

# WARM UP TO WINTER SAVINGS!

**Flexible Voucher Option! Secure your budget now and use your voucher to run a project within the next 12 months.**

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## RNAseq promotion and voucher option

### HIGH THROUGHPUT GENE EXPRESSION PROFILING

#### Service includes:

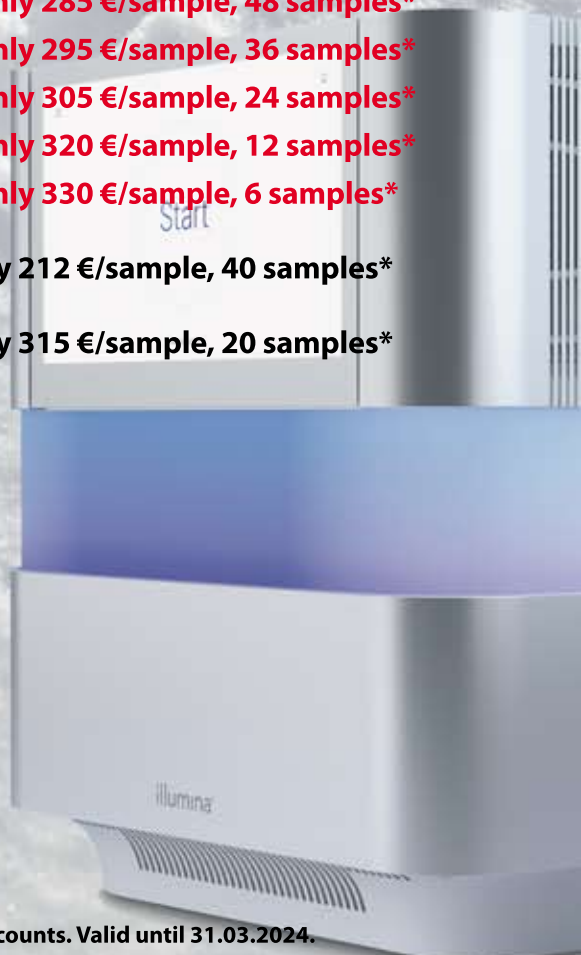
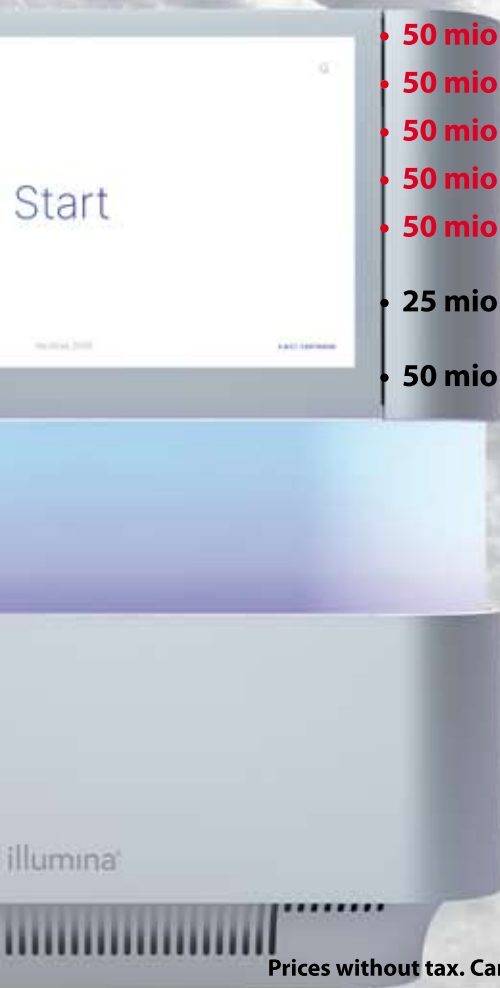


- mRNA isolation from total RNA starting from 6 samples
- NEBNext<sup>®</sup> Ultra<sup>™</sup> II Directional RNA library preparation
- Quantification and QC of library
- Sequencing of 1 x 50 nt / 2 x 150 nt with Illumina NextSeq 2000<sup>™</sup>
- Data delivery of FASTQ files via download

#### Price example:



- 25 mio PE reads<sup>1</sup> (2 x 150 nt, 3.75 Gb) for only 200 €/sample, 48 samples\*
- 25 mio PE reads<sup>1</sup> (2 x 150 nt, 3.75 Gb) for only 210 €/sample, 36 samples\*
- 25 mio PE reads<sup>1</sup> (2 x 150 nt, 3.75 Gb) for only 220 €/sample, 24 samples\*
- 25 mio PE reads<sup>1</sup> (2 x 150 nt, 3.75 Gb) for only 235 €/sample, 12 samples\*
- 25 mio PE reads<sup>1</sup> (2 x 150 nt, 3.75 Gb) for only 245 €/sample, 6 samples\*
- 50 mio PE reads<sup>1</sup> (2 x 150 nt, 7.5 Gb) for only 285 €/sample, 48 samples\*
- 50 mio PE reads<sup>1</sup> (2 x 150 nt, 7.5 Gb) for only 295 €/sample, 36 samples\*
- 50 mio PE reads<sup>1</sup> (2 x 150 nt, 7.5 Gb) for only 305 €/sample, 24 samples\*
- 50 mio PE reads<sup>1</sup> (2 x 150 nt, 7.5 Gb) for only 320 €/sample, 12 samples\*
- 50 mio PE reads<sup>1</sup> (2 x 150 nt, 7.5 Gb) for only 330 €/sample, 6 samples\*
- 25 mio SE reads<sup>1</sup> (1 x 50 nt, 1.25 Gb) for only 212 €/sample, 40 samples\*
- 50 mio SE reads<sup>1</sup> (1 x 50 nt, 2.5 Gb) for only 315 €/sample, 20 samples\*



Prices without tax. Cannot be combined with other promotions or discounts. Valid until 31.03.2024.



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#### Additional services



**Bioanalyzer check of RNA samples: Starting from 10 €/sample**

**Qubit™ check with RNA assay: Starting from 5 €/sample**

**rRNA depletion: Starting from 80 €/sample**

#### Bioinformatic services



**Bioinformatic data analysis 1:**

**RNA-Seq Alignment to reference genomes<sup>2</sup> (STAR aligner, DRAGEN)  
starting from 40 €/sample**

**Bioinformatic data analysis 1:**

**RNA-Seq Alignment to non-reference genomes (STAR aligner, DRAGEN)  
starting from 50 €/sample**

**Bioinformatic data analysis 2:**

**Pairwise comparison to identify differentially regulated genes with DESeq2  
or DRAGEN workflow  
starting from 40 €/comparison**

<sup>1</sup> 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.

