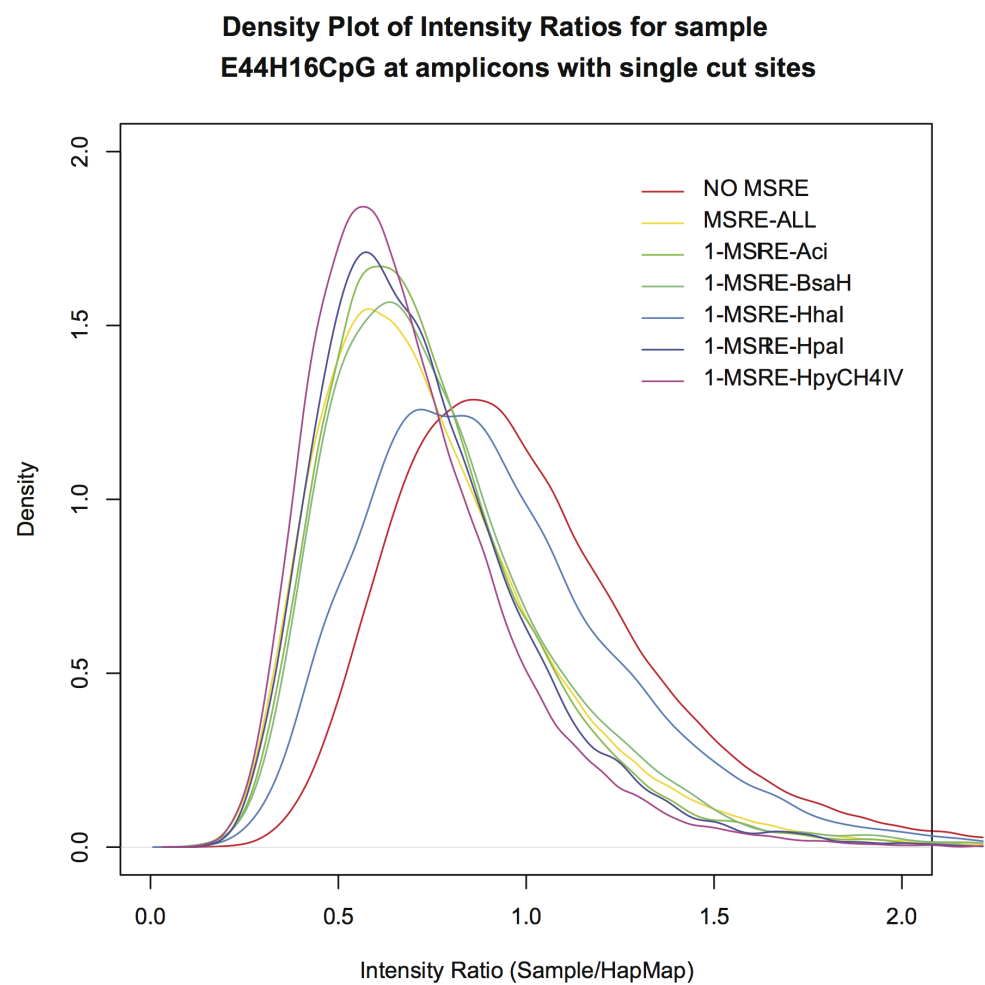
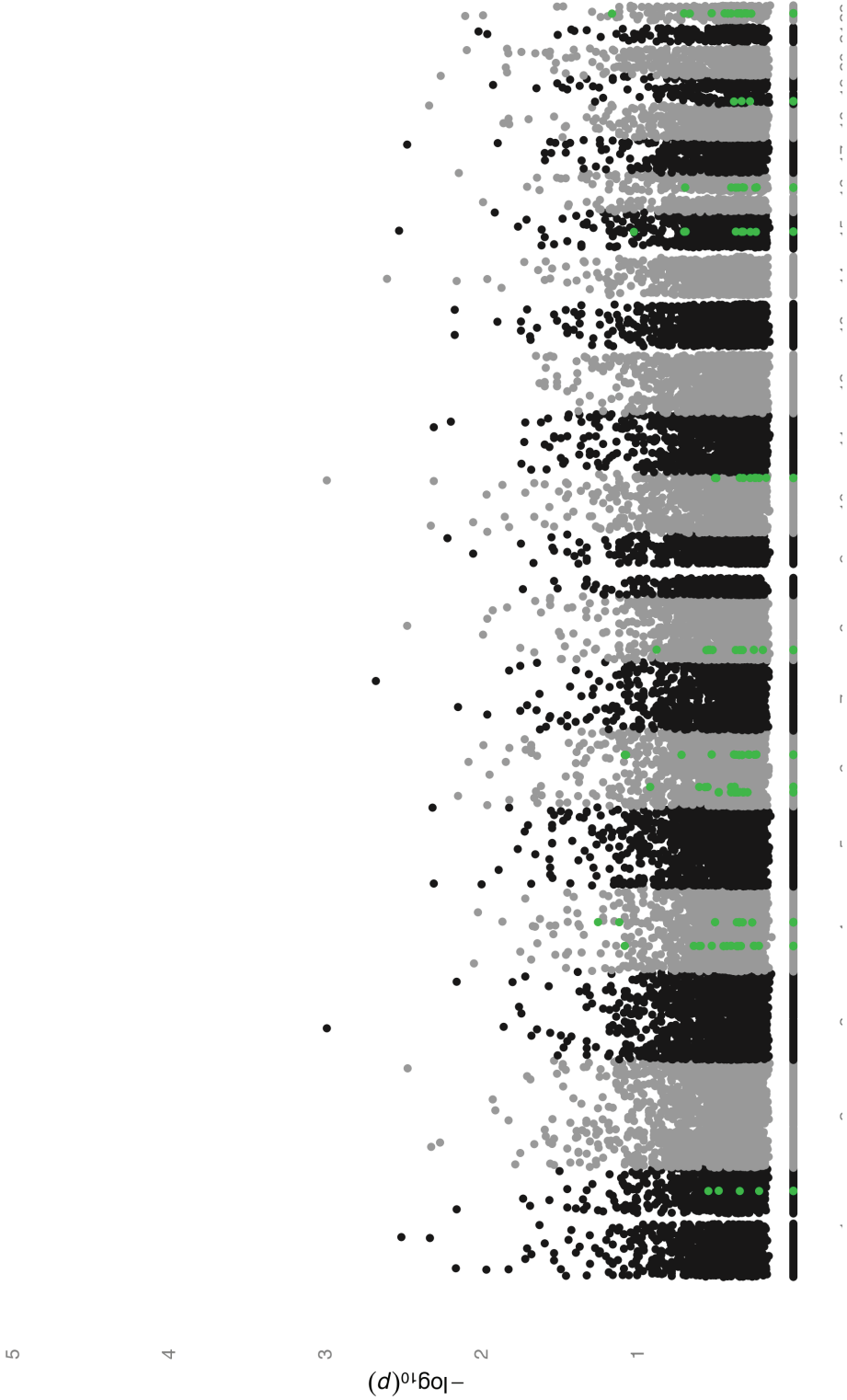


Supplemental Figure 1



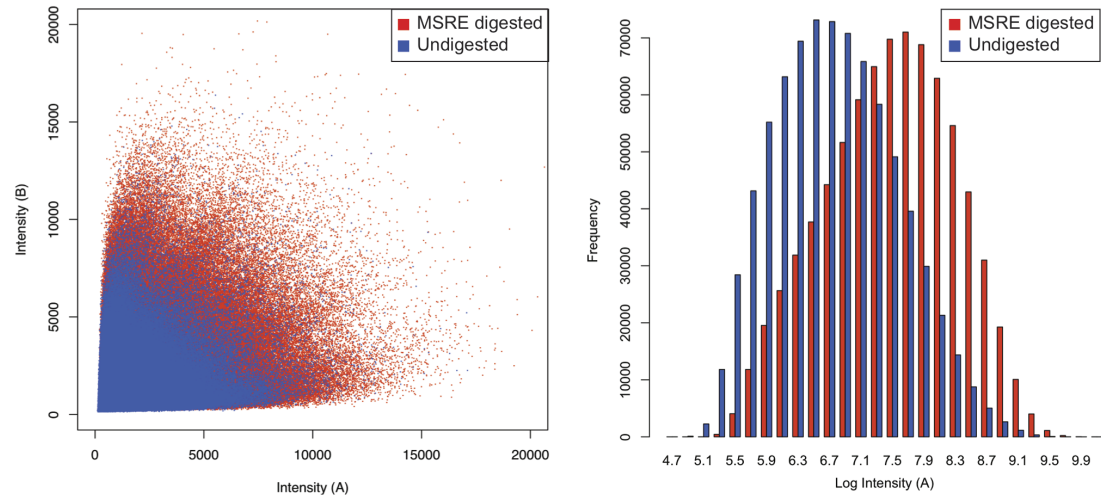
Supplemental Figure 2



Supplemental Figure 3

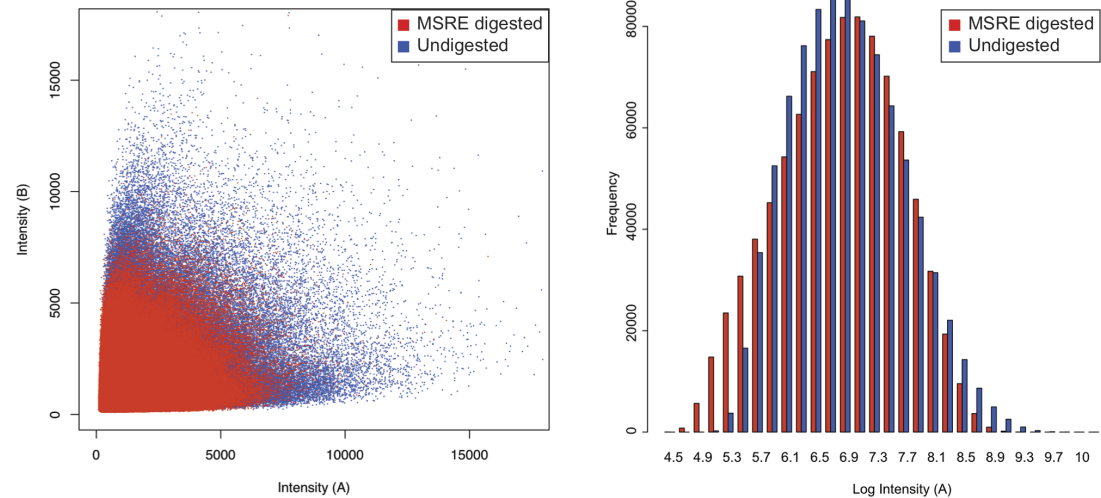
A

Unnormalized



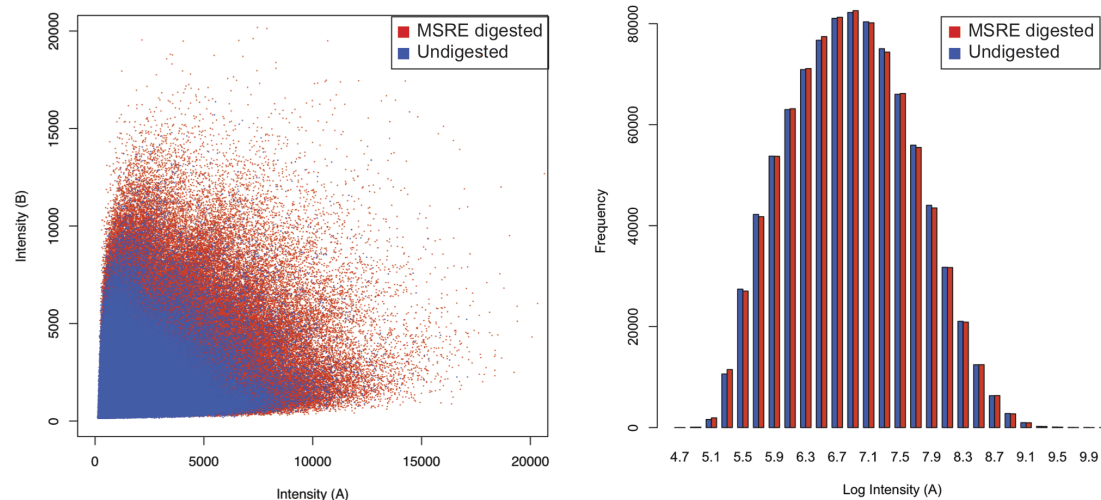
B

Median Normalized

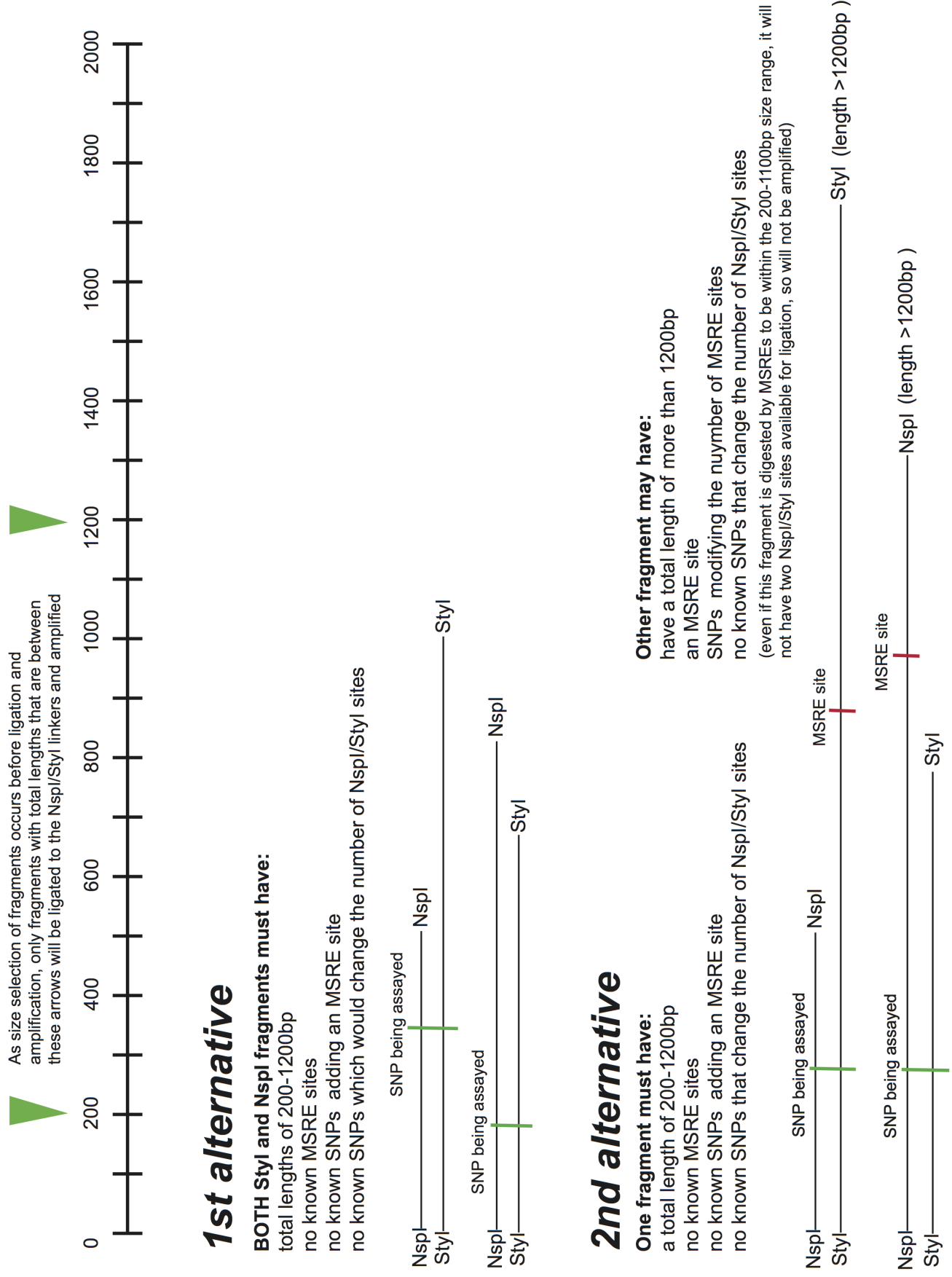


C

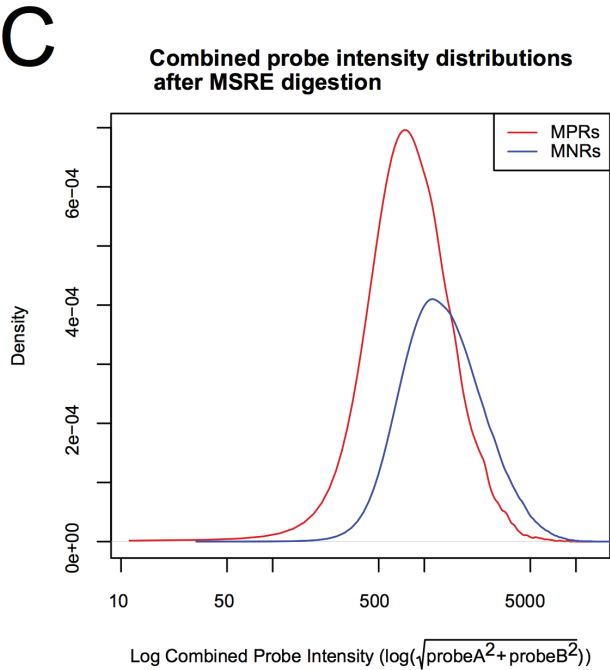
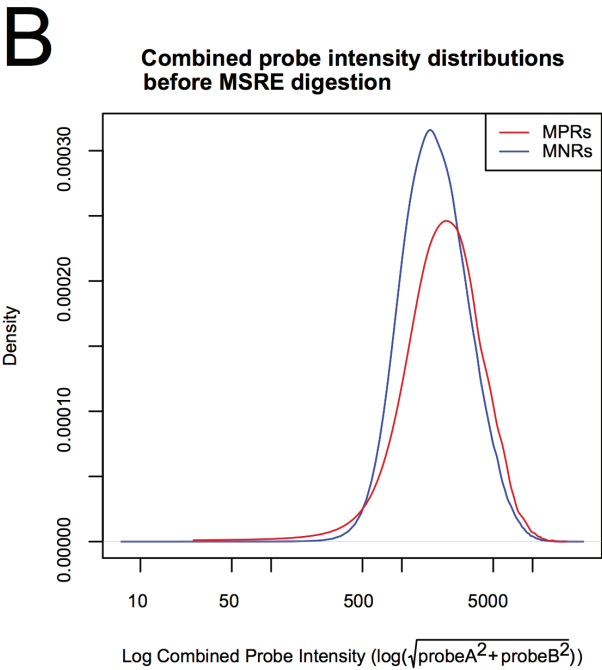
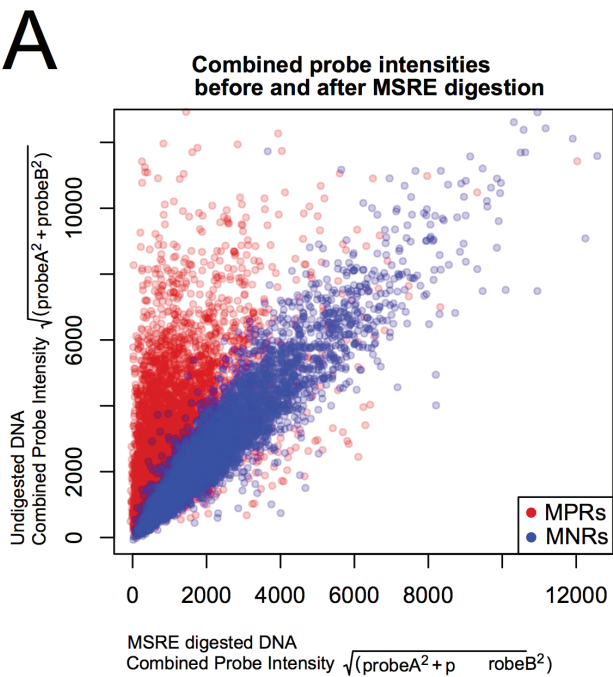
Quantile Normalized



Supplemental Figure 4

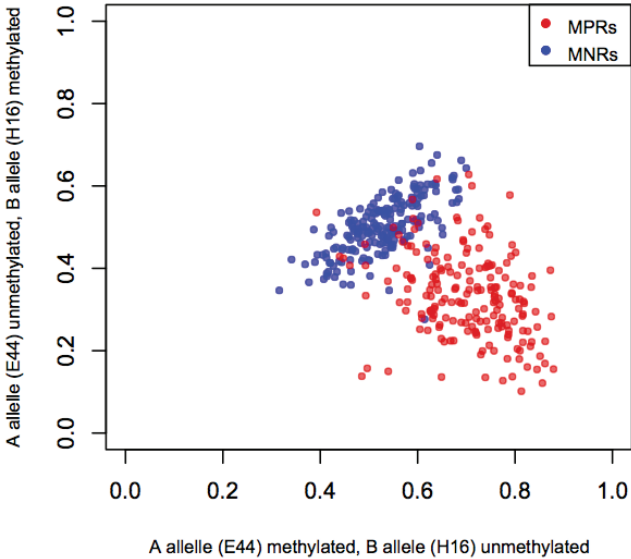


Supplemental Figure 5

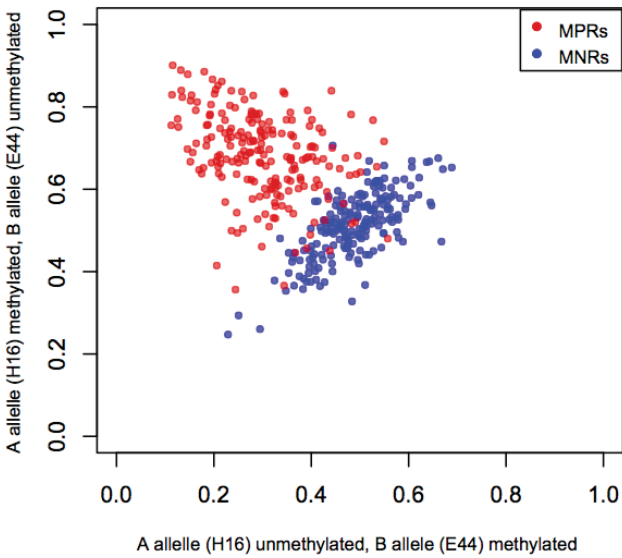


Supplemental Figure 6

A A allele frequencies for E44-AA and H16-BB genotypes from unnormalized 50:50 E44-H16 control mixes

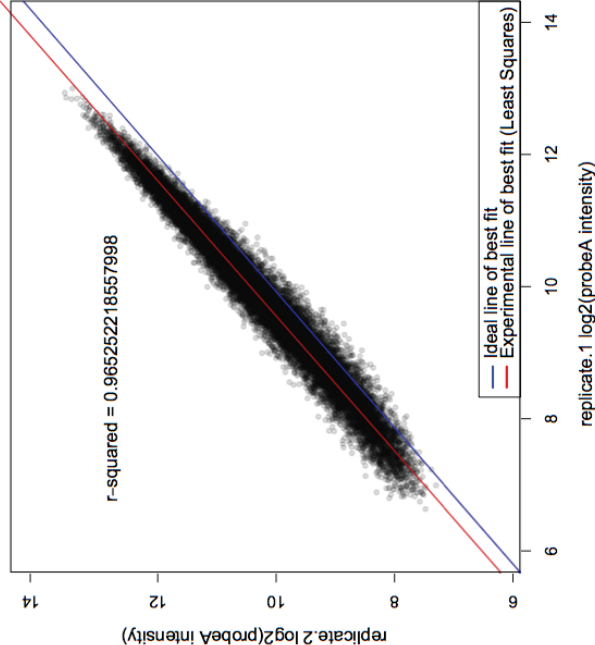


B A allele frequencies for E44-BB and H16-AA genotypes from unnormalized 50:50 E44-H16 control mixes

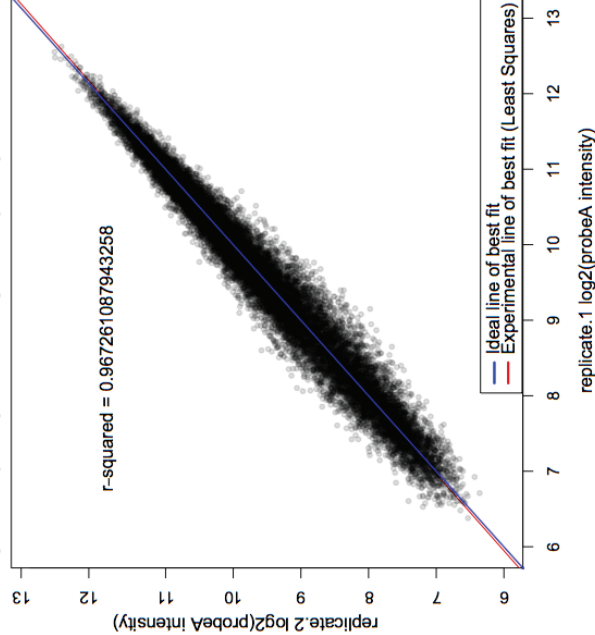


Supplemental Figure 7

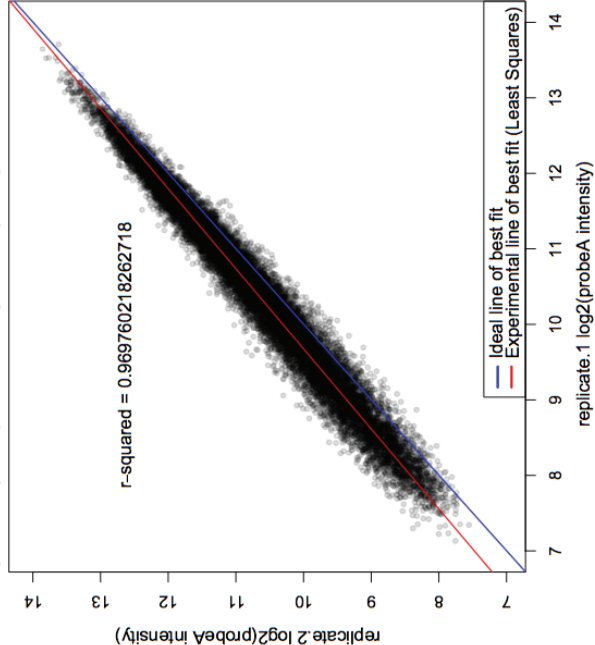
A Unnormalized ProbeA Intensities for Replicates of 1:1 Methylated(E44):Unmethylated(H16) Control Mix



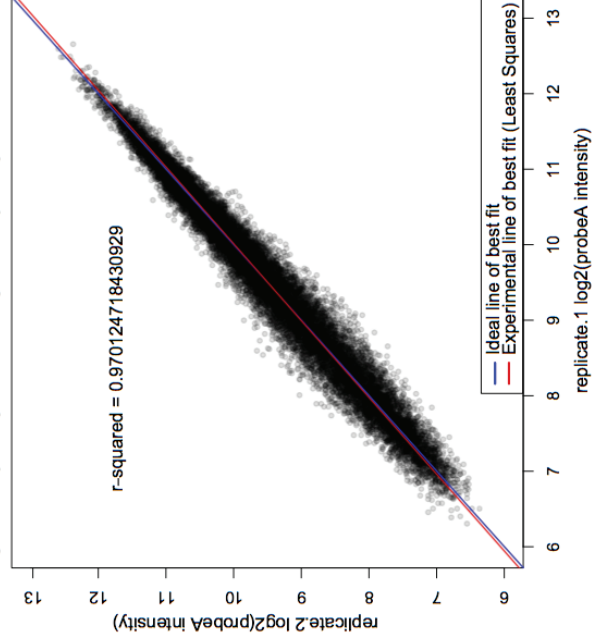
B Normalized ProbeA Intensities for Replicates of 1:1 Methylated(E44):Unmethylated(H16) Control Mix



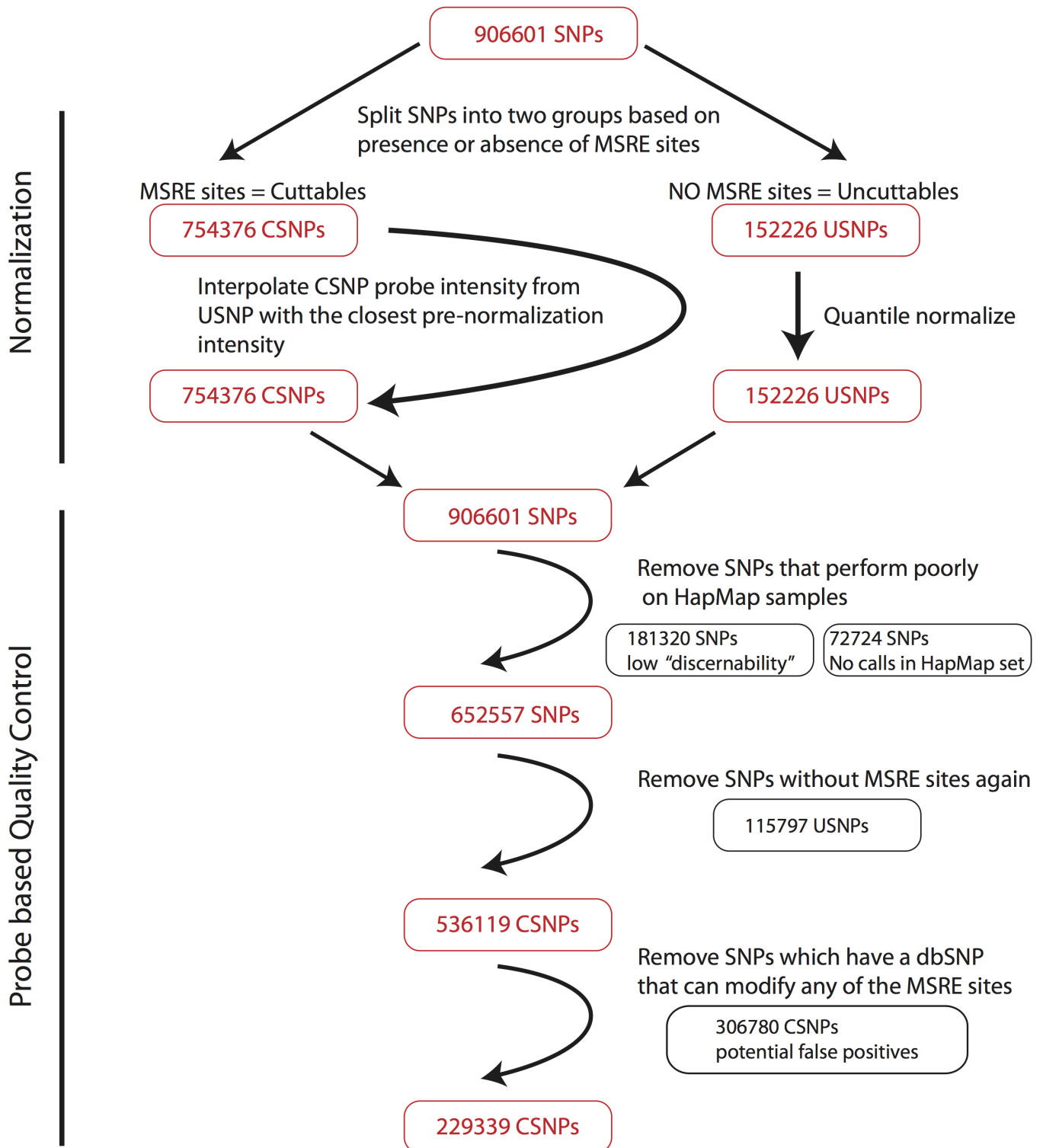
C Unnormalized ProbeA Intensities for Replicates of 1:1 Methylated(H16):Unmethylated(E44) Control Mix



D Normalized ProbeA Intensities for Replicates of 1:1 Methylated(H16):Unmethylated(E44) Control Mix

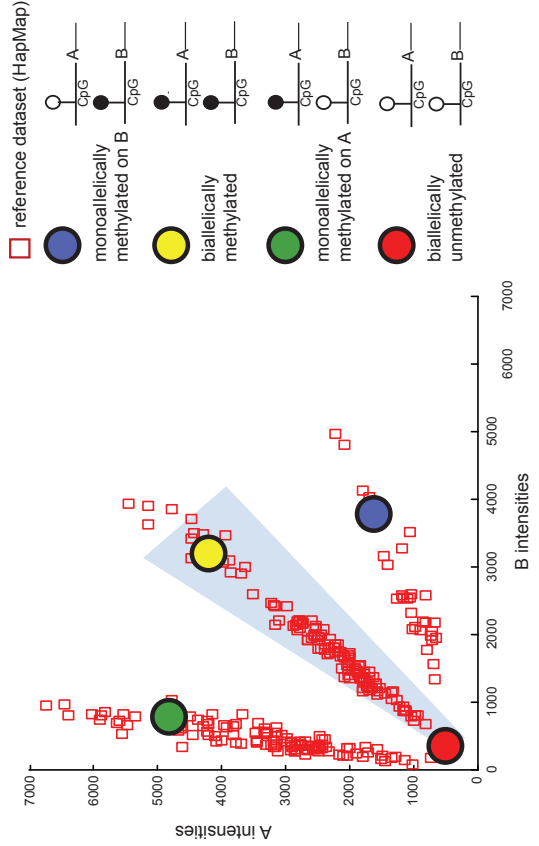


Supplemental Figure 8

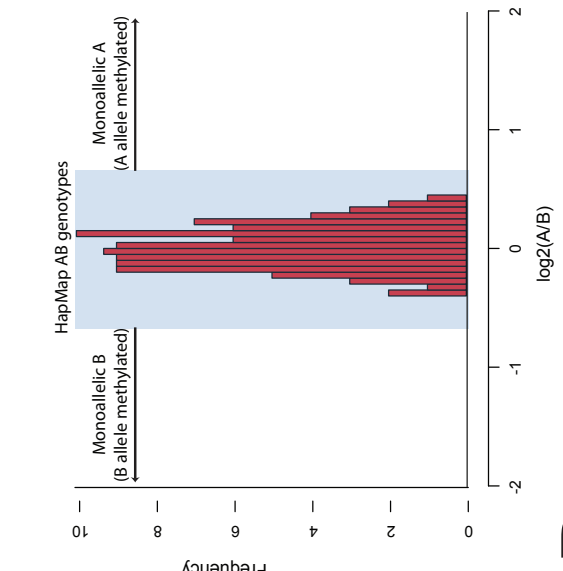


Supplemental Figure 9

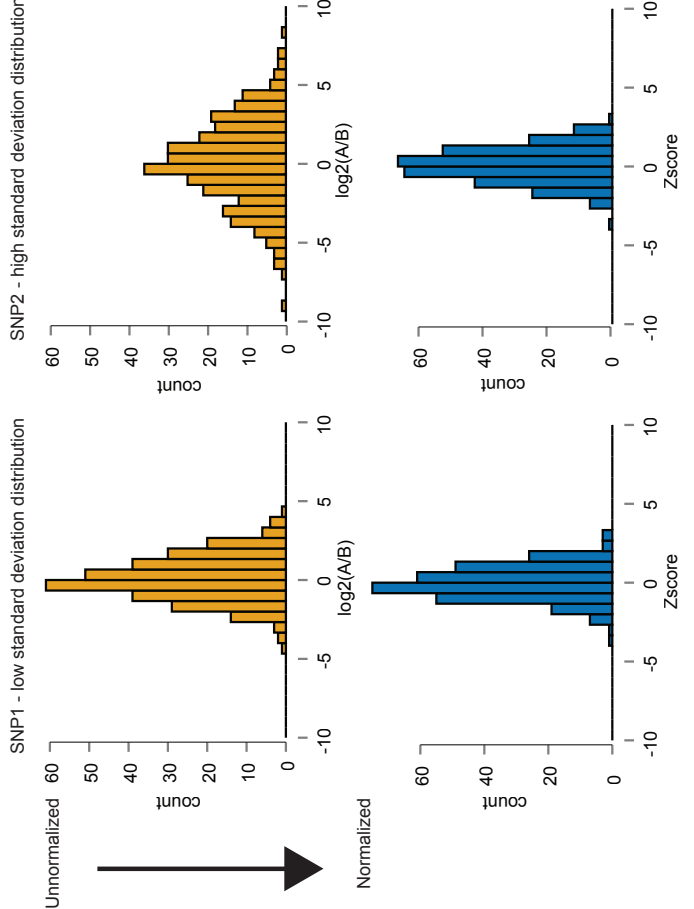
A Potential outcomes for AB genotypes



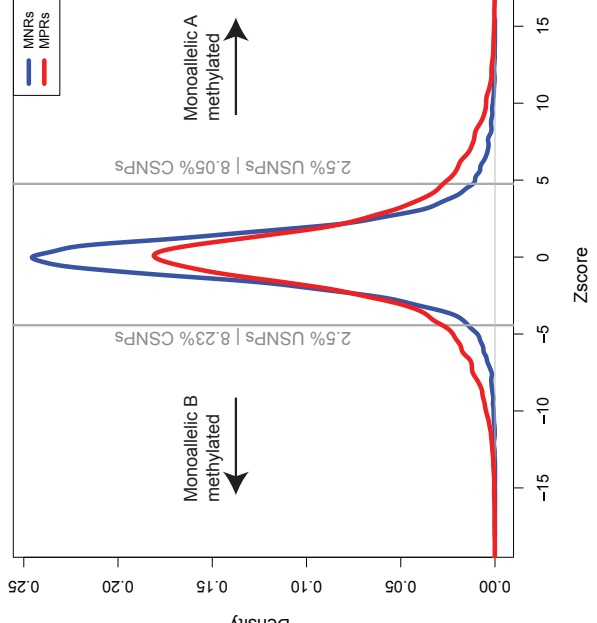
B Use A/B ratio as measure of allelic bias



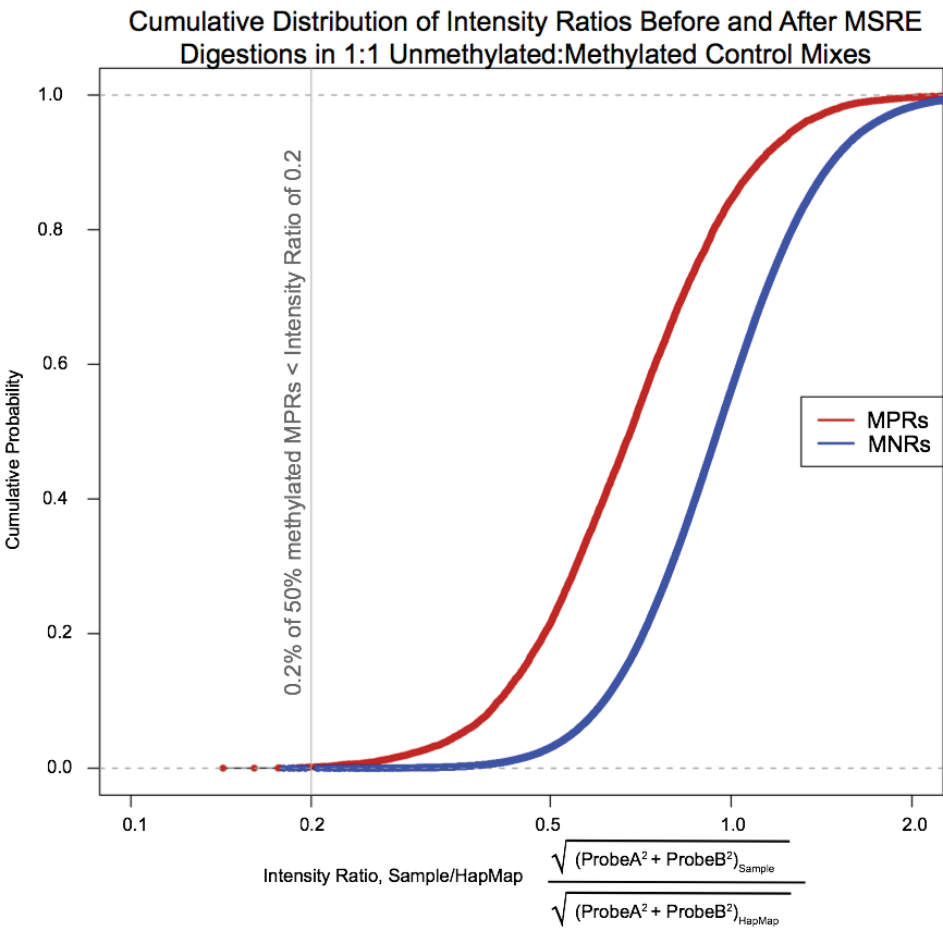
C Standard normalize A/B ratios of different probesets using HapMap Value



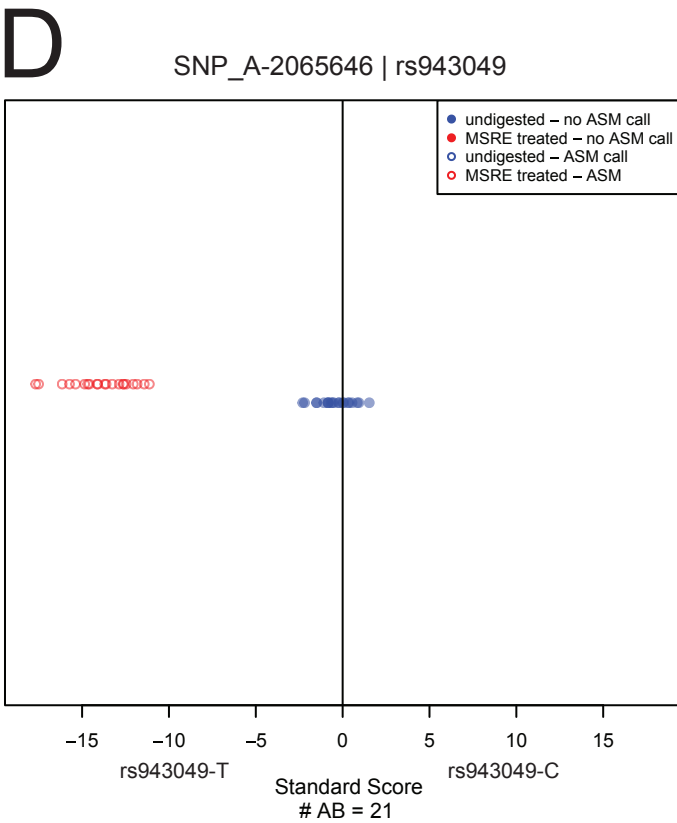
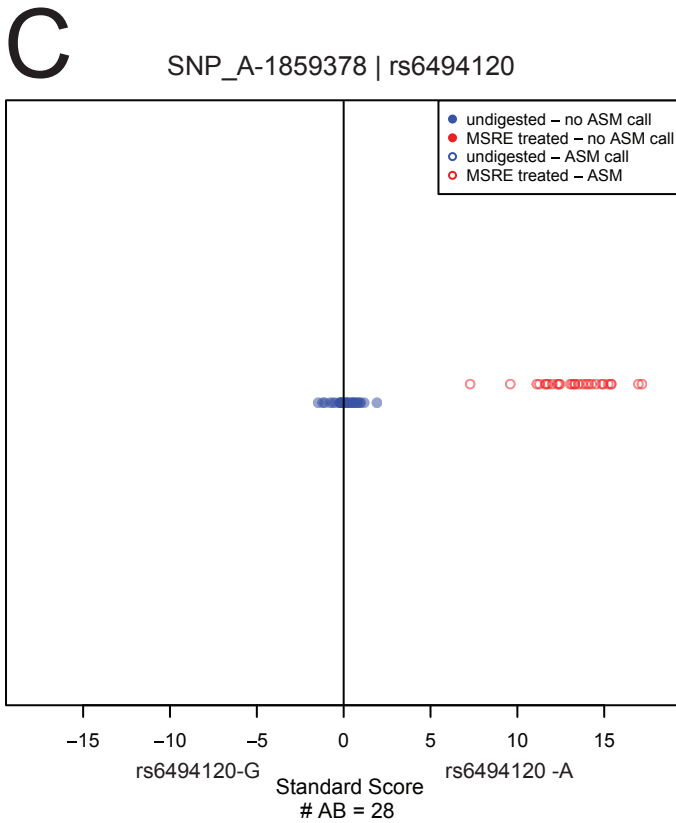
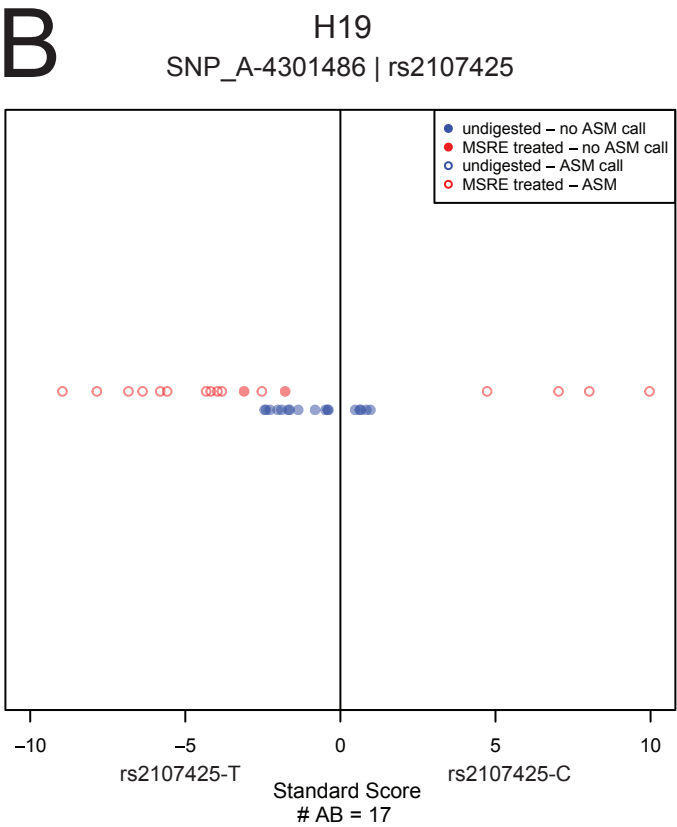
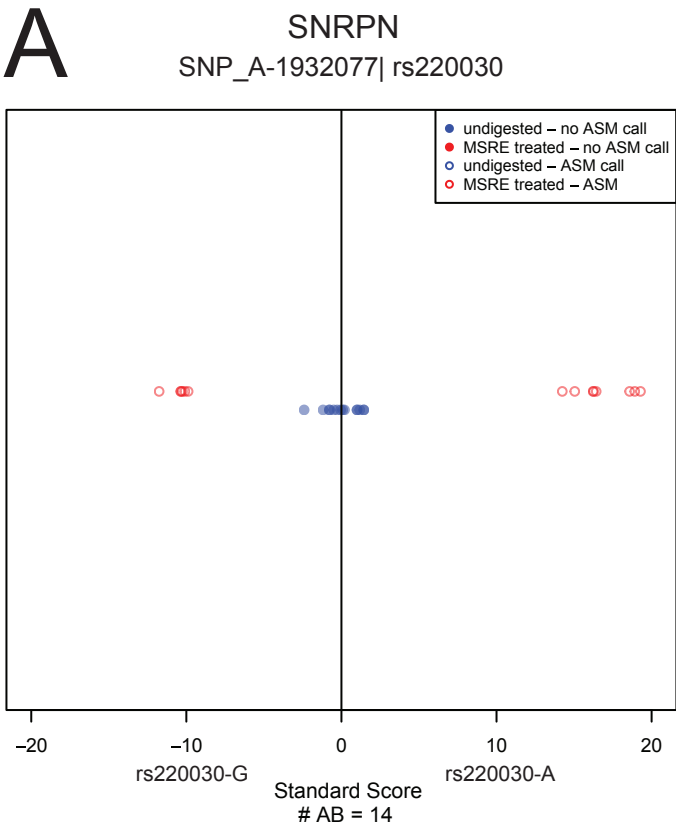
D Use MNRbased Z-scores to remove inter-sample technical variation



Supplemental Figure 10



Supplemental Figure 11



Supplemental Figure 12

