



Data Article

Data relating to sequencing statistics and the reads and genomic coverage aligning to *Taenia solium* in the cerebrospinal fluid

Xiaofei Fei^{a,1}, Chaoyang Li^{a,1}, Yun Zhang^a, Hongya Zhang^a,
 Xuewu Liu^a, Xinchao Ji^a, Yajun Shi^a, Na Liu^a, Mengli Wu^a,
 Fang Du^a, Yining Yang^a, Wen Dai^a, TingTing Liu^a, Ying He^a,
 Ting Bian^a, Huimin Zhou^a, Xingyue An^a, Zheng Cai^a, Jian Shi^b,
 Guodong Feng^{c,*}, Ming Shi^{a,*}, Gang Zhao^{a,*}

^a Department of Neurology, Xijing Hospital, The Fourth Military Medical University, 15 Changle xi Road, Xi'an 710032, China

^b Department of Neurology, The First Affiliated Hospital Of Henan University Of Science and Technology, Luoyang, Henan, China

^c Department of Neurology, Zhongshan Hospital, Fudan University, 180 Fenglin Road, Shanghai 200032, China

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ABSTRACT

This data can serve as a reference for other next-generation sequencing (NGS) of the cerebrospinal fluid (CSF). In the related research article, entitled "Next-Generation Sequencing of Cerebrospinal Fluid for the Diagnosis of Neurocysticercosis", we reported NGS of the CSF might be an auxiliary method for neurocysticercosis (NCC) patients who have complicated manifestations and courses to receive early diagnosis and treatment. In this article, we retrieved the available data about the sequencing statistics of the CSF samples and the number of unique reads and genomic coverage aligning to microorganism sequences. The data were generated by the Illumina MiniSeq system for sequencing and computational subtraction of the human host sequences was performed. Finally, the remaining sequencing data were aligned to the Mi-

* Corresponding authors.

E-mail addresses: feng.guodong@zs-hospital.sh.cn (G. Feng), biomidas@163.com (M. Shi), zhaogang@fmmu.edu.cn (G. Zhao).

¹ These authors contributed equally to this work

crobial Genome Databases. This data can serve as a reference for other NGS of the CSF.

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Specifications Table

Subject	Biochemistry, Genetics and Molecular Biology (General)
Specific subject area	Molecular Biology
Type of data	Table
How data were acquired	Illumina MiniSeq system for sequencing, computational subtraction, Burrows-Wheeler Alignment tool, Finally, Microbial Genome Databases.
Data format	Raw and filtered
Parameters for data collection	The sequencing statistics of the cerebrospinal fluid (CSF) samples and the number of unique reads and genomic coverage aligning to microorganic sequences.
Description of data collection	The data were generated by the Illumina MiniSeq system for sequencing and computational subtraction of the human host sequences was performed using a Burrows-Wheeler Alignment tool. Finally, the remaining sequencing data were aligned to the Microbial Genome Databases (ftp://ftp.ncbi.nlm.nih.gov/genomes), which are composed of 2700 whole genome sequences of viral taxa, 1494 bacterial genomes or scaffolds, 73 fungi and 48 parasites associated with human infectivity.
Data source location	Department of Neurology, Xijing Hospital, The Fourth Military Medical University, 15 Changle xi Road, Xi'an 710032, China
Data accessibility	Data are presented in this article
Related research article	Author's name: Xiaofei Fei; Chaoyang Li; Yun Zhang; Hongya Zhang; Xuewu Liu; Xinchao Ji; Yajun Shi; Na Liu; Mengli Wu; Fang Du; Yining Yang; Wen Dai; TingTing Liu; Ying He; Ting Bian; Huimin Zhou; Xingyue An; Zheng Cai; Jian Shi; Guodong Feng; Ming Shi and Gang Zhao Title: Next-Generation Sequencing of Cerebrospinal Fluid for the Diagnosis of Neurocysticercosis Journal: Clin Neurol Neurosurg DOI: 10.1016/j.clineuro.2020.105752

Value of the Data

- This data provide raw reads aligning to human and the number of reads and genomic coverage aligning to *Taenia solium* and other microorganic sequences in the CSF.
- This data can serve as a reference for the diagnosis of neurocysticercosis by the next-generation sequencing (NGS) of the CSF.
- This data can be also used by further NGS of the CSF to identify common contaminated or non-pathogenic biological sequences.

1. Data Description

The reads aligned to human/primate, non-human/primate and NCBI (National Center for Biotechnology Information) NT (Nucleotide Sequence) database (<ftp://ftp.ncbi.nlm.nih.gov/genomes>) in the CSF are given in Table 1. The Microbial Genome Databases are composed of 2700 whole genome sequences of viral taxa, 1494 bacterial genomes or scaffolds, 73 fungi and 48 parasites associated with human infectivity. The reference genomes were downloaded from

Table 1

. The Sequencing statistics aligned to human/primate, non-human/primate and NCBI NT database in the cerebrospinal fluid

Sample	% Reads Passing Quality Control	# of Raw Reads	# of Reads after Quality Filtering and Adapter Trimming	# of Reads Aligned to Human / Primate	# of Non-Human / Primate Reads	% Human / Primate Reads	# of Reads Aligned to NCBI NT database*
Case 1-1	91.73985%	693159	635903	626181	9722	98.47115%	5997
Case 1-2	79.77807%	1063672	848577	823181	25396	97.00723%	7339
Case 1-3	90.39721%	1067117	964644	957545	7099	99.26408%	3215
Case 1-4	86.63103%	902119	781515	712063	69452	91.11316%	23107
Case 2-2	91.10832%	1175863	1071309	1008891	62418	94.17367%	48977
Case 2-3	91.60472%	856970	785025	778762	6263	99.20219%	4459
Case 3-1	92.24918%	1226090	1131058	1127120	3938	99.65183%	1208
Case 3-2	91.37044%	1596953	1459143	1454141	5002	99.65720%	2467
Case 3-3	92.91249%	1275399	1185005	1180024	4981	99.57966%	2063
Case 3-4	93.21982%	1202107	1120602	1112667	7935	99.29190%	4804
Case 3-5	79.97971%	1064365	851276	726802	124474	85.37795%	95282
Case 4	91.39075%	651195	595132	577096	18036	96.96941%	9493
Case 5	91.86937%	1559191	1432419	1424446	7973	99.44339%	4581
Case 6	90.16523%	1029195	927976	906599	21377	97.69638%	11589
Case 7	91.74785%	741467	680280	484374	195906	71.20215%	186639

* Reads Aligned to NCBI NT database refer to the filtered reads aligning to the microbial genomes.

NCBI. The coverage of each species was calculated using Soap Coverage (<http://soap.genomics.org.cn>). The number of unique reads and genomic coverage of *Taenia solium* and other microorganisms in the CSF and the “no-template” controls are given in Table 2.

2. Experimental Design, Materials, and Methods [2,3]

2.1. Sample Collection and DNA Extraction

CSF samples (300 µl) were collected from 7 patients. “No-template” controls (NTCs) are sterile water which are used as negative controls. Before the extraction of DNA, 300ul sterile water was added to a sterile centrifuge tube. The operations of NTCs were identical to that of CSF samples. All operations are performed in horizontal laminar flow clean bench. DNA was extracted using the TIANamp Micro DNA Kit (DP316, Tiangen Biotech, Beijing, China). When DNA extraction reagent was added to CSF, the same reagent was added to 300ul sterile water. All operations are performed in the workbench. Proteinase K (10mL) and buffer GB (with carrier RNA; 300mL) were added in the CSF samples and NTCs. The sample was incubated at 56°C for 10 min. After adding 300 µL of cold absolute ethyl alcohol, the tube was incubated for 5min at room temperature. The liquid was transferred to a new adsorption column and washed with buffer GD and buffer PW. Finally, the DNA was dissolved with 40mL of Tris-ethylenediaminetetraacetic acid buffer.

2.2. Library construction and sequencing

The extracted DNA was sonicated into 200–300 bp fragments using a Bioruptor Pico. DNA libraries were constructed via end-repair adaptation overnight and the use of polymerase chain reaction (PCR) amplification of the extracted DNA. The purified library was diluted, mixed, denatured, re-diluted, mixed with PhiX (equal to 1% of the final DNA amount) as described in the MiniSeq System Denature and Dilute Libraries Guide, and then applied to an Illumina

Table 2
The reads aligning to microbial genomes only in the cerebrospinal fluid and the non-template controls

Data of Case 1-1		
species	coverage	unique reads
bacteria		
Mesorhizobium sp. UASWS1009	1.07102%	928
Ralstonia sp. NT80	0.71621%	422
Staphylococcus hominis	0.44053%	136
Propionibacterium acnes	0.37285%	142
Moraxella osloensis	0.36310%	110
Ralstonia sp. MD27	0.27996%	98
Burkholderia sp. A9	0.23270%	4
Staphylococcus warneri	0.21697%	66
Staphylococcus epidermidis	0.20439%	40
Burkholderia ubonensis	0.20348%	34
Burkholderia multivorans	0.19835%	92
Ralstonia sp. 5_2_56FAA	0.19063%	48
Asinibacterium sp. OR53	0.17729%	86
Burkholderia sp. lig30	0.16949%	24
Acidovorax sp. KKS102	0.14422%	30
Pantoea sp. 9140	0.10644%	70
Pantoea sp. aB	0.05827%	4
Pantoea agglomerans	0.05721%	2
Pseudomonas oryzihabitans	0.02842%	20
Pseudomonas sp. RIT-PI-a	0.02804%	18
Erwinia gerundensis	0.02618%	18
Atopobium vaginae	0.02097%	4
Arthrobacter sp. Leaf234	0.02086%	8
Lactobacillus agilis	0.02012%	6
Sanguibacter sp. Leaf3	0.01839%	10
viruses		
Burkholderia phage KS10	0.41185%	2
Staphylococcus phage StB27	0.32942%	2
Staphylococcus phage SPbeta-like	0.27011%	8
Human gammaherpesvirus 4	0.08682%	2
Paramecium bursaria Chlorella virus A1	0.07004%	2
Parasite		
Taenia solium	0.14226%	2614
Wuchereria bancrofti	0.00581%	58
Acanthamoeba palestinensis	0.00207%	4
Taenia saginata	0.00198%	0
Enterocytozoon bieneusi	0.00194%	0
Taenia multiceps	0.00143%	2
Entamoeba histolytica	0.00103%	2
Hammondia hammondi	0.00096%	4
Plasmodium gallinaceum	0.00089%	0
Theileria equi	0.00064%	0
Gregarina niphandrodes	0.00054%	0
Plasmodium malariae	0.00022%	0
Anncaliia algerae	0.00109%	0
fungi		
Malassezia globosa	0.00787%	10
Albugo laibachii	0.00068%	2
Aspergillus fischeri	0.00047%	0
Fusarium verticillioides	0.00019%	2
Data of NTC 1-1		
species	coverage	unique reads
bacteria		
Bradyrhizobium elkanii	21.88930%	28096
Mesorhizobium sp. UASWS1009	16.55630%	18192
Ralstonia sp. NT80	14.52210%	9754

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Table 2 (continued)

Staphylococcus hominis	10.42230%	3698
Ralstonia sp. MD27	8.87976%	4906
Moraxella osloensis	7.18657%	2434
Corynebacterium jeikeium	5.98909%	1270
Ralstonia sp. 5_2_56FAA	4.20281%	1410
Propionibacterium acnes	3.72993%	1482
Asinibacterium sp. OR53	3.17341%	1474
Corynebacterium afermentans	3.10861%	666
Streptomyces purpurogeneiscleroticus	3.10289%	3072
Paracoccus sphaerophysae	2.93074%	1418
Comamonadaceae bacterium CCH4-C5	2.64042%	352
Corynebacterium sp. HMSC034A01	2.48935%	376
Ralstonia pickettii	2.45672%	580
Comamonadaceae bacterium CCH12-A10	2.45636%	64
Acidovorax temperans	2.31626%	278
Staphylococcus warneri	2.29655%	684
Burkholderia sp. A9	2.28783%	62
Staphylococcus haemolyticus	2.19982%	760
Burkholderia ubonensis	2.19935%	532
Corynebacterium tuberculostrictum	2.19913%	356
Psychrobacter sp. 1501(2011)	2.16726%	994
Burkholderia sp. lig30	2.05547%	408
Brevundimonas vesicularis	1.96955%	336
Afipia broomeae	1.89598%	1128
Herbaspirillum frisingense	1.85754%	1566
Acidovorax sp. CCH12-A4	1.79300%	66
Staphylococcus epidermidis	1.79137%	384
Acidovorax delafieldii	1.78164%	240
alpha proteobacterium L41A	1.73341%	178
Corynebacterium aurimucosum	1.72909%	176
Burkholderia multivorans	1.71611%	876
Acidovorax sp. KKS102	1.61235%	180
Kocuria palustris	1.59043%	674
Pseudomonas fluorescens	1.58135%	1664
Brevundimonas nasdae	1.56017%	212
Sphingomonas sp. Ant H11	1.50154%	686
Azospira oryzae	1.46515%	812
Acidovorax sp. Root70	1.42366%	266
Burkholderia pseudomultivorans	1.23697%	170
Asticcacaulis excentricus	1.19113%	452
Burkholderia dolosa	1.14323%	128
Burkholderia territorii	1.03587%	80
Acidovorax sp. Root402	1.02996%	156
Burkholderia cenocepacia	1.01921%	74
Caulobacter vibrioides	1.00835%	654
Burkholderia vietnamiensis	0.88260%	98
Burkholderia cepacia	0.87995%	76
Burkholderia contaminans	0.86850%	66
Burkholderia paludis	0.85199%	86
Burkholderia latens	0.81089%	58
Methylotenera versatilis	0.76310%	204
Acinetobacter johnsonii	0.70205%	346
Burkholderia oklahomensis	0.51224%	66
Acinetobacter baumannii	0.03004%	2
Tepidiphilus thermophilus	0.02925%	6
Peptoniphilus lacrimalis	0.02125%	4
Gardnerella vaginalis	0.01717%	4
Serratia marcescens	0.00894%	2

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Table 2 (continued)

viruses		
Burkholderia phage KS10	12.39273%	42
Flavobacterium phage Fpv2	0.45320%	4
Paramecium bursaria Chlorella virus A1	0.35670%	5
Staphylococcus phage IME-SA4	14.68467%	67
Staphylococcus phage CNPH82	13.21050%	45
Staphylococcus phage Ipla5	12.78080%	35
Staphylococcus phage PH15	12.20680%	42
Staphylococcus phage Ipla7	8.94998%	18
Staphylococcus phage CNPx	4.27783%	10
Staphylococcus phage StB12	3.47691%	6
Staphylococcus phage StB20-like	1.07450%	3
Staphylococcus phage StB27	0.85037%	3
Staphylococcus phage PT1028	0.83317%	1
Staphylococcus phage SPbeta-like	0.80453%	19
Parasite		
Acanthamoeba palestinensis	0.00880%	34
Wuchereria bancrofti	0.00770%	46
Hammondia hammondi	0.00330%	6
Cryptosporidium hominis	0.00210%	4
Acanthamoeba mauritaniensis	0.00180%	2
Trypanosoma cruzi	0.00080%	2
Toxoplasma gondii	0.00220%	4
Enterobius vermicularis	0.00030%	3
Hammondia hammondi	0.00070%	4
Leishmania mexicana	0.00130%	4
fungi		
Malassezia globosa	0.00938%	6
Neurospora crassa	0.00170%	4
Neurospora tetrasperma	0.00147%	3
Sordaria macrospora	0.00085%	1
Talaromyces marneffeii	0.00061%	1
Aspergillus oryzae	0.00120%	6
Albugo laibachii	0.00090%	5
Data of Case 1-2		
species	coverage	unique reads
bacteria		
Burkholderia contaminans	2.21054%	2372
Burkholderia sp. A9	1.46819%	32
Propionibacterium acnes	1.22233%	476
Burkholderia ubonensis	1.12679%	258
Burkholderia sp. lig30	1.05198%	184
Burkholderia multivorans	0.86904%	476
Burkholderia pseudomultivorans	0.62819%	104
Burkholderia cenocepacia	0.59451%	50
Burkholderia cepacia	0.59443%	48
Burkholderia dolosa	0.58867%	66
Burkholderia territorii	0.52705%	28
Burkholderia vietnamiensis	0.44917%	36
Burkholderia paludis	0.44871%	40
Burkholderia latens	0.41821%	36
Burkholderia oklahomensis	0.27370%	20
Candidatus Kinetoplastibacterium crithidii	0.03528%	0
Burkholderiales bacterium YL45	0.01796%	0
Candidatus Proffittella armatura	0.01656%	0
Streptococcus sp. oral taxon 058	0.01412%	0
Formosa sp. Hel3_A1_48	0.00878%	0
[Eubacterium] nodatum	0.00765%	0
Deinococcus puniceus	0.00690%	0
Streptococcus sp. HMSC034E03	0.00663%	0
Streptococcus pasteurianus	0.00654%	0
Streptococcus macedonicus	0.00630%	0

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Table 2 (continued)

viruses		
Burkholderia phage KS10	1.76432%	0
Staphylococcus phage Slt	0.15137%	0
Staphylococcus phage phiMR11	0.15112%	0
Staphylococcus phage phiJB	0.15112%	0
Staphylococcus phage 71	0.15076%	0
Burkholderia virus phiE125	0.12178%	0
Parasite		
Taenia solium	0.02478%	334
Enterocytozoon bienewisi	0.00531%	0
Wuchereria bancrofti	0.00307%	28
Entamoeba histolytica	0.00111%	0
Taenia multiceps	0.00072%	0
Anncaliia algerae	0.00054%	0
Acanthamoeba palestinensis	0.00045%	0
Taenia saginata	0.00036%	0
Toxoplasma gondii	0.00029%	0
Hammondia hammondi	0.00028%	0
Vitrella brassicaformis	0.00019%	0
Trypanosoma congolense	0.00016%	0
Hymenolepis nana	0.00012%	0
fungi		
Malassezia globosa	0.00135%	2
Albugo laibachii	0.00037%	2
Sordaria macrospora	0.00019%	0

Data of NTC 1-2

Species	coverage	unique reads
bacteria		
Burkholderia contaminans	70.71390%	192162
Burkholderia sp. A9	18.34850%	698
Propionibacterium acnes	9.69150%	4508
Burkholderia ubonensis	9.52910%	4152
Burkholderia cepacia	9.48444%	778
Streptomyces purpureogenescleroticus	9.26422%	11520
Burkholderia sp. lig30	8.61528%	3324
Paracoccus sphaerophysae	8.27434%	4748
Burkholderia multivorans	7.99355%	10438
Burkholderia cenocepacia	7.77753%	722
Burkholderia pseudomultivorans	6.56730%	1360
Burkholderia paludis	6.23575%	752
Burkholderia terrortii	5.93721%	810
Burkholderia dolosa	5.70962%	1008
Brevundimonas vesicularis	5.46127%	1098
alpha proteobacterium L41A	5.36417%	960
Burkholderia vietnamiensis	5.00986%	758
Burkholderia latens	4.81704%	550
Moraxella osloensis	4.48765%	1750
Brevundimonas nasdae	4.26600%	620
Ralstonia sp. MD27	3.95541%	3814
Methylobacterium sp. Leaf92	3.33116%	1984
Burkholderia oklahomensis	2.55266%	532
Burkholderia sp. MSMB0266	2.39555%	502
Burkholderia thailandensis	2.36199%	356
Mitsuaria chitosanitabida	2.30286%	1550
Burkholderia pseudomallei	2.15821%	394
Polynucleobacter duraquae	2.03233%	242
Mesorhizobium sp. UASWS1009	2.02916%	2578
Staphylococcus epidermidis	1.75235%	464
Delftia sp. 670	1.59035%	350
beta proteobacterium CB	1.47058%	160

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Table 2 (continued)

Rhizobiales bacterium CCH3-A5	1.44322%	1258
Delftia tsuruhatensis	1.39544%	136
Comamonadaceae bacterium CCH4-C5	1.34171%	152
Burkholderia sp. TSV85	1.26039%	206
Limnochabitus sp. Rim47	1.25771%	524
Comamonadaceae bacterium CCH12-A10	1.22388%	28
Sphingopyxis sp. LC81	1.21113%	646
Methylobacterium sp. AMS5	1.17324%	160
Paraburkholderia graminis	1.11557%	100
Cupriavidus metallidurans	1.07216%	148
Polynucleobacter sp. MWH-Adler-W8	1.06592%	154
Polynucleobacter yangtzensis	1.06532%	116
Acidovorax sp. CCH12-A4	1.06181%	22
Acidovorax temperans	1.05237%	140
Rhodoluna laticola	1.00760%	172
Acidovorax sp. KKS102	1.00036%	100
Burkholderia glumae	0.92570%	164
Burkholderia plantarii	0.90366%	156
Acidovorax delafieldii	0.85833%	102
Acinetobacter johnsonii	0.70257%	396
Serratia marcescens	0.60362%	398
Staphylococcus warneri	0.59456%	284
Methylobacterium populi	0.51600%	72
Methylobacterium sp. MB200	0.45124%	106
Brevundimonas diminuta	0.32852%	38
Pseudomonas putida	0.30588%	34
Brevundimonas naejangsanensis	0.23745%	4
Cellvibrio sp. pealriver	0.23255%	36
Luteimonas huabeiensis	0.21588%	4
Paracoccus sp. S4493	0.19800%	24
Paracoccus sp. 228	0.17676%	18
Thermomonas hydrothermalis	0.13133%	2
Caldimonas manganoxidans	0.11231%	6
Deinococcus geothermalis	0.06766%	14
Pseudomonas pseudoalcaligenes	0.05742%	8
Tetrasphaera elongata	0.05497%	12
Microbacterium aurum	0.05443%	14
Dietzia sp. 111N12-1	0.04864%	24
Gordonia sputi	0.04593%	18
Brevibacterium casei	0.02841%	10
Xanthomonas sp. Mitacek01	0.02604%	4
viruses		
Burkholderia phage KS10	12.46273%	45
Flavobacterium phage Fpv2	0.44520%	5
Paramecium bursaria Chlorella virus A1	0.36770%	4
Staphylococcus phage IME-SA4	14.67467%	87
Staphylococcus phage CNPH82	13.21050%	45
Staphylococcus phage Ipla5	12.78080%	45
Staphylococcus phage PH15	12.88680%	42
Staphylococcus phage Ipla7	8.89998%	23
Staphylococcus phage CNPx	4.65783%	11
Staphylococcus phage StB12	3.47691%	8
Staphylococcus phage PT1028	0.43317%	0
Staphylococcus phage SPbeta-like	0.80953%	21
Parasite		
Acanthamoeba palestinensis	0.00760%	36
Wuchereria bancrofti	0.00660%	55
Hammondia hammondi	0.00330%	10
Cryptosporidium hominis	0.00240%	5
Acanthamoeba mauritaniensis	0.00100%	1
Enterobius vermicularis	0.00020%	3
Hammondia hammondi	0.00030%	1
Leishmania mexicana	0.00150%	4

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Table 2 (continued)

fungi		
Malassezia globosa	0.00945%	7
Neurospora crassa	0.00168%	5
Neurospora tetrasperma	0.00147%	5
Sordaria macrospora	0.00085%	1
Albugo laibachii	0.00110%	5
Data of Case 1-3		
species	coverage	unique reads
bacteria		
Mesorhizobium sp. UASWS1009	0.60169%	520
Burkholderia sp. A9	0.25588%	4
Comamonadaceae bacterium CCH4-C5	0.22380%	28
Burkholderia sp. lig30	0.22198%	44
Moraxella osloensis	0.20637%	84
Acidovorax temperans	0.20151%	16
Comamonadaceae bacterium CCH12-A10	0.20112%	4
Burkholderia ubonensis	0.20000%	42
Burkholderia multivorans	0.18438%	92
Asinibacterium sp. OR53	0.16400%	82
Methylobacterium versatilis	0.15945%	26
Acidovorax delafieldii	0.14580%	20
Acidovorax sp. CCH12-A4	0.13736%	0
Burkholderia dolosa	0.12890%	6
Acidovorax sp. KKS102	0.12711%	20
Buchnera aphidicola	0.03577%	4
Candidatus Methylophilum planktonicus	0.01526%	2
Streptococcus suis	0.01360%	2
Streptococcus sp. HMSC063B03	0.01279%	2
Streptococcus sp. X13SY08	0.00962%	0
Candidatus Nitrosotenuis cloacae	0.00926%	2
Coriobacteriales bacterium DNF00809	0.00883%	2
Lactobacillus frumenti	0.00865%	2
Fenollaria timonensis	0.00862%	0
Ezakiella massiliensis	0.00861%	0
viruses		
Propionibacterium phage P1.1	0.51111%	2
Rhodovirax phage P26218	0.20653%	0
Burkholderia phage KS10	0.19928%	0
Paramecium bursaria Chlorella virus A1	0.05417%	2
Parasite		
Wuchereria bancrofti	0.01117%	138
Taenia solium	0.00129%	20
Entamoeba histolytica	0.00060%	0
Acanthamoeba palestinensis	0.00055%	0
Acanthamoeba mauritaniensis	0.00038%	0
Hammondia hammondi	0.00033%	0
Toxoplasma gondii	0.00023%	0
Vitrella brassicaformis	0.00020%	0
Sordaria macrospora	0.00018%	0
Spirometra erinaceieuropaei	0.00016%	16
Sarcocystis neurona	0.00009%	2
Acanthamoeba lugdunensis	0.00008%	0
Taenia saginata	0.00007%	0
Taenia multiceps	0.00005%	0
fungi		
[Candida] glabrata		0
Fusarium verticillioides	0.00061%	4
Aspergillus oryzae	0.00050%	2
Phytophthora ramorum	0.00031%	0

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Table 2 (continued)

Data of NTC 1-3		
species	coverage	unique reads
bacteria		
Propionibacterium acnes	34.04003%	11554
Burkholderia sp. A9	12.28355%	582
Burkholderia ubonensis	9.00584%	5830
Burkholderia sp. lig30	8.51874%	4474
Moraxella osloensis	7.97496%	1552
Acidovorax sp. CCH12-A4	7.68344%	209
Comamonadaceae bacterium CCH4-C5	7.43362%	1213
Mesorhizobium sp. UASWS1009	6.71863%	3682
Acidovorax temperans	6.18504%	1086
Comamonadaceae bacterium CCH12-A10	6.17620%	400
Burkholderia multivorans	5.28967%	8881
Acidovorax sp. KKS102	4.38349%	1422
Burkholderia pseudomultivorans	4.29995%	2234
Acidovorax delafieldii	4.23114%	1467
Burkholderia dolosa	3.80671%	1668
Streptomyces purpureogeniscleroticus	3.78001%	1982
Staphylococcus epidermidis	3.26394%	669
Burkholderia territorii	3.21927%	1242
Burkholderia vietnamiensis	3.03225%	1214
Burkholderia cepacia	2.84271%	1257
Burkholderia cenocepacia	2.83904%	1263
Burkholderia latens	2.67585%	835
Burkholderia paludis	2.64373%	1292
Burkholderia contaminans	2.43925%	1041
Methylophilus sp. 42	2.14890%	308
Paludibacter propionigenes	1.97348%	582
Cutibacterium granulosum	1.92545%	253
Burkholderia oklahomensis	1.88096%	855
Acidovorax sp. Root70	1.77776%	481
Chryseobacterium gambrini	1.70283%	610
Acidovorax sp. Root402	1.68536%	480
Paraburkholderia graminis	1.67921%	33
Staphylococcus hominis	1.61241%	287
Methyloversatilis universalis	1.59867%	470
Burkholderia sp. MSMB0266	1.57836%	636
Burkholderia thailandensis	1.56916%	539
Burkholderia pseudomallei	1.53337%	617
[Propionibacterium] namnetense	1.52591%	278
Limnochabitans sp. Rim47	1.47593%	235
Corynebacterium sp. KPL1860	1.45035%	265
Sphingomonas sp. CCH10-B3	1.26080%	47
Pelomonas sp. Root1444	1.23576%	169
Cupriavidus metallidurans	1.23463%	206
Curvibacter delicatus	1.14647%	148
Acidovorax sp. GW101-3H11	1.11543%	293
Bosea vaviloviae	0.96862%	404
Xenophilus azovorans	0.92828%	16
Propionibacterium humerusii	0.85206%	190
Dyella jiangningensis	0.75250%	502
Acinetobacter johnsonii	0.58676%	176
Micrococcus luteus	0.56357%	61
Corynebacterium aurimucosum	0.50558%	72
Neisseria sp. HMSC073B07	0.47438%	65
viruses		
Burkholderia phage KS10	12.46273%	45
Flavobacterium phage Fpv2	0.44520%	5
Paramecium bursaria Chlorella virus A1	0.36770%	4
Staphylococcus phage IME-SA4	14.67467%	87
Staphylococcus phage CNPH82	13.21050%	45

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Table 2 (continued)

Staphylococcus phage Ipla5	12.78080%	45
Staphylococcus phage PH15	12.88680%	42
Staphylococcus phage Ipla7	8.89998%	23
Staphylococcus phage CNP _x	4.65783%	11
Staphylococcus phage StB12	3.47691%	8
Staphylococcus phage PT1028	0.43317%	0
Propionibacterium phage P1.1	0.80953%	21
Parasite		
Acanthamoeba palestinensis	0.00680%	30
Wuchereria bancrofti	0.00970%	66
Hammondia hammondi	0.00330%	6
Cryptosporidium hominis	0.00210%	5
Acanthamoeba mauritaniensis	0.00180%	2
Trypanosoma cruzi	0.00190%	3
Toxoplasma gondii	0.00220%	4
Enterobius vermicularis	0.00030%	3
fungi		
Malassezia globosa	0.00938%	7
Neurospora crassa	0.00170%	4
Neurospora tetrasperma	0.00177%	5
Sordaria macrospora	0.00085%	1
Albugo laibachii	0.00120%	8

Data of Case 1-4

species	coverage	unique reads
bacteria		
Burkholderia sp. A9	7.81720%	124
Burkholderia ubonensis	4.04034%	1367
Burkholderia sp. lig30	3.77586%	1022
Burkholderia contaminans	3.77353%	2157
Burkholderia multivorans	2.76210%	2158
Mesorhizobium sp. UASWS1009	2.74414%	1415
Burkholderia pseudomultivorans	1.71037%	506
Burkholderia dolosa	1.49604%	440
Ralstonia sp. MD27	1.33630%	558
Propionibacterium acnes	1.29076%	248
Burkholderia territorii	1.22983%	291
Burkholderia vietnamiensis	1.14219%	260
Burkholderia cepacia	1.03080%	316
Burkholderia cenocepacia	1.01151%	324
Burkholderia latens	0.97577%	197
Candidatus Kinetoplastibacterium galatii	0.06556%	0
Lactobacillus crispatus	0.02790%	4
Cellulosimicrobium sp. I38E	0.02219%	4
Leuconostoc lactis	0.02120%	4
Pantoea septica	0.01996%	6
Brackiella oedipodis	0.01800%	0
Gardnerella vaginalis	0.01685%	1
Corynebacterium genitalium	0.01596%	0
Nitrosomonas eutropha	0.01455%	0
Salmonella enterica	0.00303%	1
viruses		
Burkholderia phage KS10	9.18294%	19
Propionibacterium phage Kubed	0.50915%	1
Propionibacterium phage PHL009	0.39318%	1
Propionibacterium phage PHL116	0.27897%	1
Propionibacterium phage BruceLethal	0.25642%	0
Propionibacterium phage Lauchelly	0.25409%	0
Burkholderia virus phiE125	0.23982%	1
Rhodoferrax phage P26218	0.20653%	0
Staphylococcus phage StB12	0.16773%	0
Acinetobacter bacteriophage AP22	0.16168%	0

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Table 2 (continued)

Burkholderia virus Bcepil02	0.15945%	0
Pseudomonas phage PMG1	0.13883%	0
Burkholderia virus Bcep22	0.11740%	0
Salmonella phage SJ46	0.07250%	0
Invertebrate iridescent virus 31	0.06130%	1
Paramecium bursaria Chlorella virus A1	0.02335%	0
Parasite		
Wuchereria bancrofti	0.00406%	21
Acanthamoeba palestinensis	0.00088%	5
Hammondia hammondi	0.00071%	2
Anisakis simplex	0.00047%	3
Toxoplasma gondii	0.00045%	1
Enterobius vermicularis	0.00015%	0
Acanthamoeba mauritaniensis	0.00012%	1
Necator americanus	0.00008%	1
Spirometra erinaceieuropaei	0.00008%	5
Daphnia pulex	0.00008%	0
Cimex lectularius	0.00001%	0
fungi		
Malassezia globosa		8
Sordaria macrospora	0.01104%	1
Aspergillus oryzae	0.00075%	1
Aspergillus terreus	0.00040%	0
Talaromyces stipitatus	0.00026%	1

Data of NTC 1-4

species	coverage	unique reads
bacteria		
Burkholderia contaminans	17.06165%	12499
Propionibacterium acnes	14.79645%	3213
Burkholderia sp. A9	13.71155%	416
Moraxella osloensis	10.41486%	1926
Burkholderia ubonensis	7.25759%	3932
Ralstonia sp. MD27	7.19944%	3495
Burkholderia sp. lig30	6.79520%	2965
Mesorhizobium sp. UASWS1009	6.36419%	3543
Staphylococcus capitis	5.54523%	1036
Burkholderia multivorans	4.57565%	6074
Burkholderia pseudomultivorans	3.34007%	1486
Burkholderia dolosa	2.94948%	1156
Acinetobacter johnsonii	2.75123%	784
Burkholderia territorii	2.45843%	865
Burkholderia vietnamiensis	2.31264%	812
Burkholderia cepacia	2.23127%	888
Streptomyces purpurogeneiscleroticus	2.19861%	1174
Burkholderia cenocepacia	2.18833%	914
Burkholderia latens	2.07107%	558
Sphingomonas sp. Ant H11	2.05460%	689
Burkholderia paludis	2.01034%	885
Methylotenera versatilis	1.68798%	291
Paraburkholderia graminis	1.48860%	22
Pseudomonas sp. NBRC 111126	1.47376%	592
Burkholderia oklahomensis	1.47342%	588
Kocuria polaris	1.44637%	399
Acidovorax sp. Leaf160	1.33441%	358
Acidovorax delafieldii	1.33048%	365
Enterobacter hormaechei	1.20764%	433
Burkholderia sp. MSMB0266	1.20270%	459
Burkholderia thailandensis	1.18905%	403
Limnochabbits sp. Rim47	1.18635%	218
Burkholderia pseudomallei	1.17267%	430
Acidovorax sp. CCH12-A4	1.16758%	25

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Table 2 (continued)

Acidovorax sp. Root70	1.15159%	282
Acidovorax sp. KKS102	1.13274%	273
Cupriavidus metallidurans	1.10643%	156
Polynucleobacter duraquae	1.04787%	64
Azospira oryzae	0.98796%	277
Acinetobacter ursingii	0.96935%	249
Xenophilus azovorans	0.86198%	9
Methylobacterium sp. Leaf92	0.84496%	332
Dyella jiangningensis	0.73064%	362
Cupriavidus necator	0.71804%	301
Comamonadaceae bacterium CCH12-A10	0.65781%	18
Ralstonia sp. NT80	0.65181%	210
Comamonadaceae bacterium CCH4-C5	0.62873%	74
Hydrogenophaga sp. Root209	0.59192%	53
Acinetobacter pittii	0.54572%	149
Acidovorax temperans	0.48750%	59
Serratia marcescens	0.27563%	87
viruses		
Burkholderia phage KS10	12.43273%	53
Flavobacterium phage Fpv2	0.40320%	4
Paramecium bursaria Chlorella virus A1	0.36670%	6
Staphylococcus phage IME-SA4	17.78467%	67
Staphylococcus phage CNPH82	14.21050%	78
Staphylococcus phage Ipla5	18.78080%	78
Staphylococcus phage PH15	14.20680%	35
Staphylococcus phage Ipla7	8.94998%	22
Staphylococcus phage CNP _x	4.27783%	9
Propionibacterium phage Kubed	3.48991%	7
Propionibacterium phage PHL009	1.67450%	5
Propionibacterium phage PHL116	0.78037%	3
Propionibacterium phage BruceLethal	0.84517%	5
Propionibacterium phage Lauchelly	0.70453%	12
Parasite		
Acanthamoeba palestinensis	0.00890%	37
Wuchereria bancrofti	0.00670%	42
Hammondia hammondi	0.00330%	6
Cryptosporidium hominis	0.00210%	5
Acanthamoeba mauritaniensis	0.00190%	2
Trypanosoma cruzi	0.00080%	2
Toxoplasma gondii	0.00340%	5
Enterobius vermicularis	0.00040%	4
Hammondia hammondi	0.00120%	6
Leishmania mexicana	0.00140%	5
fungi		
Malassezia globosa	0.00937%	6
Neurospora crassa	0.00168%	5
Talaromyces marneffeii	0.00061%	6
Aspergillus oryzae	0.00150%	1
Albugo laibachii	0.00130%	4

Data of Case 2-2

species	coverage	unique reads
bacteria		
Burkholderia sp. A9	3.07628%	86
Burkholderia ubonensis	2.83859%	660
Burkholderia sp. lig30	2.64866%	570
Burkholderia multivorans	2.15804%	1208
Burkholderia pseudomultivorans	1.56057%	202
Burkholderia dolosa	1.49231%	162
Burkholderia territorii	1.37086%	92
Burkholderia cenocepacia	1.33809%	108
Burkholderia cepacia	1.24686%	102

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Table 2 (continued)

Burkholderia vietnamiensis	1.20625%	118
Burkholderia paludisj	1.11181%	134
Burkholderia latens	1.10139%	70
Mesorhizobium sp. UASWS1009	1.08090%	1114
Burkholderia contaminans	1.04647%	112
Paracoccus sphaerophysae	0.81007%	356
Kinetoplastibacterium blastocrithidii	0.04780%	0
Actinomyces sp. HMSC08A01	0.02886%	10
Candidatus Proffotella armatura	0.02216%	0
Candidatus Kinetoplastibacterium crithidii	0.01995%	0
Corynebacterium variabile	0.01992%	4
Aerococcus viridans	0.01991%	0
Weissella jogaejeotgali	0.01973%	0
Candidatus Kinetoplastibacterium galatii	0.01934%	0
Candidatus Kinetoplastibacterium oncopeltii	0.01851%	0
Streptococcus macedonicus	0.01668%	0
viruses		
Burkholderia phage KS10	4.26465%	16
Propionibacterium phage PHL060L00	0.50823%	2
Staphylococcus phage StB27	0.37434%	2
Burkholderia virus phiE125	0.32226%	2
Staphylococcus phage IME-SA4	0.17924%	0
Flavobacterium phage Fpv2	0.08875%	2
Paramecium bursaria Chlorella virus A1	0.02335%	0
Parasite		
Taenia solium	3.03254%	45972
Taenia saginata	0.05191%	18
Taenia multiceps	0.03624%	62
Wuchereria bancrofti	0.01077%	74
Acanthamoeba palestinensis	0.00174%	8
Hymenolepis nana	0.00150%	0
Entamoeba histolytica	0.00119%	0
Acanthamoeba mauritaniensis	0.00103%	2
Echinococcus multilocularis	0.00085%	0
Trypanosoma cruzi	0.00062%	0
Hammondia hammondi	0.00058%	2
Anncaliia algerae	0.00054%	0
Toxoplasma gondii	0.00046%	0
Schistosoma mansoni	0.00039%	0
fungi		
Malassezia globosa	0.00238%	4
Pneumocystis carinii	0.00196%	0
Sordaria macrospora	0.00094%	0
Albugo laibachii	0.00060%	2

Data of NTC 2-2

species	coverage	unique reads
bacteria		
Staphylococcus hominis	12.19550%	4564
Ralstonia sp. MD27	10.70210%	9644
Burkholderia ubonensis	8.40481%	3698
Moraxella osloensis	7.84991%	2552
Burkholderia sp. A9	7.76343%	466
Burkholderia sp. lig30	7.68243%	2762
Paracoccus sphaerophysae	7.61451%	3744
Rothia sp. ND6WE1A	7.30648%	2784
Staphylococcus haemolyticus	6.01573%	2306
Burkholderia multivorans	5.80606%	6370
Staphylococcus epidermidis	5.25386%	1058
Burkholderia pseudomultivorans	5.06785%	1126
alpha proteobacterium L41A	4.88849%	798
Brevundimonas vesicularis	4.87511%	854

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Table 2 (continued)

Burkholderia dolosa	4.71681%	818
Mesorhizobium sp. UASWS1009	4.62789%	5248
Propionibacterium acnes	4.58402%	1860
Burkholderia cenocepacia	4.31558%	560
Burkholderia territorii	4.26066%	582
Burkholderia vietnamiensis	3.87120%	662
Burkholderia cepacia	3.86708%	616
Brevundimonas nasdae	3.81090%	514
Burkholderia latens	3.56392%	356
Burkholderia paludis	3.52522%	598
Burkholderia contaminans	3.43589%	548
Corynebacterium appendicis	3.31193%	994
Streptomyces purpurogeneiscleroticus	3.21604%	3336
Acinetobacter johnsonii	2.93549%	1556
Staphylococcus warneri	2.91993%	878
Burkholderia oklahomensis	2.19710%	456
Burkholderia thailandensis	2.03216%	256
Burkholderia sp. MSMB0266	1.90831%	434
Burkholderia pseudomallei	1.85903%	332
Acidovorax delafieldii	1.46921%	190
Ralstonia sp. NT80	1.45625%	246
Sphingomonas sp. Ant H11	1.45307%	756
Methylobacterium versatilis	1.38689%	204
Corynebacterium tuberculoearicum	1.34973%	220
Acidovorax sp. KKS102	1.31939%	164
Corynebacterium aurimucosum	1.27600%	200
Acidovorax sp. Leaf160	1.25323%	654
Acidovorax sp. Root70	1.12287%	230
Burkholderia sp. TSV85	1.07564%	164
Cupriavidus metallidurans	1.05755%	198
Comamonadaceae bacterium CCH12-A10	1.05171%	16
Comamonadaceae bacterium CCH4-C5	1.02252%	96
Acidovorax sp. CCH12-A4	0.88438%	32
Acidovorax sp. Root402	0.87451%	136
Burkholderia plantarii	0.80571%	130
Acidovorax temperans	0.76659%	74
Ralstonia pickettii	0.75577%	246
Bradyrhizobium elkanii	0.71983%	762
Limnhabitans sp. Rim47	0.69754%	252
Ralstonia sp. 5_2_56FAA	0.57599%	66
Acinetobacter lwoffii	0.52177%	168
Cloacibacterium normanense	0.16745%	54
Prevotella disiens	0.01169%	2
Serratia marcescens	0.00786%	6
viruses		
Burkholderia phage KS10	12.39273%	42
Flavobacterium phage Fpv2	0.45320%	4
Paramecium bursaria Chlorella virus A1	0.35670%	5
Staphylococcus phage IME-SA4	14.68467%	67
Staphylococcus phage CNPH82	13.21050%	45
Staphylococcus phage Ipla5	12.78080%	35
Staphylococcus phage PH15	12.20680%	42
Staphylococcus phage Ipla7	8.94998%	18
Staphylococcus phage CNPx	4.27783%	10
Staphylococcus phage StB12	3.47691%	6
Staphylococcus phage StB20-like	1.07450%	3
Staphylococcus phage StB27	0.85037%	3
Staphylococcus phage PT1028	0.83317%	1
Staphylococcus phage SPbeta-like	0.80453%	19

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Table 2 (continued)

Parasite		
Acanthamoeba palestinensis	0.01080%	44
Wuchereria bancrofti	0.01070%	76
Hammondia hammondi	0.00350%	5
Cryptosporidium hominis	0.00160%	3
Acanthamoeba mauritaniensis	0.00210%	5
Trypanosoma cruzi	0.00070%	9
Toxoplasma gondii	0.00200%	3
Enterobius vermicularis	0.00130%	11
Hammondia hammondi	0.00120%	8
Leishmania mexicana	0.00050%	1
fungi		
Malassezia globosa	0.00938%	7
Neurospora crassa	0.00173%	5
Neurospora tetrasperma	0.00144%	4
Sordaria macrospora	0.00082%	2
Talaromyces marneffeii	0.00061%	1
Aspergillus oryzae	0.00150%	7
Albugo laibachii	0.00130%	8
Data of Case 2-3		
species	coverage	unique reads
bacteria		
Mesorhizobium sp. UASWS1009	0.91784%	812
Moraxella osloensis	0.50888%	156
Burkholderia sp. A9	0.33967%	4
Burkholderia ubonensis	0.25409%	58
Burkholderia multivorans	0.24535%	138
Burkholderia sp. lig30	0.22921%	34
Comamonadaceae bacterium CCH4-C5	0.22088%	22
Staphylococcus hominis	0.21209%	64
Comamonadaceae bacterium CCH12-A10	0.20514%	4
Staphylococcus warneri	0.19807%	52
Propionibacterium acnes	0.19807%	68
Acidovorax temperans	0.19201%	22
Acidovorax delafieldii	0.17649%	28
Acidovorax sp. KKS102	0.16566%	20
Herbaspirillum frisingense	0.16484%	128
Candidatus Kinetoplastibacterium crithidii	0.02737%	0
Buchnera aphidicola	0.01413%	2
Streptococcus gordonii	0.01386%	2
Thermus scotoductus	0.01274%	2
Leptotrichia shahii	0.01268%	4
Candidatus Methylopumilus planktonicus	0.01106%	0
Candidatus Aquiluna sp. IMCC13023	0.01103%	0
Lactobacillus iners	0.01049%	2
Atopobium vaginae	0.01049%	2
Mycobacterium hassiacum	0.00152%	2
viruses		
Burkholderia phage KS10	0.71476%	4
Staphylococcus phage Ipla7	0.24452%	0
Staphylococcus phage CNPx	0.23791%	0
Staphylococcus phage CNPH82	0.23722%	0
Staphylococcus phage Ipla5	0.23634%	0
Rhodoferrax phage P26218	0.20653%	0
Burkholderia virus phiE125	0.14052%	0
Paramecium bursaria Chlorella virus A1	0.07004%	2

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Table 2 (continued)

Parasite		
Wuchereria bancrofti	0.01086%	118
Taenia solium	0.00910%	162
Acanthamoeba palestinensis	0.00137%	2
Toxoplasma gondii	0.00068%	4
Entamoeba histolytica	0.00060%	0
Hammondia hammondi	0.00055%	4
Leishmania mexicana	0.00046%	0
Acanthamoeba mauritaniensis	0.00030%	0
Daphnia magna	0.00023%	0
Daphnia pulex	0.00019%	0
Taenia multiceps	0.00008%	0
Taenia saginata	0.00007%	0
Trichobilharzia regenti	0.00001%	0
fungi		
Candida glabrata	0.00098%	2
Sordaria macrospora	0.00088%	2
Malassezia globosa	0.00087%	2
Fusarium graminearum	0.00039%	2
Aspergillus oryzae	0.00029%	2
Data of NTC 2-3		
species	coverage	unique reads
bacteria		
Burkholderia ubonensis	12.17370%	7912
Burkholderia contaminans	12.10940%	10322
Mesorhizobium sp. UASWS1009	11.83390%	13442
Burkholderia sp. lig30	11.40910%	6560
Burkholderia sp. A9	11.29790%	910
Propionibacterium acnes	9.16155%	3460
Burkholderia multivorans	8.55849%	17058
Burkholderia pseudomultivorans	7.80365%	2686
Burkholderia dolosa	7.34465%	1902
Burkholderia cenocepacia	7.00066%	1386
Burkholderia territorii	6.74042%	1392
Burkholderia cepacia	6.33014%	1264
Burkholderia vietnamiensis	6.17856%	1488
Burkholderia latens	5.73374%	926
Burkholderia paludis	5.59031%	1366
Ralstonia sp. MD27	4.20060%	3402
Burkholderia oklahomensis	3.58476%	976
Acidovorax delafieldii	3.58468%	538
Burkholderia thailandensis	3.36727%	574
Acidovorax sp. KKS102	3.27177%	364
Burkholderia sp. MSMB0266	3.22183%	928
Streptomyces purpureogeneiscleroticus	3.17552%	3042
Burkholderia pseudomallei	3.13012%	752
Sphingomonas sp. Ant H11	3.04975%	1640
Acidovorax sp. Root70	2.79418%	558
Methylobacterium versatilis	2.75240%	486
Methylobacterium sp. Leaf92	2.45321%	1300
Acidovorax sp. Leaf160	2.42142%	1122
Limnhabitans sp. Rim47	2.21576%	802
Acidovorax sp. Root402	2.13516%	284
Moraxella osloensis	2.12775%	646
Thermomonas hydrothermalis	1.82230%	588
Burkholderia sp. TSV85	1.78087%	384
Rhizobiales bacterium CCH3-A5	1.71232%	1246
Methylobacterium universalis	1.42668%	474
Polynucleobacter duraquae	1.41796%	154
Polynucleobacter sp. MWH-Adler-W8	1.20835%	186
Bradyrhizobium elkanii	1.20446%	1270

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Table 2 (continued)

Kocuria palustris	0.88080%	378
Arthrobacter sp. LS16	0.78653%	434
Serratia marcescens	0.62863%	350
Aerococcus urinaeequi	0.57963%	86
Staphylococcus capitis	0.49754%	188
Sphingomonas paucimobilis	0.48782%	36
Methylophilus sp. 5	0.31586%	32
Streptococcus cristatus	0.03968%	4
Neisseria sp. HMSC073B07	0.03618%	2
Neisseria sp. HMSC074B07	0.03480%	2
Streptococcus sp. M334	0.03407%	2
Streptococcus mitis	0.03110%	2
Streptococcus gordonii	0.02959%	4
Corynebacterium matruchotii	0.02556%	10
Streptococcus sanguinis	0.02546%	2
Streptococcus pseudopneumoniae	0.02475%	2
Streptococcus oralis	0.00757%	2
Staphylococcus xylosus	0.00656%	4
viruses		
Burkholderia phage KS10	12.46273%	45
Flavobacterium phage Fpv2	0.44520%	5
Paramecium bursaria Chlorella virus A1	0.36770%	4
Staphylococcus phage IME-SA4	14.67467%	87
Staphylococcus phage CNPH82	13.21050%	45
Staphylococcus phage Ipla5	12.78080%	45
Staphylococcus phage PH15	12.88680%	42
Staphylococcus phage StB12	3.47691%	8
Staphylococcus phage PT1028	0.43317%	0
Propionibacterium phage P1.1	0.80953%	21
Parasite		
Acanthamoeba palestinensis	0.00680%	30
Wuchereria bancrofti	0.01270%	106
Hammondia hammondi	0.00330%	6
Cryptosporidium hominis	0.00210%	5
Acanthamoeba mauritaniensis	0.00170%	4
Trypanosoma cruzi	0.00180%	3
Toxoplasma gondii	0.00220%	5
Enterobius vermicularis	0.00120%	6
fungi		
Malassezia globosa	0.00956%	8
Neurospora crassa	0.00179%	5
Neurospora tetrasperma	0.00177%	6
Sordaria macrospora	0.00065%	2
Albugo laibachii	0.00120%	4

Data of Case 3-1

species	coverage	unique reads
bacteria		
Burkholderia sp. A9	0.10084%	2
Moraxella osloensis	0.06874%	24
Burkholderia multivorans	0.04319%	32
Pandoraea thiooxydans	0.04222%	0
Burkholderia sp. b14	0.03558%	0
Burkholderia ubonensis	0.03458%	6
Burkholderia sp. lig30	0.03346%	14
Polynucleobacter duraquae	0.03168%	4
Methylothera versatilis	0.02709%	0
Burkholderia contaminans	0.02371%	12
Paraburkholderia rhizoxinica	0.02211%	0
Lactobacillus acidophilus	0.02088%	2
Polynucleobacter sp. MWH-Adler-W8	0.01885%	4
Burkholderia dolosa	0.01842%	2

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Table 2 (continued)

beta proteobacterium CB	0.01809%	0
Lactobacillus gasserii	0.00792%	2
Gemella morbillorum	0.00725%	2
Megasphaera micronuciformis	0.00663%	2
Bergeyella zoohelcum	0.00643%	0
Erysipelotrichaceae bacterium MTC7	0.00605%	0
Alloprevotella rava	0.00578%	2
Negativicoccus massiliensis	0.00544%	0
Prevotella stercorea	0.00484%	0
Chryseobacterium antarcticum	0.00480%	0
viruses		
Parasite		
Taenia solium	0.08346%	1114
Wuchereria bancrofti	0.01755%	134
Taenia saginata	0.00105%	0
Taenia multiceps	0.00069%	0
Toxoplasma gondii	0.00046%	2
Entamoeba histolytica	0.00030%	0
Plasmodium vivax	0.00028%	2
Plasmodium malariae	0.00022%	0
Spirometra erinaceieuropaei	0.00012%	10
Eimeria mitis	0.00010%	0
Clonorchis sinensis	0.00003%	0
fungi		
Hamiltosporidium tvaerminnensis	0.00057%	0
Sclerotinia sclerotiorum	0.00020%	0
Allomyces macrogynus	0.00013%	0

Data of NTC 3-1

species	coverage	unique reads
bacteria		
Moraxella osloensis	4.60267%	1602
Propionibacterium acnes	2.02756%	940
Acinetobacter johnsonii	1.78572%	1074
Staphylococcus epidermidis	1.47129%	328
Polynucleobacter duraquae	1.02221%	118
beta proteobacterium CB	0.91454%	124
Staphylococcus warneri	0.88221%	370
Staphylococcus hominis	0.75899%	284
Polynucleobacter sp. MWH-Adler-W8	0.73046%	114
Chryseobacterium haifense	0.71781%	282
Burkholderia sp. A9	0.71542%	40
Burkholderia contaminans	0.53869%	572
Burkholderia multivorans	0.51537%	628
Polynucleobacter yangtzensis	0.49462%	60
Burkholderia ubonensis	0.48325%	210
Methylobacterium versatilis	0.45982%	32
Staphylococcus haemolyticus	0.42115%	160
Burkholderia sp. lig30	0.40663%	216
Staphylococcus capitis	0.34395%	90
Burkholderia sp. b14	0.28547%	4
Acinetobacter lwoffii	0.25894%	86
Burkholderia territorii	0.25855%	34
Burkholderia cepacia	0.25659%	34
Burkholderia dolosa	0.25389%	50
Burkholderia pseudomultivorans	0.25365%	54
Burkholderia latens	0.24669%	16
Burkholderia cenocepacia	0.22793%	30
Ralstonia sp. MD27	0.21679%	200
Polynucleobacter sp. MWH-Weng1-1	0.21435%	2
[Propionibacterium] namnetense	0.19896%	18

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Table 2 (continued)

Burkholderia paludis	0.19189%	20
Moraxella atlantae	0.19034%	4
Burkholderia vietnamiensis	0.18418%	26
Staphylococcus caprae	0.15180%	22
Psychrobacter sp. SHUES1	0.12428%	52
Veillonella atypica	0.11949%	4
Rhodoluna laticola	0.11787%	18
Acinetobacter radioresistens	0.11707%	4
Burkholderia oklahomensis	0.10138%	14
Corynebacterium sp. KPL1860	0.09916%	20
Staphylococcus cohnii	0.09633%	18
Acinetobacter schindleri	0.07833%	16
Acinetobacter indicus	0.07579%	6
Acinetobacter nosocomialis	0.06862%	2
Psychrobacter sp. P11F6	0.06282%	22
Cloacibacterium normanense	0.04807%	12
Dolosigranulum pigrum	0.04253%	10
Psychrobacter sp. P11G5	0.03984%	2
Acinetobacter harbinensis	0.03611%	6
Corynebacterium singulare	0.03190%	6
Corynebacterium accolens	0.02429%	6
Bradyrhizobium elkanii	0.02394%	28
Psychrobacter sp. G	0.01795%	4
Neisseria sp. oral taxon 014	0.01650%	2
Acinetobacter pittii	0.01196%	2
viruses		
Burkholderia phage KS10	12.46273%	45
Flavobacterium phage Fpv2	0.44520%	5
Staphylococcus phage PT1028	0.43317%	0
Staphylococcus phage SPbeta-like	0.80953%	21
Parasite		
Acanthamoeba palestinensis	0.00760%	36
Wuchereria bancrofti	0.01560%	96
Hammondia hammondi	0.00360%	12
Cryptosporidium hominis	0.00130%	3
Acanthamoeba mauritaniensis	0.00100%	1
Enterobius vermicularis	0.00100%	5
Hammondia hammondi	0.00030%	1
Leishmania mexicana	0.00210%	6
fungi		
Malassezia globosa	0.00979%	8
Neurospora crassa	0.00168%	5
Neurospora tetrasperma	0.00146%	6
Sordaria macrospora	0.00085%	1
Albugo laibachii	0.00150%	8

Data of Case 3-2

species	coverage	unique reads
bacteria		
Burkholderia sp. A9	0.36836%	6
Burkholderia ubonensis	0.34902%	54
Burkholderia sp. lig30	0.29985%	44
Bradyrhizobium elkanii	0.29244%	318
Burkholderia multivorans	0.24832%	120
Burkholderia pseudomultivorans	0.18167%	20
Burkholderia dolosa	0.17946%	12
Burkholderia territorii	0.16482%	18
Burkholderia cenocepacia	0.16120%	6
Burkholderia cepacia	0.14259%	12
Burkholderia paludis	0.12624%	12
Burkholderia contaminans	0.11931%	24

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Table 2 (continued)

Burkholderia latens	0.11872%	16
Burkholderia vietnamiensis	0.11297%	4
Burkholderia oklahomensis	0.07175%	10
Kinetoplastibacterium blastocritidii	0.02915%	0
Candidatus Kinetoplastibacterium galatii	0.02907%	0
Sphingopyxis sp. LPB0140	0.00754%	0
Streptococcus sp. I-P16	0.00741%	2
Rhodospirillum rubrum	0.00690%	0
Thermus scotoductus	0.00534%	2
Staphylococcus agnetis	0.00522%	0
Actinomyces sp. ICM47	0.00479%	2
Brochothrix thermosphacta	0.00419%	2
Solemya pervernica gill symbiont viruses	0.00415%	0
Burkholderia phage KS10	0.61911%	4
Parasite		
Taenia solium	0.07672%	1026
Wuchereria bancrofti	0.02276%	180
Leishmania mexicana	0.00339%	18
Taenia saginata	0.00170%	0
Taenia multiceps	0.00126%	6
Toxoplasma gondii	0.00072%	2
Entamoeba histolytica	0.00030%	0
Trichuris suis	0.00023%	0
Acanthamoeba mauritaniensis	0.00023%	0
Hammondia hammondi	0.00022%	0
Spirometra erinaceieuropaei	0.00022%	18
Enterobius vermicularis	0.00016%	2
Daphnia pulex	0.00008%	0
Fasciola hepatica	0.00001%	0
fungi		
Malassezia globosa	0.00168%	2

Data of NTC 3-2

species	coverage	unique reads
bacteria		
Burkholderia ubonensis	9.57853%	4852
Burkholderia sp. lig30	8.86285%	3832
Burkholderia sp. A9	8.67200%	542
Mesorhizobium sp. UASWS1009	8.00531%	9484
Burkholderia multivorans	6.60315%	9182
Burkholderia pseudomultivorans	5.84032%	1584
Burkholderia dolosa	5.33883%	1148
Burkholderia cenocepacia	4.99446%	792
Burkholderia territorii	4.97842%	806
Burkholderia vietnamiensis	4.51675%	854
Burkholderia cepacia	4.41761%	682
Burkholderia latens	4.15117%	500
Burkholderia paludis	4.06631%	822
Burkholderia contaminans	4.03285%	808
Propionibacterium acnes	3.98345%	1658
Burkholderia oklahomensis	2.57198%	602
Burkholderia thailandensis	2.36005%	434
Burkholderia sp. MSMB0266	2.30809%	476
Streptomyces purpurogeneiscleroticus	2.23613%	2526
Burkholderia pseudomallei	2.20894%	474
Sphingomonas sp. Ant H11	2.17519%	1192
Acidovorax delafieldii	2.15278%	326
Acidovorax sp. KKS102	2.08157%	270
Brevundimonas vesicularis	2.05936%	362
alpha proteobacterium L41A	2.02106%	278
Comamonadaceae bacterium CCH4-C5	1.97819%	226
Rhizobiales bacterium CCH3-A5	1.94178%	1568

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Table 2 (continued)

Acidovorax sp. Root70	1.71866%	352
Methylotenera versatilis	1.60144%	232
Moraxella osloensis	1.49328%	528
Acidovorax sp. Leaf160	1.26938%	682
Bradyrhizobium elkanii	1.26822%	1444
Sphingomonas echinoides	0.81389%	76
Methyloversatilis discipulorum	0.74241%	352
Staphylococcus hominis	0.51032%	196
Acinetobacter johnsonii	0.49428%	232
Afipia broomeae	0.38927%	84
Sphingomonas paucimobilis	0.27656%	14
Brevundimonas sp. BAL3	0.25902%	56
Methylobacterium populi	0.23710%	10
Afipia sp. OHSU_I-C6	0.23504%	16
Brevundimonas sp. DS20	0.20330%	20
Staphylococcus warneri	0.17526%	46
Paracoccus sp. 228	0.08994%	10
Comamonas thiooxydans	0.04206%	6
Rothia mucilaginosa	0.02486%	2
Serratia marcescens	0.01072%	10
Kocuria flava	0.00951%	4
viruses		
Burkholderia phage KS10	11.16273%	39
Flavobacterium phage Fpv2	0.44520%	5
Paramecium bursaria Chlorella virus A1	0.36770%	4
Staphylococcus phage IME-SA4	12.37467%	66
Propionibacterium phage P1.1	0.75953%	15
Parasite		
Acanthamoeba palestinensis	0.00770%	43
Wuchereria bancrofti	0.02170%	130
Hammondia hammondi	0.00300%	7
Cryptosporidium hominis	0.00210%	5
Acanthamoeba mauritaniensis	0.00160%	5
Trypanosoma cruzi	0.00180%	3
Toxoplasma gondii	0.00310%	8
Enterobius vermicularis	0.00120%	6
fungi		
Malassezia globosa	0.00967%	6
Neurospora crassa	0.00179%	5
Neurospora tetrasperma	0.00217%	7
Sordaria macrospora	0.00065%	2
Albugo laibachii	0.00120%	5

Data of Case 3-3

species	coverage	unique reads
bacteria		
Burkholderia sp. A9	0.43787%	6
Burkholderia ubonensis	0.38464%	74
Burkholderia sp. lig30	0.36030%	64
Burkholderia multivorans	0.30223%	132
Burkholderia pseudomultivorans	0.21531%	34
Burkholderia dolosa	0.21283%	20
Burkholderia territorii	0.17445%	22
Burkholderia cenocepacia	0.17331%	14
Burkholderia paludis	0.14703%	10
Burkholderia vietnamiensis	0.14694%	16
Burkholderia cepacia	0.14440%	10
Burkholderia contaminans	0.13599%	10
Burkholderia latens	0.12709%	4
Burkholderia oklahomensis	0.10530%	10
Burkholderia thailandensis	0.09303%	4

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Table 2 (continued)

Bartonella ancashensis	0.01247%	0
bacterium endosymbiont of Mortierella elongata	0.01073%	0
Solemya pervernicosa gill symbiont	0.00850%	4
Bartonella bacilliformis	0.00747%	0
Fulvamarina pelagi	0.00678%	0
Clostridiales bacterium KLE1615	0.00492%	2
Helicobacter heilmannii	0.00467%	0
Mageeibacillus indolicus	0.00448%	0
Burkholderia sp. Leaf177	0.00441%	0
Candidatus Glomeribacter gigasporarum viruses	0.00434%	0
Burkholderia phage KS10	0.79713%	2
Burkholderia virus Bcepil02	0.11959%	0
Parasite		
Taenia solium	0.04368%	592
Wuchereria bancrofti	0.01555%	108
Leishmania mexicana	0.00162%	4
Taenia saginata	0.00133%	2
Toxoplasma gondii	0.00084%	4
Trichuris suis	0.00084%	4
Taenia multiceps	0.00074%	0
Trichinella zimbabwensis	0.00029%	0
Plasmodium vivax	0.00027%	0
Leptomonas seymouri	0.00027%	0
Trichuris muris	0.00018%	0
Eimeria tenella	0.00014%	0
Sarcoptes scabiei fungi	0.00013%	0
Malassezia globosa	0.00256%	4
Sordaria macrospora	0.00019%	0

Data of NTC 3-3

species	coverage	unique reads
bacteria		
Bradyrhizobium elkanii	10.70770%	12942
Burkholderia ubonensis	9.14576%	3794
Burkholderia sp. A9	8.60309%	408
Burkholderia sp. lig30	8.47525%	3010
Burkholderia multivorans	6.32021%	6692
Burkholderia pseudomultivorans	5.51548%	1166
Burkholderia dolosa	5.10665%	916
Burkholderia territorii	4.77273%	672
Burkholderia cenocepacia	4.73794%	620
Burkholderia vietnamiensis	4.32945%	660
Burkholderia cepacia	4.19702%	614
Ralstonia sp. MD27	4.19666%	3488
Burkholderia latens	4.00264%	452
Burkholderia paludis	3.85719%	650
Burkholderia contaminans	3.65830%	488
Mesorhizobium sp. UASWS1009	2.92958%	2972
Burkholderia oklahomensis	2.42164%	484
Burkholderia thailandensis	2.26419%	276
Burkholderia sp. MSMB0266	2.18351%	350
Streptomyces purpureogeneiscleroticus	2.14049%	2136
Burkholderia pseudomallei	2.04635%	318
Propionibacterium acnes	2.03909%	802
Bacillus sp. VT-16-64	1.89532%	3728
Phyllobacterium sp. UNC302MFC05.2	1.63491%	412
Burkholderia sp. TSV85	1.12836%	124
Phyllobacterium sp. YR531	0.99762%	426
Cupriavidus metallidurans	0.87224%	124
Burkholderia glumae	0.84774%	150

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Table 2 (continued)

Burkholderia plantarii	0.84727%	140
Paraburkholderia graminis	0.82195%	30
Moraxella osloensis	0.76100%	254
Limnohabitans sp. Rim47	0.75291%	274
Dyella jiangningensis	0.67286%	466
Methylobacterium versatilis	0.64078%	68
Acidovorax temperans	0.50702%	54
Acinetobacter johnsonii	0.21199%	110
[Eubacterium] angustum	0.16539%	6
Thermomonas hydrothermalis	0.13901%	28
Chryseobacterium sp. FF12	0.12517%	8
Paracoccus sphaerophysae	0.11972%	46
[Propionibacterium] namnetense	0.11688%	20
Comamonas aquatica	0.11633%	36
Cloacibacterium normanense	0.07579%	22
Leifsonia sp. Leaf336	0.06631%	14
Micrococcus luteus	0.06260%	14
Paenarthrobacter nicotinovorans	0.03381%	8
Arthrobacter sp. LS16	0.03111%	16
Kocuria polaris	0.01722%	10
Corynebacterium stationis	0.00790%	2
viruses		
Burkholderia phage KS10	12.39273%	42
Flavobacterium phage Fpv2	0.45320%	4
Paramecium bursaria Chlorella virus A1	0.35670%	5
Staphylococcus phage IME-SA4	14.68467%	67
Staphylococcus phage CNPH82	13.21050%	45
Staphylococcus phage Ipla5	12.78080%	35
Staphylococcus phage PH15	12.20680%	42
Staphylococcus phage Ipla7	8.94998%	18
Parasite		
Acanthamoeba palestinensis	0.01080%	44
Wuchereria bancrofti	0.01270%	96
Hammondia hammondi	0.00350%	5
Cryptosporidium hominis	0.00170%	4
Acanthamoeba mauritaniensis	0.00210%	5
Trypanosoma cruzi	0.00080%	9
Toxoplasma gondii	0.00200%	6
Enterobius vermicularis	0.00100%	11
Hammondia hammondi	0.00140%	8
Leishmania mexicana	0.00130%	5
fungi		
Malassezia globosa	0.00943%	8
Neurospora crassa	0.00182%	9
Neurospora tetrasperma	0.00140%	3
Sordaria macrospora	0.00082%	2

Data of Case 3-4

species	coverage	unique reads
bacteria		
Burkholderia sp. A9	1.00709%	14
Burkholderia ubonensis	0.98022%	228
Burkholderia sp. lig30	0.79173%	146
Burkholderia multivorans	0.74839%	354
Propionibacterium acnes	0.73383%	256
Ralstonia sp. MD27	0.51143%	414
Burkholderia pseudomultivorans	0.50465%	66
Burkholderia dolosa	0.48257%	58
Burkholderia territorii	0.44845%	42
Burkholderia cenocepacia	0.41857%	30
Burkholderia vietnamiensis	0.37598%	44
Burkholderia paludis	0.35834%	20

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Table 2 (continued)

Burkholderia cepacia	0.35464%	30
Burkholderia latens	0.34386%	20
Burkholderia contaminans	0.31135%	24
Candidatus Profftella armatura	0.02302%	0
Propionibacterium sp. oral taxon 192	0.01623%	0
Buchnera aphidicola	0.01274%	2
Brochothrix thermosphacta	0.01155%	6
Exiguobacterium sp. AT1b	0.01100%	2
Weissella confusa	0.01046%	4
Atopobium deltae	0.01033%	2
Bergeyella zoohelcum	0.00917%	0
Granulicatella elegans	0.00860%	2
Pseudomonas luteola	0.00778%	6
viruses		
Burkholderia phage KS10	1.93171%	12
Propionibacterium phage Procrass1	0.39868%	2
Burkholderia virus phiE125	0.14052%	0
Escherichia virus EC6	0.13104%	0
Escherichia virus AYO145A	0.12933%	0
Salmonella virus HB2014	0.12913%	0
Salmonella virus UAB87	0.12899%	0
Paramecium bursaria Chlorella virus A1	0.02335%	0
Parasite		
Wuchereria bancrofti	0.01744%	124
Taenia solium	0.00647%	78
Toxoplasma gondii	0.00114%	2
Entamoeba histolytica	0.00089%	0
Endotrypanum monterogeii	0.00046%	0
Leishmania mexicana	0.00043%	0
Trichuris trichiura	0.00040%	0
Vitrella brassicaformis	0.00031%	0
Cyclospora cayetanensis	0.00029%	2
Naegleria fowleri	0.00025%	0
Acanthamoeba palestinensis	0.00024%	0
Acanthamoeba mauritaniensis	0.00023%	0
Trichuris muris	0.00009%	0
Chromera velia	0.00004%	0
Trichobilharzia regenti	0.00001%	0
fungi		
Malassezia globosa	0.00166%	2
Aspergillus niger	0.00022%	0
Sordaria macrospora	0.00020%	2

Data of NTC 3-4

species	coverage	unique reads
bacteria		
Ralstonia sp. MD27	54.07490%	75456
Propionibacterium acnes	26.50730%	12352
Moraxella osloensis	17.82990%	6552
Burkholderia ubonensis	11.38230%	6708
Burkholderia sp. lig30	10.67190%	5064
Burkholderia sp. A9	10.40340%	786
Burkholderia multivorans	7.74574%	11594
Burkholderia pseudomultivorans	7.10555%	2222
Ralstonia sp. NT80	7.04594%	374
Burkholderia dolosa	6.72714%	1400
Burkholderia territorii	6.17956%	1116
Burkholderia cenocepacia	6.16325%	1008
Burkholderia vietnamiensis	5.59079%	1100
Burkholderia cepacia	5.53351%	942
Burkholderia contaminans	5.29455%	1500
Burkholderia latens	5.20924%	642

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Table 2 (continued)

Burkholderia paludis	5.02586%	990
Chryseobacterium haifense	4.52775%	1546
Mesorhizobium sp. UASWS1009	4.42173%	4836
Burkholderia oklahomensis	3.26041%	804
Staphylococcus epidermidis	3.19298%	804
Streptomyces purpureogeniscleroticus	3.01688%	2892
Burkholderia thailandensis	3.00964%	492
Burkholderia sp. MSMB0266	2.88301%	594
Paracoccus sphaerophysae	2.82150%	1420
Burkholderia pseudomallei	2.81857%	542
Bradyrhizobium elkanii	2.80009%	3180
Ralstonia pickettii	2.67821%	1448
alpha proteobacterium L41A	2.50307%	374
Brevundimonas vesicularis	2.50114%	448
Acinetobacter johnsonii	2.21033%	1150
Desulfocarbo indianensis	2.13641%	16
Ralstonia sp. 5_2_56FAA	2.02035%	206
Brevundimonas nasdae	2.00738%	256
Chryseobacterium sp. FF12	1.80377%	234
Micrococcus luteus	1.73076%	34
Burkholderia sp. TSV85	1.50398%	248
[Propionibacterium] namnetense	1.45034%	294
Staphylococcus hominis	1.36621%	490
Cupriavidus metallidurans	1.34057%	126
Limnohabitans sp. Rim47	1.28398%	454
Burkholderia plantarii	1.19460%	184
Paraburkholderia graminis	1.09001%	50
Burkholderia glumae	1.08947%	196
Streptococcus sp. CCH8-G7	0.86913%	68
Thermomonas hydrothermalis	0.86666%	278
Dyella jiangningensis	0.74234%	708
Corynebacterium tuberculostearicum	0.73242%	134
Corynebacterium aurimucosum	0.56701%	72
Actinomyces oris	0.55522%	152
Actinomyces odontolyticus	0.46989%	130
Veillonella parvula	0.46043%	108
Corynebacterium afermentans	0.33454%	80
Porphyromonas somerae	0.22141%	28
Ottowia sp. oral taxon 894	0.21324%	68
Bacillus sp. VT-16-64	0.19344%	74
Phyllobacterium sp. UNC302MFCol5.2	0.12524%	6
Phyllobacterium sp. YR531	0.10552%	12
Corynebacterium ureicelerivorans	0.08345%	12
Corynebacterium striatum	0.05518%	6
Paramesorhizobium deserti	0.03794%	2
Serratia marcescens	0.03624%	28
viruses		
Burkholderia phage KS10	11.26273%	34
Flavobacterium phage Fpv2	0.44520%	5
Paramecium bursaria Chlorella virus A1	0.36770%	4
Staphylococcus phage IME-SA4	13.56467%	77
Staphylococcus phage CNPH82	13.21050%	67
Staphylococcus phage Ipla5	14.78080%	23
Staphylococcus phage PH15	13.88680%	66
Parasite		
Acanthamoeba palestinensis	0.00830%	44
Wuchereria bancrofti	0.01560%	109
Hammondia hammondi	0.00330%	11
Cryptosporidium hominis	0.00270%	6
Acanthamoeba mauritaniensis	0.00100%	1
Enterobius vermicularis	0.00050%	6
Hammondia hammondi	0.00030%	1
Leishmania mexicana	0.00160%	5

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Table 2 (continued)

fungi		
Malassezia globosa	0.00947%	7
Neurospora crassa	0.00168%	6
Neurospora tetrasperma	0.00144%	3
Sordaria macrospora	0.00085%	1
Albugo laibachii	0.00100%	4
Data of Case 3-5		
species	coverage	unique reads
bacteria		
Burkholderia contaminans	18.70960%	21516
Burkholderia sp. A9	10.11700%	480
Burkholderia ubonensis	9.44550%	3918
Burkholderia sp. lig30	8.71094%	3184
Burkholderia multivorans	6.83204%	8176
Streptomyces purpurogeneiscleroticus	6.57775%	6694
Burkholderia pseudomultivorans	5.75880%	1272
Burkholderia cenocepacia	5.36565%	658
Burkholderia dolosa	5.31402%	972
Burkholderia territorii	4.98050%	654
Burkholderia cepacia	4.94573%	726
Burkholderia vietnamiensis	4.54066%	736
Burkholderia paludis	4.27915%	724
Burkholderia latens	4.14980%	416
Mesorhizobium sp. UASWS1009	3.08087%	3280
Lactobacillus coryniformis	0.09456%	2
Candidatus Kinetoplastibacterium crithidii	0.06375%	0
Atopobium vaginae	0.04516%	8
Gardnerella vaginalis	0.03952%	0
Aerococcus viridans	0.03527%	6
Streptococcus oralis	0.03409%	4
Enterococcus malodoratus	0.03193%	18
Corynebacterium lowii	0.02990%	10
Propionibacteriaceae bacterium P6A17	0.02940%	0
Atopococcus tabaci	0.02646%	0
viruses		
Burkholderia phage KS10	13.10220%	94
Enterobacteria phage HK629	2.33675%	0
Escherichia virus Lambda	2.27826%	0
Burkholderia phage KS5	1.03932%	6
Propionibacterium phage PHL116	0.51031%	0
Propionibacterium phage Pirate	0.46372%	0
Propionibacterium phage QueenBey	0.46356%	0
Propionibacterium phage P104A	0.46304%	0
Human mastadenovirus C	0.41740%	0
Shigella phage Sf6	0.30992%	0
Shigella phage Sf11	0.29174%	0
Burkholderia virus phiE125	0.27729%	4
Propionibacterium phage BruceLethal	0.25642%	0
Propionibacterium phage Moyashi	0.25638%	0
Propionibacterium phage PHL041	0.25500%	0
Parasite		
Acanthamoeba palestinensis	0.00881%	34
Wuchereria bancrofti	0.00765%	46
Entamoeba histolytica	0.00470%	0
Enterocytozoon bienersi	0.00451%	0
Hammondia hammondi	0.00330%	6
Cryptosporidium hominis	0.00209%	4
Acanthamoeba mauritaniensis	0.00181%	2
Vitrella brassicaformis	0.00092%	0
Trypanosoma cruzi	0.00079%	2
Babesia bigemina	0.00054%	0

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Table 2 (continued)

fungi		
Sordaria macrospora	0.00231%	2
Malassezia globosa	0.00212%	4
Batrachochytrium dendrobatidis	0.00159%	0
Talaromyces marneffei	0.00129%	0
Aspergillus nidulans	0.00097%	2
Albugo laibachii	0.00090%	2
Sporisorium reilianum	0.00065%	2
Talaromyces stipitatus	0.00062%	0
Fusarium verticillioides	0.00036%	2
Aspergillus terreus	0.00026%	0
Coccidioides posadasii	0.00027%	0
Data of NTC 3-5		
species	coverage	unique reads
bacteria		
Burkholderia contaminans	56.80650%	109638
Streptomyces purpureogenesceroticus	24.69500%	30704
Burkholderia sp. A9	16.05410%	896
Burkholderia ubonensis	11.90740%	7644
Burkholderia sp. lig30	11.14240%	6124
Burkholderia multivorans	9.38219%	17226
Burkholderia cepacia	8.52934%	1194
Burkholderia cenocepacia	8.03225%	1264
Burkholderia pseudomultivorans	7.77659%	2452
Burkholderia dolosa	7.20618%	1822
Propionibacterium acnes	6.98045%	2948
Burkholderia territorii	6.88786%	1242
Burkholderia paludis	6.50903%	1362
Burkholderia vietnamiensis	6.26256%	1434
Burkholderia latens	5.81930%	844
Serratia marcescens	5.64359%	3652
Mesorhizobium sp. UASWS1009	4.28548%	4730
Burkholderia oklahomensis	3.49623%	980
Burkholderia thailandensis	3.21669%	660
Burkholderia sp. MSMB0266	3.14893%	732
Delftia tsuruhatensis	3.05396%	392
Delftia sp. 670	3.03026%	460
Burkholderia pseudomallei	2.97279%	656
Mitsuaria chitosanitabida	2.36550%	1322
Ralstonia sp. MD27	2.22214%	1752
Moraxella osloensis	2.11922%	710
Brevundimonas vesicularis	1.76609%	298
Limnohabitans sp. Rim47	1.74668%	648
Burkholderia sp. TSV85	1.72213%	346
Paracoccus sphaerophysae	1.63158%	772
alpha proteobacterium L41A	1.60633%	230
Delftia acidovorans	1.60317%	210
Methylobacterium radiotolerans	1.59919%	654
Comamonadaceae bacterium CCH4-C5	1.55371%	180
Acidovorax sp. KKS102	1.46956%	160
Comamonadaceae bacterium CCH12-A10	1.40673%	32
Acidovorax delafieldii	1.38893%	178
Brevundimonas nasdae	1.36767%	180
Polynucleobacter duraquae	1.33801%	170
Burkholderia plantarii	1.27188%	228
Acidovorax temperans	1.26872%	174
Cupriavidus metallidurans	1.26008%	246
Methylobacterium sp. Leaf92	1.23582%	600
Burkholderia glumae	1.19595%	284
Paraburkholderia graminis	1.18886%	54
Acidovorax sp. CCH12-A4	1.18354%	32

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Table 2 (continued)

Rhizobiales bacterium CCH3-A5	1.12968%	878
Methylobacterium sp. B34	1.12402%	186
Methylothera versatilis	1.08952%	144
Acidovorax sp. Root70	1.03090%	212
beta proteobacterium CB	1.02751%	114
Sphingopyxis sp. LC81	1.00728%	518
Methyloversatilis universalis	0.99189%	392
Burkholderia gladioli	0.98735%	698
Polynucleobacter sp. MWH-Adler-W8	0.95063%	176
Sphingomonas sp. Ant H11	0.90814%	438
Acinetobacter johnsonii	0.78364%	424
Staphylococcus warneri	0.27879%	88
Tetrasphaera elongata	0.06735%	34
Chryseobacterium haifense	0.03634%	6
Klebsiella pneumoniae viruses	0.01997%	12
Burkholderia phage KS10	13.36273%	44
Flavobacterium phage Fpv2	0.44520%	5
Paramecium bursaria Chlorella virus A1	0.36770%	4
Propionibacterium phage PHL116	14.67467%	87
Propionibacterium phage Pirate	17.21050%	43
Propionibacterium phage QueenBey	15.78080%	34
Propionibacterium phage P104A	16.88680%	41
Staphylococcus phage StB12	3.47691%	8
Staphylococcus phage PT1028	0.43317%	0
Propionibacterium phage P1.1	1.10953%	10
Parasite		
Acanthamoeba palestinensis	0.00660%	33
Wuchereria bancrofti	0.00870%	56
Hammondia hammondi	0.00330%	7
Cryptosporidium hominis	0.00220%	5
Acanthamoeba mauritaniensis	0.00240%	4
Trypanosoma cruzi	0.00180%	2
Toxoplasma gondii	0.00230%	5
Enterobius vermicularis	0.00120%	5
fungi		
Malassezia globosa	0.00957%	9
Neurospora crassa	0.00199%	6
Neurospora tetrasperma	0.00177%	6
Sordaria macrospora	0.00078%	8
Albugo laibachii	0.00120%	4

Data of Case 4

species	coverage	unique reads
bacteria		
Staphylococcus hominis	1.84954%	670
Burkholderia sp. A9	1.83276%	44
Burkholderia ubonensis	1.70182%	392
Burkholderia sp. lig30	1.50086%	284
Burkholderia multivorans	1.29341%	680
Burkholderia pseudomultivorans	0.94778%	128
Ralstonia sp. MD27	0.93673%	716
Burkholderia dolosa	0.85274%	98
Burkholderia territorii	0.77720%	70
Burkholderia cenocepacia	0.76887%	66
Burkholderia cepacia	0.66769%	60
Burkholderia vietnamiensis	0.65960%	70
Burkholderia paludis	0.62014%	74
Mesorhizobium sp. UASWS1009	0.58649%	588
Burkholderia latens	0.55086%	32
Lactococcus piscium	0.05453%	16

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Table 2 (continued)

Lactococcus raffinolactis	0.03024%	8
Pelobacter propionicus	0.02021%	0
Exiguobacterium sp. RIT341	0.01928%	2
Candidatus Profftella armatura	0.01699%	0
Dermacoccus nishinomiyaensis	0.01693%	0
Bacillus cellulosilyticus	0.01636%	0
Helcobacillus massiliensis	0.01443%	0
Candidatus Glomeribacter gigasporarum	0.01372%	0
Arthrobacter sp. Leaf234	0.01274%	6
viruses		
Burkholderia phage KS10	2.51096%	8
Staphylococcus phage StB12	0.53451%	4
Staphylococcus phage SPbeta-like	0.48228%	0
Enterobacteria phage Sfl	0.33603%	0
Enterobacteria phage HK542	0.33108%	0
Enterobacteria phage HK544	0.32126%	0
Escherichia virus Lambda	0.26597%	0
Burkholderia virus phiE125	0.14052%	0
Pseudomonas phage PaMx74	0.12791%	0
Flavobacterium phage Fpv2	0.11909%	2
Paramecium bursaria Chlorella virus A1	0.04669%	2
Parasite		
Wuchereria bancrofti	0.00513%	42
Acanthamoeba palestinensis	0.00197%	20
Hammondia hammondi	0.00065%	0
Trypanosoma cruzi	0.00062%	0
Anncaliia algerae	0.00054%	0
Trypanosoma grayi	0.00036%	0
Taenia solium	0.00032%	6
Toxoplasma gondii	0.00026%	4
Leishmania sp. MAR LEM2494	0.00024%	0
Anisakis simplex	0.00012%	0
Daphnia magna	0.00012%	0
Vitrella brassicaformis	0.00010%	0
Spirometra erinaceieuropaei	0.00009%	6
Necator americanus	0.00006%	0
fungi		
Sordaria macrospora	0.00104%	2
Albugo laibachii	0.00046%	2
Blastocystis hominis	0.00040%	0

Data of NTC 4

species	coverage	unique reads
bacteria		
Staphylococcus hominis	12.19550%	4564
Ralstonia sp. MD27	10.70210%	9644
Burkholderia ubonensis	8.40481%	3698
Moraxella osloensis	7.84991%	2552
Burkholderia sp. A9	7.76343%	466
Burkholderia sp. lig30	7.68243%	2762
Paracoccus sphaerophysae	7.61451%	3744
Rothia sp. ND6WE1A	7.30648%	2784
Staphylococcus haemolyticus	6.01573%	2306
Burkholderia multivorans	5.80606%	6370
Staphylococcus epidermidis	5.25386%	1058
Burkholderia pseudomultivorans	5.06785%	1126
alpha proteobacterium L41A	4.88849%	798
Brevundimonas vesicularis	4.87511%	854
Burkholderia dolosa	4.71681%	818
Mesorhizobium sp. UASWS1009	4.62789%	5248
Propionibacterium acnes	4.58402%	1860
Burkholderia cenocepacia	4.31558%	560

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Table 2 (continued)

Burkholderia territorii	4.26066%	582
Burkholderia vietnamiensis	3.87120%	662
Burkholderia cepacia	3.86708%	616
Brevundimonas nasdae	3.81090%	514
Burkholderia latens	3.56392%	356
Burkholderia paludis	3.52522%	598
Burkholderia contaminans	3.43589%	548
Corynebacterium appendicis	3.31193%	994
Streptomyces purpurogenescleroticus	3.21604%	3336
Acinetobacter johnsonii	2.93549%	1556
Staphylococcus warneri	2.91993%	878
Burkholderia oklahomensis	2.19710%	456
Burkholderia thailandensis	2.03216%	256
Burkholderia sp. MSMB0266	1.90831%	434
Burkholderia pseudomallei	1.85903%	332
Acidovorax delafieldii	1.46921%	190
Ralstonia sp. NT80	1.45625%	246
Sphingomonas sp. Ant H11	1.45307%	756
Methylobacterium versatilis	1.38689%	204
Corynebacterium tuberculostearicum	1.34973%	220
Acidovorax sp. KKS102	1.31939%	164
Corynebacterium aurimucosum	1.27600%	200
Acidovorax sp. Leaf160	1.25323%	654
Acidovorax sp. Root70	1.12287%	230
Burkholderia sp. TSV85	1.07564%	164
Cupriavidus metallidurans	1.05755%	198
Comamonadaceae bacterium CCH12-A10	1.05171%	16
Comamonadaceae bacterium CCH4-C5	1.02252%	96
Acidovorax sp. CCH12-A4	0.88438%	32
Acidovorax sp. Root402	0.87451%	136
Burkholderia plantarii	0.80571%	130
Acidovorax temperans	0.76659%	74
Ralstonia pickettii	0.75577%	246
Bradyrhizobium elkanii	0.71983%	762
Limnhabitans sp. Rim47	0.69754%	252
Ralstonia sp. 5_2_56FAA	0.57599%	66
Acinetobacter lwoffii	0.52177%	168
Cloacibacterium normanense	0.16745%	54
Prevotella disiens	0.01169%	2
Serratia marcescens	0.00786%	6
viruses		
Burkholderia phage KS10	10.96273%	34
Flavobacterium phage Fpv2	0.44520%	5
Paramecium bursaria Chlorella virus A1	0.36770%	4
Enterobacteria phage Sfl	12.37467%	67
Enterobacteria phage HK542	11.21050%	34
Enterobacteria phage HK544	16.78080%	65
Propionibacterium phage P1.1	0.80953%	19
Parasite		
Acanthamoeba palestinensis	0.00670%	31
Wuchereria bancrofti	0.08700%	46
Hammondia hammondi	0.00330%	8
Cryptosporidium hominis	0.00190%	6
Acanthamoeba mauritaniensis	0.00170%	5
Trypanosoma cruzi	0.00150%	4
Toxoplasma gondii	0.00230%	3
Enterobius vermicularis	0.00120%	6
fungi		
Malassezia globosa	0.00876%	7
Neurospora crassa	0.00179%	5
Neurospora tetrasperma	0.00178%	7
Sordaria macrospora	0.00045%	1
Albugo laibachii	0.00140%	3

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Table 2 (continued)

Data of Case 5		
species	coverage	unique reads
bacteria		
Burkholderia sp. A9	0.82290%	14
Burkholderia ubonensis	0.74907%	158
Burkholderia sp. lig30	0.70272%	124
Burkholderia multivorans	0.56438%	236
Burkholderia pseudomultivorans	0.45016%	44
Corynebacterium jeikeium	0.36015%	54
Burkholderia dolosa	0.35464%	32
Burkholderia cenocepacia	0.34338%	14
Burkholderia territorii	0.33098%	24
Burkholderia cepacia	0.30341%	24
Burkholderia latens	0.30035%	20
Burkholderia vietnamiensis	0.28130%	32
Burkholderia contaminans	0.27948%	26
Burkholderia paludis	0.26410%	18
Mesorhizobium sp. UASWS1009	0.22014%	234
Gardnerella vaginalis	0.01983%	2
Candidatus Kinetoplastibacterium galatii	0.01825%	2
Corynebacterium sp. HMSC065H09	0.01801%	2
Candidatus Profftella armatura	0.01699%	0
Turicella sp. HMSC034H07	0.01514%	0
Corynebacterium sp. HMSC062A03	0.01339%	0
Corynebacterium sp. HMSC066C02	0.01326%	0
Trueperella sp. HMSC08B05	0.01225%	0
Geothrix fermentans	0.01222%	0
viruses		
Burkholderia phage KS10	0.99641%	0
Burkholderia virus phiE125	0.14052%	0
Parasite		
Taenia solium	0.04556%	626
Wuchereria bancrofti	0.02155%	186
Enterocytozoon bieneusi	0.00194%	0
Taenia saginata	0.00103%	2
Leptomonas seymouri	0.00066%	0
Entamoeba histolytica	0.00060%	0
Anncaliia algerae	0.00054%	0
Taenia multiceps	0.00049%	2
Acanthamoeba palestinensis	0.00047%	2
Toxoplasma gondii	0.00039%	2
Leishmania tarentolae	0.00024%	0
Spirometra erinaceieuropaei	0.00019%	24
Hammondia hammondi	0.00015%	0
Dracunculus medinensis	0.00007%	0
fungi		
Malassezia globosa	0.03473%	28
Sordaria macrospora	0.00041%	2
Data of NTC 5		
species	coverage	unique reads
bacteria		
Paracoccus sphaerophysae	13.91450%	7542
Burkholderia ubonensis	10.91620%	6322
Burkholderia sp. lig30	10.28230%	4788
Burkholderia sp. A9	9.93702%	698
Ralstonia sp. MD27	8.91267%	8016
Burkholderia multivorans	7.51153%	10518
Moraxella osloensis	6.85012%	2348
Burkholderia pseudomultivorans	6.83803%	1920
Burkholderia dolosa	6.36310%	1392

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Table 2 (continued)

Brevundimonas vesicularis	5.95865%	1122
Burkholderia territorii	5.94944%	1030
Burkholderia cenocepacia	5.93886%	982
alpha proteobacterium L41A	5.87010%	960
Burkholderia vietnamiensis	5.41452%	1092
Burkholderia cepacia	5.25421%	964
Streptomyces purpureogeneiscleroticus	5.14750%	5328
Burkholderia latens	5.02917%	708
Brevundimonas nasdae	4.88906%	742
Burkholderia paludis	4.85164%	1048
Burkholderia contaminans	4.73254%	1012
Staphylococcus hominis	4.18608%	1598
Bradyrhizobium elkanii	3.61955%	4378
Burkholderia oklahomensis	3.10360%	726
Burkholderia thailandensis	2.95443%	448
Mesorhizobium sp. UASWS1009	2.86955%	3198
Burkholderia sp. MSMB0266	2.74114%	650
Burkholderia pseudomallei	2.69440%	562
Thermomonas hydrothermalis	1.90140%	628
Ralstonia sp. NT80	1.61419%	420
Burkholderia sp. TSV85	1.47854%	242
Acinetobacter johnsonii	1.40778%	718
Comamonadaceae bacterium CCH4-C5	1.27388%	146
Propionibacterium acnes	1.21901%	528
Burkholderia plantarii	1.18824%	182
Acidovorax delafieldii	1.18208%	166
Methyloversatilis universalis	1.15586%	474
Acidovorax sp. KKS102	1.11858%	120
Comamonadaceae bacterium CCH12-A10	1.10651%	30
Burkholderia glumae	1.09671%	178
Cupriavidus metallidurans	1.06383%	166
Limnohabitans sp. Rim47	1.04516%	322
Sphingomonas paucimobilis	1.04005%	586
Methyloversatilis discipulorum	1.02565%	442
Rhizobiales bacterium CCH3-A5	1.02316%	774
Staphylococcus epidermidis	0.97893%	214
Staphylococcus haemolyticus	0.96417%	342
Acidovorax sp. Root70	0.84761%	150
Sphingomonas sp. Ant H11	0.81704%	336
Methylotenera versatilis	0.67421%	68
Acidovorax sp. Root402	0.67300%	106
Acidovorax sp. Leaf160	0.35953%	148
Rothia sp. ND6WE1A	0.20422%	78
Streptococcus sp. CCH8-G7	0.01582%	2
Streptococcus sp. HMSC073F11	0.01440%	2
Serratia marcescens	0.01119%	8
Streptococcus oralis	0.00698%	2
viruses		
Burkholderia phage KS10	10.66273%	33
Flavobacterium phage Fpv2	0.44520%	4
Paramecium bursaria Chlorella virus A1	0.23770%	3
Staphylococcus phage IME-SA4	10.37467%	30
Propionibacterium phage P1.1	0.65953%	12
Parasite		
Acanthamoeba palestinensis	0.00800%	45
Wuchereria bancrofti	0.02370%	150
Hammondia hammondi	0.00300%	7
Cryptosporidium hominis	0.00220%	6
Acanthamoeba mauritaniensis	0.00160%	4
Trypanosoma cruzi	0.00180%	3
Toxoplasma gondii	0.00120%	9
Enterobius vermicularis	0.00120%	6

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Table 2 (continued)

fungi		
Malassezia globosa	0.00988%	12
Neurospora crassa	0.00189%	6
Neurospora tetrasperma	0.00227%	7
Sordaria macrospora	0.00065%	2
Albugo laibachii	0.00190%	8
Data of Case 6		
species	coverage	unique reads
bacteria		
Acinetobacter junii	3.67362%	1552
Propionibacterium acnes	1.86082%	666
Burkholderia sp. A9	1.63337%	32
Burkholderia ubonensis	1.46515%	330
Burkholderia sp. lig30	1.30212%	234
Burkholderia multivorans	1.16087%	636
Burkholderia pseudomultivorans	0.82146%	104
Burkholderia dolosa	0.74319%	46
Burkholderia cenocepacia	0.68609%	60
Burkholderia territorii	0.68137%	62
Burkholderia cepacia	0.58838%	38
Burkholderia contaminans	0.58263%	110
Burkholderia vietnamiensis	0.57924%	60
Burkholderia paludis	0.54351%	52
Burkholderia latens	0.54190%	36
Pseudomonas putida	0.50566%	368
Marinomonas aquimarina	0.08951%	2
Acinetobacter venetianus	0.03138%	0
Atopobium sp. oral taxon 199	0.02702%	0
Gardnerella vaginalis	0.02238%	0
Lactobacillus mucosae	0.02029%	0
Arthrobacter sp. Leaf234	0.01969%	8
Candidatus Liberibacter asiaticus	0.01929%	0
Shewanella sp. MR-4	0.01895%	4
viruses		
Burkholderia phage KS10	2.24791%	10
Human gammaherpesvirus 4	0.45727%	2
Pseudomonas phage PaMx74	0.25581%	2
Pseudomonas phage MP1412	0.24523%	2
Lactobacillus phage Sha1	0.18693%	2
Staphylococcus phage StB20	0.18085%	0
Parasite		
Taenia solium	0.20137%	2642
Wuchereria bancrofti	0.01339%	100
Taenia saginata	0.00331%	2
Taenia multiceps	0.00154%	2
Acanthamoeba palestinensis	0.00122%	10
Toxoplasma gondii	0.00121%	2
Babesia bigemina	0.00108%	0
Vitrella brassicaformis	0.00041%	0
fungi		
Pneumocystis jirovecii	0.00596%	6
Schizosaccharomyces pombe	0.00297%	0
Fusarium verticillioides	0.00207%	12
Malassezia globosa	0.00336%	4
Yarrowia lipolytica	0.00073%	2
Saccharomyces cerevisiae	0.00062%	0
Sordaria macrospora	0.00037%	0

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Table 2 (continued)

Data of NTC 6		
species	coverage	unique reads
bacteria		
Propionibacterium acnes	12.19170%	5332
Burkholderia ubonensis	7.63207%	3072
Burkholderia sp. A9	7.38595%	396
Burkholderia sp. lig30	7.13174%	2426
Moraxella osloensis	6.44270%	2288
Burkholderia multivorans	5.39103%	5470
Burkholderia pseudomultivorans	4.57937%	984
Burkholderia dolosa	4.22517%	708
Burkholderia cenocepacia	3.98858%	534
Burkholderia territorii	3.90938%	532
Burkholderia contaminans	3.73823%	1410
Burkholderia cepacia	3.51458%	502
Burkholderia vietnamiensis	3.44614%	568
Burkholderia latens	3.30098%	370
Burkholderia paludis	3.22433%	518
Thermomonas hydrothermalis	2.40415%	890
Burkholderia oklahomensis	1.98692%	442
Burkholderia thailandensis	1.90333%	280
Rhizobiales bacterium CCH3-A5	1.86148%	1518
Burkholderia sp. MSMB0266	1.78302%	282
Burkholderia pseudomallei	1.71428%	288
Methyloversatilis universalis	1.52909%	620
Pseudomonas sp. CFT9	1.22869%	810
Acinetobacter johnsonii	1.19179%	636
Comamonadaceae bacterium CCH4-C5	1.18539%	152
Sphingopyxis sp. LC81	1.11632%	568
Comamonadaceae bacterium CCH12-A10	1.04177%	26
beta proteobacterium CB	1.04169%	146
Polynucleobacter duraquae	1.02675%	110
Acidovorax temperans	1.00990%	134
Micrococcus luteus	1.00961%	4
Pseudomonas putida	0.97041%	912
Burkholderia sp. TSV85	0.95026%	196
Cupriavidus metallidurans	0.87502%	142
Acidovorax sp. CCH12-A4	0.86398%	28
Methyloversatilis discipulorum	0.83134%	376
Xylophilus ampelinus	0.79146%	576
[Propionibacterium] namnetense	0.77477%	198
Polynucleobacter sp. MWH-Adler-W8	0.74921%	108
Staphylococcus epidermidis	0.73200%	182
Mesorhizobium sp. UASWS1009	0.68557%	824
Ralstonia sp. MD27	0.60947%	490
Sphingomonas sp. Ant H11	0.45496%	220
Propionibacterium humerusii	0.42515%	56
Kocuria palustris	0.35688%	162
Cutibacterium granulosum	0.33911%	108
Bradyrhizobium elkanii	0.22595%	266
Delftia sp. 670	0.21119%	50
Delftia tsuruhatensis	0.20858%	4
Afiopia broomeae	0.10435%	32
Kocuria polaris	0.08646%	50
Psychrobacter sp. 1501(2011)	0.08235%	12
Stenotrophomonas sp. SKA14	0.05745%	2
Prevotella intermedia	0.05031%	20
Pseudomonas aeruginosa	0.02379%	18
Serratia marcescens	0.01451%	10

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Table 2 (continued)

viruses		
Burkholderia phage KS10	12.39273%	42
Flavobacterium phage Fpv2	0.45320%	4
Paramecium bursaria Chlorella virus A1	0.35670%	5
Staphylococcus phage IME-SA4	14.68467%	67
Staphylococcus phage PH15	12.20680%	42
Staphylococcus phage Ipla7	8.94998%	18
Parasite		
Acanthamoeba palestinensis	0.01130%	45
Wuchereria bancrofti	0.01340%	106
Hammondia hammondi	0.00350%	6
Cryptosporidium hominis	0.00170%	4
Acanthamoeba mauritaniensis	0.00210%	4
Trypanosoma cruzi	0.00080%	9
Toxoplasma gondii	0.00200%	7
Enterobius vermicularis	0.00100%	11
fungi		
Malassezia globosa	0.00988%	11
Neurospora crassa	0.00182%	10
Fusarium verticillioides	0.00188%	10
Sordaria macrospora	0.00098%	5

Data of Case 7

species	coverage	unique reads
bacteria		
Bradyrhizobium elkanii	2.63972%	2874
Ralstonia sp. MD27	2.25852%	1758
Burkholderia sp. A9	1.89506%	42
Burkholderia ubonensis	1.88076%	392
Burkholderia sp. lig30	1.66429%	314
Burkholderia multivorans	1.50462%	786
Burkholderia pseudomultivorans	1.00124%	112
Burkholderia dolosa	0.97612%	100
Moraxella osloensis	0.89112%	262
Burkholderia cenocepacia	0.88388%	72
Burkholderia territorii	0.82892%	62
Burkholderia cepacia	0.75835%	70
Burkholderia vietnamiensis	0.75451%	68
Burkholderia paludis	0.68078%	88
Burkholderia latens	0.66739%	28
Microtholunatus phosphovorus	0.11110%	86
Candidatus Kinetoplastibacterium galatii	0.03406%	0
Weissella hellenica	0.02400%	4
Knoellia subterranea	0.02260%	10
bacterium endosymbiont of Mortierella elongata	0.02204%	0
Candidatus Proffittella armatura	0.02130%	0
Streptococcus sp. HMSC063B03	0.02032%	0
Bacteroides sp. Marseille-P3166	0.01886%	0
Blattabacterium sp. (Nauphoeta cinerea)	0.01692%	0
Blattabacterium sp. (Periplaneta americana)	0.01655%	0
viruses		
Burkholderia phage KS10	2.84044%	8
Human mastadenovirus C	0.66784%	4
Enterobacteria phage HK629	0.16283%	0
Gordonia phage Schwabeltier	0.15993%	0
Escherichia virus Lambda	0.15876%	0
Burkholderia virus phiE125	0.15738%	2
Salmonella phage SJ46	0.11890%	2
Paramecium bursaria Chlorella virus A1	0.02335%	0

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Table 2 (continued)

Parasite		
Taenia solium	14.80790%	261064
Taenia saginata	0.23011%	112
Taenia multiceps	0.15579%	212
Acanthamoeba palestinensis	0.00688%	68
Wuchereria bancrofti	0.00473%	28
Hymenolepis nana	0.00428%	4
Cimex hemipterus	0.00281%	0
Enterocytozoon bieneusi	0.00194%	0
Echinococcus multilocularis	0.00156%	2
Trypanosoma cruzi	0.00145%	0
Cryptosporidium hominis	0.00128%	2
		261492
fungi		
Malassezia globosa	0.01876%	22
[Candida] glabrata	0.01215%	24
Pneumocystis carinii	0.00196%	0
Saccharomyces cerevisiae	0.00123%	2
Data of NTC 7		
species	coverage	unique reads
bacteria		
Bradyrhizobium elkanii	25.93500%	34192
Ralstonia sp. MD27	20.62190%	19060
Burkholderia ubonensis	10.47360%	4914
Burkholderia sp. A9	9.70348%	580
Burkholderia sp. lig30	9.69313%	4120
Burkholderia multivorans	7.12847%	9434
Burkholderia pseudomultivorans	6.53222%	1622
Burkholderia dolosa	5.98695%	1218
Burkholderia cenocepacia	5.61033%	816
Burkholderia territorii	5.56941%	856
Burkholderia vietnamiensis	5.08144%	832
Burkholderia cepacia	5.03973%	736
Burkholderia contaminans	4.74377%	1074
Burkholderia latens	4.66839%	534
Burkholderia paludis	4.59436%	834
Mesorhizobium sp. UASWS1009	3.34627%	3464
Propionibacterium acnes	3.28747%	1292
Streptomyces purpurogeneiscleroticus	2.95533%	2780
Burkholderia oklahomensis	2.87800%	584
Burkholderia thailandensis	2.76245%	384
Burkholderia sp. MSMB0266	2.56173%	526
Burkholderia pseudomallei	2.42884%	428
Ralstonia sp. NT80	2.09376%	88
Thermomonas hydrothermalis	1.59071%	466
Burkholderia sp. TSV85	1.36560%	184
Cupriavidus gilardii	1.19640%	692
Limnhabitans sp. Rim47	1.13696%	364
Ralstonia pickettii	1.12647%	316
Cupriavidus metallidurans	1.09302%	158
Burkholderia plantarii	1.08915%	148
Acidovorax delafieldii	1.00982%	106
Moraxella osloensis	1.00614%	330
Paraburkholderia graminis	0.97890%	32
Burkholderia glumae	0.96302%	130
Acidovorax sp. KKS102	0.87773%	80
Methylobacterium sp. Leaf92	0.87767%	408
alpha proteobacterium L41A	0.84148%	126
Ralstonia sp. 5_2_56FAA	0.83787%	56
Sphingomonas sp. Ant H11	0.82602%	314
Brevundimonas vesicularis	0.80243%	156

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Table 2 (continued)

Burkholderia gladioli	0.78890%	514
Desulfocarbo indianensis	0.78396%	8
Acidovorax sp. Root70	0.72725%	170
Brevundimonas nasdae	0.71617%	116
Xenophilus azovorans	0.70860%	10
Methylobacter versatilis	0.70601%	58
Comamonadaceae bacterium CCH12-A10	0.69941%	14
Comamonadaceae bacterium CCH4-C5	0.69602%	46
Paracoccus sphaerophysae	0.68723%	342
Dyella jiangningensis	0.67789%	590
Acidovorax sp. CCH12-A4	0.63535%	24
Ralstonia mannitolilytica	0.62904%	98
Polynucleobacter duraquae	0.60213%	72
Comamonas testosteroni	0.59597%	8
Aflipia broomeae	0.58748%	130
Paraburkholderia acidipaludis	0.56997%	150
beta proteobacterium CB	0.54665%	52
Acidovorax sp. Root402	0.53293%	104
Paraburkholderia rhizoxinica	0.50318%	2
Paraburkholderia ferrariae	0.48933%	244
Limnohabitans sp. 103DPR2	0.47128%	144
Polynucleobacter sp. MWH-Adler-W8	0.46562%	66
Burkholderia sp. SRS-W-2-2016	0.46524%	66
Staphylococcus epidermidis	0.39120%	84
Staphylococcus hominis	0.35611%	126
Staphylococcus haemolyticus	0.09685%	36
Micrococcus luteus	0.03479%	4
Rothia sp. ND6WE1A	0.01490%	4
viruses		
Burkholderia phage KS10	13.36273%	44
Flavobacterium phage Fpv2	0.44520%	5
Paramecium bursaria Chlorella virus A1	0.36770%	4
Propionibacterium phage PHL116	14.67467%	87
Propionibacterium phage Pirate	17.21050%	43
Propionibacterium phage QueenBey	15.78080%	34
Propionibacterium phage P104A	16.88680%	41
Staphylococcus phage StB12	3.47691%	8
Staphylococcus phage PT1028	0.43317%	0
Propionibacterium phage P1.1	1.10953%	10
Parasite		
Acanthamoeba palestinensis	0.00860%	45
Wuchereria bancrofti	0.00770%	46
Hammondia hammondi	0.00330%	7
Cryptosporidium hominis	0.00220%	6
Acanthamoeba mauritaniensis	0.00240%	4
Trypanosoma cruzi	0.00180%	3
Toxoplasma gondii	0.00230%	5
Enterobius vermicularis	0.00120%	7
fungi		
Malassezia globosa	0.00988%	16
Neurospora crassa	0.00126%	6
Neurospora tetrasperma	0.00157%	4
Sordaria macrospora	0.00078%	9
Albugo laibachii	0.00120%	2

NTC = no template control; coverage means genomic coverage.

MiniSeq system for sequencing with the High Output Reagent Kit (150 cycles), as described in the MiniSeq Local Run Manager Software Guide.

2.3. Data analysis

High-quality sequencing data were generated after removing short (<35 bp), low-quality, and low-complexity reads and computational subtraction of the human host sequences was performed using a Burrows-Wheeler Alignment tool [1]. Finally, the remaining sequencing data were aligned to the Microbial Genome Databases, which are composed of 2700 whole genome sequences of viral taxa, 1494 bacterial genomes or scaffolds, 73 fungi and 48 parasites associated with human infectivity. The reference genomes were downloaded from the National Center for Biotechnology Information (<ftp://ftp.ncbi.nlm.nih.gov/genomes>). The mapped data were further processed; the depth and coverage of each species was calculated using Soap Coverage (<http://soap.genomics.org.cn>).

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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References

- [1] H. Li, R. Durbin, Fast and accurate short read alignment with Burrows-Wheeler transform, *BIOINFORMATICS* 25 (2009) 1754–1760 <https://doi.org/10.1093/bioinformatics/btp324>.
- [2] P. Liu, X. Weng, J. Zhou, Next generation sequencing based pathogen analysis in a patient with neurocysticercosis: a case report, *BMC Infect Dis* 18 (2018) 113 <https://doi.org/10.1186/s12879-018-3015-y>.
- [3] S. Fan, X. Qiao, L. Liu, H. Wu, Next-Generation Sequencing of Cerebrospinal Fluid for the Diagnosis of Neurocysticercosis, *Front Neurol* 9 (2018) 471 <https://doi.org/10.3389/fneur.2018.00471>.