

Sample site	Group 1 - Fv 3	Group 2 - Fv 4	Group 3 - Fv 5	Group 4 - Fv 6	Group 5 - Fv7	After copying files to your home directory, go to your home directory and change permissions with the chmod command: cd ~ chmod -R a+w <name-of-copied-directory>
GPS location	69.72892,18.94781	69.72922,18.94847	69.72900,18.94826	69.72895,18.94828	69.72891,18.94858	
Temperature	4	5	5	4.5	4.5	
QC, assembly and binning						
Number of reads in total (R1 + R2)	4913432	5338312	4258868	4182372	6201964	
Number of contigs > 1000bp	12 290	9731	5742	73759	1481	
Total length of the contigs > 1000bp	17 057 906	13524910	7372006	9116201	2359160	
Length of the longest contig	7404	6219	5568	8944	6086	
Number of bins	7	8	5	7	13	
Completeness (%) of "best" bin	70	87.5	67.5	67.5	80	
Size (Mb) of "most complete bin	1.3	1720859	2.85	2.57	2.39	
Taxonomy of the "best" bin	Proteobacteria 85 % (kaiju)	Proteobacteria (phylum)	Proteobacteria(phylum)	Flavobacteriacea (70 %)	Cyanobacteria	
Taxonomy						
How many reads consists of 16S rRNA sequences	3046	2748	2278	2753	3838	
The most dominant taxa (16S) on Phylum level	Proteobacteria 37%	Proteobacteria (32%)	84%Bacteria(30%Proteobacteria)	Proteobacteria (31%)	Proteobacteria (24%)	
Relative abundance of the most abundant genus (16S rRNA)	catecholium 1%	Eudoraea (2%)	0.39% Eudorea	Eudoraea (2.13%)	Anabaena (1.13%)	
The most dominant taxa (Kraken) on Phylum level	Proteobacteria 49%	Proteobacteria (0.8%)	50% Proteobacteria	2 % Bacteria (Proteobacteria 1%)	Proteobacteria (48%)	
Relative abundance of the most abundant genus (Kraken)	Octadecabacter 0.4%		2% actinobacteria	Octadecabacter (0.02%)	Anabaena (9%)	
The most dominant taxa (Kaiju) on Phylum level	Proteobacteria 48%	Proteobacteria (48%)	50% Proteobacteria	Proteobacteria (42%)	Proteobacteria (36%)	
Number of reads mapped to the most abundant genera (Kaiju)	Maribacter (18539)	unclassified gammaproteobacteria (4%)	19351 (Rhodopirellula)	Lewinella (34802)	Lewinella (76439)	
Functional						
Number of protein coding sequences in the "best" bin	1709		3638		2364	
Functional profile of the "best" bin					No resistance genes, virulence genes, plasmids etc	
Antimicrobial resistance genes in the complete metagenome	0 genes identified (Abricate)		1		2 9 (no complete genes)	