UNIVERSIDADE FEDERAL DO RIO GRANDE DO SUL – UFRGS

Síndrome anual da abelha mandaçaia (*Melipona quadrifasciata*) - o papel de simbiontes, sistema imune e ambiente.

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SUMÁRIO

LISTA DE ABREVIATURAS E UNIDADES

+ssRNA: RNA fita simples de sentido positivo (*positive-sense single-stranded RNA*)

°C: graus Celsius

ABPV: vírus da paralisia aguda de abelha (*Acute bee paralysis virus*)

AMPs: peptídeos antimicrobianos

ANOVA: análise de variância

ARV-1: *Apis mellifera rhabdovirus-1*

BL: Boqueirão do Leão - RS

BLAST: ferramenta básica de busca de alinhamento local (*Basic Local Alignment Search Tool)*

BP: Bom princípio - RS

bp: pares de base (*base pairs*)

BQCV: vírus da célula de rainha negra (*Black queen cell virus*)

BU: teste incondicional de Barnard (*Barnard's Unconditional test*)

CBPV: vírus da paralisia crônica das abelhas (*Chronic bee paralysis virus*)

CCD: desordem do colapso das colônias (*Colony collapse disorder*)

CDS: sequência codificante (*Coding sequence*)

CMH: teste de Cochran-Mantel-Haenszel

CNRQ: quantidade relativa calibrada e normalizada (*Calibrated Normalized Relative Quantity*)

Cq: ciclo de quantificação (*quantification cycle*)

DEG: genes diferentemente expressos (*differentially expressed genes*)

dsDNA: DNA de fita dupla

DWV: vírus deformador da asa (*Deformed wing virus*)

E: eficiência do primer (*primer efficiency*)

fem: gene feminizador

g: gramas

GE: expressão gênica (*gene expression*)

GOX: glicose oxidase

H: saudável (*healthy*)

HDNA: amostra de DNA de abelhas saudáveis (*DNA sample from healthy bees*)

HJ: hormônio juvenil

HRNA: amostra de RNA de abelhas saudáveis (*RNA sample from healthy bees*)

IAPV: vírus da paralisia aguda israelense (*Israeli acute paralysis virus*)

Imd: via da imunodeficiência (*Immune deficiency*)

Jak/STAT: Janus quinase / transdutor de sinal e ativador da transcrição (*Janus kinase/Signal Transducer and Activator of Transcription*)

KBV: vírus de abelha da caxemira (*Kashmir bee virus*)

LSV: vírus do lago Sinai (*Lake Sinai virus*)

Ma: milhões de anos

min: minutos

mL: mililitros

mm: milímetros

mM: milimolar

MqC: *Melipona quadrifasciata cyclovirus*

MqC1: *Melipona quadrifasciata cyclovirus 1*

MqC2: *Melipona quadrifasciata cyclovirus 2*

MqD: *Melipona quadrifasciata densovirus*

MqV1a: *Melipona quadrifasciata virus 1a*

MqV1b: *Melipona quadrifasciata virus 1b*

MqV2: *Melipona quadrifasciata virus 2*

NF-κB: fator nuclear kappa-B

NGE: expressão gênica normalizada (*normalized gene expression*)

nm: nanômetros

NMDS: escala multidimensional não métrica (*non-metric multidimensional scaling*)

nt: nucleotídeos

OcNV: *Osmia cornuta nudivírus*

OTUs: unidades taxonômicas operacionais (*Operational Taxonomic Units*)

p450: citocromo p450

PA: Porto Alegre - RS

PAMPs: Padrões Moleculares Associados a Patógenos

PCA: análise de componentes principais (*Principal Component Analysis*)

PCR: reação em cadeia da polimerase (*Polymerase Chain Reaction*)

PERMANOVA: análise multivariada permutacional de variância (*Permutational Multivariate Analysis of Variance*)

PO: fenoloxidase

r.p.m: rotações por minuto

RFU: unidade de fluorescência relativa (*Relative Fluorescence Unit*)

RL: Rolante – RS

RT-qPCR: PCR quantitativa de transcrição reversa (*quantitative reverse transcription PCR*)

SBPV: vírus da paralisia lenta das abelhas (*Slow bee paralysis virus*)

SBV: vírus de abelha *Sacbrood* (*Sacbrood bee virus*)

SGE: similaridade de expressão gênica (*gene expression similarity*)

ssDNA: DNA de fita simples

−ssRNA: RNA fita simples de sentido negativo (*negative-sense single-stranded RNA)*

U: doente (*unhealthy*)

UDNA: amostra de DNA de abelhas doente (*DNA sample from unhealthy bees*)

uL: microlitros

URNA: amostra de RNA de abelhas doentes (*RNA sample from unhealthy bees*)

VDV1: *Varroa destructor virus-1*

Vg: vitelogenina

Δ : delta

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RESUMO

Todos os anos ao final do verão, no sul do Brasil, colônias manejadas da abelha sem ferrão *Melipona quadrifasciata* manifestam uma síndrome que eventualmente leva-as ao colapso. Abelhas de colônias afetadas podem apresentar sintomas como tremores e paralisia, mas a principal característica da síndrome é a repentina morte de operárias, cujos corpos são encontrados em frente ou mesmo dentro da colméia. Nesta tese descrevemos nossos achados sobre as possíveis causas dessa mortalidade avaliando os diferentes níveis de complexidade de uma abelha social, desde o indivíduo e seus microrganismos associados até o nível da colônia. Mostramos que a microbiota de *M. quadrifasciata* é altamente variável, com grandes diferenças na composição bacteriana de abelhas de diferentes colônias. Bactérias patogênicas não foram detectadas em abelhas afetadas e o padrão na composição da microbiota não indicou uma correlação entre disbiose e a ocorrência da síndrome. Mostramos também que os sintomas observados em forrageiras doentes não são causados por vírus conhecidos como patogênicos em outras abelhas. Entretanto, novos vírus que nós identificamos no viroma da *M. quadrifasciata* são mais frequentemente diagnosticados em determinados meliponários durante a síndrome, e podem estar relacionados à intensidade dos sintomas e ao colapso de certas colméias. Por fim, num monitoramento temporal feito ao longo de cinco meses no verão de 2018/2019, mostramos que a síndrome foi resultado da incapacidade de expressar genes envolvidos na detoxificação de xenobióticos e resposta imune cerca de dois meses antes da síndrome, seguido da perda de peso das forrageiras, troca nos recursos polínicos utilizados e perda da capacidade de controle do clima interno da colônia. Além da divulgação e discussão no meio científico, elaboramos também, com base nestas investigações, um guia com recomendações de manejo aos meliponicultores que, se aplicadas, podem contribuir para a prevenção da síndrome anual de *M. quadrifasciata*, bem como da perda de outras abelhas nativas.

palavras-chave: abelha, abelha sem ferrão, simbiose, microbiota, vírus, sistema imune, comportamento, saúde das abelhas.

ABSTRACT

Every year at the end of summer, in southern Brazil, managed colonies of the stingless bee *Melipona quadrifasciata* manifest a syndrome that eventually leads to their collapse. Bees from affected colonies may show symptoms such as tremors and paralysis, but the main feature of the syndrome is the sudden death of workers, whose bodies are found in front or inside the hives. In this thesis we describe our discoveries on the possible causes of this mortality evaluating the different complexity levels of an eusocial bee, from the individual and its associated microorganisms until colony level. We show that the *M. quadrifasciata* microbiota is highly variable, with large differences in community composition among bees from different colonies. Pathogenic bacteria were not detected in affected bees, and the pattern of microbiota composition did not indicate a correlation between dysbiosis and syndrome occurrence. We have also shown that the symptoms observed in unhealthy foragers are not caused by viruses known to be pathogenic in other bees. However, novel viruses that we identified in the *M. quadrifasciata*-associated virome are more often diagnosed in some meliponaries during the outbreak, and may be related to the intensity of observed symptoms and to the collapse of some colonies. Finally, on a temporal survey performed for five months during the summer of 2018/2019, we show the syndrome resulted from the inability to express genes involved in the detoxification of xenobiotics and immune response about two months before the outbreak, followed by foragers weight loss, a shift in pollen resources used, and a decrease in performance to control the nest environment. In addition to reporting our results to the scientific community, we have also prepared, based on our investigations, a guide with recommendations for the management of stingless bees that may contribute to the prevention of the *M. quadrifasciata* annual syndrome, as well the loss of other native bees.

key words: bee, stingless bee, symbiosis, microbiota, virus, immune system, behavior, bee health.

CAPÍTULO 1

Introdução e objetivos

1. Introdução

1.1 Abelhas neotropicais

Polinizadores prestam um serviço importante na manutenção de ecossistemas naturais e também para a agricultura. As abelhas fazem parte das 100.000 espécies polinizadoras de mais de 200.000 espécies de plantas. Quanto às espécies de plantas cultivadas pelo homem, as abelhas são o grupo mais importante de polinizadores (Heard 1999; Klein et al. 2007; Giannini et al. 2015).

A região neotropical é reconhecida por suportar uma fauna rica em espécies de abelhas. Estima-se para a região um número total de mais de 15.000 espécies e para o Brasil a riqueza de espécies de abelhas pode chegar a 3.000 (Silveira et al. 2002). As abelhas fazem parte da ordem Hymenoptera e, dentre as sete famílias que a compõe, Apidae é a mais rica e abundante na Mata Atlântica. Espécies da tribo Meliponini são as mais registradas neste bioma (Gonçalves e Brandão 2008). A tribo agrupa as abelhas sociais encontradas nos trópicos e regiões subtropicais, conhecidas popularmente como abelhas sem ferrão por possuírem o ferrão atrofiado. Abelhas do gênero *Melipona*, reconhecidamente monofilético, fazem parte de um clado que inclui apenas abelhas sem ferrão neotropicais (Figura 1) (Ramírez et al. 2010; Rasmussen e Cameron 2010).

1.1.2 A abelha mandaçaia

A mandaçaia (*Melipona quadrifasciata*, Lepeletier 1836, Figura 2) é a segunda espécie de abelha sem ferrão mais cultivada por meliponicultores (aqueles que criam abelhas da tribo Meliponini) (Jaffé et al. 2015). As colônias de mandaçaia são compostas por 300 a 400 indivíduos (Tóth et al. 2003) e colônias selvagens costumam nidificar em troncos ocos. O período de desenvolvimento do ovo ao adulto é de em média 40 dias. Quando adultas, operárias medem 10 a 11 mm e são mais robustas que as abelhas melíferas. A determinação das castas em abelhas do gênero *Melipona* é diferente da maioria das abelhas sem ferrão, em que as larvas determinadas a desenvolverem-se como rainhas recebem e consomem uma quantidade maior de alimento comparado aos demais ovos depositados (Kerr 1969; Hartfelder et al. 2006).

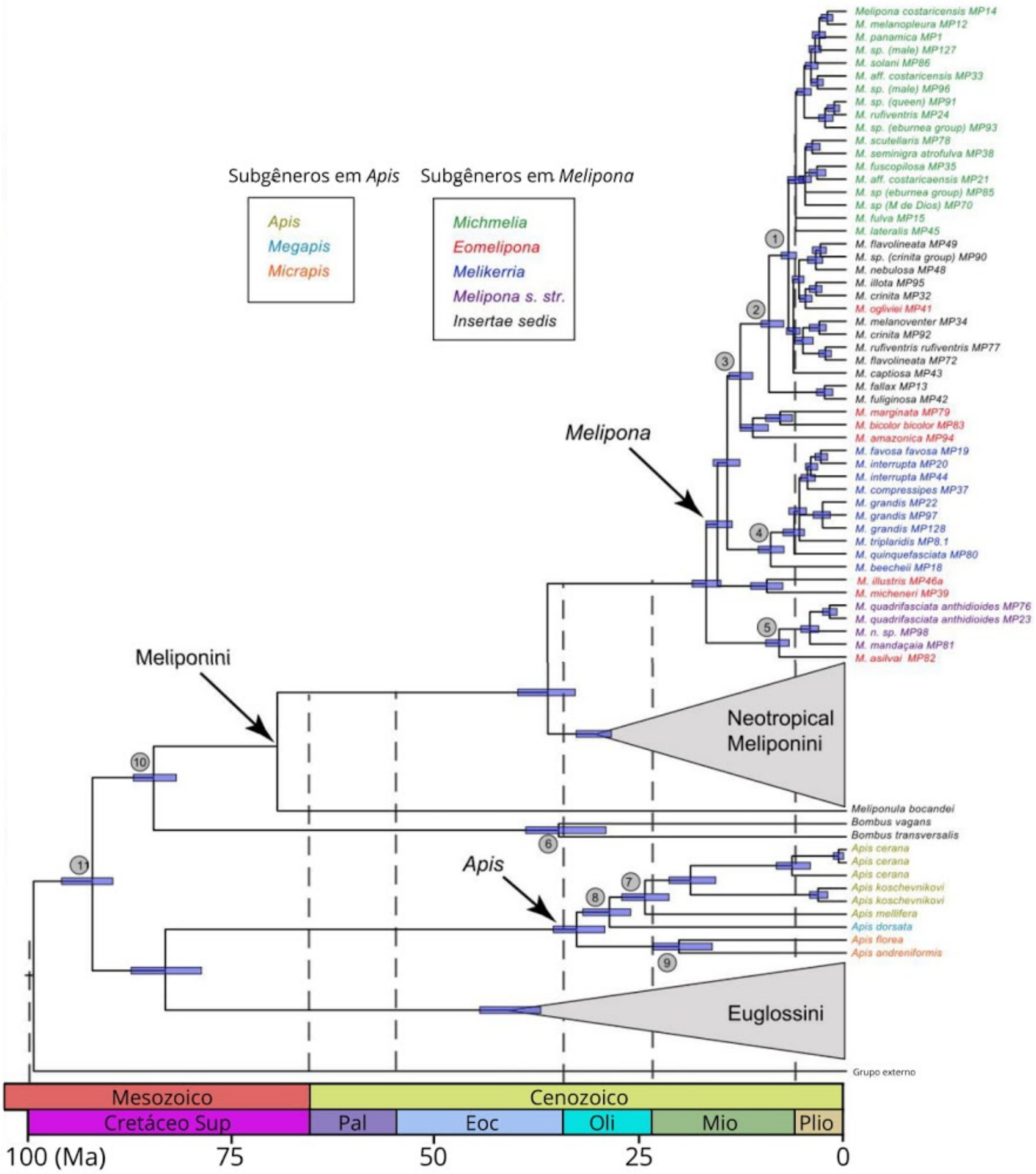

Figura 1. Análise filogenética Bayesiana baseada em cinco *loci* e cronograma com relógio-relaxado do gênero *Melipona* e grupos relacionados. Os tempos de divergência são apresentados em milhões de anos (Ma). *Melipona* compartilhou um ancestral comum durante o Mioceno, 14–17 milhões de anos atrás (adaptado de Ramírez et al. 2010).

Em *Melipona* a determinação de castas se dá por predisposição genética, seguindo um modelo de dois *loci*/dois alelos ainda não determinados (Kerr 1950; Hartfelder et al. 2006). Estudos mais recentes mostram que os níveis de transcritos do gene feminizador (*fem*) em abelhas fêmeas são provavelmente aumentados pelo hormônio juvenil (HJ), mais expresso em larvas que irão se desenvolver como rainhas, sugerindo que *fem* atua como componente de interação entre vias de determinação do sexo e das castas (de Oliveira Campos et al. 1975; Bonetti et al. 1995; Brito et al. 2015).

As abelhas sem ferrão são consideradas polinizadoras generalistas da flora nativa e também fundamentais para polinização de cultivares agrícolas. Uma característica marcante das mandaçaias, assim como outras abelhas do gênero *Melipona*, é sua capacidade de coletar pólen por vibração especialmente em flores com anteras poricidas (onde o pólen sai da antera através de poros apicais), como da família de plantas Solanaceae. A abelha pousa sobre o ápice da antera, agarra-se ao estame e contrai os músculos torácicos de forma a vibrar e liberar o pólen (Nunes-Silva et al. 2010). Devido a este comportamento, a mandaçaia é uma importante polinizadora de cultivares como o de tomate, pimentão e berinjela (Cruz et al. 2005; dos Santos et al. 2009; Nunes-Silva et al. 2013; Bartelli e Nogueira-Ferreira 2014).

A mandaçaia ocorre na Argentina, Paraguai e Brasil. No Brasil a espécie *M. quadrifasciata* é dividida em duas subespécies. No nordeste, sudeste e centro-oeste do Brasil encontra-se a subespécie *M. q. anthidioides*, com bandas amarelas interrompidas no dorso do abdômen; enquanto no centro-oeste, sudeste e sul ocorre a subespécie *M. q. quadrifasciata*, na qual as bandas dorsais são contínuas (Batalha-Filho et al. 2009). Marcadores moleculares, como regiões polimórficas do DNA (Waldschmidt et al. 2000) e regiões do DNA mitocondrial com padrões diferentes de clivagem por enzimas de restrição (Souza et al. 2008; Batalha-Filho et al. 2010) já foram descritos para auxiliar na diferenciação das subespécies e para estudos de zonas híbridas, encontradas em São Paulo e Minas Gerais. As mandaçaias híbridas possuem um padrão de coloração intermediário, com bandas dorsais interrompidas e contínuas no abdômen. A subespécie *M. q. quadrifasciata* é classificada como em perigo na lista mais atual de espécies ameaçadas do Rio Grande do Sul, elaborada pela Fundação Zoobotânica (2014) e tentativas de encontrar ninhos selvagens na região não tiveram sucesso.

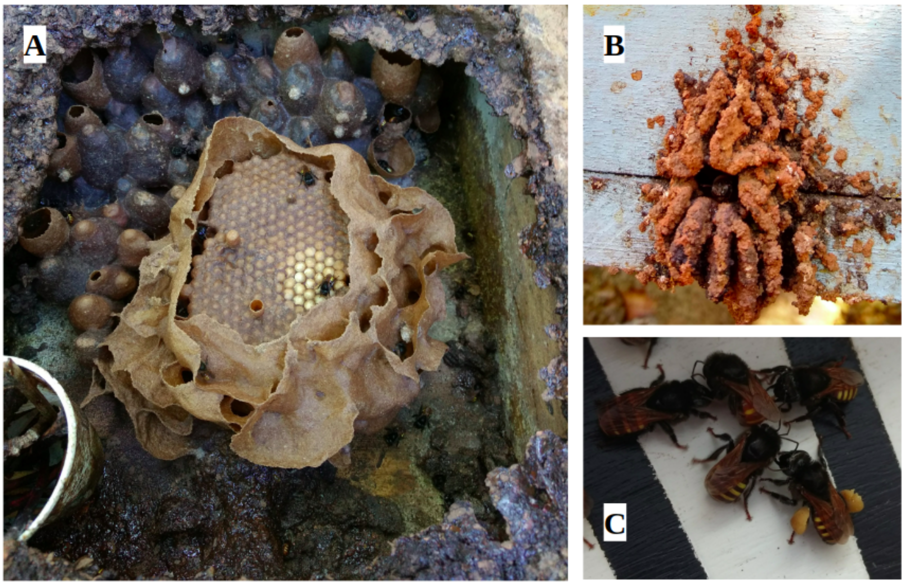

Figura 2. Características da abelha mandaçaia. (A) Parte interna de uma colônia manejada de mandaçaia, com discos de cria envoltos por cerume e no canto da caixa os potes de mel e pólen. (B) Entrada típica de um ninho de mandaçaia, feito de barro coletado por operárias. (C) Abelhas operárias da subespécie *M. q. quadrifasciata* do Rio Grande do Sul. (Fotos: Lílian Caesar)

1.2 Ameaças às abelhas e o colapso de colônias

Nas últimas décadas tem sido relatada a diminuição das populações de abelhas. Na América do Norte e Europa perdas anuais de populações de abelhas manejadas têm aumentado, podendo chegar até 40% do total de colônias (Genersch et al. 2010; Kulhanek et al. 2017). Em 2005 e 2006 apicultores dos Estados Unidos da América começaram a relatar o que passou-se a chamar de desordem do colapso de colônias (CCD, *colony collapse disorder*) (Stokstad 2007). A CCD é caracterizada pela repentina perda da população adulta de abelhas, sem que se encontrem indivíduos mortos no interior ou na proximidade das colônias. O grande número de colônias perdidas após o aparecimento da CCD levou a esforços de pesquisa principalmente voltados a gerar informações sobre cargas de patógenos em polinizadores, permitindo a identificação de possíveis ameaças emergentes à saúde das abelhas (Cox-Foster et al. 2007; Evans e Schwarz 2011; Schwarz, Huang, et al. 2015). Esse processo, no entanto, levou à conclusão de que as perdas de colônias são o resultado de vários estressores em interação, como aquecimento global e perda de habitat, má nutrição, ação de patógenos e práticas agrícolas como a utilização de pesticidas (vanEngelsdorp e Meixner 2010).

O declínio de populações selvagens de abelhas é um fato (Koh et al. 2016; Meeus et al. 2018). Na região tropical, os fatores que têm influenciado o baixo *status* de conservação de abelhas selvagens incluem a disseminação de espécies de abelhas exóticas, que competem por recursos e podem transmitir patógenos às abelhas nativas, a perda de habitat e o uso de pesticidas (Freitas et al. 2009; Guzman-Novoa et al. 2015; Ueira-Vieira et al. 2015; Maggi et al. 2016; Santos et al. 2018). A meliponicultura, por sua vez, pode ser uma atividade benéfica ao criar e manejar abelhas nativas em risco de extinção, como a *M. q. quadrifasciata* (Jaffé et al. 2015). No entanto, meliponicultores do sul do Brasil relatam uma síndrome de ocorrência anual, geralmente no final do verão, que culmina com o colapso das colônias da espécie. A síndrome difere da conhecida CCD uma vez que são encontrados indivíduos mortos nas proximidades ou até dentro das colônias. A principal característica desta síndrome é a quantidade anormal de operárias mortas em frente a colônia (Figura 3). Em alguns meliponários indivíduos de colônias afetadas podem também apresentar um comportamento alterado e tremores, incapacidade de voo e a eversão da probóscide. O colapso da colônia ocorre devido à falta de operárias para a manutenção e proteção, de modo que a colônia acaba por fim sendo invadida por parasitas como fungos e moscas. A síndrome ocorre em meliponários com ambientes heterogêneos, situados em áreas urbanas à regiões cercadas por mata conservada. Há também diferenças na intensidade dos sintomas observados nos diferentes locais, assim como nem todas as colônias de mandaçaia ficam doentes. Portanto, assim como sugerido para o declínio das populações globais de abelhas e mesmo para a CCD, esta também pode ser uma síndrome multifatorial.

1.2.1 Bactérias

Diversas bactérias patogênicas são conhecidas por infectar principalmente abelhas melíferas, dentre elas as bactérias *Paenibacillus larvae* e *Melissococcus plutonius* são as mais bem caracterizadas (Fünfhaus et al. 2018). *P. larvae* é o agente causador da cria pútrida americana (*American Foulbrood*). O sintoma típico observado após a infecção das larvas por esporos da bactéria é a degradação da larva morta (J. Brødsgaard et al. 1998; Genersch 2010),

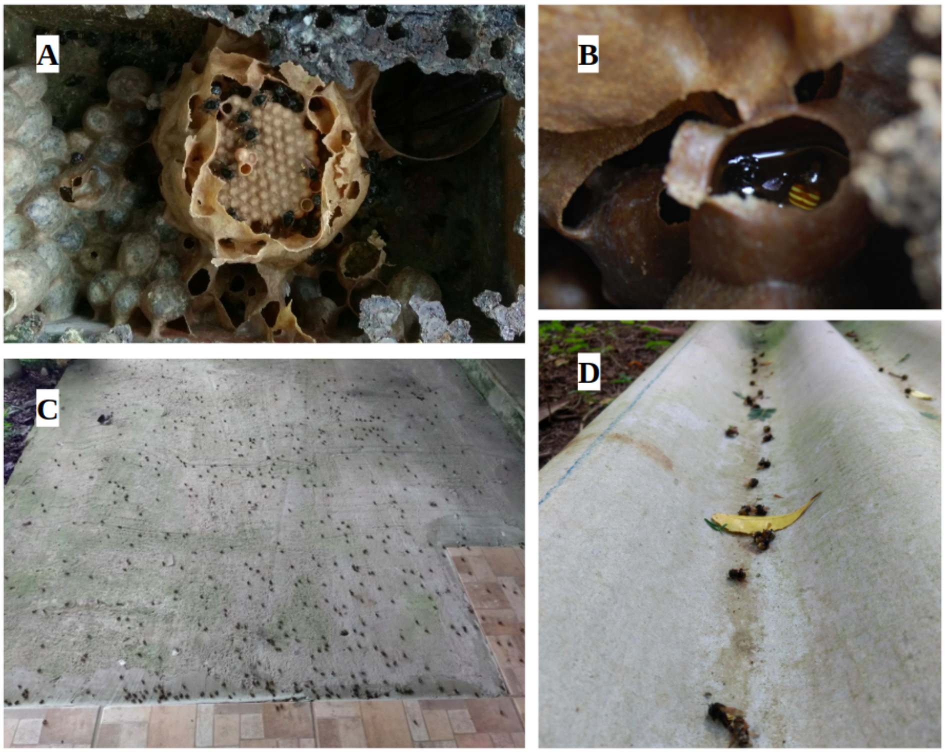

Figura 3. Imagens da síndrome anual das mandaçaias. (A) Parte interna de uma colônia manejada de mandaçaia no ínicio da síndrome. Os discos de cria, potes de pólen e mel permanecem intactos, mas no fundo da colônia começam a acumular operárias mortas ou com sintomas da síndrome, como tremores e paralisia (Foto: Lílian Caesar). (B) Nos potes de mel também passam a ser observadas operárias afogadas que não são removidas por falta de operárias para desempenhar as atividades de limpeza dentro da colônia (Foto: Lucas Kehl). (C, D) A característica mais marcante da síndrome é o grande número de operárias mortas em frente às suas colônias (Foto C: Daniel Iochims; D: Lílian Caesar).

essencial para a transmissão de esporos para larvas saudáveis, bem como para a transmissão da doença dentro e entre colônias. Já *M. plutonius* é o agente causador da doença conhecida como cria pútrida européia (*European Foulbrood*). As larvas são infectadas ao ingerirem alimento larval contaminado e quando mortas são encontradas torcidas dentro da célula de cria aberta. Sua decomposição ocorre também pela presença de invasores secundários como *P. alvei* ou *Enterococcus faecalis* (Nakamura et al. 2016; Lewkowski e Erler 2018). Ambas bactérias já foram diagnosticadas em abelhas melíferas brasileiras em estudos de monitoramento (Maggi et al. 2016), mas não há detalhes sobre os sintomas da infecção. Recentemente *M. plutonius* foi também diagnosticado em abelhas sem ferrão do gênero *Melipona* que apresentavam os sintomas da cria pútrida européia e em alguns casos estava levando ao colapso de colônias (Teixeira et al. 2020). No estudo mostram que a infecção ocorreu por meio da suplementação alimentar das colônias de abelhas sem ferrão com pólen de *Apis* contaminado.

A bactéria *Lysinibacillus sphaericus* é um conhecido patógeno de insetos, sendo inclusive usada em programas de controle de insetos vetores de doenças humanas (Lacey 2007). Apesar desta bactéria não ser, a princípio, patogênica à abelhas melíferas (West Davidson et al. 1977), ela é o agente causador da perda da prole de colônias manejadas da abelha sem ferrão australiana *Tetragonula carbonaria* (Shanks et al. 2017). Colônias afetadas parecem não ter rainhas, tem uma população reduzida de abelhas adultas e pouca atividade na entrada do ninho. As larvas infectadas apresentam descoloração ou aspecto apodrecido. No Brasil não há registros de abelhas sem ferrão infectadas por tal bactéria.

Outras bactérias patogênicas à abelhas são *Spiroplasma apis* e *S. melliferum*, que vivem intracelularmente nos tecidos do hospedeiro ou extracelularmente na hemolinfa. Abelhas infectadas por *S. apis* são incapazes de voar, rastejam no chão e tremem, além de ficarem com o abdômen inchado devido ao intestino cheio de pólen não digerido (Mouches et al. 1982; Mouches et al. 1983). A infecção por *S. melliferum* se dá na hemolinfa causando patologia em diversos tecidos e diminuindo a longevidade de abelhas adultas (Clark et al. 1985; Zheng e Chen 2014). Abelhas melíferas brasileiras, sem sintomas evidentes, já foram diagnosticadas para a infecção por ambas espécies de *Spiroplasma*, inclusive com infecções concomitantes de *S. apis* e *S. melliferum* (Schwarz et al. 2014).

A bactéria *Serratia marcescens*, encontrada tanto em plantas como animais, é também um patógeno oportunista de abelhas (Raymann et al. 2018). Está frequentemente presente em baixa densidade no intestino de abelhas adultas e já foi também isolada de ácaros parasitas e da hemolinfa de abelhas doentes ou mortas (El Sanousi et al. 1987; Burritt et al. 2016; Raymann et al. 2017). No Brasil não há relatos e falhas em colônias relacionado a infecção por esta bactérias.

1.2.2 Vírus

Até pouco tempo podíamos contar facilmente o número de vírus identificados em abelhas, principalmente em *A. mellifera* (Chen e Siede 2007; McMenamin e Genersch 2015).

Mas as recentes técnicas de sequenciamento de nova geração tem facilitado o sequenciamento de alto rendimento de transcriptomas, metagenomas e viromas, o que tem contribuído significativamente para a caracterização da diversidade de vírus associados às abelhas (Grozinger e Flenniken 2019). A maioria dos vírus de abelhas são de RNA fita simples de sentido positivo (+ssRNA). A família *Dicistroviridae* inclui vírus como: vírus da paralisia aguda israelense (IAPV, *Israeli acute paralysis virus*), vírus de abelha da caxemira (KBV, *Kashmir bee virus*), vírus da paralisia aguda de abelha (ABPV, *Acute bee paralysis virus*) e vírus da célula de rainha negra (BQCV, *Black queen cell virus*). Na família *Iflaviridae* fazem parte vírus como: vírus deformador da asa (DWV, *Deformed wing virus*), vírus *Varroa destructor*-1/DWV-B, vírus de abelha *Sacbrood* (SBV, *Sacbrood bee virus*) e vírus da paralisia lenta das abelhas (SBPV, *Slow bee paralysis virus*). Há também vírus +ssRNA taxonomicamente não classificados, como: vírus da paralisia crônica das abelhas (CBPV, *Chronic bee paralysis virus*) e vírus do lago Sinai (LSVs, *Lake Sinai virus*) (McMenamin e Flenniken 2018; Grozinger e Flenniken 2019).

Alguns destes vírus são conhecidos por causar paralisia em abelhas. O vírus SBPV acumula-se nos tecidos da parte anterior do corpo das abelhas causando a paralisia das pernas anteriores do inseto, sintoma observável apenas 12 dias após a inoculação do vírus, não sendo tão agressivo de imediato (Bailey e Woods 1974). O vírus CBPV causa sintomas semelhantes, podendo também ser observadas abelhas incapazes de voar, aglomeradas e rastejando próximas à colmeia, sem pelos e com o abdômen inchado (Bailey et al. 1983; Blanchard et al. 2007). Este vírus acumula-se principalmente no sistema nervoso da abelha melífera e infecta/aumenta sua carga viral particularmente no verão, podendo infectar e levar apenas algumas colônias de apiários ao colapso.

Em meliponários de Minas Gerais e Pernambuco, onde ocorreu uma alta mortalidade de *M. scutellaris*, o vírus ABPV foi detectado em abelhas operárias (Ueira-Vieira et al. 2015). Este vírus é considerado praticamente assintomático, mas leva rapidamente à morte de abelhas infectadas (Miranda et al. 2013). Análises filogenéticas mostraram que a linhagem de ABPV desta abelha sem ferrão derivou de sequências de ABPV de *A. mellifera* da Europa e da América do Sul (Ueira-Vieira et al. 2015). O vírus DWV e BQCV também já foi detectado em abelhas melíferas do Brasil, assim como em cinco diferentes espécies de abelhas sem ferrão (de Souza et al. 2019; Guimarães-Cestaro et al. 2020). Nestas espécies de abelha sem ferrão em que o vírus foi detectado não há evidência de sintomas, mas quando a infecção é sintomática, como observado principalmente em abelhas melíferas, este vírus leva abelhas a desenvolverem-se com asas amassadas/vestigiais e abdômen inchado, levando à morte logo após o indivíduo emergir da pupa. A transmissão deste vírus por um vetor, como o ácaro *Varroa*, leva a infecções mais virulentas e com sintomas observáveis (Ryabov et al. 2014; Wilfert et al. 2016). O DWV também já foi detectado na abelha sem ferrão *Scaptotrigona mexicana*, espécies na qual também foi detectado o vírus BQCV (Guzman-Novoa et al. 2015), que costuma causar sintomas mais evidentes nos estágios iniciais do desenvolvimento, como pré-pupas mortas em células com paredes escurecidas ou larvas com aparência pálida e o tecido endurecido (Miranda et al. 2013). Devido ao compartilhamento do ecossistema com *A. mellifera,* o próprio contato físico entre as abelhas exóticas e nativas, ou o contato com pólen de plantas visitadas por ambas as espécies, é sugerido como possível via de transmissão destes vírus (Guzman-Novoa et al. 2015).

Outros vírus identificados em abelhas incluem vírus de RNA fita simples de sentido negativo (−ssRNA), como o *Apis mellifera* rhabdovirus-1 (ARV-1) e *Apis mellifera* rhabdovirus-2 (ARV-2) (Remnant et al. 2017). Quanto aos vírus de DNA, dois vírus de DNA de fita dupla (dsDNA) foram já descritos, o Vírus filamentoso de *Apis mellifera* (Gauthier et al. 2015) e o *Osmia cornuta* nudivírus (OcNV) (Schoonvaere et al. 2018). Também foram já identificados sequências virais correspondentes a vírus de DNA de fita simples (ssDNA) das famílias *Circoviridae* e *Parvoviridae* (Galbraith et al. 2018; Schoonvaere et al. 2018). A patogenicidades destes vírus em abelhas infectadas ainda precisa ser investigada.

1.2.3 Outros inimigos naturais

Além de bactérias e vírus, outros inimigos naturais das abelhas são os ácaros, fungos e tripanossomatídeos. O ácaro *Varroa destructor*, que foi transmitido da abelha *A. ceranae*, tolerante ao parasita, à *A. mellifera*, é hoje um dos mais importantes parasitas desta espécie de abelha (Rosenkranz et al. 2010; Evans e Cook 2018). Ele se beneficia da ampla distribuição da abelha melífera, juntamente com as práticas de manejo, como a alta densidade de colônias nos apiários, para ser transmitido horizontalmente entre colônias (Seeley e Smith 2015). *Varroa* causa danos pelos efeitos diretos do seu parasitismo, como malformações durante o desenvolvimento e diminuição da performance das colônias (Garedew et al. 2004; Dainat et al. 2012). O ácaro também atua como vetor de vírus como KBV, IAPV e DWV (Chen et al. 2004; Shen et al. 2005; Di Prisco et al. 2011) e seu parasitismo tem contribuído para a emergência de estirpes virais, como do DWV, ao suprimir a resposta imune do hospedeiro desestabilizando a dinâmica de controle da infecção (Yang e Cox-Foster 2005; McMahon et al. 2016; Erban et al. 2019). Este ácaro já está espalhado por diferentes países da América Latina, incluindo o Brasil, mas até o momento não causa danos aparentes ou há evidências de sua atuação na transmissão de vírus (Strapazzon et al. 2009; de Mattos et al. 2016; Brettell e Martin 2017).

Nosema ceranae é um microsporídio parasita intracelular obrigatório de abelhas melíferas (Fries et al. 1996; Fries 2010). Nosemoses afetam larvas e abelhas adultas, causando mortalidade de abelhas e podendo levar ao colapso de colônias (Higes et al. 2007; Higes et al. 2008; Higes et al. 2009; Bromenshenk et al. 2010; Paxton 2010), apesar de ser também diagnosticada em colônias assintomáticas (Cox-Foster et al. 2007; Fernández et al. 2012). A infecção por *Nosema* pode comprometer o sistema imune, forrageamento, produção de feromônios e hormônios e síntese lipídica (Kralj e Fuchs 2010; Goblirsch et al. 2013; Mayack et al. 2015; Badaoui et al. 2017; Li et al. 2018). O parasita é transmitido por via oral pelo mel, néctar, pólen e matéria fecal das abelhas (Smith 2012). Um estudo realizado em colônias de *A. mellifera* de 20 apiários do estado de São Paulo detectou esporos do parasita em indivíduos de todas colônias, mas nenhuma evidência clara de correlação da quantidade de esporos com o declínio das colônias foi observado (Teixeira et al. 2013). Esporos de *Nosema* já foram também detectados em abelhas sem ferrão, provavelmente adquiridos em flores também visitadas por *A. mellifera* parasitadas (Porrini et al. 2017; Purkiss e Lach 2019). Em um estudo recente o patógeno, no entanto, não foi encontrado no intestino das abelhas sem ferrão, sugerindo que essas abelhas não são afetadas (Guimarães-Cestaro et al. 2020).

Os tripanossomatídeos *Crithidia mellificae* e *Lotmaria passim* são parasitas obrigatórios unicelulares que costumam infectar abelhas melíferas (Schwarz et al. 2015). *L. passim* é atualmente a espécie de tripanossomatídeo predominante em *A. mellifera* de grande parte do mundo. Para a América do Sul as informações sobre a distribuição dos tripanossomatídeos permanecem escassas, apesar de já terem sido diagnosticados (Arismendi et al. 2016; Castelli et al. 2019). Apesar de *L. passim* ter sido associado à mortalidade de abelhas (Ravoet et al. 2013), os efeitos de sua infecção ainda são pouco conhecidos. Já *C.*

bombi é um tripanossoma parasita de *Bombus* sp., e sua infecção já foi melhor caracterizada. Ele reduz drasticamente a produção de machos, o sucesso na fundação de novas colônias e tamanho delas, além de prejudicar processos cognitivos nas abelhas parasitadas (Brown et al. 2003; Gegear et al. 2006). Também induz a expressão de genes relacionados ao sistema imunológico, como os codificadores de Relish e peptídeos antimicrobianos (AMPs) (Schlüns et al. 2010; Riddell et al. 2011; Riddell et al. 2014).

1.2.5 Agroquímicos

O Brasil é o maior consumidor mundial de agroquímicos, representando aproximadamente 20% do uso total (Albuquerque et al. 2016). Em um estudo de caso recente, 90% dos apicultores brasileiros entrevistados relataram perda de colônias que acreditam ser causadas por causa do uso de agroquímicos em culturas próximas a seus apiários (Cerqueira e Figueiredo 2017). Mas enquanto países desenvolvidos têm reduzido o uso de agroquímicos na agricultura, o Brasil tem ido na contramão, facilitando ainda mais o seu uso (Santos et al. 2018). Altas doses de agroquímicos podem ter efeito letal para as abelhas, levando colônias inteiras ao colapso. Mas o efeito subletal dos agroquímicos, aquele que não leva a morte imediata das abelhas, pode também ser muito prejudicial e contribuir para falha da colônias (Desneux et al. 2007).

Agroquímicos já foram detectados em níveis residuais na prole, pólen, mel e cera de colônias de abelhas melíferas (Wu et al. 2011; Calatayud-Vernich et al. 2018; Tosi et al. 2018). Estes resíduos influenciam negativamente no crescimento, força e sobrevivência das colônias de abelhas por comprometerem o retorno de forrageiras ao lar, habilidades cognitivas e de forrageamento (Mommaerts et al. 2010; Henry et al. 2012), a motilidade espermática em machos (Thompson et al. 2005; Ciereszko et al. 2017) e a emergência, sobrevivência e reprodução de rainhas (Thompson et al. 2005; Sandrock et al. 2014; dos Santos et al. 2016). O efeito de doses subletais de agroquímicos pode também ser acentuado ao agir de forma sinergística com agroquímicos de outras classes (Spurgeon et al. 2016; Sgolastra et al. 2017), contribuir para o aumento da susceptibilidade a infecção por patógenos como *Nosema* sp. ou DWV (Alaux, Brunet, et al. 2010; Prisco et al. 2013; Aufauvre et al. 2014) e reduzir ainda mais a longevidade e sobrevivência de abelhas sob estresse nutricional (Tosi et al. 2017).

Diversos estudos experimentais têm mostrado os efeitos tóxicos de agroquímicos sob abelhas sem ferrão (Valdovinos-Núñez et al. 2009; Dorneles et al. 2017; Tomé et al. 2017; Padilha et al. 2020). Abelhas do gênero *Melipona* contaminadas sofrem uma diminuição na longevidade e mudanças no comportamento que influenciam a capacidade de forrageamento (Del Sarto et al. 2014; de Morais et al. 2018; Nocelli et al. 2019). Um estudo que investigou a suscetibilidade de *M. quadrifasciata* e *A. mellifera* aos agroquímicos Deltametrina, Metamidofós e Abamectina mostrou que a abelha nativa é, inclusive, mais suscetível do que a abelha exótica comumente usada como parâmetro para estudos de toxicidade (Del Sarto et al. 2014). Um padrão similar foi observado para a abelha sem ferrão *Partamona helleri*, mais suscetível à ação sinérgica de misturas da Deltametrina e uma formulação combinada de fungicidas comparado à *A. mellifera* (Tomé et al. 2017)

1.2.6 Perda de habitat

Cerca de um terço do território nacional já foi convertido em produção agrícola, o que tem levado à perda de grandes áreas de vegetação natural (Ferreira et al. 2012). Essa expansão está relacionada principalmente à crescente quantidade de terra usada para o cultivo de monoculturas, como a da soja, observada nos últimos anos no Brasil e outros países da América do Sul (Pacheco 2012). A invasão das florestas pelo cultivo de monoculturas afeta a saúde das abelhas pelo aumento no uso de pesticida nestes cultivares, por fragmentar habitats de nidificação e estabelecimento das colônias, e por comprometer a nutrição das abelhas uma vez que leva à perda da flora nativa que fornece diversas fontes de néctar e pólen às abelhas. Uma boa nutrição é essencial para a saúde das abelhas (Brodschneider e Crailsheim 2010). O consumo de pólen diverso, polifloral, e de boa qualidade é fisiologicamente mais saudável, contribuindo para uma maior tolerância a infecções patogênicas por garantir a disponibilidade de micronutrientes necessários e estimular a expressão de genes do sistema imune inato da abelha (Alaux, Ducloz, et al. 2010; Perry et al. 2015; Pasquale et al. 2016; Filipiak et al. 2017). Por exemplo, a alimentação com pólen polifloral aumenta a longevidade de abelhas melíferas parasitadas por *Nosema* comparado a abelhas que se alimentaram de pólen monofloral (Pasquale et al. 2013). Esta resposta também é observadas na infecção por IAPV, em que uma dieta polifloral tem o potencial de reduzir a mortalidade de abelhas infectadas (Dolezal et al. 2019).

1.3 Sistema imune e saúde da abelha

A saúde da abelha não é um tópico trivial e quando se trata de abelhas sociais, como a mandaçaia, uma colônia saudável não pode ser reduzida à ausência de patógenos ou colônias populosas. Ao estudar a saúde das abelhas deve se respeitar os diferentes níveis de complexidade do superorganismo (Figura 4), a saúde deve ser medida e investigada a nível individual, da colônia e populacional (López-Uribe et al. 2020). É o resultado da interação destes diferentes níveis que possibilitará um estado de bem-estar onde a energia é adquirida, alocada e utilizada da maneira ideal, permitindo que os indivíduos vivam mais e/ou se reproduzam mais. Nesta tese investigamos a síndrome das mandaçaias sob uma perspectiva multinível, medindo aspectos individuais (microbioma intestinal, diagnóstico de patógenos, viroma e expressão gênica), assim como medindo características da colônias (peso dos indivíduos, temperatura e umidade dentro das colônias e comportamento imune social).

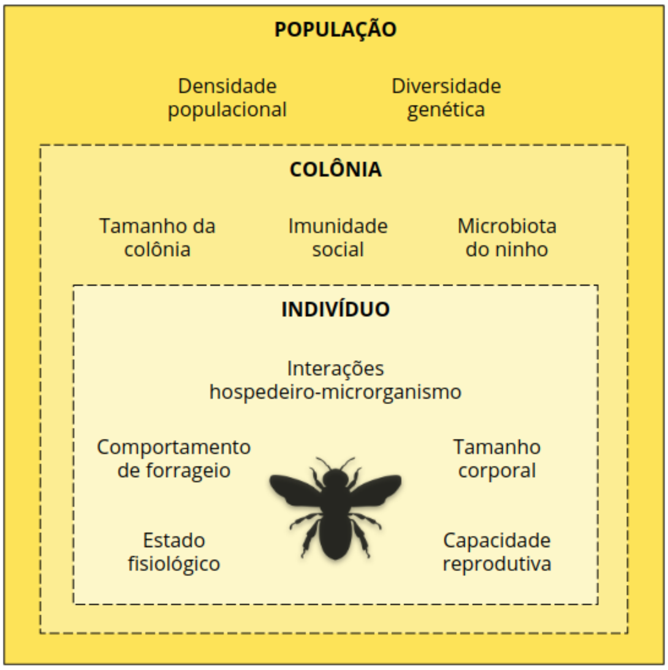

Figura 4. Os três níveis de organização biológica importantes para o estudo e discussões sobre a saúde das abelhas e, dentro de cada um, algumas das diferentes maneiras avaliá-los. As linhas pontilhadas entre os níveis representam o fluxo de informações de níveis mais específicos aos mais amplos. Por exemplo, avaliações a nível de indivíduo informam também sobre a saúde da colônia, e avaliações a nível de colônia informam também sobre a saúde a nível de população (adaptado de López-Uribe et al. 2020, ilustração da abelha de www.kindpng.com).

1.3.1 Imunidade social

A imunidade social é uma forma de defesa coletiva contra parasitas e patógenos, onde os indivíduos da colônia realizam pequenas tarefas que coletivamente têm um impacto na saúde da colônia (Cremer et al. 2007). A auto-higiene e higienização de outras abelhas da colônia é um comportamento imune social para remoção de pólen, partículas estranhas e parasitas, como ácaros, do corpo das abelhas (Jander 1976; Büchler et al. 1992; Danka e Villa 1998; Boecking e Spivak 1999). Comportamentos termorregulatórios, como a febre social gerada por abelhas operárias, são importantes no combate a patógenos sensíveis ao calor, como fungos (Simone-Finstrom et al. 2014). O comportamento higiênico envolve a detecção de células de cria com larvas mortas ou infectadas e sua remoção da colônia, evitando a disseminação de ácaros, vírus e fungos na colônia (Spivak e Gilliam 1998; Bigio et al. 2014; Toufailia et al. 2014; Al Toufailia et al. 2016). Quando a abelha adulta é quem está infectada, ela também pode abandonar a colônia para morrer fora dela, evitando a disseminação de doenças (Rueppell et al. 2010; Shorter e Rueppell 2012). Em abelhas sem ferrão podemos observar que as células de cria são preenchidas com alimento larval logo após a construção e antes da oviposição pela rainha, sendo seladas imediatamente após a oviposição (Lindauer 1976). Diferente das abelhas melíferas, em que o alimento é dado progressivamente às larvas em células de cria abertas, este comportamento impede que parasitas, como ácaros, tenham acesso à prole em desenvolvimento.

Outros comportamentos relacionados à imunidade social envolvem a auto-medicação, como o uso de resinas antimicrobianas coletadas nas plantas visitadas, que são misturadas à cera ou solo e então usadas na construção dos ninhos (Simone et al. 2009; Drescher et al. 2014; Popova et al. 2014; Drescher et al. 2017). Abelhas nutrizes também podem usar a glicose oxidase (GOX), produzida pelas abelhas que processam o néctar, no alimento larval e estoques de mel servindo como um agente antimicrobiano (Bucekova et al. 2014). A produção de GOX tem sido inclusive usada como um biomarcador de defesa imune social, apesar de sua expressão também poder variar devido a fatores genéticos e ambientais (Alaux, Ducloz, et al. 2010; López-Uribe et al. 2017; Jones et al. 2018).

1.3.2 Imunidade individual

Cada abelha de uma colônia possui resposta imune individual, podendo ser mecânica, fisiológica e imunológica. A cutícula e a membrana peritrófica revestindo o trato digestivo servem como uma primeira barreira mecânica impedindo a aderência ou entrada de microrganismos no corpo. Inibidores fisiológicos à invasão microbiana incluem alterações no pH e outras condições químicas do intestino de insetos tornando-o inóspito (Evans e Spivak 2010). Quando estas barreiras são ultrapassadas, as abelhas contam então com o sistema imune humoral (Evans et al. 2006; Wilson-Rich et al. 2008). Ele é ativado uma vez que reconhece motivos estruturais na superfície dos patógenos, os Padrões Moleculares Associados a Patógenos (PAMPs) (Brutscher et al. 2015). A sinalização desencadeada leva a ativação da resposta imune celular mediada por hemócitos, incluindo fagocitose, formação de nódulos e encapsulação da patógenos invasores, o início da cascata de fenoloxidase (PO) que regula a coagulação ou a melanização da hemolinfa, ou a síntese de AMPs (Casteels-Josson et al. 1994; Vizioli e Salzet 2002; Evans et al. 2006).

Algumas das vias da sinalização que controlam a expressão de AMPs e outros fatores antimicrobianos são Imd (*Immune Deficiency*), Jak/STAT (*Janus kinase/Signal Transducer and Activator of Transcription*) e Toll. Imd é uma via específica de resposta antimicrobiana que induz a produção de AMPs e outros genes envolvidos na defesa antimicrobiana através do fator de transcrição NF-κB Relish. A via de sinalização JAK-STAT contribui também para o sistema imune inato induzindo transdutores de sinal e ativadores de transcrição a regular efetores antimicrobianos como TEP7 (*Thioester-containing protein 7*), TEPA, TEPB e o inibidor SOCS (*Suppressor of Cytokine Signaling*). Já a ativação do complexo Toll leva a degradação do inibidor de NF-κB Cactus e então a translocação nuclear do fator de transcrição NF-κB Dorsal que por sua vez aumenta a expressão de AMPs (Royet et al. 2005; Evans et al. 2006; Brutscher et al. 2015). Estas vias desempenham um papel importante para a saúde da abelhas e a desestabilização contribui para o colapso de colônias. Um exemplo vem do parasitismo pelo o ácaro *V. destructor*, que desestabiliza a resposta imune da abelha através da supressão de NF-κB (Toll) possibilitando uma infecção mais virulenta pelo DWV (Nazzi et al. 2012).

Embora insetos não possuam anticorpos, que carregam a memória imunológica em vertebrados, eles possuem o que é chamado de imune *priming*, uma forma de imunidade transgeracional (Sadd et al. 2005; Freitak et al. 2014). Por exemplo, a prole de *A. mellifera* infectada experimentalmente por *P. larvae* tem maior resistência a uma nova infecção pelo patógeno (Hernández López et al. 2014). Posteriormente foi mostrado que a memória da infecção, que gerou resistência à prole, se dá através do transporte de fragmentos da parede celular do patógeno, contendo elicitores imunológicos, pela proteína vitelogenina (*Vg*) presente nos ovos (Salmela et al. 2015). A *Vg* também desempenha importante papel no controle do polietismo etário (Hartfelder et al. 2006; Dallacqua et al. 2007; Rodriguez Messan et al. 2018), agindo contra estresse oxidativo (Zhang et al. 2017; Park et al. 2018) e na resposta a patógenos (Alaux et al. 2011; Salmela et al. 2015; Steinmann et al. 2015). Uma menor expressão de *Vg* está associada à maturação comportamental acelerada e atividade de forrageamento em abelhas operárias, e a indução do forrageamento precoce pode também estar relacionada a uma resposta adaptativa contra transmissão de patógenos na colônia (Marco Antonio et al. 2008; Natsopoulou et al. 2016). As abelhas também possuem um sistema metabólico sofisticado que media a conversão de xenobióticos nocivos, como agroquímicos, em formas menos tóxicas. Uma das principais superfamílias enzimáticas responsáveis por esse mecanismo de desintoxicação são as monooxigenases do citocromo p450 (p450s), pertencentes à subfamília CYP9Q (Manjon et al. 2018). Já foi mostrado que p450s protegem as abelhas contra os efeitos tóxicos dos próprios inseticidas utilizados no controle de ácaros parasitas como *Varroa* (Mao et al. 2011). A expressão de p450s têm sido inclusive usada como um possível biomarcador em resposta a desafios por xenobióticos (Berenbaum e Johnson 2015; Manjon et al. 2018).

1.3.3 Microbioma de abelhas

As abelhas possuem relações com diversos simbiontes bacterianos, os quais desempenham um papel importante na saúde e homeostase do indivíduo, sendo mantidos nas populações por transmissão horizontal e vertical. A comunidade bacteriana melhor caracterizada até então é a de *A. mellifera*, que é composta por cinco grupos de bactérias: dois grupos de Proteobactérias (*Gilliamella* e *Snodgrassella*), dois grupos de Firmicutes (*Lactobacillus* Firm-4 e *Lactobacillus* Firm-5) e um de Actinobacteria (*Bifidobacterium asteroide*) (Kwong e Moran 2016). Estes grupos são também predominantes em *Bombus* e nas poucas abelhas sem ferrão já caracterizadas, sugerindo que esses *taxa* compreendem o microbioma intestinal padrão de abelhas corbiculadas (Kwong et al. 2017). Outras bactérias em menores quantidades e com nichos específicos no intestino da abelha melífera também compõem o microbioma, como *Frischella perrara*, *Bartonella apis*, *Parasaccharibacter apium* e uma bactéria relacionada à *Gluconobacter*. Enquanto *B. apis* e *F. perrana* são filotipos específicos de abelhas melíferas, Acetobacter-like parece ser um filotipo específico de abelhas sem ferrão (Kwong et al. 2017).

A riqueza e a composição da microbiota padrão influencia diretamente na saúde da abelha. Estudos experimentais mostraram que a suscetibilidade de *Bombus terrestris* ao parasita *Crithidia bombi* é predominantemente determinada pela composição da microbiota e apenas secundariamente pelo genoma do hospedeiro (Koch e Schmid-Hempel 2012). O metagenoma de *A. mellifera* sugere que as bactérias como *Snodgrassella* e *Gilliamella* auxiliam na produção de biofilmes e na comunicação celular da abelha, o que poderia contribuir para a proteção contra patógenos. Bactérias dos grupos Gamaproteobacteria, Firmicutes e Bifidobacteria estão provavelmente envolvidas com o transporte e quebra de carboidratos (Engel et al. 2012). O microbioma core também é importante pois, com a presença dessas bactérias intestinais controladas, as abelhas regulam positivamente a expressão gênica de AMPs como apidaecina e himenoptaecina, o que por sua vez estimula o sistema imunológico contra futuras infecções patogênicas (Kwong et al. 2017)**.** A disbiose, caracterizada por uma alteração na composição da microbiota padrão, pode ser causada por diversos fatores de estresse bióticos e abióticos (Hamdi et al. 2011). Pesticidas, por exemplo, podem alterar a abundância relativa de *taxa* microbianos no intestino das abelhas (Motta et al. 2018; Rouzé et al. 2019). A exposição de abelhas ao agroquímico Glifosato levou a uma diminuição na abundância relativa e absoluta de espécies dominantes da microbiota intestinal, como a bactéria *S. alvi,* e também aumentou a taxa de mortalidade de abelhas infectadas pela bactéria oportunista *S. marcescens* (Motta et al. 2018).

1.4 Objetivo

Investigar as causas da síndrome anual das mandaçaias (*Melipona quadrifasciata*) com um olhar para diferentes níveis de organização biológica da colônia e o impacto de estressores ambientais.

1.4.1 Objetivos específicos

- Caracterizar a microbiota intestinal de mandaçaias;
- Verificar a ocorrência de disbiose ou presença de bactérias patogênicas associadas a mandaçaias afetadas pela síndrome;
- Caracterizar o viroma de mandaçaias;
- Avaliar se existe uma relação entre a presença de vírus eucarióticos e a manifestação da síndrome;
- Investigar se mandaçaias adquiriram vírus da abelha exótica *A. mellifera*;
- Determinar a contribuição da genética das colônias e do ambiente para a ocorrência da síndrome;
- Mensurar a resposta imune e comportamental de mandaçaias, em nível de indivíduo e colônia, através de abordagem temporal;
- Investigar o papel de fatores ambientais no desencadeamento da síndrome anual.

CAPÍTULO 2

Report on the microbiota of *Melipona quadrifasciata* affected by a recurrent disease.

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Short Communication

Report on the microbiota of *Melipona quadrifasciata* affected by a recurrent disease

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ABSTRACT

Melipona quadrifasciata is an eusocial stingless bee traditionally used for honey production in Brazil. In the last decades, the species disappeared from the wild in Southern Brazil, being kept exclusively in managed colonies for commercial and recreational purposes. Stingless beekeepers from this region report annual losses of their colonies due to a syndrome of yet unknown causes. We investigate whether it is associated to pathogenic microorganisms already known to cause disease in bees. These results provide a starting point for future studies aimed at clarifying the relationship between the microbial community of stingless bees and their colony collapses.

1. Introduction

Stingless bees (Apidae, Meliponini) are the only highly social bees other than the true honeybees. In Brazil and other parts of South America stingless bees are by far the most abundant bee species, suggesting that they have a prominent role as pollinators in this region (Giannini et al., 2015; Heard, 1999). Before the introduction of honey bees in the 19th century, colonies of stingless bees and wasps were the only sources of honey used in Brazil (Nogueira-Neto, 1997), and stingless bee culture represents an old aboriginal tradition that helps to increase agricultural production by maintaining ecological interactions (Garibaldi et al., 2016). *Melipona quadrifasciata* is one of the most popular stingless bees cultivated in Brazil (Jaffé et al., 2015), where it is called “man daçaia”, which in the indigenous language means “beautiful vigilant”, referring to the guard that permanently protects the nest entrance. Two *M. quadrifasciata* subspecies that show significant genetic divergence are recognized by their different abdomen coloration patterns, i.e., *M. q. anthidioides*, found in the southeast and northern Brazil, and *M. q. quadrifasciata*, which occurs in the south (Batalha-Filho et al., 2010; Tavares et al., 2013).

In the southernmost sate of Brazil, Rio Grande do Sul, which corresponds to the southern limit of *M. quadrifasciata*’s geographic distribution, wild populations disappeared since more than 50 years, and the species is now regarded as endangered (Blochtein and Marques, 2003; Fundação Zoobotânica, 2014). Furthermore, numerous beekeepers from Rio Grande do Sul have been reporting annual losses of their *M. quadrifasciata* colonies. At the end of summertime, between February and April, workers become unable to fly and crawl with their proboscis everted, leading to massive deaths that ultimately end with the colony collapse. Although such collapses happen synchronously in many different localities, they can’t be connected to a common environmental factor, such as a potentially toxic flower or pesticides. Deaths occur in colonies from very dissimilar habitats.

Symbiotic bacteria are known to play an important role in bee health (Hamdi et al., 2011; Vásquez et al., 2012). Pathogens, viruses or other factors may interfere with the normal composition of bacteria associated to the bee gut epithelium (Cariveau et al., 2014;

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Cox-Foster et al., 2007) and in turn the bacterial colonization interferes with subsequent susceptibility to infections (Koch and Schmid-Hempel, 2012; Schwarz et al., 2016). The aim of the present study is to investigate whether the syndrome that annually leads to *M. quadrifasciata* colony collapses in Southern Brazil is correlated to infection with pathogenic bacteria. We describe, for the first time, the bacterial symbiont communities of this stingless bee species based on high throughput sequencing of 16S rDNA.

2. Materials and methods

2.1. Sampling and DNA extraction

M. quadrifasciata adult individuals manifesting symptoms of disease, i.e., disorientation, flight incapacity or proboscis eversion (unhealthy; n = 52) as well as without any detectable symptom (healthy; n = 24) were removed from their colonies for DNA extraction using a clean forceps. Stingless bee colonies were sampled in two summers (February/March) of 2014 and 2015 in two localities of Rio Grande do Sul, i.e., Boqueirão do Leão (30°3′9.7″S; 51°11′6.03″W) and Porto Alegre (30°4′30,3″S; 51°8′4.5″W). DNA was extracted using the DNeasy Blood & Tissue Kit (QIAGEN, Hilden, Germany) from individual abdomens, which were separated from bee bodies in aseptic conditions using sterile scalpels.

2.2. Metabarcoding of bacteria, and their possible link to disease

A segment of the bacterial 16S rDNA gene corresponding to the V1-V3 variable region was amplified from the DNA samples with modified barcoded versions of primers 27F (GAGTTTGATCNTGGCTCAG) (Lane, 1991) and 519R (GTNTTACNGCGGCKGCTG) (Turner et al., 1999) and sequenced using Illumina MiSeq technology. Reads were processed with Mothur v. 1.36.1 (Schloss et al., 2009). After filtering out low quality sequences, chimeras were removed with UCHIME (Edgar et al., 2011), as well non-bacterial sequences, based on a preliminary classification using the SILVA v123 nr database (Quast et al., 2013). Only samples containing at least 500× coverage were retained in subsequent analyses (n = 33; see Table S1). Sequences showing ⩾95% identity were clustered in Operational Taxonomic Units (OTUs). A non-metric multidimensional scaling (NMDS) of Bray-Curtis dissimilarities among bacterial communities was performed in PAST version 3.13 (Hammer et al., 2001). To investigate the dynamics of stingless bee microbiota we also performed a Permutational Multivariate Analysis of Variance (PERMANOVA) of Bray-Curtis pairwise distances, in which the factors “sampling year”, “colony” and “health status”, as well as their interactions, were tested as sources of variation in bacterial community composition. The phylogenetic affinities among principal bacterial OTUs was inferred by maximum likelihood using a dataset of known bee symbiont sequences obtained from GenBank as reference. Alignment was made with MAFTT v. 7.187 (Katoh and Standley, 2013), and phylogenetic analysis was performed with PhyML (Guindon and Gascuel, 2003) using the GTR + G + Inv model ($\alpha = 0.5$), which showed the best AIC score in ModelTest (Darriba et al., 2012). Local support values were estimated by nonparametric bootstrap based on 500 resamplings.

3. Results and discussion

The 16S rRNA amplicons from 33 *M. quadrifasciata* individuals belonging to 11 colonies (Table S1) yielded a total of 52,545 sequences (mean ± SD = 1592 ± 770 per sample) that were binned into 276 OTUs (mean ± SD = 29 ± 12 per sample). Rarefaction curves reach OTU saturation, indicating a good sampling (Fig. S1). The 32 OTUs with ⩾100 sequences (GenBank accesion numbers KX021311-KX021342) that represent 93.8% of the dataset were used for further analyses. The *M. quadrifasciata* bacterial symbiont OTUs were classified in 11 clades (Fig. 1), seven of them belonging to Firmicutes, which correspond to 73.4% of the total sampling.

Overall, the seven clades of Firmicutes and 3 OTUs of Proteobacteria belonging to the family Acetobacteriaceae are the most representative bacteria; Firmicutes Group U, Firmicutes Group Z and Acetobacteraceae correspond respectively to 23%, 23% and 16% of the total sampling. Though OTU frequencies show extensive variation across *M. quadrifasciata* individuals (Fig. 2), the factor that best explains variations in microbiota composition is the colony ($F = 2.752$; $p = 0.0006$); however no significant associations are found between year of sampling ($F = 1.112$; $p = 0.3405$) or stingless bee health status ($F = 0.854$; $p = 0.4915$) and microbiota composition. Interestingly, although main effects of sampling year and health status are not statistically significant, their interaction effect is ($F = 1.146$; $p = 0.0218$), suggesting that the effect of bee health status on microbiota composition is not the same in both years. Overall, there is a crossover effect of sampling year and health status on microbiota composition, which is possibly caused by the higher abundance of Firmicutes group U and Z bacteria in unhealthy bees on 2014, but in healthy bees of 2015 (see Fig. 2). This conclusion is also supported by NMDS, where unhealthy bees of different sampling years fall on opposite sides of coordinate 1 (Fig. S2). Therefore, we tentatively suggest that the syndrome manifested by *M. quadrifasciata* colonies may have a link to its microbiota composition, but we haven’t been able to detect it with this preliminary study. Nevertheless, no pathogenic bacteria known for the honeybee, such as *Spiroplasma*, *Melissococcus* and *Paenibacillus* that cause foulbrood disease, and mostly affect honeybee larvae (Bailey and Ball, 1991), were found in our samples.

The main bacterial OTUs identified in our study are phylogenetically related to other known bee symbionts (Fig. 1). Firmicutes group U is related to *Lactobacillus kunkeii*, and belongs to a clade of common symbionts of stingless bee species such as *Tetragonula carbonaria* and *Austroplebeia australis* (Fig. S3; Leonhardt and Kaltenpoth, 2014). Firmicutes group Z clusters with the so-called Firm-5 clade of lactic acid bacteria (Martinson et al., 2011). Different species from this clade were found in *Melipona panamica* (Koch et al., 2013), *Bombus* sp. (Praet et al., 2015) and *Apis mellifera* (Olofsson et al., 2014). The Lactobacillales and the Acetobacteraceae are mostly found in the honeybee stomach and rectum as well as in its hive products (Moran, 2015). Proteobacteria that are dominant in the honeybee ileum, such as *Gilliamella* and *Frischella* (Gammaproteobacteria) or *Snodgrassella* (Betaproteobacteria) are absent in our samples, concordant with previous studies of Meliponini microbiota (Koch et al., 2013). However, a clade of bacteria belonging to the Enterobacteriaceae (Gammaproteobacteria), which are common symbionts of the honeybee ileum, appears in low frequency in our dataset (2% of total sampling), but surprisingly in only four unhealthy individuals (Fig. 2; Table S1). The 16S sequence of this bacterium clusters with another found in the gut of *Eulaema* sp. (Euglossini) from Panama (Fig. 1), and is close to *Yokenella regensburgei* (Koch et al., 2013). Firmicutes group W, which represents 15% of our sampling, is phylogenetically related to *Streptococcus*, a bacterial genus known for causing opportunistic infections in larvae affected by foulbrood disease (Bailey et al., 1973). However, its previously reported presence in *M. panamica* (Koch et al., 2013), as well as the occurrence in healthy and unhealthy *M. quadrifasciata* individuals of the present study suggests a non-pathogenic interaction of *Streptococcus* and *Melipona*. Likewise, we haven’t been able to detect other well-known eukaryotic bee pathogens (*Nosema* or *Crithidia*) by PCR (data not shown).

The lack of any direct evidence leaves the question of what is killing *M. quadrifasciata* colonies in Southern Brazil still open. Bee-

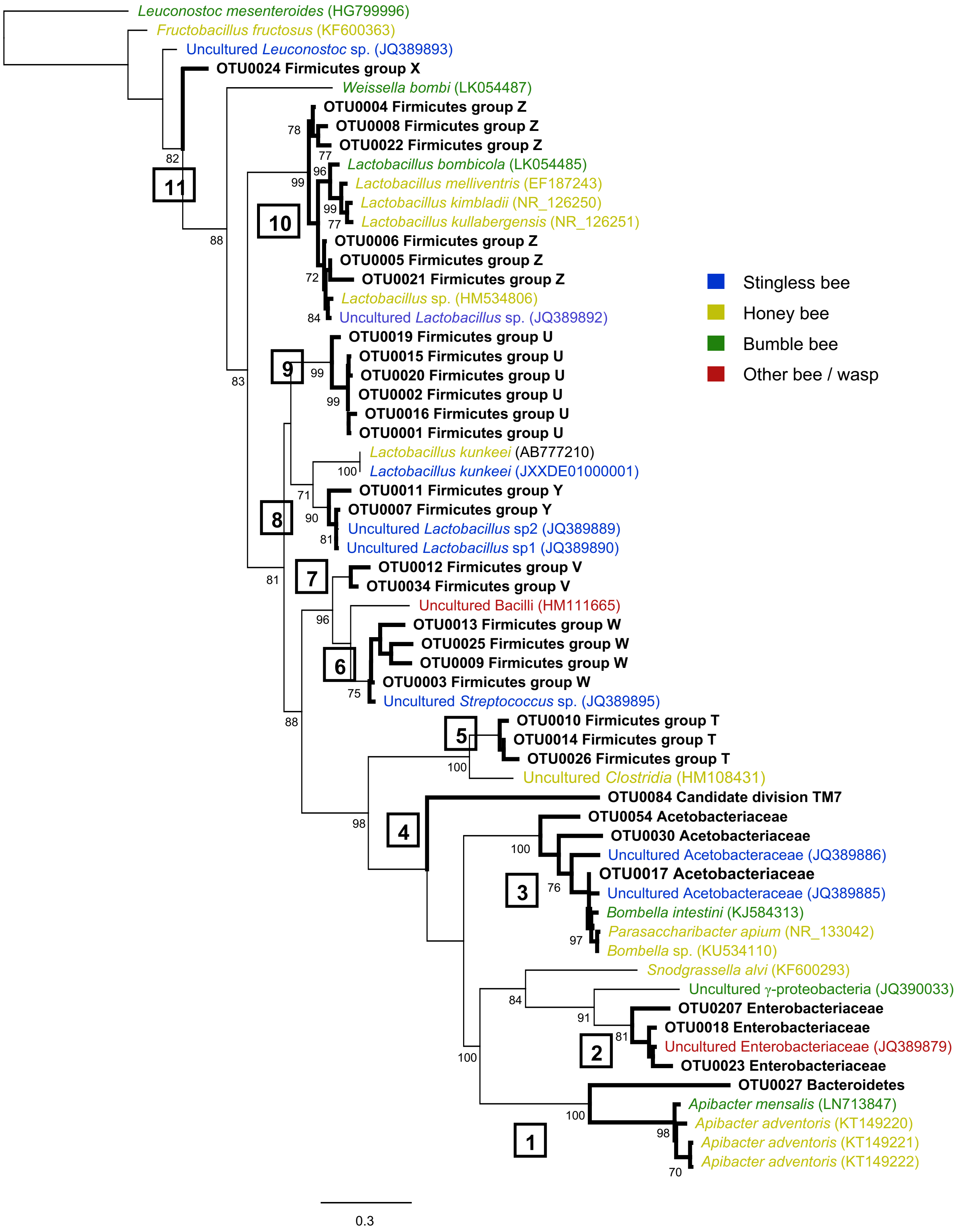

Fig. 1. Phylogenetic reconstruction based on bacterial 16S rRNA sequences. Thirty-two *Melipona quadrifasciata* symbiont OTUs belonging to 11 major clades (shown in bold) are compared to sequences from bacteria previously characterized for other bees, identified by their respective accession numbers. Bootstrap support values larger than 70% are shown at the respective branch nodes.

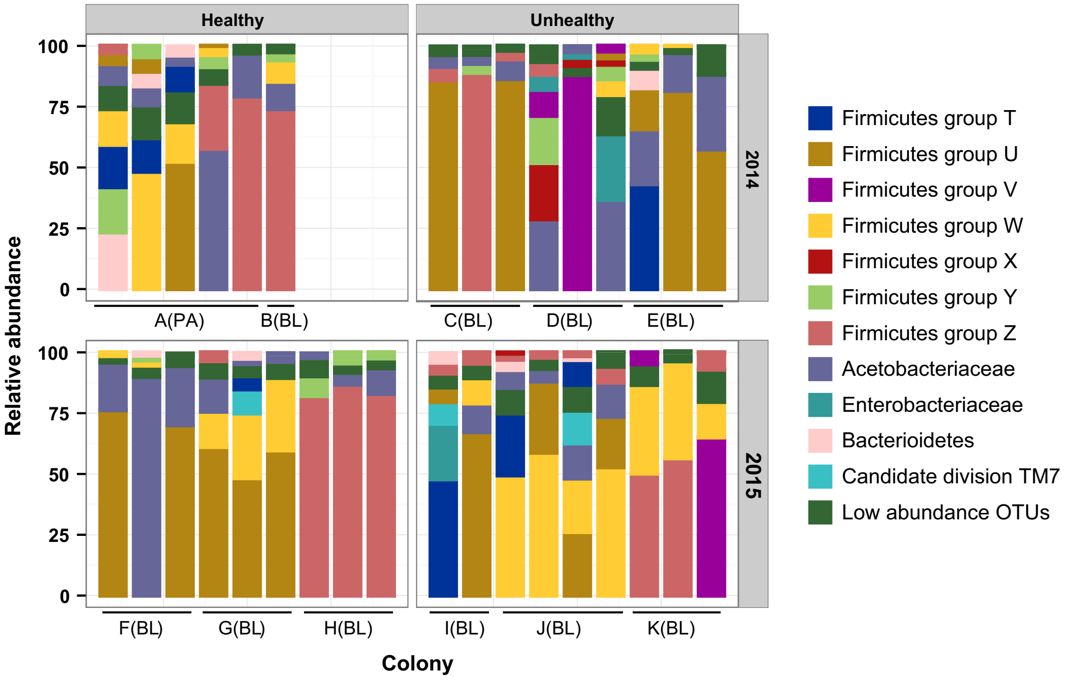

Fig. 2. Relative abundance of the 11 most representative bacterial taxa (clades) of healthy and unhealthy *Melipona quadrifasciata* sampled in two consecutive years. Letters indicate individuals from the same colony; PA and BL refer to the sampling localities, Porto Alegre and Boqueirão do Leão, respectively.

keepers learned that by preventing bees from leaving the colony, or by moving the colony to another locality, it is often possible to avoid the collapse, which makes them suspect that a toxic plant is poisoning their bees, but we observed that the pollen types in the crop of both healthy and unhealthy adults are indistinguishable (data not shown). *M. quadrifasciata* adults seem to forage mostly on *Eucalyptus* spp. – an observation corroborated by other studies on *Melipona* feeding habits in Southern Brazil (Hilgert-Moreira et al., 2014) – and on native Asteraceae, such as *Vernonanthura tweediana*, that bloom in the region in this time of the year. We think that, as already suggested for colony collapses of honeybees (Goulson et al., 2015; Nazzi et al., 2012; VanEngelsdorp et al., 2010), a synergistic effect of multiple factors, such as environmental stresses caused by climatic change, intensive management and the use of pesticides, as well as biological factors that haven't been assessed in the present study, such as viruses or other pathogens, may be at the heart of the problem.

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Appendix A. Supplementary material

Supplementary data associated with this article can be found, in the online version, at http://dx.doi.org/10.1016/j.jip.2016.11.012.

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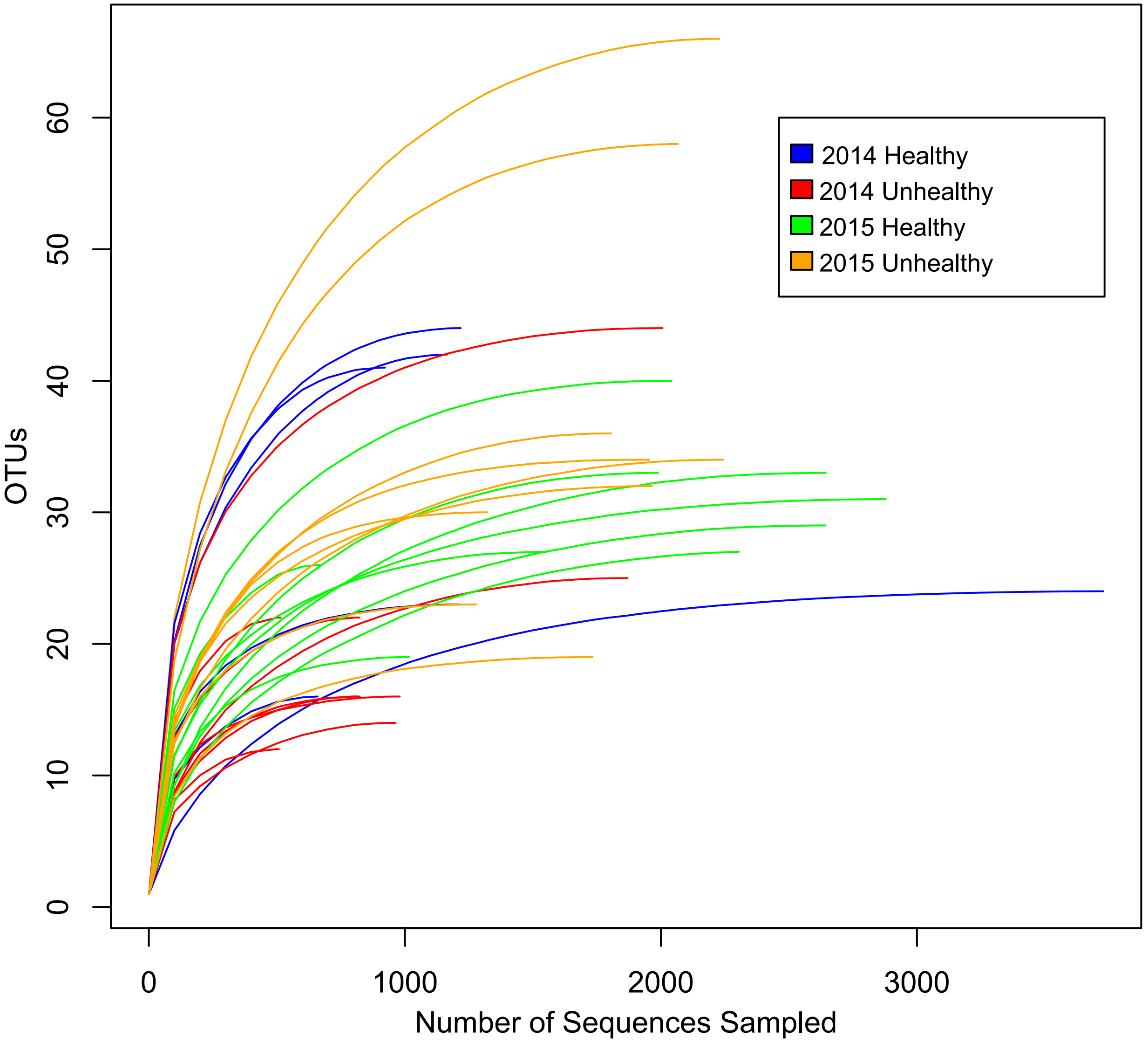
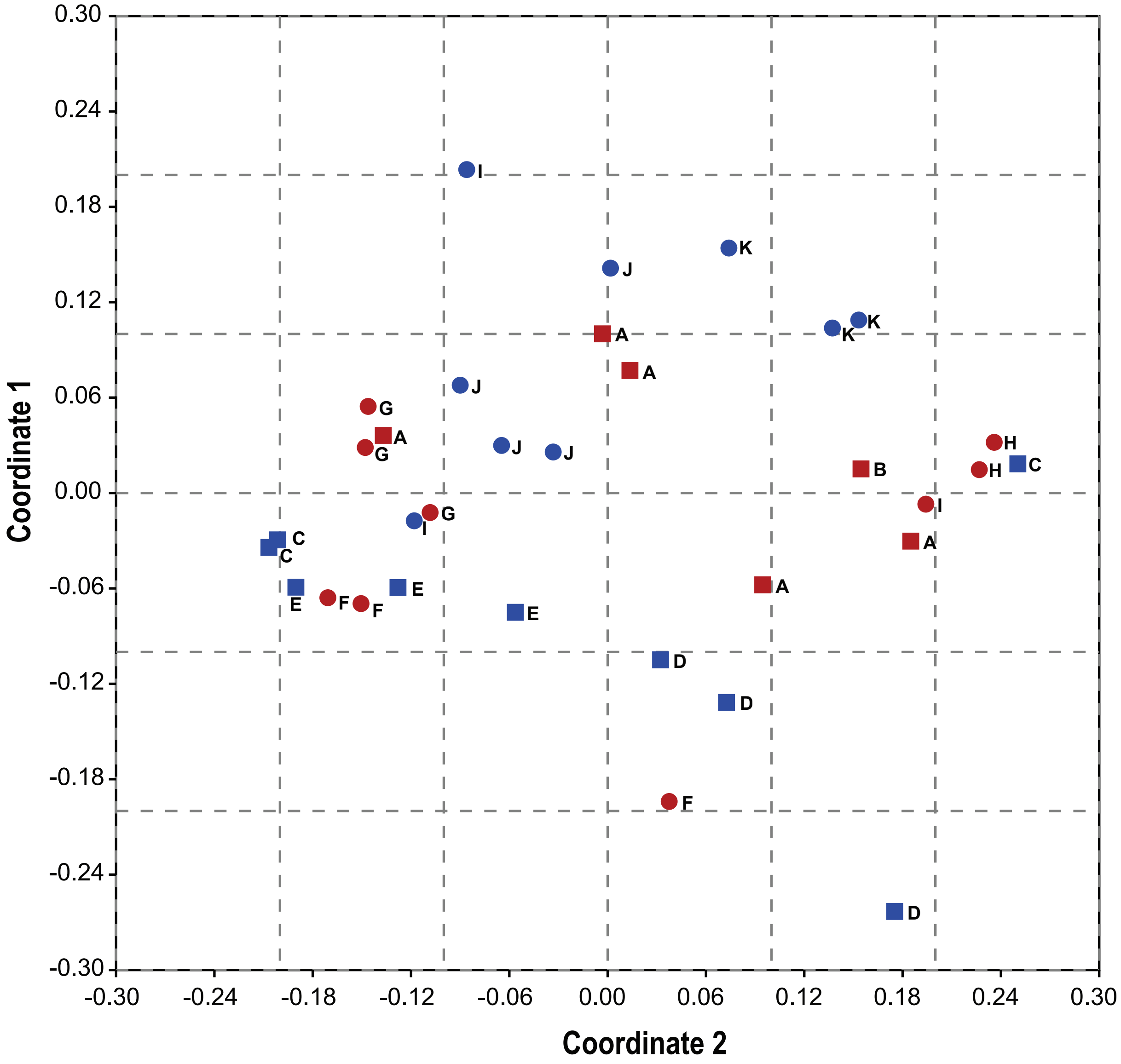
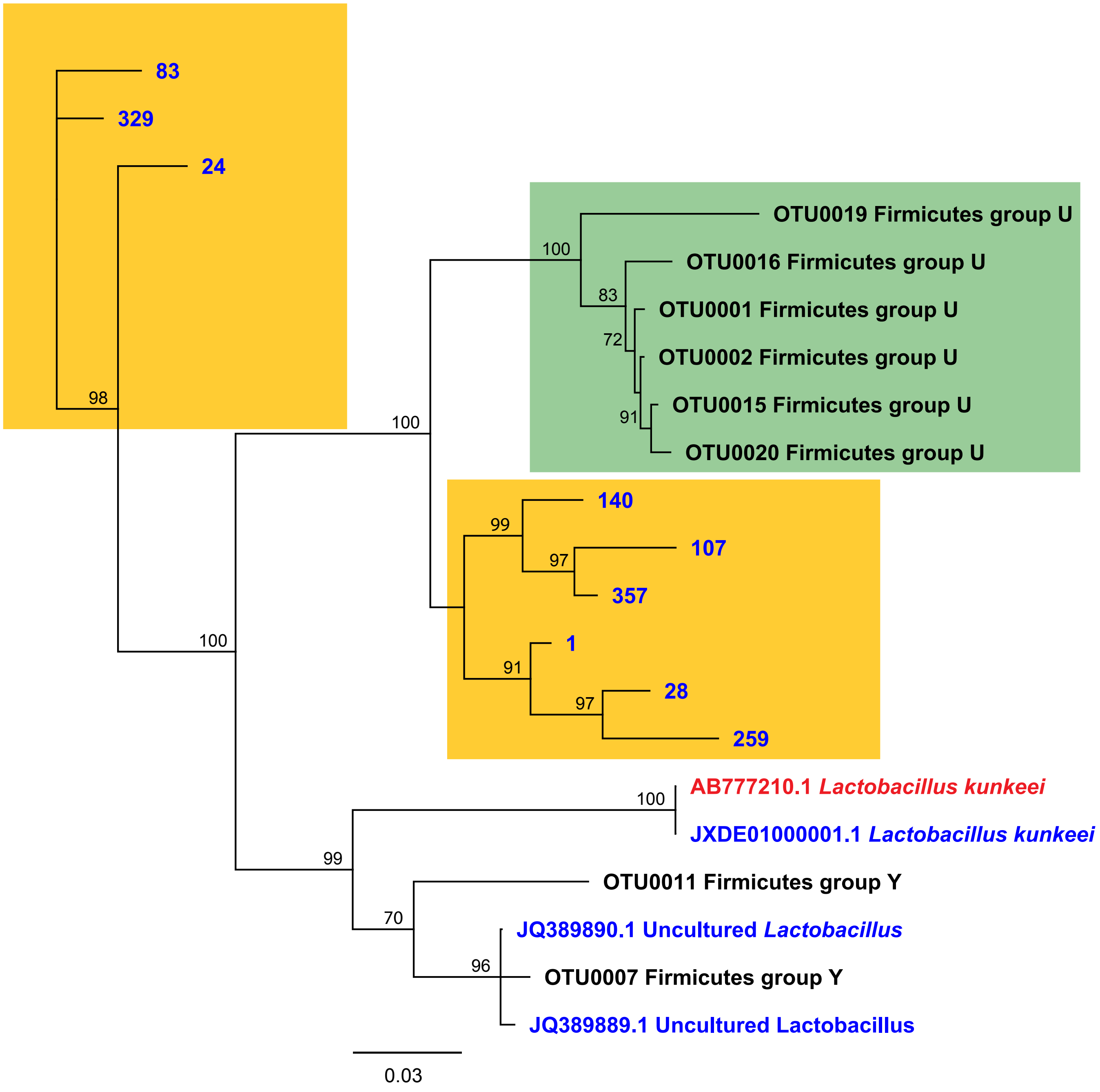


Supplementary Figure 1. Microbiota rarefaction curves. Each line represents the cumulative fraction of bacterial community represented by the OTUs sampled for each *Melipona quadrifasciata* individual.



Supplementary Figure 2. NMDS ordination plot. Microbial communities are discriminated by Bray-Curtis dissimilarity on two coordinates (stress=0.19). Samples derived from unhealthy and healthy stingless bees are shown in blue and red respectively; squares represent samples from 2014 and circles correspond to samples from 2015. Letters indicate the respective colony of each stingless bee.



Supplementary Figure 3. Phylogenetic relationships of OTUs belonging to Firmicutes group U. Yellow boxes indicate Meliponini-associated OTUs previously identified by Leonhardt and Kaltenpoth (2014) in Australian stingless bees. These bacteria belong to a sister clade of Halictidae-associated Lactobacillales (see Leonhardt and Kaltenpoth for details). Sequences obtained in our study are shown in black, whereas blue and red represent sequences obtained in other studies from stingless bees and honey bees, respectively.

Table S1

Group	Year	Local	Healthy	Colony	# Sequences	# OTUs	Shannon	Chao1	Inverse Simpson	Clade Abundance (%)											
										Firmicutes group T	Firmicutes group U	Firmicutes group V	Firmicutes group W	Firmicutes group X	Firmicutes group Y	Firmicutes group Z	Acetobacteriaceae	Enterobacteriaceae	Bacteroidetes	Candidate division TM7	Low abundance OTUs
Agr10	2014	PA	Yes	A	1166	42	2.61	42.00	8.74	17.41	4.55	0.00	14.67	0.00	18.61	2.92	8.15	0.00	23.33	0.00	10.38
Agr13	2014	PA	Yes	A	922	41	2.37	41.00	4.59	13.77	5.10	0.00	48.26	0.00	4.77	0.76	7.81	0.00	5.97	0.00	13.56
Agr14	2014	PA	Yes	A	1218	44	2.45	44.00	6.54	10.51	52.38	0.00	16.26	0.00	0.49	0.33	3.78	0.00	3.12	0.00	13.14
Agr30	2014	PA	Yes	A	1214	23	1.68	23.00	2.83	0.00	1.57	0.00	2.14	0.00	5.11	26.69	57.74	0.00	0.00	0.00	6.75
Agr33	2014	PA	Yes	A	3727	24	0.76	24.00	1.57	0.00	0.00	0.00	0.13	0.00	0.21	79.23	17.63	0.00	0.00	0.00	2.79
Wal00	2014	PA	Yes	B	659	16	1.85	16.00	5.11	0.00	0.00	0.00	8.80	0.00	3.34	74.05	11.23	0.00	0.00	0.00	2.58
Mq021	2014	BL	No	C	824	16	1.36	16.00	2.75	0.00	85.92	0.00	0.85	0.00	0.00	5.46	4.85	0.00	0.00	0.00	2.91
Mq023	2014	BL	No	C	813	16	1.27	16.00	2.61	0.00	0.25	0.00	0.86	0.00	3.69	88.93	3.69	0.00	0.00	0.00	2.58
Mq024	2014	BL	No	C	508	12	1.32	12.00	2.63	0.00	86.42	0.00	0.59	0.00	0.00	3.54	8.07	0.00	0.00	0.00	1.38
Mq1A1	2014	BL	No	D	515	22	2.26	22.00	7.39	0.00	0.78	10.68	0.97	23.11	19.42	5.24	28.74	6.21	0.00	0.00	4.85
Mq1A3	2014	BL	No	D	1870	25	0.71	25.00	1.31	0.00	0.00	88.02	0.21	3.37	0.16	0.21	1.93	2.35	0.00	0.00	3.74
Mq1A4	2014	BL	No	D	2006	44	2.56	44.00	7.91	0.00	2.34	2.29	6.48	3.09	5.98	0.00	36.69	27.02	0.00	0.00	16.10
Mq1B1	2014	BL	No	E	823	22	2.12	22.00	6.05	43.13	16.89	0.24	2.43	0.00	3.28	0.00	22.60	0.00	8.02	0.00	3.40
Mq1B2	2014	BL	No	E	964	14	1.34	14.00	2.90	0.00	81.54	0.00	1.24	0.00	0.31	0.00	15.56	0.00	0.00	0.00	1.35
Mq1B3	2014	BL	No	E	980	16	1.67	16.00	4.10	0.00	57.45	0.00	0.61	0.00	0.00	0.00	30.71	0.00	0.00	0.00	11.22
MqVD1	2015	BL	Yes	F	2304	27	1.38	27.00	3.01	0.00	76.26	0.00	1.26	0.00	0.00	0.48	19.57	0.00	0.00	0.00	2.43
MqVD2	2015	BL	Yes	F	2644	33	0.73	33.00	1.30	0.00	0.15	0.00	2.12	0.00	1.97	1.17	89.94	0.00	0.00	0.00	4.65
MqVD3	2015	BL	Yes	F	2643	29	1.48	29.00	3.27	0.00	70.07	0.00	0.38	0.00	0.00	0.76	24.33	0.00	0.00	0.00	4.46
MqVF1	2015	BL	Yes	G	669	26	2.17	26.00	5.89	0.00	61.14	0.00	14.50	0.00	0.00	3.59	14.05	0.00	0.00	0.00	6.73
MqVF2	2015	BL	Yes	G	2041	40	2.28	40.00	6.20	5.39	48.31	0.00	26.60	0.00	0.00	0.78	2.20	0.00	1.81	9.90	5.00
MqVF3	2015	BL	Yes	G	1554	27	2.00	27.00	5.04	0.00	59.72	0.00	29.79	0.00	0.00	1.03	2.83	0.00	0.00	0.00	6.63
MqVG1	2015	BL	Yes	H	2878	31	1.55	31.00	2.78	0.00	0.00	0.07	0.45	0.00	8.13	82.07	1.70	0.00	0.00	0.07	7.51
MqVG2	2015	BL	Yes	H	1989	33	1.50	33.00	2.48	0.00	0.50	0.00	0.35	0.00	3.67	86.78	4.88	0.00	0.00	0.00	3.82
MqVG3	2015	BL	Yes	H	1016	19	1.54	19.00	3.00	0.00	0.00	0.00	0.79	0.00	1.67	82.97	10.53	0.00	0.00	0.00	4.04
MqVB4	2015	BL	No	I	1806	36	2.04	36.00	4.75	47.84	6.04	0.00	0.11	0.00	0.00	4.49	0.39	22.81	3.71	8.91	5.70
MqVB5	2015	BL	No	I	1322	30	1.95	30.00	4.53	0.00	67.25	0.00	10.36	0.00	0.00	4.61	11.80	0.00	0.00	0.00	5.98
MqVE1	2015	BL	No	J	2067	58	2.12	58.00	3.97	25.45	1.02	0.00	49.44	0.00	0.10	1.50	7.40	0.00	4.21	0.39	10.50
MqVE2	2015	BL	No	J	2243	34	1.77	34.00	3.46	0.00	29.29	0.00	58.76	0.00	0.00	2.18	5.17	0.00	0.00	0.00	4.59
MqVE3	2015	BL	No	J	2228	66	2.73	66.00	9.43	10.23	26.17	0.00	21.99	0.00	0.00	1.53	14.45	0.00	1.57	13.46	10.59
MqVE4	2015	BL	No	J	1954	34	1.93	34.00	3.89	0.00	20.73	0.00	52.81	0.00	0.00	6.55	14.02	0.00	0.00	0.00	5.89
MqVH1	2015	BL	No	K	1966	32	1.91	32.00	4.27	0.00	0.20	4.53	36.42	0.00	0.00	50.20	0.10	0.00	0.00	0.00	8.55
MqVH2	2015	BL	No	K	1733	19	1.54	19.00	3.64	0.00	0.29	0.00	39.87	0.00	0.00	56.49	0.12	0.00	0.00	0.00	3.23
MqVH3	2015	BL	No	K	1279	23	1.67	23.00	2.91	0.00	0.00	65.05	14.62	0.00	0.55	6.49	0.00	0.00	0.00	0.00	13.29

CAPÍTULO 3

The virome of an endangered stingless bee suffering from annual mortality in southern Brazil

Este capítulo apresenta o seguinte artigo publicado:

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The virome of an endangered stingless bee suffering from annual mortality in southern Brazil

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Abstract

Meliponiculture – the management of stingless bee colonies – is an expanding activity in Brazil with economic, social and environmental potential. However, unlike in apiculture, the pathogens that impact on meliponiculture remain largely unknown. In southern Brazil, every year at the end of the summer, managed colonies of the stingless bee *Melipona quadrifasciata* manifest a syndrome that eventually leads to collapse. Here we characterize the *M. quadrifasciata* virome using high-throughput sequencing, with the aim of identifying potentially pathogenic viruses, and test whether they are related to the syndrome outbreaks. Two paired viromes are explored, one from healthy bees and another from unhealthy ones. Each virome is built from metagenomes assembled from sequencing reads derived either from RNA or DNA. A total of 40621 reads map to viral contigs of the unhealthy bees' metagenomes, whereas only 11 reads map to contigs identified as viruses of healthy bees. The viruses showing the largest copy numbers in the virome of unhealthy bees belong to the family *Dicistroviridae* – common pathogenic honeybee viruses – as well as *Parvoviridae* and *Circoviridae,* which have never been reported as being pathogenic in insects. Our analyses indicate that they represent seven novel viruses associated with stingless bees. PCR-based detection of these viruses in individual bees (healthy or unhealthy) from three different localities revealed a statistically significant association between viral infection and symptom manifestation in one meliponary. We conclude that although viral infections may contribute to colony collapses in the annual syndrome in some meliponaries, viruses spread opportunistically during the outbreak, perhaps due to colony weakness.

INTRODUCTION

Stingless bee management in Brazil began with indigenous South Americans, who domesticated the non-aggressive native bees as a source for honey [1]. One of these bees, *Melipona quadrifasciata*, which is distributed from the state of Paraíba in the north of Brazil through to the southernmost state, Rio Grande do Sul [2], is the second most cultivated stingless bee in Brazil [3]. In spite of being widely cultivated, natural populations of stingless bees in the neotropics have reduced drastically in recent years due to different factors, ranging from habitat fragmentation to the introduction of exotic bees [4] that not only compete for resources, but also bring new pathogens to which native bees might be susceptible. In most of southern Brazil, wild populations of the subspecies *M. q. quadrifasciata* have been disappearing for 50 years. The species is currently mostly maintained through management

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Keywords: *Melipona*; Apidae; virome; colony collapse; bee virus.

Abbreviations: ABPV, *Acute bee paralisys virus*; BLAST, Basic Local Alignment Search Tool; BQCV, *Black queen cell virus*; BU, Barnard's Uunconditional test; CCD, Colony collapse disorder; CDS, Coding sequence; CMH, Cochran-Mantel-Haenszel; DWV, *Deformed wing virus*; IAPV, *Israeli acute paralysis virus*; KBV, *Kashmir bee virus*; MqC, *Melipona quadrifasciata cyclovirus*; MqC1, *Melipona quadrifasciata cyclovirus 1*; MqC2, *Melipona quadrifasciata cyclovirus 2*; MqD, *Melipona quadrifasciata densovirus*; MqV2, *Melipona quadrifasciata virus 2*; MqV1a, *Melipona quadrifasciata virus 1a*; MqV1b, *Melipona quadrifasciata virus 1a*; SBPV, *Slow bee paralysis virus*; VDV1, *Varroa destructor virus-1*.
MK190907 (MqC1), MK190906 (MqC2), MH340498 (MqD), MH340499 (MqV1a) and MH34500 (MqV1b), MK190905 (MqV2).
Two supplementary figures and four supplementary tables are available with the online version of this article.

in this region, and is therefore considered to be endangered [5, 6]. Managing stingless bees has been crucial for conservation, but on the other hand, practices that involve hive translocation may also spread pathogens [7]. Despite advances in beekeeping legislation and monitoring, there is no official bee surveillance in Brazil and, consequently, there are no regular records on bee mortality caused by pathogens. Nevertheless, it is a common knowledge among beekeepers from different localities in southern Brazil that every year at the end of the summer – normally during the first week of March – their *M. quadrifasciata* bees begin to manifest an unusual behaviour that may include tremors, crawling with everted proboscis and paralysis [8]. Although the disease symptoms are quite variable among stingless bees from different localities, during this period it is common to find large numbers of dead bees inside or in front of hives. Mortality, and the inability of bees to perform their regular activities, sometimes lead to colony collapse. Our previous studies on the *M. quadrifasciata* syndrome searched the associated microbiota for pathogenic bacteria or imbalances in bacterial community composition that could explain the symptoms [8]. However, no consistent differences in microbiota composition were found between healthy and unhealthy bees. While *Apis mellifera* shows a highly conserved core microbiota [9], *M. quadrifasciata*'s associated bacterial community is highly variable across colonies, independent of their health status. Furthermore, no pathogenic bacteria or other common bee pathogens such as *Nosema* and *Crithidia*, were detected in unhealthy bees.

Several viruses have already been identified in *A. mellifera* in Brazil [10], mainly in samples from areas where abnormal population declines have been observed [11]. These have included *Iflaviridae* such as the *Deformed wing virus* (DWV), and *Dicistroviridae* such as the *Black queen cell virus* (BQCV), *Acute bee paralysis virus* (ABPV) and *Israeli acute paralysis virus* (IAPV) [11, 12]. Characteristic symptoms of DWV infections are the death of pupae, or adult bees with deformed wings, sometimes associated with shortened and bloated abdomens, and miscolouring [13]. However, DWV may persist in covert infections with no apparent symptoms [14, 15], in spite of having strongly deleterious effects on honeybee foraging and survival [16]. Similarly, dicistroviruses may also persist with no obvious symptoms at the individual or colony level [17]. Nevertheless, it has been shown that an increase in BQCV titre kills developing queen larvae, whose necrotic remains result in a pupal cell with a darkened colour [18]. Other viruses of this family, such as ABPV and IAPV, are known to cause paralysis [19, 20]. They are extremely virulent when injected into pupae or adults, causing disease in the honeybee with fewer than 100 viral particles [21]. Honeybees experimentally infected with IAPV develop symptoms such as crawling, disorientation and trembling wings, which progress to paralysis and death within or outside the hive [22, 23]. Furthermore, viruses with RNA genomes such as the *Iflaviridae* and *Dicistroviridae*, which show higher mutation rates, quickly evolve into many variants, allowing them to switch between different bee hosts [24–26]. An example of viral host switching between bee species is the detection of honeybee virus ABPV in managed colonies of *M. scutellaris* suffering from an unexpected increase in worker bee mortality in Brazil [27].

The main routes of virus transmission between bees are vectors such as mites or pollen resource sharing [28]. The most studied vector in honeybees is *Varroa destructor*, which transmits different lineages of DWV, *Varroa destructor virus*-1 (VDV1) and IAPV [29–31]. These and many other viruses are also transmitted within and between species via floral sources [24, 32]. Bee species sharing habitats and resources tend to have similar associated micro-organisms. A study on viral distribution via pollen sources showed that in apiaries with colonies affected by colony collapse disorder (CCD), IAPV virus was associated with *A. mellifera* as well with non-*Apis* hymenopteran pollinators [32]. At the same time, in nearby apiaries not affected by CCD, the virus was present in neither *A. mellifera* nor non-*Apis* hymenopterans. The persistence of BQCV, DWV, ABPV and *Slow bee paralysis virus* (SBPV) in wild bumblebee populations in Europe, often at putatively low levels, may also result from indirect interactions with local *A. mellifera* through the shared use of floral resources [24].

Recent studies using high-throughput sequencing technologies expanded the list of known honeybee viruses, previously restricted to the Picornavirales [33]. Among the recently identified viruses are those from the family *Rhabdoviridae* with −ssRNA genomes , ssDNA viruses belonging to the families *Circoviridae* and *Parvoviridae*, and dsDNA viruses from the family *Nudiviridae* [34–36]. These viruses were identified in honeybees displaying variable health conditions. Hence, the viromes of bees have revealed that, in addition to the complex network of host-associated bacteria [9], a very diverse range of viruses are probably acting on and interacting in the bacterial network. Different bee viruses are frequently detected in healthy and unhealthy hosts [24, 34, 35, 37]. Chronic viral infections may become harmful by increasing their loads in genetically predisposed individuals, depending on the environmental conditions [37–39], or may become symbiotic [40].

Given that the symptoms observed in *M. quadrifasciata* affected by the annual syndrome resemble those of honeybee viral diseases such as IAPV and ABPV, and given that stingless bees probably host yet unidentified viruses, some of which may have been spread by honeybees due to beekeeping practices, we focus our investigation on viruses that might be implicated in the disease. Using high-throughput sequencing to characterize the virome of *M. quadrifasciata,* we identify seven novel stingless bee viruses.

RESULTS

Viromes of healthy and unhealthy *M. quadrifasciata*

In order to find viruses associated with the *M. quadrifasciata* syndrome, worker bees from a single colony showing disease symptoms such as tremor and paralysis (unhealthy bees), as well as workers from another colony where none of the individuals showed such symptoms (healthy bees), were sampled from the same meliponary (place where stingless bees are reared). Each bee pool was macerated and underwent subsequent centrifugation steps, including an ultracentrifugation with a sucrose cushion for virus enrichment. The nucleic acids were then subjected to high-throughput sequencing, yielding the following number of paired-end reads: 640 953 (DNA sample from unhealthy bees=UDNA), 535 631 (DNA sample from healthy bees=HDNA), 582 603 (RNA sample from unhealthy bees=URNA) and 834 753 (RNA sample from healthy bees=HRNA). After assembly, viral contigs larger then 200 bp were classified based on the best BLASTX hit against the nr database, resulting in a total of 989 viral sequences. From these, only five were recovered from healthy bees (three from DNA and two from RNA), whereas all remaining 984 viral sequences were assembled from unhealthy bees.

From the total of 989 viral sequences (Table S1, available in the online version of this article), 901 were identified as bacteriophages and 17 were identified as viruses of unclassified or unknown hosts, and for the purpose of the present study, we focused on the remaining 71 sequences, which were identified as eukaryotic viruses (Fig. 1). The HRNA sample was left out of Fig. 1, since both viral contigs assembled from the RNA of healthy bees were identified as bacteriophages. Thus, the virome of healthy bees contained only three sequences from eukaryotic viruses that belonged to two different families. The virome of unhealthy bees, on the other hand, contained 38 sequences from viruses belonging to 11 different families, as well as 30 contigs showing similarity to unclassified viruses previously found in eukaryotes (Fig. 1). Using sequencing depth as a proxy for abundance, i.e. the number of copies of viruses within each virome, the most representative viruses in unhealthy bees (50–140 X depth) belonged to the families *Parvoviridae* (ssDNA genome) and *Circoviridae* (ssDNA genome). Viruses identified as *Dicistroviridae* (+ssRNA genome) that included potential honeybee pathogens showed lower sequencing depth, ranging from 8 to 15 X.

Characterization of novel *M. quadrifasciata* viruses

Seven eukaryotic viral sequences with significant length and depth were selected as candidates for further investigation: *Melipona quadrifasciata cyclovirus* (MqC), *Melipona quadrifasciata cyclovirus* 1 (MqC1) and *Melipona quadrifasciata cyclovirus* 2 (MqC2) from the family *Circoviridae*; *Melipona quadrifasciata densovirus* (MqD) from the family *Parvoviridae*; *Melipona quadrifasciata virus* 1a and 1b (MqV1a and MqV1b) from the family *Dicistroviridae*; and *Melipona quadrifasciata virus* 2 (MqV2), which is unclassified (Table S1). To evaluate whether these sequences represent already known or novel viruses, predicted proteins derived from their coding sequences (CDSs) were used for phylogenetic analyses. None of them showed sufficient similarity to other known viruses to be regarded as the same species.

The most abundant virus found in unhealthy stingless bees belonged to the family *Parvoviridae* (MqD; Table S1). The MqD sequence (4214 nt) probably represents a complete genome, encoding the non-structural (534 aa) and structural (655 aa) proteins, containing conserved domains Parvo_NS1 (cl24009, e-value 4.57e^{-10}) and Denso_VP4 (cl03545, e-value 4.83e^{-15}), respectively. Phylogenetic inference based on their concatenated amino acid sequences groups MqD with other *Parvoviridae* found mainly in insects, within the genus *Densovirus* (Fig. S1), such as the recently described *Bombus cryptarum densovirus* [34].

Two *Circoviridae* sequences from unhealthy bees also contained recognizable CDSs: MqC1 and MqC2 (Table S1). MqC1 (1587 nt) is probably a complete genome as well, from which the non-structural protein (228 aa), with a P-loop_NTPase domain (cl21455, e-value 7.94e^{-18}), and the structural protein (224 aa) are predicted. MqC2 (673 nt) is a partial virus genome bearing a partial non-structural protein (224 aa) with the P-loop_NTPase domain (e-value 3.34e^{-18}). These two viruses cluster with viruses from the family *Circoviridae* within the genus *Cyclovirus* (Fig. 2), a sister clade of the genus *Circovirus*, that were found recently in *A. mellifera* (Circo-like 1 and Circo-like 2) [35].

Two other partial viral genomes show similarity to *Dicistroviridae* viruses: MqV1a (5913 nt) and MqV1b (1236 nt) (Table S1). A single protein is predicted from each, i.e. the structural protein (1888 aa), with RNA_dep_RNAP (cd01699, e-value 9.44e^{-83}) and RNA_helicase (pfam00910, e-value 1.24e^{-31}) domains, is encoded by MqV1a, whereas the partial non-structural protein (412 aa), with RHV_like (cd00205, e-value 5.94e^{-23}) and Dicistro_VP4 (cl13011, e-value 4.36e^{-08}) domains, is predicted from MqV1b. Both proteins group these viruses within *Dicistroviridae* known to infect bees and other arthropods (Fig. 3), such as ABPV and IAPV. However, the amino acid identities between MqV1a or MqV1b proteins and known ABPV and IAPV proteins are within the order of 28–15% and 29–16 %, respectively.

MqV2 (3730 nt) shows an unclassified virus as best hit (Table S1), and encodes a non-structural protein (479 aa), which contains RT_like (cl02808, e-value 8.87e^{-11}) and RdRP_3 (cl24119, e-value 2.48e^{-05}) domains. MqV2 is related to other unclassified RNA viruses that are found to be associated with a diversity of hosts, from plants to animals such as birds, molluscs and bees (Fig. S2) [41].

Virus detection in stingless bees and honeybees

Having characterized seven novel eukaryotic viruses found in high abundance in unhealthy stingless bees, we tested whether their presence is associated with the manifestation of disease symptoms (Table S2). We reasoned that if a virus is directly implicated in the annual syndrome, it should be detected more often in unhealthy than in healthy bees of different meliponaries. Virus detection by PCR was performed by testing individual worker bees to determine if the disease symptoms were present in three different meliponiaries, using primers designed to amplify fragments of about 300 bp from each virus genome (Table 1). Table 2 summarizes the results of Cochran–Mantel–Haenszel (CMH) tests, which were used to verify the association between the detection of each candidate virus with the manifestation of symptoms, controlled

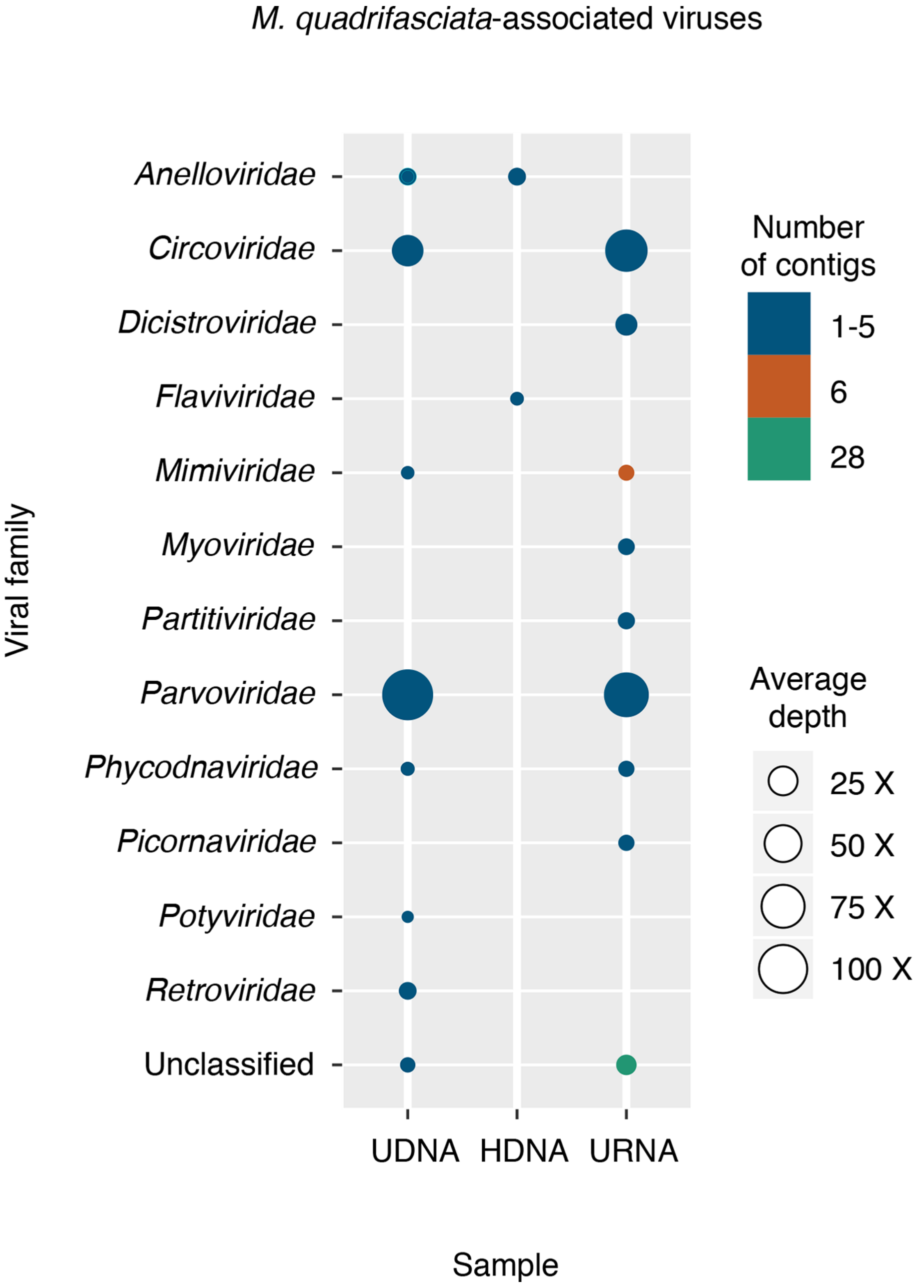

Fig. 1. Taxonomic distribution of *M. quadrifasciata* viral contigs in metagenomes of healthy (HDNA) and unhealthy bees (UDNA and URNA). Only contigs larger than 200 bp and showing best hits on eukaryotic viruses are considered in this plot. Sequences of viral families showing larger sequencing depth (larger circles) were chosen as candidates in subsequent analyses.

by locality, and the results of Barnard's unconditional (BU) tests applied to individual localities. All viruses were detected in both healthy and unhealthy bees, and only MqV1a was detected in bees from all meliponaries. None of the viruses were found to be significantly more associated with the syndrome manifestation in all localities in view of the CMH test. However, MqC, MqD and MqV1a viruses were more often associated with unhealthy bees in the Boqueirão do Leão (BL) meliponary, where *M. quadrifasciata* was sampled to build the viromes. Interestingly, the three circoviruses (MqC, MqC1 and MqC2) and the unclassified virus MqV2 were also detected in *A. mellifera* colonies from one of the sampling localities [Bom Princípio (BP)] (see Table 2).

DISCUSSION

Bee populations have been declining for some years, leading to global concern over the plight of plant pollinators [42, 43].

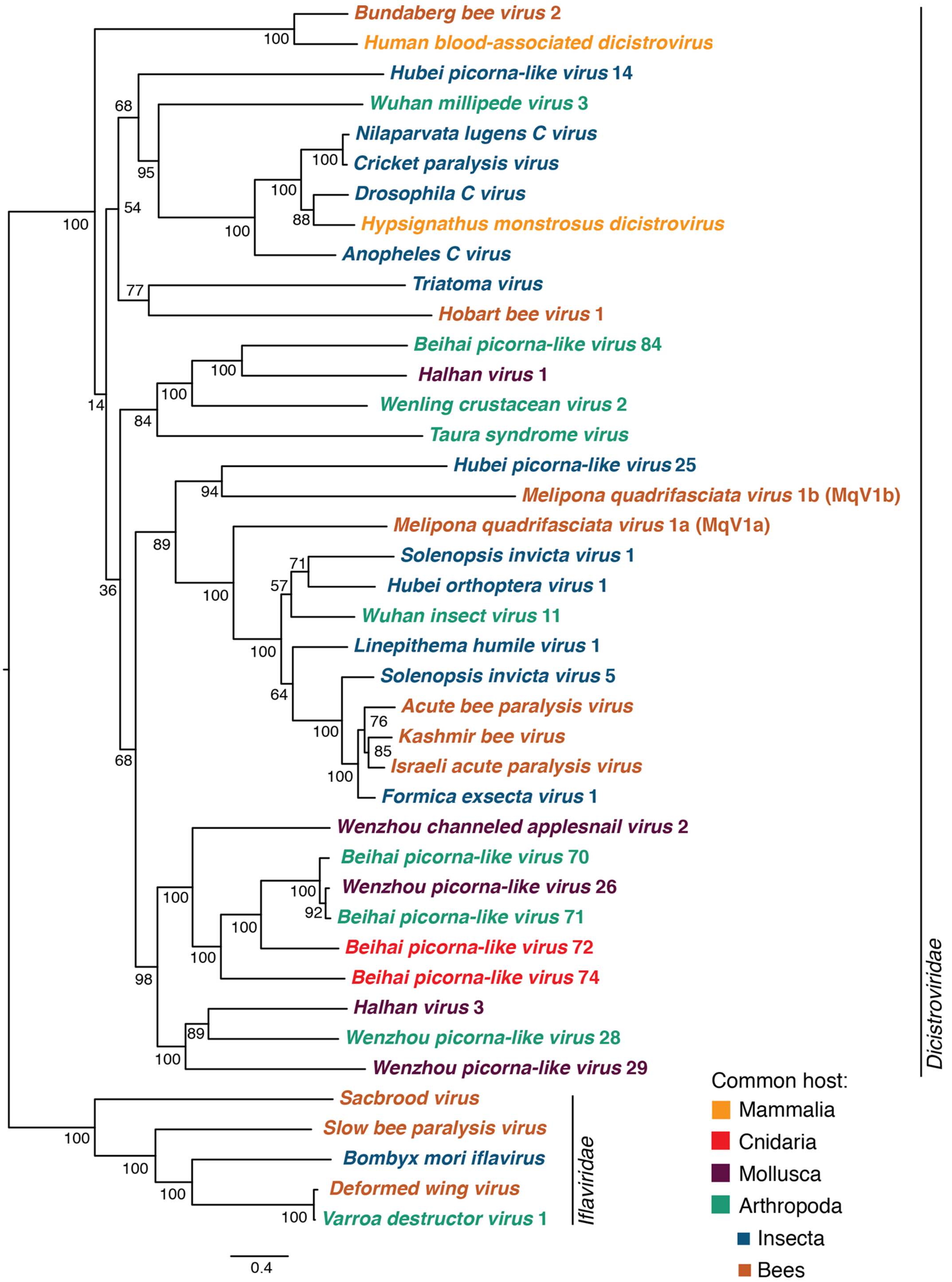

Fig. 2. Phylogenetic inference of MqC1 and MqC2 viruses (*Circoviridae*). The maximum-likelihood tree was inferred with 100 bootstrap resamples based on an alignment of 502 aa. The colours of the species names represent the viruses' common hosts (see lower right).

Viruses that are prevalent in weak colonies of honeybees are probably directly implicated in the population decline of different bee species [44–46]. For example, honeybee colonies affected by CCD, a syndrome characterized by the sudden disappearance of honeybees [47], often show higher prevalence of IAPV, ABPV or *Kashmir bee virus* (KBV) [48, 49]. The apparent spread of CCD in the USA suggests that viruses, among numerous other factors such as pesticides, stress, climate and habitat change, and other natural enemies, could cause honeybee populations to drop so much

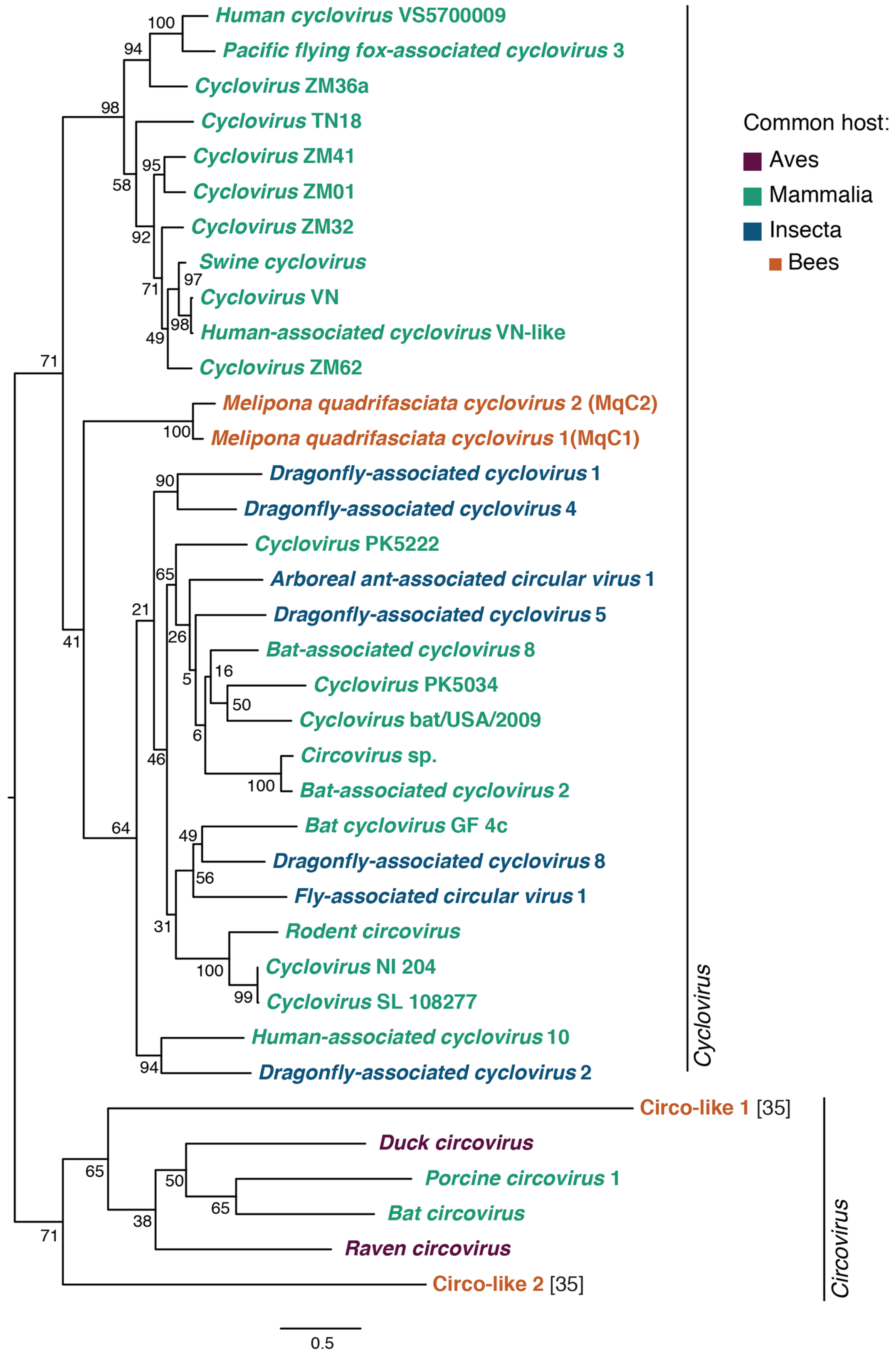

Fig. 3. Phylogenetic inference of MqV1a and MqV1b viruses (*Dicistroviridae*). The maximum-likelihood tree was inferred with 100 bootstrap resamples based on an alignment of 2748 aa. The colours of the species names represent the viruses' common hosts (see top right).

Table 1. Primer sequences designed for virus detection

Name	Sequence	Amplicon length (bp)
MqC F	5′ ACTTCTGTGCCGTTGGTAGT 3′	300
MqC R	5′ TCTCTCAAATTGCTTGCGCC 3′	
MqC1 F	5′ GCCACTTCTGTGCCGGATAT 3	304
MqC1 R	5′ TCCTTCAAAGGTGCCAGCTC 3	
MqC2 F	5′ ACTACTGGGAGCACGGAGAT 3	318
MqC2 R	5′ ATCCGTCCCACCATTCTCCT 3	
MqD F	5′ TCAAGCAGCGATTCTGGAGA 3′	300
MqD R	5′ CCACACAGGCGCTACTATTT 3′	
MqV1a F	5′ CTTCTTTGCCATCGACAAGCT 3′	300
MqV1a R	5′ TCAGCCGCAAACTTCTTCGA 3′	
MqV1b F	5′ TTAGTCTAAACGGGCCCACT 3′	300
MqV1b R	5′ TGGACATGCCCAACACTACA 3	
MqV2 F	5′ GCGCTGTATTGCATCTGGTG 3′	304
MqV2 R	5′ CGACGCGCATTTTCCTCAAT 3′	

that agricultural pollination will become unsustainable [50]. In spite of being less important with regard to crop pollination than honeybees, stingless bees and other native bees are fundamental to sustain nesting and alternative flower resources for crop pollinators, which are typically unavailable within intensively managed crop fields [51]. Moreover, the disappearance of *M. quadrifasciata* wild nests in southern Brazil is worrying because the management practices that are used to maintain bee populations in this region are not well regulated, and the trade in stingless bee colonies across the country could potentially spread viruses and other pathogens.

The seven most abundant eukaryotic viruses found in the virome of unhealthy *M. quadrifasciata* are novel viruses. Two partial dicistrovirus genomes were obtained: MqV1a and MqV1b. Although each contains one of the two CDSs of a typical dicistrovirus, our attempts to bridge them by PCR failed (data not shown), suggesting that they may indeed represent related, but different, viruses. Both show low identity to other dicistroviruses causing similar pathological symptoms in honeybees (IAPV and ABPV). Their high divergence from honeybee dicistroviruses and the lack of detection of MqV1a and b sequences in honeybees indicate that the presence of dicistroviruses in *M. quadrifasciata* does not represent a horizontal transmission event from *A. mellifera* to stingless bees, as previously suggested for ABPV infections in *M. scutellaris* [27]. Rather, our phylogenetic analyses indicate that MqV1a and b belong to an evolutionary branch that diverged from the honeybee IAPV long before other dicistroviruses found in unrelated hosts such as ants and crustaceans. Similarly, a recent study on the prevalence of DWV in *Melipona subnitida* and *A. mellifera* colonies from a single island in Brazil showed that DWV strain C, which is typically found in the stingless bee, is virtually absent in the honeybee [52]. Such dissimilar scenarios concerning the simultaneous presence of dicistroviruses in stingless bees and honeybees in Brazil probably represent different stages of the evolutionary divergence process that follows a host-switching event.

Interestingly, the most abundant *M. quadrifasciata* viruses in our study have ssDNA genomes: MqD (genus *Densovirus*, family *Parvoviridae*), MqC, MqC1 and MqC2 (genus *Cyclovirus*, family *Circoviridae*). These viral families have not been

Table 2. Candidate virus detection in *M. quadrifasciata* and *A. mellifera*. The number of *M. quadrifasciata* individuals that were positive for each virus is shown in relation to the total number of tested bees. Differences in the proportion of positive samples between healthy (H) and unhealthy (U) bees were tested for each meliponary (BL, Boqueirão do Leão; BP, Bom Princípio; and RL, Rolante) using Barnard's unconditional (BU) test and for the total number of sampled bees controlled by locality using the Cochran–Mantel–Haenszel (CMH) test. Pools of bees from three colonies of *A. mellifera* from BP were tested for the same viruses

	BL			BP			RL			CMH	*A. mellifera*		
	H	U	p£	H	U	p£	H	U	p£	p	1	2	3
MqC	8/19	40/57	0.029	0/6	0/3	NT*	1/6	0/3	0.579	0.094	+	+	+
MqC1	13/19	49/57	0.107	2/6	2/3	0.492	0/6	0/3	NT*	0.106	+	−	+
MqC2	5/19	27/57	0.122	0/6	0/3	NT*	0/6	0/3	NT*	NT**	+	+	−
MqD	6/19	6/57	0.031	0/6	0/3	NT*	0/6	0/3	NT*	NT**	−	−	−
MqV1a	0/6	4/6	0.021	8/38	7/27	0.668	0/6	2/37	0.776	0.192	−	−	−
MqV1b	1/6	3/6	0.303	3/38	5/27	0.249	0/6	0/37	NT*	0.165	−	−	−
MqV2	0/6	2/6	0.197	1/38	0/27	0.569	0/6	0/37	NT*	0.919	+	−	+

£, BU test.

*, not tested; virus not detected.

**, not tested; virus detected in a single locality.

found to be associated with other bee species until recently. Using high-throughput sequencing technologies, viruses belonging to the *Nudiviridae* (dsDNA) and *Parvoviridae* (ssDNA) were found in *Bombus* sp. [34], and *Circoviridae* viruses (ssDNA) were identified in *A. mellifera* [35], with no apparent pathological consequences. Densoviruses are known to establish both mutualistic and pathogenic relationships with their arthropod hosts [53–55]. Viruses from the genus *Cyclovirus* are not known to cause pathology in insects, but have been detected in the cerebrospinal fluid of human patients with neurological conditions [56, 57], and in secretions from patients with respiratory disease [58]. Here, the three cycloviruses were detected in honeybees sharing their habitat with *M. quadrifasciata*. It is known that the pollen resources of honeybees and *Melipona* spp. overlap in different regions of Brazil [59–61], and by foraging on the same flowers they may potentially exchange viruses. Inter-species transmission of bee viruses such as DWV, IAPV, SBPV and BQCV through pollen sources is already well documented [32, 62]. It is not possible to confirm that the *M. quadrifasciata* cycloviruses are in fact replicating within the bee body, but the high loads of DNA viruses such as MqD (136 X), MqC (107 X) and MqC1 (83 X) in the metagenome derived from a RNA sample at least suggests that they are active.

Even though no direct association was found between the manifestation of the *M. quadrifasciata* annual syndrome and the detection of the seven candidate viruses in adult stingless bees from all localities, we do not rule out the possibility that these viruses indeed play a role in the outbreaks. Our viromes were built using pools of bees from BL, where they showed the most intense disease symptoms, and three viruses (MqC, MqD and MqV1a) were found significantly more often in unhealthy bees. This indicates that viruses apparently replicate opportunistically on a local basis, and that, given the regular timing of the outbreaks on different meliponaries, the common denominator might be a higher susceptibility of bees at the end of the summer. In the case of honeybee CCD, no single factor explains the manifestation of the disorder; rather, it seems that a combination of several factors may act synergistically [50]. Known examples of synergistic interactions of honeybee viruses with other factors include *Varroa* mites that destabilize DWV–host dynamics via suppression of the honeybee NF-kB immune response [63] and pesticides that reduce honeybee resistance to viral infections [64]. Bee nutrition, which varies across landscapes and seasons, is also known to affect resistance to viruses and other pathogens [65].

In conclusion, there is no obvious answer to the question of whether or not viruses are implicated in the *M. quadrifasciata* annual syndrome. In spite of having shown a higher diversity and abundance of viruses in the virome of unhealthy bees in one of the studied meliponaries, our study suggests that viruses are not the direct cause of the syndrome, but may influence adult bee symptoms in certain localities. It is worth mentioning that eusocial bees differ from other animals in having an additional higher-level immunity referred to as social immunity [66, 67]. Because social immunity is negatively correlated with host density [68], it is possible that the annual syndrome actually represents a mechanism of density control in *M. quadrifasciata* populations at the end of the summer. Nevertheless, our study calls attention to the presence of a diversity of as yet unknown bee viruses in stingless bees, and their ability to spread across species boundaries. Given their pathogenic potential, and global concern about the decline of bee populations, viruses must be taken into account when planning management practices and conservation strategies.

METHODS

Worker bee sampling

M. quadrifasciata worker bees were collected from four different meliponaries in southern Brazil: 76 bees were taken from BL (29°18′5.47″S/52°25′57.96″W), 43 bees were taken from Rolante (RL) (29°38′19.78″S/50°26′49.77″W) and 65 bees were taken from BP (29°31′2.30″S/51°17′29.00″W). Sampling was performed in February, March and September (i.e. before, during and after the syndrome outbreak, respectively) in different years. Worker bees with symptoms such as tremors and paralysis (unhealthy) and symptomless bees (healthy) were collected using an entomological pooter, stored temporarily in sample pots and brought alive or in RNAlater (Thermo Fisher Scientific, USA) to the laboratory where they were stored individually at −80 °C until nucleic acid extraction. Healthy individuals were only collected in colonies where none of the bees presented symptoms. During the 2017 syndrome outbreak at BL, an additional 25 healthy and 25 unhealthy worker bees were collected from a colony affected by the syndrome and one not affected by it, respectively, pooled and stored in 5 ml of RNAlater (Thermo Fisher Scientific, USA) at 4 °C until nucleic acid extraction. Additionally, three pools of ~100 *A. mellifera* workers were sampled in September 2018 from different colonies of the BP location and stored as described.

Nucleic acid extraction for metagenome sequencing

Nucleic acids (RNA and DNA) were extracted from samples enriched for viral particles following the protocol of de Sales Lima and collaborators [69]. Briefly, two pools of 25 worker bees (healthy and unhealthy) were individually ground with sterile sand in 3 ml of phosphate-buffered saline (PBS). The homogenate was filtered in a cell strainer to remove bee parts (i.e. wings, legs and cuticles) and then centrifuged at 3000 r.p.m. for 15 min at 4 °C. The supernatant was collected with a syringe and filtered through a 0.45 µm filter (Sigma-Aldrich, USA) to remove bacteria-sized particles. The filtrate was transferred to a centrifuge tube in an SW-28 Ti rotor (Beckman Coulter, USA) already containing a sucrose cushion (25 % sucrose in Tris-Cl 10 mM, EDTA 1 mM) and ultracentrifuged at 27 000 r.p.m. for 4 h at 4 °C. The pellet, enriched for viral particles, was eluted in 200 µl DEPC-treated water and split into two aliquots of 100 µl each, one for DNA extraction with the universal phenol-chloroform protocol [70] and another for RNA extraction with TRIzol (Ambion, USA), following the recommendations of the manufacturers. The yield and quality of nucleic acid purification were assessed with a NanoDrop spectrophotometer (Thermo Fisher Scientific, USA) and a Qubit fluorometer (Invitrogen, USA). Aliquots of the purified RNA were used for cDNA synthesis with the High-Capacity cDNA Reverse Transcription kit (Thermo Fisher Scientific, USA). The cDNA second strand was synthesized using Klenow fragment DNA polymerase (New England Biolabs, USA). Fragment libraries were further prepared with 1 ng of purified DNA or double-stranded cDNA using the Nextera XT DNA Library Preparation kit (Illumina, USA) and paired-end sequenced (2×150 nt) using the MiSeq Reagent kit v2 (Illumina, USA) on a MiSeq instrument (Illumina, USA).

De novo assembly and contig filtering

Paired-end reads from healthy and unhealthy bee DNA and RNA fragment libraries were debarcoded and used for *de novo* assembly. Datasets derived from DNA samples were assembled with SPAdes v3.10.1 [71], whereas RNA-derived reads were assembled with Trinity v2.2.0 [72]. Within SPAdes, reads were assembled with k-mer lengths 21, 33 and 55, without a filtering step before assembly. Within Trinity, a read quality trimming step (*--trimmomatic*) was added with the default settings [73]. Contaminations were removed by building subsets (bins) of the NCBI nucleotide (nt) database with the *blastdb_aliastool* command of BLAST [74]. Contigs with significant hits (e-value cutoff $1e^{-12}$) to bins including sequences from bacteria (taxid: 2), fungi (taxid: 4751) or plants (taxid: 33090) were filtered out. Another bin was used to filter out hits against the *M. quadrifasciata* genome (LIRP00000000.1) using the same parameters.

Virome sequence analysis and candidate virus selection

For taxonomic characterization, the remaining contigs were matched with BLASTX to a viral protein database created from the virus RefSeq database (taxid: 10239). This strategy provided consistent results independently of the BLAST algorithm (BLASTX or BLASTP) or database (nr or RefSeq) used in the analyses (Table S3). Only contigs matching the viral database were retained (e-value cutoff $1e^{-5}$). False positives were then filtered out by comparing the candidate viral dataset with the total protein database (nr) from the NCBI using BLASTX, and removing contigs showing best hits to non-viral sequences. Taxonomic information for retained contigs larger than 200 bp was retrieved with taxdb. Contig depth was estimated with the depth command from Samtools v1.3.1 [75] by mapping the trimmed reads onto the virome with Bowtie 2 v2.3.1 [76], and used as a proxy for abundance. The taxonomic and sequencing depth data were used as inputs for bubble plots drawn with the ggplot2 package [77] in R. Contigs that had a sequencing depth larger than 8 X, were longer than 500 bp and showed best BLASTX hits on eukaryotic viruses were chosen as candidates for further investigation. Coding sequence prediction and annotation were performed with the prokaryotic genome annotator Prokka v1.12 [78] using the command options *--kingdom* (viruses) and *--metagenome*. To validate annotations with protein-conserved domains, predicted coding sequences were submitted to NCBI's conserved domain database (CDD) with the web application Batch CD-Search (www.ncbi.nlm.nih.gov/Structure/bwrpsb/bwrpsb.cgi; e-value cutoff $1e^{-3}$).

Phylogenetic inferences

The predicted coding sequences of six candidate viruses (all candidate viruses, except MqC, which does not have predicted protein) were used to search for similar viral sequences in GenBank (e-value cutoff $1e^{-5}$), avoiding species redundancy. These sequences, plus relevant reference sequences (see Table S4), were used for phylogenetic inferences. Sequences were aligned using MAFFT as implemented in Geneious R11 [79], removing columns with more than 60 % gaps. For each alignment, the best-fitted model of amino acid substitution was selected using ProtTest v3.4.2 [80] under corrected Akaike information criteria (AIC). Maximum-likelihood phylogenies with 100 bootstrap resamples of the alignment datasets were generated with RaxML v8.2.9 [81] and then edited and visualized with FigTree v.1.4.2 [82].

Nucleic acid extraction for PCR and RT-PCR

For PCR-based detection of viruses, the extraction of DNA, RNA or simultaneous DNA/RNA from individual bees was performed with the DNeasy Blood and Tissue kit (Qiagen, Germany), TRIzol (Ambion, USA) and the QIAamp Cador Pathogen Mini kit (Qiagen, Germany), respectively, according to the manufacturers' protocols. The nucleic acid extractions tested for the presence of RNA had been treated previously with TURBO DNase (Thermo Fisher Scientific, USA) and were then used for cDNA synthesis with the High-Capacity cDNA Reverse Transcription kit (Thermo Fisher Scientific, USA).

Virus detection by PCR and RT-PCR

Primers for virus detection were designed based on the seven candidate viral contig sequences (Table 1). An aliquot of 100–300 ng of nucleic acids purified from each of the tested samples was used as a template for PCR or RT-PCR, according to the sample type, mixed with 1 U of Platinum *Taq* DNA polymerase (Invitrogen, USA), 1× PCR buffer, 0.2 mM of each dNTP, 1.5 mM $MgCl_2$ and 0.2 µM of each forward and reverse primer in a final reaction volume of 50 µl. For MqV1a, the temperature cycling protocol used was 94 °C for 5 min, 60 °C for 1 min and 72 °C for 2 min, followed by 20 cycles of 94 °C for 1 min, 55 °C for 1 min and 72 °C for 2 min, with a touchdown of 0.5 °C per cycle, and another 20 cycles of 94 °C for 1 min, 45 °C for 1 min and 72 °C for 2 min, and a final extension step of 72 °C for 10 min. For the remaining six viruses a similar touchdown procedure was used, with primer annealing temperatures starting at 54 °C and ending at 44 °C. The amplicons were analysed by conventional agarose gel electrophoresis. To test for the association of virus detection in individual bees with the manifestation of disease symptoms we conducted CMH test with Compare2 v.3.85 from WinPep [83] and two-way Barnard's unconditional tests with the Barnard package [84] in R.

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Conflicts of interest

The authors declare that there are no conflicts of interest.

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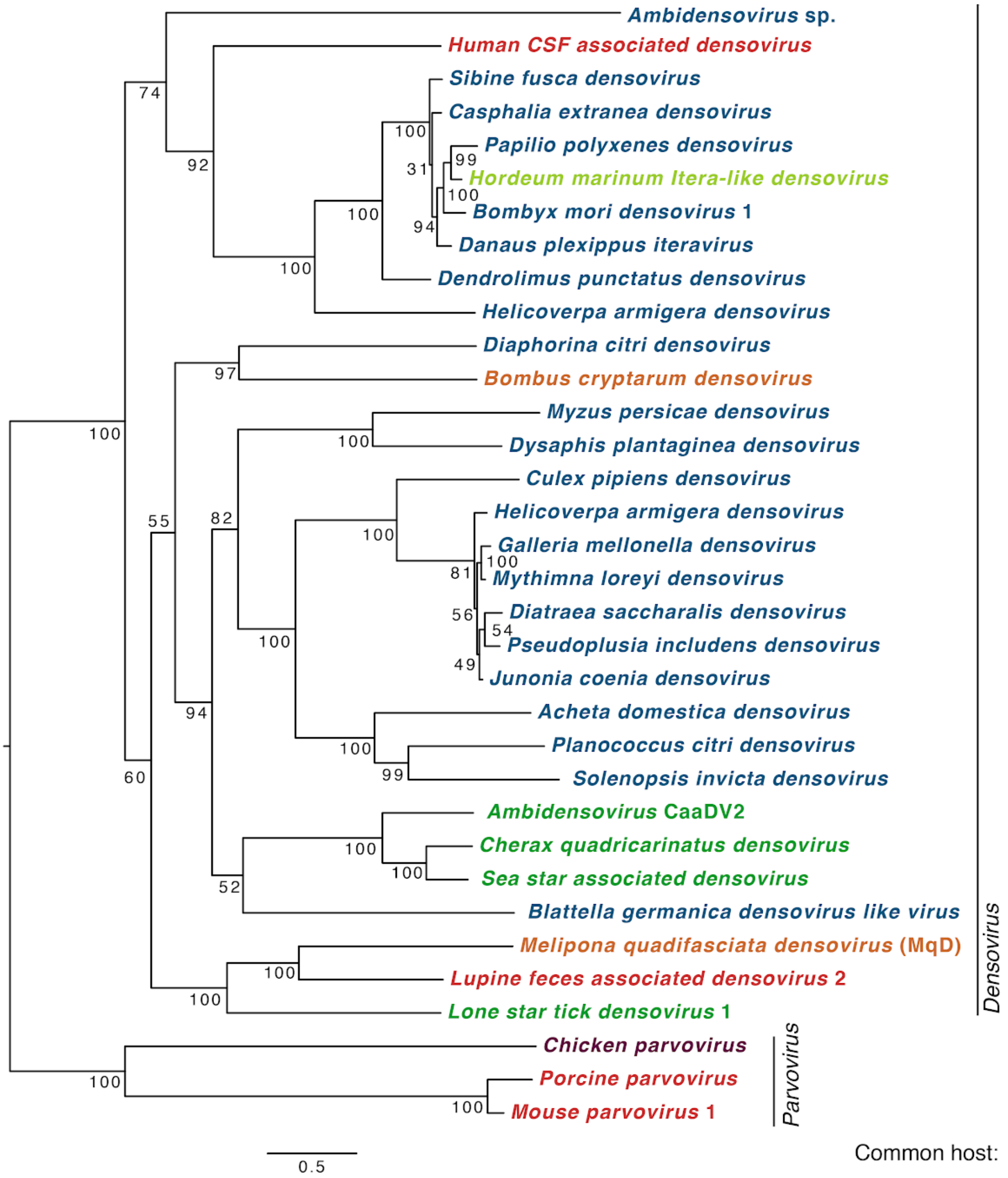
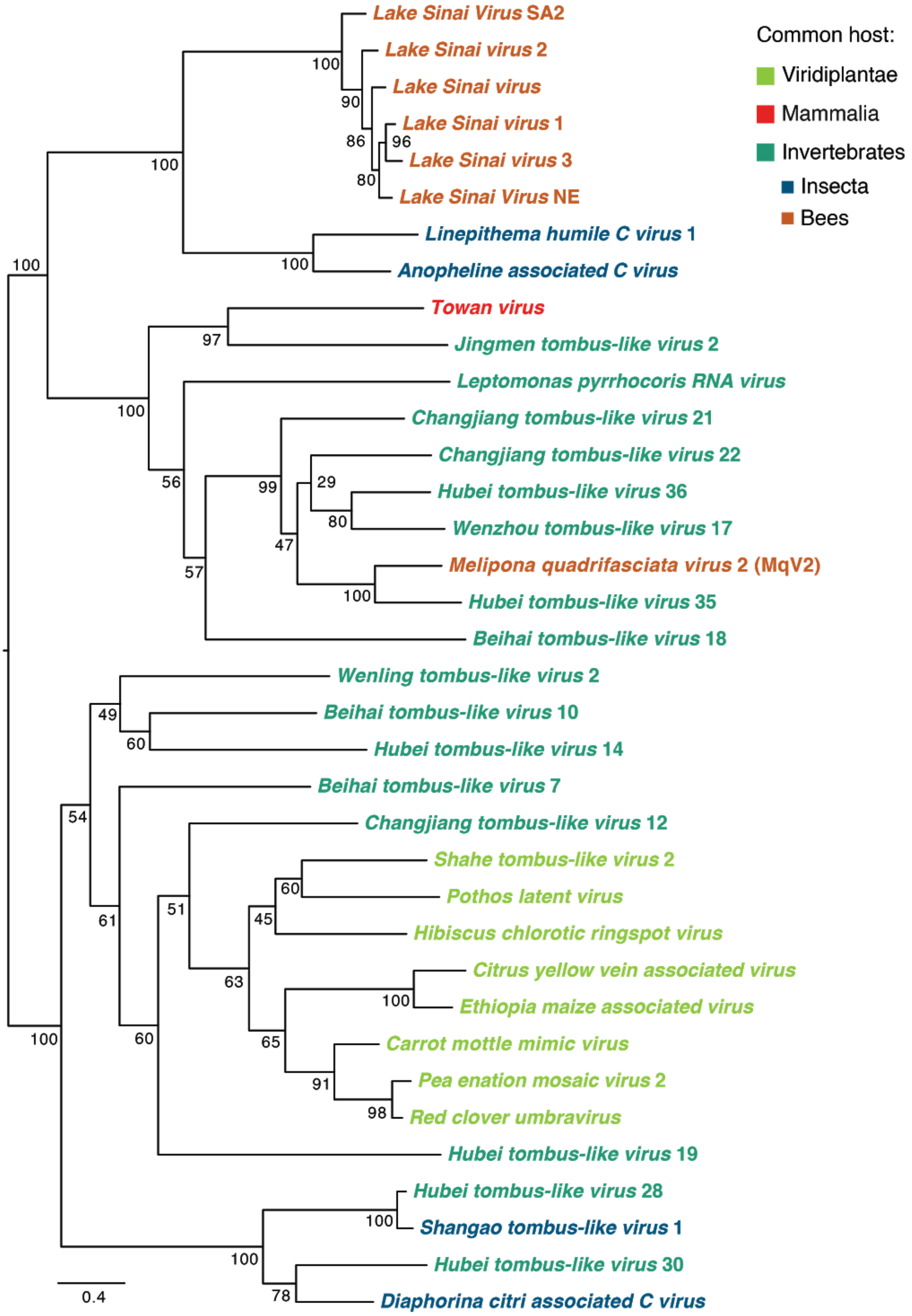


Common host:
- 🟩 Viridiplantae
- 🟪 Aves
- 🟥 Mammalia
- 🟩 Invertebrates
  - 🟦 Insecta
  - 🟧 Bees

Supplementary figure 1 - Phylogenetic inference of MqD virus (*Parvoviridae*). The maximum-likelihood tree was inferred with 100 bootstrap resamples based on an alignment of 1,310 aa. Species name colours represent the virus common host.



Supplementary figure 2 - Phylogenetic inference of MqV2 virus. The maximum-likelihood tree was inferred with 100 bootstrap resamples based on an alignment of 598 aa. Species name colours represent the virus common host.

Supplementary Table 1 - Virome of unhealthy and healthy *M. quadrifasciata*: taxonomic classification of the best hit of each contig exceeding 200 bp in the four metagenomes (UDNA = DNA from unhealthy bees, HDNA = DNA from helathy bees, URNA = RNA from unhealthy bees, HRNA = RNA from helathy bees). Contigs are ordered according their coverages. Shading color indicates two major host groups bacteria (green) and eukaryotes (purple); hihglighted in red are the contigs that were chosen to be investigated for their relation with the annual syndrome.

Name	Query (Contig name)	Length	Mean coverage	Subject	Bitscore	E-value	Staxids	Best hit species	Common host	Common host classification	Viral Order	Viral Family	Virus Molecule type
								Unhealthy bees DNA virome					
	NODE 1371 length 261 cov 5101.58	261	5937.31	gi|66395188|ref|YP 239478.1|	48.9	1.77E-07	320832	*Staphylococcus phage 66*	*Staphylococcus aureus*	Firmicutes; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
	NODE 3218 length 202 cov 2485.69	202	4616.9	gi|658607919|ref|YP 009044904.1|	103	2.02E-28	1262519	*Leuconostoc phage phiLN34*	*Leuconostoc mesenteroides*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
	NODE 67 length 1399 cov 2196.09	1399	4396.57	gi|1070100089|ref|YP 009283993.1|	179	1.45E-50	1543206	*Staphylococcus phage BP39*	*Staphylococcus aureus*	Firmicutes; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
	NODE 142 length 837 cov 2004.61	837	3448.91	gi|966201261|ref|YP 009191338.1|	112	4.28E-27	1747288	*Enterococcus phage vB IME195*	*Enterococcus faecium*	Firmicutes; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
	NODE 82 length 1231 cov 1512.21	1231	2965.47	gi|1070096635|ref|YP 009278561.1|	150	1.24E-38	1821228	*Staphylococcus phage SLPW*	*Staphylococcus aureus*	Firmicutes; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
	NODE 504 length 370 cov 1301.35	370	2793.61	gi|31072015|ref|NP 852013.1|	109	4.16E-28	230871	*Streptococcus phage C1*	*Staphylococcus aureus*	Firmicutes; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
	NODE 257 length 556 cov 1608.69	556	2771.15	gi|29565740|ref|NP 817314.1|	180	8.89E-55	204086	*Staphylococcus phage 44AHJD*	*Staphylococcus aureus*	Firmicutes; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
	NODE 38 length 2005 cov 1102.3	2005	2141.64	gi|66395192|ref|YP 239479.1|	141	1.52E-35	320832	*Staphylococcus phage 66*	*Staphylococcus aureus*	Firmicutes; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
	NODE 59 length 1601 cov 1305.56	1601	1969.64	gi|712916221|ref|YP 009103964.1|	55.8	2.64E-07	1161939	*Enterococcus phage vB Efae230P-4*	*Enterococcus faecium*	Firmicutes; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
	NODE 390 length 422 cov 1051.65	422	1902.38	gi|712916217|ref|YP 009103960.1|	101	6.56E-26	1161939	*Enterococcus phage vB Efae230P-4*	*Enterococcus faecium*	Firmicutes; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
	NODE 2661 length 219 cov 9609.49	219	1055.29	gi|327197601|ref|YP 004301292.1|	47.4	3.47E-07	764561	*Brochothrix phage NF5*	*Brochothrix thermosphacta*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
	NODE 1039 length 277 cov 6070.11	277	798.448	gi|327197601|ref|YP 004301292.1|	80.1	2.31E-18	764561	*Brochothrix phage NF5*	*Brochothrix thermosphacta*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
MqD	NODE 6 length 4214 cov 47.7802	4214	104.516	gi|56698740|ref|YP 164339.1|	173	2.00E-43	292208	*Dendrolimus punctatus densovirus*	*Dendrolimus punctatus*	Arthropoda; Metazoa; Eukaryota	unclassified	Parvoviridae	ssDNA
MqC2	NODE 181 length 673 cov 27.6828	673	59.2363	gi|663089940|ref|YP 009047065.1|	260	7.66E-87	1348500	*Cyclovirus VN*	*Homo sapiens*	Chordata; Metazoa; Eukaryota	unclassified	Circoviridae	ssDNA
	NODE 1 length 14405 cov 25.8403	14405	55.6807	gi|151266296|ref|YP 001333659.1|	206	5.92E-55	338473	*Actinomyces phage Av-1*	*Actinomyces naeslundii*	Actinobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
	NODE 482 length 379 cov 19.5957	379	39.7045	gi|607840595|ref|YP 009021845.1|	64.3	2.14E-12	1234882	*Dragonfly cyclovirus 4*	*Somatochlora meridionalis*	Arthropoda; Metazoa; Eukaryota	unclassified	Circoviridae	ssDNA
	NODE 47 length 1772 cov 19.8427	1772	38.7472	gi|658310065|ref|YP 009042257.1|	227	2.90E-64	1327934	*Cronobacter phage CR8*	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 12 length 2790 cov 15.8786	2790	32.3681	gi|966203645|ref|YP 009188960.1|	125	9.81E-31	1684115	*Cronobacter phage PBES 02*	*Cronobacter sp.*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 75 length 1310 cov 14.4797	1310	32.313	gi|363539710|ref|YP 004893995.1|	77	4.94E-17	889338	*Salmonella phage PVP-SE1*	*Salmonella enterica subsp. enterica serovar Enteritidis*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 23 length 2531 cov 15.0521	2531	31.1972	gi|593777390|ref|YP 009015235.1|	253	3.61E-73	1162290	*Cronobacter phage CR9*	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 16 length 2705 cov 15.2894	2705	28.9919	gi|730985156|ref|YP 009111241.1|	164	9.69E-45	1527519	*Escherichia phage Av-05*	*Escherichia coli O157:H7*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 208 length 612 cov 13.7487	612	27.1373	gi|410492669|ref|YP 006908871.1|	48.9	2.55E-06	1604355	*Escherichia phage ECBP2*	*Escherichia coli*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
	NODE 33 length 2212 cov 12.5535	2212	25.9118	gi|966203781|ref|YP 009189096.1|	60.5	6.08E-11	1684115	*Cronobacter phage PBES 02*	*Cronobacter sp.*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 27 length 2374 cov 11.8995	2374	22.9356	gi|363539688|ref|YP 004893973.1|	183	1.16E-50	889338	*Salmonella phage PVP-SE1*	*Salmonella enterica subsp. enterica serovar Enteritidis*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 19 length 2673 cov 11.95	2673	22.7565	gi|658310257|ref|YP 009042449.1|	374	2.27E-123	1327934	*Cronobacter phage CR8*	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 7 length 3822 cov 11.8471	3822	22.5903	gi|658310123|ref|YP 009042315.1|	394	2.74E-121	1327934	*Cronobacter phage CR8*	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 14 length 2710 cov 11.145	2710	21.4587	gi|389059870|ref|YP 006383023.1|	410	2.03E-126	1162295	*Cronobacter phage CR3*	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 91 length 1174 cov 9.41555	1174	19.7308	gi|389059880|ref|YP 006383033.1|	195	1.22E-60	1162295	*Cronobacter phage CR3*	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 95 length 1135 cov 9.35	1135	18.3885	gi|593777139|ref|YP 009014984.1|	296	5.56E-98	1162290	*Cronobacter phage CR9*	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 36 length 2088 cov 9.15199	2088	17.8252	gi|389059955|ref|YP 006383108.1|	95.1	4.75E-22	1162295	*Cronobacter phage CR3*	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 70 length 1325 cov 7.26457	1325	17.6581	gi|388570790|ref|YP 006383773.1|	51.2	6.96E-08	1187128	*Acinetobacter bacteriophage AP22*	*Acinetobacter baumannii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 9 length 2927 cov 9.01358	2927	17.6194	gi|658310137|ref|YP 009042329.1|	208	2.21E-61	1327934	*Cronobacter phage CR8*	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 110 length 998 cov 6.41569	998	17.5882	gi|682123183|ref|YP 009055504.1|	254	5.19E-81	1505225	*Acinetobacter phage YMC-13-01-C62*	*Acinetobacter baumannii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 76 length 1310 cov 9.00717	1310	17.3725	gi|389060084|ref|YP 006383237.1|	207	3.80E-64	1162295	*Cronobacter phage CR3*	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 34 length 2102 cov 8.80606	2102	17.0324	gi|593777352|ref|YP 009015197.1|	410	3.75E-138	1162290	*Cronobacter phage CR9*	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 44 length 1847 cov 8.88895	1847	16.7823	gi|593777363|ref|YP 009015208.1|	368	2.75E-122	1162290	*Cronobacter phage CR9*	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 3 length 5385 cov 8.33527	5385	16.5744	gi|448244744|ref|YP 007392464.1|	147	5.62E-37	1116482	*Pectobacterium phage phiTE*	*Pectobacterium atrosepticum SCRI1043*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 86 length 1202 cov 8.1578	1202	16.3378	gi|389059887|ref|YP 006383040.1|	238	3.03E-77	1162295	*Cronobacter phage CR3*	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 5 length 4317 cov 8.25059	4317	16.0644	gi|593777283|ref|YP 009015128.1|	88.6	1.29E-19	1162290	*Cronobacter phage CR9*	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 8 length 3348 cov 7.53325	3348	15.425	gi|563397615|ref|YP 008857379.1|	202	8.18E-57	1391428	*Enterobacteria phage 4MG*	*Escherichia coli K-12*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 24 length 2521 cov 8.03406	2521	15.386	gi|448260249|ref|YP 007348345.1|	53.9	5.33E-08	1264737	*Cronobacter phage vB CskP GAP227*	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
	NODE 132 length 891 cov 7.60646	891	15.0236	gi|593777268|ref|YP 009015113.1|	124	3.89E-35	1162290	*Cronobacter phage CR9*	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 98 length 1104 cov 7.55005	1104	14.5616	gi|563397555|ref|YP 008857319.1|	158	7.26E-45	1391428	*Enterobacteria phage 4MG*	*Escherichia coli K-12*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 607 length 347 cov 7.86301	347	14.5504	gi|593777353|ref|YP 009015198.1|	61.2	3.75E-13	1162290	*Cronobacter phage CR9*	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 22 length 2568 cov 7.01074	2568	14.1347	gi|966203769|ref|YP 009189084.1|	68.9	2.43E-13	1684115	*Cronobacter phage PBES 02*	*Cronobacter sp.*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 488 length 376 cov 4.82866	376	14.0133	gi|388570783|ref|YP 006383766.1|	201	1.51E-63	1187128	*Acinetobacter bacteriophage AP22*	*Acinetobacter baumannii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 163 length 751 cov 8.03879	751	13.7617	gi|563397604|ref|YP 008857368.1|	63.5	2.51E-12	1391428	*Enterobacteria phage 4MG*	*Escherichia coli K-12*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 1590 length 252 cov 9.17766	252	13.6667	gi|966203376|ref|YP 009187688.1|	134	3.27E-38	1719140	*Klebsiella phage vB KpnM KB57*	*Klebsiella pneumoniae*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 236 length 578 cov 7.26195	578	13.4931	gi|363539705|ref|YP 004893990.1|	49.7	9.71E-08	889338	*Salmonella phage PVP-SE1*	*Salmonella enterica subsp. enterica serovar Enteritidis*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 79 length 1265 cov 6.71157	1265	13.4324	gi|401723087|ref|YP 006589997.1|	84	3.02E-16	1136535	*Burkholderia phage DC1*	*Burkholderia cepacia*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
	NODE 28 length 2286 cov 6.76109	2286	13.0009	gi|563397519|ref|YP 008857283.1|	124	3.25E-28	1391428	*Enterobacteria phage 4MG*	*Escherichia coli K-12*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 315 length 496 cov 5.16327	496	12.8306	gi|448244797|ref|YP 007392517.1|	56.6	4.07E-09	1116482	*Pectobacterium phage phiTE*	*Pectobacterium atrosepticum SCRI1043*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 2 length 5413 cov 6.22714	5413	12.5797	gi|389059922|ref|YP 006383075.1|	528	4.31E-165	1162295	*Cronobacter phage CR3*	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 21 length 2596 cov 5.8717	2596	12.3617	gi|448244800|ref|YP 007392520.1|	514	2.06E-175	1116482	*Pectobacterium phage phiTE*	*Pectobacterium atrosepticum SCRI1043*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 652 length 334 cov 5.73835	334	12.1048	gi|593777273|ref|YP 009015118.1|	63.9	8.15E-14	1162290	*Cronobacter phage CR9*	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 747 length 315 cov 7.04231	315	11.8286	gi|593777390|ref|YP 009015235.1|	86.7	1.85E-20	1162290	*Cronobacter phage CR9*	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 26 length 2424 cov 5.68763	2424	11.1993	gi|966203664|ref|YP 009188979.1|	84.3	3.17E-16	1684115	*Cronobacter phage PBES 02*	*Cronobacter sp.*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 54 length 1661 cov 6.05168	1661	11.0319	gi|563397558|ref|YP 008857322.1|	155	3.51E-44	1391428	*Enterobacteria phage 4MG*	*Escherichia coli K-12*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 60 length 1548 cov 3.58607	1548	10.7597	gi|1070106045|ref|YP 009291896.1|	148	4.58E-67	1792222	*Acinetobacter phage LZ35*	*Acinetobacter baumannii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 42 length 1886 cov 5.55871	1886	10.7582	gi|363539667|ref|YP 004893952.1|	115	4.52E-28	889338	*Salmonella phage PVP-SE1*	*Salmonella enterica subsp. enterica serovar Enteritidis*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 367 length 440 cov 5.37662	440	10.6273	gi|448244961|ref|YP 007392681.1|	118	4.24E-34	1116482	*Pectobacterium phage phiTE*	*Pectobacterium atrosepticum SCRI1043*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 93 length 1153 cov 5.30874	1153	10.4779	gi|589889806|ref|YP 009005342.1|	59.7	2.03E-10	1455074	*Enterobacter phage PG7*	*Enterobacter cloacae*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 61 length 1497 cov 5.38003	1497	10.3447	gi|658310249|ref|YP 009042441.1|	402	3.60E-136	1327934	*Cronobacter phage CR8*	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 177 length 702 cov 4.84853	702	10.2165	gi|1070637985|ref|YP 009301963.1|	58.9	5.57E-10	1821564	*Gordonia phage Vivi2*	*Gordonia terrae*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
	NODE 18 length 2681 cov 5.18012	2681	10.169	gi|593777397|ref|YP 009015242.1|	85.5	6.81E-19	1162290	*Cronobacter phage CR9*	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 122 length 935 cov 5.39886	935	10.0235	gi|593777264|ref|YP 009015109.1|	61.2	4.12E-11	1162290	*Cronobacter phage CR9*	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 2732 length 217 cov 9.01103	217	9.90783	gi|448244885|ref|YP 007392605.1|	43.5	2.32E-06	1116482	*Pectobacterium phage phiTE*	*Pectobacterium atrosepticum SCRI1043*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 83 length 1231 cov 5.02551	1231	9.65556	gi|389060088|ref|YP 006383241.1|	263	4.47E-87	1162295	*Cronobacter phage CR3*	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 2606 length 220 cov 6.06667	220	9.55455	gi|448244974|ref|YP 007392694.1|	82.4	2.88E-20	1116482	*Pectobacterium phage phiTE*	*Pectobacterium atrosepticum SCRI1043*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 31 length 2251 cov 3.51685	2251	9.53976	gi|682123142|ref|YP 009055463.1|	170	4.16E-48	1505225	*Acinetobacter phage YMC-13-01-C62*	*Acinetobacter baumannii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 130 length 903 cov 4.64741	903	9.2835	gi|593777128|ref|YP 009014973.1|	62	7.82E-11	1162290	*Cronobacter phage CR9*	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 241 length 567 cov 5.27539	567	8.92416	gi|658310474|ref|YP 009042664.1|	178	4.23E-51	1445858	*Enterococcus phage IME-EFm1*	*Enterococcus faecium*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
	NODE 164 length 751 cov 2.38075	751	8.88948	gi|1070106098|ref|YP 009291949.1|	131	9.52E-35	1792222	*Acinetobacter phage LZ35*	*Acinetobacter baumannii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 294 length 520 cov 4.72473	520	8.51923	gi|971758015|ref|YP 009211443.1|	45.1	4.54E-06	1429794	*Pectobacterium bacteriophage PM2*	*Pectobacterium sp.*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 186 length 665 cov 4.3459	665	8.28722	gi|414086723|ref|YP 006986911.1|	94.7	3.80E-24	1141135	*Cronobacter phage vB CsaM GAP31*	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 73 length 1317 cov 4.62124	1317	8.25133	gi|448244882|ref|YP 007392602.1|	275	3.68E-91	1116482	*Pectobacterium phage phiTE*	*Pectobacterium atrosepticum SCRI1043*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 50 length 1707 cov 4.08414	1707	8.06854	gi|593777142|ref|YP 009014987.1|	629	0.00E+00	1162290	*Cronobacter phage CR9*	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 55 length 1650 cov 4.20313	1650	7.83091	gi|658310076|ref|YP 009042268.1|	176	5.95E-52	1327934	*Cronobacter phage CR8*	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 1202 length 269 cov 3.95327	269	7.67286	gi|448244896|ref|YP 007392616.1|	48.5	2.39E-07	1116482	*Pectobacterium phage phiTE*	*Pectobacterium atrosepticum SCRI1043*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 873 length 295 cov 5.02083	295	7.44068	gi|363539537|ref|YP 004893822.1|	122	4.14E-33	889338	*Salmonella phage PVP-SE1*	*Salmonella enterica subsp. enterica serovar Enteritidis*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 40 length 1902 cov 3.04169	1902	7.4285	gi|971763838|ref|YP 009216836.1|	140	1.02E-36	1229760	*Acinetobacter phage phiAC-1*	*Acinetobacter soli*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 470 length 384 cov 4.27964	384	7.23958	gi|764162029|ref|YP 009126425.1|	118	2.33E-31	1561065	*Paracoccus phage vB PmaS IMEP1*	*Paracoccus marcusii*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
	NODE 306 length 511 cov 3.29825	511	7.18982	gi|388570784|ref|YP 006383767.1|	163	6.82E-48	1187128	*Acinetobacter bacteriophage AP22*	*Acinetobacter baumannii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 111 length 995 cov 3.85426	995	7.14171	gi|593777130|ref|YP 009014975.1|	223	1.04E-72	1162290	*Cronobacter phage CR9*	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 417 length 411 cov 3.98034	411	6.91241	gi|448244953|ref|YP 007392673.1|	107	3.91E-28	1116482	*Pectobacterium phage phiTE*	*Pectobacterium atrosepticum SCRI1043*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 491 length 375 cov 3.20938	375	6.86933	gi|388570795|ref|YP 006383778.1|	92.4	2.27E-22	1187128	*Acinetobacter bacteriophage AP22*	*Acinetobacter baumannii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 229 length 586 cov 3.24482	586	6.34812	gi|658310072|ref|YP 009042264.1|	175	7.42E-55	1327934	*Cronobacter phage CR8*	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 373 length 433 cov 3.62169	433	6.34411	gi|563397525|ref|YP 008857289.1|	77	1.90E-16	1391428	*Enterobacteria phage 4MG*	*Escherichia coli K-12*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 175 length 714 cov 2.93475	714	6.23109	gi|658310294|ref|YP 009042486.1|	301	1.25E-100	1327934	*Cronobacter phage CR8*	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 291 length 525 cov 3.8	525	6.10476	gi|448244953|ref|YP 007392673.1|	92.8	5.15E-22	1116482	*Pectobacterium phage phiTE*	*Pectobacterium atrosepticum SCRI1043*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 146 length 814 cov 3.40053	814	6.03194	gi|1068512424|ref|YP 009276107.1|	83.6	1.27E-18	1647473	*Gordonia phage GRU3*	*Gordonia rubripertincta*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
	NODE 663 length 332 cov 3.24188	332	6.0241	gi|389060078|ref|YP 006383231.1|	171	1.24E-50	1162295	*Cronobacter phage CR3*	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 313 length 501 cov 2.73543	501	5.74651	gi|448244956|ref|YP 007392676.1|	88.6	1.66E-21	1116482	*Pectobacterium phage phiTE*	*Pectobacterium atrosepticum SCRI1043*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 97 length 1108 cov 2.96771	1108	5.60921	gi|389059863|ref|YP 006383016.1|	437	2.41E-151	1162295	*Cronobacter phage CR3*	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses

NODE 415 length 413 cov 2.89106	413	5.54479	gi|448244935|ref|YP 007392655.1|	126	1.16E-35	1116482	*Pectobacterium phage phiTE*	*Pectobacterium atrosepticum SCRI1043*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 1907 length 241 cov 3.22043	241	5.53112	gi|1070106045|ref|YP 009291896.1|	71.2	1.18E-15	1792222	*Acinetobacter phage LZ35*	*Acinetobacter baumannii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 703 length 323 cov 2.89179	323	5.45511	gi|971745247|ref|YP 009199435.1|	51.2	2.41E-08	1718606	*Escherichia phage phiSUSP1*	*Escherichia coli*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 530 length 365 cov 2.57742	365	5.4411	gi|157325017|ref|YP 001468443.1|	47.8	4.51E-07	40522	*Listeria phage A500*	*Listeria monocytogenes WSLC1042*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 1759 length 246 cov 3.24607	246	5.26016	gi|414086874|ref|YP 006987062.1|	85.5	1.20E-20	1141135	*Cronobacter phage vB CsaM GAP31*	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 514 length 368 cov 2.86262	368	5.18207	gi|327198375|ref|YP 004306949.1|	62	1.56E-11	59241	*Streptococcus phage Dp-1*	*Streptococcus pneumoniae*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 1513 length 255 cov 3.845	255	5.14118	gi|448244960|ref|YP 007392680.1|	144	5.78E-45	1116482	*Pectobacterium phage phiTE*	*Pectobacterium atrosepticum SCRI1043*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 301 length 514 cov 3.05229	514	5.11673	gi|389060077|ref|YP 006383230.1|	273	7.32E-92	1162295	*Cronobacter phage CR3*	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 1492 length 256 cov 2.34328	256	5.00781	gi|571798161|ref|YP 008770540.1|	80.5	1.31E-19	1406786	*Bacillus phage Page*	*Bacillus megaterium*	Firmicutes; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 1516 length 255 cov 2.6	255	5.00392	gi|514361130|ref|YP 008130364.1|	46.6	1.03E-06	1345637	*Human cyclovirus VS5700009*	*Homo sapiens*	Chordata; Metazoa; Eukaryota	unclassified	Circoviridae	ssDNA
NODE 2341 length 227 cov 3.35465	227	5	gi|593777119|ref|YP 009014964.1|	129	1.49E-36	1162290	*Cronobacter phage CR9*	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 2208 length 231 cov 2.15909	231	4.98701	gi|682123139|ref|YP 009055460.1|	90.9	6.03E-24	1505225	*Acinetobacter phage YMC-13-01-C62*	*Acinetobacter baumannii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 431 length 404 cov 1.60458	404	4.82673	gi|472340490|ref|YP 007674015.1|	142	4.55E-40	754049	*Vibrio phage pYD21-A*	*Vibrio sp. YD21*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 1471 length 257 cov 2.9505	257	4.79377	gi|448244955|ref|YP 007392675.1|	124	2.27E-35	1116482	*Pectobacterium phage phiTE*	*Pectobacterium atrosepticum SCRI1043*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 400 length 418 cov 2.00826	418	4.73684	gi|1070106029|ref|YP 009291880.1|	66.2	7.89E-13	1792222	*Acinetobacter phage LZ35*	*Acinetobacter baumannii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 608 length 347 cov 2.82534	347	4.68588	gi|939536927|ref|YP 009168411.2|	127	3.44E-36	1622234	*Citrobacter phage CVT22*	*Citrobacter sp. TM1552*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 1453 length 258 cov 2.12315	258	4.65504	gi|937456469|ref|YP 009168394.1|	123	1.24E-33	1622234	*Citrobacter phage CVT22*	*Citrobacter sp. TM1552*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 278 length 534 cov 2.40292	534	4.64794	gi|937456502|ref|YP 009168428.1|	54.7	5.62E-09	1622234	*Citrobacter phage CVT22*	*Citrobacter sp. TM1552*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 542 length 361 cov 2.5817	361	4.46814	gi|9626704|ref|NP 040974.1|	128	3.95E-37	11673	*Feline immunodeficiency virus*	*Felidae*	Chordata; Metazoa; Eukaryota	unclassified	Retroviridae	ssRNA RT
NODE 664 length 332 cov 2.11913	332	4.46386	gi|593777132|ref|YP 009014977.1|	132	3.70E-37	1162290	*Cronobacter phage CR9*	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 1337 length 263 cov 3.02404	263	4.34221	gi|62327110|ref|YP 223898.1|	137	2.02E-38	235201	*Lactobacillus phage phiJL-1*	*Lactobacillus plantarum*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 249 length 562 cov 2.46351	562	4.30071	gi|93007440|ref|YP 579204.1|	123	1.30E-32	370623	*Streptomyces phage mu1/6*	*Kitasatospora aureofaciens*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 1142 length 272 cov 3.20737	272	4.28676	gi|388570790|ref|YP 006383773.1|	42	7.15E-06	1187128	*Acinetobacter bacteriophage AP22*	*Acinetobacter baumannii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 374 length 433 cov 2.1746	433	4.27252	gi|658310265|ref|YP 009042457.1|	211	1.30E-64	1327934	*Cronobacter phage CR8*	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 366 length 441 cov 2.41451	441	4.26757	gi|1068511077|ref|YP 009274031.1|	44.3	9.87E-06	1838072	*Gordonia phage McGonagall*	*Gordonia neofelifaecis*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 466 length 386 cov 1.8429	386	4.24611	gi|658310061|ref|YP 009042253.1|	152	1.47E-44	1327934	*Cronobacter phage CR8*	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 611 length 345 cov 2.55172	345	4.23188	gi|448244898|ref|YP 007392618.1|	153	5.62E-47	1116482	*Pectobacterium phage phiTE*	*Pectobacterium atrosepticum SCRI1043*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 412 length 415 cov 1.42222	415	4.15181	gi|971763827|ref|YP 009216825.1|	125	3.77E-36	1229760	*Acinetobacter phage phiAC-1*	*Acinetobacter soli*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 654 length 334 cov 2.48746	334	4.13772	gi|418489115|ref|YP 007002969.1|	140	1.64E-40	37105	*Lactobacillus phage JCL1032*	*Lactobacillus delbrueckii subsp. lactis*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 245 length 564 cov 2.4165	564	4.13121	gi|151266305|ref|YP 001333668.1|	112	3.90E-29	338473	*Actinomyces phage Av-1*	*Actinomyces naeslundii*	Actinobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 371 length 434 cov 2.53298	434	4.1129	gi|971748496|ref|YP 009202413.1|	62	3.23E-11	1698711	*Mycobacterium phage Lolly9*	*Mycobacterium smegmatis str. MC2 155*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 3036 length 210 cov 2.52903	210	3.9619	gi|151266296|ref|YP 001333659.1|	57.4	8.65E-11	338473	*Actinomyces phage Av-1*	*Actinomyces naeslundii*	Actinobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 874 length 295 cov 2.9125	295	3.95254	gi|971747642|ref|YP 009201507.1|	57.4	3.43E-10	1739609	*Lactobacillus phage iA2*	*Lactobacillus paracasei*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 971 length 281 cov 2.73894	281	3.92171	gi|985757728|ref|YP 009223104.1|	128	6.05E-36	1567453	*Lactobacillus phage LfeSau*	*Lactobacillus fermentum*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 261 length 553 cov 2.07229	553	3.91139	gi|966203686|ref|YP 009189001.1|	86.7	2.90E-19	1684115	*Cronobacter phage PBES 02*	*Cronobacter sp.*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 3162 length 207 cov 2.63816	207	3.89855	gi|448244802|ref|YP 007392522.1|	88.6	8.57E-22	1116482	*Pectobacterium phage phiTE*	*Pectobacterium atrosepticum SCRI1043*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 2491 length 223 cov 2.02381	223	3.88341	gi|1070067156|ref|YP 009289259.1|	42.7	8.33E-06	1868596	*Pseudomonas phage MD8*	*Pseudomonas aeruginosa*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 230 length 582 cov 2.26755	582	3.86254	gi|593777381|ref|YP 009015226.1|	325	8.25E-111	1162290	*Cronobacter phage CR9*	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 547 length 359 cov 2.16118	359	3.7883	gi|682123168|ref|YP 009055489.1|	115	2.51E-31	1505225	*Acinetobacter phage YMC-13-01-C62*	*Acinetobacter baumannii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 3124 length 208 cov 2.83007	208	3.77885	gi|1102617795|ref|YP 009321540.1|	45.4	1.14E-06	1701837	*Streptococcus phage phiARI0746*	*Streptococcus pneumoniae*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 192 length 651 cov 2.01174	651	3.76651	gi|593777136|ref|YP 009014981.1|	191	1.65E-55	1162290	*Cronobacter phage CR9*	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 762 length 312 cov 2.31128	312	3.76603	gi|658310132|ref|YP 009042324.1|	147	3.21E-43	1327934	*Cronobacter phage CR8*	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 302 length 514 cov 1.49455	514	3.76265	gi|971746169|ref|YP 009200249.1|	142	1.55E-39	1636200	*Pseudoalteromonas Phage H103*	*Pseudoalteromonas marina*	Proteobacteria; Bacteria	Caudovirales	unclassified	dsDNA viruses
NODE 701 length 324 cov 2.21933	324	3.75	gi|658310273|ref|YP 009042465.1|	175	1.13E-54	1327934	*Cronobacter phage CR8*	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 1004 length 279 cov 2.26786	279	3.65591	gi|937456472|ref|YP 009168397.1|	102	3.38E-26	1622234	*Citrobacter phage CVT22*	*Citrobacter sp. TM1552*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 1145 length 272 cov 2.17051	272	3.63971	gi|318069475|ref|YP 004152328.1|	66.2	5.33E-14	942033	*Cyclovirus PKgoat21/PAK/2009*	*Capra hircus*	Chordata; Metazoa; Eukaryota	unclassified	Circoviridae	ssDNA
NODE 2826 length 215 cov 2.78125	215	3.60465	gi|971752673|ref|YP 009206702.1|	90.9	3.72E-23	1739607	*Lactobacillus phage CL1*	*Lactobacillus paracasei*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 2832 length 215 cov 1.99375	215	3.56279	gi|149408208|ref|YP 001294642.1|	87.4	2.51E-21	347327	*Pseudomonas phage PA11*	*Pseudomonas aeruginosa*	Proteobacteria; Bacteria	unclassified	unclassified	dsDNA viruses
NODE 620 length 342 cov 2.31359	342	3.54971	gi|418489114|ref|YP 007002968.1|	179	4.48E-54	37105	*Lactobacillus phage JCL1032*	*Lactobacillus delbrueckii subsp. lactis*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 550 length 358 cov 1.72277	358	3.54749	gi|29566753|ref|NP 818317.1|	82.8	6.19E-19	205879	*Mycobacterium phage Omega*	*Mycobacterium sp.*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 204 length 622 cov 2.08289	622	3.54502	gi|1070106097|ref|YP 009291948.1|	355	3.14E-122	1792222	*Acinetobacter phage LZ35*	*Acinetobacter baumannii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 645 length 336 cov 1.70107	336	3.54167	gi|764161625|ref|YP 009126057.1|	57.8	3.29E-10	1566993	*Arthrobacter phage vB ArtM-ArV1*	*Arthrobacter sp.*	Actinobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 643 length 336 cov 1.88612	336	3.54167	gi|571797869|ref|YP 008772035.1|	145	3.88E-42	1399941	*Lactobacillus phage phiJB*	*Lactobacillus delbrueckii*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 838 length 300 cov 2.43265	300	3.53667	gi|971751675|ref|YP 009205624.1|	97.1	3.92E-24	1175662	*Pseudomonas phage PaMx42*	*Pseudomonas aeruginosa*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 440 length 400 cov 2.02319	400	3.5325	gi|203454733|ref|YP 002225049.1|	62.4	1.52E-11	546805	*Mycobacterium phage Myrna*	*Mycobacterium smegmatis str. MC2 155*	Actinobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 2919 length 213 cov 2.67089	213	3.53052	gi|937456472|ref|YP 009168397.1|	63.5	7.39E-13	1622234	*Citrobacter phage CVT22*	*Citrobacter sp. TM1552*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 2115 length 234 cov 1.97207	234	3.52991	gi|658310162|ref|YP 009042354.1|	111	9.13E-30	1327934	*Cronobacter phage CR8*	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 2827 length 215 cov 2.475	215	3.52558	gi|160700666|ref|YP 001552346.1|	48.9	8.60E-08	480808	*Mycobacterium phage Giles*	*Mycobacterium smegmatis*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 1205 length 269 cov 1.70561	269	3.51301	gi|509142291|ref|YP 008061153.1|	98.2	5.99E-25	1007869	*Rhodococcus phage E3*	*Rhodococcus hoagii*	Actinobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 307 length 511 cov 1.53289	511	3.45205	gi|410491660|ref|YP 006906882.1|	58.2	1.22E-09	1150869	*Escherichia phage P13374*	*Escherichia coli O104:H4 str. CB13374*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 2957 length 212 cov 1.84713	212	3.43868	gi|530545073|ref|YP 008408677.1|	67	3.86E-14	1340826	*Mycobacterium phage Whirlwind*	*Mycobacterium sp.*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 441 length 400 cov 1.93623	400	3.4175	gi|682123168|ref|YP 009055489.1|	115	4.18E-31	1505225	*Acinetobacter phage YMC-13-01-C62*	*Acinetobacter baumannii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 516 length 368 cov 2.25879	368	3.41576	gi|526178663|ref|YP 008242242.1|	67.4	1.58E-13	1327990	*Cellulophaga phage phi14:2*	*Cellulophaga baltica*	Bacteroidetes; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 2608 length 220 cov 2.54545	220	3.40909	gi|472340490|ref|YP 007674015.1|	85.1	1.70E-20	754049	*Vibrio phage pYD21-A*	*Vibrio sp. YD21*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 1017 length 278 cov 2.3139	278	3.38129	gi|338826858|ref|YP 004678771.1|	61.6	1.32E-12	981323	*Gordonia phage GTE2*	*Nocardia; Rhodococcus; Gordonia; Rhodococcus*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 749 length 315 cov 1.99615	315	3.35556	gi|472339627|ref|YP 007673160.1|	74.3	4.33E-16	754040	*Synechococcus phage S-RIP2*	*Synechococcus sp. WH 7803*	Cyanobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 1189 length 270 cov 2.35814	270	3.32593	gi|971757354|ref|YP 009210861.1|	71.2	2.53E-15	1647301	*Mycobacterium phage Vincenzo*	*Mycobacterium smegmatis str. MC2 155*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 191 length 653 cov 1.88462	653	3.317	gi|418487743|ref|YP 007002066.1|	192	4.06E-56	1133292	*Brucella phage Tb*	*Brucella abortus 544*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 526 length 366 cov 2.39871	366	3.31421	gi|389060123|ref|YP 006383276.1|	85.5	7.08E-22	1162295	*Cronobacter phage CR3*	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 1246 length 267 cov 1.57547	267	3.31086	gi|971748726|ref|YP 009202615.1|	87.4	4.70E-21	1698356	*Mycobacterium phage Phatniss*	*Mycobacterium smegmatis str. MC2 155*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 741 length 316 cov 2.0613	316	3.31013	gi|509142290|ref|YP 008061152.1|	77.4	8.16E-18	1007869	*Rhodococcus phage E3*	*Rhodococcus hoagii*	Actinobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 1882 length 242 cov 1.79679	242	3.30992	gi|151266296|ref|YP 001333659.1|	97.1	1.46E-24	338473	*Actinomyces phage Av-1*	*Actinomyces naeslundii*	Actinobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 1422 length 259 cov 2.03922	259	3.30502	gi|971763827|ref|YP 009216825.1|	92	6.49E-24	1229760	*Acinetobacter phage phiAC-1*	*Acinetobacter soli*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 194 length 646 cov 1.59222	646	3.30495	gi|509142255|ref|YP 008061117.1|	79.7	1.82E-16	1007869	*Rhodococcus phage E3*	*Rhodococcus hoagii*	Actinobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 262 length 553 cov 1.93173	553	3.3038	gi|682123145|ref|YP 009055466.1|	81.3	1.93E-17	1505225	*Acinetobacter phage YMC-13-01-C62*	*Acinetobacter baumannii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 2112 length 234 cov 2.31285	234	3.2735	gi|359802275|ref|YP 004935741.1|	48.9	1.51E-08	319522	*Gordonia phage GTE5*	*Gordonia terrae*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 1051 length 276 cov 2.40271	276	3.27174	gi|937456475|ref|YP 009168400.1|	136	1.33E-41	1622234	*Citrobacter phage CVT22*	*Citrobacter sp. TM1552*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 1760 length 246 cov 2.31937	246	3.2561	gi|1068510648|ref|YP 009273447.1|	46.2	1.43E-06	1838084	*Gordonia phage Woes*	*Gordonia terrae*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 363 length 443 cov 1.9433	443	3.20542	gi|593777244|ref|YP 009015089.1|	66.6	7.24E-13	1162290	*Cronobacter phage CR9*	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 2407 length 225 cov 2.27059	225	3.18222	gi|151266299|ref|YP 001333662.1|	54.7	1.01E-09	338473	*Actinomyces phage Av-1*	*Actinomyces naeslundii*	Actinobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 990 length 280 cov 1.92889	280	3.17143	gi|593777143|ref|YP 009014988.1|	83.6	1.36E-20	1162290	*Cronobacter phage CR9*	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 887 length 294 cov 2.04184	294	3.15646	gi|937456472|ref|YP 009168397.1|	101	9.53E-26	1622234	*Citrobacter phage CVT22*	*Citrobacter sp. TM1552*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 2574 length 221 cov 1.8253	221	3.12217	gi|157310980|ref|YP 001468976.1|	95.9	3.42E-24	384848	*Corynebacterium phage P1201*	*Corynebacterium glutamicum*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 333 length 475 cov 1.76667	475	3.11368	gi|593777339|ref|YP 009015184.1|	89.7	1.59E-22	1162290	*Cronobacter phage CR9*	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 1518 length 255 cov 1.87	255	3.07059	gi|937456464|ref|YP 009168389.1|	47.8	3.56E-07	1622234	*Citrobacter phage CVT22*	*Citrobacter sp. TM1552*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 1243 length 267 cov 2.25	267	3.05243	gi|1070103190|ref|YP 009287804.1|	51.2	2.97E-08	1873777	*Streptomyces phage Nanodon*	*Streptomyces griseus*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 475 length 383 cov 1.16768	383	2.9765	gi|593775442|ref|YP 009013305.1|	135	3.52E-41	1089132	*Mycobacterium phage SG4*	*Mycobacterium smegmatis str. MC2 155*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 670 length 331 cov 1.9058	331	2.91843	gi|937456473|ref|YP 009168398.1|	55.1	2.80E-09	1622234	*Citrobacter phage CVT22*	*Citrobacter sp. TM1552*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 802 length 306 cov 1.48207	306	2.91503	gi|151266296|ref|YP 001333659.1|	95.5	1.22E-23	338473	*Actinomyces phage Av-1*	*Actinomyces naeslundii*	Actinobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 259 length 554 cov 1.91182	554	2.90614	gi|937456507|ref|YP 009168433.1|	253	3.25E-85	1622234	*Citrobacter phage CVT22*	*Citrobacter sp. TM1552*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 1799 length 245 cov 1.6	245	2.89796	gi|29566753|ref|NP 818317.1|	100	6.56E-26	205879	*Mycobacterium phage Omega*	*Mycobacterium sp.*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 1230 length 268 cov 1.69014	268	2.88806	gi|509142338|ref|YP 008061200.1|	94	2.91E-23	1007869	*Rhodococcus phage E3*	*Rhodococcus hoagii*	Actinobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 1338 length 263 cov 2.00962	263	2.84411	gi|966201606|ref|YP 009191792.1|	107	3.10E-28	1647385	*Delftia phage IME-DE1*	*Delftia sp. 670*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 738 length 317 cov 1.98092	317	2.83281	gi|509142305|ref|YP 008061167.1|	66.2	3.09E-13	1007869	*Rhodococcus phage E3*	*Rhodococcus hoagii*	Actinobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 235 length 579 cov 1.58779	579	2.81865	gi|53793592|ref|YP 112492.1|	51.6	3.25E-07	294631	*Flavobacterium phage 11b*	*Flavobacterium sp.*	Bacteroidetes; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 282 length 532 cov 1.28931	532	2.75188	gi|971482459|ref|YP 009193961.1|	75.5	8.77E-16	1698358	*Mycobacterium phage Brusacoram*	*Mycobacterium smegmatis str. MC2 155*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 2023 length 237 cov 2.04945	237	2.72996	gi|62327110|ref|YP 223898.1|	74.7	1.00E-16	235201	*Lactobacillus phage phiJL-1*	*Lactobacillus plantarum*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 625 length 341 cov 1.34266	341	2.72434	gi|937456476|ref|YP 009168401.1|	61.6	8.19E-13	1622234	*Citrobacter phage CVT22*	*Citrobacter sp. TM1552*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses

NODE 317 length 496 cov 1.39229	496	2.69758	gi|203460615|ref|YP 002224349.1|	98.6	1.32E-24	546808	*Mycobacterium phage Spud*	*Mycobacterium smegmatis str. MC2 155*	Actinobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 502 length 371 cov 1.63924	371	2.69003	gi|514051708|ref|YP 008126134.1|	46.6	4.52E-06	1262532	*Mycobacterium phage BTCU-1*	*Mycobacterium smegmatis*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 1019 length 278 cov 1.86547	278	2.68345	gi|593777132|ref|YP 009014977.1|	132	1.84E-37	1162290	*Cronobacter phage CR9*	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 2238 length 230 cov 2.00571	230	2.66957	gi|686983201|ref|YP 009058944.1|	73.2	3.46E-16	1543419	*Torque teno Tadarida brasiliensis virus*	*Tadarida brasiliensis*	Chordata; Metazoa; Eukaryota	unclassified	Anelloviridae	ssDNA
NODE 284 length 531 cov 1.58193	531	2.60264	gi|388570812|ref|YP 006383795.1|	95.1	5.86E-24	1187128	*Acinetobacter bacteriophage AP22*	*Acinetobacter baumannii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 812 length 304 cov 1.62249	304	2.59539	gi|151266296|ref|YP 001333659.1|	110	5.97E-29	338473	*Actinomyces phage Av-1*	*Actinomyces naeslundii*	Actinobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 2350 length 227 cov 1.51163	227	2.57269	gi|971757155|ref|YP 009210688.1|	44.7	3.84E-06	1701853	*Mycobacterium phage Serenity*	*Mycobacterium smegmatis str. MC2 155*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 418 length 411 cov 1.70506	411	2.54745	gi|372449746|ref|YP 005086972.1|	58.9	2.96E-10	1109716	*Rhodococcus phage RGL3*	*Rhodococcus globerulus*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 358 length 449 cov 1.63959	449	2.53229	gi|971763799|ref|YP 009216797.1|	164	2.39E-48	1229760	*Acinetobacter phage phiAC-1*	*Acinetobacter soli*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 1962 length 239 cov 2.07065	239	2.51464	gi|985757333|ref|YP 009222296.1|	50.8	2.63E-08	1567484	*Lactobacillus phage LfeInf*	*Lactobacillus fermentum*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 2788 length 216 cov 1.97516	216	2.49074	gi|1070103328|ref|YP 009287971.1|	83.6	6.68E-20	1891703	*Mycobacterium phage Tonenili*	*Mycobacterium smegmatis str. MC2 155*	Actinobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 1730 length 247 cov 1.94792	247	2.44534	gi|371496158|ref|YP 004957306.1|	58.5	4.18E-11	994601	*Planktothrix phage PaV-LD*	*Planktothrix agardhii HAB637*	Cyanobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 3088 length 209 cov 1.35065	209	2.43062	gi|589889559|ref|YP 009004942.1|	48.9	9.62E-08	1429768	*Erwinia phage Ea35-7*	*Erwinia amylovora*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 702 length 324 cov 1.64312	324	2.42901	gi|215401206|ref|YP 002332511.1|	162	6.65E-49	575608	*Staphylococcus phage phiSauS-IPLA88*	*Staphylococcus aureus*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 3169 length 207 cov 1.59211	207	2.40097	gi|682123182|ref|YP 009055503.1|	74.7	6.31E-17	1505225	*Acinetobacter phage YMC-13-01-C62*	*Acinetobacter baumannii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 391 length 422 cov 1.75477	422	2.37915	gi|937456472|ref|YP 009168397.1|	156	2.14E-44	1622234	*Citrobacter phage CVT22*	*Citrobacter sp. TM1552*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 2275 length 229 cov 1.68966	229	2.34934	gi|937456469|ref|YP 009168394.1|	115	6.40E-31	1622234	*Citrobacter phage CVT22*	*Citrobacter sp. TM1552*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 1494 length 256 cov 1.83085	256	2.34766	gi|1070621526|ref|YP 009302998.1|	82.8	1.56E-19	1821562	*Gordonia phage SoilAssassin*	*Gordonia terrae*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 409 length 416 cov 1.45706	416	2.33654	gi|593777123|ref|YP 009014968.1|	176	1.01E-54	1162290	*Cronobacter phage CR9*	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 1859 length 243 cov 1.83511	243	2.3251	gi|966203364|ref|YP 009187675.1|	133	5.86E-41	1719140	*Klebsiella phage vB KpnM KB57*	*Klebsiella pneumoniae*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 3043 length 210 cov 1.47742	210	2.30476	gi|937424920|ref|YP 009165756.1|	66.6	5.47E-14	1100043	*Apis mellifera filamentous virus*	*Apis mellifera*	Arthropoda; Metazoa; Eukaryota	unclassified	unclassified	dsDNA
NODE 355 length 451 cov 1.2601	451	2.28603	gi|593777121|ref|YP 009014966.1|	103	3.39E-26	1162290	*Cronobacter phage CR9*	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 1190 length 270 cov 1.7814	270	2.23333	gi|509142181|ref|YP 008061043.1|	110	4.10E-29	1007869	*Rhodococcus phage E3*	*Rhodococcus hoagii*	Actinobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 600 length 349 cov 1.10884	349	2.2235	gi|472340491|ref|YP 007674016.1|	52	3.46E-08	754049	*Vibrio phage pYD21-A*	*Vibrio sp. YD21*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 1098 length 274 cov 2.02283	274	2.20438	gi|722142304|ref|YP 009104301.1|	86.3	1.47E-20	1527515	*Idiomarinaceae phage Phi1M2-2*	*Idiomarinaceae bacterium M2-2*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 1169 length 271 cov 1.73148	271	2.19188	gi|937456498|ref|YP 009168424.1|	61.6	7.37E-12	1622234	*Citrobacter phage CVT22*	*Citrobacter sp. TM1552*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 705 length 323 cov 1.21642	323	2.16718	gi|29566640|ref|NP 818206.1|	78.6	1.31E-17	205877	*Mycobacterium phage Bxz1*	*Mycobacterium sp.*	Actinobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 1006 length 279 cov 1.70982	279	2.16129	gi|1070103030|ref|YP 009287678.1|	64.7	5.52E-13	1838137	*Propionibacterium phage PFR1*	*Propionibacterium freudenreichii*	Actinobacteria; Bacteria	unclassified	unclassified	unclassified
NODE 881 length 295 cov 1.23333	295	2.14237	gi|1068511191|ref|YP 009274208.1|	57	1.47E-11	1838071	*Gordonia phage Kvothe*	*Gordonia terrae*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 980 length 281 cov 1.16372	281	2.14235	gi|326784531|ref|YP 004324978.1|	58.9	2.58E-11	445688	*Prochlorococcus phage P-SSM7*	*Prochlorococcus marinus str. NATL1A*	Cyanobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 2414 length 225 cov 1.51765	225	2.12444	gi|564292915|ref|YP 008873609.1|	52.8	7.26E-10	1007127	*Staphylococcus phage Sb-1*	*Staphylococcus aureus*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 954 length 284 cov 1.67249	284	2.12324	gi|593775732|ref|YP 009013592.1|	76.6	4.44E-17	1089121	*Mycobacterium phage Dori*	*Mycobacterium smegmatis str. MC2 155*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 1620 length 251 cov 1.58163	251	2.11155	gi|937456504|ref|YP 009168430.1|	114	1.72E-30	1622234	*Citrobacter phage CVT22*	*Citrobacter sp. TM1552*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 943 length 286 cov 1.4026	286	2.10839	gi|388684798|ref|YP 006382678.1|	65.5	3.70E-13	1161927	*Pseudomonas phage Lu11*	*Pseudomonas putida*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 1460 length 258 cov 1.18227	258	2.10078	gi|589287688|ref|YP 009010292.1|	57.4	2.00E-10	1401669	*Erwinia phage PhiEaH1*	*Erwinia amylovora*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 2243 length 230 cov 1.42286	230	2.1	gi|1070096285|ref|YP 009277923.1|	112	5.52E-31	1887651	*Gordonia phage Nyceirae*	*Gordonia terrae*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 929 length 289 cov 0.884615	289	2.0692	gi|9626704|ref|NP 040974.1|	61.2	5.57E-12	11673	*Feline immunodeficiency virus*	*Felidae*	Chordata; Metazoa; Eukaryota	unclassified	Retroviridae	ssRNA RT
NODE 1801 length 245 cov 1.49474	245	2.05714	gi|414087615|ref|YP 006987800.1|	49.7	8.18E-08	1141139	*Enterobacteria phage vB EcoP ACG-C91*	*Escherichia coli*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 2113 length 234 cov 2.27374	234	2.05128	gi|203454750|ref|YP 002225066.1|	79	2.56E-18	546805	*Mycobacterium phage Myrna*	*Mycobacterium smegmatis str. MC2 155*	Actinobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 2056 length 236 cov 1.1105	236	2.05085	gi|1068511844|ref|YP 009275124.1|	62.4	2.36E-12	1821554	*Gordonia phage Hotorobo*	*Gordonia terrae*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 846 length 299 cov 1.32377	299	2.01672	gi|939177065|ref|YP 009172504.1|	79.3	5.88E-18	1663208	*Ostreococcus lucimarinus virus 2*	*Ostreococcus 'lucimarinus'*	Chlorophyta; Viridiplantae; Eukaryota	unclassified	Phycodnaviridae	dsDNA
NODE 755 length 314 cov 1.40541	314	2.00637	gi|460042347|ref|YP 007517785.1|	68.2	5.74E-14	1283078	*Pelagibacter phage HTVC011P*	*Candidatus Pelagibacter ubique HTCC1062*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 1080 length 275 cov 1.37727	275	2	gi|1173244297|ref|YP 009352305.1|	60.1	2.32E-11	1220717	*Rhizobium phage RHEph10*	*Rhizobium etli CFN 42*	Proteobacteria; Bacteria	unclassified	unclassified	unclassified
NODE 2211 length 231 cov 1.63636	231	1.96104	gi|937456465|ref|YP 009168390.1|	139	1.71E-41	1622234	*Citrobacter phage CVT22*	*Citrobacter sp. TM1552*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 1499 length 256 cov 1.22388	256	1.95312	gi|56693176|ref|YP 164763.1|	79.3	5.45E-19	298338	*Lactobacillus phage LP65*	*Lactobacillus plantarum*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 359 length 449 cov 1.02792	449	1.83964	gi|971748547|ref|YP 009202464.1|	47.4	3.88E-07	1698711	*Mycobacterium phage Lolly9*	*Mycobacterium smegmatis str. MC2 155*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 995 length 280 cov 1.25778	280	1.79643	gi|1070096446|ref|YP 009278373.1|	52	1.72E-08	1883372	*Erwinia phage vB EamM EarlPhillipIV*	*Erwinia amylovora*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 2679 length 219 cov 1.16463	219	1.78539	gi|849250932|ref|YP 009147766.1|	85.9	1.16E-20	1560313	*Lactococcus phage WRP3*	*Lactococcus lactis*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 1340 length 263 cov 1.36058	263	1.70342	gi|682123922|ref|YP 009056237.1|	48.9	1.73E-07	1529058	*Vibrio phage ICP2 2013 A Haiti*	*Vibrio cholerae*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 574 length 354 cov 1.08027	354	1.70056	gi|682123169|ref|YP 009055490.1|	68.2	9.78E-15	1505225	*Acinetobacter phage YMC-13-01-C62*	*Acinetobacter baumannii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 1480 length 257 cov 1.06931	257	1.6965	gi|1070064978|ref|YP 009283092.1|	74.3	1.77E-16	1815509	*Bacillus phage AR9*	*Bacillus subtilis subsp. subtilis str. 168*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 1736 length 247 cov 1.15625	247	1.63158	gi|1070101667|ref|YP 009285847.1|	75.1	5.03E-17	1844477	*Pseudomonas phage NP1*	*Pseudomonas sp.*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 1152 length 272 cov 1.02765	272	1.62868	gi|481019400|ref|YP 007877754.1|	48.1	3.29E-07	536444	*Cyanophage P-RSM1*	*Prochlorococcus marinus str. MIT 9303*	Cyanobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 1106 length 274 cov 0.940639	274	1.62774	gi|29134961|ref|NP 803591.1|	53.1	6.63E-09	169683	*Pseudomonas phage phiKZ*	*Pseudomonas aeruginosa*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 493 length 374 cov 1.1348	374	1.6123	gi|514361054|ref|YP 008130293.1|	86.3	5.27E-20	1282995	*Serratia phage Eta*	*Serratia marcescens*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 1370 length 262 cov 0.859903	262	1.60305	gi|526120194|ref|YP 008320473.1|	65.9	1.83E-13	1325731	*Flavobacterium phage 6H*	*Flavobacterium psychrophilum*	Bacteroidetes; Bacteria	unclassified	unclassified	dsDNA viruses
NODE 481 length 381 cov 1.17791	381	1.5853	gi|363539900|ref|YP 004894381.1|	49.7	3.73E-07	1094892	*Megavirus chiliensis*	*Acanthamoeba*	Longamoebia; Eukaryota	unclassified	Mimiviridae	dsDNA
NODE 1128 length 273 cov 0.958716	273	1.57143	gi|509142296|ref|YP 008061158.1|	89	1.89E-21	1007869	*Rhodococcus phage E3*	*Rhodococcus hoagii*	Actinobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 727 length 320 cov 0.977358	320	1.49687	gi|971753194|ref|YP 009207149.1|	98.2	2.13E-24	1690425	*Streptomyces phage Caliburn*	*Streptomyces griseus*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 822 length 303 cov 1.39516	303	1.49175	gi|509142319|ref|YP 008061181.1|	102	3.41E-26	1007869	*Rhodococcus phage E3*	*Rhodococcus hoagii*	Actinobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 3176 length 207 cov 1.26316	207	1.45894	gi|151266296|ref|YP 001333659.1|	51.6	8.90E-09	338473	*Actinomyces phage Av-1*	*Actinomyces naeslundii*	Actinobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 3203 length 207 cov 1.19079	207	1.45894	gi|34610177|ref|NP 919002.1|	90.5	2.18E-22	242861	*Burkholderia phage BcepNazgul*	*Burkholderia cepacia*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 774 length 311 cov 1.07422	311	1.45659	gi|937456473|ref|YP 009168398.1|	102	3.42E-26	1622234	*Citrobacter phage CVT22*	*Citrobacter sp. TM1552*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 3134 length 208 cov 1.2549	208	1.45192	gi|157310980|ref|YP 001468976.1|	82.4	1.63E-19	384848	*Corynebacterium phage P1201*	*Corynebacterium glutamicum*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 3212 length 207 cov 0.842105	207	1.44928	gi|327198319|ref|YP 004306893.1|	43.1	8.29E-06	59241	*Streptococcus phage Dp-1*	*Streptococcus pneumoniae*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 3153 length 208 cov 1.24837	208	1.44712	gi|563398140|ref|YP 008857900.1|	87	2.08E-21	1414742	*Arthrobacter phage vB ArS-ArV2*	*Arthrobacter sp.*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 3092 length 209 cov 1.24675	209	1.44498	gi|422935214|ref|YP 007005171.1|	52.8	1.40E-09	1190451	*Campylobacter phage CP21*	*Campylobacter sp.*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 3059 length 210 cov 1.23871	210	1.4381	gi|151266300|ref|YP 001333663.1|	89.7	3.81E-22	338473	*Actinomyces phage Av-1*	*Actinomyces naeslundii*	Actinobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 3201 length 207 cov 1.21711	207	1.42512	gi|448245200|ref|YP 007392917.1|	48.5	1.33E-07	1188795	*Xanthomonas citri phage CP2*	*Xanthomonas citri*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 2761 length 217 cov 1.18519	217	1.39171	gi|148724470|ref|YP 001285436.1|	44.3	4.67E-06	438482	*Synechococcus phage Syn5*	*Synechococcus sp. WH 8109*	Cyanobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 2683 length 219 cov 1.16463	219	1.37443	gi|29135112|ref|NP 803742.1|	47.4	2.76E-07	169683	*Pseudomonas phage phiKZ*	*Pseudomonas aeruginosa*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 2628 length 220 cov 1.16364	220	1.37273	gi|937424933|ref|YP 009165769.1|	70.1	3.08E-15	1100043	*Apis mellifera filamentous virus*	*Apis mellifera*	Arthropoda; Metazoa; Eukaryota	unclassified	unclassified	dsDNA
NODE 2659 length 220 cov 0.830303	220	1.36818	gi|371496158|ref|YP 004957306.1|	63.2	4.86E-13	994601	*Planktothrix phage PaV-LD*	*Planktothrix agardhii HAB637*	Cyanobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 2649 length 220 cov 1.12121	220	1.36364	gi|725949138|ref|YP 009098384.1|	49.3	5.42E-08	1194091	*Klebsiella phage NTUH-K2044-K1-1*	*Klebsiella pneumoniae*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 2579 length 221 cov 1.40964	221	1.36199	gi|1109302725|ref|YP 009325851.1|	62	2.43E-12	1917232	*Only Syngen Nebraska virus 5*	*Chlorella variabilis*	Chlorophyta; Viridiplantae; Eukaryota	unclassified	Phycodnaviridae	dsDNA
NODE 2563 length 222 cov 0.826347	222	1.35586	gi|948298241|ref|YP 009177768.1|	43.5	8.32E-06	1032473	*Aeropyrum pernix spindle-shaped virus 1*	*Aeropyrum pernix*	Crenarchaeota; Archaea	unclassified	unclassified	unclassified
NODE 2509 length 223 cov 1.14286	223	1.35426	gi|985757377|ref|YP 009222340.1|	64.3	4.16E-13	1567484	*Lactobacillus phage LfeInf*	*Lactobacillus fermentum*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 2418 length 225 cov 1.12941	225	1.34222	gi|971763817|ref|YP 009216815.1|	72.8	2.33E-17	1229760	*Acinetobacter phage phiAC-1*	*Acinetobacter soli*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 2355 length 227 cov 1.11628	227	1.3304	gi|971848936|ref|YP 009035515.1|	55.8	3.73E-10	1416334	*Lactobacillus phage phi jlb1*	*Lactobacillus gasseri ADH*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 2400 length 226 cov 1.11111	226	1.32743	gi|1068511664|ref|YP 009274976.1|	43.9	5.68E-06	1838081	*Gordonia phage Utz*	*Gordonia sp.*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 2297 length 229 cov 1.06322	229	1.31441	gi|610583977|ref|YP 008869280.1|	61.6	1.02E-12	1325372	*Edwardsiella phage PEi21*	*Edwardsiella ictaluri*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 2227 length 231 cov 1.08523	231	1.30303	gi|151266300|ref|YP 001333663.1|	62.8	1.47E-12	338473	*Actinomyces phage Av-1*	*Actinomyces naeslundii*	Actinobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
NODE 2165 length 233 cov 1.07303	233	1.29185	gi|985758405|ref|YP 009223776.1|	51.2	1.96E-08	1572712	*Geobacillus virus E3*	*Geobacillus sp.*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 2133 length 234 cov 1.07263	234	1.2906	gi|593777800|ref|YP 009015647.1|	52.8	5.40E-09	1084719	*Bacillus phage G*	*Bacillus sp.; Geobacillus sp.*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 2102 length 235 cov 1.06111	235	1.28085	gi|282598799|ref|YP 003359118.1|	45.8	1.09E-06	686439	*Clavibacter phage CMP1*	*Clavibacter michiganensis subsp. michiganensis*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 2059 length 236 cov 1.06077	236	1.27966	gi|149882831|ref|YP 001294810.1|	58.2	8.31E-11	446529	*Microbacterium phage Min1*	*Microbacterium nematophilum*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 2058 length 236 cov 1.06077	236	1.27966	gi|45597421|ref|NP 996706.1|	44.7	4.13E-06	12390	*Lactococcus phage phiLC3*	*Lactococcus lactis subsp. cremoris*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 1974 length 239 cov 1.04348	239	1.2636	gi|939177681|ref|YP 009173589.1|	47	5.52E-07	455364	*Chrysochromulina ericina virus*	*Haptolina ericina*	Prymnesiales; Eukaryota	unclassified	Phycodnaviridae	dsDNA
NODE 1890 length 242 cov 1.02674	242	1.24793	gi|1070064942|ref|YP 009283056.1|	48.5	1.86E-07	1815509	*Bacillus phage AR9*	*Bacillus subtilis subsp. subtilis str. 168*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 1871 length 243 cov 1.01064	243	1.23457	gi|1109302725|ref|YP 009325851.1|	61.6	5.32E-12	1917232	*Only Syngen Nebraska virus 5*	*Chlorella variabilis*	Chlorophyta; Viridiplantae; Eukaryota	unclassified	Phycodnaviridae	dsDNA
NODE 1851 length 244 cov 1.01058	244	1.23361	gi|1070101687|ref|YP 009285867.1|	73.6	3.06E-16	1844477	*Pseudomonas phage NP1*	*Pseudomonas sp.*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 1825 length 245 cov 0.994737	245	1.23265	gi|725949311|ref|YP 009098904.1|	63.9	1.24E-13	1357714	*Caulobacter phage Cr30*	*Caulobacter vibrioides CB15*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 1822 length 245 cov 1	245	1.22449	gi|338826904|ref|YP 004678817.1|	54.3	1.71E-09	981323	*Gordonia phage GTE2*	*Nocardia; Rhodococcus; Gordonia; Rhodococcus*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 1786 length 246 cov 1	246	1.22358	gi|593777538|ref|YP 009015381.1|	81.3	5.40E-19	1084719	*Bacillus phage G*	*Bacillus sp.; Geobacillus sp.*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
NODE 1658 length 250 cov 0.979487	250	1.204	gi|479336466|ref|YP 007869815.1|	64.7	4.39E-13	1296646	*Mycobacterium phage Butters*	*Mycobacterium smegmatis*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 1631 length 251 cov 0.979592	251	1.20319	gi|593774743|ref|YP 009012611.1|	58.2	2.74E-11	691964	*Rhodococcus phage ReqiPoco6*	*Rhodococcus hoagii*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 1609 length 252 cov 0.964467	252	1.19048	gi|431810400|ref|YP 007237282.1|	47.8	3.51E-07	1147137	*Clostridium phage phi8074-B1*	*Clostridium sporogenes*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
NODE 1564 length 254 cov 0.914573	254	1.18504	gi|310831495|ref|YP 003970138.1|	44.3	7.83E-06	693272	*Cafeteria roenbergensis virus BV-PW1*	*Cafeteria roenbergensis*	Bicosoecida; Eukaryota	unclassified	Mimiviridae	dsDNA

	NODE 1554 length 254 cov 0.959799	254	1.18504	gi|327198390|ref|YP 004326978.1|	44.7	9.45E-07	925986	*Erwinia phage phiEa104*	*Erwinia amylovora*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 1528 length 255 cov 0.96	255	1.18431	gi|56693171|ref|YP 164758.1|	81.3	6.88E-19	298338	*Lactobacillus phage LP65*	*Lactobacillus plantarum*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 1637 length 251 cov 0.954082	251	1.18327	gi|1070643172|ref|YP 009300729.1|	62	2.20E-12	1796997	*Arthrobacter phage Mudcat*	*Arthrobacter sp. ATCC 21022*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
	NODE 1502 length 256 cov 0.955224	256	1.17969	gi|509142181|ref|YP 008061043.1|	57	2.01E-10	1007869	*Rhodococcus phage E3*	*Rhodococcus hoagii*	Actinobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 1503 length 256 cov 0.955224	256	1.17969	gi|56693153|ref|YP 164740.1|	57.8	1.01E-10	298338	*Lactobacillus phage LP65*	*Lactobacillus plantarum*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 1504 length 256 cov 0.950249	256	1.17578	gi|849250941|ref|YP 009147775.1|	55.8	4.83E-10	1560313	*Lactococcus phage WRP3*	*Lactococcus lactis*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
	NODE 1485 length 257 cov 0.950495	257	1.1751	gi|966198453|ref|YP 009188253.1|	102	2.42E-26	1589733	*Cyanophage TIM40*	*Prochlorococcus marinus str. NATL2A*	Cyanobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 1481 length 257 cov 0.950495	257	1.1751	gi|803431957|ref|YP 009129267.1|	45.1	4.36E-06	46076	*Artichoke latent virus*	*Cynara cardunculus var. scolymus*	Streptophyta; Viridiplantae; Eukaryota	unclassified	Potyviridae	ssRNA +
	NODE 1466 length 258 cov 0.945813	258	1.17054	gi|971767322|ref|YP 009220192.1|	54.3	1.08E-09	461711	*Synechococcus phage S-CBP42*	*Synechococcus sp. WH 7803*	Actinobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
	NODE 1432 length 259 cov 0.941176	259	1.16602	gi|358356497|ref|YP 004934248.1|	105	4.14E-31	331278	*Yersinia phage phiR1-37*	*Yersinia enterocolitica*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 1447 length 259 cov 0.926471	259	1.15444	gi|937456460|ref|YP 009168385.1|	80.9	4.32E-20	1622234	*Citrobacter phage CVT22*	*Citrobacter sp. TM1552*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
	NODE 1362 length 262 cov 0.927536	262	1.15267	gi|971761177|ref|YP 009214523.1|	71.6	1.77E-15	1572704	*Staphylococcus phage phiIPLA-C1C*	*Staphylococcus aureus*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 1324 length 264 cov 0.91866	264	1.14394	gi|1109302725|ref|YP 009325851.1|	103	1.47E-26	1917232	*Only Syngen Nebraska virus 5*	*Chlorella variabilis*	Chlorophyta; Viridiplantae; Eukaryota	unclassified	Phycodnaviridae	dsDNA
	NODE 1369 length 262 cov 0.869565	262	1.14122	gi|985757332|ref|YP 009222295.1|	95.5	6.89E-24	1567484	*Lactobacillus phage LfeInf*	*Lactobacillus fermentum*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 1333 length 264 cov 0.913876	264	1.14015	gi|906476370|ref|YP 009160383.1|	98.6	4.86E-26	1655656	*Gokushovirinae Fen672 31*	*na*	na	unclassified	Microviridae	ssDNA viruses
	NODE 1279 length 266 cov 0.905213	266	1.13158	gi|712914779|ref|YP 009102168.1|	47.4	7.00E-07	1273738	*Escherichia phage PBECO 4*	*Escherichia coli O157*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 1254 length 267 cov 0.90566	267	1.13109	gi|1070065029|ref|YP 009283143.1|	55.5	8.19E-10	1815509	*Bacillus phage AR9*	*Bacillus subtilis subsp. subtilis str. 168*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 1251 length 267 cov 0.90566	267	1.13109	gi|593774742|ref|YP 009012610.1|	50.8	3.97E-08	691964	*Rhodococcus phage ReqiPoco6*	*Rhodococcus hoagii*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
	NODE 1160 length 272 cov 0.875576	272	1.10294	gi|906476370|ref|YP 009160383.1|	90.1	1.11E-22	1655656	*Gokushovirinae Fen672 31*	*na*	na	unclassified	Microviridae	ssDNA viruses
	NODE 1113 length 274 cov 0.876712	274	1.10219	gi|971764128|ref|YP 009217130.1|	78.2	1.06E-17	998086	*Pseudomonas phage PhiPA3*	*Pseudomonas aeruginosa*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA viruses
	NODE 1117 length 274 cov 0.872146	274	1.09854	gi|24371536|ref|NP 720276.1|	82	2.03E-19	173443	*Salmonella phage ST64T*	*Salmonella enterica*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
	NODE 1083 length 275 cov 0.872727	275	1.09818	gi|944325910|ref|YP 009174707.1|	75.5	9.53E-17	1586713	*Yellowstone lake phycodnavirus 1*	*na*	na	unclassified	Phycodnaviridae	dsDNA viruses
	NODE 1032 length 278 cov 0.860987	278	1.08633	gi|363540839|ref|YP 004894409.1|	75.5	9.51E-17	1094892	*Megavirus chiliensis*	*Acanthamoeba*	Longamoebia; Eukaryota	unclassified	Mimiviridae	dsDNA
	NODE 1036 length 278 cov 0.856502	278	1.08273	gi|1070643189|ref|YP 009300747.1|	135	6.92E-38	1796997	*Arthrobacter phage Mudcat*	*Arthrobacter sp. ATCC 21022*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA viruses
	NODE 860 length 297 cov 1.05372	297	1.0101	gi|422935909|ref|YP 007005806.1|	110	6.36E-31	1051675	*Erwinia phage vB EamP-S6*	*Erwinia amylovora*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA viruses
								Healthy bees DNA virome					
	NODE 67 length 398 cov 1.82799	398	2.88442	gi|686983201|ref|YP 009058944.1|	60.8	4.18E-08	1543419	*Torque teno Tadarida brasiliensis virus*	*Tadarida brasiliensis*	Chordata; Metazoa; Eukaryota	unclassified	Anelloviridae	ssDNA
	NODE 1120 length 225 cov 1.39412	225	2.69333	gi|333596680|gb|AEF58760.1|	66.6	4.63E-11	1034790	*Mosquito VEM Anellovirus SDBVL A*	*Culicidae*	Arthropoda; Metazoa; Eukaryota	unclassified	Anelloviridae	ssDNA
	NODE 1058 length 227 cov 1.11628	227	1.3304	gi|557680986|dbj|BAO04453.1|	166	4.36E-46	381707	*Bovine viral diarrhea virus 3*	*Bos taurus*	Chordata; Metazoa; Eukaryota	unclassified	Flaviviridae	ssRNA +
								Unhealthy bees RNA virome					
	a29119;2756 total counts: 7460053 Seed: 2 K: 25 length: 2731	2731	1251.63	gi|589892981|ref|YP 009004309.1|	405	2.23E-132	1453367	Staphylococcus phage GRCS	*Staphylococcus aureus*	Firmicutes; Bacteria	Caudovirales	Podoviridae	dsDNA
MqD	a145575;124 total counts: 517623 Seed: 5 K: 25 length: 4184	4184	136.13	gi|56698740|ref|YP 164339.1|	173	1.97E-43	292208	*Dendrolimus punctatus densovirus*	*Dendrolimus punctatus*	Arthropoda; Metazoa; Eukaryota	unclassified	Parvoviridae	ssDNA
MqC	a23;106 total counts: 85879 Seed: 2 K: 25 length: 835	835	107.419	gi|607840595|ref|YP 009021845.1|	64.3	4.27E-11	1234882	*Dragonfly cyclovirus 4*	*Erythemis simplicicollis*	Arthropoda; Metazoa; Eukaryota	unclassified	Circoviridae	ssDNA
MqC1	a87654;83 total counts: 129393 Seed: 2 K: 25 length: 1587	1587	83.0183	gi|1192699366|ref|YP 009362252.1|	276	4.64E-89	795381	*Bat cyclovirus GF-4c*	*Chiroptera*	Chordata; Metazoa; Eukaryota	unclassified	Circoviridae	ssDNA
	a116472;2 total counts: 909 Seed: 2 K: 25 length: 582	582	40.1554	gi|151266299|ref|YP 001333662.1|	90.9	8.08E-21	338473	Actinomyces phage Av-1	*Actinomyces naeslundii*	Actinobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
	a89036;2 total counts: 576 Seed: 2 K: 25 length: 260	260	27.1163	gi|151266305|ref|YP 001333668.1|	51.2	2.88E-08	338473	Actinomyces phage Av-1	*Actinomyces naeslundii*	Actinobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
MqV2	a356;26 total counts: 96963 Seed: 2 K: 25 length: 3730	3730	27.008	gi|1132371839|ref|YP 009337674.1|	342	1.65E-104	1922816	*Changjiang tombus-like virus 22*	*Astacoidea*	Arthropoda; Metazoa; Eukaryota	unclassified	unclassified	RNA
	a148797;3 total counts: 838 Seed: 3 K: 25 length: 357	357	21.7183	gi|1068512414|ref|YP 009276097.1|	58.9	1.30E-10	1647473	Gordonia phage GRU3	*Gordonia malaquae*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
	a29135;15 total counts: 37696 Seed: 18 K: 25 length: 2471	2471	20.1829	gi|388570783|ref|YP 006383766.1|	644	0.00E+00	1187128	Acinetobacter bacteriophage AP22	*Acinetobacter baumannii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
	a145736;12 total counts: 14774 Seed: 6 K: 25 length: 1211	1211	17.6201	gi|1070106045|ref|YP 009291896.1|	268	5.96E-87	1792222	Acinetobacter phage LZ35	*Acinetobacter baumannii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
	a145548;14 total counts: 225461 Seed: 2 K: 25 length: 16338	16338	14.2949	gi|593777809|ref|YP 009015656.1|	135	3.99E-30	1084719	Bacillus phage G	*Bacillus sp.; Geobacillus sp.*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
MqV1a	a115910;13 total counts: 77920 Seed: 2 K: 25 length: 5913	5913	14.2757	gi|1134955725|ref|YP 009342327.1|	721	0.00E+00	1923715	*Wuhan insect virus 11*	*Astacoidea*	Arthropoda; Metazoa; Eukaryota	Picornavirales	Dicistroviridae	ssRNA +
	a3371;13 total counts: 6188 Seed: 8 K: 25 length: 488	488	14.2336	gi|448244865|ref|YP 007392585.1|	47	2.51E-06	1116482	Pectobacterium phage phiTE	*Pectobacterium atrosepticum SCRI1043*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
	a58206;11 total counts: 43766 Seed: 5 K: 25 length: 3937	3937	13.4763	gi|966199285|ref|YP 009189380.1|	189	2.77E-48	691318	Acinetobacter phage phiAB1	*Acinetobacter baumannii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
	a61384;15 total counts: 5882 Seed: 12 K: 25 length: 421	421	12.8599	gi|23334610|ref|NP 694833.1|	47.8	2.68E-06	37138	*Galleria mellonella densovirus*	*Galleria mellonella*	Arthropoda; Metazoa; Eukaryota	unclassified	Parvoviridae	ssDNA
	a29390;11 total counts: 22460 Seed: 8 K: 25 length: 1991	1991	12.8307	gi|682123154|ref|YP 009055475.1|	375	4.00E-120	1505225	Acinetobacter phage YMC-13-01-C62	*Acinetobacter baumannii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
	a30242;10 total counts: 7809 Seed: 16 K: 25 length: 836	836	12.3361	gi|971763811|ref|YP 009216809.1|	219	6.48E-68	1229760	Acinetobacter phage phiAC-1	*Acinetobacter soli*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
	a146893;11 total counts: 7131 Seed: 11 K: 25 length: 679	679	12.2548	gi|971765187|ref|YP 009218283.1|	46.6	5.96E-06	1597976	Enterococcus phage EFDG1	*Enterococcus faecalis*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
	a30349;8 total counts: 8570 Seed: 2 K: 25 length: 1075	1075	12.2239	gi|971746169|ref|YP 009200249.1|	243	1.48E-74	1636200	Pseudoalteromonas Phage H103	*Pseudoalteromonas marina*	Proteobacteria; Bacteria	Caudovirales	unclassified	dsDNA
	a29421;6 total counts: 2661 Seed: 7 K: 25 length: 474	474	11.6068	gi|764162207|ref|YP 009126577.1|	94.4	3.05E-23	1538804	Vibrio phage VpKK5	*Vibrio parahaemolyticus*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
	a134905;2 total counts: 525 Seed: 4 K: 25 length: 248	248	11.4022	gi|593778368|ref|YP 009016208.1|	70.9	2.72E-15	691963	Rhodococcus phage ReqiPine5	*Rhodococcus hoagii*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
	a148892;2 total counts: 763 Seed: 2 K: 25 length: 492	492	11.3347	gi|22296540|ref|NP 680500.1|	58.2	8.31E-10	51369	Lactobacillus phage A2	*Lactobacillus casei*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
	a58544;8 total counts: 12547 Seed: 2 K: 25 length: 1519	1519	10.7031	gi|388570790|ref|YP 006383773.1|	52.4	3.45E-08	1187128	Acinetobacter bacteriophage AP22	*Acinetobacter baumannii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
	a146684;12 total counts: 7542 Seed: 3 K: 25 length: 676	676	10.1553	gi|682123168|ref|YP 009055489.1|	93.2	1.31E-21	1505225	Acinetobacter phage YMC-13-01-C62	*Acinetobacter baumannii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
	a149896;10 total counts: 1814 Seed: 5 K: 25 length: 212	212	9.5283	gi|388570830|ref|YP 006383813.1|	49.7	3.43E-08	1187128	Acinetobacter bacteriophage AP22	*Acinetobacter baumannii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
	a146706;9 total counts: 7470 Seed: 3 K: 25 length: 826	826	9.40436	gi|985757779|ref|YP 009223154.1|	65.5	2.71E-11	1755679	Bacillus phage BM5	*Bacillus megaterium*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
	a130237;2 total counts: 453 Seed: 2 K: 25 length: 283	283	8.97411	gi|589890583|ref|YP 009006439.1|	60.1	3.00E-11	1414739	Vibrio phage SHOU24	*Vibrio parahaemolyticus*	Proteobacteria; Bacteria	unclassified	unclassified	dsDNA
	a58401;11 total counts: 3538 Seed: 2 K: 25 length: 357	357	8.95238	gi|1132371030|ref|YP 009337019.1|	79.3	1.12E-17	1923158	*Hubei picorna-like virus 74*	*Myriapoda*	Arthropoda; Metazoa; Eukaryota	unclassified	unclassified	RNA
	a87374;9 total counts: 11851 Seed: 2 K: 25 length: 1293	1293	8.94122	gi|448244802|ref|YP 007392522.1|	101	3.19E-22	1116482	Pectobacterium phage phiTE	*Pectobacterium atrosepticum SCRI1043*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
	a59767;7 total counts: 4925 Seed: 7 K: 25 length: 701	701	8.54066	gi|1070106029|ref|YP 009291880.1|	110	9.05E-28	1792222	Acinetobacter phage LZ35	*Acinetobacter baumannii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
	a29401;4 total counts: 887 Seed: 6 K: 25 length: 246	246	8.51717	gi|589893779|ref|YP 009010488.1|	44.3	5.46E-06	1458842	Geobacillus phage GBK2	*Geobacillus kaustophilus*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
	a89639;8 total counts: 4696 Seed: 6 K: 25 length: 631	631	8.50713	gi|448244960|ref|YP 007392680.1|	149	5.05E-45	1116482	Pectobacterium phage phiTE	*Pectobacterium atrosepticum SCRI1043*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
	a92269;2 total counts: 813 Seed: 3 K: 25 length: 450	450	8.47083	gi|1070103030|ref|YP 009287678.1|	103	8.82E-26	1838137	Propionibacterium phage PFR1	*Propionibacterium freudenreichii*	Actinobacteria; Bacteria	unclassified	unclassified	unclassified
MqV1b	a87907;9 total counts: 11161 Seed: 5 K: 25 length: 1236	1236	8.45793	gi|73747918|ref|NP 851404.2|	172	2.31E-46	68876	*Kashmir bee virus*	*Apis cerana*	Arthropoda; Metazoa; Eukaryota	Picornavirales	Dicistroviridae	ssRNA +
	a90481;8 total counts: 2074 Seed: 2 K: 25 length: 295	295	8.39661	gi|966203611|ref|YP 009188926.1|	62	2.46E-12	1684115	Cronobacter phage PBES 02	*Cronobacter sp.*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
	a152844;2 total counts: 557 Seed: 2 K: 25 length: 279	279	8.32605	gi|372450020|ref|YP 005087241.1|	53.5	5.43E-09	1109714	Rhodococcus phage REQ3	*Rhodococcus hoagii*	Actinobacteria; Bacteria	unclassified	unclassified	unclassified
	a489;8 total counts: 6985 Seed: 15 K: 25 length: 899	899	8.18354	gi|414086874|ref|YP 006987062.1|	201	1.36E-61	1141135	Cronobacter phage vB CsaM GAP31	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
	a29230;7 total counts: 10358 Seed: 5 K: 25 length: 1422	1422	8.08861	gi|363539705|ref|YP 004893990.1|	79.3	1.51E-17	889338	Salmonella phage PVP-SE1	*Salmonella enterica subsp. enterica serovar Enteritidis*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
	a115755;8 total counts: 8948 Seed: 6 K: 25 length: 1124	1124	7.84431	gi|1132372007|ref|YP 009337788.1|	167	1.07E-44	1923151	*Hubei picorna-like virus 68*	*Diplopoda*	Arthropoda; Metazoa; Eukaryota	unclassified	unclassified	RNA
	a146691;5 total counts: 1437 Seed: 5 K: 25 length: 313	313	7.73464	gi|589892934|ref|YP 009004263.1|	48.9	3.44E-07	1406793	Clavibacter phage CN1A	*Clavibacter michiganensis*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
	a117376;7 total counts: 6934 Seed: 5 K: 25 length: 965	965	7.71399	gi|448244775|ref|YP 007392495.1|	198	1.08E-62	1116482	Pectobacterium phage phiTE	*Pectobacterium atrosepticum SCRI1043*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
	a117847;9 total counts: 2482 Seed: 9 K: 25 length: 315	315	7.68254	gi|226377807|ref|YP 002790856.1|	45.1	2.07E-06	632112	Lactobacillus phage Lb338-1	*Lactobacillus paracasei*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
	a147681;7 total counts: 2817 Seed: 7 K: 25 length: 407	407	7.67813	gi|971848889|ref|YP 009035468.1|	76.3	1.62E-16	1416334	Lactobacillus phage phi jlb1	*Lactobacillus gasseri ADH*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
	a87919;8 total counts: 5141 Seed: 4 K: 25 length: 682	682	7.64516	gi|1132370297|ref|YP 009336506.1|	152	1.10E-41	1923011	*Hubei orthoptera virus 3*	*Orthoptera*	Arthropoda; Metazoa; Eukaryota	unclassified	unclassified	RNA
	a3336;7 total counts: 5770 Seed: 2 K: 25 length: 797	797	7.601	gi|593777363|ref|YP 009015208.1|	228	1.59E-72	1162290	Cronobacter phage CR9	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
	a59574;7 total counts: 6078 Seed: 2 K: 25 length: 951	951	7.13985	gi|448244957|ref|YP 007392677.1|	111	3.49E-26	1116482	Pectobacterium phage phiTE	*Pectobacterium atrosepticum SCRI1043*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
	a149598;2 total counts: 319 Seed: 2 K: 25 length: 226	226	7.12708	gi|1070101683|ref|YP 009285863.1|	70.5	1.13E-15	1844477	Pseudomonas phage NP1	*Pseudomonas sp.*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
	a93244;6 total counts: 2296 Seed: 14 K: 25 length: 417	417	7.10552	gi|658310263|ref|YP 009042455.1|	74.7	7.38E-16	1327934	Cronobacter phage CR8	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
	a145610;6 total counts: 11121 Seed: 2 K: 25 length: 1836	1836	7.04194	gi|966203720|ref|YP 009189035.1|	837	0.00E+00	1684115	Cronobacter phage PBES 02	*Cronobacter sp.*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
	a145591;3 total counts: 3090 Seed: 2 K: 25 length: 1074	1074	7.01488	gi|1068358202|ref|YP 009273943.1|	212	3.08E-64	1838080	Gordonia phage Vendetta	*Gordonia terrae*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
	a147897;7 total counts: 2386 Seed: 2 K: 25 length: 366	366	7.0082	gi|571026783|ref|YP 008888536.1|	102	1.03E-25	1432856	*Formica exsecta virus 1*	*Formica exsecta*	Arthropoda; Metazoa; Eukaryota	Picornavirales	Dicistroviridae	ssRNA +
	a60807;6 total counts: 1537 Seed: 3 K: 25 length: 303	303	6.9934	gi|1132370297|ref|YP 009336506.1|	58.9	8.36E-11	1923011	*Hubei orthoptera virus 3*	*Orthoptera*	Arthropoda; Metazoa; Eukaryota	unclassified	unclassified	RNA
	a155640;3 total counts: 851 Seed: 7 K: 25 length: 279	279	6.97328	gi|418489114|ref|YP 007002968.1|	128	2.19E-35	37105	Lactobacillus phage JCL1032	*Lactobacillus delbrueckii subsp. lactis*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
	a116979;6 total counts: 11399 Seed: 2 K: 25 length: 1828	1828	6.92287	gi|389059941|ref|YP 006383094.1|	69.7	3.46E-14	1162295	Cronobacter phage CR3	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
	a73159;3 total counts: 611 Seed: 3 K: 25 length: 259	259	6.86408	gi|508178998|ref|YP 008051459.1|	44.7	2.73E-06	1327759	Streptomyces phage Sujidade	*Streptomyces lividans*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
	a125;6 total counts: 3682 Seed: 2 K: 25 length: 638	638	6.83229	gi|593777210|ref|YP 009015055.1|	141	3.60E-39	1162290	Cronobacter phage CR9	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
	a959;6 total counts: 6640 Seed: 8 K: 25 length: 1147	1147	6.79512	gi|593777239|ref|YP 009015084.1|	55.5	3.25E-08	1162290	Cronobacter phage CR9	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
	a87945;7 total counts: 2997 Seed: 7 K: 25 length: 485	485	6.74227	gi|966203439|ref|YP 009187756.1|	55.1	5.00E-09	1719140	Klebsiella phage vB KpnM KB57	*Klebsiella pneumoniae*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
	a60707;6 total counts: 1510 Seed: 4 K: 25 length: 259	259	6.73359	gi|658310123|ref|YP 009042315.1|	165	6.62E-49	1327934	Cronobacter phage CR8	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
	a146551;4 total counts: 4589 Seed: 7 K: 25 length: 1126	1126	6.56879	gi|1068511068|ref|YP 009274022.1|	132	8.70E-37	1838072	Gordonia phage McGonagall	*Gordonia neofelifaecis*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
	a13;6 total counts: 5184 Seed: 6 K: 25 length: 829	829	6.53438	gi|593777273|ref|YP 009015118.1|	74.3	4.20E-16	1162290	Cronobacter phage CR9	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
	a93128;3 total counts: 1188 Seed: 3 K: 25 length: 402	402	6.53154	gi|557307947|ref|YP 008767267.1|	55.5	4.15E-09	39103	Lactobacillus phage PL-1	*Lactobacillus paracasei*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
	a146281;6 total counts: 5714 Seed: 15 K: 25 length: 1054	1054	6.4611	gi|593777142|ref|YP 009014987.1|	506	1.59E-178	1162290	Cronobacter phage CR9	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
	a146755;4 total counts: 3333 Seed: 14 K: 25 length: 868	868	6.4252	gi|146329949|ref|YP 001210257.1|	93.6	1.23E-21	437329	Burkholderia phage BcepGomr	*Burkholderia cepacia*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
	a84;5 total counts: 4687 Seed: 10 K: 25 length: 894	894	6.39821	gi|658310256|ref|YP 009042448.1|	264	1.71E-88	1327934	Cronobacter phage CR8	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
	a87883;6 total counts: 7909 Seed: 7 K: 25 length: 1336	1336	6.38174	gi|593777139|ref|YP 009014984.1|	201	3.58E-60	1162290	Cronobacter phage CR9	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA

a146107;7 total counts: 6223 Seed: 2 K: 25 length: 980	980	6.25816	gi|448244974|ref|YP 007392694.1|	275	8.43E-92	1116482	Pectobacterium phage phiTE	*Pectobacterium atrosepticum SCRI1043*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a87678;6 total counts: 5258 Seed: 9 K: 25 length: 941	941	6.19497	gi|1068358199|ref|YP 009273940.1|	86.7	4.83E-18	1838080	Gordonia phage Vendetta	*Gordonia terrae*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a65757;2 total counts: 360 Seed: 2 K: 25 length: 257	257	6.1645	gi|939536927|ref|YP 009168411.2|	101	7.99E-27	1622234	Citrobacter phage CVT22	*Citrobacter sp. TM1552*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a88229;6 total counts: 5692 Seed: 2 K: 25 length: 1024	1024	6.16309	gi|593777125|ref|YP 009014970.1|	250	1.66E-74	1162290	Cronobacter phage CR9	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a58559;6 total counts: 3379 Seed: 5 K: 25 length: 610	610	6.14754	gi|593777283|ref|YP 009015128.1|	88.6	7.29E-22	1162290	Cronobacter phage CR9	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a30198;7 total counts: 3618 Seed: 2 K: 25 length: 524	524	6.12977	gi|1132372007|ref|YP 009337788.1|	58.2	1.62E-09	1923151	*Hubei picorna-like virus 68*	*Diplopoda*	Arthropoda; Metazoa; Eukaryota	unclassified	unclassified	RNA
a148940;7 total counts: 2435 Seed: 12 K: 25 length: 372	372	6.12097	gi|937456198|ref|YP 009167808.1|	77.8	1.65E-17	438780	Lactobacillus phage phiPYB5	*Lactobacillus fermentum*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a116141;5 total counts: 2380 Seed: 2 K: 25 length: 475	475	6.05895	gi|440789461|ref|YP 007349171.1|	56.6	6.21E-10	1262513	Serratia phage phiMAM1	*Serratia sp.*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a147164;6 total counts: 5790 Seed: 8 K: 25 length: 1028	1028	6.04767	gi|682123153|ref|YP 009055474.1|	112	9.36E-29	1505225	Acinetobacter phage YMC-13-01-C62	*Acinetobacter baumannii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a87623;6 total counts: 2023 Seed: 3 K: 25 length: 385	385	5.99481	gi|448244891|ref|YP 007392611.1|	72.4	6.67E-17	1116482	Pectobacterium phage phiTE	*Pectobacterium atrosepticum SCRI1043*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a116386;7 total counts: 5103 Seed: 11 K: 25 length: 785	785	5.9172	gi|563397698|ref|YP 008857462.1|	65.9	2.20E-13	1391428	Enterobacteria phage 4MG	*Escherichia coli K-12*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a88401;5 total counts: 4397 Seed: 4 K: 25 length: 967	967	5.88004	gi|363539710|ref|YP 004893995.1|	77	2.17E-17	889338	Salmonella phage PVP-SE1	*Salmonella enterica subsp. enterica serovar Enteritidis*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a61329;2 total counts: 582 Seed: 2 K: 25 length: 263	263	5.8699	gi|764162033|ref|YP 009126429.1|	123	2.71E-35	1561065	Paracoccus phage vB PmaS IMEP1	*Paracoccus marcusii*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a87760;5 total counts: 3323 Seed: 8 K: 25 length: 633	633	5.85624	gi|1132372007|ref|YP 009337788.1|	120	9.32E-31	1923151	*Hubei picorna-like virus 68*	*Diplopoda*	Arthropoda; Metazoa; Eukaryota	unclassified	unclassified	RNA
a59531;6 total counts: 9726 Seed: 8 K: 25 length: 1704	1704	5.82453	gi|658310294|ref|YP 009042486.1|	377	2.64E-125	1327934	Cronobacter phage CR8	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a117633;5 total counts: 2738 Seed: 6 K: 25 length: 598	598	5.75585	gi|1134599800|ref|YP 009342254.1|	105	9.39E-26	1923692	*Wuhan arthropod virus 3*	*Hexapoda*	Arthropoda; Metazoa; Eukaryota	unclassified	unclassified	RNA
a116567;5 total counts: 5007 Seed: 5 K: 25 length: 1025	1025	5.71512	gi|563397489|ref|YP 008857253.1|	95.5	2.97E-21	1391428	Enterobacteria phage 4MG	*Escherichia coli K-12*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a87688;7 total counts: 2137 Seed: 3 K: 25 length: 333	333	5.68769	gi|422937549|ref|YP 007007754.1|	57.4	4.70E-10	1127514	Aeromonas phage vB AsaM-56	*Aeromonas salmonicida*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a62989;8 total counts: 1709 Seed: 2 K: 25 length: 233	233	5.67811	gi|593777355|ref|YP 009015200.1|	82.8	1.63E-20	1162290	Cronobacter phage CR9	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a120694;7 total counts: 1942 Seed: 6 K: 25 length: 286	286	5.66667	gi|764162223|ref|YP 009126593.1|	133	3.49E-37	1538804	Vibrio phage VpKK5	*Vibrio parahaemolyticus*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a116247;6 total counts: 3553 Seed: 2 K: 25 length: 661	661	5.66263	gi|1070106098|ref|YP 009291949.1|	180	1.62E-53	1792222	Acinetobacter phage LZ35	*Acinetobacter baumannii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a146679;6 total counts: 2317 Seed: 4 K: 25 length: 440	440	5.64773	gi|1070099784|ref|YP 009283489.1|	44.7	2.08E-06	1647411	Salmonella phage NR01	*Salmonella enterica subsp. enterica serovar Typhimurium*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a1808;3 total counts: 2394 Seed: 2 K: 25 length: 818	818	5.59889	gi|971765014|ref|YP 009218007.1|	105	9.57E-25	1755682	Streptomyces phage phiSAJS1	*Streptomyces avermitilis*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a119732;5 total counts: 1999 Seed: 10 K: 25 length: 391	391	5.58568	gi|1127298679|ref|YP 009333576.1|	72.4	5.33E-15	1922550	*Beihai picorna-like virus 121*	*Ligia exotica*	Arthropoda; Metazoa; Eukaryota	unclassified	unclassified	RNA
a60775;5 total counts: 3496 Seed: 3 K: 25 length: 673	673	5.58247	gi|971763828|ref|YP 009216826.1|	168	4.65E-51	1229760	Acinetobacter phage phiAC-1	*Acinetobacter soli*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a123068;6 total counts: 1164 Seed: 3 K: 25 length: 226	226	5.5708	gi|712915520|ref|YP 009103259.1|	55.1	3.92E-10	1481187	Acinetobacter phage vB AbaP Acibel007	*Acinetobacter baumannii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a147161;2 total counts: 758 Seed: 4 K: 25 length: 357	357	5.54862	gi|712912877|ref|YP 009099732.1|	62.8	4.50E-12	1555208	Ruegeria phage DSS3-P1	*Ruegeria pomeroyi DSS-3*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a8803;6 total counts: 2129 Seed: 2 K: 25 length: 384	384	5.53224	gi|1070101651|ref|YP 009285831.1|	49.3	5.18E-07	1844477	Pseudomonas phage NP1	*Pseudomonas sp.*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a157036;2 total counts: 541 Seed: 3 K: 25 length: 258	258	5.52753	gi|1068511062|ref|YP 009274016.1|	50.8	3.25E-08	1838072	Gordonia phage McGonagall	*Gordonia neofelifaecis*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a150472;5 total counts: 1663 Seed: 2 K: 25 length: 344	344	5.50872	gi|1132370297|ref|YP 009336506.1|	137	4.39E-38	1923011	*Hubei orthoptera virus 3*	*Orthoptera*	Arthropoda; Metazoa; Eukaryota	unclassified	unclassified	RNA
a148545;5 total counts: 4407 Seed: 4 K: 25 length: 906	906	5.4713	gi|593777136|ref|YP 009014981.1|	230	8.18E-69	1162290	Cronobacter phage CR9	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a710;8 total counts: 10651 Seed: 7 K: 25 length: 1313	1313	5.46473	gi|472342361|ref|YP 007675869.1|	181	8.37E-54	754058	Vibrio phage PWH3a-P1	*Vibrio natriegens*	Proteobacteria; Bacteria	unclassified	unclassified	dsDNA
a91422;5 total counts: 7244 Seed: 6 K: 25 length: 1453	1453	5.46387	gi|593777149|ref|YP 009014994.1|	116	7.15E-27	1162290	Cronobacter phage CR9	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a12310;3 total counts: 671 Seed: 5 K: 25 length: 285	285	5.44271	gi|1070101678|ref|YP 009285858.1|	65.9	4.20E-14	1844477	Pseudomonas phage NP1	*Pseudomonas sp.*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a147994;5 total counts: 2716 Seed: 2 K: 25 length: 623	623	5.40931	gi|730985057|ref|YP 009111142.1|	86.3	4.28E-19	1527519	Escherichia phage Av-05	*Escherichia coli O157:H7*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a89524;5 total counts: 5704 Seed: 5 K: 25 length: 1090	1090	5.40367	gi|593777381|ref|YP 009015226.1|	268	2.17E-85	1162290	Cronobacter phage CR9	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a148424;6 total counts: 2706 Seed: 2 K: 25 length: 480	480	5.35113	gi|1070101665|ref|YP 009285845.1|	68.2	2.26E-13	1844477	Pseudomonas phage NP1	*Pseudomonas sp.*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a1179;5 total counts: 4904 Seed: 10 K: 25 length: 928	928	5.34914	gi|389059974|ref|YP 006383127.1|	358	2.43E-122	1162295	Cronobacter phage CR3	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a10598;3 total counts: 614 Seed: 3 K: 25 length: 239	239	5.33197	gi|1070099007|ref|YP 009281736.1|	83.6	9.35E-20	1874002	Bacillus phage Stitch	*Bacillus sp.*	Firmicutes; Bacteria	Caudovirales	Podoviridae	dsDNA
a30927;5 total counts: 1678 Seed: 2 K: 25 length: 360	360	5.32222	gi|593777375|ref|YP 009015220.1|	58.5	1.15E-11	1162290	Cronobacter phage CR9	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a146560;3 total counts: 818 Seed: 2 K: 25 length: 311	311	5.31379	gi|1068357956|ref|YP 009273286.1|	65.1	4.55E-13	1647470	Gordonia phage GMA1	*Gordonia malaquae*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a87786;4 total counts: 3868 Seed: 4 K: 25 length: 908	908	5.29846	gi|363539684|ref|YP 004893969.1|	127	1.86E-35	889338	Salmonella phage PVP-SE1	*Salmonella enterica subsp. enterica serovar Enteritidis*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a147329;4 total counts: 4586 Seed: 2 K: 25 length: 1094	1094	5.29616	gi|971763920|ref|YP 009216905.1|	56.6	2.14E-08	1522092	Clostridium phage phiCDHM19	*Clostridium sp.*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a58707;5 total counts: 7658 Seed: 3 K: 25 length: 1538	1538	5.28088	gi|389060077|ref|YP 006383230.1|	471	5.19E-164	1162295	Cronobacter phage CR3	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a29755;9 total counts: 7610 Seed: 2 K: 25 length: 902	902	5.26718	gi|1132370509|ref|YP 009336655.1|	81.6	3.01E-16	1923160	*Hubei picorna-like virus 76*	*Myriapoda*	Arthropoda; Metazoa; Eukaryota	unclassified	unclassified	RNA
a148214;5 total counts: 1378 Seed: 5 K: 25 length: 322	322	5.26618	gi|9633052|ref|NP 050160.1|	48.1	8.03E-07	12417	Lactobacillus phage phiadh	*Lactobacillus gasseri*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a61287;2 total counts: 413 Seed: 2 K: 25 length: 214	214	5.25413	gi|472339880|ref|YP 007673409.1|	46.6	5.33E-07	756282	Cellulophaga phage phiST	*Cellulophaga sp. MM#3*	Bacteroidetes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a87573;5 total counts: 8642 Seed: 3 K: 25 length: 1816	1816	5.25275	gi|730985094|ref|YP 009111179.1|	192	9.27E-53	1527519	Escherichia phage Av-05	*Escherichia coli O157:H9*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a146137;6 total counts: 2577 Seed: 8 K: 25 length: 483	483	5.21325	gi|658310154|ref|YP 009042346.1|	68.2	7.59E-15	1327934	Cronobacter phage CR8	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a66893;5 total counts: 1556 Seed: 5 K: 25 length: 353	353	5.20963	gi|593777397|ref|YP 009015242.1|	50.1	3.61E-08	1162290	Cronobacter phage CR9	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a1155;5 total counts: 2384 Seed: 2 K: 25 length: 494	494	5.19433	gi|966203777|ref|YP 009189092.1|	214	4.67E-67	1684115	Cronobacter phage PBES 02	*Cronobacter sp.*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a120203;2 total counts: 666 Seed: 2 K: 25 length: 353	353	5.18405	gi|151266302|ref|YP 001333665.1|	48.5	5.24E-07	338473	Actinomyces phage Av-1	*Actinomyces naeslundii*	Actinobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a150305;6 total counts: 1803 Seed: 2 K: 25 length: 351	351	5.1453	gi|389059922|ref|YP 006383075.1|	86.7	3.30E-20	1162295	Cronobacter phage CR3	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a147855;5 total counts: 1519 Seed: 6 K: 25 length: 339	339	5.06204	gi|571797869|ref|YP 008772035.1|	77.8	2.56E-17	1399941	Lactobacillus phage phiJB	*Lactobacillus delbrueckii*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a58916;5 total counts: 4273 Seed: 4 K: 25 length: 899	899	5.05451	gi|971762804|ref|YP 009215890.1|	53.1	6.32E-07	1296655	Bacillus phage JL	*Bacillus cereus*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a58466;5 total counts: 1329 Seed: 2 K: 25 length: 293	293	5	gi|389060116|ref|YP 006383269.1|	87.8	3.44E-23	1162295	Cronobacter phage CR3	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a150749;4 total counts: 1179 Seed: 6 K: 25 length: 342	342	4.99457	gi|472340162|ref|YP 007673689.1|	45.4	5.94E-06	754067	Salicola phage CGphi29	*Salicola sp.*	Proteobacteria; Bacteria	unclassified	unclassified	dsDNA
a29359;5 total counts: 3883 Seed: 8 K: 25 length: 780	780	4.95897	gi|1132371092|ref|YP 009337064.1|	54.3	1.91E-07	1923150	*Hubei picorna-like virus 67*	*Myriapoda*	Arthropoda; Metazoa; Eukaryota	unclassified	unclassified	RNA
a4746;5 total counts: 1034 Seed: 2 K: 25 length: 230	230	4.8913	gi|966203360|ref|YP 009187671.1|	80.5	3.67E-19	1719140	Klebsiella phage vB KpnM KB57	*Klebsiella pneumoniae*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a124153;2 total counts: 683 Seed: 2 K: 25 length: 315	315	4.88333	gi|374531230|ref|YP 005098014.1|	47.4	3.01E-07	1125653	Salmonella phage SPN1S	*Salmonella enterica subsp. enterica serovar Typhimurium*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a87707;4 total counts: 1477 Seed: 4 K: 25 length: 437	437	4.86041	gi|1132372007|ref|YP 009337788.1|	48.9	1.33E-06	1923151	*Hubei picorna-like virus 68*	*Diplopoda*	Arthropoda; Metazoa; Eukaryota	unclassified	unclassified	RNA
a87941;3 total counts: 2356 Seed: 2 K: 25 length: 744	744	4.84901	gi|985760384|ref|YP 009225904.1|	107	9.57E-26	1556290	Streptomyces phage Jay2Jay	*Streptomyces lividans*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a149502;4 total counts: 1712 Seed: 5 K: 25 length: 448	448	4.80357	gi|593777201|ref|YP 009015046.1|	131	1.61E-35	1162290	Cronobacter phage CR9	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a58735;5 total counts: 3285 Seed: 7 K: 25 length: 679	679	4.79971	gi|658310275|ref|YP 009042467.1|	121	4.10E-34	1327934	Cronobacter phage CR8	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a149443;5 total counts: 1624 Seed: 2 K: 25 length: 339	339	4.78761	gi|937456775|ref|YP 009168612.1|	52.4	2.34E-08	755164	Lactobacillus phage LBR48	*Lactobacillus brevis*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a99582;4 total counts: 853 Seed: 3 K: 25 length: 228	228	4.76754	gi|593777350|ref|YP 009015195.1|	78.2	2.40E-19	1162290	Cronobacter phage CR9	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a4252;4 total counts: 1012 Seed: 2 K: 25 length: 250	250	4.744	gi|971763827|ref|YP 009216825.1|	62	2.07E-12	1229760	Acinetobacter phage phiAC-1	*Acinetobacter soli*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a1311;5 total counts: 3847 Seed: 3 K: 25 length: 840	840	4.73333	gi|593777352|ref|YP 009015197.1|	350	2.01E-120	1162290	Cronobacter phage CR9	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a87697;5 total counts: 2755 Seed: 2 K: 25 length: 576	576	4.72396	gi|448244884|ref|YP 007392604.1|	95.5	1.98E-24	1116482	Pectobacterium phage phiTE	*Pectobacterium atrosepticum SCRI1043*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a1805;5 total counts: 3486 Seed: 4 K: 25 length: 662	662	4.71752	gi|593777128|ref|YP 009014973.1|	114	3.47E-31	1162290	Cronobacter phage CR9	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a145684;4 total counts: 4230 Seed: 2 K: 25 length: 984	984	4.71748	gi|593777123|ref|YP 009014968.1|	222	9.15E-70	1162290	Cronobacter phage CR9	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a88535;5 total counts: 3188 Seed: 2 K: 25 length: 709	709	4.70381	gi|389059863|ref|YP 006383016.1|	315	3.14E-105	1162295	Cronobacter phage CR3	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a90302;2 total counts: 441 Seed: 2 K: 25 length: 290	290	4.68771	gi|971744076|ref|YP 009198398.1|	89.4	1.55E-21	1647302	Mycobacterium phage Phayonce	*Mycobacterium smegmatis str. MC2 155*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a146301;5 total counts: 2878 Seed: 2 K: 25 length: 584	584	4.68493	gi|593777382|ref|YP 009015227.1|	147	5.11E-45	1162290	Cronobacter phage CR9	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a118198;5 total counts: 1677 Seed: 2 K: 25 length: 369	369	4.68293	gi|682123169|ref|YP 009055490.1|	68.2	9.19E-15	1505225	Acinetobacter phage YMC-13-01-C62	*Acinetobacter baumannii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a88020;5 total counts: 4331 Seed: 7 K: 25 length: 985	985	4.68223	gi|658310257|ref|YP 009042449.1|	359	7.62E-125	1327934	Cronobacter phage CR8	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a5118;5 total counts: 3299 Seed: 3 K: 25 length: 722	722	4.66759	gi|849248849|ref|YP 009146765.1|	86.3	1.70E-18	1560342	Acinetobacter phage YMC13/03/R2096	*Acinetobacter baumannii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a31892;4 total counts: 768 Seed: 2 K: 25 length: 223	223	4.66667	gi|148912835|ref|YP 001293414.1|	47.4	3.32E-07	347325	Pseudomonas phage 73	*Pseudomonas aeruginosa*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a5;8 total counts: 3485 Seed: 3 K: 25 length: 438	438	4.65982	gi|966203673|ref|YP 009188988.1|	57	2.00E-09	1684115	Cronobacter phage PBES 02	*Cronobacter sp.*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a147249;4 total counts: 1593 Seed: 6 K: 25 length: 456	456	4.64706	gi|764162033|ref|YP 009126429.1|	149	2.36E-44	1561065	Paracoccus phage vB PmaS IMEP1	*Paracoccus marcusii*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a58152;5 total counts: 2250 Seed: 9 K: 25 length: 516	516	4.62209	gi|1150146953|ref|YP 009345893.1|	176	1.16E-50	1923716	*Wuhan insect virus 12*	*Arthropoda*	Arthropoda; Metazoa; Eukaryota	unclassified	unclassified	RNA
a117622;6 total counts: 1796 Seed: 8 K: 25 length: 318	318	4.60063	gi|448244911|ref|YP 007392631.1|	118	5.04E-34	1116482	Pectobacterium phage phiTE	*Pectobacterium atrosepticum SCRI1043*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a118456;5 total counts: 4582 Seed: 2 K: 25 length: 965	965	4.5886	gi|593777143|ref|YP 009014988.1|	216	4.40E-69	1162290	Cronobacter phage CR9	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a145649;4 total counts: 2350 Seed: 5 K: 25 length: 578	578	4.58824	gi|971758015|ref|YP 009211443.1|	45.1	5.27E-06	1429794	Pectobacterium bacteriophage PM2	*Pectobacterium sp.*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a2396;5 total counts: 1764 Seed: 4 K: 25 length: 384	384	4.58701	gi|479336583|ref|YP 007869931.1|	50.1	2.92E-07	1305710	Mycobacterium phage vB MapS FF47	*Mycobacterium avium subsp. paratuberculosis*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a149871;4 total counts: 1261 Seed: 2 K: 25 length: 337	337	4.5638	gi|1132370297|ref|YP 009336506.1|	53.9	8.43E-09	1923011	*Hubei orthoptera virus 3*	*Orthoptera*	Arthropoda; Metazoa; Eukaryota	unclassified	unclassified	RNA
a147405;5 total counts: 1821 Seed: 11 K: 25 length: 384	384	4.52865	gi|1070125526|ref|YP 009293489.1|	59.3	1.69E-10	1815968	Salmonella phage SJ46	*Salmonella enterica subsp. enterica serovar Indiana*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a30645;5 total counts: 2820 Seed: 4 K: 25 length: 589	589	4.51974	gi|1068359384|ref|YP 009276387.1|	71.6	4.22E-15	1647471	Gordonia phage GMA4	*Gordonia malaquae*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a61267;3 total counts: 883 Seed: 3 K: 25 length: 293	293	4.50512	gi|448244883|ref|YP 007392603.1|	45.8	2.57E-06	1116482	Pectobacterium phage phiTE	*Pectobacterium atrosepticum SCRI1043*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a29910;2 total counts: 370 Seed: 2 K: 25 length: 214	214	4.50422	gi|764162201|ref|YP 009126571.1|	57	2.25E-11	1538804	Vibrio phage VpKK5	*Vibrio parahaemolyticus*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a2959;7 total counts: 1967 Seed: 7 K: 25 length: 303	303	4.46689	gi|526178371|ref|YP 008242193.1|	84	1.25E-20	1327993	Cellulophaga phage phi39:1	*Cellulophaga baltica*	Bacteroidetes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a6607;4 total counts: 788 Seed: 4 K: 25 length: 239	239	4.42678	gi|563397696|ref|YP 008857460.1|	60.8	1.71E-12	1391428	Enterobacteria phage 4MG	*Escherichia coli K-12*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a94219;4 total counts: 914 Seed: 7 K: 25 length: 242	242	4.42562	gi|593777353|ref|YP 009015198.1|	55.1	3.22E-11	1162290	Cronobacter phage CR9	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a116551;5 total counts: 4072 Seed: 2 K: 25 length: 889	889	4.3802	gi|389059955|ref|YP 006383108.1|	95.1	2.82E-23	1162295	Cronobacter phage CR3	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a146221;5 total counts: 2874 Seed: 2 K: 25 length: 650	650	4.35538	gi|658310280|ref|YP 009042472.1|	116	4.64E-32	1327934	Cronobacter phage CR8	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a3942;5 total counts: 1878 Seed: 8 K: 25 length: 441	441	4.34014	gi|1134599801|ref|YP 009342255.1|	48.1	2.23E-06	1923692	*Wuhan arthropod virus 3*	*Hexapoda*	Arthropoda; Metazoa; Eukaryota	unclassified	unclassified	RNA
a62123;4 total counts: 2233 Seed: 3 K: 25 length: 640	640	4.32188	gi|730985156|ref|YP 009111241.1|	139	5.75E-40	1527519	Escherichia phage Av-05	*Escherichia coli O157:H8*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a2791;4 total counts: 992 Seed: 5 K: 25 length: 304	304	4.31908	gi|658310053|ref|YP 009042245.1|	106	1.92E-27	1327934	Cronobacter phage CR8	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA

a122019;3 total counts: 1194 Seed: 3 K: 25 length: 366	366	4.31842	gi|1070620945|ref|YP 009301454.1|	64.7	7.17E-13	1821552	Gordonia phage Emalyn	*Gordonia terrae*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a149361;5 total counts: 1571 Seed: 9 K: 25 length: 310	310	4.3	gi|971763831|ref|YP 009216829.1|	76.6	5.48E-19	1229760	Acinetobacter phage phiAC-1	*Acinetobacter soli*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a147715;2 total counts: 378 Seed: 2 K: 25 length: 221	221	4.28602	gi|157168388|ref|YP 001456745.1|	65.9	1.24E-13	28358	Corynebacterium phage BFK20	*[Brevibacterium] flavum*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a88405;4 total counts: 1813 Seed: 7 K: 25 length: 464	464	4.28017	gi|593777392|ref|YP 009015237.1|	45.4	2.37E-06	1162290	Cronobacter phage CR9	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a1589;3 total counts: 1127 Seed: 6 K: 25 length: 436	436	4.27509	gi|48697198|ref|YP 024928.1|	177	5.81E-55	279280	Burkholderia phage BcepC6B	*Burkholderia cepacia*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a30965;4 total counts: 1194 Seed: 2 K: 25 length: 325	325	4.21231	gi|848469552|ref|YP 009145928.1|	70.9	4.86E-15	1220714	Rhizobium phage RHEph06	*Rhizobium etli GR56*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a375;4 total counts: 1247 Seed: 4 K: 25 length: 347	347	4.1902	gi|966203437|ref|YP 009187754.1|	120	3.60E-35	1719140	Klebsiella phage vB KpnM KB57	*Klebsiella pneumoniae*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a121594;4 total counts: 629 Seed: 6 K: 25 length: 201	201	4.15423	gi|593777201|ref|YP 009015046.1|	115	1.83E-31	1162290	Cronobacter phage CR9	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a97527;5 total counts: 2221 Seed: 2 K: 25 length: 436	436	4.15228	gi|971762140|ref|YP 009215331.1|	119	5.01E-32	1636183	Streptomyces phage YDN12	*Streptomyces griseus subsp. griseus*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a62460;5 total counts: 972 Seed: 5 K: 25 length: 206	206	4.14563	gi|389059866|ref|YP 006383019.1|	54.3	1.05E-09	1162295	Cronobacter phage CR3	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a148337;4 total counts: 1892 Seed: 2 K: 25 length: 460	460	4.12609	gi|226377831|ref|YP 002790879.1|	59.7	2.93E-10	631345	*Solenopsis invicta virus 3*	*Solenopsis invicta*	Arthropoda; Metazoa; Eukaryota	unclassified	unclassified	unclassified
a2658;5 total counts: 1125 Seed: 4 K: 25 length: 262	262	4.11832	gi|472342218|ref|YP 007675729.1|	55.5	5.44E-10	756280	Cellulophaga phage phiSM	*Cellulophaga sp. MM#3*	Bacteroidetes; Bacteria	Caudovirales	Myoviridae	dsDNA
a147066;5 total counts: 1636 Seed: 3 K: 25 length: 324	324	4.11404	gi|410491332|ref|YP 006906554.1|	122	5.20E-33	1229786	Propionibacterium phage P101A	*Cutibacterium acnes*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a146197;4 total counts: 3045 Seed: 2 K: 25 length: 808	808	4.10877	gi|971751687|ref|YP 009205612.1|	80.9	1.74E-16	1175662	Pseudomonas phage PaMx42	*Pseudomonas aeruginosa*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a146950;3 total counts: 532 Seed: 4 K: 25 length: 207	207	4.06557	gi|1070620973|ref|YP 009301483.1|	49.7	5.50E-08	1821552	Gordonia phage Emalyn	*Gordonia terrae*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a153042;2 total counts: 381 Seed: 3 K: 25 length: 239	239	4.06329	gi|41179371|ref|NP 958679.1|	63.5	1.14E-12	194699	Bordetella phage BPP-1	*Bordetella bronchiseptica*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a30547;13 total counts: 6700 Seed: 21 K: 25 length: 552	552	4.02958	gi|372449802|ref|YP 005087026.1|	221	2.13E-70	1109717	Rhodococcus phage RRH1	*Rhodococcus rhodochrous*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a119223;2 total counts: 334 Seed: 2 K: 25 length: 221	221	4.01386	gi|971762626|ref|YP 009215748.1|	93.6	2.37E-23	1718273	Pseudomonas phage PAE1	*Pseudomonas aeruginosa*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a64277;5 total counts: 1172 Seed: 5 K: 25 length: 281	281	4.01068	gi|448244878|ref|YP 007392598.1|	96.7	2.72E-24	1116482	Pectobacterium phage phiTE	*Pectobacterium atrosepticum SCRI1043*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a29235;5 total counts: 2308 Seed: 2 K: 25 length: 522	522	4.00766	gi|563397465|ref|YP 008857229.1|	188	5.09E-55	1391428	Enterobacteria phage 4MG	*Escherichia coli K-12*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a93068;2 total counts: 738 Seed: 3 K: 25 length: 357	357	4	gi|151266305|ref|YP 001333668.1|	131	8.16E-38	338473	Actinomyces phage Av-1	*Actinomyces naeslundii*	Actinobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a4907;4 total counts: 1091 Seed: 5 K: 25 length: 303	303	3.9967	gi|971765803|ref|YP 009218802.1|	119	2.35E-32	1655645	Parabacteroides phage YZ-2015b	*na*	na	unclassified	Microviridae	ssDNA
a115738;6 total counts: 2739 Seed: 8 K: 25 length: 448	448	3.97768	gi|1132371030|ref|YP 009337019.1|	93.6	4.29E-22	1923158	*Hubei picorna-like virus 74*	*Myriapoda*	Arthropoda; Metazoa; Eukaryota	unclassified	unclassified	RNA
a2021;4 total counts: 1002 Seed: 5 K: 25 length: 266	266	3.97744	gi|593777354|ref|YP 009015199.1|	100	2.88E-27	1162290	Cronobacter phage CR9	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a2748;4 total counts: 2112 Seed: 5 K: 25 length: 600	600	3.96667	gi|389059910|ref|YP 006383063.1|	81.3	8.25E-20	1162295	Cronobacter phage CR3	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a150241;4 total counts: 1761 Seed: 6 K: 25 length: 519	519	3.95568	gi|448244744|ref|YP 007392464.1|	55.5	1.25E-08	1116482	Pectobacterium phage phiTE	*Pectobacterium atrosepticum SCRI1043*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a159393;3 total counts: 506 Seed: 4 K: 25 length: 202	202	3.94022	gi|146329913|ref|YP 001210221.1|	46.6	4.79E-07	437329	Burkholderia phage BcepGomr	*Burkholderia cepacia*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a159158;4 total counts: 862 Seed: 6 K: 25 length: 226	226	3.93424	gi|9635533|ref|NP 059624.1|	121	1.03E-35	10754	Enterobacteria phage P22	*Escherichia coli*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a147402;3 total counts: 683 Seed: 2 K: 25 length: 224	224	3.92994	gi|937456460|ref|YP 009168385.1|	80.9	2.30E-20	1622234	Citrobacter phage CVT22	*Citrobacter sp. TM1552*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a150827;3 total counts: 478 Seed: 2 K: 25 length: 211	211	3.89151	gi|41179223|ref|NP 958561.1|	65.9	6.96E-15	139870	Lactobacillus prophage Lj965	*Lactobacillus johnsonii*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a148796;4 total counts: 1311 Seed: 2 K: 25 length: 335	335	3.88955	gi|388570811|ref|YP 006383794.1|	136	8.44E-38	1187128	Acinetobacter bacteriophage AP22	*Acinetobacter baumannii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a146808;5 total counts: 2402 Seed: 2 K: 25 length: 488	488	3.87955	gi|849060585|ref|YP 009152819.1|	52	1.86E-07	1540093	Bacillus phage Pookie	*Bacillus megaterium*	Firmicutes; Bacteria	Caudovirales	Podoviridae	dsDNA
a29954;4 total counts: 4678 Seed: 6 K: 25 length: 1159	1159	3.86885	gi|448244802|ref|YP 007392522.1|	179	1.16E-50	1116482	Pectobacterium phage phiTE	*Pectobacterium atrosepticum SCRI1043*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a149052;3 total counts: 1216 Seed: 6 K: 25 length: 415	415	3.86024	gi|593777266|ref|YP 009015111.1|	69.7	5.24E-16	1162290	Cronobacter phage CR9	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a59372;3 total counts: 1154 Seed: 3 K: 25 length: 355	355	3.84598	gi|422935909|ref|YP 007005806.1|	84.3	1.90E-20	1051675	Erwinia phage vB EamP-S6	*Erwinia amylovora*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a149416;3 total counts: 822 Seed: 3 K: 25 length: 265	265	3.80755	gi|410492122|ref|YP 006907308.1|	65.5	2.73E-13	57477	Bacillus phage Bastille	*Bacillus cereus*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a35779;4 total counts: 1247 Seed: 6 K: 25 length: 343	343	3.80466	gi|363539688|ref|YP 004893973.1|	99	3.52E-25	889338	Salmonella phage PVP-SE1	*Salmonella enterica subsp. enterica serovar Enteritidis*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a147425;4 total counts: 2771 Seed: 5 K: 25 length: 661	661	3.79425	gi|563397553|ref|YP 008857317.1|	121	1.46E-34	1391428	Enterobacteria phage 4MG	*Escherichia coli K-12*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a1848;3 total counts: 514 Seed: 4 K: 25 length: 200	200	3.785	gi|448260870|ref|YP 007349227.1|	49.7	4.35E-08	1204533	Bacillus phage phiAGATE	*Bacillus pumilus*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a147149;9 total counts: 15933 Seed: 14 K: 25 length: 1868	1868	3.76676	gi|418489428|ref|YP 007003245.1|	225	1.57E-67	947980	Lactobacillus phage LF1	*Lactobacillus sp.*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a35212;4 total counts: 971 Seed: 8 K: 25 length: 259	259	3.76062	gi|593777120|ref|YP 009014965.1|	134	1.25E-40	1162290	Cronobacter phage CR9	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a117265;3 total counts: 661 Seed: 2 K: 25 length: 242	242	3.73554	gi|906476396|ref|YP 009160400.1|	76.3	1.50E-17	1655659	*Gokushovirinae Fen7875 21*	*na*	na	unclassified	Microviridae	ssDNA
a146821;5 total counts: 2458 Seed: 2 K: 25 length: 524	524	3.71545	gi|589893779|ref|YP 009010488.1|	74.3	4.05E-15	1458842	Geobacillus phage GBK2	*Geobacillus kaustophilus*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a146506;4 total counts: 3410 Seed: 3 K: 25 length: 814	814	3.71007	gi|593777392|ref|YP 009015237.1|	49.3	3.60E-07	1162290	Cronobacter phage CR9	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a158898;2 total counts: 344 Seed: 2 K: 25 length: 206	206	3.68644	gi|1070099269|ref|YP 009282381.1|	47	4.56E-07	1815511	Lactobacillus phage PLE2	*Lactobacillus casei BL23*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a65;6 total counts: 4013 Seed: 2 K: 25 length: 656	656	3.65753	gi|62327110|ref|YP 223898.1|	151	2.75E-41	235201	Lactobacillus phage phiJL-1	*Lactobacillus plantarum*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a150391;2 total counts: 603 Seed: 2 K: 25 length: 285	285	3.63158	gi|508177873|ref|YP 008050946.1|	55.5	1.20E-09	1325953	Mycobacterium phage PegLeg	*Mycobacterium smegmatis str. MC2 155*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a31857;4 total counts: 705 Seed: 2 K: 25 length: 224	224	3.62054	gi|90592627|ref|YP 529887.1|	47.4	1.23E-07	363555	Lactobacillus phage KC5a	*Lactobacillus gasseri*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a152065;4 total counts: 2093 Seed: 6 K: 25 length: 561	561	3.61151	gi|1070096343|ref|YP 009277980.1|	125	4.45E-33	1654782	Propionibacterium phage QueenBey	*Cutibacterium acnes*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a2557;4 total counts: 3571 Seed: 6 K: 25 length: 1017	1017	3.59095	gi|658310132|ref|YP 009042324.1|	380	4.58E-130	1327934	Cronobacter phage CR8	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a156327;4 total counts: 1421 Seed: 2 K: 25 length: 394	394	3.59073	gi|410491739|ref|YP 006906961.1|	60.5	7.29E-11	1204525	Streptomyces phage SV1	*Streptomyces venezuelae*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a118987;6 total counts: 1591 Seed: 4 K: 25 length: 287	287	3.57491	gi|1132370375|ref|YP 009336558.1|	57.4	2.91E-10	1923009	*Hubei orthoptera virus 1*	*Orthoptera*	Arthropoda; Metazoa; Eukaryota	unclassified	unclassified	RNA
a149082;2 total counts: 673 Seed: 5 K: 25 length: 316	316	3.56835	gi|712913802|ref|YP 009100909.1|	69.7	1.41E-14	1536592	Idiomarinaceae phage 1N2-2	*Idiomarinaceae bacterium N2-2*	Proteobacteria; Bacteria	unclassified	unclassified	dsDNA
a7871;5 total counts: 1965 Seed: 6 K: 25 length: 443	443	3.56659	gi|966203781|ref|YP 009189096.1|	58.9	5.91E-12	1684115	Cronobacter phage PBES 02	*Cronobacter sp.*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a1705;3 total counts: 715 Seed: 3 K: 25 length: 280	280	3.56429	gi|448244951|ref|YP 007392671.1|	137	3.21E-39	1116482	Pectobacterium phage phiTE	*Pectobacterium atrosepticum SCRI1043*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a30141;3 total counts: 903 Seed: 9 K: 25 length: 311	311	3.54019	gi|593777348|ref|YP 009015193.1|	166	1.35E-48	1162290	Cronobacter phage CR9	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a62682;5 total counts: 1539 Seed: 2 K: 25 length: 321	321	3.51325	gi|1068512754|ref|YP 009276541.1|	75.5	6.83E-17	1838064	Gordonia phage BritBrat	*Gordonia terrae*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a36095;3 total counts: 1669 Seed: 5 K: 25 length: 594	594	3.4899	gi|593777396|ref|YP 009015241.1|	79.3	1.69E-18	1162290	Cronobacter phage CR9	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a31951;4 total counts: 1233 Seed: 2 K: 25 length: 360	360	3.48611	gi|971848926|ref|YP 009035505.1|	101	1.28E-25	1416334	Lactobacillus phage phi jlb1	*Lactobacillus gasseri ADH*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a146623;4 total counts: 2347 Seed: 5 K: 25 length: 639	639	3.46009	gi|1070638430|ref|YP 009302456.1|	48.5	4.07E-06	1792032	Bacillus phage SP-15	*Bacillus paralicheniformis ATCC 9945a*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a15378;3 total counts: 1073 Seed: 9 K: 25 length: 385	385	3.45974	gi|593777334|ref|YP 009015179.1|	127	2.03E-35	1162290	Cronobacter phage CR9	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a94606;2 total counts: 399 Seed: 3 K: 25 length: 218	218	3.45525	gi|151266296|ref|YP 001333659.1|	70.5	2.78E-15	338473	Actinomyces phage Av-1	*Actinomyces naeslundii*	Actinobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a1737;4 total counts: 1522 Seed: 2 K: 25 length: 431	431	3.45373	gi|479336583|ref|YP 007869931.1|	100	6.46E-25	1305710	Mycobacterium phage vB MapS FF47	*Mycobacterium avium subsp. paratuberculosis*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a155313;4 total counts: 679 Seed: 2 K: 25 length: 217	217	3.45205	gi|563398175|ref|YP 008857935.1|	82.8	3.62E-21	1414742	Arthrobacter phage vB ArS-ArV2	*Arthrobacter sp.*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a5597;2 total counts: 505 Seed: 4 K: 25 length: 228	228	3.44106	gi|764161561|ref|YP 009126008.1|	50.1	4.06E-08	1567472	Mycobacterium phage Malithi	*Mycobacterium smegmatis str. MC2 155*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a146603;3 total counts: 535 Seed: 5 K: 25 length: 209	209	3.43541	gi|90592612|ref|YP 529872.1|	99.4	5.51E-26	363555	Lactobacillus phage KC5a	*Lactobacillus gasseri*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a119038;2 total counts: 534 Seed: 2 K: 25 length: 349	349	3.43307	gi|1070637962|ref|YP 009301940.1|	80.1	4.96E-18	1821564	Gordonia phage Vivi2	*Gordonia terrae*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a33351;4 total counts: 1147 Seed: 8 K: 25 length: 342	342	3.42105	gi|593777136|ref|YP 009014981.1|	82.8	6.32E-19	1162290	Cronobacter phage CR9	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a31122;3 total counts: 758 Seed: 4 K: 25 length: 279	279	3.41219	gi|388570841|ref|YP 006383824.1|	57.8	9.06E-11	1187128	Acinetobacter bacteriophage AP22	*Acinetobacter baumannii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a88517;4 total counts: 850 Seed: 3 K: 25 length: 255	255	3.4	gi|90592627|ref|YP 529887.1|	70.1	2.77E-16	363555	Lactobacillus phage KC5a	*Lactobacillus gasseri*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a151992;3 total counts: 630 Seed: 4 K: 25 length: 228	228	3.3985	gi|530545495|ref|YP 008409095.1|	43.5	8.32E-06	1340824	Mycobacterium phage Hamulus	*Mycobacterium sp.*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a148430;3 total counts: 1726 Seed: 4 K: 25 length: 518	518	3.39768	gi|1070638519|ref|YP 009302545.1|	98.6	1.35E-23	1792032	Bacillus phage SP-15	*Bacillus paralicheniformis ATCC 9945a*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a36152;3 total counts: 535 Seed: 4 K: 25 length: 213	213	3.38498	gi|389059870|ref|YP 006383023.1|	76.3	2.20E-17	1162295	Cronobacter phage CR3	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a116473;2 total counts: 735 Seed: 2 K: 25 length: 320	320	3.37188	gi|593777121|ref|YP 009014966.1|	70.9	4.93E-15	1162290	Cronobacter phage CR9	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a31238;3 total counts: 1025 Seed: 2 K: 25 length: 346	346	3.36416	gi|593777132|ref|YP 009014977.1|	167	2.74E-50	1162290	Cronobacter phage CR9	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a32036;2 total counts: 452 Seed: 3 K: 25 length: 211	211	3.35965	gi|318065890|ref|YP 004123926.1|	80.9	4.44E-19	938131	Mycobacterium phage Wee	*Mycobacterium smegmatis*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a36417;4 total counts: 1098 Seed: 2 K: 25 length: 290	290	3.35862	gi|593777201|ref|YP 009015046.1|	169	6.29E-50	1162290	Cronobacter phage CR9	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a147088;3 total counts: 3047 Seed: 4 K: 25 length: 1112	1112	3.35432	gi|1070638519|ref|YP 009302545.1|	83.2	2.02E-16	1792032	Bacillus phage SP-15	*Bacillus paralicheniformis ATCC 9945a*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a122334;3 total counts: 671 Seed: 3 K: 25 length: 253	253	3.33992	gi|363539688|ref|YP 004893973.1|	70.5	2.98E-15	889338	Salmonella phage PVP-SE1	*Salmonella enterica subsp. enterica serovar Enteritidis*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a1745;3 total counts: 929 Seed: 5 K: 25 length: 327	327	3.31498	gi|658310265|ref|YP 009042457.1|	174	1.60E-51	1327934	Cronobacter phage CR8	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a87683;5 total counts: 2612 Seed: 4 K: 25 length: 604	604	3.30726	gi|526177165|ref|YP 008241014.1|	82	1.47E-17	1327976	Cellulophaga phage phi12:1	*Cellulophaga baltica*	Bacteroidetes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a147514;3 total counts: 2837 Seed: 3 K: 25 length: 1063	1063	3.29351	gi|593777809|ref|YP 009015656.1|	67.4	2.62E-11	1084719	Bacillus phage G	*Bacillus sp.; Geobacillus sp.*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a3104;4 total counts: 2592 Seed: 3 K: 25 length: 673	673	3.29272	gi|593777136|ref|YP 009014981.1|	331	2.53E-108	1162290	Cronobacter phage CR9	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a62223;3 total counts: 1272 Seed: 2 K: 25 length: 407	407	3.28747	gi|20889303|ref|NP 624351.1|	179	3.15E-55	1511847	*Fusarium solani virus 1*	*Fusarium solani*	Ascomycota; Fungi; Eukaryota	unclassified	Partitiviridae	dsRNA
a147903;4 total counts: 758 Seed: 3 K: 25 length: 231	231	3.28139	gi|593777361|ref|YP 009015206.1|	91.7	3.47E-24	1162290	Cronobacter phage CR9	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a149402;2 total counts: 424 Seed: 2 K: 25 length: 218	218	3.27236	gi|151266300|ref|YP 001333663.1|	55.1	6.37E-10	338473	Actinomyces phage Av-1	*Actinomyces naeslundii*	Actinobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a225;4 total counts: 3128 Seed: 4 K: 25 length: 886	886	3.25959	gi|448244868|ref|YP 007392588.1|	70.5	4.49E-14	1116482	Pectobacterium phage phiTE	*Pectobacterium atrosepticum SCRI1043*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a153011;3 total counts: 721 Seed: 5 K: 25 length: 272	272	3.24265	gi|682123168|ref|YP 009055489.1|	86.7	5.35E-21	1505225	Acinetobacter phage YMC-13-01-C62	*Acinetobacter baumannii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a146652;8 total counts: 9108 Seed: 2 K: 25 length: 1123	1123	3.22408	gi|589892942|ref|YP 009004271.1|	82.8	2.57E-16	1406793	Clavibacter phage CN1A	*Clavibacter michiganensis*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a58141;4 total counts: 1342 Seed: 5 K: 25 length: 361	361	3.21607	gi|448244921|ref|YP 007392641.1|	50.4	9.18E-09	1116482	Pectobacterium phage phiTE	*Pectobacterium atrosepticum SCRI1043*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a149302;2 total counts: 475 Seed: 2 K: 25 length: 279	279	3.21368	gi|422934279|ref|YP 007004320.1|	67	1.24E-14	1090133	Enterobacteria phage IME10	*Escherichia coli*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a59400;5 total counts: 3435 Seed: 4 K: 25 length: 714	714	3.20219	gi|31415799|ref|NP 852540.1|	87.4	6.51E-19	225725	Bacillus phage phBC6A51	*Bacillus cereus*	Firmicutes; Bacteria	Caudovirales	Podoviridae	dsDNA
a30839;3 total counts: 767 Seed: 2 K: 25 length: 259	259	3.20077	gi|1236513346|ref|YP 009407943.1|	52.8	7.21E-09	2018503	*Lasius niger virus 1*	*Formicidae*	Arthropoda; Metazoa; Eukaryota	unclassified	unclassified	ssRNA +
a30366;4 total counts: 813 Seed: 3 K: 25 length: 220	220	3.19091	gi|658310275|ref|YP 009042467.1|	111	2.12E-32	1327934	Cronobacter phage CR8	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a149992;6 total counts: 1933 Seed: 2 K: 25 length: 370	370	3.18966	gi|722142297|ref|YP 009104294.1|	105	2.05E-29	1527515	Idiomarinaceae phage Phi1M2-2	*Idiomarinaceae bacterium M2-2*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a64890;2 total counts: 878 Seed: 2 K: 25 length: 407	407	3.14988	gi|593777119|ref|YP 009014964.1|	197	4.37E-61	1162290	Cronobacter phage CR9	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a403;3 total counts: 703 Seed: 2 K: 25 length: 257	257	3.1462	gi|937456480|ref|YP 009168405.1|	50.1	2.36E-08	1622234	Citrobacter phage CVT22	*Citrobacter sp. TM1552*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a35722;3 total counts: 661 Seed: 2 K: 25 length: 274	274	3.12774	gi|388570784|ref|YP 006383767.1|	115	5.21E-31	1187128	Acinetobacter bacteriophage AP22	*Acinetobacter baumannii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA

a150976;4 total counts: 893 Seed: 3 K: 25 length: 229	229	3.11146	gi|219563209|ref|YP 002455801.1|	55.5	5.84E-10	578234	Lactobacillus phage Lv-1	*Lactobacillus jensenii*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a94817;4 total counts: 691 Seed: 4 K: 25 length: 200	200	3.1	gi|937456524|ref|YP 009168450.1|	62.4	1.31E-12	1622234	Citrobacter phage CVT22	*Citrobacter sp. TM1552*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a145734;3 total counts: 1072 Seed: 4 K: 25 length: 418	418	3.09569	gi|593777349|ref|YP 009015194.1|	75.9	2.34E-18	1162290	Cronobacter phage CR9	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a62821;2 total counts: 663 Seed: 2 K: 25 length: 372	372	3.09153	gi|1070103030|ref|YP 009287678.1|	105	8.36E-27	1838137	Propionibacterium phage PFR1	*Propionibacterium freudenreichii*	Actinobacteria; Bacteria	unclassified	unclassified	unclassified
a35554;4 total counts: 1833 Seed: 2 K: 25 length: 435	435	3.08389	gi|422935909|ref|YP 007005806.1|	132	1.05E-38	1051675	Erwinia phage vB EamP-S6	*Erwinia amylovora*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a31545;3 total counts: 713 Seed: 6 K: 25 length: 228	228	3.07895	gi|158079314|ref|YP 001504127.1|	67.4	2.32E-14	442493	Enterococcus phage phiEF24C	*Enterococcus faecalis*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a154746;2 total counts: 656 Seed: 4 K: 25 length: 435	435	3.06872	gi|1070639841|ref|YP 009304190.1|	63.9	8.03E-13	1821553	Gordonia phage Guacamole	*Gordonia terrae*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a150529;3 total counts: 678 Seed: 2 K: 25 length: 265	265	3.06415	gi|593777538|ref|YP 009015381.1|	111	9.90E-30	1084719	Bacillus phage G	*Bacillus sp.; Geobacillus sp.*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a154917;2 total counts: 285 Seed: 3 K: 25 length: 207	207	3.06093	gi|1102621404|ref|YP 009322238.1|	52.8	6.69E-10	1813769	Salmonella phage 64795 sal3	*Salmonella enterica*	Proteobacteria; Bacteria	unclassified	unclassified	unclassified
a64192;2 total counts: 467 Seed: 2 K: 25 length: 263	263	3.05703	gi|1070106096|ref|YP 009291947.1|	93.6	2.66E-25	1792222	Acinetobacter phage LZ35	*Acinetobacter baumannii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a87433;4 total counts: 1294 Seed: 2 K: 25 length: 343	343	3.05248	gi|682123168|ref|YP 009055489.1|	82.8	2.68E-19	1505225	Acinetobacter phage YMC-13-01-C62	*Acinetobacter baumannii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a148132;4 total counts: 936 Seed: 4 K: 25 length: 269	269	3.04516	gi|418487735|ref|YP 007002058.1|	80.9	1.24E-18	1133292	Brucella phage Tb	*Brucella abortus 544*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a148959;2 total counts: 508 Seed: 2 K: 25 length: 249	249	3.03571	gi|937456502|ref|YP 009168428.1|	43.5	7.66E-06	1622234	Citrobacter phage CVT22	*Citrobacter sp. TM1552*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a162105;2 total counts: 849 Seed: 2 K: 25 length: 395	395	3.03139	gi|149408242|ref|YP 001294521.1|	131	3.54E-36	347328	Pseudomonas phage M6	*Pseudomonas aeruginosa*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a35477;3 total counts: 1262 Seed: 4 K: 25 length: 401	401	3.02993	gi|422937532|ref|YP 007007737.1|	86.7	4.81E-20	1127514	Aeromonas phage vB AsaM-56	*Aeromonas salmonicida*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a149688;4 total counts: 1078 Seed: 2 K: 25 length: 265	265	3.01399	gi|479336582|ref|YP 007869930.1|	104	3.69E-27	1305710	Mycobacterium phage vB MapS FF47	*Mycobacterium avium subsp. paratuberculosis*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a30180;2 total counts: 792 Seed: 2 K: 25 length: 351	351	3	gi|1132370297|ref|YP 009336506.1|	139	1.05E-38	1923011	*Hubei orthoptera virus 3*	*Orthoptera*	Arthropoda; Metazoa; Eukaryota	unclassified	unclassified	RNA
a60166;3 total counts: 965 Seed: 4 K: 25 length: 366	366	2.9871	gi|543171058|ref|YP 008531119.1|	75.1	3.68E-17	1354514	Mycobacterium phage Quink	*Mycobacterium smegmatis str. MC2 155*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a58655;3 total counts: 818 Seed: 4 K: 25 length: 302	302	2.98344	gi|906476384|ref|YP 009160392.1|	103	5.69E-28	1655658	*Microviridae Fen7786 21*	*na*	na	unclassified	Microviridae	ssDNA
a59367;6 total counts: 4260 Seed: 3 K: 25 length: 784	784	2.98333	gi|764162043|ref|YP 009126439.1|	59.3	8.04E-10	1561065	Paracoccus phage vB PmaS IMEP1	*Paracoccus marcusii*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a119799;2 total counts: 1055 Seed: 6 K: 25 length: 453	453	2.97778	gi|1068359406|ref|YP 009276409.1|	248	9.59E-84	1647471	Gordonia phage GMA4	*Gordonia malaquae*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a147678;2 total counts: 645 Seed: 2 K: 25 length: 315	315	2.97143	gi|971848934|ref|YP 009035513.1|	82	4.63E-19	1416334	Lactobacillus phage phi jlb1	*Lactobacillus gasseri ADH*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a124268;3 total counts: 568 Seed: 5 K: 25 length: 216	216	2.96928	gi|151266299|ref|YP 001333662.1|	56.6	1.95E-10	338473	Actinomyces phage Av-1	*Actinomyces naeslundii*	Actinobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a62875;3 total counts: 1490 Seed: 3 K: 25 length: 454	454	2.96696	gi|1003725486|ref|YP 009237509.1|	73.9	1.69E-15	1685785	*Lake Sarah-associated circular virus-8*	*na*	na	unclassified	unclassified	unclassified
a66836;2 total counts: 431 Seed: 3 K: 25 length: 201	201	2.96517	gi|209967989|ref|YP 002296164.1|	53.1	2.54E-09	181082	*Emiliania huxleyi virus 86*	*Emiliania huxleyi*	Haptophyta; Chromalveolata; Eukaryota	unclassified	Phycodnaviridae	dsDNA
a34695;2 total counts: 691 Seed: 2 K: 25 length: 327	327	2.94792	gi|1068511239|ref|YP 009274344.1|	164	4.67E-49	1647476	Tsukamurella phage TPA4	*Tsukamurella paurometabola*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a68430;2 total counts: 500 Seed: 2 K: 25 length: 247	247	2.93927	gi|446730230|ref|YP 007173600.1|	49.7	4.89E-08	1206110	Lactobacillus phage phiAQ113	*Lactobacillus helveticus*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a39562;2 total counts: 423 Seed: 2 K: 25 length: 210	210	2.93506	gi|151266299|ref|YP 001333662.1|	54.3	1.32E-09	338473	Actinomyces phage Av-1	*Actinomyces naeslundii*	Actinobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a149738;3 total counts: 735 Seed: 3 K: 25 length: 268	268	2.9291	gi|1070620004|ref|YP 009304800.1|	59.7	1.14E-11	1605379	Acinetobacter phage vB AbaM phiAbaA1	*Acinetobacter baumannii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a149950;3 total counts: 649 Seed: 4 K: 25 length: 212	212	2.92777	gi|41179218|ref|NP 958556.1|	72	6.88E-16	139870	Lactobacillus prophage Lj965	*Lactobacillus johnsonii*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a120198;2 total counts: 774 Seed: 4 K: 25 length: 343	343	2.92711	gi|363540839|ref|YP 004894409.1|	51.6	6.09E-08	1094892	*Megavirus chiliensis*	*Acanthamoeba*	Longamoebia; Amoebozoa; Eukaryota	unclassified	Mimiviridae	dsDNA
a128023;2 total counts: 427 Seed: 3 K: 25 length: 214	214	2.92203	gi|149408253|ref|YP 001294532.1|	57.4	3.20E-11	347328	Pseudomonas phage M6	*Pseudomonas aeruginosa*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a10175;3 total counts: 723 Seed: 3 K: 25 length: 281	281	2.92171	gi|363539649|ref|YP 004893934.1|	179	6.22E-57	889338	Salmonella phage PVP-SE1	*Salmonella enterica subsp. enterica serovar Enteritidis*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a151953;6 total counts: 4135 Seed: 4 K: 25 length: 711	711	2.91603	gi|418489116|ref|YP 007002970.1|	157	4.63E-47	37105	Lactobacillus phage JCL1032	*Lactobacillus delbrueckii subsp. lactis*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a120732;4 total counts: 839 Seed: 6 K: 25 length: 244	244	2.89855	gi|1070101675|ref|YP 009285855.1|	65.5	2.38E-13	1844477	Pseudomonas phage NP1	*Pseudomonas sp.*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a60776;2 total counts: 837 Seed: 3 K: 25 length: 364	364	2.88736	gi|966203396|ref|YP 009187713.1|	120	1.49E-34	1719140	Klebsiella phage vB KpnM KB57	*Klebsiella pneumoniae*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a149322;3 total counts: 1310 Seed: 4 K: 25 length: 469	469	2.8742	gi|226377764|ref|YP 002790813.1|	103	1.70E-25	632112	Lactobacillus phage Lb338-1	*Lactobacillus paracasei*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a58672;3 total counts: 2088 Seed: 3 K: 25 length: 747	747	2.87015	gi|448244883|ref|YP 007392603.1|	123	5.97E-33	1116482	Pectobacterium phage phiTE	*Pectobacterium atrosepticum SCRI1043*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a29628;9 total counts: 8674 Seed: 2 K: 25 length: 947	947	2.86546	gi|971746169|ref|YP 009200249.1|	149	6.97E-40	1636200	Pseudoalteromonas Phage H103	*Pseudoalteromonas marina*	Proteobacteria; Bacteria	Caudovirales	unclassified	dsDNA
a34270;3 total counts: 903 Seed: 3 K: 25 length: 323	323	2.86538	gi|109522826|ref|YP 655246.1|	55.1	2.61E-09	373410	Mycobacterium phage PBI1	*Mycobacterium sp.*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a1675;3 total counts: 844 Seed: 4 K: 25 length: 302	302	2.86387	gi|1068512776|ref|YP 009276563.1|	73.6	5.63E-16	1838064	Gordonia phage BritBrat	*Gordonia terrae*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a72710;2 total counts: 497 Seed: 3 K: 25 length: 327	327	2.85321	gi|1070638959|ref|YP 009303093.1|	54.7	3.34E-09	1796994	Arthrobacter phage BarretLemon	*Arthrobacter sp. ATCC 21022*	Actinobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a4632;5 total counts: 919 Seed: 4 K: 25 length: 220	220	2.85	gi|947835102|ref|YP 009177523.1|	73.2	1.47E-16	1720495	Escherichia phage slur16	*Escherichia coli*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a59368;20 total counts: 48740 Seed: 7 K: 25 length: 2470	2470	2.83945	gi|401723087|ref|YP 006589997.1|	100	2.06E-20	1136535	Burkholderia phage DC1	*Burkholderia cepacia*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a116340;3 total counts: 783 Seed: 7 K: 25 length: 265	265	2.83774	gi|593777364|ref|YP 009015209.1|	101	1.21E-28	1162290	Cronobacter phage CR9	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a146541;4 total counts: 1219 Seed: 2 K: 25 length: 343	343	2.83544	gi|985757694|ref|YP 009222820.1|	196	2.17E-61	1573458	Pseudomonas phage PS-1	*Pseudomonas sp. 1-1-1b*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a147444;3 total counts: 542 Seed: 2 K: 25 length: 212	212	2.82075	gi|410492609|ref|YP 006907795.1|	47	5.46E-07	1136731	Bacillus phage BPS13	*Bacillus cereus*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a36038;2 total counts: 482 Seed: 5 K: 25 length: 245	245	2.81522	gi|609217172|ref|YP 008772005.1|	50.4	2.50E-08	1406790	Bacillus phage Slash	*Bacillus megaterium*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a147745;2 total counts: 436 Seed: 2 K: 25 length: 222	222	2.81013	gi|16271799|ref|NP 438136.1|	43.9	3.67E-06	173707	Temperate phage phiNIH1.1	*Streptococcus pyogenes*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a1021;4 total counts: 2717 Seed: 2 K: 25 length: 670	670	2.80909	gi|530546184|ref|YP 008409778.1|	55.1	4.47E-08	1340825	Mycobacterium phage Trouble	*Mycobacterium sp.*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a149357;2 total counts: 908 Seed: 2 K: 25 length: 416	416	2.80529	gi|1173244220|ref|YP 009352233.1|	70.5	3.55E-14	1920988	*Diabrotica virgifera virgifera virus 2*	*Diabrotica virgifera virgifera*	Arthropoda; Metazoa; Eukaryota	unclassified	unclassified	unclassified
a9077;3 total counts: 798 Seed: 3 K: 25 length: 312	312	2.79487	gi|203454733|ref|YP 002225049.1|	105	6.33E-27	546805	Mycobacterium phage Myrna	*Mycobacterium smegmatis str. MC2 155*	Actinobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a154028;3 total counts: 851 Seed: 2 K: 25 length: 308	308	2.79221	gi|448244788|ref|YP 007392508.1|	55.5	1.57E-10	1116482	Pectobacterium phage phiTE	*Pectobacterium atrosepticum SCRI1043*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a29508;2 total counts: 488 Seed: 3 K: 25 length: 290	290	2.76543	gi|971821357|ref|YP 009208706.1|	75.1	1.53E-16	1664247	Achromobacter phage phiAxp-3	*Achromobacter xylosoxidans*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a244;4 total counts: 3220 Seed: 9 K: 25 length: 772	772	2.75926	gi|1068512872|ref|YP 009276644.1|	72.8	1.03E-13	1838062	Gordonia phage Blueberry	*Gordonia terrae*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a12231;2 total counts: 723 Seed: 2 K: 25 length: 368	368	2.74728	gi|966203619|ref|YP 009188934.1|	191	2.98E-60	1684115	Cronobacter phage PBES 02	*Cronobacter sp.*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a2166;3 total counts: 570 Seed: 4 K: 25 length: 243	243	2.7426	gi|206599597|ref|YP 002242036.1|	44.3	2.24E-06	561996	Mycobacterium phage Brujita	*Mycobacterium smegmatis str. MC2 155*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a148860;2 total counts: 904 Seed: 2 K: 25 length: 419	419	2.74107	gi|971757354|ref|YP 009210861.1|	47	4.28E-06	1647301	Mycobacterium phage Vincenzo	*Mycobacterium smegmatis str. MC2 155*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a146509;3 total counts: 878 Seed: 2 K: 25 length: 312	312	2.73944	gi|9632906|ref|NP 049935.1|	49.3	2.65E-07	72638	Streptococcus phage Sfi19	*Streptococcus thermophilus*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a6034;2 total counts: 325 Seed: 3 K: 25 length: 229	229	2.73684	gi|643654753|ref|YP 009035933.1|	62	2.75E-12	1458711	Mycobacterium phage Hawkeye	*Mycobacterium smegmatis str. MC2 155*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a146213;5 total counts: 919 Seed: 4 K: 25 length: 215	215	2.72093	gi|682123142|ref|YP 009055463.1|	76.3	2.21E-18	1505225	Acinetobacter phage YMC-13-01-C62	*Acinetobacter baumannii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a67573;2 total counts: 359 Seed: 2 K: 25 length: 216	216	2.71698	gi|1068357916|ref|YP 009273246.1|	53.9	1.39E-09	1647470	Gordonia phage GMA1	*Gordonia malaquae*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a117800;2 total counts: 538 Seed: 4 K: 25 length: 250	250	2.716	gi|158079316|ref|YP 001504129.1|	77.8	1.27E-18	442493	Enterococcus phage phiEF24C	*Enterococcus faecalis*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a100422;2 total counts: 505 Seed: 3 K: 25 length: 298	298	2.71523	gi|304360708|ref|YP 003856839.1|	75.5	1.11E-16	871584	Clostridium phage phiCTP1	*Clostridium tyrobutyricum*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a38439;3 total counts: 588 Seed: 3 K: 25 length: 259	259	2.71429	gi|410491500|ref|YP 006906722.1|	45.4	2.52E-06	1177632	Salmonella phage SSU5	*Salmonella enterica subsp. enterica serovar Typhimurium str. LT2*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a35792;3 total counts: 482 Seed: 2 K: 25 length: 214	214	2.70093	gi|985757333|ref|YP 009222296.1|	84.3	2.94E-20	1567484	Lactobacillus phage LfeInf	*Lactobacillus fermentum*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a149818;4 total counts: 885 Seed: 9 K: 25 length: 248	248	2.68376	gi|418489145|ref|YP 007003001.1|	43.9	7.16E-06	37105	Lactobacillus phage JCL1032	*Lactobacillus delbrueckii subsp. lactis*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a148381;2 total counts: 727 Seed: 2 K: 25 length: 323	323	2.66667	gi|219563215|ref|YP 002455807.1|	72	2.52E-15	578234	Lactobacillus phage Lv-1	*Lactobacillus jensenii*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a148015;3 total counts: 1678 Seed: 2 K: 25 length: 590	590	2.66372	gi|1070099244|ref|YP 009282356.1|	65.1	1.28E-11	1815511	Lactobacillus phage PLE2	*Lactobacillus casei BL23*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a116951;3 total counts: 710 Seed: 2 K: 25 length: 295	295	2.66076	gi|149408270|ref|YP 001294549.1|	140	4.06E-40	347328	Pseudomonas phage M6	*Pseudomonas aeruginosa*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a1109;4 total counts: 869 Seed: 3 K: 25 length: 257	257	2.64727	gi|12248109|ref|NP 073685.1|	84.3	5.82E-20	12345	Bacillus phage GA-1	*Bacillus sp.*	Firmicutes; Bacteria	Caudovirales	Podoviridae	dsDNA
a147728;5 total counts: 1445 Seed: 4 K: 25 length: 321	321	2.64228	gi|971748336|ref|YP 009202281.1|	67	2.88E-14	1556289	Mycobacterium phage CaptainTrips	*Mycobacterium smegmatis str. MC2 155*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a123603;3 total counts: 963 Seed: 5 K: 25 length: 329	329	2.62918	gi|593777201|ref|YP 009015046.1|	114	6.22E-30	1162290	Cronobacter phage CR9	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a119065;2 total counts: 518 Seed: 2 K: 25 length: 276	276	2.62681	gi|389060247|ref|YP 006383379.1|	47.8	4.73E-07	1173297	Halocynthia phage JM-2012	*Halocynthia sp.*	Chordata; Metazoa; Eukaryota	Caudovirales	Myoviridae	dsDNA
a147413;2 total counts: 730 Seed: 2 K: 25 length: 327	327	2.6208	gi|985761436|ref|YP 009227020.1|	55.8	1.60E-09	1445810	Bacillus phage Bp8p-C	*Bacillus pumilus*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a31785;2 total counts: 650 Seed: 2 K: 25 length: 303	303	2.62046	gi|158079318|ref|YP 001504131.1|	43.5	2.75E-06	442493	Enterococcus phage phiEF24C	*Enterococcus faecalis*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a7087;2 total counts: 565 Seed: 2 K: 25 length: 297	297	2.61376	gi|29566748|ref|NP 818312.1|	87.4	9.38E-21	205879	Mycobacterium phage Omega	*Mycobacterium sp.*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a152266;2 total counts: 482 Seed: 2 K: 25 length: 241	241	2.61062	gi|966197718|ref|YP 009187316.1|	94.4	8.10E-24	936054	Enterobacteria phage VT2phi 272	*Escherichia coli O157:H7*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a33002;2 total counts: 1040 Seed: 3 K: 25 length: 450	450	2.60889	gi|593777123|ref|YP 009014968.1|	199	2.30E-63	1162290	Cronobacter phage CR9	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a150503;2 total counts: 690 Seed: 2 K: 25 length: 306	306	2.60784	gi|1070106041|ref|YP 009291892.1|	58.2	4.91E-12	1792222	Acinetobacter phage LZ35	*Acinetobacter baumannii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a4581;4 total counts: 1133 Seed: 5 K: 25 length: 322	322	2.60248	gi|658310046|ref|YP 009042238.1|	161	6.07E-48	1327934	Cronobacter phage CR8	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a65806;2 total counts: 475 Seed: 4 K: 25 length: 227	227	2.59912	gi|410492990|ref|YP 006908056.1|	55.1	8.82E-10	1126950	Bacillus phage BCP78	*Bacillus cereus*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a119001;3 total counts: 1597 Seed: 7 K: 25 length: 512	512	2.57851	gi|937456472|ref|YP 009168397.1|	122	4.26E-32	1622234	Citrobacter phage CVT22	*Citrobacter sp. TM1552*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a31557;2 total counts: 539 Seed: 3 K: 25 length: 279	279	2.57595	gi|194100416|ref|YP 002003789.1|	103	3.12E-29	532077	Klebsiella phage K11	*Klebsiella sp. 390*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a87448;54 total counts: 329658 Seed: 57 K: 25 length: 6111	6111	2.56652	gi|151266296|ref|YP 001333659.1|	206	2.14E-55	338473	Actinomyces phage Av-1	*Actinomyces naeslundii*	Actinobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a152436;4 total counts: 1325 Seed: 5 K: 25 length: 380	380	2.56332	gi|1068512699|ref|YP 009276500.1|	83.6	5.59E-19	1838066	Gordonia phage Cozz	*Gordonia terrae*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a120204;2 total counts: 495 Seed: 2 K: 25 length: 271	271	2.55807	gi|151266296|ref|YP 001333659.1|	93.2	5.80E-23	338473	Actinomyces phage Av-1	*Actinomyces naeslundii*	Actinobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a149182;2 total counts: 354 Seed: 2 K: 25 length: 228	228	2.55556	gi|1070620872|ref|YP 009301297.1|	43.9	7.15E-06	1796995	Arthrobacter phage KellEzio	*Arthrobacter sp. ATCC 21022*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a63434;2 total counts: 490 Seed: 2 K: 25 length: 331	331	2.53797	gi|399528321|ref|YP 006560244.1|	72.8	3.67E-16	1176423	Marinomonas phage P12026	*Marinomonas sp.*	Proteobacteria; Bacteria	unclassified	unclassified	dsDNA
a11210;2 total counts: 1182 Seed: 2 K: 25 length: 505	505	2.53465	gi|985757293|ref|YP 009222256.1|	64.3	8.87E-12	1567484	Lactobacillus phage LfeInf	*Lactobacillus fermentum*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a125151;3 total counts: 667 Seed: 4 K: 25 length: 284	284	2.52817	gi|985757333|ref|YP 009222296.1|	60.8	1.66E-11	1567484	Lactobacillus phage LfeInf	*Lactobacillus fermentum*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a91672;3 total counts: 1259 Seed: 4 K: 25 length: 475	475	2.51579	gi|327197763|ref|YP 004301461.1|	67.4	6.02E-13	857312	Brochothrix phage A9	*Brochothrix thermosphacta*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a149608;2 total counts: 501 Seed: 3 K: 25 length: 238	238	2.5084	gi|66391812|ref|YP 238737.1|	70.5	3.43E-15	321023	Aeromonas phage 31	*Aeromonas salmonicida*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a149056;2 total counts: 419 Seed: 2 K: 25 length: 216	216	2.49537	gi|593777708|ref|YP 009015555.1|	62.8	1.42E-12	1084719	Bacillus phage G	*Bacillus sp.; Geobacillus sp.*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a6453;2 total counts: 487 Seed: 2 K: 25 length: 236	236	2.48729	gi|1132371510|ref|YP 009337387.1|	50.1	5.72E-08	1923147	*Hubei picorna-like virus 64*	*Tetragnatha maxillosa*	Arthropoda; Metazoa; Eukaryota	unclassified	unclassified	RNA
a62167;2 total counts: 983 Seed: 3 K: 25 length: 465	465	2.47527	gi|985757306|ref|YP 009222269.1|	79.3	3.38E-17	1567484	Lactobacillus phage LfeInf	*Lactobacillus fermentum*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a34820;3 total counts: 699 Seed: 6 K: 25 length: 284	284	2.46479	gi|589892179|ref|YP 009008544.1|	86.7	1.39E-20	1458669	Acinetobacter phage IME AB3	*Acinetobacter baumannii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a120705;3 total counts: 878 Seed: 7 K: 25 length: 293	293	2.45756	gi|151266302|ref|YP 001333665.1|	68.9	7.71E-15	338473	Actinomyces phage Av-1	*Actinomyces naeslundii*	Actinobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA

a150732;2 total counts: 730 Seed: 4 K: 25 length: 327	327	2.45051	gi|966198655|ref|YP 009188488.1|	61.6	1.29E-11	1589270	Streptococcus phage Str-PAP-1	*Streptococcus parauberis*	Firmicutes; Bacteria	Caudovirales	Podoviridae	dsDNA
a30131;2 total counts: 500 Seed: 3 K: 25 length: 300	300	2.44	gi|414087049|ref|YP 006987236.1|	47.4	8.74E-07	1141136	Cronobacter phage vB CsaM GAP32	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a93248;2 total counts: 493 Seed: 4 K: 25 length: 248	248	2.43145	gi|313768216|ref|YP 004061896.1|	105	2.68E-27	880161	*Micromonas sp. RCC1109 virus MpV1*	*Micromonas pusilla*	Chlorophyta; Viridiplantae; Eukaryota	unclassified	Phycodnaviridae	dsDNA
a7992;2 total counts: 506 Seed: 2 K: 25 length: 248	248	2.42742	gi|20889303|ref|NP 624351.1|	95.1	4.89E-24	1511847	*Fusarium solani virus 1*	*Fusarium solani*	Ascomycota; Fungi; Eukaryota	unclassified	Partitiviridae	dsRNA
a147754;4 total counts: 1356 Seed: 5 K: 25 length: 347	347	2.42604	gi|1068358200|ref|YP 009273941.1|	63.9	2.15E-12	1838080	Gordonia phage Vendetta	*Gordonia terrae*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a94533;4 total counts: 673 Seed: 7 K: 25 length: 200	200	2.42568	gi|937456498|ref|YP 009168424.1|	79.7	1.27E-18	1622234	Citrobacter phage CVT22	*Citrobacter sp. TM1552*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a89575;3 total counts: 1059 Seed: 2 K: 25 length: 328	328	2.42378	gi|282599097|ref|YP 003359014.1|	48.5	1.36E-07	665032	Deftia phage phiW-14	*Delftia acidovorans*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a95022;2 total counts: 512 Seed: 2 K: 25 length: 312	312	2.42308	gi|1043372887|ref|YP 009259743.1|	64.7	6.18E-13	1676182	*Chimpanzee faeces associated microphage 2*	*na*	na	unclassified	Microviridae	ssDNA
a31208;2 total counts: 431 Seed: 3 K: 25 length: 225	225	2.42222	gi|971848665|ref|YP 009042132.1|	47	6.13E-07	1465639	*Podovirus Lau218*	*na*	na	Caudovirales	Podoviridae	dsDNA
a87520;2 total counts: 530 Seed: 2 K: 25 length: 263	263	2.40928	gi|971748533|ref|YP 009202450.1|	52.8	1.39E-09	1698711	Mycobacterium phage Lolly9	*Mycobacterium smegmatis str. MC2 155*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a32291;2 total counts: 651 Seed: 2 K: 25 length: 291	291	2.39437	gi|338826843|ref|YP 004678757.1|	125	4.69E-34	1041524	Enterobacteria phage K30	*Escherichia sp.*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a35855;2 total counts: 537 Seed: 4 K: 25 length: 252	252	2.39286	gi|509142181|ref|YP 008061043.1|	54.7	1.69E-09	1007869	Rhodococcus phage E3	*Rhodococcus hoagii*	Actinobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a906;7 total counts: 14133 Seed: 6 K: 25 length: 1980	1980	2.3758	gi|589893782|ref|YP 009010491.1|	59.7	3.12E-08	1458842	Geobacillus phage GBK2	*Geobacillus kaustophilus*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a62006;4 total counts: 686 Seed: 2 K: 25 length: 214	214	2.37383	gi|282598836|ref|YP 003359159.1|	49.7	6.76E-09	686439	Clavibacter phage CMP1	*Clavibacter michiganensis subsp. michiganensis*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a87978;3 total counts: 685 Seed: 5 K: 25 length: 251	251	2.36255	gi|29135075|ref|NP 803705.1|	48.1	2.75E-07	169683	Pseudomonas phage phiKZ	*Pseudomonas aeruginosa*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a122566;2 total counts: 607 Seed: 3 K: 25 length: 320	320	2.35625	gi|927594450|ref|YP 009165276.1|	46.2	3.52E-06	1678078	*Mollivirus sibericum*	*Acanthamoeba castellanii*	Longamoebia; Amoebozoa; Eukaryota	unclassified	unclassified	unclassified
a87947;2 total counts: 433 Seed: 3 K: 25 length: 230	230	2.33918	gi|937456514|ref|YP 009168440.1|	47.8	1.93E-07	1622234	Citrobacter phage CVT22	*Citrobacter sp. TM1552*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a67842;3 total counts: 594 Seed: 4 K: 25 length: 251	251	2.32407	gi|1102618170|ref|YP 009321910.1|	73.2	3.93E-16	1792274	Flavobacterium phage Fpv20	*Flavobacterium psychrophilum*	Bacteroidetes; Bacteria	unclassified	unclassified	unclassified
a151216;3 total counts: 567 Seed: 2 K: 25 length: 243	243	2.32099	gi|203454799|ref|YP 002225115.1|	60.5	6.17E-12	546805	Mycobacterium phage Myrna	*Mycobacterium smegmatis str. MC2 155*	Actinobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a117809;3 total counts: 563 Seed: 2 K: 25 length: 225	225	2.31556	gi|658310061|ref|YP 009042253.1|	102	1.71E-26	1327934	Cronobacter phage CR8	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a88403;2 total counts: 486 Seed: 2 K: 25 length: 290	290	2.31529	gi|937456498|ref|YP 009168424.1|	112	1.79E-29	1622234	Citrobacter phage CVT22	*Citrobacter sp. TM1552*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a58070;3 total counts: 2596 Seed: 4 K: 25 length: 848	848	2.31486	gi|448244948|ref|YP 007392668.1|	216	5.42E-71	1116482	Pectobacterium phage phiTE	*Pectobacterium atrosepticum SCRI1043*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a146862;3 total counts: 1436 Seed: 3 K: 25 length: 465	465	2.31111	gi|157168378|ref|YP 001456735.1|	144	8.02E-42	28358	Corynebacterium phage BFK20	*[Brevibacterium] flavum*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a35231;3 total counts: 562 Seed: 4 K: 25 length: 248	248	2.28629	gi|448244878|ref|YP 007392598.1|	71.6	1.49E-15	1116482	Pectobacterium phage phiTE	*Pectobacterium atrosepticum SCRI1043*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a91292;2 total counts: 562 Seed: 2 K: 25 length: 301	301	2.28571	gi|593777139|ref|YP 009014984.1|	104	7.99E-28	1162290	Cronobacter phage CR9	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a35475;2 total counts: 405 Seed: 2 K: 25 length: 230	230	2.28261	gi|29135232|ref|NP 803862.1|	63.9	7.48E-14	169683	Pseudomonas phage phiKZ	*Pseudomonas aeruginosa*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a58842;3 total counts: 703 Seed: 2 K: 25 length: 227	227	2.28194	gi|1147809662|ref|YP 009344963.1|	59.7	2.18E-11	1929150	*Enterovirus AN12*	*Bos taurus*	Chordata; Metazoa; Eukaryota	Picornavirales	Picornaviridae	ssRNA +
a63607;2 total counts: 825 Seed: 2 K: 25 length: 394	394	2.27919	gi|985760870|ref|YP 009226385.1|	49.7	1.01E-07	1296659	Paenibacillus phage Jimmer1	*Paenibacillus larvae*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a146574;4 total counts: 2199 Seed: 2 K: 25 length: 626	626	2.27473	gi|148750838|ref|YP 001285880.1|	150	2.25E-42	12348	Lactobacillus phage LL-H	*Lactobacillus delbrueckii subsp. lactis*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a90332;3 total counts: 622 Seed: 4 K: 25 length: 229	229	2.26894	gi|966198576|ref|YP 009188410.1|	44.3	2.00E-06	1647474	Gordonia phage GTE6	*Gordonia terrae*	Actinobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a147979;2 total counts: 377 Seed: 4 K: 25 length: 204	204	2.2598	gi|310831534|ref|YP 003970177.1|	53.9	1.42E-09	693272	*Cafeteria roenbergensis virus BV-PW1*	*Cafeteria roenbergensis*	Bicosoecida; Eukaryota	unclassified	Mimiviridae	dsDNA
a148421;2 total counts: 718 Seed: 4 K: 25 length: 409	409	2.25428	gi|593777612|ref|YP 009015458.1|	81.6	3.33E-18	1084719	Bacillus phage G	*Bacillus sp.; Geobacillus sp.*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a87756;2 total counts: 535 Seed: 2 K: 25 length: 294	294	2.2487	gi|372449823|ref|YP 005087046.1|	155	1.15E-45	1109713	Rhodococcus phage REQ2	*Rhodococcus hoagii*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a120792;3 total counts: 859 Seed: 3 K: 25 length: 338	338	2.2426	gi|658310047|ref|YP 009042239.1|	157	3.09E-46	1327934	Cronobacter phage CR8	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a90837;2 total counts: 749 Seed: 2 K: 25 length: 402	402	2.24129	gi|589889646|ref|YP 009005029.1|	45.1	4.97E-06	1429768	Erwinia phage Ea35-7	*Erwinia amylovora*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a5407;2 total counts: 487 Seed: 3 K: 25 length: 261	261	2.23372	gi|203454797|ref|YP 002225113.1|	62.4	3.40E-13	546805	Mycobacterium phage Myrna	*Mycobacterium smegmatis str. MC2 155*	Actinobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a73295;2 total counts: 394 Seed: 2 K: 25 length: 218	218	2.22936	gi|589889419|ref|YP 009004802.1|	53.9	1.79E-09	1429768	Erwinia phage Ea35-7	*Erwinia amylovora*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a97454;2 total counts: 421 Seed: 2 K: 25 length: 232	232	2.22845	gi|985757311|ref|YP 009222274.1|	46.2	9.92E-07	1567484	Lactobacillus phage LfeInf	*Lactobacillus fermentum*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a155663;2 total counts: 740 Seed: 2 K: 25 length: 417	417	2.21343	gi|906476413|ref|YP 009160408.1|	140	2.11E-41	1655661	*Microviridae Fen7918 21*	*na*	na	unclassified	Microviridae	ssDNA
a121517;2 total counts: 362 Seed: 4 K: 25 length: 207	207	2.21256	gi|712915791|ref|YP 009103574.1|	55.8	3.04E-10	1481186	Acinetobacter phage vB AbaM Acibel004	*Acinetobacter baumannii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a90635;3 total counts: 848 Seed: 5 K: 25 length: 312	312	2.20502	gi|41179374|ref|NP 958682.1|	87.8	6.96E-21	194699	Bordetella phage BPP-1	*Bordetella bronchiseptica*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a115758;3 total counts: 526 Seed: 3 K: 25 length: 229	229	2.17419	gi|1068512709|ref|YP 009276510.1|	63.5	8.02E-13	1838066	Gordonia phage Cozz	*Gordonia terrae*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a630;5 total counts: 1097 Seed: 5 K: 25 length: 264	264	2.17045	gi|428782719|ref|YP 007112472.1|	58.5	2.16E-11	1147158	Enterobacterial phage mEp390	*Escherichia coli*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a147453;6 total counts: 4131 Seed: 4 K: 25 length: 675	675	2.16846	gi|971741645|ref|YP 009196166.1|	244	1.01E-78	1636261	Paenibacillus phage Vegas	*Paenibacillus larvae*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a149767;2 total counts: 429 Seed: 2 K: 25 length: 260	260	2.16154	gi|363540041|ref|YP 004894551.1|	107	3.90E-28	1094892	*Megavirus chiliensis*	*Acanthamoeba*	Longamoebia; Amoebozoa; Eukaryota	unclassified	Mimiviridae	dsDNA
a147905;2 total counts: 452 Seed: 2 K: 25 length: 280	280	2.15714	gi|46401632|ref|YP 006476.1|	59.7	3.82E-11	10678	Enterobacteria phage P1	*Escherichia coli*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a89668;2 total counts: 489 Seed: 2 K: 25 length: 273	273	2.14286	gi|29134961|ref|NP 803591.1|	66.6	1.39E-13	169683	Pseudomonas phage phiKZ	*Pseudomonas aeruginosa*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a1231;2 total counts: 571 Seed: 2 K: 25 length: 341	341	2.13818	gi|1068357955|ref|YP 009273285.1|	47	1.66E-06	1647470	Gordonia phage GMA1	*Gordonia malaquae*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a4768;2 total counts: 352 Seed: 3 K: 25 length: 243	243	2.12346	gi|906476306|ref|YP 009160347.1|	99	2.84E-25	1655649	*Gokushovirinae Bog5712 52*	*na*	na	unclassified	Microviridae	ssDNA
a99443;2 total counts: 420 Seed: 2 K: 25 length: 256	256	2.12109	gi|363540687|ref|YP 004894539.1|	56.6	2.74E-10	1094892	*Megavirus chiliensis*	*Acanthamoeba*	Longamoebia; Amoebozoa; Eukaryota	unclassified	Mimiviridae	dsDNA
a33766;2 total counts: 736 Seed: 4 K: 25 length: 404	404	2.11881	gi|658310137|ref|YP 009042329.1|	174	3.70E-56	1327934	Cronobacter phage CR8	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a5135;3 total counts: 781 Seed: 6 K: 25 length: 311	311	2.10932	gi|1070106046|ref|YP 009291897.1|	44.3	9.81E-06	1792222	Acinetobacter phage LZ35	*Acinetobacter baumannii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a94289;3 total counts: 739 Seed: 2 K: 25 length: 257	257	2.10644	gi|151266296|ref|YP 001333659.1|	62.8	2.05E-12	338473	Actinomyces phage Av-1	*Actinomyces naeslundii*	Actinobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a151167;2 total counts: 478 Seed: 3 K: 25 length: 273	273	2.10256	gi|607840598|ref|YP 009021847.1|	61.6	6.34E-12	1234881	*Dragonfly cyclovirus 3*	*Erythemis simplicicollis*	Arthropoda; Metazoa; Eukaryota	unclassified	Circoviridae	ssDNA
a2130;2 total counts: 374 Seed: 2 K: 25 length: 217	217	2.09924	gi|593774692|ref|YP 009012312.1|	90.5	4.54E-23	1074309	Mycobacterium phage BigNuz	*Mycobacterium smegmatis str. MC2 155*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a151570;2 total counts: 914 Seed: 7 K: 25 length: 393	393	2.07143	gi|589287448|ref|YP 009010939.1|	48.5	9.21E-07	1465618	Salmonella phage vB SenS-Ent2	*Salmonella enterica subsp. enterica serovar Enteritidis*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a116535;3 total counts: 1708 Seed: 2 K: 25 length: 582	582	2.06701	gi|448244963|ref|YP 007392683.1|	145	5.42E-43	1116482	Pectobacterium phage phiTE	*Pectobacterium atrosepticum SCRI1043*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a157881;2 total counts: 336 Seed: 3 K: 25 length: 209	209	2.06699	gi|363540510|ref|YP 004894822.1|	57.8	6.12E-11	1094892	*Megavirus chiliensis*	*Acanthamoeba*	Longamoebia; Amoebozoa; Eukaryota	unclassified	Mimiviridae	dsDNA
a59635;4 total counts: 790 Seed: 2 K: 25 length: 231	231	2.06494	gi|226377831|ref|YP 002790879.1|	58.5	4.65E-11	631345	*Solenopsis invicta virus 3*	*Solenopsis invicta*	Arthropoda; Metazoa; Eukaryota	unclassified	unclassified	unclassified
a88597;2 total counts: 485 Seed: 2 K: 25 length: 294	294	2.04422	gi|971764182|ref|YP 009217184.1|	62.4	4.52E-12	998086	Pseudomonas phage PhiPA3	*Pseudomonas aeruginosa*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a8784;4 total counts: 778 Seed: 2 K: 25 length: 224	224	2.04151	gi|971757354|ref|YP 009210861.1|	111	1.00E-29	1647301	Mycobacterium phage Vincenzo	*Mycobacterium smegmatis str. MC2 155*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a159521;2 total counts: 405 Seed: 2 K: 25 length: 210	210	2.0381	gi|446730260|ref|YP 007173630.1|	57	1.42E-10	1206110	Lactobacillus phage phiAQ113	*Lactobacillus helveticus*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a67732;2 total counts: 346 Seed: 3 K: 25 length: 200	200	2.03382	gi|937456478|ref|YP 009168403.1|	74.3	1.20E-18	1622234	Citrobacter phage CVT22	*Citrobacter sp. TM1552*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a36496;2 total counts: 305 Seed: 2 K: 25 length: 224	224	2.00893	gi|363539688|ref|YP 004893973.1|	95.5	1.41E-24	889338	Salmonella phage PVP-SE1	*Salmonella enterica subsp. enterica serovar Enteritidis*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a87902;4 total counts: 1124 Seed: 3 K: 25 length: 327	327	2.0067	gi|472339123|ref|YP 007672659.1|	99.4	7.84E-25	885867	Prochlorococcus phage P-SSP10	*Prochlorococcus marinus str. NATL2A*	Cyanobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a72785;3 total counts: 565 Seed: 3 K: 25 length: 233	233	2	gi|151266301|ref|YP 001333664.1|	60.5	8.07E-12	338473	Actinomyces phage Av-1	*Actinomyces naeslundii*	Actinobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a147711;3 total counts: 625 Seed: 3 K: 25 length: 246	246	2	gi|151266296|ref|YP 001333659.1|	69.7	6.75E-15	338473	Actinomyces phage Av-1	*Actinomyces naeslundii*	Actinobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a32902;4 total counts: 731 Seed: 3 K: 25 length: 230	230	2	gi|371496158|ref|YP 004957306.1|	48.1	2.04E-07	994601	Planktothrix phage PaV-LD	*Planktothrix agardhii HAB637*	Cyanobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a150393;2 total counts: 755 Seed: 3 K: 25 length: 448	448	2	gi|371496158|ref|YP 004957306.1|	55.1	6.15E-09	994601	Planktothrix phage PaV-LD	*Planktothrix agardhii HAB637*	Cyanobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a91848;2 total counts: 584 Seed: 2 K: 25 length: 275	275	2	gi|22855149|ref|NP 690635.1|	100	1.23E-25	10778	Bacillus phage B103	*Bacillus subtilis*	Firmicutes; Bacteria	Caudovirales	Podoviridae	dsDNA
a129701;2 total counts: 318 Seed: 3 K: 25 length: 222	222	2	gi|41179402|ref|NP 958711.1|	47	4.84E-07	194699	Bordetella phage BPP-1	*Bordetella bronchiseptica*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a128155;2 total counts: 428 Seed: 2 K: 25 length: 234	234	2	gi|937456472|ref|YP 009168397.1|	47.4	4.86E-07	1622234	Citrobacter phage CVT22	*Citrobacter sp. TM1552*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a153571;4 total counts: 1726 Seed: 2 K: 25 length: 441	441	2	gi|170783624|ref|YP 001648906.1|	152	2.78E-46	489779	Enterobacteria phage Min27	*Escherichia coli O157:H7*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a149205;4 total counts: 1630 Seed: 2 K: 25 length: 453	453	2	gi|374531901|ref|YP 005098457.1|	59.3	2.42E-10	1131315	Erwinia phage PEp14	*Erwinia amylovora*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a95896;2 total counts: 436 Seed: 3 K: 25 length: 206	206	2	gi|194100463|ref|YP 002003836.1|	129	3.50E-36	532077	Klebsiella phage K11	*Klebsiella sp. 390*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a102495;3 total counts: 466 Seed: 3 K: 25 length: 202	202	2	gi|423261934|ref|YP 007010536.1|	77.4	2.79E-18	1161935	Salinivibrio phage CW02	*Salinivibrio costicola*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a147812;4 total counts: 986 Seed: 7 K: 25 length: 300	300	2	gi|13559835|ref|NP 112045.1|	58.2	8.91E-11	155148	Salmonella phage HK620	*Salmonella enterica*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a59102;2 total counts: 500 Seed: 3 K: 25 length: 267	267	2	gi|1070643136|ref|YP 009300693.1|	66.6	7.01E-15	1796997	Arthrobacter phage Mudcat	*Arthrobacter sp. ATCC 21022*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a151532;5 total counts: 1388 Seed: 7 K: 25 length: 292	292	2	gi|563398140|ref|YP 008857900.1|	78.6	7.89E-18	1414742	Arthrobacter phage vB ArS-ArV2	*Arthrobacter sp.*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a88277;3 total counts: 729 Seed: 2 K: 25 length: 305	305	2	gi|563398140|ref|YP 008857900.1|	55.5	1.41E-09	1414742	Arthrobacter phage vB ArS-ArV2	*Arthrobacter sp.*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a160;2 total counts: 1030 Seed: 3 K: 25 length: 495	495	2	gi|157168378|ref|YP 001456735.1|	115	7.42E-31	28358	Corynebacterium phage BFK20	*[Brevibacterium] flavum*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a152075;4 total counts: 1531 Seed: 5 K: 25 length: 416	416	2	gi|1068512754|ref|YP 009276541.1|	75.9	1.61E-16	1838064	Gordonia phage BritBrat	*Gordonia terrae*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a64364;2 total counts: 638 Seed: 2 K: 25 length: 318	318	2	gi|1068357939|ref|YP 009273269.1|	77	3.36E-18	1647470	Gordonia phage GMA1	*Gordonia malaquae*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a147174;8 total counts: 3508 Seed: 15 K: 25 length: 456	456	2	gi|1068358009|ref|YP 009273598.1|	110	5.03E-31	1647472	Gordonia phage GMA5	*Gordonia malaquae*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a3389;3 total counts: 629 Seed: 3 K: 25 length: 261	261	2	gi|1070619841|ref|YP 009304275.1|	52.8	9.71E-09	1821557	Gordonia phage Lucky10	*Gordonia terrae*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a59236;5 total counts: 2455 Seed: 9 K: 25 length: 487	487	2	gi|1068511076|ref|YP 009274030.1|	122	7.97E-34	1838072	Gordonia phage McGonagall	*Gordonia neofelifaecis*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a154144;2 total counts: 407 Seed: 4 K: 25 length: 236	236	2	gi|1070096285|ref|YP 009277923.1|	72	7.88E-16	1887651	Gordonia phage Nyceirae	*Gordonia terrae*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a95691;2 total counts: 606 Seed: 3 K: 25 length: 278	278	2	gi|1049011795|ref|YP 009269160.1|	44.7	8.35E-06	1838078	Gordonia phage Smoothie	*Gordonia terrae*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a62394;2 total counts: 387 Seed: 3 K: 25 length: 200	200	2	gi|602259748|ref|YP 009021458.1|	63.2	6.99E-13	1458670	Microbacterium phage vB MoxS-ISF9	*Microbacterium oxydans*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a67455;3 total counts: 680 Seed: 3 K: 25 length: 262	262	2	gi|593775216|ref|YP 009013081.1|	55.5	8.94E-10	1089115	Mycobacterium phage Babsiella	*Mycobacterium smegmatis str. MC2 155*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a147923;4 total counts: 1106 Seed: 2 K: 25 length: 338	338	2	gi|530545458|ref|YP 008409059.1|	114	2.67E-30	1340708	Mycobacterium phage Bobi	*Mycobacterium smegmatis str. MC2 155*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a34211;2 total counts: 505 Seed: 4 K: 25 length: 246	246	2	gi|29566045|ref|NP 817615.1|	57.4	1.57E-10	205870	Mycobacterium phage Bxz2	*Mycobacterium sp.*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a155087;2 total counts: 779 Seed: 2 K: 25 length: 423	423	2	gi|29566426|ref|NP 817992.1|	102	2.65E-25	205876	Mycobacterium phage Che9d	*Mycobacterium sp.*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a94447;2 total counts: 367 Seed: 2 K: 25 length: 212	212	2	gi|764160085|ref|YP 009124746.1|	76.3	2.47E-17	1486472	Mycobacterium phage Gaia	*Mycobacterium smegmatis str. MC2 155*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a149274;2 total counts: 1187 Seed: 3 K: 25 length: 642	642	2	gi|764160092|ref|YP 009124753.1|	71.2	1.73E-14	1486472	Mycobacterium phage Gaia	*Mycobacterium smegmatis str. MC2 155*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a29514;4 total counts: 2397 Seed: 2 K: 25 length: 651	651	2	gi|304360966|ref|YP 003857148.1|	84.3	1.15E-18	861047	Mycobacterium phage LeBron	*Mycobacterium sp.*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a59812;4 total counts: 1466 Seed: 7 K: 25 length: 392	392	2	gi|640884162|ref|YP 009031541.1|	48.5	1.63E-07	1471542	Mycobacterium phage MosMoris	*Mycobacterium smegmatis str. MC2 155*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a29198;2 total counts: 859 Seed: 5 K: 25 length: 479	479	2	gi|530545328|ref|YP 008408930.1|	143	2.07E-39	1340829	Mycobacterium phage Muddy	*Mycobacterium sp.*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA

a150626;4 total counts: 2102 Seed: 2 K: 25 length: 586	586	2	gi|971748726|ref|YP 009202615.1|	88.6	6.66E-20	1698356	Mycobacterium phage Phatniss	*Mycobacterium smegmatis str. MC2 155*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a30887;3 total counts: 2539 Seed: 2 K: 25 length: 774	774	2	gi|589893731|ref|YP 009010023.1|	89.4	2.32E-19	1458846	Mycobacterium phage RhynO	*Mycobacterium smegmatis str. MC2 155*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a146282;4 total counts: 5091 Seed: 2 K: 25 length: 1297	1297	2	gi|764160062|ref|YP 009124741.1|	274	1.24E-86	1567475	Mycobacterium phage Sbash	*Mycobacterium smegmatis str. MC2 155*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a119119;3 total counts: 778 Seed: 4 K: 25 length: 286	286	2	gi|479336632|ref|YP 007869980.1|	60.8	1.35E-11	1305710	Mycobacterium phage vB MapS FF47	*Mycobacterium avium subsp. paratuberculosis*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a151831;3 total counts: 574 Seed: 2 K: 25 length: 228	228	2	gi|530546937|ref|YP 008410526.1|	61.6	1.79E-12	1340713	Mycobacterium phage Wanda	*Mycobacterium smegmatis str. MC2 155*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a87667;2 total counts: 336 Seed: 2 K: 25 length: 219	219	2	gi|509141053|ref|YP 008059937.1|	44.7	2.96E-06	1327036	Mycobacterium phage WIVsmall	*Mycobacterium smegmatis str. MC2 155*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a31358;5 total counts: 1878 Seed: 2 K: 25 length: 404	404	2	gi|985760367|ref|YP 009225887.1|	76.6	8.27E-17	1556290	Streptomyces phage Jay2Jay	*Streptomyces lividans*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a146790;4 total counts: 3112 Seed: 6 K: 25 length: 754	754	2	gi|971765016|ref|YP 009218009.1|	63.9	8.38E-11	1755682	Streptomyces phage phiSAJS1	*Streptomyces avermitilis*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a152986;2 total counts: 486 Seed: 2 K: 25 length: 304	304	2	gi|326425096|ref|YP 004286319.1|	79	7.87E-20	981330	Tsukamurella phage TPA2	*Tsukamurella paurometabola*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a116252;11 total counts: 45454 Seed: 6 K: 25 length: 4300	4300	2	gi|22296541|ref|NP 680501.1|	62	4.31E-09	51369	Lactobacillus phage A2	*Lactobacillus casei*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a29349;2 total counts: 802 Seed: 4 K: 25 length: 384	384	2	gi|418489408|ref|YP 007003225.1|	47.4	2.32E-06	947980	Lactobacillus phage LF1	*Lactobacillus sp.*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a147077;5 total counts: 4358 Seed: 2 K: 25 length: 855	855	2	gi|195661221|ref|YP 002117689.1|	47.8	8.41E-06	496874	Lactobacillus phage Lrm1	*Lactobacillus rhamnosus*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a146940;5 total counts: 1211 Seed: 3 K: 25 length: 274	274	2	gi|571797865|ref|YP 008772031.1|	68.9	1.83E-14	1399941	Lactobacillus phage phiJB	*Lactobacillus delbrueckii*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a154177;3 total counts: 506 Seed: 3 K: 25 length: 226	226	2	gi|557307973|ref|YP 008767295.1|	78.2	5.30E-20	39103	Lactobacillus phage PL-1	*Lactobacillus paracasei*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a87642;7 total counts: 5502 Seed: 2 K: 25 length: 856	856	2	gi|557307959|ref|YP 008767281.1|	123	2.69E-33	39103	Lactobacillus phage PL-1	*Lactobacillus paracasei*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a149756;3 total counts: 714 Seed: 4 K: 25 length: 245	245	2	gi|13095906|ref|NP 076815.1|	73.2	3.76E-16	151539	Lactococcus phage bIL312	*Lactococcus lactis subsp. lactis Il1403*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a127697;2 total counts: 395 Seed: 4 K: 25 length: 226	226	2	gi|526244864|ref|YP 008320190.1|	43.5	8.01E-06	1229751	Lactococcus phage BM13	*Lactococcus lactis*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a88987;3 total counts: 1259 Seed: 2 K: 25 length: 396	396	2	gi|66395809|ref|YP 240178.1|	46.6	5.02E-06	320841	Staphylococcus phage EW	*Staphylococcus aureus*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a30153;7 total counts: 2236 Seed: 7 K: 25 length: 362	362	2	gi|971766715|ref|YP 009219657.1|	100	2.28E-26	1610872	Staphylococcus phage IME-SA4	*Staphylococcus haemolyticus*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a153673;2 total counts: 398 Seed: 4 K: 25 length: 203	203	2	gi|66394700|ref|YP 240855.1|	42.4	8.81E-06	320850	Staphylococcus phage X2	*Staphylococcus aureus*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a151174;4 total counts: 983 Seed: 4 K: 25 length: 267	267	2	gi|9632896|ref|NP 049925.1|	68.2	3.27E-15	72638	Streptococcus phage Sfi19	*Streptococcus thermophilus*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a155772;2 total counts: 737 Seed: 2 K: 25 length: 368	368	2	gi|32469465|ref|NP 862873.1|	63.9	2.80E-12	157924	Streptococcus phage SM1	*Streptococcus mitis*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a146417;4 total counts: 1476 Seed: 2 K: 25 length: 408	408	2	gi|764162029|ref|YP 009126425.1|	108	7.12E-28	1561065	Paracoccus phage vB PmaS IMEP1	*Paracoccus marcusii*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a116451;5 total counts: 4758 Seed: 5 K: 25 length: 1031	1031	2	gi|1070101634|ref|YP 009285814.1|	92	2.14E-21	1844477	Pseudomonas phage NP	*Pseudomonas sp.*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a145642;3 total counts: 725 Seed: 2 K: 25 length: 263	263	2	gi|1070101664|ref|YP 009285844.1|	80.1	7.76E-19	1844477	Pseudomonas phage NP1	*Pseudomonas sp.*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a30328;3 total counts: 1021 Seed: 4 K: 25 length: 408	408	2	gi|1070101679|ref|YP 009285859.1|	118	4.27E-33	1844477	Pseudomonas phage NP1	*Pseudomonas sp.*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a7418;5 total counts: 4292 Seed: 8 K: 25 length: 853	853	2	gi|1070101667|ref|YP 009285847.1|	262	2.14E-86	1844477	Pseudomonas phage NP1	*Pseudomonas sp.*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a118886;3 total counts: 1884 Seed: 4 K: 25 length: 577	577	2	gi|971762591|ref|YP 009215714.1|	87.4	2.35E-19	1718273	Pseudomonas phage PAE1	*Pseudomonas aeruginosa*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a122622;3 total counts: 1093 Seed: 5 K: 25 length: 344	344	2	gi|374531258|ref|YP 005098041.1|	56.6	6.11E-10	1129145	Pseudomonas phage phi297	*Pseudomonas aeruginosa*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a67923;2 total counts: 681 Seed: 4 K: 25 length: 318	318	2	gi|162135148|ref|YP 001595889.1|	63.9	1.73E-12	462590	Pseudomonas phage YuA	*Pseudomonas aeruginosa*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a29473;2 total counts: 964 Seed: 2 K: 25 length: 471	471	2	gi|162135088|ref|YP 001595829.1|	62.4	3.14E-11	462590	Pseudomonas phage YuA	*Pseudomonas aeruginosa*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a145784;8 total counts: 4517 Seed: 6 K: 25 length: 590	590	2	gi|472340490|ref|YP 007674015.1|	133	1.06E-35	754049	Vibrio phage pYD21-A	*Vibrio sp. YD21*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a58882;3 total counts: 799 Seed: 4 K: 25 length: 306	306	2	gi|764162223|ref|YP 009126593.1|	96.3	7.07E-24	1538804	Vibrio phage VpKK5	*Vibrio parahaemolyticus*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a20767;2 total counts: 277 Seed: 2 K: 25 length: 205	205	2	gi|1102619166|ref|YP 009323093.1|	58.2	2.92E-11	1883368	Synechococcus phage S-CAM7	*Synechococcus sp.*	Cyanobacteria; Bacteria	unclassified	unclassified	unclassified
a70564;3 total counts: 651 Seed: 2 K: 25 length: 228	228	2	gi|509140424|ref|YP 008059305.1|	50.4	3.02E-08	1273749	Halovirus HGTV-1	*Halogranum sp. SS5-1*	Euryarchaeota; Archaea	unclassified	unclassified	dsDNA
a147494;5 total counts: 2823 Seed: 4 K: 25 length: 627	627	2	gi|1068513125|ref|YP 009276859.1|	116	2.33E-30	1567487	Bacillus phage BalMu-1	*Bacillus alcalophilus ATCC 27647 = CGMCC 1.3604*	Firmicutes; Bacteria	unclassified	unclassified	dsDNA
a146566;4 total counts: 819 Seed: 6 K: 25 length: 210	210	2	gi|163932187|ref|YP 001642377.1|	55.1	9.19E-11	139871	Lactobacillus johnsonii prophage Lj771	*Lactobacillus johnsonii*	Firmicutes; Bacteria	unclassified	unclassified	unclassified
a9208;3 total counts: 823 Seed: 3 K: 25 length: 295	295	2	gi|163932195|ref|YP 001642385.1|	45.8	3.69E-06	139871	Lactobacillus johnsonii prophage Lj771	*Lactobacillus johnsonii*	Firmicutes; Bacteria	unclassified	unclassified	unclassified
a151847;2 total counts: 406 Seed: 2 K: 25 length: 216	216	2	gi|1070639738|ref|YP 009304106.1|	120	2.78E-33	1718278	Brucella phage BiPBO1	*Brucella inopinata*	Proteobacteria; Bacteria	unclassified	unclassified	unclassified
a4117;4 total counts: 1722 Seed: 2 K: 25 length: 498	498	2	gi|971746169|ref|YP 009200249.1|	185	2.16E-55	1636200	Pseudoalteromonas Phage H103	*Pseudoalteromonas marina*	Proteobacteria; Bacteria	Caudovirales	unclassified	dsDNA
a119264;6 total counts: 4099 Seed: 5 K: 25 length: 723	723	2	gi|481018921|ref|YP 007877278.1|	53.5	2.50E-08	573173	Vibrio phage helene 12B3	*Vibrio splendidus*	Proteobacteria; Bacteria	unclassified	unclassified	dsDNA
a89109;5 total counts: 2537 Seed: 4 K: 25 length: 541	541	1.99333	gi|93007440|ref|YP 579204.1|	103	2.09E-25	370623	Streptomyces phage mu1/6	*Kitasatospora aureofaciens*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a61764;3 total counts: 1169 Seed: 2 K: 25 length: 378	378	1.98684	gi|149882819|ref|YP 001294798.1|	107	2.50E-28	446529	Microbacterium phage Min1	*Microbacterium nematophilum*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a116831;4 total counts: 1468 Seed: 5 K: 25 length: 420	420	1.98305	gi|392972735|ref|YP 006488695.1|	47.4	2.63E-06	1118063	Staphylococcus phage SpaA1	*Staphylococcus pasteuri*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a34480;2 total counts: 589 Seed: 2 K: 25 length: 356	356	1.97753	gi|448244966|ref|YP 007392686.1|	89.4	4.71E-23	1116482	Pectobacterium phage phiTE	*Pectobacterium atrosepticum SCRI1043*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a150691;2 total counts: 408 Seed: 3 K: 25 length: 228	228	1.96789	gi|151266296|ref|YP 001333659.1|	49.7	6.78E-08	338473	Actinomyces phage Av-1	*Actinomyces naeslundii*	Actinobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a87571;2 total counts: 502 Seed: 2 K: 25 length: 232	232	1.96552	gi|906476306|ref|YP 009160347.1|	116	1.68E-31	1655649	*Gokushovirinae Bog5712 52*	*na*	na	unclassified	Microviridae	ssDNA
a159187;2 total counts: 584 Seed: 4 K: 25 length: 366	366	1.96104	gi|298103488|ref|YP 003714730.1|	71.6	6.13E-15	747763	Streptomyces phage phiSASD1	*Streptomyces avermitilis*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a149541;4 total counts: 2097 Seed: 4 K: 25 length: 524	524	1.96026	gi|971762571|ref|YP 009215694.1|	80.1	3.04E-18	1718273	Pseudomonas phage PAE1	*Pseudomonas aeruginosa*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a116854;3 total counts: 570 Seed: 3 K: 25 length: 201	201	1.9602	gi|422937534|ref|YP 007007739.1|	65.9	1.02E-13	1127514	Aeromonas phage vB AsaM-56	*Aeromonas salmonicida*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a29426;4 total counts: 3393 Seed: 5 K: 25 length: 879	879	1.96	gi|372449802|ref|YP 005087026.1|	117	2.48E-29	1109717	Rhodococcus phage RRH1	*Rhodococcus rhodochrous*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a148540;2 total counts: 364 Seed: 2 K: 25 length: 265	265	1.94717	gi|672551192|ref|YP 009052394.1|	56.2	4.90E-10	1474867	*Aureococcus anophagefferens virus*	*Aureococcus anophagefferens*	Pelagophyceae; Eukaryota	unclassified	Phycodnaviridae	dsDNA
a88247;2 total counts: 457 Seed: 3 K: 25 length: 264	264	1.94156	gi|966198557|ref|YP 009188391.1|	72	3.92E-16	1647474	Gordonia phage GTE6	*Gordonia terrae*	Actinobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a32896;3 total counts: 834 Seed: 6 K: 25 length: 310	310	1.93793	gi|192824184|ref|YP 001994825.1|	53.9	6.00E-09	540068	Mycobacterium phage Pukovnik	*Mycobacterium smegmatis str. MC2 155*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a95332;2 total counts: 393 Seed: 3 K: 25 length: 216	216	1.93716	gi|971745058|ref|YP 009199262.1|	44.3	3.95E-06	1690817	Streptomyces phage SF1	*Streptomyces flavovirens*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a147319;5 total counts: 4372 Seed: 2 K: 25 length: 958	958	1.93293	gi|9633052|ref|NP 050160.1|	129	2.57E-32	12417	Lactobacillus phage phiadh	*Lactobacillus gasseri*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a58114;4 total counts: 1409 Seed: 5 K: 25 length: 385	385	1.92949	gi|764159561|ref|YP 009124300.1|	46.2	5.09E-06	1536603	Mycobacteriophage Estave1	*Mycobacterium smegmatis str. MC2 155*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a148590;2 total counts: 421 Seed: 2 K: 25 length: 216	216	1.92949	gi|162135108|ref|YP 001595849.1|	125	1.04E-34	462590	Pseudomonas phage YuA	*Pseudomonas aeruginosa*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a125126;3 total counts: 637 Seed: 3 K: 25 length: 218	218	1.92202	gi|985757280|ref|YP 009222243.1|	66.2	8.18E-14	1567484	Lactobacillus phage LfeInf	*Lactobacillus fermentum*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a120378;2 total counts: 408 Seed: 3 K: 25 length: 232	232	1.91139	gi|937456462|ref|YP 009168387.1|	105	9.21E-28	1622234	Citrobacter phage CVT22	*Citrobacter sp. TM1552*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a7292;3 total counts: 998 Seed: 5 K: 25 length: 352	352	1.91083	gi|1070098399|ref|YP 009281132.1|	62.8	6.93E-12	1887647	Gordonia phage Ghobe	*Gordonia terrae*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a147273;4 total counts: 2465 Seed: 4 K: 25 length: 618	618	1.91083	gi|1070101668|ref|YP 009285848.1|	191	6.84E-62	1844477	Pseudomonas phage NP1	*Pseudomonas sp.*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a61414;6 total counts: 1937 Seed: 6 K: 25 length: 356	356	1.90351	gi|448260249|ref|YP 007348345.1|	53.5	1.47E-09	1264737	Cronobacter phage vB CskP GAP227	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a147384;7 total counts: 6615 Seed: 6 K: 25 length: 1012	1012	1.89937	gi|971747098|ref|YP 009201022.1|	99	7.50E-24	1567468	Mycobacterium phage Edtherson	*Mycobacterium smegmatis str. MC2 155*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a62335;2 total counts: 368 Seed: 2 K: 25 length: 245	245	1.89388	gi|56693138|ref|YP 164725.1|	86.7	9.00E-21	298338	Lactobacillus phage LP65	*Lactobacillus plantarum*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a88976;2 total counts: 428 Seed: 3 K: 25 length: 232	232	1.8875	gi|971762591|ref|YP 009215714.1|	73.6	2.67E-16	1718273	Pseudomonas phage PAE1	*Pseudomonas aeruginosa*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a5115;2 total counts: 936 Seed: 2 K: 25 length: 446	446	1.88716	gi|937456504|ref|YP 009168430.1|	70.5	3.68E-14	1622234	Citrobacter phage CVT22	*Citrobacter sp. TM1552*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a147689;2 total counts: 440 Seed: 4 K: 25 length: 279	279	1.88688	gi|971482324|ref|YP 009193827.1|	58.2	1.31E-10	1636257	Paenibacillus phage Harrison	*Paenibacillus larvae*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a6737;2 total counts: 311 Seed: 3 K: 25 length: 203	203	1.8867	gi|751868297|ref|YP 009117066.1|	52.4	5.72E-09	1592095	*Sewage-associated circular DNA virus-28*	*na*	na	unclassified	unclassified	ssDNA
a35764;2 total counts: 489 Seed: 3 K: 25 length: 238	238	1.88235	gi|448244898|ref|YP 007392618.1|	106	2.25E-29	1116482	Pectobacterium phage phiTE	*Pectobacterium atrosepticum SCRI1043*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a35784;3 total counts: 1182 Seed: 2 K: 25 length: 403	403	1.86957	gi|593775709|ref|YP 009013568.1|	77	3.24E-18	1089121	Mycobacterium phage Dori	*Mycobacterium smegmatis str. MC2 155*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a149958;3 total counts: 703 Seed: 3 K: 25 length: 237	237	1.86937	gi|41179372|ref|NP 958680.1|	50.1	5.31E-08	194699	Bordetella phage BPP-1	*Bordetella bronchiseptica*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a89052;2 total counts: 424 Seed: 2 K: 25 length: 284	284	1.84507	gi|422936959|ref|YP 007007224.1|	82	5.33E-19	1147094	Enterobacteria phage vB KleM-RaK2	*Klebsiella sp.*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a124061;2 total counts: 391 Seed: 3 K: 25 length: 266	266	1.84211	gi|56693107|ref|YP 164694.1|	46.6	1.20E-06	298338	Lactobacillus phage LP65	*Lactobacillus plantarum*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a145893;5 total counts: 2025 Seed: 4 K: 25 length: 453	453	1.84177	gi|764162201|ref|YP 009126571.1|	70.1	3.81E-15	1538804	Vibrio phage VpKK5	*Vibrio parahaemolyticus*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a146134;4 total counts: 1862 Seed: 6 K: 25 length: 471	471	1.84146	gi|937456522|ref|YP 009168448.1|	140	9.71E-42	1622234	Citrobacter phage CVT22	*Citrobacter sp. TM1552*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a34101;3 total counts: 670 Seed: 3 K: 25 length: 286	286	1.83929	gi|23455777|ref|NP 695147.1|	45.8	3.21E-06	52979	Lactobacillus phage phig1e	*Lactobacillus sp.*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a146080;6 total counts: 3259 Seed: 5 K: 25 length: 532	532	1.83544	gi|431810189|ref|YP 007237076.1|	99	1.06E-25	1206557	Yersinia phage phiR201	*Yersinia enterocolitica*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a120527;2 total counts: 458 Seed: 2 K: 25 length: 317	317	1.82258	gi|149408199|ref|YP 001294633.1|	76.3	2.63E-17	347327	Pseudomonas phage PA11	*Pseudomonas aeruginosa*	Proteobacteria; Bacteria	unclassified	unclassified	dsDNA
a32096;4 total counts: 1550 Seed: 4 K: 25 length: 413	413	1.82243	gi|764162217|ref|YP 009126587.1|	114	7.55E-32	1538804	Vibrio phage VpKK5	*Vibrio parahaemolyticus*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a148275;3 total counts: 688 Seed: 2 K: 25 length: 257	257	1.80934	gi|431810499|ref|YP 007237607.1|	55.8	6.97E-10	984186	Cronobacter phage ENT47670	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a33456;2 total counts: 799 Seed: 4 K: 25 length: 376	376	1.80851	gi|971761211|ref|YP 009214557.1|	77.4	6.49E-17	1572704	Staphylococcus phage phiIPLA-C1C	*Staphylococcus sp.*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a161001;2 total counts: 637 Seed: 2 K: 25 length: 374	374	1.80723	gi|1070621526|ref|YP 009302998.1|	85.9	6.89E-20	1821562	Gordonia phage SoilAssassin	*Gordonia terrae*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a70671;2 total counts: 355 Seed: 2 K: 25 length: 251	251	1.8008	gi|226377752|ref|YP 002790801.1|	54.7	1.73E-09	632112	Lactobacillus phage Lb338-1	*Lactobacillus paracasei*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a60296;2 total counts: 794 Seed: 2 K: 25 length: 368	368	1.79891	gi|971848699|ref|YP 009042166.1|	83.6	4.27E-19	1465639	*Podovirus Lau218*	*na*	na	Caudovirales	Podoviridae	dsDNA
a34269;3 total counts: 721 Seed: 5 K: 25 length: 231	231	1.79518	gi|151266296|ref|YP 001333659.1|	77.4	1.18E-17	338473	Actinomyces phage Av-1	*Actinomyces naeslundii*	Actinobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a152339;2 total counts: 555 Seed: 2 K: 25 length: 276	276	1.78986	gi|56693138|ref|YP 164725.1|	62.8	2.99E-12	298338	Lactobacillus phage LP65	*Lactobacillus plantarum*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a146768;5 total counts: 4038 Seed: 4 K: 25 length: 795	795	1.78698	gi|1070640003|ref|YP 009304373.1|	92.8	2.38E-21	1821565	Gordonia phage Yeezy	*Gordonia terrae*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a146540;3 total counts: 846 Seed: 6 K: 25 length: 306	306	1.78571	gi|849060525|ref|YP 009151998.1|	49.3	5.24E-08	1540098	Escherichia phage Seurat	*Escherichia coli*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a123738;2 total counts: 380 Seed: 2 K: 25 length: 245	245	1.78146	gi|937456504|ref|YP 009168430.1|	110	3.82E-29	1622234	Citrobacter phage CVT22	*Citrobacter sp. TM1552*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a58062;2819 total counts: 10018172 Seed: 3 K: 25 length: 3578	3578	1.77647	gi|589892981|ref|YP 009004309.1|	405	1.02E-129	1453367	Staphylococcus phage GRCS	*Staphylococcus aureus*	Firmicutes; Bacteria	Caudovirales	Podoviridae	dsDNA
a29989;4 total counts: 1646 Seed: 3 K: 25 length: 392	392	1.77647	gi|372449918|ref|YP 005087141.1|	115	1.57E-30	1109715	Rhodococcus phage RER2	*Rhodococcus erythropolis*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a69857;3 total counts: 502 Seed: 3 K: 25 length: 205	205	1.77576	gi|971746163|ref|YP 009200243.1|	74.3	8.20E-17	1636200	Pseudoalteromonas Phage H103	*Pseudoalteromonas marina*	Proteobacteria; Bacteria	Caudovirales	unclassified	dsDNA
a122531;2 total counts: 558 Seed: 3 K: 25 length: 319	319	1.76687	gi|981221102|ref|YP 009221538.1|	54.3	6.99E-10	1524882	Sinorhizobium phage phiLM21	*Sinorhizobium sp. LM21*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a147193;9 total counts: 7629 Seed: 2 K: 25 length: 915	915	1.76608	gi|849060162|ref|YP 009151498.1|	125	2.09E-31	1540092	Bacillus phage Pascal	*Bacillus megaterium*	Firmicutes; Bacteria	Caudovirales	Podoviridae	dsDNA
a89178;3 total counts: 481 Seed: 2 K: 25 length: 208	208	1.76442	gi|971741485|ref|YP 009196045.1|	42	7.67E-06	1572703	Staphylococcus phage phiIPLA-RODI	*Staphylococcus sp.*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a88524;2 total counts: 613 Seed: 2 K: 25 length: 299	299	1.76374	gi|589892942|ref|YP 009004271.1|	120	2.51E-32	1406793	Clavibacter phage CN1A	*Clavibacter michiganensis*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a60804;3 total counts: 1578 Seed: 3 K: 25 length: 567	567	1.7561	gi|1068359406|ref|YP 009276409.1|	221	1.39E-72	1647471	Gordonia phage GMA4	*Gordonia malaquae*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA

a147032;4 total counts: 2138 Seed: 3 K: 25 length: 573	573	1.75194	gi|1068359285|ref|YP 009275707.1|	87	9.94E-20	1622193	Gordonia phage Gsput1	*Gordonia sputi*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a115857;2 total counts: 873 Seed: 2 K: 25 length: 442	442	1.75	gi|149882840|ref|YP 001294819.1|	51.2	3.65E-08	446529	Microbacterium phage Min1	*Microbacterium nematophilum*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a88076;5 total counts: 2208 Seed: 6 K: 25 length: 460	460	1.75	gi|29566753|ref|NP 818317.1|	162	5.40E-48	205879	Mycobacterium phage Omega	*Mycobacterium sp.*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a88739;6 total counts: 2738 Seed: 12 K: 25 length: 457	457	1.75	gi|22855026|ref|NP 690786.1|	59.7	2.91E-11	10717	Bacillus phage phi105	*Bacillus subtilis*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a118768;3 total counts: 1047 Seed: 7 K: 25 length: 347	347	1.74419	gi|206600214|ref|YP 002241820.1|	90.9	3.44E-23	563123	Mycobacterium phage Ramsey	*Mycobacterium smegmatis str. MC2 155*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a119050;10 total counts: 6075 Seed: 15 K: 25 length: 629	629	1.74419	gi|593778368|ref|YP 009016208.1|	84	5.17E-18	691963	Rhodococcus phage ReqiPine5	*Rhodococcus hoagii*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a61291;3 total counts: 674 Seed: 2 K: 25 length: 236	236	1.74153	gi|388570814|ref|YP 006383797.1|	45.4	2.00E-06	1187128	Acinetobacter bacteriophage AP22	*Acinetobacter baumannii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a29416;19 total counts: 128119 Seed: 2 K: 25 length: 6724	6724	1.73988	gi|1068512423|ref|YP 009276106.1|	271	1.43E-78	1647473	Gordonia phage GRU3	*Gordonia malaquae*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a29962;5 total counts: 3288 Seed: 7 K: 25 length: 648	648	1.73563	gi|563398140|ref|YP 008857900.1|	77.4	6.86E-16	1414742	Arthrobacter phage vB ArS-ArV2	*Arthrobacter sp.*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a150174;3 total counts: 1110 Seed: 2 K: 25 length: 426	426	1.73563	gi|9635029|ref|NP 056694.1|	80.5	1.15E-17	78541	Streptococcus phage Sfi11	*Streptococcus sp.*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a116838;3 total counts: 618 Seed: 2 K: 25 length: 262	262	1.72519	gi|448244890|ref|YP 007392610.1|	45.1	1.73E-06	1116482	Pectobacterium phage phiTE	*Pectobacterium atrosepticum SCRI1043*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a88657;2 total counts: 472 Seed: 2 K: 25 length: 273	273	1.71759	gi|1068357954|ref|YP 009273284.1|	79.3	4.24E-18	1647470	Gordonia phage GMA1	*Gordonia malaquae*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a146554;3 total counts: 1817 Seed: 3 K: 25 length: 623	623	1.71591	gi|41179288|ref|NP 958506.1|	85.1	1.20E-18	139872	Lactobacillus prophage Lj928	*Lactobacillus johnsonii*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a73400;2 total counts: 365 Seed: 2 K: 25 length: 206	206	1.71341	gi|971748040|ref|YP 009201826.1|	77	1.00E-19	1739608	Lactobacillus phage CL2	*Lactobacillus paracasei*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a116936;2 total counts: 396 Seed: 2 K: 25 length: 244	244	1.71311	gi|158079460|ref|YP 001504273.1|	51.6	8.28E-09	442493	Enterococcus phage phiEF24C	*Enterococcus faecalis*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a149390;2 total counts: 452 Seed: 2 K: 25 length: 210	210	1.71023	gi|1070105036|ref|YP 009290193.1|	94	2.58E-24	1837862	Weissella phage WCP30	*Weissella sp.*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a124699;3 total counts: 522 Seed: 3 K: 25 length: 220	220	1.70455	gi|971848929|ref|YP 009035508.1|	57.8	8.20E-11	1416334	Lactobacillus phage phi jlb1	*Lactobacillus gasseri ADH*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a155933;2 total counts: 633 Seed: 4 K: 25 length: 307	307	1.68404	gi|643217946|ref|YP 009036156.1|	98.2	9.92E-25	1486659	Bacillus phage Hakuna	*Bacillus thuringiensis*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a8778;2 total counts: 444 Seed: 3 K: 25 length: 266	266	1.67039	gi|589287594|ref|YP 009010198.1|	62	5.37E-12	1401669	Erwinia phage PhiEaH1	*Erwinia amylovora*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a118240;2 total counts: 479 Seed: 2 K: 25 length: 272	272	1.66544	gi|313768166|ref|YP 004061597.1|	45.1	5.39E-06	880159	*Bathycoccus sp. RCC1105 virus BpV1*	*Bathycoccus prasinos RCC1105*	Chlorophyta; Viridiplantae; Eukaryota	unclassified	Phycodnaviridae	dsDNA
a88367;5 total counts: 3217 Seed: 4 K: 25 length: 612	612	1.66013	gi|764162223|ref|YP 009126593.1|	200	5.15E-60	1538804	Vibrio phage VpKK5	*Vibrio parahaemolyticus*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a87757;8 total counts: 9851 Seed: 3 K: 25 length: 1279	1279	1.65934	gi|970580046|ref|YP 009193590.1|	118	6.89E-31	1572743	Mannheimia phage vB MhS 535AP2	*Mannheimia haemolytica*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a3464;2 total counts: 448 Seed: 4 K: 25 length: 321	321	1.65421	gi|593777360|ref|YP 009015205.1|	60.8	1.17E-11	1162290	Cronobacter phage CR9	*Cronobacter sakazakii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a2900;3 total counts: 631 Seed: 2 K: 25 length: 257	257	1.65027	gi|151266300|ref|YP 001333663.1|	77.4	1.62E-17	338473	Actinomyces phage Av-1	*Actinomyces naeslundii*	Actinobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a119791;7 total counts: 4210 Seed: 2 K: 25 length: 595	595	1.64964	gi|157325017|ref|YP 001468443.1|	100	1.16E-26	40522	Listeria phage A500	*Listeria monocytogenes WSLC1042*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a31868;3 total counts: 2017 Seed: 5 K: 25 length: 703	703	1.64835	gi|1070619841|ref|YP 009304275.1|	74.7	1.34E-14	1821557	Gordonia phage Lucky10	*Gordonia terrae*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a64513;3 total counts: 687 Seed: 2 K: 25 length: 237	237	1.64481	gi|971748533|ref|YP 009202450.1|	48.1	5.41E-08	1698711	Mycobacterium phage Lolly9	*Mycobacterium smegmatis str. MC2 155*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a149411;3 total counts: 766 Seed: 2 K: 25 length: 252	252	1.64286	gi|414090422|ref|YP 006990535.1|	44.3	5.88E-06	1204534	Clostridium phage phiMMP02	*Clostridioides difficile*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a66453;4 total counts: 996 Seed: 5 K: 25 length: 285	285	1.63243	gi|971751675|ref|YP 009205624.1|	93.6	4.30E-23	1175662	Pseudomonas phage PaMx42	*Pseudomonas aeruginosa*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a155141;2 total counts: 477 Seed: 2 K: 25 length: 306	306	1.63072	gi|90592623|ref|YP 529883.1|	160	1.56E-46	363555	Lactobacillus phage KC5a	*Lactobacillus gasseri*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a146813;3 total counts: 3069 Seed: 9 K: 25 length: 926	926	1.62703	gi|526177379|ref|YP 008241215.1|	185	1.04E-52	1327983	Cellulophaga phage phi18:3	*Cellulophaga baltica*	Bacteroidetes; Bacteria	Caudovirales	Podoviridae	dsDNA
a96090;3 total counts: 507 Seed: 2 K: 25 length: 213	213	1.62385	gi|151266296|ref|YP 001333659.1|	64.3	3.94E-13	338473	Actinomyces phage Av-1	*Actinomyces naeslundii*	Actinobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a148252;4 total counts: 837 Seed: 3 K: 25 length: 245	245	1.61983	gi|1070096285|ref|YP 009277923.1|	59.7	2.12E-11	1887651	Gordonia phage Nyceirae	*Gordonia terrae*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a119564;3 total counts: 930 Seed: 3 K: 25 length: 345	345	1.60963	gi|1070101647|ref|YP 009285827.1|	151	4.09E-44	1844477	Pseudomonas phage NP1	*Pseudomonas sp.*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a10171;2 total counts: 387 Seed: 2 K: 25 length: 213	213	1.60932	gi|338826838|ref|YP 004678752.1|	110	2.04E-29	1041524	Enterobacteria phage K30	*Escherichia sp.*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a14779;2 total counts: 342 Seed: 3 K: 25 length: 221	221	1.60633	gi|971763757|ref|YP 009216768.1|	45.4	1.56E-06	1701405	*Gokushovirinae GNX3R*	*na*	na	unclassified	Microviridae	ssDNA
a1742;2 total counts: 564 Seed: 4 K: 25 length: 292	292	1.59788	gi|593779801|ref|YP 009017628.1|	119	4.07E-32	691965	Rhodococcus phage ReqiPepy6	*Rhodococcus hoagii*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a146533;5 total counts: 4704 Seed: 2 K: 25 length: 977	977	1.59259	gi|372449804|ref|YP 005087028.1|	180	4.15E-53	1109717	Rhodococcus phage RRH1	*Rhodococcus rhodochrous*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a146624;4 total counts: 3208 Seed: 5 K: 25 length: 758	758	1.58421	gi|849250882|ref|YP 009147716.1|	125	4.80E-33	1560313	Lactococcus phage WRP3	*Lactococcus lactis*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a35573;3 total counts: 829 Seed: 3 K: 25 length: 295	295	1.58182	gi|1070103030|ref|YP 009287678.1|	94.7	1.75E-23	1838137	Propionibacterium phage PFR1	*Propionibacterium freudenreichii*	Actinobacteria; Bacteria	unclassified	unclassified	unclassified
a150131;2 total counts: 402 Seed: 2 K: 25 length: 220	220	1.57592	gi|163932155|ref|YP 001642345.1|	47.8	9.66E-08	139871	Lactobacillus johnsonii prophage Lj771	*Lactobacillus johnsonii*	Firmicutes; Bacteria	unclassified	unclassified	unclassified
a59363;5 total counts: 3352 Seed: 10 K: 25 length: 636	636	1.57447	gi|1068358199|ref|YP 009273940.1|	151	2.89E-42	1838080	Gordonia phage Vendetta	*Gordonia terrae*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a839;6 total counts: 1702 Seed: 2 K: 25 length: 318	318	1.55862	gi|48697428|ref|YP 024813.1|	72.4	2.26E-15	279303	Actinoplanes phage phiAsp2	*Actinoplanes sp. SN223/29*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a89492;2 total counts: 518 Seed: 4 K: 25 length: 241	241	1.54772	gi|563397579|ref|YP 008857343.1|	81.3	4.79E-20	1391428	Enterobacteria phage 4MG	*Escherichia coli K-12*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a88549;2 total counts: 594 Seed: 2 K: 25 length: 296	296	1.54138	gi|939536933|ref|YP 009168408.2|	61.2	1.82E-13	1622234	Citrobacter phage CVT22	*Citrobacter sp. TM1552*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a98953;2 total counts: 444 Seed: 2 K: 25 length: 292	292	1.53082	gi|971752893|ref|YP 009206906.1|	48.5	3.81E-07	1690456	Bacillus phage TsarBomba	*Bacillus sp.*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a122345;2 total counts: 557 Seed: 3 K: 25 length: 260	260	1.53017	gi|937456522|ref|YP 009168448.1|	73.2	1.07E-16	1622234	Citrobacter phage CVT22	*Citrobacter sp. TM1552*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a146785;2 total counts: 434 Seed: 2 K: 25 length: 234	234	1.52632	gi|418489112|ref|YP 007002966.1|	62.8	2.80E-13	37105	Lactobacillus phage JCL1032	*Lactobacillus delbrueckii subsp. lactis*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a2;3069 total counts: 35374508 Seed: 6 K: 25 length: 11549	11549	1.52282	gi|712916232|ref|YP 009103975.1|	271	2.98E-75	1161939	Enterococcus phage vB Efae230P-4	*Enterococcus faecium*	Firmicutes; Bacteria	Caudovirales	Podoviridae	dsDNA
a155472;2 total counts: 356 Seed: 2 K: 25 length: 215	215	1.51256	gi|1068511238|ref|YP 009274343.1|	76.3	2.43E-17	1647476	Tsukamurella phage TPA4	*Tsukamurella paurometabola*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a90116;2 total counts: 419 Seed: 2 K: 25 length: 241	241	1.46829	gi|588295080|ref|YP 009003341.1|	44.3	5.98E-06	1392231	Streptococcus phage 20617	*Streptococcus thermophilus DSM 20617*	Firmicutes; Bacteria	unclassified	unclassified	unclassified
a117786;2 total counts: 734 Seed: 2 K: 25 length: 328	328	1.4386	gi|29566753|ref|NP 818317.1|	115	1.02E-30	205879	Mycobacterium phage Omega	*Mycobacterium sp.*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a64062;2 total counts: 761 Seed: 2 K: 25 length: 345	345	1.43478	gi|1070106098|ref|YP 009291949.1|	97.8	2.93E-24	1792222	Acinetobacter phage LZ35	*Acinetobacter baumannii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a58823;3 total counts: 507 Seed: 3 K: 25 length: 211	211	1.43128	gi|56693176|ref|YP 164763.1|	90.9	1.10E-23	298338	Lactobacillus phage LP65	*Lactobacillus plantarum*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a150645;4 total counts: 1468 Seed: 2 K: 25 length: 368	368	1.42587	gi|589286930|ref|YP 009007125.1|	47	1.62E-06	1449437	Pseudomonas phage vB PaeP Tr60 Ab31	*Pseudomonas aeruginosa*	Proteobacteria; Bacteria	unclassified	unclassified	dsDNA
a30269;2 total counts: 378 Seed: 2 K: 25 length: 201	201	1.41294	gi|56693142|ref|YP 164729.1|	64.7	2.48E-13	298338	Lactobacillus phage LP65	*Lactobacillus plantarum*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a132959;2 total counts: 344 Seed: 3 K: 25 length: 214	214	1.41121	gi|363540839|ref|YP 004894409.1|	51.2	1.65E-08	1094892	*Megavirus chiliensis*	*Acanthamoeba*	Longamoebia; Amoebozoa; Eukaryota	unclassified	Mimiviridae	dsDNA
a100241;2 total counts: 326 Seed: 2 K: 25 length: 200	200	1.41	gi|906476402|ref|YP 009160402.1|	49.7	4.41E-08	1655660	*Microviridae Fen7895 21*	*na*	na	unclassified	Microviridae	ssDNA
a152403;3 total counts: 578 Seed: 3 K: 25 length: 214	214	1.40476	gi|238801907|ref|YP 002925110.1|	60.1	1.35E-11	646413	Streptococcus phage 5093	*Streptococcus thermophilus*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a149773;2 total counts: 397 Seed: 2 K: 25 length: 215	215	1.40465	gi|848469534|ref|YP 009145910.1|	101	4.31E-27	1220714	Rhizobium phage RHEph06	*Rhizobium etli GR56*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a31;6 total counts: 1996 Seed: 2 K: 25 length: 354	354	1.40465	gi|472340490|ref|YP 007674015.1|	91.3	6.52E-22	754049	Vibrio phage pYD21-A	*Vibrio sp. YD21*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a30650;2 total counts: 350 Seed: 4 K: 25 length: 215	215	1.39394	gi|937456504|ref|YP 009168430.1|	72.4	5.38E-16	1622234	Citrobacter phage CVT22	*Citrobacter sp. TM1552*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a147551;4 total counts: 932 Seed: 5 K: 25 length: 275	275	1.38406	gi|1070098374|ref|YP 009281105.1|	119	7.95E-33	1887647	Gordonia phage Ghobes	*Gordonia terrae*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a61026;4 total counts: 679 Seed: 2 K: 25 length: 201	201	1.38308	gi|1127298444|ref|YP 009333392.1|	50.8	1.76E-08	1922548	*Beihai picorna-like virus 119*	*Echinodermata*	Metazoa; Eukaryota	unclassified	unclassified	RNA
a60343;2 total counts: 456 Seed: 3 K: 25 length: 215	215	1.3814	gi|971765481|ref|YP 009218533.1|	55.5	4.17E-10	1655644	Parabacteroides phage YZ-2015a	*Parabacteroides distasonis*	Bacteroidetes; Bacteria	unclassified	Microviridae	ssDNA
a127578;2 total counts: 402 Seed: 3 K: 25 length: 258	258	1.37688	gi|1068359282|ref|YP 009275704.1|	67.4	6.35E-14	1622193	Gordonia phage Gsput1	*Gordonia sputi*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a89766;4 total counts: 1189 Seed: 2 K: 25 length: 290	290	1.35531	gi|1068357954|ref|YP 009273284.1|	119	1.01E-32	1647470	Gordonia phage GMA1	*Gordonia malaquae*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a123522;2 total counts: 323 Seed: 2 K: 25 length: 226	226	1.32743	gi|828805703|ref|YP 009143064.1|	63.2	2.20E-14	1357423	Sinorhizobium phage phiM12	*Sinorhizobium meliloti*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a115802;49 total counts: 671701 Seed: 2 K: 25 length: 13606	13606	1.30144	gi|151266296|ref|YP 001333659.1|	206	5.56E-55	338473	Actinomyces phage Av-1	*Actinomyces naeslundii*	Actinobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a29565;2 total counts: 334 Seed: 2 K: 25 length: 235	235	1.28511	gi|712912741|ref|YP 009099611.1|	44.3	3.36E-06	1498228	Rhizobium phage vB RleM PPF1	*Rhizobium leguminosarum*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a119947;3 total counts: 890 Seed: 6 K: 25 length: 325	325	1.26619	gi|971741821|ref|YP 009196306.1|	88.2	7.08E-23	1175657	Pseudomonas phage PaMx11	*Pseudomonas aeruginosa*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a119421;2 total counts: 443 Seed: 2 K: 25 length: 231	231	1.25541	gi|29135023|ref|NP 803653.1|	47.8	3.38E-07	169683	Pseudomonas phage phiKZ	*Pseudomonas aeruginosa*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a83435;2 total counts: 293 Seed: 3 K: 25 length: 200	200	1.195	gi|56693161|ref|YP 164748.1|	43.1	8.84E-06	298338	Lactobacillus phage LP65	*Lactobacillus plantarum*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a66771;2 total counts: 457 Seed: 2 K: 25 length: 207	207	1.1751	gi|937456472|ref|YP 009168397.1|	73.9	1.38E-16	1622234	Citrobacter phage CVT22	*Citrobacter sp. TM1552*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a149072;2 total counts: 344 Seed: 2 K: 25 length: 246	246	1.1748	gi|1070064936|ref|YP 009283050.1|	45.4	2.42E-06	1815509	Bacillus phage AR9	*Bacillus subtilis subsp. subtilis str. 168*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a88391;2 total counts: 667 Seed: 4 K: 25 length: 314	314	1.17391	gi|937456472|ref|YP 009168397.1|	147	1.50E-41	1622234	Citrobacter phage CVT22	*Citrobacter sp. TM1552*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a69455;2 total counts: 495 Seed: 4 K: 25 length: 257	257	1.17121	gi|226377745|ref|YP 002790794.1|	57.4	1.64E-10	632112	Lactobacillus phage Lb338-1	*Lactobacillus paracasei*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a155316;2 total counts: 319 Seed: 3 K: 25 length: 217	217	1.17012	gi|372450006|ref|YP 005087227.1|	70.5	2.47E-15	1109714	Rhodococcus phage REQ3	*Rhodococcus hoagii*	Actinobacteria; Bacteria	unclassified	unclassified	unclassified
a29718;2 total counts: 633 Seed: 3 K: 25 length: 341	341	1.15888	gi|399528988|ref|YP 006561033.1|	65.5	7.16E-13	1204517	Pseudomonas phage MP1412	*Pseudomonas aeruginosa PAO1*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a88507;2 total counts: 354 Seed: 2 K: 25 length: 243	243	1.11111	gi|906476392|ref|YP 009160396.1|	69.7	7.00E-15	1655659	*Gokushovirinae Fen7875 21*	*na*	na	unclassified	Microviridae	ssDNA
a90174;2 total counts: 468 Seed: 2 K: 25 length: 295	295	1.01695	gi|80159718|ref|YP 398462.1|	60.1	3.55E-11	12336	Clostridium phage c-st	*Clostridium botulinum C str. Stockholm*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a100393;2 total counts: 426 Seed: 3 K: 25 length: 220	220	1	gi|937456504|ref|YP 009168430.1|	77	1.14E-17	1622234	Citrobacter phage CVT22	*Citrobacter sp. TM1552*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a152874;2 total counts: 438 Seed: 3 K: 25 length: 284	284	1	gi|327198107|ref|YP 004306637.1|	43.9	7.20E-06	767806	Enterococcus phage EFRM31	*Enterococcus faecalis*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a150194;2 total counts: 344 Seed: 4 K: 25 length: 219	219	1	gi|985760152|ref|YP 009225673.1|	83.2	7.73E-20	1662330	Rhodobacter phage RcTitan	*Rhodobacter capsulatus YW1*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a115751;2 total counts: 374 Seed: 3 K: 25 length: 209	209	1	gi|151266296|ref|YP 001333659.1|	43.9	4.85E-06	338473	Actinomyces phage Av-1	*Actinomyces naeslundii*	Actinobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a88138;3 total counts: 1332 Seed: 2 K: 25 length: 498	498	1	gi|388542678|ref|YP 006299882.1|	96.7	4.13E-24	1141526	Pseudomonas phage vB Pae-Kakheti25	*Pseudomonas aeruginosa*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a147822;7 total counts: 2845 Seed: 4 K: 25 length: 412	412	1	gi|971759891|ref|YP 009213215.1|	139	1.69E-39	1690818	Streptomyces phage SF3	*Streptomyces flavovirens*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a87966;7 total counts: 3026 Seed: 6 K: 25 length: 480	480	1	gi|1070103030|ref|YP 009287678.1|	91.3	2.87E-21	1838137	Propionibacterium phage PFR1	*Propionibacterium freudenreichii*	Actinobacteria; Bacteria	unclassified	unclassified	unclassified
a65704;5 total counts: 1073 Seed: 3 K: 25 length: 231	231	1	gi|937456511|ref|YP 009168437.1|	104	1.23E-28	1622234	Citrobacter phage CVT22	*Citrobacter sp. TM1552*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a2425;2 total counts: 289 Seed: 2 K: 25 length: 207	207	1	gi|446730251|ref|YP 007173621.1|	46.2	7.75E-07	1206110	Lactobacillus phage phiAQ113	*Lactobacillus helveticus*	Firmicutes; Bacteria	Caudovirales	Myoviridae	dsDNA
a121873;2 total counts: 283 Seed: 2 K: 25 length: 200	200	1	gi|226377831|ref|YP 002790879.1|	51.2	1.41E-08	631345	*Solenopsis invicta virus 3*	*Solenopsis invicta*	Arthropoda; Metazoa; Eukaryota	unclassified	unclassified	unclassified
a159179;2 total counts: 433 Seed: 2 K: 25 length: 221	221	1	gi|640885164|ref|YP 009032398.1|	70.9	1.98E-15	1486427	Mycobacterium phage ZoeJ	*Mycobacterium smegmatis str. MC2 155*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a154270;3 total counts: 793 Seed: 4 K: 25 length: 320	320	1	gi|151266300|ref|YP 001333663.1|	102	5.47E-26	338473	Actinomyces phage Av-1	*Actinomyces naeslundii*	Actinobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a9189;2 total counts: 334 Seed: 2 K: 25 length: 200	200	1	gi|388570795|ref|YP 006383778.1|	47.8	1.87E-07	1187128	Acinetobacter bacteriophage AP22	*Acinetobacter baumannii*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a118010;3 total counts: 772 Seed: 2 K: 25 length: 254	254	1	gi|163932184|ref|YP 001642374.1|	103	7.27E-27	139871	Lactobacillus johnsonii prophage Lj771	*Lactobacillus johnsonii*	Firmicutes; Bacteria	unclassified	unclassified	unclassified
a157762;2 total counts: 330 Seed: 2 K: 25 length: 228	228	1	gi|937456465|ref|YP 009168390.1|	124	7.26E-36	1622234	Citrobacter phage CVT22	*Citrobacter sp. TM1552*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a149949;2 total counts: 454 Seed: 3 K: 25 length: 215	215	1	gi|435844466|ref|YP 007006582.1|	53.9	1.53E-09	1161931	Agrobacterium phage 7-7-1	*Agrobacterium sp. H13-3*	Proteobacteria; Bacteria	Caudovirales	Myoviridae	dsDNA
a115736;3225 total counts: 33384215 Seed: 6 K: 25 length: 10375	10375	1	gi|966201251|ref|YP 009191328.1|	278	2.31E-77	1747288	Enterococcus phage vB IME195	*Enterococcus faecalis*	Firmicutes; Bacteria	Caudovirales	Podoviridae	dsDNA

a58124;1283 total counts: 2159833 Seed: 5 K: 25 length: 1707	1707	1	gi|66395192|ref|YP 239479.1|	160	1.08E-42	320832	Staphylococcus phage 66	*Staphylococcus aureus*	Firmicutes; Bacteria	Caudovirales	Podoviridae	dsDNA
a5806;2 total counts: 572 Seed: 3 K: 25 length: 293	293	1	gi|966198655|ref|YP 009188488.1|	57.4	3.10E-10	1589270	Streptococcus phage Str-PAP-1	*Streptococcus parauberis*	Firmicutes; Bacteria	Caudovirales	Podoviridae	dsDNA
a145743;2 total counts: 471 Seed: 2 K: 25 length: 262	262	1	gi|937456458|ref|YP 009168383.1|	63.2	4.86E-13	1622234	Citrobacter phage CVT22	*Citrobacter sp. TM1552*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a154779;3 total counts: 942 Seed: 3 K: 25 length: 323	323	1	gi|41057303|ref|NP 958202.1|	62.8	7.36E-13	10761	Shigella phage Sf6	*Shigella flexneri*	Proteobacteria; Bacteria	Caudovirales	Podoviridae	dsDNA
a62341;3 total counts: 1220 Seed: 4 K: 25 length: 422	422	1	gi|338826904|ref|YP 004678817.1|	50.1	4.09E-07	981323	Gordonia phage GTE2	*Nocardia; Rhodococcus; Gordonia*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a147877;3 total counts: 1313 Seed: 4 K: 25 length: 440	440	1	gi|530546920|ref|YP 008410509.1|	63.2	1.22E-12	1052673	Mycobacterium phage Thibault	*Mycobacterium smegmatis str. MC2 155*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a119828;3 total counts: 1364 Seed: 5 K: 25 length: 451	451	1	gi|372449813|ref|YP 005087037.1|	134	4.40E-37	1109717	Rhodococcus phage RRH1	*Rhodococcus rhodochrous*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a63661;2 total counts: 479 Seed: 2 K: 25 length: 301	301	1	gi|764162114|ref|YP 009126495.1|	62	1.20E-12	1552735	Lactobacillus phage Ldl1	*Lactobacillus delbrueckii subsp. lactis*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a151973;2 total counts: 631 Seed: 5 K: 25 length: 306	306	1	gi|327198366|ref|YP 004306940.1|	67.8	7.10E-14	59241	Streptococcus phage Dp-1	*Streptococcus pneumoniae*	Firmicutes; Bacteria	Caudovirales	Siphoviridae	dsDNA
a146202;6 total counts: 3699 Seed: 5 K: 25 length: 635	635	1	gi|146329916|ref|YP 001210224.1|	240	2.19E-76	437329	Burkholderia phage BcepGomr	*Burkholderia cepacia*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a62462;5 total counts: 1641 Seed: 3 K: 25 length: 339	339	1	gi|399528722|ref|YP 006560759.1|	92.8	1.33E-22	1132026	Burkholderia phage KL1	*Burkholderia cenocepacia*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a147376;5 total counts: 1753 Seed: 7 K: 25 length: 376	376	1	gi|62362234|ref|YP 224159.1|	118	2.71E-31	101570	Enterobacteria phage ES18	*Salmonella enterica subsp. enterica serovar Typhimurium*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a29643;2 total counts: 737 Seed: 2 K: 25 length: 321	321	1	gi|1070106097|ref|YP 009291948.1|	144	6.53E-42	1792222	Pseudomonas phage NP1	*Pseudomonas sp.*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a11418;2 total counts: 484 Seed: 3 K: 25 length: 227	227	1	gi|162135148|ref|YP 001595889.1|	114	5.43E-31	462590	Pseudomonas phage YuA	*Pseudomonas aeruginosa*	Proteobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a117147;6 total counts: 3442 Seed: 3 K: 25 length: 595	595	1	gi|372450021|ref|YP 005087242.1|	168	1.12E-48	1109714	Rhodococcus phage REQ3	*Rhodococcus hoagii*	Actinobacteria; Bacteria	unclassified	unclassified	unclassified
Healthy bees RNA virome												
a332225;2 total counts: 397 Seed: 2 K: 25 length: 219	219	2.38813	gi|1068512422|ref|YP 009276105.1|	70.1	3.92E-15	1647473	*Gordonia phage GRU3*	*Gordonia rubripertincta*	Actinobacteria; Bacteria	Caudovirales	Siphoviridae	dsDNA
a18498;2 total counts: 429 Seed: 2 K: 25 length: 236	236	2	gi|712916216|ref|YP 009103959.1|	58.9	3.34E-11	1161939	*Enterococcus phage vB Efae230P-4*	*Enterococcus faecium*	Firmicutes; Bacteria	Caudovirales	Podoviridae	dsDNA

Supplementary Table 2 - Detection of *M. quadrifasciata* viruses in stingless bee samples: samples of healthy (H) and unhealthy bees (U) of four different meliponaries in Southern of Brazil (BL = Boqueirão do Leão, BP = Bom Principio and RL = Rolante) were tested for virus presence/absence via PCR/RT-PCR. The + symbol means positive samples for the detection of the respective virus. Viruses with DNA genomes were only tested for detection in samples from which the DNA was extracted, the same for RNA viruses in samples from which the RNA was extracted (cells in gray were not tested).

Locality	Year	Syndrome period	Health	Sample type	MqC	MqC1	MqC2	MqD	MqV1a	MqV1b	MqV2
BL	2014	During	U	DNA whole body	+	+					
BL	2014	During	U	DNA whole body	+	+					
BL	2014	During	U	DNA whole body	+	+					
BL	2014	During	U	DNA whole body	+	+	+				
BL	2014	During	U	DNA whole body	+	+					
BL	2014	During	U	DNA whole body		+					
BL	2014	During	U	DNA whole body		+					
BL	2014	During	U	DNA whole body	+						
BL	2014	During	U	DNA whole body	+	+	+				
BL	2014	During	U	DNA whole body	+	+					
BL	2014	During	U	DNA whole body							
BL	2014	During	U	DNA whole body		+					
BL	2014	During	U	DNA whole body							
BL	2014	During	U	DNA whole body		+					
BL	2014	During	U	DNA whole body		+					
BL	2014	During	U	DNA whole body							
BL	2015	During	U	DNA whole body		+	+				
BL	2015	During	U	DNA whole body		+	+				
BL	2015	During	U	DNA whole body	+	+	+				
BL	2015	During	U	DNA whole body	+	+	+				
BL	2015	During	U	DNA whole body	+	+					
BL	2015	During	U	DNA whole body	+	+	+				
BL	2015	During	U	DNA whole body	+	+					
BL	2015	During	U	DNA whole body	+	+					
BL	2015	During	U	DNA whole body		+	+				
BL	2015	During	U	DNA whole body		+	+				
BL	2015	During	U	DNA whole body	+	+					
BL	2015	During	U	DNA whole body	+	+					
BL	2015	During	U	DNA whole body	+	+					
BL	2015	During	U	DNA whole body	+	+	+				
BL	2015	During	U	DNA whole body	+	+	+				
BL	2015	During	U	DNA whole body	+	+	+				
BL	2015	During	U	DNA whole body	+	+	+				
BL	2015	During	U	DNA whole body	+	+	+				
BL	2015	During	U	DNA whole body	+	+					
BL	2015	During	U	DNA whole body	+	+	+				
BL	2015	During	U	DNA whole body	+	+	+				
BL	2015	During	U	DNA whole body	+						
BL	2015	During	U	DNA whole body	+		+				
BL	2015	During	U	DNA whole body	+	+	+				
BL	2015	During	U	DNA whole body	+	+	+				
BL	2015	During	U	DNA whole body	+	+					
BL	2015	During	U	DNA whole body	+	+					
BL	2015	During	U	DNA whole body							
BL	2015	During	U	DNA whole body		+					
BL	2015	During	U	DNA whole body							
BL	2015	During	H	DNA whole body	+	+					
BL	2015	During	H	DNA whole body			+				
BL	2015	During	H	DNA whole body	+	+	+				
BL	2015	During	H	DNA whole body		+					
BL	2015	During	H	DNA whole body		+	+				
BL	2015	During	H	DNA whole body	+						
BL	2015	During	H	DNA whole body	+	+					
BL	2015	During	H	DNA whole body	+						
BL	2015	During	H	DNA whole body							
BL	2015	During	H	DNA whole body							
BL	2015	During	H	DNA whole body		+	+				
BL	2015	During	H	DNA whole body	+	+	+				

BL	2015	During	H	DNA whole body	+	+					
BL	2017	During	U	DNA/RNA whole body	+	+		+			
BL	2017	During	U	DNA/RNA whole body	+	+		+	+	+	
BL	2017	During	U	DNA/RNA whole body		+		+	+	+	
BL	2017	During	U	DNA/RNA whole body	+	+	+	+	+	+	+
BL	2017	During	U	DNA/RNA whole body	+	+	+	+	+		+
BL	2017	During	U	DNA/RNA whole body		+	+	+			
BL	2017	During	U	DNA whole body	+	+	+				
BL	2017	During	U	DNA whole body	+	+	+				
BL	2017	During	U	DNA whole body	+	+	+				
BL	2017	During	U	DNA whole body	+	+	+				
BL	2017	During	U	DNA whole body	+	+	+				
BL	2017	During	H	DNA/RNA whole body		+		+			
BL	2017	During	H	DNA/RNA whole body				+			
BL	2017	During	H	DNA/RNA whole body		+		+			
BP	2017	During	U	DNA/RNA whole body							
BP	2017	During	U	DNA/RNA whole body		+					
BP	2017	During	U	DNA/RNA whole body		+					
BP	2018	During	U	cDNA whole body							
BP	2018	During	U	cDNA whole body							
BP	2018	During	U	cDNA whole body							
BP	2018	During	U	cDNA whole body							
BP	2018	During	U	cDNA whole body					+		
BP	2018	During	U	cDNA whole body							
BP	2018	During	U	cDNA whole body					+		
BP	2018	During	U	cDNA whole body							
BP	2018	During	U	cDNA whole body							
BP	2018	During	U	cDNA whole body							
BP	2018	During	U	cDNA whole body							
BP	2018	During	U	cDNA whole body					+		
BP	2018	During	U	cDNA whole body					+	+	
BP	2018	During	U	cDNA whole body							
BP	2018	During	U	cDNA whole body						+	
BP	2018	During	U	cDNA whole body							
BP	2018	During	U	cDNA whole body							
BP	2018	During	U	cDNA whole body						+	
BP	2018	During	U	cDNA whole body							
BP	2018	During	U	cDNA whole body							
BP	2018	During	U	cDNA whole body					+		
BP	2018	During	U	cDNA whole body							
BP	2018	During	U	cDNA whole body					+	+	
BP	2018	During	U	cDNA whole body					+	+	
RL	2018	During	U	cDNA whole body							
RL	2018	During	U	cDNA whole body							
RL	2018	During	U	cDNA whole body							
RL	2018	During	U	cDNA whole body							
RL	2018	During	U	cDNA whole body							
RL	2018	During	U	cDNA whole body							
RL	2018	During	U	cDNA whole body							
RL	2018	During	U	cDNA whole body							
RL	2018	During	U	cDNA whole body							
RL	2018	During	U	cDNA whole body							
RL	2018	During	U	cDNA whole body							
RL	2018	During	U	cDNA whole body							
RL	2018	During	U	cDNA whole body							
RL	2018	During	U	cDNA whole body							
RL	2018	During	U	cDNA whole body							
RL	2018	During	U	cDNA whole body							
RL	2018	During	U	cDNA whole body							
RL	2018	During	U	cDNA whole body					+		
RL	2018	During	U	cDNA whole body							
RL	2018	During	U	cDNA whole body							
RL	2018	During	U	cDNA whole body							

RL	2018	During	U	cDNA whole body							
RL	2018	During	U	cDNA whole body							
RL	2018	During	U	cDNA whole body							
RL	2018	During	U	cDNA whole body							
RL	2018	During	U	cDNA whole body							
RL	2018	During	U	cDNA whole body							
RL	2018	During	U	cDNA whole body							
RL	2018	During	U	cDNA whole body							
RL	2018	During	U	cDNA whole body							
RL	2018	During	U	cDNA whole body							
RL	2018	During	U	cDNA whole body					+		
RL	2018	During	U	cDNA whole body							
RL	2018	During	U	cDNA whole body							
RL	2018	During	U	DNA/RNA whole body							
RL	2018	During	U	DNA/RNA whole body							
RL	2018	During	U	DNA/RNA whole body							
BL	2017	Outside	H	DNA/RNA whole body		+		+			
BL	2017	Outside	H	DNA/RNA whole body	+	+		+			
BL	2017	Outside	H	DNA/RNA whole body		+		+		+	
BP	2017	Outside	H	DNA/RNA whole body							
BP	2017	Outside	H	DNA/RNA whole body							
BP	2017	Outside	H	DNA/RNA whole body						+	
BP	2018	Outside	H	cDNA whole body							
BP	2018	Outside	H	cDNA whole body							
BP	2018	Outside	H	cDNA whole body							
BP	2018	Outside	H	cDNA whole body							
BP	2018	Outside	H	cDNA whole body							
BP	2018	Outside	H	cDNA whole body							
BP	2018	Outside	H	cDNA whole body							
BP	2018	Outside	H	cDNA whole body							
BP	2018	Outside	H	cDNA whole body							
BP	2018	Outside	H	cDNA whole body							
BP	2018	Outside	H	cDNA whole body							
BP	2018	Outside	H	cDNA whole body							
BP	2018	Outside	H	cDNA whole body							
BP	2018	Outside	H	cDNA whole body							
BP	2018	Outside	H	cDNA whole body					+		
BP	2018	Outside	H	cDNA whole body							
BP	2018	Outside	H	cDNA whole body							
BP	2018	Outside	H	cDNA whole body					+		
BP	2018	Outside	H	cDNA whole body							
BP	2018	Outside	H	cDNA whole body							
BP	2018	Outside	H	cDNA whole body							
BP	2018	Outside	H	cDNA whole body							
BP	2018	Outside	H	cDNA whole body							
BP	2018	Outside	H	cDNA whole body							+
BP	2018	Outside	H	cDNA whole body					+		
BP	2018	Outside	H	cDNA whole body					+		
BP	2018	Outside	H	cDNA whole body					+		
BP	2018	Outside	H	cDNA whole body							
BP	2018	Outside	H	cDNA whole body					+		
BP	2018	Outside	H	cDNA whole body					+		
BP	2018	Outside	H	cDNA whole body						+	
BP	2018	Outside	H	cDNA whole body					+	+	
BP	2018	Outside	H	DNA/RNA whole body		+					
BP	2018	Outside	H	DNA/RNA whole body							
BP	2018	Outside	H	DNA/RNA whole body		+					
RL	2018	Outside	H	DNA/RNA whole body	+						
RL	2018	Outside	H	DNA/RNA whole body							
RL	2018	Outside	H	DNA/RNA whole body							
RL	2018	Outside	H	DNA/RNA whole body							
RL	2018	Outside	H	DNA/RNA whole body							
RL	2018	Outside	H	DNA/RNA whole body							

Supplementary Table 3 - Tests for the choice of BLAST type to be used for the retrieval and taxonomy of contigs. A sub-sample of contigs (49 contigs of unhealthy bees RNA viroma) was used in the blastP (tab 1) and blastX tests (tab 2), both against the nr database and against the viral RefSeq. In red are highlighted the candidate viral contigs used in the study.

Translated contig (amino acids)	**BlastP against nr**						**BlastP against RefSeq**					
query acc.ver	**subject acc.ver**	**name**	**% identity**	**alignment length**	**evalue**	**bit score**	**subject acc.ver**	**name**	**% identity**	**alignment length**	**evalue**	**bit score**
115738_6_total_counts:_2739_Seed:_8_K:_25_length:_448_translation_frame_3_reverse	YP_009337019.1	hypothetical protein 1 [Hubei picorna-like virus 74]	36.4	143	3.64E-19	93.6	YP_009337019.1	hypothetical protein 1 [Hubei picorna-like virus 74]	36.4	143	4.19E-22	93.6
115755_8_total_counts:_8948_Seed:_6_K:_25_length:_1124_translation_frame_1	YP_009342254.1	hypothetical protein 1 [Wuhan arthropod virus 3]	34.9	295	6.73E-43	170	YP_009342254.1	hypothetical protein 1 [Wuhan arthropod virus 3]	34.9	295	7.76E-46	170
115910_13_total_counts:_77920_Seed:_2_K:_25_length:_5913_translation_frame_2	APG76667.1	hypothetical protein 1 [Wuhan insect virus 11]	45.7	870	0.00E+00	731	YP_009342327.1	hypothetical protein 1 [Wuhan insect virus 11]	45.9	870	0.00E+00	728
117633_5_total_counts:_2738_Seed:_6_K:_25_length:_598_translation_frame_2	YP_009337788.1	hypothetical protein [Hubei picorna-like virus 68]	37.9	190	9.68E-24	108	YP_009337788.1	hypothetical protein [Hubei picorna-like virus 68]	37.9	190	1.12E-26	108
118987_6_total_counts:_1591_Seed:_4_K:_25_length:_287_translation_frame_3	YP_009336558.1	hypothetical protein 2 [Hubei orthoptera virus 1]	28.7	87	4.70E-07	56.6	YP_009336558.1	hypothetical protein 2 [Hubei orthoptera virus 1]	28.7	87	5.42E-10	56.6
119065_2_total_counts:_518_Seed:_2_K:_25_length:_276_translation_frame_3	BAW18990.1	hypothetical protein [Ralstonia phage RP12]	38.9	90	7.70E-16	79.7	YP_009207816.1	hypothetical protein [Ralstonia phage RSF1]	30.5	82	1.85E-06	46.2
119732_5_total_counts:_1999_Seed:_10_K:_25_length:_391_translation_frame_1_reverse	YP_009333576.1	hypothetical protein 1 [Beihai picorna-like virus 121]	38.8	116	1.08E-15	82.8	YP_009333576.1	hypothetical protein 1 [Beihai picorna-like virus 121]	38.8	116	1.25E-18	82.8
121873_2_total_counts:_283_Seed:_2_K:_25_length:_200_translation_frame_1	YP_002790880.2	putative structural polyprotein [Solenopsis invicta virus 3]	39.4	66	1.12E-05	51.2	YP_002790880.2	putative structural polyprotein [Solenopsis invicta virus 3]	39.4	66	1.29E-08	51.2
145575_124_total_counts:_517623_Seed:_5_K:_25_length:_4184_translation_frame_1	**ASM93489.1**	**NS1 [Lupine feces-associated densovirus 2]**	**37.1**	**510**	**2.32E-94**	**323**	**YP_009256211.1**	**putative nonstructural protein NS1 [Diaphorina citri densovirus]**	**31.8**	**453**	**1.66E-49**	**190**
145575_124_total_counts:_517623_Seed:_5_K:_25_length:_4184_translation_frame_2_reverse	**ASM93488.1**	**VP1 [Lupine feces-associated densovirus 2]**	**34.5**	**345**	**7.41E-44**	**180**	**YP_009256212.1**	**putative structural protein [Diaphorina citri densovirus]**	**26.6**	**173**	**5.49E-06**	**53.1**
147897_7_total_counts:_2386_Seed:_2_K:_25_length:_366_translation_frame_1_reverse	5CDD_C	Chain C, Structural Polyprotein, Vp2 [ABPV]	36.2	105	9.07E-24	100	NP_066242.1	capsid protein [Acute bee paralysis virus]	39.0	105	9.54E-26	102
149357_2_total_counts:_908_Seed:_2_K:_25_length:_416_translation_frame_2	YP_009352233.1	polyprotein [Diabrotica virgifera virgifera virus 2]	29.3	133	3.93E-16	84.3	YP_009352233.1	polyprotein [Diabrotica virgifera virgifera virus 2]	29.3	133	4.53E-19	84.3
149871_4_total_counts:_1261_Seed:_2_K:_25_length:_337_translation_frame_3_reverse	YP_009336506.1	hypothetical protein 1 [Hubei orthoptera virus 3]	31.4	105	7.15E-06	53.9	YP_009336506.1	hypothetical protein 1 [Hubei orthoptera virus 3]	31.4	105	8.24E-09	53.9
150472_5_total_counts:_1663_Seed:_2_K:_25_length:_344_translation_frame_3_reverse	YP_009336506.1	hypothetical protein 1 [Hubei orthoptera virus 3]	59.8	112	2.89E-35	137	YP_009336506.1	hypothetical protein 1 [Hubei orthoptera virus 3]	59.8	112	3.33E-38	137
151167_2_total_counts:_478_Seed:_3_K:_25_length:_273_translation_frame_1_reverse	ADF80789.1	replication-association protein, partial [Cyclovirus PKbeef25]	43.8	64	1.23E-09	60.5	YP_009021847.1	replication-associated protein [Dragonfly associated cyclovirus 3]	41.3	75	1.59E-11	60.5
23_106_total_counts:_85879_Seed:_2_K:_25_length:_835_translation_frame_2_reverse	AEL28798.1	replication-associated protein [Bat circovirus ZS/Yunnan-China/2009]	61.2	49	1.31E-10	71.2	YP_009506302.1	replication-associated protein [Pacific flying fox associated cyclovirus-3]	56.3	48	5.42E-13	69.7
29359_5_total_counts:_3883_Seed:_8_K:_25_length:_780_translation_frame_3_reverse	YP_009337064.1	hypothetical protein 1 [Hubei picorna-like virus 67]	29.0	131	9.52E-05	55.1	YP_009337064.1	hypothetical protein 1 [Hubei picorna-like virus 67]	29.0	131	1.10E-07	55.1
29755_9_total_counts:_7610_Seed:_2_K:_25_length:_902_translation_frame_2	YP_009336655.1	hypothetical protein 1 [Hubei picorna-like virus 76]	29.9	281	2.55E-13	81.6	YP_009336655.1	hypothetical protein 1 [Hubei picorna-like virus 76]	29.9	281	2.94E-16	81.6
30180_2_total_counts:_792_Seed:_2_K:_25_length:_351_translation_frame_3_reverse	YP_009336506.1	hypothetical protein 1 [Hubei orthoptera virus 3]	56.6	113	8.88E-36	139	YP_009336506.1	hypothetical protein 1 [Hubei orthoptera virus 3]	56.6	113	1.02E-38	139
30198_7_total_counts:_3618_Seed:_2_K:_25_length:_524_translation_frame_1	YP_009337788.1	hypothetical protein [Hubei picorna-like virus 68]	32.6	129	2.01E-06	57.8	YP_009337788.1	hypothetical protein [Hubei picorna-like virus 68]	32.6	129	2.32E-09	57.8
30839_3_total_counts:_767_Seed:_2_K:_25_length:_259_translation_frame_3	AXA52568.1	putative RdRp [Linepithema humile polycipivirus 1]	42.7	75	1.02E-07	57.8	YP_009407943.1	RNA-dependent RNA polymerase, partial [Lasius niger virus 1]	36.6	71	7.04E-09	52.8
356_26_total_counts:_96963_Seed:_2_K:_25_length:_3730_translation_frame_2	APG76480.1	hypothetical protein 2, partial [Hubei tombus-like virus 35]	51.3	517	7.89E-169	521	YP_009337674.1	hypothetical protein 2 [Changjiang tombus-like virus 22]	39.8	487	1.40E-103	339
3942_5_total_counts:_1878_Seed:_8_K:_25_length:_441_translation_frame_2_reverse	AZB48781.1	VP1, partial [Norovirus GIII]	26.6	124	1.66E-05	52.4	YP_009237901.1	VP1 [Norovirus GIII]	30.9	81	4.50E-06	47
58152_5_total_counts:_2250_Seed:_9_K:_25_length:_516_translation_frame_2_reverse	YP_009345893.1	hypothetical protein [Wuhan insect virus 12]	50.0	164	9.85E-48	176	YP_009345893.1	hypothetical protein [Wuhan insect virus 12]	50.0	164	1.14E-50	176
58401_11_total_counts:_3538_Seed:_2_K:_25_length:_357_translation_frame_1_reverse	YP_009337019.1	hypothetical protein 1 [Hubei picorna-like virus 74]	36.2	116	9.52E-15	79.3	YP_009337019.1	hypothetical protein 1 [Hubei picorna-like virus 74]	36.2	116	1.10E-17	79.3
58842_3_total_counts:_703_Seed:_2_K:_25_length:_227_translation_frame_1_reverse	AEK82102.1	polyprotein [Human parechovirus 2]	43.5	69	3.19E-09	61.6	YP_009508969.1	protein 2C [Dromedary camel enterovirus 19CC]	37.1	70	5.19E-12	61.2
59635_4_total_counts:_790_Seed:_2_K:_25_length:_231_translation_frame_1_reverse	YP_009337388.1	hypothetical protein 2 [Hubei picorna-like virus 64]	58.7	46	9.04E-10	63.2	YP_009337388.1	hypothetical protein 2 [Hubei picorna-like virus 64]	58.7	46	1.04E-12	63.2
60807_6_total_counts:_1537_Seed:_3_K:_25_length:_303_translation_frame_2	YP_009336506.1	hypothetical protein 1 [Hubei orthoptera virus 3]	34.8	92	7.09E-08	58.9	YP_009336506.1	hypothetical protein 1 [Hubei orthoptera virus 3]	34.8	92	8.17E-11	58.9
61026_4_total_counts:_679_Seed:_2_K:_25_length:_201_translation_frame_3	YP_009333392.1	hypothetical protein 1 [Beihai picorna-like virus 119]	38.6	44	1.49E-05	50.8	YP_009333392.1	hypothetical protein 1 [Beihai picorna-like virus 119]	38.6	44	1.71E-08	50.8
61384_15_total_counts:_5882_Seed:_12_K:_25_length:_421_translation_frame_2_reverse	ASM93488.1	VP1 [Lupine feces-associated densovirus 2]	37.8	119	1.80E-19	93.6	NP_694830.1	structural protein VP1 [Galleria mellonella densovirus]	34.2	79	2.00E-06	48.1
62223_3_total_counts:_1272_Seed:_2_K:_25_length:_407_translation_frame_2_reverse	NP_624351.1	capsid protein [Fusarium solani virus 1]	70.8	120	2.67E-52	179	NP_624351.1	capsid protein [Fusarium solani virus 1]	70.8	120	3.08E-55	179
6453_2_total_counts:_487_Seed:_2_K:_25_length:_236_translation_frame_3	YP_009337387.1	hypothetical protein 1 [Hubei picorna-like virus 64]	53.3	60	2.82E-13	73.2	YP_009337387.1	hypothetical protein 1 [Hubei picorna-like virus 64]	53.3	60	3.25E-16	73.2
7992_2_total_counts:_506_Seed:_2_K:_25_length:_248_translation_frame_3_reverse	NP_624351.1	capsid protein [Fusarium solani virus 1]	60.8	74	4.14E-21	95.1	NP_624351.1	capsid protein [Fusarium solani virus 1]	60.8	74	4.78E-24	95.1
87654_83_total_counts:_129393_Seed:_2_K:_25_length:_1587_translation_frame_1	**YP_004152328.1**	**Cap protein [Cyclovirus PKgoat21/PAK/2009]**	**37.5**	**168**	**6.00E-22**	**104**	**YP_004152328.1**	**Cap protein [Cyclovirus PKgoat21/PAK/2009]**	**37.5**	**168**	**6.92E-25**	**104**
87654_83_total_counts:_129393_Seed:_2_K:_25_length:_1587_translation_frame_2_reverse	**YP_008130363.1**	**replication association protein [Human cyclovirus VS5700009]**	**57.1**	**226**	**6.48E-88**	**281**	**YP_008130363.1**	**replication association protein [Human cyclovirus VS5700009]**	**57.1**	**226**	**7.47E-91**	**281**
87760_5_total_counts:_3323_Seed:_8_K:_25_length:_633_translation_frame_2	YP_009337788.1	hypothetical protein [Hubei picorna-like virus 68]	36.1	208	7.90E-28	120	YP_009337788.1	hypothetical protein [Hubei picorna-like virus 68]	36.1	208	9.11E-31	120
87907_9_total_counts:_11161_Seed:_5_K:_25_length:_1236_translation_frame_2_reverse	AAR19088.1	structural polyprotein, partial [Kashmir bee virus]	32.2	404	3.53E-44	174	NP_851404.2	structural polyprotein, partial [Kashmir bee virus]	31.4	408	2.26E-46	172
87919_8_total_counts:_5141_Seed:_4_K:_25_length:_682_translation_frame_3	YP_009336506.1	hypothetical protein 1 [Hubei orthoptera virus 3]	36.5	208	4.19E-39	154	YP_009336506.1	hypothetical protein 1 [Hubei orthoptera virus 3]	36.5	208	4.83E-42	154

Contig (nucleotide)	**BLASTx againt nr**							**BLASTx againt RefSeq**				
query acc.ver	**subject acc.ver**	**name**	**% identity**	**alignment length**	**evalue**	**bit score**	**frame**	**name**	**% identity**	**alignment length**	**evalue**	**bit score**
115738_6_total_counts:_2739_Seed:_8_K:_25_length:_448	YP_009337019.1	hypothetical protein 1 [Hubei picorna-like virus 74]	36.4	143	4.04E-19	93.6	-3/0	hypothetical protein 1 [Hubei picorna-like virus 74]	36.4	143	1.10E-23	93.6
115755_8_total_counts:_8948_Seed:_6_K:_25_length:_1124	YP_009342254.1	hypothetical protein 1 [Wuhan arthropod virus 3]	34.9	295	9.48E-43	170	1/0	hypothetical protein 1 [Wuhan arthropod virus 3]	34.9	295	2.58E-47	170
115910_13_total_counts:_77920_Seed:_2_K:_25_length:_5913	APG76667.1	hypothetical protein 1 [Wuhan insect virus 11]	45.7	870	0.00E+00	726	2/0	hypothetical protein 1 [Wuhan insect virus 11]	45.9	870	0.00E+00	723
117633_5_total_counts:_2738_Seed:_6_K:_25_length:_598	YP_009337788.1	hypothetical protein [Hubei picorna-like virus 68]	37.9	190	1.08E-23	108	2/0	hypothetical protein [Hubei picorna-like virus 68]	37.9	190	2.93E-28	108
118987_6_total_counts:_1591_Seed:_4_K:_25_length:_287	ATO59710.1	structural polyprotein [Solenopsis invicta virus 5]	33.8	74	2.65E-07	57.4	3/0	hypothetical protein 2 [Hubei orthoptera virus 1]	28.7	87	7.47E-12	57.4
119065_2_total_counts:_518_Seed:_2_K:_25_length:_276	BAW18990.1	hypothetical protein [Ralstonia phage RP12]	38.9	90	8.56E-16	79.7	3/0	hypothetical protein [Ralstonia phage RSF1]	30.5	82	2.06E-06	46.2
119732_5_total_counts:_1999_Seed:_10_K:_25_length:_391	YP_009333576.1	hypothetical protein 1 [Beihai picorna-like virus 121]	41.8	98	5.02E-12	72.4	-1/0	hypothetical protein 1 [Beihai picorna-like virus 121]	41.8	98	1.36E-16	72.4
121873_2_total_counts:_283_Seed:_2_K:_25_length:_200	YP_002790880.2	putative structural polyprotein [Solenopsis invicta virus 3]	39.4	66	1.25E-05	51.2	1/0	putative structural polyprotein [Solenopsis invicta virus 3]	39.4	66	3.39E-10	51.2
145575_124_total_counts:_517623_Seed:_5_K:_25_length:_4184	ASM93489.1	NS1 [Lupine feces-associated densovirus 2]	40.6	433	8.62E-94	321	1/0	putative nonstructural protein NS1 [Diaphorina citri densovirus]	31.8	453	1.27E-53	198
147897_7_total_counts:_2386_Seed:_2_K:_25_length:_366	5CDD_C	Chain C, Structural Polyprotein, Vp2 [IAPV]	36.2	105	1.01E-23	100	-1/0	ORF2 [Israeli acute paralysis virus]	36.2	105	3.67E-26	99.4
149357_2_total_counts:_908_Seed:_2_K:_25_length:_416	YP_009352233.1	polyprotein [Diabrotica virgifera virgifera virus 2]	29.3	133	3.35E-11	70.5	2/0	hypothetical protein 1 [Hubei orthoptera virus 3]	23.4	128	9.05E-14	64.7
149871_4_total_counts:_1261_Seed:_2_K:_25_length:_337	YP_009336506.1	hypothetical protein 1 [Hubei orthoptera virus 3]	31.4	105	7.94E-06	53.9	-3/0	hypothetical protein 1 [Hubei orthoptera virus 3]	31.4	105	2.16E-10	53.9
150472_5_total_counts:_1663_Seed:_2_K:_25_length:_344	YP_009336506.1	hypothetical protein 1 [Hubei orthoptera virus 3]	59.8	112	4.13E-35	137	-3/0	hypothetical protein 1 [Hubei orthoptera virus 3]	59.8	112	1.12E-39	137
151167_2_total_counts:_478_Seed:_3_K:_25_length:_273	ADF80789.1	replication-association protein, partial [Cyclovirus PKbeef25]	43.8	64	5.46E-10	61.6	-1/0	replication-associated protein [Dragonfly associated cyclovirus 3]	41.3	75	1.62E-13	61.6
23_106_total_counts:_85879_Seed:_2_K:_25_length:_835	AEL28798.1	replication-associated protein [Bat circovirus ZS/Yunnan-China/2009]	61.2	49	4.30E-10	69.7	-2/0	rolling circle replication initiator protein [Cyclovirus ZM36a]	56.3	48	2.63E-13	65.9
29359_5_total_counts:_3883_Seed:_8_K:_25_length:_780								hypothetical protein 1 [Hubei picorna-like virus 67]	29.0	131	4.89E-09	54.3
29755_9_total_counts:_7610_Seed:_2_K:_25_length:_902	YP_009336655.1	hypothetical protein 1 [Hubei picorna-like virus 76]	29.9	281	2.84E-13	81.6	2/0	hypothetical protein 1 [Hubei picorna-like virus 76]	29.9	281	7.72E-18	81.6
30180_2_total_counts:_792_Seed:_2_K:_25_length:_351	YP_009336506.1	hypothetical protein 1 [Hubei orthoptera virus 3]	56.6	113	9.86E-36	139	-3/0	hypothetical protein 1 [Hubei orthoptera virus 3]	56.6	113	2.68E-40	139
30198_7_total_counts:_3618_Seed:_2_K:_25_length:_524	YP_009337788.1	hypothetical protein [Hubei picorna-like virus 68]	32.6	129	1.52E-06	58.2	1/0	hypothetical protein [Hubei picorna-like virus 68]	32.6	129	4.15E-11	58.2
30839_3_total_counts:_767_Seed:_2_K:_25_length:_259	AXA52568.1	putative RdRp [Linepithema humile polycipivirus 1]	42.7	75	1.13E-07	57.8	3/0	RNA-dependent RNA polymerase, partial [Lasius niger virus 1]	36.6	71	1.85E-10	52.8
356_26_total_counts:_96963_Seed:_2_K:_25_length:_3730	APG76480.1	hypothetical protein 2, partial [Hubei tombus-like virus 35]	51.3	517	1.33E-170	525	2/0	hypothetical protein 2 [Changjiang tombus-like virus 22]	39.8	487	4.23E-106	342
3942_5_total_counts:_1878_Seed:_8_K:_25_length:_441	AMD33538.1	capsid protein [Norovirus GI]	30.6	111	2.55E-05	53.5	-2/0	VP1 [Norovirus GIII]	30.9	81	1.30E-07	47
58152_5_total_counts:_2250_Seed:_9_K:_25_length:_516	YP_009345893.1	hypothetical protein [Wuhan insect virus 12]	50.0	164	1.09E-47	176	-2/0	hypothetical protein [Wuhan insect virus 12]	50.0	164	2.98E-52	176
58401_11_total_counts:_3538_Seed:_2_K:_25_length:_357	YP_009337019.1	hypothetical protein 1 [Hubei picorna-like virus 74]	36.2	116	1.06E-14	79.3	-1/0	hypothetical protein 1 [Hubei picorna-like virus 74]	36.2	116	2.88E-19	79.3
58842_3_total_counts:_703_Seed:_2_K:_25_length:_227	AEK82102.1	polyprotein [Human parechovirus 2]	43.5	69	3.54E-09	61.6	-1/0	2C [Sichuan takin enterovirus]	35.7	70	5.99E-12	56.6
59635_4_total_counts:_790_Seed:_2_K:_25_length:_231	YP_009337388.1	hypothetical protein 2 [Hubei picorna-like virus 64]	58.7	46	3.18E-09	62	-1/0	hypothetical protein 2 [Hubei picorna-like virus 64]	58.7	46	8.65E-14	62
60807_6_total_counts:_1537_Seed:_3_K:_25_length:_303	YP_009336506.1	hypothetical protein 1 [Hubei orthoptera virus 3]	34.8	92	7.88E-08	58.9	2/0	hypothetical protein 1 [Hubei orthoptera virus 3]	34.8	92	2.14E-12	58.9
61026_4_total_counts:_679_Seed:_2_K:_25_length:_201	YP_009333392.1	hypothetical protein 1 [Beihai picorna-like virus 119]	38.6	44	1.65E-05	50.8	3/0	hypothetical protein 1 [Beihai picorna-like virus 119]	38.6	44	4.50E-10	50.8
61384_15_total_counts:_5882_Seed:_12_K:_25_length:_421	ASM93488.1	VP1 [Lupine feces-associated densovirus 2]	37.8	119	2.00E-19	93.6	-2/0	structural protein VP4 [Galleria mellonella densovirus]	31.5	89	6.87E-08	47.8
62223_3_total_counts:_1272_Seed:_2_K:_25_length:_407	NP_624351.1	capsid protein [Fusarium solani virus 1]	70.8	120	2.96E-52	179	-2/0	putative coat protein [Gremmeniella abietina RNA virus MS1]	48.3	120	1.58E-36	127
6453_2_total_counts:_487_Seed:_2_K:_25_length:_236	YP_009337387.1	hypothetical protein 1 [Hubei picorna-like virus 64]	53.3	60	5.39E-05	50.1	3/0	hypothetical protein 1 [Hubei picorna-like virus 64]	53.3	60	1.47E-09	50.1
7992_2_total_counts:_506_Seed:_2_K:_25_length:_248	NP_624351.1	capsid protein [Fusarium solani virus 1]	60.8	74	4.60E-21	95.1	-3/0	capsid protein [Penicillium stoloniferum virus S]	34.9	63	5.82E-06	40
87654_83_total_counts:_129393_Seed:_2_K:_25_length:_1587	AIZ46815.1	replication associated protein [Swine cyclovirus]	58.3	228	1.25E-86	278	-2/0	putative Rep [Bat cyclovirus GF-4c]	57.5	233	1.19E-90	276
87760_5_total_counts:_3323_Seed:_8_K:_25_length:_633	YP_009337788.1	hypothetical protein [Hubei picorna-like virus 68]	36.1	208	8.78E-28	120	2/0	hypothetical protein [Hubei picorna-like virus 68]	36.1	208	2.39E-32	120
87907_9_total_counts:_11161_Seed:_5_K:_25_length:_1236	AAR19088.1	structural polyprotein, partial [Kashmir bee virus]	32.2	404	3.93E-44	174	-2/0	hypothetical protein 2 [Hubei picorna-like virus 25]	31.7	366	1.14E-44	163
87919_8_total_counts:_5141_Seed:_4_K:_25_length:_682	YP_009336506.1	hypothetical protein 1 [Hubei orthoptera virus 3]	36.5	208	1.04E-38	152	3/0	hypothetical protein 1 [Hubei orthoptera virus 3]	36.5	208	2.82E-43	152

Supplementary Table 4 - Accession number (ID) of the sequences used in phylogenetic inferences.

IDs	Species
MqV2 phylogeny	
YP_009388491.1	*Lake Sinai Virus SA2*
ASS83296.1_	*Lake Sinai virus 2*
AJR19138.1	*Lake Sinai virus*
ASS83254.1	*Lake Sinai virus 1*
AYP65068.1	*Lake Sinai virus 3*
YP_009388495.1	*Lake Sinai Virus NE*
AXA52557.1	*Linepithema humile C virus 1*
YP_009011225.1	*Anopheline-associated C virus*
AOG30801.1	*Towan virus*
YP_009344965.1	*Jingmen tombus-like virus 2*
ASN64759.1	*Leptomonas pyrrhocoris RNA virus*
YP_009337040.1	*Changjiang tombus-like virus 21*
YP_009337674.1	*Changjiang tombus-like virus 22*
YP_009337712.1	*Hubei tombus-like virus 36*
YP_009342273.1	*Wenzhou tombus-like virus 17*
APG76480.1	*Hubei tombus-like virus 35*
YP_009336952.1	*Beihai tombus-like virus 18*
YP_009337190.1	*Wenling tombus-like virus 2*
YP_009336894.1	*Beihai tombus-like virus 10*
YP_009336965.1	*Hubei tombus-like virus 14*
YP_009337688.1	*Beihai tombus-like virus 7*
YP_009337155.1	*Changjiang tombus-like virus 12*
YP_009336861.1	*Shahe tombus-like virus 2*
BAU09527.1	*Pothos latent virus*
NP_619671.1	*Hibiscus chlorotic ringspot virus*
AGG23390.1	*Citrus yellow vein-associated virus*
AWS06679.1	*Ethiopia maize-associated virus*
ACJ03575.1	*Carrot mottle mimic virus*
NP_620846.3	*Pea enation mosaic virus 2*
AXN55932.1	*Red clover umbravirus*
YP_009336880.1	*Hubei tombus-like virus 19*
YP_009337113.1	*Hubei tombus-like virus 28*
APG76298.1	*Shangao tombus-like virus 1*
YP_009333257.1	*Hubei tombus-like virus 30*
ALV85423.1	*Diaphorina citri-associated C virus*
MqC1 and MqC2 phylogeny	
YP_008130364.1/YP_008130363.1	*Human cyclovirus VS5700009*
AMH87656.1/AMH87655.1	*Pacific flying fox-associated cyclovirus 3*
YP_009104365.1/YP_009104366.1	*Cyclovirus ZM36a*
ADD62479.1/ADD62480.1	*Cyclovirus TN18*
BAP81876.1/BAP81877.1	*Cyclovirus ZM41*
BAP81871.1/BAP81870.1	*Cyclovirus ZM01*
BAP81869.1/BAP81868.1	*Cyclovirus ZM32*
AIZ46815.1/AIZ46816.1	*Swine cyclovirus*
AGO59220.1/AGO59219.1	*Cyclovirus VN*
AIZ46821.1/AIZ46822.1	*Human cyclovirus VN-like*
BAP81882.1/BAP81883.1	*Cyclovirus ZM62*

ADY17984.1/ADY17985.1	*Dragonfly-associated cyclovirus 1*
YP_009513184.1/YP_009513183.1	*Dragonfly-associated cyclovirus 4*
YP_009506320.1/YP_009506319.1	*Cyclovirus PK5222*
AXL65887.1/AXL65888.1	*Arboreal ant-associated circular virus 1*
AFS65280.1/AFS65281.1	*Dragonfly-associated cyclovirus 5*
YP_009506293.1	*Bat-associated cyclovirus 8*
YP_009506324.1/YP_009506323.1	*Cyclovirus PK5034*
YP_004152332.1/YP_004152331.1	*Cyclovirus bat/USA/2009*
ARO38287.1/ARO38286.1	*Circovirus sp*
YP_009506285.1/YP_009506286.1	*Bat-associated cyclovirus 2*
YP_009362253.1/YP_009362252.1	*Bat cyclovirus GF 4c*
YP_009506313.1/YP_009506314.1	*Dragonfly-associated cyclovirus 8*
AXL65889.1/AXL65890.1	*Fly-associated circular virus 1*
ATP66708.1	*Rodent circovirus*
AKE49354.1/AKE49355.1	*Cyclovirus NI 204*
YP_009506329.1/YP_009506330.1	*Cyclovirus SL 108277*
YP_009021871.2/YP_009021870.2	*Human-associated cyclovirus 10*
AFS65290.1/AFS65289.1	*Dragonfly-associated cyclovirus 2*
Ref [35]	*Circo-like 1*
YP_271918.1/YP_271921.1	*Duck circovirus*
NP_065678.1/NP_065679	*Porcine circovirus*
YP_009423856.1/YP_009423857.1	*Bat circovirus*
YP_764455.1/YP_764456.1	*Raven circovirus*
Ref [35]	*Circo-like 2*

MqV1a and MqV1b phylogeny

AWK77852.1/AWK77853.1	*Bundaberg bee virus 2*
AWK23470.1/AWK23471.1	*Human blood-associated dicistrovirus*
YP_009337313.1/YP_009337314.1	*Hubei picorna-like virus 14*
YP_009345054.1/YP_009345055.1	*Wuhan millipede virus 3*
AIY53985.1/AIY53986.1	*Nilaparvata lugens C virus*
AKA63263.1/AKA63264.1	*Cricket paralysis virus*
NP_044945.1/NP_044946.1	*Drosophila C virus*
AZR39355.1/AZR39356.1	*Hypsignathus monstrosus dicistrovirus*
YP_009252204.1/YP_009252205.1	*Anopheles C virus*
NP_620562.1/NP_620563.1	*Triatoma virus*
AWK77884.1/AWK77885.1	*Hobart bee virus 1*
YP_009333496.1/YP_009333497.1	*Beihai picorna-like virus 84*
AYN75548.1/AYN75549.1	*Halhan virus 1*
YP_009336690.1/YP_009336691.1	*Wenling crustacean virus 2*
AFO53688.1/AFO53689.1	*Taura syndrome virus*
YP_009337654.1/YP_009337655.1	*Hubei picorna-like virus 25*
YP.164440.1/YP.164441.1	*Solenopsis invicta virus 1*
YP_009336557.1/YP_009336558.1	*Hubei orthoptera virus 1*
APG76667.1/APG76668.1	*Wuhan insect virus 11*
AXA52579.1/AXA52580.1	*Linepithema humile virus 1*
ATO59709.1/ATO59710.1	*Solenopsis invicta virus 5*
NP_066241.1/NP_066242.1	*Acute bee paralysis virus*
AHL83499.1/AHL83500.1	*Kashmir bee virus*
ABY57949.1/ABY57950.1	*Israeli acute paralysis virus*
YP_008888535.1/YP_008888536.1	*Formica exsecta virus 1*
YP_009336777.1/YP_009336778.1	*Wenzhou channeled applesnail virus 2*

APG76699.1/APG76700.1	*Beihai picorna-like virus 70*
YP_009337682.1/YP_009337683.1	*Wenzhou picorna-like virus 26*
YP_009333456.1/YP_009333457.1	*Beihai picorna-like virus 71*
APG76793.1/APG76794.1	*Beihai picorna-like virus 72*
APG78016.1/APG78017.1	*Beihai picorna-like virus 74*
AYN75554.1/AYN75555.1	*Halhan virus 3*
YP_009336994.1/YP_009336995.1	*Wenzhou picorna-like virus 28*
APG78539.1/APG78540.1	*Wenzhou picorna-like virus 29*
NP_049374.1	*Sacbrood virus*
YP_003622540.1	*Slow bee paralysis virus*
YP_009162630.1	*Bombyx mori iflavirus*
NP_853560.2	*Deformed wing virus*
YP.145791.1/	*Varroa destructor virus 1*

MqD phylogeny

AWV66973.1/AWV66974.1	*Ambidensovirus sp.*
ANG55951.1/ANG55948.1	*Human CSF-associated densovirus*
YP_006576512.1/YP_006576514.1	*Sibine fusca densovirus*
NP_694838.1/NP_694840.1	*Casphalia extranea densovirus*
YP_006589928.1/YP_006589930.1	*Papilio polyxenes densovirus*
AIT71975.1/AIT71974	*Hordeum marinum Itera-like densovirus*
NP_542609.1/NP_542611.1	*Bombyx mori densovirus 1*
YP_009021036.1/YP_009021038.1	*Danaus plexippus plexippus iteravirus*
YP.164339.1/YP.164341.1	*Dendrolimus punctatus densovirus*
YP_004678720.1/YP_004678721.1	*Helicoverpa armigera densovirus*
YP_009256211.1/YP_009256212.1	*Diaphorina citri densovirus*
AVH76852.1/AVH76854.1	*Bombus cryptarum densovirus*
NP_874376.1/NP_874377.1	*Myzus persicae densovirus*
YP_009362129.1/YP_009362131.1	*Dysaphis plantaginea densovirus*
YP_002887625.1/YP_002887627.1	*Culex pipiens densovirus*
AFK91980.1/AFK91983.1	*Helicoverpa armigera densovirus*
NP_899650.1/NP_694830.1	*Galleria mellonella densovirus*
NP_958099.1/NP_958101.1	*Mythimna loreyi densovirus*
NP_046813.1/NP_046815.1	*Diatraea saccharalis densovirus*
YP_007003823.1/YP_007003825.1	*Pseudoplusia includens densovirus*
NP_694824.1/NP_694823.1	*Junonia coenia densovirus*
AGO32210.1/AGO32212.1	*Acheta domestica densovirus*
NP_694843.1/NP_694842.1	*Planococcus citri densovirus*
YP_008766862.1/YP_008766863.1	*Solenopsis invicta densovirus*
ARI46485.1/ARI46488.1	*Ambidensovirus CaaDV2*
YP_009134732.1/YP_009134734.1	*Cherax quadricarinatus densovirus*
YP_009507340.1/YP_009507339.1	*Sea star-associated densovirus*
AFC75858.1/AFC75860.1	*Blattella germanica densovirus-like virus*
ASM93489.1/ASM93488.1	*Lupine feces-associated densovirus 2*
ASU47551.1/ASU47552.1	*Lone star tick densovirus 1*
AYG77882.1/AYG77881.1/AYG77880.1	*Chicken parvovirus*
NP_757371.1/NP_757369.1	*Porcine parvovirus*
AAA61405.1/AAA61406.1	*Mouse parvovirus 1*

CAPÍTULO 4

Delayed effects of low gene expression, and behavioral changes associated with a stingless bee annual syndrome

Este capítulo apresenta o seguinte artigo em preparação para publicação:

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Delayed effects of low gene expression, and behavioral changes associated with a stingless bee annual syndrome

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Abstract

Bee populations are declining around the world and what appears to be at the root of colony failure is the combination of different sub-lethal factors, such as habitat loss, malnutrition and agrochemicals. In Brazil, an annual syndrome affects colonies of the stingless bee *Melipona quadrifasciata*, causing the sudden death of workers. In our previous studies, no pathogen was consistently associated with the disease. Here we conducted an integrative and temporal survey on *M. quadrifasciata* managed colonies in order to further investigate the causes behind the syndrome by measuring individual- and colony-level traits. We suggest that both the lack of genetic variation in bee populations and environmental stressors contribute to disease outcomes. We have found that the incapacity to express important health-related genes (*cytochrome p450*, *vitellogenin*, *phenoloxidase*) two months before the outbreak is associated with symptom manifestation, suggesting poor metabolization of xenobiotics and weak immune responses in colonies that became unhealthy. Concomitantly, we observed a weight loss in foragers, change in pollen resources stored in bee colonies and a decrease in performance to control nest environment. Our findings corroborate theoretical studies proposing that bee collapses result from positive density dependence influenced by the combination of diverse sub-lethal factors, such as competition for resources, pathogens and agrochemicals.

Key-words: bee health, colony collapse, sub-lethal effects.

Introduction

The worldwide decrease in bee populations observed in the last decade is a matter of great concern. Colony collapses in North America and Europe, where numbers are better documented, are on average twice as high as historically (Genersch et al. 2010; Kulhanek et al. 2017). Some of these losses can be explained by the presence of pathogens or infectious agents (Evans and Schwarz 2011; Schwarz et al. 2015). Additionally, several other interacting stressors, such as climate change, habitat loss, malnutrition, agrochemicals and colony management practices were shown to reduce the fitness of bee populations (vanEngelsdorp and Meixner 2010; Goulson et al. 2015). Theoretical studies indicate that although multifactorial stresses could cause colony failure, this failure is most likely a result of a critical level of stress from the accumulation of sub-lethal factors, even without synergistic effects (Bryden et al. 2013). Mathematical models demonstrate that the reason why some colonies collapse while others do not, despite suffering from the same sub-lethal stresses, involves colony density (Khoury et al. 2011; Bryden et al. 2013).

Sub-lethal factors are those that do not cause the immediate death of individuals, but reduce individual fitness by cumulative or synergistic effects, eventually causing death later on. Such delayed effects are reported for many bee populations. Colonies of *Apis mellifera* parasitized by *Varroa destructor* and infected by *Deformed wing virus* (DWV) during summer and autumn are more susceptible to collapse in winter, probably due to immunosuppression caused by pathogens (Dainat et al. 2012; Barroso-Arévalo et al. 2019). Honey bee workers reared in pollen-stressed colonies develop completely, but as adults they are less likely to waggle dance, and, if they dance, the information about food location is less precise (Scofield and Mattila 2015). Bumblebee workers have impaired learning performance when exposed to sub-lethal doses of agrochemicals during any developmental stage (Smith et al. 2020). Delayed effects of gene expression may as well represent sub-lethal factors that contribute to the collapse of bee colonies. In *A. mellifera* the decrease in the expression of *defensin*, which encodes an antimicrobial peptide, was correlated to colony collapse months after (Barroso-Arévalo et al. 2019). Furthermore, the combination of low *defensin* expression with a decrease in the expression of *relish*, a gene that belongs to the immune deficiency (IMD) signalling pathway, results in a reduced chance of bee colony survival in a future infection with DWV and *Varroa* (Barroso-Arévalo et al. 2019). Honey bee colonies are also more likely to successfully overwinter if workers express more vitellogenin (*Vg*), which regulates immune function and longevity, in fall (Dainat et al. 2012; Steinmann et al. 2015).

In southern Brazil, beekeepers report an annual syndrome that usually occurs in late summer (frequently in March), often leading to the collapse of managed colonies of the stingless bee *Melipona quadrifasciata* (Díaz et al. 2017; Caesar et al. 2019). The main feature of this syndrome is the sudden death of worker bees. In some localities affected workers show a number of neurologic symptoms, such as tremors and paralysis, suggesting the implication of viruses. However, although the virome of unhealthy bees includes novel viruses related to those causing similar symptoms in *A. mellifera*, such as viruses from the family *Dicistroviridae* (Genersch and Aubert 2010; Caesar et al. 2019), they were not found consistently associated to unhealthy bees (Caesar et al. 2019). No pathogenic bacteria, *Nosema* or *Crithidia* were identified as causative agents of the syndrome either (Díaz et al. 2017).

Pollinator health is a complex trait. The absence of pathogens is not a sufficient condition for bee health, and social bees show an additional level of epidemiological complexity besides the individual and the population, i.e., the colony (López-Uribe et al. 2020). The use of biomarkers for each of these levels of complexity contributes to investigations on bee health and disorders. At the individual level, gene expression indicates the effect of certain factors, as for example the expression of cytochrome p450 genes, which indicates a response to xenobiotics. At the colony level, conventional measures, such as colony size, reveal about colony performance (López-Uribe et al. 2020).

Here we report an integrative and temporal study designed to investigate the factors underlying the annual syndrome of *M. quadrifasciata*. Our survey was conducted on three pairs of sister colonies kept in two separate localities, in order to determine the contribution of both the colony genetic background as well as the environment to the syndrome manifestation, measuring individual- and colony-level traits.

Materials and Methods

(a) Searching for genes differentially expressed during the syndrome

Initially, three *M. quadrifasciata* colonies were selected for transcriptomic analyses aiming to identify genes with differential gene expression during the syndrome. Two were sampled during the outbreak in March 2018 in meliponaries from Bom Princípio (BP; 29°31′2.30″S/51°17′29.00″W) and Estância Velha (EV; 29°38'50.316"S/51°10'23.592"W). Both colonies were manifesting syndrome symptoms, such as dead bees in front of the colony, or bees presenting tremors and paralysis. A third colony showed no symptoms during the outbreak, and was sampled in April (after the outbreak) in BP. Three bees from each colony (labeled U1, U2 and H, respectively) were collected and used for RNA extraction and transcriptome sequencing.

Total RNA of individual bees was extracted with TRIzol™ Reagent (Thermo Fisher Scientific, USA), following the manufacturer's recommendations. RNA yield was assessed with Qubit fluorometer (Invitrogen, USA) and the integrity was checked on a 1% agarose gel. For sequencing, aliquots of 2 µg RNA treated with TURBO DNase (Thermo Fisher Scientific, USA) from three foragers were pooled with respective colony samples and stored at -80 ºC until use. Transcripts were purified by polyA-tail selection, followed by library construction using TruSeq Stranded mRNA Library Prep Kit (Illumina, EUA). Single-end sequencing (read length = 150 nt) was performed on an Illumina NextSeq instrument, producing about 100 million reads per sample.

Trimmomatic v.0.36 was run with default parameters to remove low quality reads

(Bolger et al. 2014). Gene expression (*GE*) was estimated with *depth* command from Samtools v.1.3.1 (Li et al. 2009) by mapping the trimmed reads onto *M. quadrifasciata* genome (GenBank assembly accession: GCA_001276565.1) with GSNAP v. 2018-07-04 (Wu et al. 2016) and recovering the number of reads per gene. To normalize gene expression (*NGE*) among the three transcriptomes the following formula was used:

$$NGE = (100{,}000{,}000/n^{o}\ of\ mapped\ reads) * GE$$

Next, the similarity in gene expression (*SGE*) between transcriptomes was estimated by comparing *NGE* from healthy and unhealthy samples with the following formula:

$$SGE\ = (H + U)/(2 * max)$$

Where *H* is the *NGE* of healthy transcriptome, *U* is the *NGE* of one unhealthy transcriptome, and *max* is the largest *NGE* value between *H* and *U* being compared. The result ranges between 0.5 and 1, and genes were regarded as differentially expressed (DEGs) when the *SGE* was equal or lower than 0.7 in both comparisons of *H vs. U* transcriptomes. Hypothetical genes among DEGs were re-annotated with BLASTp versus nr database (cut-off 1e-5) (Altschul et al. 1990). DEGs with putative roles in bee health were selected for relative quantification with RT-qPCR or by enzymatic assay (see below).

(b) Monitoring bee colonies before, during and after an outbreak

In order to monitor key changes in several bee biological features, observations were made in colonies under semi-controlled conditions during six months in two localities, *i.e.,* Bom Principio (BP; 29°31′2.30″S/51°17′29.00″W) and Porto Alegre (PA; 30°2'4.7292"S/ 51°13'3.5724"W). The BP meliponary is located inside a small agricultural property where agrochemicals are regularly used. PA colonies were kept in the vicinity of a secondary forest located inside the University Campus. To control for genetic factors contributing to the syndrome, three colonies from BP (named BP1, BP2 and BP3) were divided in February 2018, resulting in three pairs of sister colonies. After six months, when both paired colonies became mature, the three sister colonies (named PA1, PA2 and PA3) were translocated to PA, and all colonies were then monitored monthly from December 2018 (Summer) to May 2019 (Autumn). Each colony was equipped with a datalogger device (model U23-001 HOBO Pro v2, version 3.6.2, ONSET, Brazil) to record within-hive temperature and humidity. Records were made daily every six hours during the experiment and downstream analyses were conducted with the daily lowest temperature (6 a.m.) and the highest humidity (12 p.m.).

(c) Pollen resources used by stingless bees

Aliquots of pollen stored by worker bees were collected with tweezers every month and stored in the laboratory at 4 °C. Because there was sometimes no stored pollen within hives, or storage inaccessible for sampling, a few other colonies from both meliponaries were sampled as well. Pollen was chemically processed by acetolysis (Erdtman 1952). Four slides were mounted for each sample with glycerin gelatine (Salgado-Labouriau 2007) and around 500 pollen grains were identified at the family, genus or species level. The number of pollen grains per plant family was quantified for each sample.

(d) Bee weight and glucose oxidase assay

With an entomological sucker, five foragers were collected monthly from each of the six colonies between December 2018 and April 2019. Bees were brought to the laboratory alive, weighted, decapitated and heads stored separately from the remaining body at -80 °C. SpectraMax M2e fluorescence microplate reader was used to quantify glucose oxidase (GOX) activity using the Amplex® Red Glucose/Glucose Oxidase Assay Kit (Thermo Fisher Scientific, USA). Five heads per colony were pooled and macerated in 400µL of phosphate-buffered saline, centrifuged for 1 min at 5000 rpm and two separated aliquots of 10µL from the homogenate was used to estimate GOX activity. Fluorescence was measured with 544 nm excitation and 590 nm emission every minute and the linear slope of the reaction was calculated up to 20 min. The results are expressed as Relative Fluorescence Unit (RFU)/min/µL and normalized for body weight.

(e) Relative quantification of gene expression

Other five foragers were removed monthly from the experimental colonies between January and April 2019. They were transferred individually to separate vials containing 200 µL of RNAlater (Thermo Fisher Scientific, USA) and stored at -80 °C for RNA extraction and gene expression analysis by RT-qPCR. Total RNA was extracted from the whole body and quantified as previously explained. An aliquot of 1 µg RNA from each forager was used as input for first strand cDNA synthesis with the High-Capacity Reverse Transcription kit (Thermo Fisher Scientific, USA).

Five genes found differentially expressed in the initial transcriptomic analyses, and with a putative role in bee health were selected for monitoring worker bee expression patterns during the experiment: two vitellogenin domain-containing proteins (*Vg1 and Vg2),* RHD domain-containing protein (putative nuclear factor kappa-B; *NF-kB),* putative cytochrome p450 *(p450)* and phenoloxidase subunit 1 (*PO*; supplementary material, Table S1). Primer3 implemented in Geneious R11 (Kearse et al. 2012) was used to design primers based on the sequence of each of these genes in *M. quadrifasciata* genome (supplementary material, Table S2). Actin (*act*) and 40S ribosomal protein S5 (*rps5*) were used as reference for gene expression normalization (Evans et al. 2006; Brito et al. 2015; Freitas et al. 2019). StepOnePlus™ Real-Time PCR System (Applied Biosystems) was used for the RT-qPCR assays. Amplifications were carried out in 25 µL reaction solutions containing 12.5 µL cDNA (diluted to 1:30), 0.2 X SYBR™ Green I Nucleic Acid Gel Stain (Thermo Fisher Scientific, USA), 0.25 U of Platinum Taq DNA polymerase (Invitrogen, USA), 1 X PCR buffer (Tris-HCl 200 mM, pH 8,4, KCl 500 mM), 3 mM MgCl2, 0.1 mM of each dNTP, 0.2 µM of each specific primer.

Primer amplification efficiency (*E*) was calculated with qBASE+ software (Hellemans et al. 2007) from the slope of a five-point 1:10 serial dilution of calibrator cDNA samples, as follows: *E* = 10 (- 1/slope) (supplementary material, Table S2). Experimental setup of qPCR involved the sample maximization method (Hellemans et al. 2007), with three technical replicates for each sample, and inter-run calibrator samples were considered in calculations for run-to-run variation effects. For template quantification the qBASE+ pipeline was used (Hellemans et al. 2007), by first calculating the means and standard deviations of quantification cycle (Cq) values of technical replicates and relativizing Cq values based on the gene specific amplification efficiency. Next, the sample specific normalization factors were calculated by taking the geometric mean of the relative quantities of the two reference genes (*act* and *rps5*). The normalized Cq values were finally rescaled in relation to the sample with the lowest relative quantity (Hellemans et al. 2007), expressed in the form of calibrated normalized relative quantities (CNRQs), and used for statistical analyses.

(f) Statistical analyses

To identify differences in weight measures during the course of the monitoring survey, one-way ANOVA using “month” as factor was performed. In order to identify whether temperature and humidity were different among colonies during the outbreak period, specifically in those that became unhealthy, a t-test was conducted with data from March. Pearson’s correlation coefficient between foragers weight and nest temperature and humidity was calculated with PAST v.4.0 (Hammer et al. 2001). To access monthly extremes of temperature (t) and humidity (h) suffered by colonies, which also reflect the performance of worker bees in controlling their nest environment, a variable called delta (Δ = maximum value - minimum value) was calculated. The Δs were tested for their fit to normality and variance homogeneity using Shapiro's ($P < 0.05$) and Bartlett's ($P < 0.05$) tests, respectively. Box-Cox transformation with package MASS (Venables and Ripley 2002) in R (R Core Team 2019) was used for non-normal and non-homogeneous data. Differences in Δt and Δh were tested with one-way ANOVA using "month" and "colony" as factors. T-test and variance analyses were performed in R (R core team 2019), and the laercio package was used for mean comparisons with Tukey's test (Silva 2015).

Expression data of the selected genes was also tested for normality distribution and variance, with Box-Cox transformation used for non-normal and non-homogeneous data as mentioned above. To identify differences in our measures during the course of the monitoring survey, one-way ANOVA using "month" and "colony" as factors was performed for each variable. Similarly, a one-way ANOVA was used with each variable, to check for the differences within the "health status" of colonies (whether or not the syndrome manifested itself in March) and within the "intensity" of syndrome, since two of the affected colonies showed only mild effects of the syndrome (see below). Finally, a one-way ANOVA was performed for variables using "sister colonies" as factors to assess putative genetic effects on all variables, assuming that sister colonies*, i.e.,* obtained by division, are more related genetically than non-sister colonies. Considering that the syndrome occurs always in March, and that colonies have been monitored from January until April, a two-way ANOVA using either "colony", "sister colony", "health status" or "intensity" combined with "month" as factors was also performed for each variable, to identify interactions in specific periods during the course of our survey. Variance analyses and Tukey's test were performed in R (R core team 2019) as mentioned above. We used PAST v. 4.0 (Hammer et al. 2001) to evaluate combined variations in expression patterns of the five genes with one-way and two-way PERMANOVA, using Euclidean distances and 9999 permutations, in a procedure similar as described above for each gene individually.

Principal component analysis (PCA) was performed with PAST v. 4.0 (Hammer et al. 2001) to identify possible temporal patterns from combined variables measured from stingless bee colonies that eventually culminate with the syndrome. Two PCAs were run, discriminating variables that represent traits expressed at the level of individual bees, such as gene expression, from those that are manifested at the colony level, such as social immunity, stored pollen, weight, temperature and humidity. Raw data used in our statistical analyses are provided as supplementary material (Table S3).

Results

(a) Transcriptomic overview of differentially expressed genes

Transcriptome sequencing yielded 99,766,936, 102,034,731, 135,982,124, single-end high quality-trimmed reads for U1, U2 and H, respectively. From all reads, 87-99% mapped against the *M. quadrifasciata* genome. The comparison between transcriptomes of healthy and unhealthy bees revealed 558 DEGs, from which 212 were hypothetical genes. Based on BLAST hits of the hypothetical genes to characterized genes from the *nr* database, 108/212 *M. quadrifasciata* DEGs were re-annotated (supplementary material, Table S1).

From total DEGs, 493 were down-regulated and 44 were up-regulated in unhealthy bees transcriptomes. Interestingly, among the most differentially expressed genes are genes involved in developmental processes, such as sensory organ development, methylation and behavior (supplementary material, Table S1). Only 21 DEGs showed inconsistent expression patterns. Looking for genes known for their role in bee health, five DEGs (*Vg1*: WN51_06142, *Vg2*: WN51_14077, *NF-kB*: WN51_13409, *p450*: WN51_04136 and *PO*: WN51_02761) were chosen for gene expression quantification using RT-qPCR and since five other DEGs (WN51_09191, WN51_04932, WN51_04931, WN51_07421, WN51_04930) that encode glucose dehydrogenase/oxidase are putatively involved in social immunity, the enzyme was quantified at the protein level.

(b) Behavioral changes of worker bees

Among the six colonies monitored in our study, four manifested symptoms of the syndrome in March 2019. Colonies BP2 and BP3 manifested the strongest symptoms, with some bees showing tremors and often paralysis, and high mortality of workers (~ 100 dead bees found in front of the hives). Their respective sister colonies PA2 and PA3 maintained in a separate locality became slightly unhealthy, since fewer deaths were observed in front of the hives (~ 10 dead bees) and bees did not manifest abnormal behavior. We rule out the possibility that the unhealthy bees died due to lethal doses of agrochemicals, since residue analyses conducted by NSF International Laboratories (Porto Alegre, Brazil) did not indicate contamination by agrochemical compounds in three pools of ~20 bees from unhealthy colonies (supplementary material, Table S4). Sister colonies BP1 and PA1 did not manifest the syndrome, suggesting that the genetic component predisposing to disease. We found a marked reduction in forager weight from January until March ($P < 0.0005$), when the syndrome occurred (Figure 1). The lowest average weight was reached in March, and was higher in colonies that remained healthy during the outbreak (0.064 g), as compared to slightly unhealthy (0.063 g) and unhealthy (0.060 g) colonies, although the differences are not statistically significant. From January to February we observed a sudden change in the pollen stored by worker bees, *i.e.,* its composition shifted from mostly *Eucalyptus* sp. to mostly *Mimosa bimucronata* (Figure 1).

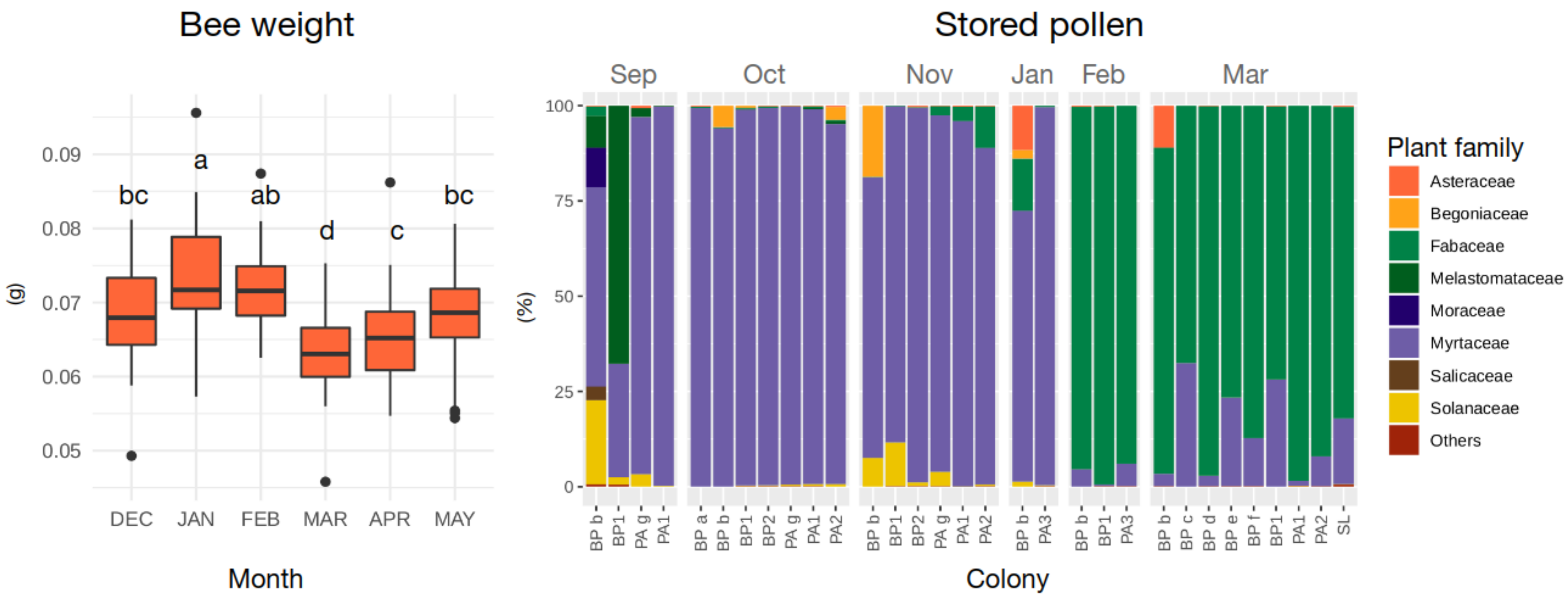

Figure 1: Changes in forager weight and stored pollen. (a) On the left a boxplot showing the temporal reduction in average forager weight. Lower case letters above bars represent significant differences ($P < 0.05$). **(b)** Barplot showing temporal variation in the percentage of pollen stored by workers, evidencing the change between January and February.

Bee weight reduction was accompanied by a similar reduction in the internal temperature of colonies ($r = 0.63$, $P = 0.0083$), and increase in humidity ($r = -0.51$, $P = 0.0431$). This pattern was more pronounced in colonies that became unhealthy during syndrome outbreak, such as sister colonies 2 (BP2 and PA2; $P < 0.0005$). Furthermore, temperature was lower ($P = 0.0006$) and humidity was higher ($P < 0.0005$) inside unhealthy colonies when the syndrome symptoms were first observed (Figure 2). Higher differences in daily temperature within colonies occurred in December and March ($P < 0.0005$), and BP colonies, which showed the most intense syndrome symptoms, had the highest differences in daily humidity ($P = 0.0022$, Figure 2).

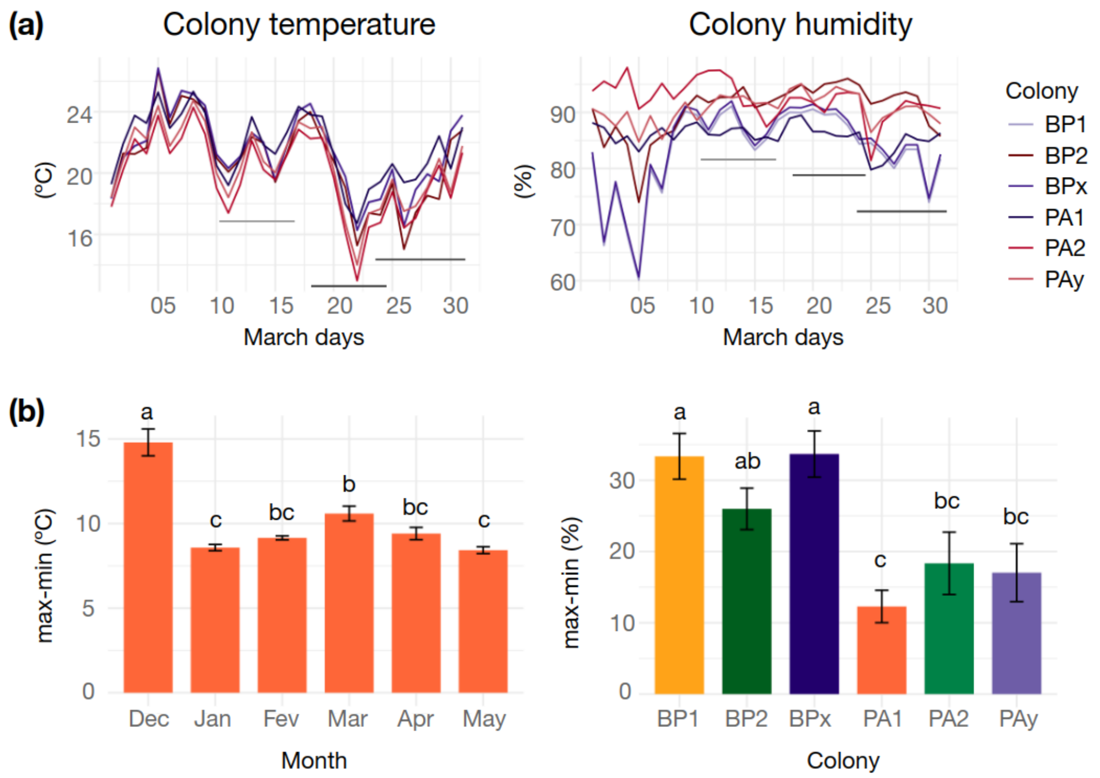

Figure 2: Temperature and humidity fluctuation. (a) Plot of the minimum daily temperature and maximum daily humidity in March. Horizontal bars indicate the days of syndrome manifestation, with higher (dark gray) or lower (light gray) intensity. Colonies affected by the syndrome (shades of red) show the lowest temperatures and highest humidities, especially during the outbreak period. **(b)** Barplot of the average monthly difference in maximum *vs.* minimum temperature (left) and average monthly difference in maximum *vs.* minimum humidity in different colonies (right). Bars indicate the standard error, and distinct lower case letters represent significant differences ($P < 0.05$).

(c)Temporal variation in forager gene expression

Transcriptome analysis revealed a large number of DEGs in unhealthy foragers, some of which are already known for their role in immunity and health of other bee species. Table 1 summarizes the genes selected for expression quantification in foragers sampled from the six colonies monitored in our study, their putative biological roles and the hypotheses behind their use as biomarkers for different aspects of colony health.

Table 1: Bee health-related genes differentially expressed in transcriptomes (*SGE*), comparing both unhealthy transcriotmes (U1 and U2) to the healthy (H). ANOVA results on data from the temporal survey comparing gene expression between colonies (C), months (M), sister colonies (SC), health status (HS) and syndrome intensity (I). Temporal variation in effects of C, SC, HS and I are shown as well (Interactions). For more details on the statistically significant comparisons, see electronic supplementary material (Figure S1).

				SGE		**Effect**					**Interactions**			
Gene	**Role**	**Hypothesis**	**References**	**U1**	**U2**	**C**	**M**	**SC**	**HS**	**I**	**CxM**	**SCxM**	**HSxM**	**IxM**
p450	Metabolism/detoxification of xenobiotics.	Increase in *p450* expression may indicate response to agrochemicals exposure.	Berenbaum and Johnson 2015.	0.67 (H > U)	0.59 (H > U)	ns	$P = 0.0243$	ns	ns	ns	$P = 0.0103$	ns	$P = 0.0213$	$P = 0.0205$
Vg1	Increase life span, antioxidant and immune function. Involved also in caste and task determination.	Increase in *Vg* expression may indicate better colony nutrition and performance.	Seehuus et al. 2006; Alaux et al. 2011.	0.57 (H < U)	0.63 (H > U)	ns	ns	ns	ns	ns	$P < 0.0005$	ns	ns	$P = 0.0023$
Vg2				0.60 (H > U)	0.53 (H > U)	$P = 0.0386$	ns	ns	ns	ns	$P < 0.0005$	$P = 0.0392$	$P = 0.0182$	$P = 0.0114$
PO	Activates melanogenesis.	Increase in *PO* expression may indicate a response to wound healing and defense against parasites.	Schmid-Hempel 2005.	0.69 (H < U)	0.65 (H > U)	$P = 0.0577$	ns	ns	ns	ns	ns	$P = 0.0149$	$P = 0.0163$	ns
NF-kB	Regulates humoral immune response (*e.g.* AMPs synthesis), but also cell survival and proliferation.	Increase in *NF-kB* expression may indicates a response to viral infection.	Nazzi et al. 2012; Ganesan et al. 2011.	0.62 (H > U)	0.56 (H > U)	ns	ns	$P = 0.022$	$P = 0.0303$	ns	$P = 0.0345$	$P = 0.0151$	ns	ns
GOX	Antimicrobial agent secreted by eusocial bees in larval food and honey stocks.	Colonies that secrete more GOX may indicate a stronger social immunity.	López-Uribe et al. 2017	0.59 – 0.66 (H > U)	0.50 – 0.62 (H > U)	ns	ns	ns	ns	ns	ns	ns	ns	ns
Combined expression pattern						$P = 0.0202$	ns	ns	ns	ns	$P < 0.0005$	$P = 0.008$	$P = 0.0541$	$P < 0.0005$

ns = not significant

Significant variation in *p450* expression was found across months, with peaks in March in both healthy and unhealthy colonies, and in January only in healthy colonies. In March foragers from healthy colonies expressed more *p450* compared to unhealthy colonies, similarly to what was found in our transcriptome analyses (Figure 3).

Vg2 and *PO* had similar patterns of expression during the course of the survey. Both showed significant differences between colonies (Table 1), with BP1 and BP2 showing the highest and lowest expression, respectively, on average (supplementary material, Figure S1). Furthermore, similarly to *p450*, bees that remained healthy during the outbreak period showed the highest expression in January (Figure 3). *Vg1* did not show association with the factors analyzed in our study (Table 1). Taking into account the hypotheses raised on Table 1, the lower expression of *p450*, *Vg2* and *PO* in bees that later became unhealthy suggests delayed effects in the response to xenobiotics, poor nutrition and weak immunity.

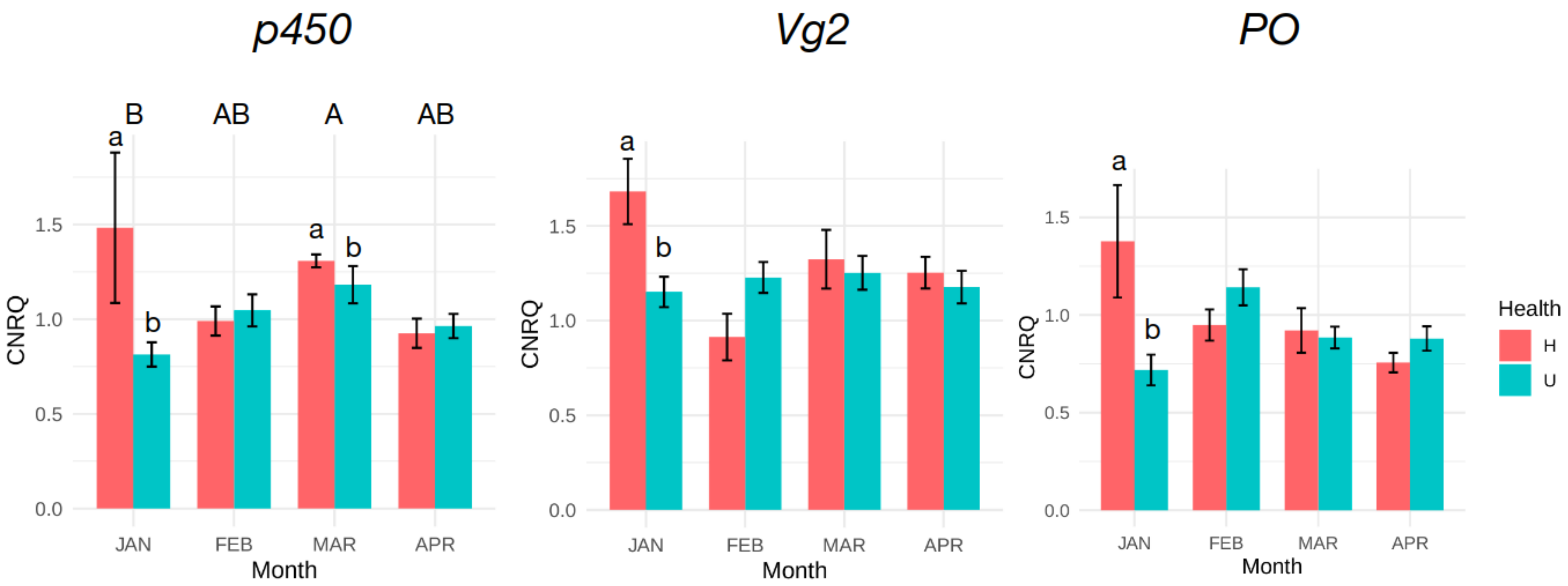

Figure 3: Relative expression of *p450*, *Vg2* and *PO*. Barplot comparing gene expression in foragers from healthy colonies (H), with those from colonies that showed signs of disease during syndrome outbreak (U)**.** Bars indicate the standard error; distinct uppercase letters designate differences among months and distinct lowercase letters indicate differences between healthy and unhealthy colonies within each month, according to Tukey's test ($P < 0.05$). Only significant differences are indicated by letters.

Among the five genes analyzed in our study, *NF-kB* was unique for showing significant differences in expression between pairs of sister colonies, suggesting a strong genetic influence on expression (Table 1). Although *NF-kB* is more expressed in healthy foragers on average (supplementary material, Figure S1), this effect is not consistent across months. The amount of GOX secreted by worker bees as part of their social immunity remained stable over the months, suggesting a constitutive expression pattern (with one outlier, see supplementary material, Figure S2).

(d) Combined analyses of traits

Considering that all measures performed in our longitudinal survey represent phenotypes, we ran PCA analyses in order to identify differences between months and colony health status. Therefore, we discriminated traits expressed at the individual bee from those expressed at the level of the whole colony. We considered that while gene expression patterns are observed at the individual level, stored pollen composition, as well as within-colony temperature and humidity represent colony-level traits. Similarly, although GOX is expressed at the level of the individual, it is part of a social behavior used to fight against potentially pathogenic microorganisms. Forager weight was also regarded as a colony level trait, considering that a positive correlation exists between bee weight and colony density (Jones et al. 2018). Overall, variation in individual-level traits does not explain the temporal changes that eventually culminate with the syndrome, even though *p450*, *Vg2* and *PO* are among genes that most contribute to data our distribution (Figure 4). Colony-level traits behave as better indicators of health, with factors daily highest humidity, daily humidity difference and daily lowest temperature explaining most of the data distribution (Figure 4).

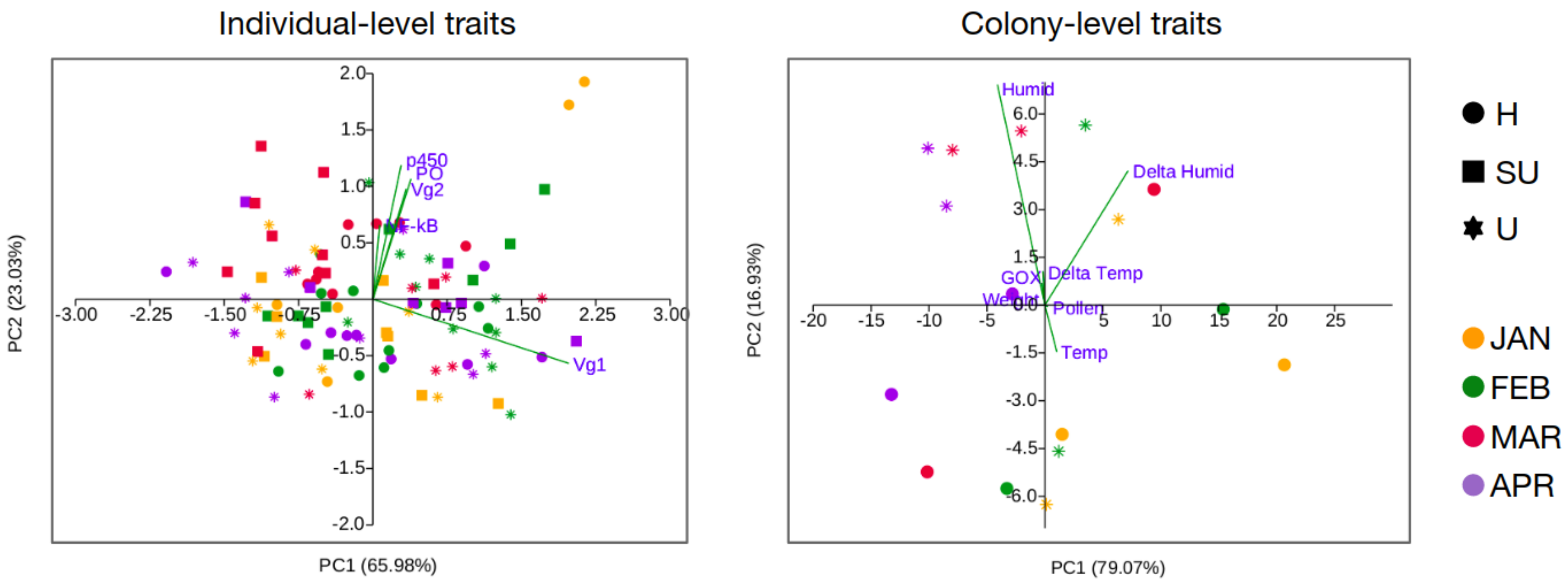

Figure 4: Principal component analysis (PCA) with individual- and colony-level traits. On the left, the plot shows the distribution of individuals according to the expression of five genes quantified by real time PCR. On the right the plot shows the distribution of colonies according to characteristics measured at the colony level. Symbols refer to healthy (H), slightly unhealthy (SU) and unhealthy (U) colonies. Samples from different months are plotted with distinct colors.

Discussion

Our temporal survey on six *M. quadrifasciata* managed colonies revealed that both genetic and environmental factors underlie the annual syndrome reported by beekeepers in Southern Brazil. Sister colonies (genetic relatedness of 0.375; see (Oliveira et al. 2015) presented a similar health status during the 2019 syndrome outbreak, even though they have been kept in different localities. Though, the symptoms of worker bees were stronger in two affected colonies kept nearby an agricultural setting.

(a) Bee domestication and responses to environmental factors

Domestication leads to the loss of genetic variation and gene expression diversity (Liu et al. 2019). The stingless bee *M. quadrifasciata* is a highly domesticated species, whose wild nests virtually disappeared in Southern Brazil (Fundação Zoobotânica 2014). The species is intensively managed for colony trading in the region, with some meliponaries maintaining up to 50 colonies. The practice of colony division is being performed since decades, and became more common with recent trade intensification (Jaffé et al. 2015). We suspect that the general use of this management practice, associated with the concomitant loss of wild nests, may have reduced the genetic diversity of *M. quadrifasciata* populations in Southern Brazil.

Reduced genetic variation may have affected stingless bee populations to properly respond to environmental stresses, such as pesticides, pathogens and competition for food resources with other bees, especially *A. mellifera*. By analyzing the differential gene expression of healthy *vs.* unhealthy *M. quadrifasciata* worker bees, and focusing on a subset of key genes, we suggest that the syndrome is manifested by bees' incapacity to respond to environmental stresses. We show that the expression of *M. quadrifasciata* genes homologous to *A. mellifera* genes related to health and immunity is significantly lower in foragers from colonies that became unhealthy two months before the outbreak period. In *A. mellifera* cytochrome p450 acts in detoxification of xenobiotics (Berenbaum and Johnson 2015), vitellogenin, besides being involved in caste and task determination, also protects against oxidative stress, enhances longevity and is a biomarker for good nutrition (Hartfelder et al. 2006; Seehuus et al. 2006; Alaux et al. 2011); and phenoloxidase activates melanogenesis needed for parasites defense and response to wound healing (Schmid-Hempel 2005).

Melipona development takes around 40 days from egg to adult (Alves et al. 2009), thus the *M. quadrifasciata* foragers sampled in March were juveniles in January. This may explain the observed delayed effect of gene expression. Considering the whole period, *PO* and *Vg2* showed similar patterns of gene expression with significant differences between colonies, and sister colonies responding similarly to the different environmental factors (*PO* interaction P = 0.0149, *Vg2* interaction P = 0.0392; supplementary material, Figure S1). It may also indicate a functional relationship between the *Vg2* and *PO*. *Vg2* encodes a secreted protein, with a putative signal peptide (Piulachs et al. 2003). The functional relationship between *Vg2* and *PO* suggests its role as a regulator of immune function.

We did not see any consistent relationship of *NF-kB* expression and the syndrome outbreak. In *A. mellifera* this gene was shown to be involved in the response against viral infections (Nazzi et al. 2012), and was used in our study to test the hypothesis that colonies fail for not being able to control viral proliferation. We have previously shown that although viruses did not seem to determine the outcome of the syndrome in all meliponaries, the relationship between the presence of viruses and the syndrome manifestation varies across localities (Caesar et al. 2019). In our transcriptome analyses we found an increase in the expression of *NF-kB* in healthy foragers, but the temporal survey using real time PCR quantification revealed the opposite result (Table 1; supplementary material, Figure S1). Our survey suggests that there might be a stronger genetic component in the variation of *NF-kB* expression (Table 1; supplementary material, Figure S1), which could mean that this gene is less responsive to the stressors faced by our bees. Furthermore, the *M. quadrifasciata* genome contains another *NF-kB*-related gene (WN51_01536), bringing into question whether the gene chosen in our study indeed represents the *Apis* ortholog.

(b) Sub-lethal effects

Among the five genes analyzed in our survey, only *p450* showed a significantly higher level of expression during the outbreak period (Table 1, Figure 3). In honey bees, bumblebees and solitary bees, cytochrome p450 functions as a detoxifying agent and determine the sensitivity to agrochemicals (Manjon et al. 2018; Beadle et al. 2019). Even though we did not detect lethal doses of agrochemicals in colonies affected by the syndrome, Southern Brazil is the region where they are most used in agriculture (Pignati et al. 2017). Furthermore, the significant interaction of *p450* expression levels and month, with healthy foragers sampled in January showing the highest levels of expression, suggests that a poor metabolization of xenobiotics in January possibly results in sub-lethal effects that contribute to forager impairment later on. Our transcriptome analysis also suggests neurological and behavioral changes in bees affected by the syndrome, such as lower expressions of ADP/ATP translocase (WN51_03592), pheromone-binding protein (WN51_03399), chaoptin (WN51_11844) and neuropeptide (WN51_06770; supplementary material, Table S2). It was already shown that *M. q. anthidioides* and bumblebees, that had contact with neonicotinoids at juvenile stages, showed reduced brain development resulting in compromised mobility and learning performance in adults, thus affecting major colony activities such as foraging (Tomé et al. 2012; Smith et al. 2020).

Another sub-lethal effect suggested by our study is the exposure to pathogens. Similarly to *p450*, we detected a significantly reduced expression of *PO* in January in foragers from colonies that later manifest the syndrome. January might be characterized by a higher density of pollinators in general, including *A. mellifera*, creating opportunities for getting in contact with a larger diversity of pathogens. Stingless bees from Brazil sharing foraging areas with honey bees were found contaminated with viruses and the microsporidium *N. ceranae,* suggesting the occurrence of spillover from *A. mellifera* (Guimarães-Cestaro et al. 2020). To fight against pathogens *PO* was found up-regulated in honey bee larvae infected with *Paenibacillus larvae* (Chan et al. 2009), in pupae infested with *Varroa* (Tesovnik et al. 2017) and in *Apis* infected by *Deformed wing virus* (Mazzei et al. 2016). Considering that *Vg2* expression pattern at the colony level was similar to *PO*, we think that its function is also related to immunity. *Vg1*, on the other hand, was the gene with the highest relative expression in our study (*Vg1* CNRQ: 0.8 - 4.9; *Vg2* CNRQ: 0.4 - 2.3), but with no clear connection to the syndrome. Vitellogenin (*Vg*) plays an important role promoting longevity in honey bees (Münch et al. 2013), but homologous genes that diverged from *Vg* have specialized functions. In *A. mellifera*, *Vg-like-A* responds more to inflammatory and oxidative conditions and *vg-like-B* responds more to oxidative stress (Salmela et al. 2016). There are at least 3 paralogous vitellogenin genes in *M. quadrifasciata* genome (WN51_13813, WN51_04373, WN51_14077) and they might correspond to *Vgs* with specialized functions too.

Finally, pollen stress might have been an additional factor with sub-lethal effects. We detected weight loss of foragers from January to March (Figure 1), suggesting poor nutrition and/or developmental acceleration. Furthermore, we detected an abrupt change in pollen stored by worker bees, which shifted from mostly *Eucalyptus* to mostly *Mimosa* between January and February. Such a shift may result from competitive exclusion, since *M. quadrifasciata* apparently competes with *A. mellifera* for flowers (Wilms and Wiechers 1997). Similarly to agrochemicals, pollen stress can also lead to neurological impairment, as suggested by the compromised foraging and recruitment performance of honey bee workers if they were reared as larvae in a pollen-limited colony environment (Scofield and Mattila 2015). Moreover, pollen-stressed workers are known to become lighter, dying sooner, and some of them do not even perform the forage activity (Scofield and Mattila 2015). Two months after *M. quadrifasciata* starts to use *Mimosa*, which begins to bloom in February, we noticed a gradual recovery in foragers weight (Figure 1). In *A. mellifera*, which suffered reduction in head mass, immune system depletion and increase in DWV titles caused by antibiotics, the supply with pollen helped to recover body mass and immune response as by increasing *Vg* expression (Li et al. 2019).

(c) Individual level *vs*. colony level traits

It is now well established that combined sub-lethal effects are at the root of colony failures (Bryden et al. 2013; Lu et al. 2020). PCA of the factors evaluated in our study suggest that colony-level traits provide a better description of differences between health and disease in the *M. quadrifasciata* syndrome (figure 4), but such traits are themselves consequences of biological processes that occur at the individual level. Bee weight is a known proxy for colony density (Jones et al. 2018). Similarly, nest temperature and humidity are controlled by worker bees through specialized behaviors (Jones and Oldroyd 2006; Ayton et al. 2016), which are influenced by different sub-lethal factors that we inferred from our gene expression survey at the individual level. Surprisingly, social immunity evaluated in our study by the amount of glucose oxidase in the heads of worker bees was not affected by the factors that stimulate other immune responses assessed in our study such as *PO*. Nevertheless, this result is in agreement with previous findings showing that GOX is constitutively secreted by *A. mellifera* workers (López-Uribe et al. 2017). Honey bee nurses secrete it into larval jelly and foragers into honey (Bucekova et al. 2014).

Although four of the six colonies surveyed in our study manifested some degree of syndrome symptoms, none of them collapsed during the outbreak period. We think that the annual collapses reported for *M. quadrifasciata* colonies in Southern Brazil result from positive density dependence influenced by the combination of diverse sub-lethal factors, as suggested by mathematical modeling studies (Khoury et al. 2011; Bryden et al. 2013). Unfortunately, the complexity of causes behind colony collapses worldwide entangle efforts to sustain pollination services. Based on our findings, actions such as limiting the use of agrochemicals in the vicinity of managed colonies and providing natural polyfloral resources through the conservation of native forests, could help to prevent the annual *M. quadrifasciata* syndrome, and the loss of other native bee species.

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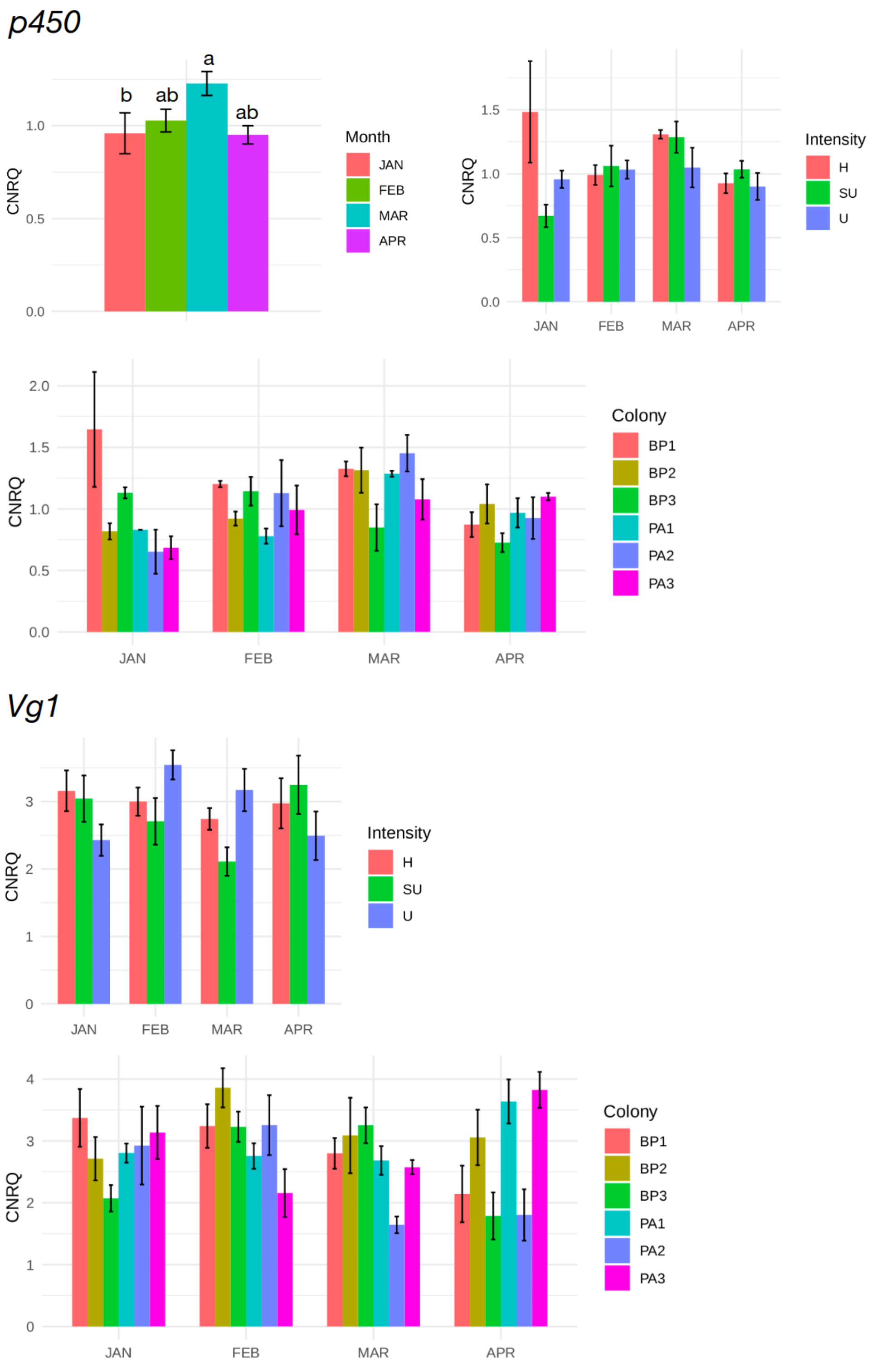
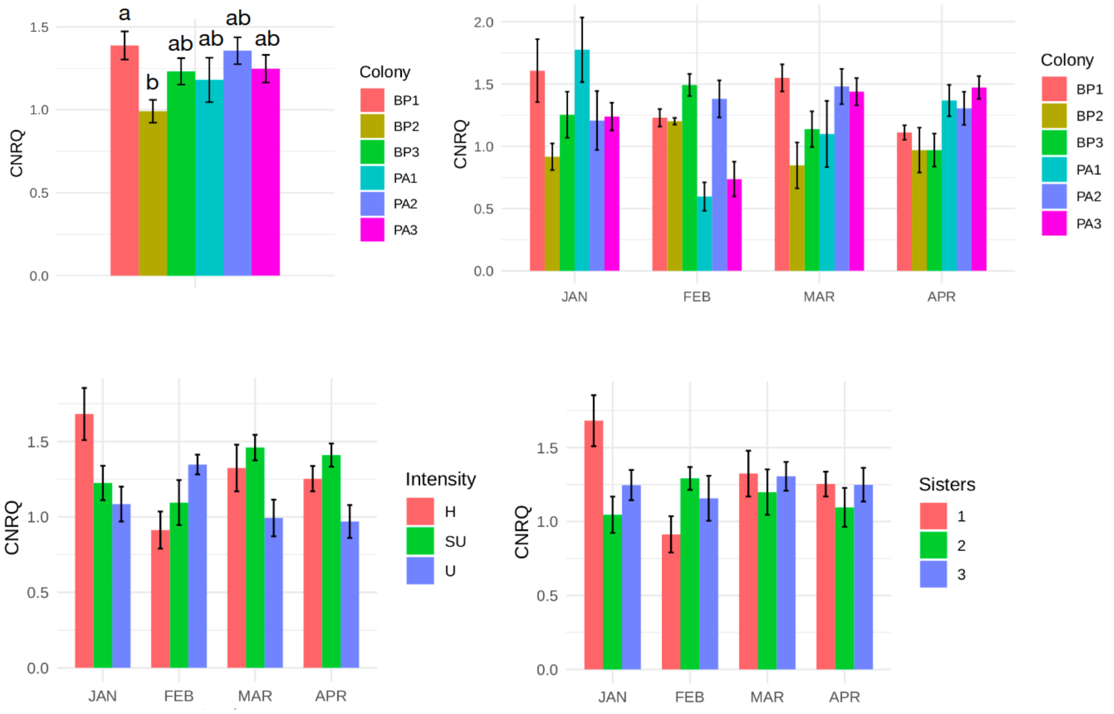


Figure S1: Relative gene expression of *p450, Vg1, Vg2, PO* and *NF-kB*. Barplots refer to comparisons that revealed statistical significance in variance analyses ($P < 0.05$) listed on Table 1.

Vg2



PO

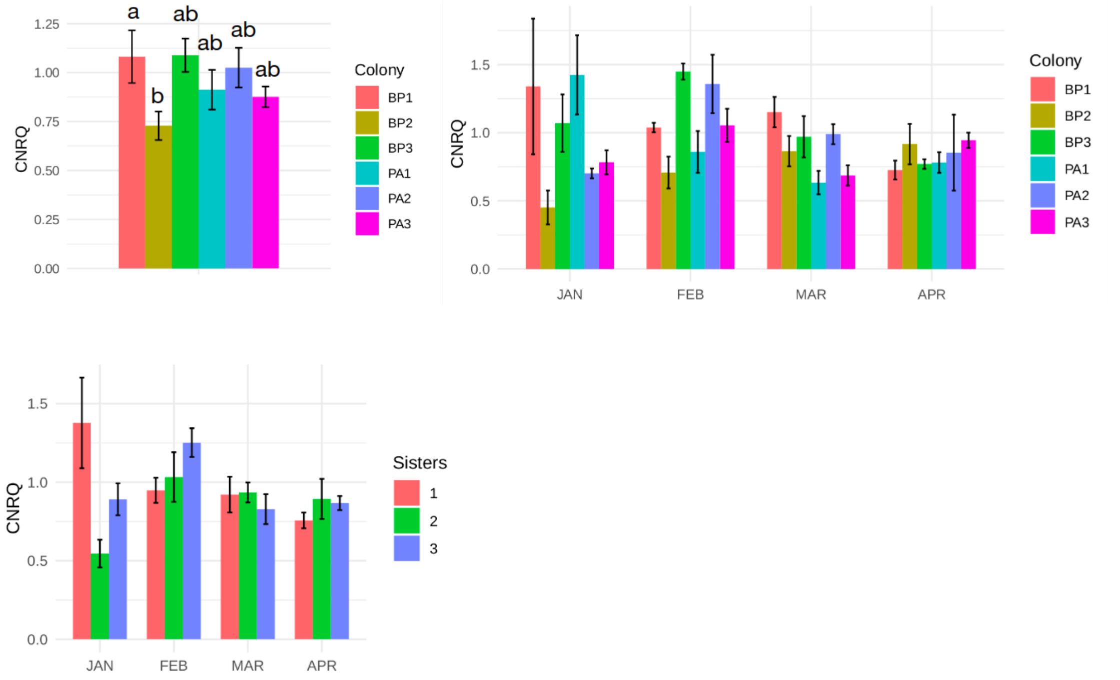


Figure S1: (Continuation).

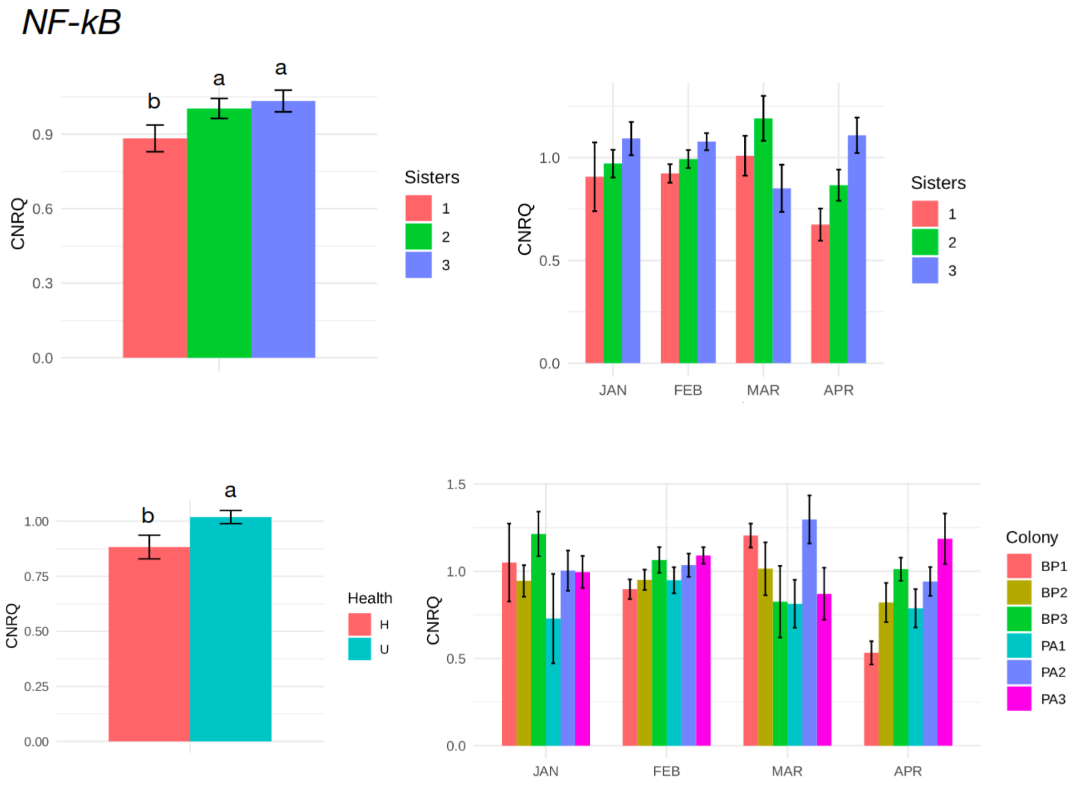


Figure S1: (Continuation).

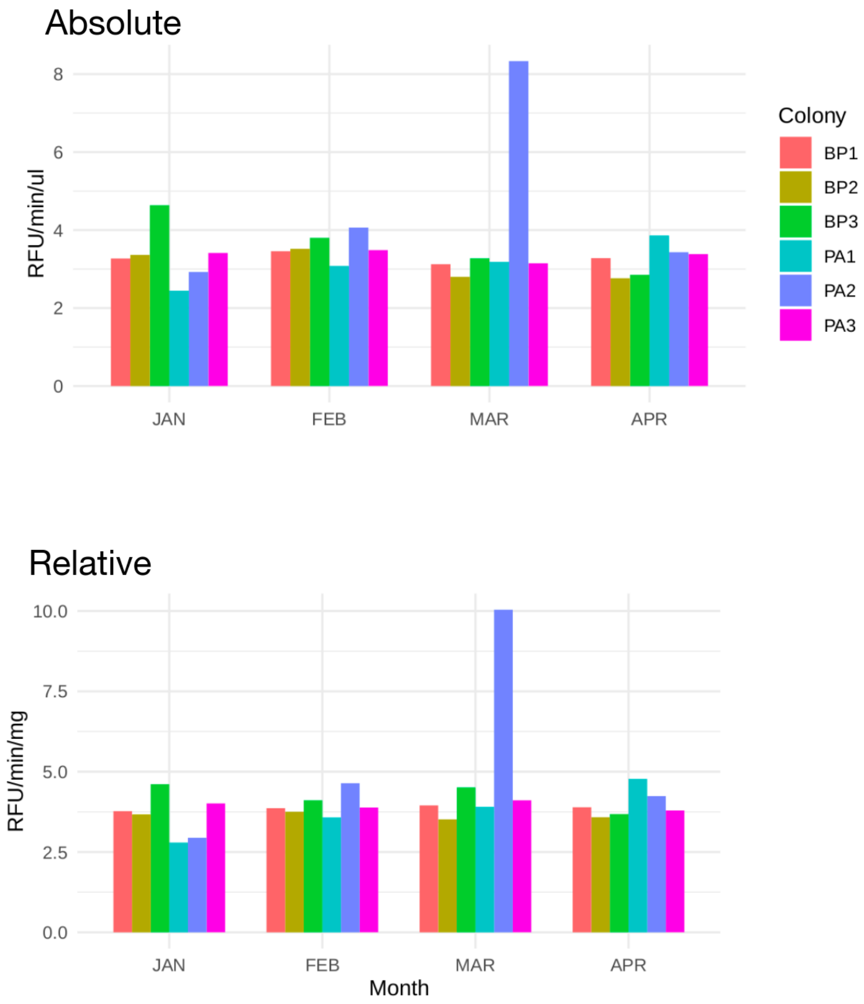


Figure S2: Glucose oxidase (GOX) activity in each colony and month. Above the absolute quantification and below the quantification relative to foragers weight of respective colony.

Table S1(a): list of differently expressed genes comparing U1 (unhealthy bees from Bom Princípio), U2 (unhealthy bees from Estância Velha) e H (healthy bees from Bom Princípio) transcriptomes and their respective normalized gene expression (NGE) and similarity in gene expression (SGE). Most differently expressed genes are above (light red) and genes chosen for quantification by RT-qPCR or enzymatic assay are also highlighted (green).

Protein	NGE U1	NGE U2	NGE H	SGE U1	SGE U2	Biological process
WN51_11205_hypothetical_protein	0.04	0.05	28.69	0.50	0.50	
WN51_05670_hypothetical_protein	0.13	104.14	27.59	0.50	0.63	
WN51_04193_jmjC_domain-containing_protein_4_isoform_X2	0.51	15.14	54.81	0.50	0.64	cellular process, metabolic process, viral RNA genome replication, localization, regulation of cell cycle.
WN51_07902_hypothetical_protein	0.27	0.12	23.85	0.51	0.50	
WN51_03592_ADP/ATP_translocase_4	0.45	0.02	22.13	0.51	0.50	cellular process, biological regulation, cellular component organization, localization, response to stimulus, developmental process, chemical synaptic transmission, determination of adult lifespan, reproductive process, locomotion, synaptic growth at neuromuscular junction, viral process, metabolic process.
WN51_12208_hypothetical_protein	0.98	0.00	47.54	0.51	0.50	
WN51_03399_Pheromone-binding_protein-related_protein_3	0.68	6.93	32.98	0.51	0.60	multicellular organismal process, behavior, response to pheromone, courtship behavior, multicellular organism reproduction, cellular process, biological regulation, copper ion transport, metabolic process, cellular component organization.
WN51_04637_protein_amnionless-like	2.66	0.04	114.01	0.51	0.50	cellular process, metabolic process, developmental process, regulation of biological process, actin cytoskeleton reorganization, multicellular organism development.
WN51_11844_Chaoptin	1.23	10.03	49.75	0.51	0.60	cellular process, cellular component organization, locomotion, sensory organ development, regulation of biological process, response to stimulus, homophilic cell adhesion via plasma membrane adhesion molecules, visual perception, metabolic process.
WN51_06770_Neuropeptide_FF_receptor_2	0.93	0.04	34.41	0.51	0.50	biological regulation, cellular process, response to stimulus, mating behavior and sex discrimination, multicellular organismal process, methylation.
WN51_13573_hypothetical_protein	0.56	0.56	20.61	0.51	0.51	
WN51_04190_putative_cytochrome_P450_12a5,_mitochondrial	0.78	0.22	21.50	0.52	0.51	
WN51_12311_Papilin	1.57	2.78	42.73	0.52	0.53	
WN51_12392_hypothetical_protein	1.16	78.75	30.63	0.52	0.69	
WN51_06061_Cubilin	4.54	1.76	107.10	0.52	0.51	
WN51_00353_Pituitary_homeobox_like_protein_Ptx1	0.93	0.08	21.51	0.52	0.50	
WN51_11275_probable_JmjC_domain-containing_histone_demethylation_protein_2C	1.78	4.33	41.11	0.52	0.55	
WN51_06580_hypothetical_protein	1.04	67.82	24.02	0.52	0.68	
WN51_09379_hypothetical_protein	1.65	0.00	37.90	0.52	0.50	
WN51_03763_Myogenic_factor_5	3.18	0.49	70.28	0.52	0.50	
WN51_03684_Reticulocyte-binding_protein_2_like_protein_a	1.11	81.06	24.05	0.52	0.65	
WN51_07801_Protein_yellow	0.98	2.02	20.75	0.52	0.55	
WN51_09070_orcokinin_peptides-like_isoform_X2	1.24	184.57	25.89	0.52	0.57	
WN51_09378_Homeobox_protein_araucan	1.17	4.03	24.22	0.52	0.58	
WN51_00177_hypothetical_protein	3.13	19.87	63.77	0.52	0.66	
WN51_05941_Knirps-related_protein	1.41	7.42	28.08	0.53	0.63	
WN51_10836_hypothetical_protein	1.26	9.49	24.47	0.53	0.69	
WN51_00173_hypothetical_protein	3.35	5.85	64.50	0.53	0.55	
WN51_05104_Fatty_acid_synthase	3.41	1.09	64.72	0.53	0.51	
WN51_08196_Protein_trachealess	1.32	8.65	24.75	0.53	0.67	
WN51_14534_cAMP-specific_3",5"-cyclic_phosphodiesterase	1.96	5.10	36.03	0.53	0.57	
WN51_12044_hypothetical_protein	2.18	2.44	36.45	0.53	0.53	
WN51_12673_1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase epsilon-1	1.90	106.74	31.38	0.53	0.65	
WN51_09419_hypothetical_protein	1.96	6.70	32.32	0.53	0.60	
WN51_07675_hypothetical_protein	2.92	1.56	45.12	0.53	0.52	
WN51_00523_hypothetical_protein	2.48	5.38	38.08	0.53	0.57	
WN51_02326_Sodium_channel_protein_para	4.35	13.22	60.89	0.54	0.61	
WN51_05779_Chitin_deacetylase-like_5	4.32	10.79	59.95	0.54	0.59	
WN51_00399_transposase	3.00	0.00	40.19	0.54	0.50	
WN51_07143_hypothetical_protein	6.93	32.47	90.06	0.54	0.68	
WN51_07303_HEAT_repeat-containing_protein_2	3.43	16.48	42.44	0.54	0.69	
WN51_03377_Cytochrome_c_oxidase_subunit_6B1	2.56	0.00	31.21	0.54	0.50	
WN51_13754_hypothetical_protein	4.02	13.99	48.40	0.54	0.64	
WN51_12010_hypothetical_protein	2.44	10.23	29.30	0.54	0.67	
WN51_12072_X-linked_retinitis_pigmentosa_GTPase_regulator	1.88	2.37	22.53	0.54	0.55	
WN51_04441_chloride_channel_CLIC-like_protein_1_isoform_X6	6.40	0.00	74.93	0.54	0.50	
WN51_14585_B1_protein	11.74	8.52	135.64	0.54	0.53	
WN51_07674_thyrotroph_embryonic_factor_isoform_X2	2.43	7.82	28.10	0.54	0.64	
WN51_08604_hypothetical_protein	10.00	21.85	113.07	0.54	0.60	
WN51_12846_hypothetical_protein	6.77	10.72	76.10	0.54	0.57	
WN51_00042_NADH-ubiquinone_oxidoreductase_chain_5	85.99	149.61	7.68	0.54	0.53	
WN51_00468_BBSome-interacting_protein_1	10.89	12.99	120.37	0.55	0.55	
WN51_07556_hypothetical_protein	7.63	1.22	83.97	0.55	0.51	
WN51_14222_hypothetical_protein	5.16	180.11	56.28	0.55	0.66	

WN51_00859_hypothetical_protein	10.13	1.14	109.13	0.55	0.51
WN51_11173_Torso-like_protein	7.70	5.86	82.73	0.55	0.54
WN51_01027_Organic_cation_transporter_1	6.16	12.35	64.87	0.55	0.60
WN51_02439_hypothetical_protein	31.11	24.67	2.96	0.55	0.56
WN51_09281_mucin-5AC-like_isoform_X3	8.25	20.91	84.93	0.55	0.62
WN51_03560_Synaptotagmin-14	2.09	83.75	21.38	0.55	0.63
WN51_01741_low_density_lipoprotein_receptor_adapter_protein_1-like_isoform_X3	3.76	5.24	38.38	0.55	0.57
WN51_03220_DnaJ_like_protein_subfamily_C_member_14	5.54	0.17	56.53	0.55	0.50
WN51_02823_adoMet-dependent_rRNA_methyltransferase_SPB1_isoform_X1	2.73	6.07	27.43	0.55	0.61
WN51_05305_Sensory_neuron_membrane_protein_1	8.23	9.69	82.36	0.55	0.56
WN51_00428_F-box/LRR-repeat_protein_14	2.95	3.60	29.41	0.55	0.56
WN51_04933_titin	6.26	12.60	61.91	0.55	0.60
WN51_04269_Tensin	8.21	17.65	80.43	0.55	0.61
WN51_12588_calphotin-like	7.78	12.78	75.68	0.55	0.58
WN51_14147_hypothetical_protein	2.12	0.94	20.15	0.55	0.52
WN51_12744_patched_domain-containing_protein_3_isoform_X2	5.99	1.80	56.55	0.55	0.52
WN51_01239_hypothetical_protein	10.12	0.35	95.05	0.55	0.50
WN51_14148_hypothetical_protein	3.30	0.00	30.93	0.55	0.50
WN51_14599_Protein_brown	14.08	7.18	128.92	0.55	0.53
WN51_08948_Mitochondrial_thiamine_pyrophosphate_carrier	9.19	25.08	80.90	0.56	0.66
WN51_06500_Ras-specific_guanine_nucleotide-releasing_factor_1	4.18	138.51	36.77	0.56	0.63
WN51_14628_RNA_pseudouridylate_synthase_domain-containing_protein_2	8.48	17.95	72.02	0.56	0.62
WN51_01490_hypothetical_protein	4.38	7.71	36.65	0.56	0.61
WN51_03687_Putative_polypeptide_N-acetylgalactosaminyltransferase_9	2.94	0.14	24.26	0.56	0.50
WN51_03909_hypothetical_protein	12.59	29.79	103.68	0.56	0.64
WN51_11144_Carboxypeptidase_D	8.93	14.59	72.54	0.56	0.60
WN51_05679_MAM_domain-containing_glycosylphosphatidylinositol_anchor_protein_1	13.33	8.55	106.02	0.56	0.54
WN51_08080_Glutamate_synthase_2_[NADH],_chloroplastic	15.92	5.12	126.16	0.56	0.52
WN51_07276_SCO-spondin	2.96	6.77	23.24	0.56	0.65
WN51_06649_Retinol_dehydrogenase_10-A	15.93	5.61	124.64	0.56	0.52
WN51_04261_Protein_abrupt	4.23	9.74	33.08	0.56	0.65
WN51_14382_Low-density_lipoprotein_receptor-related_protein_2	7.78	9.57	60.48	0.56	0.58
WN51_04327_Putative_zinc_metalloproteinase_T16A9.4	5.97	15.53	46.18	0.56	0.67
WN51_01357_Methylenetetrahydrofolate_reductase	6.59	12.99	50.08	0.57	0.63
WN51_01017_high_molecular_weight_rhoptry_protein_2,_putative	11.25	1.92	85.31	0.57	0.51
WN51_10562_Heart-_and_neural_crest_derivatives-expressed_protein_2	4.48	4.81	33.86	0.57	0.57
WN51_11848_Molybdenum_cofactor_sulfurase	12.33	6.32	92.34	0.57	0.53
WN51_09653_Histone_H2A	112.79	67.19	15.09	0.57	0.61
WN51_12862_ribonuclease_P/MRP_protein_subunit_POP5	3.52	0.00	26.09	0.57	0.50
WN51_01295_serine-rich_adhesin_for_platelets-like	15.78	1.25	116.69	0.57	0.51
WN51_02793_Cuticlin-1	7.88	4.74	58.11	0.57	0.54
WN51_14278_Histone-lysine_N-methyltransferase_SETMAR	3.77	0.01	27.82	0.57	0.50
WN51_14055_Vitellogenin-6	8.82	4.39	64.19	0.57	0.53
WN51_13358_Cytochrome_P450_6a2	13.20	30.87	95.14	0.57	0.66
WN51_09750_Homeobox_protein_MOX-2	60.47	23.50	8.40	0.57	0.68
WN51_06720_UPF0193_protein_EVG1	2.98	0.03	21.34	0.57	0.50
WN51_07515_Elongation_of_very_long_chain_fatty_acids_protein_7	8.06	8.06	57.56	0.57	0.57
WN51_02336_Multiple_PDZ_domain_protein	7.36	10.24	52.20	0.57	0.60
WN51_06361_Neuron_navigator_2	4.29	9.06	30.43	0.57	0.65
WN51_03256_Branched-chain-amino-acid_aminotransferase,_cytosolic	15.14	12.66	107.10	0.57	0.56
WN51_00618_Solute_carrier_organic_anion_transporter_family_member_3A1	3.90	3.13	27.42	0.57	0.56
WN51_14090_G/T_mismatch-specific_thymine_DNA_glycosylase	8.83	15.25	61.88	0.57	0.62
WN51_04406_division_abnormally_delayed_protein	12.68	11.47	88.76	0.57	0.56
WN51_07086_Receptor-type_tyrosine-protein_phosphatase_kappa	15.16	17.69	104.79	0.57	0.58
WN51_10823_Acyl-CoA_Delta(11)_desaturase	93.84	56.96	13.59	0.57	0.62
WN51_11601_MATH_and_LRR_domain-containing_protein_PFE0570w-like	5.36	0.05	36.85	0.57	0.50
WN51_06142_Vitellogenin [Vg1]	167.60	6.83	24.40	0.57	0.64
WN51_00299_Microtubule-associatedA	5.53	6.00	37.73	0.57	0.58
WN51_01963_ABC_transporter_G_family_member_23	17.99	3.18	122.40	0.57	0.51
WN51_09925_1-acyl-sn-glycerol-3-phosphate_acyltransferase_alpha	14.54	38.20	97.22	0.57	0.70
WN51_07017_Gamma-aminobutyric_acid_type_B_receptor_subunit_1	3.09	64.49	20.67	0.57	0.66
WN51_12667_Glycoprotein_3-alpha-L-fucosyltransferase_A	7.73	16.67	51.61	0.57	0.66
WN51_00306_hypothetical_protein	6.09	2.93	40.68	0.57	0.54
WN51_10563_Nose_resistant_to_fluoxetine_protein_6	13.71	1.68	91.48	0.57	0.51
WN51_02144_Utrophin	6.99	4.92	46.53	0.58	0.55
WN51_03774_UBX_domain-containing_protein_6	16.56	32.51	110.32	0.58	0.65
WN51_13725_hypothetical_protein	33.10	26.27	4.98	0.58	0.59
WN51_06050_dirigent_protein_10-like	35.03	51.30	5.29	0.58	0.55
WN51_12041_Tyrosine_aminotransferase	9.65	21.92	63.69	0.58	0.67
WN51_13753_tRNA_2-thiocytidine_biosynthesis_protein_TtcA	16.60	30.92	109.46	0.58	0.64
WN51_02659_hypothetical_protein	11.74	8.38	77.37	0.58	0.55
WN51_02937_Galanin_receptor_type_1	7.24	6.30	47.45	0.58	0.57
WN51_13283_hypothetical_protein	7.24	16.12	47.41	0.58	0.67
WN51_02934_pyroglutamylated_Rfamide_peptide_receptor-like_isoform_X2	5.80	13.09	37.74	0.58	0.67
WN51_13311_Tolloid-like_protein_2	18.69	3.22	121.31	0.58	0.51
WN51_08474_Xin_actin-binding_repeat-containing_protein_2	51.44	20.37	7.99	0.58	0.70
WN51_08417_skin_secretory_protein_xP2-like	3.46	1.41	22.17	0.58	0.53
WN51_12032_Spermine_oxidase	20.43	29.54	3.21	0.58	0.55
WN51_06482_hypothetical_protein	6.87	17.25	43.64	0.58	0.70
WN51_09251_Choline_O-acetyltransferase	3.28	66.20	20.83	0.58	0.66
WN51_04902_Spondin-1	19.01	23.42	120.10	0.58	0.60
WN51_01650_zinc_finger_protein_395	4.36	3.47	27.55	0.58	0.56
WN51_14190_Protein_trapped_in_endoderm-1	5.46	2.24	34.40	0.58	0.53
WN51_11332_hypothetical_protein	4.84	0.00	30.35	0.58	0.50
WN51_03729_Glutamate_receptor,_ionotropic_kainate_1	7.06	2.81	44.15	0.58	0.53
WN51_12996_Phospholipase_A2	4.37	7.05	27.35	0.58	0.63

WN51_08056_Protein_SDA1_like_protein	7.83	8.55	48.65	0.58	0.59
WN51_01347_Sn1-specific_diacylglycerol_lipase_alpha	10.37	24.29	64.18	0.58	0.69
WN51_04639_hypothetical_protein	4.67	1.58	28.75	0.58	0.53
WN51_12447_Regulator_of_microtubule_dynamics_protein_1	9.94	7.85	61.13	0.58	0.56
WN51_09769_myb-like_protein_M	10.98	16.46	67.48	0.58	0.62
WN51_11769_Krueppel-like_factor_15	11.63	5.90	70.16	0.58	0.54
WN51_11350_Pupal_cuticle_protein_C1B	27.16	114.58	4.53	0.58	0.52
WN51_11255_SPRY_domain-containing_SOCS_box_protein_1	11.95	19.22	71.44	0.58	0.63
WN51_11040_Transmembrane_protein_60	16.98	33.54	101.52	0.58	0.67
WN51_14249_Neuroparsin-A	8.75	137.62	52.16	0.58	0.69
WN51_06495_Insulin_enhancer_protein_ISL-1	3.76	3.57	22.38	0.58	0.58
WN51_06607_Anoctamin-4	3.88	0.19	23.08	0.58	0.50
WN51_12146_Fibrillin-2	8.58	19.42	50.62	0.58	0.69
WN51_10745_DmX-like_protein_2	6.81	14.23	39.95	0.59	0.68
WN51_02141_Dystrophin,_isoforms_A/C/F/G/H	5.39	8.06	31.55	0.59	0.63
WN51_02729_tRNA_pseudouridine(38/39)_synthase	10.61	20.10	61.52	0.59	0.66
WN51_03453_Thyrotropin-releasing_hormone-degrading_ectoenzyme	5.40	9.17	31.22	0.59	0.65
WN51_01652_zinc_finger_protein_395_isoform_X2	8.79	14.66	50.76	0.59	0.64
WN51_09085_MIEF1_upstream_open_reading_frame_protein	13.80	6.76	79.35	0.59	0.54
WN51_06599_hypothetical_protein	4.24	0.06	23.91	0.59	0.50
WN51_10599_Steroid_receptor_seven-up,_isoform_A	12.02	11.10	67.46	0.59	0.58
WN51_13136_hypothetical_protein	4.03	5.48	22.58	0.59	0.62
WN51_10737_Neurotrimin	4.04	74.49	22.61	0.59	0.65
WN51_06946_Outer_row_dynein_assembly_protein_16_like_protein	5.05	6.72	28.22	0.59	0.62
WN51_11278_hypothetical_protein	4.64	0.94	25.80	0.59	0.52
WN51_13943_hypothetical_protein	7.77	6.47	43.08	0.59	0.58
WN51_13564_Histone_H2A	37.88	27.71	6.84	0.59	0.62
WN51_09191_Glucose_dehydrogenase_[acceptor]	13.12	0.22	72.50	0.59	0.50
WN51_08603_hypothetical_protein	7.67	8.74	41.97	0.59	0.60
WN51_00378_Fatty-acid_amide_hydrolase_2-A	3.82	2.38	20.92	0.59	0.56
WN51_06963_Cytochrome_P450_4C1	20.77	0.35	113.44	0.59	0.50
WN51_04629_Insulin-like_peptide	55.13	39.55	10.09	0.59	0.63
WN51_07629_TWiK_family_of_potassium_channels_protein_7	7.39	8.86	40.26	0.59	0.61
WN51_02660_hypothetical_protein	15.95	9.42	86.21	0.59	0.55
WN51_00316_extracellular_serine/threonine_protein_CG31145	19.25	29.60	103.94	0.59	0.64
WN51_05693_Protein_slit	5.57	4.72	30.05	0.59	0.58
WN51_08457_Glycerol-3-phosphate_acyltransferase_1,_mitochondrial	23.07	22.86	123.67	0.59	0.59
WN51_09416_hypothetical_protein	14.51	18.26	77.79	0.59	0.62
WN51_10023_Inositol-pentakisphosphate_2-kinase	6.00	12.37	32.10	0.59	0.69
WN51_04694_Leucine-rich_repeats_and_immunoglobulin-like_domains_protein_3	6.14	6.82	32.80	0.59	0.60
WN51_12743_Patched_domain-containing_protein_3	12.65	6.91	67.39	0.59	0.55
WN51_06247_Synaptotagmin-like_protein_3	12.85	6.92	68.28	0.59	0.55
WN51_01489_Mushroom_body_large-type_Kenyon_cell-specific_protein_1	15.36	28.60	81.40	0.59	0.68
WN51_10135_Prostacyclin_receptor	8.01	7.53	42.26	0.59	0.59
WN51_07094_putative_cytochrome_P450_6a14	11.15	18.31	58.66	0.60	0.66
WN51_05958_Frizzled-5	10.45	19.42	54.92	0.60	0.68
WN51_01966_max_dimerization_protein_1-like	4.65	8.66	24.27	0.60	0.68
WN51_01099_C-myc_promoter-binding_protein	8.09	2.84	42.05	0.60	0.53
WN51_10147_hypothetical_protein	15.36	4.67	79.31	0.60	0.53
WN51_00156_Leucine-rich_repeat-containing_protein_15	14.11	12.14	72.74	0.60	0.58
WN51_14508_Endothelin-converting_enzyme_2	5.34	79.69	27.50	0.60	0.67
WN51_05738_thyroid_adenoma-associated_protein	6.44	7.41	33.14	0.60	0.61
WN51_07866_Krueppel-like_factor_5	5.22	6.95	26.83	0.60	0.63
WN51_14274_Elongation_of_very_long_chain_fatty_acids_protein_6	8.78	0.75	45.01	0.60	0.51
WN51_13329_hypothetical_protein	5.92	6.67	30.26	0.60	0.61
WN51_08594_Monocarboxylate_transporter_12	5.20	3.45	26.55	0.60	0.56
WN51_07552_hypothetical_protein	12.08	5.56	61.45	0.60	0.55
WN51_12174_Heparan-sulfate_6-O-sulfotransferase_2	22.40	31.81	113.85	0.60	0.64
WN51_07501_serine/threonine-protein_kinase_KIPK1	4.52	1.55	22.83	0.60	0.53
WN51_07944_hypothetical_protein	42.12	36.04	8.37	0.60	0.62
WN51_10602_COUP_transcription_factor_2	16.54	24.79	83.28	0.60	0.65
WN51_07615_Calcitonin_receptor	12.82	5.86	63.58	0.60	0.55
WN51_08079_Putative_glutamate_synthase_[NADPH]	26.55	17.72	131.49	0.60	0.57
WN51_13883_Dual_specificity_tyrosine-phosphorylation-regulated_kinase_2	11.91	9.97	58.80	0.60	0.58
WN51_14102_hypothetical_protein	5.31	10.39	26.06	0.60	0.70
WN51_02106_Protein_bowel	104.53	0.01	21.34	0.60	0.50
WN51_09518_POU_domain_protein_CF1A	16.72	13.90	81.51	0.60	0.59
WN51_07261_Sphingomyelin_phosphodiesterase	13.44	8.32	64.88	0.60	0.56
WN51_09744_glutamyl-tRNA(Gln)_amidotransferase_subunit_C,_mitochondrial	14.79	19.63	71.35	0.60	0.64
WN51_02228_Phosphatidylinositol_3-kinase_regulatory_subunit_alpha	12.74	2.88	61.43	0.60	0.52
WN51_14077_Vitellogenin [Vg2]	13.35	3.95	64.27	0.60	0.53
WN51_13921_Low_molecular_weight_phosphotyrosine_protein_phosphatase	16.64	27.43	79.95	0.60	0.67
WN51_14597_ABC_transporter_G_family_member_15	10.40	1.52	49.73	0.60	0.52
WN51_00058_hypothetical_protein	16.20	0.35	76.73	0.61	0.50
WN51_06535_hypothetical_protein	30.99	0.07	146.68	0.61	0.50
WN51_08002_Tetratricopeptide_repeat_protein	5.60	0.04	26.52	0.61	0.50
WN51_06308_kinase_protein	8.11	6.87	38.30	0.61	0.59
WN51_10892_DC-STAMP_domain-containing_protein_1	13.74	10.16	64.80	0.61	0.58
WN51_12982_Beta-1,3-galactosyltransferase_1	20.35	36.12	95.37	0.61	0.69
WN51_04941_otolith_matrix_protein_OMM-64_isoform_X5	6.04	7.70	28.11	0.61	0.64
WN51_12498_Tyrosine-protein_phosphatase_69D	16.84	18.95	78.06	0.61	0.62
WN51_03604_neuroendocrine_convertase_2	4.39	6.16	20.22	0.61	0.65
WN51_02029_E3_ubiquitin-protein_ligase_MARCH3	121.71	0.00	26.59	0.61	0.50
WN51_06851_Vacuolar_protein_sorting-associated_protein_13A	12.76	20.67	58.13	0.61	0.68
WN51_02945_DNA_primase_small_subunit	24.69	5.98	112.46	0.61	0.53
WN51_10011_hypothetical_protein	61.58	100.51	13.54	0.61	0.57

WN51_13647_Down_syndrome_cell_adhesion_molecule-like_protein_Dscam2	4.63	55.28	21.00	0.61	0.69
WN51_00860_Ferrochelatase,_mitochondrial	25.71	45.28	116.37	0.61	0.69
WN51_08505_digestive_organ_expansion_factor_homolog	12.66	10.99	57.11	0.61	0.60
WN51_03686_Putative_polypeptide_N-acetylgalactosaminyltransferase_9	8.28	10.08	37.25	0.61	0.64
WN51_05974_hypothetical_protein	12.59	5.77	56.51	0.61	0.55
WN51_10495_DNA_ligase_4	5.69	2.25	25.55	0.61	0.54
WN51_09974_probable_endochitinase	8.79	1.83	39.36	0.61	0.52
WN51_12753_Hemocytin	15.77	10.89	70.37	0.61	0.58
WN51_12215_Ectopic_P_granules_protein_5_like_protein	6.22	11.03	27.72	0.61	0.70
WN51_02497_Esterase_FE4	27.07	7.35	120.15	0.61	0.53
WN51_04222_putative_ATP-dependent_RNA_helicase_DHX36	11.02	13.81	48.88	0.61	0.64
WN51_07555_Scavenger_receptor_class_B_member_1	19.65	3.02	86.73	0.61	0.52
WN51_01391_MMS19_nucleotide_excision_repair_protein_like_protein	16.83	28.57	73.42	0.61	0.69
WN51_07212_hypothetical_protein	4.73	68.48	20.64	0.61	0.65
WN51_05976_hypothetical_protein	15.16	11.25	65.95	0.61	0.59
WN51_01238_hypothetical_protein	15.89	11.42	68.69	0.62	0.58
WN51_04932_Glucose_dehydrogenase_[acceptor]	14.49	15.73	62.44	0.62	0.63
WN51_10858_nucleolar_protein_4-like_isoform_X3	4.96	1.23	21.35	0.62	0.53
WN51_09212_Folylpolyglutamate_synthase,_mitochondrial	19.60	14.18	84.15	0.62	0.58
WN51_07030_Brain-specific_angiogenesis_inhibitor_1-associated_protein_2	10.26	5.45	43.54	0.62	0.56
WN51_01857_hypothetical_protein	45.13	29.85	10.70	0.62	0.68
WN51_08963_putative_palmitoyltransferase_ZDHHC24	14.61	24.31	61.61	0.62	0.70
WN51_10802_Transcription_factor_Sox-6	6.16	3.11	25.96	0.62	0.56
WN51_00609_Protein_artemis	5.25	8.37	22.11	0.62	0.69
WN51_02802_Vacuolar_protein_sorting-associated_protein_41_like_protein	15.96	17.61	67.10	0.62	0.63
WN51_00902_GTP-binding_protein_RAD	6.65	89.89	27.91	0.62	0.66
WN51_07978_Bifunctional_ATP-dependent_dihydroxyacetone_kinase/FAD-AMP_lyase_(cyclizing)	34.14	44.68	143.10	0.62	0.66
WN51_09876_Nudix_hydrolase_8	22.09	21.63	91.61	0.62	0.62
WN51_03061_SIFamide-related_peptide	13.13	157.38	54.41	0.62	0.67
WN51_13409_nuclear_factor_NF-kappa-B_p100_subunit_isoform_X1 [NF-kB]	24.47	12.17	100.80	0.62	0.56
WN51_08329_protein_arginine_n-methyltransferase_7-like_protein	12.82	20.57	52.80	0.62	0.69
WN51_04168_flagellar_attachment_zone_protein_1-like	11.25	3.10	46.29	0.62	0.53
WN51_06228_Rhodopsin	7.73	3.28	31.70	0.62	0.55
WN51_11791_probable_JmjC_domain-containing_histone_demethylation_protein_2C_isoform_X7	8.33	0.00	34.04	0.62	0.50
WN51_12324_hypothetical_protein	10.58	15.55	43.22	0.62	0.68
WN51_00877_NADH-ubiquinone_oxidoreductase_chain_5	136.79	144.31	33.55	0.62	0.62
WN51_01656_Diuretic_hormone_receptor	5.99	0.04	24.38	0.62	0.50
WN51_05041_Tubulin_polyglutamylase_ttll6	14.14	14.95	57.25	0.62	0.63
WN51_14507_Ecdysone_receptor	12.17	17.15	49.23	0.62	0.67
WN51_07502_Dual_specificity_testis-specific_protein_kinase_2	11.29	7.79	45.45	0.62	0.59
WN51_12622_hypothetical_protein	7.17	0.01	28.84	0.62	0.50
WN51_04103_cytochrome_b5_reductase_4	17.05	25.86	68.60	0.62	0.69
WN51_03842_Fibrous_sheath-interacting_protein_2	7.52	3.52	30.17	0.62	0.56
WN51_12413_Growth_arrest-specific_protein_1	18.96	14.12	75.44	0.63	0.59
WN51_08607_Solute_carrier_family_35_member_F5	17.64	13.74	70.07	0.63	0.60
WN51_12661_hypothetical_protein	9.62	12.16	38.18	0.63	0.66
WN51_13012_hypothetical_protein	23.24	0.10	91.74	0.63	0.50
WN51_00352_Pituitary_homeobox_2	7.43	2.81	29.22	0.63	0.55
WN51_06480_hypothetical_protein	13.18	10.28	51.67	0.63	0.60
WN51_01744_DNA_replication_licensing_factor_MCM8	13.13	15.61	51.35	0.63	0.65
WN51_05564_Importin-4	28.42	13.82	110.64	0.63	0.56
WN51_07206_Sperm-associated_antigen_6	19.70	6.78	76.44	0.63	0.54
WN51_03196_Scavenger_receptor_class_B_member_1	28.79	3.96	110.96	0.63	0.52
WN51_12043_Accumulation-associated_protein	34.58	19.85	133.25	0.63	0.57
WN51_06534_mitochondrial_sodium/hydrogen_exchanger_9B2_isoform_X1	27.03	8.58	103.52	0.63	0.54
WN51_13316_hypothetical_protein	19.76	15.81	75.44	0.63	0.60
WN51_10025_Neurofibromin	12.69	13.96	48.34	0.63	0.64
WN51_09908_Protein_vav	24.03	29.20	91.39	0.63	0.66
WN51_04065_Proton-coupled_amino_acid_transporter_4	102.95	4.81	27.11	0.63	0.59
WN51_08463_Exportin-7	19.76	11.58	75.01	0.63	0.58
WN51_07270_Alpha-(1,3)-fucosyltransferase_11	23.36	32.18	88.18	0.63	0.68
WN51_10270_Alpha-tocopherol_transfer_protein-like	140.66	2.72	37.27	0.63	0.54
WN51_07734_Organic_cation_transporter_protein	12.85	9.62	48.47	0.63	0.60
WN51_08597_Lamin-B_receptor	19.25	23.58	72.63	0.63	0.66
WN51_07643_Vacuolar_protein_sorting-associated_protein_18_like_protein	12.18	13.84	45.92	0.63	0.65
WN51_00365_Mothers_against_decapentaplegic_like_protein_6	16.87	8.62	63.62	0.63	0.57
WN51_00789_Sperm-associated_antigen_1	9.22	4.13	34.73	0.63	0.56
WN51_06011_Ankyrin_repeat,_SAM_and_basic_leucine_zipper_domain-containing_protein_1	20.89	26.94	78.61	0.63	0.67
WN51_14401_putative_uncharacterized_protein_DDB_G0291812	17.26	0.00	64.88	0.63	0.50
WN51_08046_Slowpoke-binding_protein	97.38	77.86	26.00	0.63	0.67
WN51_00948_PR_domain_zinc_finger_protein_10	13.59	13.16	50.89	0.63	0.63
WN51_05301_leucine-rich_repeat-containing_protein	31.98	41.16	119.53	0.63	0.67
WN51_04062_Protein_mago_nashi	35.24	50.91	131.59	0.63	0.69
WN51_06987_coilin_isoform_X1	6.90	4.46	25.67	0.63	0.59
WN51_09651_Glycerate_kinase	30.51	15.46	113.55	0.63	0.57
WN51_00300_rho-associated_protein_kinase_2-like	7.90	5.95	29.38	0.63	0.60
WN51_05259_Putative_odorant_receptor_13a	10.59	9.26	39.27	0.63	0.62
WN51_08169_UDP-galactose_translocator	18.19	10.64	67.43	0.63	0.58
WN51_04148_Protein_hid-1_like_protein	18.09	26.57	66.76	0.64	0.70
WN51_14702_Talin-1	11.99	16.90	44.22	0.64	0.69
WN51_00025_Fatty_acyl-CoA_reductase_1	19.38	8.38	71.49	0.64	0.56
WN51_09162_transmembrane_protein_164	24.75	35.11	90.88	0.64	0.69
WN51_11210_Regulator_of_microtubule_dynamics_protein_1	22.48	22.26	82.45	0.64	0.63
WN51_09516_Major_facilitator_superfamily_domain-containing_protein_6-A	16.38	14.41	60.08	0.64	0.62
WN51_00890_unpaired-like_protein	115.34	5.56	31.59	0.64	0.59
WN51_08716_33_kDa_inner_dynein_arm_light_chain,_axonemal	8.55	6.58	31.13	0.64	0.61

WN51_00669_Protein_bride_of_sevenless	24.82	21.82	90.33	0.64	0.62
WN51_07079_hypothetical_protein	39.38	14.69	142.61	0.64	0.55
WN51_01275_BCL-6_corepressor	8.66	6.99	31.27	0.64	0.61
WN51_11927_Sodium/potassium/calcium_exchanger_5	17.16	9.71	61.90	0.64	0.58
WN51_03071_BarH-like_1_homeobox_protein	20.55	16.97	73.89	0.64	0.61
WN51_12051_nuclear_receptor_coactivator_1-like_isoform_X8	7.21	2.86	25.86	0.64	0.56
WN51_07273_Protein_singed	56.64	53.43	15.79	0.64	0.65
WN51_03199_transmembrane_protein_KIAA1109_isoform_X1	9.20	7.60	32.80	0.64	0.62
WN51_05254_hypothetical_protein	26.90	30.77	95.30	0.64	0.66
WN51_07771_hypothetical_protein	9.19	5.43	32.54	0.64	0.58
WN51_06276_Cytosolic_endo-beta-N-acetylglucosaminidase	26.60	14.58	94.16	0.64	0.58
WN51_03699_Arginine_kinase	54.57	41.67	15.42	0.64	0.69
WN51_10378_Alpha-1,2-mannosyltransferase_ALG9	10.81	12.22	38.21	0.64	0.66
WN51_04513_Gamma-secretase_subunit_PEN-2	38.56	44.53	135.97	0.64	0.66
WN51_08272_Histone-lysine_N-methyltransferase_SETD2	6.39	0.03	22.50	0.64	0.50
WN51_14209_Zinc_finger_MYND_domain-containing_protein	9.31	6.90	32.62	0.64	0.61
WN51_00014_hypothetical_protein	22.27	2.76	78.01	0.64	0.52
WN51_00684_hypothetical_protein	27.24	26.26	95.16	0.64	0.64
WN51_10242_Phosphatidylinositol_4-phosphate_3-kinase_C2_domain-containing_subunit_beta	9.30	11.82	32.43	0.64	0.68
WN51_09964_Inhibitor_of_nuclear_factor_kappa-B_kinase_subunit_beta	11.50	8.21	40.10	0.64	0.60
WN51_00554_Rap1_GTPase-GDP_dissociation_stimulator_1-B	30.55	36.67	106.45	0.64	0.67
WN51_07725_Ras-related_protein_Rab-8A	8.59	11.60	29.91	0.64	0.69
WN51_06307_kinase_protein	9.06	6.41	31.49	0.64	0.60
WN51_03811_apomucin_isoform_X2	25.41	8.01	88.24	0.64	0.55
WN51_13085_zinc_finger_protein_37-like	15.70	20.42	54.52	0.64	0.69
WN51_01803_putative_maltase_H	154.00	9.62	44.45	0.64	0.61
WN51_05900_Bifunctional_heparan_sulfate_N-deacetylase/N-sulfotransferase	26.14	9.78	90.31	0.64	0.55
WN51_00583_3-hydroxyisobutyryl-CoA_hydrolase,_mitochondrial	18.00	13.85	62.02	0.65	0.61
WN51_14659_RB1-inducible_coiled-coil_protein_1	16.41	13.45	56.42	0.65	0.62
WN51_11231_DNA_repair_protein_RAD51_like_protein_4	25.26	20.57	86.62	0.65	0.62
WN51_03215_zinc_finger_protein_2_homolog	15.85	20.01	54.27	0.65	0.68
WN51_00356_TELO2-interacting_protein_1_like_protein	16.33	11.29	55.89	0.65	0.60
WN51_12869_CUGBP_Elav-like_family_member_2_isoform_X2	7.34	0.49	25.09	0.65	0.51
WN51_07982_Protein_doublesex	17.42	10.75	59.56	0.65	0.59
WN51_10105_Coiled-coil_domain-containing_protein	25.17	22.83	85.81	0.65	0.63
WN51_06479_hypothetical_protein	12.04	13.35	41.02	0.65	0.66
WN51_02785_Serine/threonine-protein_phosphatase_6_regulatory_ankyrin_repeat_subunit_A	14.36	8.12	48.77	0.65	0.58
WN51_06099_GPI_mannosyltransferase_3	22.71	28.07	77.01	0.65	0.68
WN51_13417_Stearoyl-CoA_desaturase_5	32.59	3.01	110.54	0.65	0.51
WN51_09166_hypothetical_protein	6.11	0.00	20.72	0.65	0.50
WN51_12346_hypothetical_protein	7.61	10.30	25.77	0.65	0.70
WN51_07600_Ecdysone-inducible_protein_E75	21.26	20.63	72.03	0.65	0.64
WN51_00588_Protocadherin-15	7.26	9.05	24.57	0.65	0.68
WN51_00693_E3_ubiquitin-protein_ligase_RFWD2	35.65	47.73	120.25	0.65	0.70
WN51_02967_probable_serine/threonine-protein_kinase_clkA	6.66	6.55	22.47	0.65	0.65
WN51_14679_Zinc_finger_protein_ush	16.47	10.56	55.53	0.65	0.60
WN51_08468_Kinesin-like_protein_KIF9	12.30	15.31	41.35	0.65	0.69
WN51_09665_transmembrane_protein_104_homolog_isoform_X2	27.12	8.01	91.14	0.65	0.54
WN51_05288_Arf-GAP_with_SH3_domain,_ANK_repeat_and_PH_domain-containing_protein_1	13.31	3.04	44.68	0.65	0.53
WN51_03839_hypothetical_protein	11.89	15.75	39.91	0.65	0.70
WN51_08541_Myosin-VIIa	11.55	2.64	38.68	0.65	0.53
WN51_09365_B(0,+)-type_amino_acid_transporter_1	29.12	5.54	97.10	0.65	0.53
WN51_12472_Division_abnormally_delayed_protein	19.44	5.30	64.78	0.65	0.54
WN51_14201_Inhibin_beta_A_chain	40.80	33.61	135.72	0.65	0.62
WN51_11674_Eyes_absent_like_protein_4	63.60	73.29	19.15	0.65	0.63
WN51_06311_kinase_protein	23.69	9.06	78.61	0.65	0.56
WN51_11527_Putative_amino_acid_permease_F13H10.3	18.16	5.74	60.27	0.65	0.55
WN51_13112_hypothetical_protein	29.50	28.57	97.85	0.65	0.65
WN51_00138_tRNA_(guanine-N(7)-)-methyltransferase	20.25	22.22	67.13	0.65	0.67
WN51_07249_Ubiquitin-conjugating_enzyme_E2-24_kDa	11.02	5.86	36.44	0.65	0.58
WN51_04931_Glucose_dehydrogenase_[acceptor]	38.38	11.63	126.88	0.65	0.55
WN51_08964_Sulfhydryl_oxidase_1	18.77	23.68	62.01	0.65	0.69
WN51_02307_Alpha-1,3/1,6-mannosyltransferase_ALG2	30.22	29.90	99.48	0.65	0.65
WN51_13282_Sorbin_and_SH3_domain-containing_protein_1	19.50	23.20	63.93	0.65	0.68
WN51_13404_Protein_ST7_like_protein	29.62	32.15	96.73	0.65	0.67
WN51_06451_Beta-1,4-N-acetylgalactosaminyltransferase_bre-4	37.09	15.32	121.07	0.65	0.56
WN51_00307_inward_rectifier_potassium_channel_4-like_isoform_X3	25.30	30.17	82.53	0.65	0.68
WN51_09503_Metallo-beta-lactamase_domain-containing_protein_1	15.82	12.25	51.61	0.65	0.62
WN51_12172_Atrial_natriuretic_peptide-converting_enzyme	13.93	4.40	45.26	0.65	0.55
WN51_11225_Protein-tyrosine_sulfotransferase	17.84	17.25	57.82	0.65	0.65
WN51_06068_POU_domain,_class_2,_transcription_factor_1	72.88	2.84	22.52	0.65	0.56
WN51_08229_pancreatic_triacylglycerol_lipase-like	11.07	6.90	35.77	0.65	0.60
WN51_00146_Inositol_hexakisphosphate_and_diphosphoinositol-pentakisphosphate_kinase	12.98	16.06	41.78	0.66	0.69
WN51_12257_Putative_aldehyde_dehydrogenase_family_7_member_A1_like_protein	41.28	21.63	132.55	0.66	0.58
WN51_06938_hypothetical_protein	8.10	6.18	25.99	0.66	0.62
WN51_11156_Patatin-like_phospholipase_domain-containing_protein_2	36.81	15.92	118.01	0.66	0.57
WN51_06644_Neuronal_acetylcholine_receptor_subunit_alpha-6	41.02	34.28	131.49	0.66	0.63
WN51_07421_Glucose_dehydrogenase_[acceptor]	42.85	29.98	137.22	0.66	0.61
WN51_10727_Argininosuccinate_lyase	16.82	9.38	53.80	0.66	0.59
WN51_07235_Gamma-tubulin_complex_component_6	12.94	16.01	41.31	0.66	0.69
WN51_13046_hypothetical_protein	16.11	3.28	51.43	0.66	0.53
WN51_13561_Integral_membrane_protein	9.49	5.82	30.17	0.66	0.60
WN51_07527_Nuclear_RNA_export_factor_2	15.84	18.20	50.37	0.66	0.68
WN51_06344_hypothetical_protein	21.06	53.67	6.62	0.66	0.56
WN51_09224_Ecdysone-induced_protein_74EF_isoform_A	9.69	0.17	30.75	0.66	0.50
WN51_12089_Neuroguidin-A	40.00	11.03	126.15	0.66	0.54

WN51_00427_Putative_phosphatidate_phosphatase	18.32	6.55	57.71	0.66	0.56
WN51_07512_Elongation_of_very_long_chain_fatty_acids_protein_7	42.52	6.64	133.80	0.66	0.52
WN51_10732_Calpain-7	29.38	36.45	91.97	0.66	0.70
WN51_01317_hypothetical_protein	22.63	22.28	70.77	0.66	0.66
WN51_03184_Leucine-rich_repeat-containing_protein_34	7.64	8.41	23.84	0.66	0.68
WN51_03412_hypothetical_protein	8.12	6.29	25.34	0.66	0.62
WN51_05716_DNA_polymerase_epsilon_catalytic_subunit_A	6.52	8.07	20.30	0.66	0.70
WN51_08546_Membrane_magnesium_transporter_1	36.35	40.66	113.10	0.66	0.68
WN51_09852_Receptor_expression-enhancing_protein_6	26.65	9.71	82.90	0.66	0.56
WN51_11642_E3_ubiquitin-protein_ligase_MARCH5	38.69	18.68	120.09	0.66	0.58
WN51_04930_Glucose_dehydrogenase_[acceptor]	31.41	24.08	97.42	0.66	0.62
WN51_04468_Tyrosine_kinase_receptor_Cad96Ca	8.47	4.87	26.24	0.66	0.59
WN51_13882_Dual_specificity_tyrosine-phosphorylation-regulated_kinase_2	28.28	28.08	9.15	0.66	0.66
WN51_13027_hypothetical_protein	27.44	20.38	84.71	0.66	0.62
WN51_04474_nucleoporin_GLE1	12.93	105.87	39.87	0.66	0.69
WN51_07790_N-lysine_methyltransferase_SMYD2-A	7.35	5.68	22.61	0.66	0.63
WN51_02781_Dymeclin	18.53	4.91	56.90	0.66	0.54
WN51_02076_putative_cytochrome_P450_6a20	67.82	7.08	22.16	0.66	0.66
WN51_04016_COMM_domain-containing_protein_5	24.68	10.78	75.49	0.66	0.57
WN51_10552_putative_cytochrome_P450_49a1	7.75	2.87	23.66	0.66	0.56
WN51_12624_hypothetical_protein	24.41	0.00	74.24	0.66	0.50
WN51_12632_UDP-N-acetylglucosamine_transferase_subunit_ALG14_like_protein	24.24	25.78	73.65	0.66	0.68
WN51_08499_hypothetical_protein	10.09	9.66	30.55	0.67	0.66
WN51_11935_Cytochrome_b-c1_complex_subunit_Rieske,_mitochondrial	72.87	74.42	24.10	0.67	0.66
WN51_02250_Cytokine_receptor	25.22	12.62	75.98	0.67	0.58
WN51_03117_Ring_canal_kelch_like_protein	20.87	9.26	62.63	0.67	0.57
WN51_00145_Dolichyldiphosphatase_1	41.65	14.21	124.56	0.67	0.56
WN51_00106_hypothetical_protein	39.60	26.31	118.36	0.67	0.61
WN51_08427_hypothetical_protein	148.23	141.69	49.66	0.67	0.68
WN51_14285_Putative_odorant_receptor_9a	27.85	18.24	83.06	0.67	0.61
WN51_02321_F-box/WD_repeat-containing_protein_5	27.58	18.71	82.17	0.67	0.61
WN51_06908_hypothetical_protein	23.13	21.64	68.59	0.67	0.66
WN51_00309_hypothetical_protein	15.07	2.12	44.64	0.67	0.52
WN51_08334_Putative_E3_ubiquitin-protein_ligase_SINAT1	24.32	14.99	71.99	0.67	0.60
WN51_12596_E3_ubiquitin-protein_ligase_HUWE1	7.76	6.01	22.96	0.67	0.63
WN51_10241_hypothetical_protein	30.87	3.32	91.21	0.67	0.52
WN51_02961_WD_repeat-containing_protein_6	14.09	13.40	41.57	0.67	0.66
WN51_04074_Longitudinals_lacking_protein,_isoforms_A/B/D/L	135.65	17.20	45.99	0.67	0.69
WN51_08370_bromodomain-containing_protein_DDB_G0270170_isoform_X1	16.50	9.02	48.64	0.67	0.59
WN51_04160_hypothetical_protein	24.32	0.06	71.54	0.67	0.50
WN51_02742_Methyltransferase-like_protein_13	33.80	35.92	99.09	0.67	0.68
WN51_11236_hypothetical_protein	9.13	0.61	26.72	0.67	0.51
WN51_03211_Protein_spaetzle	21.85	17.59	63.88	0.67	0.64
WN51_04908_Putative_homeodomain_transcription_factor	26.81	15.76	77.86	0.67	0.60
WN51_02301_cell_wall_protein_DAN4-like	19.16	21.86	55.57	0.67	0.70
WN51_03434_Neuronal_PAS_domain-containing_protein_2	35.45	28.39	102.70	0.67	0.64
WN51_10123_hypothetical_protein	75.65	10.09	26.15	0.67	0.69
WN51_09894_GDP-D-glucose_phosphorylase_1	10.38	0.04	29.95	0.67	0.50
WN51_04638_Cyclic_AMP-responsive_element-binding_protein_3-like_protein_1	21.11	4.09	60.77	0.67	0.53
WN51_04203_myoneurin-like	24.62	2.75	70.79	0.67	0.52
WN51_07823_Serine/threonine-protein_kinase-transforming_protein_mos	58.48	8.09	20.34	0.67	0.70
WN51_13065_Chitooligosaccharidolytic_beta-N-acetylglucosaminidase	35.26	16.63	101.24	0.67	0.58
WN51_03396_Mucosa-associated_lymphoid_tissue_lymphoma_translocation_protein_1	35.44	35.96	101.42	0.67	0.68
WN51_06460_Phosphatidylinositol_3,4,5-trisphosphate_3-phosphatase_and_dual-specificity_protein_phosp	14.02	12.04	40.10	0.67	0.65
WN51_14217_putative_ATP-dependent_RNA_helicase_DHX35	25.61	19.38	73.13	0.68	0.63
WN51_12003_hypothetical_protein	43.38	46.35	123.87	0.68	0.69
WN51_07268_Tubulin-specific_chaperone_D	31.55	17.96	90.09	0.68	0.60
WN51_12063_Endothelin-converting_enzyme_1	33.77	11.33	96.28	0.68	0.56
WN51_10698_Protein_flightless-1	18.55	3.19	52.89	0.68	0.53
WN51_09671_zinc_finger_protein_616-like	35.45	31.57	100.84	0.68	0.66
WN51_07632_Ceramide_synthase_6	37.95	1.97	107.89	0.68	0.51
WN51_08967_5-formyltetrahydrofolate_cyclo-ligase	42.32	15.14	120.09	0.68	0.56
WN51_02692_Integrator_complex_subunit_2	11.71	10.41	33.15	0.68	0.66
WN51_04136_cytochrome_p450_315a1 [p450]	37.19	19.59	105.14	0.68	0.59
WN51_06378_Peritrophin-1	23.37	46.97	8.28	0.68	0.59
WN51_04370_Insulin-like_growth_factor-binding_protein_complex_acid_labile_subunit	10.82	3.43	30.52	0.68	0.56
WN51_12698_Methyl-CpG-binding_domain_protein_5	17.89	6.51	50.41	0.68	0.56
WN51_08557_hypothetical_protein	14.77	1.95	41.61	0.68	0.52
WN51_08178_Regulator_of_telomere_elongation_helicase_1_like_protein	13.14	8.56	37.00	0.68	0.62
WN51_02202_F-box_only_protein_28	34.43	35.62	96.86	0.68	0.68
WN51_02453_1-phosphatidylinositol_4,5-bisphosphate_phosphodiesterase_gamma-1	21.30	18.64	59.91	0.68	0.66
WN51_07179_Histone-lysine_N-methyltransferase_ash1	19.29	9.24	54.14	0.68	0.59
WN51_05801_PDZ_and_LIM_domain_protein_Zasp	24.39	24.58	67.55	0.68	0.68
WN51_05255_hypothetical_protein	27.57	13.32	76.24	0.68	0.59
WN51_01442_Kv_channel-interacting_protein_2	11.08	84.04	30.62	0.68	0.68
WN51_08788_Exocyst_complex_component_1	24.68	26.77	68.01	0.68	0.70
WN51_01303_putative_beta-hexosaminidase_fdl	39.15	30.57	107.82	0.68	0.64
WN51_04675_Endoplasmic_reticulum_metallopeptidase_1	34.81	20.01	95.82	0.68	0.60
WN51_02872_Chloride_channel_protein_2	40.84	33.52	112.04	0.68	0.65
WN51_12294_early_endosome_antigen_1-like	21.03	16.23	57.67	0.68	0.64
WN51_12218_Werner_Syndrome-like_exonuclease	17.32	15.29	47.48	0.68	0.66
WN51_05287_Arf-GAP_with_SH3_domain,_ANK_repeat_and_PH_domain-containing_protein_1	15.72	11.80	43.04	0.68	0.64
WN51_05068_hypothetical_protein	188.54	192.83	68.96	0.68	0.68
WN51_01056_Chaoptin	10.72	8.30	29.18	0.68	0.64
WN51_00121_gag-pol_polyprotein	12.79	10.00	34.74	0.68	0.64
WN51_12893_putative_cation-transporting_ATPase_13A1	36.72	9.43	99.72	0.68	0.55

WN51_11015_putative_Ufm1-specific_protease_2	35.69	29.61	96.75	0.68	0.65
WN51_03038_serine/arginine_repetitive_matrix_protein_1	18.26	18.49	49.45	0.68	0.69
WN51_04527_hypothetical_protein	10.93	0.13	29.52	0.69	0.50
WN51_03497_DNA-directed_RNA_polymerase_I_subunit_RPA1	18.95	12.04	51.11	0.69	0.62
WN51_09473_Thiamine_transporter_2	37.31	38.60	100.39	0.69	0.69
WN51_01666_E3_ubiquitin-protein_ligase_UBR3	18.45	16.08	49.65	0.69	0.66
WN51_08602_hypothetical_protein	25.45	26.81	68.47	0.69	0.70
WN51_09392_Codanin-1	37.24	35.64	100.19	0.69	0.68
WN51_12623_hypothetical_protein	20.32	10.85	54.59	0.69	0.60
WN51_12395_Cytochrome_b561	51.70	25.62	138.70	0.69	0.59
WN51_11680_Leucine-rich_repeat-containing_protein_47	36.21	12.62	96.83	0.69	0.57
WN51_13123_Protein_bric-a-brac_1	14.98	12.98	40.05	0.69	0.66
WN51_11182_Zinc_finger_protein_32	27.40	7.64	73.24	0.69	0.55
WN51_10480_Oxidation_resistance_protein_1	31.09	32.10	82.88	0.69	0.69
WN51_06007_Polypeptide_N-acetylgalactosaminyltransferase_35A	25.05	22.71	66.77	0.69	0.67
WN51_03293_WD_repeat-containing_protein_CG11141	42.97	30.45	114.42	0.69	0.63
WN51_00448_Anoctamin-1	36.16	23.37	96.25	0.69	0.62
WN51_10240_Homeobox_protein_CDX-4	25.72	1.09	68.46	0.69	0.51
WN51_10725_histone-lysine_N-methyltransferase_PRDM9-like_isoform_X2	14.97	9.56	39.83	0.69	0.62
WN51_02791_Neogenin	14.42	10.18	38.32	0.69	0.63
WN51_05589_hypothetical_protein	10.93	141.85	28.99	0.69	0.60
WN51_09295_General_receptor_for_phosphoinositides_1-associated_scaffold_protein	47.34	77.58	17.95	0.69	0.62
WN51_05803_Phospholipase_A2	40.84	25.97	107.72	0.69	0.62
WN51_01359_EKC/KEOPS_complex_subunit_LAGE3-like_isoform_X2	31.96	24.45	84.31	0.69	0.64
WN51_07807_Optomotor-blind_protein	24.74	60.22	9.40	0.69	0.58
WN51_06835_Transient_receptor_potential_cation_channel_trpm	20.88	20.76	54.89	0.69	0.69
WN51_14065_hypothetical_protein	68.10	155.97	25.93	0.69	0.58
WN51_04172_tRNA_pseudouridine_synthase-like_1	25.13	10.54	65.97	0.69	0.58
WN51_00537_ubiquitin_carboxyl-terminal_hydrolase_MINDY-3_homolog	48.19	32.11	126.35	0.69	0.63
WN51_09658_Broad-complex_core_protein_isoforms_1/2/3/4/5	29.10	23.26	76.23	0.69	0.65
WN51_02055_Hemicentin-2	9.28	3.45	24.29	0.69	0.57
WN51_02351_Xanthine_dehydrogenase	44.35	14.89	115.83	0.69	0.56
WN51_12047_Collagen_alpha-1(IV)_chain	41.93	38.68	109.38	0.69	0.68
WN51_09547_Chromodomain_Y_protein	15.47	9.63	40.30	0.69	0.62
WN51_02353_protein_PFC0760c-like_isoform_X1	33.64	29.60	87.64	0.69	0.67
WN51_05459_Rap_guanine_nucleotide_exchange_factor_2	25.14	14.04	65.36	0.69	0.61
WN51_11677_Trafficking_protein_particle_complex_subunit_2-like_protein	45.24	41.47	117.37	0.69	0.68
WN51_03129_Peroxisomal_membrane_protein_PEX16	14.36	6.93	37.24	0.69	0.59
WN51_02679_Facilitated_trehalose_transporter_Tret1	53.48	8.28	138.57	0.69	0.53
WN51_05977_hypothetical_protein_	36.71	18.10	95.02	0.69	0.60
WN51_01286_Low-density_lipoprotein_receptor-related_protein_11	9.50	9.47	24.55	0.69	0.69
WN51_05425_FGFR1_oncogene_partner	10.58	2.47	27.35	0.69	0.55
WN51_02096_Protein_bowel	10.98	4.26	28.35	0.69	0.58
WN51_14616_Ubiquitin_carboxyl-terminal_hydrolase_CYLD	41.92	23.79	108.19	0.69	0.61
WN51_14191_Laminin_subunit_beta-1	25.20	17.94	64.94	0.69	0.64
WN51_10265_RING_finger_protein_121	38.55	17.58	99.32	0.69	0.59
WN51_06788_Glycine_dehydrogenase_[decarboxylating],_mitochondrial	37.86	29.66	97.46	0.69	0.65
WN51_11575_Protein_polybromo-1	13.95	2.80	35.90	0.69	0.54
WN51_03972_Ubiquitin-protein_ligase_E3B	33.26	28.86	85.59	0.69	0.67
WN51_02317_Alanine--tRNA_ligase,_cytoplasmic	29.07	23.27	74.71	0.69	0.66
WN51_08164_Histone-lysine_N-methyltransferase_SETMAR	12.54	11.00	32.21	0.69	0.67
WN51_09678_DNA_polymerase_delta_small_subunit	41.45	42.37	106.46	0.69	0.70
WN51_09813_hypothetical_protein	23.31	15.63	59.64	0.70	0.63
WN51_07208_dynactin,_150_kDa_isoform_isoform_X1	10.06	3.36	25.73	0.70	0.57
WN51_06102_RNA-binding_protein_fusilli_isoform_X1	47.64	12.76	121.86	0.70	0.55
WN51_10127_hypothetical_protein	15.40	7.58	39.40	0.70	0.60
WN51_06891_Transcription_factor_GATA-4	32.49	12.66	82.98	0.70	0.58
WN51_02455_Membralin	47.99	11.40	122.53	0.70	0.55
WN51_14372_Vacuolar_protein_sorting-associated_protein_72_like_protein	36.04	12.81	91.94	0.70	0.57
WN51_05212_Alpha-1-macroglobulin	50.91	40.57	129.86	0.70	0.66
WN51_11422_hypothetical_protein	16.56	15.22	42.15	0.70	0.68
WN51_07209_Cullin-1	37.08	21.18	94.31	0.70	0.61
WN51_03418_hypothetical_protein	11.55	3.02	29.36	0.70	0.55
WN51_14303_Putative_ATP-dependent_RNA_helicase_DHX33	17.39	11.06	44.21	0.70	0.63
WN51_13651_Tyrosine-protein_phosphatase_99A	26.10	6.25	66.33	0.70	0.55
WN51_02113_cGMP-dependent_protein_kinase_1	27.49	12.85	69.85	0.70	0.59
WN51_12587_hypothetical_protein	20.75	20.45	8.17	0.70	0.70
WN51_07601_hypothetical_protein	21.40	19.73	54.14	0.70	0.68
WN51_07159_proline-rich_protein_12-like	64.77	82.98	25.62	0.70	0.65
WN51_11543_Prestin	45.06	35.50	113.62	0.70	0.66
WN51_13233_Leucine-rich_repeat-containing_protein_26	52.87	12.06	133.18	0.70	0.55
WN51_02761_Phenoloxidase_subunit_1 [PO]	69.09	8.65	27.56	0.70	0.66
WN51_10202_Calcium-binding_mitochondrial_carrier_protein_Aralar1	41.57	35.61	104.20	0.70	0.67
WN51_00999_E3_ubiquitin-protein_ligase_MYLIP	36.20	11.37	90.61	0.70	0.56

Table S1(b): annotation of hypothetical genes according to the best BLASTp hit.

Query	WN51	Accession	Description	E-value	Query coverage	Bit-Score	% Pairwise Identity	Grade	Hit end	Hit start	Query end	Query start	Max Sequence Length	Min Sequence Length	Sequence Length
gi|925682931|gb|KOX79557.1|	WN51_02823	XP_020722090	adoMet-dependent rRNA methyltransferase SPB1 isoform X1	3.87E-74	59.67%	242	69.2%	64.4%	311	105	284	69	216	207	221
gi|925674026|gb|KOX71504.1|	WN51_03811	XP_011638228	apomucin isoform X2	0.00E+00	100.00%	868	47.2%	75.0%	1328	54	1293	1	1293	1275	1373
KOX70641.1	WN51_03699	PBC31636	Arginine kinase	0.00E+00	83.00%	839	77.3%	80.2%	555	20	547	1	547	536	551
gi|925683615|gb|KOX80193.1|	WN51_08370	XP_006561066	bromodomain-containing protein DDB G0270170 isoform X1	0.00E+00	53.35%	1181	61.9%	57.6%	1179	1	1188	1	1188	1179	1268
gi|925678801|gb|KOX75800.1|	WN51_12588	XP_023709364	calphotin-like	3.72E-87	83.25%	285	44.7%	66.6%	537	149	411	59	389	353	407
gi|925676235|gb|KOX73488.1|	WN51_14534	PBC26964	CAMP-specific 3’,5’-cyclic phosphodiesterase	3.65E-151	76.89%	444	72.8%	74.8%	380	42	389	54	339	336	349
gi|925674286|gb|KOX71732.1|	WN51_02301	XP_025993928	cell wall protein DAN4-like	0.00E+00	92.24%	935	58.6%	75.4%	935	22	980	77	914	904	950
gi|925681137|gb|KOX77893.1|	WN51_05779	KOB79386	Chitin deacetylase-like 5	0.00E+00	43.51%	743	76.1%	59.8%	2227	1817	951	513	439	411	439
gi|925672223|gb|KOX69927.1|	WN51_04441	XP_012243282	chloride channel CLIC-like protein 1 isoform X6	6.53E-18	96.83%	86	67.2%	57.0%	78	18	61	1	61	61	61
gi|925681443|gb|KOX78188.1|	WN51_09547	PBC29602	Chromodomain Y protein	0.00E+00	99.59%	1398	67.1%	83.3%	1264	1	1226	1	1264	1226	1297
gi|925682391|gb|KOX79057.1|	WN51_10105	EZA61334	Coiled-coil domain-containing protein	0.00E+00	100.00%	1478	79.2%	89.6%	939	6	908	1	934	908	937
gi|925670942|gb|KOX68819.1|	WN51_06987	XP_012176075	coilin isoform X1	1.21E-64	42.58%	232	42.9%	46.3%	325	5	336	4	333	321	347
gi|925678384|gb|KOX75419.1|	WN51_12869	XP_025154382	CUGBP Elav-like family member 2 isoform X2	2.11E-16	28.07%	89	59.8%	18.9%	91	7	193	130	85	64	87
gi|925670708|gb|KOX68617.1|	WN51_04103	XP_017755415	cytochrome b5 reductase 4	5.83E-16	65.85%	83	61.0%	38.4%	77	1	81	1	81	77	82
gi|925670741|gb|KOX68650.1|	**WN51_04136**	**KMQ90601**	**cytochrome p450 315a1**	**0.00E+00**	**81.07%**	**527**	**57.4%**	**69.2%**	**439**	**1**	**522**	**99**	**439**	**424**	**439**
gi|925670835|gb|KOX68726.1|	WN51_06963	OAD62263	Cytochrome P450 4C1	2.31E-30	87.13%	122	59.1%	73.1%	88	1	88	1	88	88	88
gi|925682056|gb|KOX78746.1|	WN51_08505	XP_017792183	digestive organ expansion factor homolog	8.67E-63	95.06%	216	69.9%	82.5%	155	1	154	1	155	154	156
KOX68156.1	WN51_06050	XP_015190994	dirigent protein 10-like	1.16E-16	25.54%	85	84.5%	30.0%	124	54	268	198	71	71	71
gi|925672190|gb|KOX69894.1|	WN51_04406	XP_017759273	division abnormally delayed protein	4.17E-39	58.97%	150	77.3%	68.1%	619	523	92	1	97	92	97
gi|925683053|gb|KOX79679.1|	WN51_02945	PBC29248	DNA primase small subunit	6.40E-116	89.66%	365	67.0%	78.3%	836	540	290	5	297	286	300
gi|925674510|gb|KOX71943.1|	WN51_03220	OAD59427	DnaJ like protein subfamily C member 14	7.05E-23	53.95%	104	53.7%	53.6%	78	1	109	28	82	78	82
gi|925676602|gb|KOX73805.1|	WN51_13883	OAD53296	Dual specificity tyrosine-phosphorylation-regulated kinase 2	0.00E+00	88.22%	541	79.8%	84.0%	596	276	363	42	322	321	322
gi|925682549|gb|KOX79206.1|	WN51_07208	XP_003400403	dynactin, 150 kDa isoform isoform X1	1.24E-139	88.12%	406	78.4%	83.3%	264	1	267	1	267	264	269
gi|925678523|gb|KOX75550.1|	WN51_12294	XP_006620391	early endosome antigen 1-like	7.88E-49	100.00%	176	65.7%	82.9%	935	796	115	1	140	115	140
gi|925675681|gb|KOX72991.1|	WN51_01359	XP_024227411	EKC/KEOPS complex subunit LAGE3-like isoform X2	4.12E-19	100.00%	82	92.9%	71.4%	90	49	42	1	42	42	42
gi|925677246|gb|KOX74413.1|	WN51_00316	XP_015439231	extracellular serine/threonine protein CG31145	1.98E-90	37.77%	309	52.0%	44.9%	345	6	778	484	340	295	342
gi|925677757|gb|KOX74866.1|	WN51_00378	KOX74867	Fatty-acid amide hydrolase 2-A	6.18E-49	35.54%	169	98.8%	67.2%	109	24	90	5	86	86	86
gi|925684448|gb|KOX80942.1|	WN51_00860	KYN39468	Ferrochelatase, mitochondrial	3.78E-25	85.22%	109	60.0%	72.6%	103	4	98	1	100	98	100
gi|925670773|gb|KOX68682.1|	WN51_04168	XP_024226552	flagellar attachment zone protein 1-like	3.29E-178	74.11%	531	63.4%	68.8%	725	239	587	153	487	435	487
gi|925684763|gb|KOX81213.1|	WN51_00121	PIK41367	gag-pol polyprotein	8.64E-14	71.43%	72	64.4%	42.9%	64	20	45	1	45	45	45
gi|925683045|gb|KOX79671.1|	WN51_02937	OAD54970	Galanin receptor type 1	1.09E-22	93.24%	95	63.8%	78.2%	69	1	69	1	69	69	69
gi|925680615|gb|KOX77420.1|	WN51_09744	XP_012237451	glutamyl-tRNA(Gln) amidotransferase subunit C, mitochondrial	6.35E-20	100.00%	86	79.6%	64.8%	135	87	49	1	49	49	49
gi|925674743|gb|KOX72155.1|	WN51_01017	XP_028860879	high molecular weight rhoptry protein 2, putative	1.22E-13	92.31%	74	58.1%	50.2%	659	598	64	5	62	60	62
gi|925684952|gb|KOX81390.1|	WN51_10725	XP_014482497	histone-lysine N-methyltransferase PRDM9-like isoform X2	0.00E+00	100.00%	616	56.3%	78.2%	647	1	735	1	735	647	751
gi|925668660|gb|KOX67365.1|	WN51_08272	KYM93355	Histone-lysine N-methyltransferase SETD2	0.00E+00	92.25%	594	49.4%	71.1%	790	1	786	61	790	726	806
gi|925669866|gb|KOX67927.1|	WN51_08164	KOX70315	Histone-lysine N-methyltransferase SETMAR	1.09E-27	78.13%	106	96.0%	87.1%	50	1	50	1	50	50	50
gi|925677026|gb|KOX74210.1|	WN51_13561	PBC33385	Integral membrane protein	0.00E+00	96.32%	951	96.8%	96.6%	493	25	489	19	471	469	471
gi|925677237|gb|KOX74404.1|	WN51_00307	XP_006611024	inward rectifier potassium channel 4-like isoform X3	4.30E-35	100.00%	136	70.3%	85.2%	117	1	104	1	117	104	118
gi|925673645|gb|KOX71170.1|	WN51_04193	XP_015182352	jmjC domain-containing protein 4 isoform X2	5.14E-58	88.61%	202	48.2%	69.3%	518	297	236	27	222	210	222
gi|925671345|gb|KOX69154.1|	WN51_06307	PBC29048	kinase protein	7.45E-157	97.28%	458	54.6%	76.0%	398	10	405	12	394	389	399
gi|925671346|gb|KOX69155.1|	WN51_06308	PBC29048	kinase protein	5.38E-82	93.87%	261	50.4%	72.1%	240	1	245	1	245	240	246
gi|925671349|gb|KOX69158.1|	WN51_06311	PBC29048	kinase protein	3.55E-167	61.60%	493	60.0%	60.8%	398	10	638	246	393	389	395
gi|925684379|gb|KOX80881.1|	WN51_05301	KMQ96186	leucine-rich repeat-containing protein	0.00E+00	95.32%	619	42.3%	72.7%	1022	9	1068	51	1018	1014	1100
gi|925673972|gb|KOX71467.1|	WN51_01741	XP_003486183	low density lipoprotein receptor adapter protein 1-like isoform X3	7.83E-50	27.05%	184	70.4%	48.7%	117	15	523	382	142	103	142
gi|925676272|gb|KOX73513.1|	WN51_01286	OAD62934	Low-density lipoprotein receptor-related protein 11	0.00E+00	99.51%	4336	66.9%	83.2%	3324	1	3252	1	3324	3252	3389
gi|925679334|gb|KOX76270.1|	WN51_11601	XP_028522768	MATH and LRR domain-containing protein PFE0570w-like	8.42E-134	73.92%	406	54.7%	64.3%	409	2	579	152	428	408	437
gi|925684156|gb|KOX80678.1|	WN51_01966	XP_020289855	max dimerization protein 1-like	4.11E-15	37.40%	79	89.1%	38.3%	248	205	123	78	46	44	46
gi|925677229|gb|KOX74396.1|	WN51_00299	PBC28359	Microtubule-associatedA	1.19E-57	97.27%	195	82.4%	89.8%	108	1	107	1	108	107	108
gi|925682637|gb|KOX79283.1|	WN51_09085	XP_012168616	MIEF1 upstream open reading frame protein	2.86E-22	69.33%	91	84.6%	76.3%	52	1	52	1	52	52	52
gi|925671907|gb|KOX69648.1|	WN51_06534	XP_017760200	mitochondrial sodium/hydrogen exchanger 9B2 isoform X1	1.99E-137	92.25%	411	81.7%	87.0%	234	1	262	1	262	234	263
gi|925680830|gb|KOX77616.1|	WN51_09281	XP_014613093	mucin-5AC-like isoform X3	2.36E-164	100.00%	473	76.3%	88.1%	394	26	327	1	369	327	371
gi|925680640|gb|KOX77445.1|	WN51_09769	XP_017759425	myb-like protein M	0.00E+00	100.00%	774	66.3%	83.1%	674	1	650	1	674	650	724
gi|925673655|gb|KOX71180.1|	WN51_04203	XP_011146613	myoneurin-like	0.00E+00	93.57%	802	51.9%	72.7%	913	57	945	59	887	857	933
gi|925673520|gb|KOX71063.1|	WN51_03604	XP_017757624	neuroendocrine convertase 2	1.42E-64	81.87%	220	80.3%	81.1%	142	1	140	1	142	140	142
gi|925683345|gb|KOX79949.1|	WN51_06361	KOC60556	Neuron navigator 2	0.00E+00	80.81%	781	62.4%	71.6%	718	1	907	154	754	718	774
gi|925678013|gb|KOX75102.1|	**WN51_13409**	**XP_020721409**	**nuclear factor NF-kappa-B p100 subunit isoform X1**	**7.06E-81**	**99.46%**	**267**	**68.2%**	**83.8%**	**221**	**21**	**183**	**1**	**201**	**183**	**201**
gi|925678716|gb|KOX75724.1|	WN51_12051	XP_017886597	nuclear receptor coactivator 1-like isoform X8	2.71E-15	38.54%	80	100.0%	44.3%	42	6	51	15	37	37	37
gi|925680436|gb|KOX77252.1|	WN51_10858	XP_017761695	nucleolar protein 4-like isoform X3	1.82E-119	38.96%	371	84.3%	61.6%	256	74	220	11	210	183	210
gi|925672255|gb|KOX69959.1|	WN51_04474	XP_014222438	nucleoporin GLE1	6.89E-34	100.00%	129	42.6%	75.0%	217	1	183	1	217	183	223
KOX78400.1	WN51_07807	KOX69571	Optomotor-blind protein	7.02E-14	28.57%	77	90.0%	34.3%	246	207	140	101	40	40	40
KOX79268.1	WN51_09070	XP_016908608	orcokinin peptides-like isoform X2	1.80E-21	98.44%	91	74.6%	82.0%	151	90	63	1	63	62	63
gi|925671926|gb|KOX69659.1|	WN51_04941	XP_016920258	otolith matrix protein OMM-64 isoform X5	6.01E-34	59.69%	138	63.2%	61.5%	154	52	166	50	117	103	117
gi|925668618|gb|KOX67323.1|	WN51_08229	XP_003491818	pancreatic triacylglycerol lipase-like	1.80E-17	24.89%	91	75.9%	25.4%	58	1	204	150	58	55	58
gi|925678537|gb|KOX75555.1|	WN51_12744	XP_012173032	patched domain-containing protein 3 isoform X2	3.31E-33	89.55%	130	95.0%	92.3%	163	104	67	8	60	60	60
gi|925683973|gb|KOX80512.1|	WN51_12996	EFN73746	Phospholipase A2	0.00E+00	100.00%	1965	75.0%	87.5%	1655	169	1448	1	1487	1448	1534
gi|925684585|gb|KOX81049.1|	WN51_09974	XP_012241960	probable endochitinase	8.20E-14	98.97%	73	38.6%	49.5%	178	68	96	1	111	96	114
gi|925679998|gb|KOX76857.1|	WN51_11275	XP_017762615	probable JmjC domain-containing histone demethylation protein 2C	4.74E-77	51.32%	278	65.2%	58.2%	630	318	385	75	313	311	330
gi|925679118|gb|KOX76076.1|	WN51_11791	XP_020719953	probable JmjC domain-containing histone demethylation protein 2C isoform X7	1.41E-29	74.32%	120	96.4%	85.3%	55	1	55	1	55	55	55
gi|925675323|gb|KOX72673.1|	WN51_02967	XP_017754637	probable serine/threonine-protein kinase clkA	1.53E-131	100.00%	397	54.7%	77.3%	468	1	446	1	468	446	472
gi|925682500|gb|KOX79157.1|	WN51_07159	XP_012230880	proline-rich protein 12-like	0.00E+00	94.86%	586	73.0%	83.9%	463	48	428	23	416	406	419
gi|925673566|gb|KOX71102.1|	WN51_04637	XP_012241714	protein amnionless-like	1.34E-37	89.55%	143	68.6%	79.1%	480	366	134	15	120	115	121
gi|925683574|gb|KOX80152.1|	WN51_08329	KMQ98432	protein arginine n-methyltransferase 7-like protein	6.88E-21	78.45%	100	37.3%	47.0%	148	10	146	5	142	139	142
gi|925670667|gb|KOX68576.1|	WN51_04062	PBC26721	Protein mago nashi	3.56E-36	90.38%	132	66.0%	78.2%	232	133	94	1	100	94	100
gi|925674337|gb|KOX71783.1|	WN51_02353	XP_026298819	protein PFC0760c-like isoform X1	6.12E-55	89.74%	189	54.0%	71.9%	264	14	271	1	271	251	272
gi|925678062|gb|KOX75138.1|	WN51_14285	KOX76482	Putative odorant receptor 9a	1.06E-138	89.24%	446	62.5%	75.9%	2111	1773	352	38	339	315	339
gi|925676102|gb|KOX73355.1|	WN51_14401	XP_012340372	putative uncharacterized protein DDB G0291812	6.77E-22	56.32%	99	95.9%	74.4%	95	47	59	11	49	49	49
gi|925683042|gb|KOX79668.1|	WN51_02934	XP_017760635	pyroglutamylated Rfamide peptide receptor-like isoform X2	1.19E-102	49.75%	328	60.3%	55.0%	398	119	478	175	304	280	317
gi|925681592|gb|KOX78319.1|	WN51_07725	PBC31987	Ras-related protein Rab-8A	0.00E+00	94.91%	513	92.0%	93.4%	261	1	261	1	261	261	261
gi|925680723|gb|KOX77528.1|	WN51_09852	OAD61849	Receptor expression-enhancing protein 6	0.00E+00	98.07%	1230	86.5%	92.3%	738	41	725	15	711	698	711
gi|925677230|gb|KOX74397.1|	WN51_00300	XP_026300706	rho-associated protein kinase 2-like	1.62E-29	48.31%	121	67.4%	57.9%	87	2	86	1	86	86	86
gi|925678377|gb|KOX75412.1|	WN51_12862	XP_003489234	ribonuclease P/MRP protein subunit POP5	2.68E-17	93.24%	80	61.4%	52.3%	139	72	69	1	69	68	70
gi|925680347|gb|KOX77175.1|	WN51_10265	XP_018406366	RING finger protein 121	0.00E+00	87.50%	515	80.4%	83.9%	318	18	344	44	301	301	301

gi|925670220|gb|KOX68208.1|	WN51_06102	XP_012249361	RNA-binding protein fusilli isoform X1	2.67E-63	71.59%	217	95.3%	83.4%	709	583	164	39	127	126	127
gi|925676281|gb|KOX73522.1|	WN51_01295	XP_017795855	serine-rich adhesin for platelets-like	0.00E+00	98.63%	1146	55.7%	77.2%	1294	133	1162	13	1162	1150	1221
gi|925674453|gb|KOX71893.1|	WN51_03038	XP_012287305	serine/arginine repetitive matrix protein 1	2.64E-25	71.84%	109	63.2%	67.5%	793	718	101	28	76	74	76
gi|925681936|gb|KOX78640.1|	WN51_07501	XP_003402214	serine/threonine-protein kinase KIPK1	0.00E+00	92.93%	645	65.2%	79.1%	570	1	486	1	570	486	583
gi|925675160|gb|KOX72529.1|	WN51_03061	XP_016909675	SIFamide-related peptide	3.57E-41	80.65%	139	84.0%	82.3%	75	1	93	19	75	75	75
gi|925683662|gb|KOX80240.1|	WN51_08417	XP_017764944	skin secretory protein xP2-like	1.68E-110	93.58%	339	80.4%	87.0%	388	4	405	27	385	379	388
gi|925672473|gb|KOX70162.1|	WN51_04902	KOC65037	Spondin-1	5.83E-38	94.32%	144	81.9%	88.1%	115	33	88	6	83	83	83
gi|925669918|gb|KOX67966.1|	WN51_08002	EZA56707	Tetratricopeptide repeat protein	3.23E-45	87.77%	167	66.4%	77.1%	496	360	127	6	137	122	137
gi|925681096|gb|KOX77852.1|	WN51_05738	XP_012167972	thyroid adenoma-associated protein	0.00E+00	97.79%	592	80.0%	88.9%	1301	947	354	1	355	354	355
gi|925669744|gb|KOX67821.1|	WN51_07674	XP_012347802	thyrotroph embryonic factor isoform X2	2.06E-54	76.00%	183	94.7%	85.4%	96	2	120	26	95	95	95
gi|925671918|gb|KOX69651.1|	WN51_04933	XP_025074166	titin	0.00E+00	74.10%	617	41.4%	62.1%	1161	17	1066	17	1145	1050	1189
gi|925680538|gb|KOX77343.1|	WN51_09665	XP_012166150	transmembrane protein 104 homolog isoform X2	1.60E-156	68.35%	460	76.9%	72.7%	502	198	395	126	305	270	308
gi|925668978|gb|KOX67439.1|	WN51_09162	XP_017753925	transmembrane protein 164	0.00E+00	90.03%	548	84.9%	87.5%	298	1	331	34	298	298	298
gi|925674489|gb|KOX71922.1|	WN51_03199	XP_011343539	transmembrane protein KIAA1109 isoform X1	0.00E+00	99.98%	9001	86.5%	93.2%	5035	1	4992	1	5035	4992	5057
gi|925677668|gb|KOX74792.1|	WN51_00399	AAB49410	transposase	4.19E-20	98.31%	85	67.2%	57.8%	60	3	58	1	58	58	58
gi|925679603|gb|KOX76518.1|	WN51_12498	OAD62167	Tyrosine-protein phosphatase 69D	2.45E-89	64.04%	301	76.3%	70.2%	1712	1525	202	16	188	187	190
gi|925677440|gb|KOX74582.1|	WN51_00537	XP_003490264	ubiquitin carboxyl-terminal hydrolase MINDY-3 homolog	3.88E-123	98.35%	365	96.1%	97.2%	179	1	179	1	179	179	179
gi|925674198|gb|KOX71660.1|	WN51_03774	KYM85472	UBX domain-containing protein 6	1.54E-26	83.74%	113	56.5%	70.1%	108	1	103	1	108	103	108
gi|925684478|gb|KOX80972.1|	WN51_00890	AFC60675	unpaired-like protein	5.75E-97	97.31%	293	64.0%	80.6%	274	54	217	1	221	217	222
gi|925673312|gb|KOX70866.1|	WN51_03293	XP_011067560	WD repeat-containing protein CG11141	0.00E+00	99.45%	1017	71.3%	85.4%	736	1	728	1	736	728	743
gi|925676926|gb|KOX74129.1|	WN51_14209	PBC25517	Zinc finger MYND domain-containing protein	1.52E-89	44.44%	290	73.4%	58.9%	501	322	413	230	184	180	184
gi|925674505|gb|KOX71938.1|	WN51_03215	XP_015435743	zinc finger protein 2 homolog	0.00E+00	94.58%	1157	79.4%	87.0%	718	1	716	1	718	716	728
gi|925677514|gb|KOX74651.1|	WN51_13085	XP_011639980	zinc finger protein 37-like	0.00E+00	99.29%	829	53.5%	76.4%	756	6	851	7	845	751	858
gi|925673882|gb|KOX71377.1|	WN51_01650	XP_017754344	zinc finger protein 395	4.25E-114	82.59%	347	90.7%	86.7%	194	1	185	1	194	185	194
gi|925673884|gb|KOX71379.1|	WN51_01652	XP_020724307	zinc finger protein 395 isoform X2	5.40E-133	93.24%	395	89.4%	91.3%	556	353	222	16	207	204	207
gi|925680544|gb|KOX77349.1|	WN51_09671	XP_003693701	zinc finger protein 616-like	0.00E+00	100.00%	513	89.3%	94.6%	289	1	287	1	289	287	289

Table S2: list of primers used for RT-qPCR assays.

Primer	Sequence	ID	Fragment size (pb)	Annealing temperature (ºC) *	Efficiency (E)
Vg1 F	ACGACAAGACACCATCCACC	KOX68248.1 /	136	60	2.114±0.062
Vg1 R	CTTCCTACGCGCAGATCCAT				
Vg2 F	CAGGCTGAAACTAGACGGCA	KOX73997.1 /	137	60	2.104±0.109
Vg2 R	TGTCATGCACGGTACTGCTT				
NF-kB F	TCTGGATCCTGCAGTAATACGA	KOX75102.1 /	103	50	1.988±0.021
NF-kB R	ATCTTGACCAGCATCTCTACGG				
P450 F	TTGGAGGAAATTCGTTGCGTC	KOX68650.1 /	129	50	2.055±0.025
P450 R	TCCTCAGCTCGGATACCTTCAT				
PO F	TTTCCAAGCACGTTGATACCC	KOX79496.1 /	120	50	2.057±0.125
PO R	TCAAGATCTGGAAAGATGGCG				
rps5 F	ATAATTCACCTGTTGACCGGG	KOX78800.1 /	148	60	1.897±0.035
rps5 R	TTACTCGTCGTAGCGGAGAAA				
Act F	CTGCTGGAAGGTGGACAGAG	Brito et al. 2015.	138	50	1.884±059
Act R	GCCGATCGTATGCAGAAGGA				

***qPCR conditions:** 95 °C for 3 min followed by 40 cycles of 95 °C for 15 sec, 60 °C (for rps5, Vg1 and Vg2) or 50 °C (for act, PO, NF-kB and P450) for 30 sec and 72 °C for 30 sec. The amplification specificity was confirmed by melting curve analysis (95 °C for 15 sec, 60 °C for 1 min and a continuous raise in temperature to 95 °C at 0.3 °C/sec ramp rate followed by 95 °C for 15 sec).

Table S3(a): calibrated normalized relative quantities (CNRQs) of gene expression for five health-related bee genes. For each sample there is information from the Month, Health in March (H = healthy, U = unhealthy, Intensity (H = healthy, SU = slightly unhealthy, U = unhealthy, Locality (BP = meliponary in Bom Princípio, PA = meliponary in Porto Alegre), Sisters (1 = colonies BP1 and PA1, 2 = colonies BP2 and PA2, 3 = colonies BP3 and PA3) and Colony.

Month	Health in March	Intensity	Locality	Sisters	Colony	NF-kB	p450	PO	Vg1	Vg2
APR	H	H	BP	1	BP1	0.40393	0.68156	0.62291	2.30409	1.21100
APR	H	H	BP	1	BP1	0.49486	0.91759	0.75866	2.78038	1.16520
APR	H	H	BP	1	BP1	0.51081	0.75520	0.90834	2.68193	1.12127
APR	H	H	BP	1	BP1	0.71951	1.13653	0.61239	0.80512	0.94431
APR	U	U	BP	2	BP2	0.49571	0.54405	0.57382	2.15483	0.29769
APR	U	U	BP	2	BP2	0.73196	0.92746	0.83528	4.02957	0.90546
APR	U	U	BP	2	BP2	0.81841	1.12291	0.95468	1.98528	1.20335
APR	U	U	BP	2	BP2	0.86493	1.07878	0.76386	4.11033	1.14243
APR	U	U	BP	2	BP2	1.19265	1.52828	1.45653	3.00167	1.29949
APR	U	U	BP	3	BP3	0.84810	0.82940	0.73560	1.63140	1.08661
APR	U	U	BP	3	BP3	0.97722	0.50283	0.87123	1.61803	0.58382
APR	U	U	BP	3	BP3	1.06376	0.74974	0.71002	2.85523	1.02761
APR	U	U	BP	3	BP3	1.15887	0.82268	0.76193	1.04493	1.18115
APR	H	H	PA	1	PA1	0.60806	1.00171	0.94383	4.63445	1.45137
APR	H	H	PA	1	PA1	0.61272	0.78342	0.58713	3.18476	1.22451
APR	H	H	PA	1	PA1	0.70325	0.79097	0.80850	3.93723	1.25030
APR	H	H	PA	1	PA1	0.81130	0.84617	0.62507	2.54957	1.09589
APR	H	H	PA	1	PA1	1.20330	1.41889	0.94163	3.88383	1.81578
APR	U	SU	PA	2	PA2	0.78643	0.92944	0.97721	2.21866	1.28203
APR	U	SU	PA	2	PA2	0.96854	0.63022	0.32152	NaN	1.08747
APR	U	SU	PA	2	PA2	1.06952	1.21748	1.26286	1.38856	1.54639
APR	U	SU	PA	3	PA3	0.80914	1.11853	1.14126	4.93630	1.43340
APR	U	SU	PA	3	PA3	0.90577	1.03001	0.99472	3.26563	1.37499
APR	U	SU	PA	3	PA3	1.21623	1.13177	0.84885	3.62170	1.32607
APR	U	SU	PA	3	PA3	1.47475	1.03625	0.88811	3.76915	1.39518
APR	U	SU	PA	3	PA3	1.52514	1.18454	0.85083	3.53806	1.83276
FEB	H	H	BP	1	BP1	0.76028	1.25627	1.01126	2.65872	1.05540
FEB	H	H	BP	1	BP1	0.78092	1.22612	1.05259	4.05905	1.14897
FEB	H	H	BP	1	BP1	0.93026	1.10565	1.16402	2.24251	1.39994
FEB	H	H	BP	1	BP1	0.95416	1.20392	0.99822	3.31675	1.14920
FEB	H	H	BP	1	BP1	1.06014	1.21981	0.96403	3.92704	1.39389
FEB	U	U	BP	2	BP2	0.77611	0.73801	0.33652	4.50375	1.17110
FEB	U	U	BP	2	BP2	0.90836	0.97417	0.59170	4.20709	1.23665
FEB	U	U	BP	2	BP2	0.96147	0.89965	0.71688	2.69329	1.11045
FEB	U	U	BP	2	BP2	0.97089	0.90928	1.00416	3.72209	1.25183
FEB	U	U	BP	2	BP2	1.13867	1.08658	0.88982	4.16470	1.23829
FEB	U	U	BP	3	BP3	0.91174	1.17937	1.55670	3.00213	1.34081
FEB	U	U	BP	3	BP3	0.95301	1.06870	1.22893	4.04815	1.58224
FEB	U	U	BP	3	BP3	1.01468	1.19193	1.42675	3.30598	1.48822
FEB	U	U	BP	3	BP3	1.12005	0.77627	1.50121	3.24259	1.27729
FEB	U	U	BP	3	BP3	1.32552	1.50106	1.52947	2.54451	1.77481
FEB	H	H	PA	1	PA1	0.69974	0.67245	0.96946	3.13858	0.69615
FEB	H	H	PA	1	PA1	0.89655	0.71890	0.24830	2.16123	0.65533
FEB	H	H	PA	1	PA1	0.96277	0.81484	1.00835	3.16287	0.63907
FEB	H	H	PA	1	PA1	1.03705	0.68380	1.00425	2.94774	0.15975

FEB	H	H	PA	1	PA1	1.14693	1.00413	1.06463	2.37282	0.83289
FEB	U	SU	PA	2	PA2	0.82417	1.21281	1.50307	3.77168	1.37775
FEB	U	SU	PA	2	PA2	0.94122	0.52800	0.84997	1.88611	1.07685
FEB	U	SU	PA	2	PA2	1.08991	1.44593	1.64496	4.05538	1.60738
FEB	U	SU	PA	2	PA2	1.13557	0.53498	0.86608	2.30362	1.03911
FEB	U	SU	PA	2	PA2	1.18294	1.91891	1.92203	4.25835	1.80484
FEB	U	SU	PA	3	PA3	0.94980	0.91465	0.85386	2.19873	0.78099
FEB	U	SU	PA	3	PA3	1.05728	0.90186	0.82027	0.67346	NaN
FEB	U	SU	PA	3	PA3	1.06825	0.88541	1.02837	2.44390	0.86088
FEB	U	SU	PA	3	PA3	1.13985	1.73046	1.49921	2.87407	0.97242
FEB	U	SU	PA	3	PA3	1.23820	0.52761	1.06986	2.59854	0.33361
JAN	H	H	BP	1	BP1	0.37127	NaN	1.28160	3.55489	1.44594
JAN	H	H	BP	1	BP1	0.79236	0.61127	0.11911	2.64655	1.08757
JAN	H	H	BP	1	BP1	1.01856	1.10064	0.37454	1.98306	1.11360
JAN	H	H	BP	1	BP1	1.51512	2.44836	2.54207	4.37752	2.34298
JAN	H	H	BP	1	BP1	1.55136	2.42430	2.38124	4.29870	2.04590
JAN	U	U	BP	2	BP2	0.71417	0.71919	0.59688	3.74611	0.83746
JAN	U	U	BP	2	BP2	0.80112	0.62632	0.46447	2.55849	0.86880
JAN	U	U	BP	2	BP2	0.97809	0.89465	0.09376	1.90109	0.59685
JAN	U	U	BP	2	BP2	0.99047	0.84732	0.28709	2.08675	1.04941
JAN	U	U	BP	2	BP2	1.23933	1.00088	0.81547	3.27345	1.22975
JAN	U	U	BP	3	BP3	0.93298	1.06957	0.67682	1.79251	0.71114
JAN	U	U	BP	3	BP3	1.10896	1.12940	1.13665	2.18712	1.33554
JAN	U	U	BP	3	BP3	1.28247	1.06699	1.39808	1.68420	1.17887
JAN	U	U	BP	3	BP3	1.53135	1.25788	NaN	2.62480	1.17820
JAN	U	U	BP	3	BP3	NaN	NaN	NaN	NaN	1.86391
JAN	H	H	PA	1	PA1	0.12789	NaN	1.37761	3.09950	2.07374
JAN	H	H	PA	1	PA1	0.66631	NaN	1.37910	2.73021	1.71248
JAN	H	H	PA	1	PA1	0.74127	NaN	2.17882	NaN	2.24292
JAN	H	H	PA	1	PA1	1.37855	0.83050	0.76219	2.58040	1.07201
JAN	U	SU	PA	2	PA2	0.77554	1.09550	NaN	4.63275	1.63251
JAN	U	SU	PA	2	PA2	0.95132	0.42822	0.73009	1.96430	0.61312
JAN	U	SU	PA	2	PA2	0.96355	0.78150	0.63044	1.99150	1.04367
JAN	U	SU	PA	2	PA2	1.32419	0.30406	0.74546	3.11081	1.53931
JAN	U	SU	PA	3	PA3	0.74546	0.58250	0.69443	4.33833	1.10272
JAN	U	SU	PA	3	PA3	0.90377	0.82394	0.89278	1.72744	1.32499
JAN	U	SU	PA	3	PA3	0.91116	0.62447	0.47443	3.59957	0.90087
JAN	U	SU	PA	3	PA3	1.20689	0.96052	0.92592	2.93313	1.56133
JAN	U	SU	PA	3	PA3	1.21183	0.43547	0.92755	3.08372	1.30555
MAR	H	H	BP	1	BP1	1.00237	1.18329	0.75738	2.21579	1.12978
MAR	H	H	BP	1	BP1	1.11375	1.40617	1.14949	2.45166	1.60400
MAR	H	H	BP	1	BP1	1.22787	1.18323	1.40423	2.71378	1.68929
MAR	H	H	BP	1	BP1	1.27892	1.47250	1.11996	3.65666	1.74396
MAR	H	H	BP	1	BP1	1.40087	1.38446	1.32351	2.95647	1.57923
MAR	U	U	BP	2	BP2	0.71132	0.95508	0.79277	3.66182	0.78778
MAR	U	U	BP	2	BP2	1.16379	1.55710	1.16630	4.53431	1.20592
MAR	U	U	BP	2	BP2	1.16816	1.43266	0.63443	2.09140	1.03616
MAR	U	U	BP	2	BP2	NaN	NaN	0.86603	2.06460	0.35814
MAR	U	U	BP	3	BP3	0.37412	0.33498	0.51874	2.45968	0.92161
MAR	U	U	BP	3	BP3	0.59895	0.79401	1.07109	3.78976	0.90351
MAR	U	U	BP	3	BP3	1.06476	1.12739	1.17176	3.22656	1.21752

MAR	U	U	BP	3	BP3	1.26362	1.13792	1.12021	3.53408	1.51012
MAR	H	H	PA	1	PA1	0.28170	NaN	NaN	2.84397	0.04623
MAR	H	H	PA	1	PA1	0.83792	1.30258	0.84565	2.27927	1.26173
MAR	H	H	PA	1	PA1	0.92956	1.32466	0.47103	2.48985	1.29336
MAR	H	H	PA	1	PA1	0.97290	1.30035	0.51909	2.29260	1.40017
MAR	H	H	PA	1	PA1	1.04688	1.21635	0.69896	3.51554	1.49378
MAR	U	SU	PA	2	PA2	0.80296	0.93231	0.88155	1.38305	1.17709
MAR	U	SU	PA	2	PA2	1.19940	1.57735	0.77582	1.77445	1.13982
MAR	U	SU	PA	2	PA2	1.42161	1.32443	1.00711	1.51384	1.50673
MAR	U	SU	PA	2	PA2	1.49562	1.75613	1.18692	1.43628	1.76001
MAR	U	SU	PA	2	PA2	1.56496	1.67173	1.09681	2.11148	1.81762
MAR	U	SU	PA	3	PA3	0.45121	0.60011	0.47875	1.86376	1.04327
MAR	U	SU	PA	3	PA3	0.57028	NaN	NaN	2.92598	1.58267
MAR	U	SU	PA	3	PA3	1.07956	1.14165	0.78750	2.35862	1.38272
MAR	U	SU	PA	3	PA3	1.09680	1.23807	0.80069	3.43498	1.66468
MAR	U	SU	PA	3	PA3	1.15657	1.33334	0.67823	2.29559	1.52276

Table S3(b): Lowest daily temperature and highest daily humidity for each colony. In addition to the information on the previous tab, there is also information on Syndrome days (NO = without syndrome symptoms, YES = with syndrome symptoms).

Month	Health in March	Syndrome days	Locality	Sisters	Colony	Day	Temperature morning	Humidity noon
DEC	H	NO	BP	1	BP1	12/01/18	23.09	93.98
DEC	H	NO	BP	1	BP1	12/02/18	18.27	92.51
DEC	H	NO	BP	1	BP1	12/03/18	13.59	92.24
DEC	H	NO	BP	1	BP1	12/04/18	13.31	84.24
DEC	H	NO	BP	1	BP1	12/05/18	15.92	85.18
DEC	H	NO	BP	1	BP1	12/06/18	15.99	82.13
DEC	H	NO	BP	1	BP1	12/07/18	17.03	79.95
DEC	H	NO	BP	1	BP1	12/08/18	11.42	74.54
DEC	H	NO	BP	1	BP1	12/09/18	14.7	71.63
DEC	H	NO	BP	1	BP1	12/10/18	20.56	70.54
DEC	H	NO	BP	1	BP1	12/11/18	19.32	70.36
DEC	H	NO	BP	1	BP1	12/12/18	26.57	69.08
DEC	H	NO	BP	1	BP1	12/13/18	23.4	72.89
DEC	H	NO	BP	1	BP1	12/14/18	25.38	61.4
DEC	H	NO	BP	1	BP1	12/15/18	24.34	79.95
DEC	H	NO	BP	1	BP1	12/16/18	25.11	75.6
DEC	H	NO	BP	1	BP1	12/17/18	26.38	53.68
DEC	H	NO	BP	1	BP1	12/18/18	25.4	84.71
DEC	H	NO	BP	1	BP1	12/19/18	24.29	78.09
DEC	H	NO	BP	1	BP1	12/20/18	24.85	71.29
DEC	H	NO	BP	1	BP1	12/21/18	23.69	88.29
DEC	H	NO	BP	1	BP1	12/22/18	23.09	70.34
DEC	H	NO	BP	1	BP1	12/23/18	22.73	72.29
DEC	H	NO	BP	1	BP1	12/24/18	21.8	77.69
DEC	H	NO	BP	1	BP1	12/25/18	21.25	67.45
DEC	H	NO	BP	1	BP1	12/26/18	22.75	60.4
DEC	H	NO	BP	1	BP1	12/27/18	22.01	58.1
DEC	H	NO	BP	1	BP1	12/28/18	24.85	55.17
DEC	H	NO	BP	1	BP1	12/29/18	22.2	54.2
DEC	H	NO	BP	1	BP1	12/30/18	24.58	52.7
DEC	H	NO	BP	1	BP1	12/31/18	28.39	71.3
JAN	H	NO	BP	1	BP1	01/01/19	26.28	54.94
JAN	H	NO	BP	1	BP1	01/02/19	28.59	53.39
JAN	H	NO	BP	1	BP1	01/03/19	30.95	70.51
JAN	H	NO	BP	1	BP1	01/04/19	23.47	86.47
JAN	H	NO	BP	1	BP1	01/05/19	22.8	86.57
JAN	H	NO	BP	1	BP1	01/06/19	23.47	72.87
JAN	H	NO	BP	1	BP1	01/07/19	27.88	71.15
JAN	H	NO	BP	1	BP1	01/08/19	25.48	72
JAN	H	NO	BP	1	BP1	01/09/19	26.13	80.39
JAN	H	NO	BP	1	BP1	01/10/19	24.75	81.1
JAN	H	NO	BP	1	BP1	01/11/19	24.53	86.55
JAN	H	NO	BP	1	BP1	01/12/19	23.91	89.9
JAN	H	NO	BP	1	BP1	01/13/19	24.92	77.49
JAN	H	NO	BP	1	BP1	01/14/19	25.09	81.18
JAN	H	NO	BP	1	BP1	01/15/19	26.79	66.39
JAN	H	NO	BP	1	BP1	01/16/19	25.5	72.47
JAN	H	NO	BP	1	BP1	01/17/19	27.36	84.21
JAN	H	NO	BP	1	BP1	01/18/19	22.66	87.92

JAN	H	NO	BP	1	BP1	01/19/19	25.67	90.29
JAN	H	NO	BP	1	BP1	01/20/19	22.51	88.06
JAN	H	NO	BP	1	BP1	01/21/19	23.76	90.94
JAN	H	NO	BP	1	BP1	01/22/19	22.06	74.14
JAN	H	NO	BP	1	BP1	01/23/19	24	67.39
JAN	H	NO	BP	1	BP1	01/24/19	26.4	68.36
JAN	H	NO	BP	1	BP1	01/25/19	23.69	67.14
JAN	H	NO	BP	1	BP1	01/26/19	25.07	66.49
JAN	H	NO	BP	1	BP1	01/27/19	25.94	64.19
JAN	H	NO	BP	1	BP1	01/28/19	25.62	55.48
JAN	H	NO	BP	1	BP1	01/29/19	27.11	57.7
JAN	H	NO	BP	1	BP1	01/30/19	27.55	53.01
JAN	H	NO	BP	1	BP1	01/31/19	27.33	56.19
FEB	H	NO	BP	1	BP1	02/01/19	24.97	64.75
FEB	H	NO	BP	1	BP1	02/02/19	25.48	75.77
FEB	H	NO	BP	1	BP1	02/03/19	23.52	86.07
FEB	H	NO	BP	1	BP1	02/04/19	19.87	85.19
FEB	H	NO	BP	1	BP1	02/05/19	20.37	79.39
FEB	H	NO	BP	1	BP1	02/06/19	18.08	77.51
FEB	H	NO	BP	1	BP1	02/07/19	20.1	74.68
FEB	H	NO	BP	1	BP1	02/08/19	22.01	67.61
FEB	H	NO	BP	1	BP1	02/09/19	23.45	61.55
FEB	H	NO	BP	1	BP1	02/10/19	26.89	75.38
FEB	H	NO	BP	1	BP1	02/11/19	25.19	75.64
FEB	H	NO	BP	1	BP1	02/12/19	24.15	84.37
FEB	H	NO	BP	1	BP1	02/13/19	18.65	85.79
FEB	H	NO	BP	1	BP1	02/14/19	20.08	71.54
FEB	H	NO	BP	1	BP1	02/15/19	24.22	88.33
FEB	H	NO	BP	1	BP1	02/16/19	22.61	88.68
FEB	H	NO	BP	1	BP1	02/17/19	22.15	79.83
FEB	H	NO	BP	1	BP1	02/18/19	23.26	78.94
FEB	H	NO	BP	1	BP1	02/19/19	22.47	80.61
FEB	H	NO	BP	1	BP1	02/20/19	23.71	72.2
FEB	H	NO	BP	1	BP1	02/21/19	21.68	72.51
FEB	H	NO	BP	1	BP1	02/22/19	21.13	69.72
FEB	H	NO	BP	1	BP1	02/23/19	24.27	63.44
FEB	H	NO	BP	1	BP1	02/24/19	27.36	54.4
FEB	H	NO	BP	1	BP1	02/25/19	24.48	85.73
FEB	H	NO	BP	1	BP1	02/26/19	21.27	86.35
FEB	H	NO	BP	1	BP1	02/27/19	19.79	86.6
FEB	H	NO	BP	1	BP1	02/28/19	19.37	84.08
MAR	H	NO	BP	1	BP1	03/01/19	18.32	82.11
MAR	H	NO	BP	1	BP1	03/02/19	20.98	66.29
MAR	H	NO	BP	1	BP1	03/03/19	21.75	76.9
MAR	H	NO	BP	1	BP1	03/04/19	22.08	68.22
MAR	H	NO	BP	1	BP1	03/05/19	26.82	60.11
MAR	H	NO	BP	1	BP1	03/06/19	23.62	79.93
MAR	H	NO	BP	1	BP1	03/07/19	25.36	75.67
MAR	H	NO	BP	1	BP1	03/08/19	25.14	86.5
MAR	H	NO	BP	1	BP1	03/09/19	24.39	90.21
MAR	H	NO	BP	1	BP1	03/10/19	21.2	89.53
MAR	H	NO	BP	1	BP1	03/11/19	20.29	86.07
MAR	H	NO	BP	1	BP1	03/12/19	21.06	89.58
MAR	H	NO	BP	1	BP1	03/13/19	22.61	91.13

MAR	H	NO	BP	1	BP1	03/14/19	21.99	86.2
MAR	H	NO	BP	1	BP1	03/15/19	19.51	83.28
MAR	H	NO	BP	1	BP1	03/16/19	21.77	85.28
MAR	H	NO	BP	1	BP1	03/17/19	24.05	88.64
MAR	H	NO	BP	1	BP1	03/18/19	24.51	90.02
MAR	H	NO	BP	1	BP1	03/19/19	22.82	89.96
MAR	H	NO	BP	1	BP1	03/20/19	21.32	90.58
MAR	H	NO	BP	1	BP1	03/21/19	19.75	89.58
MAR	H	NO	BP	1	BP1	03/22/19	16.25	89.72
MAR	H	NO	BP	1	BP1	03/23/19	18.08	87.71
MAR	H	NO	BP	1	BP1	03/24/19	18.27	84.39
MAR	H	NO	BP	1	BP1	03/25/19	20.22	84.57
MAR	H	NO	BP	1	BP1	03/26/19	16.53	82.58
MAR	H	NO	BP	1	BP1	03/27/19	18.89	80.03
MAR	H	NO	BP	1	BP1	03/28/19	19.91	83.41
MAR	H	NO	BP	1	BP1	03/29/19	19.44	83.41
MAR	H	NO	BP	1	BP1	03/30/19	22.73	73.98
MAR	H	NO	BP	1	BP1	03/31/19	23.76	81.74
APR	H	NO	BP	1	BP1	04/01/19	23.14	85.57
APR	H	NO	BP	1	BP1	04/02/19	22.13	81.2
APR	H	NO	BP	1	BP1	04/03/19	24.36	73.4
APR	H	NO	BP	1	BP1	04/04/19	24.51	77.87
APR	H	NO	BP	1	BP1	04/05/19	24.82	83.98
APR	H	NO	BP	1	BP1	04/06/19	21.25	87.99
APR	H	NO	BP	1	BP1	04/07/19	22.06	89.17
APR	H	NO	BP	1	BP1	04/08/19	21.41	87.78
APR	H	NO	BP	1	BP1	04/09/19	17.13	87.42
APR	H	NO	BP	1	BP1	04/10/19	16.94	86.89
APR	H	NO	BP	1	BP1	04/11/19	20.32	83.4
APR	H	NO	BP	1	BP1	04/12/19	21.77	87.51
APR	H	NO	BP	1	BP1	04/13/19	20.98	88.58
APR	H	NO	BP	1	BP1	04/14/19	20.58	82.95
APR	H	NO	BP	1	BP1	04/15/19	22.18	85.69
APR	H	NO	BP	1	BP1	04/16/19	23.11	89.76
APR	H	NO	BP	1	BP1	04/17/19	20.96	89.97
APR	H	NO	BP	1	BP1	04/18/19	19.1	85.81
APR	H	NO	BP	1	BP1	04/19/19	18.68	88.05
APR	H	NO	BP	1	BP1	04/20/19	20.67	88.34
APR	H	NO	BP	1	BP1	04/21/19	22.32	90.14
APR	H	NO	BP	1	BP1	04/22/19	19.46	88.94
APR	H	NO	BP	1	BP1	04/23/19	20.08	83.65
APR	H	NO	BP	1	BP1	04/24/19	21.15	81.12
APR	H	NO	BP	1	BP1	04/25/19	22.75	89.3
APR	H	NO	BP	1	BP1	04/26/19	23.04	92.34
APR	H	NO	BP	1	BP1	04/27/19	23.3	92.02
APR	H	NO	BP	1	BP1	04/28/19	22.32	92.18
APR	H	NO	BP	1	BP1	04/29/19	18.7	91.76
APR	H	NO	BP	1	BP1	04/30/19	16.06	89.8
MAY	H	NO	BP	1	BP1	05/01/19	20.41	89.57
MAY	H	NO	BP	1	BP1	05/02/19	17.89	87.32
MAY	H	NO	BP	1	BP1	05/03/19	20.91	75.16
MAY	H	NO	BP	1	BP1	05/04/19	24.1	91.96
MAY	H	NO	BP	1	BP1	05/05/19	24.27	89.2
MAY	H	NO	BP	1	BP1	05/06/19	23.3	91.27

MAY	H	NO	BP	1	BP1	05/07/19	20.37	91.23
MAY	H	NO	BP	1	BP1	05/08/19	16.39	87.56
MAY	H	NO	BP	1	BP1	05/09/19	20.37	92.31
MAY	H	NO	BP	1	BP1	05/10/19	22.32	89.1
MAY	H	NO	BP	1	BP1	05/11/19	21.08	90.24
MAY	H	NO	BP	1	BP1	05/12/19	18.03	92.17
MAY	H	NO	BP	1	BP1	05/13/19	19.46	91.51
MAY	H	NO	BP	1	BP1	05/14/19	18.46	91.77
MAY	H	NO	BP	1	BP1	05/15/19	19.08	98.24
MAY	H	NO	BP	1	BP1	05/16/19	20.96	75
MAY	H	NO	BP	1	BP1	05/17/19	20.89	61.56
MAY	H	NO	BP	1	BP1	05/18/19	21.39	69.02
MAY	H	NO	BP	1	BP1	05/19/19	22.27	71.12
MAY	H	NO	BP	1	BP1	05/20/19	22.94	74.21
MAY	H	NO	BP	1	BP1	05/21/19	23.81	75.2
MAY	H	NO	BP	1	BP1	05/22/19	22.44	79.89
DEC	U	NO	BP	2	BP2	12/01/18	24.17	94.02
DEC	U	NO	BP	2	BP2	12/02/18	18.18	91.25
DEC	U	NO	BP	2	BP2	12/03/18	14.79	93.68
DEC	U	NO	BP	2	BP2	12/04/18	14.22	91.84
DEC	U	NO	BP	2	BP2	12/05/18	16.58	87.05
DEC	U	NO	BP	2	BP2	12/06/18	16.89	88.02
DEC	U	NO	BP	2	BP2	12/07/18	17.56	84.48
DEC	U	NO	BP	2	BP2	12/08/18	12.1	85.13
DEC	U	NO	BP	2	BP2	12/09/18	15.53	84.08
DEC	U	NO	BP	2	BP2	12/10/18	20.94	80.28
DEC	U	NO	BP	2	BP2	12/11/18	19.98	73.05
DEC	U	NO	BP	2	BP2	12/12/18	27.41	69.59
DEC	U	NO	BP	2	BP2	12/13/18	23.88	81.62
DEC	U	NO	BP	2	BP2	12/14/18	25.4	75.69
DEC	U	NO	BP	2	BP2	12/15/18	22.2	79.16
DEC	U	NO	BP	2	BP2	12/16/18	23.81	87.32
DEC	U	NO	BP	2	BP2	12/17/18	25.19	73.74
DEC	U	NO	BP	2	BP2	12/18/18	23.67	84.05
DEC	U	NO	BP	2	BP2	12/19/18	22.54	89.26
DEC	U	NO	BP	2	BP2	12/20/18	22.9	85.73
DEC	U	NO	BP	2	BP2	12/21/18	21.82	91.04
DEC	U	NO	BP	2	BP2	12/22/18	21.84	92.23
DEC	U	NO	BP	2	BP2	12/23/18	21.18	90.85
DEC	U	NO	BP	2	BP2	12/24/18	20.1	86.93
DEC	U	NO	BP	2	BP2	12/25/18	19.98	84.57
DEC	U	NO	BP	2	BP2	12/26/18	22.27	83.16
DEC	U	NO	BP	2	BP2	12/27/18	21.06	81.39
DEC	U	NO	BP	2	BP2	12/28/18	24.22	76.03
DEC	U	NO	BP	2	BP2	12/29/18	21.41	74.64
DEC	U	NO	BP	2	BP2	12/30/18	23.3	67.66
DEC	U	NO	BP	2	BP2	12/31/18	26.72	76.24
JAN	U	NO	BP	2	BP2	01/01/19	25.11	75.66
JAN	U	NO	BP	2	BP2	01/02/19	27.8	68.32
JAN	U	NO	BP	2	BP2	01/03/19	30.09	68.24
JAN	U	NO	BP	2	BP2	01/04/19	21.34	80.29
JAN	U	NO	BP	2	BP2	01/05/19	21.37	85.6
JAN	U	NO	BP	2	BP2	01/06/19	21.99	87.72
JAN	U	NO	BP	2	BP2	01/07/19	26.94	81.67

JAN	U	NO	BP	2	BP2	01/08/19	24.17	84.46
JAN	U	NO	BP	2	BP2	01/09/19	25.21	81.37
JAN	U	NO	BP	2	BP2	01/10/19	23.88	85.26
JAN	U	NO	BP	2	BP2	01/11/19	23.3	89.08
JAN	U	NO	BP	2	BP2	01/12/19	22.61	90.71
JAN	U	NO	BP	2	BP2	01/13/19	23.79	93.51
JAN	U	NO	BP	2	BP2	01/14/19	23.71	91.2
JAN	U	NO	BP	2	BP2	01/15/19	25.91	84.3
JAN	U	NO	BP	2	BP2	01/16/19	25.87	89.12
JAN	U	NO	BP	2	BP2	01/17/19	27.63	90.04
JAN	U	NO	BP	2	BP2	01/18/19	22.59	94.31
JAN	U	NO	BP	2	BP2	01/19/19	25.74	94.97
JAN	U	NO	BP	2	BP2	01/20/19	22.25	96.08
JAN	U	NO	BP	2	BP2	01/21/19	23.47	96.17
JAN	U	NO	BP	2	BP2	01/22/19	22.32	94.94
JAN	U	NO	BP	2	BP2	01/23/19	24.29	90.59
JAN	U	NO	BP	2	BP2	01/24/19	26.33	88.88
JAN	U	NO	BP	2	BP2	01/25/19	24.12	87.95
JAN	U	NO	BP	2	BP2	01/26/19	25.43	83.11
JAN	U	NO	BP	2	BP2	01/27/19	26.52	77.35
JAN	U	NO	BP	2	BP2	01/28/19	26.09	77.24
JAN	U	NO	BP	2	BP2	01/29/19	27.24	76.08
JAN	U	NO	BP	2	BP2	01/30/19	27.7	72.01
JAN	U	NO	BP	2	BP2	01/31/19	27.41	74.92
FEB	U	NO	BP	2	BP2	02/01/19	25.19	83.92
FEB	U	NO	BP	2	BP2	02/02/19	25.7	86.83
FEB	U	NO	BP	2	BP2	02/03/19	23.42	92.12
FEB	U	NO	BP	2	BP2	02/04/19	20.32	94.11
FEB	U	NO	BP	2	BP2	02/05/19	20.72	93.56
FEB	U	NO	BP	2	BP2	02/06/19	18.87	93.61
FEB	U	NO	BP	2	BP2	02/07/19	20.51	92.55
FEB	U	NO	BP	2	BP2	02/08/19	22.23	87.52
FEB	U	NO	BP	2	BP2	02/09/19	23.59	83.71
FEB	U	NO	BP	2	BP2	02/10/19	26.62	83.56
FEB	U	NO	BP	2	BP2	02/11/19	25.11	88.49
FEB	U	NO	BP	2	BP2	02/12/19	23.86	91.25
FEB	U	NO	BP	2	BP2	02/13/19	18.75	92.2
FEB	U	NO	BP	2	BP2	02/14/19	20.34	91.27
FEB	U	NO	BP	2	BP2	02/15/19	23.93	91.54
FEB	U	NO	BP	2	BP2	02/16/19	22.47	94.1
FEB	U	NO	BP	2	BP2	02/17/19	21.8	91.93
FEB	U	NO	BP	2	BP2	02/18/19	22.94	91.95
FEB	U	NO	BP	2	BP2	02/19/19	22.2	92.22
FEB	U	NO	BP	2	BP2	02/20/19	23.64	89.52
FEB	U	NO	BP	2	BP2	02/21/19	21.8	87.15
FEB	U	NO	BP	2	BP2	02/22/19	21.37	82.5
FEB	U	NO	BP	2	BP2	02/23/19	24.41	76.96
FEB	U	NO	BP	2	BP2	02/24/19	27.43	67.11
FEB	U	NO	BP	2	BP2	02/25/19	24.2	84.45
FEB	U	NO	BP	2	BP2	02/26/19	20.89	89.3
FEB	U	NO	BP	2	BP2	02/27/19	19.6	91.9
FEB	U	NO	BP	2	BP2	02/28/19	19.13	93.01
MAR	U	NO	BP	2	BP2	03/01/19	18.41	90.7
MAR	U	NO	BP	2	BP2	03/02/19	21.29	83.77

MAR	U	NO	BP	2	BP2	03/03/19	21.25	87.52
MAR	U	NO	BP	2	BP2	03/04/19	21.65	84.3
MAR	U	NO	BP	2	BP2	03/05/19	26.74	73.99
MAR	U	NO	BP	2	BP2	03/06/19	23.21	84.19
MAR	U	NO	BP	2	BP2	03/07/19	25.04	85.83
MAR	U	NO	BP	2	BP2	03/08/19	24.82	86.73
MAR	U	NO	BP	2	BP2	03/09/19	24.15	90.73
MAR	U	NO	BP	2	BP2	03/10/19	20.98	93
MAR	U	NO	BP	2	BP2	03/11/19	20.08	91.77
MAR	U	NO	BP	2	BP2	03/12/19	20.89	92.66
MAR	U	NO	BP	2	BP2	03/13/19	22.35	92.71
MAR	U	NO	BP	2	BP2	03/14/19	21.96	94.53
MAR	U	NO	BP	2	BP2	03/15/19	19.41	90.88
MAR	U	NO	BP	2	BP2	03/16/19	21.27	91.58
MAR	U	NO	BP	2	BP2	03/17/19	23.42	92.58
MAR	U	NO	BP	2	BP2	03/18/19	24	93.62
MAR	U	NO	BP	2	BP2	03/19/19	22.2	94.95
MAR	U	NO	BP	2	BP2	03/20/19	20.79	93.48
MAR	U	NO	BP	2	BP2	03/21/19	19.06	95.04
MAR	U	NO	BP	2	BP2	03/22/19	15.27	95.39
MAR	U	NO	BP	2	BP2	03/23/19	17.39	96.03
MAR	U	YES	BP	2	BP2	03/24/19	17.27	94.87
MAR	U	YES	BP	2	BP2	03/25/19	19.32	91.52
MAR	U	YES	BP	2	BP2	03/26/19	15.03	92.09
MAR	U	YES	BP	2	BP2	03/27/19	17.42	93.07
MAR	U	YES	BP	2	BP2	03/28/19	18.53	93.61
MAR	U	YES	BP	2	BP2	03/29/19	18.3	92.89
MAR	U	YES	BP	2	BP2	03/30/19	22.18	87.61
MAR	U	NO	BP	2	BP2	03/31/19	22.8	85.76
APR	U	NO	BP	2	BP2	04/01/19	22.32	90.07
APR	U	NO	BP	2	BP2	04/02/19	21.49	87.16
APR	U	NO	BP	2	BP2	04/03/19	23.91	86.26
APR	U	NO	BP	2	BP2	04/04/19	23.88	83.09
APR	U	NO	BP	2	BP2	04/05/19	23.69	85.45
APR	U	NO	BP	2	BP2	04/06/19	20.17	89.52
APR	U	NO	BP	2	BP2	04/07/19	20.98	91.1
APR	U	NO	BP	2	BP2	04/08/19	20.41	93.38
APR	U	NO	BP	2	BP2	04/09/19	19.79	87.41
APR	U	NO	BP	2	BP2	04/10/19	16.46	91.91
APR	U	NO	BP	2	BP2	04/11/19	19.98	89.54
APR	U	NO	BP	2	BP2	04/12/19	20.89	89.25
APR	U	NO	BP	2	BP2	04/13/19	20.17	92.01
APR	U	NO	BP	2	BP2	04/14/19	19.79	92.77
APR	U	NO	BP	2	BP2	04/15/19	21.7	90.37
APR	U	NO	BP	2	BP2	04/16/19	22.39	91.36
APR	U	NO	BP	2	BP2	04/17/19	20.41	93.84
APR	U	NO	BP	2	BP2	04/18/19	18.37	95.14
APR	U	NO	BP	2	BP2	04/19/19	18.18	93.94
APR	U	NO	BP	2	BP2	04/20/19	20.03	92.42
APR	U	NO	BP	2	BP2	04/21/19	21.63	93.36
APR	U	NO	BP	2	BP2	04/22/19	18.65	93.85
APR	U	NO	BP	2	BP2	04/23/19	19.41	95.42
APR	U	NO	BP	2	BP2	04/24/19	19.89	97.06
APR	U	NO	BP	2	BP2	04/25/19	21.94	94.36

APR	U	NO	BP	2	BP2	04/26/19	22.37	94.97
APR	U	NO	BP	2	BP2	04/27/19	22.35	95.94
APR	U	NO	BP	2	BP2	04/28/19	21.6	97.42
APR	U	NO	BP	2	BP2	04/29/19	17.82	98.06
APR	U	NO	BP	2	BP2	04/30/19	15.61	98.57
MAY	U	NO	BP	2	BP2	05/01/19	19.46	97.81
MAY	U	NO	BP	2	BP2	05/02/19	17.01	98.83
MAY	U	NO	BP	2	BP2	05/03/19	20.17	97.25
MAY	U	NO	BP	2	BP2	05/04/19	22.99	97.23
MAY	U	NO	BP	2	BP2	05/05/19	23.42	96.73
MAY	U	NO	BP	2	BP2	05/06/19	22.49	97.69
MAY	U	NO	BP	2	BP2	05/07/19	19.46	99.1
MAY	U	NO	BP	2	BP2	05/08/19	15.41	99.84
MAY	U	NO	BP	2	BP2	05/09/19	19.32	99.22
MAY	U	NO	BP	2	BP2	05/10/19	21.41	97.86
MAY	U	NO	BP	2	BP2	05/11/19	20.17	98.86
MAY	U	NO	BP	2	BP2	05/12/19	16.75	100
MAY	U	NO	BP	2	BP2	05/13/19	18.41	100
MAY	U	NO	BP	2	BP2	05/14/19	17.63	100
MAY	U	NO	BP	2	BP2	05/15/19	18.03	100
MAY	U	NO	BP	2	BP2	05/16/19	20.96	77.15
MAY	U	NO	BP	2	BP2	05/17/19	20.91	62.9
MAY	U	NO	BP	2	BP2	05/18/19	21.41	70.05
MAY	U	NO	BP	2	BP2	05/19/19	22.27	72.49
MAY	U	NO	BP	2	BP2	05/20/19	22.97	75.33
MAY	U	NO	BP	2	BP2	05/21/19	23.88	76.02
MAY	U	NO	BP	2	BP2	05/22/19	22.47	84.17
DEC	U	NO	BP	4	BP extra x	12/01/18	23.12	94.9
DEC	U	NO	BP	4	BP extra x	12/02/18	18.3	93.41
DEC	U	NO	BP	4	BP extra x	12/03/18	13.61	93.14
DEC	U	NO	BP	4	BP extra x	12/04/18	13.32	85.07
DEC	U	NO	BP	4	BP extra x	12/05/18	15.94	86.01
DEC	U	NO	BP	4	BP extra x	12/06/18	16.01	82.93
DEC	U	NO	BP	4	BP extra x	12/07/18	17.06	80.73
DEC	U	NO	BP	4	BP extra x	12/08/18	11.44	75.27
DEC	U	NO	BP	4	BP extra x	12/09/18	14.72	72.33
DEC	U	NO	BP	4	BP extra x	12/10/18	20.58	71.23
DEC	U	NO	BP	4	BP extra x	12/11/18	19.35	71.05
DEC	U	NO	BP	4	BP extra x	12/12/18	26.61	69.76
DEC	U	NO	BP	4	BP extra x	12/13/18	23.43	73.6
DEC	U	NO	BP	4	BP extra x	12/14/18	25.42	62
DEC	U	NO	BP	4	BP extra x	12/15/18	24.37	80.73
DEC	U	NO	BP	4	BP extra x	12/16/18	25.15	76.33
DEC	U	NO	BP	4	BP extra x	12/17/18	26.41	54.2
DEC	U	NO	BP	4	BP extra x	12/18/18	25.44	85.54
DEC	U	NO	BP	4	BP extra x	12/19/18	24.32	78.86
DEC	U	NO	BP	4	BP extra x	12/20/18	24.88	71.99
DEC	U	NO	BP	4	BP extra x	12/21/18	23.72	89.15
DEC	U	NO	BP	4	BP extra x	12/22/18	23.12	71.03
DEC	U	NO	BP	4	BP extra x	12/23/18	22.76	73
DEC	U	NO	BP	4	BP extra x	12/24/18	21.83	78.45
DEC	U	NO	BP	4	BP extra x	12/25/18	21.28	68.11
DEC	U	NO	BP	4	BP extra x	12/26/18	22.78	60.99
DEC	U	NO	BP	4	BP extra x	12/27/18	22.04	58.67

DEC	U	NO	BP	4	BP extra x	12/28/18	24.88	55.71
DEC	U	NO	BP	4	BP extra x	12/29/18	22.23	54.73
DEC	U	NO	BP	4	BP extra x	12/30/18	24.62	53.22
DEC	U	NO	BP	4	BP extra x	12/31/18	28.43	71.99
JAN	U	NO	BP	4	BP extra x	01/01/19	26.32	55.48
JAN	U	NO	BP	4	BP extra x	01/02/19	28.63	53.92
JAN	U	NO	BP	4	BP extra x	01/03/19	30.99	71.2
JAN	U	NO	BP	4	BP extra x	01/04/19	23.5	87.31
JAN	U	NO	BP	4	BP extra x	01/05/19	22.83	87.42
JAN	U	NO	BP	4	BP extra x	01/06/19	23.5	73.58
JAN	U	NO	BP	4	BP extra x	01/07/19	27.91	71.85
JAN	U	NO	BP	4	BP extra x	01/08/19	25.51	72.7
JAN	U	NO	BP	4	BP extra x	01/09/19	26.17	81.18
JAN	U	NO	BP	4	BP extra x	01/10/19	24.78	81.89
JAN	U	NO	BP	4	BP extra x	01/11/19	24.57	87.4
JAN	U	NO	BP	4	BP extra x	01/12/19	23.94	90.78
JAN	U	NO	BP	4	BP extra x	01/13/19	24.95	78.25
JAN	U	NO	BP	4	BP extra x	01/14/19	25.12	81.98
JAN	U	NO	BP	4	BP extra x	01/15/19	26.83	67.04
JAN	U	NO	BP	4	BP extra x	01/16/19	25.54	73.18
JAN	U	NO	BP	4	BP extra x	01/17/19	27.4	85.03
JAN	U	NO	BP	4	BP extra x	01/18/19	22.69	88.78
JAN	U	NO	BP	4	BP extra x	01/19/19	25.71	91.17
JAN	U	NO	BP	4	BP extra x	01/20/19	22.54	88.92
JAN	U	NO	BP	4	BP extra x	01/21/19	23.79	91.83
JAN	U	NO	BP	4	BP extra x	01/22/19	22.09	74.86
JAN	U	NO	BP	4	BP extra x	01/23/19	24.04	68.04
JAN	U	NO	BP	4	BP extra x	01/24/19	26.44	69.03
JAN	U	NO	BP	4	BP extra x	01/25/19	23.72	67.79
JAN	U	NO	BP	4	BP extra x	01/26/19	25.1	67.14
JAN	U	NO	BP	4	BP extra x	01/27/19	25.98	64.82
JAN	U	NO	BP	4	BP extra x	01/28/19	25.66	56.02
JAN	U	NO	BP	4	BP extra x	01/29/19	27.15	58.26
JAN	U	NO	BP	4	BP extra x	01/30/19	27.59	53.53
JAN	U	NO	BP	4	BP extra x	01/31/19	27.37	56.74
FEB	U	NO	BP	4	BP extra x	02/01/19	25	65.38
FEB	U	NO	BP	4	BP extra x	02/02/19	25.51	76.52
FEB	U	NO	BP	4	BP extra x	02/03/19	23.55	86.91
FEB	U	NO	BP	4	BP extra x	02/04/19	19.89	86.02
FEB	U	NO	BP	4	BP extra x	02/05/19	20.39	80.17
FEB	U	NO	BP	4	BP extra x	02/06/19	18.11	78.27
FEB	U	NO	BP	4	BP extra x	02/07/19	20.13	75.41
FEB	U	NO	BP	4	BP extra x	02/08/19	22.04	68.27
FEB	U	NO	BP	4	BP extra x	02/09/19	23.48	62.16
FEB	U	NO	BP	4	BP extra x	02/10/19	26.93	76.12
FEB	U	NO	BP	4	BP extra x	02/11/19	25.22	76.38
FEB	U	NO	BP	4	BP extra x	02/12/19	24.18	85.2
FEB	U	NO	BP	4	BP extra x	02/13/19	18.68	86.63
FEB	U	NO	BP	4	BP extra x	02/14/19	20.11	72.24
FEB	U	NO	BP	4	BP extra x	02/15/19	24.25	89.19
FEB	U	NO	BP	4	BP extra x	02/16/19	22.64	89.55
FEB	U	NO	BP	4	BP extra x	02/17/19	22.19	80.61
FEB	U	NO	BP	4	BP extra x	02/18/19	23.29	79.71
FEB	U	NO	BP	4	BP extra x	02/19/19	22.5	81.4

FEB	U	NO	BP	4	BP extra x	02/20/19	23.75	72.9
FEB	U	NO	BP	4	BP extra x	02/21/19	21.71	73.22
FEB	U	NO	BP	4	BP extra x	02/22/19	21.16	70.4
FEB	U	NO	BP	4	BP extra x	02/23/19	24.3	64.06
FEB	U	NO	BP	4	BP extra x	02/24/19	27.4	54.94
FEB	U	NO	BP	4	BP extra x	02/25/19	24.52	86.57
FEB	U	NO	BP	4	BP extra x	02/26/19	21.3	87.19
FEB	U	NO	BP	4	BP extra x	02/27/19	19.82	87.45
FEB	U	NO	BP	4	BP extra x	02/28/19	19.39	84.9
MAR	U	NO	BP	4	BP extra x	03/01/19	18.34	82.92
MAR	U	NO	BP	4	BP extra x	03/02/19	21.01	66.94
MAR	U	NO	BP	4	BP extra x	03/03/19	21.78	77.65
MAR	U	NO	BP	4	BP extra x	03/04/19	22.11	68.89
MAR	U	NO	BP	4	BP extra x	03/05/19	26.86	60.7
MAR	U	NO	BP	4	BP extra x	03/06/19	23.65	80.71
MAR	U	NO	BP	4	BP extra x	03/07/19	25.39	76.41
MAR	U	NO	BP	4	BP extra x	03/08/19	25.17	87.35
MAR	U	NO	BP	4	BP extra x	03/09/19	24.42	91.09
MAR	U	NO	BP	4	BP extra x	03/10/19	21.23	90.41
MAR	U	NO	BP	4	BP extra x	03/11/19	20.32	86.91
MAR	U	NO	BP	4	BP extra x	03/12/19	21.09	90.46
MAR	U	NO	BP	4	BP extra x	03/13/19	22.64	92.02
MAR	U	NO	BP	4	BP extra x	03/14/19	22.02	87.05
MAR	U	NO	BP	4	BP extra x	03/15/19	19.54	84.09
MAR	U	NO	BP	4	BP extra x	03/16/19	21.8	86.11
MAR	U	NO	BP	4	BP extra x	03/17/19	24.08	89.51
MAR	U	NO	BP	4	BP extra x	03/18/19	24.54	90.9
MAR	U	NO	BP	4	BP extra x	03/19/19	22.86	90.84
MAR	U	NO	BP	4	BP extra x	03/20/19	21.35	91.46
MAR	U	NO	BP	4	BP extra x	03/21/19	19.77	90.46
MAR	U	NO	BP	4	BP extra x	03/22/19	16.27	90.6
MAR	U	NO	BP	4	BP extra x	03/23/19	18.11	88.56
MAR	U	NO	BP	4	BP extra x	03/24/19	18.3	85.22
MAR	U	NO	BP	4	BP extra x	03/25/19	20.25	85.4
MAR	U	NO	BP	4	BP extra x	03/26/19	16.56	83.38
MAR	U	NO	BP	4	BP extra x	03/27/19	18.92	80.81
MAR	U	NO	BP	4	BP extra x	03/28/19	19.94	84.23
MAR	U	NO	BP	4	BP extra x	03/29/19	19.46	84.23
MAR	U	NO	BP	4	BP extra x	03/30/19	22.76	74.7
MAR	U	NO	BP	4	BP extra x	03/31/19	23.79	82.54
APR	U	NO	BP	4	BP extra x	04/01/19	23.17	86.41
APR	U	NO	BP	4	BP extra x	04/02/19	22.16	81.99
APR	U	NO	BP	4	BP extra x	04/03/19	24.4	74.12
APR	U	NO	BP	4	BP extra x	04/04/19	24.54	78.63
APR	U	NO	BP	4	BP extra x	04/05/19	24.86	84.8
APR	U	NO	BP	4	BP extra x	04/06/19	21.28	88.85
APR	U	NO	BP	4	BP extra x	04/07/19	22.09	90.04
APR	U	NO	BP	4	BP extra x	04/08/19	21.44	88.64
APR	U	NO	BP	4	BP extra x	04/09/19	17.15	88.27
APR	U	NO	BP	4	BP extra x	04/10/19	16.96	87.74
APR	U	NO	BP	4	BP extra x	04/11/19	20.35	84.21
APR	U	NO	BP	4	BP extra x	04/12/19	21.8	88.36
APR	U	NO	BP	4	BP extra x	04/13/19	21.01	89.44
APR	U	NO	BP	4	BP extra x	04/14/19	20.61	83.76

APR	U	NO	BP	4	BP extra x	04/15/19 22.21	86.53
APR	U	NO	BP	4	BP extra x	04/16/19 23.14	90.63
APR	U	NO	BP	4	BP extra x	04/17/19 20.99	90.85
APR	U	NO	BP	4	BP extra x	04/18/19 19.13	86.65
APR	U	NO	BP	4	BP extra x	04/19/19 18.7	88.92
APR	U	NO	BP	4	BP extra x	04/20/19 20.7	89.2
APR	U	NO	BP	4	BP extra x	04/21/19 22.35	91.02
APR	U	NO	BP	4	BP extra x	04/22/19 19.49	89.81
APR	U	NO	BP	4	BP extra x	04/23/19 20.11	84.47
APR	U	NO	BP	4	BP extra x	04/24/19 21.18	81.91
APR	U	NO	BP	4	BP extra x	04/25/19 22.78	90.17
APR	U	NO	BP	4	BP extra x	04/26/19 23.07	93.24
APR	U	NO	BP	4	BP extra x	04/27/19 23.34	92.92
APR	U	NO	BP	4	BP extra x	04/28/19 22.35	93.08
APR	U	NO	BP	4	BP extra x	04/29/19 18.73	92.66
APR	U	NO	BP	4	BP extra x	04/30/19 16.08	90.68
MAY	U	NO	BP	4	BP extra x	05/01/19 20.44	90.44
MAY	U	NO	BP	4	BP extra x	05/02/19 17.92	88.17
MAY	U	NO	BP	4	BP extra x	05/03/19 20.94	75.9
MAY	U	NO	BP	4	BP extra x	05/04/19 24.13	92.86
MAY	U	NO	BP	4	BP extra x	05/05/19 24.3	90.07
MAY	U	NO	BP	4	BP extra x	05/06/19 23.34	92.17
MAY	U	NO	BP	4	BP extra x	05/07/19 20.39	92.12
MAY	U	NO	BP	4	BP extra x	05/08/19 16.42	88.42
MAY	U	NO	BP	4	BP extra x	05/09/19 20.39	93.21
MAY	U	NO	BP	4	BP extra x	05/10/19 22.35	89.97
MAY	U	NO	BP	4	BP extra x	05/11/19 21.11	91.12
MAY	U	NO	BP	4	BP extra x	05/12/19 18.06	93.08
MAY	U	NO	BP	4	BP extra x	05/13/19 19.49	92.4
MAY	U	NO	BP	4	BP extra x	05/14/19 18.49	92.67
MAY	U	NO	BP	4	BP extra x	05/15/19 19.11	99.2
MAY	U	NO	BP	4	BP extra x	05/16/19 20.99	75.73
MAY	U	NO	BP	4	BP extra x	05/17/19 20.92	62.17
MAY	U	NO	BP	4	BP extra x	05/18/19 21.42	69.7
MAY	U	NO	BP	4	BP extra x	05/19/19 22.31	71.81
MAY	U	NO	BP	4	BP extra x	05/20/19 22.98	74.94
MAY	U	NO	BP	4	BP extra x	05/21/19 23.84	75.93
MAY	U	NO	BP	4	BP extra x	05/22/19 22.47	80.67
DEC	H	NO	PA	1	PA1	12/01/18 23.91	86.54
DEC	H	NO	PA	1	PA1	12/02/18 18.15	82.41
DEC	H	NO	PA	1	PA1	12/03/18 16.08	78.45
DEC	H	NO	PA	1	PA1	12/04/18 16.34	74.65
DEC	H	NO	PA	1	PA1	12/05/18 20.6	78.77
DEC	H	NO	PA	1	PA1	12/06/18 18.06	79.01
DEC	H	NO	PA	1	PA1	12/07/18 17.49	73.93
DEC	H	NO	PA	1	PA1	12/08/18 13.88	78.23
DEC	H	NO	PA	1	PA1	12/09/18 16.37	81.34
DEC	H	NO	PA	1	PA1	12/10/18 20.27	77.26
DEC	H	NO	PA	1	PA1	12/11/18 21.77	74.26
DEC	H	NO	PA	1	PA1	12/12/18 26.55	76.73
DEC	H	NO	PA	1	PA1	12/13/18 24.17	80.96
DEC	H	NO	PA	1	PA1	12/14/18 23.98	78.82
DEC	H	NO	PA	1	PA1	12/15/18 23.62	81.4
DEC	H	NO	PA	1	PA1	12/16/18 24.36	83.49

DEC	H	NO	PA	1	PA1	12/17/18	25.45	71.51
DEC	H	NO	PA	1	PA1	12/18/18	24.15	80.64
DEC	H	NO	PA	1	PA1	12/19/18	23.59	83.16
DEC	H	NO	PA	1	PA1	12/20/18	24.36	82.62
DEC	H	NO	PA	1	PA1	12/21/18	22.78	85.73
DEC	H	NO	PA	1	PA1	12/22/18	23.91	86.06
DEC	H	NO	PA	1	PA1	12/23/18	22.51	83.05
DEC	H	NO	PA	1	PA1	12/24/18	20.63	81.69
DEC	H	NO	PA	1	PA1	12/25/18	20.41	80.2
DEC	H	NO	PA	1	PA1	12/26/18	23.69	80.04
DEC	H	NO	PA	1	PA1	12/27/18	23.18	79.34
DEC	H	NO	PA	1	PA1	12/28/18	22.87	79.42
DEC	H	NO	PA	1	PA1	12/29/18	24.53	73.83
DEC	H	NO	PA	1	PA1	12/30/18	24.77	76
DEC	H	NO	PA	1	PA1	12/31/18	27.11	77.15
JAN	H	NO	PA	1	PA1	01/01/19	26.74	79.72
JAN	H	NO	PA	1	PA1	01/02/19	26.82	77.26
JAN	H	NO	PA	1	PA1	01/03/19	29.59	74.56
JAN	H	NO	PA	1	PA1	01/04/19	22.66	83.85
JAN	H	NO	PA	1	PA1	01/05/19	21.77	83.9
JAN	H	NO	PA	1	PA1	01/06/19	22.87	81.71
JAN	H	NO	PA	1	PA1	01/07/19	27.01	76.99
JAN	H	NO	PA	1	PA1	01/08/19	24.44	78.6
JAN	H	NO	PA	1	PA1	01/09/19	26.06	78.32
JAN	H	NO	PA	1	PA1	01/10/19	25.02	79.88
JAN	H	NO	PA	1	PA1	01/11/19	25.87	80.35
JAN	H	NO	PA	1	PA1	01/12/19	23.79	84.08
JAN	H	NO	PA	1	PA1	01/13/19	24.58	85.84
JAN	H	NO	PA	1	PA1	01/14/19	25.84	80.77
JAN	H	NO	PA	1	PA1	01/15/19	25.89	82.07
JAN	H	NO	PA	1	PA1	01/16/19	25.33	81.64
JAN	H	NO	PA	1	PA1	01/17/19	27.83	83.08
JAN	H	NO	PA	1	PA1	01/18/19	23.57	87.29
JAN	H	NO	PA	1	PA1	01/19/19	24.82	89.13
JAN	H	NO	PA	1	PA1	01/20/19	20.87	90.56
JAN	H	NO	PA	1	PA1	01/21/19	23.09	89.31
JAN	H	NO	PA	1	PA1	01/22/19	22.11	88.76
JAN	H	NO	PA	1	PA1	01/23/19	24.05	86.45
JAN	H	NO	PA	1	PA1	01/24/19	27.73	83.03
JAN	H	NO	PA	1	PA1	01/25/19	23.57	84.45
JAN	H	NO	PA	1	PA1	01/26/19	25.04	81.85
JAN	H	NO	PA	1	PA1	01/27/19	24.27	80.66
JAN	H	NO	PA	1	PA1	01/28/19	25.31	78.75
JAN	H	NO	PA	1	PA1	01/29/19	26.38	73.07
JAN	H	NO	PA	1	PA1	01/30/19	27.06	71.35
JAN	H	NO	PA	1	PA1	01/31/19	28.15	70.24
FEB	H	NO	PA	1	PA1	02/01/19	24.77	79.51
FEB	H	NO	PA	1	PA1	02/02/19	25.4	82.15
FEB	H	NO	PA	1	PA1	02/03/19	22.44	84.87
FEB	H	NO	PA	1	PA1	02/04/19	19.46	83.07
FEB	H	NO	PA	1	PA1	02/05/19	18.25	81.66
FEB	H	NO	PA	1	PA1	02/06/19	19.46	80.53
FEB	H	NO	PA	1	PA1	02/07/19	21.32	80.9
FEB	H	NO	PA	1	PA1	02/08/19	22.73	80.9

FEB	H	NO	PA	1	PA1	02/09/19	23.86	79.57
FEB	H	NO	PA	1	PA1	02/10/19	27.7	73.33
FEB	H	NO	PA	1	PA1	02/11/19	24.87	80.34
FEB	H	NO	PA	1	PA1	02/12/19	23.62	81.06
FEB	H	NO	PA	1	PA1	02/13/19	19.2	82.38
FEB	H	NO	PA	1	PA1	02/14/19	21.56	80.88
FEB	H	NO	PA	1	PA1	02/15/19	23.5	80.73
FEB	H	NO	PA	1	PA1	02/16/19	22.59	85.03
FEB	H	NO	PA	1	PA1	02/17/19	21.75	84.89
FEB	H	NO	PA	1	PA1	02/18/19	24.24	82.58
FEB	H	NO	PA	1	PA1	02/19/19	23.57	82.09
FEB	H	NO	PA	1	PA1	02/20/19	24.32	81.23
FEB	H	NO	PA	1	PA1	02/21/19	22.71	79.21
FEB	H	NO	PA	1	PA1	02/22/19	23.74	79.06
FEB	H	NO	PA	1	PA1	02/23/19	24.75	80.77
FEB	H	NO	PA	1	PA1	02/24/19	25.91	76.49
FEB	H	NO	PA	1	PA1	02/25/19	23.88	84.09
FEB	H	NO	PA	1	PA1	02/26/19	20.84	87.7
FEB	H	NO	PA	1	PA1	02/27/19	19.84	88.64
FEB	H	NO	PA	1	PA1	02/28/19	18.18	87.87
MAR	H	NO	PA	1	PA1	03/01/19	19.27	88.15
MAR	H	NO	PA	1	PA1	03/02/19	21.89	87.31
MAR	H	NO	PA	1	PA1	03/03/19	23.76	84.47
MAR	H	NO	PA	1	PA1	03/04/19	23.26	85.78
MAR	H	NO	PA	1	PA1	03/05/19	25.28	83
MAR	H	NO	PA	1	PA1	03/06/19	22.94	85.86
MAR	H	NO	PA	1	PA1	03/07/19	23.88	87.24
MAR	H	NO	PA	1	PA1	03/08/19	25.33	85.14
MAR	H	NO	PA	1	PA1	03/09/19	23.95	87.54
MAR	H	NO	PA	1	PA1	03/10/19	20.48	88.25
MAR	H	NO	PA	1	PA1	03/11/19	19.2	86.04
MAR	H	NO	PA	1	PA1	03/12/19	20.94	85.93
MAR	H	NO	PA	1	PA1	03/13/19	23.67	87.13
MAR	H	NO	PA	1	PA1	03/14/19	21.84	87.29
MAR	H	NO	PA	1	PA1	03/15/19	21.25	85.1
MAR	H	NO	PA	1	PA1	03/16/19	22.66	85.61
MAR	H	NO	PA	1	PA1	03/17/19	24.34	84.88
MAR	H	NO	PA	1	PA1	03/18/19	23.81	88.94
MAR	H	NO	PA	1	PA1	03/19/19	23.71	89.5
MAR	H	NO	PA	1	PA1	03/20/19	21.18	86.59
MAR	H	NO	PA	1	PA1	03/21/19	17.99	86.57
MAR	H	NO	PA	1	PA1	03/22/19	16.73	85.81
MAR	H	NO	PA	1	PA1	03/23/19	18.94	85.71
MAR	H	NO	PA	1	PA1	03/24/19	19.44	86.48
MAR	H	NO	PA	1	PA1	03/25/19	20.6	79.79
MAR	H	NO	PA	1	PA1	03/26/19	19.39	80.53
MAR	H	NO	PA	1	PA1	03/27/19	19.58	82.79
MAR	H	NO	PA	1	PA1	03/28/19	20.63	86.16
MAR	H	NO	PA	1	PA1	03/29/19	22.42	85.17
MAR	H	NO	PA	1	PA1	03/30/19	20.29	84.86
MAR	H	NO	PA	1	PA1	03/31/19	22.99	86.29
APR	H	NO	PA	1	PA1	04/01/19	24.41	87.29
APR	H	NO	PA	1	PA1	04/02/19	22.15	85.97
APR	H	NO	PA	1	PA1	04/03/19	24.82	84.19

APR	H	NO	PA	1	PA1	04/04/19	24.87	84.81
APR	H	NO	PA	1	PA1	04/05/19	24.92	86.04
APR	H	NO	PA	1	PA1	04/06/19	20.72	87.41
APR	H	NO	PA	1	PA1	04/07/19	22.18	89.82
APR	H	NO	PA	1	PA1	04/08/19	19.94	90.43
APR	H	NO	PA	1	PA1	04/09/19	16.32	89.14
APR	H	NO	PA	1	PA1	04/10/19	17.96	88.63
APR	H	NO	PA	1	PA1	04/11/19	20.08	86.98
APR	H	NO	PA	1	PA1	04/12/19	23.33	87.87
APR	H	NO	PA	1	PA1	04/13/19	21.82	89.58
APR	H	NO	PA	1	PA1	04/14/19	23.35	89.36
APR	H	NO	PA	1	PA1	04/15/19	21.96	87.52
APR	H	NO	PA	1	PA1	04/16/19	22.23	87.96
APR	H	NO	PA	1	PA1	04/17/19	18.53	90.78
APR	H	NO	PA	1	PA1	04/18/19	17.63	91.27
APR	H	NO	PA	1	PA1	04/19/19	18.37	91.03
APR	H	NO	PA	1	PA1	04/20/19	20.01	89.87
APR	H	NO	PA	1	PA1	04/21/19	22.59	90.16
APR	H	NO	PA	1	PA1	04/22/19	19.44	90.33
APR	H	NO	PA	1	PA1	04/23/19	20.44	90.48
APR	H	NO	PA	1	PA1	04/24/19	21.41	89.84
APR	H	NO	PA	1	PA1	04/25/19	24.03	89.29
APR	H	NO	PA	1	PA1	04/26/19	23.83	91.46
APR	H	NO	PA	1	PA1	04/27/19	23.83	92.16
APR	H	NO	PA	1	PA1	04/28/19	21.65	92.45
APR	H	NO	PA	1	PA1	04/29/19	18.13	91.54
APR	H	NO	PA	1	PA1	04/30/19	14.7	91.63
MAY	H	NO	PA	1	PA1	05/01/19	20.39	90.78
MAY	H	NO	PA	1	PA1	05/02/19	16.42	89.8
MAY	H	NO	PA	1	PA1	05/03/19	19.6	89.82
MAY	H	NO	PA	1	PA1	05/04/19	23.83	92.27
MAY	H	NO	PA	1	PA1	05/05/19	22.92	92.79
MAY	H	NO	PA	1	PA1	05/06/19	22.85	92.75
MAY	H	NO	PA	1	PA1	05/07/19	18.22	93.55
MAY	H	NO	PA	1	PA1	05/08/19	14.65	92.54
MAY	H	NO	PA	1	PA1	05/09/19	20.2	91.9
MAY	H	NO	PA	1	PA1	05/10/19	21.32	91.35
MAY	H	NO	PA	1	PA1	05/11/19	21.68	93.14
MAY	H	NO	PA	1	PA1	05/12/19	16.8	94.21
MAY	H	NO	PA	1	PA1	05/13/19	18.51	93.89
MAY	H	NO	PA	1	PA1	05/14/19	17.72	94.25
MAY	H	NO	PA	1	PA1	05/15/19	18.94	94.18
MAY	H	NO	PA	1	PA1	05/16/19	17.99	94.64
MAY	H	NO	PA	1	PA1	05/17/19	14.86	93.84
MAY	H	NO	PA	1	PA1	05/18/19	15.06	91.7
MAY	H	NO	PA	1	PA1	05/19/19	18.01	90.42
MAY	H	NO	PA	1	PA1	05/20/19	16.75	89.74
MAY	H	NO	PA	1	PA1	05/21/19	21.03	89.53
MAY	H	NO	PA	1	PA1	05/22/19	20.37	91.78
DEC	U	NO	PA	2	PA2	12/01/18	21.41	99.32
DEC	U	NO	PA	2	PA2	12/02/18	16.08	100
DEC	U	NO	PA	2	PA2	12/03/18	13.28	99.75
DEC	U	NO	PA	2	PA2	12/04/18	13.52	99.17
DEC	U	NO	PA	2	PA2	12/05/18	17.58	96.47

DEC	U	NO	PA	2	PA2	12/06/18	15.77	95.1
DEC	U	NO	PA	2	PA2	12/07/18	15.44	93.16
DEC	U	NO	PA	2	PA2	12/08/18	11.27	92.64
DEC	U	NO	PA	2	PA2	12/09/18	13.43	92.04
DEC	U	NO	PA	2	PA2	12/10/18	17.51	90
DEC	U	NO	PA	2	PA2	12/11/18	19.32	85.13
DEC	U	NO	PA	2	PA2	12/12/18	24.48	81.99
DEC	U	NO	PA	2	PA2	12/13/18	21.94	80.27
DEC	U	NO	PA	2	PA2	12/14/18	22.18	79.48
DEC	U	NO	PA	2	PA2	12/15/18	21.75	80.24
DEC	U	NO	PA	2	PA2	12/16/18	22.32	82.27
DEC	U	NO	PA	2	PA2	12/17/18	23.04	78.3
DEC	U	NO	PA	2	PA2	12/18/18	22.13	79.74
DEC	U	NO	PA	2	PA2	12/19/18	21.65	82.05
DEC	U	NO	PA	2	PA2	12/20/18	22.42	80.25
DEC	U	NO	PA	2	PA2	12/21/18	21.37	83.7
DEC	U	NO	PA	2	PA2	12/22/18	22.13	86.8
DEC	U	NO	PA	2	PA2	12/23/18	20.44	84.51
DEC	U	NO	PA	2	PA2	12/24/18	18.51	82.74
DEC	U	NO	PA	2	PA2	12/25/18	18.63	80.88
DEC	U	NO	PA	2	PA2	12/26/18	21.89	77.49
DEC	U	NO	PA	2	PA2	12/27/18	21.08	77.83
DEC	U	NO	PA	2	PA2	12/28/18	20.98	76.7
DEC	U	NO	PA	2	PA2	12/29/18	22.99	63.07
DEC	U	NO	PA	2	PA2	12/30/18	22.68	72.3
DEC	U	NO	PA	2	PA2	12/31/18	25.14	72.54
JAN	U	NO	PA	2	PA2	01/01/19	24.8	75.66
JAN	U	NO	PA	2	PA2	01/02/19	24.7	74.4
JAN	U	NO	PA	2	PA2	01/03/19	27.58	71.04
JAN	U	NO	PA	2	PA2	01/04/19	21.06	73.68
JAN	U	NO	PA	2	PA2	01/05/19	19.89	76.3
JAN	U	NO	PA	2	PA2	01/06/19	20.98	78.62
JAN	U	NO	PA	2	PA2	01/07/19	24.73	77.36
JAN	U	NO	PA	2	PA2	01/08/19	22.42	78.82
JAN	U	NO	PA	2	PA2	01/09/19	24.2	77.47
JAN	U	NO	PA	2	PA2	01/10/19	23.3	77.68
JAN	U	NO	PA	2	PA2	01/11/19	24.03	76.47
JAN	U	NO	PA	2	PA2	01/12/19	22.27	79.25
JAN	U	NO	PA	2	PA2	01/13/19	22.8	81.92
JAN	U	NO	PA	2	PA2	01/14/19	24.2	80.21
JAN	U	NO	PA	2	PA2	01/15/19	24.48	80.41
JAN	U	NO	PA	2	PA2	01/16/19	24.15	81.61
JAN	U	NO	PA	2	PA2	01/17/19	26.65	81.95
JAN	U	NO	PA	2	PA2	01/18/19	23.04	86.28
JAN	U	NO	PA	2	PA2	01/19/19	24.17	87.22
JAN	U	NO	PA	2	PA2	01/20/19	20.22	88.69
JAN	U	NO	PA	2	PA2	01/21/19	22.44	89.13
JAN	U	NO	PA	2	PA2	01/22/19	21.41	88.19
JAN	U	NO	PA	2	PA2	01/23/19	23.06	85.3
JAN	U	NO	PA	2	PA2	01/24/19	26.38	83.39
JAN	U	NO	PA	2	PA2	01/25/19	22.61	84.78
JAN	U	NO	PA	2	PA2	01/26/19	23.86	83.47
JAN	U	NO	PA	2	PA2	01/27/19	23.18	80.93
JAN	U	NO	PA	2	PA2	01/28/19	24.46	79.02

JAN	U	NO	PA	2	PA2	01/29/19	25.67	76
JAN	U	NO	PA	2	PA2	01/30/19	26.16	74.49
JAN	U	NO	PA	2	PA2	01/31/19	26.84	72.22
FEB	U	NO	PA	2	PA2	02/01/19	23.57	74.65
FEB	U	NO	PA	2	PA2	02/02/19	24.12	77.53
FEB	U	NO	PA	2	PA2	02/03/19	21.51	81.06
FEB	U	NO	PA	2	PA2	02/04/19	18.63	81.13
FEB	U	NO	PA	2	PA2	02/05/19	17.37	80.14
FEB	U	NO	PA	2	PA2	02/06/19	18.51	80.64
FEB	U	NO	PA	2	PA2	02/07/19	19.89	80.59
FEB	U	NO	PA	2	PA2	02/08/19	20.84	79.76
FEB	U	NO	PA	2	PA2	02/09/19	22.42	77.52
FEB	U	NO	PA	2	PA2	02/10/19	26.23	73.3
FEB	U	NO	PA	2	PA2	02/11/19	23.42	76.91
FEB	U	NO	PA	2	PA2	02/12/19	22.61	79.03
FEB	U	NO	PA	2	PA2	02/13/19	17.84	80.96
FEB	U	NO	PA	2	PA2	02/14/19	20.1	80.6
FEB	U	NO	PA	2	PA2	02/15/19	22.06	80.98
FEB	U	NO	PA	2	PA2	02/16/19	20.75	83.18
FEB	U	NO	PA	2	PA2	02/17/19	20.17	82.89
FEB	U	NO	PA	2	PA2	02/18/19	22.87	82.08
FEB	U	NO	PA	2	PA2	02/19/19	22.18	82.41
FEB	U	NO	PA	2	PA2	02/20/19	22.85	83.32
FEB	U	NO	PA	2	PA2	02/21/19	21.32	79.79
FEB	U	NO	PA	2	PA2	02/22/19	22.06	78.73
FEB	U	NO	PA	2	PA2	02/23/19	23.33	75.99
FEB	U	NO	PA	2	PA2	02/24/19	24.2	71.45
FEB	U	NO	PA	2	PA2	02/25/19	22.56	79.21
FEB	U	NO	PA	2	PA2	02/26/19	19.79	83.23
FEB	U	NO	PA	2	PA2	02/27/19	18.53	87
FEB	U	NO	PA	2	PA2	02/28/19	17.08	91.23
MAR	U	NO	PA	2	PA2	03/01/19	17.8	93.82
MAR	U	NO	PA	2	PA2	03/02/19	20.2	95.54
MAR	U	NO	PA	2	PA2	03/03/19	22.23	94.35
MAR	U	NO	PA	2	PA2	03/04/19	21.27	98.01
MAR	U	NO	PA	2	PA2	03/05/19	23.76	90.62
MAR	U	NO	PA	2	PA2	03/06/19	21.29	92.19
MAR	U	NO	PA	2	PA2	03/07/19	22.27	95.16
MAR	U	NO	PA	2	PA2	03/08/19	24.29	92.38
MAR	U	NO	PA	2	PA2	03/09/19	22.56	94.47
MAR	U	YES	PA	2	PA2	03/10/19	19.01	96.7
MAR	U	YES	PA	2	PA2	03/11/19	17.39	97.45
MAR	U	YES	PA	2	PA2	03/12/19	19.22	97.51
MAR	U	YES	PA	2	PA2	03/13/19	22.11	96.05
MAR	U	YES	PA	2	PA2	03/14/19	20.22	91.11
MAR	U	YES	PA	2	PA2	03/15/19	19.56	91.28
MAR	U	YES	PA	2	PA2	03/16/19	21.18	87.43
MAR	U	NO	PA	2	PA2	03/17/19	22.85	89.64
MAR	U	NO	PA	2	PA2	03/18/19	22.25	92.62
MAR	U	NO	PA	2	PA2	03/19/19	22.32	92.62
MAR	U	NO	PA	2	PA2	03/20/19	19.7	91.78
MAR	U	NO	PA	2	PA2	03/21/19	16.15	90
MAR	U	NO	PA	2	PA2	03/22/19	12.97	93.3
MAR	U	NO	PA	2	PA2	03/23/19	16.46	93.56

MAR	U	NO	PA	2	PA2	03/24/19	16.77	93.33
MAR	U	NO	PA	2	PA2	03/25/19	18.77	81.44
MAR	U	NO	PA	2	PA2	03/26/19	16.42	88.34
MAR	U	NO	PA	2	PA2	03/27/19	17.06	90.07
MAR	U	NO	PA	2	PA2	03/28/19	18.91	92.06
MAR	U	NO	PA	2	PA2	03/29/19	20.51	91.48
MAR	U	NO	PA	2	PA2	03/30/19	18.37	91.19
MAR	U	NO	PA	2	PA2	03/31/19	21.34	90.74
APR	U	NO	PA	2	PA2	04/01/19	22.66	90.2
APR	U	NO	PA	2	PA2	04/02/19	20.46	88.77
APR	U	NO	PA	2	PA2	04/03/19	23.21	87.16
APR	U	NO	PA	2	PA2	04/04/19	23.23	86.01
APR	U	NO	PA	2	PA2	04/05/19	23.52	84.66
APR	U	NO	PA	2	PA2	04/06/19	19.56	88.71
APR	U	NO	PA	2	PA2	04/07/19	20.77	91.09
APR	U	NO	PA	2	PA2	04/08/19	18.87	92.38
APR	U	NO	PA	2	PA2	04/09/19	15.01	93.29
APR	U	NO	PA	2	PA2	04/10/19	16.13	93.86
APR	U	NO	PA	2	PA2	04/11/19	18.56	93.94
APR	U	NO	PA	2	PA2	04/12/19	21.84	92.52
APR	U	NO	PA	2	PA2	04/13/19	20.2	94.26
APR	U	NO	PA	2	PA2	04/14/19	21.84	94.58
APR	U	NO	PA	2	PA2	04/15/19	20.56	93.87
APR	U	NO	PA	2	PA2	04/16/19	20.51	93.91
APR	U	NO	PA	2	PA2	04/17/19	16.61	95.66
APR	U	NO	PA	2	PA2	04/18/19	16.15	96.58
APR	U	NO	PA	2	PA2	04/19/19	16.61	97.33
APR	U	NO	PA	2	PA2	04/20/19	18.49	97.03
APR	U	NO	PA	2	PA2	04/21/19	20.87	96.52
APR	U	NO	PA	2	PA2	04/22/19	17.89	97.09
APR	U	NO	PA	2	PA2	04/23/19	18.68	97.38
APR	U	NO	PA	2	PA2	04/24/19	19.79	98.09
APR	U	NO	PA	2	PA2	04/25/19	22.32	96.91
APR	U	NO	PA	2	PA2	04/26/19	22.23	97.64
APR	U	NO	PA	2	PA2	04/27/19	22.3	98.06
APR	U	NO	PA	2	PA2	04/28/19	20.6	98.3
APR	U	NO	PA	2	PA2	04/29/19	16.87	99.19
APR	U	NO	PA	2	PA2	04/30/19	13.45	99.61
MAY	U	NO	PA	2	PA2	05/01/19	18.68	98.58
MAY	U	NO	PA	2	PA2	05/02/19	14.96	99
MAY	U	NO	PA	2	PA2	05/03/19	17.84	99.57
MAY	U	NO	PA	2	PA2	05/04/19	22.23	98.09
MAY	U	NO	PA	2	PA2	05/05/19	21.58	98.47
MAY	U	NO	PA	2	PA2	05/06/19	21.75	98
MAY	U	NO	PA	2	PA2	05/07/19	17.37	98.58
MAY	U	NO	PA	2	PA2	05/08/19	13.76	99.35
MAY	U	NO	PA	2	PA2	05/09/19	18.79	98.46
MAY	U	NO	PA	2	PA2	05/10/19	20.01	97.7
MAY	U	NO	PA	2	PA2	05/11/19	20.46	97.81
MAY	U	NO	PA	2	PA2	05/12/19	15.96	98.8
MAY	U	NO	PA	2	PA2	05/13/19	17.46	98.45
MAY	U	NO	PA	2	PA2	05/14/19	16.99	99.15
MAY	U	NO	PA	2	PA2	05/15/19	17.89	98.69
MAY	U	NO	PA	2	PA2	05/16/19	17.08	99.38

MAY	U	NO	PA	2	PA2	05/17/19	14.27	100
MAY	U	NO	PA	2	PA2	05/18/19	14.39	99.71
MAY	U	NO	PA	2	PA2	05/19/19	17.18	99.07
MAY	U	NO	PA	2	PA2	05/20/19	16.03	98.86
MAY	U	NO	PA	2	PA2	05/21/19	19.94	97.94
MAY	U	NO	PA	2	PA2	05/22/19	19.22	96.25
DEC	U	NO	PA	5	PA extra y	12/01/18	23.5	92.2
DEC	U	NO	PA	5	PA extra y	12/02/18	18.49	94.5
DEC	U	NO	PA	5	PA extra y	12/03/18	16.32	93.55
DEC	U	NO	PA	5	PA extra y	12/04/18	16.18	93.91
DEC	U	NO	PA	5	PA extra y	12/05/18	19.84	89.78
DEC	U	NO	PA	5	PA extra y	12/06/18	18.03	88.95
DEC	U	NO	PA	5	PA extra y	12/07/18	17.61	87.94
DEC	U	NO	PA	5	PA extra y	12/08/18	14.03	87.26
DEC	U	NO	PA	5	PA extra y	12/09/18	15.84	87.03
DEC	U	NO	PA	5	PA extra y	12/10/18	19.7	84.12
DEC	U	NO	PA	5	PA extra y	12/11/18	21.32	76.66
DEC	U	NO	PA	5	PA extra y	12/12/18	26.11	75.51
DEC	U	NO	PA	5	PA extra y	12/13/18	23.38	78.31
DEC	U	NO	PA	5	PA extra y	12/14/18	23.35	81.94
DEC	U	NO	PA	5	PA extra y	12/15/18	22.9	81.9
DEC	U	NO	PA	5	PA extra y	12/16/18	23.38	82.39
DEC	U	NO	PA	5	PA extra y	12/17/18	24.51	73.26
DEC	U	NO	PA	5	PA extra y	12/18/18	23.33	79.97
DEC	U	NO	PA	5	PA extra y	12/19/18	22.54	82.94
DEC	U	NO	PA	5	PA extra y	12/20/18	23.69	82.51
DEC	U	NO	PA	5	PA extra y	12/21/18	22.23	87.04
DEC	U	NO	PA	5	PA extra y	12/22/18	23.35	87.7
DEC	U	NO	PA	5	PA extra y	12/23/18	21.94	85
DEC	U	NO	PA	5	PA extra y	12/24/18	19.89	84.74
DEC	U	NO	PA	5	PA extra y	12/25/18	19.96	82.57
DEC	U	NO	PA	5	PA extra y	12/26/18	22.92	82.12
DEC	U	NO	PA	5	PA extra y	12/27/18	22.23	78.54
DEC	U	NO	PA	5	PA extra y	12/28/18	22.3	73.7
DEC	U	NO	PA	5	PA extra y	12/29/18	24.1	62.63
DEC	U	NO	PA	5	PA extra y	12/30/18	23.95	72.06
DEC	U	NO	PA	5	PA extra y	12/31/18	26.43	75.76
JAN	U	NO	PA	5	PA extra y	01/01/19	25.89	72.43
JAN	U	NO	PA	5	PA extra y	01/02/19	26.11	71.55
JAN	U	NO	PA	5	PA extra y	01/03/19	28.87	72.3
JAN	U	NO	PA	5	PA extra y	01/04/19	21.87	80.38
JAN	U	NO	PA	5	PA extra y	01/05/19	21.37	81.87
JAN	U	NO	PA	5	PA extra y	01/06/19	22.27	80.4
JAN	U	NO	PA	5	PA extra y	01/07/19	26.06	78.05
JAN	U	NO	PA	5	PA extra y	01/08/19	23.81	77.47
JAN	U	NO	PA	5	PA extra y	01/09/19	25.31	78.54
JAN	U	NO	PA	5	PA extra y	01/10/19	24.39	79.61
JAN	U	NO	PA	5	PA extra y	01/11/19	25.23	81.14
JAN	U	NO	PA	5	PA extra y	01/12/19	23.04	84.57
JAN	U	NO	PA	5	PA extra y	01/13/19	23.86	84.66
JAN	U	NO	PA	5	PA extra y	01/14/19	25.45	78.89
JAN	U	NO	PA	5	PA extra y	01/15/19	25.55	78.7
JAN	U	NO	PA	5	PA extra y	01/16/19	25.11	79.69
JAN	U	NO	PA	5	PA extra y	01/17/19	26.92	80.53

JAN	U	NO	PA	5	PA extra y	01/18/19 23.04	84.2
JAN	U	NO	PA	5	PA extra y	01/19/19 24.34	86.57
JAN	U	NO	PA	5	PA extra y	01/20/19 20.34	87.59
JAN	U	NO	PA	5	PA extra y	01/21/19 22.54	87.71
JAN	U	NO	PA	5	PA extra y	01/22/19 21.46	86.92
JAN	U	NO	PA	5	PA extra y	01/23/19 23.18	83.65
JAN	U	NO	PA	5	PA extra y	01/24/19 26.74	80.46
JAN	U	NO	PA	5	PA extra y	01/25/19 22.9	82.01
JAN	U	NO	PA	5	PA extra y	01/26/19 24.2	79.54
JAN	U	NO	PA	5	PA extra y	01/27/19 23.52	76.45
JAN	U	NO	PA	5	PA extra y	01/28/19 25.02	71.83
JAN	U	NO	PA	5	PA extra y	01/29/19 26.3	66.88
JAN	U	NO	PA	5	PA extra y	01/30/19 26.55	64.92
JAN	U	NO	PA	5	PA extra y	01/31/19 27.26	68.39
FEB	U	NO	PA	5	PA extra y	02/01/19 24.1	74.23
FEB	U	NO	PA	5	PA extra y	02/02/19 24.48	76.95
FEB	U	NO	PA	5	PA extra y	02/03/19 21.75	81.38
FEB	U	NO	PA	5	PA extra y	02/04/19 18.84	81.36
FEB	U	NO	PA	5	PA extra y	02/05/19 17.51	80.92
FEB	U	NO	PA	5	PA extra y	02/06/19 18.65	81.35
FEB	U	NO	PA	5	PA extra y	02/07/19 20.22	81.27
FEB	U	NO	PA	5	PA extra y	02/08/19 21.06	80.85
FEB	U	NO	PA	5	PA extra y	02/09/19 22.63	78.34
FEB	U	NO	PA	5	PA extra y	02/10/19 26.52	72.42
FEB	U	NO	PA	5	PA extra y	02/11/19 23.62	77.57
FEB	U	NO	PA	5	PA extra y	02/12/19 22.75	79.58
FEB	U	NO	PA	5	PA extra y	02/13/19 17.99	81.47
FEB	U	NO	PA	5	PA extra y	02/14/19 20.27	81.66
FEB	U	NO	PA	5	PA extra y	02/15/19 22.13	80.53
FEB	U	NO	PA	5	PA extra y	02/16/19 20.87	83.4
FEB	U	NO	PA	5	PA extra y	02/17/19 20.32	84.57
FEB	U	NO	PA	5	PA extra y	02/18/19 22.99	83.93
FEB	U	NO	PA	5	PA extra y	02/19/19 22.27	84.52
FEB	U	NO	PA	5	PA extra y	02/20/19 23.06	84.51
FEB	U	NO	PA	5	PA extra y	02/21/19 21.6	83.49
FEB	U	NO	PA	5	PA extra y	02/22/19 22.37	81.89
FEB	U	NO	PA	5	PA extra y	02/23/19 23.74	80.12
FEB	U	NO	PA	5	PA extra y	02/24/19 24.56	74.3
FEB	U	NO	PA	5	PA extra y	02/25/19 22.94	82.66
FEB	U	NO	PA	5	PA extra y	02/26/19 20.01	88.43
FEB	U	NO	PA	5	PA extra y	02/27/19 18.89	89.57
FEB	U	NO	PA	5	PA extra y	02/28/19 17.63	90.31
MAR	U	NO	PA	5	PA extra y	03/01/19 18.41	90.64
MAR	U	NO	PA	5	PA extra y	03/02/19 20.84	89.54
MAR	U	NO	PA	5	PA extra y	03/03/19 22.99	87.57
MAR	U	NO	PA	5	PA extra y	03/04/19 22.23	90.13
MAR	U	NO	PA	5	PA extra y	03/05/19 24.39	84.77
MAR	U	NO	PA	5	PA extra y	03/06/19 21.77	89.38
MAR	U	NO	PA	5	PA extra y	03/07/19 22.99	85.22
MAR	U	NO	PA	5	PA extra y	03/08/19 24.75	89.05
MAR	U	NO	PA	5	PA extra y	03/09/19 23.4	91.8
MAR	U	NO	PA	5	PA extra y	03/10/19 19.98	88.6
MAR	U	NO	PA	5	PA extra y	03/11/19 18.41	90.94
MAR	U	NO	PA	5	PA extra y	03/12/19 20.22	93.06

MAR	U	NO	PA	5	PA extra y	03/13/19	22.68	92.59
MAR	U	NO	PA	5	PA extra y	03/14/19	20.75	92.93
MAR	U	NO	PA	5	PA extra y	03/15/19	20.03	91.57
MAR	U	NO	PA	5	PA extra y	03/16/19	21.82	91.72
MAR	U	NO	PA	5	PA extra y	03/17/19	23.33	90.71
MAR	U	YES	PA	5	PA extra y	03/18/19	22.92	94.17
MAR	U	YES	PA	5	PA extra y	03/19/19	23.02	95.11
MAR	U	YES	PA	5	PA extra y	03/20/19	20.22	91.93
MAR	U	YES	PA	5	PA extra y	03/21/19	16.75	92.94
MAR	U	YES	PA	5	PA extra y	03/22/19	14	94.57
MAR	U	YES	PA	5	PA extra y	03/23/19	17.37	93.78
MAR	U	YES	PA	5	PA extra y	03/24/19	17.65	93.31
MAR	U	NO	PA	5	PA extra y	03/25/19	19.58	86.45
MAR	U	NO	PA	5	PA extra y	03/26/19	17.51	89
MAR	U	NO	PA	5	PA extra y	03/27/19	17.84	90.09
MAR	U	NO	PA	5	PA extra y	03/28/19	19.06	91.08
MAR	U	NO	PA	5	PA extra y	03/29/19	20.94	91.11
MAR	U	NO	PA	5	PA extra y	03/30/19	18.75	89.69
MAR	U	NO	PA	5	PA extra y	03/31/19	21.77	87.99
APR	U	NO	PA	5	PA extra y	04/01/19	22.94	87.78
APR	U	NO	PA	5	PA extra y	04/02/19	20.77	87.28
APR	U	NO	PA	5	PA extra y	04/03/19	23.59	82.02
APR	U	NO	PA	5	PA extra y	04/04/19	23.57	79.89
APR	U	NO	PA	5	PA extra y	04/05/19	23.67	82.48
APR	U	NO	PA	5	PA extra y	04/06/19	19.98	85.67
APR	U	NO	PA	5	PA extra y	04/07/19	21.03	87.93
APR	U	NO	PA	5	PA extra y	04/08/19	19.13	88.36
APR	U	NO	PA	5	PA extra y	04/09/19	15.29	89.47
APR	U	NO	PA	5	PA extra y	04/10/19	16.37	88.78
APR	U	NO	PA	5	PA extra y	04/11/19	18.94	88.43
APR	U	NO	PA	5	PA extra y	04/12/19	22.18	86.66
APR	U	NO	PA	5	PA extra y	04/13/19	20.56	87.85
APR	U	NO	PA	5	PA extra y	04/14/19	22.3	88.79
APR	U	NO	PA	5	PA extra y	04/15/19	20.72	87.93
APR	U	NO	PA	5	PA extra y	04/16/19	20.7	88.57
APR	U	NO	PA	5	PA extra y	04/17/19	16.75	91.17
APR	U	NO	PA	5	PA extra y	04/18/19	16.27	92.38
APR	U	NO	PA	5	PA extra y	04/19/19	16.94	93.19
APR	U	NO	PA	5	PA extra y	04/20/19	18.82	93
APR	U	NO	PA	5	PA extra y	04/21/19	21.1	92.41
APR	U	NO	PA	5	PA extra y	04/22/19	18.11	93.27
APR	U	NO	PA	5	PA extra y	04/23/19	18.79	93.22
APR	U	NO	PA	5	PA extra y	04/24/19	19.94	93.83
APR	U	NO	PA	5	PA extra y	04/25/19	22.49	93.18
APR	U	NO	PA	5	PA extra y	04/26/19	22.54	94.06
APR	U	NO	PA	5	PA extra y	04/27/19	22.44	94.54
APR	U	NO	PA	5	PA extra y	04/28/19	20.72	95.31
APR	U	NO	PA	5	PA extra y	04/29/19	16.99	95.88
APR	U	NO	PA	5	PA extra y	04/30/19	13.35	96.12
MAY	U	NO	PA	5	PA extra y	05/01/19	18.77	95.47
MAY	U	NO	PA	5	PA extra y	05/02/19	14.79	95.7
MAY	U	NO	PA	5	PA extra y	05/03/19	17.77	96.17
MAY	U	NO	PA	5	PA extra y	05/04/19	22.27	95.43
MAY	U	NO	PA	5	PA extra y	05/05/19	21.6	96.16

MAY	U	NO	PA	5	PA extra y	05/06/19	21.89	96.16
MAY	U	NO	PA	5	PA extra y	05/07/19	17.32	96.72
MAY	U	NO	PA	5	PA extra y	05/08/19	13.59	97.44
MAY	U	NO	PA	5	PA extra y	05/09/19	18.72	96.45
MAY	U	NO	PA	5	PA extra y	05/10/19	20.01	95.55
MAY	U	NO	PA	5	PA extra y	05/11/19	20.46	95.98
MAY	U	NO	PA	5	PA extra y	05/12/19	15.92	97.14
MAY	U	NO	PA	5	PA extra y	05/13/19	17.42	96.75
MAY	U	NO	PA	5	PA extra y	05/14/19	16.84	97.48
MAY	U	NO	PA	5	PA extra y	05/15/19	17.89	97.3
MAY	U	NO	PA	5	PA extra y	05/16/19	16.99	97.97
MAY	U	NO	PA	5	PA extra y	05/17/19	14.03	98.46
MAY	U	NO	PA	5	PA extra y	05/18/19	14.12	98.22
MAY	U	NO	PA	5	PA extra y	05/19/19	17.01	97.73
MAY	U	NO	PA	5	PA extra y	05/20/19	15.87	98.49
MAY	U	NO	PA	5	PA extra y	05/21/19	19.87	97.21
MAY	U	NO	PA	5	PA extra y	05/22/19	19.22	95.74

Table S3(c): whole bee weight.

Month	**Health in march**	**Intensity**	**Locality**	**Sisters**	**Colony**	**Weight (g)**
APR	H	H	BP	1	BP1	0.0695
APR	H	H	BP	1	BP1	0.0611
APR	H	H	BP	1	BP1	0.0679
APR	H	H	BP	1	BP1	0.0635
APR	H	H	BP	1	BP1	0.0751
DEC	H	H	BP	1	BP1	0.0594
DEC	H	H	BP	1	BP1	0.0642
DEC	H	H	BP	1	BP1	0.0642
DEC	H	H	BP	1	BP1	0.0648
DEC	H	H	BP	1	BP1	0.0493
FEB	H	H	BP	1	BP1	0.0716
FEB	H	H	BP	1	BP1	0.0679
FEB	H	H	BP	1	BP1	0.0664
FEB	H	H	BP	1	BP1	0.0731
FEB	H	H	BP	1	BP1	0.0789
JAN	H	H	BP	1	BP1	0.0694
JAN	H	H	BP	1	BP1	0.0744
JAN	H	H	BP	1	BP1	0.0573
JAN	H	H	BP	1	BP1	0.0743
JAN	H	H	BP	1	BP1	0.0716
MAY	H	H	BP	1	BP1	0.0689
MAY	H	H	BP	1	BP1	0.0588
MAY	H	H	BP	1	BP1	0.0695
MAY	H	H	BP	1	BP1	0.0708
MAY	H	H	BP	1	BP1	0.0674
MAR	H	H	BP	1	BP1	0.0619
MAR	H	H	BP	1	BP1	0.0633
MAR	H	H	BP	1	BP1	0.0650
MAR	H	H	BP	1	BP1	0.0649
MAR	H	H	BP	1	BP1	0.0613
APR	U	U	BP	2	BP2	0.0644
APR	U	U	BP	2	BP2	0.0663
APR	U	U	BP	2	BP2	0.0625
APR	U	U	BP	2	BP2	0.0547
APR	U	U	BP	2	BP2	0.0608
DEC	U	U	BP	2	BP2	0.0588
DEC	U	U	BP	2	BP2	0.0798
DEC	U	U	BP	2	BP2	0.0678
DEC	U	U	BP	2	BP2	0.0660
DEC	U	U	BP	2	BP2	0.0718
FEB	U	U	BP	2	BP2	0.0750
FEB	U	U	BP	2	BP2	0.0810
FEB	U	U	BP	2	BP2	0.0657
FEB	U	U	BP	2	BP2	0.0746
FEB	U	U	BP	2	BP2	0.0790
JAN	U	U	BP	2	BP2	0.0792
JAN	U	U	BP	2	BP2	0.0655
JAN	U	U	BP	2	BP2	0.0789
JAN	U	U	BP	2	BP2	0.0736

JAN	U	U	BP	2	BP2	0.0694
MAY	U	U	BP	2	BP2	0.0557
MAY	U	U	BP	2	BP2	0.0668
MAY	U	U	BP	2	BP2	0.0711
MAY	U	U	BP	2	BP2	0.0635
MAY	U	U	BP	2	BP2	0.0544
MAR	U	U	BP	2	BP2	0.0680
MAR	U	U	BP	2	BP2	0.0670
MAR	U	U	BP	2	BP2	0.0592
MAR	U	U	BP	2	BP2	0.0574
MAR	U	U	BP	2	BP2	0.0671
APR	U	U	BP	3	BP3	0.0647
APR	U	U	BP	3	BP3	0.0681
APR	U	U	BP	3	BP3	0.0624
APR	U	U	BP	3	BP3	0.0581
APR	U	U	BP	3	BP3	0.0567
DEC	U	U	BP	3	BP3	0.0683
DEC	U	U	BP	3	BP3	0.0681
DEC	U	U	BP	3	BP3	0.0694
DEC	U	U	BP	3	BP3	0.0655
DEC	U	U	BP	3	BP3	0.0707
FEB	U	U	BP	3	BP3	0.0715
FEB	U	U	BP	3	BP3	0.0776
FEB	U	U	BP	3	BP3	0.0776
FEB	U	U	BP	3	BP3	0.0706
FEB	U	U	BP	3	BP3	0.0726
JAN	U	U	BP	3	BP3	0.0956
JAN	U	U	BP	3	BP3	0.0691
JAN	U	U	BP	3	BP3	0.0849
JAN	U	U	BP	3	BP3	0.0811
JAN	U	U	BP	3	BP3	0.0717
MAY	U	U	BP	3	BP3	0.0554
MAY	U	U	BP	3	BP3	0.0551
MAY	U	U	BP	3	BP3	0.0665
MAY	U	U	BP	3	BP3	0.0684
MAY	U	U	BP	3	BP3	0.0629
MAR	U	U	BP	3	BP3	0.0588
MAR	U	U	BP	3	BP3	0.0560
MAR	U	U	BP	3	BP3	0.0567
MAR	U	U	BP	3	BP3	0.0597
MAR	U	U	BP	3	BP3	0.0593
JAN	H	H	PA	1	PA1	0.0669
JAN	U	SU	PA	2	PA2	0.0841
JAN	U	SU	PA	3	PA3	0.0701
APR	H	H	PA	1	PA1	0.0686
APR	H	H	PA	1	PA1	0.0688
APR	H	H	PA	1	PA1	0.0652
APR	H	H	PA	1	PA1	0.0558
APR	H	H	PA	1	PA1	0.0652
DEC	H	H	PA	1	PA1	0.0611
DEC	H	H	PA	1	PA1	0.0736

DEC	H	H	PA	1	PA1	0.0747
DEC	H	H	PA	1	PA1	0.0812
DEC	H	H	PA	1	PA1	0.0725
FEB	H	H	PA	1	PA1	0.0633
FEB	H	H	PA	1	PA1	0.0718
FEB	H	H	PA	1	PA1	0.0707
FEB	H	H	PA	1	PA1	0.0755
FEB	H	H	PA	1	PA1	0.0635
JAN	H	H	PA	1	PA1	0.0711
JAN	H	H	PA	1	PA1	0.0617
JAN	H	H	PA	1	PA1	0.0787
JAN	H	H	PA	1	PA1	0.0716
MAY	H	H	PA	1	PA1	0.0764
MAY	H	H	PA	1	PA1	0.0760
MAY	H	H	PA	1	PA1	0.0806
MAY	H	H	PA	1	PA1	0.0757
MAY	H	H	PA	1	PA1	0.0700
MAR	H	H	PA	1	PA1	0.0626
MAR	H	H	PA	1	PA1	0.0608
MAR	H	H	PA	1	PA1	0.0712
MAR	H	H	PA	1	PA1	0.0668
MAR	H	H	PA	1	PA1	0.0650
APR	U	SU	PA	2	PA2	0.0657
APR	U	SU	PA	2	PA2	0.0606
APR	U	SU	PA	2	PA2	0.0591
APR	U	SU	PA	2	PA2	0.0666
APR	U	SU	PA	2	PA2	0.0717
DEC	U	SU	PA	2	PA2	0.0720
DEC	U	SU	PA	2	PA2	0.0756
DEC	U	SU	PA	2	PA2	0.0654
DEC	U	SU	PA	2	PA2	0.0774
DEC	U	SU	PA	2	PA2	0.0801
FEB	U	SU	PA	2	PA2	0.0726
FEB	U	SU	PA	2	PA2	0.0744
FEB	U	SU	PA	2	PA2	0.0715
FEB	U	SU	PA	2	PA2	0.0692
FEB	U	SU	PA	2	PA2	0.0625
JAN	U	SU	PA	2	PA2	0.0764
JAN	U	SU	PA	2	PA2	0.0736
JAN	U	SU	PA	2	PA2	0.0802
JAN	U	SU	PA	2	PA2	0.0833
MAY	U	SU	PA	2	PA2	0.0806
MAY	U	SU	PA	2	PA2	0.0757
MAY	U	SU	PA	2	PA2	0.0721
MAY	U	SU	PA	2	PA2	0.0652
MAY	U	SU	PA	2	PA2	0.0695
MAR	U	SU	PA	2	PA2	0.0633
MAR	U	SU	PA	2	PA2	0.0622
MAR	U	SU	PA	2	PA2	0.0615
MAR	U	SU	PA	2	PA2	0.0697
MAR	U	SU	PA	2	PA2	0.0753

APR	U	SU	PA	3	PA3	0.0577
APR	U	SU	PA	3	PA3	0.0688
APR	U	SU	PA	3	PA3	0.0728
APR	U	SU	PA	3	PA3	0.0862
APR	U	SU	PA	3	PA3	0.0713
DEC	U	SU	PA	3	PA3	0.0645
DEC	U	SU	PA	3	PA3	0.0655
DEC	U	SU	PA	3	PA3	0.0601
DEC	U	SU	PA	3	PA3	0.0785
DEC	U	SU	PA	3	PA3	0.0633
FEB	U	SU	PA	3	PA3	0.0674
FEB	U	SU	PA	3	PA3	0.0874
FEB	U	SU	PA	3	PA3	0.0633
FEB	U	SU	PA	3	PA3	0.0715
FEB	U	SU	PA	3	PA3	0.0695
JAN	U	SU	PA	3	PA3	0.0657
JAN	U	SU	PA	3	PA3	0.0672
JAN	U	SU	PA	3	PA3	0.0655
JAN	U	SU	PA	3	PA3	0.0717
MAY	U	SU	PA	3	PA3	0.0676
MAY	U	SU	PA	3	PA3	0.0667
MAY	U	SU	PA	3	PA3	0.0698
MAY	U	SU	PA	3	PA3	0.0780
MAY	U	SU	PA	3	PA3	0.0655
MAR	U	SU	PA	3	PA3	0.0684
MAR	U	SU	PA	3	PA3	0.0628
MAR	U	SU	PA	3	PA3	0.0458
MAR	U	SU	PA	3	PA3	0.0635
MAR	U	SU	PA	3	PA3	0.0659

Table S3(d): glucose oxidase (GOX) activity from a five-head pool, represented by the Relative Fluorescence Unit per min/μL and /g

Month	Health in March	Intensity	Locality	Sisters	Colony	RFU/min/uL	RFU/min/g
APR	H	H	BP	1	BP1	3.28	3.89
APR	U	U	BP	2	BP2	2.76	3.58
APR	U	U	BP	3	BP3	2.85	3.68
APR	H	H	PA	1	PA1	3.86	4.77
APR	U	SU	PA	2	PA2	3.43	4.24
APR	U	SU	PA	3	PA3	3.38	3.79
FEB	H	H	BP	1	BP1	3.46	3.86
FEB	U	U	BP	2	BP2	3.52	3.75
FEB	U	U	BP	3	BP3	3.80	4.11
FEB	H	H	PA	1	PA1	3.08	3.57
FEB	U	SU	PA	2	PA2	4.06	4.64
FEB	U	SU	PA	3	PA3	3.49	3.89
JAN	H	H	BP	1	BP1	3.27	3.77
JAN	U	U	BP	2	BP2	3.36	3.67
JAN	U	U	BP	3	BP3	4.64	4.61
JAN	H	H	PA	1	PA1	2.44	2.79
JAN	U	SU	PA	2	PA2	2.93	2.94
JAN	U	SU	PA	3	PA3	3.41	4.01
MAR	H	H	BP	1	BP1	3.12	3.95
MAR	U	U	BP	2	BP2	2.80	3.52
MAR	U	U	BP	3	BP3	3.28	4.51
MAR	H	H	PA	1	PA1	3.18	3.90
MAR	U	SU	PA	2	PA2	8.33	10.04
MAR	U	SU	PA	3	PA3	3.15	4.11

Table S3(e): taxonomic characterization (at Family and/or genus level) of stored pollen of different colonies.

				Eucalyptus	**Myrtaceae**	**Pleroma cf. granulosa**	**Asteraceae**	**Solanum**	**Parapiptadenia rigida**	**Moraceae**	**Allophylus edulis**	**Salix humboldtiana**	**Sebastiania commersoniana**
Month	**Health in March**	**Locality**	**Colony**	**Myrtaceae**	**Myrtaceae**	**Melastomataceae**	**Asteraceae**	**Solanaceae**	**Fabaceae**	**Moraceae**	**Sapindaceae**	**Salicaceae**	**Euphorbioideae**
FEB	H	BP	BP b	1	26	0	0	0	0	0	0	0	0
FEB	H	BP	BP1	1	1	0	0	0	0	0	0	0	0
FEB	H	PA	PA3	26	8	0	0	0	0	0	0	0	0
JAN	H	BP	BP b	175	204	0	0	7	0	0	0	0	0
JAN	H	PA	PA3	1	522	0	0	1	1	0	1	0	0
MAR	U	BP	BP e	55	13	0	0	0	0	0	0	0	0
MAR	U	BP	BP f	148	1	0	0	0	0	0	0	0	0
MAR	H	BP	BP b	11	8	0	0	0	0	0	0	0	0
MAR	H	BP	BP1	53	103	0	0	0	0	0	0	0	0
MAR	U	BP	BP c	177	22	0	0	0	0	0	0	0	0
MAR	U	BP	BP d	10	9	0	0	0	0	0	0	0	0
MAR	H	PA	PA1	4	5	0	0	1	0	0	0	0	0
MAR	U	PA	PA2	1	56	0	0	0	0	0	0	0	0
MAR	U	SL	SL	1	98	0	1	1	1	0	1	0	0
NOV	H	BP	BP b	4	540	0	0	56	0	0	0	0	0
NOV	H	BP	BP1	1	500	0	0	65	0	0	0	0	0
NOV	U	BP	BP2	1	508	0	1	5	0	0	0	0	0
NOV	U	PA	PA g	365	259	0	1	25	15	0	0	0	0
NOV	H	PA	PA1	119	456	0	1	0	21	0	0	0	0
NOV	U	PA	PA2	431	48	0	1	2	59	0	0	0	0
OCT	H	BP	BP a	94	533	0	0	0	1	0	0	0	0
OCT	H	BP	BP b	11	592	0	0	0	1	0	0	0	0
OCT	H	BP	BP1	248	335	1	0	1	1	0	0	0	0
OCT	U	BP	BP2	4	530	0	0	1	0	0	0	0	0
OCT	U	PA	PA g	560	36	0	1	2	1	0	0	0	0
OCT	H	PA	PA1	205	350	2	1	3	1	0	0	0	0
OCT	U	PA	PA2	154	377	4	1	4	1	0	0	0	0
SET	H	BP	BP b	109	124	37	1	98	11	46	3	16	0
SET	H	BP	BP1	8	111	271	0	8	0	0	0	0	2
SET	U	PA	PA g	109	175	7	2	10	0	0	0	0	0
SET	H	PA	PA1	146	260	1	0	1	0	0	0	0	0

Table S3(e, continuation): taxonomic characterization (at Family and/or genus level) of stored pollen of different colonies.

				Triporado	**Mimosa**	**Begonia**	**tipo Syagrus romanzo**	**Mimosa bimucronata**	**Matayba elaegnoides**	**Caesalpinia cf. peltophoroides**	**Casearia sylvestris**	**Senna**	**Trichilia pallens**
Month	**Health in March**	**Locality**	**Colony**	**Outro**	**Fabaceae**	**Begoniaceae**	**Arecaceae**	**Fabaceae**	**Asteraceae**	**Fabaceae**	**Salicaceae**	**Fabaceae**	**Meliaceae**
FEB	H	BP	BP b	0	559	0	2	0	0	0	0	1	0
FEB	H	BP	BP1	0	525	0	0	0	0	0	0	0	0
FEB	H	PA	PA3	0	545	0	0	0	0	0	0	0	0
JAN	H	BP	BP b	0	73	12	21	0	0	0	0	0	0
JAN	H	PA	PA3	0	0	0	0	0	0	0	0	1	0
MAR	U	BP	BP e	0	472	0	0	0	0	0	0	0	0
MAR	U	BP	BP f	0	491	0	0	0	0	0	0	0	0
MAR	H	BP	BP b	0	506	0	62	0	0	0	0	0	0
MAR	H	BP	BP1	0	396	0	0	0	0	0	0	1	0
MAR	U	BP	BP c	0	414	0	0	0	0	0	0	0	0
MAR	U	BP	BP d	0	668	0	0	0	0	0	0	0	0
MAR	H	PA	PA1	0	685	0	0	0	0	0	0	1	0
MAR	U	PA	PA2	0	674	0	0	0	0	0	0	0	0
MAR	U	SL	SL	0	468	0	0	1	0	0	0	0	0
NOV	H	BP	BP b	0	0	138	0	0	0	0	0	1	0
NOV	H	BP	BP1	0	0	0	0	0	0	0	0	1	0
NOV	U	BP	BP2	0	0	0	0	0	0	0	0	1	0
NOV	U	PA	PA g	0	0	0	0	0	0	0	0	1	1
NOV	H	PA	PA1	0	0	0	0	0	1	1	1	0	0
NOV	U	PA	PA2	1	0	0	0	0	0	0	0	0	0
OCT	H	BP	BP a	0	0	0	1	0	0	0	0	1	0
OCT	H	BP	BP b	0	0	36	0	0	0	0	0	1	0
OCT	H	BP	BP1	0	0	3	0	0	0	0	0	1	0
OCT	U	BP	BP2	0	0	0	0	0	0	0	0	1	0
OCT	U	PA	PA g	1	0	0	0	0	0	0	0	0	0
OCT	H	PA	PA1	1	1	0	0	0	0	0	0	0	0
OCT	U	PA	PA2	0	0	19	1	1	0	0	0	0	0
SET	H	BP	BP b	0	0	0	0	0	0	0	0	0	0
SET	H	BP	BP1	0	0	0	0	0	0	0	0	0	0
SET	U	PA	PA g	0	0	0	0	0	0	0	0	0	0
SET	H	PA	PA1	0	0	0	0	0	0	0	0	0	0

Table S3(e, continuation): taxonomic characterization (at Family and/or genus level) of stored pollen of different colonies.

				tipo Butia	**Euphorbia**	**Indeterminado**	**Senna tipo 2 (pequeno)**	**Plantago**	**Ligustrum cf. lucidum**	**Handroanthus cf. chrysotrichus**	**Tricolpado**	**Bauhinia**
Month	**Health in March**	**Locality**	**Colony**	**Arecaceae**	**Euphorbiaceae**	**Outro**	**Fabaceae**	**Plantaginaceae**	**Oleaceae**	**Bignoniaceae**	**Outro**	**Fabaceae**
FEB	H	BP	BP b	0	0	0	0	0	0	0	0	0
FEB	H	BP	BP1	1	0	0	0	0	0	1	0	0
FEB	H	PA	PA3	0	0	0	0	0	0	1	0	1
JAN	H	BP	BP b	41	0	0	0	0	0	0	0	0
JAN	H	PA	PA3	0	0	0	0	0	0	0	0	0
MAR	U	BP	BP e	0	0	0	0	0	0	1	0	0
MAR	U	BP	BP f	0	0	0	0	0	0	1	0	0
MAR	H	BP	BP b	3	0	0	0	0	0	1	0	0
MAR	H	BP	BP1	1	0	0	0	0	0	0	0	0
MAR	U	BP	BP c	0	0	0	0	0	0	0	0	0
MAR	U	BP	BP d	1	0	0	0	0	0	0	1	0
MAR	H	PA	PA1	0	0	0	0	0	0	1	0	0
MAR	U	PA	PA2	0	0	0	0	0	0	1	0	0
MAR	U	SL	SL	1	0	0	0	0	1	1	0	0
NOV	H	BP	BP b	0	0	0	0	0	0	0	0	0
NOV	H	BP	BP1	0	0	0	0	0	1	0	0	0
NOV	U	BP	BP2	1	0	0	0	1	0	0	0	0
NOV	U	PA	PA g	0	0	0	0	0	0	0	0	0
NOV	H	PA	PA1	0	0	0	0	0	0	0	0	0
NOV	U	PA	PA2	0	0	0	0	0	0	0	0	0
OCT	H	BP	BP a	1	0	0	0	0	0	0	0	0
OCT	H	BP	BP b	0	0	0	0	0	0	0	0	0
OCT	H	BP	BP1	0	1	0	0	0	0	0	0	0
OCT	U	BP	BP2	1	0	1	1	0	0	0	0	0
OCT	U	PA	PA g	0	0	0	0	0	0	0	0	0
OCT	H	PA	PA1	0	0	0	0	0	0	0	0	0
OCT	U	PA	PA2	0	0	0	0	0	0	0	0	0
SET	H	BP	BP b	0	0	0	0	0	0	0	0	0
SET	H	BP	BP1	0	0	0	0	0	0	0	0	0
SET	U	PA	PA g	0	0	0	0	0	0	0	0	0
SET	H	PA	PA1	0	0	0	0	0	0	0	0	0

Table S4: Detection limits of high performance liquid chromatography coupled with sequential mass spectrometry

Parameter	**Unit**	**Quantification limit**
3 - Hydroxy carbofuran	mg/kg	0.01
Abamectin	mg/kg	0.01
Acephate	mg/kg	0.01
Acetamiprid	mg/kg	0.01
Acetochlor	mg/kg	0.01
Acrinathrin	mg/kg	0.01
Aldicarb (SUM)	mg/kg	0.01
Aldicarb sulfoxide	mg/kg	0.01
Aldicarb sulphone	mg/kg	0.01
Ametryn	mg/kg	0.01
Amicarbazone	mg/kg	0.01
Aminocarb	mg/kg	0.01
Amitraz	mg/kg	0.01
Anilazine	mg/kg	0.01
Atrazine	mg/kg	0.1
Azaconazole	mg/kg	0.01
Azimsulfuron	mg/kg	0.02
Azinphos ethyl	mg/kg	0.01
Azinphos methyl	mg/kg	0.01
Azocyclotin	mg/kg	0.01
Benalaxyl	mg/kg	0.01
Benfuracarb	mg/kg	0.01
Bitertanol	mg/kg	0.01
Boscalid	mg/kg	0.01
Bromacyl	mg/kg	0.01
Bupirimate	mg/kg	0.01
Buprofezin	mg/kg	0.01
Cadusafos	mg/kg	0.01
Carbaryl	mg/kg	0.01
Carbendazin (Benomyl, thiophanate methyl)	mg/kg	0.01
Carbofuran	mg/kg	0.01
Carbophenothion	mg/kg	0.01
Carbosulfan	mg/kg	0.01
Carboxin	mg/kg	0.01
Carfentrazone ethyl	mg/kg	0.01
Carpropamid	mg/kg	0.01
Chlorimuron ethyl	mg/kg	0.01
Chlorpyrifos (dursban/lorsba)	mg/kg	0.01
Chlorthiophos	mg/kg	0.01
Clothianidin	mg/kg	0.01
Coumaphos	mg/kg	0.01
Cyanazine	mg/kg	0.01
Cyanofenphos	mg/kg	0.01
Cyazofamid	mg/kg	0.01
Cyproconazole	mg/kg	0.01
Dichlofluanid	mg/kg	0.01
Dichlorvos	mg/kg	0.01
Diclofop methyl	mg/kg	0.01

Dicrotophos	mg/kg	0.01
Difenoconazole 1, 2	mg/kg	0.01
Diflubenzuron	mg/kg	0.01
Dimethanamid	mg/kg	0.01
Dimethoate	mg/kg	0.01
Dimethomorph (SUM)	mg/kg	0.01
Diniconazole	mg/kg	0.01
Disulfoton sulfone	mg/kg	0.01
Disulfoton sulfoxide	mg/kg	0.01
Diuron	mg/kg	0.01
Dodemorph	mg/kg	0.01
EPN	mg/kg	0.01
Epoxiconazole	mg/kg	0.01
Ethiofencarb	mg/kg	0.01
Ethiofencarb-sulfone	mg/kg	0.01
Ethion (nialate)	mg/kg	0.01
Ethiprole	mg/kg	0.01
Ethoprophos	mg/kg	0.01
Ethoxysulfuron	mg/kg	0.01
Etoxazole	mg/kg	0.01
Etrimfos	mg/kg	0.01
Famoxadone	mg/kg	0.01
Fenamidone	mg/kg	0.01
Fenamiphos sulfone	mg/kg	0.01
Fenamiphos sulfoxide	mg/kg	0.01
Fenarimol	mg/kg	0.01
Fenbuconazole	mg/kg	0.01
Fenhexamid	mg/kg	0.01
Fenoxycarb	mg/kg	0.01
Fenpropimorph	mg/kg	0.01
Fenpyroximate	mg/kg	0.01
Fenthion	mg/kg	0.01
Fenthion sulfone	mg/kg	0.01
Fenthion sulfoxide	mg/kg	0.01
Fipronil	mg/kg	0.03
Flazasulforon	mg/kg	0.01
Flufenacet	mg/kg	0.01
Flufenoxuron	mg/kg	0.01
Fluopicolide	mg/kg	0.1
Fluquinconazole	mg/kg	0.01
Flusilazol	mg/kg	0.01
Flutolanil	mg/kg	0.01
Fomezafen	mg/kg	0.01
Fonofos (SUM)	mg/kg	0.01
Fostiazate	mg/kg	0.01
Furathiocarb	mg/kg	0.01
Hexaconazole	mg/kg	0.01
Hexazinone	mg/kg	0.01
Hexythiazox	mg/kg	0.01
Imazalil	mg/kg	0.01
Imazapic	mg/kg	0.01

Imazapyr	mg/kg	0.01
Imazaquim	mg/kg	0.01
Imibenconazole	mg/kg	0.01
Imidacloprid	mg/kg	0.01
Indoxacarb	mg/kg	0.01
Iprovalicarb	mg/kg	0.01
Isofenphos	mg/kg	0.01
Isoxaflutole	mg/kg	0.01
Linuron	mg/kg	0.01
Lufenuron	mg/kg	0.01
Malaoxon	mg/kg	0.01
Metalaxyl (SUM)	mg/kg	0.01
Metconazole	mg/kg	0.01
Methamidophos	mg/kg	0.01
Methidathion	mg/kg	0.01
Methiocarb	mg/kg	0.01
Methiocarb sulfone	mg/kg	0.01
Methiocarb sulfoxide	mg/kg	0.01
Methobromuron	mg/kg	0.01
Methomyl	mg/kg	0.01
Metribuzin	mg/kg	0.01
Metsulfuron methyl	mg/kg	0.01
Mevinphos (SUM)	mg/kg	0.01
Monocrotophos	mg/kg	0.01
Monuron	mg/kg	0.01
Myclobutanil	mg/kg	0.03
Napropamide	mg/kg	0.01
Novaluron	mg/kg	0.01
Omethoate	mg/kg	0.01
Oxadixyl	mg/kg	0.01
Oxamyl	mg/kg	0.01
Oxasulfuron	mg/kg	0.01
Oxycarboxin	mg/kg	0.01
Paclobutrazol	mg/kg	0.01
Paraoxon ethyl	mg/kg	0.01
Paraoxon methyl	mg/kg	0.01
Penconazole	mg/kg	0.01
Pencycuron	mg/kg	0.01
Pendimenthalin	mg/kg	0.01
Phorate	mg/kg	0.01
Phosalone	mg/kg	0.01
Phosmet	mg/kg	0.01
Phosphamidon (SUM)	mg/kg	0.01
Picoxystrobin	mg/kg	0.01
Pirimicarb	mg/kg	0.01
Pirimiphos ethyl	mg/kg	0.01
Pirimiphos methyl	mg/kg	0.01
Prochloraz	mg/kg	0.01
Profenophos	mg/kg	0.01
Promecarb	mg/kg	0.01
Prometon	mg/kg	0.01

Prometryn	mg/kg	0.01
Propamocarb	mg/kg	0.01
Propargite	mg/kg	0.01
Propiconazole I, II	mg/kg	0.1
Propoxur	mg/kg	0.01
Pymetrozine	mg/kg	0.01
Pyraclostrobin	mg/kg	0.01
Pyrazophos	mg/kg	0.01
Pyrethrins	mg/kg	0.01
Pyridaben	mg/kg	0.01
Pyridaphenthion	mg/kg	0.01
Pyrifenox	mg/kg	0.01
Pyrimethanil	mg/kg	0.01
Pyriproxyfen	mg/kg	0.01
Quinoxyfen	mg/kg	0.01
Quizalofpop-p-ethyl	mg/kg	0.01
Rotenone	mg/kg	0.01
Simazine	mg/kg	0.01
Spinosad	mg/kg	0.01
Spiroxamine	mg/kg	0.01
Sulfentrazone	mg/kg	0.01
Sulfometuron-methyl	mg/kg	0.01
Sulfotep	mg/kg	0.01
Sulprofos	mg/kg	0.01
Tebuconazole	mg/kg	0.01
Tebufenozide	mg/kg	0.01
Tetraconazole	mg/kg	0.01
Thiabendazole	mg/kg	0.01
Thiacloprid	mg/kg	0.01
Thiamethoxam	mg/kg	0.01
Thiobencarb	mg/kg	0.01
Thiodicarb	mg/kg	0.01
Thionazin	mg/kg	0.01
Thiophanate methyl	mg/kg	0.01
Tolylfluanid	mg/kg	0.01
Triadimefon	mg/kg	0.01
Triadimenol	mg/kg	0.01
Triazophos	mg/kg	0.01
Trichlorfon	mg/kg	0.01
Tricyclazole	mg/kg	0.01
Tridemorph	mg/kg	0.01
Trifloxystrobin	mg/kg	0.01
Triflumizole	mg/kg	0.01
Triflumuron	mg/kg	0.01
Triticonazole	mg/kg	0.01
Vamidathion	mg/kg	0.01
Penoxulam	µg/kg	0.01

CAPÍTULO 5

Recomendações para o manejo da mandaçaia no RS

Este capítulo apresenta um folder de divulgação científica direcionado, principalmente, aos meliponicultores.

Recomendações para o manejo da abelha mandaçaia no RS

por Lílian Caesar e Karen Luisa Haag

A mandaçaia (*Melipona quadrifasciata*) é uma abelha sem ferrão amplamente distribuída no Brasil e, desde os aborígenes, cultivada para a obtenção de mel. No nosso Estado, Rio Grande do Sul (RS), ocorre uma subespécie desta abelha (*M. q. quadrifasciata*) que é evolutivamente divergente da mandaçaia do norte do Brasil (*M. q. anthidioides*, encontrada a partir do Estado de São Paulo). Isso significa que, embora muito parecidas, estas duas subespécies possuem adaptações próprias ao seu habitat (clima, flores utilizadas, etc) e também uma composição genética diferente.

No RS há vários anos ou talvez décadas, não se encontram mais ninhos da mandaçaia na natureza, com poucas exceções. Toda colônia de mandaçaia cultivada hoje no RS foi então obtida de outra colônia por divisão, um processo que vem acontecendo por muitas gerações. Portanto, pode-se considerar que a mandaçaia no RS é uma abelha domesticada, assim como a *Apis mellifera,* que foi introduzida da Europa e depois africanizou-se. A diferença entre a *A. mellifera* e a mandaçaia, no que diz respeito à domesticação, é que a abelha africanizada ainda tem a capacidade de enxamear e produzir ninhos silvestres, apesar da domesticação. Trata-se de uma abelha muito bem adaptada ao nosso ambiente, que forma colônias gigantescas comparativamente as nossas abelhas nativas e com extrema capacidade competitiva quanto à utilização de recursos.

Anualmente no RS os meliponicultores observam que uma grande quantidade de colônias de mandaçaias adoece sempre no final do verão (normalmente em março). A doença pode ser tão severa que toda a colônia entra em colapso, lembrando bastante uma doença séria da *A. mellifera* chamada de "Desordem do Colapso das Colméias" (CCD), frequente nos Estados Unidos desde 2006. Até hoje não existe uma causa única que explique a CCD, mas alguns fatores importantes são a varroa, os vírus e os agroquímicos. No caso da mandaçaia, diferentes possibilidades foram levantadas pelos meliponicultores, como a toxicidade de alguma(s) planta(s) e os agroquímicos.

Por isso, nosso grupo de pesquisas do Laboratório de Genômica Evolutiva do Departamento de Genética da UFRGS, em colaboração com vários outros pesquisadores desta e de outras instituições, tem direcionado esforços no sentido de investigar as causas envolvidas na mortalidade anual das mandaçaias no nosso Estado.

Resumidamente, as conclusões dos nossos trabalhos – alguns deles já publicados em revistas científicas de alto nível – são as seguintes:

1. Há uma contínua **perda de peso** das forrageiras **entre janeiro e março**. A perda de peso das forrageiras está correlacionada ao tamanho da colônia em abelhas sociais de uma forma geral, então isso nos permite concluir que abelhas individuais, bem como a colmeia, enfraquecem neste período.

2. No período que antecede a síndrome também há uma **mudança nos hábitos alimentares** das mandaçaias, pois o pólen predominantemente armazenado nas colônias a partir de fevereiro deixa de ser de eucaliptos e passa a ser do maricá. É possível que a mandaçaia esteja sendo excluída pelo seus competidores - incluindo as *A. mellifera* - das áreas contendo as flores do eucalipto, e passa a coletar pólen de maricá que entra em floração em fevereiro.

3. Outra observação importante é que as abelhas doentes - e também as abelhas saudáveis, isto é, aquelas que não apresentam sintomas da doença - **podem abrigar os mais variados vírus**. Alguns desses vírus ocorrem também na *A. mellifera*, indicando que o contato direto - ou indireto, através das flores que ambas visitam - entre as duas espécies de abelhas permite a transmissão dos vírus uma à outra. **Em alguns meliponários** do RS as mandaçaias de colônias doentes apresentam **sintomas muito semelhantes aos sintomas neurológicos causados por infecções virais** em outras abelhas - raramente estes sintomas são também observados em outras espécies de abelha sem ferrão na mesma época. No entanto esses sintomas observados nas mandaçaias não são generalizados, variando enormemente entre colônias de distintos meliponários. O que todos os meliponários que observam a síndrome têm em comum é uma **mortalidade alta e incomum em março da espécie *M. quadrifasciata*.**

4. É possível que a maior vulnerabilidade das mandaçaias em relação às outras abelhas nativas e a *A. mellifera* tenha relação com o **afrouxamento da seleção relacionado a algumas práticas de manejo,** as quais não necessariamente favorecem as abelhas no seu ambiente natural. Por exemplo, se por várias gerações as abelhas foram acostumadas a receber alimento regularmente, com o passar de muitas gerações poderá haver uma piora no desempenho destas abelhas em procurar alimento por conta própria.

5. Outro aspecto a ser levado em consideração é o **uso de agroquímicos** nas áreas de forrageio das abelhas. Mesmo que elas não estejam sujeitas a doses letais desses agentes químicos, podem haver efeitos subletais que irão se manifestar com o passar do tempo. Esses efeitos podem ser tardios e também cumulativos (vão se tornando cada vez mais graves). Um estudo recente feito na Europa mostrou que a presença de doses muito baixas de um pesticida em larvas e pupas das abelhas leva a um baixo desenvolvimento dos órgãos do sistema nervoso necessários para que a abelha quando adulta desempenhe suas atividades normais. (...)

(continuação) O forrageio é um comportamento que requer inteligência e reflexo. O mau funcionamento do sistema nervoso diminui o desempenho da forrageira, e consequentemente a nutrição da colônia.

6. Acompanhando três pares de colônias de mandaçaias em dois locais diferentes, nós observamos **efeitos tardios do mal funcionamento de genes relacionados com a detoxificação de compostos, bem como com a imunidade e a saúde geral das abelhas.** Isto sugere que não apenas podem estar ocorrendo efeitos subletais devido a exposição das mandaçaias a agroquímicos, como também uma perda na capacidade de defender-se de seus inimigos naturais, como vírus e outros parasitas.

Dadas as conclusões listadas acima, nossos estudos nos levam a sugerir as seguintes **medidas profiláticas no manejo das mandaçaias no RS**, que podem ser ampliadas ao manejo de outras abelhas sem ferrão, com o intuito de fortalecer as colônias e diminuir a incidência da síndrome:

1. Cultivar as abelhas em **condições similares ao ambiente natural**, procurando não fornecer alimento desnecessariamente e não alterando o microclima natural das colônias, como a temperatura. Desta forma, com o passar das gerações, diminuirão os possíveis efeitos danosos de algumas práticas de manejo.

2. **Não introduzir abelhas de outros locais** indiscriminadamente. Muito embora a mistura de abelhas originárias de locais distintos possa contribuir para aumentar a variabilidade genética, há o grande risco de serem introduzidos patógenos contra os quais as mandaçaias de populações locais não apresentam defesa.

3. Prover **quantidade de pasto apícola proporcional à quantidade de abelhas cultivadas** com o intuito de diminuir a competição por alimento. Esta recomendação é ainda mais importante se as mandaçaias estiverem sendo mantidas na proximidade de colônias de *A. mellifera*.

4. **Evitar o uso de agroquímicos** nas áreas de forrageio das mandaçaias.

5. As recomendações 3 e 4 são particularmente importantes nos meses anteriores à síndrome (**a partir de janeiro**), levando em consideração os efeitos tardios observados nos nossos estudos, que podem culminar com a síndrome.

Mais informações em: http://www.ufrgs.br/genomicaevolutiva/manejo-de-abelhas

SUGESTÕES PARA LEITURA

Título em português: Relato sobre a microbiota de *Melipona quadrifasciata* afetada por doença recorrente
Título original: Report on the microbiota of *Melipona quadrifasciata* affected by a recurrent disease
Link oficial: https://www.sciencedirect.com/science/article/abs/pii/S002220111630218X?via%3Dihub
Destaques: Neste trabalho mostramos que as principais bactérias associadas ao intestino de mandaçaia são parecidas àquelas que estão também no de *Apis*, desempenhando funções importantes para a saúde da abelha. Também mostramos que não estão presentes bactérias patogênicas já conhecidas por infectar outras abelhas, nem mesmo nas colônias afetadas pela síndrome. Não foram também detectados, nas mesmas colônias doentes e saudáveis avaliadas, patógenos como *Nosema* ou *Crithidia* (um tripanossomatídeo).

Título em português: O viroma de uma abelha sem ferrão em risco de extinção que sofre de uma mortalidade anual no sul do Brasil
Título original: The virome of an endangered stingless bee suffering from annual mortality in southern Brazil
Link oficial: https://www.microbiologyresearch.org/content/journal/jgv/10.1099/jgv.0.001273#tab7
Destaques: Neste trabalho mostramos que mandaçaias afetadas pela síndrome carregam muito mais vírus que as saudáveis. Dentre eles vírus, sete novos vírus foram descritos e dois deles são parecidos com vírus patogênicos de abelhas melíferas (que causam tremores e paralisia nelas). Estes vírus não são a causa principal da síndrome, mas alguns deles estão mais associados a abelhas doentes em um meliponário, onde os sintomas da síndrome foram mais intensos, e podem estar contribuindo para o colapso de colônias neste local.

Título em português: Definindo a saúde dos polinizadores: uma abordagem holística baseada em fatores ecológicos, genéticos e fisiológicos
Título original: Defining pollinator health: A Holistic Approach Based on Ecological, Genetic, and Physiological Factors
Link oficial: https://www.annualreviews.org/doi/abs/10.1146/annurev-animal-020518-115045
Destaques: Nesta revisão os autores discutem que a saúde dos polinizadores não pode ser reduzida à ausência de doença ou colônias cheias de indivíduos, mas sim um estado que permite que os indivíduos vivam mais e/ou se reproduzam mais, mesmo na presença de patógenos pelo ambiente. Também falam sobre o uso de biomarcadores padronizados para avaliar a saúde nos diferentes níveis de complexidade das abelhas sociais: a nível individual (ex: tamanho corporal, microbiota intestinal, fisiologia), da colônia (ex: imunidade social, tamanho da colônia) e da população (ex: diversidade genética). Reforçam que estas medidas de saúde usando biomarcadores podem guiar decisões sobre o manejo de colônias, sobre a conservação de abelhas selvagens e políticas ambientais.

Título em português: As práticas meliponícolas e a distância geográfica, não o uso da terra, direcionam o fluxo gênico nas abelhas tropicais
Título original: Beekeeping practices and geographic distance, not land use, drive gene flow across tropical bees
Link oficial: https://onlinelibrary.wiley.com/doi/abs/10.1111/mec.13852
Destaques: Neste trabalho os autores mostram que o fluxo de genes (quando uma população recebe genes de outra) ocorre pela diminuição do isolamento geográfico devido ao manejo e troca de colônias, o que não é observado nas colônias selvagens. Isto pode levar à mistura entre espécies, resultando na substituição completa das características da espécie original. Também mostram que o que mantém o alto fluxo de genes nas abelhas sem ferrão são ambientes com paisagens heterogêneas, como florestas nativas conservadas. Por isso, os autores sugerem que para a preservação das abelhas haja regulação das práticas de meliponicultura para manter o fluxo gênico natural, como também melhorar os habitats amigáveis aos polinizadores.

Título em português: Cria pútrida européia em abelhas sem ferrão (Apidae: Meliponini) no Brasil: doença antiga, ameaça renovada
Título original: European Foulbrood in stingless bees (Apidae: Meliponini) in Brazil: old disease, renewed threat
Link oficial: https://www.sciencedirect.com/science/article/abs/pii/S002220112030063X
Destaques: Neste estudo foi detectado pela primeira vez a bactéria patogênica *Melissococcus plutonius* e os sintomas da cria pútrida européia em espécies de *Melipona*, o que estava levando à morte da prole e em alguns casos ao colapso de colônias. Essa bactéria infectou as colônias através do pólen de *Apis* contaminado e usado para alimentar as abelhas sem ferrão. Para evitar a transmissão de patógenos, os autores recomendam que meliponicultores evitem a introdução de rainhas, enxames ou colônias em meliponários sem considerar critérios sanitários; evitem o uso de utensílios contaminados, desinfetando apropriadamente, e que limitem o uso de suplementos à base de pólen para sustentar colônias de *Melipona*.

Título em português: Particionamento de recursos florais entre abelhas nativas do gênero *Melipona* e a abelha africanizada introduzida na floresta tropical atlântica brasileira
Título original: Floral resource partitioning between native *Melipona* bees and the introduced Africanized honey bee in the Brazilian Atlantic rain forest
Link oficial: https://www.apidologie.org/articles/apido/abs/1997/05/Apidologie_0044-8435_1997_28_6_ART0002/Apidologie_0044-8435_1997_28_6_ART0002.html
Destaques: Neste estudo os autores mostram que *Melipona* e *Apis mellifera* na Mata Atlântica competem por recursos das mesmas flores, principalmente do grupo Myrtaceae (como o Eucalipto). O pico de coleta de pólen por *Melipona* foi justamente no período em que a *Apis* competiu menos por esses recursos. Isso por que enquanto *Melipona* usa poucas plantas como recurso, principalmente Myrtaceae e Melastomataceae, a *Apis mellifera* usa mais plantas, como Myrtaceae, Asteraceae, Euphorbiaceae e Arecaceae para pólen e Cunoniaceae, Rubiaceae e Myrtaceae para néctar.

Título em português: A exposição a inseticidas durante o desenvolvimento da prole ou no início da idade adulta reduz o crescimento cerebral e prejudica a aprendizagem de abelhas adultas.
Título original: Insecticide exposure during brood or early-adult development reduces brain growth and impairs adult learning in bumblebees
Link oficial: https://royalsocietypublishing.org/doi/10.1098/rspb.2019.2442
Destaques: Neste trabalho os autores mostram que houve uma redução no desenvolvimento de partes do cérebro de abelhas que foram expostas a agroquímicos (neonicotinóides) durante qualquer um dos estágios do desenvolvimento. Essa malformação não foi revertida mesmo quando a abelha não teve mais contato com o agroquímico. Estas abelhas também apresentaram uma resposta menor ao oferecimento de açúcar e dificuldade na aprendizagem.

Título em português: Abordagens ecológicas e evolutivas para o manejo de doenças de abelhas
Título original: Ecological and evolutionary approaches to managing honeybee disease
Link oficial: https://www.nature.com/articles/s41559-017-0246-z
Destaques: Neste trabalho os autores mostram que apiários muito populosos aumentam a chance de espalhar parasitas entre colônias, assim como colônias muito populosas podem ter dificuldade de desempenhar a imunidade social contra parasitas. Também mostram como a translocação de colônias leva novos patógenos a outros apiários e contribui para seleção de parasitas mais virulentos. Para evitar isso, os autores sugerem conservar a diversidade genotípica das colônias; disponibilizar maior diversidade alimentar e diminuir a dependência das colônias por açúcares processados; promover "estoque de sobreviventes", ou seja, manter colônias naturalmente resistentes e permitir que colônias com baixa resistência a parasitas morram naturalmente ao invés de forçar medicações.

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PERGUNTAS FREQUENTES

A síndrome é causada por alguma planta tóxica (ex: lanceta ou mata-campo)?
Análises do tipo de pólen coletado por mandaçaias de dois meliponários do RS, onde a síndrome ocorreu, não detectaram a presença de pólen de lanceta ou mata-campo, então estas plantas não são os agentes causadores da síndrome. Com esta análise percebemos que houve uma troca do consumo de pólen de eucalipto para pólen de maricá próximo ao período da síndrome. O maricá é uma planta nativa da região e não é tóxica para insetos. Esta troca pode ser resultado da competição por recursos com outros polinizadores e por isso, ao começar a florada de maricá, a mandaçaia passa a usá-lo como recurso.

Não seria então causada pelo besouro vaquinha que está nas plantas que a mandaçaia visita?
Não. Ao longo de nossas análises o besouro vaquinha (*Astylus variegatus*) não foi observado parasitando colônias de mandaçaias, nem mesmo mandaçaias que estavam forrageando. Este besouro também não está associado a plantas que a mandaçaia costuma visitar, como o eucalipto.

A síndrome é causada por agrotóxicos?
Análises de resíduos de colônias afetadas pela síndrome não detectaram agrotóxicos. No entanto, em um experimento recente que fizemos, observamos um mal funcionamento de um gene relacionado à detoxificação de compostos químicos nas colônias que adoeceram no período da síndrome. Este resultado sugere que embora as abelhas não morram imediatamente por doses altas de agroquímicos, as dose sub-letais podem estar contribuindo para a síndrome.

Esta síndrome é uma forma de controle populacional antes do inverno?
De fato a abelha mandaçaia não costuma fazer diapausa, que é uma forma de diminuir a atividade da colônia durante o inverno quando há menos recursos. No entanto, a síndrome já foi observada em colônias grandes, mas também em colônias jovens/pequenas, o que vai contra esta ideia. Também, os sintomas observados em mandaçaias de alguns meliponários (tremores e paralisia) sugerem algum problema neurológico causado por um parasita ou composto químico tóxico.

A síndrome afeta apenas mandaçaias?
A mandaçaia é a principal abelha afetada por esta síndrome. Em alguns meliponários, embora não em todos os anos, já foram observados sintomas similares em outras abelhas sem ferrão, como a *Melipona bicolor*, *M. seminigra*, *M. scutellaris* e *Scaptotrigona postica*. Amostras destas espécies já foram coletadas para futuras análises.

A síndrome ocorre também em outros estados além do RS?
Sim. Além do Rio Grande do Sul, a síndrome também ocorre em meliponários de Santa Catarina. Há também relatos de mortalidade de mandaçaias em março no Paraná, Minas Gerais, Rio de Janeiro e Bahia, embora não possamos garantir que seja exatamente a mesma síndrome.

Fechar a colônia antes do período da síndrome evita a alta mortalidade?
Até o momento não realizamos experimentos controlados testando os efeitos de fechar as colônias no início de março para prevenir a síndrome. Por isso, não podemos recomendar esta prática. O que se sabe são relatos de meliponicultores que ao fechar as colônias notaram que elas não adoeceram. Esta prática pode estar evitando o contato das abelhas com algum agente que contribua para a ocorrência da síndrome e também estimulando cuidados internos na colônia. Nossa estratégia é entender a síndrome para então pensar em estratégias de prevenção.

Carvão ativado é uma solução para a síndrome?

Para os efeitos do carvão ativado em colônias de mandaçaia também não realizamos experimentos controlados e, portanto, não recomendamos a aplicação como um remédio. O que se sabe no momento são relatos de meliponicultores que observam que algumas colônias que receberam uma solução de carvão ativado não adoeceram. Reforçamos que nossa estratégia é entender a síndrome para então pensar em estratégias de prevenção, assim também não precisaremos medicar as colônias.

A síndrome é pilhagem?

Não. A pilhagem é o furto entre colônias, principalmente nas colônias menores ou mais fracas, o que pode levar a brigas entre indivíduos e decapitação. Nada disso foi observado ao longo de nossos estudos sobre a síndrome, pelo contrário, as colônias somente são invadidas por parasitas (como outras abelhas ou forídeos) quando já morreram muitas operárias.

A síndrome é causada por forídeos?

Não, embora forídeos possam se aproveitar do enfraquecimento das colônias para invadi-las, contribuindo para o colapso final da colônia.

CAPÍTULO 6

Discussão e conclusão

6. Discussão e conclusão

Doenças de abelhas e o colapso de suas colônias tem desafiado pesquisadores na busca dos fatores causais. Embora a CCD explique apenas uma parte do colapso de colônias nos EUA, ela ficou conhecida pelo grande esforço feito por parte de diversos laboratórios para encontrar a causa da desordem (Williams et al. 2010). Os estudos foram primeiramente conduzidos com o intuito de buscar um agente causador único, mas o que foi encontrado até o momento é que múltiplos fatores podem estar envolvidos no colapso, como patógenos, desnutrição e agroquímicos (Cox-Foster et al. 2007; vanEngelsdorp et al. 2009; VanEngelsdorp et al. 2010). Efeitos subletais destes diversos fatores, agindo ou não de forma sinergística, passaram a explicar grande parte do colapso de colônias pelo mundo (Bryden et al. 2013; Goulson et al. 2015). O que aumenta ainda mais o desafio do estudo do colapso de colônias é também a complexidade inerente às abelhas sociais, pois as respostas de como estes fatores agem podem estar no nível do indivíduo, da colônia ou mesmo da população (López-Uribe et al. 2020).

O estudo sobre a mortalidade anual de mandaçaias no RS se mostrou também bastante desafiador. Ao longo de nossas observações e amostragens percebemos que a síndrome, apesar de sazonal, ocorre em meliponários com distintos contextos ambientais e mostram uma variedade de sintomas com diferentes intensidades. Também não são todas as colônias de mandaçaias que são afetadas. A dificuldade de observarmos um fator em comum em todos locais e colônias afetadas indicava a possibilidade da ação de múltiplos fatores para o desfecho da síndrome. Investigando aspectos chave da saúde das mandaçaias, em nível de indivíduo e de colônia, identificamos alguns fatores relacionados à ocorrência da síndrome.

Primeiramente investigamos o papel do microbioma bacteriano das abelhas na ocorrência da síndrome (Díaz et al. 2017; Capítulo 2). Nosso estudo foi o primeiro a caracterizar a microbiota de uma abelha nativa do Brasil, a qual se mostrou bastante diversa e composta principalmente por bactérias do grupo Firmicutes (como diferentes tipos de *Lactobacillus*), assim como em *A. mellifera*. Entretanto, diferentemente da abelha melífera, que possui alta conservação nos grupos de bactérias associadas ao intestino (Martinson et al. 2011), *M. quadrifasciata* apresenta grande variação na composição da microbiota entre abelhas de diferentes colônias (Díaz et al. 2017). É possível que tais padrões tenham relação com o processo de domesticação que a *A. mellifera* já sofre há mais tempo e mais intensamente (Zheng et al. 2018). Concluímos com esta investigação que a síndrome anual não é causada por alguma bactéria patogênica e também não parece estar relacionada à disbiose. Ou seja, não há diferença na composição geral da microbiota comparando abelhas doentes e saudáveis, apesar dos resultados sugerirem que a composição da microbiota nos diferentes *status* de saúde é dependente do ano. No entanto, não podemos descartar que a falta de algum padrão claro esteja relacionado a grande variação na microbiota. Um estudo acompanhando flutuações na composição da microbiota temporalmente poderia complementar os achados deste trabalho e faz parte das perspectivas desta tese. Já temos o DNA abdominal de 120 amostras de mandaçaia (ANEXO I), coletadas entre 2018-2019 para o estudo do Capítulo 4 (5 operárias/colônia/localidade/mês, utilizadas para pesagem e quantificação da atividade de GOX), a serem submetidas à amplificação de fragmentos de 16S (bactérias) e ITS (fungos) por PCR, sequenciamento e análises comparativas.

A partir da observação dos sintomas de mandaçaias afetadas pela síndrome, direcionamos as investigações para a possibilidade de uma infecção viral (Caesar et al. 2019; Capítulo 3). Tremores, paralisia e incapacidade de voar são alguns dos sintomas que podem ser observados em operárias de colônias afetadas. Tais sintomas assemelham-se aos observados em infecções por dicistrovírus em *Apis* spp. (McMenamin e Genersch 2015), mas nenhum destes vírus (ex: ABPV, IAPV, KBV) foi detectado nas mandaçaias. Porém, novos vírus da família *Dicistroviridae* (MqV1a e MqV1b) foram descritos, assim como da família *Circoviridae* (MqC, MqC1 e MqC2) e *Densoviridae* (MqD). Nenhum deles foi consistentemente relacionado à ocorrência da síndrome, mas alguns destes novos vírus foram mais detectados em um meliponário onde os sintomas observados durante a síndrome foram mais intensos (Caesar et al. 2019). Uma investigação envolvendo a quantificação da densidade da infecção viral poderia contribuir para entender a sua relação com os sintomas observados e faz parte das perspectivas desta tese. Amostras de colônias do meliponário onde observam-se sintomas mais intensos nas forrageiras afetadas foram coletadas durante a síndrome de 2019 e armazenadas a -80 ºC (ANEXO II) para futura extração de DNA ou RNA, síntese de cDNA e quantificação absoluta dos vírus por qPCR.

Outro achado interessante desta etapa do estudo foi a detecção de vírus da mandaçaia também em *A. mellifera*. Embora não possamos confirmar a direção da transmissão dos vírus, este dado chama atenção para a ocorrência de troca de patógenos entre abelhas exóticas e nativas.

A ausência de algum patógeno consistemente associado às abelhas de colônias que sofreram mortalidade nos levou então a uma investigação integrativa sobre o *status* de saúde das colônias no período que engloba a síndrome. Avaliamos diversas características das mandaçaias tanto em nível de indivíduo quanto de colônia (Caesar et al. *em preparação;* Capítulo 4). Planejamos este estudo de forma a discriminar a contribuição genética da colônia bem como do ambiente para o desfecho da síndrome. As características em nível de colônia foram as que mais explicaram o *status* de saúde, como a perda do controle da umidade e temperatura, principalmente em colônias afetadas pela síndrome. Tais traços, no entanto, são consequência de diversos processos biológicos que ocorrem em nível individual. Nós verificamos que forrageiras das colônias que adoeceram tiveram uma menor expressão de genes relacionados, na abelha modelo *A. mellifera*, à capacidade de detoxificação de agroquímicos (*p450*) e resposta imune (*Vg* e *PO*). Assim como observado em outros eventos de colapso de colônias, sugerimos com este estudo que o efeito subletal de estressores como agroquímicos, competição por recursos e exposição a patógenos possam estar na raiz desta síndrome.

Todos estes achados foram usados como base para a elaboração de um manual de recomendações aos meliponicultores (Capítulo 5), os quais trouxeram aos pesquisadores o problema da síndrome anual das mandaçaias. A meliponicultura é uma atividade que tem tomado proporções cada vez maiores no Brasil, sendo que até 2015 estimava-se que haviam mais de 5.000 meliponicultores (Jaffé et al. 2015). A criação e manejo de abelhas sem ferrão pode ajudar comunidades como uma forma de renda adicional através da venda de produtos das colônias, e também incentiva a proteção de habitats naturais como fontes de alimento e locais de nidificação para as abelhas, assim como contribui na prestação de serviços de polinização da flora selvagem e de cultivares agrícolas (Slaa et al. 2006; Jaffé et al. 2015). A legislação atual, em nível nacional, impõe algumas regras aos meliponicultores, como o registro daqueles que possuem mais de 50 colônias, a comercialização de colônias e produtos derivados apenas mediante autorização e restringe a translocação de colônias entre regiões (CONAMA, 2004). No entanto, além destas normas não serem suficientes para a preservação das espécies nativas, elas também não são estritamente seguidas, principalmente pela burocracia envolvida, como relatam os meliponicultores (Jaffé et al. 2015).

A translocação de colônias, por exemplo, é uma prática comum e um dos fatores que mais influencia nos padrões de diversidade genética entre espécies de abelhas sem ferrão das Américas (Jaffé et al. 2016). Alguns meliponicultores costumam comprar colônias de outras regiões do Brasil com o objetivo de fortalecer as colônias. No entanto, esta prática pode levar à homogeneização do perfil genético das populações e perda de adaptações locais importantes para a sobrevivência da espécie, como uma maior resistência a baixas temperaturas ou a agroquímicos (Jaffé et al. 2016). Nós observamos que a síndrome anual das mandaçaias tem um componente genético, ou seja, há colônias mais suscetíveis aos efeitos subletais de estressores ambientais e também mais resistes. A homogeneização do perfil genético das populações pode levar à perda do perfil genético destas colônias que respondem melhor aos fatores que contribuem para a ocorrência da síndrome. Por outro lado, certos genótipos também estão sendo grandemente expandidos através da comercialização de colméias obtidas por divisão, uma prática comum para obtenção de novas colônias (Jaffé et al. 2015). A mistura de genótipos através da translocação de colônias, combinada com a sua expansão pela divisão, altera completamente a estrutura genética das populações de abelhas sem ferrão. Esta prática pode ter afetado mais intensamente a mandaçaia, que é uma das espécies mais manejada historicamente (Jaffé et al. 2015). Isto, associado ao fato de que não há mais ninhos silvestres, com indivíduos capazes de fornecer genes as colônias manejadas, sugere que a questão genética é um fator importante para a ocorrência da síndrome.

Outro impacto resultante da translocação de colônias é a introdução de patógenos. Estudos realizados em diferentes estados do Brasil detectaram recentemente a presença de microsporídios, bactérias e vírus potencialmente patogênicos em abelhas sem ferrão (de Souza et al. 2019; Guimarães-Cestaro et al. 2020; Teixeira et al. 2020). Embora nem todas as colônias nas quais estes patógenos foram detectados apresentavam sintomas típicos de cada infecção, em outros contextos a infecção por eles pode levar a diferentes desfechos. Sabe-se, por exemplo, que o DWV é mais virulento no inverno, levando ao colapso de inúmeras colônias de *A. mellifera* na Europa (Natsopoulou et al. 2017). Desta forma, caso este vírus seja trazido para o sul do Brasil, onde o inverno é mais rigoroso, ele poderia ser mais virulento e causar sintomas observáveis e danosos a diversas colônias. Além disso, há evidências de troca de patógenos entre abelhas sem ferrão e *A. mellifera*, inclusive em nosso estudo, sugerindo que ambas possam ser afetadas com a introdução de novos patógenos (Caesar et al. 2019; de Souza et al. 2019; Guimarães-Cestaro et al. 2020).

Outra prática bastante usada na meliponicultura é a suplementação alimentar de colônias, principalmente em períodos de maior escassez de recursos. Nós constatamos que a perda de peso das abelhas, possivelmente relacionada a competição por recursos, é um fator implicado na ocorrência da síndrome das mandaçaias. Porém, ao mesmo tempo que fornecer alimento às abelhas pode fortalecer as colônias para o período da síndrome, a suplementação alimentar também irá mascarar colônias geneticamente suscetíveis à mortalidade anual. Além disso, a dieta natural das abelhas é bastante equilibrada, enquanto o néctar fornece a principal fonte de carboidratos, o pólen fornece proteínas, lipídios e outros micronutrientes (Vaudo et al. 2015). Em *A. mellifera* e *B. terrestris* já foi mostrado que a atividade de forrageio é altamente regulada de acordo com as necessidades das colônias (Paoli et al. 2014; Stabler et al. 2015). Portanto, o uso de xarope e pólen apícola como suplementação alimentar deve ser evitado, e se for feito, é de extrema importância que o meliponicultor tome medidas sanitárias adequadas. Um estudo recente, que diagnosticou pela primeira vez a bactéria *M. plutonius* e os sintomas da doença conhecida como cria pútrida européia em *Melipona* spp., mostrou a presença do patógeno no pólen apícola oferecido às colônias que se infectaram (Teixeira et al. 2020).

A melhor forma de garantir a qualidade nutricional das colônias é promover pasto apícola diverso nos arredores do meliponário, proporcional à quantidade de colônias manejadas, como através da preservação de matas nativas (Vaudo et al. 2015). Com isso também será possível amenizar os efeitos da competição por recursos. Um estudo conduzido em região de Mata Atlântica mostrou que *M. quadrifasciata* e *A. mellifera* competem pelos recursos das mesmas flores, e o pico de coleta da abelha sem ferrão ocorreu quando a abelha melífera não estava competindo pelo mesmo recurso (Wilms e Wiechers 1997). Com uma menor sobreposição dessas duas espécies também haverá uma diminuição no risco da troca de patógenos.

Outro fator de risco às mandaçaias, e mesmo a outras abelhas sem ferrão, é o uso de agroquímicos. Nossos resultados indicam diferenças entre colônias na capacidade de detoxificação destes compostos, o que por sua vez influencia no desfecho da síndrome. Por mais que os agroquímicos sejam ministrados de forma correta e nenhuma letalidade seja observada no período de aplicação, efeitos subletais podem afetar a saúde das colônias, e apenas tardiamente serem observados os efeitos. Em *B. terrestris* expostas à neonicotinóides durante qualquer um dos estágios do desenvolvimento há uma redução no desenvolvimento de partes do cérebro das abelhas que, apenas semanas depois, quando adultas, apresentaram uma resposta menor ao oferecimento de açúcar e dificuldade na aprendizagem (Smith et al. 2020). Portanto, é importante evitar o uso de agroquímicos nas proximidades do meliponário ou áreas de forrageio.

Por fim, concluímos que a síndrome anual das mandaçaias é resultado da combinação de efeitos subletais de múltiplos fatores, como a genética da colônia, competição por recursos, exposição a patógenos e agroquímicos. Nós acreditamos que há formas de amenizar os efeitos da mortalidade anual das mandaçaias, e que preservando a espécie *M. quadrifasciata* estaremos também contribuindo para a manutenção de outras abelhas sem ferrão que possam estar sofrendo pela ação dos mesmos fatores.

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ANEXO I

ID amostra	Status de saúde	Colônia	Amostra da colônia	Mês	DNA ng/ul	260/280
41	saudável	PA1	1	Jan	63,8	2,13
42	saudável	PA1	2	Jan	65	2,19
43	saudável	PA1	3	Jan	120,2	2,13
44	saudável	PA1	4	Jan	75,3	2,1
45	saudável	PA1	5	Jan	106,7	2,17
51	doente	PA2	1	Jan	71,5	2,15
52	doente	PA2	2	Jan	107,3	2,18
53	doente	PA2	3	Jan	128,4	2,15
54	doente	PA2	4	Jan	116,1	2,15
55	doente	PA2	5	Jan	139,1	2,12
56	doente	PA3	1	Jan	178,4	2,19
57	doente	PA3	2	Jan	199,7	2,21
58	doente	PA3	3	Jan	261,2	2,18
59	doente	PA3	4	Jan	278,7	2,13
60	doente	PA3	5	Jan	274,4	2,17
61	doente	BP3	1	Jan	245,5	2,16
62	doente	BP3	2	Jan	213,1	2,16
63	doente	BP3	3	Jan	267,2	2,14
64	doente	BP3	4	Jan	303,4	2,16
65	doente	BP3	5	Jan	226,7	2,21
66	doente	BP2	1	Jan	126,3	2,08
67	doente	BP2	2	Jan	118,1	2,12
68	doente	BP2	3	Jan	146,7	2,19
69	doente	BP2	4	Jan	84,3	2,19
70	doente	BP2	5	Jan	114,4	2,06
76	saudável	BP1	1	Jan	74,7	2,17
77	saudável	BP1	2	Jan	115	2,17
78	saudável	BP1	3	Jan	111,3	2,13
79	saudável	BP1	4	Jan	106,2	2,17
80	saudável	BP1	5	Jan	66,2	2,2
81	saudável	PA1	1	Fev	76,6	2,09
82	saudável	PA1	2	Fev	36,6	1,94
83	saudável	PA1	3	Fev	61,5	2,1
84	saudável	PA1	4	Fev	119,4	2,04
85	saudável	PA1	5	Fev	37,3	1,83
91	doente	PA2	1	Fev	59	2,15
92	doente	PA2	2	Fev	78,2	2,17
93	doente	PA2	3	Fev	74,1	2,28
94	doente	PA2	4	Fev	64,6	2,29
95	doente	PA2	5	Fev	70,3	2,24
96	doente	PA3	1	Fev	98,6	2,24
97	doente	PA3	2	Fev	158,5	2,17
98	doente	PA3	3	Fev	179,4	2,2
99	doente	PA3	4	Fev	152,9	2,21
100	doente	PA3	5	Fev	191	2,18
101	saudável	BP1	1	Fev	156,5	2,18
102	saudável	BP1	2	Fev	113,5	2,19
103	saudável	BP1	3	Fev	115,8	2,15
104	saudável	BP1	4	Fev	123,4	1,92
105	saudável	BP1	5	Fev	179,8	2,19
111	doente	BP2	1	Fev	106,3	2,19
112	doente	BP2	2	Fev	108,7	2,13
113	doente	BP2	3	Fev	61,8	1,98
114	doente	BP2	4	Fev	155,3	2,14
115	doente	BP2	5	Fev	111,8	2,14

116	saudável	BP1	1	Fev	102,6	2,12
117	saudável	BP1	2	Fev	71,5	2,18
118	saudável	BP1	3	Fev	111	2,15
119	saudável	BP1	4	Fev	77,9	2,04
120	saudável	BP1	5	Fev	58,3	1,97
121	saudável	PA1	1	Mar	100	2,25
122	saudável	PA1	2	Mar	100,8	2,24
123	saudável	PA1	3	Mar	132,2	2,25
124	saudável	PA1	4	Mar	160,6	2,23
125	saudável	PA1	5	Mar	152,8	2,14
131	doente	PA2	1	Mar	275,5	2,22
132	doente	PA2	2	Mar	153,3	2,25
133	doente	PA2	3	Mar	129,7	2,22
134	doente	PA2	4	Mar	141,3	2,25
135	doente	PA2	5	Mar	339,7	2,21
136	doente	PA3	1	Mar	148,8	2,13
137	doente	PA3	2	Mar	151,7	2,31
138	doente	PA3	3	Mar	150,8	2,27
139	doente	PA3	4	Mar	87,4	2,22
140	doente	PA3	5	Mar	113,6	2,25
141	doente	BP3	1	Abr	149,6	2,09
142	doente	BP3	2	Abr	118,8	2,25
143	doente	BP3	3	Abr	125,8	2,23
144	doente	BP3	4	Abr	149	2,3
145	doente	BP3	5	Abr	106,1	2,26
146	doente	BP2	1	Abr	115,5	2,24
147	doente	BP2	2	Abr	141,7	2,25
148	doente	BP2	3	Abr	102,6	2,3
149	doente	BP2	4	Abr	84,6	2,33
150	doente	BP2	5	Abr	73,7	2,36
156	saudável	BP1	1	Abr	90,9	2,36
157	saudável	BP1	2	Abr	146,9	2,27
158	saudável	BP1	3	Abr	118,2	2,32
159	saudável	BP1	4	Abr	48,6	2,29
160	saudável	BP1	5	Abr	138,6	2,34
161	saudável	PA1	1	Abr	54,4	2,12
162	saudável	PA1	2	Abr	42,6	2,33
163	saudável	PA1	3	Abr	59,5	2,16
164	saudável	PA1	4	Abr	100,3	2,27
165	saudável	PA1	5	Abr	40,6	2,29
171	doente	PA2	1	Abr	38,5	2,17
172	doente	PA2	2	Abr	80	2,38
173	doente	PA2	3	Abr	60,6	2,21
174	doente	PA2	4	Abr	35,3	2,21
175	doente	PA2	5	Abr	59,8	2,24
176	doente	PA3	1	Abr	60,6	2,14
177	doente	PA3	2	Abr	54,7	2,17
178	doente	PA3	3	Abr	64,6	2,24
179	doente	PA3	4	Abr	60,3	2,16
180	doente	PA3	5	Abr	78,2	2,36
181	saudável	BP1	1	Mar	176,7	2,26
182	saudável	BP1	2	Mar	149	2,31
183	saudável	BP1	3	Mar	127,6	2,23
184	saudável	BP1	4	Mar	137,6	2,28
185	saudável	BP1	5	Mar	135,3	2,28
191	doente	BP2	1	Mar	79,2	2,2
192	doente	BP2	2	Mar	80,7	2,3

193	doente	BP2	3	Mar	99,1	2,28
194	doente	BP2	4	Mar	165,3	2,28
195	doente	BP2	5	Mar	105,5	2,38
196	doente	BP3	1	Mar	133,7	2,29
197	doente	BP3	2	Mar	89,8	2,29
198	doente	BP3	3	Mar	82,8	2,23
199	doente	BP3	4	Mar	140,8	2,3
200	doente	BP3	5	Mar	62,1	2,33

ANEXO II

Colônia	**Espécie**	**Status de saúde**	**Operárias**	**Larvas**	**Pupas**	**Ovos**	**Rainhas**	**Ácaros**	**Formigas**	**Fezes**	**Mel**	**Pólen**
BLA	*M. quadrifasciata*	Doentes	5		10			x		x	x	
BLB	*M. quadrifasciata*	Doentes	5		10			x	x	x	x	x
BLC	*M. quadrifasciata*	Doentes - com carvão ativado	5		10			x			x	x
BLD	*M. bicolor*	Doentes	5		5				x		x	x
BLE	*M. scutellaris*	Doentes	5		6			x	x		x	x
BLF	*M. seminigra*	Saudáveis	5							x	x	x
BLG	*M. seminigra*	Doentes	5		10			x		x	x	x
BLH	*M. scutellaris*	Doentes - com carvão ativado	5		4					x	x	x
BLI	*S. postica*	Doentes	5		5						x	x
BLJ	*M. quadrifasciata*	Saudáveis – no cativeiro	5		10			x			x	
BLK	*M. quadrifasciata*	Saudáveis – no cativeiro	5	10				x			x	
BLL	*M. scutellaris*	Saudáveis – no cativeiro	5									
BLM	*M. seminigra*	Saudáveis – no cativeiro	5					x			x	
BLN	*A. melifera*	Saudáveis	5									x
BLO	*A. melifera*	Saudáveis	5									x
BLP	*A. melifera*	Saudáveis	5									x
BLQ	*M. quadrifasciata*	Doentes	5	10	10	10	1				x	x
BLR	*M. quadrifasciata*	Doentes	5	10	10	10	1				x	x