

Description

Using RNA-seq (Mortazavi *et al.*, 2008), high-resolution genome-wide maps of the mouse transcriptome in various mouse (C57BL/6) tissues, primary cells, cell lines of different developmental stage and age groups were generated.

Display Conventions and Configuration

This is a composite track that contains multiple data types (*views*). For each view, there are multiple subtracks that display individually on the browser. Instructions for configuring composite tracks are [here](#). This track contains the following views:

Signal

Density graph (wiggle) of signal enrichment based on processed data.

Alignments

Mappings of short reads to the genome. See the [SAM Format Specification](#) for more information on the SAM/BAM file format.

Metadata for a particular subtrack can be found by clicking the down arrow in the list of subtracks.

Additional views are available on the Downloads page.

Methods

Cells were grown according to the approved [ENCODE cell culture protocols](#).

RNA-seq

RNA samples from tissues and primary cells were extracted from Trizol® according to protocol (Invitrogen). Long PolyA+ RNA was purified with the Dynabeads mRNA purification kit (Invitrogen). The mRNA libraries were prepared for strand-specific sequencing as described previously (Parkhomchuk *et al.*, 2009).

Sequencing and Analysis

Samples were sequenced on Illumina Genome Analyzer II, Genome Analyzer IIx and HiSeq 2000 platforms for 36 cycles. Image analysis, base calling and alignment to the mouse genome version NCBI37/mm9 were performed using Illumina's RTA. Alignment to the mouse genome was performed using TopHat (Trapnell *et al.*, 2009). Wig files were generated by TopHat and expression levels were calculated with Cufflinks (Trapnell *et al.*, 2010).

Release Notes

This is Release 2 (Mar 2012). It contains a total of 22 RNA-seq experiments with the addition of 12 new experiments.

Credits

These data were generated and analyzed in [Bing Ren's laboratory](#) at the Ludwig Institute for Cancer Research.

Contact: [Yin Shen](#)

References

- Mortazavi A, Williams BA, McCue K, Schaeffer L, Wold B. [Mapping and quantifying mammalian transcriptomes by RNA-Seq](#). *Nat Methods*. 2008 Jul;5(7):621-8.
- Parkhomchuk D, Borodina T, Amstislavskiy V, Banaru M, Hallen L, Krobitch S, Lehrach H, Soldatov A. [Transcriptome analysis by strand-specific sequencing of complementary DNA](#). *Nucleic Acids Res*. 2009 Oct;37(18):e123.
- Trapnell C, Pachter L, Salzberg SL. [TopHat: discovering splice junctions with RNA-Seq](#). *Bioinformatics*. 2009 May 1;25(9):1105-11.
- Trapnell C, Williams BA, Pertea G, Mortazavi A, Kwan G, van Baren MJ, Salzberg SL, Wold BJ, Pachter L. [Transcript assembly and quantification by RNA-Seq reveals unannotated transcripts and isoform switching during cell differentiation](#). *Nat Biotechnol*. 2010 May;28(5):511-5.

Data Release Policy

Data users may freely use ENCODE data, but may not, without prior consent, submit publications that use an unpublished ENCODE dataset until nine months following the release of the dataset. This date is listed in the *Restricted Until* column, above. The full data release policy for ENCODE is available [here](#).