Description

The tracks show enrichment of RNA sequence tags generated by high throughput sequencing (RNA-seq) and mapped to the human genome. Double stranded cDNA was synthesized from polyadenylated RNA (polyA+) . PCR amplified, adapter ligated cDNA, 150-300nt long, was sequenced on an Illumina GA sequencer.

Where designated, cell lines received specific treatments prior to RNA isolation. As indicated, K562 cells were treated with either interferon-a or interferon-g for 30 minutes or 6 hours. These experiments were carried out in conjunction with ChIP-Seq experiments on the transcription factors STAT1 and STAT2 in order to examine the effects that inducers of a specific transcriptional response might have on gene expression and on transcription factor binding site discovery. K562 cells were treated with a-amanitin in order to examine the effects of RNA polymerase II inhibition on RNA polymerase III-mediated transcription.

This track shows *expression* data generated as confirmation of the SYDH TFBS tracks currently available on genome-preview.

Display Conventions and Configuration

This is a composite track that contains multiple data types (*views*). Instructions for configuring composite tracks are here.

Raw Signal

Density graph (wiggle) of signal enrichment.

Alignments

The Alignments view shows reads mapped to the genome and indicates where bases may mismatch. The alignment file follows the standard SAM format of Bowtie output with the following additions: the custom tags X0 X1 XN XM XO XG XT XA XS XF XE are present. These tags are described by the BWA specifications. See the Bowtie Manual for more information about the SAM Bowtie output (including other tags) and the SAM Format Specification for more information on the SAM/BAM file format.

Methods

Cells were grown according to the approved ENCODE cell culture protocols. Total RNA was extracted using TRIzol reagents (15596-018, Life Tech), following the manufacturer's protocol. For polyA+ samples, polyadenylated RNA was purified using the MicroPoly(A) Purist kit (AM1919, Life Tech) and fragmented using RNA Fragmentation Reagent (AM8740, Life Tech). Illumina adapters were ligated to double stranded cDNA which was synthesized using reagents from Life Tech (11917-010).

PCR amplified adapter ligated cDNA (150-300 bp) was sequenced using Illumina GA. Sequence reads of 27-33nt long with 0-2 mismatches were mapped to the genome. The signal height corresponds to the number of overlapping fragments at each nucleotide position in the genome.

Samples originally mapped to the hg18 version of the human genome were remapped to hg19 using the BWA aligner, version 0.5.7.

Credits

These data were generated and analyzed by the labs of Michael Snyder, Mark Gerstein and Sherman Weissman at Yale University; Peggy Farnham at USC; and Kevin Struhl at Harvard.

Contact: Gerstein Lab.

References

Nagalakshmi U, Wang Z, Waern K, Shou C, Raha D, Gerstein M, Snyder M. The transcriptional landscape of the yeast genome defined by RNA sequencing. *Science*. 2008 Jun 6;320(5881):1344-9.

Raha D, Wang Z, Moqtaderi Z, Wu L, Zhong G, Gerstein M, Struhl K, Snyder M. Close association of RNA polymerase II and many transcription factors with Pol III genes. *Proc Natl Acad Sci U S A.* 2010 Feb 23;107(8):3639-44.

Wu JQ, Habegger L, Noisa P, Szekely A, Qiu C, Hutchison S, Raha D, Egholm M, Lin H, Weissman S *et al*. Dynamic transcriptomes during neural differentiation of human embryonic stem cells revealed by short, long, and paired-end sequencing. *Proc Natl Acad Sci U S A.* 2010 Mar 16;107(11):5254-9.

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 on the track configuration page and the download page. The full data release policy for ENCODE is available here.