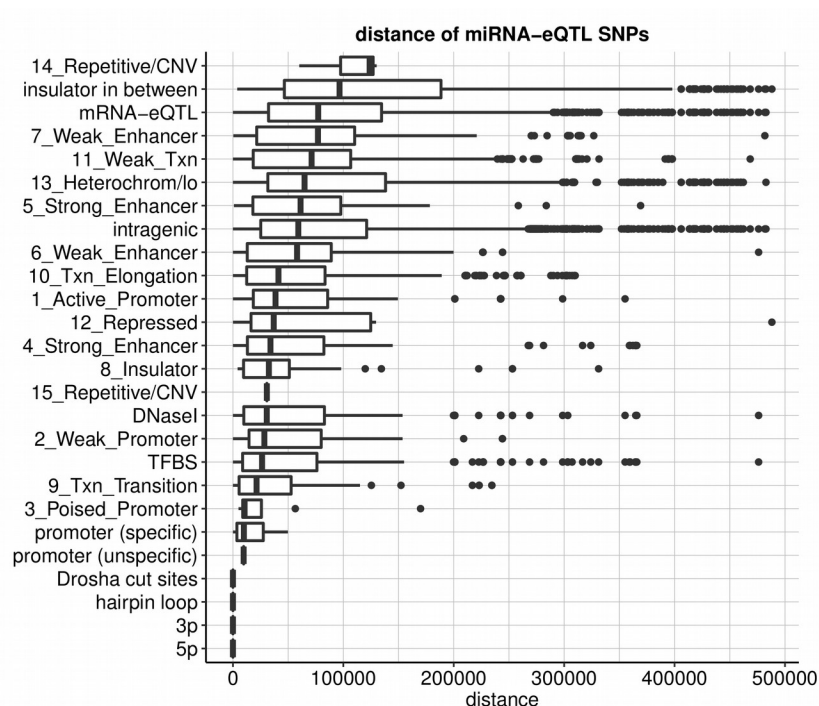
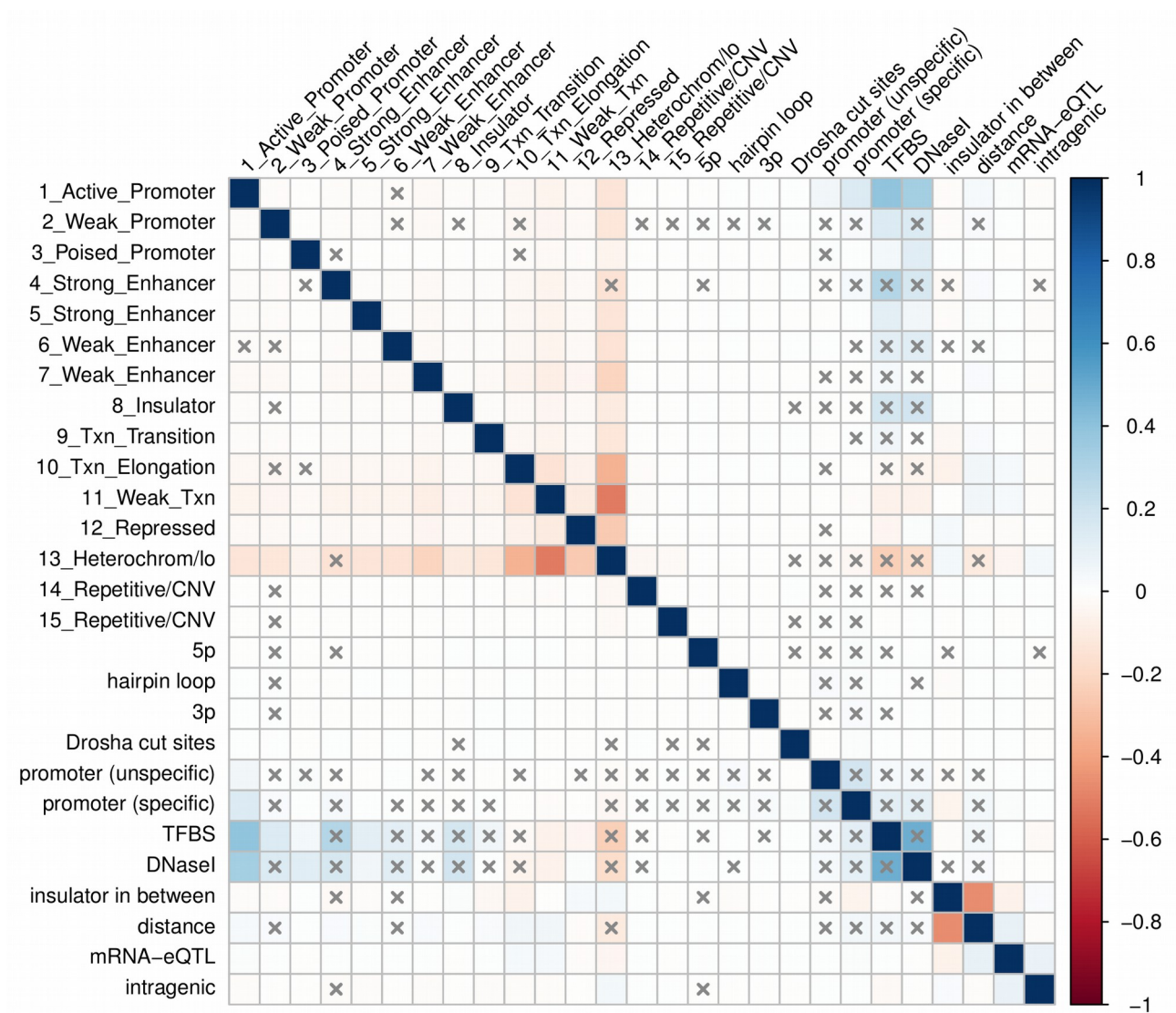


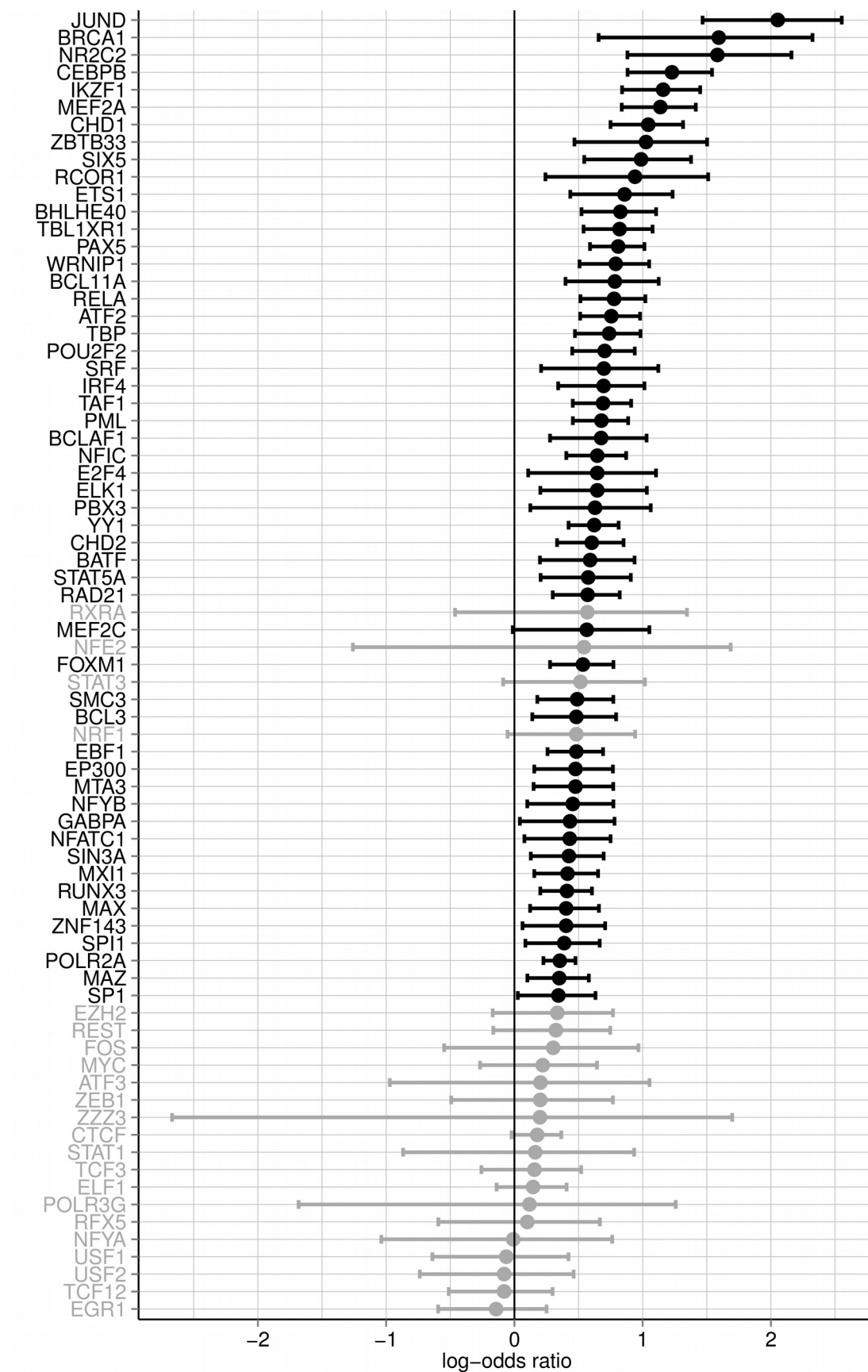
**Figure S1A.** Distance of all SNPs overlapping a feature with respect to the pre-miRNAs.



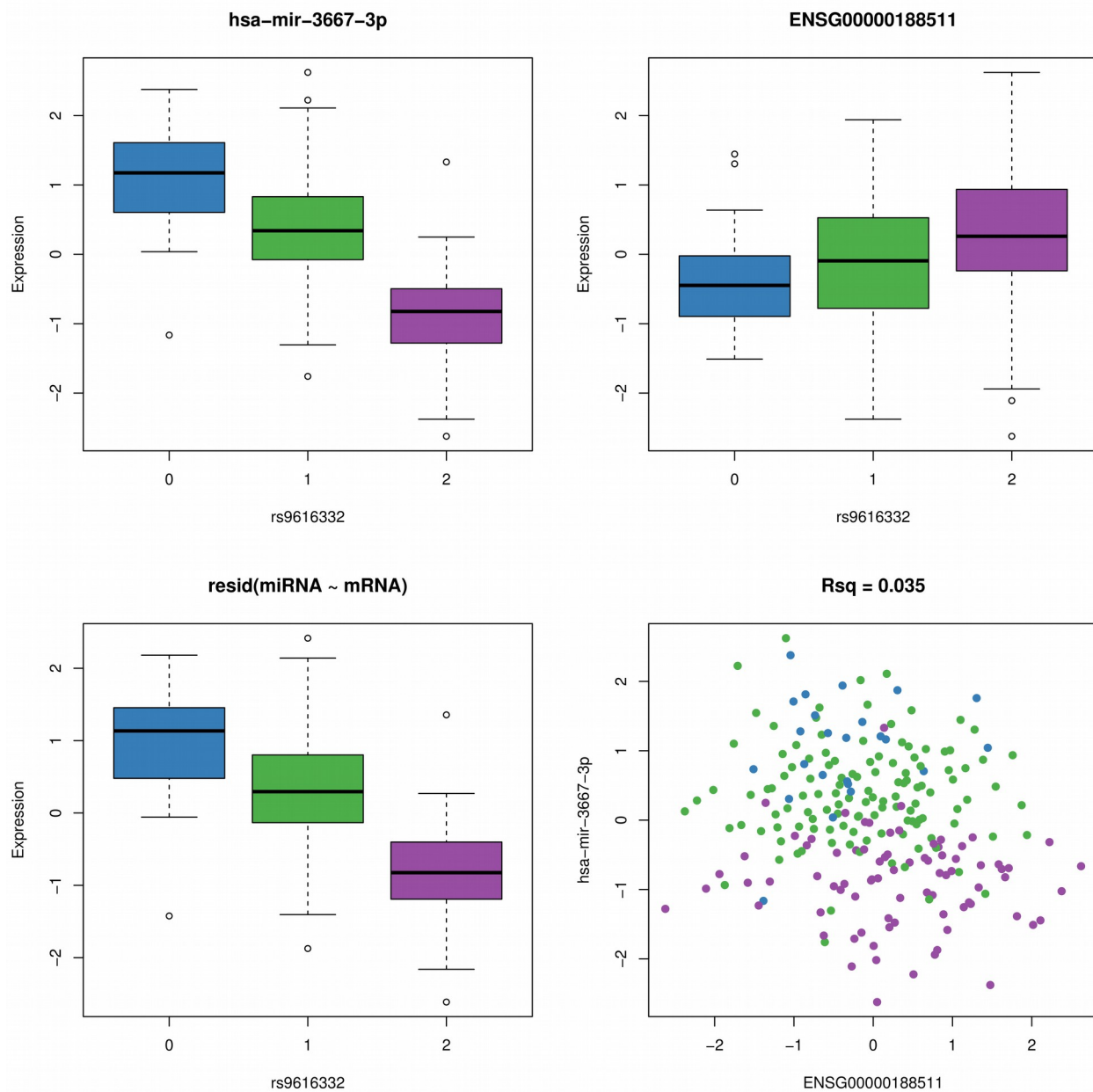
**Figure S1B.** Distance of miRNA-eQTL SNPs overlapping a feature with respect to the pre-miRNAs.



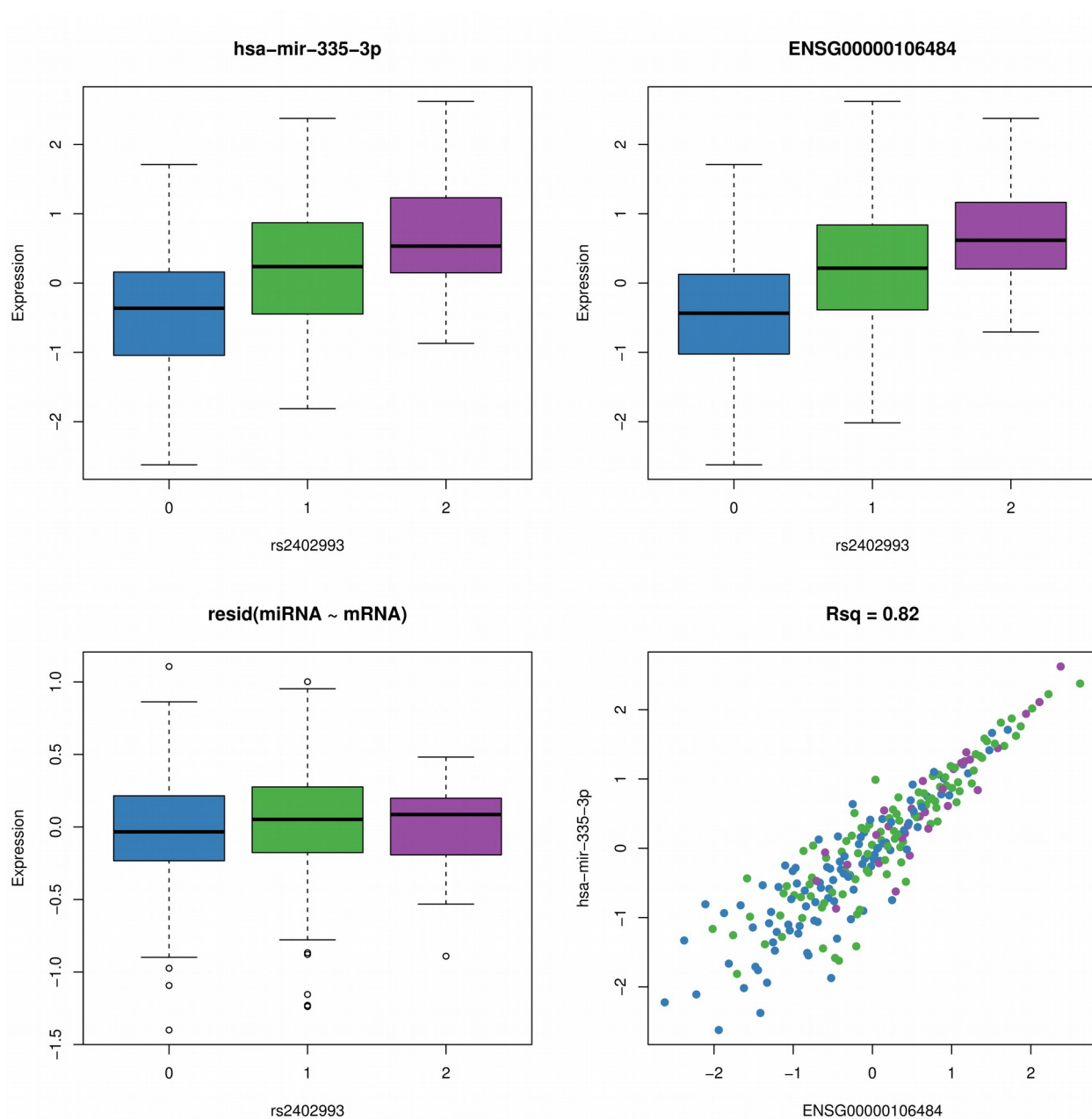
**Figure S1C. Pearson's product moment correlation coefficient for all feature pairs.** Crossed-out entries are not significant ( $p > 0.05$ ).



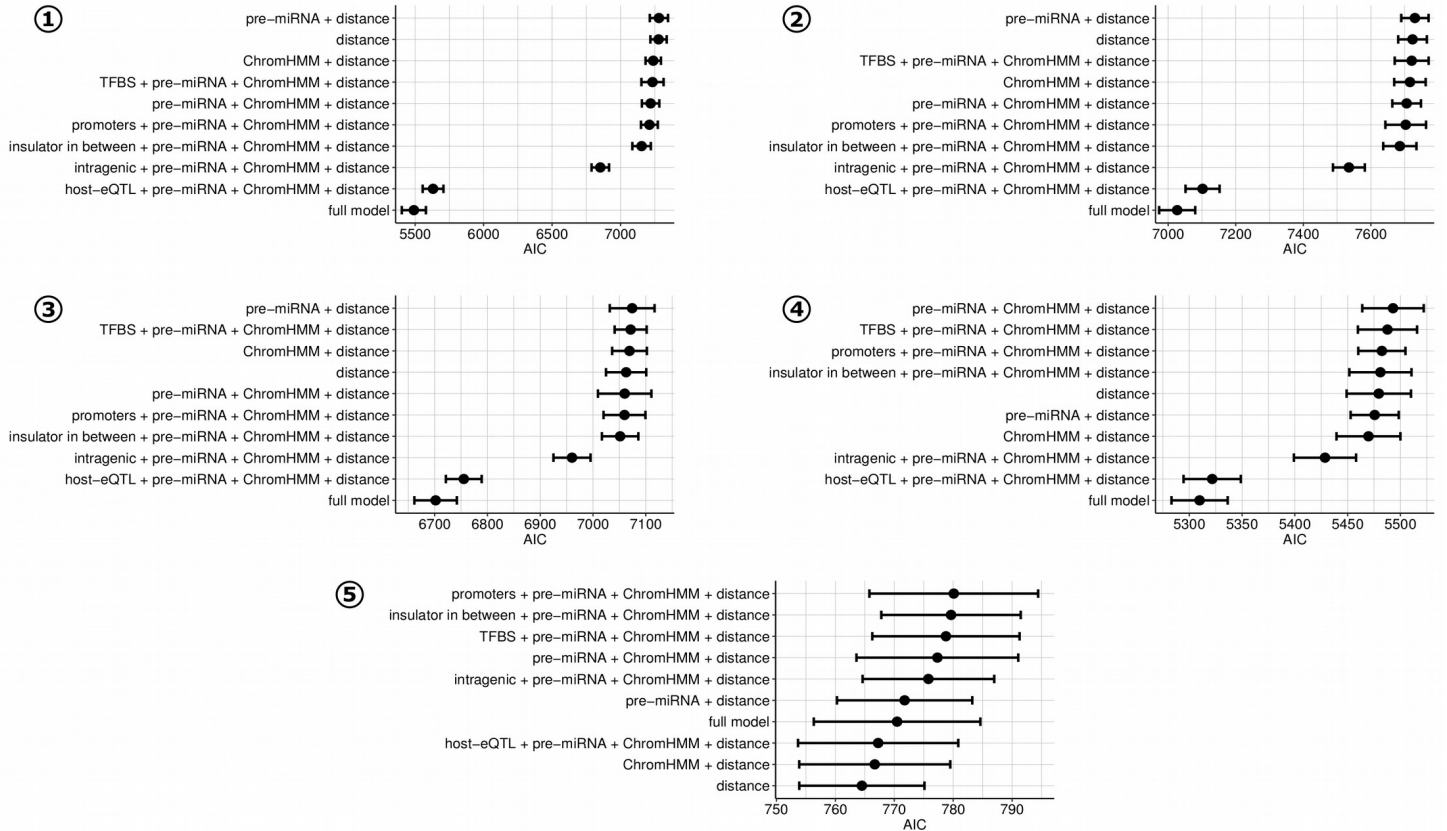
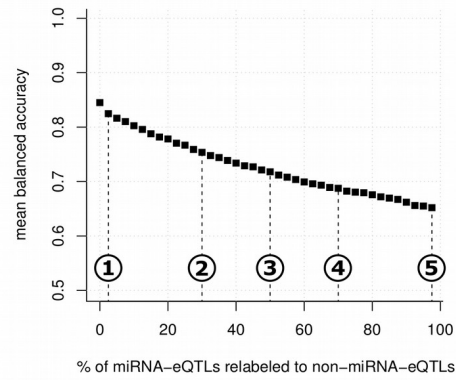
**Figure S1D. TFBS selection and log-odds ratios.** For each TF a separate logistic regression was performed, always including the distance as a second feature. Insignificant log-odds ratios are shown greyed ( $p > 0.05$ ). Error bars illustrate 95% confidence intervals.



**Figure S1E. Example of an independent miRNA and mRNA eQTL.** Boxplots and scatterplot depict the miRNA and host gene expression (scaled and processed as described in the section 'MiRNA – Host Gene Independence Analysis' in Methods) for the three different genotypes of the respective eQTL.



**Figure S1F. Example of a shared miRNA and mRNA eQTL.** Boxplots and scatterplot depict the miRNA and host gene expression (scaled and processed as described in the section 'MiRNA – Host Gene Independence Analysis' in Methods) for the three different genotypes of the respective eQTL.



**Figure S1G. Effect of randomly relabeling miRNA-eQTLs as non-miRNA-eQTLs to address the fact that not all miRNA-eQTLs used in the model are causal SNPs.** The top panel shows the mean balanced accuracy (y-axis) for 25 random samples when relabeling a fraction of the eQTLs (x-axis). The dashed lines marked by circled numbers indicate fractions for which a model selection according to the AIC was performed. Results of the model selection are shown below marked by the corresponding circled numbers. These plots are analogous to Figure 3A in the main text.