Table S3: PCR mixtures for DGGE analysis of Archaeal 16S rDNA, Bacterial 16S rDNA and Fungal ITS region

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| PCR-DGGE primers (5’- 3’) | PCR mixtures | Thermal conditions |
| ***Archaeal 16S* rDNA**A2F - TTCCGGTTGATCCYGCCGGA(DeLong, 1992)U1406F - ACGGGCGGTGTGTRC(Koga *et al*., 1993) | 0.2mM dNTPs, 1x buffer (Roche), 0.25µl BSA , 0.5µl DMSO, 0.5µM each primer, 0.2U Taq polymerase (Roche)  | 95ºC 5 min94ºC 1 min, 57.5ºC 30 s, 72ºC 4 min, 35 cyclesfinal extension of 72ºC 7 min |
| ARC344 (\*ACGGGGCGCAGCAG GCGCGA)(Bano *et al*., 2004)517r (ATTACCGCGGCTGCTGG)(Bano *et al*., 2004) | 0.2mM dNTPs, 1x buffer (Roche), 0.4µM each primer, 0.5U Taq polymerase (Roche)  | 94ºC 5min94ºC 45s, 65ºC-62ºC 45s 7 cycles72ºC 30s94ºC 45s, 62ºC-55ºC 45s 6 cycles72ºC 30s94ºC 45s, 55ºC 45s 30 cycles72ºC 30s72ºC 10 min |
| ***Bacterial 16S*** F968 (\*AACGCGAAGAACCTTAC)(Gomes *et al*., 2001)R1401.1b (CGGTGTGTACAAGAC CCGGGAACG)(Brons *and van Elsas*, 2008) | 0.2mM dNTPs, 3.75mM MgCl2, 1x buffer (Bioline), 1% formamide, 0.2µM each primer, 2.5U Taq polymerase (Bioline) | 95ºC 5 min 60ºC 1’( - 1º /cycle, until 55ºC); 72ºC 2 min 10 cycles94ºC 1 min, 55ºC 1 min, 72ºC 2 min 20 cycles 72ºC 10 min |
| ***ITS region***EF4 (GGAAGGGRTGTATTTATTAG)(Smit *et al*., 1999)ITS4 (TCCTCCGCTTATTGATATGC)(White *et al*., 1990)ITS1f (\*CTTGGTCATTTAGAGGA AGTA)(Gardes and Bruns, 1993) ITS-2 (GCTGCGTTCTTCATCGAT GC)(White *et al*., 1990) | 0.2 dNTPs, 2.0 mM MgCl2, 1x buffer (Bioline), 0.025µl T4 gene protein, 0.4µM each primer, 2.5U Taq polymerase (Bioline)0.25mM dNTPs, 2.0mM MgCl2, 1x buffer (Bioline), 0.4µM each primer, 2.5U Taq polymerase (Bioline) | 94ºC 5min94ºC 30s, 55ºC 30s, 72ºC 1 min 30s, 34 cycles72ºC 5 min94º C 5min94º C 30s, 55º C 30s, 72ºC 30s, 34 cycles72º C 5 min |

\* Means that a GC-clamp is present (Muyzer *et al*., 2001)