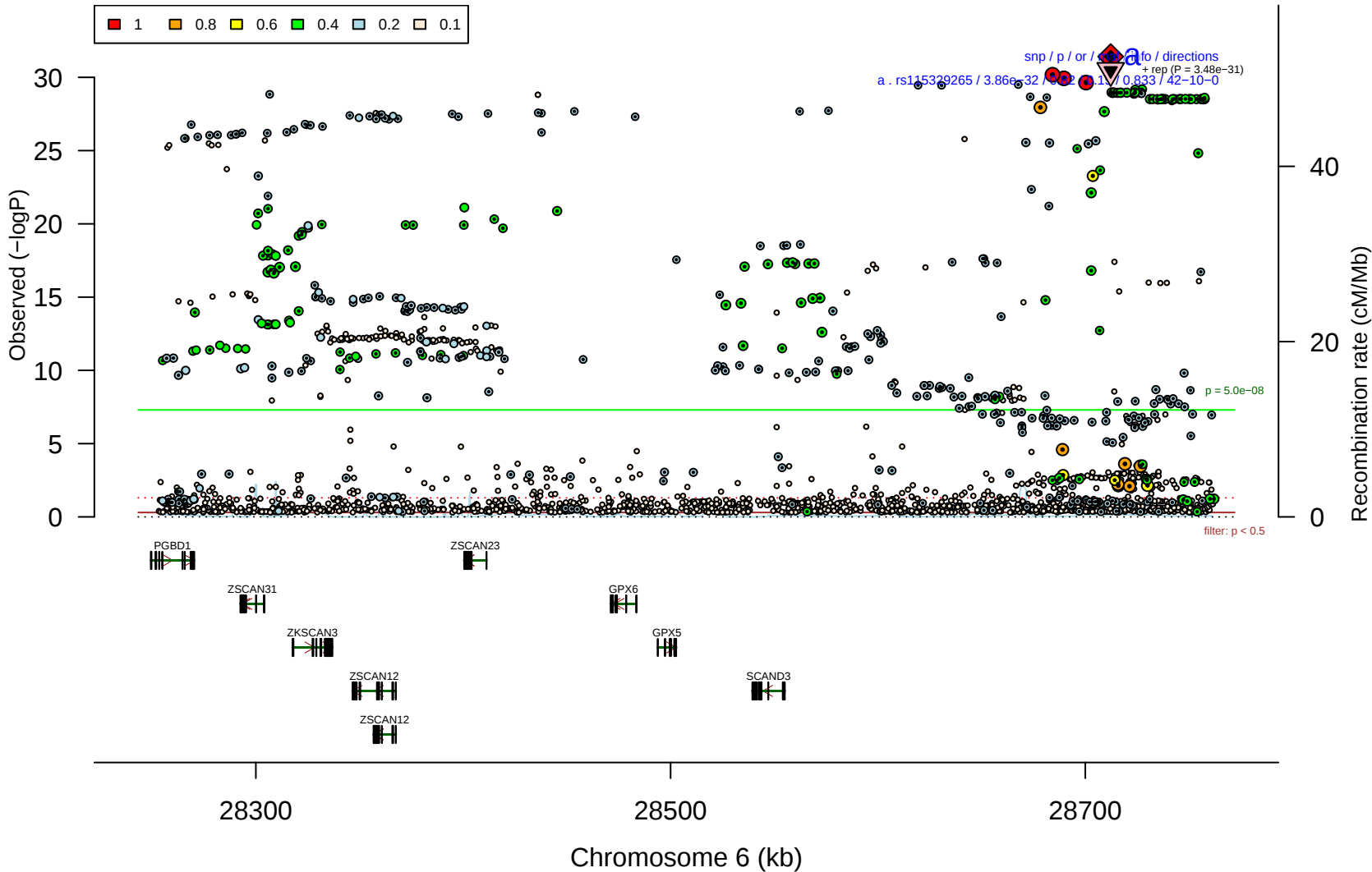


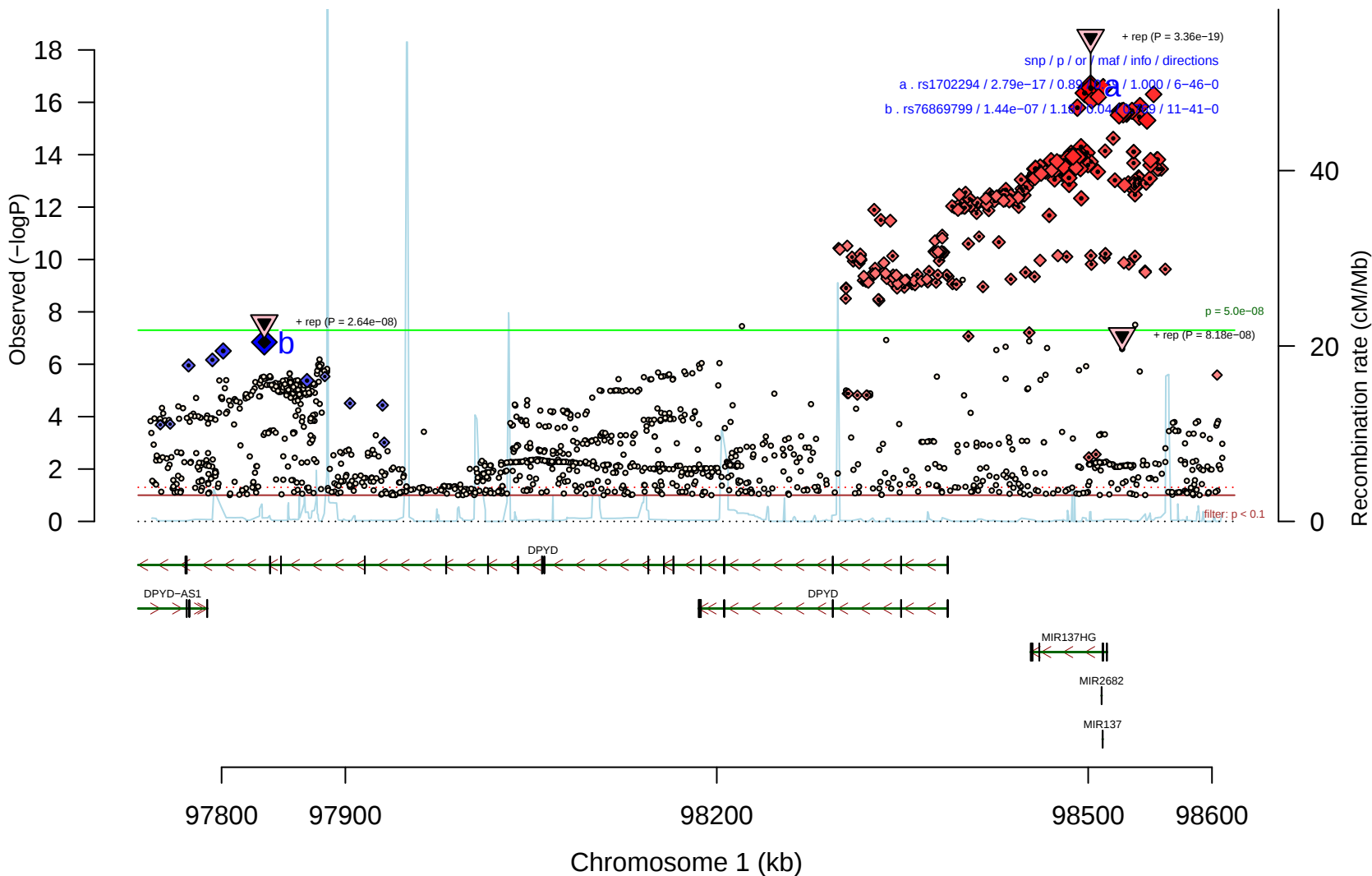
Supplementary Figure 1: Region Plots

Regional plots of loci defined and ordered as in Supplementary Table 2. The x-axis is chromosomal position (in kb) and the y-axis is significance of association represented as $-\log_{10}(P)$. The green line shows the genome-wide significance level (5×10^{-8}). Dot size is proportional to LD between the plotted SNP and the index SNP defining the associated region. Colour scheme: If only a single index SNP in the region, colouring is based on degree of LD to the single index SNP as represented by R^2 . Legend for R^2 is given in upper left corner (e.g. region 5 = PGC_SCZ52.reg5). If a locus contains multiple independent index SNPs (e.g. region 4 = PGC_SCZ52.reg4), each index SNP is denoted by a different colour. LD to each index SNP is denoted by the intensity of the same colour. Markers present in 1000 Genomes Project data but not in HapMap3 have a black centre. Details of index SNPs are given in the upper right corner (labelled with letters): snp=SNP (or indel) name, p=association p-value, or=odds ratio for the minor allele, maf=minor allele frequency, info=imputation quality, direction denotes the consistency of the allelic association enrichment across the 52 studies N_one_direction – N_other_direction - missing. Triangles denote p-values after inclusion of extension data (also indicated by +rep) and are only available for index SNPs. Green lines in lower half: genes based on UCSC (April 2013 freeze) with black vertical lines for exons. Arrow heads denote the direction of transcription. To minimize complexity, in some plots we exclude SNPs with association P values above certain thresholds (indicated by filter: $p < x$). The blue line denotes regional recombination rates derived from HapMap.

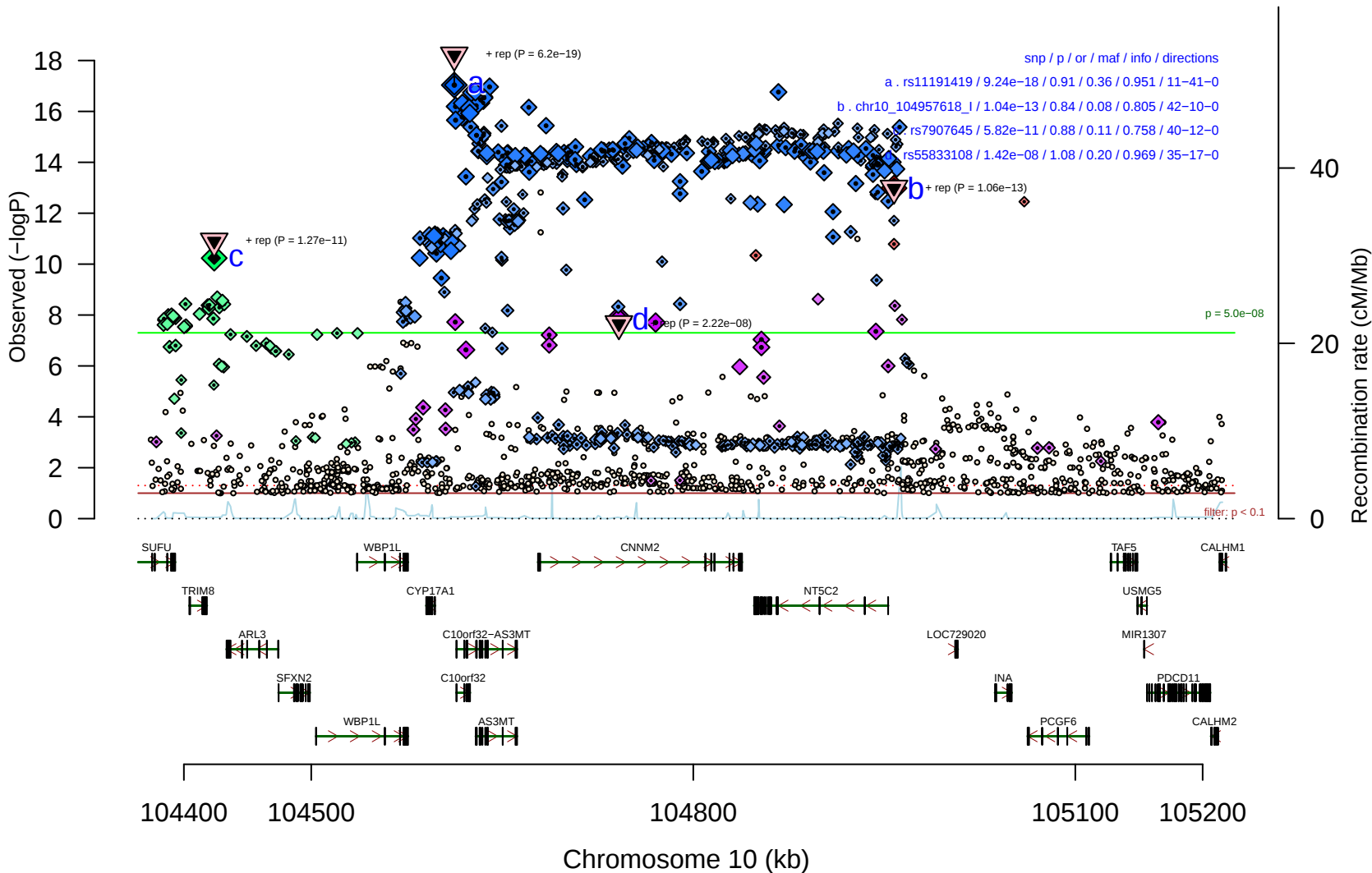
PGC_SCZ52.reg1



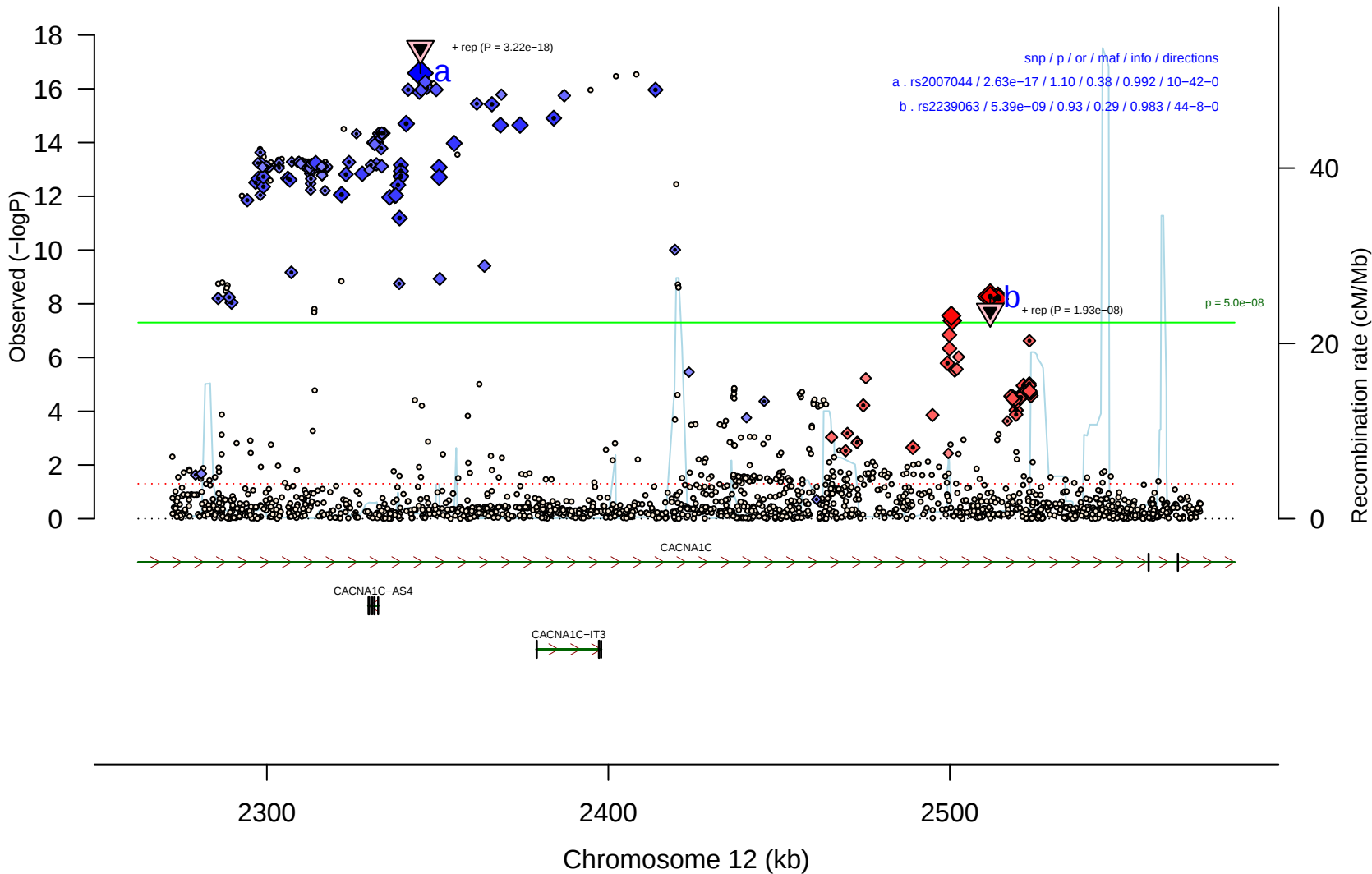
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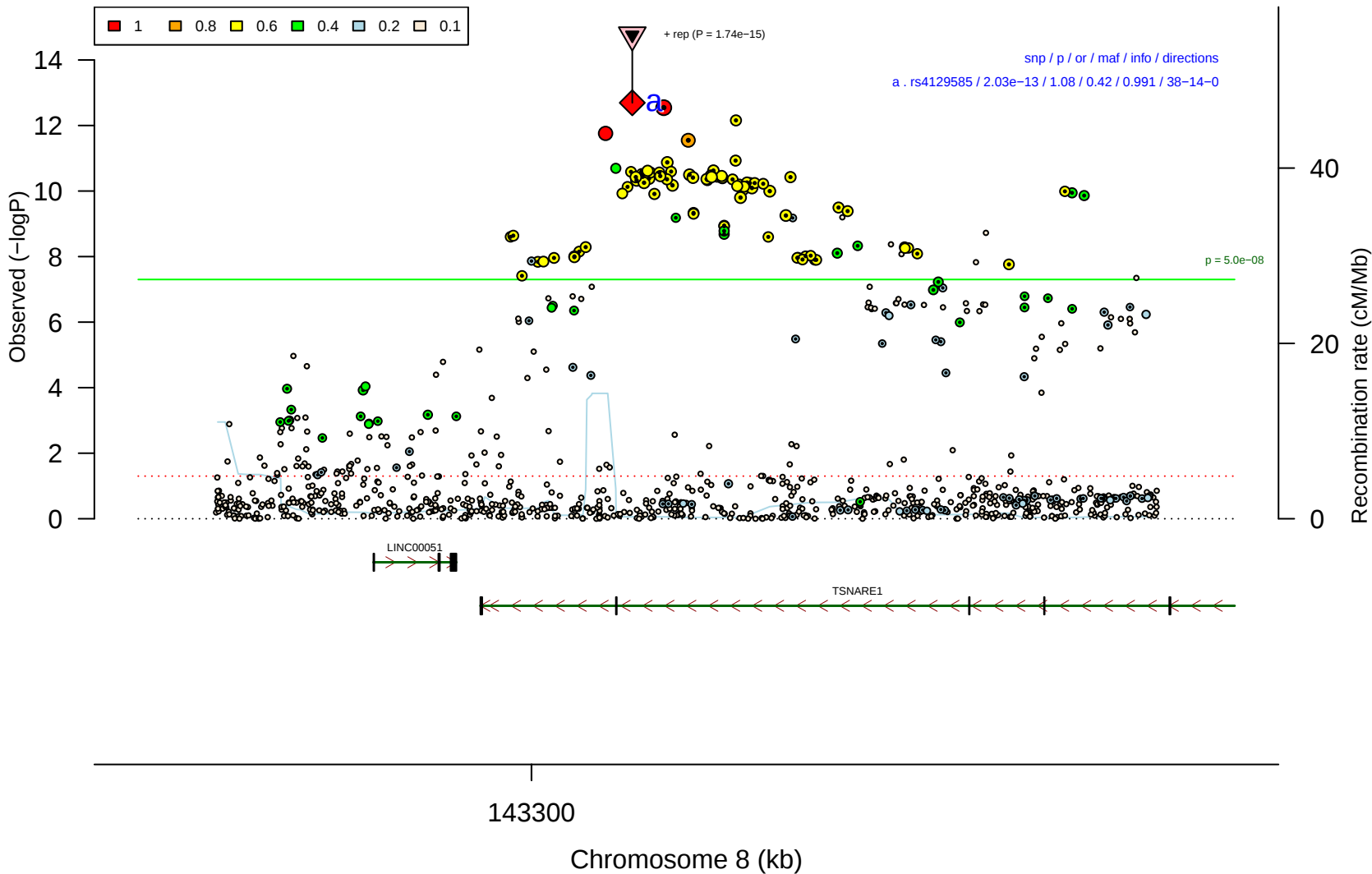
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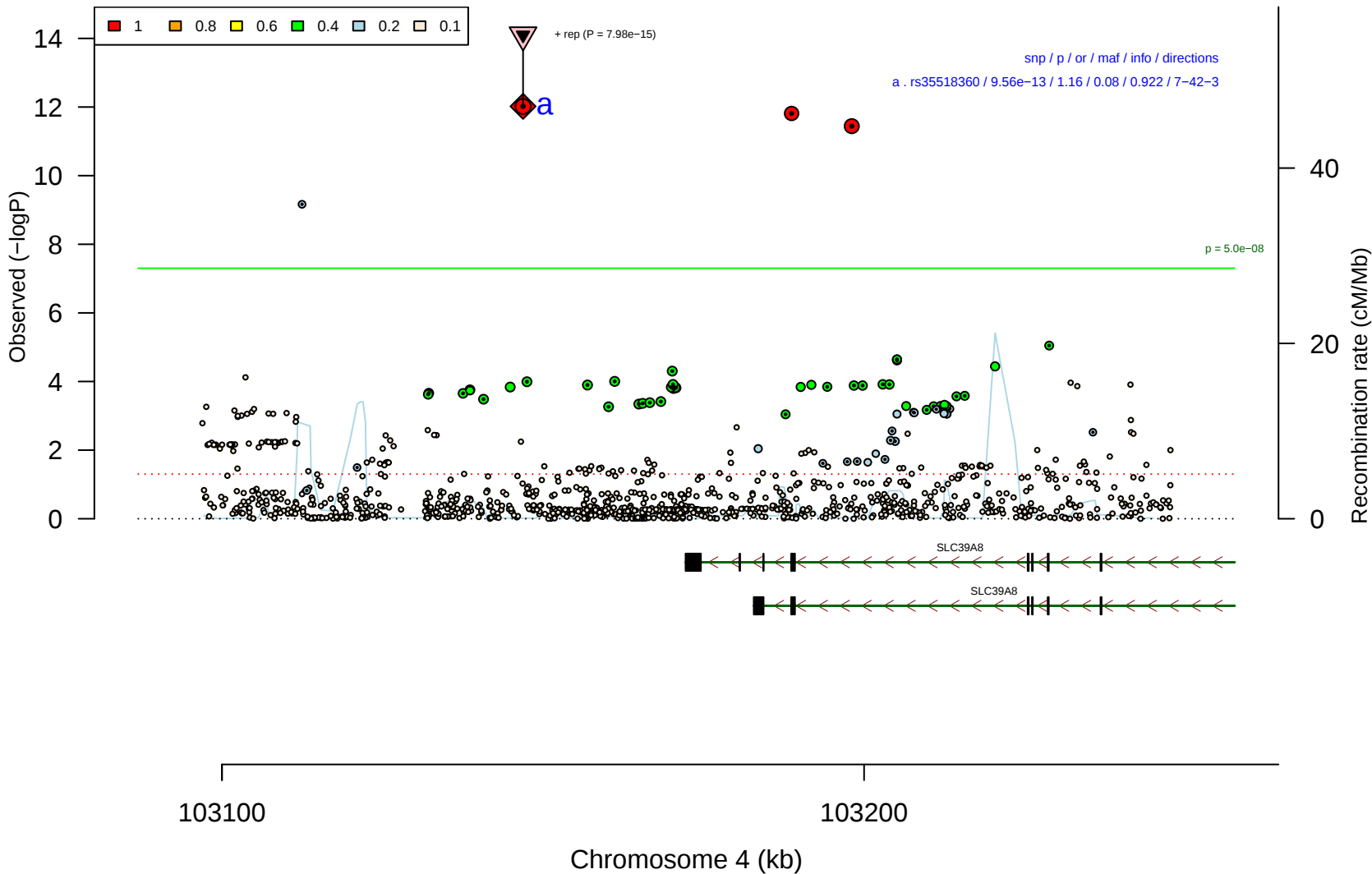
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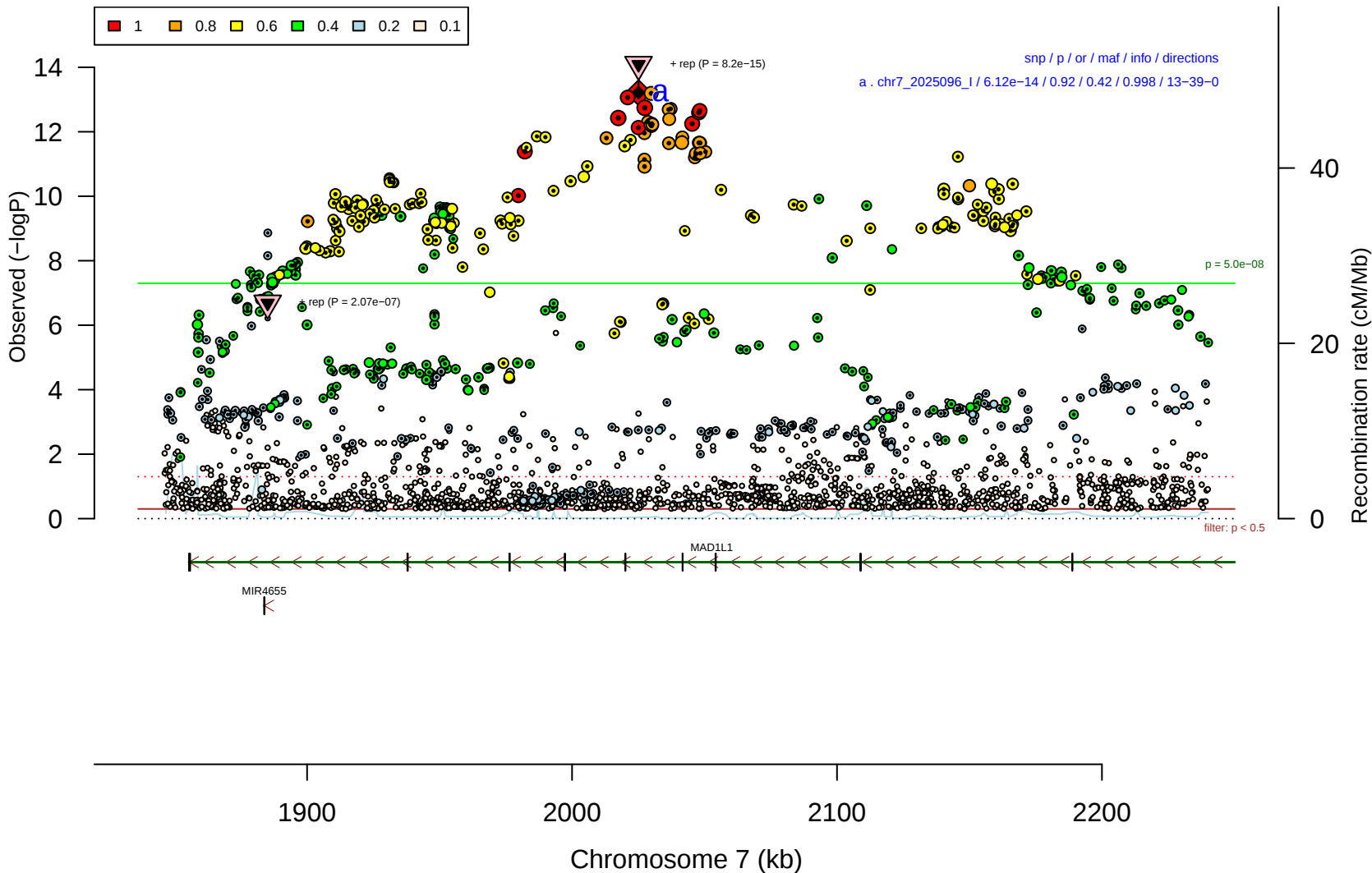
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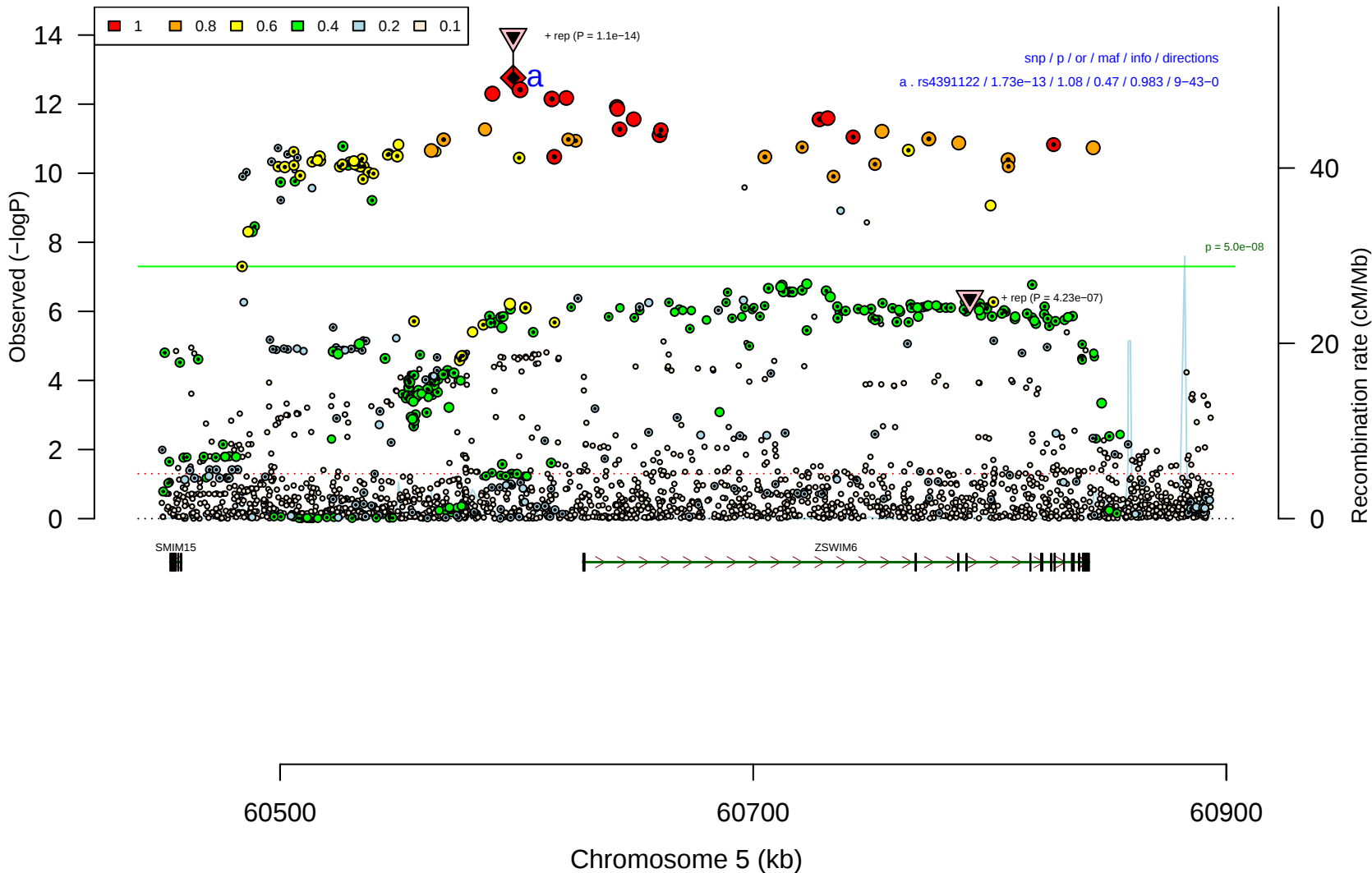
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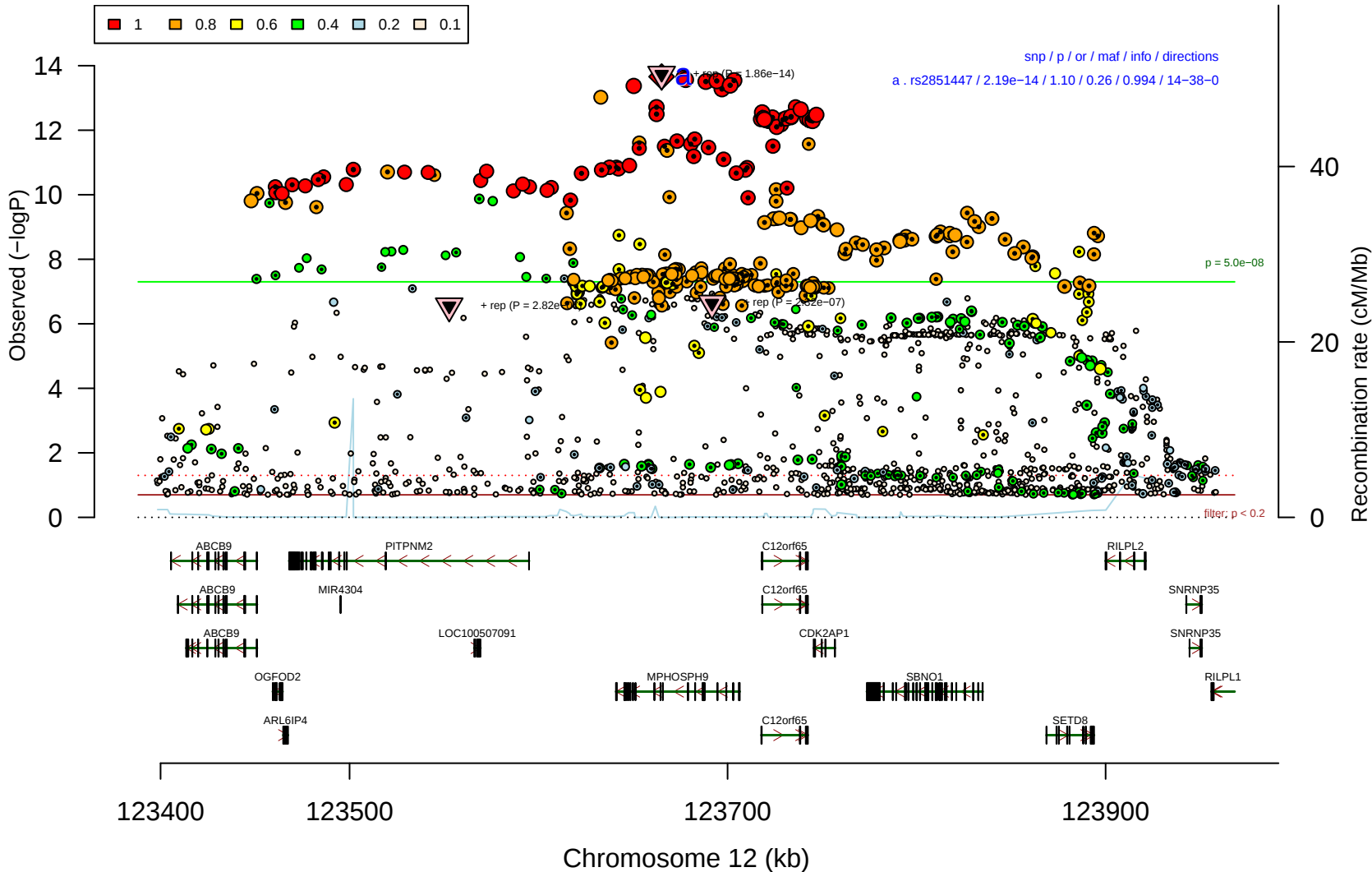
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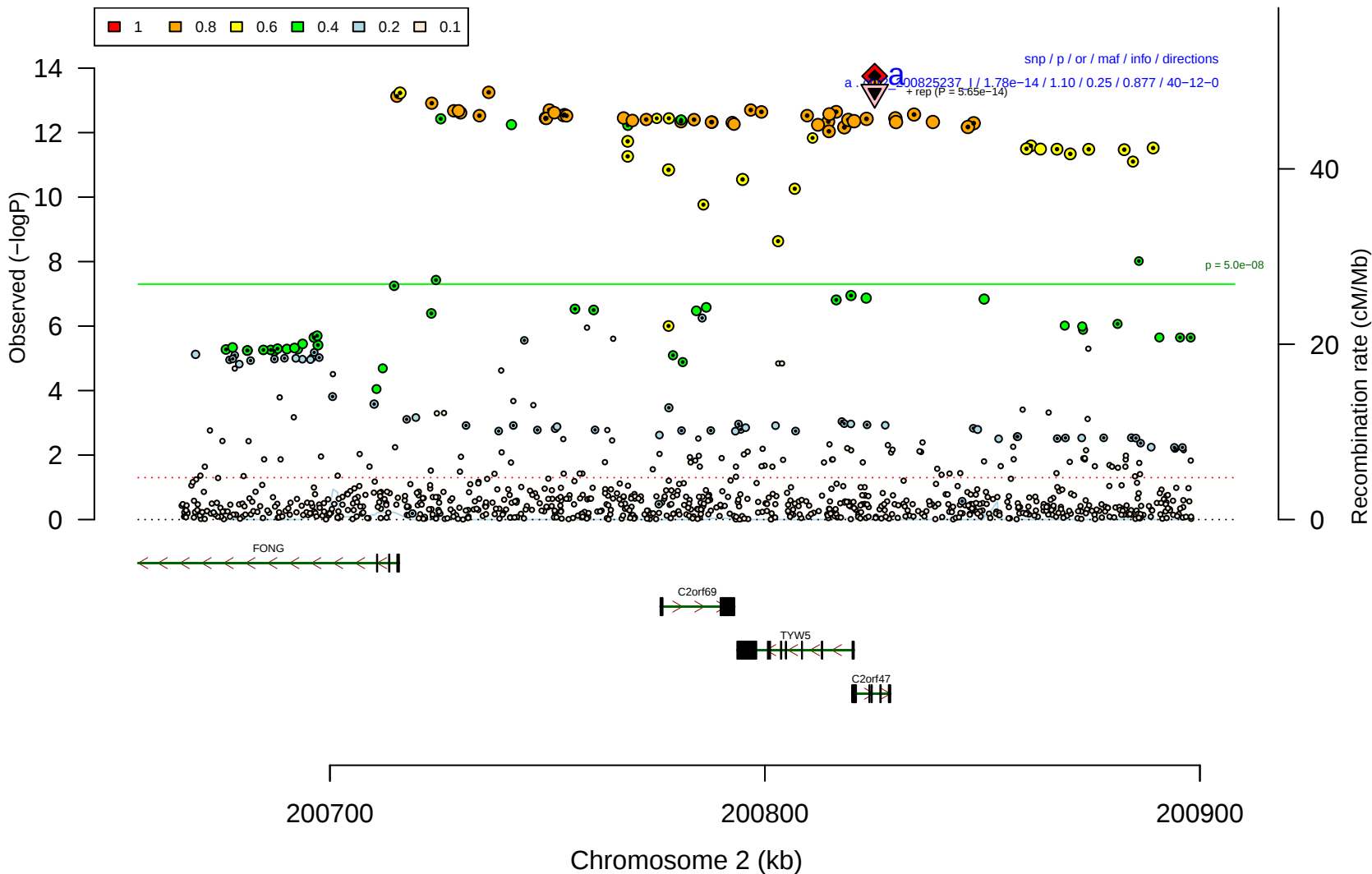
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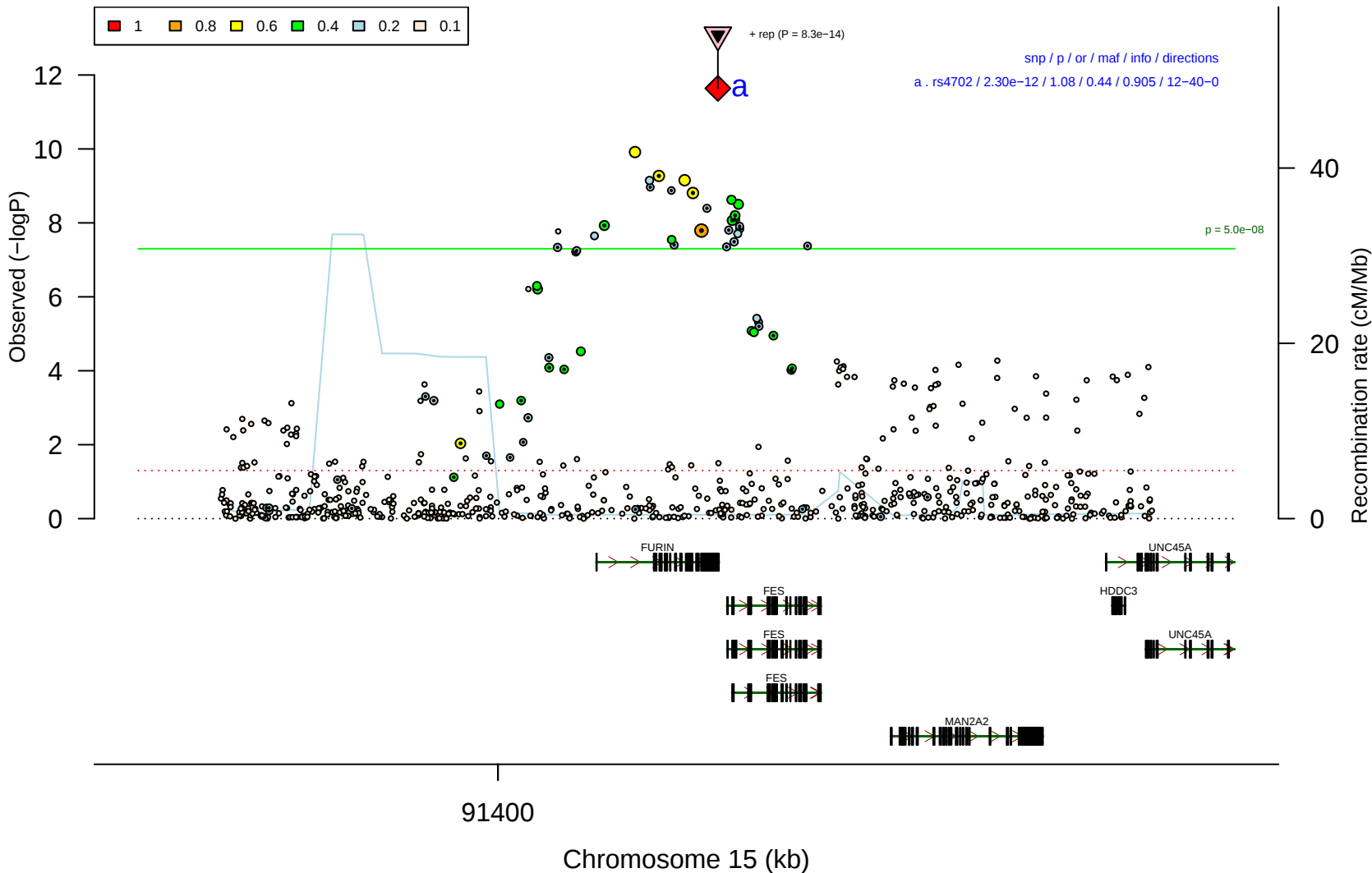
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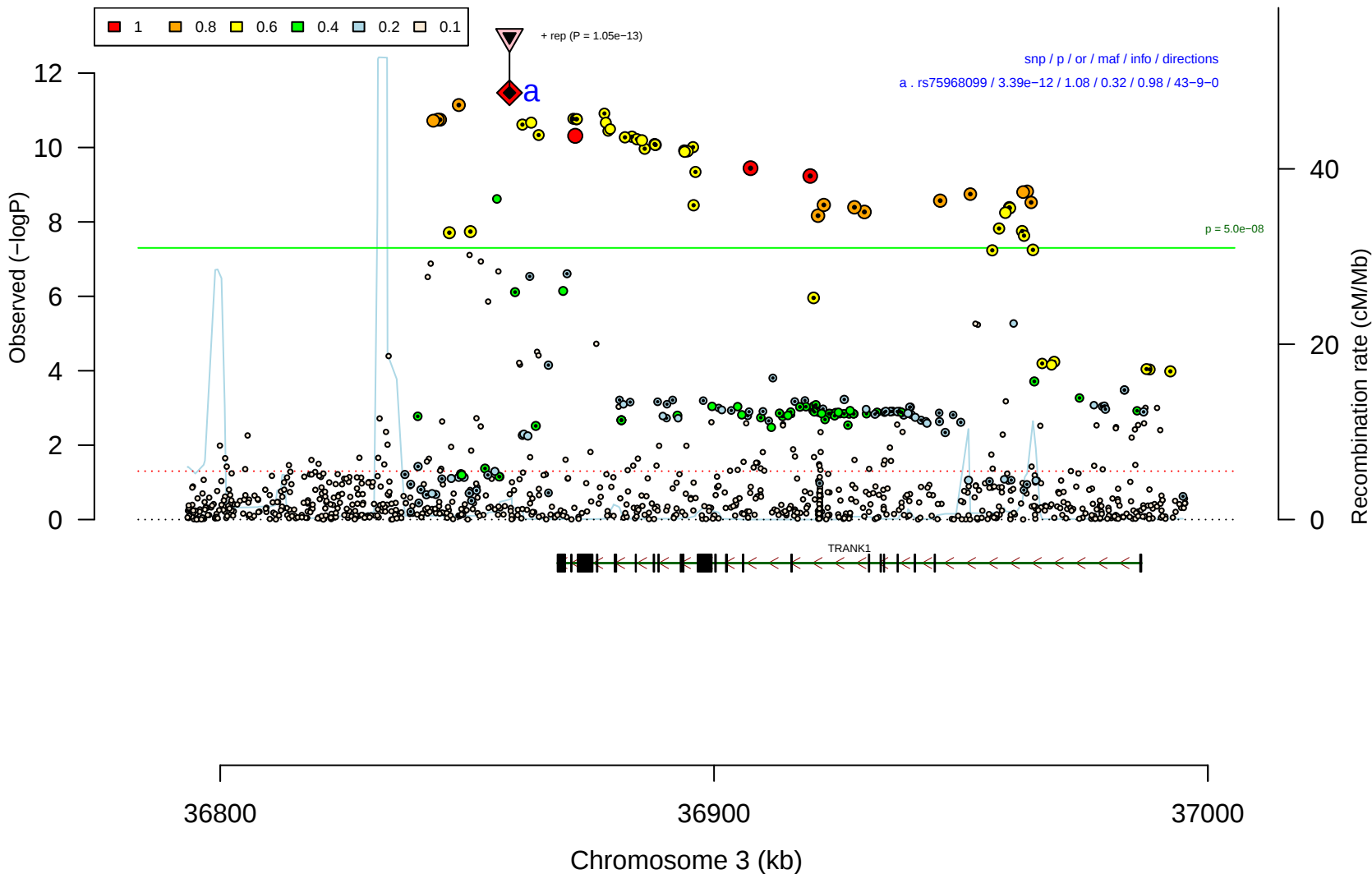
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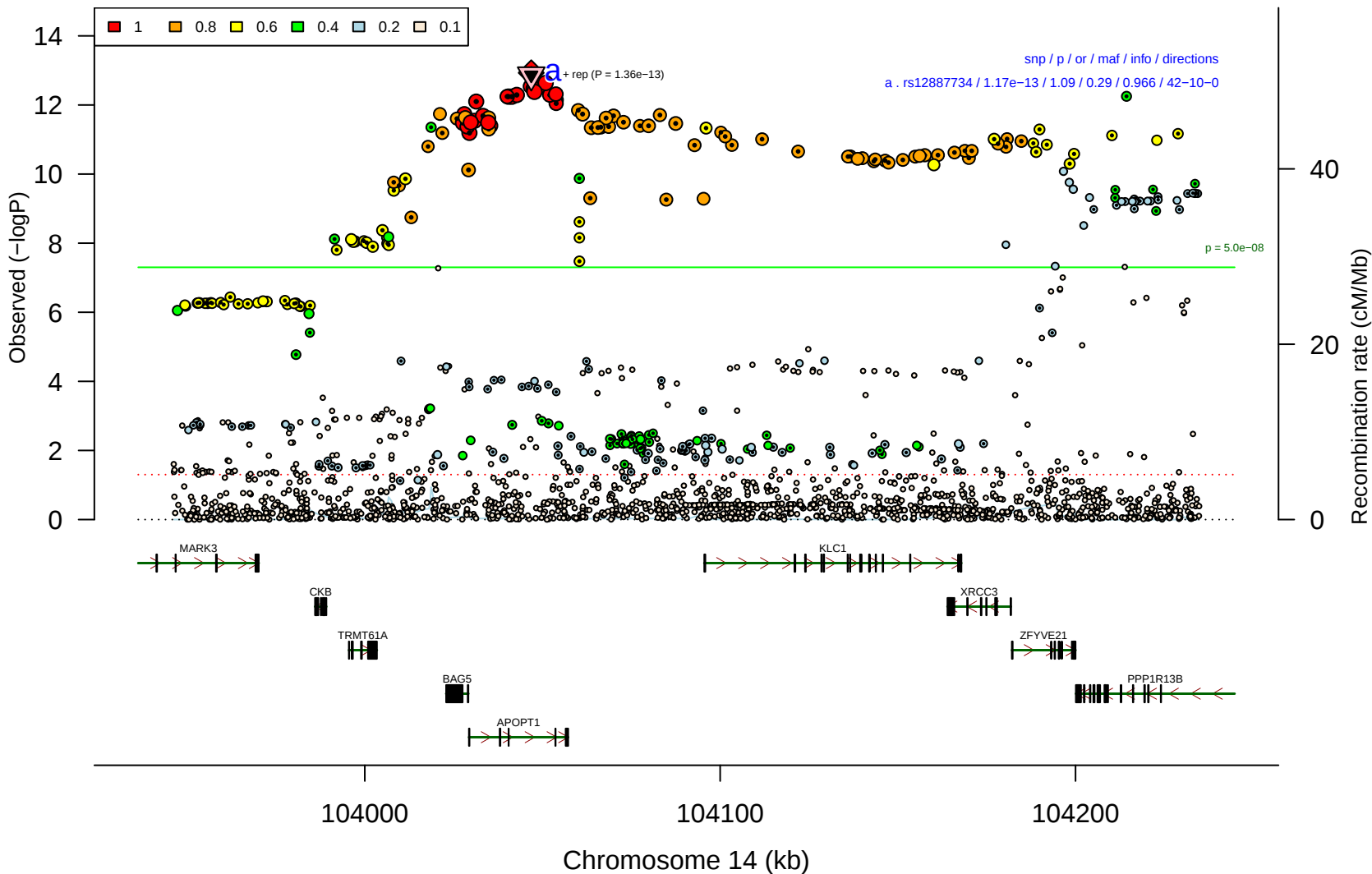
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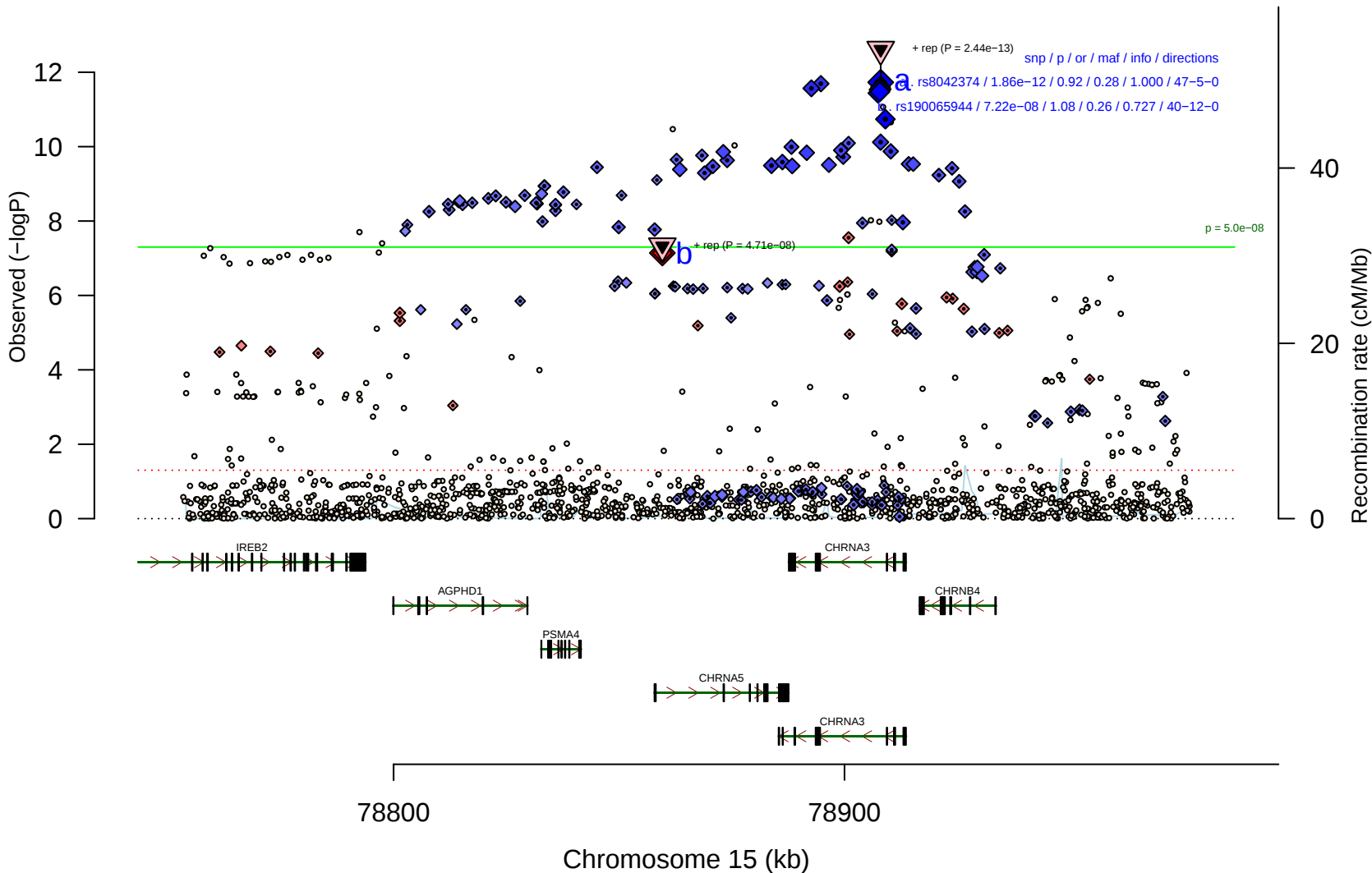
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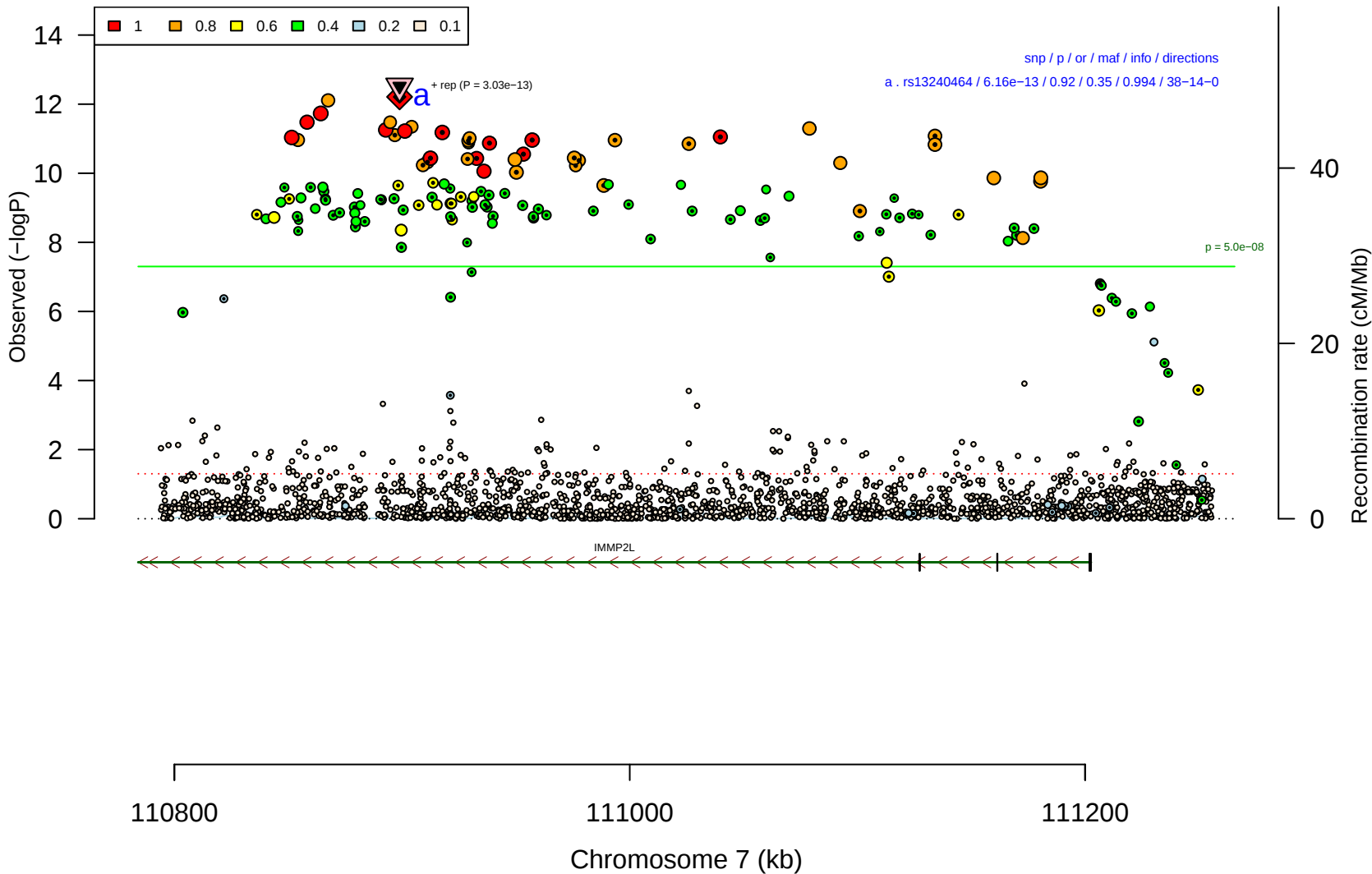
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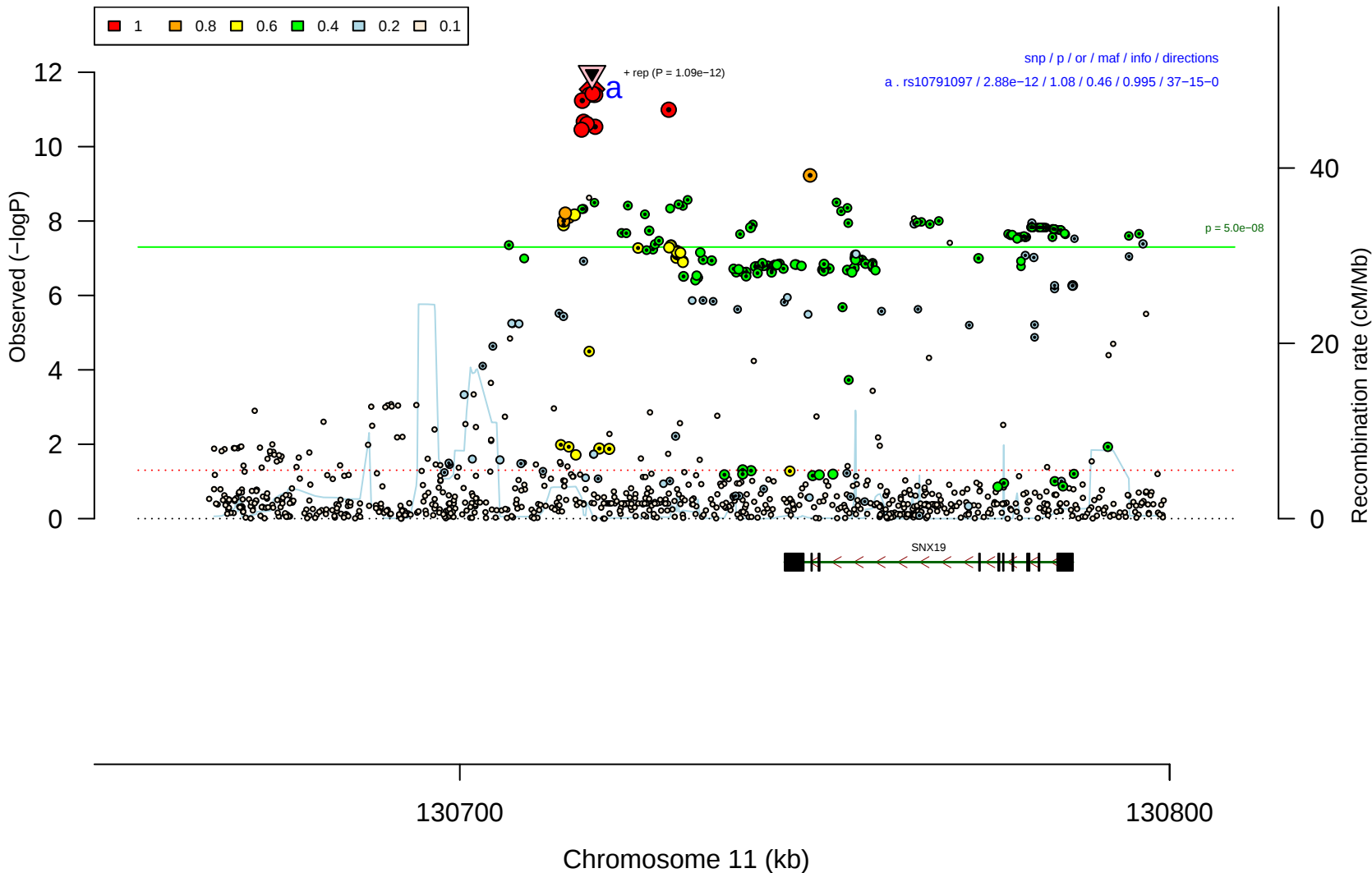
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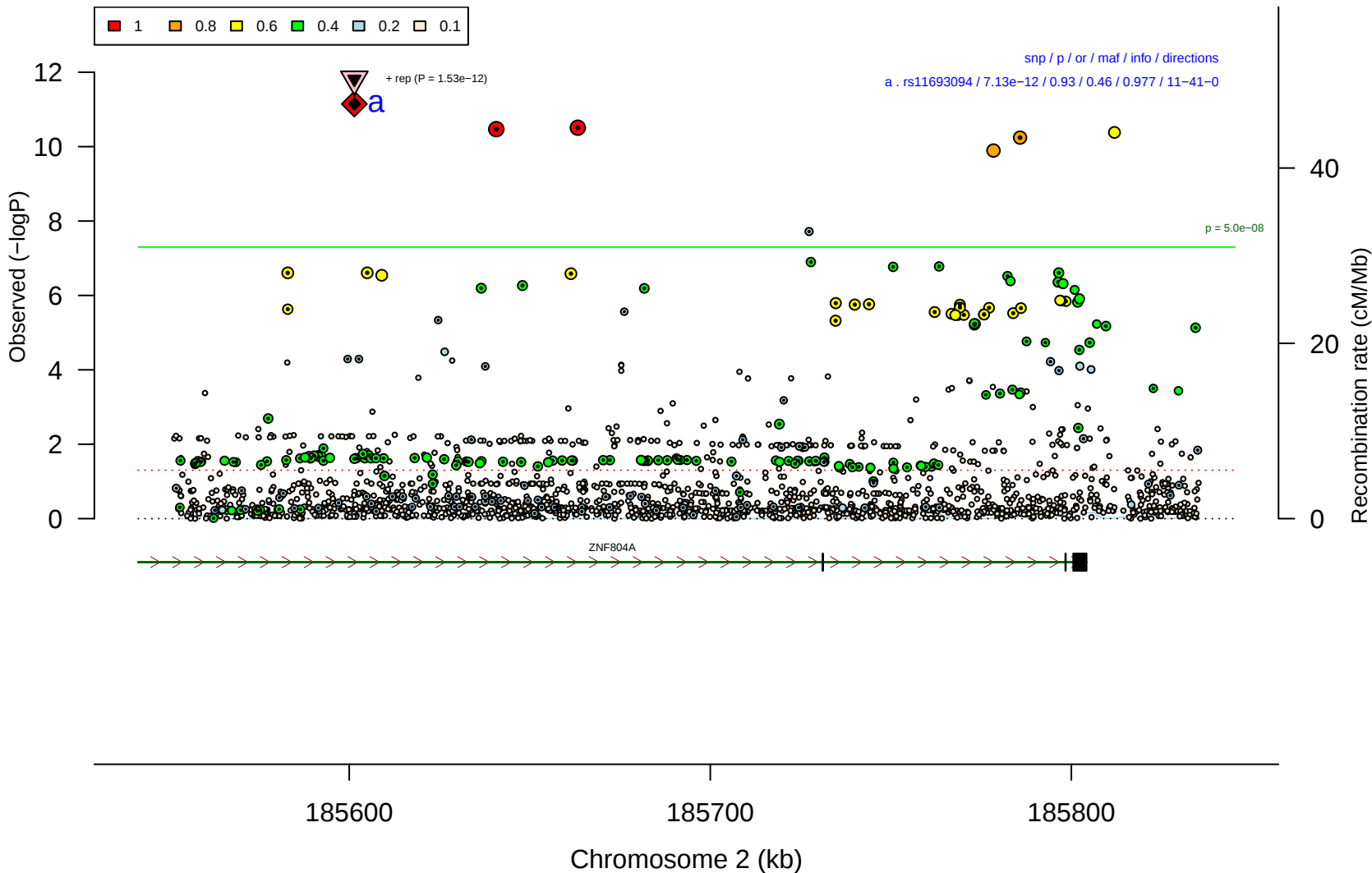
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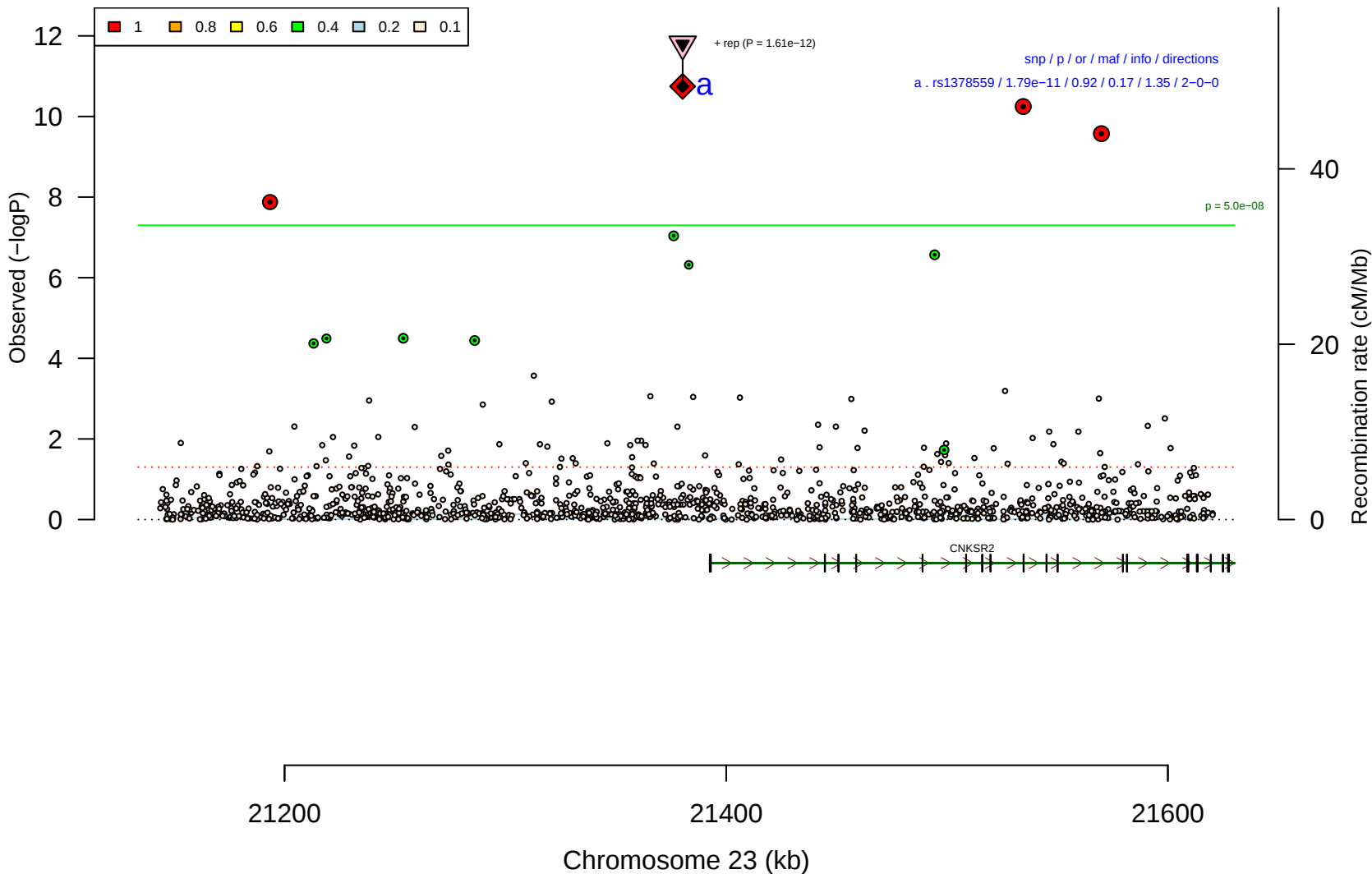
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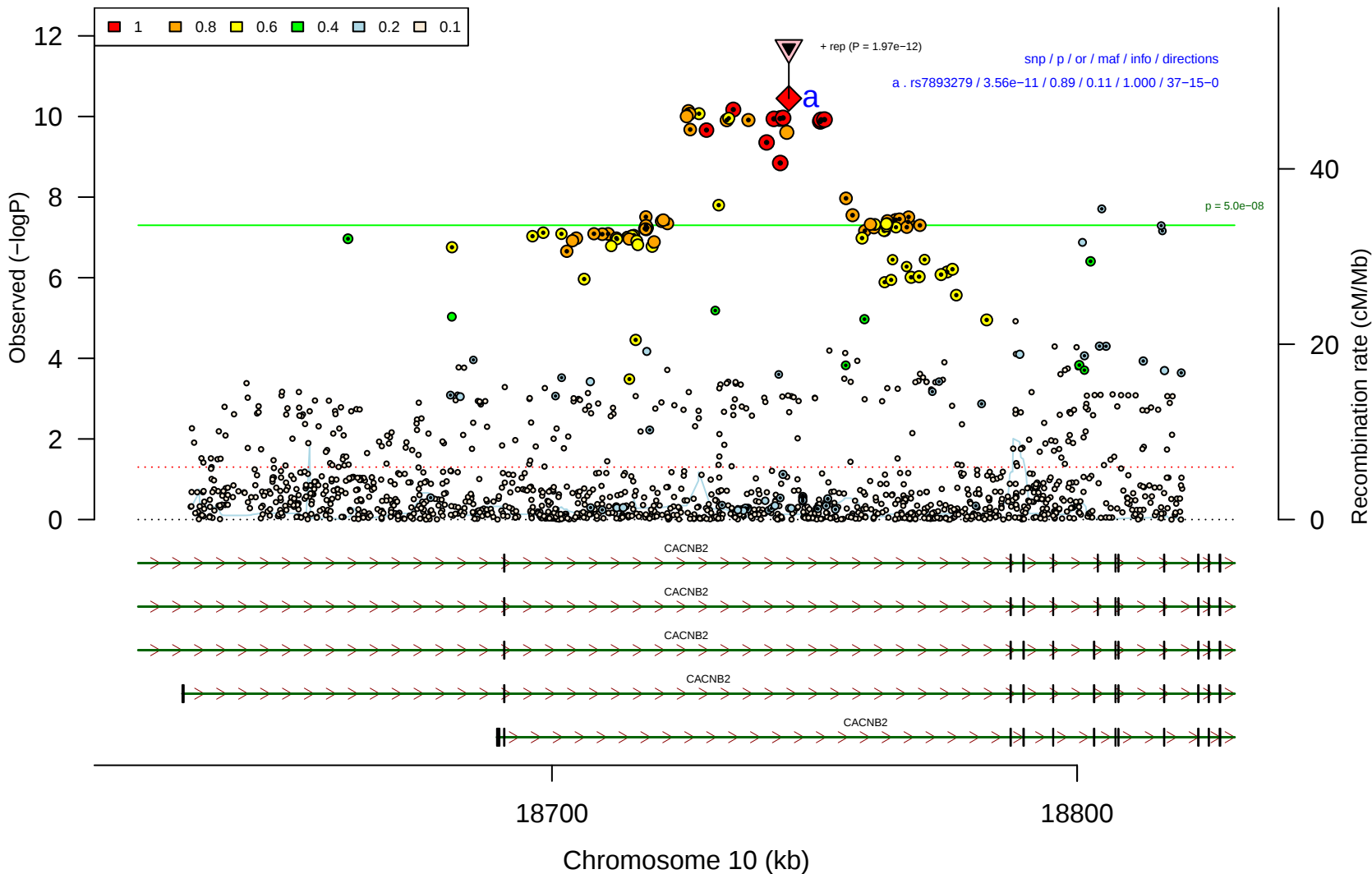
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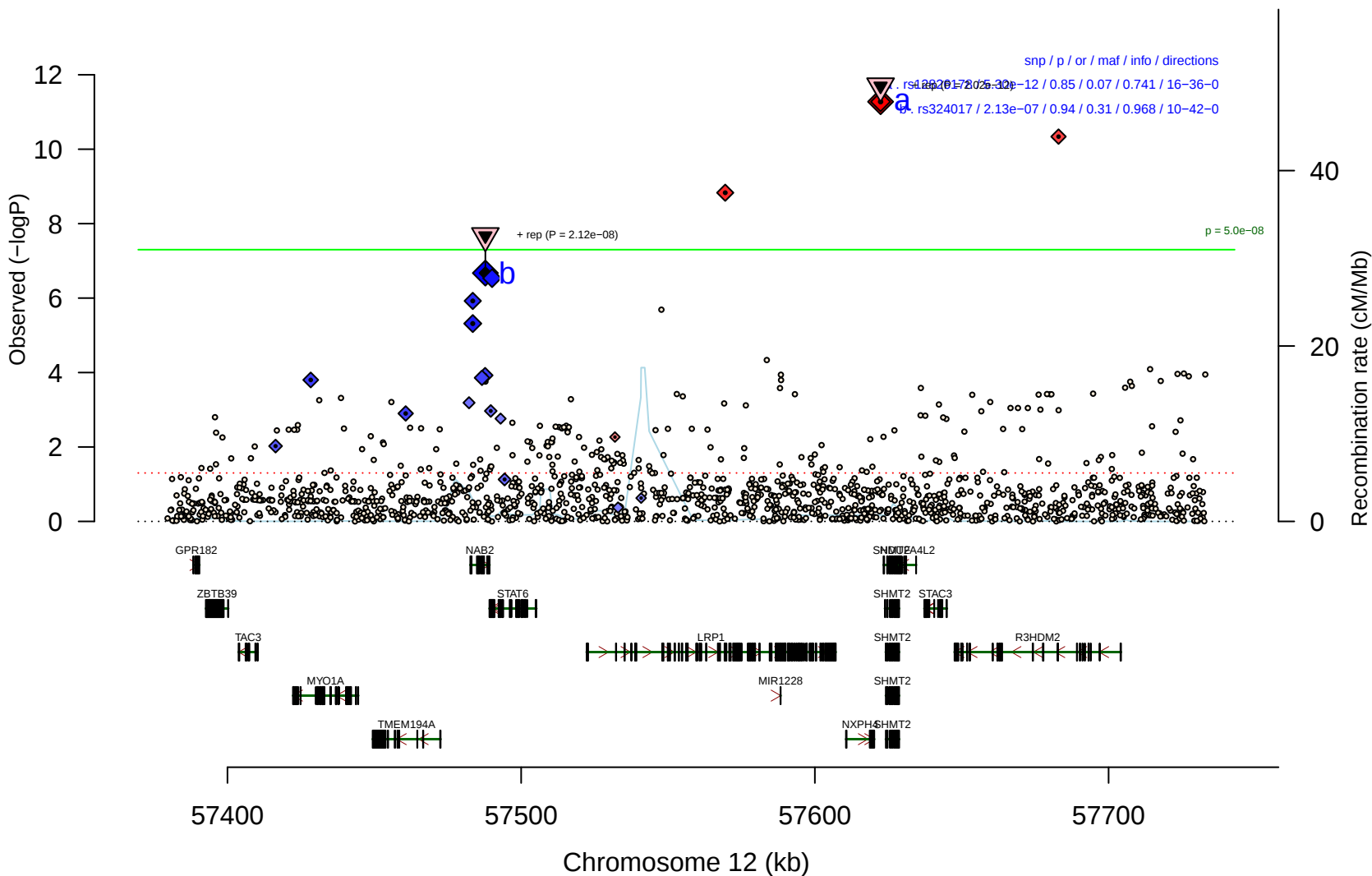
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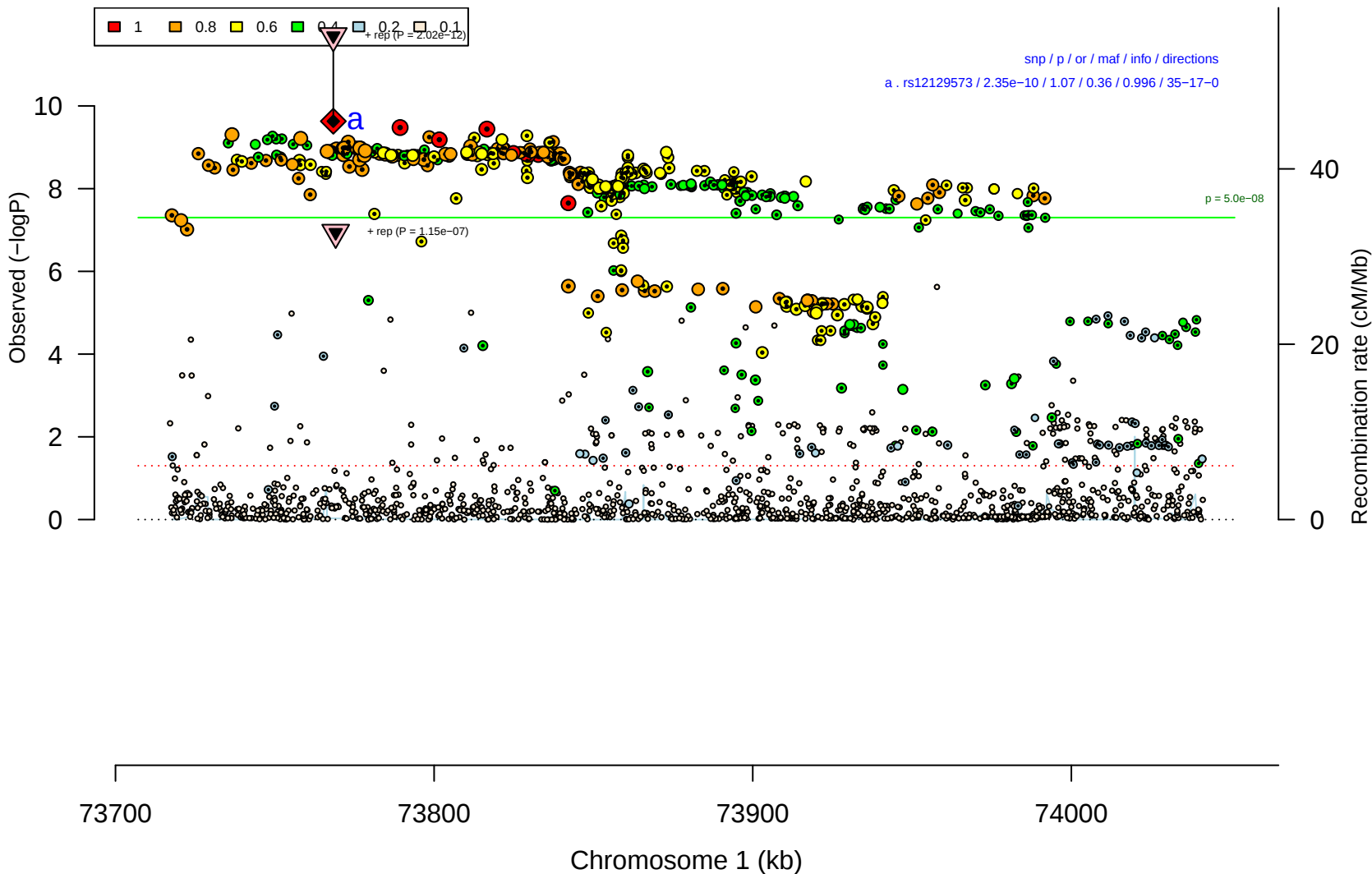
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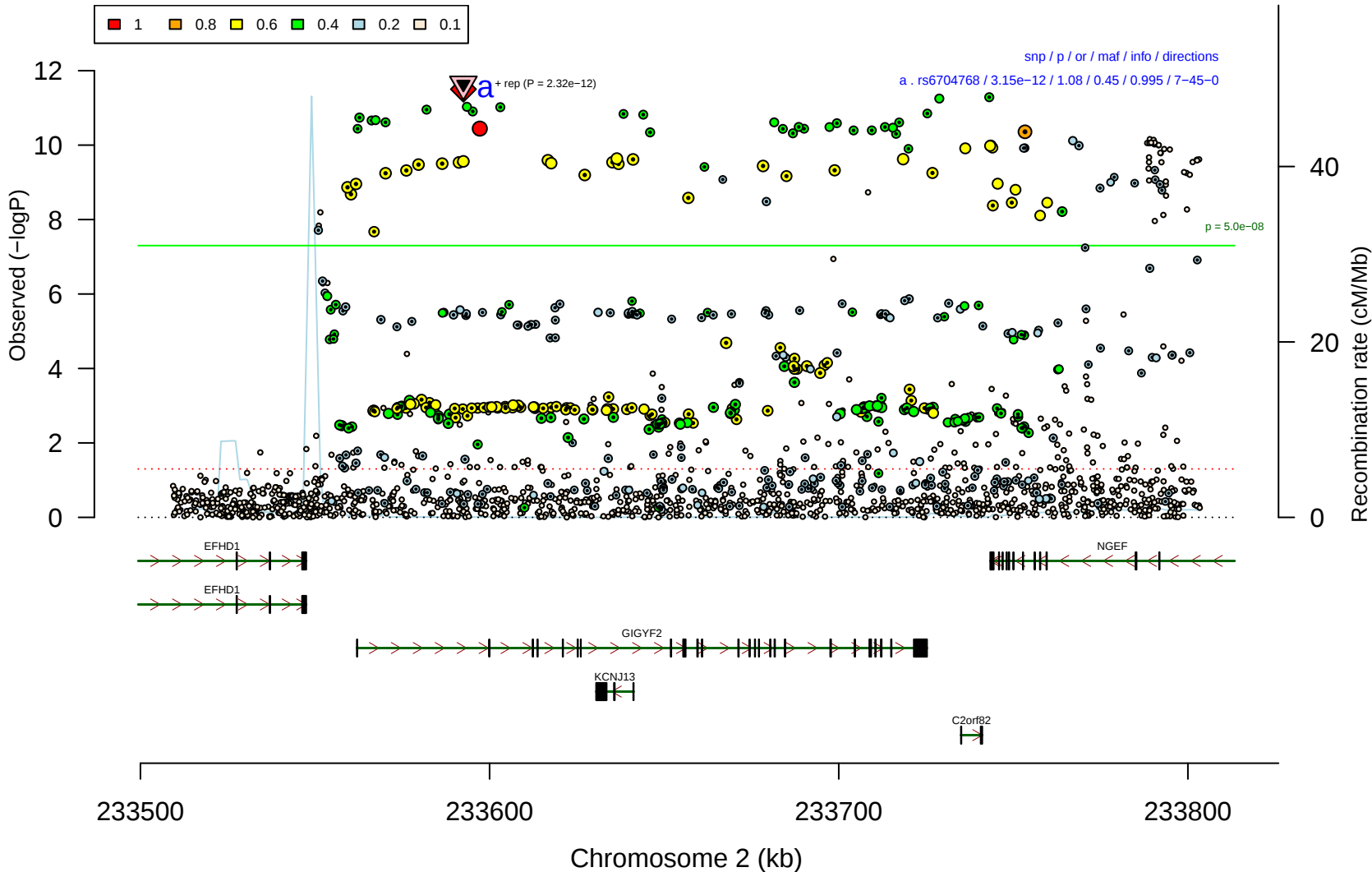
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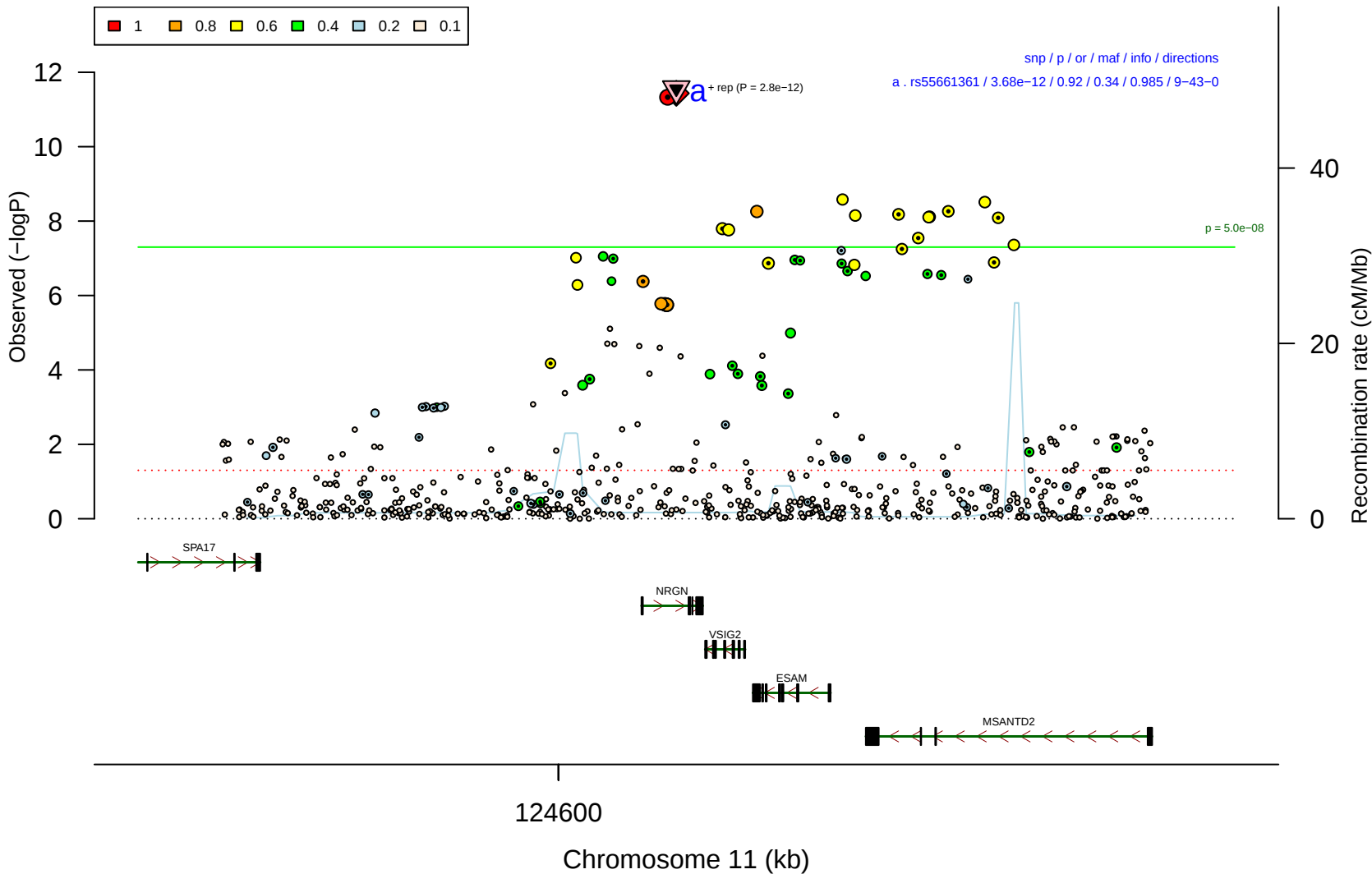
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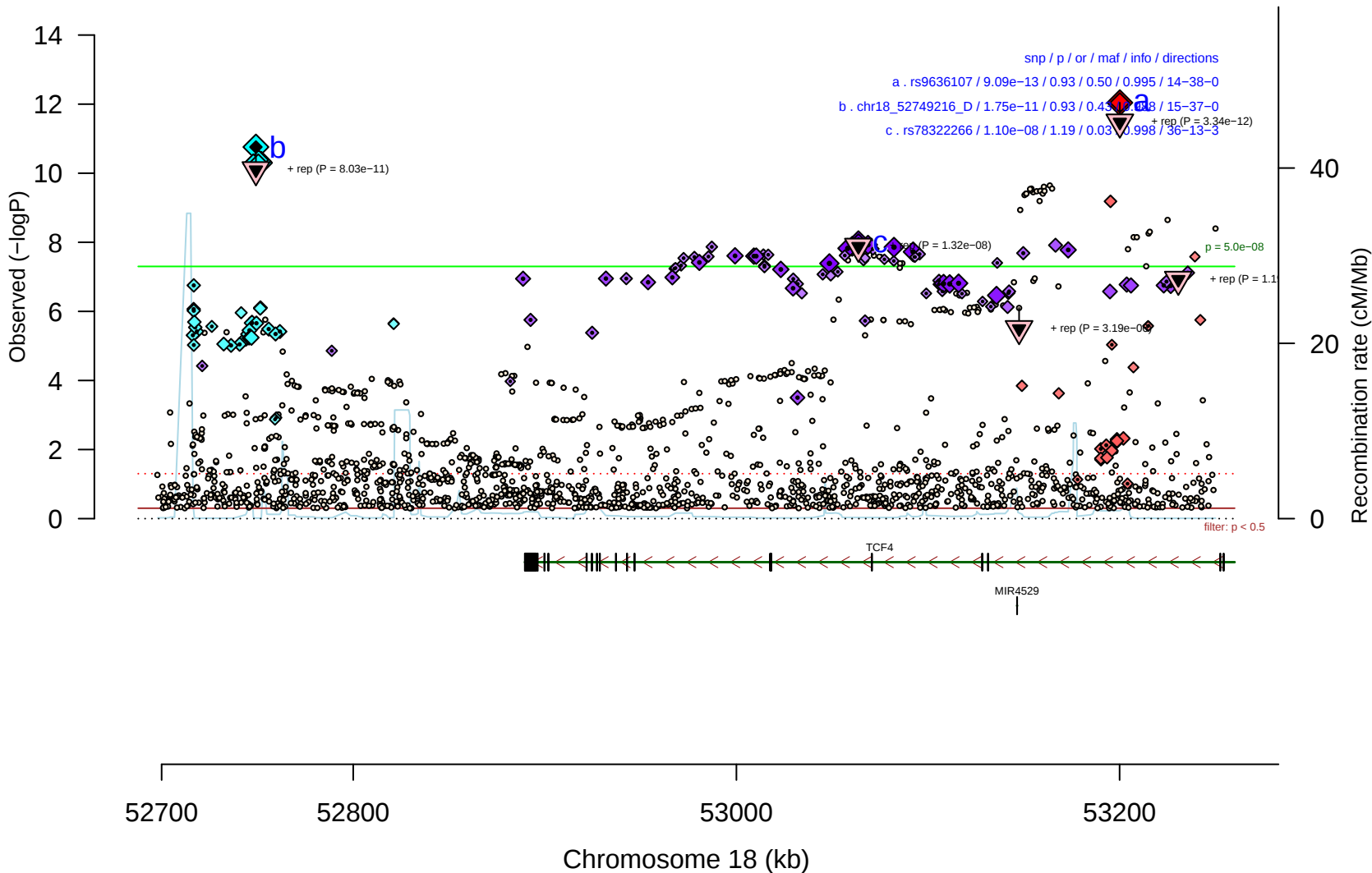
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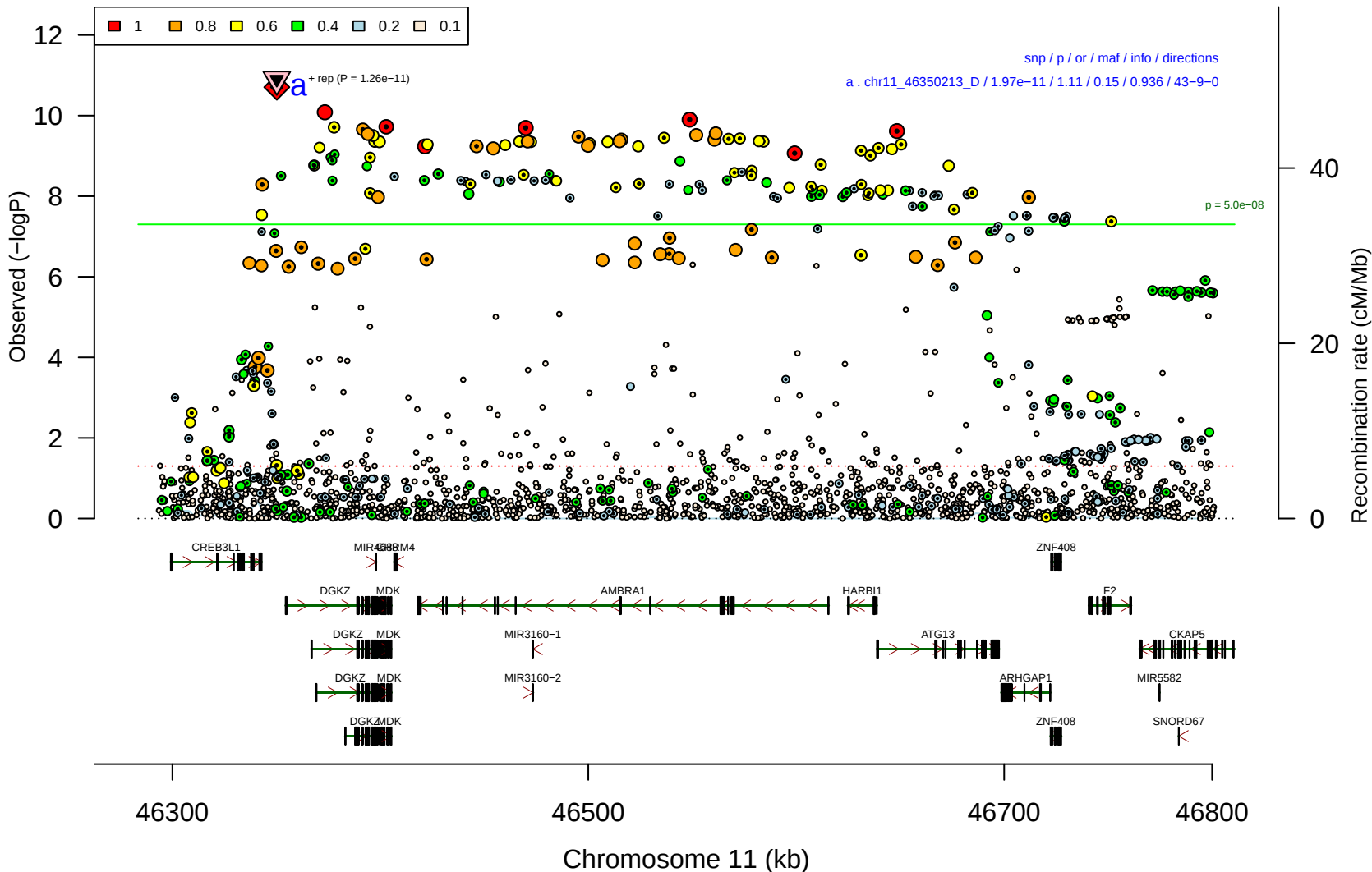
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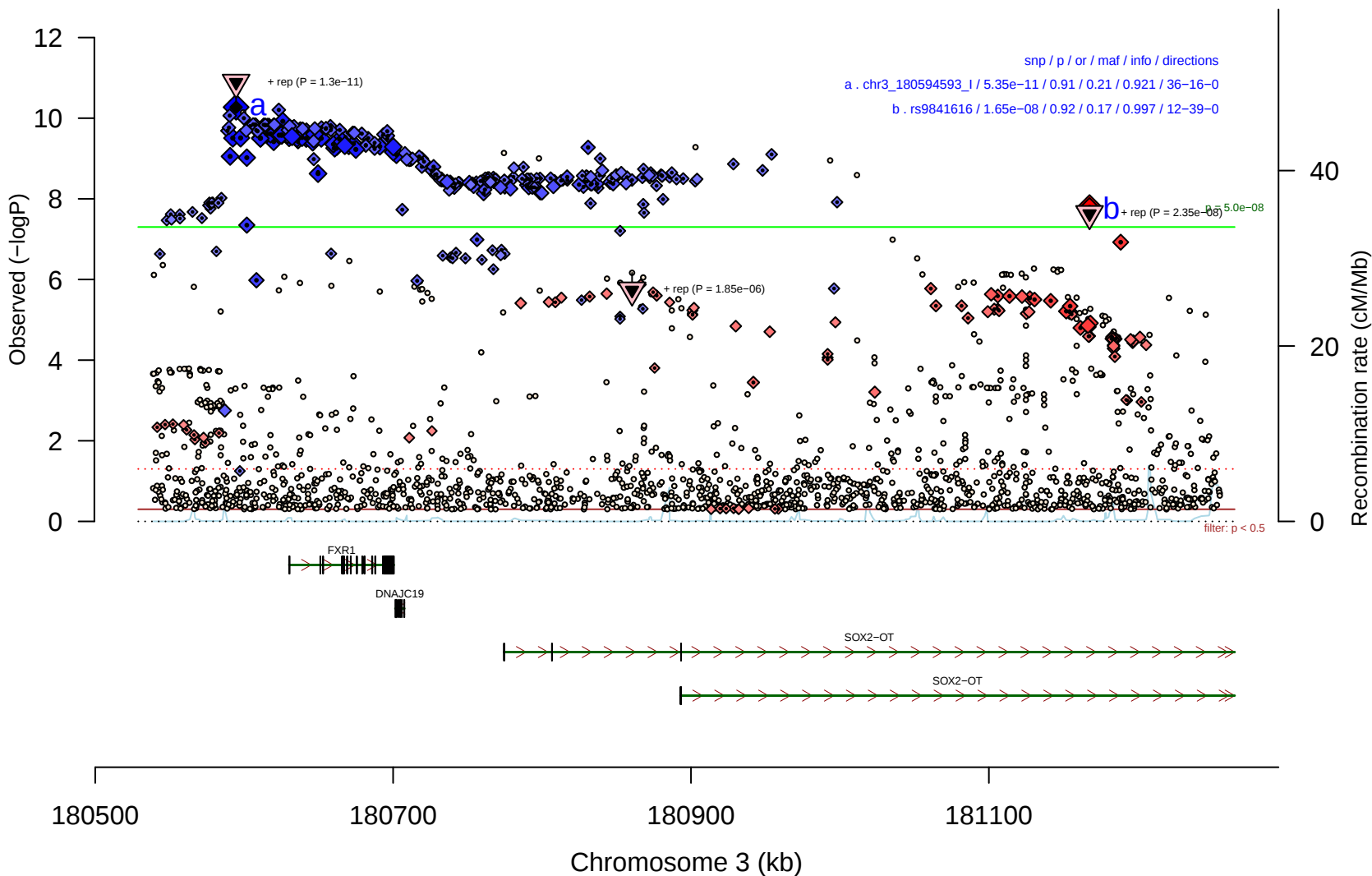
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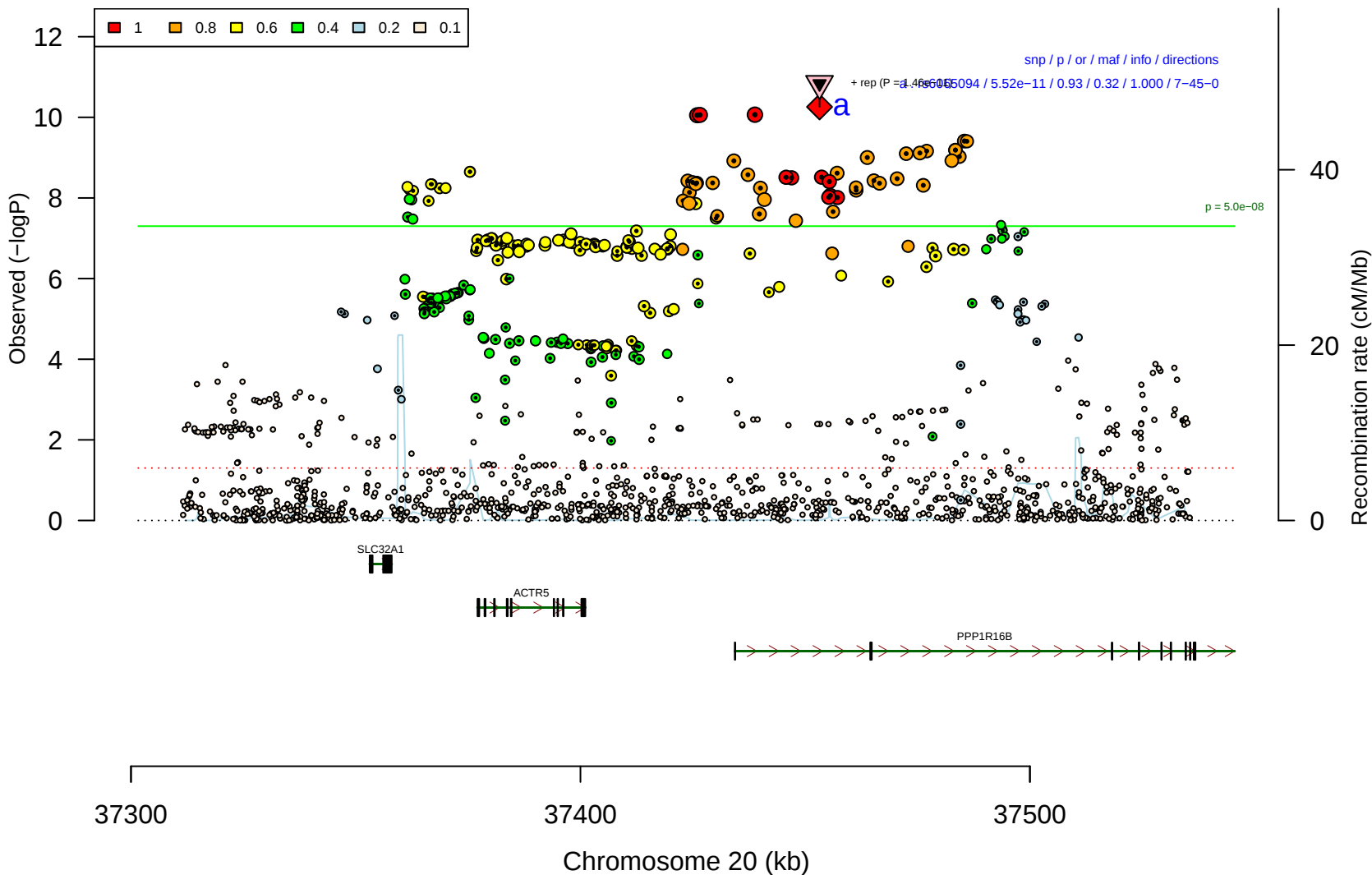
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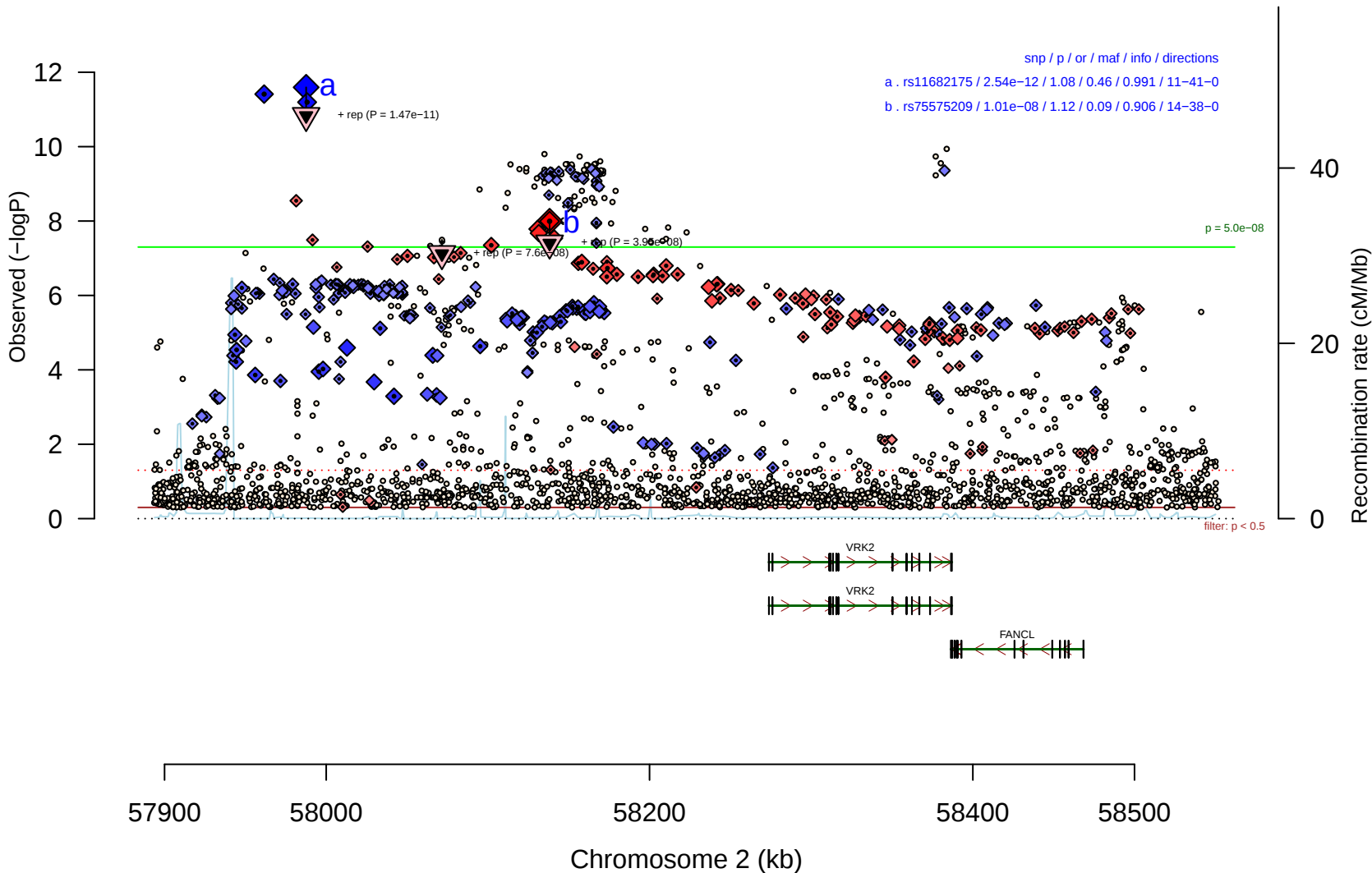
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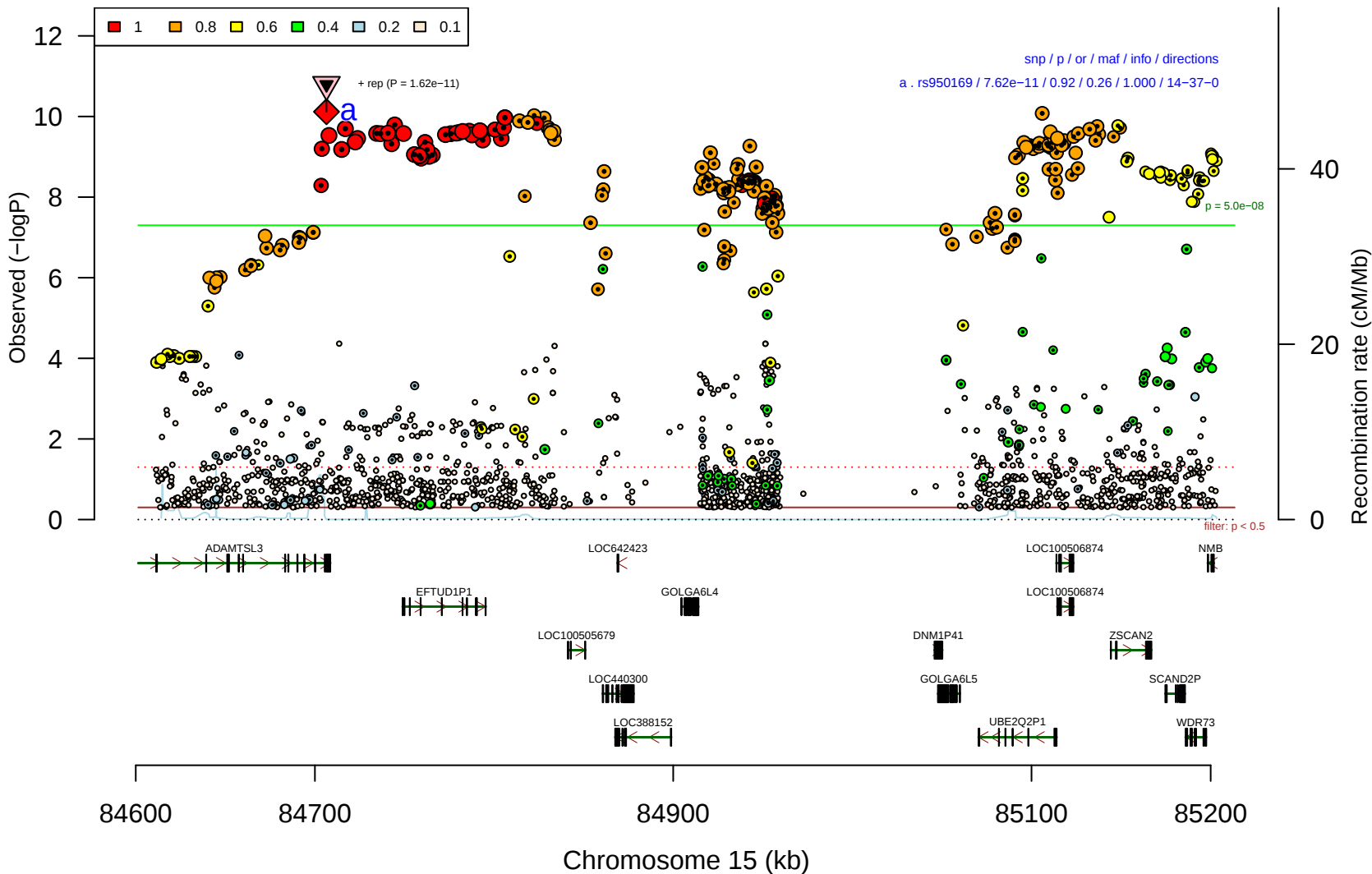
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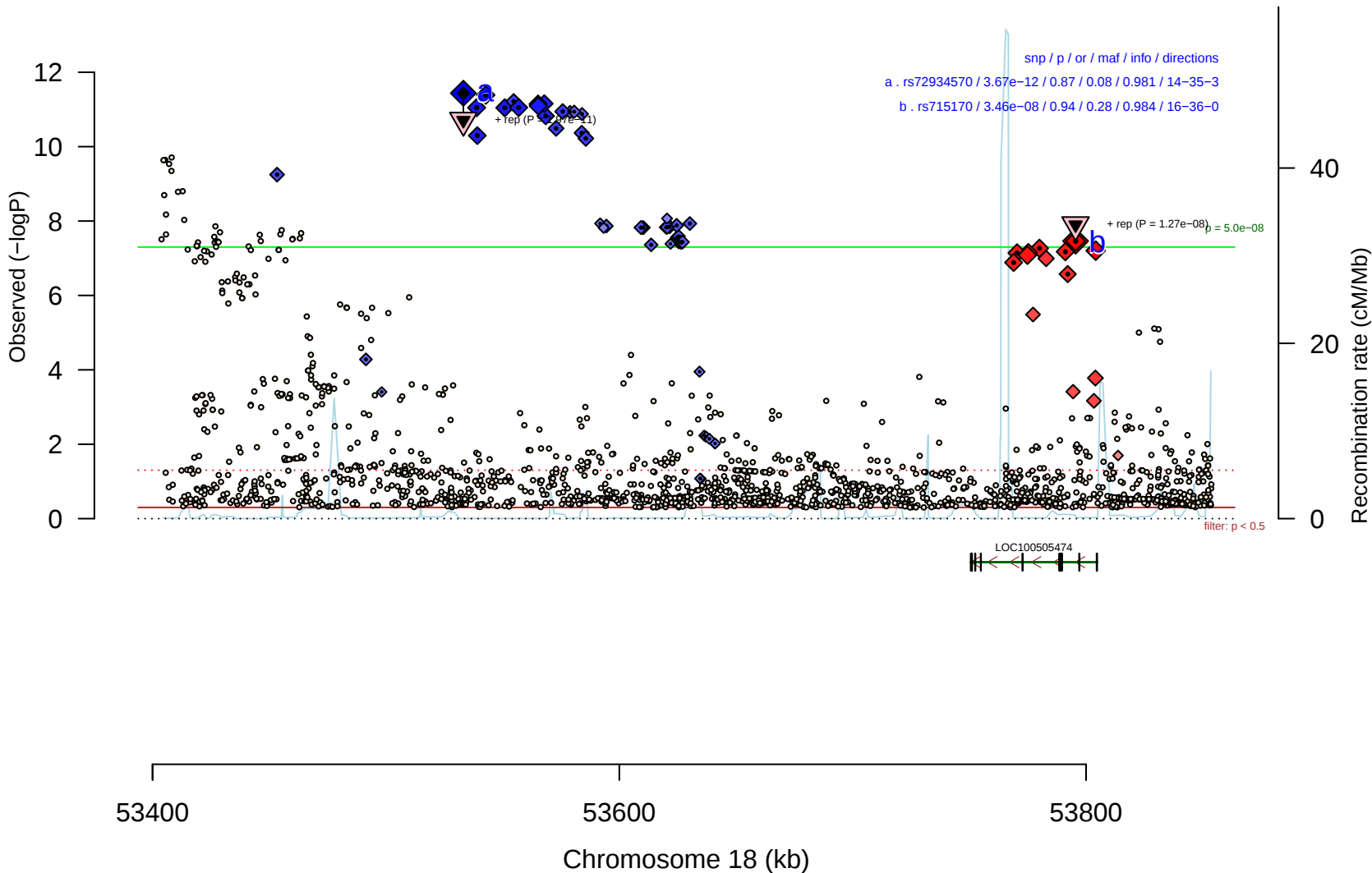
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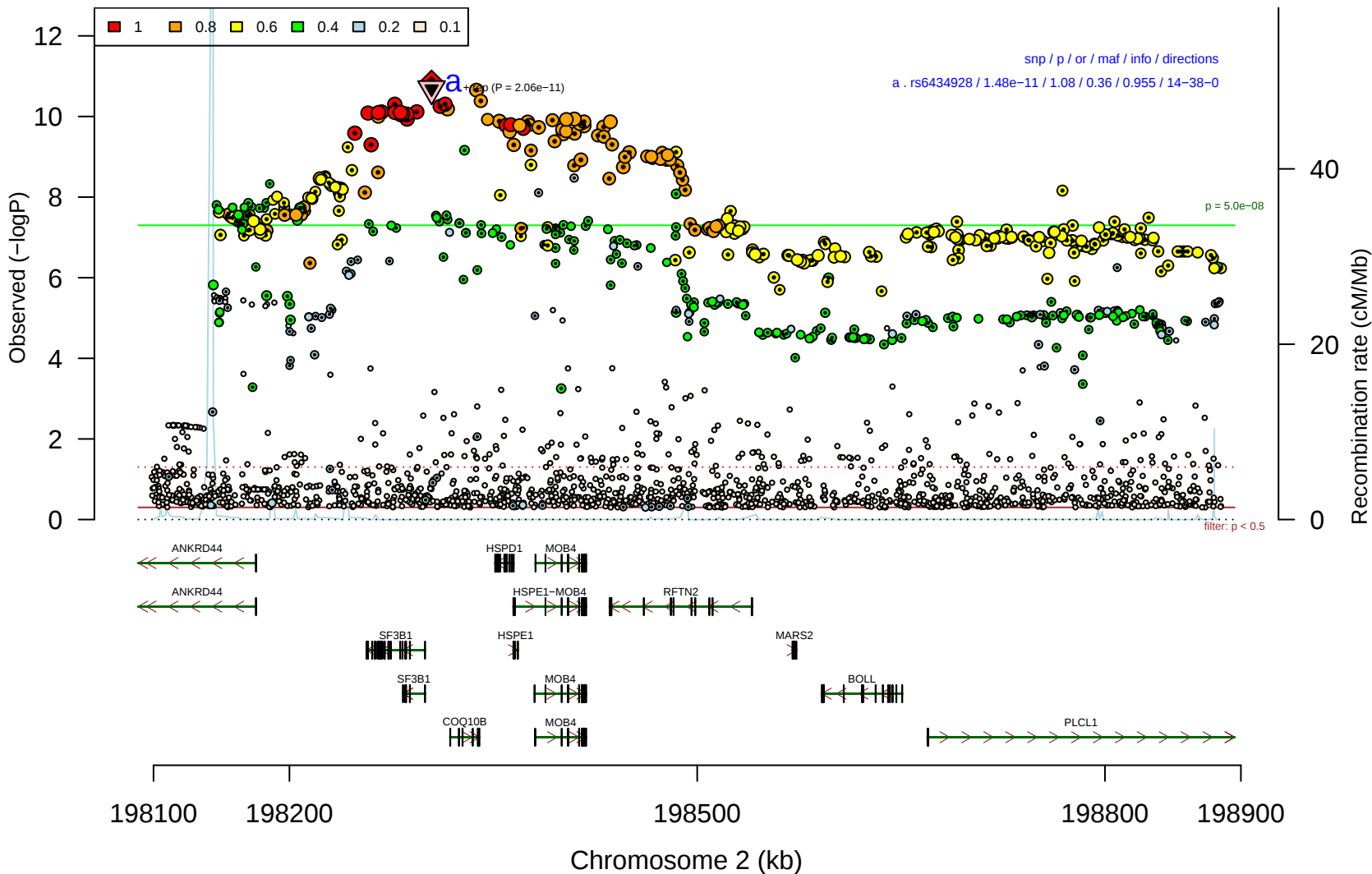
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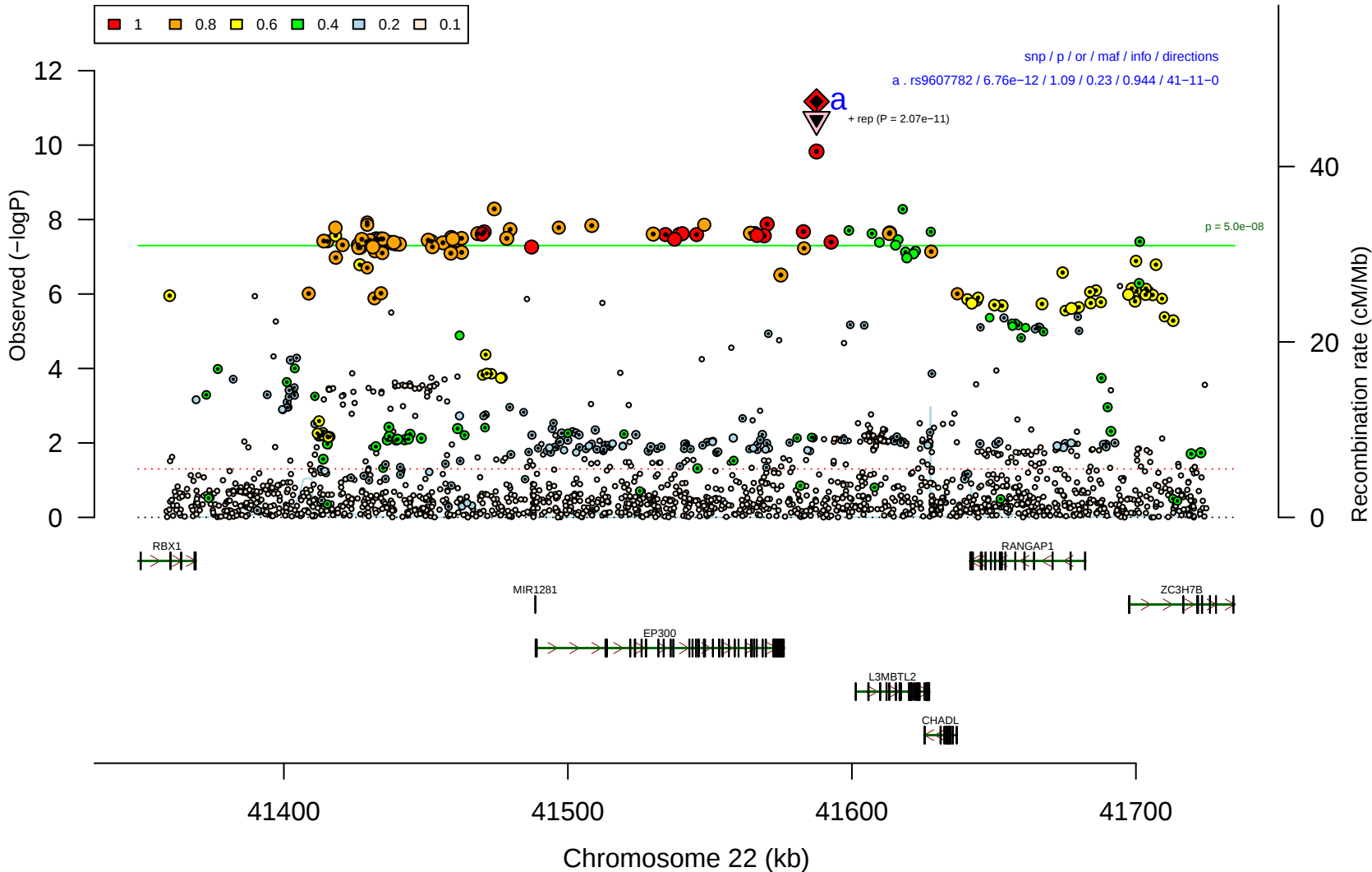
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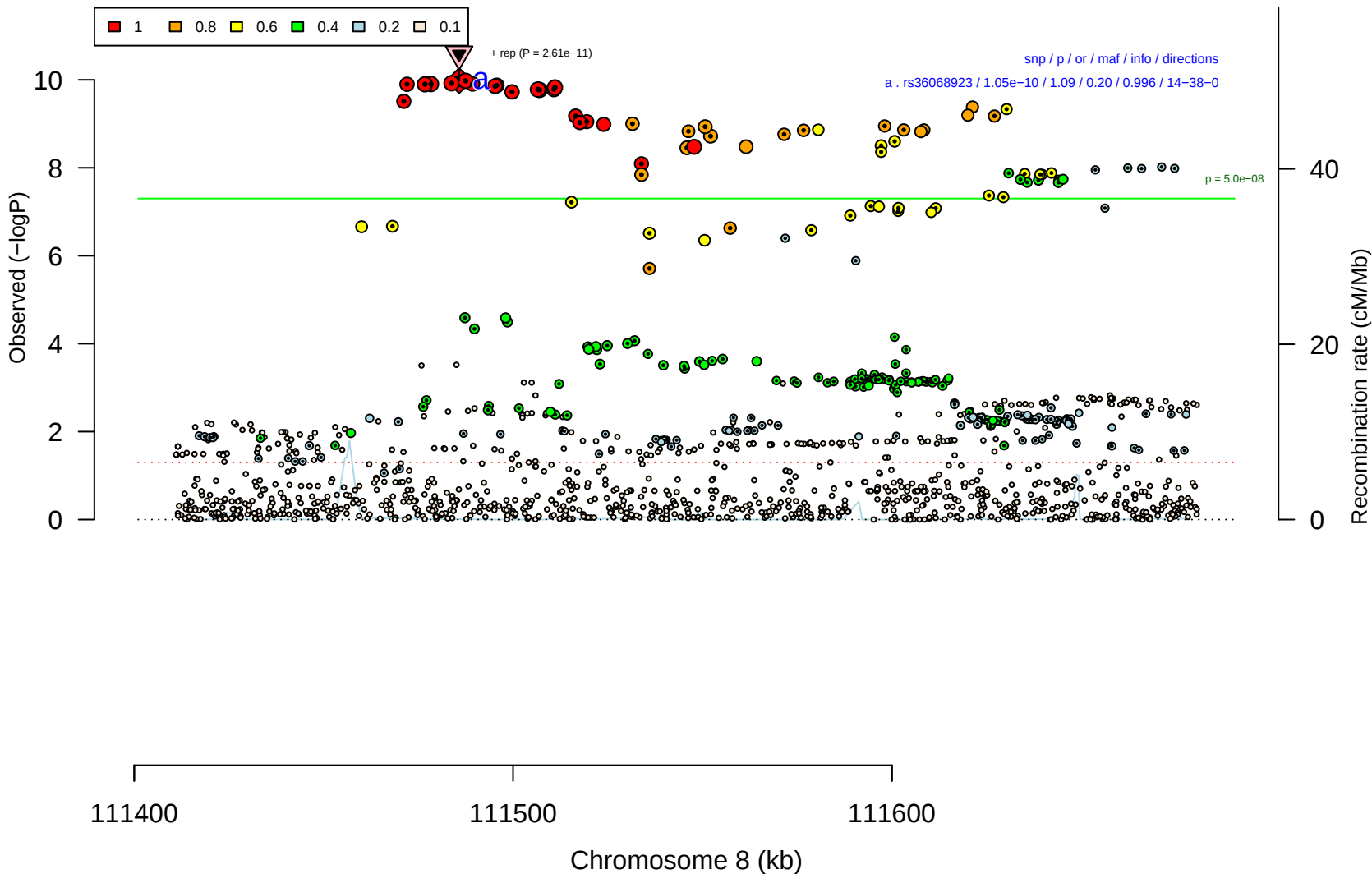
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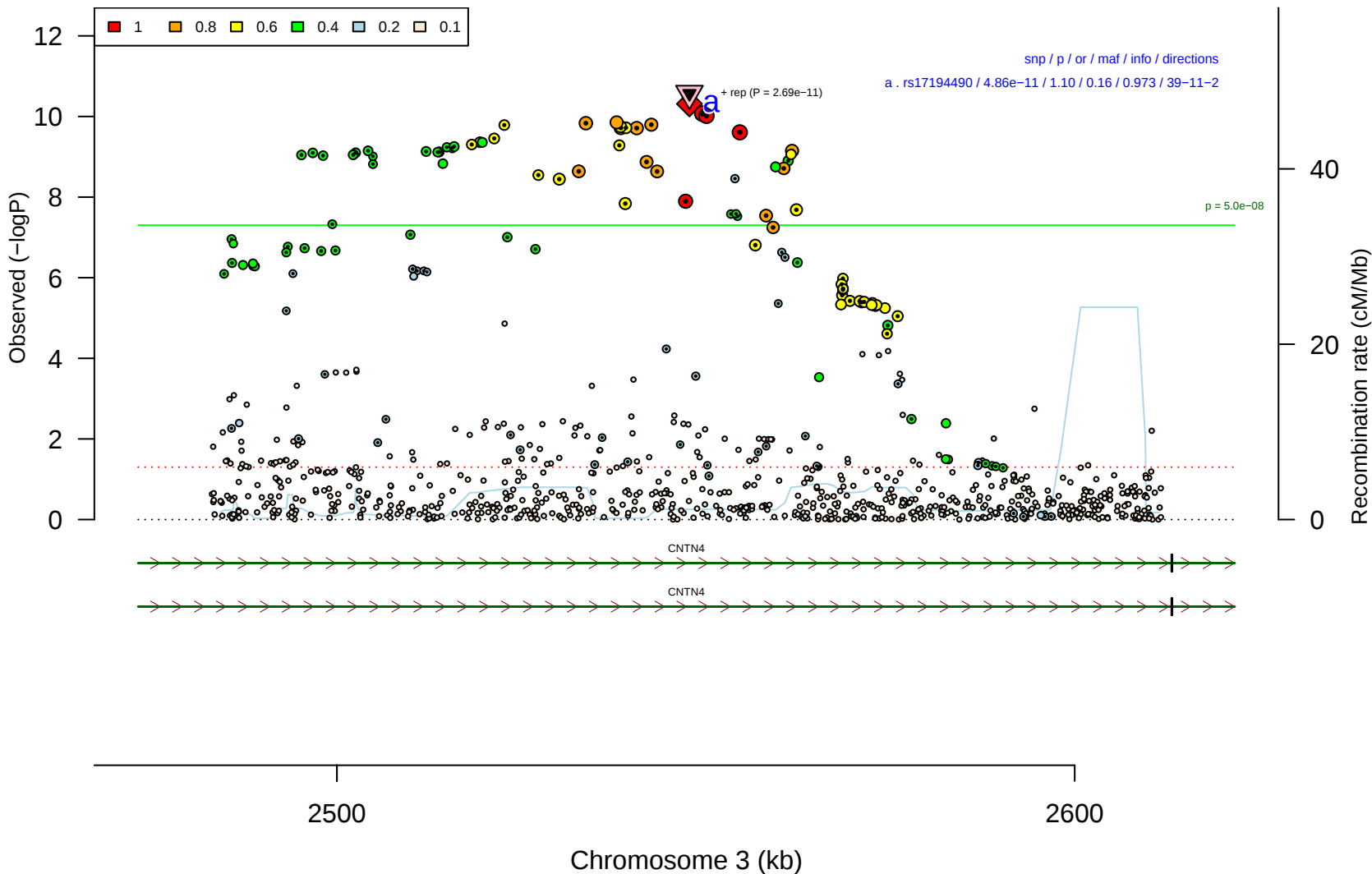
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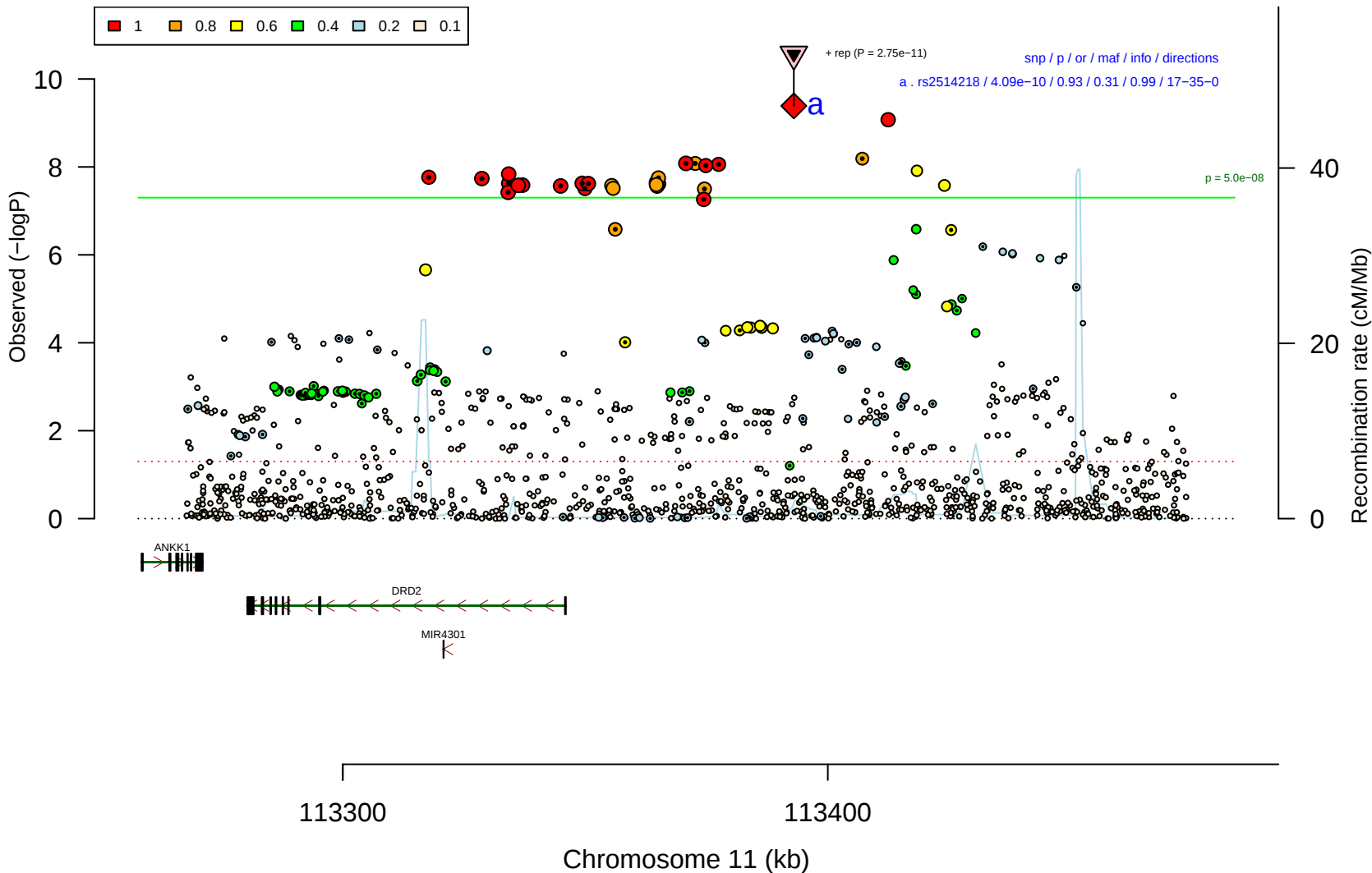
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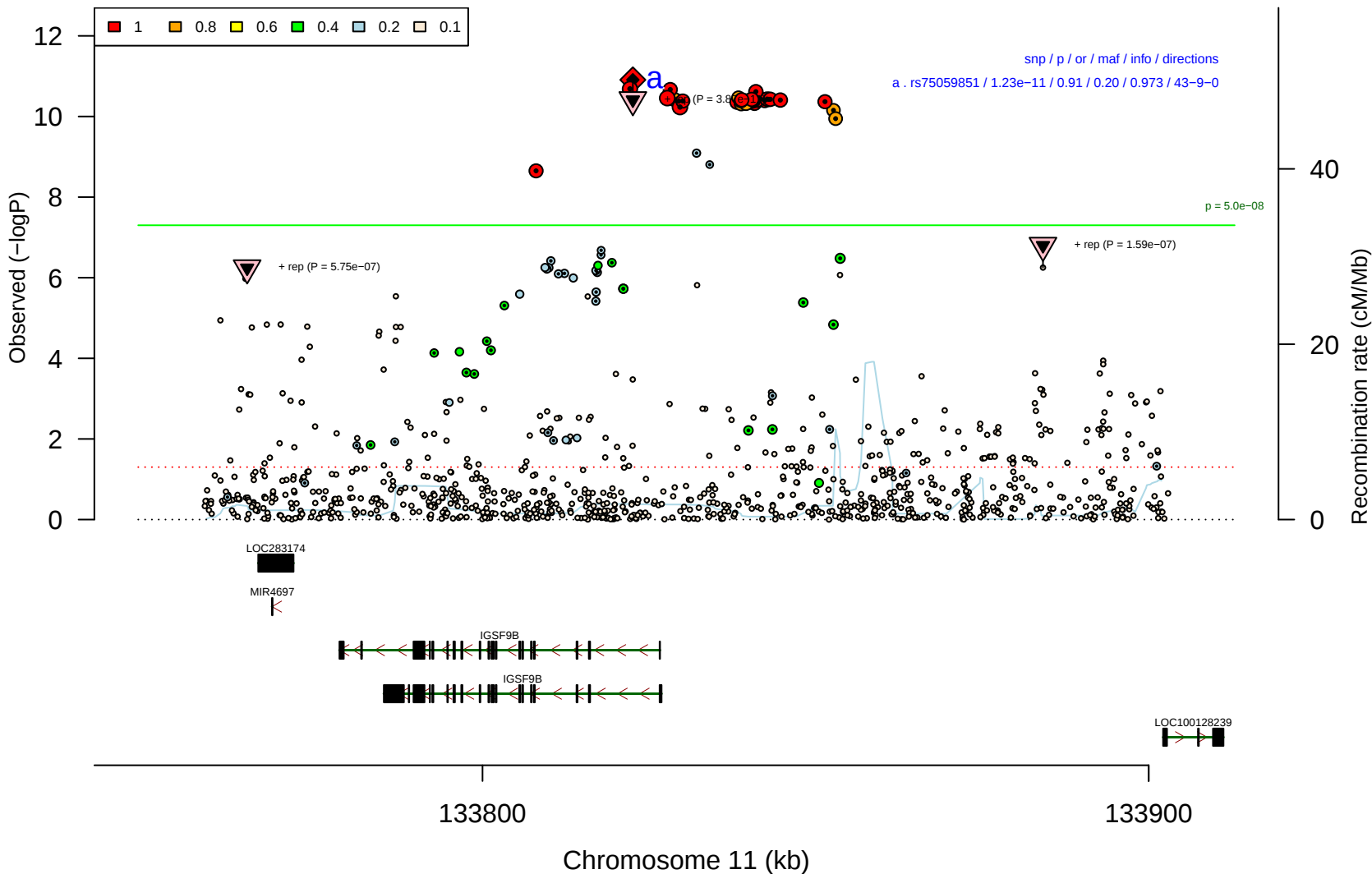
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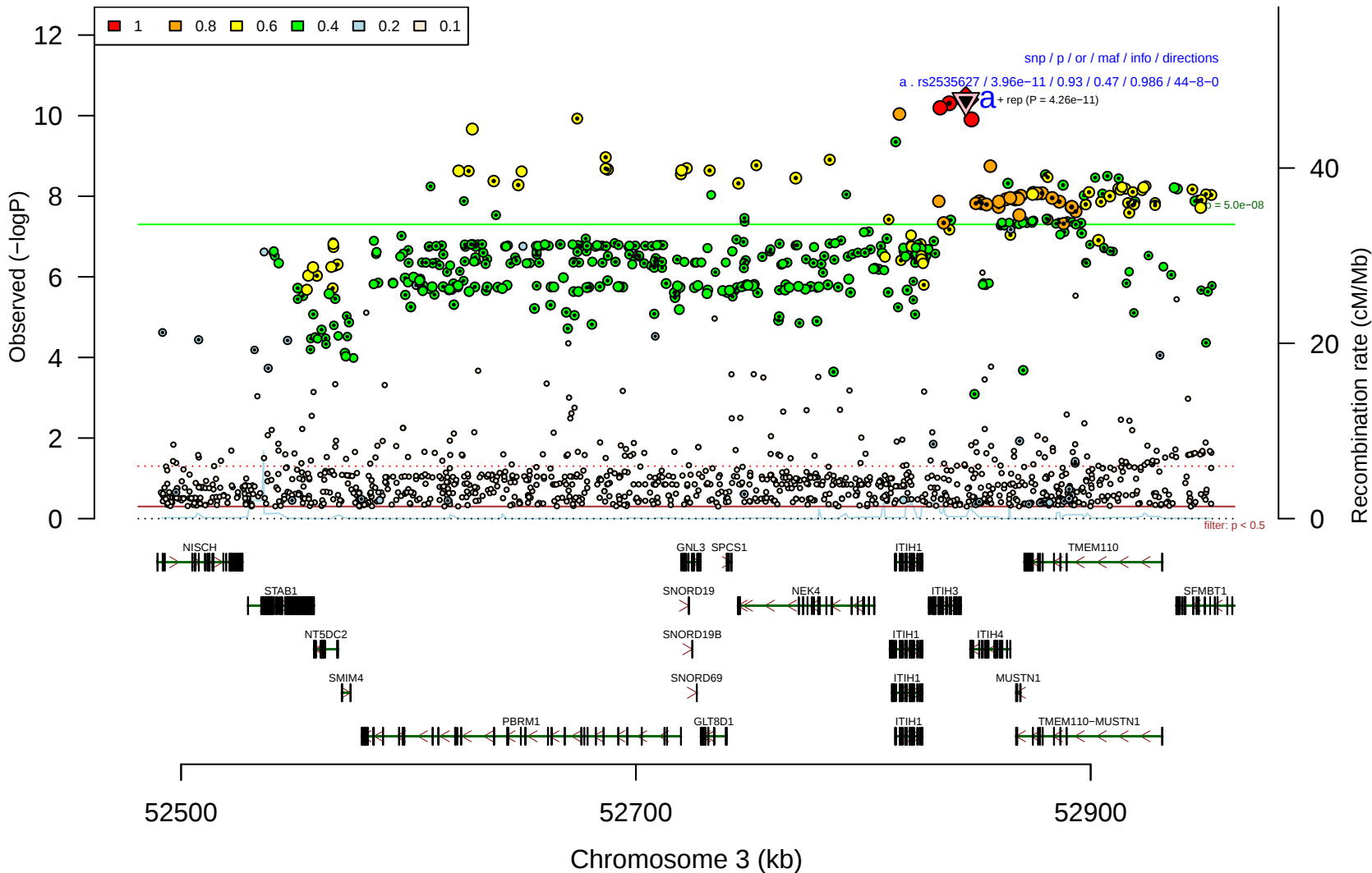
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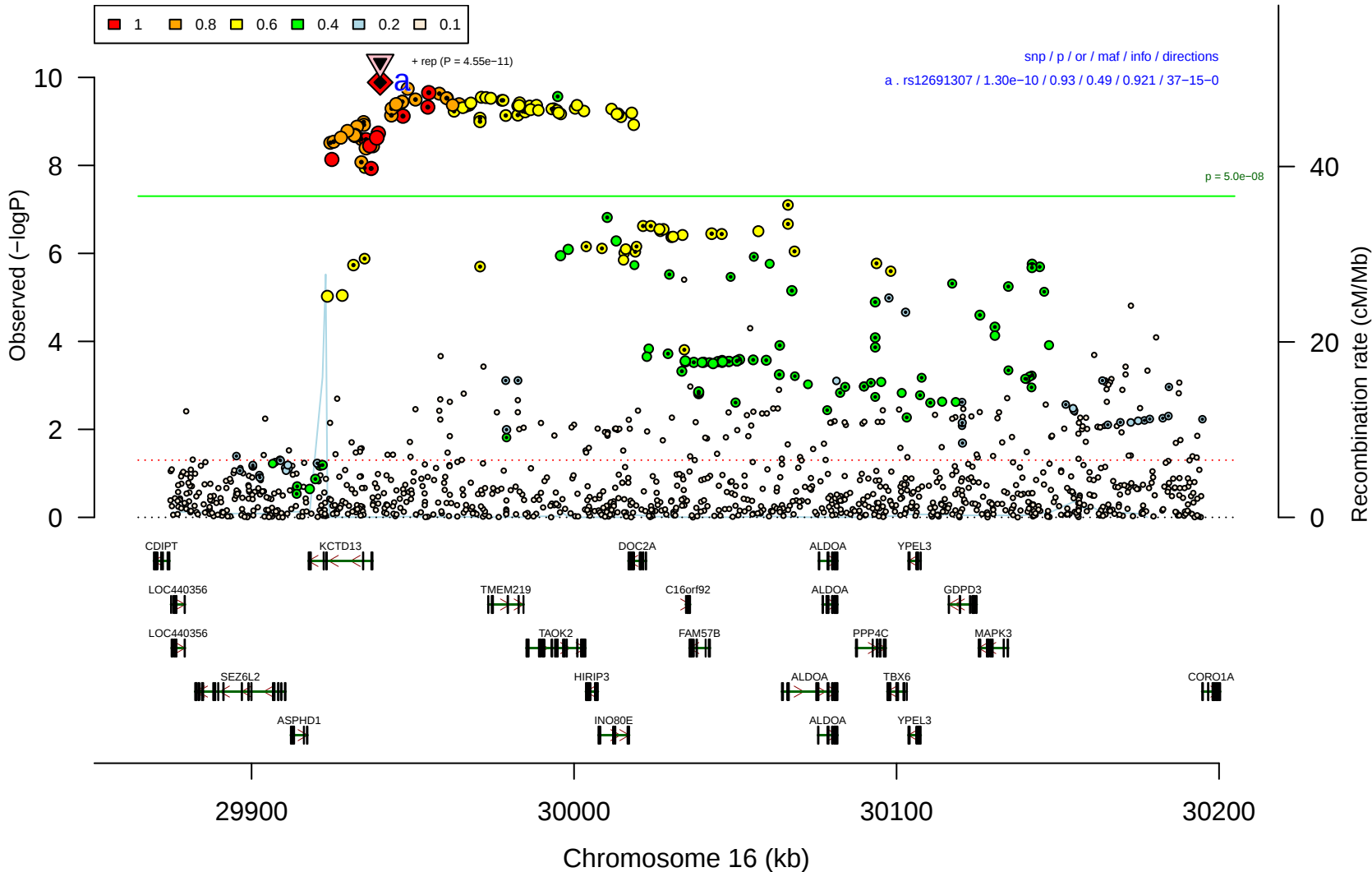
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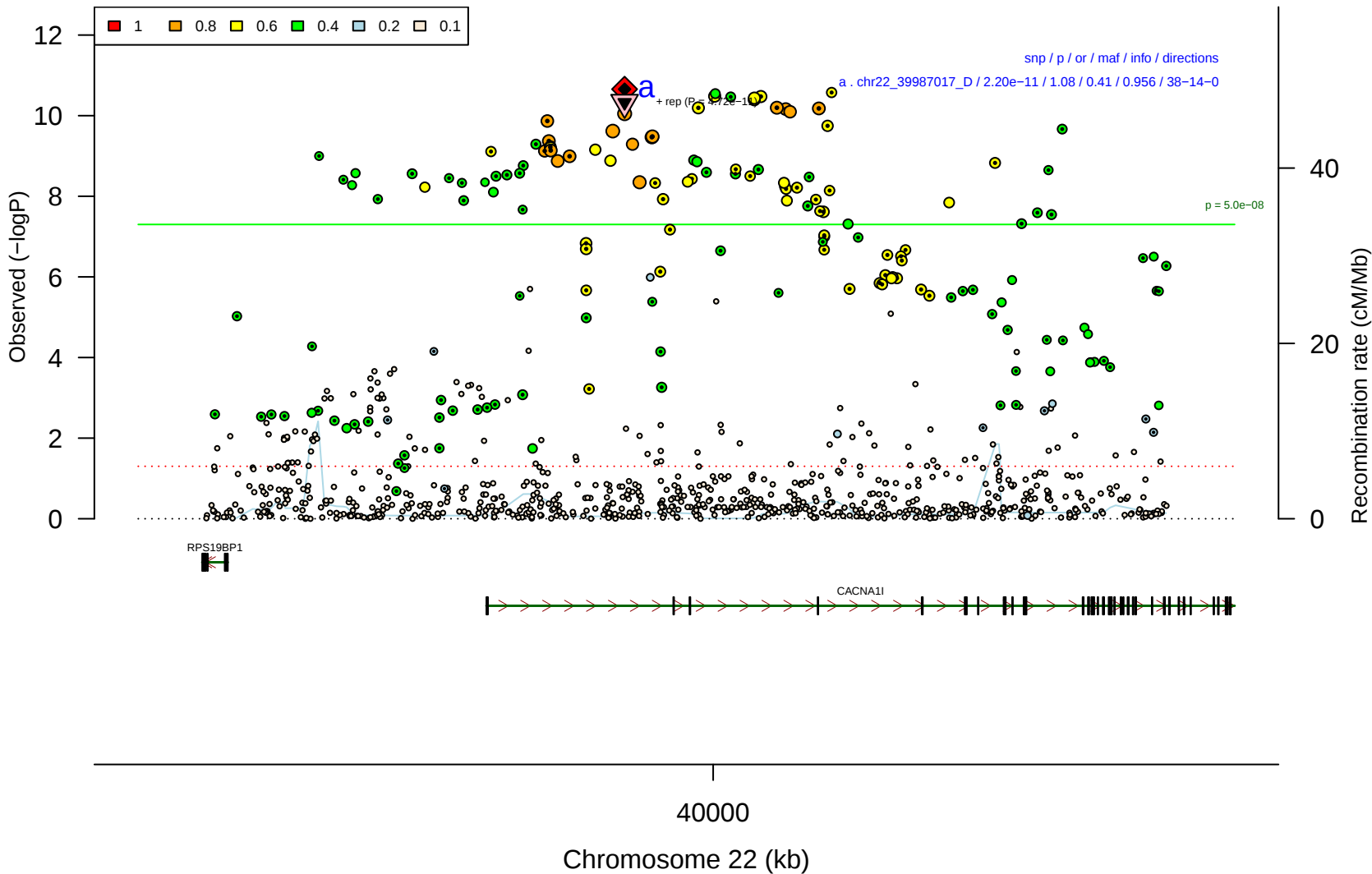
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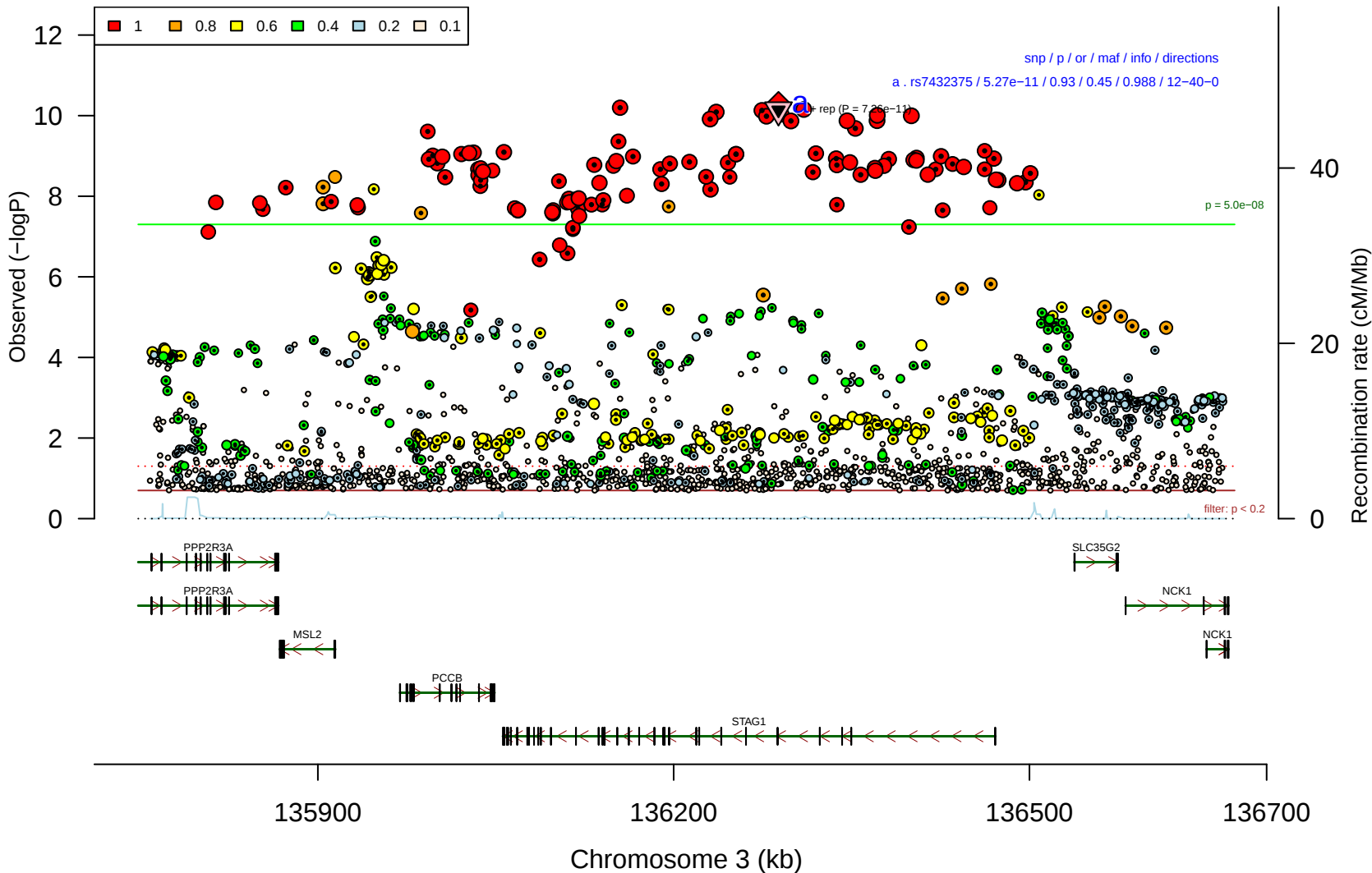
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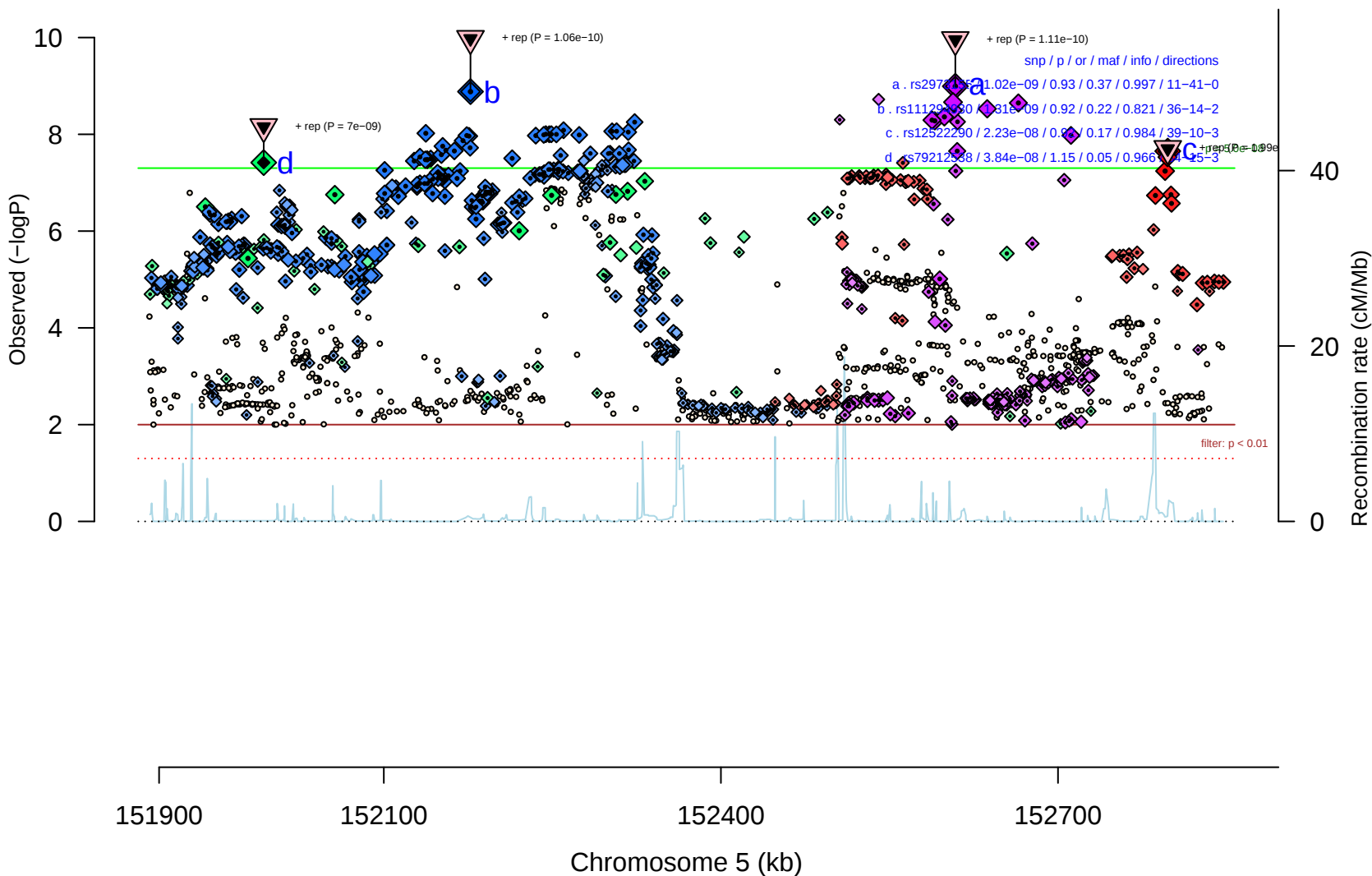
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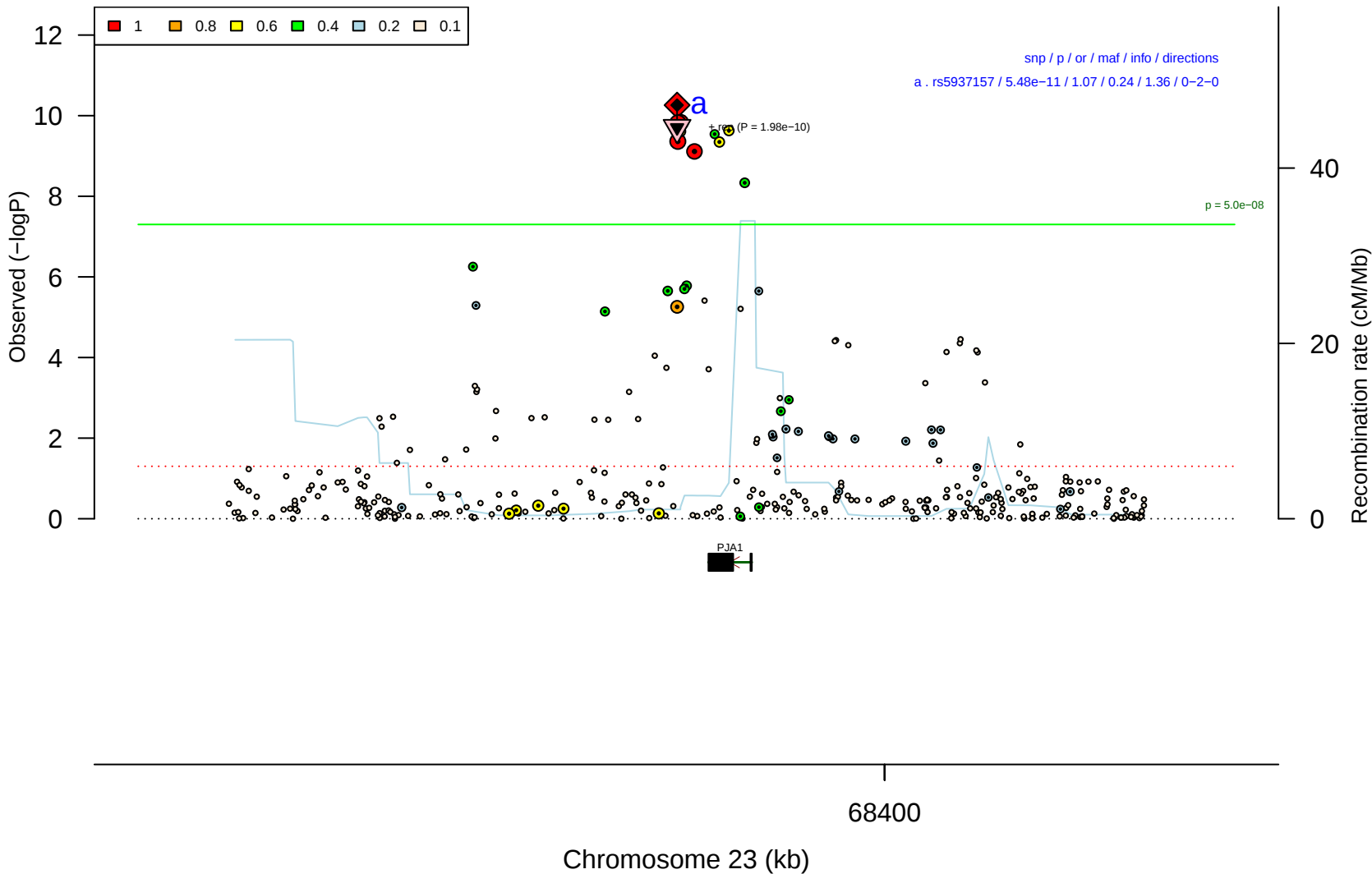
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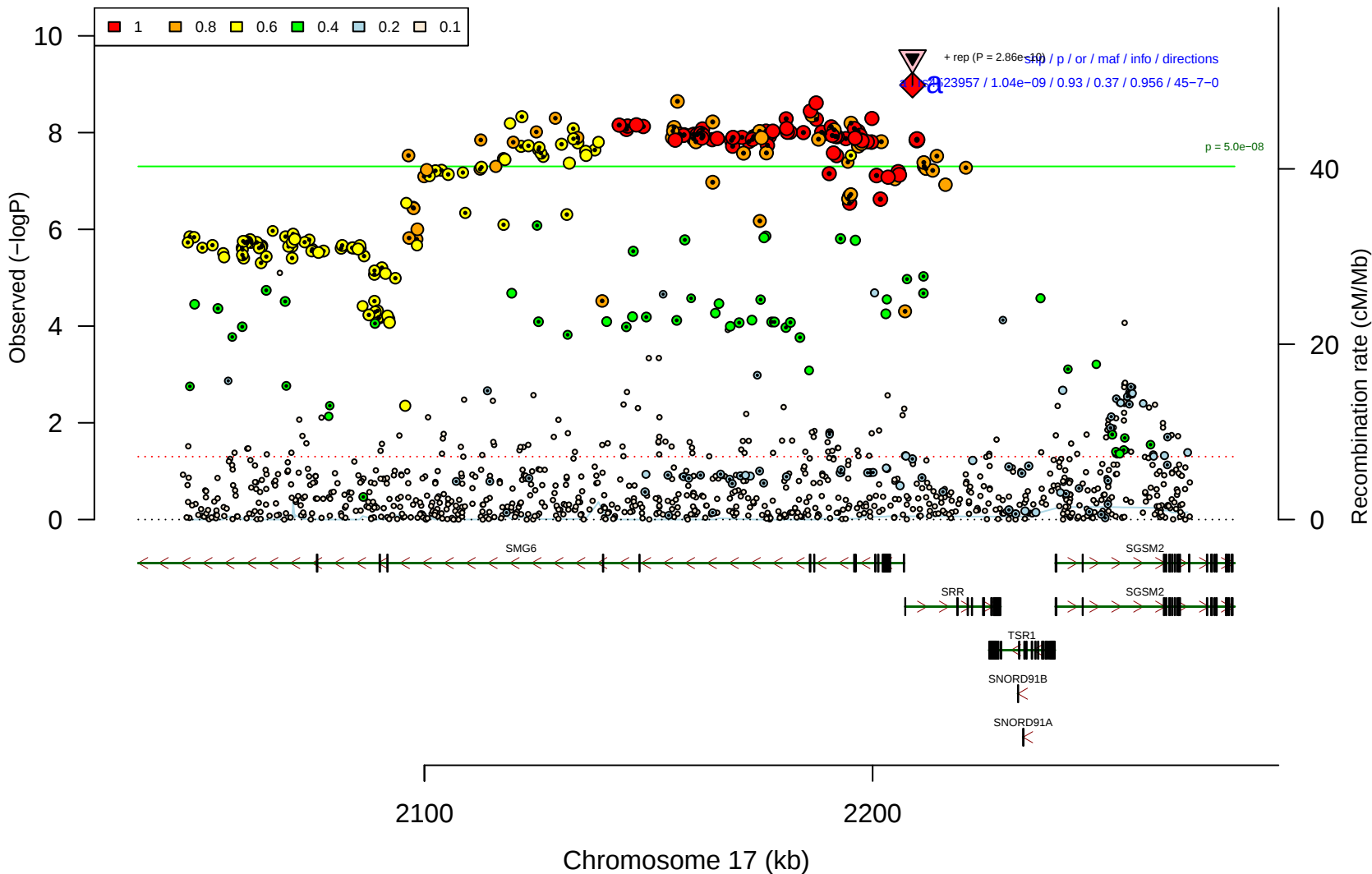
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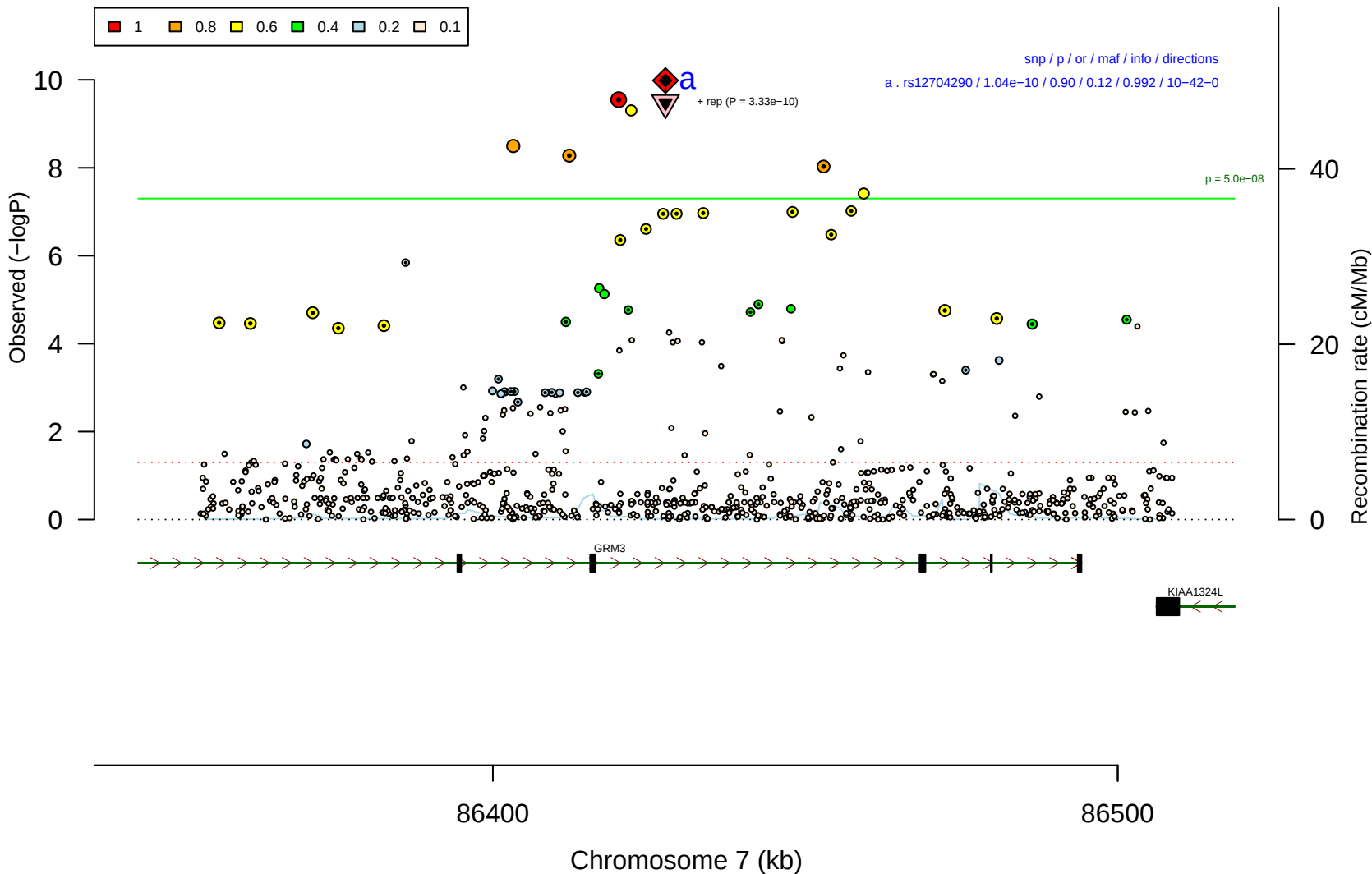
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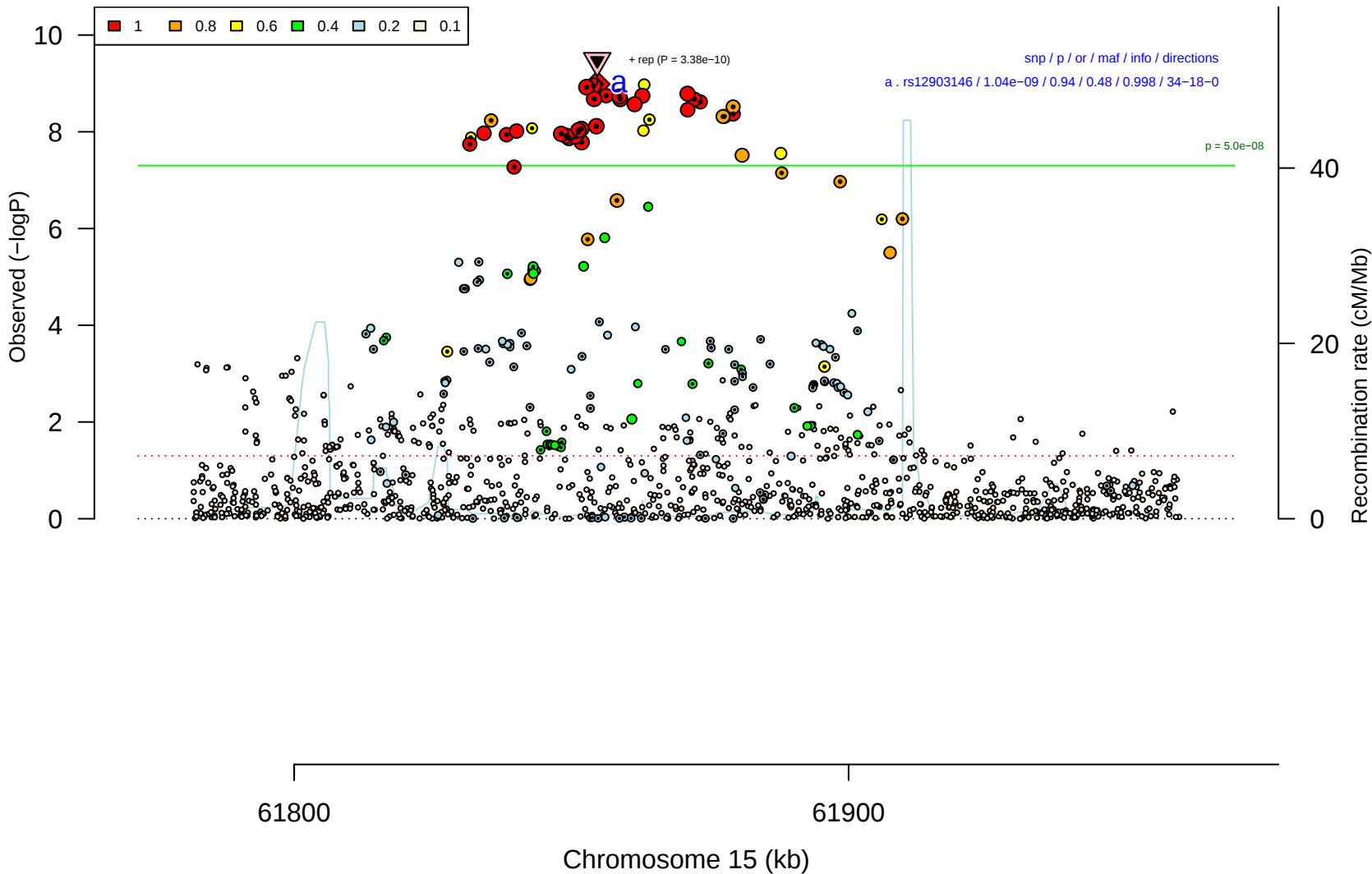
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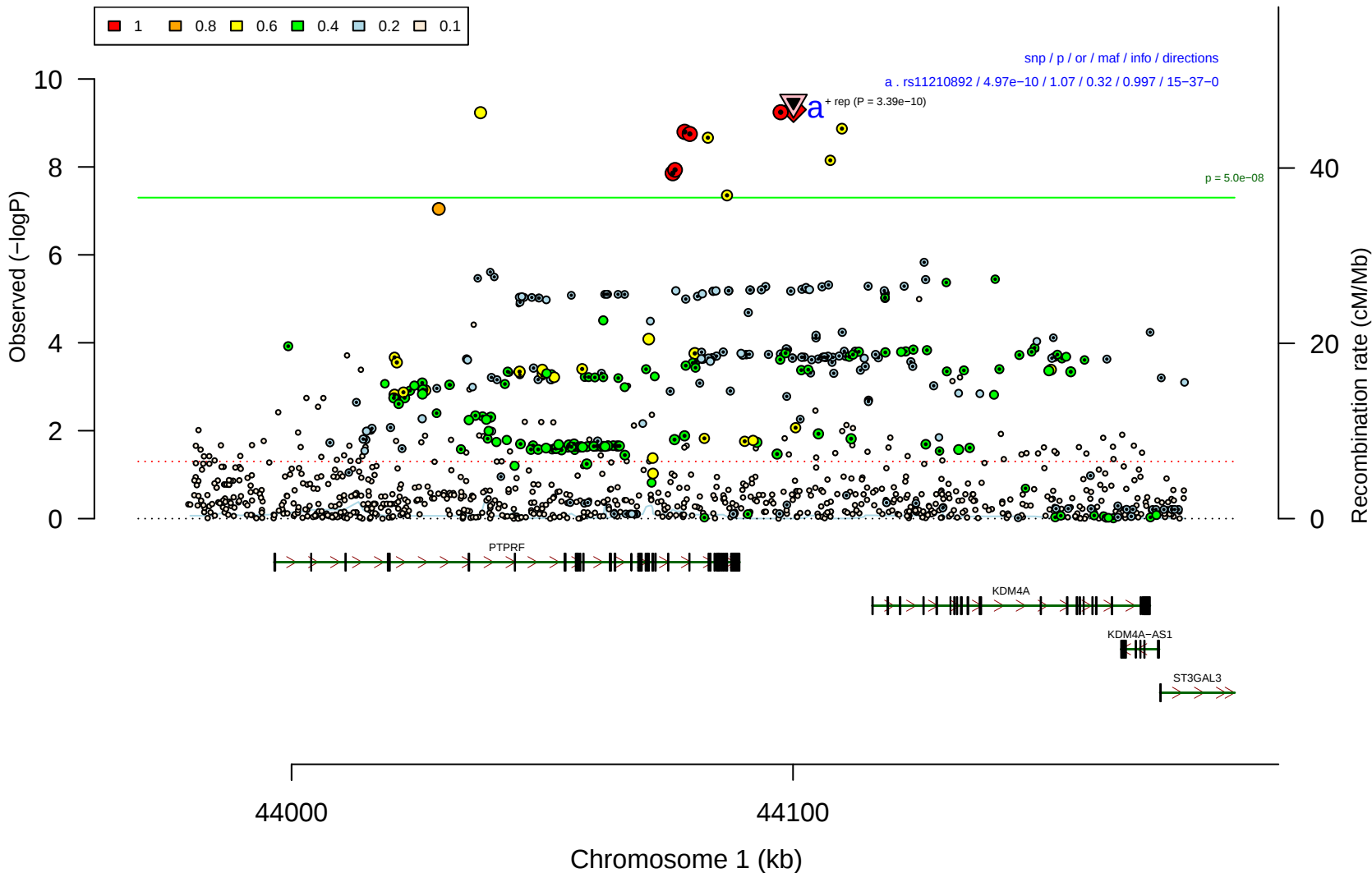
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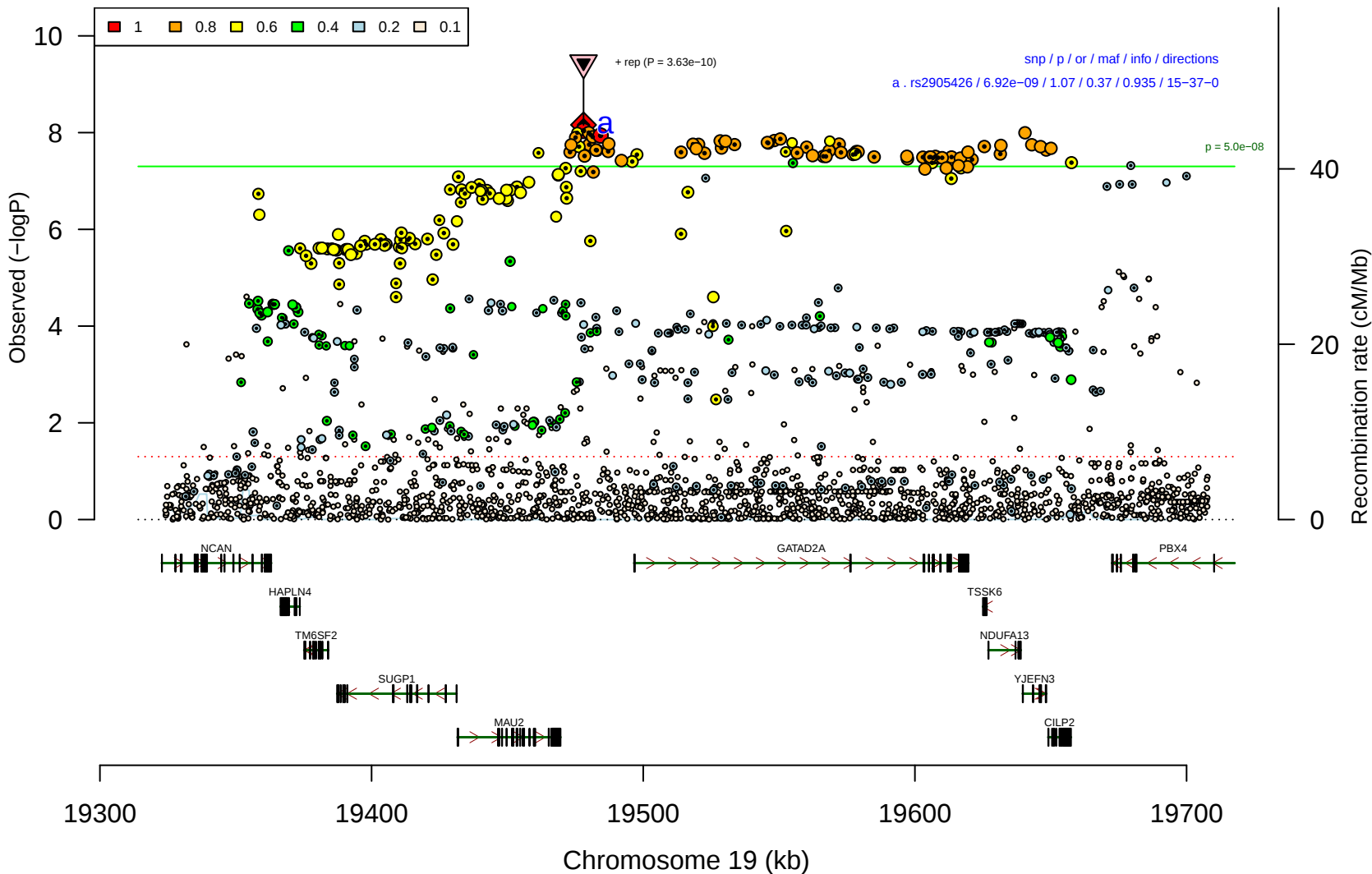
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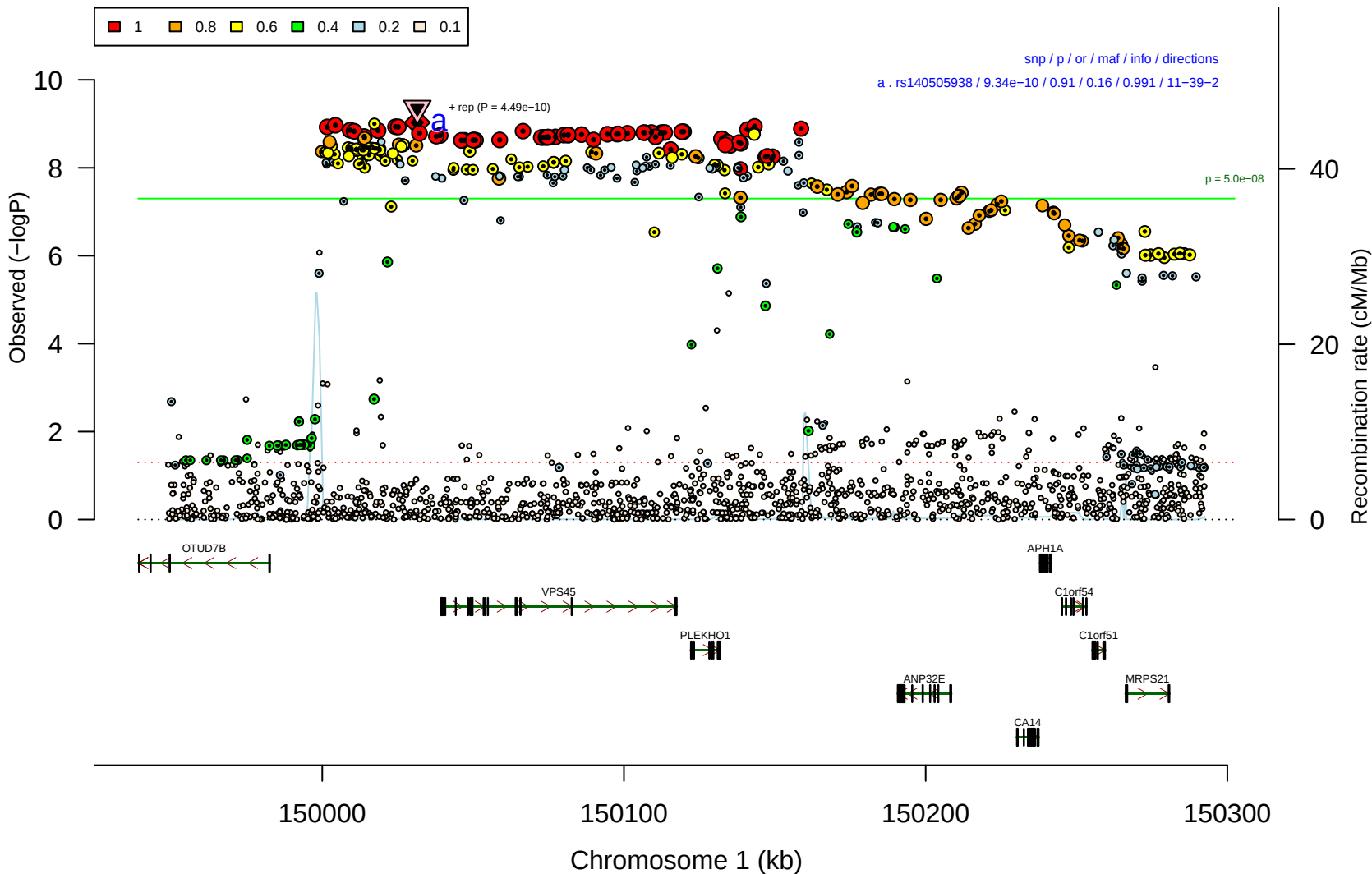
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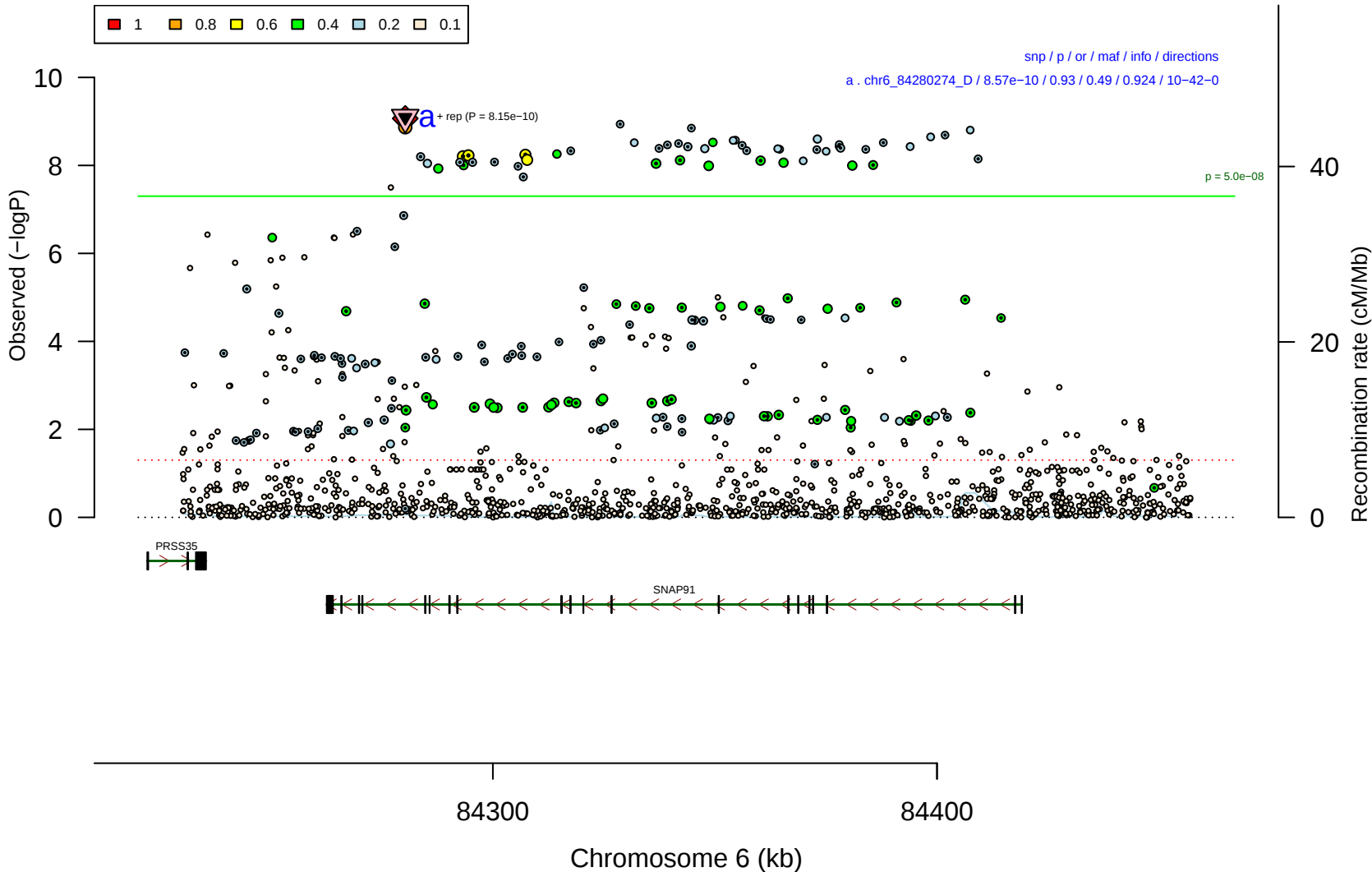
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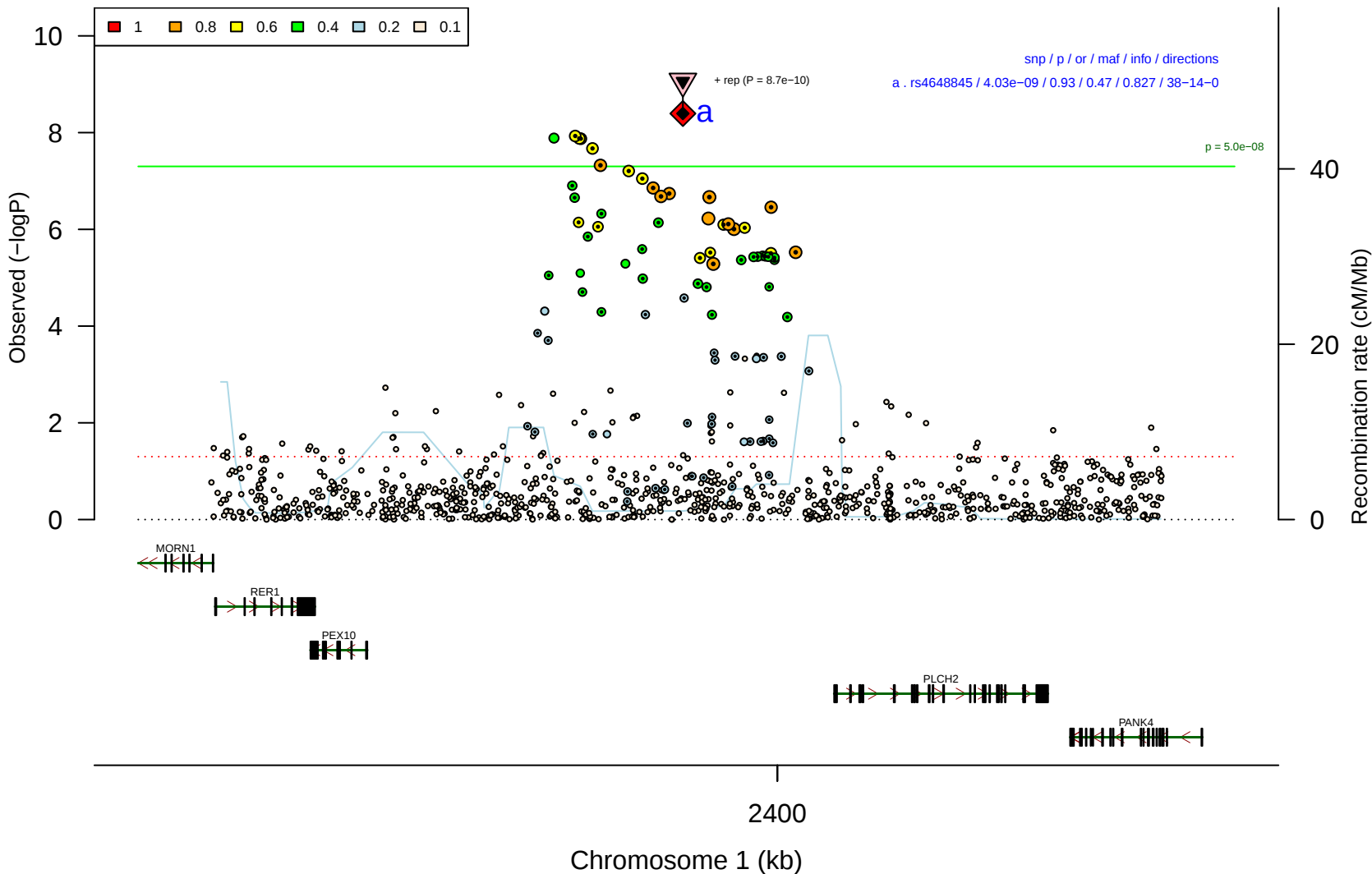
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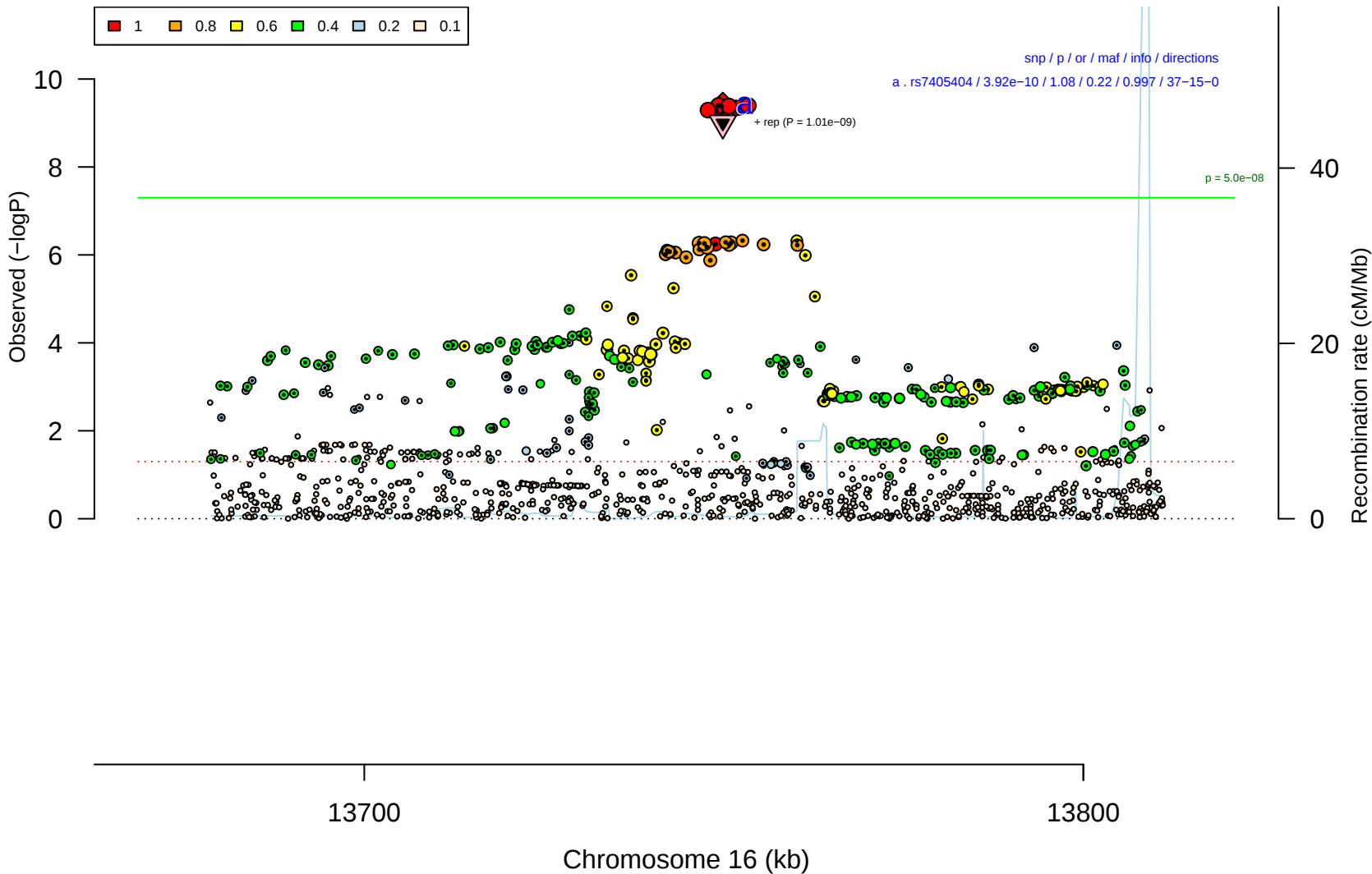
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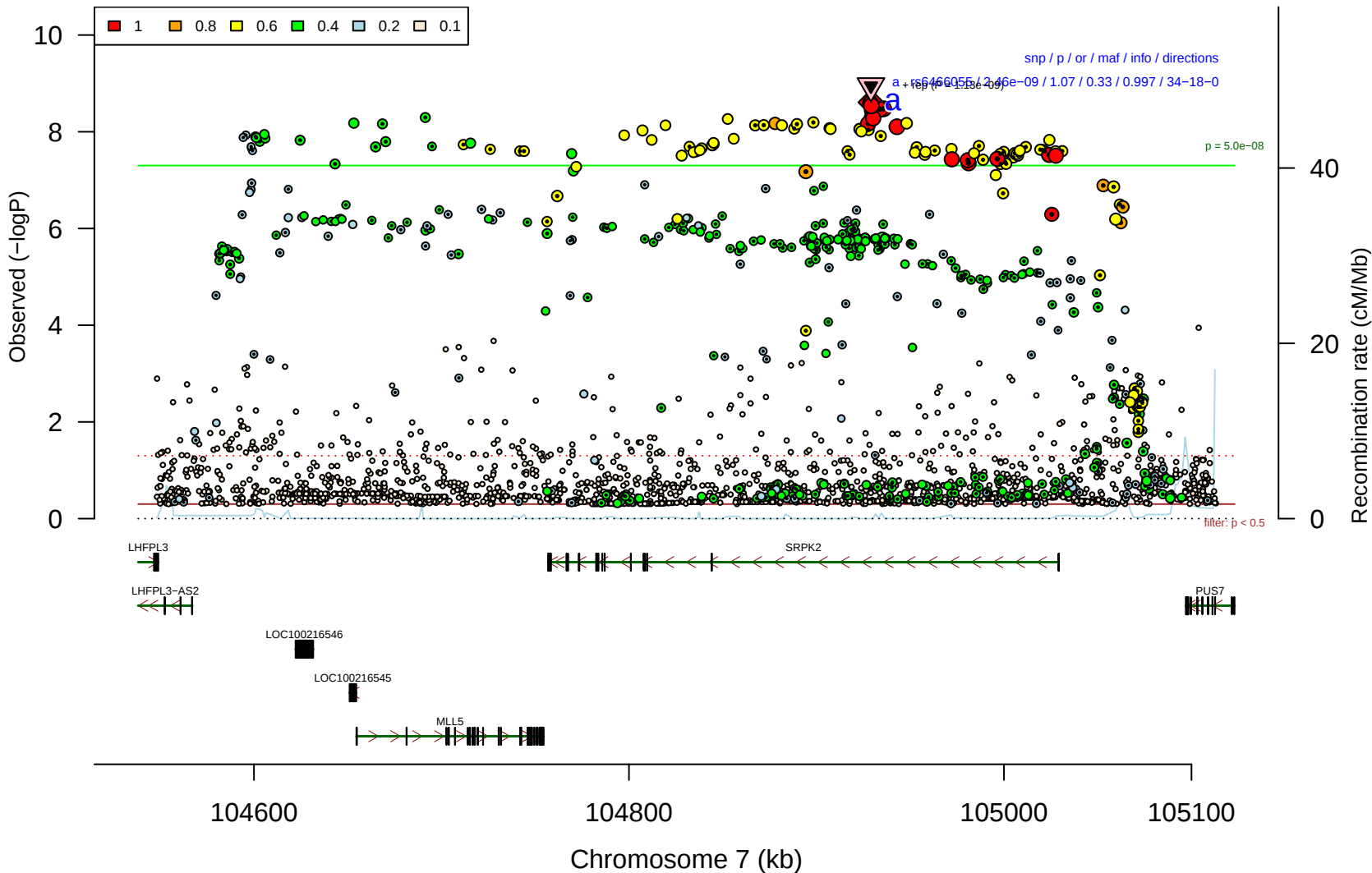
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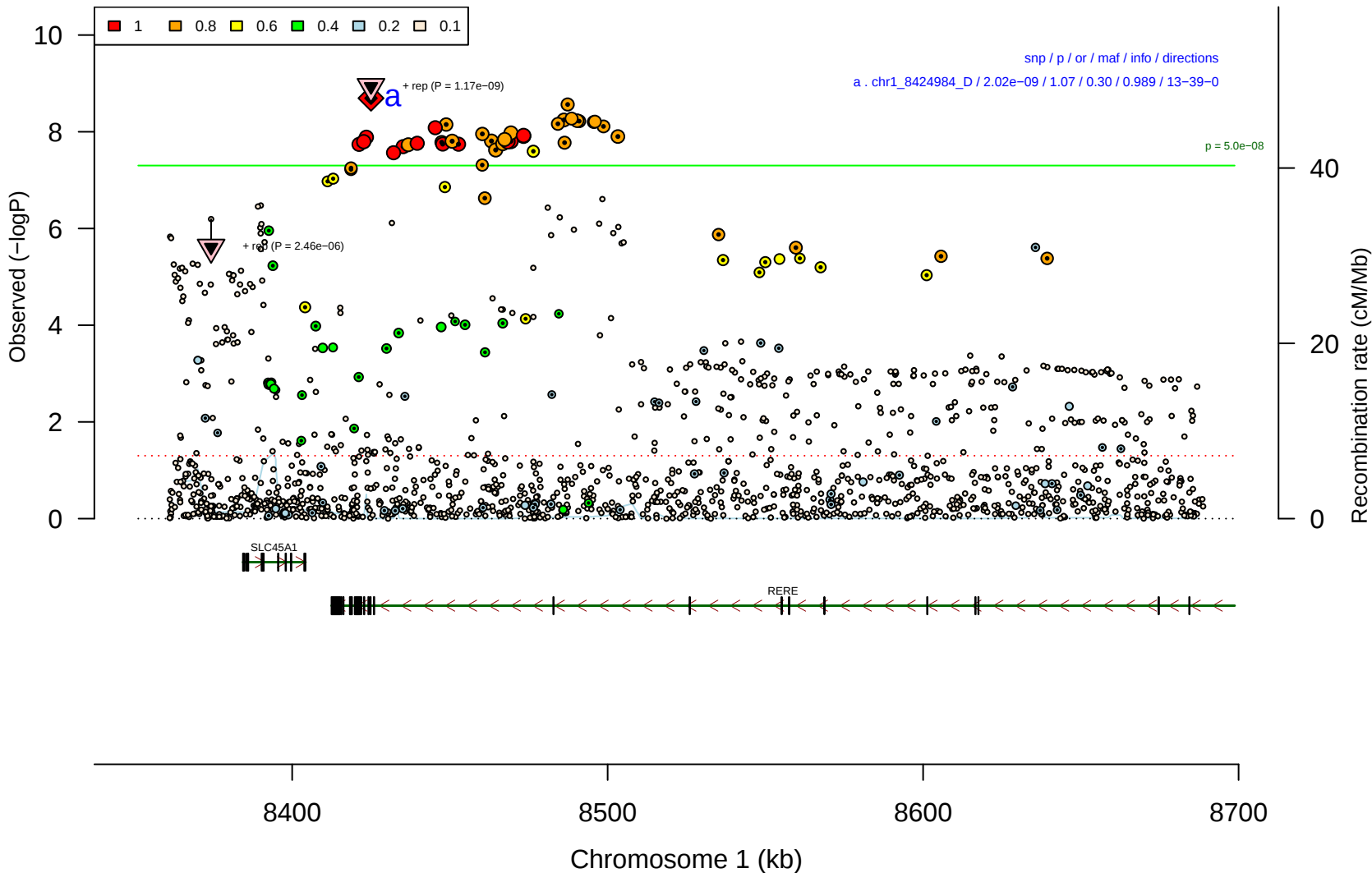
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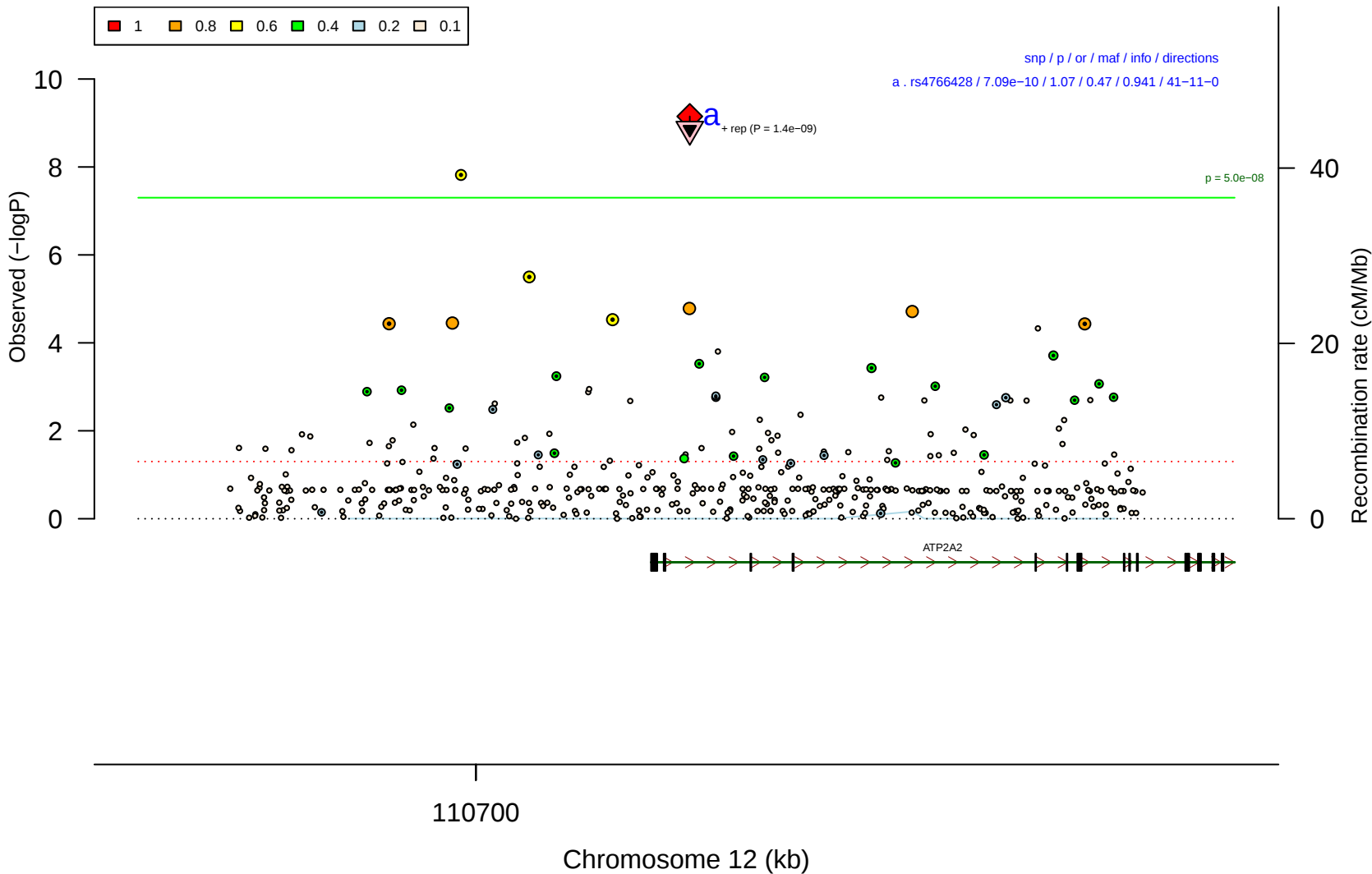
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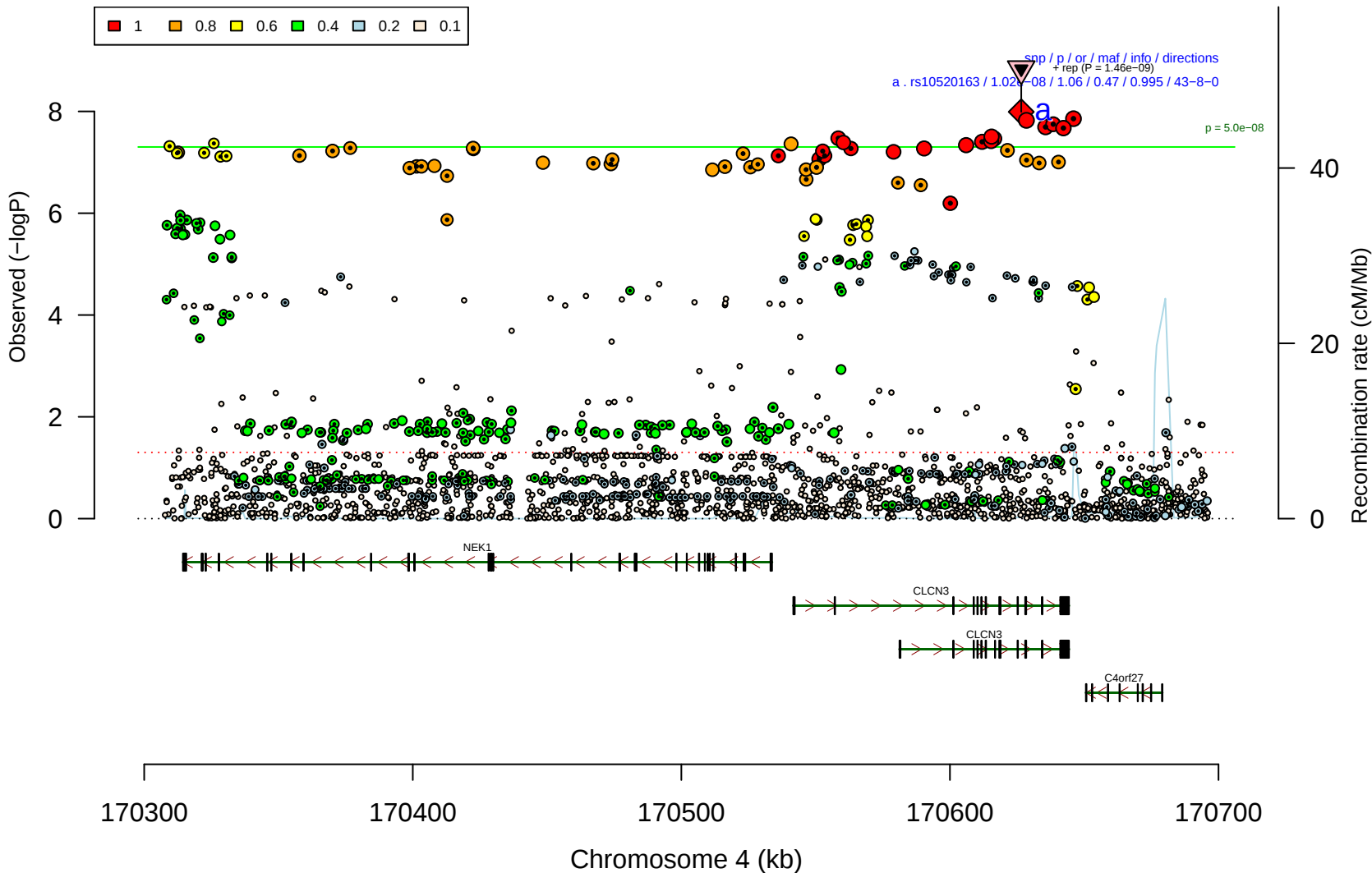
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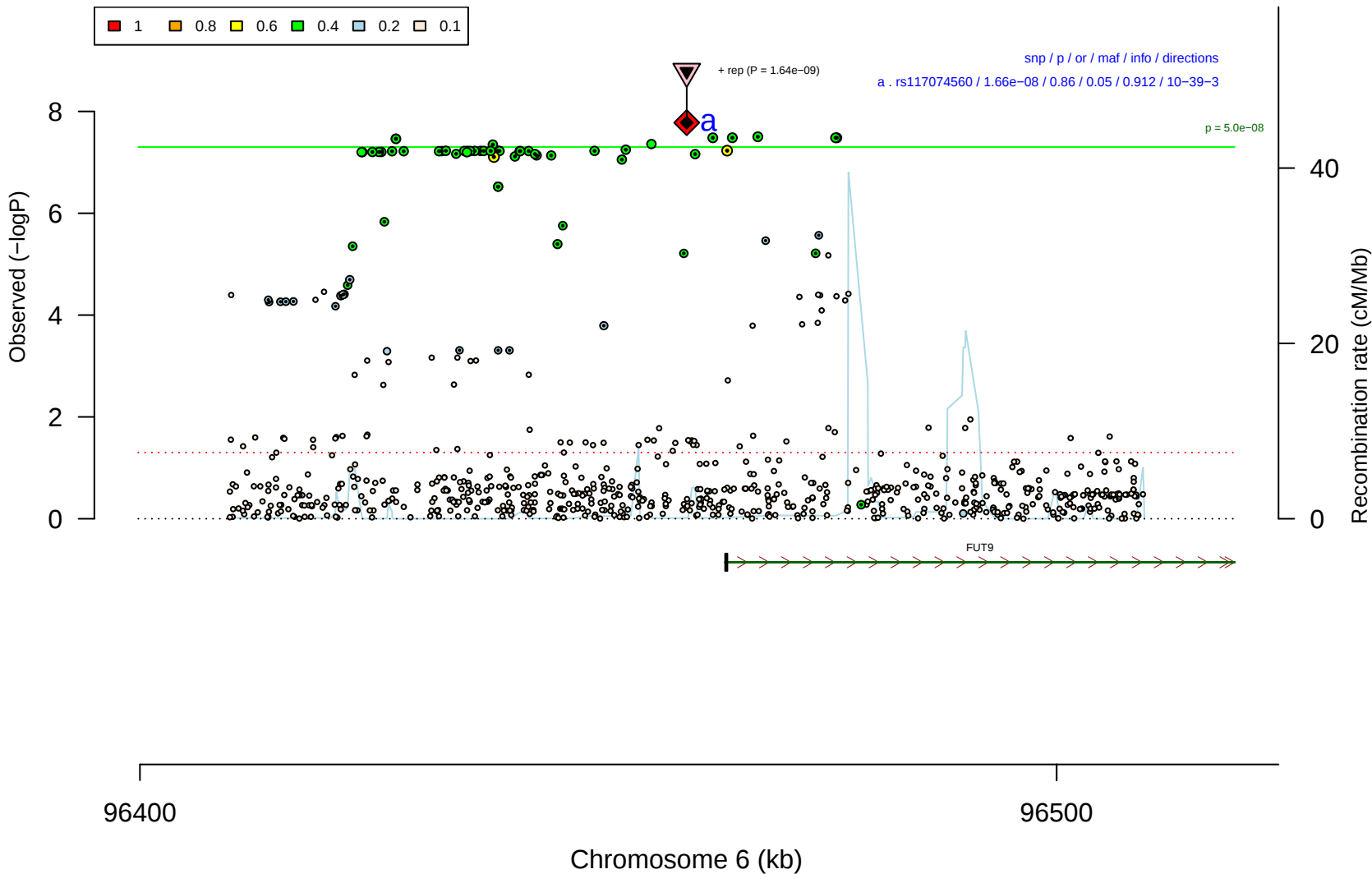
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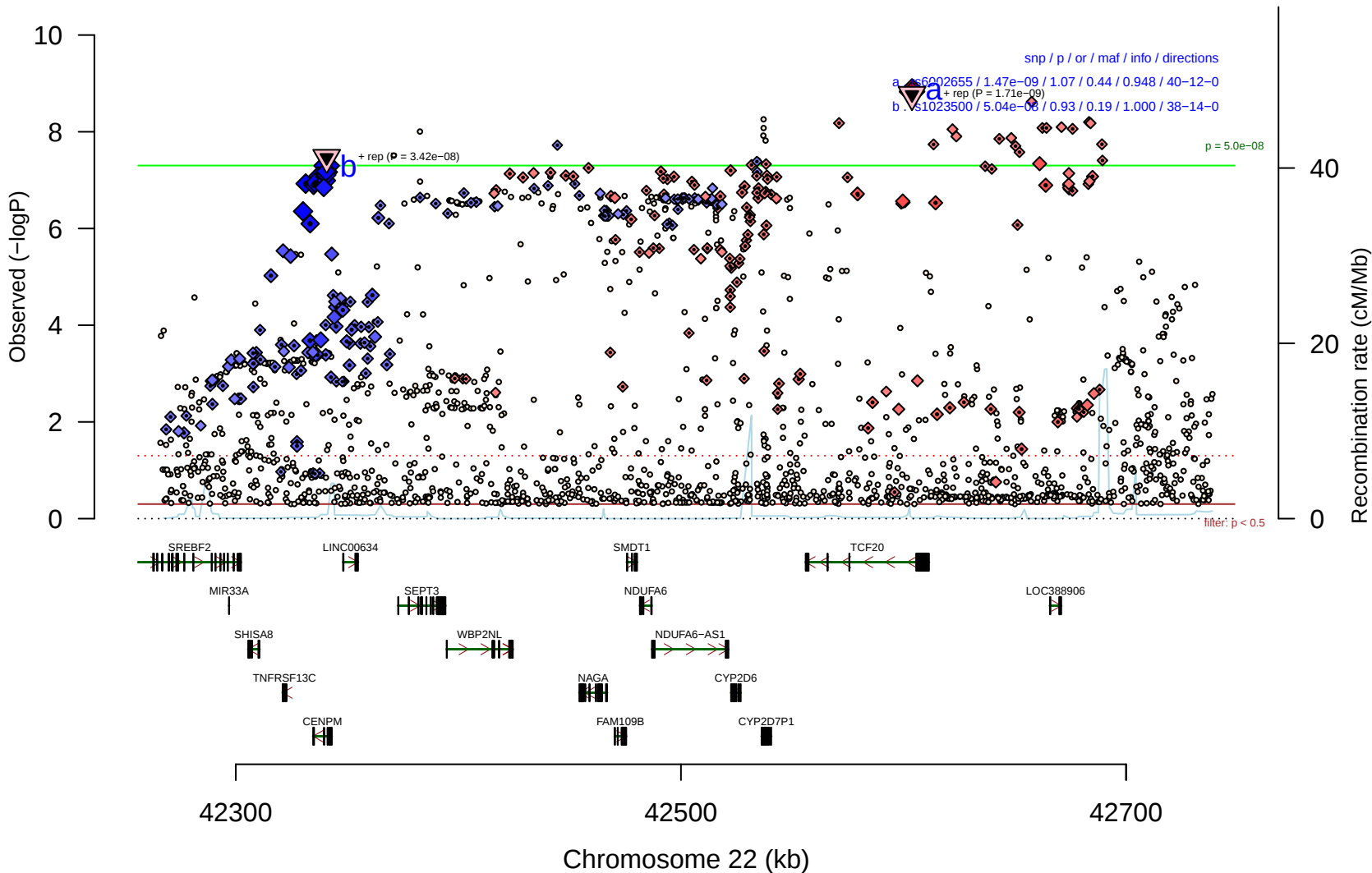
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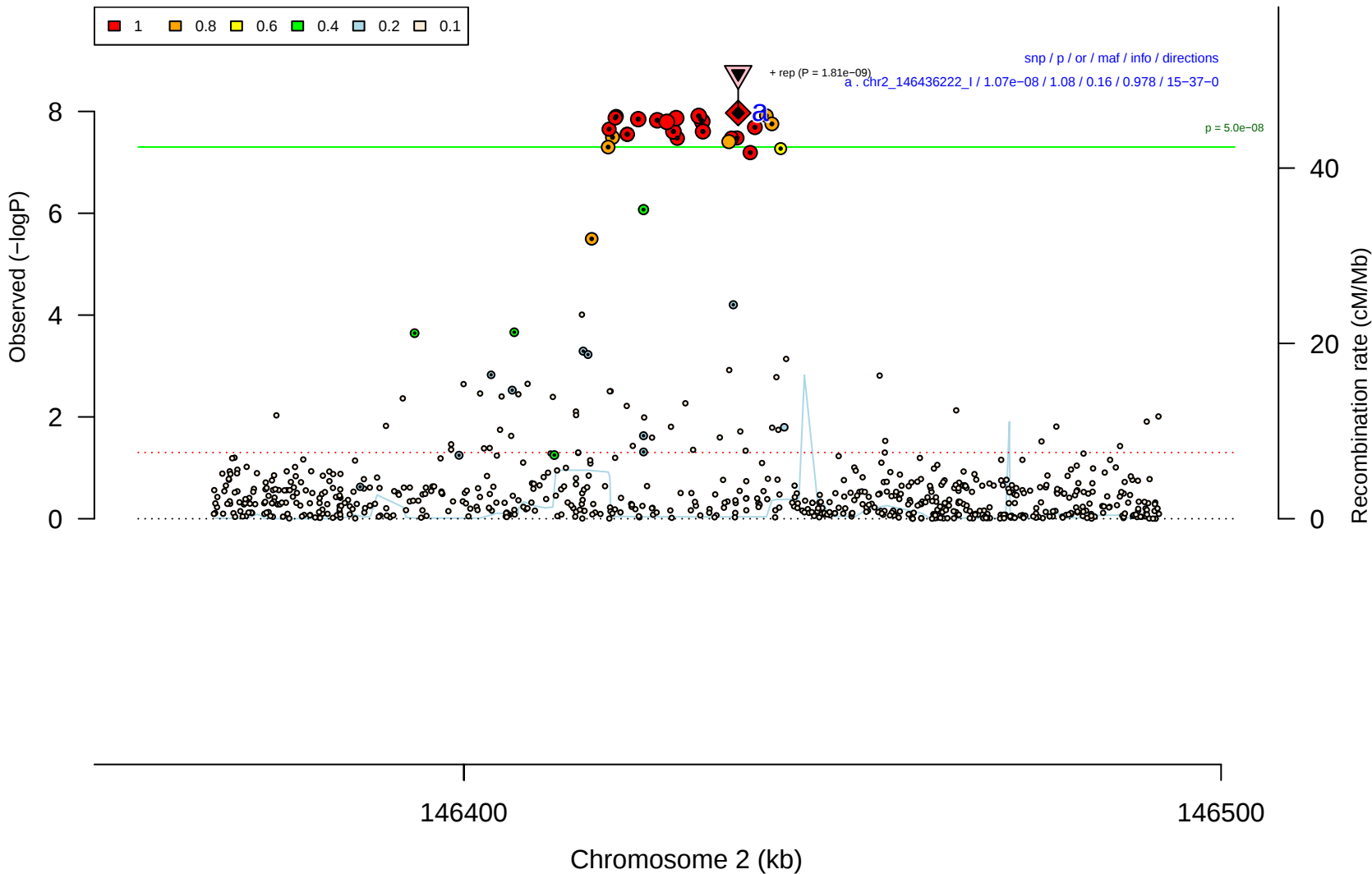
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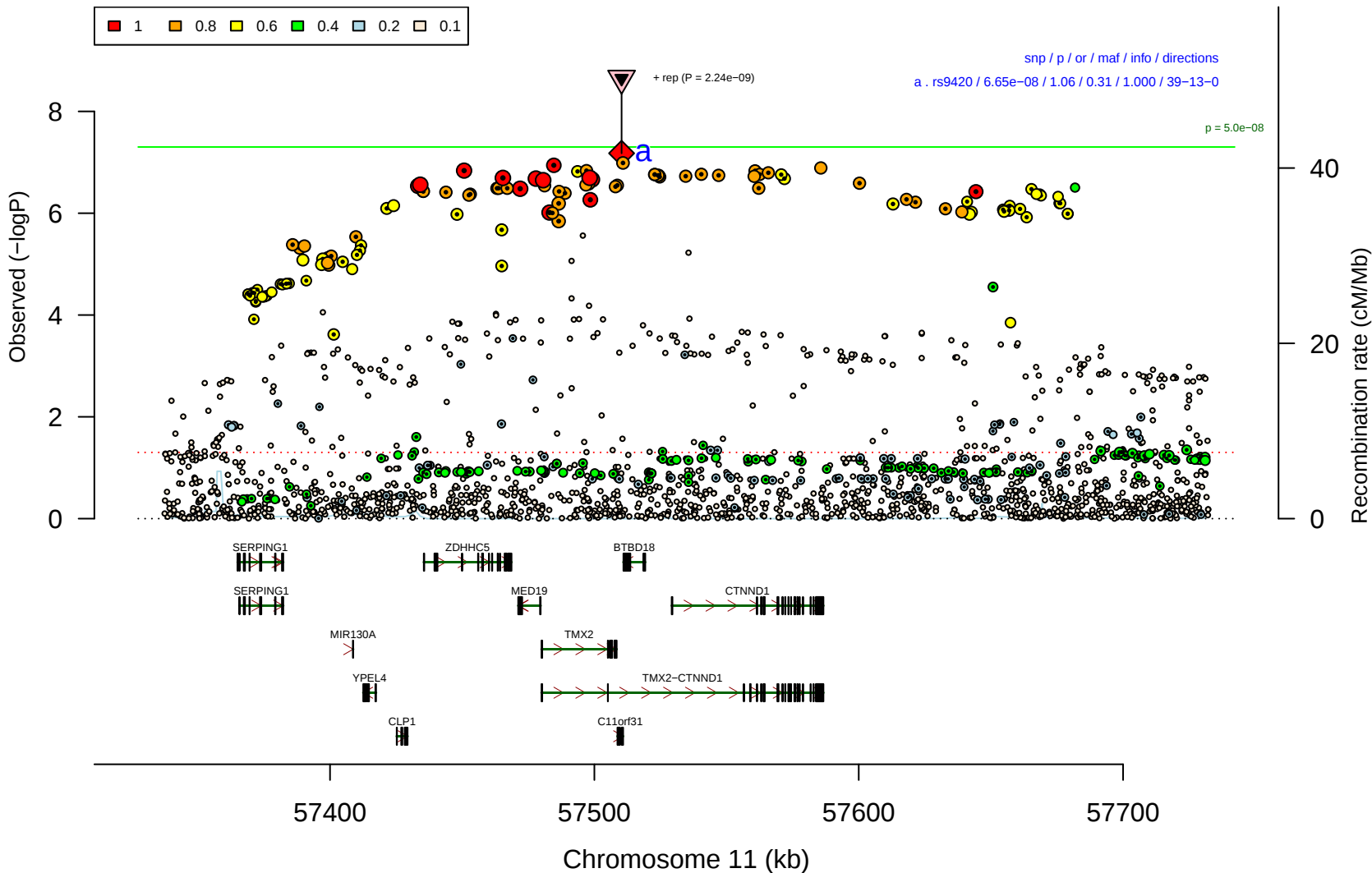
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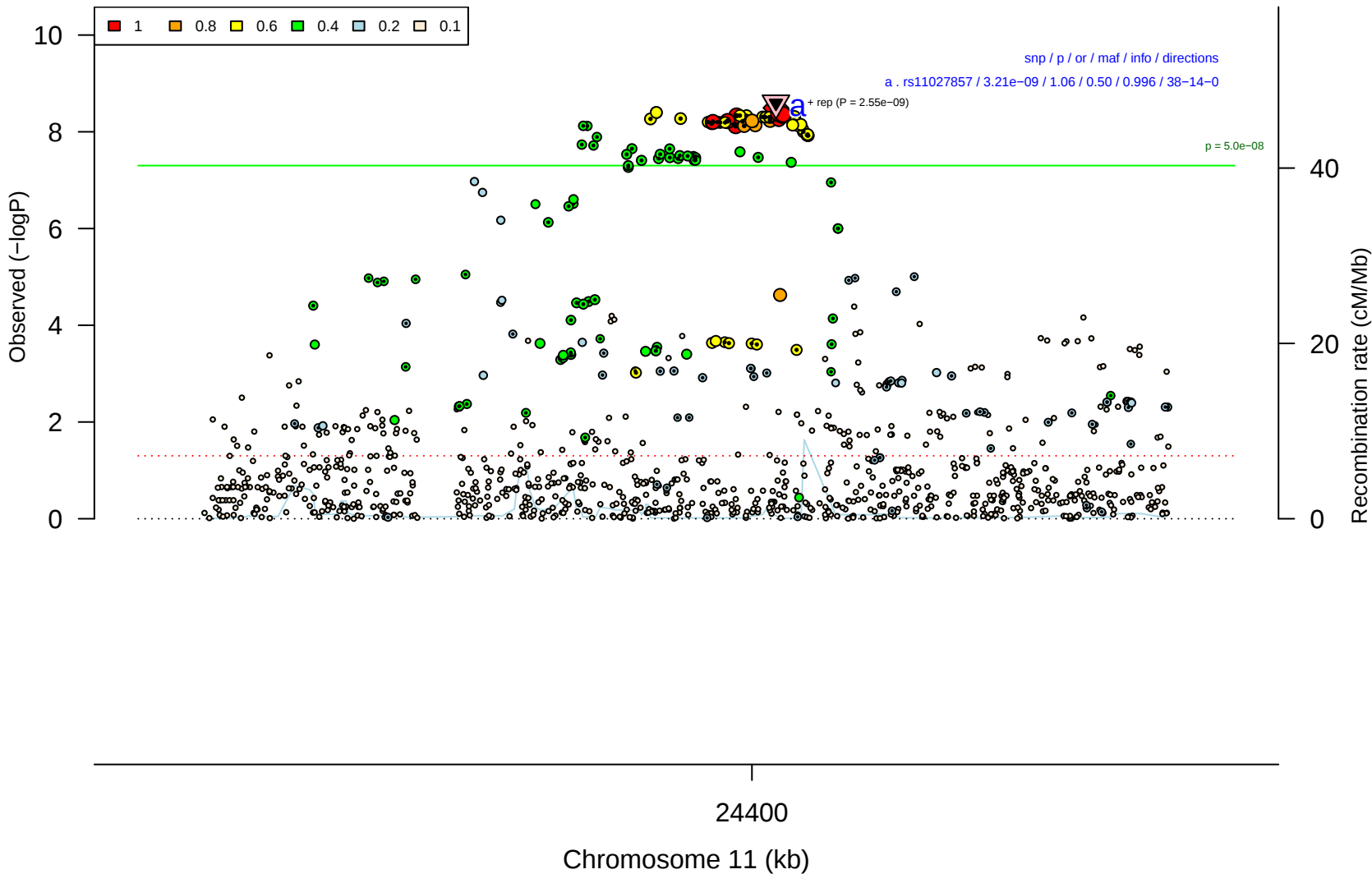
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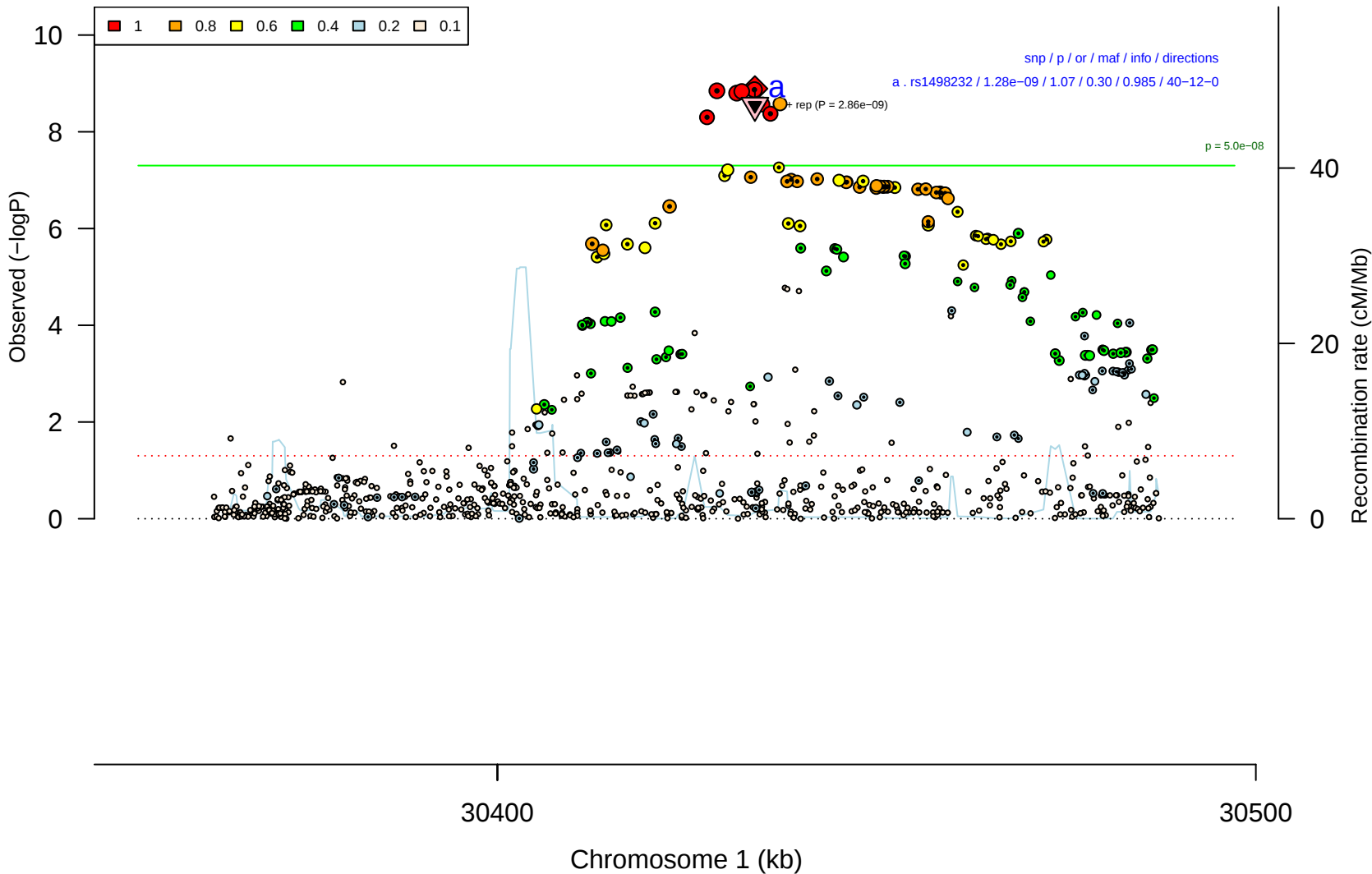
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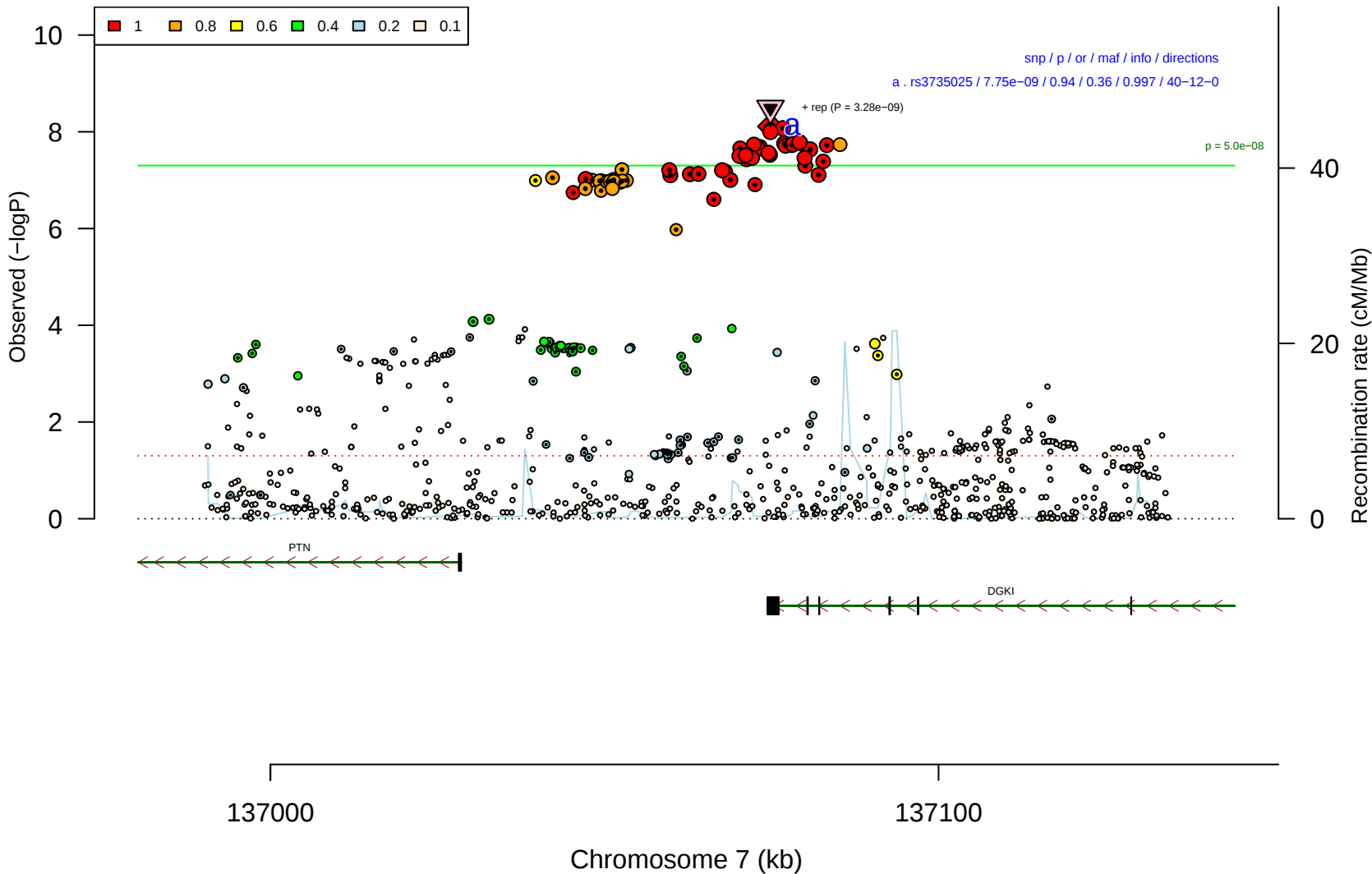
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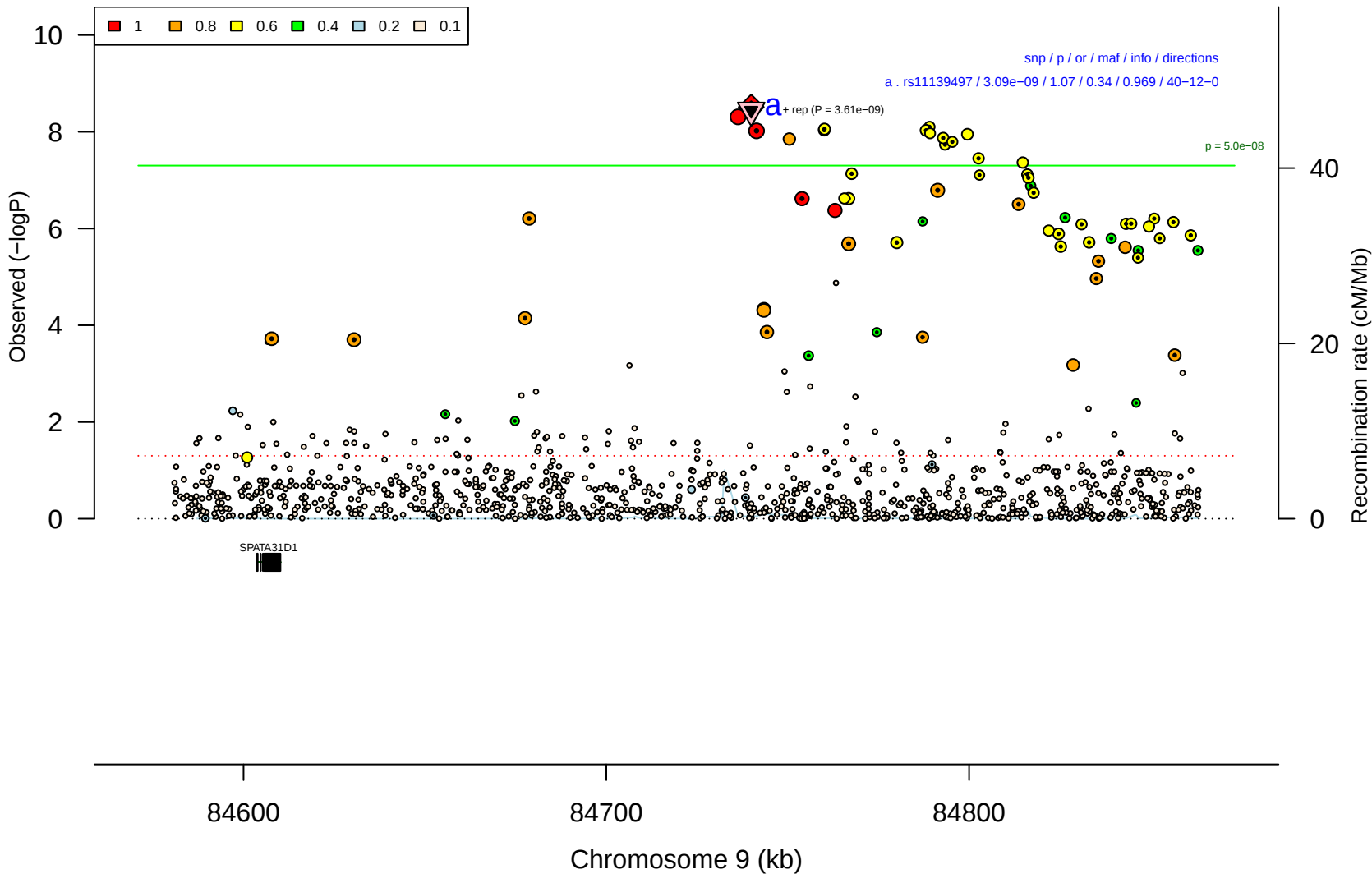
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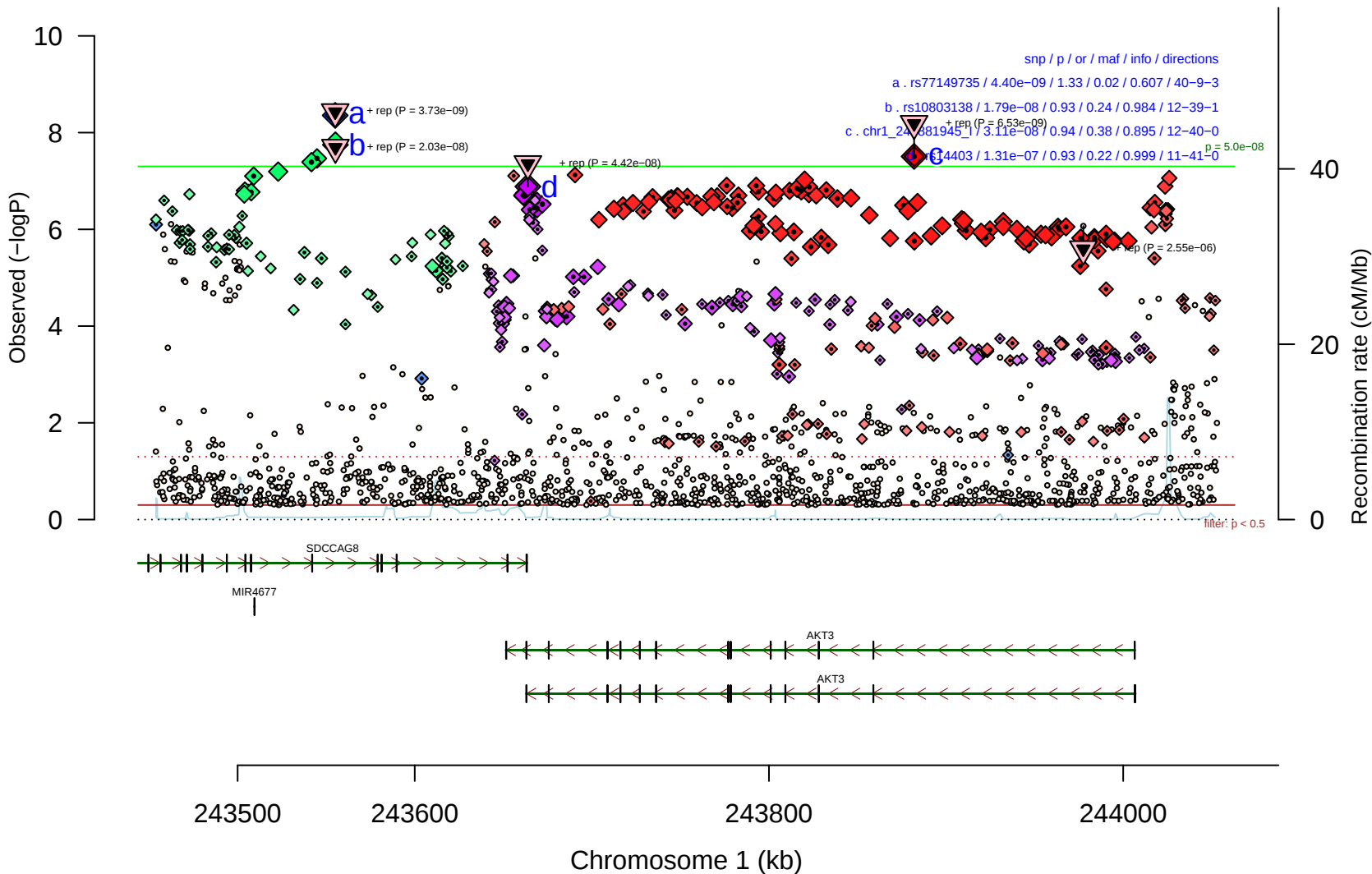
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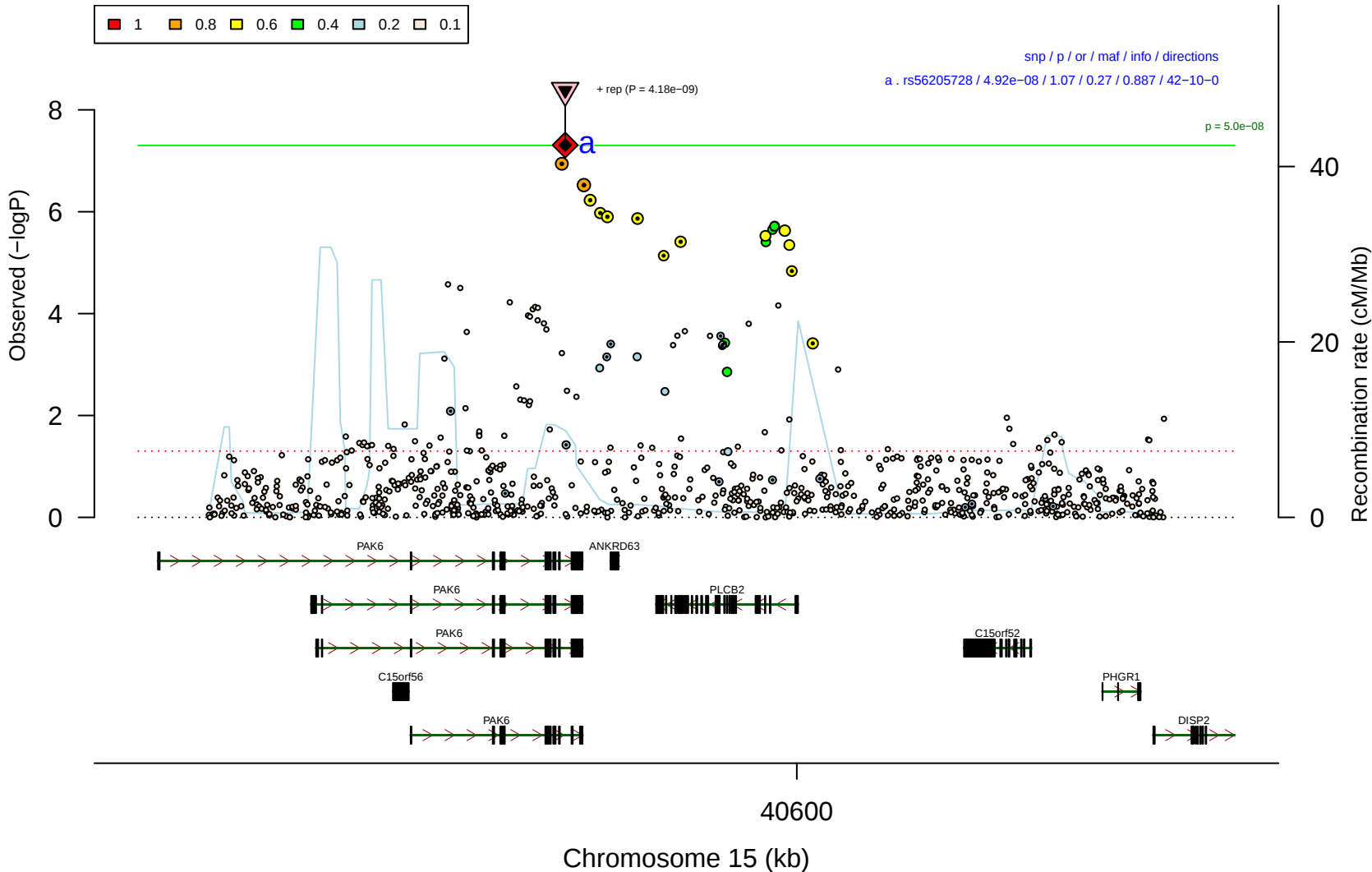
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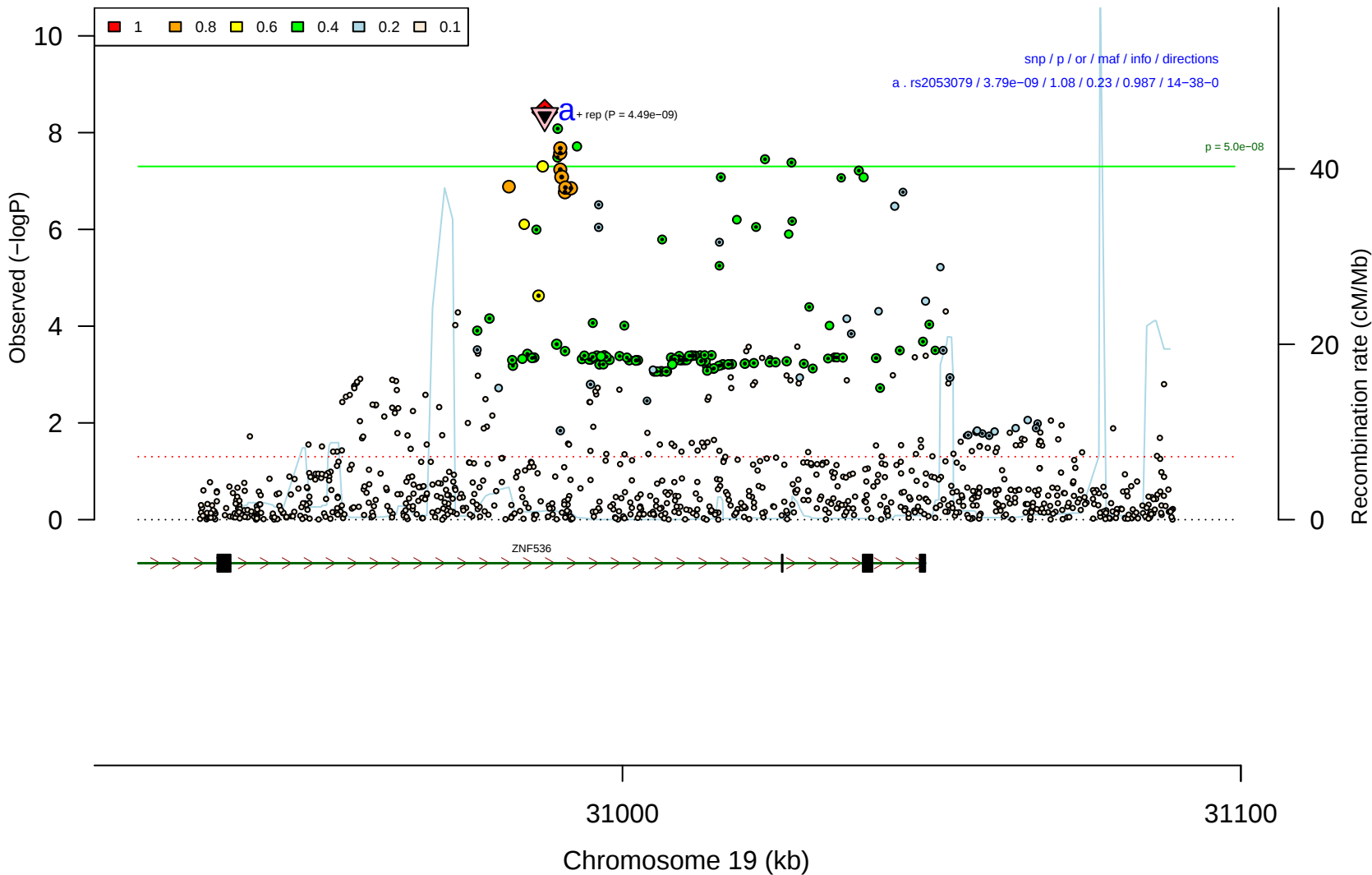
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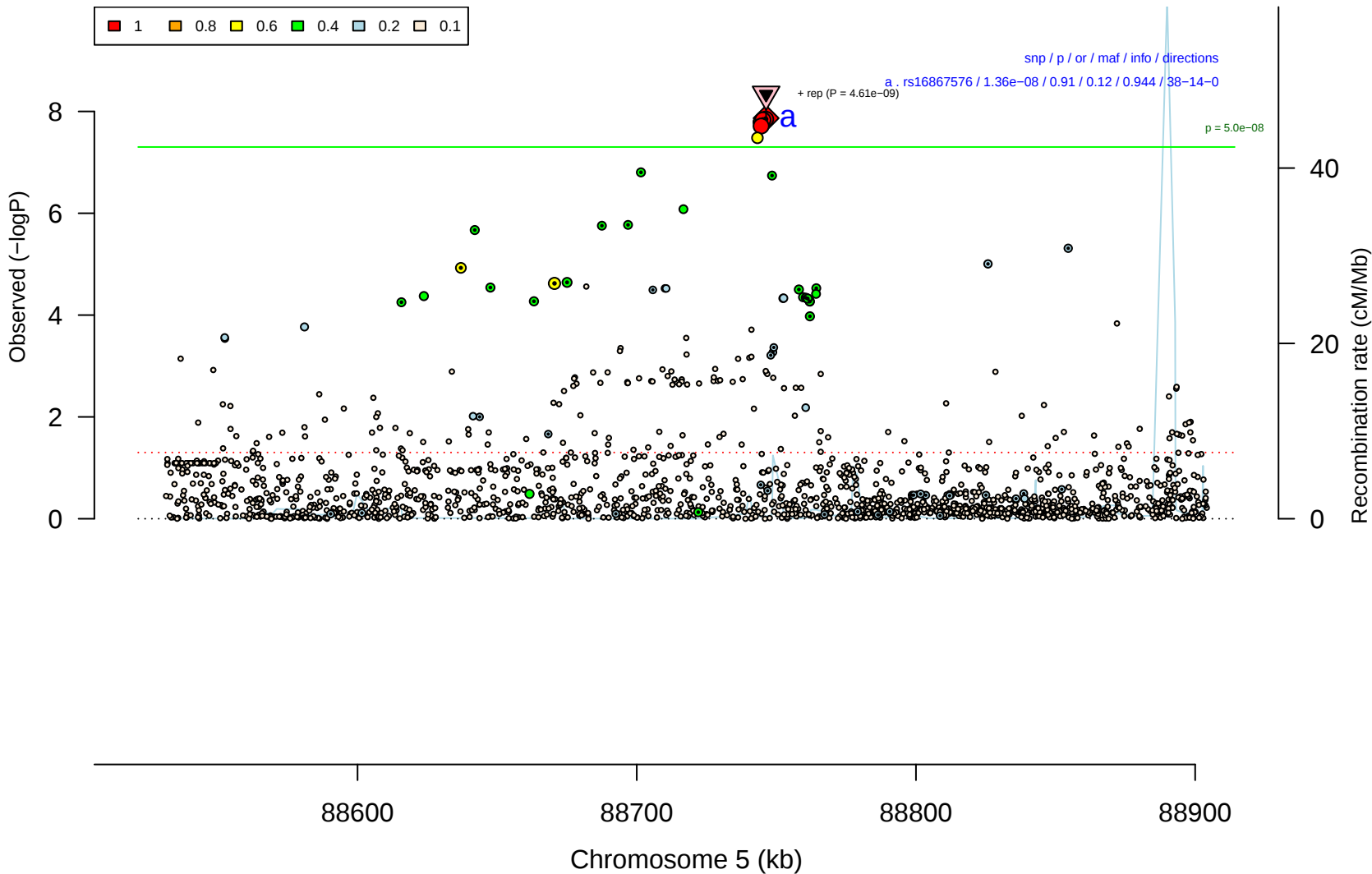
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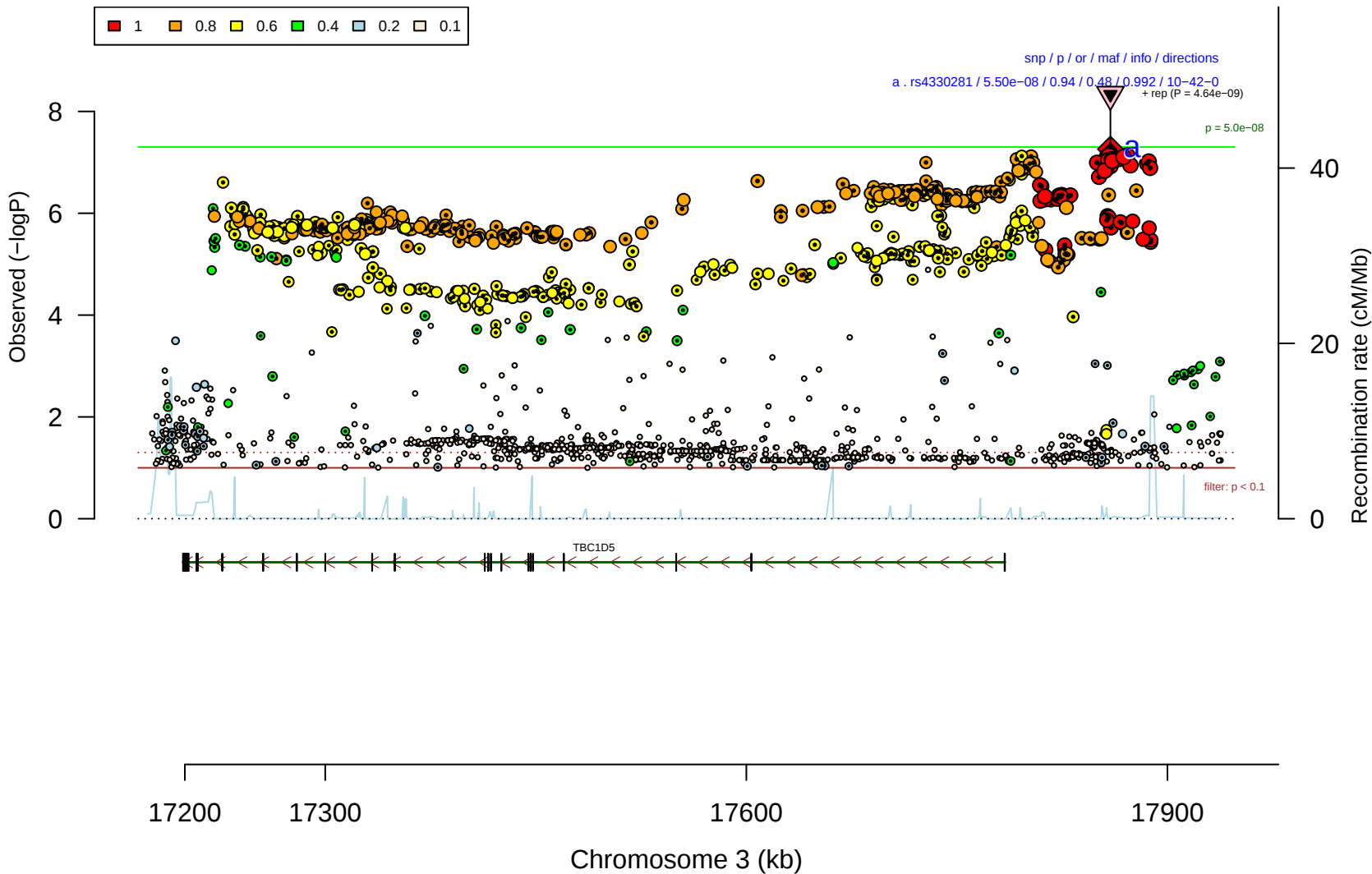
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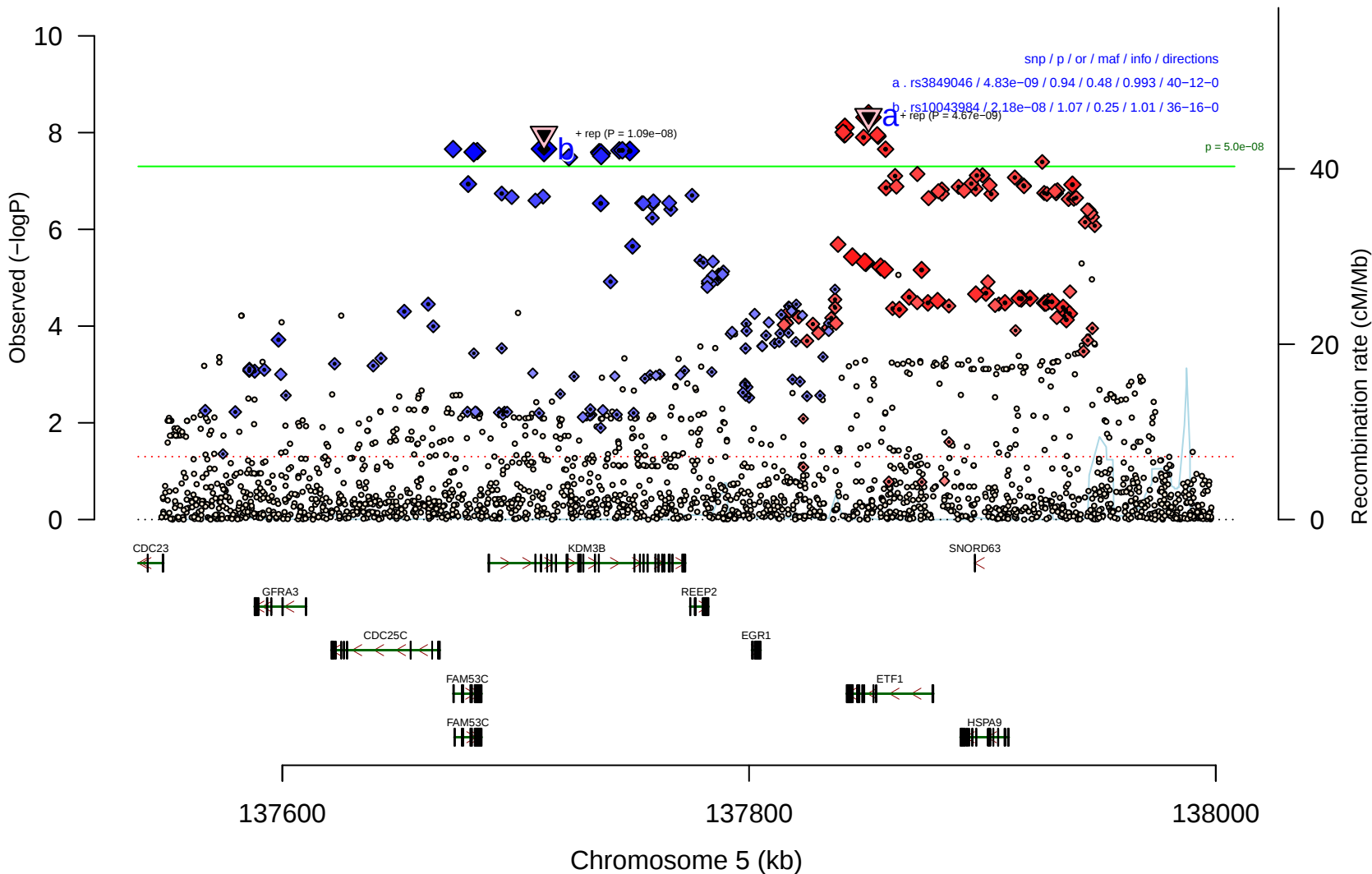
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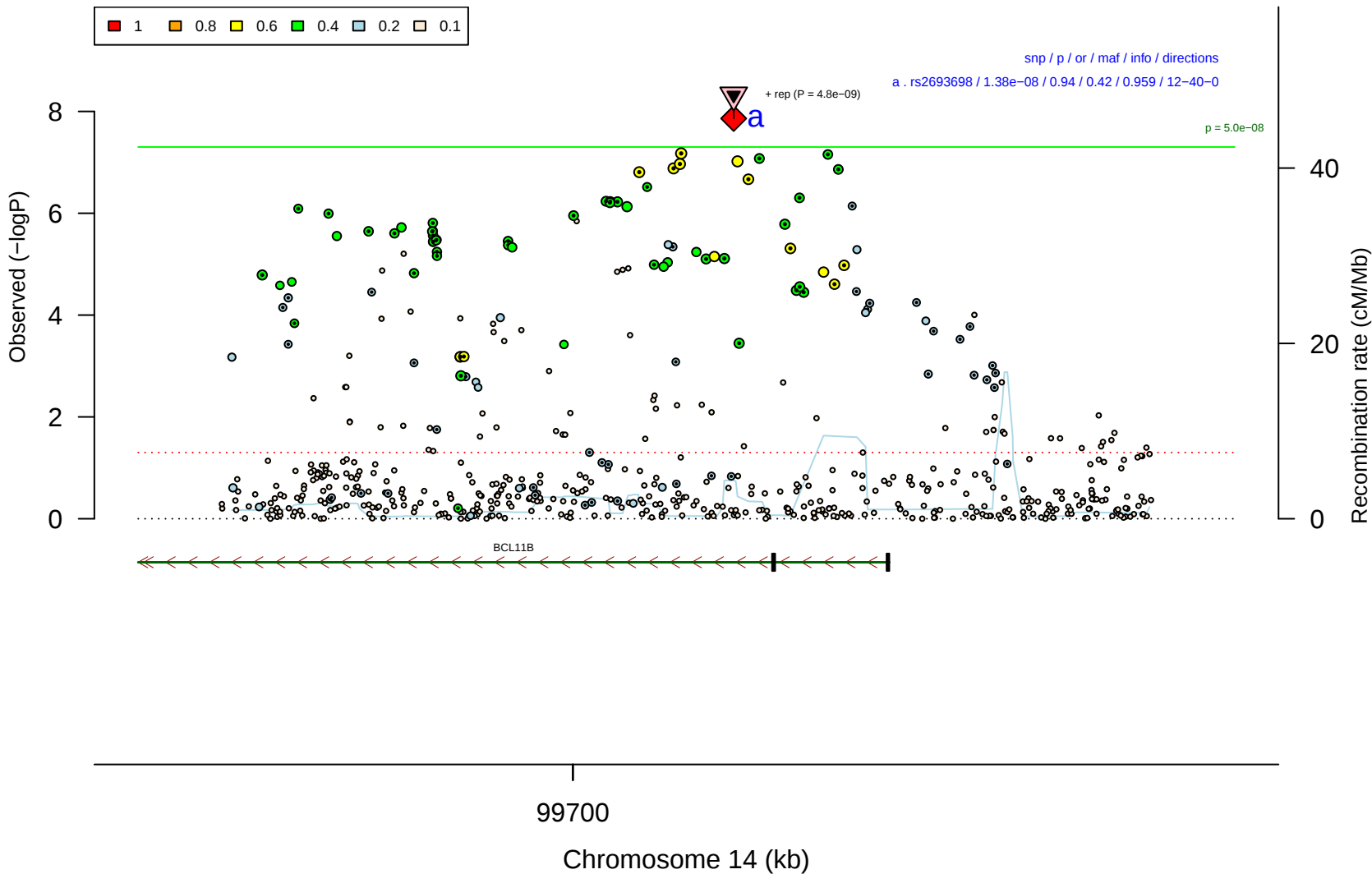
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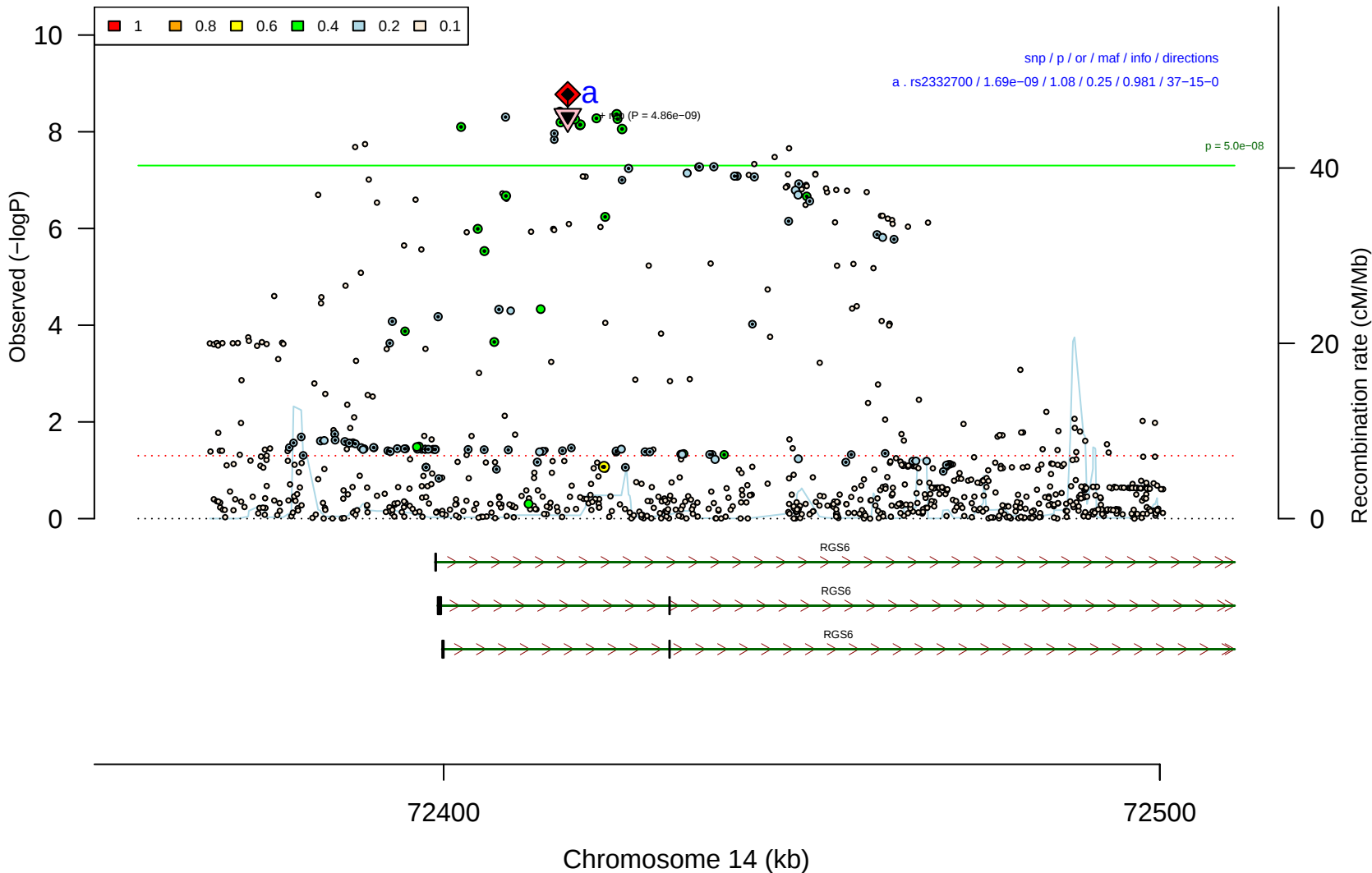
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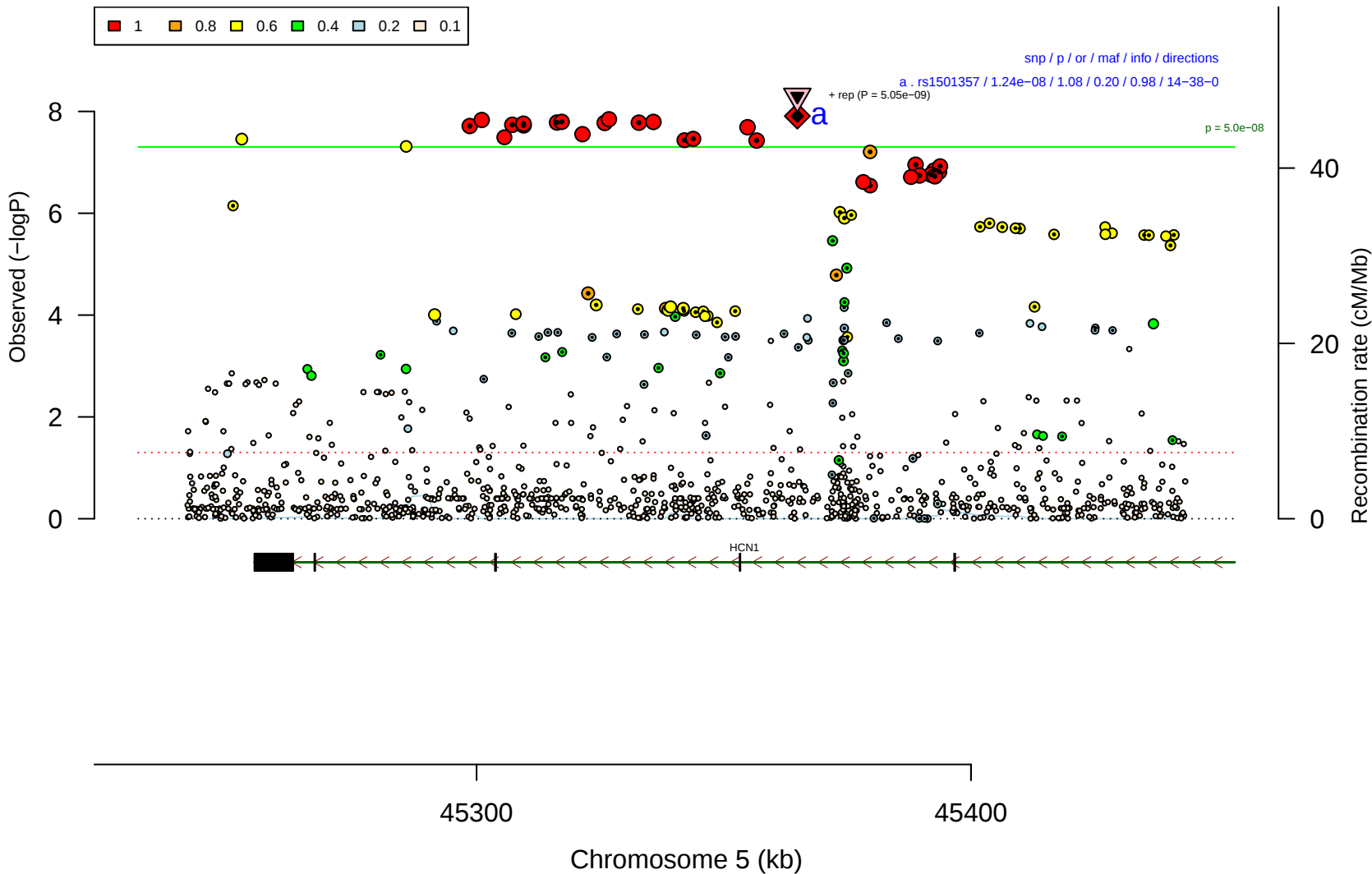
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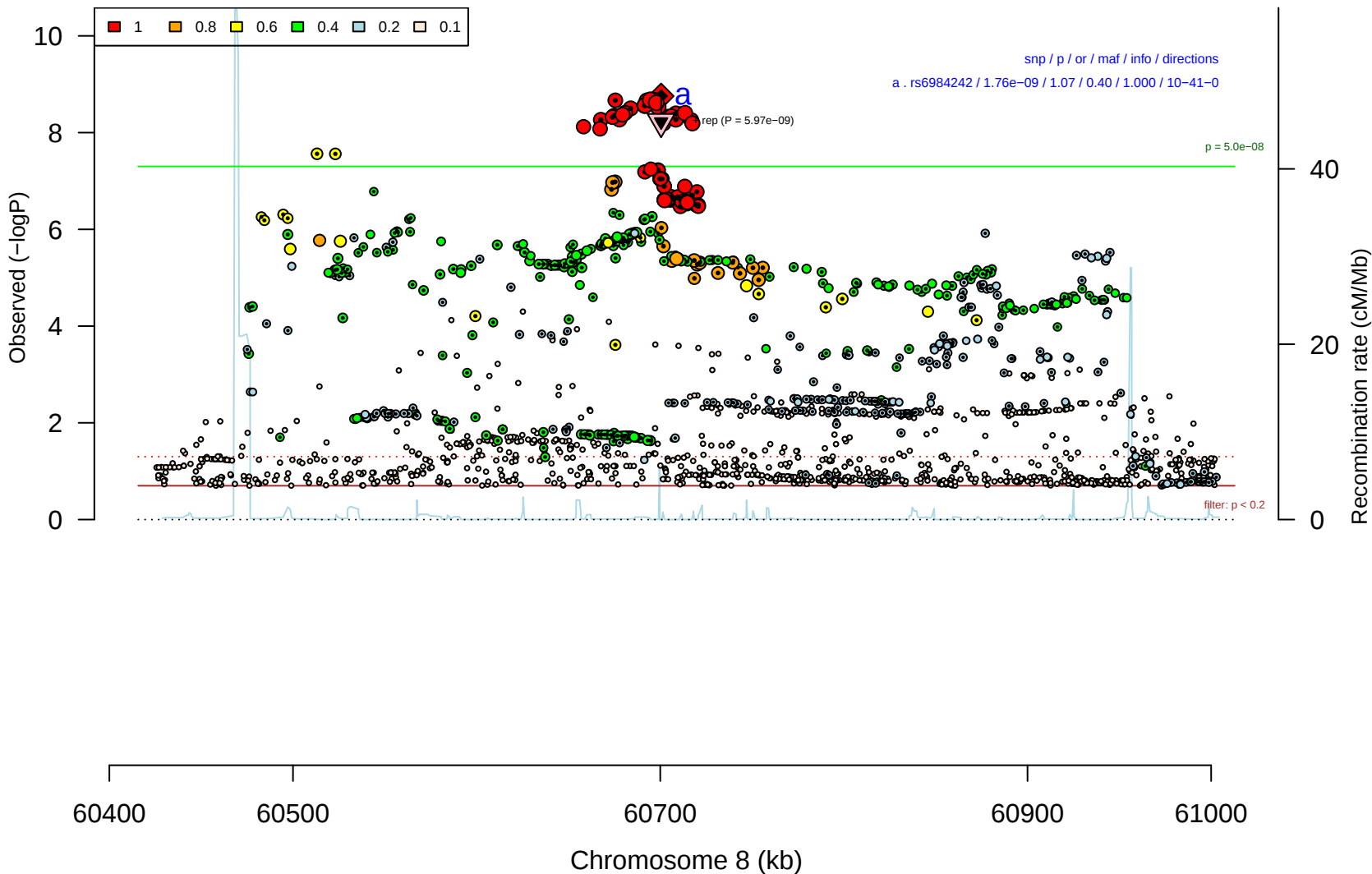
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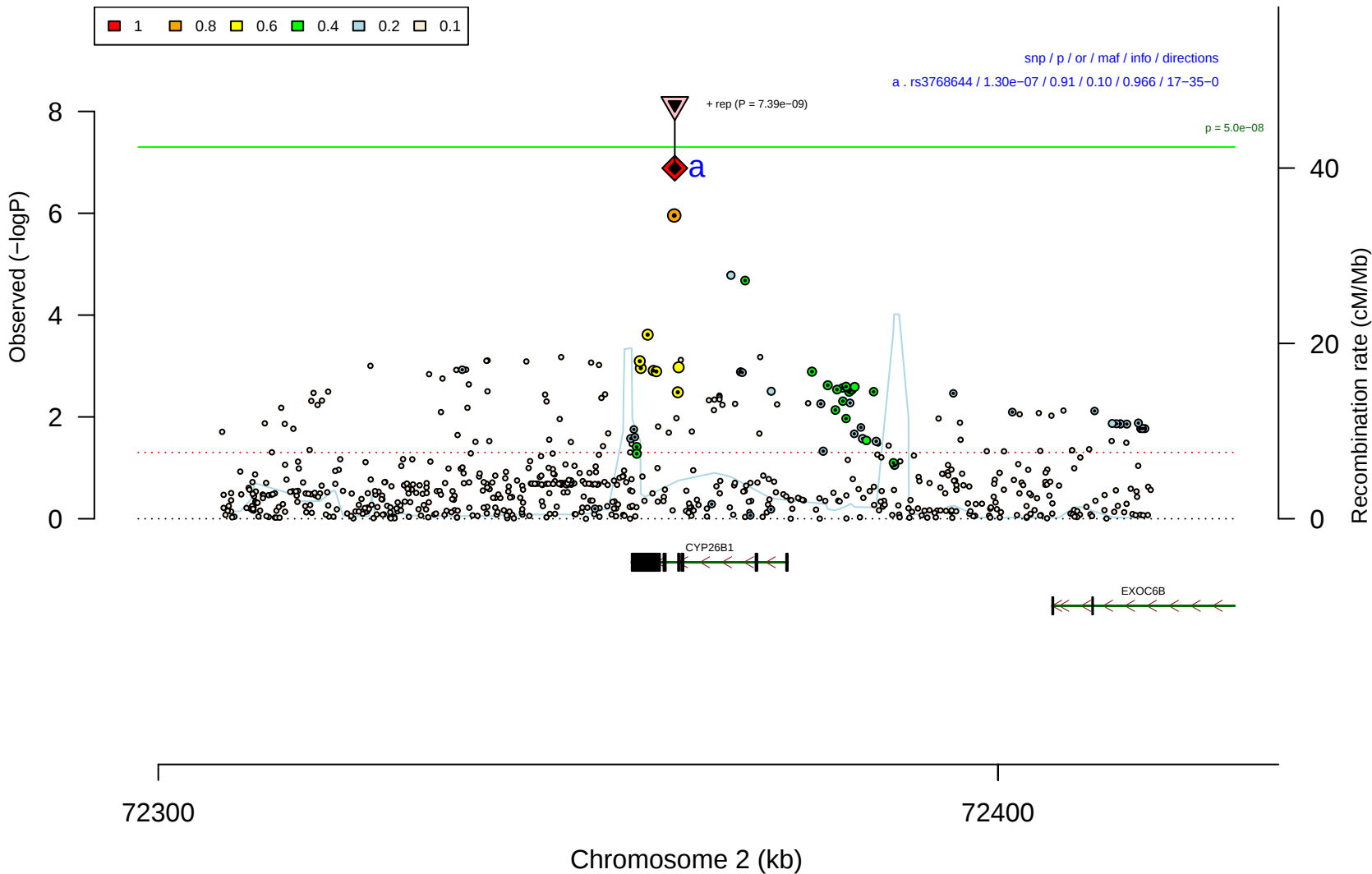
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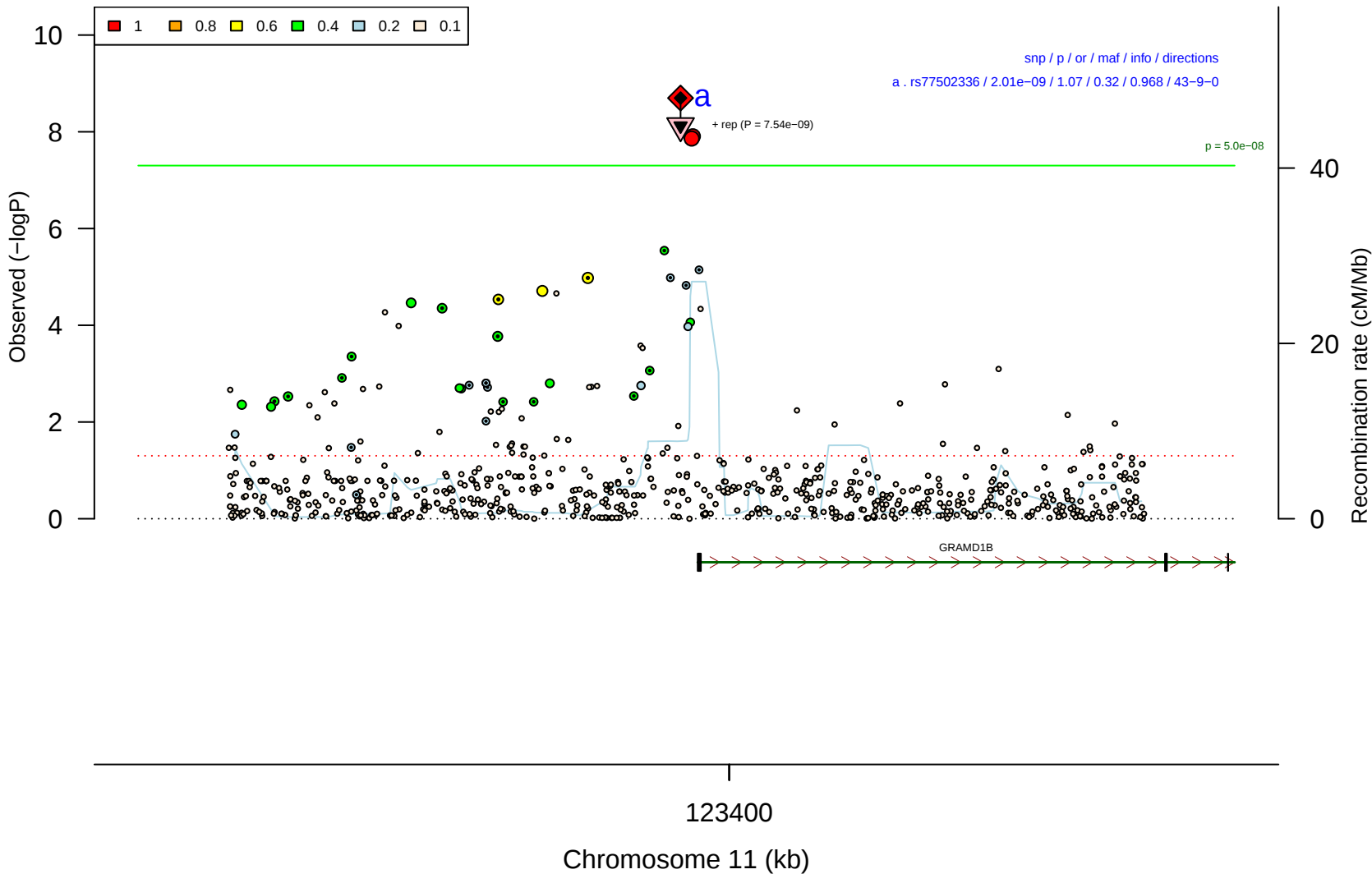
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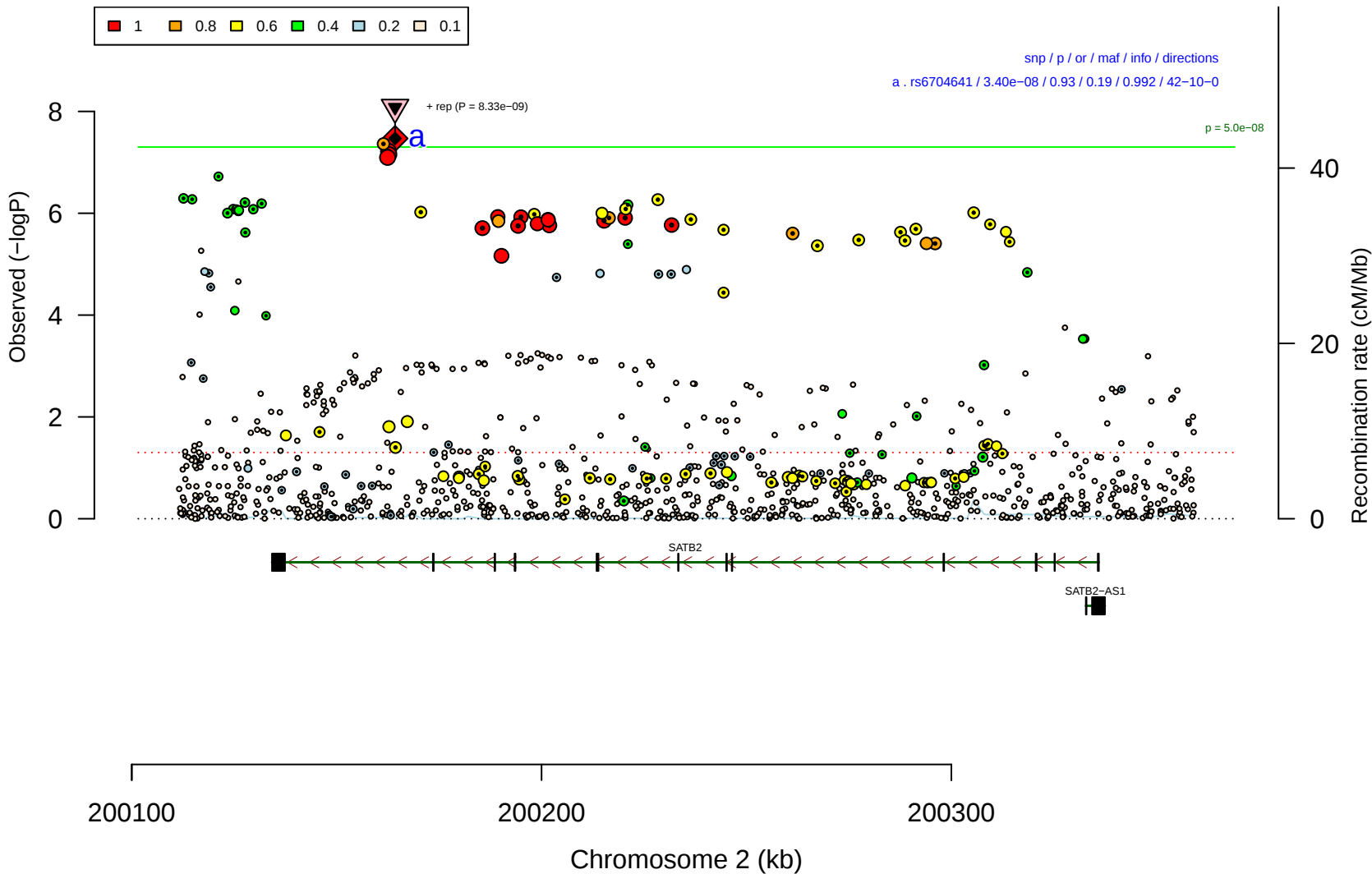
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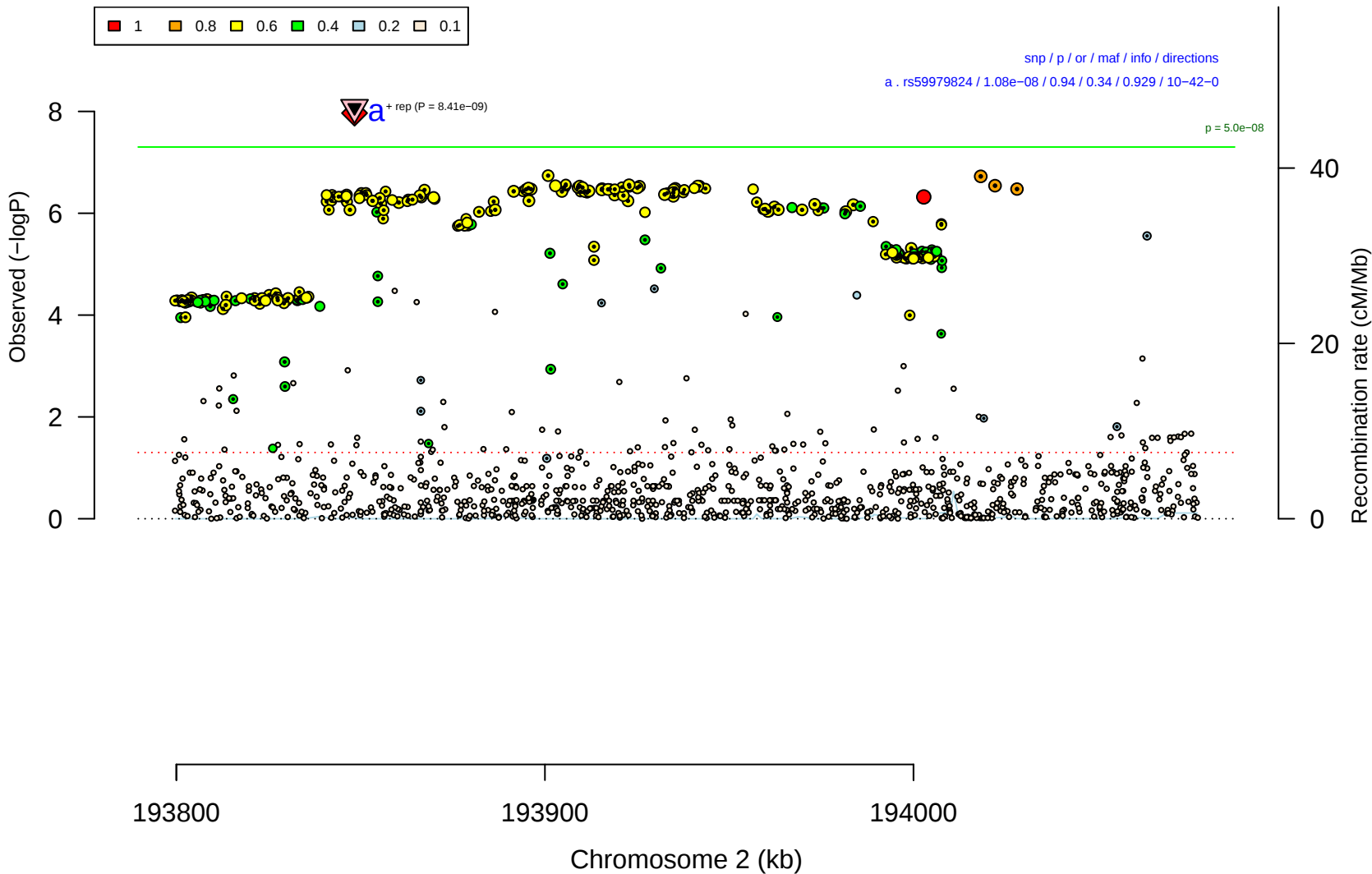
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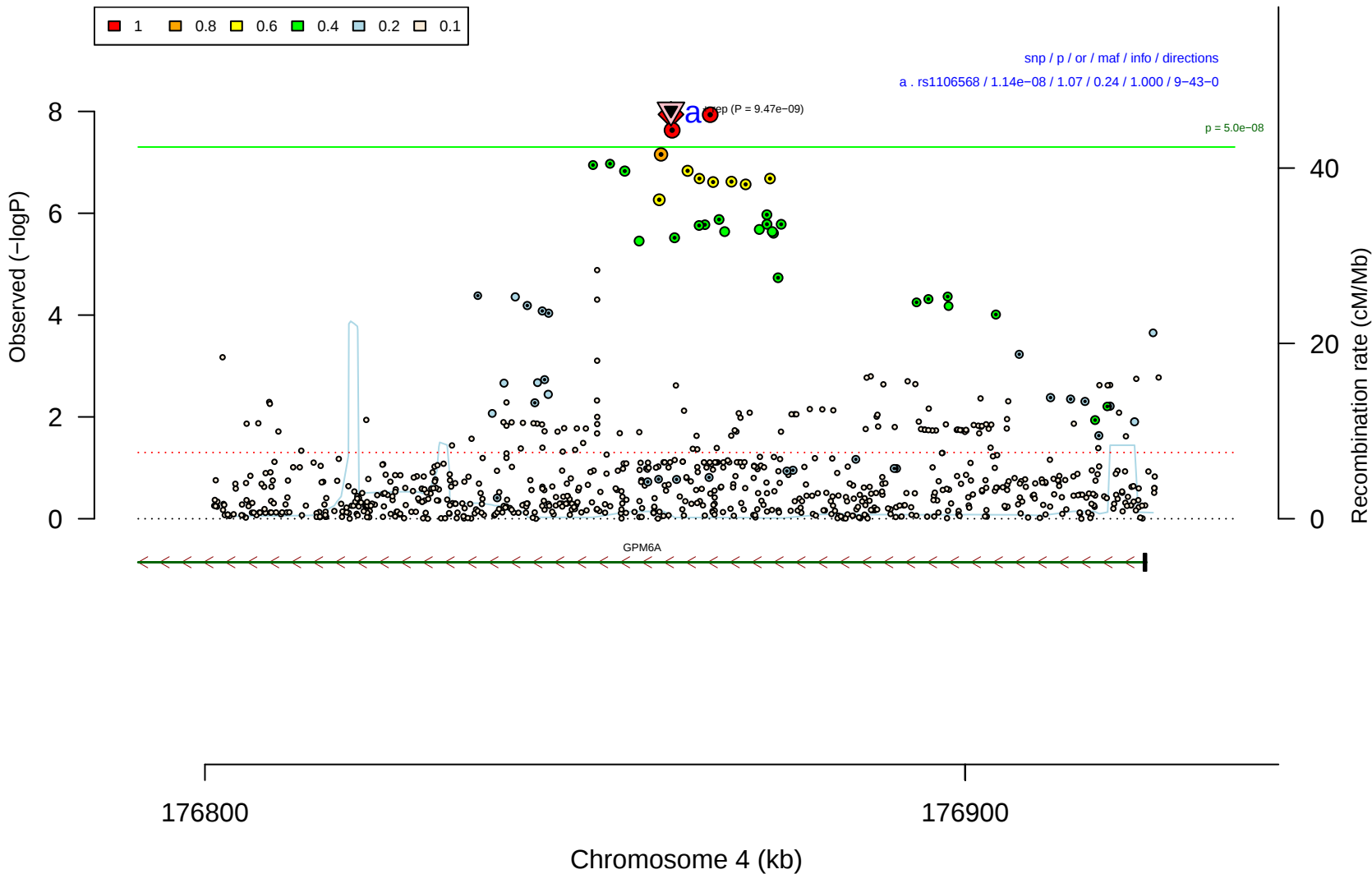
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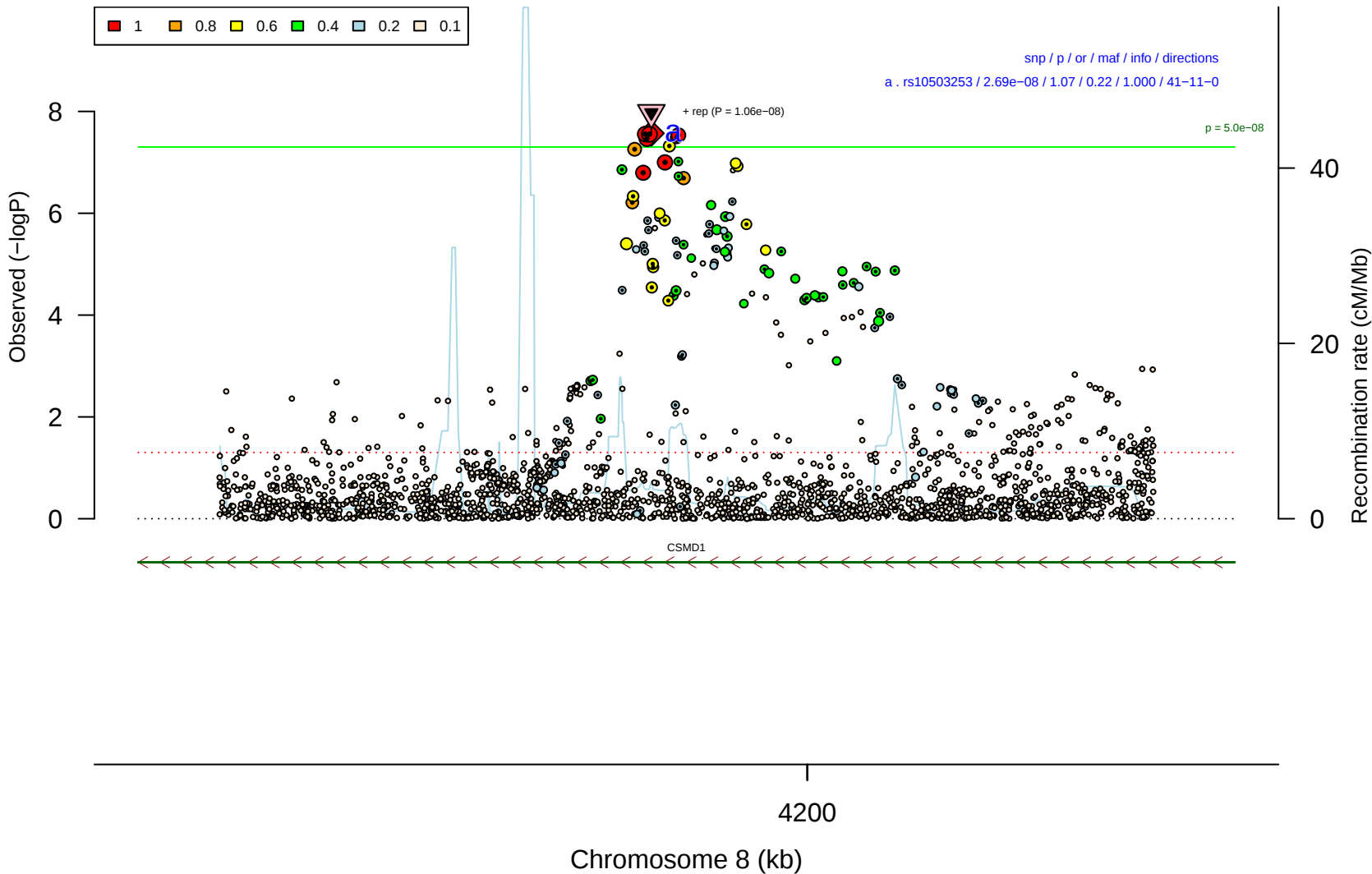
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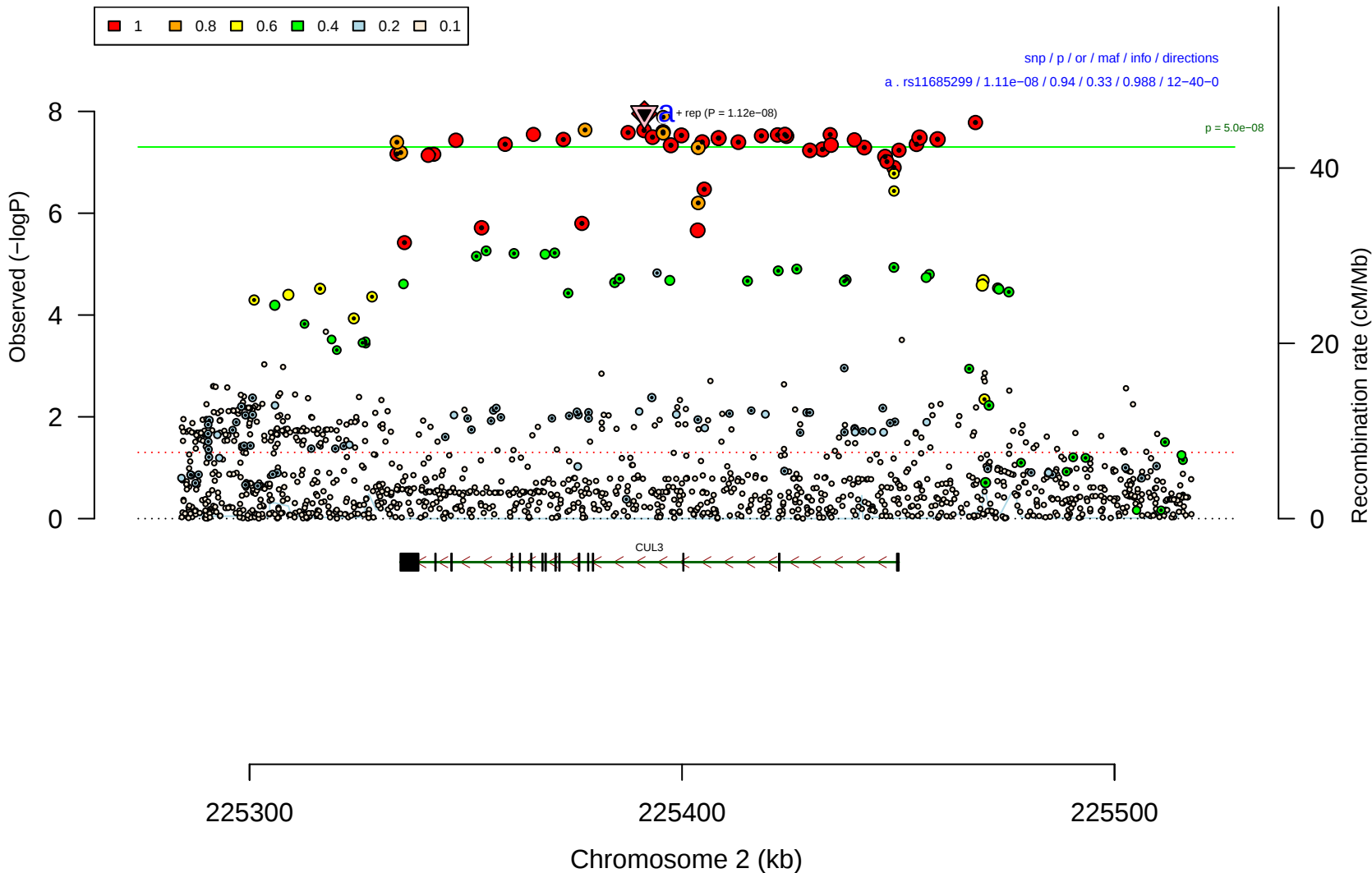
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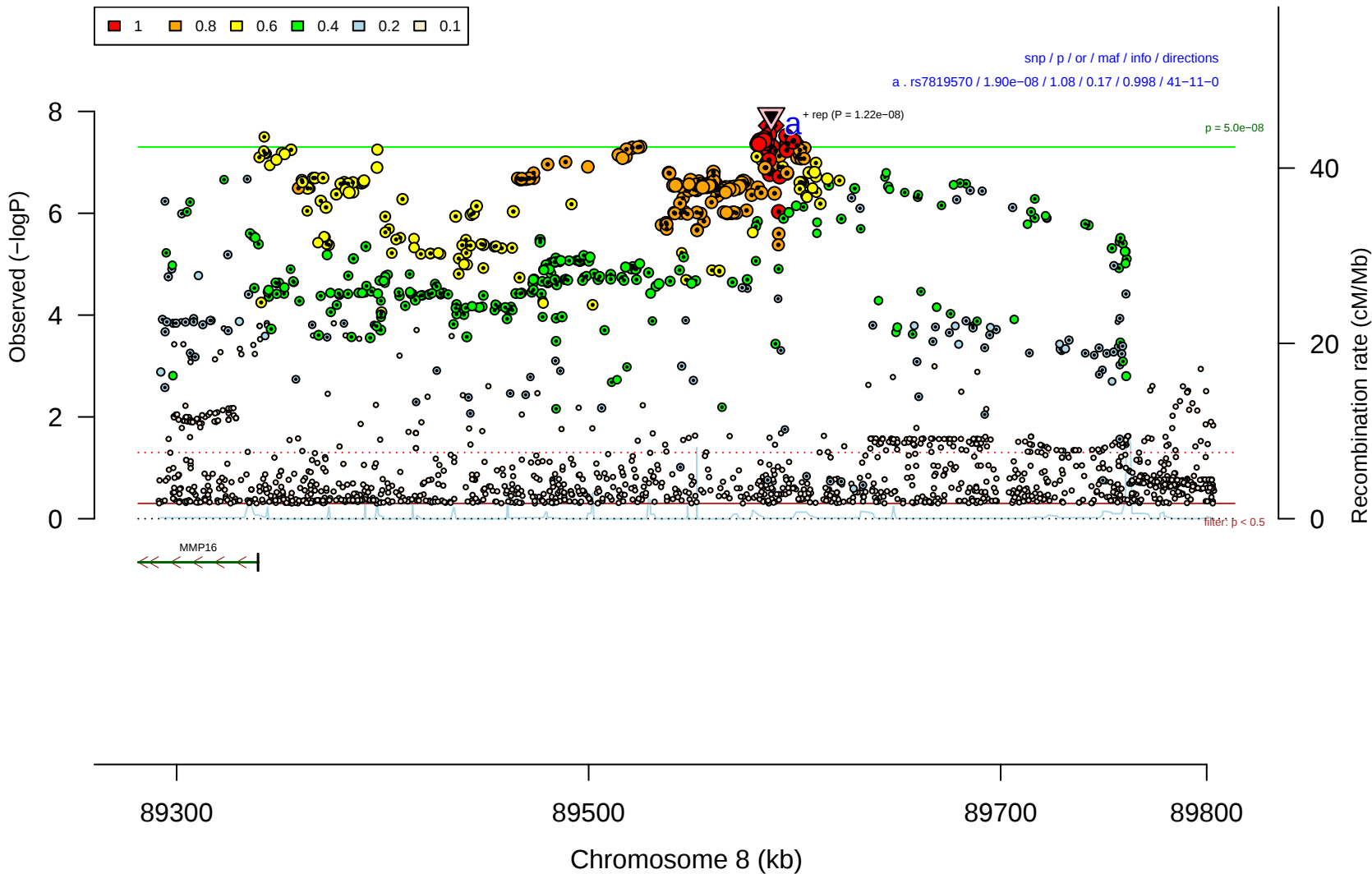
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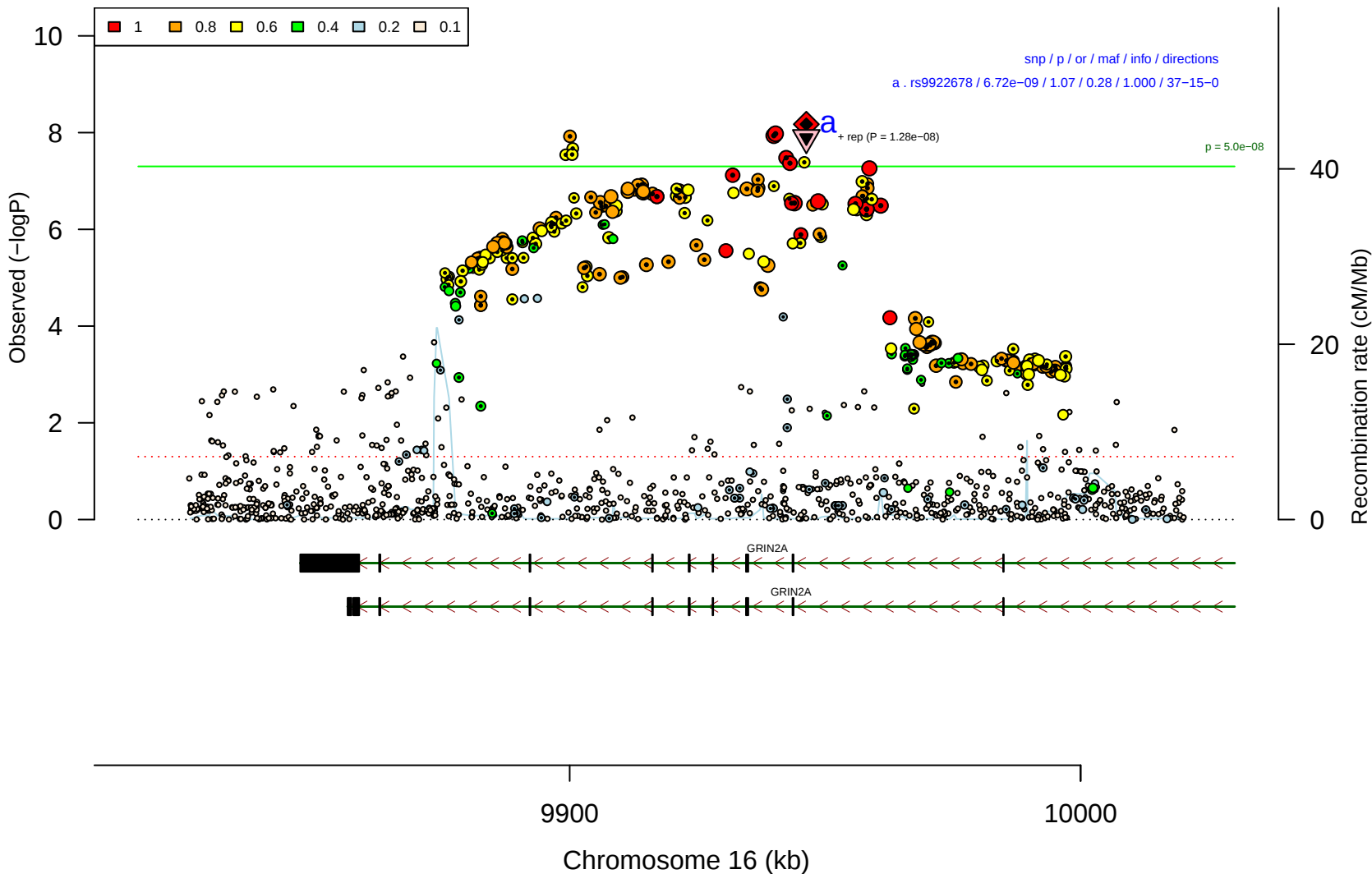
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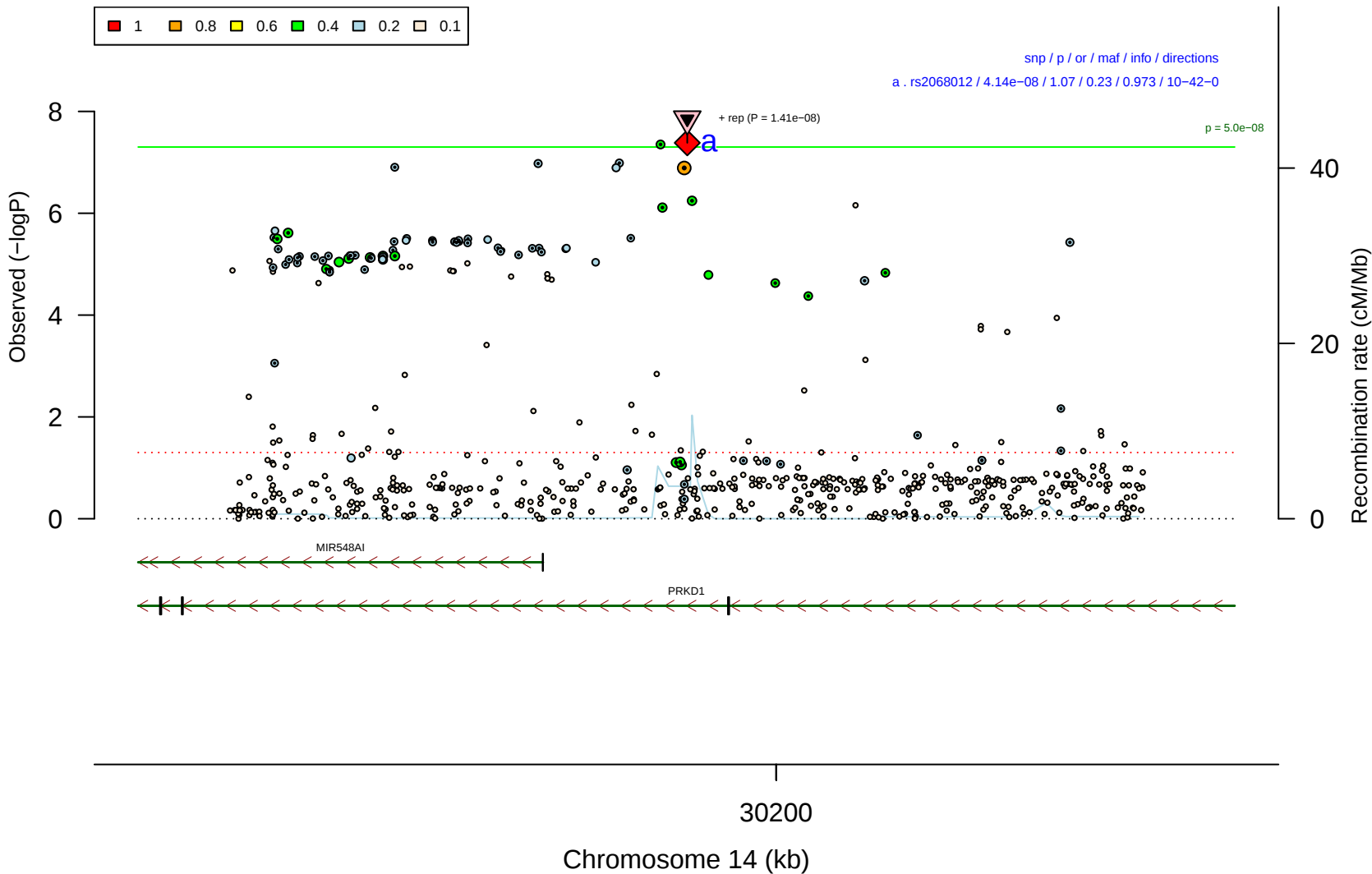
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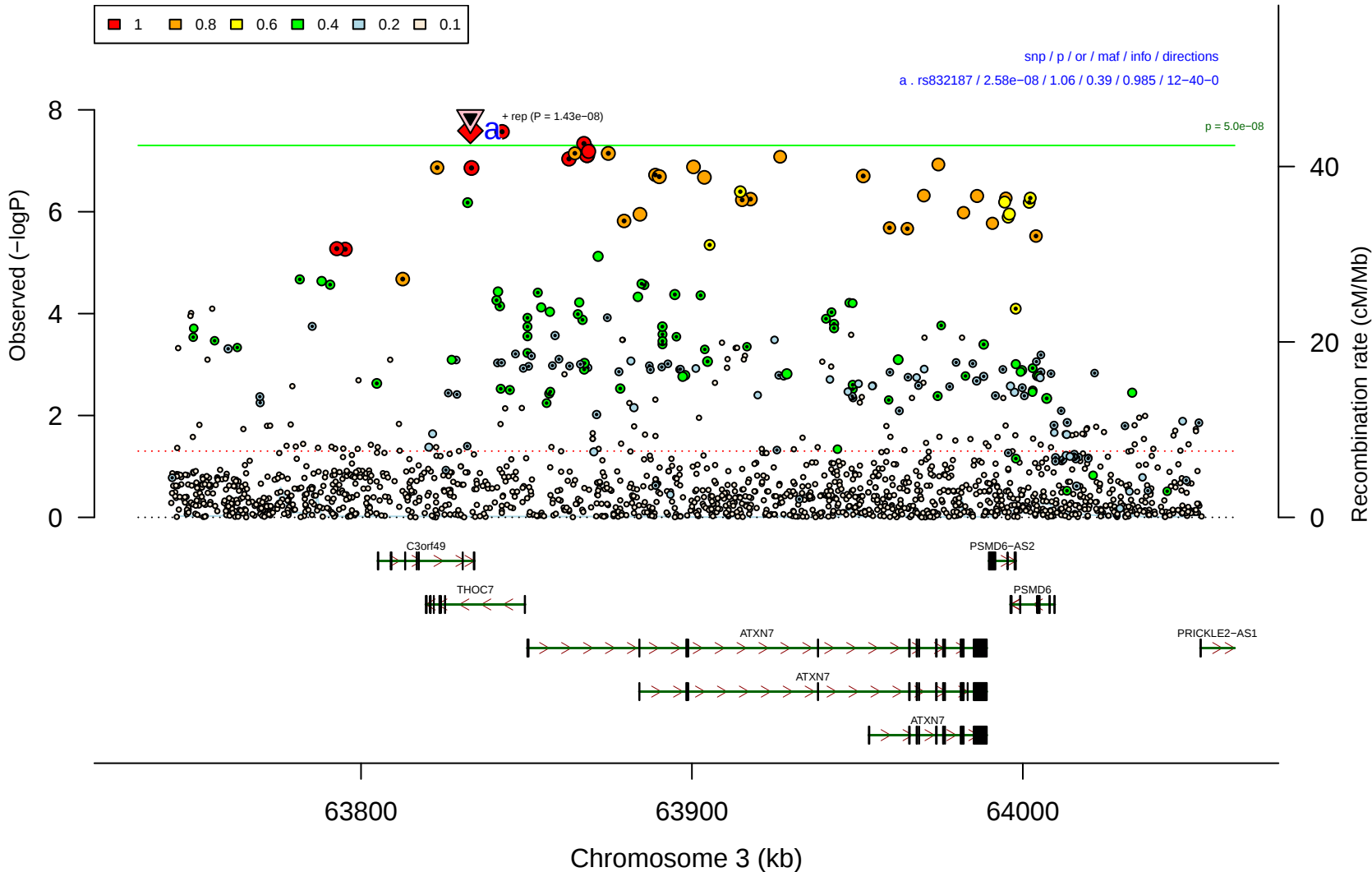
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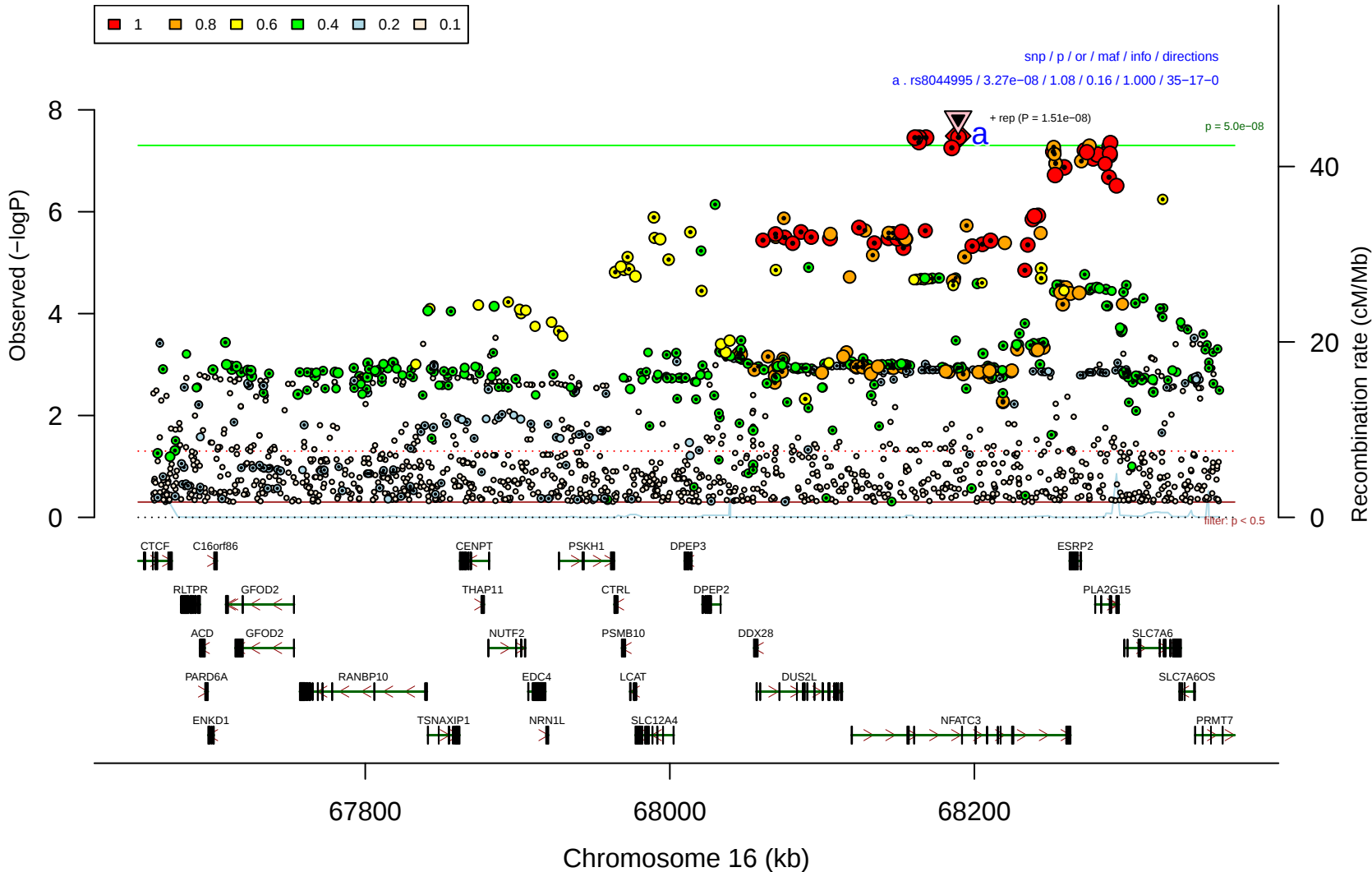
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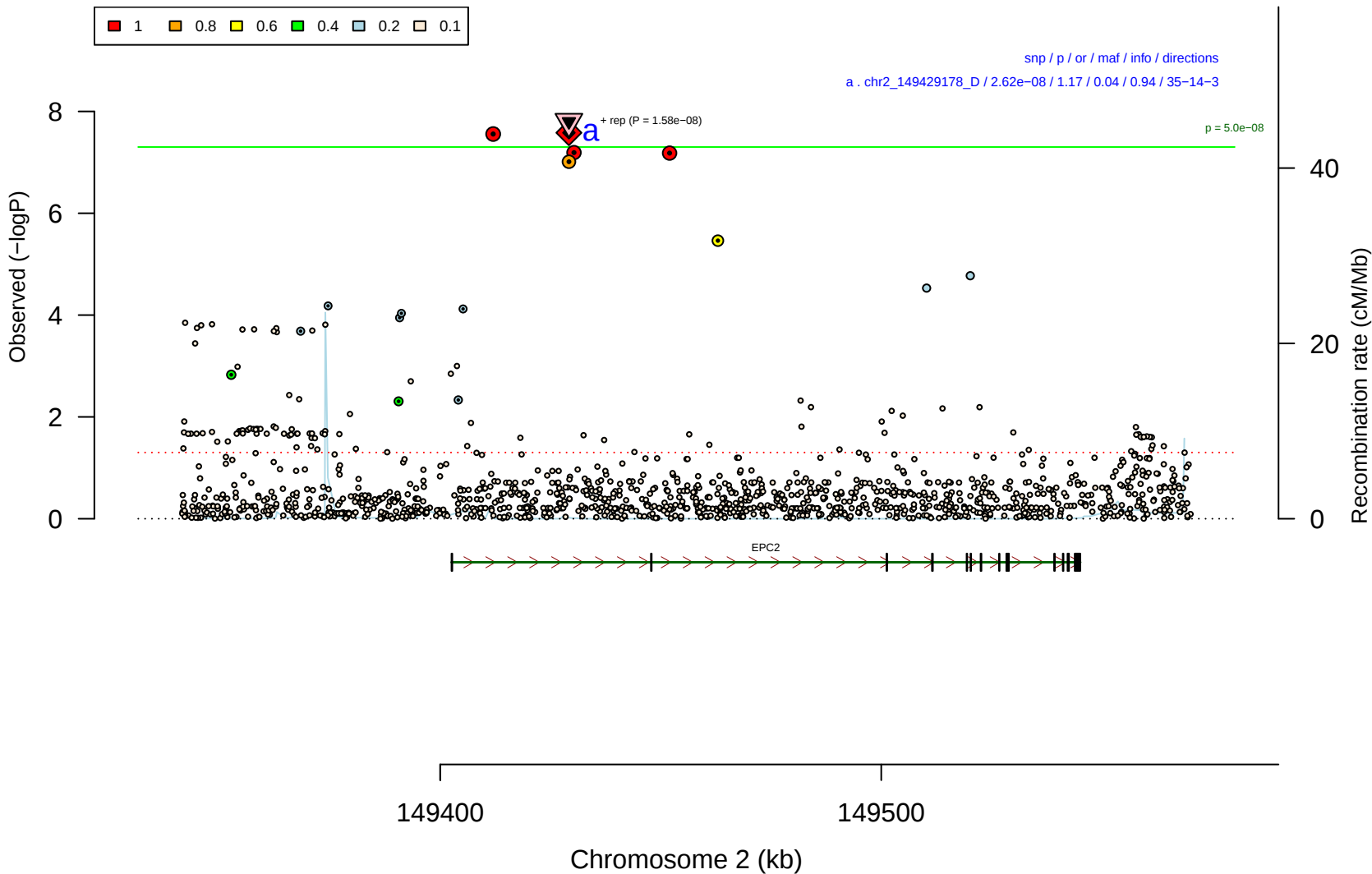
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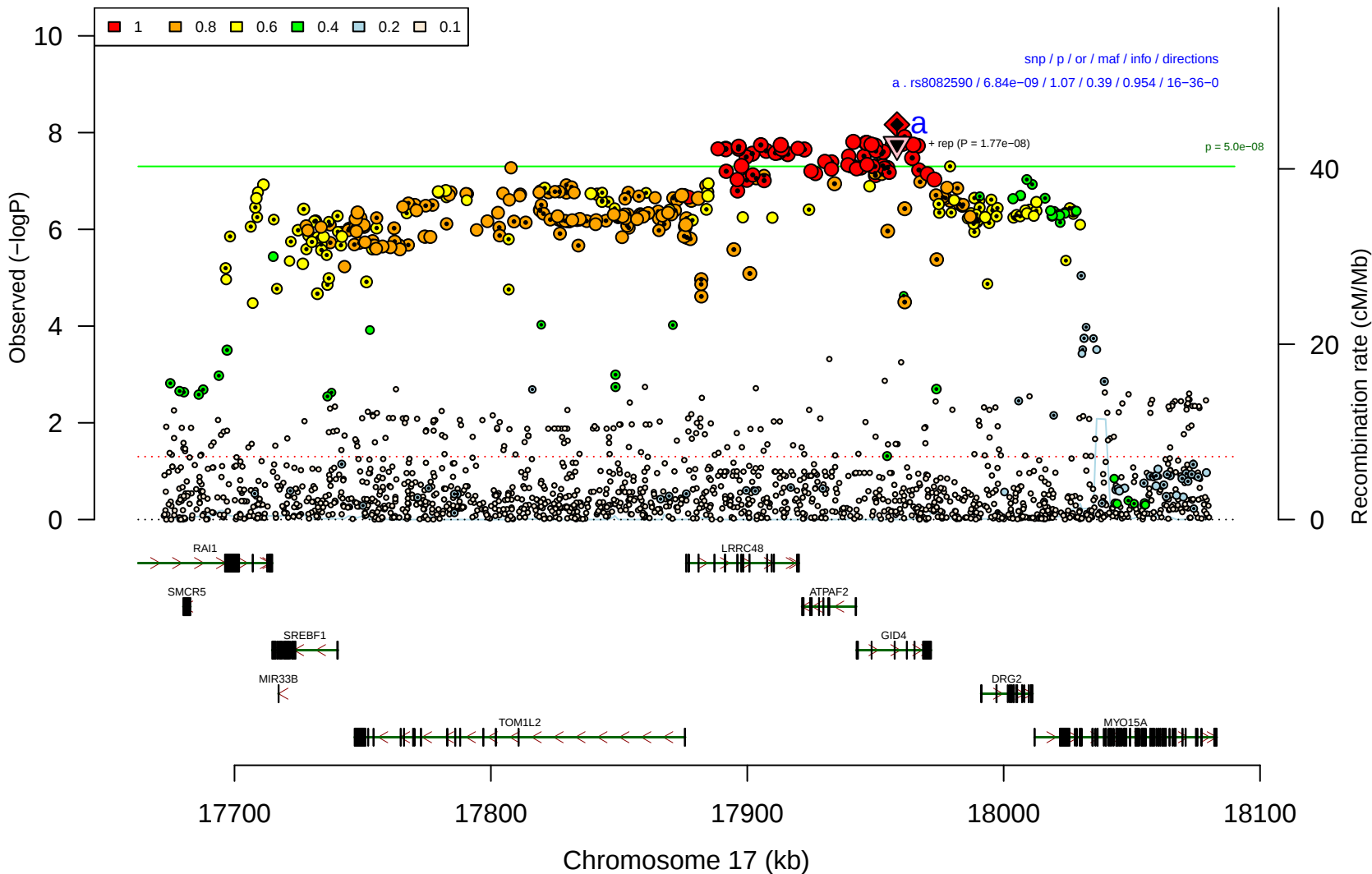
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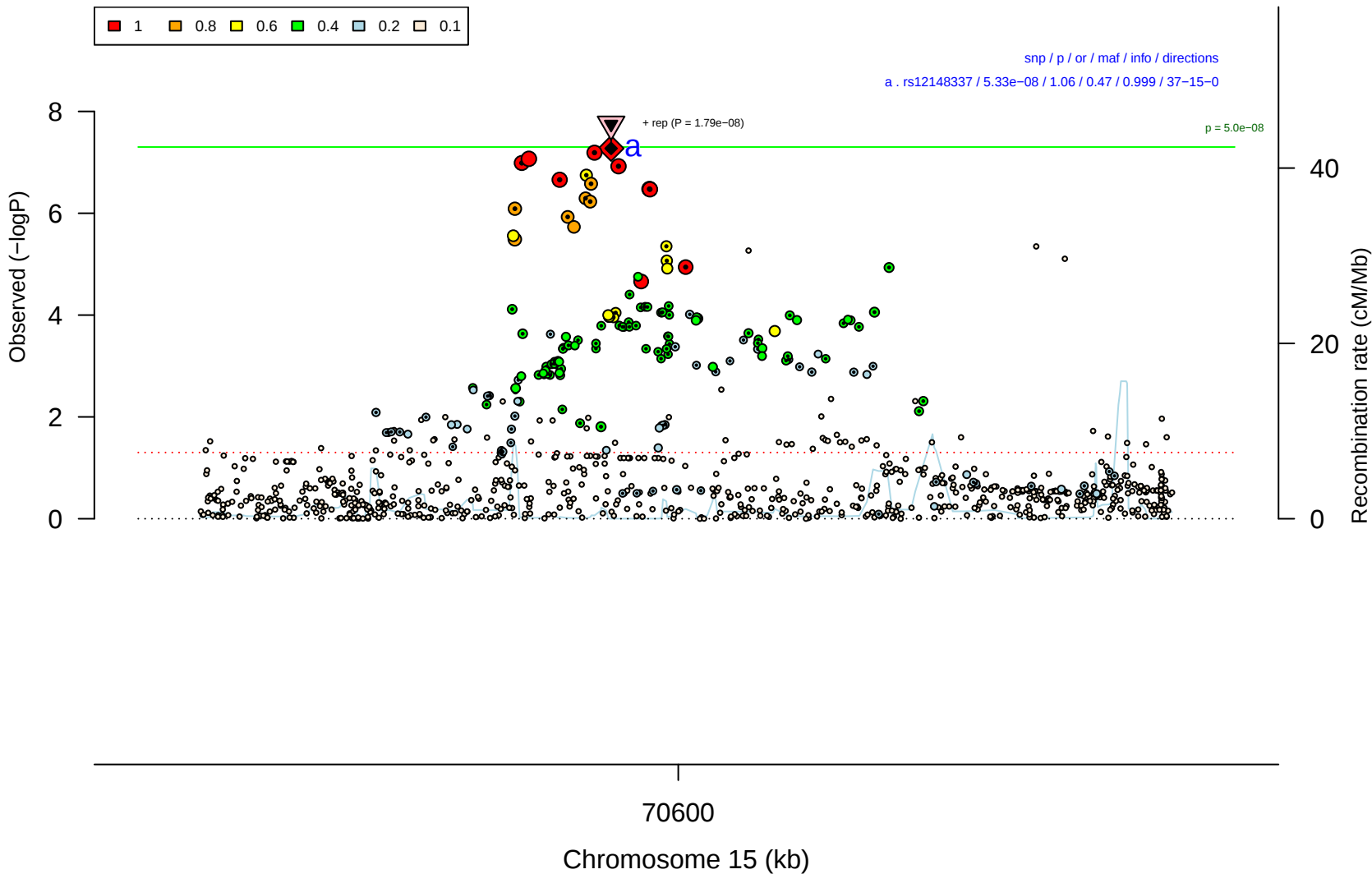
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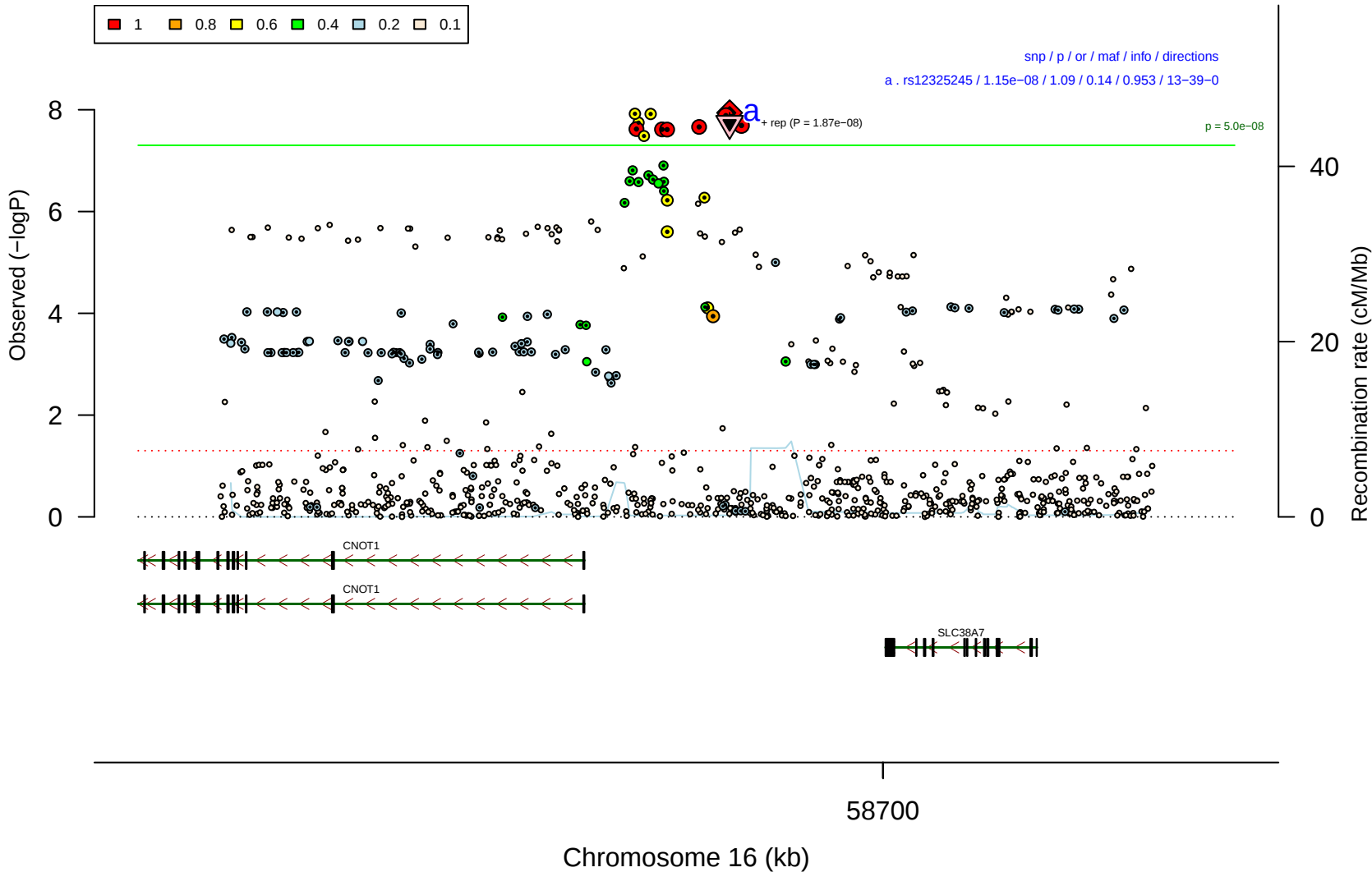
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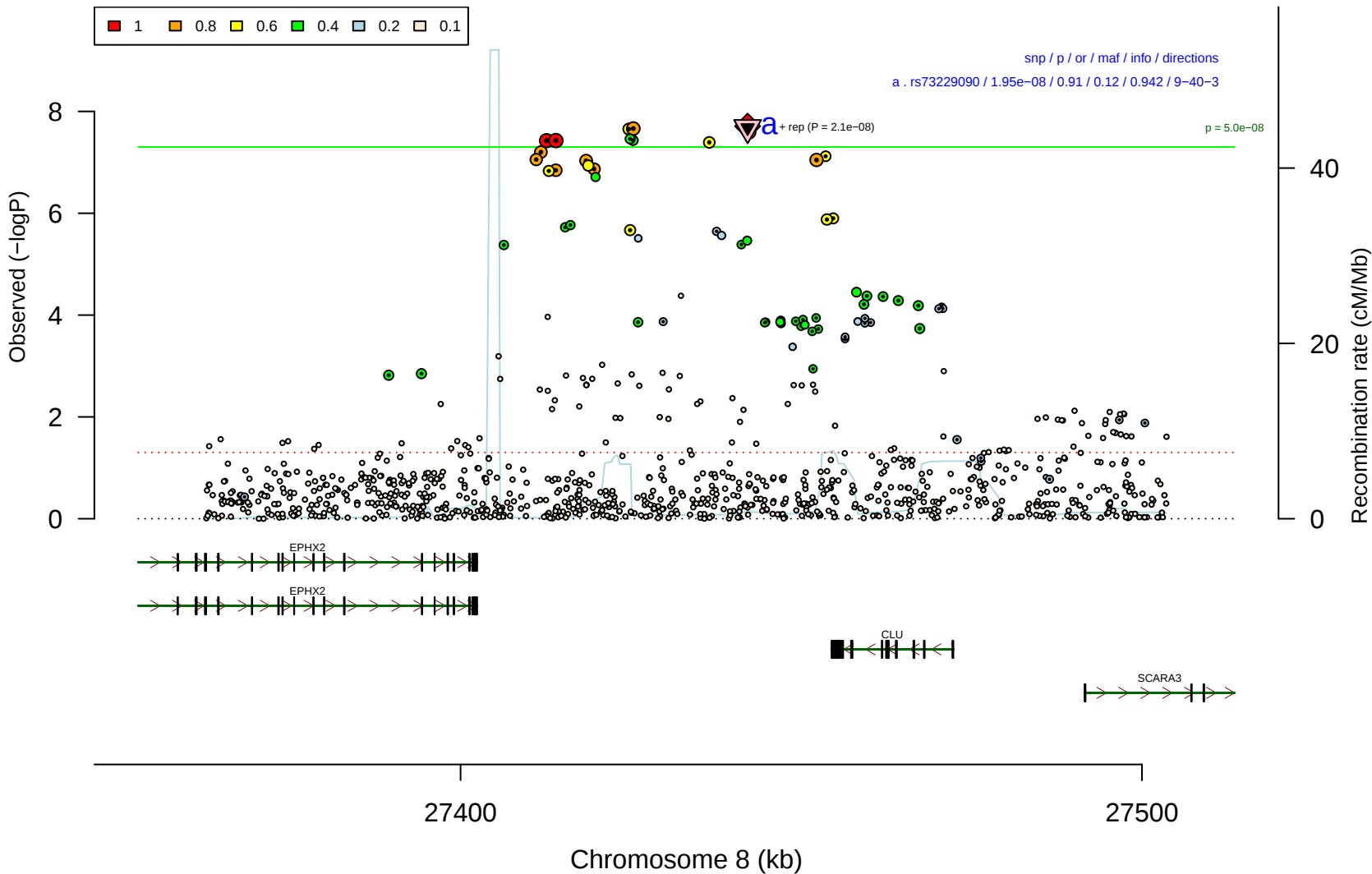
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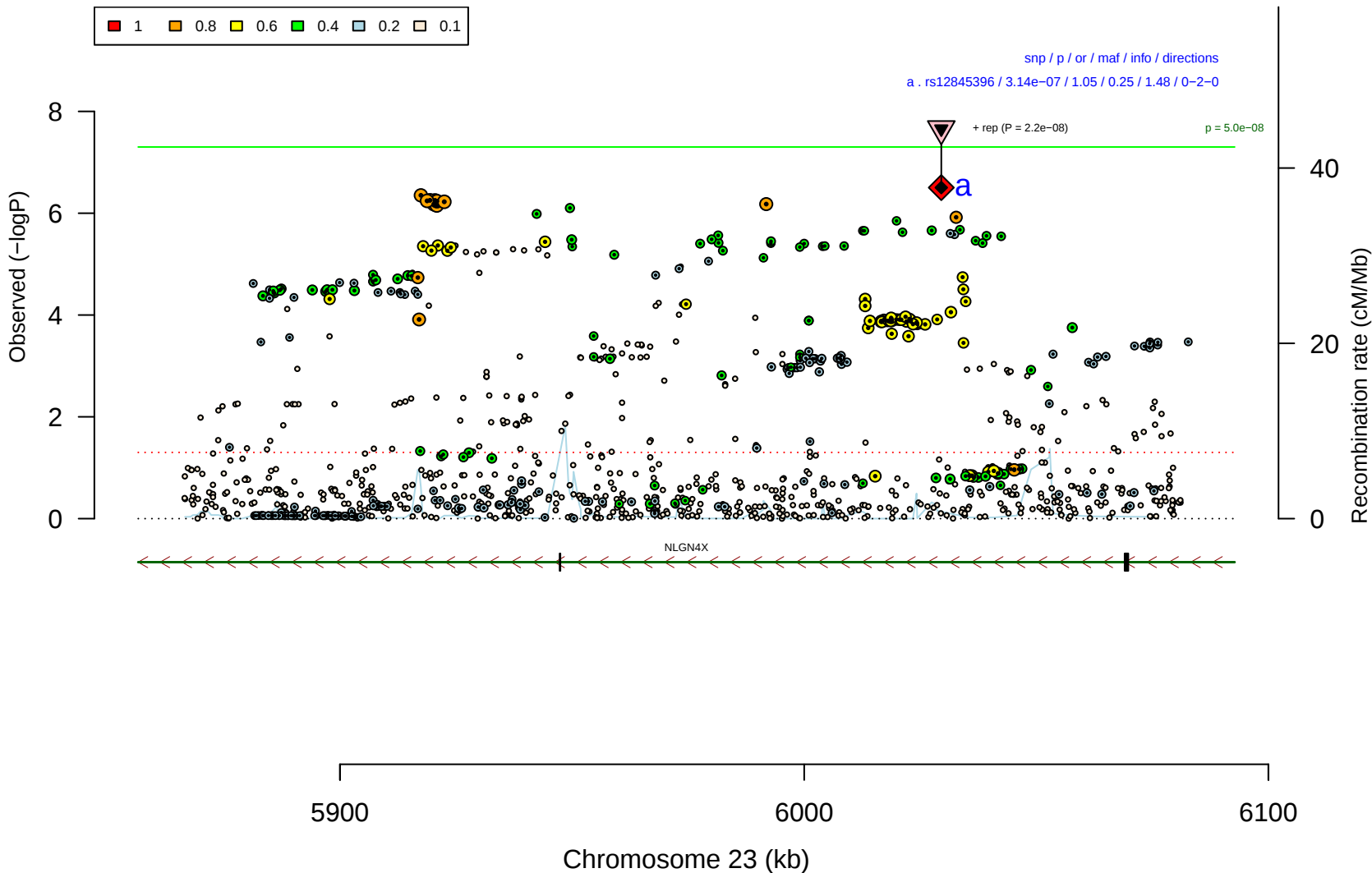
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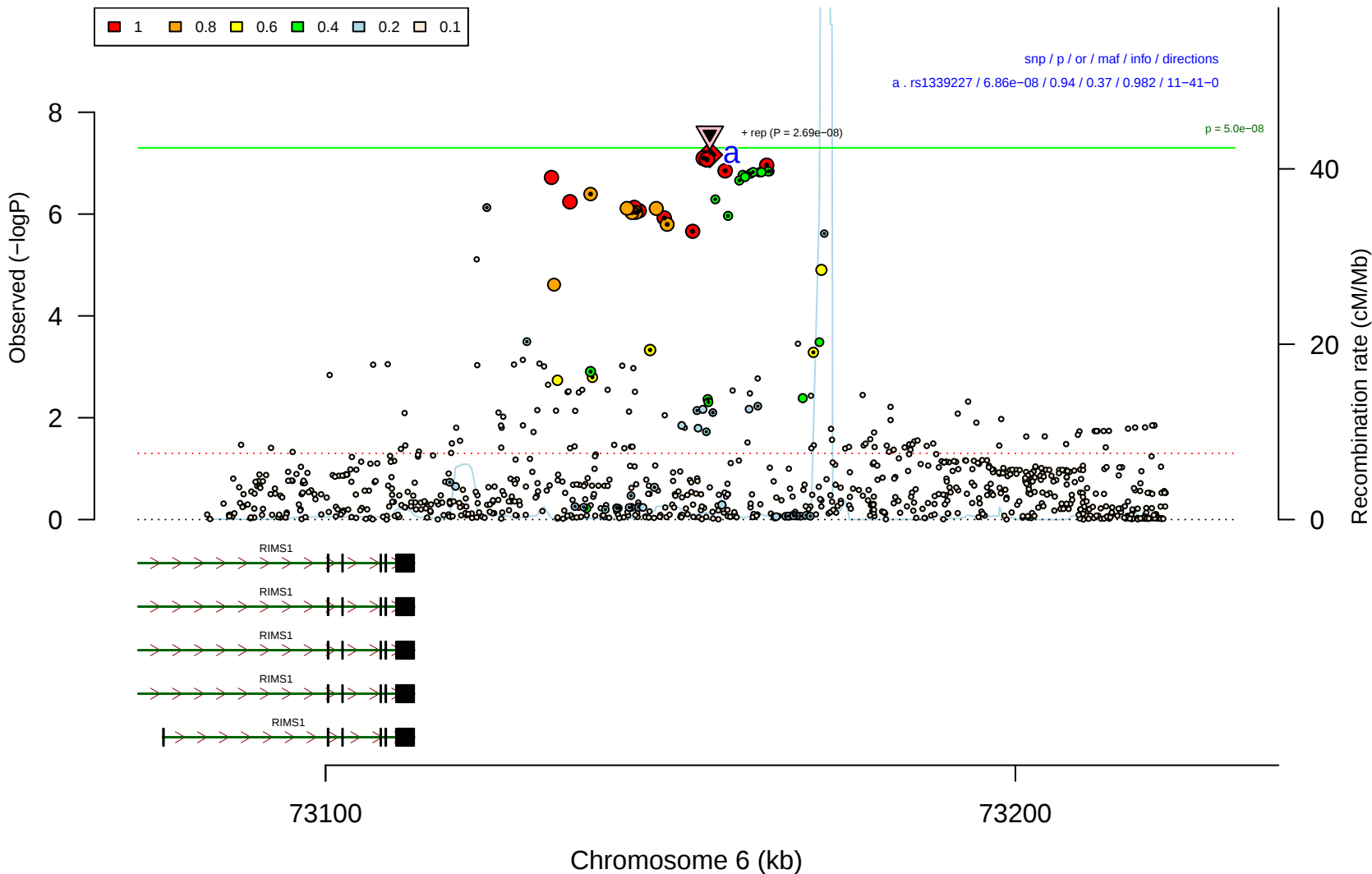
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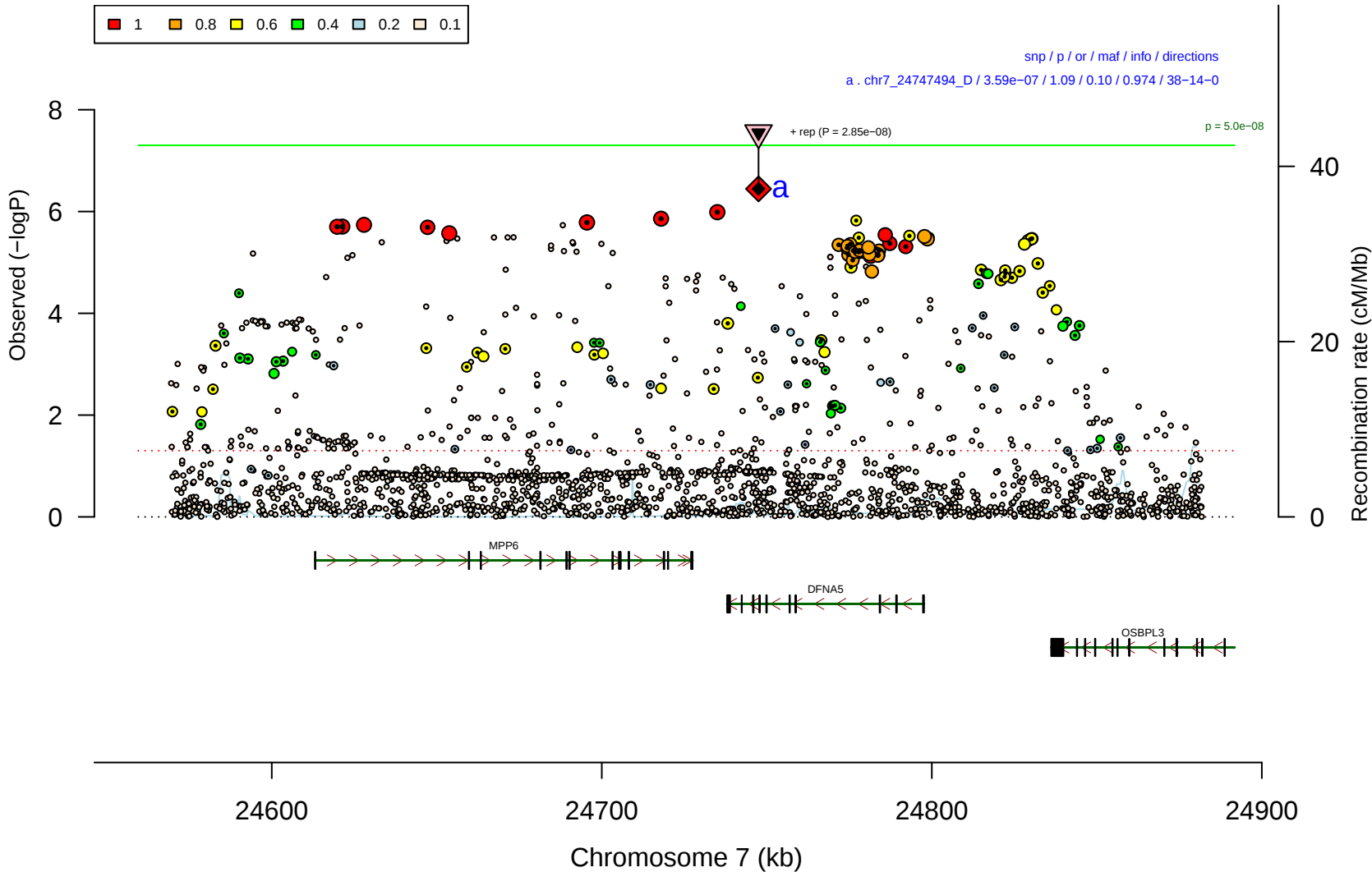
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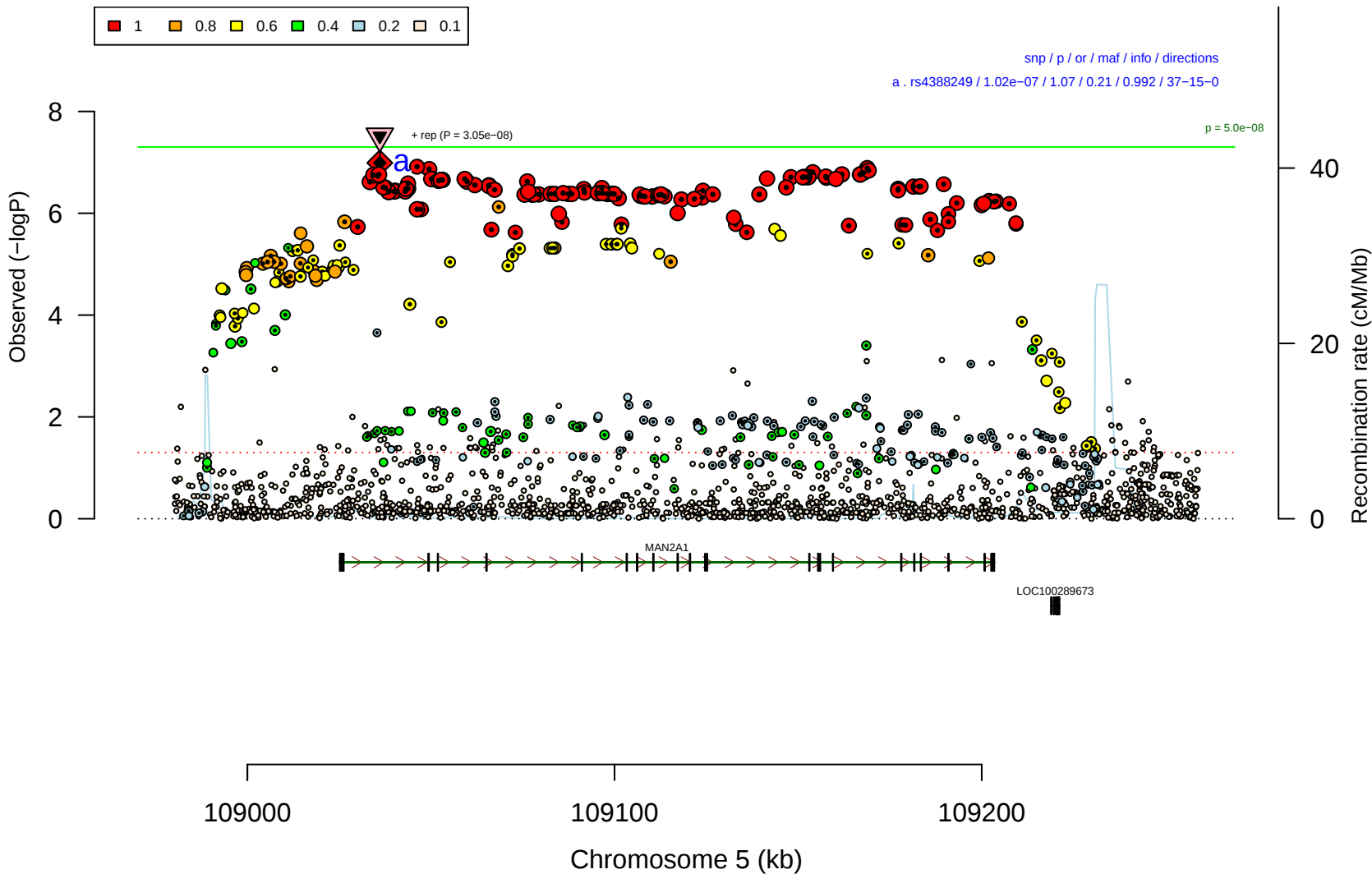
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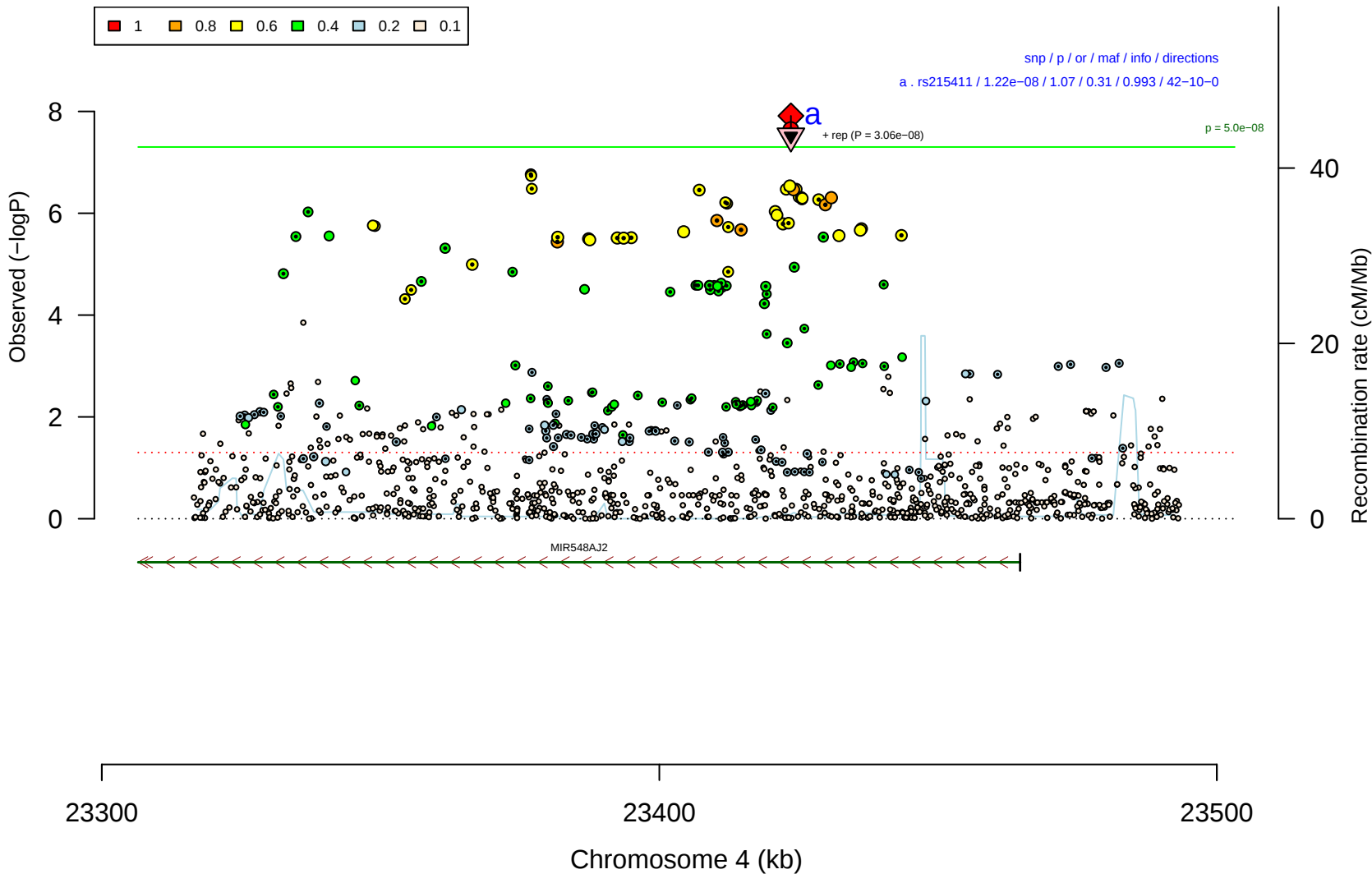
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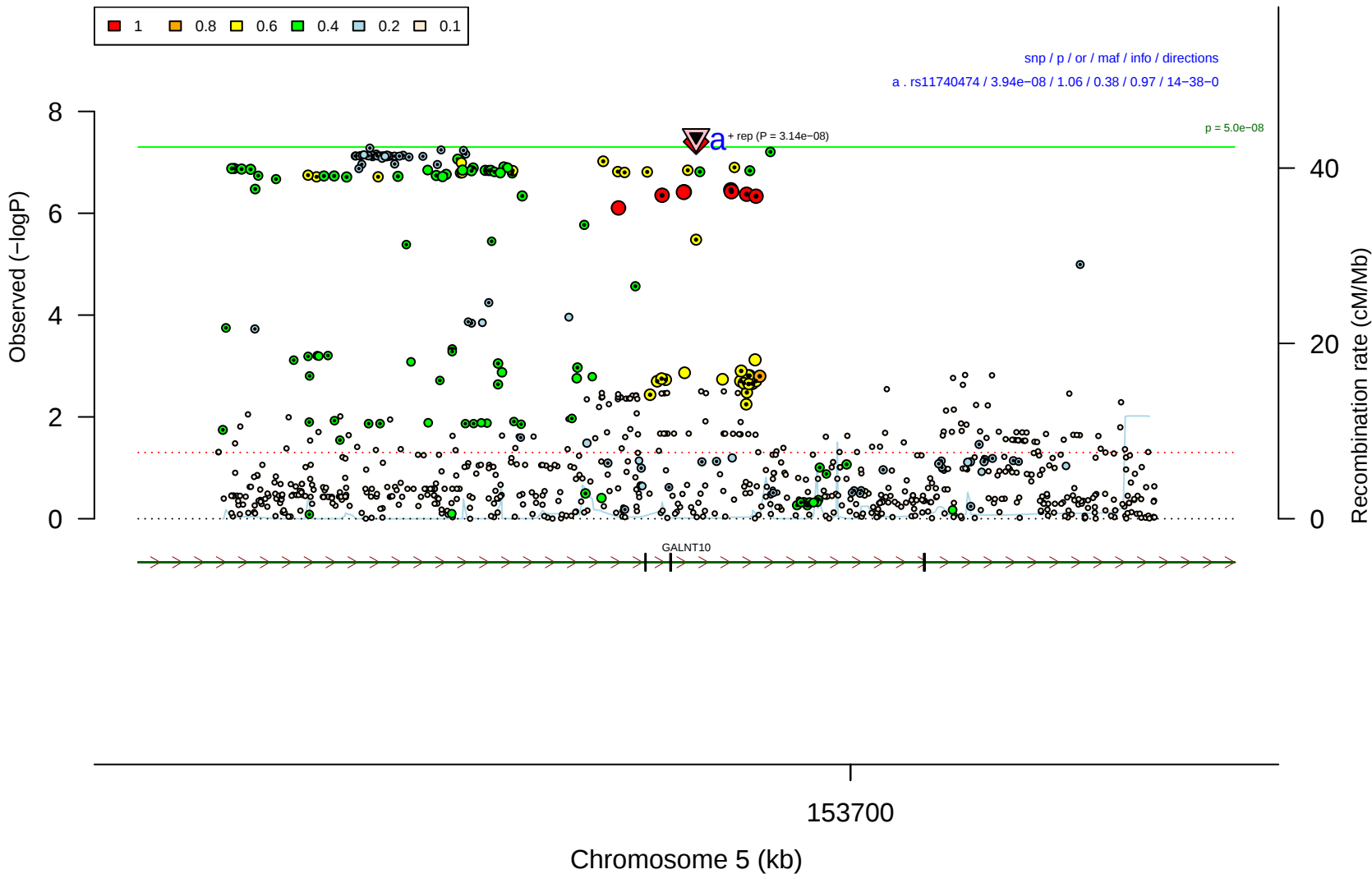
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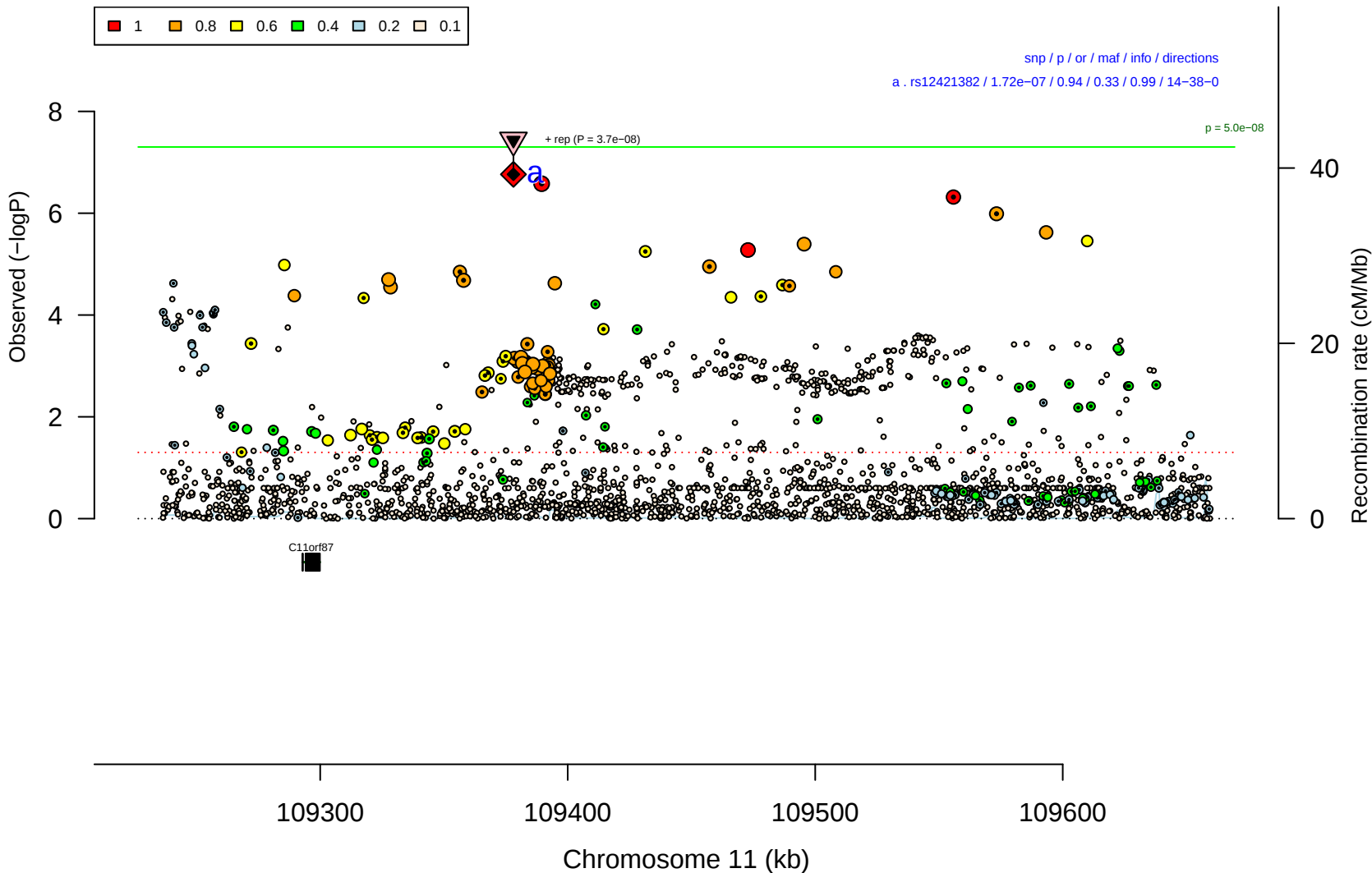
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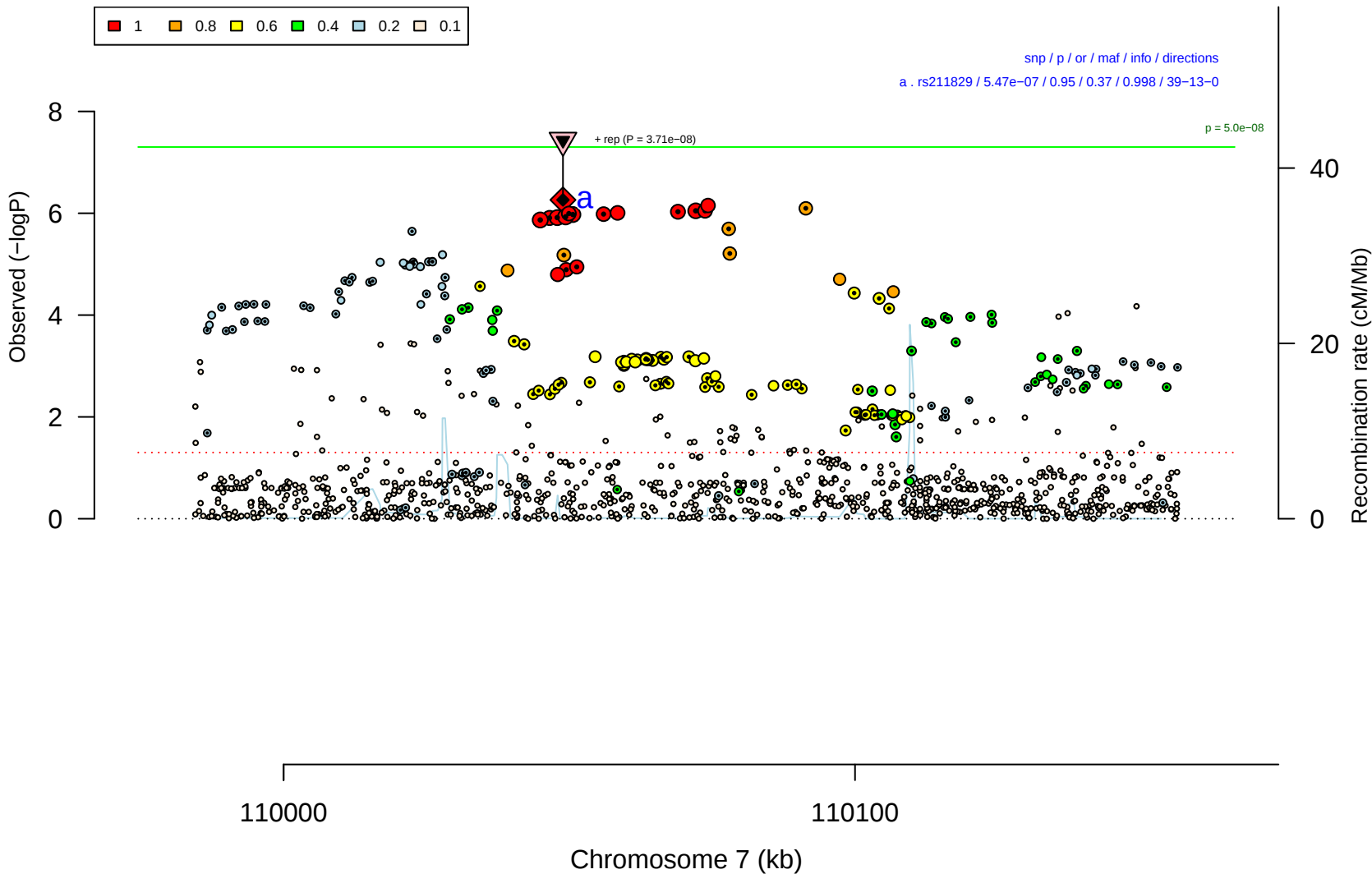
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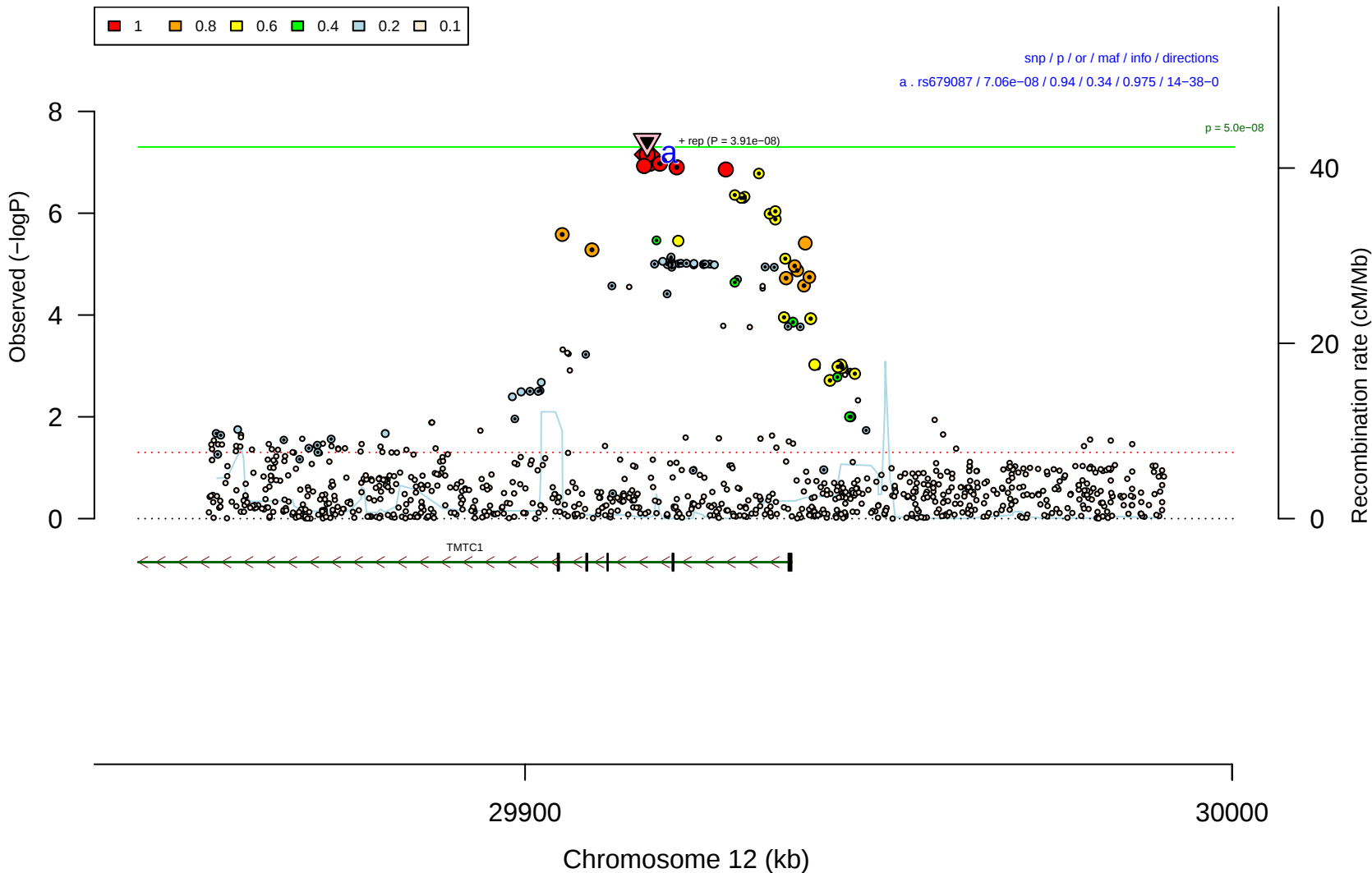
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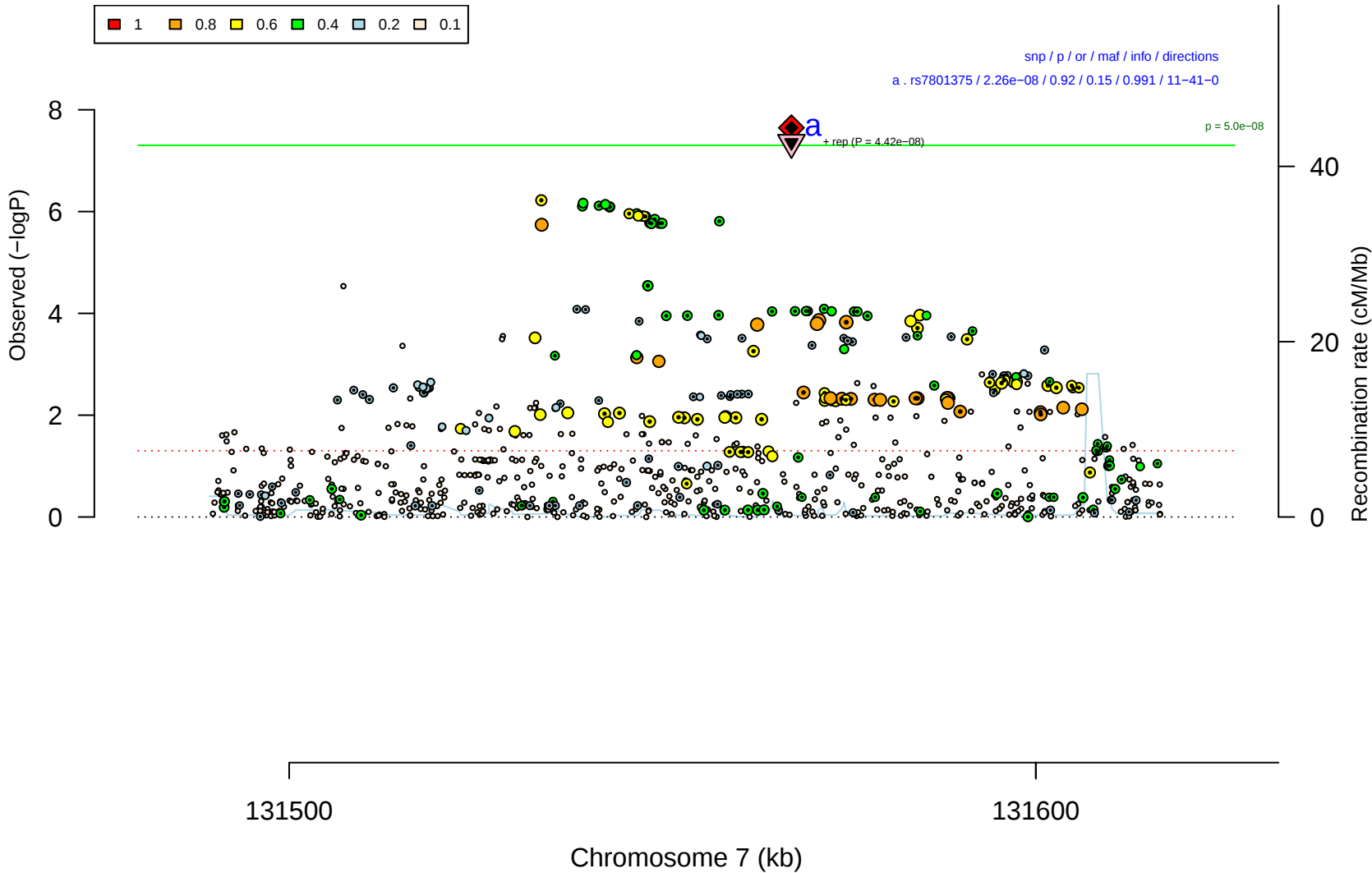
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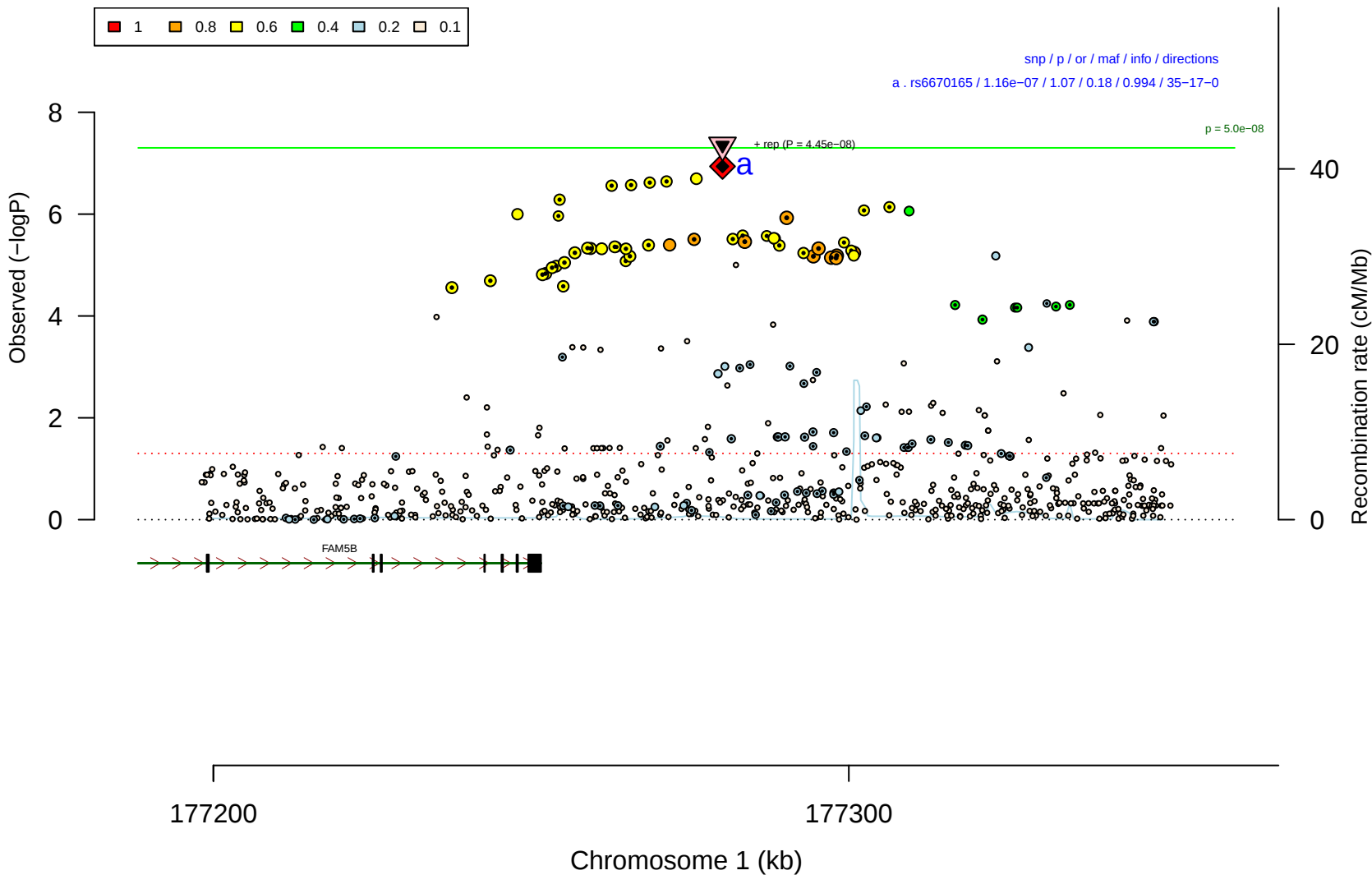
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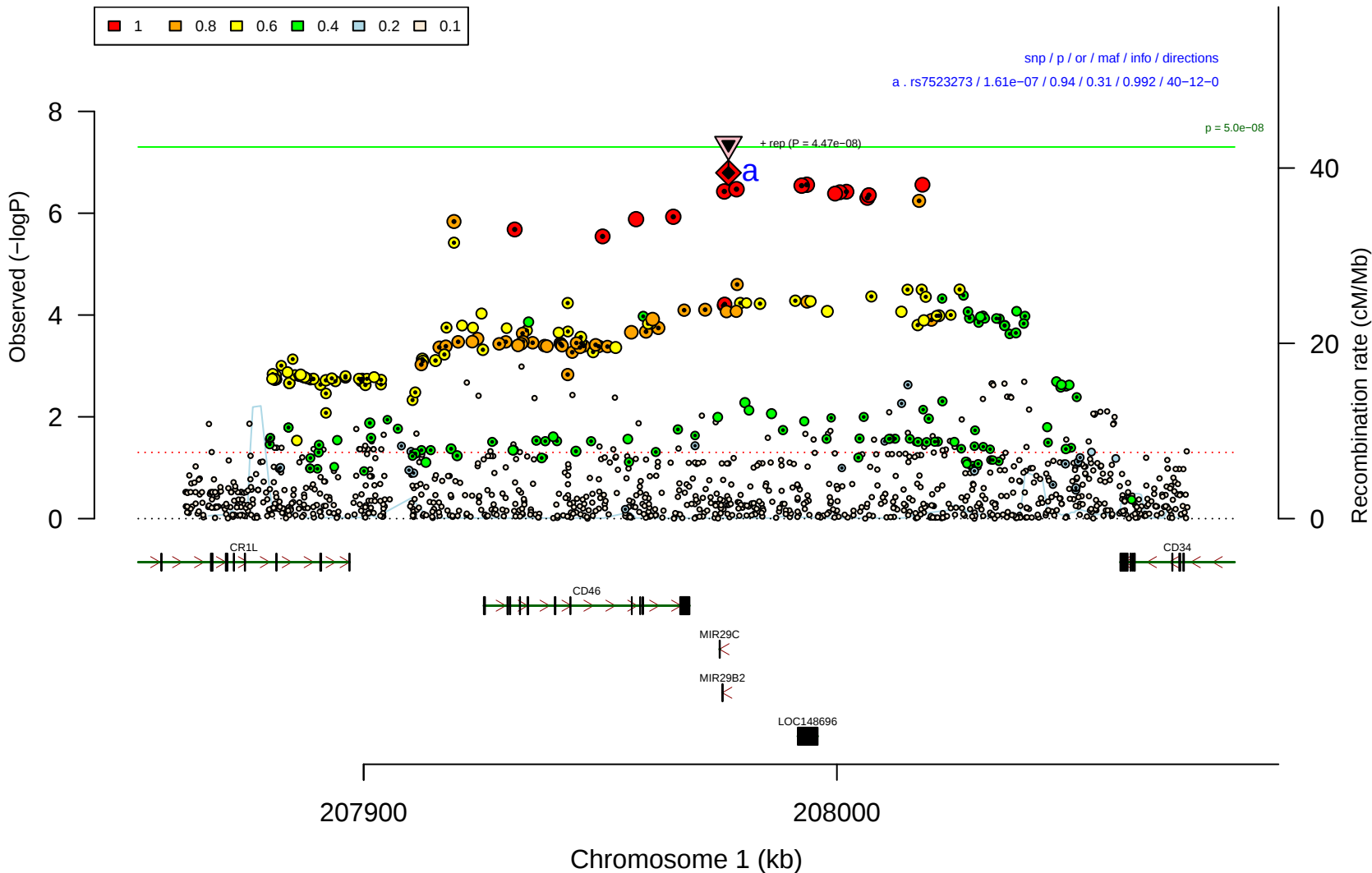
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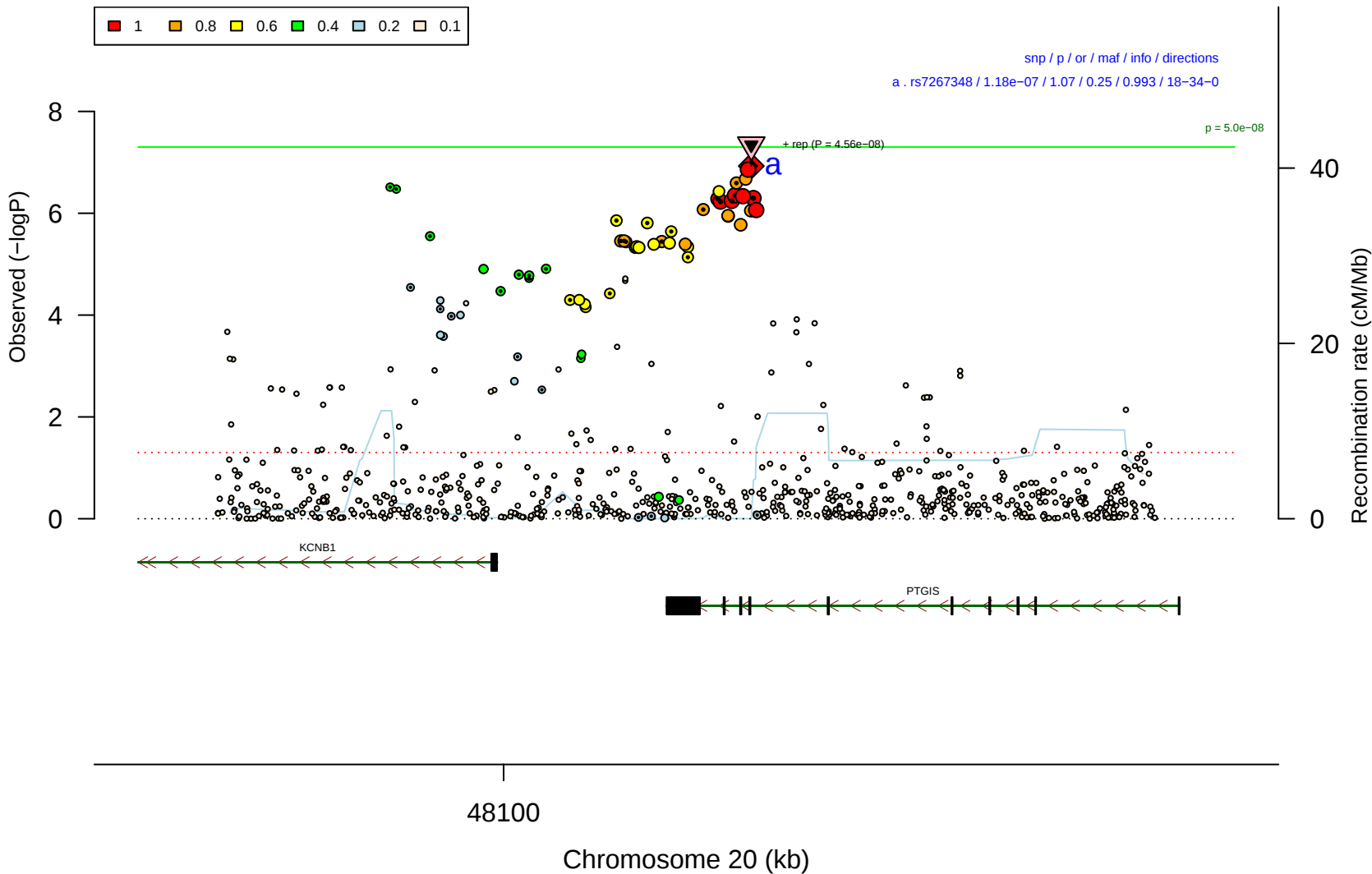
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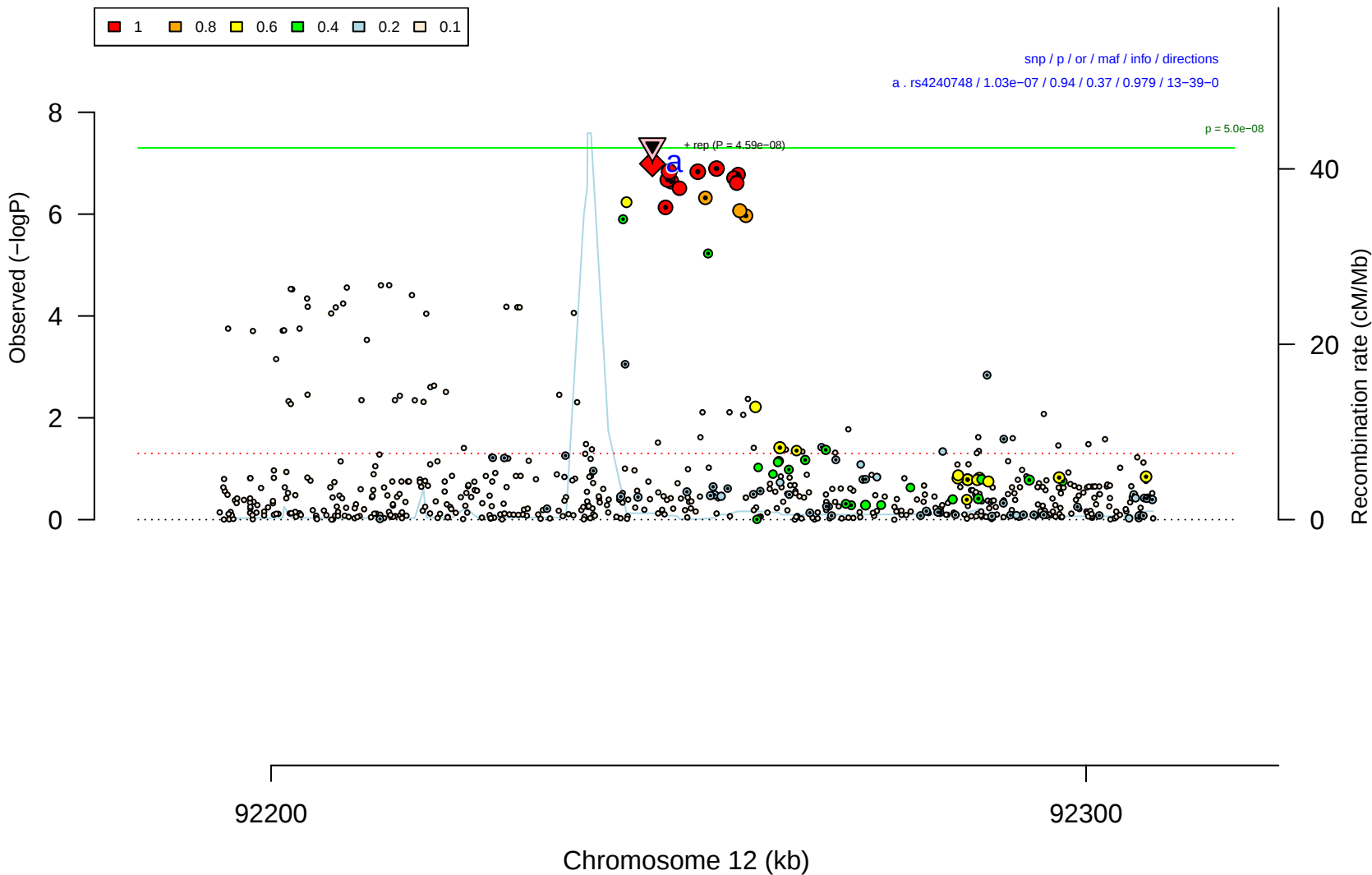
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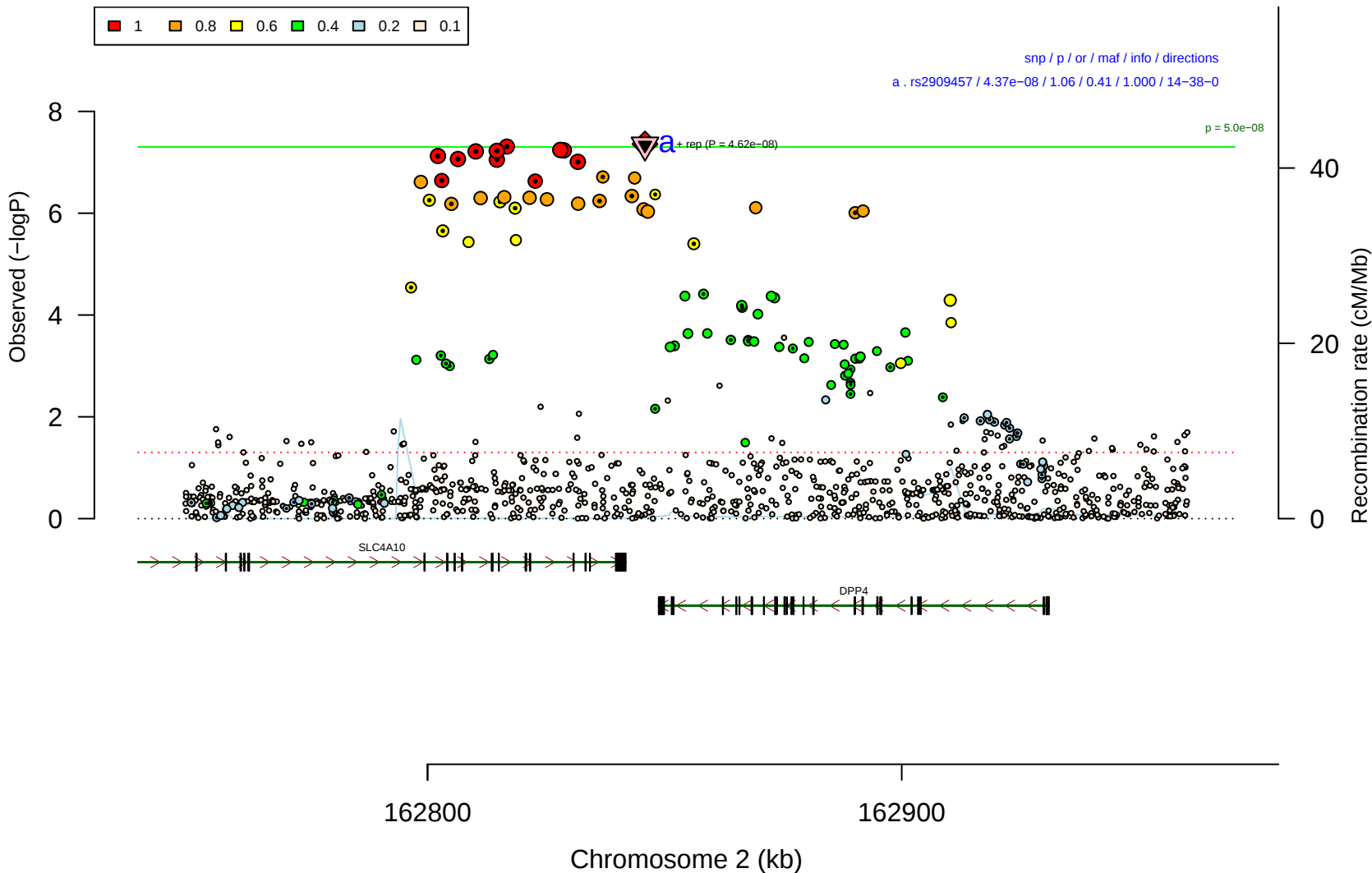
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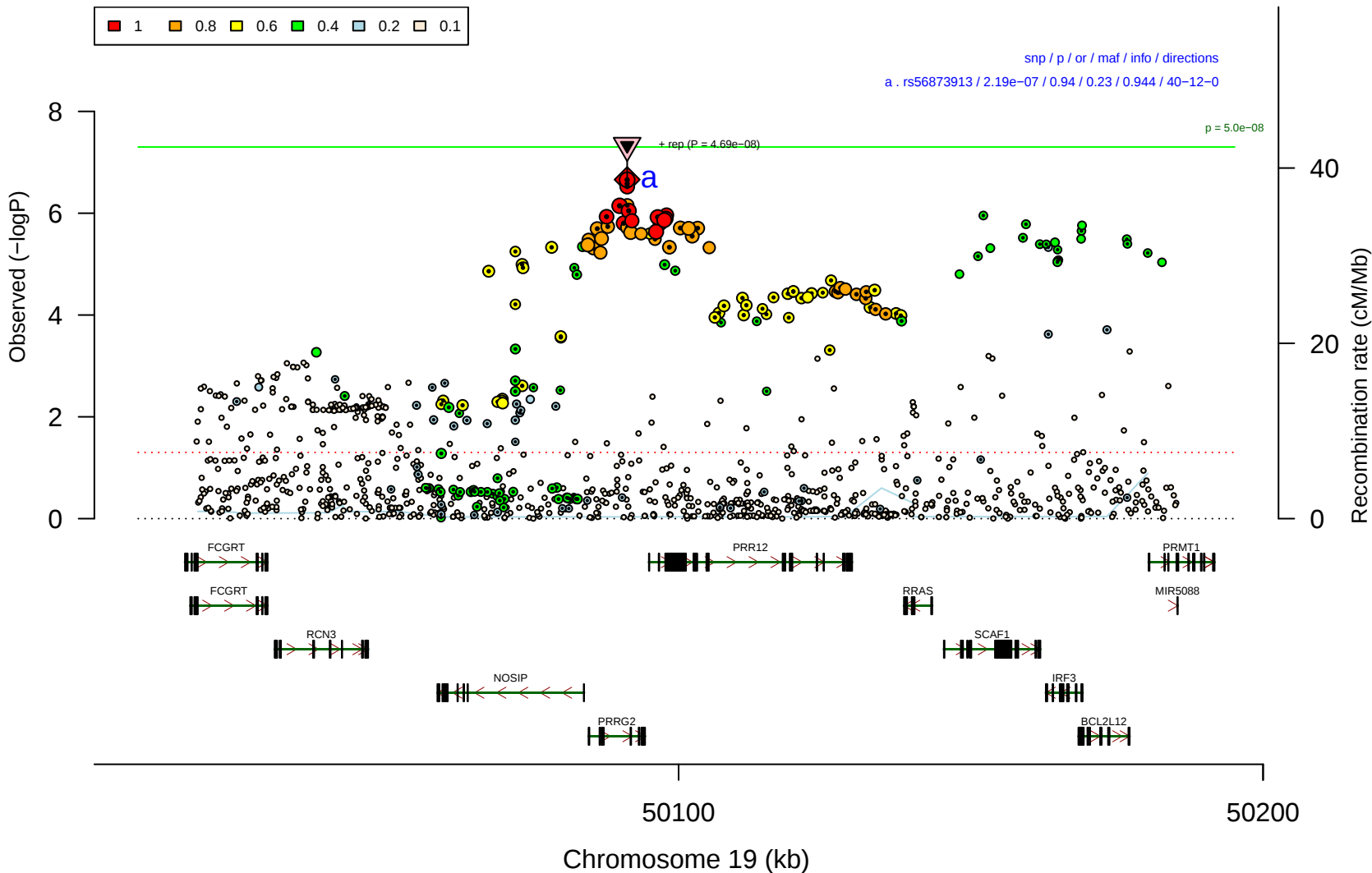
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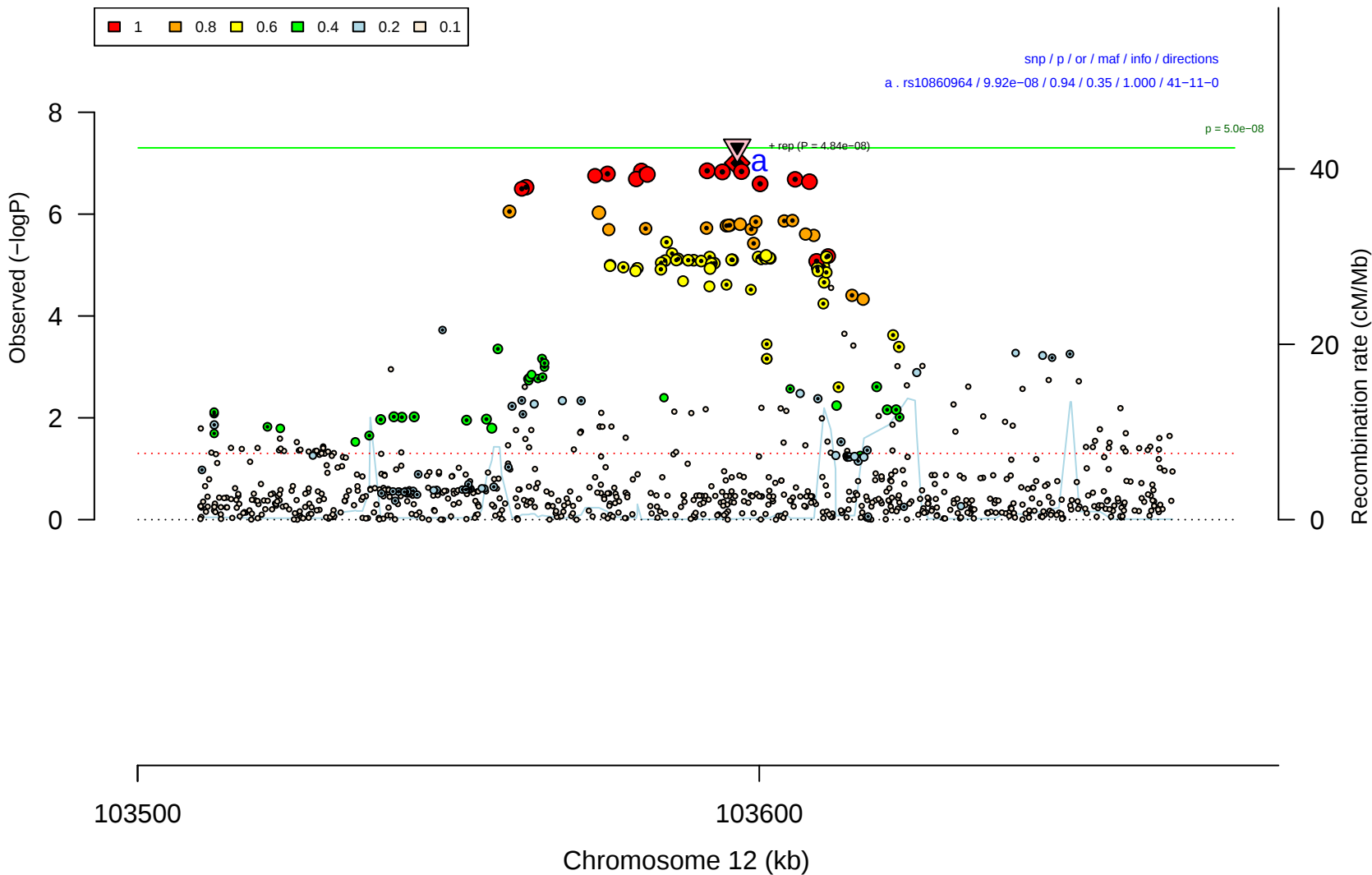
PGC_SCZ52.reg105



PGC_SCZ52.reg106



PGC_SCZ52.reg107



PGC_SCZ52.reg108

