

Supporting information:

Supplementary tables:


Table S3. List of primer assays

Primer assay	
Hs_YAP1_1_SG	(NM_001195044)
Hs_FOXA2_1_SG	(NM_021784)
Hs_AMOTL2_1_SG	(NM_016201)
Hs_TEAD2_1_SG	(NM_001256658)
Hs_SMAD4_1_SG	(NM_005359)
Hs_NF2_1_SG	(NM_000268)
Hs_GAPDH_1_SG	(NM_001256799)
Hs_miR-650_1	(MIMAT0003320)
Hs_miR-1205_1	(MIMAT0005869)
Hs_SNORD72_11	(MS00033719)
Human RPARP-AS	(ENST00000473970)
Human SRD5A3-AS	(ENST00000433175)

Supplementary figures:

A. YAP1

UniProtKB:M3Y746	YAP1	involved_in	GO:0035329	   hippo signaling	ECO:0000265	GO_REF:0000107	UniProtKB:P46938	9669	Ensembl
					   IEA		more...	Mustela putorius furo	
UniProtKB:M3Y746	YAP1	involved_in	GO:0042060	   wound healing	ECO:0000265	GO_REF:0000107	UniProtKB:P46938	9669	Ensembl
					   IEA		more...	Mustela putorius furo	
UniProtKB:M3Y746	YAP1	involved_in	GO:0042127	   regulation of cell population proliferation	ECO:0000265	GO_REF:0000107	UniProtKB:P46938	9669	Ensembl
					   IEA		more...	Mustela putorius furo	

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YAP1 ↔ Non-alcoholic Fatty Liver Disease

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Filter by		Association type		Filter	
		ALL			
1-50 of 83 results.					
First		Previous		1 2 Next Last	
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 3 chemicals: Choline Dietary Fats Methionine	
2.	✓	Song Y, et al. Chrysin ameliorates hepatic steatosis induced by a diet deficient in methionine and choline by inducing the secretion of hepatocyte nuclear factor 4α-dependent very low-density lipoprotein. J Biochem Mol Toxicol. 2020 Jul;34(7):e22497.		Inferred via 2 chemicals: Choline Methionine	
3.	✓	Thongrak 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	
4.	✓	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	
5.	✓	Han X, et al. Acanthoic acid modulates lipogenesis in nonalcoholic fatty liver disease via FXR/LXRα-dependent manner. Chem Biol Interact. 2019 Sep 25;311:108794.		Inferred via 1 chemical: Dietary Fats	
6.	✓	Kus E, et al.		Inferred via 1 chemical: Dietary Fats	

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SuperPathway	Contained pathways
1. Hippo signaling pathway	 Hippo signaling pathway
2. Hippo signaling pathway - multiple species	 Hippo signaling pathway - multiple species
3. Signaling by Hippo	 Signaling by Hippo

GenesLikeMe


Genes that share pathways with YAP1: view


Pathways by source for YAP1 Gene


1 Sino Biological pathway for YAP1 Gene


 AKT Signaling Pathway


2 Biosystems pathways for YAP1 Gene

 ErbB4 signaling events


 Mesodermal Commitment Pathway


 Rac1/Pak1/p38/MMP-2 pathway


 IGF-beta receptor signaling

 TGF-beta Signaling Pathway


3 Qiagen pathways for YAP1 Gene

 14-3-3 and Regulation of BAD Activity

 14-3-3 Induced Intracellular Signaling

 Akt Signaling

4 Cell Signaling Technology pathways for YAP1 Gene

 Glucose / Energy Metabolism

B: SMAD4

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

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SMAD4 ↔ Non-alcoholic Fatty Liver Disease

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Filter by

Association type

ALL

Filter

1-50 of 81 results.

First

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1

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Last

	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;133:110930.	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. Acantholic acid modulates lipogenesis in nonalcoholic fatty liver disease via FXR/LXRs-dependent manner. Chem Biol Interact. 2019 Sep 25;311:108704.	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

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SuperPathway	Contained pathways
1 Hippo signaling pathway	Hippo signaling pathway

 GenesLikeMe

Genes that share pathways with SMAD4: [view](#)

C: NF2

UniProtKB:P46662	NF2	acts_upstream_of_or_within	GO:0046426 (P) (M) (I) (C) (E) (D) (S) (O) (T) (F) (G) (H) (J) (K) (L) (M) (N) (O) (P) (Q) (R) (S) (T) (U) (V) (W) (X) (Y) (Z) (AA) (AB) (AC) (AD) (AE) (AF) (AG) (AH) (AI) (AJ) (AK) (AL) (AM) (AN) (AO) (AP) (AQ) (AR) (AS) (AT) (AU) (AV) (AW) (AX) (AY) (AZ) (BA) (BB) (BC) (BD) (BE) (BF) (BG) (BH) (BI) (BJ) (BK) (BL) (BM) (BN) (BO) (BP) (BQ) (BR) (BS) (BT) (BU) (BV) (BW) (BX) (BY) (BZ) (CA) (CB) (CC) (CD) (CE) (CF) (CG) (CH) (CI) (CJ) (CK) (CL) (CM) (CN) (CO) (CP) (CQ) (CR) (CS) (CT) (CU) (CV) (CW) (CX) (CY) (CZ) (DA) (DB) (DC) (DD) (DE) (DF) (DG) (DH) (DI) (DJ) (DK) (DL) (DM) (DN) (DO) (DP) (DQ) (DR) (DS) (DT) (DU) (DV) (DW) (DX) (DY) (DZ) (EA) (EB) (EC) (ED) (EE) (EF) (EG) (EH) (EI) (EJ) (EK) (EL) (EM) (EN) (EO) (EP) (EQ) (ER) (ES) (ET) (EU) (EV) (EW) (EX) (EY) (EZ) (FA) (FB) (FC) (FD) (FE) (FF) (FG) (FH) (FI) (FJ) (FK) (FL) (FM) (FN) (FO) (FP) (FQ) (FR) (FS) (FT) (FU) (FV) (FW) (FX) (FY) (FZ) (GA) (GB) (GC) (GD) (GE) (GF) (GG) (GH) (GI) 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NF2

Non-alcoholic Fatty Liver Disease

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Association type

ALL

Filter

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First

Previous

1

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	Reference	Association
1	<div><div>✓</div><div>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.</div></div>	Inferred via 1 chemical: Dietary Fats
2	<div><div>✓</div><div>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.</div></div>	Inferred via 1 chemical: Dietary Fats
3	<div><div>✓</div><div>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.</div></div>	Inferred via 1 chemical: Dietary Fats
4	<div><div>✓</div><div>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.</div></div>	Inferred via 1 chemical: Dietary Fats

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Filter:

(2 results)

	SuperPathway	Contained pathways
1	Hippo signaling pathway	Hippo signaling pathway
2	Hippo signaling pathway - multiple species	Hippo signaling pathway - multiple species

GenesLikeMe

Genes that share pathways with NF2: view

Pathways by source for NF2 Gene

2 BioSystems pathways for NF2 Gene

1 Qiagen pathway for NF2 Gene

D: AMOTL2

UniProtKB:F6SBP4	amotl2	part_of	GO:0031410 cytoplasmic vesicle	ECO:0000318 IBA	PMID:21873635	MGI:MGI:108440 more...	8364 Xenopus tropicalis	GO_Central
UniProtKB:F6SBP4	amotl2	involved_in	GO:0035329 hippo signaling	ECO:0000318 IBA	PMID:21873635	PANTHER:PTN000381812 more...	8364 Xenopus tropicalis	GO_Central

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AMOTL2 ↔ **Non-alcoholic Fatty Liver Disease**

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Filter by: Association type: ALL Filter

1 25 of 25 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	Failler KA, et al. Convergence of hepcidin deficiency, systemic iron overloading, heme accumulation, and KLF-EBF/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. Biulchim 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

genecards.org/cgi-bin/carddisp.pl?gene=AMOTL2&keywords=amotl2#pathways_interactions

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Pathways & Interactions for AMOTL2 Gene

SuperPathways for AMOTL2 Gene

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Filter: (1 result)

SuperPathway	Contained pathways
1 Signaling by Hippo	Signaling by Hippo













GenesLikeMe Genes that share pathways with AMOTL2: [view](#)

Pathways by source for AMOTL2 Gene

2 Reactome pathways for AMOTL2 Gene

1 KEGG pathway for AMOTL2 Gene

E: FOXA2

UniProtKB:Q7T1R4	foxa2	enables	GO:0008134    transcription factor binding	ECO:0000256  IEA	GO_REF:0000002	InterPro:IPR013638	8364 Xenopus tropicalis	InterPro
UniProtKB:Q7T1R4	foxa2	enables	GO:0019904    protein domain specific binding	ECO:0000256  IEA	GO_REF:0000002	InterPro:IPR013638	8364 Xenopus tropicalis	InterPro
UniProtKB:Q7T1R4	foxa2	involved_in	GO:0030154    cell differentiation	ECO:0000318  IBA	PMID:21873635	MGI:MGI:1347466 more...	8364 Xenopus tropicalis	GO_Central

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GPS-Prot Interaction Network for FOXA2

SIGNOR [curated interactions for FOXA2 Gene](#) [?](#)


 Activates: [DLK1](#)
 Inactivates: [OTX2](#)
 Is activated by: [CTNNB1](#)
 Is inactivated by: [NANOG](#), [POU5F1](#), [CHUK](#)

Gene Ontology (GO) - Biological Process for FOXA2 Gene [?](#)

Filter: (2 results)

GO ID	Qualified GO term	Evidence	PubMed IDs
GO:0030154	cell differentiation	IBA	21873635
GO:0071542	dopaminergic neuron differentiation	TAS	24431302

 **GenesLikeMe** Genes that share ontologies with FOXA2: [view](#) [?](#)

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FOXA2 ↔ Non-alcoholic Fatty Liver Disease

This gene-disease association may be inferred in part via [curated interactions](#) between [FOXA2](#) and any chemicals listed below, and a curated association between those chemicals and [Non-alcoholic Fatty Liver Disease](#).

Filter by Association type ALL Filter

	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. <i>Food Chem Toxicol.</i> 2020 Jan;135:110930.		Inferred via 2 chemicals: Choline Methionine
2. ✓ Song Y, et al. Chrysin ameliorates hepatic steatosis induced by a diet deficient in methionine and choline by inducing the secretion of hepatocyte nuclear factor 4α-dependent very low-density lipoprotein. <i>J Biochem Mol Toxicol.</i> 2020 Jul;34(7):e22497.		Inferred via 2 chemicals: Choline Methionine
3. ✓ Lake AD, et al. Folate receptor-beta expression as a diagnostic target in human & rodent nonalcoholic steatohepatitis. <i>Toxicol Appl Pharmacol.</i> 2019 Apr 1;368:49-54.		Inferred via 2 chemicals: Choline Methionine
4. ✓ Li MH, et al. RLA8-A New and Highly Effective Quadruple PPAR-γ and GPR40 Agonist to Reverse Nonalcoholic Steatohepatitis and Fibrosis. <i>J Pharmacol Exp Ther.</i> 2019 Apr;369(1):67-77.		Inferred via 2 chemicals: Choline Methionine
5. ✓ Pogribny IP, et al. Epigenetically mediated inhibition of S-adenosylhomocysteine hydrolase and the associated dysregulation of 1-carbon metabolism in nonalcoholic steatohepatitis and hepatocellular carcinoma. <i>FASEB J.</i> 2018 Mar;32(3):1591-1601.		Inferred via 4 chemicals: Choline Folic Acid Methionine Streptozotcin
6. ✓ Willebrords J, et al.		Inferred via 1 chemical: Choline

F: TEAD2

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SIGNOR

curated interactions for FOXA2 Gene

Activates: DLK1

Inactivates: OTX2

Is activated by: CTNNB1

Is inactivated by: NANOG, POU5F1, CHUK

Gene Ontology (GO) - Biological Process for FOXA2 Gene

Filter: (2 results)

GO ID	Qualified GO term	Evidence	PubMed IDs
GO:0030154	cell differentiation	IBA	21873635
GO:0071542	dopaminergic neuron differentiation	TAS	24431302

GenesLikeMe

Genes that share ontologies with FOXA2: view

UniProtKB:ADA2J8K2K7	TEAD2	involved_in	GO:0035329 (P) hippo signaling	ECO:0000318 IBA	PMID:21873635	MGI:MGI:101876 more...	9598 Pan troglodytes	GO_Central
UniProtKB:ADA2J8K2K7	TEAD2	enables	GO:0001228 (F)	ECO:0000318	PMID:21873635	MGI:MGI:101876	9598 Pan	GO_Central

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TEAD2 ↔ Non-alcoholic Fatty Liver Disease

This gene-disease association may be inferred in part via curated interactions between TEAD2 and any chemicals listed below, and a curated association between those chemicals and Non-alcoholic Fatty Liver Disease.

Filter by Association type ALL Filter

1-14 of 14 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-ERBa/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. Nault R, et al.	Inferred via 1 chemical:

Figures S1. Validation of the relation between key hub genes to NAFLD, cell proliferation/differentiation and Hippo pathway by public databases.

YAP1 & miR-650

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mRWalk

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YAP1

Entrezid 10413
 Genesymbol YAP1
 Alias COB1:YAP;YAP2;YAP65.YKI
 Description Homo sapiens Yes associated protein 1 (YAP1), transcript variant X1, mRNA.
 Chromosome 11
 Ensemblid ENSG00000137693

Transcripts:

Refseq	Ensemblid	Length	Startcode	Endcode
NM_001282101	ENST00000416947	9408	389	1915
NM_001282100	ENST00000397274	9360	389	1867
NM_001130145	ENST00000282441	9396	389	1903
NM_001189044	ENST00000314339	9348	389	1893
XM_001282098	ENST00000348877	9294	389	1801
NM_001282098	ENST00000429886	9248	389	1793
NM_006106	ENST0000026343	9234	389	1741
NM_001130940	ENST00000244752	4093	225	1000

Interactions:

Mirna	Refseqid	Genesymbol	Score	Position	Binding Site	Au	Nc	N Pairings	Targetscan	Mirdb	Mirbase
hsa-miR-650-3p	NM_001130145	YAP1	0.92	CCS	1794,1823	0.93	-7.163	19	—	—	—
hsa-miR-650-1-3p	NM_001130145	YAP1	0.92	3'UTR	2732,2762	0.68	-5.18	21	—	—	—
hsa-miR-650-1-5p	NM_001130145	YAP1	0.92	CCS	1391,1400	0.92	-7.163	19	—	—	—
hsa-miR-650-1-3p	NM_001130145	YAP1	0.92	3'UTR	2334,2357	0.68	-5.18	21	—	—	—
hsa-miR-650-1-3p	NM_001130145	YAP1	0.92	CCS	1452,1461	0.92	-7.163	19	—	—	—
hsa-miR-650-1-3p	NM_001130145	YAP1	0.92	3'UTR	2573,2588	0.68	-5.18	21	—	—	—
hsa-miR-650-5a	NM_001130145	YAP1	0.85	CCS	1044,1077	0.5	-7.14	19	—	—	—
hsa-miR-650	NM_001130145	YAP1	0.83	3'UTR	290,418	0.41	-11.412	16	—	—	—
hsa-miR-649b-3p	NM_001130145	YAP1	0.92	3'UTR	2642,2676	0.9	-8.97	19	—	—	—
hsa-miR-649b-3p	NM_001130145	YAP1	0.92	3'UTR	2651,2671	0.9	-8.87	19	—	—	—

← ... 592 593 594 595 596 597 598 599 600 601 602 ... →

YAP1 & miR-1205

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YAP1

Entrezid 10413
 Genesymbol YAP1
 Alias COB1:YAP;YAP2;YAP65.YKI
 Description Homo sapiens Yes associated protein 1 (YAP1), transcript variant X1, mRNA.
 Chromosome 11
 Ensemblid ENSG00000137693

Transcripts:

Refseq	Ensemblid	Length	Startcode	Endcode
NM_001282101	ENST00000416947	9408	389	1915
NM_001282100	ENST00000397274	9360	389	1867
NM_001130145	ENST00000282441	9396	389	1903
NM_001189044	ENST00000314339	9348	389	1893
NM_001282098	ENST00000348877	9294	389	1801
NM_001282098	ENST00000429886	9248	389	1793
NM_006106	ENST0000026343	9234	389	1741
NM_001130940	ENST00000244752	4093	225	1000

Interactions:

Mirna	Refseqid	Genesymbol	Score	Position	Binding Site	Au	Nc	N Pairings	Targetscan	Mirdb	Mirbase
hsa-miR-1207-3p	NM_001130145	YAP1	1.00	3'UTR	2149,2180	0.94	-9.498	12	—	—	—
hsa-miR-1207-3p	NM_001282101	YAP1	1.00	3'UTR	2177,2192	0.94	-9.498	12	—	—	—
hsa-miR-1205	NM_001282101	YAP1	0.83	CCS	1690,1716	0.9	-8.762	17	—	—	—
hsa-miR-1205	NM_001282101	YAP1	0.92	CCS	1428,1447	0.9	-8.354	16	—	—	—
hsa-miR-1205	NM_001130145	YAP1	0.92	CCS	1414,1438	0.9	-8.354	16	—	—	—
hsa-miR-1205	NM_001130145	YAP1	0.92	3'UTR	4010,4239	0.9	-13.227	18	—	—	—
hsa-miR-1205	NM_001282100	YAP1	0.85	CCS	1642,1668	0.9	-8.762	17	—	—	—
hsa-miR-1205	NM_001282100	YAP1	0.96	CCS	1393,1399	0.4	-8.304	14	—	—	—
hsa-miR-1205	NM_001130145	YAP1	0.85	3'UTR	3962,3987	0.6	-13.227	18	—	—	—
hsa-miR-1205	NM_001130145	YAP1	0.85	CCS	1371,1387	0.46	-8.304	14	—	—	—

← ... 2069 2070 2071 2072 2073 2074 2075 2076 2077 2078 2079 ... →

SMAD4 & miR-650

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SMAD4

Entrezid 4000
Genesymbol SMAD4
Alias DPC4,IP-MADH4,MYHRS
Description Homo sapiens SMAD family member 4 (SMAD4), mRNA.
Chromosome10
Ensemblid ENSG00000141046

Transcripts:

Refseq	Ensemblid	Length	Startcode	Endcode
NM_003359	ENST00000242988	8789	339	2197

Interactions:

Mirna	Refseqid	Genesymbol	Score	Position	Binding Site	Au	Me	N Pairings	Targetscan	Mirdb	Mirtarbase
hsa-miR-647	NM_005359	SMAD4	1.00	3UTR	5515-5537	0.6	-6.97	18	—	—	—
hsa-miR-647	NM_005359	SMAD4	1.00	3UTR	4314-4332	0.44	-6.878	13	—	—	—
hsa-miR-648	NM_005359	SMAD4	1.00	3UTR	5523-5574	0.56	-2.793	17	—	—	—
hsa-miR-649	NM_005359	SMAD4	0.82	CDS	1244-1287	0.46	-6.512	18	—	—	—
hsa-miR-649	NM_005359	SMAD4	1.00	3UTR	4684-4689	0.79	-12.874	15	—	—	—
hsa-miR-6499-5b	NM_005359	SMAD4	1.00	3UTR	7313-7333	0.5	-5.839	17	—	—	—
hsa-miR-650	NM_005359	SMAD4	0.92	3UTR	4802-4827	0.65	-6.97	19	—	—	—
hsa-miR-650	NM_005359	SMAD4	0.92	3UTR	7023-7028	0.54	-4.027	19	—	—	—
hsa-miR-650	NM_005359	SMAD4	0.92	3UTR	8207-8224	0.48	-7.743	19	—	—	—
hsa-miR-6500-3p	NM_005359	SMAD4	0.85	CDS	1832-1948	0.44	-4.026	19	—	—	—

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SMAD4 & miR-1205

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HOME FAQ RESOURCES ABOUT

SMAD4

Entrezid 4000
Genesymbol SMAD4
Alias DPC4,IP-MADH4,MYHRS
Description Homo sapiens SMAD family member 4 (SMAD4), mRNA.
Chromosome10
Ensemblid ENSG00000141046

Transcripts:

Refseq	Ensemblid	Length	Startcode	Endcode
NM_003359	ENST00000242988	8789	339	2197

Interactions:

Mirna	Refseqid	Genesymbol	Score	Position	Binding Site	Au	Me	N Pairings	Targetscan	Mirdb	Mirtarbase
hsa-miR-1202	NM_005359	SMAD4	0.92	3UTR	231-266	0.15	-9.418	16	—	—	—
hsa-miR-1203	NM_005359	SMAD4	1.00	3UTR	5295-5321	0.36	-8.823	18	—	—	—
hsa-miR-1204	NM_005359	SMAD4	1.00	3UTR	7896-7914	0.72	-6.97	15	—	—	—
hsa-miR-1205	NM_005359	SMAD4	0.92	3UTR	2204-2227	0.65	-12.408	16	—	LINK	—
hsa-miR-1205	NM_005359	SMAD4	0.85	3UTR	625-97	0.28	-6.246	12	—	LINK	—
hsa-miR-1207-3p	NM_005359	SMAD4	0.92	3UTR	7456-7493	0.62	-6.597	15	—	—	—
hsa-miR-1207-5p	NM_005359	SMAD4	0.92	3UTR	4256-4402	0.4	-5.495	20	—	—	—
hsa-miR-1208	NM_005359	SMAD4	0.85	3UTR	9271-9289	0.87	-7.961	16	—	—	—
hsa-miR-12113	NM_005359	SMAD4	0.92	3UTR	5542-5555	0.33	-13.973	14	—	—	—
hsa-miR-12114	NM_005359	SMAD4	1.00	3UTR	2640-2655	0.52	-6.212	14	—	—	—

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Export

NF2 & miR-650

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NF2

Entrezid 4771

Genesymbol NF2

Alias ACN,BANF,SCH

Description Homo sapiens neurofibromin 2 (NF2), transcript variant 8, mRNA.

Chromosome22

Ensemblid ENSG00000186575

Transcripts:

Refseq	Ensemblid	Length	Startcod	Endcod
NM_181832	ENST00000397789	6106	444	2216
NM_016418	ENST00000670396	6091	444	2216
NM_000269	ENST00000338641	6046	444	2231
NM_181833	ENST00000413209	4756	444	841
NM_181829	ENST00000361452	5968	444	2093
NM_181828	ENST00000361676	5965	444	2093
NM_181830	ENST00000333387	5842	444	1967
NM_181823	ENST00000403999	3126	444	2216
NM_181831	ENST00000334961	2217	444	1967

Interactions:

Mirna	Refseqid	Genesymbol	Score	Position	Binding Site	Au	Me	N Pairings	Targetscan	Widb	Wistarbase
hsa-miR-646	NM_181832	NF2	0.85	CDS	1784,1805	0.38	-10.782	14	—	—	—
hsa-miR-647	NM_181832	NF2	1.00	3'UTR	2809,3824	0.4	-7.017	16	—	—	—
hsa-miR-648	NM_181832	NF2	1.00	3'UTR	3671,3694	0.33	-9.814	16	—	—	—
hsa-miR-649	NM_181832	NF2	1.00	3'UTR	3554,3575	0.43	-9.236	17	—	—	—
hsa-miR-649	NM_181832	NF2	0.92	3'UTR	3565,3586	0.5	-9.847	18	—	—	—
hsa-miR-649	NM_181832	NF2	0.85	3'UTR	4869,4887	0.38	-10.874	15	—	—	—
hsa-miR-650	NM_181832	NF2	0.92	3'UTR	3970,3990	0.47	-9.18	19	—	Link	—
hsa-miR-650-3p	NM_181832	NF2	0.97	3'UTR	4642,4655	0.57	-9.593	13	—	—	—
hsa-miR-652-5p	NM_181832	NF2	0.85	3'UTR	3599,3623	0.37	-10.117	15	—	—	—
hsa-miR-652-5p	NM_181832	NF2	0.85	3'UTR	3023,3043	0.32	-12.442	15	—	—	—

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NF2 & miR-1205

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NF2

Entrezid 4771

Genesymbol NF2

Alias ACN,BANF,SCH

Description Homo sapiens neurofibromin 2 (NF2), transcript variant 8, mRNA.

Chromosome22

Ensemblid ENSG00000186575

Transcripts:

Refseq	Ensemblid	Length	Startcod	Endcod
NM_181832	ENST00000397789	6106	444	2216
NM_016418	ENST00000670396	6091	444	2216
NM_000269	ENST00000338641	6046	444	2231
NM_181833	ENST00000413209	4756	444	841
NM_181829	ENST00000361452	5968	444	2093
NM_181828	ENST00000361676	5965	444	2093
NM_181830	ENST00000333387	5842	444	1967
NM_181823	ENST00000403999	3126	444	2216
NM_181831	ENST00000334961	2217	444	1967

Interactions:

Mirna	Refseqid	Genesymbol	Score	Position	Binding Site	Au	Me	N Pairings	Targetscan	Widb	Wistarbase
hsa-miR-1205	NM_181829	NF2	1.00	3'UTR	2096,2116	0.47	-10.966	17	—	—	—
hsa-miR-1205	NM_181828	NF2	0.92	CDS	887,904	0.4	-10.109	14	—	—	—
hsa-miR-1205	NM_181828	NF2	0.84	CDS	1808,1927	0.37	-9.938	17	—	—	—
hsa-miR-1205	NM_181828	NF2	0.92	CDS	1678,1696	0.37	-8.236	15	—	—	—
hsa-miR-1205	NM_181830	NF2	1.00	3'UTR	2093,2113	0.47	-10.966	17	—	—	—
hsa-miR-1205	NM_181830	NF2	0.84	CDS	1788,1804	0.37	-9.938	17	—	—	—
hsa-miR-1205	NM_181830	NF2	0.92	CDS	1833,1873	0.37	-8.236	15	—	—	—
hsa-miR-1205	NM_181830	NF2	1.00	3'UTR	1970,1990	0.47	-10.966	17	—	—	—
hsa-miR-1205	NM_181829	NF2	0.84	CDS	2034,2053	0.37	-9.938	17	—	—	—
hsa-miR-1205	NM_181829	NF2	0.92	CDS	1804,1822	0.37	-8.236	15	—	—	—

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
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AMOTL2

Entrezid [01421](#)
 GeneSymbol [AMOTL2](#)
 Alias [LCOP](#)

Description [Homo sapiens angiotensin like 2 \(AMOTL2\), transcript variant 1, mRNA.](#)
 Chromosome [1](#)
 Ensemblid [ENS00000114019](#)

Transcripts:

RefSeq	EnsemblId	Length	Startcod	Endcod
NM_001278683	ENST00000251424	4991	118	2821
NM_001278683	ENST00000231348	4989	306	2839
NM_0148201	ENST00000249883	5008	306	2848
MIM_R067135X	ENST00000242020	6442	338	3386

Interactions:

Homo	RefSeqid	GeneSymbol	Score	Position	Binding Site	Au	Me	N Pairings	TargetScan	Hotdo	Hotbase
hsa-mir-6499-3p	NM_001278683	AMOTL2	0.82	CDS	1614..1637	0.31	-8.762	19	--	--	--
hsa-mir-6499-3p	NM_016301	AMOTL2	0.82	CDS	1614..1637	0.31	-8.762	19	--	--	--
hsa-mir-6499-3p	XM_006713654	AMOTL2	0.82	CDS	1387..1390	0.31	-8.762	19	--	--	--
hsa-mir-6499-3p	XM_006713654	AMOTL2	0.83	CDS	479..701	0.23	-9.894	17	--	--	--
hsa-mir-6499-3p	XM_006713654	AMOTL2	0.82	UTR	148..211	0.28	-9.113	16	--	--	--
hsa-mir-6499-3p	NM_001278683	AMOTL2	0.92	UTR	228..239	0.28	-9.113	16	--	--	--
hsa-mir-6499-3p	NM_016301	AMOTL2	0.92	UTR	228..239	0.28	-9.113	16	--	--	--
hsa-mir-650	NM_016301	AMOTL2	0.92	CDS	1041..1063	0.41	-8.283	18	--	--	--
hsa-mir-650	NM_016301	AMOTL2	0.92	CDS	1395..1409	0.37	-8.14	18	--	--	--
hsa-mir-650	NM_001278683	AMOTL2	0.92	CDS	1041..1063	0.41	-8.283	18	--	--	--

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AMOTL2

Entrezid [51421](#)
 Genesymbol [AMOTL2](#)
 Alias [LCCP](#)
 Description [Homo sapiens angiotensin like 2 \(AMOTL2\), transcript variant 1, mRNA](#)
 Chromosome [3](#)
 Ensemblid [ENSG00000114919](#)

Transcripts:

Refseq	Ensemblid	Length	Startcode	Endcode
NM_001278683	ENST00000145114	4991	118	2631
NM_001278683	ENST00000131148	4999	304	2639
NM_014201	ENST00000249883	3008	304	2640
XM_008713654	ENST00000422455	4440	239	2399

Interactions:

Mirna	Refseqid	Genesymbol	Score	Position	Binding Site	Au	Ma	N Pairings	Targetscan	Mirdb	Mirbase
hsa-miR-125b	NM_006713654	AMOTL2	0.92	CD8	1282-1279	0.43	-0.97	18	—	—	—
hsa-miR-125b	NM_006713654	AMOTL2	0.85	CD8	677-704	0.26	-0.938	17	—	—	—
hsa-miR-125b	NM_006713654	AMOTL2	0.92	CD8	360-380	0.29	-0.97	17	—	—	—
hsa-miR-125b	NM_001278683	AMOTL2	1.00	CD8	1402-1426	0.43	-0.97	18	—	—	—
hsa-miR-125b	NM_001278683	AMOTL2	0.90	CD8	407-427	0.29	-0.97	17	—	—	—
hsa-miR-125b	NM_001278683	AMOTL2	1.00	CD8	1385-1412	0.43	-0.97	18	—	—	—
hsa-miR-125b	NM_001278683	AMOTL2	0.92	CD8	393-413	0.29	-0.97	17	—	—	—
hsa-miR-125b	NM_014201	AMOTL2	1.00	CD8	1402-1426	0.43	-0.97	18	—	—	—
hsa-miR-125b	NM_014201	AMOTL2	0.92	CD8	407-427	0.29	-0.97	17	—	—	—
hsa-miR-125b	NM_014201	AMOTL2	0.85	3p76	4095-4124	0.71	-0.938	20	—	—	—

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FOXA2 & miR-650

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FOXA2

Entrezid 5170

GeneSymbol FOXA2

Alias HNF3B,TCF3B

Description Homo sapiens forkhead box A2 (FOXA2), transcript variant 2, mRNA.

Chromosome20

Ensemblid ENSG00000125708

Transcripts:

Refseq	Ensemblid	Length	Startcod	Endcod
NM_133675	ENST00000271115	2415	191	1564
NM_021784	ENST0000419308	2426	186	1577

Interactions:

Mirna	Refseqid	GeneSymbol	Score	Position	Binding Site	Au	Me	N Pairings	Targetscan	Winds	Mirabase
hsa-miR-649	NM_021784	FOXA2	1.00	CDS	1395.1366	5.4	-10.319	14	—	—	—
hsa-miR-648	NM_133675	FOXA2	1.00	CDS	1397.1393	5.4	-10.319	14	—	—	—
hsa-miR-647	NM_021784	FOXA2	0.88	5'UTR	42.60	0.28	-7.934	17	—	—	—
hsa-miR-647	NM_021784	FOXA2	0.92	5'UTR	126.126	0.33	-5.026	17	—	—	—
hsa-miR-648	NM_021784	FOXA2	0.89	CDS	899.874	0.37	-7.914	12	—	—	—
hsa-miR-648	NM_133675	FOXA2	0.89	CDS	840.861	0.37	-7.914	12	—	—	—
hsa-miR-6499-5p	NM_133675	FOXA2	0.89	CDS	1168.202	0.16	-10.816	16	—	—	—
hsa-miR-6499-5p	NM_021784	FOXA2	0.86	CDS	1161.1215	0.16	-10.816	16	—	—	—
hsa-miR-6499-5p	NM_021784	FOXA2	0.89	CDS	243.272	0.38	-4.879	20	—	—	—
hsa-miR-650	NM_021784	FOXA2	1.00	5'UTR	2370.2393	0.69	-3.793	17	—	—	—

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FOXA2 & miR-1205

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ABOUT

FOXA2

Entrezid 5170

GeneSymbol FOXA2

Alias HNF3B,TCF3B

Description Homo sapiens forkhead box A2 (FOXA2), transcript variant 2, mRNA.

Chromosome20

Ensemblid ENSG00000125708

Transcripts:

Refseq	Ensemblid	Length	Startcod	Endcod
NM_133675	ENST00000271115	2415	191	1564
NM_021784	ENST0000419308	2426	186	1577

Interactions:

Mirna	Refseqid	GeneSymbol	Score	Position	Binding Site	Au	Me	N Pairings	Targetscan	Winds	Mirabase
hsa-miR-1204	NM_021784	FOXA2	0.89	CDS	1037.1032	0.32	-11.336	12	—	—	—
hsa-miR-1205	NM_021784	FOXA2	1.00	5'UTR	1076.1081	0.39	-5.743	18	—	—	—
hsa-miR-1205	NM_133675	FOXA2	1.00	5'UTR	1843.1876	0.39	-5.743	13	—	—	—
hsa-miR-1207-3p	NM_133675	FOXA2	0.89	CDS	1138.1108	0.29	-5.743	13	—	—	—
hsa-miR-1207-3p	NM_021784	FOXA2	0.92	5'UTR	131.135	0.37	-6.251	17	—	—	—
hsa-miR-1208	NM_021784	FOXA2	0.89	5'UTR	180.225	0.38	-11.252	16	—	—	—
hsa-miR-12115	NM_133675	FOXA2	0.92	CDS	1934.1981	0.47	-5.481	20	—	—	—
hsa-miR-12115	NM_021784	FOXA2	1.00	CDS	1937.1984	0.47	-5.481	22	—	—	—
hsa-miR-12116	NM_133675	FOXA2	1.00	CDS	828.864	0.39	-6.251	20	—	—	—
hsa-miR-12116	NM_021784	FOXA2	0.92	5'UTR	84.109	0.42	-6.251	17	—	—	—

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TEAD2 & miR-650

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TEAD2
 Entrezid: 5453
 GeneSymbol: TEAD2
 Alias: ETP, TEAD-2, TEF-4, TEF4
 Description: Homo sapiens TEA domain transcription factor 2 (TEAD2), transcript variant 8, mRNA.
 Chromosome: 19
 Ensemblid: ENSG00000074219

Transcripts:

Refseq	Ensemblid	Length	Startcod	Endcod
NM_001256662	ENST00000339648	1967	259	1218
NM_003998	ENST00000311227	2220	92	1439
NM_001256659	ENST00000377214	2183	92	1444
NM_001256660	ENST00000339648	2236	132	1487
NM_001256659	ENST00000401918	2237	136	1488
NM_001256661	ENST00000399815	2211	107	1482

Interactions:

Mirna	Refseqid	GeneSymbol	Score	Position	Binding Site	Au	Me	N Pairings	Targetscan	Mirdb	Mirtarbase
hsa-miR-650	NM_001256662	TEAD2	1.00	3UTR	1977-1913	0.48	-3.793	20	—	—	—
hsa-miR-650	NM_001256659	TEAD2	0.85	3UTR	1847-1883	0.48	-3.793	20	—	—	—
hsa-miR-650	NM_001256659	TEAD2	0.82	3UTR	1823-1839	0.48	-3.793	20	—	—	—
hsa-miR-650	NM_001256660	TEAD2	0.83	3UTR	1846-1882	0.48	-3.793	20	—	—	—
hsa-miR-6500-3p	NM_001256660	TEAD2	0.85	3UTR	1428-1468	0.37	-7.641	16	—	—	—
hsa-miR-6500-3p	NM_001256662	TEAD2	0.85	3UTR	1199-1180	0.37	-7.641	16	—	—	—
hsa-miR-6500-3p	NM_001256661	TEAD2	0.83	3UTR	1390-1424	0.37	-7.641	16	—	—	—
hsa-miR-6500-3p	NM_001256659	TEAD2	0.82	3UTR	1385-1406	0.37	-7.641	16	—	—	—
hsa-miR-6500-3p	NM_001256658	TEAD2	0.85	3UTR	1418-1490	0.37	-7.641	16	—	—	—
hsa-miR-6500-3p	NM_003998	TEAD2	0.82	3UTR	1360-1387	0.37	-7.641	16	—	—	—

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TEAD2 & miR-1205

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mRWalk

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TEAD2
 Entrezid: 5453
 GeneSymbol: TEAD2
 Alias: ETP, TEAD-2, TEF-4, TEF4
 Description: Homo sapiens TEA domain transcription factor 2 (TEAD2), transcript variant 8, mRNA.
 Chromosome: 19
 Ensemblid: ENSG00000074219

Transcripts:

Refseq	Ensemblid	Length	Startcod	Endcod
NM_001256662	ENST00000339648	1967	259	1218
NM_003998	ENST00000311227	2220	92	1439
NM_001256659	ENST00000377214	2183	92	1444
NM_001256660	ENST00000339648	2236	132	1487
NM_001256659	ENST00000401918	2237	136	1488
NM_001256661	ENST00000399815	2211	107	1482

Interactions:

Mirna	Refseqid	GeneSymbol	Score	Position	Binding Site	Au	Me	N Pairings	Targetscan	Mirdb	Mirtarbase
hsa-miR-1204	NM_003998	TEAD2	1.00	3UTR	280-248	0.43	-9.518	19	—	—	—
hsa-miR-1204	NM_001256660	TEAD2	0.82	3UTR	280-278	0.43	-9.518	19	—	—	—
hsa-miR-1205	NM_001256660	TEAD2	0.86	3UTR	497-494	0.41	-9.518	19	—	—	—
hsa-miR-1204	NM_001256662	TEAD2	0.85	3UTR	808-827	0.34	-7.757	16	—	—	—
hsa-miR-1205	NM_001256662	TEAD2	0.82	3UTR	1842-1876	0.5	-9.938	19	—	—	—
hsa-miR-1205	NM_001256660	TEAD2	0.82	3UTR	2111-2140	0.5	-9.938	19	—	—	—
hsa-miR-1205	NM_001256660	TEAD2	0.82	3UTR	281-323	0.44	-9.968	19	—	—	—
hsa-miR-1205	NM_001256659	TEAD2	0.82	3UTR	2112-2146	0.5	-9.938	19	—	—	—
hsa-miR-1205	NM_001256659	TEAD2	0.82	3UTR	282-327	0.44	-9.968	19	—	—	—
hsa-miR-1205	NM_001256659	TEAD2	0.82	3UTR	2088-2102	0.5	-9.938	19	—	—	—

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Figures S2. Validation of the interaction between the selected m-RNAs and retrieved mi-RNAs from mirwalk.

miR-650 & SRD5A3-AS1

Input form	Web services	Help & Documentation	Bioinformatics Tools FA
EMBOSS_001	301	accttgattctactaaaaaaaaaGGATCCTTCAACTtcaacaataat	350
hsa-miR-650	1	-----	0
EMBOSS_001	351	aacacaagggagTGAAGAAAAACACTTTCTAAGGAAATCTCTCTGAG	400
hsa-miR-650	1	-----	0
EMBOSS_001	401	CTACCATCCTGCTAGGGAGAGCCTGAAAGCAGAATGCTGACTTGACTAGC	450
hsa-miR-650	1	-----	0
EMBOSS_001	451	TCTGGTCAATGAAAGAAATCACCAGTGGAAAGGTACCAGGGGGCTTTCT	500
hsa-miR-650	1	-----	0
EMBOSS_001	501	CAAAAGAGAGGGACAGTAAACTGCAAGATGAACAACTCAATGCCATCCAG	550
hsa-miR-650	1	-----	0
EMBOSS_001	551	GTCTGGATGAGAAAGAACAGTCGAGAGACTGAGTTTCAGGAGTGGAAACA	600
hsa-miR-650	1	-----AGGAGG--- .	6
EMBOSS_001	601	CTCAAAGCATCATCTTCCACTTTCTTCTCCGGCTGCTAGGAAGAAGGGAA	650
hsa-miR-650	7	----CAG-CGCUCUCAGGAC----- .. :..	21
EMBOSS_001	651	AAACACAGACCTTCTGAGGACCTGCGGAGCAAACTGAGTTTCAGAAAA	700
hsa-miR-650	22	-----	21
EMBOSS_001	701	GCAAACAGGGACTTCCCTCTGCGCAGCAGGAAGCAGTTAGCCTAGTCGGA	750
hsa-miR-650	--	-----	--

miR-650 & RPARP-AS1

Input form	Web services	Help & Documentation	Bioinformatics Tools FAQ
hsa-miR-650	1	-----	0
EMBOSS_001	1	tttttttttttttttttttagagacagggtttcgccatgttgccctag	50
hsa-miR-650	1	-----	0
EMBOSS_001	51	gctggtctccaacctggtctcctgggctcaagcgatccgccgcctcggc	100
hsa-miR-650	1	-----	0
EMBOSS_001	101	ctcccacagtgtctgggattccaggcgtgagctaccgcgccggccTATTT	150
hsa-miR-650	1	-----	0
EMBOSS_001	151	ACTTTTCTTACTAAGCTGGGGATCACCGTCGCCCTCGGCTTGGCAGGAAG	200
hsa-miR-650	1	-----AGGAGG--CAGCGCUCUCAG----GAC----- 	21
EMBOSS_001	201	GCGGGGGTGCAAGAAGAAAAGAGGTACAGAACACCAGAGGTGCCCTCGA	250
hsa-miR-650	22	-----	21
EMBOSS_001	251	TTCCGTCTTGCACTTGCCCTTCTCCACCGTCCAGCAATAAAGCGAGAGA	300
hsa-miR-650	22	-----	21
EMBOSS_001	301	AACAAGTGCAGGAACTGGCCGGCAGTCATGGGAGAAGCCAAAAAGACAG	350
hsa-miR-650	22	-----	21

miR-1205 & SRD5A3-AS1

Input form	Web services	Help & Documentation	Bioinformatics Tools FAQ
EMBOSS_001	151	gcatcatatcatgatcatctacagtccactgaggagaatagcagacgag	200
hsa-miR-1205	1	-----	0
EMBOSS_001	201	Aggccagggtgcagtgcataatcccagcactttgggagactgagatggg	250
hsa-miR-1205	1	-----	0
EMBOSS_001	251	aagatcgcttgaggccaggagtgcaagaccagcctgggcaacacagcaag	300
hsa-miR-1205	1	-----	0
EMBOSS_001	301	accttgattctactaaaaaaaaaGGATCCTTCAACTtcaacaataat	350
hsa-miR-1205	1	-----	0
EMBOSS_001	351	aacacaagggaagTGAAGAAAAACACTTTCTAAGGAATCTCTCTGAG	400
hsa-miR-1205	1	-----UCUGC-AGGGUUUGCUUUGAG-----	20
EMBOSS_001	401	CTACCATCCTGCTAGGGAGAGCCTGAAAGCAGAATGCTGACTTGACTAGC	450
hsa-miR-1205	21	-----	20
EMBOSS_001	451	TCTGGTCAATGAAAGAAATCACCAGTGGAAGGCTACCAGGGGGCTTTCT	500
hsa-miR-1205	21	-----	20
EMBOSS_001	501	CAAAAGAGAGGAGCACTAAACTGAAATGAAAGTCAATGCGATGAG	550

miR-1205 & RPARP-AS1

Input form	Web services	Help & Documentation	Bioinformatics Tools FAQ
hsa-miR-1205	1	-----	0
EMBOSS_001	1201	gttatattacatgaccaggagaagtaagggttcagatggcagtaagggt	1250
hsa-miR-1205	1	-----	0
EMBOSS_001	1251	gctaattgggctgaccttaagataaggagatgatcctggattatctgggtg	1300
hsa-miR-1205	1	-----	0
EMBOSS_001	1301	gacccaatgtaatcacaagggtccttaactgtggaatagtgggtggctg	1350
hsa-miR-1205	1	-----	0
EMBOSS_001	1351	agtcagaggcagatgatgcaatgactgaaagacttaaccagccatcacc	1400
hsa-miR-1205	1	-----UCUG-----CAGGGUUUGCUUUGAG-----	20
EMBOSS_001	1401	ggctttgaatacggagacggtcatgagccagggaatgcaggcaggctct	1450
hsa-miR-1205	21	-----	20
EMBOSS_001	1451	gggagctgaaaaaagcaagaaatggattctccccctggagcctccagaag	1500
hsa-miR-1205	21	-----	20
EMBOSS_001	1501	ggatgcggtcctgccaaaccttgtcagtgagccatttcagattttctgac	1550
hsa-miR-1205	21	-----	20
EMBOSS_001	1551	ttcaggactgtaagaaaataaacttgcttgttttcagcca	1592
#	-----		

Figures S3. Validation of the interaction between the retrieved mi-RNAs and retrieved lncRNAs.