## END OF YEAR PROMOTION 2020!

Flexible Voucher Option. Transfer your Funds and Budget to 2021!

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

## **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 NextSeg 500™
  - Data delivery of FASTQ files via download

## **Output:**

- 25 mio PE reads¹ (2 x 150 nt, 3.75 Gb) for only 325 €/sample, 24 samples\*
- 25 mio PE reads¹ (2 x 150 nt, 3.75 Gb) for only 350 €/sample, 12 samples\*
- 25 mio PE reads¹ (2 x 150 nt, 3.75 Gb) for only 370 €/sample, 6 samples\*
- 50 mio PE reads¹ (2 x 150 nt, 7.5 Gb) for only 495 €/sample, 24 samples\*
- 50 mio PE reads¹ (2 x 150 nt, 7.5 Gb) for only 515 €/sample, 12 samples\*
- 50 mio PE reads¹(2 x 150 nt, 7.5 Gb) for only 535 €/sample, 6 samples\*
- 25 mio SE reads¹ (1 x 75 nt, 1.875 Gb) for only 310 €/sample, 24 samples\*
- 25 mio SE reads¹ (1 x 75 nt, 1.875 Gb) for only 330 €/sample, 12 samples\*
- 25 mio SE reads¹ (1 x 75 nt, 1.875 Gb) for only 350 €/sample, 6 samples\*
- 50 mio SE reads¹ (1 x 75 nt, 3.75 Gb) for only 460 €/sample, 24 samples\*
- 50 mio SE reads<sup>1</sup> (1 x 75 nt, 3.75 Gb) for only 480 €/sample, 12 samples\*
- 50 mio SE reads<sup>1</sup> (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<sup>2</sup> (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<sup>™</sup> check with RNA assay: Starting from 20 €/sample

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

<sup>2</sup> 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.



