

Table S1. Primer sequences

Primer	Forward Sequence (5'-3')	Reverse Sequence (3'-5')	NCBI Accession number
GAPDH	CTGGGCTACACTGAGCACC	AAGTGGTCGTTGAGGGCAATG	NM_001357943.2
VCAM-1	AATGCCTGGGAAGATGGTCG	GATGTGGTCCCCTCATTCGT	NM_001078.4
ICAM-1	TATAAAGGATCACGCGCCCC	AACAACCTGGGCTGGTCACA	NM_000201
E-Selectin	CTGGCAGTTCCGGGAAAGAT	AGCCAGAGGAGAAATGGTGC	NM_000450.2
NFκB-p65	GCGAGAGGAGCACAGATACC	AGGGGTTGTTGTTGGTCTGG	NM_001145138.1
JAM-C	GCAATCGAACCCCAAGTGGTA	GTCACCTGGCTTCACTCAATTT	NM_001205329.1
VE-Cadherin	CACGCCTCTGTCATGTACCA	TGTACTTGGTCTGGGTGAAGA	NM_001795.5
P120 Catenin	GGGCCAAGAAGGGCAAAGA	GCTGAGGCTTCTAGGATGGC	NM_001085458.2
ESAM	TAAGCCCGCTGTCCAATACC	TGGGCCTTGCAGACATAGAC	NM_138961.3

Primer sequences utilized in mRNA analysis via qPCR. Primers were synthesized by Integrated DNA Technologies (Coralville, Iowa, USA). All primers were first checked for suitability in target species using the NCBI NIH PrimerBLAST system (available at <https://www.ncbi.nlm.nih.gov/tools/primer-blast/>). Subject to their suitability the primers were then QC checked using the Sequence Manipulation Suite available at (www.bioinformatics.org/sms2/pcr_primer_stats.html) prior to their use.