SPRING PROMOTION 2020!
Flexible Voucher Option!
Buy now and perform this or any other project within 12 months.

****

RNAseq promotion and voucher option
HIGH THROUGHPUT GENE EXPRESSION PROFILING FOR 6, 12 OR 24 SAMPLES

(Leiopicus medius)

Service includes:
- mRNA isolation from total RNA for 6, 12 or 24 samples
- NEBNext® Ultra™ II Directional RNA library preparation
- Quantification and QC of library
- Sequencing of 1 x 75 nt / 2 x 150 nt with Illumina NextSeq 500™
- Data delivery of FASTQ files via download

Output:
- 25 mio PE reads[1] (2 x 150 nt, 3.75 Gb) for only 325 €/sample, 24 samples*
- 25 mio PE reads[1] (2 x 150 nt, 3.75 Gb) for only 350 €/sample, 12 samples*
- 25 mio PE reads[1] (2 x 150 nt, 3.75 Gb) for only 370 €/sample, 6 samples*

- 50 mio PE reads[1] (2 x 150 nt, 7.5 Gb)   for only 495 €/sample, 24 samples*
- 50 mio PE reads[1] (2 x 150 nt, 7.5 Gb)   for only 515 €/sample, 12 samples*
- 50 mio PE reads[1] (2 x 150 nt, 7.5 Gb)   for only 535 €/sample, 6 samples*

- 25 mio SE reads[1] (1 x 75 nt, 1.875 Gb) for only 310 €/sample, 24 samples*
- 25 mio SE reads[1] (1 x 75 nt, 1.875 Gb) for only 330 €/sample, 12 samples*
- 25 mio SE reads[1] (1 x 75 nt, 1.875 Gb) for only 350 €/sample, 6 samples*

- 50 mio SE reads[1] (1 x 75 nt, 3.75 Gb)   for only 460 €/sample, 24 samples*
- 50 mio SE reads[1] (1 x 75 nt, 3.75 Gb)   for only 480 €/sample, 12 samples*
- 50 mio SE reads[1] (1 x 75 nt, 3.75 Gb)   for only 500 €/sample, 6 samples*

Optional: Bioinformatic services

Bioinformatic data analysis 1: RNA-Seq Alignment to reference genomes[2] (STAR aligner, Manta, Salomon, Strelka2) starting from 70 €/sample

Bioinformatic data analysis 2: Pairwise comparison to identify differentially regulated genes with DESeq2 workflow starting from 120 €/comparison

Bioanalyzer check of RNA samples: Starting from 40 €/sample

Qubit™ check with RNA assay: Starting from 20 €/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

* Samples must be delivered as batch.

Star★SEQ