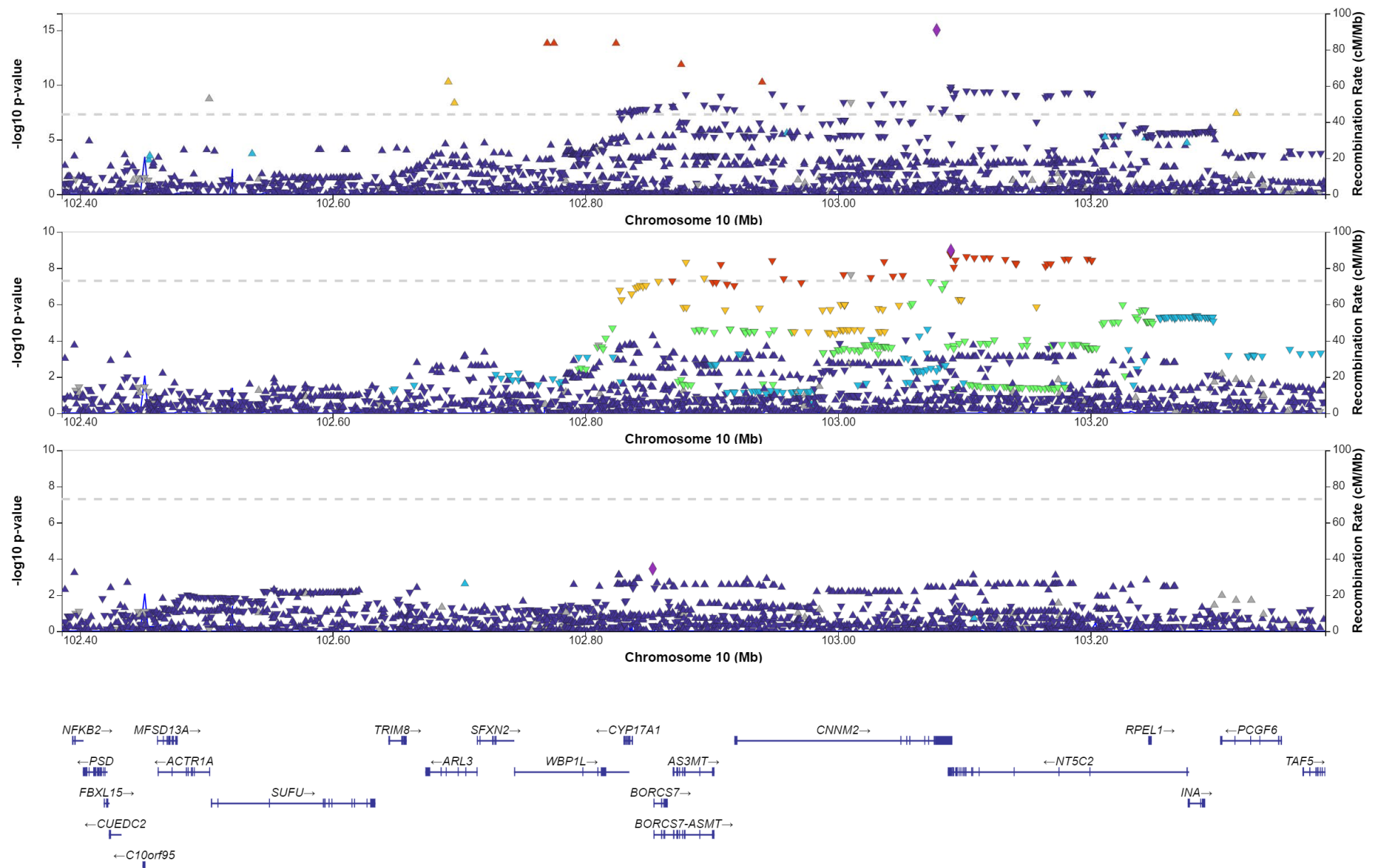**Fig S5.** HEALS iAs% Conditional Association Results

Fig S5. HEALS iAs% Conditional Association Results

Results of a post-imputation genetic association study of iAS% in the 10q24.32 region in HEALS. P-values were generated with linear models adjusted for age, sex, and kinship. The top panel represents overall association results, the second shows p-values from models adjusted for the initial lead SNP, and the bottom panel shows the result of models adjusted for both previously identified variants. Three lead variants were identified in this analysis: chr10:103078084 (rs145537350), chr10:103089387 (rs12573221) and chr10:102853348. We further note that the primary and secondary signals are identical to two signals identified in the analysis of DMA%.