Results

Quantitative PCR was performed for seven target genes in order to compare to RNA-Seq analysis. There was a significant difference in expression between the two locations (BBC and DH) for 6 of the genes by qPCR and 4 of the genes by RNA-Seq (see Table 2 for p-values). In all cases the RNA-Seq results showed a greater fold difference than the qPCR results (Figure 1). For three of the genes examined, serine protease inhibitor (*dpgn*), glutathione S transferase A (*gsta*) and steroid 17-alpha-hydroxylase (*cyp17A*), expression was significantly higher in the DH library by RNA-Seq and qPCR analysis. High mobility group protein (*hmgp*) was expressed higher in the BBC library by RNA-Seq, and corroborated with qPCR results. Metalloproteinase inhibitor 3 (*timp3*) was determined not to be differentially expressed using either approach. Two of the genes selected, calmodulin-like protein (*call*) and gonadotropin-releasing hormone II receptor (*gnrr2*), were not differentially expressed between the two libraries as determined by RNA-Seq analysis, however expression results from qPCR indicated significantly higher expression in DH samples.