RNAsequencing with Illumina NextSeq 500™

LIBRARY, SEQUENCING-RUN AND BIOINFORMATICS

Services includes:



- mRNA isolation from total RNA
- TruSeq stranded RNA library preparation
- Quantification and QC of library
- Sequencing of 1 x 75 / 2 x 150 nt with Illumina Next Seg 500™
- Data delivery of FASTQ and bioinformatic analysis files via download

Output:

- 50 mio SE reads² (1 x 75 nt, 3.75 Gb) for only 750,- €/sample
- 25 mio PE reads² (2 x 150 nt, 3.75 Gb) for only 790,- €/sample
- 50 mio PE reads² (2 x 150 nt, 7.5 Gb) for only 990,- €/sample



• Bioinformatic data analysis: RNA-Seq Alignment to reference genomes¹ (TopHat, FPKM/RPKM, Variants, Fusion)

Price valid from the very first sample!

HIGH TROUGHPUT GENE EXPRESSION PROFILING FOR 6 AND 12 SAMPLES

Services includes:



- mRNA isolation from total RNA for 6 or 12 samples
- TruSeg stranded RNA library preparation
- Quantification and QC of library
- Sequencing of 2 x 150 nt with Illumina Next Seq 500™
- Data delivery of FASTQ files via download



Output:

- 25 mio PE reads² (2 x 150 nt, 3.75 Gb) for only 450,- €/sample, 12 samples
- 25 mio PE reads² (2 x 150 nt, 3.75 Gb) for only 550,- €/sample, 6 samples
- 50 mio PE reads² (2 x 150 nt, 7.5 Gb) for only 650,- €/sample, 12 samples
- 50 mio PE reads² (2 x 150 nt, 7.5 Gb) for only 750,-€/sample, 6 samples





Bioinformatic data analysis 1: RNA-Seq Alignment to reference genomes¹ (TopHat, FPKM/RPKM, Variants, Fusion) 80,- €/sample Bioinformatic data analysis 2: Pairwise comparison to identify differentially regulated genes with Cufflinks workflow 175,- €/comparison Bioanalyzer check of RNA samples: 40,- €/sample

² data output can vary 5-10% depending on the nature of starting material and according to Illumina specifications



¹ Available reference genomes include: *H. sapiens* hg19, *H. sapiens* hg38, *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