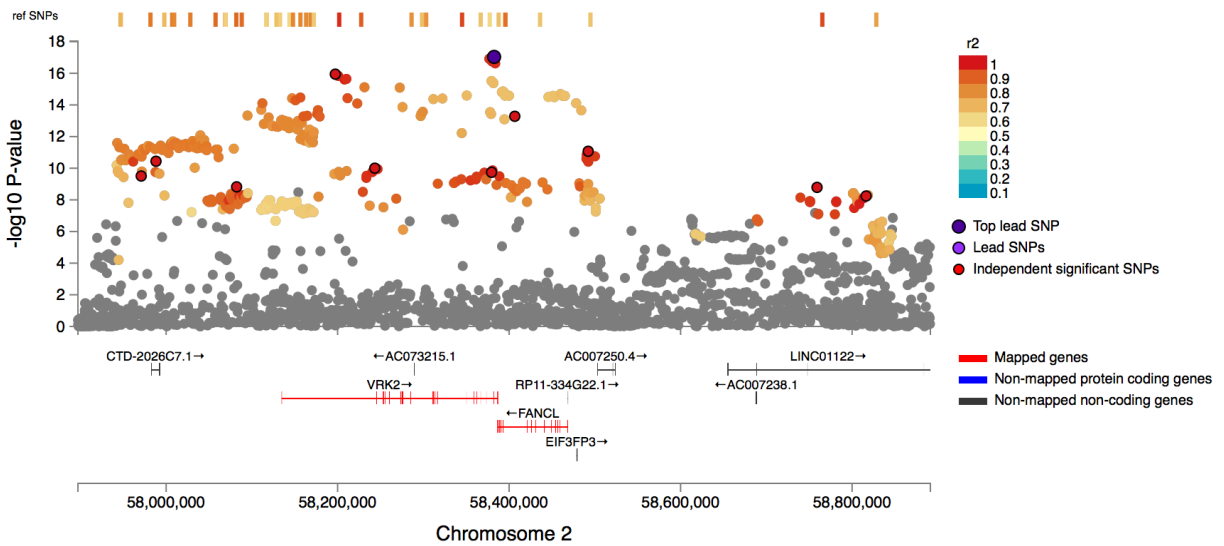


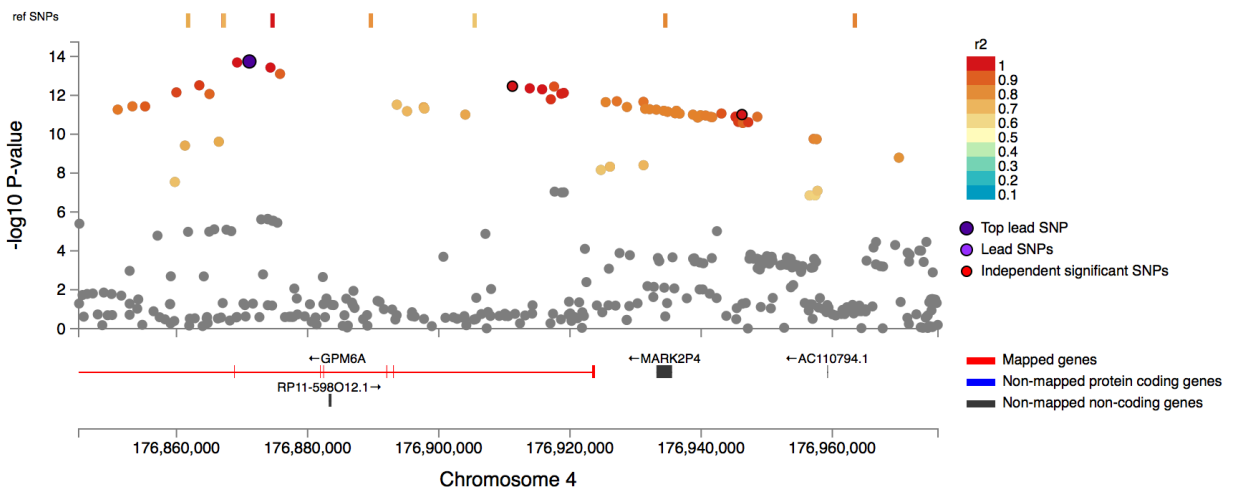
Regional association plots

Regional association plots are presented below for each of the 68 genomic loci associated with rhythm that surpassed the threshold for genome-wide significance. Plots were generated for each locus using FUMA, from the rhythm summary statistics (which had undergone two rounds of LD pruning, first at $r^2=0.6$ [independent SNPs], and another round of pruning at $r^2 = 0.1$, kb=250). In each plot, the top independent SNP for each locus is depicted as “Top lead SNP”, with a navy circle.

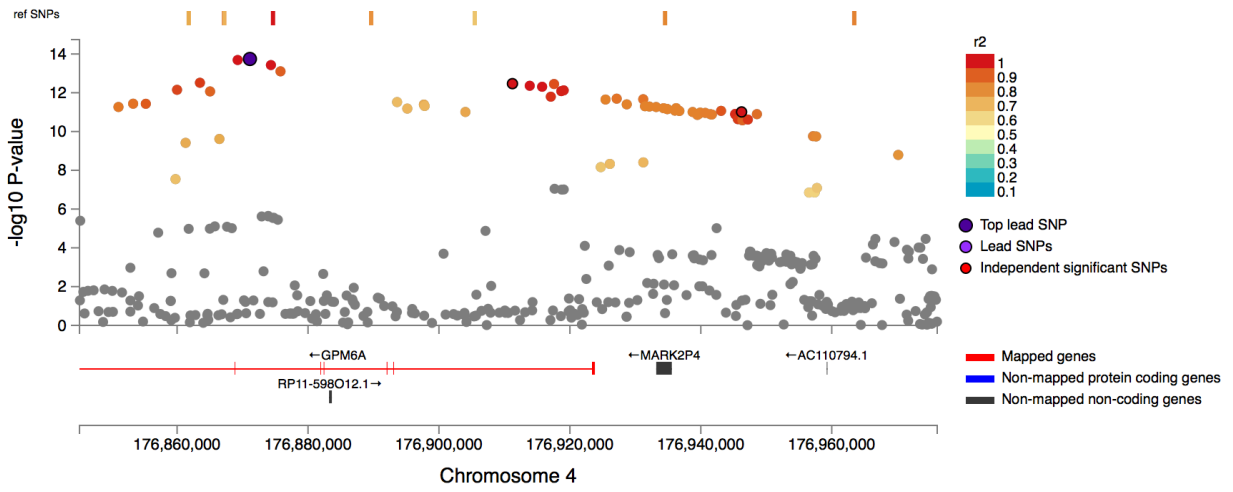
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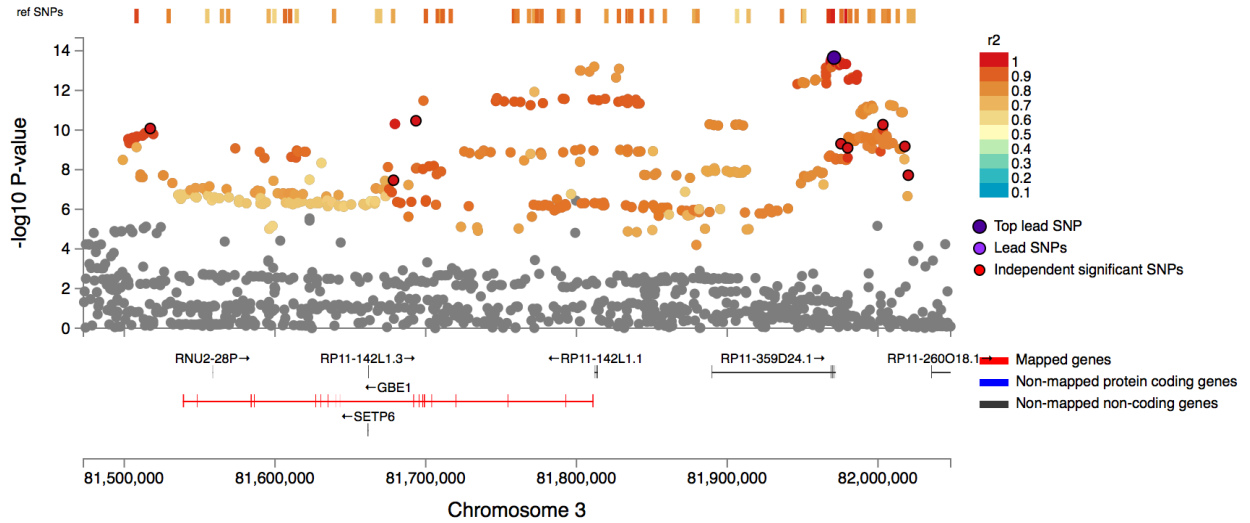
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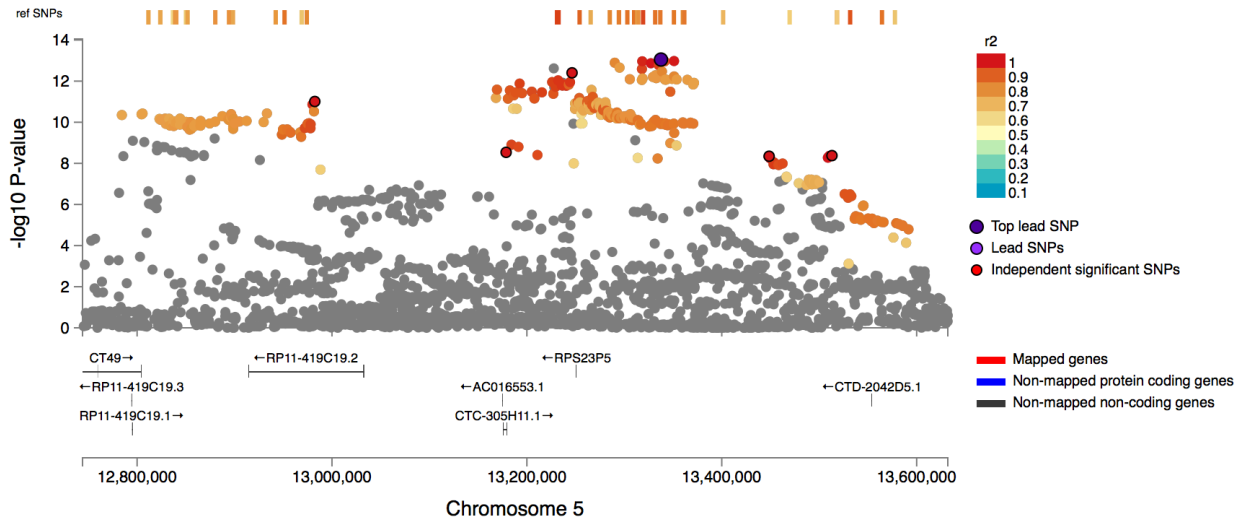
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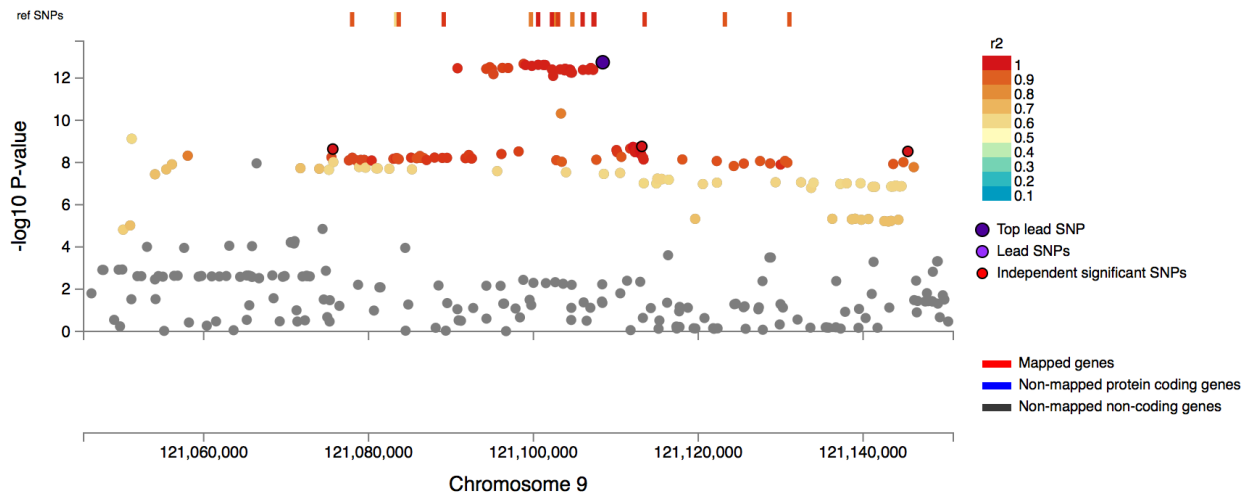
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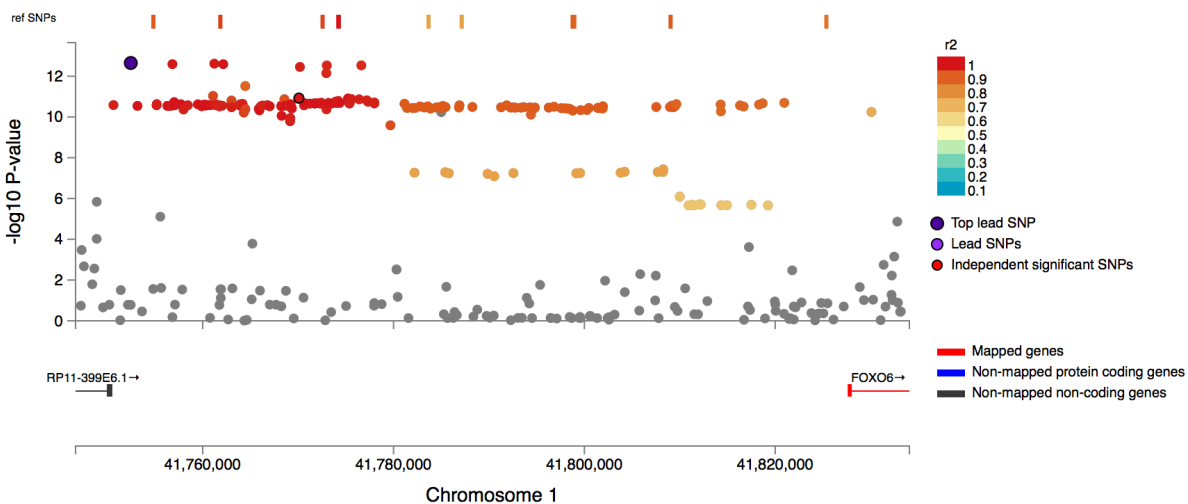
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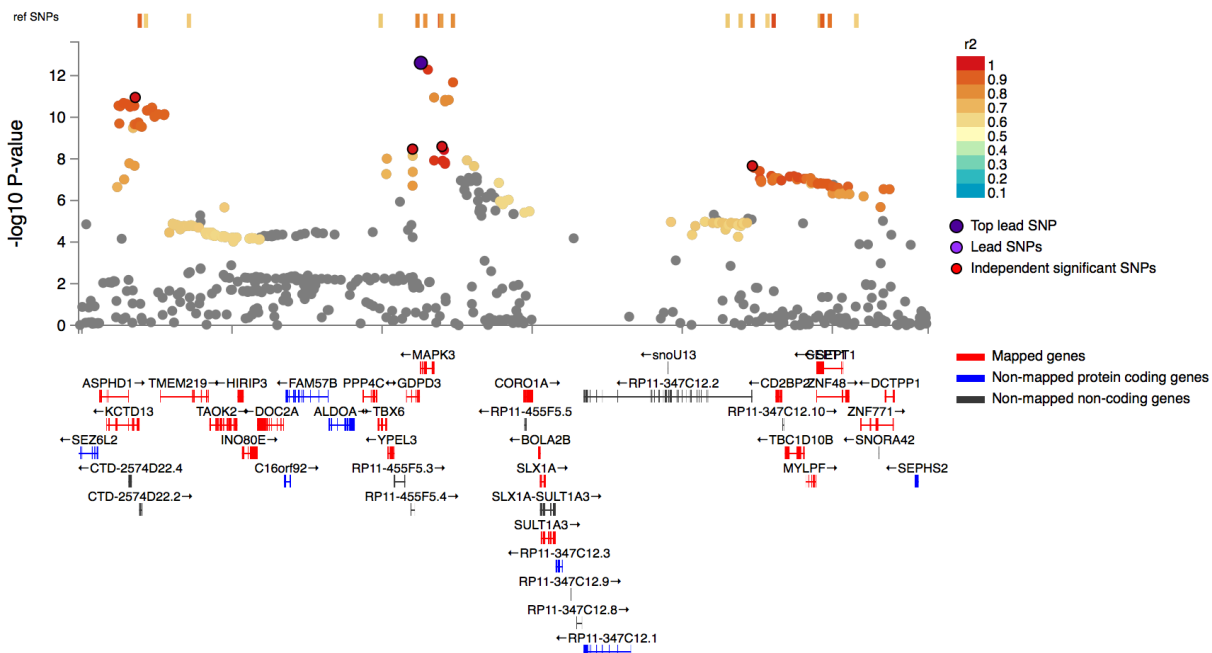
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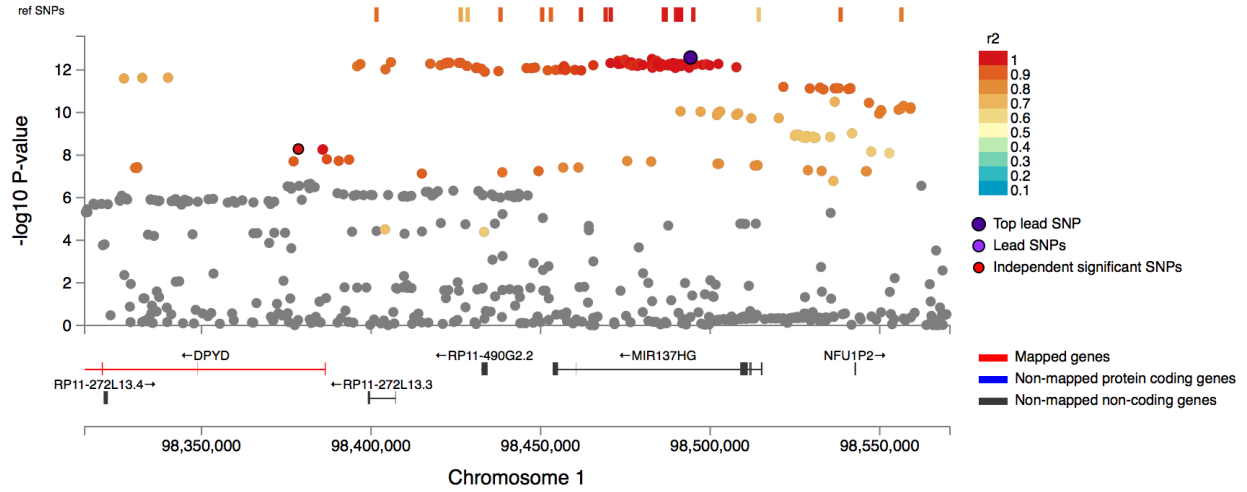
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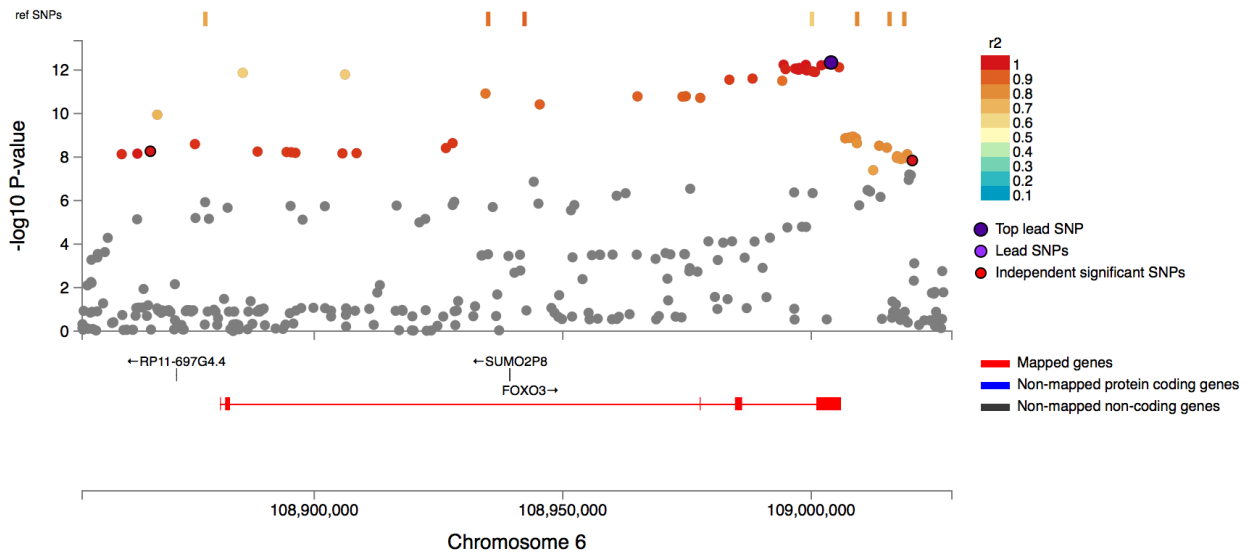
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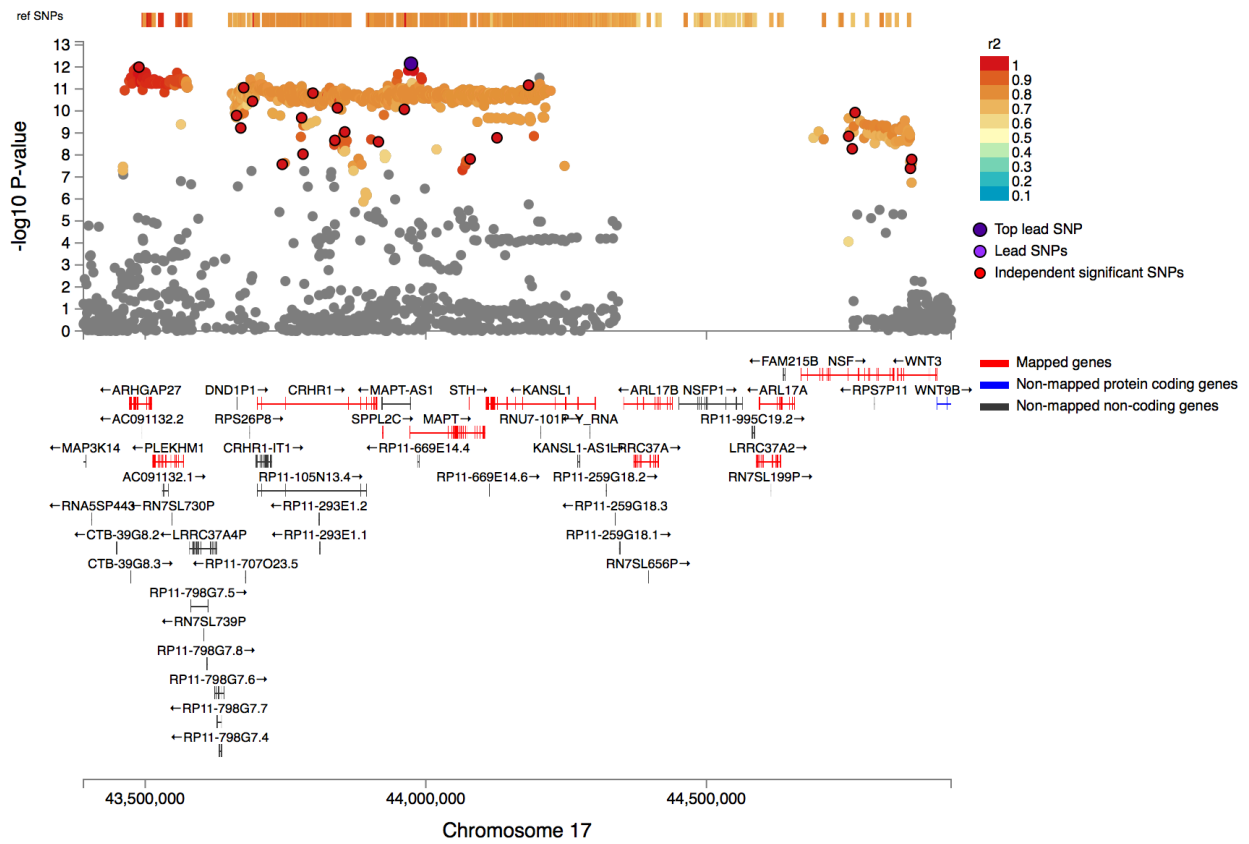
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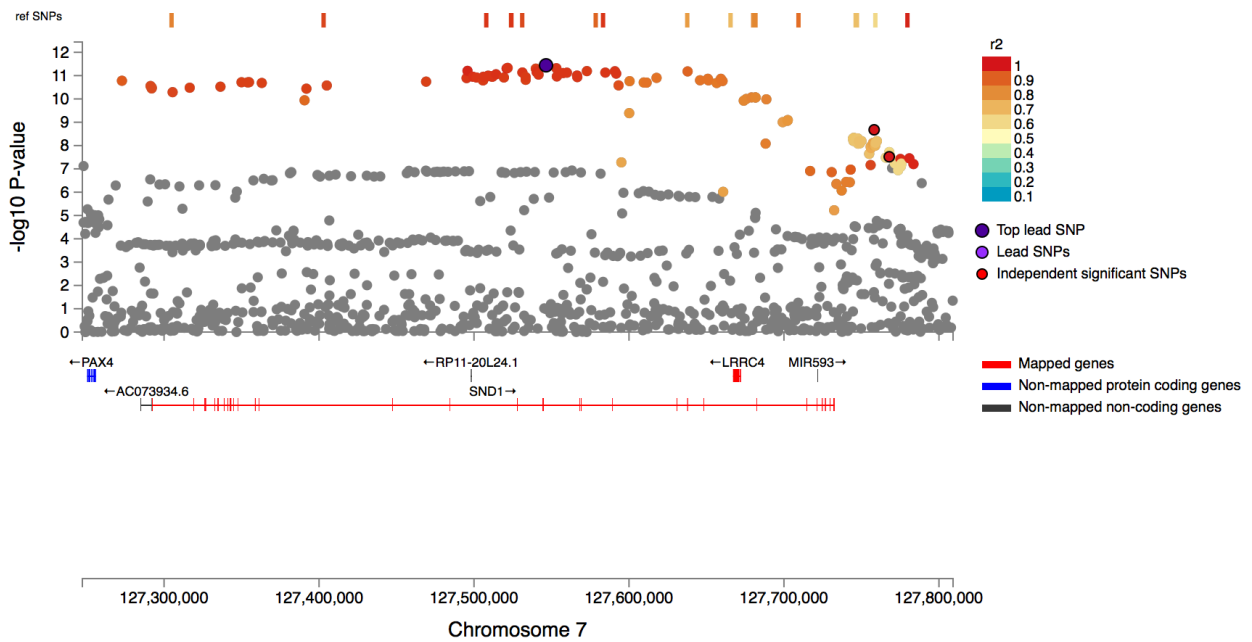
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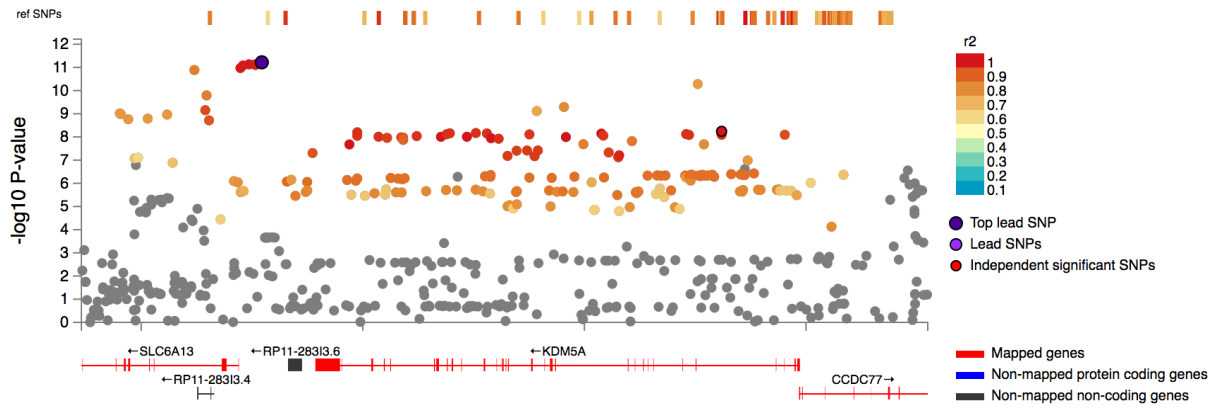
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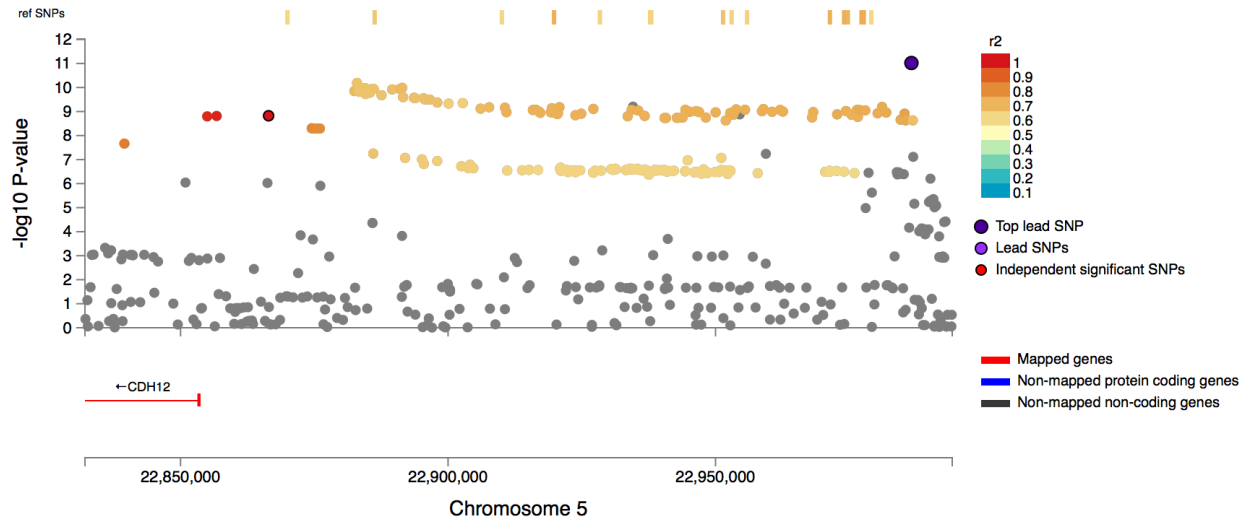
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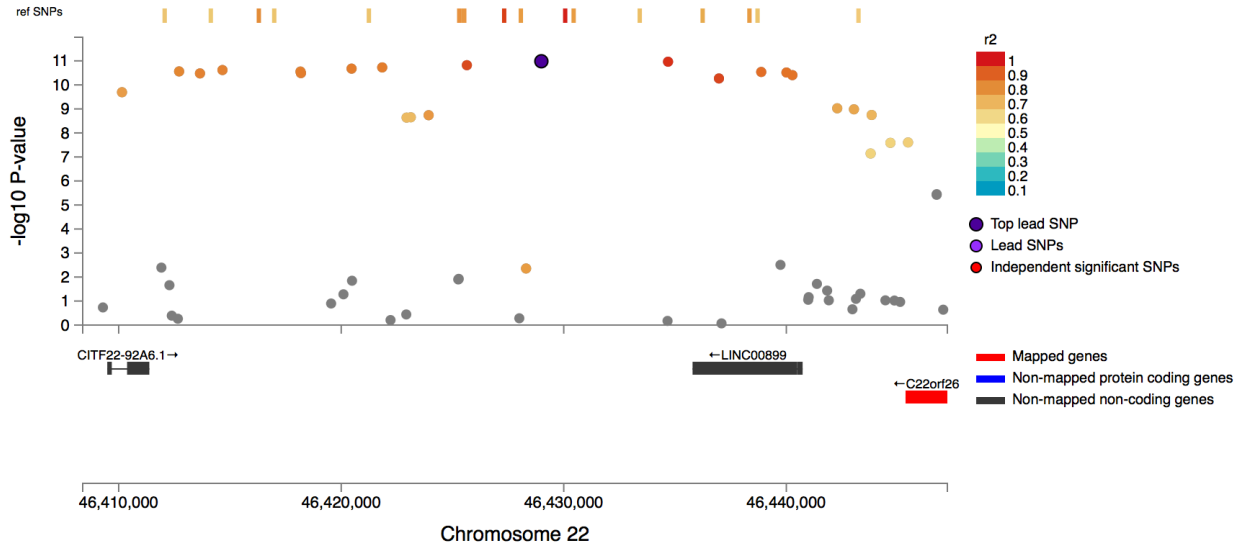
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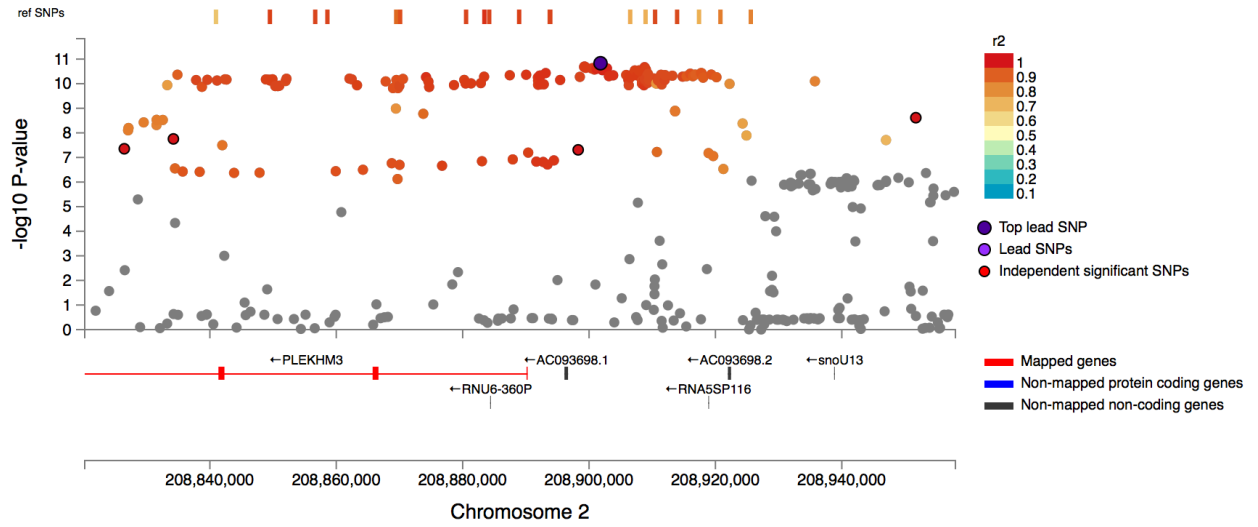
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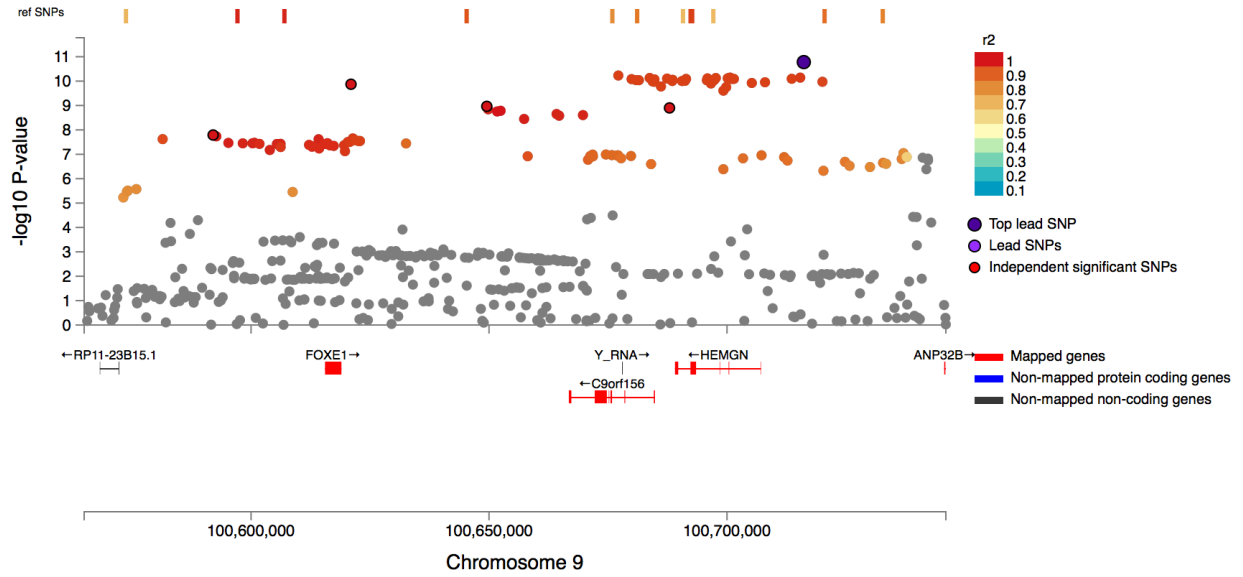
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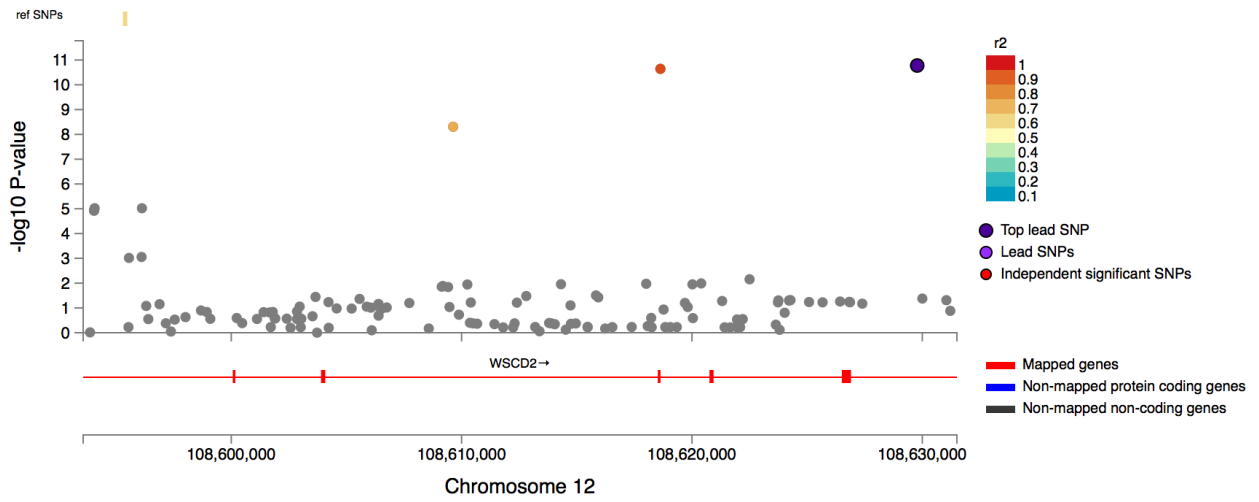
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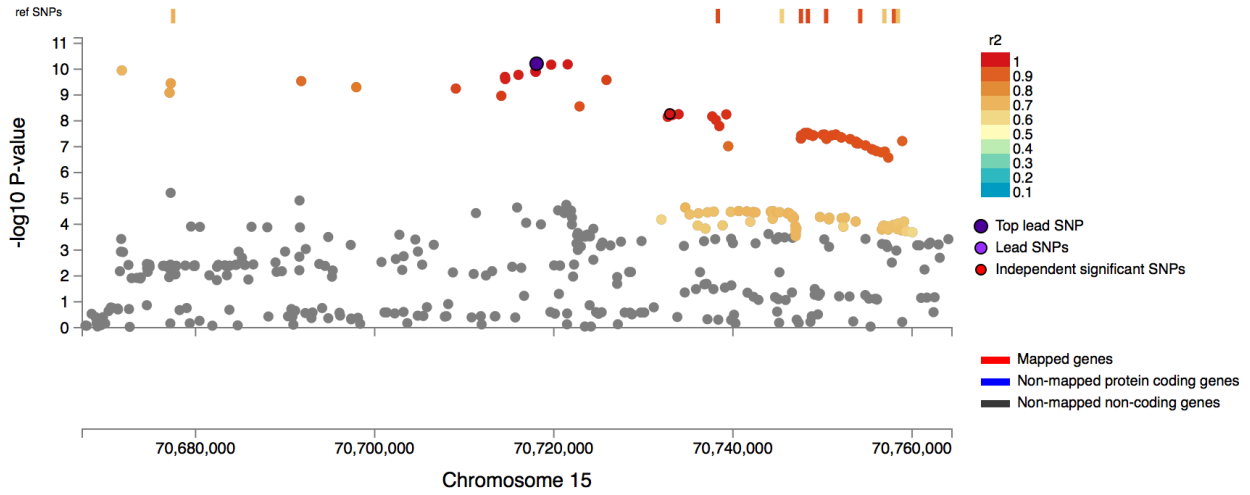
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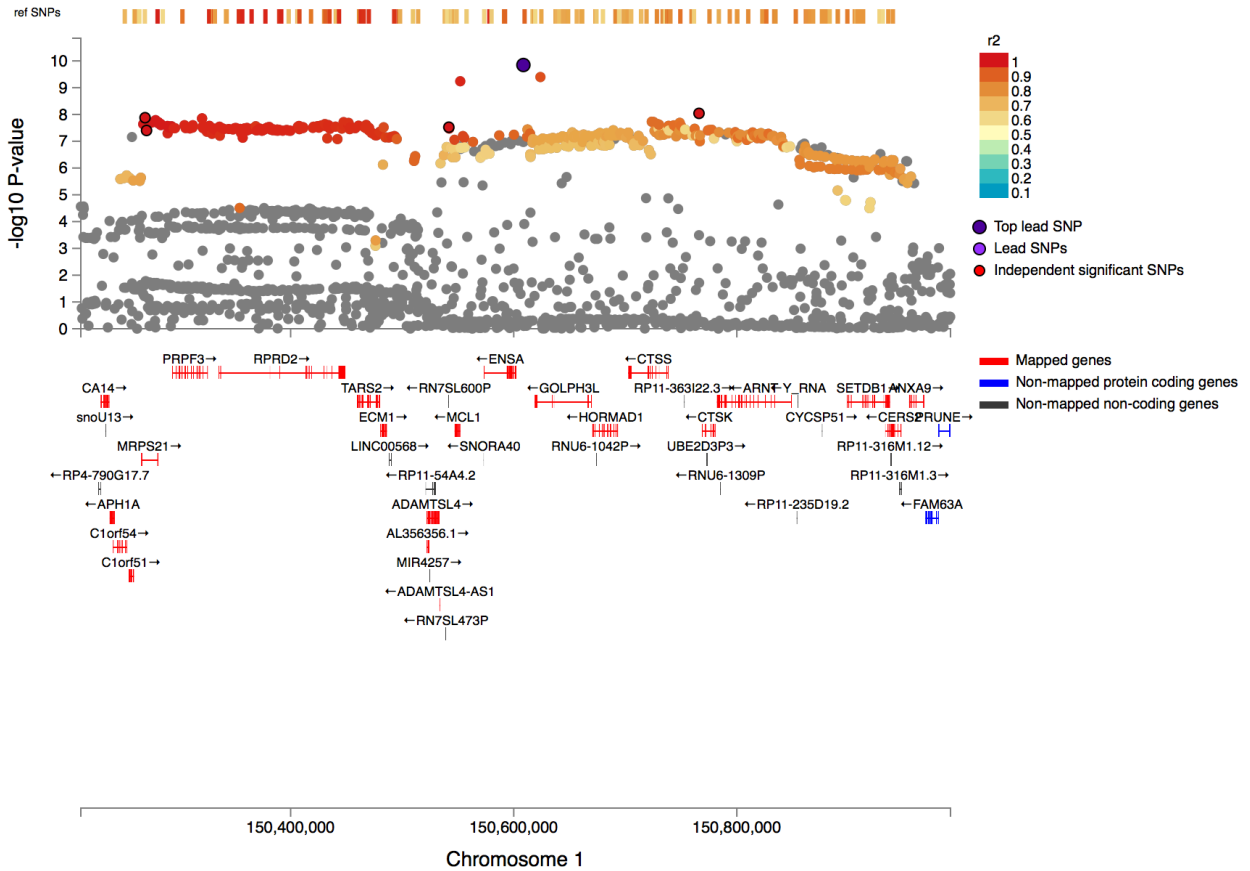
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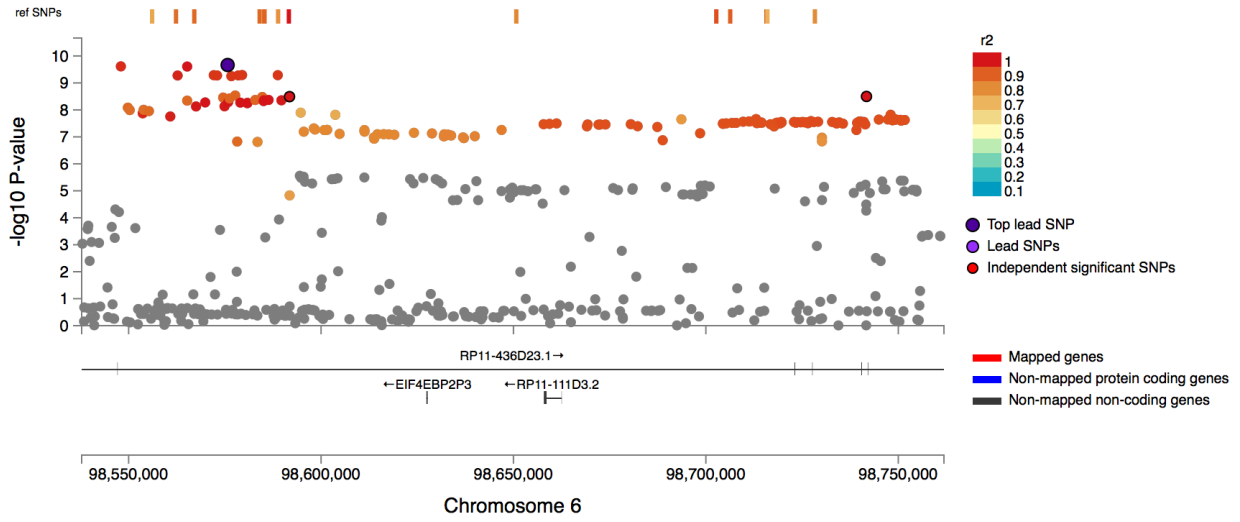
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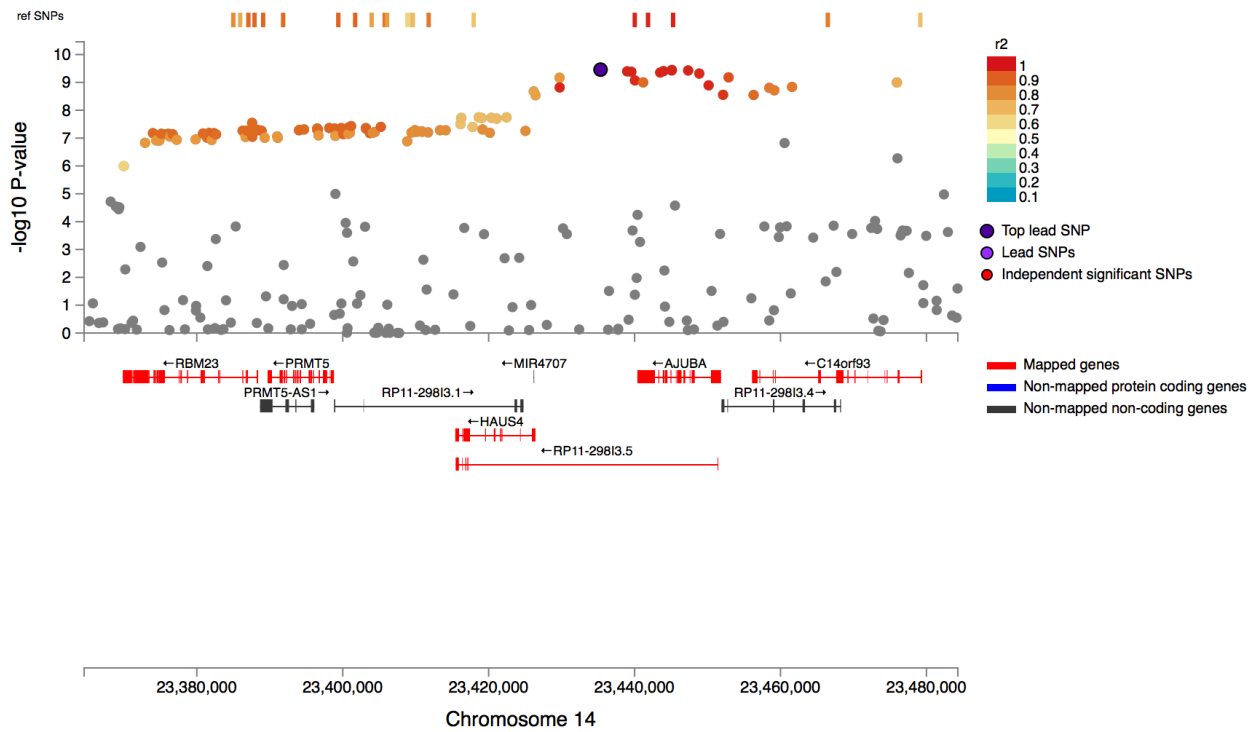
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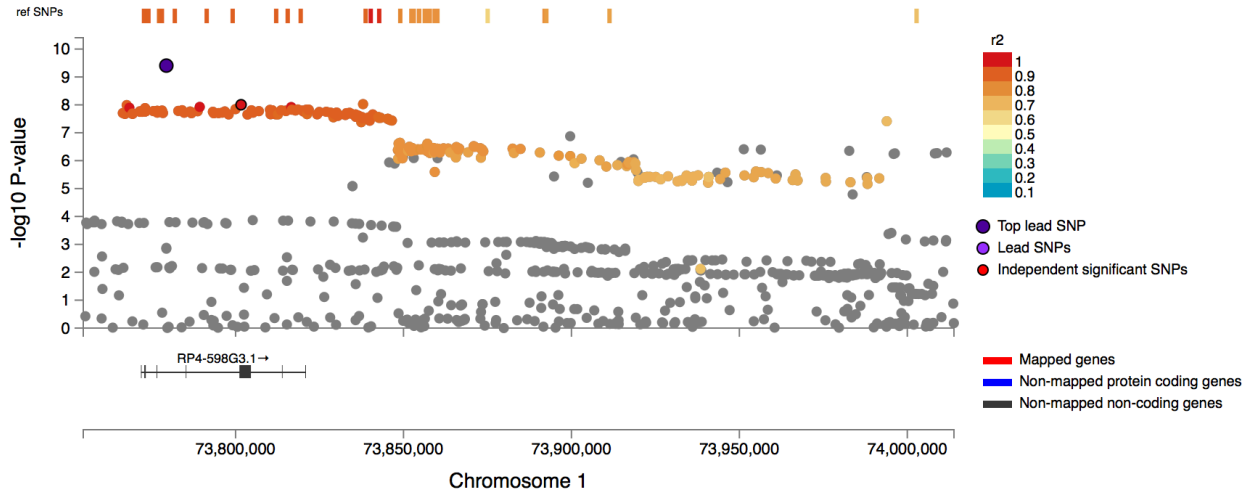
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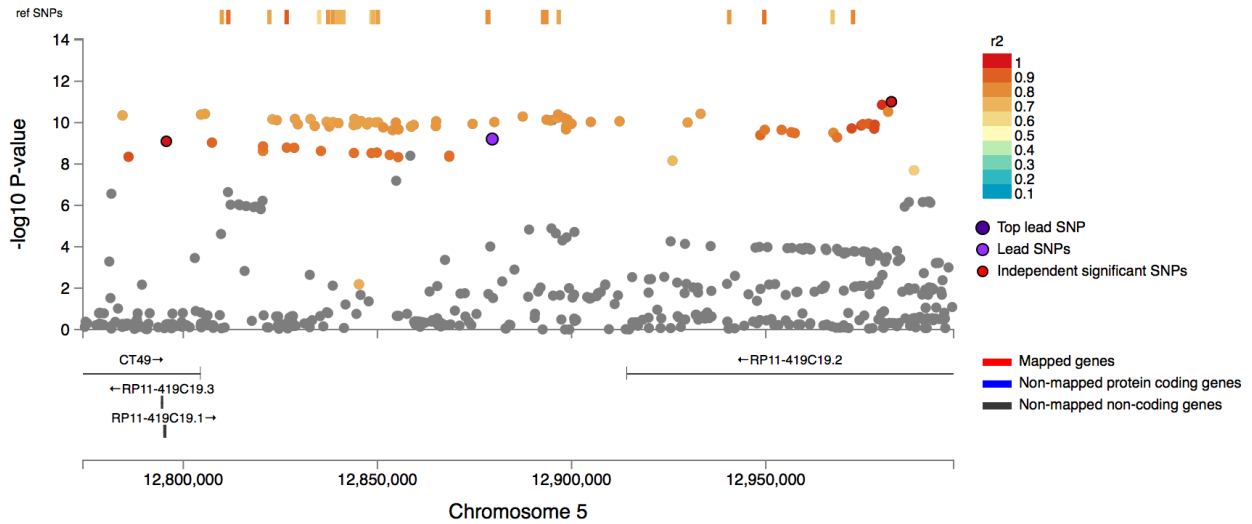
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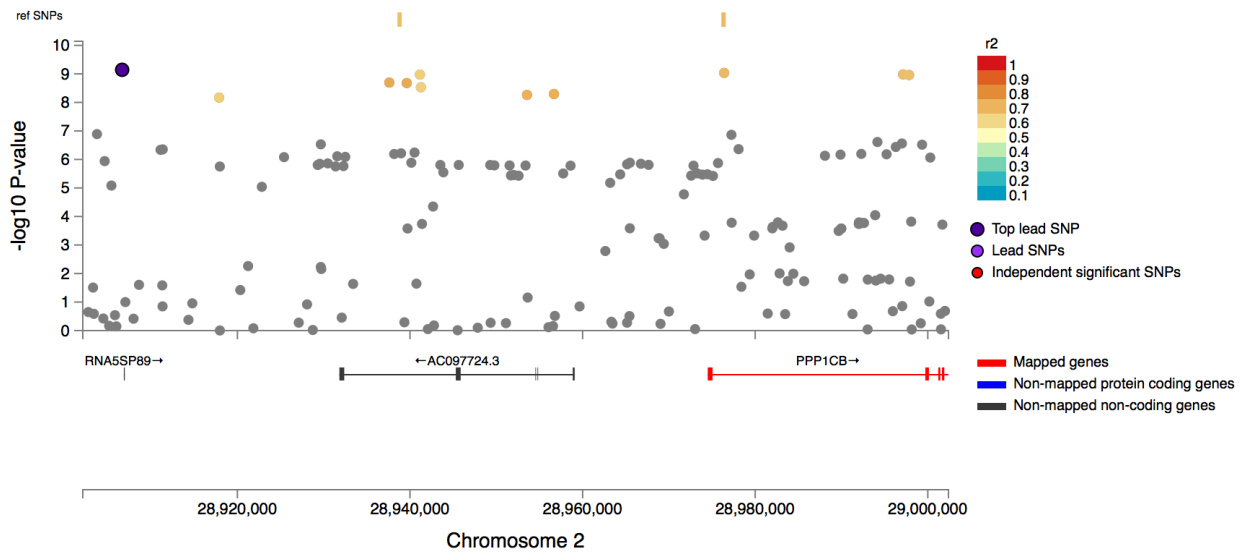
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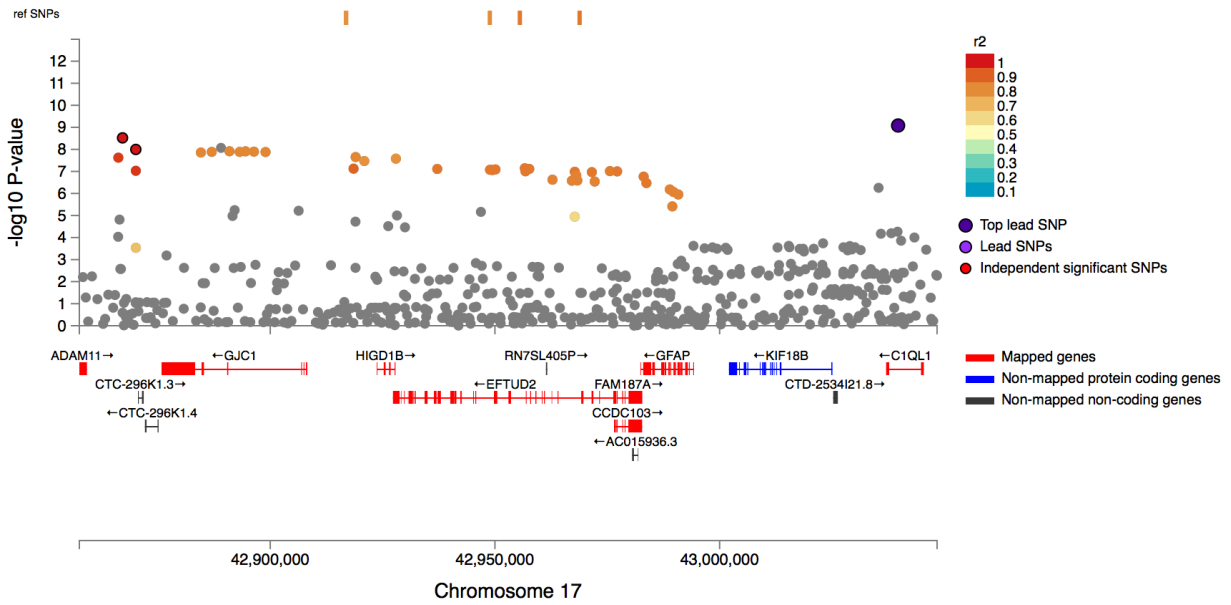
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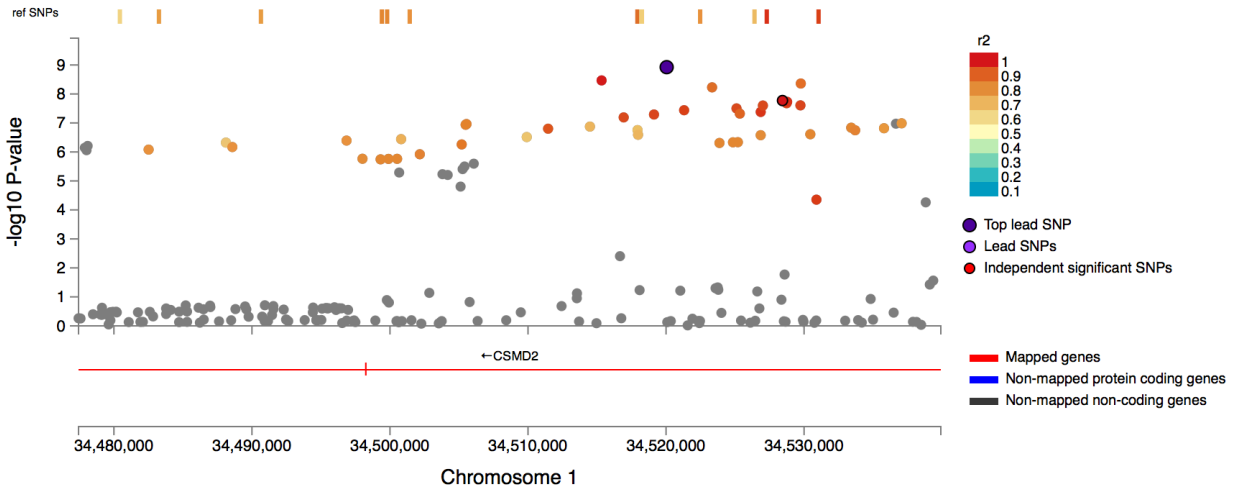
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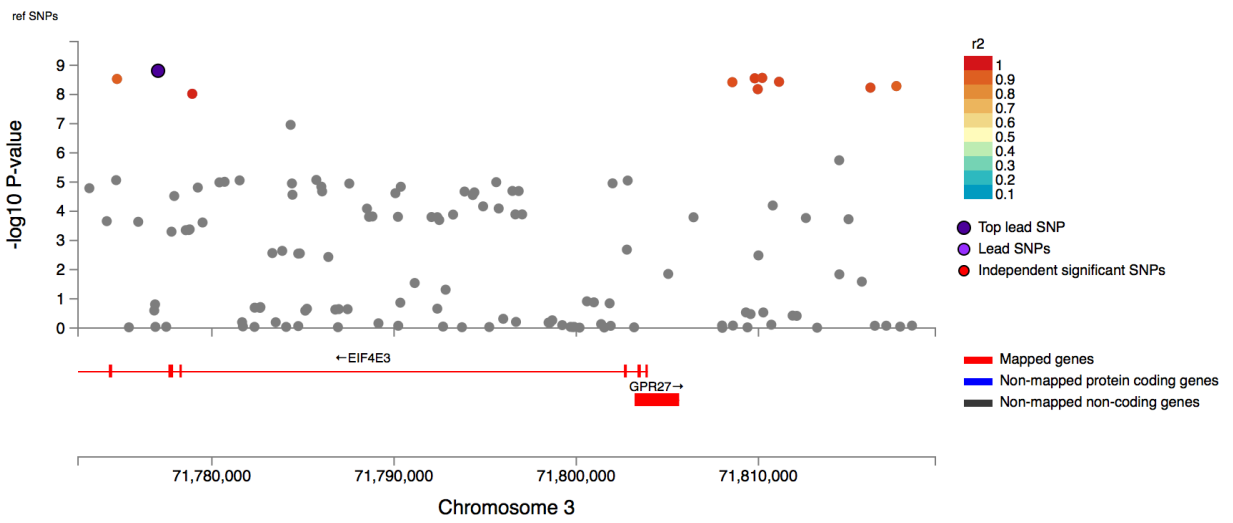
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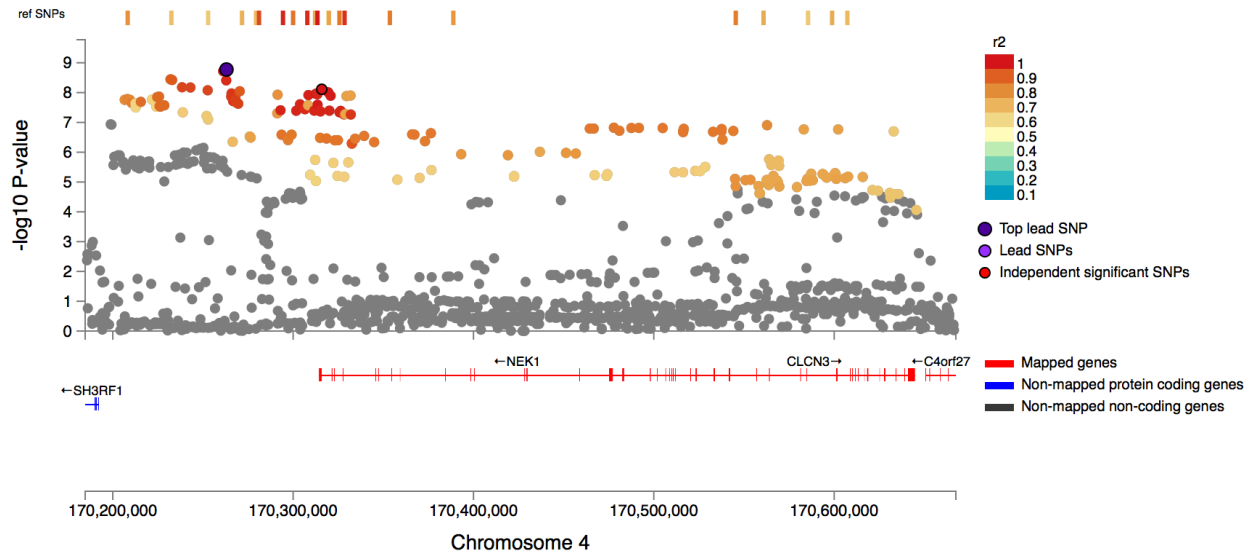
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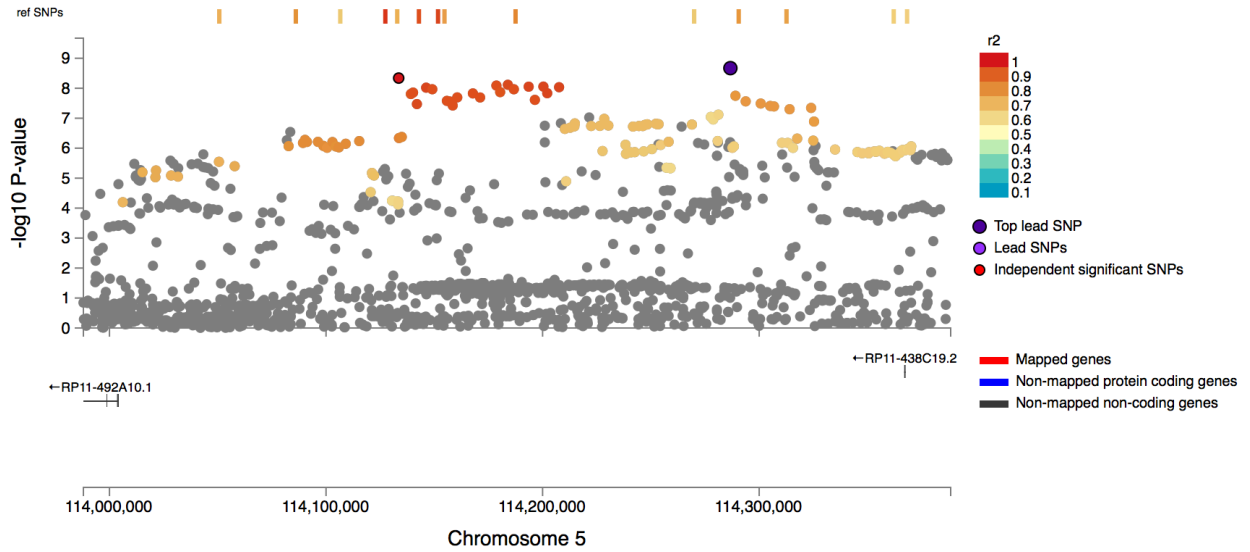
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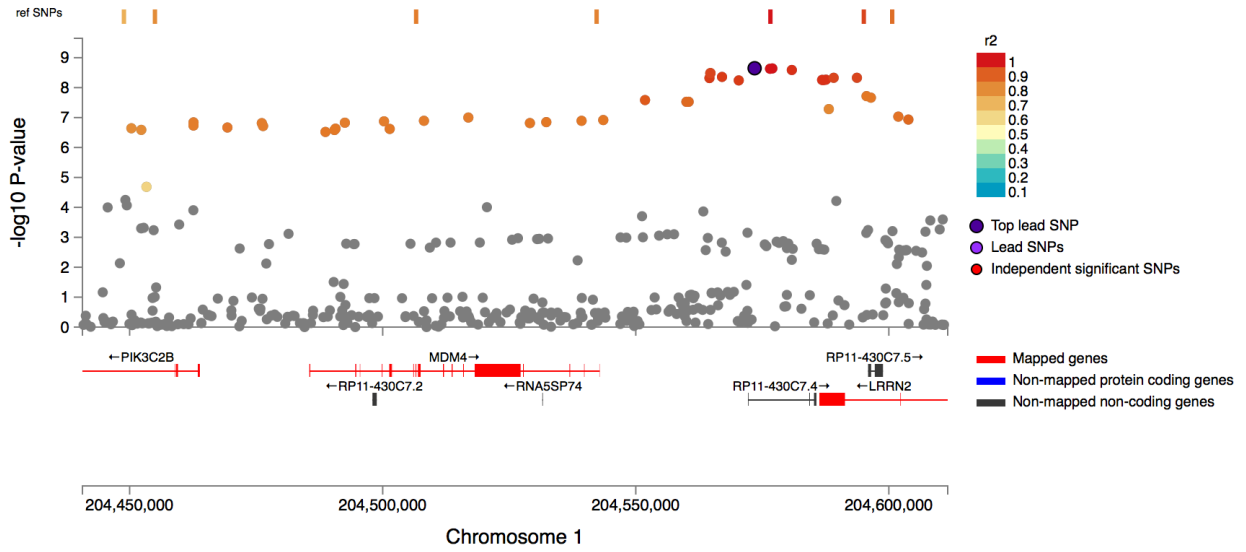
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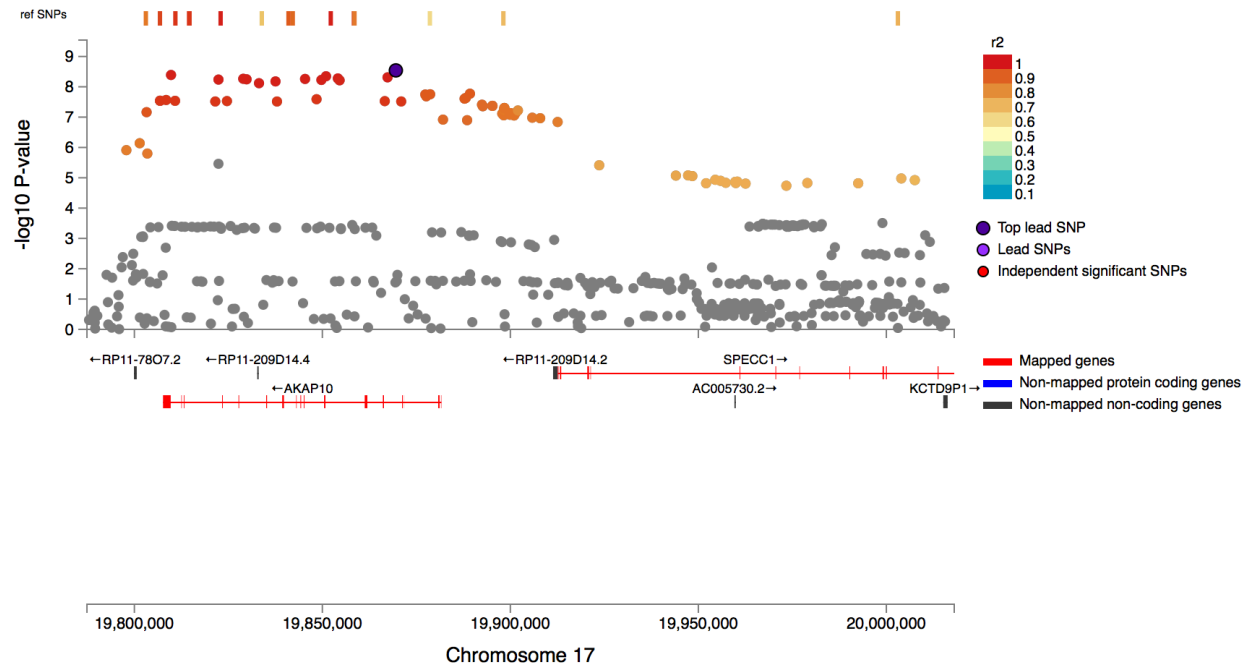
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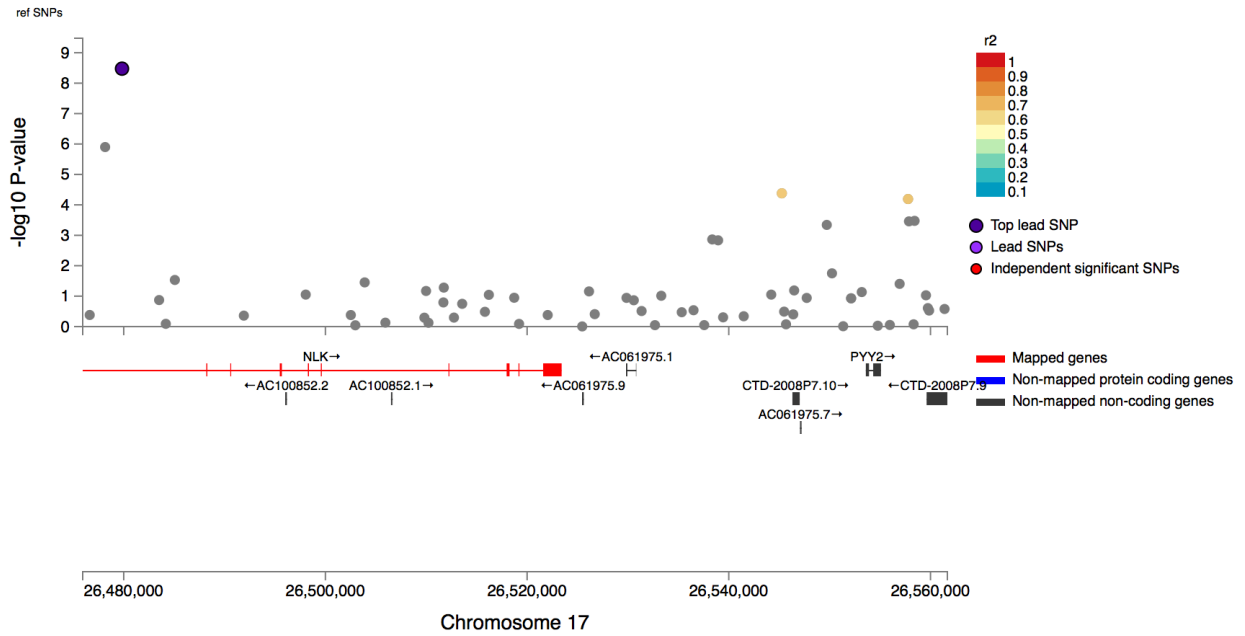
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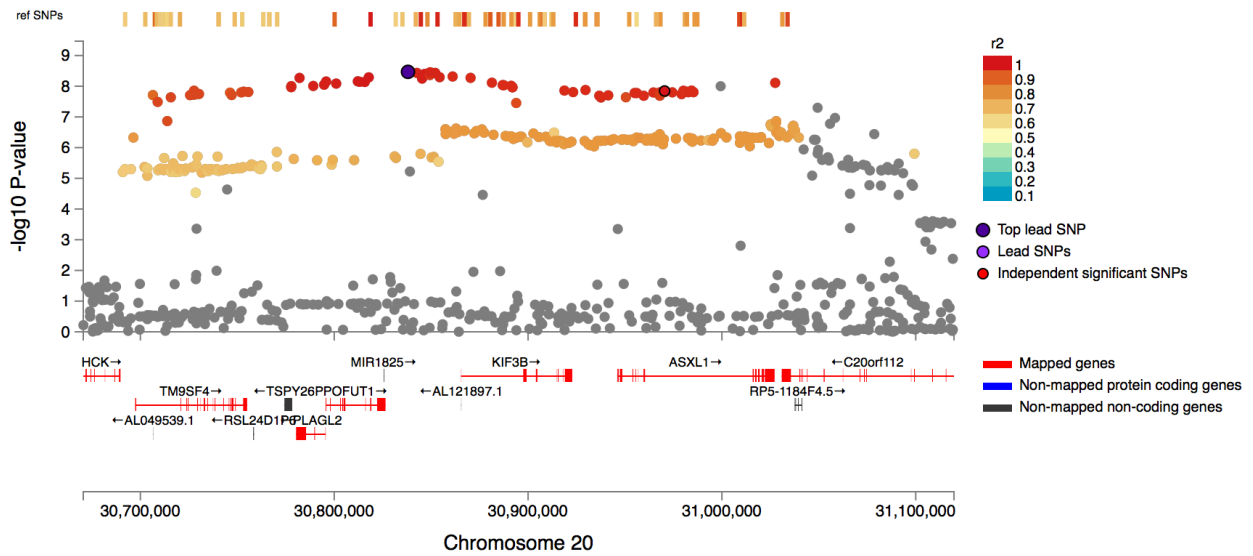
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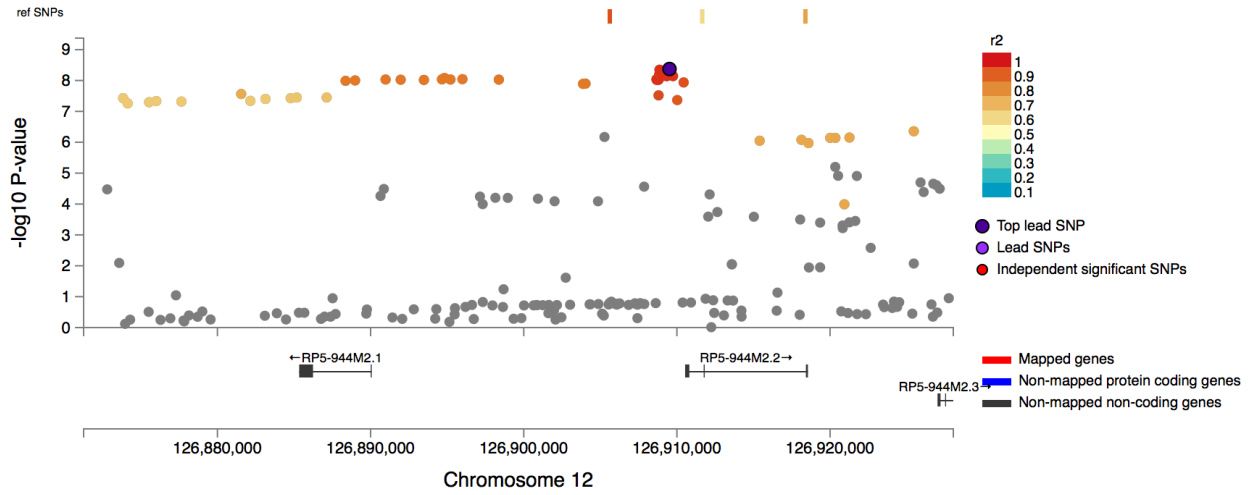
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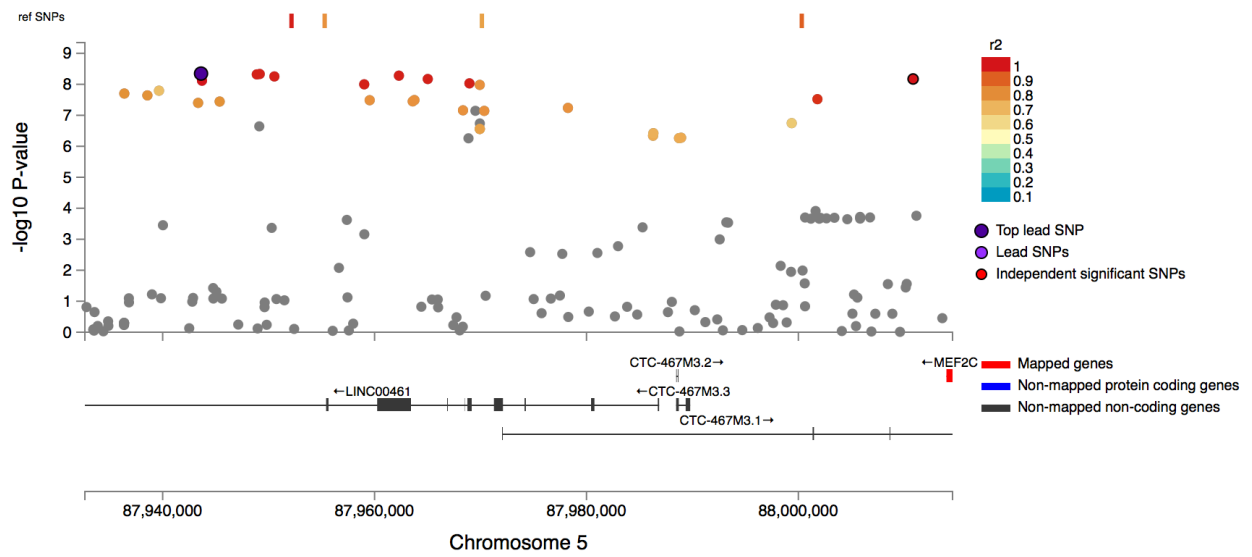
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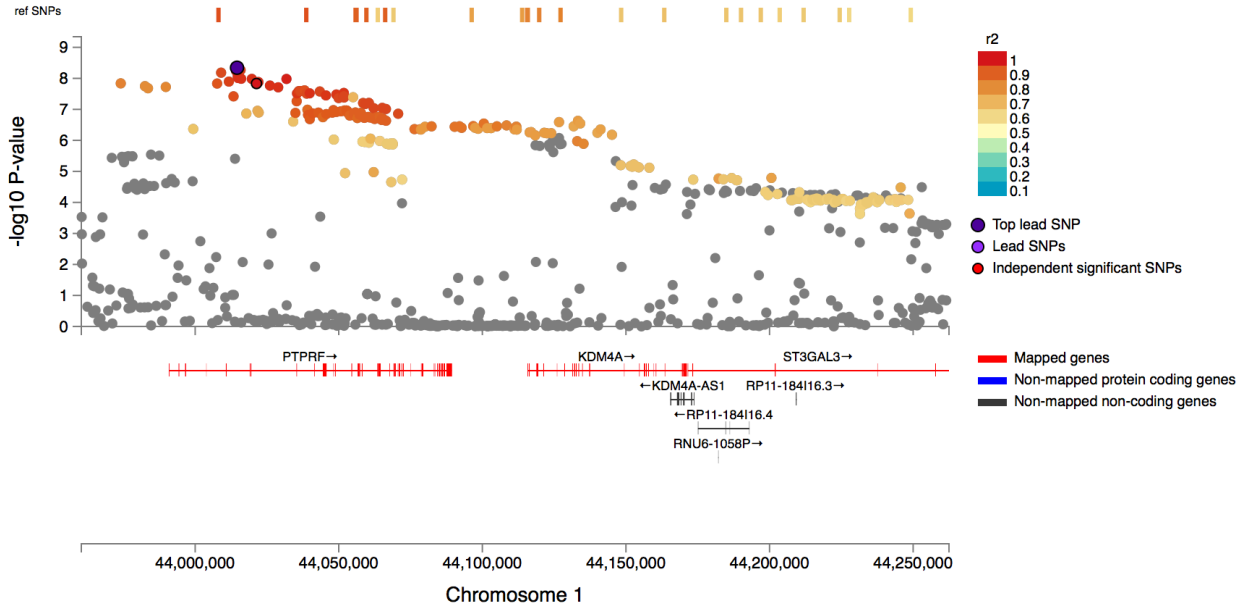
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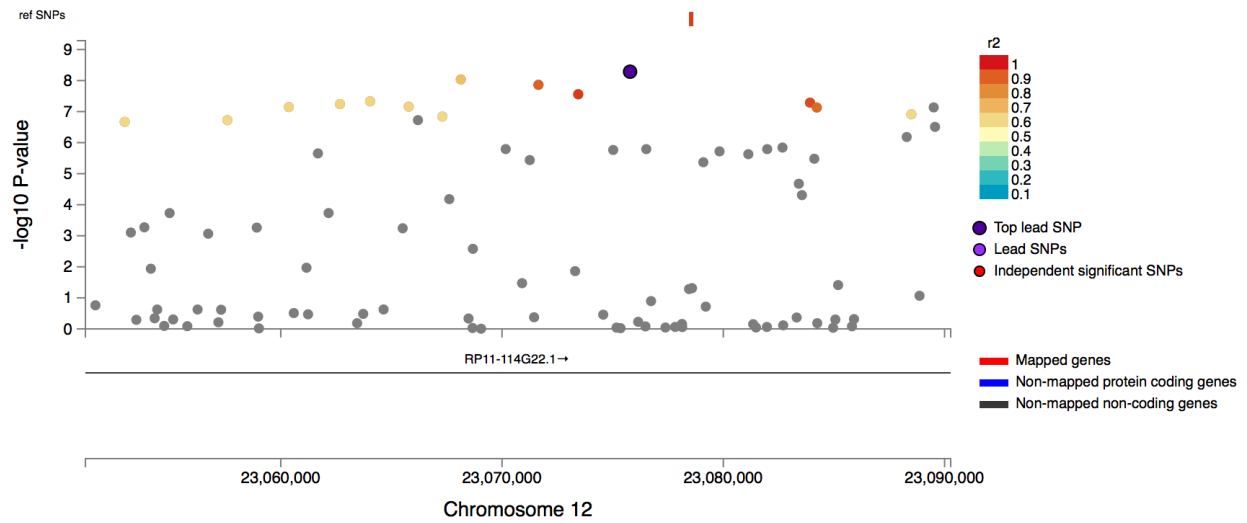
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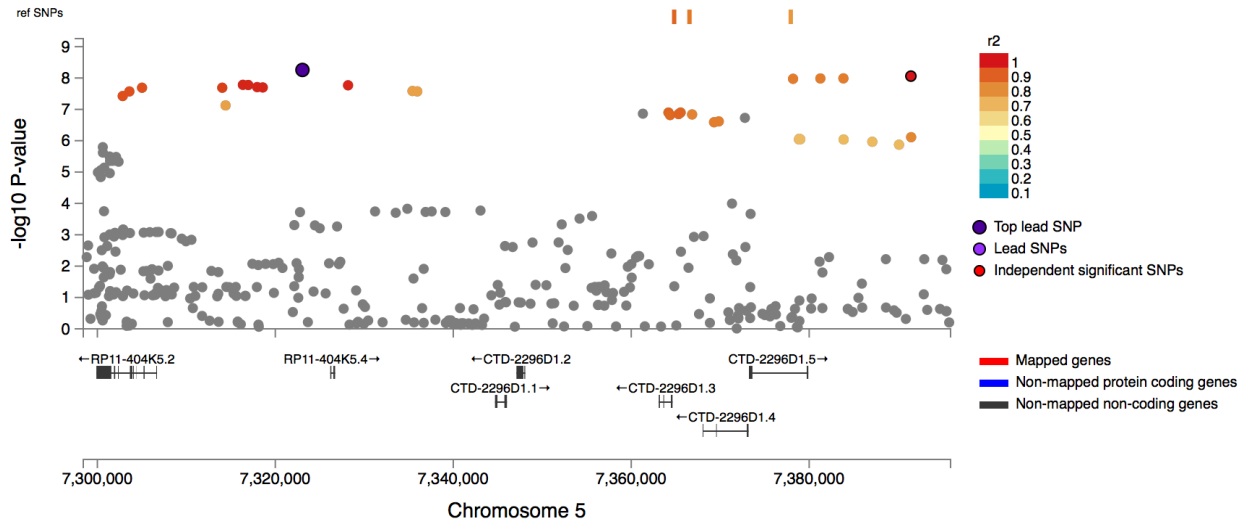
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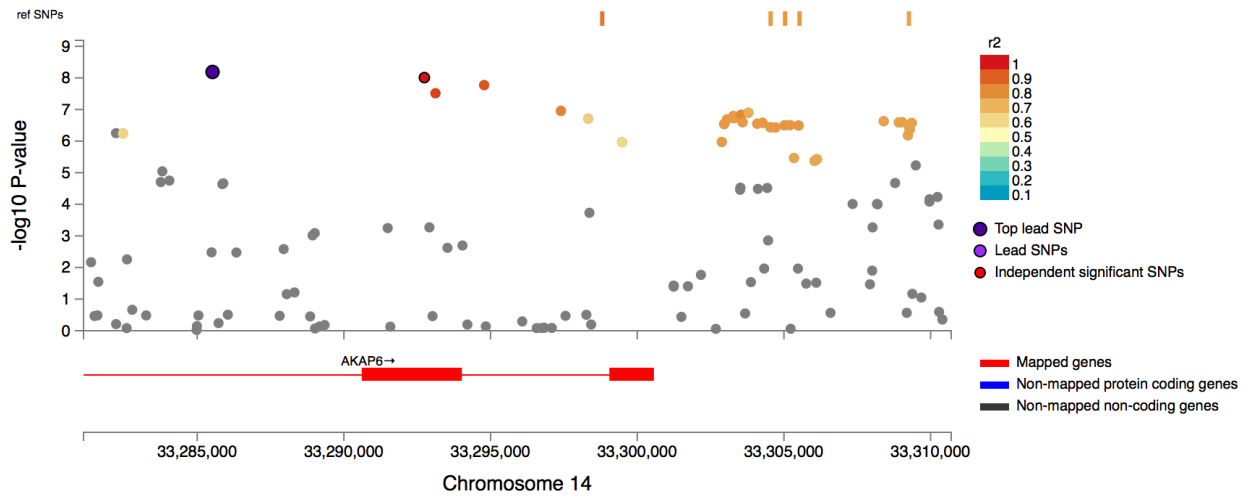
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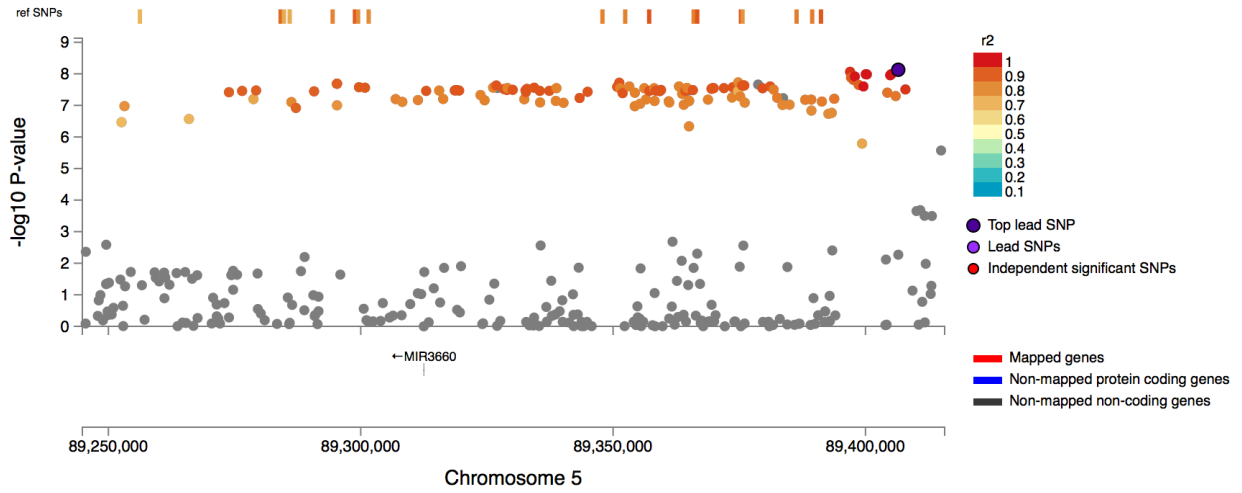
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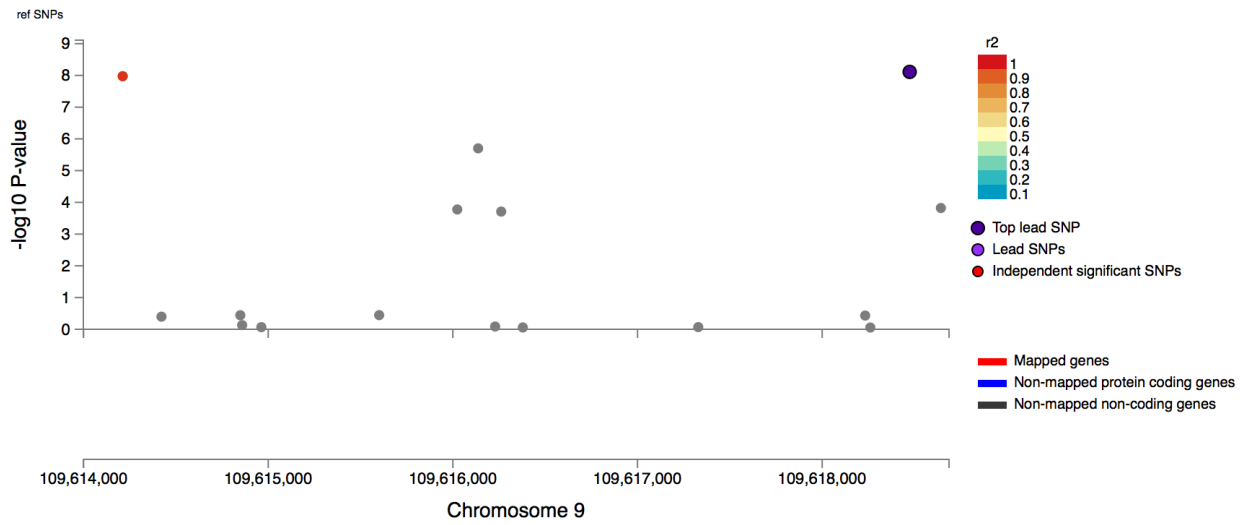
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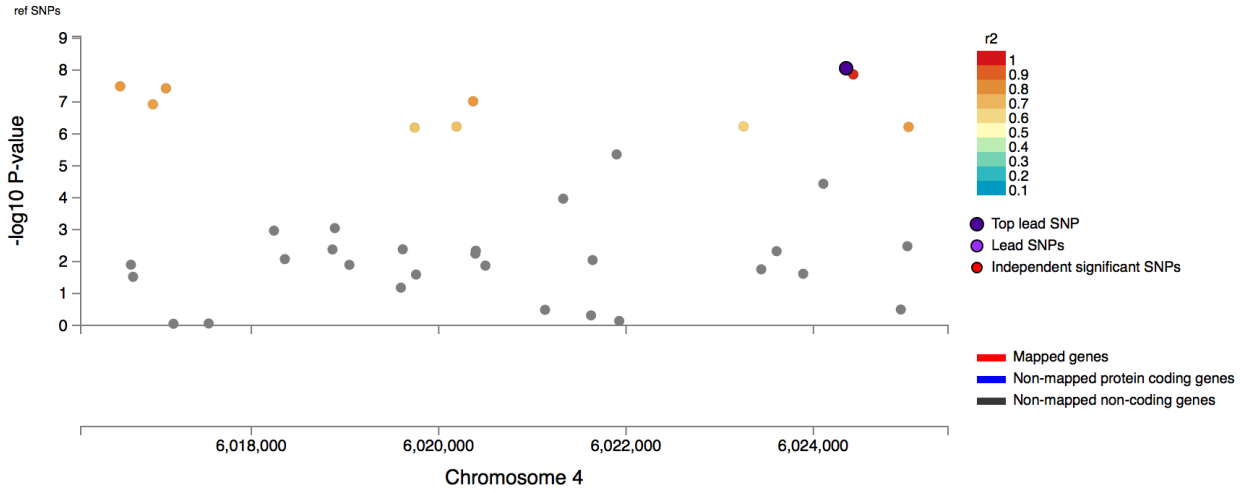
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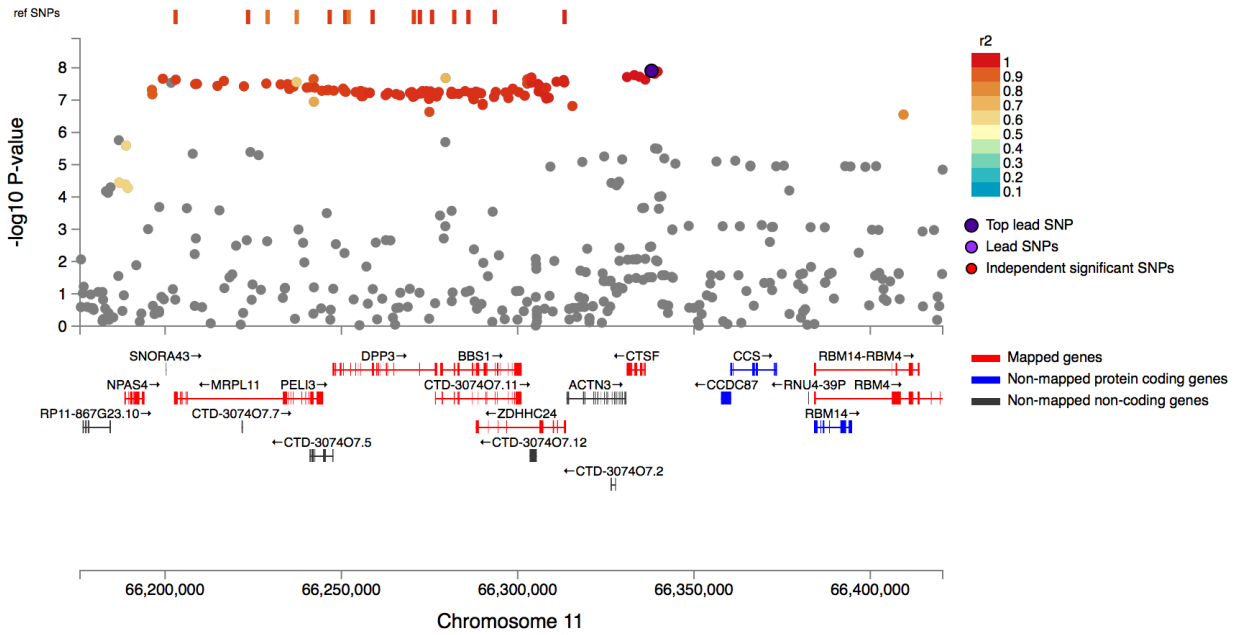
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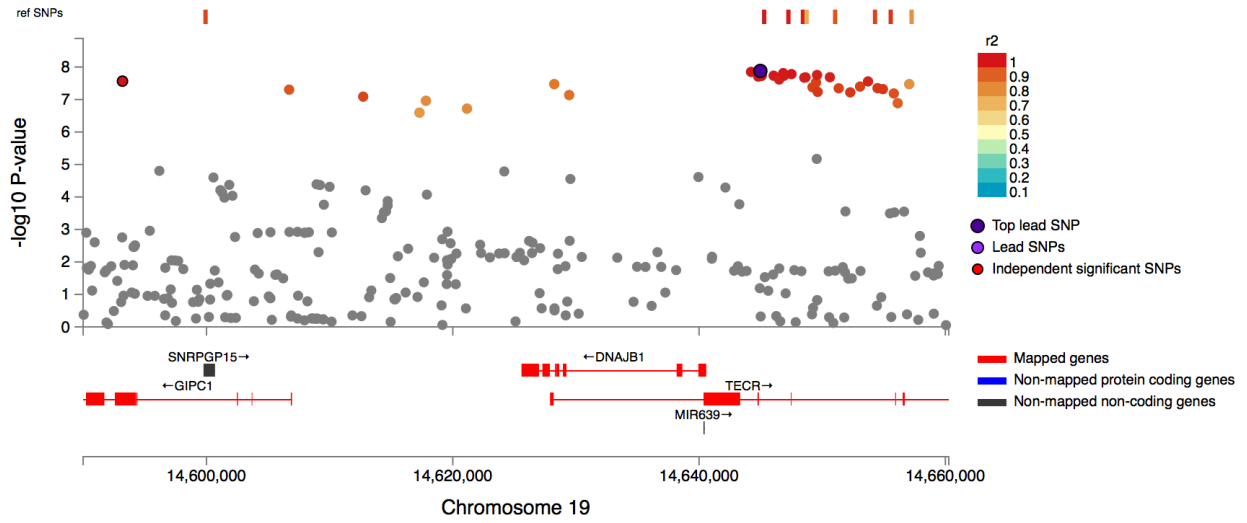
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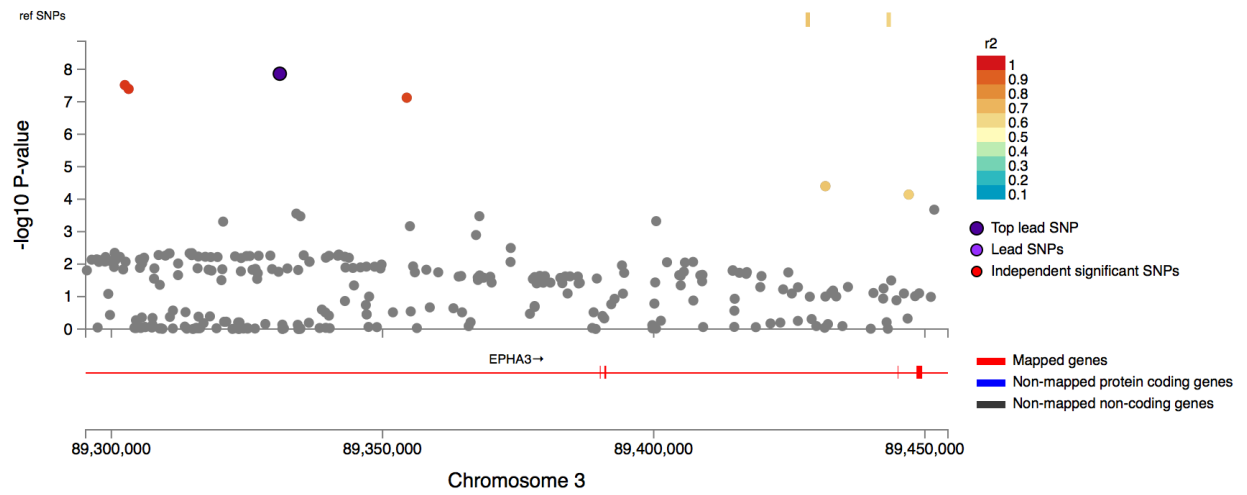
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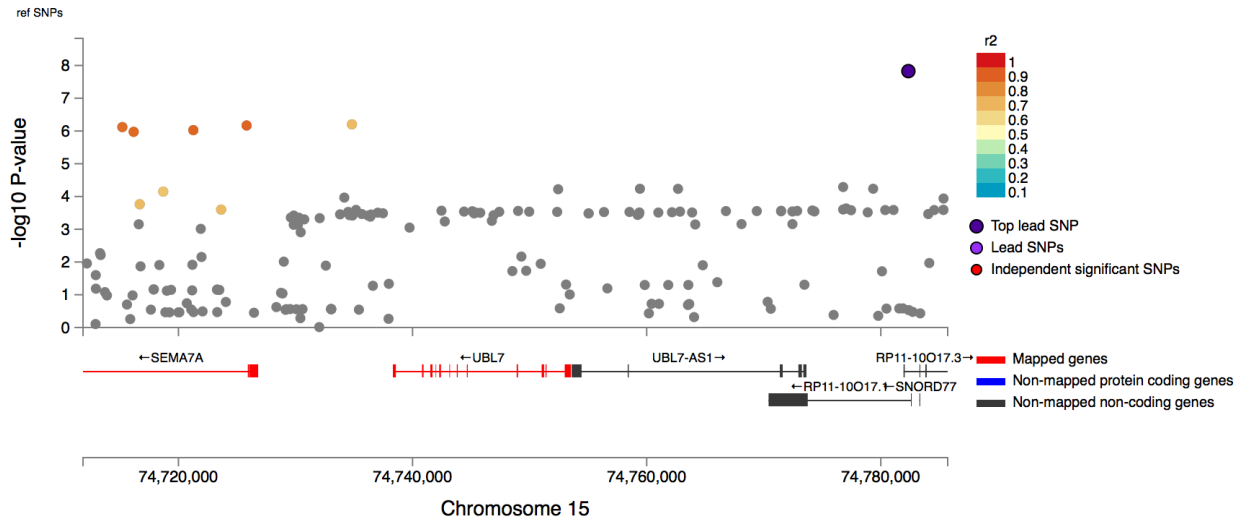
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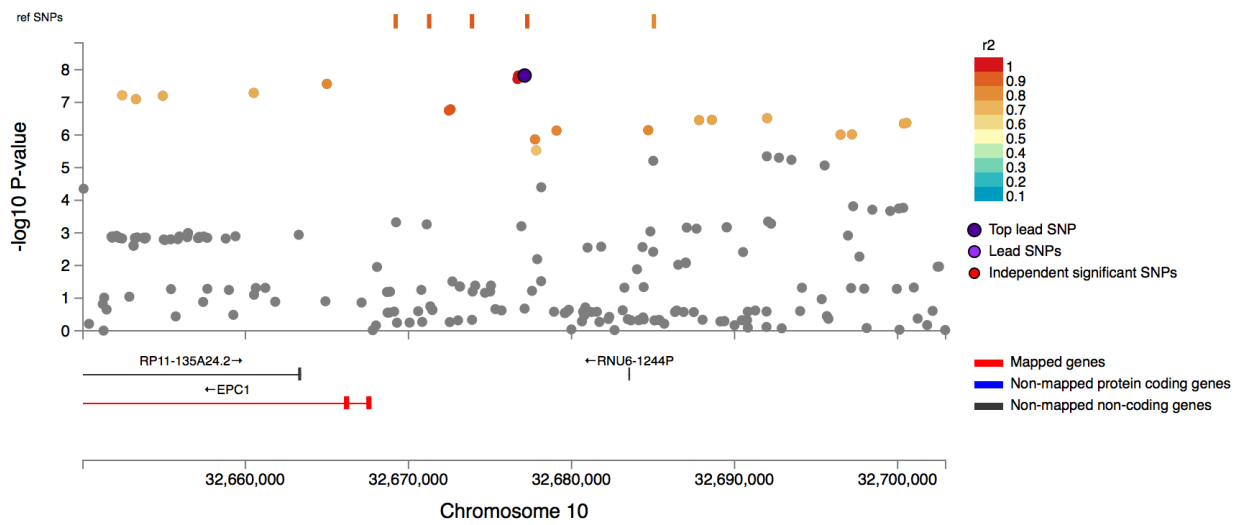
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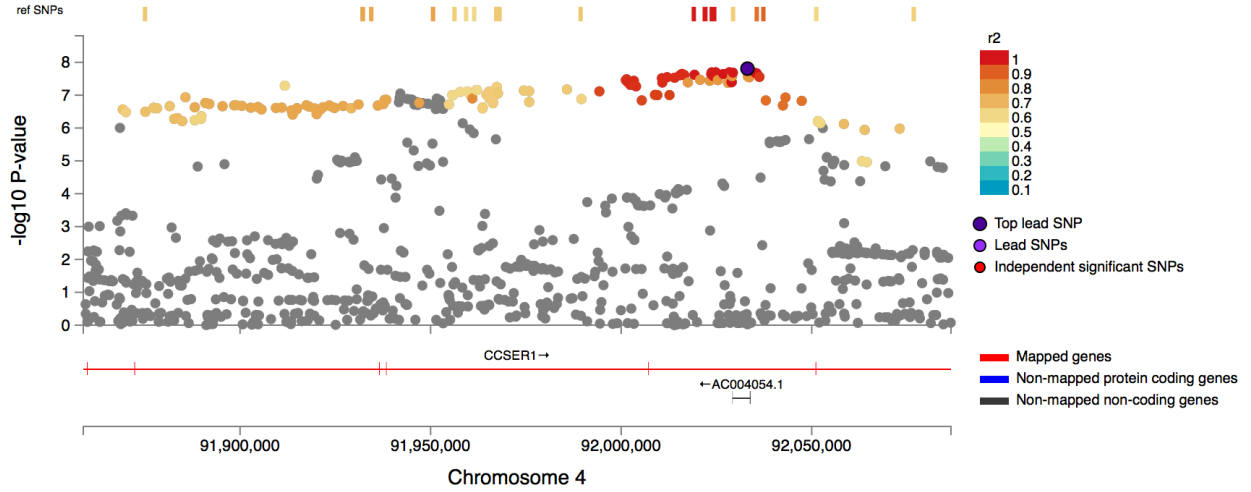
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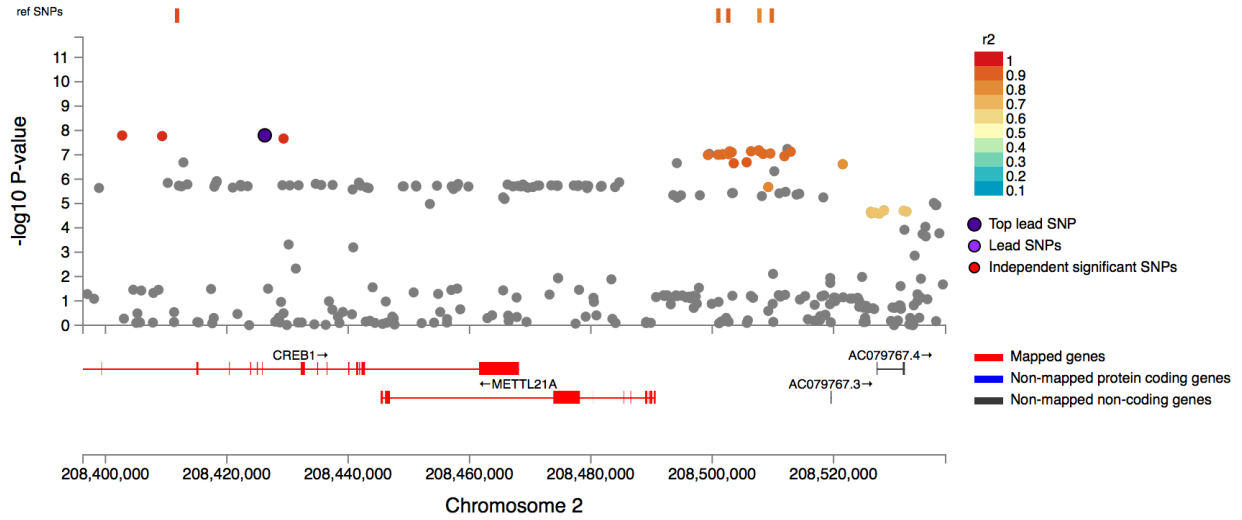
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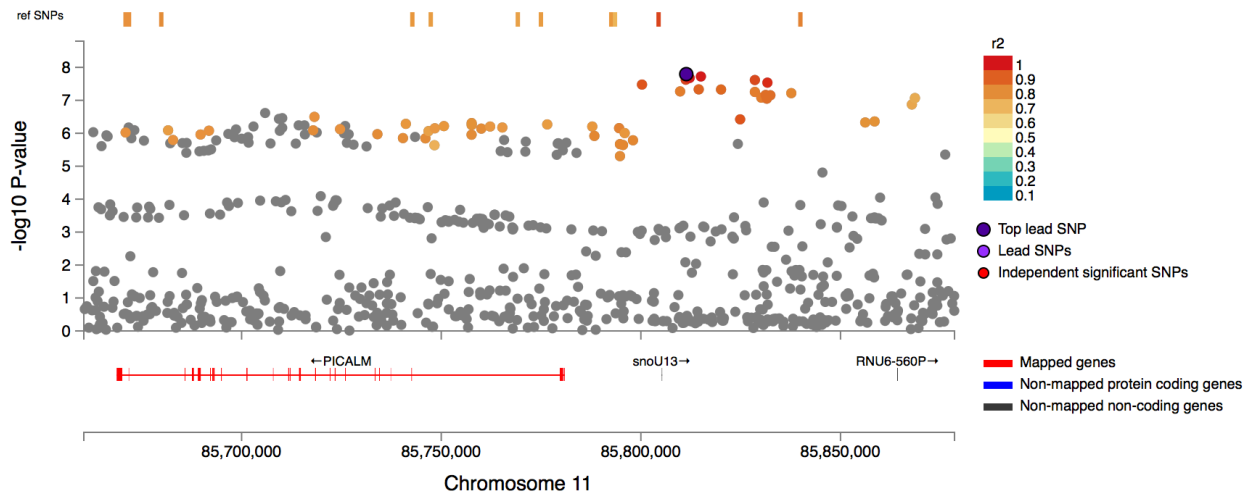
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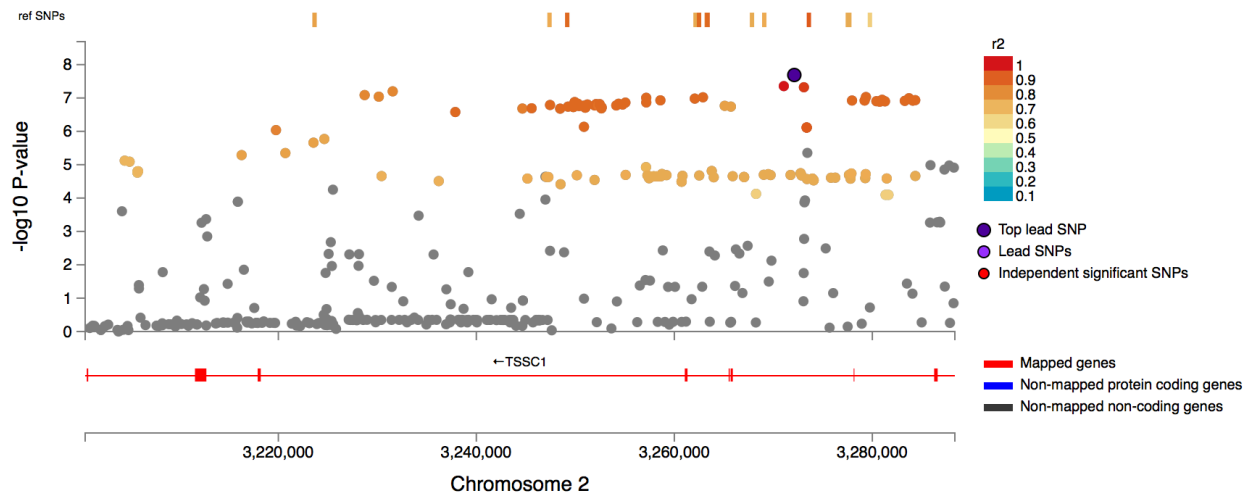
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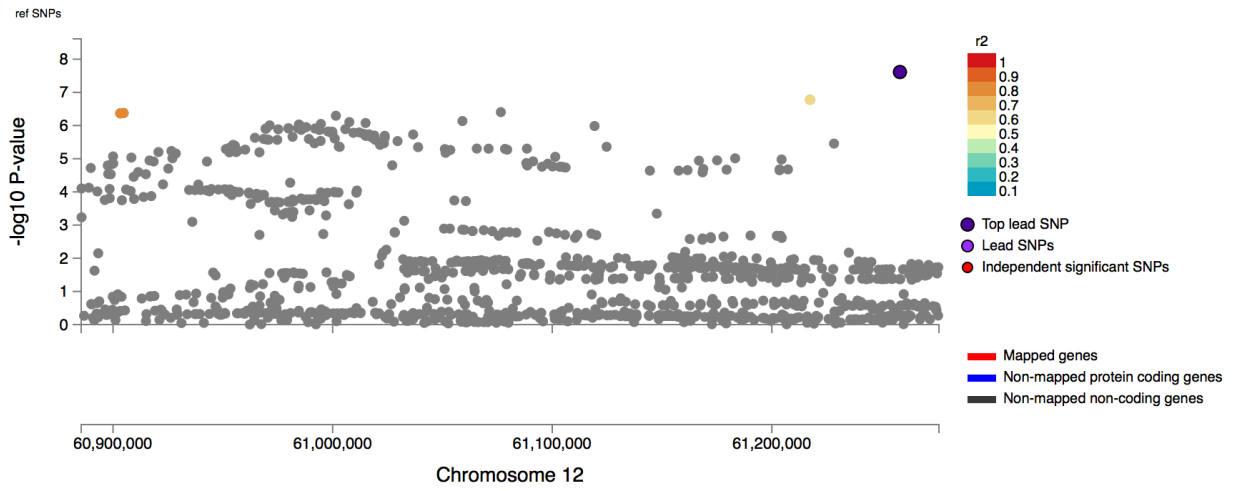
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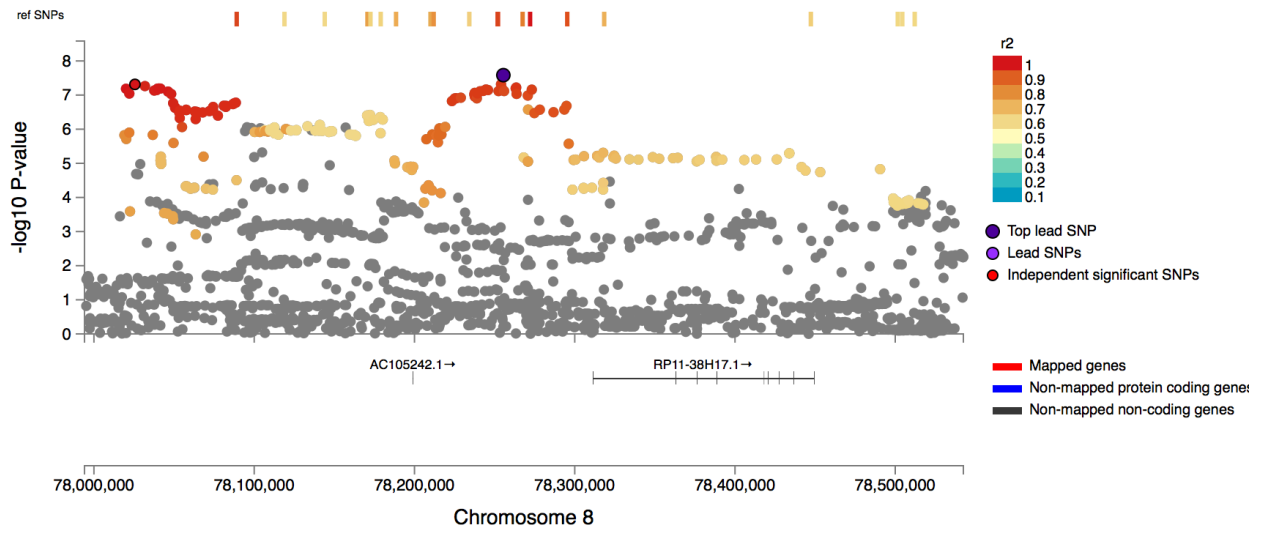
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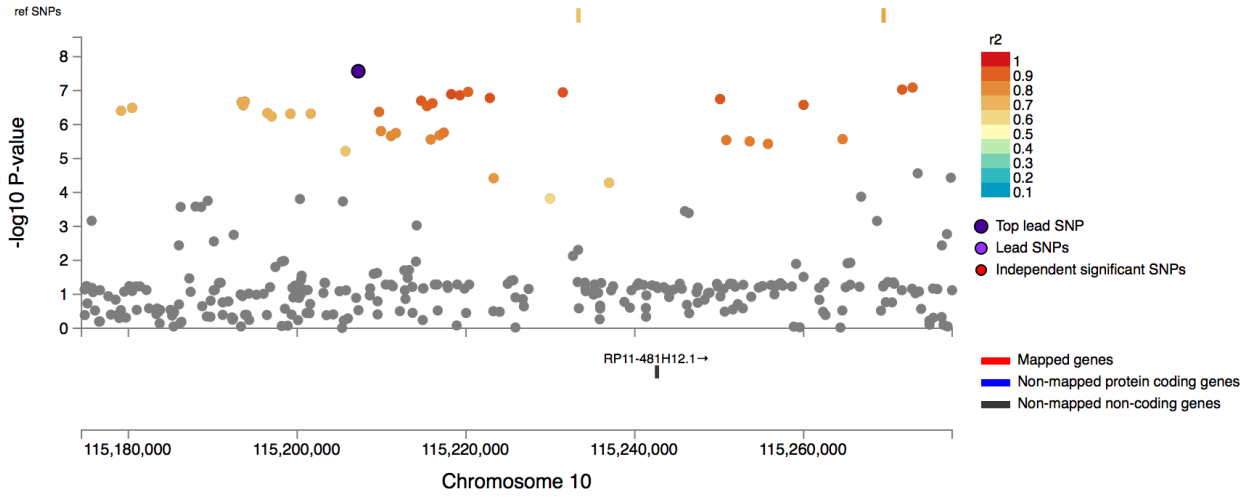
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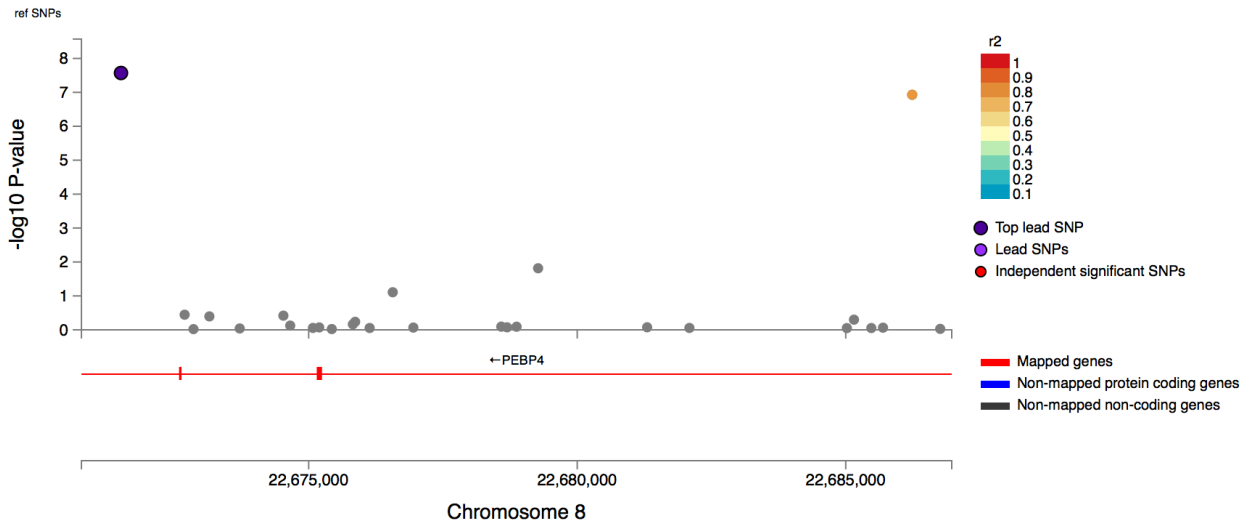
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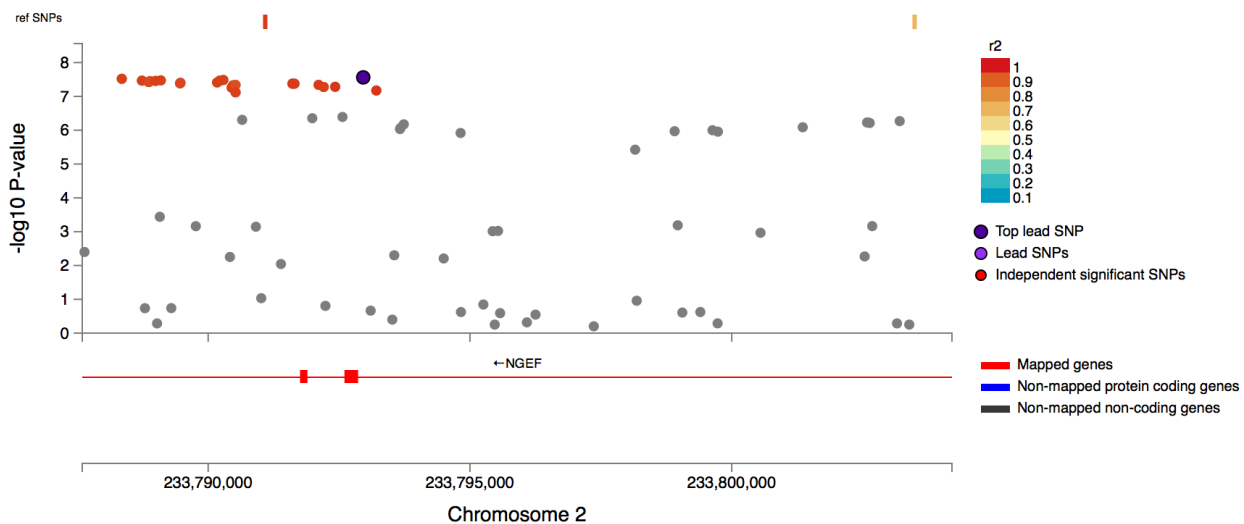
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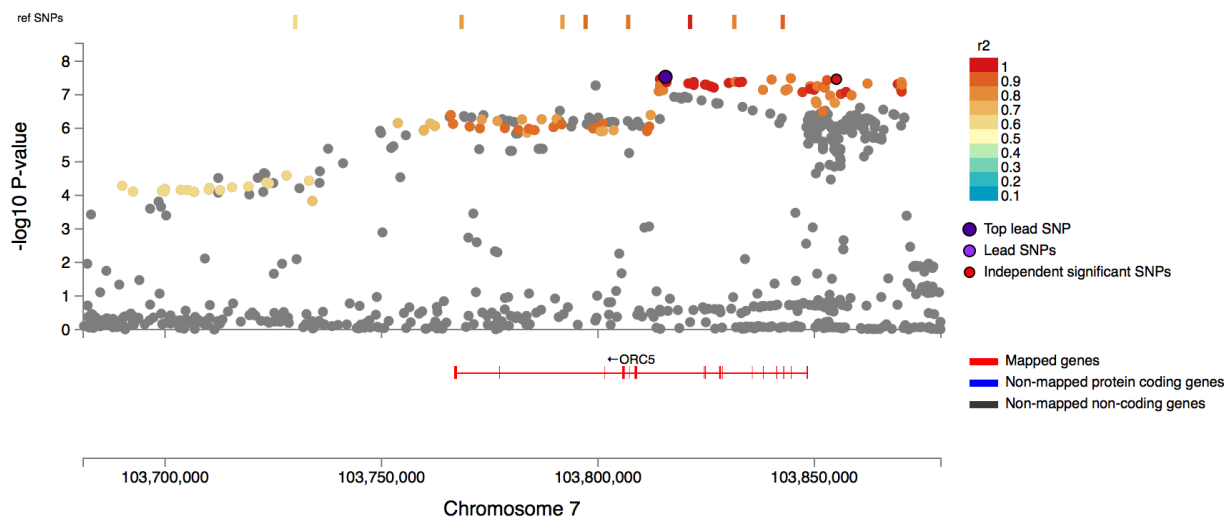
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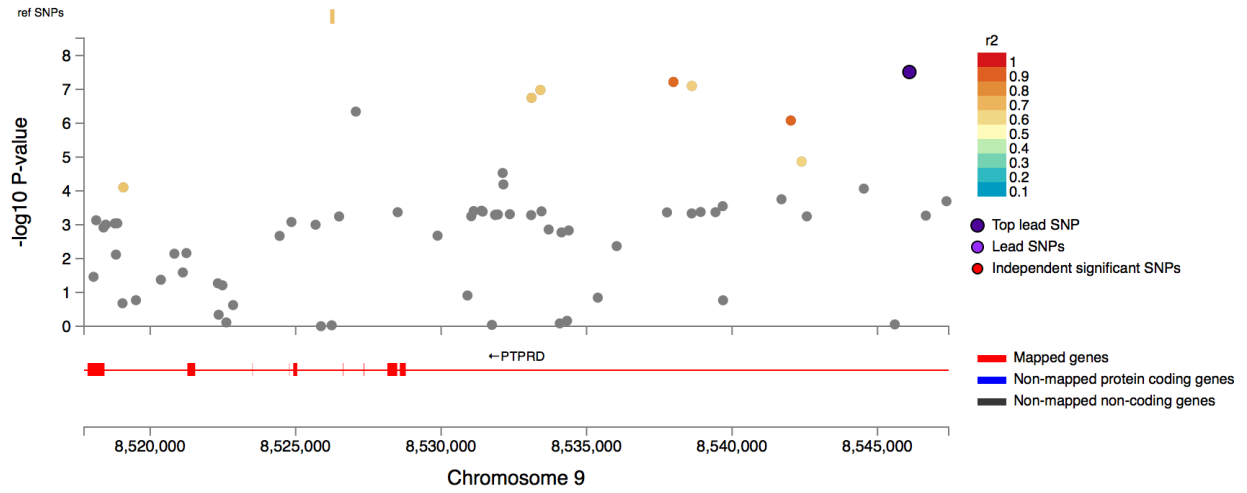
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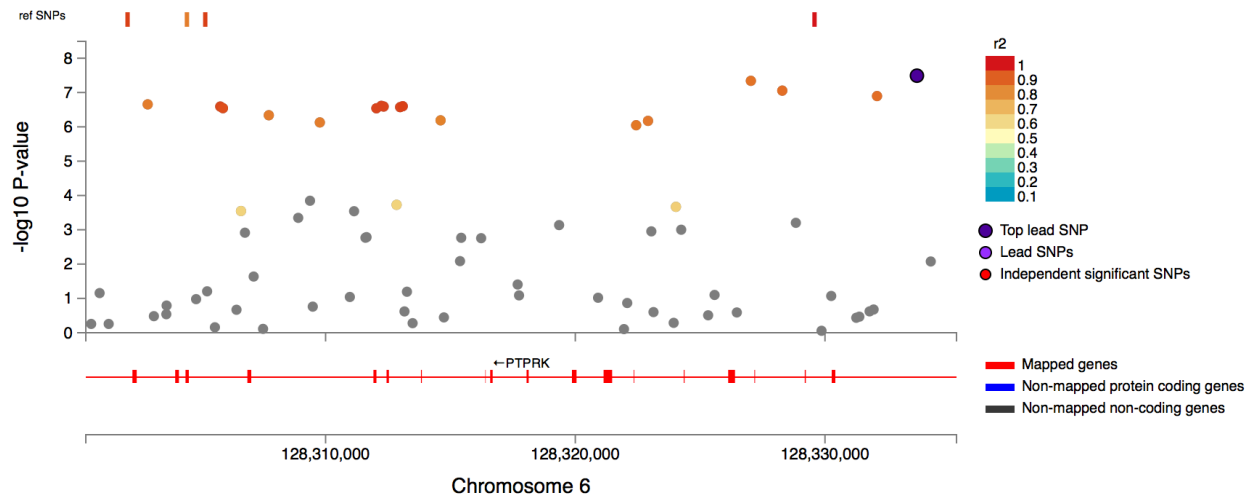
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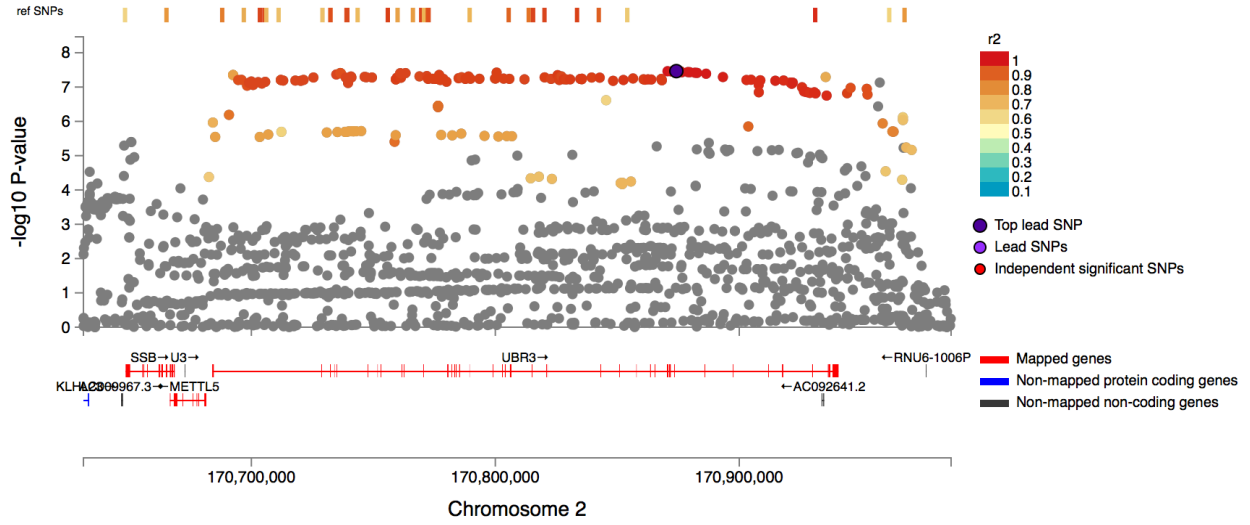
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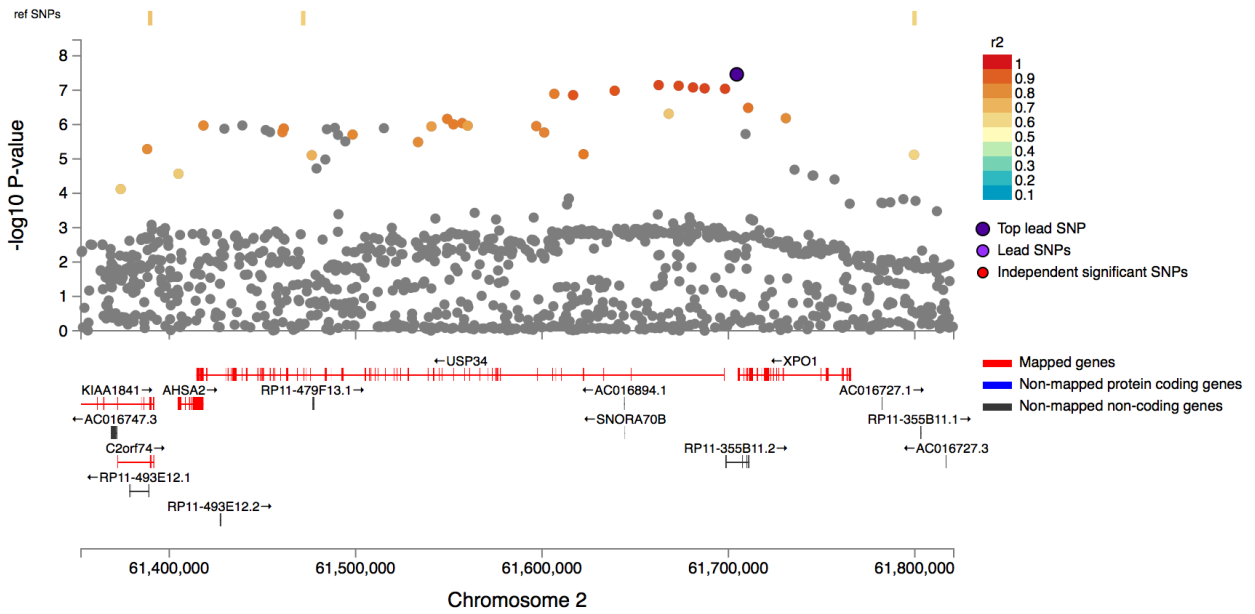
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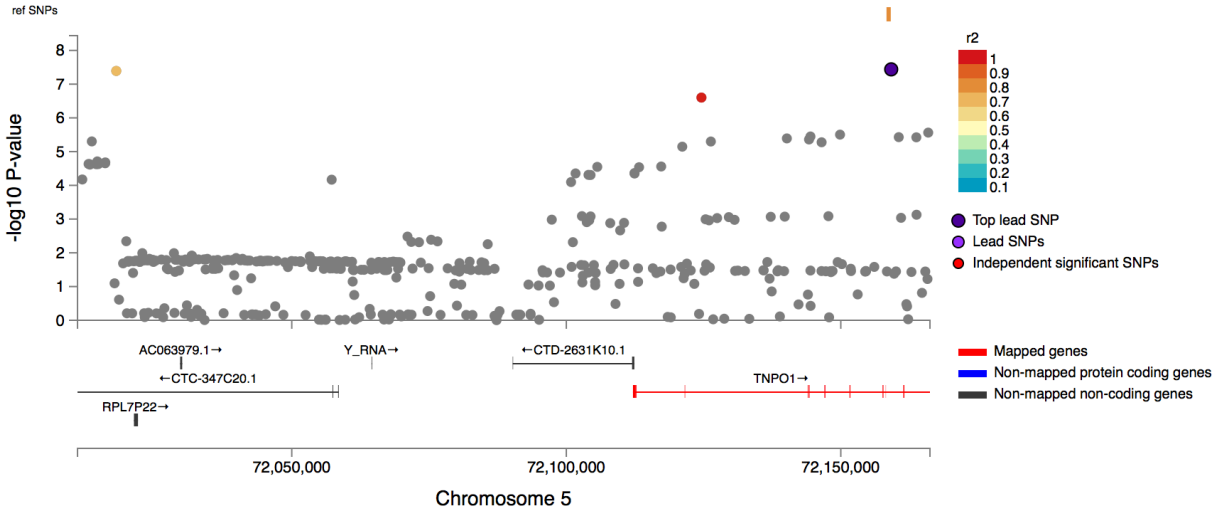
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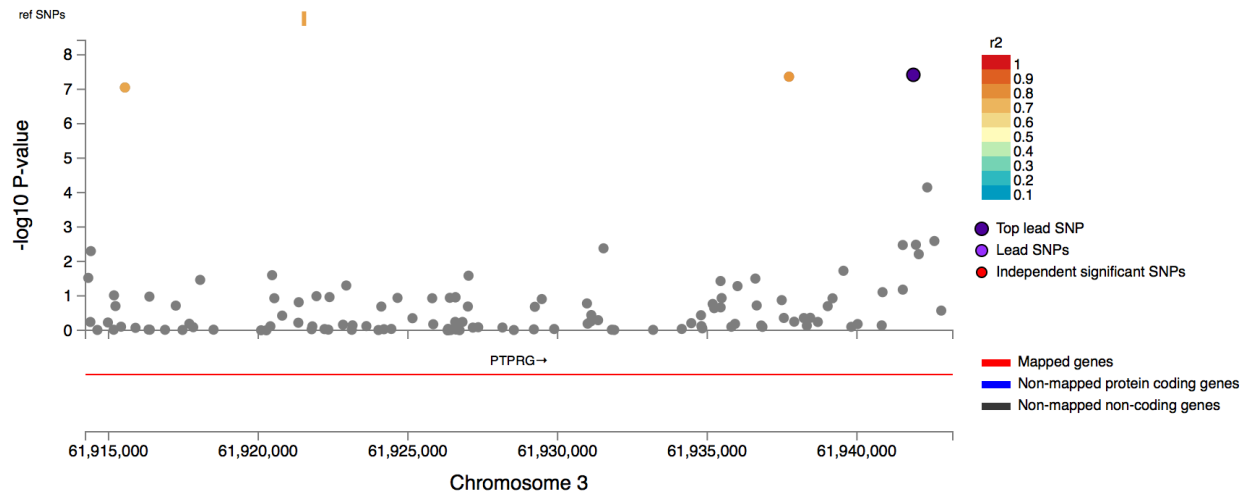
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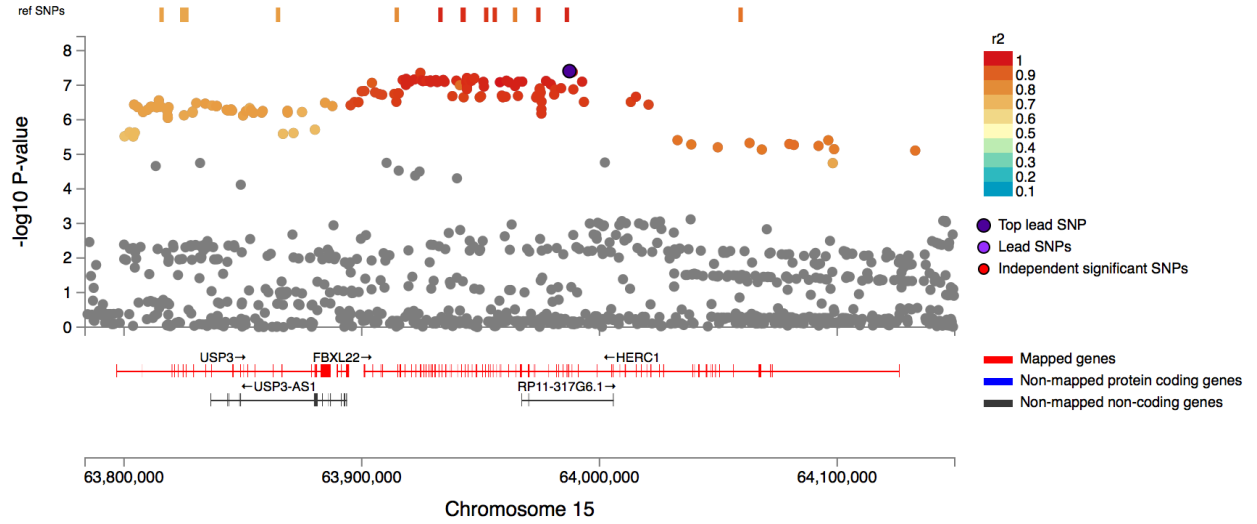
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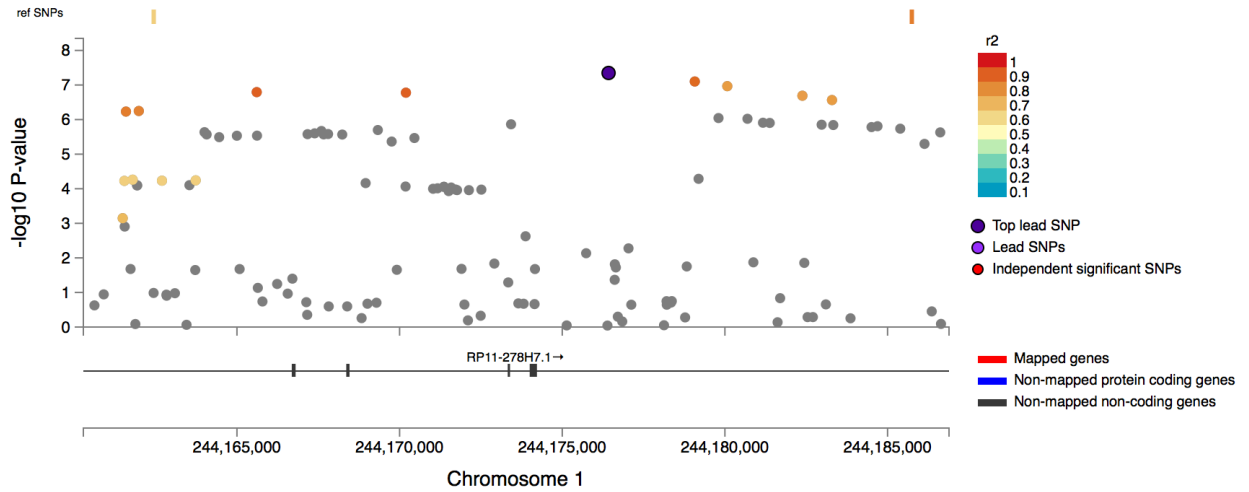
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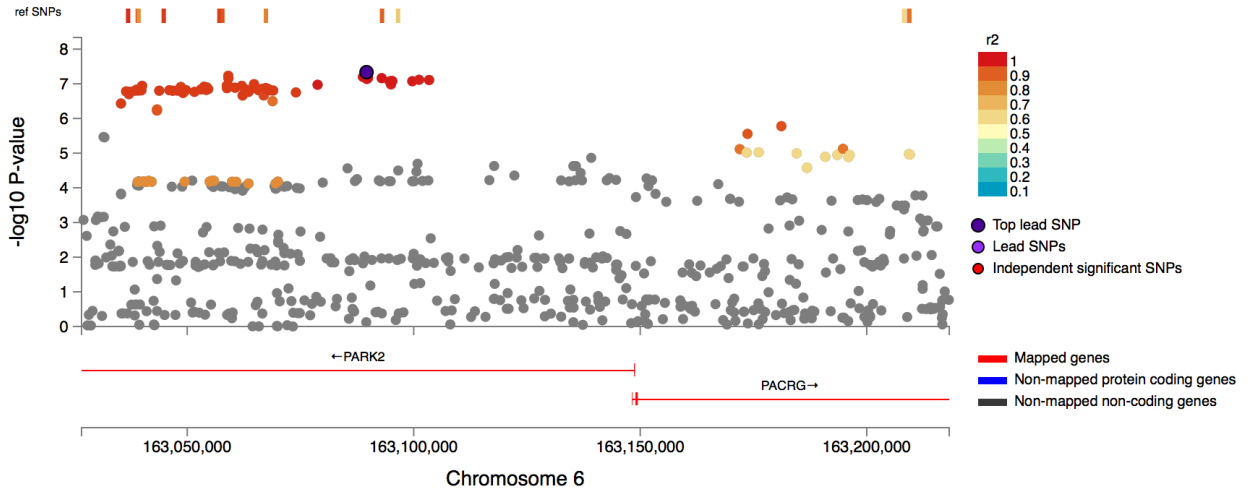
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