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

Genomics Study Specifications

**Study Name**: Open chromatin in human pancreatic islets (FAIRE-seq)

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**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


**Synopsis**

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

- 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.

Find Locations

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

Repositories

Stoeckert Lab

- Request this resource
- Stock #: Not provided
- Availability Notes: Not provided

Comments

There are no comments for this entry.

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