

(A) MFE secondary structure

(B) Centroid secondary structure

(C)

(D)

(E)

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Supplemental Table 1 Information regarding the primers used.

Primers Names	Primer sequences (5' to 3')	Size (bp)	Reference sequences	Application
<i>oar-lncRSFD1</i>	F: GCCTAGTCTGTGTCTTCACAAAAG R: CAGTTATGTTAGCCTTCCACACAG	112	<i>lncRSFD1</i>	mRNA expression profile
<i>oar-PDE4DIP</i>	F: AGCGGAAAGAACGGATGCTG R: AGCAGGCCCTGAATCTCCAT	85	XM_027973716.2	
<i>oar-GAPDH</i>	F: CCTGCCAAGTATGATGAGAT R: TGAGTGTCTGCTGTTGAAGT	119	NM_001190390.1	
<i>mmu-PPARγ</i>	F: GTGCCAGTTTTCGATCCGTAGA R: GGCCAGCATCGTGTAGATGA	142	NM_011146.4	
<i>mmu-FABP4</i>	F: CAGAAGTGGGATGGAAAGTCG R: CGACTGACTATTGTAGTGTTTGA	169	NM_024406.4	qRT-PCR
<i>mmu-C/EBPα</i>	F: CAAGAACAGCAACGAGTACCG R: GTCACTGGTCAACTCCAGCAC	124	NM_001287514.1	
<i>mmu-PDK4</i>	F: AAACCCAAGCCACATTGGAAGTA R: CGCAGAGCATCTTTGCACAC	89	NM_013743.2	
<i>mmu-FASN</i>	F: ATTGGCTCCACCAAATCCAAC R: CCCATGCTCCAGGGATAACAG	90	NM_007988.3	
<i>mmu-CyclinE</i>	F: CCGTCTTGAATTGGGGCAATA R: GAGCTTATAGACTTCGCACACC	167	NM_007633.2	
<i>mmu-PCNA</i>	F: GAACCTCACCAGCATGTCCA R: ATTCACCCGACGGCATCTTT	221	NM_011045.2	
<i>mmu-P21</i>	F: CCTGGTGATGTCCGACCTG R: CCATGAGCGCATCGCAATC	103	NM_007669.5	
<i>mmu-β-actin</i>	F: GGCTGTATTCCCCTCCATCG R: CCAGTTGGTAACAATGCCATGT	154	NM_007393.5	
REases				
Pro-R	CCGCTCGAGGGGCCTCTTGCATGTCACTTA		<i>XhoI</i>	
Pro-F1	CGGGGTACCGACCACTGACAGAGCACCTATT	2957		luciferase
Pro-F2	CGGGGTACCGGTCTGCCTCTGAATGAGCTT	2125		reporter
Pro-F3	CGGGGTACCTCTGATTCTTTCTTTCTGAGCC	1599	<i>KpnI</i>	vector
Pro-F4	CGGGGTACCCCCCATCTCCTCATCAAGTAAACA	1275		construction
Pro-F5	CGGGGTACCACAAAAGCCATCCTCTTTCTTCCA	1140		
Pro-F6	CGGGGTACCCTTGACAGGCTCTCACCACAA	947		

Note, REases means restriction endonuclease. The underlined letter indicates the restriction site.

Supplemental Table2 Mature sequences of miRNAs adsorbed by *lncRSFD1* in different species.

miRNAs	Names	Species	Mature Sequences (5'→3')
miR-30a-3p	oar-miR-30a-3p	Ovis aries	CUUUCAGUCGGAUGUUUGCAG
	chi-miR-30a-3p	Capra hircus	CUUUCAGUCGGAUGUUUGCAG
	gga-miR-30a-3p	Gallus gallus	CUUUCAGUCGGAUGUUUGCAGC
	ssc-miR-30a-3p	Sus scrofa	CUUUCAGUCGGAUGUUUGCAGC
	hsa-miR-30a-3p	Homo sapiens	CUUUCAGUCGGAUGUUUGCAGC
	mml-miR-30a-3p	Macaca mulatta	CUUUCAGUCGGAUGUUUGCAGC
	ggo-miR-30a-3p	Gorilla gorilla	CUUUCAGUCGGAUGUUUGCAGC
	mmu-miR-30a-3p	Mus musculus	CUUUCAGUCGGAUGUUUGCAGC
	rno-miR-30a-3p	Rattus norvegicus	CUUUCAGUCGGAUGUUUGCAGC
miR-329	oar-miR-329b-5p	Ovis aries	GAGGUUUUCUGGGUUUCUGUUUC
	bta-miR-329b	Bos taurus	AGAGGUUUUCUGGGUUUCUGUUU
	pal-miR-329b-5p	Pteropus alecto	AGAGGUUUUCUGGGUUUCUGUUU
	cfa-miR-329a	Canis familiaris	AGAGGUUUUCUGGGUUUCUGUUU
miR-431	oar-miR-431	Ovis aries	UGUCUUGCAGGCCGUCAUGCAGG
	bta-miR-431	Bos taurus	UGUCUUGCAGGCCGUCAUGCAGG
	hsa-miR-431-5p	Homo sapiens	UGUCUUGCAGGCCGUCAUGCA
	mml-miR-431	Macaca mulatta	UGUCUUGCAGGCCGUCAUGCA
	mmu-miR-431-5p	Mus musculus	UGUCUUGCAGGCCGUCAUGCA
	rno-miR-431	Rattus norvegicus	UGUCUUGCAGGCCGUCAUGCA
	cpo-miR-431-5p	Cavia porcellus	UGUCUUGCAGGCCGUCAUGCA

Supplemental Table 3 Prediction of the promoter region of *IncRSFD1* using BDGP and Softberry.

Software	Start	End	Score	Promoter Sequence
BDGP	425	475	0.91	AGGGAGAGTCTATGAAAAAGGAGCTTCTGGAAGTGAAGAAC C AAACT ATCC
	1291	1341	0.99	TATGCCACTATATAAAAAAAGTATGGAAAGATGCCACCTA A CAAGTT GAT
	2156	2206	0.82	GGGCCACTTCTATATGTGCCTGTTTCAAGCTAAGCATATC T TTTCCTGG G
	2593	2643	0.94	ACCGGAGGTCCTTAAAACAGCAGGAAGGATGGGCCTGTGC C CCTTCT TCA
	2699	2749	0.85	TGGAAGGGGTCATAGATATGGCCTCGTGCGCAGGGTGAAA G GCAGA GGGC
	2753	2803	0.83	CCTGCACTTGAGGAATAACAAGGCAGGGTGCCCGTGGCTC A GCTCTA AGG
	3430	3480	0.89	GATATATATTTATATATGTTGCTATAGTGCTGTGTGGAAG G CTAACATA A
	Position	LDF	TATA box	
Soft- berry	2191	+1.997	2166	+4.820 TATATGTG
	2633	+0.373	2603	+4.049 CTAAAAAC
	1331	-0.513	1299	+7.629 TATATAAA