

Table S1 : The predicted target miRNAs of Hsa_circ_0001451 through Circular RNA Interactome

CircRNA	CircRNA (Top) - miRNA (Bottom)	Context score	context score percentile
Mirbase ID	pairing		
hsa_circ_0001451 (5' ... 3')	GCACACUGCAAGGAAUGGUGAAG CGACCCACCUCUCCACCACUU	-0.091	80
hsa-miR-197 (3' ... 5')			
hsa_circ_0001451 (5' ... 3')	AGAUGAAGAACAUGCUGGUGAAC CGACCCACCUCUCCACCACUU	-0.109	84
hsa-miR-197 (3' ... 5')			
hsa_circ_0001451 (5' ... 3')	AGGAAGAUGAAGAACAUGCUGGU GUUGUUUUAGUGACUACGACCU	0.173	90
hsa-miR-338-3p (3' ... 5')			
hsa_circ_0001451 (5' ... 3')	AGAACAGAUGAAUCGUGUGGUAG GGCACCAAGAUGGGACACCAU	-0.089	78
hsa-miR-140-3p (3' ... 5')			

Table S2 : The predicted target mRNA of the three miRNAs through starBase v2.0

miRNA	Gene	miRDB	miRTarBase	TargetScan	Sum
hsa-mir-338-3p	SGTB	1	1	1	3
hsa-mir-140-5p	RALA	1	1	1	3

hsa-mir-338-3p	MRPS23	1	1	1	3
hsa-mir-338-3p	ARHGEF28	1	1	1	3
hsa-mir-197-3p	MED16	1	1	1	3
hsa-mir-140-5p	VEGFA	1	1	1	3
hsa-mir-140-5p	RAB10	1	1	1	3
hsa-mir-140-5p	FZD6	1	1	1	3
hsa-mir-197-3p	CKS1B	1	1	1	3
hsa-mir-197-3p	RBM27	1	1	1	3
hsa-mir-338-3p	NOVA1	1	1	1	3
hsa-mir-140-5p	MMD	1	1	1	3
hsa-mir-140-5p	GLRX5	1	1	1	3
hsa-mir-338-3p	PFAS	1	1	1	3
hsa-mir-197-3p	GGT7	1	1	1	3
hsa-mir-140-5p	ARIH1	1	1	1	3
hsa-mir-140-5p	PDGFRA	1	1	1	3
hsa-mir-197-3p	GOLGB1	1	1	1	3
hsa-mir-140-5p	TSC22D2	1	1	1	3
hsa-mir-140-5p	PHACTR2	1	1	1	3
hsa-mir-338-3p	ACVR1	1	1	1	3
hsa-mir-197-3p	HNRNPD	1	1	1	3
hsa-mir-197-3p	SAMD8	1	1	1	3
hsa-mir-197-3p	ACVR1B	1	1	1	3
hsa-mir-338-3p	ZDHHC18	1	1	1	3
hsa-mir-338-3p	ZWINT	1	1	1	3
hsa-mir-197-3p	TTPAL	1	1	1	3
hsa-mir-140-5p	STRADB	1	1	1	3
hsa-mir-197-3p	TAOK1	1	1	1	3
hsa-mir-197-3p	CHIC2	1	1	1	3
hsa-mir-140-5p	LAMC1	1	1	1	3
hsa-mir-338-3p	NRP1	1	1	1	3
hsa-mir-140-5p	VEZF1	1	1	1	3
hsa-mir-140-5p	TSPAN12	1	1	1	3
hsa-mir-197-3p	SYNGR1	1	1	1	3

hsa-mir-140-5p	RPUSD2	1	1	1	3
hsa-mir-140-5p	YOD1	1	1	1	3
hsa-mir-140-5p	PRDM1	1	1	1	3
hsa-mir-140-5p	KLK10	1	1	1	3
hsa-mir-197-3p	SS18	1	1	1	3
hsa-mir-338-3p	PREX2	1	1	1	3
hsa-mir-338-3p	ORC4	1	1	1	3
hsa-mir-140-5p	HDAC7	1	1	1	3
hsa-mir-140-5p	FGF9	1	1	1	3
hsa-mir-140-5p	CAPN1	1	1	1	3
hsa-mir-140-5p	2-Sep	1	1	1	3
hsa-mir-140-5p	TGFBR1	1	1	1	3
hsa-mir-140-5p	MED13	1	1	1	3

Table S3 : Gene Ontology (GO) enrichment analysis

Category	Term	PValue	Genes	FDR
GOTERM_B P_FAT	GO:0035295~tube development	0.00002 64	NRP1, FGF9, TGFBR1, VEGFA, PDGFRA, FZD6, ACVR1	0.03959 4293
GOTERM_B P_FAT	GO:0007167~enzyme linked receptor protein signaling pathway	0.00003 32	SS18, ACVR1B, NRP1, FGF9, TGFBR1, VEGFA, PDGFRA, ACVR1	0.04993 8993
GOTERM_B P_FAT	GO:0043009~chordate embryonic development	0.00025 1	ACVR1B, FGF9, TGFBR1, PDGFRA, PRDM1, FZD6, ACVR1	0.37679 1327
GOTERM_B P_FAT	GO:0048514~blood vessel morphogenesis	0.00025 6	NRP1, FGF9, TGFBR1, VEGFA, VEZF1, ACVR1	0.38333 6096
GOTERM_B P_FAT	GO:0009792~embryo nic development ending in birth or egg hatching	0.00026 4	ACVR1B, FGF9, TGFBR1, PDGFRA, PRDM1, FZD6, ACVR1	0.39552 4072

GOTERM_B	GO:0001568~blood	0.00050	NRP1, FGF9, TGFBR1,	0.76025
P_FAT	vessel development	8	VEGFA, VEZF1, ACVR1	3851
GOTERM_B	GO:0001944~vasculat	0.00056	NRP1, FGF9, TGFBR1,	0.84839
P_FAT	ure development	7	VEGFA, VEZF1, ACVR1	6813
GOTERM_B	GO:0001525~angioge	0.00068	NRP1, FGF9, VEGFA,	1.02594
P_FAT	nesis	6	VEZF1, ACVR1	1432
GOTERM_B	GO:0008284~positive	0.00082	NRP1, FGF9, TGFBR1,	1.23018
P_FAT	regulation of cell proliferation	3	VEGFA, PDGFRA, LAMC1, CAPN1	5271
GOTERM_B	GO:0048568~embryo	0.00120	FGF9, TGFBR1, VEGFA,	1.78988
P_FAT	nic organ development	1336	PRDM1, FZD6	8303
GOTERM_B	GO:0001701~in utero	0.00130	ACVR1B, TGFBR1,	1.94718
P_FAT	embryonic development	7887	PDGFRA, PRDM1, ACVR1	6948
GOTERM_B	GO:0001569~patterni	0.00147	NRP1, VEGFA, ACVR1	2.19977
P_FAT	ng of blood vessels	932		7727
GOTERM_B	GO:0051270~regulatio	0.00183	NRP1, TGFBR1, VEGFA,	2.72234
P_FAT	n of cell motion	5303	PDGFRA, HDAC7	4501
GOTERM_B	GO:0051272~positive	0.00239	TGFBR1, VEGFA,	3.54007
P_FAT	regulation of cell motion	5955	PDGFRA, HDAC7	7205
GOTERM_B	GO:0030324~lung	0.00246	FGF9, TGFBR1, VEGFA,	3.64208
P_FAT	development	6202	PDGFRA	063
GOTERM_B	GO:0030323~respirato	0.00268	FGF9, TGFBR1, VEGFA,	3.95853
P_FAT	ry tube development	4573	PDGFRA	1097
GOTERM_B	GO:0007169~transme	0.00314	SS18, NRP1, FGF9,	4.62850
P_FAT	mbrane receptor protein tyrosine kinase signaling pathway	9126	VEGFA, PDGFRA	7909
GOTERM_B	GO:0060541~respirato	0.00315	FGF9, TGFBR1, VEGFA,	4.63889
P_FAT	ry system development	635	PDGFRA	0404

GOTERM_B	GO:0035239~tube	0.00497	NRP1, VEGFA, FZD6,	7.21841
P_FAT	morphogenesis	4059	ACVR1	7546
GOTERM_B	GO:0050679~positive	0.00558		8.06543
P_FAT	regulation of epithelial cell proliferation	1225	FGF9, VEGFA, LAMC1	761
GOTERM_B	GO:0048754~branchin	0.01358		18.5799
P_FAT	g morphogenesis of a tube	7261	NRP1, VEGFA, ACVR1	8277
GOTERM_B	GO:0050678~regulatio	0.01606		21.6021
P_FAT	n of epithelial cell proliferation	7359	FGF9, VEGFA, LAMC1	3729
GOTERM_B	GO:0001763~morpho	0.01737		23.1528
P_FAT	genesis of a branching structure	4774	NRP1, VEGFA, ACVR1	3235
GOTERM_B		0.01770	CKS1B, ACVR1B,	23.5368
P_FAT	GO:0007049~cell cycle	2323	SEPT2, ZWINT, KLK10, STRADB, ACVR1	2028
GOTERM_B	GO:0007242~intracell	0.01822	SS18, MED16, ZWINT,	24.1491
P_FAT	ular signaling cascade	7812	TGFBR1, PREX2, RALA, MED13, STRADB, RAB10	1504
GOTERM_B	GO:0042127~regulatio	0.01885	NRP1, FGF9, TGFBR1,	24.8690
P_FAT	n of cell proliferation	079	VEGFA, PDGFRA, LAMC1, CAPN1	7274
GOTERM_B	GO:0030949~positive	0.01899		25.0328
P_FAT	regulation of vascular endothelial growth factor receptor signaling pathway	3276	FGF9, VEGFA	4091
GOTERM_B	GO:0060037~pharyng	0.01899		25.0328
P_FAT	eal system development	3276	TGFBR1, ACVR1	4091

GOTERM_B	GO:0051489~regulation of filopodium assembly	0.01899		25.0328
P_FAT		3276	TGFBR1, RALA	4091
GOTERM_B	GO:0051491~positive regulation of filopodium assembly	0.01899		25.0328
P_FAT		3276	TGFBR1, RALA	4091
GOTERM_B	GO:0048839~inner ear development	0.01965		25.7844
P_FAT		0924	FGF9, PDGFRA, FZD6	0925
GOTERM_B	GO:0046777~protein amino acid autophosphorylation	0.02253		29.0015
P_FAT		8226	ACVR1B, TGFBR1, PDGFRA	8984
GOTERM_B	GO:0043536~positive regulation of blood vessel endothelial cell migration	0.02435		30.9588
P_FAT		5146	VEGFA, HDAC7	5086
GOTERM_B	GO:0030947~regulation of vascular endothelial growth factor receptor signaling pathway	0.02435		30.9588
P_FAT		5146	FGF9, VEGFA	5086
GOTERM_B	GO:0007423~sensory organ development	0.02437		30.9779
P_FAT		3106	FGF9, VEGFA, PDGFRA, FZD6	4478
GOTERM_B	GO:0030335~positive regulation of cell migration	0.02455		31.1708
P_FAT		4829	VEGFA, PDGFRA, HDAC7	5766
GOTERM_B	GO:0031344~regulation of cell projection organization	0.02455		31.1708
P_FAT		4829	NRP1, TGFBR1, RALA	5766
GOTERM_B	GO:0032925~regulation of activin receptor signaling pathway	0.02702		33.7441
P_FAT		5377	ACVR1B, ACVR1	0827
GOTERM_B	GO:0043583~ear development	0.02771		34.4441
P_FAT		3005	FGF9, PDGFRA, FZD6	7852

GOTERM_B	GO:0040017~positive	0.02935	VEGFA, PDGFRA,	36.0836
P_FAT	regulation of	0512	HDAC7	1374
	locomotion			
GOTERM_B	GO:0048010~vascular	0.02968		36.4171
P_FAT	endothelial growth	8498	NRP1, PDGFRA	9681
	factor receptor			
	signaling pathway			
GOTERM_B	GO:0007178~transme	0.03216	ACVR1B, TGFBR1,	38.8111
P_FAT	mbrane receptor	3802	ACVR1	7791
	protein			
	serine/threonine			
	kinase signaling			
	pathway			
GOTERM_B	GO:0030198~extracell	0.03273	TGFBR1, PDGFRA,	39.3551
P_FAT	ular matrix	8845	LAMC1	5231
	organization			
GOTERM_B	GO:0006468~protein	0.03391	ACVR1B, TAOK1,	40.4530
P_FAT	amino acid	423	TGFBR1, PDGFRA,	1857
	phosphorylation		STRADB, ACVR1	
GOTERM_B	GO:0003006~reprodu	0.03439	FGF9, VEGFA, PDGFRA,	40.8962
P_FAT	ctive developmental	4481	ACVR1	3425
	process			
GOTERM_B	GO:0010595~positive	0.03499		41.4447
P_FAT	regulation of	3479	VEGFA, HDAC7	2423
	endothelial cell			
	migration			
GOTERM_B	GO:0007389~pattern	0.03607	NRP1, TGFBR1, VEGFA,	42.4224
P_FAT	specification process	4299	ACVR1	0642
GOTERM_B	GO:0016477~cell	0.03920	NRP1, TGFBR1,	45.1681
P_FAT	migration	3969	LAMC1, ACVR1	7294
GOTERM_B	GO:0051094~positive	0.03991	ACVR1B, FGF9,	45.7771
P_FAT	regulation of	7874	HDAC7, ACVR1	4378

	developmental			
	process			
GOTERM_B	GO:0043489~RNA	0.04027		46.0753
P_FAT	stabilization	0235	VEGFA, HNRNPD	8053
GOTERM_B	GO:0048255~mRNA	0.04027		46.0753
P_FAT	stabilization	0235	VEGFA, HNRNPD	8053
	GO:0043535~regulatio			
GOTERM_B	n of blood vessel	0.04289		48.2517
P_FAT	endothelial cell	8075	VEGFA, HDAC7	545
	migration			
	GO:0002053~positive			
GOTERM_B	regulation of	0.04551		50.3404
P_FAT	mesenchymal cell	8914	FGF9, VEGFA	4259
	proliferation			
	GO:0009967~positive			
GOTERM_B	regulation of signal	0.04625	ACVR1B, FGF9,	50.9119
P_FAT	transduction	3997	TGFBR1, VEGFA	7941
	GO:0045137~develop			
GOTERM_B	ment of primary sexual	0.04703		51.5146
P_FAT	characteristics	7883	FGF9, VEGFA, PDGFRA	9245
	GO:0010464~regulatio			
GOTERM_B	n of mesenchymal cell	0.04813		52.3449
P_FAT	proliferation	2769	FGF9, VEGFA	7154
	GO:0018107~peptidyl			
GOTERM_B	-threonine	0.04813		52.3449
P_FAT	phosphorylation	2769	ACVR1B, TGFBR1	7154
	GO:0060491~regulatio			
GOTERM_B	n of cell projection	0.04813		52.3449
P_FAT	assembly	2769	TGFBR1, RALA	7154
	GO:0048179~activin			
GOTERM_C	receptor complex	0.00772		8.37631
C_FAT		5891	ACVR1B, ACVR1	3549
	GO:0005604~baseme			
GOTERM_C	nt membrane	0.01717		17.7510
C_FAT		6374	FGF9, VEGFA, LAMC1	1882

GOTERM_C	GO:0043235~receptor	0.03590	ACVR1B, TGFBR1,	33.7969
C_FAT	complex	6244	ACVR1	7922
GOTERM_C	GO:0044420~extracell	0.03647	FGF9, VEGFA, LAMC1	34.2343
C_FAT	ular matrix part	2639		4584
GOTERM_M	GO:0005025~transfor			
F_FAT	ming growth factor	0.00011	ACVR1B, TGFBR1,	0.13243
F_FAT	beta receptor activity,	1	ACVR1	114
	type I			
GOTERM_M	GO:0005024~transfor	0.00111	ACVR1B, TGFBR1,	1.31561
F_FAT	ming growth factor	2285	ACVR1	5047
	beta receptor activity			
GOTERM_M	GO:0004675~transme			
F_FAT	mbrane receptor	0.00111	ACVR1B, TGFBR1,	1.31561
F_FAT	protein	2285	ACVR1	5047
	serine/threonine			
	kinase activity			
GOTERM_M	GO:0019838~growth	0.00302	ACVR1B, TGFBR1,	3.53899
F_FAT	factor binding	3287	PDGFRA, ACVR1	4591
			ACVR1B, NRP1,	
GOTERM_M	GO:0004672~protein	0.00593	TAOK1, TGFBR1,	6.84277
F_FAT	kinase activity	877	PDGFRA, STRADB,	5118
			ACVR1	
GOTERM_M	GO:0046332~SMAD	0.00716	ACVR1B, TGFBR1,	8.20288
F_FAT	binding	6631	ACVR1	8509
GOTERM_M	GO:0016361~activin	0.01104	ACVR1B, ACVR1	12.3821
F_FAT	receptor activity, type I	6651		6803
GOTERM_M	GO:0017002~activin	0.01652	ACVR1B, ACVR1	17.9871
F_FAT	receptor activity	5396		1111
GOTERM_M	GO:0005021~vascular	0.02197	NRP1, PDGFRA	23.2342
F_FAT	endothelial growth	4627		8729
	factor receptor activity			

GOTERM_M	GO:0050431~transforming growth factor	0.02739	TGFBR1, ACVR1	28.1464
F_FAT	beta binding	4499		8303
GOTERM_M	GO:0005161~platelet-derived growth factor	0.03009	VEGFA, PDGFRA	30.4836
F_FAT	receptor binding	3474		855
GOTERM_M	GO:0048185~activin	0.03009	ACVR1B, ACVR1	30.4836
F_FAT	binding	3474	ACVR1B, SEPT2, TAOK1, TGFBR1,	855
GOTERM_M	GO:0000166~nucleotide binding	0.03613	PDGFRA, HNRNP, RALA, STRADB, RBM27, RAB10, PFAS, ACVR1	35.4651
F_FAT		5047		8984

Table S4 : Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway analysis

Category	Term	PValue	Genes	FDR
KEGG_PATH	hsa05200:Pathways in cancer	1.18926E-06	CKS1B, ACVR1B, FGF9, TGFBR1, VEGFA, PDGFRA, RALA, LAMC1, FZD6	0.001067
WAY				852
KEGG_PATH	hsa05212:Pancreatic cancer	0.001096	ACVR1B, TGFBR1, VEGFA, RALA	0.980025
WAY		227		552
KEGG_PATH	hsa05210:Colorectal cancer	0.001714	ACVR1B, TGFBR1, PDGFRA, FZD6	1.528929
WAY		434		339
KEGG_PATH	hsa04060:Cytokine-cytokine receptor interaction	0.005987	ACVR1B, TGFBR1, VEGFA, PDGFRA, ACVR1	5.249746
WAY		652		84
KEGG_PATH	hsa04010:MAPK signaling pathway	0.006403	ACVR1B, TAOK1, FGF9, TGFBR1, PDGFRA	5.605304
WAY		765		215

KEGG_PATH	hsa04350:TGF-	0.026296		21.28084
WAY	beta signaling pathway	843	ACVR1B, TGFBR1, ACVR1	204
