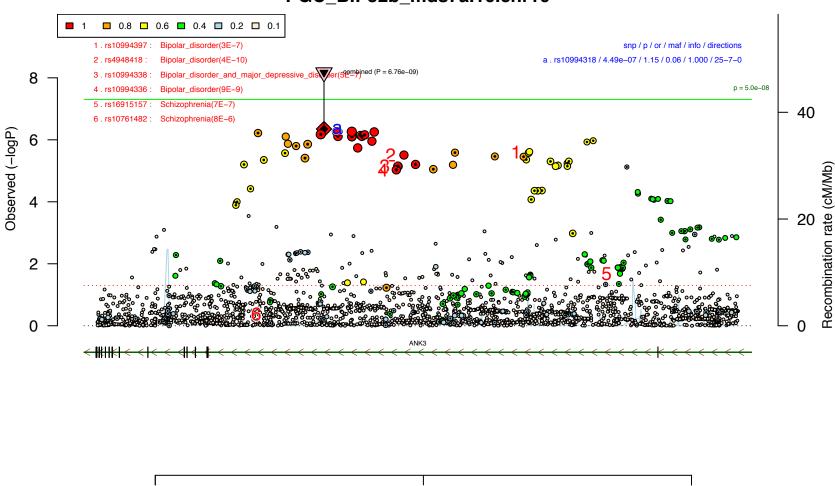
Supplemental Data 1-3. Regional association plots (1), forest plots for discovery GWAS studies (2) and forest plots for follow-up studies (3), for all 31 lead SNPs in the 30 genome-wide significant loci. Each multi-figure PDF below is a separate supplemental data piece.

Supplemental Data 1. Regional association plots.

Supplemental Data 2. Forest plots of the 32 primary GWAS datasets.

Supplemental Data 3. Forest plots of the 7 followup datasets.

PGC_BIP32b_mds7a.10.chr10



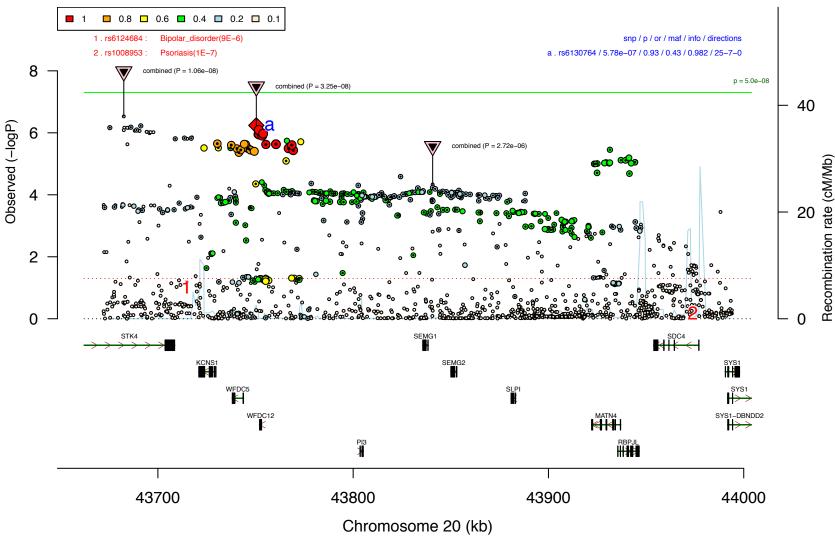
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Chromosome 10 (kb)

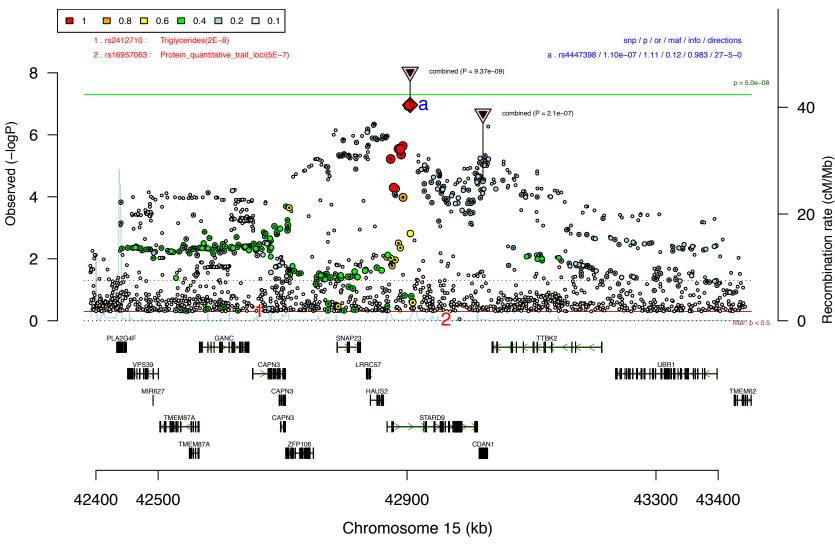
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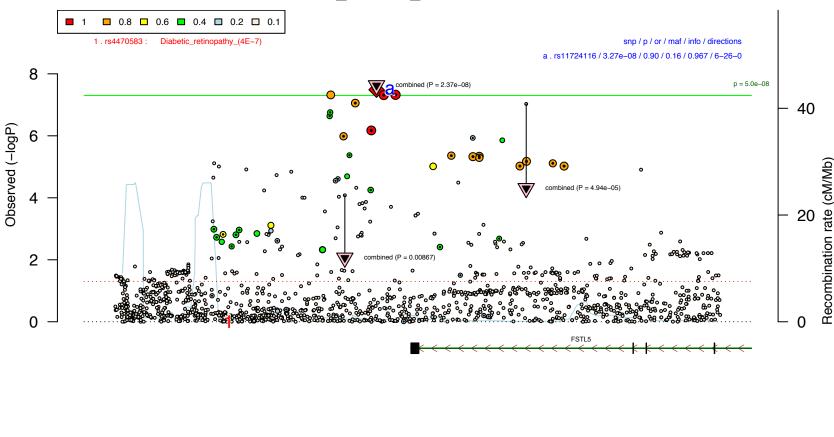
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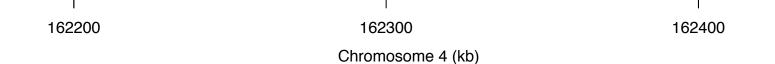


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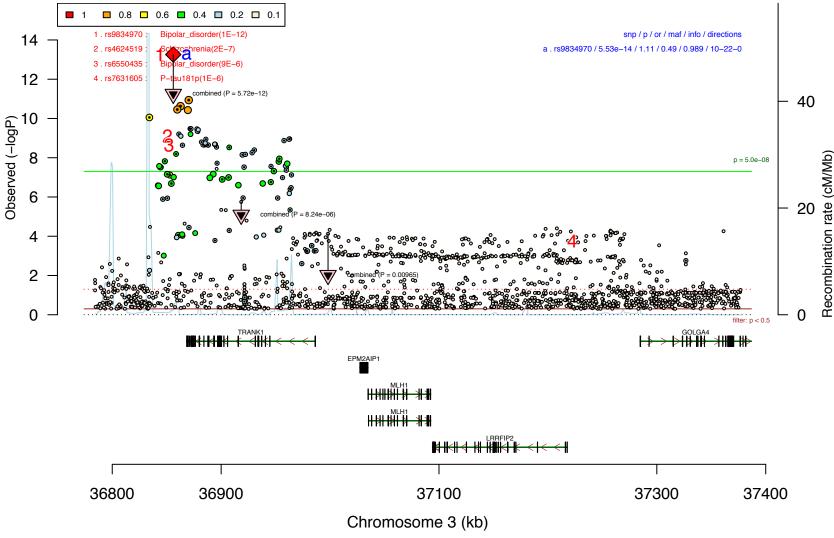


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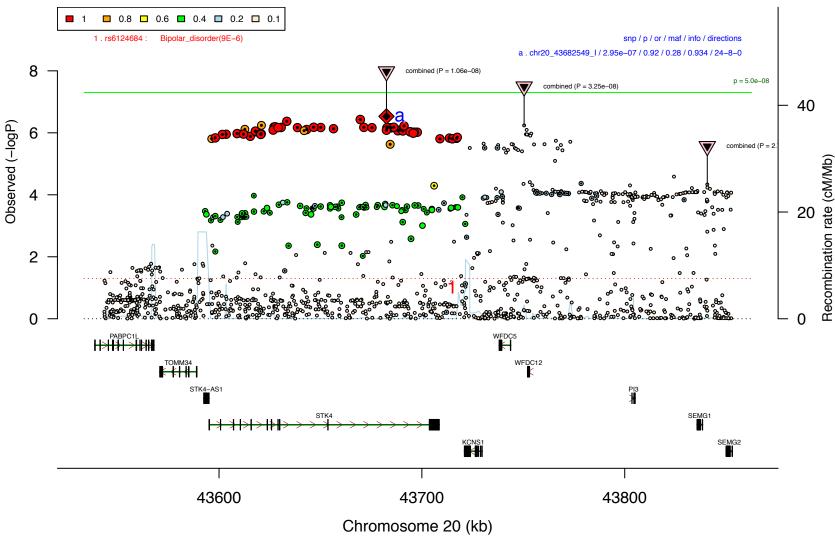




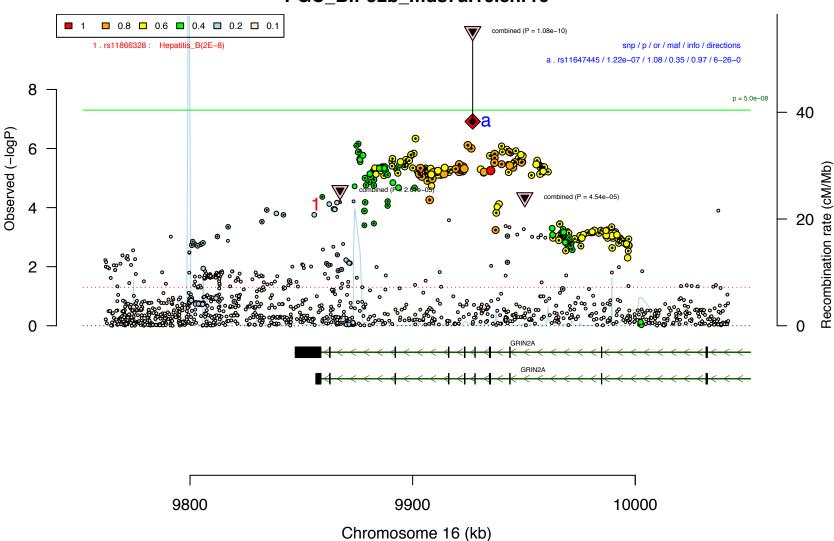
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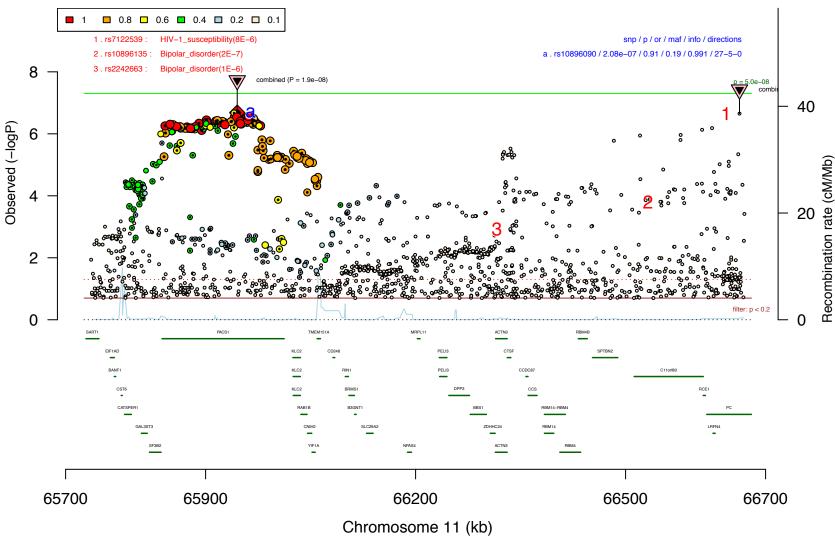
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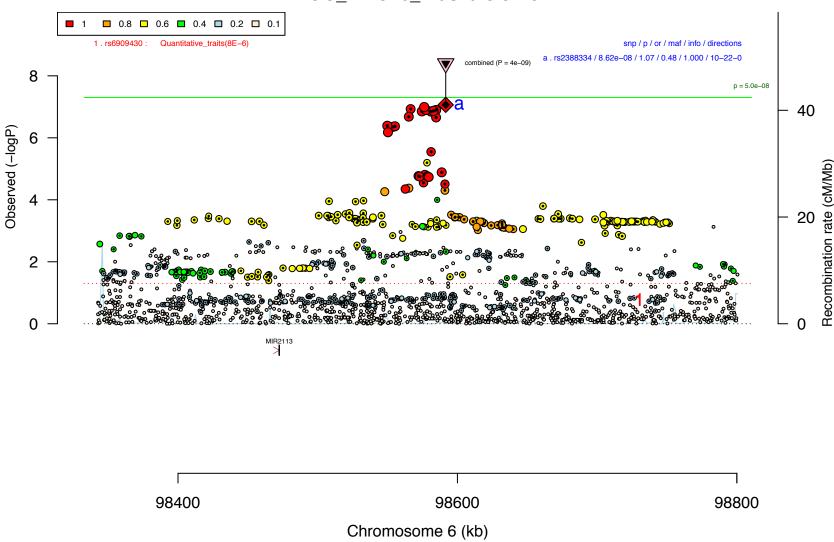
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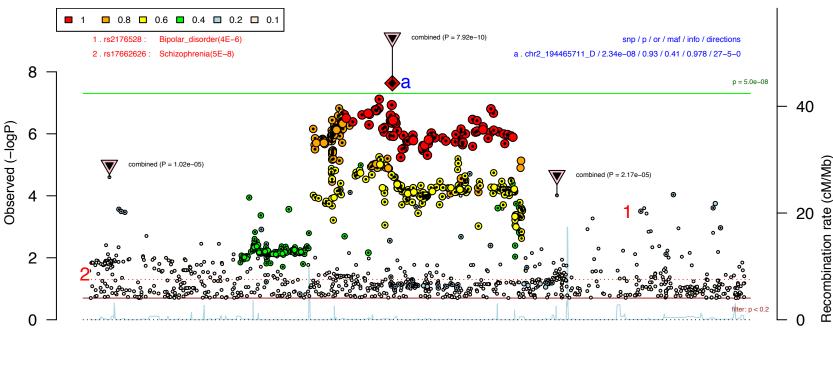
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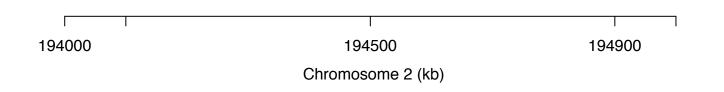


PGC_BIP32b_mds7a.6.chr6



PGC_BIP32b_mds7a.2.chr2

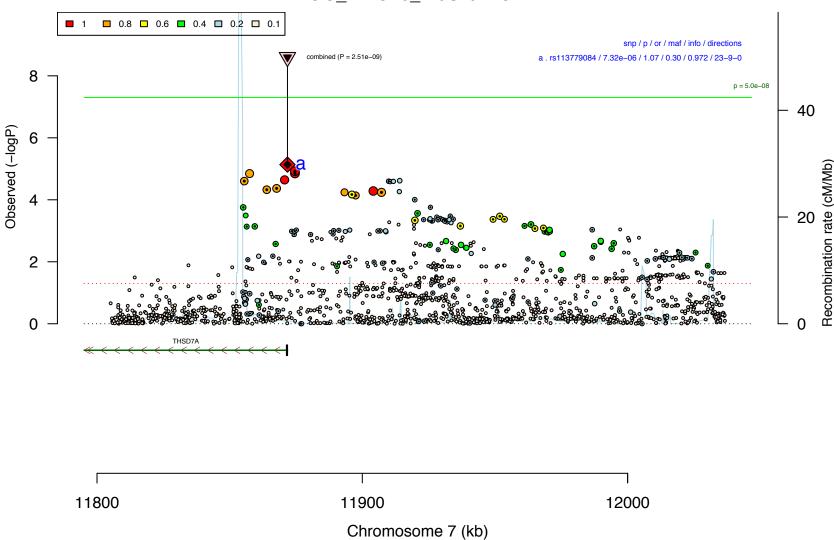


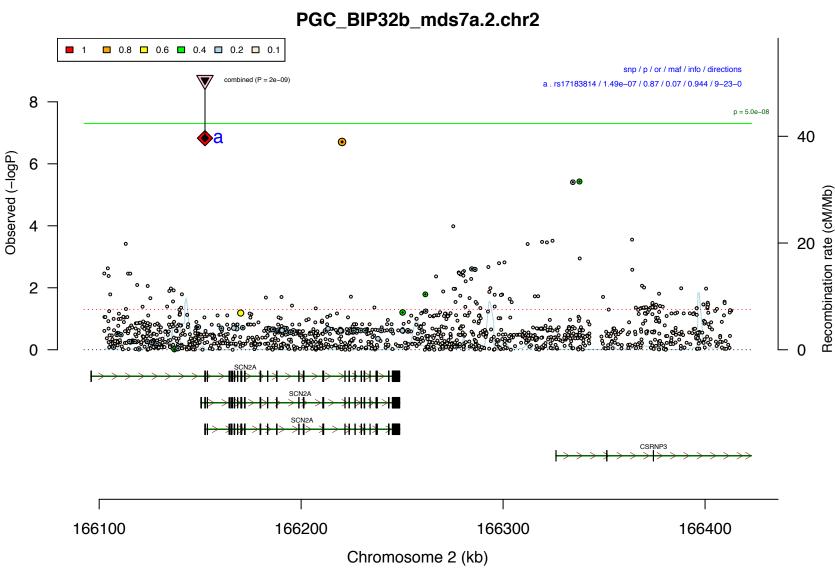


PGC_BIP32b_mds7a.3.chr3 **■** 0.8 **■** 0.6 **■** 0.4 **■** 0.2 **■** 0.1 snp / p / or / maf / info / directions a . rs3804640 / 9.26e-08 / 0.93 / 0.47 / 0.993 / 26-6-0 8 combined (P = 1.99e-08) p = 5.0e - 0840 Observed (-logP) Recombination rate (cM/Mb) 20 2 0 107800 107900 108000 107700

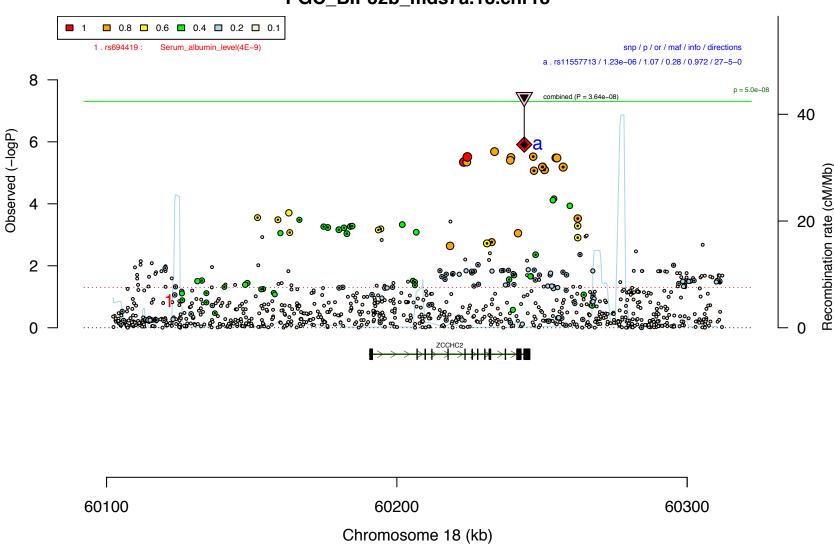
Chromosome 3 (kb)

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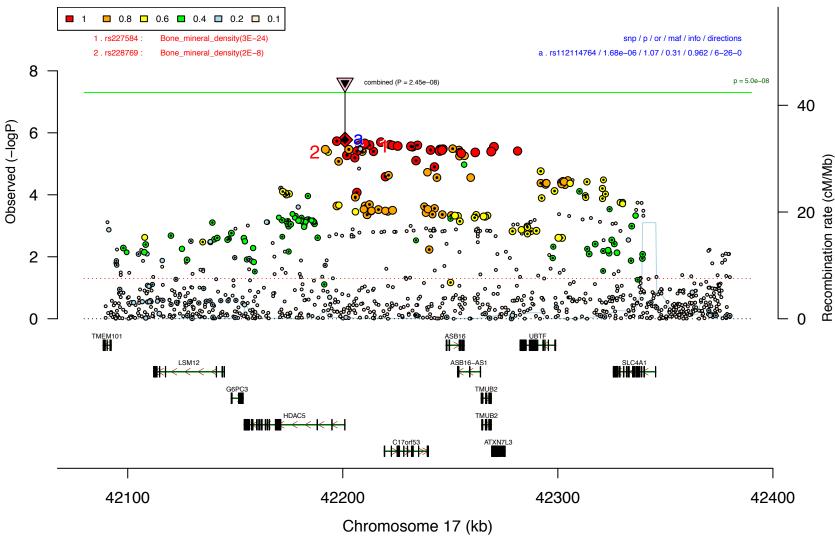




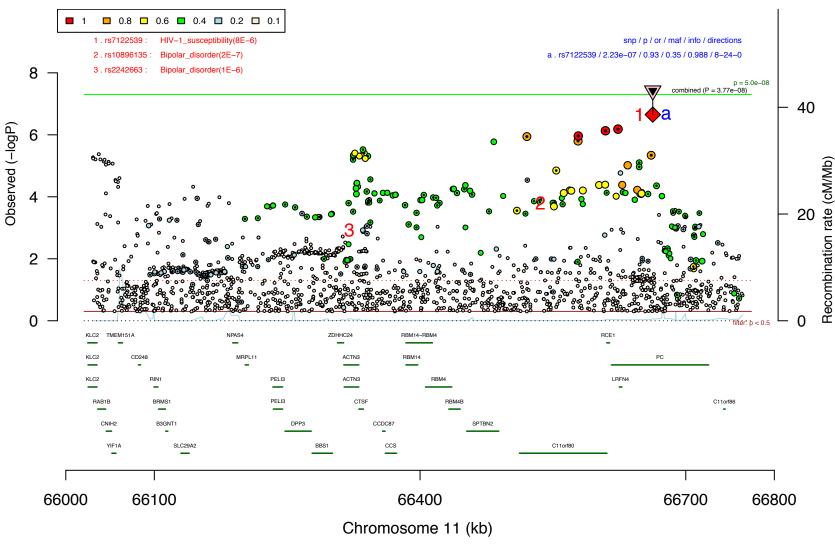
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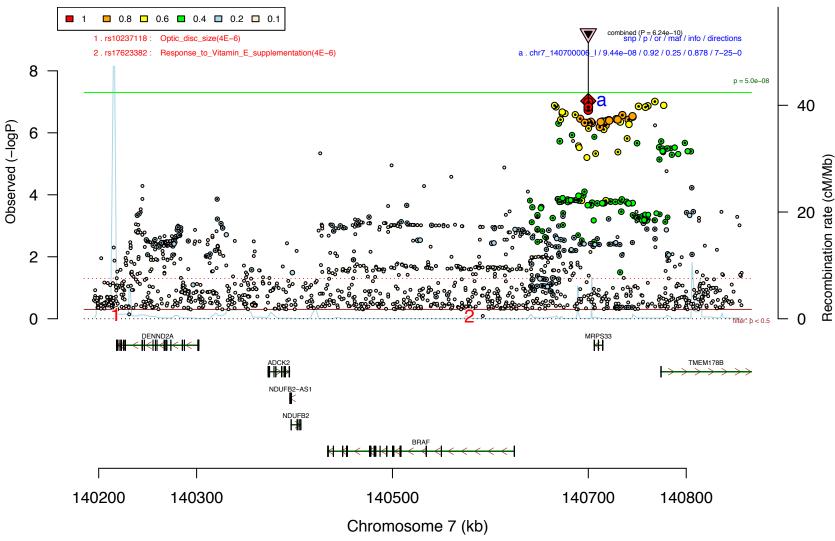
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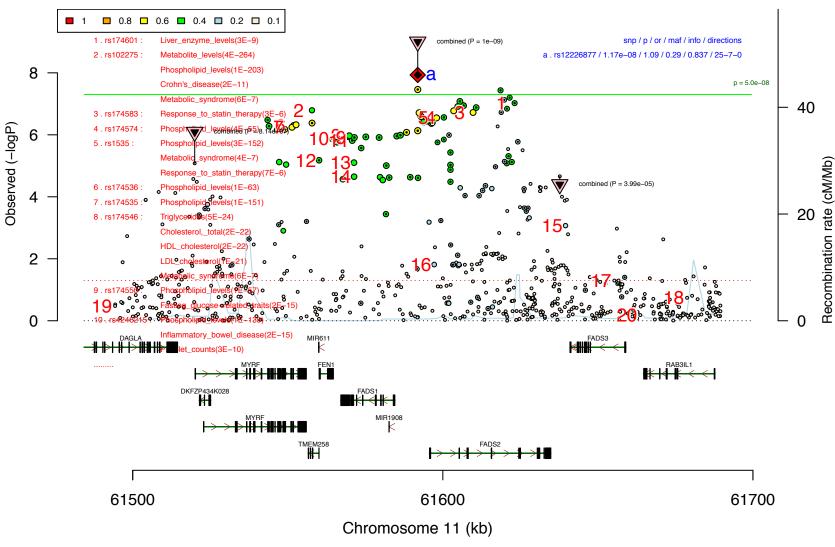
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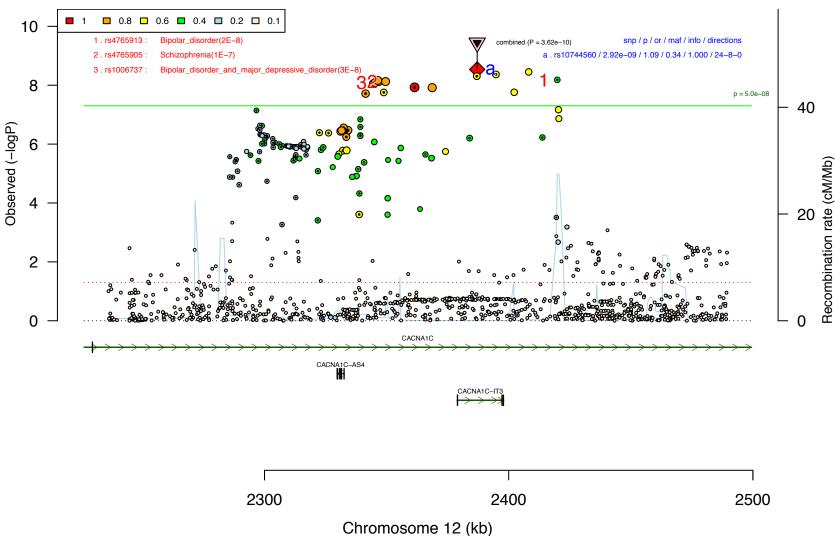
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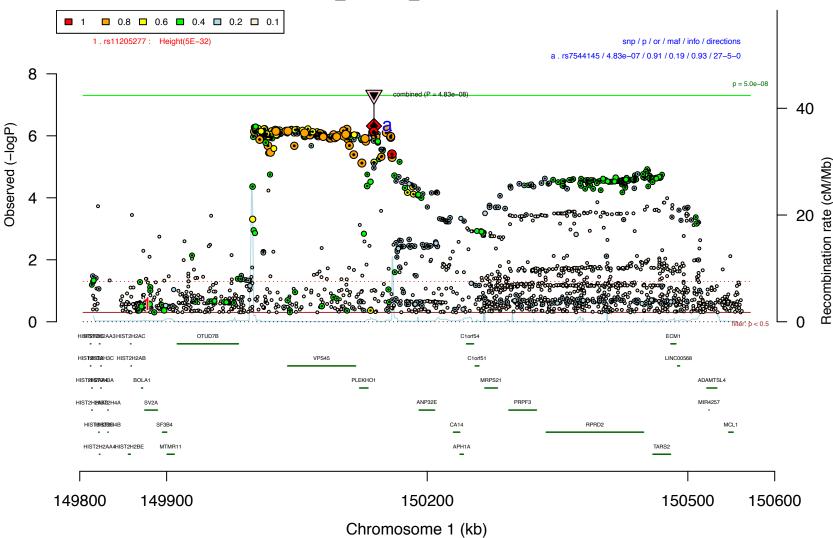
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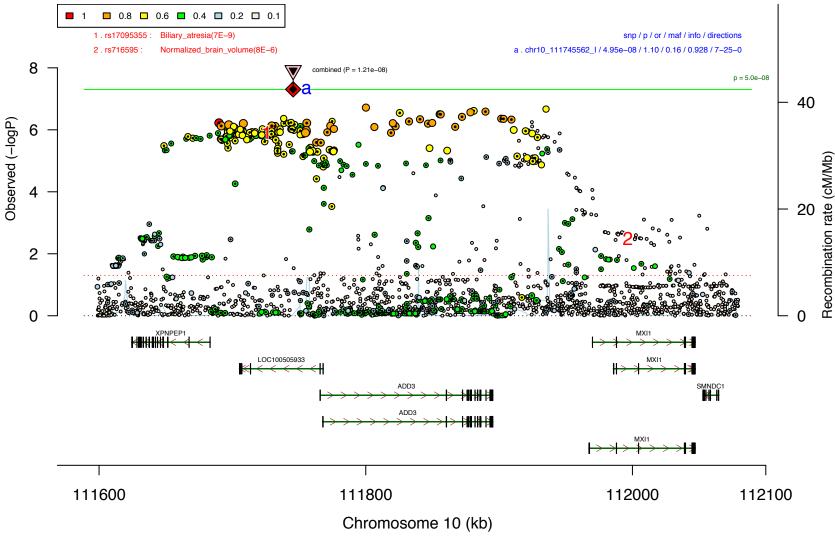
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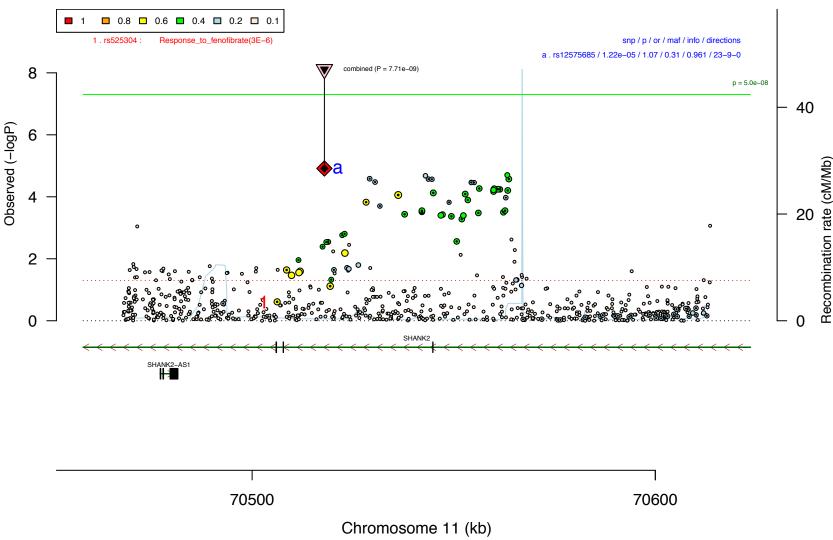
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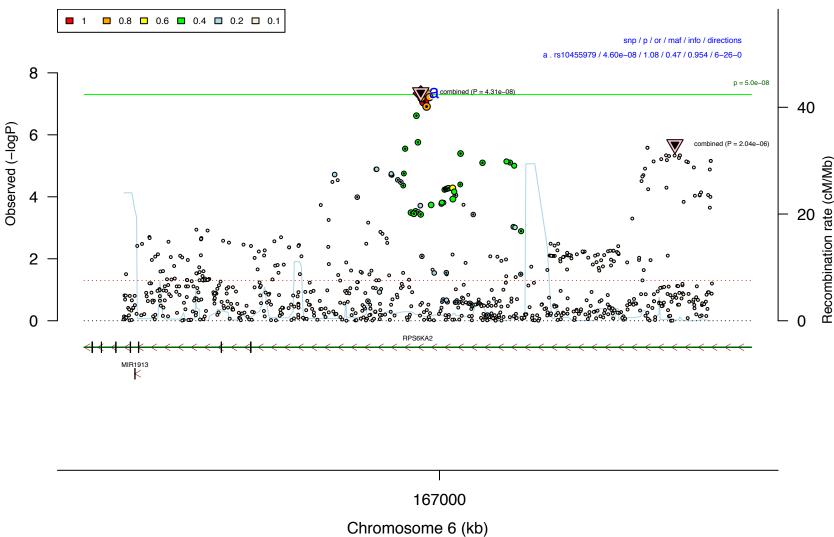
PGC_BIP32b_mds7a.10.chr10



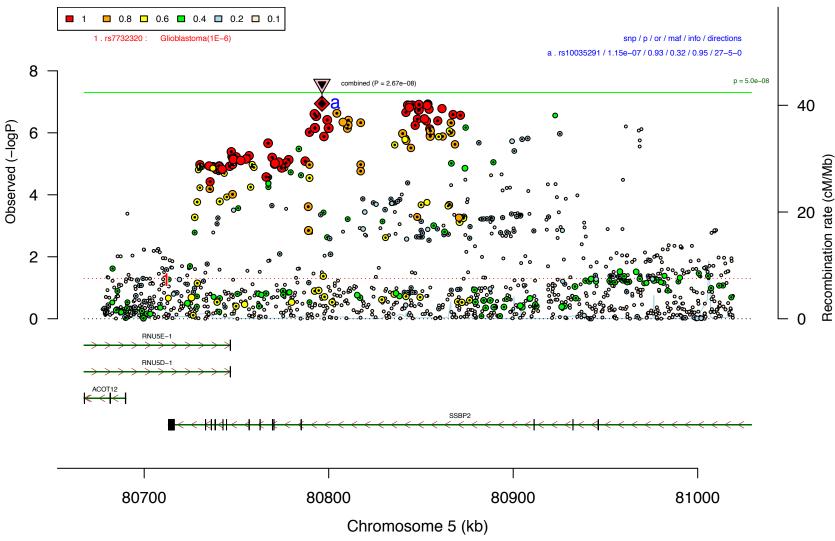
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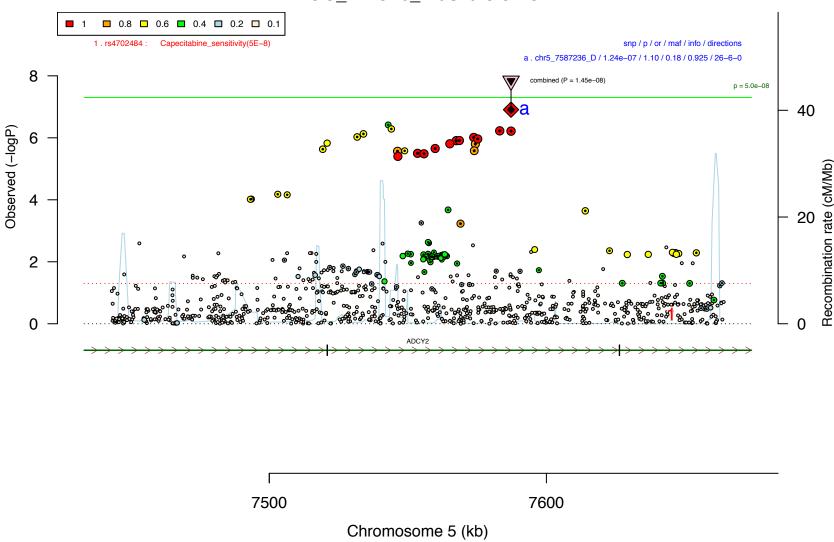
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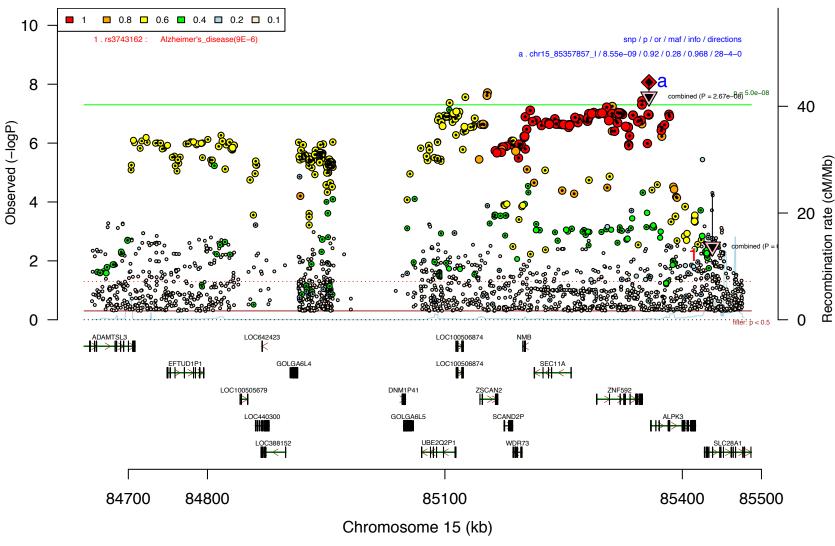
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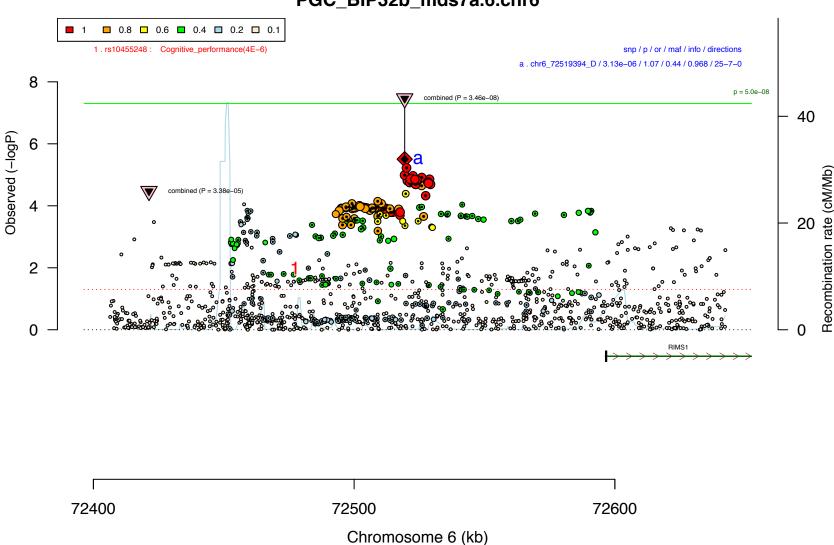
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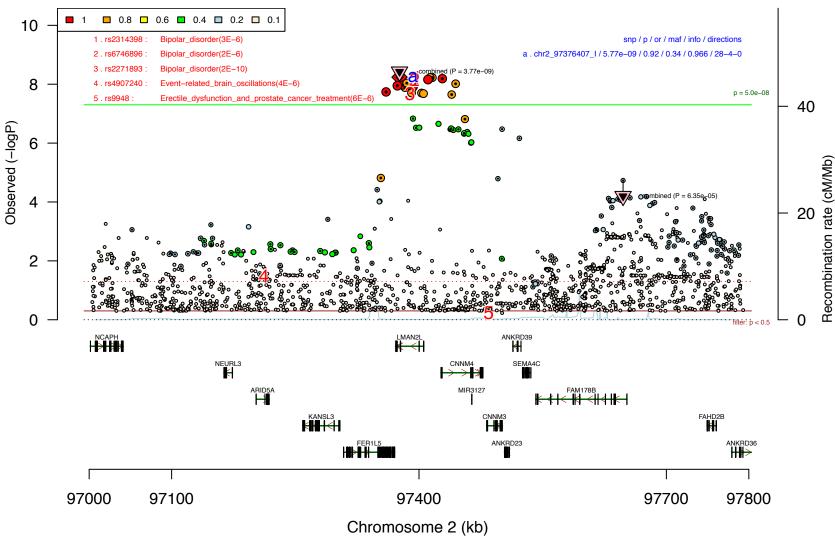
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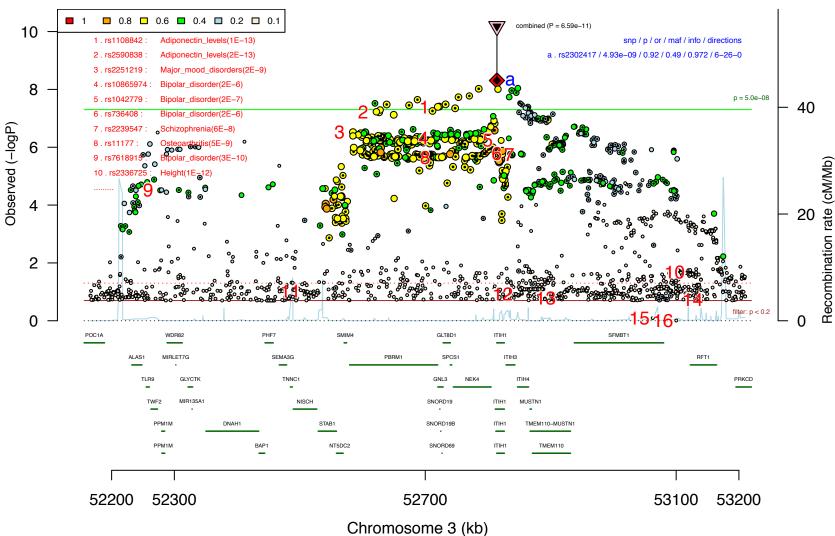
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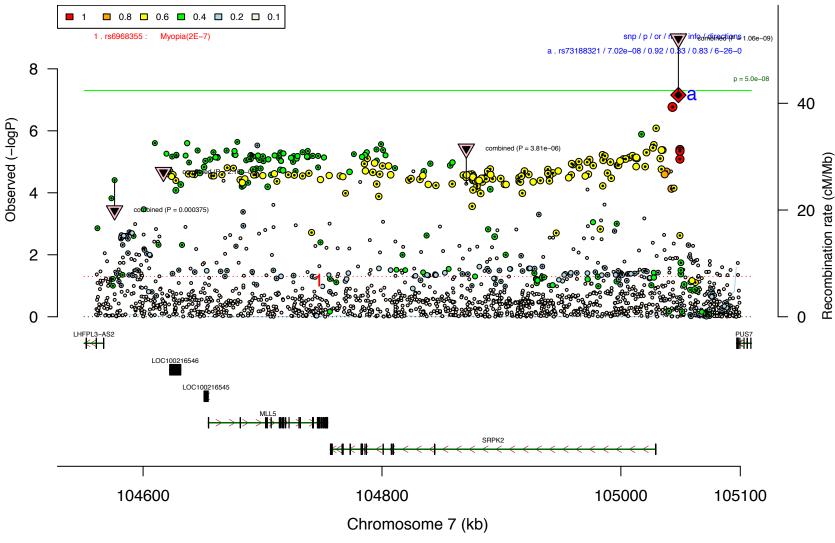
PGC_BIP32b_mds7a.2.chr2



PGC_BIP32b_mds7a.3.chr3



PGC_BIP32b_mds7a.7.chr7



PGC_BIP32b_mds7a.19.chr19

