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Open chromatin in human pancreatic islets (FAIRE-seq) - Study GBCO4075**Genomics Study Specifications**

Study Name	Open chromatin in human pancreatic islets (FAIRE-seq)
Contact Name	Kyle J. Gaulton (University of North Carolina at Chapel Hill)
Publication	http://www.ncbi.nlm.nih.gov/pubmed/20118932
My Strategies	Return to My Strategies page
Classification	Tissue expression, surveys and comparisons
Links	 Biomaterials Graph  GEO
BCBC Release Date	January 04, 2011
Public Release Date	January 04, 2011
Citation	Gaulton KJ, Nammo T, Pasquali L, Simon JM, Giresi PG, Fogarty MP, Panhuis TM, Mieczkowski P, Secchi A, Bosco D, Berney T, Montanya E, Mohlke KL, Lieb JD, Ferrer J. A map of open chromatin in human pancreatic islets . Nat Genet. 2010. 42:255-9

Synopsis

Study Description	Goals	
Approaches	Results	Conclusions
Related Studies		

The goal of this experiment was to identify active regulatory DNA in human pancreatic islets. This was accomplished using high-throughput sequencing of genomic regions isolated using FAIRE from three purified pancreatic islet samples. FAIRE-seq data were technically validated by comparing to gene expression patterns determined by hybridizing the FAIRE samples to a tiling DNA microarray. Comparison between islet and non-islet cell lines revealed ~3,300 physically linked clusters of open chromatin sites, many encompassing single genes with islet-specific expression. By mapping sequence variants to open chromatin sites, we were also able to identify an association between rs7903146, a TCF7L2 intronic variant, and type 2 diabetes.

Platform types	Open chromatin FAIRE-Seq, Epigenomic
Platforms	Not available
Study Design Type	<ul style="list-style-type: none"> cell_type_comparison_design
Study Factors	Show study factors
Study Assays	Show study assays


Access to Study Data

This Study Data is publicly available to all users.


Gene List(s)

There are no gene lists currently available for this study.

Genome Browser**Access Status**

 This resource is publicly viewable.


Request this Resource


 Request from a repository

Primary contributor: [Stoeckert Lab](#)

Resource Tags

ctcf, faire-seq, tcf7l2

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Resource History & Actions

Approved on Jan 04, 2011
Last modified on Aug 02, 2011

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Related resources**BCBC**

No matching resources

Other Consortia

No matching resources

Data courtesy of [dkCOIN](#). Only public resources are displayed.

Browse related tracks on the genome browser by clicking on the link(s) below:

[View tracks for this study in the region around the INS gene](#)

[Open Chromatin Peak Calls and Coverage](#)

Lists of Locations

Use the following form(s) to refine the parameters and add the list of genomic sequences corresponding to peak calls to a strategy. Depending on your choices, these searches may be slow.

Open Chromatin in Human Islets (Sample 3; F-Seq Peak Calls from MAQ Aligned FAIRE-Seq)

Retrieve:

Whole Genome

Peaks in a Region of Interest (specify below):

Enter a region (e.g., chr:start-stop) or enter just the chromosome (e.g., chr12 or chrX) to search for peaks on a single chromosome. Select the "Whole Genome" option or leave the text box blank to return all results from this analysis.

Open Chromatin in Human Islets (Sample 3; MACS Peak Calls from MAQ Aligned FAIRE-Seq)

Repositories

Stoeckert Lab

Stock #: *Not provided*

Availability Notes: *Not provided*

Comments

There are no comments for this entry.

