Resource Summary Report

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SpliceTrap

RRID:SCR_006728
Type: Tool

Proper Citation

SpliceTrap (RRID:SCR_006728)

Resource Information

URL: http://rulai.cshl.edu/splicetrap/

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Description: A statistic tool for quantifying exon inclusion ratios in paired-end RNA-seq data, with broad applications for the study of alternative splicing. SpliceTrap approaches to exon inclusion level estimation as a Bayesian inference problem. For every exon it quantifies the extent to which it is included, skipped or subjected to size variations due to alternative 3?/5? splice sites or Intron Retention. In addition, SpliceTrap can quantify alternative splicing within a single cellular condition, with no need of a background set of reads.

Abbreviations: SpliceTrap

Resource Type: software resource

Defining Citation: PMID:21896509

Keywords: bio.tools

Funding:

Resource Name: SpliceTrap

Resource ID: SCR_006728

Alternate IDs: biotools:splicetrap, OMICS_01292

Alternate URLs: https://bio.tools/splicetrap

Record Creation Time: 20220129T080237+0000

Record Last Update: 20250410T065450+0000

Ratings and Alerts

No rating or validation information has been found for SpliceTrap.

No alerts have been found for SpliceTrap.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 16 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Fronk AD, et al. (2024) Development and validation of AI/ML derived splice-switching oligonucleotides. Molecular systems biology, 20(6), 676.

Teng P, et al. (2023) The human lncRNA GOMAFU suppresses neuronal interferon response pathways affected in neuropsychiatric diseases. Brain, behavior, and immunity, 112, 175.

Yang P, et al. (2021) Alternative splicing level related to intron size and organism complexity. BMC genomics, 22(1), 853.

Vuong CK, et al. (2018) Rbfox1 Regulates Synaptic Transmission through the Inhibitory Neuron-Specific vSNARE Vamp1. Neuron, 98(1), 127.

Liu H, et al. (2018) Alternative splicing analysis in human monocytes and macrophages reveals MBNL1 as major regulator. Nucleic acids research, 46(12), 6069.

Johnston WL, et al. (2017) C. elegans SUP-46, an HNRNPM family RNA-binding protein that prevents paternally-mediated epigenetic sterility. BMC biology, 15(1), 61.

Das DK, et al. (2017) Fibronectin and androgen receptor expression data in prostate cancer obtained from a RNA-sequencing bioinformatics analysis. Data in brief, 11, 131.

Fang J, et al. (2017) Ubiquitination of hnRNPA1 by TRAF6 links chronic innate immune signaling with myelodysplasia. Nature immunology, 18(2), 236.

Tan JH, et al. (2017) The combinatorial control of alternative splicing in C. elegans. PLoS

genetics, 13(11), e1007033.

Arun G, et al. (2016) Differentiation of mammary tumors and reduction in metastasis upon Malat1 lncRNA loss. Genes & development, 30(1), 34.

de Bruin RG, et al. (2016) Quaking promotes monocyte differentiation into pro-atherogenic macrophages by controlling pre-mRNA splicing and gene expression. Nature communications, 7, 10846.

Giudice J, et al. (2016) Neonatal cardiac dysfunction and transcriptome changes caused by the absence of Celf1. Scientific reports, 6, 35550.

Ragle JM, et al. (2015) Coordinated tissue-specific regulation of adjacent alternative 3' splice sites in C. elegans. Genome research, 25(7), 982.

Linares AJ, et al. (2015) The splicing regulator PTBP1 controls the activity of the transcription factor Pbx1 during neuronal differentiation. eLife, 4, e09268.

Viner C, et al. (2014) Validation of predicted mRNA splicing mutations using high-throughput transcriptome data. F1000Research, 3, 8.

Gelfman S, et al. (2013) DNA-methylation effect on cotranscriptional splicing is dependent on GC architecture of the exon-intron structure. Genome research, 23(5), 789.