LICR RNA-seq Track Settings

RNA-seq from ENCODE/LICR (▲All Expression and Regulation tracks)

Maximum display mode: full ▾ Submit Cancel   Reset to defaults

Select views (Help):
Signal ▾ full ▾   Alignments ▾ hide ▾

Select subtracks by cell line and age:

List subtracks: ⦿ only selected/visible   ○ all   (8 of 88 selected)   Top↑

		Cell Line↓1	views↓2	Age↓3	Rep↓4	Track Name↓5		Restricted Until
☑	full Configure	Heart	Signal	Embryonic day 14.5	1	Heart Embryonic day 14.5 RNA-seq Signal Rep 1 from ENCODE/LICR ▲	Schema	2012-10-04

Principal Investigator on grant: Ren
Lab producing data: Ren - LICR
Experiment (Assay) type: RNA-seq
View - Peaks or Signals: Signal
Cell, tissue or DNA sample: Heart
Strain of organism: C57BL/6
Sex of donor organism: U
Age of donor organism: Embryonic day 14.5
Cellular compartment: cell
RNA Extract: Long PolyA+ RNA
Paired/Single reads lengths: 1x36
Replicate number: 1
ENCODE Data Freeze: ENCODE Mar 2012 Freeze
UCSC Accession: wgEncodeEM002391
Date submitted to UCSC: 2012-01-05
Date restrictions end: 2012-10-04
Submission ID: 5422
GEO sample accession: GSM929724
Lab specific details: 4/29/11 Lane 1
Sequencing Platform: Illumina HiSeq 2000
Lab specific informatics: TopHat
Tissue Source Type: Individual
tableName: wgEncodeLicrRnaSeqHeartCellPapUE14halfC57bl6SigRep1
fileName: wgEncodeLicrRnaSeqHeartCellPapUE14halfC57bl6SigRep1.bigWig

| ☑ | full Configure | Heart | Signal | Embryonic day 14.5 | 2 | Heart Embryonic day 14.5 RNA-seq Signal Rep 2 from ENCODE/LICR ▲ | Schema | 2012-10-04 |

Principal Investigator on grant: Ren
Lab producing data: Ren - LICR
Experiment (Assay) type: RNA-seq
View - Peaks or Signals: Signal
Cell, tissue or DNA sample: Heart
Strain of organism: C57BL/6
Sex of donor organism: U
Age of donor organism: Embryonic day 14.5
Cellular compartment: cell
RNA Extract: Long PolyA+ RNA
Paired/Single reads lengths: 1x36
Replicate number: 2
ENCODE Data Freeze: ENCODE Mar 2012 Freeze
UCSC Accession: wgEncodeEM002391
Date submitted to UCSC: 2012-01-05
Date restrictions end: 2012-10-04
Submission ID: 5422
GEO sample accession: GSM929724
Lab specific details: 4/29/11 Lane 1
Sequencing Platform: Illumina HiSeq 2000
Lab specific informatics: TopHat
Tissue Source Type: Individual
tableName: wgEncodeLicrRnaSeqHeartCellPapUE14halfC57bl6SigRep2
fileName: wgEncodeLicrRnaSeqHeartCellPapUE14halfC57bl6SigRep2.bigWig

| ☑ | full Configure | Limb | Signal | Embryonic day 14.5 | 1 | Limb Embryonic day 14.5 RNA-seq Signal Rep 1 from ENCODE/LICR ▲ | Schema | 2012-10-03 |

Principal Investigator on grant: Ren
Lab producing data: Ren - LICR
Experiment (Assay) type: RNA-seq
View - Peaks or Signals: Signal
Cell, tissue or DNA sample: Limb
Strain of organism: C57BL/6
Sex of donor organism: U
Age of donor organism: Embryonic day 14.5
Cellular compartment: cell
RNA Extract: Long PolyA+ RNA
Paired/Single reads lengths: 1x36
Replicate number: 1
ENCODE Data Freeze: ENCODE Mar 2012 Freeze
UCSC Accession: wgEncodeEM002387
Date submitted to UCSC: 2012-01-04
Date restrictions end: 2012-10-03
Submission ID: 5396
GEO sample accession: GSM929713
Lab specific details: 11/10/10 Lane 5
Sequencing Platform: Illumina HiSeq 2000
Lab specific informatics: TopHat
Tissue Source Type: Individual
tableName: wgEncodeLicrRnaSeqLimbCellPapUE14halfC57bl6SigRep1
fileName: wgEncodeLicrRnaSeqLimbCellPapUE14halfC57bl6SigRep1.bigWig

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			Cell Line↓1	views↓2	Age↓3	Rep↓4	Track Name↓5		Restricted Until

☑ full ⚙ Configure Limb   Signal   Embryonic day 14.5   2   Limb Embryonic day 14.5 RNA-seq Signal Rep 2 from ENCODE/LICR ▲   Schema   2012-10-03

Principal Investigator on grant: Ren
Lab producing data: Ren - LICR
Experiment (Assay) type: RNA-seq
View - Peaks or Signals: Signal
Cell, tissue or DNA sample: Limb
Strain of organism: C57BL/6
Sex of donor organism: U
Age of donor organism: Embryonic day 14.5
Cellular compartment: cell
RNA Extract: Long PolyA+ RNA
Paired/Single reads lengths: 1x36
Replicate number: 2
ENCODE Data Freeze: ENCODE Mar 2012 Freeze
UCSC Accession: wgEncodeEM002387
Date submitted to UCSC: 2012-01-04
Date restrictions end: 2012-10-03
Submission ID: 5396
GEO sample accession: GSM929713
Lab specific details: 11/10/10 Lane 5
Sequencing Platform: Illumina HiSeq 2000
Lab specific informatics: TopHat
Tissue Source Type: Individual
tableName: wgEncodeLicrRnaSeqLimbCellPapUE14halfC57bl6SigRep2
fileName: wgEncodeLicrRnaSeqLimbCellPapUE14halfC57bl6SigRep2.bigWig

☑ full ⚙ Configure Liver   Signal   Embryonic day 14.5   1   Liver Embryonic day 14.5 RNA-seq Signal Rep 1 from ENCODE/LICR ▲   Schema   2012-10-04

Principal Investigator on grant: Ren
Lab producing data: Ren - LICR
Experiment (Assay) type: RNA-seq
View - Peaks or Signals: Signal
Cell, tissue or DNA sample: Liver
Strain of organism: C57BL/6
Sex of donor organism: U
Age of donor organism: Embryonic day 14.5
Cellular compartment: cell
RNA Extract: Long PolyA+ RNA
Paired/Single reads lengths: 1x36
Replicate number: 1
ENCODE Data Freeze: ENCODE Mar 2012 Freeze
UCSC Accession: wgEncodeEM002392
Date submitted to UCSC: 2012-01-05
Date restrictions end: 2012-10-04
Submission ID: 5423
GEO sample accession: GSM929721
Lab specific details: 11/10/10 Lane 5
Sequencing Platform: Illumina HiSeq 2000
Lab specific informatics: TopHat
Tissue Source Type: Individual
tableName: wgEncodeLicrRnaSeqLiverCellPapUE14halfC57bl6SigRep1
fileName: wgEncodeLicrRnaSeqLiverCellPapUE14halfC57bl6SigRep1.bigWig

☑ full ⚙ Configure Liver   Signal   Embryonic day 14.5   2   Liver Embryonic day 14.5 RNA-seq Signal Rep 2 from ENCODE/LICR ▲   Schema   2012-10-04

Principal Investigator on grant: Ren
Lab producing data: Ren - LICR
Experiment (Assay) type: RNA-seq
View - Peaks or Signals: Signal
Cell, tissue or DNA sample: Liver
Strain of organism: C57BL/6
Sex of donor organism: U
Age of donor organism: Embryonic day 14.5
Cellular compartment: cell
RNA Extract: Long PolyA+ RNA
Paired/Single reads lengths: 1x36
Replicate number: 2
ENCODE Data Freeze: ENCODE Mar 2012 Freeze
UCSC Accession: wgEncodeEM002392
Date submitted to UCSC: 2012-01-05
Date restrictions end: 2012-10-04
Submission ID: 5423
GEO sample accession: GSM929721
Lab specific details: 11/10/10 Lane 5
Sequencing Platform: Illumina HiSeq 2000
Lab specific informatics: TopHat
Tissue Source Type: Individual
tableName: wgEncodeLicrRnaSeqLiverCellPapUE14halfC57bl6SigRep2
fileName: wgEncodeLicrRnaSeqLiverCellPapUE14halfC57bl6SigRep2.bigWig

☑ full ⚙ Configure Whole Brain Signal   Embryonic day 14.5   1   Whole Brain Embryonic day 14.5 RNA-seq Signal Rep 1 from ENCODE/LICR ▲   Schema   2012-10-03

Principal Investigator on grant: Ren
Lab producing data: Ren - LICR
Experiment (Assay) type: RNA-seq
View - Peaks or Signals: Signal
Cell, tissue or DNA sample: Whole Brain
Strain of organism: C57BL/6
Sex of donor organism: U
Age of donor organism: Embryonic day 14.5
Cellular compartment: cell
RNA Extract: Long PolyA+ RNA
Paired/Single reads lengths: 1x36
Replicate number: 1
ENCODE Data Freeze: ENCODE Mar 2012 Freeze
UCSC Accession: wgEncodeEM002390
Date submitted to UCSC: 2012-01-04
Date restrictions end: 2012-10-03
Submission ID: 5397
GEO sample accession: GSM929723
Lab specific details: 11/10/10 Lane 5
Sequencing Platform: Illumina HiSeq 2000
Lab specific informatics: TopHat
Tissue Source Type: Individual
tableName: wgEncodeLicrRnaSeqWbrainCellPapUE14halfC57bl6SigRep1
fileName: wgEncodeLicrRnaSeqWbrainCellPapUE14halfC57bl6SigRep1.bigWig

☑ full ⚙ Configure Whole Brain Signal   Embryonic day 14.5   2   Whole Brain Embryonic day 14.5 RNA-seq Signal Rep 2 from ENCODE/LICR ▲   Schema   2012-10-03

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Restriction Policy

Cell Line↓1	views↓2	Age↓3	Rep↓4	Track Name↓5	Restricted Until

Principal Investigator on grant: Ren
Lab producing data: Ren - LICR
Experiment (Assay) type: RNA-seq
View - Peaks or Signals: Signal
Cell, tissue or DNA sample: Whole Brain
Strain of organism: C57BL/6
Sex of donor organism: U
Age of donor organism: Embryonic day 14.5
Cellular compartment: cell
RNA Extract: Long PolyA+ RNA
Paired/Single reads lengths: 1x36
Replicate number: 2
ENCODE Data Freeze: ENCODE Mar 2012 Freeze
UCSC Accession: wgEncodeEM002390
Date submitted to UCSC: 2012-01-04
Date restrictions end: 2012-10-03
Submission ID: 5397
GEO sample accession: GSM929723
Lab specific details: 11/10/10 Lane 5
Sequencing Platform: Illumina HiSeq 2000
Lab specific informatics: TopHat
Tissue Source Type: Individual
tableName: wgEncodeLicrRnaSeqWbrainCellPapUE14halfC57bl6SigRep2
fileName: wgEncodeLicrRnaSeqWbrainCellPapUE14halfC57bl6SigRep2.bigWig

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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. PMID: 18516045

Parkhomchuk D, Borodina T, Amstislavskiy V, Banaru M, Hallen L, Krobitsch S, Lehrach H, Soldatov A. Transcriptome analysis by strand-specific sequencing of complementary DNA. *Nucleic Acids Res*. 2009 Oct;37(18):e123. PMID: 19620212; PMC: PMC2764448

Trapnell C, Pachter L, Salzberg SL. TopHat: discovering splice junctions with RNA-Seq. *Bioinformatics*. 2009 May 1;25(9):1105-11. PMID: 19289445; PMC: PMC2672628

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. PMID: 20436464; PMC: PMC3146043

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.

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