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## Transcriptome profiling of human pancreatic cell lineage specification reveals functional signaling pathways and lncRNAs for cell fate determination - Study GBCO4594

**Genomics Study Specifications**

<b>Study Name</b>	Transcriptome profiling of human pancreatic cell lineage specification reveals functional signaling pathways and lncRNAs for cell fate determination
<b>Contact Name</b>	<a href="#">Yi Zhang</a> (Harvard University)
<b>Publication</b>	Not provided
<b>My Strategies</b>	<a href="#">Return to My Strategies page</a>
<b>Classification</b>	Cell differentiation; Tissue expression, surveys and comparisons
<b>Links</b>	<a href="#">Biomaterials Graph</a> <a href="#">ArrayExpress</a>
<b>BCBC Release Date</b>	April 16, 2013
<b>Citation</b>	unavailable
<b>Synopsis</b>	<div style="border: 1px solid #ccc; padding: 5px;"> <div style="display: flex; justify-content: space-between; border-bottom: 1px solid #ccc;"> <span style="background-color: #e91e63; color: white; padding: 2px 5px;">Study Description</span> <span>Goals</span> </div> <div style="display: flex; justify-content: space-between; border-bottom: 1px solid #ccc;"> <span>Approaches</span> <span>Results</span> <span>Conclusions</span> </div> <div style="display: flex; justify-content: space-between;"> <span>Related Studies</span> </div> <p>To guide the beta cell differentiation process in vitro, a complete understanding of the transcriptome and their regulatory network during the differentiation process is essential. Using RNA-seq, we have performed the transcriptome profiling of human embryonic stem cells (ESCs), purified ESC-derivate definitive endoderm (DE), pancreatic progenitors (PP), as well as sorted human primary pancreatic alpha cells, beta cells and exocrine cells.</p> </div>
<b>Platform types</b>	Expression, Expression RNA-Seq
<b>Platforms</b>	Not available
<b>Study Design Type</b>	<ul style="list-style-type: none"> <li>development_or_differentiation_design</li> </ul>
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**Access to Study Data**

To access the Study Data you must "Request this Resource" (below) and the supplier must fill your Request. Then Beta Cell Genomics will contact you with details on how to access the data.

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To access this study's gene list(s) you must "Request this Resource" (below) and the supplier must fill your Request.


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Zhang Lab

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**Availability Notes:** Not provided

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