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Transcriptional and epigenetic profiling of the progression of hESCs to beta cells - Study GBCO4314

Genomics Study Specifications

Study Name	Transcriptional and epigenetic profiling of the progression of hESCs to beta cells
Contact Name	Maike Sander (University of California, San Diego)
Publication	http://www.ncbi.nlm.nih.gov/pubmed/23318056
My Strategies	Return to My Strategies page
Classification	Cell differentiation; Differentiation of insulin-producing cells
Links	Biomaterials Graph ArrayExpress
BCBC Release Date	December 13, 2011
Public Release Date	February 12, 2013
Citation	Xie R, Everett LJ, Lim HW, Patel NA, Schug J, Kroon E, Kelly OG, Wang A, D'Amour KA, Robins AJ, Won KJ, Kaestner KH, Sander M. Dynamic chromatin remodeling mediated by polycomb proteins orchestrates pancreatic differentiation of human embryonic stem cells. Cell Stem Cell. 2013. 12:224-37
Synopsis	Study Description | Goals | Approaches | Results | Conclusions | Related Studies To characterize the epigenetic programs that underlie pancreas differentiation, we have generated genome-scale maps of H3K4me3, H3K4me1 and H3K27me3 patterns by ChIP-seq and determined expression profiles by RNA-seq from undifferentiated human ESCs, three intermediate differentiated stages (definitive endoderm, primitive gut tube, and posterior foregut), pancreatic progenitors and in vitro-differentiated polyhormonal cells. Antibodies against CD142 and CD200 were used to select for targeted pancreatic and endocrine populations at the end of the culture. Pancreatic endoderm was subsequently transplanted for further differentiation into mature insulin-producing beta-cells and compared to sorted polyhormonal cells by RNA-seq and ChIP-seq analysis.
Platform types	Expression, Epigenomic, Expression RNA-Seq, Histone modification ChIP-Seq
Platforms	*Not available*
Study Design Type	• cell_type_comparison_design • development_or_differentiation_design • is_expressed_design • organism_part_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.

Access Status

This resource is publicly viewable.

Request this Resource

Request from a repository

Primary contributor: Sander Lab

Resource Tags

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Resource History & Actions

Approved on Dec 13, 2011
Last modified on Feb 26, 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.

Gene List(s)

Browse related gene lists by clicking on the link(s) below:

hESC-DE Gene Signature	Browse hESC-derived definitive endoderm signature genes
hESC-GT Gene Signature	Browse hESC-derived gut tube signature genes
hESC-PF Gene Signature	Browse hESC-derived posterior foregut signature genes
hESC-PE Gene Signature	Browse hESC-derived pancreatic endoderm signature genes
hESC-FE Gene Signature	Browse hESC-derived functional endocrine cell signature genes
hESC-DE Signature:bivalent resolved to H3K4me3	Browse hESC-derived definitive endoderm signature genes resolved from bivalent in hESCs to H3K4me3 at the definitive endoderm stage
hESC-PE Signature:bivalent resolved to H3K4me3	Browse hESC-derived pancreatic endoderm signature genes resolved from bivalent in hESCs to H3K4me3 at the late pancreatic endoderm stage
hESC-FE Signature:bivalent resolved to H3K4me3	Browse hESC-derived functional endocrine signature genes resolved from bivalent at the pancreatic endocrine stage to H3K4me3 after engraftment in mice
hESC-FE Signature: H3K4me3 acquired	Browse hESC-derived functional endocrine cell signature genes with no modification at the pancreatic endoderm stage acquiring H3K4me3 after engraftment in mice
hESC-FE v hESC-PH Cells	Browse genes more highly expressed in hESC-derived functional endocrine cells than in polyhormonal cells
hESC-FE up: H3K4me3 not acquired in PH	Browse genes with higher expression in hESC-derived functional endocrine cells relative to polyhormonal cells failing to acquire H3K4me3 during the transition from pancreatic endoderm to polyhormonal cells
hESC-FE up: H3K27me3 retained in PH	Browse genes with higher expression in hESC-derived functional endocrine cells relative to polyhormonal cells retaining H3K27me3 repression during the transition from pancreatic endoderm to polyhormonal cells

Genome Browser

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

hESC, culture day 0, in the region around the SOX17 gene	RNA-Seq Expression Coverage; H3K4me3, H3K27me3 and Input Peak Calls and Coverage
hESC-derived definitive endoderm in the region around the SOX17 gene	RNA-Seq Expression Coverage; H3K4me3, H3K27me3 and Input Peak Calls and Coverage
hESC-derived gut tube in the region around the SOX17 gene	RNA-Seq Expression Coverage; H3K4me3, H3K27me3 and Input Peak Calls and Coverage
hESC-derived posterior foregut in the region around the SOX17 gene	RNA-Seq Expression Coverage; H3K4me3, H3K27me3 and Input Peak Calls and Coverage
hESC-derived pancreatic endoderm in the region around the PDX1 gene	RNA-Seq Expression Coverage; H3K4me3, H3K27me3 and Input Peak Calls and Coverage
hESC-derived CD142+ late pancreatic endoderm in the region around the PDX1 gene	RNA-Seq Expression Coverage; H3K4me3, H3K27me3 and Input Peak Calls and Coverage
hESC-derived CD200+ polyhormonal cells in the region around the PDX1 gene	RNA-Seq Expression Coverage; H3K4me3, H3K27me3 and Input Peak Calls and Coverage
hESC-derived endocrine cells functionally matured in-vivo in the region around the PDX1 gene	RNA-Seq Expression Coverage; H3K4me3, H3K27me3 and Input Peak Calls and Coverage
Fetal pancreas in the region around the PDX1 gene	RNA-Seq Expression Coverage; H3K4me3, H3K27me3 and Input 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.

H3K4me3 ESC peak calls (culture day 0)

Retrieve:

Whole Genome
Peaks in a Region of Interest (specify below):
chr8

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

- H3K27me3 ESC peak calls (culture day 0)
- H3K4me3 ESC directed to Definitive Endoderm peak calls (culture day 2)
- H3K27me3 ESC directed to Definitive Endoderm peak calls (culture day 2)
- H3K4me3 ESC directed to Primitive Gut Tube peak calls (culture day 5)
- H3K27me3 ESC directed to Primitive Gut Tube peak calls (culture day 5)
- H3K4me3 ESC directed to Posterior Foregut peak calls (culture day 7)
- H3K27me3 ESC directed to Posterior Foregut peak calls (culture day 7)
- H3K4me3 ESC directed to Pancreatic Endoderm peak calls (culture day 10)
- H3K27me3 ESC directed to Pancreatic Endoderm peak calls (culture day 10)
- H3K4me3 CD142+ late pancreatic endoderm from ESC peak calls (culture day 13)
- H327me3 CD142+ late pancreatic endoderm from ESC peak calls (culture day 13)
- H3K4me3 CD200+ polyhormonal cells from ESC peak calls (culture day 13)
- H3K27me3 CD200+ polyhormonal cells from ESC peak calls (culture day 13)
- H3K4me3 in vivo-matured Endocrine Cells peak calls
- H3K27me3 in vivo-matured Endocrine Cells peak calls

Repositories

Sander Lab

Request this resource

Stock #: *Not provided*
Availability Notes: *Not provided*

Stoeckert Lab

Request this resource

Stock #: *Not provided*
Availability Notes: *Not provided*

Comments

There are no comments for this entry.

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