Probematch search was restricted to region relative to positions in E. coli: 300 to 850
RDP Release 11, Update 1 :: October 2013

		DegePrime				EMP	
Taxonomic group	**Number of sequences**	**341F**	**341'F**	**515'F**	**805R**	**515F**	**806R**
domain Bacteria	1534872	0.96	0.93	0.93	0.90	0.93	0.91
phylum "Actinobacteria"	204784	0.97	0.97	0.72	0.71	0.72	0.71
phylum "Aquificae"	1279	0.97	0.97	0.97	0.95	0.97	0.95
phylum "Bacteroidetes"	182923	0.97	0.97	0.97	0.96	0.97	0.95
phylum "Caldiserica"	263	0.98	0.98	0.00	0.97	0.00	0.95
phylum "Chlamydiae"	563	0.76	0.01	0.01	0.96	0.01	0.96
phylum "Chlorobi"	1531	0.95	0.95	0.62	0.95	0.62	0.95
phylum "Chloroflexi"	25804	0.89	0.76	0.96	0.35	0.96	0.59
phylum "Chrysiogenetes"	13	0.85	0.85	1.00	1.00	1.00	1.00
phylum "Deferribacteres"	734	0.99	0.99	0.98	0.96	0.98	0.93
phylum "Deinococcus-Thermus"	2556	0.97	0.97	0.98	0.97	0.98	0.97
phylum "Dictyoglomi"	36	1.00	1.00	0.97	1.00	0.97	1.00
phylum "Elusimicrobia"	326	0.97	0.98	0.98	0.94	0.98	0.95
phylum "Fibrobacteres"	462	0.96	0.96	0.98	0.96	0.98	0.96
phylum "Fusobacteria"	10194	0.95	0.95	0.97	0.97	0.97	0.97
phylum "Gemmatimonadetes"	2152	0.98	0.98	0.97	0.93	0.97	0.93
phylum "Lentisphaerae"	1978	0.94	0.00	0.98	0.96	0.97	0.93
phylum "Nitrospira"	2258	0.98	0.98	0.97	0.95	0.97	0.95
phylum "Planctomycetes"	14348	0.81	0.01	0.93	0.94	0.93	0.91
phylum "Proteobacteria"	454358	0.98	0.98	0.97	0.94	0.97	0.94
phylum "Spirochaetes"	10644	0.92	0.92	0.97	0.86	0.97	0.79
phylum "Synergistetes"	1649	0.98	0.98	0.97	0.94	0.97	0.94
phylum "Tenericutes"	4064	0.94	0.94	0.93	0.96	0.93	0.93
phylum "Thermodesulfobacteria"	166	0.96	0.96	0.96	0.99	0.96	0.99
phylum "Thermotogae"	777	0.97	0.97	0.97	0.94	0.97	0.94
phylum BRC1	477	0.94	0.94	0.96	0.97	0.96	0.97
phylum OD1	411	0.68	0.00	0.00	0.88	0.00	0.84
phylum OP11	150	0.21	0.01	0.27	0.00	0.27	0.00
phylum SR1	466	0.95	0.96	0.97	0.97	0.97	0.97
phylum TM7	2596	0.97	0.97	0.00	0.88	0.00	0.81
phylum WS3	672	0.96	0.98	0.97	0.97	0.97	0.97
phylum "Armatimonadetes"	1576	0.29	0.05	0.97	0.91	0.97	0.91
phylum "Verrucomicrobia"	12387	0.98	0.00	0.96	0.93	0.96	0.93
phylum "Acidobacteria"	27092	0.98	0.97	0.98	0.95	0.98	0.95
phylum Firmicutes	483681	0.97	0.96	0.97	0.96	0.97	0.96
phylum Cyanobacteria/Chloroplast	30775	0.93	0.93	0.98	0.95	0.98	0.91
unclassified_Bacteria	50727	0.84	0.66	0.88	0.86	0.88	0.84
domain Archaea	78684	0.00	0.90	0.96	0.94	0.53	0.93
phylum "Crenarchaeota"	20677	0.00	0.89	0.97	0.93	0.00	0.93
phylum "Euryarchaeota"	41963	0.00	0.93	0.96	0.95	0.94	0.94
phylum "Korarchaeota"	221	0.00	0.93	0.95	0.93	0.29	0.94
phylum "Nanoarchaeota"	138	0.00	0.00	0.00	0.00	0.00	0.00
phylum "Thaumarchaeota"	0	NA	NA	NA	NA	NA	NA
unclassified_Archaea	15685	0.00	0.85	0.96	0.93	0.16	0.93

Primer Name	**Primer sequence**	**Reference**
341F (DegePrime)	CCTACGGGNGGCWGCAG	Herlemann, D. et al, ISMEj 2011; this work
341'F (DegePrime)	CCTAHGGGRBGCAGCAG	This work
515'F (DegePrime)	GTGBCAGCMGCCGCGGTAA	This work
805R (DegePrime)	GACTACHVGGGTATCTAATCC	Herlemann, D. et al, ISMEj 2011; this work
515F (EMP)	GTGCCAGCMGCCGCGGTAA	Caporaso, J.G. et al, PNAS 2011
806R (EMP)	GGACTACHVGGGTWTCTAAT	Caporaso, J.G. et al, PNAS 2011

Supplementary table 1. Taxonomic coverage of primers as deduced by the Probe Match tool in RDP (http://rdp.cme.msu.edu/). The search was conducted against release 11 update 1 of RDP and including only sequences spanning E.coli postions 300 to 850 and only including sequences with good quality scores.

	Primer sequence	Moose	Marine	Moose	Marine
		Total 16S reads			
		21233	20953		
		Matched reads		%matched relative to degenerate primer	
341F	CCTACGGG[ACTG]GGC[AT]GCAG	872	2155	100	100
	CCTACGGG[A]GGC[A]GCAG	837	2079	95.99	96.47
	CCTACGGG[A]GGC[T]GCAG	21	12	2.41	0.56
	CCTACGGG[C]GGC[A]GCAG	8	8	0.92	0.37
	CCTACGGG[C]GGC[T]GCAG	0	1	0.00	0.05
	CCTACGGG[G]GGC[A]GCAG	4	20	0.46	0.93
	CCTACGGG[G]GGC[T]GCAG	0	1	0.00	0.05
	CCTACGGG[T]GGC[A]GCAG	2	27	0.23	1.25
	CCTACGGG[T]GGC[T]GCAG	0	7	0.00	0.32
515'F	GTG[TCG]CAGC[AC]GCCGCGGTAA	878	2432	100	100
	GTG[C]CAGC[A]GCCGCGGTAA	873	2392	99.43	98.36
	GTG[C]CAGC[C]GCCGCGGTAA	3	6	0.34	0.25
	GTG[G]CAGC[A]GCCGCGGTAA	2	14	0.23	0.58
	GTG[G]CAGC[C]GCCGCGGTAA	0	5	0.00	0.21
	GTG[T]CAGC[A]GCCGCGGTAA	0	12	0.00	0.49
	GTG[T]CAGC[C]GCCGCGGTAA	0	3	0.00	0.12
805R	GGATTAGATACCC[CTG][AGT]GTAGTC	764	1287	100	100
	GGATTAGATACCC[C][A]GTAGTC	10	59	1.31	4.58
	GGATTAGATACCC[C][G]GTAGTC	65	48	8.51	3.73
	GGATTAGATACCC[C][T]GTAGTC	0	21	0.00	1.63
	GGATTAGATACCC[G][A]GTAGTC	0	11	0.00	0.85
	GGATTAGATACCC[G][G]GTAGTC	4	7	0.52	0.54
	GGATTAGATACCC[G][T]GTAGTC	0	0	0.00	0.00
	GGATTAGATACCC[T][A]GTAGTC	16	0	2.09	0.00
	GGATTAGATACCC[T][G]GTAGTC	668	1132	87.43	87.96
	GGATTAGATACCC[T][T]GTAGTC	1	9	0.13	0.70

Supplementary table 2. In silico matching of primer sequences to 16S sequence reads from the two shotgun metagenomes.
Total 16S reads are all reads extracted with sortmeRNA. These 100 bp reads are distribured over the 16S gene, only a subset of them overlap with the primers. Matched reads are reads that perfectly match (forward or reverse complementary) to the primer.

References

Herlemann DP, Labrenz M, Jurgens K, Bertilsson S, Waniek JJ, Andersson AF. 2011. Transitions in bacterial communities along the 2000 km salinity gradient of the Baltic Sea. ISME J 5:1571-1579.

Caporaso JG, Lauber CL, Walters WA, Berg-Lyons D, Lozupone CA, Turnbaugh PJ, Fierer N, Knight R. 2011. Global patterns of 16S rRNA diversity at a depth of millions of sequences per sample. Proc Natl Acad Sci U S A 108 Suppl 1:4516-4522.