



Figure 1. Probe selection in gene expression estimation. Pink probes that map to variant a and b are used for gene expression summarization. Grey probes are discarded as they only target fragments from variant b.

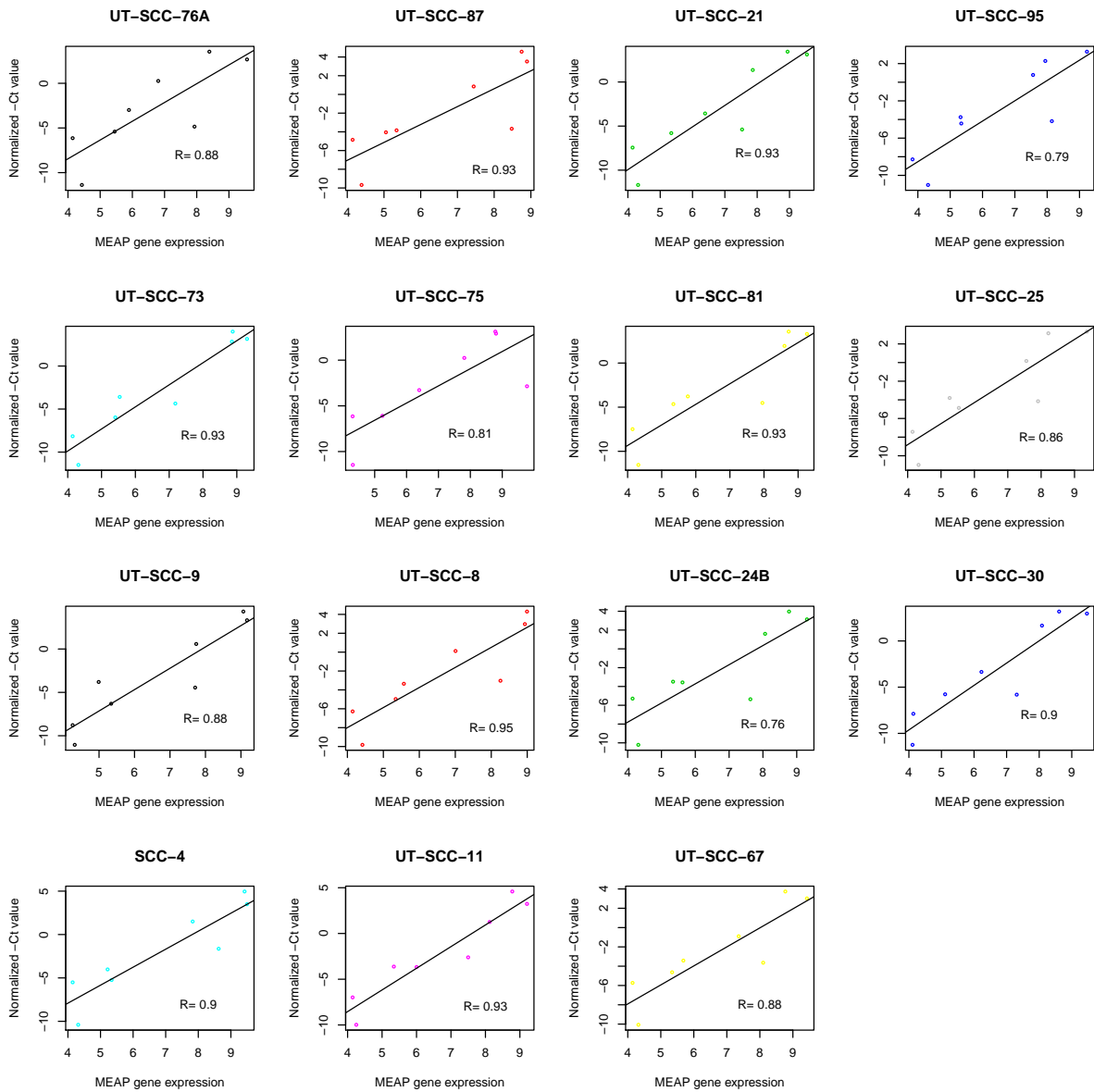


Figure 2. Gene expression correlation. qPCR -Ct values are correlated with expression values. Spearman correlation between MEAP gene expression and qPCR normalized -Ct values for eight reference genes from 15 cell lines shows our gene expression summarization method is accurate and reliable.

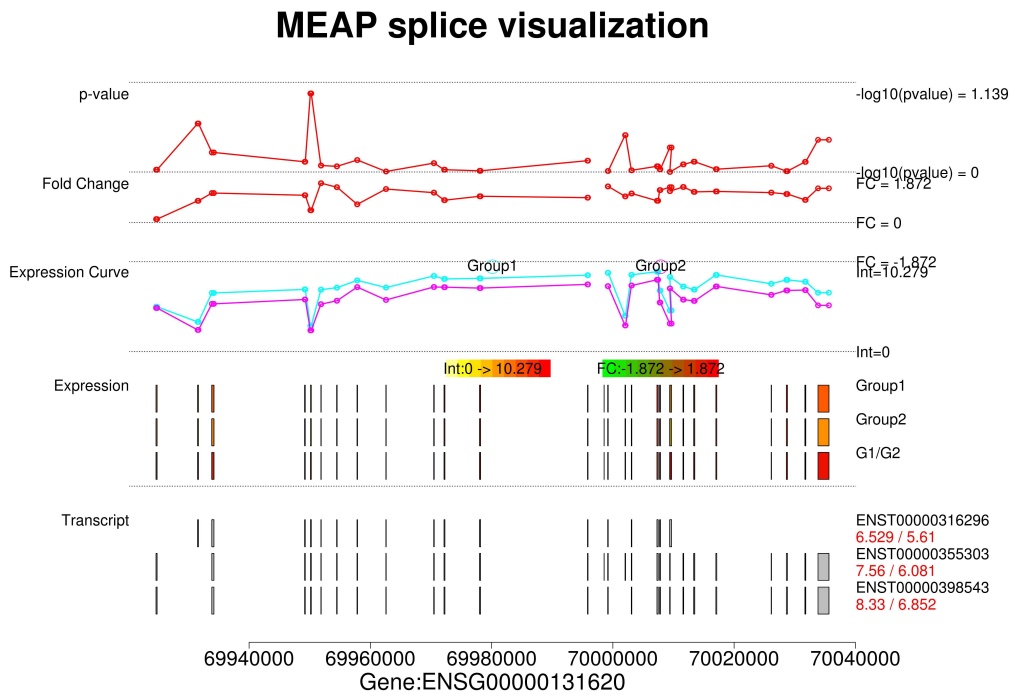


Figure 3. MEAP splice visualization plot for gene *ANO1*.

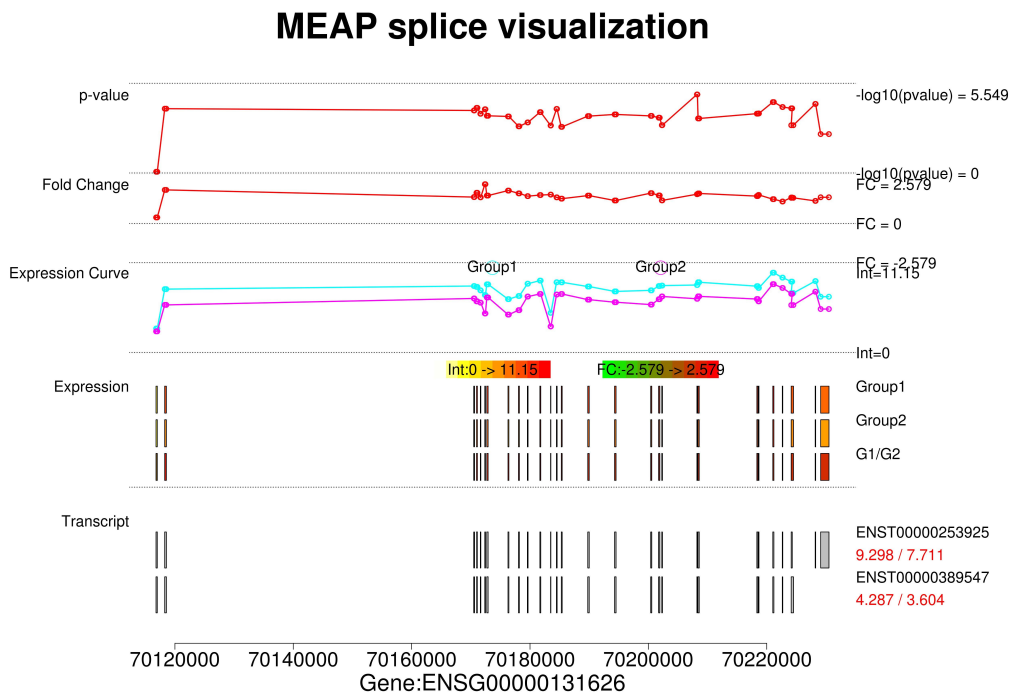


Figure 4. MEAP splice visualization plot for gene *PPF1A1*.