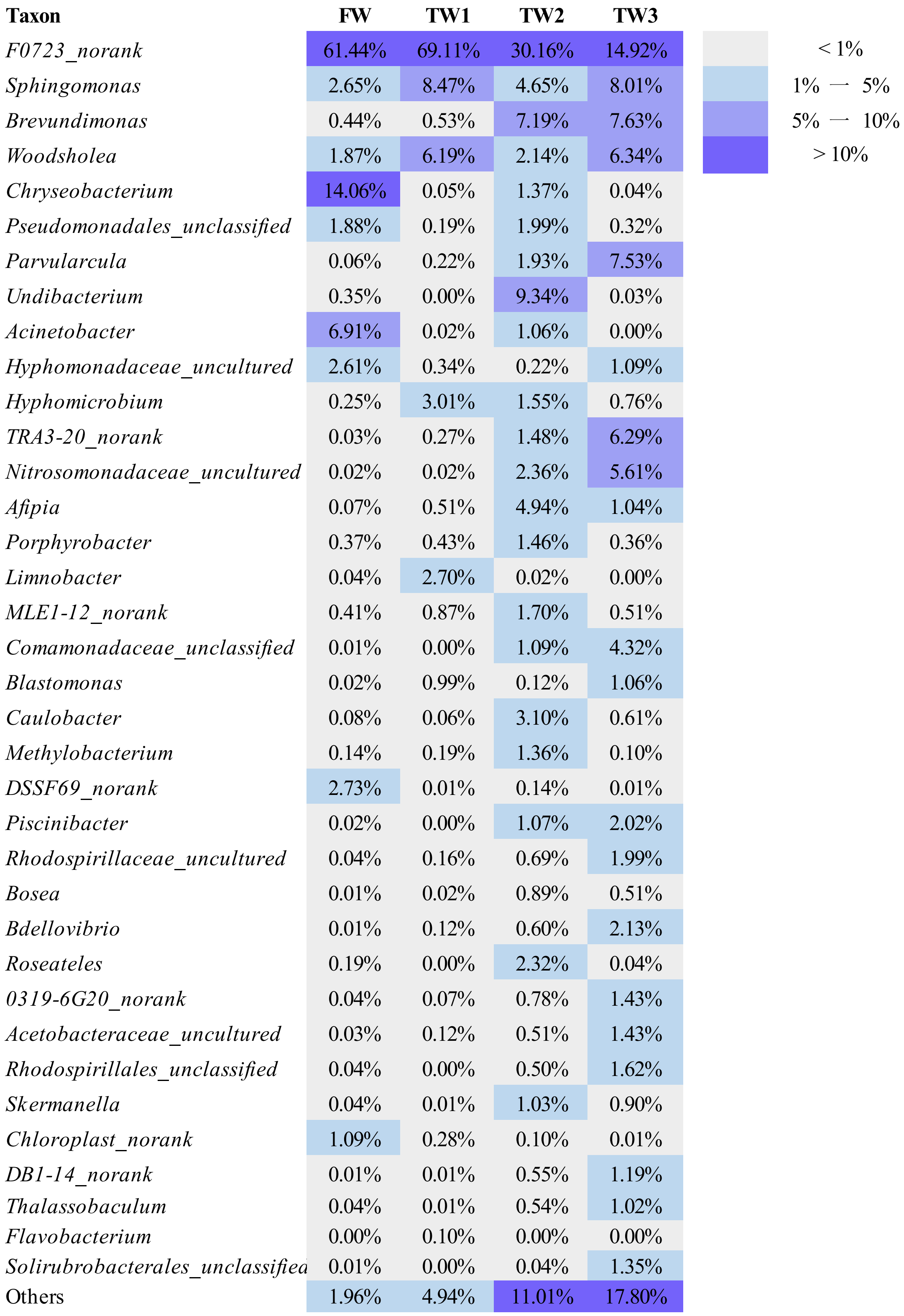
Supplementary Material



Taxon	FW	TW1	TW2	TW3
F0723_norank	61.44%	69.11%	30.16%	14.92%
Sphingomonas	2.65%	8.47%	4.65%	8.01%
Brevundimonas	0.44%	0.53%	7.19%	7.63%
Woodsholea	1.87%	6.19%	2.14%	6.34%
Chryseobacterium	14.06%	0.05%	1.37%	0.04%
Pseudomonadales_unclassified	1.88%	0.19%	1.99%	0.32%
Parvularcula	0.06%	0.22%	1.93%	7.53%
Undibacterium	0.35%	0.00%	9.34%	0.03%
Acinetobacter	6.91%	0.02%	1.06%	0.00%
Hyphomonadaceae_uncultured	2.61%	0.34%	0.22%	1.09%
Hyphomicrobium	0.25%	3.01%	1.55%	0.76%
TRA3-20_norank	0.03%	0.27%	1.48%	6.29%
Nitrosomonadaceae_uncultured	0.02%	0.02%	2.36%	5.61%
Afipia	0.07%	0.51%	4.94%	1.04%
Porphyrobacter	0.37%	0.43%	1.46%	0.36%
Limnobacter	0.04%	2.70%	0.02%	0.00%
MLE1-12_norank	0.41%	0.87%	1.70%	0.51%
Comamonadaceae_unclassified	0.01%	0.00%	1.09%	4.32%
Blastomonas	0.02%	0.99%	0.12%	1.06%
Caulobacter	0.08%	0.06%	3.10%	0.61%
Methylobacterium	0.14%	0.19%	1.36%	0.10%
DSSF69_norank	2.73%	0.01%	0.14%	0.01%
Piscinibacter	0.02%	0.00%	1.07%	2.02%
Rhodospirillaceae_uncultured	0.04%	0.16%	0.69%	1.99%
Bosea	0.01%	0.02%	0.89%	0.51%
Bdellovibrio	0.01%	0.12%	0.60%	2.13%
Roseateles	0.19%	0.00%	2.32%	0.04%
0319-6G20_norank	0.04%	0.07%	0.78%	1.43%
Acetobacteraceae_uncultured	0.03%	0.12%	0.51%	1.43%
Rhodospirillales_unclassified	0.04%	0.00%	0.50%	1.62%
Skermanella	0.04%	0.01%	1.03%	0.90%
Chloroplast_norank	1.09%	0.28%	0.10%	0.01%
DB1-14_norank	0.01%	0.01%	0.55%	1.19%
Thalassobaculum	0.04%	0.01%	0.54%	1.02%
Flavobacterium	0.00%	0.10%	0.00%	0.00%
Solirubrobacterales_unclassified	0.01%	0.00%	0.04%	1.35%
Others	1.96%	4.94%	11.01%	17.80%

< 1%
1% → 5%
5% → 10%
> 10%

Fig. S1 The bacterial community composition of FW, TW1, TW2 and TW3 at the genus level

Table S1 The results of correlation analysis between bacterial diversity indexes and water quality parameters

Parameters	Pearson Corr.	
	Chao	Shannon
Temperature	-0.90	-0.83
Turbidity	0.73*	0.45
Ammonia	0.54	0.23
COD_{Mn}	0.76	0.50
DOC	0.97	0.86
TBC	0.83	0.85
RC	-0.96*	-0.89

Note: * $P < 0.05$

Table S2 The representative OTUs might closely related with opportunistic pathogens

Genrea	**OTU ID**	**FW**	**DW1**	**DW2**	**DW3**	**DNA Sequence**
Acinetobacter	OTU214	5	0	0	0	GTGGGGAATATTGGACAATGGGCGCAAGCCTGATCCAGCCATGCCGCGTgtgtgAAGAAGGCCTTATGGTTGTAAAGCACTTTAAGCGAGGAGGAGGCTACTTTAGTTAATACCTAGAGATAGTGGACGTTACTCGCAGAATAAGCACCGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGATTTACTGGGCGTAAAGCgcgcgTAGGCGGCTAATTAAGTCAAATGTGAAATCCCCGAGCTTAACTTGGGAATTGCATTCGATACTGGTTAGCTAGAGTGTGGGAGAGGATGGTAGAATTCCAGGTGTAGCGGTGAAATGCGTAGAGATCTGGAGGAATACCGATGGCGAAGGCAGCCATCTGGCCTAACACTGACGCTGAGGTGCGAAAGCATGGGGAGCAAACAGGATTAGATACCCTTGTAGTCC
	OTU307	51	2	3	0	GTGGGGAATATTGGACAATGGggggAACCCTGATCCAGCCATGCCGCGTgtgtgAAGAAGGCCTTATGGTTGTAAAGCACTTTAAGCGAGGAGGAGGCTACTGAGACTAATACTCTTGGATAGTGGACGTTACTCGCAGAATAAGCACCGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGAGGGTGCGAGCGTTAATCGGATTTACTGGGCGTAAAGCGTGCGTAGGCGGCTTtttAAGTCGGATGTGAAATCCCCGAGCTTAACTTGGGAATTGCATTCGATACTGGGAAGCTAGAGTATGGGAGAGGATGGTAGAATTCCAGGTGTAGCGGTGAAATGCGTAGAGATCTGGAGGAATACCGATGGCGAAGGCAGCCATCTGGCCTAATACTGACGCTGAGGTACGAAAGCATGGGGAGCAAACAGGATTAGAAACCCTAGTAGTCC
	OTU36	2493	7	330	0	GTGGGGAATATTGGACAATGGggggAACCCTGATCCAGCCATGCCGCGTgtgtgAAGAAGGCCTTTTGGTTGTAAAGCACTTTAAGCGAGGAGGAGGCTACCTAGATTAATACTTTAGGATAGTGGACGTTACTCGCAGAATAAGCACCGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGAGGGTGCGAGCGTTAATCGGATTTACTGGGCGTAAAGCGTGCGTAGGCGGCCAATTAAGTCAAATGTGAAATCCCCGAGCTTAACTTGGGAATTGCATTCGATACTGGTTGGCTAGAGTATGGGAGAGGATGGTAGAATTCCAGGTGTAGCGGTGAAATGCGTAGAGATCTGGAGGAATACCGATGGCGAAGGCAGCCATCTGGCCTAATACTGACGCTGAGGTACGAAAGCATGGGGAGCAAACAGGATTAGAAACCCTGGTAGTCC
	Total	**2549**	**9**	**333**	**0**	
Legionella	OTU19	0	1	3	0	GTGGGGAATATTGGACAATGGggggAACCCTGATCCAGCAATGCCGCGTgtgtgAAGAAGGCCTGAGGGTTGTAAAGCACTTTCAGTGGGGAGGAGGATTGATTGGTTAAGAGCTGGTTAGTTGGACGTTACCCACAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGCGAGCGTTAATCGGAATTACTGGGCGTAAAGGGTGCGTAGGTGGTTTAGTAAGTTATCTGTGAAATTCCTGGGCTTAACCTAGGGTGGTCAGATAAGACTGCAAGACTCGAGTATGGGAGAGGGTAGTGGAATTTCCGGTGTAGCGGTGAAATGCGTAGAGATCGGAAGGAACACCAGTGGCGAAGGCGGCTACCTGGCCTAATACTGACACTGAGGCACGAAAGCGTGGGGAGCAAACAGGATT

Genrea	OTU ID	FW	DW1	DW2	DW3	DNA Sequence
						AGAAACCCTGGTAGTCC
	OTU9	0	2	7	1	GTGGGGAATATTGGACAATGGgggCAACCCTGATCCAGCAATGCCGCGTgtgtgAAGAAGGCCTGAGGGTTGTAAAGCACTTTCAGTGGGGAGGAGGTTATTTAGGTTAAGAGCTAGAGTAATGGACGTTACCCACAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGAGTGCGTAGGTGGTTGAATAAGTTATCTGTGAAATCCCTGGGCTTAACCTGGGCAGGTCAGATGATACTGTTTAACTCGAGTATGGGAGAGGGTAGTGGAATTTCCGGTGTAGCGGTGAAATGCGTAGAGATCGGAAGGAACACCAGTGGCGAAGGCGGCTACCTGGCCTAATACTGACACTGAGGCACGAAAGCGTGGGGAGCAAACAGGATTAGAAACCCCTGTAGTCC
	OTU80	0	12	0	0	GTGGGGAATATTGGACAATGGggggAACCCTGATCCAGCAATGCCGCGTgtgtgAAGAAGGCCTGAGGGTTGTAAAGCACTTTCAGTGGGGAGGAGGGTTGTCAGGTTAAGAGCTAGATGACTGGACGTTACCCACAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGCGAGCGTTAATCGGAATTACTGGGCGTAAAGGGTGCGTAGGTTGTCTGTTAAGTTATCTGTGAAATCCCTGGGCTTAACCTGGGCAGGTCAGATAAGACTGATGGACTCGAGTATGGGAGAGGGTAGTGGAATTTCCGGTGTAGCGGTGAAATGCGTAGAGATCGGAAGGAACACCAGTGGCGAAGGCGGCTACCTGGCCTAATACTGACACTGAGGCACGAAAGCGTGGGGAGCAAACAGGATTAGAAACCCTTGTAGTCC
	OTU205	1	0	21	0	GTGGGGAATATTGGACAATGGggggAACCCTGATCCAGCAATGCCGCGTgtgtgAAGAAGGCCTGAGGGTTGTAAAGCACTTTCAGTGGGGAGGAGGGTTGATAGGTTAAGAGCTAATTAACTGGACGTTACCCACAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGGGTGCGTAGGTGGTTGATTAAGTTATCTGTGAAATTCCCGGGCTCAACCTGGGCGTGTCAGATAAGACTGGTTAACTTGAGTATGGGAGAGGGTAGTGGAATTTCCGGTGTAGCGGTGAAATGCGTAGAGATCGGAAGGAACACCAGTGGCGAAGGCGGCTACCTGGCCTAATACTGACACTGAGGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTAGTAGTCC
	Total	**1**	**15**	**31**	**1**	
Mycobacterium	OTU86	12	3	0	2	GTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGCGTGGgggATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGACGAAGCGCAAGTGACGGTACCTGCAGAAGAAGCACCGGCCAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCGAGCGTTGTCCGGAATTACTGGGCGTAAAGAGCTCGTAGGTGGTTTGTCGCGTTGTTCGTGAAATCTCACGGCTTAACTGTGAGCGTGCGGGCGATACGGGCAGACTTGAGTACTGCAGGGGAGACTGGAATTCCTGGTGTAGCGGTGGAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGGTCTCTGGGCAGTAACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGAAACCCGAGTAGTCC

Genrea	OTU ID	FW	DW1	DW2	DW3	DNA Sequence
	OTU343	0	82	5	1	GTGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCGACGCCGCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGTAGGGACGAAGCGCAAGTGACGGTACCTATAGAAGAAGGACCGGCCAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTCCGAGCGTTGTCCGGAATTACTGGGCGTAAAGAGCTCGTAGGTGGTTTGTCGCGTTGTTCGTGAAAACTCACAGCTCAACTGTGGGCGTGCGGGCGATACGGGCAGACTTGAGTACTGCAGGGGAGACTGGAATTCCTGGTGTAGCGGTGGAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGGTCTCTGGGCAGTAACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCCAGTAGTCC
	Total	**12**	**85**	**5**	**3**	
Pseudomonas	OTU240	14	0	2	0	GTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGCCGCGTgtgtgAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGGAGGAAGGGTTGTAGATTAATACTCTGCAATTTTGACGTTACCGACAGAATAAGCACCGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCgcgcgTAGGTGGTTTGTTAAGTTGGATGTGAAATCCCCGGGCTCAACCTGGGAACTGCATCCAAAACTGGCAAGCTAGAGTATGGTAGAGGGTGGTGGAATTTCCTGTGTAGCGGTGAAATGCGTAGATATAGGAAGGAACACCAGTGGCGAAGGCGACCACCTGGACTGATACTGACACTGAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGAAACCCCAGTAGTCC
	OTU230	180	7	0	5	GTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGCCGCGTgtgtgAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGGAGGAAGGGCATTAACCTAATACGTTAGTGTTTTGACGTTACCGACAGAATAAGCACCGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCgcgcgTAGGTGGTTCGTTAAGTTGGATGTGAAATCCCCGGGCTCAACCTGGGAACTGCATCCAAAACTGGCGAGCTAGAGTAGGGCAGAGGGTGGTGGAATTTCCTGTGTAGCGGTGAAATGCGTAGATATAGGAAGGAACACCAGTGGCGAAGGCGACCACCTGGGCTCATACTGACACTGAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGAAACCCCAGTAGTCC
	Total	**194**	**7**	**2**	**5**	
Sphingomonas	OTU28	0	6	4	0	GTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCAATGCCGCGTGAGTGATGAAGGCCTTAGGGTTGTAAAGCTCTTTTACCCGGGAAGATAATGACCGTACCGGGAGAATAAGCCCCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGAGGgggCTAGCGTTATTCGGAATTACTGGGCGTAAAGCgcgcgTAGGCGGTTtttCAAGTCAGAGGTGAAAGCCTGGAGCTCAACTCCAGAATTGCCTTTGAAACTGGATCACTAGAGTCTTGGAGAGGTCAGTGGAATTCCGAGTGTAGAGGTGAAATTCGTAGATATTCGGAAGAACACCAGTGGCGAAGGCGACTGACTGGACAAGTACTGACGCTGAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGAAACCCGAGTAGTCC

Genrea	OTU ID	FW	DW1	DW2	DW3	DNA Sequence
	OTU144	6	35	3	0	GTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCAATGCCGCGTGAGTGATGAAGGCCTTAGGGTTGTAAAGCTCTTTTACCCGGGATGATAATGACAGTACCGGGAGAATAAGCTCCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGAGCTAGCGTTATTCGGAATTACTGGGCGTAAAGCGCACGTAGGCGGCTTTGTAAGTAAGAGGTGAAAGCCCAGAGCTCAACTCTGGAATTGCCTTTTAGACTGCATCGCTTGAATCATGGAGAGGTCAGTGGAATTCCGAGTGTAGAGGTGAAATTCGTAGATATTCGGAAGAACACCAGTGGCGAAGGCGGCTGACTGGACATGTATTGACGCTGAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGAAACCCTGGTAGTCC
	OTU320	80	34	100	75	GTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCAATGCCGCGTGAGTGATGAAGGCCCTAGGGTTGTAAAGCTCTTTTACCCGGGAAGATAATGACTGTACCGGGAGAATAAGCCCCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGAGGgggCTAGCGTTGTTCGGAATTACTGGGCGTAAAGCGCACGTAGGCGGCTTTGTAAGTCAGAGGTGAAAGCCTGGAGCTCAACTCCAGAACTGCCTTTGAGACTGCATCGCTTGAATCCAGGAGAGGTCAGTGGAATTCCGAGTGTAGAGGTGAAATTCGTAGATATTCGGAAGAACACCAGTGGCGAAGGCGGCTGACTGGACTGGTATTGACGCTGAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGAAACCCTTGTAGTCC
	OTU337	141	2105	289	604	GTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCAATGCCGCGTGAGTGATGAAGGCCTTAGGGTTGTAAAGCTCTTTTACCCGGGATGATAATGACAGTACCGGGAGAATAAGCTCCGGCTAACTTCGTGCCAGCAGCCGCGGTAATACGAGGGGAGCTAGCGTTATTCGGAATTACTGGGCGTAAAGCGCACGTAGGCGGCTTTGTAAGTTAGAGGTGAAAGCCCGGGGCTCAACTCCGGAATTGCCTTTAAGACTGCATCGCTTGAATCCAGGAGAGGTGAGTGGAATTCCGAGTGTAGAGGTGAAATTCGTAGATATTCGGAAGAACACCAGTGGCGAAGGCGGCTCACTGGACTGGTATTGACGCTGAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCGGGTAGTCC
	OTU3	750	1154	1063	1512	GTGGGGAATATTGGACAATGGGCGCAAGCCTGATCCAGCCATGCCGCGTGAGTGATGAAGGCCTTAGGGTTGTAAAGCTCTTTTACCCGGGAAGATAATGACTGTACCGGGAGAATAAGCTCCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGAGCTAGCGTTGTTCGGAATTACTGGGCGTAAAGCGCACGTAGGCGGCTTTGTAAGTTAGAGGTGAAAGCCTGGAGCTCAACTCCAGAATTGCCTTTAAGACTGCATCGCTTGAATCCAGGAGAGGTGAGTGGAATTCCGAGTGTAGAGGTGAAATTCGTAGATATTCGGAAGAACACCAGTGGCGAAGGCGGCTCACTGGACTGGTATTGACGCTGAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCCAGTAGTCC
	Total	**977**	**3334**	**1459**	**2191**	
Staphylococcus	OTU339	8	1	0	0	GTAGGGAATCTTCCGCAATGGGCGAAAGCCTGACGGAGCAACGCCGCGTGAGTGATGAAGGTCTTCGGATCGTAAAACTCTGTTATCAGGGAAGAACAAATGTGTAAGTAACTGTGCACATCTTGACGGTACCTGATCAGAAAGCCACGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGCgcgcgTAGGCGGTTttttAAGTCTGATGTGAAAGCCCACGGCTCAACCGTGGAGGGTCATTGGAAACTGGAAAACTTGAGTGCAGAAGAGGAAAGTGGAATTCCATGTGTAGCGGTGAAATGCGCAGAG

Genrea	**OTU ID**	**FW**	**DW1**	**DW2**	**DW3**	**DNA Sequence**
						ATATGGAGGAACACCAGTGGCGAAGGCGACTTTCTGGTCTGTAACTGACGCTGATGTGCGAAAGCGTGGGGATCAAACAGGATTAGAAACCCTAGTAGTCC
	Total	**8**	**1**	**0**	**0**	