

NGS Promotion at StarSEQ: 16S and ITS Microbiome Analysis

**“All in One Microbiome” Packages:
High Throughput Amplicon Generation, Sequencing and Analysis**

Choose your option of Amplicon sequencing:



Bacterial microbiome analysis:

16S V4 region, Primer combination: 515F – 806R¹

16S V4-V5 region, Primer combination: 515F – 909R¹

Fungal microbiome analysis:

ITS ITS 1 region, Primer combination: ITS1F – ITS2²

Send us your gDNA samples and make use of our “All in One” Service:



- Quality control
- Single step amplicon generation with reduced bias
- Double indexing, quality check, quantification, normalization and pooling of amplicons
- Illumina MiSeq sequencing: 2 x 300 nt paired-end sequencing with V3 chemistry
- Output: 30-40 M reads (including 25 % PhiX to balance the composition of bases)
- De-multiplexing of reads
- Free 16S metagenomics analysis (Illumina App)
- Data delivery via FTP server



Package A: 48 samples only 75 € per sample

Package B: 96 samples only 50 € per sample

Package C: 192 samples only 32 € per sample

**Please contact us if you are interested in further service options
or other gene regions and we will find YOUR optimal solution!**
microbiome@starseq.com



Primer sequence references:

¹Apprill A, McNally S, Parsons R, Weber L. 2015. Minor revision to V4 region SSU rRNA 806R gene primer greatly increases detection of SAR11 bacterioplankton. *Aquat Microb Ecol* 75:129–137. Parada AE, Needham DM, Fuhrman JA. Every base matters: assessing small subunit rRNA primers for marine microbiomes with mock communities, time series and global field samples. *Environ Microbiol*. 2016;18: 1403–1414.

²White, T. J., T. Bruns, S. Lee, and J. W. Taylor. 1990. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. Pp. 315-322 In: *PCR Protocols: A Guide to Methods and Applications*. Academic Press, New York, NY. Gardes, M., and T. D. Bruns. 1993. ITS primers with enhanced specificity for basidiomycetes - application to the identification of mycorrhizae and rusts. *Mol. Ecol*. 2: 113-118.

Sequencing of your ready to load 16S libraries:



- Illumina MiSeq sequencing: 2 x 300 nt paired-end sequencing with V3 chemistry
- Output 30-40 M reads (including 25 % PhiX to balance the composition of bases)
- De-multiplexing of reads
- Free 16S metagenomics analysis (Illumina App)
- Data delivery via FTP server

Only 2600 €

Optimize your research with our 16S/ITS workflow solutions



From sample prep to library prep to sequencing and bioinformatics. StarSEQ offers a complete and comprehensive workflow for various 16S/ITS applications. Sequencing of the hypervariable regions of the 16S rRNA gene is the gold-standard for identification and classification of bacteria communities within a given sample.

StarSEQ is using established gold-standard primer sequences to target regions covering the hypervariable regions V3-V4, V4 and V4-V5. In contrast to common used methods, StarSEQ has designed its own single-step technique for contemporaneous amplification, indexing and adapting of samples to reduce the bias caused during PCR.

Applications:

- Environmental Metagenomics (soil, water, air)
- Human or Animal Microbiome (skin, stool, blood, swab)
- Sterility Monitoring
- Detection of Contamination
- Monitoring of Biogas Plant
- Biosafety Monitoring
- Food Quality
- Clinical Samples

**You have no time/staff for routine preparation of gDNA
from your collected samples?**

**As an additional service we offer also the purification of gDNA
from various starting material.**

Prices without tax. Cannot be combined with other promotions or discounts. Valid until 31.03.2017