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## Whole transcriptome analysis of Sox17.Epi and Endo cells in mouse embryos - Study GBCO4275

**Genomics Study Specifications**

<b>Study Name</b>	Whole transcriptome analysis of Sox17.Epi and Endo cells in mouse embryos
<b>Contact Name</b>	<a href="#">Mark Magnuson</a> (Vanderbilt University)
<b>Publication</b>	<a href="http://www.ncbi.nlm.nih.gov/pubmed/22865702">http://www.ncbi.nlm.nih.gov/pubmed/22865702</a>
<b>My Strategies</b>	<a href="#">Return to My Strategies page</a>
<b>Classification</b>	Pancreas development and growth; Tissue expression, surveys and comparisons
<b>Links</b>	 <a href="#">Biomaterials Graph</a>  <a href="#">ArrayExpress</a>
<b>BCBC Release Date</b>	December 13, 2011
<b>Public Release Date</b>	July 23, 2012
<b>Citation</b>	Choi E, Kraus MR, Lemaire LA, Yoshimoto M, Vemula S, Potter LA, Manduchi E, Stoeckert CJ, Grapin-Botton A, Magnuson MA. <a href="#">Dual lineage-specific expression of Sox17 during mouse embryogenesis</a> . Stem Cells. 2012. 30:2297-308

**Synopsis**

Study Description	Goals
Approaches	Results
Conclusions	
Related Studies	

This experiment has been done to understand the dynamics of gene expression in Sox17.Epi and Endo cells using multiplex RNA-Seq technology. Sox17.Epi (Sox17<sup>GFP+EpCAM+</sup>) and Sox17.Endo (Sox17<sup>GFP+EpCAM-</sup>) cells were isolated by FACS from E9.5 mouse embryos. The spatial comparison between Sox17.Epi versus Sox17.Endo provides insight into which genes are differentially of specifically expressed in two populations.

<b>Platform types</b>	Expression, Expression RNA-Seq
<b>Platforms</b>	<i>Not available</i>
<b>Study Design Type</b>	<ul style="list-style-type: none"> <li>cell_type_comparison_design</li> <li>transcript_identification_design</li> </ul>
<b>Study Factors</b>	<a href="#">Show study factors</a>
<b>Study Assays</b>	<a href="#">Show study assays</a>


**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: [Magnuson Lab](#)

**Resource Tags**

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**Resource History & Actions**

Approved on Dec 13, 2011  
 Last modified on Nov 20, 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.

|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): Endo

[Find Genes](#)

## 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 Onecut1 gene](#)      RNA-Seq Expression Coverage

## Lists of Locations

*There are no genomic location datasets currently available for this study.*


## Repositories

### Magnuson Lab

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


### Stoeckert Lab

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

## Comments

*There are no comments for this entry.*

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