

Characterization of the promoter region of the bovine acyl-CoA synthetase 1 gene: Roles of E2F1, Sp1, KLF15, and E2F4

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Table S1.**Primers used in the expression and functional analysis of the ACSL1 promoter**

Reaction	primer	Primer sequence(5'-3')	Binding region	Size (bp)
qRT-PCR	ACSL1 forward	CTTCGCAGTGGCATCAATTAG	+53285/+53305	178
	ACSL1 reverse	GTCCGTAGCCTTCGTAGAAC	+55111/+55131	--
	β-actin forward	CATCGGCAATGAGCGGTTCC	--	147
	β-actin reverse	ACCGTGTGGCGTAGAGGTC	--	--
Promoter cloning	ACSL1 promoter forward	TGGCAAACACTAGTACACCACAGACC	-1933/-1909	1954
	ACSL1 promoter reverse	CTGTCACTACAGCCCACTG	+3/+21	--
	ACSL1 promoter forward 1	GAGCTCT GGCAAACACTAGTACACCACAGACC	-1933/-1909	1954
	ACSL1 promoter forward 2	GAGCTCTT GCTGTACCACGTGCAGGAG	-1634/-1613	1655
	ACSL1 promoter forward 3	GAGCTCGGTC CGGAACAGTCAGATATG	-1328/-1307	1349
	ACSL1 promoter forward 4	GAGCTCC AGTAGAGGTTATCTGTAC	-1034/-1014	1055
	ACSL1 promoter forward 5	GAGCTC AGAAGTGGCAGGTGGAC	-730/-712	751
	ACSL1 promoter forward 6	GAGCTCGCCT GTGGATGAAGGTGGAAG	-436/-415	457
	ACSL1 promoter forward 7	GAGCTCTT GTGAAATCCAGGCAGTCC	-325/-304	346
	ACSL1 promoter forward 8	GAGCTCC GAGCTCGCGGGGCGGAGCGGGGC	-140/-120	161
	ACSL1 promoter forward 9	GAGCTCC GAGCTCTGCAGCGAGCGGCTGGAGCG	-80/-120	101
	ACSL1 promoter reverse 1	CTCGAGCT GTCACTACAGCCCACTG	+3/+21	--
5' RACE	R1	CGGGAACACCTCGTACGACTCGG	+20843/+35338	507
	R2	GTAGTGACGGCCGTGGAGGTGAC	+39636/+39660	289
Site-directed mutagenesis	E2F1 forward	GCAGGGCCGCGGTGAGG AAA GGGCTGAGACGGGG	-209/-176	346
	E2F1 reverse	CCCCGTCTCAGCC TTT CCTACGGCGCCCTGC	--	--
	Sp1 forward	GCGGGGTCCGAGCG TTT CGGGGCGGGCCCGG	-175/-143	346
	Sp1 reverse	CCGGCCCCCGCCCG AAA CGCTCGGACCCCGC	--	--
	KLF15 forward	GGTCCGAGCGGGCC AAA GCGGGCCGGGGGGC	-170/-138	346
	KLF15 reverse	GCCCCCGGCCCG TTT GCCCGCTCGGACC	--	--
	E2F4 forward	CCGAGCGGGCCGGG TTT GGCCGGGGCGGGG	-167/-134	346
	E2F4 reverse	CCCCCCCCCGCC AAA CCCCCGCCCGCTCGG	--	--
	KLF15-Sp1 forward	GCGGGGTCCGAGCG TTTCCAAA GCGGGCCCGG	-175/-143	346
	KLF15-Sp1 reverse	CCGGCCCCCG TTTGGAAA CGCTCGGACCCCGC	--	--
	E2F4-Sp1 forward	GCGGGGTCCGAGCG TTTCCGGTT GGCCCGG	-175/-143	346
	E2F4-Sp1 reverse	CCGGCC AAA CCCCCG AAA CGCTCGGACCCCGC	--	--
	KLF15- E2F4 forward	CCGAGCGGGCC AAA G TTT GGCCGGGGCGGGG	-167/-134	346
	KLF15- E2F4 reverse	CCCCCCCCCGCC AAACTTT GGCCCCGCTCGG	--	--
EMSA	E2F1 forward	GCAGGGCCGCGGTGAG GGGGG GCTGAGACGGGG	-209/-176	346
	E2F1 reverse	CCCCGTCTCAGC CCGCC CCTACGGCGCCCTGC	--	--
	Sp1 forward	GCGGGGTCCGAGCG GGGCC GGGGCGGGCCCGG	-175/-143	346
	Sp1 reverse	CCGGCCCCCGCC GGCCC CGCTCGGACCCCGC	--	--
	KLF15 forward	GGTCCGAGCGGGCC GGGGC GGGGCCGGGGGGC	-170/-138	346
	KLF15 reverse	GCCCCCGGCC CGCCC GGCCCCGCTCGGACC	--	--
	E2F4 forward	CCGAGCGGGCCGGG GCGG GGCCGGGGCGGGG	-167/-134	346
	E2F4 reverse	CCCCCCCCCGCC CCGC CCCGCCCGCTCGG	--	--