Table S1. Sequencing results of samples

Sample A.

Database	Organism	Unique Matches Frequency	Unique Matches	% Unique Matches	% Total Matches	Relative Abundance	Above_Threshold
Bacteria	Pseudomonas_aeruginosa_38661 Branch	36	34	21.25	15.3	65.11	Y
Bacteria	Streptococcus_australis_ATCC_700641	2085	1883	2.34	2.39	12.34	Y
Bacteria	Streptococcus_sp_I_G2	471	416	1.1	1.22	5.376	Y
Bacteria	Propionibacterium_acnes_HL082PA2	47	41	1.98	2.52	4.487	Y
Bacteria	Klebsiella_pneumoniae_35366 Branch	28	25	1.11	1.28	3.872	Y
Bacteria	Enterobacter_sp_MGH_33	208	207	0.93	1.02	2.259	N
Bacteria	Enterococcus_faecalis_4475 Branch	16	16	1.62	1.62	2.125	N
Bacteria	Bacteroides_fragilis_str_1242 Branch	19	16	0.33	1.05	0.6042	N
Bacteria	Serratia_liquefaciens_ATCC_27592	319	311	0.16	0.18	0.4145	N
Bacteria	Bacteroides_plebeius_DSM_17135	275	275	0.14	0.14	0.3573	N
Bacteria	Staphylococcus_epidermidis_VCU071	23	23	0.22	0.38	0.3222	N
Bacteria	Bifidobacterium_breve_JCM_7019	65	65	0.17	0.17	0.3211	N
Bacteria	Bacteroides_1055 Branch	34	34	0.03	0.04	0.1942	N
Bacteria	Faecalibacterium_prausnitzii_27369 Branch	78	78	0.07	0.09	0.1903	N
Bacteria	Streptococcus_parasanguinis_ATCC_903	39	38	0.1	0.11	0.175	N
Bacteria	Anaerococcus_42657 Branch	26	25	0.1	0.1	0.1713	N
Bacteria	Clostridium_paraputrificum_AGR2156	101	99	0.08	0.08	0.1667	N
Bacteria	Streptococcus_infantis_ATCC_700779	44	37	0.09	0.09	0.1571	N
Bacteria	Clostridiales_Order_18 2486_26738 Branch	43	43	0.06	0.06	0.119	N
Bacteria	Bacteroides_caccae_924 Branch	71	71	0.04	0.04	0.09074	N
Bacteria	Klebsiella_variicola_strain_DSM_15968	12	12	0.09	1.03	0.09996	N
Bacteria	Acinetobacter_johnsonii_SH046	45	43	0.06	0.06	0.09934	N
Bacteria	Alistipes_putredinis_DSM_17216	80	80	0.05	0.05	0.09281	N
Bacteria	Klebsiella_35782 Branch	21	21	0.03	0.04	0.09153	N
Bacteria	Bacteroides_sp_1_1_6	32	32	0.06	0.05	0.09152	N
Bacteria	Bacteroides_stercoris_ATCC_43183	38	38	0.05	0.06	0.08162	N
Bacteria	Bacteroides_880 Branch	24	24	0.02	0.02	0.06029	N
Bacteria	Bacteroides_vulgatus_dnLKV7	23	23	0.05	0.07	0.07613	N
Bacteria	Bacteroides_824 Branch	12	12	0.05	0.07	0.07117	N
Bacteria	Halomonas_sp_KM_1	73	70	0.04	0.04	0.07041	N
Bacteria	Bifidobacterium_bifidum_LMG_13195	12	12	0.05	0.04	0.06303	N
Bacteria	Veillonella_parvula_ATCC_17745	14	14	0.05	0.05	0.05737	N
Bacteria	Acinetobacter_lwoffii_WJ10621	29	26	0.04	0.04	0.05521	N
Bacteria	Bacteroides_eggerthii_DSM_20697	23	23	0.03	0.04	0.04821	N
Bacteria	Rothia_dentocariosa_20586 Branch	18	18	0.02	0.02	0.04457	N
Bacteria	Corynebacterium_striatum_ATCC_6940	48	45	0.03	0.03	0.04511	N

Sample A cont.

Virus	Pseudomonas_phage_Pf1	421	356	13.86	13.86	75	Y
Virus	Propionibacterium_phage_PHL113M01	107	79	2.25	2.95	18.57	Y
Virus	Rosellinia_necatrix_partitivirus_2	122	10	0.58	0.58	5.926	N
Virus	Enterococcus_phage_phiFL4A	31	31	0.16	0.16	0.4951	N

Respiratory Virus	no calls detected above threshold

Fungi	no calls detected above threshold

Protist	Sarcocystis_neurona_strain_SN1	2279	268	0.55	0.23	74.58	Y
Protist	Plasmodium_gaboni_strain_Pgk	980	48	0.09	0.09	19.62	Y
Protist	Toxoplasma_gondii_GT1	156	17	0.07	0.02	5.798	Y

Antibiotic Resistance	MDR-Efflux-pump_mexG	66	50	38.46	38.46		N
Antibiotic Resistance	MDR-Efflux-pump_mexQ	376	301	31.58	31.58		N
Antibiotic Resistance	MDR-Efflux-pump_opmE	114	109	28.53	28.53		N
Antibiotic Resistance	Repressor-of-efflux-complex_nfxB	68	45	25.28	25.28		N
Antibiotic Resistance	Sensor-protein_soxR	35	31	25	25		N
Antibiotic Resistance	MDR-Efflux-pump_opmH	126	101	24.57	24.57		N
Antibiotic Resistance	Macrolide_mel	65	65	18.79	24.43		N
Antibiotic Resistance	MDR-Efflux-pump_mexB	256	245	24.04	24.04		N
Antibiotic Resistance	Outer-membrane-factor_oprM	150	99	23.86	23.86		N
Antibiotic Resistance	Phenicol_catB7	45	45	23.44	23.44		N
Antibiotic Resistance	Beta-lactam-resistance_bla 244_1197_740 Branch	60	60	23.08	23.08		N
Antibiotic Resistance	Repressor-of-mexJK_mexL	56	44	22.68	22.68		N
Antibiotic Resistance	MDR-Efflux-pump_mexD	284	232	21.95	21.95		N
Antibiotic Resistance	MDR-Efflux-pump_mexM	72	66	20.62	20.62		N

Sample A cont.

Antibiotic Resistance	MDR-Efflux-pump_mexP	57	57	17.81	17.81	N
Antibiotic Resistance	Efflux-pump_triB	49	49	17.63	17.63	N
Antibiotic Resistance	Beta-lactam-resistance_blaOXA_50	70	70	17.24	17.24	N
Antibiotic Resistance	MDR-Efflux-pump_mexC	63	49	16.44	16.44	N
Antibiotic Resistance	Inner-membrane-transporter_mexF	160	153	14.97	14.97	N
Antibiotic Resistance	Repressor_nalC	28	28	14.58	14.58	N
Antibiotic Resistance	Beta-lactam_cfxA_2366 Branch	67	67	14.5	14.19	N
Antibiotic Resistance	MDR-Efflux-pump_mexJ	40	40	14.03	14.03	N
Antibiotic Resistance	Efflux-pump_triA	43	43	13.83	13.83	N
Antibiotic Resistance	MDR-Efflux-pump_mexN	127	127	13.54	13.54	N
Antibiotic Resistance	Aminoglycoside_aph3'_IIa	38	38	13.52	13.52	N
Antibiotic Resistance	MDR-Efflux-pump_oprJ	61	54	13.47	13.47	N
Antibiotic Resistance	MDR-Efflux-pump_mexI	167	123	13.18	13.18	N
Antibiotic Resistance	AR 215_778_2296 Branch	33	33	12.99	12.99	N
Antibiotic Resistance	MDR-Efflux-pump_mexH	39	39	12.3	12.3	N
Antibiotic Resistance	Suppressor-of-MexT_mexS	36	36	11.8	11.8	N
Antibiotic Resistance	MDR-Efflux-pump_oprN	43	43	11.38	11.38	N
Antibiotic Resistance	Repressor-of-efflux-complex_phoP	57	57	11.22	11.22	N
Antibiotic Resistance	MDR-Efflux-pump_opmD	44	40	11.05	11.05	N
Antibiotic Resistance	Efflux-pump_triC	138	101	10.25	10.25	N
Antibiotic Resistance	Involved-in-polymyxin-resistance_pmrB	83	83	9.87	9.87	N
Antibiotic Resistance	Membrane-fusion-protein_mexA	25	25	7.12	7.12	N
Antibiotic Resistance	MDR-Efflux-pump_mexE	24	24	6.8	6.8	N
Antibiotic Resistance	Sensor-protein_phoQ	67	62	6.22	6.22	N
Antibiotic Resistance	AR 214_989_2085 Branch	58	47	5.5	5.5	N

Virulence Factor	Pseudomonas_aeruginosa_GENE_xcpV	90	57	57	57	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_fliQ	48	38	56.72	56.72	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_lasI	163	105	52.24	52.24	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_pilM	176	141	49.82	49.82	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_lasA	166	145	47.39	47.39	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_pilP	91	74	45.12	45.12	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_Alg44	150	118	44.7	44.7	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_fliJ	46	40	42.1	42.1	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_rhlA	161	109	41.92	41.92	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_pilO	102	82	41.41	41.41	Y

Sample A cont.

Virulence Factor	Pseudomonas_aeruginosa_GENE_pchR	97	84	38.71	38.71	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_mucC	63	41	38.32	38.32	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_xcpX	96	70	37.04	37.04	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_fliD	208	180	36.15	36.15	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_fliM	127	109	35.05	35.05	N
Virulence Factor	Pseudomonas_aeruginosa_GeneID_PA0072	105	88	34.78	34.78	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_fleQ	142	141	34.14	34.3	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_fleR	134	133	33.93	33.93	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_pchG	91	88	33.46	33.46	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_lasR	70	70	32.26	32.26	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_fliP	68	68	32.08	32.08	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_fimT	43	43	31.85	31.85	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_flhB	107	85	31.48	31.48	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_waaC	77	77	31.3	31.3	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_Alg8	130	130	30.95	30.95	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_algU	60	60	30.3	30.3	N
Virulence Factor	Pseudomonas_aeruginosa_GeneID_PA0086	75	65	30.23	30.23	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_xcpW	47	47	30.13	30.13	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_pilK	99	70	30.04	30.04	N
Virulence Factor	Pseudomonas_aeruginosa_GeneID_PA0084	152	135	29.93	29.93	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_fliE	29	29	29.59	29.59	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_pilY2	29	29	29.59	29.59	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_plcH	231	160	28.93	28.93	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_algL	77	77	28.84	28.84	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_pchB	22	22	28.57	28.57	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_fleN	73	73	28.52	28.52	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_pilI	38	38	28.36	28.36	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_pvdE	134	118	28.03	28.03	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_algR	72	59	27.83	27.83	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_xcpR	102	89	27.64	27.64	N
Virulence Factor	Pseudomonas_aeruginosa_GeneID_PA0079	108	100	27.32	27.32	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_pilV	58	46	26.44	26.44	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_flgJ	77	77	26.28	26.28	N
Virulence Factor	Pseudomonas_aeruginosa_GeneID_PA0082	71	67	26.27	26.27	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_flgD	49	49	25.39	25.39	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_algD	89	87	25.36	25.36	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_chpB	96	68	25.19	25.19	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_flhA	157	157	25.12	25.12	N

Sample A cont.

Virulence Factor	Pseudomonas_aeruginosa_GENE_fimV	146	146	25	25	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_flgC	44	32	25	25	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_xcpZ	26	26	25	25	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_vgrG1	105	103	24.82	24.82	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_pilQ	259	149	24.71	24.71	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_pilJ	139	139	24.51	24.51	N
Virulence Factor	Pseudomonas_aeruginosa_GeneID_PAP4746	67	56	24.35	24.35	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_algE	83	83	23.58	23.58	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_hcp1	37	29	23.58	23.58	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_pchH	99	95	23.57	23.57	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_pilD	59	59	23.23	23.23	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_phzM	125	69	23.08	23.08	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_exoT	141	90	22.96	22.96	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_pilC	117	88	22.62	22.62	N
Virulence Factor	Pseudomonas_aeruginosa_GeneID_PA0083	32	32	22.22	22.22	N
Virulence Factor	Pseudomonas_aeruginosa_GeneID_PA0075	44	39	22.16	22.16	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_pchF	111	90	22.11	22.11	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_algI	91	91	21.93	21.93	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_algK	100	63	21.88	21.88	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_algG	93	91	21.51	21.51	N
Virulence Factor	Streptococcus_pyogenes_GENE_msrD	159	117	21.47	21.47	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_aprA	86	86	21.13	21.13	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_mucA	31	31	20.53	20.53	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_fliR	43	43	20.09	20.09	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_flgH	44	39	19.8	19.8	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_exoS	96	79	18.81	18.81	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_pilA	28	28	18.79	18.79	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_xcpS	80	53	18.53	18.53	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_rhlL	31	31	18.34	18.34	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_pchA	62	62	17.97	17.97	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_pilR	80	70	17.5	17.5	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_pchE	78	64	17.39	17.39	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_waaP	42	40	17.17	17.17	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_xcpQ	80	78	17.03	17.03	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_fliF	88	88	16.96	16.96	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_mucB	39	39	16.96	16.96	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_waaA	47	47	16.61	16.61	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_algQ	22	22	16.54	16.54	N

Sample A cont.

Virulence Factor	Pseudomonas_aeruginosa_GeneID_PA0087	19	19	16.52	16.52	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_pilH	18	18	16.51	16.51	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_flgK	101	89	16.48	16.48	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_fliC	51	51	16.04	16.04	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_wzy	115	90	15.99	15.99	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_pilS	79	68	15.93	15.93	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_pvdA	51	45	15.73	15.73	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_algJ	45	44	15.66	15.66	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_ppkA	78	78	15.35	15.35	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_toxA	85	73	15.3	15.3	N
Virulence Factor	Pseudomonas_aeruginosa_GeneID_PA0088	87	74	15.16	15.16	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_algZ	45	45	15.15	15.15	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_pilB	97	87	14.85	14.85	N
Virulence Factor	Pseudomonas_aeruginosa_GeneID_PA0081	62	53	14.4	14.4	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_fliH	30	30	14.29	14.29	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_lasB	45	45	13.8	13.8	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_pilX	24	24	13.71	13.71	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_flhF	41	41	13.49	13.49	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_pilT	37	37	13.21	13.21	N
Virulence Factor	Pseudomonas_aeruginosa_GeneID_PA0073	21	21	12.65	12.65	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_icmF1	64	64	12.62	12.62	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_pilF	28	28	12.5	12.5	N
Virulence Factor	Enterobacter_GENE_tpx	38	38	12.3	12.3	N
Virulence Factor	Bacteroides_fragilis_GENE_mobA	18	18	12.08	12.08	N
Virulence Factor	Pseudomonas_aeruginosa_GeneID_PA0078	46	33	11.7	11.7	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_clpV1	46	46	11.7	11.7	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_exoY	42	42	11.63	11.63	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_chpD	17	17	11.33	11.33	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_chpE	16	16	11.27	11.27	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_pchC	18	18	11.04	11.04	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_fptA	53	53	10.19	10.19	N
Virulence Factor	Bacteroides_fragilis_GENE_mobB	41	41	9.88	9.88	N
Virulence Factor	Pseudomonas_aeruginosa_GeneID_PA0076	15	15	9.38	9.38	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_pchI	29	29	9.18	9.18	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_fimU	29	15	9.09	9.09	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_pchD	34	34	9.02	9.02	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_pilW	20	20	8.51	8.51	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_xcpP	16	16	8.47	8.47	N

Sample A cont.

Virulence Factor	Pseudomonas_aeruginosa_GENE_waaF	32	23	8.36	8.36	N
Virulence Factor	Enterobacter_GENE_espf_2378 Branch	41	41	8.28	8.28	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_algB	35	29	7.84	8.09	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_flgG	18	18	7.38	7.38	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_algX	24	24	7.21	7.21	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_xcpY	22	16	6.9	6.9	N
Virulence Factor	Bacteroides_fragilis_GENE_rteA	55	55	6.12	6.12	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_phzS	18	18	6	6	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_flgE	22	22	5.33	5.33	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_algA	22	22	5.06	5.06	N

Sample B.

Database	Organism	Unique Matches Frequency	Unique Matches	% Unique Matches	% Total Matches	Relative Abundance	Above_Threshold
Bacteria	Bacteroides_fragilis_str_1242 Branch	66	63	1.28	1.85	81.37	Y
Bacteria	Lactobacillus_5304 Branch	22	22	0.18	0.18	3.508	N
Bacteria	Bacteroides_819 Branch	17	17	0.04	0.04	1.735	N
Bacteria	Bacteroides_stercoris_ATCC_43183	81	79	0.1	0.13	2.705	N
Bacteria	Bifidobacterium_longum_subsp_infantis_EK3	52	52	0.11	0.13	2.619	N
Bacteria	Bacteroides_caccae_924 Branch	93	93	0.05	0.05	1.688	N
Bacteria	Clostridiales_Order_18 2486_26738 Branch	47	47	0.06	0.06	1.621	N
Bacteria	Bacteroides_eggerthii_1_2_48FAA	36	36	0.05	0.08	1.125	N
Bacteria	Bacteroides_thetaiotaomicron_dnLKV9	44	40	0.04	0.04	0.919	N
Bacteria	Faecalibacterium_cf_prausnitzii_KLE1255	58	58	0.03	0.04	0.8062	N
Bacteria	Faecalibacterium_prausnitzii_SL3_3	32	32	0.03	0.06	0.6653	N
Bacteria	Alistipes_1161 Branch	35	35	0.02	0.02	0.621	N
Bacteria	Bacteroides_dorei_isolate_HS1_L_1_B_010	13	13	0.04	0.02	0.6202	N
Virus	Rosellinia_necatrix_partitivirus_2	259	10	0.58	0.58	66.19	Y
Virus	Pseudomonas_phage_Pf1	48	48	1.87	1.87	33.81	Y
Respiratory Virus	no calls detected above threshold						
Fungi	no calls detected above threshold						
Protist	Sarcocystis_neurona_strain_SN1	4549	397	0.82	0.35	96.2	Y
Protist	Toxoplasma_gondii_CtCo5	366	10	0.02	0.01	3.799	Y

Sample B cont.

Antibiotic Resistance	Repressor-of-efflux-complex_nfxB	43	43	24.16	24.16	N
Antibiotic Resistance	Outer-membrane-factor_oprM	35	35	8.43	8.43	N

Virulence Factor	Escherichia_coli_GENE_mcmA	38	38	18.63	18.63	N
Virulence Factor	Pseudomonas_aeruginosa_GeneID_PA0086	17	17	7.91	7.91	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_fimV	40	40	6.85	6.85	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_flgK	34	34	6.3	6.3	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_pilK	14	14	6.01	6.01	N

Sample C.

Database	Organism	Unique Matches Frequency	Unique Matches	% Unique Matches	% Total Matches	Relative Abundance	Above Threshold
Bacteria	Propionibacterium_20956 Branch	42	29	0.24	0.17	47.14	N
Bacteria	Staphylococcus_aureus_11902 Branch	10	10	0.27	0.36	27.27	N
Bacteria	StaphEpidermidis 242_6162 Branch	18	16	0.15	0.13	18.86	N
Bacteria	Staphylococcus_hominis_6333 Branch	23	16	0.05	0.04	6.729	N
Virus	no calls detected above threshold						
Respiratory Virus	no calls detected above threshold						
Fungi	no calls detected above threshold						
Protist	no calls detected above threshold						
Antibiotic Resistance	no calls detected above threshold						
Virulence Factor	Staphylococcus_aureus_GI_33390919	66	38	19.1	20.45		N
Virulence Factor	Staphylococcus_aureus_GeneID_SAS0111	62	62	16.45	16.45		N
Virulence Factor	Staphylococcus_aureus_GeneID_SASa1133	48	48	10.88	10.88		N
Virulence Factor	Staphylococcus_aureus_GeneID_SASa2284	33	33	7.47	7.47		N

Sample D.

Database	Organism	Unique Matches Frequency	Unique Matches	% Unique Matches	% Total Matches	Relative Abundance	Above Threshold
Bacteria	Georgenia_sp_SUBG003	271	15	0.01	0.01	53.9	N
Bacteria	Dermacoccus_20818 Branch	33	28	0.02	0.02	27.33	N
Bacteria	candidate_division_TM7_single_cell_isolate_TM7a	21	16	0.02	0.02	18.77	N

Virus	no calls detected above threshold
Fungi	no calls detected above threshold
Protist	no calls detected above threshold
Antibiotic Resistance	no calls detected above threshold
Virulence Factor	no calls detected above threshold

Sample E.

Database	Organism	Taxonomy	Unique Matches Frequency	Unique Matches	% Unique Matches	% Total Matches	Relative Abundance	Above_Threshold
Bacteria	Faecalibacterium_27364	Branch	3	3	0.22	0.22	100	N
Virus	no calls detected above threshold							
Fungi	no calls detected above threshold							
Protist	no calls detected above threshold							
Antibiotic Resistance	no calls detected above threshold							
Virulence Factor	no calls detected above threshold							

Sample 1.

Database	Organism	Unique Matches Frequency	Unique Matches	% Unique Matches	% Total Matches	Relative Abundance	Above Threshold
Bacteria	Propionibacterium_sp_KPL1854	28	28	3.51	19.58	57.04	Y
Bacteria	Clostridium_autoethanogenum_DSM_10061	1536	1212	3.2	6.96	10.81	Y
Bacteria	Clostridium_ljungdahlii_DSM_13528	2013	1575	3.2	6.73	10.78	Y
Bacteria	Lachnospiraceae_bacterium_A4	5178	4737	2.42	2.42	6.602	Y
Bacteria	Oscillibacter_sp_1_3	1532	1405	0.71	0.73	1.6	N
Bacteria	Staphylococcus_6058 Branch	13	13	0.78	0.79	0.9093	N
Bacteria	Firmicutes_bacterium_ASF500	1063	931	0.51	0.51	1.093	N
Bacteria	Enterococcus_faecalis_EnGen_5094 Branch	19	17	0.86	0.71	0.7987	N
Bacteria	Lactococcus_lactis_subsp_cremoris_4115 Branch	54	53	0.17	0.17	0.526	N
Bacteria	Clostridium_sp_ASF502	645	604	0.31	0.31	0.606	N
Bacteria	Propionibacterium_acnes_SK182B_JCVI	563	538	0.31	0.31	0.6035	N
Bacteria	Enterococcus_faecium_1_231_501	35	34	0.51	0.69	0.5678	N
Bacteria	Pseudomonas_aeruginosa_strain_AZPAE14829	23	23	0.56	0.33	0.5484	N
Bacteria	Anaerotruncus_sp_G32012	594	528	0.28	0.29	0.5396	N
Bacteria	Peptoclostridium_difficile_27096 Branch	14	10	0.65	0.65	0.5335	N
Bacteria	Oscillibacter_valericigenes_Sjm18_20	543	525	0.27	0.28	0.5116	N
Bacteria	Eubacterium_plexicaudatum_ASF492	555	509	0.26	0.28	0.5021	N
Bacteria	Dorea_sp_5_2	477	434	0.22	0.22	0.4179	N
Bacteria	Staphylococcus_hominis_6333 Branch	32	32	0.1	0.09	0.298	N
Bacteria	Erysipelotrichaceae_bacterium_6_1_45	70	66	0.2	0.19	0.2671	N
Bacteria	Streptococcus_thermophilus_2097 Branch	18	16	0.07	0.08	0.2191	N
Bacteria	Finegoldia_magna_42689 Branch	14	14	0.07	0.06	0.1689	N
Bacteria	Megasphaera_elsdenii_14260 Branch	89	83	0.1	0.1	0.2073	N
Bacteria	Corynebacterium_accolens_ATCC_49725	60	51	0.15	0.15	0.1897	N
Bacteria	Stenotrophomonas_maltophilia_JV3	201	195	0.12	0.12	0.1882	N
Bacteria	Geobacillus_stearothermophilus_strain_12847 Branch	75	75	0.13	0.17	0.1687	N
Bacteria	Delftia_acidovorans_SPH_1	126	124	0.11	0.15	0.1631	N
Bacteria	Acinetobacter_junii_41991 Branch	15	15	0.14	0.09	0.1374	N
Bacteria	Eubacterium_sp_14_2	172	164	0.09	0.09	0.1418	N
Bacteria	Prevotella_copri_DSM_18205	178	165	0.09	0.09	0.1385	N
Bacteria	Staphylococcus_capitis_QN1	11	11	0.18	0.18	0.1373	N

.Sample 1 cont.

Bacteria	Kocuria_rhizophila_P7_4	109	109	0.09	0.18	0.1363	N
Bacteria	Lactobacillus_johnsonii_NCC_533	28	26	0.12	0.14	0.1261	N
Bacteria	Christensenella_timonensis_Marseille_P2437	142	126	0.07	0.1	0.1075	N
Bacteria	Clostridiales_26672 Branch	48	47	0.04	0.04	0.07718	N
Bacteria	Streptococcus_2988 Branch	24	21	0.07	0.07	0.0871	N
Bacteria	Prevotella_bivia_853 Branch	24	24	0.03	0.03	0.09634	N
Bacteria	Propionibacterium_granulosum_TM11	34	34	0.09	0.11	0.09473	N
Bacteria	Rothia_mucilaginosa_20589 Branch	29	29	0.07	0.06	0.0805	N
Bacteria	Acidovorax_25090 Branch	68	68	0.05	0.05	0.08147	N
Bacteria	Oscillibacter_ruminantium_GH1	116	115	0.06	0.08	0.08546	N
Bacteria	Clostridiales_Order_18 3421_27046 Branch	85	81	0.05	0.07	0.08036	N
Bacteria	Corynebacterium_sp_GD7	104	97	0.06	0.06	0.08245	N
Bacteria	Klebsiella_35782 Branch	20	19	0.03	0.04	0.08021	N
Bacteria	Prevotella_disiens_JCM_6334_ATCC_29426	26	26	0.08	0.08	0.0762	N
Bacteria	Delftia_sp_670	41	41	0.06	0.13	0.0756	N
Bacteria	Achromobacter_xylosoxidans_X02736	88	88	0.05	0.06	0.07242	N
Bacteria	Pseudomonas_syringae_pv_pisi_str_PP1	67	14	0.04	0.03	0.0668	N
Bacteria	Clostridium_scatologenes	89	70	0.05	0.05	0.06651	N
Bacteria	Rothia_dentocariosa_20586 Branch	29	29	0.04	0.04	0.0595	N
Bacteria	Mycobacterium_abscessus_MAB_082312_2273	82	82	0.04	0.04	0.05694	N
Bacteria	Lactobacillus_sakei_5706 Branch	17	17	0.03	0.03	0.05689	N
Bacteria	Bacillus_cereus_VD102	16	16	0.06	0.08	0.0554	N
Bacteria	Clostridium_carboxidivorans_P7	68	54	0.04	0.08	0.05563	N
Bacteria	Peptoniphilus_harei_ACS_146_V_Sch2b	36	36	0.05	0.05	0.05439	N
Bacteria	Porphyromonas_bennonis_DSM_23058_JCM_16335	51	50	0.04	0.04	0.04825	N
Bacteria	Facklamia_hominis_4212 Branch	18	18	0.03	0.03	0.04161	N
Bacteria	Corynebacterium_pseudogenitalium_ATCC_33035	39	39	0.04	0.04	0.04359	N
Bacteria	Dolosigranulum_pigrum_ATCC_51524	50	42	0.04	0.04	0.04345	N
Bacteria	Clostridium_methylpentosum_DSM_5476	73	64	0.03	0.05	0.04337	N
Bacteria	Intestinimonas_butyriciproducens	67	64	0.03	0.03	0.04237	N
Bacteria	Phascolarctobacterium_succinatutens_YIT_12067	37	37	0.04	0.03	0.0393	N
Bacteria	Bacteroides_uniformis_dnLKV2	34	30	0.04	0.02	0.03861	N
Bacteria	GlobalTree 4354 Node_14006	14	14	0.02	0.02	0.03628	N

.Sample 1 cont.

Bacteria	Carnobacterium_maltaromaticum_5850 Branch	12	12	0.01	0.01	0.03495	N
Bacteria	Staphylococcus_6307 Branch	37	36	0.03	0.03	0.03514	N
Bacteria	Prevotella_sp_P5_60	15	12	0.04	0.11	0.03482	N
Bacteria	Prevotella_corporis_DSM_18810_JCM_8529	53	47	0.03	0.03	0.03471	N
Bacteria	Lactococcus_raffinolactis_4877	40	38	0.03	0.03	0.03078	N
Bacteria	Pseudoflavonifractor_capillosus_ATCC_29799	54	49	0.03	0.03	0.03095	N
Bacteria	Caulobacter_sp_JGI_0001013_D04	13	10	0.04	0.02	0.03058	N
Bacteria	Clostridium_acetobutylicum_27843 Branch	12	10	0.01	0.01	0.03006	N
Bacteria	Staphylococcus_lugdunensis_6250 Branch	14	14	0.01	0.01	0.02991	N

Virus	Murine_type_C_retrovirus	48	48	2.08	1.76	37.36	Y
Virus	Streptococcus_phage_DT1	70	70	0.96	0.85	15.7	N
Virus	Lactococcus_phage_BK5_T	89	89	0.71	0.55	12.21	N
Virus	Propionibacterium_phage_P100D	31	25	0.68	0.68	9.1	N
Virus	PreXMRV_1	18	18	0.77	0.68	8.76	N
Virus	Human_adenovirus_C	15	15	0.35	1.04	3.771	N
Virus	Enterobacteria_phage_9g	50	50	0.18	0.18	2.766	N
Virus	Yersinia_phage_L_413C	14	14	0.22	0.2	2.292	N
Virus	Phage_phi_OH2	29	29	0.17	0.17	2.257	N
Virus	Staphylococcus_phage_StB20	33	33	0.16	0.16	2.121	N
Virus	Pseudomonas_phage_vB_PaeP_Tr60_Ab31	27	17	0.1	0.1	1.349	N
Virus	Cronobacter_phage_CR_2542 Branch	32	32	0.09	0.08	1.251	N
Virus	Bacillus_phage_Waukesha92	12	12	0.11	0.1	1.058	N

Fungi	Malassezia_restricta_CBS_7877	127	122	0.19	0.19	100	N

Protist	Plasmodium_yoelii_yoelii	1114	492	0.89	0.41	81.18	Y

.Sample 1 cont.

Protist	Plasmodium_berghei_ANKA	342	169	0.26	0.26	18.82	Y
Antibiotic Resistance	Tetracycline_tetW	297	220	13.46	13.46		N
Antibiotic Resistance	Tetracycline_tet40	23	23	25.28	9.14		N
Antibiotic Resistance	Tetracycline_tetO	68	68	7.82	7.82		N
Antibiotic Resistance	Macrolide_vgaA_2099 Branch	53	53	6.12	6.12		N
Virulence Factor	Enterobacter_aerogenes_GENE_upf54.8	35	35	37.23	37.23		N
Virulence Factor	Bacillus_anthracis_GeneID_BASa3239	57	57	12.58	12.58		N
Virulence Factor	Staphylococcus_lentus_GENE_pre	59	59	11.97	11.97		N

Sample 15.

Database	Organism	Unique Matches Frequency	Unique Matches	% Unique Matches	% Total Matches	Relative Abundance	Above Threshold
Bacteria	Propionibacterium_sp_KPL1854	42	33	4.14	46.31	48.59	Y
Bacteria	Propionibacterium_acnes_KPA171202	26	22	2.95	46.34	43.83	Y
Bacteria	Staphylococcus_epidermidis_AG42	35	35	1.27	2.85	2.433	Y
Bacteria	Staphylococcus_capitis_QN1	91	89	1.44	0.88	0.7921	N
Bacteria	Lactobacillus_5619 Branch	140	119	0.52	0.52	0.6061	N
Bacteria	Clostridium_ljungdahlii_DSM_13528	276	272	0.55	1.09	0.4009	N
Bacteria	Streptococcus_thermophilus_2097 Branch	30	30	0.14	0.17	0.1917	N
Bacteria	Clostridium_autoethanogenum_DSM_100	153	153	0.4	1.1	0.2627	N
Bacteria	Staphylococcus_hominis_6333 Branch	86	81	0.26	0.27	0.2034	N
Bacteria	Kocuria_rhizophila_P7_4	341	308	0.27	0.46	0.2016	N
Bacteria	StaphEpidermidis 242_6162 Branch	37	28	0.26	1.84	0.1734	N
Bacteria	Propionibacterium_granulosum_TM11	94	87	0.22	0.31	0.1303	N
Bacteria	Peptoniphilus_rhinitidis_1_13	122	112	0.18	0.18	0.1104	N
Bacteria	Prevotella_bivia_DNF_857 Branch	17	14	0.22	0.12	0.1062	N
Bacteria	Peptoniphilus_harei_ACS_146_V_Sch2b	120	120	0.16	0.16	0.1006	N
Bacteria	Prevotella_disiens_JCM_6334_ATCC_2942	67	63	0.18	0.18	0.09915	N
Bacteria	Acinetobacter_junii_SH205	49	37	0.15	0.46	0.07901	N
Bacteria	Propionibacterium_humerusii_20948 Bran	15	15	0.01	0.01	0.06725	N
Bacteria	Pseudomonas_fluorescens_NZ007	186	180	0.09	0.09	0.06202	N
Bacteria	Corynebacterium_sp_GD7	174	156	0.09	0.09	0.06205	N
Bacteria	Roseomonas_23661 Branch	100	95	0.05	0.05	0.04951	N
Bacteria	Lactococcus_lactis_subsp_cremoris_4115	31	29	0.09	0.09	0.05344	N
Bacteria	Acidovorax_sp_JS42	125	122	0.09	0.19	0.05523	N
Bacteria	Rothia_dentocariosa_M567	93	93	0.08	0.13	0.04919	N
Bacteria	Stenotrophomonas_maltophilia_JV3	136	130	0.08	0.08	0.04916	N
Bacteria	Staphylococcus_sp_6240 Branch	93	83	0.08	0.08	0.04848	N
Bacteria	Acidovorax_ebreus_TPSY	102	94	0.08	0.19	0.04766	N
Bacteria	Prevotella_sp_P_1307 Branch	87	87	0.07	0.07	0.04334	N
Bacteria	Delftia_acidovorans_SPH_1	97	87	0.08	0.12	0.04592	N
Bacteria	Prevotella_corporis_DSM_18810_JCM_85	129	117	0.07	0.07	0.04427	N
Bacteria	Corynebacterium_pseudogenitalium_ATC	79	77	0.08	0.08	0.0429	N

Sample 15 cont.

Bacteria	Streptococcus_sp_2_1_36FAA	53	53	0.08	0.09	0.04101	N
Bacteria	Corynebacterium_tuberculostearicum_SK1	69	68	0.07	0.07	0.04019	N
Bacteria	Streptococcus_mitis_strain_SK271	14	14	0.11	0.1	0.03928	N
Bacteria	Finegoldia_magna_ATCC_53516	53	51	0.07	0.12	0.03533	N
Bacteria	Micrococcus_luteus_strain_RIT324w	30	30	0.08	0.09	0.03511	N
Bacteria	Staphylococcus_6338 Branch	18	18	0.09	0.14	0.03354	N
Bacteria	GlobalTree 4354 Node_14006	21	19	0.03	0.03	0.02828	N
Bacteria	Lactobacillus_sakei_5706 Branch	23	23	0.04	0.04	0.02913	N
Bacteria	Caulobacter_sp_JGI_0001013_D04	19	19	0.07	0.04	0.02832	N
Bacteria	Staphylococcus_6215 Branch	16	13	0.05	0.07	0.02682	N
Bacteria	Serratia_marcescens_s_35630 Branch	45	36	0.04	0.04	0.0241	N
Bacteria	Varibaculum_cambriense_DSM_15806	70	56	0.04	0.05	0.02517	N
Bacteria	Anaerococcus_senegalensis_JC48	29	28	0.05	0.05	0.02436	N
Bacteria	Haemophilus_sputorum_38065 Branch	29	28	0.03	0.03	0.0234	N
Bacteria	Dolosigranulum_pigrum_ATCC_51524	56	54	0.05	0.05	0.02412	N
Bacteria	Corynebacterium_tuscaniense_DNF00037	76	76	0.04	0.04	0.02375	N
Bacteria	Burkholderia_sp_2385	21	21	0.06	0.06	0.02365	N
Bacteria	Atopobium_vaginae_DSM_15829	52	51	0.05	0.04	0.02356	N
Bacteria	Prevotella_timonensis_4401737_DSM_22	54	53	0.04	0.05	0.02293	N
Bacteria	Dialister_micraerophilus_DSM_19965	19	19	0.06	0.06	0.02283	N
Bacteria	Gemella_sanguinis_M325	29	24	0.05	0.04	0.02242	N
Bacteria	Delftia_sp_670	39	29	0.05	0.12	0.02239	N
Bacteria	Leuconostoc_5987 Branch	40	40	0.04	0.05	0.02191	N
Bacteria	Peptoniphilus_lacrimalis_DSM_7455	11	11	0.07	0.05	0.02152	N
Bacteria	Propionibacterium_20926 Branch	17	17	0.03	0.04	0.02123	N
Bacteria	Pseudomonas_syringae_pv_pisi_str_PP1	58	10	0.03	0.02	0.02095	N
Bacteria	Achromobacter_xylosoxidans_X02736	67	62	0.04	0.05	0.0203	N
Bacteria	Corynebacterium_aurimucosum_ATCC_70	61	59	0.03	0.03	0.01792	N
Bacteria	Rothia_mucilaginosa_M508	38	38	0.04	0.09	0.01768	N
Bacteria	Staphylococcus_cohnii_hu_01	12	10	0.05	0.05	0.01741	N
Bacteria	Dermacoccus_20818 Branch	41	41	0.03	0.03	0.01593	N
Bacteria	Ruminococcus_flavefaciens_MA2007	63	57	0.03	0.03	0.01685	N
Bacteria	Facklamia_hominis_CCUG_36813	18	18	0.04	0.07	0.01616	N

Sample 15 cont.

Bacteria	Ochrobactrum_anthropi_22533 Branch	14	14	0.04	0.02	0.01572	N
Bacteria	Gemella_haemolysans_ATCC_10379	29	29	0.03	0.03	0.01462	N
Bacteria	Anaerococcus_vaginalis_ATCC_51170	14	14	0.04	0.03	0.01455	N
Bacteria	Anaerococcus_prevotii_DSM_20548	28	26	0.03	0.03	0.01433	N
Bacteria	Staphylococcus_warneri_6227 Branch	20	20	0.03	0.04	0.01427	N
Bacteria	Actinomyces_sp_oral_taxon_448_str_F04	45	45	0.03	0.03	0.01369	N
Bacteria	Porphyromonas_bennonis_DSM_23058_J	40	35	0.03	0.03	0.01342	N
Bacteria	Mycobacterium_abscessus_MAB_082312_	50	50	0.03	0.03	0.01307	N
Bacteria	Peptoniphilus_sp_oral_taxon_375_str_F04	24	24	0.03	0.03	0.01306	N
Bacteria	Microbacterium_laevaniformans_OR221	34	30	0.03	0.03	0.0127	N

Virus	Propionibacterium_phage_PHL111M01	46	38	1.06	0.96	76.06	Y
Virus	Human_adenovirus_313 Branch	34	17	0.55	0.55	11.96	N
Virus	Staphylococcus_phage_StB20	48	48	0.23	0.23	4.589	N
Virus	Lactococcus_phage_ul36	26	26	0.22	0.21	3.817	N
Virus	Streptococcus_phage_DT1	18	17	0.23	0.25	3.576	N

Fungi	Malassezia_restricta_CBS_7877	414	401	0.61	0.61	100	N

Protist	no calls detected above threshold

Antibiotic Resistance	Macrolide_vgaA_2099 Branch	167	118	13.63	13.63		N
Antibiotic Resistance	MDR-Efflux-pump_mexC	23	23	7.72	7.72		N
Antibiotic Resistance	Macrolide_ermX	78	40	7.11	7.11		N
Antibiotic Resistance	Macrolide_ermC	50	50	5.59	5.59		N

Sample 15 cont.

Virulence Factor	Staphylococcus_aureus_GI_1527 Branch	45	33	30.27	30.27	N
Virulence Factor	Staphylococcus_lentus_GENE_repL	55	55	25.46	25.46	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_pilN	33	33	21.29	21.29	N
Virulence Factor	Pseudomonas_aeruginosa_GeneID_PA007	59	30	18.07	18.07	N
Virulence Factor	Enterobacter_aerogenes_GENE_trbP	36	36	17.91	17.91	N
Virulence Factor	Pseudomonas_aeruginosa_GeneID_PA008	87	87	17.83	17.83	N
Virulence Factor	Staphylococcus_aureus_GI_33390940	65	65	15.37	15.37	N
Virulence Factor	Staphylococcus_lentus_GENE_ermC	50	50	15.02	15.02	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_fliC	40	40	12.58	12.58	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_lasA	33	33	10.78	10.78	N
Virulence Factor	Enterobacter_aerogenes_GENE_trbG	24	24	10.62	10.62	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_clpV1	39	39	9.92	9.92	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_flgL	24	24	5.75	5.75	N
Virulence Factor	Bacteroides_fragilis_GENE_rteA	49	49	5.45	5.45	N

Microbial DNA free water.

Database	Organism	Unique Matches Frequency	Unique Matches	% Unique Matches	% Total Matches	Relative Abundance	Above_Threshold
Bacteria	Bacteroides_vulgatus_ATCC_8482	235163	7376	25.6	31.46	15.94	Y
Bacteria	Bacteroides_sp_3_1_40A	41098	2899	19.66	13.93	7.813	Y
Bacteria	Bacteroides_uniformis_ATCC_8492	98060	6915	31.12	82.63	4.519	Y
Bacteria	Faecalibacterium_cf_prausnitzii_KLE1255	1874026	105177	58.68	59.77	6.71	Y
Bacteria	Bacteroides_eggerthii_DSM_20697	688558	24260	34.66	73.53	5.578	Y
Bacteria	Ruminococcus_bicirculans	1585034	73047	42.6	42.62	5.409	Y
Bacteria	Faecalibacterium_prausnitzii_M21_2	607678	23492	24.61	46.19	3.97	Y
Bacteria	Alistipes_putredinis_DSM_17216	893803	118128	68.13	68.13	3.782	Y
Bacteria	Bacteroides_dorei_isolate_HS1_L_1_B_010	102321	3152	9.27	16.03	1.667	Y
Bacteria	Ruminococcus_bromii_L2_63	466391	79375	55.39	55.38	2.521	Y
Bacteria	Bacteroides_massiliensis_B84634_Timone_84634_	267530	120570	61.24	61.49	1.811	Y
Bacteria	Phascolarctobacterium_sp_CAG_207	285291	102999	67.05	67.05	2.072	Y
Bacteria	Parabacteroides_sp_D25	121	28	14.07	46.07	1.347	Y
Bacteria	Parabacteroides_distasonis_str_3776_D15_i_1025	977	142	16.63	3.87	1.732	Y
Bacteria	Bacteroides_clarus_YIT_12056	277396	112295	57.04	57.04	1.724	Y
Bacteria	Alistipes_onderdonkii_WAL_8169_DSM_19147	193207	21370	26.45	42.78	1.654	Y
Bacteria	Ruminococcus_sp_5_1_39BFAA	49367	22877	30.44	33.5	1.606	Y
Bacteria	Blautia_wexlerae_DSM_19850	48992	23434	25.89	28.03	1.507	Y
Bacteria	Bacteroidales_bacterium_ph8	213018	94828	52.26	51.19	1.439	Y
Bacteria	Bacteroides_ovatus_CL03T12C18	31099	15812	25.14	29.64	1.215	Y
Bacteria	Bifidobacterium_stercoris_21370 Branch	1613	960	3.1	3.1	1.192	Y
Bacteria	Oscillibacter_sp_ER4	197475	66281	38.46	37.91	1.162	Y
Bacteria	Porphyromonas_sp_31_2	8271	2278	11.62	37.9	0.8415	Y
Bacteria	Roseburia_inulinivorans_DSM_16841	142984	71436	40.53	40.55	1.061	Y
Bacteria	Ruminococcus_obeum_ATCC_29174	114486	68370	41.74	41.74	1.049	Y
Bacteria	Eubacterium_hallii_DSM_3353	101122	60009	39.91	39.9	0.9729	Y
Bacteria	Alistipes_sp_AL_1	165901	13182	14.7	38.29	0.9636	Y
Bacteria	Bifidobacterium_adolescentis_strain_BBMN23	5318	2875	11.32	16.95	0.8801	Y
Bacteria	Bacteroides_salyersiae_CL02T12C01	53332	23770	30.74	60.81	0.8528	Y
Bacteria	Bacteroides_thetaiotaomicron_VPI_5482	35092	10485	21.8	57.34	0.8223	Y
Bacteria	Bacteroides_xylanisolvens_CL03T12C04	20541	11137	13.38	14.4	0.7779	Y

Microbial DNA free water.cont.

Bacteria	Parabacteroides_merdae_CL03T12C32	34118	17131	14.3	23.36	0.7802	Y
Bacteria	Candidatus_Bacteroides_timonensis_AP1	58693	24283	12.35	12.76	0.7533	Y
Bacteria	Bacteroides_fragilis_str_3725_D9_ii	128	46	6.57	30.03	0.3302	Y
Bacteria	Eubacterium_eligens_ATCC_27750	72875	35699	27.51	27.57	0.6791	Y
Bacteria	Lachnospiraceae_bacterium_5_1_63FAA	5178	3841	12.02	14.84	0.6669	Y
Bacteria	Bacteroides_sartorii_JCM_16497	12473	1154	1.05	1.84	0.3916	Y
Bacteria	butyrate_producing_bacterium_SSC_2	247	204	3.36	3.85	0.6094	Y
Bacteria	Bacteroides_cellulosilyticus_CL02T12C19	32150	12440	11.92	14.25	0.601	Y
Bacteria	Eubacterium_biforme_DSM_3989	50302	30397	25.31	25.31	0.5764	Y
Bacteria	Alistipes_shahii_WAL_8301	63885	38643	20.79	20.45	0.5418	Y
Bacteria	Catenibacterium_mitsuokai_DSM_15897	62975	25800	19.59	19.59	0.5076	Y
Bacteria	Anaerostipes_hadrus_DSM_3319	2286	1651	6.2	9.47	0.471	Y
Bacteria	Collinsella_sp_4_8_47FAA	23874	16006	12.69	12.69	0.4395	Y
Bacteria	Collinsella_aerofaciens_ATCC_25986	23311	15673	11.45	11.45	0.4095	Y
Bacteria	Dorea_longicatena_AGR2136	34572	25357	16.89	16.92	0.4059	Y
Bacteria	Dorea_formicigenerans_ATCC_27755	8810	6052	8.84	8.83	0.3743	Y
Bacteria	Bifidobacterium_sp_12_1_47BFAA	87	78	1.04	1.04	0.362	Y
Bacteria	Bilophila_wadsworthia_ATCC_49260	19977	12527	13.26	37.62	0.3558	Y
Bacteria	Bifidobacterium_longum_subsp_longum_7_1B	190	165	6.49	8.18	0.3165	Y
Bacteria	Butyricimonas_virosa_DSM_23226	51881	23970	12.17	12.4	0.2975	Y
Bacteria	Oscillospiraceae_bacterium_VE202_24	12840	9432	12.97	30.35	0.2816	Y
Bacteria	Blautia_sp_KLE_1732	7940	5228	6.65	6.64	0.2798	Y
Bacteria	Clostridium_sp_SS2_1	508	381	6.01	16.19	0.2592	Y
Bacteria	Roseburia_intestinalis_XB6B4	9220	4753	8.77	17.85	0.2524	Y
Bacteria	Subdoligranulum_sp_4_3_54A2FAA	26803	23384	11.89	11.89	0.2393	Y
Bacteria	Enterococcus_faecium_4290 Branch	590	478	19.1	18.72	0.2387	Y
Bacteria	Roseburia_hominis_A2_183	26436	20407	10.38	10.38	0.2287	Y
Bacteria	Clostridiales_bacterium_VE202_14	20446	18677	10.31	10.31	0.2002	Y
Bacteria	Peptoclostridium_difficile_Y358	643	103	14.17	12.05	0.1473	Y
Bacteria	Dorea_sp_AGR2135	2581	1649	3.28	6.1	0.1438	Y
Bacteria	Coprococcus_catus_GD_7	15172	12707	7.41	7.41	0.1423	Y
Bacteria	Bilophila_sp_4_1_30	13601	8926	5.82	29.13	0.1322	Y
Bacteria	Bacteroides_stercorirosoris_JCM_17103	19541	7800	3.96	5.58	0.132	Y

Microbial DNA free water.cont.

Bacteria	Intestinimonas_butyriciproducens	13697	12594	6.4	6.74	0.1248	Y
Bacteria	Christensenella_timonensis_Marseille_P2437	38853	2144	1.19	1.32	0.1202	Y
Bacteria	Bacteroides_intestinalis_DSM_17393	10947	4190	2.13	3.89	0.1143	Y
Bacteria	Flavonifractor_plautii_ATCC_29863	3023	2458	4.65	26.84	0.1097	Y
Bacteria	Bifidobacterium_pseudocatenulatum_IPLA36007	2776	2322	5.68	9.03	0.1096	Y
Bacteria	Acidaminococcus_14354 Branch	15	13	3.78	5.4	0.09331	Y
Bacteria	Bacteroides_rodentium_JCM_16496	11631	2577	1.31	20.87	0.06034	Y
Bacteria	Haemophilus_parainfluenzae_T3T1	2730	2418	2.91	2.94	0.08172	Y
Bacteria	Tyzzerella_nexilis_DSM_1787	23318	2446	1.59	1.69	0.07346	Y
Bacteria	Eubacterium_ventriosum_ATCC_27560	5895	4900	3.75	3.86	0.06474	Y
Bacteria	Parabacteroides_1355 Branch	2485	2283	1.35	2.31	0.0647	Y
Bacteria	Clostridium_orbiscindens_1_3_50AFAA	1718	1345	2.73	26.76	0.06178	Y
Bacteria	Blautia_hydrogenotrophica_DSM_10507	6675	6275	3.37	3.37	0.05787	Y
Bacteria	Bifidobacterium_ruminantium	106	52	4.06	0.39	0.0565	Y
Bacteria	Acidaminococcus_sp_BV3L6	773	609	2.37	5.02	0.05162	Y
Bacteria	Clostridium_clostridioforme_90A7	1212	1140	1.36	2.43	0.04182	Y
Bacteria	Prevotella_bivia_DNF00650	2357	71	0.5	0.07	0.04551	Y
Bacteria	Bacteroides_oleiciplenus_YIT_12058	7835	2950	1.5	2.26	0.044	Y
Bacteria	Bacteroides_caccae_CL03T12C61	5230	1607	2.55	3.62	0.04371	Y
Bacteria	Intestinibacter_bartlettii_DSM_16795	1455	1342	2.07	2.07	0.04104	Y
Bacteria	Clostridium_bolteae_90A9	1020	326	3.92	2.35	0.03737	Y
Bacteria	Bifidobacterium_catenulatum_DSM_16992_JCM_1	1663	948	1.24	1.24	0.03905	Y
Bacteria	Clostridiales_Order_18 2469_26631 Branch	681	224	0.17	0.18	0.01398	Y
Bacteria	Eubacterium_rectale_DSM_17629	5893	1387	2.79	3.22	0.03834	Y
Bacteria	Prevotella_sp_P4_76	3759	99	0.35	0.19	0.03824	Y
Bacteria	Clostridium_citroniae_WAL_17108	4559	4357	2.21	2.25	0.03747	Y
Bacteria	Bacteroides_stercoris_ATCC_43183	7183	1211	1.54	1.32	0.03589	Y
Bacteria	Prevotella_tannerae_ATCC_51259	15915	570	0.35	0.35	0.03579	Y
Bacteria	Senegalimassilia_anaerobia_JC110	3771	3549	2.22	2.22	0.03573	Y
Bacteria	Christensenella_minuta_DSM22607	15506	1025	0.55	0.68	0.03378	Y
Bacteria	Ruminococcus_gnavus_ATCC_29149	1035	626	1.68	1.69	0.02982	Y
Bacteria	Alistipes_finegoldii_DSM_17242	5628	791	0.92	0.69	0.02962	Y
Bacteria	Butyrivibrio_crossotus_DSM_2876	5370	1429	1.04	1.23	0.02605	Y

Microbial DNA free water.cont.

Bacteria	Anaerotruncus_colihominis_DSM_17241	3605	1091	1.86	1.39	0.02567	Y
Bacteria	Streptococcus_sp_I_P16	629	604	1.5	2.36	0.02524	Y
Bacteria	Parabacteroides_goldsteinii_CL02T12C30	2568	1993	1.32	2.35	0.02522	Y
Bacteria	Ruminococcus_albus_8	13513	511	0.26	0.26	0.02474	Y
Bacteria	Ruminococcus_torques_L2_14	4194	1870	1.29	1.29	0.02441	Y
Bacteria	Alistipes_timonensis_JC136	9209	1415	0.74	0.74	0.02414	Y
Bacteria	Bacteroides_finegoldii_DSM_17565	6354	1279	0.82	0.6	0.02223	Y
Bacteria	Alistipes_senegalensis_JC50	7920	1374	0.7	0.71	0.02103	Y
Bacteria	Eubacterium_sp_3_1_31	2382	1186	1.5	1.51	0.0191	Y
Bacteria	Subdoligranulum_variabile_DSM_15176	5209	1784	0.91	0.92	0.01909	Y
Bacteria	Clostridium_asparagiforme_DSM_15981	1742	1564	1.01	1.72	0.01883	Y
Bacteria	Parabacteroides_johnsonii_DSM_18315	4332	1635	1.77	15.65	0.01879	Y
Bacteria	Holdemania_massiliensis_AP2	2182	2103	1.23	1.23	0.01867	Y
Bacteria	Barnesiella_viscericola_DSM_18177	9382	661	0.34	0.35	0.01853	Y
Bacteria	Ruminococcus_lactaris_CC59_002D	876	407	1.05	0.52	0.01851	Y
Bacteria	Bacteroides_faecis_MAJ27	5298	1651	0.84	8.45	0.01833	Y
Bacteria	Ruminococcaceae_bacterium_D16	5601	1404	0.75	0.78	0.01804	Y
Bacteria	Ruminococcus_flavefaciens_FD_1	9024	503	0.26	0.26	0.01682	Y
Bacteria	Pseudoflavonifractor_capillosus_ATCC_29799	2803	2021	1.03	1.03	0.01659	Y
Bacteria	Pseudomonas_aeruginosa_38657 Branch	16	16	2.66	2.66	0.01506	Y
Bacteria	Bacteroides_acidifaciens_JCM_10556	7439	629	0.32	0.38	0.01498	Y
Bacteria	Coprococcus_comes_ATCC_27758	2946	1237	0.76	0.8	0.014	N
Bacteria	Bacteroides_coprocola_DSM_17136	7209	486	0.25	0.26	0.01368	N
Bacteria	Clostridium_cf_saccharolyticum_K10	2141	893	1.5	0.53	0.01366	N
Bacteria	Ruminococcus_champanellensis_18P13_JCM_170	3447	1204	0.67	0.67	0.01321	N
Bacteria	Prevotella_988 Branch	833	28	0.03	0.02	0.01185	N
Bacteria	Bacteroides_pectinophilus_ATCC_43243	3385	880	0.58	0.75	0.01289	N
Bacteria	Eubacterium_ramulus_ATCC_29099	3661	1040	0.58	0.6	0.0126	N
Bacteria	Clostridium_hathewayi_DSM_13479	2176	1512	0.77	0.93	0.01208	N
Bacteria	Erysipelotrichaceae_bacterium_6_1_45	2630	333	1.02	0.97	0.01188	N
Bacteria	Kandleria_vitulina_42625 Branch	81	27	0.04	0.04	0.008502	N
Bacteria	Bacteroides_barnesiae_DSM_18169_JCM_13652	6168	404	0.2	0.22	0.01133	N
Bacteria	Bacteroides_nordii_WAL_11050_JCM_12987	2721	172	0.22	0.48	0.01107	N

Microbial DNA free water.cont.

Bacteria	Eubacterium_desmolans_ATCC_43058	2559	1174	0.62	0.62	0.01091	N
Bacteria	Eubacterium_siraeum_V10Sc8a	1798	473	0.53	0.54	0.01076	N
Bacteria	Bacteroides_plebeius_DSM_17135	4698	678	0.34	0.34	0.01074	N
Bacteria	Veillonella_sp_oral_taxon_158_str_F0412	979	955	0.74	0.87	0.01002	N
Bacteria	Fusobacterium_varium_ATCC_27725	789	770	0.77	0.76	0.01001	N
Bacteria	Bacteroides_gallinarum_DSM_18171_JCM_13658	3956	729	0.37	0.37	0.009873	N
Bacteria	Blautia_hansenii_DSM_20583	1012	228	0.5	0.3	0.009766	N
Bacteria	Clostridium_symbiosum_WAL_14673	462	179	0.69	0.61	0.009703	N
Bacteria	Streptococcus_salivarius_M18	235	227	0.89	1.69	0.009547	N
Bacteria	Prevotella_copri_DSM_18205	5357	210	0.11	0.12	0.009064	N
Bacteria	Citrobacter_freundii_UCI_32	565	561	0.72	0.85	0.008937	N
Bacteria	Veillonella_dispar_ATCC_17748	823	802	0.64	0.78	0.008462	N
Bacteria	Prevotella_stercorea_DSM_18206	4981	257	0.13	0.14	0.008448	N
Bacteria	Bacteroides_coprophilus_DSM_18228_JCM_13818	4809	259	0.13	0.13	0.008196	N
Bacteria	Odoribacter_splanchnicus_DSM_20712	4904	214	0.11	0.11	0.008071	N
Bacteria	Eubacterium_dolichum_DSM_3991	1210	598	0.51	0.51	0.007845	N
Bacteria	Coprobacillus_sp_8_2_54BFAA	462	80	0.39	0.38	0.007708	N
Bacteria	Odoribacter_laneus_YIT_12061	3989	242	0.12	0.12	0.006918	N
Bacteria	Rikenella_microfusus_DSM_15922	3169	396	0.22	0.23	0.006913	N
Bacteria	Clostridium_innocuum	1273	146	0.23	0.23	0.006824	N
Bacteria	Anaerofustis_stercorihominis_DSM_17244	635	631	0.54	0.54	0.006772	N
Bacteria	Streptococcus_agalactiae_MRI_Z1_039	25	25	1.37	1.11	0.006715	N
Bacteria	Bacteroides_salanitronis_DSM_18170	3409	330	0.17	0.17	0.006449	N
Bacteria	Blautia_producta	1041	815	0.41	0.43	0.005774	N
Bacteria	Tannerella_sp_6_1_58FAA_CT1	1045	220	0.28	0.29	0.005726	N
Bacteria	Klebsiella_pneumoniae_MGH_34763 Branch	21	21	0.9	1.4	0.005534	N
Bacteria	Clostridium_methylpentosum_DSM_5476	922	774	0.39	0.39	0.005344	N
Bacteria	Prevotella_disiens_DNF00882	868	30	0.08	0.08	0.005122	N
Bacteria	Paraprevotella_xylaniphila_YIT_11841	2578	313	0.16	0.14	0.005066	N
Bacteria	Parabacteroides_gordonii_DSM_23371	2073	433	0.22	0.39	0.005024	N
Bacteria	Clostridium_butyricum_27022 Branch	22	16	0.04	0.04	0.003547	N
Bacteria	Bacteroides_paurosaccharolyticus_JCM_15092	1347	436	0.26	0.26	0.004647	N
Bacteria	Propionibacterium_20956 Branch	18	18	0.15	0.12	0.004189	N

Microbial DNA free water.cont.

Bacteria	Butyricicoccus_pullicaecorum_1_2	959	575	0.29	0.3	0.004206	N
Bacteria	Bifidobacterium_kashiwanohense_PV20_2	467	399	0.34	0.42	0.004184	N
Bacteria	Bifidobacterium_bifidum_21470 Branch	17	14	0.02	0.02	0.001683	N
Bacteria	Catonella_morbi_ATCC_51271	896	374	0.24	0.24	0.00374	N
Bacteria	Coprococcus_sp_ART55_1	738	352	0.25	0.27	0.00355	N
Bacteria	Streptococcus_parasanguinis	136	132	0.37	0.53	0.003546	N
Bacteria	Actinomyces_sp_ICM47	505	495	0.29	0.29	0.003522	N
Bacteria	Firmicutes_bacterium_ASF500	594	434	0.24	0.24	0.003077	N
Bacteria	Alloprevotella_rava_F0323	1853	70	0.04	0.04	0.003071	N
Bacteria	Bifidobacterium_angulatum_21376 Branch	441	278	0.19	0.19	0.002949	N
Bacteria	Bacteroides_pyogenes_JCM_10003	200	64	0.22	0.14	0.002873	N
Bacteria	bacterium_LF_3	479	250	0.21	0.21	0.002833	N
Bacteria	Streptococcus_australis_ATCC_700641	213	210	0.26	0.3	0.002762	N
Bacteria	Bacteroides_faecichinchillae_JCM_17102	1326	217	0.11	0.19	0.002661	N
Bacteria	Lactobacillus_ruminis_ATCC_25644	332	50	0.13	0.09	0.002595	N
Bacteria	Hallella_seregens_ATCC_51272	768	29	0.04	0.02	0.002427	N
Bacteria	Streptococcus_suis_EA1832_92	501	198	0.17	0.17	0.002401	N
Bacteria	Bacteroides_fluxus_YIT_12057	1001	247	0.13	0.41	0.002374	N
Bacteria	Clostridium_scindens_ATCC_35704	150	96	0.22	0.19	0.002235	N
Bacteria	Faecalitalea_cylindroides_ATCC_27803	175	101	0.19	0.13	0.002105	N
Bacteria	Sharpea_azabuensis_DSM_18934	647	153	0.12	0.12	0.002095	N
Bacteria	Lachnospira_multipara_ATCC_19207	639	148	0.11	0.26	0.002063	N
Bacteria	Clostridium_celatum_DSM_1785	302	208	0.18	0.47	0.00206	N
Bacteria	Bacteroides_helcogenes_P_36_108	1050	172	0.09	0.09	0.002031	N
Bacteria	Kluyvera_ascorbata_ATCC_33433	346	340	0.17	0.17	0.001987	N
Bacteria	Coprococcus_eutactus_ATCC_27759	706	144	0.1	0.15	0.001907	N
Bacteria	Haemophilus_haemolyticus_HK386	95	75	0.19	0.17	0.001716	N
Bacteria	Cellulomonas_carbonis_T26	811	124	0.07	0.07	0.001707	N
Bacteria	Marvinbryantia_formatexigens_DSM_14469	531	225	0.12	0.12	0.001621	N
Bacteria	Holdemania_filiformis_DSM_12042	494	199	0.11	0.11	0.001583	N
Bacteria	Clostridium_saccharolyticum_WM1	511	205	0.11	0.11	0.001514	N
Bacteria	Clostridiales_genomosp_BVAB3_str_27783 Branch	326	62	0.07	0.07	0.001403	N
Bacteria	Escherichia_coli_32006 Branch	17	17	0.23	0.27	0.001471	N

Microbial DNA free water.cont.

Bacteria	Solobacterium_moorei_F0204	145	71	0.13	0.08	0.001414	N
Bacteria	Anaerostipes_sp_3_2_56FAA	93	85	0.15	0.16	0.001363	N
Bacteria	Clostridium_aminophilum_DSM_10710	482	182	0.09	0.09	0.001331	N
Bacteria	bacterium_OL_1	263	193	0.12	0.12	0.001312	N
Bacteria	Butyricimonas_synergistica_DSM_23225	443	182	0.09	0.41	0.001281	N
Bacteria	Anaerotruncus_sp_G32012	406	184	0.1	0.1	0.001272	N
Bacteria	Prevotella_melaninogenica_DNF00666	285	83	0.09	0.07	0.001261	N
Bacteria	Prevotella_bergensis_DSM_17361	468	171	0.09	0.09	0.001254	N
Bacteria	Oscillibacter_ruminantium_GH1	355	198	0.1	0.12	0.001247	N
Bacteria	Eubacterium_limosum_KIST612	228	208	0.11	0.1	0.0012	N
Bacteria	Phascolarctobacterium_succinatutens_CAG_287	633	34	0.03	0.04	0.001187	N
Bacteria	Streptococcus_pleomorphus_DSM_20574	268	102	0.09	0.09	0.001139	N
Bacteria	Clostridium_leptum_DSM_753	427	145	0.08	0.08	0.001126	N
Bacteria	Klebsiella_35336 Branch	53	51	0.08	0.08	0.001059	N
Bacteria	Johnsonella_ignava_ATCC_51276	217	118	0.09	0.09	0.001066	N
Bacteria	Collinsella_stercoris_DSM_13279	231	154	0.09	0.09	0.001048	N
Bacteria	Enterobacter_28635 Branch	78	77	0.06	0.06	0.001032	N
Bacteria	Oribacterium_sinus_F0268	156	133	0.1	0.1	0.001008	N
Bacteria	Bifidobacterium_breve_HPH0326	26	20	0.15	0.15	0.0009668	N
Bacteria	Negativicoccus_succinicivorans_DORA_17_25	73	66	0.11	0.11	0.0009493	N
Bacteria	Clostridium_perfringens_SM101	42	42	0.13	0.18	0.0009484	N
Bacteria	Dialister_succinatiphilus_YIT_11850	155	133	0.09	0.09	0.0009179	N
Bacteria	Prevotella_multisaccharivorax_DSM_17128	712	40	0.02	0.02	0.0009034	N
Bacteria	Clostridium_saccharogumia_DSM_17460	126	88	0.09	0.09	0.0008725	N
Bacteria	Peptostreptococcus_stomatis_DSM_17678	99	99	0.09	0.1	0.0008692	N
Bacteria	Haemophilus_sputorum_CCUG_13788	29	28	0.13	0.26	0.000865	N
Bacteria	Porphyromonas_cangingivalis_strain_COT_109_OH	187	13	0.03	0.03	0.0008131	N
Bacteria	Pediococcus_5758 Branch	32	32	0.08	0.08	0.0007383	N
Bacteria	Shuttleworthia_sp_MSX8B	112	44	0.07	0.05	0.0007842	N
Bacteria	Paraprevotella_clara_YIT_11840	276	123	0.06	0.06	0.0007751	N
Bacteria	Enterococcus_gilvus_ATCC_BAA_350	255	127	0.06	0.06	0.0007697	N
Bacteria	Clostridium_27666 Branch	75	37	0.05	0.05	0.0006614	N
Bacteria	Peptostreptococcus_sp_MV1	197	56	0.06	0.06	0.0007579	N

Microbial DNA free water.cont.

Bacteria	Selenomonas_bovis_14321 Branch	65	34	0.05	0.05	0.0005958	N
Bacteria	Enterobacter_cloacae_strain_Ecl1	26	26	0.11	0.39	0.0007409	N
Bacteria	Prevotella_baroniae_1366 Branch	239	32	0.02	0.02	0.0006029	N
Bacteria	Prevotella_bryantii_B14	256	15	0.02	0.01	0.0007167	N
Bacteria	Veillonella_atypica_ACS_134_V_Col7a	34	34	0.1	0.32	0.0007072	N
Bacteria	Lactobacillus_5619 Branch	14	14	0.06	0.06	0.0006345	N
Bacteria	Haemophilus_pittmaniae_HK_85	99	92	0.08	0.11	0.0007025	N
Bacteria	Eggerthella_lenta_1_1_60AFAA	53	29	0.09	0.07	0.0007002	N
Bacteria	Megasphaera_sp_14257 Branch	251	83	0.05	0.05	0.0006941	N
Bacteria	Butyrivibrio_fibrisolvens_27746 Branch	74	14	0.02	0.02	0.0005765	N
Bacteria	Citrobacter_sp_30_2	64	62	0.08	0.5	0.0006891	N
Bacteria	Eubacterium_sulci_ATCC_35585	77	75	0.08	0.08	0.0006872	N
Bacteria	Bacteroidaceae_bacterium_MS4	406	67	0.03	0.03	0.0006657	N
Bacteria	Gemella_sanguinis_M325	42	42	0.09	0.11	0.0006618	N
Bacteria	Olsenella_sp_oral_taxon_809_str_F0356	117	104	0.07	0.07	0.0006538	N
Bacteria	Collinsella_intestinalis_DSM_13280	156	85	0.06	0.06	0.0006454	N
Bacteria	Lachnoanaerobaculum_sp_OBRC5_5	63	48	0.08	0.05	0.0006428	N
Bacteria	Prevotella_dentasini_JCM_15908	456	42	0.02	0.02	0.0006317	N
Bacteria	Atopobium_sp_ICM58	78	76	0.07	0.07	0.0006305	N
Bacteria	Oribacterium_27619 Branch	31	26	0.05	0.07	0.0005359	N
Bacteria	Bifidobacterium_dentium_21436 Branch	21	21	0.1	0.1	0.0006263	N
Bacteria	Eubacterium_plexicaudatum_ASF492	239	100	0.05	0.05	0.0006247	N
Bacteria	Prevotella_corporis_DSM_18810_JCM_8529	410	33	0.02	0.02	0.0006018	N
Bacteria	Bacteroides_graminisolvens_DSM_19988_JCM_15	429	48	0.02	0.03	0.0006018	N
Bacteria	Oribacterium_parvum_ACB_27622 Branch	106	61	0.06	0.06	0.0005937	N
Bacteria	Streptococcus_vestibularis_ATCC_49124	20	20	0.1	0.26	0.0005876	N
Bacteria	Oscillibacter_valericigenes_Sjm18_20	194	102	0.05	0.08	0.0005792	N
Bacteria	Bifidobacterium_merycicum_21467 Branch	118	97	0.06	0.06	0.0005753	N
Bacteria	Prevotella_timonensis_S9_PR14	200	41	0.04	0.03	0.0005688	N
Bacteria	Gordonibacter_pamelaeae_7_10_1_b	124	105	0.06	0.06	0.0005659	N
Bacteria	Prevotella_buccalis_ATCC_35310	405	24	0.02	0.02	0.0005631	N
Bacteria	Porphyromonadaceae_bacterium_OUH_334697	57	16	0.06	0.06	0.0005592	N
Bacteria	Lachnospiraceae_oral_taxon_107_str_F0167	178	57	0.04	0.04	0.0005485	N

Microbial DNA free water.cont.

Bacteria	Streptococcus_infantis_ATCC_700779	33	32	0.08	0.08	0.0005445	N
Bacteria	Rothia_mucilaginosa_DY_18	74	74	0.06	0.12	0.0005441	N
Bacteria	Bifidobacterium_saeculare_DSM_6531_LMG_1493	124	33	0.04	0.04	0.000512	N
Bacteria	Citrobacter_28747 Branch	25	25	0.08	0.08	0.0005081	N
Bacteria	Terrisporobacter_sp_08_306576	81	74	0.06	0.06	0.0005061	N
Bacteria	Pseudobutyrivibrio_27608 Branch	29	14	0.04	0.04	0.0004142	N
Bacteria	Lactobacillus_salivarius_CECT_5713	13	13	0.1	0.05	0.0005059	N
Bacteria	Actinomyces_odontolyticus_21164 Branch	36	34	0.05	0.05	0.0004422	N
Bacteria	Coprobacter_fastidiosus_NSB1	128	23	0.03	0.03	0.0004771	N
Bacteria	Lachnobacterium_bovis_C6A12	17	12	0.08	0.04	0.0004601	N
Bacteria	Prevotella_oralis_CC98A	207	24	0.02	0.01	0.0004583	N
Bacteria	Collinsella_tanakaei_YIT_12063	103	81	0.05	0.05	0.0004414	N
Bacteria	Succinispira_mobilis_DSM_6222	157	37	0.03	0.03	0.0004415	N
Bacteria	Bacteroides_reticulotermitis_JCM_10512	275	49	0.03	0.03	0.0004333	N
Bacteria	Enorma_massiliensis_phI	127	63	0.04	0.04	0.0004214	N
Bacteria	Haemophilus_sp_oral_taxon_851_str_F0397	28	27	0.06	0.07	0.0004129	N
Bacteria	Clostridium_spiroforme_DSM_1552	65	52	0.05	0.05	0.000405	N
Bacteria	Oribacterium_sp_oral_taxon_078_str_F0263	56	39	0.05	0.04	0.0003927	N
Bacteria	Ruminococcus_gauvreauii_DSM_19829	132	76	0.04	0.04	0.0003934	N
Bacteria	Lachnoanaerobaculum_saburreum_DSM_3986	75	27	0.04	0.03	0.0003706	N
Bacteria	Sutterella_wadsworthensis_2_1_59BFAA	197	36	0.02	0.03	0.0003643	N
Bacteria	Acidaminococcus_fermentans_DSM_20731	134	50	0.03	0.08	0.0003551	N
Bacteria	Peptostreptococcaceae_bacterium_VA2	56	51	0.04	0.06	0.0003383	N
Bacteria	Bacteroides_propionicifaciens_DSM_1333 Branch	16	12	0.01	0.01	0.0003384	N
Bacteria	Porphyromonas_bennonis_DSM_23058_JCM_1633	97	42	0.03	0.03	0.0003322	N
Bacteria	Veillonella_parvula_ACS_068_V_Sch12	17	17	0.05	0.18	0.0003207	N
Bacteria	Citrobacter_werkmanii_NBRC_105721	68	67	0.04	0.07	0.0003124	N
Bacteria	Prevotella_scopos_JCM_17725	246	18	0.01	0.01	0.0003131	N
Bacteria	Enterobacter_sp_5_4	14	14	0.06	0.44	0.0003057	N
Bacteria	Candidatus_Soleaferrea_massiliensis_AP7	101	63	0.03	0.03	0.0003044	N
Bacteria	Burkholderiales_Order_15 6184 Node_25062	147	25	0.02	0.02	0.0003049	N
Bacteria	Prevotella_denticola_1011 Branch	101	12	0.01	0.01	0.0002745	N
Bacteria	Butyrivibrio_sp_27738 Branch	62	25	0.02	0.02	0.0002292	N

Microbial DNA free water.cont.

Bacteria	Porphyromonas_asaccharolytica_780 Branch	52	17	0.02	0.02	0.0002511	N
Bacteria	Prevotella_brevis_ATCC_19188	167	18	0.01	0.02	0.0002776	N
Bacteria	Prevotella_falsenii_DSM_22864_JCM_15124	226	16	0.01	0.01	0.0002587	N
Bacteria	Aggregatibacter_segnis_ATCC_33393	43	38	0.03	0.03	0.0002533	N
Bacteria	Olsenella_uli_MSTE5	30	19	0.04	0.05	0.0002508	N
Bacteria	Clostridium_hylemonae_DSM_15053	115	47	0.02	0.03	0.0002518	N
Bacteria	Olsenella_profusa_F0195	64	51	0.03	0.03	0.0002384	N
Bacteria	Slackia_piriformis_YIT_12062	49	44	0.03	0.03	0.0002354	N
Bacteria	Clostridium_sordellii_26858 Branch	19	18	0.02	0.03	0.0002239	N
Bacteria	Clostridium_sporosphaeroides_DSM_1294	102	44	0.02	0.02	0.0002317	N
Bacteria	Clostridium_27788 Branch	67	38	0.02	0.02	0.0002206	N
Bacteria	Pseudobutyrivibrio_ruminis_AD2017	96	31	0.02	0.03	0.000227	N
Bacteria	Eubacterium_cellulosolvens_LD2006	80	47	0.03	0.03	0.0002236	N
Bacteria	Actinomyces_graevenitzii_F0530	33	33	0.03	0.07	0.0002222	N
Bacteria	Robinsoniella_27415 Branch	58	32	0.02	0.02	0.0001822	N
Bacteria	Campylobacter_hominis_ATCC_BAA_381	24	24	0.03	0.03	0.0002118	N
Bacteria	bacterium_MS4	126	32	0.02	0.02	0.0002068	N
Bacteria	Eubacterium_xylanophilum_ATCC_35991	95	24	0.02	0.02	0.0002059	N
Bacteria	Porphyromonas_somerae_DSM_23386	151	13	0.01	0.01	0.0002054	N
Bacteria	Atopobium_rimae_ATCC_49626	35	35	0.03	0.03	0.0002026	N
Bacteria	Atopobium_parvulum_DNF00906	20	20	0.03	0.03	0.0002001	N
Bacteria	Allobaculum_stercoricanis_DSM_13633	50	27	0.02	0.02	0.0001946	N

Virus	Shigella_phage_SfIV	134	134	1.54	1.81	30.23	Y
Virus	Pseudomonas_phage_Pf1	42	42	1.64	1.64	19.83	N
Virus	Enterobacteria_phage_YYZ_2008	109	109	1.78	1.78	18.26	N
Virus	Stx2_converting_phage_1717	70	70	0.9	0.76	12.3	N
Virus	Streptococcus_phage_20617	114	114	0.58	0.58	8.829	N
Virus	Propionibacterium_phage_P105	24	24	0.68	0.69	7.115	N
Virus	Escherichia_phage_TL_2011b	41	41	0.29	0.21	3.441	N

Microbial DNA free water.cont.

Respiratory Virus no calls detected above threshold

Fungi	Enterocytozoon_bieneusi_H348	57	37	0.17	0.17	100	N

Protist	Cyclospora_cayetanensis_strain_CHN_HEN01	919	22	0.03	0.03	100	Y

Antibiotic Resistance	Tetracycline_tet_32	1885	208	100	100		Y
Antibiotic Resistance	Macrolide_lnuB	146	16	100	100		Y
Antibiotic Resistance	Beta-lactam-resistance_blaOXA_347	15572	322	100	100		Y
Antibiotic Resistance	Beta-lactam_cfxA4	89	15	100	100		Y
Antibiotic Resistance	Beta-lactam_cfxA_2367 Branch	716	15	100	100		Y
Antibiotic Resistance	Aminoglycoside_aac6'_aph2''	103980	871	100	100		Y
Antibiotic Resistance	Aminoglycoside_aph3'_III	1277	359	99.45	99.45		Y
Antibiotic Resistance	Tetracycline_tet40	555	74	81.32	96.89		Y
Antibiotic Resistance	Plasmid-mediated-aminoglycoside-resistance_npm	838	336	96.83	96.83		Y
Antibiotic Resistance	Tetracycline_tetQ	216997	1854	96.21	96.21		Y
Antibiotic Resistance	Aminoglycoside_sat4A	15	10	100	95.68		Y
Antibiotic Resistance	beta_lactamase_CblA_1	5338	361	95.25	95.25		Y
Antibiotic Resistance	Aminoglycoside_aadA_2151 Branch	11	11	78.57	94.53		Y
Antibiotic Resistance	Dihydrofolate-reductase_dfrF	1822	250	94.34	94.34		Y
Antibiotic Resistance	Transporter-gene_lsaE	2935	766	92.74	92.74		Y
Antibiotic Resistance	Tetracycline_tet32	1565	307	74.33	90.85		Y
Antibiotic Resistance	Macrolide_ermF	39869	500	89.13	89.41		Y
Antibiotic Resistance	Sulphonamide_sul_2049 Branch	758	341	88.11	88.11		Y
Antibiotic Resistance	Macrolide_lnuC	1188	229	87.74	87.74		Y

Microbial DNA free water.cont.

Antibiotic Resistance	Phenicol_catP	27	15	53.57	85.32	Y
Antibiotic Resistance	Tetracycline_tetO	11758	705	81.13	81.13	Y
Antibiotic Resistance	Phenicol_cmlA_2475 Branch	34	20	100	77.93	Y
Antibiotic Resistance	Aminoglycoside_aph4_Ia	443	277	75.27	75.27	Y
Antibiotic Resistance	Aminoglycoside_aadA_2142 Branch	48	48	68.57	75	Y
Antibiotic Resistance	Aminoglycoside_aac3_IVa	375	209	74.11	74.11	Y
Antibiotic Resistance	Macrolide_ermB	47142	393	64.11	70.39	Y
Antibiotic Resistance	Tetracycline_tetW	59165	1139	69.66	69.66	Y
Antibiotic Resistance	Macrolide_mefB	557	349	60.8	60.8	Y
Antibiotic Resistance	Sulphonamide_sul2	8505	284	54.3	54.3	Y
Antibiotic Resistance	Tetracycline_tet44	2600	777	53.85	53.85	Y
Antibiotic Resistance	Aminoglycoside_a_2394 Branch	349	161	77.03	52.87	Y
Antibiotic Resistance	Tetracycline_tetX	15297	620	51.33	51.33	Y
Antibiotic Resistance	Aminoglycoside_aac6'_Im	114	112	42.75	42.75	Y
Antibiotic Resistance	Macrolide_ermG	193	193	39.63	39.63	N
Antibiotic Resistance	Tetracycline_tetBP	619	415	38.25	38.25	N
Antibiotic Resistance	Tetracycline_tetM	6833	1089	37.36	37.54	N
Antibiotic Resistance	Aminoglycoside_aph_2302 Branch	211	129	32.01	32.01	N
Antibiotic Resistance	Macrolide_mefA	10158	331	22.55	22.55	N
Antibiotic Resistance	Macrolide_ermQ	194	99	21.29	21.29	N
Antibiotic Resistance	Aminoglycoside_ant2''_Ia	41	37	71.15	15.29	N
Antibiotic Resistance	Phenicol_catB4	62	35	70	15.02	N
Antibiotic Resistance	Repressor_nalC	28	28	14.58	14.58	N
Antibiotic Resistance	Beta-lactam_cfxA6	2440	57	11.38	13.11	N
Antibiotic Resistance	Tetracycline_tetD	62	62	9.32	9.32	N
Antibiotic Resistance	Sensor-kinase_cpxA	69	49	8.86	8.86	N
Antibiotic Resistance	Beta-lactam-resistance_bla 244_1197_740 Branch	25	22	8.46	8.46	N
Antibiotic Resistance	MDR-Efflux-pump_mdtP	45	45	8.02	8.02	N
Antibiotic Resistance	Involved-in-polymyxin-resistance_pmrC	82	52	7.28	7.28	N
Antibiotic Resistance	Membrane-fusion-protein_emrK	33	33	6.51	6.51	N
Antibiotic Resistance	MDR-protein_mdtH	26	26	5.5	5.5	N

Microbial DNA free water.cont.

Virulence Factor	Bacteroides_fragilis_GENE_tetQ	142218	710	100	100	Y
Virulence Factor	Bacteroides_fragilis_GI_46242796	144678	1506	100	100	Y
Virulence Factor	Bacteroides_fragilis_GENE_rteA	110440	899	100	100	Y
Virulence Factor	Bacteroides_fragilis_GENE_exc	77579	745	100	100	Y
Virulence Factor	Bacteroides_fragilis_GENE_bmhA	85582	944	100	100	Y
Virulence Factor	Bacteroides_fragilis_GI_46242807	45665	493	100	100	Y
Virulence Factor	Bacteroides_fragilis_GENE_int	37792	348	100	100	Y
Virulence Factor	Bacteroides_fragilis_GENE_mobC	52717	765	100	100	Y
Virulence Factor	Bacteroides_fragilis_GENE_rteB	36881	454	100	100	Y
Virulence Factor	Bacteroides_fragilis_GI_46242797	34338	473	100	100	Y
Virulence Factor	Bacteroides_fragilis_GENE_mobB	30766	415	100	100	Y
Virulence Factor	Bacteroides_fragilis_GI_46242808	17673	135	100	100	Y
Virulence Factor	Bacteroides_fragilis_GI_46242805	19794	190	100	100	Y
Virulence Factor	Bacteroides_fragilis_GI_46242799	18284	170	100	100	Y
Virulence Factor	Bacteroides_fragilis_GI_46242810	12795	93	100	100	Y
Virulence Factor	Bacteroides_fragilis_GENE_rteC	16352	196	100	100	Y
Virulence Factor	Bacteroides_fragilis_GENE_mobA	13831	149	100	100	Y
Virulence Factor	Bacteroides_fragilis_GI_46242809	10771	121	100	100	Y
Virulence Factor	Bacteroides_fragilis_GI_46242811	8436	74	100	100	Y
Virulence Factor	Bacteroides_fragilis_GENE_rhuM	8144	95	100	100	Y
Virulence Factor	Bacteroides_fragilis_GENE_traA	9195	219	100	100	Y
Virulence Factor	Bacteroides_fragilis_GENE_traC	5725	125	100	100	Y
Virulence Factor	Bacteroides_fragilis_GENE_traF	3332	60	100	100	Y
Virulence Factor	Bacteroides_fragilis_GI_46242774	2773	263	100	100	Y
Virulence Factor	Vibrio_cholerae_GENE_intI1	16	13	100	100	Y
Virulence Factor	Proteus_mirabilis_GENE_tnpA	22	20	100	100	Y
Virulence Factor	Enterococcus_faecium_GENE_ermB	49002	351	100	100	Y
Virulence Factor	Enterococcus_faecium_GI_21886747	1893	27	100	100	Y
Virulence Factor	Enterococcus_faecium_GI_21886746	1906	56	100	100	Y
Virulence Factor	Parabacteroides_distasonis_GI_32395281	874	22	100	100	Y
Virulence Factor	Bacteroides_vulgatus_GI_33413459	3966	95	100	100	Y
Virulence Factor	Staphylococcus_aureus_GENE_AACA-APHD	66843	568	100	100	Y

Microbial DNA free water.cont.

Virulence Factor	Staphylococcus_aureus_GI_33390945	3968	66	100	100	Y
Virulence Factor	Bacteroides_thetaiotaomicron_GeneID_BTV3705	2403	143	100	100	Y
Virulence Factor	Bacteroides_thetaiotaomicron_GeneID_BTV1816	466	138	100	100	Y
Virulence Factor	Bacteroides_thetaiotaomicron_GeneID_BTV3502	304	85	100	100	Y
Virulence Factor	Enterococcus_faecium_GENE_sat4	354	164	99.39	99.39	Y
Virulence Factor	Bacteroides_fragilis_GI_37812496	35914	512	96.79	96.79	Y
Virulence Factor	Bacteroides_thetaiotaomicron_GeneID_BTV0319	326	150	96.77	96.77	Y
Virulence Factor	Bacteroides_fragilis_GENE_traB	5835	155	95.09	95.09	Y
Virulence Factor	Bacteroides_fragilis_GENE_traM	10910	401	92.61	92.61	Y
Virulence Factor	Bacteroides_fragilis_GENE_traI	5705	209	92.07	92.07	Y
Virulence Factor	Bacteroides_fragilis_GI_46242772	696	84	91.3	91.3	Y
Virulence Factor	Bacteroides_thetaiotaomicron_GeneID_BTV1572	301	185	89.81	89.81	Y
Virulence Factor	Bacteroides_fragilis_GENE_traE	3652	87	89.69	89.69	Y
Virulence Factor	Bacteroides_fragilis_GENE_traH	2214	103	89.57	89.57	Y
Virulence Factor	Bacteroides_thetaiotaomicron_GeneID_BTV0525	1720	848	89.17	89.17	Y
Virulence Factor	Bacteroides_fragilis_GENE_traD	10294	234	88.64	88.64	Y
Virulence Factor	Enterococcus_faecium_GI_21886752	1140	294	88.29	88.29	Y
Virulence Factor	Bacteroides_thetaiotaomicron_GeneID_BTV3480	351	133	88.08	88.08	Y
Virulence Factor	Bacteroides_uniformis_GI_436818	2631	201	87.77	87.77	Y
Virulence Factor	Bacteroides_fragilis_GENE_traJ	7180	310	84.93	84.93	Y
Virulence Factor	Bacteroides_fragilis_GENE_lys	4565	146	84.88	84.88	Y
Virulence Factor	Bacteroides_fragilis_GENE_traO	943	154	84.61	84.61	Y
Virulence Factor	Bacteroides_fragilis_GENE_traQ	4310	125	83.89	83.89	Y
Virulence Factor	Parabacteroides_distasonis_GI_32395282	4621	76	82.61	82.61	Y
Virulence Factor	Bacteroides_thetaiotaomicron_GeneID_BTV2148	603	337	82.4	82.4	Y
Virulence Factor	Bacteroides_fragilis_GENE_traP	1523	222	81.62	81.62	Y
Virulence Factor	Bacteroides_thetaiotaomicron_GeneID_BTV3482	1254	691	81.49	81.49	Y
Virulence Factor	Bacteroides_thetaiotaomicron_GeneID_BTV0526	472	353	81.34	81.34	Y
Virulence Factor	Bacteroides_thetaiotaomicron_GeneID_BTV3481	1273	568	80.8	80.8	Y
Virulence Factor	Bacteroides_thetaiotaomicron_GeneID_BTV2147	568	343	79.22	79.22	Y
Virulence Factor	Bacteroides_fragilis_GENE_yahA	1986	86	78.9	78.9	Y
Virulence Factor	Bacteroides_thetaiotaomicron_GeneID_BTV0320	329	232	78.11	78.11	Y
Virulence Factor	Streptococcus_pyogenes_GI_52345264	3093	268	77.01	77.01	Y

Microbial DNA free water.cont.

Virulence Factor	Bacteroides_fragilis_GENE_traN	9884	219	75.78	75.78	Y
Virulence Factor	Bacteroides_thetaiotaomicron_GeneID_BTV1573	838	400	75.33	75.33	Y
Virulence Factor	Bacteroides_thetaiotaomicron_GeneID_BTV0318	728	369	73.36	73.36	Y
Virulence Factor	Bacteroides_thetaiotaomicron_GeneID_BTV3476	1600	711	72.92	72.92	Y
Virulence Factor	Bacteroides_fragilis_GENE_traG	20058	643	71.84	71.84	Y
Virulence Factor	Bacteroides_fragilis_GENE_traK	5827	139	71.28	71.28	Y
Virulence Factor	Bacteroides_thetaiotaomicron_GeneID_BTV0528	286	175	70.85	70.85	Y
Virulence Factor	Bacteroides_thetaiotaomicron_GeneID_BTV2143	732	397	70.26	70.26	Y
Virulence Factor	Bacteroides_thetaiotaomicron_GeneID_BTV2145	1368	619	69.94	69.94	Y
Virulence Factor	Bacteroides_thetaiotaomicron_GeneID_BTV1815	309	182	67.66	67.66	Y
Virulence Factor	Bacteroides_fragilis_GENE_traL	1561	54	66.67	66.67	Y
Virulence Factor	Bacteroides_thetaiotaomicron_GeneID_BTV4099	1190	527	65.63	65.63	Y
Virulence Factor	Bacteroides_thetaiotaomicron_GeneID_BTV3246	1320	511	64.03	64.03	Y
Virulence Factor	Enterobacter_aerogenes_GENE_tniA	452	284	63.25	63.25	Y
Virulence Factor	Bacteroides_thetaiotaomicron_GeneID_BTV2144	178	136	58.87	58.87	Y
Virulence Factor	Bacteroides_thetaiotaomicron_GeneID_BTV1571	152	72	58.54	58.54	Y
Virulence Factor	Bacteroides_thetaiotaomicron_GeneID_BTV1809	821	456	58.24	58.24	Y
Virulence Factor	Bacteroides_thetaiotaomicron_GeneID_BTV4098	429	207	55.8	55.8	Y
Virulence Factor	Bacteroides_thetaiotaomicron_GeneID_BTV3244	536	233	55.08	55.08	Y
Virulence Factor	Enterococcus_faecium_GENE_aadE	419	189	53.54	53.54	Y
Virulence Factor	Bacteroides_thetaiotaomicron_GeneID_BTV3490	262	119	52.89	52.89	Y
Virulence Factor	Enterococcus_faecium_GI_21886751	668	191	51.76	51.76	Y
Virulence Factor	Bacteroides_thetaiotaomicron_GeneID_BTV2038	523	225	51.02	51.02	Y
Virulence Factor	Bacteroides_thetaiotaomicron_GeneID_BTV3245	173	112	50.68	50.68	Y
Virulence Factor	Bacteroides_thetaiotaomicron_GeneID_BTV1810	170	83	49.4	49.4	Y
Virulence Factor	Bacteroides_thetaiotaomicron_GeneID_BTV2146	859	335	48.48	48.48	Y
Virulence Factor	Bacteroides_thetaiotaomicron_GeneID_BTV1813	475	276	48.25	48.25	Y
Virulence Factor	Bacteroides_thetaiotaomicron_GeneID_BTV1811	113	62	47.69	47.69	Y
Virulence Factor	Bacteroides_thetaiotaomicron_GeneID_BTV4100	41	41	47.13	47.13	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_intI1	24	23	46	46	Y
Virulence Factor	Bacteroides_thetaiotaomicron_GeneID_BTV1812	243	133	41.3	41.3	Y
Virulence Factor	Bacteroides_thetaiotaomicron_GeneID_BTV0527	201	110	39.43	39.43	N
Virulence Factor	Streptococcus_pyogenes_GENE_mefA	5549	189	39.05	39.05	N

Microbial DNA free water.cont.

Virulence Factor	Bacteroides_thetaiotaomicron_GeneID_BTV1214	146	100	35.97	35.97	N
Virulence Factor	Bacteroides_thetaiotaomicron_GeneID_BTV1213	322	161	33.54	33.54	N
Virulence Factor	Bacteroides_thetaiotaomicron_GeneID_BTV1814	391	157	28.34	28.34	N
Virulence Factor	Enterococcus_faecalis_GI_8100672	66	29	26.85	26.85	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_pilP	52	44	26.83	26.83	N
Virulence Factor	Bacteroides_fragilis_GI_46242769	389	38	25.68	25.68	N
Virulence Factor	Pseudomonas_aeruginosa_GeneID_PA0080	20	20	24.69	24.69	N
Virulence Factor	Enterococcus_faecalis_GI_48190	651	141	22.35	22.35	N
Virulence Factor	Streptococcus_pyogenes_GI_52345271	36	36	20.69	20.69	N
Virulence Factor	Klebsiella_oxytoca_GI_4775482	50	50	18.45	18.45	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_tnpA	614	337	15.81	15.81	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_lasR	29	29	13.36	13.36	N
Virulence Factor	Pseudomonas_aeruginosa_GeneID_PA0087	15	15	13.04	13.04	N
Virulence Factor	Streptococcus_pyogenes_GI_52345272	18	18	12.77	12.77	N
Virulence Factor	Enterococcus_faecalis_GENE_mobB	70	70	12.19	12.19	N
Virulence Factor	Enterococcus_faecalis_GI_8100663	110	78	12.17	12.17	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_algB	42	42	11.35	11.59	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_flgI	33	33	11.11	11.11	N
Virulence Factor	Enterococcus_faecalis_GI_8100671	69	49	11.01	11.01	N
Virulence Factor	Enterococcus_faecalis_GI_8100673	109	12	10	10	N
Virulence Factor	Bacteroides_fragilis_GI_46242770	470	14	9.79	9.79	N
Virulence Factor	Yersinia_pestis_GENE_ybtU	28	28	7.57	7.57	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_pchI	23	23	7.28	7.28	N
Virulence Factor	Yersinia_pestis_GENE_ybtS	37	37	7.26	7.26	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_algX	24	24	7.21	7.21	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_fliM	22	22	7.07	7.07	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_xcpQ	41	32	6.99	6.99	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_fliG	18	18	6.54	6.54	N
Virulence Factor	Yersinia_pestis_GENE_ybtX	28	28	6.11	6.11	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_clpV1	23	23	5.85	5.85	N
Virulence Factor	Enterobacter_aerogenes_GENE_tnpA	46	27	5.3	5.3	N

Microbial DNA free water.cont.

Staphylococcus aureus control.

Database	Organism	Unique Matches Frequency	Unique Matches	% Unique Matches	% Total Matches	Relative Abundance	Above Threshold
Bacteria	Staphylococcus_aureus_1801_2_2011	234	65	25.29	72.1	99.85	Y
Bacteria	Propionibacterium_20956 Branch	48	48	0.33	0.29	0.05375	N
Bacteria	Chlamydia_psittaci_06_1683	17	17	0.62	0.62	0.02123	N
Bacteria	Staphylococcus_6209 Branch	35	27	0.06	0.06	0.008317	N
Bacteria	Staphylococcus_epidermidis_NIHLM_6071	54	18	0.19	0.15	0.01039	N
Bacteria	Staphylococcus_warneri_6227 Branch	18	14	0.02	0.04	0.008516	N
Bacteria	Staphylococcus_lugdunensis_6250 Branch	101	71	0.06	0.06	0.00527	N
Bacteria	Staphylococcus_simiae_CCM_7213	242	165	0.12	0.12	0.00778	N
Bacteria	Lactococcus_lactis_subsp_cremoris_4136	16	16	0.15	0.26	0.004974	N
Bacteria	Staphylococcus_s_6275 Branch	50	36	0.03	0.04	0.003523	N
Bacteria	Stenotrophomonas_maltophilia_strain_53	118	113	0.07	0.08	0.003772	N
Bacteria	Staphylococcus_capitis_6320 Branch	49	26	0.05	0.07	0.00355	N
Bacteria	Staphylococcus_sp_E463	43	22	0.07	0.06	0.003167	N
Bacteria	Xanthomonas_campestris_37936 Branch	29	28	0.04	0.04	0.002382	N
Bacteria	Staphylococcus_6307 Branch	53	35	0.03	0.03	0.002192	N
Bacteria	Staphylococcus_6310 Branch	37	30	0.03	0.03	0.00198	N
Bacteria	Staphylococcus_caprae_M23864_W1	70	55	0.04	0.04	0.001917	N
Bacteria	Bradyrhizobium_sp_BTAi1	75	71	0.04	0.04	0.001845	N
Bacteria	Geobacillus_sp_WCH70	66	61	0.04	0.04	0.001777	N
Bacteria	Delftia_25859 Branch	21	21	0.04	0.04	0.001636	N
Bacteria	Staphylococcus_6285 Branch	71	36	0.03	0.03	0.001708	N
Bacteria	Acidovorax_25090 Branch	38	38	0.03	0.03	0.001385	N
Bacteria	Halomonas_sp_KM_1	55	53	0.03	0.03	0.001287	N
Bacteria	Staphylococcus_6247 Branch	26	17	0.02	0.03	0.001178	N
Bacteria	Staphylococcus_gallinarum_strain_DSM_2	59	37	0.02	0.02	0.001141	N
Virus	Staphylococcus_phage_phi2958PVL	179313	452	35.85	35.85	72.11	Y
Virus	Staphylococcus_prophage_phiPV83	29539	128	1.87	1.83	27.87	Y
Virus	Pseudomonas_phage_Pf1	45	45	1.75	1.75	0.01149	N

Staphylococcus aureus cont.

Virus	Lactococcus_phage_TP901_1	71	43	0.35	0.34	0.002618	N
Respiratory Viru	no calls detected above threshold						
Fungi	no calls detected above threshold						
Protist	no calls detected above threshold						
Antibiotic Resis	Response-regulator_arlS	191173	788	100	100		Y
Antibiotic Resis	MDR-Efflux-pump_sav1866	375190	951	100	100		Y
Antibiotic Resis	Aminoglycoside_aph	107249	414	100	100		Y
Antibiotic Resis	Tetracycline_tet_38	24503	189	93.1	98.1		Y
Antibiotic Resis	Regulator_mgrA	2163	210	93.33	93.33		Y
Antibiotic Resis	arlR	48130	332	93	93		Y
Antibiotic Resis	Phenicol_dha1	163958	539	87.5	87.5		Y
Antibiotic Resis	Repressor-of-MepA_mepR	40211	166	78.3	78.3		Y
Antibiotic Resis	Aminoglycoside_aac3_Ik	17483	178	72.95	72.95		Y
Antibiotic Resis	Tetracycline_tet38	102	46	12.57	64.48		Y
Antibiotic Resis	Macrolide_ermC	1785577	553	61.86	61.86		Y
Antibiotic Resis	Efflux-pump_mepA	3849	482	54.59	54.59		Y
Antibiotic Resis	mprF	244034	1392	53.83	53.83		Y
Antibiotic Resis	Signal-transcuding-protein_mecR1	98234	544	53.6	53.6		Y
Antibiotic Resis	Beta-lactam-resistance_blaTEM_157	13	13	52	52		Y
Antibiotic Resis	Beta-lactam_mecA	4443	54	20.45	47.61		Y
Antibiotic Resis	Fosfomycin_fosB	100626	225	42.61	42.61		Y

Staphylococcus aureus cont.

Antibiotic Resis	Quinolone_norA	18440	600	34.54	34.54	N
Antibiotic Resis	Aminoglycoside_aac3_Ia	24	17	25.76	15.05	N
Antibiotic Resis	MDR-Efflux-pump_mexG	17	17	13.08	13.08	N
Antibiotic Resis	Efflux-pump_amrA	11	11	18.97	10.58	N
Antibiotic Resis	Inner-membrane-transporter_mexF	119	106	10.37	10.37	N
Antibiotic Resis	MDR-Efflux-pump_oprN	36	36	9.52	9.52	N
Antibiotic Resis	MDR-Efflux-pump_mexB	93	93	9.13	9.13	N
Antibiotic Resis	Efflux-pump_triB	24	24	8.63	8.63	N
Antibiotic Resis	AR 214_989_2085 Branch	72	72	8.43	8.43	N
Antibiotic Resis	MDR-Efflux-pump_opmH	34	34	8.27	8.27	N
Antibiotic Resis	MDR-Efflux-pump_mexC	23	23	7.72	7.72	N
Antibiotic Resis	MDR-Efflux-pump_opmE	29	29	7.59	7.59	N
Antibiotic Resis	Macrolide_erm33	18	18	35.29	6.54	N
Antibiotic Resis	MDR-transporter_emrE	19	15	6.02	6.02	N
Antibiotic Resis	MDR-Efflux-pump_mexQ	55	55	5.77	5.77	N
Antibiotic Resis	Involved-in-polymyxin-resistance_pmrB	45	45	5.35	5.35	N
Antibiotic Resis	MDR-Efflux-pump_mexN	50	50	5.33	5.33	N
Antibiotic Resis	Efflux-pump_triC	52	52	5.28	5.28	N
Antibiotic Resis	MDR-Efflux-pump_oprJ	21	21	5.24	5.24	N

Virulence Factc	Staphylococcus_aureus_GeneID_SASa064	128952	418	100	100	Y
Virulence Factc	Staphylococcus_aureus_GeneID_SAS1010	94565	279	100	100	Y
Virulence Factc	Staphylococcus_aureus_GeneID_SASa011	107982	409	100	100	Y
Virulence Factc	Staphylococcus_aureus_GENE_1593 Branc	293	15	100	100	Y
Virulence Factc	Staphylococcus_aureus_GeneID_SASa113	64218	441	100	100	Y
Virulence Factc	Staphylococcus_aureus_GeneID_SAS1009	42507	452	100	100	Y
Virulence Factc	Staphylococcus_aureus_GENE_isdB	8799	63	100	100	Y
Virulence Factc	Staphylococcus_aureus_GeneID_SASa064	30354	469	100	100	Y
Virulence Factc	Staphylococcus_aureus_GeneID_SAS1013	47814	406	99.02	99.02	Y
Virulence Factc	Staphylococcus_aureus_GeneID_SASd069	120543	283	98.95	98.95	Y
Virulence Factc	Staphylococcus_aureus_GeneID_SASa011	7058	737	97.88	97.88	Y

Staphylococcus aureus cont.

Virulence Factc	Staphylococcus_aureus_GeneID_SASa073	114382	364	97.59	97.59	Y
Virulence Factc	Staphylococcus_aureus_GENE_isdD	91976	566	97.25	97.25	Y
Virulence Factc	Staphylococcus_aureus_GeneID_SASa064	257399	463	96.66	96.66	Y
Virulence Factc	Staphylococcus_aureus_GeneID_SAS0117	6237	521	96.66	96.66	Y
Virulence Factc	Staphylococcus_aureus_GeneID_SASa073	107281	524	96.5	96.5	Y
Virulence Factc	Staphylococcus_aureus_GeneID_SASa228	118521	425	96.15	96.15	Y
Virulence Factc	Staphylococcus_aureus_GENE_sspB2	46445	269	88.2	94.87	Y
Virulence Factc	Staphylococcus_aureus_GeneID_SAS1014	169640	331	94.57	94.57	Y
Virulence Factc	Staphylococcus_aureus_GeneID_SASa255	154830	771	94.14	94.14	Y
Virulence Factc	Staphylococcus_aureus_GENE_aur	212356	749	93.98	93.98	Y
Virulence Factc	Staphylococcus_aureus_GeneID_SASa073	130847	415	93.89	93.89	Y
Virulence Factc	Staphylococcus_aureus_GeneID_SAS1730	6421	198	93.4	93.4	Y
Virulence Factc	Staphylococcus_aureus_GENE_set_1582 E	3712	285	95.96	93.24	Y
Virulence Factc	Staphylococcus_aureus_GeneID_SASa011	64538	415	92.84	92.84	Y
Virulence Factc	Staphylococcus_aureus_GENE_set_1668 E	70766	175	92.59	92.59	Y
Virulence Factc	Staphylococcus_aureus_GENE_scn	78981	184	92.46	92.46	Y
Virulence Factc	Staphylococcus_aureus_GENE_map	78731	350	84.54	92.12	Y
Virulence Factc	Staphylococcus_aureus_GENE_esxA	1824	146	91.82	91.82	Y
Virulence Factc	Staphylococcus_aureus_GeneID_SAS0111	63804	342	90.72	90.72	Y
Virulence Factc	Staphylococcus_aureus_GeneID_SASa012	2145	233	88.26	88.26	Y
Virulence Factc	Staphylococcus_aureus_GeneID_SAS1008	118747	836	85.05	86.04	Y
Virulence Factc	Staphylococcus_aureus_GeneID_SASa012	93877	294	85.71	85.71	Y
Virulence Factc	Staphylococcus_aureus_GENE_cap5L	5413	20	35.09	84.87	Y
Virulence Factc	Staphylococcus_aureus_GeneID_SAS1015	6939	132	84.61	84.61	Y
Virulence Factc	Staphylococcus_aureus_GeneID_SAS0122	52689	199	83.97	83.97	Y
Virulence Factc	Staphylococcus_aureus_GENE_cap5H	156161	356	82.03	82.03	Y
Virulence Factc	Staphylococcus_aureus_GENE_cap8G	24	19	42.22	81.7	Y
Virulence Factc	Staphylococcus_aureus_GeneID_SAS0119	26116	606	81.45	81.45	Y
Virulence Factc	Staphylococcus_aureus_GENE_sak	126234	281	80.98	80.98	Y
Virulence Factc	Staphylococcus_aureus_GeneID_SAS0115	63472	357	80.77	80.77	Y
Virulence Factc	Staphylococcus_aureus_GENE_ic_1660 Br	69680	75	70.75	80.57	Y
Virulence Factc	Staphylococcus_aureus_GENE_cap8D	41	33	15.57	80.48	Y
Virulence Factc	Staphylococcus_aureus_GeneID_SASa012	91554	636	80	80	Y

Staphylococcus aureus cont.

Virulence Factc	Staphylococcus_aureus_GENE_lukS_PV	8196	475	67.19	79.95	Y
Virulence Factc	Staphylococcus_aureus_GENE_essA	98884	293	78.98	78.98	Y
Virulence Factc	Staphylococcus_lentus_GENE_ermC	967799	263	78.98	78.98	Y
Virulence Factc	Staphylococcus_aureus_GENE_splD	3074	24	26.97	78.68	Y
Virulence Factc	Staphylococcus_aureus_GENE_hld	22182	57	77.03	77.03	Y
Virulence Factc	Staphylococcus_aureus_GENE_sdrH	165171	477	73.61	73.61	Y
Virulence Factc	Staphylococcus_aureus_GENE_nuc	8978	676	71.76	71.76	Y
Virulence Factc	Staphylococcus_aureus_GENE_cap5J	100315	658	70.83	71.14	Y
Virulence Factc	Staphylococcus_aureus_GENE_cap5D	10684	14	33.33	70.96	Y
Virulence Factc	Staphylococcus_aureus_GENE_icaD	95502	187	69.78	70.65	Y
Virulence Factc	Staphylococcus_aureus_GENE_cap5E	358	37	24.03	70.01	Y
Virulence Factc	Staphylococcus_aureus_GENE_sspC	42711	237	69.91	69.91	Y
Virulence Factc	Staphylococcus_aureus_GENE_cap_1631 I	16355	63	30.43	69.72	Y
Virulence Factc	Staphylococcus_aureus_GENE_cap5O	26552	106	51.21	69.55	Y
Virulence Factc	Staphylococcus_aureus_GENE_cap5P	2622	78	41.49	69.23	Y
Virulence Factc	Staphylococcus_aureus_GENE_hlb	144128	590	68.61	68.61	Y
Virulence Factc	Staphylococcus_aureus_GENE_cap5G	138	39	20.1	67.74	Y
Virulence Factc	Staphylococcus_aureus_GeneID_SAS0121	100149	354	66.92	66.92	Y
Virulence Factc	Staphylococcus_aureus_GENE_cap5I	188642	654	66.67	66.67	Y
Virulence Factc	Staphylococcus_aureus_GENE_cap5K	223890	768	65.64	65.93	Y
Virulence Factc	Staphylococcus_aureus_GENE_esxB	57006	167	65.75	65.75	Y
Virulence Factc	Staphylococcus_aureus_GENE_esaC	51914	358	64.5	64.5	Y
Virulence Factc	Staphylococcus_aureus_GeneID_SASa080	18217	279	63.41	63.41	Y
Virulence Factc	Staphylococcus_aureus_GENE_capC	19	15	14.71	63.17	Y
Virulence Factc	Staphylococcus_aureus_GENE_cap5F	25	22	16.42	62.51	Y
Virulence Factc	Staphylococcus_aureus_GENE_icaR	100963	345	61.94	61.94	Y
Virulence Factc	Staphylococcus_aureus_GENE_set9	67	37	13.81	61.44	Y
Virulence Factc	Staphylococcus_aureus_GENE_capD	97555	537	47.19	60.68	Y
Virulence Factc	Staphylococcus_aureus_GENE_SEnt_1536	15	15	26.32	60.44	Y
Virulence Factc	Staphylococcus_aureus_GENE_spa	388207	1486	58.43	59.1	Y
Virulence Factc	Staphylococcus_aureus_GI_33390919	1863	123	61.81	58.77	Y
Virulence Factc	Staphylococcus_aureus_GENE_cap5N	1650	99	39.29	57.93	Y
Virulence Factc	Staphylococcus_aureus_GENE_esaB	44563	122	56.22	56.22	Y

Staphylococcus aureus cont.

Virulence Factc	Staphylococcus_aureus_GENE_eap	131395	314	54.99	54.99	Y
Virulence Factc	Staphylococcus_aureus_GENE_capO	105	38	11.24	54.81	Y
Virulence Factc	Staphylococcus_aureus_GENE_hlgA	239927	543	66.14	54.58	Y
Virulence Factc	Staphylococcus_aureus_GENE_eap_map	54665	155	24.45	53.58	Y
Virulence Factc	Staphylococcus_aureus_GENE_sdrE	244487	1553	46.43	52.87	Y
Virulence Factc	Staphylococcus_aureus_GENE_cap1A	261	21	52.5	52.5	Y
Virulence Factc	Staphylococcus_aureus_GENE_isdF	12436	30	51.72	51.72	Y
Virulence Factc	Staphylococcus_aureus_GENE_isb	63960	356	39.03	49.13	Y
Virulence Factc	Staphylococcus_aureus_GENE_lip	37336	567	41.97	46.4	Y
Virulence Factc	Staphylococcus_aureus_GENE_geh	100116	1123	42.91	45.56	Y
Virulence Factc	Staphylococcus_aureus_GENE_cap5M	44285	232	48.33	44.47	Y
Virulence Factc	Staphylococcus_aureus_GENE_atl	516584	2300	43.84	43.84	Y
Virulence Factc	Staphylococcus_aureus_GENE_icaA	93134	665	43.27	43.56	Y
Virulence Factc	Staphylococcus_aureus_GENE_splA	80579	392	42.89	42.89	Y
Virulence Factc	Staphylococcus_aureus_GENE_fib	39092	135	20.15	42.1	Y
Virulence Factc	Staphylococcus_aureus_GENE_ebh	2646725	17702	41.59	41.59	Y
Virulence Factc	Staphylococcus_aureus_GENE_ebpS	214444	873	41.51	41.51	Y
Virulence Factc	Staphylococcus_aureus_GENE_lukF_PV	99724	516	28.12	40.95	Y
Virulence Factc	Staphylococcus_aureus_GENE_hla	120250	547	40.13	40.13	Y
Virulence Factc	Staphylococcus_aureus_GENE_icaB	17016	477	39	39	N
Virulence Factc	Staphylococcus_aureus_GENE_essB	398308	903	38.81	38.81	N
Virulence Factc	Staphylococcus_aureus_GENE_esaA	273526	1846	38.53	38.53	N
Virulence Factc	Staphylococcus_aureus_GENE_capA	42	38	6.53	37.5	N
Virulence Factc	Staphylococcus_aureus_GENE_sdrC	301209	1564	29.11	36.66	N
Virulence Factc	Staphylococcus_aureus_GENE_sdrD	520624	2217	30.53	36.18	N
Virulence Factc	Staphylococcus_aureus_GENE_essC	624297	2703	36.09	36.09	N
Virulence Factc	Pseudomonas_aeruginosa_GENE_flhB	93	93	34.44	34.44	N
Virulence Factc	Staphylococcus_aureus_GENE_clfA	388885	1879	32.53	33.92	N
Virulence Factc	Staphylococcus_aureus_GENE_clfB	310484	1557	31.54	32.68	N
Virulence Factc	Pseudomonas_aeruginosa_GENE_flgH	63	63	31.98	31.98	N
Virulence Factc	Staphylococcus_aureus_GENE_hlgB	126891	565	34.49	31.59	N
Virulence Factc	Pseudomonas_aeruginosa_GENE_chpD	60	47	31.33	31.33	N
Virulence Factc	Staphylococcus_aureus_GENE_hlgC	130451	595	31.02	31.02	N

Staphylococcus aureus cont.

Virulence Factc	Staphylococcus_aureus_GENE_cap5C	42	17	17.35	30.77	N
Virulence Factc	Pseudomonas_aeruginosa_GeneID_PA007	95	77	30.43	30.43	N
Virulence Factc	Pseudomonas_aeruginosa_GENE_Alg44	79	79	29.92	29.92	N
Virulence Factc	Pseudomonas_aeruginosa_GENE_algK	97	86	29.86	29.86	N
Virulence Factc	Staphylococcus_aureus_GENE_sspA	86541	570	36.33	29.83	N
Virulence Factc	Staphylococcus_aureus_GENE_vwb	614929	1983	29.5	29.5	N
Virulence Factc	Staphylococcus_aureus_GENE_fnbA	393645	1216	25.34	29.3	N
Virulence Factc	Staphylococcus_aureus_GENE_splB	49516	398	27.95	28.57	N
Virulence Factc	Pseudomonas_aeruginosa_GENE_fimU	46	46	27.88	27.88	N
Virulence Factc	Pseudomonas_aeruginosa_GENE_phzM	82	82	27.42	27.42	N
Virulence Factc	Pseudomonas_aeruginosa_GENE_fleN	106	70	27.34	27.34	N
Virulence Factc	Staphylococcus_aureus_GENE_splE	60197	277	25.77	27.15	N
Virulence Factc	Staphylococcus_aureus_GENE_splC	62832	436	25.86	25.86	N
Virulence Factc	Pseudomonas_aeruginosa_GENE_xcpY	76	60	25.86	25.86	N
Virulence Factc	Staphylococcus_aureus_GI_33390948	929	13	7.18	24.48	N
Virulence Factc	Pseudomonas_aeruginosa_GENE_pilK	72	57	24.46	24.46	N
Virulence Factc	Staphylococcus_aureus_GENE_hysA	356224	1076	22.05	24.4	N
Virulence Factc	Pseudomonas_aeruginosa_GENE_rhlL	41	41	24.26	24.26	N
Virulence Factc	Pseudomonas_aeruginosa_GENE_pilT	66	66	23.57	23.57	N
Virulence Factc	Pseudomonas_aeruginosa_GENE_fliH	46	46	21.91	21.91	N
Virulence Factc	Staphylococcus_aureus_GENE_eta	106766	551	21.75	21.75	N
Virulence Factc	Pseudomonas_aeruginosa_GENE_mucC	23	23	21.49	21.49	N
Virulence Factc	Pseudomonas_aeruginosa_GENE_fliM	65	65	20.9	20.9	N
Virulence Factc	Pseudomonas_aeruginosa_GENE_flhF	63	63	20.72	20.72	N
Virulence Factc	Pseudomonas_aeruginosa_GENE_algD	88	69	20.12	20.12	N
Virulence Factc	Pseudomonas_aeruginosa_GENE_algI	80	80	19.28	19.28	N
Virulence Factc	Pseudomonas_aeruginosa_GENE_algZ	89	57	19.19	19.19	N
Virulence Factc	Pseudomonas_aeruginosa_GeneID_PA008	47	47	19.03	19.03	N
Virulence Factc	Pseudomonas_aeruginosa_GENE_algX	59	59	17.72	17.72	N
Virulence Factc	Staphylococcus_aureus_GENE_set17	13	13	17.57	17.57	N
Virulence Factc	Pseudomonas_aeruginosa_GeneID_PA008	19	19	16.52	16.52	N
Virulence Factc	Pseudomonas_aeruginosa_GENE_mucB	36	36	15.65	15.65	N
Virulence Factc	Pseudomonas_aeruginosa_GeneID_PA007	57	57	15.57	15.57	N

Staphylococcus aureus cont.

Virulence Factc	Staphylococcus_aureus_GENE_SEntK	10	10	11.63	14.66	N
Virulence Factc	Pseudomonas_aeruginosa_GENE_fliN	19	19	13.67	13.67	N
Virulence Factc	Pseudomonas_aeruginosa_GeneID_PA008	56	50	13.59	13.59	N
Virulence Factc	Pseudomonas_aeruginosa_GeneID_PAP47	31	31	13.48	13.48	N
Virulence Factc	Pseudomonas_aeruginosa_GeneID_PA008	60	60	13.3	13.3	N
Virulence Factc	Pseudomonas_aeruginosa_GENE_pilX	23	23	13.14	13.14	N
Virulence Factc	Pseudomonas_aeruginosa_GENE_fliG	35	35	12.73	12.73	N
Virulence Factc	Staphylococcus_aureus_GENE_set13	48	42	11.8	11.8	N
Virulence Factc	Pseudomonas_aeruginosa_GENE_fliI	38	38	11.66	11.66	N
Virulence Factc	Pseudomonas_aeruginosa_GeneID_PA007	18	18	11.25	11.25	N
Virulence Factc	Pseudomonas_aeruginosa_GENE_lasA	34	34	11.11	11.11	N
Virulence Factc	Staphylococcus_aureus_GENE_set12	37	32	10.85	10.85	N
Virulence Factc	Pseudomonas_aeruginosa_GENE_pchG	28	28	10.65	10.65	N
Virulence Factc	Pseudomonas_aeruginosa_GENE_chpC	12	12	9.6	9.6	N
Virulence Factc	Pseudomonas_aeruginosa_GeneID_PA007	27	27	9.57	9.57	N
Virulence Factc	Staphylococcus_aureus_GENE_lukD	79	16	9.52	9.42	N
Virulence Factc	Pseudomonas_aeruginosa_GENE_pchR	19	19	8.76	8.76	N
Virulence Factc	Pseudomonas_aeruginosa_GENE_exoT	34	33	8.42	8.42	N
Virulence Factc	Pseudomonas_aeruginosa_GENE_pchA	28	28	8.12	8.12	N
Virulence Factc	Pseudomonas_aeruginosa_GENE_fptA	42	42	8.08	8.08	N
Virulence Factc	Pseudomonas_aeruginosa_GENE_pilB	46	46	7.85	7.85	N
Virulence Factc	Staphylococcus_aureus_GENE_SEnt_1655	246	40	18.26	7.42	N
Virulence Factc	Pseudomonas_aeruginosa_GENE_waaA	41	21	7.42	7.42	N
Virulence Factc	Pseudomonas_aeruginosa_GeneID_PA008	36	36	7.38	7.38	N
Virulence Factc	Pseudomonas_aeruginosa_GeneID_PA008	15	15	6.98	6.98	N
Virulence Factc	Pseudomonas_aeruginosa_GENE_fliF	72	36	6.94	6.94	N
Virulence Factc	Pseudomonas_aeruginosa_GENE_xcpP	13	13	6.88	6.88	N
Virulence Factc	Staphylococcus_aureus_GENE_set_1611 E	14	14	7.22	6.76	N
Virulence Factc	Pseudomonas_aeruginosa_GENE_algJ	19	19	6.76	6.76	N
Virulence Factc	Pseudomonas_aeruginosa_GENE_algE	23	23	6.53	6.53	N
Virulence Factc	Pseudomonas_aeruginosa_GENE_algA	28	28	6.44	6.44	N
Virulence Factc	Pseudomonas_aeruginosa_GENE_pchD	23	23	6.1	6.1	N
Virulence Factc	Pseudomonas_aeruginosa_GENE_xcpQ	26	26	5.68	5.68	N

Staphylococcus aureus cont.

Virulence Factc	Pseudomonas_aeruginosa_GENE_fliC	18	18	5.66	5.66	N
Virulence Factc	Pseudomonas_aeruginosa_GENE_aprA	33	23	5.65	5.65	N
Virulence Factc	Pseudomonas_aeruginosa_GENE_xcpR	18	18	5.59	5.59	N
Virulence Factc	Pseudomonas_aeruginosa_GENE_ppkA	28	28	5.51	5.51	N
Virulence Factc	Pseudomonas_aeruginosa_GENE_pilQ	33	33	5.47	5.47	N
Virulence Factc	Pseudomonas_aeruginosa_GENE_flgJ	16	16	5.46	5.46	N
Virulence Factc	Pseudomonas_aeruginosa_GENE_fleQ	22	22	5.33	5.31	N
Virulence Factc	Pseudomonas_aeruginosa_GENE_algG	22	22	5.2	5.2	N
Virulence Factc	Pseudomonas_aeruginosa_GENE_exoS	21	21	5	5	N

Pseudomonas aeruginosa control.

Database	Organism	Unique Matches Frequency	Unique Matches	% Unique Matches	% Total Matches	Relative Abundance	Above Threshold
Bacteria	Pseudomonas_aeruginosa_strain_AZPAE14876	4188	111	4.53	4.53	91.61	Y
Bacteria	Pseudomonas_otitidis	45	32	1.95	1.95	5.78	Y
Bacteria	Pseudomonas_sp_2_1_26	92	79	1.04	1.04	2.229	Y
Bacteria	Ralstonia_pickettii_12D	1769	1611	1.87	1.86	0.1848	Y
Bacteria	Propionibacterium_20956 Branch	30	30	0.2	0.19	0.06475	Y
Bacteria	Leifsonia_aquatica_ATCC_14665	1517	1147	0.65	0.66	0.06057	N
Bacteria	Ralstonia_24678 Branch	40	33	0.24	0.24	0.01137	N
Bacteria	Streptomyces_pluripotens_strain_MUSC_137	43	43	0.13	0.08	0.006152	N
Bacteria	Pseudomonas_thermotolerans_39784 Branch	134	101	0.07	0.07	0.005385	N
Bacteria	Streptococcus_mutans_2662 Branch	17	17	0.14	0.14	0.005484	N
Bacteria	Lactococcus_lactis_subsp_cremoris_4115 Branc	28	27	0.09	0.08	0.004413	N
Bacteria	Pseudomonadaceae_Family 4039_40175 Branch	61	50	0.04	0.04	0.00403	N
Bacteria	Pseudomonas_alcaligenes_39473 Branch	112	75	0.04	0.04	0.00333	N
Bacteria	alpha_proteobacterium_SCGC_AAA027_C06	17	17	0.09	0.16	0.003399	N
Bacteria	Pseudomonas_denitrificans_ATCC_13867	116	96	0.05	0.05	0.002929	N
Bacteria	Pseudomonas_knackmussii_B13	119	92	0.05	0.05	0.002829	N
Bacteria	Pseudomonas_39662 Branch	28	21	0.03	0.05	0.002029	N
Bacteria	Pseudomonas_azotifigens_DSM_17556	99	69	0.04	0.04	0.002111	N
Bacteria	Synechococcus_sp_CB0101	57	57	0.04	0.04	0.002035	N
Bacteria	Pseudomonas_nitroreducens_TX1	84	66	0.03	0.05	0.001879	N
Bacteria	Pseudomonas_resinovorans_NBRC_106553	79	66	0.03	0.03	0.001846	N
Bacteria	Azotobacter_chroococcum_NCIMB_8003	86	64	0.03	0.03	0.00184	N
Bacteria	Pseudomonas_39733 Branch	37	25	0.02	0.02	0.001403	N
Bacteria	Leifsonia_xyli_subsp_cynodontis_DSM_46306	60	53	0.03	0.05	0.001658	N
Bacteria	Pseudomonas_39821 Branch	37	31	0.02	0.02	0.001341	N
Bacteria	Acidovorax_sp_JS42	151	21	0.02	0.04	0.001645	N
Bacteria	Pseudomonas_mendocina_39458 Branch	18	16	0.01	0.01	0.00135	N
Bacteria	Pseudomonas_pseudoalcaligenes_KF707	78	52	0.03	0.03	0.001479	N
Bacteria	Pseudomonas_fulva_12_X	36	32	0.03	0.02	0.001217	N

Pseudomonas aeruginosa cont.

Virus	Pseudomonas_phage_Pf1	68101	2400	93.46	93.46	95.51	Y
Virus	Myoviridae_Family_5 1127_7583 Branch	112	68	28.94	28.94	4.454	Y
Virus	Shigella_phage_SfI_7665 Branch	32	32	1.37	0.61	0.03672	N

Respiratory Virus no calls detected above threshold

Fungi no calls detected above threshold

Protist no calls detected above threshold

Antibiotic Resistance	Repressor-of-efflux-complex_nfxB	7154	178	100	100		Y
Antibiotic Resistance	Sensor-protein_soxR	13199	124	100	100		Y
Antibiotic Resistance	MDR-Efflux-pump_mexG	17413	130	100	100		Y
Antibiotic Resistance	Phenicol_catB7	10450	192	100	100		Y
Antibiotic Resistance	MDR-Efflux-pump_oprN	31524	378	100	100		Y
Antibiotic Resistance	Outer-membrane-factor_oprM	22427	415	100	100		Y
Antibiotic Resistance	Efflux-pump_triA	21657	306	98.39	98.39		Y
Antibiotic Resistance	MDR-Efflux-pump_mexC	22619	292	97.99	97.99		Y
Antibiotic Resistance	Efflux-pump_triB	15347	272	97.84	97.84		Y
Antibiotic Resistance	Repressor_nalD	7710	204	96.68	96.68		Y
Antibiotic Resistance	MDR-Efflux-pump_mexN	51788	906	96.59	96.59		Y
Antibiotic Resistance	Efflux-pump_triC	41560	951	96.55	96.55		Y
Antibiotic Resistance	MDR-Efflux-pump_mexI	58333	899	96.36	96.36		Y
Antibiotic Resistance	Efflux-pump_amrB	2173	65	82.28	95.71		Y

Pseudomonas aeruginosa cont.

Antibiotic Resistance MDR-Efflux-pump_mexJ	14780	271	95.09	95.09	Y
Antibiotic Resistance MDR-Efflux-pump_oprJ	41966	380	94.76	94.76	Y
Antibiotic Resistance Aminoglycoside_aac3_Ia	4043	56	84.85	94.62	Y
Antibiotic Resistance MDR-Efflux-pump_opmD	32487	340	93.92	93.92	Y
Antibiotic Resistance Inner-membrane-transporter_mexF	69556	958	93.74	93.74	Y
Antibiotic Resistance MDR-Efflux-pump_opmE	29100	356	93.19	93.19	Y
Antibiotic Resistance Repressor-of-mexJK_mexL	10400	178	91.75	91.75	Y
Antibiotic Resistance MDR-Efflux-pump_mexD	51503	953	90.16	90.16	Y
Antibiotic Resistance Repressor_nalC	3532	173	90.1	90.1	Y
Antibiotic Resistance MDR-Efflux-pump_mexB	37061	917	89.99	89.99	Y
Antibiotic Resistance MDR-Efflux-pump_mexE	2344	317	89.8	89.8	Y
Antibiotic Resistance MDR-Efflux-pump_mexM	13455	287	89.69	89.69	Y
Antibiotic Resistance MDR-Efflux-pump_mexH	6004	284	89.59	89.59	Y
Antibiotic Resistance Efflux-pump_amrA	6895	53	91.38	89.42	Y
Antibiotic Resistance MDR-Efflux-pump_mexQ	45078	852	89.4	89.4	Y
Antibiotic Resistance Suppressor-of-MexT_mexS	12255	271	88.85	88.85	Y
Antibiotic Resistance MDR-Efflux-pump_opmH	11924	360	87.59	87.59	Y
Antibiotic Resistance Beta-lactam-resistance_bla 244_1197_740 Branc	8073	225	86.54	86.54	Y
Antibiotic Resistance Membrane-fusion-protein_mexA	15131	290	82.62	82.62	Y
Antibiotic Resistance MDR-Efflux-pump_mexP	6601	249	77.81	77.81	Y
Antibiotic Resistance Aminoglycoside_aac1	19	13	25	77.33	Y
Antibiotic Resistance Aminoglycoside_aph3'_IIb	11440	136	63.85	63.85	Y
Antibiotic Resistance Beta-lactam-resistance_blaOXA_50	15759	253	62.31	62.31	Y
Antibiotic Resistance Involved-in-polymyxin-resistance_pmrB	20535	397	47.21	47.21	Y
Antibiotic Resistance Aminoglycoside_aph3'_Ib	272	139	44.13	44.13	Y
Antibiotic Resistance polymyxin-and-cationic-antimicrobial-peptides_ar	22195	548	38.89	38.89	N
Antibiotic Resistance Involved-in-polymyxin-resistance_pmrA	20198	173	38.88	38.88	N
Antibiotic Resistance Sensor-protein_phoQ	15856	371	37.25	37.25	N
Antibiotic Resistance MDR-transporter_emrE	8466	92	36.95	36.95	N
Antibiotic Resistance Repressor-of-efflux-complex_phoP	4759	178	35.04	35.04	N
Antibiotic Resistance MDR-transporter_emrY	143	143	18.79	18.79	N
Antibiotic Resistance MDR-Efflux-pump_mdtE	112	83	18.36	18.36	N
Antibiotic Resistance Regulator_cpxR	55	45	15.36	15.36	N

Pseudomonas aeruginosa cont.

Antibiotic Resistance	Repressor-for-mdr-efflux-pump_emrR	30	30	13.22	13.22	N
Antibiotic Resistance	Involved-in-polymyxin-resistance_pmrF	53	53	12.77	12.77	N
Antibiotic Resistance	Inner-membrane-transporter_acrF	190	152	11.5	11.5	N
Antibiotic Resistance	MDR-Efflux-pump_mdtD	64	57	10.07	10.07	N
Antibiotic Resistance	MDR-protein_mdtH	70	43	9.09	9.09	N
Antibiotic Resistance	Beta-lactam-resistance_blaAmpC	110	80	8.97	8.97	N
Antibiotic Resistance	Transporter-for-efflux-complex_mdtF	136	110	8.59	8.59	N
Antibiotic Resistance	Membrane-fusion-protein_emrK	95	43	8.48	8.48	N
Antibiotic Resistance	Involved-in-polymyxin-resistance_pmrE	44	44	8.02	8.02	N
Antibiotic Resistance	Involved-in-polymyxin-resistance_pmrC	55	55	7.7	7.7	N
Antibiotic Resistance	Beta-lactam_pbp4_Ecoli	35	35	6.54	6.54	N
Antibiotic Resistance	MDR-transporter_mdtK	72	36	6.44	6.44	N

Virulence Factor	Pseudomonas_aeruginosa_GENE_flhB	35386	270	100	100	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_fleN	29275	256	100	100	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_fliH	25109	210	100	100	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_fliR	24642	214	100	100	Y
Virulence Factor	Pseudomonas_aeruginosa_GeneID_PA0089	25451	247	100	100	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_waaA	25646	283	100	100	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_xcpY	23373	232	100	100	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_phzM	26100	299	100	100	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_Alg44	20998	264	100	100	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_algJ	20079	281	100	100	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_algD	21891	343	100	100	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_chpD	14904	150	100	100	Y
Virulence Factor	Pseudomonas_aeruginosa_GeneID_PA0076	15173	160	100	100	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_fliM	19788	311	100	100	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_pchC	13316	163	100	100	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_fliO	9464	79	100	100	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_pilN	12824	155	100	100	Y
Virulence Factor	Pseudomonas_aeruginosa_GeneID_PA0087	10697	115	100	100	Y

Pseudomonas aeruginosa cont.

Virulence Factor	Pseudomonas_aeruginosa_GENE_flgC	9836	128	100	100	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_fimU	10556	165	100	100	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_hcp1	9094	123	100	100	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_xcpP	10658	189	100	100	Y
Virulence Factor	Pseudomonas_aeruginosa_GeneID_PA0073	9826	166	100	100	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_flgF	8683	236	100	100	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_algF	6029	135	100	100	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_pilI	4713	134	100	100	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_xcpV	3204	100	100	100	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_algQ	1112	133	100	100	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_pilH	804	109	100	100	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_pilG	680	124	100	100	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_algI	30332	414	99.76	99.76	Y
Virulence Factor	Pseudomonas_aeruginosa_GeneID_PA0078	27874	281	99.65	99.65	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_algK	19517	287	99.65	99.65	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_fliG	6414	274	99.64	99.64	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_pilE	5448	129	99.23	99.23	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_xcpT	572	118	99.16	99.16	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_flgD	1109	191	98.96	98.96	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_pilK	12598	230	98.71	98.71	Y
Virulence Factor	Pseudomonas_aeruginosa_GeneID_PA0075	1522	173	98.29	98.29	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_mucB	11763	226	98.26	98.26	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_algA	32454	427	98.16	98.16	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_pchE	22284	361	98.1	98.1	Y
Virulence Factor	Pseudomonas_aeruginosa_GeneID_PA0081	18093	361	98.1	98.1	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_icmF1	17690	497	98.03	98.03	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_pvdS	971	142	97.93	97.93	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_pilJ	35546	555	97.88	97.88	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_algG	26699	414	97.87	97.87	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_pchH	42674	394	97.77	97.77	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_clpV1	10686	384	97.71	97.71	Y
Virulence Factor	Pseudomonas_aeruginosa_GeneID_PA0082	29402	249	97.65	97.65	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_plcH	32439	540	97.65	97.65	Y

Pseudomonas aeruginosa cont.

Virulence Factor	Pseudomonas_aeruginosa_GENE_algZ	32191	290	97.64	97.64	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_flgI	14113	290	97.64	97.64	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_waaC	23998	240	97.56	97.56	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_lasB	13146	318	97.55	97.55	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_fimV	37193	569	97.43	97.43	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_pchB	5211	75	97.4	97.4	Y
Virulence Factor	Pseudomonas_aeruginosa_GeneID_PA0079	26718	356	97.27	97.27	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_pilU	19175	321	97.27	97.27	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_xcpS	11211	278	97.2	97.2	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_xcpZ	1677	101	97.11	97.11	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_waaF	6830	267	97.09	97.09	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_pchF	23997	395	97.05	97.05	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_fliQ	345	65	97.01	97.01	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_pilR	3175	388	97	97	Y
Virulence Factor	Pseudomonas_aeruginosa_GeneID_PA0072	18975	245	96.84	96.84	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_pchA	16252	331	95.94	95.94	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_fleQ	28979	396	95.88	95.89	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_xcpQ	39052	439	95.85	95.85	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_fliJ	2447	91	95.79	95.79	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_algR	9143	203	95.75	95.75	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_algP	2178	89	95.7	95.7	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_flgG	6059	233	95.49	95.49	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_algB	20118	352	95.13	95.15	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_aprA	14323	387	95.09	95.09	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_phzS	4620	285	95	95	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_flgH	24116	187	94.92	94.92	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_rhlB	10687	335	94.9	94.9	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_pilY2	4101	93	94.9	94.9	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_algE	18185	334	94.89	94.89	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_pilX	15741	166	94.86	94.86	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_waaP	6278	221	94.85	94.85	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_toxA	33332	451	94.55	94.55	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_pilV	7718	164	94.25	94.25	Y

Pseudomonas aeruginosa cont.

Virulence Factor	Pseudomonas_aeruginosa_GENE_fliN	5494	131	94.24	94.24	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_fliF	25015	489	94.22	94.22	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_xcpX	5685	178	94.18	94.18	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_flhF	15755	284	93.42	93.42	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_mucA	5081	141	93.38	93.38	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_chpE	8367	132	92.96	92.96	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_xcpR	6257	296	91.93	91.93	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_ExcC	14262	113	91.87	91.87	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_xcpU	10249	123	91.79	91.79	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_pchI	17916	290	91.77	91.77	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_pchR	2805	199	91.71	91.71	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_lasR	925	199	91.71	91.71	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_flhA	34491	573	91.68	91.68	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_fleR	6851	359	91.58	91.58	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_lasI	6441	184	91.54	91.54	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_pilM	10010	259	91.52	91.52	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_pilO	1038	181	91.41	91.41	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_algL	8039	244	91.39	91.39	Y
Virulence Factor	Pseudomonas_aeruginosa_GeneID_PA0088	9679	446	91.39	91.39	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_pilP	6879	148	90.24	90.24	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_fliP	10677	191	90.09	90.09	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_Alg8	20966	378	90	90	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_chpB	3288	243	90	90	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_vgrG1	33424	373	89.88	89.88	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_pilF	1973	201	89.73	89.73	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_mucC	6222	96	89.72	89.72	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_chpC	8152	112	89.6	89.6	Y
Virulence Factor	Pseudomonas_aeruginosa_GeneID_PA0084	37714	403	89.36	89.36	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_pchG	17638	235	89.35	89.35	Y
Virulence Factor	Pseudomonas_aeruginosa_GeneID_PA0086	7053	192	89.3	89.3	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_rhlA	12373	232	89.23	89.23	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_exoS	9594	371	88.33	88.33	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_pilD	17286	224	88.19	88.19	Y

Pseudomonas aeruginosa cont.

Virulence Factor	Pseudomonas_aeruginosa_GENE_flgJ	7575	258	88.06	88.06	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_fliI	7485	287	88.04	88.04	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_algX	16161	291	87.39	87.39	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_flgE	17009	360	87.17	87.17	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_pilT	15490	242	86.43	86.43	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_pilQ	28663	519	86.07	86.07	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_fptA	7657	447	85.96	85.96	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_pilS	12917	367	85.95	85.95	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_lasA	3559	263	85.95	85.95	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_ppkA	16738	436	85.83	85.83	Y
Virulence Factor	Pseudomonas_aeruginosa_GeneID_PA0083	695	123	85.42	85.42	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_pilA	637	126	84.56	84.56	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_pchD	17058	318	84.35	84.35	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_pvdE	1585	353	83.85	83.85	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_algU	991	166	83.84	83.84	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_waaG	14811	231	83.7	83.7	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_fliE	5525	81	82.65	82.65	Y
Virulence Factor	Pseudomonas_aeruginosa_GeneID_PAP1713	939	84	80.77	80.77	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_exoT	8289	316	80.61	80.61	Y
Virulence Factor	Pseudomonas_aeruginosa_GeneID_PA0080	1798	65	80.25	80.25	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_pvdA	5651	227	79.37	79.37	Y
Virulence Factor	Pseudomonas_aeruginosa_GeneID_PAP4746	583	182	79.13	79.13	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_xcpW	7093	122	78.21	78.21	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_rhlL	5766	132	78.11	78.11	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_pilW	12861	181	77.02	77.02	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_fpvA	1813	457	76.81	76.81	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_PilZ	771	71	76.34	76.6	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_rhlR	1233	153	76.12	76.12	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_exoY	3136	273	75.62	75.62	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_fimT	1269	102	75.56	75.56	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_pilB	20094	410	69.97	69.97	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_accC1	191	33	67.35	67.35	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_qacEdelta1	2882	18	58.06	58.06	Y

Pseudomonas aeruginosa cont.

Virulence Factor	Pseudomonas_aeruginosa_GENE_flgK	4953	282	52.22	52.22	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_flgL	511	170	40.77	40.77	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_pilC	6955	157	40.36	40.36	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_wzy	726	227	40.32	40.32	Y
Virulence Factor	Pseudomonas_aeruginosa_GENE_fliC	811	121	38.05	38.05	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_fliD	280	154	30.92	30.92	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_pilY1	1104	134	30.45	30.45	N
Virulence Factor	Escherichia_coli_GENE_ompA	42	42	14.24	14.24	N
Virulence Factor	Salmonella_Typhimurium_GENE_tetA	68	41	12.61	12.61	N
Virulence Factor	Pseudomonas_aeruginosa_GENE_wzz	47	30	7.35	7.35	N

Table S2. Microbiomes for comparison with PJI communities

Sample Type	Accession Number	Study
Skin (left retroauricular crease)	SRS019015	Metagenomics of human microbiome
Skin (left retroauricular crease)	SRS024482	Metagenomics of human microbiome
Skin (right retroauricular crease)	SRS019081	Metagenomics of human microbiome
Skin (right retroauricular crease)	SRS045606	Metagenomics of human microbiome
Skin (right retroauricular crease)	SRS046688	Metagenomics of human microbiome
Skin (right retroauricular crease)	SRS052988	Metagenomics of human microbiome
Skin (right retroauricular crease)	SRS058221	Metagenomics of human microbiome
Saliva	SRS013942	Metagenomics of human microbiome
Saliva	SRS014468	Metagenomics of human microbiome
Saliva	SRS014692	Metagenomics of human microbiome
Saliva	SRS015055	Metagenomics of human microbiome
Saliva	SRS019120	Metagenomics of human microbiome
Stool	SRS014459	Metagenomics of human microbiome
Stool	SRS016056	Metagenomics of human microbiome
Stool	SRS018656	Metagenomics of human microbiome
Stool	SRS019582	Metagenomics of human microbiome
Stool	SRS022137	Metagenomics of human microbiome
Plaque (subgingival plaque)	SRS013950	Metagenomics of human microbiome
Plaque (subgingival plaque)	SRS014107	Metagenomics of human microbiome
Plaque (subgingival plaque)	SRS014477	Metagenomics of human microbiome
Plaque (subgingival plaque)	SRS015064	Metagenomics of human microbiome
Plaque (subgingival plaque)	SRS019129	Metagenomics of human microbiome
Plaque (supragingival plaque)	SRS014894	Metagenomics of human microbiome
Plaque (supragingival plaque)	SRS015378	Metagenomics of human microbiome
Plaque (supragingival plaque)	SRS019333	Metagenomics of human microbiome
Plaque (supragingival plaque)	SRS022083	Metagenomics of human microbiome
Throat	SRS013948	Metagenomics of human microbiome
Throat	SRS014689	Metagenomics of human microbiome
Throat	SRS019027	Metagenomics of human microbiome
Throat	SRS019127	Metagenomics of human microbiome
Tongue	SRS013818	Metagenomics of human microbiome
Tongue	SRS015064	Metagenomics of human microbiome
Tongue	SRS045127	Metagenomics of human microbiome
Tongue	SRS052227	Metagenomics of human microbiome
Vagina (vagina interrior forinx)	SRS014465	Metagenomics of human microbiome
Vagina (vagina interrior forinx)	SRS015071	Metagenomics of human microbiome
Vagina (mid vagina)	SRS014466	Metagenomics of human microbiome
Vagina (mid vagina)	SRS015072	Metagenomics of human microbiome