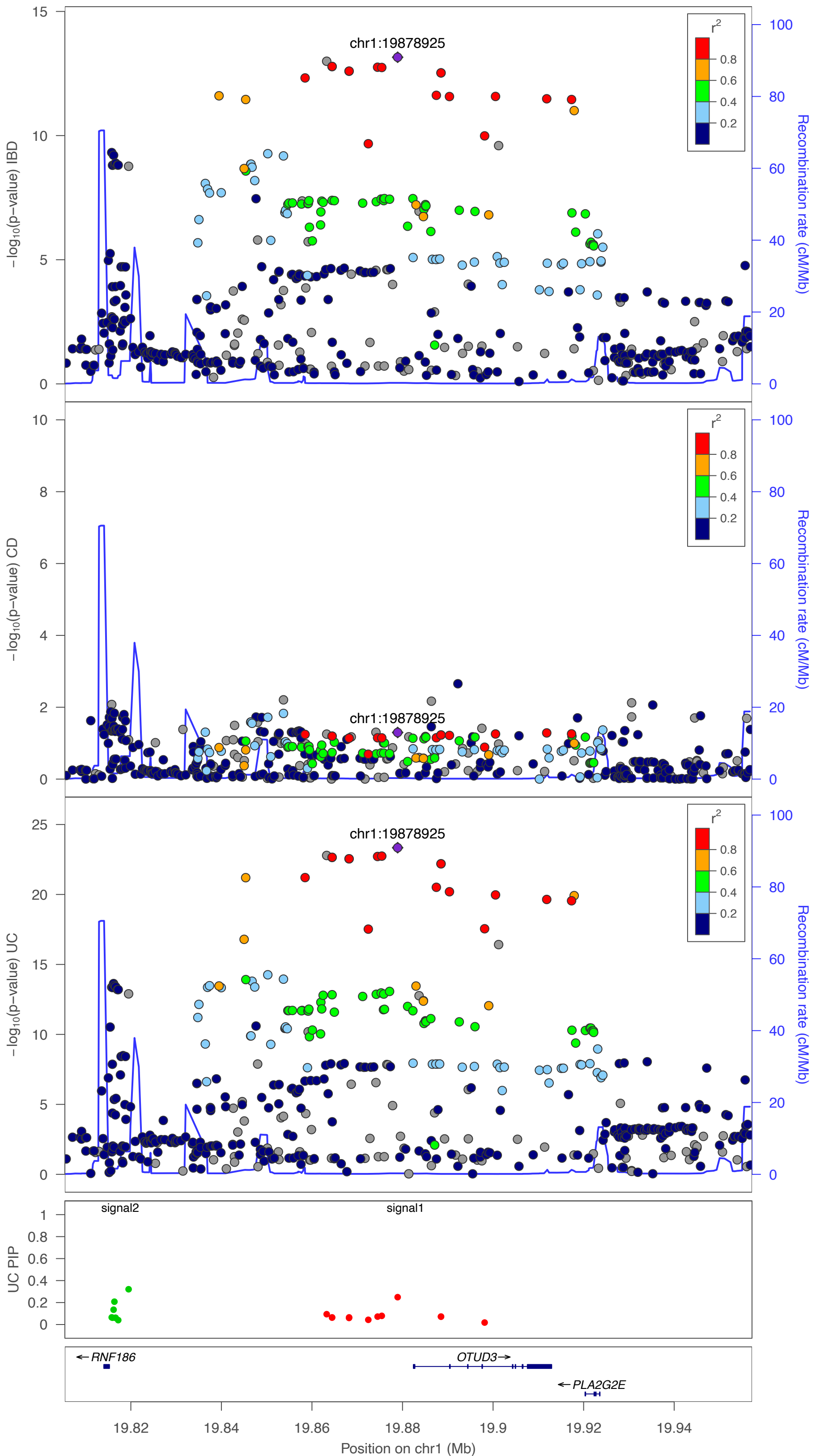
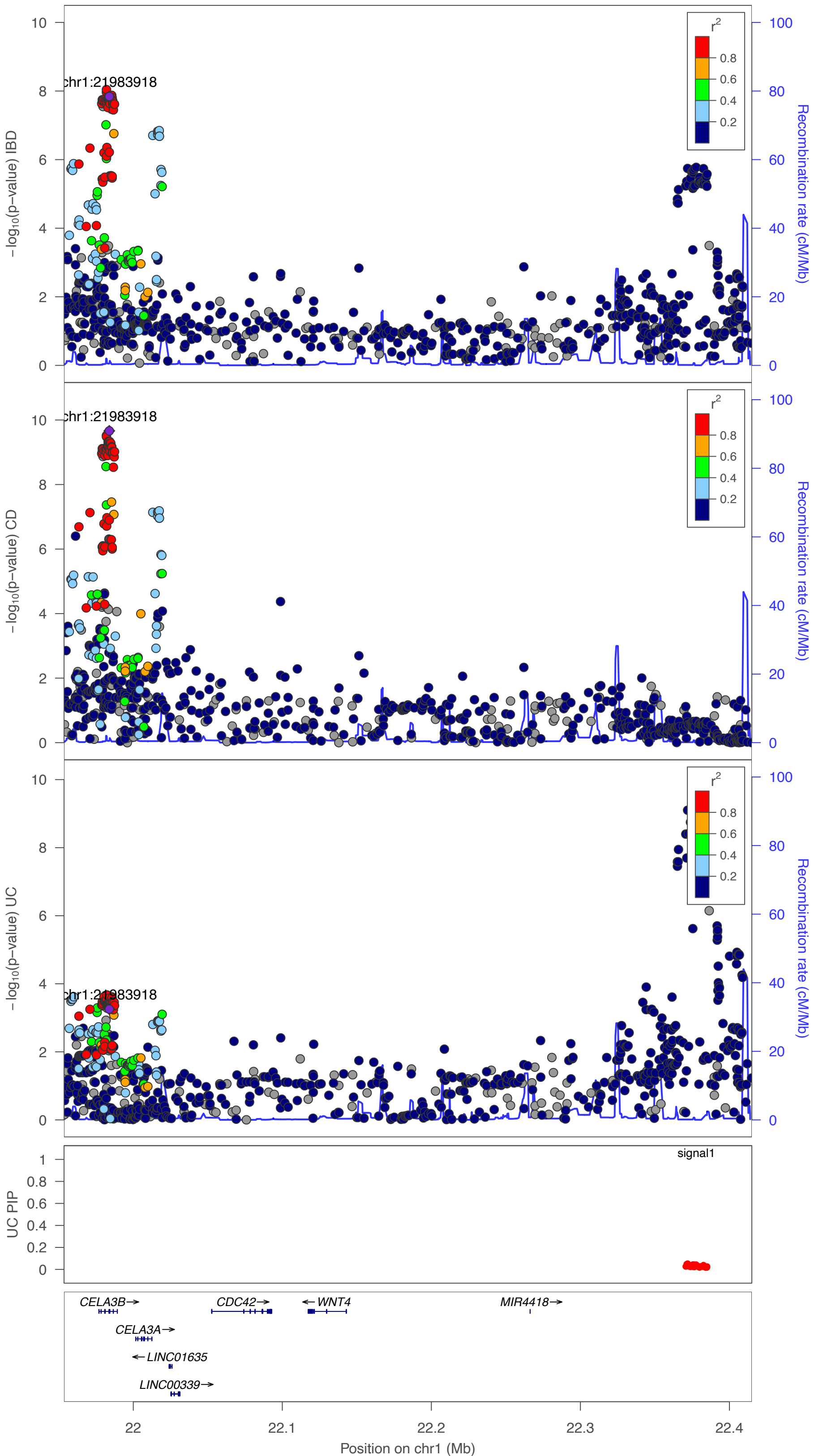


Supplementary Data 2. Regional association plot for IBD-associated loci in EAS. The title of each page shows the disease subtype and the index variant of the locus. In each regional association plot, the purple diamond indicates the index variant of the locus. Different colors indicate the magnitude of LD with the index variant measured as R^2 using EAS subjects from the 1000 Genomes Project Phase 3. P-value: original P-value from the fixed-effect meta-analysis (two-tailed). When fine-mapping was performed in the region, fine-mapping results were plotted below the association plots. In fine-mapping plots, different colors indicate different association signals (credible sets). PIP: posterior inclusion probability.

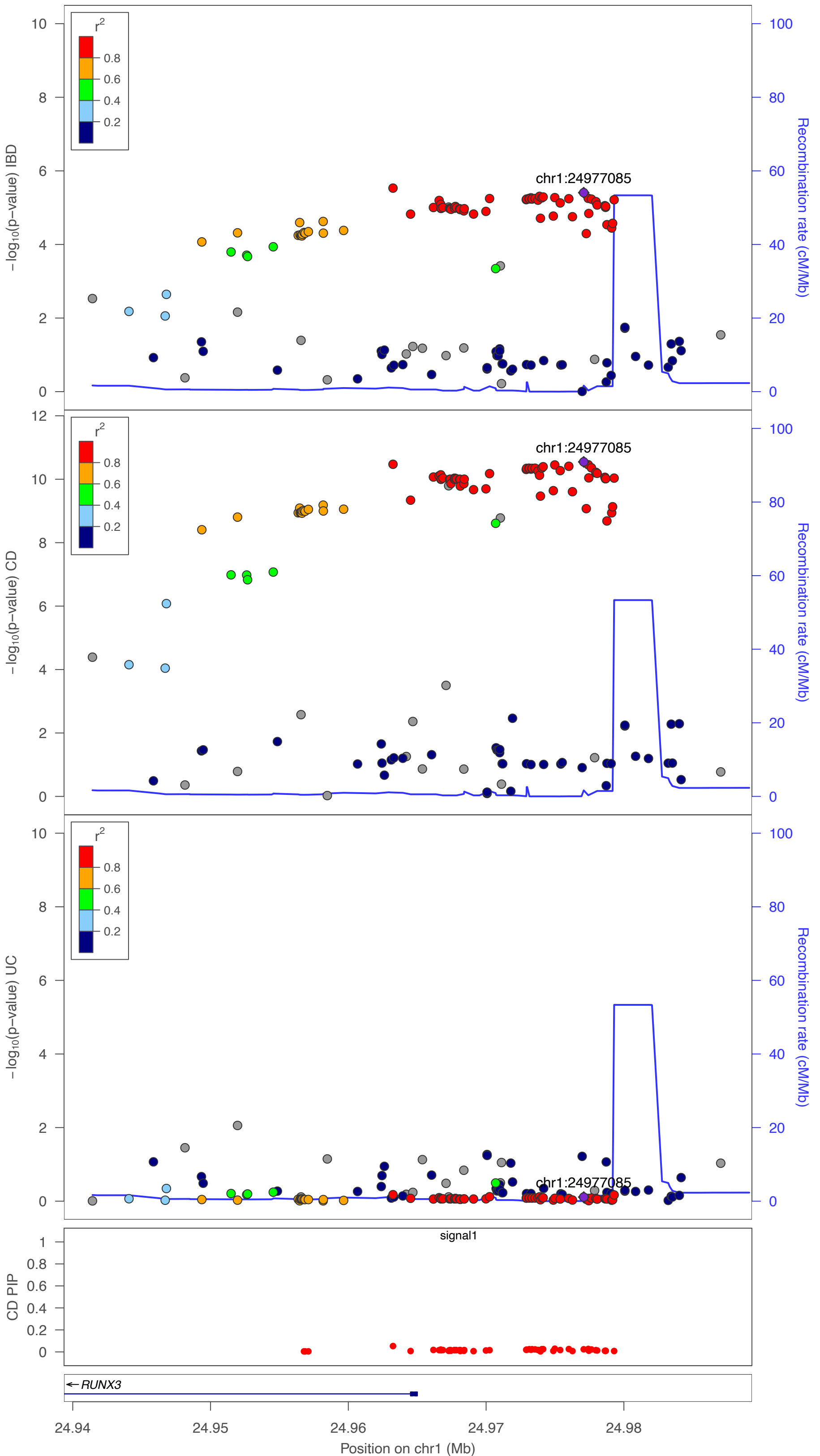
UC chr1:19878925:A:G



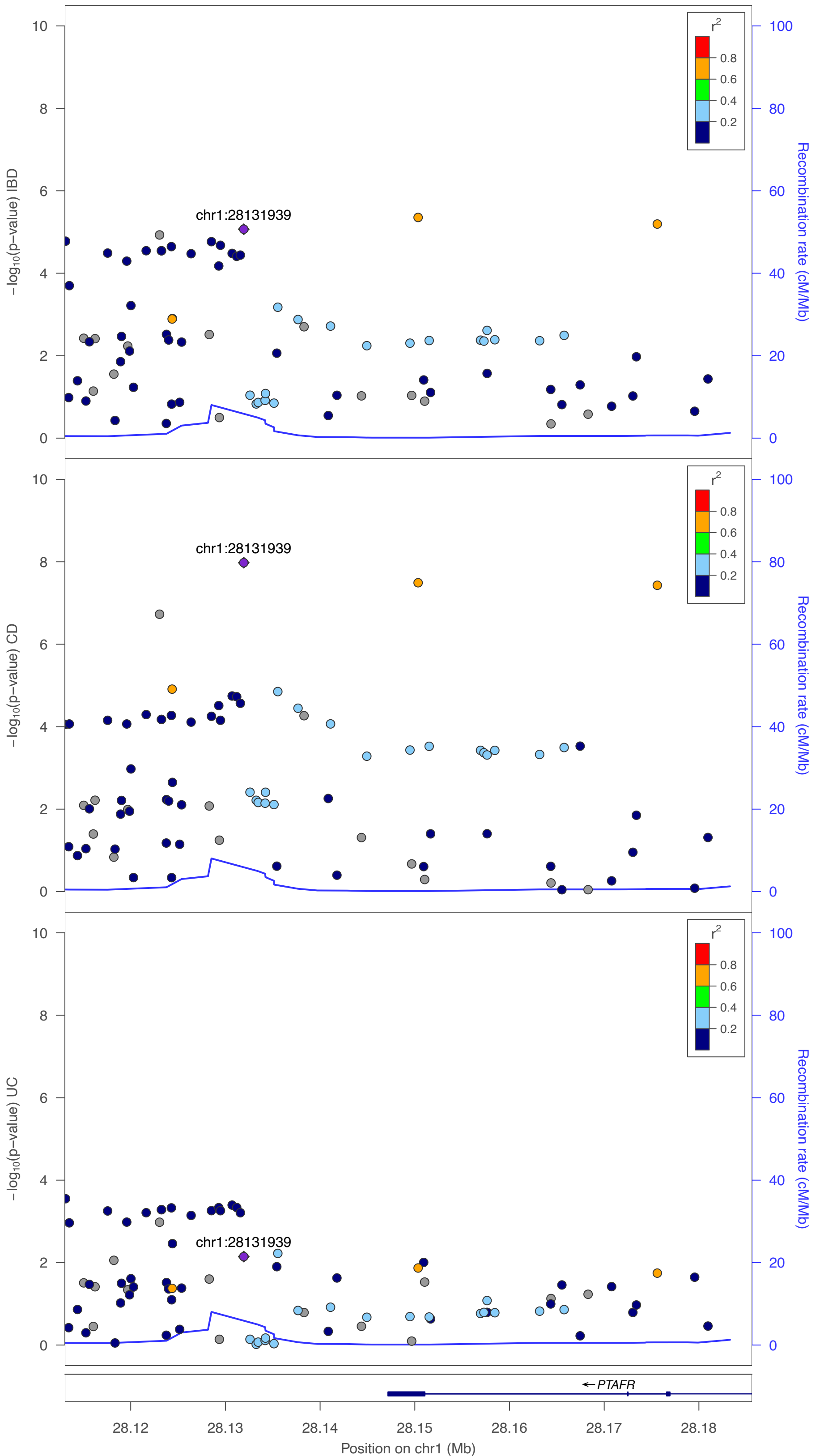
IBD chr1:21983918:A:G



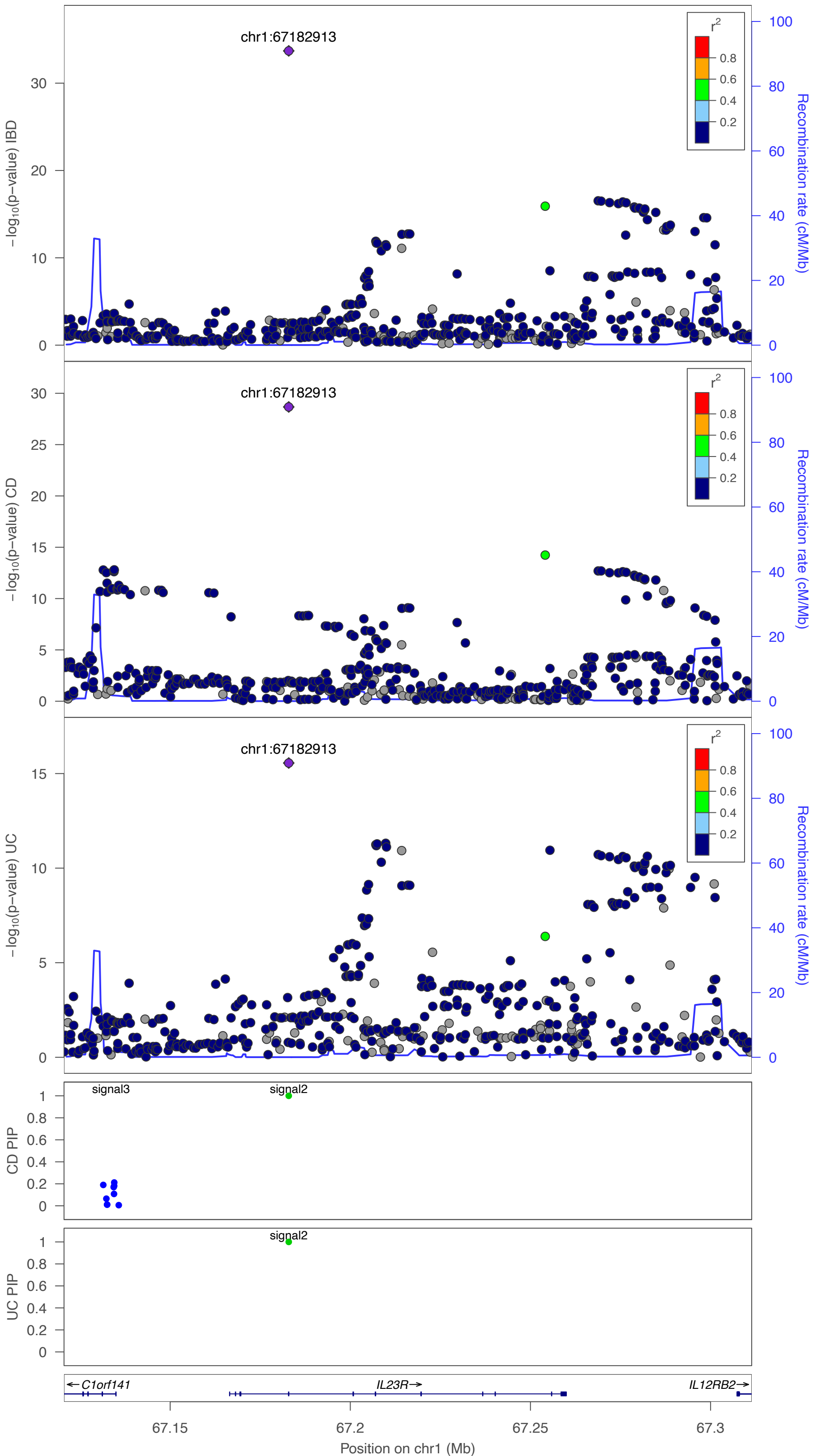
CD chr1:24977085:A:G



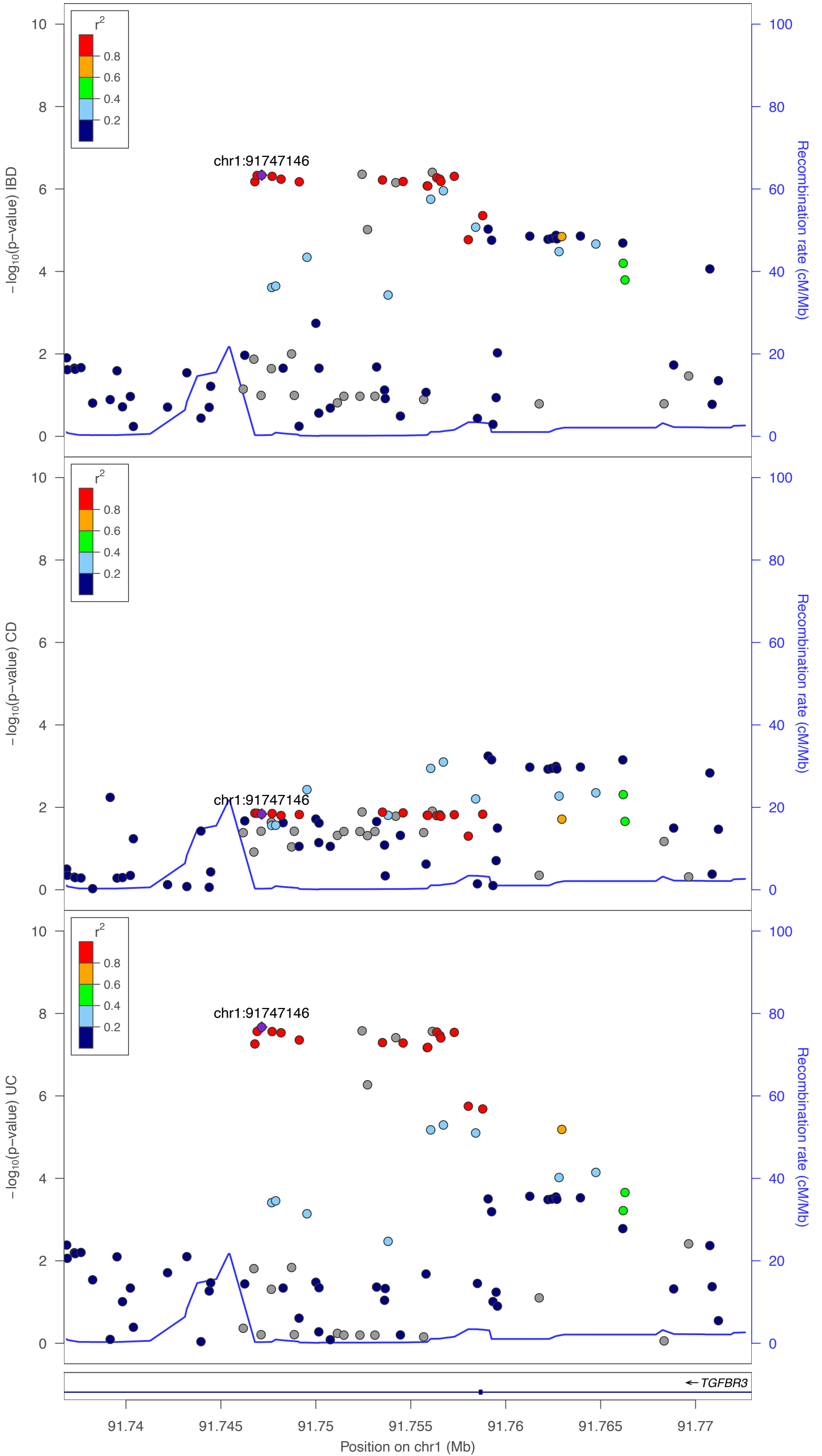
CD chr1:28131939:C:T



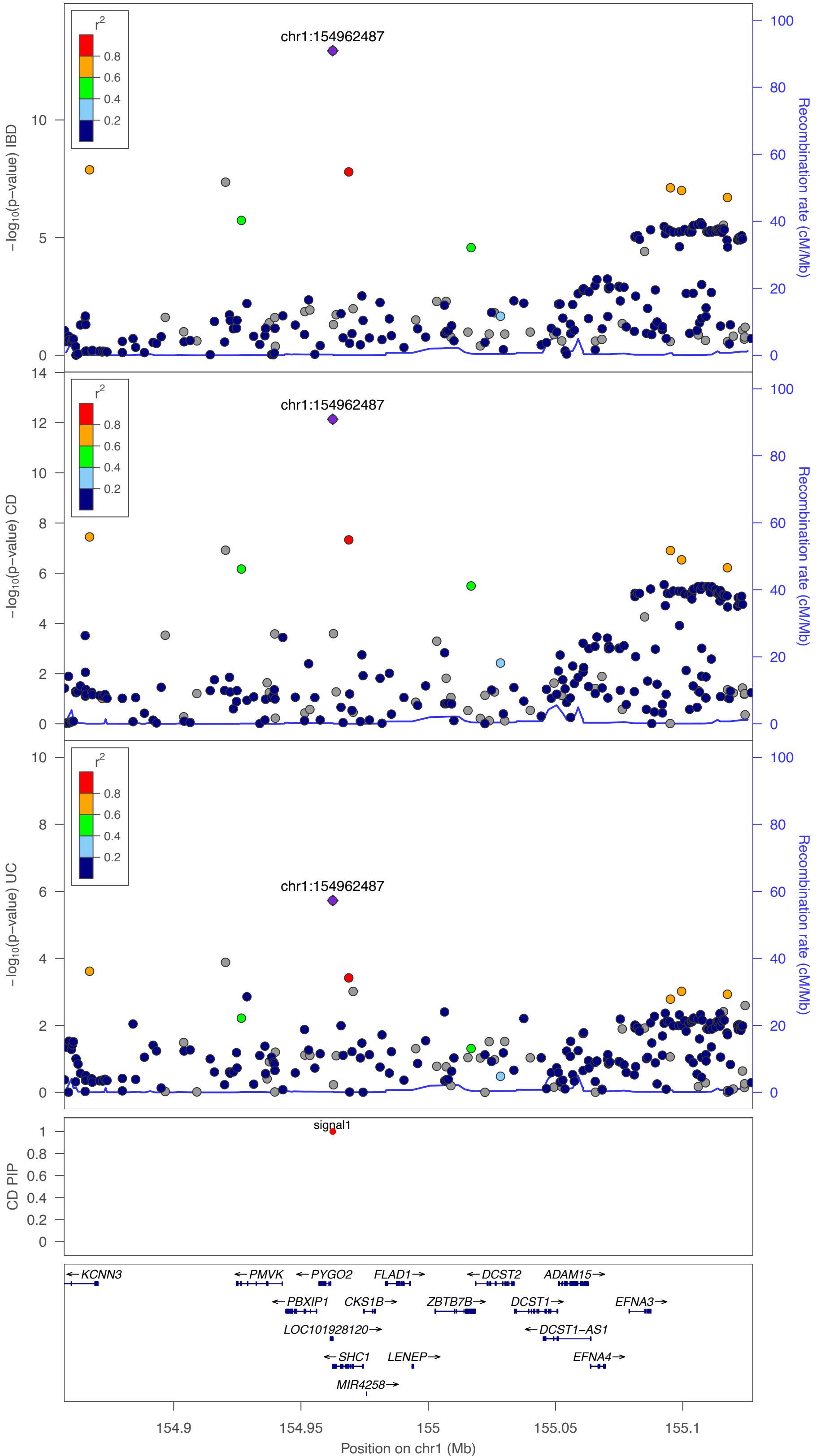
IBD chr1:67182913:G:A



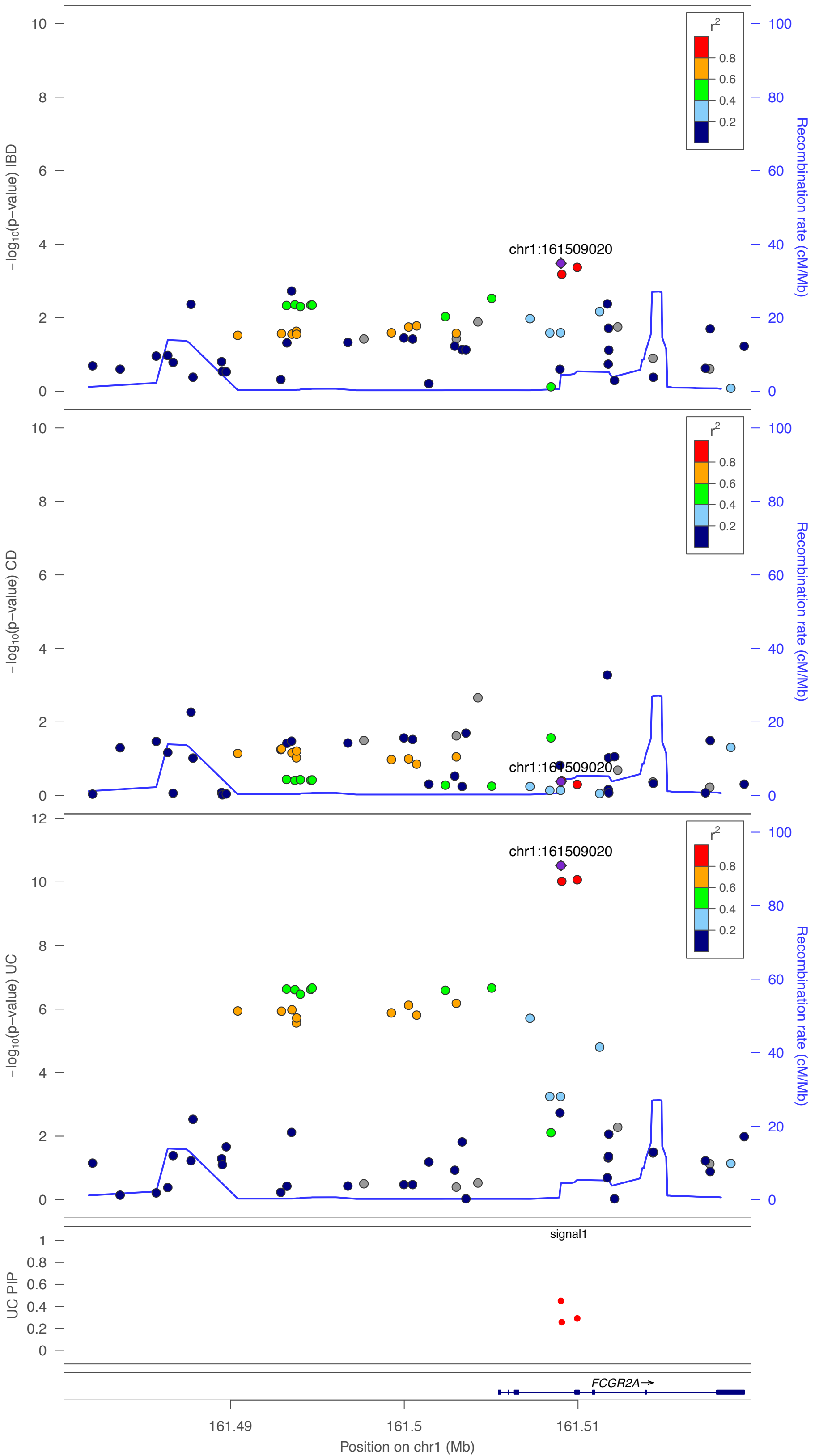
UC chr1:91747146:C:T



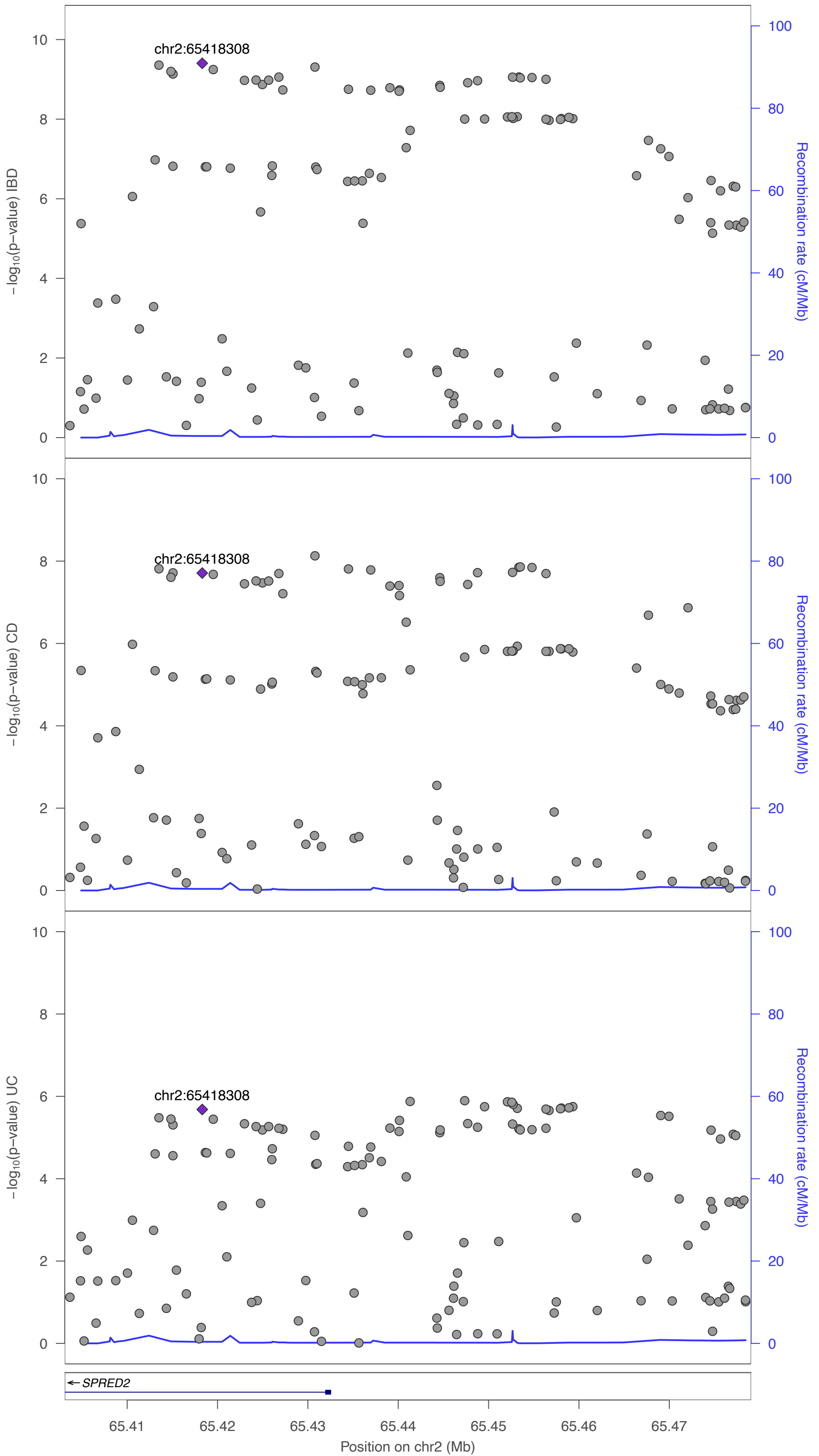
IBD chr1:154962487:G:A



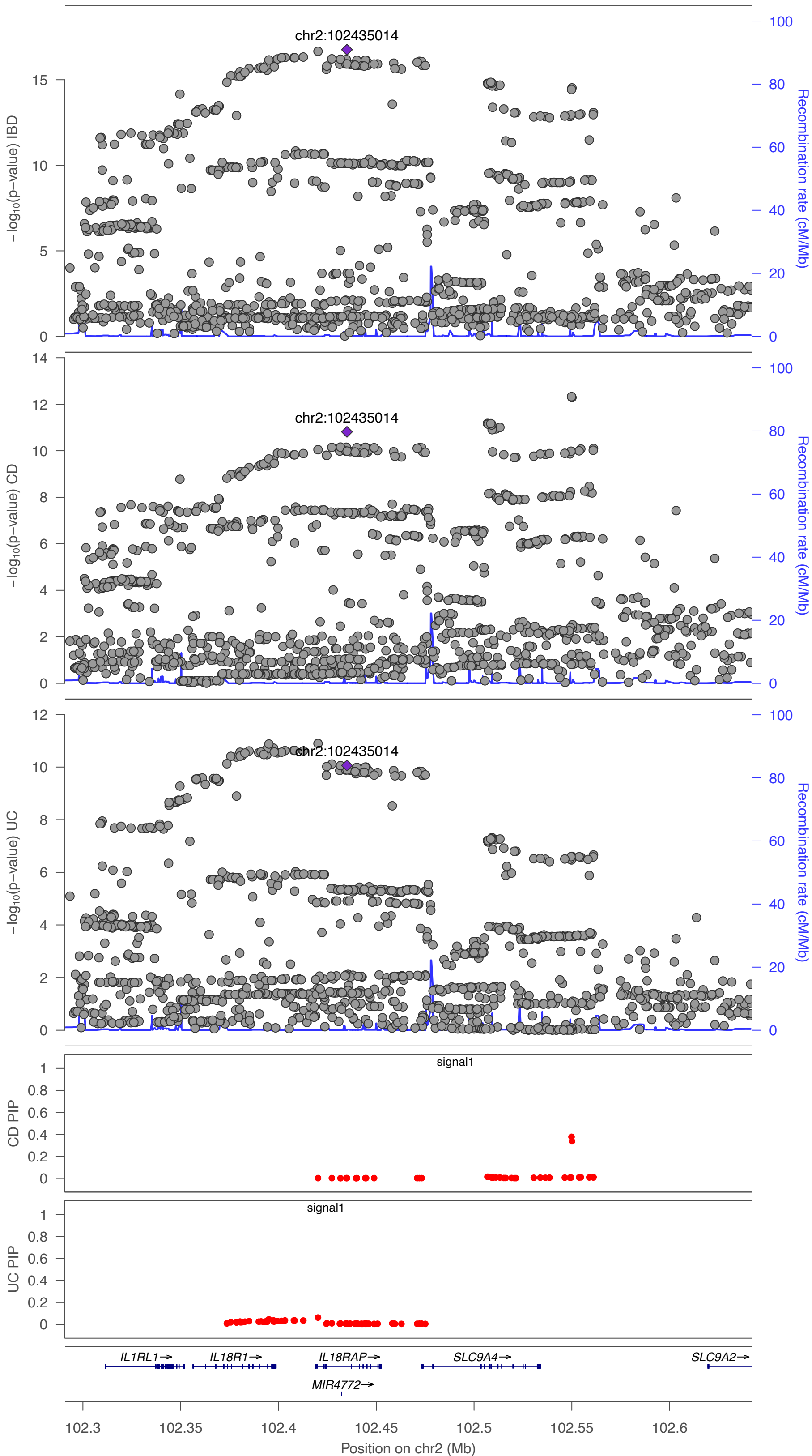
UC chr1:161509020:G:A



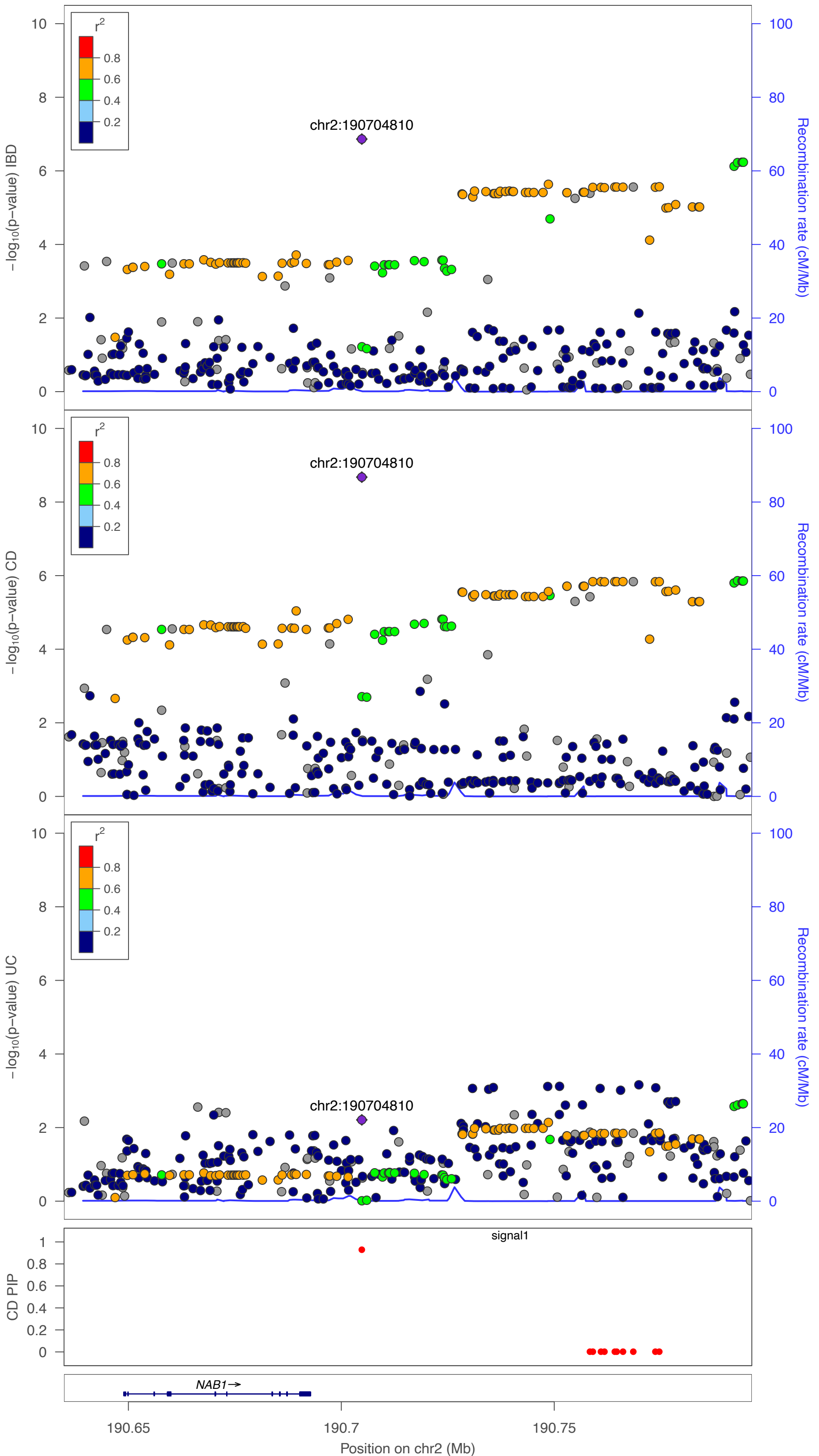
IBD chr2:65418308:A:AC



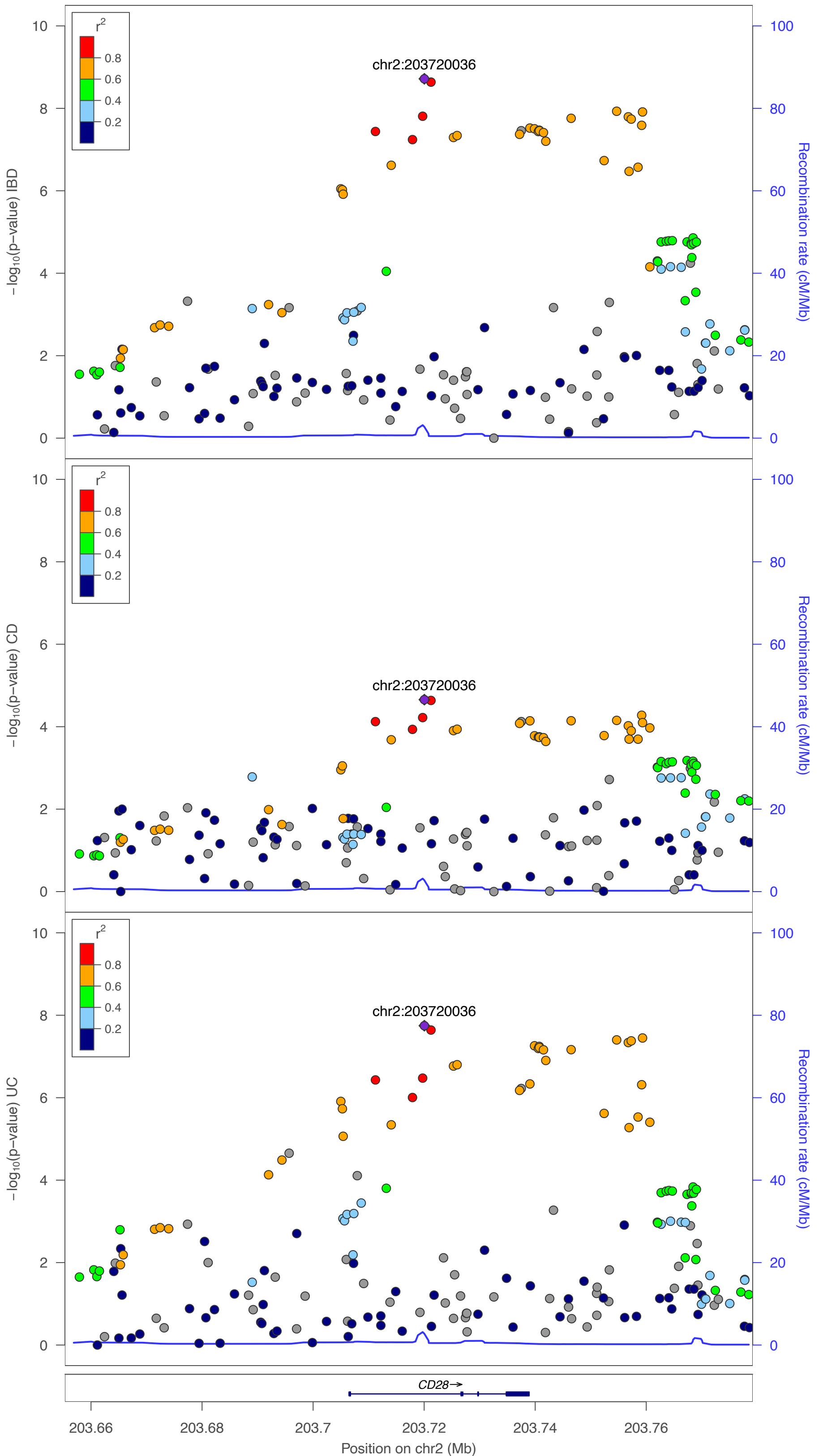
IBD chr2:102435014:TA:T



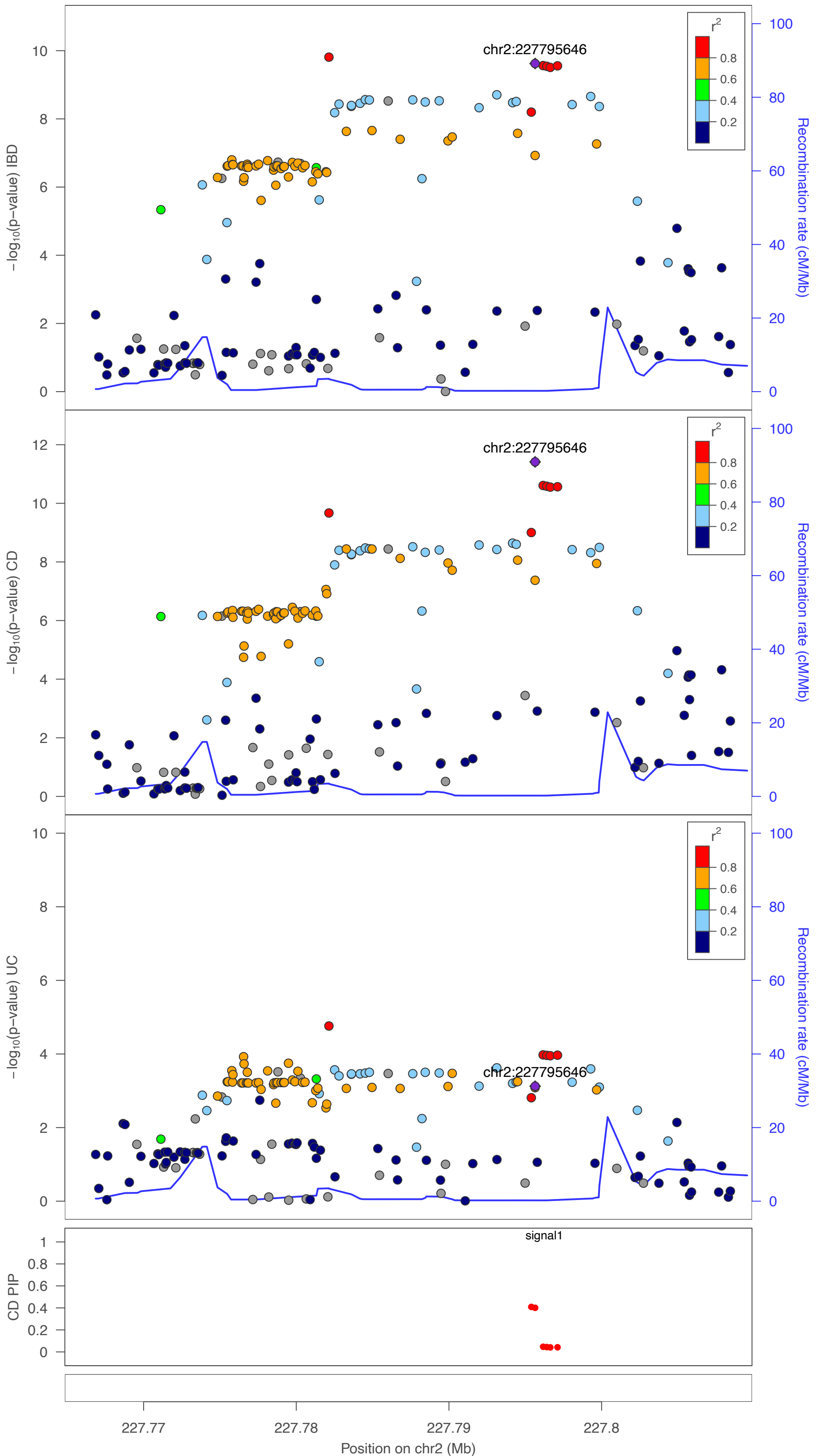
CD chr2:190704810:C:T



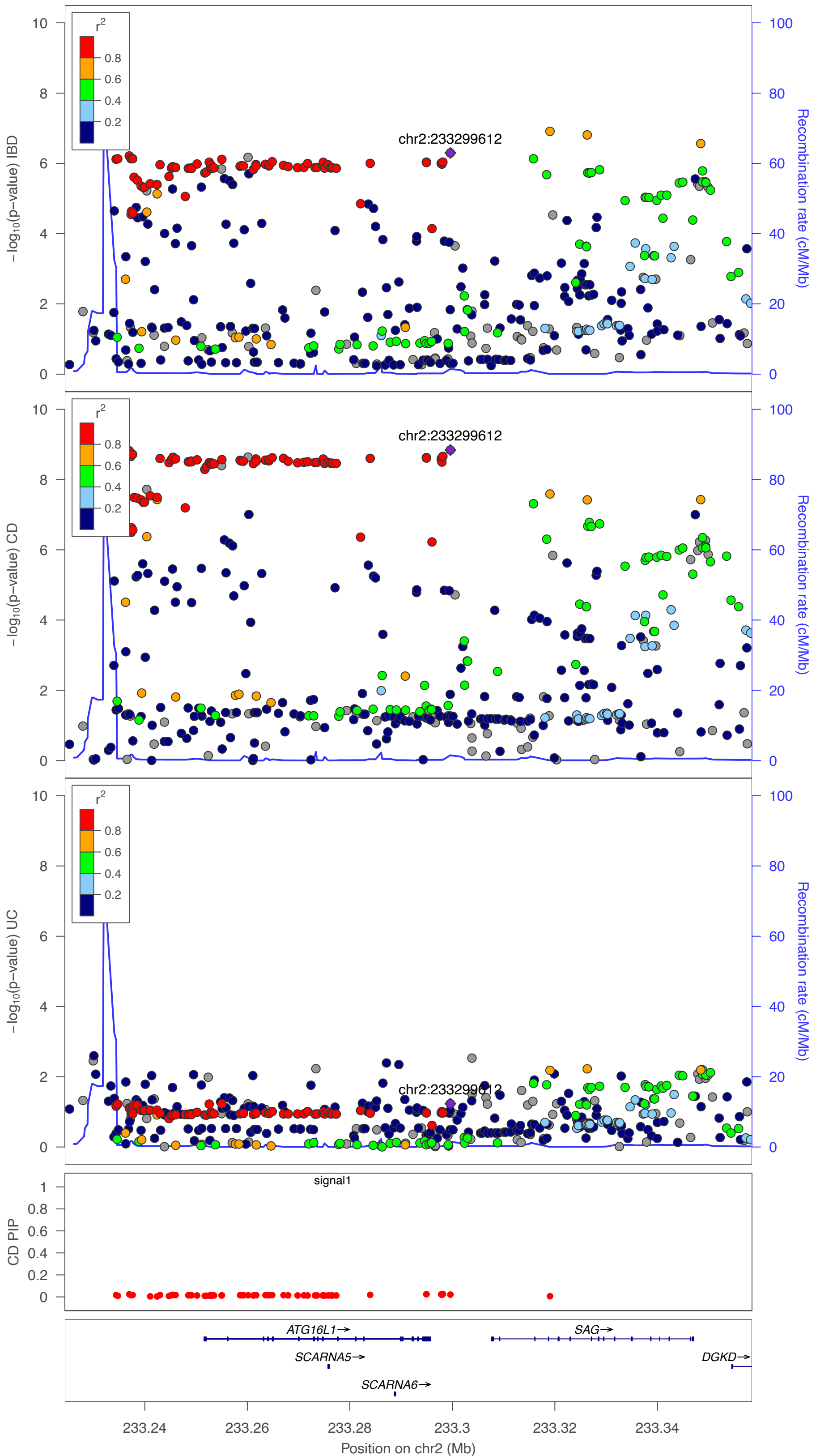
IBD chr2:203720036:T:C



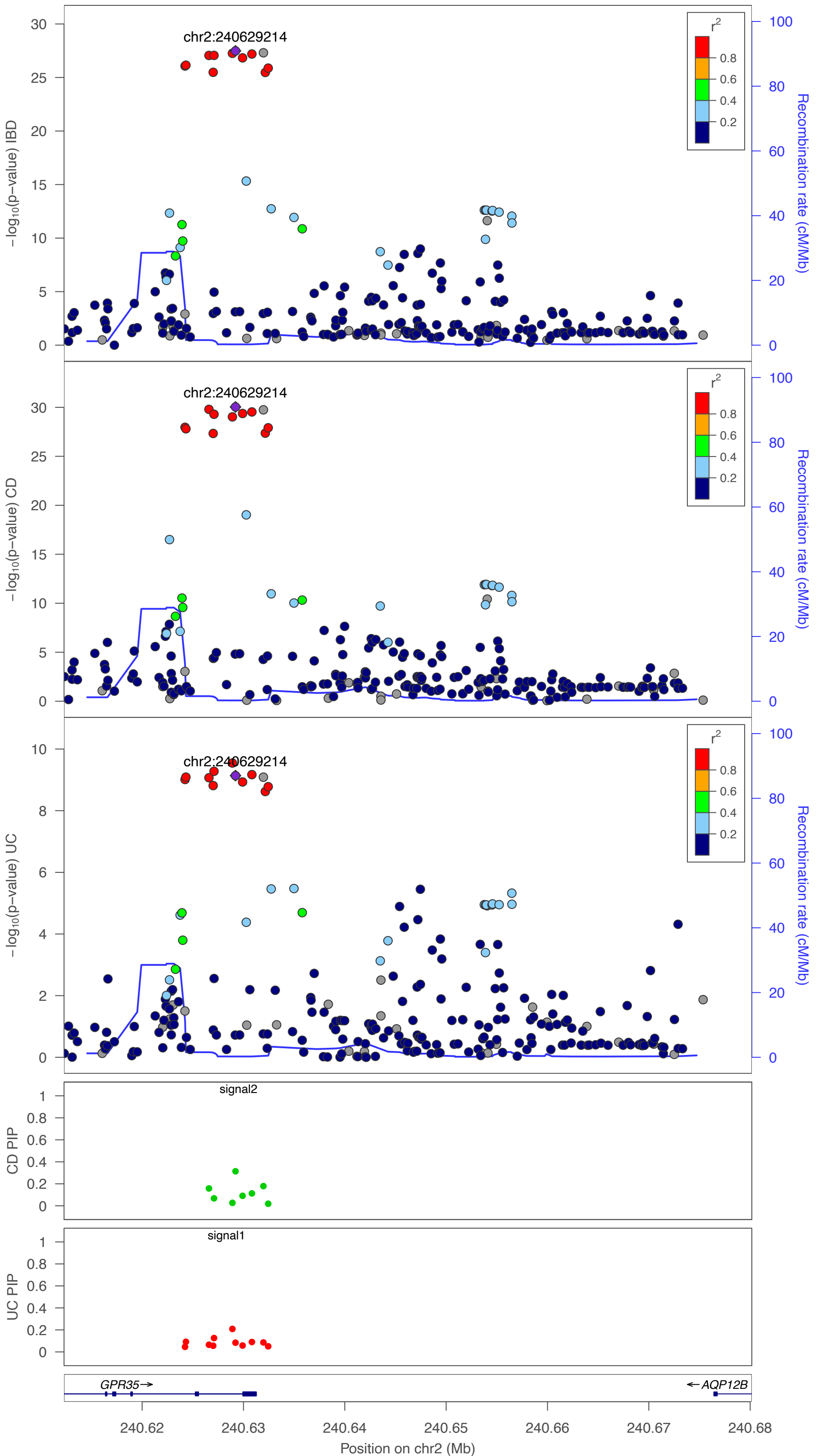
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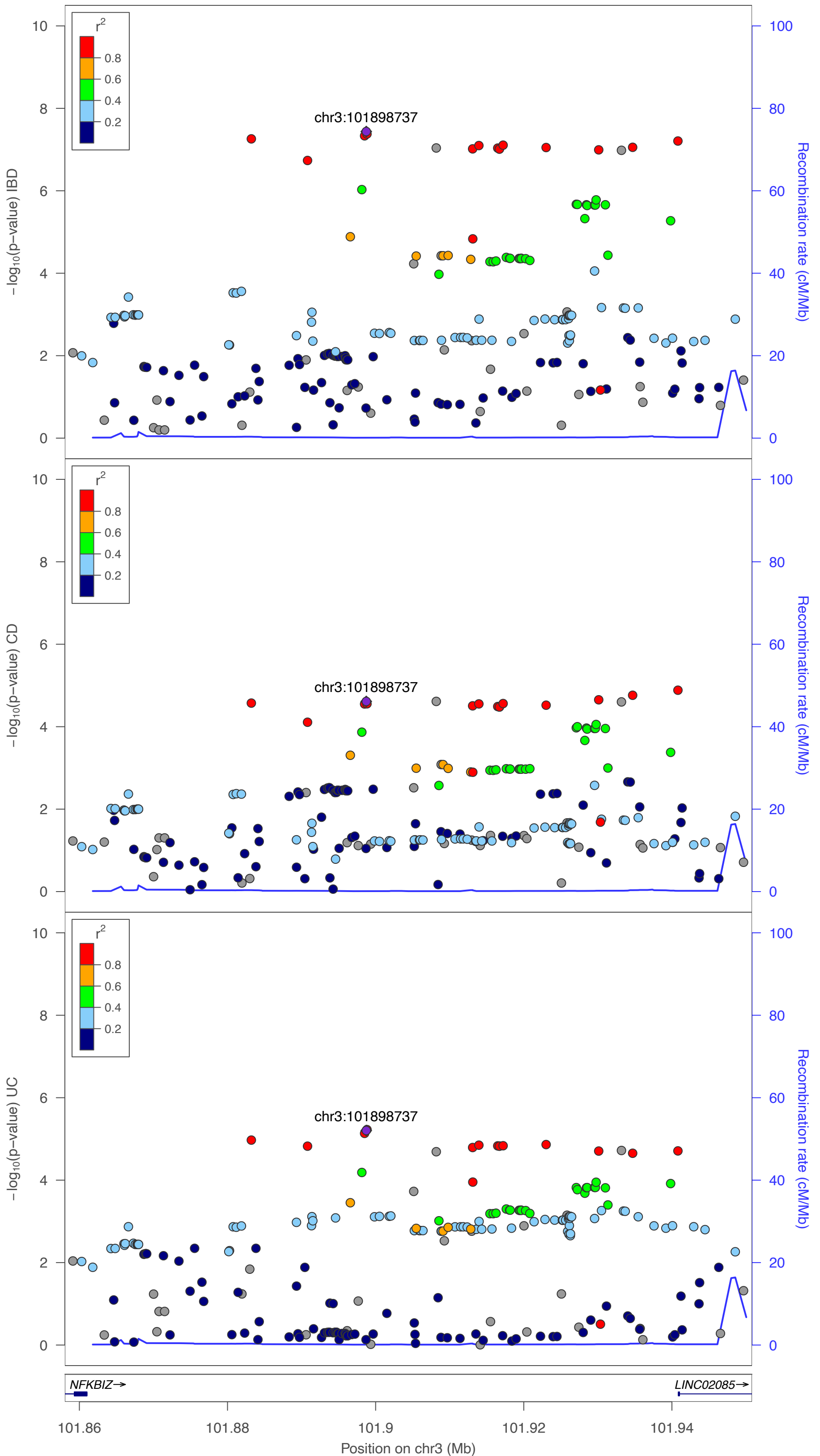
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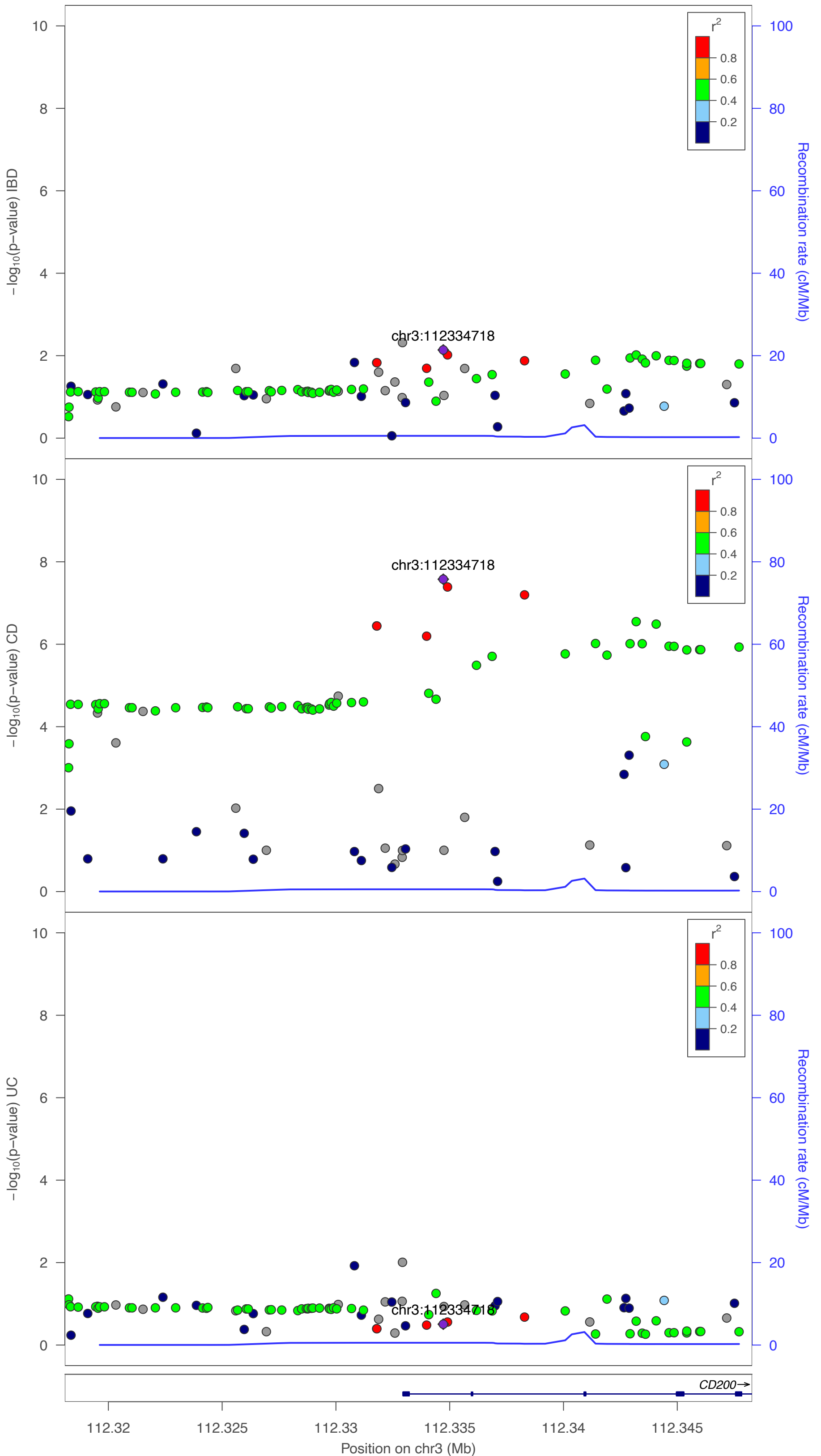
IBD chr2:240629214:A:G



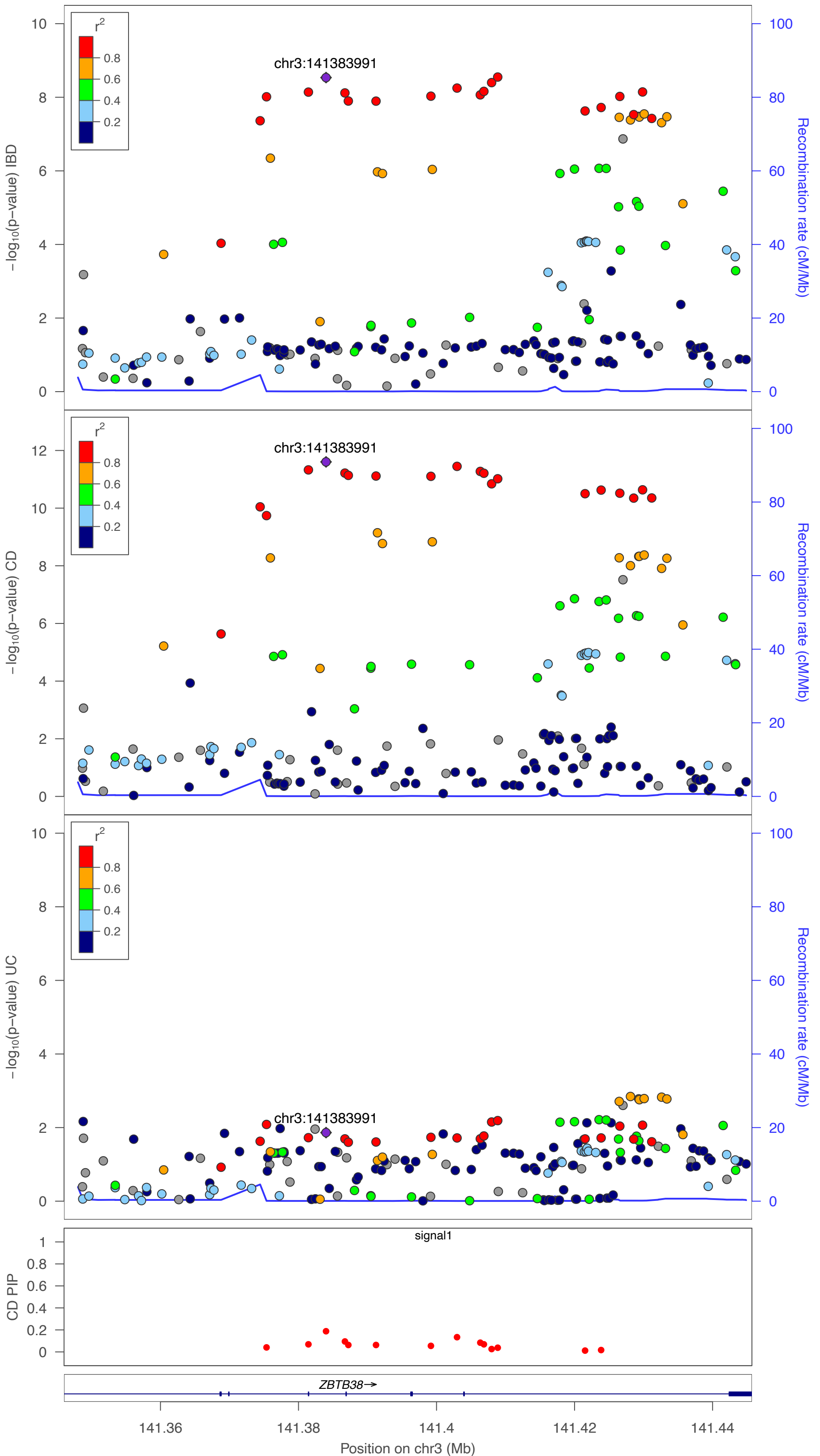
IBD chr3:101898737:G:C



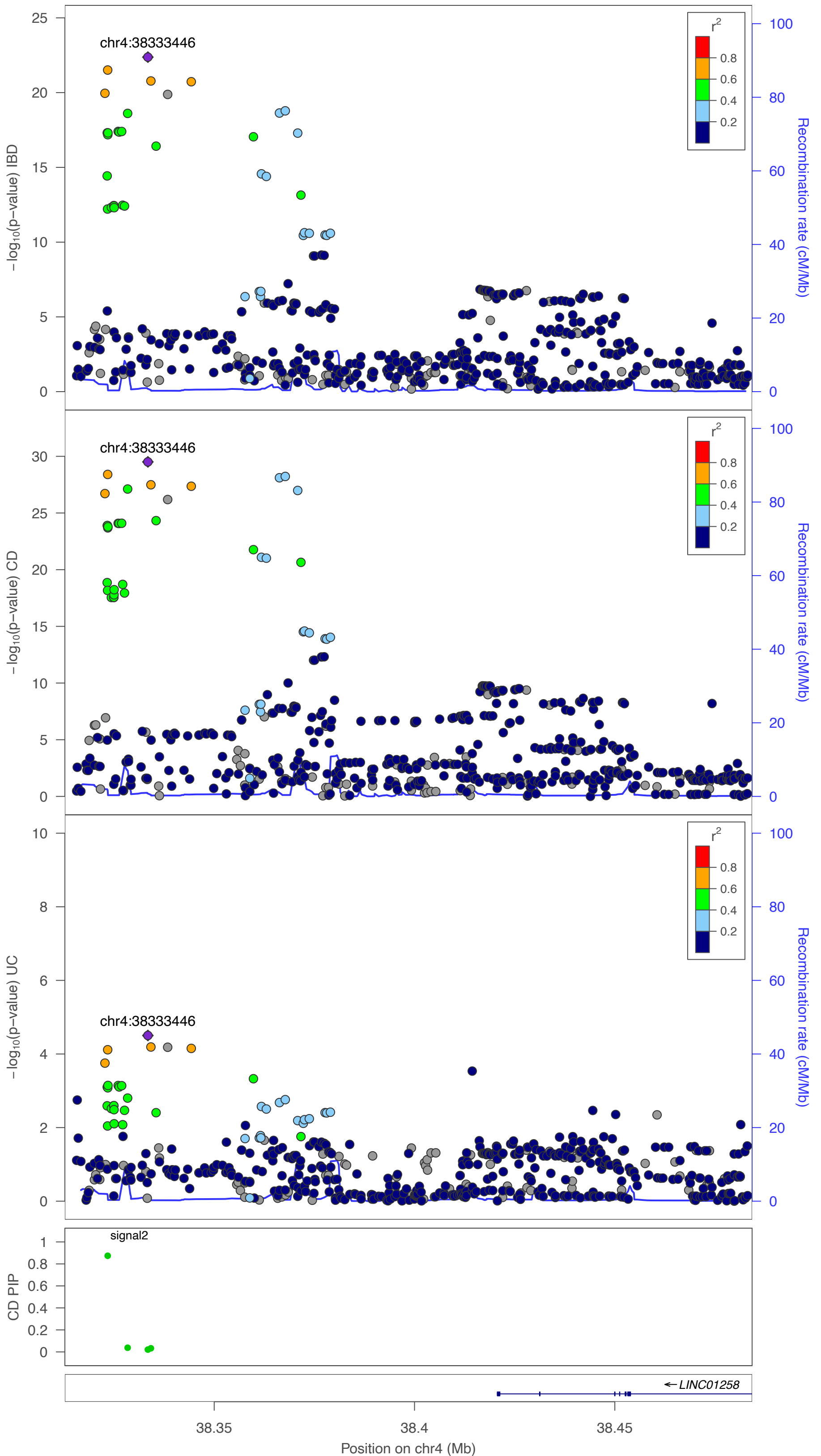
CD chr3:112334718:G:A



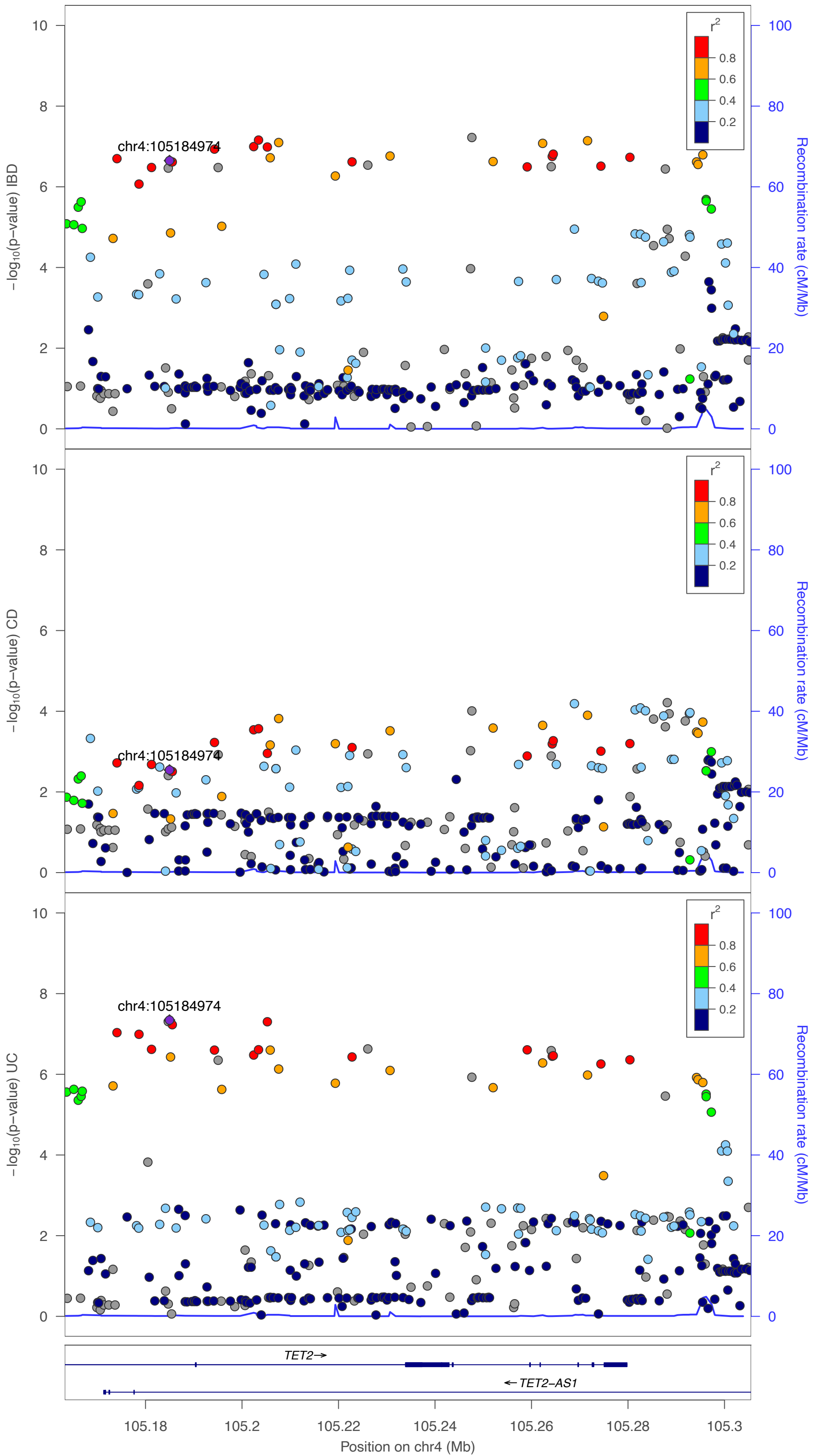
CD chr3:141383991:G:A



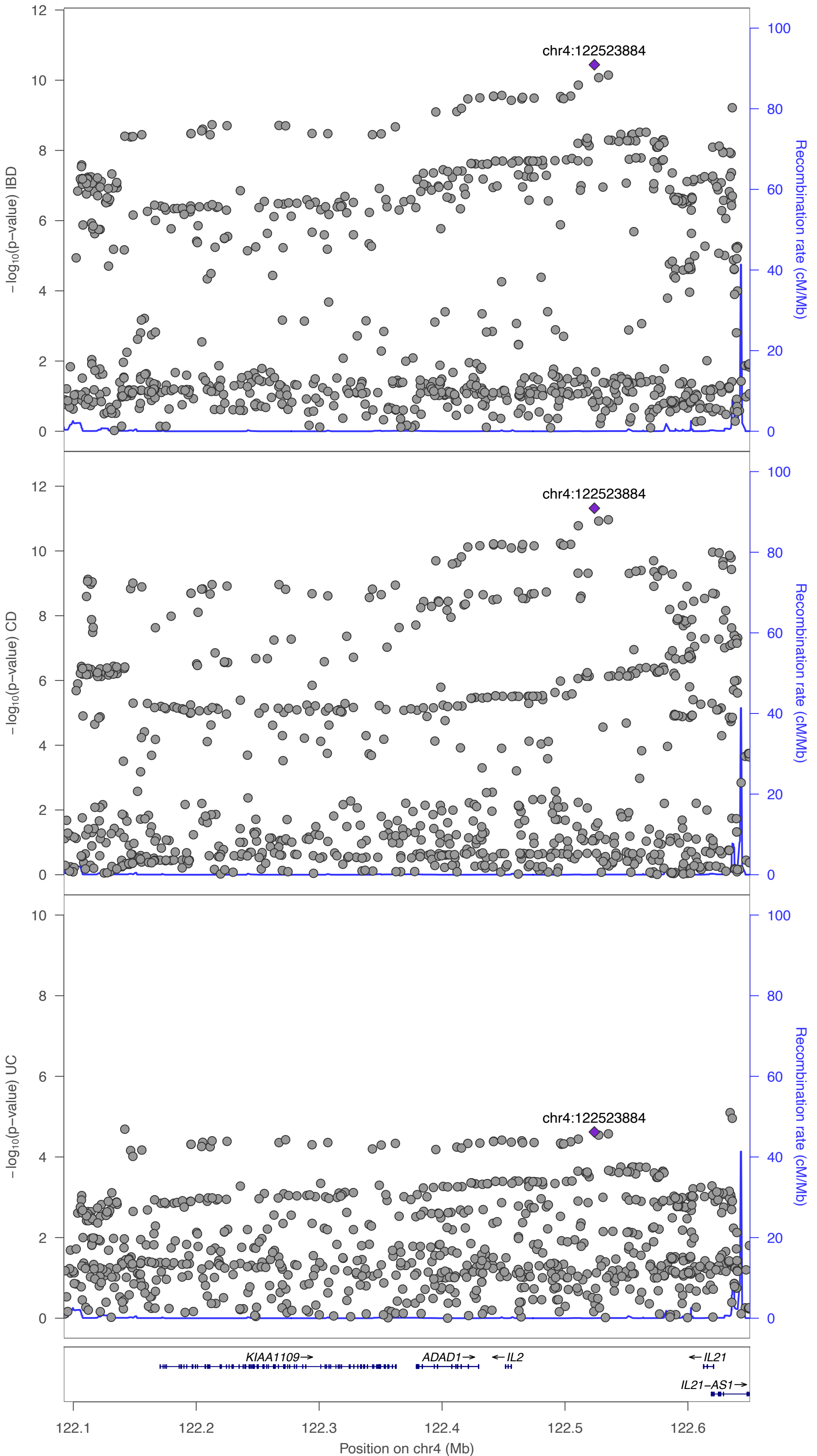
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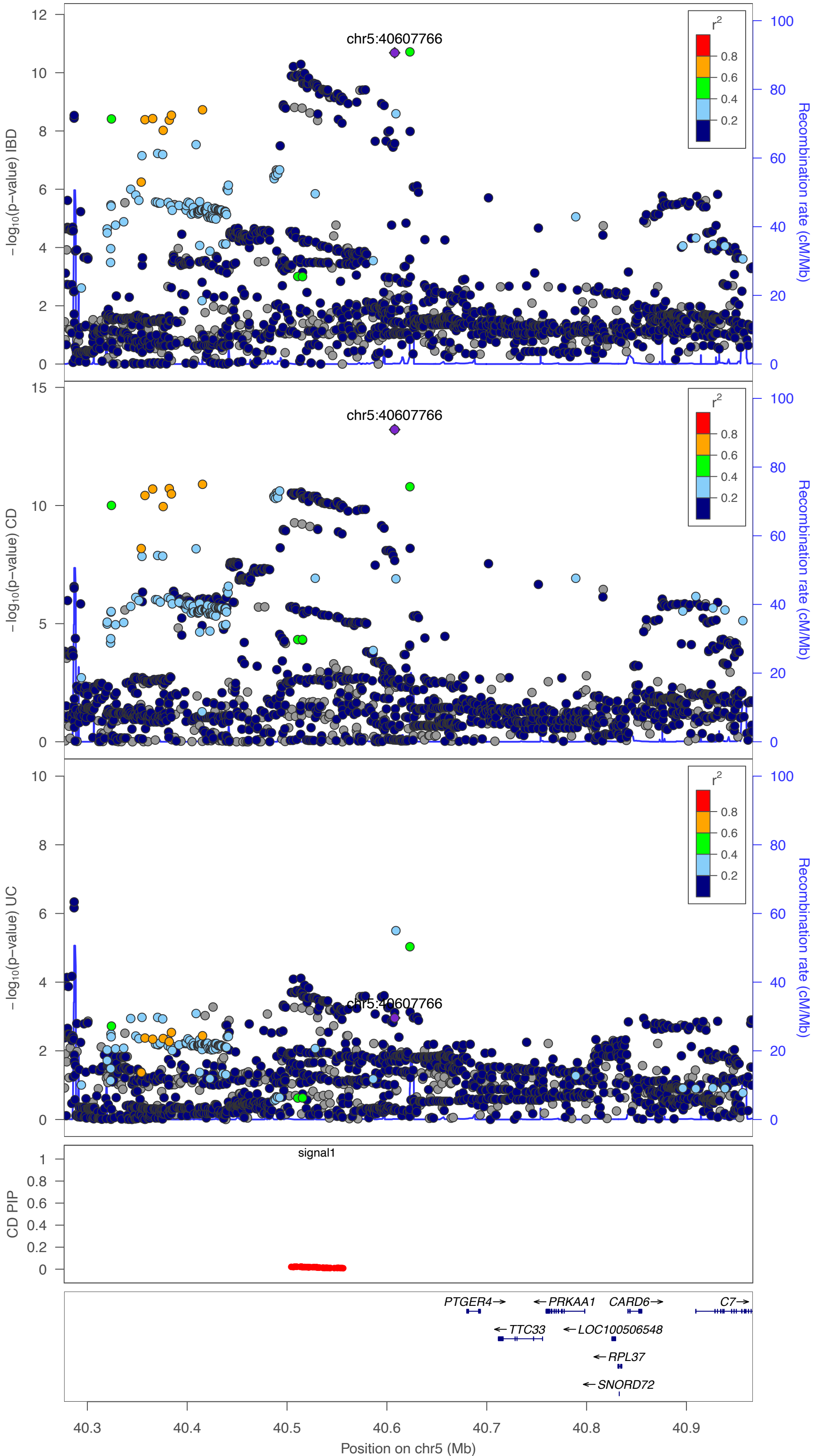
UC chr4:105184974:G:C



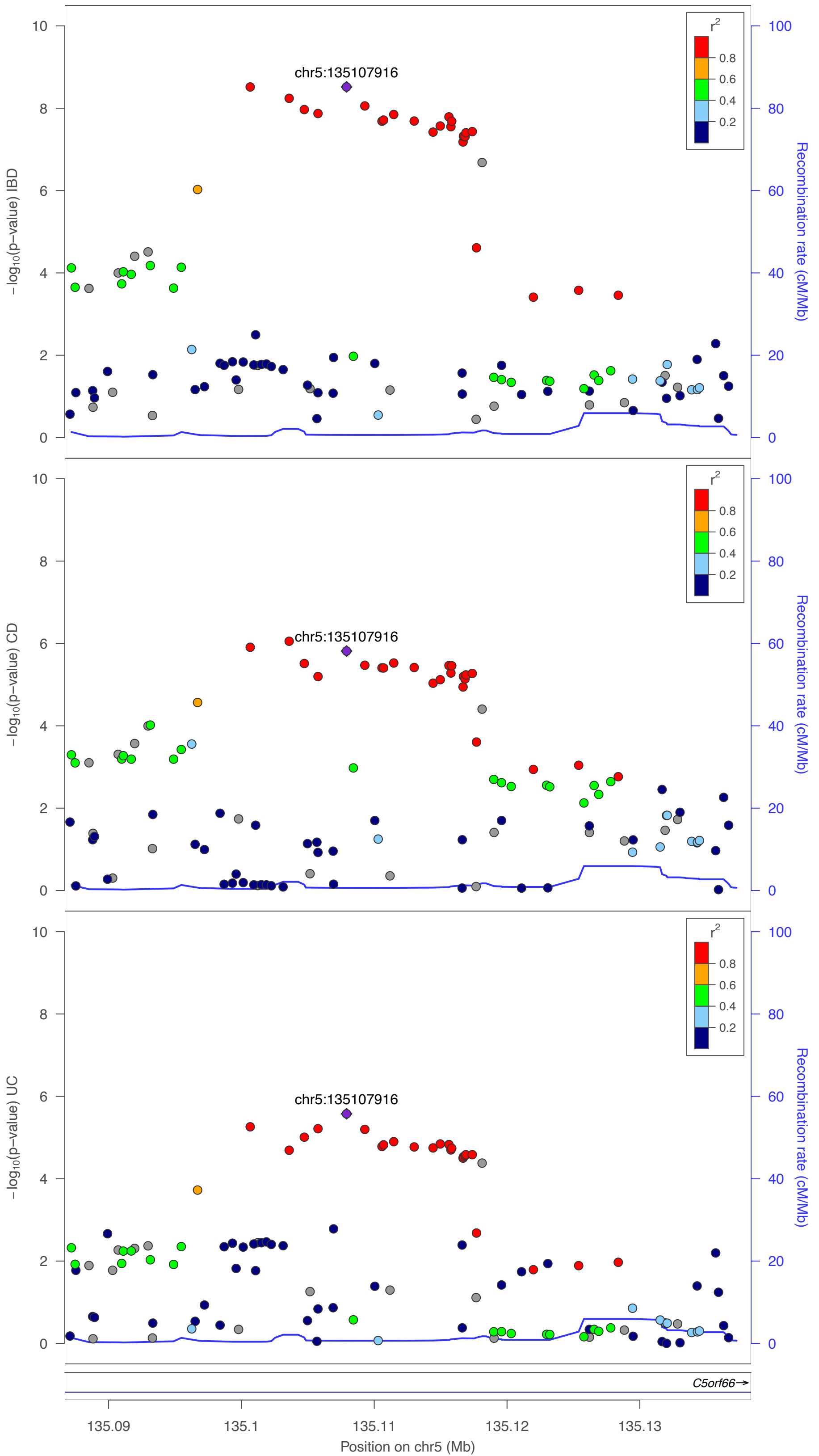
IBD chr4:122523884:G:GT



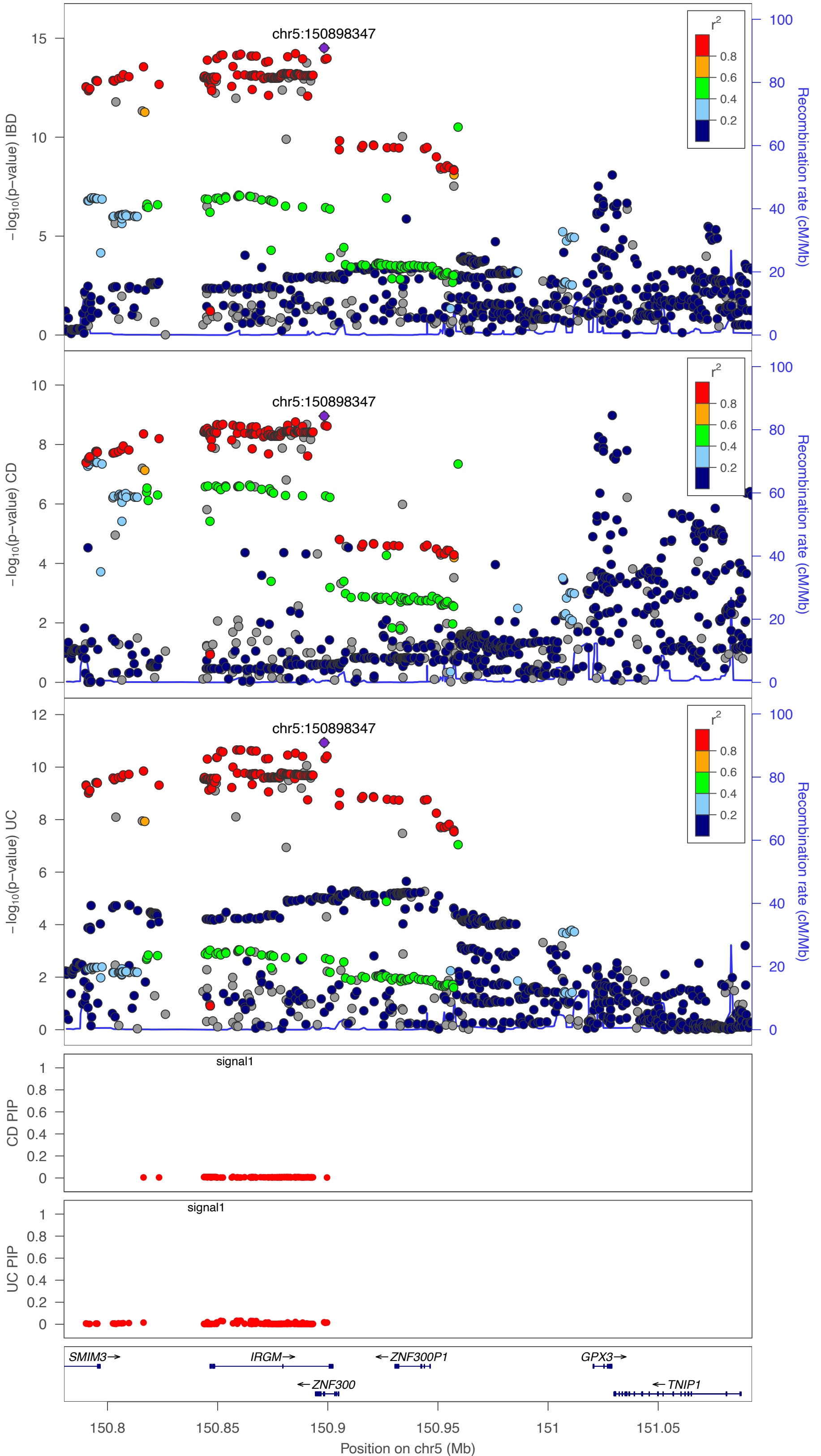
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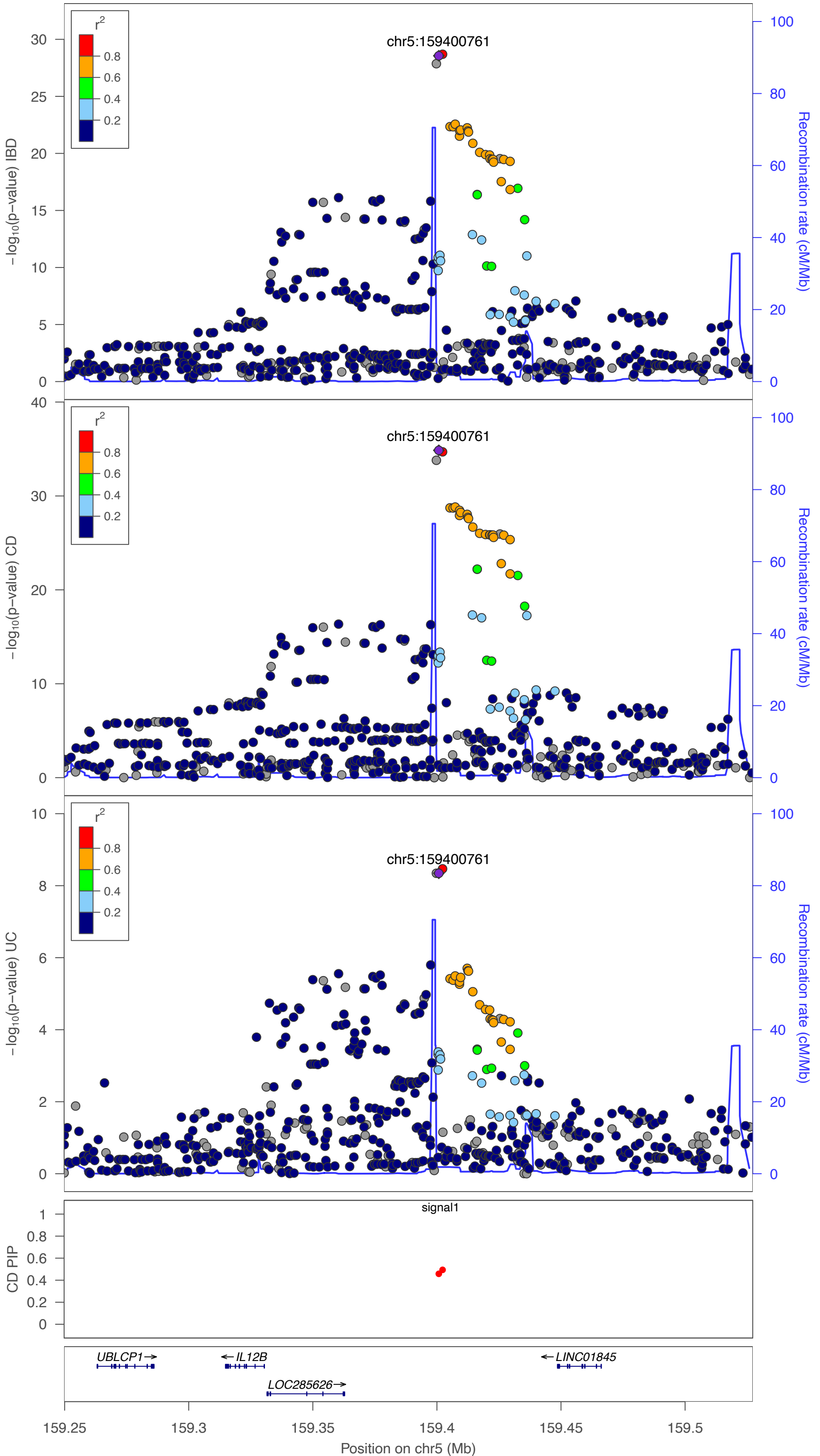
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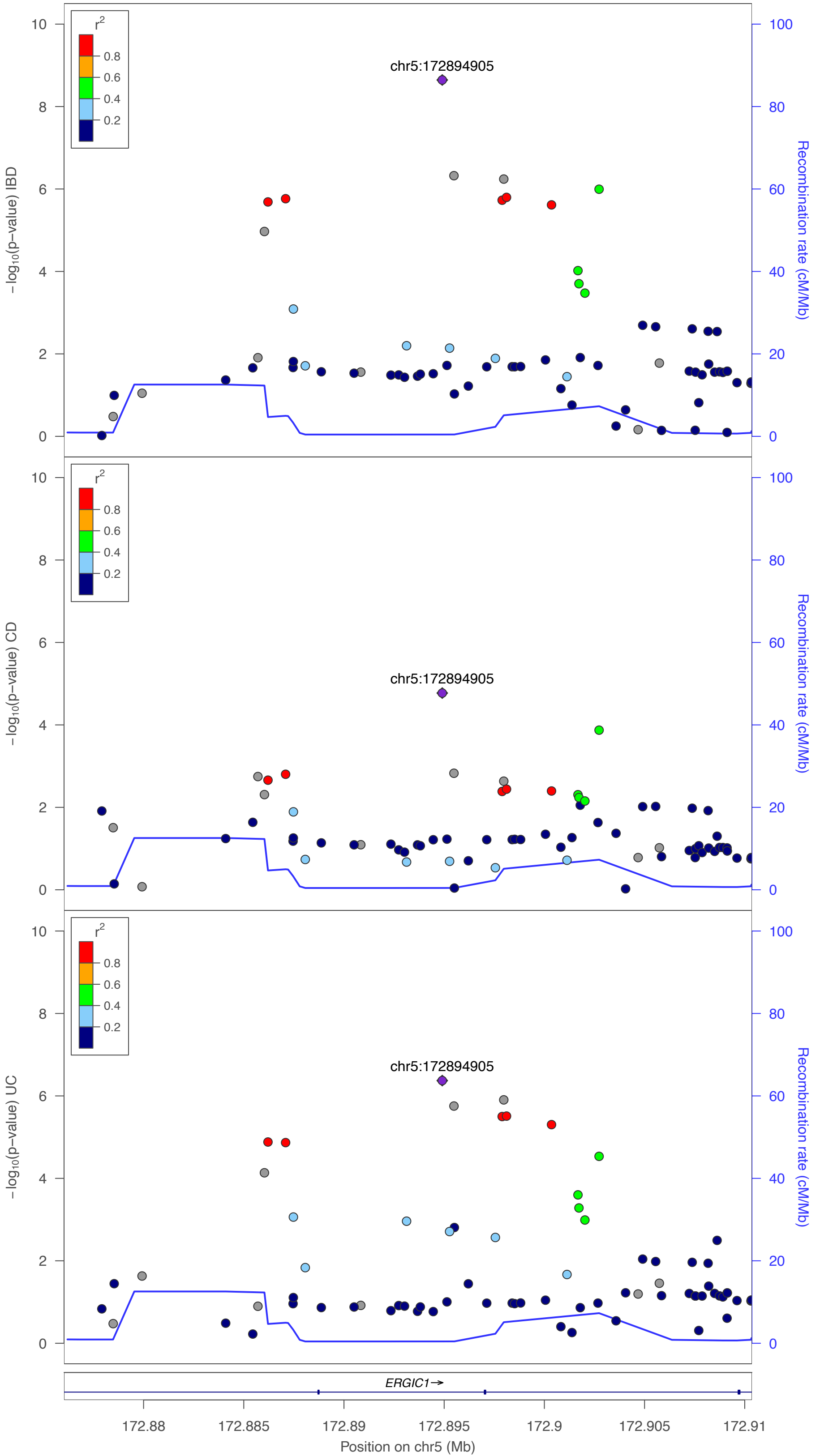
IBD chr5:150898347:A:G



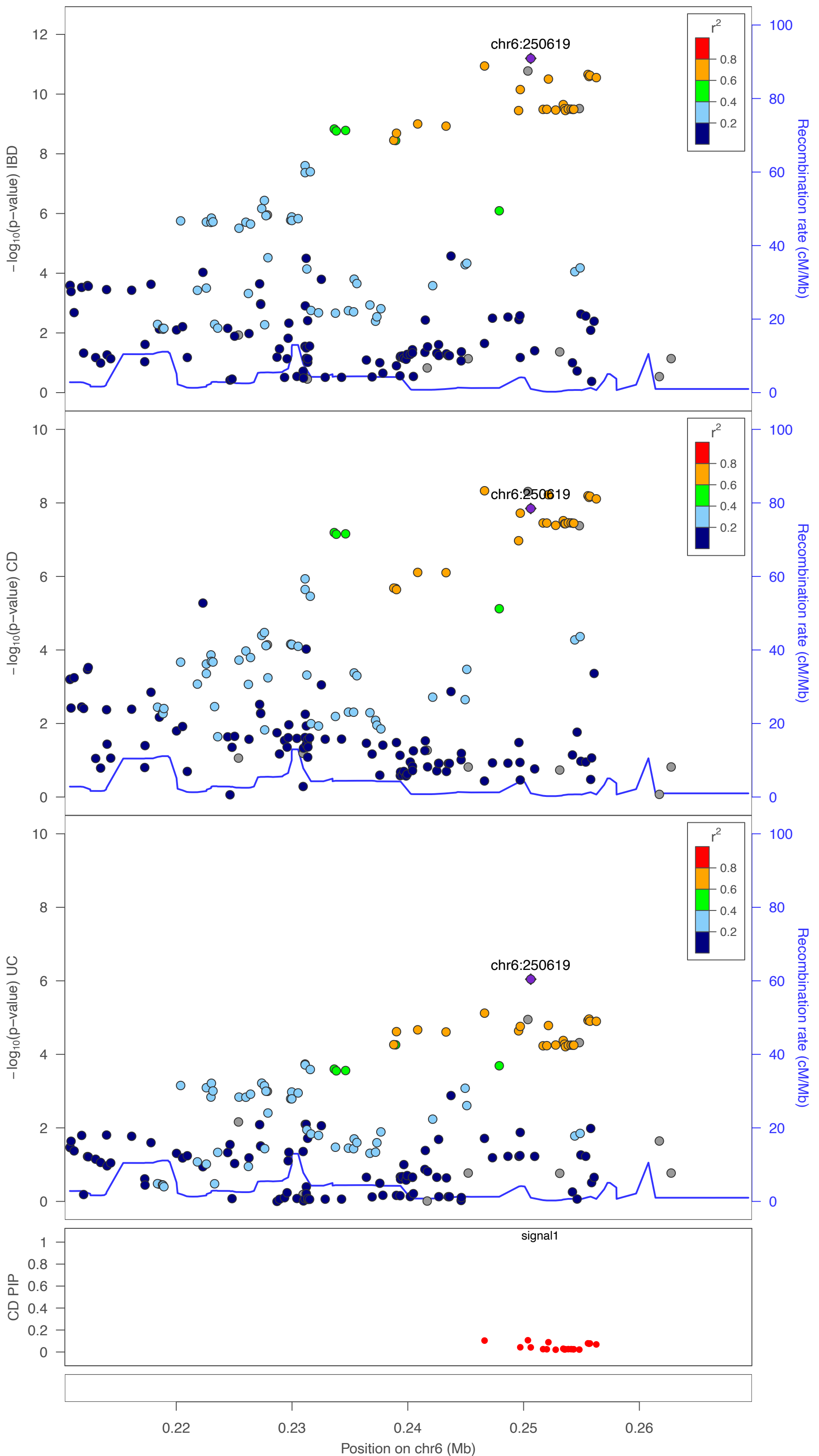
IBD chr5:159400761:C:A



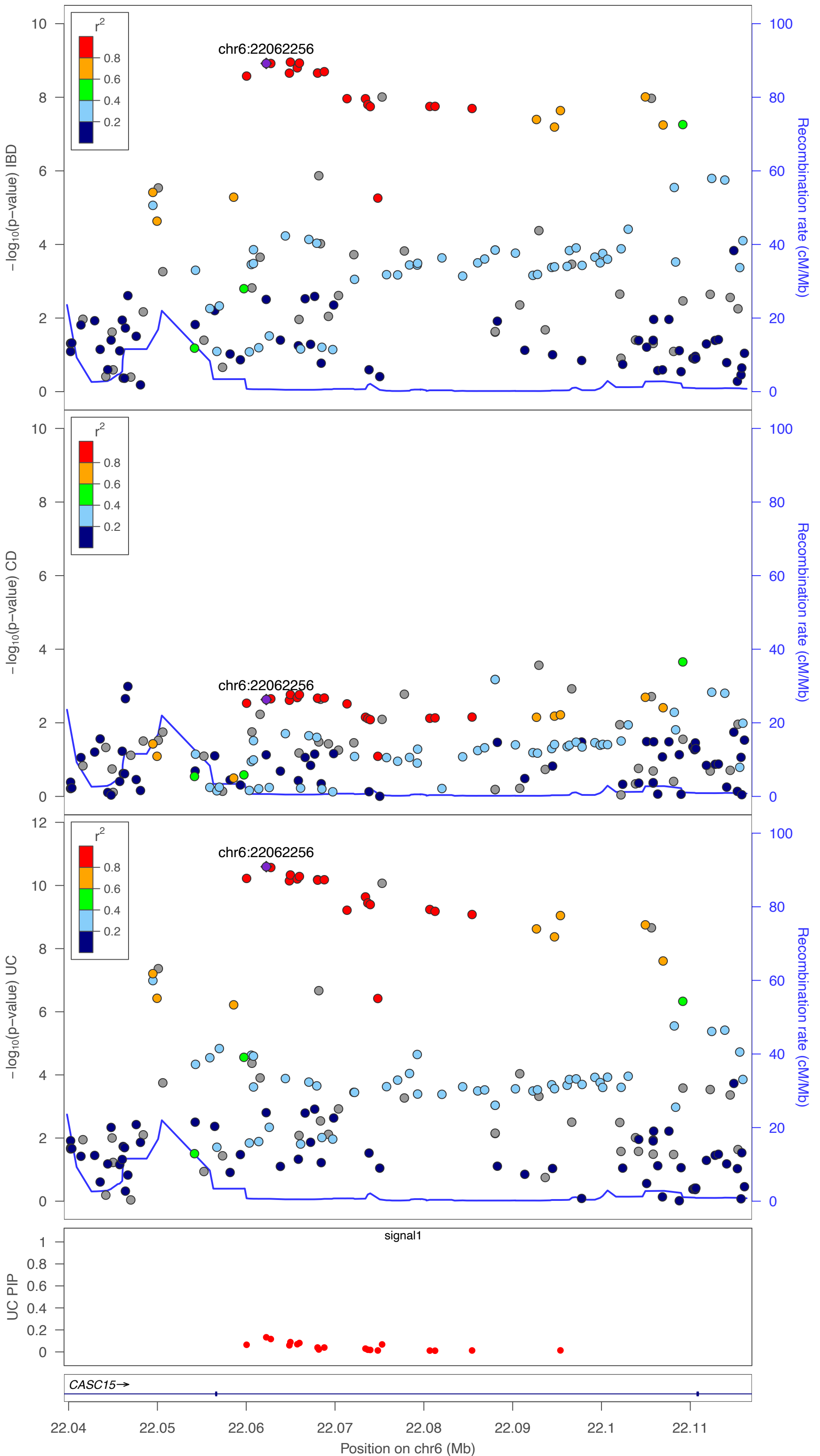
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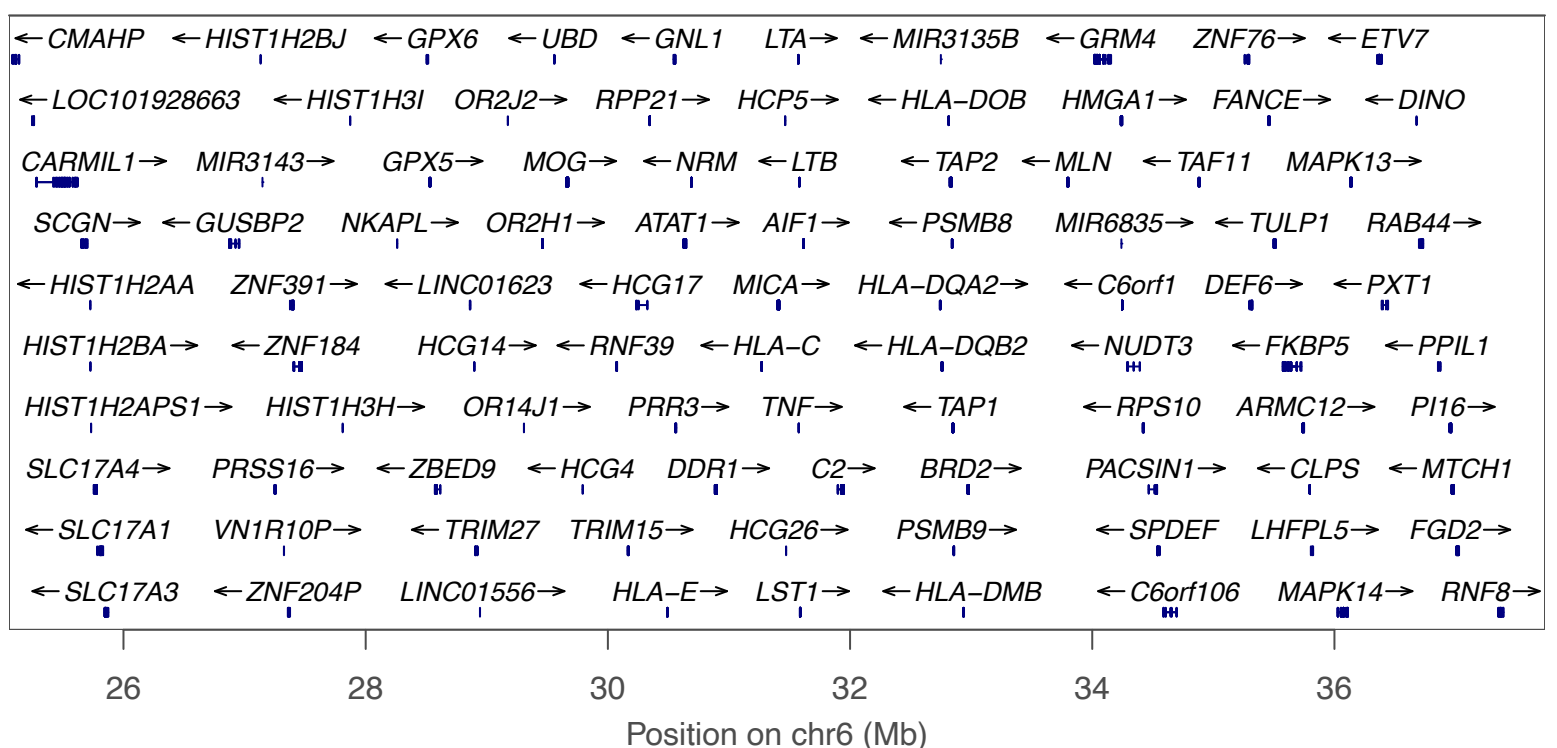
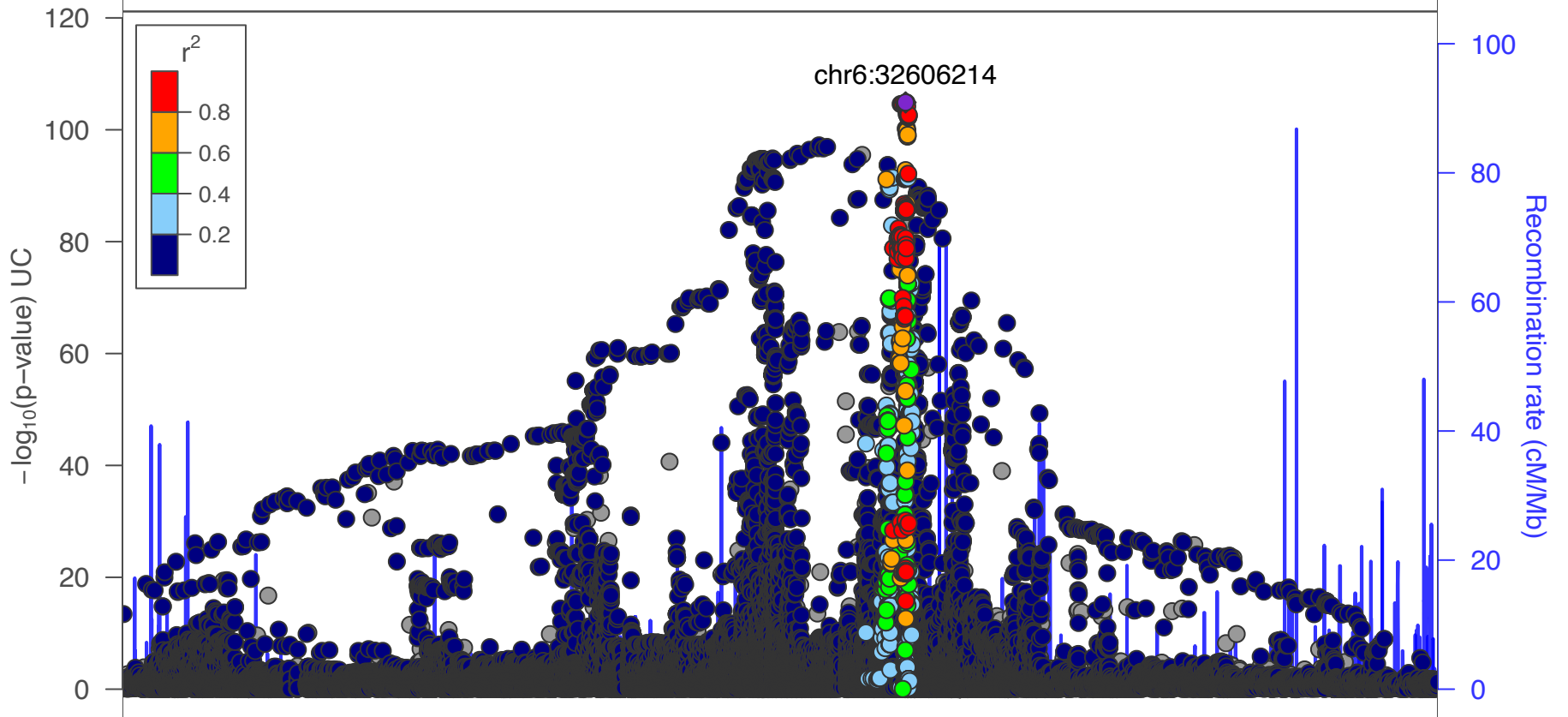
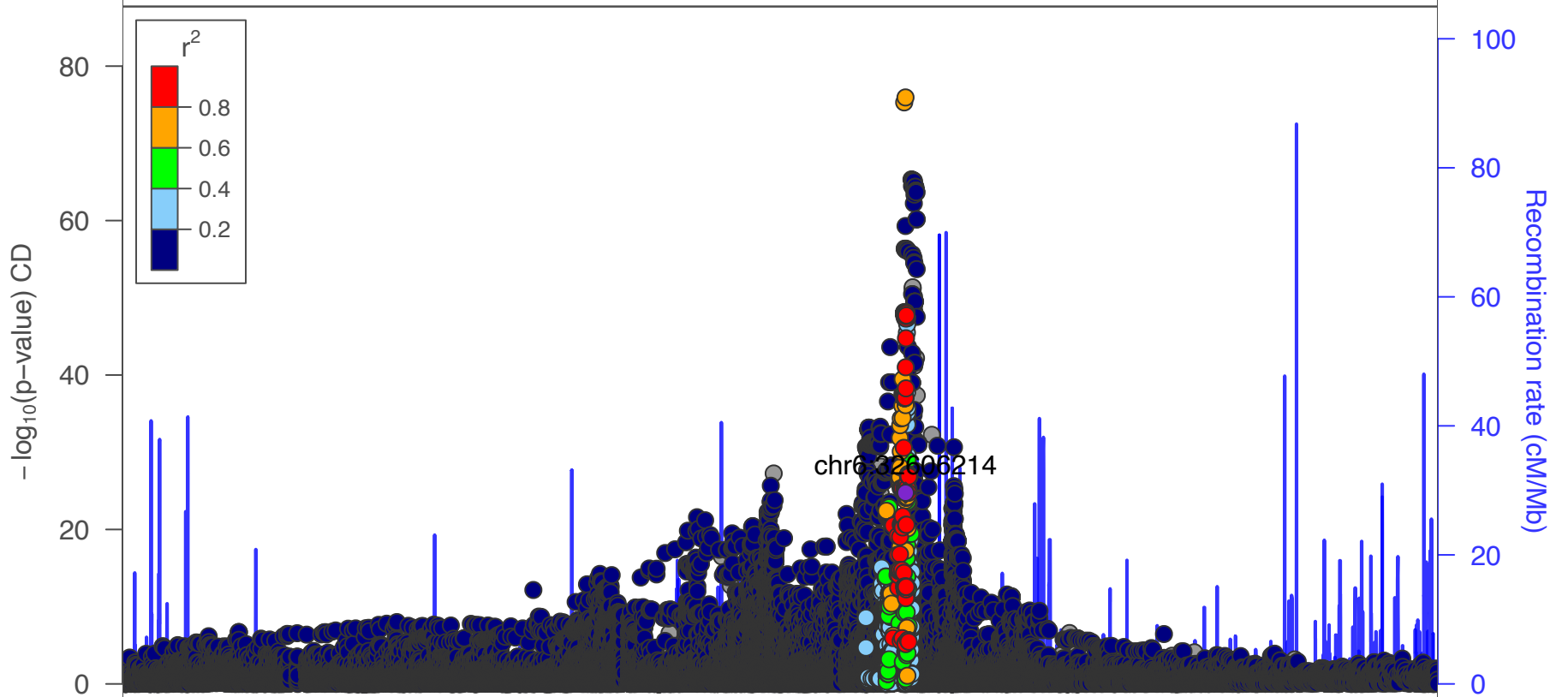
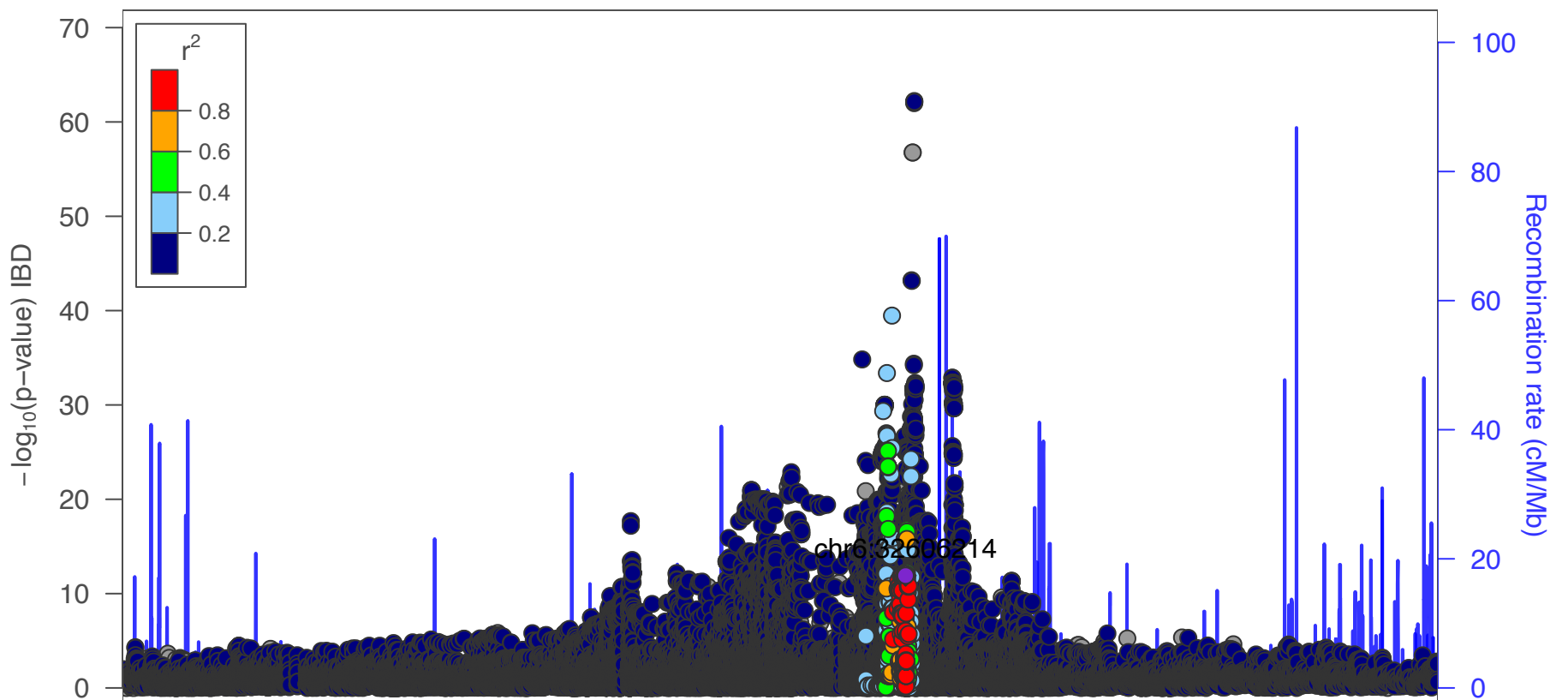
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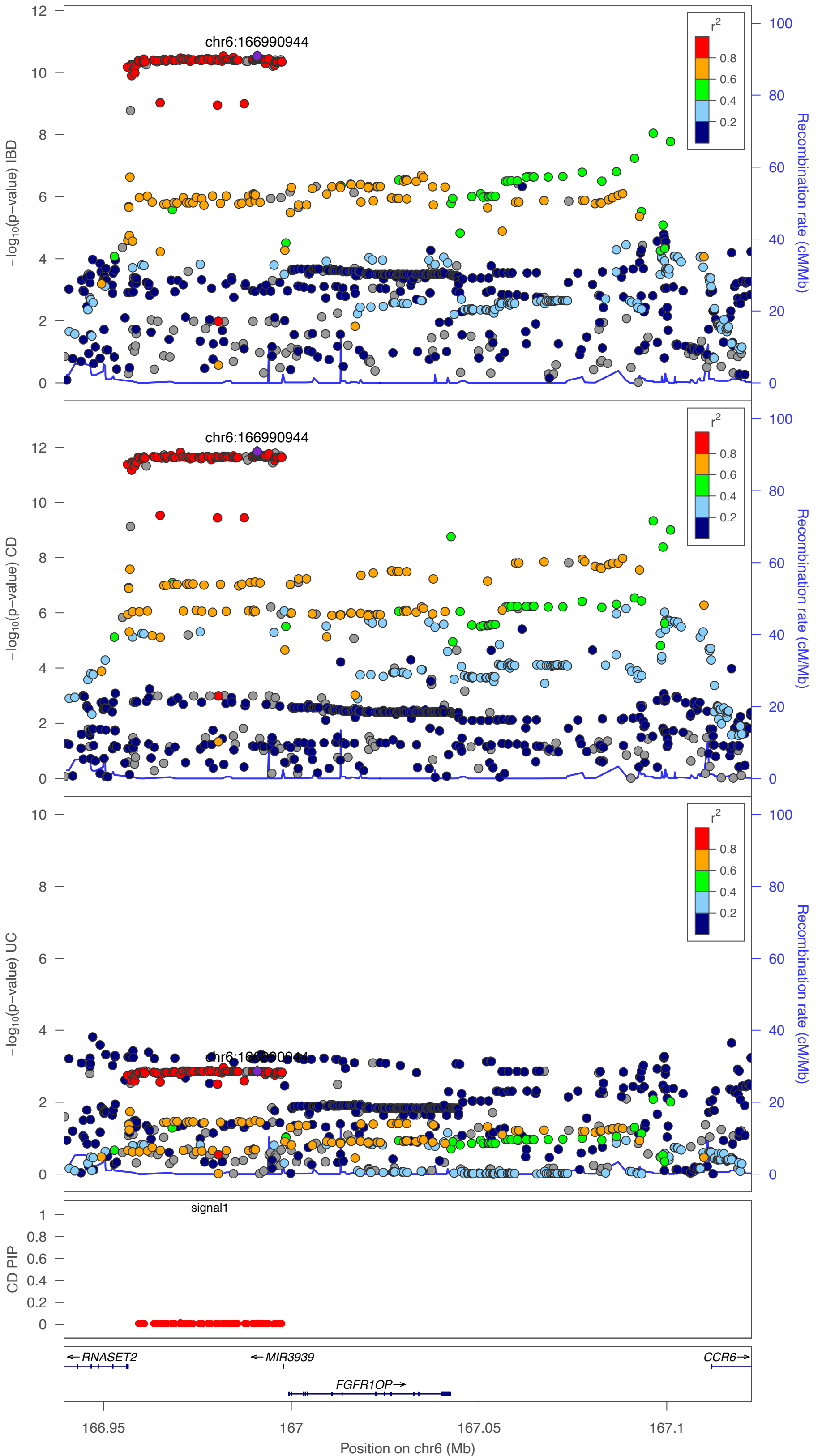
UC chr6:22062256:C:A



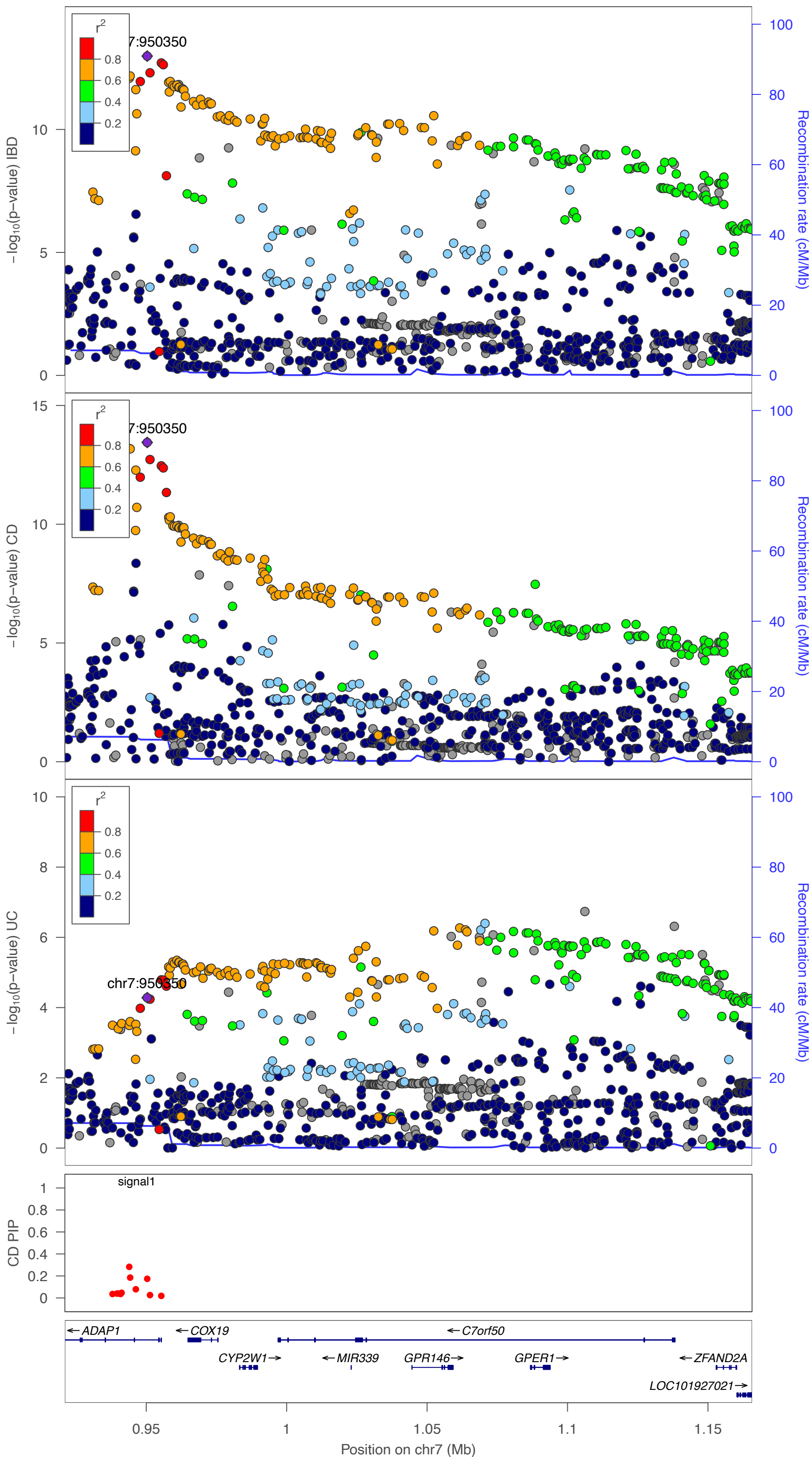
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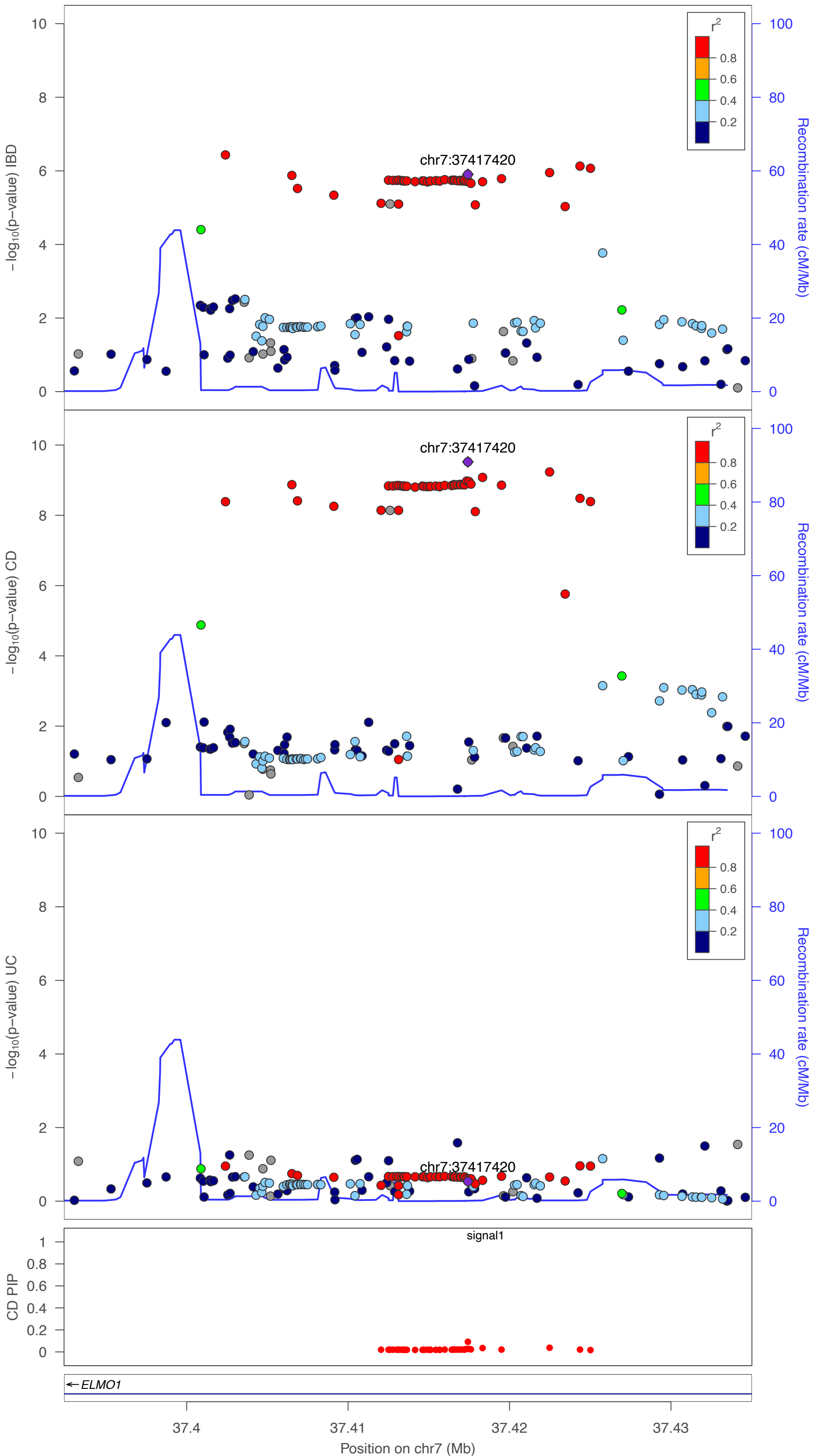
CD chr6:166990944:C:T



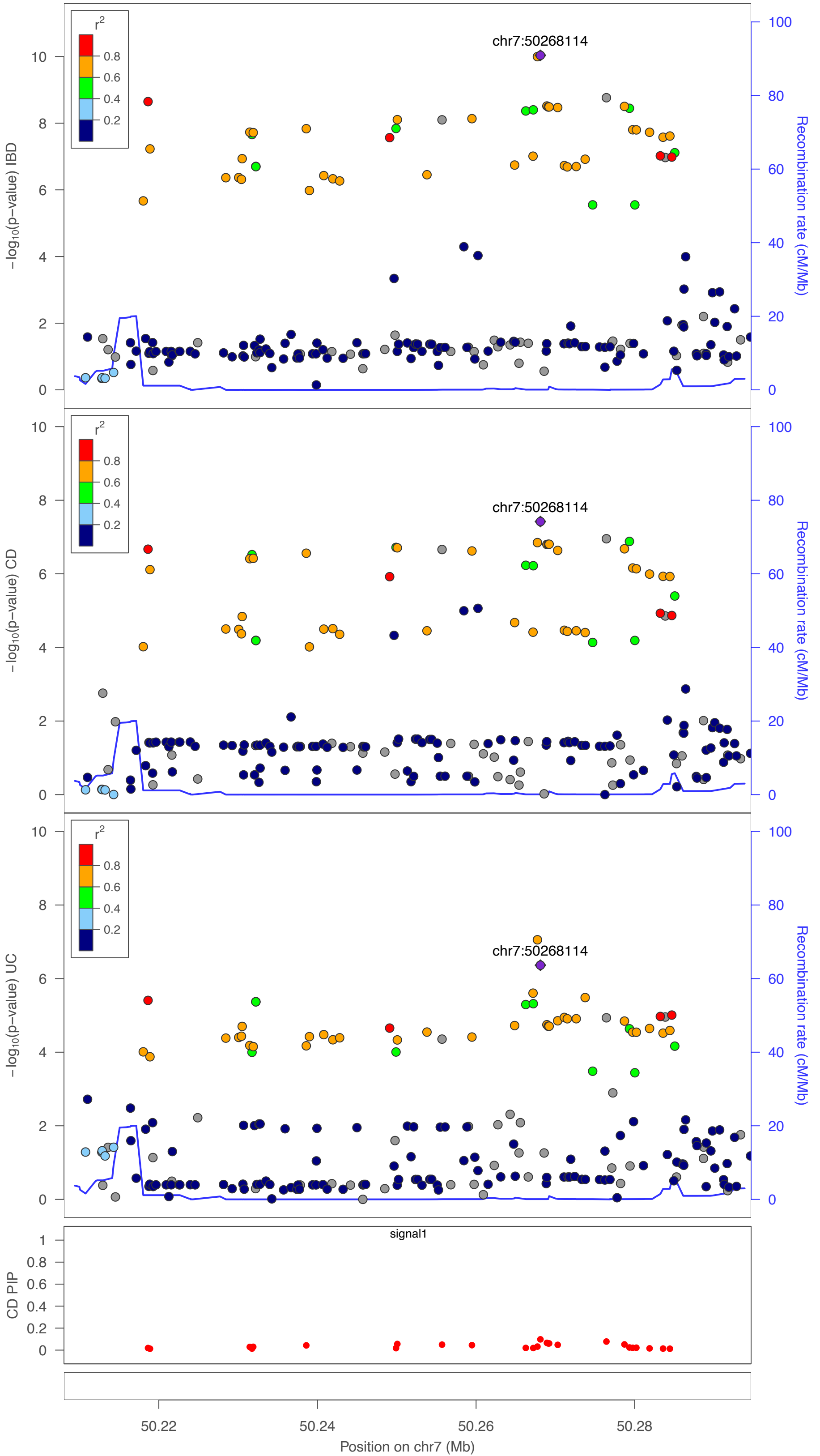
IBD chr7:950350:G:A



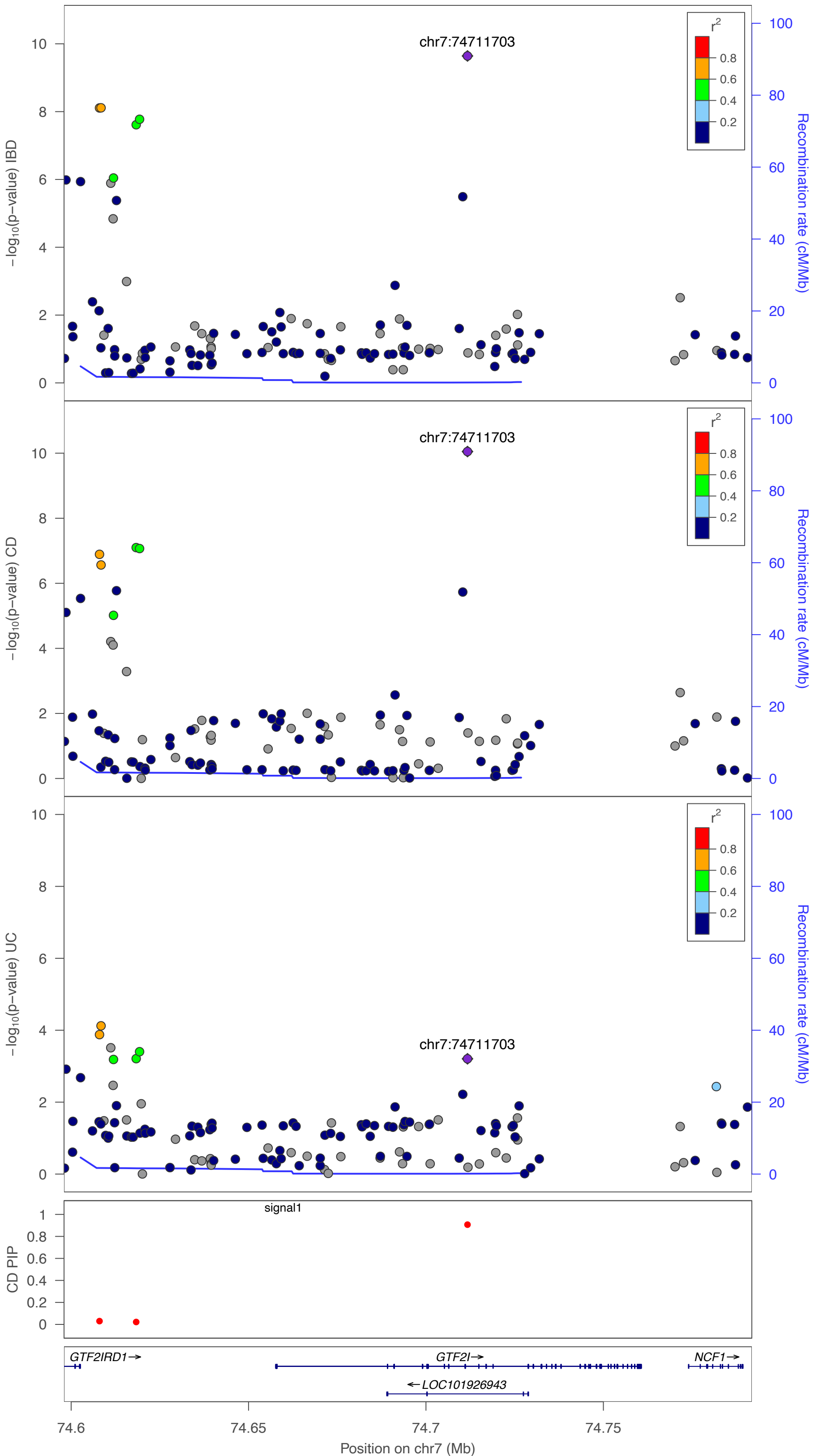
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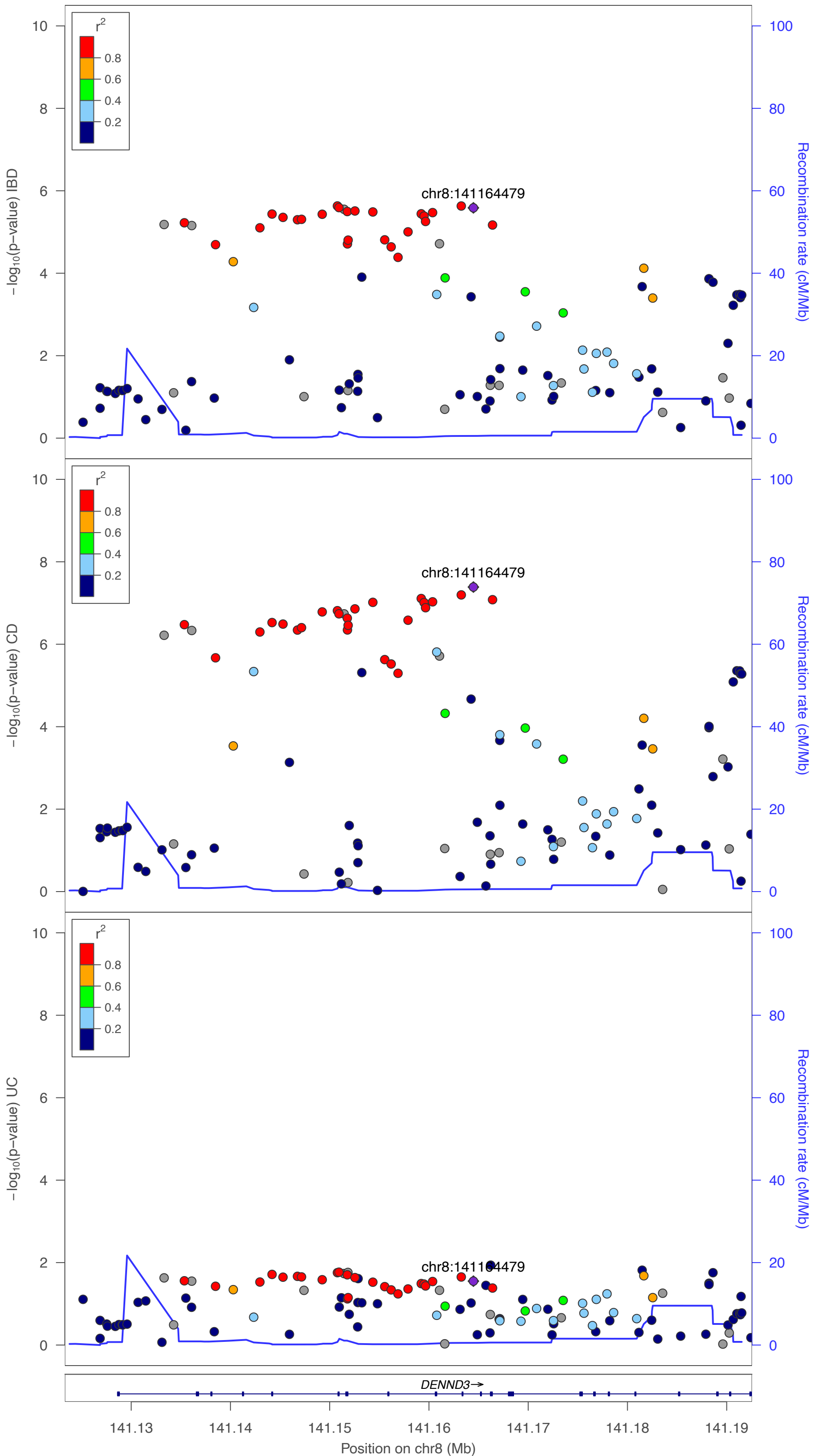
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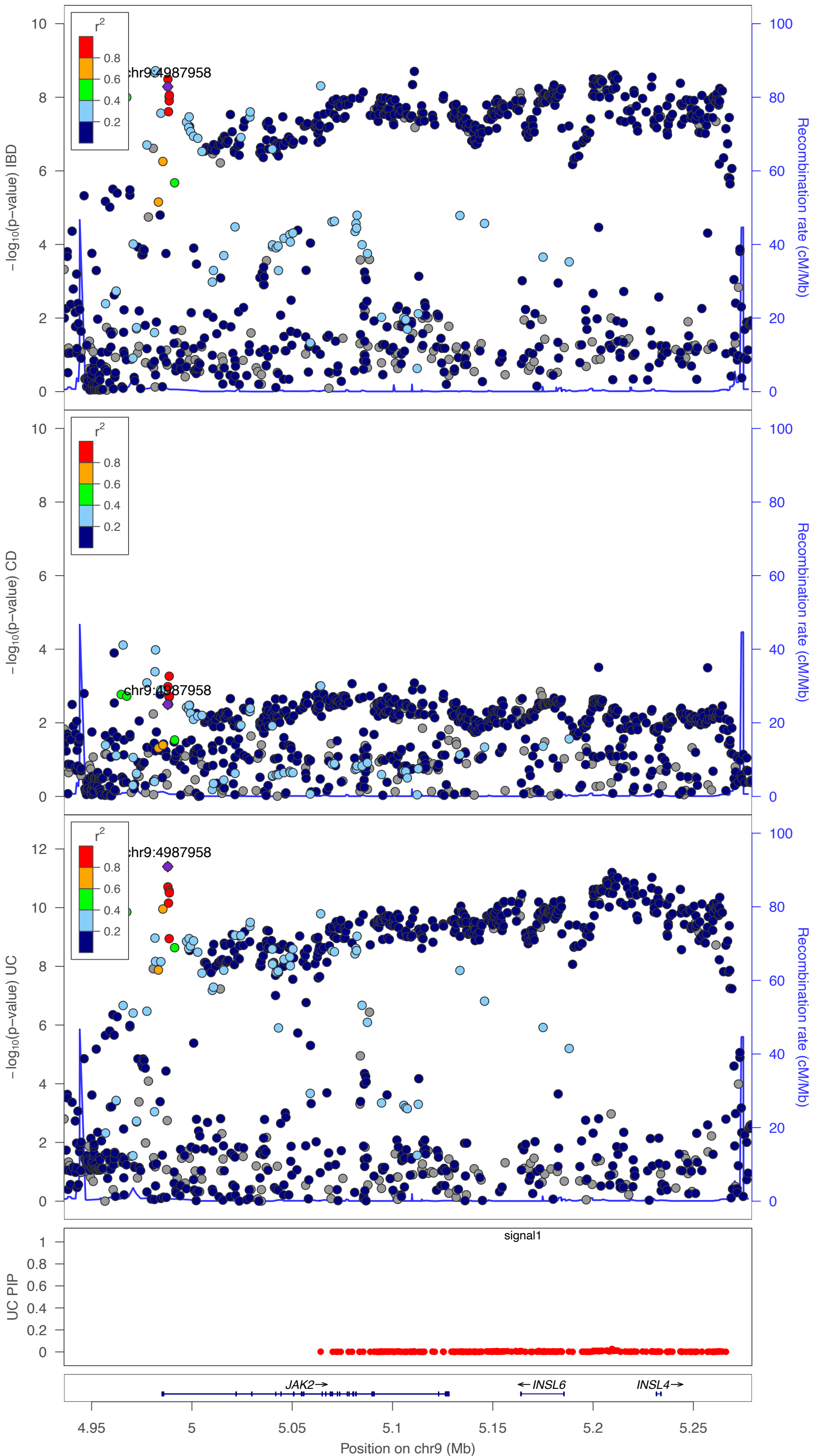
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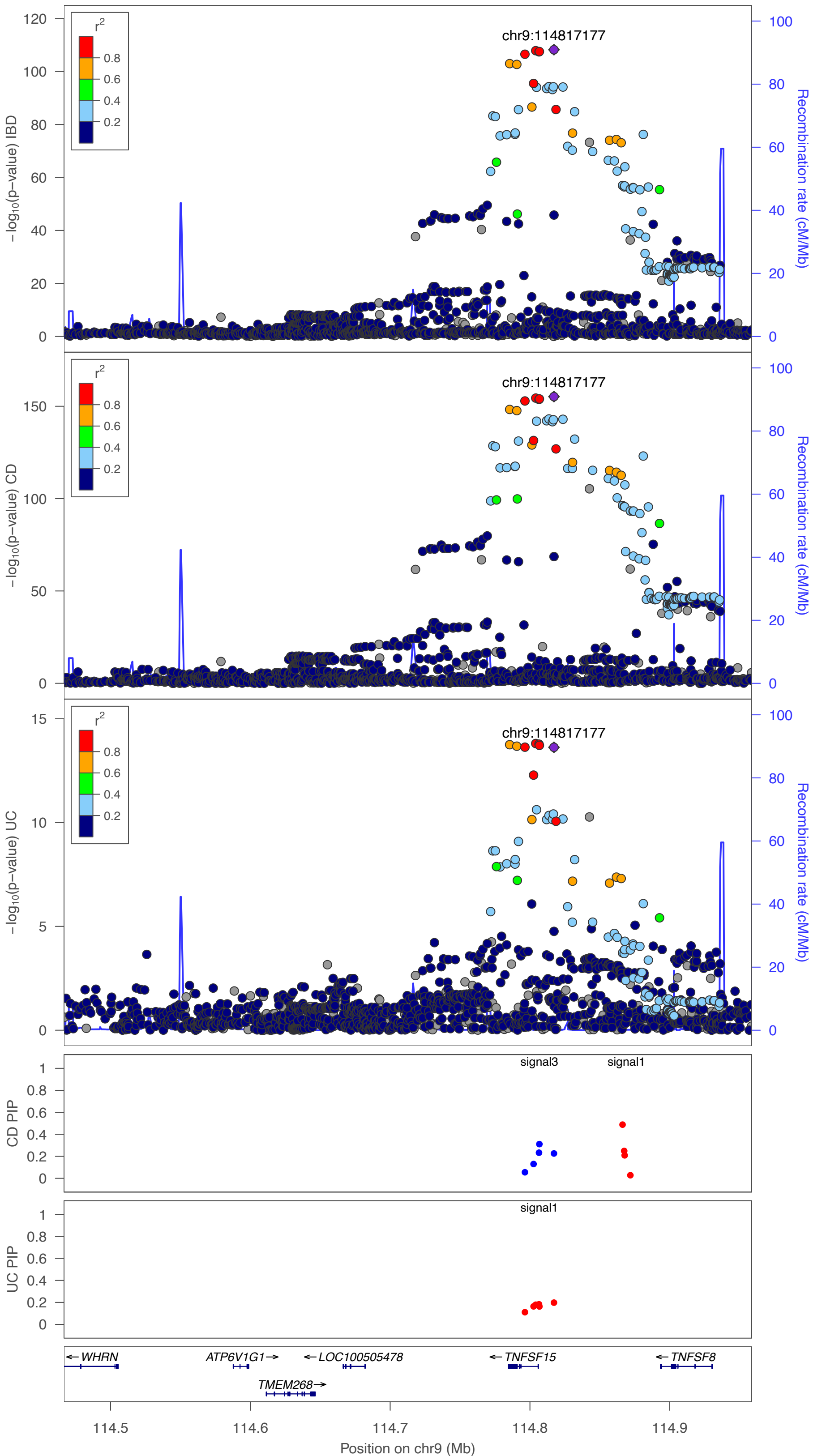
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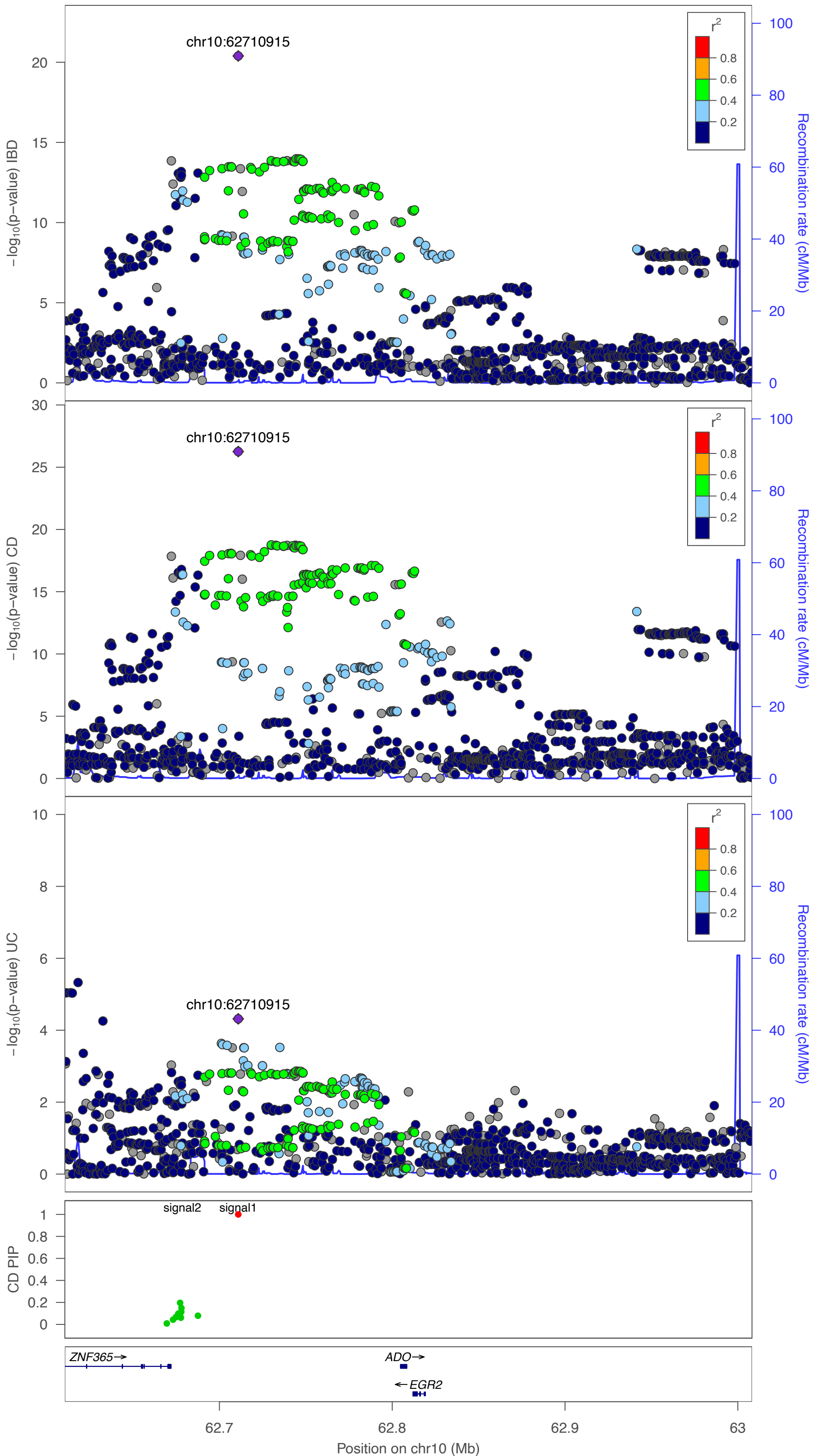
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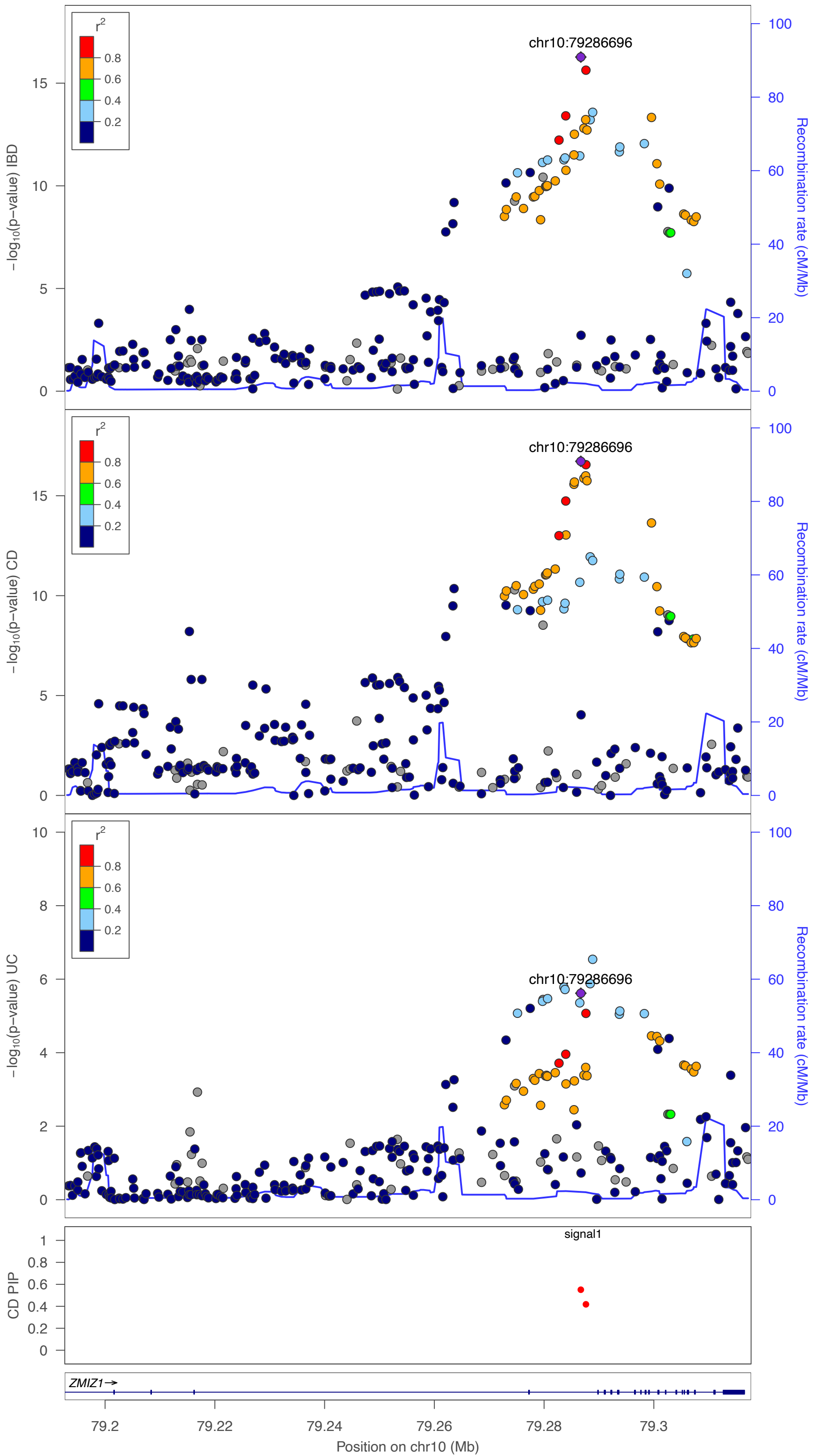
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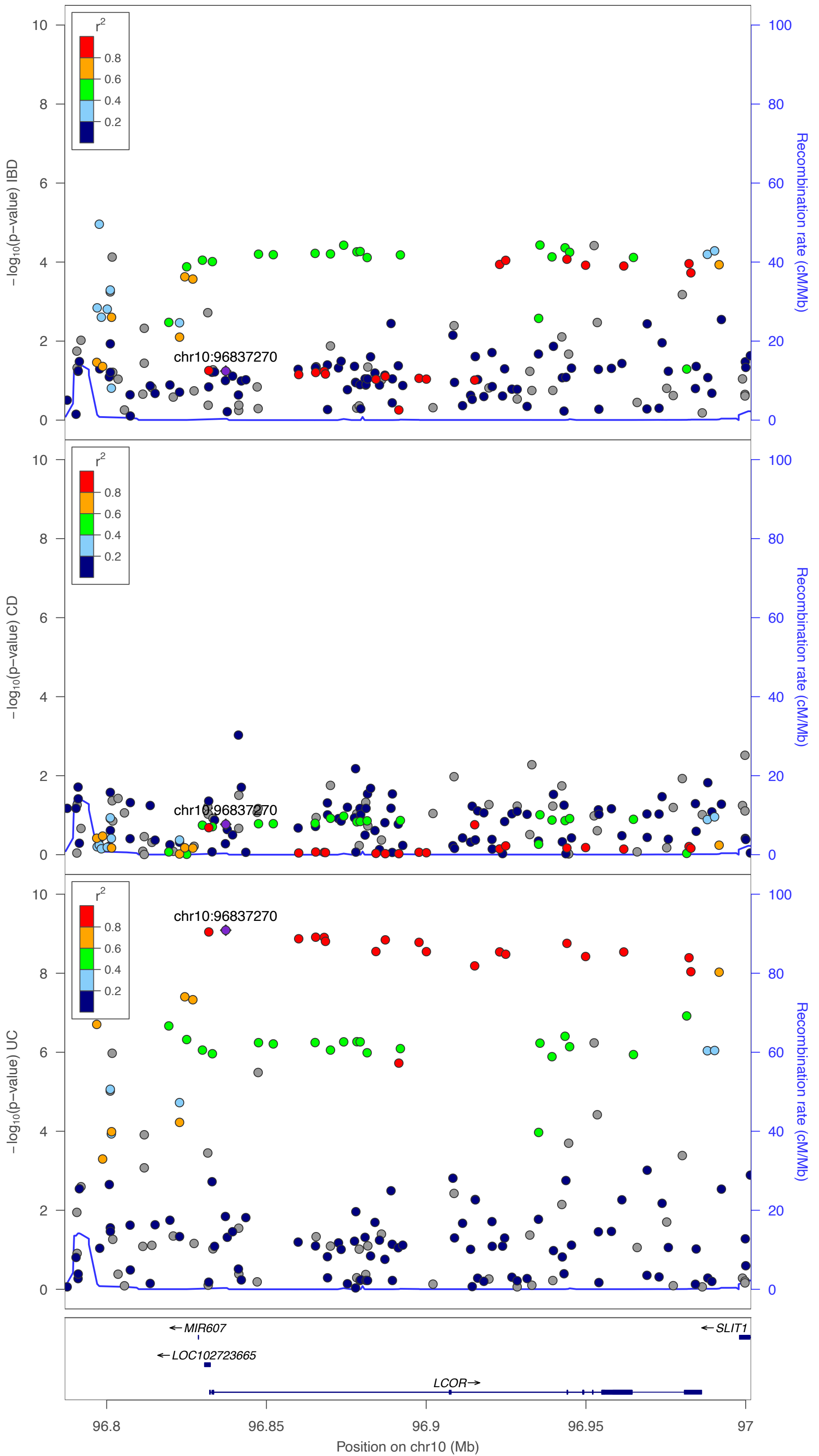
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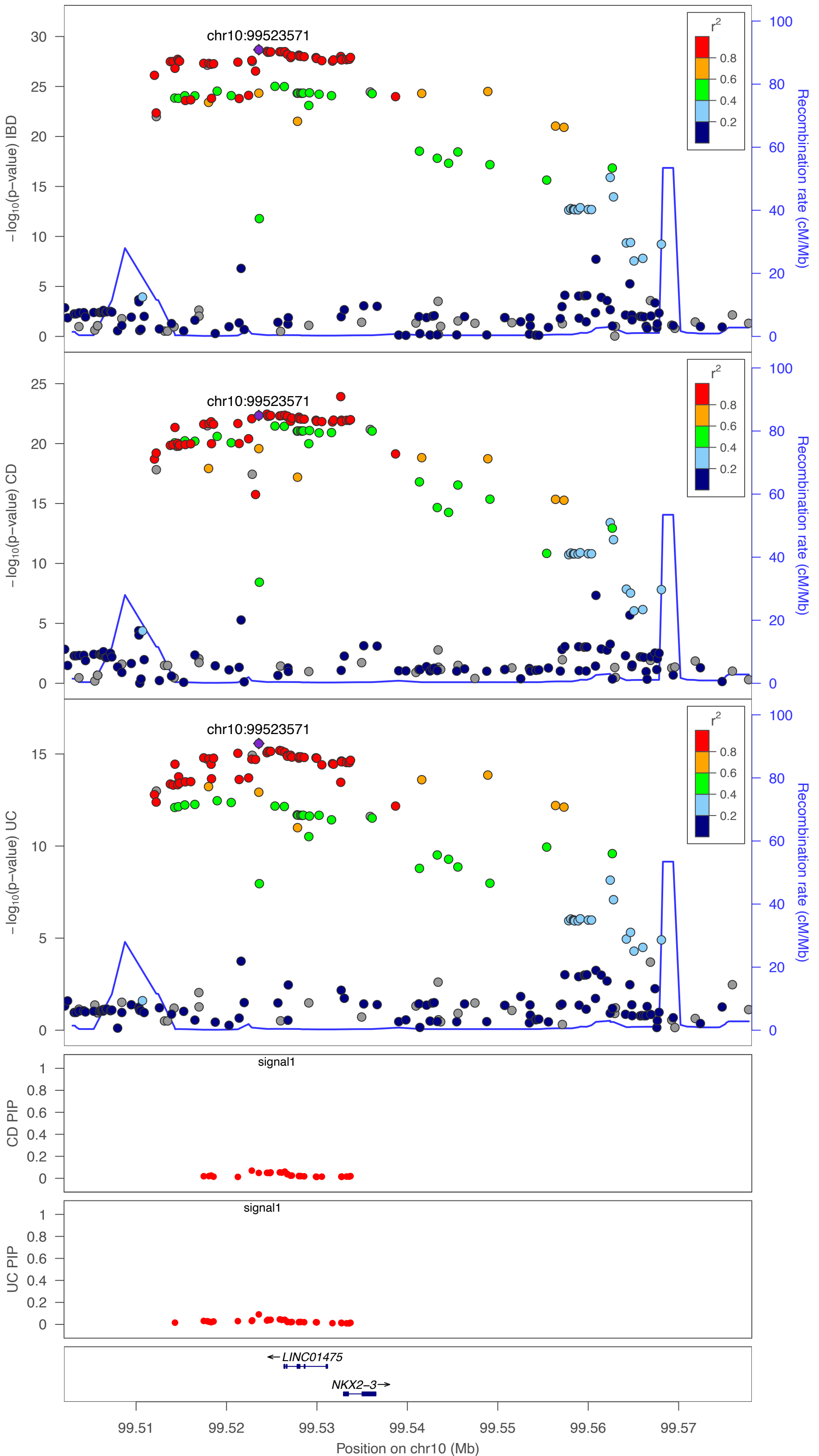
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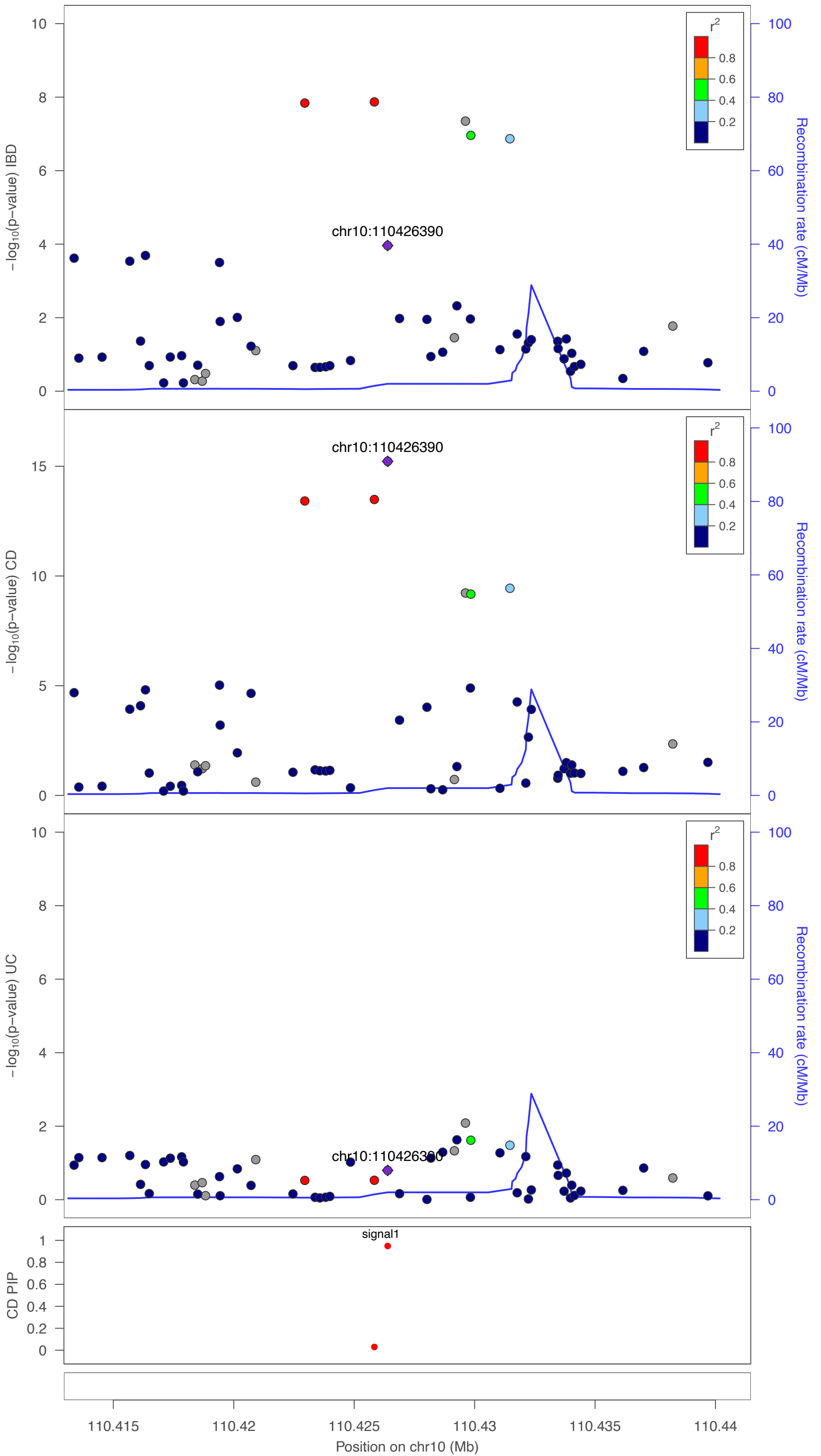
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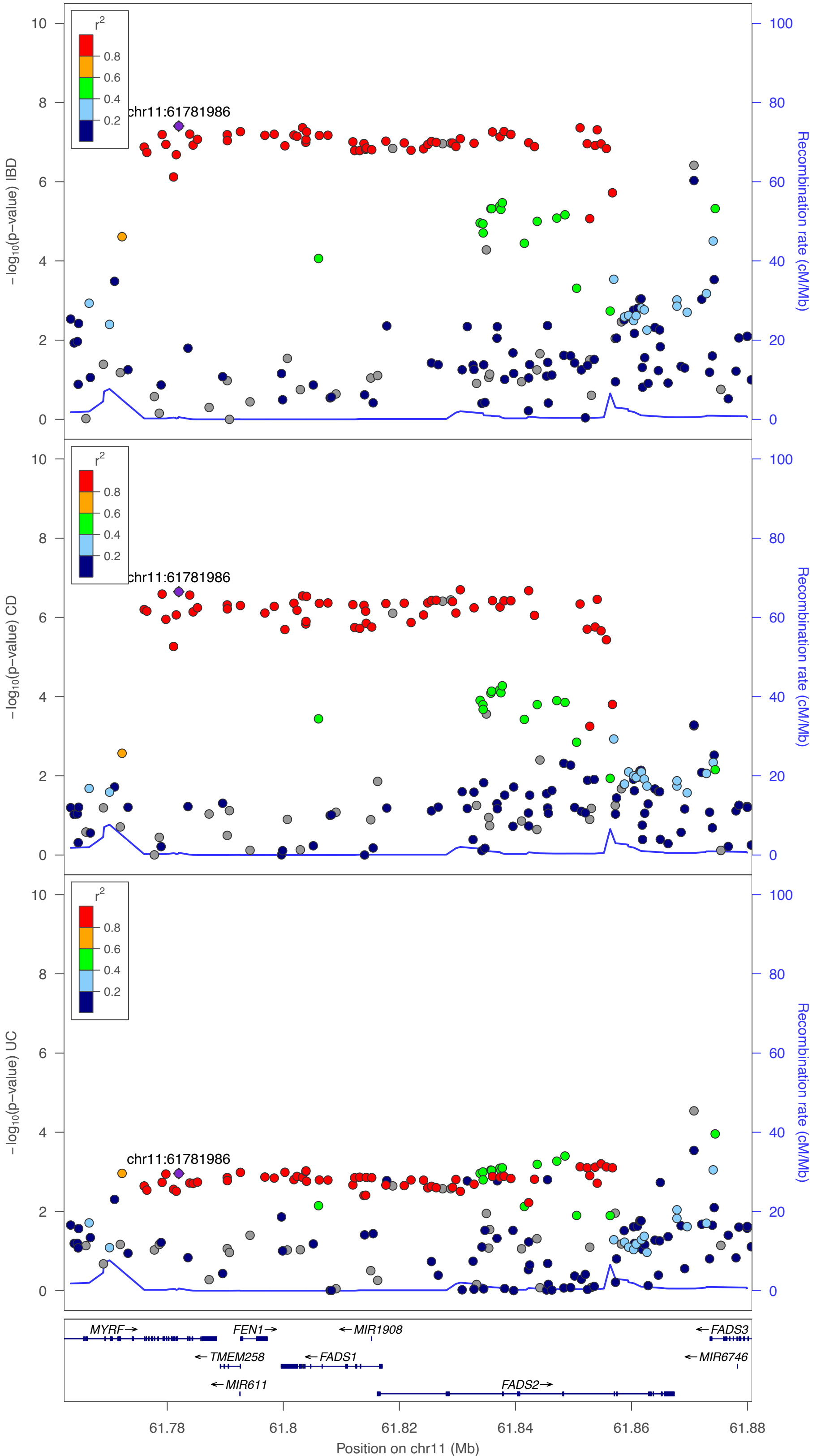
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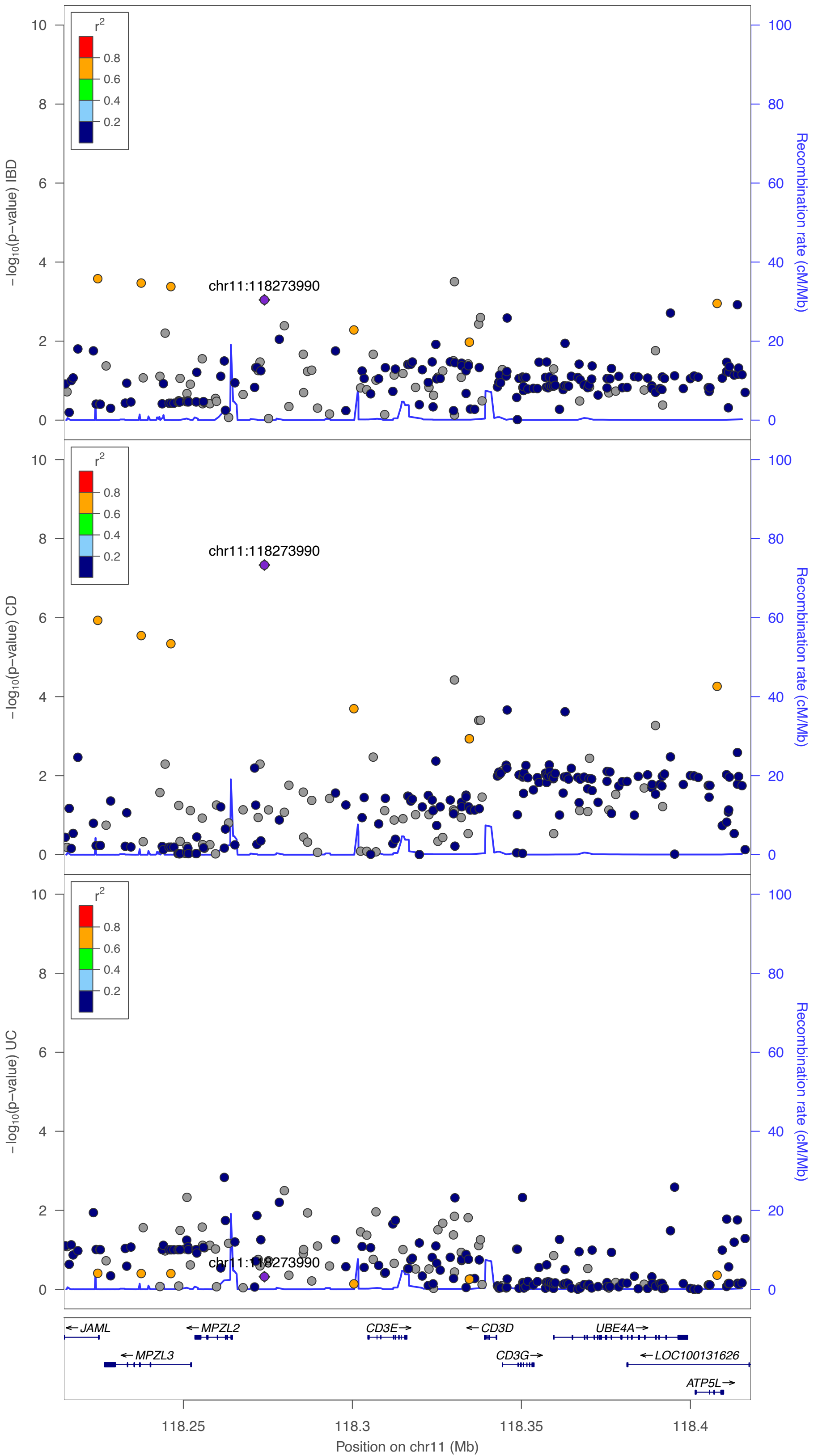
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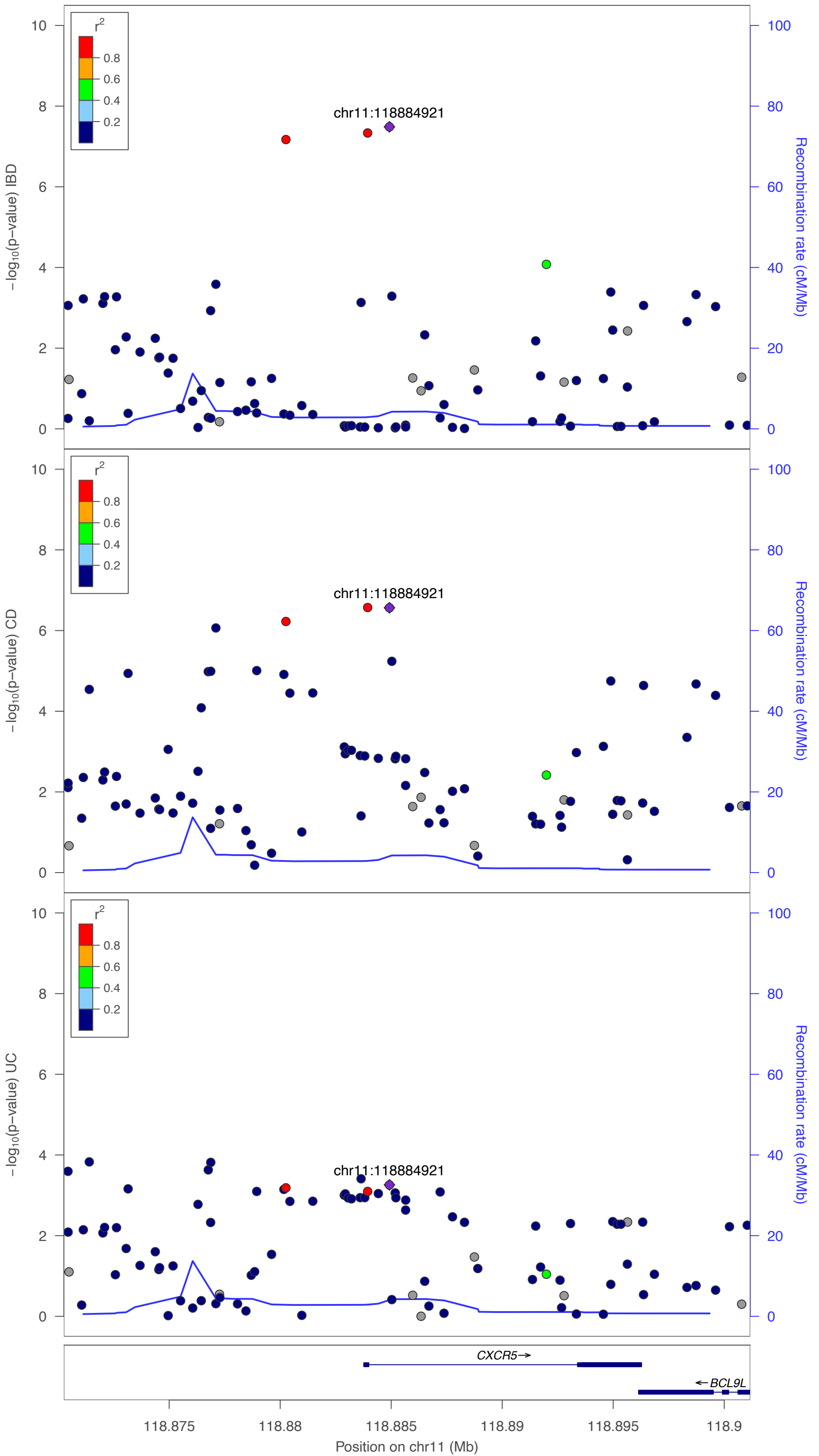
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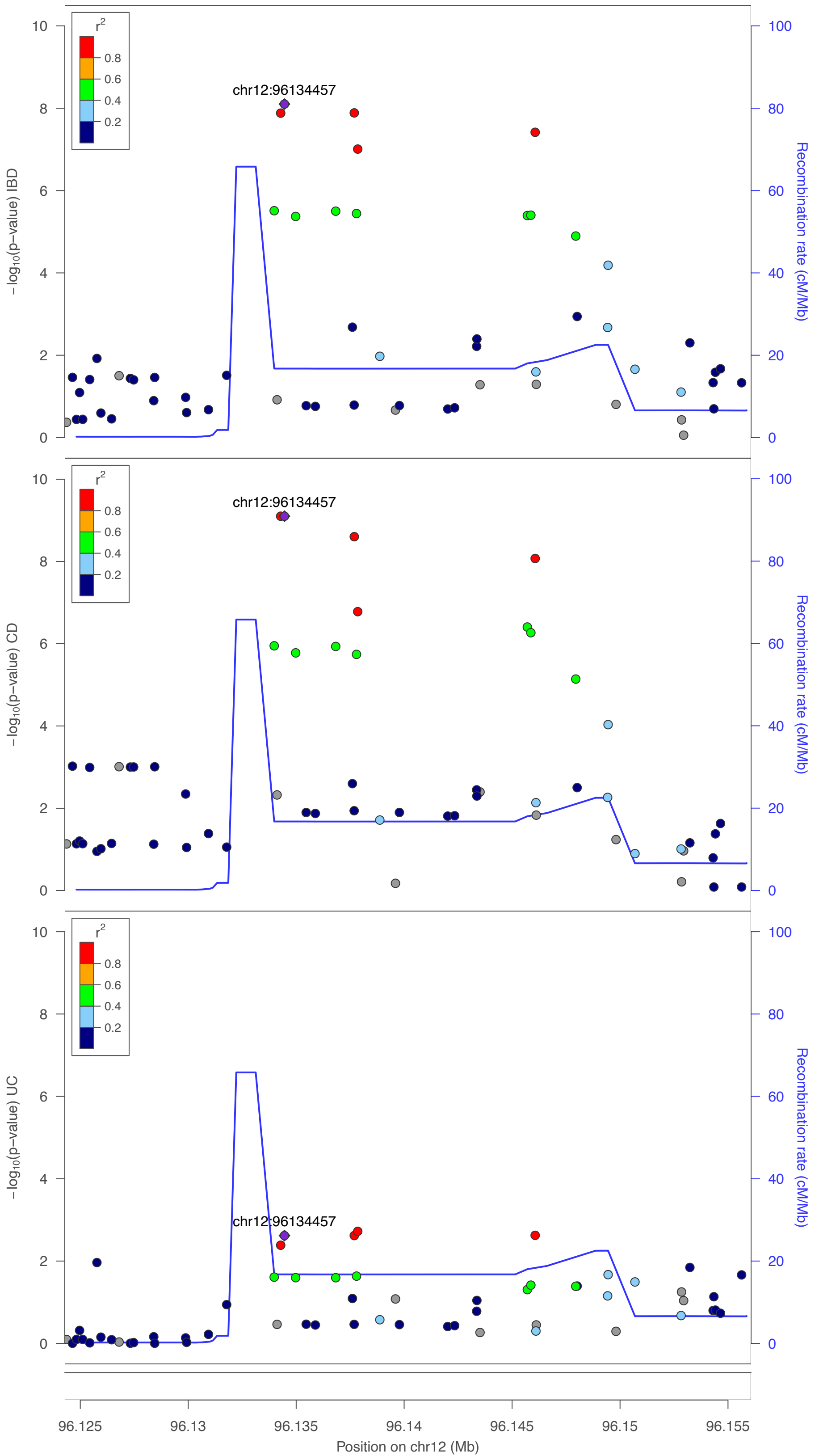
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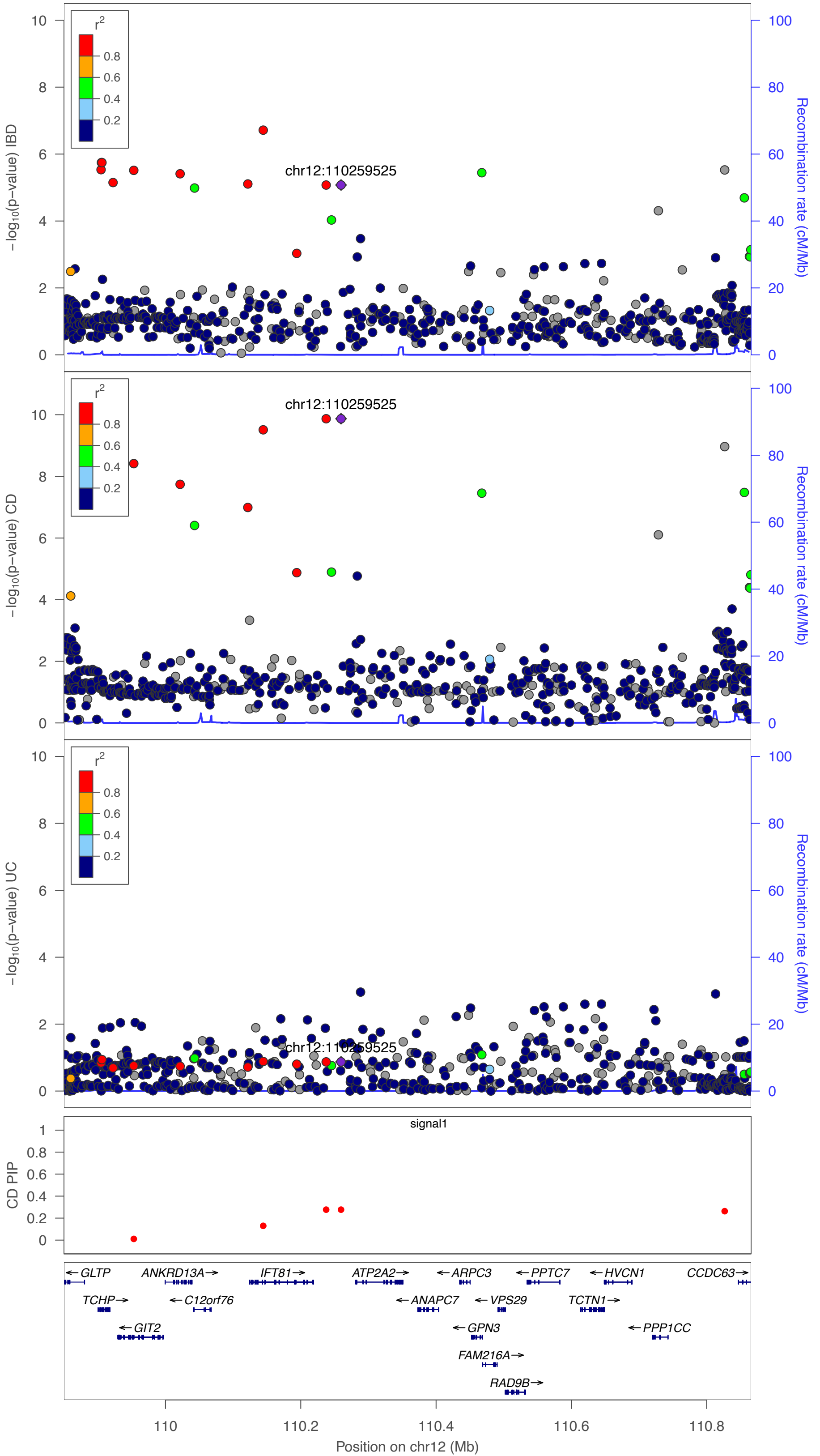
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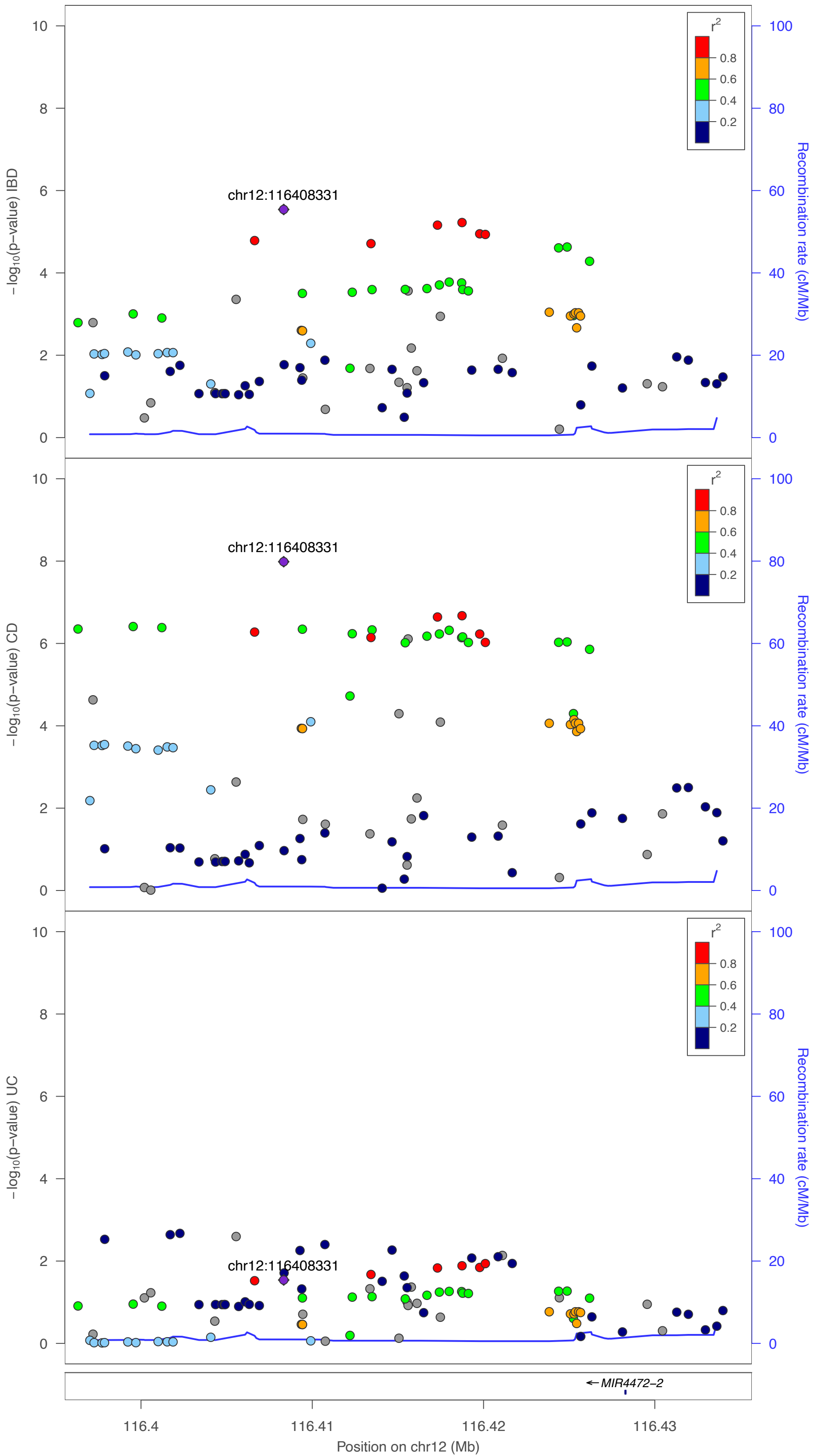
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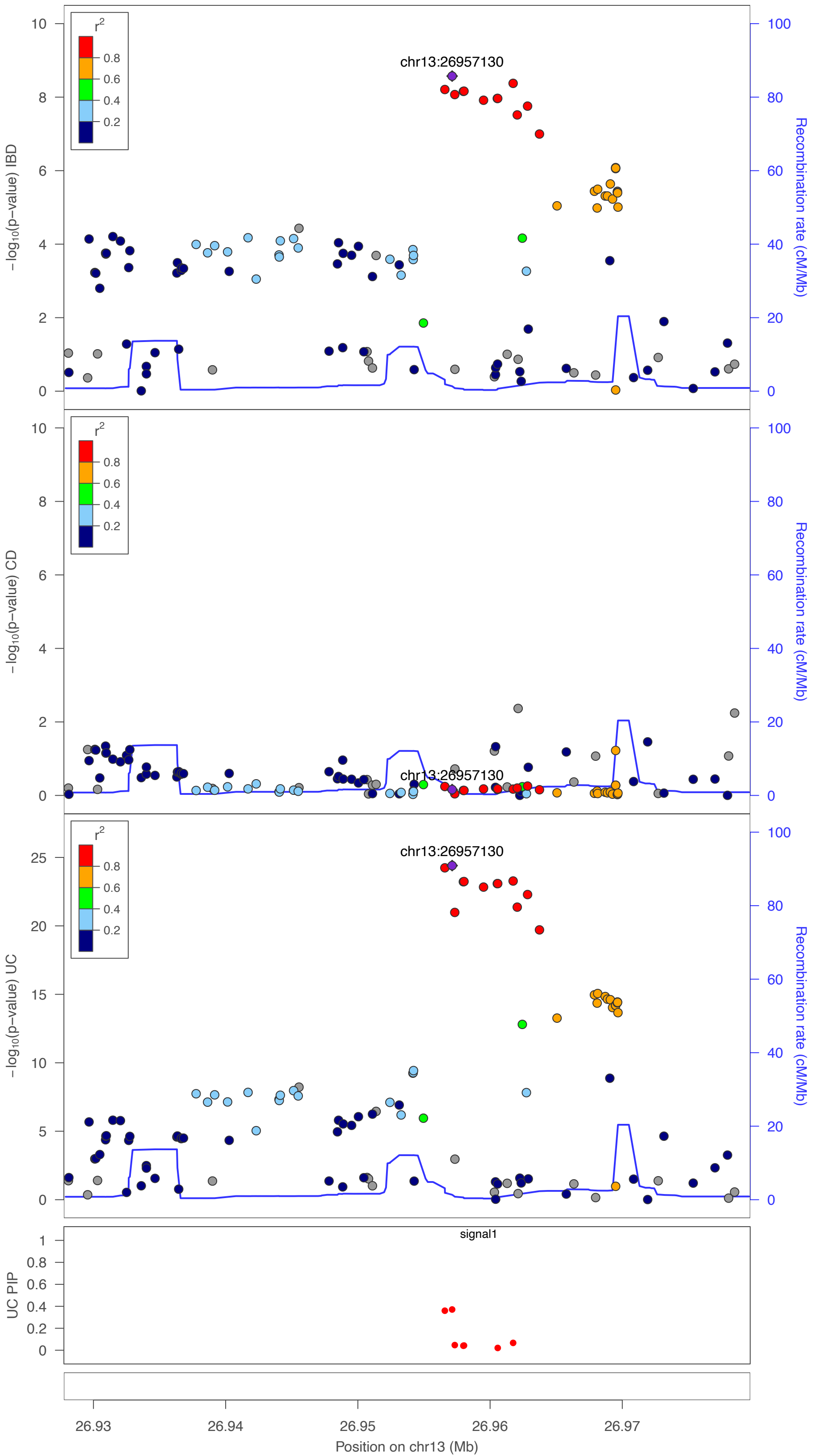
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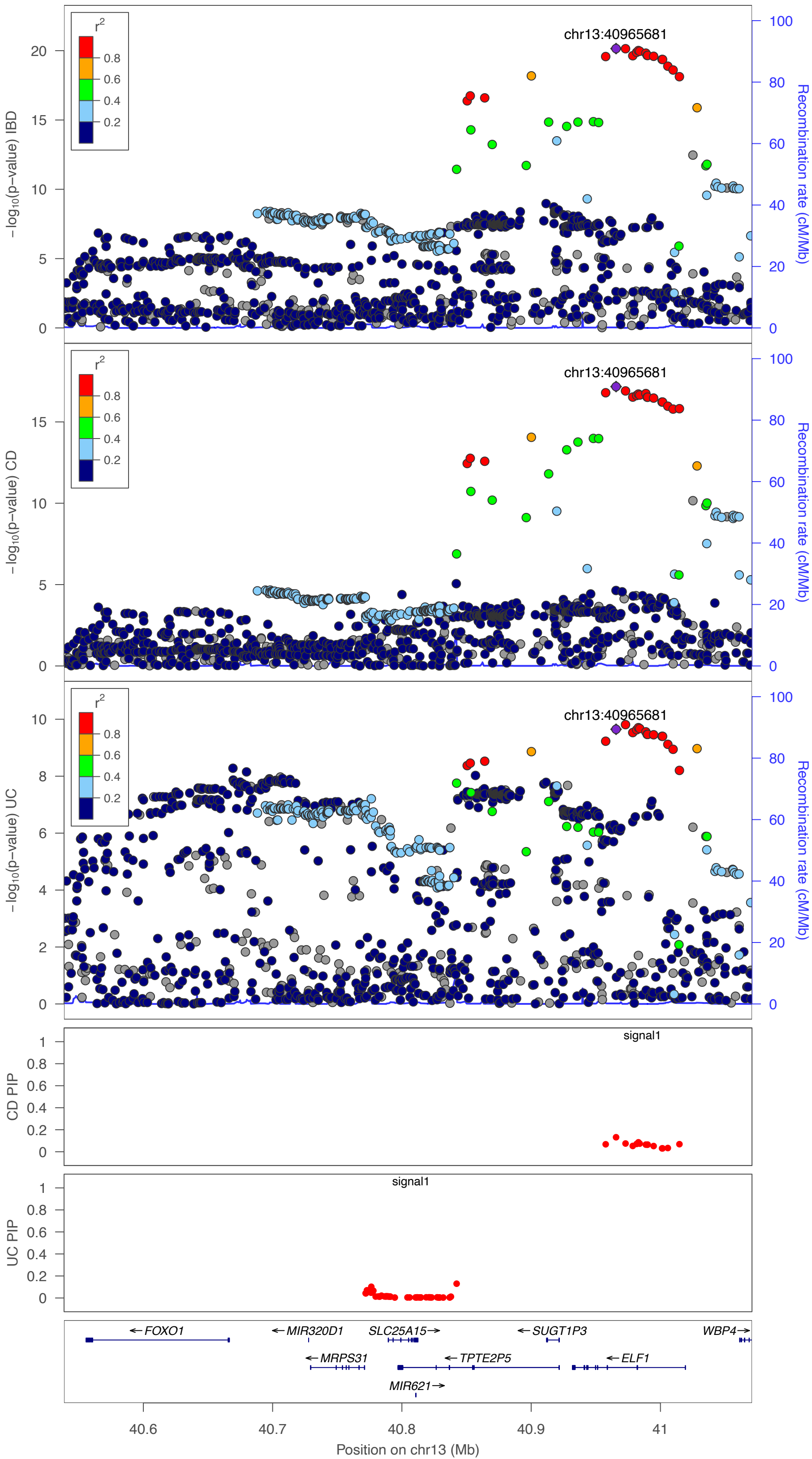
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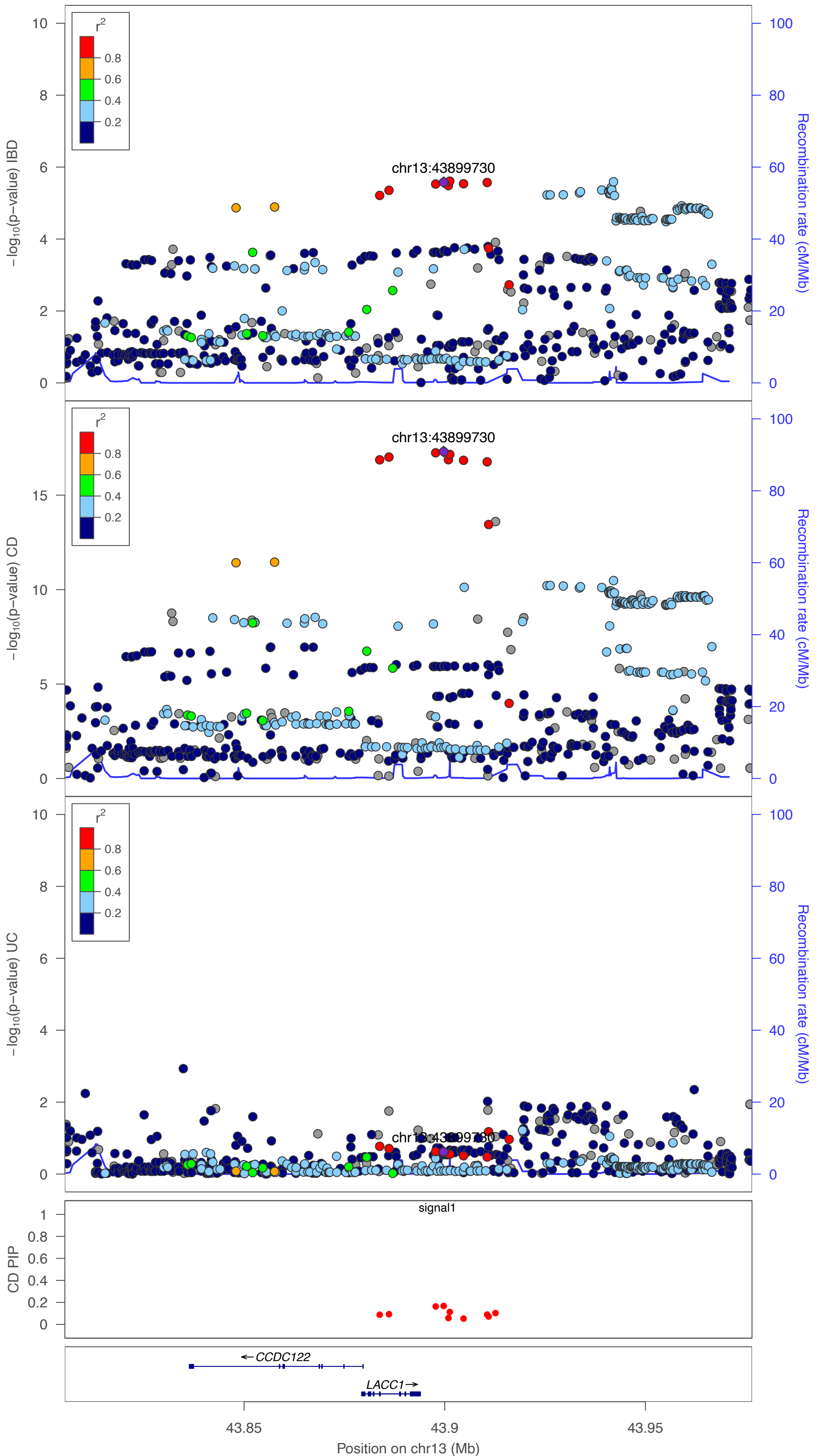
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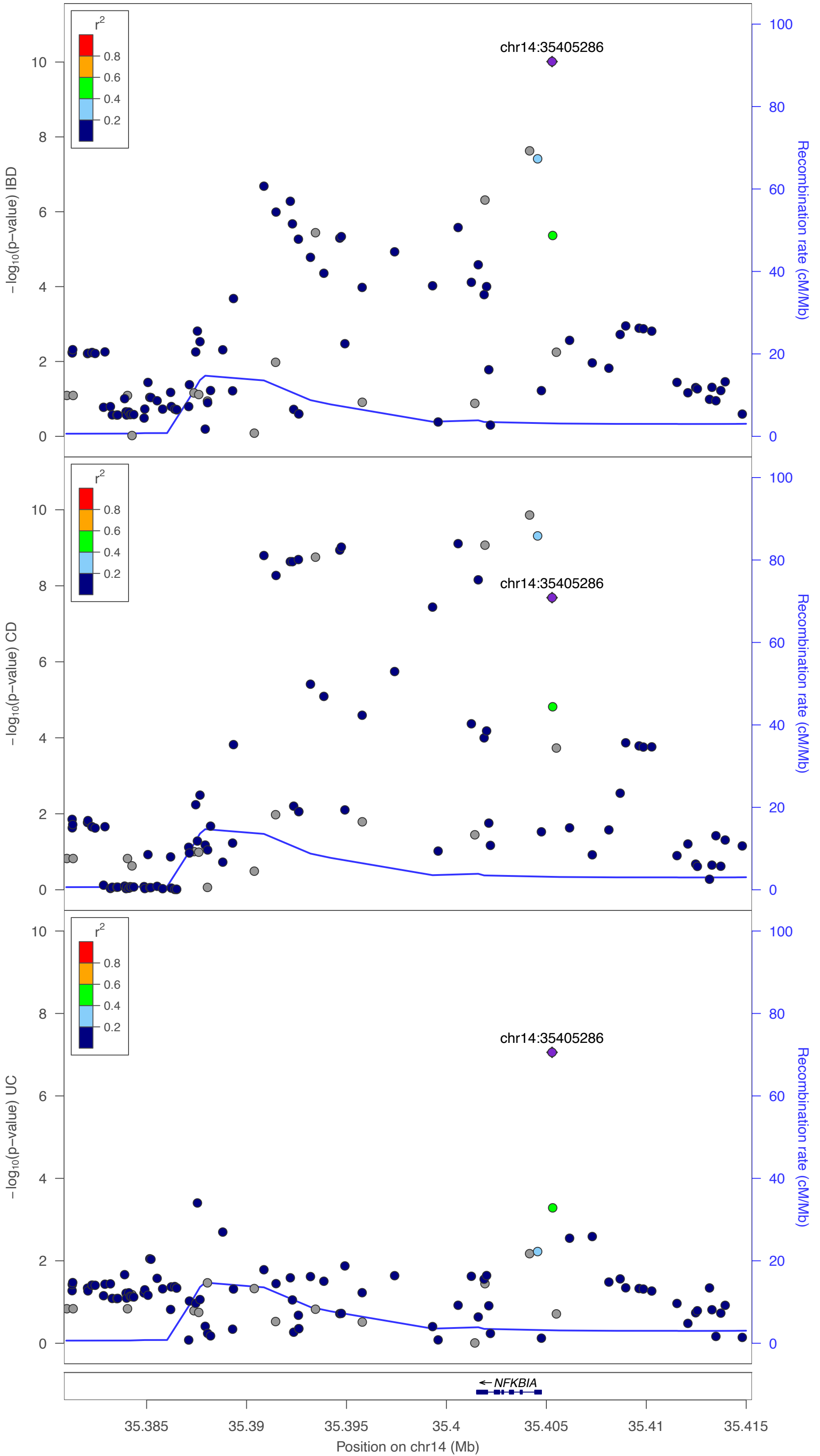
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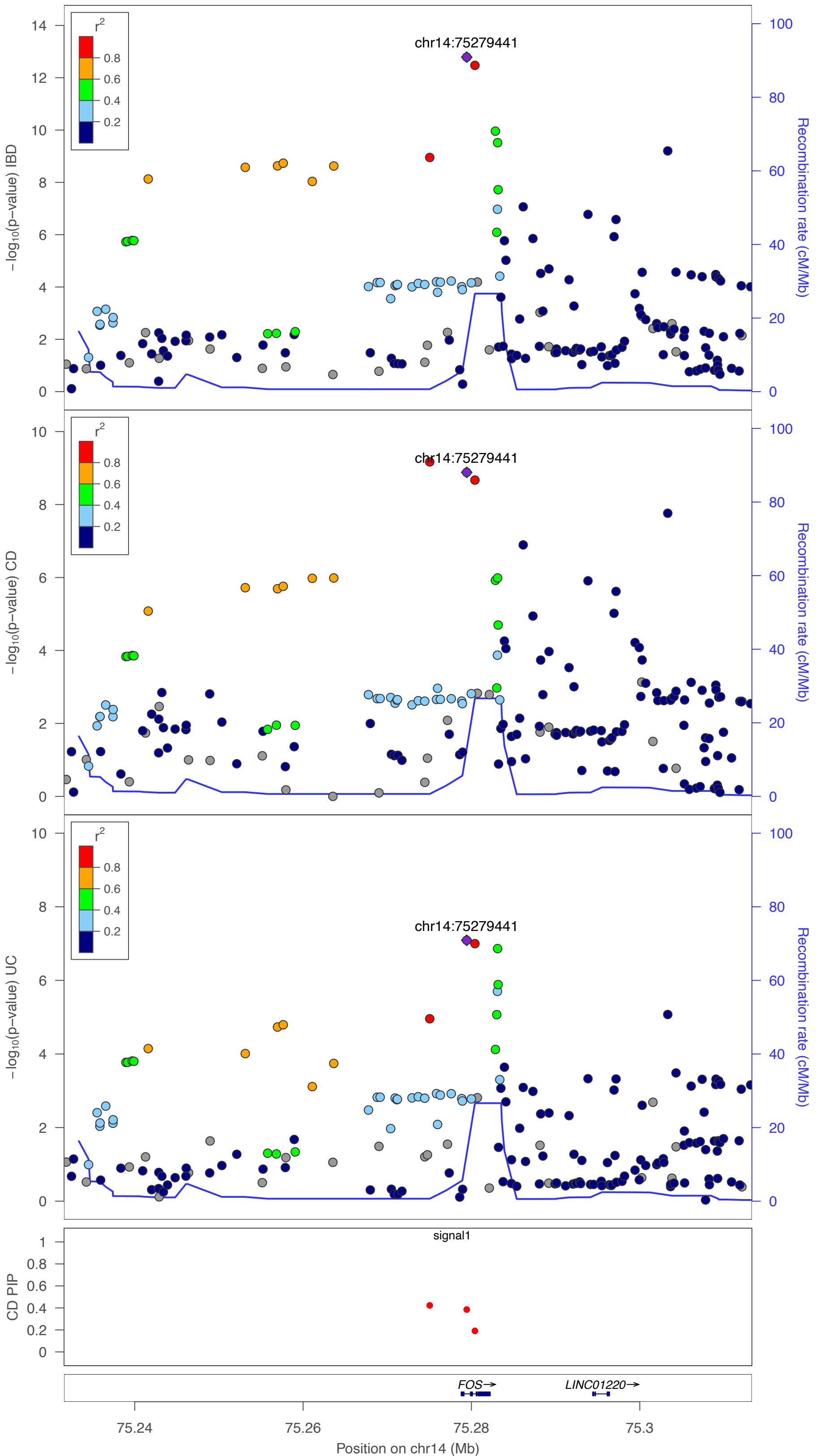
CD chr13:43899730:G:T



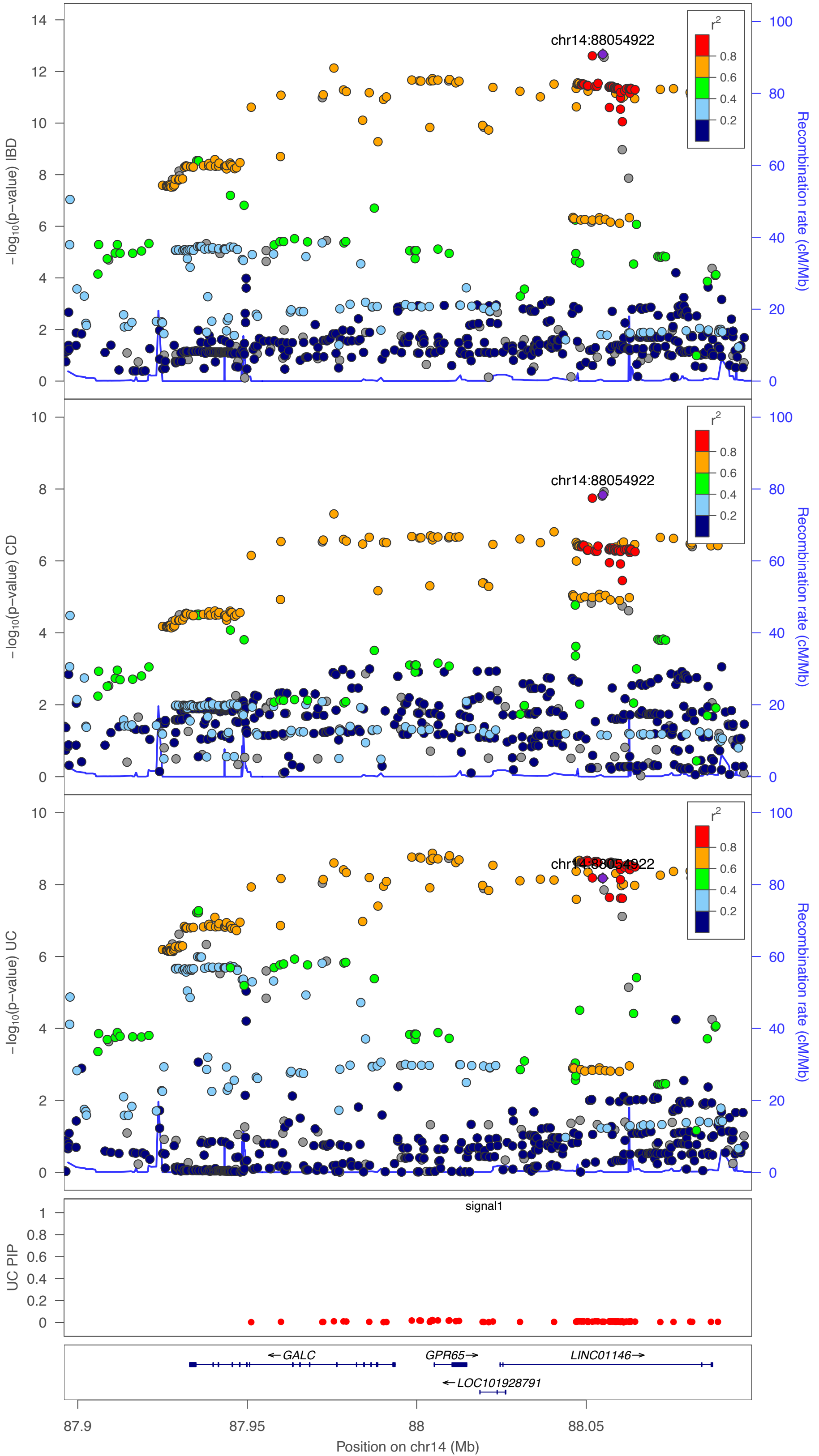
IBD chr14:35405286:G:A



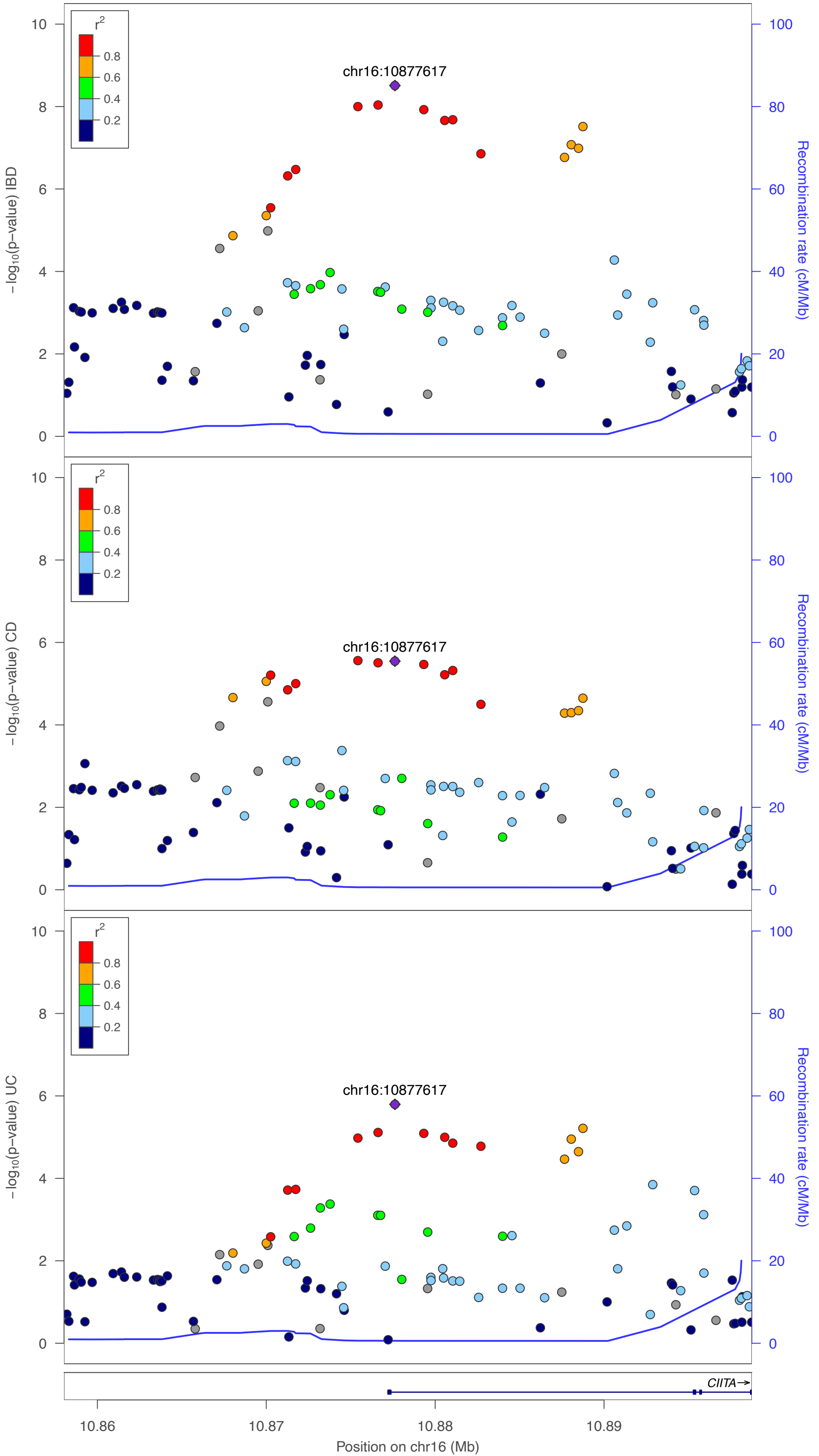
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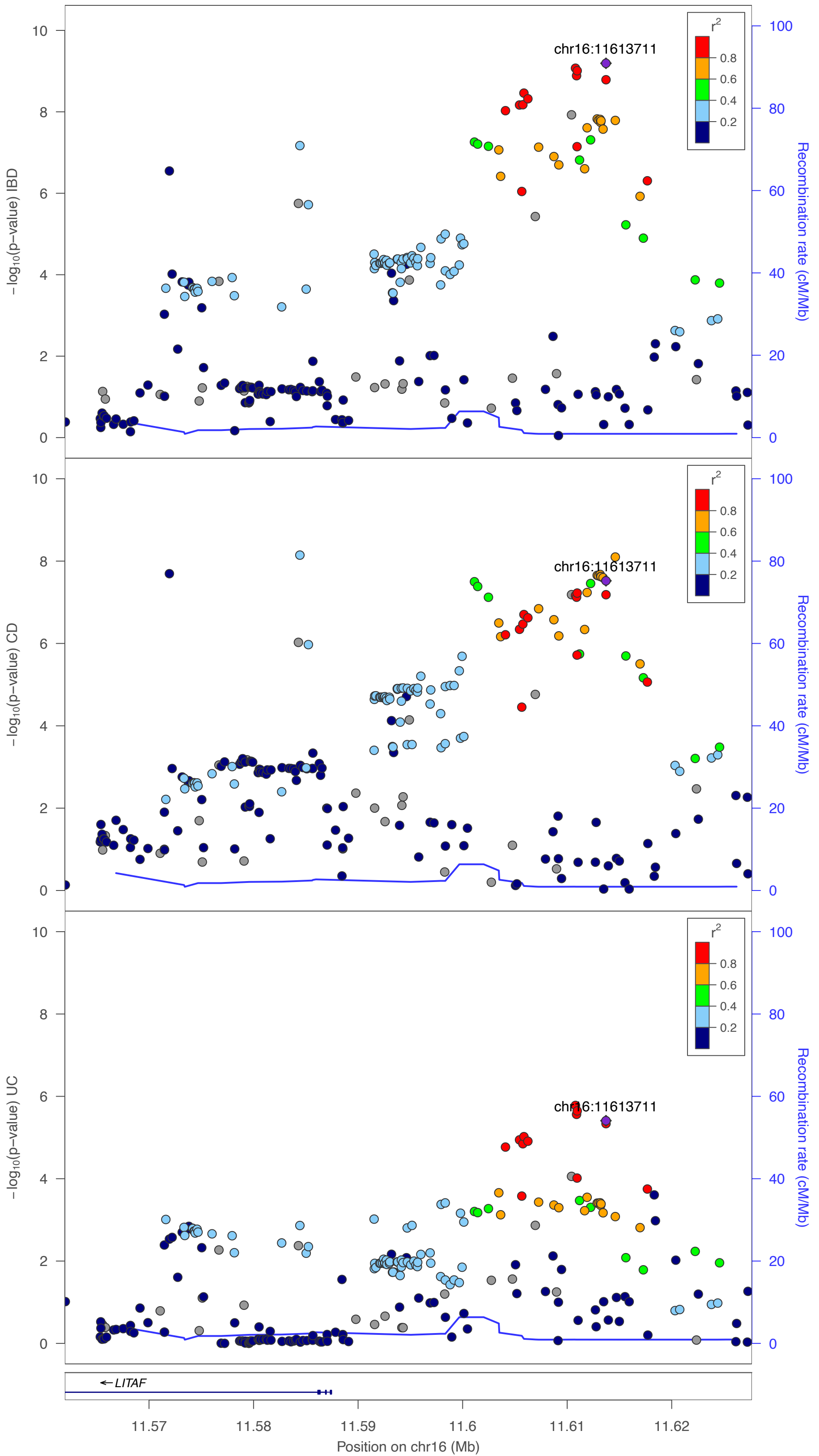
IBD chr14:88054922:A:G



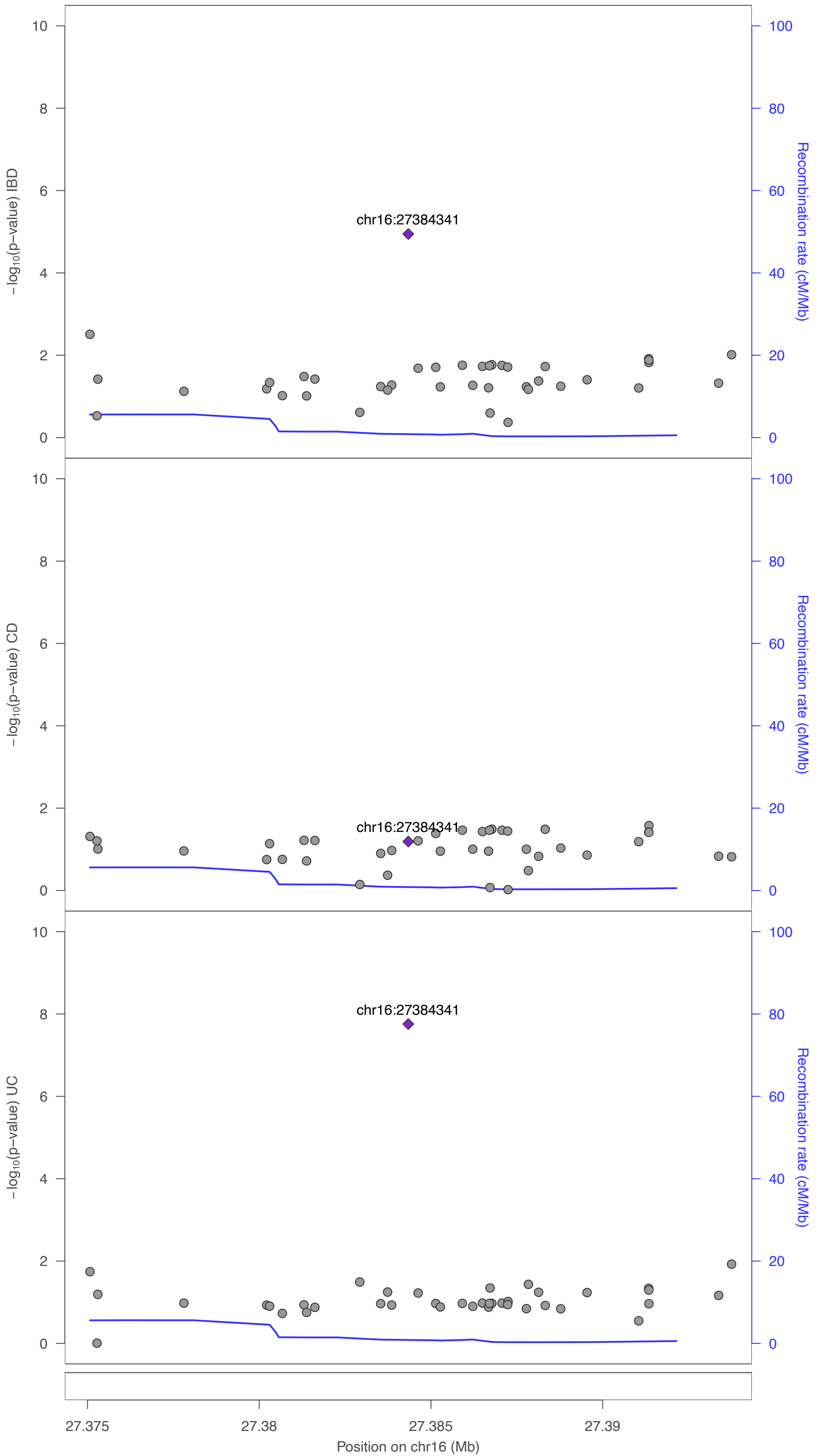
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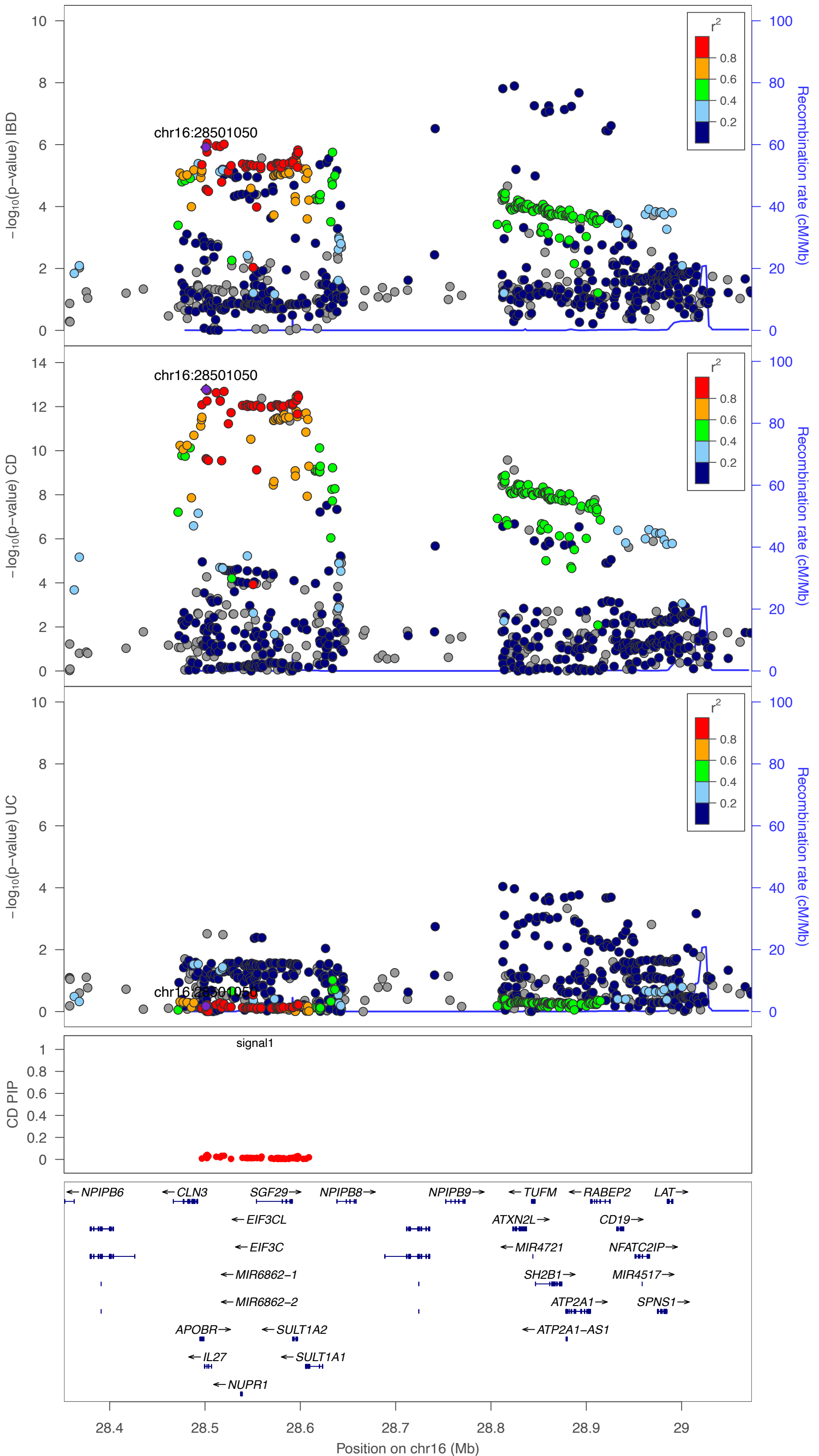
IBD chr16:11613711:G:A



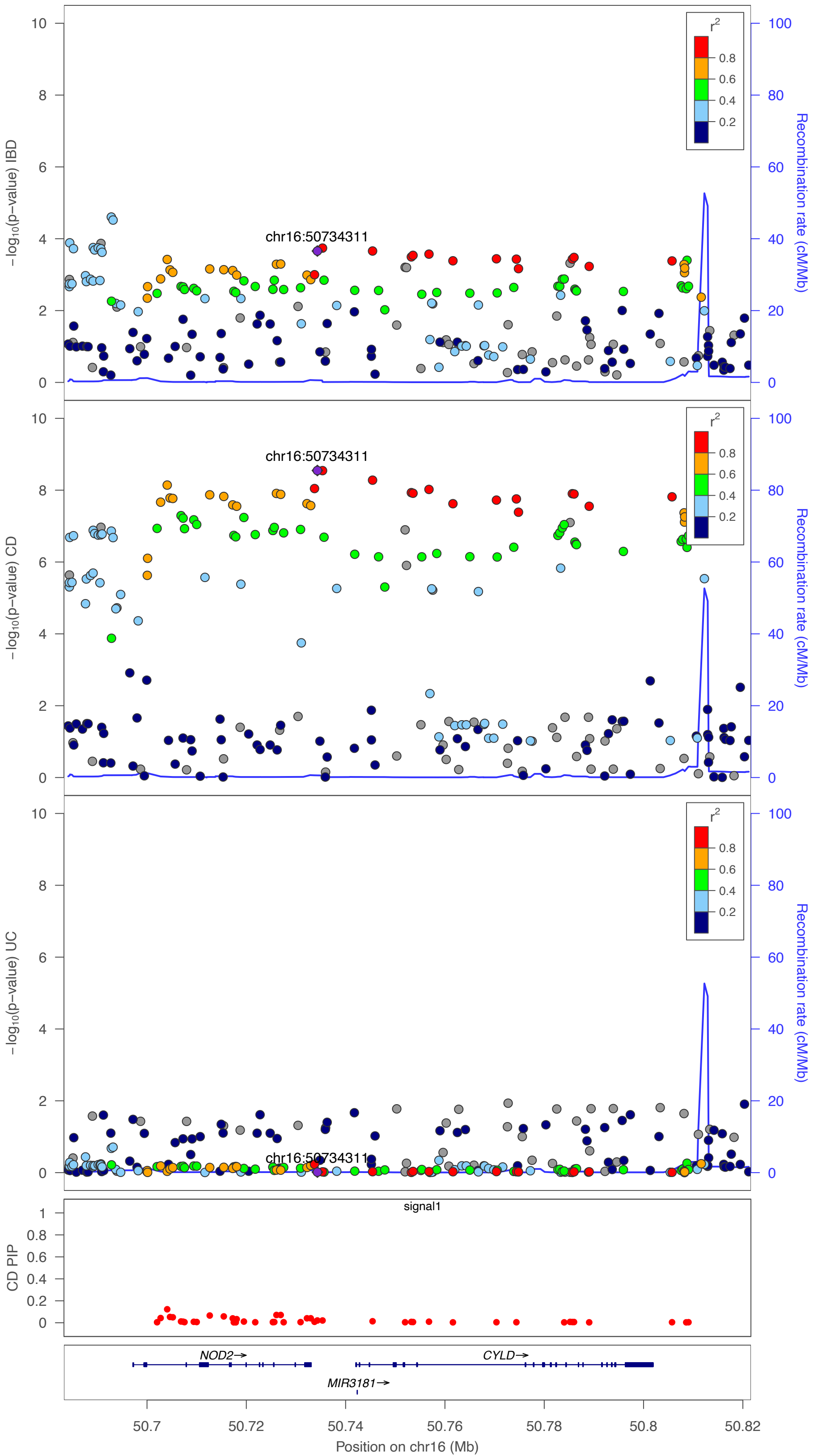
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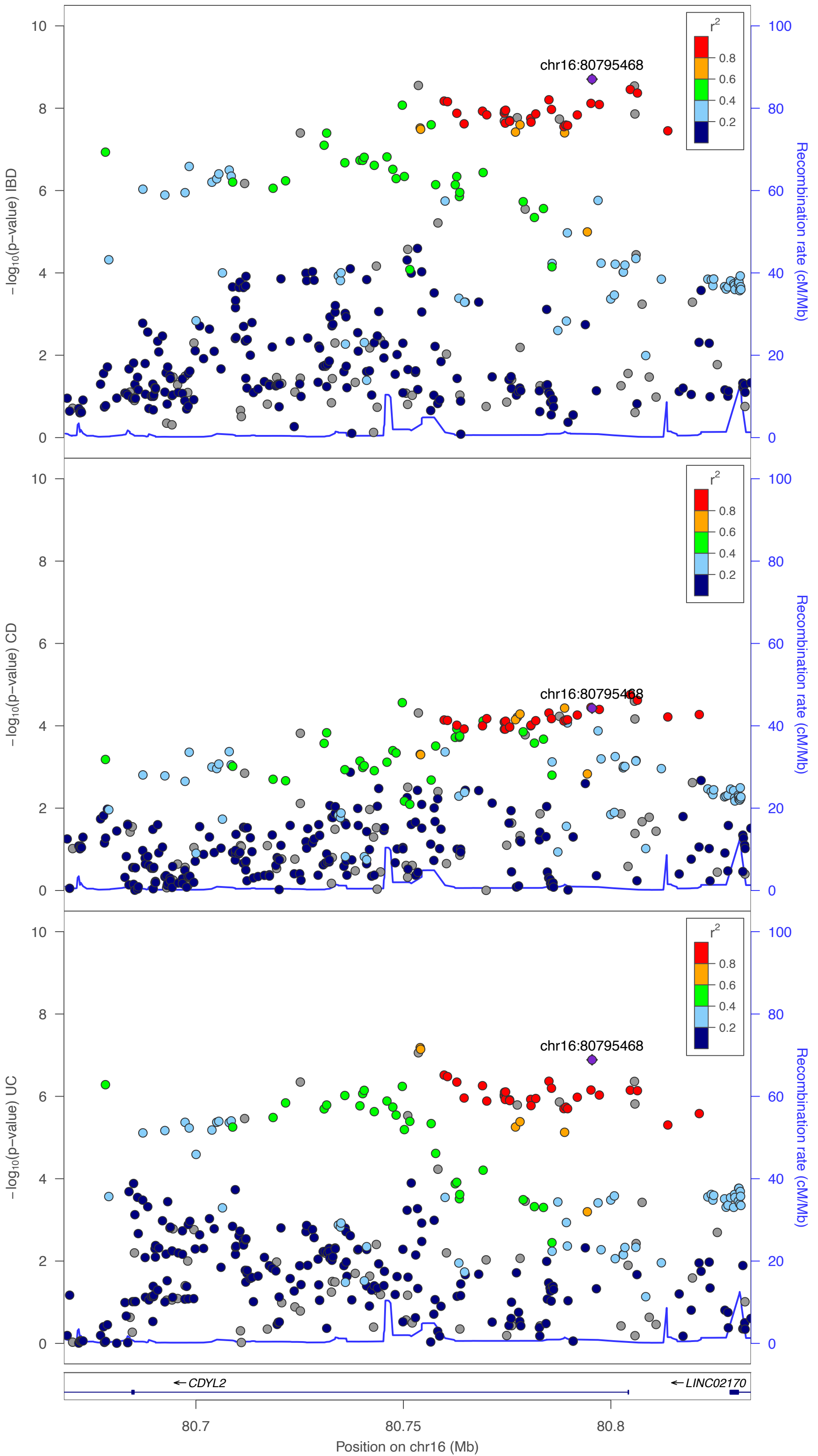
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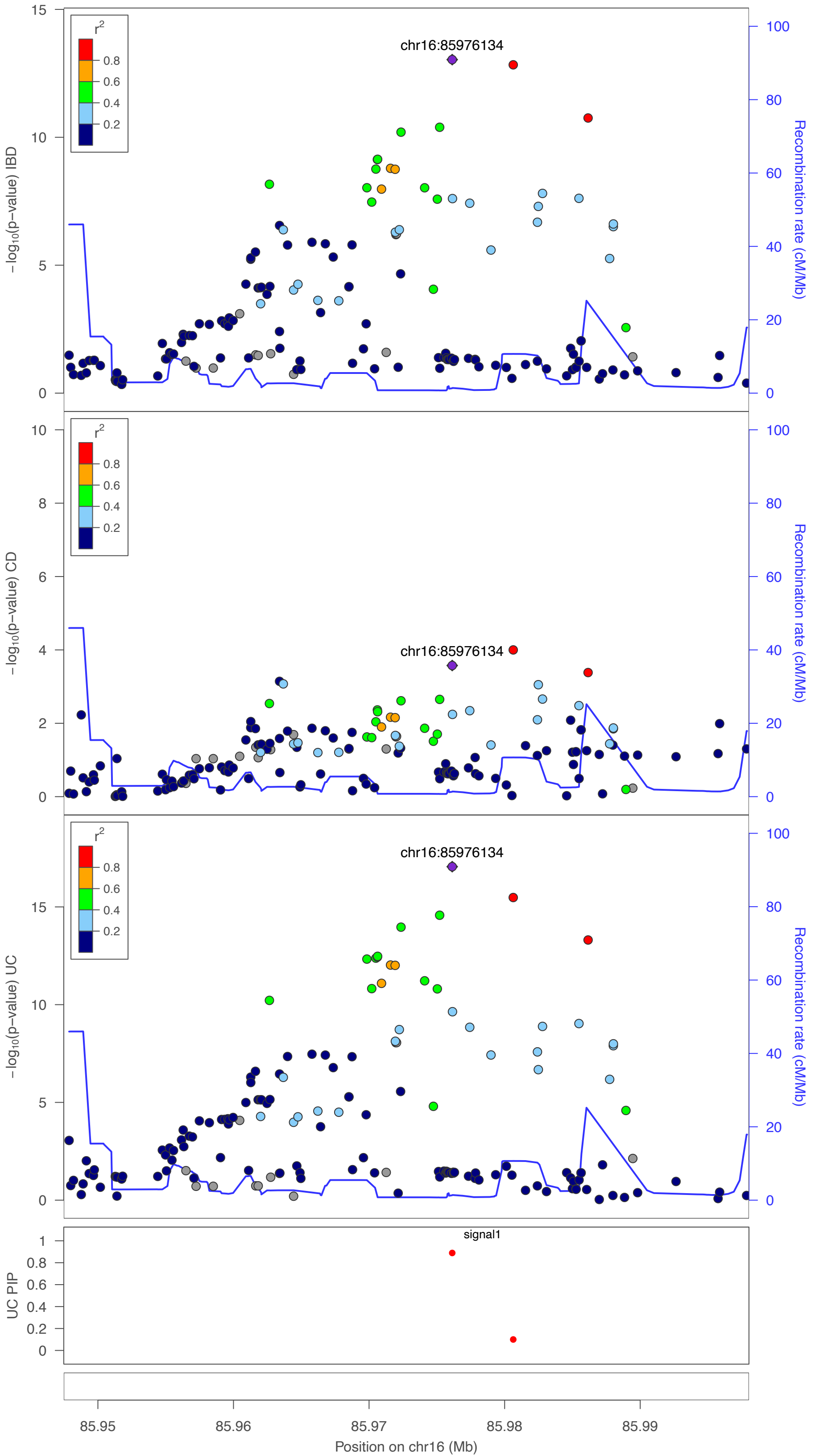
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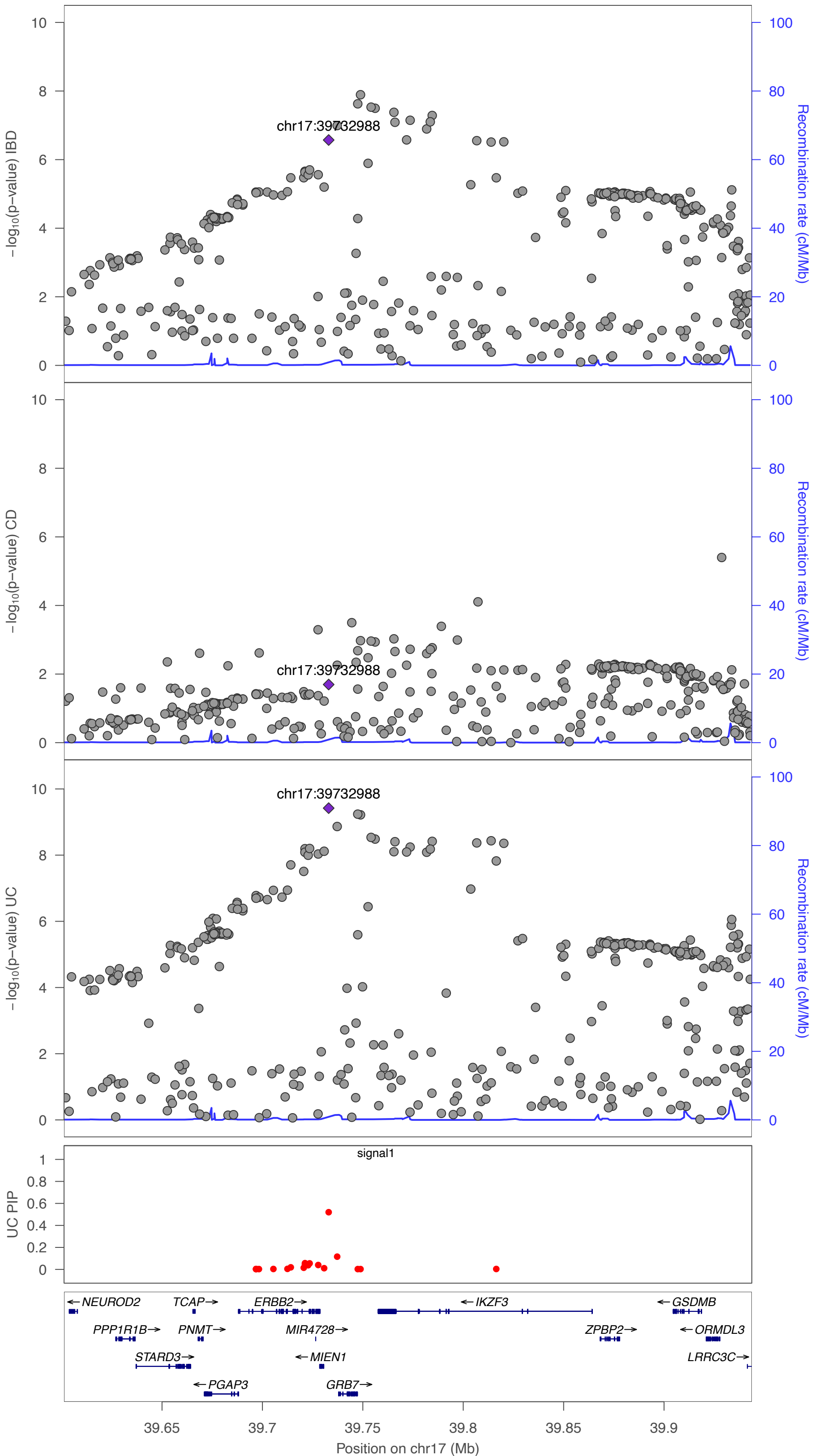
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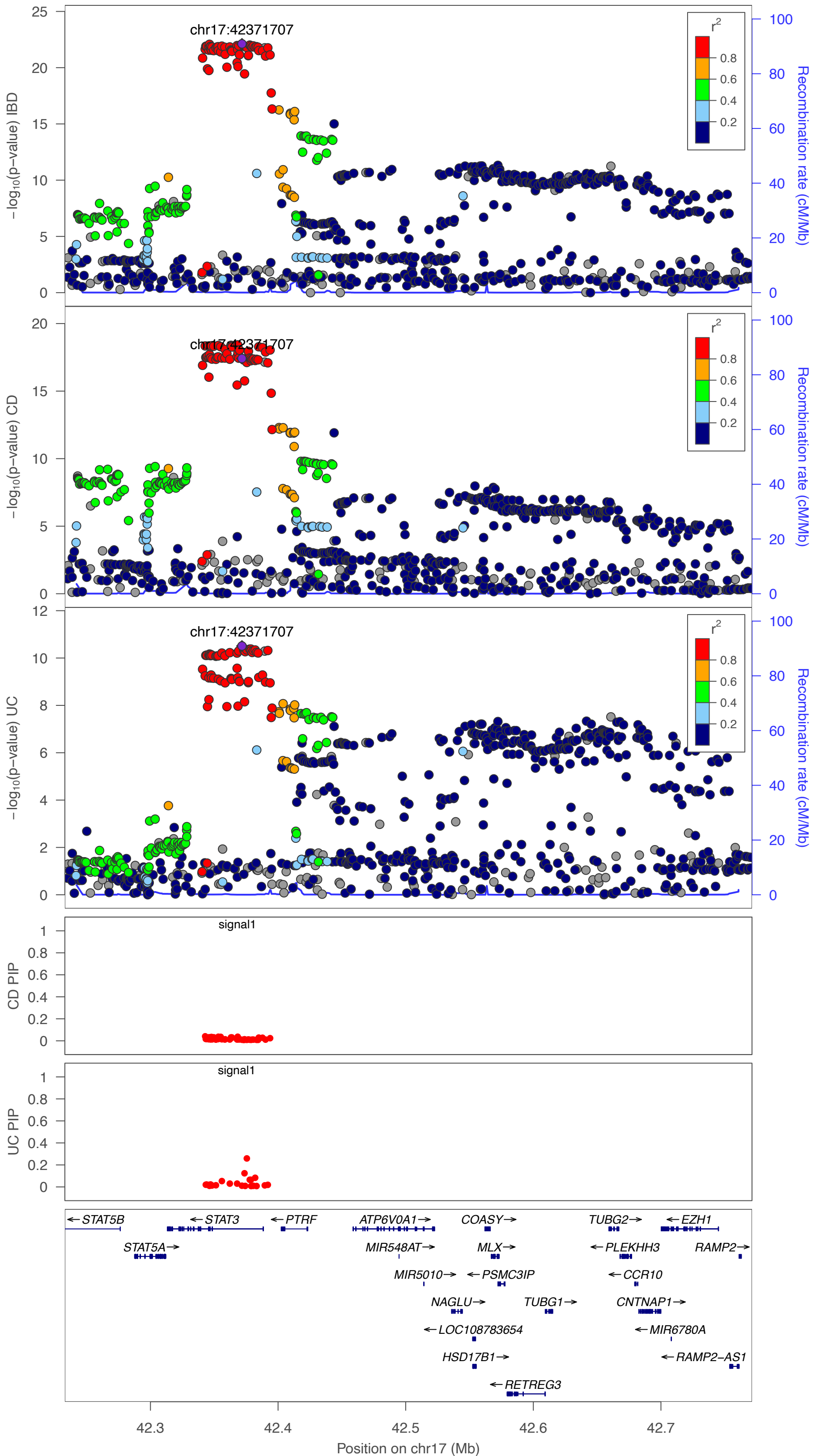
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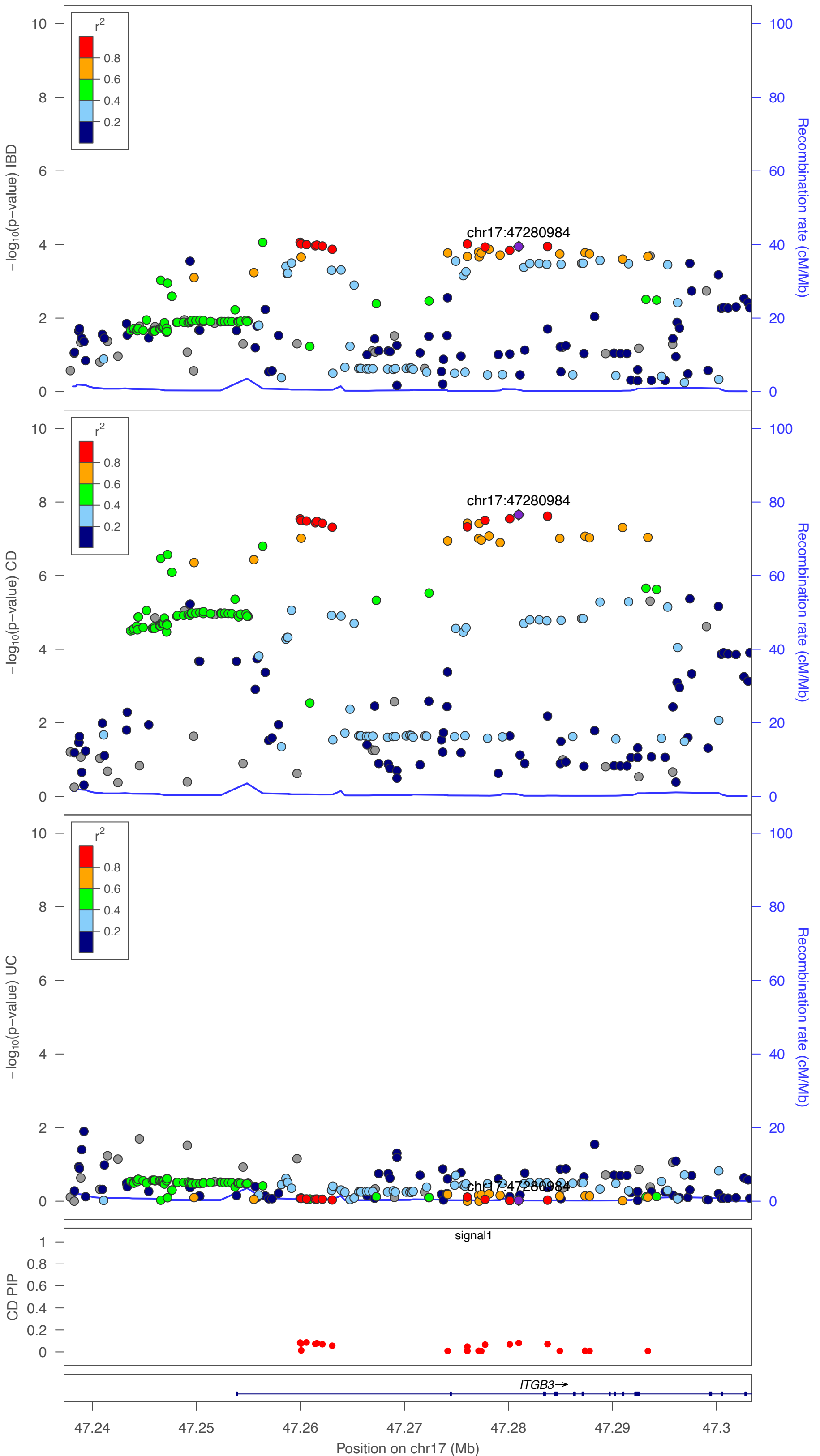
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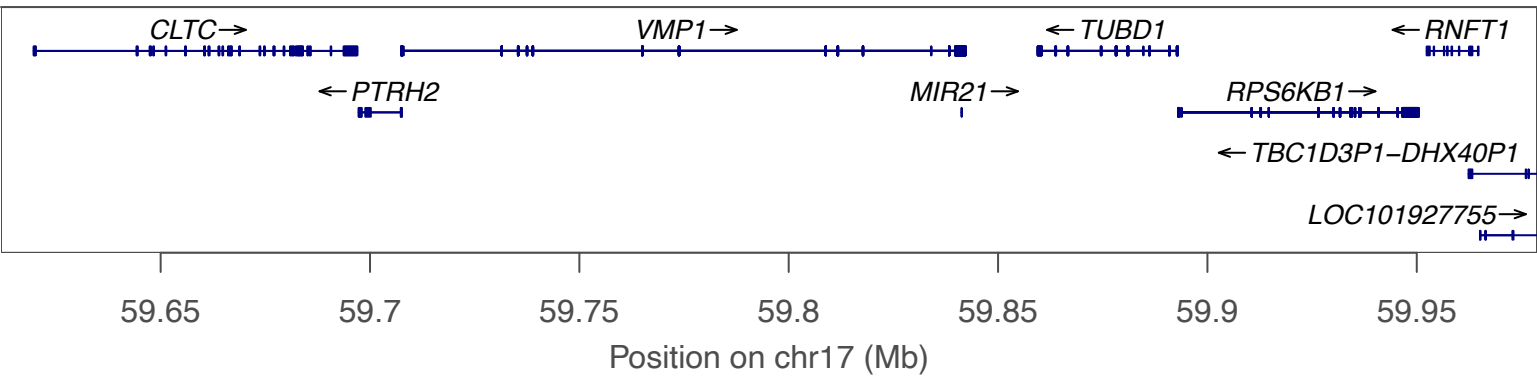
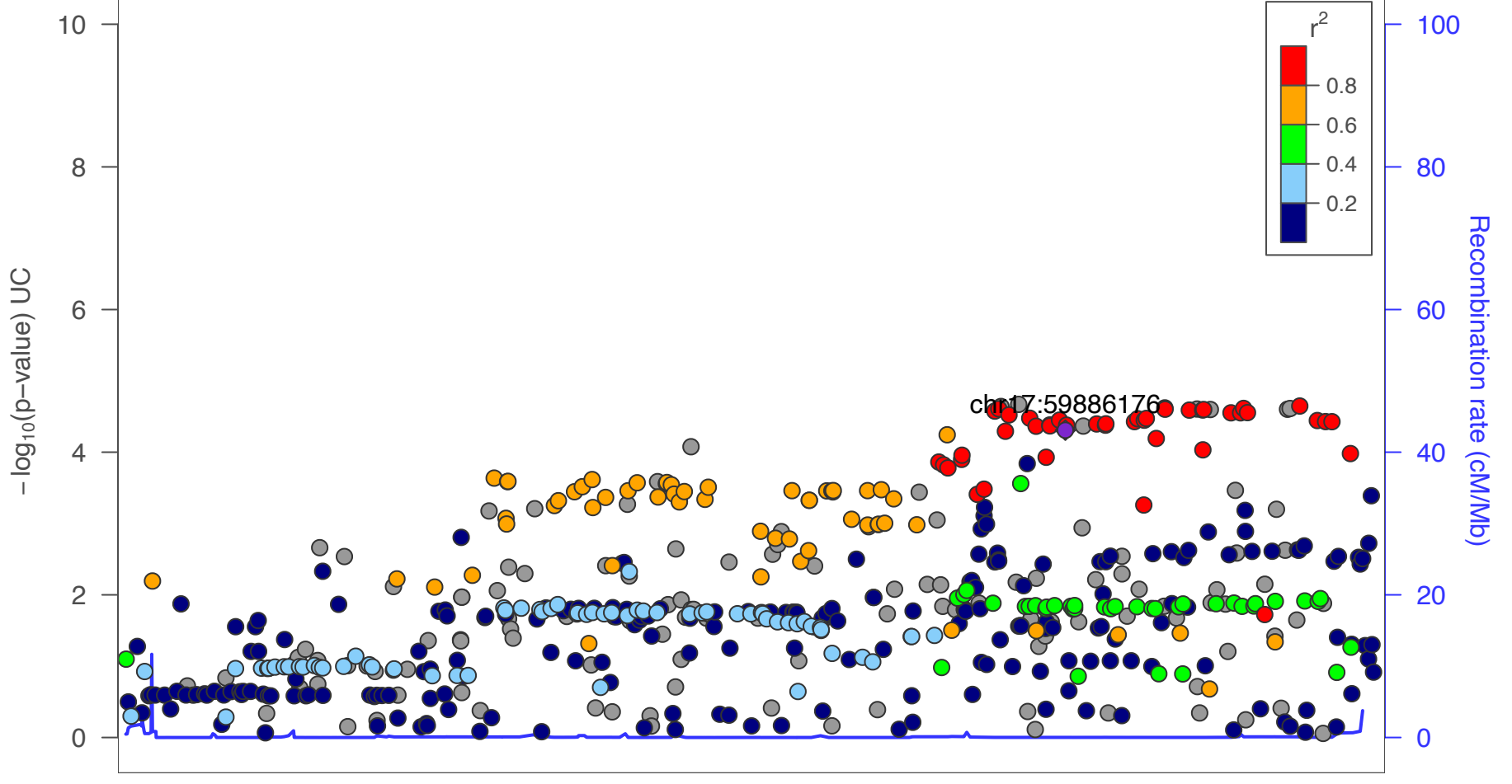
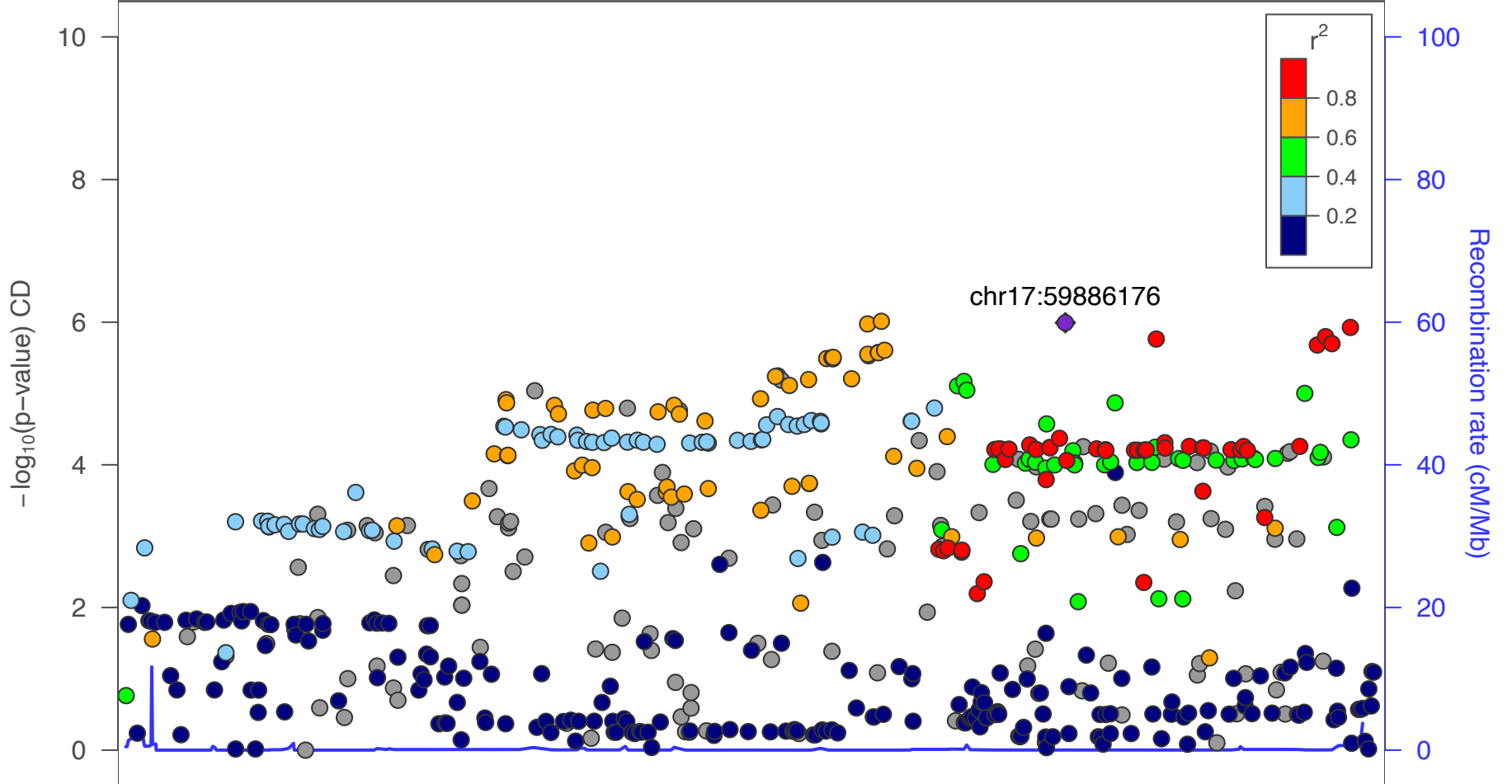
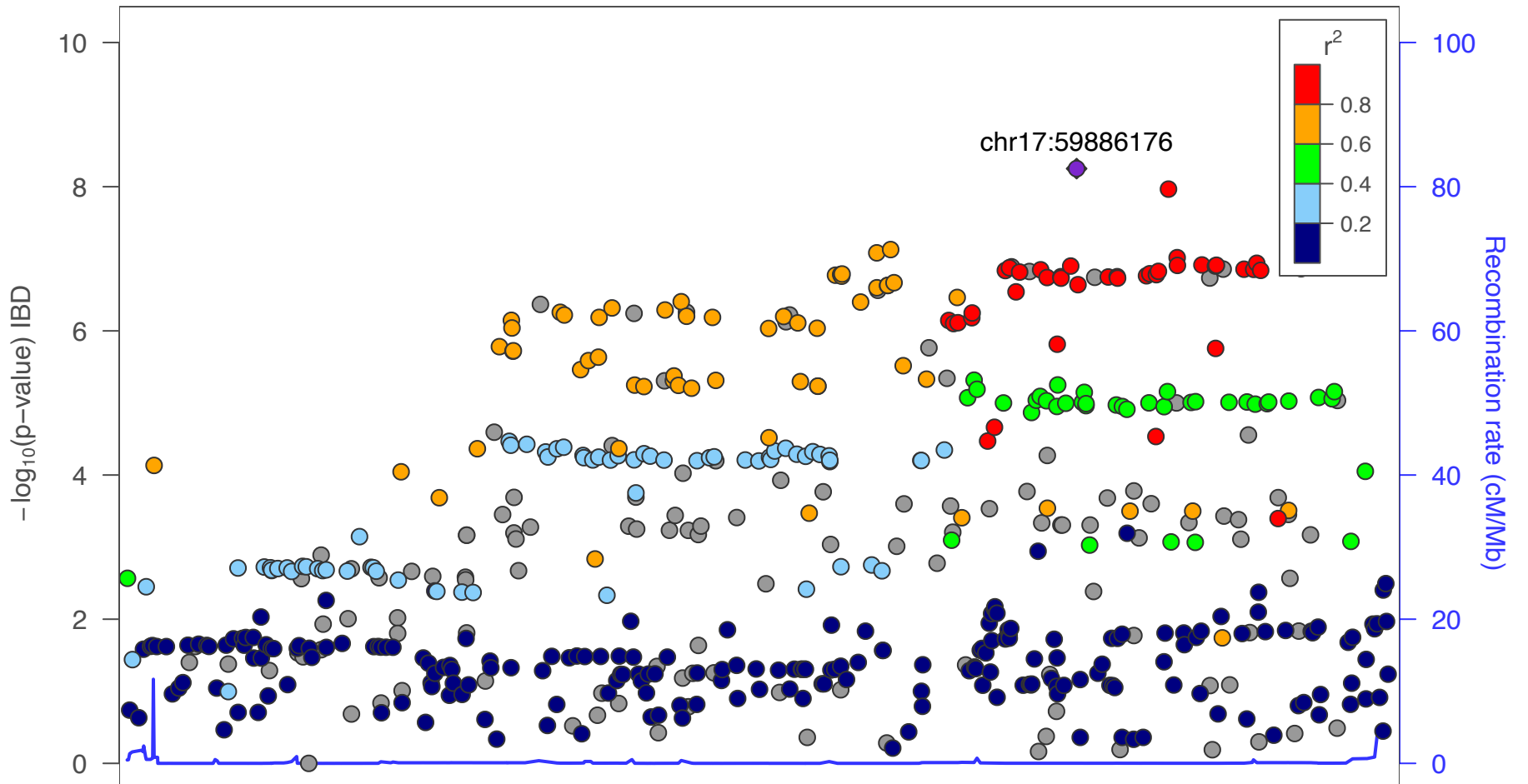
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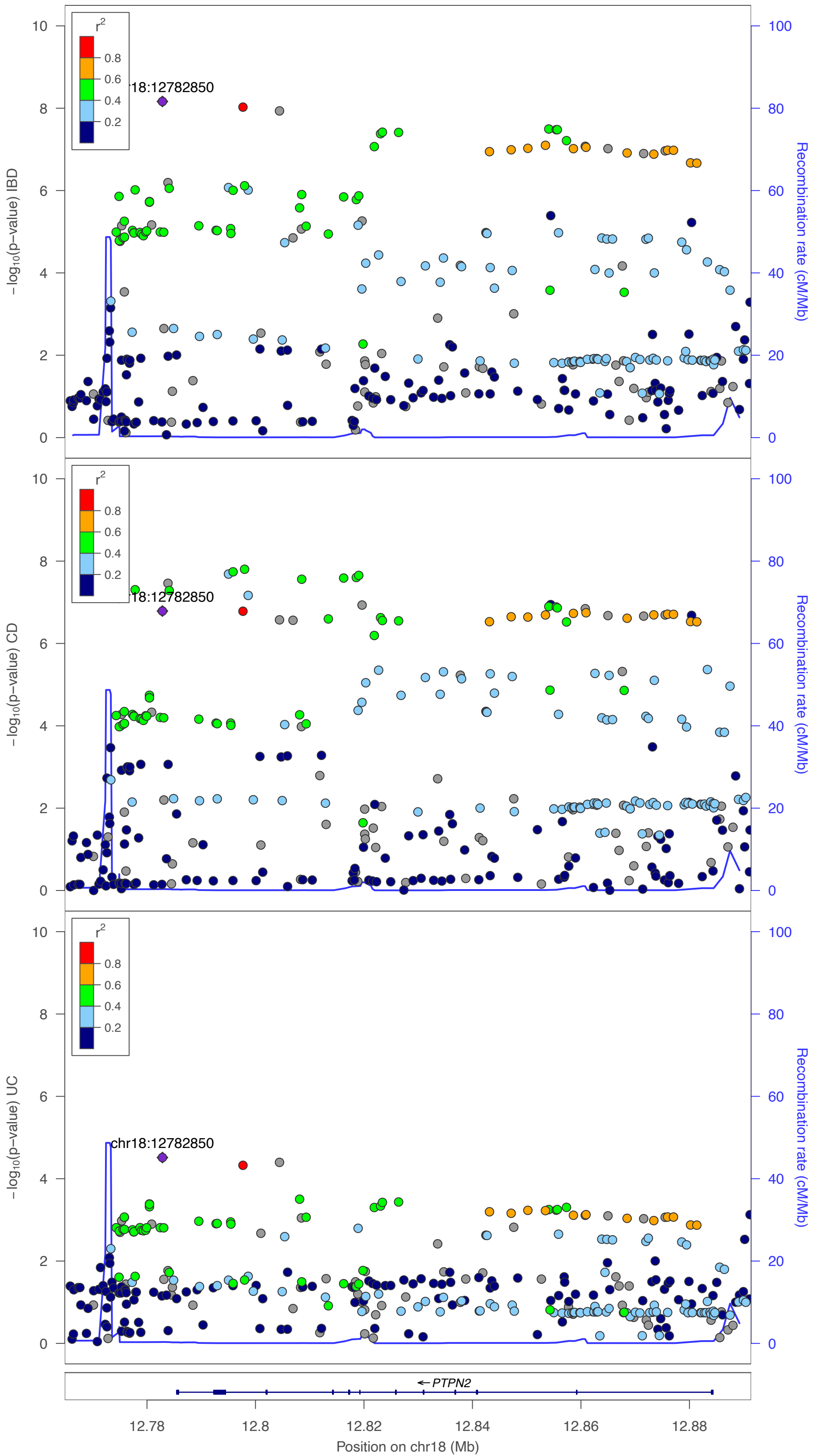
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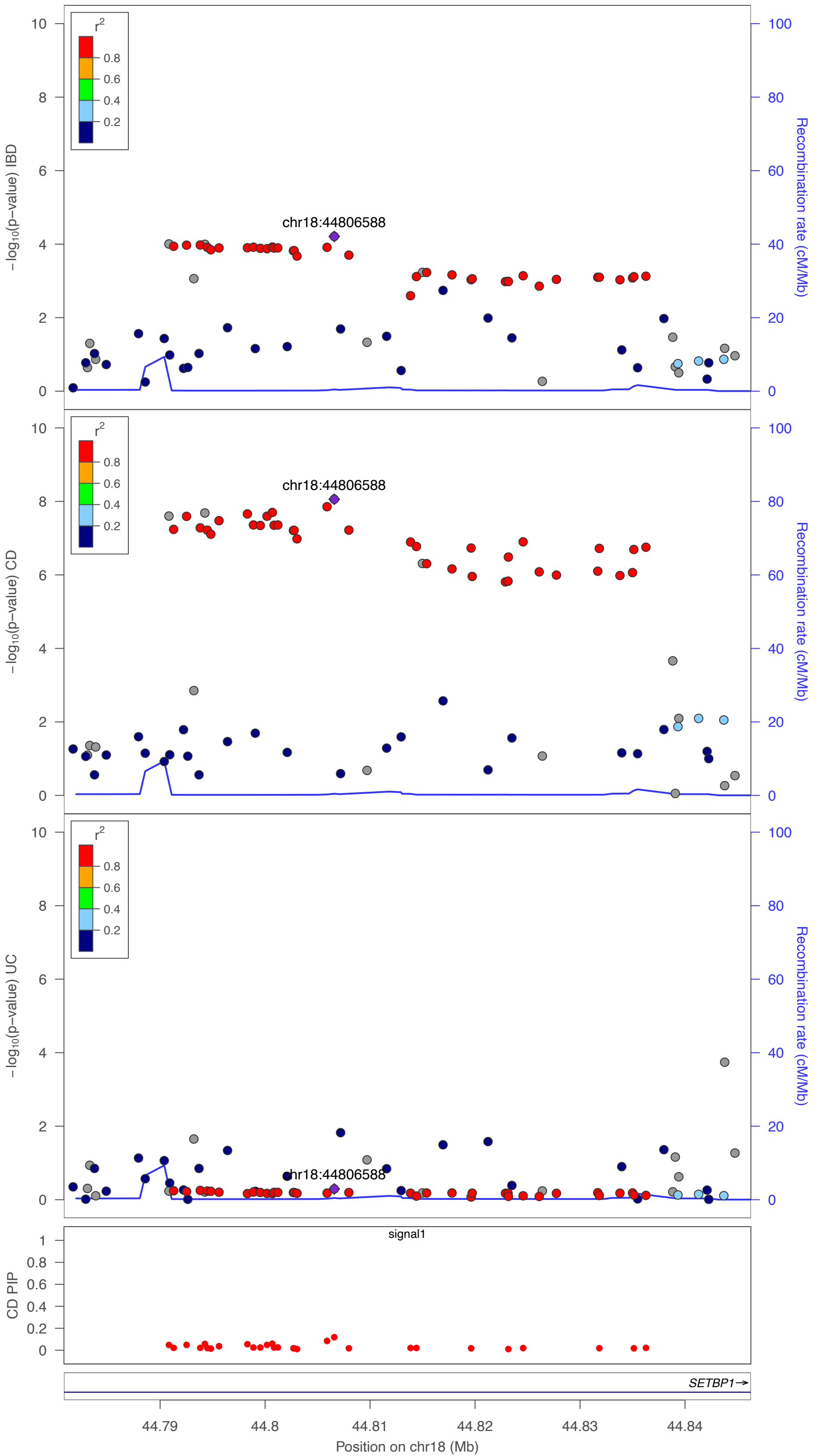
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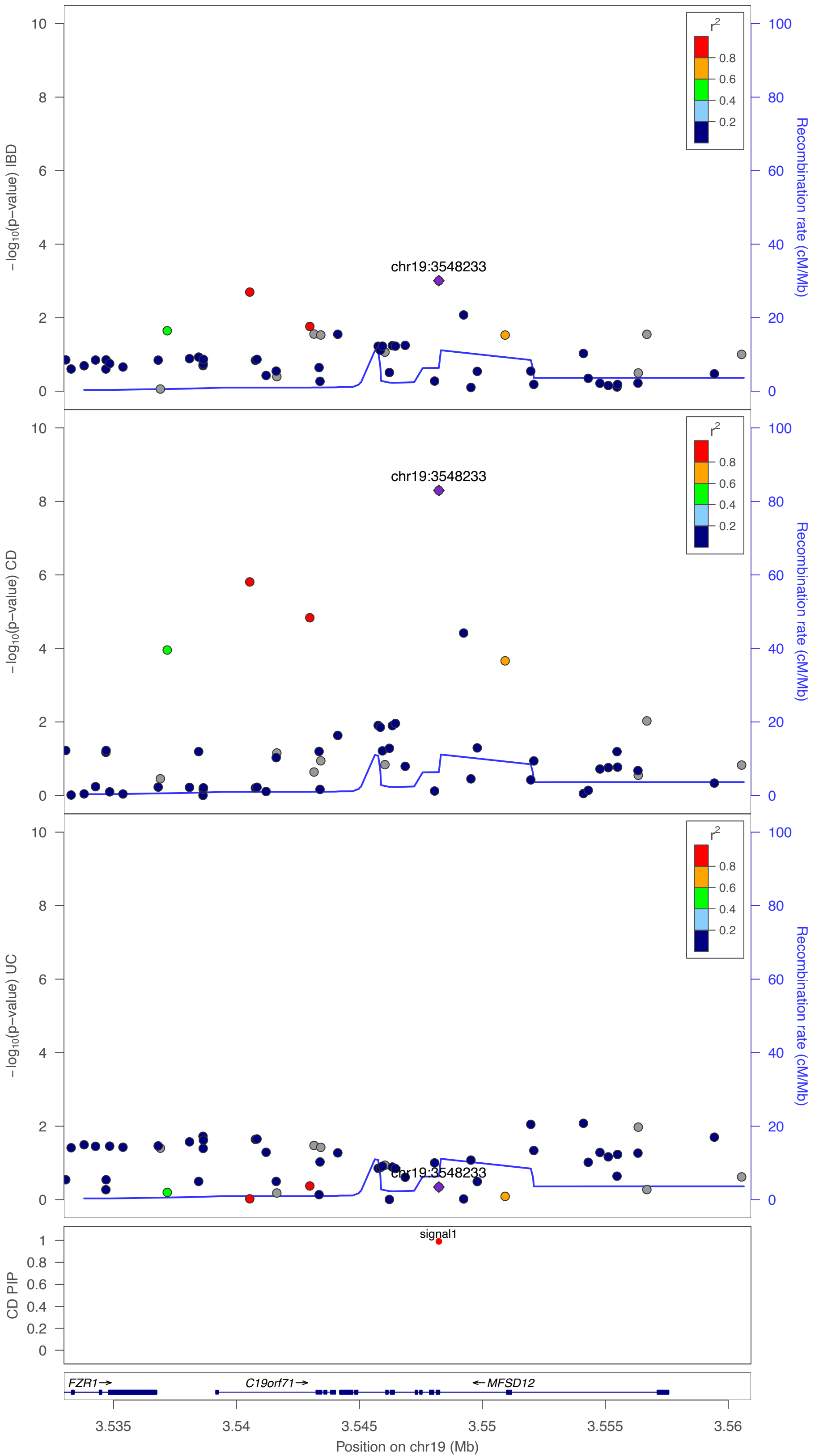
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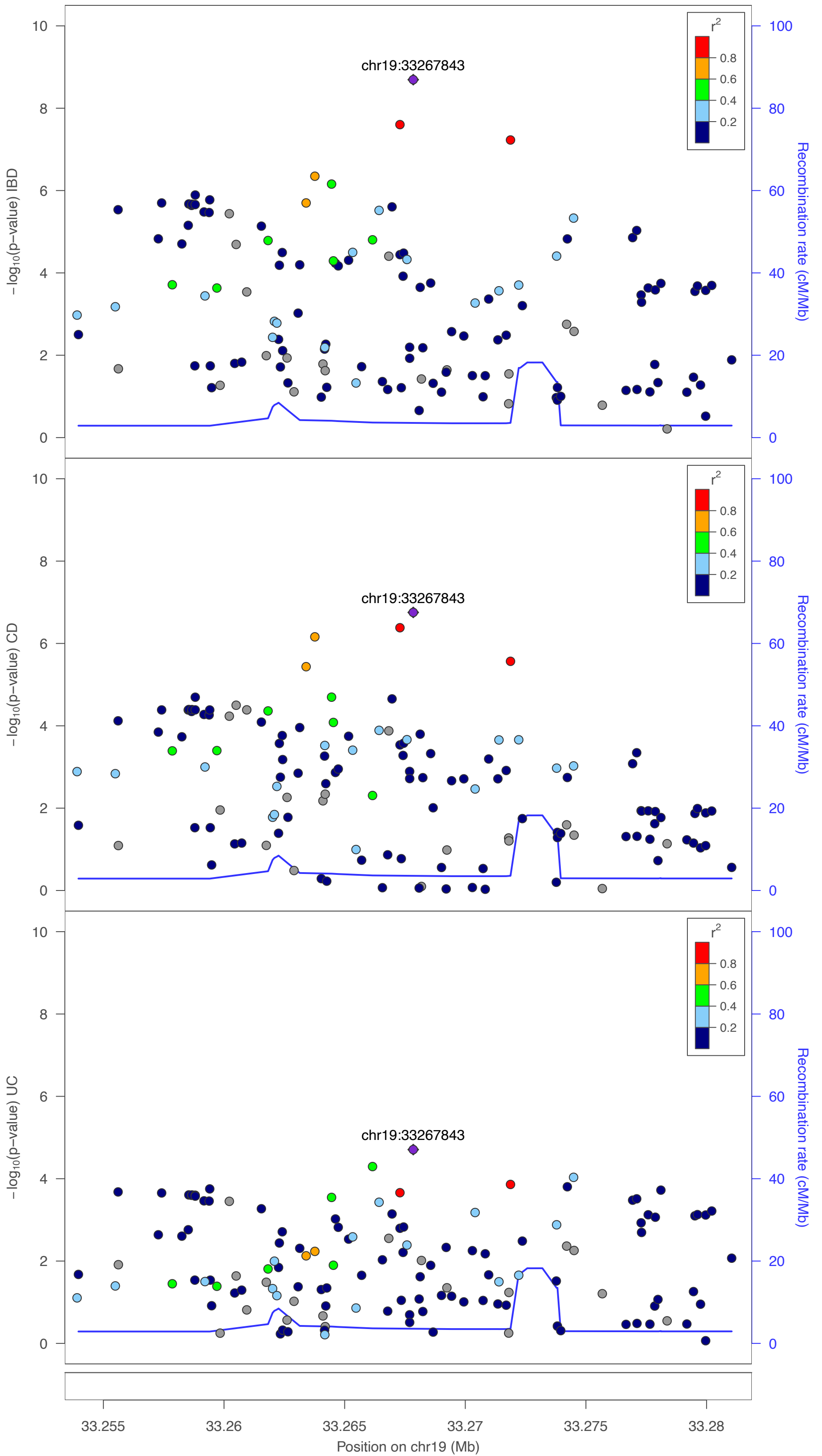
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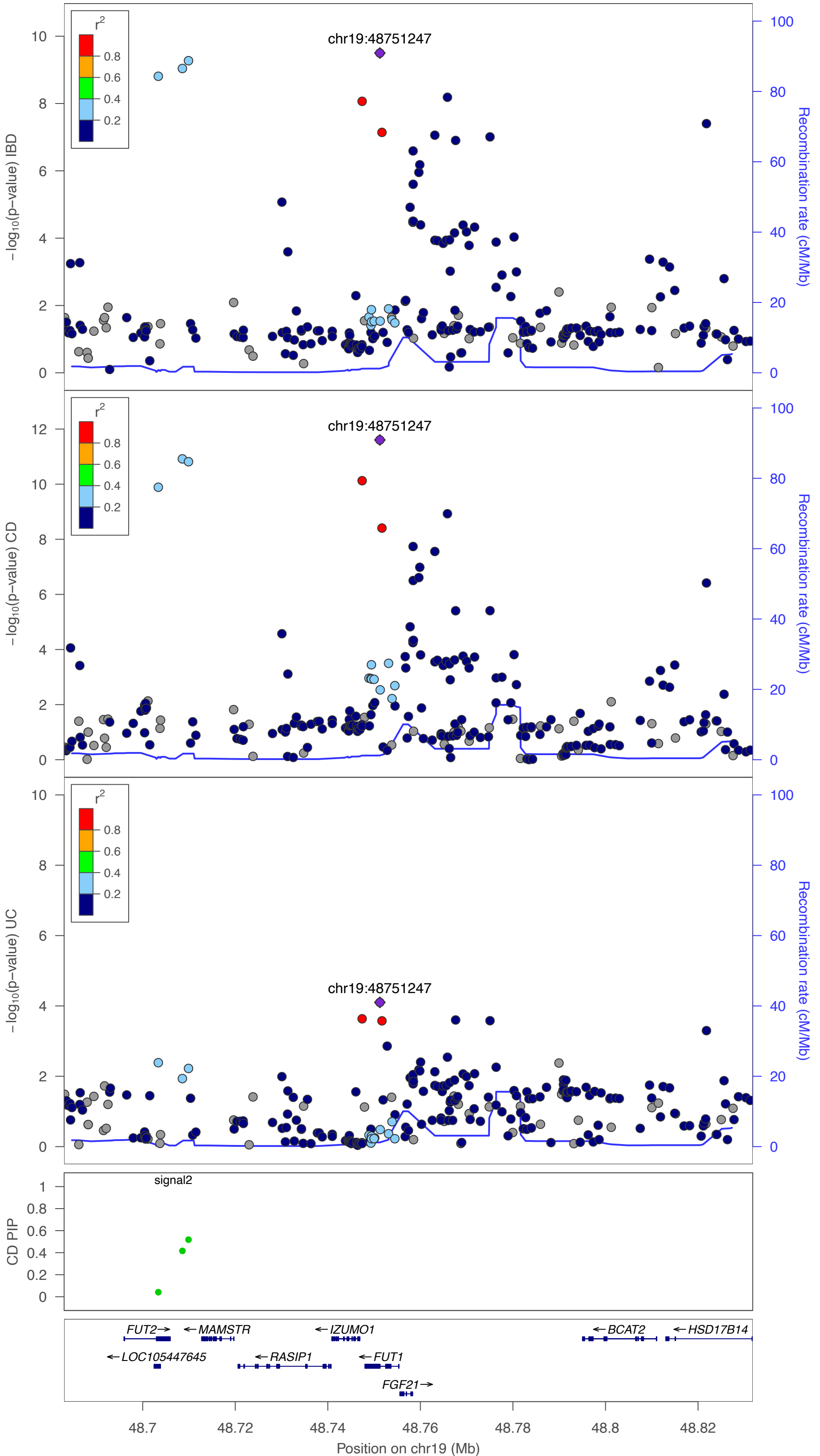
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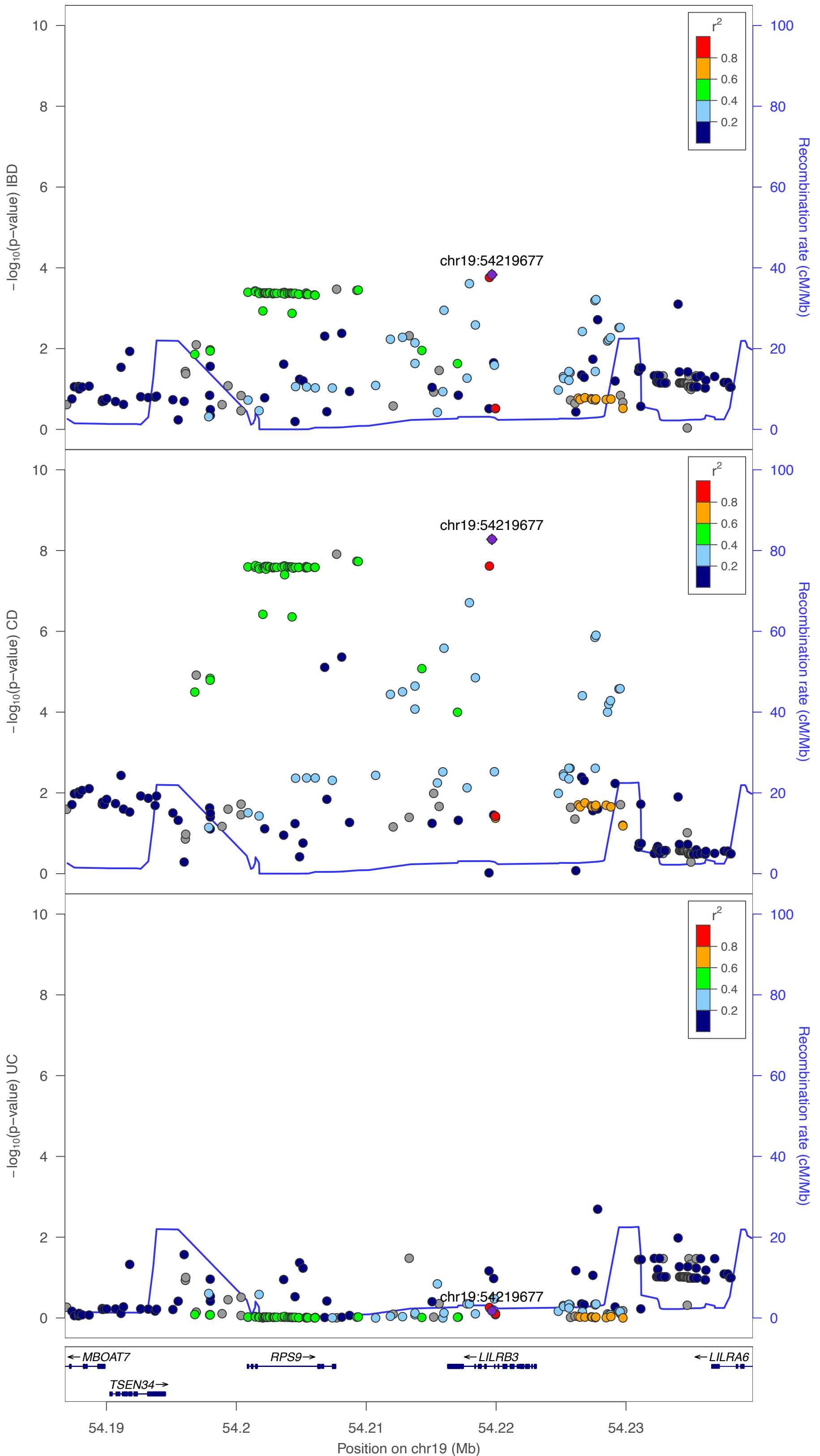
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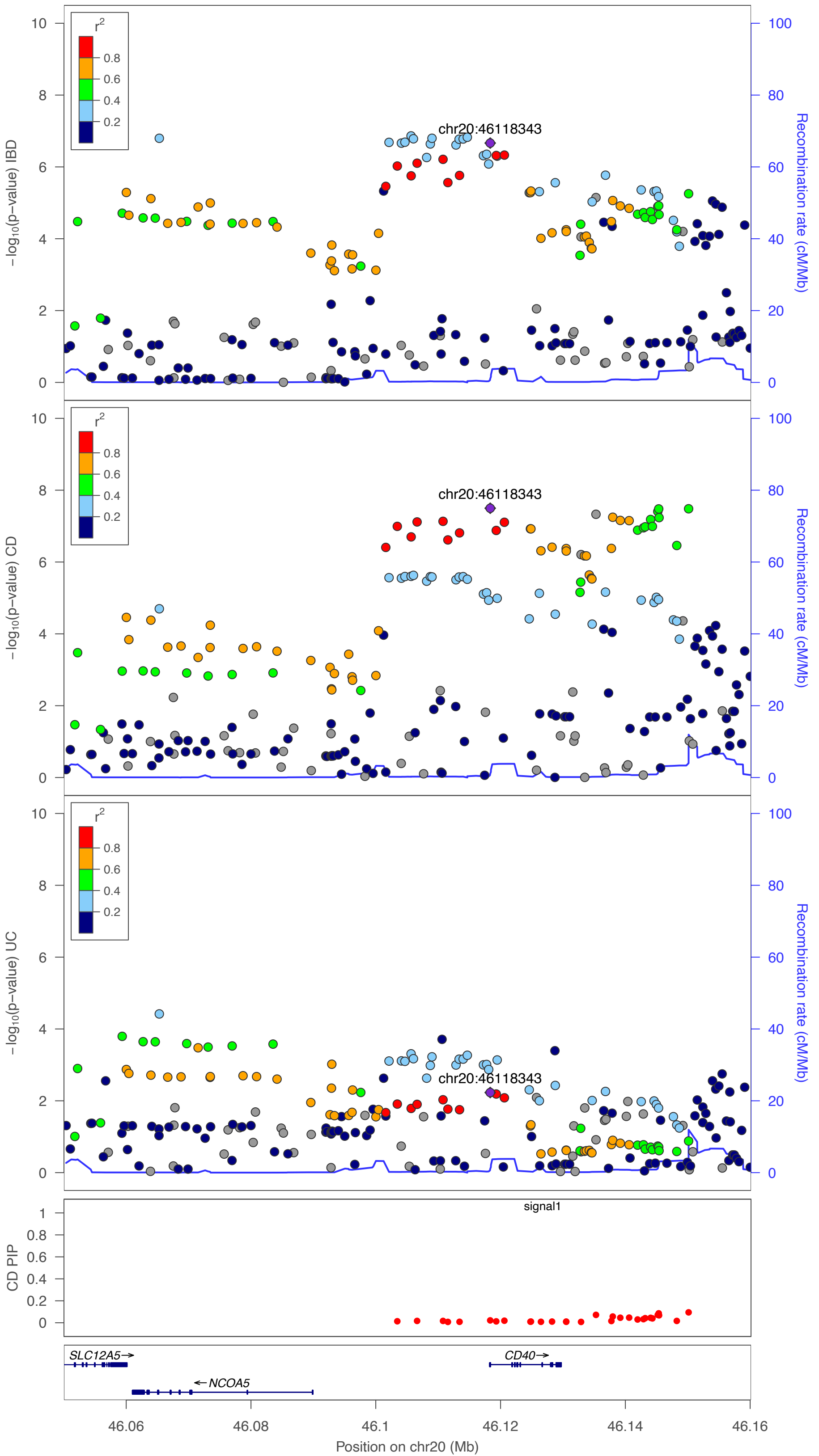
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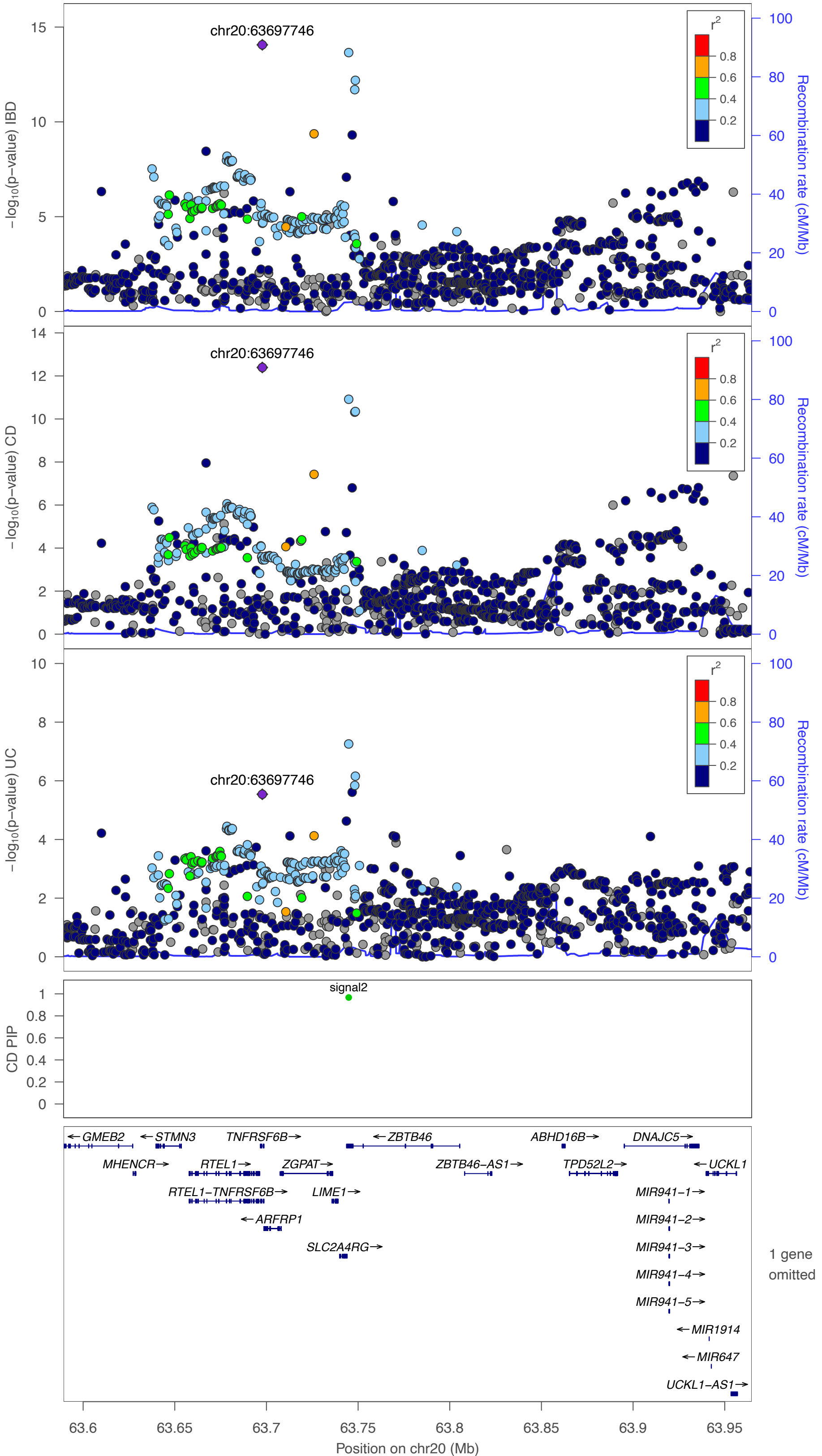
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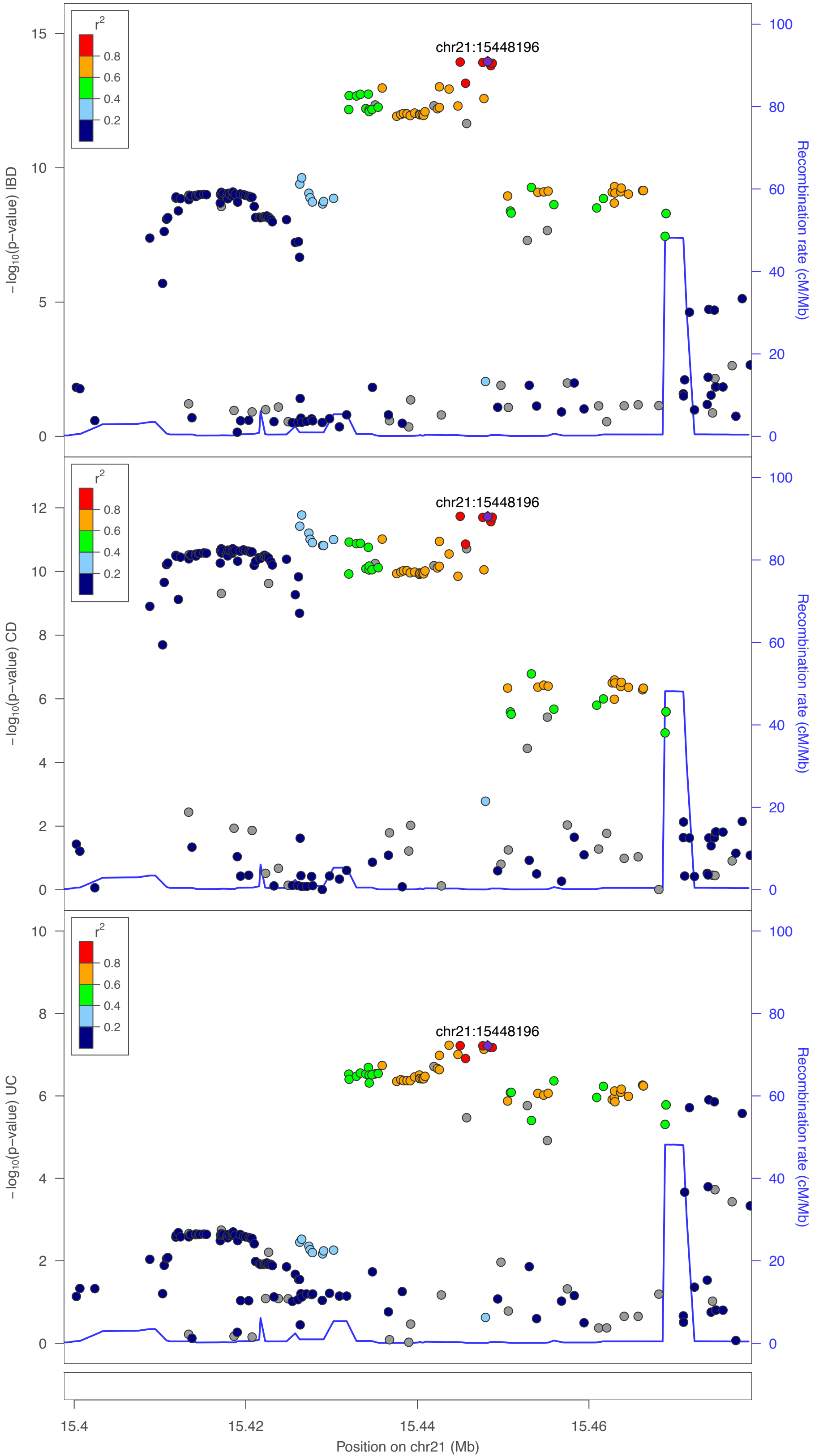
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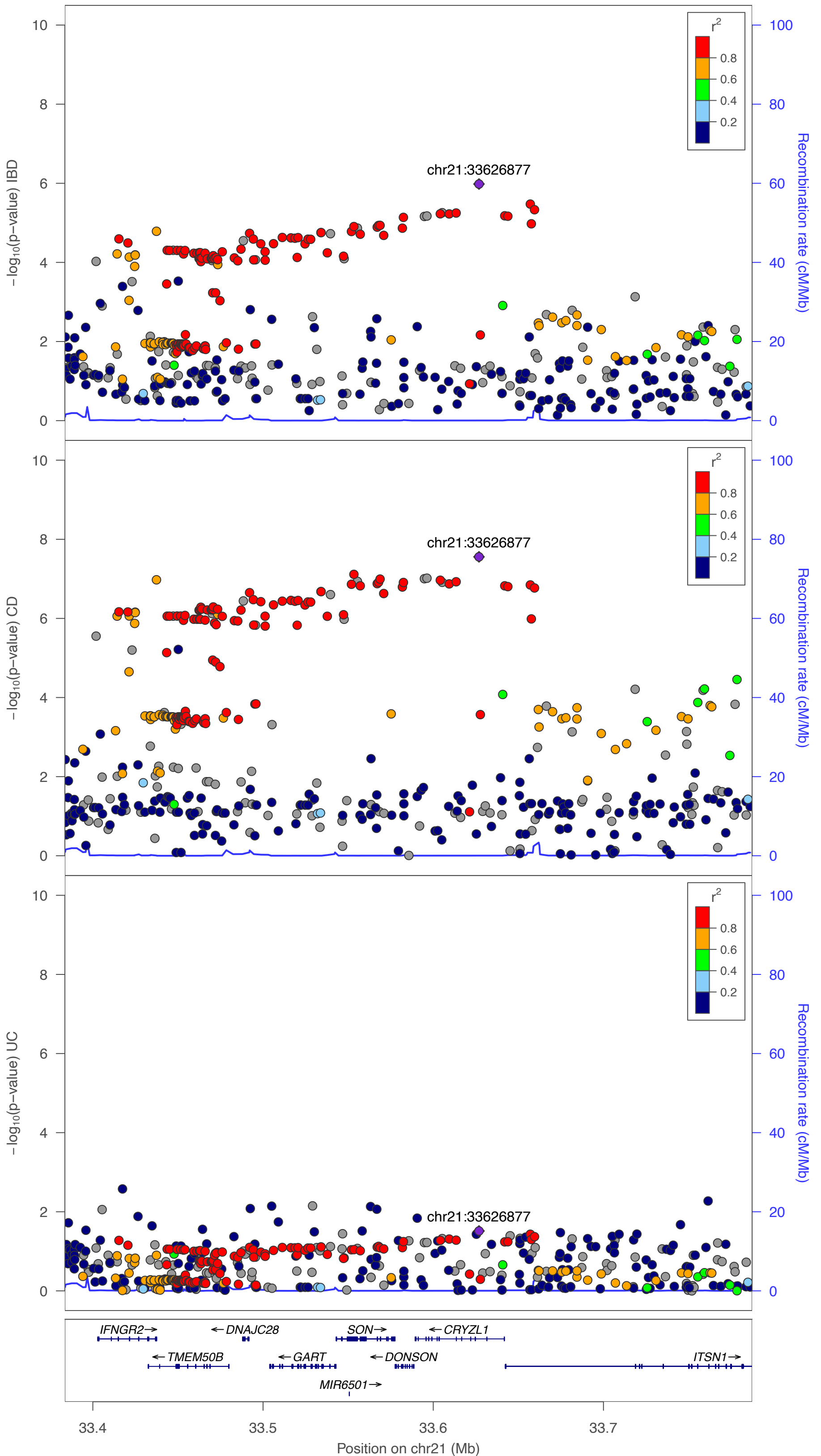
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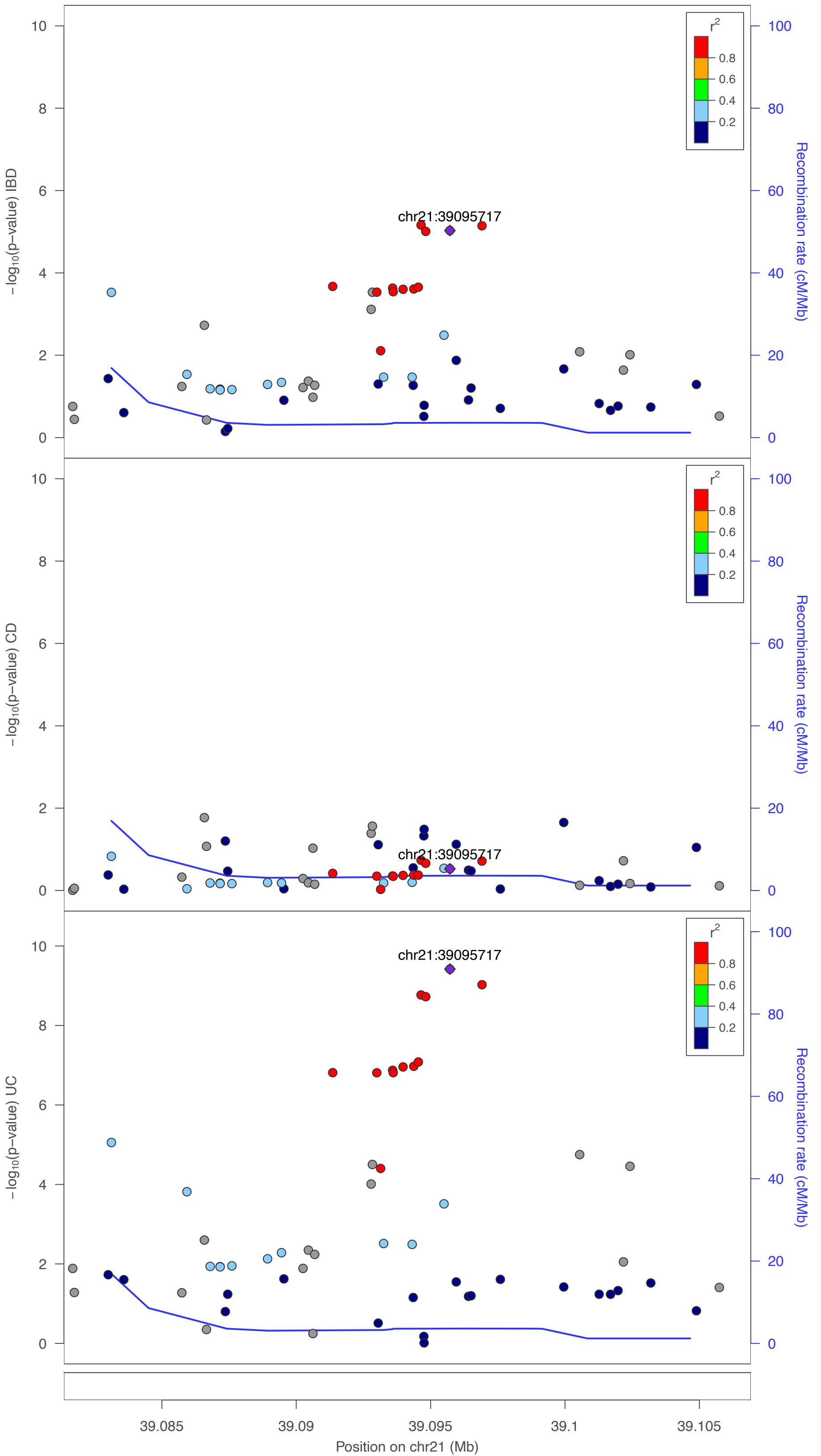
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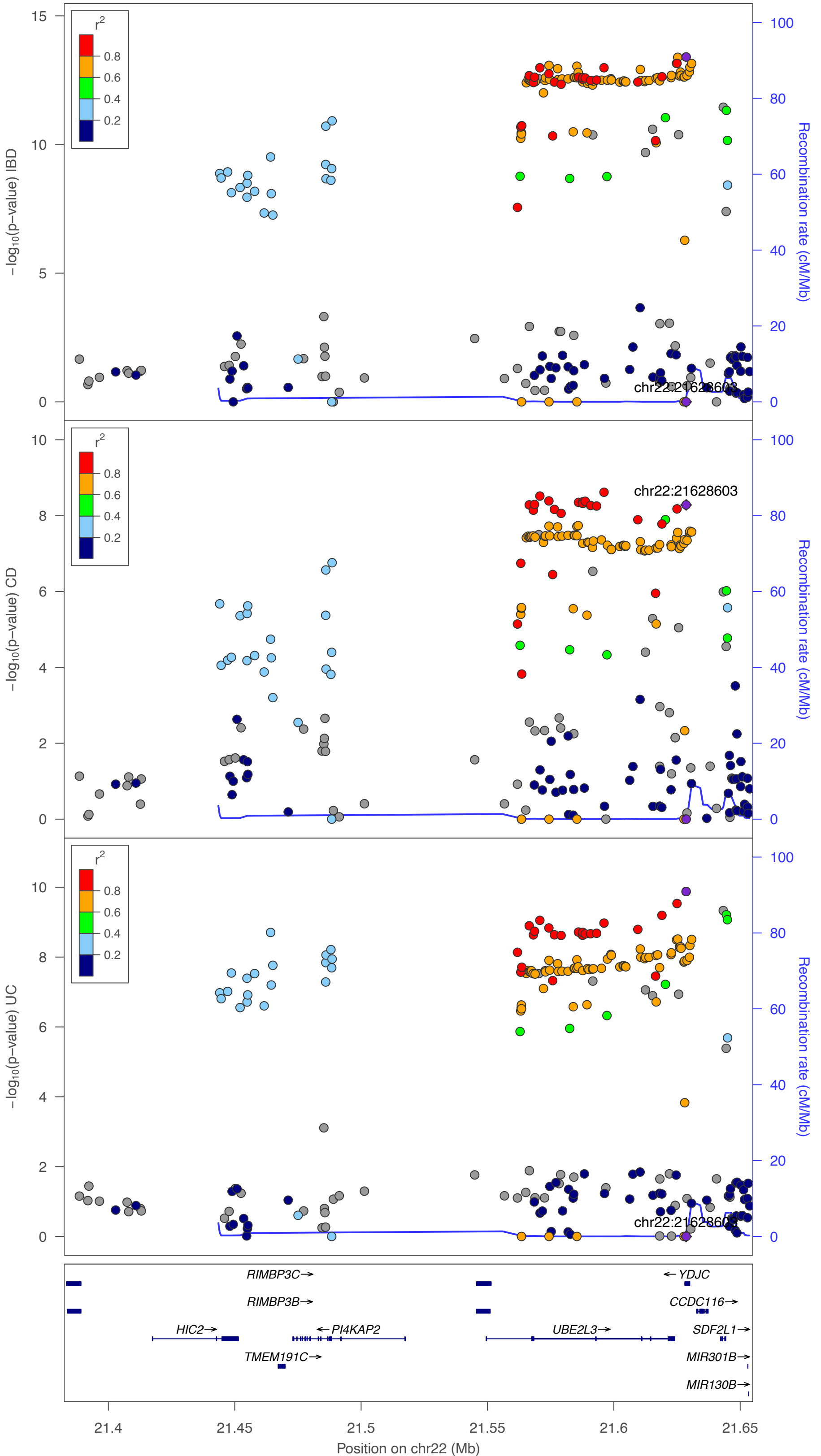
CD chr21:33626877:A:G



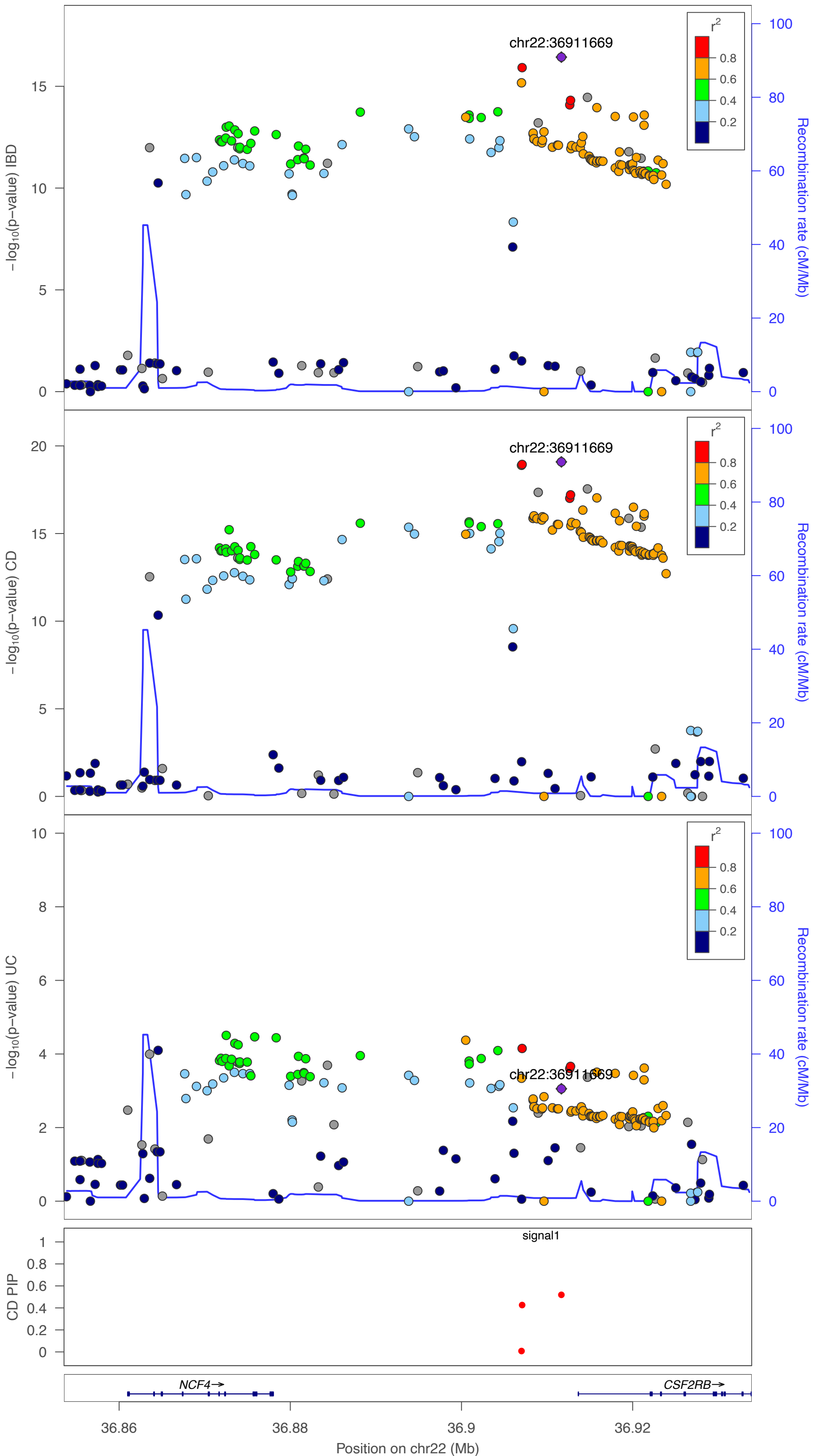
UC chr21:39095717:T:C



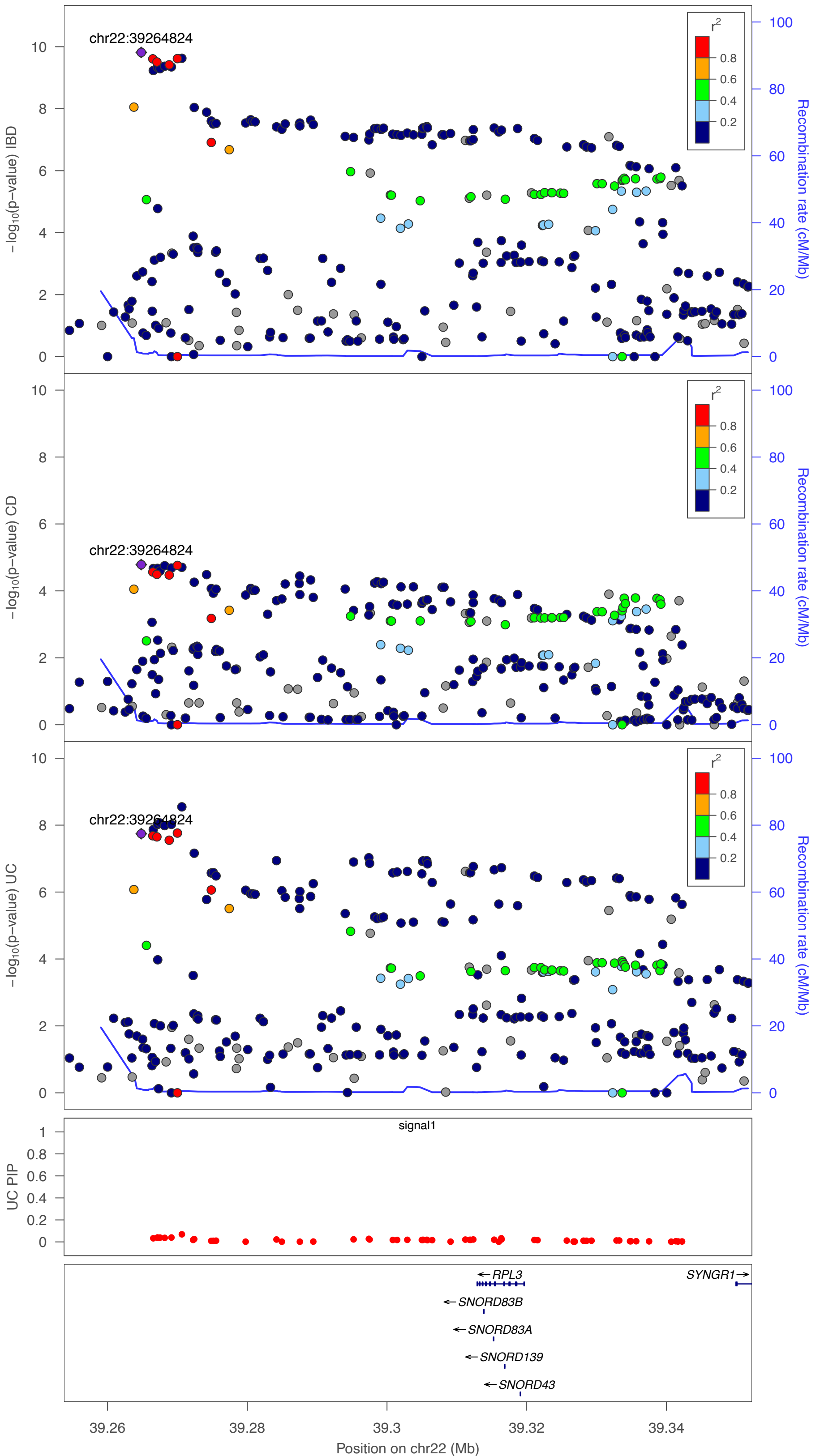
IBD chr22:21628603:C:T



CD chr22:36911669:C:T



IBD chr22:39264824:T:C



CD chrX:136605401:A:C

