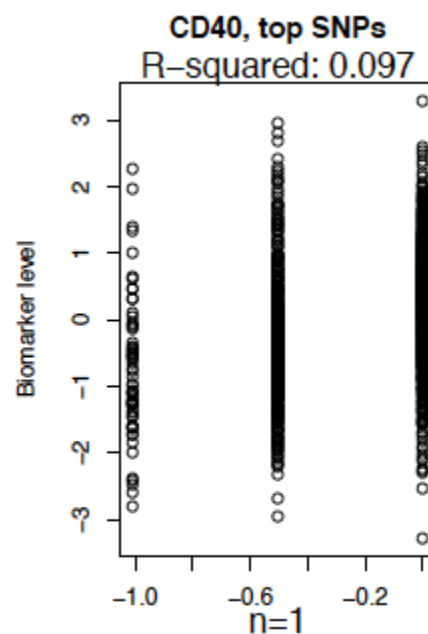
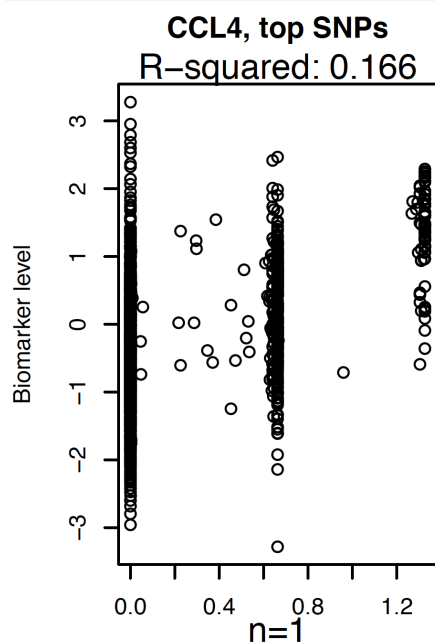
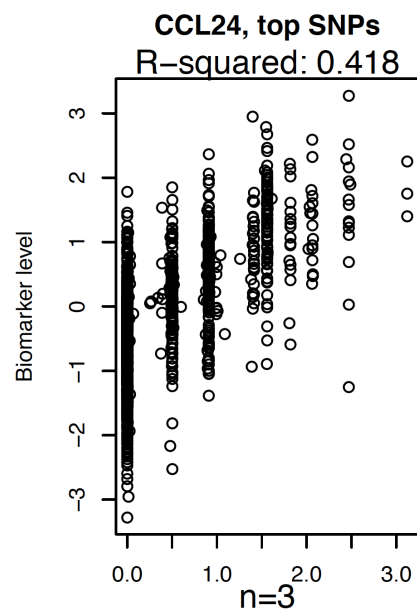
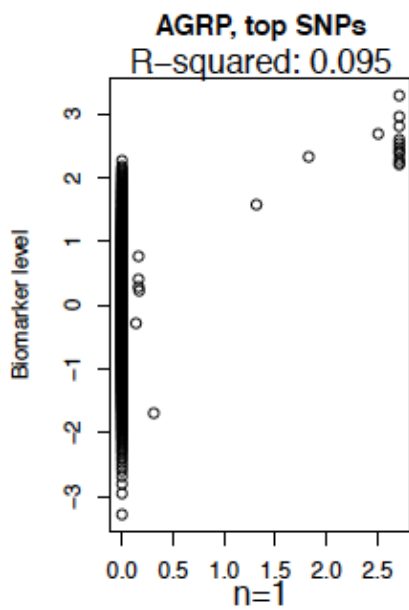
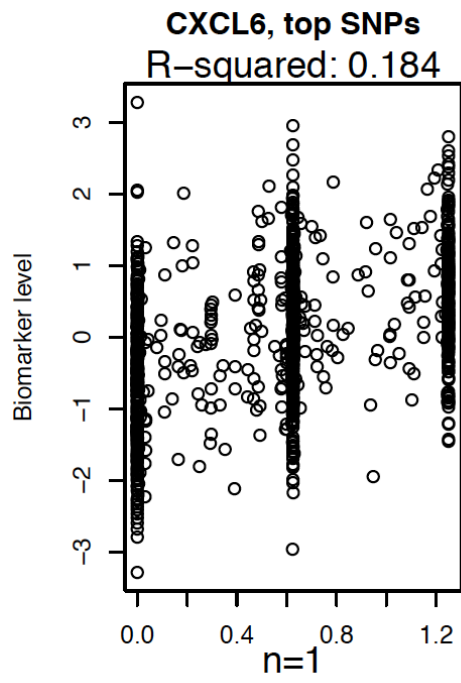
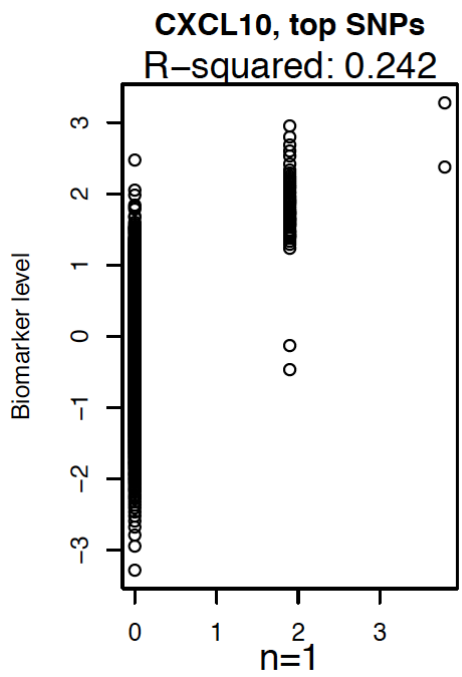
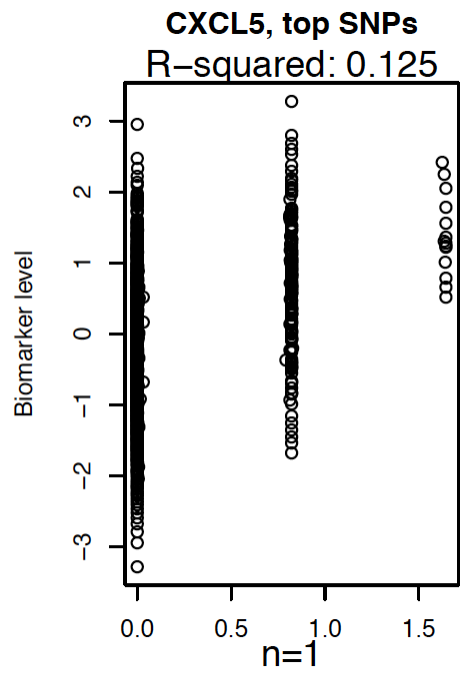
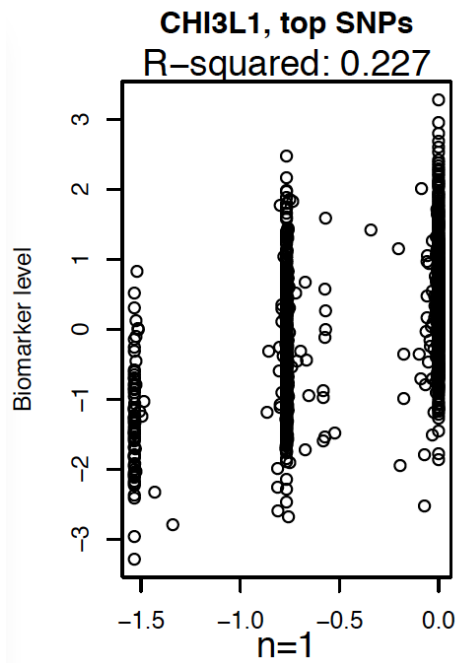
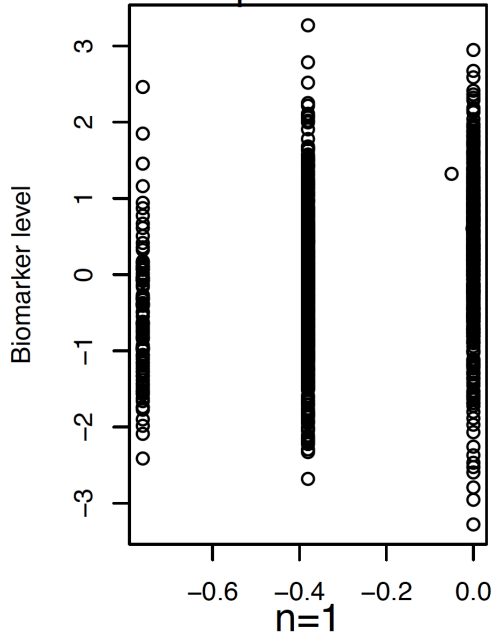


Supplemental Fig S6. Allelic effects on biomarker levels. The X-axis represents the weighted (by the regression coefficients) allelic effects by the top GWAS SNPs and the Y-axis is the measured biomarker level for each individual. For biomarkers with more than one independent SNP, all independent cis-SNPs are included, and N indicates the number of SNPs included. R -squared is the fraction of the variance in biomarker levels explained by all (N) variants. For biomarkers with $N=1$, most individuals are in either of three clusters that correspond to individuals being homozygous for the minor or major allele or individuals being heterozygous. Dosage values for the imputed genotypes are used, and therefore, some individuals are located outside the three clusters. For biomarkers with more than one SNP included as IVs; more than three clusters are observed which agrees with the higher number of possible allele-combinations

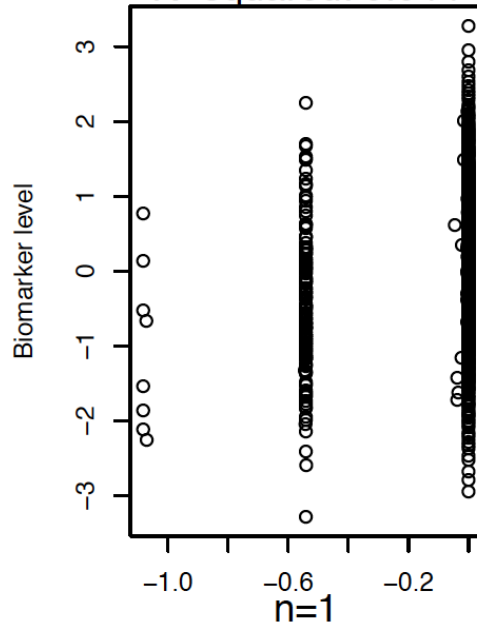




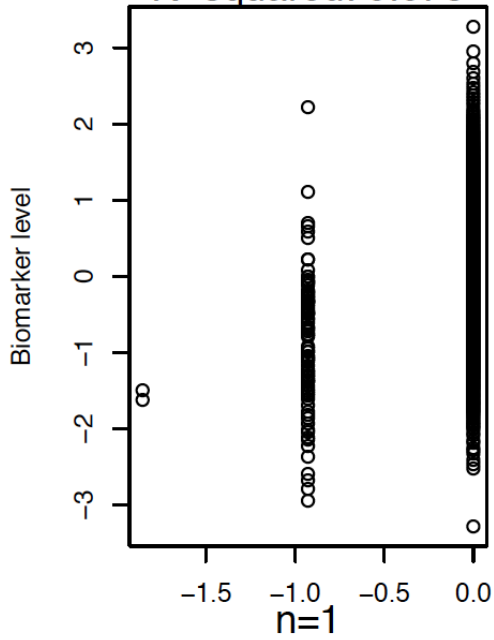
Cystatin_B, top SNPs
R-squared: 0.064



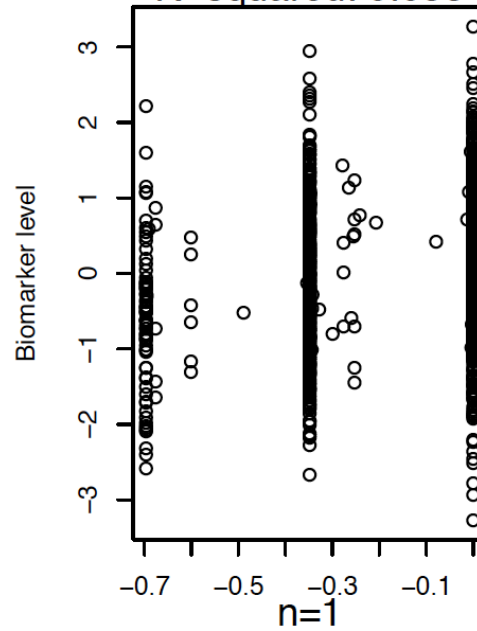
Galectin-3, top SNPs
R-squared: 0.044

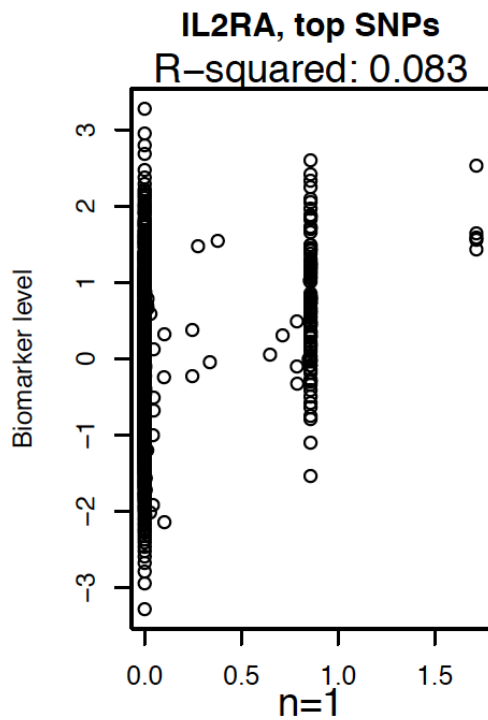
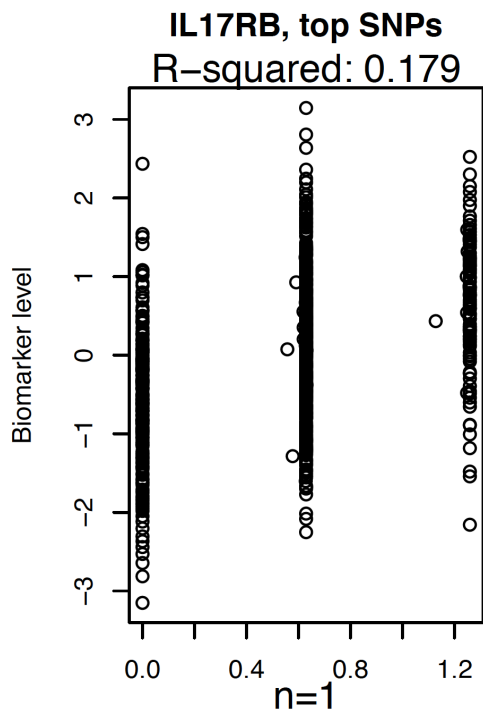
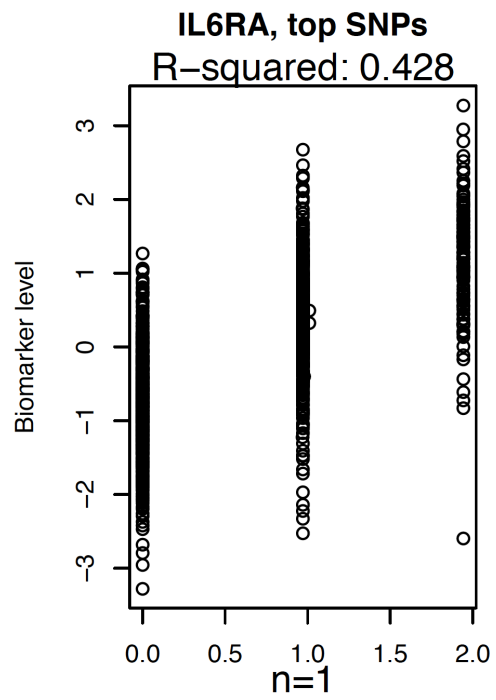
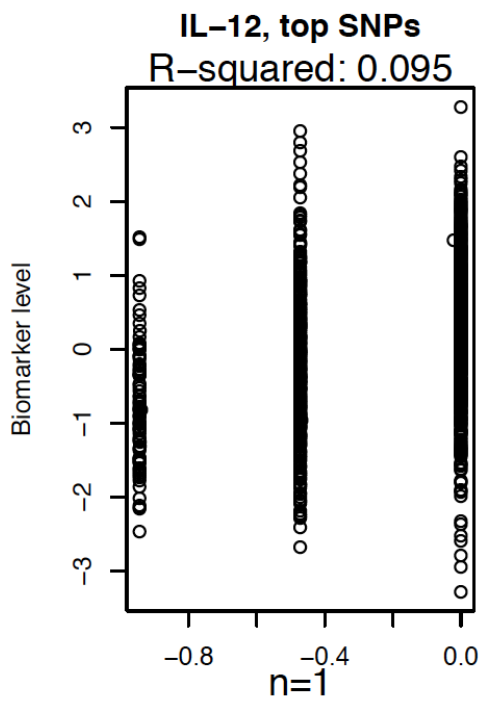


Ep-CAM, top SNPs
R-squared: 0.078

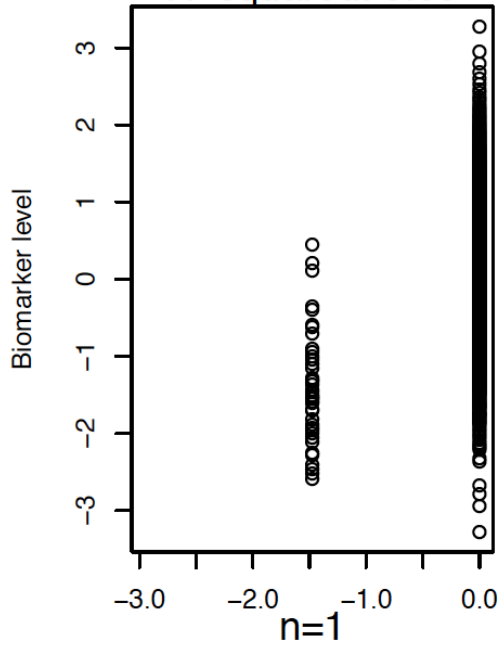


HSP_27, top SNPs
R-squared: 0.055

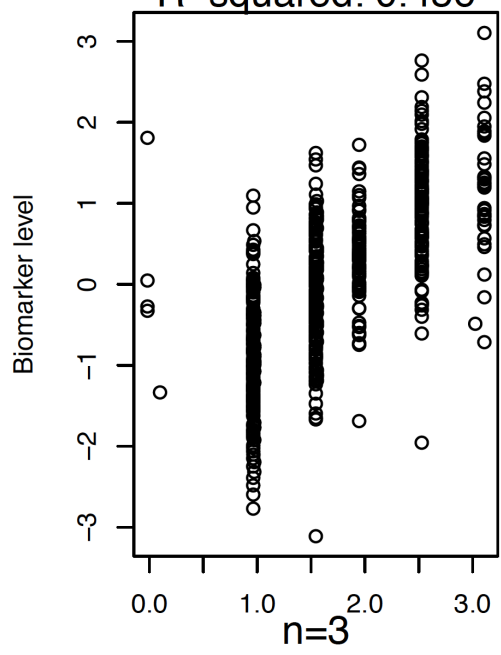




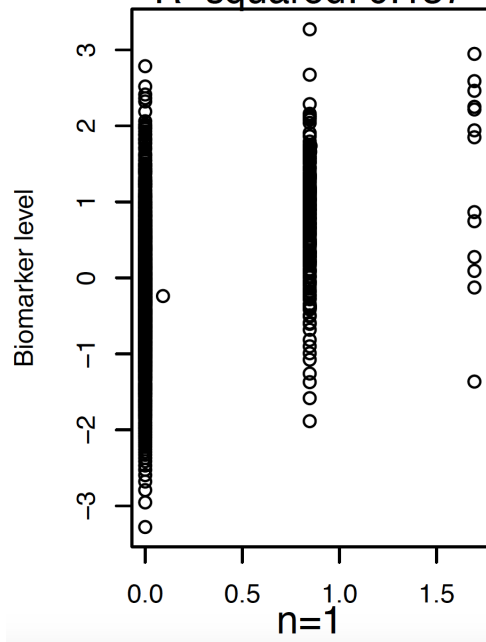
Kallikrein-11, top SNPs
R-squared: 0.09



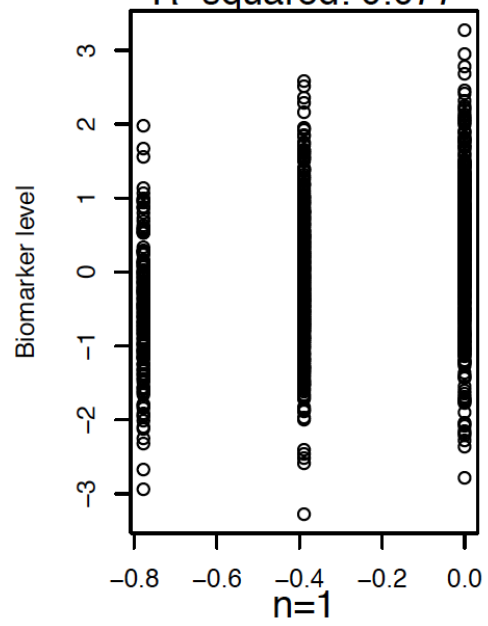
MIC-A, top SNPs
R-squared: 0.456

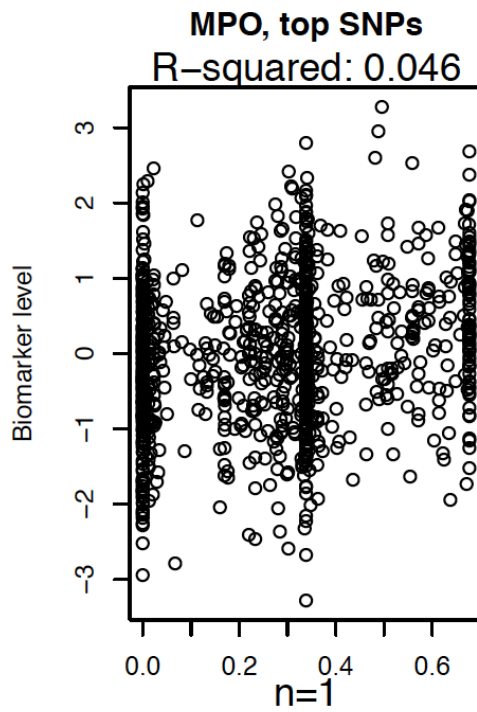
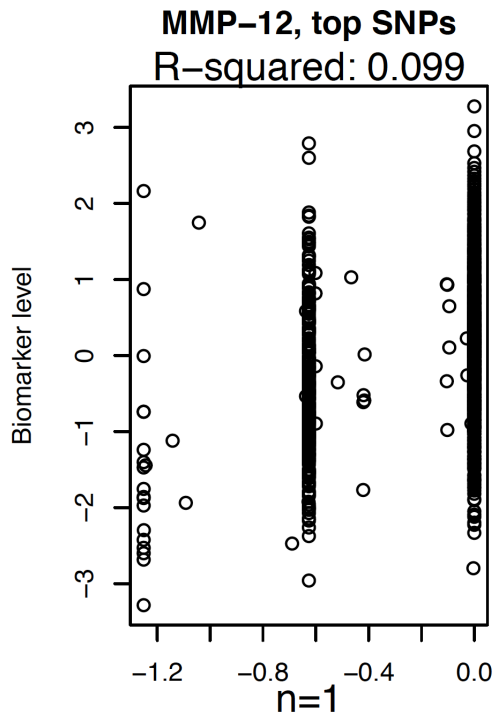
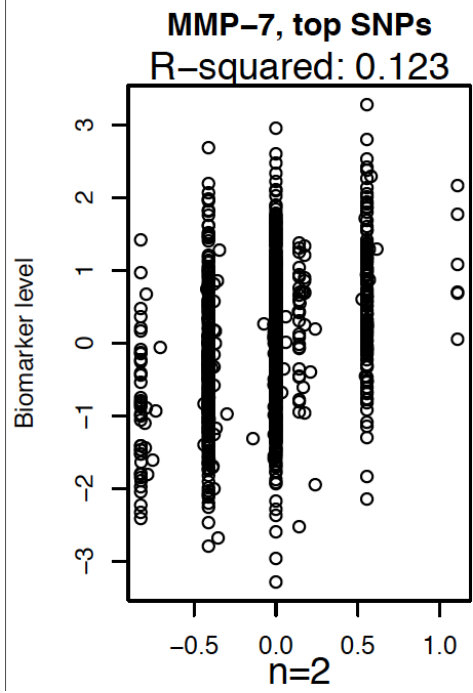
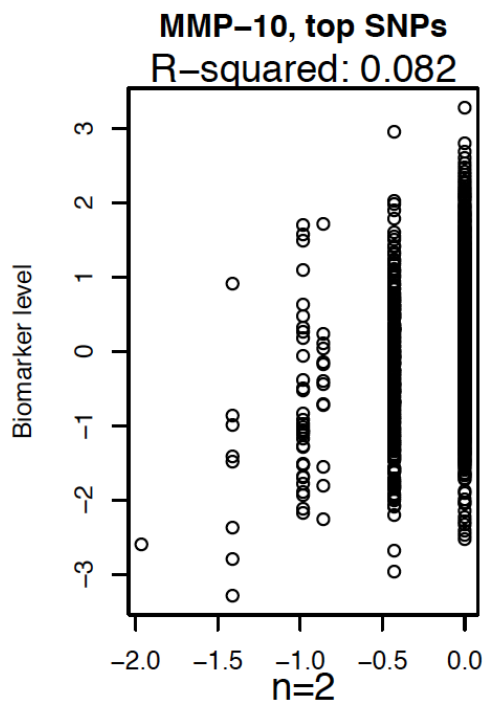


MIA, top SNPs
R-squared: 0.137

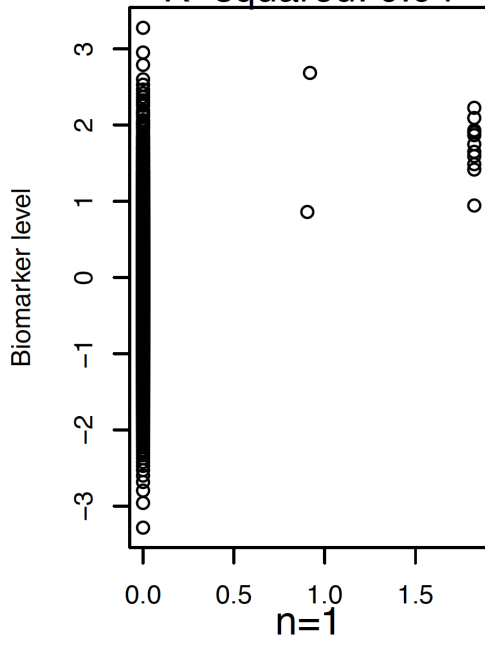


MMP-1, top SNPs
R-squared: 0.077

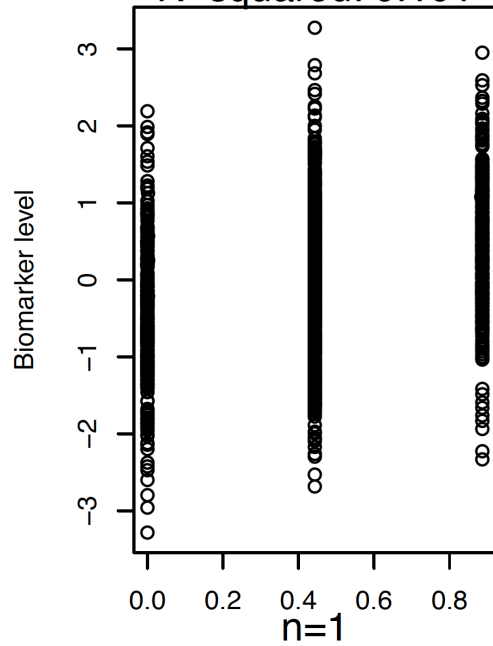




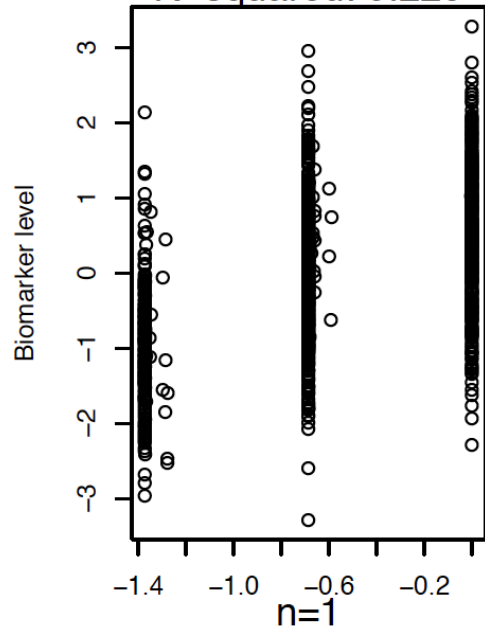
RETN, top SNPs
R-squared: 0.04



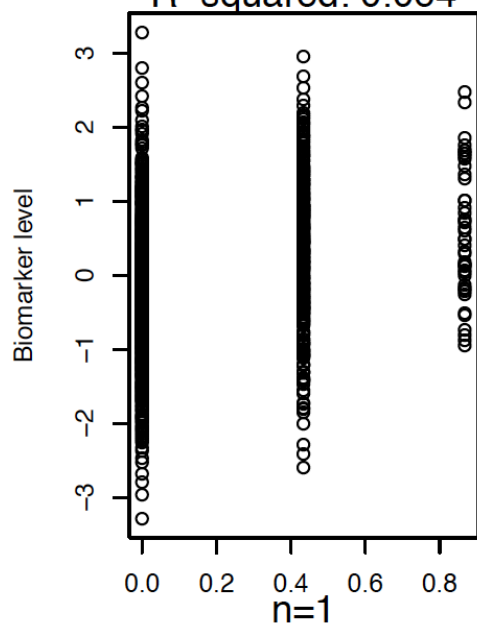
TIM, top SNPs
R-squared: 0.101



ST2, top SNPs
R-squared: 0.229



TM, top SNPs
R-squared: 0.064



VEGFR-2, top SNPs
R-squared: 0.079

