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

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 2 x 150 nt with Illumina NextSeq 2000™
- Bioinformatic data analysis 1: RNA-Seq Alignment to reference genomes[2] (STAR aligner, DRAGEN)
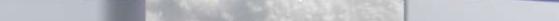- Data delivery of FASTQ and bioinformatic analysis files via download

Output:

- 25 mio PE reads[1] (2 x 150 nt, 3.75 Gb)   for only   265 €/sample
- 50 mio PE reads[1] (2 x 150 nt, 7.5 Gb)   for only   350 €/sample
- 75 mio PE reads[1] (2 x 150 nt, 11.25 Gb)   for only   435 €/sample
- 100 mio PE reads[1] (2 x 150 nt, 15 Gb)   for only   520 €/sample

Optional: Bioinformatic services

- Bioinformatic data analysis 2: Pairwise comparison to identify differentially regulated genes with DESeq2 or DRAGEN workflow starting from 70 €/comparison
- Bioinformatic data analysis 3: RNA-Seq Alignment to non-standard genomes from 80 €/sample
- Bioinformatic data analysis 4: Differential expression of novel and reference transcripts of none-standard genome from 70 €/sample
- rRNA depletion: from 90 €/sample

Sequencing prices valid from the very first sample!

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[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

Star★SEQ