

Table S1. Swine specific oligonucleotide forward (F) and reverse (R) primer sequence (5'-3'), amplicon length of the evaluated genes, and primer efficiency in the standard curve on qPCR.

Target name	GenBank ID	Primer (5'-3')	Amplicon	Efficiency (%)	Melting temperature	Reference
<i>PGR</i>	NM_001166488.1	F: 5' AACACCAAACCCGACACTTC 3' R: 5' CGAAAACCTGGCAGTGACTT 3'	107 bp	89.80	80.22	This study
<i>VEGF</i>	X81380	F: 5' CGAAGTGGTGAAGTTCATGG 3' R: 5' ACACAGGACGGCTTGAAGAT 3'	120 bp	99.07	83.96	This study
<i>FLT1</i>	AJ245445.1	F: 5' ACCCCGGAAATCTATCAGATCA 3' R: 5' GGTCGCCTAGTTTTTCCACAAG 3'	94 bp	87.97	79.63	This study
<i>KDR</i>	AJ245446.1	F: 5' CTCAGCAGGATGGCAAAGACTA 3' R: 5' GGGGTCACACACTTCCTCTTCT 3'	128 bp	86.90	81.56	This study
<i>STAR</i>	NM213755	F: 5' CAGACTTTGGAGAGATGCCTGA 3' R: 5' ATCCCTTGAGGTCAATGCTGAG 3'	138 bp	90.10	86.48	This study
<i>CYP11A1</i>	NM_214427.1	F: 5' CCTGCCAAGACATTGGTACAAG 3' R: 3' AGGTCCCTTTCTTTACCCAACC 3'	113 bp	86.41	84.39	This study
<i>HSD3B1</i>	NM_001004049.1	F: 5' TGGTCATCCACACTGCCTCTAT 3' R: 5' GGAGCTGGGTACCTTTCACATT 3'	90 bp	91.11	83.2	This study
<i>LHCGR</i>	XM_021085888.1	F: 5' CATAACCACCGTACCAGCAA 3' R: 5' TTCAGCTCCAGGGAAATCAG 3'	135 bp	98.80	78.13	This study
<i>HSD11B2</i>	AF414125	F: 5' GCGAAAGCTTCCCACTGAAC 3' R: 5' AGGGTCTGTTTGGGCTCATG 3'	59 bp	102.63	83.2	[1]

NR3C1	AF141371	F: 5' GATCATGACCGCACTCAACATG 3' R: 5' TTGCCTTTGCCCATTTTCAC 3'	68 bp	97.11	82.31	[1]
NR3C2	XM_013978840.2	F: 5' TTGCCTTGAGCTGGAGATCG 3' R: 5' GAACTGCAGGCTGATCTGGT 3'	143 bp	106.17	82.01	[1]
TNF	NM_214022.1	F: 5' GCCCTTCCACCAACGTTTTTC 3' R: 5' CAAGGGCTCTTGATGGCAGA 3'	97 bp	—	—	This study
IFNG	NM_213948.1	F: 5' GCGCAAAGCCATCAGTGAAC 3' R: 5' GCTCTCTGGCCTTGGAACAT 3'	105 bp	—	—	This study
IL1B	XM_021085847.1	F: 5' TTTGAAGAAGAGCCCATCATCC 3' R: 5' CCAGCCAGCACTAGAGATTG 3'	119 bp	97.98	81.41	[2]
UBB	U72496.1	F: 5' ACCAGCAGCGTCTGATTTTTT 3' R: 5' CAAGTGCAGGGTGGACTCTT 3'	92 bp	100.03	82.61	[3]

References

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Table S2. Comparisons between independent variables and the interactions, for each of the evaluated genes.

Target gene	Housing	Challenge	Housing*Challenge
<i>IL1B</i>	0.261	0.543	0.221
<i>LHCGR</i>	0.027*	0.187	0.661
<i>CYP11A1</i>	0.108	0.473	0.141
<i>PGR</i>	0.067	0.897	0.492
<i>FLT1</i>	0.598	0.024*	0.144
<i>NR3C2</i>	0.256	0.214	0.081
<i>HSD11B2</i>	0.162	0.835	0.238
<i>STAR</i>	0.015*	0.577	0.060
<i>VEGF</i>	0.167	0.044*	0.314
<i>KDR</i>	0.292	0.487	0.513
<i>NR3C1</i>	0.479	0.602	0.687
<i>HSD3B1</i>	0.251	0.013*	0.493

*Significant differences ($p < 0.05$) were represented by an asterisk.