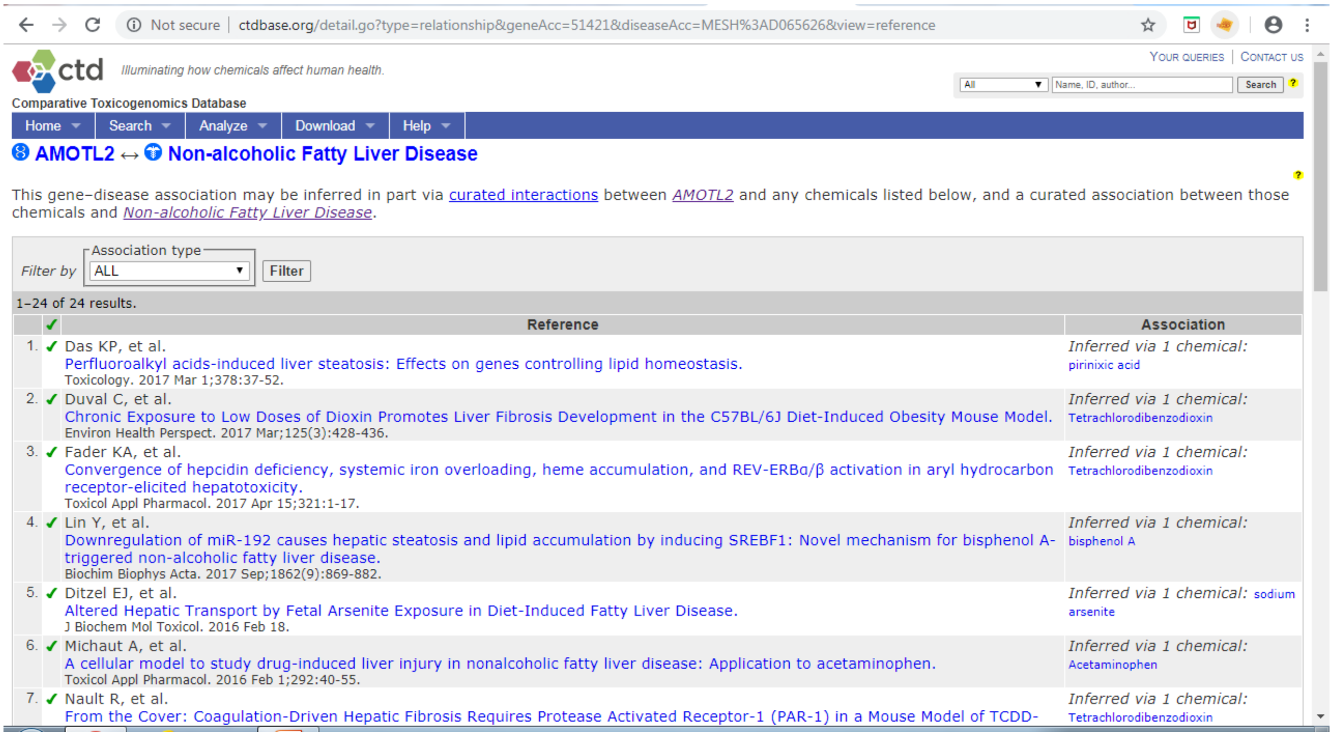
Supplementary Materials:



AMOTL2 ↔ Non-alcoholic Fatty Liver Disease

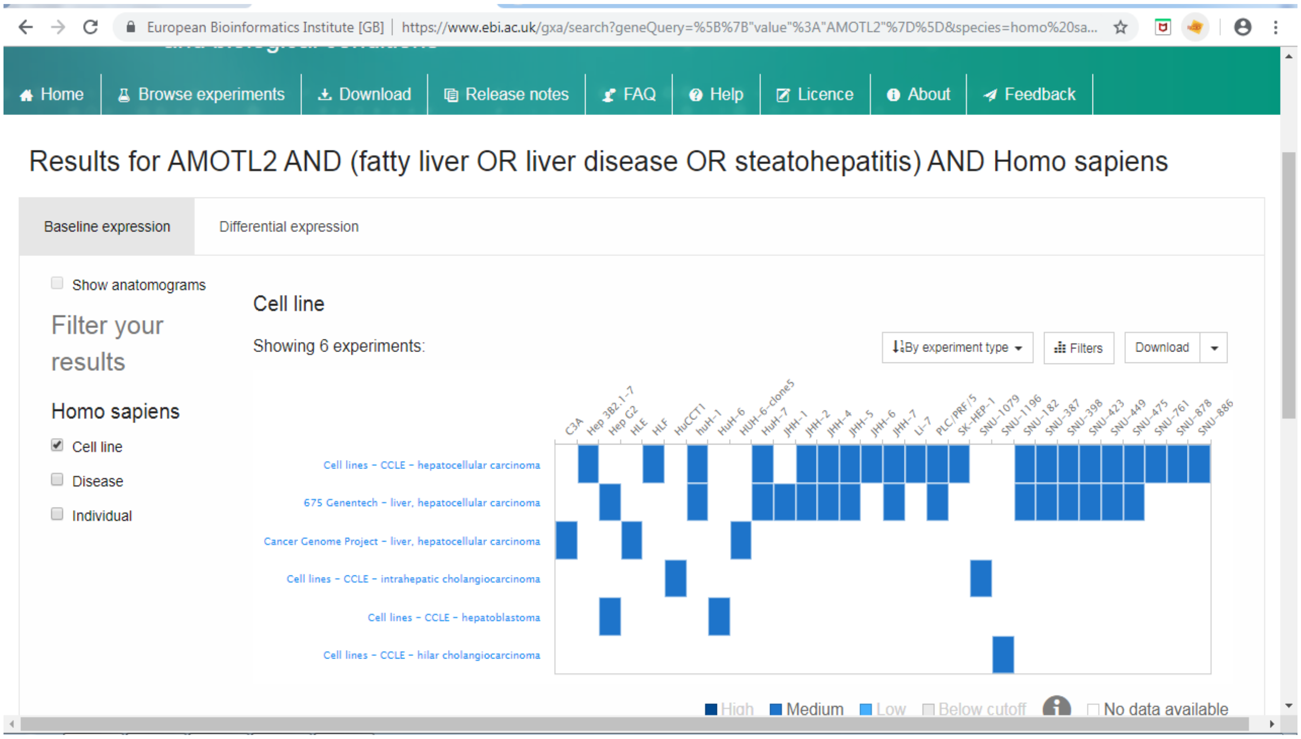
This gene–disease association may be inferred in part via curated interactions between *AMOTL2* and any chemicals listed below, and a curated association between those chemicals and *Non-alcoholic Fatty Liver Disease*.

Filter by Association type: ALL ▾ Filter

1–24 of 24 results.

	✓	Reference	Association
1.	✓	Das KP, et al. Perfluoroalkyl acids-induced liver steatosis: Effects on genes controlling lipid homeostasis. Toxicology. 2017 Mar 1;378:37-52.	*Inferred via 1 chemical:* pirinixic acid
2.	✓	Duval C, et al. Chronic Exposure to Low Doses of Dioxin Promotes Liver Fibrosis Development in the C57BL/6J Diet-Induced Obesity Mouse Model. Environ Health Perspect. 2017 Mar;125(3):428-436.	*Inferred via 1 chemical:* Tetrachlorodibenzodioxin
3.	✓	Fader KA, et al. Convergence of hepcidin deficiency, systemic iron overloading, heme accumulation, and REV-ERBα/β activation in aryl hydrocarbon receptor-elicited hepatotoxicity. Toxicol Appl Pharmacol. 2017 Apr 15;321:1-17.	*Inferred via 1 chemical:* Tetrachlorodibenzodioxin
4.	✓	Lin Y, et al. Downregulation of miR-192 causes hepatic steatosis and lipid accumulation by inducing SREBF1: Novel mechanism for bisphenol A-triggered non-alcoholic fatty liver disease. Biochim Biophys Acta. 2017 Sep;1862(9):869-882.	*Inferred via 1 chemical:* bisphenol A
5.	✓	Ditzel EJ, et al. Altered Hepatic Transport by Fetal Arsenite Exposure in Diet-Induced Fatty Liver Disease. J Biochem Mol Toxicol. 2016 Feb 18.	*Inferred via 1 chemical:* sodium arsenite
6.	✓	Michaut A, et al. A cellular model to study drug-induced liver injury in nonalcoholic fatty liver disease: Application to acetaminophen. Toxicol Appl Pharmacol. 2016 Feb 1;292:40-55.	*Inferred via 1 chemical:* Acetaminophen
7.	✓	Nault R, et al. From the Cover: Coagulation-Driven Hepatic Fibrosis Requires Protease Activated Receptor-1 (PAR-1) in a Mouse Model of TCDD-	*Inferred via 1 chemical:* Tetrachlorodibenzodioxin

Figure S1A: Print screen shows correlation between AMOTL2 and NAFLD/NASH using Comparative Toxicogenomics Database, http://ctdbase.org/detail.go?type=relationship&geneAcc=51421&diseaseAcc=MESH%3AD065626&view=reference



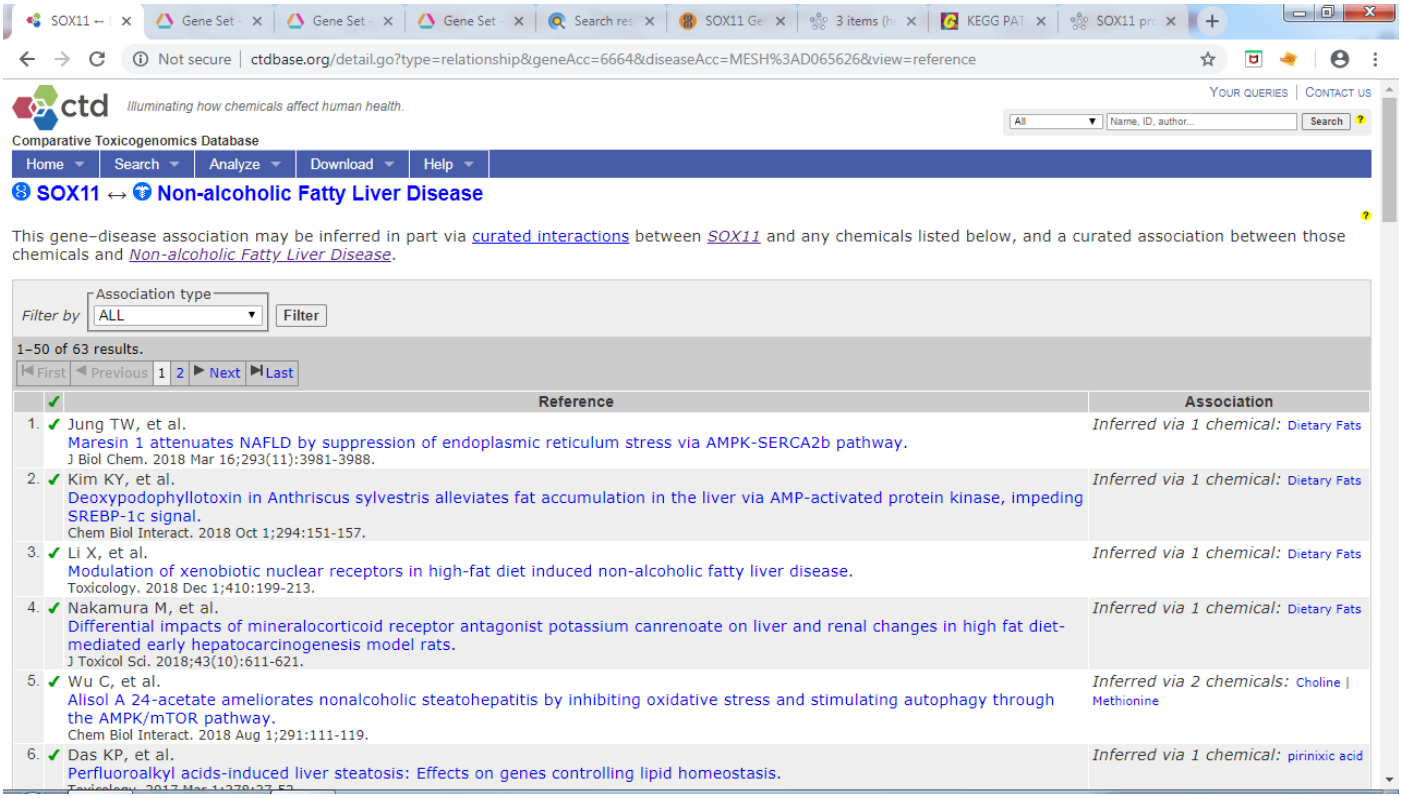
Results for AMOTL2 AND (fatty liver OR liver disease OR steatohepatitis) AND Homo sapiens

Filter your results — Homo sapiens: ☑ Cell line ☐ Disease ☐ Individual

Cell line

Showing 6 experiments:

Figure S1B: Print screen shows correlation between AMOTL2 and NAFLD/NASH using Gene atlas database, https://www.ebi.ac.uk/gxa/search?geneQuery=%5B%7B%22value%22%3A%22AMOTL2%22%7D%5D&species=homo%20sapiens&conditionQuery=%5B%7B%22value%22%3A%22fatty%20liver%22%7D%2C%7B%22value%22%3A%22liver%20disease%22%7D%2C%7B%22value%22%3A%22steatohepatitis%22%7D%5D&bs=%7B%22homo%20sapiens%22%3A%5B%22CELL_LINE%22%5D%7D&ds=%7B%22kingdom%22%3A%5B%22animals%22%5D%7D#baseline



SOX11 ↔ Non-alcoholic Fatty Liver Disease

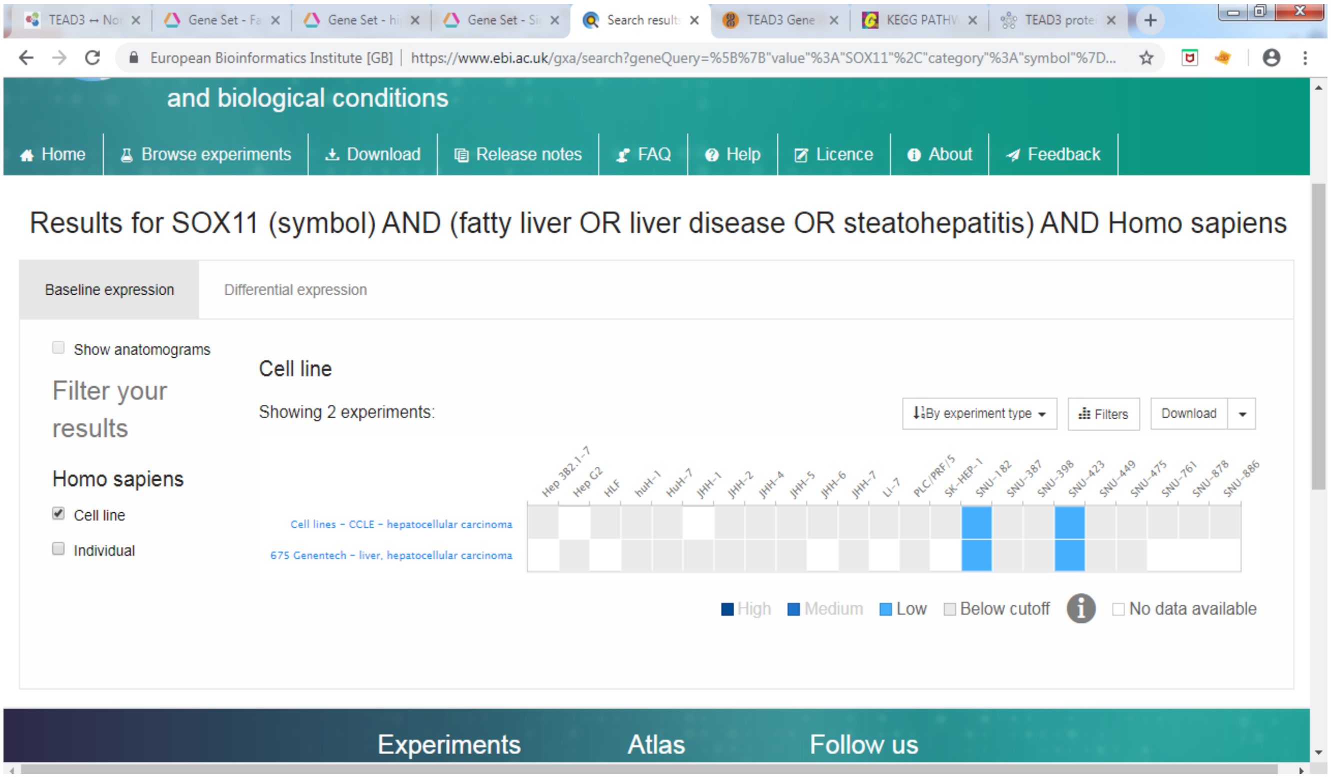
This gene–disease association may be inferred in part via curated interactions between *SOX11* and any chemicals listed below, and a curated association between those chemicals and *Non-alcoholic Fatty Liver Disease*.

Filter by Association type: ALL ▾ Filter

1–50 of 63 results.

	✓	Reference	Association
1.	✓	Jung TW, et al. Maresin 1 attenuates NAFLD by suppression of endoplasmic reticulum stress via AMPK-SERCA2b pathway. J Biol Chem. 2018 Mar 16;293(11):3981-3988.	*Inferred via 1 chemical:* Dietary Fats
2.	✓	Kim KY, et al. Deoxypodophyllotoxin in Anthriscus sylvestris alleviates fat accumulation in the liver via AMP-activated protein kinase, impeding SREBP-1c signal. Chem Biol Interact. 2018 Oct 1;294:151-157.	*Inferred via 1 chemical:* Dietary Fats
3.	✓	Li X, et al. Modulation of xenobiotic nuclear receptors in high-fat diet induced non-alcoholic fatty liver disease. Toxicology. 2018 Dec 1;410:199-213.	*Inferred via 1 chemical:* Dietary Fats
4.	✓	Nakamura M, et al. Differential impacts of mineralocorticoid receptor antagonist potassium canrenoate on liver and renal changes in high fat diet-mediated early hepatocarcinogenesis model rats. J Toxicol Sci. 2018;43(10):611-621.	*Inferred via 1 chemical:* Dietary Fats
5.	✓	Wu C, et al. Alisol A 24-acetate ameliorates nonalcoholic steatohepatitis by inhibiting oxidative stress and stimulating autophagy through the AMPK/mTOR pathway. Chem Biol Interact. 2018 Aug 1;291:111-119.	*Inferred via 2 chemicals:* Choline | Methionine
6.	✓	Das KP, et al. Perfluoroalkyl acids-induced liver steatosis: Effects on genes controlling lipid homeostasis.	*Inferred via 1 chemical:* pirinixic acid

Figure S1C :Print screen shows correlation between SOX11 and NAFLD/NASH using Comparative Toxicogenomics Database, http://ctdbase.org/detail.go?type=relationship&geneAcc=6664&diseaseAcc=MESH%3AD065626&view=reference



Results for SOX11 (symbol) AND (fatty liver OR liver disease OR steatohepatitis) AND Homo sapiens

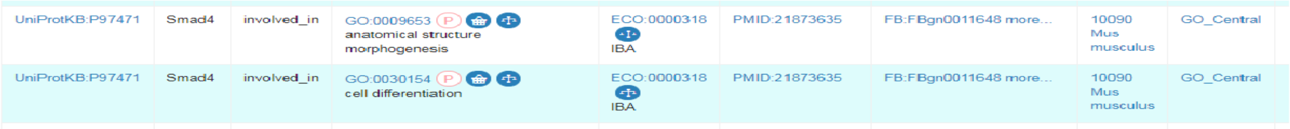
Cell line

Showing 2 experiments:

	Hep 3B2.1-7	Hep G2	HLF	huH-1	HuH-7	JHH-1	JHH-2	JHH-4	JHH-5	JHH-6	JHH-7	Li-7	PLC/PRF/5	SK-HEP-1	SNU-182	SNU-387	SNU-398	SNU-423	SNU-449	SNU-475	SNU-761	SNU-878	SNU-886
Cell lines – CCLE – hepatocellular carcinoma	▨	☐	▨	▨	▨	☐	▨	▨	▨	▨	▨	▨	▨	▨	🟦	▨	▨	🟦	▨	▨	▨	▨	▨
675 Genentech – liver, hepatocellular carcinoma	☐	▨	☐	▨	▨	▨	▨	▨	▨	☐	▨	☐	▨	☐	🟦	▨	▨	🟦	▨	▨	☐	☐	☐

■ High ■ Medium 🟦 Low ▨ Below cutoff ☐ No data available

Figure S1D:Print screen shows correlation between SOX11 and NAFLD/NASH using Gene atlas database, https://www.ebi.ac.uk/gxa/search?geneQuery=%5B%7B%22value%22%3A%22SOX11%22%2C%22category%22%3A%22symbol%22%7D%5D&species=homo%20sapiens&conditioQuery=%5B%7B%22value%22%3A%22fatty%20liver%22%7D%2C%7B%22value%22%3A%22liver%20disease%22%7D%2C%7B%22value%22%3A%22steatohepatitis%22%7D%5D&bs=%7B%22homo%20sapiens%22%3A%5B%22CELL_LINE%22%5D%7D#baseline



UniProtKB:P97471	Smad4	involved_in	GO:0009653 anatomical structure morphogenesis	ECO:0000318 IBA	PMID:21873635	FB:FBgn0011648 more…	10090 Mus musculus	GO_Central
UniProtKB:P97471	Smad4	involved_in	GO:0030154 cell differentiation	ECO:0000318 IBA	PMID:21873635	FB:FBgn0011648 more…	10090 Mus musculus	GO_Central

SMAD4 ↔ Non-alcoholic Fatty Liver Disease

This gene–disease association may be inferred in part via curated interactions between *SMAD4* and any chemicals listed below, and a curated association between those chemicals and *Non-alcoholic Fatty Liver Disease*.

Filter by Association type: ALL

1–50 of 81 results.

	✓	Reference	Association
1.	✓	Kim JW, et al. Cigarette smoking differentially regulates inflammatory responses in a mouse model of nonalcoholic steatohepatitis depending on exposure time point. Food Chem Toxicol. 2020 Jan;135:110930.	*Inferred via 1 chemical:* Dietary Fats
2.	✓	Thongnak L, et al. Effects of dapagliflozin and statins attenuate renal injury and liver steatosis in high-fat/high-fructose diet-induced insulin resistant rats. Toxicol Appl Pharmacol. 2020 Jun 1;396:114997.	*Inferred via 1 chemical:* Dietary Fats
3.	✓	Han HY, et al. Preventive Effect of Citrus aurantium Peel Extract on High-Fat Diet-Induced Non-alcoholic Fatty Liver in Mice. Biol Pharm Bull. 2019;42(2):255-260.	*Inferred via 1 chemical:* Dietary Fats
4.	✓	Han X, et al. Acanthoic acid modulates lipogenesis in nonalcoholic fatty liver disease via FXR/LXRs-dependent manner. Chem Biol Interact. 2019 Sep 25;311:108794.	*Inferred via 1 chemical:* Dietary Fats
5.	✓	Kus E, et al. LSEC Fenestrae Are Preserved Despite Pro-inflammatory Phenotype of Liver Sinusoidal Endothelial Cells in Mice on High Fat Diet.	*Inferred via 1 chemical:* Dietary Fats

Pathways & Interactions for SMAD4 Gene

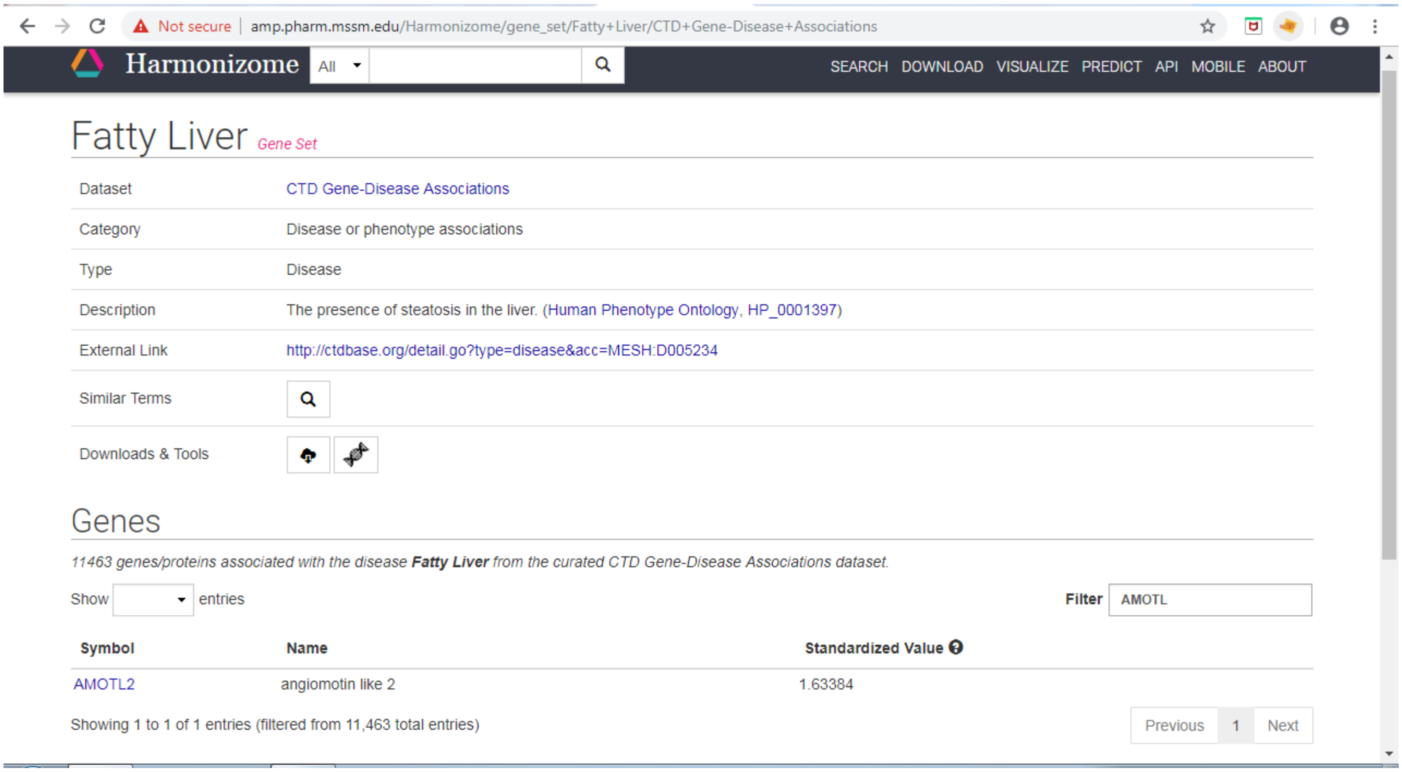
PathCards SuperPathways for SMAD4 Gene

Filter: (1 result)

	SuperPathway	Contained pathways	
1	Hippo signaling pathway	Hippo signaling pathway	-

GenesLikeMe Genes that share pathways with SMAD4: view

Figure S1E: Print screen shows correlation between SMAD4 and NAFLD/NASH using Comparative Toxicogenomics Database,



Fatty Liver *Gene Set*

Dataset	CTD Gene-Disease Associations
Category	Disease or phenotype associations
Type	Disease
Description	The presence of steatosis in the liver. (Human Phenotype Ontology, HP_0001397)
External Link	http://ctdbase.org/detail.go?type=disease&acc=MESH:D005234
Similar Terms	
Downloads & Tools	

Genes

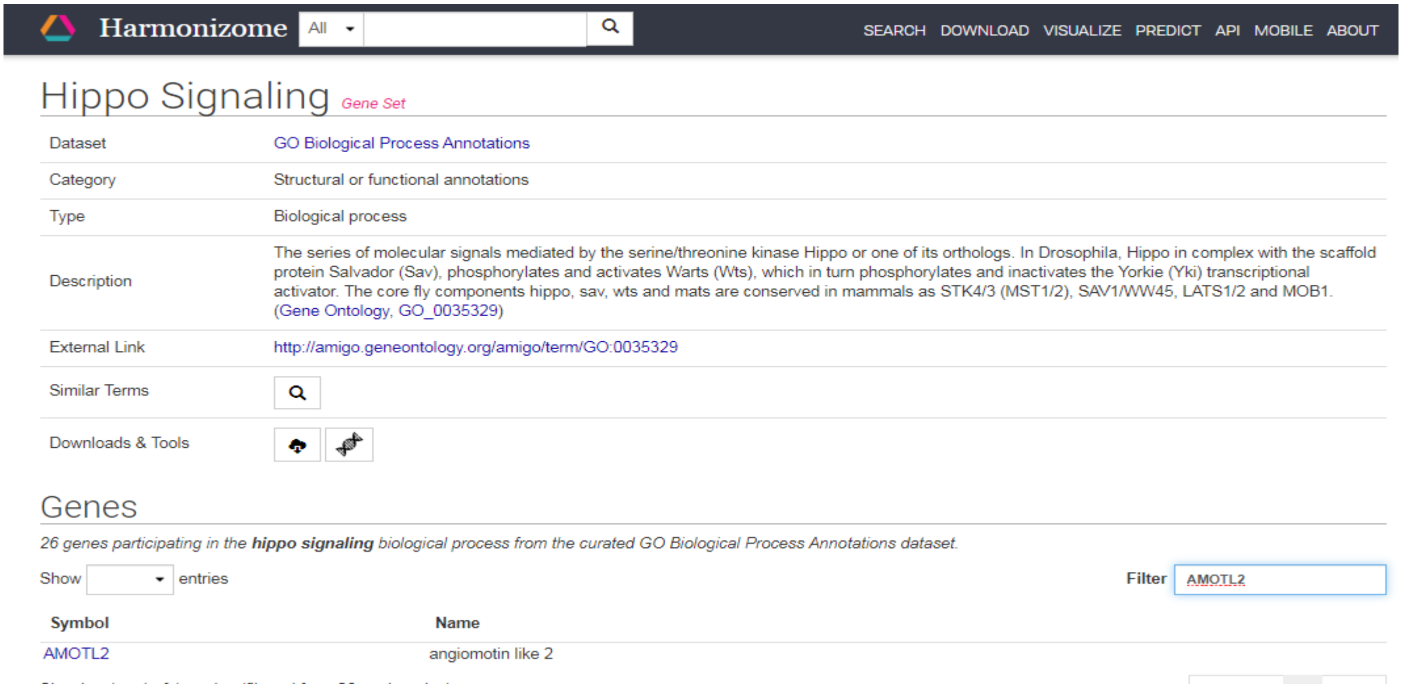
*11463 genes/proteins associated with the disease **Fatty Liver** from the curated CTD Gene-Disease Associations dataset.*

Show entries | **Filter** AMOTL

Symbol	Name	Standardized Value
AMOTL2	angiomotin like 2	1.63384

Showing 1 to 1 of 1 entries (filtered from 11,463 total entries)

Figure S2A; Print screen shows correlation between AMOTL2 and Fatty liver using Harmonizome database: http://amp.pharm.mssm.edu/Harmonizome/gene_set/Fatty+Liver/CTD+Gene-Disease+Associations



Hippo Signaling *Gene Set*

Dataset	GO Biological Process Annotations
Category	Structural or functional annotations
Type	Biological process
Description	The series of molecular signals mediated by the serine/threonine kinase Hippo or one of its orthologs. In Drosophila, Hippo in complex with the scaffold protein Salvador (Sav), phosphorylates and activates Warts (Wts), which in turn phosphorylates and inactivates the Yorkie (Yki) transcriptional activator. The core fly components hippo, sav, wts and mats are conserved in mammals as STK4/3 (MST1/2), SAV1/WW45, LATS1/2 and MOB1. (Gene Ontology, GO_0035329)
External Link	http://amigo.geneontology.org/amigo/term/GO:0035329
Similar Terms	
Downloads & Tools	

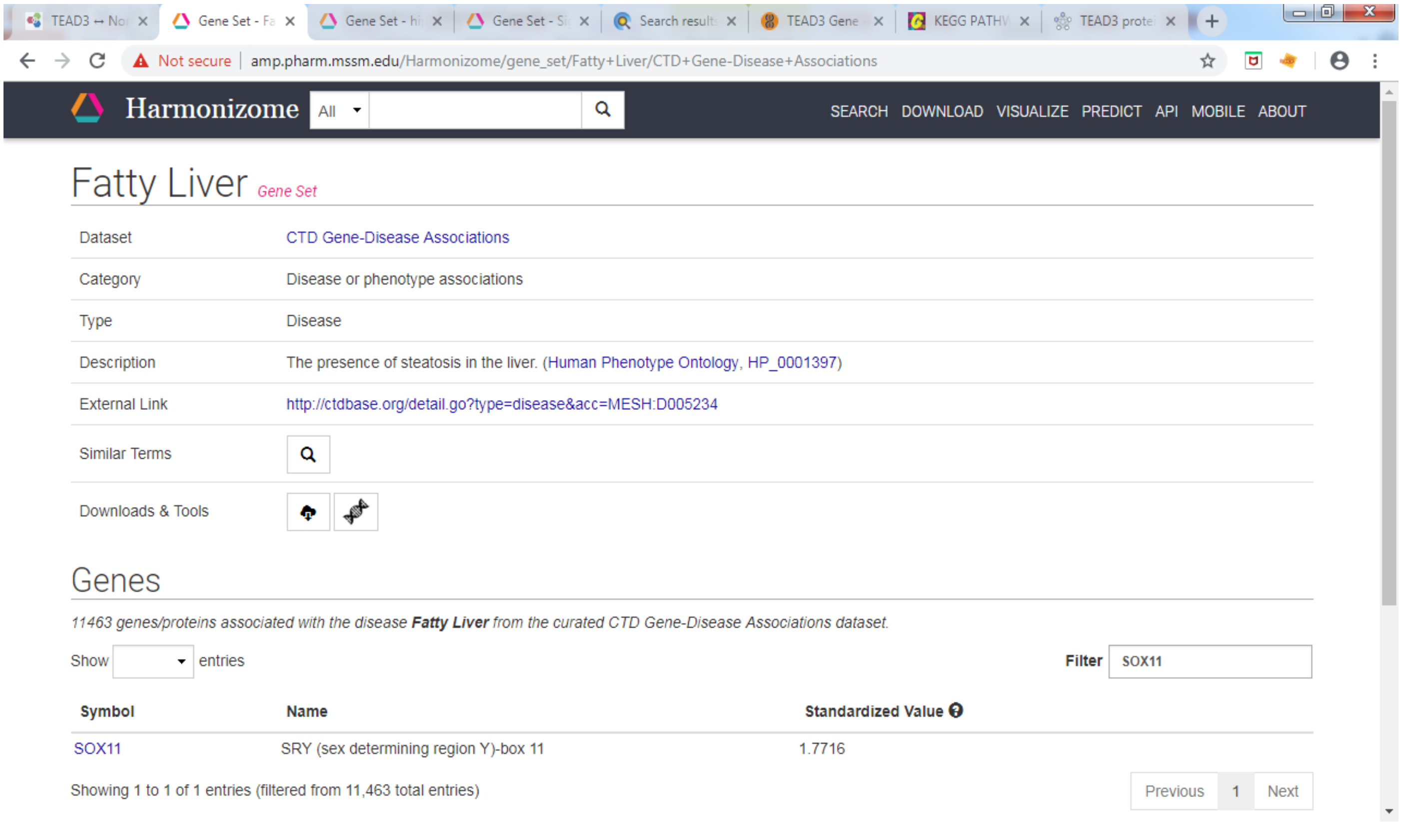
Genes

*26 genes participating in the **hippo signaling** biological process from the curated GO Biological Process Annotations dataset.*

Show entries | **Filter** AMOTL2

Symbol	Name
AMOTL2	angiomotin like 2

Figure S2B; Print screen shows correlation between AMOTL2 and Hippo signaling using Harmonizome



Fatty Liver *Gene Set*

Dataset	CTD Gene-Disease Associations
Category	Disease or phenotype associations
Type	Disease
Description	The presence of steatosis in the liver. (Human Phenotype Ontology, HP_0001397)
External Link	http://ctdbase.org/detail.go?type=disease&acc=MESH:D005234
Similar Terms	
Downloads & Tools	

Genes

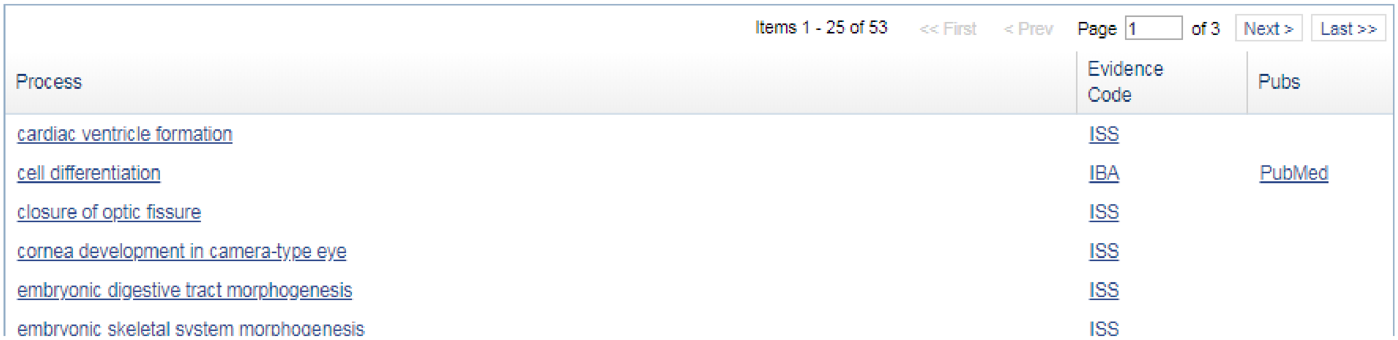
11463 genes/proteins associated with the disease ***Fatty Liver*** *from the curated CTD Gene-Disease Associations dataset.*

Show entries **Filter** SOX11

Symbol	Name	Standardized Value
SOX11	SRY (sex determining region Y)-box 11	1.7716

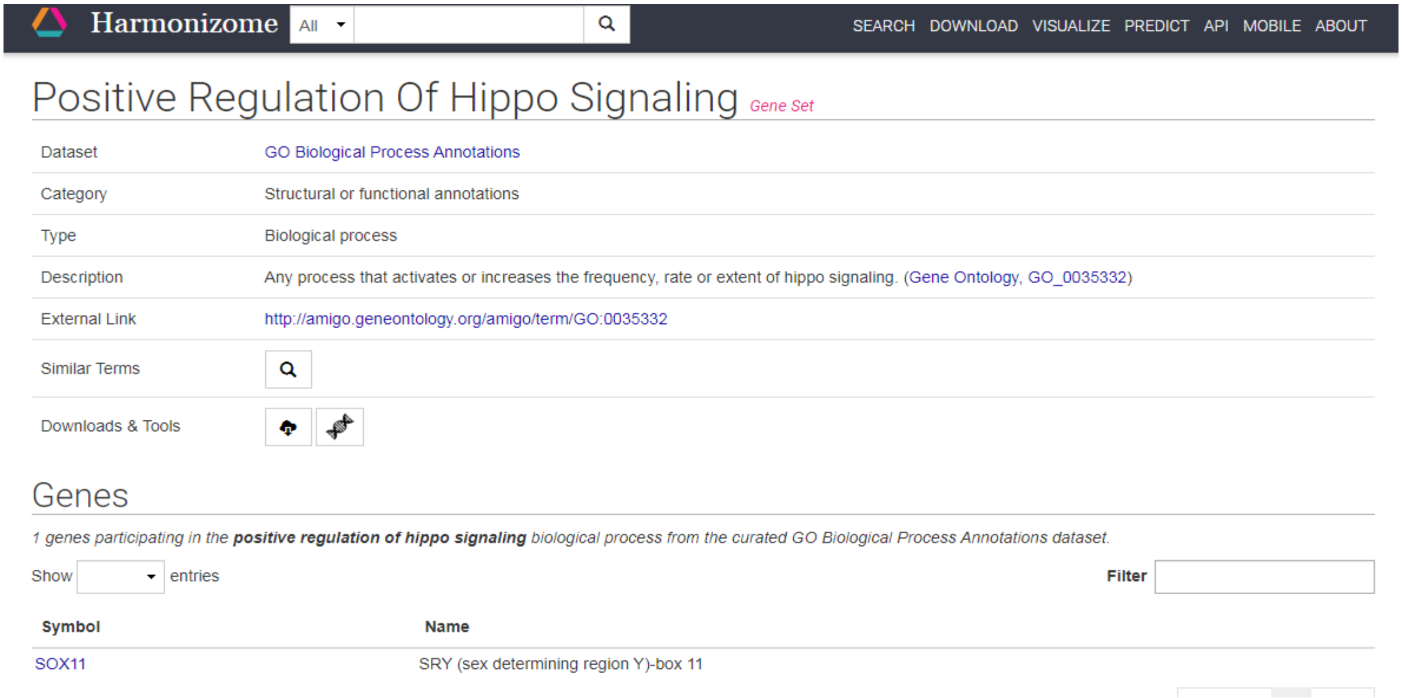
Showing 1 to 1 of 1 entries (filtered from 11,463 total entries)

Figure S2C; Print screen shows correlation between SOX11 and Fatty liver using Harmonizome, http://amp.pharm.mssm.edu/Harmonizome/gene_set/Fatty+Liver/CTD+Gene-Disease+Associations



Process	Evidence Code	Pubs
cardiac ventricle formation	ISS	
cell differentiation	IBA	PubMed
closure of optic fissure	ISS	
cornea development in camera-type eye	ISS	
embryonic digestive tract morphogenesis	ISS	
embryonic skeletal system morphogenesis	ISS	

Figure S2D: Print screen shows correlation between SOX11 and Hippo signaling using ncbi Gene, https://www.ncbi.nlm.nih.gov/gene/6664



Positive Regulation Of Hippo Signaling Gene Set

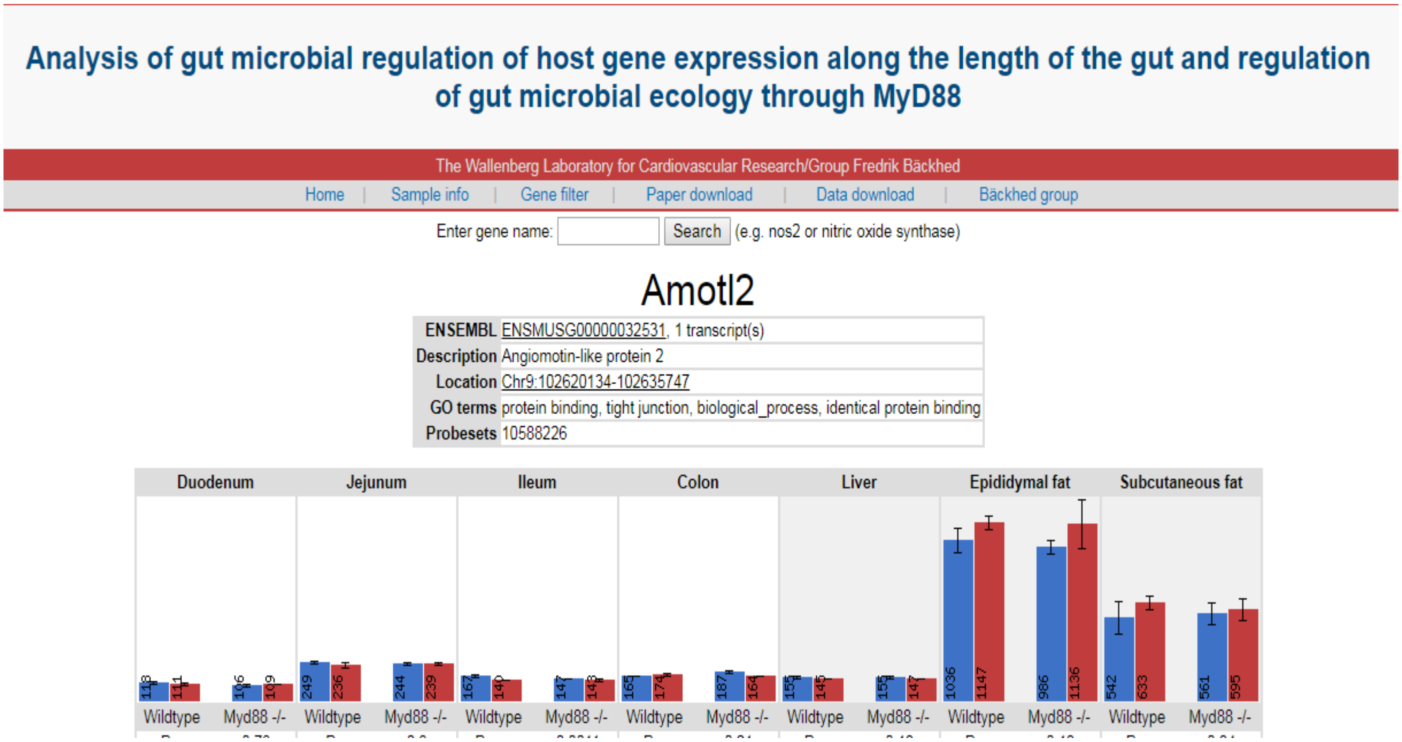
Dataset	GO Biological Process Annotations
Category	Structural or functional annotations
Type	Biological process
Description	Any process that activates or increases the frequency, rate or extent of hippo signaling. (Gene Ontology, GO_0035332)
External Link	http://amigo.geneontology.org/amigo/term/GO:0035332
Similar Terms	
Downloads & Tools	

Genes

*1 genes participating in the **positive regulation of hippo signaling** biological process from the curated GO Biological Process Annotations dataset.*

Symbol	Name
SOX11	SRY (sex determining region Y)-box 11

Figure S2E: Print screen shows correlation between SOX11 and Hippo signaling using Harmonizome, http://amp.pharm.mssm.edu/Harmonizome/gene_set/positive+regulation+of+hippo+signaling/GO+Biological+Process+Annotations

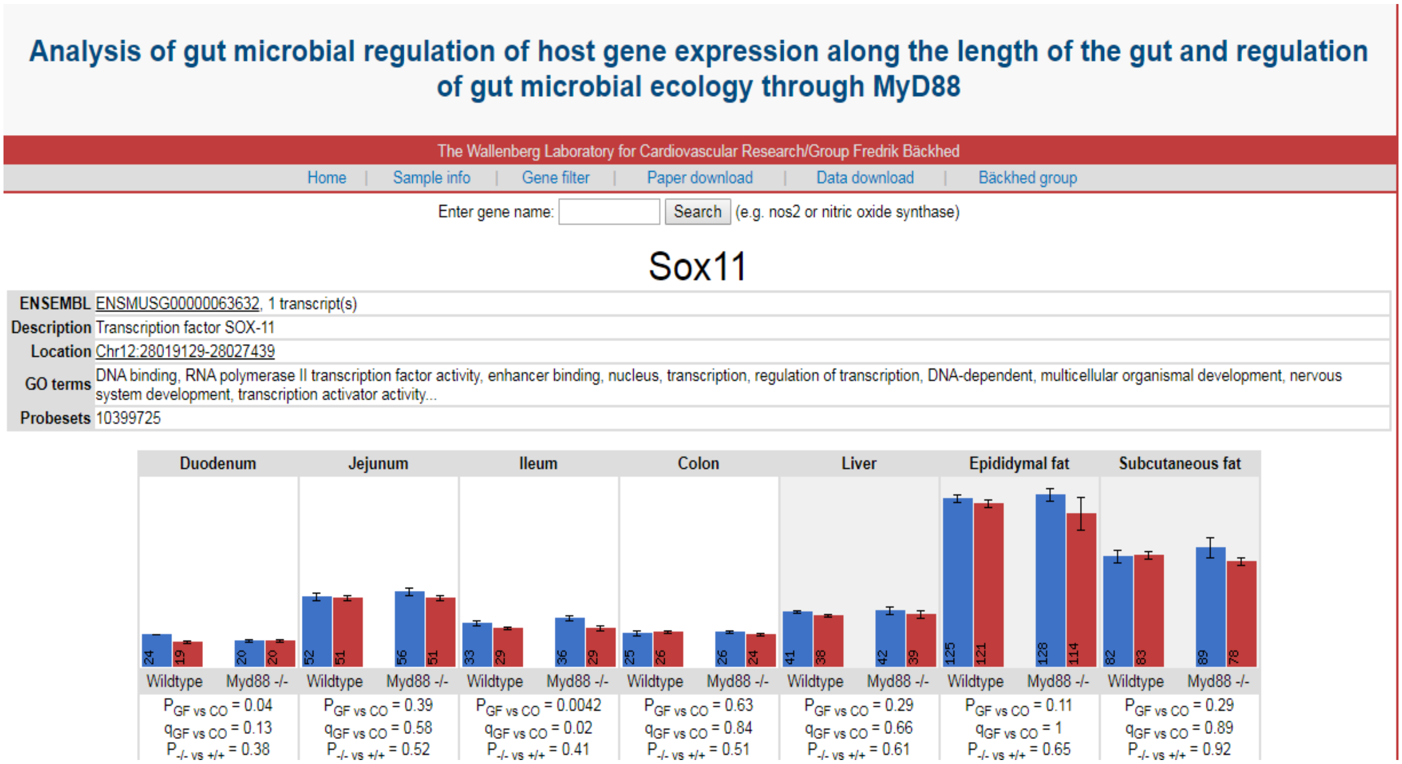


Analysis of gut microbial regulation of host gene expression along the length of the gut and regulation of gut microbial ecology through MyD88

Amotl2

ENSEMBL	ENSMUSG00000032531, 1 transcript(s)
Description	Angiomotin-like protein 2
Location	Chr9:102620134-102635747
GO terms	protein binding, tight junction, biological_process, identical protein binding
Probesets	10588226

Figure S3A: Print screen shows Gut microbiota/ AMOTL2 crosstalk using Encyclopedia of gut microbiota regulated genes, http://microbiota.wall.gu.se/larsson/view_gene.php?gene=8913.



Analysis of gut microbial regulation of host gene expression along the length of the gut and regulation of gut microbial ecology through MyD88

The Wallenberg Laboratory for Cardiovascular Research/Group Fredrik Bäckhed

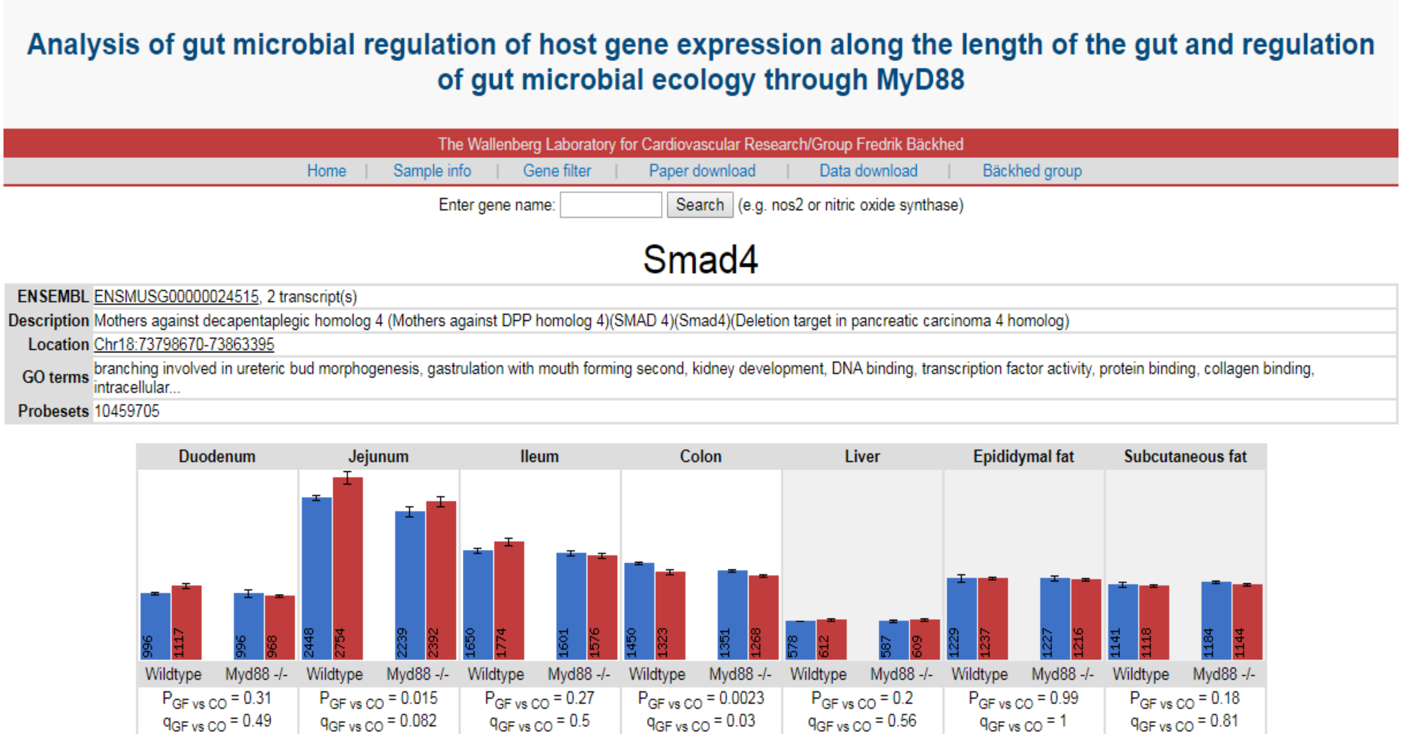
Sox11

ENSEMBL	ENSMUSG00000063632, 1 transcript(s)
Description	Transcription factor SOX-11
Location	Chr12:28019129-28027439
GO terms	DNA binding, RNA polymerase II transcription factor activity, enhancer binding, nucleus, transcription, regulation of transcription, DNA-dependent, multicellular organismal development, nervous system development, transcription activator activity...
Probesets	10399725

Duodenum	Jejunum	Ileum	Colon	Liver	Epididymal fat	Subcutaneous fat
$P_{GF\ vs\ CO}$ = 0.04	$P_{GF\ vs\ CO}$ = 0.39	$P_{GF\ vs\ CO}$ = 0.0042	$P_{GF\ vs\ CO}$ = 0.63	$P_{GF\ vs\ CO}$ = 0.29	$P_{GF\ vs\ CO}$ = 0.11	$P_{GF\ vs\ CO}$ = 0.29
$q_{GF\ vs\ CO}$ = 0.13	$q_{GF\ vs\ CO}$ = 0.58	$q_{GF\ vs\ CO}$ = 0.02	$q_{GF\ vs\ CO}$ = 0.84	$q_{GF\ vs\ CO}$ = 0.66	$q_{GF\ vs\ CO}$ = 1	$q_{GF\ vs\ CO}$ = 0.89
$P_{-/-\ vs\ +/+}$ = 0.38	$P_{-/-\ vs\ +/+}$ = 0.52	$P_{-/-\ vs\ +/+}$ = 0.41	$P_{-/-\ vs\ +/+}$ = 0.51	$P_{-/-\ vs\ +/+}$ = 0.61	$P_{-/-\ vs\ +/+}$ = 0.65	$P_{-/-\ vs\ +/+}$ = 0.92

Figure S3B: Print screen shows Gut microbiota/ SOX11 crosstalk using Encyclopedia of gut microbiota regulated genes,

http://microbiota.wall.gu.se/larsson/view_gene.php?gene=17626



Analysis of gut microbial regulation of host gene expression along the length of the gut and regulation of gut microbial ecology through MyD88

The Wallenberg Laboratory for Cardiovascular Research/Group Fredrik Bäckhed

Smad4

ENSEMBL	ENSMUSG00000024515, 2 transcript(s)
Description	Mothers against decapentaplegic homolog 4 (Mothers against DPP homolog 4)(SMAD 4)(Smad4)(Deletion target in pancreatic carcinoma 4 homolog)
Location	Chr18:73798670-73863395
GO terms	branching involved in ureteric bud morphogenesis, gastrulation with mouth forming second, kidney development, DNA binding, transcription factor activity, protein binding, collagen binding, intracellular...
Probesets	10459705

Duodenum	Jejunum	Ileum	Colon	Liver	Epididymal fat	Subcutaneous fat
$P_{GF\ vs\ CO}$ = 0.31	$P_{GF\ vs\ CO}$ = 0.015	$P_{GF\ vs\ CO}$ = 0.27	$P_{GF\ vs\ CO}$ = 0.0023	$P_{GF\ vs\ CO}$ = 0.2	$P_{GF\ vs\ CO}$ = 0.99	$P_{GF\ vs\ CO}$ = 0.18
$q_{GF\ vs\ CO}$ = 0.49	$q_{GF\ vs\ CO}$ = 0.082	$q_{GF\ vs\ CO}$ = 0.5	$q_{GF\ vs\ CO}$ = 0.03	$q_{GF\ vs\ CO}$ = 0.56	$q_{GF\ vs\ CO}$ = 1	$q_{GF\ vs\ CO}$ = 0.81

Figure S3C: Print screen shows Gut microbiota/ SMAD4 crosstalk using Encyclopedia of gut microbiota regulated genes, http://microbiota.wall.gu.se/larsson/view_gene.php?gene=4475

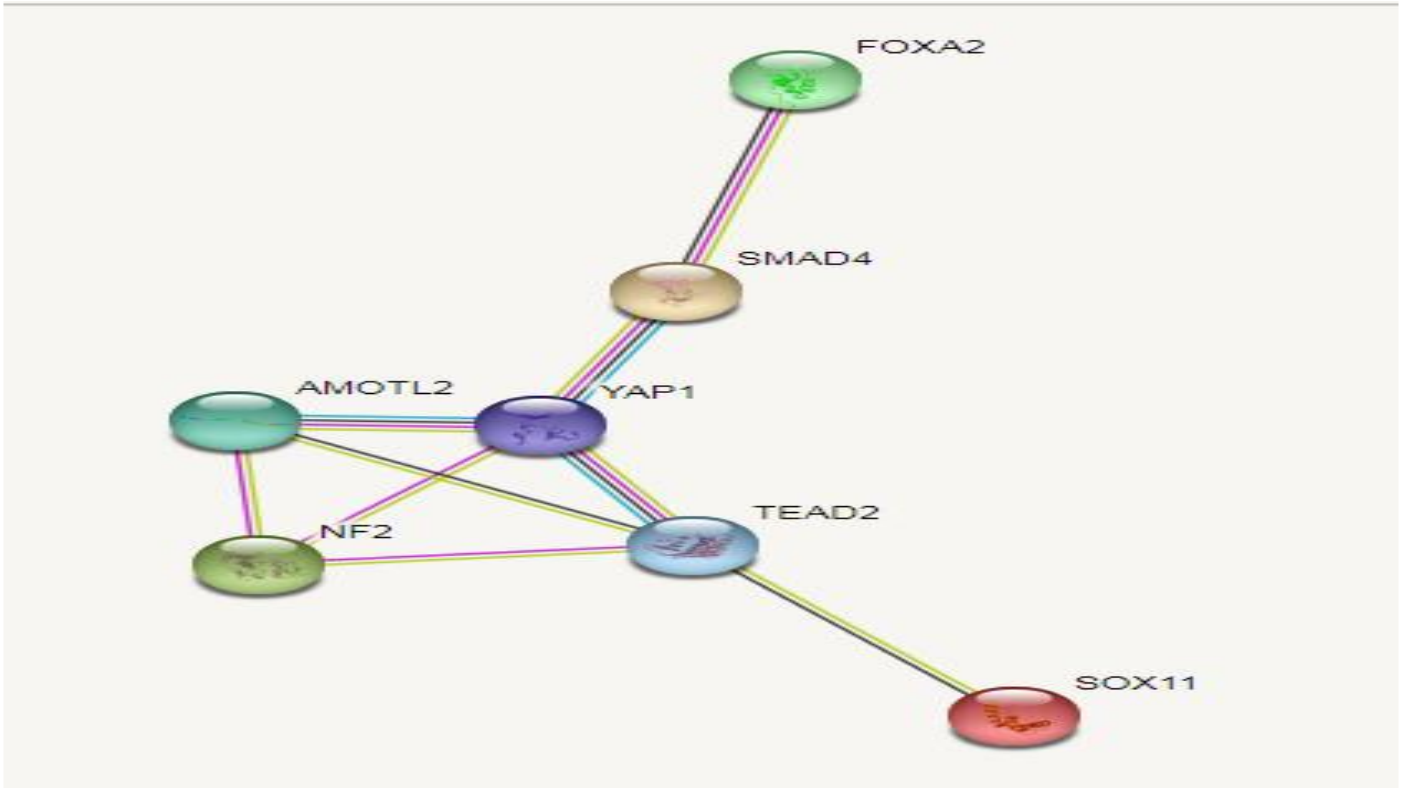


Figure S4A: print screen shows protein-protein interaction between the selected mRNAs and HIPPO target effectors by STRING database. https://string-db.org/cgi/network.pl?taskId=w75m42gDhIJ1

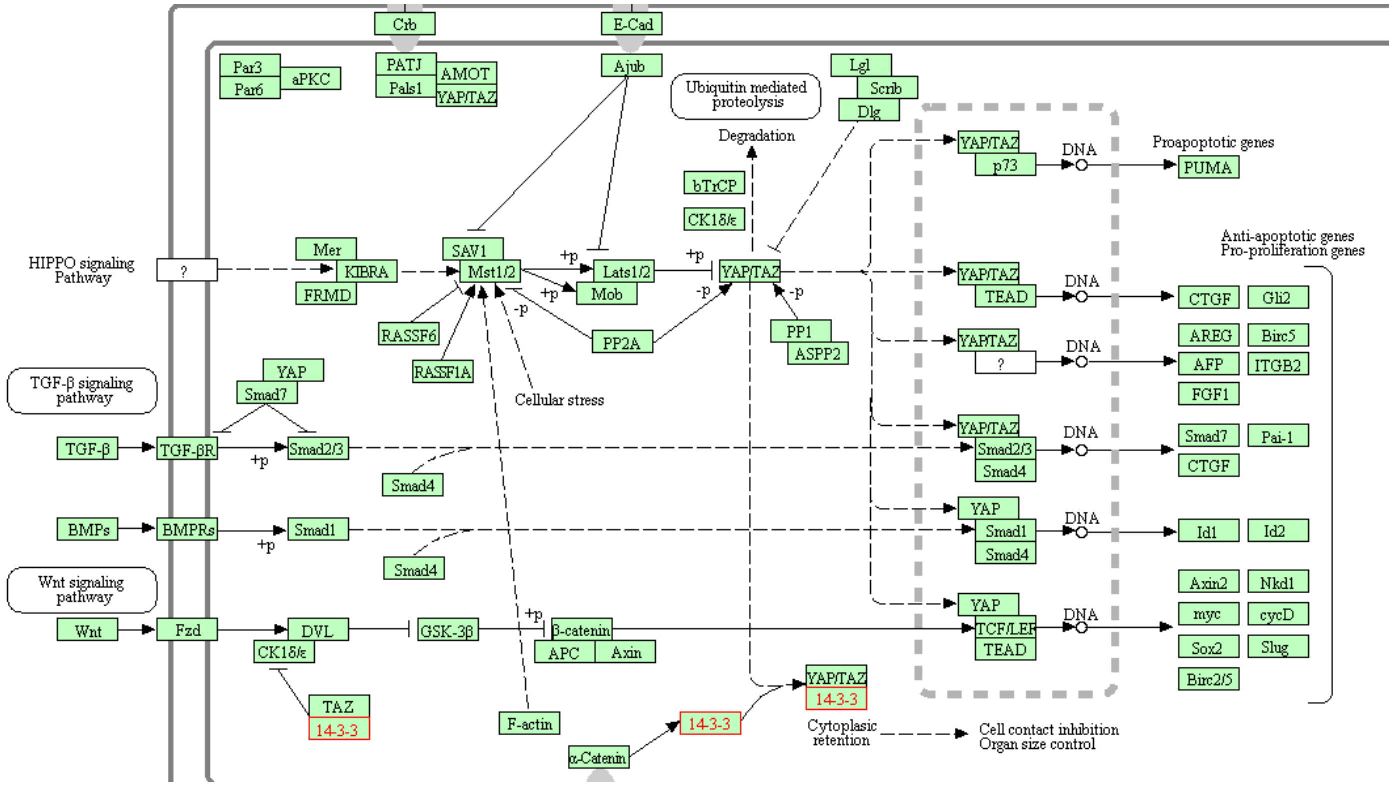
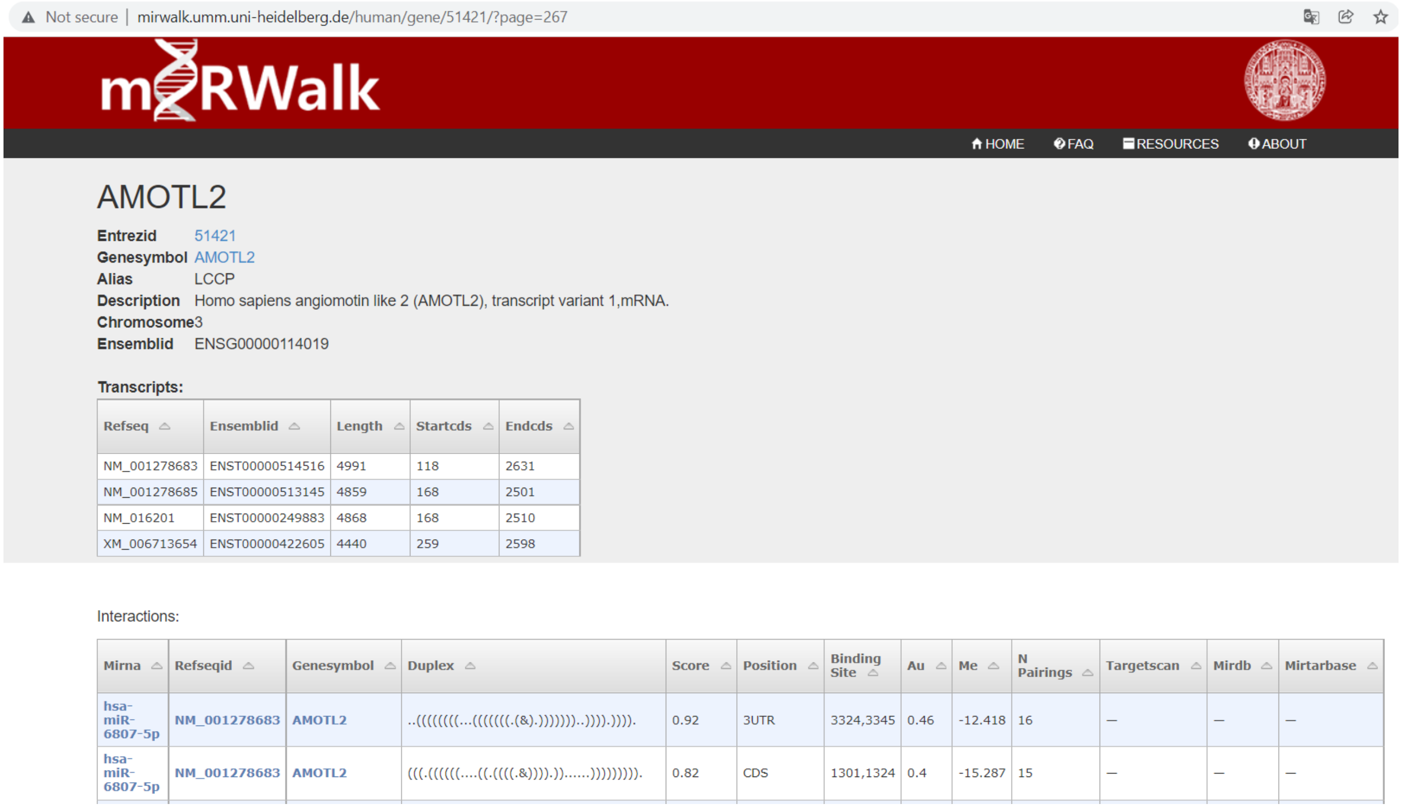


Figure S4B: print screen shows protein-protein interaction between the selected mRNAs and HIPPO target effectors by KEGG pathway of hippo.

https://www.kegg.jp/kegg-bin/show_pathway?select_scale=1.0&query=+YWHAB&map=hsa04390&scale=&orgs=&auto_image=&show_description=hide&multi_query=



AMOTL2

Entrezid 51421
Genesymbol AMOTL2
Alias LCCP
Description Homo sapiens angiomotin like 2 (AMOTL2), transcript variant 1,mRNA.
Chromosome 3
Ensemblid ENSG00000114019

Transcripts:

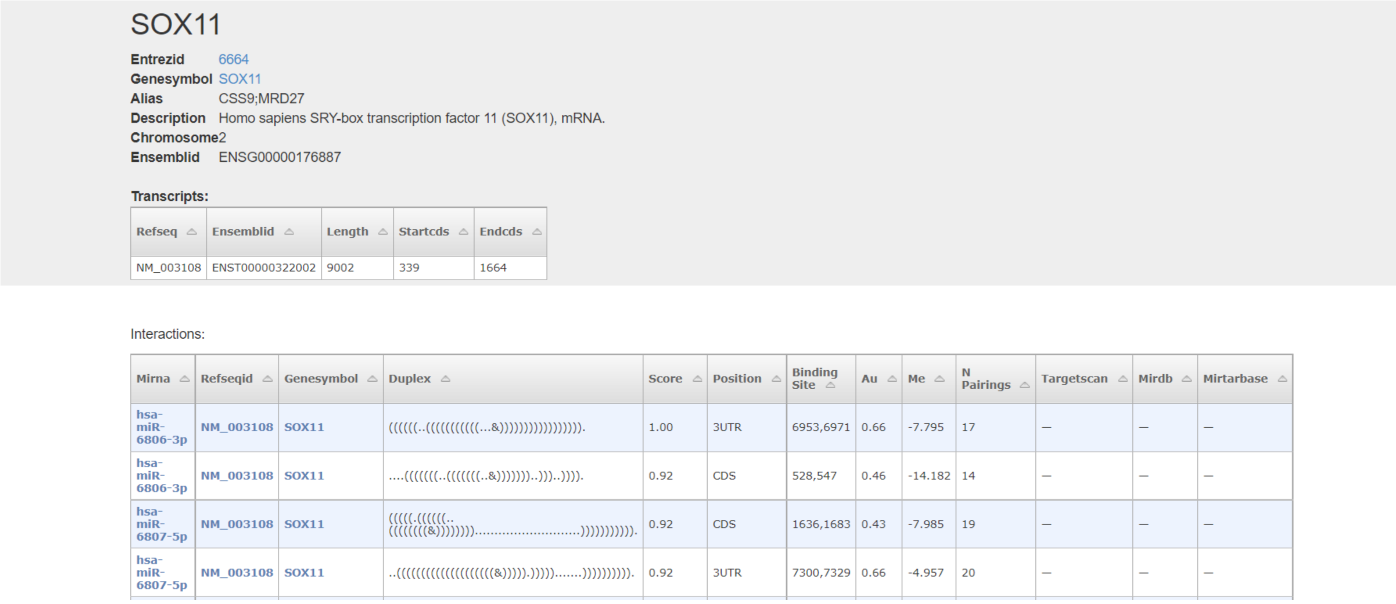
Refseq	Ensemblid	Length	Startcds	Endcds
NM_001278683	ENST00000514516	4991	118	2631
NM_001278685	ENST00000513145	4859	168	2501
NM_016201	ENST00000249883	4868	168	2510
XM_006713654	ENST00000422605	4440	259	2598

Interactions:

Mirna	Refseqid	Genesymbol	Duplex	Score	Position	Binding Site	Au	Me	N Pairings	Targetscan	Mirdb	Mirtarbase
hsa-miR-6807-5p	NM_001278683	AMOTL2	..((((((((...(((((((.(&).)))))))..)))).)))).	0.92	3UTR	3324,3345	0.46	-12.418	16	—	—	—
hsa-miR-6807-5p	NM_001278683	AMOTL2	(((.((((((....((.((((.&)))).))......))))))))).	0.82	CDS	1301,1324	0.4	-15.287	15	—	—	—

Figure S5A:AMOTL2 mRNA is a direct target of miRNA-6807-5p that was retrieved from miRwalk database. It shows direct interaction between miRNA-6807-5p and AMOTL2 mRNA.

http://mirwalk.umm.uni-heidelberg.de/human/gene/51421/?page=267


SOX11

Entrezid 6664
Genesymbol SOX11
Alias CSS9;MRD27
Description Homo sapiens SRY-box transcription factor 11 (SOX11), mRNA.
Chromosome 2
Ensemblid ENSG00000176887

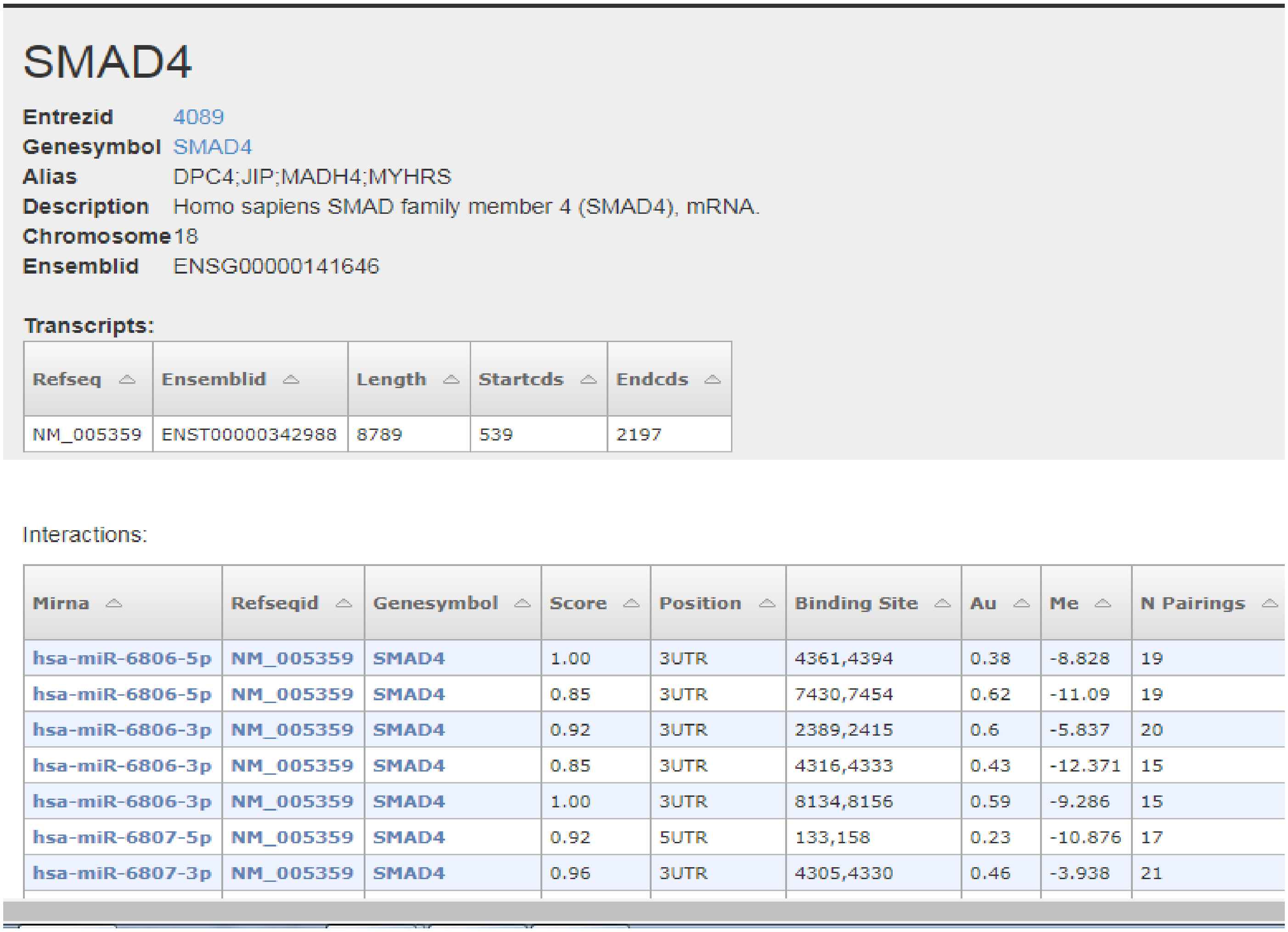
Transcripts:

Refseq	Ensemblid	Length	Startcds	Endcds
NM_003108	ENST00000322002	9002	339	1664

Interactions:

Mirna	Refseqid	Genesymbol	Duplex	Score	Position	Binding Site	Au	Me	N Pairings	Targetscan	Mirdb	Mirtarbase
hsa-miR-6806-3p	NM_003108	SOX11	((((((..(((((((((((...&))))))))))))))))).	1.00	3UTR	6953,6971	0.66	-7.795	17	—	—	—
hsa-miR-6806-3p	NM_003108	SOX11	....(((((((..(((((((..&)))))))..)))..)))).	0.92	CDS	528,547	0.46	-14.182	14	—	—	—
hsa-miR-6807-5p	NM_003108	SOX11	(((((.((((((..((((((((&))))))))........................))))))))))).	0.92	CDS	1636,1683	0.43	-7.985	19	—	—	—
hsa-miR-6807-5p	NM_003108	SOX11	..((((((((((((((((((((&))))).)))))......))))))))))).	0.92	3UTR	7300,7329	0.66	-4.957	20	—	—	—

Figure S5B: SOX11 mRNA is a direct target of miRNA-6807-5p that was retrieved from miRwalk database. It shows direct interaction between miRNA-6807-5p and SOX11 mRNA. http://mirwalk.umm.uni-heidelberg.de/human/gene/6664/?page=204



SMAD4

Entrezid	4089
Genesymbol	SMAD4
Alias	DPC4;JIP;MADH4;MYHRS
Description	Homo sapiens SMAD family member 4 (SMAD4), mRNA.
Chromosome	18
Ensemblid	ENSG00000141646

Transcripts:

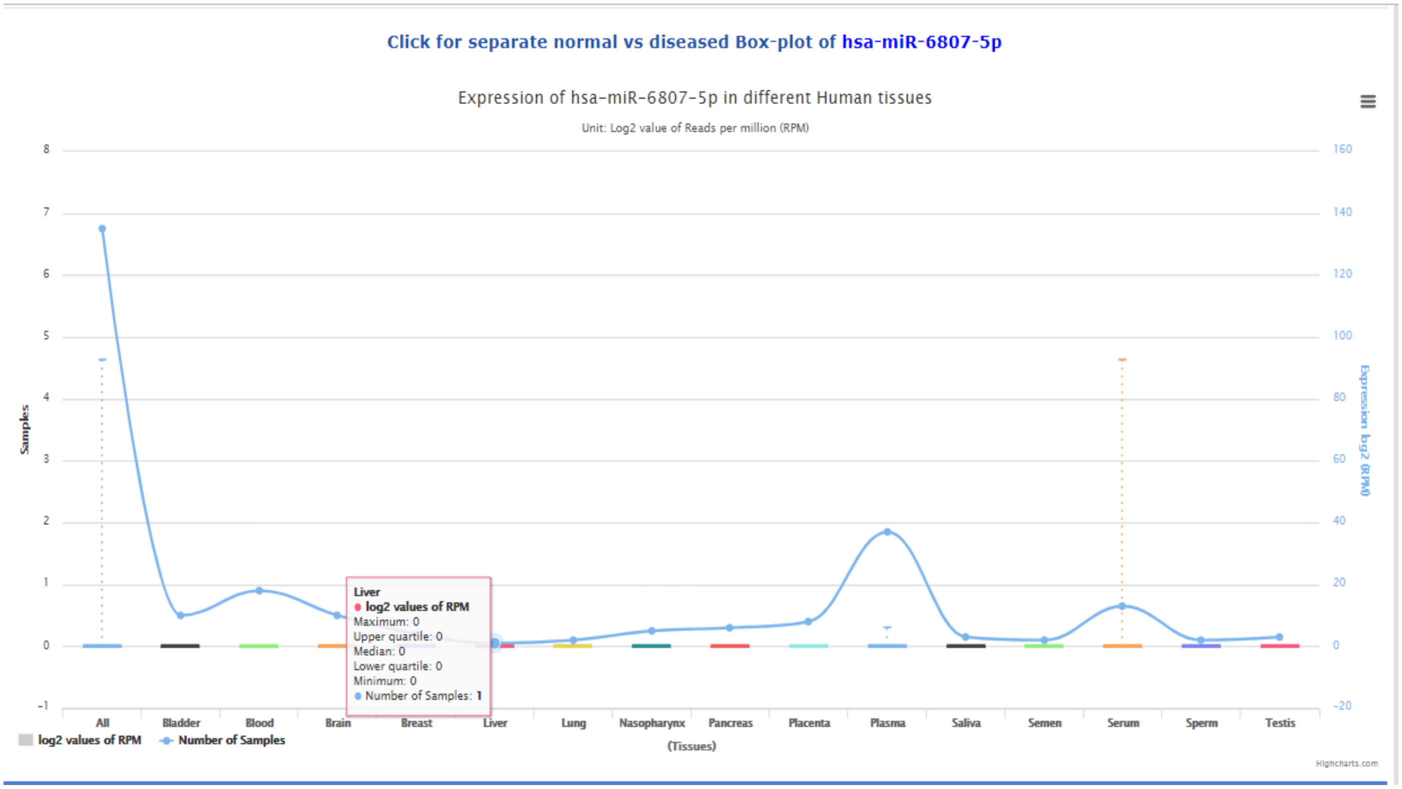
Refseq	Ensemblid	Length	Startcds	Endcds
NM_005359	ENST00000342988	8789	539	2197

Interactions:

Mirna	Refseqid	Genesymbol	Score	Position	Binding Site	Au	Me	N Pairings
hsa-miR-6806-5p	NM_005359	SMAD4	1.00	3UTR	4361,4394	0.38	-8.828	19
hsa-miR-6806-5p	NM_005359	SMAD4	0.85	3UTR	7430,7454	0.62	-11.09	19
hsa-miR-6806-3p	NM_005359	SMAD4	0.92	3UTR	2389,2415	0.6	-5.837	20
hsa-miR-6806-3p	NM_005359	SMAD4	0.85	3UTR	4316,4333	0.43	-12.371	15
hsa-miR-6806-3p	NM_005359	SMAD4	1.00	3UTR	8134,8156	0.59	-9.286	15
hsa-miR-6807-5p	NM_005359	SMAD4	0.92	5UTR	133,158	0.23	-10.876	17
hsa-miR-6807-3p	NM_005359	SMAD4	0.96	3UTR	4305,4330	0.46	-3.938	21

Figure S5C:SMAD4 mRNA is a direct target of miRNA-6807-5p that was retrieved from miRwalk database. It shows direct interaction between miRNA-6807-5p and SMAD4 Mrna.

http://mirwalk.umm.uni-heidelberg.de/human/gene/16399/?page=277

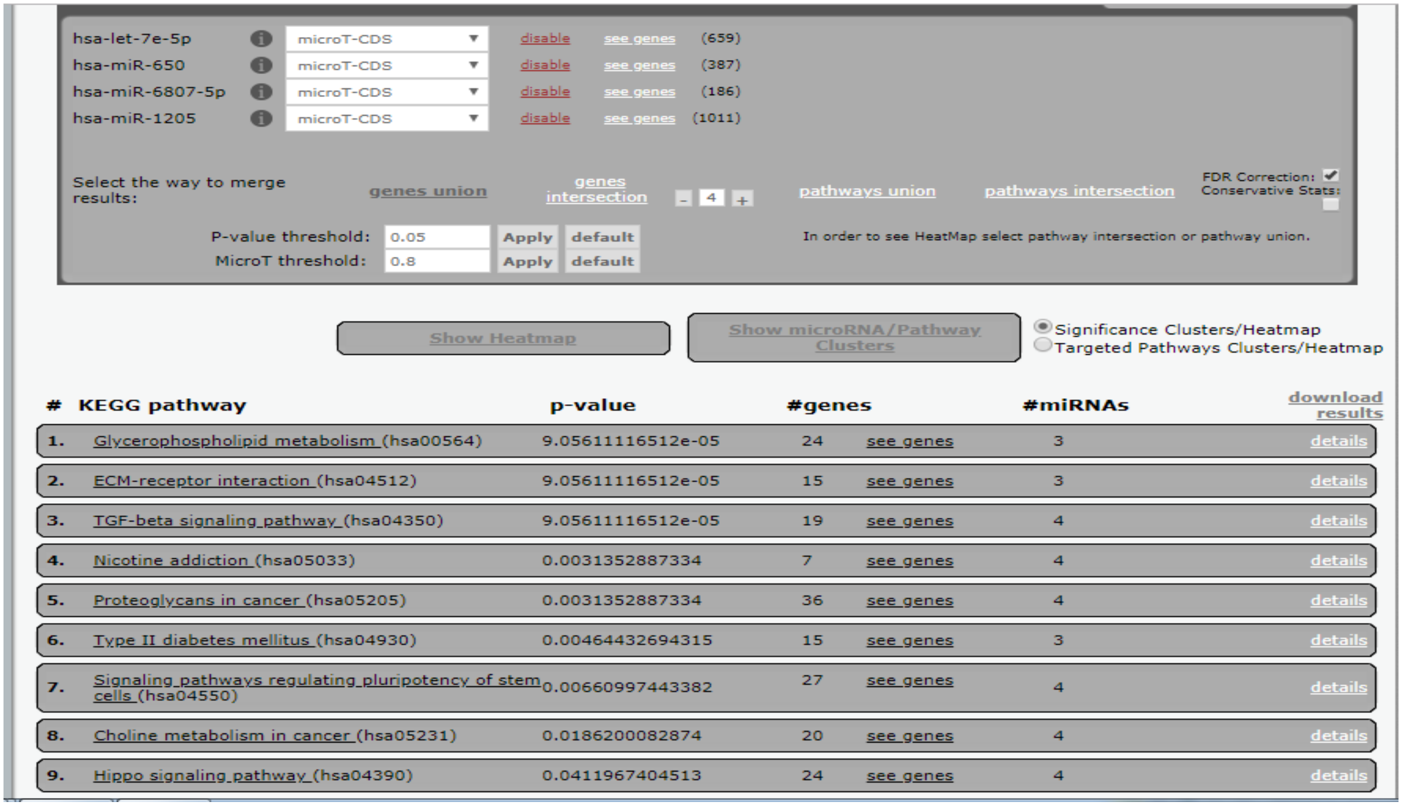


Click for separate normal vs diseased Box-plot of hsa-miR-6807-5p

Liver
● log2 values of RPM
Maximum: 0
Upper quartile: 0
Median: 0
Lower quartile: 0
Minimum: 0
● Number of Samples: 1

Figure S6A: Gene expression of has-miR-6807-5p in liver that was retrieved from miRmine database

http://guanlab.ccmb.med.umich.edu/mirmine/single.php?mirna=hsa-miR-6807-5p&tissue=liver&cline=



hsa-let-7e-5p	microT-CDS	disable	see genes	(659)
hsa-miR-650	microT-CDS	disable	see genes	(387)
hsa-miR-6807-5p	microT-CDS	disable	see genes	(186)
hsa-miR-1205	microT-CDS	disable	see genes	(1011)

Select the way to merge results: genes union genes intersection - 4 + pathways union pathways intersection

FDR Correction: ☑
Conservative Stats: ☐

P-value threshold: 0.05
MicroT threshold: 0.8

In order to see HeatMap select pathway intersection or pathway union.

● Significance Clusters/Heatmap
○ Targeted Pathways Clusters/Heatmap

#	KEGG pathway	p-value	#genes		#miRNAs	
1.	Glycerophospholipid metabolism (hsa00564)	9.05611116512e-05	24	see genes	3	details
2.	ECM-receptor interaction (hsa04512)	9.05611116512e-05	15	see genes	3	details
3.	TGF-beta signaling pathway (hsa04350)	9.05611116512e-05	19	see genes	4	details
4.	Nicotine addiction (hsa05033)	0.0031352887334	7	see genes	4	details
5.	Proteoglycans in cancer (hsa05205)	0.0031352887334	36	see genes	4	details
6.	Type II diabetes mellitus (hsa04930)	0.00464432694315	15	see genes	3	details
7.	Signaling pathways regulating pluripotency of stem cells (hsa04550)	0.00660997443382	27	see genes	4	details
8.	Choline metabolism in cancer (hsa05231)	0.0186200082874	20	see genes	4	details
9.	Hippo signaling pathway (hsa04390)	0.0411967404513	24	see genes	4	details

Figure S6B: Print screen shows pathway enrichment analysis of has-miR-6807-5p that was done by DIANA database tools: miRpath, http://snf-515788.vm.okeanos.grnet.gr/. It highlights the role of this miRNA in Hippo signaling.