*Primers*

Primers were designed using NCBI Primer-BLAST, with selection for ideal target specificity, PCR product size (less than 200 bp, and when possible less than 100 bp), primer annealing temperature (60°C), and PCR product melting temperature (less than 93°C). When possible, primers were designed to either span exon/intron junctions or have an intervening intron greater than 1000 base-pairs. Primers were experimentally validated for mRNA and target specificity and optimized for efficiency (92-99%) across 6-logs input template concentration. **NOTE:** Some genes are single-exon and require genomic DNA digestion prior to cDNA generation for accurate mRNA expression analysis.

*Quantitative PCR*

PCR reactions consisted of 1X PowerUp SYBR Green Master Mix (Thermo Fisher Scientific), 0.5 μM forward and reverse primers, 5-20 ng cDNA (mRNA analysis) or 25-50 ng DNA (mitochondrial or genomic DNA analysis) in a total reaction volume of 10 μL. Reactions were amplified as technical duplicates or triplicates on a QuantStudio 3 real-time PCR system (Thermo Fisher Scientific). The instrument cover was set to 105°C and the PCR program included a hold stage for a UNG enzyme activity (1 cycle: 50°C/2 min, 95°C/2 min), a PCR stage (45 cycles: 95°C/1 sec, 60°C/20 sec with data collection), and a final melting curve stage (95°C/1 sec, 60°C/20 sec, 95°C/1 sec with a temperature transition of 0.15°C/sec and continuous data acquisition during the melting transition). Data were analyzed using the Thermo Fisher Cloud analysis platform with an efficiency-corrected relative quantification (2^ΔΔCq) methodology utilizing *Tbp* as a reference gene for mRNA analysis.