

Supplementary Table S1. GenBank accession number, sequence and amplicon size of primers used to analyze gene expression by quantitative PCR.

Accession no.	Gene	Primers ¹	Primers (5'-3')	Length (bp) ²
NM_175781.1	<i>ITGB2</i>	F.1231	GACACCCTGAAAGTCACCTACGA	108
		R.1338	GAAGGTGATCGGGACGTTGAT	
BC146107.1	<i>TLN1</i>	F.942	TTCCTGCCCAAGGAGTATGTG	100
		R.1041	AGCGTACCTTGGCCTCAATCT	
XM_015460928.1	<i>LGALS8</i>	F.576	CCCGGTCATCCCCTATGTTG	100
		R.675	CTGGAACCTGTCCGAGTCAC	
XM_003586675.4	<i>LCN2</i>	F.393	ACAGTGCGGGTGGTGAACA	100
		R.492	TCCCGTAAAGGGTGATCTTGA	
NM_180998.2	<i>LTF</i>	F.631	CCAGGGAGCTGTGGCTAAAT	135
		R.765	AAGTATGGTTCCCGGGAGGA	
NM_001113725.2	<i>S100A8</i>	F.19	ATTTTGGGGAGACCTGGTGG	124
		R.142	ACGGCGTGGTAATTCCTTT	
NM_174197.2	<i>TLR2</i>	F.3182	CCATGTCTGGAGAGGGTGTT	102
		R.3283	GGGGACACAAAACAGCACTT	
NM_174814.2	<i>YWHAZ</i>	F.	TGAAAATGAAAGGAGACTACTACCG	84
		R.	GCTGTGACTGGTCCACAATC	
NM_173979.3	<i>ACTB</i>	F.258	ACCAACTGGGACGACATGGA	149
		R.406	GTCTCGAACATGATCTGGGTCAT	
NM_174178.2	<i>SDHA</i>	F.	CTGAAGCAGGTTTCAACACG	113
		R.	GTTGTCCTCCTCCATGTTCC	
NM_174093.1	<i>IL1B</i>	F.30	ATTCTCTCCAGCCAACCTTCATT	100
		R.129	TTCTCGTCACTGTAGTAAGCCATCA	
NM_001206735.1	<i>IL1R</i>	F.897	CCCGGGCGATAAAGCTGATT	104
		R.1000	AAGCCAGGATCCCAAGACCA	
NM_173966.3	<i>TNF</i>	F.174	CCAGAGGGAAGAGCAGTCCC	114
		R.287	TCGGCTACAACGTGGGCTAC	
NM_001034034.2	<i>GAPDH</i>	F.908	TTGTCTCCTGCGACTTCAACA	103
		R.1010	TCGTACCAGGAAATGAGCTTGAC	

¹ Primer direction (F – forward; R – reverse) and hybridization position on the sequence are highlighted.

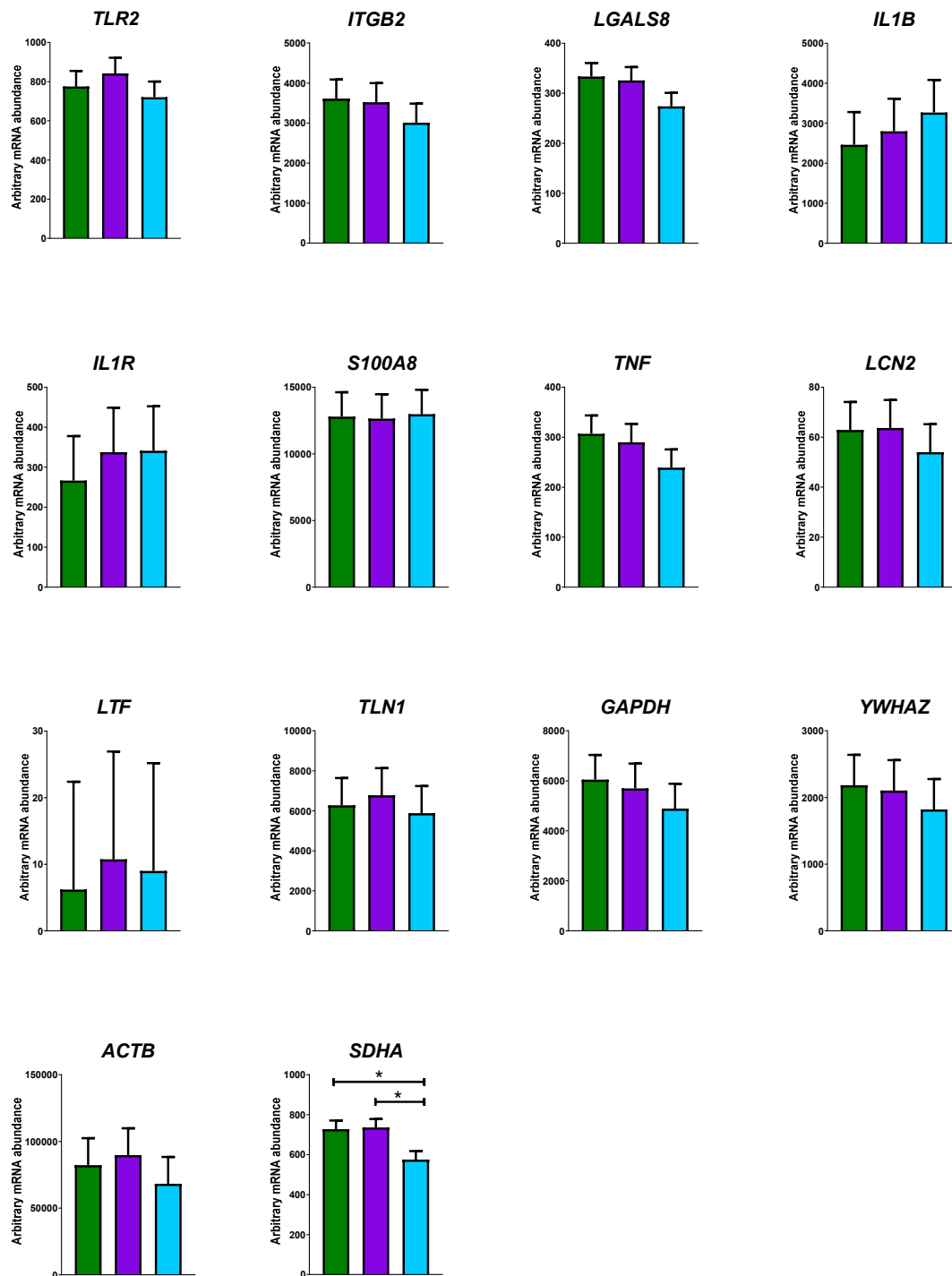
² Amplicon size in base pair (bp).

Supplementary Table S2. Sequencing results obtained from PCR product of *Bos taurus* specific primers for genes under investigation.

Gene	Sequence
<i>ITGB2</i>	ATCGAATCGCAGGTGGACAGCCCAGAGGGACTGCGACGGCGTCCAGATCAAC GTCCCGATCACCTTCAAGAGGG
<i>TLN1</i>	ACCCCGTCCGCAATTCCTTCTCTACGTGCAGGCACGAGATGCCTAGGAAATGG CTCCCATCCTGTCTCCTCTGCTAAAGGCC
<i>LGALS</i> 8	AGCTTGGAACGTTGATTGTACTACGTGGGCATGTTTCCTAGTGACTCGGACAGG TTCCAGA
<i>LCN2</i>	CATAGTGTACTTCAAGAAGGTTCAAAGGAAAAAGACGTACTTCAAGATCACCC TTTACGGGAA
<i>LTF</i>	CTCTTTGGCTCTCCCCCGGCCAGAGGGACCTGCTGTTCAAAGACTCTGCTCTT GGTT
<i>S100A</i> 8	GTGTGCCATTAACCTCCCTGATTGACGTCTACCACAAGTACTCCCTGAAAAAAG GGAATTACCACGCC
<i>TLR2</i>	TTAAAAGAGTCACAATAGAAAGCTTAAGGTTTTTCTGGTTCCTTGTTTCACAA CATTTAAATTCGGCGTTAGAATATTTGGATCGTCATAAAAACTTA
<i>ACTB</i>	CACTTCTACACGAGCTGCGTGTGGCCCCCTGAGGAGCACCCCGTGCTGCTGAC CGAGGCCCCCTCTGAACCCCAAGGCCAACCGTGAGAAGATGACCCAGATCAT GTTCAGAGACA
<i>GAPD</i> <i>H</i>	TCTACCTTCGATGCTGGGGCTGGCATTGCCCTCAACGACCACTTTGTCAAGCTC ATTCCTGGTACGAA
<i>IL1B</i>	ACAGCCATGGCACCGTACCTGAACCCATCAACGAAATGATCGGCTTACGTCAC AGTGGACAGAGCACAATAGCACCCCC
<i>IL1R</i> <i>TNF</i>	TGTGAGTCCAGCTAATGAGACAATGGAAGTGGTCTTGGGATCCTGGCTTACAG TCACTCTCCGGGGCAGCTCCGGTGGTGGGACTCGTATGCCAATGCCCTCATGG AA

Supplementary Table S3. Average of the amplification efficiencies of the gene used in the study.

Gene	Efficiency
<i>ACTB</i>	1.72
<i>GAPDH</i>	1.82
<i>IL1B</i>	1.78
<i>IL1R</i>	1.87
<i>ITGB2</i>	1.82
<i>LCN2</i>	1.84
<i>LGALS8</i>	1.84
<i>LTF</i>	1.86
<i>S100A8</i>	1.82
<i>SDHA</i>	1.83
<i>TLN1</i>	1.79
<i>TLR2</i>	1.83
<i>TNF</i>	1.77
<i>YWHAZ</i>	1.83



Supplementary Figure S1. Least square means \pm SEM of the arbitrary mRNA abundance of genes in leukocytes isolated from blood of mid-lactating Holstein cows collected in Li-heparin (green columns), K-EDTA (purple columns), or Na-citrate (light blue columns) tubes; * indicate significant difference between anticoagulants ($p < 0.05$)