Table S1. The primers sequences used in qPCR analysis.

Gen	GenBank accession code	Primers sequences	
Gapdh	NM_017008	F:5′-TGCCAAGTATGATGACATCAAGAAG-3′	R:5′-AGCCCAGGATGCCCTTTAGT-3′
Nos1	NM_052799.1	F:5′-CCAATGTTCACAAAAAACGAGTCT-3′	R:5′-TCGGCTGGACTTAGGGCTTT-3′
Nos2	NM_012611.3	F:5′-TGCTAATGCGGAAGGTCATG-3′	R:5′-GCTTCCGACTTTCCTGTCTCA-3′
Nos3	NM_021838.2	F:5′-CACAAGAGTTACAAAATCCGATTCA-3′	R:5′-TCTGTGTTACTGGATTCCTTCCTTT-3′
Gucy1a3	NM_017090.2	F:5′-AACACCGGCTAATAAGGAGGAAA-3′	R:5′-ACTCCCCCGTGATCTTGAGA-3′
Gucy1b3	NM_012769.2	F:5′-AGAAGAGGCCTGTACCTGAGTGA-3′	R:5′-TTTGTACTCCTCCCGGAACTGT-3′
Prkg1	NM_001105731.3	F:5′-CCCACGGACACAAGCAATTT-3′	R:5′-CCCAGCCTGAGTTGTCATCA-3′
Pde5a	NM_133584.1	F:5′-GCTGGATGGCTGCAGGAA-3′	R: 5′-CCCCATTAAGGAGCGTCTTCT-3′

Primers were design by Primer Express 3.0 software (Applied Biosystems) using full genes sequences from NCBI GenBank (http://www.ncbi.nlm.nih.gov/nuccore). F - forward, R - reverse.