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Genome-wide Analysis of Histone Modifications in Normal Human Islets - Study GBCO3918

Genomics Study Specifications

Study Name	Genome-wide Analysis of Histone Modifications in Normal Human Islets
Contact Name	Reena Bhandare (Department of Genetics, University of Pennsylvania)
Publication	http://www.ncbi.nlm.nih.gov/pubmed/20181961
My Strategies	Return to My Strategies page
Classification	Tissue expression, surveys and comparisons
Links	 Biomaterials Graph  ArrayExpress
BCBC Release Date	July 21, 2010
Public Release Date	July 21, 2010
Citation	Bhandare R, Schug J, Le Lay J, Fox A, Smirnova O, Liu C, Naji A, Kaestner KH. Genome-wide analysis of histone modifications in human pancreatic islets . Genome Res. 2010. 20:428-33

Synopsis**Study Description**

Goals

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Related Studies

This experiment used ChIP-seq technology to create a genome-wide profile of histone marks in normal human pancreatic islets. In the current work we analyzed two histone marks associated with gene expression (H3K4me3, H3K4me1) and marks associated with gene repression (H3K27me3). Each mark was analyzed using samples obtained from four donors (n=4). Chromatin Immunoprecipitations (ChIPs) for histone marks were performed using specific anti-histone antibodies. Enrichment of each sample was calculated with respect to its individual input using qPCR. Samples were sequenced with Solexa and sequenced DNA from both Input (n=4) and ChIP (n = 4) samples were aligned to the NCBI Genome Build 36.1 Hg18 to determine regions that were enriched for binding by modified histones.

Platform types	Histone modification ChIP-Seq, Epigenomic
Platforms	<i>Not available</i>
Study Design Type	<ul style="list-style-type: none"> binding_site_identification_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.

Access Status

 This resource is publicly viewable.

Request this Resource


 Request from a repository

Primary contributor: [Kaestner Lab](#)

Resource Tags

GAPDH, GCG, H3K27me3, H3K4me1, H3K4me3, HOXB7, HOXB 9, Illumina Genome Analyzer, INS, MAFB, PDX1

 [Login to edit tags](#)

 [Read more about tags](#)

Resource History & Actions

Approved on Jul 21, 2010
Last modified on Jan 17, 2012

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Related resources

BCBC

No matching resources

Other Consortia

No matching resources

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

Genome Browser

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](#)

H3K4me1, H3K4me2, H3K4me3, and H3K27me3 Peak Calls

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.

H3K4me2 Histone Modification in Normal Human Islets (GLITR Pipeline:Pooled Unique-Best-Match Reads)

Retrieve:

Whole Genome

Peaks in a Region of Interest (specify below):

chr5

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


H3K4me3 Histone Modification in Normal Human Islets (GLITR Pipeline:Pooled Unique-Best-Match Reads)

H3K27me3 Histone Modification in Normal Human Islets (GLITR Pipeline:Pooled Unique-Best-Match Reads)

H3K4me1 Histone Modification in Normal Human Islets (GLITR Pipeline:Pooled Unique-Best-Match Reads)

Repositories

Kaestner Lab


 Request this resource

Stock #: *Not provided*

Availability Notes: *Not provided*

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