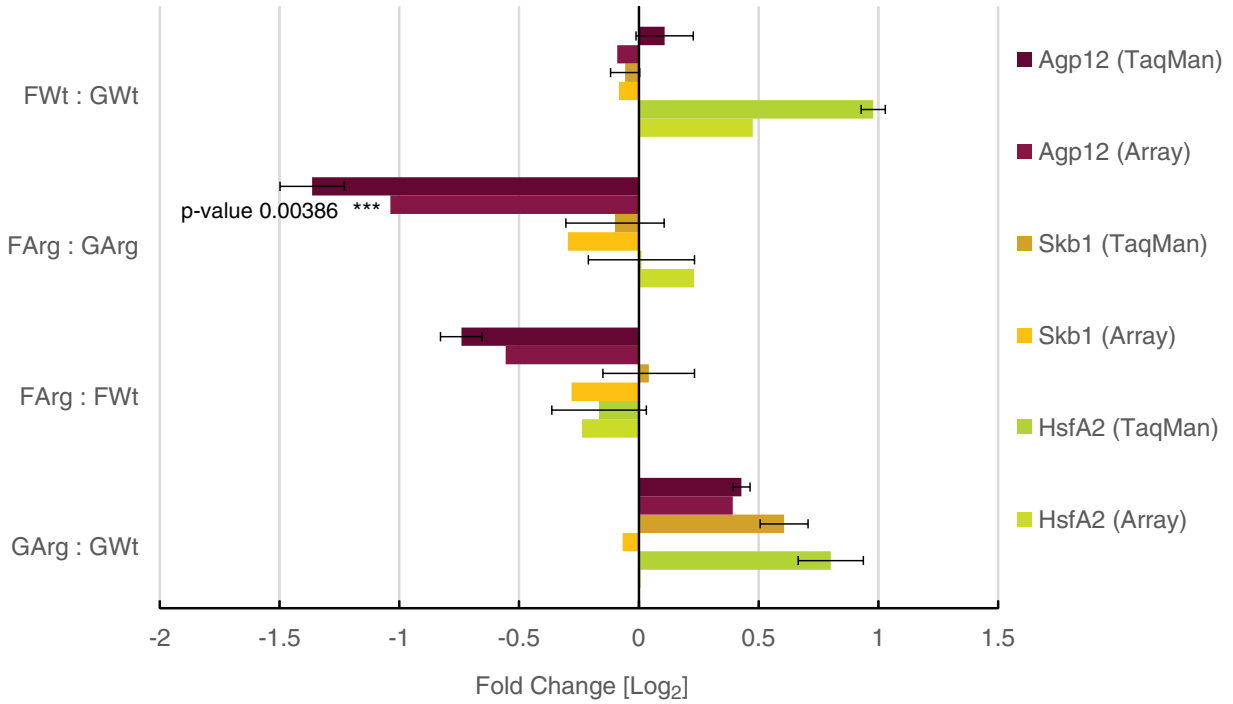


Target gene expression in RT-qPCR vs Microarray



SUPPLEMENTARY FIG. S2. Quantitative analyses. The transcript abundance for three representative genes, Agp12, Skb1, HsfA2 is shown for four comparison groups as measured in RT-qPCR (darker shades) or in microarrays (lighter shade). The individual gene transcript abundance was first normalized to the Ubq11 transcript abundance, and then the relative transcript abundance was calculated appropriately for each of the four comparison groups (labeled on the left side of the plot area). The x axis represents the fold change of gene expression in the comparison group calculated as a log₂ function. The RT-qPCR error bars represent the standard error of the mean of the log₂ fold change. The microarray data is labeled with asterisks and the value of the p-value is indicated only if significant.