

Table 1 Primer sequences for qRT-PCR

Species	Gene	Primer Sequence (5'-3')	Size (bp)
<i>P.ovis</i>	β -actin	F: TGAATTGCCTGATGGTCAAG R: TGGCGAACAAGTCTTTACGG	92
	<i>PsoCRT</i>	F: GCCGATGCAGATTGGTCA R: TGCATGTTTGTATGCCTTT	120
	PQ498351	F: CTTTGTCAAGCTCATTTCTCTGG R: TCTTCCTCTTGTGCTCTTGC	133
	GAPDH	F: CTTTGTCAAGCTCATTTCTCTGG R: TCTTCCTCTTGTGCTCTTGC	133
Human (HaCaT)	NM_001256799.3	F: AACCTCTTCGAGGCACAAGG R: GTCCTGGAAGGAGCACTTCAT	197
	IL-1 β	F: TCCTTCTCCACAAACATGTAACAA R: TCACCAGGCAAGTCTCCTCA	143
	NM_000576.3	F: GCCCATGTTGTAGCAAACCC R: TGAGGTACAGGCCCTCTGAT	133
	IL-6	F: GAGTGTGGAGACCATCAAGGA R: TGGACATTCAAGTCAGTTACCGAA	114
	NM_001318095.2	F: CACCTTCGAGTCTGTGGCTT R: CCACATCTTCTCCAAAGCTTAAA	149
	TNF- α	F: CGCAAGAAATCCCGTCCCT R: GCAACGCGAGTCTGTGTTTT	108
	NM_000594.4	F: CAGCTCTACCGAAAGCCACT R: GAGCCAGGTGAAGCACGAAA	112
	IFN- γ	F: GCCTTACTGTGAGTCTGGTTGA R: GACAGGCACCTTCTGGCAT	183
	NM_000619.3	F: GAGTGTGGAGACCATCAAGGA R: TGGACATTCAAGTCAGTTACCGAA	114
	IL-36	F: CACCTTCGAGTCTGTGGCTT R: CCACATCTTCTCCAAAGCTTAAA	149
	XM_054341389.1	F: CGCAAGAAATCCCGTCCCT R: GCAACGCGAGTCTGTGTTTT	108
	VEGF	F: CAGCTCTACCGAAAGCCACT R: GAGCCAGGTGAAGCACGAAA	112
	NM_001025367.3	F: GCCTTACTGTGAGTCTGGTTGA R: GACAGGCACCTTCTGGCAT	183
	CCL27	F: GAGCCAGGTGAAGCACGAAA R: GACAGGCACCTTCTGGCAT	112
	NM_006664.4	F: GCCTTACTGTGAGTCTGGTTGA R: GACAGGCACCTTCTGGCAT	183
	IVL	F: GAGCCAGGTGAAGCACGAAA R: GACAGGCACCTTCTGGCAT	112
	NM_005547.4	F: CGGCAAATCCTGAAGAATCCA R: GTGCTTTCTGTGCTTGTGTCC	189
	FLG	F: CGGCAAATCCTGAAGAATCCA R: GTGCTTTCTGTGCTTGTGTCC	189
	NM_002016.2	F: GGCATGGAGTCGTGTGGCATC R: CGTGTGGCGTACAGGTCCTTG	90
	β -actin	F: GGCATGGAGTCGTGTGGCATC R: CGTGTGGCGTACAGGTCCTTG	90
Rabbit	NM001101683.1	F: TCGTGCAATCCTAAAGAACCC R: ATGCCTTTTGTGCTTTTCGCT	190
	FLG	F: TCGTGCAATCCTAAAGAACCC R: ATGCCTTTTGTGCTTTTCGCT	190
	XM_008264430.3	F: GGCACAACAGATCGCTTTGG R: CAGGTCATTTTCATTGCCACTGT	131
	IL-1 β	F: GGCACAACAGATCGCTTTGG R: CAGGTCATTTTCATTGCCACTGT	131
	NM_001082201.1	F: GACGACCACGATCCACTTCA R: AGAGCCCATGAAATTCCGCA	115
	IL-6	F: GACGACCACGATCCACTTCA R: AGAGCCCATGAAATTCCGCA	115
	NM_001082064.2	F: ACAGCCACTGTCAAACAAGC R: GAGCCAGATGAAGCACGAAAG	101
	CCL27	F: ACAGCCACTGTCAAACAAGC R: GAGCCAGATGAAGCACGAAAG	101
	XM_002707938.4	F: CGCAAGAAATCCCGTCCCT R: GCCTCGGCTTGTACATCT	163
	VEGF	F: CGCAAGAAATCCCGTCCCT R: GCCTCGGCTTGTACATCT	163
	XM_051854688.1	F: GCCTCGGCTTGTACATCT R: TCGTGCAATCCTAAAGAACCC	190
	FLG	F: TCGTGCAATCCTAAAGAACCC R: ATGCCTTTTGTGCTTTTCGCT	190
	XM_008264430.3	F: AAGTCGGCCCCGGATCAATAG R: AGGAAGGGGACCCCGAAG	126
	LOR	F: AAGTCGGCCCCGGATCAATAG R: AGGAAGGGGACCCCGAAG	126
	XM_002715344.5	F: AAGTCGGCCCCGGATCAATAG R: AGGAAGGGGACCCCGAAG	126