

Figure S1. Distribution of MAF for exonic and all variants (top); distribution of MAF for exonic and all variants with MAF<0.05 (middle); distribution of INDEL size for exonic and all variants (bottom).

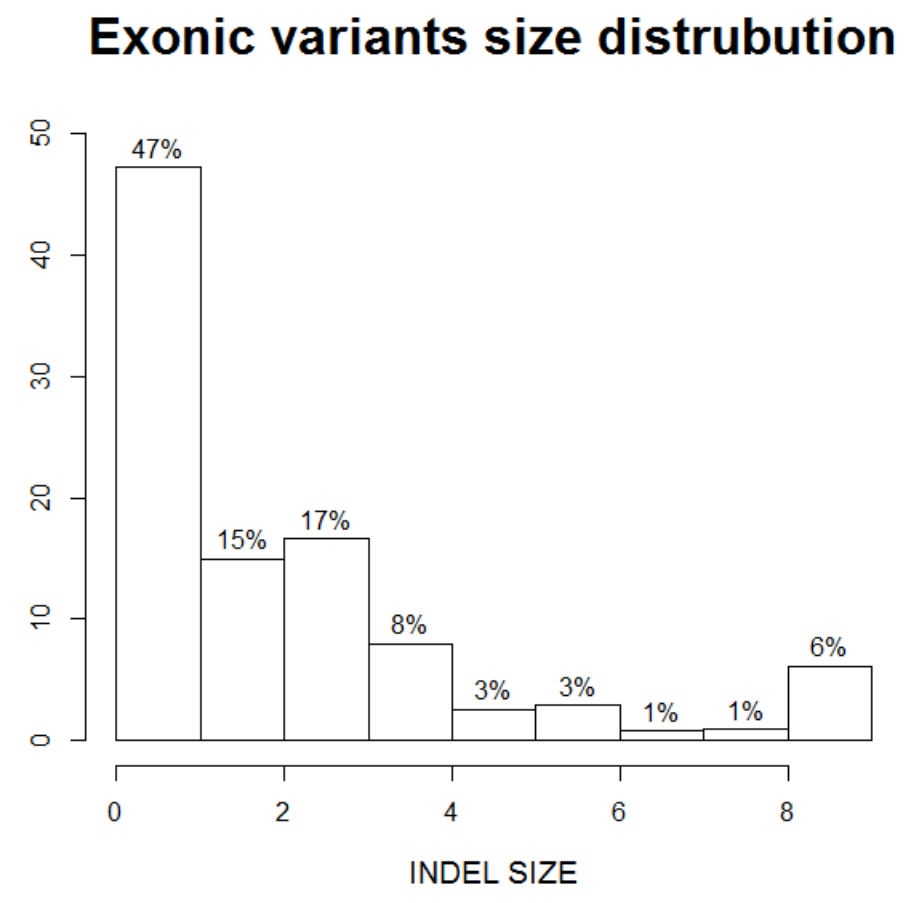
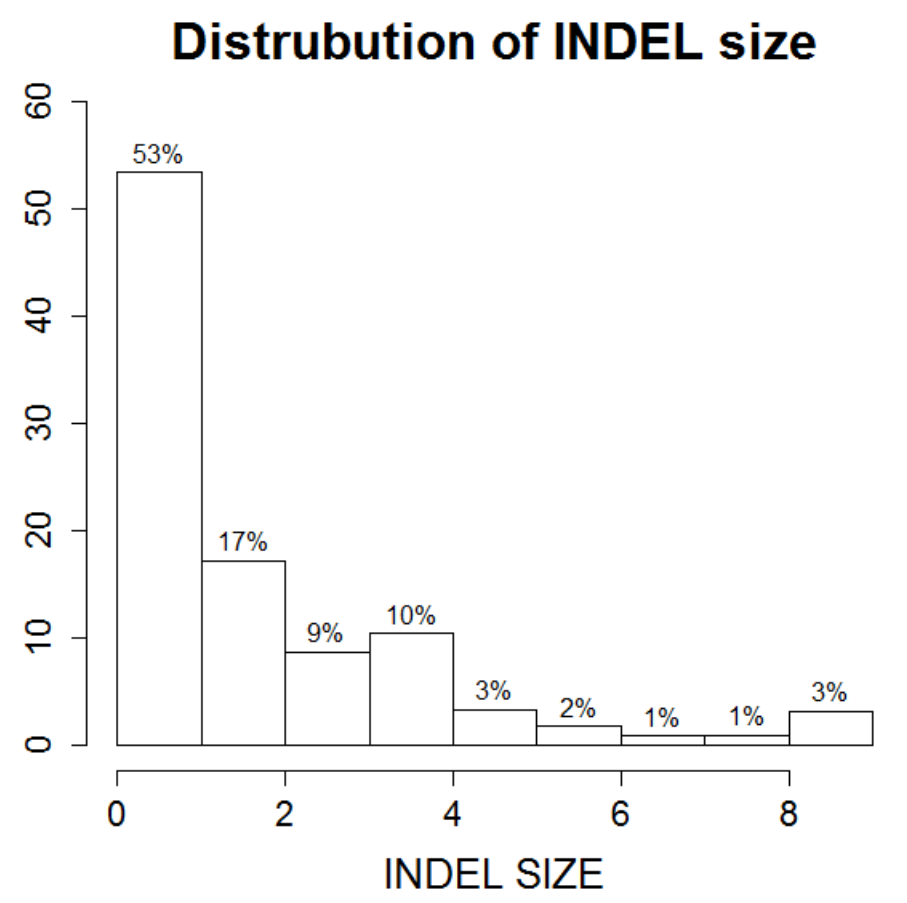
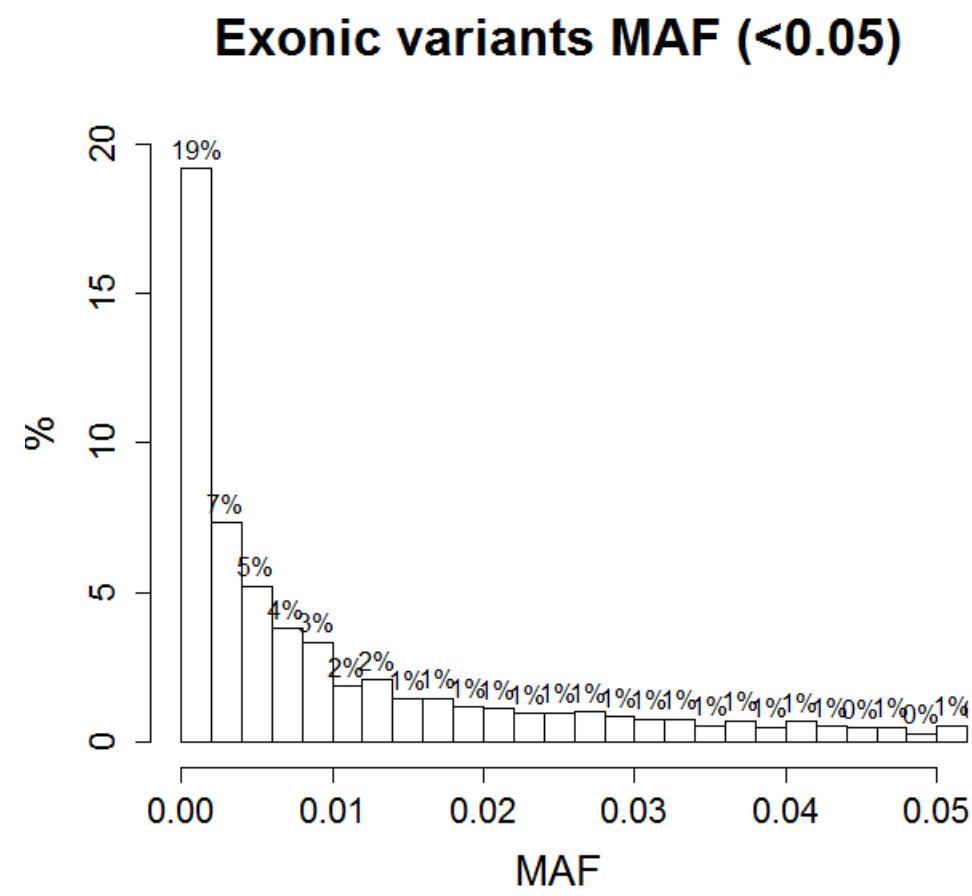
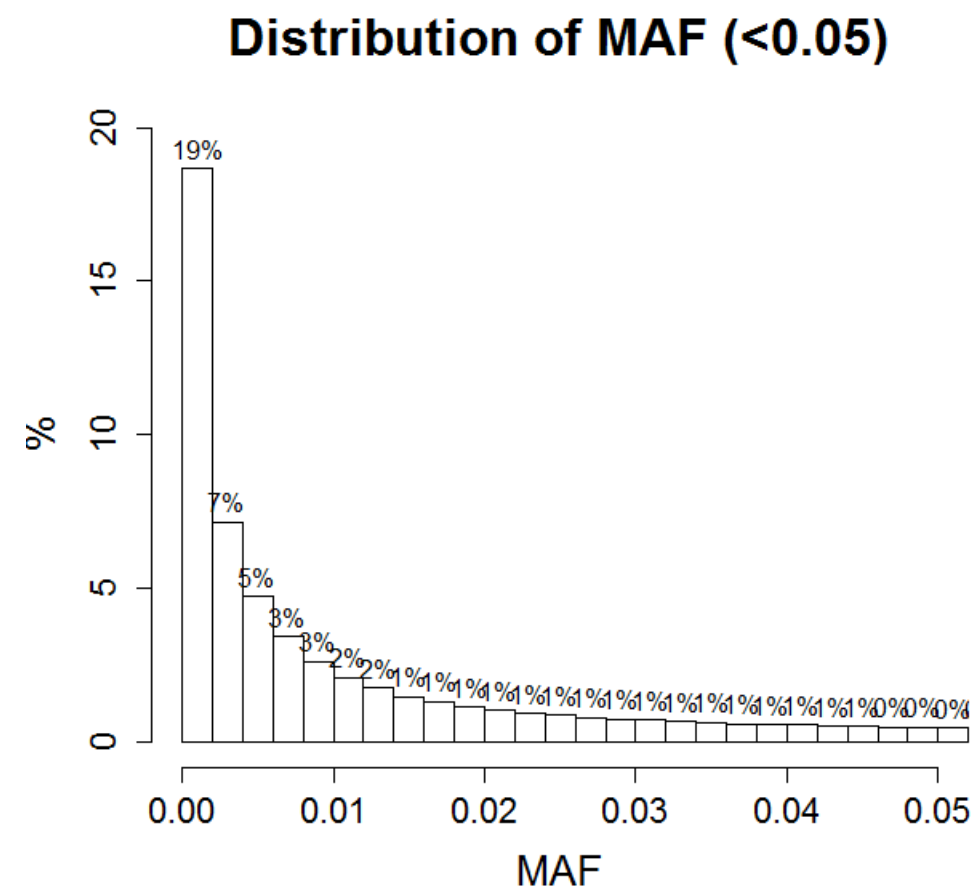
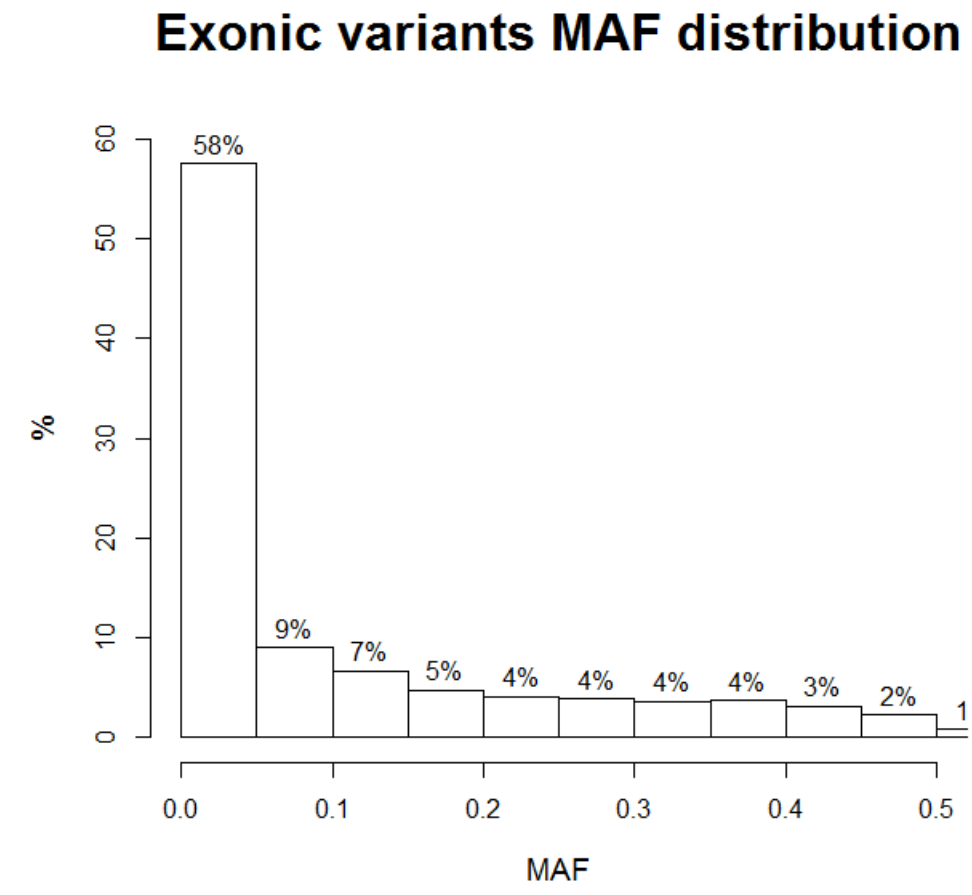
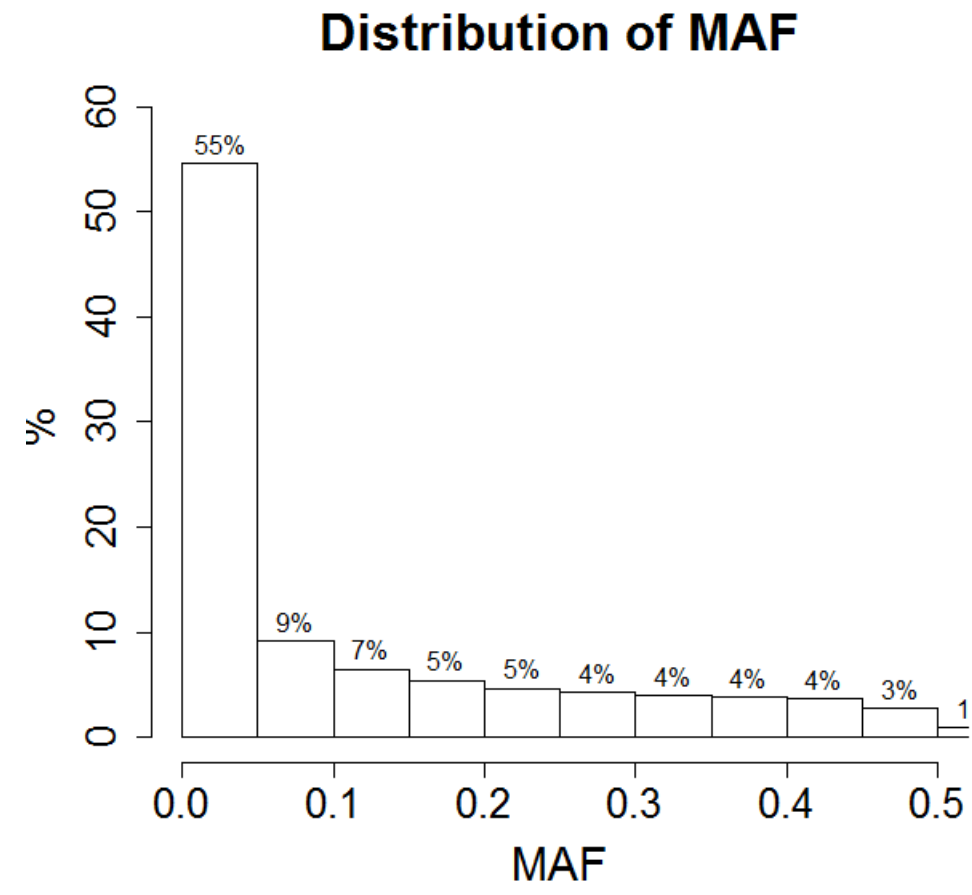


Figure S2. Kappa value stratified by INDEL sizes (top) and function annotations (bottom).

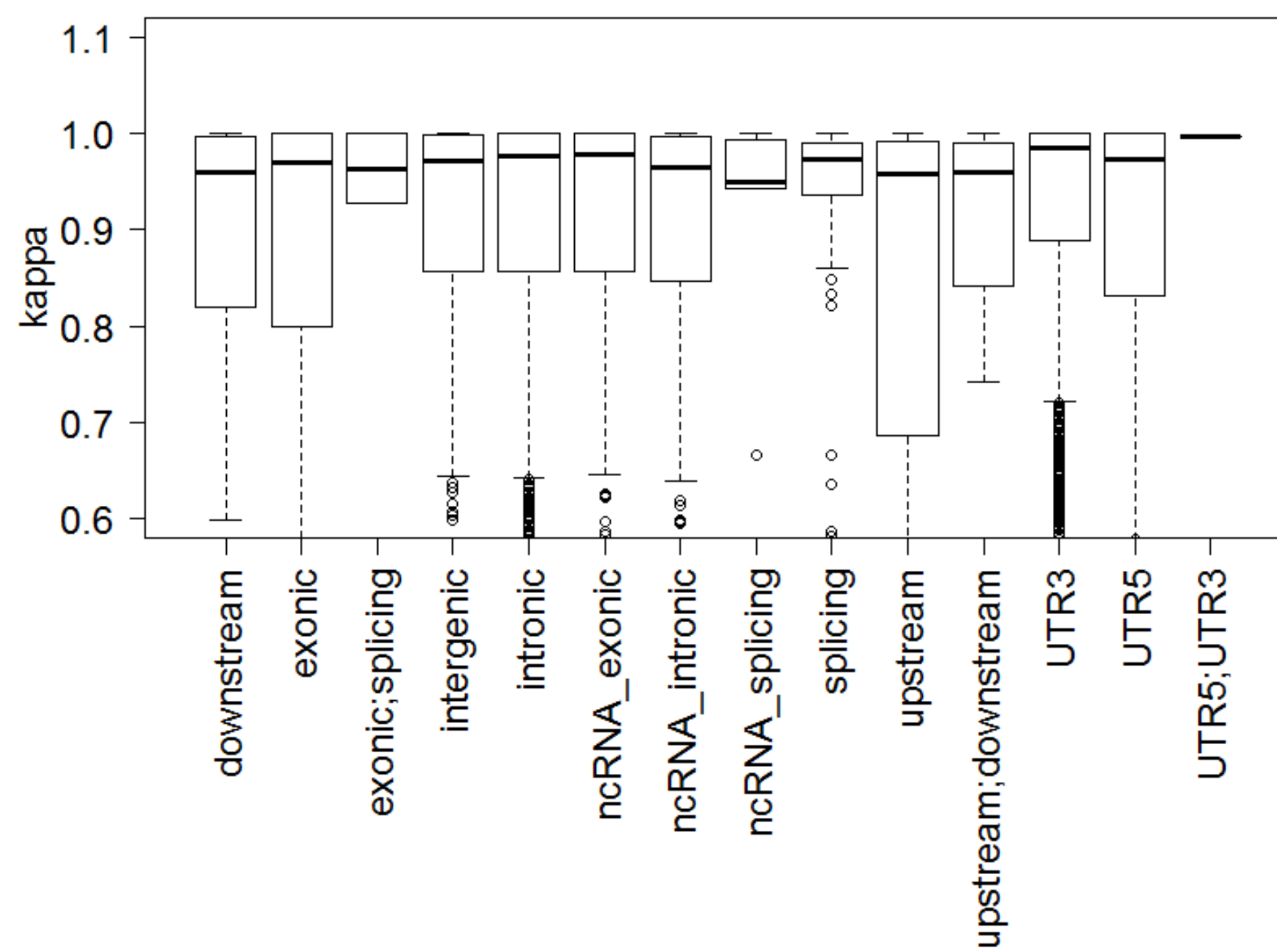
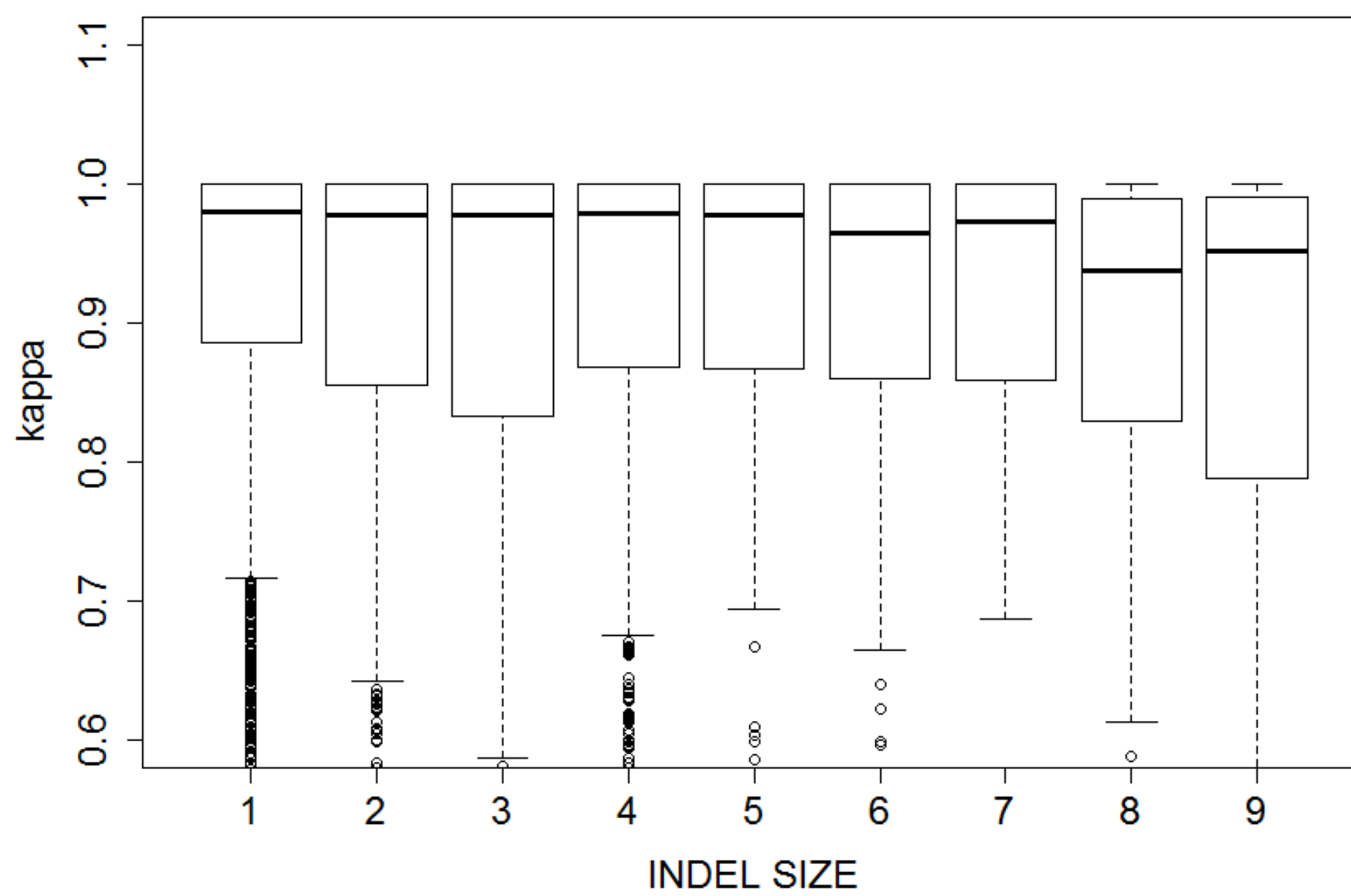


Figure S3. Regional plot for CETP association signal with HDL.

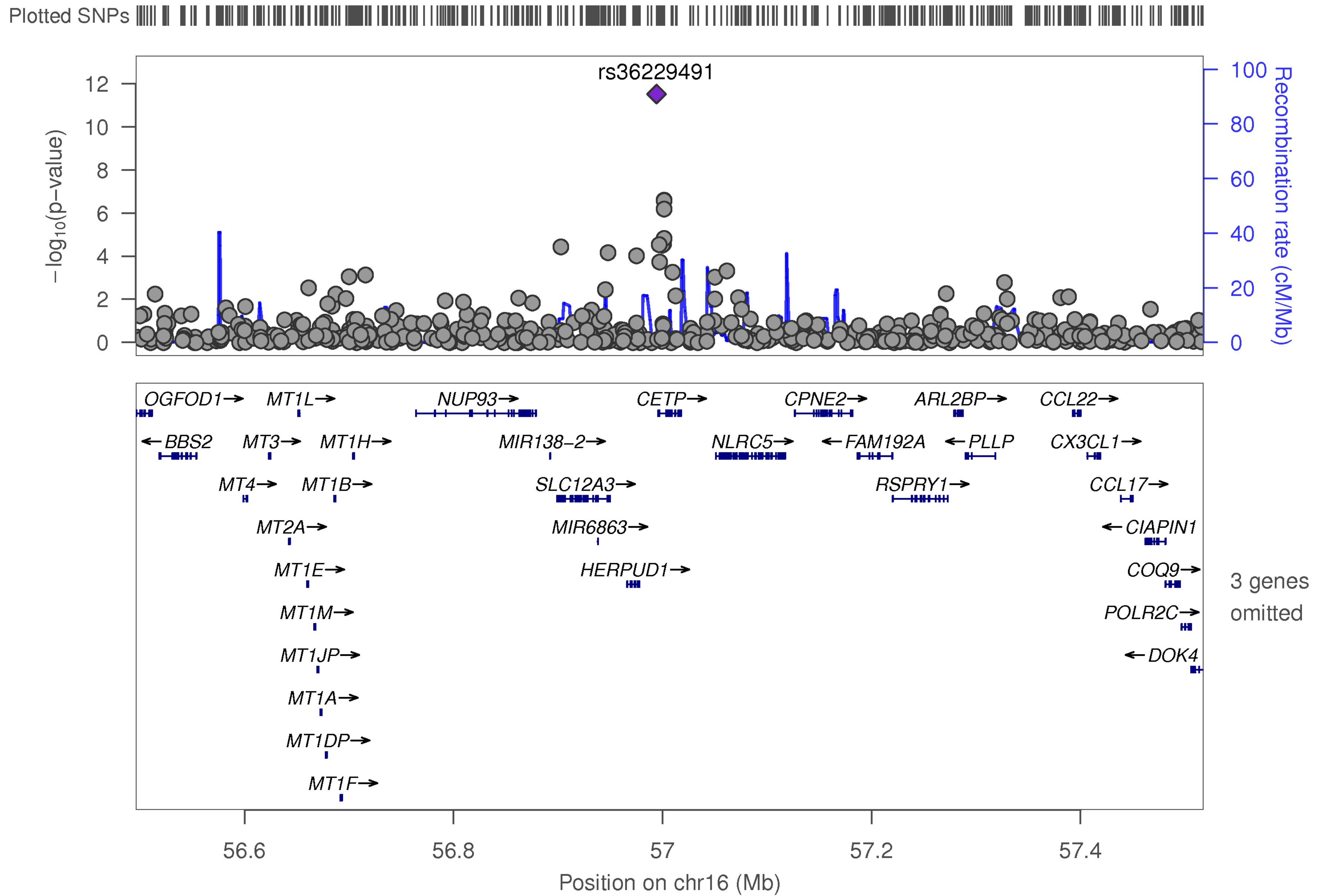


Figure S4. a. For variants associated ($P < 0.005$) and linked ($\text{LOD} > 1$) with HDL, the comparison of INDEL size distributions (top), function annotations (middle) and MAF (bottom). b. For variants associated ($P < 0.005$) and linked ($\text{LOD} > 1$) with TG, the comparison of INDEL size distributions (top), function annotations (middle) and MAF (bottom).

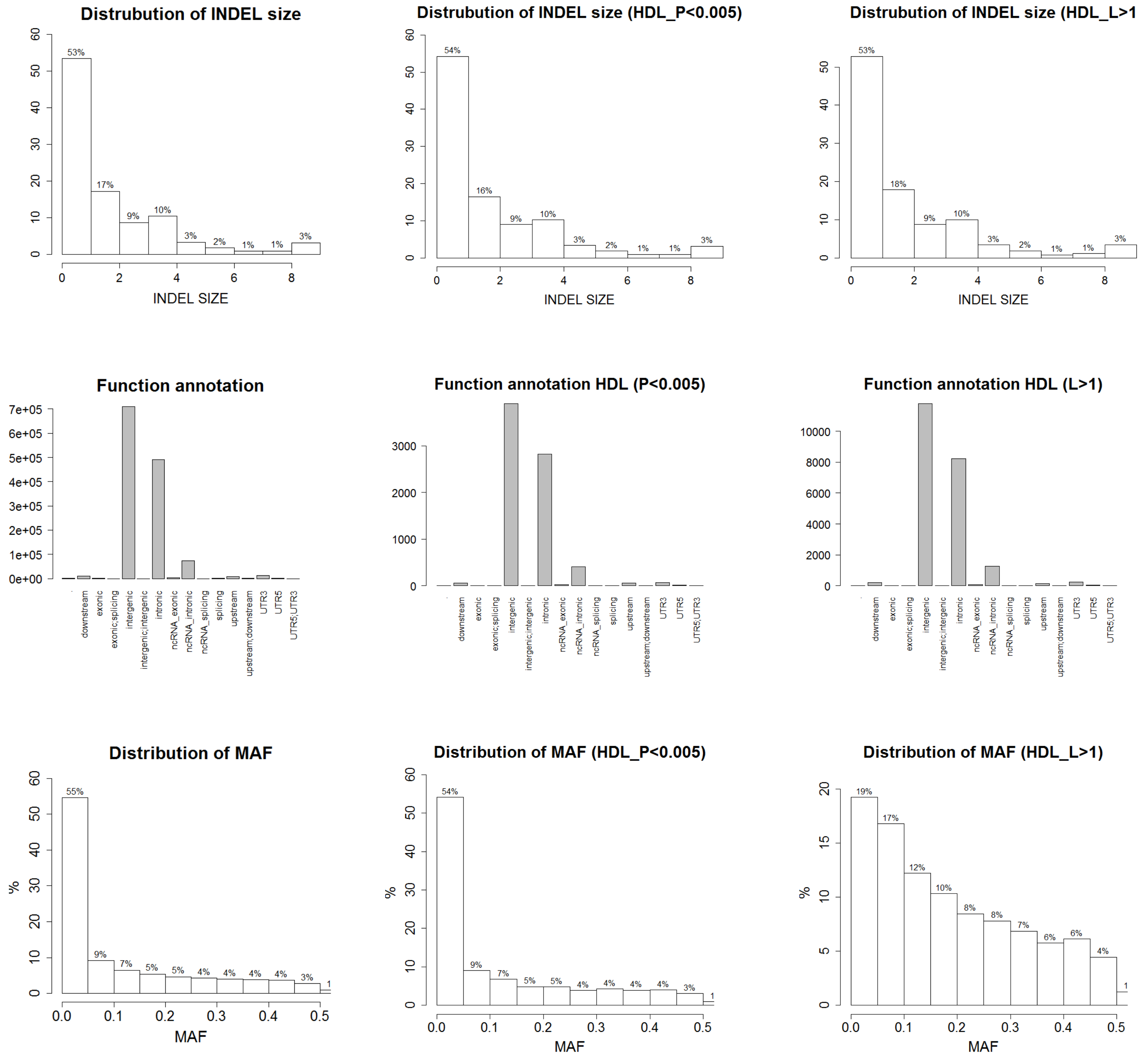


Figure S4. a. For variants associated ($P < 0.005$) and linked ($\text{LOD} > 1$) with HDL, the comparison of INDEL size distributions (top), function annotations (middle) and MAF (bottom). b. For variants associated ($P < 0.005$) and linked ($\text{LOD} > 1$) with TG, the comparison of INDEL size distributions (top), function annotations (middle) and MAF (bottom).

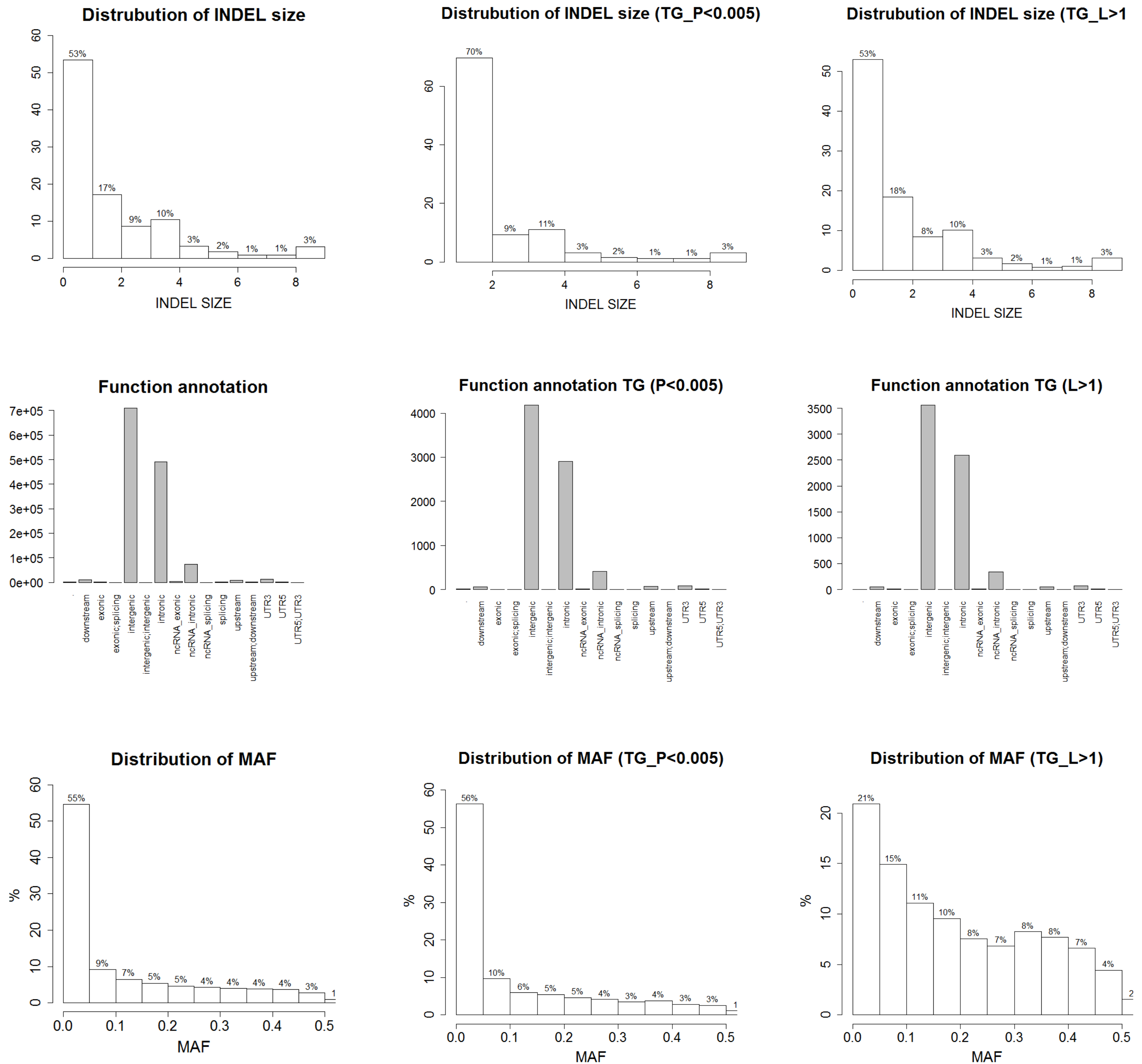


Figure S5. Scatter plots, opposed plots, and QQ plots (with and without 1% MAF cut off) for genome-wide association and linkage results for Structural Variants. For scatter plots, x-axis represents the $-\log_{10}(P)$ for association, y-axis represents the LOD score.

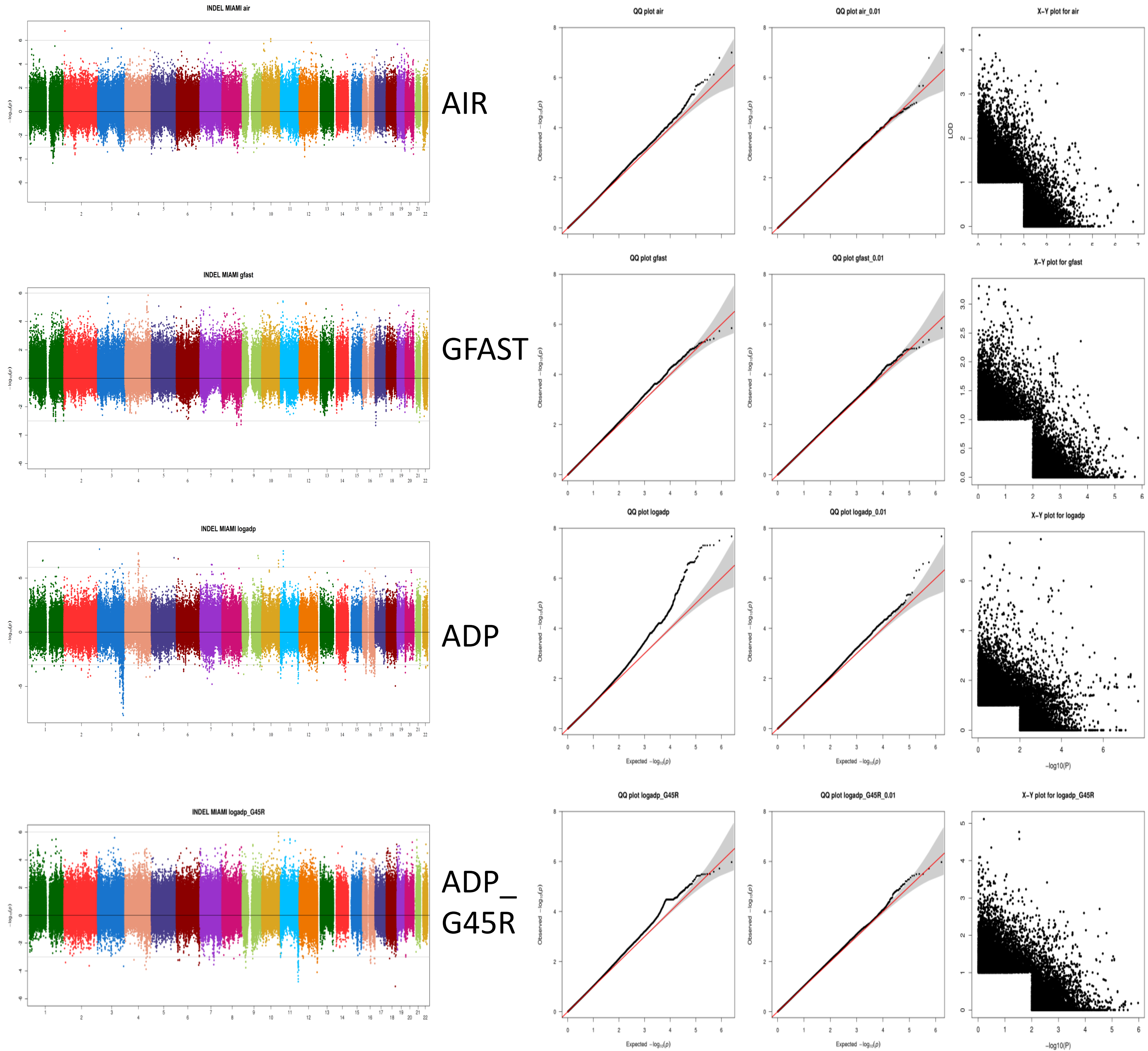


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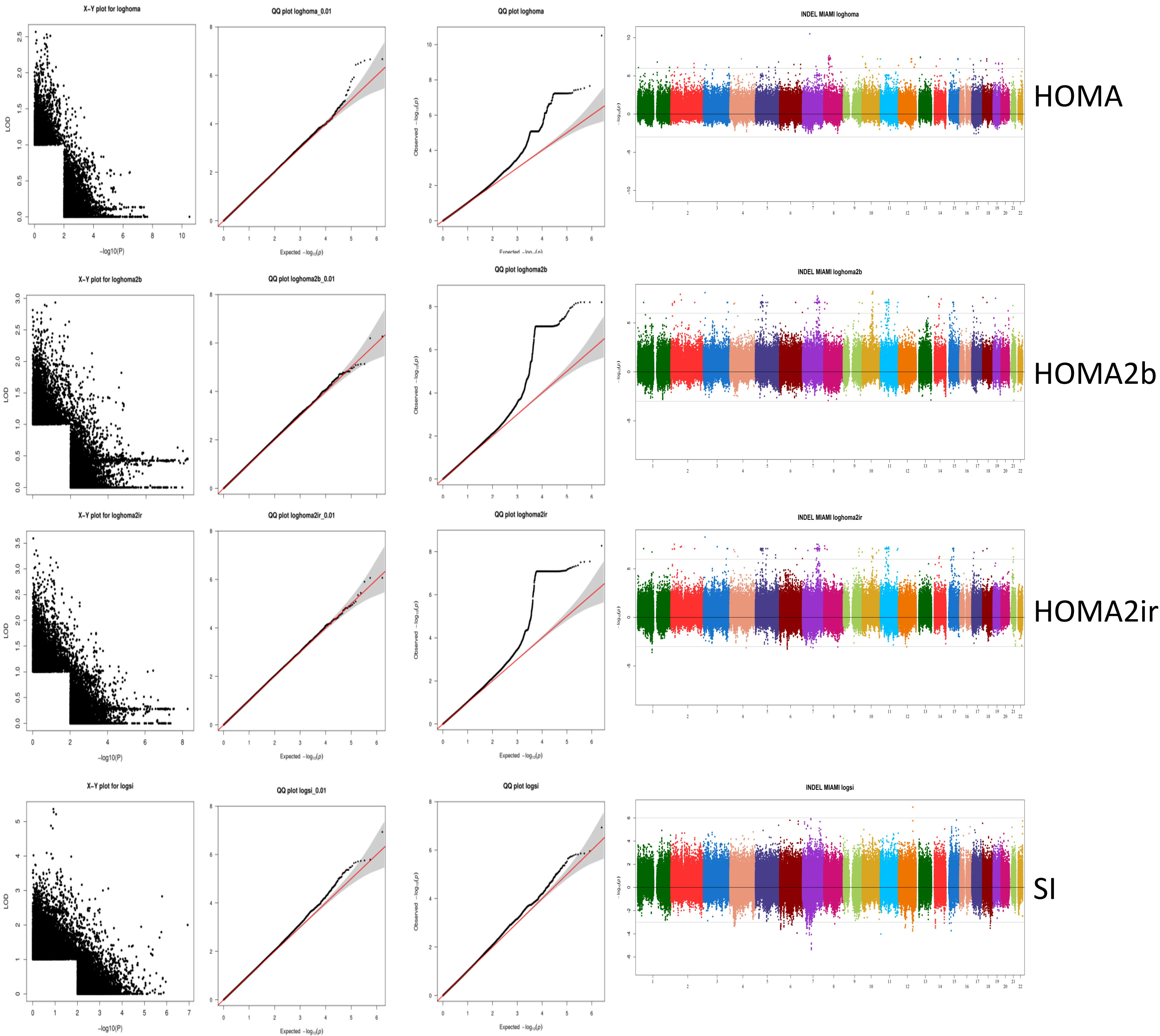


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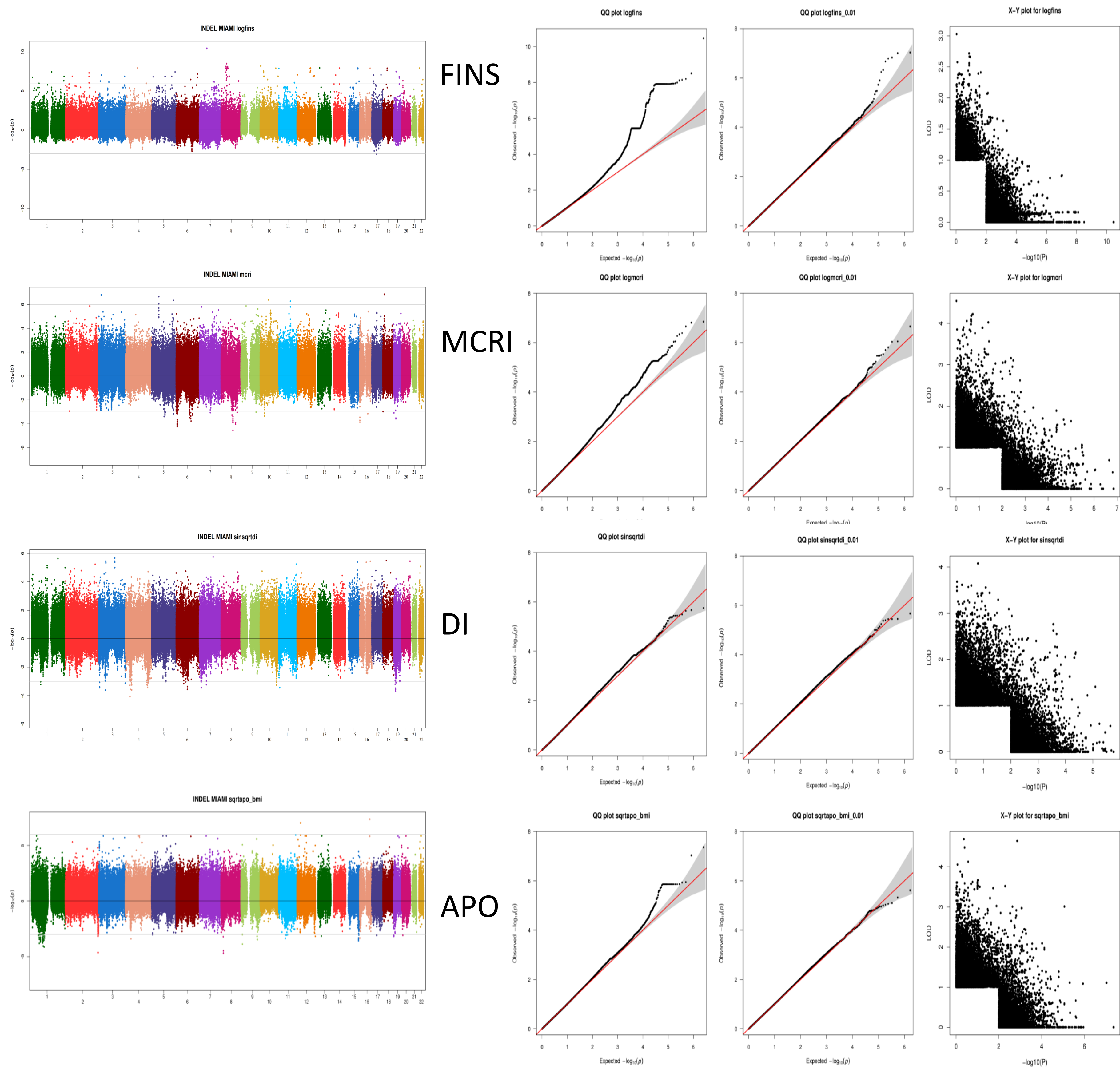


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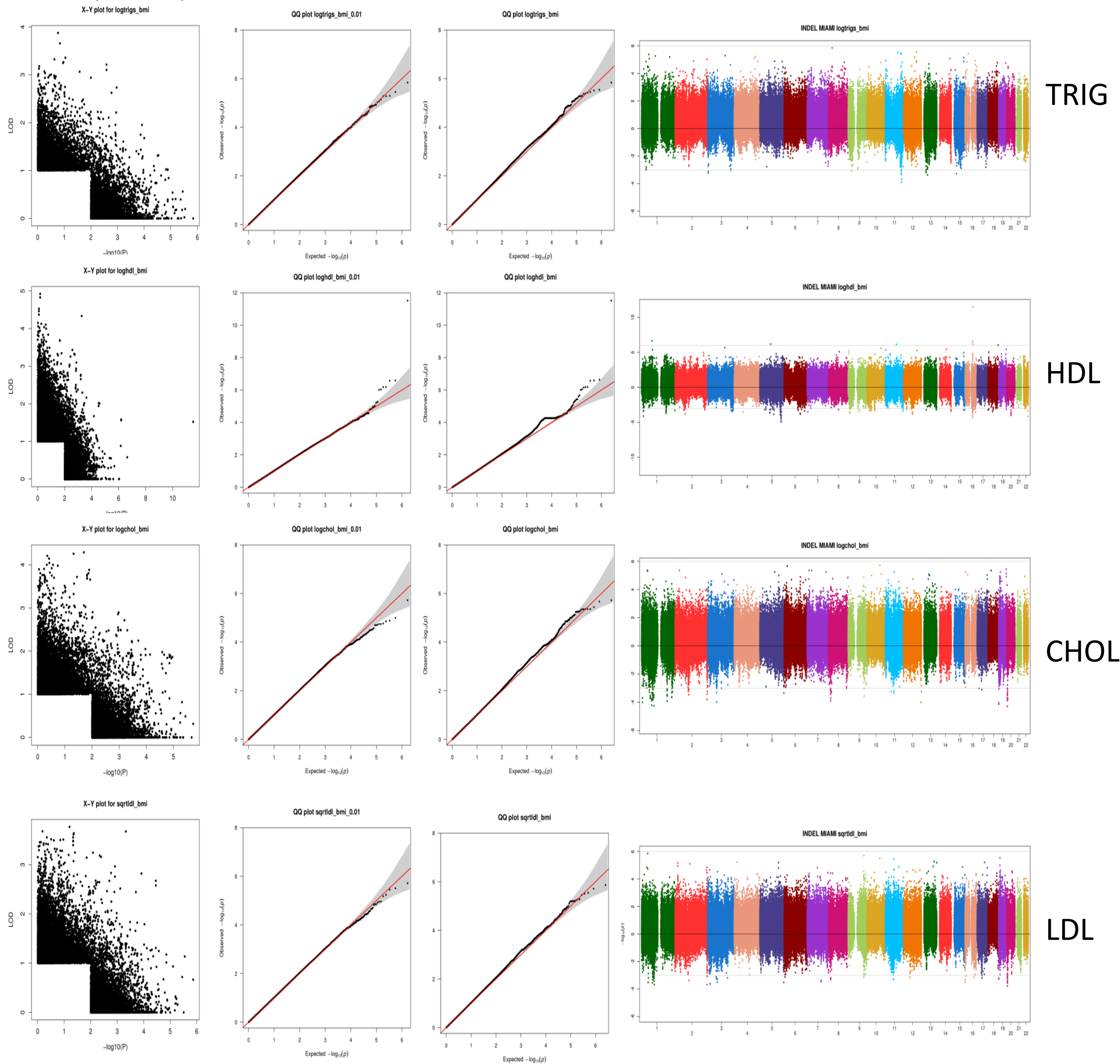
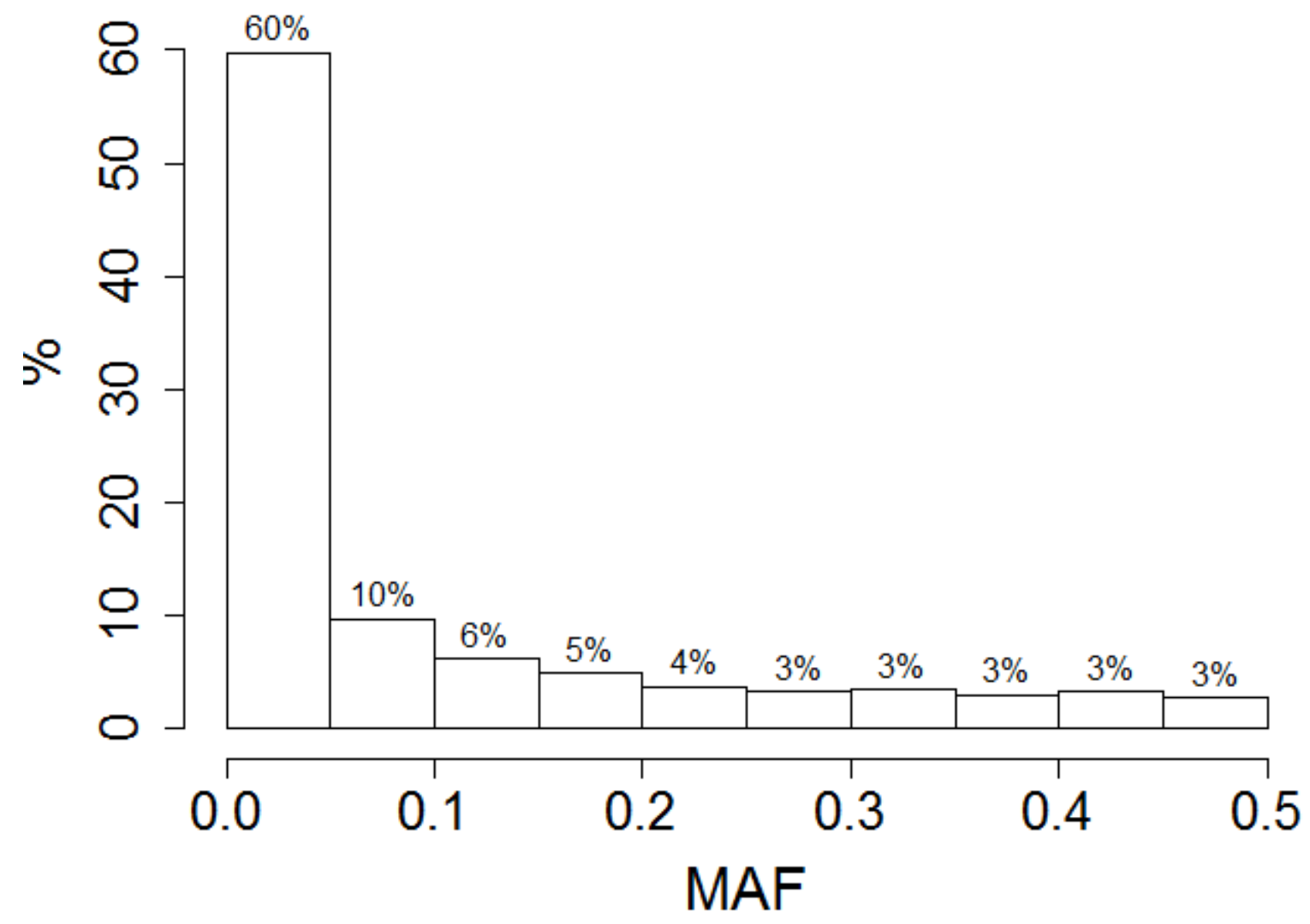


Figure S6. For exome sequencing and GWAS imputed INDELS overlapping and non-overlapping variants, the distribution of MAF (top) and INDEL size (bottom).

Distribution of MAF (overlapping)



Distribution of MAF (non-overlapping)

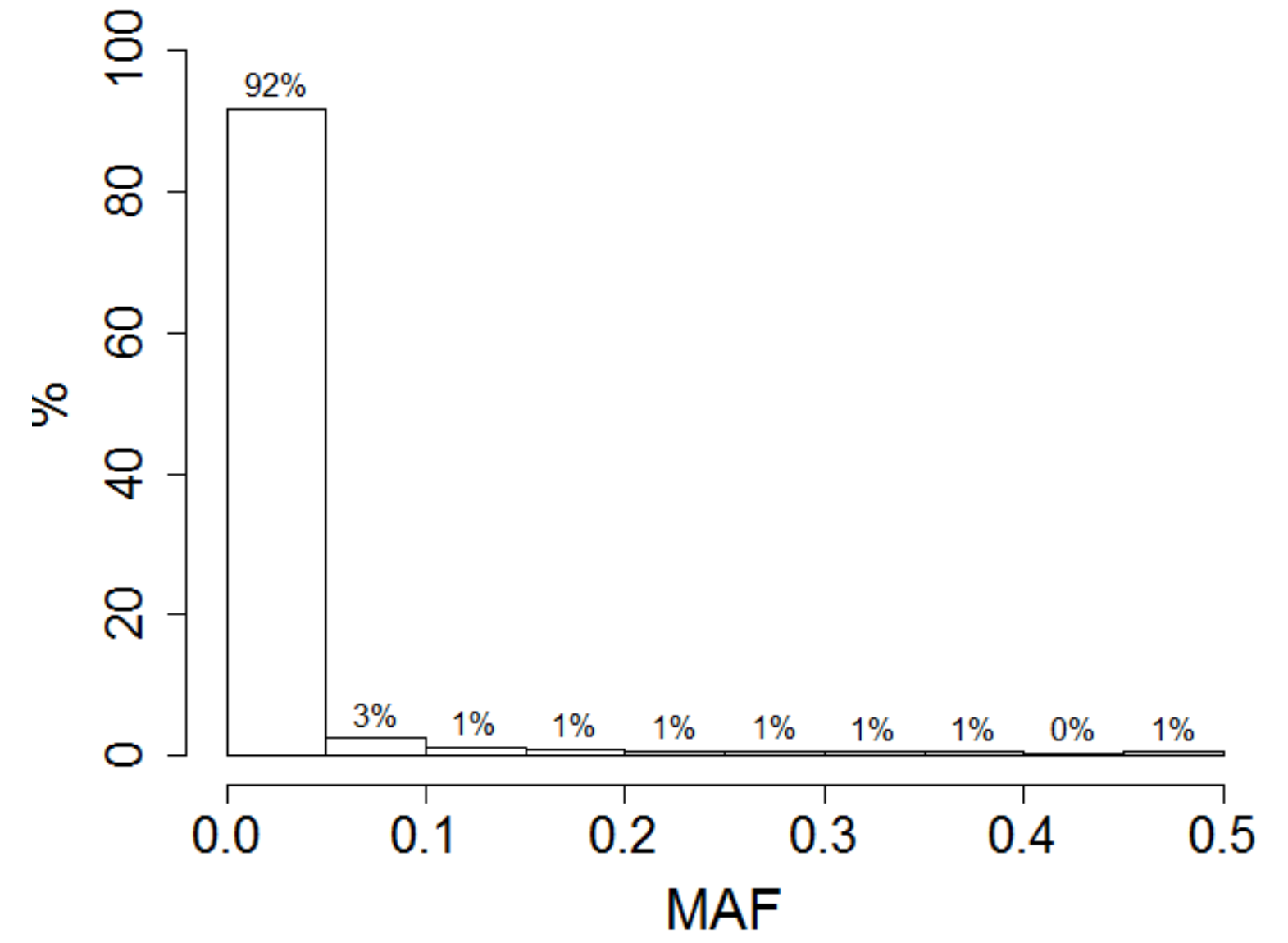


Figure S7. Opposed plot of association and linkage results for a. Adiponectin; b. SG; c. HOMA_B; d. HOMA_{1R}. Association manhattan plot on the top and linkage results were plotted on the bottom.

