Resource Summary Report

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FANTOM DB

RRID:SCR_002678
Type: Tool

Proper Citation

FANTOM DB (RRID:SCR_002678)

Resource Information

URL: http://fantom.gsc.riken.jp/4/

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Description: The FANTOM consortium is an international collaborative research project initiated and organized by the RIKEN Omics Science Center. In earlier FANTOM efforts we cloned and annotated 103,000 full-length cDNAs from mouse and distributed them to researchers throughout the world. FANTOM1-3 focused on identifying the transcribed components of mammalian cells. This work improved estimates of the total number of genes and their alternative transcript isoforms in both human and mouse, expanded gene families, and revealed that a large fraction of the transcriptome is non-coding. In addition, with the development of Cap Analysis of Gene Expression (CAGE) FANTOM3 could map a large fraction of transcription start sites and revise our models of promoter structure. This updated web resource provides the previous FANTOM results mapped to current genome builds and presents the results of FANTOM4. In FANTOM4 the focus has changed to understanding how these components work together in the context of a biological network. Using deepCAGE (deep sequencing with CAGE) we monitored the dynamics of transcription start site (TSS) usage during a time course of monocytic differentiation in the acute myeloid leukemia cell line THP-1. This allowed us to identify active promoters, monitor their relative expression and define relevant regions for carrying out transcription factor binding site predictions. Computational methods were then used to build a network model of gene expression in this leukemia and the transcription factors key to its regulation. This work gives the first picture of the wiring between genes involved in acute myeloid leukemia and provides a strategy for identifying key factors that determine cell fates. In addition to the network, FANTOM4 data was used in two additional analyses. The first identified a novel class of short RNAs associated with transcription start sites and the second focused on the role of repetitive element expression in the transcriptome. TOOLS *Genome Browser: graphical display of genomic features, such as promoters, exon structures, H3K9 acetylation, transcription factors positioning on the genome, coupled with gene and promoter activities.

*EdgeExpressDB: regulatory interactions, such as transcriptional regulation, post-transcriptional silencing with miRNA, and PPI, coupled with gene and promoter activities. *SwissRegulon: FANTOM4 TF regulation is predicted using Motif Activity Response Analysis (MARA) developed by Erik van Nimwegen at Biozentrum. Follow the link to carry out MARA on your own dataset. *Custom Tracks on the UCSC Genome Browser: FANTOM4 tracks on the UCSC Genome Browser Database. *The RIKEN integrated database of mammals: Integration of FANTOM4 data with other mammalian resources, in particular, produced by RIKEN.

Abbreviations: FANTOM DB

Synonyms: FANTOM: Functional Annotation of Mouse, FANTOM2, FANTOM1, Functional Annotation of the Mammalian Genome, FANTOM4, FANTOM3, FANTOM, Functional Annotation of Mouse

Resource Type: material resource, biomaterial supply resource

Defining Citation: PMID:20211142

Keywords: cdna clone, mouse, mouse cdna, human, bio.tools

Funding:

Availability: Public

Resource Name: FANTOM DB

Resource ID: SCR_002678

Alternate IDs: nif-0000-02833, biotools:fantom

Alternate URLs: http://fantom3.gsc.riken.jp/, https://bio.tools/fantom

Record Creation Time: 20220129T080214+0000

Record Last Update: 20250517T055543+0000

Ratings and Alerts

No rating or validation information has been found for FANTOM DB.

No alerts have been found for FANTOM DB.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 19 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Company C, et al. (2024) Logical design of synthetic cis-regulatory DNA for genetic tracing of cell identities and state changes. Nature communications, 15(1), 897.

Wedenoja S, et al. (2020) Fetal HLA-G mediated immune tolerance and interferon response in preeclampsia. EBioMedicine, 59, 102872.

Umegaki Y, et al. (2018) Palladin Is a Neuron-Specific Translational Target of mTOR Signaling That Regulates Axon Morphogenesis. The Journal of neuroscience : the official journal of the Society for Neuroscience, 38(21), 4985.

Chen H, et al. (2018) Reply re: "Autologous Fat Graft (AFG) for the Treatment of Sighted Posttraumatic Enophthalmos and Sunken Upper Eyelid". Ophthalmic plastic and reconstructive surgery, 34(6), 604.

Chen H, et al. (2018) Fast-Evolving Human-Specific Neural Enhancers Are Associated with Aging-Related Diseases. Cell systems, 6(5), 604.

Espinal-Enríquez J, et al. (2017) The Transcriptional Network Structure of a Myeloid Cell: A Computational Approach. International journal of genomics, 2017, 4858173.

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Horlbeck MA, et al. (2016) Compact and highly active next-generation libraries for CRISPR-mediated gene repression and activation. eLife, 5.

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Kubosaki A, et al. (2010) The combination of gene perturbation assay and ChIP-chip reveals functional direct target genes for IRF8 in THP-1 cells. Molecular immunology, 47(14), 2295.

Kawaji H, et al. (2009) The FANTOM web resource: from mammalian transcriptional landscape to its dynamic regulation. Genome biology, 10(4), R40.

Balwierz PJ, et al. (2009) Methods for analyzing deep sequencing expression data: constructing the human and mouse promoterome with deepCAGE data. Genome biology, 10(7), R79.

Xavier CP, et al. (2009) Structural and functional diversity of novel coronin 1C (CRN2) isoforms in muscle. Journal of molecular biology, 393(2), 287.