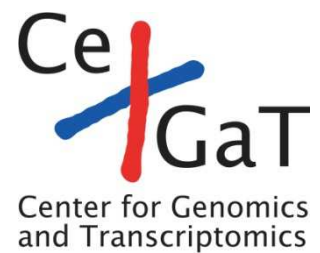


# Next-Generation-Sequencing



## Whole Exome Sequencing

- We offer Exome Sequencing on the brand new SOLiD 4 System (available since April 2010)
- Whole Exome Enrichment is performed with Agilent Whole Exome Sure Select Technology
- Required are only 3µg of gDNA
- More than 37Mb of the Human Genome are covered incl. all exons
- In addition, more than 700 miRNA and more than 300 other non-coding RNA are also covered
- Approx 80 million mappable reads with readlength of 50 basepairs are generated
- Identification of SNPs and mutations
- Turn-Around-Time is less than two months after receipt of gDNA

### Prices (excl. VAT) - valid until end of 2010:

One sample	EUR 8.900 / sample
Four samples	EUR 7.500 / sample
Eight samples	EUR 5.625 / sample

Prices include Consulting, Enrichment, Library Preparation, and Sequencing on SOLiD 4 System



**AB** applied biosystems<sup>®</sup>  
by life technologies<sup>®</sup>

## Whole Transcriptome Sequencing

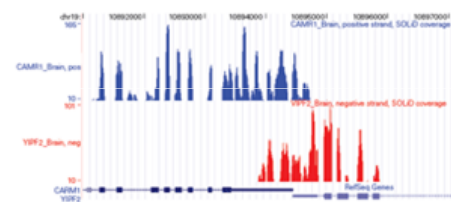
- Expression of all coding and non-coding RNAs
- Identification of alternative splicing events
- Expressed SNPs (single nucleotide polymorphisms) or mutations
- Translocations and fusion transcripts
- Identify allele specific expression patterns
- Strand specific read distribution

### Prices (excl. VAT) - valid until end of 2010:

One sample	EUR 3.500 / sample
Four samples	EUR 3.000 / sample
Eight samples	EUR 2.875 / sample

Prices include Consulting, Library Preparation, and Sequencing on SOLiD 4 System

Lit: Cloonan and Grimmond, Transcriptome Content and Dynamics at single nucleotide resolution. Genome Biol. 2008



## Micro RNA Sequencing

- Discover novel RNA without the probe bias of microarrays
- Robust method for hypothesis-neutral, whole genome analysis of expression patterns

### Prices (excl. VAT) - valid until end of 2010:

One sample	EUR 2.900 / sample
Four samples	EUR 2.500 / sample
Eight samples	EUR 2.250 / sample

Prices include Consulting, Library Preparation, and Sequencing on SOLiD 4 System

Lit: Tan et al., mRNA SEQ whole transcriptome analysis of a single cell. Nature Methods 2009

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