

IT CAN ONLY GET BETTER PROMOTION 2021



Flexible Voucher Option! Buy now and perform this or any other project within 12 months.

RNAseq promotion and voucher option

LOW THROUGHPUT RNA ANALYSIS: LIBRARY, SEQUENCING-RUN AND BIOINFORMATICS

Service includes:

- Quality and quantity check of total RNA
- mRNA isolation from total RNA starting from 1 sample
- NEBNext[®] Ultra[™] II Directional RNA library preparation
- Quantification and QC of library
- Sequencing of 1 x 50 nt / 2 x 150 nt with Illumina NextSeq 2000[™]
- Bioinformatic data analysis 1: RNA-Seq Alignment to reference genomes² (STAR aligner, DRAGEN)
- Data delivery of FASTQ and bioinformatic analysis files via download



Output:

- 25 mio PE reads¹ (2 x 150 nt, 3.75 Gb) for only 305.50 €/sample
- 50 mio PE reads¹ (2 x 150 nt, 7.5 Gb) for only 401 €/sample
- 75 mio PE reads¹ (2 x 150 nt, 11.25 Gb) for only 496.50 €/sample
- 100 mio PE reads¹ (2 x 150 nt, 15 Gb) for only 592 €/sample

Optional: Bioinformatic services

- **Bioinformatic data analysis 2:** Pairwise comparison to identify differentially regulated genes with DESeq2 or DRAGEN workflow starting from 120 €/comparison
- **Bioinformatic data analysis 3:** RNA-Seq Alignment to non-standard genomes from 100 €/sample
- **Bioinformatic data analysis 4:** Differential expression of novel and reference transcripts from 120 €/sample
- rRNA depletion: from 150 €/sample

Sequencing prices valid from the very first sample!

¹ Depending on the nature of starting material and according to Illumina specifications the data output can vary 5-10%.

² Available reference genomes include: *H. sapiens* hg19, *H. sapiens* GRCh38Decoy, *M. musculus* mm10, *M. musculus* UCSC mm9, *R. norvegicus* rn5, *D. melanogaster* dm3, *B. taurus* bosTau6, *S. scrofa* susScr3, *G. gallus* galGal4, *D. rerio* danRer7, *C. elegans* ce10, *Z. mays* AGPv3, *A. thaliana* TAIR10, *O. sativa* japonica IRGSP-1.0, *S. cerevisiae* R64-1-1