Supplementary Table S1

V3_F_modified	aatgatacggcgaccaccgagatctacactctttccctacacgacgctcttccgatctNNNNCCTACGGGAGGCAGCAG
V4_1R	caagcagaagacggcatacgagat**CGTGAT**gtgactggagttcagacgtgtgctcttccgatctGGACTACHVGGGTWTCTAAT
V4_2R	caagcagaagacggcatacgagat**ACATCG**gtgactggagttcagacgtgtgctcttccgatctGGACTACHVGGGTWTCTAAT
V4_3R	caagcagaagacggcatacgagat**GCCTAA**gtgactggagttcagacgtgtgctcttccgatctGGACTACHVGGGTWTCTAAT
V4_4R	caagcagaagacggcatacgagat**TGGTCA**gtgactggagttcagacgtgtgctcttccgatctGGACTACHVGGGTWTCTAAT
V4_5R	caagcagaagacggcatacgagat**CACTGT**gtgactggagttcagacgtgtgctcttccgatctGGACTACHVGGGTWTCTAAT
V4_6R	caagcagaagacggcatacgagat**ATTGGC**gtgactggagttcagacgtgtgctcttccgatctGGACTACHVGGGTWTCTAAT
V4_7R	caagcagaagacggcatacgagat**GATCTG**gtgactggagttcagacgtgtgctcttccgatctGGACTACHVGGGTWTCTAAT
V4_8R	caagcagaagacggcatacgagat**TCAAGT**gtgactggagttcagacgtgtgctcttccgatctGGACTACHVGGGTWTCTAAT
V4_9R	caagcagaagacggcatacgagat**CTGATC**gtgactggagttcagacgtgtgctcttccgatctGGACTACHVGGGTWTCTAAT
V4_10R	caagcagaagacggcatacgagat**AAGCTA**gtgactggagttcagacgtgtgctcttccgatctGGACTACHVGGGTWTCTAAT
V4_11R	caagcagaagacggcatacgagat**GTAGCC**gtgactggagttcagacgtgtgctcttccgatctGGACTACHVGGGTWTCTAAT
V4_12R	caagcagaagacggcatacgagat**TACAAG**gtgactggagttcagacgtgtgctcttccgatctGGACTACHVGGGTWTCTAAT
V4_13R	caagcagaagacggcatacgagat**CGTACT**gtgactggagttcagacgtgtgctcttccgatctGGACTACHVGGGTWTCTAAT
V4_14R	caagcagaagacggcatacgagat**GACTGA**gtgactggagttcagacgtgtgctcttccgatctGGACTACHVGGGTWTCTAAT
V4_15R	caagcagaagacggcatacgagat**GCTCAA**gtgactggagttcagacgtgtgctcttccgatctGGACTACHVGGGTWTCTAAT
V4_16R	caagcagaagacggcatacgagat**TCGCTT**gtgactggagttcagacgtgtgctcttccgatctGGACTACHVGGGTWTCTAAT

Nucleotide sequences of primers used in the construction of libraries for Illumina sequencing. Lowercase letters denote adapter sequences necessary for binding to the flowcell, underlined lowercase are binding sites for the Illumina sequencing primers, bold uppercase highlight the index sequences (additional indexes can be found in the paper by Bartram et al.). Regular uppercase are the V3 and V4 region primers (341F on for the forward primer and 806R for the reverse primers). The inclusion of four maximally degenerated bases ("NNNN") maximizes diversity during the first four bases of the run. Diversity is important for identifying unique clusters and base-calling accuracy [11, 12].

References

- Bokulich NA, Joseph CM, Allen G, Benson AK, Mills DA (2012) Next-generation sequencing reveals significant bacterial diversity of botrytized wine. PLoS One 7:e36357, DOI:10.1371/journal.pone.0036357
- Bartram AK, Lynch MD, Stearns JC, Moreno-Hagelsieb G, Neufeld JD (2011) Generation of multimillion-sequence 16S rRNA gene libraries from complex microbial communities by assembling paired-end illumina reads. Appl Environ Microbiol 77:3846-3852, DOI:10.1128/AEM.02772-10