RNA-seq of Ins+, Ucn3+/- cell populations within developmental mouse islets using MARIS - Study GBCO4762

Genomics Study Specifications

Study Name: RNA-seq of Ins+, Ucn3+/- cell populations within developmental mouse islets using MARIS
Contact Name: David Gifford (MIT)
Publication: Not provided

My Strategies: Return to My Strategies page
Classification: Tissue expression, surveys and comparisons; Pancreas development and growth

Links:
- Biomaterials Graph
- ArrayExpress

BCBC Release Date: April 01, 2014
Citation: unavailable

Synopsis:
The aim of this experiment was to observe the transcriptional profile of individual populations of cells in mouse islets throughout development. MARIS was used to isolate Ins+ islet cells at E18.5 and P13, and further separate Ucn3- and Ucn3+ populations at the transition point P4 and P5.

Platform types: Expression RNA-Seq, Expression
Platforms: Not available
Study Design Type: development_or_differentiation_design
Study Factors:
- Show study factors

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.

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

Repositories:
Melton Lab
- Request this resource
Stock #: Not provided
Availability Notes: Not provided

Stoeckert Lab
- Request this resource
Stock #: Not provided
Availability Notes: Not provided