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RNA-seq comparison: before/after MARIS protocol and library construction technique test - Study GBCO4763

Genomics Study Specifications

Study Name	RNA-seq comparison: before/after MARIS protocol and library construction technique test
Contact Name	David Gifford (MIT)
Publication	http://www.ncbi.nlm.nih.gov/pubmed/24594682
My Strategies	Return to My Strategies page
Classification	Tissue expression, surveys and comparisons; Cell differentiation; Differentiation of insulin-producing cells
Links	Biomaterials Graph ArrayExpress
BCBC Release Date	April 01, 2014
Citation	Hrvatin S, Deng F, O'Donnell CW, Gifford DK, Melton DA. MARIS: method for analyzing RNA following intracellular sorting. PLoS One. 2014. 9:e89459
Synopsis	Study Description | Goals | Approaches | Results | Conclusions | Related Studies The aim of this experiment was to determine the amount of RNA-seq signal degradation that results from MARIS and to test how well 4 different RNA-seq library construction techniques perform on partially degraded RNA.
Platform types	Expression, Expression RNA-Seq
Platforms	*Not available*
Study Design Type	• optimization_design • quality_control_testing_design
Study Factors	Show study factors
Study Assays	Show study assays

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

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

Stoeckert Lab

Stock #: *Not provided*

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Request from a **repository**

Primary contributor: **Melton Lab**

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Approved on Apr 01, 2014
Last modified on Apr 15, 2014

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Data courtesy of dkCOIN. Only public resources are displayed.

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Availability Notes: *Not provided*

Comments

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