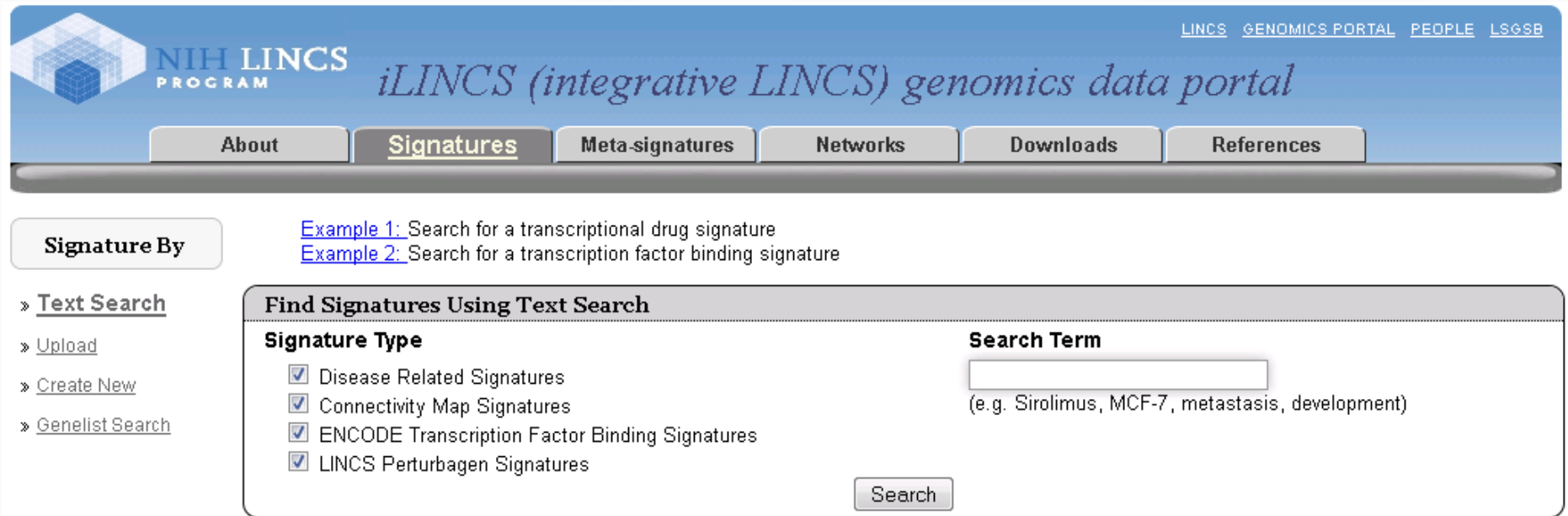


# <http://LincsGenomics.org>



The screenshot shows the iLINCS (integrative LINCS) genomics data portal. The header features the NIH LINCS PROGRAM logo and the text "iLINCS (integrative LINCS) genomics data portal". Navigation links include LINCS, GENOMICS PORTAL, PEOPLE, and LSGSB. A menu bar contains buttons for About, Signatures (highlighted), Meta-signatures, Networks, Downloads, and References.

On the left, a "Signature By" section lists options: Text Search, Upload, Create New, and Genelist Search. The "Text Search" option is selected.

The main content area is titled "Find Signatures Using Text Search". It includes a "Signature Type" section with four checked options: Disease Related Signatures, Connectivity Map Signatures, ENCODE Transcription Factor Binding Signatures, and LINCS Perturbagen Signatures. To the right is a "Search Term" input field with a placeholder text "(e.g. Sirolimus, MCF-7, metastasis, development)". A "Search" button is located at the bottom right of the search area.

Mario Medvedovic, Siva Sivaganesan, John Reichard, Mukta Phatak, Wen Niu, Jing Chen, Vineet Joshi



# Placing LINCS perturbagen signatures in the context of other “genome-scale” signatures

## Signature:

*“genome-wide” (for each gene) list of “scores” (activity level) and “p-values” (statistical significance)*

## Signature types:

*Differential gene expression signatures (log-ratio, p-value)*

*Transcription factor binding signatures (score, probability of binding)*

**(Poster by Jing Chen)**



# Libraries of pre-computed signatures

***LINCS Perturbagen Signatures***: transcriptional signatures of “perturbagen” activity constructed based on Broad L1000 assay data.

***Disease Related Signatures***: transcriptional signatures constructed by analysis of GEO GDS collection

***ENCODE Transcription Factor Binding Signatures***: transcription factor (TF) binding signatures constructed using ENCODE ChIP-seq data

***Connectivity Map Signature***: transcriptional signatures of “perturbagen” activity based on CMAP 2 data.



# Genomics datasets that can be used to create custom signatures

*~3,000 genomics datasets with ~100,000 transcriptional profiles*

*GEO GDS data collection of human, mouse and rat datasets*

*TCGA RNA-seq data*

*Custom curated datasets of interest*





**Find or construct a genome scale signatures**



**Find concordant signatures**



**Establish biological model of concordance**



# Finding pre-computed signatures and their concordant signatures

Signatures

Text S

Upload

Create

Genelis

## Signatures Concordant with the Selected Signature

Concordant Signatures in Library: Connectivity Map Signatures

<input type="checkbox"/>	Signature ID	Perturbagen (2)	Concentration	Cell
<input checked="" type="checkbox"/>	<a href="#">CMAP_48</a>	estradiol	0.00000001, 0.00000001	MCF7
<input checked="" type="checkbox"/>	<a href="#">CMAP_42</a>	estradiol	0.00000001	MCF7
<input type="checkbox"/>	<a href="#">CMAP_173</a>	tretinoin	0.000001, 0.0000134	MCF7
<input type="checkbox"/>	<a href="#">CMAP_225</a>	genistein	0.000001, 0.00001	MCF7
<input type="checkbox"/>	<a href="#">CMAP_3647</a>	estropipate	0.0000092	MCF7
<input checked="" type="checkbox"/>	<a href="#">CMAP_38</a>	estradiol	0.00000001	MCF7
<input type="checkbox"/>	<a href="#">CMAP_168</a>	tretinoin	0.000001	MCF7
<input type="checkbox"/>	<a href="#">CMAP_4646</a>	equilin	0.000015	MCF7
<input type="checkbox"/>	<a href="#">CMAP_4874</a>	etynodiol	0.0000104	MCF7
<input type="checkbox"/>	<a href="#">CMAP_172</a>	tretinoin	0.0000134	MCF7
<input type="checkbox"/>	<a href="#">CMAP_996</a>	naringenin	0.0000146	MCF7
<input type="checkbox"/>	<a href="#">CMAP_220</a>	genistein	0.00001	MCF7
<input type="checkbox"/>	<a href="#">CMAP_5086</a>	dienestrol	0.000015	MCF7
<input type="checkbox"/>	<a href="#">CMAP_1812</a>	lynestrenol	0.000014	MCF7
<input type="checkbox"/>	<a href="#">CMAP_7</a>	metformin	0.00001, 0.0000001, 0.00000001	MCF7
<input type="checkbox"/>	<a href="#">CMAP_4221</a>	epitiostanol	0.000013	MCF7
<input checked="" type="checkbox"/>	<a href="#">CMAP_248</a>	fulvestrant	0.00000001	MCF7
<input type="checkbox"/>	<a href="#">CMAP_4760</a>	butyl hydroxybenzoate	0.0000206	MCF7
<input type="checkbox"/>	<a href="#">CMAP_3911</a>	diethylstilbestrol	0.000015	MCF7
<input type="checkbox"/>	<a href="#">CMAP_4634</a>	aminophylline	0.0000096	MCF7
<input checked="" type="checkbox"/>	<a href="#">CMAP_255</a>	fulvestrant	0.00000001, 0.000001	MCF7
<input type="checkbox"/>	<a href="#">CMAP_3329</a>	isotretinoin	0.0000134	MCF7
<input type="checkbox"/>	<a href="#">CMAP_4858</a>	prasterone	0.0000122	MCF7
<input checked="" type="checkbox"/>	<a href="#">CMAP_127</a>	raloxifene	0.0000078	MCF7
<input type="checkbox"/>	<a href="#">CMAP_3429</a>	epiandrosterone	0.0000138	MCF7
<input type="checkbox"/>	<a href="#">CMAP_864</a>	corticosterone	0.0000116	MCF7

Functional TreeView: http://eh3.uc.edu/tmp/TreeViewMon\_Mar\_18\_09:53:49\_2013\_5...

File Settings Analysis Export Window Help

View Stat  
NODEID:  
NODE18  
CORREL  
0.39979

Usage Hints  
Click to select node  
- use arrow keys to navigate tree

estradiol, MCF7, estradiol, 0.0000146, control  
estradiol, MCF7, estradiol, 0.00000001, control  
estradiol, MCF7, estradiol, 0.0000000001, 0.00000001, 0.0000146, control  
estradiol, MCF7, estradiol, 0.0000000001, control  
raloxifene, MCF7, raloxifene, 0.0000078, control  
fulvestrant, MCF7, fulvestrant, 0.0000000001, control  
fulvestrant, MCF7, fulvestrant, 0.0000000001, 0.000001, control

4886: NPY1R: neuropeptide  
55540: IL17RB: interleukin  
6478: SIAH2: siah E3 ubiquitin  
26353: HSPB8: heat shock  
2296: FOXO1: forkhead box  
3487: IGFBP4: insulin-like growth factor  
595: CCND1: cyclin D1  
5979: RET: ret proto-oncogene  
2274: FHL2: four and a half  
6446: SGK1: serum/glucocorticoid-inducible kinase  
51195: RAPGEFL1: Rap guanine nucleotide exchange factor  
5366: PMAIP1: phorbol-12-13-myristate 13-acetate  
11098: PRSS23: protease  
23678: SGK3: serum/glucocorticoid-inducible kinase  
3717: JAK2: Janus kinase  
55638: SYBU: syntabulin (serine/threonine phosphatase)  
54981: NMRK1: nicotinic

Functional Information



# Finding signatures enriched for a gene list

**Signature By**

- » [Text Search](#)
- » [Upload](#)
- » [Create New](#)
- » [Genelist Search](#)

## Analysis Results

Datasets concordant with the custom signature are listed under "Concordant Signatures in Library". Repeat analysis by creating a different signature and/or choosing different signature type.

Differential Expression Signature	
<b>Sample Grouping Factor</b>	<b>Numerator</b>
PAM50Call	LumA
<b>Description</b>	<b>Reference</b>
919 mRNA-seq breast invasive carcinoma (BRCA) samples from TCGA project. The data was processed using the version 2 of the TCGA pipeline based on RSEM methodology. The dataset was downloaded from UCSC Cancer Genomics Browser.	Collins FS, Barke the genes involved complex landscape Mar;296(3):50-7. <a href="#">PubMed</a> source=ID=TCGA_BRCA_

**Interactive Tree Browsing \***

- [Original Data](#)
- [Centered Data](#)

**Static Heatmaps (pdf)**

- [Legend for all the heatmaps](#)
- [Statistical Analysis](#)
- [Original Data](#)
- [Centered Data](#)

**Data Download**

\* Unless the original data is in the form of log-transformed ratios, non-centered TreeView might not be very informative

**STITCH 3.1** [Input Page](#) [Downloads](#) [Help/Info](#)

[GO!](#)

- Confidence view
- Evidence view
- Actions view
- Interactive → [advanced](#)
- Show stereo-isomers
- Combine stereo-isomers
- Chemical link
- Add nodes
- Remove nodes
- Save

## Signatures Concordant with the Selected Signature

Concordant Signatures in Library: LINCS Perturbagen Signatures			
Displaying 5 records out of a total of 598 <span style="margin-left: 10px;"><a href="#">Display All</a></span> <span style="margin-left: 10px;"><a href="#">Export</a></span> <span style="margin-left: 10px;"><a href="#">Group Analysis</a></span>			
Signature ID	Perturbagen (?)	Concentration	Cell
<a href="#">LINCSCP_2904</a>	<a href="#">WORTMANNIN</a>	10nm	PC3
<a href="#">LINCSCP_2902</a>	<a href="#">WORTMANNIN</a>	10nm	MCF
<a href="#">LINCSCP_660</a>	<a href="#">WORTMANNIN</a>	10nm	A549
<a href="#">LINCSCP_420</a>	<a href="#">TESTOSTERONE PROPIONATE</a>	10nm	VCA
<a href="#">LINCSCP_2263</a>	<a href="#">METOCLOPRAMIDE HYDROCHLORIDE</a>	10nm	VCA

**Name:** NCGC00185091-01  
**LINCS ID:** LSM-2203  
**PubChem CID:** [46725878](#)  
**LINCS facility ID:** BRD-K09902554

**MW:** 272.4  
**TPSA:** 29.5  
**RD:** 1  
**Lipinski Rule of 5:** true  
**Bioavailability:** true

**MF:** C14H12N2S2  
**Logp:** 3.65  
**HBA:** 2  
**Lipinski Rule of 3:** false  
**Lead Likeness:** true

**Logd:** 2.22  
**HBD:** 1

CENTER for  
COMPUTATIONAL  
SCIENCE

NIH LINCS  
PROGRAM



**NIH LINCS  
PROGRAM**

[LINCS](#) [GENOMICS PORTAL](#) [PEOPLE](#) [LSGSB](#)

## iLINCS (*integrative LINCS*) genomics data portal

About
**Signatures**
Meta-signatures
Networks
Downloads
References

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**Signature By**

- > [Text Search](#)
- > [Upload](#)
- > [Create New](#)
- > [Genelist Search](#)

### Details Of Selected Signature

SignatureID	Perturbagen	Concentration
LINCSCP_3321	SALICIN	10nm

### Signatures Concordant with the Selected Signature

**Concordant Signatures in Library: Disease Related Signatures**  
 Displaying all 5 records    Export    Group Analysis

Signature ID	Dataset	Factor	Level 1				
<a href="#">GDS_4845</a>	<a href="#">gdsGDS1412</a>	protocol	hormone replacement therapy				
<a href="#">GDS_5031</a>	<a href="#">gdsGDS1993</a>	time	2 wk	3 wk	-0.25	1	
<a href="#">GDS_5029</a>	<a href="#">gdsGDS1993</a>	time	1 wk	3 wk	-0.23	1	
<a href="#">GDS_4222</a>	<a href="#">gdsGDS2396</a>	cell.type	stem cell				
<a href="#">GDS_4303</a>	<a href="#">gdsGDS1816</a>	cell.type	mesenchymal				

**Concordant Signatures in Library: LINCS Perturbagen Signatures**  
 Displaying 5 records out of a total of 265    Display All    Export    Group An

Signature ID	Perturbagen (?)	Concentrat
<a href="#">LINCSCP_2144</a>	<a href="#">CILOSTAZOL (STITCH)</a>	10nm
<a href="#">LINCSCP_829</a>	<a href="#">Naringenine (STITCH)</a>	10nm
<a href="#">LINCSCP_219</a>	<a href="#">CARBINOXAMINE MALEATE (STITCH)</a>	10nm
<a href="#">LINCSCP_588</a>	<a href="#">NAFRONYL OXALATE (STITCH)</a>	10nm
<a href="#">LINCSCP_1295</a>	<a href="#">BRD-K20482099-001-01-1 (STITCH)</a>	10nm

STITCH 3.1

Input Page Downloads Help/For search in Homo sapiens

STRUCTURE Suggest Model: Default

Name: NCG000185091-01  
 LINCS ID: LSM-2203  
 PubChem CID: [46925878](#)  
 LINCS facility ID: BRD-K09902564  
 MW: 272.4 MF: C<sub>14</sub>H<sub>12</sub>N<sub>2</sub>O<sub>2</sub>  
 TPSA: 29.5 Logp: 3.65  
 RB: 1 HBA: 2  
 Lipinski Rule of 5: true Lipinski Rule of 3: false  
 Bioavailability: true Lead Likeness: true

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