

**My Account**

Login  
Create Account

**Resources**

View All (813)  
Adenoviruses (137)  
Antibodies (175)  
Bioimages (67)  
Genomics Studies (145)  
mESC Lines (68)  
Mouse Strains (120)  
Miscellaneous (46)  
Protocols (55)  
Research Data (4)  
Resource Tags (389)  
Visualization (9)



**Research & Cores**

Core Facilities (5)  
Research Highlights (5)  
Research Networks  
Research Objectives

**Information**

About the BCBC  
BCBC Events  
Branding & Logos  
Career Opportunities  
Health  
NIH hESC Registry  
Policies & Guidelines  
Member Publications  
Research Programs  
Research Investigators  
Member Directory  
Tutorials

**Brown preadipocyte IRS knockout profiling 1 - Study GBCO2330****Genomics Study Specifications**

<b>Study Name</b>	Brown preadipocyte IRS knockout profiling 1
<b>Contact Name</b>	<a href="#">Ronald C Kahn</a> (Joslin Diabetes Center and Harvard Medical School)
<b>Publication</b>	<a href="http://www.ncbi.nlm.nih.gov/pubmed/15895078">http://www.ncbi.nlm.nih.gov/pubmed/15895078</a>
<b>My Strategies</b>	<a href="#">Return to My Strategies page</a>
<b>Classification</b>	Cell differentiation
<b>Links</b>	 <a href="#">Biomaterials Graph</a>  <a href="#">ArrayExpress</a>
<b>BCBC Release Date</b>	February 20, 2006
<b>Public Release Date</b>	February 20, 2006
<b>Citation</b>	Tseng YH, Butte AJ, Kokkotou E, Yechoor VK, Taniguchi CM, Kriauciunas KM, Cypess AM, Niinobe M, Yoshikawa K, Patti ME, Kahn CR. <a href="#">Prediction of preadipocyte differentiation by gene expression reveals role of insulin receptor substrates and neclin</a> . Nat Cell Biol. 2005. 7:601-11

**Synopsis**

<b>Study Description</b>	Goals	
Approaches	Results	Conclusions
Related Studies		

Brown preadipocytes were grown to confluence and synchronized by overnight serum starvation. Four independent RNA samples were analyzed from each IRS KO cell line and three independent clones of WT cells were separately analyzed as controls. Splitting of the samples resulted in a total 28 microarrays. 15 mg of adjusted cRNA were hybridized to Affymetrix U74A-v2 arrays.

<b>Platform types</b>	Expression microarray, Expression
<b>Platforms</b>	<a href="#">Show platform Affymetrix MG_U74A</a>
<b>Study Design Type</b>	<ul style="list-style-type: none"> <li>genetic_modification_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)**

There are no gene lists currently available for this study.


**Genome Browser**

There are no genome browser tracks currently available for this study.


**Lists of Locations**

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

**Access Status**

 This resource is publicly viewable.


**Request this Resource**

 Request from a repository

Primary contributor: [Stoeckert Lab](#)

**Resource Tags**

 Login to edit tags

 Read more about tags

**Resource History & Actions**

Approved on Feb 20, 2006  
Last modified on Aug 02, 2011

 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.

## Repositories


Stoeckert Lab

 Request this resource

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

## Comments

*There are no comments for this entry.*

 Login to add comments

[Home](#) · [Your Account](#) · [News & Events](#) · [Resources](#) · [Policies & Guidelines](#) · [About Us](#) · [FAQ](#) · [Site Map](#)

© 2002-2015 Beta Cell Biology Consortium - All Rights Reserved. [Terms of usage and disclaimer.](#)

