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Supplementary figure S1

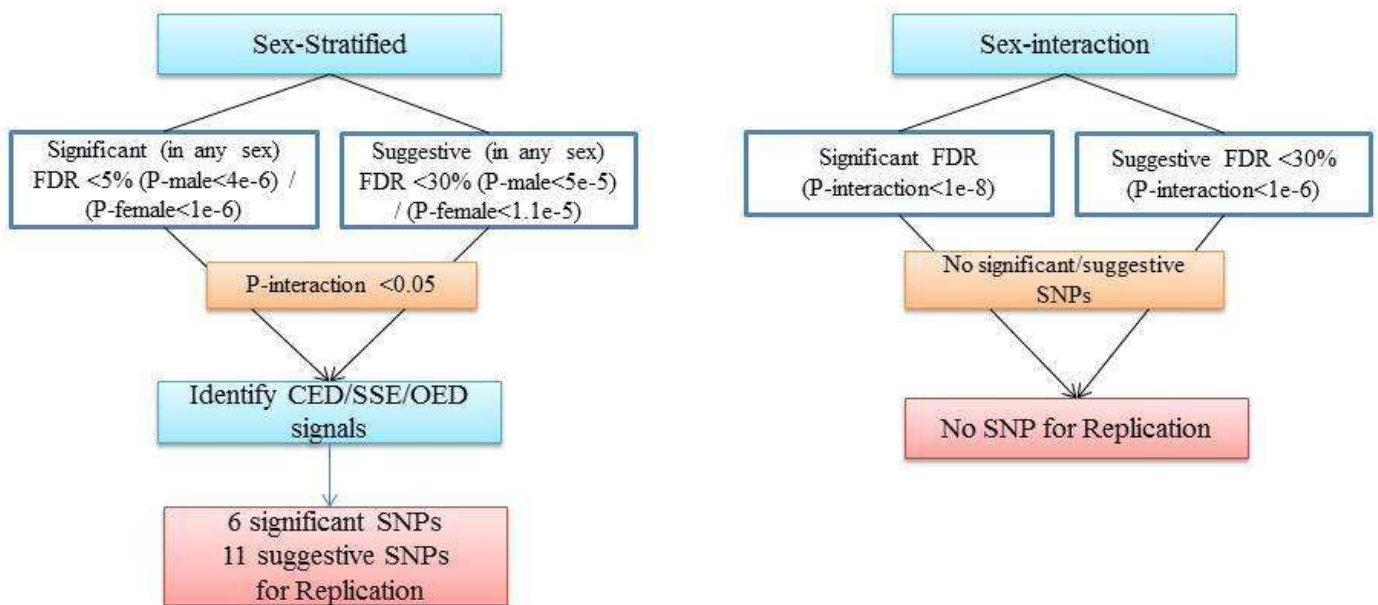
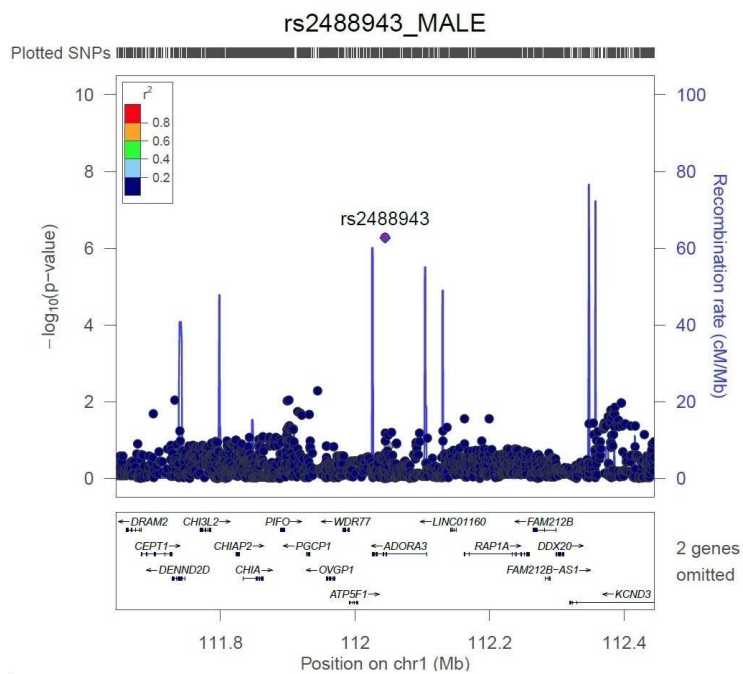
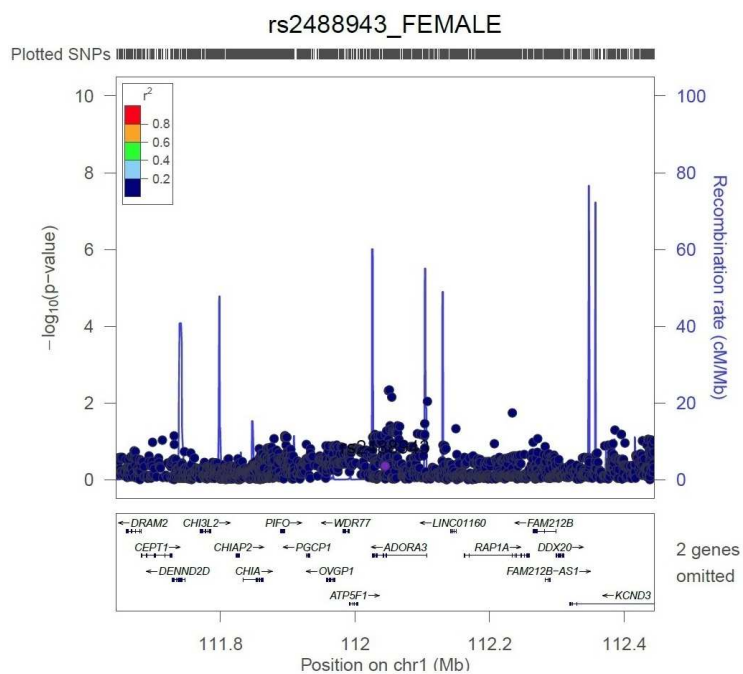


Fig: Criteria for selection of SNPs to carry forward for replication

Fig S2 Regional plot of SNP(s) without LD cluster in hg19 1000gEUR



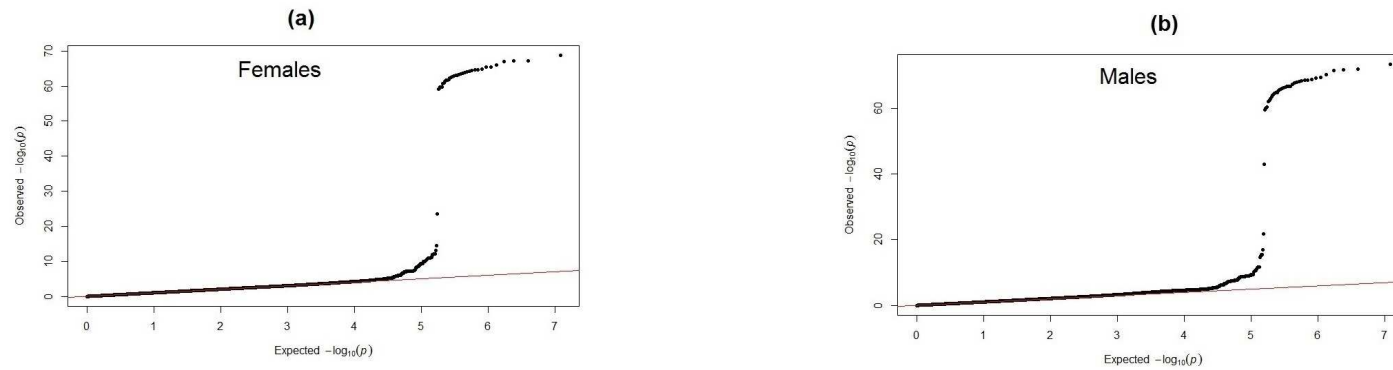


Fig S3: Quantile-Quantile plots of GWAS P-values in (a) female and (b) male datasets

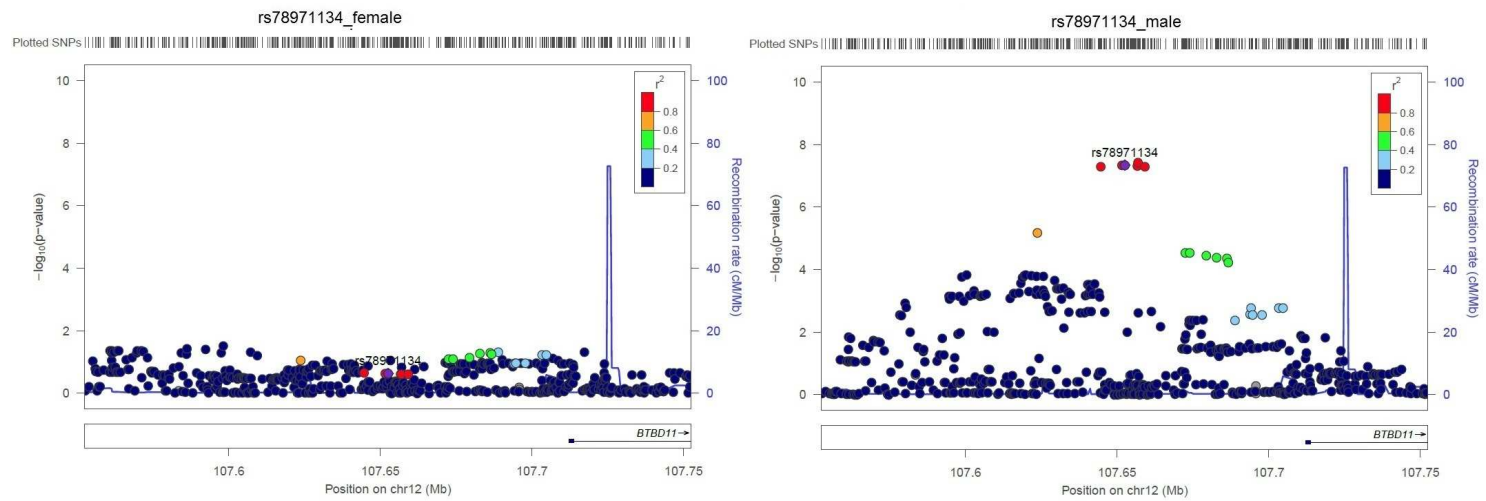
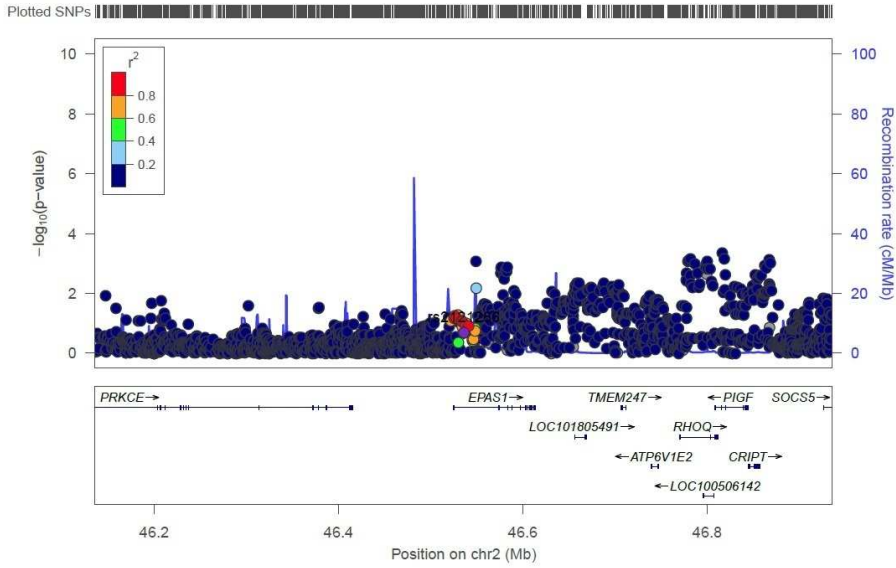


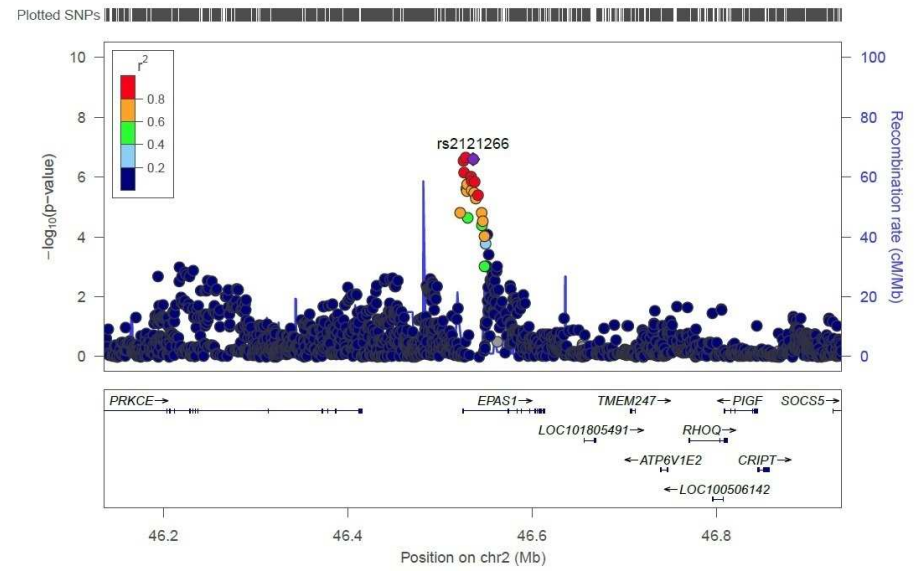
Fig S4(a) Regional LD plot of the significant SNPs in the discovery series

Fig S4(a) Regional LD plot of the significant SNPs in the discovery series

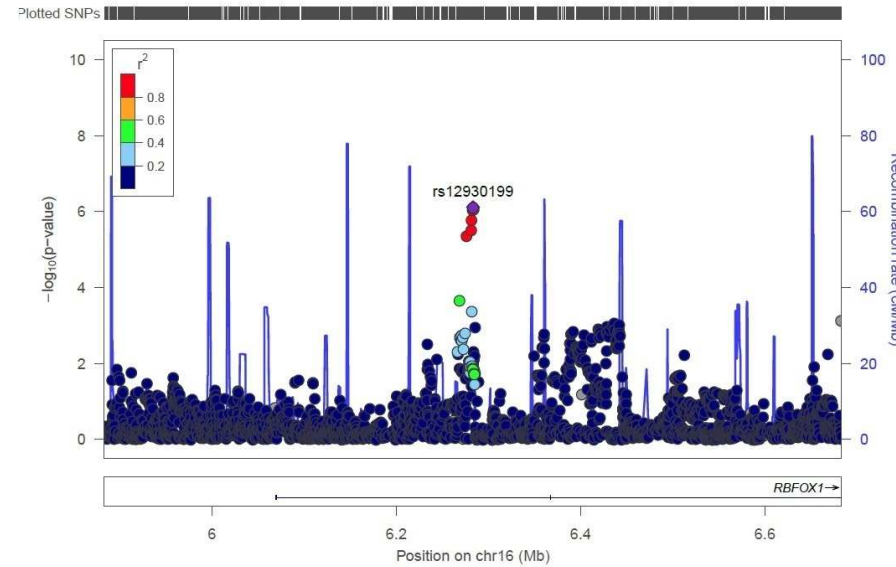
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rs2121266_male



rs12930199_female



rs12930199_male

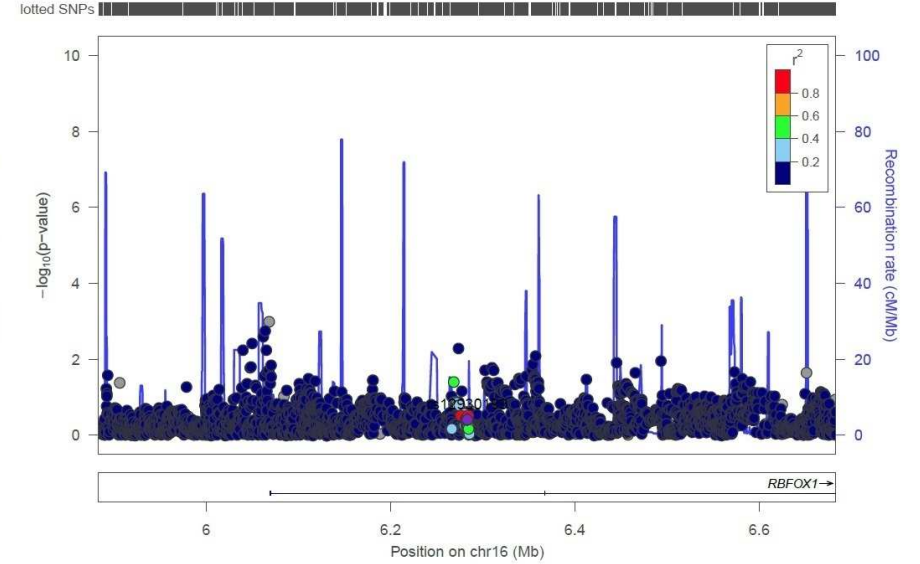


Fig S4(a) Regional LD plot of the significant SNPs in the discovery series

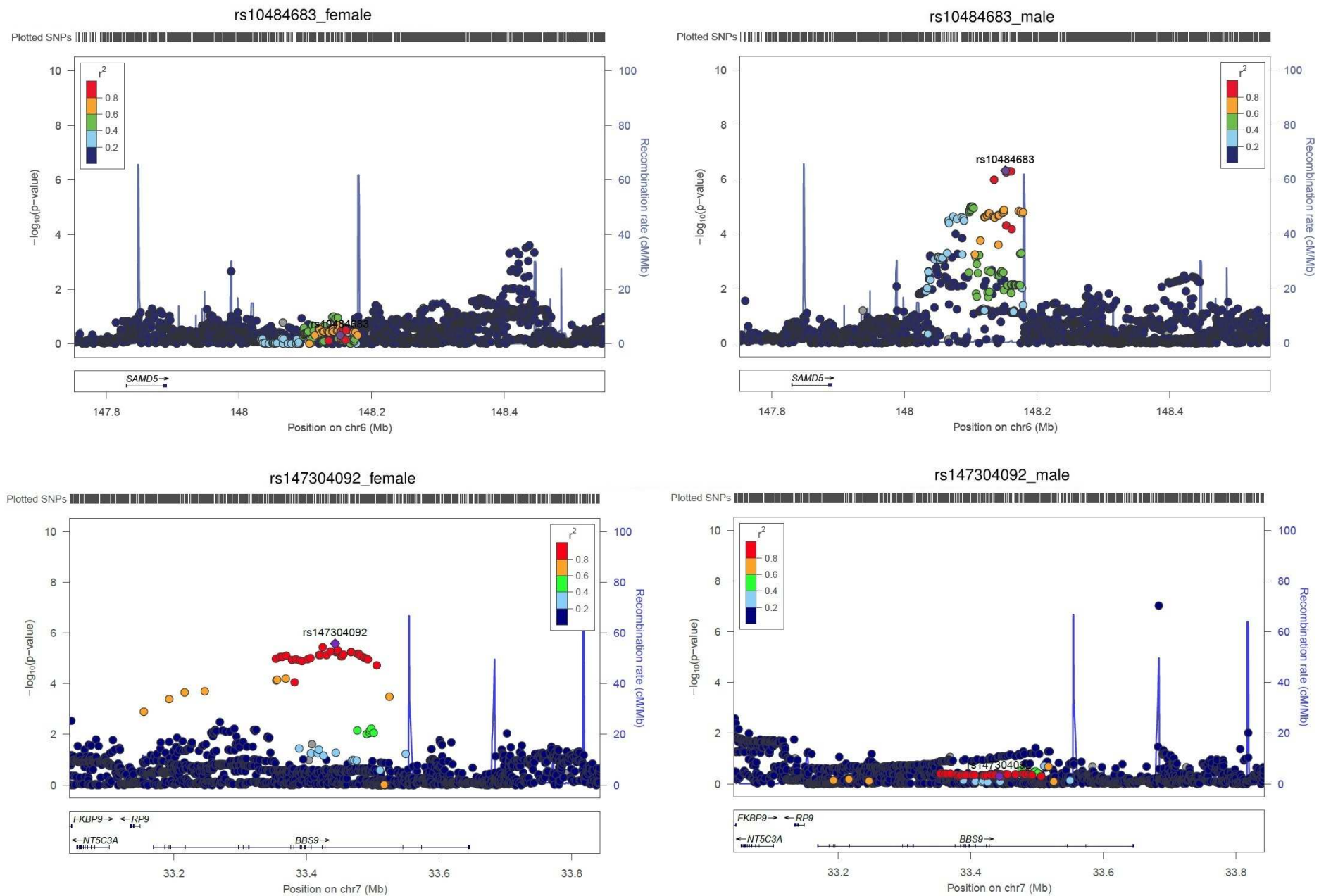


Fig S4(b) Regional plot of the suggestive SNPs in the discovery series

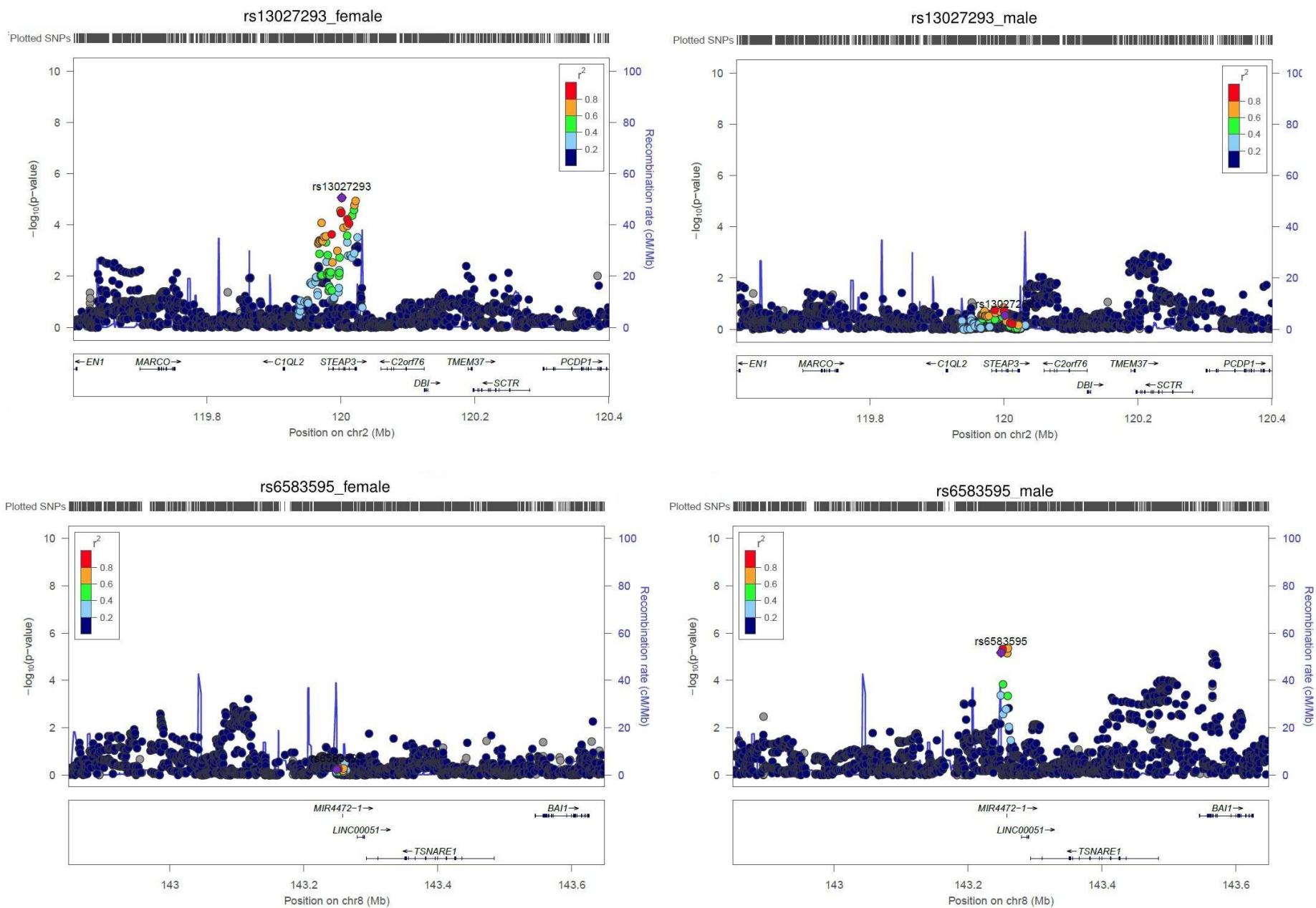
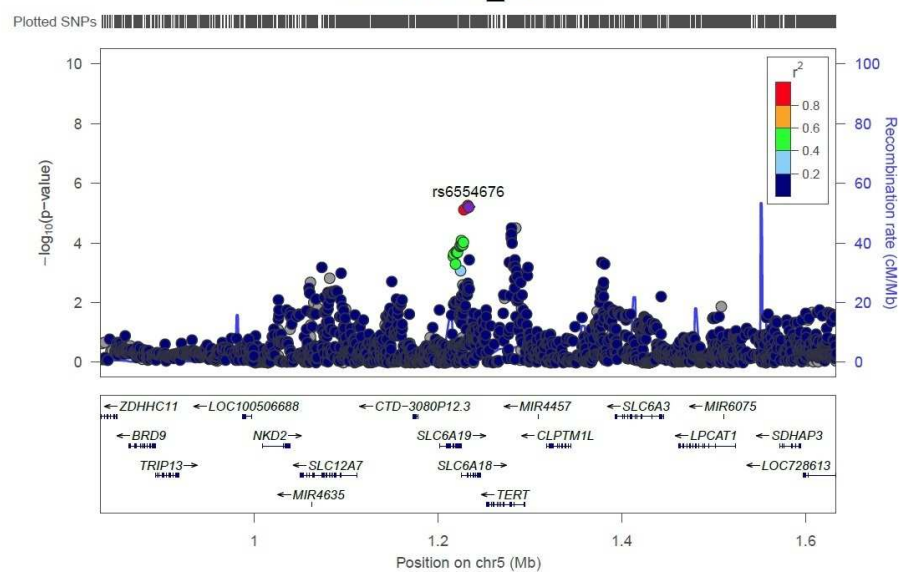
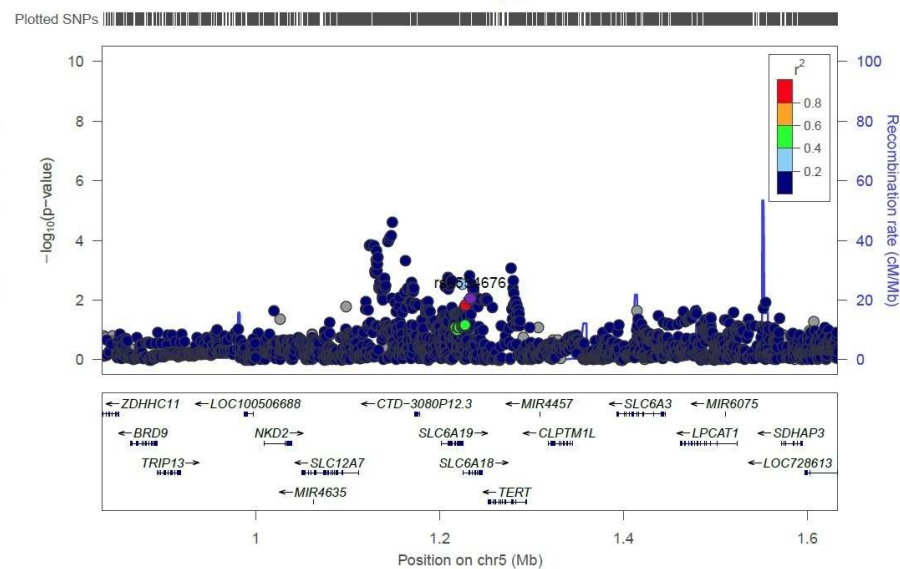


Fig S4(b) Regional plot of the suggestive SNPs in the discovery series

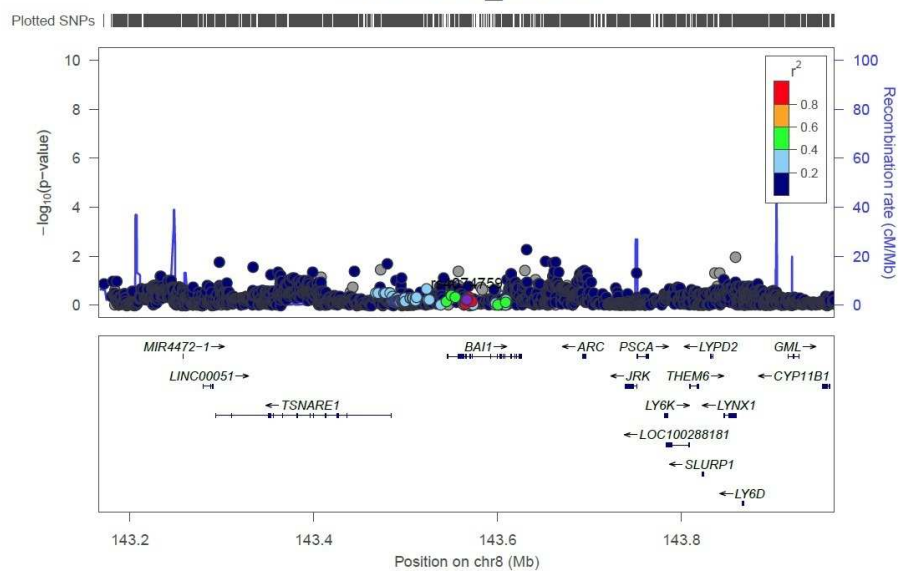
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rs6554676_male



rs4074759_female



rs4074759_male

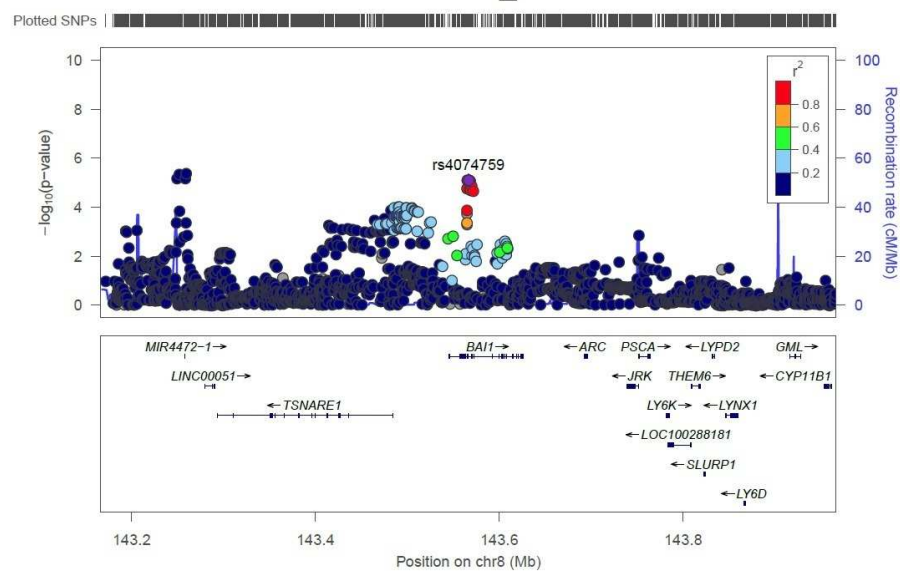
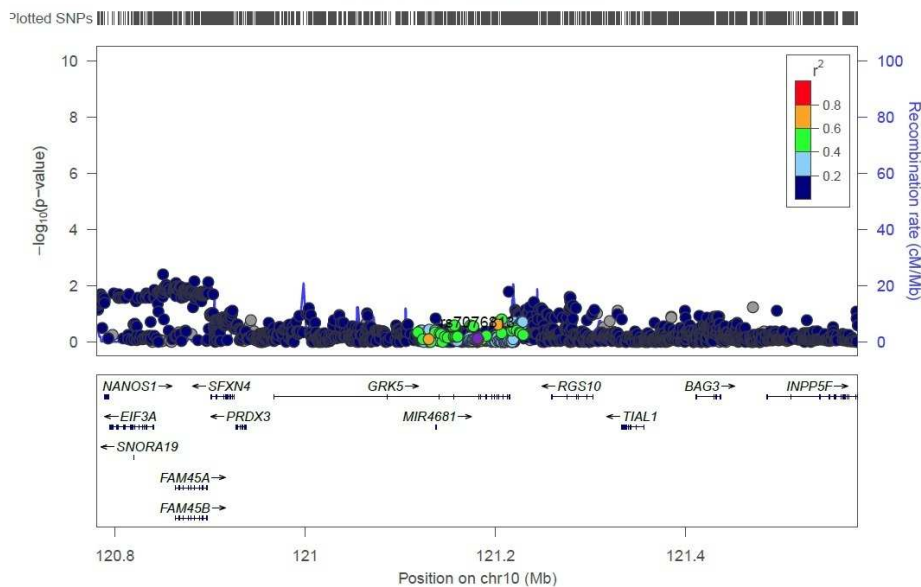
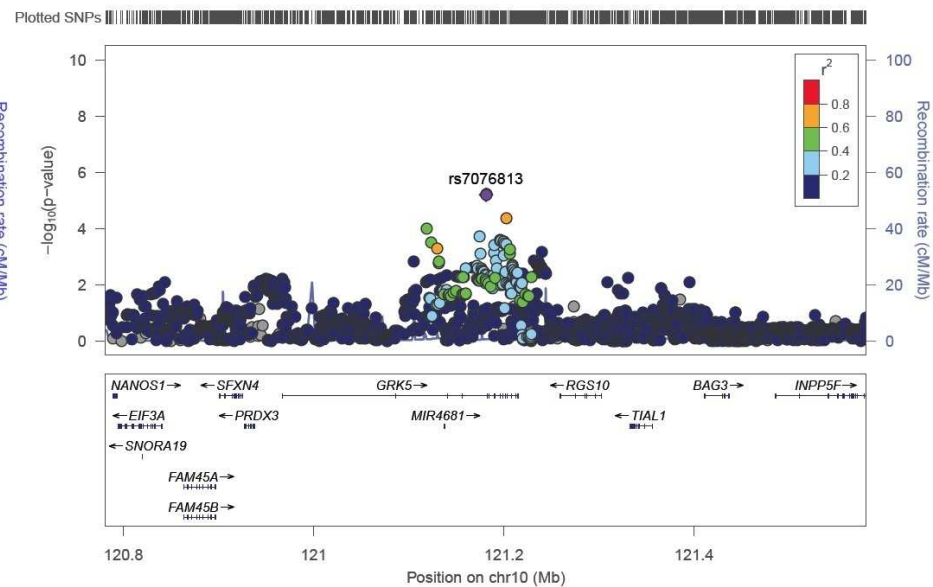


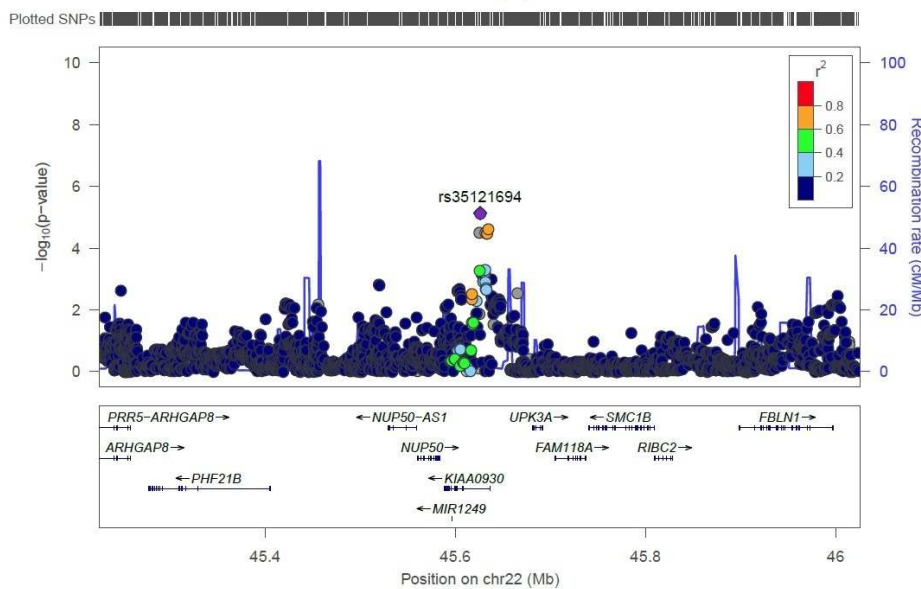
Fig S4(b) Regional plot of the suggestive SNPs in the discovery series
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rs7076813_male



rs35121694_female



rs35121694_male

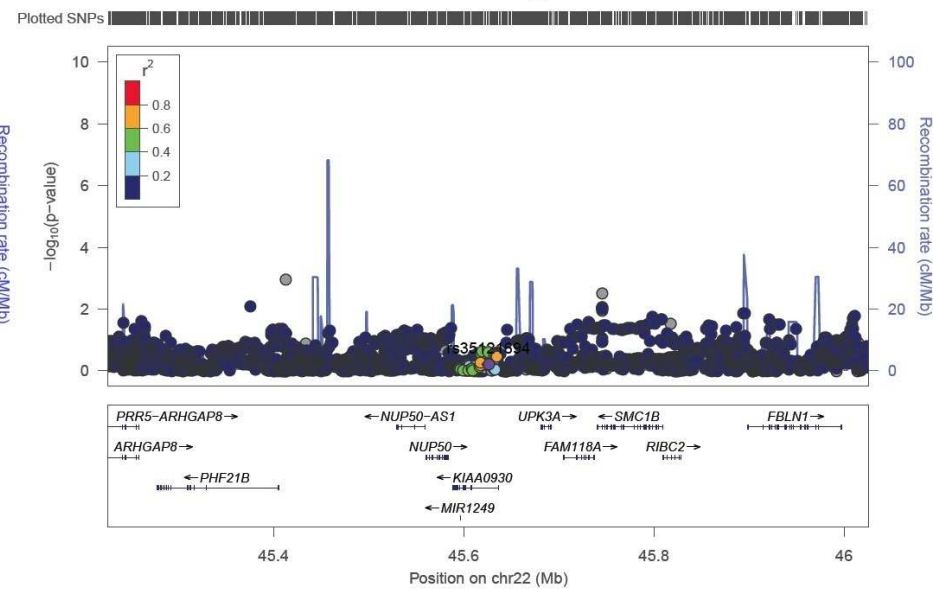
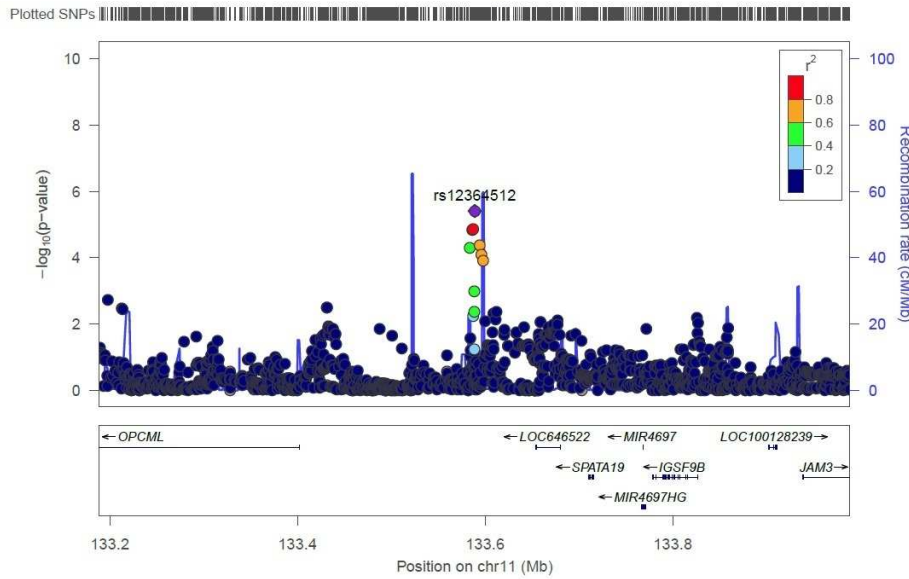
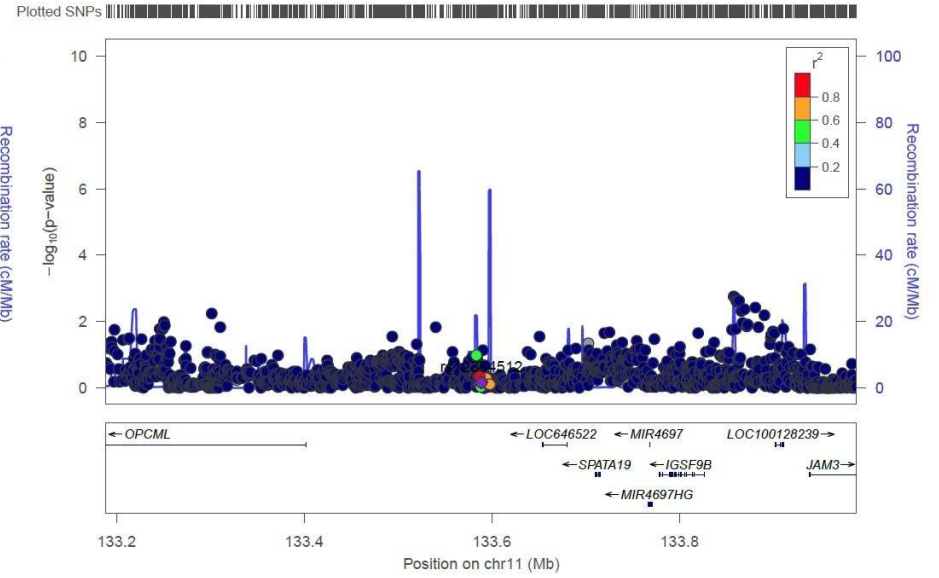


Fig S4(b) Regional plot of the suggestive SNPs in the discovery series

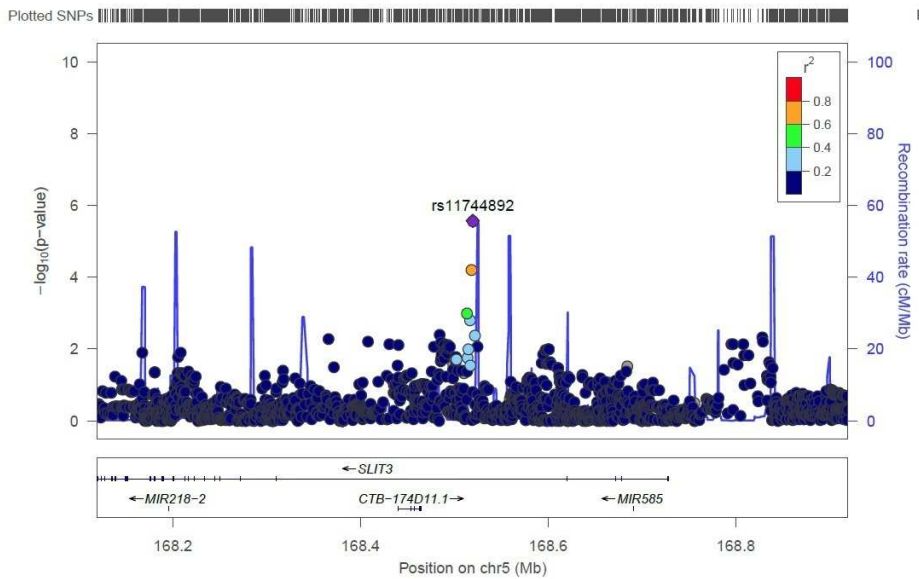
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rs12364512_male



rs11744892_female



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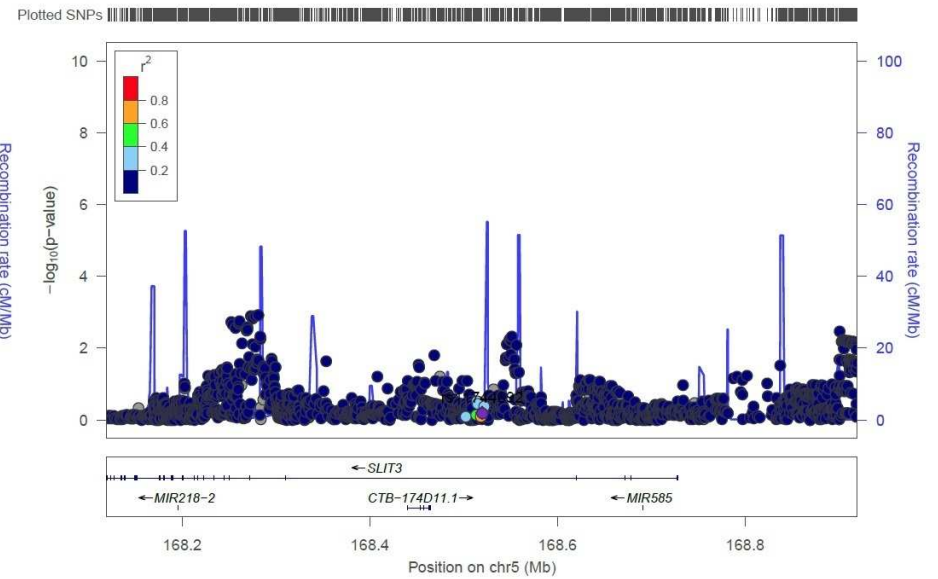
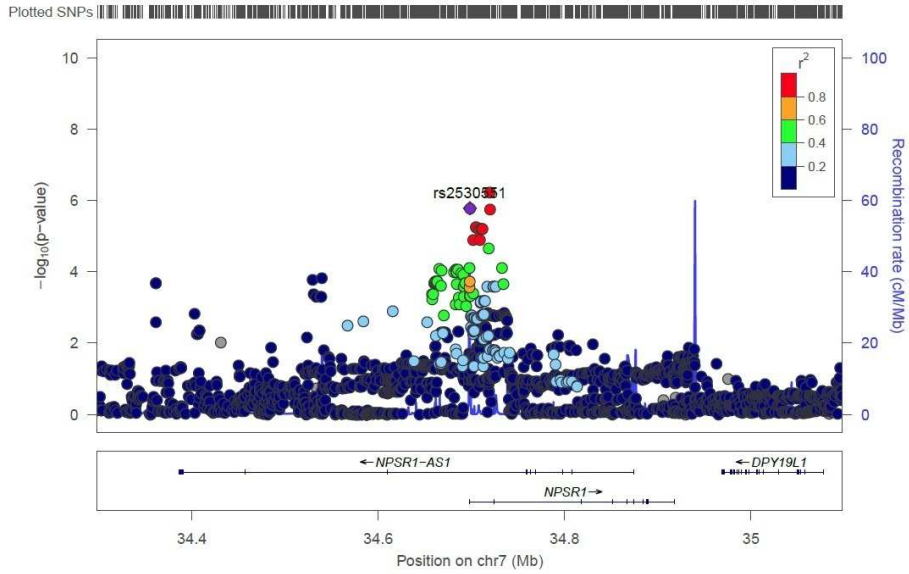
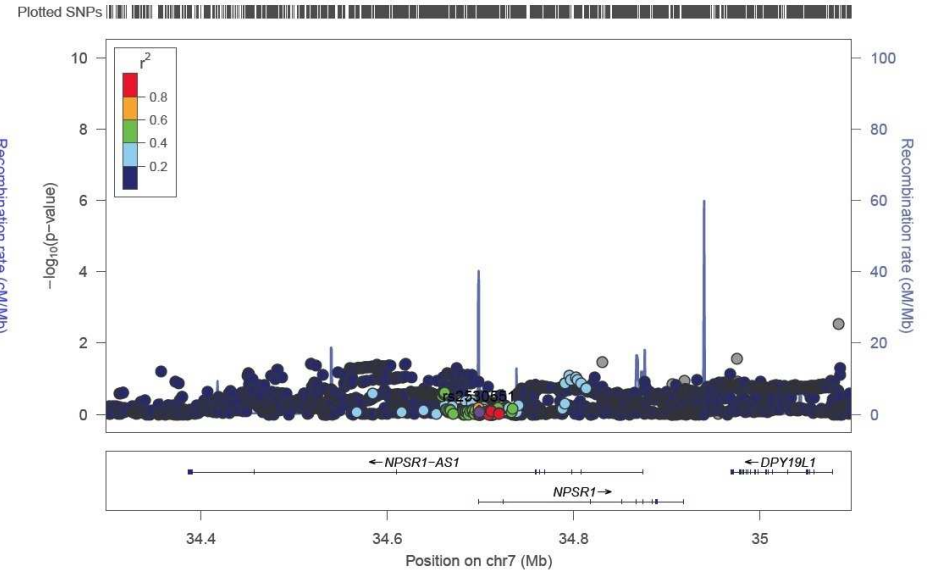


Fig S4(b) Regional plot of the suggestive SNPs in the discovery series

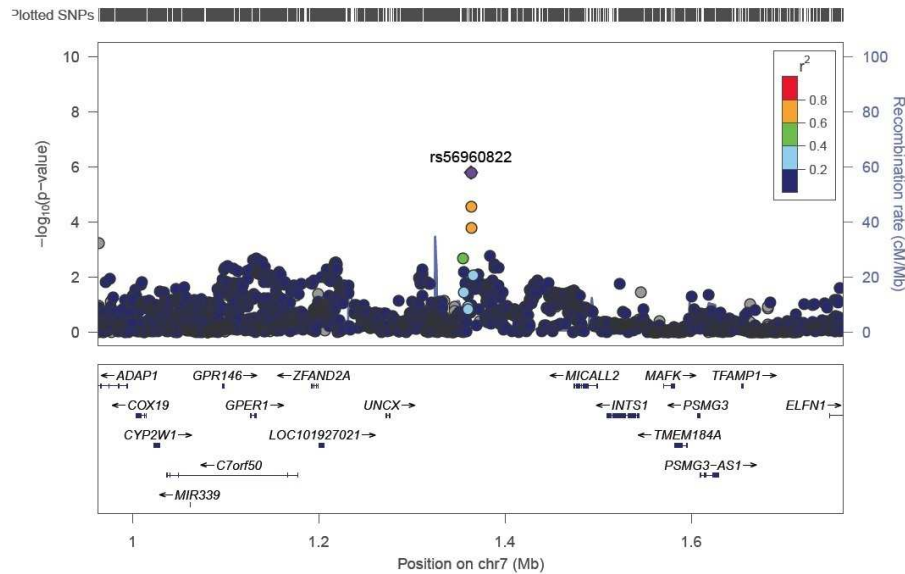
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rs2530551_male



rs56960822_female



rs56960822_male

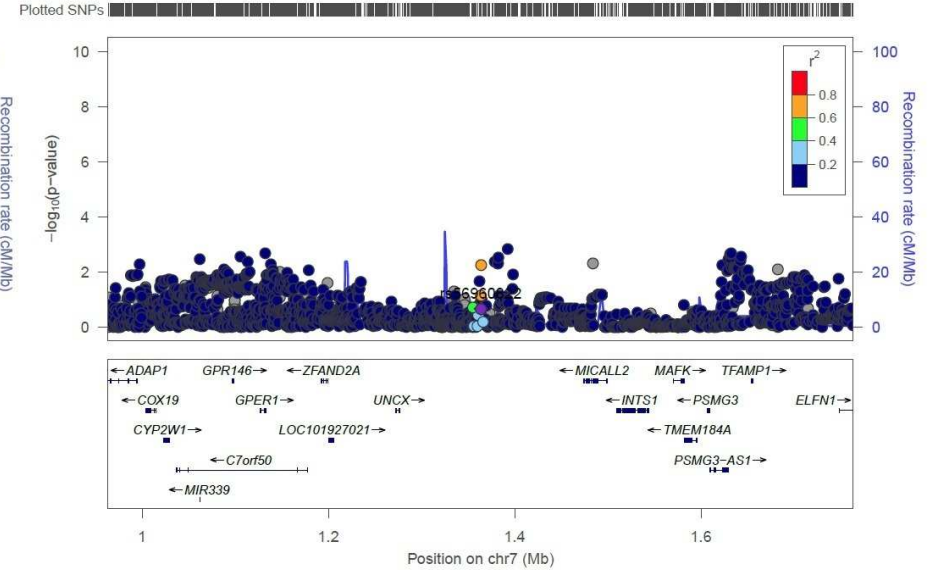


Fig S5(a) Quantile-quantile plot of sex x genotype interaction from the discovery series

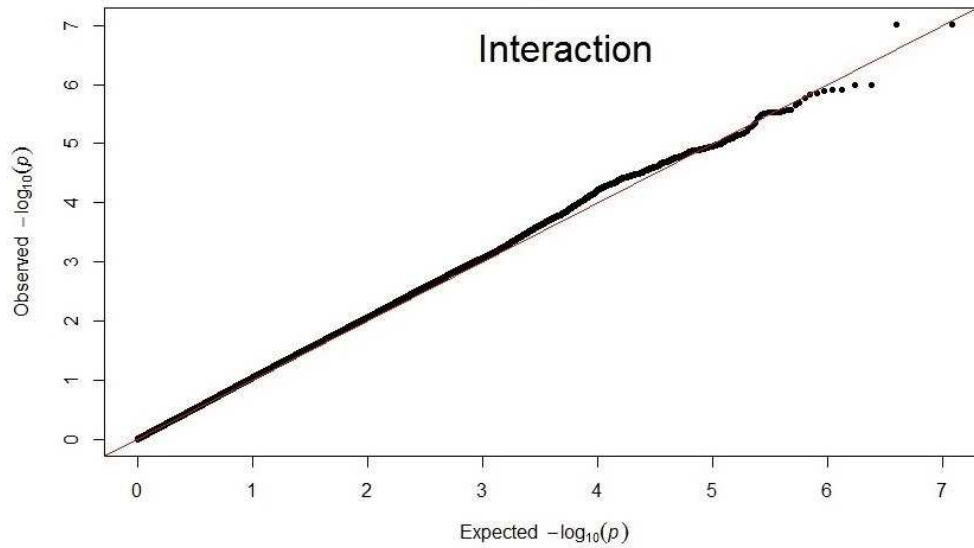
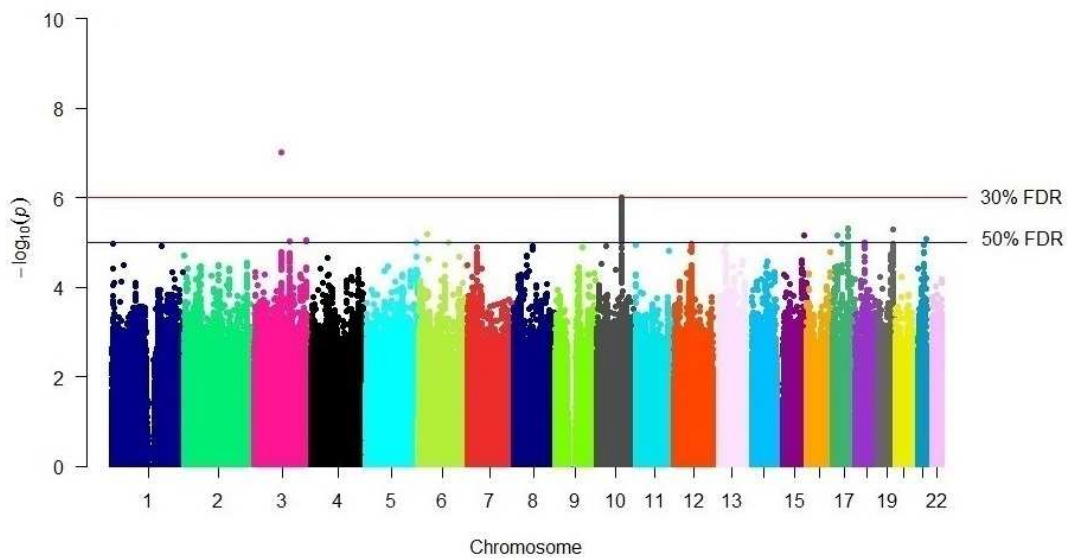


Fig S5(b) Manhattan plot of sex x genotype interaction from the discovery series



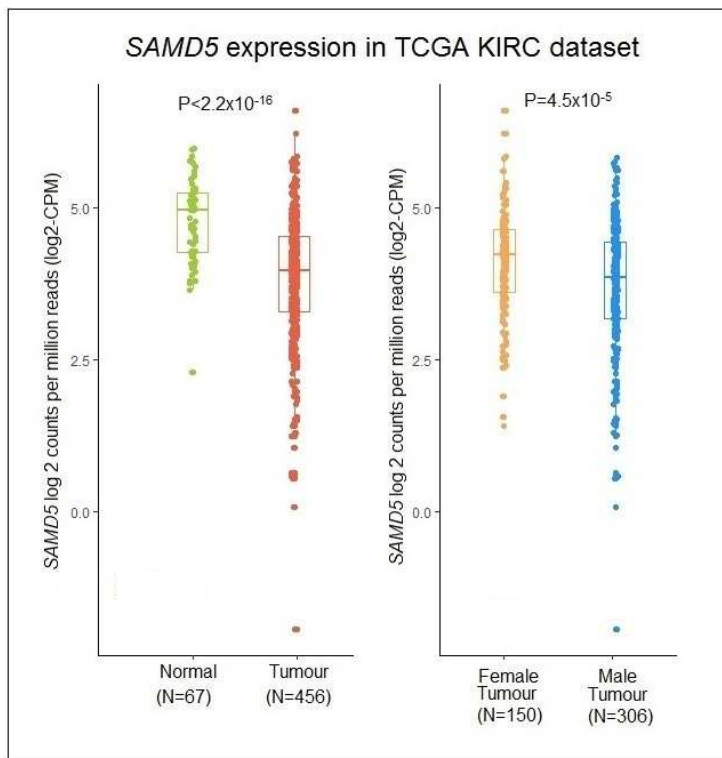
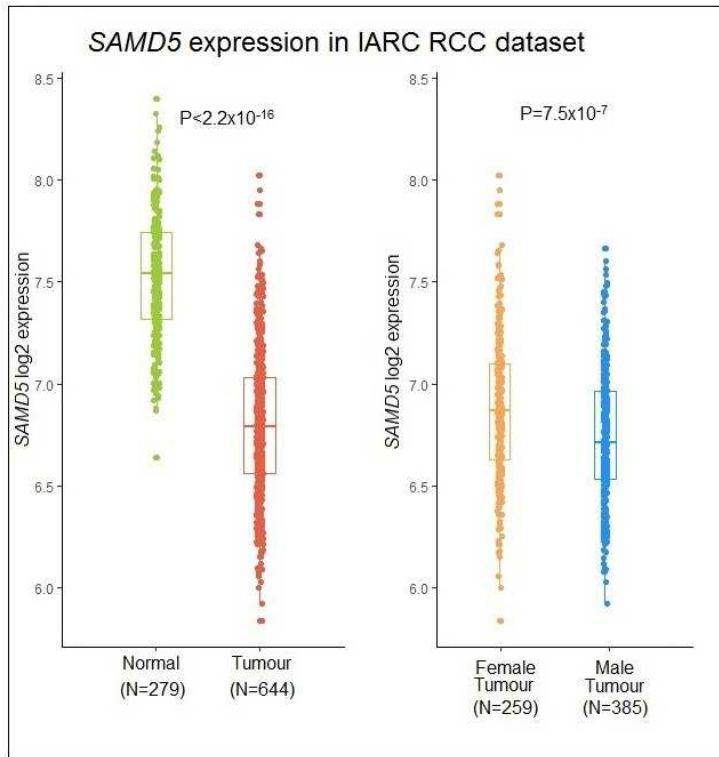


Fig S6: Comparison of SAMD5 expression in IARC and TCGA datasets. P-values are from two sample T-test

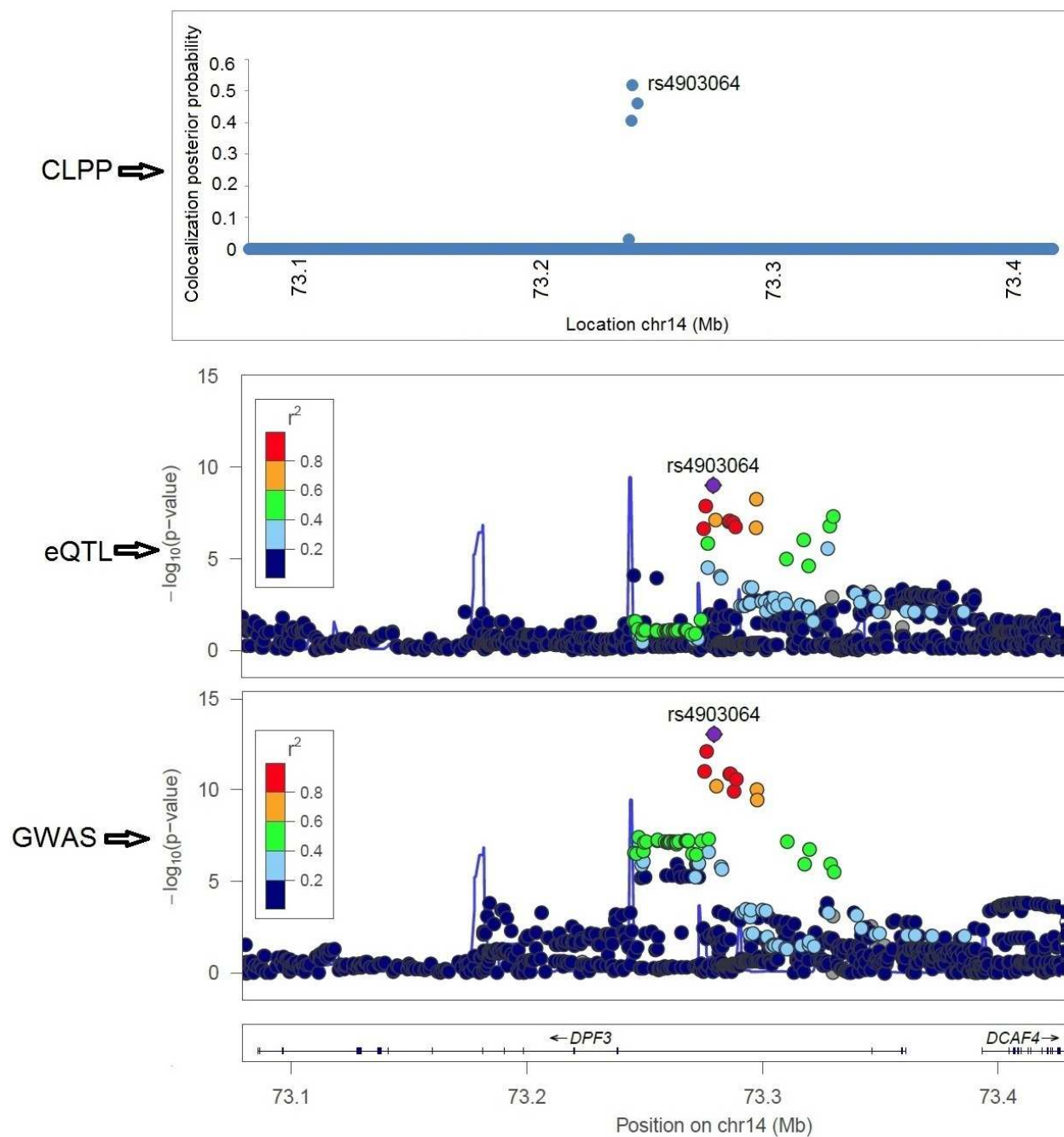


Fig S7 : Figure showing colocalization of GWAS and eQTL plots. Colocalization posterior probability (CLPP) is the probability that the same variant is causal in both GWAS and eQTL.