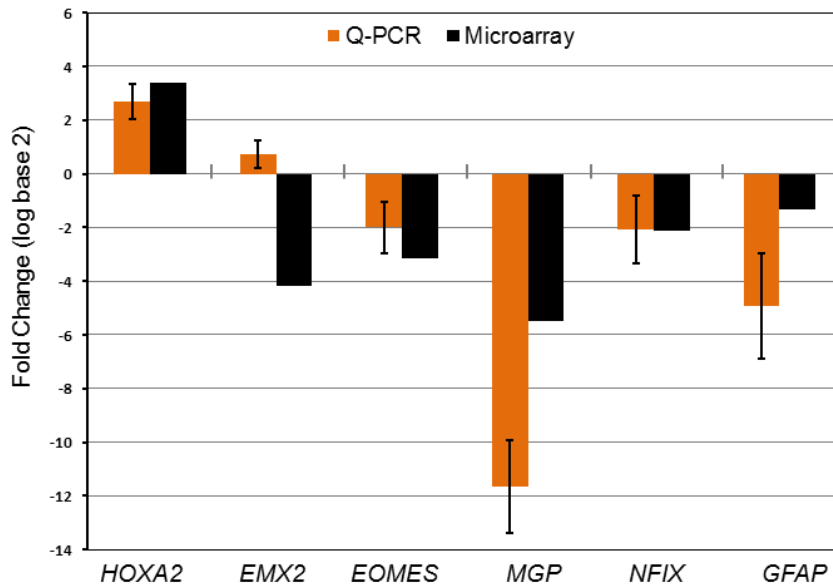


Supplementary Figure 1



Supplementary Figure 1. Validation of microarray data by qRT-PCR. A selection of genes with the differential fold change (log base 2) in gene expression detected by microarray (black bars) and qRT-PCR (orange bars). Data analysis was performed using the Comparative Ct ($\Delta\Delta C_t$) method normalised to GAPDH. Each data point represents a minimum of two individual reactions. Standard error of the mean is indicated. Correlation of 83% (5/6). All primers were designed to cross exon-exon junctions and are listed in Supplementary Table 1.