DataSheet

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Biology for a better world

GeneChip® Mouse Transcriptome Assay 1.0

One experiment – multiple layers of biology

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Mouse Transcriptome Assay 1.0 is the most powerful and flexible tool for measuring a broad range of expression changes across the whole mouse transcriptome quickly, easily, and cost-effectively.

Analysis flexibility

Multiple levels of analysis to choose from

- Confidently identify global gene-level expression patterns
- Precisely measure transcript isoforms and alternative splicing events
- Accurately detect rare transcripts without compromising performance
- Decode the role of non-coding RNA in expression regulation
- Generate robust expression profiles from various sample types, including fresh and fresh frozen tissues, blood, and FFPE samples

Data to insights in minutes

A solution designed for the biologist

- Generate lists of differential expression changes in minutes with intuitive, highly visual data analysis software solutions
- Explore gene expression and its regulation
- Simplify interpretation of complex alternative splicing events
- Focus on your genes or pathways of interest with just a few clicks

Mouse models have proven to be an invaluable tool for studying biomolecular interactions and human disease. The mouse genome is comparable to that of human and can be easily manipulated to model human disease states by replacing or inactivating genes with an altered or inactive version. Although human and mouse gene-level expression signatures can be highly similar, many investigators experience difficulties in translating preclinical research in mouse models to clinical human studies.

Some of these challenges can be explained by experimental manipulations in mouse models resulting in extensive alterations at not only gene-level expression but also at the population level of transcript isoforms generated by alternative splicing events. These changes can significantly impact the interpretation and translatability of mouse data to human studies. Detailed analysis of altered gene-level and transcript isoform expression can provide valuable insight into understanding the molecular basis of the development and the pathological mechanisms underlying disease.

Are you missing the data that you need?

Many common technologies fail to capture the true variation in the transcriptome in a single experiment. The design of traditional microarrays and the low-read depth typically used in RNA-Seq experiments result in the detection of expression changes only at the gene-level or at the 3′ end of the gene. This approach misses important coding and non-coding gene-level and transcript isoform expression changes critical to interpreting the real biological implications and replicating findings in humans.

One experiment – multiple answers

Mouse Transcriptome Assay 1.0 is designed to accelerate preclinical human disease research and increase the successful translation of discoveries in mouse models to human studies by providing a rich data set sufficient to decipher changes at multiple levels in a single experiment. With approximately ten detection probes per exon and four probes per exon-exon splice junction, Mouse Transcriptome Assay 1.0 generates the most complete, accurate, and reproducible whole-transcriptome expression data with the flexibility to select the analysis level required to answer your biological questions—gene-level, transcript-level, protein-coding, or non-coding RNA—you decide. In addition, Mouse Transcriptome Assay 1.0 is designed to work with a wide range of common sample types, including fresh and fresh frozen tissue, blood, and FFPE samples.

A complete solution that rapidly takes you from samples to meaningful results

To get to biological insights simply, quickly, and seamlessly, Mouse Transcriptome 1.0 Assay includes intuitive analysis software that transforms the high-quality expression data generated by the assay into biologically meaningful information in minutes. Affymetrix® Transcriptome Analysis Console (TAC) Software is designed for the biologist to rapidly perform statistical analysis and visualization of global expression changes as well as focused analysis on specific pathways and to explore non-coding RNA relationships with mRNA. TAC Software also enables the easy and rapid analysis of alternative splicing events without the challenges of mapping, filtering, aligning, and interpreting hundreds of millions of data points for every sample in your experiment.

Accelerate your preclinical studies with Mouse Transcriptome Assay 1.0.

Array content summary

Array protein coding content	Number
Genes (transcript clusters)	>23,000
Transcripts	>114,000
Exons	>332,000
Exon clusters	>215,000

Array non-protein coding content (non-coding RNA, pseudogenes, rRNA, etc.)	Number
Genes (transcript clusters)	>55,000
Transcripts	>101,000
Exons	>222,000
Exon clusters	>162,000

Array coding and non-protein coding content (counts already included in above numbers)	Number
Genes (transcript clusters)	>12,000
Transcripts	>1,000
Exons	>66,000
Exon clusters	>80,000

Controls	
ERCC probe set[1, 2]	155
Background probes	Antigenomic set
Poly-A controls[2]	*dap, lys, phe, thr*
Hybridization controls	bioB, bioC, bioD, creX

[1] Probe sets interrogating external RNA controls present in the Ambion® ERCC RNA Spike-In Control Mixes, P/N 4456740 and 4456739.

[2] This array contains probe sets for both ERCC and Poly-A spike-in controls. Sequence homology between the two control mixes will result in cross-hybridization of target to the control probes on the array. It is important to use only one control probe set when processing the array (ERCC or Poly-A controls), but not both.

Data sources used to design and annotate the array
RefSeq
Ensembl
UCSC Known Genes
Vertebrate Genome Annotation (Vega) database
MGC Mammalian Gene Collection
MGI: Mouse Genome Informatics from Jackson Lab
NONCODE
lncRNA db
Intergenic noncoding RNA from Luo, *et al* [1]

[1] Luo H., *et al.* Comprehensive characterization of 10,571 mouse large intergenic noncoding RNAs from whole transcriptome sequencing. *PLoS ONE* **8**(8):e70835 (2013). doi:10.1371/journal.pone.0070835

Specifications

Sensitivity	≥1:100,000 (≥1.5 pM)
Correlation coefficient (intra-lot)	≥0.99
Detectable fold change	2-fold for 1:100,000 vs 1:50,000
Dynamic range	~3 logs
Total RNA input required	50–500 ng
Probe feature size	5 µm
Probe length	25-mer
Probes per gene (median)[1]	30
Target RNA orientation[2]	Sense target

[1] Single and double exon genes were brought up to a minimum of 30 probes total per gene.

[2] The probes tiled on the array are designed in the anti-sense orientation, requiring sense-strand labeled targets to be hybridized to the array.

Ordering information*

Part number	Description	Details
902513 902514	GeneChip® Mouse Transcriptome Assay 1.0 Kit (compatible with intact RNA and blood tissue)	Sufficient for 10 samples Sufficient for 30 samples
902515 902516	GeneChip® Mouse Transcriptome Assay 1.0 Kit for FFPE Sample	Sufficient for 12 samples Sufficient for 24 samples
900720	GeneChip® Hybridization, Wash, and Stain Kit	Sufficient for 30 reactions

*Assay configurations exist for high-throughput automation. For more information, please visit www.affymetrix.com

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