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

### Genomics Study Specifications

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

**Synopsis****Study Description**

## Goals

## Approaches

## Results

## Conclusions

## 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** *Not available*

**Study Design Type**

- 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](#)

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### Resource History & Actions

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

 [Login to edit or request an edit](#)

### 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):

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.


### 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*

## Comments

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