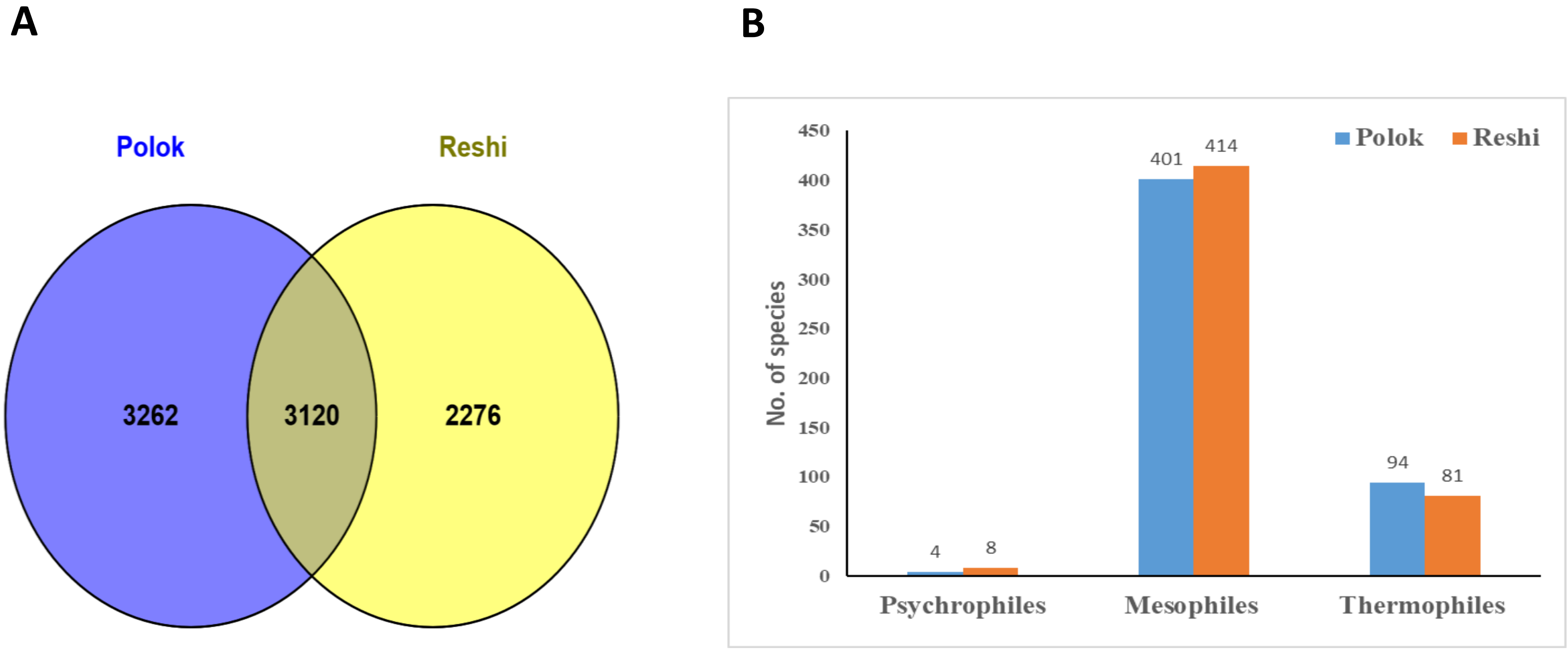
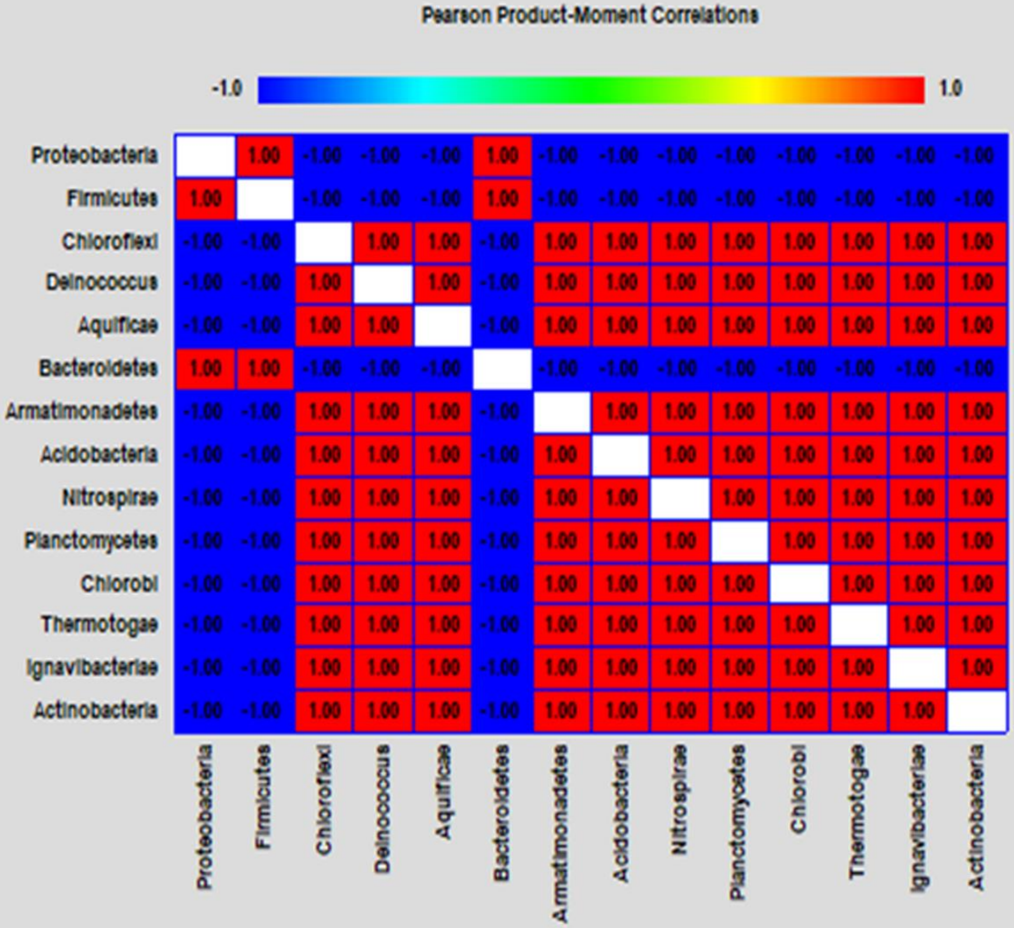


Fig. S1. (A) Species count commonly and exclusively present in Polok and Reshi, (B) Total number of mesophiles, thermophiles and psychrophiles in Polok and Reshi.



	Proteobacteria	Firmicutes	Chloroflexi	Deinococcus	Aquificae	Bacteroidetes	Armatimonadetes	Acidobacteria	Nitrospirae	Planctomycetes	Chlorobi	Thermotogae	Ignavibacteriae	Actinobacteria
Proteobacteria		1.00	-1.00	-1.00	-1.00	1.00	-1.00	-1.00	-1.00	-1.00	-1.00	-1.00	-1.00	-1.00
Firmicutes	1.00		-1.00	-1.00	-1.00	1.00	-1.00	-1.00	-1.00	-1.00	-1.00	-1.00	-1.00	-1.00
Chloroflexi	-1.00	-1.00		1.00	1.00	-1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Deinococcus	-1.00	-1.00	1.00		1.00	-1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Aquificae	-1.00	-1.00	1.00	1.00		-1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Bacteroidetes	1.00	1.00	-1.00	-1.00	-1.00		-1.00	-1.00	-1.00	-1.00	-1.00	-1.00	-1.00	-1.00
Armatimonadetes	-1.00	-1.00	1.00	1.00	1.00	-1.00		1.00	1.00	1.00	1.00	1.00	1.00	1.00
Acidobacteria	-1.00	-1.00	1.00	1.00	1.00	-1.00	1.00		1.00	1.00	1.00	1.00	1.00	1.00
Nitrospirae	-1.00	-1.00	1.00	1.00	1.00	-1.00	1.00	1.00		1.00	1.00	1.00	1.00	1.00
Planctomycetes	-1.00	-1.00	1.00	1.00	1.00	-1.00	1.00	1.00	1.00		1.00	1.00	1.00	1.00
Chlorobi	-1.00	-1.00	1.00	1.00	1.00	-1.00	1.00	1.00	1.00	1.00		1.00	1.00	1.00
Thermotogae	-1.00	-1.00	1.00	1.00	1.00	-1.00	1.00	1.00	1.00	1.00	1.00		1.00	1.00
Ignavibacteriae	-1.00	-1.00	1.00	1.00	1.00	-1.00	1.00	1.00	1.00	1.00	1.00	1.00		1.00
Actinobacteria	-1.00	-1.00	1.00	1.00	1.00	-1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	

Fig. S2. Pearson product moment correlation plot at phylum level.

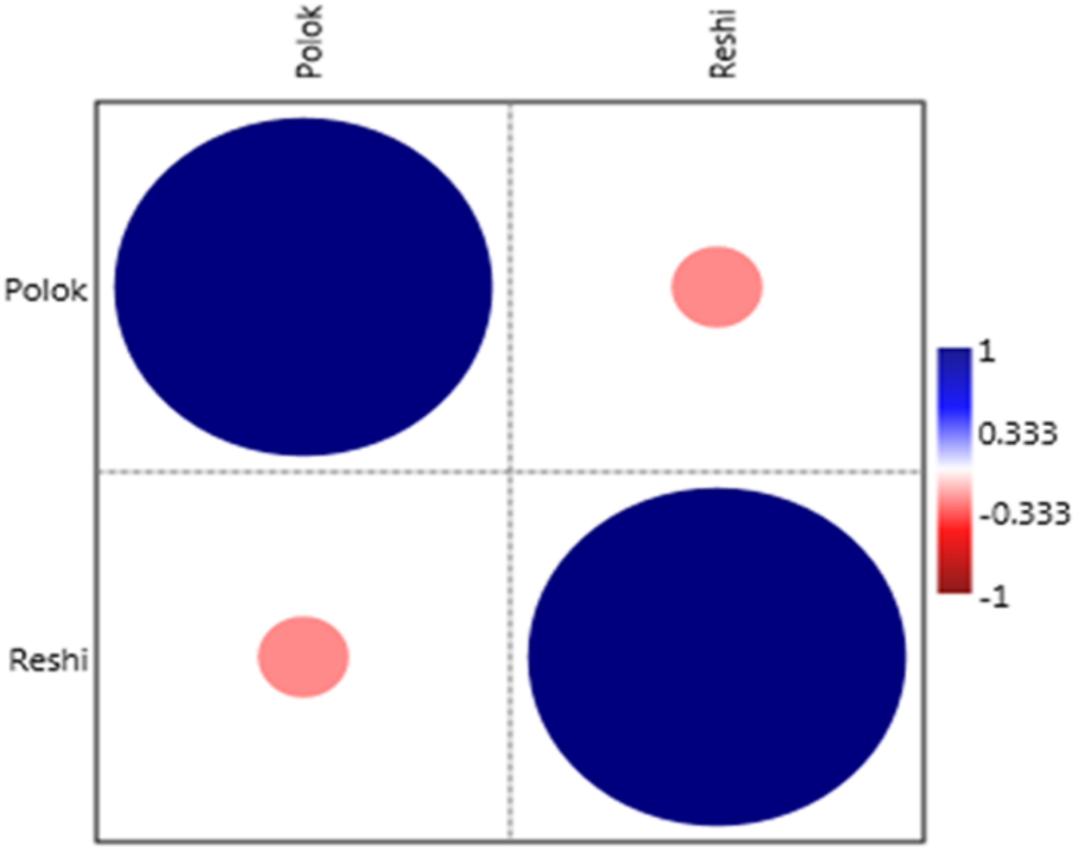


Fig. S3. Relative abundance of microbial species in Polok and Reshi hot springs.

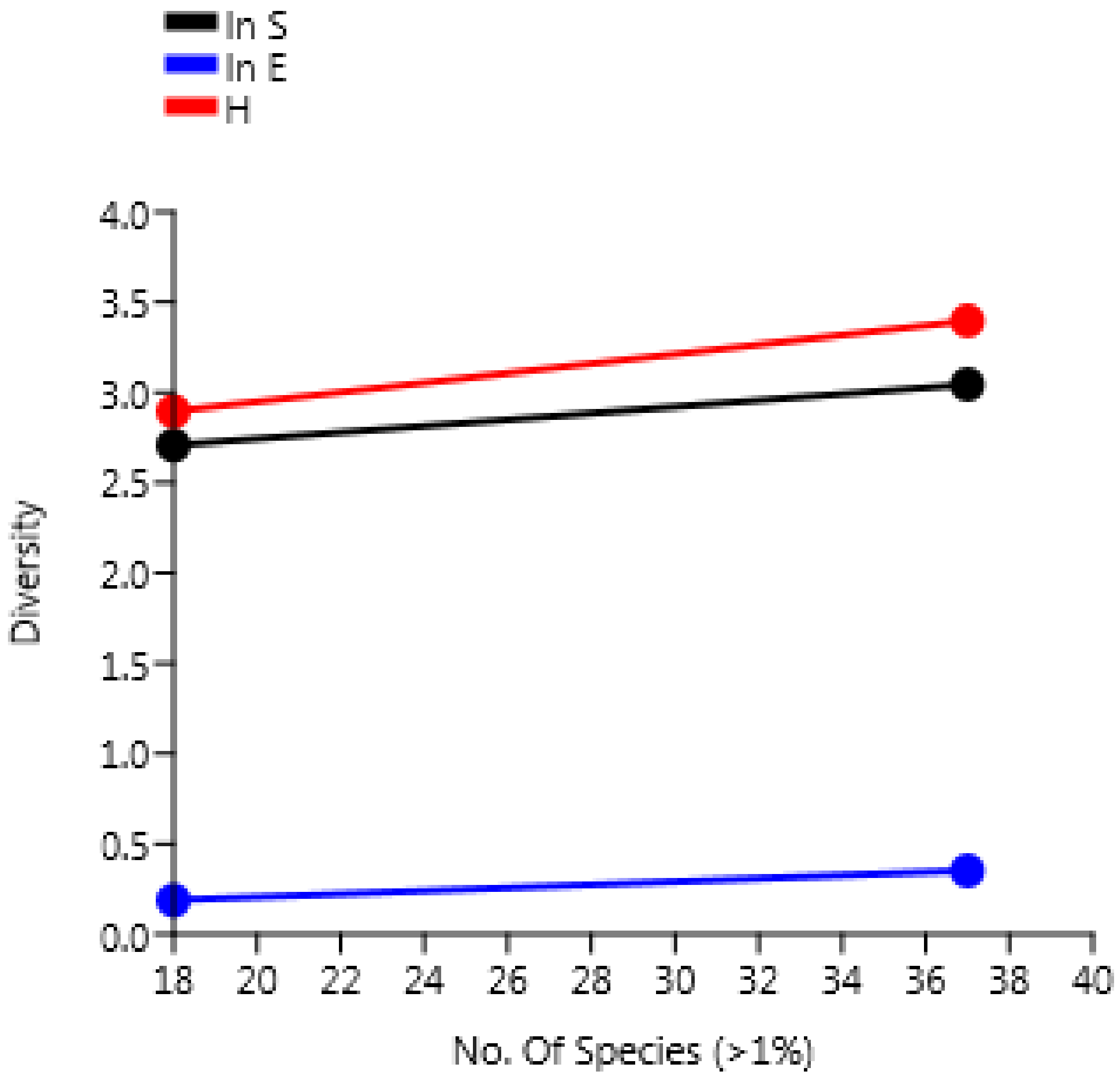


Fig. S4. SHE analysis of microbial species distribution in Polok and Reshi.

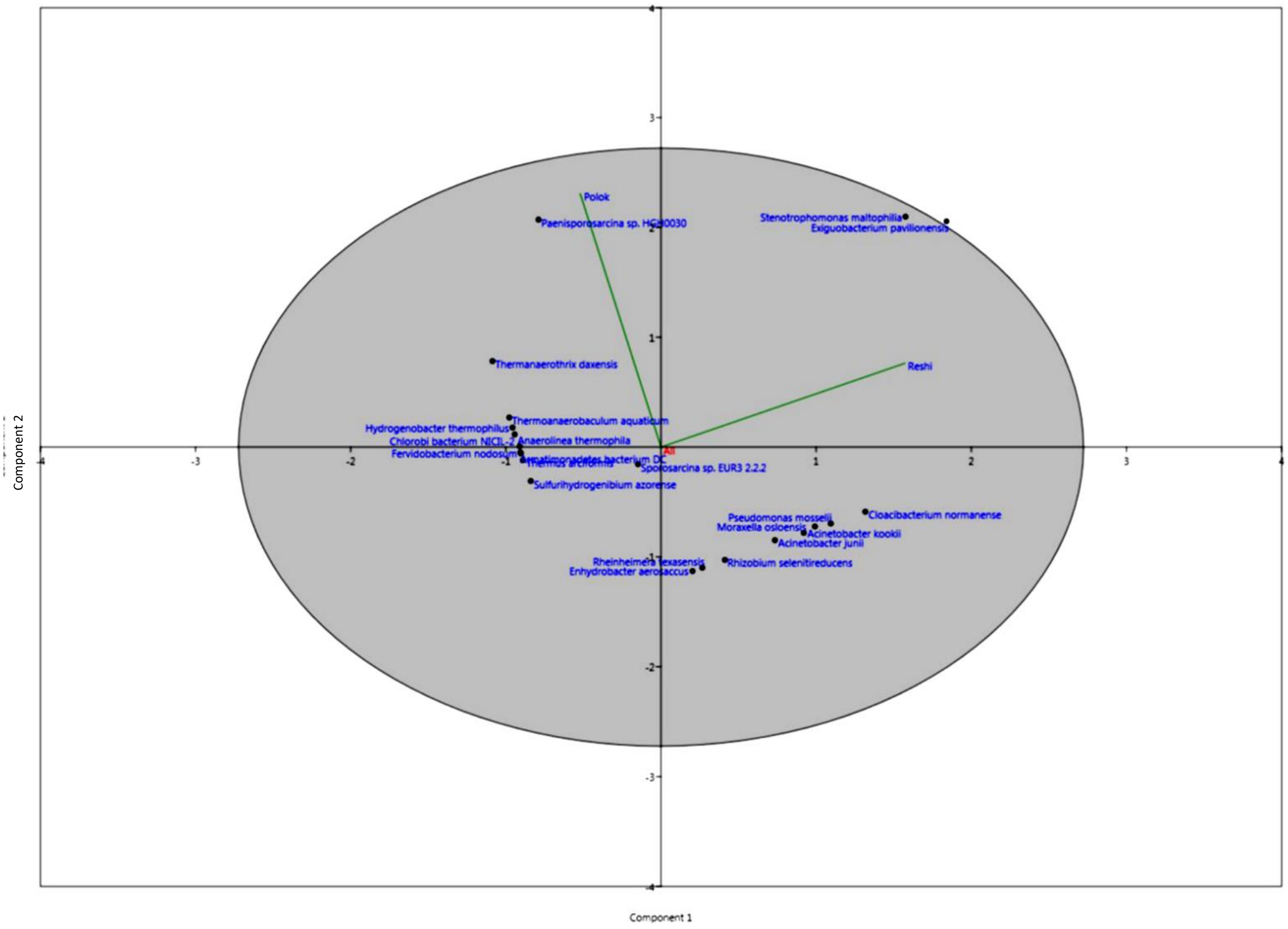


Fig. S5. Principle component analysis (PCA) at species level.

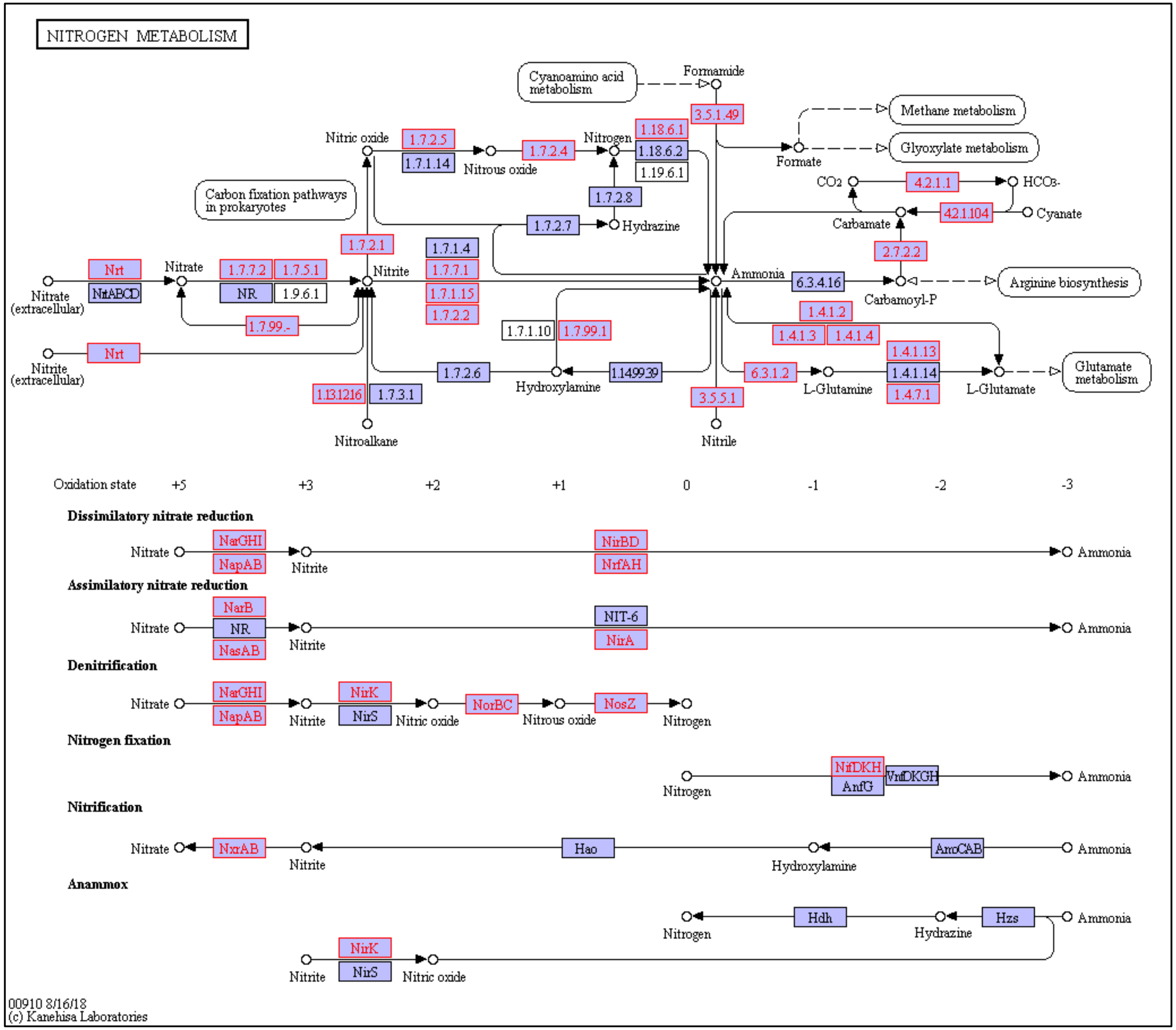


Fig. S6. Metagenomic genes mapped to nitrogen metabolism.

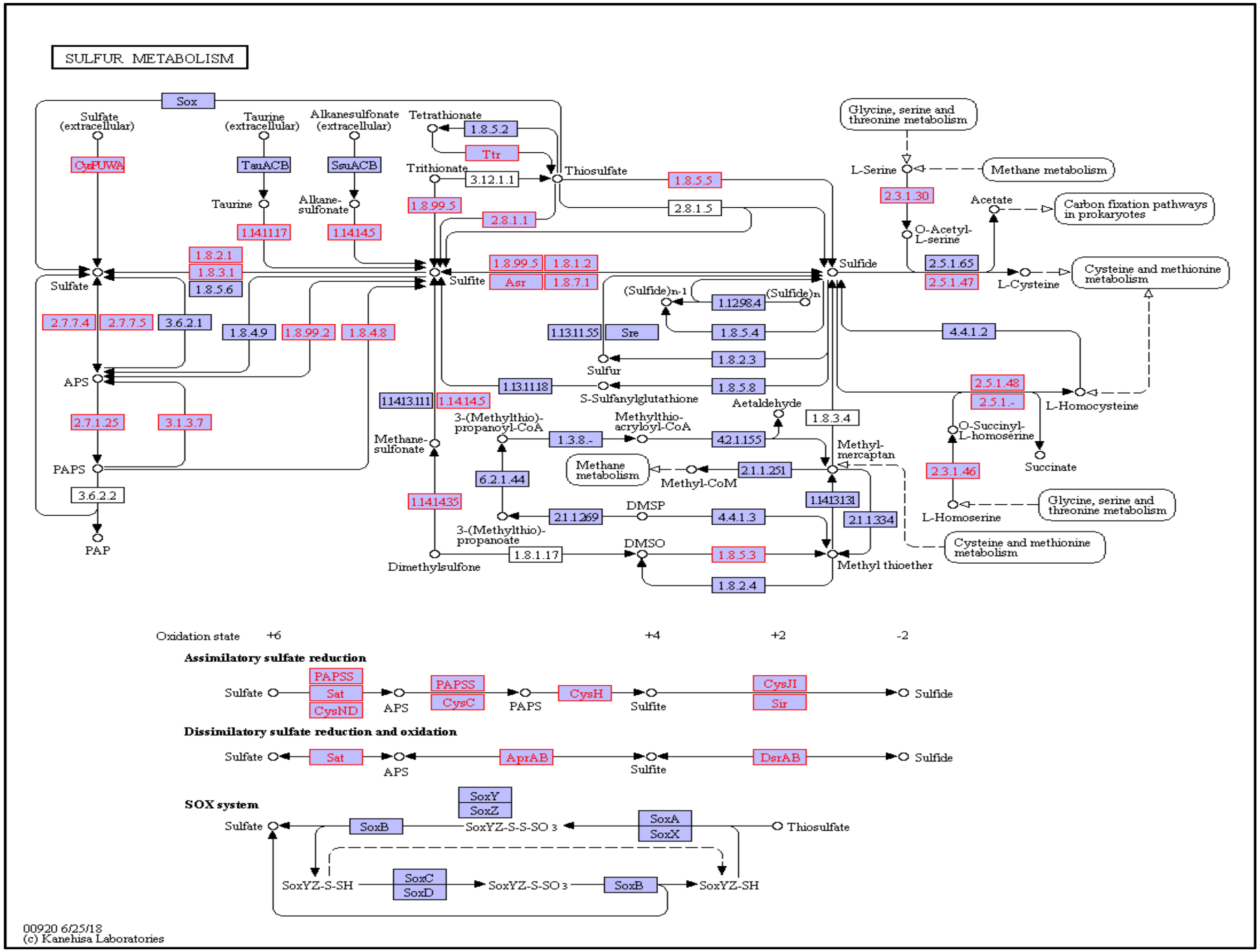


Fig. S7. Metagenomic genes mapped to sulphur metabolism.

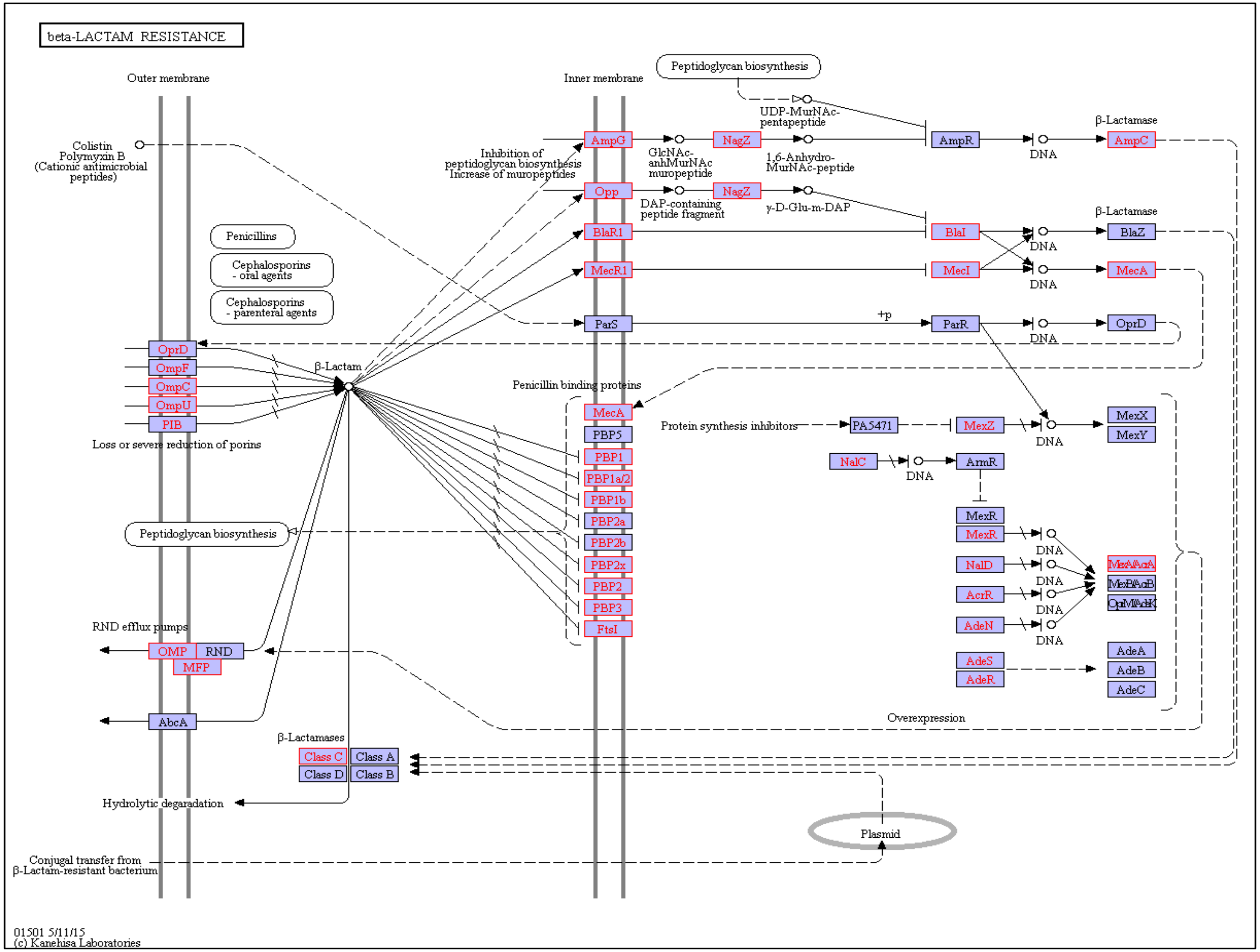


Fig. S8. Metagenomic genes mapped to beta-Lactam resistance pathway.

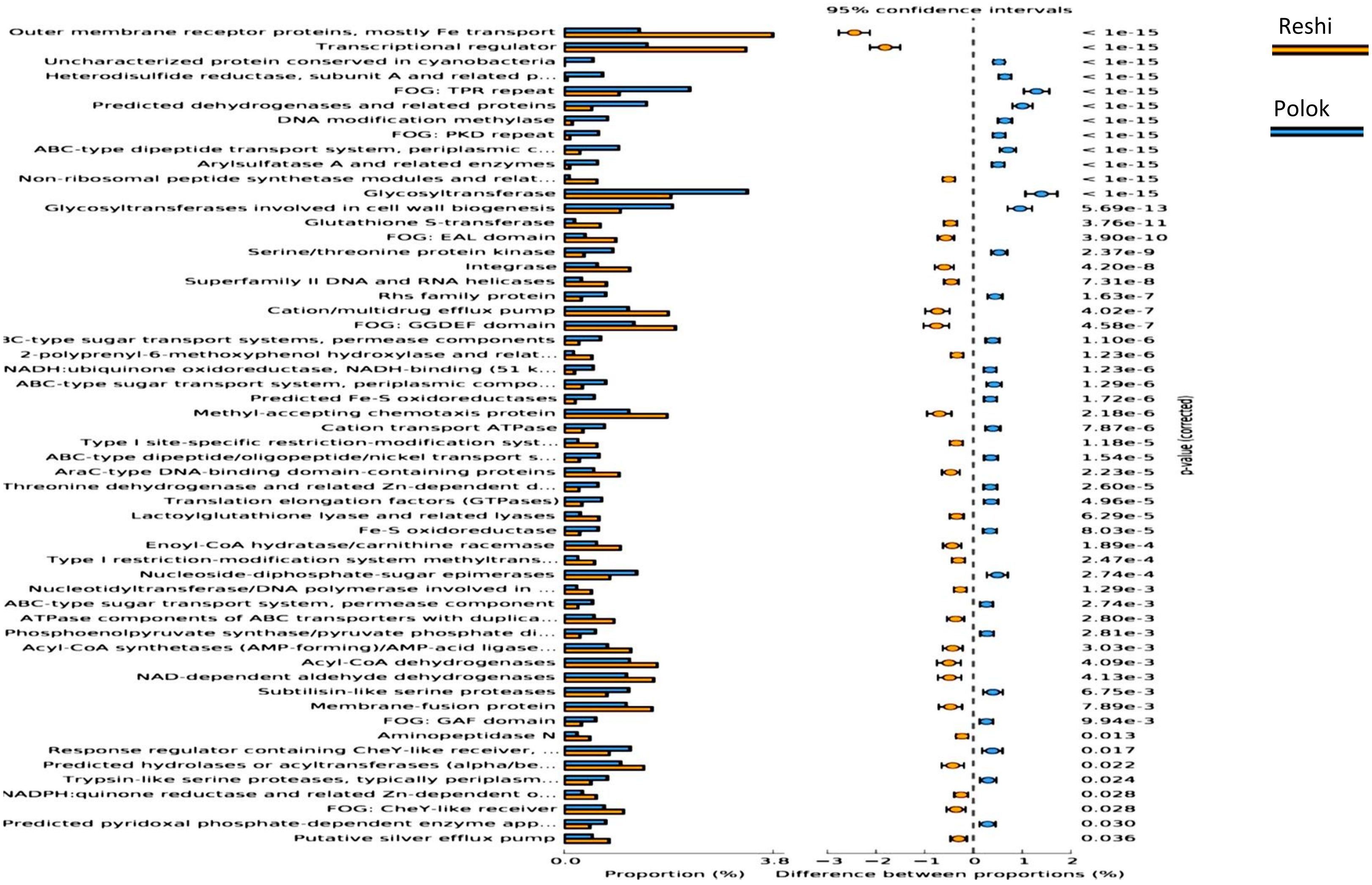


Fig. S9. ORFs mapped to top 100 COG functions in the metagenome. Differential proportion of ORFs is statistically validated by STAMP tool using Fisher exact test with Bonferroni correction. The details of ORF distribution are given in Table S17.