

Additional file 1, Supplementary table S1: Stability of the expression levels of reference genes

Tissue	Gene	GS	Infected	Fold^a	p^b
Liver	<i>SFRS4</i>	9991 ± 435	9174 ± 763	0.92	0.40
	<i>ACTB</i>	240189 ± 14225	413546 ± 61026	1.72	0.055
	<i>CLIC1</i>	5029 ± 579	8788 ± 1022	1.75	0.02
	<i>RPLA35A</i>	250703 ± 3446	425551 ± 61529	1.70	0.03
Udder	<i>SFRS4</i>	7143 ± 922	9591 ± 632	1.34	0.06
	<i>ACTB</i>	45225 ± 1775	150757 ± 15931	3.33	0.00
	<i>CLIC1</i>	11184 ± 2106	128123 ± 16900	11.4	0.00

Values are mean values (± S.E.M.) of copy numbers, relative to the same amount of cDNA input in every sample. GS (Gold standard), n=6; Infected (*E. coli*, 24 h), n=5; ^aFold, fold change of mean values (infected vs GS samples); ^bP value of difference (Student's t-test).

Additional file 1; Supplementary Table S2A: Primers for real time quantitative PCR.

Gene	Accession#	cDNA generation (5'-)	Forward primer (5'-)	Reverse primer (5'-)	Amplicon (bp)
SCD1	NM_173959.4	GCAGCAAGTGGGCCGGCAT	CACGCAAAGCAGGCTCAGGA	GCATCTGGGCTCTCAGACACT	110
ACACA	NM_174224.2	TTTCAAGAGAAGTTCTGGGAGCT	GTTCTCATTGCCAACAATGGCA	CAGCCAGCCCAAAGCTGCTTGAC	266
C/EBP α	NM_176784.2	GCAGTTGCCCATGGCCTTG	GCAAGAGCCGGGACAAGG	TCGGGCAGCTGACGGAAG	151
C/EBP β	NM_176788.1	5'-TTTTTTTTTTTTTTTTTTTTTN	GACAAGCACAGCGACGAGTACA	CGACAGTTGCTCCACCTTCTTC	198
C/EBP δ	NM_174267.2	5'-TTTTTTTTTTTTTTTTTTTTTN	AACCCGCTGCCTTCTACGA	CCCGCTTTGTGGTTGCTGT	152
NFYA	NM_001014956.1	5'-TTTTTTTTTTTTTTTTTTTTTN	AGGCGGACGATTTTTCTCT	AGTGGGAAACTGTGAGGAAT	150
SREBP1a	NM_001113302.1	CAGCTTCTGCCGCTGCCAGA	GCCAGCCTGGCAATGTGTGA	CAGGTACACAGGAGCAGCT	103
NF- κ B (p65)	NM_001080242.2	AAGTTGATGGTGCTGAGAGATG	TTTTTCACAAGCTGACGTGCAC	GCTCTGAAGGTCTCGTACGT	211
NF- κ B (p50)	NM_001076409.1	CACTGTCCCCGTTCTCATC	GTCAAACCTCCAGAATGGCAGA	GAAATCCTCTCTGTTTAGGTTGCTC	179
SFRS4	NM_001101231.1	CTTGTGGGCATCTGCATAAGTC	ATGGCAGTTACGGTTCTGGAC	CCTGCCTGACGCATATAATCC	156

The source files used to derive the primers are indicated (accession#).

Additional file 1; Supplementary Table S2B: Primers for plasmid constructs, chromatin assay and 5'RACE experiment.

Primer name	Sequence (5'-3') ^{*,#}	Applications
pf1	AGCT <u>GGTACCG</u> GAGCAACACCTGCCAGAC	WT promoter construct (PL)
pf2	AGCT <u>GGTACCG</u> TGACCATTGGCTGAACCTCT	WT promoter construct (PS)
pr2	AGCT <u>AAGCTT</u> GCATCTGGGCTCTCAGACACT	WT promoter construct (PL and PS)
mpf3	CGAAATGGCCAGTTATG <u>CCGAAGGCAATTCCAAACAACG</u>	Mutation for distal site
mpr4	TGCCTTCGGCATAACTGGCCATTCGTGGAGAAAGGAC	Mutation for distal site
mpf5	CGAATAAAAGAGGACATATG <u>TGTTACGGGACACAGTCACCCCCT</u>	Mutation for proximal site
mpr6	CGTAACACATATGTCCTCTTTTATTCGTTCCAACAAG	Mutation for proximal site
pfA	GGGAAAGGCCATTTTCGTGGAG	CHART-PCR for area A
prA	ATTGATTGGCTGCTGTGACCAT	CHART-PCR for area A
pfB	GTGCCATCCATTTGCGAATTG	CHART-PCR for area B
prB	GGCTCGGCGCAATCTGCTGT	CHART-PCR for area B
pfC	CTCCCACGGTGAACCAACTCT	CHART-PCR for area C
prC	GCATCTGGGCTCTCAGACACT	CHART-PCR for area C
Rpf1	GGACACTGACATGGACTGAAGGAGTA	5'RACE nested
Rpf2	CGACTGGAGCACGAGGACTGA	5'RACE
Rpr1	GGCTCCCAAGTGTAACAGAGAC	5'RACE nested
Rpr2	TGCAGGTGGGGATCAATGTGA	5'RACE

*, Mutated nucleotides are shown as bold letters.

#, Underlined are artificially introduced restriction site.

Additional file 1, Supplementary Table S3A: mRNA levels in Tissues.

TFs	Liver			MG			
	GS	Infected	fold inductio n vs GS	GS	Neighbo r	Infected	fold inductio n vs GS
CEBP- β	49 \pm 5	164 \pm 41*	3.32	36 \pm 6	59 \pm 7	301 \pm 30**	8.36
CEBP- α	832 \pm 96	1509 \pm 186*	1.81	85 \pm 6	160 \pm 10	245 \pm 38**	2.88
CEBP- δ	51 \pm 6	79 \pm 7*	1.55	16 \pm 4	43 \pm 9	163 \pm 26**	10.18
NFYA	409 \pm 18	578 \pm 64*	1.41	461 \pm 65	629 \pm 39	774 \pm 63**	1.68
SREBP1 a	881 \pm 143	505 \pm 39*	0.57	2538 \pm 635	979 \pm 122	880 \pm 102*	0.35
p65	115 \pm 5	215 \pm 27**	1.86	117 \pm 16	196 \pm 11	242 \pm 19**	2.07
p50	655 \pm 35	939 \pm 81*	1.43	1956 \pm 302	2822 \pm 89	5962 \pm 463**	3.05

Values are mean (\pm S.E.M.) copy numbers relative to 75 ng of total RNA used as input for cDNA generation; MG, mammary gland; TF, transcription factor; GS or Infected, tissues gold standard or infected cows; Neighbor, sterile udder quarter neighboring an infected one.

Additional file 3, Supplementary Table S3B: mRNA levels in model cells.

TF	HepG2	MAC-T
	Mean \pm SEM	Mean \pm SEM
SREBP1a	21 \pm 9	453 \pm 51
C/EBP- α	41 \pm 6	173 \pm 6
C/EBP- β	160 \pm 10	76 \pm 3