS, NRPS, T3PKS	20,435	130,140	109,706	Bacillaene (100%)
Trans-AT-PKS	349,293	437,499	88,207	Macrolactin H (100%)
Lanthipeptide	602,798	631,687	28,890	-
NRPS	205,658	271,065	65,408	Surfactin (78%)
PKS-Like	62,897	104,141	41,245	Butirosin A/Butirosin B (7%)
Terpene	186,177	206,917	20,741	Unknown
T3PKS	1	26,394	26,394	Unknown
Terpene	95,059	116,942	21,884	Unknown
NRPS	139,672	178,102	38,431	Plipastatin (46%)
NRPS, beta-lactone, *trans*-AT-PKS	1	87,619	87,619	Fengycin (80%)
Fengycin	1	9,487	9,487	Fengycin (13%)

MSKC: Most similar known cluster in the MiBig database, where the numbers in parenthesis are the percentage of similarity.

Table S10. Secondary metabolite gene clusters of *B. velezensis* B15 detected by AntiSMASH.

Type	From	To	Size (nt)	Metabolite/MSKC
PKS-like	63,692	104,936	41,245	Butirosin A/Butirosin B (7%)
Terpene	187,740	208,480	20,741	-
NRPS, beta-lactone, *trans*-AT-PKS	3	99,803	99,801	Fengycin (86%)
Trans-AT-PKS-like, *trans*-AT-PKS, NRPS, T3PKS	162,026	272,134	110,109	Bacillaene (100%)
Other	42,529	83,947	41,419	Bacilysin (100%)
Terpene	49,157	71,040	21,884	-
T3PKS	134,507	175,607	41,101	-
Trans-AT-PKS-like	291,468	337,314	41,847	Difficidin (53%)
Thiopeptide, LAP	92,101	121,834	29,734	-
NRPS	133,234	198,641	65,408	Surfactin (91%)
Trans-AT-PKS-like	185,896	220,367	34,472	Difficidin (46%)
NRPS, bacteriocin	134,660	186,452	51,793	Bacillibactin (100%)
Trans-AT-PKS	1	81,573	81,573	Macrolactin H (100%)
Trans-AT-PKS-like	1	22,938	22,938	Difficidin (26%)

NRPS	1	13,471	13,471	Fengycin (20%)

MSKC: Most similar known cluster in the MiBig database, where the numbers in parenthesis are the percentage of similarity.

Capítulo 2 - Larval gut microbiome of *Pelidnota luridipes* (Coleoptera: Scarabaeidae): high bacterial diversity, different metabolic profiles on gut chambers and species with probiotic potential

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Larval gut microbiome of *Pelidnota luridipes* (Coleoptera: Scarabaeidae): high bacterial diversity, different metabolic profiles on gut chambers and species with probiotic potential

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Abstract

Pelidnota luridipes Blanchard (1850) is a tropical beetle of the family Scarabaeidae, whose larvae live on wood without parental care. Microbiota of mid- and hindgut of larvae was evaluated by culture-dependent and independent methods, and the results show a diverse microbiota, with most species of bacteria and fungi shared between midgut and hindgut. We isolated 272 bacterial and 29 yeast isolates, identified in 57 and 7 species, respectively, while using metabarcoding, we accessed 1,481 and 267 OTUs of bacteria and fungi, respectively. The composition and abundance of bacteria and fungi differed between mid- and hindgut, with a tendency for higher richness and diversity of yeasts in the midgut, and bacteria on the hindgut. Some taxa are abundant in the intestine of *P. luridipes* larvae, such as *Firmicutes, Bacteroidetes, Proteobacteria*, and *Actinobacteria*; as well as *Saccharomycetales* and *Trichosporonales* yeasts. Mid- and hindgut metabolic profiles differ (e.g. biosynthesis of amino acids, cofactors, and lipopolysaccharides) with higher functional diversity in the hindgut. Isolates have different functional traits such as secretion of hydrolytic enzymes and antibiosis against pathogens. *Apiotrichum siamense* L29A and *Bacillus* sp. BL17B protected larvae of the moth *Galleria mellonella* (Linnaeus, 1758), against infection by the pathogens *Listeria monocytogenes* ATCC19111 and *Pseudomonas aeruginosa* ATCC 9027. This is the first work with the larval microbiome of a Rutelini beetle, demonstrating its diversity and potential in prospecting microbial products as probiotics. The functional role of microbiota for the nutrition and adaptability of *P. luridipes* larvae needs to be evaluated in the future.

Keywords: metabarcoding, saproxylic beetles, grub, Rutelinae, probiotics, lytic enzymes

Key Points:

- Gut microbiome of *P. luridipes* larvae is dominated by *Firmicutes* and *Bacteroidetes*.
- Yeasts *Spathaspora* and *Candida* are abundant in larval gut.
- *Apiotrichum siamense* L29A e *Bacillus* sp. BL17B showed probiotic features.

Introduction

Microbes and insects share and modify environments, and the association between them is complex, diverse, and ancient. Throughout their diversification, insects have generated niches occupied by symbiotic and/or parasitic microbiota (Dillon and Dillon 2004; Blackwell 2017) that are associated with different parts of their body, especially the cuticle and the gut (Mattoso et al. 2012; Stefanini 2018). Temporally, the host-associated microbiota can be transient - momentarily acquired from habitat or food (Santos-Garcia et al. 2020) - or represented by resident species, constituting a community that can be relatively stable (Douglas 2015). Microbial communities associated with insect guts have interesting functional traits for the insect, such as substrate fermentation (Lemke et al. 2003), secretion of lytic enzymes (Sheng et al. 2015), and detoxification of toxic compounds (Adams et al 2013; Ceja-Navarro et al. 2015). Conversely, insects contribute to the dispersion of microbes (Madden et al. 2018; Jacquemyn et al. 2021), facilitate microbial action on comminuted foods (Brune 2014; Ulyshen 2016), and provide a favourable micro-habitat to microbial growth (Blackwell 2017). These microbes can supplement nutrients, such as sterols (Nasir and Noda 2003) and essential amino acids (Douglas 2013; Ayayee et al. 2016; Alonso-Pernas et al. 2017b), required for maintenance and insect growth on nutritionally poor substrates such as wood or flour. Biological nitrogen fixation by the microbial community is capable of ameliorating the carbon:nitrogen (C:N) balance in some groups of termites (Brune and Dietrich 2015), for example. In general, not only termites, but other wood boring insects have the potential to accelerate the release of immobilised nitrogen in fungal tissues and to promote the activity of nitrogen-fixing prokaryotes, incorporating it into their biomass and increasing the amount of this element in the environment (Ulyshen 2015). Microbial biomass of the gut itself can be a nutritional source for insects, as occurs in termites and passalids (Reyes Castillo 1970; Nalepa et al. 2001).

The gut of insects has three main segments, the stomodeum (foregut) directly connected to the mouth, the mesodeum (midgut), and the proctodeum (hindgut) (Holtof et al. 2019). These regions vary anatomically according to the group and their diet, with several groups also having crypts, caeca, or enlargements that promote the persistence of microorganisms inside the tube (Engel and Moran 2013). In addition to anatomical differences, the intestinal compartments have varying functions and pH, constituting different environments in which microbial colonisation occurs. In termites, the wood crushed by mandibulae and by the gizzard crosses an alkaline midgut facilitating the extraction of hemicelluloses (Terra 1990) that are hydrolysed by the microbiota of the proctodeal chamber (Brune and Dietrich 2015). Similarly, xylophagous beetles (e.g. family Scarabaeidae) have an expansion of the midgut with alkaline pH, ranging from 8.38 in *Odontotaenius disjunctus* (Illiger, 1800) (Ceja-Navarro et al. 2014) to 10.7 in *Trypoxylus dichotomus* (Linnaeus, 1771) (Wada et al. 2014); in addition to a large chamber in the hindgut that hosts a very diverse microbial community (Egert et al. 2005; Arias-Cordero

et al. 2012; Alonso-Pernas et al. 2017a; Shelomi et al. 2019). The bacterial phyla most often found in these beetles are *Proteobacteria* (mainly classes γ and β), *Firmicutes, Bacteroidetes* and *Actinobacteria* (Egert et al. 2005; El-Sayed and Ibrahim 2015; Ziganshina et al. 2018). Although most studies focus on bacterial communities, some authors frequently indicate Saccharomycetes yeasts in the insect guts, and less frequently *Basidiomycota* yeasts (Ziganshina et al. 2018).

This diverse microbiota is an important repository of species for the development of biotechnological products and processes (Ankrah and Douglas 2018). It can bear enzymes of industrial interest for textile processing, paper recycling, production of nutritional supplements, for the food industry, for the production of alcohol from lignocellulosic materials (Berasategui et al. 2016), antimicrobial compounds for pest management and medical applications (Xie et al. 2019), and probiotic microbial strains (Honey Chandran and Keerthi 2018; Borah et al. 2019).

Probiotics can be defined as live microorganisms that, when administered in adequate amounts, have health benefits to the host (Hill et al. 2014). However, this definition has been updated to include dead, inactivated, disrupted cells or even cell metabolites that have shown probiotic effects (Zendeboodi et al. 2020). Probiotic effects are species or lineage-specific (McFarland et al. 2018), and may work for a limited number of indications (Sniffen et al. 2018). Therefore, it is necessary to prospect for new broader spectrum probiotics or for functions not yet covered. Probiotics act mainly by reinforcing the epithelial barrier, adhering to the intestinal mucosa (and inhibiting pathogen adhesion), inhibiting pathogens by competitive exclusion, producing antimicrobial molecules, and modulating the immune system (Bermudez-Brito et al. 2012), although the exact mechanisms are not fully known (Cremon et al. 2018). In addition to these mechanisms, probiotic strains can secrete useful vitamins and enzymes to the host (Daliri and Lee 2015; Dawood et al. 2019), increase enterocyte renewal and regulate intestinal transit (Hill et al. 2014). Some probiotic strains have specific effects against certain gastrointestinal pathogens, neutralise carcinogenic compounds, and even have neurological, immunological, and endocrine effects (Zendeboodi et al. 2020).

Antibiosis against gastrointestinal pathogens is an extremely desirable feature for probiotics, as it helps to avoid the use of antibiotics and their growing microbial resistance. Microorganisms isolated from insects and other animals are potential probiotics, such as *Lactobacillus kunkeei* (isolated from bee intestine) which is capable of inhibiting *Pseudomonas aeruginosa* in larvae of the moth *Galleria mellonella* (Linnaeus, 1758) (Fernández et al. 2017). Other studies demonstrate the *in vitro* and *in vivo* inhibition of pathogens that cause vaginal dysbiosis (Pino et al. 2021) and mastitis (Bousmaha-Marroki et al. 2021), in humans. Probiotics for animal production can combine pathogen inhibition to the production of nutrients for the animal (Dawood et al. 2019), like three isolates of *Lactococcus lactis* subsp. *lactis* which, inhibit *Salmonella* Heidelberg (a serovar from *S. enterica*) and *Staphylococcus aureus*, and also secrete folate and riboflavin, essential for the development of chickens (Sabo et al. 2020).

Pelidnota luridipes is a beetle of the family Scarabaeidae (subfamily Rutelinae) of mostly unknown biology (Morón and Deloya 2002; Lunz et al. 2011; Rodrigues and Falco 2011). As far as it is known, there are no published studies on either the species and genus microbiota. *Pelidnota* adults are usually caught at light or in fruit traps at the beginning of the rainy season (Moore et al. 2017). Adults live for a few weeks and feed on flowers, fruits, and buds - in some species, adults do not feed (Ritcher 1966; Morón and Deloya 2002; Lunz et al. 2011; Rodrigues and Falco 2011; Moore et al. 2017). *Pelidnota* larvae feed on wood, humus, or roots and spend most of their development in the third instar (Rodrigues and Falco 2011). They resemble grubs, rhizophagous pests of the subfamilies Dynastinae and Melolonthinae (Scholtz and Grebennikov 2016). Larvae of these families and other Scarabaeidae usually have an expanded midgut with an alkaline pH (Wada et al. 2014), as well as an even bulkier fermentation chamber in the hindgut, which pH is close to neutral (Areekul 1957; Zheng et al. 2012; Wada et al. 2014). Within these chambers, the pH and availability of O_2 vary, creating microhabitats exploited by the associated microbiota (Ceja-Navarro et al. 2014) in Dynastinae, Melolonthinae as well as other closely related families. Larvae in this group harbour microbes able to ferment sugars such as cellulose and xylose (Selim et al. 2020) and are also able to recycle nitrogen waste which is later absorbed by the insect (Cadete et al. 2009; Alonso-Pernas et al. 2017b), in addition to secreting several enzymes of biotechnological interest (Egert et al. 2005; Handique et al. 2017; Wales et al. 2018).

In this work, we used cultivation-dependent and independent methods to analyse the structure of the bacteria and fungi communities associated with the gut of *P. luridipes* larvae, in addition to evaluating functional traits and probiotic potential of cultivable isolates. We aim to unveil and understand microbial diversity in the gut of a tropical beetle larva that lives under a very poor diet, and check for the presence of species featuring interesting antimicrobial and/or enzymatic properties that may help larvae thrive on decaying wood, and may be of biotechnological interest.

Material and Methods

Insect collection and processing

Third instar larvae of *Pelidnota luridipes* were found and collected manually during April 2018 on a decaying log in a forest fragment in the municipality of Cuiabá, Mato Grosso, Brazil (15.606750 S, 56.047229W) (access number on Sisgen A9C82C6). Larvae were transported to the laboratory inside their substrate to avoid potential contamination or stress to the animals. Insect vouchers (three larvae) were deposited at the Entomology Section of the Universidade Federal de Mato Grosso (UFMT) Zoological Collection (CEMT). Five larvae were kept in individual plastic pots containing fragments of wood and soil from the site until the emergence of adults for identification. A couple of emerged adults were kept for breeding in plastic containers and for obtaining eggs. The remaining adults were deposited at CEMT (CEMT 00042724-40725). Three third

instar larvae obtained from these eggs were dissected and mid- and hindgut were separated and macerated in 3 mL of ultrapure water for pH measuring.

Isolation and identification of cultivable microorganisms from larval guts

Initially, larvae (Online Resource 1, Fig. S1a) were superficially disinfected with 70% alcohol for 1 min, and rinsed three times in a sterile phosphate buffer (PBS) (81mM Na2HPO4, 19mM NaH2PO4, 150mM NaCl, pH 7.4). Then, larvae were dissected in a laminar flow hood (Online Resource 1, Fig. S1b). The guts of five larvae were processed without separation of midgut and hindgut initially, only for plating and cultivation of microorganisms. Afterwards, three other larvae were processed, individualising the two digestive chambers for enumeration and isolation of microorganisms and for total DNA extraction.

The mass of whole tubes and chambers was measured on an analytical scale. Sequentially, the materials were macerated in Eppendorf tubes containing PBS buffer for isolation of cultivable microbes. A fraction of the macerate obtained from each gut chamber was stored at -20ºC for total DNA extraction. The macerates were plated on TSA 10% with nystatin, ACA with nystatin (100 µg / mL) and YPD culture medium with chloramphenicol (100 µg / mL). Plates were incubated at 28º C and observed daily. The colonies were purified and morphotyped, and then stored in 20% glycerol at -20ºC.

Isolates were identified by extracting their DNA (Bio-Rad Instagene Matrix Kit) and amplifying the regions 16S of bacterial rDNA with the 1492R-P027F oligos (Lane 1991) and yeasts' ITS rDNA with the ITS1-ITS4 oligos (White et al. 1990) by PCR. The amplicons were purified enzymatically with ExoSap-it PCR Product Cleanup Reagent (GE Healthcare) and Sanger sequenced using the BigDye™ Terminator Cycle Sequencing kit. Sequences were filtered and edited in BioEdit version 7.2.6.1 and aligned for molecular identification in NCBI with BLASTn algorithm (Altschul and Gish, W. Miller, E. W. Myers 1990). The identification considered sharing at least 97% the identity with the sequences deposited in GenBank (Janda and Abbott 2007). Sequences were deposited in GenBank with access numbers MW142049 to 142152, MW147750 to 147755 and MW165500 to 165513 (Online Resource 2, Table S1).

Sequencing and metabarcoding of gut samples

We extracted and purified total DNA from larval gut macerates with the DNEasy Power Soil kit (Qiagen), according to the manufacturer's instructions and using the equivalent of 50 mg of intestine. We identified the communities of bacteria and fungi in the samples by next generation sequencing on Illumina - MiSeq platform (2 × 300 bp), according to the manufacturer's recommendations. The 16S rRNA genes were amplified with primers S-D-Bact-0341-b-S-17 (5′-CCTACGGGNGGCWGCAG-3′) e S-D-Bact-0785-a-A-21

(5′-GACTACHVGGGTATCTAATCC-3′) that flank the hypervariable regions V3 and V4 (Klindworth et al. 2013). The nRLSU-U (nuclear ribosomal large subunit rDNA) region of the fungal 28S rDNA gene was amplified using primers U1 and U2 (Huang et al. 2014).

Sequences were processed using USEARCH v11.0.667 (Edgar 2010). First, the paired-end raw readings were joined with overlap criteria: identity higher than 90% and less than 30 differences between the ends of pairs. Then, the adapters were eliminated and the reads selected by final size of 400 bp (16S) and 210 bp (nRLSU-U).

Sequences were filtered using the criterion of expected average errors ("max_EE" = 02 average errors per sequence) and were not replicated, obtaining representative sequences for each OTU. OTUs represented by only one read were eliminated (Debroas et al. 2017). Subsequently, the unreplicated sequences went through grouping or clustering, recruiting in a single group all sequences with up to 97% similarity (Yoon et al. 2017). The chimeric sequences were removed with the UCHIME algorithm (Edgar et al. 2011) implemented in USEARCH. The counting matrices were obtained with the "usearch_global" algorithm. Finally, the taxonomy of the non-replicated sequences was predicted using the SINTAX algorithm, implemented in USEARCH. We used an 80% confidence bootstrap to predict a taxonomic level for an OTU. The database for taxonomic prediction was made with the combination of the Ribosomal Database Project - RDP (http://rdp.cme.msu.edu/), added with mitochondrial sequences from the NT bank - National Center for Biotechnology Information - NCBI and the SILVA database (Yarza et al. 2014) . For further analysis, we removed the sequences classified as chloroplasts and mitochondria. Sequences were deposited in GenBank under accession numbers PRJNA718877.

Evaluation of probiotic functional traits of isolates

Stocked bacteria and yeasts were previously activated in LB and YPD broth, respectively, at 28 ºC under agitation of 100 rpm for 24 h. The isolated strains were characterised by their ability to secrete hydrolytic enzymes: cellulases, proteases, pectinases, amylases, esterases (Carrim et al. 2006); ligninases (growth and production of halos in medium with tannic acid: tannic acid, 5 g / L; malt extract, 15 g / L; agar 40 g / L) and by phosphate solubilisation (Katznelson and Bose 1959). The growth and production of halos (or precipitate, in the case of esterase) was evaluated semi-quantitatively by scales of 0 (absence) and 1 to 3 (relative size of halos: small, medium and large).

Antagonistic antibiotic activity of the isolates was determined by the overlay method (Pugsley and Oudega 1987). Liquid cultures of the isolates were inoculated in Petri dishes containing LB agar and inactivated with chloroform vapour after 24 h of growth. Then, an over-layer of semi-solid LB medium (0.8% agar) containing 50µL of culture of the pathogenic strain (OD 600nm 0.8) was deposited on the inactivated cultures. After half an hour at 4º C, plates were incubated at 37º C for 24 h. Antagonistic activity was determined by the

size of the inhibition halo on the pathogens: *Escherichia coli* ATCC25922, *Listeria monocytogenes* ATCC19111, *Pseudomonas aeruginosa* ATCC9027, *Salmonella enterica* serovar Typhimurium ATCC14028, *Yersinia enterocolitica* IAL2449, *Shigella flexneri* ATCC12022, *Staphylococcus aureus* ATCC6538. Inhibition of pathogenic yeasts *Candida albicans* 159 and *Candida tropicalis* 160 (clinical isolates obtained from Hospital Universitário Julio Muller) were also tested. Pathogen inhibition halos were used to calculate qualitative inhibition scores (number of inhibited pathogen species) and total scores (total sum of halo values).

The ability of the isolates to grow at different pHs was determined in liquid medium in 96-well microplates at 28º C. Cellular growth in liquid LB at pH 2, 4, 7 and 8 was measured in a spectrophotometer by the optical density at 600 nm for 48 h. Finally, the ability of the isolates to grow in the presence of bile salts was determined in Petri dishes containing TSA 10% or YMA medium with 0.3% bile salts (Sedláčková et al. 2015). *Saccharomyces boulardii* (Repoflor® - Legrand) and *Bacillus clausii* (Enterogermina Plus® - Sanofi commercial probiotic strains were used as a reference in all tests.

Evaluation of antagonistic activity *in vivo* in *Galleria mellonella* larvae

The antagonistic activity of the isolates against pathogenic microorganisms was evaluated in *Galleria mellonella (Linnaeus, 1758)* larvae (Scalfaro et al. 2017). Initially, we selected strains that inhibited at least two pathogenic species or strains that showed a quantitative inhibition score higher than 5. The strains identified as pathogenic species were eliminated from the selection. At the end, seven species were selected for the assays with *G. mellonella* (Table 1).

Table 1. Characterisation of the isolates selected for *in vivo* antibiosis assay in *Galleria mellonella* larvae.

Isolate	Functional Traits							Growth					Antibiosis halos *in vitro* (mm)									
	PT	ES	CEL	PEC	AM	LG	SB	PO_4	pH2	pH4	pH7	pH8	CA	CT	EC	PA	SF	ST	YE	LM	SA	Halo Sums
Apiotrichum siamense L29A	0	0	0	0	2	0	2	0	1	1	1	1	0	0	0	9	0	0	0	8	0	17
Bacillus paranthracis B73	3	2	2	0	3	0	0	0	0	0	1	1	0	0	0	14	0	0	0	14	0	28
Bacillus pumilus B34	1	0	1	1	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	14	18	32
Bacillus sp. BL17B	3	0	3	2	3	0	1	0	0	0	1	1	0	0	0	0	3	0	10	0	20	33
Bacillus thuringiensis B27B	3	3	0	1	2	1	3	1	1	0	1	1	0	0	0	18	0	0	0	15	26	59
Bacillus velezensis BL14	3	0	2	2	2	0	0	0	0	0	1	1	0	0	19	0	11	10	34	0	45	119
Xanthomonas maliensis B6B	0	0	1	0	0	0	3	2	0	0	1	1	0	0	14	0	15	16	0	0	0	45
Bacillus clausii – comercial	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0
Saccharomyces boulardii – comercial	0	0	0	0	0	0	0	1	0	0	1	1	0	0	0	0	0	0	0	0	0	0

Functional traits indicated by halo semi-quantitative measure: PT: Protease, ES: Esterase, CEL: Cellulase, PEC: Pectinase, AM: Amylase, LG: Ligninase, SB: Growth in medium with bile salts, PO_4: Phosphate solubilisation. Growth in culture medium with different pHs: 0 - Non-growth and 1- Growth. Halos of in vitro antibiosis: CA: *Candida albicans* 159, CT: *Candida tropicalis* 160, EC: *Escherichia coli* ATCC25922, PA: *Pseudomonas aeruginosa* ATCC9027, *Shigella flexneri* ATCC12022, *Salmonella enterica* serovar Typhimurium ATCC14028, YE: *Yersinia enterocolitica* IAL2449, LM: *Listeria monocytogenes* ATCC19111, *Staphylococcus aureus* ATCC6538.

Initially, the concentration of pathogen cells capable of killing *G. mellonella* larvae was determined. Larvae were bred in laboratory conditions according to Harding et al. (2013). *Listeria monocytogenes* ATCC19111, *Shigella flexneri* ATCC12022 and *P. aeruginosa* ATCC9027 were activated in BHI broth at 37 ºC, under agitation (100 rpm for 24 h). Cells were collected by centrifugation (5,000 rpm, for 5 min) and the pellet was rinsed twice in a sterile saline solution (NaCl 0.8%). The cell pellet was resuspended in saline, and optical density at 600nm OD was adjusted using a spectrophotometer. Five healthy larvae, weighing between 0.2-0.3 g, were chosen at random and subject to injections (in the left third pseudo-leg) with 10µL of the microbial cell suspension. Larvae were incubated at 37 ºC in the dark and evaluated daily for mortality and melanisation up to seven days (Megaw et al. 2015; Champion et al. 2018). Control treatments consisted of larvae injected or not with sterile saline solution and uninjected larvae. The pathogenicity of the seven selected strains (Table 1) was determined similarly to the procedure described previously.

The protective effect on *G. mellonella* larvae was evaluated by co-injection of selected strains and pathogenic bacteria. Cell suspensions were prepared as described above. Initially, a volume of 10 µL of cell suspensions of the selected species (Table 1) was injected into the third left pro-leg of ten *G. mellonella* larvae. Control treatments were set up with commercial probiotics. After keeping larvae at 37 ºC for 2 h, 10 µL of cell suspensions of the pathogens was injected into the third right pro-leg of larvae. Larvae were incubated at 37 ºC in the dark, and the rate of death and melanisation was monitored daily for 7 days. Survival analysis were performed by comparisons by treatment pairs (co-injection treatment vs. pathogen treatment) using the Log rank test (Mantel-Cox) in the GraphPad Prism 6.0 software.

Statistical analyses

Diversity of communities identified by cultivation dependent and independent methods was estimated and compared between the mid- and hindgut. Alpha diversity parameters (Richness, equitability, Shannon and Simpson index) were estimated using Fossil (Vavrek 2011) and Vegan (Oksanen 2017) packages in R (R Core Team 2020). Differences in beta diversity between microbial communities between mid- and hindgut were evaluated by composition (Jaccard index) and abundance (Bray-Curtis index) of the different taxa using transformed abundance data (ln + 1). Similarities were visualised via NMDS (Non-Metric Multidimensional Scaling Analysis).

Differences in community composition were visualised by Venn diagrams using the BioInformatics and Evolutionary Genomics online tool (http://bioinformatics.psb.ugent.be/webtools/Venn/). We used Mann-Whitney U tests to determine whether the gut chamber influences the relative abundance of cultivable and non-cultivable microorganisms. Metabolic functions of bacterial communities identified from the 16S rRNA

sequences were predicted by annotating OTU pathways against the KEGG database using PICRUST v. 1.1.4 (Phylogenetic Investigation of Communities by Reconstruction of Unobserved State) (Langille et al. 2013). Analyses were performed on the Microbiome Analyst platform (Chong et al. 2020). Data were filtered using the standard procedure and normalized by Cumulative sum scaling (CSS). Cluster analyses were performed using the Bray-Curtis distance matrix and Ward clustering algorithm. Differential abundance analysis of the KO descriptors was determined by the edgeR algorithm ($p < 0.05$). The differentially abundant descriptors between mid and hindgut of *P. luridipes* were mapped in the metabolic pathways using the website https://www.genome.jp/kegg/ko.html.

Results

Gut microbial community of *Pelidnota luridipes* analysed by culture-dependent method

The midgut and hindgut of *P. luridipes* larvae differ in their pH. Contents of the midgut were more alkaline (pH 10.44 ± 1.13) in relation to the material collected from the hindgut (pH 7.65 ± 0.15) (t= 4,209, p-value= 0.048). Counting with the initial plating tests, we obtained a total of 125 bacterial isolates, 147 actinobacteria and 29 yeasts, for a total of 302 isolates from eight larvae. We identified 64 species of cultivable microorganisms, 22 of which are actinobacterial, 35 bacterial and seven yeast species (Online Resource 2, Table S1). From this total, when considering only the second isolation with separation of mid and hindgut, we obtained 60 bacterial isolates, 59 actinobacteria and nine yeasts (Online Resource 2, Table S1).

There were no significant differences between the alpha diversity indices estimated for the microbial communities between the mid- and hindgut of *P. luridipes* (t test, $p < 0.05$) (Table 2). The NMDS analysis indicates a separation between the chambers in the composition (Jaccard Distance) and abundance (Bray-Curtis Distance) of bacteria and yeasts, with a more evident separation between the bacterial communities (Online Resource 1, Figs. S2 and S3).

Considering each species, there were no significant differences in relative abundance between mid- and hindgut by the Mann-Whitney U test ($p < 0.05$). Although we did not observe any statistically significant differences in alpha diversity, the data indicate a tendency for higher richness and diversity of yeasts in the midgut in relation to hindgut, and the opposite is observed in bacterial communities which tend to be more rich and diverse in the hindgut (Fig. 1).

Table 2. Abundance and alpha diversity measures of cultivable microbial community of mid- and hindgut of *Pelidnota luridipes*.

Group	Measure	Midgut	Hindgut	*p* value
Bacteria	Abundance (log UFC/mg)	4.23 ±2.35	2.98 ± 1.30	0.45
	Shannon	1.04 ± 0.33	1.46 ± 0.49	0.29
	Richness	14.33 ± 11.59	15.33 ± 2.52	0.90
	Eveness	0.59 ± 0.32	0.54 ±0.20	0.84
	Simpson	0.49 ± 0.06	0.69 ±0.14	0.84
Yeasts	Abundance (log UFC/mg)	2.98 ± 1.18	3.3 ± 1.3	0.58
	Shannon	0.69 ± 0.73	0.51 ± 0.45	0.72
	Richness	3.33 ± 1.53	2.67 ± 1.53	0.57
	Eveness	0.49 ± 0.46	0.62 ± 0.06	0.85
	Simpson	0.38 ± 0.37	0.34 ± 0.29	0.34
Total	Abundance (log UFC/mg)	7.22 ± 3.08	9 ± 0.96	0.47
	Shannon	0.8 ± 0.84	0.93 ± 0.93	0.47
	Richness	17.67 ± 12.5	18.00 ± 3.61	0.97
	Eveness	0.31 ± 0.27	0.31 ± 0.32	0.53
	Simpson	0.33 ± 0.3	0.44 ± 0.40	0.13

Of the six classes of bacteria identified, *Gammaproteobacteria* (68.90%) and *Bacilli* (24.01%) abundantly colonise the intestine of *P. luridipes* larvae (Online Resource 2, Table S2). The classes *Alphaproteobacteria* and *Flavobacteria* were exclusive to the midgut. We detected 28 genera (midgut: 21; hindgut: 16), with *Citrobacter* (midgut: 46.41%; hindgut: 77.15%), *Enterococcus* (midgut: 35.86%; hindgut: 5.54%), *Lactococcus* (midgut: 1.11%; hindgut: 7.31%) and *Sporosarcina* (midgut: 8.94%; hindgut: 0.30%) being the most abundant (Online Resource 2, Table S2).

We isolated 50 species of bacteria (midgut: 31; hindgut: 34), and the most abundant were *Citrobacter amalonaticus* (66.38%), *Enterococcus termitis* (10.47%), and *Lactococcus* sp. (5.41%) (Fig. 1). The most common species of the midgut were *Citrobacter amalonaticus* (46.41%), *Enterococcus termitis* (35.76%) and *Sporosarcina contaminans*. (8.94%); while *Citrobacter amalonaticus* (74.63%), *Lactococcus* sp. (7.31%) and *Enterococcus hirae*. (5.54%) were more abundant in the hindgut (Online Resource 1, Fig. 1 and Online Resource 2, Table S2).

Yeasts contributed to only 2.3% of the average abundance of cultivable microorganisms, and are represented by species of the orders *Saccharomycetales* (99.74% of CFUs/mg of yeasts) and *Trichosporonales* (0.26% of CFUs/mg of yeasts) (Fig. 1 and Online Resource 2, Table S3). *Spathaspora* (29.34% of yeast CFUs in the midgut and 58.31% in the hindgut) was the most abundant genus among the yeasts identified, followed by *Candida* (16.58% of the yeasts in the midgut against 30.49% of hindgut), *Scheffersomyces* (45.64% of the yeasts of midgut against 10.58% of hindgut) and *Meyerozyma* (exclusive of midgut, 8.29%) (Fig. 1 and Online Resource 2, Table S3). *Apiotrichum* (0.15% of yeasts of midgut versus 0.31% of hindgut) was the least abundant

genus in the counts. Only *Candida* was represented by three species, with all other genera represented by one species each (Fig. 1 and Online Resource 2, Table S3).

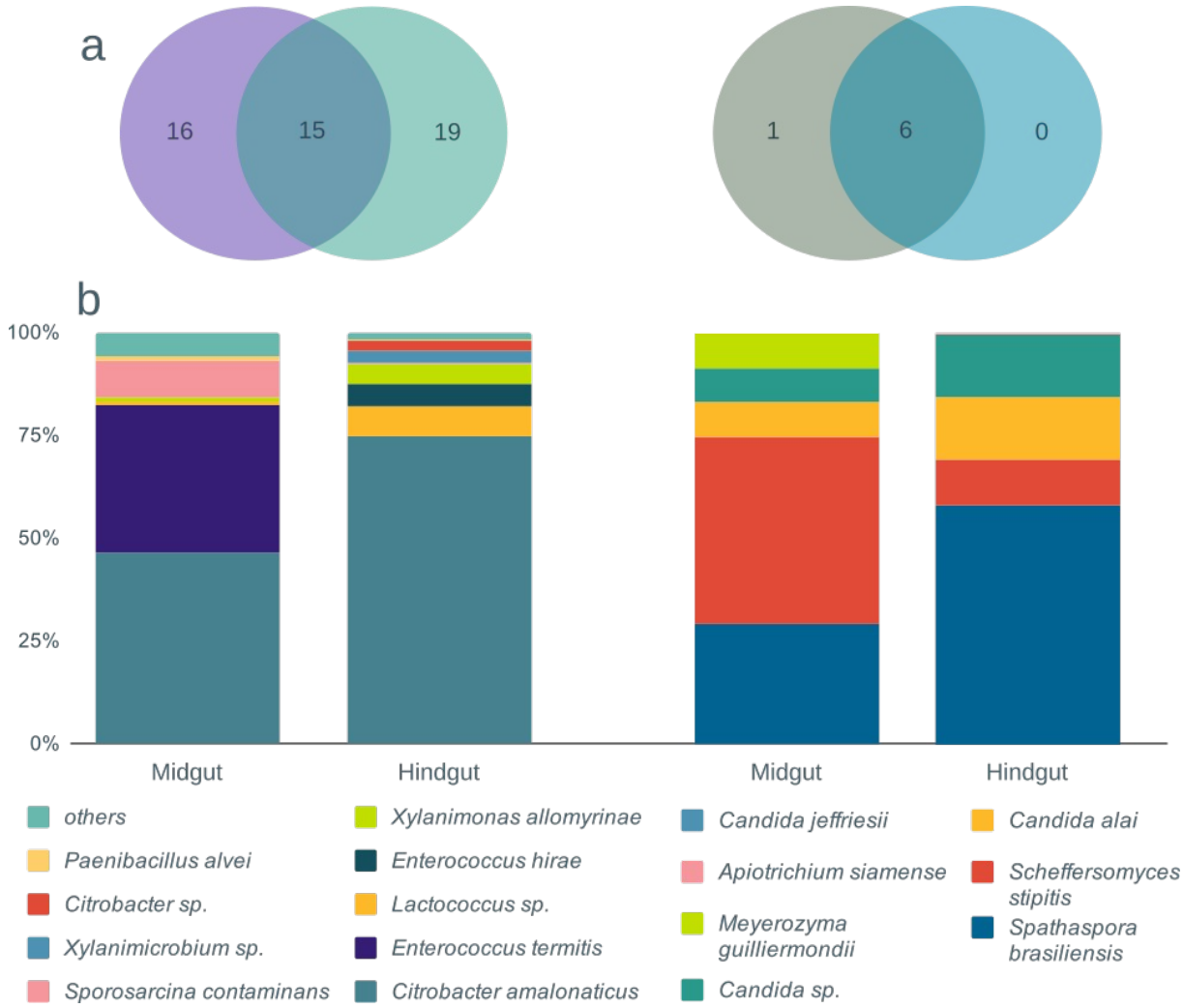


Fig. 1 Richness (a) and relative abundance (b) of cultivable bacterial (left) and yeast (right) species in the mid- and hindgut of *Pelidnota luridipes*

Analysis of the non-cultivable microbial community of mid and hindgut of *P. luridipes*

After the quality and size filtering procedures, the 1,009,086 total reads were distributed in 345,316 bacterial and 788,973 fungal reads (Table 3).

Table 3. Total number of sequences from gut chambers of *Pelidnota luridipes* according to the parameters of the different sequencing phases.

Group	Sample*	R1	R2	Merged	Trimmed	Filtered	Mapped	OTUs
Bacteria	P6A	113,911	113,911	80,998	80,822	75,838	64,608	1,023
	P7A	106,886	106,886	72,496	72,371	67,014	54,365	271
	P8A	125,811	125,811	90,462	90,009	85,127	51,413	1,154
	P6R	128,594	128,594	94,009	93,530	88,876	53,716	1,005
	P7R	147,871	147,871	108,905	108,099	102,601	58,607	1,120
	P8R	169,305	169,305	124,272	123,165	116,906	62,607	1,235
Fungi	P6A	146,351	146,351	131,195	131,055	130,115	127,024	130
	P7A	142,304	142,304	125,214	125,100	124,229	121,233	122
	P8A	135,853	135,853	121,200	121,164	120,313	118,516	171
	P6R	150,142	150,142	134,599	134,553	133,717	128,748	86
	P7R	141,815	141,815	126,601	126,356	125,439	123,000	106
	P8R	195,376	195,376	174,322	174,185	173,019	170,452	141

*Samples refer to animal codes (P6, P7, P8) combined with chamber source (A: midgut, R: hindgut).

The main difference between the two compartments is shown in diversity (Shannon index) of phyla, genera and bacterial OTUs. Hindgut showed higher values in relation to midgut (test t, $p < 0.01$) (Table 4). In addition, hindgut showed higher evenness of bacterial phyla (test t, $p < 0.05$) (Table 4). We found no differences in the parameters of alpha diversity in the fungal community (order, family and OTU) (test t, $p < 0.05$) (Table 4). Bacterial community tends to have higher richness in the hindgut, while the fungal community tends to be more rich in the midgut (Table 4, Figs. 2 and 4), similarly to what we observed with cultivation dependent methods.

Table 4. Diversity of uncultivable microorganisms for the two gut chambers of *Pelidnota luridipes*.

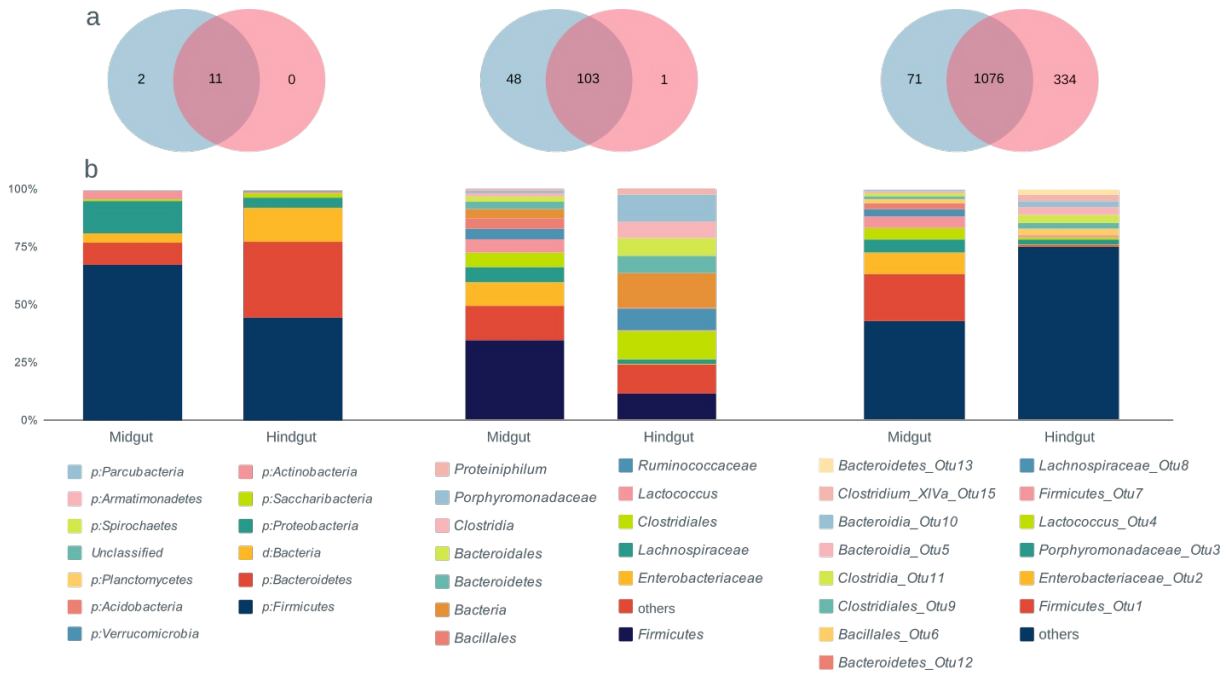
Bacteria	Phylla			Genera			OTUs		
	Midgut	Hindgut	*p*	Midgut	Hindgut	*p*	Anterior	Hindgut	*p*
Richness	7.33 ± 2.08	6.67 ± 0.58	0.64	106.33 ± 35.23	75.00 ± 14.73	0.26	662.00 ± 427.17	991.00 ± 116.05	0.31
Shannon	0.69 ± 0.06	0.93 ± 0.05	**0.01**	2.03 ± 0.04	2.61 ± 0.03	**0.0001335**	2.63 ± 0.54	4.96 ± 0.10	**0.01**
Chao1	7.33 ± 2.08	6.67 ± 0.58	0.64	116.58 ± 30.03	107.21 ± 31.19	0.73	842.47 ± 403.15	1091.96 ± 98.03	0.40
Eveness	0.37 ± 0.03	0.50 ± 0.01	**0.02**	0.51 ±0.09	0.62 ± 0.01	0.15	0.54 ± 0.13	0.74 ± 0.04	0.11
Fungi	Orders			Families			OTUs		
	Midgut	Hindgut	*p*	Midgut	Hindgut	*p*	Midgut	Hindgut	*p*
Richness	38.67 ± 3.79	31.67 ± 3.21	0.07	43.67 ±9.71	50.33 ± 8.39	0.42	137.00 ± 26.15	105.67 ± 25.11	0.21
Shannon	1.48 ± 0.04	1.25 ± 0.51	0.51	1.28 ±0.54	1.54 ± 0.01	0.48	2.60 ± 0.08	2.07 ± 0.67	0.31
Chao1	39.00 ± 3.61	32.6 ± 4.16	0.12	45.08 ±9.66	57.83 ± 0.14	0.14	186.61 ± 94.01	117.34 ± 25.95	0.14
Eveness	0.45 ± 0.05	0.39 ± 0.17	0.63	0.33 ± 0.13	0.46 ± 0.05	0.22	0.55 ± 0.02	0.47 ± 0.15	0.48

* Values are mean and standard deviation of the indices. Values were compared by an unpaired t test.

The two compartments share 11 bacterial phyla, *Parcubacteria* and *Armatimonadetes* are midgut exclusive (Fig. 2). Approximately 4.1% and 14.9% of the reads from the mid and hindguts, respectively, could not be classified at the phylum level. Only the abundances of the *Firmicutes* and *Bacteroidetes* reads were statistically different between the compartments (t test, $p < 0.05$). The most abundant phyla in both chambers are *Firmicutes* (67.75% of the reads from the midgut against 44.95% reads from the hindgut), *Bacteroidetes* (9.51% - midgut against 32.71% - hindgut), and *Proteobacteria* (14.31% - midgut against 4.53 % - hindgut) (Fig. 2). An unidentified phylum of the *Bacteria* Domain had 4.06% of the reads from midgut and 14.98% of the reads from hindgut. Midgut had 48 exclusive genera (Fig. 2), and only one taxon (*Clostridiaceae*1) was foregut-exclusive, with an abundance of about 0.036%.

We obtained 1,481 bacterial OTUs with different abundances between the two chambers of *P. luridipes'* gut, and 1,076 of the OTUs are shared between both (Fig. 2; Online Resource 2, Table S4). Exclusive OTUs are enriched in the hindgut (Fig. 2). Considering the total OTUs, some stand out for their relative abundance, such as *Firmicutes*_OTU1 representing 10.47% of total reads (20.3% in the midgut and 0.65% in the hindgut), *Enterobacteriaceae*_OTU2 with 4.79% (9.4% in the midgut, 0.2 % in the hindgut), *Porphyromonadaceae*_OTU3 (3.94% of total; 5.7% in the midgut, 2.17% in the midgut) and *Lactococcus*_OTU4 (3.01% of total; 5.03% in the midgut, 1% in the hindgut) (Fig. 2, and Online Resource 2, Table S4).

About 118 OTUs showed relative frequency (RF) equal to or higher than 0.1% of the total reads, represented by *Actinobacteria* (3 OTUs), *Bacteroidetes* (83 OTUs), *Candidatus_Saccharibacteria* (2 OTUs), *Firmicutes* (64 OTUs), *Proteobacteria* (9 OTUs), *Verrucomicrobia* (1 OTUs), and without specific phylum (14 OTUs) (Online Resource 2, Table S4). We identified 19 families (55 OTUs) and 13 genera (17 OTUs) among the selected OTUs (FR> 0.1) (Table 5). Among OTUs with abundance higher than 0.1%, we observed 15 OTUs absent in the midgut and only three not detected in the hindgut (*Bacteroidetes*_OTU12, *Providencia*_OTU34 and *Paenibacillus*_OTU78) (Table 5). The most abundant OTUs in the midgut were *Firmicutes*_OTU1, *Enterobacteriaceae*_OTU2, *Porphyromonadaceae*_OTU3, *Lactococcus*_OTU4 and *Firmicutes*_OTU7; while *Bacteroidia*_OTU5, *Clostridia*_OTU11, *Bacillales*_OTU6, *Clostridium*_XlVa_OTU15 and *Clostridiales*_OTU9 were the most abundant in the hindgut.



397 **Fig. 2** Richness (a) and relative abundance (b) of phyla, genera and OTUs of bacteria detected by
398 metabarcoding in the gut chambers of *Pelidnota luridipes*

Table 5. Bacterial OTUs with a relative frequency higher than 0.1% present in the gut chambers of *Pelidnota luridipes* with relative abundance higher than 0.1%.

	Relative abundance				Classification					
#OTU	Total	MG	HG	MG/HG	Domain	Phyllum	Class	Order	Family	Genus
Otu132	0.13	0.04	0.22	0.2	*Bacteria*	*Proteobacteria*	*Gammaproteobacteria*	*Pseudomonadales*	*Moraxellaceae*	*Acinetobacter*
Otu79	0.15	0.29	0.02	18.29	*Bacteria*	*Firmicutes*	*Bacilli*	*Bacillales*	*Bacillaceae_1*	*Bacillus*
Otu92	0.12	0.22	0.02	9.6	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Peptostreptococcaceae*	*Clostridium_XI*
Otu15	1.53	0	3.05	0	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Lachnospiraceae*	*Clostridium_XlVa*
Otu54	0.27	0.3	0.25	1.19	*Bacteria*	*Proteobacteria*	*Deltaproteobacteria*	*Desulfovibrionales*	*Desulfovibrionaceae*	*Desulfovibrio*
Otu106	0.12	0.07	0.16	0.47	*Bacteria*	*Proteobacteria*	*Deltaproteobacteria*	*Desulfovibrionales*	*Desulfovibrionaceae*	*Desulfovibrio*
Otu22	0.75	0.84	0.67	1.25	*Bacteria*	*Bacteroidetes*	*Bacteroidia*	*Bacteroidales*	*Porphyromonadaceae*	*Dysgonomonas*
Otu66	0.2	0.3	0.11	2.79	*Bacteria*	*Bacteroidetes*	*Bacteroidia*	*Bacteroidales*	*Porphyromonadaceae*	*Dysgonomonas*
Otu61	0.19	0.27	0.1	2.58	*Bacteria*	*Bacteroidetes*	*Bacteroidia*	*Bacteroidales*	*Porphyromonadaceae*	*Dysgonomonas*
Otu32	0.9	0.8	1.01	0.8	*Bacteria*	*Firmicutes*	*Bacilli*	*Lactobacillales*	*Enterococcaceae*	*Enterococcus*
Otu37	0.48	0.26	0.7	0.37	*Bacteria*	*Actinobacteria*	*Actinobacteria*	*Actinomycetales*	*Microbacteriaceae*	*Gryllotalpicola*
Otu4	3.02	5.03	1.01	4.99	*Bacteria*	*Firmicutes*	*Bacilli*	*Lactobacillales*	*Streptococcaceae*	*Lactococcus*
Otu130	0.12	0.21	0.02	9.89	*Bacteria*	*Firmicutes*	*Bacilli*	*Bacillales*	*Planococcaceae*	*Lysinibacillus*
Otu78	0.26	0.51	0	-	*Bacteria*	*Firmicutes*	*Bacilli*	*Bacillales*	*Paenibacillaceae_1*	*Paenibacillus*
Otu14	1.38	1.4	1.37	1.02	*Bacteria*	*Bacteroidetes*	*Bacteroidia*	*Bacteroidales*	*Porphyromonadaceae*	*Proteiniphilum*
Otu30	0.46	0.46	0.47	0.98	*Bacteria*	*Bacteroidetes*	*Bacteroidia*	*Bacteroidales*	*Porphyromonadaceae*	*Proteiniphilum*
Otu34	0.53	1.07	0	-	*Bacteria*	*Proteobacteria*	*Gammaproteobacteria*	*Enterobacteriales*	*Enterobacteriaceae*	*Providencia*
Otu1	10.47	20.28	0.65	31.01	*Bacteria*	*Firmicutes*	U	U	U	U
Otu2	4.79	9.38	0.2	47.44	*Bacteria*	*Proteobacteria*	*Gammaproteobacteria*	*Enterobacteriales*	*Enterobacteriaceae*	U
Otu3	3.95	5.73	2.17	2.64	*Bacteria*	*Bacteroidetes*	*Bacteroidia*U	*Bacteroidales*	*Porphyromonadaceae*	U
Otu7	2.83	4.95	0.72	6.87	*Bacteria*	*Firmicutes*	U	U	U	U
Otu6	2.43	1.75	3.11	0.56	*Bacteria*	*Firmicutes*	*Bacilli*	*Bacillales*	NI	U
Otu5	2.26	1.06	3.46	0.31	*Bacteria*	*Bacteroidetes*	*Bacteroidia*	U	U	U
Otu11	2.18	1.15	3.2	0.36	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu9	1.92	1.34	2.51	0.53	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu10	1.63	0.76	2.5	0.3	*Bacteria*	*Bacteroidetes*	*Bacteroidia*	U	U	U
Otu8	1.6	3.19	0.01	315.11	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Lachnospiraceae*	U
Otu12	1.33	2.66	0	-	*Bacteria*	*Bacteroidetes*	U	U	U	U
Otu13	1.12	0	2.24	0	*Bacteria*	*Bacteroidetes*	U	U	U	U
Otu18	1.07	1.66	0.49	3.41	*Bacteria*	*Firmicutes*	U	U	U	U
Otu23	1.05	0.93	1.17	0.79	*Bacteria*	*Bacteroidetes*	*Bacteroidia*	*Bacteroidales*	*Porphyromonadaceae*	U

Otu19	0.97	0.49	1.45	0.34	*Bacteria*	*Bacteroidetes*	U	U	U	U
Otu16	0.93	1.13	0.72	1.56	*Bacteria*	U	U	U	U	U
Otu24	0.88	0.21	1.55	0.14	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu17	0.88	1.36	0.39	3.45	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu26	0.85	0	1.7	0	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu21	0.81	1.49	0.13	11.41	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Lachnospiraceae*	U
Otu28	0.81	0	1.62	0	*Bacteria*	*Firmicutes*	U	U	U	U
Otu20	0.79	0	1.59	0	*Bacteria*	*Bacteroidetes*	U	U	U	U
Otu45	0.74	0.83	0.64	1.3	*Bacteria*	U	U	U	U	U
Otu29	0.68	0	1.36	0	*Bacteria*	*Firmicutes*	U	U	U	U
Otu42	0.66	0.48	0.84	0.56	*Bacteria*	*Actinobacteria*	*Actinobacteria*	*Actinomycetales*	*Promicromonosporaceae*	U
Otu25	0.61	0.86	0.37	2.36	*Bacteria*	U	U	U	U	U
Otu48	0.61	0.43	0.79	0.55	*Bacteria*	*Bacteroidetes*	*Bacteroidia*	*Bacteroidales*	*Porphyromonadaceae*	U
Otu27	0.57	0.6	0.54	1.11	*Bacteria*	*Bacteroidetes*	*Bacteroidia*	*Bacteroidales*	*Bacteroidaceae*	U
Otu33	0.5	0.21	0.79	0.26	*Bacteria*	*Proteobacteria*	*Deltaproteobacteria*	*Desulfovibrionales*	U	U
Otu36	0.49	0	0.99	0	*Bacteria*	*Bacteroidetes*	*Bacteroidia*	*Bacteroidales*	*Porphyromonadaceae*	U
Otu31	0.49	0.43	0.56	0.77	*Bacteria*	*Bacteroidetes*	*Bacteroidia*	*Bacteroidales*	U	U
Otu41	0.46	0.8	0.13	6.36	*Bacteria*	*Candidatus_Saccharibacteria*	U	U	U	U
Otu49	0.44	0.59	0.28	2.06	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu38	0.43	0.04	0.83	0.05	*Bacteria*	*Bacteroidetes*	*Bacteroidia*	*Bacteroidales*	*Bacteroidaceae*	U
Otu35	0.43	0.21	0.65	0.32	*Bacteria*	*Firmicutes*	U	U	U	U
Otu40	0.42	0.01	0.84	0.01	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu46	0.42	0.25	0.6	0.41	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu43	0.38	0	0.77	0	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu47	0.38	0.32	0.44	0.72	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu39	0.37	0.35	0.38	0.91	*Bacteria*	*Candidatus_Saccharibacteria*	*Saccharibacteria_genera_incertae_sedis*	U	U	U
Otu80	0.33	0.19	0.47	0.41	*Bacteria*	*Firmicutes*	U	U	U	U
Otu50	0.33	0.5	0.16	3.19	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu44	0.32	0.14	0.5	0.28	*Bacteria*	*Bacteroidetes*	*Bacteroidia*	*Bacteroidales*	*Porphyromonadaceae*	U
Otu81	0.32	0.13	0.51	0.25	*Bacteria*	*Bacteroidetes*	U	U	U	U
Otu82	0.31	0	0.62	0	*Bacteria*	*Proteobacteria*	*Gammaproteobacteria*	*Enterobacteriales*	*Enterobacteriaceae*	U
Otu55	0.3	0	0.6	0	*Bacteria*	*Firmicutes*	U	U	U	U

Otu86	0.3	0.2	0.41	0.48	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu52	0.3	0.04	0.57	0.07	*Bacteria*	*Firmicutes*	U	U	U	U
Otu51	0.3	0.27	0.32	0.84	*Bacteria*	*Bacteroidetes*	*Bacteroidia*	*Bacteroidales*	*Bacteroidaceae*	U
Otu59	0.28	0.06	0.49	0.13	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu57	0.27	0.08	0.47	0.16	*Bacteria*	*Firmicutes*	U	U	U	U
Otu72	0.25	0	0.5	0	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu75	0.25	0.11	0.39	0.27	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu53	0.25	0	0.49	0	*Bacteria*	*Proteobacteria*	*Epsilonproteobacteria*	*Campylobacterales*	*Campylobacteraceae*	U
Otu56	0.25	0.22	0.27	0.81	*Bacteria*	U	U	U	U	U
Otu90	0.25	0.27	0.22	1.19	*Bacteria*	U	U	U	U	U
Otu71	0.24	0.21	0.27	0.78	*Bacteria*	U	U	U	U	U
Otu58	0.24	0.19	0.29	0.66	*Bacteria*	*Bacteroidetes*	*Bacteroidia*	*Bacteroidales*	*Rikenellaceae*	U
Otu62	0.23	0.06	0.4	0.15	*Bacteria*	*Bacteroidetes*	U	U	U	U
Otu60	0.23	0.05	0.4	0.13	*Bacteria*	U	U	U	U	U
Otu879	0.23	0	0.45	0	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Lachnospiraceae*	U
Otu63	0.21	0.21	0.21	1	*Bacteria*	*Verrucomicrobia*	*Opitutae*	*Opitutales*	U	U
Otu119	0.21	0.17	0.25	0.68	*Bacteria*	*Firmicutes*	U	U	U	U
Otu70	0.2	0.02	0.39	0.04	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu67	0.2	0.2	0.2	0.99	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu73	0.19	0.24	0.14	1.68	*Bacteria*	U	U	U	U	U
Otu76	0.19	0	0.37	0.01	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu85	0.18	0.1	0.27	0.37	*Bacteria*	*Firmicutes*	U	U	U	U
Otu65	0.18	0.12	0.24	0.51	*Bacteria*	U	U	U	U	U
Otu112	0.18	0	0.36	0	*Bacteria*	*Firmicutes*	U	U	U	U
Otu64	0.17	0	0.35	0	*Bacteria*	*Bacteroidetes*	U	U	U	U
Otu77	0.17	0.14	0.2	0.71	*Bacteria*	*Firmicutes*	*Negativicutes*	*Selenomonadales*	*Veillonellaceae*	U
Otu74	0.17	0.13	0.2	0.65	*Bacteria*	*Bacteroidetes*	U	U	U	U
Otu68	0.16	0.01	0.32	0.02	*Bacteria*	*Firmicutes*	U	U	U	U
Otu133	0.16	0.07	0.25	0.29	*Bacteria*	*Firmicutes*	*Negativicutes*	U	U	U
Otu83	0.16	0.12	0.2	0.61	*Bacteria*	U	U	U	U	U
Otu120	0.16	0.13	0.18	0.7	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Syntrophomonadaceae*	U
Otu89	0.16	0	0.31	0	*Bacteria*	U	U	U	U	U
Otu165	0.15	0.06	0.24	0.25	*Bacteria*	U	U	U	U	U
Otu69	0.14	0.25	0.03	8.33	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu91	0.14	0.03	0.25	0.12	*Bacteria*	*Firmicutes*	U	U	U	U

Otu94	0.14	0.03	0.25	0.14	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu123	0.13	0.05	0.21	0.22	*Bacteria*	*Actinobacteria*	*Actinobacteria*	*Actinomycetales*	U	U
Otu141	0.13	0.05	0.21	0.22	*Bacteria*	*Proteobacteria*	*Deltaproteobacteria*	*Desulfovibrionales*	U	U
Otu95	0.13	0.08	0.17	0.49	*Bacteria*	*Firmicutes*	U	U	U	U
Otu84	0.13	0.23	0.02	13.06	*Bacteria*	*Firmicutes*	*Negativicutes*	*Selenomonadales*	*Veillonellaceae*	U
Otu93	0.13	0	0.25	0	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu88	0.12	0.15	0.1	1.44	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu97	0.12	0.06	0.19	0.32	*Bacteria*	U	U	U	U	U
Otu101	0.12	0.07	0.17	0.42	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu98	0.12	0	0.23	0	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu145	0.12	0.13	0.1	1.28	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu87	0.12	0	0.23	0.01	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu195	0.11	0.17	0.05	3.28	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu246	0.11	0.13	0.09	1.42	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu99	0.11	0.01	0.21	0.03	*Bacteria*	*Firmicutes*	U	U	U	U
Otu108	0.11	0.16	0.06	2.82	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu96	0.11	0.16	0.05	3.4	*Bacteria*	*Firmicutes*	U	U	U	U
Otu103	0.1	0.05	0.15	0.31	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu122	0.1	0.08	0.12	0.71	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu117	0.1	0.13	0.07	1.92	*Bacteria*	U	U	U	U	U

Total: OTU's relative abundance in relation to the total bacterial OTUs. MG and HG: OTU's relative abundance in the midgut and hindgut respectively. MG/HG: Relative abundance of OTU in the midgut divided by relative abundance of OTU in the hindgut. U: unidentified taxon

Of the 267 OTUs of fungi, 244 OTUs were identified as *Ascomycota*, *Basidiomycota*, *Mortierellomycota* and *Mucoromycota*, and identification of the phylum of 23 other OTUs was not possible (Online Resource 2, Table S5). Taxonomic attribution allowed identification of 87 genera of fungi in the gut of *P. luridipes* (Online Resource 2, Table S5).

Most orders, families and fungal OTUs are shared between the mid- and hindgut, with a decrease in the number of exclusive taxa from the mid- to the hindgut (Fig. 3, and Online Resource 2, Table S5). *P. luridipes* gut chambers are colonised by yeasts of the order *Saccharomycetales* (57% of the reads in the midgut and 65% of the reads in the hindgut), and by *Trichosporonales* (4% in the previous, 9% in the later), and the same pattern was observed for the *Debaryomycetaceae* (71.8% in the midgut, 51% in the hindgut) and *Trichosporonaceae* (2.8% in the midgut, 10.2% in the hindgut) families.

Midgut had a higher number of fungal OTUs, with 90 of these OTUs being exclusive (Fig. 3, Online Resource 2, Table S5). OTUs *Candida*_OTU1 (24.63% in the midgut, 32.80% in the hindgut) and *Spathaspora*_OTU2 (25.97% in the midgut, 24.53% in the hindgut) represent over 50% of all reads detected in the intestine of *P. luridipes* (Fig. 4, and Online Resource 2, Table S8). Other OTUs stand out as *Apiotrichum*_OTU4 (3.9% in the midgut, 9.03% in the hindgut) and *Scheffersomyces*_OTU3 (5.1% in the midgut, 5.8% in the hindgut) (Online Resource 2, Table S5).

Fifty-two OTUs stand out for their relative abundance, higher than 0.1% ,and are distributed in the *Ascomycota* (44 OTUs), *Basidiomycota* (5 OTUs), *Mucoromycota* (1 OTU- *Umbelopsis*_OTU48) and two OTUs of unidentified phyla (*Fungi*_OTU16 and *Fungi*_OTU43) . Among these OTUs there are eight classes: *Sordariomycetes* (14 OTUs), *Agaricomycetes* (3), *Leotiomycetes* (6), *Dothideomycetes* (2), *Eurotiomycetes* (7), *Saccharomycetes* (6), *Umbelopsidomycetes* (1), and *Tremellomycetes* (1), in addition to another 12 OTUs whose classes have not been identified (Table 6). The *Basidiomycota*_OTU28, *Ascomycota*_OTU29 and *Nais*_OTU30 taxa are exclusive to the midgut (Table 6).

Some OTUs were more abundant in the midgut than in the hindgut: *Hyphoderma*_OTU23 (20.6 times more abundant in the midgut), *Sordariomycetes*_OTU18 (10.6x), *Leotiomycetes*_OTU45 (9.5x) and other 16 OTUs with minor differences. Among OTUs more abundant in the hindgut, were *Ascomycetes*_OTU19 (23.5 times more abundant in hindgut) and *Ascomycetes*_OTU37 (7.5x).

Microbial communities of bacteria and fungi identified by culture independent methods are also visually very different in composition (Jaccard index) and abundance (Bray-Curtis index) in the ordering by NMDS (Online Resource 1, Fig. S2).

Fig. 3 Richness (a) and relative abundance (b) of order, family and OTUs of fungi detected by metabarcoding in the gut chambers of *Pelidnota luridipes*

435 **Table 6.** Fungal OTUs with relative abundance higher than 0.1% in the gut chambers of *Pelidnota luridipes.*

	Relative abundance				Classification					
#OTU ID	Total	MG	HG	MG/HG	Kingdom	Phyllum	Class	Order	Family	Genus
OTU1	28.72	24.63	32.8	0.75	*Fungi*	*Ascomycota*	*Saccharomycetes*	*Saccharomycetales*	*Debaryomycetaceae*	*Candida*
OTU10	1.16	0.3	2.03	0.15	*Fungi*	*Ascomycota*	U	U	U	U
OTU11	0.89	0.45	1.33	0.33	*Fungi*	*Ascomycota*	*Dothideomycetes*	U	U	U
OTU12	1.19	2.1	0.28	7.64	*Fungi*	*Ascomycota*	*Dothideomycetes*	*Aulographales*	*Rhizodiscinaceae*	*Rhizodiscina*
OTU13	1	0.32	1.68	0.19	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Xenospadicoidales*	*Xenospadicoidaceae*	*Spadicoides*
OTU132	1.04	0.89	1.2	0.74	*Fungi*	*Ascomycota*	*Saccharomycetes*	*Saccharomycetales*	*Debaryomycetaceae*	*Spathaspora*
OTU14	0.92	0.71	1.12	0.64	*Fungi*	*Ascomycota*	*Eurotiomycetes*	*Eurotiales*	*Thermoascaceae*	*Byssochlamys*
OTU140	0.16	0.15	0.17	0.85	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Hypocreales*	*Hypocreaceae*	*Trichoderma*
OTU15	0.92	1.02	0.82	1.25	*Fungi*	*Ascomycota*	*Sordariomycetes,*	*Hypocreales*	*Hypocreaceae*	U
OTU16	1.47	1.13	1.8	0.63	*Fungi*	*Fungi_OTU16*	U	U	U	U
OTU17	0.77	1.13	0.42	2.73	*Fungi*	*Ascomycota*	*Sordariomycetes*	U	U	U
OTU172	0.49	0.42	0.57	0.74	*Fungi*	*Ascomycota*	*Saccharomycetes*	*Saccharomycetales*	*Debaryomycetaceae*	*Candida*
OTU18	0.88	1.6	0.15	10.56	*Fungi*	*Ascomycota*	*Sordariomycetes*	U	U	U
OTU185	0.17	0.21	0.12	1.77	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Hypocreales*	*Hypocreaceae*	*Trichoderma*
OTU19	0.44	0.04	0.85	0.04	*Fungi*	*Ascomycota*	U	U	U	U
OTU198	0.11	0.08	0.13	0.61	*Fungi*	*Ascomycota*	*Eurotiomycetes*	*Chaetothyriales*	*Herpotrichiellaceae*	*Exophiala*
OTU2	25.25	25.97	24.54	1.06	*Fungi*	*Ascomycota*	*Saccharomycetes*	*Saccharomycetales*	*Debaryomycetaceae*	*Spathaspora*
OTU20	0.54	0.3	0.78	0.38	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Coniochaetales*	U	U
OTU21	0.52	0.64	0.4	1.61	*Fungi*	*Ascomycota*	U	U	U	U

OTU22	0.42	0.39	0.44	0.87	*Fungi*	*Ascomycota*	*Leotiomycetes*	*Helotiales*	U	U
OTU23	0.39	0.75	0.04	20.64	*Fungi*	*Basiodiomycota*	*Agaricomycetes*	*Polyporales*	*Hyphodermataceae*	*Hyphoderma*
OTU24	0.35	0.16	0.54	0.3	*Fungi*	*Ascomycota*	*Eurotiomycetes*	*Eurotiales*	*Aspergillaceae*	*Aspergillus*
OTU248	0.45	0.45	0.45	1.01	*Fungi*	*Ascomycota*	*Saccharomycetes*	*Saccharomycetales*	*Debaryomycetaceae*	*Scheffersomyces*
OTU25	0.31	0.27	0.35	0.77	*Fungi*	*Ascomycota*	*Eurotiomycetes*	*Eurotiales*	*Aspergillaceae*	*Aspergillus*
OTU26	0.29	0.48	0.1	4.65	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Xylariales*	*Hypoxylaceae*	*Hypoxylon*
OTU27	0.38	0.58	0.19	2.98	*Fungi*	*Ascomycota*	*Sordariomycetes*	U	U	U
OTU28	0.3	0.61	0	-	*Fungi*	*Basiodiomycota*	U	U	U	U
OTU29	0.23	0.45	0	-	*Fungi*	*Ascomycota*	U	U	U	U
OTU3	5.46	5.11	5.82	0.88	*Fungi*	*Ascomycota*	*Saccharomycetes*	*Saccharomycetales*	*Debaryomycetaceae*	*Scheffersomyces*
OTU30	0.21	0.43	0	-	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Microascales*	*Halosphaeriaceae*	*Nais*
OTU31	0.19	0.27	0.11	2.38	*Fungi*	*Ascomycota*	*Sordariomycetes*	U	U	U
OTU32	0.19	0.34	0.04	8.54	*Fungi*	*Basiodiomycota*	*Agaricomycetes*	*Hymenochaetales*	*Rickenellaceae*	*Sidera*
OTU33	0.2	0.27	0.13	2.12	*Fungi*	*Ascomycota*	*Eurotiomycetes*	*Eurotiales*	*Aspergillaceae*	*Aspergillus*
OTU34	0.19	0.17	0.22	0.75	*Fungi*	*Ascomycota*	*Leotiomycetes*	*Erysiphales*	*Erysiphaceae*	*Leveillula*
OTU35	0.15	0.14	0.16	0.87	*Fungi*	*Ascomycota*	*Eurotiomycetes*	*Chaetothyriales*	*Herpotrichiellaceae*	*Exophiala*
OTU36	0.17	0.24	0.09	2.55	*Fungi*	*Ascomycota*	U	U	U	U
OTU37	0.25	0.06	0.45	0.13	*Fungi*	*Ascomycota*	U	U	U	U
OTU38	0.3	0.14	0.45	0.31	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Microascales*	*Microascaceae*	*Microascus*
OTU39	0.15	0.25	0.04	5.7	*Fungi*	*Ascomycota*	*Leotiomycetes*	*Erysiphales*	U	U
OTU4	6.52	4	9.04	0.44	*Fungi*	*Basiodiomycota*	*Tremellomycetes*	*Trichosporonales*	*Trichosporonaceae*	*Apiotrichum*
OTU40	0.14	0.15	0.12	1.31	*Fungi*	*Ascomycota*	*Eurotiomycetes*	*Chaetothyriales*	*Herpotrichiellaceae*	*Fonsecaea*

OTU41	0.12	0.12	0.12	1.02	*Fungi*	*Ascomycota*	*Sordariomycetes*	U	U	U
OTU42	0.15	0.25	0.04	6.52	*Fungi*	*Ascomycota*	*Leotiomycetes*	*Helotiales*	U	U
OTU43	0.12	0.16	0.07	2.13	*Fungi*	*Fungi_OTU43*	U	U	U	U
OTU44	0.11	0.16	0.06	2.61	*Fungi*	*Ascomycota*	U	U	U	U
OTU45	0.11	0.21	0.02	9.46	*Fungi*	*Ascomycota*	*Leotiomycetes*	U	U	U
OTU48	0.11	0.1	0.12	0.82	*Fungi*	*Mucoromycota*	*Umbelopsidomycetes*	*Umbelopsidales*	*Umbelopsidaceae*	*Umbelopsis*
OTU5	2.57	2.68	2.45	1.1	*Fungi*	*Ascomycota*	*Leotiomycetes*	*Erysiphales*	*Erysiphaceae*	*Leveillula*
OTU6	3.67	5.01	2.34	2.14	*Fungi*	*Ascomycota*	U	U	U	U
OTU7	3.24	4.85	1.63	2.97	*Fungi*	*Basiodiomycota*	*Agaricomycetes*	*Corticiales*	*Corticiaceae*	*Subulicystidium*
OTU8	1.81	3.17	0.45	7	*Fungi*	*Ascomycota*	*Sordariomycetes*	U	U	U
OTU9	1.58	2.63	0.53	4.96	*Fungi*	*Ascomycota*	U	U	U	U

Total: OTU's relative abundance in relation to total fungal OTUs. MG and HG: OTU's relative abundance in the mid and hindgut, respectively. MG/HG: Relative abundance of the OTU in the midgut divided by the relative abundance of OTU in the hindgut. U: Unidentified taxon.

Functional profile of microbial community on gut chambers

The KEGG Orthology (KO) descriptors identified 12 metabolic pathways that are important in the bacterial gut microbiome of *P. luridipes*. Pathways Biosynthesis of amino acids, Porphyrin and chlorophyll metabolism, 2- oxocarboxylic acid metabolism and lipopolysaccharide biosynthesis were highly significative (p FDR <0.0001) (Online Resource 2, Table S6).

We obtained 2575 KO (KEGG Orthology) descriptors differentially abundant between the two gut chambers (Online Resource 2, Table S9) ($p < 0.05$), with 47% and 53% of these descriptors being more abundant in the mid- and hindgut, respectively (Online Resource 2, Table S9). Mid- and hindgut also have distinct functional profiles shown by the separation into two groups in the cluster analysis using the KO identifiers (Online Resource 1, Fig. S3). Functions attributed to the selected KOs (15 highest and lowest values of log2FC) relate to different functions and metabolic pathways according to the analysed gut chamber (Online Resource 2, Table S7). Midgut presents KO identifiers involved with the secretion system, chemotaxis and metabolism of glutathione and purines; while in the hindgut we observed a differential abundance of KOs involved with amino acid metabolism and O antigen biosynthesis.

The KEGG pathway map revealed the distribution of the 2,575 descriptors in 242 paths mapped, with 160 and 211 routes being specifically distributed in the mid- and hindgut, respectively (Online Resource 2, Table S10). The higher diversity of routes mapped in the hindgut indicated that in 68 of the routes the number of KO descriptors is at least twice as high as the number of the midgut (Online Resource 2, Table S10).

The midgut did not present KO descriptors for metabolic pathways such as Ribosome, Amino sugar and nucleotide sugar metabolism, Aminoacyl-tRNA biosynthesis, Cell cycle - *Caulobacter*, Streptomycin biosynthesis, Nitrotoluene degradation, Base excision repair, Other glycan degradation, Biosynthesis of various secondary metabolites, HIF-1 signaling pathway, while descriptors for Phosphotransferase system were detected exclusively in the midgut (Online Resource 2, Table S10).

Evaluation of functional traits and antibiosis *in vivo* in *Galleria mellonella* larvae

We evaluated different functional traits of 169 isolates of bacteria and yeasts from the gut of *P. luridipes*. *Candida albicans* 159 and *Candida tropicalis* 160 were not inhibited by any of the isolates. In contrast, 49.3% and 37.3% of the mid- and hindgut isolates, respectively, are antagonistic to pathogenic bacteria (Online Resource 2, Table S1). Most of the microorganisms (94.7%) could grow in culture medium at pH 7 and 8, while few managed to grow at pH 2 (3.5%) and 4 (12.9%). The secretion of ligninase and cellulase was detected in a smaller proportion of the strains in relation to the secretion of other enzymes such as, protease, esterase,

pectinase and amylase (Online Resource 2, Table S1). The midgut had a higher percentage of positive isolates for almost all enzymes (Online Resource2, Table S8), except esterase, which had practically the same percentage of positives in both chambers. The midgut had a higher percentage of positive isolates for growth in medium with bile salts and for PO_4 solubilisation, as well as a higher percentage of isolates able to grow at pH 2 and 4, and the hindgut, at pH 7 and 8 (Online Resource 2, Table S8).

From the seven strains selected for the *in vivo* antibiosis assay, *Bacillus methylotrophicus* BL14, *Xanthomonas maliensis* B6B, *Bacillus thuringiensis* B27B, *Bacillus pumilus* B34 and *Bacillus paranthracis* B73 had their tests interrupted because they showed pathogenicity to *Galleria mellonella* larvae in the tested dose (10 µLof cell suspension 0.1 OD 600nm). Pathogenicity was verified by the high mortality rate (> 50%) and melanisation of the larvae. Strains *Apiotrichum siamense* L29A and *Bacillus* sp. BL17B showed no signs of pathogenicity against the larvae.

Bacillus sp. BL17B (OD 0.05) efficiently controlled *S. flexneri* ATCC12022 in *G. mellonella* larvae (Comparison of the mortality curve using the Mantel-Cox log-rank test, *p*: 0.0001) (Table 7, and Online Resource 1, Fig. S4). We observed no difference in the mortality curve between treatments of *G. mellonella* larvae infected with *Bacillus clausii* + *S. flexneri* ATCC12022 and the control treatments infected only with *S. flexneri* ATCC12022 (Mantel-Cox, *p*> 0.05). *Apiotrichum siamense* L29A (OD 0.1) protects *G. mellonella* larvae against pathogenic bacteria *L. monocytogenes* ATCC19111 (ODs 0.05 and 0.1) and *Pseudomonas aeruginosa* ATCC9027 (OD 0.4) (Mantel-Cox, *p* <0.05) (Table 7, and Online Resource 1, Figs. S5 and S6), reducing the mortality rate relative to the control (larvae infected only with pathogen) (Mantel-Cox, *p* <0.05) (Table 7). Commercial probiotic *Saccharomyces boullardii* (OD 0.05 and 0.1) was able to protect larvae only against *L. monocytogenes* ATCC19111 (OD 0.1) compared to the control (Mantel-Cox, p <0.05). *A. siamense* L29A (OD 0.05) + P. aeruginosa ATCC9027 (OD 0.5), *S. boullardii* (OD 0.1) + *L. monocytogenes* ATCC19111 (OD 0.05) and *S. boullardii* (OD 0.1) + *P. aeruginosa* ATCC9027 (OD 0.5) induced a higher mortality rate in the larvae compared with the control treatment (larvae infected only with pathogen) (Mantel-Cox, p <0.05) (Table 7).

Table 7. Survival analysis of *Galleria mellonella* larvae infected with pathogens and probiotic strains.

Co-Inoculation Treatment			Control Treatment			*p***
Isolate	OD_{600}	Pathogen	OD_{600}	Pathogen	OD_{600}	
Apiotrichum siamense L29A	0.05	LM	0.05	LM	0.05	>0.05
Apiotrichum siamense L29A	0.05	LM	0.1	LM	0.1	>0.05
Apiotrichum siamense L29A	0.05	PA	0.4	PA	0.4	>0.05
Apiotrichum siamense L29A	0.05	PA	0.5	PA	0.5	0.03
Apiotrichum siamense L29A	0.1	LM	0.05	LM	0.05	0.01
Apiotrichum siamense L29A	0.1	LM	0.1	LM	0.1	0.02
Apiotrichum siamense L29A	0.1	PA	0.4	PA	0.4	0.04
Apiotrichum siamense L29A	0.1	PA	0.5	PA	0.5	>0.05
Saccharomyces boullardii	0.05	LM	0.05	LM	0.05	>0.05
Saccharomyces boullardii	0.05	LM	0.1	LM	0.1	0.02
Saccharomyces boullardii	0.05	PA	0.4	PA	0.4	>0.05
Saccharomyces boullardii	0.05	PA	0.5	PA	0.5	>0.05
Saccharomyces boullardii	0.1	LM	0.05	LM	0.05	0.02
Saccharomyces boullardii	0.1	LM	0.1	LM	0.1	0.01
Saccharomyces boullardii	0.1	PA	0.4	PA	0.4	>0.05
Saccharomyces boullardii	0.1	PA	0.5	PA	0.5	<0.0001
Bacillus sp. BL17B	0.05	SF	0.4	SF	0.4	>0.05
Bacillus sp. BL17B	0.05	SF	0.5	SF	0.5	<0.0001
Bacillus sp. BL17B	0.1	SF	0.4	SF	0.4	0.0024
Bacillus sp. BL17B	0.1	SF	0.5	SF	0.5	>0.05
Bacillus clausii	0.05	SF	0.4	SF	0.4	<0.0001
Bacillus clausii	0.05	SF	0.5	SF	0.5	>0.05
Bacillus clausii	0.1	SF	0.4	SF	0.4	>0.05
Bacillus clausii	0.1	SF	0.5	SF	0.5	>0.05

*Pathogen: LM: *Listeria monocytogenes* ATCC19111, PA: *Pseudomonas aeruginosa* ATCC9027*, SF: *S. flexneri* ATCC12022. **Survival analysis, Log-rank Mantel-Cox test. Significant *p*-values in bold are for treatments with higher mortality than control. *Saccharomyces boullardii* and *Bacillus clausii* are commercial strains.

Discussion

We used culture dependent and independent methods to access and describe the associated microbiome of the gut of *P. luridipes* larvae. This species has evident gut macroanoatomic and pH distinctions between the mid- and hindgut. The results obtained by dependent and independent cultivation methods are convergent, indicating differences in the composition and abundance of bacteria and fungi between the mid- and hindgut. Microbiota associated with *P. luridipes* larvae, in addition to secreting different hydrolytic enzymes and antibiosis against pathogenic bacteria, also has strains such as *Apiotrichum siamense* L29A and *Bacillus* sp. BL17B, which are able to protect *Galleria mellonella* larvae against pathogens.

Cultivation dependent and independent methods are intended to describe and understand the dynamics of microbial communities in different environments. High-throughput sequencing techniques allow in-depth access to hyper-diverse communities, and although cultivation-dependent methods access a limited number of microbial diversity, the cultivation of microorganisms is essential in the development of microbial products and processes, as well as in the evaluation of functionality and microbial ecology (Pascoal et al. 2021). Using metabarcoding, we identified 11 bacterial phyla and four fungal phyla (*Ascomycota, Basidiomycota, Mortierellomycota* and *Mucoromycota*) associated with the gut of *P. luridipes* larvae, while only *Firmicutes* bacteria, *Proteobacteria*, *Flavobacteria* and *Actinobacteria*, and yeasts *Ascomycota* and *Basidomycota* were detected by cultivation methods. Metabarcoding data indicate higher abundance of *Firmicutes* and *Bacteroidetes* in the midgut than in the hindgut, respectively. There are records of all these phyla associated with the gut of beetle larvae (Ebert et al., 2021; Podgwaite et al. 2013; Rojas-Jiménez et al. 2015; Wang & Rozen, 2017; Shelomi et al. 2019 and 2020). It is not uncommon for microorganisms grown in a culture media not to be observed by independent culture methods and vice versa due to the limitations of each technique (Wang et al. 2015).

The interaction of the intestinal microbiota is very dynamic, and balanced between transient and persistent species (Shade & Handelsman 2012; Bhatt et al. 2018). The individual variation in these microbial communities tends to be high, since this is an open system, with a constant flow of microorganisms originating mainly from food intake (Brune and Dietrich 2015). Other factors such as the proximity between competitors and mutualists in the gut, microbial adhesion in the epithelial cells and the genetic variation of the host influence this complex dynamics between transient and persistent species (Douglas 2014). These factors may be important in the intraspecific variation of microbial communities, especially for insects that do not have mechanisms for sharing microorganisms such as trophalaxis (Brune 2014) or coprophagy (Rosas et al. 2018) as is the case of *P. luridipes* larvae. Environmental pH acts directly on microbial survival and growth rate, and therefore directly influences species composition, abundance and activity in edaphic microbial communities (Zheng et al. 2020; Wan et al. 2020; Bang-Andreasen et al. 2021), as well as in the microbiota associated with animal guts (Koziolek et al. 2015; Lkhagva et al. 2021). As observed in *P. luridipes* larvae, the guts of other insects have along their length, anatomical divisions with variations in pH. In many Scarabaeidae and termites, the midgut is very alkaline and the hindgut is more neutral, which suggests that the digestion process is compartmentalised (Brune and Emerson 1995; Watanabe et al. 2010; Wada et al. 2014). This variation in pH may explain part of the variation in composition, abundance and diversity observed in the intestine of *P. luridipes* larvae.

Richness and diversity of bacterial species (cultivable) and OTUs (metabarcoding) tends to increase along the passage of the intestinal content, while the fungi community has an inverse profile, which differentiates the composition and abundance of microorganisms associated with the gut chambers larvae of *P. luridipes*. A similar observation was made in relation to the chambers of the beetle *Odontotaenius disjunctus* (Illiger, 1800)

(Ceja-Navarro et al. 2019).

The result obtained here that the majority of the diversity of bacteria and yeasts is shared between the two gut compartiments has also been reported in other beetle species (Shelomi et al. 2020). Richness of cultivable species in the intestine of *P. luridipes* larvae (57 bacterial species and seven yeasts) is higher when we compare the larvae of other coleopterans such as *Oryctes rhinoceros* (16 bacterial species and 3 fungi) (Scarabaeidae: Dynastinae) (Shelomi et al. 2020), *Nicrophorus vespilloides* Herbst, 1783 (28 bacterial species and 1 yeast) (Silphidae: Necrophorinae) (Wang and Rozen. 2017), *Anaplophora glabripennis* (Motschulsky, 1854) (Cerambycidae: Lamiinae) (22 bacterial species) (Podgwaite et al. 2013), and xylophagous Scarabaeidae larvae (18 bacterial species and 18 fungi). However, both cultive-dependent and metabarcoding studies with Scarabaeidae larvae vary widely in terms of methodology, making comparisons difficult. Other larvae from this family, such as the coprophagus *Copris incertus* Say, 1835 (Scarabaeinae), are less species rich but more diverse (Suarez-Moo et al., 2020). Ziganshina et al. (2018) found approximately 470 bacterial OTUs and 50 fungal OTUs in *Oryctes nasicornis* (Linnaeus, 1758), a species of a genus overall closer to *Pelidnota*. In the same work, the authors found between 168 to 433 OTUs of bacteria and between 23 and 39 OTUs of fungi in the hindgut of *Amphimallon solstitiale* (Linnaeus, 1758) (Melolonthinae). The diversity measured by the Shannon index, however, was higher for both beetle species in terms of fungi and bacteria however, the authors did not separate mid- and hindgut of *O. nasicornis*. *Firmicutes, Bacteroidetes, Proteobacteria* and *Actinobacteria* are the most abundant phyla in the compartiments of *P. luridipes*, and are frequently reported in larvae of *Oryctes nasicornis* and *Amphimallon solstitiale* (Ziganshina et al. 2018), in addition to being dominant in other species of wood insects (Jang and Kikuchi 2020).

The phyla *Parcubacteria* and *Armatimonadetes* were exclusive to the midgut, despite being in very low abundance. In fact, few studies with beetles report the presence of these phyla, and the majority of these report them in very low abundance (Guerrero et al., 2016; Kaczmarczyk-Ziemba et al., 2020). There are studies that detect these phyla in other insects, but always with a relative abundance of less than 1% (Costa et al., 2012; Muturi et al., 2017; Sharma et al., 2011). *Citrobacter* (Enterobacteriaceae) is abundant among cultivable strains obtained from *P. luridipes* larvae and can play an important functional role in hydrolysis of the ingested substrate or production of nitrogenous compounds for the larva. This genus is often described in the digestive tract of beetles such as the melolontines *Melolontha melolontha* (Linnaeus, 1758) (Skowronek et al. 2020) and *Holotrichia parallella* (Motschulsky, 1854) (Zhang et al. 2018), and also the dynastine *Oryctes* (El-Sayed and Ibrahim 2015; Shelomi et al. 2019). *Citrobacter* is usually related to cellulose degradation (Huang et al. 2012; Muhammad et al. 2017; Handique et al. 2017) and nitrogen fixation in termites (French et al. 1976). The genus also dominates the intestinal microbial community of larvae of the weevils (Curculionidae) *Conorhynchus palumbus* (Olivier, 1807) and *Menecleonus virgatus* Schoenherr, 1832 two Lixinae beetles that live in the Negev desert, Israel, reaching 71% of OTUs (Meng et al. 2019). The authors of the work make the assumption that their

dominance would play a role in the survival of the larvae in the desert environment, by probably helping to fix nitrogen.

Firmicutes_OTU1, *Enterobacteriaceae_OTU2*, *Porphyromonadaceae_OTU3*, and *Lactococcus_OTU4* were the most abundant OTUs in the gut of *P. luridipes*. They belong to groups also abundant in other larvae, and on species that feed on lignocellulosic material (Ziganshina et al., 2018; 2018; Shelomi et al., 2019; Alonso-Pernas et al., 2017a; Tagliavia et al., 2014). The *Enterobacteriaceae* family also has representatives able to fix nitrogen (Rizo et al., 2020) and degrade carbohydrates, such as *Citrobacter, Klebsiella*, and *Enterobacter* (Huang et al., 2012). In larvae of *Cotinis nitida* (Linnaeus, 1764) (rhizophagous Melolonthidae) living in soils experimentally contaminated with phenanthrene, *Porphyromonadaceae* tend to proliferate (Jung et al., 2020). The genera of *Dysgonomonas* and *Proteiniphilum* (*Porphyromonadaceae*) were also found in our samples, with higher abundance in the midgut. These have also been found in species of the coprophagus *Euoniticellus* (Scarabaeinae)from several countries (Parker et al., 2020), with a higher abundance of *Dysgonomonas*. Few studies approach the role of the *Porphyromonadaceae* family outside of humans however, Parker et al. (2020) propose that the genus *Dysgonomonas* may be related to the production of antifungal compounds in *Euoniticellus*. Luo et al. (2020) found four dominant genera in the microbiome of the bamboo weevil *Cyrtotrachelus buqueti* Guérin-Méneville, 1844 (Dryophthorinae), among them, *Dysgonomonas* and *Lactococcus*. The authors also analysed the genomes of species of this genus and found several genes for glycosyl hydrolases and carbohydrate esterases, indicating that both genera may be involved in carbohydrate metabolism. *Lactococcus* is a genus of lactic acid bacteria (LAB), of fermentative metabolism (Daliri and Lee, 2015). In termites, lactic acid produced in the fermentation of lignocellulosic substrates is converted into acetate and then into short-chain fatty acids, which can be absorbed by the insect (Brune, 2014). In *P. luridipes*, our cultivated *Lactococcus* produce proteases, esterases, ligninases, and some solubilises PO_4. The four most abundant OTUs are in higher numbers in the midgut of *P. luridipes*, and they are possibly involved in carbohydrate metabolism, but further studies are needed to understand their role.

Saccharomycetales and *Trichosporonales* were the main orders of yeasts identified in the gut of *P. luridipes* larvae, regardless of the method used. These orders exist in larvae of *Oryctes nasicornis* and *Amphimallon solstitiale* (Ziganshina et al. 2018). *Spathaspora brasiliensis* is a very abundant yeast in the gut of *P. luridipes* larvae. This species is reported in decaying wood (Cadete et al. 2013) and the genus is often isolated from wood and xylophagous insects (Wang et al. 2016; Morais et al. 2017). *Spathaspora* has several species able to convert D-xylose to ethanol and/or xylitol, with potential application in the food and energy industries (Cadete et al. 2009; Hou 2012; Cadete et al. 2013; Morais et al. 2020; Selim et al. 2020). *Candida, Scheffersomyces, Meyerozyma,* and *Apiotrichum* are present in the microbiota associated with *P. luridipes* and have species able to ferment xylose (Trichez et al. 2019; Morais et al. 2020). The genus *Apiotrichum*, which we were able to isolate, is an oleaginous yeast, with several species that accumulate lipids in the cytoplasm (Akindumila and Glatz 1998;

Aliyu et al. 2020; Morais et al. 2020). All of these genera have already been reported from beetle larvae or decaying wood (Cadete et al., 2013; da Silveira et al., 2020; Trichez et al., 2019; Wang et al., 2016). The functional traits of these yeasts may have a role in larval nutrition, either in the form of fermentative properties of these yeasts or even in the possible digestion of their cells by the larvae. This should be subject to further studies, since, part of the nutrients obtained by insects comes from the microbial biomass itself (Alonso-Pernas et al. 2017b), either by re-ingestion by trophallaxis (Brune and Dietrich 2015) or by larvae being fed by the adults with wood mixed with faeces, as seen in the Passalidae (Reyes Castillo 1970). In the case of *P. luridipes*, no subsocial behaviour is known. Since the adults die before the larvae hatch, parental care is absent, making this type of behaviour somewhat impossible. Therefore, the functional role of these species of bacteria and yeasts in larval nutrition needs to be further investigated.

The inference of the functional profile via PICRUST indicates a metabolic profile consistent with a gut microbiome of an insect subject to poor nutrition from plant food. The abundance of metabolic pathways linked to the metabolism of amino acids and cofactors is consistent with the hypothesis that microorganisms help supplement nutrients that are poor in the diet or that the larva cannot synthesize. Indeed, other studies indicate that the microbiota associated with the gut has an important role in the synthesis of nutrients for the host (Douglas 2018), such as with the published works with larvae of *Melolontha melolontha* (Alonso-Pernas et al. 2017b) and the weevil *Cryptorhynchus lapathi* (Linnaeus, 1758) (Cryptorhynchinae) (Jing et al. 2020). PICRUST functional prediction demonstrated a distinct profile between mid- and hindgut of *P. luridipes* indicating that some metabolic pathways such as amino acid and cofactor metabolism, nitrogen metabolism, hydrolases, sugar metabolism and nucleotides occur preferentially in the hindgut. Metabolic functions related to amino acid metabolism, antibiotic biosynthesis, nitrogen metabolism, and polysaccharide hydrolysis have been inferred in the microbiota associated with the gut of beetle larvae such as *C. incertus* (Suárez-Moo et al. 2020) and *Euoniticellus* (Shukla et al., 2016). This functional profile indicates that the microbiota in larval guts helps larvae in various ways, such as producing nutrients (vitamins, amino acids, co-factors), antibiotics, enzymes involved in the detoxification and processing of ingested foods (Douglas, 2009). The data inferred by PICRUST must be looked under the limitations of the metabolic prediction via 16S (Langille et al. 2013), and need validation in future experiments.

The functionalities evaluated *in vitro* indicate that *P. luridipes* larvae harbour microbes able to hydrolyse polysaccharides (cellulose, pectin, and starch), proteins, lignin, and solubilise phosphate. Bacteria associated with the gut of *Holotrichia paralella* (Melolonthinae) and *Pachnoda marginata* (Drury, 1773) (Cetoniinae) secrete cellulases that aid in the digestion of plant material (Cazemier et al. 2003; Huang et al. 2012), as well as *Bacteroidetes* and *Firmicutes* present in *H. parallela* (Sheng et al. 2015) and the yeasts *Candida tropicalis* and *Candida xylanilytica* isolated from *Oryctes rhinocerus* (Shelomi and Chen 2020).

Like *A. siamense* L29A and *Bacillus* sp. BL17B, other microbes with probiotic characteristics have

already been isolated from insect guts (Callegari et al., 2020; Fernandez et al., 2017; Grau et al., 2017; Mathialagan et al., 2018; Yao et al., 2017), as well as microbes that produce antimicrobial compounds (Amer et al., 2021). The ability to grow with bile salts and inhibit gastrointestinal pathogens are important functional traits in the development of probiotics (de Melo Pereira, 2018; Plaza-Diaz, 2020). *G. mellonella* has been widely used in infection tests thanks to the similarity of its innate immune response to that of vertebrates and the ease of obtaining a high number of larvae at a low cost, with simple management (Hernandez et al., 2019; Ramarao et al., 2012; Tsai et al., 2016). More recently, the larva has also been proposed as an appropriate organism for testing probiotics (Scalfaro et al., 2017; Fernández et al., 2017; Jorjão et al., 2018). In our tests, *A. siamense* L29A and *Bacillus* sp. BL17B reduced *G. mellonella* larval mortality when injected before injection of the pathogens *L. monocytogenes* ATCC19111, *P. aeruginosa* ATCC 9027, and *S. flexneri* ATCC 12022, although not in all concentrations. The isolates performed similarly or better than the commercial strains, e.g. *Saccharomyces boulardii* only protected the larva against *L. monocytogenes* ATCC19111, while *A. siamense* L29A also protected it against both *L. monocytogenes* ATCC19111 and *P. aeruginosa* ATCC 9027. The mechanisms involved in the protection of *G. mellonella* larvae may involve stimulation of the host's immune response, competitive exclusion of the pathogen, or production of antimicrobial substances (de Melo Pereira, 2018; Plaza-Diaz, 2020). These mechanisms need to be elucidated in future tests, including protection of mammals against gastrointestinal pathogens. Inhibition of pathogens *in vitro* is evidence that *A. siamense* L29A and *Bacillus* sp. BL17B produce antibacterial substances, but it does not exclude other possibilities. The commercial probiotics tested had no activity *in vitro* against any of the pathogens tested. The enzymatic profile of *A. siamense* L29A and *Bacillus* sp. BL17B was also broader than that of commercial probiotics, especially for *Bacillus* sp. BL17B, which produced protease, cellulase, amylase, and pectinase. Inhibition of other pathogens by *Bacillus* sp. BL17B *in vitro* is also a positive characteristic, which should be tested in future studies in mammals, since the pathogens in question - *Salmonella enterica serovar* Typhimurium ATCC14028, *Yersinia enterocolitica* IAL2449, and *Staphylococcus aureus* ATCC6538 - were not pathogenic to the larva.

In conclusion, this is the first report of the microbiota associated with the intestines of the larvae of the beetle *Pelidnota luridipes*, and, as far as we know, it is the first for Rutelini. The data obtained by dependent and independent cultivation methods are convergent, indicating that the communities of bacteria and fungi have different profiles between mid- and hindgut. The microbiota of *P. luridipes* is mainly composed of bacteria from the *Firmicutes, Bacteroidetes, Proteobacteria,* and yeasts *Saccharomycetales* and *Trichosporonales*. In addition to the difference in composition and abundance, gut chambers have microbes with different metabolic profiles that may correlate with the colonisation and function of microorganisms in each habitat. The microbiota associated with *P. luridipes* larvae is an important repository for prospecting strains with probiotic potentials, such as *Apiotrichum siamense* L29A and *Bacillus* sp. BL17B, that protected *Galleria mellonella* larvae against pathogenic bacteria. The mechanisms of action of antibiosis need to be elucidated in the future, as well as other

tests of safety and resistance to stomach conditions, and a finer prospection of these strains metabolic properties. New collections in different environments and breeding and experiments on *P. luridipes* and closer species may support new studies to differentiate the microbiota associated with the stage of development, as well as to determine transient and resident species in the intestine of this beetle.

References

Adams AS, Aylward FO, Adams SM, Erbilgin N, Aukema BH, Currie CR, Suen G, Raffa KF (2013) Mountain pine beetles colonizing historical and naïve host trees are associated with a bacterial community highly enriched in genes contributing to terpene metabolism. Appl Environ Microbiol 79:3468–3475 . https://doi.org/10.1128/AEM.00068-13

Akindumila F, Glatz BA (1998) Growth and oil production of *Apiotrichum curvatum* in tomato juice. J Food Prot 61:1515–1517 . https://doi.org/10.4315/0362-028X-61.11.1515

Aliyu H, Gorte O, de Maayer P, Neumann A, Ochsenreither K (2020) Genomic insights into the lifestyles, functional capacities and oleagenicity of members of the fungal family Trichosporonaceae. Sci Rep 10:1–12 . https://doi.org/10.1038/s41598-020-59672-2

Alonso-Pernas P, Arias-Cordero E, Novoselov A, Ebert C, Rybak J, Kaltenpoth M, Westermann M, Neugebauer U, Boland W (2017a) Bacterial community and PHB-accumulating bacteria associated with the wall and specialized niches of the hindgut of the forest cockchafer (*Melolontha hippocastani*). Front Microbiol 8:1–13 . https://doi.org/10.3389/fmicb.2017.00291

Alonso-Pernas P, Bartram S, Arias-Cordero EM, Novoselov AL, Halty-deLeon L, Shao Y, Boland W (2017b) *In Vivo* Isotopic Labeling of Symbiotic Bacteria Involved in Cellulose Degradation and Nitrogen Recycling within the Gut of the Forest Cockchafer (*Melolontha hippocastani*). Front Microbiol 8:1–15 . https://doi.org/10.3389/fmicb.2017.01970

Altschul SF, Gish, W. Miller, E. W. Myers and DJL (1990) Basic local alignment search tool. J Mol Biol 215:403–410

Amer A, Hamdy B, Mahmoud D, Elanany M, Rady M, Alahmadi T, Alharbi S, Alashaal S (2021) Antagonistic activity of bacteria isolated from the *Periplaneta americana L.* gut against some multidrug-resistant human pathogens. Antibiotics 10:1–16

Ankrah NYD, Douglas AE (2018) Nutrient factories: metabolic function of beneficial microorganisms associated with insects. Environ Microbiol 20:2002–2011 . https://doi.org/10.1111/1462-2920.14097

Areekul S (1957) The comparative internal larval anatomy of several genera of Scarabaeidae (Coleoptera). Ann Entomol Soc Am 50:562–577

Arévalo-Villena M, Fernandez-Pacheco P, Castillo N, Bevilacqua A, Briones Pérez A (2018) Probiotic capability in yeasts: Set-up of a screening method. LWT - Food Sci Technol 89:657–665 . https://doi.org/10.1016/j.lwt.2017.11.047

Arias-Cordero E, Platzer M, Boland W, Reichwald K, Ping L, Delb H, Reichwald K, Delb H, Platzer M, Boland W (2012) Comparative Evaluation of the Gut Microbiota Associated with the Below- and Above-Ground Life Stages (Larvae and Beetles) of the Forest Cockchafer, *Melolontha hippocastani*. PLoS One 7:e51557 . https://doi.org/10.1371/journal.pone.0051557

Ayayee PA, Larsen T, Rosa C, Felton GW, Ferry JG, Hoover K (2016) Essential amino acid supplementation by gut microbes of a wood-feeding cerambycid. Environ Entomol 45:66–73 . https://doi.org/10.1093/ee/nvv153

Berasategui A, Shukla S, Salem H, Kaltenpoth M (2016) Potential applications of insect symbionts in biotechnology. Appl Microbiol Biotechnol 100:1567–1577 . https://doi.org/10.1007/s00253-015-7186-9

Bermudez-Brito M, Plaza-Díaz J, Muñoz-Quezada S, Gómez-Llorente C, Gil A (2012) Probiotic mechanisms of action. Ann Nutr Metab 61:160–174 . https://doi.org/10.1159/000342079

Bhatt P, Kumaresan V, Palanisamy R, Ravichandran G, Mala K, Amin SMN, Arshad A, Yusoff FM, Arockiaraj J (2018) A mini review on immune role of chemokines and its receptors in snakehead murrel *Channa striatus*. Fish Shellfish Immunol 72:670–678 . https://doi.org/10.1016/j.fsi.2017.11.036

Blackwell M (2017) Made for Each Other: Ascomycete Yeasts and Insects. In: The Fungal Kingdom. American Society of Microbiology, pp 945–962

Borah D, Gogoi P, Agarwal D, Khataniar A (2019) Characterization of a Newly Isolated Probiotic Strain from *Oecophylla smaragdina*, an Edible Insect Popular Among the Indigenous Communities of Northeast India. Indian J Microbiol 59:39–50 . https://doi.org/10.1007/s12088-018-0758-5

Bousmaha-Marroki L, Boutillier D, Marroki A, Grangette C (2021) In Vitro Anti-staphylococcal and Anti-inflammatory Abilities of *Lacticaseibacillus rhamnosus* from Infant Gut Microbiota as Potential Probiotic Against Infectious Women Mastitis. Probiotics Antimicrob Proteins. https://doi.org/10.1007/s12602-021-09755-x

Brune A (2014) Symbiotic digestion of lignocellulose in termite guts. Nat Rev Microbiol 12:168–180 . https://doi.org/10.1038/nrmicro3182

Brune A, Emerson D (1995) The Termite Gut Microflora as an Oxygen Sink : Microelectrode Determination of Oxygen and pH Gradients in Guts of Lower and Higher Termites. 61:2681–2687

Fernández F, Aldea P, Fuentes JAA, Berríos P, Trombert ANN, Carreño A, Salas D, Fuentes JAA, Salas D, Carreño A, Aldea P, Fernández F, Trombert ANN (2017) Inhibitory effect of biofilm-forming *Lactobacillus kunkeei* strains against virulent *Pseudomonas aeruginosa* in vitro and in honeycomb moth (*Galleria mellonella*) infection model . Benef Microbes 9:257–268 . https://doi.org/10.3920/bm2017.0048

Cadete RM, Melo MA, Zilli JE, Vital MJS, Mouro A, Prompt AH, Gomes FCO, Stambuk BU, Lachance MA, Rosa CA (2013) *Spathaspora brasiliensis* sp. nov., *Spathaspora suhii* sp. nov., *Spathaspora roraimanensis* sp. nov. and *Spathaspora xylofermentans* sp. nov., four novel d-xylose-fermenting yeast species from Brazilian Amazonian forest. Antonie van Leeuwenhoek, Int J Gen Mol Microbiol 103:421–431 . https://doi.org/10.1007/s10482-012-9822-z

Cadete RM, Rosa CA (2018) The yeasts of the genus *Spathaspora*: potential candidates for second-generation biofuel production. Yeast 35:191–199 . https://doi.org/10.1002/yea.3279

Cadete RM, Santos RO, Melo MA, Mouro A, Gonçalves DL, Stambuk BU, Gomes FCO, Lachance MA, Rosa CA (2009) *Spathaspora arborariae* sp. nov., a d-xylose-fermenting yeast species isolated from rotting wood in Brazil. FEMS Yeast Res 9:1338–1342 . https://doi.org/10.1111/j.1567-1364.2009.00582.x

Callegari M, Jucker C, Fusi M, Leonardi MG, Daffonchio D, Borin S, Savoldelli S, Crotti E (2020) Hydrolytic Profile of the Culturable Gut Bacterial Community Associated With *Hermetia illucens*. Front Microbiol 11:1–13 . https://doi.org/10.3389/fmicb.2020.01965

Carrim AJI, Edweis CB, Gonçalves Vieira JD (2006) Enzymatic activity of endophytic bacterial isolates of *Jacaranda decurrens* Cham. (Carobinha-do-campo). Brazilian Arch Biol Technol 49:353–359 . https://doi.org/10.1590/s1516-89132006000400001

Cazemier AE, Verdoes JC, Reubsaet FAG, Hackstein JHP, van der Drift C, Op den Camp HJM (2003) *Promicromonospora pachnodae* sp. nov., a member of the (hemi)cellulolytic hindgut flora of larvae of the scarab beetle *Pachnoda marginata*. Antonie van Leeuwenhoek, Int J Gen Mol Microbiol 83:135–148 . https://doi.org/10.1023/A:1023325817663

Ceja-Navarro JA, Karaoz U, Bill M, Hao Z, White RA, Arellano A, Ramanculova L, Filley TR, Berry TD, Conrad ME, Blackwell M, Nicora CD, Kim YM, Reardon PN, Lipton MS, Adkins JN, Pett-Ridge J, Brodie EL (2019) Gut anatomical properties and microbial functional assembly promote lignocellulose

deconstruction and colony subsistence of a wood-feeding beetle. Nat Microbiol 4:864–875 . https://doi.org/10.1038/s41564-019-0384-y

Ceja-Navarro JA, Nguyen NH, Karaoz U, Gross SR, Herman DJ, Andersen GL, Bruns TD, Pett-Ridge J, Blackwell M, Brodie EL (2014) Compartmentalized microbial composition, oxygen gradients and nitrogen fixation in the gut of *Odontotaenius disjunctus*. ISME J 8:6–18 . https://doi.org/10.1038/ismej.2013.134

Ceja-Navarro JA, Vega FE, Karaoz U, Hao Z, Jenkins S, Lim HC, Kosina P, Infante F, Northen TR, Brodie EL (2015) Gut microbiota mediate caffeine detoxification in the primary insect pest of coffee. Nat Commun 6:1–9 . https://doi.org/10.1038/ncomms8618

Champion O, Titball R, Bates S (2018) Standardization of *G. mellonella* larvae to provide reliable and reproducible results in the study of fungal pathogens. J Fungi 4:108 . https://doi.org/10.3390/jof4030108

Chong J, Liu P, Zhou G, Xia J (2020) Using MicrobiomeAnalyst for comprehensive statistical, functional, and meta-analysis of microbiome data. Nat Protoc 15:799–821 . https://doi.org/10.1038/s41596-019-0264-1

Costa PS, Oliveira PL, Chartone-Souza E, Nascimento AMA (2013) Phylogenetic diversity of prokaryotes associated with the mandibulate nasute termite *Cornitermes cumulans* and its mound. Biol Fertil Soils 49:567–574 . https://doi.org/10.1007/s00374-012-0742-x

Cremon C, Barbaro MR, Ventura M, Barbara G (2018) Pre- and probiotic overview. Curr Opin Pharmacol 43:87–92 . https://doi.org/10.1016/j.coph.2018.08.010

Daliri EB-M, Lee BH (2015) New perspectives on probiotics in health and disease. Food Sci Hum Wellness 4:56–65 . https://doi.org/10.1016/j.fshw.2015.06.002

Dawood MAO, Koshio S, Abdel-Daim MM, Van Doan H (2019) Probiotic application for sustainable aquaculture. Rev Aquac 11:907–924 . https://doi.org/10.1111/raq.12272

da Silveira FA, Fernandes TAR, Bragança CRS, Balbino TR, Diniz RHS, Passos FML, da Silveira WB (2020) Isolation of xylose-assimilating yeasts and optimization of xylitol production by a new *Meyerozyma guilliermondii* strain. Int Microbiol 23:325–334 . https://doi.org/10.1007/s10123-019-00105-0

Debroas D, Domaizon I, Humbert J-F, Jardillier L, Lepère C, Oudart A, Taïb N (2017) Overview of freshwater microbial eukaryotes diversity: a first analysis of publicly available metabarcoding data. FEMS Microbiol Ecol 93: . https://doi.org/10.1093/femsec/fix023

de Melo Pereira GV, de Oliveira Coelho B, Magalhães Júnior AI, Thomaz-Soccol V, Soccol CR (2018) How to select a probiotic? A review and update of methods and criteria. Biotechnol Adv 36:2060–2076 . https://doi.org/10.1016/j.biotechadv.2018.09.003

Dillon RJ, Dillon VM (2004) The gut bacteria of insects: Nonpathogenic Interactions. Annu Rev Entomol 49:71–92 . https://doi.org/10.1146/annurev.ento.49.061802.123416

do Espírito Santo EPT, Monteiro RC, da Costa ARF, Marques-da-Silva SH (2020) Molecular Identification, Genotyping, Phenotyping, and Antifungal Susceptibilities of Medically Important *Trichosporon*, *Apiotrichum*, and *Cutaneotrichosporon* Species. Mycopathologia 185:307–317 . https://doi.org/10.1007/s11046-019-00407-x

Douglas AE (2009) The microbial dimension in insect nutritional ecology. Funct Ecol 23:38–47 . https://doi.org/10.1111/j.1365-2435.2008.01442.x

Douglas AE (2015) Multiorganismal Insects: Diversity and Function of Resident Microorganisms. Annu Rev Entomol 60:17–34 . https://doi.org/10.1146/annurev-ento-010814-020822

Douglas AE (2013) Microbial Brokers of Insect-Plant Interactions Revisited. J Chem Ecol 39:952–961 . https://doi.org/10.1007/s10886-013-0308-x

Douglas AE (2014) The molecular basis of bacterial-insect symbiosis. J Mol Biol 426:3830–3837 . https://doi.org/10.1016/j.jmb.2014.04.005

Douglas AE (2018) Omics and the metabolic function of insect–microbial symbioses. Curr Opin Insect Sci 29:1–6 . https://doi.org/10.1016/j.cois.2018.05.012

Edgar RC (2010) Search and clustering orders of magnitude faster than BLAST. Bioinformatics 26:2460–2461 . https://doi.org/10.1093/bioinformatics/btq461

Edgar RC, Haas BJ, Clemente JC, Quince C, Knight R (2011) UCHIME improves sensitivity and speed of chimera detection. Bioinformatics 27:2194–2200 . https://doi.org/10.1093/bioinformatics/btr381

Egert M, Stingl U, Bruun LD, Pommerenke B, Brune A, Friedrich MW (2005) Structure and topology of microbial communities in the major gut compartments of *Melolontha melolontha* larvae (Coleoptera: Scarabaeidae). Appl Environ Microbiol 71:4556–4566 . https://doi.org/10.1128/AEM.71.8.4556-4566.2005

El-Sayed WS, Ibrahim RA (2015) Diversity and phylogenetic analysis of endosymbiotic bacteria of the date palm root borer *Oryctes agamemnon* (Coleoptera: Scarabaeidae). BMC Microbiol 15:1–10 . https://doi.org/10.1186/s12866-015-0422-8

Engel P, Moran NA (2013) The gut microbiota of insects - diversity in structure and function. FEMS Microbiol Rev 37:699–735 . https://doi.org/10.1111/1574-6976.12025

Fernández F, Aldea P, Fuentes JAA, Berríos P, Trombert ANN, Carreño A, Salas D, Fuentes JAA, Salas D, Carreño A, Aldea P, Fernández F, Trombert ANN (2017) Inhibitory effect of biofilm-forming *Lactobacillus kunkeei* strains against virulent *Pseudomonas aeruginosa* in vitro and in honeycomb moth (*Galleria mellonella*) infection model . Benef Microbes 9:257–268 . https://doi.org/10.3920/bm2017.0048

French JR, Turner GL, Bradbury JF (1976) Nitrogen fixation by bacteria from the hindgut of termites. J Gen Microbiol 96:202–206 . https://doi.org/10.1099/00221287-95-2-202

Gales A, Chatellard L, Abadie M, Bonnafous A, Auer L, Carrère H, Godon JJ, Hernandez-Raquet G, Dumas C (2018) Screening of phytophagous and xylophagous insects guts microbiota abilities to degrade lignocellulose in bioreactor. Front Microbiol 9:1–14 . https://doi.org/10.3389/fmicb.2018.02222

Guerrero E Ben, Soria M, Salvador R, Ceja-Navarro JA, Campos E, Brodie EL, Talia P (2016) Effect of different lignocellulosic diets on bacterial microbiota and hydrolytic enzyme activities in the gut of the cotton boll weevil (*Anthonomus grandis*). Front Microbiol 7:1–13 . https://doi.org/10.3389/fmicb.2016.02093

Grau T, Vilcinskas A, Joop G (2017) Probiotic *Enterococcus mundtii* isolate protects the model insect *Tribolium castaneum* against *Bacillus thuringiensis*. Front Microbiol 8:1–10 . https://doi.org/10.3389/fmicb.2017.01261

Handique G, Phukan A, Bhattacharyya B, Baruah AALH, Rahman SW, Baruah R (2017) Characterization of cellulose degrading bacteria from the larval gut of the white grub beetle *Lepidiota mansueta* (Coleoptera: Scarabaeidae). Arch Insect Biochem Physiol 94:1–8 . https://doi.org/10.1002/arch.21370

Harding CR, Schroeder GN, Collins JW, Frankel G (2013) Use of *Galleria mellonella* as a model organism to study *Legionella pneumophila* infection. J Vis Exp. https://doi.org/10.3791/50964

Hernandez RJ, Hesse E, Dowling AJ, Coyle NM, Feil EJ, Gaze WH, Vos M (2019) Using the wax moth larva *Galleria mellonella* infection model to detect emerging bacterial pathogens. PeerJ 2019: . https://doi.org/10.7717/peerj.6150

Hill C, Guarner F, Reid G, Gibson GR, Merenstein DJ, Pot B, Morelli L, Canani RB, Flint HJ, Salminen S, Calder PC, Sanders ME (2014) The International Scientific Association for Probiotics and Prebiotics

consensus statement on the scope and appropriate use of the term probiotic. Nat Rev Gastroenterol &Amp; Hepatol 11:506

Holtof M, Lenaerts C, Cullen D, Vanden Broeck J (2019) Extracellular nutrient digestion and absorption in the insect gut. Cell Tissue Res 377:397–414 . https://doi.org/10.1007/s00441-019-03031-9

Honey Chandran C, Keerthi TR (2018) Probiotic potency of *Lactobacillus plantarum* KX519413 and KX519414 isolated from honey bee gut. FEMS Microbiol Lett 365:1–8 . https://doi.org/10.1093/femsle/fnx285

Hou X (2012) Anaerobic xylose fermentation by *Spathaspora passalidarum*. Appl Microbiol Biotechnol 94:205–214 . https://doi.org/10.1007/s00253-011-3694-4

Huang S, Sheng P, Zhang H (2012) Isolation and identification of cellulolytic bacteria from the gut of *Holotrichia parallela* larvae (Coleoptera: Scarabaeidae). Int J Mol Sci 13:2563–2577 . https://doi.org/10.3390/ijms13032563

Huang CL, Jian FY, Huang HJ, Chang WC, Wu WL, Hwang CC, Lee RH, Chiang TY (2014) Deciphering mycorrhizal fungi in cultivated *Phalaenopsis* microbiome with next-generation sequencing of multiple barcodes. Fungal Divers 66:77–88 . https://doi.org/10.1007/s13225-014-0281-x

Jacquemyn H, Pozo MI, Álvarez-Pérez S, Lievens B, Fukami T (2021) Yeast–nectar interactions: metacommunities and effects on pollinators. Curr Opin Insect Sci 44:35–40 . https://doi.org/10.1016/j.cois.2020.09.014

Janda JM, Abbott SL (2007) 16S rRNA gene sequencing for bacterial identification in the diagnostic laboratory: Pluses, perils, and pitfalls. J Clin Microbiol 45:2761–2764 . https://doi.org/10.1128/JCM.01228-07

Jang S, Kikuchi Y (2020) Impact of the insect gut microbiota on ecology, evolution, and industry. Curr Opin Insect Sci 41:33–39 . https://doi.org/10.1016/j.cois.2020.06.004

Jing TZ, Qi FH, Wang ZY (2020) Most dominant roles of insect gut bacteria: Digestion, detoxification, or essential nutrient provision? Microbiome 8:1–20 . https://doi.org/10.1186/s40168-020-00823-y

Jorjão AL, de Oliveira FE, Leão MVP, Jorge AOC, de Oliveira LD (2018) Effect of *Lactobacillus rhamnosus* on the response of *Galleria mellonella* against *Staphylococcus aureus* and *Escherichia coli* infections. Arch Microbiol 200:383–389 . https://doi.org/10.1007/s00203-017-1441-7

Jung CM, Carr M, Fleischman E, Roesch CJ (2020) Response of the green June beetle and its gut microbiome to RDX and phenanthrene. Int J Environ Sci Technol. https://doi.org/10.1007/s13762-020-02960-1

Kaczmarczyk-Ziemba A, Zagaja M, Wagner GK, Pietrykowska-Tudruj E, Saniec B (2020) First Insight into Microbiome Profiles of Myrmecophilous Beetles and Their Host , Red Wood. Insects 11:1–19

Katznelson H, Bose B (1959) Metabolic activity and phosphate-dissolving capability of bacterial isolates from wheat roots, rhizosphere, and non-rhizosphere soil. Can J Microbiol 5:79–85 . https://doi.org/10.1139/m59-010

Koziolek M, Grimm M, Becker D, Iordanov V, Zou H, Shimizu J, Wanke C, Garbacz G, Weitschies W (2015) Investigation of pH and Temperature Profiles in the GI Tract of Fasted Human Subjects Using the Intellicap® System. J Pharm Sci 104:2855–2863 . https://doi.org/10.1002/jps.24274

Klindworth A, Pruesse E, Schweer T, Peplies J, Quast C, Horn M, Glöckner FO (2013) Evaluation of general 16S ribosomal RNA gene PCR primers for classical and next-generation sequencing-based diversity studies. Nucleic Acids Res 41:1–11 . https://doi.org/10.1093/nar/gks808

Lane D (1991) 16S/23S rRNA sequencing. In: In: Stachebrandt E, Goodfellow M (eds) Wiley C (ed) Nucleic acid techniques in bacterial systematics

Langille MGI, Zaneveld J, Caporaso JG, McDonald D, Knights D, Reyes JA, Clemente JC, Burkepile DE, Vega Thurber RL, Knight R, Beiko RG, Huttenhower C (2013) Predictive functional profiling of microbial communities using 16S rRNA marker gene sequences. Nat Biotechnol 31:814–821 . https://doi.org/10.1038/nbt.2676

Lemke T, Stingl U, Egert M, Friedrich MW, Brune A (2003) Physicochemical Conditions and Microbial Activities in the Highly Alkaline Gut of the Humus-Feeding Larva of *Pachnoda ephippiata* (Coleoptera : Scarabaeidae). 69:6650–6658 . https://doi.org/10.1128/AEM.69.11.6650

Lkhagva E, Chung HJ, Hong J, Tang WHW, Lee S Il, Hong ST, Lee S (2021) The regional diversity of gut microbiome along the GI tract of male C57BL/6 mice. BMC Microbiol 21:1–13 . https://doi.org/10.1186/s12866-021-02099-0

Lunz AM, Vaz-De-Mello FZ, Monteiro OMO, Mello FZV de, Monteiro OMO (2011) *Pelidnota filippiniae* Soula, 2009 (Coleoptera: Melolonthidae: Rutelinae): um novo desfolhador de acácia-australiana, *Racosperma mangium* (Willd.) Pedley (Fabaceae), na Amazônia Oriental, Brasil. Acta Amaz 41:439–442 . https://doi.org/10.1590/s0044-59672011000300017

Luo C, Li Y, Chen Y, Fu C, Long W, Xiao X, Liao H, Yang Y (2019) Bamboo lignocellulose degradation by gut symbiotic microbiota of the bamboo snout beetle *Cyrtotrachelus buqueti*. Biotechnol Biofuels 12:1–16 . https://doi.org/10.1186/s13068-019-1411-1

Mathialagan M, Thangaraj Edward YSJ, David PMM, Senthilkumar M, Srinivasan MR, Mohankumar S (2018) Isolation, Characterization and Identification of Probiotic Lactic Acid Bacteria (LAB) from Honey Bees. Int J Curr Microbiol Appl Sci 7:894–906 . https://doi.org/10.20546/ijcmas.2018.704.096

Mattoso TC, Moreira DDO, Samuels RI (2012) Symbiotic bacteria on the cuticle of the leaf-cutting ant *Acromyrmex subterraneus subterraneus* protect workers from attack by entomopathogenic fungi. Biol Lett 8:461–464 . https://doi.org/10.1098/rsbl.2011.0963

McFarland L V., Evans CT, Goldstein EJC (2018) Strain-specificity and disease-specificity of probiotic efficacy: A systematic review and meta-analysis. Front Med 5: . https://doi.org/10.3389/fmed.2018.00124

Megaw J, Thompson TP, Lafferty RA, Gilmore BF (2015) Galleria mellonella as a novel in vivo model for assessment of the toxicity of 1-alkyl-3-methylimidazolium chloride ionic liquids. Chemosphere 139:197–201 . https://doi.org/10.1016/j.chemosphere.2015.06.026

Meng F, Bar-Shmuel N, Shavit R, Behar A, Segoli M (2019) Gut bacteria of weevils developing on plant roots under extreme desert conditions. BMC Microbiol 19:1–13 . https://doi.org/10.1186/s12866-019-1690-5

Mohammed WS, Ziganshina EE, Shagimardanova EI, Gogoleva NE, Ziganshin AM (2018) Comparison of intestinal bacterial and fungal communities across various xylophagous beetle larvae (Coleoptera: Cerambycidae). Sci Rep 8:1–12 . https://doi.org/10.1038/s41598-018-27342-z

Molnar O, Schatzmayr G, Fuchs E, Prillinger H (2004) *Trichosporon mycotoxinivorans* sp. nov., a new yeast species useful in biological detoxification of various mycotoxins. Syst Appl Microbiol 27:661–671 . https://doi.org/10.1078/0723202042369947

Moore MRM, Jameson MML, Garner BBH, Audibert C, Smith AABT, Seidel M (2017) Synopsis of the pelidnotine scarabs (Coleoptera, Scarabaeidae, Rutelinae, Rutelini) and annotated catalog of the species and subspecies. Zookeys 666:1–349 . https://doi.org/10.3897/zookeys.666.9191

Morais CG, Batista TM, Kominek J, Borelli BM, Furtado C, Moreira RG, Franco GR, Rosa LH, Fonseca C, Hittinger CT, Lachance MA, Rosa CA (2017) *Spathaspora boniae* sp. nov., a D-xylose-fermenting species in the *Candida albicans/Lodderomyces* clade. Int J Syst Evol Microbiol 67:3798–3805 . https://doi.org/10.1099/ijsem.0.002186

Morais CG, Sena LMF, Lopes MR, Santos ARO, Barros KO, Alves CR, Uetanabaro APT, Lachance MA, Rosa CA (2020) Production of ethanol and xylanolytic enzymes by yeasts inhabiting rotting wood isolated in sugarcane bagasse hydrolysate. Fungal Biol 124:639–647 . https://doi.org/10.1016/j.funbio.2020.03.005

Morón MAÁ, Deloya C (2002) Observaciones sobre el ciclo de vida de *Pelidnota (Pelidnota) virescens* Burmeister, 1844 (Coleoptera: Melolonthidae; Rutelinae). Acta Zoológica Mex 85:109–118

Muhammad A, Fang Y, Hou Y, Shi Z (2017) The gut entomotype of red palm weevil *Rhynchophorus ferrugineus* Olivier (Coleoptera: Dryophthoridae) and their effect on host nutrition metabolism. Front Microbiol 8:1–15 . https://doi.org/10.3389/fmicb.2017.02291

Muturi EJ, Ramirez JL, Rooney AP, Kim CH (2017) Comparative analysis of gut microbiota of mosquito communities in central Illinois. PLoS Negl Trop Dis 11:1–18 . https://doi.org/10.1371/journal.pntd.0005377

Nakase T, Jindamorakot S, Sugita T, Hiroko SA, Wanchern K (2006) *Trichosporon siamense* sp. nov. isolated from insect frass in Thailand. 106–109 . https://doi.org/10.1007/s10267-005-0277-1

Nalepa CA, Bignell DE, Bandi C (2001) Detritivory, coprophagy, and the evolution of digestive mutualisms in Dictyoptera. Insectes Soc 48:194–201 . https://doi.org/10.1007/PL00001767

Nasir H, Noda H (2003) Yeast-like symbiotes as a sterol source in anobiid beetles (Coleoptera, Anobiidae): Possible metabolic pathways from fungal sterols to 7-dehydrocholesterol. Arch Insect Biochem Physiol 52:175–182 . https://doi.org/10.1002/arch.10079

Oksanen J (2017) Vegan: ecological diversity. R Packag Version 24-4 11

Parker ES, Newton ILG, Moczek AP (2020) (My Microbiome) Would Walk 10,000 miles: Maintenance and Turnover of Microbial Communities in Introduced Dung Beetles. Microb Ecol 80:435–446 . https://doi.org/10.1007/s00248-020-01514-9

Pino A, Rapisarda AMC, Vitale SG, Cianci S, Caggia C, Randazzo CL, Cianci A (2021) A clinical pilot study on the effect of the probiotic *Lacticaseibacillus rhamnosus* TOM 22.8 strain in women with vaginal dysbiosis. Sci Rep 11:1–12 . https://doi.org/10.1038/s41598-021-81931-z

Plaza-Diaz J, Ruiz-Ojeda FJ, Gil-Campos M, Gil A (2019) Mechanisms of Action of Probiotics. Adv Nutr 10:S49–S66 . https://doi.org/10.1093/advances/nmy063

Podgwaite JD, D'Amico V, Zerillo RT, Schoenfeldt H (2013) Bacteria associated with larvae and adults of the Asian longhorned beetle (Coleoptera: Cerambycidae). J Entomol Sci 48:128–138 . https://doi.org/10.18474/0749-8004-48.2.128

Pugsley A, Oudega B (1987) Methods of studying colicinas and their plasmids. Oxford

R Core Team (2020) R: a Language and Environment for Statistical Computing.

Ramarao N, Nielsen-Leroux C, Lereclus D (2012) The insect *Galleria mellonella* as a powerful infection model to investigate bacterial pathogenesis. J Vis Exp 1–7 . https://doi.org/10.3791/4392

Rakic Martinez M, Wiedmann M, Ferguson M, Datta AR (2017) Assessment of *Listeria monocytogenes* virulence in the *Galleria mellonella* insect larvae model. PLoS One 12:1–17 . https://doi.org/10.1371/journal.pone.0184557

Reyes Castillo P (1970) Coleoptera, Passalidae: Morfologia y division en grandes grupos: géneros americanos. Folia Entomol. Mex. 20–22:1–240

Rizo J, Rogel MA, Guillén D, Wacher C, Martinez-Romero E, Encarnación S, Sánchez S, Rodríguez-Sanoja R (2020) Nitrogen fixation in pozol, a traditional fermented beverage. Appl Environ Microbiol 86:1–15 . https://doi.org/10.1128/AEM.00588-20

Ritcher PO (1966) White grubs and their allies. A study of North American Scarabaeoid Larvae. Oregon State University Press., Corvallis.

Rodrigues R, Falco S (2011) Aspectos biológicos de *Pelidnota fulva* Blanchard, 1850 (Coleoptera, Scarabaeidae, Rutelinae). Biota Neotrop 11:157–160

Rojas-Jiménez K, Hernández M (2015) Isolation of fungi and bacteria associated with the guts of tropical wood-feeding coleoptera and determination of their lignocellulolytic activities. Int J Microbiol 2015: . https://doi.org/10.1155/2015/285018

Rosas T, García-Ferris C, Domínguez-Santos R, Llop P, Latorre A, Moya A (2018) Rifampicin treatment of *Blattella germanica* evidences a fecal transmission route of their gut microbiota. FEMS Microbiol Ecol 94:1–12 . https://doi.org/10.1093/femsec/fiy002

Sabo S da S, Mendes MA, Araújo E da S, Muradian LB de A, Makiyama EN, LeBlanc JG, Borelli P, Fock RA, Knöbl T, Oliveira RP de S (2020) Bioprospecting of probiotics with antimicrobial activities against *Salmonella* Heidelberg and that produce B-complex vitamins as potential supplements in poultry nutrition. Sci Rep 10:1–14 . https://doi.org/10.1038/s41598-020-64038-9

Santos-Garcia D, Mestre-Rincon N, Zchori-Fein E, Morin S (2020) Inside out: microbiota dynamics during host-plant adaptation of whiteflies. ISME J 847–856 . https://doi.org/10.1038/s41396-019-0576-8

Scalfaro C, Iacobino A, Nardis C, Franciosa G (2017) *Galleria mellonella* as an in vivo model for assessing the protective activity of probiotics against gastrointestinal bacterial pathogens. FEMS Microbiol Lett 364:1–6 . https://doi.org/10.1093/femsle/fnx064

Scholtz CH, Grebennikov V V (2016) Scarabaeoidea Latreille, 1802. In: Beutel RG, Leschen RAB (eds) Handbook of Zoology: Teilband/Part 38 Volume 1: Morphology and Systematics (Archostemata, Adephaga, Myxophaga, Polyphaga partim), 2nd edn. de Gruyter, Berlin/Boston, pp 443–526

Sedláčková P, Horáčková Š, Shi T, Kosová M, Plocková M (2015) Two different methods for screening of bile salt hydrolase activity in *Lactobacillus* strains. Czech J Food Sci 33:13–18 . https://doi.org/10.17221/299/2014-CJFS

Selim KA, Easa SM, El-Diwany AI (2020) The xylose metabolizing yeast *Spathaspora passalidarum* is a promising genetic treasure for improving bioethanol production. Fermentation 6:1–12 . https://doi.org/10.3390/FERMENTATION6010033

Shade A, Handelsman J (2012) Beyond the Venn diagram: The hunt for a core microbiome. Environ Microbiol 14:4–12 . https://doi.org/10.1111/j.1462-2920.2011.02585.x

Sharma P, Sharma S, Maurya RK, De T Das, Thomas T, Lata S, Singh N, Pandey KC, Valecha N, Dixit R (2011) Salivary glands harbor more diverse microbial communities than gut in Anopheles culicifacies. Appl Environ Microbiol 77:586–596 . https://doi.org/10.1128/AEM.01080-10

Shelomi M, Chen MJ (2020) Culturing-enriched metabarcoding analysis of the Oryctes rhinoceros gut microbiome. Insects 11:1–13 . https://doi.org/10.3390/insects11110782

Shelomi M, Lin SS, Liu LY (2019) Transcriptome and microbiome of coconut rhinoceros beetle (Oryctes rhinoceros) larvae. BMC Genomics 20:1–13 . https://doi.org/10.1186/s12864-019-6352-3

Skowronek M, Sajnaga E, Pleszczyńska M, Kazimierczak W, Lis M, Wiater A (2020) Bacteria from the midgut of common cockchafer (*Melolontha melolontha* L.) larvae exhibiting antagonistic activity against bacterial symbionts of entomopathogenic nematodes: Isolation and molecular identification. Int J Mol Sci 21: . https://doi.org/10.3390/ijms21020580

Sniffen JC, McFarland L V., Evans CT, Goldstein EJC (2018) Choosing an appropriate probiotic product for your patient: An evidence-based practical guide. PLoS One 13:1–22 . https://doi.org/10.1371/journal.pone.0209205

Stefanini I (2018) Yeast-insect associations: It takes guts. Yeast 35:315–330 . https://doi.org/10.1002/yea.3309

Tanahashi M, Hawes CJ (2016) The presence of a mycangium in European *Sinodendron cylindricum* (Coleoptera: Lucanidae) and the associated yeast symbionts. J Insect Sci. https://doi.org/10.1093/jisesa/iew054

Terra WR (1990) Evolution of digestive systems of insects. Annu Rev Entomol Vol 35 181–200 . https://doi.org/10.1146/annurev.ento.35.1.181

Tokuda G, Watanabe H (2007) Hidden cellulases in termites: Revision of an old hypothesis. Biol Lett 3:336–339 . https://doi.org/10.1098/rsbl.2007.0073

Trichez D, Steindorff AS, Soares CEVF, Formighieri EF, Almeida JRM (2019) Physiological and comparative genomic analysis of new isolated yeasts *Spathaspora* sp. JA1 and *Meyerozyma caribbica* JA9 reveal insights into xylitol production. FEMS Yeast Res 19:1–15 . https://doi.org/10.1093/femsyr/foz034

Tsai CJY, Loh JMS, Proft T (2016) *Galleria mellonella* infection models for the study of bacterial diseases and for antimicrobial drug testing. Virulence 7:214–229 . https://doi.org/10.1080/21505594.2015.1135289

Ulyshen MD (2016) Wood decomposition as influenced by invertebrates. Biol Rev 91:70–85 . https://doi.org/10.1111/brv.12158

Ulyshen MD (2015) Insect-mediated nitrogen dynamics in decomposing wood. Ecol Entomol 40:97–112 . https://doi.org/10.1111/een.12176

Vavrek MJ (2011) Fossil: palaeoecological and palaeogeographical analysis tools. Palaeontol Electron 14:

Wada N, Sunairi M, Anzai H, Iwata R, Yamane A, Nakajima M (2014) Glycolytic Activities in the Larval Digestive Tract of *Trypoxylus dichotomus* (Coleoptera: Scarabaeidae). Insects 5:351–363 . https://doi.org/10.3390/insects5020351

Wang Y, Ren Y-C, Zhang Z-T, Ke T, Hui F-L (2016) *Spathaspora allomyrinae* sp. nov., a D-xylose- fermenting yeast species isolated from a scarabeid beetle *Allomyrina dichotoma*. Int J Syst Evol Microbiol 66:2008–2012 . https://doi.org/10.1099/ijsem.0.000979

Wang Y, Rozen DE (2017) Gut microbiota colonization and *Nicrophorus vespilloides* throughout development. Appl Environ Microbiol 83:1–13

Wang Y, Zhang Y (2015) Investigation of gut-associated bacteria in *Tenebrio molitor* (Coleoptera: Tenebrionidae) larvae using culture-dependent and DGGE methods. Ann Entomol Soc Am 108:941–949 . https://doi.org/10.1093/aesa/sav079

Watanabe H, Tokuda G (2010) Cellulolytic Systems in Insects. Annu Rev Entomol 55:609–632 . https://doi.org/10.1146/annurev-ento-112408-085319

White T, Bruns T, Lee S, Taylor J (1990) Amplification and Direct Sequencing of Fungal Ribosomal RNA Genes for Phylogenetics. In: Gurr S (ed) PCR Protocols: A guide to Methods and Applications. Academic Press, Inc., pp 315–322

Xie S, Lan Y, Sun C, Shao Y (2019) Insect microbial symbionts as a novel source for biotechnology. World J Microbiol Biotechnol 35:0 . https://doi.org/10.1007/s11274-019-2599-8

Yao M, Zhang H, Cai P, Gu X, Wang D, Ji Q (2017) Enhanced fitness of a *Bactrocera cucurbitae* genetic sexing strain based on the addition of gut-isolated probiotics (*Enterobacter* spec.) to the larval diet. Entomol Exp Appl 162:197–203 . https://doi.org/10.1111/eea.12529

Yao S, Xiong L, Chen X, Li H, Chen X (2020) Comparative study of lipid production from cellulosic ethanol fermentation wastewaters by four oleaginous yeasts. Prep Biochem Biotechnol 0:1–9 . https://doi.org/10.1080/10826068.2020.1852416

Yarza P, Yilmaz P, Pruesse E, Glöckner FO, Ludwig W, Schleifer K, Whitman WB, Euzéby J, Amann R, Rosselló-móra R (2014) Uniting the classification of cultured and uncultured Bacteria and Archaea using 16S rRNA gene sequences. Nat Publ Gr 12:635–645 . https://doi.org/10.1038/nrmicro3330

Yoon S-H, Ha S-M, Kwon S, Lim J, Kim Y, Seo H, Chun J (2017) Introducing EzBioCloud: a taxonomically united database of 16S rRNA gene sequences and whole-genome assemblies. Int J Syst Evol Microbiol 67:1613—1617 . https://doi.org/10.1099/ijsem.0.001755

Yong H Sen, Song SL, Chua KO, Lim PE (2017) High Diversity of Bacterial Communities in Developmental Stages of *Bactrocera carambolae* (Insecta: Tephritidae) Revealed by Illumina MiSeq Sequencing of 16S rRNA Gene. Curr Microbiol 74:1076–1082 . https://doi.org/10.1007/s00284-017-1287-x

Zhang Z, Yuan Y, Ali MW, Peng T, Peng W, Raza MF, Zhao Y, Zhang H (2018) Cultivable anaerobic and aerobic bacterial communities in the fermentation chambers of *Holotrichia parallela* (coleoptera: scarabaeidae) larvae. 1–18

Zheng W, Zhao Y, Zhang H (2012) Morphology and ultrastructure of the hindgut fermentation chamber of a melolonthine beetle *Holotrichia parallela* (Coleoptera: Scarabaeidae) during larval development. Micron 43:638–642 . https://doi.org/10.1016/j.micron.2011.11.009

Zheng F, Zhu D, Chen QL, Bi QF, Yang XR, O'Connor P, Zhu YG (2020) The driving factors of nematode gut microbiota under long-term fertilization. FEMS Microbiol Ecol 96:1–11 . https://doi.org/10.1093/femsec/fiaa037

Ziganshina EE, Mohammed WS, Shagimardanova EI, Vankov PY, Gogoleva NE, Ziganshin AM (2018) Fungal, Bacterial, and Archaeal Diversity in the Digestive Tract of Several Beetle Larvae (Coleoptera). Biomed Res Int 2018:1–15 . https://doi.org/10.1155/2018/6765438

Figures and Tables

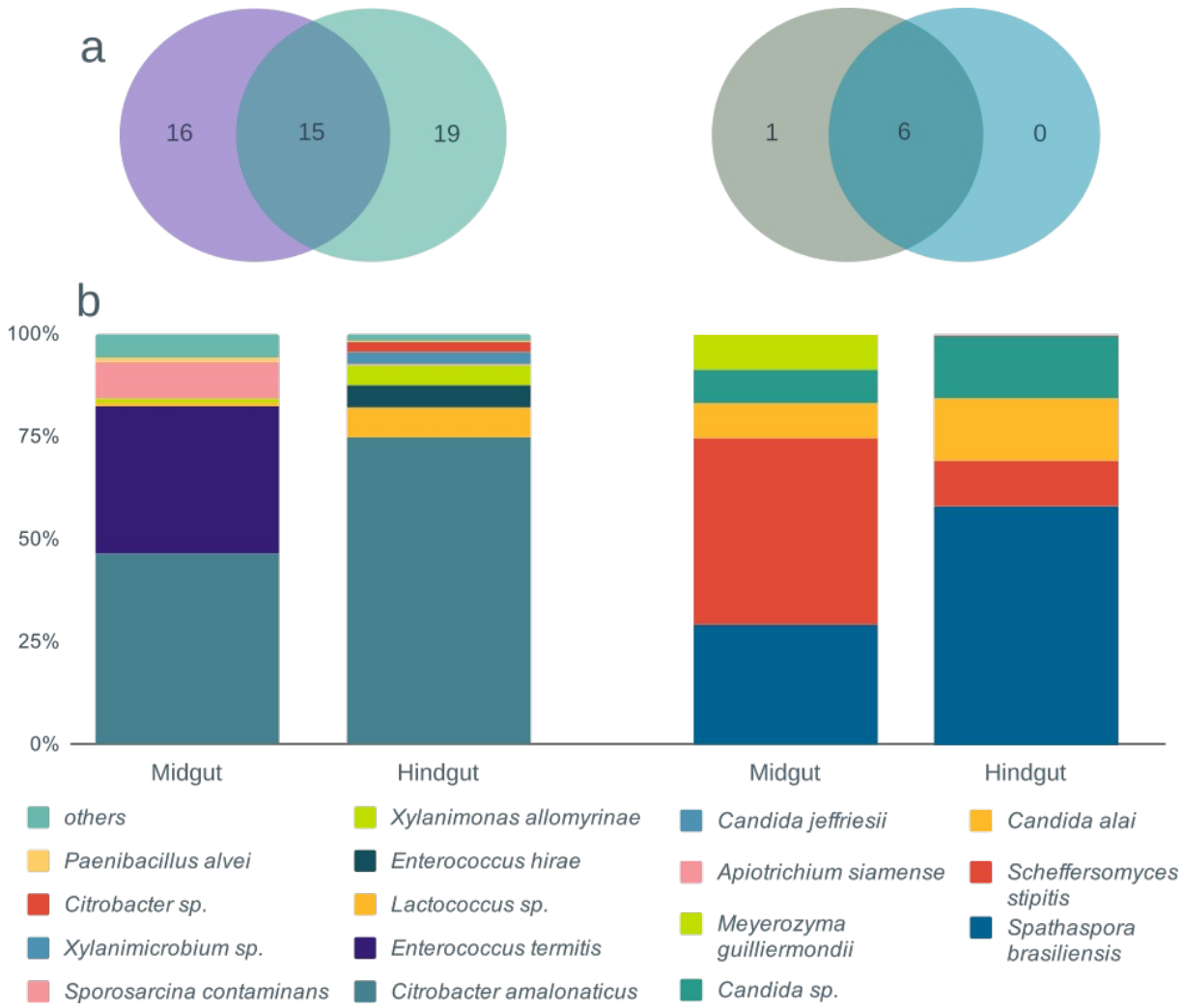


Fig. 1 Richness (a) and relative abundance (b) of cultivable bacterial (left) and yeast (right) species in the mid- and hindgut of *Pelidnota luridipes*

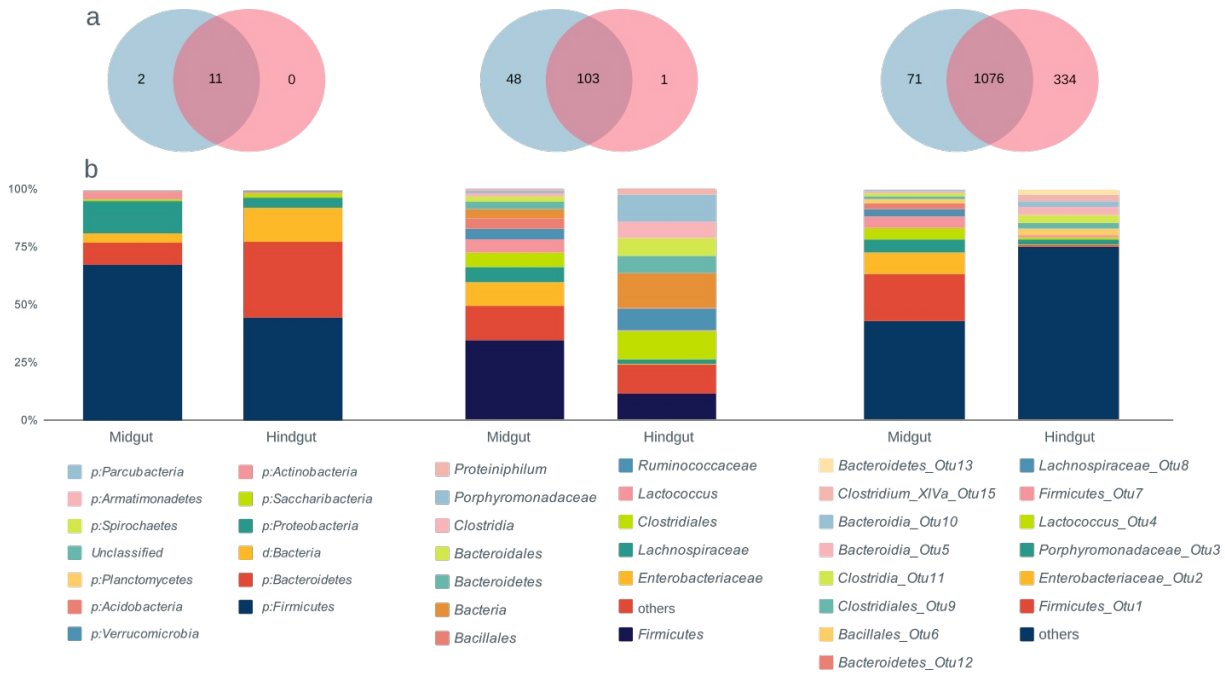


Fig. 2 Richness (a) and relative abundance (b) of phyla, genera and OTUs of bacteria detected by metabarcoding in the gut chambers of *Pelidnota luridipes*

Fig. 3 Richness (a) and relative abundance (b) of order, family and OTUs of fungi detected by metabarcoding in the gut chambers of *Pelidnota luridipes*

Table 1. Characterisation of the isolates selected for *in vivo* antibiosis assay in *Galleria mellonella* larvae.

Isolate	Functional Traits							Growth					Antibiosis halos *in vitro* (mm)									
	PT	ES	CEL	PEC	AM	LG	SB	PO_4	pH2	pH4	pH7	pH8	CA	CT	EC	PA	SF	ST	YE	LM	SA	Halo Sums
Apiotrichum siamense L29A	0	0	0	0	2	0	2	0	1	1	1	1	0	0	0	9	0	0	0	8	0	17
Bacillus paranthracis B73	3	2	2	0	3	0	0	0	0	0	1	1	0	0	0	14	0	0	0	14	0	28
Bacillus pumilus B34	1	0	1	1	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	14	18	32
Bacillus sp. BL17B	3	0	3	2	3	0	1	0	0	0	1	1	0	0	0	0	3	0	10	0	20	33
Bacillus thuringiensis B27B	3	3	0	1	2	1	3	1	1	0	1	1	0	0	0	18	0	0	0	15	26	59
Bacillus velezensis BL14	3	0	2	2	2	0	0	0	0	0	1	1	0	0	19	0	11	10	34	0	45	119
Xanthomonas maliensis B6B	0	0	1	0	0	0	3	2	0	0	1	1	0	0	14	0	15	16	0	0	0	45
Bacillus clausii – comercial	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0
Saccharomyces boulardii – comercial	0	0	0	0	0	0	0	1	0	0	1	1	0	0	0	0	0	0	0	0	0	0

Functional traits indicated by halo semi-quantitative measure: PT: Protease, ES: Esterase, CEL: Cellulase, PEC: Pectinase, AM: Amylase, LG: Ligninase, SB: Growth in medium with bile salts, PO_4: Phosphate solubilisation. Growth in culture medium with different pHs: 0 - Non-growth and 1- Growth. Halos of in vitro antibiosis: CA: *Candida albicans* 159, CT: *Candida tropicalis* 160, EC: *Escherichia coli* ATCC25922, PA: *Pseudomonas aeruginosa* ATCC9027, *Shigella flexneri* ATCC12022, *Salmonella enterica* serovar Typhimurium ATCC14028, YE: *Yersinia enterocolitica* IAL2449, LM: *Listeria monocytogenes* ATCC19111, *Staphylococcus aureus* ATCC6538

Table 2. Abundance and alpha diversity measures of cultivable microbial community of mid- and hindgut of *Pelidnota luridipes*.

Group	Measure	Midgut	Hindgut	*p* value
Bacteria	Abundance (log UFC/mg)	4.23 ±2.35	2.98 ± 1.30	0.45
	Shannon	1.04 ± 0.33	1.46 ± 0.49	0.29
	Richness	14.33 ± 11.59	15.33 ± 2.52	0.90
	Eveness	0.59 ± 0.32	0.54 ±0.20	0.84
	Simpson	0.49 ± 0.06	0.69 ±0.14	0.84
Yeasts	Abundance (log UFC/mg)	2.98 ± 1.18	3.3 ± 1.3	0.58
	Shannon	0.69 ± 0.73	0.51 ± 0.45	0.72
	Richness	3.33 ± 1.53	2.67 ± 1.53	0.57
	Eveness	0.49 ± 0.46	0.62 ± 0.06	0.85
	Simpson	0.38 ± 0.37	0.34 ± 0.29	0.34
Total	Abundance (log UFC/mg)	7.22 ± 3.08	9 ± 0.96	0.47
	Shannon	0.8 ± 0.84	0.93 ± 0.93	0.47
	Richness	17.67 ± 12.5	18.00 ± 3.61	0.97
	Eveness	0.31 ± 0.27	0.31 ± 0.32	0.53
	Simpson	0.33 ± 0.3	0.44 ± 0.40	0.13

Table 3. Total number of sequences from gut chambers of *Pelidnota luridipes* according to the parameters of the different sequencing phases.

Group	Sample*	R1	R2	Merged	Trimmed	Filtered	Mapped	OTUs
Bacteria	P6A	113,911	113,911	80,998	80,822	75,838	64,608	1,023
	P7A	106,886	106,886	72,496	72,371	67,014	54,365	271
	P8A	125,811	125,811	90,462	90,009	85,127	51,413	1,154
	P6R	128,594	128,594	94,009	93,530	88,876	53,716	1,005
	P7R	147,871	147,871	108,905	108,099	102,601	58,607	1,120
	P8R	169,305	169,305	124,272	123,165	116,906	62,607	1,235
Fungi	P6A	146,351	146,351	131,195	131,055	130,115	127,024	130
	P7A	142,304	142,304	125,214	125,100	124,229	121,233	122
	P8A	135,853	135,853	121,200	121,164	120,313	118,516	171
	P6R	150,142	150,142	134,599	134,553	133,717	128,748	86
	P7R	141,815	141,815	126,601	126,356	125,439	123,000	106
	P8R	195,376	195,376	174,322	174,185	173,019	170,452	141

*Samples refer to animal codes (P6, P7, P8) combined with chamber source (A: midgut, R: hindgut).

Table 4. Diversity of uncultivable microorganisms for the two gut chambers of *Pelidnota luridipes*.

Bacteria	Phylla			Genera			OTUs		
	Midgut	Hindgut	*p*	Midgut	Hindgut	*p*	Anterior	Hindgut	*p*
Richness	7.33 ± 2.08	6.67 ± 0.58	0.64	106.33 ± 35.23	75.00 ± 14.73	0.26	662.00 ± 427.17	991.00 ± 116.05	0.31
Shannon	0.69 ± 0.06	0.93 ± 0.05	**0.01**	2.03 ± 0.04	2.61 ± 0.03	**0.0001335**	2.63 ± 0.54	4.96 ± 0.10	**0.01**
Chao1	7.33 ± 2.08	6.67 ± 0.58	0.64	116.58 ± 30.03	107.21 ± 31.19	0.73	842.47 ± 403.15	1091.96 ± 98.03	0.40
Eveness	0.37 ± 0.03	0.50 ± 0.01	**0.02**	0.51 ±0.09	0.62 ± 0.01	0.15	0.54 ± 0.13	0.74 ± 0.04	0.11
Fungi	Orders			Families			OTUs		
	Midgut	Hindgut	*p*	Midgut	Hindgut	*p*	Midgut	Hindgut	*p*
Richness	38.67 ± 3.79	31.67 ± 3.21	0.07	43.67 ±9.71	50.33 ± 8.39	0.42	137.00 ± 26.15	105.67 ± 25.11	0.21
Shannon	1.48 ± 0.04	1.25 ± 0.51	0.51	1.28 ±0.54	1.54 ± 0.01	0.48	2.60 ± 0.08	2.07 ± 0.67	0.31
Chao1	39.00 ± 3.61	32.6 ± 4.16	0.12	45.08 ±9.66	57.83 ± 0.14	0.14	186.61 ± 94.01	117.34 ± 25.95	0.14
Eveness	0.45 ± 0.05	0.39 ± 0.17	0.63	0.33 ± 0.13	0.46 ± 0.05	0.22	0.55 ± 0.02	0.47 ± 0.15	0.48

* Values are mean and standard deviation of the indices. Values were compared by an unpaired t test.

Table 5. Bacterial OTUs with a relative frequency higher than 0.1% present in the gut chambers of *Pelidnota luridipes* with relative abundance higher than 0.1%.

	Relative abundance				Classification					
#OTU	Total	MG	HG	MG/HG	Domain	Phyllum	Class	Order	Family	Genus
Otu132	0.13	0.04	0.22	0.2	*Bacteria*	*Proteobacteria*	*Gammaproteobacteria*	*Pseudomonadales*	*Moraxellaceae*	*Acinetobacter*
Otu79	0.15	0.29	0.02	18.29	*Bacteria*	*Firmicutes*	*Bacilli*	*Bacillales*	*Bacillaceae_1*	*Bacillus*
Otu92	0.12	0.22	0.02	9.6	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Peptostreptococcaceae*	*Clostridium_XI*
Otu15	1.53	0	3.05	0	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Lachnospiraceae*	*Clostridium_XlVa*
Otu54	0.27	0.3	0.25	1.19	*Bacteria*	*Proteobacteria*	*Deltaproteobacteria*	*Desulfovibrionales*	*Desulfovibrionaceae*	*Desulfovibrio*
Otu106	0.12	0.07	0.16	0.47	*Bacteria*	*Proteobacteria*	*Deltaproteobacteria*	*Desulfovibrionales*	*Desulfovibrionaceae*	*Desulfovibrio*
Otu22	0.75	0.84	0.67	1.25	*Bacteria*	*Bacteroidetes*	*Bacteroidia*	*Bacteroidales*	*Porphyromonadaceae*	*Dysgonomonas*
Otu66	0.2	0.3	0.11	2.79	*Bacteria*	*Bacteroidetes*	*Bacteroidia*	*Bacteroidales*	*Porphyromonadaceae*	*Dysgonomonas*
Otu61	0.19	0.27	0.1	2.58	*Bacteria*	*Bacteroidetes*	*Bacteroidia*	*Bacteroidales*	*Porphyromonadaceae*	*Dysgonomonas*
Otu32	0.9	0.8	1.01	0.8	*Bacteria*	*Firmicutes*	*Bacilli*	*Lactobacillales*	*Enterococcaceae*	*Enterococcus*
Otu37	0.48	0.26	0.7	0.37	*Bacteria*	*Actinobacteria*	*Actinobacteria*	*Actinomycetales*	*Microbacteriaceae*	*Gryllotalpicola*
Otu4	3.02	5.03	1.01	4.99	*Bacteria*	*Firmicutes*	*Bacilli*	*Lactobacillales*	*Streptococcaceae*	*Lactococcus*
Otu130	0.12	0.21	0.02	9.89	*Bacteria*	*Firmicutes*	*Bacilli*	*Bacillales*	*Planococcaceae*	*Lysinibacillus*
Otu78	0.26	0.51	0	-	*Bacteria*	*Firmicutes*	*Bacilli*	*Bacillales*	*Paenibacillaceae_1*	*Paenibacillus*
Otu14	1.38	1.4	1.37	1.02	*Bacteria*	*Bacteroidetes*	*Bacteroidia*	*Bacteroidales*	*Porphyromonadaceae*	*Proteiniphilum*
Otu30	0.46	0.46	0.47	0.98	*Bacteria*	*Bacteroidetes*	*Bacteroidia*	*Bacteroidales*	*Porphyromonadaceae*	*Proteiniphilum*
Otu34	0.53	1.07	0	-	*Bacteria*	*Proteobacteria*	*Gammaproteobacteria*	*Enterobacteriales*	*Enterobacteriaceae*	*Providencia*
Otu1	10.47	20.28	0.65	31.01	*Bacteria*	*Firmicutes*	U	U	U	U
Otu2	4.79	9.38	0.2	47.44	*Bacteria*	*Proteobacteria*	*Gammaproteobacteria*	*Enterobacteriales*	*Enterobacteriaceae*	U
Otu3	3.95	5.73	2.17	2.64	*Bacteria*	*Bacteroidetes*	*Bacteroidia*U	*Bacteroidales*	*Porphyromonadaceae*	U
Otu7	2.83	4.95	0.72	6.87	*Bacteria*	*Firmicutes*	U	U	U	U
Otu6	2.43	1.75	3.11	0.56	*Bacteria*	*Firmicutes*	*Bacilli*	*Bacillales*	NI	U
Otu5	2.26	1.06	3.46	0.31	*Bacteria*	*Bacteroidetes*	*Bacteroidia*	U	U	U
Otu11	2.18	1.15	3.2	0.36	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu9	1.92	1.34	2.51	0.53	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu10	1.63	0.76	2.5	0.3	*Bacteria*	*Bacteroidetes*	*Bacteroidia*	U	U	U
Otu8	1.6	3.19	0.01	315.11	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Lachnospiraceae*	U
Otu12	1.33	2.66	0	-	*Bacteria*	*Bacteroidetes*	U	U	U	U
Otu13	1.12	0	2.24	0	*Bacteria*	*Bacteroidetes*	U	U	U	U
Otu18	1.07	1.66	0.49	3.41	*Bacteria*	*Firmicutes*	U	U	U	U
Otu23	1.05	0.93	1.17	0.79	*Bacteria*	*Bacteroidetes*	*Bacteroidia*	*Bacteroidales*	*Porphyromonadaceae*	U

Otu19	0.97	0.49	1.45	0.34	*Bacteria*	*Bacteroidetes*	U	U	U	U
Otu16	0.93	1.13	0.72	1.56	*Bacteria*	U	U	U	U	U
Otu24	0.88	0.21	1.55	0.14	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu17	0.88	1.36	0.39	3.45	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu26	0.85	0	1.7	0	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu21	0.81	1.49	0.13	11.41	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Lachnospiraceae*	U
Otu28	0.81	0	1.62	0	*Bacteria*	*Firmicutes*	U	U	U	U
Otu20	0.79	0	1.59	0	*Bacteria*	*Bacteroidetes*	U	U	U	U
Otu45	0.74	0.83	0.64	1.3	*Bacteria*	U	U	U	U	U
Otu29	0.68	0	1.36	0	*Bacteria*	*Firmicutes*	U	U	U	U
Otu42	0.66	0.48	0.84	0.56	*Bacteria*	*Actinobacteria*	*Actinobacteria*	*Actinomycetales*	*Promicromonosporaceae*	U
Otu25	0.61	0.86	0.37	2.36	*Bacteria*	U	U	U	U	U
Otu48	0.61	0.43	0.79	0.55	*Bacteria*	*Bacteroidetes*	*Bacteroidia*	*Bacteroidales*	*Porphyromonadaceae*	U
Otu27	0.57	0.6	0.54	1.11	*Bacteria*	*Bacteroidetes*	*Bacteroidia*	*Bacteroidales*	*Bacteroidaceae*	U
Otu33	0.5	0.21	0.79	0.26	*Bacteria*	*Proteobacteria*	*Deltaproteobacteria*	*Desulfovibrionales*	U	U
Otu36	0.49	0	0.99	0	*Bacteria*	*Bacteroidetes*	*Bacteroidia*	*Bacteroidales*	*Porphyromonadaceae*	U
Otu31	0.49	0.43	0.56	0.77	*Bacteria*	*Bacteroidetes*	*Bacteroidia*	*Bacteroidales*	U	U
Otu41	0.46	0.8	0.13	6.36	*Bacteria*	*Candidatus_Saccharibacteria*	U	U	U	U
Otu49	0.44	0.59	0.28	2.06	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu38	0.43	0.04	0.83	0.05	*Bacteria*	*Bacteroidetes*	*Bacteroidia*	*Bacteroidales*	*Bacteroidaceae*	U
Otu35	0.43	0.21	0.65	0.32	*Bacteria*	*Firmicutes*	U	U	U	U
Otu40	0.42	0.01	0.84	0.01	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu46	0.42	0.25	0.6	0.41	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu43	0.38	0	0.77	0	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu47	0.38	0.32	0.44	0.72	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu39	0.37	0.35	0.38	0.91	*Bacteria*	*Candidatus_Saccharibacteria*	*Saccharibacteria_genera_incertae_sedis*	U	U	U
Otu80	0.33	0.19	0.47	0.41	*Bacteria*	*Firmicutes*	U	U	U	U
Otu50	0.33	0.5	0.16	3.19	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu44	0.32	0.14	0.5	0.28	*Bacteria*	*Bacteroidetes*	*Bacteroidia*	*Bacteroidales*	*Porphyromonadaceae*	U
Otu81	0.32	0.13	0.51	0.25	*Bacteria*	*Bacteroidetes*	U	U	U	U
Otu82	0.31	0	0.62	0	*Bacteria*	*Proteobacteria*	*Gammaproteobacteria*	*Enterobacteriales*	*Enterobacteriaceae*	U
Otu55	0.3	0	0.6	0	*Bacteria*	*Firmicutes*	U	U	U	U

Otu86	0.3	0.2	0.41	0.48	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu52	0.3	0.04	0.57	0.07	*Bacteria*	*Firmicutes*	U	U	U	U
Otu51	0.3	0.27	0.32	0.84	*Bacteria*	*Bacteroidetes*	*Bacteroidia*	*Bacteroidales*	*Bacteroidaceae*	U
Otu59	0.28	0.06	0.49	0.13	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu57	0.27	0.08	0.47	0.16	*Bacteria*	*Firmicutes*	U	U	U	U
Otu72	0.25	0	0.5	0	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu75	0.25	0.11	0.39	0.27	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu53	0.25	0	0.49	0	*Bacteria*	*Proteobacteria*	*Epsilonproteobacteria*	*Campylobacterales*	*Campylobacteraceae*	U
Otu56	0.25	0.22	0.27	0.81	*Bacteria*	U	U	U	U	U
Otu90	0.25	0.27	0.22	1.19	*Bacteria*	U	U	U	U	U
Otu71	0.24	0.21	0.27	0.78	*Bacteria*	U	U	U	U	U
Otu58	0.24	0.19	0.29	0.66	*Bacteria*	*Bacteroidetes*	*Bacteroidia*	*Bacteroidales*	*Rikenellaceae*	U
Otu62	0.23	0.06	0.4	0.15	*Bacteria*	*Bacteroidetes*	U	U	U	U
Otu60	0.23	0.05	0.4	0.13	*Bacteria*	U	U	U	U	U
Otu879	0.23	0	0.45	0	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Lachnospiraceae*	U
Otu63	0.21	0.21	0.21	1	*Bacteria*	*Verrucomicrobia*	*Opitutae*	*Opitutales*	U	U
Otu119	0.21	0.17	0.25	0.68	*Bacteria*	*Firmicutes*	U	U	U	U
Otu70	0.2	0.02	0.39	0.04	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu67	0.2	0.2	0.2	0.99	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu73	0.19	0.24	0.14	1.68	*Bacteria*	U	U	U	U	U
Otu76	0.19	0	0.37	0.01	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu85	0.18	0.1	0.27	0.37	*Bacteria*	*Firmicutes*	U	U	U	U
Otu65	0.18	0.12	0.24	0.51	*Bacteria*	U	U	U	U	U
Otu112	0.18	0	0.36	0	*Bacteria*	*Firmicutes*	U	U	U	U
Otu64	0.17	0	0.35	0	*Bacteria*	*Bacteroidetes*	U	U	U	U
Otu77	0.17	0.14	0.2	0.71	*Bacteria*	*Firmicutes*	*Negativicutes*	*Selenomonadales*	*Veillonellaceae*	U
Otu74	0.17	0.13	0.2	0.65	*Bacteria*	*Bacteroidetes*	U	U	U	U
Otu68	0.16	0.01	0.32	0.02	*Bacteria*	*Firmicutes*	U	U	U	U
Otu133	0.16	0.07	0.25	0.29	*Bacteria*	*Firmicutes*	*Negativicutes*	U	U	U
Otu83	0.16	0.12	0.2	0.61	*Bacteria*	U	U	U	U	U
Otu120	0.16	0.13	0.18	0.7	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Syntrophomonadaceae*	U
Otu89	0.16	0	0.31	0	*Bacteria*	U	U	U	U	U
Otu165	0.15	0.06	0.24	0.25	*Bacteria*	U	U	U	U	U
Otu69	0.14	0.25	0.03	8.33	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu91	0.14	0.03	0.25	0.12	*Bacteria*	*Firmicutes*	U	U	U	U

Otu94	0.14	0.03	0.25	0.14	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu123	0.13	0.05	0.21	0.22	*Bacteria*	*Actinobacteria*	*Actinobacteria*	*Actinomycetales*	U	U
Otu141	0.13	0.05	0.21	0.22	*Bacteria*	*Proteobacteria*	*Deltaproteobacteria*	*Desulfovibrionales*	U	U
Otu95	0.13	0.08	0.17	0.49	*Bacteria*	*Firmicutes*	U	U	U	U
Otu84	0.13	0.23	0.02	13.06	*Bacteria*	*Firmicutes*	*Negativicutes*	*Selenomonadales*	*Veillonellaceae*	U
Otu93	0.13	0	0.25	0	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu88	0.12	0.15	0.1	1.44	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu97	0.12	0.06	0.19	0.32	*Bacteria*	U	U	U	U	U
Otu101	0.12	0.07	0.17	0.42	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu98	0.12	0	0.23	0	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu145	0.12	0.13	0.1	1.28	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu87	0.12	0	0.23	0.01	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu195	0.11	0.17	0.05	3.28	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu246	0.11	0.13	0.09	1.42	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu99	0.11	0.01	0.21	0.03	*Bacteria*	*Firmicutes*	U	U	U	U
Otu108	0.11	0.16	0.06	2.82	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu96	0.11	0.16	0.05	3.4	*Bacteria*	*Firmicutes*	U	U	U	U
Otu103	0.1	0.05	0.15	0.31	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu122	0.1	0.08	0.12	0.71	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu117	0.1	0.13	0.07	1.92	*Bacteria*	U	U	U	U	U

Total: OTU's relative abundance in relation to the total bacterial OTUs. MG and HG: OTU's relative abundance in the midgut and hindgut respectively. MG/HG: Relative abundance of OTU in the midgut divided by relative abundance of OTU in the hindgut. U: unidentified taxon

Table 6. Fungal OTUs with relative abundance higher than 0.1% in the gut chambers of *Pelidnota luridipes.*

	Relative abundance				Classification					
#OTU ID	Total	MG	HG	MG/HG	Kingdom	Phyllum	Class	Order	Family	Genus
OTU1	28.72	24.63	32.8	0.75	*Fungi*	*Ascomycota*	*Saccharomycetes*	*Saccharomycetales*	*Debaryomycetaceae*	*Candida*
OTU10	1.16	0.3	2.03	0.15	*Fungi*	*Ascomycota*	U	U	U	U
OTU11	0.89	0.45	1.33	0.33	*Fungi*	*Ascomycota*	*Dothideomycetes*	U	U	U
OTU12	1.19	2.1	0.28	7.64	*Fungi*	*Ascomycota*	*Dothideomycetes*	*Aulographales*	*Rhizodiscinaceae*	*Rhizodiscina*
OTU13	1	0.32	1.68	0.19	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Xenospadicoidales*	*Xenospadicoidaceae*	*Spadicoides*
OTU132	1.04	0.89	1.2	0.74	*Fungi*	*Ascomycota*	*Saccharomycetes*	*Saccharomycetales*	*Debaryomycetaceae*	*Spathaspora*
OTU14	0.92	0.71	1.12	0.64	*Fungi*	*Ascomycota*	*Eurotiomycetes*	*Eurotiales*	*Thermoascaceae*	*Byssochlamys*
OTU140	0.16	0.15	0.17	0.85	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Hypocreales*	*Hypocreaceae*	*Trichoderma*
OTU15	0.92	1.02	0.82	1.25	*Fungi*	*Ascomycota*	*Sordariomycetes,*	*Hypocreales*	*Hypocreaceae*	U
OTU16	1.47	1.13	1.8	0.63	*Fungi*	*Fungi_OTU16*	U	U	U	U
OTU17	0.77	1.13	0.42	2.73	*Fungi*	*Ascomycota*	*Sordariomycetes*	U	U	U
OTU172	0.49	0.42	0.57	0.74	*Fungi*	*Ascomycota*	*Saccharomycetes*	*Saccharomycetales*	*Debaryomycetaceae*	*Candida*
OTU18	0.88	1.6	0.15	10.56	*Fungi*	*Ascomycota*	*Sordariomycetes*	U	U	U
OTU185	0.17	0.21	0.12	1.77	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Hypocreales*	*Hypocreaceae*	*Trichoderma*
OTU19	0.44	0.04	0.85	0.04	*Fungi*	*Ascomycota*	U	U	U	U
OTU198	0.11	0.08	0.13	0.61	*Fungi*	*Ascomycota*	*Eurotiomycetes*	*Chaetothyriales*	*Herpotrichiellaceae*	*Exophiala*
OTU2	25.25	25.97	24.54	1.06	*Fungi*	*Ascomycota*	*Saccharomycetes*	*Saccharomycetales*	*Debaryomycetaceae*	*Spathaspora*
OTU20	0.54	0.3	0.78	0.38	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Coniochaetales*	U	U
OTU21	0.52	0.64	0.4	1.61	*Fungi*	*Ascomycota*	U	U	U	U

OTU22	0.42	0.39	0.44	0.87	*Fungi*	*Ascomycota*	*Leotiomycetes*	*Helotiales*	U	U
OTU23	0.39	0.75	0.04	20.64	*Fungi*	*Basiodiomycota*	*Agaricomycetes*	*Polyporales*	*Hyphodermataceae*	*Hyphoderma*
OTU24	0.35	0.16	0.54	0.3	*Fungi*	*Ascomycota*	*Eurotiomycetes*	*Eurotiales*	*Aspergillaceae*	*Aspergillus*
OTU248	0.45	0.45	0.45	1.01	*Fungi*	*Ascomycota*	*Saccharomycetes*	*Saccharomycetales*	*Debaryomycetaceae*	*Scheffersomyces*
OTU25	0.31	0.27	0.35	0.77	*Fungi*	*Ascomycota*	*Eurotiomycetes*	*Eurotiales*	*Aspergillaceae*	*Aspergillus*
OTU26	0.29	0.48	0.1	4.65	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Xylariales*	*Hypoxylaceae*	*Hypoxylon*
OTU27	0.38	0.58	0.19	2.98	*Fungi*	*Ascomycota*	*Sordariomycetes*	U	U	U
OTU28	0.3	0.61	0	-	*Fungi*	*Basiodiomycota*	U	U	U	U
OTU29	0.23	0.45	0	-	*Fungi*	*Ascomycota*	U	U	U	U
OTU3	5.46	5.11	5.82	0.88	*Fungi*	*Ascomycota*	*Saccharomycetes*	*Saccharomycetales*	*Debaryomycetaceae*	*Scheffersomyces*
OTU30	0.21	0.43	0	-	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Microascales*	*Halosphaeriaceae*	*Nais*
OTU31	0.19	0.27	0.11	2.38	*Fungi*	*Ascomycota*	*Sordariomycetes*	U	U	U
OTU32	0.19	0.34	0.04	8.54	*Fungi*	*Basiodiomycota*	*Agaricomycetes*	*Hymenochaetales*	*Rickenellaceae*	*Sidera*
OTU33	0.2	0.27	0.13	2.12	*Fungi*	*Ascomycota*	*Eurotiomycetes*	*Eurotiales*	*Aspergillaceae*	*Aspergillus*
OTU34	0.19	0.17	0.22	0.75	*Fungi*	*Ascomycota*	*Leotiomycetes*	*Erysiphales*	*Erysiphaceae*	*Leveillula*
OTU35	0.15	0.14	0.16	0.87	*Fungi*	*Ascomycota*	*Eurotiomycetes*	*Chaetothyriales*	*Herpotrichiellaceae*	*Exophiala*
OTU36	0.17	0.24	0.09	2.55	*Fungi*	*Ascomycota*	U	U	U	U
OTU37	0.25	0.06	0.45	0.13	*Fungi*	*Ascomycota*	U	U	U	U
OTU38	0.3	0.14	0.45	0.31	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Microascales*	*Microascaceae*	*Microascus*
OTU39	0.15	0.25	0.04	5.7	*Fungi*	*Ascomycota*	*Leotiomycetes*	*Erysiphales*	U	U
OTU4	6.52	4	9.04	0.44	*Fungi*	*Basiodiomycota*	*Tremellomycetes*	*Trichosporonales*	*Trichosporonaceae*	*Apiotrichum*
OTU40	0.14	0.15	0.12	1.31	*Fungi*	*Ascomycota*	*Eurotiomycetes*	*Chaetothyriales*	*Herpotrichiellaceae*	*Fonsecaea*

OTU41	0.12	0.12	0.12	1.02	*Fungi*	*Ascomycota*	*Sordariomycetes*	U	U	U
OTU42	0.15	0.25	0.04	6.52	*Fungi*	*Ascomycota*	*Leotiomycetes*	*Helotiales*	U	U
OTU43	0.12	0.16	0.07	2.13	*Fungi*	*Fungi_OTU43*	U	U	U	U
OTU44	0.11	0.16	0.06	2.61	*Fungi*	*Ascomycota*	U	U	U	U
OTU45	0.11	0.21	0.02	9.46	*Fungi*	*Ascomycota*	*Leotiomycetes*	U	U	U
OTU48	0.11	0.1	0.12	0.82	*Fungi*	*Mucoromycota*	*Umbelopsidomycetes*	*Umbelopsidales*	*Umbelopsidaceae*	*Umbelopsis*
OTU5	2.57	2.68	2.45	1.1	*Fungi*	*Ascomycota*	*Leotiomycetes*	*Erysiphales*	*Erysiphaceae*	*Leveillula*
OTU6	3.67	5.01	2.34	2.14	*Fungi*	*Ascomycota*	U	U	U	U
OTU7	3.24	4.85	1.63	2.97	*Fungi*	*Basiodiomycota*	*Agaricomycetes*	*Corticiales*	*Corticiaceae*	*Subulicystidium*
OTU8	1.81	3.17	0.45	7	*Fungi*	*Ascomycota*	*Sordariomycetes*	U	U	U
OTU9	1.58	2.63	0.53	4.96	*Fungi*	*Ascomycota*	U	U	U	U

Total: OTU's relative abundance in relation to total fungal OTUs. MG and HG: OTU's relative abundance in the mid and hindgut, respectively. MG/HG: Relative abundance of the OTU in the midgut divided by the relative abundance of OTU in the hindgut. U: Unidentified taxon.

Table 7. Survival analysis of *Galleria mellonella* larvae infected with pathogens and probiotic strains.

Co-Inoculation Treatment			Control Treatment			*p***
Isolate	OD_{600}	Pathogen	OD_{600}	Pathogen	OD_{600}	
Apiotrichum siamense L29A	0.05	LM	0.05	LM	0.05	>0.05
Apiotrichum siamense L29A	0.05	LM	0.1	LM	0.1	>0.05
Apiotrichum siamense L29A	0.05	PA	0.4	PA	0.4	>0.05
Apiotrichum siamense L29A	0.05	PA	0.5	PA	0.5	0.03
Apiotrichum siamense L29A	0.1	LM	0.05	LM	0.05	0.01
Apiotrichum siamense L29A	0.1	LM	0.1	LM	0.1	0.02
Apiotrichum siamense L29A	0.1	PA	0.4	PA	0.4	0.04
Apiotrichum siamense L29A	0.1	PA	0.5	PA	0.5	>0.05
Saccharomyces boullardii	0.05	LM	0.05	LM	0.05	>0.05
Saccharomyces boullardii	0.05	LM	0.1	LM	0.1	0.02
Saccharomyces boullardii	0.05	PA	0.4	PA	0.4	>0.05
Saccharomyces boullardii	0.05	PA	0.5	PA	0.5	>0.05
Saccharomyces boullardii	0.1	LM	0.05	LM	0.05	0.02
Saccharomyces boullardii	0.1	LM	0.1	LM	0.1	0.01
Saccharomyces boullardii	0.1	PA	0.4	PA	0.4	>0.05
Saccharomyces boullardii	0.1	PA	0.5	PA	0.5	<0.0001
Bacillus sp. BL17B	0.05	SF	0.4	SF	0.4	>0.05
Bacillus sp. BL17B	0.05	SF	0.5	SF	0.5	<0.0001
Bacillus sp. BL17B	0.1	SF	0.4	SF	0.4	0.0024
Bacillus sp. BL17B	0.1	SF	0.5	SF	0.5	>0.05
Bacillus clausii	0.05	SF	0.4	SF	0.4	<0.0001
Bacillus clausii	0.05	SF	0.5	SF	0.5	>0.05
Bacillus clausii	0.1	SF	0.4	SF	0.4	>0.05
Bacillus clausii	0.1	SF	0.5	SF	0.5	>0.05

Pathogen: LM: *Listeria monocytogenes* ATCC19111, PA: *Pseudomonas aeruginosa* ATCC9027*, SF: *S. flexneri* ATCC12022. **Survival analysis, Log-rank Mantel-Cox test. Significant *p*-values in bold are for treatments with higher mortality than control. *Saccharomyces boullardii* and *Bacillus clausii* are commercial strains

Anexo 2 - Material Suplementar do Capítulo 2

Supplementary Material

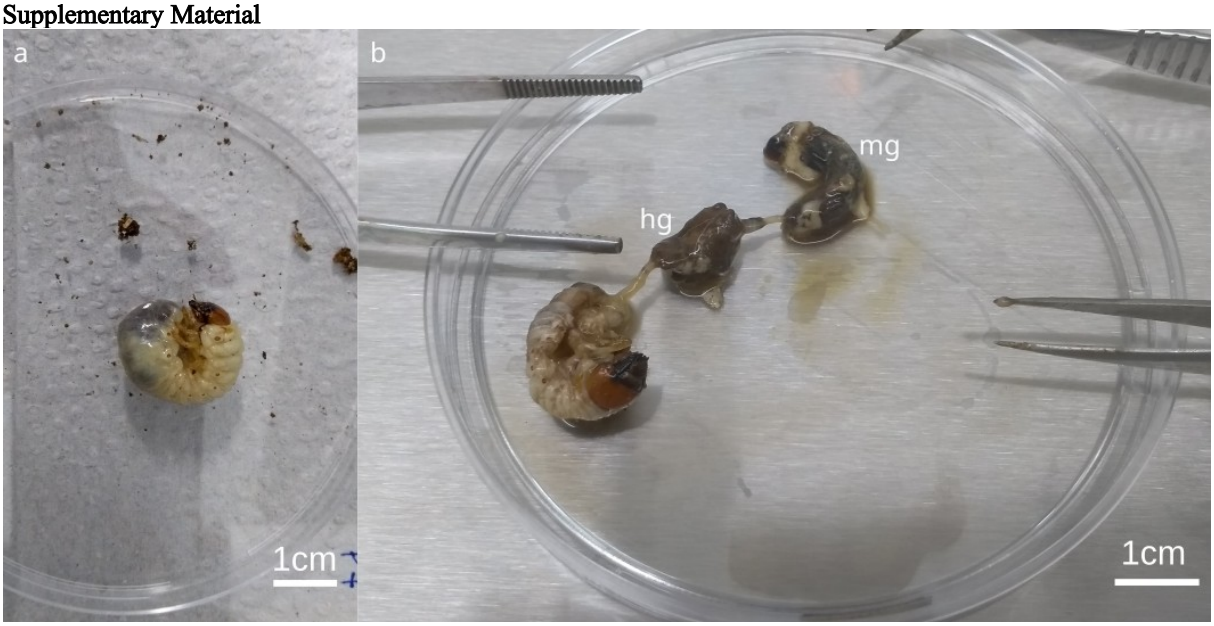


Fig. S1. Third instar larvae of *Pelidnota luridipes.*
a. Live larva. b. Dissected larva showing gut compartments. mg: Midgut. hg: Hindgut

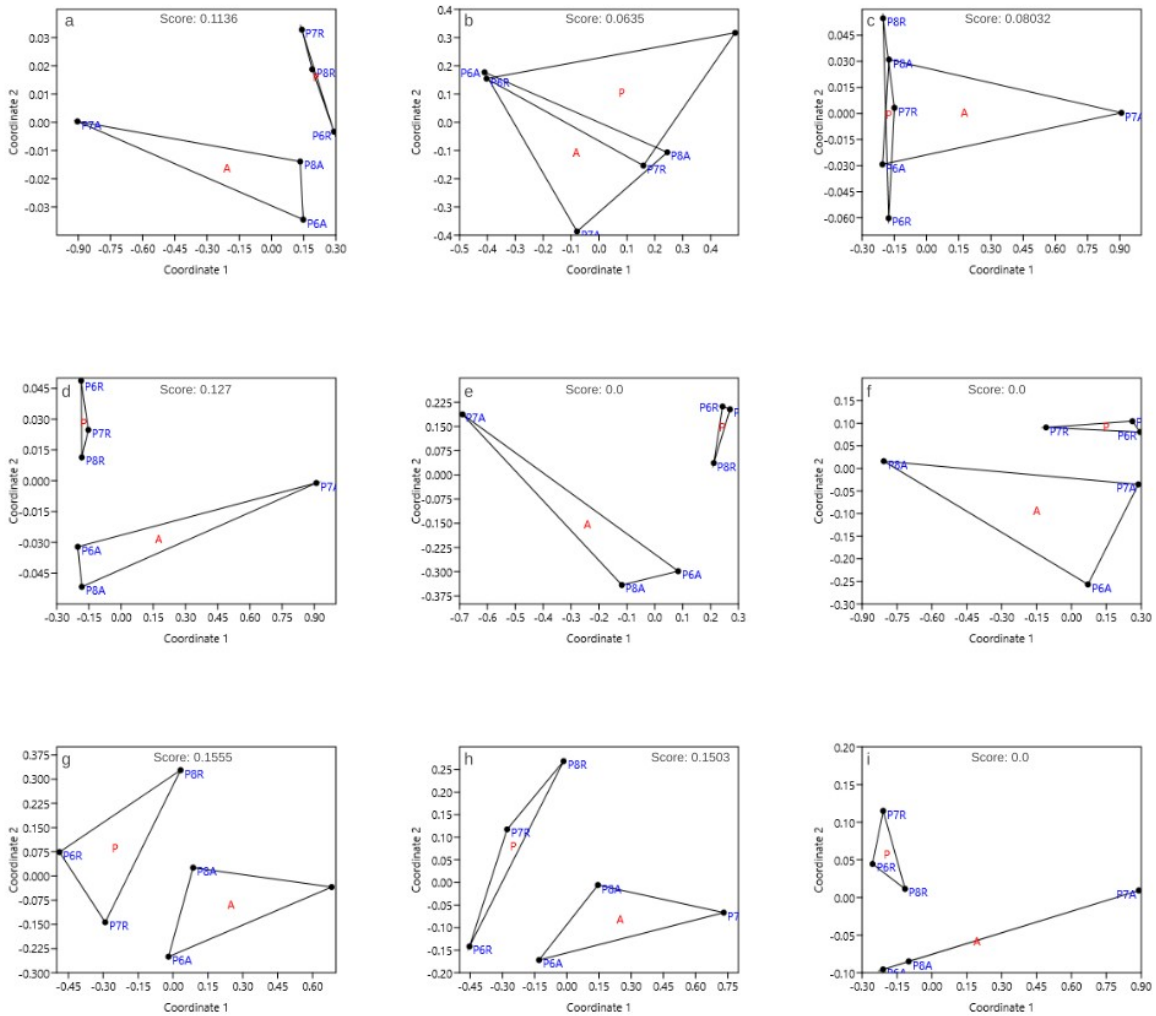


Fig. S2. NMDS ordinations of cultivable (first row) and uncultivable (second and third row) microbial communities from *P. luridipes* using Bray-Curtis distances .
a-c: bacterial, yeast and total species; d-f: bacterial phyla, genera and OTUs; g-i: fungal orders, families and OTUs

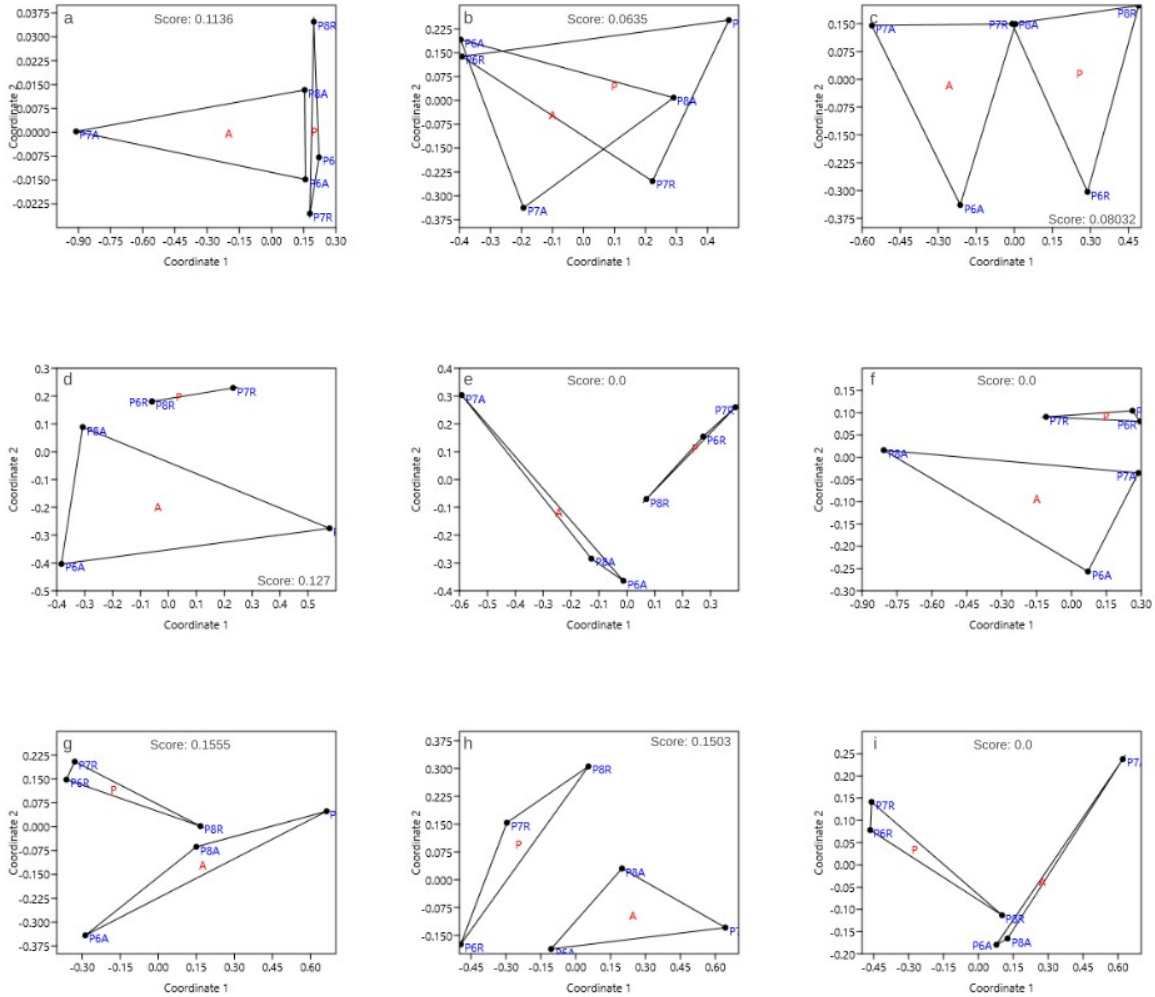


Fig. S3. NMDS ordinations of cultivable (first row) and uncultivable (second and third row) microbial communities from *P. luridipes* using Jaccard distances.
a-c: bacterial, yeast and total species; d-f: bacterial phyla, genera and OTUs; g-i: fungal orders, families and OTUs

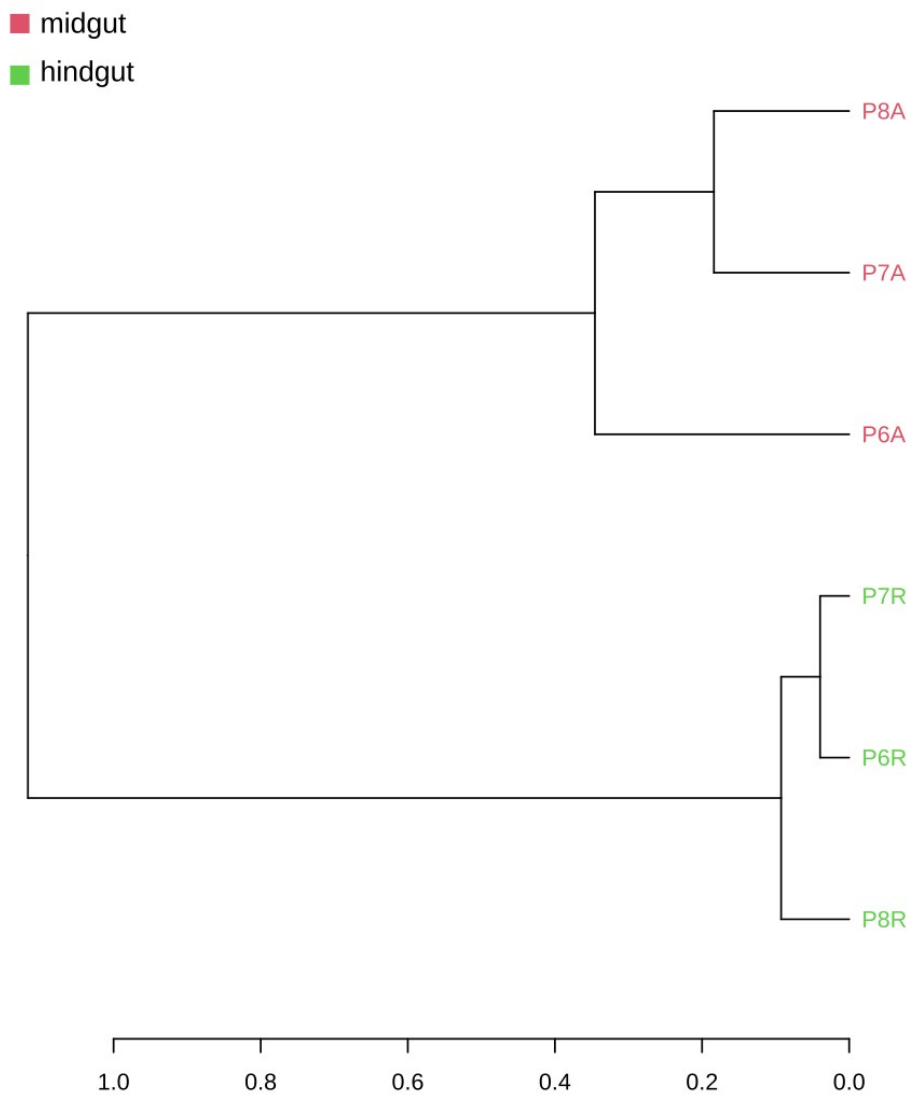


Fig. S4. Hierarchical clustering of KO descriptors predicted for the bacterial community of *P. luridipes* using Bray-Curtis distance and Ward algorithm

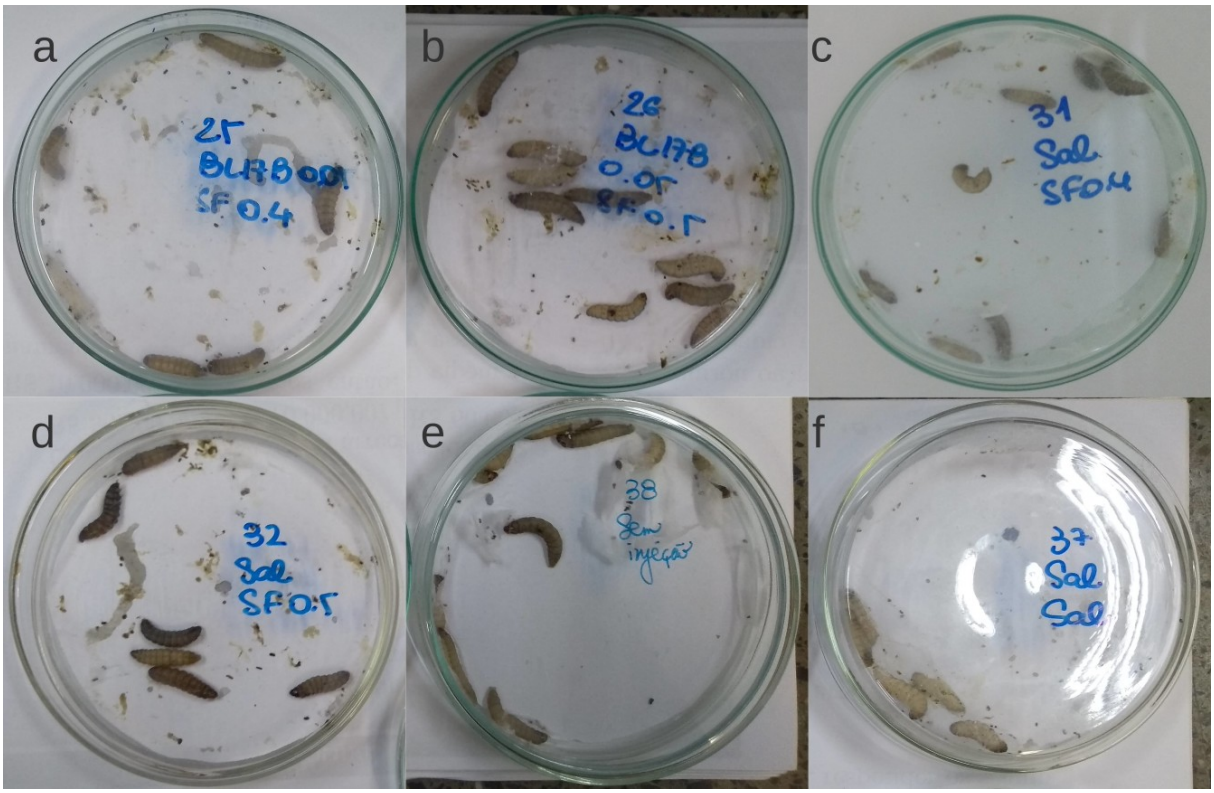


Fig. S5. Seven day plates of *Galleria mellonella* on confrontation tests with *Bacillus* sp. BL17B (BL17B) and *S. flexneri* ATCC 12022 (SF).
a. BL17B (OD 0.05) with SF (OD 0.4). b. BL17B (OD 0.05) with SF (OD 0.5). Pathogen control: c. Saline and SF on OD 0.4. d. Saline and SF on DO 0.5. e. Uninjected control and f. Saline Control

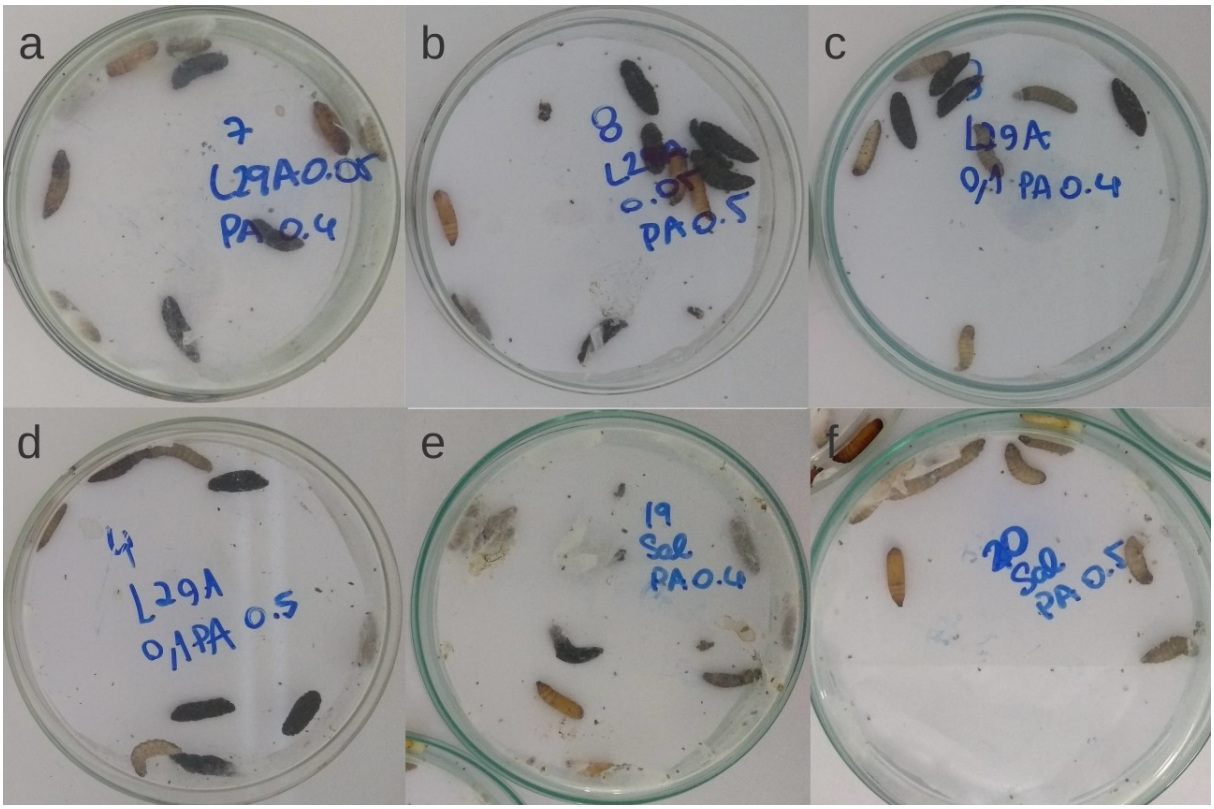


Fig. S6. Seven day plates of *G. mellonella* on confrontation tests with *A. siamense* L29A (L29A) and *P.* aeruginosa ATCC 9027 (PA).
a. L29A (OD 0.05) with PA (OD 0.4). b. L29A (OD 0.05) with PA (OD 0.5). c. L29A (OD 0.1) with PA (OD 0.4). d. L29A (OD 0.1) with PA na (OD 0.5). Pathogen Control: e. Saline with PA (OD 0.4) OD and f. Saline with PA (OD 0.5)

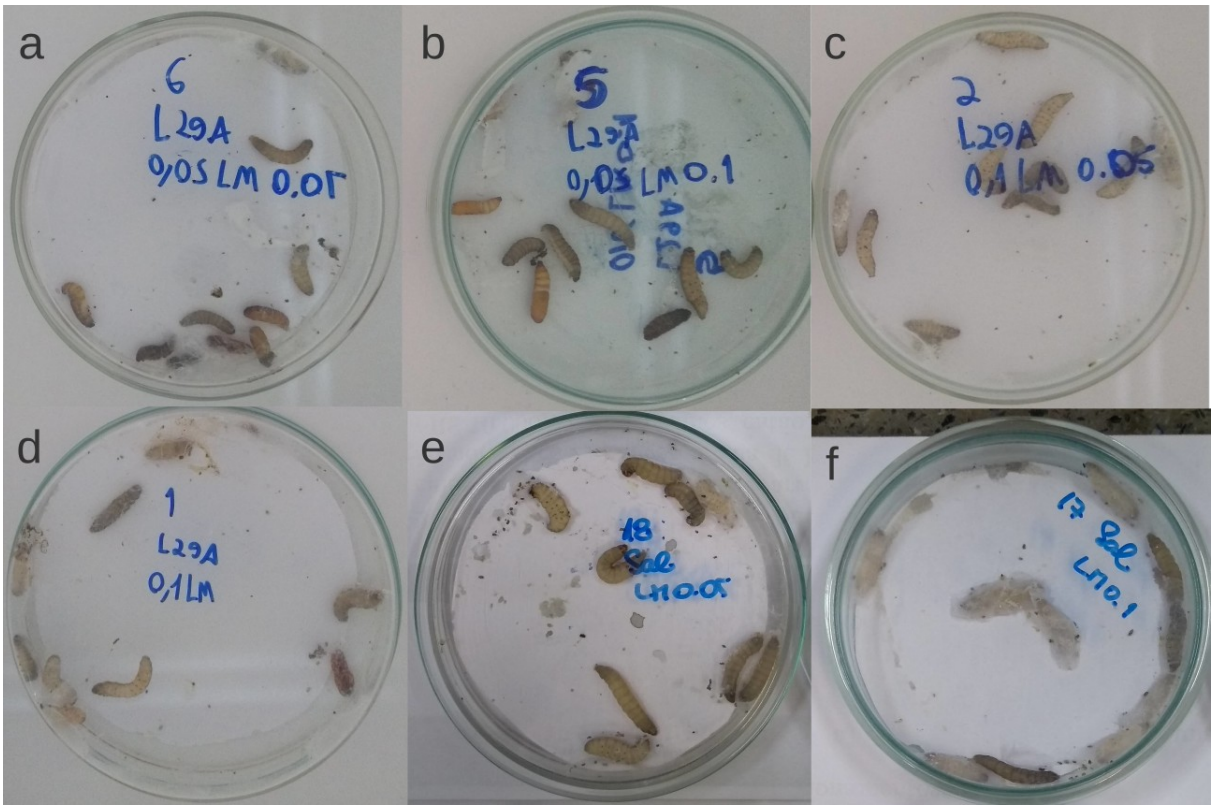


Fig. S7. Seven day plates of *G. mellonella* on confrontation tests with *A. siamense* L29A (L29A) and *L. monocytogenes* ATCC 1911 (LM).
a. L29A (OD 0.05) with LM (OD 0.05). b. L29A (OD 0.05) with LM (OD 0.1). c. L29A (OD 0.1) with LM (OD 0.05). d. L29A (OD 0.1) with LM (OD 0.1). Pathogen Controls: e. Saline with LM (OD 0.05) and f. Saline with LM (DO 0.1)

Table S1. Functional traits of microbial isolates from *Pelidnota luridipes*

Isolate	Source	Grp	GenBank	UFC/mg MG	UFC/mg HG	Halo									Growth			
						prt	est	cel	pec	aml	lgn	PO_4	Inib	SB	pH2	pH4	pH7	pH8
Alcaligenes faecalis BL27	MG	bac	MW142152	3.09	0.00	0	0	0	0	0	0	0	0	0	0	0	1	1
***Apiotrichum siamense* L29A**	**HG**	**lev**	**MW165509**	**0.00**	**42.20**	**0**	**0**	**0**	**0**	**2**	**0**	**0**	**3**	**2**	**1**	**1**	**1**	**1**
***Apiotrichum siamense* L30A**	**MG and HG**	**lev**	**MW138108**	**1.67**	**4.27**	**0**	**0**	**0**	**0**	**2**	**0**	**0**	**2**	**2**	**1**	**1**	**1**	**1**
***Apiotrichum siamense* L30B**	**MG and HG**	**lev**	**MW165510**	**1.67**	**4.27**	**0**	**0**	**0**	**0**	**2**	**0**	**0**	**2**	**1**	**0**	**0**	**1**	**1**
Apiotrichum siamense L43	MG	lev	MW138107	0.56	0.00	0	0	0	0	2	0	0	1	2	1	1	1	1
Apiotrichum siamense L43A	MG	lev	MW138107	0.56	0.00	0	0	0	0	1	0	0	1	2	1	1	1	1
***Apiotrichum siamense* L44**	**MG**	**lev**	**MW165512**	**1.11**	**0.00**	**0**	**0**	**0**	**0**	**2**	**0**	**0**	**2**	**2**	**0**	**1**	**1**	**1**
***Apiotrichum siamense* L45**	**MG**	**lev**	**MW165513**	**1.11**	**0.00**	**0**	**0**	**0**	**0**	**2**	**0**	**0**	**2**	**2**	**1**	**1**	**1**	**1**
***Apiotrichum siamense* L38A**	**MG and HG**	**lev**	**MW165511**	**4.44**	**4.63**	**0**	**2**	**0**	**1**	**1**	**0**	**0**	**2**	**2**	**0**	**1**	**1**	**1**
***Apiotrichum siamense* L40**	**HG**	**lev**	**MW165508**	**0.00**	**1.16**	**0**	**0**	**0**	**0**	**2**	**0**	**0**	**3**	**2**	**0**	**1**	**1**	**1**
***Apiotrichum siamense* LB13**	**WG**	**lev**	**MW165507**	**-**	**-**	**0**	**0**	**0**	**0**	**2**	**0**	**0**	**2**	**2**	**0**	**0**	**1**	**1**
Bacillus cereus B62	MG and HG	bac	MW142079	462.96	347.22	3	2	1	0	3	0	1	0	0	0	0	1	1
***Bacillus cereus* B38A**	**WG**	**bac**	**MW142137**	**-**	**-**	**3**	**2**	**2**	**0**	**3**	**0**	**0**	**2**	**3**	**0**	**1**	**1**	**1**
Bacillus cereus B38B	WG	bac	MW142137	-	-	0	2	0	0	0	0	0	0	3	0	0	1	1
Bacillus cereus B38C	WG	bac	MW142137	-	-	0	0	0	0	1	0	0	0	0	0	0	1	1
Bacillus cereus B62	MG and HG	bac	MW142069	462.96	347.22	3	2	0	0	0	0	2	1	0	0	0	1	1
***Bacillus paranthracis* B73**	**MG and HG**	**bac**	**MW142143**	**154.32**	**115.74**	**3**	**2**	**2**	**0**	**3**	**0**	**0**	**2**	**0**	**0**	**0**	**1**	**1**
Bacillus paranthracis B73B	MG and HG	bac	MW142144	154.32	115.74	3	2	2	0	2	0	0	0	0	0	0	1	1
***Bacillus pumilus* B34**	**WG**	**bac**	**MW142134**	**-**	**-**	**1**	**0**	**1**	**1**	**0**	**0**	**0**	**2**	**0**	**0**	**0**	**1**	**1**
***Bacillus* sp. BL17B**	**WG**	**bac**	**MW147750**	**-**	**-**	**3**	**0**	**3**	**2**	**3**	**0**	**0**	**5**	**1**	**0**	**0**	**1**	**1**
***Bacillus subtilis* BL2**	**MG and HG**	**bac**	**MW142061**	**23.95**	**4.63**	**3**	**0**	**3**	**2**	**3**	**0**	**0**	**3**	**0**	**0**	**0**	**1**	**1**
***Bacillus subtilis* BL24A**	**MG**	**bac**	**MW142053**	**4.12**	**0.00**	**3**	**0**	**3**	**2**	**3**	**0**	**0**	**3**	**0**	**0**	**0**	**1**	**1**
***Bacillus subtilis* BL24B**	**MG**	**bac**	**MW142053**	**4.12**	**0.00**	**3**	**0**	**3**	**2**	**3**	**0**	**0**	**4**	**0**	**0**	**0**	**1**	**1**
***Bacillus subtilis* BL26**	**MG**	**bac**	**MW142051**	**6.17**	**0.00**	**3**	**0**	**3**	**2**	**3**	**0**	**0**	**3**	**0**	**0**	**0**	**1**	**1**
***Bacillus subtilis* BL37**	**WG**	**bac**	**MW142060**	**-**	**-**	**3**	**0**	**3**	**2**	**3**	**0**	**0**	**5**	**2**	**0**	**0**	**1**	**1**
***Bacillus subtilis* BL39**	**HG**	**bac**	**MW142059**	**0.00**	**6.94**	**3**	**0**	**3**	**2**	**3**	**0**	**0**	**4**	**0**	**0**	**0**	**1**	**1**
***Bacillus thuringiensis* B18**	**MG**	**bac**	**MW142080**	**154.32**	**0.00**	**3**	**2**	**1**	**0**	**3**	**1**	**1**	**2**	**1**	**0**	**0**	**1**	**1**
Bacillus thuringiensis B18B	MG	bac	MW142080	154.32	0.00	1	2	0	1	3	1	0	1	1	0	0	1	1
Bacillus thuringiensis B27A	WG	bac	MW142109	-	-	0	0	0	1	0	0	2	0	2	0	0	1	1
***Bacillus thuringiensis* B27B**	**WG**	**bac**	**MW142109**	**-**	**-**	**3**	**3**	**0**	**1**	**2**	**1**	**1**	**2**	**3**	**1**	**0**	**1**	**1**
***Bacillus velezensis* BL14**	**WG**	**bac**	**MW142055**	**-**	**-**	**3**	**0**	**2**	**2**	**2**	**0**	**0**	**5**	**0**	**0**	**0**	**1**	**1**
Burkholderia cenocepacia B69a	MG	bac	MW142075	308.64	0.00	3	3	0	0	0	0	0	0	0	0	0	1	1
Candida alai B53	MG and HG	lev	MW142077	925.925	4,022.99	0	0	0	1	0	0	0	0	2	0	1	1	1
Candida jeffriesii L5C	MG and HG	lev	MW165506	1.52	0.77	0	0	0	0	0	0	0	0	2	0	1	1	1
Candida sp. B53C	MG and HG	lev	MW165503	925.925	4,022.99	1	0	0	1	0	0	0	0	1	0	0	1	1
Chryseobacterium gwangjuense A138	MG	bac	MW142142	1,543.21	0.00	1	3	0	0	0	0	3	0	0	0	0	1	1
Chryseobacterium gwangjuense	MG	bac	MW142076	308.64	0.00	3	3	0	0	0	0	0	1	0	0	0	0	0

B69b																		
***Citrobacter amalonaticus* B2B**	**MG and HG**	**bac**	**MW142078**	**38,858.02**	**279,522.79**	**0**	**1**	**0**	**1**	**3**	**0**	**2**	**2**	**1**	**0**	**0**	**1**	**1**
Citrobacter amalonaticus B2C	MG and HG	bac	MW142078	38,858.02	279,522.79	1	2	0	2	0	0	1	1	1	0	0	1	0
Citrobacter amalonaticus B79A	MG and HG	bac	MW142146	22,160.49	385.80	0	0	0	1	0	0	1	1	2	0	0	1	1
Citrobacter amalonaticus B79B	MG and HG	bac	MW142102	22,160.49	385.80	0	0	0	1	0	0	1	0	2	0	0	1	1
Citrobacter koseri B101	HG	bac	MW142065	0.00	1,709.40	1	0	0	1	0	0	3	0	2	0	0	1	1
Citrobacter koseri B60	HG	bac	MW142070	0.00	766.28	0	0	0	1	0	0	1	0	2	0	0	1	1
Citrobacter sp. B1A	HG	bac	MW142050	0.00	8,237.55	0	1	0	0	0	0	2	1	1	0	0	1	1
Citrobacter sp. B1B	HG	bac	MW142050	0.00	8,237.55	0	1	0	1	0	0	2	1	1	0	0	1	1
***Cytobacillus kochii* B75**	**MG**	**bac**	**MW142145**	**1,543.21**	**0.00**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**3**	**1**	**0**	**0**	**1**	**1**
Enterococcus hirae B76	MG and HG	bac	MW142073	14,176.95	284.90	0	3	0	0	0	0	1	0	0	0	0	0	1
Enterococcus hirae B76A	MG and HG	bac	MW142073	14,176.95	284.90	0	1	0	0	0	0	1	0	1	0	0	1	1
Enterococcus hirae B76B	MG and HG	bac	MW142072	14,176.95	284.90	0	0	0	0	0	0	0	0	0	0	0	1	1
Enterococcus hirae B96A	HG	bac	MW142064	0.00	20,370.37	0	0	0	1	0	0	3	0	2	0	0	1	1
Enterococcus hirae B96B	HG	bac	MW142064	0.00	20,370.37	0	0	0	1	0	0	3	0	1	0	0	1	1
Enterococcus termitis B89A	MG	bac	MW724806	34,444.44	0.00	0	0	0	0	0	0	1	0	2	0	0	1	1
Enterococcus termitis B89B	MG	bac	MW725072	34,444.44	0.00	0	0	0	0	0	0	1	0	0	0	0	1	1
Galactobacter valiniphilus B91A	MG	bac	MW725071	555.56	0.00	1	0	0	0	0	0	2	0	0	0	0	1	1
***Galactobacter valiniphilus* B91C**	**MG**	**bac**	**MW142057**	**555.56**	**0.00**	**1**	**2**	**1**	**0**	**1**	**0**	**2**	**2**	**3**	**0**	**0**	**1**	**1**
Isoptericola dokdonensis B56B	HG	act	MW142100	0.00	191.57	0	0	1	0	0	0	1	0	2	0	0	1	1
Kitasatospora sp. A61A	MG	act	MW142104	308.6419753	0.00	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Kitasatospora sp. A61B	MG	act	MW142104	308.64	0.00	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
***Klebsiella michiganensis* B7**	**WG**	**bac**	**MW142049**	**-**	**-**	**0**	**0**	**0**	**0**	**1**	**0**	**2**	**2**	**2**	**0**	**0**	**1**	**1**
Klebsiella michiganensis B71	MG	bac	MW725073	1,152.26	0.00	0	0	0	1	0	0	1	0	0	0	0	1	1
Kosakonia cowanii B116A	MG	bac	MW142097	2,469.14	0.00	0	0	0	1	0	0	3	0	0	0	0	1	1
***Lactococcus garvieae* B9**	**WG**	**bac**	**MW142135**	**-**	**-**	**1**	**0**	**0**	**0**	**0**	**0**	**2**	**2**	**3**	**0**	**0**	**1**	**1**
Lactococcus sp. B10A	MG and HG	bac	MW142105	843.62	18,287.04	1	0	0	0	0	0	1	1	1	0	0	1	1
Lactococcus sp. B10B	MG and HG	bac	MW142105	843.62	18,287.04	3	2	0	0	0	1	1	1	1	0	0	1	1
Lactococcus sp. B10C	MG and HG	bac	MW142105	843.62	18,287.04	1	2	0	0	0	0	2	1	0	0	0	1	1
Lactococcus taiwanensis B81	MG	bac	MW142147	925.93	0.00	0	0	0	0	0	0	0	1	0	0	0	0	0
Luteimicrobium album B11A	HG	act	MW147752	0.00	766.28	1	0	0	2	0	0	0	1	0	0	0	1	1
Luteimicrobium album B11B	HG	act	MW147752	0.00	766.28	0	0	0	1	0	0	1	0	3	0	0	1	1
***Lysinibacillus fusiformis* B63**	**WG**	**bac**	**MW142136**	**-**	**-**	**2**	**1**	**0**	**0**	**0**	**0**	**1**	**2**	**2**	**0**	**0**	**1**	**1**
Lysinibacillus fusiformis B84	HG	bac	MW142068	0.00	231.48	0	0	0	0	0	0	0	0	0	0	0	1	1
Lysinibacillus fusiformis B84B	HG	bac	MW142068	0.00	231.48	3	0	0	1	0	0	1	1	0	0	0	1	1
Lysinibacillus xylanilyticus B85B	HG	bac	MW142067	0.00	231.48	0	1	0	0	0	0	0	0	0	0	0	1	1
Lysinibacillus xylanilyticus B85	HG	bac	MW142066	0.00	231.48	0	1	0	0	0	0	0	0	0	0	0	1	1
Meyerozyma guilliermondii L48	MG	lev	MW165501	617.28	0.00	2	0	0	0	0	0	0	0	2	0	1	1	1
Microbacterium natoriense B72A	MG	act	MW142074	1,728.40	0.00	1	0	0	1	3	0	0	0	0	0	0	1	1
Mycobacterium porcinum A121	HG	act	MW142088	0.00	46.30	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Bacillus clausii- comercial	comercial	-	-	-	-	0	0	0	0	0	0	0	0	0	0	0	1	1

Saccharomyces boulardii-comercial	comercial	-	-	-	-	0	0	0	0	0	0	1	0	2	0	0	1	1
unidentified A10B	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A12	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A126	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A129A1	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A129A2	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A130	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A131A	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A133	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A142	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A143	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A143B	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A144	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A147	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A150	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A151	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A152	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A153	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A155	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A157	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A163A	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A164A	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A165A	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A167A	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A169A	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A171A	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A171B	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A172A	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A173	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A175	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A175B	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A177	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A181	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A185	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A186	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A187	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A190	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A19C	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A1B	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A20	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND

unidentified A20B	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A24B	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A24C	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A24D	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A24E	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A25A	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A25C	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A27A	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A27B	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A27C	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A28	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A29	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A29B	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A29C	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A2A	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A31	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A31B	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A33	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A35	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A39	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A39B	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A40	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A41	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A42	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A43	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A44	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A44B	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A46	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A48	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A49	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A49A	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A4B	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A4C	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A50	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A51	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A51B	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A52	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A53	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A54	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A55A	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A55B	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND

unidentified A56	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A57	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A5C	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A60	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A62	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A63	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A82A	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A97A	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified A97B	WG	act	-	-	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
unidentified B109A	WG	bac	-	-	-	3	3	0	0	0	0	1	1	3	0	0	1	1
unidentified B109B	WG	bac	-	-	-	3	3	0	0	0	0	3	1	3	0	0	1	1
unidentified B112A	WG	bac	-	-	-	0	2	0	0	0	0	3	0	2	0	0	1	1
unidentified B114A	WG	bac	-	-	-	0	2	0	1	0	0	3	0	3	0	0	1	1
unidentified B115	WG	bac	-	-	-	0	0	1	1	0	0	3	0	3	0	0	1	1
unidentified B120	WG	bac	-	-	-	3	3	0	0	0	0	3	1	3	0	0	1	1
unidentified B14	WG	bac	-	-	-	0	0	0	0	0	0	0	0	0	0	0	1	0
unidentified B144A	WG	bac	-	-	-	0	0	0	1	0	0	0	0	2	0	0	1	1
unidentified B15	WG	bac	-	-	-	1	0	0	0	0	0	0	1	2	0	0	1	1
unidentified B19	WG	bac	-	-	-	3	2	0	0	3	0	1	1	0	0	0	1	1
unidentified B20	WG	bac	-	-	-	1	0	0	1	0	0	0	1	0	0	0	1	0
unidentified B21	WG	bac	-	-	-	0	0	0	0	0	0	1	0	0	0	0	1	1
unidentified B22	WG	bac	-	-	-	0	1	0	0	0	0	1	0	1	0	0	1	1
unidentified B31B	WG	bac	-	-	-	1	1	0	1	0	0	1	1	3	0	0	1	1
unidentified B32	WG	bac	-	-	-	0	1	0	1	0	0	2	1	3	0	0	1	1
unidentified B37	WG	bac	-	-	-	3	2	1	0	0	0	1	1	3	0	0	1	1
unidentified B41B	WG	bac	-	-	-	0	0	0	0	0	0	0	0	0	0	0	1	1
unidentified B42	WG	bac	-	-	-	0	0	0	0	0	0	0	0	3	0	0	1	1
unidentified B43	WG	bac	-	-	-	0	0	0	0	0	0	0	0	0	0	0	1	1
unidentified B44	WG	bac	-	-	-	1	0	0	0	1	0	1	0	0	0	0	1	1
unidentified B46B	WG	bac	-	-	-	1	0	0	0	1	0	0	0	3	0	0	1	1
unidentified B47	WG	bac	-	-	-	0	2	0	1	0	0	1	0	0	0	0	1	1
unidentified B48	WG	bac	-	-	-	0	0	0	1	0	0	1	0	1	0	0	1	1
unidentified B49	WG	bac	-	-	-	0	0	2	1	3	0	1	0	0	0	0	1	1
unidentified B4A	WG	bac	-	-	-	3	3	0	1	1	0	1	1	3	0	0	1	1
unidentified B4B	WG	bac	-	-	-	3	3	0	0	1	0	1	1	3	0	0	1	1
unidentified B4C	WG	bac	-	-	-	3	3	0	0	1	0	2	1	3	0	0	1	1
unidentified B5	WG	bac	-	-	-	2	3	1	3	3	0	1	0	0	0	0	1	1
unidentified B61	WG	bac	-	-	-	0	0	0	0	1	0	0	0	0	0	0	0	1
unidentified B61	WG	bac	-	-	-	0	0	0	0	0	0	1	0	0	0	0	0	1
unidentified B64	WG	bac	-	-	-	0	1	0	0	0	0	0	0	2	0	0	1	1
unidentified B65	WG	bac	-	-	-	0	1	0	0	0	0	0	0	0	0	0	1	1

unidentified B66	WG	bac	-	-	-	0	0	0	0	0	0	1	1	0	0	0	1	1
unidentified B67	WG	bac	-	-	-	2	1	0	3	1	0	0	1	0	0	0	1	0
unidentified B67	WG	bac	-	-	-	0	0	0	0	0	0	0	0	0	0	0	0	0
unidentified B87	WG	bac	-	-	-	3	3	0	1	1	0	1	0	3	0	0	1	1
unidentified B88	WG	bac	-	-	-	0	0	0	1	0	0	1	1	3	0	0	1	1
unidentified B94A	WG	bac	-	-	-	0	1	0	0	0	0	3	0	0	0	0	1	1
unidentified BL22	WG	bac	-	-	-	2	0	0	0	0	0	0	1	1	0	0	1	1
unidentified BL3	WG	bac	-	-	-	1	0	0	2	2	0	0	0	0	0	0	1	1
unidentified BL35	WG	bac	-	-	-	3	2	0	3	2	0	0	1	0	0	1	1	1
unidentified BL36	WG	bac	-	-	-	0	0	0	0	0	0	1	0	1	0	0	1	1
unidentified BL4	WG	bac	-	-	-	0	0	1	2	0	0	0	0	3	0	0	1	1
unidentified BL49	WG	bac	-	-	-	0	0	0	0	1	0	0	0	2	0	1	1	1
unidentified BL8A	WG	bac	-	-	-	0	0	0	0	0	0	0	0	2	0	1	1	1
unidentified BL8B	WG	bac	-	-	-	0	0	0	0	2	0	0	0	2	0	1	1	1
unidentified L21	WG	lev	-	-	-	0	0	0	0	0	0	0	0	1	0	1	1	1
unidentified L23	WG	lev	-	-	-	1	0	0	0	0	0	0	0	1	0	0	1	1
unidentified L28	WG	lev	-	-	-	0	0	0	0	0	0	0	1	2	0	1	1	1
unidentified L32	WG	lev	-	-	-	0	0	0	0	1	0	0	1	2	0	1	1	1
unidentified L34	WG	lev	-	-	-	0	0	0	0	2	0	0	1	2	0	0	1	1
unidentified L4	WG	lev	-	-	-	0	0	0	0	0	0	0	0	0	0	0	1	1
unidentified L4B	WG	lev	-	-	-	0	0	0	0	0	0	0	0	2	0	1	1	1
unidentified L50	WG	lev	-	-	-	2	0	0	0	0	0	0	0	2	0	0	1	1
unidentified L51	WG	lev	-	-	-	0	0	0	0	0	0	0	0	1	0	0	1	1
Nocardiopsis alba A103A	HG	act	MW142091	0.00	231.48	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Oceanobacillus aidingensis B53B	MG and HG	bac	MW142077	925.925	4,022.99	1	1	0	1	3	0	2	0	0	0	0	1	1
***Ochrobactrum ciceri* BL24**	**MG**	**bac**	**MW142132**	**4.12**	**0.00**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**2**	**2**	**0**	**0**	**1**	**1**
Paenibacillus alvei B57	HG	bac	MW142071	0.00	1,149.43	0	0	0	0	2	0	0	1	0	0	0	1	1
Paenibacillus alvei B70	MG and HG	bac	MW142103	4,938.27	231.48	1	0	0	0	0	0	0	0	0	0	0	1	1
Paenibacillus alvei B71B	MG	bac	MW724809	1,152.26	0.00	0	0	0	1	0	0	1	0	0	0	0	0	1
Paenibacillus alvei B79C	MG and HG	bac	MW142107	22,160.49	385.80	0	3	0	0	0	0	1	0	0	0	0	1	1
Paenibacillus alvei B83	HG	bac	MW142148	0.00	694.44	0	0	0	0	0	0	0	0	0	0	0	1	1
Paenibacillus alvei B90A	MG	bac	MW724805	1,111.11	0.00	1	0	0	2	0	0	1	0	0	0	0	1	1
Paenibacillus alvei B90B	MG	bac	MW724805	1,111.11	0.00	1	0	0	2	3	0	0	0	0	0	0	1	1
Paraburkholderia caballeronis B56A	HG	bac	MW142099	0.00	191.57	0	0	0	0	0	0	1	0	0	0	0	1	1
***Pseudomonas aeruginosa* B17**	**WG**	**bac**	**MW142138**	**-**	**-**	**3**	**1**	**1**	**0**	**0**	**0**	**2**	**2**	**3**	**0**	**0**	**1**	**1**
***Pseudomonas citronellolis* B71A**	**MG**	**bac**	**MW724811**	**1,152.26**	**0.00**	**0**	**0**	**0**	**0**	**0**	**0**	**1**	**2**	**3**	**0**	**0**	**1**	**1**
Raoultella ornithinolytica B78A	MG	bac	MW142098	617.28	0.00	0	0	1	3	1	0	1	1	3	0	0	1	1
***Rothia kristinae* BL11**	**WG**	**bac**	**MW142151**	**-**	**-**	**1**	**0**	**0**	**0**	**1**	**0**	**0**	**4**	**0**	**0**	**1**	**1**	**1**
Scheffersomyces stipitis L5A	MG and HG	lev	MW165504	1.52	0.77	0	0	0	0	0	0	0	1	2	0	0	1	1
Scheffersomyces stipitis L5B	MG and HG	lev	MW165505	1.52	0.77	0	0	0	0	0	0	0	0	2	0	0	1	1

Serratia marcescens **B86**	**WG**	**bac**	**MW142106**	**-**	**-**	**3**	**2**	**1**	**0**	**0**	**0**	**1**	**2**	**3**	**0**	**0**	**1**	**1**
Serratia **sp. B30**	**WG**	**bac**	**MW147751**	**-**	**-**	**3**	**3**	**0**	**1**	**0**	**0**	**2**	**2**	**3**	**0**	**0**	**1**	**1**
Spathaspora brasiliensis L18	HG	lev	MW165502	0.00	498.08	1	0	0	0	0	0	0	0	1	0	0	1	1
Spathaspora brasiliensis L1A	MG and HG	lev	MW165500	1,087.97	4,881.63	0	0	0	0	0	0	0	0	1	0	0	1	1
Spathaspora brasiliensis **L1B**	**MG and HG**	**lev**	**MW165500**	**1,087.97**	**4,881.63**	**3**	**0**	**2**	**3**	**3**	**0**	**0**	**4**	**0**	**0**	**0**	**1**	**1**
Spathaspora brasiliensis L25B	MG	lev	MW138109	9.26	0.00	0	0	0	0	0	0	0	0	2	0	0	1	1
Sporosarcina contaminans **B92A**	**MG**	**bac**	**MW142056**	**1,111.11**	**0.00**	**1**	**2**	**1**	**0**	**0**	**0**	**3**	**2**	**3**	**0**	**0**	**1**	**1**
Sporosarcina contaminans B92B	MG	bac	MW724804	1,111.11	0.00	0	0	0	0	0	0	2	0	0	0	0	1	1
Sporosarcina contaminans B93A	MG	bac	MW724807	12,777.78	0.00	0	0	0	0	0	0	1	0	1	0	0	1	1
Sporosarcina contaminans B93B	MG	bac	MW724807	12,777.78	0.00	0	2	0	0	0	0	0	1	0	0	0	1	1
Sporosarcina contaminans B93C	MG	bac	MW724807	12,777.78	0.00	0	1	0	0	0	0	3	1	2	0	0	1	1
Sporosarcina contaminans B98A	HG	bac	MW142063	0.00	2,279.20	1	0	0	1	0	0	3	0	2	0	0	1	1
Streptomyces antibioticus A108	HG	act	MW142090	0.00	462.96	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Streptomyces antibioticus A158	HG	act	MW142095	0.00	76.63	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Streptomyces atratus A123C	MG and HG	act	MW142118	200.62	69.44	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Streptomyces atratus A71A	HG	act	MW142140	0.00	28.49	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Streptomyces atratus A72A	MG and HG	act	MW142139	1.11	28.49	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Streptomyces atratus A79A	MG and HG	act	MW142084	0.56	14.25	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Streptomyces atratus A79B	MG and HG	act	MW142083	0.56	14.25	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Streptomyces costaricanus A94B	MG	act	MW142150	55.56	0.00	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Streptomyces diastaticus A96	MG	act	MW756916	1.11	0.00	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Streptomyces drozdowiczii A118	HG	act	MW142089	0.00	23.15	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Streptomyces flavogriseus A110A	HG	act	MW142116	0.00	231.48	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Streptomyces flavogriseus A161	HG	act	MW142115	0.00	76.63	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Streptomyces flavogriseus A82	MG and HG	act	MW142113	1.67	13.28	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Streptomyces flavogriseus A82	MG and HG	act	MW142114	1.67	13.28	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Streptomyces flavogriseus A83A	MG and HG	act	MW142111	2.22	24.29	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Streptomyces griseofuscus A81	HG	act	MW142082	0.00	1.42	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Streptomyces misionensis A116A	MG and HG	act	MW142128	1,604.94	514.85	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Streptomyces misionensis A149	MG	act	MW142117	30.86	0.00	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Streptomyces misionensis A66B	MG and HG	act	MW142086	77.78	142.59	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Streptomyces misionensis A73	MG and HG	act	MW142092	2.47	129.49	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Streptomyces rochei A104A	MG and HG	act	MW142130	87.54	412.81	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Streptomyces rochei A104B	MG and HG	act	MW142131	87.54	412.81	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Streptomyces rochei A134A	MG	act	MW142052	617.28	0.00	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Streptomyces rochei A148A	MG	act	MW147755	61.73	0.00	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Streptomyces rochei A159	HG	act	MW142094	0.00	38.31	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Streptomyces rochei A70A	HG	act	MW142133	0.00	28.49	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Streptomyces rochei A76A	HG	act	MW142149	0.00	113.96	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Streptomyces rochei A78	HG	act	MW142087	0.00	74.79	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Streptomyces rochei A80	MG and HG	act	MW142101	11.11	1.42	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND

Streptomyces sanglieri A119	HG	act	MW142112	0.00	23.15	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Streptomyces sp. A104C	MG and HG	act	MW142129	87.54	412.81	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Streptomyces sp. A15	MG and HG	act	MW142096	61.73	383.14	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Streptomyces sp. A58	HG	act	MW142093	0.00	766.28	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Streptomyces sp. A74C	MG and HG	act	MW753133	6.67	114.25	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Streptomyces sp. A75	HG	act	MW142085	0.00	28.49	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Streptomyces sp. A85	HG	act	MW142081	0.00	0.28	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Streptomyces sp. A86	HG	act	MW147753	0	0.28	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Streptomyces thermosacchari A102	HG	act	MW142119	0.00	231.48	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Xanthomonas maliensis B6A	WG	bac	MW142058	-	-	0	0	0	1	0	0	2	0	0	0	0	1	1
***Xanthomonas maliensis* B6B**	**WG**	**bac**	**MW142058**	**-**	**-**	**0**	**0**	**1**	**0**	**0**	**0**	**2**	**4**	**3**	**0**	**0**	**1**	**1**
Xilanimicrobium sp. A67A	HG	act	MW147754	0	284.9	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Xylanimicrobium sp. B58A	HG	act	MW142125	0.00	11,494.25	0	2	0	0	0	0	1	0	1	0	0	1	1
Xylanimicrobium sp. B58B	HG	act	MW142124	0.00	11,494.25	0	0	0	0	0	0	0	0	1	0	0	1	1
Xylanimonas allomyrinae B51A	HG	act	MW142122	0.00	5,172.41	0	0	0	0	0	0	3	0	0	0	0	0	0
Xylanimonas allomyrinae B51B	HG	act	MW142122	0.00	5,172.41	0	0	0	0	0	0	1	0	2	0	0	1	1
Xylanimonas allomyrinae B52	HG	act	MW142121	0.00	13,409.96	0	0	0	0	0	0	1	0	0	0	0	1	1
Xylanimonas allomyrinae B54	HG	act	MW142123	0.00	3,831.42	1	2	0	1	0	0	2	0	0	0	0	1	1
Xylanimonas allomyrinae B55A	MG and HG	act	MW142126	1,028.81	2,681.99	0	0	0	0	0	0	0	0	1	0	0	1	1
Xylanimonas allomyrinae B55B	MG and HG	act	MW142108	1,028.81	2,681.99	0	0	0	0	0	0	0	0	0	0	1	1	1
Xylanimonas allomyrinae B55C	MG and HG	act	MW142127	1,028.81	2,681.99	0	0	0	0	0	0	0	0	0	0	0	1	1
Xylanimonas allomyrinae B59	HG	act	MW142110	0.00	383.14	0	0	0	0	0	0	1	0	0	0	0	1	1
Xylanimonas allomyrinae B80	MG	act	MW142120	308.64	0.00	1	0	0	0	0	0	2	0	2	0	0	1	1

Isolates in bold were selected on the first pathogen antagonism screening. Grp: Group. GenBank: Accession number on GenBank. Prt: protease. Est: Esterase. Cel: Cellulase. Pec: Pectinase. Aml: Amylase. Lgn: Ligninase. PO_4: Phosphate solubilisation. Inib: Pathogen Inhibition. ND: Not determined (isolate not subject to tests)

Table S2. Relative Frequency (%) of cultivable bacteria on gut compartiments of *Pelidnota luridipes*

Species	Class	Total	Midgut	Hindgut
Galactobacter valiniphilus	Actinobacteria	0.1047	0.3576	0
Isoptericola dokdonensis	Actinobacteria	0.018	0	0.0255
Kitasatospora sp.	Actinobacteria	0.0582	0.1987	0
Luteimicrobium album	Actinobacteria	0.1444	0	0.2042
Microbacterium natoriense	Actinobacteria	0.1629	0.5563	0
Mycobacterium porcinum	Actinobacteria	0.0044	0	0.0062
Nocardiopsis alba	Actinobacteria	0.0218	0	0.0308
Streptomyces antibioticus	Actinobacteria	0.0508	0	0.0719
Streptomyces atratus	Actinobacteria	0.0237	0.0312	0.0206
Streptomyces diastaticus	Actinobacteria	0.0001	0.0004	0
Streptomyces drozdowiczii	Actinobacteria	0.0022	0	0.0031
Streptomyces flavogriseus	Actinobacteria	0.03	0.0018	0.0417
Streptomyces griseofuscus	Actinobacteria	0.0001	0	0.0002
Streptomyces misionensis	Actinobacteria	0.1664	0.2742	0.1217
Streptomyces rochei	Actinobacteria	0.1957	0.3103	0.1483
Streptomyces sanglieri	Actinobacteria	0.0022	0	0.0031
Streptomyces sp. *1*	Actinobacteria	0.0221	0.0021	0.0304
Streptomyces sp. *3*	Actinobacteria	0	0	0
Streptomyces sp. *4*	Actinobacteria	0	0	0
Streptomyces sp. *6*	Actinobacteria	0.0722	0	0.1021
Streptomyces sp.*5*	Actinobacteria	0.0419	0.0199	0.051
Streptomyces thermosacchari	Actinobacteria	0.0218	0	0.0308
Xylanimicrobium sp.	Actinobacteria	2.1928	0	3.1003
Xylanimonas allomyrinae	Actinobacteria	3.7132	1.0928	4.7977
Ochrobactrum ciceri	Alphaproteobacteria	0.0004	0.0013	0
Bacillus cereus	Bacilli	0.0654	0	0.0925
Bacillus paranthracis	Bacilli	0.0509	0.0993	0.0308
Bacillus subtilis	Bacilli	0.0047	0.0123	0.0015
Bacillus thuringiensis	Bacilli	0.1163	0.3974	0
Cytobacillus kochii	Bacilli	0.1454	0.4967	0
Enterococcus hirae	Bacilli	3.9481	0.0993	5.541
Enterococcus termitis	Bacilli	10.4692	35.7644	0
Lactococcus sp.	Bacilli	5.4073	0.8146	7.3081
Lactococcus taiwanensis	Bacilli	0.0872	0.298	0
Lysinibacillus fusiformis	Bacilli	0.0436	0	0.0617
Lysinibacillus xylanilyticus	Bacilli	0.0436	0	0.0617
Oceanobacillus aidingensis	Bacilli	0.3109	0.1987	0.3573
Paenibacillus alvei	Bacilli	0.5135	1.0862	0.2765
Sporosarcina contaminans	Bacilli	2.832	8.9411	0.3036
Alcaligenes faecalis	Betaproteobacteria	0.0003	0.001	0
Burkholderia cenocepacia	Betaproteobacteria	0.0582	0.1987	0
Paraburkholderia caballeronis	Betaproteobacteria	0.018	0	0.0255
Chryseobacterium gwangjuense	Flavobacteria	0.1745	0.5961	0
Citrobacter amalonaticus	Gammaproteobacteria	66.3674	46.4142	74.6257
Citrobacter koseri	Gammaproteobacteria	0.2333	0	0.3298
Citrobacter sp.	Gammaproteobacteria	1.5522	0	2.1947
Klebsiella michiganensis	Gammaproteobacteria	0.1086	0.3709	0
Kosakonia cowanii	Gammaproteobacteria	0.2326	0.7948	0
Pseudomonas citronellolis	Gammaproteobacteria	0.1086	0.3709	0

Raoultella ornithinolytica	Gammaproteobacteria	0.0582	0.1987	0

Tabela S3. Relative Frequency (%) of cultivable yeasts on gut compartiments of *Pelidnota luridipes*

Species	Total	Midgut	Hindgut
Apiotrichum siamense	0.27	0.15	0.31
Candida alai	13.17	8.29	15.24
Candida jeffriesii	0.01	0.01	0.01
Candida sp.	13.17	8.29	15.24
Meyerozyma guilliermondii	2.46	8.29	0
Scheffersomyces stipitis	21.22	45.64	10.89
Spathaspora brasiliensis	49.69	29.34	58.31

Tabela S4. Absolute and Relative abundance of bacterial OTUs on gut compartiments of *P. luridipes*

#OTU	Absolute abundance									Relative abundance			Classification					
	P6A	P7A	P8A	P6R	P7R	P8R	Total	Midgut	Hindgut	Total	Midgut	Hindgut	Domain	Phylum	Class	Order	Family	Genus
Otu1	12951	176	4921	28	434	120	18630.0000	18048.0000	582.0000	10.4690	20.2839	0.6541	*Bacteria*	*Firmicutes*	U	U	U	U
Otu10	412	253	10	902	301	1021	2899.0000	675.0000	2224.0000	1.6291	0.7586	2.4995	*Bacteria*	*Bacteroidetes*	*Bacteroidia*	U	U	U
Otu100	2	14	0	35	1	95	147.0000	16.0000	131.0000	0.0826	0.0180	0.1472	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1000	0	1	0	12	1	9	23.0000	1.0000	22.0000	0.0129	0.0011	0.0247	*Bacteria*	U	U	U	U	U
Otu1001	0	0	0	0	10	7	17.0000	0.0000	17.0000	0.0096	0.0000	0.0191	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1002	0	4	0	3	0	7	14.0000	4.0000	10.0000	0.0079	0.0045	0.0112	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1003	4	4	0	1	2	0	11.0000	8.0000	3.0000	0.0062	0.0090	0.0034	*Bacteria*	U	U	U	U	U
Otu1004	1	0	1	1	5	0	8.0000	2.0000	6.0000	0.0045	0.0022	0.0067	*Bacteria*	*Planctomycetes*	*Planctomycetia*	*Planctomycetales*	*Planctomycetaceae*	*Aquisphaera*
Otu1005	0	4	0	3	0	4	11.0000	4.0000	7.0000	0.0062	0.0045	0.0079	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1006	0	0	3	0	6	0	9.0000	3.0000	6.0000	0.0051	0.0034	0.0067	*Bacteria*	*Actinobacteria*	*Actinobacteria*	*Actinomycetales*	*Microbacteriaceae*	*Agromyces*
Otu1007	1	1	0	3	3	3	11.0000	2.0000	9.0000	0.0062	0.0022	0.0101	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1008	0	0	0	0	7	0	7.0000	0.0000	7.0000	0.0039	0.0000	0.0079	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	*Rhizobiales*	U	U
Otu1009	1	0	0	5	0	0	6.0000	1.0000	5.0000	0.0034	0.0011	0.0056	*Bacteria*	*Firmicutes*	U	U	U	U
Otu101	5	57	1	88	1	61	213.0000	63.0000	150.0000	0.1197	0.0708	0.1686	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1010	0	0	0	1	0	2	3.0000	0.0000	3.0000	0.0017	0.0000	0.0034	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1011	6	0	6	0	23	2	37.0000	12.0000	25.0000	0.0208	0.0135	0.0281	*Bacteria*	*Actinobacteria*	*Actinobacteria*	U	U	U
Otu1012	0	0	0	8	0	10	18.0000	0.0000	18.0000	0.0101	0.0000	0.0202	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1013	0	0	0	13	0	8	21.0000	0.0000	21.0000	0.0118	0.0000	0.0236	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1014	0	0	1	0	2	0	3.0000	1.0000	2.0000	0.0017	0.0011	0.0022	*Bacteria*	*Actinobacteria*	*Actinobacteria*	U	U	U
Otu1015	0	1	0	4	0	6	11.0000	1.0000	10.0000	0.0062	0.0011	0.0112	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1016	1	4	0	1	1	8	15.0000	5.0000	10.0000	0.0084	0.0056	0.0112	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1017	4	0	0	0	2	1	7.0000	4.0000	3.0000	0.0039	0.0045	0.0034	*Bacteria*	U	U	U	U	U
Otu1018	2	7	0	2	0	4	15.0000	9.0000	6.0000	0.0084	0.0101	0.0067	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1019	0	3	0	2	3	2	10.0000	3.0000	7.0000	0.0056	0.0034	0.0079	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu102	9	53	0	45	2	24	133.0000	62.0000	71.0000	0.0747	0.0697	0.0798	*Bacteria*	U	U	U	U	U
Otu1020	0	0	0	0	13	1	14.0000	0.0000	14.0000	0.0079	0.0000	0.0157	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1021	0	2	0	0	0	4	6.0000	2.0000	4.0000	0.0034	0.0022	0.0045	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1022	0	0	0	6	10	3	19.0000	0.0000	19.0000	0.0107	0.0000	0.0214	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1023	1	5	0	0	0	2	8.0000	6.0000	2.0000	0.0045	0.0067	0.0022	*Bacteria*	U	U	U	U	U
Otu1024	2	0	0	12	10	1	25.0000	2.0000	23.0000	0.0140	0.0022	0.0258	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1025	0	0	0	9	1	1	11.0000	0.0000	11.0000	0.0062	0.0000	0.0124	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1026	2	0	0	0	3	1	6.0000	2.0000	4.0000	0.0034	0.0022	0.0045	*Bacteria*	*Proteobacteria*	*Gammaproteobacteria*	U	U	U
Otu1027	0	0	0	10	1	0	11.0000	0.0000	11.0000	0.0062	0.0000	0.0124	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1028	0	3	0	0	2	6	11.0000	3.0000	8.0000	0.0062	0.0034	0.0090	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1029	0	3	0	2	0	3	8.0000	3.0000	5.0000	0.0045	0.0034	0.0056	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U

Otu103	9	34	0	25	1	111	180.0000	43.0000	137.0000	0.1011	0.0483	0.1540	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1030	0	0	0	1	6	1	8.0000	0.0000	8.0000	0.0045	0.0000	0.0090	*Bacteria*	U	U	U	U	U
Otu1031	10	0	0	0	1	0	11.0000	10.0000	1.0000	0.0062	0.0112	0.0011	*Bacteria*	*Proteobacteria*	*Gammaproteobacteria*	U	U	U
Otu1032	0	4	0	0	0	4	8.0000	4.0000	4.0000	0.0045	0.0045	0.0045	*Bacteria*	U	U	U	U	U
Otu1033	0	2	0	0	0	4	6.0000	2.0000	4.0000	0.0034	0.0022	0.0045	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1034	0	0	0	27	9	39	75.0000	0.0000	75.0000	0.0421	0.0000	0.0843	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1035	0	2	0	2	0	5	9.0000	2.0000	7.0000	0.0051	0.0022	0.0079	*Bacteria*	U	U	U	U	U
Otu1036	0	4	0	6	1	2	13.0000	4.0000	9.0000	0.0073	0.0045	0.0101	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1037	0	4	0	11	0	6	21.0000	4.0000	17.0000	0.0118	0.0045	0.0191	*Bacteria*	*Proteobacteria*	*Deltaproteobacteria*	*Desulfovibrionales*	U	U
Otu1038	1	1	0	9	0	4	15.0000	2.0000	13.0000	0.0084	0.0022	0.0146	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1039	6	0	0	0	3	0	9.0000	6.0000	3.0000	0.0051	0.0067	0.0034	*Bacteria*	*Proteobacteria*	*Deltaproteobacteria*	*Myxococcales*	U	U
Otu104	40	98	0	3	12	20	173.0000	138.0000	35.0000	0.0972	0.1551	0.0393	*Bacteria*	*Candidatus_Saccharibacteria bacteria*	*Saccharibacteria_genera_incertae_sedis*	U	U	U
Otu1040	1	10	0	0	0	0	11.0000	11.0000	0.0000	0.0062	0.0124	0.0000	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1041	0	1	0	1	2	5	9.0000	1.0000	8.0000	0.0051	0.0011	0.0090	*Bacteria*	U	U	U	U	U
Otu1042	0	0	0	1	2	1	4.0000	0.0000	4.0000	0.0022	0.0000	0.0045	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	
Otu1043	0	0	0	0	9	0	9.0000	0.0000	9.0000	0.0051	0.0000	0.0101	*Bacteria*	*Proteobacteria*	*Gammaproteobacteria*	U	U	U
Otu1044	0	0	0	0	15	2	17.0000	0.0000	17.0000	0.0096	0.0000	0.0191	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1045	0	4	0	1	0	5	10.0000	4.0000	6.0000	0.0056	0.0045	0.0067	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1046	0	0	0	20	0	0	20.0000	0.0000	20.0000	0.0112	0.0000	0.0225	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1047	0	0	1	0	4	1	6.0000	1.0000	5.0000	0.0034	0.0011	0.0056	*Bacteria*	*Actinobacteria*	*Actinobacteria*	*Actinomycetales*	*Microbacteriaceae*	U
Otu1048	2	0	5	0	10	1	18.0000	7.0000	11.0000	0.0101	0.0079	0.0124	*Bacteria*	*Actinobacteria*	*Actinobacteria*	*Actinomycetales*	U	U
Otu1049	1	3	0	2	1	6	13.0000	4.0000	9.0000	0.0073	0.0045	0.0101	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu105	5	78	0	19	1	71	174.0000	83.0000	91.0000	0.0978	0.0933	0.1023	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1050	2	1	0	1	0	5	9.0000	3.0000	6.0000	0.0051	0.0034	0.0067	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1051	2	3	0	2	0	5	12.0000	5.0000	7.0000	0.0067	0.0056	0.0079	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1052	7	0	2	0	3	0	12.0000	9.0000	3.0000	0.0067	0.0101	0.0034	*Bacteria*	*Candidatus_Saccharibacteria bacteria*	*Saccharibacteria_genera_incertae_sedis*	U	U	U
Otu1053	0	0	0	0	0	14	14.0000	0.0000	14.0000	0.0079	0.0000	0.0157	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1054	2	0	0	7	0	0	9.0000	2.0000	7.0000	0.0051	0.0022	0.0079	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1055	2	2	0	1	0	0	5.0000	4.0000	1.0000	0.0028	0.0045	0.0011	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1056	3	0	0	0	0	0	3.0000	3.0000	0.0000	0.0017	0.0034	0.0000	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	*Rhodospirillales*	*Rhodospirillaceae*	U
Otu1057	0	2	0	3	5	2	12.0000	2.0000	10.0000	0.0067	0.0022	0.0112	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1058	1	4	0	0	0	1	6.0000	5.0000	1.0000	0.0034	0.0056	0.0011	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1059	0	3	0	1	1	2	7.0000	3.0000	4.0000	0.0039	0.0034	0.0045	*Bacteria*	U	U	U	U	U
Otu106	6	60	0	75	3	61	205.0000	66.0000	139.0000	0.1152	0.0742	0.1562	*Bacteria*	*Proteobacteria*	*Deltaproteobacteria*	*Desulfovibrionales*	*Desulfovibrionaceae*	*Desulfovibrio*
Otu1060	0	0	0	0	8	4	12.0000	0.0000	12.0000	0.0067	0.0000	0.0135	*Bacteria*	U	U	U	U	U

Otu1061	0	0	0	5	8	1	14.0000	0.0000	14.0000	0.0079	0.0000	0.0157	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1062	0	2	0	3	0	4	9.0000	2.0000	7.0000	0.0051	0.0022	0.0079	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1063	0	0	0	8	2	0	10.0000	0.0000	10.0000	0.0056	0.0000	0.0112	*Bacteria*	U	U	U	U	U
Otu1064	0	0	0	0	12	0	12.0000	0.0000	12.0000	0.0067	0.0000	0.0135	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	*Rhizobiales*	*Bradyrhizobiaceae*	*Bosea*
Otu1065	1	1	0	6	0	2	10.0000	2.0000	8.0000	0.0056	0.0022	0.0090	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1066	1	1	0	1	0	1	4.0000	2.0000	2.0000	0.0022	0.0022	0.0022	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu1067	5	0	0	0	4	0	9.0000	5.0000	4.0000	0.0051	0.0056	0.0045	*Bacteria*	*Armatimonadetes*	U	U	U	U
Otu1068	0	5	0	0	0	0	5.0000	5.0000	0.0000	0.0028	0.0056	0.0000	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1069	0	0	0	7	3	0	10.0000	0.0000	10.0000	0.0056	0.0000	0.0112	*Bacteria*	U	U	U	U	U
Otu107	5	114	0	32	1	17	169.0000	119.0000	50.0000	0.0950	0.1337	0.0562	*Bacteria*	*Proteobacteria*	*Deltaproteobacteria*	U	U	U
Otu1070	0	1	0	0	0	4	5.0000	1.0000	4.0000	0.0028	0.0011	0.0045	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1071	1	0	0	6	3	2	12.0000	1.0000	11.0000	0.0067	0.0011	0.0124	*Bacteria*	U	U	U	U	U
Otu1072	1	6	0	0	2	0	9.0000	7.0000	2.0000	0.0051	0.0079	0.0022	*Bacteria*	U	U	U	U	U
Otu1073	0	4	0	2	0	2	8.0000	4.0000	4.0000	0.0045	0.0045	0.0045	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1074	0	2	0	5	1	3	11.0000	2.0000	9.0000	0.0062	0.0022	0.0101	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1075	2	2	0	1	4	1	10.0000	4.0000	6.0000	0.0056	0.0045	0.0067	*Bacteria*	U	U	U	U	U
Otu1076	0	2	0	0	0	0	2.0000	2.0000	0.0000	0.0011	0.0022	0.0000	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1077	0	0	0	18	6	2	26.0000	0.0000	26.0000	0.0146	0.0000	0.0292	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1078	0	0	0	2	5	29	36.0000	0.0000	36.0000	0.0202	0.0000	0.0405	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1079	2	6	0	0	0	0	8.0000	8.0000	0.0000	0.0045	0.0090	0.0000	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu108	13	128	0	25	14	11	191.0000	141.0000	50.0000	0.1073	0.1585	0.0562	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1080	1	0	0	7	0	11	19.0000	1.0000	18.0000	0.0107	0.0011	0.0202	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1081	8	0	0	0	0	0	8.0000	8.0000	0.0000	0.0045	0.0090	0.0000	*Bacteria*	*Proteobacteria*	*Betaproteobacteria*	*Burkholderiales*	*Oxalobacteraceae*	U
Otu1082	0	0	0	2	2	2	6.0000	0.0000	6.0000	0.0034	0.0000	0.0067	*Bacteria*	U	U	U	U	U
Otu1083	0	2	0	2	0	4	8.0000	2.0000	6.0000	0.0045	0.0022	0.0067	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1084	1	3	0	1	1	4	10.0000	4.0000	6.0000	0.0056	0.0045	0.0067	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu1085	0	0	0	0	7	5	12.0000	0.0000	12.0000	0.0067	0.0000	0.0135	*Bacteria*	U	U	U	U	U
Otu1086	0	4	0	4	2	4	14.0000	4.0000	10.0000	0.0079	0.0045	0.0112	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1087	0	5	0	1	0	4	10.0000	5.0000	5.0000	0.0056	0.0056	0.0056	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1088	0	0	0	0	2	1	3.0000	0.0000	3.0000	0.0017	0.0000	0.0034	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1089	0	0	0	2	2	6	10.0000	0.0000	10.0000	0.0056	0.0000	0.0112	*Bacteria*	U	U	U	U	U
Otu109	1	125	0	26	0	2	154.0000	126.0000	28.0000	0.0865	0.1416	0.0315	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1090	0	0	1	0	7	0	8.0000	1.0000	7.0000	0.0045	0.0011	0.0079	*Bacteria*	*Bacteroidetes*	*Flavobacteriia*	*Flavobacteriales*	*Flavobacteriaceae*	U
Otu1091	0	0	0	3	0	0	3.0000	0.0000	3.0000	0.0017	0.0000	0.0034	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1092	0	0	0	1	0	9	10.0000	0.0000	10.0000	0.0056	0.0000	0.0112	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1093	0	1	0	1	6	0	8.0000	1.0000	7.0000	0.0045	0.0011	0.0079	*Bacteria*	U	U	U	U	U
Otu1094	7	0	0	0	1	0	8.0000	7.0000	1.0000	0.0045	0.0079	0.0011	*Bacteria*	*Proteobacteria*	*Betaproteobacteria*	*Burkholderiales*	*Burkholderiaceae*	*Burkholderia*
Otu1095	6	3	0	7	1	3	20.0000	9.0000	11.0000	0.0112	0.0101	0.0124	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1096	0	1	0	4	2	2	9.0000	1.0000	8.0000	0.0051	0.0011	0.0090	*Bacteria*	U	U	U	U	U
Otu1097	0	1	0	1	1	0	3.0000	1.0000	2.0000	0.0017	0.0011	0.0022	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu1098	0	1	0	1	0	2	4.0000	1.0000	3.0000	0.0022	0.0011	0.0034	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U

Otu1099	1	2	0	4	1	0	8.0000	3.0000	5.0000	0.0045	0.0034	0.0056	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu11	418	598	5	2226	434	190	3871.0000	1021.0000	2850.0000	2.1753	1.1475	3.2031	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu110	8	75	0	24	0	23	130.0000	83.0000	47.0000	0.0731	0.0933	0.0528	*Bacteria*	U	U	U	U	U
Otu1100	0	0	0	1	1	1	3.0000	0.0000	3.0000	0.0017	0.0000	0.0034	*Bacteria*	U	U	U	U	U
Otu1101	0	0	0	0	13	7	20.0000	0.0000	20.0000	0.0112	0.0000	0.0225	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1102	2	1	0	0	3	0	6.0000	3.0000	3.0000	0.0034	0.0034	0.0034	*Bacteria*	*Actinobacteria*	*Actinobacteria*	*Gaiellales*	*Gaiellaceae*	U
Otu1103	2	0	0	0	14	0	16.0000	2.0000	14.0000	0.0090	0.0022	0.0157	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	*Rhizobiales*	U	U
Otu1104	0	0	0	0	4	2	6.0000	0.0000	6.0000	0.0034	0.0000	0.0067	*Bacteria*	*Actinobacteria*	*Actinobacteria*	*Actinomycetales*	U	U
Otu1105	0	0	0	7	1	0	8.0000	0.0000	8.0000	0.0045	0.0000	0.0090	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1106	0	3	0	2	1	1	7.0000	3.0000	4.0000	0.0039	0.0034	0.0045	*Bacteria*	U	U	U	U	U
Otu1107	0	2	0	1	1	1	5.0000	2.0000	3.0000	0.0028	0.0022	0.0034	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1108	0	0	0	1	6	4	11.0000	0.0000	11.0000	0.0062	0.0000	0.0124	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1109	2	0	0	0	14	0	16.0000	2.0000	14.0000	0.0090	0.0022	0.0157	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	*Rhizobiales*	*Xanthobacteraceae*	*Labrys*
Otu111	8	80	0	40	0	46	174.0000	88.0000	86.0000	0.0978	0.0989	0.0967	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu1110	0	2	0	2	5	0	9.0000	2.0000	7.0000	0.0051	0.0022	0.0079	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1111	0	0	0	0	1	1	2.0000	0.0000	2.0000	0.0011	0.0000	0.0022	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1112	0	0	0	5	2	5	12.0000	0.0000	12.0000	0.0067	0.0000	0.0135	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*		
Otu1113	3	0	0	0	0	0	3.0000	3.0000	0.0000	0.0017	0.0034	0.0000	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	*Rhodospirillales*	*Rhodospirillaceae*	U
Otu1114	1	2	0	0	0	3	6.0000	3.0000	3.0000	0.0034	0.0034	0.0034	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1115	0	1	0	6	0	2	9.0000	1.0000	8.0000	0.0051	0.0011	0.0090	*Bacteria*	U	U	U	U	U
Otu1116	0	0	0	0	0	5	5.0000	0.0000	5.0000	0.0028	0.0000	0.0056	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu1117	0	0	0	0	3	3	6.0000	0.0000	6.0000	0.0034	0.0000	0.0067	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1118	2	8	0	0	4	6	20.0000	10.0000	10.0000	0.0112	0.0112	0.0112	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1119	0	1	0	2	0	5	8.0000	1.0000	7.0000	0.0045	0.0011	0.0079	*Bacteria*	*Firmicutes*	U	U	U	U
Otu112	0	0	0	194	88	34	316.0000	0.0000	316.0000	0.1776	0.0000	0.3551	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1120	0	0	0	0	2	3	5.0000	0.0000	5.0000	0.0028	0.0000	0.0056	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu1121	0	0	0	3	0	0	3.0000	0.0000	3.0000	0.0017	0.0000	0.0034	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1122	0	0	0	0	1	4	5.0000	0.0000	5.0000	0.0028	0.0000	0.0056	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1123	0	0	0	0	3	0	3.0000	0.0000	3.0000	0.0017	0.0000	0.0034	*Bacteria*	U	U	U	U	U
Otu1124	2	0	0	0	1	0	3.0000	2.0000	1.0000	0.0017	0.0022	0.0011	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	U	U	U
Otu1125	0	0	3	0	0	0	3.0000	3.0000	0.0000	0.0017	0.0034	0.0000	*Bacteria*	*Proteobacteria*	*Deltaproteobacteria*	*Myxococcales*	U	U
Otu1126	0	3	0	4	5	3	15.0000	3.0000	12.0000	0.0084	0.0034	0.0135	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1127	0	1	0	1	4	0	6.0000	1.0000	5.0000	0.0034	0.0011	0.0056	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1128	0	0	0	2	1	4	7.0000	0.0000	7.0000	0.0039	0.0000	0.0079	*Bacteria*	U	U	U	U	U
Otu1129	2	0	0	0	1	0	3.0000	2.0000	1.0000	0.0017	0.0022	0.0011	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	*Alphaproteobacteria_incertae_sedis*	U	U
Otu113	0	0	0	51	78	14	143.0000	0.0000	143.0000	0.0804	0.0000	0.1607	*Bacteria*	U	U	U	U	U

Otu1130	1	6	0	2	2	0	11.0000	7.0000	4.0000	0.0062	0.0079	0.0045	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1131	0	1	0	5	0	1	7.0000	1.0000	6.0000	0.0039	0.0011	0.0067	*Bacteria*	U	U	U	U	U
Otu1132	0	0	0	4	2	2	8.0000	0.0000	8.0000	0.0045	0.0000	0.0090	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1133	0	0	0	1	2	1	4.0000	0.0000	4.0000	0.0022	0.0000	0.0045	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu1134	0	0	3	0	0	0	3.0000	3.0000	0.0000	0.0017	0.0034	0.0000	*Bacteria*	*Actinobacteria*	U	U	U	U
Otu1135	1	7	0	0	0	0	8.0000	8.0000	0.0000	0.0045	0.0090	0.0000	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1136	0	0	0	2	0	5	7.0000	0.0000	7.0000	0.0039	0.0000	0.0079	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1137	0	1	0	2	0	1	4.0000	1.0000	3.0000	0.0022	0.0011	0.0034	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1138	1	0	0	4	0	1	6.0000	1.0000	5.0000	0.0034	0.0011	0.0056	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1139	0	1	0	2	0	0	3.0000	1.0000	2.0000	0.0017	0.0011	0.0022	*Bacteria*	*Firmicutes*	U	U	U	U
Otu114	0	0	170	5	0	0	175.0000	170.0000	5.0000	0.0983	0.1911	0.0056	*Bacteria*	*Firmicutes*	*Erysipelotrichia*	*Erysipelotrichales*	*Erysipelotrichaceae*	U
Otu1140	0	0	0	2	0	0	2.0000	0.0000	2.0000	0.0011	0.0000	0.0022	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1141	0	0	0	2	0	1	3.0000	0.0000	3.0000	0.0017	0.0000	0.0034	*Bacteria*	U	U	U	U	U
Otu1142	0	2	0	1	0	1	4.0000	2.0000	2.0000	0.0022	0.0022	0.0022	*Bacteria*	U	U	U	U	U
Otu1143	0	0	0	5	1	2	8.0000	0.0000	8.0000	0.0045	0.0000	0.0090	*Bacteria*	U	U	U	U	U
Otu1144	1	2	0	1	2	6	12.0000	3.0000	9.0000	0.0067	0.0034	0.0101	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	*Ruminococcus*
Otu1145	0	0	0	1	2	1	4.0000	0.0000	4.0000	0.0022	0.0000	0.0045	*Bacteria*	*Firmicutes*	*Erysipelotrichia*	*Erysipelotrichales*	*Erysipelotrichaceae*	*Erysipelothrix*
Otu1146	0	0	0	0	0	2	2.0000	0.0000	2.0000	0.0011	0.0000	0.0022	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1147	0	0	0	0	0	16	16.0000	0.0000	16.0000	0.0090	0.0000	0.0180	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu1148	1	0	0	0	3	0	4.0000	1.0000	3.0000	0.0022	0.0011	0.0034	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	U	U	U
Otu1149	2	1	0	3	1	7	14.0000	3.0000	11.0000	0.0079	0.0034	0.0124	*Bacteria*	*Firmicutes*	U	U	U	U
Otu115	121	1	0	0	54	0	176.0000	122.0000	54.0000	0.0989	0.1371	0.0607	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	*Sphingomonadales*	*Sphingomonadaceae*	*Sphingomonas*
Otu1150	0	1	0	2	0	1	4.0000	1.0000	3.0000	0.0022	0.0011	0.0034	*Bacteria*	*Firmicutes*	*Negativicutes*	U	U	U
Otu1151	0	4	0	0	1	2	7.0000	4.0000	3.0000	0.0039	0.0045	0.0034	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1152	0	1	0	1	4	3	9.0000	1.0000	8.0000	0.0051	0.0011	0.0090	*Bacteria*	U	U	U	U	U
Otu1153	0	0	0	0	3	0	3.0000	0.0000	3.0000	0.0017	0.0000	0.0034	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	*Rhizobiales*	U	U
Otu1154	0	0	0	0	7	0	7.0000	0.0000	7.0000	0.0039	0.0000	0.0079	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1155	0	0	0	2	3	1	6.0000	0.0000	6.0000	0.0034	0.0000	0.0067	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1156	2	7	0	0	0	0	9.0000	9.0000	0.0000	0.0051	0.0101	0.0000	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1157	0	0	0	0	2	0	2.0000	0.0000	2.0000	0.0011	0.0000	0.0022	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	*Sphingomonadales*	*Sphingomonadaceae*	*Sphingobium*
Otu1158	0	0	0	0	2	0	2.0000	0.0000	2.0000	0.0011	0.0000	0.0022	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	*Rhodospirillales*	U	U
Otu1159	0	0	1	0	3	0	4.0000	1.0000	3.0000	0.0022	0.0011	0.0034	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	*Rhizobiales*	U	U
Otu116	0	20	0	84	3	47	154.0000	20.0000	134.0000	0.0865	0.0225	0.1506	*Bacteria*	*Proteobacteria*	*Deltaproteobacteria*	*Desulfovibrionales*	*Desulfovibrionaceae*	*Desulfovibrio*
Otu1160	0	0	0	14	0	3	17.0000	0.0000	17.0000	0.0096	0.0000	0.0191	*Bacteria*	U	U	U	U	U
Otu1161	5	0	0	0	6	0	11.0000	5.0000	6.0000	0.0062	0.0056	0.0067	*Bacteria*	U	U	U	U	U
Otu1162	0	1	5	0	0	0	6.0000	6.0000	0.0000	0.0034	0.0067	0.0000	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Lachnospiraceae*	*Clostridium_XlVa*
Otu1164	15	26	0	0	16	8	65.0000	41.0000	24.0000	0.0365	0.0461	0.0270	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1165	0	3	0	0	0	2	5.0000	3.0000	2.0000	0.0028	0.0034	0.0022	*Bacteria*	U	U	U	U	U
Otu1166	2	0	0	0	0	0	2.0000	2.0000	0.0000	0.0011	0.0022	0.0000	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Peptostreptococcaceae*	U

Otu1167	0	0	0	11	4	1	16.0000	0.0000	16.0000	0.0090	0.0000	0.0180	*Bacteria*	U	U	U	U	U
Otu1168	0	0	0	3	0	0	3.0000	0.0000	3.0000	0.0017	0.0000	0.0034	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1169	1	2	0	0	0	0	3.0000	3.0000	0.0000	0.0017	0.0034	0.0000	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu117	11	106	0	42	0	19	178.0000	117.0000	61.0000	0.1000	0.1315	0.0686	*Bacteria*	U	U	U	U	U
Otu1170	2	1	1	3	2	0	9.0000	4.0000	5.0000	0.0051	0.0045	0.0056	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu1171	0	0	0	0	2	1	3.0000	0.0000	3.0000	0.0017	0.0000	0.0034	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	*Rhodospirillales*	*Acetobacteraceae*	U
Otu1172	4	0	1	0	2	0	7.0000	5.0000	2.0000	0.0039	0.0056	0.0022	*Bacteria*	*Acidobacteria*	*Acidobacteria_Gp10*	*Gp10*	U	U
Otu1173	0	0	0	2	0	0	2.0000	0.0000	2.0000	0.0011	0.0000	0.0022	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1174	1	0	0	0	6	0	7.0000	1.0000	6.0000	0.0039	0.0011	0.0067	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1175	0	1	0	0	1	0	2.0000	1.0000	1.0000	0.0011	0.0011	0.0011	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu1176	1	0	0	5	1	1	8.0000	1.0000	7.0000	0.0045	0.0011	0.0079	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu1177	5	0	0	0	3	0	8.0000	5.0000	3.0000	0.0045	0.0056	0.0034	*Bacteria*	*Bacteroidetes*	*Cytophagia*	*Cytophagales*	U	U
Otu1178	1	3	0	0	0	2	6.0000	4.0000	2.0000	0.0034	0.0045	0.0022	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1179	6	0	0	0	7	0	13.0000	6.0000	7.0000	0.0073	0.0067	0.0079	*Bacteria*	*Actinobacteria*	*Actinobacteria*	*Actinomycetales*	*Nocardioidaceae*	*Nocardioides*
Otu118	1	7	0	27	2	122	159.0000	8.0000	151.0000	0.0893	0.0090	0.1697	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1180	1	5	0	0	0	1	7.0000	6.0000	1.0000	0.0039	0.0067	0.0011	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1181	0	0	0	1	0	5	6.0000	0.0000	6.0000	0.0034	0.0000	0.0067	*Bacteria*	U	U	U	U	U
Otu1182	0	2	1	1	3	1	8.0000	3.0000	5.0000	0.0045	0.0034	0.0056	*Bacteria*	*Planctomycetes*	*Planctomycetia*	*Planctomycetales*	*Planctomycetaceae*	U
Otu1183	0	0	0	4	4	2	10.0000	0.0000	10.0000	0.0056	0.0000	0.0112	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1184	0	3	0	2	0	5	10.0000	3.0000	7.0000	0.0056	0.0034	0.0079	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1185	1	0	0	1	1	5	8.0000	1.0000	7.0000	0.0045	0.0011	0.0079	*Bacteria*	U	U	U	U	U
Otu1186	1	1	0	2	0	4	8.0000	2.0000	6.0000	0.0045	0.0022	0.0067	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1187	0	2	0	4	1	2	9.0000	2.0000	7.0000	0.0051	0.0022	0.0079	*Bacteria*	U	U	U	U	U
Otu1188	0	0	0	0	3	1	4.0000	0.0000	4.0000	0.0022	0.0000	0.0045	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1189	1	1	0	2	0	5	9.0000	2.0000	7.0000	0.0051	0.0022	0.0079	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu119	73	75	0	76	21	121	366.0000	148.0000	218.0000	0.2057	0.1663	0.2450	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1190	0	0	1	0	4	1	6.0000	1.0000	5.0000	0.0034	0.0011	0.0056	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1191	0	0	0	2	1	0	3.0000	0.0000	3.0000	0.0017	0.0000	0.0034	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1192	1	9	0	3	1	0	14.0000	10.0000	4.0000	0.0079	0.0112	0.0045	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1193	0	0	0	4	0	1	5.0000	0.0000	5.0000	0.0028	0.0000	0.0056	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1194	0	0	0	6	0	0	6.0000	0.0000	6.0000	0.0034	0.0000	0.0067	*Bacteria*	U	U	U	U	U
Otu1195	0	0	0	0	3	0	3.0000	0.0000	3.0000	0.0017	0.0000	0.0034	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	U	U	U
Otu1196	0	0	0	2	1	2	5.0000	0.0000	5.0000	0.0028	0.0000	0.0056	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1197	2	0	0	0	4	0	6.0000	2.0000	4.0000	0.0034	0.0022	0.0045	*Bacteria*	*Proteobacteria*	*Betaproteobacteria*	*Burkholderiales*	*Burkholderiaceae*	*Burkholderia*
Otu1198	2	0	0	0	2	2	6.0000	2.0000	4.0000	0.0034	0.0022	0.0045	*Bacteria*	U	U	U	U	U
Otu1199	0	0	0	2	0	0	2.0000	0.0000	2.0000	0.0011	0.0000	0.0022	*Bacteria*	*Firmicutes*	U	U	U	U
Otu12	1665	698	0	0	0	0	2363.0000	2363.0000	0.0000	1.3279	2.6557	0.0000	*Bacteria*	*Bacteroidetes*	U	U	U	U
Otu120	14	100	0	49	6	109	278.0000	114.0000	164.0000	0.1562	0.1281	0.1843	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Syntrophomonadaceae*	U

Otu1200	0	2	0	4	3	0	9.0000	2.0000	7.0000	0.0051	0.0022	0.0079	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu1201	1	0	0	0	3	0	4.0000	1.0000	3.0000	0.0022	0.0011	0.0034	*Bacteria*	*Planctomycetes*	*Planctomycetia*	*Planctomycetales*	*Planctomycetaceae*	*Planctomicrobium*
Otu1202	0	0	0	0	1	1	2.0000	0.0000	2.0000	0.0011	0.0000	0.0022	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Lachnospiraceae*	*Lachnospiracea_incertae_sedis*
Otu1203	1	0	0	0	3	0	4.0000	1.0000	3.0000	0.0022	0.0011	0.0034	*Bacteria*	*Verrucomicrobia*	*Spartobacteria*	*Spartobacteria_genera_incertae_sedis*	U	U
Otu1204	0	0	0	1	2	5	8.0000	0.0000	8.0000	0.0045	0.0000	0.0090	*Bacteria*	U	U	U	U	U
Otu1205	1	0	0	3	1	2	7.0000	1.0000	6.0000	0.0039	0.0011	0.0067	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu1206	0	1	0	1	1	3	6.0000	1.0000	5.0000	0.0034	0.0011	0.0056	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1207	0	0	0	0	1	3	4.0000	0.0000	4.0000	0.0022	0.0000	0.0045	*Bacteria*	U	U	U	U	U
Otu1208	5	0	0	0	0	0	5.0000	5.0000	0.0000	0.0028	0.0056	0.0000	*Bacteria*	*Bacteroidetes*	*Flavobacteriia*	*Flavobacteriales*	*Flavobacteriaceae*	*Flavobacterium*
Otu1209	1	5	0	0	0	0	6.0000	6.0000	0.0000	0.0034	0.0067	0.0000	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu121	0	0	158	0	0	0	158.0000	158.0000	0.0000	0.0888	0.1776	0.0000	*Bacteria*	*Firmicutes*	*Bacilli*	*Lactobacillales*	*Streptococcaceae*	*Lactococcus*
Otu1210	0	0	1	0	1	0	2.0000	1.0000	1.0000	0.0011	0.0011	0.0011	*Bacteria*	*Candidatus_Saccharibacteria*	*Saccharibacteria_genera_incertae_sedis*	U	U	U
Otu1211	1	0	1	0	9	0	11.0000	2.0000	9.0000	0.0062	0.0022	0.0101	*Bacteria*	*Actinobacteria*	*Actinobacteria*	*Actinomycetales*	*Micrococcaceae*	U
Otu1212	0	1	0	0	13	1	15.0000	1.0000	14.0000	0.0084	0.0011	0.0157	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1213	5	0	0	0	0	0	5.0000	5.0000	0.0000	0.0028	0.0056	0.0000	*Bacteria*	*Acidobacteria*	*Acidobacteria_Gp1*	U	U	U
Otu1214	0	0	3	0	6	0	9.0000	3.0000	6.0000	0.0051	0.0034	0.0067	*Bacteria*	*Actinobacteria*	*Actinobacteria*	U	U	U
Otu1215	0	0	0	7	3	1	11.0000	0.0000	11.0000	0.0062	0.0000	0.0124	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1216	0	2	0	4	0	2	8.0000	2.0000	6.0000	0.0045	0.0022	0.0067	*Bacteria*	U	U	U	U	U
Otu1217	0	2	0	0	0	6	8.0000	2.0000	6.0000	0.0045	0.0022	0.0067	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1218	0	5	0	0	1	0	6.0000	5.0000	1.0000	0.0034	0.0056	0.0011	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu122	13	62	0	6	5	94	180.0000	75.0000	105.0000	0.1011	0.0843	0.1180	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu1221	1	4	0	0	4	2	11.0000	5.0000	6.0000	0.0062	0.0056	0.0067	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1222	0	4	0	7	22	34	67.0000	4.0000	63.0000	0.0377	0.0045	0.0708	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu1223	0	3	0	2	1	0	6.0000	3.0000	3.0000	0.0034	0.0034	0.0034	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1224	0	3	0	1	0	4	8.0000	3.0000	5.0000	0.0045	0.0034	0.0056	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1225	0	0	0	4	0	0	4.0000	0.0000	4.0000	0.0022	0.0000	0.0045	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1227	0	4	0	0	0	2	6.0000	4.0000	2.0000	0.0034	0.0045	0.0022	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1228	0	0	0	2	0	0	2.0000	0.0000	2.0000	0.0011	0.0000	0.0022	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1229	0	0	0	4	2	0	6.0000	0.0000	6.0000	0.0034	0.0000	0.0067	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu123	7	7	28	2	178	10	232.0000	42.0000	190.0000	0.1304	0.0472	0.2135	*Bacteria*	*Actinobacteria*	*Actinobacteria*	*Actinomycetales*	U	U
Otu1230	1	2	0	0	1	4	8.0000	3.0000	5.0000	0.0045	0.0034	0.0056	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1231	2	0	0	0	8	0	10.0000	2.0000	8.0000	0.0056	0.0022	0.0090	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	*Rhizobiales*	*Hyphomicrobiaceae*	U
Otu1232	0	0	0	0	3	0	3.0000	0.0000	3.0000	0.0017	0.0000	0.0034	*Bacteria*	U	U	U	U	U
Otu1233	2	3	0	2	2	0	9.0000	5.0000	4.0000	0.0051	0.0056	0.0045	*Bacteria*	U	U	U	U	U
Otu1234	3	0	0	0	0	0	3.0000	3.0000	0.0000	0.0017	0.0034	0.0000	*Bacteria*	*Parcubacteria*	U	U	U	U
Otu1235	0	0	0	3	1	2	6.0000	0.0000	6.0000	0.0034	0.0000	0.0067	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1236	0	0	0	0	4	0	4.0000	0.0000	4.0000	0.0022	0.0000	0.0045	*Bacteria*	*Planctomycetes*	*Planctomycetia*	*Planctomycetales*	*Planctomycetaceae*	U

Otu1237	0	0	0	0	5	1	6.0000	0.0000	6.0000	0.0034	0.0000	0.0067	*Bacteria*	U	U	U	U	U
Otu1238	0	0	0	0	2	0	2.0000	0.0000	2.0000	0.0011	0.0000	0.0022	*Bacteria*	*Actinobacteria*	*Actinobacteria*	*Actinomycetales*	*Micromonosporaceae*	U
Otu1239	0	0	0	0	9	1	10.0000	0.0000	10.0000	0.0056	0.0000	0.0112	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu124	0	0	171	3	0	0	174.0000	171.0000	3.0000	0.0978	0.1922	0.0034	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	*Clostridium_IV*
Otu1240	0	0	0	2	1	1	4.0000	0.0000	4.0000	0.0022	0.0000	0.0045	*Bacteria*	U	U	U	U	U
Otu1241	3	0	0	0	1	0	4.0000	3.0000	1.0000	0.0022	0.0034	0.0011	*Bacteria*	U	U	U	U	U
Otu1242	0	0	0	0	2	5	7.0000	0.0000	7.0000	0.0039	0.0000	0.0079	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1243	0	1	0	4	0	2	7.0000	1.0000	6.0000	0.0039	0.0011	0.0067	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1244	0	2	0	2	0	2	6.0000	2.0000	4.0000	0.0034	0.0022	0.0045	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1245	0	0	0	12	4	2	18.0000	0.0000	18.0000	0.0101	0.0000	0.0202	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1246	0	0	0	7	0	0	7.0000	0.0000	7.0000	0.0039	0.0000	0.0079	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1247	0	12	0	6	2	2	22.0000	12.0000	10.0000	0.0124	0.0135	0.0112	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu1248	0	1	0	6	0	7	14.0000	1.0000	13.0000	0.0079	0.0011	0.0146	*Bacteria*	U	U	U	U	U
Otu1249	0	0	0	9	5	0	14.0000	0.0000	14.0000	0.0079	0.0000	0.0157	*Bacteria*	*Firmicutes*	U	U	U	U
Otu125	0	3	0	129	1	26	159.0000	3.0000	156.0000	0.0893	0.0034	0.1753	*Bacteria*	U	U	U	U	U
Otu1250	0	2	0	1	1	1	5.0000	2.0000	3.0000	0.0028	0.0022	0.0034	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1251	2	4	0	2	0	5	13.0000	6.0000	7.0000	0.0073	0.0067	0.0079	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1252	0	1	0	1	0	2	4.0000	1.0000	3.0000	0.0022	0.0011	0.0034	*Bacteria*	U	U	U	U	U
Otu1253	0	0	0	0	3	0	3.0000	0.0000	3.0000	0.0017	0.0000	0.0034	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1254	0	3	0	2	0	4	9.0000	3.0000	6.0000	0.0051	0.0034	0.0067	*Bacteria*	U	U	U	U	U
Otu1255	0	0	0	1	0	4	5.0000	0.0000	5.0000	0.0028	0.0000	0.0056	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1256	3	1	0	0	0	0	4.0000	4.0000	0.0000	0.0022	0.0045	0.0000	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1257	2	6	0	0	0	0	8.0000	8.0000	0.0000	0.0045	0.0090	0.0000	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1258	0	1	0	0	1	0	2.0000	1.0000	1.0000	0.0011	0.0011	0.0011	*Bacteria*	U	U	U	U	U
Otu1259	1	3	0	3	0	7	14.0000	4.0000	10.0000	0.0079	0.0045	0.0112	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu126	9	19	0	67	3	46	144.0000	28.0000	116.0000	0.0809	0.0315	0.1304	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1260	0	0	0	0	3	3	6.0000	0.0000	6.0000	0.0034	0.0000	0.0067	*Bacteria*	U	U	U	U	U
Otu1261	0	0	0	6	0	3	9.0000	0.0000	9.0000	0.0051	0.0000	0.0101	*Bacteria*	U	U	U	U	U
Otu1262	0	5	0	1	0	0	6.0000	5.0000	1.0000	0.0034	0.0056	0.0011	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1263	0	1	0	3	0	1	5.0000	1.0000	4.0000	0.0028	0.0011	0.0045	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1264	0	0	0	0	3	1	4.0000	0.0000	4.0000	0.0022	0.0000	0.0045	*Bacteria*	*Planctomycetes*	*Planctomycetia*	*Planctomycetales*	*Planctomycetaceae*	U
Otu1265	1	0	0	0	1	0	2.0000	1.0000	1.0000	0.0011	0.0011	0.0011	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1266	1	3	0	0	0	7	11.0000	4.0000	7.0000	0.0062	0.0045	0.0079	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1267	1	5	0	0	0	1	7.0000	6.0000	1.0000	0.0039	0.0067	0.0011	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1268	1	1	0	2	0	5	9.0000	2.0000	7.0000	0.0051	0.0022	0.0079	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1269	1	0	0	0	0	1	2.0000	1.0000	1.0000	0.0011	0.0011	0.0011	*Bacteria*	U	U	U	U	U
Otu127	1	7	0	19	5	72	104.0000	8.0000	96.0000	0.0584	0.0090	0.1079	*Bacteria*	U	U	U	U	U
Otu1270	5	0	0	0	0	0	5.0000	5.0000	0.0000	0.0028	0.0056	0.0000	*Bacteria*	*Bacteroidetes*	*Sphingobacteriia*	*Sphingobacteriales*	*Chitinophagaceae*	U
Otu1271	2	0	0	1	0	1	4.0000	2.0000	2.0000	0.0022	0.0022	0.0022	*Bacteria*	U	U	U	U	U
Otu1272	0	0	0	0	1	2	3.0000	0.0000	3.0000	0.0017	0.0000	0.0034	*Bacteria*	U	U	U	U	U
Otu1273	2	0	0	0	4	0	6.0000	2.0000	4.0000	0.0034	0.0022	0.0045	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1274	2	4	0	1	1	3	11.0000	6.0000	5.0000	0.0062	0.0067	0.0056	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1275	0	0	0	5	0	2	7.0000	0.0000	7.0000	0.0039	0.0000	0.0079	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1276	0	0	0	7	3	0	10.0000	0.0000	10.0000	0.0056	0.0000	0.0112	*Bacteria*	U	U	U	U	U

Otu1277	1	1	0	1	0	6	9.0000	2.0000	7.0000	0.0051	0.0022	0.0079	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1278	0	0	0	4	1	1	6.0000	0.0000	6.0000	0.0034	0.0000	0.0067	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1279	2	0	0	4	2	2	10.0000	2.0000	8.0000	0.0056	0.0022	0.0090	*Bacteria*	*Firmicutes*	U	U	U	U
Otu128	27	10	1	27	3	69	137.0000	38.0000	99.0000	0.0770	0.0427	0.1113	*Bacteria*	U	U	U	U	U
Otu1280	0	0	0	0	14	2	16.0000	0.0000	16.0000	0.0090	0.0000	0.0180	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1281	0	0	0	1	3	0	4.0000	0.0000	4.0000	0.0022	0.0000	0.0045	*Bacteria*	U	U	U	U	U
Otu1282	0	0	0	0	2	0	2.0000	0.0000	2.0000	0.0011	0.0000	0.0022	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	*Rhizobiales*	U	U
Otu1283	4	0	0	0	1	0	5.0000	4.0000	1.0000	0.0028	0.0045	0.0011	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	U	U	U
Otu1285	0	4	0	4	0	1	9.0000	4.0000	5.0000	0.0051	0.0045	0.0056	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1286	0	0	1	0	5	0	6.0000	1.0000	5.0000	0.0034	0.0011	0.0056	*Bacteria*	*Bacteroidetes*	*Flavobacteriia*	*Flavobacteriales*	*Flavobacteriaceae*	*Myroides*
Otu1287	0	2	0	1	1	6	10.0000	2.0000	8.0000	0.0056	0.0022	0.0090	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1288	0	0	15	0	0	0	15.0000	15.0000	0.0000	0.0084	0.0169	0.0000	*Bacteria*	*Proteobacteria*	*Gammaproteobacteria*	*Enterobacteriales*	*Enterobacteriaceae*	U
Otu1289	0	3	0	0	0	5	8.0000	3.0000	5.0000	0.0045	0.0034	0.0056	*Bacteria*	*Firmicutes*	U	U	U	U
Otu129	1	22	0	66	14	57	160.0000	23.0000	137.0000	0.0899	0.0258	0.1540	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1290	0	0	0	2	1	1	4.0000	0.0000	4.0000	0.0022	0.0000	0.0045	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1291	0	0	0	0	0	3	3.0000	0.0000	3.0000	0.0017	0.0000	0.0034	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1292	0	2	0	4	0	2	8.0000	2.0000	6.0000	0.0045	0.0022	0.0067	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Syntrophomonadaceae*	U
Otu1293	0	1	0	1	0	0	2.0000	1.0000	1.0000	0.0011	0.0011	0.0011	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1294	0	0	0	0	4	0	4.0000	0.0000	4.0000	0.0022	0.0000	0.0045	*Bacteria*	U	U	U	U	U
Otu1295	3	0	0	0	4	1	8.0000	3.0000	5.0000	0.0045	0.0034	0.0056	*Bacteria*	*Candidatus_Saccharibacteria*	*Saccharibacteria_genera_incertae_sedis*	U	U	U
Otu1296	0	0	0	2	4	2	8.0000	0.0000	8.0000	0.0045	0.0000	0.0090	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1297	0	1	0	2	4	5	12.0000	1.0000	11.0000	0.0067	0.0011	0.0124	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Lachnospiraceae*	U
Otu1298	0	0	0	0	5	3	8.0000	0.0000	8.0000	0.0045	0.0000	0.0090	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu1299	0	0	0	3	1	2	6.0000	0.0000	6.0000	0.0034	0.0000	0.0067	*Bacteria*	U	U	U	U	U
Otu13	0	0	0	0	287	1710	1997.0000	0.0000	1997.0000	1.1222	0.0000	2.2444	*Bacteria*	*Bacteroidetes*	U	U	U	U
Otu130	2	2	184	1	16	2	207.0000	188.0000	19.0000	0.1163	0.2113	0.0214	*Bacteria*	*Firmicutes*	*Bacilli*	*Bacillales*	*Planococcaceae*	*Lysinibacillus*
Otu1300	0	0	0	1	3	1	5.0000	0.0000	5.0000	0.0028	0.0000	0.0056	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1301	7	0	0	0	1	0	8.0000	7.0000	1.0000	0.0045	0.0079	0.0011	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	*Rhodospirillales*	U	U
Otu1302	3	0	0	0	0	0	3.0000	3.0000	0.0000	0.0017	0.0034	0.0000	*Bacteria*	*Verrucomicrobia*	*Subdivision3*	*Subdivision3_genera_ incertae_sedis*	U	U
Otu1303	1	0	0	0	1	0	2.0000	1.0000	1.0000	0.0011	0.0011	0.0011	*Bacteria*	*Bacteroidetes*	*Cytophagia*	U	U	U
Otu1304	4	0	0	0	3	0	7.0000	4.0000	3.0000	0.0039	0.0045	0.0034	*Bacteria*	*Candidatus_Saccharibacteria*	*Saccharibacteria_genera_incertae_sedis*	U	U	U
Otu1306	0	2	0	0	0	1	3.0000	2.0000	1.0000	0.0017	0.0022	0.0011	*Bacteria*	*Actinobacteria*	*Actinobacteria*	*Actinomycetales*	*Propionibacteriaceae*	U
Otu1307	2	5	0	0	10	0	17.0000	7.0000	10.0000	0.0096	0.0079	0.0112	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1308	0	0	0	0	7	2	9.0000	0.0000	9.0000	0.0051	0.0000	0.0101	*Bacteria*	U	U	U	U	U

Otu1309	0	2	0	4	1	4	11.0000	2.0000	9.0000	0.0062	0.0022	0.0101	*Bacteria*	*Firmicutes*	U	U	U	U
Otu131	18	81	0	23	3	42	167.0000	99.0000	68.0000	0.0938	0.1113	0.0764	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1310	0	0	0	0	5	2	7.0000	0.0000	7.0000	0.0039	0.0000	0.0079	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1311	0	1	0	0	0	3	4.0000	1.0000	3.0000	0.0022	0.0011	0.0034	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1312	0	0	0	0	8	4	12.0000	0.0000	12.0000	0.0067	0.0000	0.0135	*Bacteria*	U	U	U	U	U
Otu1313	0	1	0	0	2	1	4.0000	1.0000	3.0000	0.0022	0.0011	0.0034	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1314	3	2	0	0	0	0	5.0000	5.0000	0.0000	0.0028	0.0056	0.0000	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu1315	0	2	0	0	0	8	10.0000	2.0000	8.0000	0.0056	0.0022	0.0090	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1316	0	0	1	0	3	0	4.0000	1.0000	3.0000	0.0022	0.0011	0.0034	*Bacteria*	*Actinobacteria*	*Actinobacteria*	*Actinomycetales*	*Microbacteriaceae*	U
Otu1317	0	0	0	0	4	0	4.0000	0.0000	4.0000	0.0022	0.0000	0.0045	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1318	0	1	0	0	0	1	2.0000	1.0000	1.0000	0.0011	0.0011	0.0011	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1319	1	1	0	3	1	2	8.0000	2.0000	6.0000	0.0045	0.0022	0.0067	*Bacteria*	U	U	U	U	U
Otu132	1	0	37	0	168	26	232.0000	38.0000	194.0000	0.1304	0.0427	0.2180	*Bacteria*	*Proteobacteria*	*Gammaproteobacteria*	*Pseudomonadales*	*Moraxellaceae*	*Acinetobacter*
Otu1320	0	0	0	2	0	6	8.0000	0.0000	8.0000	0.0045	0.0000	0.0090	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1321	0	0	0	0	0	4	4.0000	0.0000	4.0000	0.0022	0.0000	0.0045	*Bacteria*	U	U	U	U	U
Otu1322	0	0	0	4	1	2	7.0000	0.0000	7.0000	0.0039	0.0000	0.0079	*Bacteria*	U	U	U	U	U
Otu1323	1	0	0	0	3	0	4.0000	1.0000	3.0000	0.0022	0.0011	0.0034	*Bacteria*	*Candidatus_Saccharibacteria*	*Saccharibacteria_genera_incertae_sedis*	U	U	U
Otu1325	0	0	0	2	0	1	3.0000	0.0000	3.0000	0.0017	0.0000	0.0034	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1326	4	0	0	0	0	1	5.0000	4.0000	1.0000	0.0028	0.0045	0.0011	*Bacteria*	U	U	U	U	U
Otu1327	1	2	0	0	0	4	7.0000	3.0000	4.0000	0.0039	0.0034	0.0045	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1328	0	2	0	1	0	4	7.0000	2.0000	5.0000	0.0039	0.0022	0.0056	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1329	1	2	0	1	4	0	8.0000	3.0000	5.0000	0.0045	0.0034	0.0056	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu133	12	52	0	28	149	42	283.0000	64.0000	219.0000	0.1590	0.0719	0.2461	*Bacteria*	*Firmicutes*	*Negativicutes*	U	U	U
Otu1330	0	1	0	9	0	0	10.0000	1.0000	9.0000	0.0056	0.0011	0.0101	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1331	9	0	0	0	1	0	10.0000	9.0000	1.0000	0.0056	0.0101	0.0011	*Bacteria*	*Bacteroidetes*	*Flavobacteriia*	*Flavobacteriales*	*Cryomorphaceae*	*Fluviicola*
Otu1332	0	0	0	4	0	0	4.0000	0.0000	4.0000	0.0022	0.0000	0.0045	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Lachnospiraceae*	*Clostridium_XlVa*
Otu1333	3	1	0	0	0	0	4.0000	4.0000	0.0000	0.0022	0.0045	0.0000	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
0,00%	0	5	0	1	0	1	7.0000	5.0000	2.0000	0.0039	0.0056	0.0022	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Lachnospiraceae*	U
Otu1336	5	0	0	0	0	0	5.0000	5.0000	0.0000	0.0028	0.0056	0.0000	*Bacteria*	*Proteobacteria*	*Gammaproteobacteria*	U	U	U
Otu1337	0	1	0	1	0	5	7.0000	1.0000	6.0000	0.0039	0.0011	0.0067	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1338	0	4	0	0	2	2	8.0000	4.0000	4.0000	0.0045	0.0045	0.0045	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Lachnospiraceae*	U
Otu1339	0	5	0	0	0	0	5.0000	5.0000	0.0000	0.0028	0.0056	0.0000	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu134	18	19	0	55	4	33	129.0000	37.0000	92.0000	0.0725	0.0416	0.1034	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1340	3	0	0	0	8	0	11.0000	3.0000	8.0000	0.0062	0.0034	0.0090	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	*Rhizobiales*	U	U
Otu1341	6	0	0	0	5	0	11.0000	6.0000	5.0000	0.0062	0.0067	0.0056	*Bacteria*	*Proteobacteria*	*Deltaproteobacteria*	*Myxococcales*	U	U
Otu1342	2	0	0	0	0	0	2.0000	2.0000	0.0000	0.0011	0.0022	0.0000	*Bacteria*	*Proteobacteria*	*Deltaproteobacteria*	*Myxococcales*	U	U
Otu1343	6	0	2	0	7	2	17.0000	8.0000	9.0000	0.0096	0.0090	0.0101	*Bacteria*	*Actinobacteria*	*Actinobacteria*	*Actinomycetales*	*Micromonosporaceae*	U
Otu1344	1	0	0	0	1	0	2.0000	1.0000	1.0000	0.0011	0.0011	0.0011	*Bacteria*	*Firmicutes*	U	U	U	U

Otu1345	0	3	0	2	0	3	8.0000	3.0000	5.0000	0.0045	0.0034	0.0056	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1346	0	0	0	1	0	3	4.0000	0.0000	4.0000	0.0022	0.0000	0.0045	*Bacteria*	*Proteobacteria*	*Deltaproteobacteria*	*Desulfovibrionales*	U	U
Otu1347	0	0	0	1	2	3	6.0000	0.0000	6.0000	0.0034	0.0000	0.0067	*Bacteria*	U	U	U	U	U
Otu1348	1	0	0	3	7	4	15.0000	1.0000	14.0000	0.0084	0.0011	0.0157	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1349	6	0	0	0	2	0	8.0000	6.0000	2.0000	0.0045	0.0067	0.0022	*Bacteria*	*Bacteroidetes*	*Flavobacteriia*	*Flavobacteriales*	*Flavobacteriaceae*	*Flavobacterium*
Otu135	18	42	0	96	3	1	160.0000	60.0000	100.0000	0.0899	0.0674	0.1124	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu1350	0	1	0	0	0	4	5.0000	1.0000	4.0000	0.0028	0.0011	0.0045	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1351	3	0	0	0	0	0	3.0000	3.0000	0.0000	0.0017	0.0034	0.0000	*Bacteria*	*Actinobacteria*	*Actinobacteria*	*Actinomycetales*	*Micromonosporaceae*	U
Otu1352	0	0	0	1	2	0	3.0000	0.0000	3.0000	0.0017	0.0000	0.0034	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1353	5	0	0	0	0	0	5.0000	5.0000	0.0000	0.0028	0.0056	0.0000	*Bacteria*	U	U	U	U	U
Otu1354	0	3	0	0	1	0	4.0000	3.0000	1.0000	0.0022	0.0034	0.0011	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1355	0	6	0	2	0	9	17.0000	6.0000	11.0000	0.0096	0.0067	0.0124	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu1356	0	1	0	1	0	1	3.0000	1.0000	2.0000	0.0017	0.0011	0.0022	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1357	1	3	0	3	1	2	10.0000	4.0000	6.0000	0.0056	0.0045	0.0067	*Bacteria*	U	U	U	U	U
Otu1358	1	0	0	0	4	0	5.0000	1.0000	4.0000	0.0028	0.0011	0.0045	*Bacteria*	*Acidobacteria*	*Acidobacteria_Gp6*	*Gp6*	U	U
Otu1359	0	0	0	6	0	2	8.0000	0.0000	8.0000	0.0045	0.0000	0.0090	*Bacteria*	U	U	U	U	U
Otu136	5	35	1	63	39	10	153.0000	41.0000	112.0000	0.0860	0.0461	0.1259	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1360	0	0	0	2	2	4	8.0000	0.0000	8.0000	0.0045	0.0000	0.0090	*Bacteria*	U	U	U	U	U
Otu1361	0	2	0	1	0	2	5.0000	2.0000	3.0000	0.0028	0.0022	0.0034	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1362	3	0	0	0	1	0	4.0000	3.0000	1.0000	0.0022	0.0034	0.0011	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	*Rhodospirillales*	U	U
Otu1363	0	0	0	0	2	0	2.0000	0.0000	2.0000	0.0011	0.0000	0.0022	*Bacteria*	*Candidatus_Saccharibacteria*	U	U	U	U
Otu1364	1	0	0	6	0	0	7.0000	1.0000	6.0000	0.0039	0.0011	0.0067	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1365	0	4	0	0	0	2	6.0000	4.0000	2.0000	0.0034	0.0045	0.0022	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1366	2	2	0	0	0	0	4.0000	4.0000	0.0000	0.0022	0.0045	0.0000	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1367	0	0	0	0	4	0	4.0000	0.0000	4.0000	0.0022	0.0000	0.0045	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	*Rhizobiales*	*Rhizobiaceae*	*Rhizobium*
Otu1368	0	4	0	2	4	0	10.0000	4.0000	6.0000	0.0056	0.0045	0.0067	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1369	0	0	3	0	0	0	3.0000	3.0000	0.0000	0.0017	0.0034	0.0000	*Bacteria*	*Firmicutes*	U	U	U	U
Otu137	52	1	13	4	56	8	134.0000	66.0000	68.0000	0.0753	0.0742	0.0764	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	*Rhizobiales*	*Rhizobiaceae*	*Rhizobium*
Otu1370	4	0	0	0	2	1	7.0000	4.0000	3.0000	0.0039	0.0045	0.0034	*Bacteria*	*Candidatus_Saccharibacteria*	*Saccharibacteria_genera_incertae_sedis*	U	U	U
Otu1371	2	3	0	0	2	0	7.0000	5.0000	2.0000	0.0039	0.0056	0.0022	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1372	0	0	3	0	1	0	4.0000	3.0000	1.0000	0.0022	0.0034	0.0011	*Bacteria*	*Actinobacteria*	*Actinobacteria*	U	U	U
Otu1373	1	0	3	0	3	1	8.0000	4.0000	4.0000	0.0045	0.0045	0.0045	*Bacteria*	*Actinobacteria*	*Actinobacteria*	*Actinomycetales*	*Mycobacteriaceae*	*Mycobacterium*
Otu1374	0	10	0	1	0	0	11.0000	10.0000	1.0000	0.0062	0.0112	0.0011	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1375	1	0	1	0	2	0	4.0000	2.0000	2.0000	0.0022	0.0022	0.0022	*Bacteria*	*Proteobacteria*	*Deltaproteobacteria*	*Myxococcales*	U	U
Otu1377	0	4	0	0	0	1	5.0000	4.0000	1.0000	0.0028	0.0045	0.0011	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U

Otu1378	0	4	0	0	0	4	8.0000	4.0000	4.0000	0.0045	0.0045	0.0045	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1379	2	0	1	0	1	0	4.0000	3.0000	1.0000	0.0022	0.0034	0.0011	*Bacteria*	*Planctomycetes*	U	U	U	U
Otu138	0	0	0	0	90	68	158.0000	0.0000	158.0000	0.0888	0.0000	0.1776	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Lachnospiraceae*	U
Otu1380	0	0	0	6	0	8	14.0000	0.0000	14.0000	0.0079	0.0000	0.0157	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1381	2	0	0	0	11	0	13.0000	2.0000	11.0000	0.0073	0.0022	0.0124	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	*Rhizobiales*	U	U
Otu1382	0	0	0	1	0	2	3.0000	0.0000	3.0000	0.0017	0.0000	0.0034	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1383	0	2	0	1	0	0	3.0000	2.0000	1.0000	0.0017	0.0022	0.0011	*Bacteria*	U	U	U	U	U
Otu1384	3	3	0	0	0	3	9.0000	6.0000	3.0000	0.0051	0.0067	0.0034	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1385	3	0	1	0	2	0	6.0000	4.0000	2.0000	0.0034	0.0045	0.0022	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	*Caulobacterales*	*Caulobacteraceae*	U
Otu1386	1	8	0	3	1	1	14.0000	9.0000	5.0000	0.0079	0.0101	0.0056	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1387	0	0	4	0	0	0	4.0000	4.0000	0.0000	0.0022	0.0045	0.0000	*Bacteria*	*Actinobacteria*	*Actinobacteria*	*Actinomycetales*	*Nakamurellaceae*	*Nakamurella*
Otu1388	0	0	0	0	3	6	9.0000	0.0000	9.0000	0.0051	0.0000	0.0101	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1389	1	0	0	0	2	0	3.0000	1.0000	2.0000	0.0017	0.0011	0.0022	*Bacteria*	*Proteobacteria*	*Gammaproteobacteria*	*Xanthomonadales*	*Xanthomonadaceae*	U
Otu139	1	23	0	52	3	47	126.0000	24.0000	102.0000	0.0708	0.0270	0.1146	*Bacteria*	U	U	U	U	U
Otu1390	0	1	0	0	15	2	18.0000	1.0000	17.0000	0.0101	0.0011	0.0191	*Bacteria*	U	U	U	U	U
Otu1391	0	0	0	0	3	1	4.0000	0.0000	4.0000	0.0022	0.0000	0.0045	U	U	U	U	U	U
Otu1392	0	1	0	0	0	3	4.0000	1.0000	3.0000	0.0022	0.0011	0.0034	*Bacteria*	U	U	U	U	U
Otu1393	1	0	2	0	7	0	10.0000	3.0000	7.0000	0.0056	0.0034	0.0079	*Bacteria*	*Actinobacteria*	*Actinobacteria*	U	U	U
Otu1394	0	0	0	1	0	4	5.0000	0.0000	5.0000	0.0028	0.0000	0.0056	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1395	4	0	1	0	3	0	8.0000	5.0000	3.0000	0.0045	0.0056	0.0034	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	U	U	U
Otu1396	0	1	0	3	1	4	9.0000	1.0000	8.0000	0.0051	0.0011	0.0090	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1397	4	0	0	0	0	0	4.0000	4.0000	0.0000	0.0022	0.0045	0.0000	*Bacteria*	U	U	U	U	U
Otu1399	1	3	0	3	0	0	7.0000	4.0000	3.0000	0.0039	0.0045	0.0034	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu14	513	733	0	841	12	363	2462.0000	1246.0000	1216.0000	1.3835	1.4004	1.3666	*Bacteria*	*Bacteroidetes*	*Bacteroidia*	*Bacteroidales*	*Porphyromonadaceae*	*Proteiniphilum*
Otu140	3	80	0	30	0	61	174.0000	83.0000	91.0000	0.0978	0.0933	0.1023	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1400	1	0	0	0	1	1	3.0000	1.0000	2.0000	0.0017	0.0011	0.0022	*Bacteria*	*Verrucomicrobia*	*Spartobacteria*	U	U	U
Otu1401	0	1	0	2	0	0	3.0000	1.0000	2.0000	0.0017	0.0011	0.0022	*Bacteria*	*Proteobacteria*	U	U	U	U
Otu1402	0	0	0	0	3	0	3.0000	0.0000	3.0000	0.0017	0.0000	0.0034	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1403	0	0	0	0	6	1	7.0000	0.0000	7.0000	0.0039	0.0000	0.0079	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1404	4	0	0	0	0	0	4.0000	4.0000	0.0000	0.0022	0.0045	0.0000	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	*Alphaproteobacteria_incertae_sedis*	*Rhizomicrobium*	U
Otu1405	3	0	2	0	6	2	13.0000	5.0000	8.0000	0.0073	0.0056	0.0090	*Bacteria*	*Actinobacteria*	*Actinobacteria*	*Actinomycetales*	*Mycobacteriaceae*	*Mycobacterium*
Otu1406	0	0	0	1	1	11	13.0000	0.0000	13.0000	0.0073	0.0000	0.0146	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1407	8	0	0	0	1	0	9.0000	8.0000	1.0000	0.0051	0.0090	0.0011	*Bacteria*	*Proteobacteria*	*Gammaproteobacteria*	U	U	U
Otu1408	0	1	0	0	1	2	4.0000	1.0000	3.0000	0.0022	0.0011	0.0034	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1409	1	3	0	0	1	0	5.0000	4.0000	1.0000	0.0028	0.0045	0.0011	*Bacteria*	*Firmicutes*	U	U	U	U

Otu141	9	32	0	89	41	58	229.0000	41.0000	188.0000	0.1287	0.0461	0.2113	*Bacteria*	*Proteobacteria*	*Deltaproteobacteria*	*Desulfovibrionales*	U	U
Otu1410	0	0	0	1	1	3	5.0000	0.0000	5.0000	0.0028	0.0000	0.0056	*Bacteria*	U	U	U	U	U
Otu1412	1	0	0	0	0	5	6.0000	1.0000	5.0000	0.0034	0.0011	0.0056	*Bacteria*	U	U	U	U	U
Otu1413	2	0	0	0	6	2	10.0000	2.0000	8.0000	0.0056	0.0022	0.0090	*Bacteria*	*Candidatus_Saccharibacteria*	*Saccharibacteria_genera_incertae_sedis*	U	U	U
Otu1414	0	0	0	0	9	1	10.0000	0.0000	10.0000	0.0056	0.0000	0.0112	*Bacteria*	*Firmicutes*	*Bacilli*	*Lactobacillales*	*Leuconostocaceae*	U
Otu1415	1	1	0	0	0	2	4.0000	2.0000	2.0000	0.0022	0.0022	0.0022	*Bacteria*	*Verrucomicrobia*	*Spartobacteria*	U	U	U
Otu1416	2	0	0	0	2	0	4.0000	2.0000	2.0000	0.0022	0.0022	0.0022	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	*Caulobacterales*	*Caulobacteraceae*	*Asticcacaulis*
Otu1417	0	7	0	0	0	0	7.0000	7.0000	0.0000	0.0039	0.0079	0.0000	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1418	0	4	0	0	3	3	10.0000	4.0000	6.0000	0.0056	0.0045	0.0067	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1419	0	0	0	1	2	0	3.0000	0.0000	3.0000	0.0017	0.0000	0.0034	*Bacteria*	*Candidatus_Saccharibacteria*	*Saccharibacteria_genera_incertae_sedis*	U	U	U
Otu142	21	57	0	50	6	13	147.0000	78.0000	69.0000	0.0826	0.0877	0.0775	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1420	0	0	0	0	0	2	2.0000	0.0000	2.0000	0.0011	0.0000	0.0022	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1421	0	0	0	1	8	2	11.0000	0.0000	11.0000	0.0062	0.0000	0.0124	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1422	1	4	0	2	0	4	11.0000	5.0000	6.0000	0.0062	0.0056	0.0067	*Bacteria*	U	U	U	U	U
Otu1423	0	0	0	1	1	23	25.0000	0.0000	25.0000	0.0140	0.0000	0.0281	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1424	0	0	0	2	2	2	6.0000	0.0000	6.0000	0.0034	0.0000	0.0067	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1425	2	0	0	0	9	1	12.0000	2.0000	10.0000	0.0067	0.0022	0.0112	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	*Rhizobiales*	*Roseiarcaceae*	U
Otu1426	0	0	0	2	1	1	4.0000	0.0000	4.0000	0.0022	0.0000	0.0045	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu1427	0	0	0	2	2	2	6.0000	0.0000	6.0000	0.0034	0.0000	0.0067	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1428	0	0	0	1	0	1	2.0000	0.0000	2.0000	0.0011	0.0000	0.0022	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu1429	1	2	0	0	0	0	3.0000	3.0000	0.0000	0.0017	0.0034	0.0000	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu143	3	27	0	34	4	31	99.0000	30.0000	69.0000	0.0556	0.0337	0.0775	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1430	2	3	0	2	6	5	18.0000	5.0000	13.0000	0.0101	0.0056	0.0146	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1431	0	1	0	2	3	1	7.0000	1.0000	6.0000	0.0039	0.0011	0.0067	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu1432	0	0	0	5	0	3	8.0000	0.0000	8.0000	0.0045	0.0000	0.0090	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1433	0	0	1	0	1	2	4.0000	1.0000	3.0000	0.0022	0.0011	0.0034	*Bacteria*	*Actinobacteria*	*Actinobacteria*	*Actinomycetales*	*Mycobacteriaceae*	*Mycobacterium*
Otu1434	0	4	0	0	0	0	4.0000	4.0000	0.0000	0.0022	0.0045	0.0000	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu1435	0	1	3	0	2	0	6.0000	4.0000	2.0000	0.0034	0.0045	0.0022	*Bacteria*	*Acidobacteria*	*Acidobacteria_Gp16*	*Gp16*	U	U
Otu1436	0	0	0	3	2	0	5.0000	0.0000	5.0000	0.0028	0.0000	0.0056	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1437	0	0	0	0	14	11	25.0000	0.0000	25.0000	0.0140	0.0000	0.0281	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1438	1	0	0	0	1	0	2.0000	1.0000	1.0000	0.0011	0.0011	0.0011	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	U	U	U
Otu1439	1	3	0	0	4	0	8.0000	4.0000	4.0000	0.0045	0.0045	0.0045	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu144	64	0	0	0	46	6	116.0000	64.0000	52.0000	0.0652	0.0719	0.0584	*Bacteria*	*Bacteroidetes*	*Flavobacteriia*	*Flavobacteriales*	*Flavobacteriaceae*	U
Otu1440	1	0	0	0	4	0	5.0000	1.0000	4.0000	0.0028	0.0011	0.0045	*Bacteria*	*Bacteroidetes*	U	U	U	U
Otu1441	0	3	0	2	0	2	7.0000	3.0000	4.0000	0.0039	0.0034	0.0045	*Bacteria*	U	U	U	U	U
Otu1442	1	0	0	4	1	1	7.0000	1.0000	6.0000	0.0039	0.0011	0.0067	*Bacteria*	U	U	U	U	U

Otu1443	0	0	0	1	1	4	6.0000	0.0000	6.0000	0.0034	0.0000	0.0067	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1444	2	0	0	0	4	0	6.0000	2.0000	4.0000	0.0034	0.0022	0.0045	*Bacteria*	U	U	U	U	U
Otu1445	0	0	0	0	3	0	3.0000	0.0000	3.0000	0.0017	0.0000	0.0034	*Bacteria*	*Verrucomicrobia*	*Spartobacteria*	*Terrimicrobium*	U	U
Otu1446	1	4	0	0	0	3	8.0000	5.0000	3.0000	0.0045	0.0056	0.0034	*Bacteria*	U	U	U	U	U
Otu1447	5	0	0	0	0	0	5.0000	5.0000	0.0000	0.0028	0.0056	0.0000	*Bacteria*	*Candidatus_Saccharibacteria*	*Saccharibacteria_genera_incertae_sedis*	U	U	U
Otu1448	3	4	0	2	0	2	11.0000	7.0000	4.0000	0.0062	0.0079	0.0045	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1449	0	0	1	4	3	0	8.0000	1.0000	7.0000	0.0045	0.0011	0.0079	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu145	6	109	0	26	22	42	205.0000	115.0000	90.0000	0.1152	0.1292	0.1011	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1450	1	3	0	0	0	4	8.0000	4.0000	4.0000	0.0045	0.0045	0.0045	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1451	0	1	0	0	0	3	4.0000	1.0000	3.0000	0.0022	0.0011	0.0034	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu1452	2	1	0	0	3	0	6.0000	3.0000	3.0000	0.0034	0.0034	0.0034	*Bacteria*	*Verrucomicrobia*	*Spartobacteria*	U	U	U
Otu1453	3	0	0	0	0	0	3.0000	3.0000	0.0000	0.0017	0.0034	0.0000	*Bacteria*	*Bacteroidetes*	U	U	U	U
Otu1454	0	0	0	3	1	2	6.0000	0.0000	6.0000	0.0034	0.0000	0.0067	*Bacteria*	U	U	U	U	U
Otu1455	0	0	1	0	2	0	3.0000	1.0000	2.0000	0.0017	0.0011	0.0022	*Bacteria*	*Actinobacteria*	*Actinobacteria*	*Solirubrobacterales*	U	U
Otu1456	8	0	0	0	0	0	8.0000	8.0000	0.0000	0.0045	0.0090	0.0000	*Bacteria*	*Verrucomicrobia*	*Subdivision3*	*Subdivision3_genera_ incertae_sedis*	U	U
Otu1457	0	2	0	1	0	1	4.0000	2.0000	2.0000	0.0022	0.0022	0.0022	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1458	5	0	0	0	0	0	5.0000	5.0000	0.0000	0.0028	0.0056	0.0000	*Bacteria*	*Acidobacteria*	*Acidobacteria_Gp3*	*Gp3*	U	U
Otu1459	0	1	0	0	1	2	4.0000	1.0000	3.0000	0.0022	0.0011	0.0034	*Bacteria*	*Firmicutes*	U	U	U	U
Otu146	8	40	0	12	4	55	119.0000	48.0000	71.0000	0.0669	0.0539	0.0798	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1460	0	0	0	0	1	2	3.0000	0.0000	3.0000	0.0017	0.0000	0.0034	*Bacteria*	U	U	U	U	U
Otu1461	0	0	0	0	0	6	6.0000	0.0000	6.0000	0.0034	0.0000	0.0067	*Bacteria*	U	U	U	U	U
Otu1462	0	0	0	0	5	7	12.0000	0.0000	12.0000	0.0067	0.0000	0.0135	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1463	0	1	0	2	0	5	8.0000	1.0000	7.0000	0.0045	0.0011	0.0079	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1464	1	0	0	0	3	0	4.0000	1.0000	3.0000	0.0022	0.0011	0.0034	*Bacteria*	*Proteobacteria*	U	U	U	U
Otu1465	1	1	0	1	0	0	3.0000	2.0000	1.0000	0.0017	0.0022	0.0011	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1466	0	1	0	2	0	3	6.0000	1.0000	5.0000	0.0034	0.0011	0.0056	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1467	1	3	0	0	0	2	6.0000	4.0000	2.0000	0.0034	0.0045	0.0022	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1468	1	1	0	1	2	1	6.0000	2.0000	4.0000	0.0034	0.0022	0.0045	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu147	2	6	0	51	46	13	118.0000	8.0000	110.0000	0.0663	0.0090	0.1236	*Bacteria*	U	U	U	U	U
Otu1470	0	6	0	2	0	2	10.0000	6.0000	4.0000	0.0056	0.0067	0.0045	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1471	0	0	0	2	1	8	11.0000	0.0000	11.0000	0.0062	0.0000	0.0124	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu1472	2	0	0	0	1	0	3.0000	2.0000	1.0000	0.0017	0.0022	0.0011	*Bacteria*	*Verrucomicrobia*	*Spartobacteria*	*Spartobacteria_genera_incertae_sedis*	U	U
Otu1473	0	2	0	1	0	0	3.0000	2.0000	1.0000	0.0017	0.0022	0.0011	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1474	0	0	0	0	0	2	2.0000	0.0000	2.0000	0.0011	0.0000	0.0022	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1475	0	4	0	1	1	0	6.0000	4.0000	2.0000	0.0034	0.0045	0.0022	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1476	0	0	0	1	0	4	5.0000	0.0000	5.0000	0.0028	0.0000	0.0056	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U

Otu1477	0	0	0	0	2	0	2.0000	0.0000	2.0000	0.0011	0.0000	0.0022	*Bacteria*	*Candidatus_Saccharibacteria_genera_incertae_sedis*	*Saccharibacteria_genera_incertae_sedis*	U	U	U
Otu1478	5	0	0	0	1	0	6.0000	5.0000	1.0000	0.0034	0.0056	0.0011	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	*Rhodospirillales*	*Acetobacteraceae*	U
Otu1479	3	0	0	0	0	0	3.0000	3.0000	0.0000	0.0017	0.0034	0.0000	*Bacteria*	*Bacteroidetes*	*Sphingobacteriia*	*Sphingobacteriales*	U	U
Otu148	8	107	0	25	0	24	164.0000	115.0000	49.0000	0.0922	0.1292	0.0551	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1480	0	0	1	2	0	3	6.0000	1.0000	5.0000	0.0034	0.0011	0.0056	*Bacteria*	U	U	U	U	U
Otu1481	0	0	0	1	7	2	10.0000	0.0000	10.0000	0.0056	0.0000	0.0112	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1482	3	0	0	0	0	0	3.0000	3.0000	0.0000	0.0017	0.0034	0.0000	*Bacteria*	*Proteobacteria*	*Betaproteobacteria*	U	U	U
Otu1483	3	0	0	0	3	0	6.0000	3.0000	3.0000	0.0034	0.0034	0.0034	*Bacteria*	*Candidatus_Saccharibacteria_genera_incertae_sedis*	*Saccharibacteria_genera_incertae_sedis*	U	U	U
Otu1484	0	1	0	1	0	0	2.0000	1.0000	1.0000	0.0011	0.0011	0.0011	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu1485	0	0	0	8	0	0	8.0000	0.0000	8.0000	0.0045	0.0000	0.0090	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1486	0	0	0	5	0	1	6.0000	0.0000	6.0000	0.0034	0.0000	0.0067	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1487	0	3	0	4	0	8	15.0000	3.0000	12.0000	0.0084	0.0034	0.0135	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu1488	0	0	0	2	0	2	4.0000	0.0000	4.0000	0.0022	0.0000	0.0045	*Bacteria*	*Firmicutes*	U	U	U	U
Otu1489	3	0	0	0	4	0	7.0000	3.0000	4.0000	0.0039	0.0034	0.0045	*Bacteria*	*Verrucomicrobia*	*Spartobacteria*	*Spartobacteria_genera_incertae_sedis*	U	U
Otu149	23	0	2	0	100	12	137.0000	25.0000	112.0000	0.0770	0.0281	0.1259	*Bacteria*	*Proteobacteria*	*Gammaproteobacteria*	*Enterobacteriales*	*Enterobacteriaceae*	U
Otu1490	3	0	0	0	0	0	3.0000	3.0000	0.0000	0.0017	0.0034	0.0000	*Bacteria*	U	U	U	U	U
Otu1491	2	0	0	0	2	1	5.0000	2.0000	3.0000	0.0028	0.0022	0.0034	*Bacteria*	*Acidobacteria*	*Acidobacteria_Gp1*	U	U	U
Otu1492	2	0	0	0	0	0	2.0000	2.0000	0.0000	0.0011	0.0022	0.0000	*Bacteria*	*Acidobacteria*	*Acidobacteria_Gp3*	U	U	U
Otu1493	2	1	0	0	0	3	6.0000	3.0000	3.0000	0.0034	0.0034	0.0034	*Bacteria*	*Firmicutes*	U	U	U	U
Otu15	0	0	0	0	2531	185	2716.0000	0.0000	2716.0000	1.5262	0.0000	3.0525	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Lachnospiraceae*	*Clostridium_XlVa*
Otu150	0	11	1	36	1	43	92.0000	12.0000	80.0000	0.0517	0.0135	0.0899	*Bacteria*	*Firmicutes*	U	U	U	U
Otu151	59	4	2	1	101	6	173.0000	65.0000	108.0000	0.0972	0.0731	0.1214	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	*Rhizobiales*	U	U
Otu152	0	153	0	7	2	11	173.0000	153.0000	20.0000	0.0972	0.1720	0.0225	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu153	3	33	0	35	2	48	121.0000	36.0000	85.0000	0.0680	0.0405	0.0955	*Bacteria*	*Proteobacteria*	*Deltaproteobacteria*	*Desulfovibrionales*	*Desulfovibrionaceae*	U
Otu154	1	7	0	26	3	73	110.0000	8.0000	102.0000	0.0618	0.0090	0.1146	*Bacteria*	*Proteobacteria*	*Betaproteobacteria*	*Burkholderiales*	*Comamonadaceae*	U
Otu155	37	72	0	3	18	17	147.0000	109.0000	38.0000	0.0826	0.1225	0.0427	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu156	70	8	4	0	22	2	106.0000	82.0000	24.0000	0.0596	0.0922	0.0270	*Bacteria*	*Proteobacteria*	*Gammaproteobacteria*	*Pseudomonadales*	*Pseudomonadaceae*	*Pseudomonas*
Otu157	13	28	0	22	3	34	100.0000	41.0000	59.0000	0.0562	0.0461	0.0663	*Bacteria*	U	U	U	U	U
Otu158	96	26	6	1	1	0	130.0000	128.0000	2.0000	0.0731	0.1439	0.0022	*Bacteria*	*Actinobacteria*	*Actinobacteria*	*Actinomycetales*	*Streptomycetaceae*	*Streptomyces*
Otu159	3	40	0	50	4	29	126.0000	43.0000	83.0000	0.0708	0.0483	0.0933	*Bacteria*	*Proteobacteria*	*Deltaproteobacter*	*Desulfovibrionales*	*Desulfovibrionaceae*	U

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Otu16	690	311	3	633	3	9	1649.0000	1004.0000	645.0000	0.9266	1.1284	0.7249	*Bacteria*	U	U	U	U	U
Otu160	0	7	0	30	1	77	115.0000	7.0000	108.0000	0.0646	0.0079	0.1214	*Bacteria*	*Firmicutes*	U	U	U	U
Otu161	1	65	0	28	4	50	148.0000	66.0000	82.0000	0.0832	0.0742	0.0922	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu162	0	0	0	27	1	78	106.0000	0.0000	106.0000	0.0596	0.0000	0.1191	*Bacteria*	*Acidobacteria*	*Acidobacteria_Gp3*	*Gp3*	U	U
Otu163	1	48	0	40	1	51	141.0000	49.0000	92.0000	0.0792	0.0551	0.1034	*Bacteria*	U	U	U	U	U
Otu164	0	0	108	0	0	0	108.0000	108.0000	0.0000	0.0607	0.1214	0.0000	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Lachnospiraceae*	U
Otu165	11	42	1	30	36	148	268.0000	54.0000	214.0000	0.1506	0.0607	0.2405	*Bacteria*	U	U	U	U	U
Otu166	1	14	0	46	0	35	96.0000	15.0000	81.0000	0.0539	0.0169	0.0910	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu167	2	0	0	50	18	33	103.0000	2.0000	101.0000	0.0579	0.0022	0.1135	*Bacteria*	*Firmicutes*	U	U	U	U
Otu168	0	14	0	89	0	6	109.0000	14.0000	95.0000	0.0613	0.0157	0.1068	*Bacteria*	*Firmicutes*	U	U	U	U
Otu169	4	18	0	49	0	27	98.0000	22.0000	76.0000	0.0551	0.0247	0.0854	*Bacteria*	*Proteobacteria*	*Deltaproteobacteria*	*Desulfovibrionales*	U	U
Otu17	1041	170	0	328	15	8	1562.0000	1211.0000	351.0000	0.8778	1.3610	0.3945	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu170	5	29	0	37	17	6	94.0000	34.0000	60.0000	0.0528	0.0382	0.0674	*Bacteria*	*Firmicutes*	U	U	U	U
Otu171	0	0	0	0	105	11	116.0000	0.0000	116.0000	0.0652	0.0000	0.1304	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu172	14	48	0	32	5	41	140.0000	62.0000	78.0000	0.0787	0.0697	0.0877	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Clostridiales_Incertae_Sedis_XIII*	*Anaerovorax*
Otu173	0	11	0	46	3	39	99.0000	11.0000	88.0000	0.0556	0.0124	0.0989	*Bacteria*	*Firmicutes*	U	U	U	U
Otu174	10	27	0	15	1	42	95.0000	37.0000	58.0000	0.0534	0.0416	0.0652	*Bacteria*	U	U	U	U	U
Otu175	5	16	0	13	35	57	126.0000	21.0000	105.0000	0.0708	0.0236	0.1180	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu176	9	71	0	21	5	28	134.0000	80.0000	54.0000	0.0753	0.0899	0.0607	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu177	0	2	0	0	94	23	119.0000	2.0000	117.0000	0.0669	0.0022	0.1315	*Bacteria*	*Firmicutes*	U	U	U	U
Otu178	1	73	0	12	2	10	98.0000	74.0000	24.0000	0.0551	0.0832	0.0270	*Bacteria*	*Firmicutes*	U	U	U	U
Otu179	14	40	2	59	5	3	123.0000	56.0000	67.0000	0.0691	0.0629	0.0753	*Bacteria*	*Firmicutes*	U	U	U	U
Otu18	1383	65	30	9	368	57	1912.0000	1478.0000	434.0000	1.0744	1.6611	0.4878	*Bacteria*	*Firmicutes*	U	U	U	U
Otu180	3	15	0	24	5	69	116.0000	18.0000	98.0000	0.0652	0.0202	0.1101	*Bacteria*	*Firmicutes*	U	U	U	U
Otu181	0	26	0	83	0	19	128.0000	26.0000	102.0000	0.0719	0.0292	0.1146	*Bacteria*	*Proteobacteria*	*Deltaproteobacteria*	*Desulfovibrionales*	U	U
Otu182	2	18	0	12	5	71	108.0000	20.0000	88.0000	0.0607	0.0225	0.0989	*Bacteria*	*Firmicutes*	*Negativicutes*	U	U	U
Otu183	1	0	1	0	113	8	123.0000	2.0000	121.0000	0.0691	0.0022	0.1360	*Bacteria*	*Candidatus_Saccharibacteria*	*Saccharibacteria_genera_incertae_sedis*	U	U	U
Otu184	11	22	0	60	2	11	106.0000	33.0000	73.0000	0.0596	0.0371	0.0820	*Bacteria*	U	U	U	U	U
Otu185	11	23	0	11	0	13	58.0000	34.0000	24.0000	0.0326	0.0382	0.0270	*Bacteria*	U	U	U	U	U
Otu186	3	4	0	52	7	15	81.0000	7.0000	74.0000	0.0455	0.0079	0.0832	*Bacteria*	U	U	U	U	U

Otu187	2	4	0	65	14	10	95.0000	6.0000	89.0000	0.0534	0.0067	0.1000	*Bacteria*	*Proteobacteria*	*Deltaproteobacteria*	*Desulfovibrionales*	*Desulfovibrionaceae*	*Desulfovibrio*
Otu188	18	51	0	0	18	3	90.0000	69.0000	21.0000	0.0506	0.0775	0.0236	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu189	12	29	0	53	8	30	132.0000	41.0000	91.0000	0.0742	0.0461	0.1023	*Bacteria*	*Bacteroidetes*	U	U	U	U
Otu19	233	206	0	217	37	1039	1732.0000	439.0000	1293.0000	0.9733	0.4934	1.4532	*Bacteria*	*Bacteroidetes*	U	U	U	U
Otu190	0	0	0	84	0	6	90.0000	0.0000	90.0000	0.0506	0.0000	0.1011	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu191	9	3	28	1	98	6	145.0000	40.0000	105.0000	0.0815	0.0450	0.1180	*Bacteria*	*Actinobacteria*	*Actinobacteria*	*Actinomycetales*	U	U
Otu192	3	46	2	54	14	1	120.0000	51.0000	69.0000	0.0674	0.0573	0.0775	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu193	0	0	0	0	98	29	127.0000	0.0000	127.0000	0.0714	0.0000	0.1427	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu194	9	48	0	28	2	57	144.0000	57.0000	87.0000	0.0809	0.0641	0.0978	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu195	14	137	0	4	38	4	197.0000	151.0000	46.0000	0.1107	0.1697	0.0517	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu196	20	33	1	30	2	2	88.0000	54.0000	34.0000	0.0495	0.0607	0.0382	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu197	79	0	1	0	1	0	81.0000	80.0000	1.0000	0.0455	0.0899	0.0011	*Bacteria*	*Proteobacteria*	*Gammaproteobacteria*	*Xanthomonadales*	*Xanthomonadaceae*	*Pseudoxanthomonas*
Otu198	5	6	0	54	3	30	98.0000	11.0000	87.0000	0.0551	0.0124	0.0978	*Bacteria*	U	U	U	U	U
Otu199	5	18	0	30	5	51	109.0000	23.0000	86.0000	0.0613	0.0258	0.0967	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu2	35	0	8314	0	159	17	8525.0000	8349.0000	176.0000	4.7906	9.3833	0.1978	*Bacteria*	*Proteobacteria*	*Gammaproteobacteria*	*Enterobacteriales*	*Enterobacteriaceae*	U
Otu20	0	0	0	1412	0	0	1412.0000	0.0000	1412.0000	0.7935	0.0000	1.5869	*Bacteria*	*Bacteroidetes*	U	U	U	U
Otu200	21	16	0	28	8	30	103.0000	37.0000	66.0000	0.0579	0.0416	0.0742	*Bacteria*	*Bacteroidetes*	*Bacteroidia*	*Bacteroidales*	U	U
Otu201	13	27	0	44	8	29	121.0000	40.0000	81.0000	0.0680	0.0450	0.0910	*Bacteria*	*Firmicutes*	*Negativicutes*	U	U	U
Otu202	2	11	0	27	36	20	96.0000	13.0000	83.0000	0.0539	0.0146	0.0933	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu203	0	0	2	0	53	32	87.0000	2.0000	85.0000	0.0489	0.0022	0.0955	*Bacteria*	*Proteobacteria*	*Gammaproteobacteria*	*Xanthomonadales*	*Xanthomonadaceae*	*Stenotrophomonas*
Otu204	21	23	0	15	1	73	133.0000	44.0000	89.0000	0.0747	0.0495	0.1000	*Bacteria*	*Firmicutes*	U	U	U	U
Otu205	4	59	0	35	1	19	118.0000	63.0000	55.0000	0.0663	0.0708	0.0618	*Bacteria*	U	U	U	U	U
Otu206	0	44	0	4	3	24	75.0000	44.0000	31.0000	0.0421	0.0495	0.0348	*Bacteria*	*Actinobacteria*	*Actinobacteria*	U	U	U
Otu207	29	34	0	4	10	1	78.0000	63.0000	15.0000	0.0438	0.0708	0.0169	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu208	4	18	0	25	0	43	90.0000	22.0000	68.0000	0.0506	0.0247	0.0764	*Bacteria*	*Firmicutes*	U	U	U	U
Otu209	0	1	0	39	13	14	67.0000	1.0000	66.0000	0.0377	0.0011	0.0742	*Bacteria*	U	U	U	U	U
Otu21	69	1254	1	116	0	0	1440.0000	1324.0000	116.0000	0.8092	1.4880	0.1304	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Lachnospiraceae*	U
Otu210	6	70	0	5	0	27	108.0000	76.0000	32.0000	0.0607	0.0854	0.0360	*Bacteria*	*Firmicutes*	U	U	U	U
Otu211	4	16	0	38	2	14	74.0000	20.0000	54.0000	0.0416	0.0225	0.0607	*Bacteria*	*Bacteroidetes*	U	U	U	U
Otu212	1	10	0	1	19	28	59.0000	11.0000	48.0000	0.0332	0.0124	0.0539	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu213	0	0	1	60	3	10	74.0000	1.0000	73.0000	0.0416	0.0011	0.0820	*Bacteria*	*Firmicutes*	U	U	U	U
Otu214	19	20	0	15	5	32	91.0000	39.0000	52.0000	0.0511	0.0438	0.0584	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu215	1	0	0	42	64	20	127.0000	1.0000	126.0000	0.0714	0.0011	0.1416	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu216	7	41	0	11	1	30	90.0000	48.0000	42.0000	0.0506	0.0539	0.0472	*Bacteria*	*Proteobacteria*	*Betaproteobacteria*	*Burkholderiales*	U	U
Otu217	4	25	0	41	25	15	110.0000	29.0000	81.0000	0.0618	0.0326	0.0910	*Bacteria*	U	U	U	U	U

Otu218	6	21	0	16	4	26	73.0000	27.0000	46.0000	0.0410	0.0303	0.0517	*Bacteria*	*Firmicutes*	U	U	U	U
Otu219	0	32	0	17	0	31	80.0000	32.0000	48.0000	0.0450	0.0360	0.0539	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu22	263	471	10	323	74	200	1341.0000	744.0000	597.0000	0.7536	0.8362	0.6710	*Bacteria*	*Bacteroidetes*	*Bacteroidia*	*Bacteroidales*	*Porphyromonadaceae*	*Dysgonomonas*
Otu220	1	14	0	37	0	42	94.0000	15.0000	79.0000	0.0528	0.0169	0.0888	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu221	1	4	0	57	11	3	76.0000	5.0000	71.0000	0.0427	0.0056	0.0798	*Bacteria*	U	U	U	U	U
Otu222	6	6	0	4	36	38	90.0000	12.0000	78.0000	0.0506	0.0135	0.0877	*Bacteria*	*Firmicutes*	U	U	U	U
Otu223	0	0	0	20	0	40	60.0000	0.0000	60.0000	0.0337	0.0000	0.0674	*Bacteria*	*Firmicutes*	U	U	U	U
Otu224	16	23	0	22	11	2	74.0000	39.0000	35.0000	0.0416	0.0438	0.0393	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu225	0	0	0	0	97	18	115.0000	0.0000	115.0000	0.0646	0.0000	0.1292	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Lachnospiraceae*	U
Otu226	0	0	1	66	16	6	89.0000	1.0000	88.0000	0.0500	0.0011	0.0989	*Bacteria*	*Firmicutes*	U	U	U	U
Otu227	2	5	0	19	8	30	64.0000	7.0000	57.0000	0.0360	0.0079	0.0641	*Bacteria*	*Firmicutes*	U	U	U	U
Otu228	37	8	0	6	35	1	87.0000	45.0000	42.0000	0.0489	0.0506	0.0472	*Bacteria*	*Proteobacteria*	*Betaproteobacteria*	*Burkholderiales*	*Burkholderiaceae*	*Burkholderia*
Otu229	7	32	0	15	6	41	101.0000	39.0000	62.0000	0.0568	0.0438	0.0697	*Bacteria*	U	U	U	U	U
Otu23	242	584	1	556	68	420	1871.0000	827.0000	1044.0000	1.0514	0.9295	1.1733	*Bacteria*	*Bacteroidetes*	*Bacteroidia*	*Bacteroidales*	*Porphyromonadaceae*	U
Otu230	34	4	1	0	24	3	66.0000	39.0000	27.0000	0.0371	0.0438	0.0303	*Bacteria*	*Proteobacteria*	*Betaproteobacteria*	*Burkholderiales*	*Burkholderiaceae*	*Burkholderia*
Otu231	7	48	0	29	1	22	107.0000	55.0000	52.0000	0.0601	0.0618	0.0584	*Bacteria*	*Firmicutes*	U	U	U	U
Otu232	0	12	0	31	5	29	77.0000	12.0000	65.0000	0.0433	0.0135	0.0731	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu233	27	33	0	0	2	2	64.0000	60.0000	4.0000	0.0360	0.0674	0.0045	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu234	16	42	0	11	0	33	102.0000	58.0000	44.0000	0.0573	0.0652	0.0495	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu235	1	4	0	69	1	66	141.0000	5.0000	136.0000	0.0792	0.0056	0.1528	*Bacteria*	*Firmicutes*	U	U	U	U
Otu236	0	0	0	71	0	0	71.0000	0.0000	71.0000	0.0399	0.0000	0.0798	*Bacteria*	U	U	U	U	U
Otu237	0	0	0	27	0	29	56.0000	0.0000	56.0000	0.0315	0.0000	0.0629	*Bacteria*	U	U	U	U	U
Otu238	2	30	0	20	3	26	81.0000	32.0000	49.0000	0.0455	0.0360	0.0551	*Bacteria*	*Firmicutes*	U	U	U	U
Otu239	2	1	0	76	0	1	80.0000	3.0000	77.0000	0.0450	0.0034	0.0865	*Bacteria*	U	U	U	U	U
Otu24	6	181	2	893	296	193	1571.0000	189.0000	1382.0000	0.8828	0.2124	1.5532	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu240	0	0	62	10	6	4	82.0000	62.0000	20.0000	0.0461	0.0697	0.0225	*Bacteria*	*Firmicutes*	U	U	U	U
Otu241	3	21	0	19	22	20	85.0000	24.0000	61.0000	0.0478	0.0270	0.0686	*Bacteria*	U	U	U	U	U
Otu242	1	16	0	27	6	32	82.0000	17.0000	65.0000	0.0461	0.0191	0.0731	*Bacteria*	U	U	U	U	U
Otu243	0	7	0	34	9	2	52.0000	7.0000	45.0000	0.0292	0.0079	0.0506	*Bacteria*	*Firmicutes*	U	U	U	U
Otu244	2	9	0	38	2	47	98.0000	11.0000	87.0000	0.0551	0.0124	0.0978	*Bacteria*	*Firmicutes*	U	U	U	U
Otu245	6	3	8	0	37	4	58.0000	17.0000	41.0000	0.0326	0.0191	0.0461	*Bacteria*	*Actinobacteria*	*Actinobacteria*	*Actinomycetales*	*Microbacteriaceae*	U
Otu246	21	94	0	18	3	60	196.0000	115.0000	81.0000	0.1101	0.1292	0.0910	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu247	9	28	1	29	8	8	83.0000	38.0000	45.0000	0.0466	0.0427	0.0506	*Bacteria*	*Proteobacteria*	*Betaproteobacteria*	*Burkholderiales*	U	U
Otu248	31	9	0	15	2	15	72.0000	40.0000	32.0000	0.0405	0.0450	0.0360	*Bacteria*	*Bacteroidetes*	*Bacteroidia*	*Bacteroidales*	*Rikenellaceae*	*Alistipes*
Otu249	33	0	0	4	30	4	71.0000	33.0000	38.0000	0.0399	0.0371	0.0427	*Bacteria*	*Acidobacteria*	*Acidobacteria_Gp1*	*Edaphobacter*	U	U
Otu25	70	698	0	90	4	231	1093.0000	768.0000	325.0000	0.6142	0.8631	0.3653	*Bacteria*	U	U	U	U	U

Otu250	11	1	1	2	49	10	74.0000	13.0000	61.0000	0.0416	0.0146	0.0686	*Bacteria*	*Candidatus_Saccharibacteria_genera_incertae_sedis*	*Saccharibacteria_genera_incertae_sedis*	U	U	U
Otu251	1	23	0	6	0	34	64.0000	24.0000	40.0000	0.0360	0.0270	0.0450	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu252	3	30	0	17	0	16	66.0000	33.0000	33.0000	0.0371	0.0371	0.0371	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu253	0	10	0	12	0	35	57.0000	10.0000	47.0000	0.0320	0.0112	0.0528	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu254	0	5	0	2	50	66	123.0000	5.0000	118.0000	0.0691	0.0056	0.1326	*Bacteria*	*Firmicutes*	*Negativicutes*	U	U	U
Otu255	0	3	1	16	43	6	69.0000	4.0000	65.0000	0.0388	0.0045	0.0731	*Bacteria*	U	U	U	U	U
Otu256	0	35	0	5	2	13	55.0000	35.0000	20.0000	0.0309	0.0393	0.0225	*Bacteria*	*Firmicutes*	U	U	U	U
Otu257	1	30	0	32	0	31	94.0000	31.0000	63.0000	0.0528	0.0348	0.0708	*Bacteria*	*Firmicutes*	U	U	U	U
Otu258	1	3	0	9	15	25	53.0000	4.0000	49.0000	0.0298	0.0045	0.0551	*Bacteria*	U	U	U	U	U
Otu259	0	2	0	7	9	47	65.0000	2.0000	63.0000	0.0365	0.0022	0.0708	*Bacteria*	*Firmicutes*	U	U	U	U
Otu26	0	0	0	1	1388	121	1510.0000	0.0000	1510.0000	0.8485	0.0000	1.6971	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu260	2	5	0	20	35	18	80.0000	7.0000	73.0000	0.0450	0.0079	0.0820	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu261	3	3	0	14	30	16	66.0000	6.0000	60.0000	0.0371	0.0067	0.0674	*Bacteria*	*Firmicutes*	U	U	U	U
Otu262	4	27	0	2	14	18	65.0000	31.0000	34.0000	0.0365	0.0348	0.0382	*Bacteria*	*Firmicutes*	U	U	U	U
Otu263	7	5	0	51	1	3	67.0000	12.0000	55.0000	0.0377	0.0135	0.0618	*Bacteria*	*Firmicutes*	U	U	U	U
Otu264	0	0	89	1	0	0	90.0000	89.0000	1.0000	0.0506	0.1000	0.0011	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu265	1	20	0	21	0	25	67.0000	21.0000	46.0000	0.0377	0.0236	0.0517	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu266	5	32	0	8	7	12	64.0000	37.0000	27.0000	0.0360	0.0416	0.0303	*Bacteria*	*Firmicutes*	U	U	U	U
Otu267	2	4	0	52	0	22	80.0000	6.0000	74.0000	0.0450	0.0067	0.0832	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu268	18	9	1	49	9	32	118.0000	28.0000	90.0000	0.0663	0.0315	0.1011	*Bacteria*	*Bacteroidetes*	*Bacteroidia*	U	U	U
Otu269	6	26	0	5	5	22	64.0000	32.0000	32.0000	0.0360	0.0360	0.0360	*Bacteria*	U	U	U	U	U
Otu27	201	333	0	30	12	440	1016.0000	534.0000	482.0000	0.5709	0.6002	0.5417	*Bacteria*	*Bacteroidetes*	*Bacteroidia*	*Bacteroidales*	*Bacteroidaceae*	U
Otu270	9	20	0	2	6	24	61.0000	29.0000	32.0000	0.0343	0.0326	0.0360	*Bacteria*	U	U	U	U	U
Otu271	7	23	0	2	8	15	55.0000	30.0000	25.0000	0.0309	0.0337	0.0281	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu272	6	16	0	6	0	40	68.0000	22.0000	46.0000	0.0382	0.0247	0.0517	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu273	2	16	0	16	2	26	62.0000	18.0000	44.0000	0.0348	0.0202	0.0495	*Bacteria*	*Firmicutes*	U	U	U	U
Otu274	0	4	0	24	0	24	52.0000	4.0000	48.0000	0.0292	0.0045	0.0539	*Bacteria*	U	U	U	U	U
Otu275	6	38	0	8	1	15	68.0000	44.0000	24.0000	0.0382	0.0495	0.0270	*Bacteria*	*Firmicutes*	U	U	U	U
Otu276	0	1	0	5	30	18	54.0000	1.0000	53.0000	0.0303	0.0011	0.0596	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu277	20	19	0	14	1	26	80.0000	39.0000	41.0000	0.0450	0.0438	0.0461	*Bacteria*	U	U	U	U	U
Otu278	0	0	0	56	8	2	66.0000	0.0000	66.0000	0.0371	0.0000	0.0742	*Bacteria*	*Firmicutes*	U	U	U	U
Otu279	0	0	0	34	21	7	62.0000	0.0000	62.0000	0.0348	0.0000	0.0697	*Bacteria*	U	U	U	U	U
Otu28	0	0	0	0	1330	107	1437.0000	0.0000	1437.0000	0.8075	0.0000	1.6150	*Bacteria*	*Firmicutes*	U	U	U	U
Otu280	10	33	0	9	0	0	52.0000	43.0000	9.0000	0.0292	0.0483	0.0101	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu281	4	2	0	10	37	2	55.0000	6.0000	49.0000	0.0309	0.0067	0.0551	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu282	18	32	0	3	60	17	130.0000	50.0000	80.0000	0.0731	0.0562	0.0899	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu283	0	0	0	1	35	4	40.0000	0.0000	40.0000	0.0225	0.0000	0.0450	*Bacteria*	U	U	U	U	U
Otu284	1	14	0	14	5	17	51.0000	15.0000	36.0000	0.0287	0.0169	0.0405	*Bacteria*	U	U	U	U	U
Otu285	13	28	0	14	3	4	62.0000	41.0000	21.0000	0.0348	0.0461	0.0236	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu286	7	1	0	17	58	7	90.0000	8.0000	82.0000	0.0506	0.0090	0.0922	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U

Otu287	2	39	0	5	3	13	62.0000	41.0000	21.0000	0.0348	0.0461	0.0236	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu288	5	12	0	18	6	10	51.0000	17.0000	34.0000	0.0287	0.0191	0.0382	*Bacteria*	*Proteobacteria*	*Deltaproteobacteria*	*Desulfovibrionales*	*Desulfovibrionaceae*	*Desulfovibrio*
Otu289	1	15	0	13	3	34	66.0000	16.0000	50.0000	0.0371	0.0180	0.0562	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu29	0	0	0	0	1106	108	1214.0000	0.0000	1214.0000	0.6822	0.0000	1.3644	*Bacteria*	*Firmicutes*	U	U	U	U
Otu290	24	33	0	1	0	0	58.0000	57.0000	1.0000	0.0326	0.0641	0.0011	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu291	4	69	0	22	5	12	112.0000	73.0000	39.0000	0.0629	0.0820	0.0438	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu292	3	9	0	14	4	24	54.0000	12.0000	42.0000	0.0303	0.0135	0.0472	*Bacteria*	U	U	U	U	U
Otu293	0	0	1	0	3	56	60.0000	1.0000	59.0000	0.0337	0.0011	0.0663	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu294	21	0	0	0	20	2	43.0000	21.0000	22.0000	0.0242	0.0236	0.0247	*Bacteria*	*Bacteroidetes*	*Flavobacteriia*	*Flavobacteriales*	*Flavobacteriaceae*	*Chryseobacterium*
Otu295	42	0	1	0	19	1	63.0000	43.0000	20.0000	0.0354	0.0483	0.0225	*Bacteria*	*Bacteroidetes*	*Sphingobacteriia*	*Sphingobacteriales*	*Chitinophagaceae*	*Taibaiella*
Otu296	14	49	0	13	4	6	86.0000	63.0000	23.0000	0.0483	0.0708	0.0258	*Bacteria*	*Firmicutes*	U	U	U	U
Otu297	4	17	0	17	0	27	65.0000	21.0000	44.0000	0.0365	0.0236	0.0495	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu298	0	0	0	0	97	9	106.0000	0.0000	106.0000	0.0596	0.0000	0.1191	*Bacteria*	*Firmicutes*	*Bacilli*	*Lactobacillales*	*Enterococcaceae*	*Enterococcus*
Otu299	2	17	0	12	66	48	145.0000	19.0000	126.0000	0.0815	0.0214	0.1416	*Bacteria*	*Firmicutes*	U	U		U
Otu3	246	4851	1	622	59	1250	7029.0000	5098.0000	1931.0000	3.9499	5.7296	2.1702	*Bacteria*	*Bacteroidetes*	*Bacteroidia*	*Bacteroidales*	*Porphyromonadaceae*	U
Otu30	285	120	0	0	101	313	819.0000	405.0000	414.0000	0.4602	0.4552	0.4653	*Bacteria*	*Bacteroidetes*	*Bacteroidia*	*Bacteroidales*	*Porphyromonadaceae*	*Proteiniphilum*
Otu300	16	29	0	2	2	0	49.0000	45.0000	4.0000	0.0275	0.0506	0.0045	*Bacteria*	*Firmicutes*	U	U	U	U
Otu301	5	20	0	43	3	33	104.0000	25.0000	79.0000	0.0584	0.0281	0.0888	*Bacteria*	*Proteobacteria*	*Deltaproteobacteria*	U	U	U
Otu302	0	0	0	8	2	41	51.0000	0.0000	51.0000	0.0287	0.0000	0.0573	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu303	3	45	0	11	4	35	98.0000	48.0000	50.0000	0.0551	0.0539	0.0562	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu304	0	21	0	14	1	35	71.0000	21.0000	50.0000	0.0399	0.0236	0.0562	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu305	4	30	0	11	5	11	61.0000	34.0000	27.0000	0.0343	0.0382	0.0303	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu306	4	11	0	17	1	36	69.0000	15.0000	54.0000	0.0388	0.0169	0.0607	*Bacteria*	U	U	U	U	U
Otu307	0	33	0	31	4	24	92.0000	33.0000	59.0000	0.0517	0.0371	0.0663	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu308	7	34	0	7	16	7	71.0000	41.0000	30.0000	0.0399	0.0461	0.0337	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu309	16	19	0	13	0	21	69.0000	35.0000	34.0000	0.0388	0.0393	0.0382	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu31	281	99	0	167	216	112	875.0000	380.0000	495.0000	0.4917	0.4271	0.5563	*Bacteria*	*Bacteroidetes*	*Bacteroidia*	*Bacteroidales*	U	U
Otu310	0	0	0	0	4	59	63.0000	0.0000	63.0000	0.0354	0.0000	0.0708	*Bacteria*	U	U	U	U	U
Otu311	0	23	0	16	2	11	52.0000	23.0000	29.0000	0.0292	0.0258	0.0326	*Bacteria*	U	U	U	U	U
Otu312	2	13	0	43	6	18	82.0000	15.0000	67.0000	0.0461	0.0169	0.0753	*Bacteria*	U	U	U	U	U
Otu313	7	16	0	21	1	14	59.0000	23.0000	36.0000	0.0332	0.0258	0.0405	*Bacteria*	U	U	U	U	U
Otu314	0	44	0	1	1	3	49.0000	44.0000	5.0000	0.0275	0.0495	0.0056	*Bacteria*	*Actinobacteria*	*Actinobacteria*	*Actinomycetales*	*Propionibacteriaceae*	U
Otu315	6	24	0	23	0	2	55.0000	30.0000	25.0000	0.0309	0.0337	0.0281	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu316	17	27	0	0	2	0	46.0000	44.0000	2.0000	0.0258	0.0495	0.0022	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu317	6	23	0	10	10	3	52.0000	29.0000	23.0000	0.0292	0.0326	0.0258	*Bacteria*	*Firmicutes*	U	U	U	U
Otu318	0	0	79	4	15	0	98.0000	79.0000	19.0000	0.0551	0.0888	0.0214	*Bacteria*	*Firmicutes*	*Erysipelotrichia*	*Erysipelotrichales*	*Erysipelotrichaceae*	U
Otu319	0	0	0	0	29	20	49.0000	0.0000	49.0000	0.0275	0.0000	0.0551	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu32	2	0	712	16	827	52	1609.000	714.0000	895.000	0.9042	0.8025	1.0059	*Bacteria*	*Firmicutes*	*Bacilli*	*Lactobacillales*	*Enterococcaceae*	*Enterococcus*

							0		0									
Otu320	3	10	0	6	6	10	35.0000	13.0000	22.0000	0.0197	0.0146	0.0247	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu321	16	27	0	3	4	1	51.0000	43.0000	8.0000	0.0287	0.0483	0.0090	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu322	20	0	2	0	47	0	69.0000	22.0000	47.0000	0.0388	0.0247	0.0528	*Bacteria*	*Actinobacteria*	*Actinobacteria*	*Actinomycetales*	*Nocardioidaceae*	*Nocardioides*
Otu323	7	15	1	11	7	1	42.0000	23.0000	19.0000	0.0236	0.0258	0.0214	*Bacteria*	U	U	U	U	U
Otu324	5	38	0	66	8	21	138.0000	43.0000	95.0000	0.0775	0.0483	0.1068	*Bacteria*	U	U	U	U	U
Otu325	46	0	0	0	29	0	75.0000	46.0000	29.0000	0.0421	0.0517	0.0326	*Bacteria*	*Proteobacteria*	U	U	U	U
Otu326	0	1	0	10	8	25	44.0000	1.0000	43.0000	0.0247	0.0011	0.0483	*Bacteria*	*Firmicutes*	U	U	U	U
Otu327	10	9	0	7	20	5	51.0000	19.0000	32.0000	0.0287	0.0214	0.0360	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu328	16	4	0	1	38	4	63.0000	20.0000	43.0000	0.0354	0.0225	0.0483	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu329	0	0	12	0	49	4	65.0000	12.0000	53.0000	0.0365	0.0135	0.0596	*Bacteria*	*Proteobacteria*	*Gammaproteobacteria*	*Pseudomonadales*	*Moraxellaceae*	*Acinetobacter*
Otu33	23	162	0	351	39	314	889.0000	185.0000	704.0000	0.4996	0.2079	0.7912	*Bacteria*	*Proteobacteria*	*Deltaproteobacteria*	*Desulfovibrionales*	U	U
Otu330	18	1	4	2	123	7	155.0000	23.0000	132.0000	0.0871	0.0258	0.1484	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	*Rhizobiales*	*Bradyrhizobiaceae*	U
Otu331	0	1	0	7	5	54	67.0000	1.0000	66.0000	0.0377	0.0011	0.0742	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu332	0	2	0	11	15	22	50.0000	2.0000	48.0000	0.0281	0.0022	0.0539	*Bacteria*	U	U	U	U	U
Otu333	2	14	0	27	18	8	69.0000	16.0000	53.0000	0.0388	0.0180	0.0596	*Bacteria*	U	U	U	U	U
Otu334	1	15	0	1	1	30	48.0000	16.0000	32.0000	0.0270	0.0180	0.0360	*Bacteria*	*Firmicutes*	U	U	U	U
Otu335	0	0	108	0	1	0	109.0000	108.0000	1.0000	0.0613	0.1214	0.0011	*Bacteria*	*Firmicutes*	*Bacilli*	*Bacillales*	*Paenibacillaceae_1*	*Paenibacillus*
Otu336	7	50	0	6	0	12	75.0000	57.0000	18.0000	0.0421	0.0641	0.0202	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu337	1	48	0	5	1	7	62.0000	49.0000	13.0000	0.0348	0.0551	0.0146	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu338	1	6	0	5	1	13	26.0000	7.0000	19.0000	0.0146	0.0079	0.0214	*Bacteria*	U	U	U	U	U
Otu339	0	0	0	0	40	8	48.0000	0.0000	48.0000	0.0270	0.0000	0.0539	*Bacteria*	U	U	U	U	U
Otu34	0	0	948	0	0	0	948.0000	948.0000	0.0000	0.5327	1.0654	0.0000	*Bacteria*	*Proteobacteria*	*Gammaproteobacteria*	*Enterobacteriales*	*Enterobacteriaceae*	*Providencia*
Otu340	19	3	1	0	29	1	53.0000	23.0000	30.0000	0.0298	0.0258	0.0337	*Bacteria*	*Candidatus_Saccharibacteria_bacteria*	*Saccharibacteria_genera_incertae_sedis*	U	U	U
Otu341	3	24	0	9	0	28	64.0000	27.0000	37.0000	0.0360	0.0303	0.0416	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu342	38	0	0	0	3	0	41.0000	38.0000	3.0000	0.0230	0.0427	0.0034	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	*Sphingomonadales*	*Sphingomonadaceae*	*Sphingomonas*
Otu343	6	15	0	9	0	10	40.0000	21.0000	19.0000	0.0225	0.0236	0.0214	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu344	1	17	0	32	1	27	78.0000	18.0000	60.0000	0.0438	0.0202	0.0674	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu345	6	32	0	35	0	11	84.0000	38.0000	46.0000	0.0472	0.0427	0.0517	*Bacteria*	*Proteobacteria*	*Deltaproteobacteria*	*Desulfovibrionales*	*Desulfovibrionaceae*	*Desulfovibrio*
Otu346	16	32	0	24	2	10	84.0000	48.0000	36.0000	0.0472	0.0539	0.0405	*Bacteria*	U	U	U	U	U
Otu347	15	0	0	0	44	9	68.0000	15.0000	53.0000	0.0382	0.0169	0.0596	*Bacteria*	*Bacteroidetes*	*Flavobacteriia*	*Flavobacteriales*	*Flavobacteriaceae*	*Chryseobacterium*
Otu348	4	41	0	5	0	5	55.0000	45.0000	10.0000	0.0309	0.0506	0.0112	*Bacteria*	*Firmicutes*	U	U	U	U
Otu349	12	8	0	2	6	1	29.0000	20.0000	9.0000	0.0163	0.0225	0.0101	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu35	18	165	0	270	2	305	760.0000	183.0000	577.0000	0.4271	0.2057	0.6485	*Bacteria*	*Firmicutes*	U	U	U	U
Otu350	3	0	0	36	1	8	48.0000	3.0000	45.0000	0.0270	0.0034	0.0506	*Bacteria*	*Firmicutes*	U	U	U	U
Otu351	0	0	0	19	4	13	36.0000	0.0000	36.0000	0.0202	0.0000	0.0405	*Bacteria*	*Firmicutes*	U	U	U	U
Otu352	4	48	0	0	0	0	52.0000	52.0000	0.0000	0.0292	0.0584	0.0000	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U

Otu353	0	0	0	8	3	41	52.0000	0.0000	52.0000	0.0292	0.0000	0.0584	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu354	2	6	0	11	0	32	51.0000	8.0000	43.0000	0.0287	0.0090	0.0483	*Bacteria*	*Firmicutes*	U	U	U	U
Otu355	0	0	0	29	3	45	77.0000	0.0000	77.0000	0.0433	0.0000	0.0865	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu356	5	17	0	5	2	24	53.0000	22.0000	31.0000	0.0298	0.0247	0.0348	*Bacteria*	*Proteobacteria*	*Deltaproteobacteria*	*Desulfovibrionales*	*Desulfovibrionaceae*	*Desulfovibrio*
Otu357	0	0	0	6	3	37	46.0000	0.0000	46.0000	0.0258	0.0000	0.0517	*Bacteria*	U	U	U	U	U
Otu358	0	0	0	0	3	51	54.0000	0.0000	54.0000	0.0303	0.0000	0.0607	*Bacteria*	*Proteobacteria*	*Betaproteobacteria*	U	U	U
Otu359	9	4	2	0	27	5	47.0000	15.0000	32.0000	0.0264	0.0169	0.0360	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	*Rhizobiales*	U	U
Otu36	0	0	0	0	126	751	877.0000	0.0000	877.0000	0.4928	0.0000	0.9856	*Bacteria*	*Bacteroidetes*	*Bacteroidia*	*Bacteroidales*	*Porphyromonadaceae*	U
Otu360	9	1	2	2	24	3	41.0000	12.0000	29.0000	0.0230	0.0135	0.0326	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	*Rhizobiales*	U	U
Otu361	9	9	1	2	2	7	30.0000	19.0000	11.0000	0.0169	0.0214	0.0124	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu362	15	4	0	4	32	4	59.0000	19.0000	40.0000	0.0332	0.0214	0.0450	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	U	U	U
Otu363	0	0	0	46	10	1	57.0000	0.0000	57.0000	0.0320	0.0000	0.0641	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu364	2	8	0	7	1	15	33.0000	10.0000	23.0000	0.0185	0.0112	0.0258	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu365	4	1	0	0	48	3	56.0000	5.0000	51.0000	0.0315	0.0056	0.0573	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	*Rhizobiales*	U	U
Otu366	2	14	0	10	0	28	54.0000	16.0000	38.0000	0.0303	0.0180	0.0427	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu367	28	0	0	0	21	2	51.0000	28.0000	23.0000	0.0287	0.0315	0.0258	*Bacteria*	*Bacteroidetes*	*Sphingobacteriia*	*Sphingobacteriales*	*Chitinophagaceae*	U
Otu368	0	0	0	0	44	27	71.0000	0.0000	71.0000	0.0399	0.0000	0.0798	*Bacteria*	*Firmicutes*	U	U	U	U
Otu369	4	21	0	13	3	22	63.0000	25.0000	38.0000	0.0354	0.0281	0.0427	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu37	46	26	156	17	572	32	849.0000	228.0000	621.0000	0.4771	0.2562	0.6979	*Bacteria*	*Actinobacteria*	*Actinobacteria*	*Actinomycetales*	*Microbacteriaceae*	*Gryllotalpicola*
Otu370	0	0	0	0	22	14	36.0000	0.0000	36.0000	0.0202	0.0000	0.0405	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu371	16	4	0	2	1	2	25.0000	20.0000	5.0000	0.0140	0.0225	0.0056	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu372	21	5	0	0	8	9	43.0000	26.0000	17.0000	0.0242	0.0292	0.0191	*Bacteria*	*Firmicutes*	U	U	U	U
Otu373	1	11	0	12	8	13	45.0000	12.0000	33.0000	0.0253	0.0135	0.0371	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu374	4	16	0	6	1	12	39.0000	20.0000	19.0000	0.0219	0.0225	0.0214	*Bacteria*	U	U	U	U	U
Otu375	0	0	0	3	3	33	39.0000	0.0000	39.0000	0.0219	0.0000	0.0438	*Bacteria*	U	U	U	U	U
Otu376	12	21	0	4	3	0	40.0000	33.0000	7.0000	0.0225	0.0371	0.0079	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu377	0	10	0	38	0	12	60.0000	10.0000	50.0000	0.0337	0.0112	0.0562	*Bacteria*	*Actinobacteria*	*Actinobacteria*	*Actinomycetales*	U	U
Otu378	1	7	0	8	0	33	49.0000	8.0000	41.0000	0.0275	0.0090	0.0461	*Bacteria*	*Proteobacteria*	*Betaproteobacteria*	U	U	U
Otu379	4	10	0	49	3	77	143.0000	14.0000	129.0000	0.0804	0.0157	0.1450	*Bacteria*	*Firmicutes*	U	U	U	U
Otu38	23	11	3	216	353	166	772.0000	37.0000	735.0000	0.4338	0.0416	0.8261	*Bacteria*	*Bacteroidetes*	*Bacteroidia*	*Bacteroidales*	*Bacteroidaceae*	U
Otu380	0	5	0	3	17	2	27.0000	5.0000	22.0000	0.0152	0.0056	0.0247	*Bacteria*	*Firmicutes*	U	U	U	U
Otu381	9	6	0	11	6	7	39.0000	15.0000	24.0000	0.0219	0.0169	0.0270	*Bacteria*	*Proteobacteria*	U	U	U	U
Otu382	0	4	0	6	0	29	39.0000	4.0000	35.0000	0.0219	0.0045	0.0393	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu383	0	11	1	38	0	1	51.0000	12.0000	39.0000	0.0287	0.0135	0.0438	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu384	5	24	0	10	0	9	48.0000	29.0000	19.0000	0.0270	0.0326	0.0214	*Bacteria*	*Firmicutes*	U	U	U	U

Otu385	9	11	0	7	4	10	41.0000	20.0000	21.0000	0.0230	0.0225	0.0236	*Bacteria*	U	U	U	U	U
Otu386	8	39	0	5	1	0	53.0000	47.0000	6.0000	0.0298	0.0528	0.0067	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu387	0	0	0	2	0	35	37.0000	0.0000	37.0000	0.0208	0.0000	0.0416	*Bacteria*	U	U	U	U	U
Otu388	4	12	0	17	8	13	54.0000	16.0000	38.0000	0.0303	0.0180	0.0427	*Bacteria*	*Firmicutes*	U	U	U	U
Otu389	2	5	0	10	2	7	26.0000	7.0000	19.0000	0.0146	0.0079	0.0214	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu39	109	201	0	79	31	230	650.0000	310.0000	340.0000	0.3653	0.3484	0.3821	*Bacteria*	*Candidatus_Saccharibacteria_genera_incertae_sedis*	*Saccharibacteria_genera_incertae_sedis*	U	U	U
Otu390	30	7	0	17	12	2	68.0000	37.0000	31.0000	0.0382	0.0416	0.0348	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu391	0	0	0	54	1	2	57.0000	0.0000	57.0000	0.0320	0.0000	0.0641	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu392	33	21	0	0	5	1	60.0000	54.0000	6.0000	0.0337	0.0607	0.0067	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu393	14	18	1	5	5	0	43.0000	33.0000	10.0000	0.0242	0.0371	0.0112	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu394	0	0	28	0	0	0	28.0000	28.0000	0.0000	0.0157	0.0315	0.0000	*Bacteria*	*Firmicutes*	U	U	U	U
Otu395	0	0	0	3	0	29	32.0000	0.0000	32.0000	0.0180	0.0000	0.0360	*Bacteria*	*Firmicutes*	U	U	U	U
Otu396	6	7	0	17	11	7	48.0000	13.0000	35.0000	0.0270	0.0146	0.0393	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu397	0	0	0	0	0	47	47.0000	0.0000	47.0000	0.0264	0.0000	0.0528	*Bacteria*	*Actinobacteria*	*Actinobacteria*	*Actinomycetales*	U	U
Otu398	5	25	0	0	11	2	43.0000	30.0000	13.0000	0.0242	0.0337	0.0146	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu399	0	2	1	22	24	3	52.0000	3.0000	49.0000	0.0292	0.0034	0.0551	*Bacteria*	*Firmicutes*	U	U	U	U
Otu4	65	3	4409	249	492	156	5374.0000	4477.0000	897.0000	3.0199	5.0316	1.0081	*Bacteria*	*Firmicutes*	*Bacilli*	*Lactobacillales*	*Streptococcaceae*	*Lactococcus*
Otu40	0	5	1	3	615	131	755.0000	6.0000	749.0000	0.4243	0.0067	0.8418	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu400	0	2	0	12	1	19	34.0000	2.0000	32.0000	0.0191	0.0022	0.0360	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Peptococcaceae_1*	U
Otu401	3	2	0	19	0	6	30.0000	5.0000	25.0000	0.0169	0.0056	0.0281	*Bacteria*	U	U	U	U	U
Otu402	3	10	0	38	4	13	68.0000	13.0000	55.0000	0.0382	0.0146	0.0618	*Bacteria*	U	U	U	U	U
Otu403	24	0	1	0	7	1	33.0000	25.0000	8.0000	0.0185	0.0281	0.0090	*Bacteria*	*Proteobacteria*	*Gammaproteobacteria*	*Xanthomonadales*	*Xanthomonadaceae*	*Pseudoxanthomonas*
Otu404	2	36	0	12	0	18	68.0000	38.0000	30.0000	0.0382	0.0427	0.0337	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu405	2	8	0	2	0	13	25.0000	10.0000	15.0000	0.0140	0.0112	0.0169	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu406	4	1	3	0	19	8	35.0000	8.0000	27.0000	0.0197	0.0090	0.0303	*Bacteria*	U	U	U	U	U
Otu407	0	0	0	0	5	25	30.0000	0.0000	30.0000	0.0169	0.0000	0.0337	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu408	3	51	0	15	0	8	77.0000	54.0000	23.0000	0.0433	0.0607	0.0258	*Bacteria*	*Firmicutes*	*Negativicutes*	U	U	U
Otu409	1	4	0	14	6	6	31.0000	5.0000	26.0000	0.0174	0.0056	0.0292	*Bacteria*	*Firmicutes*	U	U	U	U
Otu41	91	620	1	48	27	37	824.0000	712.0000	112.0000	0.4630	0.8002	0.1259	*Bacteria*	*Candidatus_Saccharibacteria*	U	U	U	U
Otu410	1	1	0	5	0	31	38.0000	2.0000	36.0000	0.0214	0.0022	0.0405	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu411	0	3	0	17	0	23	43.0000	3.0000	40.0000	0.0242	0.0034	0.0450	*Bacteria*	*Firmicutes*	U	U	U	U
Otu412	0	2	0	18	0	16	36.0000	2.0000	34.0000	0.0202	0.0022	0.0382	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu413	1	1	0	7	5	21	35.0000	2.0000	33.0000	0.0197	0.0022	0.0371	*Bacteria*	U	U	U	U	U
Otu414	1	4	0	28	1	4	38.0000	5.0000	33.0000	0.0214	0.0056	0.0371	*Bacteria*	U	U	U	U	U
Otu415	1	3	0	17	10	5	36.0000	4.0000	32.0000	0.0202	0.0045	0.0360	*Bacteria*	*Firmicutes*	U	U	U	U
Otu416	4	10	0	24	10	15	63.0000	14.0000	49.0000	0.0354	0.0157	0.0551	*Bacteria*	U	U	U	U	U
Otu417	7	2	0	1	18	7	35.0000	9.0000	26.0000	0.0197	0.0101	0.0292	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	*Sphingomonadales*	*Sphingomonadaceae*	*Sphingobium*
Otu418	6	8	1	0	11	9	35.0000	15.0000	20.0000	0.0197	0.0169	0.0225	*Bacteria*	U	U	U	U	U

Otu419	0	1	0	2	0	9	12.0000	1.0000	11.0000	0.0067	0.0011	0.0124	*Bacteria*	U	U	U	U	U
Otu42	76	136	211	38	650	63	1174.0000	423.0000	751.0000	0.6597	0.4754	0.8440	*Bacteria*	*Actinobacteria*	*Actinobacteria*	*Actinomycetales*	*Promicromonosporacea e*	U
Otu420	0	4	0	7	1	22	34.0000	4.0000	30.0000	0.0191	0.0045	0.0337	*Bacteria*	*Firmicutes*	U	U	U	U
Otu421	14	14	0	1	12	6	47.0000	28.0000	19.0000	0.0264	0.0315	0.0214	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu422	1	1	0	3	0	21	26.0000	2.0000	24.0000	0.0146	0.0022	0.0270	*Bacteria*	*Firmicutes*	U	U	U	U
Otu423	1	7	0	7	1	5	21.0000	8.0000	13.0000	0.0118	0.0090	0.0146	*Bacteria*	U	U	U	U	U
Otu424	0	10	0	1	0	8	19.0000	10.0000	9.0000	0.0107	0.0112	0.0101	*Bacteria*	*Firmicutes*	U	U	U	U
Otu425	13	19	0	19	4	2	57.0000	32.0000	25.0000	0.0320	0.0360	0.0281	*Bacteria*	U	U	U	U	U
Otu426	3	0	0	3	0	24	30.0000	3.0000	27.0000	0.0169	0.0034	0.0303	*Bacteria*	*Firmicutes*	U	U	U	U
Otu427	22	20	0	3	2	1	48.0000	42.0000	6.0000	0.0270	0.0472	0.0067	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	*Clostridium_IV*
Otu428	2	12	0	2	0	27	43.0000	14.0000	29.0000	0.0242	0.0157	0.0326	*Bacteria*	*Firmicutes*	U	U	U	U
Otu429	0	12	0	13	1	19	45.0000	12.0000	33.0000	0.0253	0.0135	0.0371	*Bacteria*	U	U	U	U	U
Otu43	0	0	0	12	513	160	685.0000	0.0000	685.0000	0.3849	0.0000	0.7699	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu430	1	3	0	17	2	19	42.0000	4.0000	38.0000	0.0236	0.0045	0.0427	*Bacteria*	U	U	U	U	U
Otu431	1	15	0	13	4	10	43.0000	16.0000	27.0000	0.0242	0.0180	0.0303	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu432	10	33	0	5	2	6	56.0000	43.0000	13.0000	0.0315	0.0483	0.0146	*Bacteria*	*Firmicutes*	U	U	U	U
Otu433	8	21	0	6	1	5	41.0000	29.0000	12.0000	0.0230	0.0326	0.0135	*Bacteria*	U	U	U	U	U
Otu434	12	8	0	4	0	0	24.0000	20.0000	4.0000	0.0135	0.0225	0.0045	*Bacteria*	U	U	U	U	U
Otu435	1	20	0	40	22	15	98.0000	21.0000	77.0000	0.0551	0.0236	0.0865	*Bacteria*	U	U	U	U	U
Otu436	9	17	0	1	2	5	34.0000	26.0000	8.0000	0.0191	0.0292	0.0090	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu437	0	1	0	20	4	7	32.0000	1.0000	31.0000	0.0180	0.0011	0.0348	*Bacteria*	U	U	U	U	U
Otu438	2	7	0	16	0	14	39.0000	9.0000	30.0000	0.0219	0.0101	0.0337	*Bacteria*	*Proteobacteria*	*Deltaproteobacteria*	U	U	U
Otu439	0	0	1	17	9	3	30.0000	1.0000	29.0000	0.0169	0.0011	0.0326	*Bacteria*	U	*U*	U	U	U
Otu44	36	87	0	68	26	348	565.0000	123.0000	442.0000	0.3175	0.1382	0.4968	*Bacteria*	*Bacteroidetes*	*Bacteroidia*	*Bacteroidales*	*Porphyromonadaceae*	U
Otu440	1	5	0	10	1	14	31.0000	6.0000	25.0000	0.0174	0.0067	0.0281	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu441	0	5	0	37	2	4	48.0000	5.0000	43.0000	0.0270	0.0056	0.0483	*Bacteria*	*Firmicutes*	U	U	U	U
Otu442	0	12	0	8	2	6	28.0000	12.0000	16.0000	0.0157	0.0135	0.0180	*Bacteria*	*Firmicutes*	U	U	U	U
Otu443	1	1	2	0	25	2	31.0000	4.0000	27.0000	0.0174	0.0045	0.0303	*Bacteria*	*Actinobacteria*	*Actinobacteria*	*Actinomycetales*	*Nocardioidaceae*	*Nocardioides*
Otu444	3	22	0	4	0	15	44.0000	25.0000	19.0000	0.0247	0.0281	0.0214	*Bacteria*	*Firmicutes*	U	U	U	U
Otu445	4	5	0	4	1	10	24.0000	9.0000	15.0000	0.0135	0.0101	0.0169	*Bacteria*	U	U	U	U	U
Otu446	0	6	0	20	3	14	43.0000	6.0000	37.0000	0.0242	0.0067	0.0416	*Bacteria*	U	U	U	U	U
Otu447	0	10	0	13	0	10	33.0000	10.0000	23.0000	0.0185	0.0112	0.0258	*Bacteria*	*Proteobacteria*	*Deltaproteobacteria*	*Desulfovibrionales*	*Desulfovibrionaceae*	*Desulfovibrio*
Otu448	0	3	0	14	0	11	28.0000	3.0000	25.0000	0.0157	0.0034	0.0281	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu449	1	5	0	9	3	19	37.0000	6.0000	31.0000	0.0208	0.0067	0.0348	*Bacteria*	U	U	U	U	U
Otu45	73	667	0	106	44	420	1310.0000	740.0000	570.0000	0.7361	0.8317	0.6406	*Bacteria*	U	U	U	U	U
Otu450	1	3	0	7	0	14	25.0000	4.0000	21.0000	0.0140	0.0045	0.0236	*Bacteria*	U	U	U	U	U
Otu451	0	15	0	41	0	24	80.0000	15.0000	65.0000	0.0450	0.0169	0.0731	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu452	0	0	0	1	14	13	28.0000	0.0000	28.0000	0.0157	0.0000	0.0315	*Bacteria*	*Firmicutes*	U	U	U	U
Otu453	2	5	0	18	13	6	44.0000	7.0000	37.0000	0.0247	0.0079	0.0416	*Bacteria*	*Firmicutes*	U	U	U	U

Otu454	0	0	0	11	13	16	40.0000	0.0000	40.0000	0.0225	0.0000	0.0450	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu455	10	20	0	10	11	2	53.0000	30.0000	23.0000	0.0298	0.0337	0.0258	*Bacteria*	*Firmicutes*	U	U	U	U
Otu456	4	15	0	6	0	14	39.0000	19.0000	20.0000	0.0219	0.0214	0.0225	*Bacteria*	*Firmicutes*	U	U	U	U
Otu457	5	8	0	7	30	32	82.0000	13.0000	69.0000	0.0461	0.0146	0.0775	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu458	0	0	0	0	40	6	46.0000	0.0000	46.0000	0.0258	0.0000	0.0517	*Bacteria*	*Firmicutes*	U	U	U	U
Otu459	0	0	0	0	2	32	34.0000	0.0000	34.0000	0.0191	0.0000	0.0382	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu46	65	153	0	24	358	153	753.0000	218.0000	535.0000	0.4231	0.2450	0.6013	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu460	2	7	0	7	25	3	44.0000	9.0000	35.0000	0.0247	0.0101	0.0393	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu461	5	6	0	5	3	22	41.0000	11.0000	30.0000	0.0230	0.0124	0.0337	*Bacteria*	*Firmicutes*	U	U	U	U
Otu462	1	7	0	31	0	4	43.0000	8.0000	35.0000	0.0242	0.0090	0.0393	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu463	0	5	0	24	0	17	46.0000	5.0000	41.0000	0.0258	0.0056	0.0461	*Bacteria*	U	U	U	U	U
Otu464	1	19	0	18	7	8	53.0000	20.0000	33.0000	0.0298	0.0225	0.0371	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu465	2	19	0	0	4	9	34.0000	21.0000	13.0000	0.0191	0.0236	0.0146	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu466	8	0	0	0	0	0	8.0000	8.0000	0.0000	0.0045	0.0090	0.0000	*Bacteria*	*Proteobacteria*	*Gammaproteobacteria*	*Pseudomonadales*	*Pseudomonadaceae*	*Pseudomonas*
Otu467	2	13	0	11	0	3	29.0000	15.0000	14.0000	0.0163	0.0169	0.0157	*Bacteria*	U	U	U	U	U
Otu468	1	4	0	1	1	10	17.0000	5.0000	12.0000	0.0096	0.0056	0.0135	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Lachnospiraceae*	U
Otu469	3	5	1	22	5	0	36.0000	9.0000	27.0000	0.0202	0.0101	0.0303	*Bacteria*	U	U	U	U	U
Otu47	11	270	0	179	148	66	674.0000	281.0000	393.0000	0.3787	0.3158	0.4417	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu470	0	0	0	0	7	10	17.0000	0.0000	17.0000	0.0096	0.0000	0.0191	*Bacteria*	*Firmicutes*	U	U	U	U
Otu471	8	10	0	6	2	10	36.0000	18.0000	18.0000	0.0202	0.0202	0.0202	*Bacteria*	U	U	U	U	U
Otu472	1	23	0	6	0	10	40.0000	24.0000	16.0000	0.0225	0.0270	0.0180	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu473	5	6	0	0	3	20	34.0000	11.0000	23.0000	0.0191	0.0124	0.0258	*Bacteria*	U	U	U	U	U
Otu474	0	0	0	15	0	29	44.0000	0.0000	44.0000	0.0247	0.0000	0.0495	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Syntrophomonadaceae*	U
Otu475	2	3	0	3	0	16	24.0000	5.0000	19.0000	0.0135	0.0056	0.0214	*Bacteria*	U	U	U	U	U
Otu476	8	0	0	0	35	1	44.0000	8.0000	36.0000	0.0247	0.0090	0.0405	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	*Rhizobiales*	U	U
Otu477	8	3	2	9	16	15	53.0000	13.0000	40.0000	0.0298	0.0146	0.0450	*Bacteria*	*Firmicutes*	U	U	U	U
Otu478	0	0	1	8	4	9	22.0000	1.0000	21.0000	0.0124	0.0011	0.0236	*Bacteria*	*Firmicutes*	U	U	U	U
Otu479	1	4	1	18	4	9	37.0000	6.0000	31.0000	0.0208	0.0067	0.0348	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu48	83	302	0	366	25	308	1084.0000	385.0000	699.0000	0.6091	0.4327	0.7856	*Bacteria*	*Bacteroidetes*	*Bacteroidia*	*Bacteroidales*	*Porphyromonadaceae*	U
Otu480	14	1	0	1	29	3	48.0000	15.0000	33.0000	0.0270	0.0169	0.0371	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	*Rhodospirillales*	*Reyranella*	U
Otu481	0	0	0	6	25	7	38.0000	0.0000	38.0000	0.0214	0.0000	0.0427	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu482	0	0	2	2	35	12	51.0000	2.0000	49.0000	0.0287	0.0022	0.0551	*Bacteria*	*Firmicutes*	U	U	U	U
Otu483	0	14	0	3	21	4	42.0000	14.0000	28.0000	0.0236	0.0157	0.0315	*Bacteria*	U	U	U	U	U
Otu484	0	0	0	6	15	9	30.0000	0.0000	30.0000	0.0169	0.0000	0.0337	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu485	0	0	0	1	2	20	23.0000	0.0000	23.0000	0.0129	0.0000	0.0258	*Bacteria*	U	U	U	U	U
Otu486	1	7	0	5	6	10	29.0000	8.0000	21.0000	0.0163	0.0090	0.0236	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu487	1	2	0	12	9	11	35.0000	3.0000	32.0000	0.0197	0.0034	0.0360	*Bacteria*	*Firmicutes*	U	U	U	U
Otu488	0	0	0	18	13	4	35.0000	0.0000	35.0000	0.0197	0.0000	0.0393	*Bacteria*	*Firmicutes*	U	U	U	U
Otu489	4	0	1	0	14	0	19.0000	5.0000	14.0000	0.0107	0.0056	0.0157	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	*Sphingomonadales*	*Sphingomonadaceae*	U

Otu49	29	20	473	18	161	74	775.0000	522.0000	253.0000	0.4355	0.5867	0.2843	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu490	5	4	0	2	0	7	18.0000	9.0000	9.0000	0.0101	0.0101	0.0101	*Bacteria*	U	U	U	U	U
Otu491	3	21	0	6	0	14	44.0000	24.0000	20.0000	0.0247	0.0270	0.0225	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu492	3	25	0	9	4	3	44.0000	28.0000	16.0000	0.0247	0.0315	0.0180	*Bacteria*	*Firmicutes*	U	U	U	U
Otu493	0	5	0	7	6	4	22.0000	5.0000	17.0000	0.0124	0.0056	0.0191	*Bacteria*	U	U	U	U	U
Otu494	3	6	0	24	1	13	47.0000	9.0000	38.0000	0.0264	0.0101	0.0427	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu495	1	11	0	4	1	16	33.0000	12.0000	21.0000	0.0185	0.0135	0.0236	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu496	2	9	0	10	12	6	39.0000	11.0000	28.0000	0.0219	0.0124	0.0315	*Bacteria*	*Firmicutes*	U	U	U	U
Otu497	0	0	0	9	0	13	22.0000	0.0000	22.0000	0.0124	0.0000	0.0247	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu498	0	0	0	0	6	25	31.0000	0.0000	31.0000	0.0174	0.0000	0.0348	*Bacteria*	U	U	U	U	U
Otu499	0	0	33	0	0	0	33.0000	33.0000	0.0000	0.0185	0.0371	0.0000	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Clostridiaceae_1*	*Clostridium_sensu_stricto*
Otu5	290	652	4	2196	332	550	4024.0000	946.0000	3078.0000	2.2613	1.0632	3.4593	*Bacteria*	*Bacteroidetes*	*Bacteroidia*	U	U	U
Otu50	82	360	1	44	8	87	582.0000	443.0000	139.0000	0.3271	0.4979	0.1562	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu500	3	3	23	0	26	0	55.0000	29.0000	26.0000	0.0309	0.0326	0.0292	*Bacteria*	*Actinobacteria*	*Actinobacteria*	*Actinomycetales*	U	U
Otu501	1	5	0	6	2	21	35.0000	6.0000	29.0000	0.0197	0.0067	0.0326	*Bacteria*	U	U	U	U	U
Otu502	0	8	0	10	0	22	40.0000	8.0000	32.0000	0.0225	0.0090	0.0360	*Bacteria*	U	U	U	U	U
Otu503	0	1	0	5	2	8	16.0000	1.0000	15.0000	0.0090	0.0011	0.0169	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu504	2	16	0	12	0	17	47.0000	18.0000	29.0000	0.0264	0.0202	0.0326	*Bacteria*	*Firmicutes*	U	U	U	U
Otu505	0	0	0	3	19	13	35.0000	0.0000	35.0000	0.0197	0.0000	0.0393	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu506	3	10	0	13	0	0	26.0000	13.0000	13.0000	0.0146	0.0146	0.0146	*Bacteria*	*Firmicutes*	U	U	U	U
Otu507	23	2	0	0	1	0	26.0000	25.0000	1.0000	0.0146	0.0281	0.0011	*Bacteria*	U	U	U	U	U
Otu508	0	0	0	0	58	6	64.0000	0.0000	64.0000	0.0360	0.0000	0.0719	*Bacteria*	U	U	U	U	U
Otu509	0	0	0	34	2	0	36.0000	0.0000	36.0000	0.0202	0.0000	0.0405	*Bacteria*	U	U	U	U	U
Otu51	68	172	0	91	9	187	527.0000	240.0000	287.0000	0.2961	0.2697	0.3226	*Bacteria*	*Bacteroidetes*	*Bacteroidia*	*Bacteroidales*	*Bacteroidaceae*	U
Otu510	8	7	0	18	0	0	33.0000	15.0000	18.0000	0.0185	0.0169	0.0202	*Bacteria*	*Firmicutes*	U	U	U	U
Otu511	0	0	0	6	8	15	29.0000	0.0000	29.0000	0.0163	0.0000	0.0326	*Bacteria*	U	U	U	U	U
Otu512	9	16	0	3	12	23	63.0000	25.0000	38.0000	0.0354	0.0281	0.0427	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu513	2	3	0	14	6	0	25.0000	5.0000	20.0000	0.0140	0.0056	0.0225	*Bacteria*	*Firmicutes*	U	U	U	U
Otu514	0	1	0	7	6	18	32.0000	1.0000	31.0000	0.0180	0.0011	0.0348	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu515	0	5	0	7	0	26	38.0000	5.0000	33.0000	0.0214	0.0056	0.0371	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu516	0	1	0	9	16	7	33.0000	1.0000	32.0000	0.0185	0.0011	0.0360	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu517	6	0	0	0	3	0	9.0000	6.0000	3.0000	0.0051	0.0067	0.0034	*Bacteria*	*Bacteroidetes*	*Sphingobacteriia*	*Sphingobacteriales*	*Chitinophagaceae*	U
Otu518	0	0	0	0	30	0	30.0000	0.0000	30.0000	0.0169	0.0000	0.0337	*Bacteria*	*Bacteroidetes*	*Bacteroidia*	*Bacteroidales*	*Porphyromonadaceae*	*Dysgonomonas*
Otu519	0	0	0	0	5	20	25.0000	0.0000	25.0000	0.0140	0.0000	0.0281	*Bacteria*	U	U	U	U	U
Otu52	7	24	2	5	364	135	537.0000	33.0000	504.0000	0.3018	0.0371	0.5664	*Bacteria*	*Firmicutes*	U	U	U	U
Otu520	0	4	0	7	1	16	28.0000	4.0000	24.0000	0.0157	0.0045	0.0270	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu522	5	1	0	1	9	0	16.0000	6.0000	10.0000	0.0090	0.0067	0.0112	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu523	3	11	0	6	0	3	23.0000	14.0000	9.0000	0.0129	0.0157	0.0101	*Bacteria*	*Firmicutes*	*Negativicutes*	U	U	U
Otu524	2	5	0	5	0	10	22.0000	7.0000	15.0000	0.0124	0.0079	0.0169	*Bacteria*	*Firmicutes*	U	U	U	U
Otu525	0	1	0	8	0	11	20.0000	1.0000	19.0000	0.0112	0.0011	0.0214	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U

Otu526	0	3	0	8	0	11	22.0000	3.0000	19.0000	0.0124	0.0034	0.0214	*Bacteria*	U	U	U	U	U
Otu527	16	10	0	3	0	3	32.0000	26.0000	6.0000	0.0180	0.0292	0.0067	*Bacteria*	U	U	U	U	U
Otu528	0	8	0	0	9	10	27.0000	8.0000	19.0000	0.0152	0.0090	0.0214	*Bacteria*	*Firmicutes*	U	U	U	U
Otu529	0	0	36	0	18	0	54.0000	36.0000	18.0000	0.0303	0.0405	0.0202	*Bacteria*	*Bacteroidetes*	*Flavobacteriia*	*Flavobacteriales*	*Flavobacteriaceae*	*Elizabethkingia*
Otu53	1	1	0	163	5	271	441.0000	2.0000	439.0000	0.2478	0.0022	0.4934	*Bacteria*	*Proteobacteria*	*Epsilonproteobacteria*	*Campylobacterales*	*Campylobacteraceae*	U
Otu530	0	0	0	7	23	3	33.0000	0.0000	33.0000	0.0185	0.0000	0.0371	*Bacteria*	*Firmicutes*	U	U	U	U
Otu531	4	2	5	0	15	3	29.0000	11.0000	18.0000	0.0163	0.0124	0.0202	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	*Rhizobiales*	*Hyphomicrobiaceae*	*Hyphomicrobium*
Otu532	0	14	0	4	8	15	41.0000	14.0000	27.0000	0.0230	0.0157	0.0303	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu533	1	19	0	2	1	13	36.0000	20.0000	16.0000	0.0202	0.0225	0.0180	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu534	17	22	0	2	0	4	45.0000	39.0000	6.0000	0.0253	0.0438	0.0067	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu535	0	0	0	36	7	0	43.0000	0.0000	43.0000	0.0242	0.0000	0.0483	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu536	2	7	0	10	0	5	24.0000	9.0000	15.0000	0.0135	0.0101	0.0169	*Bacteria*	U	U	U	U	U
Otu537	5	16	0	1	13	2	37.0000	21.0000	16.0000	0.0208	0.0236	0.0180	*Bacteria*	*Firmicutes*	*Negativicutes*	U	U	U
Otu538	0	0	0	8	11	9	28.0000	0.0000	28.0000	0.0157	0.0000	0.0315	*Bacteria*	*Firmicutes*	U	U	U	U
Otu539	1	0	0	0	24	2	27.0000	1.0000	26.0000	0.0152	0.0011	0.0292	*Bacteria*	*Proteobacteria*	*Gammaproteobacteria*	*Aeromonadales*	*Aeromonadaceae*	*Aeromonas*
Otu54	36	228	0	154	7	60	485.0000	264.0000	221.0000	0.2725	0.2967	0.2484	*Bacteria*	*Proteobacteria*	*Deltaproteobacteria*	*Desulfovibrionales*	*Desulfovibrionaceae*	*Desulfovibrio*
Otu540	0	0	0	7	3	2	12.0000	0.0000	12.0000	0.0067	0.0000	0.0135	*Bacteria*	U	U	U	U	U
Otu541	0	0	0	16	0	3	19.0000	0.0000	19.0000	0.0107	0.0000	0.0214	*Bacteria*	*Firmicutes*	U	U	U	U
Otu542	0	0	1	0	31	3	35.0000	1.0000	34.0000	0.0197	0.0011	0.0382	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu543	0	0	0	14	9	4	27.0000	0.0000	27.0000	0.0152	0.0000	0.0303	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu544	0	8	0	16	2	4	30.0000	8.0000	22.0000	0.0169	0.0090	0.0247	*Bacteria*	U	U	U	U	U
Otu545	0	13	0	3	0	10	26.0000	13.0000	13.0000	0.0146	0.0146	0.0146	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu546	1	6	0	1	11	1	20.0000	7.0000	13.0000	0.0112	0.0079	0.0146	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu547	0	3	0	4	12	1	20.0000	3.0000	17.0000	0.0112	0.0034	0.0191	*Bacteria*	U	U	U	U	U
Otu548	0	0	1	6	26	17	50.0000	1.0000	49.0000	0.0281	0.0011	0.0551	*Bacteria*	U	U	U	U	U
Otu549	0	11	0	6	2	11	30.0000	11.0000	19.0000	0.0169	0.0124	0.0214	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu55	0	2	0	167	331	40	540.0000	2.0000	538.0000	0.3034	0.0022	0.6047	*Bacteria*	*Firmicutes*	U	U	U	U
Otu550	3	10	0	10	1	4	28.0000	13.0000	15.0000	0.0157	0.0146	0.0169	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu551	4	9	0	18	10	20	61.0000	13.0000	48.0000	0.0343	0.0146	0.0539	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu552	0	4	0	7	9	0	20.0000	4.0000	16.0000	0.0112	0.0045	0.0180	*Bacteria*	U	U	U	U	U
Otu553	1	2	0	3	7	8	21.0000	3.0000	18.0000	0.0118	0.0034	0.0202	*Bacteria*	U	U	U	U	U
Otu554	5	8	0	4	1	0	18.0000	13.0000	5.0000	0.0101	0.0146	0.0056	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu555	2	10	0	2	1	15	30.0000	12.0000	18.0000	0.0169	0.0135	0.0202	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu556	0	1	0	7	13	3	24.0000	1.0000	23.0000	0.0135	0.0011	0.0258	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu557	1	13	0	1	4	5	24.0000	14.0000	10.0000	0.0135	0.0157	0.0112	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu558	0	4	0	9	5	7	25.0000	4.0000	21.0000	0.0140	0.0045	0.0236	*Bacteria*	U	U	U	U	U
Otu559	10	0	0	0	14	0	24.0000	10.0000	14.0000	0.0135	0.0112	0.0157	*Bacteria*	*Bacteroidetes*	*Sphingobacteriia*	*Sphingobacteriales*	*Chitinophagaceae*	*Terrimonas*
Otu56	52	143	0	36	20	186	437.0000	195.0000	242.0000	0.2456	0.2192	0.2720	*Bacteria*	U	U	U	U	U
Otu560	2	0	6	0	12	0	20.0000	8.0000	12.0000	0.0112	0.0090	0.0135	*Bacteria*	*Planctomycetes*	*Planctomycetia*	*Planctomycetales*	*Planctomycetaceae*	U
Otu561	0	0	0	18	11	2	31.0000	0.0000	31.0000	0.0174	0.0000	0.0348	*Bacteria*	*Firmicutes*	U	U	U	U

Otu562	0	11	0	6	0	8	25.0000	11.0000	14.0000	0.0140	0.0124	0.0157	*Bacteria*	U	U	U	U	U
Otu563	1	1	3	1	13	0	19.0000	5.0000	14.0000	0.0107	0.0056	0.0157	*Bacteria*	*Actinobacteria*	*Actinobacteria*	*Actinomycetales*	*Nocardioidaceae*	*Nocardioides*
Otu564	0	0	0	19	7	9	35.0000	0.0000	35.0000	0.0197	0.0000	0.0393	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu565	0	4	0	8	0	22	34.0000	4.0000	30.0000	0.0191	0.0045	0.0337	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu566	2	8	0	3	12	0	25.0000	10.0000	15.0000	0.0140	0.0112	0.0169	*Bacteria*	U	U	U	U	U
Otu567	3	15	0	7	1	8	34.0000	18.0000	16.0000	0.0191	0.0202	0.0180	*Bacteria*	U	U	U	U	U
Otu568	0	0	0	2	4	13	19.0000	0.0000	19.0000	0.0107	0.0000	0.0214	*Bacteria*	U	U	U	U	U
Otu569	3	16	0	1	0	12	32.0000	19.0000	13.0000	0.0180	0.0214	0.0146	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu57	26	41	1	79	67	271	485.0000	68.0000	417.0000	0.2725	0.0764	0.4687	*Bacteria*	*Firmicutes*	U	U	U	U
Otu570	0	0	0	0	12	18	30.0000	0.0000	30.0000	0.0169	0.0000	0.0337	*Bacteria*	*Firmicutes*	U	U	U	U
Otu571	2	10	0	6	1	13	32.0000	12.0000	20.0000	0.0180	0.0135	0.0225	*Bacteria*	U	U	U	U	U
Otu572	1	1	0	4	0	5	11.0000	2.0000	9.0000	0.0062	0.0022	0.0101	*Bacteria*	U	U	U	U	U
Otu573	0	1	0	7	9	16	33.0000	1.0000	32.0000	0.0185	0.0011	0.0360	*Bacteria*	*Firmicutes*	U	U	U	U
Otu574	5	0	1	0	7	0	13.0000	6.0000	7.0000	0.0073	0.0067	0.0079	*Bacteria*	*Bacteroidetes*	*Cytophagia*	*Cytophagales*	U	U
Otu575	1	13	0	13	6	6	39.0000	14.0000	25.0000	0.0219	0.0157	0.0281	*Bacteria*	*Firmicutes*	U	U	U	U
Otu576	0	1	0	3	3	7	14.0000	1.0000	13.0000	0.0079	0.0011	0.0146	*Bacteria*	*Firmicutes*	U	U	U	U
Otu577	10	9	0	3	0	0	22.0000	19.0000	3.0000	0.0124	0.0214	0.0034	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu578	15	7	0	0	0	0	22.0000	22.0000	0.0000	0.0124	0.0247	0.0000	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu579	9	3	0	0	11	1	24.0000	12.0000	12.0000	0.0135	0.0135	0.0135	*Bacteria*	*Candidatus_Saccharibacteria*	*Saccharibacteria_genera_incertae_sedis*	U	U	U
Otu58	64	106	0	107	97	55	429.0000	170.0000	259.0000	0.2411	0.1911	0.2911	*Bacteria*	*Bacteroidetes*	*Bacteroidia*	*Bacteroidales*	*Rikenellaceae*	U
Otu580	0	0	0	3	0	19	22.0000	0.0000	22.0000	0.0124	0.0000	0.0247	*Bacteria*	*Firmicutes*	U	U	U	U
Otu581	0	6	0	7	0	4	17.0000	6.0000	11.0000	0.0096	0.0067	0.0124	*Bacteria*	*Proteobacteria*	*Deltaproteobacteria*	*Desulfovibrionales*	*Desulfovibrionaceae*	*Desulfovibrio*
Otu582	0	0	0	1	2	11	14.0000	0.0000	14.0000	0.0079	0.0000	0.0157	*Bacteria*	*Firmicutes*	U	U	U	U
Otu583	11	29	0	0	1	0	41.0000	40.0000	1.0000	0.0230	0.0450	0.0011	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu584	0	2	0	17	0	0	19.0000	2.0000	17.0000	0.0107	0.0022	0.0191	*Bacteria*	U	U	U	U	U
Otu585	2	9	0	10	8	1	30.0000	11.0000	19.0000	0.0169	0.0124	0.0214	*Bacteria*	U	U	U	U	U
Otu586	0	1	0	10	2	2	15.0000	1.0000	14.0000	0.0084	0.0011	0.0157	*Bacteria*	U	U	U	U	U
Otu587	9	12	0	7	0	10	38.0000	21.0000	17.0000	0.0214	0.0236	0.0191	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu588	4	27	0	2	0	8	41.0000	31.0000	10.0000	0.0230	0.0348	0.0112	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu589	22	12	0	4	0	0	38.0000	34.0000	4.0000	0.0214	0.0382	0.0045	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu59	4	51	0	102	8	327	492.0000	55.0000	437.0000	0.2765	0.0618	0.4911	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu590	7	41	0	8	2	6	64.0000	48.0000	16.0000	0.0360	0.0539	0.0180	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu591	0	15	0	1	0	8	24.0000	15.0000	9.0000	0.0135	0.0169	0.0101	*Bacteria*	U	U	U	U	U
Otu592	1	7	0	0	2	3	13.0000	8.0000	5.0000	0.0073	0.0090	0.0056	*Bacteria*	*Actinobacteria*	*Actinobacteria*	*Actinomycetales*	*Propionibacteriaceae*	U
Otu593	11	11	0	0	1	1	24.0000	22.0000	2.0000	0.0135	0.0247	0.0022	*Bacteria*	U	U	U	U	U
Otu594	1	0	0	0	23	0	24.0000	1.0000	23.0000	0.0135	0.0011	0.0258	*Bacteria*	*Bacteroidetes*	*Flavobacteriia*	*Flavobacteriales*	*Flavobacteriaceae*	U
Otu595	0	0	26	0	0	0	26.0000	26.0000	0.0000	0.0146	0.0292	0.0000	*Bacteria*	*Bacteroidetes*	*Flavobacteriia*	*Flavobacteriales*	*Flavobacteriaceae*	*Chryseobacterium*
Otu596	0	0	0	1	7	1	9.0000	0.0000	9.0000	0.0051	0.0000	0.0101	*Bacteria*	*Firmicutes*	U	U	U	U
Otu597	0	0	0	12	2	14	28.0000	0.0000	28.0000	0.0157	0.0000	0.0315	*Bacteria*	U	U	U	U	U
Otu598	0	0	0	7	8	3	18.0000	0.0000	18.0000	0.0101	0.0000	0.0202	*Bacteria*	U	U	U	U	U

Otu599	3	3	0	0	13	9	28.0000	6.0000	22.0000	0.0157	0.0067	0.0247	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu6	864	120	574	84	2441	240	4323.0000	1558.0000	2765.0000	2.4293	1.7510	3.1075	*Bacteria*	*Firmicutes*	*Bacilli*	*Bacillales*	U	U
Otu60	11	34	0	180	5	174	404.0000	45.0000	359.0000	0.2270	0.0506	0.4035	*Bacteria*	U	U	U	U	U
Otu600	0	5	0	4	0	17	26.0000	5.0000	21.0000	0.0146	0.0056	0.0236	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu601	0	0	1	22	4	7	34.0000	1.0000	33.0000	0.0191	0.0011	0.0371	*Bacteria*	*Firmicutes*	U	U	U	U
Otu602	2	1	0	22	0	13	38.0000	3.0000	35.0000	0.0214	0.0034	0.0393	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Peptococcaceae_2*	U
Otu603	1	12	0	6	4	4	27.0000	13.0000	14.0000	0.0152	0.0146	0.0157	*Bacteria*	*Firmicutes*	U	U	U	U
Otu604	1	4	0	10	5	8	28.0000	5.0000	23.0000	0.0157	0.0056	0.0258	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu605	8	25	0	0	2	7	42.0000	33.0000	9.0000	0.0236	0.0371	0.0101	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu606	0	0	0	32	0	0	32.0000	0.0000	32.0000	0.0180	0.0000	0.0360	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Clostridiaceae_1*	U
Otu607	0	3	0	0	2	18	23.0000	3.0000	20.0000	0.0129	0.0034	0.0225	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu608	4	20	0	2	2	10	38.0000	24.0000	14.0000	0.0214	0.0270	0.0157	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu609	0	3	0	9	3	17	32.0000	3.0000	29.0000	0.0180	0.0034	0.0326	*Bacteria*	U	U	U	U	U
Otu61	95	143	2	36	6	51	333.0000	240.0000	93.0000	0.1871	0.2697	0.1045	*Bacteria*	*Bacteroidetes*	*Bacteroidia*	*Bacteroidales*	*Porphyromonadaceae*	*Dysgonomonas*
Otu610	0	0	1	5	1	5	12.0000	1.0000	11.0000	0.0067	0.0011	0.0124	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu611	4	11	0	1	0	1	17.0000	15.0000	2.0000	0.0096	0.0169	0.0022	*Bacteria*	*Firmicutes*	U	U	U	U
Otu612	4	14	0	10	10	15	53.0000	18.0000	35.0000	0.0298	0.0202	0.0393	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu613	2	5	0	1	0	4	12.0000	7.0000	5.0000	0.0067	0.0079	0.0056	*Bacteria*	*Firmicutes*	U	U	U	U
Otu614	4	10	0	6	2	11	33.0000	14.0000	19.0000	0.0185	0.0157	0.0214	*Bacteria*	U	U	U	U	U
Otu615	0	0	1	0	22	0	23.0000	1.0000	22.0000	0.0129	0.0011	0.0247	*Bacteria*	*Proteobacteria*	*Gammaproteobacteria*	*Pseudomonadales*	*Moraxellaceae*	*Acinetobacter*
Otu616	1	1	0	29	17	5	53.0000	2.0000	51.0000	0.0298	0.0022	0.0573	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu617	1	7	0	6	0	3	17.0000	8.0000	9.0000	0.0096	0.0090	0.0101	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu618	9	0	0	0	24	1	34.0000	9.0000	25.0000	0.0191	0.0101	0.0281	*Bacteria*	*Verrucomicrobia*	U	U	U	U
Otu619	0	1	0	1	7	9	18.0000	1.0000	17.0000	0.0101	0.0011	0.0191	*Bacteria*	U	U	U	U	U
Otu62	29	25	0	111	188	61	414.0000	54.0000	360.0000	0.2326	0.0607	0.4046	*Bacteria*	*Bacteroidetes*	U	U	U	U
Otu620	0	1	0	0	25	6	32.0000	1.0000	31.0000	0.0180	0.0011	0.0348	*Bacteria*	*Firmicutes*	U	U	U	U
Otu621	0	13	0	7	0	10	30.0000	13.0000	17.0000	0.0169	0.0146	0.0191	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu622	2	2	0	10	3	3	20.0000	4.0000	16.0000	0.0112	0.0045	0.0180	*Bacteria*	*Firmicutes*	U	U	U	U
Otu623	0	5	0	2	0	3	10.0000	5.0000	5.0000	0.0056	0.0056	0.0056	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu624	6	0	0	0	26	1	33.0000	6.0000	27.0000	0.0185	0.0067	0.0303	*Bacteria*	*Actinobacteria*	*Actinobacteria*	*Actinomycetales*	*Nocardioidaceae*	U
Otu625	0	0	0	12	0	0	12.0000	0.0000	12.0000	0.0067	0.0000	0.0135	*Bacteria*	U	U	U	U	U
Otu626	0	0	0	1	21	8	30.0000	0.0000	30.0000	0.0169	0.0000	0.0337	*Bacteria*	U	U	U	U	U
Otu627	0	0	0	5	0	13	18.0000	0.0000	18.0000	0.0101	0.0000	0.0202	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu628	0	5	0	4	0	5	14.0000	5.0000	9.0000	0.0079	0.0056	0.0101	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu629	1	7	0	3	0	15	26.0000	8.0000	18.0000	0.0146	0.0090	0.0202	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu63	41	149	0	73	17	100	380.0000	190.0000	190.0000	0.2135	0.2135	0.2135	*Bacteria*	*Verrucomicrobia*	*Opitutae*	*Opitutales*	U	U
Otu630	0	1	0	3	0	21	25.0000	1.0000	24.0000	0.0140	0.0011	0.0270	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu631	1	3	0	0	1	13	18.0000	4.0000	14.0000	0.0101	0.0045	0.0157	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu632	0	0	0	0	6	8	14.0000	0.0000	14.0000	0.0079	0.0000	0.0157	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	*Rhizobiales*	*Phyllobacteriaceae*	U

Otu633	0	6	0	7	0	16	29.0000	6.0000	23.0000	0.0163	0.0067	0.0258	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu634	12	2	1	0	3	0	18.0000	15.0000	3.0000	0.0101	0.0169	0.0034	*Bacteria*	*Proteobacteria*	*Betaproteobacteria*	*Burkholderiales*	*Burkholderiaceae*	*Burkholderia*
Otu635	6	1	0	0	11	1	19.0000	7.0000	12.0000	0.0107	0.0079	0.0135	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	*Rhodospirillales*	*Reyranella*	U
Otu636	0	0	0	7	1	2	10.0000	0.0000	10.0000	0.0056	0.0000	0.0112	*Bacteria*	U	U	U	U	U
Otu637	7	3	0	0	26	2	38.0000	10.0000	28.0000	0.0214	0.0112	0.0315	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Lachnospiraceae*	U
Otu638	0	0	0	14	2	3	19.0000	0.0000	19.0000	0.0107	0.0000	0.0214	*Bacteria*	*Firmicutes*	U	U	U	U
Otu639	0	0	0	0	12	5	17.0000	0.0000	17.0000	0.0096	0.0000	0.0191	*Bacteria*	*Firmicutes*	U	U	U	U
Otu64	0	0	0	0	19	292	311.0000	0.0000	311.0000	0.1748	0.0000	0.3495	*Bacteria*	*Bacteroidetes*	U	U	U	U
Otu640	0	0	1	4	13	1	19.0000	1.0000	18.0000	0.0107	0.0011	0.0202	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Lachnospiraceae*	U
Otu641	2	15	0	3	0	1	21.0000	17.0000	4.0000	0.0118	0.0191	0.0045	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu642	0	8	0	7	1	4	20.0000	8.0000	12.0000	0.0112	0.0090	0.0135	*Bacteria*	*Firmicutes*	U	U	U	U
Otu643	1	2	0	2	3	7	15.0000	3.0000	12.0000	0.0084	0.0034	0.0135	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu644	2	16	0	0	0	0	18.0000	18.0000	0.0000	0.0101	0.0202	0.0000	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu645	0	3	0	7	1	12	23.0000	3.0000	20.0000	0.0129	0.0034	0.0225	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu646	6	8	0	2	1	3	20.0000	14.0000	6.0000	0.0112	0.0157	0.0067	*Bacteria*	U	U	U	U	U
Otu647	2	4	0	2	0	4	12.0000	6.0000	6.0000	0.0067	0.0067	0.0067	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu648	3	6	0	5	1	0	15.0000	9.0000	6.0000	0.0084	0.0101	0.0067	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu649	3	3	0	1	5	0	12.0000	6.0000	6.0000	0.0067	0.0067	0.0067	*Bacteria*	U	U	U	U	U
Otu65	25	81	1	145	4	61	317.0000	107.0000	210.0000	0.1781	0.1203	0.2360	*Bacteria*	U	U	U	U	U
Otu650	0	3	0	4	0	11	18.0000	3.0000	15.0000	0.0101	0.0034	0.0169	*Bacteria*	U	U	U	U	U
Otu651	6	8	0	10	0	2	26.0000	14.0000	12.0000	0.0146	0.0157	0.0135	*Bacteria*	U	U	U	U	U
Otu652	1	0	1	21	2	0	25.0000	2.0000	23.0000	0.0140	0.0022	0.0258	*Bacteria*	U	U	U	U	U
Otu653	0	13	0	12	4	4	33.0000	13.0000	20.0000	0.0185	0.0146	0.0225	*Bacteria*	U	U	U	U	U
Otu654	7	0	1	0	11	0	19.0000	8.0000	11.0000	0.0107	0.0090	0.0124	*Bacteria*	*Candidatus_Saccharibacteria*	*Saccharibacteria_genera_incertae_sedis*	U	U	U
Otu655	0	0	0	1	9	3	13.0000	0.0000	13.0000	0.0073	0.0000	0.0146	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu656	0	0	0	19	0	0	19.0000	0.0000	19.0000	0.0107	0.0000	0.0214	*Bacteria*	*Proteobacteria*	*Betaproteobacteria*	*Burkholderiales*	*Comamonadaceae*	U
Otu657	0	1	0	3	0	11	15.0000	1.0000	14.0000	0.0084	0.0011	0.0157	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu658	0	6	0	2	0	12	20.0000	6.0000	14.0000	0.0112	0.0067	0.0157	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu659	4	14	0	5	0	12	35.0000	18.0000	17.0000	0.0197	0.0202	0.0191	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu66	59	207	2	65	13	18	364.0000	268.0000	96.0000	0.2045	0.3012	0.1079	*Bacteria*	*Bacteroidetes*	*Bacteroidia*	*Bacteroidales*	*Porphyromonadaceae*	*Dysgonomonas*
Otu660	4	5	0	3	1	1	14.0000	9.0000	5.0000	0.0079	0.0101	0.0056	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu661	4	21	0	2	0	0	27.0000	25.0000	2.0000	0.0152	0.0281	0.0022	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu662	3	8	0	6	0	5	22.0000	11.0000	11.0000	0.0124	0.0124	0.0124	*Bacteria*	U	U	U	U	U
Otu663	0	21	0	14	4	14	53.0000	21.0000	32.0000	0.0298	0.0236	0.0360	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu664	11	0	0	0	10	0	21.0000	11.0000	10.0000	0.0118	0.0124	0.0112	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	*Rhodospirillales*	*Rhodospirillaceae*	U
Otu665	0	2	0	16	1	1	20.0000	2.0000	18.0000	0.0112	0.0022	0.0202	*Bacteria*	U	U	U	U	U
Otu666	1	4	0	3	2	5	15.0000	5.0000	10.0000	0.0084	0.0056	0.0112	*Bacteria*	U	U	U	U	U
Otu667	4	1	2	0	15	1	23.0000	7.0000	16.0000	0.0129	0.0079	0.0180	*Bacteria*	*Proteobacteria*	*Alphaproteobacte*	*Rhizobiales*	U	U

														ria			
Otu668	8	0	0	5	14	2	29.0000	8.0000	21.0000	0.0163	0.0090	0.0236	*Bacteria*	*Firmicutes*	*Clostridia*		U	U
Otu669	11	11	0	2	0	0	24.0000	22.0000	2.0000	0.0135	0.0247	0.0022	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu67	25	150	0	34	7	135	351.0000	175.0000	176.000	0.1972	0.1967	0.1978	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
									0									
Otu670	0	0	0	3	16	2	21.0000	0.0000	21.0000	0.0118	0.0000	0.0236	*Bacteria*	*Firmicutes*	U	U	U	U
Otu671	1	4	0	13	6	1	25.0000	5.0000	20.0000	0.0140	0.0056	0.0225	*Bacteria*	U	U	U	U	U
Otu672	0	0	0	0	6	18	24.0000	0.0000	24.0000	0.0135	0.0000	0.0270	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu673	0	0	0	9	2	1	12.0000	0.0000	12.0000	0.0067	0.0000	0.0135	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu674	11	0	0	0	8	0	19.0000	11.0000	8.0000	0.0107	0.0124	0.0090	*Bacteria*	*Proteobacteria*	*Alphaproteobacte*	*Sphingomonadales*	U	U
															ria			
Otu675	4	5	0	16	3	6	34.0000	9.0000	25.0000	0.0191	0.0101	0.0281	*Bacteria*	*Proteobacteria*	*Deltaproteobacter*	*Desulfovibrionales*	U	U
															ia			
Otu676	0	4	0	14	8	1	27.0000	4.0000	23.0000	0.0152	0.0045	0.0258	*Bacteria*	*Firmicutes*	U	U	U	U
Otu677	13	12	0	2	2	2	31.0000	25.0000	6.0000	0.0174	0.0281	0.0067	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu678	8	9	0	0	3	0	20.0000	17.0000	3.0000	0.0112	0.0191	0.0034	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu679	2	6	0	0	0	7	15.0000	8.0000	7.0000	0.0084	0.0090	0.0079	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu68	2	3	1	283	0	1	290.0000	6.0000	284.000	0.1630	0.0067	0.3192	*Bacteria*	*Firmicutes*	U	U	U	U
									0									
Otu680	0	6	0	5	0	2	13.0000	6.0000	7.0000	0.0073	0.0067	0.0079	*Bacteria*	U	U	U	U	U
Otu681	1	3	0	5	1	5	15.0000	4.0000	11.0000	0.0084	0.0045	0.0124	*Bacteria*	*Firmicutes*	U	U	U	U
Otu682	5	7	0	0	3	2	17.0000	12.0000	5.0000	0.0096	0.0135	0.0056	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu683	0	6	0	16	1	19	42.0000	6.0000	36.0000	0.0236	0.0067	0.0405	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu684	0	0	0	0	20	2	22.0000	0.0000	22.0000	0.0124	0.0000	0.0247	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu685	5	25	0	13	1	15	59.0000	30.0000	29.0000	0.0332	0.0337	0.0326	*Bacteria*	U	U	U	U	U
Otu686	0	10	0	11	0	8	29.0000	10.0000	19.0000	0.0163	0.0112	0.0214	*Bacteria*	U	U	U	U	U
Otu687	1	5	0	21	11	1	39.0000	6.0000	33.0000	0.0219	0.0067	0.0371	*Bacteria*	*Firmicutes*	U	U	U	U
Otu688	2	0	0	2	0	5	9.0000	2.0000	7.0000	0.0051	0.0022	0.0079	*Bacteria*	*Firmicutes*	U	U	U	U
Otu689	2	0	0	0	3	0	5.0000	2.0000	3.0000	0.0028	0.0022	0.0034	*Bacteria*	U	U	U	U	U
Otu69	169	56	0	6	19	2	252.0000	225.0000	27.0000	0.1416	0.2529	0.0303	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu690	9	8	0	1	0	0	18.0000	17.0000	1.0000	0.0101	0.0191	0.0011	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu691	0	5	0	2	4	1	12.0000	5.0000	7.0000	0.0067	0.0056	0.0079	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu692	2	3	0	6	5	2	18.0000	5.0000	13.0000	0.0101	0.0056	0.0146	*Bacteria*	U	U	U	U	U
Otu693	0	0	0	2	18	4	24.0000	0.0000	24.0000	0.0135	0.0000	0.0270	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu694	0	0	0	11	5	0	16.0000	0.0000	16.0000	0.0090	0.0000	0.0180	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu695	1	7	0	2	0	5	15.0000	8.0000	7.0000	0.0084	0.0090	0.0079	*Bacteria*	*Firmicutes*	U	U	U	U
Otu696	0	0	0	25	0	0	25.0000	0.0000	25.0000	0.0140	0.0000	0.0281	*Bacteria*	U	U	U	U	U
Otu697	7	9	0	1	2	3	22.0000	16.0000	6.0000	0.0124	0.0180	0.0067	*Bacteria*	U	U	U	U	U
Otu698	5	0	0	0	4	0	9.0000	5.0000	4.0000	0.0051	0.0056	0.0045	*Bacteria*	*Bacteroidetes*	*Flavobacteriia*	*Flavobacteriales*	*Flavobacteriaceae*	*Flavobacterium*
Otu699	0	6	0	10	0	7	23.0000	6.0000	17.0000	0.0129	0.0067	0.0191	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu7	826	21	355	4	585	52	5043.000	4402.000	641.000	2.8339	4.9473	0.7204	*Bacteria*	*Firmicutes*	U	U	U	U
			5				0	0	0									
Otu70	1	14	0	9	6	328	358.0000	15.0000	343.000	0.2012	0.0169	0.3855	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
									0									
Otu700	2	5	0	2	9	0	18.0000	7.0000	11.0000	0.0101	0.0079	0.0124	*Bacteria*	U	U	U	U	U
Otu701	0	2	0	14	13	0	29.0000	2.0000	27.0000	0.0163	0.0022	0.0303	*Bacteria*	*Firmicutes*	U	U	U	U

Otu702	0	1	0	17	2	2	22.0000	1.0000	21.0000	0.0124	0.0011	0.0236	*Bacteria*	*Firmicutes*	U	U	U	U
Otu703	0	5	0	2	0	5	12.0000	5.0000	7.0000	0.0067	0.0056	0.0079	*Bacteria*	*Firmicutes*	U	U	U	U
Otu704	1	9	0	3	0	6	19.0000	10.0000	9.0000	0.0107	0.0112	0.0101	*Bacteria*	U	U	U	U	U
Otu705	0	0	0	1	20	9	30.0000	0.0000	30.0000	0.0169	0.0000	0.0337	*Bacteria*	*Firmicutes*	U	U	U	U
Otu706	6	4	0	0	2	0	12.0000	10.0000	2.0000	0.0067	0.0112	0.0022	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu707	2	4	0	1	0	9	16.0000	6.0000	10.0000	0.0090	0.0067	0.0112	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu708	1	2	0	0	3	6	12.0000	3.0000	9.0000	0.0067	0.0034	0.0101	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu709	8	0	0	0	14	1	23.0000	8.0000	15.0000	0.0129	0.0090	0.0169	*Bacteria*	*Verrucomicrobia*	*Spartobacteria*	U	U	U
Otu71	69	120	1	42	37	164	433.0000	190.0000	243.0000	0.2433	0.2135	0.2731	*Bacteria*	U	U	U	U	U
Otu710	0	2	0	2	1	17	22.0000	2.0000	20.0000	0.0124	0.0022	0.0225	*Bacteria*	U	U	U	U	U
Otu711	5	0	0	0	18	1	24.0000	5.0000	19.0000	0.0135	0.0056	0.0214	*Bacteria*	*Verrucomicrobia*	*Subdivision3*	*Subdivision3_genera_ incertae_sedis*	U	U
Otu712	0	10	0	2	1	4	17.0000	10.0000	7.0000	0.0096	0.0112	0.0079	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu713	0	0	0	18	0	0	18.0000	0.0000	18.0000	0.0101	0.0000	0.0202	*Bacteria*	*Firmicutes*	U	U	U	U
Otu714	0	7	0	8	4	8	27.0000	7.0000	20.0000	0.0152	0.0079	0.0225	*Bacteria*	U	U	U	U	U
Otu715	0	3	0	20	0	0	23.0000	3.0000	20.0000	0.0129	0.0034	0.0225	*Bacteria*	U	U	U	U	U
Otu716	0	0	19	0	0	0	19.0000	19.0000	0.0000	0.0107	0.0214	0.0000	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Lachnospiraceae*	U
Otu717	0	6	0	3	2	13	24.0000	6.0000	18.0000	0.0135	0.0067	0.0202	*Bacteria*	*Firmicutes*	U	U	U	U
Otu718	6	0	1	0	11	0	18.0000	7.0000	11.0000	0.0101	0.0079	0.0124	*Bacteria*	*Candidatus_Saccharibacteria*	*Saccharibacteria_genera_incertae_sedis*	U	U	U
Otu719	2	1	0	9	9	4	25.0000	3.0000	22.0000	0.0140	0.0034	0.0247	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu72	0	0	0	0	250	197	447.0000	0.0000	447.0000	0.2512	0.0000	0.5024	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu720	0	1	0	6	0	10	17.0000	1.0000	16.0000	0.0096	0.0011	0.0180	*Bacteria*	U	U	U	U	U
Otu721	0	1	1	0	17	0	19.0000	2.0000	17.0000	0.0107	0.0022	0.0191	*Bacteria*	*Actinobacteria*	*Actinobacteria*	*Actinomycetales*	*Nocardioidaceae*	*Nocardioides*
Otu722	0	1	0	6	0	19	26.0000	1.0000	25.0000	0.0146	0.0011	0.0281	*Bacteria*	*Firmicutes*	U	U	U	U
Otu723	0	3	0	7	0	5	15.0000	3.0000	12.0000	0.0084	0.0034	0.0135	*Bacteria*	*Firmicutes*	U	U	U	U
Otu724	2	6	0	1	0	3	12.0000	8.0000	4.0000	0.0067	0.0090	0.0045	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Lachnospiraceae*	U
Otu725	1	1	3	0	5	2	12.0000	5.0000	7.0000	0.0067	0.0056	0.0079	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	*Rhodospirillales*	*Acetobacteraceae*	U
Otu726	0	3	0	10	1	0	14.0000	3.0000	11.0000	0.0079	0.0034	0.0124	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu727	3	0	0	4	0	0	7.0000	3.0000	4.0000	0.0039	0.0034	0.0045	*Bacteria*	U	U	U	U	U
Otu728	2	2	0	14	1	1	20.0000	4.0000	16.0000	0.0112	0.0045	0.0180	*Bacteria*	U	U	U	U	U
Otu729	1	0	0	5	2	0	8.0000	1.0000	7.0000	0.0045	0.0011	0.0079	*Bacteria*	U	U	U	U	U
Otu73	17	196	0	64	4	59	340.0000	213.0000	127.0000	0.1911	0.2394	0.1427	*Bacteria*	U	U	U	U	U
Otu730	3	24	0	0	0	0	27.0000	27.0000	0.0000	0.0152	0.0303	0.0000	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Lachnospiraceae*	U
Otu731	7	15	0	43	1	23	89.0000	22.0000	67.0000	0.0500	0.0247	0.0753	*Bacteria*	U	U	U	U	U
Otu732	0	0	0	0	12	2	14.0000	0.0000	14.0000	0.0079	0.0000	0.0157	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu733	0	4	0	7	0	1	12.0000	4.0000	8.0000	0.0067	0.0045	0.0090	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu734	0	0	0	2	13	1	16.0000	0.0000	16.0000	0.0090	0.0000	0.0180	*Bacteria*	U	U	U	U	U
Otu735	0	0	1	6	7	15	29.0000	1.0000	28.0000	0.0163	0.0011	0.0315	*Bacteria*	*Firmicutes*	U	U	U	U

Otu736	0	0	0	0	5	11	16.0000	0.0000	16.0000	0.0090	0.0000	0.0180	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu737	1	3	0	2	1	15	22.0000	4.0000	18.0000	0.0124	0.0045	0.0202	*Bacteria*	*Firmicutes*	U	U	U	U
Otu738	0	3	0	0	0	10	13.0000	3.0000	10.0000	0.0073	0.0034	0.0112	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu739	17	0	0	0	4	0	21.0000	17.0000	4.0000	0.0118	0.0191	0.0045	*Bacteria*	*Bacteroidetes*	U	U	U	U
Otu74	74	45	0	63	9	110	301.0000	119.0000	182.0000	0.1691	0.1337	0.2045	*Bacteria*	*Bacteroidetes*	U	U	U	U
Otu740	8	6	0	0	0	0	14.0000	14.0000	0.0000	0.0079	0.0157	0.0000	*Bacteria*	*Bacteroidetes*	U	U	U	U
Otu741	0	2	0	6	0	10	18.0000	2.0000	16.0000	0.0101	0.0022	0.0180	*Bacteria*	*Firmicutes*	U	U	U	U
Otu742	0	3	0	1	0	5	9.0000	3.0000	6.0000	0.0051	0.0034	0.0067	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Lachnospiraceae*	U
Otu743	1	12	0	3	0	2	18.0000	13.0000	5.0000	0.0101	0.0146	0.0056	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu744	7	1	0	1	0	3	12.0000	8.0000	4.0000	0.0067	0.0090	0.0045	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu745	6	0	0	0	2	0	8.0000	6.0000	2.0000	0.0045	0.0067	0.0022	*Bacteria*	*Bacteroidetes*	U	U	U	U
Otu746	1	2	0	4	2	1	10.0000	3.0000	7.0000	0.0056	0.0034	0.0079	*Bacteria*	U	U	U	U	U
Otu747	0	0	0	8	0	0	8.0000	0.0000	8.0000	0.0045	0.0000	0.0090	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu748	1	3	0	2	2	1	9.0000	4.0000	5.0000	0.0051	0.0045	0.0056	*Bacteria*	*Firmicutes*	U	U	U	U
Otu749	0	4	0	11	0	8	23.0000	4.0000	19.0000	0.0129	0.0045	0.0214	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu75	5	89	0	42	12	296	444.0000	94.0000	350.0000	0.2495	0.1056	0.3934	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu750	2	5	0	5	1	4	17.0000	7.0000	10.0000	0.0096	0.0079	0.0112	*Bacteria*	*Firmicutes*	U	U	U	U
Otu751	1	0	0	0	3	0	4.0000	1.0000	3.0000	0.0022	0.0011	0.0034	*Bacteria*	*Planctomycetes*	*Planctomycetia*	*Planctomycetales*	*Planctomycetaceae*	U
Otu752	0	0	0	11	1	2	14.0000	0.0000	14.0000	0.0079	0.0000	0.0157	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu753	0	4	0	3	0	8	15.0000	4.0000	11.0000	0.0084	0.0045	0.0124	*Bacteria*	*Firmicutes*	U	U	U	U
Otu754	0	10	0	1	0	9	20.0000	10.0000	10.0000	0.0112	0.0112	0.0112	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu755	2	2	0	0	15	1	20.0000	4.0000	16.0000	0.0112	0.0045	0.0180	*Bacteria*	*Planctomycetes*	U	U	U	U
Otu756	0	0	0	0	20	4	24.0000	0.0000	24.0000	0.0135	0.0000	0.0270	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu757	0	0	0	2	5	5	12.0000	0.0000	12.0000	0.0067	0.0000	0.0135	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu758	0	0	0	0	11	5	16.0000	0.0000	16.0000	0.0090	0.0000	0.0180	*Bacteria*	*Firmicutes*	U	U	U	U
Otu759	1	5	0	2	0	7	15.0000	6.0000	9.0000	0.0084	0.0067	0.0101	*Bacteria*	*Firmicutes*	U	U	U	U
Otu76	2	2	0	0	278	54	336.0000	4.0000	332.0000	0.1888	0.0045	0.3731	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu760	1	1	0	8	6	6	22.0000	2.0000	20.0000	0.0124	0.0022	0.0225	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu761	0	0	0	12	0	5	17.0000	0.0000	17.0000	0.0096	0.0000	0.0191	*Bacteria*	U	U	U	U	U
Otu762	2	4	0	2	0	11	19.0000	6.0000	13.0000	0.0107	0.0067	0.0146	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu763	0	2	0	1	4	1	8.0000	2.0000	6.0000	0.0045	0.0022	0.0067	*Bacteria*	*Proteobacteria*	*Deltaproteobacteria*	*Desulfovibrionales*	*Desulfovibrionaceae*	U
Otu764	3	5	0	3	0	1	12.0000	8.0000	4.0000	0.0067	0.0090	0.0045	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Lachnospiraceae*	U
Otu765	0	0	1	13	0	3	17.0000	1.0000	16.0000	0.0096	0.0011	0.0180	*Bacteria*	U	U	U	U	U
Otu766	0	3	0	8	0	3	14.0000	3.0000	11.0000	0.0079	0.0034	0.0124	*Bacteria*	*Firmicutes*	U	U	U	U
Otu767	1	1	0	7	0	8	17.0000	2.0000	15.0000	0.0096	0.0022	0.0169	*Bacteria*	*Firmicutes*	*Clostridia*		U	U
Otu768	0	0	0	3	6	3	12.0000	0.0000	12.0000	0.0067	0.0000	0.0135	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu769	0	0	0	3	0	8	11.0000	0.0000	11.0000	0.0062	0.0000	0.0124	*Bacteria*	U	U	U	U	U
Otu77	21	107	0	106	6	69	309.0000	128.0000	181.0000	0.1736	0.1439	0.2034	*Bacteria*	*Firmicutes*	*Negativicutes*	*Selenomonadales*	*Veillonellaceae*	U
Otu770	0	0	0	0	13	2	15.0000	0.0000	15.0000	0.0084	0.0000	0.0169	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Eubacteriaceae*	*Anaerofustis*
Otu771	1	0	1	1	4	1	8.0000	2.0000	6.0000	0.0045	0.0022	0.0067	*Bacteria*	*Actinobacteria*	*Actinobacteria*	*Actinomycetales*	*Mycobacteriaceae*	*Mycobacterium*
Otu772	0	5	0	5	2	8	20.0000	5.0000	15.0000	0.0112	0.0056	0.0169	*Bacteria*	*Actinobacteria*	*Actinobacteria*	*Actinomycetales*	U	U

Otu773	0	2	1	11	1	0	15.0000	3.0000	12.0000	0.0084	0.0034	0.0135	*Bacteria*	*Firmicutes*	U	U	U	U
Otu774	4	0	0	0	0	0	4.0000	4.0000	0.0000	0.0022	0.0045	0.0000	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	U	U	U
Otu775	1	5	0	1	1	2	10.0000	6.0000	4.0000	0.0056	0.0067	0.0045	*Bacteria*	U	U	U	U	U
Otu776	0	1	0	2	1	5	9.0000	1.0000	8.0000	0.0051	0.0011	0.0090	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu777	0	0	12	0	0	0	12.0000	12.0000	0.0000	0.0067	0.0135	0.0000	*Bacteria*	*Firmicutes*	U	U	U	U
Otu778	0	0	0	0	14	1	15.0000	0.0000	15.0000	0.0084	0.0000	0.0169	*Bacteria*	*Planctomycetes*	*Planctomycetia*	*Planctomycetales*	*Planctomycetaceae*	*Planctomicrobium*
Otu779	4	0	3	0	17	0	24.0000	7.0000	17.0000	0.0135	0.0079	0.0191	*Bacteria*	*Actinobacteria*	*Actinobacteria*	U	U	U
Otu78	0	0	455	0	0	0	455.0000	455.0000	0.0000	0.2557	0.5114	0.0000	*Bacteria*	*Firmicutes*	*Bacilli*	*Bacillales*	*Paenibacillaceae_1*	*Paenibacillus*
Otu780	9	0	0	0	3	0	12.0000	9.0000	3.0000	0.0067	0.0101	0.0034	*Bacteria*	*Spirochaetes*	*Spirochaetia*	*Spirochaetales*	*Spirochaetaceae*	*Spirochaeta*
Otu781	0	1	0	2	0	2	5.0000	1.0000	4.0000	0.0028	0.0011	0.0045	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu782	3	5	0	0	1	1	10.0000	8.0000	2.0000	0.0056	0.0090	0.0022	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu783	0	0	0	11	2	14	27.0000	0.0000	27.0000	0.0152	0.0000	0.0303	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu784	0	0	0	4	1	3	8.0000	0.0000	8.0000	0.0045	0.0000	0.0090	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu785	13	0	0	0	0	1	14.0000	13.0000	1.0000	0.0079	0.0146	0.0011	*Bacteria*	*Acidobacteria*	*Acidobacteria_Gp1*	U	U	U
Otu786	0	0	0	14	1	12	27.0000	0.0000	27.0000	0.0152	0.0000	0.0303	*Bacteria*	U	U	U	U	U
Otu787	0	2	0	5	3	9	19.0000	2.0000	17.0000	0.0107	0.0022	0.0191	*Bacteria*	*Firmicutes*	U	U	U	U
Otu788	4	0	0	0	3	3	10.0000	4.0000	6.0000	0.0056	0.0045	0.0067	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	*Rhodospirillales*	*Acetobacteraceae*	U
Otu789	0	5	0	4	3	3	15.0000	5.0000	10.0000	0.0084	0.0056	0.0112	*Bacteria*	*Firmicutes*	U	U	U	U
Otu79	109	6	141	6	6	2	270.0000	256.0000	14.0000	0.1517	0.2877	0.0157	*Bacteria*	*Firmicutes*	*Bacilli*	*Bacillales*	*Bacillaceae_1*	*Bacillus*
Otu790	5	4	0	5	1	6	21.0000	9.0000	12.0000	0.0118	0.0101	0.0135	*Bacteria*	*Firmicutes*	U	U	U	U
Otu791	0	1	0	3	5	6	15.0000	1.0000	14.0000	0.0084	0.0011	0.0157	U	U	U	U	U	U
Otu792	12	0	0	0	4	0	16.0000	12.0000	4.0000	0.0090	0.0135	0.0045	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	*Caulobacterales*	*Caulobacteraceae*	*Asticcacaulis*
Otu793	0	4	0	4	1	18	27.0000	4.0000	23.0000	0.0152	0.0045	0.0258	*Bacteria*	U	U	U	U	U
Otu794	0	8	0	4	1	2	15.0000	8.0000	7.0000	0.0084	0.0090	0.0079	*Bacteria*	*Firmicutes*	U	U	U	U
Otu795	6	10	0	3	2	0	21.0000	16.0000	5.0000	0.0118	0.0180	0.0056	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu796	0	0	0	15	0	0	15.0000	0.0000	15.0000	0.0084	0.0000	0.0169	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu797	1	0	0	1	4	0	6.0000	1.0000	5.0000	0.0034	0.0011	0.0056	*Bacteria*	U	U	U	U	U
Otu798	0	8	0	1	1	0	10.0000	8.0000	2.0000	0.0056	0.0090	0.0022	*Bacteria*	U	U	U	U	U
Otu799	0	0	0	5	4	1	10.0000	0.0000	10.0000	0.0056	0.0000	0.0112	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu8	10	1	2825	0	8	1	2845.0000	2836.0000	9.0000	1.5987	3.1873	0.0101	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Lachnospiraceae*	U
Otu80	16	154	1	144	2	271	588.0000	171.0000	417.0000	0.3304	0.1922	0.4687	*Bacteria*	*Firmicutes*	U	U	U	U
Otu800	0	0	0	1	7	8	16.0000	0.0000	16.0000	0.0090	0.0000	0.0180	*Bacteria*	U	U	U	U	U
Otu801	2	0	0	0	0	0	2.0000	2.0000	0.0000	0.0011	0.0022	0.0000	*Bacteria*	*Proteobacteria*	*Deltaproteobacteria*	*Bdellovibrionales*	*Bacteriovoracaceae*	*Peredibacter*
Otu802	0	0	14	2	0	0	16.0000	14.0000	2.0000	0.0090	0.0157	0.0022	*Bacteria*	*Firmicutes*	U	U	U	U
Otu803	4	9	0	5	3	1	22.0000	13.0000	9.0000	0.0124	0.0146	0.0101	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu804	0	0	0	0	13	11	24.0000	0.0000	24.0000	0.0135	0.0000	0.0270	*Bacteria*	*Firmicutes*	U	U	U	U
Otu805	14	0	0	0	6	0	20.0000	14.0000	6.0000	0.0112	0.0157	0.0067	*Bacteria*	*Proteobacteria*	*Gammaproteobacteria*	U	U	U
Otu806	0	8	0	1	1	7	17.0000	8.0000	9.0000	0.0096	0.0090	0.0101	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U

Otu807	0	0	0	4	0	4	8.0000	0.0000	8.0000	0.0045	0.0000	0.0090	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu808	1	8	0	2	0	4	15.0000	9.0000	6.0000	0.0084	0.0101	0.0067	*Bacteria*	*Firmicutes*	U	U	U	U
Otu809	0	1	0	14	1	0	16.0000	1.0000	15.0000	0.0090	0.0011	0.0169	*Bacteria*	U	U	U	U	U
Otu81	52	60	0	311	63	78	564.0000	112.0000	452.0000	0.3169	0.1259	0.5080	*Bacteria*	*Bacteroidetes*	U	U	U	U
Otu810	0	0	0	3	6	1	10.0000	0.0000	10.0000	0.0056	0.0000	0.0112	*Bacteria*	*Firmicutes*	U	U	U	U
Otu811	1	3	0	1	1	0	6.0000	4.0000	2.0000	0.0034	0.0045	0.0022	*Bacteria*	U	U	U	U	U
Otu812	1	6	0	9	0	1	17.0000	7.0000	10.0000	0.0096	0.0079	0.0112	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu813	0	0	0	0	11	1	12.0000	0.0000	12.0000	0.0067	0.0000	0.0135	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu814	0	7	0	11	3	2	23.0000	7.0000	16.0000	0.0129	0.0079	0.0180	*Bacteria*	*Firmicutes*	U	U	U	U
Otu815	0	0	0	2	0	6	8.0000	0.0000	8.0000	0.0045	0.0000	0.0090	*Bacteria*	*Firmicutes*	U	U	U	U
Otu816	1	10	0	7	1	17	36.0000	11.0000	25.0000	0.0202	0.0124	0.0281	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu817	9	13	0	1	0	0	23.0000	22.0000	1.0000	0.0129	0.0247	0.0011	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu818	0	0	0	0	0	21	21.0000	0.0000	21.0000	0.0118	0.0000	0.0236	*Bacteria*	U	U	U	U	U
Otu819	0	9	0	3	2	2	16.0000	9.0000	7.0000	0.0090	0.0101	0.0079	*Bacteria*	*Firmicutes*	U	U	U	U
Otu82	0	0	0	0	499	55	554.0000	0.0000	554.0000	0.3113	0.0000	0.6226	*Bacteria*	*Proteobacteria*	*Gammaproteobacteria*	*Enterobacteriales*	*Enterobacteriaceae*	U
Otu820	0	0	0	3	7	1	11.0000	0.0000	11.0000	0.0062	0.0000	0.0124	*Bacteria*	U	U	U	U	U
Otu821	3	0	0	0	3	0	6.0000	3.0000	3.0000	0.0034	0.0034	0.0034	*Bacteria*	*Bacteroidetes*	*Sphingobacteriia*	*Sphingobacteriales*	*Sphingobacteriaceae*	*Mucilaginibacter*
Otu822	0	3	0	5	9	6	23.0000	3.0000	20.0000	0.0129	0.0034	0.0225	*Bacteria*	*Firmicutes*	U	U	U	U
Otu823	2	0	0	0	11	1	14.0000	2.0000	12.0000	0.0079	0.0022	0.0135	*Bacteria*	*Proteobacteria*	*Deltaproteobacteria*	*Bdellovibrionales*	*Bdellovibrionaceae*	*Bdellovibrio*
Otu824	0	0	0	2	1	6	9.0000	0.0000	9.0000	0.0051	0.0000	0.0101	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu825	5	0	0	0	6	0	11.0000	5.0000	6.0000	0.0062	0.0056	0.0067	*Bacteria*	*Candidatus_Saccharibacteria*	*Saccharibacteria_genera_incertae_sedis*	U	U	U
Otu826	3	5	0	4	4	1	17.0000	8.0000	9.0000	0.0096	0.0090	0.0101	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu827	0	0	0	1	6	4	11.0000	0.0000	11.0000	0.0062	0.0000	0.0124	*Bacteria*	*Firmicutes*	U	U	U	U
Otu828	0	0	0	0	8	2	10.0000	0.0000	10.0000	0.0056	0.0000	0.0112	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu829	1	0	0	0	1	12	14.0000	1.0000	13.0000	0.0079	0.0011	0.0146	*Bacteria*	U	U	U	U	U
Otu83	15	92	0	50	2	122	281.0000	107.0000	174.0000	0.1579	0.1203	0.1956	*Bacteria*	U	U	U	U	U
Otu830	1	0	0	0	8	1	10.0000	1.0000	9.0000	0.0056	0.0011	0.0101	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	*Rhizobiales*	U	U
Otu831	0	1	0	5	0	6	12.0000	1.0000	11.0000	0.0067	0.0011	0.0124	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu832	0	0	0	2	0	6	8.0000	0.0000	8.0000	0.0045	0.0000	0.0090	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu833	1	4	0	6	0	11	22.0000	5.0000	17.0000	0.0124	0.0056	0.0191	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu834	1	7	0	0	0	1	9.0000	8.0000	1.0000	0.0051	0.0090	0.0011	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu835	1	7	0	0	0	6	14.0000	8.0000	6.0000	0.0079	0.0090	0.0067	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu836	0	1	0	2	1	4	8.0000	1.0000	7.0000	0.0045	0.0011	0.0079	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu837	3	0	1	0	6	0	10.0000	4.0000	6.0000	0.0056	0.0045	0.0067	*Bacteria*	*Actinobacteria*	*Actinobacteria*	U	U	U
Otu838	0	22	0	0	0	2	24.0000	22.0000	2.0000	0.0135	0.0247	0.0022	*Bacteria*	*Firmicutes*	U	U	U	U
Otu839	3	1	0	7	3	1	15.0000	4.0000	11.0000	0.0084	0.0045	0.0124	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu84	9	200	0	6	2	8	225.0000	209.0000	16.0000	0.1264	0.2349	0.0180	*Bacteria*	*Firmicutes*	*Negativicutes*	*Selenomonadales*	*Veillonellaceae*	U
Otu840	0	0	0	2	0	4	6.0000	0.0000	6.0000	0.0034	0.0000	0.0067	*Bacteria*	U	U	U	U	U
Otu841	0	8	0	3	0	6	17.0000	8.0000	9.0000	0.0096	0.0090	0.0101	*Bacteria*	*Firmicutes*	U	U	U	U

Otu842	0	0	0	3	6	2	11.0000	0.0000	11.0000	0.0062	0.0000	0.0124	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu843	6	0	0	0	4	1	11.0000	6.0000	5.0000	0.0062	0.0067	0.0056	*Bacteria*	*Proteobacteria*	*Betaproteobacteria*	*Burkholderiales*	*Comamonadaceae*	U
Otu844	0	0	0	21	0	0	21.0000	0.0000	21.0000	0.0118	0.0000	0.0236	*Bacteria*	*Firmicutes*	U	U	U	U
Otu845	3	5	0	1	5	8	22.0000	8.0000	14.0000	0.0124	0.0090	0.0157	*Bacteria*	*Firmicutes*	*Negativicutes*	U	U	U
Otu846	2	2	0	2	0	7	13.0000	4.0000	9.0000	0.0073	0.0045	0.0101	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu847	1	5	0	4	0	0	10.0000	6.0000	4.0000	0.0056	0.0067	0.0045	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu848	0	1	0	0	0	11	12.0000	1.0000	11.0000	0.0067	0.0011	0.0124	*Bacteria*	*Firmicutes*	*Negativicutes*	U	U	U
Otu849	0	0	0	0	20	0	20.0000	0.0000	20.0000	0.0112	0.0000	0.0225	*Bacteria*	*Proteobacteria*	*Betaproteobacteria*	*Burkholderiales*	*Comamonadaceae*	U
Otu85	27	60	1	137	48	51	324.0000	88.0000	236.0000	0.1821	0.0989	0.2652	*Bacteria*	*Firmicutes*	U	U	U	U
Otu850	4	6	0	0	1	0	11.0000	10.0000	1.0000	0.0062	0.0112	0.0011	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu851	4	5	0	3	17	11	40.0000	9.0000	31.0000	0.0225	0.0101	0.0348	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu852	0	0	0	0	4	2	6.0000	0.0000	6.0000	0.0034	0.0000	0.0067	*Bacteria*	U	U	U	U	U
Otu853	1	6	0	0	0	4	11.0000	7.0000	4.0000	0.0062	0.0079	0.0045	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu854	0	0	0	15	0	0	15.0000	0.0000	15.0000	0.0084	0.0000	0.0169	*Bacteria*	U	U	U	U	U
Otu855	7	11	0	0	0	0	18.0000	18.0000	0.0000	0.0101	0.0202	0.0000	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu856	1	18	0	4	3	14	40.0000	19.0000	21.0000	0.0225	0.0214	0.0236	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu857	0	0	0	12	2	6	20.0000	0.0000	20.0000	0.0112	0.0000	0.0225	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu858	0	0	0	2	20	8	30.0000	0.0000	30.0000	0.0169	0.0000	0.0337	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu859	1	9	1	4	0	5	20.0000	11.0000	9.0000	0.0112	0.0124	0.0101	*Bacteria*	U	U	U	U	U
Otu86	37	135	4	128	51	185	540.0000	176.0000	364.0000	0.3034	0.1978	0.4091	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu860	0	0	0	13	0	0	13.0000	0.0000	13.0000	0.0073	0.0000	0.0146	*Bacteria*	*Firmicutes*	U	U	U	U
Otu861	0	3	0	4	2	2	11.0000	3.0000	8.0000	0.0062	0.0034	0.0090	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu862	8	0	0	0	1	0	9.0000	8.0000	1.0000	0.0051	0.0090	0.0011	*Bacteria*	*Bacteroidetes*	*Cytophagia*	*Cytophagales*	U	U
Otu863	0	0	0	6	0	0	6.0000	0.0000	6.0000	0.0034	0.0000	0.0067	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu864	5	5	0	0	1	0	11.0000	10.0000	1.0000	0.0062	0.0112	0.0011	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Lachnospiraceae*	U
Otu865	4	7	0	5	1	3	20.0000	11.0000	9.0000	0.0112	0.0124	0.0101	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu866	0	0	0	5	0	0	5.0000	0.0000	5.0000	0.0028	0.0000	0.0056	*Bacteria*	*Firmicutes*	U	U	U	U
Otu867	0	0	0	0	1	5	6.0000	0.0000	6.0000	0.0034	0.0000	0.0067	*Bacteria*	U	U	U	U	U
Otu868	2	0	0	0	2	0	4.0000	2.0000	2.0000	0.0022	0.0022	0.0022	*Bacteria*	*Bacteroidetes*	*Flavobacteriia*	*Flavobacteriales*	*Flavobacteriaceae*	*Flavobacterium*
Otu869	1	3	0	6	0	1	11.0000	4.0000	7.0000	0.0062	0.0045	0.0079	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu87	1	2	0	129	11	62	205.0000	3.0000	202.0000	0.1152	0.0034	0.2270	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu870	0	0	0	2	4	3	9.0000	0.0000	9.0000	0.0051	0.0000	0.0101	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu871	3	5	0	11	0	0	19.0000	8.0000	11.0000	0.0107	0.0090	0.0124	*Bacteria*	*Firmicutes*	U	U	U	U
Otu872	4	0	1	0	3	1	9.0000	5.0000	4.0000	0.0051	0.0056	0.0045	*Bacteria*	*Candidatus_Saccharibacteria_bacteria*	*Saccharibacteria_genera_incertae_sedis*	U	U	U
Otu873	0	0	0	9	0	0	9.0000	0.0000	9.0000	0.0051	0.0000	0.0101	*Bacteria*	U	U	U	U	U
Otu874	10	0	0	0	0	0	10.0000	10.0000	0.0000	0.0056	0.0112	0.0000	*Bacteria*	*Bacteroidetes*	*Sphingobacteriia*	*Sphingobacteriales*	*Chitinophagaceae*	U
Otu875	4	1	0	0	17	1	23.0000	5.0000	18.0000	0.0129	0.0056	0.0202	*Bacteria*	*Spirochaetes*	*Spirochaetia*	*Spirochaetales*	*Spirochaetaceae*	U
Otu876	0	0	1	11	0	1	13.0000	1.0000	12.0000	0.0073	0.0011	0.0135	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu877	4	0	0	0	6	0	10.0000	4.0000	6.0000	0.0056	0.0045	0.0067	*Bacteria*	*Proteobacteria*	*Alphaproteobacte*	*Rhodospirillales*	*Acetobacteraceae*	U

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Otu878	0	0	0	1	0	1	2.0000	0.0000	2.0000	0.0011	0.0000	0.0022	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu879	0	0	0	0	225	176	401.0000	0.0000	401.0000	0.2253	0.0000	0.4507	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Lachnospiraceae*	U
Otu88	12	119	0	28	5	58	222.0000	131.0000	91.0000	0.1248	0.1472	0.1023	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu880	2	5	0	4	5	0	16.0000	7.0000	9.0000	0.0090	0.0079	0.0101	*Bacteria*	U	U	U	U	U
Otu881	3	7	0	1	0	7	18.0000	10.0000	8.0000	0.0101	0.0112	0.0090	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu882	5	0	0	0	4	0	9.0000	5.0000	4.0000	0.0051	0.0056	0.0045	*Bacteria*	*Proteobacteria*	*Gammaproteobacteria*	*Xanthomonadales*	U	U
Otu883	0	1	0	2	2	3	8.0000	1.0000	7.0000	0.0045	0.0011	0.0079	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu884	5	0	0	0	2	4	11.0000	5.0000	6.0000	0.0062	0.0056	0.0067	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu885	0	0	0	1	6	2	9.0000	0.0000	9.0000	0.0051	0.0000	0.0101	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu886	3	0	0	0	8	0	11.0000	3.0000	8.0000	0.0062	0.0034	0.0090	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	*Rhizobiales*	U	U
Otu887	4	0	0	0	1	0	5.0000	4.0000	1.0000	0.0028	0.0045	0.0011	*Bacteria*	U	U	U	U	U
Otu888	2	0	0	0	14	0	16.0000	2.0000	14.0000	0.0090	0.0022	0.0157	*Bacteria*	*Planctomycetes*	*Planctomycetia*	*Planctomycetales*	*Planctomycetaceae*	U
Otu889	0	0	1	0	6	0	7.0000	1.0000	6.0000	0.0039	0.0011	0.0067	*Bacteria*	*Proteobacteria*	*Gammaproteobacteria*	*Enterobacteriales*	*Enterobacteriaceae*	U
Otu89	0	0	0	1	174	103	278.0000	0.0000	278.0000	0.1562	0.0000	0.3124	*Bacteria*	U	U	U	U	U
Otu890	2	0	0	0	2	0	4.0000	2.0000	2.0000	0.0022	0.0022	0.0022	*Bacteria*	U	U	U	U	U
Otu891	0	0	0	0	1	6	7.0000	0.0000	7.0000	0.0039	0.0000	0.0079	*Bacteria*	*Firmicutes*	U	U	U	U
Otu892	0	0	0	0	4	3	7.0000	0.0000	7.0000	0.0039	0.0000	0.0079	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu893	1	0	0	0	3	1	5.0000	1.0000	4.0000	0.0028	0.0011	0.0045	*Bacteria*	*Actinobacteria*	*Actinobacteria*	*Actinomycetales*	*Nocardioidaceae*	*Aeromicrobium*
Otu894	0	0	0	4	0	2	6.0000	0.0000	6.0000	0.0034	0.0000	0.0067	*Bacteria*	U	U	U	U	U
Otu895	3	0	0	0	3	0	6.0000	3.0000	3.0000	0.0034	0.0034	0.0034	*Bacteria*	*Bacteroidetes*	*Sphingobacteriia*	*Sphingobacteriales*	*Chitinophagaceae*	*Sediminibacterium*
Otu896	0	1	0	6	6	2	15.0000	1.0000	14.0000	0.0084	0.0011	0.0157	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu897	1	5	0	0	0	0	6.0000	6.0000	0.0000	0.0034	0.0067	0.0000	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu898	0	0	0	7	1	2	10.0000	0.0000	10.0000	0.0056	0.0000	0.0112	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu899	6	0	0	0	13	0	19.0000	6.0000	13.0000	0.0107	0.0067	0.0146	*Bacteria*	U	U	U	U	U
Otu9	190	997	5	2027	144	58	3421.0000	1192.0000	2229.0000	1.9224	1.3397	2.5051	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu90	63	174	0	111	46	42	436.0000	237.0000	199.0000	0.2450	0.2664	0.2237	*Bacteria*	U	U	U	U	U
Otu900	0	1	0	4	0	5	10.0000	1.0000	9.0000	0.0056	0.0011	0.0101	*Bacteria*	U	U	U	U	U
Otu901	0	2	0	3	0	0	5.0000	2.0000	3.0000	0.0028	0.0022	0.0034	*Bacteria*	U	U	U	U	U
Otu902	5	0	0	0	5	0	10.0000	5.0000	5.0000	0.0056	0.0056	0.0056	*Bacteria*	U	U	U	U	U
Otu903	0	3	0	6	0	2	11.0000	3.0000	8.0000	0.0062	0.0034	0.0090	*Bacteria*	*Firmicutes*	U	U	U	U
Otu904	0	0	0	1	1	6	8.0000	0.0000	8.0000	0.0045	0.0000	0.0090	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu905	2	1	0	1	2	4	10.0000	3.0000	7.0000	0.0056	0.0034	0.0079	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu906	0	3	0	3	0	5	11.0000	3.0000	8.0000	0.0062	0.0034	0.0090	*Bacteria*	U	U	U	U	U
Otu907	1	7	1	9	11	13	42.0000	9.0000	33.0000	0.0236	0.0101	0.0371	*Bacteria*	*Firmicutes*	U	U	U	U
Otu908	0	6	0	1	0	7	14.0000	6.0000	8.0000	0.0079	0.0067	0.0090	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu909	1	6	0	5	2	0	14.0000	7.0000	7.0000	0.0079	0.0079	0.0079	*Bacteria*	*Firmicutes*	U	U	U	U
Otu91	12	15	0	92	79	52	250.0000	27.0000	223.0000	0.1405	0.0303	0.2506	*Bacteria*	*Firmicutes*	U	U	U	U

Otu910	0	0	0	1	10	2	13.0000	0.0000	13.0000	0.0073	0.0000	0.0146	*Bacteria*	U	U	U	U	U
Otu911	0	0	0	0	5	0	5.0000	0.0000	5.0000	0.0028	0.0000	0.0056	*Bacteria*			U	U	U
Otu912	1	0	0	0	7	0	8.0000	1.0000	7.0000	0.0045	0.0011	0.0079	*Bacteria*	*Candidatus_Saccharibacteria*	*Saccharibacteria_genera_incertae_sedis*	U	U	U
Otu913	0	0	0	0	4	6	10.0000	0.0000	10.0000	0.0056	0.0000	0.0112	*Bacteria*	U	U	U	U	U
Otu914	4	5	0	0	2	3	14.0000	9.0000	5.0000	0.0079	0.0101	0.0056	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu915	1	0	0	1	0	3	5.0000	1.0000	4.0000	0.0028	0.0011	0.0045	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu916	10	11	0	1	2	1	25.0000	21.0000	4.0000	0.0140	0.0236	0.0045	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu917	1	6	0	1	0	0	8.0000	7.0000	1.0000	0.0045	0.0079	0.0011	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu918	0	4	0	1	0	1	6.0000	4.0000	2.0000	0.0034	0.0045	0.0022	*Bacteria*	*Firmicutes*	U	U	U	U
Otu919	4	0	0	0	0	0	4.0000	4.0000	0.0000	0.0022	0.0045	0.0000	*Bacteria*	*Verrucomicrobia*	*Opitutae*	*Opitutales*	*Opitutaceae*	*Opitutus*
Otu92	0	0	192	0	20	0	212.0000	192.0000	20.0000	0.1191	0.2158	0.0225	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Peptostreptococcaceae*	*Clostridium_XI*
Otu920	0	1	0	14	0	3	18.0000	1.0000	17.0000	0.0101	0.0011	0.0191	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu921	0	0	0	0	6	6	12.0000	0.0000	12.0000	0.0067	0.0000	0.0135	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu922	0	3	0	2	0	18	23.0000	3.0000	20.0000	0.0129	0.0034	0.0225	*Bacteria*	*Firmicutes*	U	U	U	U
Otu923	0	0	0	1	5	3	9.0000	0.0000	9.0000	0.0051	0.0000	0.0101	*Bacteria*	*Firmicutes*	U	U	U	U
Otu924	1	5	0	0	1	1	8.0000	6.0000	2.0000	0.0045	0.0067	0.0022	*Bacteria*	*Firmicutes*	U	U	U	U
Otu925	0	6	0	0	4	2	12.0000	6.0000	6.0000	0.0067	0.0067	0.0067	*Bacteria*	*Firmicutes*	U	U	U	U
Otu926	0	5	0	1	0	1	7.0000	5.0000	2.0000	0.0039	0.0056	0.0022	*Bacteria*	U	U	U	U	U
Otu927	0	0	0	2	1	8	11.0000	0.0000	11.0000	0.0062	0.0000	0.0124	*Bacteria*	*Firmicutes*	U	U	U	U
Otu928	1	0	0	2	0	6	9.0000	1.0000	8.0000	0.0051	0.0011	0.0090	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu929	6	0	0	0	11	1	18.0000	6.0000	12.0000	0.0101	0.0067	0.0135	*Bacteria*	U	U	U	U	U
Otu93	0	0	1	74	135	14	224.0000	1.0000	223.0000	0.1259	0.0011	0.2506	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu930	3	3	0	1	0	5	12.0000	6.0000	6.0000	0.0067	0.0067	0.0067	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu931	0	0	0	5	1	0	6.0000	0.0000	6.0000	0.0034	0.0000	0.0067	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu932	2	0	1	0	7	4	14.0000	3.0000	11.0000	0.0079	0.0034	0.0124	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	*Rhizobiales*	U	U
Otu933	3	5	0	0	0	2	10.0000	8.0000	2.0000	0.0056	0.0090	0.0022	*Bacteria*	*Firmicutes*	U	U	U	U
Otu934	4	3	1	1	0	1	10.0000	8.0000	2.0000	0.0056	0.0090	0.0022	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu935	0	0	0	0	10	3	13.0000	0.0000	13.0000	0.0073	0.0000	0.0146	*Bacteria*	*Actinobacteria*	*Actinobacteria*	*Actinomycetales*	U	U
Otu936	0	0	1	0	6	0	7.0000	1.0000	6.0000	0.0039	0.0011	0.0067	*Bacteria*	*Actinobacteria*	*Actinobacteria*	*Actinomycetales*	U	U
Otu937	0	0	1	4	3	0	8.0000	1.0000	7.0000	0.0045	0.0011	0.0079	*Bacteria*	*Firmicutes*			U	U
Otu938	3	0	0	0	1	0	4.0000	3.0000	1.0000	0.0022	0.0034	0.0011	*Bacteria*	*Bacteroidetes*	*Sphingobacteriia*	*Sphingobacteriales*	*Sphingobacteriaceae*	*Mucilaginibacter*
Otu939	0	0	0	16	1	0	17.0000	0.0000	17.0000	0.0096	0.0000	0.0191	*Bacteria*	U	U	U	U	U
Otu94	10	19	1	4	137	79	250.0000	30.0000	220.0000	0.1405	0.0337	0.2473	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu940	0	0	1	0	5	3	9.0000	1.0000	8.0000	0.0051	0.0011	0.0090	*Bacteria*	*Proteobacteria*	*Betaproteobacteria*	*Burkholderiales*	*Alcaligenaceae*	*Achromobacter*
Otu941	2	0	0	0	3	0	5.0000	2.0000	3.0000	0.0028	0.0022	0.0034	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	*Rhodospirillales*	*Rhodospirillaceae*	U
Otu942	0	6	0	1	0	2	9.0000	6.0000	3.0000	0.0051	0.0067	0.0034	*Bacteria*	U	U	U	U	U
Otu943	0	0	0	8	0	2	10.0000	0.0000	10.0000	0.0056	0.0000	0.0112	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu944	0	1	0	5	0	4	10.0000	1.0000	9.0000	0.0056	0.0011	0.0101	*Bacteria*	*Firmicutes*	U	U	U	U

Otu945	1	9	0	6	1	1	18.0000	10.0000	8.0000	0.0101	0.0112	0.0090	*Bacteria*	*Firmicutes*	U	U	U	U
Otu946	4	1	0	1	1	1	8.0000	5.0000	3.0000	0.0045	0.0056	0.0034	*Bacteria*	*Firmicutes*	U	U	U	U
Otu947	0	0	1	0	5	1	7.0000	1.0000	6.0000	0.0039	0.0011	0.0067	*Bacteria*	U	U	U	U	U
Otu948	1	1	0	1	2	2	7.0000	2.0000	5.0000	0.0039	0.0022	0.0056	*Bacteria*	*Firmicutes*	*Negativicutes*	*Selenomonadales*	U	U
Otu949	1	0	0	1	7	4	13.0000	1.0000	12.0000	0.0073	0.0011	0.0135	*Bacteria*	*Verrucomicrobia*	*Opitutae*	*Opitutales*	*Opitutaceae*	U
Otu95	26	49	0	73	10	69	227.0000	75.0000	152.0000	0.1276	0.0843	0.1708	*Bacteria*	*Firmicutes*	U	U	U	U
Otu950	2	5	0	2	1	0	10.0000	7.0000	3.0000	0.0056	0.0079	0.0034	*Bacteria*	U	U	U	U	U
Otu951	0	0	0	3	7	0	10.0000	0.0000	10.0000	0.0056	0.0000	0.0112	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu952	3	0	0	0	4	0	7.0000	3.0000	4.0000	0.0039	0.0034	0.0045	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	*Rhodospirillales*	*Acetobacteraceae*	U
Otu953	0	0	0	2	0	1	3.0000	0.0000	3.0000	0.0017	0.0000	0.0034	*Bacteria*	*Firmicutes*	U	U	U	U
Otu954	1	1	0	6	5	4	17.0000	2.0000	15.0000	0.0096	0.0022	0.0169	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu955	2	3	0	0	0	0	5.0000	5.0000	0.0000	0.0028	0.0056	0.0000	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu956	1	0	0	0	1	0	2.0000	1.0000	1.0000	0.0011	0.0011	0.0011	*Bacteria*	*Candidatus_Saccharibacteria*	*Saccharibacteria_genera_incertae_sedis*	U	U	U
Otu957	2	10	0	0	1	0	13.0000	12.0000	1.0000	0.0073	0.0135	0.0011	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu958	1	6	0	11	0	2	20.0000	7.0000	13.0000	0.0112	0.0079	0.0146	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu959	1	2	0	10	0	2	15.0000	3.0000	12.0000	0.0084	0.0034	0.0135	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu96	68	78	0	38	2	3	189.0000	146.0000	43.0000	0.1062	0.1641	0.0483	*Bacteria*	*Firmicutes*	U	U	U	U
Otu960	0	2	0	6	0	6	14.0000	2.0000	12.0000	0.0079	0.0022	0.0135	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu961	1	1	0	0	0	3	5.0000	2.0000	3.0000	0.0028	0.0022	0.0034	*Bacteria*	*Firmicutes*	U	U	U	U
Otu962	0	0	0	0	0	19	19.0000	0.0000	19.0000	0.0107	0.0000	0.0214	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu963	0	0	0	0	1	3	4.0000	0.0000	4.0000	0.0022	0.0000	0.0045	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu964	0	1	9	0	7	3	20.0000	10.0000	10.0000	0.0112	0.0112	0.0112	*Bacteria*	*Planctomycetes*	*Planctomycetia*	*Planctomycetales*	*Planctomycetaceae*	U
Otu965	4	0	0	0	15	0	19.0000	4.0000	15.0000	0.0107	0.0045	0.0169	*Bacteria*	*Actinobacteria*	*Actinobacteria*	U	U	U
Otu966	0	0	0	0	4	0	4.0000	0.0000	4.0000	0.0022	0.0000	0.0045	*Bacteria*	U	U	U	U	U
Otu967	0	0	0	0	7	4	11.0000	0.0000	11.0000	0.0062	0.0000	0.0124	*Bacteria*	*Firmicutes*	U	U	U	U
Otu968	3	13	0	1	0	3	20.0000	16.0000	4.0000	0.0112	0.0180	0.0045	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu969	7	0	0	0	2	0	9.0000	7.0000	2.0000	0.0051	0.0079	0.0022	*Bacteria*	U	U	U	U	U
Otu97	13	40	0	77	69	22	221.0000	53.0000	168.0000	0.1242	0.0596	0.1888	*Bacteria*	U	U	U	U	U
Otu970	0	0	2	0	5	0	7.0000	2.0000	5.0000	0.0039	0.0022	0.0056	*Bacteria*	*Actinobacteria*	*Actinobacteria*	*Acidimicrobiales*	*Iamiaceae*	*Aquihabitans*
Otu971	0	6	0	0	0	0	6.0000	6.0000	0.0000	0.0034	0.0067	0.0000	*Bacteria*	U	U		U	U
Otu972	2	0	0	0	5	1	8.0000	2.0000	6.0000	0.0045	0.0022	0.0067	*Bacteria*	*Candidatus_Saccharibacteria*	*Saccharibacteria_genera_incertae_sedis*	U	U	U
Otu973	0	0	0	7	0	0	7.0000	0.0000	7.0000	0.0039	0.0000	0.0079	*Bacteria*	U	U	U	U	U
Otu974	0	0	3	0	14	0	17.0000	3.0000	14.0000	0.0096	0.0034	0.0157	*Bacteria*	*Actinobacteria*	*Actinobacteria*	*Solirubrobacterales*	U	U
Otu975	4	0	0	0	4	0	8.0000	4.0000	4.0000	0.0045	0.0045	0.0045	*Bacteria*	U	U	U	U	U
Otu976	0	1	0	1	0	2	4.0000	1.0000	3.0000	0.0022	0.0011	0.0034	*Bacteria*	*Firmicutes*	U	U	U	U
Otu977	0	0	0	2	0	3	5.0000	0.0000	5.0000	0.0028	0.0000	0.0056	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu978	1	0	0	0	13	1	15.0000	1.0000	14.0000	0.0084	0.0011	0.0157	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	*Rhizobiales*	U	U

Otu979	0	0	3	0	0	0	3.0000	3.0000	0.0000	0.0017	0.0034	0.0000	*Bacteria*	*Bacteroidetes*	*Sphingobacteriia*	*Sphingobacteriales*	*Sphingobacteriaceae*	*Sphingobacterium*
Otu98	0	0	0	0	129	80	209.0000	0.0000	209.0000	0.1174	0.0000	0.2349	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu980	0	0	8	0	1	0	9.0000	8.0000	1.0000	0.0051	0.0090	0.0011	*Bacteria*	*Bacteroidetes*	*Sphingobacteriia*	*Sphingobacteriales*	*Sphingobacteriaceae*	*Sphingobacterium*
Otu981	0	0	0	9	0	1	10.0000	0.0000	10.0000	0.0056	0.0000	0.0112	*Bacteria*	U	U	U	U	U
Otu982	0	0	0	3	1	3	7.0000	0.0000	7.0000	0.0039	0.0000	0.0079	*Bacteria*	U	U	U	U	U
Otu983	0	1	0	1	0	3	5.0000	1.0000	4.0000	0.0028	0.0011	0.0045	*Bacteria*	*Firmicutes*	U	U	U	U
Otu984	0	1	0	0	0	8	9.0000	1.0000	8.0000	0.0051	0.0011	0.0090	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu985	0	4	0	8	1	0	13.0000	4.0000	9.0000	0.0073	0.0045	0.0101	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu986	4	2	0	2	0	7	15.0000	6.0000	9.0000	0.0084	0.0067	0.0101	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu987	1	4	0	1	0	4	10.0000	5.0000	5.0000	0.0056	0.0056	0.0056	*Bacteria*	*Firmicutes*	U	U	U	U
Otu988	0	0	0	0	7	2	9.0000	0.0000	9.0000	0.0051	0.0000	0.0101	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	U
Otu989	0	0	0	0	5	0	5.0000	0.0000	5.0000	0.0028	0.0000	0.0056	*Bacteria*	*Proteobacteria*	*Alphaproteobacteria*	*Rhizobiales*	*Xanthobacteraceae*	*Ancylobacter*
Otu99	1	5	0	48	6	136	196.0000	6.0000	190.0000	0.1101	0.0067	0.2135	*Bacteria*	*Firmicutes*	U	U	U	U
Otu990	0	7	0	6	3	4	20.0000	7.0000	13.0000	0.0112	0.0079	0.0146	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu991	0	2	0	7	0	7	16.0000	2.0000	14.0000	0.0090	0.0022	0.0157	*Bacteria*	*Firmicutes*	*Clostridia*	U	U	U
Otu992	0	0	0	0	12	3	15.0000	0.0000	15.0000	0.0084	0.0000	0.0169	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu993	6	0	0	0	6	0	12.0000	6.0000	6.0000	0.0067	0.0067	0.0067	*Bacteria*	*Bacteroidetes*	*Sphingobacteriia*	*Sphingobacteriales*	*Sphingobacteriaceae*	U
Otu994	0	10	0	2	6	4	22.0000	10.0000	12.0000	0.0124	0.0112	0.0135	*Bacteria*	*Firmicutes*	U	U	U	U
Otu995	1	1	0	0	9	1	12.0000	2.0000	10.0000	0.0067	0.0022	0.0112	*Bacteria*	U	U	U	U	U
Otu996	0	1	0	0	1	4	6.0000	1.0000	5.0000	0.0034	0.0011	0.0056	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U
Otu997	0	0	0	6	0	4	10.0000	0.0000	10.0000	0.0056	0.0000	0.0112	*Bacteria*	*Firmicutes*	U	U	U	U
Otu998	0	0	0	3	1	3	7.0000	0.0000	7.0000	0.0039	0.0000	0.0079	*Bacteria*	*Firmicutes*	U	U	U	U
Otu999	3	1	0	2	3	2	11.0000	4.0000	7.0000	0.0062	0.0045	0.0079	*Bacteria*	*Firmicutes*	*Clostridia*	*Clostridiales*	U	U

P6A to P8A: midgut samples. P6R to P8R: hindgut samples. U: Unidentified taxon

Table S5. Absolute and Relative abundance of fungal OTUs in *Pelidnota luridipes* gut

OTU ID	Abundância Absoluta									Abundância Relativa			Classificação					
	P6A	P7A	P8A	P6R	P7R	P8R	Total	Midgut	Hindgut	Total	Midgut	Hindgut	Kingdom	Phylum	Class	Order	Family	Genus
OTU1	36880.0000	30228.0000	20459.0000	56508.0000	36250.0000	23861.0000	204186.0000	87567.0000	116619.0000	28.7165	24.6305	32.8021	*Fungi*	*Ascomycota*	*Saccharomycetes*	*Saccharomycetales*	*Debaryomycetaceae*	*Candida*
OTU10	219.0000	4.0000	833.0000	192.0000	2940.0000	4082.0000	8270.0000	1056.0000	7214.0000	1.1631	0.2970	2.0291	*Fungi*	*Ascomycota*	U	U	U	U
OTU100	0.0000	0.0000	0.0000	0.0000	0.0000	60.0000	60.0000	0.0000	60.0000	0.0084	0.0000	0.0169	*Fungi*	*Basidiomycota*	U	U	U	U
OTU101	0.0000	118.0000	0.0000	0.0000	0.0000	0.0000	118.0000	118.0000	0.0000	0.0166	0.0332	0.0000	*Fungi*	*Ascomycota*	U	U	U	U
OTU102	1.0000	7.0000	1.0000	0.0000	99.0000	3.0000	111.0000	9.0000	102.0000	0.0156	0.0025	0.0287	*Fungi*	*Ascomycota*	*Dothideomycetes*	*Capnodiales*	*Mycosphaerellaceae*	*Davidiella*
OTU103	81.0000	0.0000	0.0000	0.0000	0.0000	0.0000	81.0000	81.0000	0.0000	0.0114	0.0228	0.0000	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Ophiostomatales*	*Ophiostomataceae*	*Hawksworthiomyces*
OTU104	0.0000	0.0000	20.0000	0.0000	79.0000	0.0000	99.0000	20.0000	79.0000	0.0139	0.0056	0.0222	*Fungi*	*Ascomycota*	*Dothideomycetes*	*Mycosphaerellales*	*Dissoconiaceae*	*Ramichloridium*
OTU105	8.0000	7.0000	3.0000	2.0000	4.0000	62.0000	86.0000	18.0000	68.0000	0.0121	0.0051	0.0191	*Fungi*	*Ascomycota*	*Sordariomycetes*	U	U	U
OTU106	3.0000	1.0000	1.0000	3.0000	92.0000	0.0000	100.0000	5.0000	95.0000	0.0141	0.0014	0.0267	*Fungi*	*Ascomycota*	*Dothideomycetes*	*Dothideales*	*Saccotheciaceae*	*Aureobasidium*
OTU107	0.0000	0.0000	21.0000	0.0000	70.0000	0.0000	91.0000	21.0000	70.0000	0.0128	0.0059	0.0197	*Fungi*	*Ascomycota*	*Eurotiomycetes*	*Eurotiales*	*Aspergillaceae*	*Aspergillus*
OTU108	50.0000	0.0000	48.0000	0.0000	0.0000	13.0000	111.0000	98.0000	13.0000	0.0156	0.0276	0.0037	*Fungi*	*Ascomycota*	U	U	U	U
OTU109	81.0000	0.0000	0.0000	0.0000	0.0000	0.0000	81.0000	81.0000	0.0000	0.0114	0.0228	0.0000	*Fungi*	*Fungi_OTU109*	U	U	U	U
OTU11	510.0000	149.0000	924.0000	439.0000	52.0000	4250.0000	6324.0000	1583.0000	4741.0000	0.8894	0.4453	1.3335	*Fungi*	*Ascomycota*	*Dothideomycetes*	U	U	U
OTU110	0.0000	0.0000	0.0000	0.0000	101.0000	0.0000	101.0000	0.0000	101.0000	0.0142	0.0000	0.0284	*Fungi*	*Ascomycota*	*Dothideomycetes*	U	U	U
OTU111	0.0000	0.0000	0.0000	0.0000	78.0000	0.0000	78.0000	0.0000	78.0000	0.0110	0.0000	0.0219	*Fungi*	*Ascomycota*	*Saccharomycetes*	*Saccharomycetales*	*Trichomonascaceae*	*Sugiyamaella*
OTU112	0.0000	0.0000	0.0000	0.0000	0.0000	77.0000	77.0000	0.0000	77.0000	0.0108	0.0000	0.0217	*Fungi*	*Fungi_OTU112*	U	U	U	U
OTU113	1.0000	1.0000	1.0000	0.0000	0.0000	68.0000	71.0000	3.0000	68.0000	0.0100	0.0008	0.0191	*Fungi*	*Ascomycota*	*Dothideomycetes*	*Capnodiales*	*Mycosphaerellaceae*	*Davidiella*
OTU1	78.0000	0.0000	0.0000	0.0000	14.0000	0.0000	92.0000	78.0000	14.0000	0.012	0.021	0.003	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Chaetosphaeri*	*Chaetosphaeriaceae*	*Chaetosphaeria*

14										9	9	9				*ales*		
OTU115	72.0000	0.0000	0.0000	0.0000	0.0000	0.0000	72.0000	72.0000	0.0000	0.0101	0.0203	0.0000	*Fungi*	*Basidiomycota*	*Microbotryomycetes*	*Sporidiobolales*	*Sporidiobolaceae*	*Rhodotorula*
OTU116	57.0000	0.0000	0.0000	0.0000	0.0000	31.0000	88.0000	57.0000	31.0000	0.0124	0.0160	0.0087	*Fungi*	U	U	U	U	U
OTU117	0.0000	0.0000	103.0000	0.0000	0.0000	0.0000	103.0000	103.0000	0.0000	0.0145	0.0290	0.0000	*Fungi*	*Ascomycota*	*Dothideomycetes*	*Pleosporales*	*Thyridariaceae*	*Roussoella*
OTU118	2.0000	7.0000	3.0000	0.0000	56.0000	0.0000	68.0000	12.0000	56.0000	0.0096	0.0034	0.0158	*Fungi*	*Basidiomycota*	*Malasseziomycetes*	*Malasseziales*	*Malasseziaceae*	*Malassezia*
OTU119	89.0000	0.0000	0.0000	0.0000	0.0000	0.0000	89.0000	89.0000	0.0000	0.0125	0.0250	0.0000	*Fungi*	*Ascomycota*	*Leotiomycetes*	U	U	U
OTU12	3223.0000	2903.0000	1357.0000	239.0000	140.0000	601.0000	8463.0000	7483.0000	980.0000	1.1902	2.1048	0.2757	*Fungi*	*Ascomycota*	*Dothideomycetes*	*Aulographales*	*Rhizodiscinaceae*	*Rhizodiscina*
OTU120	0.0000	0.0000	0.0000	0.0000	0.0000	48.0000	48.0000	0.0000	48.0000	0.0068	0.0000	0.0135	*Fungi*	*Ascomycota*	*Eurotiomycetes*	*Chaetothyriales*	*Herpotrichiellaceae*	*Exophiala*
OTU121	0.0000	31.0000	20.0000	0.0000	0.0000	20.0000	71.0000	51.0000	20.0000	0.0100	0.0143	0.0056	*Fungi*	*Ascomycota*	U	U	U	U
OTU122	3.0000	0.0000	67.0000	0.0000	0.0000	0.0000	70.0000	70.0000	0.0000	0.0098	0.0197	0.0000	*Fungi*	*Ascomycota*	*Dothideomycetes*	*Pleosporales*	*Pleosporaceae*	*Alternaria*
OTU123	18.0000	0.0000	11.0000	0.0000	1.0000	31.0000	61.0000	29.0000	32.0000	0.0086	0.0082	0.0090	*Fungi*	*Ascomycota*	*Dothideomycetes*	*Pleosporales*	*Massarinaceae*	*Massarina*
OTU124	0.0000	79.0000	0.0000	0.0000	0.0000	0.0000	79.0000	79.0000	0.0000	0.0111	0.0222	0.0000	*Fungi*	*Basidiomycota*	U	U	U	U
OTU125	43.0000	26.0000	0.0000	0.0000	0.0000	0.0000	69.0000	69.0000	0.0000	0.0097	0.0194	0.0000	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Hypocreales*	*Cordycipitaceae*	*Lecanicillium*
OTU126	38.0000	0.0000	34.0000	2.0000	0.0000	0.0000	74.0000	72.0000	2.0000	0.0104	0.0203	0.0006	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Hypocreales*	*Ophiocordycipitaceae*	*Harposporium*
OTU127	46.0000	0.0000	40.0000	0.0000	0.0000	0.0000	86.0000	86.0000	0.0000	0.0121	0.0242	0.0000	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Microascales*	*Microascaceae*	*Scedosporium*
OTU128	0.0000	0.0000	9.0000	40.0000	0.0000	0.0000	49.0000	9.0000	40.0000	0.0069	0.0025	0.0113	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Xylariales*	*Xylariaceae*	U
OTU129	0.0000	16.0000	1.0000	0.0000	0.0000	26.0000	43.0000	17.0000	26.0000	0.0060	0.0048	0.0073	*Fungi*	*Fungi_OTU129*	U	U	U	U
OTU13	770.0000	17.0000	356.0000	1798.0000	3705.0000	461.0000	7107.0000	1143.0000	5964.0000	0.9995	0.3215	1.6775	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Xenospadicoidales*	*Xenospadicoidaceae*	*Spadicoides*
OTU130	60.0000	2.0000	4.0000	0.0000	1.0000	1.0000	68.0000	66.0000	2.0000	0.0096	0.0186	0.0006	*Fungi*	*Ascomycota*	*Dothideomycetes*	*Pleosporales*	*Lophiostomataceae*	*Lophiostoma*
OTU131	0.0000	0.0000	14.0000	0.0000	40.0000	0.0000	54.0000	14.0000	40.0000	0.0076	0.0039	0.0113	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Hypocreales*	*Nectriaceae*	*Dialonectria*
OTU1	1253.00	1115.000	781.0000	2222.00	1145.000	898.0000	7414.000	3149.00	4265.000	1.042	0.885	1.199	*Fungi*	*Ascomycota*	*Saccharomycete*	*Saccharomyce*	*Debaryomycetaceae*	*Spathaspora*

32	00	0		00	0		0	00	0	7	7	6			*s*	*tales*		
OTU133	0.0000	14.0000	20.0000	2.0000	0.0000	5.0000	41.0000	34.0000	7.0000	0.0058	0.0096	0.0020	*Fungi*	*Ascomycota*	*Dothideomycetes*	*Capnodiales*	*Mycosphaerellaceae*	*Davidiella*
OTU134	31.0000	0.0000	13.0000	1.0000	0.0000	42.0000	87.0000	44.0000	43.0000	0.0122	0.0124	0.0121	*Fungi*	*Ascomycota*	*Dothideomycetes*	*Botryosphaeriales*	*Botryosphaeriaceae*	U
OTU135	0.0000	60.0000	0.0000	0.0000	0.0000	0.0000	60.0000	60.0000	0.0000	0.0084	0.0169	0.0000	*Fungi*	*Basidiomycota*	*Agaricomycetes*	*Atheliales*	*Atheliaceae*	*Myriococcum*
OTU136	0.0000	10.0000	17.0000	0.0000	0.0000	27.0000	54.0000	27.0000	27.0000	0.0076	0.0076	0.0076	*Fungi*	*Basidiomycota*	U	U	U	U
OTU137	0.0000	0.0000	39.0000	0.0000	0.0000	0.0000	39.0000	39.0000	0.0000	0.0055	0.0110	0.0000	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Hypocreales*	*Stachybotryaceae*	*Albifimbria*
OTU138	0.0000	54.0000	0.0000	0.0000	0.0000	0.0000	54.0000	54.0000	0.0000	0.0076	0.0152	0.0000	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Trichosphaeriales*	*Trichosphaeriales_Incertae_sedis*	*Nigrospora*
OTU139	0.0000	60.0000	0.0000	0.0000	0.0000	0.0000	60.0000	60.0000	0.0000	0.0084	0.0169	0.0000	*Fungi*	*Basidiomycota*	*Agaricomycetes*	*Russulales*	*Wrightoporiaceae*	*Wrightoporia*
OTU14	371.0000	990.0000	1177.0000	261.0000	1155.0000	2577.0000	6531.0000	2538.0000	3993.0000	0.9185	0.7139	1.1231	*Fungi*	*Ascomycota*	*Eurotiomycetes*	*Eurotiales*	*Thermoascaceae*	*Byssochlamys*
OTU140	82.0000	71.0000	368.0000	55.0000	2.0000	559.0000	1137.0000	521.0000	616.0000	0.1599	0.1465	0.1733	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Hypocreales*	*Hypocreaceae*	*Trichoderma*
OTU141	0.0000	0.0000	0.0000	0.0000	0.0000	32.0000	32.0000	0.0000	32.0000	0.0045	0.0000	0.0090	*Fungi*	*Ascomycota*	U	U	U	U
OTU142	44.0000	0.0000	6.0000	0.0000	0.0000	0.0000	50.0000	50.0000	0.0000	0.0070	0.0141	0.0000	*Fungi*	*Ascomycota*	*Eurotiomycetes*	*Eurotiales*	*Aspergillaceae*	*Aspergillus*
OTU143	0.0000	0.0000	0.0000	0.0000	51.0000	1.0000	52.0000	0.0000	52.0000	0.0073	0.0000	0.0146	*Fungi*	*Ascomycota*	*Dothideomycetes*	U	*Pleurotremataceae*	*Pleurotrema*
OTU144	0.0000	0.0000	25.0000	2.0000	0.0000	0.0000	27.0000	25.0000	2.0000	0.0038	0.0070	0.0006	*Fungi*	*Basidiomycota*	U	U	U	U
OTU145	36.0000	0.0000	0.0000	0.0000	0.0000	0.0000	36.0000	36.0000	0.0000	0.0051	0.0101	0.0000	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Xylariales*	*Xylariaceae*	*Annulohypoxylon*
OTU146	0.0000	0.0000	44.0000	0.0000	0.0000	0.0000	44.0000	44.0000	0.0000	0.0062	0.0124	0.0000	*Fungi*	*Ascomycota*	*Sordariomycetes*	U	U	U
OTU147	0.0000	0.0000	5.0000	0.0000	0.0000	33.0000	38.0000	5.0000	33.0000	0.0053	0.0014	0.0093	*Fungi*	*Ascomycota*	U	U	U	U
OTU148	0.0000	34.0000	0.0000	0.0000	0.0000	0.0000	34.0000	34.0000	0.0000	0.0048	0.0096	0.0000	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Hypocreales*	*Clavicipitaceae*	*Pochonia*
OTU149	1.0000	0.0000	13.0000	0.0000	0.0000	23.0000	37.0000	14.0000	23.0000	0.0052	0.0039	0.0065	*Fungi*	*Ascomycota*	*Dothideomycetes*	*Capnodiales*	*Mycosphaerellaceae*	*Davidiella*
OTU15	2658.0000	450.0000	514.0000	339.0000	1827.0000	737.0000	6525.0000	3622.0000	2903.0000	0.9177	1.0188	0.8165	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Hypocreales*	*Hypocreaceae*	U
OTU1	0.0000	45.0000	0.0000	0.0000	0.0000	0.0000	45.0000	45.0000	0.0000	0.006	0.012	0.000	*Fungi*	*Ascomycota*	*Eurotiomycetes*	*Eurotiales*	*Aspergillaceae*	*Aspergillus*

50										3	7	0						
OTU151	0.0000	41.0000	0.0000	0.0000	0.0000	0.0000	41.0000	41.0000	0.0000	0.0058	0.0115	0.0000	*Fungi*	*Mucoromycota*	*Mucoromycetes*	*Mucorales*	*Cunninghamellaceae*	*Absidia*
OTU152	0.0000	0.0000	0.0000	0.0000	0.0000	32.0000	32.0000	0.0000	32.0000	0.0045	0.0000	0.0090	*Fungi*	*Ascomycota*	*Eurotiomycetes*	*Eurotiales*	*Aspergillaceae*	*Aspergillus*
OTU153	0.0000	0.0000	27.0000	0.0000	0.0000	0.0000	27.0000	27.0000	0.0000	0.0038	0.0076	0.0000	*Fungi*	*Ascomycota*	*Dothideomycetes*	*Pleosporales*	U	U
OTU154	42.0000	0.0000	0.0000	0.0000	0.0000	0.0000	42.0000	42.0000	0.0000	0.0059	0.0118	0.0000	*Fungi*	*Ascomycota*	U	U	U	U
OTU155	23.0000	0.0000	0.0000	0.0000	0.0000	0.0000	23.0000	23.0000	0.0000	0.0032	0.0065	0.0000	*Fungi*	*Basidiomycota*	U	U	U	U
OTU156	0.0000	0.0000	0.0000	0.0000	0.0000	13.0000	13.0000	0.0000	13.0000	0.0018	0.0000	0.0037	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Hypocreales*	*Stachybotryaceae*	*Sirastachys*
OTU157	0.0000	0.0000	1.0000	49.0000	0.0000	0.0000	50.0000	1.0000	49.0000	0.0070	0.0003	0.0138	*Fungi*	*Ascomycota*	*Eurotiomycetes*	*Eurotiales*	*Thermoascaceae*	*Paecilomyces*
OTU158	0.0000	0.0000	0.0000	0.0000	0.0000	15.0000	15.0000	0.0000	15.0000	0.0021	0.0000	0.0042	*Fungi*	*Ascomycota*	U	U	U	U
OTU159	0.0000	24.0000	0.0000	0.0000	0.0000	0.0000	24.0000	24.0000	0.0000	0.0034	0.0068	0.0000	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Sordariales*	U	U
OTU16	1048.0000	2144.0000	840.0000	91.0000	4226.0000	2074.0000	10423.0000	4032.0000	6391.0000	1.4659	1.1341	1.7976	*Fungi*	*Fungi_OTU16*	U	U	U	U
OTU160	0.0000	0.0000	0.0000	1.0000	40.0000	0.0000	41.0000	0.0000	41.0000	0.0058	0.0000	0.0115	*Fungi*	*Basidiomycota*	U	U	U	U
OTU161	16.0000	0.0000	19.0000	0.0000	0.0000	0.0000	35.0000	35.0000	0.0000	0.0049	0.0098	0.0000	*Fungi*	*Ascomycota*	*Sordariomycetes*	U	U	U
OTU162	1.0000	0.0000	1.0000	30.0000	2.0000	1.0000	35.0000	2.0000	33.0000	0.0049	0.0006	0.0093	*Fungi*	*Ascomycota*	U	U	U	U
OTU163	0.0000	27.0000	0.0000	0.0000	0.0000	0.0000	27.0000	27.0000	0.0000	0.0038	0.0076	0.0000	*Fungi*	*Ascomycota*	*Sordariomycetes*	U	U	U
OTU164	21.0000	0.0000	13.0000	0.0000	0.0000	0.0000	34.0000	34.0000	0.0000	0.0048	0.0096	0.0000	*Fungi*	*Ascomycota*	*Eurotiomycetes*	*Chaetothyriales*	*Herpotrichiellaceae*	U
OTU165	30.0000	0.0000	0.0000	1.0000	0.0000	0.0000	31.0000	30.0000	1.0000	0.0044	0.0084	0.0003	*Fungi*	*Basidiomycota*	U	U	U	U
OTU167	0.0000	0.0000	0.0000	0.0000	0.0000	15.0000	15.0000	0.0000	15.0000	0.0021	0.0000	0.0042	*Fungi*	*Ascomycota*	*Eurotiomycetes*	*Eurotiales*	*Aspergillaceae*	*Penicillium*
OTU168	0.0000	25.0000	0.0000	0.0000	0.0000	0.0000	25.0000	25.0000	0.0000	0.0035	0.0070	0.0000	*Fungi*	*Ascomycota*	*Sordariomycetes*	U	U	U
OTU169	0.0000	0.0000	20.0000	0.0000	0.0000	0.0000	20.0000	20.0000	0.0000	0.0028	0.0056	0.0000	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Xylariales*	U	U
OTU1	3181.00	0.0000	849.0000	21.0000	1454.00	1.0000	5506.000	4030.00	1476.000	0.774	1.133	0.415	*Fungi*	*Ascomycota*	*Sordariomycetes*	U	U	U

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OTU170	0.0000	11.0000	13.0000	0.0000	0.0000	0.0000	24.0000	24.0000	0.0000	0.0034	0.0068	0.0000	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Pleurotheciales*	*Pleurotheciaceae*	*Pleurothecium*
OTU171	18.0000	0.0000	3.0000	0.0000	0.0000	0.0000	21.0000	21.0000	0.0000	0.0030	0.0059	0.0000	*Fungi*	*Ascomycota*	*Eurotiomycetes*	*Chaetothyriales*	*Herpotrichiellaceae*	*Exophiala*
OTU172	638.0000	514.0000	340.0000	1034.0000	590.0000	392.0000	3508.0000	1492.0000	2016.0000	0.4934	0.4197	0.5671	*Fungi*	*Ascomycota*	*Saccharomycetes*	*Saccharomycetales*	*Debaryomycetaceae*	*Candida*
OTU173	32.0000	0.0000	0.0000	0.0000	0.0000	0.0000	32.0000	32.0000	0.0000	0.0045	0.0090	0.0000	*Fungi*	*Ascomycota*	*Sordariomycetes*	U	U	U
OTU174	0.0000	0.0000	20.0000	0.0000	0.0000	0.0000	20.0000	20.0000	0.0000	0.0028	0.0056	0.0000	*Fungi*	*Ascomycota*	*Dothideomycetes*	*Pleosporales*	*Pleosporaceae*	*Alternaria*
OTU175	0.0000	0.0000	0.0000	0.0000	13.0000	0.0000	13.0000	0.0000	13.0000	0.0018	0.0000	0.0037	*Fungi*	*Fungi_OTU175*	U	U	U	U
OTU176	0.0000	0.0000	19.0000	0.0000	0.0000	0.0000	19.0000	19.0000	0.0000	0.0027	0.0053	0.0000	*Fungi*	*Ascomycota*	*Dothideomycetes*	*Pleosporales*	*Pleosporaceae*	*Alternaria*
OTU177	0.0000	30.0000	9.0000	0.0000	0.0000	0.0000	39.0000	39.0000	0.0000	0.0055	0.0110	0.0000	*Fungi*	*Fungi_OTU177*	U	U	U	U
OTU178	0.0000	0.0000	0.0000	0.0000	0.0000	18.0000	18.0000	0.0000	18.0000	0.0025	0.0000	0.0051	*Fungi*	*Ascomycota*	*Eurotiomycetes*	*Chaetothyriales*	*Herpotrichiellaceae*	*Fonsecaea*
OTU179	20.0000	0.0000	0.0000	0.0000	0.0000	0.0000	20.0000	20.0000	0.0000	0.0028	0.0056	0.0000	*Fungi*	*Ascomycota*	*Leotiomycetes*	U	U	U
OTU18	334.0000	2595.0000	2762.0000	96.0000	89.0000	354.0000	6230.0000	5691.0000	539.0000	0.8762	1.6007	0.1516	*Fungi*	*Ascomycota*	*Sordariomycetes*	U	U	U
OTU180	0.0000	0.0000	19.0000	0.0000	0.0000	0.0000	19.0000	19.0000	0.0000	0.0027	0.0053	0.0000	*Fungi*	*Basidiomycota*	*Agaricomycetes*	*Trechisporales*	*Hydnodontaceae*	*Sistotremastrum*
OTU181	0.0000	1.0000	17.0000	0.0000	0.0000	2.0000	20.0000	18.0000	2.0000	0.0028	0.0051	0.0006	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Chaetosphaeriales*	U	U
OTU182	1.0000	0.0000	8.0000	0.0000	0.0000	22.0000	31.0000	9.0000	22.0000	0.0044	0.0025	0.0062	*Fungi*	*Fungi_OTU182*	U	U	U	U
OTU183	15.0000	0.0000	0.0000	0.0000	0.0000	0.0000	15.0000	15.0000	0.0000	0.0021	0.0042	0.0000	*Fungi*	*Basidiomycota*	*Agaricomycetes*	*Agaricales*	*Agaricaceae*	*Lacrymaria*
OTU184	0.0000	0.0000	0.0000	12.0000	0.0000	0.0000	12.0000	0.0000	12.0000	0.0017	0.0000	0.0034	*Fungi*	*Ascomycota*	U	U	U	U
OTU185	0.0000	203.0000	558.0000	165.0000	0.0000	266.0000	1192.0000	761.0000	431.0000	0.1676	0.2141	0.1212	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Hypocreales*	*Hypocreaceae*	*Trichoderma*
OTU186	0.0000	0.0000	37.0000	0.0000	0.0000	0.0000	37.0000	37.0000	0.0000	0.0052	0.0104	0.0000	*Fungi*	*Ascomycota*	*Leotiomycetes*	*Erysiphales*	*Erysiphaceae*	*Leveillula*
OTU187	0.0000	0.0000	13.0000	0.0000	0.0000	0.0000	13.0000	13.0000	0.0000	0.0018	0.0037	0.0000	*Fungi*	*Basidiomycota*	*Agaricomycetes*	*Agaricales*	*Pluteaceae*	*Pluteus*
OTU1	0.0000	25.0000	0.0000	0.0000	0.0000	0.0000	25.0000	25.0000	0.0000	0.003	0.007	0.000	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Hypocreales*	*Ophiocordycipitaceae*	*Ophiocordycep*

88										5	0	0						*s*
OTU189	0.0000	0.0000	11.0000	0.0000	0.0000	0.0000	11.0000	11.0000	0.0000	0.0015	0.0031	0.0000	*Fungi*	*Ascomycota*	U	U	U	U
OTU19	1.0000	0.0000	127.0000	0.0000	0.0000	3013.0000	3141.0000	128.0000	3013.0000	0.4417	0.0360	0.8475	*Fungi*	*Ascomycota*	U	U	U	U
OTU190	16.0000	0.0000	0.0000	0.0000	0.0000	1.0000	17.0000	16.0000	1.0000	0.0024	0.0045	0.0003	*Fungi*	*Ascomycota*	*Dothideomycetes*	*Pleosporales*	*Lindgomycetaceae*	*Hongkongmyces*
OTU191	0.0000	0.0000	0.0000	0.0000	0.0000	11.0000	11.0000	0.0000	11.0000	0.0015	0.0000	0.0031	*Fungi*	*Ascomycota*	*Dothideomycetes*	*Pleosporales*	*Biatriosporaceae*	*Biatriospora*
OTU192	0.0000	0.0000	15.0000	0.0000	0.0000	0.0000	15.0000	15.0000	0.0000	0.0021	0.0042	0.0000	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Hypocreales*	*Clavicipitaceae*	*Metapochonia*
OTU193	19.0000	18.0000	1.0000	0.0000	0.0000	0.0000	38.0000	38.0000	0.0000	0.0053	0.0107	0.0000	*Fungi*	*Ascomycota*	*Orbiliomycetes*	*Orbiliales*	U	U
OTU194	0.0000	0.0000	12.0000	0.0000	0.0000	0.0000	12.0000	12.0000	0.0000	0.0017	0.0034	0.0000	*Fungi*	*Ascomycota*	*Dothideomycetes*	U	U	U
OTU195	0.0000	22.0000	4.0000	0.0000	0.0000	2.0000	28.0000	26.0000	2.0000	0.0039	0.0073	0.0006	*Fungi*	*Fungi_OTU195*	U	U	U	U
OTU196	0.0000	16.0000	0.0000	0.0000	0.0000	0.0000	16.0000	16.0000	0.0000	0.0023	0.0045	0.0000	*Fungi*	*Fungi_OTU196*	U	U	U	U
OTU197	0.0000	0.0000	10.0000	0.0000	0.0000	0.0000	10.0000	10.0000	0.0000	0.0014	0.0028	0.0000	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Hypocreales*	*Nectriaceae*	*Xenoacremonium*
OTU198	41.0000	0.0000	245.0000	0.0000	0.0000	466.0000	752.0000	286.0000	466.0000	0.1058	0.0804	0.1311	*Fungi*	*Ascomycota*	*Eurotiomycetes*	*Chaetothyriales*	*Herpotrichiellaceae*	*Exophiala*
OTU199	6.0000	0.0000	7.0000	0.0000	8.0000	3.0000	24.0000	13.0000	11.0000	0.0034	0.0037	0.0031	*Fungi*	*Basidiomycota*	*Malasseziomycetes*	*Malasseziales*	*Malasseziaceae*	*Malassezia*
OTU2	25271.0000	43270.0000	23785.0000	37790.0000	29467.0000	19989.0000	179572.0000	92326.0000	87246.0000	25.2548	25.9691	24.5402	*Fungi*	*Ascomycota*	*Saccharomycetes*	*Saccharomycetales*	*Debaryomycetaceae*	*Spathaspora*
OTU20	478.0000	54.0000	518.0000	358.0000	1232.0000	1189.0000	3829.0000	1050.0000	2779.0000	0.5385	0.2953	0.7817	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Coniochaetales*	U	U
OTU200	8.0000	0.0000	1.0000	1.0000	0.0000	0.0000	10.0000	9.0000	1.0000	0.0014	0.0025	0.0003	*Fungi*	*Ascomycota*	*Sordariomycetes*	U	U	U
OTU201	4.0000	1.0000	16.0000	0.0000	0.0000	1.0000	22.0000	21.0000	1.0000	0.0031	0.0059	0.0003	*Fungi*	*Ascomycota*	*Dothideomycetes*	*Capnodiales*	*Mycosphaerellaceae*	*Davidiella*
OTU202	0.0000	11.0000	0.0000	0.0000	0.0000	0.0000	11.0000	11.0000	0.0000	0.0015	0.0031	0.0000	*Fungi*	*Fungi_OTU202*	U	U	U	U
OTU203	3.0000	2.0000	2.0000	1.0000	4.0000	2.0000	14.0000	7.0000	7.0000	0.0020	0.0020	0.0020	*Fungi*	*Ascomycota*	*Dothideomycetes*	*Capnodiales*	*Mycosphaerellaceae*	*Davidiella*
OTU204	0.0000	0.0000	11.0000	0.0000	0.0000	0.0000	11.0000	11.0000	0.0000	0.0015	0.0031	0.0000	*Fungi*	*Ascomycota*	*Eurotiomycetes*	*Chaetothyriales*	*Herpotrichiellaceae*	*Cladophialophora*
OTU2	0.0000	0.0000	0.0000	0.0000	8.0000	0.0000	8.0000	0.0000	8.0000	0.001	0.000	0.002	*Fungi*	*Ascomycota*	U	U	U	U

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OTU206	0.0000	0.0000	18.0000	0.0000	0.0000	0.0000	18.0000	18.0000	0.0000	0.0025	0.0051	0.0000	*Fungi*	*Ascomycota*	U	U	U	U
OTU207	0.0000	0.0000	12.0000	0.0000	0.0000	0.0000	12.0000	12.0000	0.0000	0.0017	0.0034	0.0000	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Hypocreales*	*Nectriaceae*	*Fusarium*
OTU208	0.0000	0.0000	12.0000	0.0000	0.0000	0.0000	12.0000	12.0000	0.0000	0.0017	0.0034	0.0000	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Microascales*	*Halosphaeriaceae*	*Aniptodera*
OTU209	0.0000	0.0000	15.0000	0.0000	0.0000	0.0000	15.0000	15.0000	0.0000	0.0021	0.0042	0.0000	*Fungi*	*Ascomycota*	*Eurotiomycetes*	*Chaetothyriales*	*Trichomeriaceae*	*Trichomerium*
OTU21	1183.0000	575.0000	524.0000	180.0000	574.0000	667.0000	3703.0000	2282.0000	1421.0000	0.5208	0.6419	0.3997	*Fungi*	*Ascomycota*	U	U	U	U
OTU210	1.0000	6.0000	0.0000	0.0000	0.0000	0.0000	7.0000	7.0000	0.0000	0.0010	0.0020	0.0000	*Fungi*	*Basidiomycota*	U	U	U	U
OTU211	0.0000	0.0000	17.0000	0.0000	0.0000	0.0000	17.0000	17.0000	0.0000	0.0024	0.0048	0.0000	*Fungi*	*Ascomycota*	*Sordariomycetes*	U	U	U
OTU212	0.0000	0.0000	13.0000	0.0000	0.0000	0.0000	13.0000	13.0000	0.0000	0.0018	0.0037	0.0000	*Fungi*	*Ascomycota*	U	U	U	U
OTU213	6.0000	0.0000	0.0000	0.0000	0.0000	0.0000	6.0000	6.0000	0.0000	0.0008	0.0017	0.0000	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Togniniales*	*Togniniaceae*	*Phaeoacremonium*
OTU214	0.0000	0.0000	13.0000	0.0000	0.0000	0.0000	13.0000	13.0000	0.0000	0.0018	0.0037	0.0000	*Fungi*	*Basidiomycota*	*Tremellomycetes*	*Tremellales*	*Bulleribasidiaceae*	*Dioszegia*
OTU215	0.0000	0.0000	11.0000	0.0000	1.0000	0.0000	12.0000	11.0000	1.0000	0.0017	0.0031	0.0003	*Fungi*	*Ascomycota*	*Eurotiomycetes*	*Chaetothyriales*	*Trichomeriaceae*	*Trichomerium*
OTU216	9.0000	0.0000	1.0000	2.0000	0.0000	1.0000	13.0000	10.0000	3.0000	0.0018	0.0028	0.0008	*Fungi*	*Ascomycota*	U	U	U	U
OTU217	5.0000	0.0000	0.0000	0.0000	0.0000	0.0000	5.0000	5.0000	0.0000	0.0007	0.0014	0.0000	*Fungi*	*Ascomycota*	U	U	U	U
OTU218	0.0000	0.0000	9.0000	0.0000	0.0000	0.0000	9.0000	9.0000	0.0000	0.0013	0.0025	0.0000	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Hypocreales*	*Clavicipitaceae*	U
OTU219	0.0000	0.0000	5.0000	0.0000	0.0000	0.0000	5.0000	5.0000	0.0000	0.0007	0.0014	0.0000	*Fungi*	*Ascomycota*	*Dothideomycetes*	*Pleosporales*	*Pleosporaceae*	*Alternaria*
OTU22	496.0000	252.0000	629.0000	382.0000	631.0000	563.0000	2953.0000	1377.0000	1576.0000	0.4153	0.3873	0.4433	*Fungi*	*Ascomycota*	*Leotiomycetes*	*Helotiales*	U	U
OTU220	2.0000	4.0000	5.0000	1.0000	3.0000	1.0000	16.0000	11.0000	5.0000	0.0023	0.0031	0.0014	*Fungi*	*Ascomycota*	*Dothideomycetes*	*Capnodiales*	*Mycosphaerellaceae*	*Davidiella*
OTU221	0.0000	0.0000	7.0000	0.0000	0.0000	0.0000	7.0000	7.0000	0.0000	0.0010	0.0020	0.0000	*Fungi*	*Fungi_OTU221*	U	U	U	U
OTU222	8.0000	0.0000	0.0000	0.0000	0.0000	0.0000	8.0000	8.0000	0.0000	0.0011	0.0023	0.0000	*Fungi*	*Basidiomycota*	U	U	U	U
OTU2	0.0000	0.0000	4.0000	0.0000	0.0000	0.0000	4.0000	4.0000	0.0000	0.000	0.001	0.000	*Fungi*	*Fungi_OTU2*	U	U	U	U

23										6	1	0		*23*				
OTU24	11.0000	0.0000	5.0000	0.0000	0.0000	0.0000	16.0000	16.0000	0.0000	0.0023	0.0045	0.0000	*Fungi*	*Ascomycota*	*Eurotiomycetes*	*Onygenales*	*Arthrodermataceae*	*Trichophyton*
OTU25	0.0000	11.0000	0.0000	0.0000	0.0000	0.0000	11.0000	11.0000	0.0000	0.0015	0.0031	0.0000	*Fungi*	*Ascomycota*	*Dothideomycetes*	*Hysteriales*	U	U
OTU26	0.0000	9.0000	0.0000	0.0000	0.0000	0.0000	9.0000	9.0000	0.0000	0.0013	0.0025	0.0000	*Fungi*	*Basidiomycota*	*Agaricomycetes*	*Agaricales*	*Schizophyllaceae*	*Schizophyllum*
OTU27	0.0000	0.0000	0.0000	1.0000	11.0000	3.0000	15.0000	0.0000	15.0000	0.0021	0.0000	0.0042	*Fungi*	*Fungi_OTU227*	U	U	U	U
OTU28	0.0000	0.0000	7.0000	0.0000	0.0000	0.0000	7.0000	7.0000	0.0000	0.0010	0.0020	0.0000	*Fungi*	*Ascomycota*	*Saccharomycetes*	*Saccharomycetales*	*Debaryomycetaceae*	*Candida*
OTU29	3.0000	0.0000	0.0000	0.0000	0.0000	2.0000	5.0000	3.0000	2.0000	0.0007	0.0008	0.0006	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Xylariales*	*Amphisphaeriaceae*	*Pestalotiopsis*
OTU23	1275.0000	265.0000	1122.0000	6.0000	123.0000	0.0000	2791.0000	2662.0000	129.0000	0.3925	0.7488	0.0363	*Fungi*	*Basidiomycota*	*Agaricomycetes*	*Polyporales*	*Hyphodermataceae*	*Hyphoderma*
OTU30	0.0000	0.0000	0.0000	0.0000	0.0000	2.0000	2.0000	0.0000	2.0000	0.0003	0.0000	0.0006	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Xylariales*	*Xylariaceae*	U
OTU31	3.0000	2.0000	3.0000	1.0000	2.0000	1.0000	12.0000	8.0000	4.0000	0.0017	0.0023	0.0011	*Fungi*	*Ascomycota*	*Dothideomycetes*	*Pleosporales*	*Lophiostomataceae*	*Massarina*
OTU32	0.0000	4.0000	0.0000	0.0000	0.0000	0.0000	4.0000	4.0000	0.0000	0.0006	0.0011	0.0000	*Fungi*	*Ascomycota*	U	U	U	U
OTU33	0.0000	0.0000	0.0000	0.0000	0.0000	4.0000	4.0000	0.0000	4.0000	0.0006	0.0000	0.0011	*Fungi*	*Basidiomycota*	*Malasseziomycetes*	U	U	U
OTU34	3.0000	0.0000	0.0000	0.0000	2.0000	0.0000	5.0000	3.0000	2.0000	0.0007	0.0008	0.0006	*Fungi*	*Ascomycota*	U	U	U	U
OTU35	2.0000	0.0000	0.0000	0.0000	0.0000	0.0000	2.0000	2.0000	0.0000	0.0003	0.0006	0.0000	*Fungi*	*Basidiomycota*	U	U	U	U
OTU36	0.0000	6.0000	3.0000	0.0000	0.0000	0.0000	9.0000	9.0000	0.0000	0.0013	0.0025	0.0000	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Hypocreales*	*Nectriaceae*	*Fusicolla*
OTU37	0.0000	0.0000	0.0000	0.0000	9.0000	1.0000	10.0000	0.0000	10.0000	0.0014	0.0000	0.0028	*Fungi*	*Fungi_OTU237*	U	U	U	U
OTU38	0.0000	0.0000	0.0000	0.0000	0.0000	4.0000	4.0000	0.0000	4.0000	0.0006	0.0000	0.0011	*Fungi*	*Fungi_OTU238*	U	U	U	U
OTU39	0.0000	0.0000	0.0000	0.0000	5.0000	0.0000	5.0000	0.0000	5.0000	0.0007	0.0000	0.0014	*Fungi*	*Fungi_OTU239*	U	U	U	U
OTU24	130.0000	68.0000	374.0000	167.0000	887.0000	871.0000	2497.0000	572.0000	1925.0000	0.3512	0.1609	0.5415	*Fungi*	*Ascomycota*	*Eurotiomycetes*	*Eurotiales*	*Aspergillaceae*	*Aspergillus*
OTU40	0.0000	0.0000	5.0000	0.0000	1.0000	0.0000	6.0000	5.0000	1.0000	0.0008	0.0014	0.0003	*Fungi*	*Fungi_OTU240*	U	U	U	U
OTU2	0.0000	0.0000	1.0000	0.0000	1.0000	0.0000	2.0000	1.0000	1.0000	0.000	0.000	0.000	*Fungi*	*Ascomycota*	*Dothideomycete*	*Capnodiales*	*Mycosphaerellaceae*	*Davidiella*

41										3	3	3			*s*			
OTU242	0.0000	0.0000	0.0000	0.0000	0.0000	6.0000	6.0000	0.0000	6.0000	0.0008	0.0000	0.0017	*Fungi*	*Ascomycota*	U	U	U	U
OTU243	0.0000	3.0000	0.0000	0.0000	1.0000	0.0000	4.0000	3.0000	1.0000	0.0006	0.0008	0.0003	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Glomerellales*	*Glomerellaceae*	*Colletotrichum*
OTU244	0.0000	0.0000	1.0000	0.0000	1.0000	0.0000	2.0000	1.0000	1.0000	0.0003	0.0003	0.0003	*Fungi*	*Ascomycota*	U	U	U	U
OTU245	0.0000	5.0000	0.0000	0.0000	0.0000	0.0000	5.0000	5.0000	0.0000	0.0007	0.0014	0.0000	*Fungi*	*Basidiomycota*	*Agaricomycetes*	*Agaricales*	*Psathyrellaceae*	*Coprinellus*
OTU246	0.0000	1.0000	1.0000	0.0000	0.0000	2.0000	4.0000	2.0000	2.0000	0.0006	0.0006	0.0006	*Fungi*	*Ascomycota*	*Sordariomycetes*	U	U	U
OTU247	0.0000	0.0000	4.0000	0.0000	0.0000	0.0000	4.0000	4.0000	0.0000	0.0006	0.0011	0.0000	*Fungi*	*Basidiomycota*	U	U	U	U
OTU248	634.0000	351.0000	612.0000	516.0000	357.0000	709.0000	3179.0000	1597.0000	1582.0000	0.4471	0.4492	0.4450	*Fungi*	*Ascomycota*	*Saccharomycetes*	*Saccharomycetales*	*Debaryomycetaceae*	*Scheffersomyces*
OTU249	1.0000	1.0000	1.0000	0.0000	0.0000	2.0000	5.0000	3.0000	2.0000	0.0007	0.0008	0.0006	*Fungi*	*Ascomycota*	*Dothideomycetes*	*Capnodiales*	*Mycosphaerellaceae*	*Davidiella*
OTU25	305.0000	487.0000	153.0000	54.0000	1021.0000	155.0000	2175.0000	945.0000	1230.0000	0.3059	0.2658	0.3460	*Fungi*	*Ascomycota*	*Eurotiomycetes*	*Eurotiales*	*Aspergillaceae*	*Aspergillus*
OTU250	3.0000	2.0000	0.0000	2.0000	0.0000	1.0000	8.0000	5.0000	3.0000	0.0011	0.0014	0.0008	*Fungi*	*Ascomycota*	U	U	U	U
OTU251	0.0000	0.0000	3.0000	0.0000	0.0000	0.0000	3.0000	3.0000	0.0000	0.0004	0.0008	0.0000	*Fungi*	*Ascomycota*	*Eurotiomycetes*	*Chaetothyriales*	*Herpotrichiellaceae*	*Minimelanolocus*
OTU252	0.0000	0.0000	3.0000	0.0000	0.0000	0.0000	3.0000	3.0000	0.0000	0.0004	0.0008	0.0000	*Fungi*	*Fungi_OTU252*	U	U	U	U
OTU253	0.0000	0.0000	0.0000	0.0000	5.0000	0.0000	5.0000	0.0000	5.0000	0.0007	0.0000	0.0014	*Fungi*	*Basidiomycota*	U	U	U	U
OTU254	0.0000	0.0000	0.0000	23.0000	0.0000	48.0000	71.0000	0.0000	71.0000	0.0100	0.0000	0.0200	*Fungi*	*Basidiomycota*	U	U	U	U
OTU255	0.0000	0.0000	0.0000	1.0000	1.0000	1.0000	3.0000	0.0000	3.0000	0.0004	0.0000	0.0008	*Fungi*	*Fungi_OTU255*	U	U	U	U
OTU256	0.0000	0.0000	7.0000	0.0000	0.0000	0.0000	7.0000	7.0000	0.0000	0.0010	0.0020	0.0000	*Fungi*	*Ascomycota*	*Lecanoromycetes*	U	U	U
OTU257	0.0000	0.0000	3.0000	0.0000	0.0000	0.0000	3.0000	3.0000	0.0000	0.0004	0.0008	0.0000	*Fungi*	*Ascomycota*	U	U	U	U
OTU259	4.0000	0.0000	0.0000	0.0000	1.0000	0.0000	5.0000	4.0000	1.0000	0.0007	0.0011	0.0003	*Fungi*	*Ascomycota*	U	U	U	U
OTU26	1416.0000	0.0000	278.0000	147.0000	140.0000	77.0000	2058.0000	1694.0000	364.0000	0.2894	0.4765	0.1024	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Xylariales*	*Hypoxylaceae*	*Hypoxylon*
OTU2	0.0000	0.0000	3.0000	0.0000	1.0000	1.0000	5.0000	3.0000	2.0000	0.000	0.000	0.000	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Diaporthales*	*Diaporthaceae*	*Diaporthe*

60										7	8	6						
OTU261	0.0000	0.0000	0.0000	2.0000	0.0000	0.0000	2.0000	0.0000	2.0000	0.0003	0.0000	0.0006	*Fungi*	*Fungi_OTU261*	U	U	U	U
OTU262	1.0000	0.0000	1.0000	0.0000	0.0000	0.0000	2.0000	2.0000	0.0000	0.0003	0.0006	0.0000	*Fungi*	*Ascomycota*	U	U	U	U
OTU263	0.0000	0.0000	0.0000	0.0000	1.0000	2.0000	3.0000	0.0000	3.0000	0.0004	0.0000	0.0008	*Fungi*	*Ascomycota*	U	U	U	U
OTU264	57.0000	182.0000	26.0000	0.0000	164.0000	0.0000	429.0000	265.0000	164.0000	0.0603	0.0745	0.0461	*Fungi*	*Basidiomycota*	*Agaricomycetes*	*Russulales*	*Russulaceae*	*Russula*
OTU265	0.0000	0.0000	3.0000	0.0000	0.0000	2.0000	5.0000	3.0000	2.0000	0.0007	0.0008	0.0006	*Fungi*	*Ascomycota*	U	U	U	U
OTU266	1.0000	2.0000	1.0000	1.0000	0.0000	0.0000	5.0000	4.0000	1.0000	0.0007	0.0011	0.0003	*Fungi*	*Basidiomycota*	U	U	U	U
OTU267	4.0000	0.0000	20.0000	2.0000	51.0000	67.0000	144.0000	24.0000	120.0000	0.0203	0.0068	0.0338	*Fungi*	*Ascomycota*	U	U	U	U
OTU268	0.0000	0.0000	0.0000	0.0000	0.0000	3.0000	3.0000	0.0000	3.0000	0.0004	0.0000	0.0008	*Fungi*	*Ascomycota*	U	U	U	U
OTU27	377.0000	283.0000	1385.0000	8.0000	205.0000	474.0000	2732.0000	2045.0000	687.0000	0.3842	0.5752	0.1932	*Fungi*	*Ascomycota*	*Sordariomycetes*	U	U	U
OTU28	0.0000	2156.0000	0.0000	0.0000	0.0000	0.0000	2156.0000	2156.0000	0.0000	0.3032	0.6064	0.0000	*Fungi*	*Basidiomycota*	U	U	U	U
OTU29	0.0000	1617.0000	0.0000	0.0000	0.0000	0.0000	1617.0000	1617.0000	0.0000	0.2274	0.4548	0.0000	*Fungi*	*Ascomycota*	U	U	U	U
OTU3	9532.0000	1892.0000	6746.0000	5576.0000	4443.0000	10660.0000	38849.0000	18170.0000	20679.0000	5.4637	5.1108	5.8165	*Fungi*	*Ascomycota*	*Saccharomycetes*	*Saccharomycetales*	*Debaryomycetaceae*	*Scheffersomyces*
OTU30	0.0000	1515.0000	0.0000	0.0000	0.0000	0.0000	1515.0000	1515.0000	0.0000	0.2131	0.4261	0.0000	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Microascales*	*Halosphaeriaceae*	*Nais*
OTU31	47.0000	880.0000	35.0000	23.0000	301.0000	81.0000	1367.0000	962.0000	405.0000	0.1923	0.2706	0.1139	*Fungi*	*Ascomycota*	*Sordariomycetes*	U	U	U
OTU32	1094.0000	46.0000	81.0000	0.0000	142.0000	1.0000	1364.0000	1221.0000	143.0000	0.1918	0.3434	0.0402	*Fungi*	*Basidiomycota*	*Agaricomycetes*	*Hymenochaetales*	*Rickenellaceae*	*Sidera*
OTU33	32.0000	827.0000	95.0000	121.0000	290.0000	39.0000	1404.0000	954.0000	450.0000	0.1975	0.2683	0.1266	*Fungi*	*Ascomycota*	*Eurotiomycetes*	*Eurotiales*	*Aspergillaceae*	*Aspergillus*
OTU34	226.0000	281.0000	81.0000	50.0000	263.0000	475.0000	1376.0000	588.0000	788.0000	0.1935	0.1654	0.2216	*Fungi*	*Ascomycota*	*Leotiomycetes*	*Erysiphales*	*Erysiphaceae*	*Leveillula*
OTU35	151.0000	64.0000	294.0000	0.0000	80.0000	503.0000	1092.0000	509.0000	583.0000	0.1536	0.1432	0.1640	*Fungi*	*Ascomycota*	*Eurotiomycetes*	*Chaetothyriales*	*Herpotrichiellaceae*	*Exophiala*
OTU36	141.0000	214.0000	492.0000	30.0000	266.0000	36.0000	1179.0000	847.0000	332.0000	0.1658	0.2382	0.0934	*Fungi*	*Ascomycota*	U	U	U	U
OTU3	24.0000	0.0000	188.0000	63.0000	885.000	639.0000	1799.000	212.000	1587.000	0.253	0.059	0.446	*Fungi*	*Ascomycota*	U	U	U	U

7					0		0	0	0	0	6	4						
OTU38	87.0000	341.0000	73.0000	42.0000	1340.0000	226.0000	2109.0000	501.0000	1608.0000	0.2966	0.1409	0.4523	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Microascales*	*Microascaceae*	*Microascus*
OTU39	739.0000	52.0000	109.0000	33.0000	59.0000	66.0000	1058.0000	900.0000	158.0000	0.1488	0.2531	0.0444	*Fungi*	*Ascomycota*	*Leotiomycetes*	*Erysiphales*	U	U
OTU4	4505.0000	1475.0000	8238.0000	3956.0000	12395.0000	15781.0000	46350.0000	14218.0000	32132.0000	6.5186	3.9992	9.0380	*Fungi*	*Basidiomycota*	*Tremellomycetes*	*Trichosporonales*	*Trichosporonaceae*	*Apiotrichum*
OTU40	25.0000	177.0000	348.0000	18.0000	0.0000	402.0000	970.0000	550.0000	420.0000	0.1364	0.1547	0.1181	*Fungi*	*Ascomycota*	*Eurotiomycetes*	*Chaetothyriales*	*Herpotrichiellaceae*	*Fonsecaea*
OTU41	176.0000	138.0000	125.0000	247.0000	40.0000	144.0000	870.0000	439.0000	431.0000	0.1224	0.1235	0.1212	*Fungi*	*Ascomycota*	*Sordariomycetes*	U	U	U
OTU42	141.0000	69.0000	696.0000	0.0000	139.0000	0.0000	1045.0000	906.0000	139.0000	0.1470	0.2548	0.0391	*Fungi*	*Ascomycota*	*Leotiomycetes*	*Helotiales*	U	U
OTU43	34.0000	466.0000	64.0000	20.0000	141.0000	104.0000	829.0000	564.0000	265.0000	0.1166	0.1586	0.0745	*Fungi*	*Fungi_OTU43*	U	U	U	U
OTU44	0.0000	0.0000	571.0000	0.0000	207.0000	12.0000	790.0000	571.0000	219.0000	0.1111	0.1606	0.0616	*Fungi*	*Ascomycota*	U	U	U	U
OTU45	325.0000	0.0000	413.0000	78.0000	0.0000	0.0000	816.0000	738.0000	78.0000	0.1148	0.2076	0.0219	*Fungi*	*Ascomycota*	*Leotiomycetes*	U	U	U
OTU46	45.0000	37.0000	62.0000	55.0000	247.0000	171.0000	617.0000	144.0000	473.0000	0.0868	0.0405	0.1330	*Fungi*	*Basidiomycota*	U	U	U	U
OTU47	250.0000	0.0000	38.0000	3.0000	214.0000	88.0000	593.0000	288.0000	305.0000	0.0834	0.0810	0.0858	*Fungi*	*Mortierellomycota*	*Mortierellomycetes*	*Mortierellales*	U	U
OTU48	0.0000	305.0000	42.0000	84.0000	0.0000	341.0000	772.0000	347.0000	425.0000	0.1086	0.0976	0.1195	*Fungi*	*Mucoromycota*	*Umbelopsidomycetes*	*Umbelopsidales*	*Umbelopsidaceae*	*Umbelopsis*
OTU49	0.0000	221.0000	0.0000	67.0000	244.0000	0.0000	532.0000	221.0000	311.0000	0.0748	0.0622	0.0875	*Fungi*	*Ascomycota*	*Eurotiomycetes*	*Eurotiales*	*Aspergillaceae*	*Aspergillus*
OTU5	1391.0000	5049.0000	3102.0000	1573.0000	3074.0000	4065.0000	18254.0000	9542.0000	8712.0000	2.5672	2.6839	2.4505	*Fungi*	*Ascomycota*	*Leotiomycetes*	*Erysiphales*	*Erysiphaceae*	*Leveillula*
OTU50	51.0000	0.0000	18.0000	0.0000	323.0000	79.0000	471.0000	69.0000	402.0000	0.0662	0.0194	0.1131	*Fungi*	*Basidiomycota*	U	U	U	U
OTU51	114.0000	158.0000	72.0000	0.0000	0.0000	134.0000	478.0000	344.0000	134.0000	0.0672	0.0968	0.0377	*Fungi*	*Ascomycota*	*Eurotiomycetes*	*Chaetothyriales*	*Herpotrichiellaceae*	*Phialophora*
OTU52	44.0000	266.0000	37.0000	8.0000	0.0000	60.0000	415.0000	347.0000	68.0000	0.0584	0.0976	0.0191	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Chaetosphaeriales*	*Chaetosphaeriaceae*	*Tainosphaeria*
OTU53	14.0000	183.0000	41.0000	17.0000	31.0000	104.0000	390.0000	238.0000	152.0000	0.0548	0.0669	0.0428	*Fungi*	*Ascomycota*	*Eurotiomycetes*	*Eurotiales*	*Aspergillaceae*	*Penicillium*
OTU54	33.0000	87.0000	20.0000	0.0000	238.0000	28.0000	406.0000	140.0000	266.0000	0.0571	0.0394	0.0748	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Xylariales*	*Xylariaceae*	*Biscogniauxia*
OTU5	3.0000	0.0000	59.0000	96.0000	39.0000	127.0000	324.0000	62.0000	262.0000	0.045	0.017	0.073	*Fungi*	*Ascomycota*	U	U	U	U

5										6	4	7						
OTU56	71.0000	41.0000	3.0000	24.0000	137.0000	63.0000	339.0000	115.0000	224.0000	0.0477	0.0323	0.0630	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Hypocreales*	*Sarocladiaceae*	*Sarocladium*
OTU57	84.0000	0.0000	124.0000	16.0000	16.0000	46.0000	286.0000	208.0000	78.0000	0.0402	0.0585	0.0219	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Togniniales*	*Togniniaceae*	U
OTU58	0.0000	0.0000	0.0000	0.0000	272.0000	0.0000	272.0000	0.0000	272.0000	0.0383	0.0000	0.0765	*Fungi*	*Ascomycota*	U	U	U	U
OTU59	0.0000	0.0000	19.0000	40.0000	160.0000	34.0000	253.0000	19.0000	234.0000	0.0356	0.0053	0.0658	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Chaetosphaeriales*	*Chaetosphaeriaceae*	*Chloridium*
OTU6	4975.0000	5451.0000	7389.0000	1036.0000	1055.0000	6219.0000	26125.0000	17815.0000	8310.0000	3.6742	5.0109	2.3374	*Fungi*	*Ascomycota*	U	U	U	U
OTU60	50.0000	219.0000	72.0000	0.0000	0.0000	67.0000	408.0000	341.0000	67.0000	0.0574	0.0999	0.0188	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Sordariales*	*Chaetomiaceae*	*Chaetomium*
OTU61	0.0000	280.0000	3.0000	0.0000	0.0000	10.0000	293.0000	283.0000	10.0000	0.0412	0.0796	0.0028	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Glomerellales*	U	U
OTU62	147.0000	0.0000	25.0000	0.0000	0.0000	24.0000	196.0000	172.0000	24.0000	0.0276	0.0484	0.0068	*Fungi*	*Ascomycota*	*Sordariomycetes*	U	U	U
OTU63	0.0000	121.0000	37.0000	0.0000	54.0000	42.0000	254.0000	158.0000	96.0000	0.0357	0.0444	0.0270	*Fungi*	*Ascomycota*	*Eurotiomycetes*	*Chaetothyriales*	*Herpotrichiellaceae*	*Exophiala*
OTU64	78.0000	57.0000	63.0000	36.0000	0.0000	0.0000	234.0000	198.0000	36.0000	0.0329	0.0557	0.0101	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Trichosphaeriales*	U	U
OTU65	209.0000	0.0000	0.0000	0.0000	0.0000	0.0000	209.0000	209.0000	0.0000	0.0294	0.0588	0.0000	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Hypocreales*	*Cordycipitaceae*	*Simplicillium*
OTU66	22.0000	0.0000	21.0000	97.0000	61.0000	0.0000	201.0000	43.0000	158.0000	0.0283	0.0121	0.0444	*Fungi*	*Basidiomycota*	*Agaricomycetes*	*Russulales*	*Lachnocladiaceae*	*Asterostroma*
OTU67	2.0000	105.0000	36.0000	3.0000	50.0000	14.0000	210.0000	143.0000	67.0000	0.0295	0.0402	0.0188	*Fungi*	*Basidiomycota*	*Agaricomycetes*	*Cantharellales*	*Botryobasidiaceae*	*Botryobasidium*
OTU68	39.0000	0.0000	30.0000	0.0000	0.0000	130.0000	199.0000	69.0000	130.0000	0.0280	0.0194	0.0366	*Fungi*	*Basidiomycota*	*Agaricomycetes*	U	U	U
OTU69	193.0000	2.0000	41.0000	0.0000	0.0000	7.0000	243.0000	236.0000	7.0000	0.0342	0.0664	0.0020	*Fungi*	*Ascomycota*	*Eurotiomycetes*	*Sclerococcales*	*Dactylosporaceae*	*Fusichalara*
OTU7	3105.0000	4089.0000	10057.0000	1098.0000	524.0000	4182.0000	23055.0000	17251.0000	5804.0000	3.2424	4.8523	1.6325	*Fungi*	*Basidiomycota*	*Agaricomycetes*	*Corticiales*	*Corticiaceae*	*Subulicystidium*
OTU70	107.0000	0.0000	119.0000	33.0000	18.0000	58.0000	335.0000	226.0000	109.0000	0.0471	0.0636	0.0307	*Fungi*	*Ascomycota*	*Dothideomycetes*	*Pleosporales*	*Lophiostomataceae*	*Massarina*
OTU71	88.0000	86.0000	52.0000	0.0000	0.0000	0.0000	226.0000	226.0000	0.0000	0.0318	0.0636	0.0000	*Fungi*	*Ascomycota*	*Orbiliomycetes*	*Orbiliales*	*Orbiliaceae*	*Hyalorbilia*
OTU72	0.0000	208.0000	0.0000	0.0000	0.0000	0.0000	208.0000	208.0000	0.0000	0.0293	0.0585	0.0000	*Fungi*	*Basidiomycota*	*Agaricomycetes*	*Geastrales*	*Geastraceae*	*Geastrum*
OTU7	0.0000	59.0000	142.0000	0.0000	6.0000	101.0000	308.0000	201.000	107.0000	0.043	0.056	0.030	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Hypocreales*	*Nectriaceae*	*Fusarium*

3								0		3	5	1					
OTU74	0.0000	0.0000	0.0000	29.0000	0.0000	258.0000	287.0000	0.0000	287.0000	0.0404	0.0000	0.0807	*Fungi*	*Basidiomycota*	*Agaricomycetes*	U	U	U
OTU75	0.0000	0.0000	0.0000	0.0000	133.0000	0.0000	133.0000	0.0000	133.0000	0.0187	0.0000	0.0374	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Ophiostomatales*	*Ophiostomataceae*	*Phialocephala*
OTU76	39.0000	124.0000	10.0000	5.0000	0.0000	12.0000	190.0000	173.0000	17.0000	0.0267	0.0487	0.0048	*Fungi*	*Ascomycota*	*Saccharomycetes*	*Saccharomycetales*	*Debaryomycetaceae*	*Meyerozyma*
OTU77	0.0000	0.0000	0.0000	0.0000	58.0000	54.0000	112.0000	0.0000	112.0000	0.0158	0.0000	0.0315	*Fungi*	*Ascomycota*	*Eurotiomycetes*	*Eurotiales*	*Aspergillaceae*	*Aspergillus*
OTU78	113.0000	1.0000	1.0000	0.0000	0.0000	0.0000	115.0000	115.0000	0.0000	0.0162	0.0323	0.0000	*Fungi*	*Ascomycota*	*Sordariomycetes*	U	U	U
OTU79	0.0000	162.0000	0.0000	0.0000	0.0000	0.0000	162.0000	162.0000	0.0000	0.0228	0.0456	0.0000	*Fungi*	*Ascomycota*	*Leotiomycetes*	*Erysiphales*	*Erysiphaceae*	U
OTU8	5584.0000	1.0000	5701.0000	325.0000	459.0000	829.0000	12899.0000	11286.0000	1613.0000	1.8141	3.1745	0.4537	*Fungi*	*Ascomycota*	*Sordariomycetes*	U	U	U
OTU80	0.0000	0.0000	0.0000	0.0000	107.0000	0.0000	107.0000	0.0000	107.0000	0.0150	0.0000	0.0301	*Fungi*	*Ascomycota*	U	U	U	U
OTU81	0.0000	162.0000	0.0000	0.0000	0.0000	3.0000	165.0000	162.0000	3.0000	0.0232	0.0456	0.0008	*Fungi*	*Ascomycota*	U	U	U	U
OTU82	0.0000	132.0000	0.0000	0.0000	0.0000	0.0000	132.0000	132.0000	0.0000	0.0186	0.0371	0.0000	*Fungi*	*Ascomycota*	*Dothideomycetes*	*Capnodiales*	*Mycosphaerellaceae*	*Davidiella*
OTU83	0.0000	146.0000	0.0000	0.0000	0.0000	0.0000	146.0000	146.0000	0.0000	0.0205	0.0411	0.0000	*Fungi*	*Ascomycota*	U	U	U	U
OTU84	0.0000	0.0000	14.0000	0.0000	0.0000	124.0000	138.0000	14.0000	124.0000	0.0194	0.0039	0.0349	*Fungi*	*Ascomycota*	*Dothideomycetes*	*Tubeufiales*	*Tubeufiaceae*	*Helicoarctatus*
OTU85	0.0000	9.0000	0.0000	0.0000	129.0000	0.0000	138.0000	9.0000	129.0000	0.0194	0.0025	0.0363	*Fungi*	*Ascomycota*	*Dothideomycetes*	*Pleosporales*	*Pleosporaceae*	*Alternaria*
OTU86	0.0000	34.0000	166.0000	0.0000	0.0000	19.0000	219.0000	200.0000	19.0000	0.0308	0.0563	0.0053	*Fungi*	*Ascomycota*	*Dothideomycetes*	*Pleosporales*	*Pleosporaceae*	
OTU87	0.0000	0.0000	28.0000	0.0000	0.0000	98.0000	126.0000	28.0000	98.0000	0.0177	0.0079	0.0276	*Fungi*	*Ascomycota*	*Orbiliomycetes*	*Orbiliales*	*Orbiliaceae*	*Drechslerella*
OTU88	0.0000	127.0000	0.0000	0.0000	0.0000	0.0000	127.0000	127.0000	0.0000	0.0179	0.0357	0.0000	*Fungi*	*Ascomycota*	*Sordariomycetes*	U	U	U
OTU89	0.0000	0.0000	0.0000	0.0000	0.0000	87.0000	87.0000	0.0000	87.0000	0.0122	0.0000	0.0245	*Fungi*	*Basidiomycota*	*Microbotryomycetes*	U	U	U
OTU9	104.0000	109.0000	9120.0000	324.0000	317.0000	1242.0000	11216.0000	9333.0000	1883.0000	1.5774	2.6251	0.5296	*Fungi*	*Ascomycota*	U	U	U	U
OTU90	36.0000	71.0000	4.0000	1.0000	13.0000	10.0000	135.0000	111.0000	24.0000	0.0190	0.0312	0.0068	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Xylariales*	*Amphisphaeriaceae*	*Pestalotiopsis*
OTU9	0.0000	1.0000	4.0000	1.0000	56.0000	22.0000	84.0000	5.0000	79.0000	0.011	0.001	0.022	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Trichosphaeria*	U	U

1										8	4	2				*les*		
OTU92	0.0000	0.0000	0.0000	1.0000	106.0000	0.0000	107.0000	0.0000	107.0000	0.0150	0.0000	0.0301	*Fungi*	*Ascomycota*	U	U	U	U
OTU93	98.0000	0.0000	0.0000	0.0000	0.0000	0.0000	98.0000	98.0000	0.0000	0.0138	0.0276	0.0000	*Fungi*	*Ascomycota*	*Sordariomycetes*	U	U	U
OTU94	0.0000	50.0000	0.0000	0.0000	0.0000	57.0000	107.0000	50.0000	57.0000	0.0150	0.0141	0.0160	*Fungi*	*Ascomycota*	*Dothideomycetes*	*Pleosporales*	*Lophiostomataceae*	*Massarina*
OTU95	0.0000	0.0000	0.0000	0.0000	121.0000	0.0000	121.0000	0.0000	121.0000	0.0170	0.0000	0.0340	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Hypocreales*	*Cordycipitaceae*	*Simplicillium*
OTU96	39.0000	38.0000	9.0000	36.0000	25.0000	10.0000	157.0000	86.0000	71.0000	0.0221	0.0242	0.0200	*Fungi*	*Ascomycota*	U	U	U	U
OTU97	0.0000	0.0000	0.0000	0.0000	0.0000	80.0000	80.0000	0.0000	80.0000	0.0113	0.0000	0.0225	*Fungi*	*Ascomycota*	*Sordariomycetes*	U	U	U
OTU98	93.0000	0.0000	23.0000	0.0000	0.0000	10.0000	126.0000	116.0000	10.0000	0.0177	0.0326	0.0028	*Fungi*	*Ascomycota*	*Sordariomycetes*	*Hypocreales*	*Nectriaceae*	*Calonectria*
OTU99	0.0000	62.0000	14.0000	0.0000	0.0000	30.0000	106.0000	76.0000	30.0000	0.0149	0.0214	0.0084	*Fungi*	*Ascomycota*	*Saccharomycetes*	*Saccharomycetales*	*Saccharomycetaceae*	*Saccharomyces*

P6A to P8A: midgut samples. P6R to P8R: hindgut samples. U: Unidentified taxon.

Tabela S6. Metabolic pathways identified by KO descriptors of *Pelidnota luridipes* gut microbiome

Pathway	Total	Expected	Hits	*p*-value	FDR
Biosynthesis of amino acids	223	0	55	0	0
Porphyrin and chlorophyll metabolism	76	0	22	0	0
2-Oxocarboxylic acid metabolism	67	0	17	0	0
Lipopolysaccharide biosynthesis	17	998	8	0	0
Valine, leucine and isoleucine biosynthesis	15	881	7	0	0
Histidine metabolism	38	0	10	0	0
Phenylalanine, tyrosine and tryptophan biosynthesis	70	0	13	0	0
Thiamine metabolism	23	0	7	0	0
Pantothenate and CoA biosynthesis	29	0	7	0	0
Cysteine and methionine metabolism	78	0	12	0	0
Glycine, serine and threonine metabolism	91	0	13	0	0
Arginine and proline metabolism	126	0	16	0	0
C5-Branched dibasic acid metabolism	21	0	5	0	0
Amino sugar and nucleotide sugar metabolism	126	0	14	0	163
Lysine biosynthesis	46	0	7	0	172
One carbon pool by folate	27	0	5	0	177
D-Arginine and D-ornithine metabolism	4	235	2	19	177
Carbon metabolism	299	0	26	0	213
Folate biosynthesis	31	0	5	0	269

Tabela S7. KEGG pathway map predicted by PICRUST differentially represented in bacterial communities found in midgut and hindgut of *Pelidnota luridipes*. (discriminant KEGG terms according to KO Database - https://www.genome.jp/kegg/ko.html)

KO	log2FC	logCPM	Pvalues	FDR	Definition
K14061	-8.4226	4.6977	2.44E-05	0.00047902	universal stress protein F
K11016	-7.7864	2.0579	5.88E-05	0.00095911	hemolysin
K11017	-7.7864	2.0579	5.91E-05	0.00095911	hemolysin activation/secretion protein
K05811	-7.7542	3.3579	0.00030677	0.0032099	putative lipoprotein
K05877	-7.7519	3.3548	0.00036905	0.0037191	methyl-accepting chemotaxis protein IV
K08308	-7.7501	3353	0.00037038	0.0037256	membrane-bound lytic murein transglycosylase
K13041	-7.5939	3.1985	0.00040285	0.0039292	two-component system, LuxR family, response regulator TtrR
K07351	-7.5931	3.1975	0.00042177	0.0040492	fimbrial protein
K07348	-7.5931	3.1975	0.00042182	0.0040492	minor fimbrial subunit
K01460	-7.5911	3.1956	0.00042482	0.0040575	glutathionylspermidine amidase/synthetase
K08163	-7.5911	3.1956	0.00042565	0.0040575	MFS transporter, DHA1 family, multidrug resistance protein
K07350	-7.5911	3.1956	0.00042565	0.0040575	minor fimbrial subunit
K08154	-7452	3.3644	0.00049263	0.0043399	MFS transporter, DHA1 family, 2-module integral membrane pump EmrD
K00892	-7.4499	3.3619	0.00052979	0.0044246	inosine kinase
K14588	-7.4498	3.3619	0.00052767	0.0044154	blue copper oxidase
K17899	5.3445	1.2415	0.00014271	0.0018066	D-ornithine 4,5-aminomutase subunit alpha
K09944	5579	1.5899	0.00024022	0.0027165	uncharacterized protein
K07097	5579	1.5899	0.00024101	0.0027198	uncharacterized protein
K18284	5.6826	1.1945	0.00080103	0.0053033	adenosylhomocysteine/aminodeoxyfutalosine nucleosidase
K18992	6.9599	1.1767	0.00011061	0.0014828	TetR/AcrR family transcriptional regulator, cmeABC operon repressor
K05927	6.9599	1.1767	0.00011073	0.0014828	quinone-reactive Ni/Fe-hydrogenase small subunit
K17251	6.9599	1.1767	0.00011083	0.0014828	protein glycotransferase
K05922	6.9599	1.1767	0.00011092	0.0014828	quinone-reactive Ni/Fe-hydrogenase large subunit
K08077	6.9599	1.1767	0.00011106	0.0014828	UDP-sugar diphosphatase
K15896	6.9599	1.1767	0.00011116	0.0014828	UDP-4-amino-4,6-dideoxy-N-acetyl-beta-L-altrosamine N-acetyltransferase
K15899	6.9599	1.1767	0.00011116	0.0014828	pseudaminic acid cytidylyltransferase
K07288	6.9599	1.1767	0.00011126	0.0014828	uncharacterized membrane protein
K15897	6.9599	1.1767	0.0001113	0.0014828	UDP-2,4-diacetamido-2,4,6-trideoxy-beta-L-altropyranose hydrolase
K06882	6.9599	1.1767	0.0001113	0.0014828	uncharacterized protein
K15895	6.9599	1.1767	0.00011131	0.0014828	UDP-4-amino-4,6-dideoxy-L-N-acetyl-beta-L-altrosamine transaminase

Table S8. Proportion (%) of isolates presenting funtional traits according to gut source

Funtional trait	Midgut	Hingut	Total
Amilase	34.3	23.7	31.2
Cellulase	17.9	11.9	15.9
Esterase	32.8	32.2	32.9
Ligninase	4.5	1.7	2.4
Pectinase	31.3	35.6	33.5
Protease	41.8	32.2	40
Bile Salts	52.2	54.2	58.2
PO_4 solubilization	44.8	50.8	48.8
Growth on pH2	6	3.4	3.5
Growth on pH4	14.9	11.9	12.9
Growth on pH7	94	96.6	94.7
Growth on pH8	95.5	96.6	94.7
Pathogen Inhibition	49.3	37.3	44.7

Tabela S9. Comparison of predicted KO identifiers using PICRUSt between midgut and hindgut of *Pelidnota luridipes*. Negative and positive log2FC values indicate higher abundance in the mid and hindgut, respectively

KO	log2FC	logCPM	*p*-values	FDR
K14061	-8.4226	4.6977	2.4381e-05	0.00047902
K11016	-7.7864	2.0579	5.8764e-05	0.00095911
K11017	-7.7864	2.0579	5.9129e-05	0.00095911
K05811	-7.7542	3.3579	0.00030677	0.0032099
K05877	-7.7519	3.3548	0.00036905	0.0037191
K08308	-7.7501	3353	0.00037038	0.0037256
K13041	-7.5939	3.1985	0.00040285	0.0039292
K07351	-7.5931	3.1975	0.00042177	0.0040492
K07348	-7.5931	3.1975	0.00042182	0.0040492
K01460	-7.5911	3.1956	0.00042482	0.0040575
K08163	-7.5911	3.1956	0.00042565	0.0040575
K07350	-7.5911	3.1956	0.00042565	0.0040575
K08154	-7452	3.3644	0.00049263	0.0043399
K00892	-7.4499	3.3619	0.00052979	0.0044246
K14588	-7.4498	3.3619	0.00052767	0.0044154
K11021	-7.4493	2122	4.4184e-05	0.00077849
K03788	-7.2917	3.2055	0.00060524	0.0046363
K11929	-7272	2.8806	0.00050525	0.0043862
K13631	-7.2696	2.8781	0.00050935	0.0043881
K05952	-7.2483	2.0792	0.00019115	0.0022746
K03812	-7.1625	3.2162	0.00031371	0.00327
K05984	-7.0523	2.6651	0.0004716	0.0042699
K08723	-7049	2.6614	0.00051596	0.0043986
K06141	-7.0455	2.6572	0.00061402	0.0046363
K07781	-7.0427	2.6544	0.00061428	0.0046363
K03468	-7.0427	2.6544	0.00061429	0.0046363
K12147	-7.0427	2.6544	0.00061446	0.0046363
K16703	-7.0427	2.6544	0.00061513	0.0046363
K16710	-7.0427	2.6544	0.0006168	0.0046363
K02467	-7.0426	2.6544	0.00061167	0.0046363
K07701	-7.0426	2.6544	0.00061271	0.0046363
K09475	-7.0426	2.6544	0.00061289	0.0046363
K15548	-7.0426	2.6544	0.000613	0.0046363
K05594	-7.0426	2.6544	0.00061302	0.0046363
K02468	-7.0426	2.6544	0.00061317	0.0046363
K03971	-7.0426	2.6544	0.0006132	0.0046363
K12945	-7.0426	2.6544	0.00061353	0.0046363
K08137	-7.0426	2.6544	0.00061365	0.0046363
K12290	-7.0426	2.6544	0.0006138	0.0046363
K19587	-7.0387	2.6504	0.00062872	0.0046557
K11941	-6.9779	2675	0.0004762	0.004277
K10011	-6.9651	3.4036	0.00042842	0.0040767
K05798	-6.9351	3.2216	0.00057117	0.0046287
K07026	-6923	2.6181	0.00090149	0.0057495
K08353	-6915	2348	0.00051609	0.0043986
K12660	-6.9114	2.3449	0.00047295	0.0042699
K19354	-6.9102	2343	0.00053298	0.004431
K19709	-6.9102	2343	0.00053517	0.0044378
K19697	-6.9102	2343	0.00053542	0.0044378
K17466	-6.9101	2343	0.00052317	0.0044154
K17467	-6.9101	2343	0.0005256	0.0044154
K17468	-6.9101	2343	0.00052788	0.0044154
K17473	-6.9101	2343	0.00053067	0.0044252

K18862	-6.9101	2343	0.00053183	0.0044281
K11264	-6.91	2343	0.00051339	0.0043986
K13923	-6.91	2343	0.00051441	0.0043986
K16324	-6.91	2343	0.00051699	0.0043986
K17463	-6.91	2343	0.00051824	0.0044022
K17465	-6.91	2343	0.0005207	0.0044154
K06146	-6.9099	2343	0.00050287	0.0043806
K07319	-6.9099	2343	0.00050559	0.0043862
K07821	-6.9099	2343	0.00050832	0.0043862
K08277	-6.9099	2343	0.00051106	0.0043959
K04025	-6.9098	2343	0.00049477	0.0043518
K05245	-6.9098	2343	0.00049746	0.0043614
K05887	-6.9098	2343	0.00050016	0.0043729
K03755	-6.9097	2343	0.00048413	0.0043137
K04016	-6.9097	2343	0.00048677	0.0043302
K04020	-6.9097	2343	0.00048943	0.0043397
K04022	-6.9097	2343	0.00049209	0.0043399
K03276	-6.9096	2343	0.00047409	0.004273
K03278	-6.9096	2343	0.00047626	0.004277
K03279	-6.9096	2343	0.00047887	0.0042879
K03329	-6.9096	2343	0.0004815	0.0043043
K02080	-6.9095	2343	0.00046724	0.0042699
K02173	-6.9095	2343	0.0004698	0.0042699
K02850	-6.9095	2343	0.00047192	0.0042699
K03277	-6.9064	2.3399	0.00047083	0.0042699
K02840	-6.9064	2.3399	0.00047118	0.0042699
K00785	-6.9064	2.3399	0.00047146	0.0042699
K11200	-6.9064	2.3399	0.00047166	0.0042699
K07358	-6.9064	2.3399	0.00047176	0.0042699
K15722	-6.9063	2.3399	0.00046594	0.0042699
K14587	-6.9063	2.3399	0.00046682	0.0042699
K13654	-6.9063	2.3399	0.0004677	0.0042699
K13243	-6.9063	2.3399	0.00046858	0.0042699
K12684	-6.9063	2.3399	0.00046947	0.0042699
K11922	-6.9063	2.3399	0.00047066	0.0042699
K07352	-6.9063	2.3399	0.00047066	0.0042699
K03836	-6.9063	2.3399	0.00047073	0.0042699
K16136	-6.8843	3.3639	0.00096812	0.0060433
K08348	-6.8427	4.2241	0.00054084	0.0044623
K08478	-6.8156	2.0401	0.00064831	0.0046997
K03815	-6.7812	2.3602	0.0004058	0.0039332
K10984	-6.7793	2354	0.00059011	0.0046363
K10985	-6.7793	2354	0.000593	0.0046363
K10986	-6.7793	2354	0.0005957	0.0046363
K17464	-6.7793	2354	0.00059849	0.0046363
K08297	-6.7792	2354	0.00058725	0.0046363
K11203	-6.7783	2.3951	0.00064565	0.0046997
K13683	-6.7772	2.3944	0.00061272	0.0046363
K16076	-6.7762	2.3928	0.00067969	0.0046997
K11201	-6.7762	2.3928	0.0006804	0.0046997
K15831	-6.7727	2.3894	0.0006734	0.0046997
K15832	-6.7727	2.3894	0.00067442	0.0046997
K15833	-6.7727	2.3894	0.00067545	0.0046997
K16695	-6.7727	2.3894	0.0006764	0.0046997
K18140	-6.7727	2.3894	0.00067715	0.0046997
K16711	-6.7727	2.3894	0.0006774	0.0046997

K18141	-6.7727	2.3894	0.00067806	0.0046997
K19234	-6.7727	2.3894	0.00068019	0.0046997
K18142	-6.7727	2.3894	0.00068028	0.0046997
K18325	-6.7727	2.3894	0.00068162	0.0046997
K19148	-6.7727	2.3894	0.00068169	0.0046997
K18479	-6.7727	2.3894	0.00068239	0.0046997
K19688	-6.7727	2.3894	0.00068304	0.0046997
K19238	-6.7727	2.3894	0.00068318	0.0046997
K14064	-6.7726	2.3894	0.00066193	0.0046997
K15735	-6.7726	2.3894	0.0006648	0.0046997
K15827	-6.7726	2.3894	0.00066757	0.0046997
K15828	-6.7726	2.3894	0.00066913	0.0046997
K15829	-6.7726	2.3894	0.00067054	0.0046997
K12943	-6.7725	2.3894	0.0006478	0.0046997
K12944	-6.7725	2.3894	0.00065025	0.0046997
K13620	-6.7725	2.3894	0.00065374	0.0046997
K13629	-6.7725	2.3894	0.00065674	0.0046997
K13650	-6.7725	2.3894	0.00065736	0.0046997
K13632	-6.7725	2.3894	0.00065821	0.0046997
K13630	-6.7725	2.3894	0.00065903	0.0046997
K13684	-6.7725	2.3894	0.00065969	0.0046997
K11732	-6.7724	2.3894	0.00063647	0.0046915
K11938	-6.7724	2.3894	0.00063897	0.0046953
K12151	-6.7724	2.3894	0.00064214	0.0046953
K12299	-6.7724	2.3894	0.00064527	0.0046997
K07470	-6.7723	2.3894	0.00062282	0.0046458
K07592	-6.7723	2.3894	0.00062527	0.0046465
K07796	-6.7723	2.3894	0.0006269	0.0046524
K08225	-6.7723	2.3894	0.00062906	0.0046557
K09612	-6.7723	2.3894	0.00063128	0.0046658
K11685	-6.7723	2.3894	0.00063349	0.0046759
K04333	-6.7722	2.3894	0.00061068	0.0046363
K04334	-6.7722	2.3894	0.00061391	0.0046363
K04336	-6.7722	2.3894	0.0006171	0.0046363
K07229	-6.7722	2.3894	0.00061996	0.0046427
K02814	-6.7721	2.3894	0.00059912	0.0046363
K02815	-6.7721	2.3894	0.00059978	0.0046363
K02972	-6.7721	2.3894	0.00060297	0.0046363
K03712	-6.7721	2.3894	0.00060521	0.0046363
K03838	-6.7721	2.3894	0.00060804	0.0046363
K02255	-6772	2.3894	0.0005875	0.0046363
K02317	-6772	2.3894	0.00058993	0.0046363
K02430	-6772	2.3894	0.00059202	0.0046363
K02506	-6772	2.3894	0.00059412	0.0046363
K02812	-6772	2.3894	0.00059639	0.0046363
K00885	-6.7719	2.3894	0.00058325	0.0046363
K00932	-6.7719	2.3894	0.00058456	0.0046363
K01169	-6.7719	2.3894	0.00058588	0.0046363
K10906	-6.7693	2.3869	0.00057577	0.0046363
K11530	-6.7671	2.3846	0.00059431	0.0046363
K05804	-6.7603	4.7089	0.00038494	0.0038155
K11391	-6.7473	2.6688	0.00089714	0.0057447
K08279	-6.7149	2.4187	0.00037452	0.0037466
K03819	-6.7089	2.4109	0.00054924	0.004491
K03756	-6.7012	2.4026	0.00064133	0.0046953
K04337	-6659	2.4406	0.00052497	0.0044154

K04335	-6659	2.4406	0.00052521	0.0044154
K01406	-6.6531	2.5489	0.00025962	0.0028361
K03290	-6.6254	2.4065	0.0006632	0.0046997
K01671	-6.6241	2.4043	0.00081248	0.0053596
K07811	-6.5848	2.3659	0.00081752	0.005367
K11932	-6.5822	4.2491	0.00051202	0.0043973
K16347	-6.5816	2.4027	0.0006633	0.0046997
K07812	-6.58	2361	0.00083944	0.0054639
K04018	-6.5799	2361	0.00083563	0.0054596
K12528	-6.5767	2.3579	0.00081354	0.0053601
K12529	-6.5767	2.3579	0.00081707	0.005367
K13480	-6.5767	2.3579	0.00081994	0.0053764
K16346	-6.5767	2.3579	0.00082378	0.0053886
K04064	-6.5619	2.6849	0.00066058	0.0046997
K05517	-6553	2.7306	0.00074555	0.0050039
K02100	-6.5212	1.4398	0.00015739	0.0019406
K15834	-6.48	2.4068	0.0010178	0.0062188
K03485	-6.4799	2.4068	0.00099966	0.0061977
K02079	-6.4799	2.4068	0.0010009	0.0061985
K05775	-6.4799	2.4068	0.0010052	0.0062101
K05880	-6.4799	2.4068	0.0010099	0.0062122
K09900	-6.4799	2.4068	0.0010111	0.0062122
K13636	-6.4799	2.4068	0.0010119	0.0062122
K07784	-6.4799	2.4068	0.0010122	0.0062122
K15830	-6.4799	2.4068	0.0010151	0.0062188
K07686	-6407	3.8891	0.0010611	0.0064073
K01407	-6388	3.4085	0.0021328	0.0098609
K05839	-6.3879	3.4085	0.0020688	0.0098481
K05790	-6.3879	3.4085	0.0020753	0.0098481
K04067	-6.3879	3.4085	0.0020817	0.0098481
K02853	-6.3879	3.4085	0.0020878	0.0098481
K02682	-6.3879	3.4085	0.0020938	0.0098488
K02681	-6.3879	3.4085	0.0021002	0.0098488
K02679	-6.3879	3.4085	0.0021066	0.0098511
K02507	-6.3879	3.4085	0.002113	0.0098554
K02504	-6.3879	3.4085	0.0021198	0.0098556
K02425	-6.3879	3.4085	0.0021262	0.0098556
K12582	-6.3878	3.4085	0.0020046	0.0097934
K12288	-6.3878	3.4085	0.0020079	0.0097953
K12148	-6.3878	3.4085	0.0020141	0.0097961
K11923	-6.3878	3.4085	0.0020185	0.009809
K11751	-6.3878	3.4085	0.0020249	0.0098154
K09917	-6.3878	3.4085	0.00203	0.0098164
K09911	-6.3878	3.4085	0.0020327	0.0098164
K08682	-6.3878	3.4085	0.0020386	0.0098338
K07676	-6.3878	3.4085	0.0020434	0.0098338
K06144	-6.3878	3.4085	0.0020494	0.0098481
K06006	-6.3878	3.4085	0.0020557	0.0098481
K05997	-6.3878	3.4085	0.0020625	0.0098481
K19162	-6.3877	3.4085	0.0019665	0.0097471
K16868	-6.3877	3.4085	0.0019725	0.009759
K16704	-6.3877	3.4085	0.0019779	0.009759
K16693	-6.3877	3.4085	0.0019821	0.009762
K15974	-6.3877	3.4085	0.0019886	0.0097633
K14762	-6.3877	3.4085	0.0019951	0.009782
K13301	-6.3877	3.4085	0.0020013	0.0097865

K18988	-6.3705	3.4148	0.00046921	0.0042699
K03720	-6.3631	3.4164	0.001721	0.0089825
K12500	-6352	3.4258	0.0010301	0.0062793
K15922	-6.3419	2.5714	0.0010787	0.0064676
K02505	-6.2815	3414	0.0018989	0.0095616
K12152	-6.2767	3.4222	0.0017865	0.0091746
K07357	-6.2739	3.2305	0.00283	0.01164
K09998	-6.2722	3.4171	0.0021574	0.0098612
K09997	-6.2722	3.4171	0.0021631	0.0098612
K09910	-6.2722	3.4171	0.0021675	0.0098612
K09907	-6.2722	3.4171	0.0021716	0.0098612
K09904	-6.2722	3.4171	0.0021782	0.0098612
K09896	-6.2722	3.4171	0.002179	0.0098612
K09897	-6.2722	3.4171	0.0021818	0.0098612
K09899	-6.2722	3.4171	0.0021845	0.0098612
K09894	-6.2722	3.4171	0.0021849	0.0098612
K09891	-6.2722	3.4171	0.0021915	0.0098612
K03603	-6.2722	3.4171	0.002196	0.0098612
K09802	-6.2722	3.4171	0.0021975	0.0098612
K07648	-6.2722	3.4171	0.0021986	0.0098612
K07251	-6.2722	3.4171	0.0022018	0.0098612
K05809	-6.2722	3.4171	0.0022024	0.0098612
K06080	-6.2722	3.4171	0.0022027	0.0098612
K03591	-6.2722	3.4171	0.002203	0.0098612
K07479	-6.2722	3.4171	0.0022048	0.0098612
K06957	-6.2722	3.4171	0.0022061	0.0098612
K07269	-6.2722	3.4171	0.002207	0.0098612
K07186	-6.2722	3.4171	0.0022077	0.0098612
K03573	-6.2722	3.4171	0.0022081	0.0098612
K03632	-6.2722	3.4171	0.0022085	0.0098612
K05803	-6.2722	3.4171	0.0022101	0.0098612
K05590	-6.2722	3.4171	0.0022116	0.0098612
K03840	-6.2722	3.4171	0.0022118	0.0098612
K02344	-6.2722	3.4171	0.0022122	0.0098612
K05368	-6.2722	3.4171	0.0022151	0.0098612
K03674	-6.2722	3.4171	0.0022158	0.0098612
K03804	-6.2722	3.4171	0.0022169	0.0098612
K03764	-6.2722	3.4171	0.0022169	0.0098612
K01146	-6.2722	3.4171	0.0022188	0.0098612
K03633	-6.2722	3.4171	0.0022193	0.0098612
K04770	-6.2722	3.4171	0.0022211	0.0098612
K19226	-6.2721	3.4171	0.0020855	0.0098481
K18657	-6.2721	3.4171	0.0020897	0.0098481
K18446	-6.2721	3.4171	0.0020951	0.0098488
K15723	-6.2721	3.4171	0.0021012	0.0098488
K12961	-6.2721	3.4171	0.0021069	0.0098511
K12525	-6.2721	3.4171	0.0021102	0.0098511
K12149	-6.2721	3.4171	0.0021165	0.0098554
K11926	-6.2721	3.4171	0.0021231	0.0098556
K11925	-6.2721	3.4171	0.0021292	0.0098556
K11107	-6.2721	3.4171	0.0021357	0.0098609
K10748	-6.2721	3.4171	0.0021407	0.0098612
K10000	-6.2721	3.4171	0.0021455	0.0098612
K09999	-6.2721	3.4171	0.0021516	0.0098612
K19304	-6272	3.4171	0.0020588	0.0098481
K19230	-6272	3.4171	0.0020649	0.0098481

K19229	-6272	3.4171	0.0020704	0.0098481
K19228	-6272	3.4171	0.0020746	0.0098481
K19227	-6272	3.4171	0.0020799	0.0098481
K16322	-6.2599	4.0022	0.00074573	0.0050039
K00835	-6.25	3.4249	0.001781	0.0091686
K13498	-6.2499	3.4249	0.0017751	0.0091518
K02521	-6.2473	3422	0.0019755	0.009759
K08350	-6.2367	3.2597	0.0025512	0.010894
K08349	-6.2367	3.2597	0.0025546	0.010894
K14187	-6.2337	3.4381	0.0013837	0.0076342
K03645	-6.2308	3424	0.0014892	0.0080534
K01175	-6.2216	3425	0.0021347	0.0098609
K09893	-6.2213	3.5258	0.00049078	0.0043399
K11750	-6.2161	3.4194	0.0022461	0.0099049
K03490	-6.2108	2.4005	0.0011479	0.0066988
K19789	-6.1925	3.4244	0.0020846	0.0098481
K07773	-6.1914	3.4233	0.0021242	0.0098556
K02466	-6.1871	2.6771	0.0022093	0.0098612
K00387	-6.1867	0.86083	0.00048844	0.004338
K12973	-6.1838	3.4438	0.0017558	0.0090732
K12243	-6.1827	0.66849	0.00094588	0.0059452
K06079	-6.1799	3.2662	0.0027575	0.011442
K02560	-6.1661	3.4257	0.0022446	0.0099049
K07751	-6.1661	3.4257	0.0022486	0.0099049
K09901	-6.1661	3.4257	0.0022527	0.0099148
K09476	-6.1629	3.9018	0.002028	0.0098164
K06074	-6.1198	3.2669	0.0029097	0.011832
K06073	-6.1198	3.2669	0.0029114	0.011832
K19236	-6.1198	3.2669	0.0029115	0.011832
K06212	-6.1198	3.2669	0.0029124	0.011832
K09161	-6.1198	3.2669	0.0029151	0.011832
K08162	-6.1198	3.2669	0.0029152	0.011832
K06866	-6.1198	3.2669	0.0029158	0.011832
K19778	-6.1182	3276	0.00075486	0.0050404
K03623	-6.1171	3.7583	0.00093987	0.0059211
K14055	-6.1127	3.4314	0.0014405	0.0078447
K08227	-6.1113	3.4209	0.001369	0.0075991
K03834	-6.1092	3.2863	0.0022955	0.010071
K02742	-6.0888	3.4599	0.0010616	0.0064073
K13014	-6.0855	3.4565	0.0011353	0.0066749
K12963	-6.0855	3.4565	0.001137	0.0066749
K09890	-6.0855	3.4565	0.001137	0.0066749
K07806	-6.0855	3.4565	0.0011376	0.0066749
K09908	-6.0855	3.4565	0.0011377	0.0066749
K06899	-6.0855	3.4565	0.0011377	0.0066749
K06219	-6.0855	3.4565	0.0011405	0.0066841
K05851	-6.0855	3.4565	0.0011444	0.0066988
K05787	-6.0855	3.4565	0.0011479	0.0066988
K03112	-6.0855	3.4565	0.0011488	0.0066988
K01766	-6.0832	3.4542	0.0011656	0.0067572
K02565	-6.0828	3.4284	0.0017281	0.0089853
K09918	-6.0781	2.7565	0.00086576	0.0056028
K03828	-6.0772	3.5427	0.00090368	0.0057495
K12981	-6.0764	2.3782	0.0010714	0.0064482
K07757	-6.0716	2.9071	0.0020251	0.0098154
K07349	-6.0712	3.4112	0.0026971	0.011271

K09898	-6.0648	3.4612	0.0011141	0.0066041
K07490	-6.0624	3.2733	0.0019385	0.0096843
K11606	-6.0607	3.4624	0.00040116	0.0039235
K18918	-6.0476	0.57736	0.00012017	0.0015816
K18800	-6.0454	3.4915	0.00079398	0.0052694
K15545	-6.0059	3.4217	0.0032006	0.012742
K07674	-6.0003	3.1498	0.0031764	0.012673
K02848	-5.9855	2.4475	0.00077063	0.0051331
K06157	-5.9706	2.3695	0.002677	0.01123
K07724	-5.9688	4746	0.0014275	0.0078046
K08993	-5.9497	3.4703	0.0010411	0.0063185
K03516	-5.9339	2.9635	0.0026049	0.011055
K18164	-5.9007	0.073606	0.00059872	0.0046363
K09994	-5848	2.6881	0.0025427	0.010867
K05937	-5.8389	1.0857	0.0026702	0.011227
K07345	-5.8204	6.1922	1.5039e-05	0.00033527
K07237	-5.8188	3464	0.0011792	0.0067631
K07236	-5.8188	3464	0.0011808	0.0067631
K06159	-5.8129	2.9665	0.0036128	0.013877
K07685	-5.8082	3.4543	0.0013204	0.0073893
K11106	-5.8062	2.7643	0.00092252	0.005832
K06858	-5.7967	3.3155	0.0024453	0.010575
K03837	-5.7915	4.0668	0.00014894	0.0018701
K04338	-5.7809	2.6116	0.0015386	0.008247
K02441	-5.7789	3.4787	0.0010036	0.0062077
K03532	-5.7514	2.3921	0.0026208	0.011099
K13735	-5.7465	3.4529	0.0047193	0.015815
K06197	-5.7435	2.4946	0.0011492	0.0066988
K03675	-5.7371	2.7049	0.0042974	0.015473
K18336	-5.7355	0.52434	0.00063839	0.0046953
K00813	-5734	3.4907	0.0006565	0.0046997
K02345	-5.7159	3.4627	0.0041799	0.0152
K02750	-5.7148	2.6984	0.002783	0.011507
K13256	-5.7143	3.6916	0.00025522	0.0028101
K18837	-5.7127	2.7467	0.003881	0.014523
K12974	-5.7094	2.7435	0.0038863	0.014523
K03425	-5.7094	2.7435	0.0038874	0.014523
K12975	-5.7094	2.7435	0.0038879	0.014523
K18324	-5.7094	2.7435	0.0038898	0.014523
K12289	-5.7094	2.7435	0.0038939	0.014523
K09996	-5.7094	2.7435	0.0038945	0.014523
K07643	-5.7094	2.7435	0.0038952	0.014523
K11736	-5.7062	2.7403	0.0039507	0.01465
K02532	-5.7055	3.6308	0.0013005	0.0072853
K06214	-5.7041	2.6429	0.0016427	0.0086777
K11911	-5.6736	2.5034	0.0042384	0.015362
K12984	-5652	2.5198	0.0032792	0.01296
K14051	-5.6198	2.4621	0.0011269	0.0066544
K09906	-5.6137	3.5102	0.0043242	0.015498
K18838	-5.6016	2.7603	0.0044213	0.015624
K08219	-5.5983	2.7571	0.0044407	0.015624
K02562	-5.5983	2.7571	0.0044419	0.015624
K18765	-5.5983	2.7571	0.0044446	0.015624
K07266	-5.5956	1.5249	0.00014289	0.0018066
K09477	-5.5838	2.4782	0.001114	0.0066041
K08992	-5.5657	3515	0.0045306	0.015647

K07274	-5.5628	4.0193	0.0041769	0.015199
K06211	-5.5576	3.4314	0.0018543	0.0094538
K08485	-5.5519	3.5183	0.0045665	0.015677
K04099	-5.5476	0.34268	0.0006709	0.0046997
K06205	-5.5457	3514	0.00082118	0.005378
K19303	-5.5434	2.7662	0.0030295	0.012214
K00840	-5537	2.8366	0.0046809	0.015763
K15835	-5.5364	2.1297	0.0064459	0.018618
K11192	-5.5363	2.1297	0.0064308	0.018594
K10038	-5.5334	2.7509	0.0051199	0.016127
K08160	-5.5325	2859	0.0039984	0.014746
K04775	-5.5282	2791	0.0030792	0.012368
K16210	-5528	3.4787	0.0038728	0.014523
K01216	-5.5241	-0.28126	0.0012448	0.0070676
K05525	-5.5241	-0.28126	0.0012517	0.0070846
K11607	-5.5216	3.5147	0.00090472	0.0057495
K11604	-5.5216	3.5147	0.00090508	0.0057495
K11605	-5.5216	3.5147	0.00090527	0.0057495
K14591	-5.5212	2.7607	0.0014818	0.0080213
K19235	-5.4968	2.7706	0.0050414	0.016028
K08344	-5496	3.2694	0.0018152	0.0093006
K10972	-5.4787	2.4536	0.0051712	0.01613
K12678	-5.4762	5.2282	0.0018758	0.0095193
K04017	-5475	2.45	0.0051782	0.01613
K07690	-5.4638	2.6618	0.0011571	0.0067236
K14338	-5.4614	3.1423	0.001176	0.0067631
K04691	-5455	3.5552	0.0027237	0.011348
K09916	-5455	3.5552	0.0027286	0.011359
K19775	-5.4549	2.4959	0.0047999	0.015875
K07700	-5.4549	2.4959	0.0048018	0.015875
K07702	-5.4549	2.4959	0.0048029	0.015875
K18326	-5.4549	2.4959	0.0048048	0.015875
K11744	-5.4549	2.4959	0.0048067	0.015875
K08318	-5.4549	2.4959	0.0048084	0.015875
K14062	-5.4549	2.4959	0.0048098	0.015875
K12265	-5.4549	2.4959	0.0048103	0.015875
K13918	-5.4549	2.4959	0.0048113	0.015875
K08320	-5.4549	2.4959	0.004813	0.015875
K18923	-5.4436	2.5486	0.0033785	0.013219
K04081	-5.4372	2.5106	0.0043113	0.015488
K07740	-5.4337	2.8187	0.0030473	0.012274
K18148	-5.4311	2.3396	0.0050766	0.016065
K02783	-5.4296	4.5523	0.00039015	0.0038465
K07810	-5.4155	2.7145	0.0015768	0.0084023
K11382	-5.4148	2.4353	0.0033858	0.013228
K01825	-5.4046	3.5598	0.0027094	0.011297
K02846	-5.3772	2744	0.0014927	0.0080644
K15737	-5.3665	2736	0.0012436	0.0070676
K03651	-5.3628	3.5828	0.0024999	0.010752
K19334	-5.3461	2512	0.0055336	0.016644
K13638	-5.3377	3.4405	0.0018314	0.0093662
K09923	-5.3361	3.4885	0.0011813	0.0067631
K08153	-5.3274	3.2603	0.0028514	0.011693
K05789	-5.3047	2.4773	0.0037551	0.014273
K12962	-5.3034	3.5505	0.00075289	0.0050334
K16234	-5.3007	2.2491	0.004067	0.014871

K11710	-5.2942	1.7232	0.00066234	0.0046997
K07235	-5.2877	3.5623	0.0024512	0.010592
K07347	-5.2861	6.3626	2.6208e-05	0.00050761
K04103	-5.2803	3635	0.00050091	0.0043729
K04013	-5.2611	2.4866	0.006577	0.018917
K04014	-5.2611	2.4866	0.0065862	0.018924
K04015	-5.2611	2.4866	0.0065899	0.018924
K05802	-5.2542	4368	0.00042504	0.0040575
K05792	-5.2525	2.4782	0.0022603	0.0099402
K02485	-5.2096	3539	0.0046382	0.015724
K00068	-5.2049	3.5692	0.0025956	0.011024
K13938	-5.1923	2.5848	0.003832	0.014435
K08317	-5.1876	1.2835	0.0030813	0.012368
K03668	-5.1616	2.9085	0.0039655	0.014675
K01096	-5.1609	3.6871	0.00067241	0.0046997
K07070	-5.1572	3.6151	0.0015878	0.008443
K01085	-5.1495	3.4529	0.010523	0.027203
K11258	-5.1479	3.5303	0.0053695	0.016421
K03184	-5.1467	3.5291	0.0054061	0.016459
K02336	-5.1319	3.5527	0.00065856	0.0046997
K01545	-5.1283	0.52018	0.00052531	0.0044154
K06155	-5.1232	2.7668	0.0042615	0.015399
K03288	-5.1217	2.6593	0.0011515	0.0067053
K07703	-5.0971	2.6861	0.0057719	0.017134
K07014	-5.0955	3.4657	0.010216	0.026621
K08312	-5.0821	3.5784	0.0036655	0.01402
K13053	-5.0817	3.4931	0.0060752	0.017783
K19231	-5.0499	2.5304	0.001998	0.0097865
K13794	-5.0418	2.4552	0.0056513	0.016877
K09961	-5.0046	2226	0.0012866	0.0072371
K02839	-4.9968	2.6681	0.0032649	0.012922
K16348	-4992	2.8304	0.0025571	0.010894
K03207	-4.9837	2.5097	0.0022824	0.010021
K13040	-4.9798	3.2337	0.018127	0.040885
K07136	-4963	3.7533	0.00040464	0.0039327
K19611	-4.9517	3.4972	0.0073261	0.020531
K04774	-4.9316	3.6583	0.0012723	0.007179
K08997	-4.9294	2.9138	0.011101	0.028294
K11250	-4.9279	3.4482	0.0023005	0.010085
K13255	-4.9167	2.6047	0.0021455	0.0098612
K01771	-4913	0.90098	0.0012143	0.006916
K07807	-4.8886	-0.12355	0.0020095	0.0097953
K08324	-4886	2.9509	0.0053201	0.016345
K11535	-4.8768	4.1944	0.00031718	0.0032999
K09909	-4.8743	2.9259	0.011803	0.029518
K10938	-4.8739	-0.13609	0.0015753	0.0084023
K00884	-4.8561	4.1228	0.0013323	0.0074483
K07678	-4.8542	2.9725	0.0074872	0.020907
K00316	-4851	-0.15624	0.0011731	0.0067631
K03548	-4.8497	3.3563	0.0040497	0.014863
K07265	-4.8344	0.9235	0.0033506	0.013128
K07346	-4.8336	5.1752	0.00018579	0.0022205
K15524	-4.8242	2.7034	0.010019	0.026208
K19734	-4.8197	2.5535	0.013553	0.0329
K18843	-4.8185	2602	0.0033175	0.013041
K11733	-4817	4277	0.00030468	0.0032003

K09912	-4816	3.6528	0.0055632	0.016687
K00998	-4.8075	3.4746	0.013639	0.033035
K02753	-4.7904	2.5237	0.0069449	0.019695
K03528	-4.7877	3.6712	0.0054713	0.016561
K15396	-4.7874	3.6887	0.0051464	0.01613
K03683	-4.7865	3.6878	0.0051812	0.01613
K09895	-4.7864	3.6878	0.0051699	0.01613
K07153	-4.7846	3.6591	0.0058178	0.017205
K09902	-4.7828	3.6573	0.0059121	0.017418
K05796	-4.7821	3299	0.0084609	0.023015
K01194	-4.7606	4.0765	0.00025402	0.0028029
K05835	-4759	2.6818	0.013097	0.03203
K09712	-4.7584	2.6971	0.004286	0.015452
K06880	-4.7485	3.5713	0.0028203	0.011617
K00484	-4.7306	2.2961	0.0019651	0.0097471
K05793	-4.7258	2232	0.011683	0.029338
K15662	-4.7249	1.7695	0.004317	0.015488
K03607	-4.72	3.4675	0.013829	0.033417
K07312	-4.7168	3.4909	0.0057054	0.016992
K07689	-4.7118	3.4965	0.0030279	0.012214
K04753	-4.7114	3.4463	0.0064147	0.018558
K08351	-4.7108	3.1501	0.003685	0.014041
K07283	-4.7093	3.1419	0.0031088	0.012449
K15536	-4.7027	2696	0.013957	0.033612
K13695	-4.6893	3.4648	0.0048182	0.015882
K02680	-4.6871	3.4532	0.0052385	0.016239
K05777	-4.6846	2485	0.0047696	0.015875
K05778	-4.6846	2485	0.0047853	0.015875
K05779	-4.6846	2485	0.0047935	0.015875
K06986	-4.6737	1064	0.0022224	0.0098612
K02526	-4.6709	4126	0.0017019	0.0089079
K00118	-4.6586	-0.075729	0.0017502	0.0090602
K00247	-4.6554	3307	0.021722	0.047044
K11933	-4.6515	3.3032	0.022403	0.048119
K07306	-4.6505	4.7699	0.001437	0.007841
K02791	-4.6468	4.5894	0.0027036	0.011281
K07069	-4.6449	7.1148	5.3315e-07	4.2815e-05
K19000	-4.6382	3.4747	0.0046161	0.015724
K10857	-4.6223	3.2079	0.0020854	0.0098481
K11921	-4.5885	2.8476	0.0024158	0.010489
K03759	-4.5803	2.4382	0.020084	0.044039
K11738	-4.5731	2.9507	0.0040444	0.014863
K05785	-4.5705	3.5511	0.0068277	0.019451
K13889	-4.5691	3.1793	0.0036563	0.014005
K12700	-4.5573	2.7082	0.0052822	0.016291
K08194	-4.5543	2.6499	0.0028942	0.011832
K13891	-4552	3.0713	0.0036097	0.013875
K19430	-4.5315	1.8259	0.0017257	0.0089853
K03472	-4.5233	3.5777	0.012815	0.031472
K03658	-4.5193	3506	0.019865	0.043681
K13795	-4519	2.6101	0.0046976	0.01578
K05791	-4.5183	2.4596	0.0046035	0.015724
K07310	-4.5157	2.3949	0.012331	0.030587
K08298	-4.5157	2.3949	0.012354	0.030615
K03807	-4.5155	2.9734	0.010644	0.027397
K06149	-4.5144	3.5218	0.0038322	0.014435

K16209	-4.5131	0.040995	0.0054282	0.01649
K05526	-4.5079	3.0173	0.0031077	0.012449
K15984	-4.5021	3605	0.011763	0.029445
K12685	-4.5007	2.2705	0.0099317	0.026018
K13890	-4.4913	3.0882	0.0038527	0.014493
K09920	-4.4841	3.0146	0.010842	0.027794
K08314	-4.4673	2.5774	0.01245	0.030783
K03533	-4.4639	2.4169	0.01194	0.029805
K11905	-4.4628	2.7312	0.0032716	0.01294
K06447	-4.4549	3.4163	0.0014761	0.0079983
K11910	-4.4474	2.6884	0.0033979	0.013257
K06609	-4.44	0.61844	0.0033091	0.013035
K07400	-4.4271	3.6947	0.0034777	0.013462
K17203	-4.4237	2.8807	0.0038122	0.01442
K17204	-4.4208	2.8779	0.0038289	0.014435
K17202	-4.4208	2.8779	0.0038457	0.014477
K13657	-4.4175	0.0020232	0.002324	0.010171
K01994	-4.4058	7.2139	1.3322e-07	3.3154e-05
K06328	-4.4058	7.2139	1.3332e-07	3.3154e-05
K06426	-4.4058	7.2139	1.3349e-07	3.3154e-05
K13853	-4.3973	7.2161	1.5271e-07	3.3154e-05
K06386	-4.3953	7.2277	1.1849e-07	3.3154e-05
K11636	-4389	3.7062	0.0032539	0.012888
K07640	-4.3882	3.5326	0.008749	0.023645
K06305	-4.3859	7195	1.5432e-07	3.3154e-05
K07637	-4.3782	3.5506	0.0044602	0.015624
K00367	-4.3755	-0.9725	0.001293	0.0072635
K15540	-4.3755	3.6651	0.0025313	0.010838
K02182	-4.3725	3.0143	0.0028698	0.01175
K08368	-4.3487	2.8189	0.0050681	0.016063
K18333	-4.3405	0.55658	0.0018829	0.0095402
K01484	-4.2895	3.1776	0.0033736	0.013209
K00879	-4.2809	2.6441	0.013707	0.033156
K18654	-4.2715	1.3403	0.0073342	0.020543
K18653	-4.2715	1.3403	0.0073423	0.020555
K13283	-4.2707	3.2023	0.0031273	0.012505
K17850	-4269	3.8003	0.0012939	0.0072635
K01184	-4.2638	0.52153	0.0036835	0.014041
K11787	-4.2524	0.06286	0.0059155	0.017418
K07675	-4.2454	4.1486	0.0012063	0.0068921
K19168	-4.2304	3.7345	0.008883	0.023936
K07285	-4.2293	3.5696	0.0058577	0.017313
K13892	-4.2245	3.0666	0.0048109	0.015875
K06887	-4.2185	2.9449	0.0057129	0.016998
K06078	-4.2121	3.4914	0.012586	0.031051
K01027	-4.2067	0.10069	0.0055631	0.016687
K11202	-4.1994	3.8877	0.015324	0.036376
K15468	-4.1974	1.9823	0.0020425	0.0098338
K13796	-4.1939	2738	0.0051705	0.01613
K12661	-4.1901	2.7877	0.0039092	0.014557
K12536	-4.1699	2.5042	0.013902	0.033514
K12537	-4.1699	2.5042	0.013904	0.033514
K07230	-4.1653	3483	0.0063184	0.018347
K07311	-4.1632	2.4978	0.016463	0.038296
K18697	-4.1427	3.0445	0.0073554	0.020581
K12538	-4.1372	2.4599	0.015609	0.036906

K00137	-4.1367	2.9101	0.0057532	0.017088
K07660	-4.1345	3.6395	0.0047129	0.015814
K00055	-4.1301	0.23856	0.0034686	0.013437
K10014	-4.1086	3.0369	0.0048003	0.015875
K07264	-4.0939	3968	0.0060332	0.017688
K01387	-4.0911	2647	0.012363	0.030622
K00322	-4.0901	3.7425	0.0052675	0.016281
K08990	-4.0842	3.8434	0.0019524	0.0097039
K06918	-4.0842	3.8434	0.001956	0.0097124
K02236	-4.0838	7.3297	4.3708e-08	3.3154e-05
K09982	-4.0736	2.7906	0.0058774	0.017362
K03810	-4.0724	4.9256	0.00037852	0.0037796
K07771	-4.0721	3.4834	0.01081	0.027733
K19585	-4.0717	2.6567	0.011205	0.028487
K16514	-4.0681	1.6132	0.0014094	0.0077446
K07677	-4.0669	3.6688	0.005161	0.01613
K11534	-4.0639	3.7509	0.003821	0.01443
K15509	-4.0619	1572	0.0015682	0.0083813
K08481	-4.0599	-0.95129	0.0040563	0.014863
K18889	-4.0563	3.4875	0.011346	0.028757
K18890	-4.0563	3.4875	0.01136	0.02878
K05358	-4.0537	1.1652	0.010343	0.026849
K19222	-4.0478	3.5693	0.0038815	0.014523
K11734	-4.0438	3.8818	0.0033085	0.013035
K19586	-4.0412	2.8792	0.0076584	0.021266
K00216	-4.0384	3.3456	0.0078633	0.021703
K03805	-4.0314	2.6501	0.010034	0.026235
K05365	-4.0238	3.7516	0.0079503	0.02191
K00673	-4.0176	3.4962	0.0016787	0.0088121
K01252	-4.0138	3.3564	0.0080252	0.022038
K08313	-4.0109	2.5738	0.016772	0.038867
K02855	-4.0085	2.7139	0.0071773	0.020228
K06312	-4.0069	2.3438	0.0096893	0.025481
K02617	-4.0061	0.51051	0.0044013	0.01561
K12291	-3.9939	0.75357	0.014631	0.034988
K13727	-3991	1.3725	0.0032369	0.012847
K14063	-3.9737	-1.3177	0.0011731	0.0067631
K11477	-3.9667	1.4488	0.0018626	0.0094727
K02024	-3965	3.5411	0.0086404	0.02341
K01521	-3.9582	2.9684	0.0097946	0.025733
K06445	-3.9574	4.0341	0.0020758	0.0098481
K11940	-3.9543	3.9737	0.0014533	0.0078907
K14189	-3.9519	1528	0.0043834	0.015585
K02362	-3.9518	2.5548	0.011746	0.029445
K13633	-3.9455	2.7809	0.0095518	0.025179
K14348	-3.9425	2.7054	0.022613	0.048473
K02364	-3.9412	2.6812	0.013882	0.033504
K08319	-3.9308	0.6126	0.016147	0.037674
K14414	-3.9298	3.3626	0.014017	0.033729
K01101	-3.9283	7.3604	9.6137e-08	3.3154e-05
K16842	-3.9234	0.91012	0.019694	0.043409
K02465	-3.9152	0.59609	0.022195	0.04788
K19615	-3.9142	-1.1989	0.0016795	0.0088121
K06222	-3.9127	3.6672	0.0066972	0.019132
K11031	-3906	3.1873	0.01499	0.035706
K02798	-3905	3.7986	0.0054729	0.016561

K10831	-3899	3.0474	0.0081037	0.02222
K11066	-3.8893	3.7863	0.0047994	0.015875
K13928	-3886	-1.0708	0.00093404	0.005898
K16077	-3.8749	0.79672	0.017003	0.039318
K17938	-3.8564	3.2125	0.008496	0.023087
K10538	-3.8553	3.1592	0.006635	0.019004
K16839	-3.8386	0.95076	0.018884	0.042246
K13525	-3.8348	1.4268	0.0068302	0.019451
K03777	-3.8331	3.8829	0.0038897	0.014523
K10537	-3.8278	3.1666	0.0068957	0.019576
K02170	-3.8248	4.1309	0.0039724	0.01469
K11183	-3.8243	3.3189	0.0076486	0.021266
K08484	-3823	4.2446	0.00083773	0.0054639
K19147	-3.8119	1.1068	0.0068508	0.019495
K08970	-3.8025	2.9169	0.0094376	0.024968
K01569	-3.7942	2.3698	0.0043906	0.015589
K15736	-3.7932	2.9002	0.011792	0.029503
K03312	-3.7814	7.3357	1.0989e-06	6.0205e-05
K04033	-3.7641	2.7434	0.01064	0.027397
K07589	-3.7572	2.6432	0.015822	0.037283
K04780	-3756	2053	0.018487	0.041537
K18954	-3.7504	3.0678	0.0070015	0.019815
K14054	-3.7473	2.6045	0.016899	0.039129
K02363	-3745	3.4748	0.0074093	0.020722
K10017	-3.7449	3.1551	0.0078401	0.021674
K10016	-3.7449	3.1551	0.007844	0.021674
K10015	-3.7449	3.1551	0.007845	0.021674
K09160	-3.7447	4.1763	0.0012469	0.0070721
K05982	-3741	3904	0.0049981	0.016019
K09914	-3.7409	3.1433	0.0088457	0.023871
K07308	-3.7391	4.8928	0.0090496	0.024234
K14060	-3.7388	1.3307	0.0043059	0.015483
K07109	-3.7385	3.9777	0.010347	0.026849
K07396	-3.7331	2.4849	0.011591	0.029175
K00880	-3.7275	2.8264	0.020537	0.044834
K16080	-3.7182	2.3236	0.012181	0.030283
K01575	-3717	4.3568	0.0037669	0.014298
K07281	-3.7127	-1.9656	0.0081277	0.022275
K12957	-3709	3.0684	0.015366	0.036459
K06136	-3.7084	2.8529	0.0057948	0.017174
K08299	-3.7082	3.1052	0.0080074	0.022014
K11747	-3692	4.2051	0.0030669	0.012344
K07664	-3.6919	3.6605	0.010414	0.026996
K00032	-3.6672	-1.7731	0.0053267	0.016345
K01182	-3.6653	7.4029	3.4497e-07	3.7684e-05
K06946	-3.6567	2.6069	0.020533	0.044834
K01185	-3.6431	3.7053	0.0052512	0.01625
K10539	-3.63	3.1971	0.0098153	0.025752
K12988	-3.6253	-0.74208	0.0058909	0.017393
K08724	-3.6165	7.3939	0	3.4274e-05
K08195	-3.6011	4.1549	0.0016106	0.0085244
K00450	-3.5975	3116	0.0089383	0.024005
K08172	-3.5943	2.7078	0.018081	0.040808
K03346	-3.5875	7.4309	2.4059e-07	3.5814e-05
K02167	-3.5871	3.8139	0.006515	0.018778
K09516	-3.5816	-0.98294	0.010701	0.027489

K19707	-3.5792	2.0813	0.005623	0.01681
K11144	-3.5683	7.4324	2.4694e-07	3.5814e-05
K11735	-3.5619	3.2944	0.011597	0.029177
K09976	-3.5545	7.4339	3.1024e-07	3.6882e-05
K08226	-3.5509	0.42363	0.016413	0.038196
K03535	-3548	3.7553	0.0059034	0.017418
K04065	-3.5411	3.8112	0.0078315	0.021669
K13421	-3.5361	0.13262	0.0093494	0.024801
K02243	-3.5353	7.4162	3.4439e-07	3.7684e-05
K18692	-3.5353	7.4162	3.4445e-07	3.7684e-05
K02598	-3.5235	3.7684	0.0052155	0.016195
K07261	-3.5219	3.4623	0.0071188	0.020095
K11249	-3.5219	-0.1514	0.0090557	0.024234
K10681	-3.5137	2.1116	0.017599	0.040052
K01576	-3.5108	2.9229	0.0092826	0.024648
K15552	-3.4937	3.3487	0.011275	0.028616
K07498	-3491	3.9835	0.005497	0.016588
K11037	-3.4907	1.5354	0.017955	0.040693
K11036	-3.4907	1.5354	0.017973	0.040697
K06325	-3.4907	1.5354	0.017993	0.040712
K15551	-3.4904	3.2529	0.012522	0.030921
K16924	-3.4876	3.5951	0.018645	0.041789
K16509	-3.4792	7594	1.8817e-07	3.3154e-05
K02240	-3.4707	7.4215	4.0965e-07	3.9956e-05
K01782	-3467	4.3095	0.0017517	0.0090602
K11635	-3.4642	4.2589	0.001738	0.0090169
K00855	-3.4516	3.7887	0.0084245	0.022938
K12507	-3.4494	2.6868	0.019912	0.043713
K16258	-3.4462	0.63223	0.010895	0.027912
K08680	-3.4417	4.7403	0.00029557	0.0031468
K03291	-3.4398	4.1624	0.0035797	0.013789
K18983	-3434	1.8766	0.0064592	0.018647
K19270	-3.4317	4.9846	0.00029451	0.0031418
K19429	-3.4295	1.0102	0.0065632	0.018895
K16066	-3.4274	3653	0.011435	0.028935
K16074	-3.4259	4.1011	0.0030121	0.012178
K13075	-3.4236	0.56154	0.019398	0.042991
K14989	-3.4236	0.56154	0.019406	0.042991
K18591	-3.4236	0.56154	0.019408	0.042991
K09124	-3.4236	0.56154	0.019413	0.042991
K11034	-3.4236	0.56154	0.019416	0.042991
K14988	-3.4236	0.56154	0.019422	0.042991
K16901	-3.4236	0.56154	0.019425	0.042991
K08777	-3.4236	0.56154	0.019439	0.042991
K06307	-3.4236	0.56154	0.019441	0.042991
K06335	-3.4236	0.56154	0.019448	0.042991
K16654	-3.4236	0.56154	0.01945	0.042991
K06372	-3.4236	0.56154	0.019455	0.042991
K05338	-3.4236	0.56154	0.019457	0.042991
K19349	-3.4236	0.56154	0.019459	0.042991
K08603	-3.4236	0.56154	0.019462	0.042991
K19428	-3.4236	0.56154	0.019465	0.042991
K05339	-3.4236	0.56154	0.019468	0.042991
K02249	-3.4236	0.56154	0.01948	0.042991
K01408	-3.4236	0.56154	0.019504	0.043026
K07687	-3.4135	4.0105	0.0062482	0.018192

K06330	-3.4093	0.58089	0.018943	0.042295
K16135	-3.4048	2.7166	0.022043	0.047598
K05281	-3.4006	0.66481	0.011437	0.028935
K18478	-3.3862	2.8443	0.02229	0.04798
K07487	-3.3832	0.57606	0.018054	0.040798
K06979	-3.3713	0.59524	0.016733	0.038809
K16692	-3.3707	3.4004	0.01235	0.030615
K00471	-3.3706	-1.8225	0.0063048	0.018327
K01727	-3.3696	3.1562	0.019284	0.042921
K06198	-3.3663	4.0994	0.01213	0.030183
K11737	-3.3652	4.3639	0.0016755	0.0088121
K07029	-3.3614	7.5309	1.8136e-07	3.3154e-05
K19419	-3.3606	0.94819	0.008199	0.022425
K02688	-3.3561	3.5311	0.018217	0.041031
K04568	-3.3485	4.1138	0.0044322	0.015624
K08152	-3.3424	3.6053	0.017498	0.039905
K19295	-3.3391	-1.0916	0.0085614	0.023242
K14266	-3.3378	4.0688	0.010358	0.026863
K04080	-3.3362	4.4361	0.00059803	0.0046363
K02777	-3.3342	7.5409	1.2988e-07	3.3154e-05
K08715	-3.3294	1.4056	13	0.031827
K07340	-3.3281	4.1544	0.0051661	0.01613
K09970	-3.3265	3.4704	0.0090493	0.024234
K01641	-3.3255	4.0629	0.022257	0.047956
K09823	-3.3141	4.4114	0.00085613	0.0055537
K18925	-3.3051	4.0861	0.0034638	0.013428
K03583	-3.2975	4.0365	0.0065015	0.018749
K06948	-3.2899	7.4591	2.3093e-06	8.8828e-05
K00370	-3.2741	4.2988	0.0075477	0.021044
K12372	-3.2588	3.8325	0.0090657	0.024241
K12371	-3.2581	3.8319	0.009089	0.024287
K12370	-3.2581	3.8319	0.0090931	0.024287
K12369	-3.2581	3.8319	0.0091015	0.024297
K09945	-3.2514	2.8026	0.014701	0.035126
K18297	-3.2511	0.10641	0.014525	0.034781
K10212	-3.2391	-0.0099102	0.016102	0.037618
K13060	-3.2388	3.1366	0.017529	0.039938
K07711	-3.2388	3.5971	0.023462	0.049864
K09859	-3.2345	-0.2707	0.010739	0.027564
K15915	-3.2165	-1.2936	0.022624	0.048478
K11906	-3.2115	3.4226	0.016545	0.038432
K10013	-3.2037	3.1303	0.019101	0.042585
K07140	-3.2012	4.2795	0.002764	0.011455
K01195	-3.1967	1.0674	0.01634	0.038044
K10561	-3.1909	3.5617	0.011563	0.029131
K17737	-3.1896	0.59326	0.020489	0.044782
K06203	-3.1798	4.1221	0.0066277	0.018993
K09984	-3.1793	2.8018	0.015569	0.036845
K09971	-3.1652	3.5112	0.011077	0.028271
K19701	-3.1606	1.2482	0.010975	0.02809
K13926	-3.1603	3.7475	0.011101	0.028294
K14470	-3.16	1.0101	0.01813	0.040885
K19290	-3.1559	-1.2443	0.01155	0.029124
K01139	-3.1531	4.0271	0.010705	0.027489
K12368	-3153	4178	0.0051982	0.01615
K03862	-3.1513	2.9932	0.015879	0.0374

K11892	-3.1506	4.0842	0.0077894	0.021575
K06139	-3.1505	2.3459	0.010701	0.027489
K09021	-3.1404	-0.9423	0.006296	0.018321
K00158	-3.1401	4.1157	0.0047223	0.015815
K19591	-3.1336	-1.3648	0.010128	0.02643
K09972	-3.1315	3.5918	0.0094577	0.024968
K11617	-3.1304	4.7897	0.00073316	0.0049561
K04062	-3.1266	3.7831	0.020663	0.045091
K07645	-3.1244	4.2099	0.011587	0.029175
K18924	-3.1114	3.9117	0.0060458	0.017716
K16169	-3.1078	4.7147	0.0011764	0.0067631
K03095	-3.1078	4.7147	0.0011789	0.0067631
K17950	-3.1054	1.3609	0.011688	0.029338
K00383	-3.0994	5.3379	0.00061568	0.0046363
K19005	-3.0994	4.8653	0.00089847	0.0057464
K02399	-3.0978	3.6873	0.019475	0.042991
K03732	-3.0966	3.7978	0.017231	0.039456
K06138	-3.0948	2.3756	0.012986	0.031807
K01222	-3.0903	5.3606	0.00030571	0.0032049
K16869	-3.0891	4152	0.0045977	0.015724
K03693	-3.0869	4633	0.0017289	0.0089853
K07113	-3.0866	4.8306	0.00045537	0.0042699
K11622	-3083	3.6673	0.008043	0.022076
K09020	-3082	-0.99152	0.0073212	0.020531
K16515	-3.0811	1.6396	0.012592	0.031051
K02781	-3.07	4.2915	0.023261	0.049571
K02765	-3.0645	7.4311	4.5832e-06	0.00014064
K06443	-3.0602	1.4086	0.023554	0.049967
K03638	-3.0588	4.6171	0.00043585	0.004133
K16516	-3.0588	1.2752	0.011537	0.029107
K09964	-3055	1.3805	0.018068	0.040798
K08178	-3.0546	1883	0.011619	0.029219
K02822	-3.0535	5.6877	0.0039199	0.014574
K05994	-3.0534	-0.77442	0.018943	0.042295
K07733	-3.05	4.4385	0.0045237	0.015638
K11073	-3.0487	4.0564	0.0057805	0.01715
K03919	-3.0436	4.0339	0.0098309	0.025778
K18382	-3.0422	-0.91772	0.0071897	0.020237
K07684	-3.0422	3.7273	0.016549	0.038432
K05685	-3.0354	4.2922	0.011448	0.028949
K04712	-3.0348	-1.0355	0.017979	0.040697
K14056	-3.0322	-1.7895	0.011555	0.029124
K01716	-3.0313	4.1392	0.0082709	0.022588
K05275	-3.0311	1.0173	0.018335	0.041246
K00883	-3031	4.1308	0.0079064	0.021799
K00564	-3.0303	7.6992	5.8553e-07	4.2815e-05
K11616	-3.0236	0.90936	0.012484	0.03084
K17736	-3.0226	-1.3532	0.01342	0.032651
K00146	-3019	2.1055	0.017063	0.039333
K08996	-3.0121	1.6826	0.015823	0.037283
K03933	-3.0096	4.4703	0.0049152	0.016019
K19425	-3.0085	0.92725	0.019049	0.042485
K12555	-3007	4.8582	0.00091392	0.0057843
K05774	-3.0069	3367	0.022308	0.04798
K11102	-3.0065	4.2506	0.0049227	0.016019
K02043	-3.0056	3.3212	0.022733	0.048692

K17713	-3.0018	3.8999	0.01556	0.036839
K06884	-2.9973	3.7251	0.010539	0.027219
K01200	-2.9958	7356	1.0743e-05	0.00025403
K07586	-2.9942	7.5028	3.7185e-06	0.00012285
K02508	-2.9916	-1.5958	0.011761	0.029445
K11075	-2.9879	3.8165	0.0090323	0.024219
K17224	-2.9839	-0.21913	0.014715	0.035144
K18104	-2.9833	3.8028	0.0084597	0.023015
K05823	-2.9814	4.0412	0.0071649	0.020204
K06165	-2.9809	3372	0.023516	0.049959
K14647	-2.9781	3.4495	0.016099	0.037618
K02248	-2.9718	4.5936	0.0019056	0.0095777
K02244	-2.9718	4.5936	0.0019078	0.0095777
K09806	-2.9654	4.0276	0.012957	0.031778
K00999	-2964	-0.49776	0.010294	0.026773
K00675	-2.9537	4.3948	0.0017218	0.0089825
K10560	-2.9509	3.5308	0.017124	0.039333
K16164	-2.9483	-0.21149	0.011741	0.029445
K05549	-2.9454	1.4149	0.017134	0.039333
K01795	-2.9345	-1527	0.017255	0.039482
K19292	-2.9344	-1527	0.017059	0.039333
K17061	-2.9344	-1527	0.017077	0.039333
K18300	-2.9344	-1527	0.017082	0.039333
K19291	-2.9344	-1527	0.017083	0.039333
K17060	-2.9344	-1527	0.017087	0.039333
K19744	-2.9344	-1527	0.017095	0.039333
K16081	-2.9344	-1527	0.017102	0.039333
K13007	-2.9344	-1527	0.017117	0.039333
K14268	-2.9344	-1527	0.017122	0.039333
K19293	-2.9344	-1527	0.017126	0.039333
K11916	-2.9344	-1527	0.017136	0.039333
K19296	-2.9344	-1527	0.017139	0.039333
K11383	-2.9344	-1527	0.017153	0.039348
K11914	-2.9344	-1527	0.017172	0.039375
K08985	-2.9344	-1527	0.017184	0.039388
K08085	-2.9344	-1527	0.017219	0.039451
K02625	-2.9344	-1527	0.017236	0.039456
K03482	-2933	-1867	0.013649	0.033045
K02086	-2.9297	7497	8.6756e-06	0.00021699
K11891	-2924	4.1572	0.012053	0.030047
K02246	-2.9235	4.5703	0.0021829	0.0098612
K08234	-2919	5.1888	0.00054646	0.0044817
K09018	-2.9168	-0.70113	0.010298	0.026773
K05783	-2.9109	1.3716	0.017975	0.040697
K02819	-2.9083	5.1299	0.002343	0.01023
K07401	-2.9083	1.9865	0.016497	0.038344
K11076	-2908	3.8543	0.010099	0.02638
K00448	-2.9069	3.4749	0.018369	0.041307
K01919	-2.9032	7.5048	1.9999e-05	0.00041853
K02779	-2.9031	4.6007	0.0092718	0.024632
K06879	-2.8985	3.8708	0.019841	0.043679
K11904	-2.8975	5.3328	0.00054249	0.0044625
K00354	-2.8914	3.7208	0.010502	0.027174
K17228	-2.8914	1.9125	0.015643	0.036967
K07074	-2.8839	4.5342	0.0026214	0.011099
K02859	-2.8807	3.9717	0.0097764	0.025697

K05550	-2.8786	1.4333	0.019925	0.043724
K03048	-2878	7509	6.9128e-06	0.000186
K12256	-2.8776	1.6385	0.02322	0.049522
K14205	-2.8767	4.8436	0.0010653	0.0064226
K02804	-2.8762	5137	0.00073874	0.0049876
K05916	-2.8663	4781	0.00088844	0.0057023
K02821	-2.8626	5.6076	0.0020879	0.0098481
K01857	-2.86	4.1678	0.011177	0.028435
K00662	-2859	7.3274	7.2963e-05	0.0011194
K13052	-2.8584	7.5442	8.8167e-06	0.0002189
K00694	-2.8581	3.6217	0.015754	0.037185
K03475	-2.8537	5.5629	0.0089331	0.024005
K19745	-2.8447	4.5402	0.0022243	0.0098612
K08964	-2.8442	3.7535	0.012472	0.030825
K03471	-2.8408	7.4987	1.1832e-05	0.00027148
K10896	-2.8406	-0.76441	0.013101	0.03203
K18354	-2.8406	-0.76441	0.013116	0.032054
K10848	-2.8406	-0.76441	0.013139	0.032094
K04046	-2.8399	4.4204	0.0028192	0.011617
K01631	-2.8358	3.5223	0.021433	0.046473
K01226	-2.8352	5.0194	0.0028032	0.011582
K02478	-2835	4.4801	0.013363	0.03254
K19572	-2.8347	-1.1197	0.013833	0.033417
K13281	-2.8329	7.3851	7.2914e-05	0.0011194
K08965	-2.8317	3.4453	0.019894	0.043703
K03888	-2.8309	3.5785	0.014182	0.034078
K03887	-2.8309	3.5785	0.014243	0.034196
K09932	-2.8307	3.7724	0.015907	0.037435
K15975	-2.8289	5.3492	0.00035178	0.0036049
K08967	-2.8231	3735	0.013193	0.032184
K17472	-2822	3.5521	0.015648	0.036967
K09969	-2.8217	4.0825	0.0099968	0.026176
K13531	-2.82	3.5477	0.015907	0.037435
K11210	-2.82	3.5477	0.015939	0.037487
K02826	-2.82	3.5477	0.015983	0.037489
K02829	-2.82	3.5477	0.015985	0.037489
K02828	-2.82	3.5477	0.015988	0.037489
K06349	-2.82	3.5477	0.015989	0.037489
K06294	-2.82	3.5477	0.015991	0.037489
K02827	-2.82	3.5477	0.015994	0.037489
K06314	-2.82	3.5477	0.015999	0.037489
K00491	-2.8165	3.5556	0.015811	0.037283
K03886	-2.8142	3.5607	0.01558	0.036854
K08168	-2.8039	3.4476	0.020846	0.045381
K06956	-2.8024	7.4994	3.5265e-05	0.00064421
K15973	-2.8003	4.9297	0.0026728	0.01123
K17829	-2.7992	0.27414	0.022505	0.048281
K08969	-2.7962	3.5269	0.016974	0.039267
K08966	-2.7948	3.5256	0.017036	0.039333
K02497	-2.7948	3.5256	0.017064	0.039333
K13639	-2.7947	3.5476	0.023255	0.049571
K03392	-2.7866	1.8739	0.017644	0.040138
K18456	-2.7858	-0.11396	0.022297	0.04798
K08139	-2.7827	-0.17152	0.022047	0.047598
K02298	-2.7785	4.4223	0.0031798	0.012678
K13490	-2.7741	-0.68564	0.017511	0.03992

K19610	-2774	-1.1427	0.022309	0.04798
K18093	-2774	-1.1427	0.022312	0.04798
K19609	-2774	-1.1427	0.022356	0.048035
K07223	-2.7707	4.2302	0.013947	0.033603
K18221	-2.7681	-1289	0.018479	0.041535
K05875	-2.7649	4.2099	0.023392	0.049784
K07823	-2.7646	-0.098398	0.022175	0.047855
K03713	-2.7638	4.7576	0.0028068	0.011588
K04766	-2.7614	3555	0.017673	0.040187
K02761	-2.7595	7105	0.0010391	0.0063129
K07290	-2.7545	3.5444	0.022355	0.048035
K15125	-2.7518	4407	0.012638	0.031123
K03673	-2.7503	4.5574	0.0080123	0.022014
K01589	-2.7427	7.7818	6.7125e-06	0.0001815
K00364	-2.7421	5.0907	0.0021634	0.0098612
K02759	-2.74	6.6233	0.00086081	0.0055774
K01690	-2.7351	4.1359	0.01128	0.028617
K02300	-2.7181	4.3675	0.0050226	0.016028
K02297	-2.7181	4.3675	0.0050699	0.016063
K00130	-2.7118	4.9796	0.00098323	0.0061167
K13488	-2.7051	-0.96579	0.02287	0.048967
K13487	-2.7051	-0.96579	0.022897	0.049007
K06408	-2.7043	7.4378	5.1707e-05	0.00088257
K00917	-2.7008	4.2584	0.021966	0.047498
K13489	-2.6995	-0.85383	0.020723	0.045203
K08989	-2.6915	3.9839	0.013809	0.033388
K00449	-2.6794	3.6073	0.021922	0.047458
K01851	-2.6783	-1259	0.017534	0.039938
K13491	-2.6764	-0.81866	0.022461	0.048223
K11896	-2.6758	4.0143	0.022487	0.048262
K02760	-2.6738	6.9599	0.0011148	0.0066041
K07697	-2.6672	4.3534	0.0044752	0.015624
K03808	-2.6665	4653	0.0053095	0.016345
K18098	-2.6641	-0.5082	0.021233	0.046149
K09975	-2.6616	4.1405	0.017298	0.039549
K02082	-2.6562	4.7974	0.0070737	0.019996
K07789	-2.6511	4.4785	0.0044713	0.015624
K06304	-2.6416	3.5015	0.022978	0.049161
K08994	-2.6388	4207	0.012844	0.031531
K09023	-2.6388	-0.047228	0.023374	0.049774
K00517	-2.6376	3.9043	0.014817	0.035372
K11074	-2.6354	4.2295	0.011088	0.028287
K19267	-2632	4.6438	0.0025564	0.010894
K16079	-2.6192	4.6049	0.0096702	0.025455
K03486	-2.6082	4.7746	0.0055059	0.016604
K07788	-2.6007	4.4122	0.0066167	0.018987
K01531	-2.5908	5.1495	0.01023	0.026645
K06350	-2.5852	3633	0.022572	0.048406
K01299	-2582	7593	2.2381e-05	0.00045444
K01788	-2.5767	7.7539	0,01	0.00026295
K00167	-2.5695	4.2172	0.012322	0.030578
K00166	-2.5615	4.1957	0.012851	0.031534
K09699	-2.5529	4.1616	0.013887	0.033504
K08167	-2.5467	4.4624	0.0094295	0.024966
K03761	-2542	3882	0.023556	0.049967
K09781	-2.5403	4.3463	0.011904	0.029744

K06286	-2.5277	4883	0.0055185	0.016626
K06019	-2.5164	7.4011	0.00025052	0.0027868
K06191	-2.5068	5.2435	0.0061606	0.018004
K01479	-2.5009	5.0089	0.0016486	0.0086917
K00480	-2.4994	3.9411	0.02163	0.046883
K02250	-2.4905	4.2566	0.012191	0.030294
K01223	-2.4761	8.2164	0	3.9594e-05
K05539	-2.4631	4.3107	0.014896	0.03553
K03119	-2.4627	4.4749	0.0057836	0.01715
K02423	-2.4613	4.5136	0.0092401	0.024571
K05836	-2.4459	4.0999	0.020345	0.044557
K07300	-2.4439	5.1529	0.0017265	0.0089853
K04752	-2.4382	4488	0.0071504	0.020173
K13771	-2428	4.6888	0.0049811	0.016019
K04091	-2.4261	4.62	0.0037937	0.01437
K05800	-2.4237	4.3692	0.011212	0.028487
K11209	-2.4211	5.3495	0.00098297	0.0061167
K07708	-2.4181	4.4597	0.0087668	0.02367
K09763	-2.4105	4.1458	0.021083	0.045841
K07275	-2.3955	4.4319	0.011068	0.028263
K01070	-2.3869	4.4288	0.010936	0.028003
K14392	-2.3825	4.5012	0.012295	0.030538
K02444	-2.3678	4.3847	0.015174	0.036082
K03185	-2.3629	4.6765	0.0054876	0.016581
K03746	-2.3555	4.7862	0.0089184	0.024005
K03809	-2.3466	4.6411	0.0052794	0.016291
K00841	-2.3464	4.8989	0.00968	0.025468
K01304	-2.3241	7.7085	5.6768e-05	0.0009396
K07119	-2.3161	4.9663	0.0028236	0.011622
K01894	-2.3155	4.4873	0.011029	0.028204
K00108	-2306	4.9981	0.0030299	0.012214
K03643	-2.3043	4.4177	0.01439	0.034519
K04755	-2.2969	5.0724	0.0034944	0.013517
K11618	-2.2939	4974	0.0089304	0.024005
K02054	-2.2872	5.7605	0.0010786	0.0064676
K05822	-2.2753	4.4284	0.016602	0.038539
K10806	-2.2645	4.3978	0.016037	0.037561
K06938	-2.2601	4.4394	0.013504	0.032812
K01497	-2.2557	4.6257	0.017697	0.040224
K14188	-2251	4.7284	0.0095271	0.025126
K01664	-2.2463	5.3757	0.0043923	0.015589
K04565	-2.23	5.3402	0.0031193	0.012482
K03762	-2.2267	4.4796	0.017319	0.039563
K09862	-2.2239	4.4571	0.015771	0.037211
K07659	-2.2066	4.3754	0.020809	0.04535
K03739	-2.1971	4.6488	0.013159	0.032116
K06190	-2.1854	4.4753	0.016079	0.037612
K06726	-2.1839	5.4335	0.011529	0.029106
K07638	-2.1833	4428	0.018299	0.041182
K05527	-2.1758	4.5313	0.014678	0.035086
K02339	-2.1713	4.5247	0.01501	0.035738
K10805	-2169	5.2813	0.0053789	0.01643
K17716	-2.1689	7.4342	0.0035231	0.013619
K02064	-2.1667	4.6186	0.018602	0.041725
K02063	-2.1667	4.6186	0.018619	0.041747
K16925	-2.1659	4825	0.016479	0.038318

K02168	-2.1517	4.6102	0.023074	0.049309
K11719	-2.1447	4.4399	0.020472	0.044763
K03367	-2.1413	4.6593	0.015251	0.036234
K02062	-2.1383	4622	0.020333	0.044549
K03782	-2.1375	4.5064	0.013377	0.032561
K07177	-2.1367	5.5219	0.0042854	0.015452
K03740	-2.1349	4.7512	0.012963	0.031779
K02800	-2.1205	4.9717	0.016281	0.037922
K06221	-2.12	5.1756	0.010002	0.026176
K01048	-2.1127	5122	0.0079959	0.022002
K15772	-2.1093	7.8715	0.00088534	0.0056946
K10974	-2106	4.5577	0.021335	0.046354
K02245	-2.1055	4.9621	0.019383	0.042991
K03071	-2.1035	4.4784	0.020991	0.045677
K11939	-2.0958	5.0747	0.012037	0.030022
K16301	-2.0958	4.8046	0.017452	0.039818
K07224	-2.0922	4.8433	0.017849	0.040503
K00799	-2.0843	7.0539	0.00021735	0.0025205
K00285	-2.0825	5.6098	0.0024877	0.010716
K07245	-2074	5.1973	0.0088587	0.023895
K12262	-2068	4.77	0.0098162	0.025752
K10111	-2.0617	4.6269	0.012109	0.030159
K02200	-2.0614	4.5994	0.017268	0.039496
K00568	-2061	4.7624	0.014879	0.035505
K04085	-2.0544	4.9796	0.011414	0.028902
K01637	-2.0484	5.6098	0.0039485	0.01465
K07222	-2.0466	4.5547	0.016065	0.037612
K15770	-2.0347	7.9639	0.00058745	0.0046363
K00009	-2.0156	4.6551	0.023532	0.049967
K02299	-2.0155	4588	0.019605	0.04323
K02302	-2.0089	5.1724	0.0092399	0.024571
K03566	-1.9877	5.4124	0.0058169	0.017205
K03449	-1.9872	5.4335	0.007616	0.021213
K11103	-1.9849	5.1854	0.011143	0.028375
K00101	-1.9839	4.7701	0.013361	0.03254
K02053	-1.9702	5.9928	0.0021712	0.0098612
K08224	-1.9461	4.8099	0.017894	0.040587
K07693	-1.9397	5.2382	0.010619	0.027385
K01119	-1.9374	7.8032	0.0024366	0.010554
K00121	-1.9262	5.5211	0.0053246	0.016345
K15771	-1.9247	7.9213	0.0021569	0.0098612
K08987	-1.9196	5.1754	0.015965	0.037489
K05838	-1914	5.3109	0.010615	0.027385
K03417	-1.9017	4.9796	0.019015	0.042426
K00574	-1897	5.6974	0.0065811	0.018919
K09771	-1.8953	4.5749	0.023445	0.049847
K03893	-1.8839	5.1321	0.014973	0.035682
K00381	-1.8828	4.8614	0.016814	0.038948
K09780	-1877	4.9959	0.016721	0.038799
K07778	-1.8745	5.1325	0.016238	0.037854
K00116	-1.8601	5.3775	0.011518	0.0291
K01061	-1.8347	5299	0.011683	0.029338
K00758	-1.8292	5.1117	0.021959	0.047498
K07570	-1.8235	7.7128	0.0020121	0.0097953
K19577	-1.7712	5.8477	0.011915	0.029757
K00140	-1.7559	5.5126	0.010178	0.02655

K07156	-1.7522	5.3866	0.022228	0.047911
K00156	-1.7244	5.3958	0.01777	0.040358
K00135	-1723	6.8939	0.0026763	0.01123
K00325	-1.7188	5.2097	0.019851	0.043679
K06994	-1.7134	6.3376	0.0076454	0.021266
K00362	-1.7024	5.1597	0.023397	0.049784
K00299	-1693	5.5219	0.016229	0.037849
K00242	-1.6711	5.3411	0.02079	0.045332
K03592	-1.6646	7.6917	0.0098521	0.025822
K06916	-1.6637	5367	0.020382	0.044621
K02012	-1.6629	7.8961	0.0036337	0.013936
K02446	-1.6626	7702	0.006987	0.019784
K03929	-1.6513	5.4335	0.01804	0.040784
K00324	-1.6426	5.5934	0.015417	0.036565
K00982	-1.6317	5.4093	0.023089	0.04932
K00526	-1.6198	8.1486	0.0019509	0.0097039
K07305	-1.6103	6.4736	0.0086463	0.023414
K00851	-1.5986	6.2712	0.016075	0.037612
K08974	-1.5762	7.8673	0.0092033	0.024515
K00249	-1.5159	5.9319	0.022037	0.047598
K00344	-1512	6.4738	0.010455	0.027065
K02010	-1.4966	7.9313	0.009052	0.024234
K03700	-1.4863	8002	0.0063847	0.018495
K00674	-1.4637	8.0091	0.0092056	0.024515
K17074	-1.4607	8.6649	0.0060069	0.01764
K01255	-1.2082	8.1855	0.023063	0.049304
K02032	0.75196	10202	0.016742	0.038814
K02057	0.75582	10862	0.017797	0.040402
K02056	0.76875	9.8874	0.020511	0.044813
K02028	0.78474	10579	0.020825	0.045352
K02029	0.79496	10691	0.018948	0.042295
K11189	0.83552	9.7753	0.023161	0.049435
K02016	0.86864	10973	0.012098	0.030146
K00655	0.87453	10031	0.012978	0.031802
K03466	0.87464	10.04	0.010844	0.027794
K06180	0.87582	11092	0.019259	0.042882
K01356	0.89251	9.6767	0.01692	0.03916
K00763	0.89438	9.7178	0.019476	0.042991
K03530	0.90327	10458	0.022218	0.047908
K00820	0.90424	9.8388	0.018888	0.042246
K07025	0.90705	10148	0.014264	0.03423
K00805	0.90714	9.7292	0.017121	0.039333
K19302	0.90901	9.9527	0.010659	0.027423
K08884	0.91018	10028	0.0077268	0.021434
K03439	0.91043	9.7178	0.018793	0.042104
K02013	911	10.95	0.0077834	0.021569
K00847	0.91151	9.7629	0.017309	0.039557
K03699	0.91183	9.5588	0.023367	0.049774
K01142	0.91571	9.8616	0.014456	0.03466
K03100	0.91739	10748	0.009804	0.025745
K01996	0.91919	9.8083	0.011112	0.028308
K02036	0.92133	9.8406	0.01415	0.034018
K03569	0.92574	10494	0.014075	0.033852
K03442	0.92629	9.6893	0.020398	0.044638
K01995	0.93005	9.7925	0.010336	0.026846
K08998	0.9311	9.6173	0.018522	0.041594

K01953	0.93335	9.8924	0.013267	0.032335
K01424	0.93677	9.6852	0.018152	0.04092
K05592	0.94445	9.7635	0.013243	0.032292
K14155	0.94555	9.7555	0.011225	0.028504
K07658	0.94564	9.6418	0.021365	0.046381
K03217	0.95288	9937	0.0072195	0.020305
K01624	0.95298	9985	0.0063039	0.018327
K02030	0.95423	10961	0.0039839	0.014723
K02109	0.95468	9.8883	0.010448	0.027057
K03496	0.95506	10672	0.0067125	0.019161
K01489	0.95517	9752	0.013571	0.0329
K02945	0.95691	9.7838	0.015707	0.037092
K01778	0.95698	9.7604	0.014018	0.033729
K01998	0.96073	9.8741	0.0063795	0.018495
K00059	0.96146	11311	0.0028401	0.011664
K00014	0.96236	9.9358	0.0066799	0.019112
K01951	0.9627	9.9445	0.0063863	0.018495
K00012	0.96832	9625	0.018847	0.042189
K06959	0.9701	9.6751	0.014615	0.034981
K01997	0.97423	9.8679	0.0060275	0.017681
K03324	0.97538	9.7383	0.012758	0.031389
K02495	0.97552	10674	0.0062093	0.018117
K01952	0.97624	10264	0.004154	0.015126
K00286	0.97764	9.8565	0.0092707	0.024632
K02954	0.97765	9.9098	0.0063597	0.018457
K00088	0.97819	9.9452	0.0053175	0.016345
K00876	0.97888	9906	0.0082844	0.022613
K04486	0.98212	9.4944	0.017716	0.040252
K01586	0.98382	9.8892	0.0090247	0.024211
K02111	0.98388	9.8241	0.011762	0.029445
K03630	0.98404	9.8562	0.012431	0.030764
K02108	0.98434	9.8239	0.011753	0.029445
K00134	0.98456	9.9932	0.0054044	0.016459
K02114	0.98486	9821	0.011821	0.029549
K11754	0.9869	9.8948	0.0070765	0.019996
K00973	0.98695	9.7912	0.015258	0.036234
K02115	0.98741	9.8229	0.011532	0.029106
K00948	0.98815	9.9334	0.0050388	0.016028
K01710	0.98835	9783	0.013882	0.033504
K01449	0.98865	9.5094	0.014942	0.035624
K02110	0.99019	9.8259	0.011153	0.028386
K01893	0.99023	9662	0.013569	0.0329
K01465	0.99121	9.9369	0.0057486	0.017083
K03544	0.9916	9.9098	0.0060244	0.017681
K00567	0.99192	9.7195	0.010643	0.027397
K02040	0.99223	9.9392	0.0050907	0.016082
K05810	0.99282	9.6176	0.012591	0.031051
K02039	0.99309	9.7438	0.0090671	0.024241
K06217	0.99351	9.8738	0.0086763	0.023484
K01921	0.99448	9.9695	0.0042563	0.015399
K00873	0.99752	9.9028	0.0063815	0.018495
K03686	0.99941	10028	0.004296	0.015473
K01956	0.99948	9.8441	0.0093475	0.024801
K02335	0.99992	9.9081	0.0051653	0.01613
K07052	1.0008	10243	0.0037851	0.014347
K02356	1001	9.8968	0.0061031	0.017855

K01619	1.0024	9.7777	0.0089217	0.024005
K02493	1.0025	9.9087	0.0050638	0.016063
K01759	1.0036	9.9524	0.0032503	0.012883
K09458	1.0048	9.9743	0.005537	0.016645
K01992	1005	12412	0.0033336	0.013071
K09761	1.0052	9.8004	0.010638	0.027397
K00382	1.0055	9.9831	0.0048343	0.015925
K02909	1.0059	9.8982	0.0055968	0.016741
K01735	1.0084	9.8626	0.0079937	0.022002
K00661	1.0089	9.6368	0.010587	0.027327
K01887	1.0092	9906	0.0046591	0.015737
K03629	1.0093	9.8197	0.0081514	0.022328
K01835	1.0123	9.8053	0.0088942	0.023955
K00067	1013	9.6744	0.01344	0.032685
K03168	1.0139	9.8872	0.0055884	0.016725
K01934	1014	9.7942	0.0078312	0.021669
K00640	1.0145	9.8575	0.0083925	0.022863
K01868	1.0162	9.8968	0.0052494	0.01625
K01756	1.0165	9.8914	0.0055338	0.016644
K06173	1017	10.01	0.0034258	0.013347
K00891	1.0172	9.9891	0.0043857	0.015585
K04069	1.0175	10687	0.0047234	0.015815
K01972	1.0177	9.9182	0.0047376	0.015837
K10773	1.0183	9.8922	0.0057369	0.017058
K03438	1.0196	9.9973	0.003994	0.01474
K01104	1.0212	10412	0.0019731	0.009759
K00859	1022	9.8472	0.0074816	0.020902
K02834	1.0222	9836	0.0071046	0.020065
K04078	1.0249	9.9082	0.0044929	0.015624
K04771	1025	9.9874	0.0026348	0.011139
K12267	1.0253	9.29	0.020999	0.045677
K01866	1.0255	9.9141	0.0040677	0.014871
K03091	1.0276	11507	0.0031455	0.012568
K00858	1.0276	9.8894	0.0050366	0.016028
K06158	1.0281	9.8445	0.011068	0.028263
K04077	1.0285	9.8982	0.0050099	0.016019
K03565	1.0286	9.7892	0.008308	0.022666
K01783	1029	9.8921	0.004904	0.016015
K01714	1.0291	10252	0.0027373	0.011387
K00981	1.0301	9.8896	0.0048389	0.015925
K01448	1.0304	10949	0.0027489	0.011427
K01265	1.0306	10.26	0.0022091	0.0098612
K01937	1.0311	9.8813	0.0052709	0.016281
K01803	1.0315	9.9107	0.0040572	0.014863
K01776	1032	9.8213	0.0068592	0.019503
K07107	1.0327	9.9961	0.0040602	0.014864
K01867	1.0334	9.8874	0.0049886	0.016019
K01733	1.0339	9.9071	0.0049719	0.016019
K01881	1.0346	9.8852	0.0051857	0.01613
K00761	1.0346	9.8262	0.0069698	0.019756
K03665	1.0352	9.8775	0.0053241	0.016345
K03657	1.0359	10963	0.0025861	0.010992
K02283	1.0361	8.5921	0.021941	0.04748
K12573	1.0363	9757	0.0094569	0.024968
K03210	1.0371	9.8192	0.0078504	0.021678
K07699	1.0384	9.4781	0.0096025	0.025289

K03624	1.0387	9983	0.0034595	0.01342
K03783	1.0387	9.7009	0.010509	0.027178
K06997	1.0389	9.8832	0.0049647	0.016019
K00600	1.0396	9.8864	0.0049572	0.016019
K03631	1.0398	9.8516	0.0065657	0.018895
K03218	1.04	9.8773	0.0046609	0.015737
K01151	1.0407	9.7006	0.0081654	0.022356
K00942	1.0409	9.8952	0.0041954	0.015246
K08303	1041	10715	0.0042434	0.01537
K01892	1.0416	9.8823	0.0049388	0.016019
K00075	1.0418	9.8783	0.0049485	0.016019
K03595	1.0422	9.8556	0.0064441	0.018618
K00688	1.0426	9956	0.0030818	0.012368
K09903	1.0432	9.8815	0.0048398	0.015925
K02968	1.0452	9.8652	0.0066273	0.018993
K01872	1.0454	10094	0.0024373	0.010554
K00826	1.0454	9.9788	0.0036802	0.014041
K02824	1.0454	9631	0.0089765	0.024093
K03101	1.0459	9.9135	0.0030209	0.012204
K09811	1046	9.8353	0.005996	0.017617
K00762	1.0461	9.8917	0.0046544	0.015737
K01875	1.0463	9.8805	0.0046742	0.015755
K03470	1.0463	9.8576	0.0061576	0.018004
K01491	1.0468	9.8826	0.0046646	0.015737
K03723	1.0476	9.8801	0.0047255	0.015815
K02563	1.0479	9.8795	0.004741	0.015838
K03076	1.0483	9.8799	0.0046638	0.015737
K09748	1.0489	9.8235	0.0066928	0.019129
K02343	1.0492	9.8651	0.0056657	0.016901
K07089	1.0493	9.5234	0.015121	0.035972
K09816	1.0498	9.7459	0.0081839	0.022395
K03284	1.0502	9.9957	0.004352	0.015537
K01810	1.0505	9.8571	0.0056702	0.016905
K03703	1051	9.8803	0.0045971	0.015724
K00700	1051	9.7892	0.0072918	0.020477
K01945	1.0511	9.8634	0.005531	0.016644
K01870	1.0513	9.8698	0.0054042	0.016459
K00800	1.0514	9.8811	0.0046757	0.015755
K00057	1.0515	9879	0.0045178	0.015635
K07478	1.0517	9.8823	0.0042656	0.015399
K04043	1.0519	9.8832	0.0044379	0.015624
K00969	1.0522	9.8871	0.0044484	0.015624
K01939	1.0523	9.8782	0.0045521	0.015647
K02860	1.0523	9.8547	0.0055819	0.016715
K03531	1.0524	9875	0.0054889	0.016581
K03106	1.0526	9.8635	0.0055084	0.016604
K03070	1.0528	9.8921	0.0041164	0.015029
K04485	1.0531	9.8382	0.0067143	0.019161
K09817	1.0532	9.7491	0.0079851	0.021994
K04068	1.0532	9642	0.0083656	0.022801
K11991	1.0533	9.8533	0.0059151	0.017418
K01869	1.0534	9.8784	0.0044782	0.015624
K00554	1.0536	9.8783	0.004373	0.01558
K01889	1.0537	9.8645	0.0054409	0.016492
K02518	1054	9.8819	0.0044435	0.015624
K02902	1054	9.8779	0.004534	0.015647

K00133	1.0541	9.8793	0.0043784	0.01558
K01873	1.0542	9.8777	0.0045747	0.015691
K01736	1.0545	9.8772	0.0047541	0.015872
K03584	1.0546	9.8671	0.0056446	0.016866
K02886	1.0547	9.8775	0.0045385	0.015647
K02996	1.0547	9.8775	0.0045397	0.015647
K02600	1.0547	9.8775	0.0045437	0.015647
K03551	1.0547	9.8775	0.0045439	0.015647
K03625	1.0547	9.8775	0.0045499	0.015647
K01924	1.0548	9.8874	0.0044873	0.015624
K03536	1.0548	9.8578	0.005818	0.017205
K03702	1.0551	9.8783	0.0044435	0.015624
K03177	1.0551	9.8735	0.0055669	0.016689
K07447	1.0552	9861	0.0054402	0.016492
K03043	1.0554	9.8822	0.0043329	0.015498
K00919	1.0554	9.8614	0.0062454	0.018192
K01000	1.0555	9878	0.0045129	0.015635
K09710	1.0555	9.8752	0.005435	0.016492
K02986	1.0556	9.8782	0.0044299	0.015624
K02895	1056	9.8773	0.0045025	0.015624
K02838	1.0562	9.8624	0.005325	0.016345
K03977	1.0562	9.8624	0.00533	0.016346
K03110	1.0562	9.8624	0.0053339	0.016349
K02341	1.0562	9.8738	0.0054322	0.016492
K02990	1.0564	9.8728	0.0055481	0.016659
K02519	1.0565	9.8817	0.0044167	0.015624
K02916	1.0566	9.8623	0.0053522	0.016385
K06207	1.0568	9875	0.0053547	0.016385
K03501	1.0572	9.8601	0.0053478	0.016382
K03553	1.0575	9.8774	0.0044279	0.015624
K06187	1.0577	9.8759	0.0050947	0.016085
K04096	1.0578	9.8773	0.0044906	0.015624
K01929	1.0578	9.8764	0.0044986	0.015624
K03664	1058	9.8765	0.0044952	0.015624
K02528	1058	9.8764	0.0044979	0.015624
K01056	1058	9.8766	0.0045018	0.015624
K00954	1058	9.8762	0.0050468	0.016036
K03687	1.0581	9.8765	0.0044855	0.015624
K04066	1.0581	9.8764	0.0044904	0.015624
K02963	1.0581	9.8765	0.0044906	0.015624
K02836	1.0581	9.8764	0.0044907	0.015624
K02935	1.0582	9.8764	0.0044834	0.015624
K02338	1.0582	9.8764	0.0046244	0.015724
K03550	1.0582	9.8762	0.0050076	0.016019
K01933	1.0582	9.8758	0.0050746	0.016065
K03979	1.0583	9.8764	0.004614	0.015724
K02994	1.0583	9.8764	0.0046159	0.015724
K03685	1.0583	9.8764	0.0046161	0.015724
K03596	1.0583	9.8764	0.0046185	0.015724
K02967	1.0583	9.8764	0.0046227	0.015724
K02982	1.0583	9.8764	0.0046253	0.015724
K02988	1.0583	9.8764	0.0046293	0.015724
K02965	1.0583	9.8764	0.00463	0.015724
K02992	1.0583	9.8764	0.0046354	0.015724
K02961	1.0583	9.8764	0.004643	0.015724
K02952	1.0583	9.8764	0.0046436	0.015724

K02950	1.0583	9.8764	0.0047333	0.015832
K02946	1.0583	9.8764	0.0047756	0.015875
K02939	1.0583	9.8764	0.0047848	0.015875
K02931	1.0583	9.8764	0.0048677	0.016007
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K02892	1.0583	9.8764	0.0049083	0.016015
K02878	1.0583	9.8764	0.004937	0.016019
K02881	1.0583	9.8764	0.0049373	0.016019
K02879	1.0583	9.8764	0.0049394	0.016019
K02876	1.0583	9.8764	0.004948	0.016019
K02887	1.0583	9.8763	0.0049715	0.016019
K02357	1.0583	9.8764	0.0049746	0.016019
K02863	1.0583	9.8764	0.0049854	0.016019
K02871	1.0583	9.8764	0.0049909	0.016019
K02867	1.0583	9.8764	0.0049909	0.016019
K02835	1.0583	9.8763	0.0049992	0.016019
K02904	1.0583	9.8763	0.0050049	0.016019
K02888	1.0583	9.8763	0.005005	0.016019
K00962	1.0583	9.8763	0.0050091	0.016019
K01890	1.0583	9.8763	0.0050106	0.016019
K02956	1.0585	9.8763	0.0049887	0.016019
K02864	1.0585	9.8763	0.0049965	0.016019
K01925	1.0587	9906	0.0045054	0.015624
K02340	1.0587	9.8756	0.0051062	0.016098
K02959	1.0588	9.8762	0.0049945	0.016019
K01883	1059	9.8785	0.0042653	0.015399
K02911	1.0591	9.8773	0.004374	0.01558
K01923	1.0594	9.8806	0.0042271	0.015331
K02890	1.0594	9.8759	0.005024	0.016028
K02520	1.0594	9.8656	0.0051623	0.01613
K01588	1.0595	9.8775	0.0043186	0.015488
K04075	1.0598	9.8757	0.005037	0.016028
K06942	1.0599	9.8779	0.0043326	0.015498
K00783	1.06	9.7697	0.0068529	0.019495
K02337	1.0601	9.9261	0.0038699	0.014523
K00604	1.0601	9.8882	0.0039223	0.014574
K03601	1.0604	9.8666	0.0054134	0.016463
K01775	1.0605	10067	0.0020104	0.0097953
K06941	1.0612	9916	0.0036339	0.013936
K02907	1.0612	9.8411	0.005939	0.017478
K03602	1.0614	9.8663	0.005425	0.016489
K11175	1.0618	9.8599	0.0052453	0.01625
K02874	1.0619	9.8752	0.0050983	0.016087
K00925	1.0621	9.8756	0.0046058	0.015724
K01591	1.0626	9.8745	0.0051235	0.016129
K03046	1.0628	9.8818	0.0041379	0.015078
K00927	1.0631	9.8748	0.0048095	0.015875
K03075	1.0631	9.8747	0.0050696	0.016063
K03040	1.0637	9.8832	0.0040566	0.014863
K00609	1065	9.8927	0.0037662	0.014298
K02314	1.0659	9937	0.0032267	0.01282
K02316	1.0659	9887	0.0040114	0.014774

K01620	1.0665	9.6952	0.0077677	0.021537
K02503	1.0669	9.8748	0.0049669	0.016019
K00939	1.0672	9.8868	0.003875	0.014523
K01689	1.0681	9.9144	0.0028941	0.011832
K01990	1.0682	12646	0.0015264	0.0081977
K01179	1.0683	9.7091	0.0048913	0.016015
K00760	1.0684	9.8743	0.0050123	0.016019
K06925	1.0685	9.8569	0.005031	0.016028
K00645	1.0686	9.8687	0.0051837	0.01613
K03469	1069	9.8661	0.0057136	0.016998
K03671	1.0691	10811	0.0033121	0.013035
K15633	1.0691	9605	0.0082496	0.022552
K07082	1.0696	9.8558	0.0048839	0.016015
K03524	1.0709	9.8951	0.0033124	0.013035
K01874	1.0714	9.9023	0.0034313	0.013359
K01938	1.0743	9.6314	0.0068093	0.019411
K03073	1.0747	9.8664	0.0053904	0.016439
K01358	1.0753	10219	0.0014364	0.007841
K00806	1076	9.8883	0.0032274	0.01282
K07444	1076	9.6334	0.0084919	0.023087
K11753	1.0779	9.9021	0.0032389	0.012847
K04567	1.0788	9.8824	0.0035455	0.013676
K09815	1.0792	9.8285	0.0059698	0.017549
K02970	1.0797	9.8225	0.0059508	0.017503
K01520	1.0799	9.8248	0.0050636	0.016063
K03695	1.0816	9.8401	0.0045764	0.015691
K02948	1082	9.8687	0.0046466	0.015725
K01926	1.0827	9.7047	0.0066188	0.018987
K02238	1.0829	9925	0.0026289	0.011122
K00949	1.0852	9.6293	0.0062435	0.018192
K01880	1.0855	9.6789	0.0069084	0.019602
K14742	1.0871	9.7163	0.0068789	0.019539
K02914	1.0885	9.8423	0.0044464	0.015624
K03495	1.0894	9.8237	0.0053769	0.01643
K00648	1.0903	10181	0.0029479	0.011953
K03572	1.0906	9.8302	0.0053815	0.01643
K03650	1.0906	9.8225	0.0054917	0.016581
K06287	1.0921	9.8646	0.0047715	0.015875
K02346	1.0929	10055	0.0011123	0.0066041
K06400	1.0929	9.2798	0.018065	0.040798
K03437	1.0941	9.9069	0.0031912	0.012714
K00764	1.0951	10029	0.0018583	0.0094594
K03555	1.0957	9.8337	0.005146	0.01613
K00789	1.0958	9.9599	0.0019068	0.0095777
K02313	1.0963	9.9076	0.0027002	0.011275
K01791	1.0967	9.6291	0.0076531	0.021266
K03615	1.0976	9.6894	0.0066407	0.01901
K00656	1.0977	10.07	0.0028478	0.011687
K03978	1.0979	9.81	0.0049072	0.016015
K00566	1.0986	9.9284	0.0023626	0.010307
K09812	1.0997	9.8964	0.0022018	0.0098612
K07560	1.0997	9834	0.0043762	0.01558
K16264	1.0997	7.8347	0.023434	0.049843
K07566	1.1003	9.8506	0.0043615	0.01556
K00991	1.1006	9.8032	0.0045198	0.015635
K00528	1.1008	9.8069	0.005579	0.016715

K13038	1.1024	9853	0.0040107	0.014774
K00602	1.1029	9.9331	0.0026433	0.011161
K03527	1.1057	9.8686	0.004206	0.015275
K05366	1.1074	9.9318	0.0027703	0.011472
K07462	1.1095	9.8346	0.0042622	0.015399
K01808	1.1096	9863	0.0040416	0.014863
K11749	1.1102	9.8469	0.0044702	0.015624
K01534	1.1103	9.9085	0.001175	0.0067631
K03570	1.1109	9.8262	0.0043485	0.015534
K01662	1.1113	9.8646	0.0041283	0.015063
K01770	1.1113	9.7597	0.0051075	0.016098
K03545	1.1126	10084	0.0018255	0.0093447
K00773	1.1129	9.8471	0.0043164	0.015488
K03526	1.1131	9.84	0.0046855	0.015764
K03742	1.1141	9.7399	0.0053878	0.016439
K00099	1117	9823	0.0043368	0.015502
K12410	1118	9.7947	0.004515	0.015635
K00703	1.1182	9.7567	0.0052272	0.016222
K00527	1.1188	9.8843	0.0023355	0.010205
K02003	1.1198	12189	0.00089217	0.0057195
K02601	1.1205	9.9556	0.0019285	0.0096548
K02358	1.1221	10016	0.0018353	0.0093775
K03823	1.1225	8.6365	0.010057	0.026283
K06973	1.1245	9659	0.0059124	0.017418
K01876	1.1289	9.9776	0.0013399	0.0074681
K01719	1.1295	8.0115	0.015943	0.037487
K06178	1.1325	9.8152	0.0039567	0.014652
K01886	1.1338	9.6378	0.0068642	0.019507
K03310	1.1356	10099	0.00069605	0.0047642
K03613	1136	9.5789	0.0060559	0.017736
K03734	1.1389	9.8733	0.0030803	0.012368
K13789	1.1422	9.7752	0.0036862	0.014041
K06949	1.1429	10088	0.0016772	0.0088121
K03424	1.1448	10161	0.0014394	0.0078447
K07456	1.1481	9731	0.0039893	0.014733
K03617	1.1499	9.6065	0.0050364	0.016028
K07088	1.1505	10159	0.00044985	0.0042363
K00215	1.1505	9.9915	0.0014164	0.0077599
K03722	1.1521	8.2373	0.018831	0.04217
K01512	1.1523	8.1665	0.018897	0.042249
K04487	1.1535	10442	0.00036579	0.0037137
K01752	1.1552	10346	0.00062049	0.0046427
K06168	1.1565	9.8803	0.0022271	0.0098657
K04079	1.1565	9.7503	0.0038228	0.01443
K03786	1.1598	9.8172	0.0032837	0.012969
K01548	1.1603	7.9455	0.023146	0.049423
K09022	1.1642	9.8288	0.0026442	0.011161
K09936	1.1658	8.1416	0.023171	0.049438
K02371	1.1667	9.6621	0.0044081	0.015624
K02355	1.1672	10851	0.0014431	0.0078505
K04758	1.1682	10787	0.00074171	0.0049907
K01679	1.1702	7.7605	0.018212	0.041031
K01462	1.1717	10429	0.0004539	0.0042671
K18332	1.1719	9.3934	0.01027	0.026738
K01493	1.1731	9.7571	0.0034526	0.013412
K03614	1.1767	9643	0.0037968	0.014371

K07043	1.1768	9724	0.0029896	0.012105
K17828	1.1793	9.7699	0.0030023	0.012147
K07112	1.1803	8.1605	0.019856	0.043679
K03497	1.1816	10882	0.00061838	0.0046396
K05808	1183	9.7957	0.0032992	0.013021
K06966	1183	8.3755	0.010277	0.026743
K03498	1.1856	10106	0.00070202	0.0047991
K18707	1.1857	9.7284	0.0039125	0.014557
K02823	1.1863	9.7657	0.0028554	0.0117
K06881	1187	9.7903	0.0027761	0.011487
K10439	1.1873	9192	0.0046899	0.015764
K01903	1.1873	7.7519	0.019875	0.043685
K01006	1.1885	9731	0.0033314	0.013071
K06409	1.1892	9.8101	0.0019313	0.0096599
K18682	1.1938	9.7969	0.0025091	0.01078
K00266	1.1972	10156	0.00067974	0.0046997
K01153	1.1976	9.7901	0.0020565	0.0098481
K06153	1.2006	10123	0.00062431	0.0046458
K03169	1.2096	10066	0.00056475	0.0045835
K05601	1.2113	9.6546	0.0035423	0.013674
K00784	1.2132	8.3224	0.009496	0.025057
K02078	1.2194	10472	0.00030415	0.0032003
K01950	1.2219	9.7859	0.0025675	0.01093
K01338	1.2229	9.9237	0.0013365	0.0074639
K00334	1.2246	9.7592	0.0040481	0.014863
K10441	1.2261	9.0428	0.0043033	0.015483
K06969	1.2314	10067	0.00071101	0.0048423
K17759	1.2366	9706	0.0023776	0.010364
K06381	1.2388	9.7916	0.00093917	0.0059211
K00338	1.2409	7.5247	0.016257	0.037883
K02428	1.2417	10168	0.00074868	0.0050114
K07238	1.2453	9.9414	0.00057504	0.0046363
K00945	1.2475	10214	0.00036877	0.0037191
K03701	1248	10169	0.0006575	0.0046997
K00791	1.2506	10104	0.00071541	0.0048662
K01091	1.2533	10457	0.00013816	0.0017631
K07056	1.2556	10131	0.00066991	0.0046997
K07636	1.2583	10119	0.0013639	0.007583
K00615	1.2619	10734	0.00015679	0.0019375
K00257	1.2621	7.9526	0.018224	0.041031
K07071	1.2623	7.7793	0.012619	0.031103
K00951	1.2656	10115	0.00062395	0.0046458
K00046	1.2686	8.1004	0.007494	0.020916
K00342	1.2714	7582	0.012368	0.030622
K02470	1277	10379	0.00015635	0.0019365
K03525	1.2779	9.9058	0.00058933	0.0046363
K00666	1.2786	8.3321	0.0080828	0.022174
K03856	1.2799	9.6879	0.00094347	0.0059369
K01079	1.2827	7.3755	0.01743	0.039783
K06603	1.2831	7.0786	0.019776	0.043555
K02020	1.2837	8.4031	0.0063182	0.018347
K00339	1.2839	7.6053	0.012657	0.031154
K02469	1.2842	10381	0.00014941	0.0018717
K00928	1.2856	10295	0.0002557	0.0028101
K00340	1.2864	7.6701	0.013547	0.0329
K00341	1.2865	7.6267	0.012037	0.030022

K01902	1.2876	7.8549	0.01054	0.027219
K02049	1.2886	10344	0.00011076	0.0014828
K01495	1.2886	8.6124	0.0035555	0.013705
K02650	1.2911	6.8812	0.023054	0.049304
K03427	1.2929	9.9146	0.00035933	0.0036686
K03655	1.2973	10322	0.00025034	0.0027868
K01190	1.3046	10215	0.0010991	0.0065612
K01676	1.3073	7.6106	0.014625	0.034988
K00265	1.3074	7765	0.0085198	0.02314
K07568	1.3083	10098	0.00054206	0.0044625
K03667	1309	7.2221	0.015255	0.036234
K01419	1.3099	7.2218	0.015434	0.03659
K02051	1.3111	10241	0.00010485	0.0014499
K01738	1.3137	10338	7.5445e-05	0.0011479
K01955	1.3148	10347	0.00031865	0.0033088
K02413	1.3215	7764	0.0092155	0.02453
K01409	1.3256	10225	0.00010619	0.0014647
K00845	1326	10336	0.00025299	0.0028014
K01745	1.3281	7.9627	0.0088682	0.023908
K01154	1329	9.9593	0.00025337	0.0028014
K07090	1.3327	10817	5.0973e-05	0.00087278
K03737	1.3328	9802	0.00096339	0.0060206
K02418	1.3336	7.8899	0.010429	0.027023
K01661	1.3365	7.6612	0.0083587	0.022793
K02034	1.3375	10302	9.1224e-05	0.0013078
K02551	1.3391	7.6602	0.0082576	0.022563
K00790	1.3424	10513	5.6055e-05	0.00093346
K07105	1.3445	8.0699	0.0054531	0.01652
K02050	1.3494	10385	6.3309e-05	0.001017
K03415	1.3524	7.5489	0.0078783	0.021733
K02004	1.3531	12202	9.0302e-05	0.0013014
K01915	1.3587	10603	6.9446e-05	0.0010837
K03499	1.3604	10525	5.8075e-05	0.00095407
K07058	1.3629	9.3252	0.00068741	0.0047228
K08600	1.3702	7.9123	0.0069833	0.019783
K10716	1.3709	7.7758	0.0072501	0.020381
K07718	1.3718	9.4105	0.0018994	0.0095616
K02426	1374	7.8321	0.0062371	0.018188
K03711	1.3784	10477	0.00012852	0.0016677
K09685	1.3826	6.8442	0.019166	0.042695
K07258	1.3856	10635	1.5286e-05	0.00033802
K01802	1.3856	7.9479	0.0071905	0.020237
K02031	1.3866	9.5475	0.00043373	0.0041201
K00275	1.3876	7.4574	0.012785	0.031443
K07259	1.3919	7.5172	0.0072845	0.020467
K02407	1.3989	8.4385	0.0033188	0.013041
K06972	1.4017	7.0338	0.010671	0.027441
K03271	1.4075	6.9182	0.019899	0.043703
K07777	1.4092	6.9955	0.015465	0.03663
K02033	1.4129	10.3	5.0114e-05	0.00086317
K01468	1.4196	7.65	0.005231	0.016225
K03798	1.42	10526	2.7303e-05	0.00052326
K01712	1.4205	7.7085	0.0049413	0.016019
K07053	1.4248	10364	3.8152e-05	0.00068774
K00208	1.4295	8.1068	0.0025766	0.01096
K01633	1.4338	8.1266	0.0025369	0.010851

K02035	1.4342	10634	2.8977e-05	0.00054955
K05349	1.4343	10609	0.00022323	0.0025723
K07667	1.4372	8.7959	0.0017608	0.0090903
K03924	1.4381	9.6548	0.00018258	0.002187
K02018	1.4401	8.4373	0.0017843	0.0091746
K06910	1.4409	7.4855	0.0094504	0.024968
K00868	1.4421	8.9058	0.0019443	0.0096937
K01665	1.4439	7.6791	0.0065308	0.018814
K00337	1.4451	7.7472	0.0046196	0.015724
K07720	1.4458	9697	0.00021498	0.0024983
K01812	1.4471	7.9621	0.0029085	0.011832
K03797	1.4485	10348	0.00017633	0.002145
K03299	1.4493	7.3969	0.0086153	0.023353
K01811	1.4521	7.5405	0.0093984	0.024895
K00241	1.4553	8.1482	0.0020516	0.0098481
K06199	1.4566	8724	0.00064072	0.0046953
K09770	1.4569	7.3923	0.0050899	0.016082
K02396	1.4575	8.7783	0.00097391	0.0060725
K07646	1.4606	8.9049	0.00095547	0.0059849
K00657	1.4618	8.0332	0.0019857	0.0097633
K01533	1.4635	8.0545	0.0036841	0.014041
K00240	1.4672	8.2097	0.0017761	0.0091518
K18349	1.4701	7.2172	0.021418	0.04646
K00940	1.4712	8.4524	0.0011117	0.0066041
K03455	1.4724	8.0059	0.0033315	0.013071
K01192	1.4765	6847	0.021707	0.04703
K03640	1.4768	7.1332	0.011635	0.029245
K09793	1485	7.1557	0.010108	0.02639
K01610	1.4864	8.1666	0.0018911	0.0095581
K00001	1.4881	7.3872	0.013155	0.032116
K02411	1.4928	8.2481	0.0011078	0.0066041
K00024	1.4951	8.1804	0.0015891	0.008443
K06934	1.4978	6.2498	0.018011	0.040734
K06113	1.4994	7.1987	0.012163	0.030253
K02619	1.5017	7.5794	0.0054125	0.016463
K06223	1.5042	6.9234	0.0071915	0.020237
K03639	1.5056	8.6628	0.00077613	0.0051635
K03980	1.5074	7.8897	0.0017088	0.0089318
K00850	1.5105	10758	9.0232e-06	0.00022301
K03644	1.5133	8.2178	0.0019763	0.009759
K01613	1.5149	8.4855	0.0010515	0.0063624
K03088	1.5156	12601	1.1939e-05	0.00027171
K01971	1.5164	8.0629	0.0036083	0.013875
K03750	1.5189	8582	0.0013794	0.0076258
K02017	1.52	8.3088	0.0013821	0.0076332
K03306	1.52	8.1409	0.0019214	0.0096283
K19055	1.5234	8.3737	0.0011089	0.0066041
K01935	1.5371	7.4074	0.008759	0.023661
K07078	1.5377	7.3208	0.010316	0.026806
K02548	1.5443	8031	0.0013748	0.0076152
K04518	1.5464	8.0372	0.0011666	0.0067572
K01751	1.5476	6.3266	0.013561	0.0329
K19265	1.5477	8.2082	0.0016581	0.0087336
K02041	1.5489	6.3844	0.0093654	0.024822
K01749	1.5514	8.6669	0.00050793	0.0043862
K04762	1.5528	7.8055	0.0023322	0.010199

K01207	1553	9.1329	0.00020526	0.002403
K00796	1.5532	8.8643	0.00024219	0.0027275
K01687	1.5544	9.7513	0,02	0.00043365
K03118	1.5573	8.3838	0.00088475	0.0056946
K01537	1.5574	10483	9.2743e-06	0.00022514
K07386	1566	7.62	0.002272	0.0099838
K17103	1567	8436	0.00091006	0.0057704
K01673	1.5673	8.7775	0.0005475	0.0044835
K03637	1.5709	8.5517	0.00060253	0.0046363
K01271	1.5719	8.4211	0.00066193	0.0046997
K15532	1.5726	7.0859	0.020043	0.043965
K03801	1.5758	7.9393	0.0019451	0.0096937
K00639	1.5766	8.2285	0.0024791	0.010687
K10979	1.5769	7.9281	0.003437	0.013371
K16053	1.5844	7.2538	0.003425	0.013347
K00433	1.5862	7.2989	0.00732	0.020531
K03590	1.5889	8.3753	0.00058285	0.0046363
K00872	1.5913	8.5977	0.00040415	0.0039327
K01647	1.5922	9.7122	0,02	0.00045102
K03587	1.5924	8.2527	0.00087379	0.0056414
K07260	1.5952	8.3908	0.0024741	0.010674
K00104	1.5971	7.6117	0.0026816	0.011234
K00330	1.5972	7.9308	0.0020704	0.0098481
K00331	1.5979	7.9215	0.0020713	0.0098481
K09955	1.5983	8.2106	0.0022485	0.0099049
K07735	1606	7.2733	0.0036752	0.014041
K02647	1.6061	8.7288	0.0002457	0.0027606
K03811	1.6061	7.7477	0.0018863	0.0095484
K00616	1.6073	9.1948	0.00012333	0.0016116
K07149	1.6079	7084	0.012794	0.031449
K00077	1.6081	9.4586	5.9032e-05	0.00095911
K02406	1609	9.4031	5.8166e-05	0.00095407
K07220	1609	7.9453	0.0020617	0.0098481
K07130	1.6101	6.1096	0.0091263	0.02435
K02843	1.6108	6.6744	0.0087001	0.023536
K01567	1.6117	7.7403	0.0013733	0.0076152
K01524	1614	9.0036	0.00017864	0.0021547
K02397	1.6208	8.4016	0.00055533	0.004534
K00343	1.6238	7.8085	0.0013761	0.0076152
K00606	1.6248	8.9211	0.00011846	0.0015629
K00281	1.6255	7.7766	0.0014639	0.0079405
K02190	1.6255	7.4454	0.0023832	0.01038
K07652	1626	7.6851	0.0014143	0.0077561
K01840	1.6316	8.1218	0.0018934	0.0095581
K03313	1.6342	7.5417	0.0015037	0.0081079
K18968	1.6377	5.8493	0.021373	0.046381
K03594	1.6385	7.6848	0.0028113	0.011598
K03814	1.6414	7.4421	0.0075212	0.020981
K03610	1.6417	8383	0.00044089	0.0041735
K07271	1.6427	7.3992	0.0052657	0.016281
K03706	1.6482	8.2297	0.00064558	0.0046997
K01579	1.6492	8.6375	0.00015024	0.0018736
K03183	1.6493	8367	0.00047687	0.004277
K13653	1.6516	9.9797	8.8296e-05	0.0012778
K03832	1653	8.7463	0.0010325	0.0062871
K11928	1.6535	8.2159	0.00029613	0.0031468

K03116	1.6541	8.5796	0.00038418	0.0038155
K01438	1.6575	7.5578	0.0015121	0.0081449
K00819	1.6578	7.2079	0.004332	0.015498
K07738	1.66	9.1845	6.5994e-05	0.0010459
K17723	1.6613	6.1079	0.0076624	0.021266
K01652	1.6616	10166	7.7049e-07	5.0704e-05
K03148	1.6687	6.3202	0.020444	0.044719
K02404	1.6689	7.6927	0.00074747	0.0050094
K00074	1.6718	9.3241	2.0589e-05	0.00042917
K00970	1.6749	7.9937	0.0010519	0.0063624
K07126	1.6759	8.4268	0.00033468	0.0034426
K04767	1.6768	6.3687	0.0074145	0.020726
K01308	1.6793	6.4698	0.0064657	0.018656
K09922	1.6794	6523	0.0073228	0.020531
K07496	1681	6.6468	0.0045476	0.015647
K01761	1.6816	7.4655	0.00353	0.013636
K01585	1.6816	7.3599	0.0044347	0.015624
K00817	1.6851	9.6476	5.1613e-06	0.00015321
K02401	1.6907	8.6373	8.6996e-05	0.0012671
K03589	1.6923	9.2389	4.7695e-05	0.00082965
K01897	1694	9.9751	3.0374e-05	0.00057012
K01464	1.6943	7.6671	0.0015913	0.0084436
K11085	1.6994	8.2776	0.00050652	0.0043862
K01918	1.7001	8.9893	5.2799e-05	0.0008984
K03179	1.7002	7.9633	0.00081482	0.0053621
K03409	1.7009	5.8686	0.016091	0.037618
K04759	1.7064	10786	1.0307e-06	0,06
K01845	1707	9.0063	0,07	0.0011091
K01698	1.7105	8.6404	0.00019994	0.0023587
K15372	1.7139	5.8765	0.020815	0.04535
K07443	1714	8536	0.00018844	0.0022473
K02398	1.7145	8336	0.00030009	0.0031765
K00798	1.7154	7.8833	0.0012975	0.0072763
K01999	1.7188	9.7641	8.1754e-06	0.00020866
K19350	1.7191	7.8417	0.0019813	0.009762
K00318	1.7191	6958	0.0062	0.0181
K11358	1.7279	7.4096	0.0010062	0.0062101
K01696	1728	9.3253	2.4292e-05	0.00047899
K14445	1.7323	5.6776	0.019145	0.042664
K03559	1.7332	8.1973	0.00083903	0.0054639
K00004	1.7349	5.8337	0.013479	0.032764
K01653	1.7432	9.6903	2.6966e-06	0.0001002
K02415	1.7439	7.3634	0.00094886	0.0059502
K03654	1.7445	9.7369	3.3052e-06	0.0001156
K03281	1.7459	7.8477	0.00088619	0.0056946
K02389	1.7478	8.7039	8.1316e-05	0.0012102
K05311	1.7483	7.0265	0.0015811	0.0084169
K05595	1.7484	7973	0.00079591	0.0052758
K00031	1.7487	9.2253	2.3082e-05	0.00046351
K07154	1.7497	7.6839	0.001096	0.0065588
K01805	1.7511	7.5976	0.0010975	0.0065588
K02851	1.7515	8.6538	0,05	0.00090649
K02654	1.7535	9.1371	3.8057e-05	0.00068774
K00831	1.7537	9.3853	1.1826e-05	0.00027148
K03628	1.7545	9.2263	0,03	0.00062374
K11927	1.7558	8422	0.0003731	0.0037392

K06975	1.7564	8.8428	0.00011464	0.0015198
K03752	1.7576	7.8183	0.00064083	0.0046953
K01737	1.7577	8.7642	9.3835e-05	0.0013382
K03453	1.76	7.8332	0.00069186	0.0047474
K03800	1.7607	9.1936	2.8908e-05	0.00054955
K03518	1.7653	8.2155	0.001877	0.0095193
K00558	1.7664	9.7303	1.4799e-06	7.0908e-05
K04749	1.7719	7.0949	0.0013395	0.0074681
K00937	1.7761	9.0832	2.7149e-05	0.00052214
K18928	1.7767	7.3153	0.002514	0.01078
K06894	1.7774	7425	0.0028353	0.011653
K03406	1.7776	11.48	2.2087e-07	3.5482e-05
K07114	1.7785	9.0934	0.00049167	0.0043399
K06919	1.7808	6.6213	0.0032203	0.012811
K03303	1.7809	6.6726	0.0026562	0.011195
K00989	1.7813	8.4552	6.6066e-05	0.0010459
K02409	1.7814	8.7459	5.9176e-05	0.00095911
K01790	1.7818	9.1951	4.2088e-05	0.00074397
K11473	1782	6.5661	0.0039491	0.01465
K00620	1.7854	9.0632	0,03	0.00054123
K01755	1.7856	9.4665	6.4342e-06	0.00017749
K02067	1.7864	8.1888	0.00073988	0.0049892
K06926	1.7878	5.6831	0.016128	0.037645
K18929	1.7887	7.3107	0.0022392	0.0099032
K02585	1.7887	5.9156	0.013614	0.03299
K04562	1789	7.8171	0.00026972	0.0029173
K09765	1.7899	8.2609	0.00012171	0.001598
K01008	1.7924	8.13	0.00032949	0.003402
K09153	1.7935	7.0244	0.0036359	0.013936
K05776	1794	6.7264	0.0053201	0.016345
K02422	1.7951	9134	1.7893e-05	0.00038629
K03413	1.7968	9.5017	5.4359e-06	0.00015697
K02042	1.7988	7.0993	0.0017026	0.0089079
K07343	1.7992	6.9867	0.0042164	0.015302
K03320	1.8006	9.6033	2.5973e-06	9.7168e-05
K03402	1.8024	9.3611	1.3234e-05	0.00029993
K04656	1.8058	6.5259	0.0053193	0.016345
K07668	1.8124	7.8682	0.00024984	0.0027868
K07091	1.8128	7.8688	0.00084029	0.0054639
K00766	1816	9.1453	2.0665e-05	0.00042917
K01975	1821	8.5337	0.0001787	0.0021547
K02203	1822	6.1058	0.0055437	0.016656
K00878	1.8231	8.9627	1.8451e-05	0.00039523
K08722	1.8251	7525	0.001165	0.0067572
K01715	1.8264	8172	5.5937e-05	0.00093346
K04761	1.8264	7.3719	0.0010174	0.0062188
K07729	1831	9.7777	3.5111e-06	0.00011912
K03833	1.8326	6115	0.0094511	0.024968
K01991	1835	8.2605	0.0015261	0.0081977
K11752	1836	9.1369	1.1178e-05	0.00026204
K02492	1.8368	8.5724	8.2078e-05	0.0012182
K10541	1.8381	6.9032	0.0045628	0.015674
K04061	1.8387	8.1463	0.0002222	0.0025659
K10542	1.84	6.9049	0.0044854	0.015624
K02279	1.8408	6.6633	0.002532	0.010838
K01895	1.8434	9.0614	3.3419e-05	0.0006146

K15727	1847	7.2756	0.013067	0.031976
K19158	1847	5.7502	0.017901	0.040587
K01958	1.8471	7.8102	0.00038989	0.0038465
K02591	1.8497	6.0071	0.0093662	0.024822
K01077	1.8499	8.3009	7.8787e-05	0.0011805
K02437	1.8525	8.9947	3.0581e-05	0.00057203
K03186	1.8525	7.8016	0.00036249	0.0036896
K03652	1.8546	8.0274	0.00117	0.0067626
K00029	1.8559	7845	0.0010968	0.0065588
K05364	1.8563	8.3645	6.4166e-05	0.0010278
K04654	1.8583	6.2439	0.0067903	0.019367
K02400	1.8585	9.1171	9.4054e-06	0.00022731
K00610	1.8624	8.3251	8.3447e-05	0.0012285
K00030	1.8637	6.3294	0.012116	0.030162
K01007	1865	7051	0.002248	0.0099049
K00794	1.8652	9.2007	0,01	0.0002248
K01034	1.8661	7.5303	0.00075593	0.0050414
K00946	1.8662	8.3149	0.00016802	0.0020577
K02517	1.8664	8.1658	0.00020792	0.0024215
K00793	1867	9.1524	1.0527e-05	0.00025
K02006	1.8692	7.5509	0.0007064	0.0048229
K06196	1.8697	8.7494	4.5784e-05	0.00079896
K00008	1.8698	7.9709	0.00010718	0.0014746
K00147	1.8709	9.5453	1.7144e-06	7.4319e-05
K00931	1.8724	9545	0	7.3471e-05
K08218	1.8756	7.1564	0.0012399	0.0070543
K00058	1876	10103	6.1528e-08	3.3154e-05
K00853	1.8767	6.9286	0.0019891	0.0097633
K05540	1.8795	7.2799	0.0004111	0.0039672
K02044	1.8798	6.7864	0.00094841	0.0059502
K01657	1.8814	9371	4.9735e-06	0.00014988
K18369	1.8847	6.0168	0.0066859	0.01912
K02837	1.8852	9.3055	3.0878e-06	0.00010881
K01681	1.8866	9558	2.9281e-06	0.00010662
K00239	1.8867	8.8463	4.4352e-05	0.00077894
K06905	1.8874	5.3943	0.014231	0.034183
K08744	1.8897	7.7776	0.00035758	0.0036575
K04773	1.8913	8.1483	0.00024859	0.0027824
K08679	1.8918	6.6595	0.0031603	0.012618
K01693	1.8931	9.1886	8.6595e-06	0.00021699
K06897	1.8937	8.0711	8.7347e-05	0.0012689
K07814	1.8944	7.7516	0.00037274	0.0037392
K02066	1.8967	8.3056	0.00050118	0.0043729
K03608	1.8978	8.2948	0,08	0.0011805
K05606	1.8984	7.9005	0.00071971	0.0048833
K03696	1.8995	9.5586	1.5685e-06	7.3225e-05
K02408	1.9002	9.0087	0,01	0.0002248
K02421	1.9006	9.0094	9.8704e-06	0.00023542
K07175	1.9006	8.0444	0.00039725	0.0039095
K03925	1.9027	9.5412	1.7757e-06	7.6054e-05
K02897	1.9028	8.9616	1.9514e-05	0.00040993
K02556	1.9043	9.2261	6.4873e-06	0.00017806
K03474	1.9051	7.8025	0.00091067	0.0057704
K00652	1.9061	7.9841	0.00030378	0.0032003
K02662	1.9062	7.0888	0.0019397	0.0096843
K13652	1.9067	6.1858	0.0041356	0.015078

K05367	1.9069	7333	0.0012137	0.006916
K02416	1911	9.0401	8.2232e-06	0.00020891
K01695	1.9116	9.4717	1.6455e-06	7.3402e-05
K02417	1.9126	9.0804	6.9653e-06	0.00018649
K03517	1913	9.3043	1.1007e-05	0.00025914
K19117	1.9137	5.4029	0.0076617	0.021266
K19119	1914	5408	0.0076067	0.021198
K19118	1914	5408	0.007639	0.021266
K06872	1.9158	8.1588	0.00028851	0.003096
K02419	1.9173	9.0821	6.4284e-06	0.00017749
K02420	1.9202	9093	5.9899e-06	0.00016692
K01129	1.9213	9543	7.5511e-07	5.0298e-05
K07402	1922	8.7391	4.4965e-05	0.00078718
K12257	1.9245	8.9034	0,02	0.00046645
K02387	1.9254	9.0672	6.5765e-06	0.00017956
K02410	1.9257	9.0594	6.6078e-06	0.00017956
K01818	1.9262	6.7047	0.0012699	0.007173
K01480	1.9264	8.5326	1.6508e-05	0.00036067
K00633	1.9274	5.0168	0.018595	0.041725
K02412	1.9281	9.1026	5.5776e-06	0.00015867
K00941	1.9297	9.2722	2.9828e-06	0.00010714
K01940	1.9314	9.5595	5.9477e-07	4.2815e-05
K00788	1.9326	9.5579	5.8291e-07	4.2815e-05
K02405	1.9333	9.0793	5.3665e-06	0.00015614
K06920	1.9337	7.9863	8.2372e-05	0.0012193
K00930	1.9344	9.5534	6.6534e-07	4.6591e-05
K02669	1.9358	9.2165	5.1983e-06	0.00015348
K00145	1.9365	9.5589	5.9574e-07	4.2815e-05
K00605	1937	8.9927	2.2771e-05	0.00046066
K11720	1.9372	8.0126	0.00017843	0.0021547
K00013	1.9379	9.5435	0	4.6235e-05
K01057	1939	7.4406	0.0013647	0.007583
K03412	1.9396	9.0924	4.58e-06	0.00014064
K01704	1.9402	9.5572	5.5317e-07	4.2815e-05
K02500	1.9413	9.5585	5.8664e-07	4.2815e-05
K00575	1.9435	9.1485	3.4135e-06	0.00011726
K03340	1.9436	8.2072	9.7399e-05	0.0013818
K09810	1.9438	8.0004	0.00041296	0.0039781
K02501	1.9439	9.5513	5.8298e-07	4.2815e-05
K14761	1.9496	8.9366	7.4994e-06	0.00019884
K08301	1.9526	9.0426	1.1288e-05	0.00026295
K02557	1.9568	9.5209	9.7967e-07	5.7537e-05
K07979	1.9578	9.6895	2.0477e-06	8.3465e-05
K09118	1.9585	6.6226	0.0012757	0.0071907
K07181	1.9585	6.5569	0.0024971	0.010748
K01596	1962	7699	0.00036682	0.0037172
K15460	1962	7.6047	0.0010258	0.0062602
K01667	1.9628	7.4774	0.0014525	0.0078907
K01649	1.9633	10019	0	2.1047e-05
K00705	1964	9.3271	3.3229e-06	0.0001156
K02429	1.9642	8.1639	0.00061462	0.0046363
K05837	1.9658	9.6051	2.6637e-07	3.5814e-05
K06209	1.9677	8.5518	1.8815e-05	0.00039833
K02388	1.9683	9149	3.5516e-06	0.00011974
K11755	1.9703	9.2747	1.6338e-06	7.3402e-05
K08982	1.9711	5.9746	0.009189	0.024495

K02523	1.9718	7.9402	0.00040154	0.0039235
K00767	1.9723	9.4554	4.1445e-06	0.00013238
K03521	1.9734	9765	5.3126e-07	4.2815e-05
K12340	1.9734	8.3907	0.00049657	0.0043605
K01658	1.9744	9.1912	7.6489e-06	0.00020086
K06179	1.9756	8.9376	5.3096e-06	0.00015592
K02536	1.9768	8.1929	0.00038425	0.0038155
K03563	1.9777	9.0558	0	0.0001387
K00821	1978	8.9286	5.4892e-06	0.00015697
K14652	1979	9.1705	9.4591e-06	0.0002276
K15923	1.9793	7.6899	0.00056376	0.0045828
K03407	1.9813	9.1944	2.2956e-06	8.8828e-05
K13018	1.9815	5.9261	0.021994	0.04754
K02687	1.9825	9.5173	4.1713e-07	3.9971e-05
K03609	1.9827	8.9764	5.3741e-06	0.00015614
K18014	1.9834	5.6896	0.0051553	0.01613
K04751	1.9848	8.6447	0,04	0.00066579
K01703	1.9858	9.5614	0	4.2815e-05
K18640	1.9866	8346	0.00012232	0.0016021
K00294	1.9875	7.1699	0.0013499	0.007516
K00018	1988	8.0882	3.0044e-05	0.00056635
K02390	1.9883	9.1315	3.0011e-06	0.00010714
K02171	1.9899	7.2106	0.0014049	0.0077279
K02065	1.9916	8.1894	0.0002401	0.0027165
K07813	1.9917	8144	5.4389e-05	0.00091421
K01372	1.9922	7.6466	0.00040614	0.0039332
K00052	1.9923	9.5789	0	3.9956e-05
K03770	1.9927	7.8663	0.00029707	0.0031506
K07403	1.9945	7.3485	0.0012096	0.0069036
K00226	1.9947	7653	0.00047238	0.0042699
K07277	1.9953	8.0603	0.00026055	0.0028405
K03708	1.9959	7.8179	5.4397e-05	0.00091421
K00053	1.9967	9.5315	5.3926e-07	4.2815e-05
K00765	1.9971	9.5069	7.1315e-07	0,05
K09155	1.9984	7.2157	0.0022232	0.0098612
K05807	1.9987	7.8496	0.00027639	0.0029776
K06306	1.9989	8.3684	7.1148e-05	0.001104
K02502	1.9995	9.1251	3.7744e-06	0.00012345
K07003	2.0007	8318	5.7137e-05	0.00094285
K07183	2.0008	9.0865	5.4663e-06	0.00015697
K01814	2.0015	9.5015	4.4363e-07	4.0684e-05
K00833	2.0022	7.3851	0.00030364	0.0032003
K00278	2.0039	9.5426	1.1126e-06	6.0205e-05
K06391	2.0053	7.2543	0.00053748	0.0044413
K19294	2.0055	8.8789	2.5847e-05	0.00050241
K09808	2.0057	8.7789	9.4513e-05	0.0013444
K00797	2.0061	8.6658	7.6896e-06	0.00020096
K06923	2.0075	8.5325	3.5553e-05	0.0006473
K06042	2.0079	8.4794	7.7851e-06	0.00020249
K00854	2.0112	9.3668	7.4102e-07	4.9969e-05
K03558	2.0125	7.7767	0.00026295	0.0028553
K09704	2.0131	6.9168	0.0037056	0.014095
K06167	2014	7.6469	0.00052627	0.0044154
K07588	2.0147	7.9766	0.00014981	0.0018725
K18350	2.0151	7.0686	0.0036601	0.01401
K05825	2.0154	6.8106	0.00061589	0.0046363

K03522	2018	9.7694	4.5436e-07	4.0684e-05
K04652	2.0196	7.7452	0.00022068	0.0025537
K03688	2.0201	7974	7.3343e-05	0.0011221
K06208	2.0205	6.7335	0.00051701	0.0043986
K03269	2.0213	7.5434	0.00044191	0.004176
K03826	2.0217	6.9882	0.0015923	0.0084436
K07037	2.0242	8.5067	2.3434e-05	0.00046544
K01035	2.0248	7.5704	0.00036849	0.0037191
K03585	2.0267	8.8074	0.00017319	0.0021115
K12952	2.0272	7.1454	0.0017383	0.0090169
K18139	2.0273	6.3277	0.015098	0.035933
K03154	2.0274	9059	3.8484e-06	0.00012512
K01993	2.0291	8.6278	5.0254e-05	0.00086317
K00050	2.0308	5.7313	0.019732	0.043475
K00856	2.0319	5.1606	0.011001	0.028144
K06871	2.0362	9.4975	0	3.7129e-05
K00782	2.0362	7.6	0.00040131	0.0039235
K06861	2.0389	8.0506	0.00019354	0.0022981
K04041	2041	8.4698	1.6024e-05	0.00035292
K05989	2.0417	7.6152	0.0014955	0.0080717
K01627	2.0425	7.9764	0.00019409	0.0022996
K09251	2.0438	6.3204	0.0010092	0.0062122
K03152	2.0454	8.9535	2.3082e-06	8.8828e-05
K01885	2.0478	9.7284	3.1061e-07	3.6882e-05
K08217	2.0501	6.7791	0.0003856	0.0038155
K07736	2.0507	9.0491	0	0.00014988
K03408	2.0509	9.5805	2.7487e-07	3.5814e-05
K04651	2.0513	7.91	8.8429e-05	0.0012778
K02014	2052	10.48	4.3887e-06	0.00013776
K01241	2.0527	7.3312	0.00081055	0.0053578
K01740	2.0531	10207	6.4047e-09	1.8065e-05
K00297	2.0542	9.3493	1.3646e-06	6.7759e-05
K02122	2.0545	8.7021	0,03	0.00059711
K00172	2.0551	5.8784	0.0017456	0.0090458
K00091	2.0551	5.8092	0.014496	0.034726
K00595	2.0554	8.4095	7.2874e-06	0.00019416
K02304	2.0572	8.4074	1.4564e-05	0.00032603
K02189	2061	8.4637	4.9011e-06	0.00014872
K09778	2.0613	5.1876	0.017378	0.039682
K19221	2064	9.1776	9.2194e-07	0,06
K15342	2065	8.4344	5.7638e-06	0.00016145
K09888	2.0658	9.4603	4.5286e-07	4.0684e-05
K02527	2.0658	7.9255	0.00017756	0.0021547
K00912	2.0665	7951	0.00022862	0.0026178
K07391	2.0674	9.5886	2.6711e-07	3.5814e-05
K00748	2.0674	7.9612	0.00017255	0.0021084
K01817	2.0675	9.3774	1.7823e-06	7.6054e-05
K06310	2.0686	6594	0.0010179	0.0062188
K00262	2.0687	9.6374	1.3133e-07	3.3154e-05
K01847	2069	8.6947	0.00017927	0.0021568
K00950	2.0696	8.6985	1.5235e-05	0.00033802
K00169	2.0698	5.8172	0.0020728	0.0098481
K04070	2.0722	8.3357	8.7002e-06	0.00021699
K02588	2.0731	6509	0.001157	0.0067236
K19049	2.0737	4.8179	0.021352	0.046371
K07460	2.0744	9.5681	2.1802e-07	3.5482e-05

K01609	2.0762	9.3998	1.4537e-06	0,07
K05934	2.0783	8.4698	4.3508e-06	0.00013758
K07216	2.0807	7.6499	5.6267e-05	0.00093413
K02586	2.0808	5.8994	0.0128	0.031451
K01599	2.0834	8.8199	1.5191e-06	7.2151e-05
K03307	2.0837	9.3463	8.5037e-07	5.5294e-05
K07406	2.0848	5.7716	0.0020253	0.0098154
K00283	2.0861	8.0828	7.7894e-05	0.0011753
K00548	2.0871	9.8263	8.0825e-08	3.3154e-05
K09777	2.0873	8.5871	3.3735e-06	0.00011662
K02392	2.0875	10012	6.6149e-09	1.8065e-05
K07263	2.0881	7.8131	0.00048381	0.0043137
K03775	2.0888	7658	0.00025298	0.0028014
K00282	2.0896	8.0931	7.7271e-05	0.0011691
K06041	2.0906	7.9213	9.1201e-05	0.0013078
K00818	2.0935	8.2686	6.0365e-05	0.00097261
K03327	2.0955	8.4263	9.2193e-06	0.0002248
K09181	2.0958	7.3721	0.00027102	0.0029255
K00131	2.0997	7.1231	0.012627	0.03111
K08978	2.1021	7.9636	0.00029227	0.0031301
K07171	2.1023	9.5702	4.3021e-07	4.0514e-05
K03149	2.1025	8.4875	2.2981e-05	0.00046318
K15726	2.1032	7.7522	0.0028966	0.011832
K00097	2.1039	8.6221	1.1361e-05	0.00026295
K00651	2105	9.2196	5.0209e-07	4.2815e-05
K03113	2.1054	7.5918	0.00027732	0.0029818
K00677	2.1061	8.1191	0.00010144	0.0014243
K12343	2.1146	4.4914	0.017599	0.040052
K00768	2.1172	8.8325	9.6415e-07	5.7241e-05
K07011	2.1186	8.5078	0.00072533	0.0049153
K01711	2.1193	7.8803	0.00033408	0.0034426
K02361	2.1202	7.2495	0.00069283	0.0047481
K02315	2.1215	9.4279	2.7662e-07	3.5814e-05
K02217	2124	8.8159	1.2456e-06	6.2996e-05
K09457	2.1261	7.6938	0.00046524	0.0042699
K02224	2.1266	8.7352	2.3462e-06	8.9615e-05
K15635	2.1267	7.7334	0,03	0.00056635
K16881	2.1282	6.4878	0.00045661	0.0042699
K03605	2.1284	6.2225	0.0029018	0.011832
K09749	2.1288	8.1987	5.6127e-06	0.00015884
K01012	2.1301	9.5683	1.7106e-07	3.3154e-05
K03561	2.1301	8.8656	8.6496e-05	0.0012666
K01628	2.1367	8.8725	1.8413e-06	7.6527e-05
K01284	2.1389	8.4383	5.4111e-05	0.00091421
K12524	2.1407	7382	0.00019934	0.0023567
K01089	2141	7.1741	0.00040963	0.00396
K03205	2.1441	9.7567	2.0709e-06	8.3788e-05
K07315	2.1452	7.0559	0.00022782	0.0026142
K05946	2147	8.1944	1.1879e-05	0.00027148
K04074	2151	8.9327	3.8845e-06	0.00012555
K00634	2152	7.2833	0.00038522	0.0038155
K03411	2154	8.9475	1.7995e-06	7.6195e-05
K03147	2.1545	8.9565	9.1425e-07	0,06
K07045	2.1546	8.4952	6.5958e-05	0.0010459
K00979	2.1549	8068	7.1417e-05	0.001105
K06411	2155	8.6354	4.3578e-06	0.00013758

K04653	2.1553	7.6787	6.5456e-05	0.0010454
K03410	2.1556	8.8756	2.1967e-06	8.6945e-05
K06395	2.1581	7755	0.00024614	0.0027606
K11785	2.1588	5.4285	0.0038149	0.01442
K04076	2.1591	6.9504	0.0002667	0.0028903
K08963	2.1605	8.7279	1.2192e-06	6.2291e-05
K07133	2.1608	9.8159	4.1114e-05	0.00072911
K07168	2.1616	4.5193	0.020108	0.044072
K02007	2.1637	8.3477	9.6385e-06	0.0002309
K13626	2.1641	8.9632	1.8181e-06	7.6389e-05
K06382	2.1641	8.8055	2.9072e-06	0.00010657
K03718	2.1665	8.0776	6.7055e-05	0.001058
K03666	2.1671	8.7265	2.2336e-06	0,09
K11615	2.1674	5448	0.0056599	0.016893
K07166	2.1678	8.9519	1.2203e-06	6.2291e-05
K03325	2.1727	8.2697	0.00036275	0.0036896
K09157	2.1758	8.9628	1.0889e-06	6.0205e-05
K15778	2.1768	5.4755	0.0087283	0.023601
K01611	2178	8.6722	4.0267e-06	0.00012938
K01026	2.1794	7.6412	4.9944e-05	0.00086317
K18856	2.1796	6.7159	0.0040299	0.014832
K03839	2.1797	8.1604	7.8573e-05	0.0011805
K02005	2.1809	9.9124	4.6714e-07	4.1153e-05
K08307	2.1809	7.8213	0.00012854	0.0016677
K03802	2.1809	4.7484	0.023538	0.049967
K01849	2183	5.2927	0.002759	0.011442
K00929	2.1857	7.6226	0.0015318	0.0082187
K06438	2.1862	8.8484	2.1279e-06	8.4837e-05
K07576	2.1866	8598	1.8929e-06	7.7735e-05
K00971	2.1885	8.7776	8.3558e-06	0.00021129
K03771	2.1926	8.5489	0.00011829	0.0015629
K05936	2.1931	8.8944	1.0782e-06	6.0205e-05
K06864	2.1974	8.46	0	0.00012037
K11105	2.1979	7664	4.0923e-05	0.00072808
K03296	2.1985	9.4494	4.8901e-05	0.00084794
K10540	2.1988	7.8256	0.00023848	0.002708
K09764	2.1996	7.4337	0.00034107	0.0035018
K06397	2.2027	8.8783	0	7.3402e-05
K06396	2203	8.8789	1.6249e-06	7.3402e-05
K06392	2203	8.8789	1.6304e-06	7.3402e-05
K06283	2.2044	8878	1.6375e-06	7.3402e-05
K00184	2.2047	6.1757	0.01892	0.042284
K06385	2.2057	8.9612	1.1796e-06	6.1362e-05
K02008	2.2068	8.2592	7.8327e-06	0.00020276
K06394	2.2081	8847	1.8494e-06	7.6527e-05
K11690	2.2099	5.7975	0.0037819	0.014345
K04084	2.2103	7.8036	0.00014377	0.0018136
K11614	2.2106	5.3812	0.0048868	0.016015
K08309	2.2109	8.4043	5.0216e-06	0.00014988
K16927	2.2113	7.3714	0.00025808	0.0028298
K01571	2.2125	8.8326	2.9961e-06	0.00010714
K14441	2.2139	9.5155	1.5515e-07	3.3154e-05
K03074	2.2153	8.8945	0	0.00010814
K07079	2.2193	9.4954	2.9619e-07	3.6768e-05
K07723	2.2208	6.7972	0.00012576	0.0016394
K03072	2.2216	8.9267	2.7735e-06	0.00010236

K06393	2223	8.8735	1.5661e-06	7.3225e-05
K06390	2223	8.8735	1.6814e-06	7.3471e-05
K03270	2.2237	7.9799	7.6746e-05	0.0011644
K07164	2.2248	7.9381	0.00023214	0.0026474
K08641	2.2265	7.2815	4.0235e-05	0.00071819
K11783	2.2273	5.3053	0.0037042	0.014095
K15987	2.2295	9.3508	1.1231e-06	6.0205e-05
K18691	2.2298	7.6054	0.00022666	0.0026064
K07085	2.2313	7.5653	2.6913e-05	0.00051943
K07713	2.2331	7351	0.00040076	0.0039235
K02499	2.2335	8.9828	9.4648e-07	0,06
K04477	2.2352	8.4621	5.6749e-06	0.00015977
K02614	2.2374	6.9164	0.00013497	0.0017387
K16089	2.2375	8.6204	7.3657e-05	0.0011238
K02385	2.2377	8.7647	2.4951e-06	9.4642e-05
K13542	2.2419	8916	0	0,06
K15024	2.2421	7.4973	8.0597e-05	0.0012028
K07787	2.2444	6.9439	0.00052238	0.0044154
K04516	2.2445	7.5666	0.00020703	0.0024162
K05515	2.2508	9.7919	3.5614e-08	3.3154e-05
K07005	2.2526	9624	3.0165e-08	3.3154e-05
K06423	2.2563	7.1782	7.0169e-05	0.0010919
K01251	2.2586	8.8475	5.9685e-05	0.0009645
K12251	2.2589	7277	0.00086958	0.0056209
K02227	2.2601	9.2028	1.3285e-07	3.3154e-05
K07316	2.2653	6.3151	0.0013955	0.0076836
K00757	2.2663	8.4786	1.1353e-06	6.0205e-05
K03473	2267	7166	0.0001522	0.0018936
K11537	2.2672	6.9874	0.00025852	0.0028298
K00248	2.2675	7.9944	1.7361e-05	0.0003778
K03092	2.2683	9.3167	4.8813e-07	0,04
K02233	2272	9.2165	1.6108e-07	3.3154e-05
K18866	2.2756	5.9722	0.0016916	0.008867
K03612	2.2775	9.2719	9.8854e-08	3.3154e-05
K08999	2.2782	7.8607	0.00071752	0.0048745
K18348	2279	5.9828	0.0016467	0.0086902
K04720	2.2799	8.8566	3.6924e-07	3.8865e-05
K02124	2.2813	9.0541	1.1304e-06	6.0205e-05
K02123	2.2813	9.0541	1.1328e-06	6.0205e-05
K02231	2.2815	9.1927	1.3846e-07	3.3154e-05
K00348	2.2825	7.2903	0.00023217	0.0026474
K02377	2.2843	7.7864	0.000202	0.0023779
K06284	2.2855	8889	4.8772e-06	0.00014872
K01159	2.2888	9.4256	4.0421e-07	3.9956e-05
K02226	2.2912	9.2233	1.5346e-07	3.3154e-05
K05895	2.2946	7.7713	1.8576e-05	0.00039523
K00721	2.2955	8.8966	9.7738e-05	0.001383
K02232	2.2958	9.1821	1.2464e-07	3.3154e-05
K11381	2.2966	5.9979	0.0080116	0.022014
K19405	2.3007	7921	6.7213e-05	0.001058
K06384	2.3018	7.8471	5.5591e-05	0.0009314
K02188	2302	8.7018	1.8248e-07	3.3154e-05
K07322	2.3022	7.7247	0.00020341	0.0023893
K02118	2.3053	9.1848	9.4197e-07	0,06
K02120	2.3053	9.1848	9.4396e-07	0,06
K02117	2.3054	9.1847	9.3696e-07	0,06

K03394	2.3117	8.6356	5.7413e-07	4.2815e-05
K11784	2.3158	5.7815	0.0010354	0.0062977
K03660	2.3176	8652	1.3486e-06	6.7577e-05
K12373	2.3196	9.1246	2.0901e-06	8.3941e-05
K07705	2.3197	7.3404	0.00015899	0.0019558
K11645	2.3216	6.8236	0.00056383	0.0045828
K13688	2.3235	5.8659	0.0094499	0.024968
K03150	2.3274	9.2612	9.6063e-08	3.3154e-05
K10206	2.3282	9.0446	2.8137e-07	3.5814e-05
K14534	2.3369	7243	6.7485e-05	0.0010592
K11782	2.3385	5.7915	0.00090077	0.0057495
K03093	2342	6.3529	0.00032703	0.0033894
K19271	2.3433	7.6439	3.3364e-05	0.0006146
K01639	2.3526	7.0368	3.9284e-05	0.00070351
K18346	2.3537	6.9671	0.000156	0.0019365
K00170	2359	5.7754	0.00062372	0.0046458
K12960	2.3618	8.3187	3.7001e-07	3.8865e-05
K18285	2.3619	5828	0.00077753	0.0051665
K02119	2.3654	8.5861	1.8596e-05	0.00039523
K00772	2.3723	6.8562	0.004088	0.014936
K01572	2.3776	9.44	6.8887e-07	4.7628e-05
K19165	2.3785	5.7006	0.0025144	0.01078
K02334	2.3911	9.0462	1.8584e-05	0.00039523
K01206	2.3914	9.0712	2.5709e-05	0.00050151
K06143	2.3922	6.6742	0.00029429	0.0031418
K03606	2.3958	7.1955	0.00013649	0.00175
K01173	2.4056	6.1003	0.0018555	0.0094538
K13993	2.4124	9.4836	2.1257e-05	0.00043814
K00812	2.4255	9.5281	2.2109e-05	0.00045102
K02009	2.4286	7.6611	1.9485e-05	0.00040993
K07075	2.4311	6.3932	0.001812	0.0092932
K00171	2.4323	5.4723	0.00071006	0.0048419
K07571	2437	8.7168	0	6.1362e-05
K19411	2.4375	8.3586	0,02	0.00038629
K06001	2.4384	8.7389	2.4018e-07	3.5814e-05
K17992	2.4468	8.1194	9.2304e-05	0.0013198
K06206	2.4511	8.7948	1.0618e-06	6.0205e-05
K06402	2.4529	8165	2.5804e-06	9.7168e-05
K01156	2.4554	6.2451	0.00081122	0.0053578
K01615	2.4575	5.7983	0.001072	0.0064482
K09007	2.4646	5.2619	0.0039562	0.014652
K03803	2.4757	8.5446	1.6456e-07	3.3154e-05
K00983	2.4762	6.0556	0.016118	0.037639
K08678	2.4825	7.2296	0.0016325	0.0086321
K04655	2485	7.5406	7.9912e-06	0.00020589
K03385	2.5001	7.1682	0.00013368	0.0017261
K02103	2.5022	5.7205	0.00026235	0.0028545
K14475	2.5072	5.7085	0.014486	0.034718
K07012	2.5139	7.9462	3.4629e-06	0.00011821
K00895	2515	7.2115	8.4092e-05	0.0012347
K18234	2515	7.3898	0.00011187	0.0014867
K07590	2.5168	8.0777	1.4592e-06	0,07
K06898	2519	8.3603	2.3207e-05	0.00046375
K09121	2.5228	8.3613	2.1385e-05	0.00043912
K18330	2.5243	8.7452	0,07	0.0010617
K06142	2529	9.2967	1.6171e-05	0.00035472

K17073	2.5298	6.4943	0.0013899	0.0076605
K07464	2.5302	8.0393	4.4728e-06	0.00013881
K16363	2.5378	7.5688	0.0048963	0.016015
K06383	2.5408	8.6201	1.4311e-06	7.0422e-05
K01163	2.5443	9.1857	7.7051e-08	3.3154e-05
K01144	2.5558	7.5144	0.0048816	0.016015
K03773	2.5561	8.7283	8.1035e-06	0.0002078
K11051	2.5577	5.6801	0.011327	0.028722
K11050	2.5609	5.6795	0.011213	0.028487
K00350	2.5781	7.2437	0.00010052	0.0014151
K05970	2.5794	8.1814	0.0022339	0.0098876
K01278	2.5812	8.3224	0.0020325	0.0098164
K00351	2.5814	7.2431	0.00010269	0.0014345
K00349	2.5814	7.2431	0.00010355	0.0014402
K00347	2.5814	7.2431	0.00010363	0.0014402
K00346	2.5852	7.2425	0.00010456	0.0014495
K01583	2.5915	5.7526	0.013658	0.033053
K00844	2.5995	4.8769	0.012448	0.030783
K01912	2.6008	9.0583	2.8195e-07	3.5814e-05
K05516	2.6234	7.4155	7.5623e-06	0.00019954
K01848	2.6243	4.7624	0.0027543	0.01144
K02474	2626	7.5189	0.0017872	0.0091746
K00174	2.6398	9.8883	3.7188e-06	0.00012285
K00175	2.6421	9.8827	3.7336e-06	0.00012285
K02666	2.6452	5.5029	0.0019895	0.0097633
K07219	2.6572	6.7586	0.00031087	0.0032466
K09797	2.6822	5.5061	0.0029627	0.012005
K08676	2.6892	6.7029	0.0050198	0.016028
K03738	2.6963	6.0036	0.018528	0.041594
K07138	2.6995	8.1847	1.4313e-05	0.00032173
K16212	2.7156	6.4614	0.0019525	0.0097039
K07099	2.7166	8.2186	1.4133e-05	0.00031899
K09163	2.7194	7.7239	3.3079e-05	0.00061247
K01960	2.7306	7.5849	0.0012516	0.0070846
K01277	2734	7.4708	0.0070739	0.019996
K02121	2742	8.1562	0.00020546	0.002403
K07405	2.75	7.5194	0.0056747	0.01691
K05979	2.7622	7.3585	0.00013714	0.0017543
K00290	2.7705	8.6191	0.00014863	0.0018701
K03931	2.7764	6.6713	0.0034594	0.01342
K13747	2.7892	8.6441	0.00013564	0.0017432
K19091	2.8006	6.4395	2.4773e-05	0.00048497
K06990	2804	4.9843	0.015441	0.03659
K07706	2.8141	6.8294	0.0046892	0.015764
K02241	2.8199	7.1372	2.3264e-05	0.00046375
K00177	2.8729	9.2056	0.00044866	0.0042325
K00179	2888	8.2661	0.00010203	0.001429
K00180	2.8933	8.2769	9.9026e-05	0.0013976
K03332	2.8933	6.8006	0.00067399	0.0046997
K02587	2.9063	4.4268	0.0095777	0.025236
K02594	2.9167	5.1364	0.0024048	0.010449
K15876	2.9205	7.1208	0.0058078	0.017203
K00176	2.9229	9.1602	0.00032851	0.0033983
K13043	2.9349	7.0353	0.00084143	0.0054648
K01787	2.9663	6.9492	8.6995e-05	0.0012671
K13963	2.9725	7.2466	0.00013042	0.001688

K03465	2.9947	7.3689	3.8987e-05	0.00070048
K17489	3.0153	0.069969	0.0091301	0.02435
K00096	3.0277	5.6565	0.001076	0.0064657
K09789	3.0279	5.3353	0.0034421	0.013381
K01186	3.0332	6881	0.0001411	0.0017965
K08282	3042	4.3423	0.0089392	0.024005
K09011	3.0627	7.1763	0.0020014	0.0097865
K00603	3.0657	7.1024	0.00010939	0.0014828
K00196	3.0657	6.9303	0.0015746	0.0084023
K05773	3.0692	4.6164	0.0039101	0.014557
K00198	3.0869	7.2552	0.00072983	0.0049397
K00194	3.0885	1.2214	0.011514	0.0291
K05772	3.1017	4.6714	0.0033929	0.013247
K03077	3.1067	6.2913	0.00117	0.0067626
K18831	3.1117	6.0553	0.0012639	0.0071463
K01654	3.1154	5.4513	0.00087511	0.0056432
K03390	3197	5.9812	0.0024254	0.010522
K03389	3.1981	5.9865	0.0023025	0.010085
K07182	3.2083	4.0253	0.004919	0.016019
K15864	3.2131	-0.44819	0.012319	0.030578
K19090	3.2542	0.04155	0.011041	0.02822
K03388	3.2734	6.0854	0.001605	0.0085028
K02482	3.3193	5.6124	0.0036043	0.013874
K02590	3.3848	4.2444	0.0085796	0.02327
K02589	3.3848	4.2444	0.0085802	0.02327
K02626	3.3953	4.4098	0.0052731	0.016281
K01622	3.4083	-0.22599	0.0031072	0.012449
K01399	3417	-0.77767	0.0061923	0.018087
K02481	3.4313	7.5852	0.0005569	0.00454
K11527	3.4443	4.9969	0.0020417	0.0098338
K00968	3.4646	4.3116	0.010193	0.026574
K10819	3.4672	4352	0.0021091	0.0098511
K09740	3.4873	4.4296	0.0023935	0.010417
K07457	3.5077	4.9405	0.0018969	0.0095616
K07076	3.5439	1.6706	0.0050895	0.016082
K03620	3.5441	4.4572	0.0046395	0.015724
K02584	3.5609	5.4179	0.0005076	0.0043862
K19727	3.5908	-0.79124	0.0051491	0.01613
K19726	3.5908	-0.79124	0.0051519	0.01613
K19725	3.5908	-0.79124	0.0051634	0.01613
K19723	3.5908	-0.79124	0.0051723	0.01613
K12826	3.5908	-0.79124	0.0051763	0.01613
K19741	3.5908	-0.79124	0.0051831	0.01613
K00043	3.5908	-0.79124	0.0051911	0.016138
K11384	3.6074	3.4994	0.0054855	0.016581
K14138	3.6143	1.0235	0.006398	0.018519
K06857	3.7096	4.5468	0.001049	0.0063589
K09729	3.7371	5.4812	8.2825e-05	0.0012227
K07257	3.7505	4.3877	0.0015506	0.0083036
K07321	3.7898	4.9301	3.2113e-05	0.00059711
K03941	3.8143	-0.33455	0.0018927	0.0095581
K17229	3.8143	-0.33455	0.0019101	0.0095805
K01746	3.8698	1.0691	0.0049577	0.016019
K19714	3.8905	4.1105	0.0049745	0.016019
K09126	3.9312	1.7121	0.0033828	0.013226
K15023	4.1016	3.2463	0.0026821	0.011234

K00197	4.1016	3.2463	0.002684	0.011234
K15022	4104	0.05704	0.0018697	0.0094997
K14088	4.1128	4.3518	0.00046754	0.0042699
K06027	4.1552	0.24552	0.0021268	0.0098556
K14086	4.1928	4.5295	0.00016665	0.0020454
K09138	4.2411	0.39352	0.0025123	0.01078
K11261	4.2666	5.5469	0.00018128	0.0021762
K03851	4.3322	3.4507	0.0051325	0.01613
K14089	4.3397	4.1729	0.00057897	0.0046363
K14087	4.3632	4.1682	0.00054342	0.0044634
K11646	4.3664	4.1725	0.0024384	0.010554
K09141	4368	4421	0.0011937	0.0068274
K16846	4.3712	4.0837	0.0026507	0.01118
K16845	4.3712	4.0837	0.002666	0.011219
K00534	4.3839	4.0831	0.0026097	0.011067
K08352	4.3864	4.3014	0.00074194	0.0049907
K14090	4.3984	4.1854	0.0021947	0.0098612
K07151	4.4016	4.1259	0.0024022	0.010447
K07469	4.4195	4.1887	0.0015614	0.0083529
K06873	4.4264	3.9306	0.0026662	0.011219
K18008	4.4267	4.1598	0.0020999	0.0098488
K14091	4.4267	4.1598	0.0021008	0.0098488
K07096	4.4267	4.1598	0.0021025	0.0098488
K06951	4.4267	4.1598	0.0021155	0.0098554
K00437	4.4267	4.1598	0.0021285	0.0098556
K16915	4474	4.31	0.00095681	0.0059863
K11181	4.4769	4.3034	0.00099006	0.0061521
K11180	4.4769	4.3034	0.00099875	0.0061977
K16886	4.4824	4.2735	0.0011168	0.0066091
K16885	4.4824	4.2735	0.0011258	0.0066544
K09133	4.5004	2596	0.0047134	0.015814
K19134	4.5376	1.5408	0.0015157	0.0081562
K13819	4.5503	4.4198	0.00067806	0.0046997
K16180	4.5954	-0.11613	0.0014124	0.0077531
K16182	4.5954	-0.11613	0.0014207	0.0077756
K07488	4.6113	3.8219	0.0018398	0.0093914
K05299	4.6183	3.6087	0.00053649	0.0044398
K00183	4.7202	0.66485	0.0012849	0.0072351
K15898	4.7311	1.6795	0.00058277	0.0046363
K16181	4.7359	-0.64362	0.00023737	0.0027011
K17248	4909	1.2123	0.0024663	0.010649
K09860	4.9801	1.2169	0.0026915	0.011256
K17898	5.3445	1.2415	0.00014229	0.0018066
K17899	5.3445	1.2415	0.00014271	0.0018066
K09944	5579	1.5899	0.00024022	0.0027165
K07097	5579	1.5899	0.00024101	0.0027198
K18284	5.6826	1.1945	0.00080103	0.0053033
K18992	6.9599	1.1767	0.00011061	0.0014828
K05927	6.9599	1.1767	0.00011073	0.0014828
K17251	6.9599	1.1767	0.00011083	0.0014828
K05922	6.9599	1.1767	0.00011092	0.0014828
K08077	6.9599	1.1767	0.00011106	0.0014828
K15896	6.9599	1.1767	0.00011116	0.0014828
K15899	6.9599	1.1767	0.00011116	0.0014828
K07288	6.9599	1.1767	0.00011126	0.0014828
K15897	6.9599	1.1767	0.0001113	0.0014828

K06882	6.9599	1.1767	0.0001113	0.0014828
K15895	6.9599	1.1767	0.00011131	0.0014828

Tabela S10. KEGG pathway map predicted by PICRUST differentially represented in bacterial communities found in mid and hindgut of *Pelidnota luridipes*
(Discriminant KEGG terms according to KO Database - https://www.genome.jp/kegg/ko.html)

Pathway	Midgut	Hindgut	Total	Midgut/ Hindgut
ko00860 Porphyrin and chlorophyll metabolism	2	30	32	15
ko00340 Histidine metabolism	1	15	16	15
ko00720 Carbon fixation pathways in prokaryotes	3	42	45	14
ko00730 Thiamine metabolism	1	14	15	14
ko03018 RNA degradation	1	14	15	14
ko01502 Vancomycin resistance	1	13	14	13
ko01210 2-Oxocarboxylic acid metabolism	2	25	27	0
ko00900 Terpenoid backbone biosynthesis	1	11	12	11
ko00630 Glyoxylate and dicarboxylate metabolism	2	21	23	0
ko01230 Biosynthesis of amino acids	10	104	114	0
ko00541 O-Antigen nucleotide sugar biosynthesis	2	20	22	10
ko00020 Citrate cycle TCA cycle	3	26	29	0
ko00061 Fatty acid biosynthesis	1	8	9	8
ko02040 Flagellar assembly	4	31	35	0
ko00770 Pantothenate and CoA biosynthesis	2	15	17	0
ko01240 Biosynthesis of cofactors	18	128	146	0
ko03420 Nucleotide excision repair	1	7	8	7
ko00710 Carbon fixation in photosynthetic organisms	2	13	15	0
ko00220 Arginine biosynthesis	2	12	14	6
ko01200 Carbon metabolism	16	91	107	0
ko02030 Bacterial chemotaxis	3	17	20	0
ko00550 Peptidoglycan biosynthesis	4	21	25	0
ko00260 Glycine, serine and threonine metabolism	5	26	31	0
ko00250 Alanine, aspartate and glutamate metabolism	4	20	24	5
ko03060 Protein export	3	15	18	5
ko00290 Valine, leucine and isoleucine biosynthesis	2	10	12	5
ko00261 Monobactam biosynthesis	1	5	6	5
ko00780 Biotin metabolism	2	9	11	0
ko00670 One carbon pool by folate	3	13	16	0
ko00910 Nitrogen metabolism	3	12	15	4
ko00660 C5-Branched dibasic acid metabolism	2	8	10	4
ko00430 Taurine and hypotaurine metabolism	1	4	5	4
ko00625 Chloroalkane and chloroalkene degradation	1	4	5	4
ko04142 Lysosome	1	4	5	4
ko05134 Legionellosis	1	4	5	4
ko00400 Phenylalanine, tyrosine and tryptophan biosynthesis	6	23	29	0
ko00680 Methane metabolism	9	33	42	0
ko01110 Biosynthesis of secondary metabolites	65	235	300	0
ko00750 Vitamin B6 metabolism	2	7	9	0
ko00300 Lysine biosynthesis	5	16	21	0
ko00010 Glycolysis / Gluconeogenesis	11	33	44	3
ko00620 Pyruvate metabolism	10	30	40	3
ko00600 Sphingolipid metabolism	1	3	4	3
ko00785 Lipoic acid metabolism	1	3	4	3
ko00960 Tropane, piperidine and pyridine alkaloid biosynthesis	1	3	4	3
ko01523 Antifolate resistance	1	3	4	3
ko03020 RNA polymerase	1	3	4	3
ko04141 Protein processing in endoplasmic reticulum	1	3	4	3
ko04212 Longevity regulating pathway - worm	1	3	4	3
ko05415 Diabetic cardiomyopathy	1	3	4	3

ko05418 Fluid shear stress and atherosclerosis	1	3	4	3
ko00270 Cysteine and methionine metabolism	10	28	38	0
ko03430 Mismatch repair	5	14	19	0
ko03030 DNA replication	4	11	15	0
ko03440 Homologous recombination	6	16	22	0
ko00790 Folate biosynthesis	7	18	25	0
ko00040 Pentose and glucuronate interconversions	4	10	14	0
ko00240 Pyrimidine metabolism	11	27	38	0
ko00190 Oxidative phosphorylation	14	29	43	0
ko01100 Metabolic pathways	261	529	790	0
ko00472 D-Arginine and D-ornithine metabolism	1	2	3	2
ko00531 Glycosaminoglycan degradation	1	2	3	2
ko00940 Phenylpropanoid biosynthesis	1	2	3	2
ko00950 Isoquinoline alkaloid biosynthesis	1	2	3	2
ko04146 Peroxisome	1	2	3	2
ko04714 Thermogenesis	1	2	3	2
ko05010 Alzheimer disease	1	2	3	2
ko05131 Shigellosis	1	2	3	2
ko00330 Arginine and proline metabolism	10	18	28	0
ko00983 Drug metabolism - other enzymes	5	9	14	0
ko01212 Fatty acid metabolism	5	9	14	0
ko01120 Microbial metabolism in diverse environments	81	143	224	0
ko00650 Butanoate metabolism	14	24	38	0
ko00230 Purine metabolism	17	29	46	0
ko05111 Biofilm formation - Vibrio cholerae	6	10	16	0
ko00450 Selenocompound metabolism	3	5	8	0
ko00030 Pentose phosphate pathway	11	18	29	0
ko00640 Propanoate metabolism	14	22	36	0
ko02024 Quorum sensing	20	31	51	0
ko03070 Bacterial secretion system	10	15	25	0
ko00401 Novobiocin biosynthesis	2	3	5	0
ko00440 Phosphonate and phosphinate metabolism	2	3	5	0
ko03320 PPAR signaling pathway	2	3	5	0
ko00130 Ubiquinone and other terpenoid-quinone biosynthesis	9	13	22	0
ko00760 Nicotinate and nicotinamide metabolism	8	10	18	0
ko00360 Phenylalanine metabolism	5	6	11	0
ko00410 beta-Alanine metabolism	5	6	11	0
ko04122 Sulfur relay system	5	6	11	0
ko00564 Glycerophospholipid metabolism	7	8	15	0
ko01501 beta-Lactam resistance	8	9	17	1125
ko00540 Lipopolysaccharide biosynthesis	14	15	29	0
ko00051 Fructose and mannose metabolism	20	21	41	0
ko00740 Riboflavin metabolism	5	5	10	1
ko00473 D-Alanine metabolism	2	2	4	1
ko00561 Glycerolipid metabolism	2	2	4	1
ko00643 Styrene degradation	1	1	2	1
ko04070 Phosphatidylinositol signaling system	1	1	2	1
ko04213 Longevity regulating pathway - multiple species	1	1	2	1
ko05016 Huntington disease	1	1	2	1
ko05020 Prion disease	1	1	2	1
ko00500 Starch and sucrose metabolism	14	13	27	0
ko00280 Valine, leucine and isoleucine degradation	9	8	17	0
ko00310 Lysine degradation	8	6	14	0
ko00052 Galactose metabolism	10	7	17	0
ko00920 Sulfur metabolism	13	9	22	0
ko00627 Aminobenzoate degradation	6	4	10	0

ko02010 ABC transporters	70	45	115	0
ko02020 Two-component system	91	57	148	0
ko00350 Tyrosine metabolism	8	4	12	0
ko00053 Ascorbate and aldarate metabolism	6	3	9	0
ko00071 Fatty acid degradation	6	3	9	0
ko00626 Naphthalene degradation	2	1	3	0
ko00830 Retinol metabolism	2	1	3	0
ko00980 Metabolism of xenobiotics by cytochrome P450	2	1	3	0
ko00982 Drug metabolism - cytochrome P450	2	1	3	0
ko00998 Biosynthesis of various secondary metabolites - part 2	2	1	3	0
ko05014 Amyotrophic lateral sclerosis	2	1	3	0
ko05022 Pathways of neurodegeneration - multiple diseases	2	1	3	0
ko02025 Biofilm formation - Pseudomonas aeruginosa	11	5	16	0
ko00380 Tryptophan metabolism	7	3	10	0
ko02026 Biofilm formation - Escherichia coli	20	8	28	0
ko00480 Glutathione metabolism	7	2	9	0
ko00562 Inositol phosphate metabolism	4	1	5	0
ko01503 Cationic antimicrobial peptide resistance	29	6	35	0
ko05133 Pertussis	5	1	6	0
ko00362 Benzoate degradation	11	2	13	0
ko01220 Degradation of aromatic compounds	11	2	13	0
ko00510 N-Glycan biosynthesis	13	2	15	0
ko01053 Biosynthesis of siderophore group nonribosomal peptides	7	1	8	0
ko03010 Ribosome	0	53	53	0
ko00520 Amino sugar and nucleotide sugar metabolism	0	31	31	0
ko00970 Aminoacyl-tRNA biosynthesis	0	22	22	0
ko04112 Cell cycle - Caulobacter	0	10	10	0
ko00521 Streptomycin biosynthesis	0	8	8	0
ko00633 Nitrotoluene degradation	0	8	8	0
ko03410 Base excision repair	0	8	8	0
ko00195 Photosynthesis	0	6	6	0
ko00511 Other glycan degradation	0	6	6	0
ko00997 Biosynthesis of various secondary metabolites - part 3	0	5	5	0
ko04066 HIF-1 signaling pathway	0	5	5	0
ko00523 Polyketide sugar unit biosynthesis	0	4	4	0
ko04626 Plant-pathogen interaction	0	4	4	0
ko04922 Glucagon signaling pathway	0	4	4	0
ko05132 Salmonella infection	0	4	4	0
ko05230 Central carbon metabolism in cancer	0	4	4	0
ko00333 Prodigiosin biosynthesis	0	3	3	0
ko00460 Cyanoamino acid metabolism	0	3	3	0
ko00471 D-Glutamine and D-glutamate metabolism	0	3	3	0
ko04217 Necroptosis	0	3	3	0
ko04621 NOD-like receptor signaling pathway	0	3	3	0
ko04910 Insulin signaling pathway	0	3	3	0
ko04931 Insulin resistance	0	3	3	0
ko05152 Tuberculosis	0	3	3	0
ko00332 Carbapenem biosynthesis	0	2	2	0
ko00405 Phenazine biosynthesis	0	2	2	0
ko00513 Various types of N-glycan biosynthesis	0	2	2	0
ko00524 Neomycin, kanamycin and gentamicin biosynthesis	0	2	2	0
ko00525 Acarbose and validamycin biosynthesis	0	2	2	0
ko00603 Glycosphingolipid biosynthesis - globo and isoglobo series	0	2	2	0
ko00966 Glucosinolate biosynthesis	0	2	2	0

ko03013 RNA transport	0	2	2	0
ko03450 Non-homologous end-joining	0	2	2	0
ko04151 PI3K-Akt signaling pathway	0	2	2	0
ko04152 AMPK signaling pathway	0	2	2	0
ko04216 Ferroptosis	0	2	2	0
ko04727 GABAergic synapse	0	2	2	0
ko04920 Adipocytokine signaling pathway	0	2	2	0
ko04930 Type II diabetes mellitus	0	2	2	0
ko05012 Parkinson disease	0	2	2	0
ko05200 Pathways in cancer	0	2	2	0
ko05417 Lipid and atherosclerosis	0	2	2	0
ko00140 Steroid hormone biosynthesis	0	1	1	0
ko00542 O-Antigen repeat unit biosynthesis	0	1	1	0
ko00572 Arabinogalactan biosynthesis - Mycobacterium	0	1	1	0
ko00604 Glycosphingolipid biosynthesis - ganglio series	0	1	1	0
ko00908 Zeatin biosynthesis	0	1	1	0
ko01051 Biosynthesis of ansamycins	0	1	1	0
ko01055 Biosynthesis of vancomycin group antibiotics	0	1	1	0
ko03008 Ribosome biogenesis in eukaryotes	0	1	1	0
ko03040 Spliceosome	0	1	1	0
ko04016 MAPK signaling pathway - plant	0	1	1	0
ko04068 FoxO signaling pathway	0	1	1	0
ko04138 Autophagy - yeast	0	1	1	0
ko04210 Apoptosis	0	1	1	0
ko04612 Antigen processing and presentation	0	1	1	0
ko04657 IL-17 signaling pathway	0	1	1	0
ko04659 Th17 cell differentiation	0	1	1	0
ko04721 Synaptic vesicle cycle	0	1	1	0
ko04723 Retrograde endocannabinoid signaling	0	1	1	0
ko04724 Glutamatergic synapse	0	1	1	0
ko04914 Progesterone-mediated oocyte maturation	0	1	1	0
ko04915 Estrogen signaling pathway	0	1	1	0
ko04919 Thyroid hormone signaling pathway	0	1	1	0
ko04932 Non-alcoholic fatty liver disease	0	1	1	0
ko04934 Cushing syndrome	0	1	1	0
ko04940 Type I diabetes mellitus	0	1	1	0
ko04962 Vasopressin-regulated water reabsorption	0	1	1	0
ko04964 Proximal tubule bicarbonate reclamation	0	1	1	0
ko04973 Carbohydrate digestion and absorption	0	1	1	0
ko04974 Protein digestion and absorption	0	1	1	0
ko05120 Epithelial cell signaling in Helicobacter pylori infection	0	1	1	0
ko05130 Pathogenic Escherichia coli infection	0	1	1	0
ko05143 African trypanosomiasis	0	1	1	0
ko05146 Amoebiasis	0	1	1	0
ko05165 Human papillomavirus infection	0	1	1	0
ko05203 Viral carcinogenesis	0	1	1	0
ko05205 Proteoglycans in cancer	0	1	1	0
ko05206 MicroRNAs in cancer	0	1	1	0
ko05211 Renal cell carcinoma	0	1	1	0
ko05215 Prostate cancer	0	1	1	0
ko05231 Choline metabolism in cancer	0	1	1	0
ko02060 Phosphotransferase system	33	0	33	0
ko05150 Staphylococcus aureus infection	5	0	5	0
ko00364 Fluorobenzoate degradation	4	0	4	0
ko00622 Xylene degradation	4	0	4	0
ko00281 Geraniol degradation	3	0	3	0

ko00624 Polycyclic aromatic hydrocarbon degradation	3	0	3	0
ko00072 Synthesis and degradation of ketone bodies	2	0	2	0
ko00623 Toluene degradation	2	0	2	0
ko00903 Limonene and pinene degradation	2	0	2	0
ko00906 Carotenoid biosynthesis	2	0	2	0
ko00930 Caprolactam degradation	2	0	2	0
ko01040 Biosynthesis of unsaturated fatty acids	2	0	2	0
ko03460 Fanconi anemia pathway	2	0	2	0
ko05204 Chemical carcinogenesis	2	0	2	0
ko00253 Tetracycline biosynthesis	1	0	1	0
ko00361 Chlorocyclohexane and chlorobenzene degradation	1	0	1	0
ko00404 Staurosporine biosynthesis	1	0	1	0
ko00621 Dioxin degradation	1	0	1	0
ko00902 Monoterpenoid biosynthesis	1	0	1	0
ko00943 Isoflavonoid biosynthesis	1	0	1	0
ko00944 Flavone and flavonol biosynthesis	1	0	1	0
ko01054 Nonribosomal peptide structures	1	0	1	0
ko01524 Platinum drug resistance	1	0	1	0
ko04071 Sphingolipid signaling pathway	1	0	1	0
ko04113 Meiosis - yeast	1	0	1	0
ko04918 Thyroid hormone synthesis	1	0	1	0
ko05100 Bacterial invasion of epithelial cells	1	0	1	0
ko05135 Yersinia infection	1	0	1	0
ko05200 Pathways in cancer	1	0	1	0
ko05219 Bladder cancer	1	0	1	0
ko05225 Hepatocellular carcinoma	1	0	1	0

Conclusão Geral

Com este trabalho, podemos concluir que as interações entre insetos e microrganismos são uma fonte muito importante de aplicações biotecnológicas. A miríade de interações positivas e negativas entre microrganismos e insetos é um ponto de partida para a busca e desenvolvimento de produtos biotecnológicos.

A prospecção de bactérias do gênero *Bacillus* capazes de controlar as larvas de *Aedes aegypti* se mostrou bem-sucedida: obtivemos quatro isolados com boa capacidade larvicida e baixa toxicidade a organismos não alvo, portadores de genes para uma série de lipopeptídeos e outros compostos potencialmente larvicidas e que podem ainda ser usados para outras aplicações. A exploração *in silico* dos genes de metabolismo secundário e a anotação do genoma de *Bacillus safensis* BacI67, *Bacillus paranthracis* C21, *B. velezensis* B15 e B64a mostram a versatilidade destas espécies e nos ajudarão a desenhar novos estudos que ajudem a otimizar as condições de cultivo e obter sobrenadantes e extratos lipopeptídicos mais potentes.

O estudo da comunidade microbiana intestinal de *P. luridipes*, uma larva de besouro saproxílica, mostrou uma comunidade microbiana diversa e heterogênea, com variações entre as câmaras, que possivelmente ajudam a larva a crescer em um meio pobre em nutrientes. Obtivemos bactérias e leveduras com potencial probiótico e outras capazes de inibir patógenos e secretar enzimas líticas. Novos testes de segurança e de resistência a condições estomacais precisam ser feitos com *Apiotrichum siamense* L29A e *Bacillus* sp. BL17BA, mas a sua capacidade de proteger as larvas de *Galleria mellonella* de patógenos é animadora. A predição funcional a partir dos dados de metabarcoding mostra que ainda há possibilidades biotecnológicas a explorar: a microbiota das câmaras tem perfis que sugerem a existência de genes relacionados uma série de funções de interesse biotecnológico, como metabolismo de aminoácidos e cofatores, degradação de xenobióticos e degradação de carboidratos.

Conhecer e entender a diversidade de espécies e interações microbianas em um sistema como o do intestino de insetos é importante ainda para aumentar a probabilidade de acessar de microrganismos que escapam às técnicas tradicionais. Futuras explorações com técnicas de cultivo mais modernas, específicas e de maior rendimento podem se beneficiar desse conhecimento, ajudando a acessar microrganismos com outras potencialidades.

Anexo 3 – Normas para publicação no Journal of Invertebrate Pathology

https://www.elsevier.com/journals/journal-of-invertebrate-pathology/0022-2011/guide-for-authors (Acessadas em em 15/05/2021)

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Slifka MK, Whitton JL (2000) Clinical implications of dysregulated cytokine production. J Mol Med. doi:10.1007/s001090000086

Book

South J, Blass B (2001) The future of modern genomics. Blackwell, London

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Cartwright J (2007) Big stars have weather too. IOP Publishing PhysicsWeb. http://physicsweb.org/articles/news/11/6/16/1. Accessed 26 June 2007

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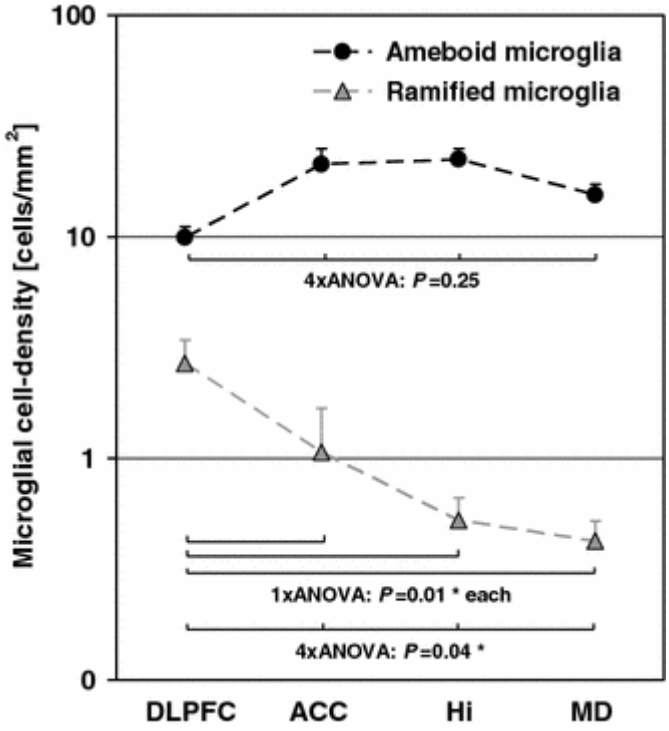

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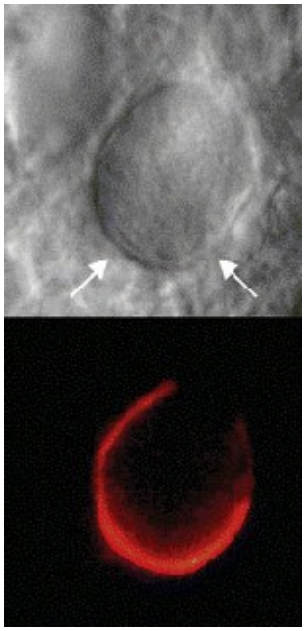

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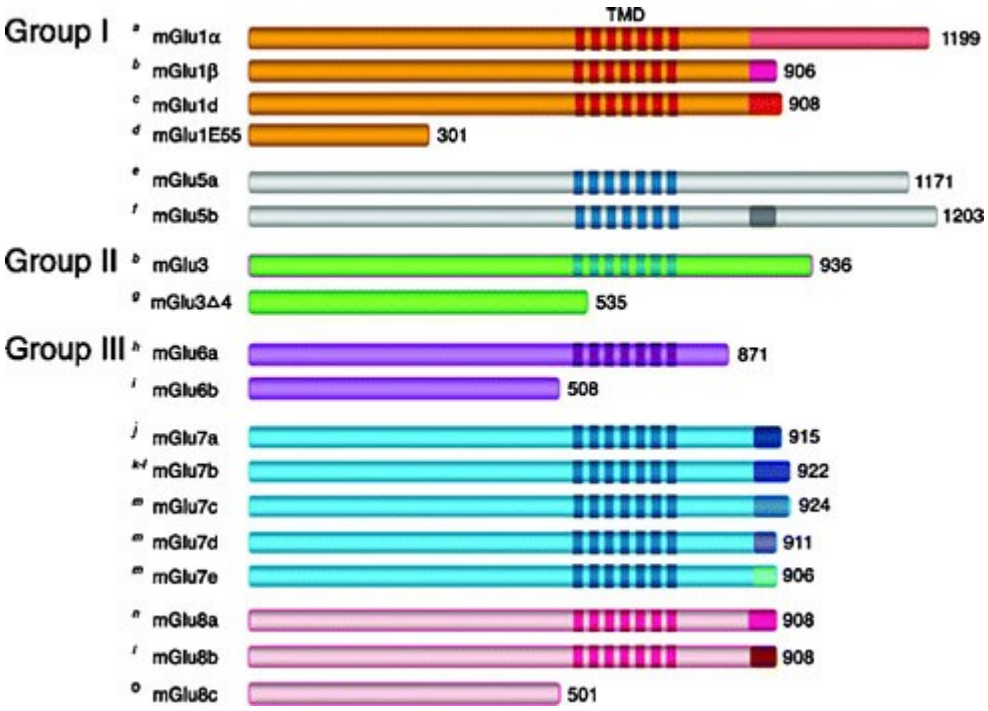

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