

Available GAST Reference Databases

Each of the SSU rRNA regions have been exported to separate reference files to match the expected amplicon sequences. The forward and reverse primers are not included in the reference files, as these will be influenced by the primer sequences used for the amplification over the original DNA sequence. The exceptions are the V3-V5 785F-a and the V6-V4 565F-a sequences. The V3-V5 and the V6-V4 amplification products are longer than can be sequenced with the Roche GS-FLX / Titanium (as of May, 2011). To ensure consistent sequence trimming for alignments and other downstream analyses, we have trimmed the sequence to an internal conserved sequence within the read length. These sequences are true to the DNA and have been maintained as part of the reference sequence sets.

SSU rRNA Region	Forward Primer	Reverse Primer
refv3	341F CCTACGGGAGGCAGCAG	533R TTACCGCGGCTGCTGGCAC
refv3a	341F CCTACGGGRSGCAGCAG	531R GCCAGCMGCCGCGGT
refv3v5	341F CCTACGGGAGGCAGCAG	785F-a** GGATTAGATACCC
refv4v6	565F-a** TGGGCGTAAAG	1064R CGACAGCCATGCANCACCT
refv5	784F GGMTTAGATACCC	926R CCGTCAATTCNTTTRAGT
refv6a	958F AATTGGANTCAACGCCGG	1064R CGRCRGCCATGYACCWC
refv6	967F CAACGCGAAGAACCTTACC	1064R CGACAGCCATGCANCACCT
refv9	1389F TTGTACACACCGCCC	1510R CCTTCNGCAGGTTCACCTAC

** Anchors used for trimming rather than primers used for amplification.