

Supplemental Table S1. List of primers used for the quantification of microbial populations by ddPCR

Primer name	Primer Sequence	Amplicon size	Target group	Reference
16S bacteria Fwd	5'GACTCCTACGGGAGGCAG3'	From 175 to 200 pb	α -bacteria γ -bacteria Firmicutes Bacteroidetes Actinobacteria <i>etc.</i>	Petrova <i>et al.</i> [1]
16S bacteria Rev	5'GTATTACCGCGGCTGCTG3'			
23S bacteria Fwd	5'GAGTAGGACGGAGCACGAG3'	161 pb	α -bacteria γ -bacteria Firmicutes Bacteroidetes Actinobacteria <i>etc.</i>	Petrova <i>et al.</i> [1]
23S bacteria Rev	5'CTTGTACGCATACGGTTTCAG3'			
16S archaea Fwd	5'AATTGGCGGGGGAGCAC3'	From 137 to 144 pb	Archaeas: Euryarchaeota and Crenarchaeota including: <i>Methanosphaera stadtmanae</i> , <i>Methanobrevibacter</i> sp., <i>Methanosarcina</i> sp.	Bayer <i>et al.</i> [2]
16S archaea Rev	5'GGCCATGCACCWCCTCTC3'			
16S RO Fwd	5'GGGGCTAATACCGGATAGATGATT3'	459 bp	<i>Methanobrevibacter</i> RO group that includes: <i>M. ruminantium</i> , <i>M. olleyae</i>	Danielsson <i>et al.</i> [3]
16S RO Rev	5'CGACCTCAAGTTCAACAGTATCAC3'			
16S SGMT Fwd	5'TCCGTAGCCGGTTTAATAAGTCT3'	From 611 to 614 pb	<i>Methanobrevibacter</i> SGMT group that includes: <i>M. smithii</i> , <i>M. gottschalkii</i> , <i>M. millerae</i> , <i>M. thaueri</i>	Danielsson <i>et al.</i> [3]
16S SGMT Rev	5'TTCCTCCTATTTATCATAGGCGG3'			
<i>mrcA</i> Fwd	5'TTCGGTGGATCDCARAGRGC3'	160 bp	<i>methyl co-enzyme M reductase alpha subunit (mcrA)</i> gene	Denman <i>et al.</i> [4]
<i>mrcA</i> Rev	5'GBARGTCGWAWCCGTAGAATCC3'			
18S fungi Fwd	5'GAGGAAGTAAAAGTCGTAACAAGGTTTC3'	From 110 to 188 pb	Mainly anaerobic fungi including <i>Neocallimastix</i> sp., <i>Orpinomyces</i> sp., <i>Anaeromyces</i> sp.	Denman and McSweeney [5]
18S fungi Rev	5'CAAATTCACAAAGGGTAGGATGATT3'			
18S protozoa Fwd	5'CTTTCGATGGTAGTGTATTGGACTAC3'	From 1363 to 1459 bp	Several protozoa including <i>Epiphyllum</i> sp.	Karnati <i>et al.</i> [6]
18S protozoa Rev	5'TGATCCTTCTGCAGGTTACCTAC3'			

References

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