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Transcriptional and epigenetic high throughput sequencing of human and mouse pancreatic islet-cells - Study GBCO4514

Genomics Study Specifications

Study Name	Transcriptional and epigenetic high throughput sequencing of human and mouse pancreatic islet-cells
Contact Name	Jorge Ferrer (Hospital Clinic de Barcelona)
Publication	http://www.ncbi.nlm.nih.gov/pubmed/23040067
My Strategies	Return to My Strategies page
Classification	Tissue expression, surveys and comparisons
Links	 Biomaterials Graph  ArrayExpress
BCBC Release Date	November 06, 2012
Public Release Date	November 06, 2012
Citation	Morán I, Akerman I, van de Bunt M, Xie R, Benazra M, Nammo T, Arnes L, Nakić N, García-Hurtado J, Rodríguez-Seguí S, Pasquali L, Sauty-Colace C, Beucher A, Scharfmann R, van Arensbergen J, Johnson PR, Berry A, Lee C, Harkins T, Gmyr V, Pattou F, Kerr-Conte J, Piemonti L, Berney T, Hanley N, Gloyn AL, Sussel L, Langman L, Brayman KL, Sander M, McCarthy MI, Ravassard P, Ferrer J. Human β cell transcriptome analysis uncovers lncRNAs that are tissue-specific, dynamically regulated, and abnormally expressed in type 2 diabetes . Cell Metab. 2012. 16:435-48

Synopsis

Study Description	Goals	
Approaches	Results	Conclusions
Related Studies		

The aim of this experiment was to obtain a detailed transcriptional landscape of human and mouse islet-cells, including strand information, as well an epigenetic map of transcriptionally active chromatin.

Platform types	Epigenomic, Histone modification ChIP-Seq, Expression, TF Binding, TF Binding ChIP-Seq, Expression RNA-Seq
Platforms	<i>Not available</i>
Study Design Type	<ul style="list-style-type: none"> is_expressed_design species_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)

Use the following form(s) to refine the parameters and add the gene list to a strategy:

Access Status

 This resource is publicly viewable.

Request this Resource

 Request from a repository

Primary contributor: [Ferrer Lab](#)

Resource Tags

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 [Read more about tags](#)

Resource History & Actions

Approved on Nov 06, 2012
Last modified on Nov 19, 2013

 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.

|Fold Change| Greater Than:

Confidence Level:

High Confidence All Results

For a microarray experiment a result with high confidence has a confidence level of at least 80%.

For a ChIP-chip experiment a result with high confidence has a confidence level of at least 90% and all fold changes are positive.

Reference (Denominator):

NA

Genome Browser

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

[View tracks for this study in the region near the PROX1 gene](#) RNA-Seq Expression Coverage (Islets, Beta Cells, Acinar Cells); Pol II Binding Peak Calls (Islets); H3K4me3, H3K36me3 and Input Peak Calls and Coverage (Islets)

[View tracks for this study in the region near the Prox1 gene](#) RNA-Seq Expression Coverage (Islets)

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.

▼ H3K36me3 Histone Modification in Human Islets, Sample HI 32 (Modified MACS Peak Calls)

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.

▶ H3K36me3 Histone Modification in Human Islets, Sample HI 25 (Modified MACS Peak Calls)

▶ Pol II Binding in Human Islets, Sample HI 32 (Modified MACS Peak Calls)

▶ H3K4me3 Histone Modification in Human Islets, Sample HI 21 (Modified MACS Peak Calls)


▶ H3K4me3 Histone Modification in Human Islets, Sample HI 25 (Modified MACS Peak Calls)

▶ H3K4me3 Histone Modification in Human Islets, Sample HI 32 (Modified MACS Peak Calls)

▶ Long non-coding RNAs in Human Islets

Repositories

Ferrer Lab


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Stock #: Not provided

Availability Notes: Not provided

Comments

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