

Supplementary Table 2. Relative abundance (percentage) of EMIRGE outputs reconstructed from the different libraries.

Taxa	Metagenome		Metatranscriptome - Night time				Metatranscriptome - Day time			
			Total RNA ^a		DSN Treated ^b		Total RNA		DSN Treated	
	Abundance (%)	OTUs	Abundance (%)	OTUs	Abundance (%)	OTUs	Abundance (%)	OTUs	Abundance (%)	OTUs
Archaea	0.6	2	0.3	2	0.6	2	0.3	1	0.1	1
Acidobacteria	1.5	16	1.8	480	5.8	428	3.4	7	0.1	1
Actinobacteria_Acidimicrobiales	0.9	9	1.0	180	2.7	171	3.0	5	0.2	2
Actinobacteria_Actinomycetales	18.2^c	50	8.7	496	18.9	459	BDL	0	2.7	35
Actinobacteria_others	BDL	0	0.3	42	0.6	34	BDL	0	BDL	0
Actinobacteria_Rubrobacteridae	7.2	26	4.2	219	10.8	206	BDL	0	1.2	12
Bacteroidetes	4.4	23	1.7	202	1.7	156	0.5	2	0.7	9
Chloroflexi	1.5	8	2.2	205	3.3	148	BDL	0	0.6	12
Cyanobacteria_Microcoleus	44.3	7	36.8	83	6.4	49	69.3	12	23.6	30
Cyanobacteria_others	3.5	12	13.9	143	2.5	63	13.2	13	5.6	21
Firmicutes	1.6	9	4.7	146	5.0	86	1.6	3	1.0	8
Gemmatimonadetes	BDL	0	2.0	108	1.1	75	1.6	2	1.0	5
Planctomycetes	1.0	7	4.1	477	11.7	442	0.3	1	0.5	8
Proteobacteria_Alphaproteobacteria	13.3	62	8.1	765	10.4	538	5.1	8	39.0	48
Proteobacteria_Betaproteobacteria	0.4	6	1.5	251	2.2	169	1.5	1	1.1	11
Proteobacteria_Deltaproteobacteria	0.4	3	2.3	238	5.1	150	BDL	0	0.1	2
Proteobacteria_Gammaproteobacteria	BDL ^d	0	0.2	59	0.4	51	BDL	0	BDL	0
Proteobacteria_others	BDL	0	0.1	35	0.3	29	BDL	0		0
Verrucomicrobia	0.1	1	0.7	146	1.7	193	BDL	0	0.1	1
Bacteria_other	1.2	10	3.4	258	2.3	192	0.1	1	22.6	7
Fungi	BDL	0	1.3	80	5.3	80	BDL	0	BDL	0
Nematoda	BDL	0	0.0	9	0.2	17	BDL	0	BDL	0
Plantae	BDL	0	0.1	18	0.2	19	BDL	0	BDL	0

Protozoa	BDL	0	0.1	24	0.3	21	BDL	0	BDL	0
Eukaryotes_other	BDL	0	0.2	44	0.7	51	BDL	0	BDL	0
Total		251		4710		3829		56		213

^aTotal RNA, metatranscriptomic libraries constructed with total cDNA.

^bDSN Treated, metatranscriptomic libraries constructed with cDNA treated with double strand nuclease.

^cNumbers in bold represent the three most abundant taxa per library.

^dBDL, below detection limit