INGENUITY
PATHWAY ANALYSIS

Analysis Name: Diff_genes_heatmap_LSECS-iPSC-suplfile-2 - 2019-02-27 12:39 PM
Analysis Creation Date: 2019-02-27
Build version: 486617M
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Experiment Metadata

Name	Value

Analysis Settings

Reference set: Ingenuity Knowledge Base (Genes Only)
Relationship to include: Direct and Indirect
Includes Endogenous Chemicals
Optional Analyses: My Pathways My List

Filter Summary:
Consider only molecules and/or relationships where
(species = Human) AND
(confidence = Experimentally Observed OR High (predicted)) AND
(tissues/cell lines = HepG2 OR Microvascular endothelial cells OR Other Stem cells OR Stem cells not otherwise specified OR Hep3B OR Hepatoma Cell Lines not otherwise specified OR Embryonic stem cells OR HuH7 OR HUVEC cells OR Mesenchymal stem cells OR Endothelial cells not otherwise specified OR Other Hepatoma Cell Lines OR Liver OR Other Endothelial cells) AND

(mol. types = biologic drug OR chemical - endogenous mammalian OR chemical - endogenous non-mammalian OR chemical - kinase inhibitor OR chemical - other OR chemical - protease inhibitor OR chemical drug OR chemical reagent OR chemical toxicant OR complex OR cytokine OR disease OR enzyme OR function OR G-protein coupled receptor OR group OR growth factor OR ion channel OR kinase OR ligand-dependent nuclear receptor OR mature microRNA OR microRNA OR other OR peptidase OR phosphatase OR transcription regulator OR translation regulator OR transmembrane receptor OR transporter) AND
(data sources = An Open Access Database of Genome-wide Association Results OR BIND OR BioGRID OR Catalogue Of Somatic Mutations In Cancer (COSMIC) OR Chemical Carcinogenesis Research Information System (CCRIS) OR ClinicalTrials.gov OR ClinVar OR Cognia OR DIP OR DrugBank OR Gene Ontology (GO) OR GVK Biosciences OR Hazardous Substances Data Bank (HSDB) OR HumanCyc OR Ingenuity Expert Findings OR Ingenuity ExpertAssist Findings OR IntAct OR Interactome studies OR MIPS OR miRBase OR miRecords OR Mouse Genome Database (MGD) OR Obesity Gene Map Database OR Online Mendelian Inheritance in Man (OMIM) OR TarBase OR TargetScan Human)

Top Canonical Pathways

Name	p-value	Overlap
EIF2 Signaling	5.17E-05	33.3 % 55/165
Axonal Guidance Signaling	2.04E-04	28.8 % 87/302
Factors Promoting Cardiogenesis in Vertebrates	4.16E-04	38.0 % 27/71
Hepatic Fibrosis / Hepatic Stellate Cell Activation	5.00E-04	32.4 % 45/139
Actin Cytoskeleton Signaling	2.14E-03	30.6 % 44/144

Top Upstream Regulators

Name	p-value	Predicted Activation

COL18A1	5.69E-05	Inhibited
ERG	7.55E-05	Activated
IFNA2	1.06E-03	Activated
TGFB1	2.80E-03	
CLOCK	3.40E-03	

Top Diseases and Bio Functions

Diseases and Disorders

Name	p-value range	# Molecules
Cancer	4.12E-02 - 8.33E-09	681
Organismal Injury and Abnormalities	4.12E-02 - 8.33E-09	711
Gastrointestinal Disease	4.12E-02 - 1.11E-08	688
Hepatic System Disease	4.12E-02 - 1.52E-06	655
Infectious Diseases	2.96E-02 - 1.47E-03	39

Molecular and Cellular Functions

Name	p-value range	# Molecules
Cellular Movement	4.12E-02 - 2.07E-06	121
Cell Death and Survival	4.35E-02 - 2.46E-05	92
Cell-To-Cell Signaling and Interaction	4.48E-02 - 2.13E-04	49
Cellular Development	4.81E-02 - 9.40E-04	139
Cellular Function and Maintenance	3.54E-02 - 9.40E-04	78

Physiological System Development and Function

Name	p-value range	# Molecules
Cardiovascular System Development and Function	4.12E-02 - 6.22E-06	150
Organismal Development	4.81E-02 - 3.67E-05	112
Tissue Development	3.54E-02 - 9.40E-04	99
Hematological System Development and Function	4.48E-02 - 1.21E-02	19
Lymphoid Tissue Structure and Development	2.07E-02 - 1.25E-02	7

Top Tox Functions

Assays: Clinical Chemistry and Hematology

Name	p-value range	# Molecules
Increased Levels of Albumin	2.03E-01 - 2.03E-01	1

Hepatotoxicity

Name	p-value range	# Molecules
Liver Hyperplasia/Hyperproliferation	4.97E-01 - 2.66E-06	640
Liver Steatosis	5.96E-01 - 3.50E-02	4
Liver Adhesion	4.12E-02 - 4.12E-02	2

Hepatocellular Peroxisome Proliferation	2.03E-01 - 2.03E-01	1
Liver Inflammation/Hepatitis	5.96E-01 - 2.03E-01	8

Top Regulator Effect Networks

ID	Regulators	Disease & Functions	Consistency Score
1	VEGFA	Binding of blood cells,Cell movement	3.674
2	COL18A1	Binding of blood cells	-3.402

Top Networks

ID	Associated Network Functions	Score
1	Cell Death and Survival, Cellular Movement, Cellular Development	20
2	Cellular Movement, Cell Death and Survival, Cancer	20
3	Cellular Assembly and Organization, Cellular Function and Maintenance, Cell-To-Cell Signaling and Interaction	12
4	Cellular Movement, Immune Cell Trafficking, Cellular Assembly and Organization	8

5	Cellular Movement, Cardiovascular System Development and Function, Organismal Development	7

Top Tox Lists

Name	p-value	Overlap
Renal Necrosis/Cell Death	1.79E-05	28.6 % 120/419
Hepatic Fibrosis	5.99E-05	37.4 % 37/99
Cardiac Hypertrophy	1.52E-04	29.5 % 81/275
Genes associated with Chronic Allograft Nephropathy (Human)	4.66E-03	50.0 % 9/18
Liver Proliferation	4.88E-03	27.9 % 58/208

Top My Lists

Top My Pathways

Name	p-value	Overlap
Network 1: 3T3 adj	4.10E-02	31.4 % 16/51
TNFupstream 3T3adj	2.62E-01	30.8 % 4/13
CHI3L1 upstream	3.65E-01	50.0 % 1/2
Network 3 3T3Adj	4.30E-01	21.2 % 28/132
Network 4 3T3adj	1.00E00	14.8 % 13/88

Top Analysis-Ready Molecules

Expr Log Ratio

Molecules	Expr. Value	Chart
CD93	↑ 9.822	
ROBO4	↑ 9.410	
FLI1	↑ 9.332	
MEOX2	↑ 9.285	
APLN	↑ 9.267	
PECAM1	↑ 9.135	
LYVE1	↑ 9.037	
ERG	↑ 8.969	
GMFG	↑ 8.961	
ZEB1	↑ 8.921	

Expr Log Ratio

Molecules	Expr. Value	Chart
LIN28A	↓ -9.881	
VCAN	↓ -9.291	
TDGF1	↓ -8.757	
GRID2	↓ -8.542	
CACNA2D3	↓ -8.062	

NLGN1	↓	-7.825
VASH2	↓	-7.750
EPCAM	↓	-7.728
SFRP2	↓	-7.724
DNMT3B	↓	-7.346