

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

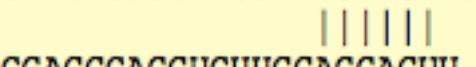
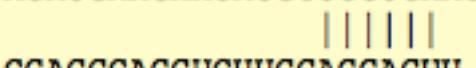
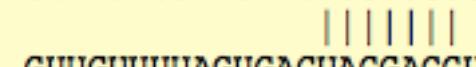
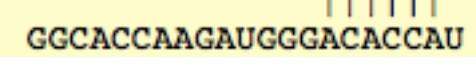
Mirbase ID	CircRNA (5' ... 3')	CircRNA (Top) - miRNA (Bottom) pairing	Context score	context score percentile
hsa_circ_0001451				
hsa-miR-197	(3' ... 5')	GCACACUGCAAGGAAUGGUGAAG  CGACCCACCUCUUCCACCAUU	-0.091	80
hsa_circ_0001451	(5' ... 3')	AGAUGAAGAACACAUGCUGGUGAAC  CGACCCACCUCUUCCACCAUU	-0.109	84
hsa_circ_0001451	(3' ... 5')			
hsa-miR-338-3p	(5' ... 3')	AGGAAGAUGAAGAACACAUGCUGGU  GUUGUUUUAGUGACUACGACCU	0.173	90
hsa_circ_0001451	(3' ... 5')			
hsa-miR-140-3p	(5' ... 3')	AGAACAGAUGAACUAGUGGGACACCAU  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	HNRNPDL	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	GO:0035295~tube	0.00002	NRP1, FGF9, TGFBR1,	0.03959
P_FAT	development	64	VEGFA, PDGFRA, FZD6,	4293
			ACVR1	
GOTERM_B	GO:0007167~enzyme	0.00003	SS18, ACVR1B, NRP1,	0.04993
P_FAT	linked receptor protein	32	FGF9, TGFBR1, VEGFA,	8993
	signaling pathway		PDGFRA, ACVR1	
GOTERM_B	GO:0043009~chordate	0.00025	ACVR1B, FGF9,	0.37679
P_FAT	embryonic	1	TGFBR1, PDGFRA,	1327
	development		PRDM1, FZD6, ACVR1	
GOTERM_B	GO:0048514~blood	0.00025	NRP1, FGF9, TGFBR1,	0.38333
P_FAT	vessel morphogenesis	6	VEGFA, VEZF1, ACVR1	6096
	GO:0009792~embryo			
GOTERM_B	nic development	0.00026	ACVR1B, FGF9,	0.39552
P_FAT	ending in birth or egg	4	TGFBR1, PDGFRA,	4072
	hatching		PRDM1, FZD6, ACVR1	

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

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

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

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

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

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

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

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

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

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