TrueQuant MACE-Seq

Massive Analysis of cDNA Ends

3' mRNA Sequencing with UMIs and UDIs for Gene Expression Analyses

Key Features

- **Sensitivity** Libraries can be generated with 10 pg of total RNA - single cell
- **Fast** Convenient library preparation in 3.5 h
- **FFPE suitable** Reliable gene expression even from degraded RNA
- **Low Costs** Needs only about 10% of the reads compared to full-length RNA-Seq
- **Reliable** GenXPro-patented Unique Molecular Identifiers (UMIs) for PCR-bias elimination (TrueQuant)
- **Resolution** Measures all poly-A transcripts
- **Throughput** 96 samples can be processed in parallel with Unique Dual Indices (UDIs)
- **Bioinformatics optional**

Comparison to hexamer-based RNA-Seq

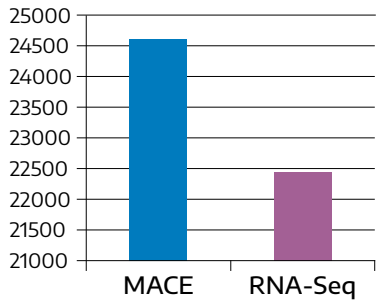
TrueQuant MACE-Seq - 3' End Fragment

Longer 3' ends compared to hexamer-based method.
Ideal for degraded RNA (FFPE)
1 read = 1 transcript: lower costs

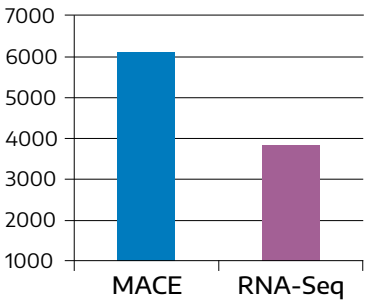
RNA-Seq - Hexamers

Not the entire RNA fragment is sequenced.
Loss of shorter, degraded and smallRNAs

Number of different transcripts identified with MACE-Seq and RNA-Seq from human placenta RNA *



Number of loci covered with >30x for determination of alleles *



* at 20 Mio reads for either technique

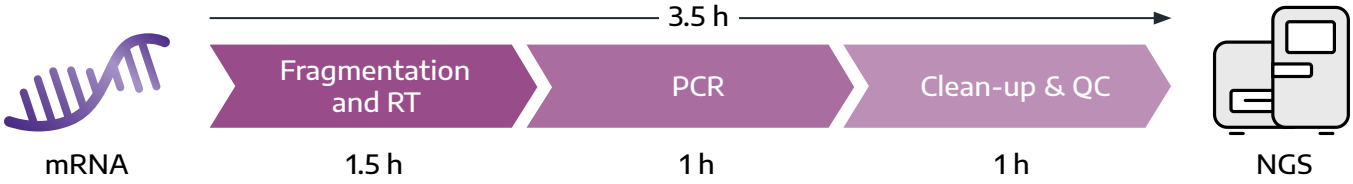
MACE-Seq Full-Service or Kits

GenXPro
Molecular Data for Research & Health

Applications

- **Gene Expression Profiling**
- **Analyses of FFPE-derived RNA**
- **Liquid Biopsies** For e.g. biomarker studies
- **Single cell sequencing**
- **Analyses of Alternative Poly-Adenylation (APA)**
- **Allele Identification** Genotyping by Sequencing (GBS) & molecular markers for breeding

Timeline



Kits and Services

MACE kits are available for 6x – 96x reactions and include UMIs and UDIs, ready to be used on the latest Illumina platforms. No additional reagents are needed for MACE-Seq library preparation from total RNA. Our MACE-Seq and other services are available for RNA or any tissue, cells, FFPE samples or liquid biopsies.

Bioinformatics Analysis
optional as a service

- Demultiplexing
- Cleaning of raw-reads
- UMI-Deduplication
- Differential Expression Analysis
- Gene Set Enrichment Analysis (GSEA)
- Pathway- and GO-enrichment
- Custom bioinformatics solutions for model and non-model organisms

For orders of service or kits please visit our website
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