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Genome-wide Association Analysis Identifies 30 New Susceptibility Loci for Schizophrenia

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Abstract

We conducted a genome-wide association study (GWAS) with replication in 36,180 Chinese individuals and performed further trans-ancestry meta-analyses with data from the Psychiatry Genomics Consortium (PGC2). ~95% of the genome-wide significant (GWS) index alleles (or their proxies) from the PGC2 study were overrepresented in Chinese cases, including ~50% achieved nominal significance, and ~75% continued to show GWS in the trans-ancestry analysis. The Chinese-only analysis identified seven GWS loci, three of these were also GWS in the trans-ancestry analyses which identified 109 GWS loci, yielding a total of 113 GWS loci (30 are novel) in at least one of these analyses. We observed considerable improvements in the fine-mapping resolution at many susceptibility loci. Our results provides several lines of evidence supporting candidate genes at many loci and highlights some pathways for further research. Together, our findings provide novel insight into the genetic architecture and biological etiology of schizophrenia.

Introduction

Schizophrenia (OMIM:181500) is a chronic, severe, and disabling brain disorder that affects approximately 1% of the worldwide population and imposes an enormous burden on society[1,2]. It is a highly heritable psychiatric disorder (an estimated heritability of 70–85%[3]) with a substantial polygenic component including thousands of common alleles with small effects that contribute to disease risk[4]. Approximately 33-50% of the genetic risk of schizophrenia can be captured by common alleles in current genome-wide association studies (GWASs)[5]. The evidence so far suggests many risk alleles for common schizophrenia-associated genetic loci may be shared across ancestry groups, but others may be population-specific because of differing causal variants or linkage disequilibrium (LD) patterns in populations of different ancestries[6]. Previous GWASs have identified more than 110 schizophrenia-associated loci and have substantially advanced our understanding of this condition[5,7-13]. In particular, the most recent and largest schizophrenia GWAS (from the Schizophrenia Working group of the Psychiatric Genomics Consortium, PGC2) which, with discovery and extension, included a total of 36,989 cases and 113,075 controls, identified 128 independent genome-wide significant associations spanning 108 loci[7].

However, a large proportion of the genetic factors underlying schizophrenia remain unknown. The vast majority of the heritability of schizophrenia is not yet attributable to specific loci, only 3.5% of liability being explained by GWS loci[7]. Moreover, to date, most GWAS participants with schizophrenia are of European descent. Thus, although the PGC2 report included samples from East Asia, the proportions were small (approximately 5% and 3% for cases and controls respectively). Large-scale GWASs using samples of non-European descent are essential for extending our understanding of the genetic architecture of schizophrenia in the human population as a whole, for testing the generalizability of the results from European populations for this global disorder[6], and to identify population specific risk factors should they exist.

To identify additional schizophrenia susceptibility loci and gain a better understanding of the genes and biological pathways implicated in schizophrenia, we performed a GWAS of 7,699 cases and 18,327 controls of Chinese ancestry, as well as a trans-ancestry GWAS meta-analysis with PGC2 (43,175 cases and 65,166 controls in total). The candidate loci found in each analysis were then studied in an independent replication sample of 4,384 cases and 5,770 controls of Chinese ancestry.

Results

Results of Chinese GWAS screening

We first conducted a GWAS for schizophrenia in the Chinese population (in comparison to the discovery phase of our prior GWAS report[10], the number of cases were doubled and the number of controls were tripled). After systematic quality control (QC) analysis and imputation to the 1000 Genomes Project data (online **Methods**), we assessed the associations of 5,107,227 genetic variants in 7,699 cases and 18,327 controls (**Supplementary Table 1**). The primary GWAS comprised three samples that were genotyped on different platforms: 4,175 cases and 10,470 controls using Affymetrix Genome-Wide Human SNP Array 6.0 (SNP6.0); 2,472 cases and 5,928 controls using the Affymetrix Axiom^{TM} Genome-Wide CHB1 Array Plate (CHB1); and 1,052 cases and 1,929 controls using CHB1 or the Illumina 1M Array (1M). Principal component analysis (PCA) was used to assess population substructure (**Supplementary Figure 1** and online **Methods**). For each subset, association testing was conducted using logistic regression including ancestry principal components (PCs) as covariates to adjust for population stratification. The results were combined using inverse variance weighted meta-analysis (based on a fixed-effects model). The genomic inflation factor (λ_{GC}) was 1.22, and λ_{1000} was 1.02. We conducted LD score regression analysis[14] to distinguish the relative contributions of confounding bias and polygenicity. The LD score regression intercept was 1.07 (s.e. = 0.01), and the slope was greater than zero, suggesting the majority of the increase in the mean χ^2 statistic is from polygenic architecture rather than population stratification, which is consistent with the previously documented polygenic nature of schizophrenia inheritance[7,15]. However, given this modest elevation in the intercept, we further corrected the meta-analysis statistics for residual test-statistic inflation[14,16] (online **Methods**). Quantile-quantile and Manhattan plots are shown in **Supplementary Figures 2** & **3**. We observed 66 GWS variants in a region previously reported as associated with schizophrenia (2p16.1)[11,12] in this analysis (**Fig. 1**).

The proportion of variance in susceptibility to schizophrenia explained by genome-wide SNP genotypes based on individuals of Han Chinese ancestry (online **Methods**) was estimated to be 31.5% (s.e. 1.9%), assuming a population risk of 0.01. This is similar to the corresponding estimate for European samples (33%)[5]. This result provides further evidence of the highly polygenic nature of schizophrenia[7,15].

Results of the Chinese and PGC2 genome-wide meta-analysis

We performed a meta-analysis of the Chinese (7,699 cases and 18,327 controls) and PGC2 (35,476 cases and 46,839 controls) GWAS samples to explore the effects of power and heterogeneity. A total of 4,303,605 genetic variants were common to the two datasets and were retained in the combined analysis. For combining the data, we used a fixed-effect model but for variants with pronounced heterogeneity (I^2 >75%)[17], we used a random-effects model to allow for the possibility that the presence of heterogeneity might result in test-statistic inflation. In our final result, the genomic inflation factor (λ_{GC}) was 1.50, and λ_{1000} was less than 1.01. The deviation of the observed statistics from the null hypothesis is less than expected under a polygenic model for schizophrenia[7,18]. Quantile-quantile and Manhattan plots are shown in **Supplementary Figures 4** & **5**. In the combined analysis, we detected 5,618 SNPs surpassing the GWS threshold for association with schizophrenia. These SNPs map to 104 physically distinct associated regions as defined by clumping the variants using r^2 > 0.1, and merging the LD-independent variants within 250kb (**Fig. 1** and **Supplementary Table 2**).

Results of the combined-analysis with replication samples

We then obtained association results from an independent Chinese cohort of 4,384 cases and 5,770 controls (**Supplementary Table 1**)[19] for LD-independent SNPs with $P < 1 \times 10^{-5}$ in the Chinese-only GWAS meta-analysis or with $P < 5 \times 10^{-7}$ in the Chinese and PGC2 GWAS meta-analysis (online **Methods**).

The combined analysis of the Chinese GWAS and replication samples resulted in a dataset of 12,083 cases and 24,097 controls. Seven loci achieved GWS for association with schizophrenia in the meta-analysis of Chinese-ancestry individuals. Of these loci, three have been previously reported to be associated with schizophrenia (**Supplementary Figure 6**), and the other four are novel: rs2073499 at 3p21.31 (OR = 0.899, fixed-effects meta-analysis $P = 2.61 \times 10^{-8}$), rs7757969 at 6q21 (OR = 1.110, $P = 4.82 \times 10^{-8}$), rs4479915 at 6q27 (OR = 0.876, $P = 4.82 \times 10^{-9}$) and rs11534004 at 7q31.1 (OR = 0.890, $P = 1.71 \times 10^{-8}$) (**Fig. 2**). Four additional loci achieved significance at $P < 1 \times 10^{-5}$ in the Chinese GWAS meta-analysis and gave nominal evidence of replication ($P < 0.05$), but failed to achieve GWS in the combined analysis. Results for all tested SNPs are presented in **Supplementary Table 3**.

The combined results of the trans-ancestry meta-analysis (43,175 cases and 65,166 controls) and replication samples (4,384 cases and 5,770 controls) identified a total of 109 GWS loci (**Supplementary Table 4** and **Supplementary Data 1**). Of the 109 loci, 83 had been previously reported, and 26 loci were novel.

Taken together, the above analyses identified 124 SNPs that were GWS associated with schizophrenia. The SNPs map to 113 physically distinct loci: four loci were GWS only in the Chinese-only analysis, 106 were GWS only in the trans-ancestry analysis, and three were present in both analyses (**Supplementary Table 5**). Of the 113 associated loci, 30 have not been previously reported (**Table 1**), four of which were GWS in the Chinese sample but not the trans-ancestry analysis. In addition, at three of the previously reported loci, the GWS SNPs in present study are in low LD with the previously identified GWS SNPs ($r^2 < 0.1$ in both the European and Chinese populations), which might suggest independent signals in these regions (**Supplementary Table 5**).

Similarities and differences across ancestries

Of the 108 loci (128 index SNPs) identified in the PGC2 report[7], we were able to investigate 103 loci (117 index SNPs or their proxies) that are common in both PGC2 and Chinese datasets (**Supplementary Table 6**). Of these, the PGC2-associated risk alleles were overrepresented in Chinese cases at 109 SNPs (from 98 loci), and at 58 of them (from 56 loci), this overrepresentation achieved nominal significance ($P < 0.05$). In trans-ancestry meta-analyses, 85 SNPs at 78 loci continued to show GWS. It is known that random-effects model might be overly conservative[20], and therefore on an exploratory basis, we performed a fixed-effect model meta-analysis for all these SNPs regardless of the existence of heterogeneity. Under the fixed-effect model, an additional eight SNPs (93 in total) at eight loci (86 loci in total) exhibited GWS in the combined analysis. However, the results for the GWS SNPs indicated by fixed-effect meta-analysis and with evidence of heterogeneity should be interpreted with caution. Nevertheless, this finding suggests that the schizophrenia susceptibility loci identified in European samples are applicable to the Chinese sample. Meanwhile, the trans-ancestry meta-analyses also confirmed two GWS loci (8p12 and 7q11.22) identified in our previous reports[10,21].

As to the seven GWS index SNPs analyzed in the Chinese-only analysis in this study, three replicated at $P < 0.05$ in the PGC2 dataset, but showed significant heterogeneity (I^2 >75%) across populations and did not reach GWS in trans-ancestry meta-analyses. In addition, one of the index SNPs (rs78681500) was absent in the PGC2 dataset due to its rarity (minor allele frequency, MAF < 1%). Of the 117 GWS index SNPs identified in the trans-ancestry analysis, all showed the same direction of effect across ancestries, and I^2 was less than 75%.

We next assessed the genome-wide congruence of risk alleles across the PGC2 and Chinese GWAS datasets for LD clumped independent SNPs[22]. For the schizophrenia-associated SNPs ($P \leq 0.0001$) identified in the Chinese dataset, we observed a highly significant excess of directional concordance in the PGC2 dataset (67.7%, binomial test $P = 3.06 \times 10^{-7}$). For the SNPs demonstrating weaker evidence of an association with schizophrenia ($0.0001 < P \leq 0.05$), we also observed an excess of consistency in the direction of effect. In contrast, for the SNPs with no evidence of association ($P > 0.5$), there was no enrichment in coincident risk alleles across ethnic groups (**Supplementary Table 7**). We repeated this analysis by identifying the schizophrenia risk alleles at SNPs in the PGC2 dataset and assessing concordance in the direction of the effect in the Chinese dataset, and a very similar pattern was found (**Supplementary Table 7**). We were convinced of a significant excess in directional concordance across ancestry groups for the SNPs with evidence of a schizophrenia association.

Potential biological mechanisms of the associated loci

To determine the likely causal genes of schizophrenia-associated genetic loci, we considered each of the following to represent evidence supporting the causality of a gene within a locus (online **Methods**): (1) being the gene nearest the index SNP[23]; (2) containing a missense mutation and being in high LD ($r^2 > 0.8$) with the GWS SNPs[23]; (3) prioritization using DEPICT [24], (4) *cis*-eQTL (cis-acting expression quantitative trait loci) genes for the index SNPs[23,25-28], or (5) prioritization by the summary-data-based mendelian randomization (SMR) analysis[29]. Using these criteria, 247 genes were prioritized from the schizophrenia risk loci, and 85 had more than one line of supporting evidence (we defined them as 'prioritized candidate genes') (**Supplementary Table 8**). We first focused on those in the newly identified loci (**Table 1**). As expected, some of these genes were plausibly biologically relevant. The index SNP rs2247870 (NP_115495.3:p.Val5876Ile) at 5q14.3 (No. 37 GWS locus) is a missense variant in *ADGRV1* (also known as *GPR98*), which encodes a member of the G-protein coupled receptor (GPCR) superfamily and is expressed in the central nervous system. Multiple lines of evidence suggest that GPCRs play critical roles in major psychiatric disorders (including schizophrenia) and their treatment[30]. A variant in *GPR98* has been found to be associated with the response to antipsychotic treatment[31]. *FYN* (No. 49 GWS locus) encodes a membrane-associated tyrosine kinase. FYN plays a critical role in neuronal apoptosis and is involved in brain development and synaptic transmission[32,33]. Decreased expression of FYN protein has been observed in the platelets of schizophrenic patients[34]. The result from whole blood eQTL analysis[27] indicated that the schizophrenia risk allele identified in this study (rs7757969-C) correlated with a lower expression of *FYN* ($P = 1.71 \times 10^{-7}$, with false discovery rate (FDR) < 0.05 and in the credible interval covered by the 99% credible set), which is consistent with previous finding. The estimate (b_{XY}) for the effect of gene expression on schizophrenia risk under the SMR analysis is -0.70 ($P_{\mathrm{SMR}} = 7.55 \times 10^{-4}$). *MAGI2* (No. 54 GWS locus) encodes a synaptic scaffolding molecule, which is essential for the development and maintenance of synapses[35]. Synaptic dysfunction has been suggested to play an important role in schizophrenia[36]. Common variants in *MAGI2* were found to be associated with cognitive impairment in schizophrenic patients[37]. Although it is currently difficult to pinpoint a causal gene that is responsible for a given locus, the prioritized genes could be considered as the most likely candidates for further research to unravel the plausible biological mechanisms for the associations.

Improved fine-mapping resolution at the associated loci

We sought to refine the localization of likely functional variants in the schizophrenia associated loci using a previously published approach[38,39]. We derived Bayesian credibility sets in different datasets and evaluated the evidence for improved fine-mapping resolution through trans-ancestry meta-analysis. For the 99% credible SNP sets, the trans-ancestry dataset produced the smallest spanned regions for about 80% (n = 88) of the tested loci (**Supplementary Table 9**), including 11 loci with a spanned region less than 30 kb. At 53 of the 88 loci, the number of genes that overlapped with the trans-ancestry interval defined by credible set was two or less. Of those overlapped genes mapping to the credible intervals in the 53 loci, 49.1% was were in the list of 'prioritized candidate genes', while the proportion is 12.4% and 5.1% for the PGC2 and Chinese analysis, respectively.

We also conducted fine-mapping analysis using PAINTOR by leveraging the functional annotation data and LD information in multi-ancestry cohorts[40-42]. We integrated the primary functional categories (coding, UTR, promoter, DNase hypersensitivity site (DHS), intronic and intergenic) proposed by Gusev *et al.*[41]. A total of 62 variants achieved a posterior probability of greater than 0.80 in at least one of the single-population and trans-ancestry analyses (**Supplementary Table 10**). Of them, 38 variants have higher posterior probability in the trans-ethnic analysis than in the single-population analyses, including an additional 16 variants that achieved a trans-ancestry posterior probability of greater than 0.80 but had a posterior probability lower than 0.80 in the single-population analyses. Eleven (68.8%) of these 16 variants had at least one hit in the selected eQTL studies in HaploReg V4.1[23] (**Supplementary Table 11**). For example, at No. 80 GWS locus, rs12541 with a posterior probability of 0.926 (**Supplementary Figure 7a**) lies in the UTR region of *ESAM*, and correlates with its expression in whole blood ($P = 3.62 \times 10^{-8}$ and in the 99% credible set interval)[27]. A further example is for No. 103 GWS locus, rs3814883 with a posterior probability of 0.911 (**Supplementary Figure 7b**) is a synonymous variant of *TAOK2* and also an eQTL SNP for several genes in different tissues[23] (**Supplementary Table 12**). It might also be correlated with the expression of *SEZ6L2* in the brain cerebellum and frontal cortex ($P = 2.37 \times 10^{-8}$ and 5.03×10^{-8}, respectively)[26]. TAOK2 was found to affect basal dendrite development in cortical neurons[43]. SEZ6L2 was identified as a Cathepsin D transport receptor and was involved in neurite outgrowth[44]. To further explore the regulatory nature in the context of cell-type specific epigenome, we also integrated the reference epigenomes of seven highlighted marks for 127 human tissues and cell types produced by the Roadmap Epigenomics Project[45] (online **Methods**). Of the top 100 enriched cell-type specific epigenomic annotations for schizophrenia associations in the current and PGC2 analyses[7], over 40 are brain and neural-related (**Supplementary Table 13**). In the further PAINTOR fine-mapping analyses with the top 100 epigenomic annotations, many SNPs obtained higher posterior probabilities and some of them were raised to a value of greater than 0.80, indicating potential biologically relevant cell types for these associations (**Supplementary Table 14**). For example, rs6670165, a candidate causal SNP at No. 7 GWS locus, mapped to enhancers and promoters active in several brain regions. The identification of these SNPs suggests an important benefit of the trans-ancestry fine-mapping signal in functional annotation data. However, it should also be noted that 14 variants had a posterior probability of greater than 0.80 in the single-population analyses but reduced to less than 0.8 in the trans-ancestry analysis (**Supplementary Table 10**).

Biological pathways and gene sets

To identify pathways and gene sets in the trans-ancestry meta-analysis, we performed an enrichment analysis using MAGMA[46]. We identified one gene set, “Regulation of Insulin Secretion by Glucagon-like Peptide 1” (from the Reactome database), that was statistically significantly enriched (MAGMA competitive $P = 5.14 \times 10^{-7}$, **Fig. 3**). The MAGMA pathway analysis also highlighted several other pathways. Two of the previously highlighted schizophrenia associated pathways, “Postsynaptic Density”[47] and “Voltage-gated Calcium Channel Complex”[7], also ranked highly in our analysis, with P values of 9.01×10^{-4} and 1.32×10^{-3}, respectively (**Supplementary Table 15**).

Polygenic risk score profiling

Polygenic scoring analyses were proposed to predict the case-control status in a target dataset based on the results from a training GWAS[4]. To assess the overlap between the common variant signal in the European and Chinese populations, and provide estimates of the proportions of variance additionally explained by the Chinese samples, we conducted a polygenic scoring analysis. We randomly selected approximately 1,000 cases and 1,000 controls from the Chinese sample as the target sample, and four training datasets were used: the PGC2 European only dataset (EUR49), the full PGC2 dataset, the Chinese sample but excluding the target sample and the Chinese and PGC2 combined datasets (**Fig. 4**). The risk-profile SNPs (P thresholds, $P_T = 5 \times 10^{-8}$, 1×10^{-6}, 0.0001, 0.001, 0.01, 0.05, 0.1, 0.2, 0.5 and 1) from the European only dataset alone could explain approximately 1.11% to 2.34% of the variance in the case-control status of the Chinese sample on the liability scale[48] (assuming a population risk of 0.01). When the Asian samples were included, the PGC2 dataset could explain approximately 1.52% to 3.51% of the variance. The Chinese dataset alone could explain approximately 0.10% to 8.15% of the variance. In almost all situations, the combined dataset (PGC2+Chinese) explained larger proportions of variance (approximately 1.89% to 8.28%). For $P_T = 5 \times 10^{-8}$, the proportion of the explained variance increased from 1.20% (EUR49), 1.52% (PGC2) and 0.10% (Chinese) to 1.89% (PGC2+Chinese); for $P_T = 0.05$, it is increased from 2.34% (EUR49), 3.09% (PGC2) and 6.16% (Chinese) to 7.86% (PGC2+Chinese). To evaluate the increased variance explained by the newly identified GWS loci, we performed an additional polygenic risk score profiling trained on the full dataset (GWAS but excluding the target sample, and replication) and restricted to the newly identified loci when Chinese sample included. It indicated that these novel loci could explain 1.34% of the variance, 30% of which was contributed by the loci from the Chinese-only analysis.

Correlations between two psychiatric disorders in Chinese

Strong evidence of shared genetic etiology between schizophrenia and other psychiatric disorders (such as bipolar disorder and major depressive disorder) was observed in European samples[49,50]. The degree of shared variation across the psychiatry disorders in Chinese samples is unclear. We estimated the genetic correlation for schizophrenia and major depressive disorder, two diseases with Chinese GWAS data of large sample size available, using LD Score regression[14]. We observed a statistically significant genetic correlation between schizophrenia and major depressive disorder in Chinese sample ($r_g = 0.43$, s.e.= 0.08, LD score regression $P = 5.87 \times 10^{-8}$), which is consistent with the finding ($r_g = \sim 0.40$) in the European samples[49].

Discussion

In the large GWAS analysis of schizophrenia in Chinese ancestry, we identified seven GWS loci, four of which were novel. In general, alleles identified as associated at sub-threshold levels of significance in the Chinese dataset were also enriched in cases in the schizophrenia GWAS from PGC2 supporting the validity of combining the two datasets. The trans-ancestry meta-analyses of the Chinese and PGC2 data identified 109 GWS risk loci, three of which were GWS in the Chinese only analysis. Our analyses confirmed most of the previously identified schizophrenia loci and identified 30 novel loci.

We observed a significant excess in the directional consistency of schizophrenia risk alleles across ancestry groups, even at SNPs demonstrating only weak evidence of an association. These findings indicated that the majority of schizophrenia risk loci are shared across these two ancestral populations, and trans-ancestry meta-analysis provided a powerful means for identifying new loci and narrowing the association intervals. Polygenic scoring analysis also demonstrated notable increases in the explained variance in case-control status (PGC2+Chinese training to Chinese target compared with PGC2 to Chinese target or Chinese training to Chinese target). However, this analysis also suggested that variants identified in European samples could partially explain the genetic variance of schizophrenia in Chinese populations. Notably, estimates of the proportion of explained variance in liability were lower than those in European populations[7], similar to previous reports on cross-ethnic analyses[4,51]. Such lower estimates might be a result of differences in the allele frequencies and LD patterns between different populations[4].

It has been suggested that there are also population-specific risk alleles for schizophrenia[6] and that if so, cross-ancestry analyses might suffer from attenuated power compared with studies of individuals with a recent shared ancestry. We found that some GWS loci in the PGC2 report failed to be GWS in the PGC2 and Chinese combined analysis. Moreover, most of the GWS SNPs identified in the analysis of Chinese samples only showed strong heterogeneity across ancestries, though three of them achieved nominal significance with the same sign in the PGC2 dataset. Another SNP fell within the previous PGC2 identified locus, but it was rare (MAF < 1%) in European populations. Thus, further trans-ancestry fine-mapping, by leveraging the differences in the LD structure among diverse populations, could be an efficient approach to identify the causal variants underlying such associations and also distinguish population-specific loci. Indeed, we also observed considerable improvements in the fine-mapping resolution at several susceptibility loci.

Our use of fine mapping tools and functional annotations to dissect schizophrenia-associated loci identified numerous candidate genes with several lines of supporting evidence, including genes that have previously been implicated in schizophrenia (e.g., *FYN* and *MAGI2*) and novel genes (e.g., *EMX1* and *BNIP3L*) within the novel loci. Moreover, pathway analyses highlighted several pathways that contribute to schizophrenia pathogenesis, including previously described pathways (the voltage-gated calcium channel pathway and postsynaptic density) and a new pathway (Regulation of Insulin Secretion by Glucagon-like Peptide 1). The latter has not been highlighted in previous genetic studies of schizophrenia, but evidence from other types of investigation has linked insulin signaling to the pathophysiology of schizophrenia. Previous epidemiological data suggest that individuals with schizophrenia have an increased prevalence of metabolic syndrome compared with the general population or healthy controls[52,53]. Moreover, increased prevalence rates of impaired glucose metabolism have been observed in drug-naive patients with schizophrenia[54]. A proteomic analysis showed that several proteins involved in energy metabolism are altered in the brains of schizophrenia patients[55]. Our results provided further support for a role for insulin related energy metabolism in the etiology of schizophrenia.

In summary, the Chinese (n = 36,180) and multi-ancestry (n = 118,495) GWAS meta-analysis and follow-up replication studies identified 113 GWS risk loci for schizophrenia, 30 of which are novel. Our results demonstrated added value from trans-ancestry meta-analysis for fine mapping loci associated with schizophrenia and highlighted the existence of shared genetic risk across populations. In addition to the confirmation of known genetic architectures, our comprehensive analyses provide further biological insights into the etiology of schizophrenia, facilitating further mechanistic studies to assess the pathogenesis of this complex disorder.

URLs

PGC, http://pgc.unc.edu; EIGENSTRAT, https://github.com/DReichLab/EIG/tree/master/EIGENSTRAT; SHAPEIT, https://mathgen.stats.ox.ac.uk/genetics_software/shapeit/shapeit.html; IMPUTE2, http://mathgen.stats.ox.ac.uk/impute/impute_v2.html; 1000 Genomes Project, http://www.1000genomes.org/; The NIH Roadmap Epigenomics Mapping Consortium, http://www.roadmapepigenomics.org/; HaploReg v4.1, http://archive.broadinstitute.org/mammals/haploreg/haploreg_v4.1.php; PLINK, https://www.cog-genomics.org/plink2/; PUBMED, http://www.ncbi.nlm.nih.gov/pubmed/; NHGRI-EBI GWAS Catalog, https://www.ebi.ac.uk/gwas/; UCSC, http://genome.ucsc.edu/; GeneCards, http://www.genecards.org/; LDSC, https://github.com/bulik/ldsc/; Price lab web, https://www.hsph.harvard.edu/alkes-price/software/.

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Author Contributions

Y. Shi conceived and designed the experiments, and supervised all aspects of the work; J. Chen, Y. Xu, L. He, D. Zhang, W. Yue, P. Wang, P. Yang, B. Liu, W. Sun, Q. Xu, W. Ji, G. Feng, Q. Yi, C. Li and X. Li performed sample collection and phenotyping; J. Chen, H. Yu, J. Zhou, B. Chen, Y. Liu, J. Wang, J. Ji, M. Wang, Q. Wang, Z. Wen, Wenjin Li, K. Liu, F. Huang, J. Zhou, G. He, Weidong Li, C. Wan and B. Li performed the experiments and data management; Z. Li, H. Yu, Z. Song, J. Shen, S.R., P.F.S. and M.C.O. performed bioinformatics and statistical analyses; Y. Shi and Z. Li interpreted the main findings; Y. Shi and Z. Li drafted the manuscript; Y. Shi, L. He, Z. Li, Y. Xu, X. Li and P.F.S. gained the funding support; All authors revised and approved the final manuscript.

Competing Financial Interests

We declare that the authors have no competing interests as defined by Springer Nature, or other interests that might be perceived to influence the results and/or discussion reported in this paper.

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Figure legends

Figure 1. Comparison of Manhattan plots for the Chinese and tran-ancestry analyses. Manhattan plot of results from the Chinese-only (7,699 cases and 18,327 controls) and PGC2+Chinese trans-ancestry (43,175 cases and 65,166 controls) analyses. $-\log_{10} P$ values for PGC2+Chinese trans-ancestry analyses and $\log_{10} P$ values for Chinese-only analyses are shown.

Figure 2. Regional plots for novel genome-wide significant loci in Chinese. a) rs2073499 at 3p21.31, b) rs7757969 at 6q21, c) rs4479915 at 6q27 and d) rs11534004 at 7q31.1. $-\log_{10} P$ values are shown for SNPs for the region 500 kb on either side of the marker SNPs. The index SNP is shown in purple, and the r^2 values of the other SNPs are indicated by color. The r^2 values are established based on the 1000 Genome data (Nov2014). *P* for the GWAS stage is shown in circle, and for the meta-analysis combining all data sets is shown in square. The genes within the relevant regions are annotated and shown as arrows.

Figure 3. Interaction network of the schizophrenia associated pathway (Glucagon-like Peptide-1 regulates insulin secretion). The network shows functional interactions for the genes in Glucagon-like Peptide-1 regulates insulin secretion pathway from the Reactome database. Each node represents a gene and each edge represents a functional interaction. The node size corresponds to the gene size. The node color corresponds to significance of the gene based on the MAGMA analysis, and the green-to-red gradient corresponds to non-significance to high significance.

Figure 4. Polygenic risk score profiling analysis. Polygenic risk score profile analysis using approximately 1,000 randomly selected cases and 1,000 controls from the Chinese sample as a target and deriving risk alleles from three training data sets: the PGC2 European-only (EUR49) data set (light blue), the full PGC2 data set (blue), the Chinese sample but excluding the target sample (light red) and the Chinese and

PGC2 data sets combined (red). The *x* axis shows ten P-value thresholds ($P_T = 5 \times 10^{-8}$, 1×10^{-6}, 0.0001, 0.001, 0.01, 0.05, 0.1, 0.2, 0.5 and 1). The *y* axis is the estimate of the proportion of variance explained on the liability scale, which is converted from Nagelkerke's pseudo R^2 (computed by comparison of a full model including covariates and polygenic risk scores to a reduced model including covariates only).

Table 1. Novel Schizophrenia GWS loci and notable genes.

Chr.	SNP	Position	*P* value	Notable gene(s)[a]
2	rs999494	73157395	2.40E-10	*EMX1* (N, D)
2	rs62152284	104984387	5.86E-09	*LOC100287010* (N)
2	rs6430491	134840967	9.55E-10	*MIR3679* (N)
3	rs10510653	32058559	2.54E-08	*GPD1L* (Q), *ZNF860* (N)
3	rs2073499	50374293	2.61E-08	*HYAL3* (Q), *RASSF1* (N)
4	rs11722779	103827488	3.40E-08	*BDH2* (Q), *CENPE* (Q), *CISD2* (Q), *KRT8P46* (Q), *LRRC37A15P* (Q), *NHEDC1* (N), *SLC9B1* (Q)
5	rs10940346	49806042	1.11E-08	*EMB* (N, Q)
5	rs2247870	90151589	2.54E-08	*ADGRV1* (N, M, D)
5	rs2764766	127213625	1.94E-08	*LINC01184* (N)
6	rs6903570	64866857	2.70E-08	*EYS* (N), *PHF3* (D), *PTP4A1* (D)
6	rs160593	105466332	7.69E-09	*HACE1* (Q), *LIN28B* (N, Q)
6	rs7757969	112132032	4.82E-08	*FYN* (N, Q)
6	rs4479915	165075601	4.82E-09	*C6orf118* (N)
7	rs323167	78336677	4.47E-08	*MAGI2* (N, D)
7	rs11534004	113467444	1.71E-08	*PPP1R3A* (N, M)
8	rs17687067	17036201	3.39E-12	*MTMR7* (Q), *VPS37A* (Q), *ZDHHC2* (N, D, Q)
8	rs73219805	26272768	1.94E-11	*BNIP3L* (N, D), *PPP2R2A* (D), *SDAD1P1* (Q)
10	rs111364339	64857872	5.37E-09	*JMJD1C* (D), *NRBF2* (N)
12	rs28607014	117708611	1.75E-08	*NOS1* (N)
14	rs10148671	29469373	4.46E-08	*LINC01551* (N)
14	rs2383377	33257914	2.36E-08	*AKAP6* (N, D), *NPAS3* (D)
14	rs8012642	84669481	4.66E-08	*FLRT2* (N)
15	rs783540	83254708	3.05E-08	*AP3B2* (D, Q), *CPEB1* (N, Q)
15	rs758129	89900887	2.87E-08	*MIR9-3* (N), *POLG* (D), *RLBP1* (Q)
16	rs6500596	4470027	5.24E-09	*CDIP1* (Q), *CORO7* (N, D, Q), *DNAJA3* (M, Q), *NMRAL1* (Q, S)
16	rs8058130	64371163	4.77E-08	*CDH11* (N)
17	rs56007784	1290950	1.16E-09	*YWHAE* (N)
17	rs72843506	19946287	3.73E-08	*AKAP10* (D), *CCDC144CP* (Q), *SPECC1* (N, D, Q), *USP32P3* (Q)
17	rs35065479	55736735	2.31E-08	*TSPOAP1-AS1* (Q), *MSI2* (N)
18	rs56775891	77575613	1.85E-08	*KCNG2* (N, Q, S)
18	rs28735056	77622879	4.60E-10	*KCNG2* (N)

Genomic position was based on the UCSC hg19/NCBI Build 37. [a]Notable genes from gene nearest to the index SNP (N); Schizophrenia-associated variant is in strong LD ($r^2 \geq 0.8$) with a missense variant in the indicated gene (M); genes prioritized by DEPICT (D); genes for which the mRNA levels showed cis-genetic linkage with the index SNPs (Q); genes prioritized by SMR analysis (S).

Methods

Recruitment of research subjects

As in our previous study[10], all cases of Chinese ancestry were inpatients or outpatients with > 2-year history of schizophrenia recruited from mental health centers in China who were interviewed by two independent psychiatrists and diagnosed according to Diagnostic and Statistical Manual of Mental Disorders (DSM)-IV criteria. All cases met the following 2 criteria: preoccupation with one or more delusions and frequent auditory hallucinations. However, none of the following symptoms was prominent: disorganized speech, disorganized or catatonic behavior or flat or inappropriate effects. The controls were randomly selected from Han Chinese volunteers (from hospitals and a community survey) who were asked to reply to a written invitation to evaluate their medical histories. Lists of potential control subjects were screened for suitability as volunteers by excluding subjects with major mental illnesses. All participants provided written informed consent. Approval was received for our study from the Ethics Committee of Human Genetic Resources at Bio-X Institutes of Shanghai Jiao Tong University, in accordance with the tenets of the Declaration of Helsinki. We confirm that our study is compliant with the ‘Guidance of the Ministry of Science and Technology (MOST) for the Review and Approval of Human Genetic Resources'.

Genotyping, quality control and genotype imputation of the Chinese GWAS data

Several different genome-wide genotyping platforms were used in this study: Affymetrix Genome-Wide Human SNP Array 6.0 (SNP6.0), Affymetrix Axiom™ Genome-Wide CHB1 Array Plate (CHB1) and Illumina 1M Array (1M).

For the SNP6.0 chips, the genotype calls were generated together using the Affymetrix Axiom™ Analysis according to the Best Practices Workflow for SNP6.0. Sample QC filtering of the GWAS data was first performed by excluding arrays with Contrast QC measurements < 0.4 (a metric developed by Affymetrix Inc. for SNP6.0 QC, n = 197). Step 1 genotyping was run on all CEL files passing QC over a subset of 20,000 SNPs, and samples with a call rate ≤ 97% were excluded (n = 285). The remaining samples were used for the Step 2 genotyping analysis. SNP polisher was then performed for SNP QC, and the SNPs in the recommended categories (PolyHighRes, MonoHighRes, NoMinorHom and Hemizygous) were retained. Sex was established via genotyping and evaluated for each of the subjects, and samples with inconsistent sex (compared with the sample record) were removed (n = 79). Heterozygosity rates were calculated with the intent of removing deviations that exceeded 6 standard deviations from the mean (n = 0). PLINK's identity-by-descent (IBD) analysis was used to detect cryptic relatedness[56] (see **URLs**). When a pair of individuals had PI_HAT > 0.2, the member of the pair with the lower call rate was excluded from the analysis (n = 259). SNPs with call rates < 97% (n = 28,040), MAF < 1% (n = 185,439) or significant deviation from Hardy-Weinberg equilibrium (HWE) in controls (HWE $P \leq 1 \times 10^{-6}$, n = 20,344) were excluded. We also excluded population outliers based on PCA analysis. After applying quality control criteria, a set of 590,413 SNPs for 14,645 individuals were generated for genotype imputation.

For the CHB1 chips, the genotype calls were generated together according to the Axiom® Genotyping Solution Data Analysis Guide. Briefly, arrays with DQC (Dish QC, a single-sample metric developed by Affymetrix for Axiom QC) values < 0.82 were first excluded (n = 181). Samples that had surpassed DQC values were used for genotype calling with a subset of probe sets. Samples with a call rate < 97% or in a non-passing plate (an average call rate of passing samples < 98.5%) were also excluded (n = 276). The post-QC samples were then co-clustered, and genotype calls were produced by the Axiom Genotyping Algorithm v1 (Axiom GT1) algorithm. SNP QC was also executed using the SNP polisher procedure, and the SNPs in the recommended categories were retained. Sex, relatedness and PCA outlier checking procedures were also conducted for sample QC as described above (n = 289). SNPs with call rates < 97% (n = 56,735), MAF < 1% (n = 206) or significant deviations from HWE in controls (HWE $P \leq 1 \times 10^{-6}$, n = 18,849) were excluded. After applying quality control criteria, a set of 555,058 SNPs for 9,580 individuals were generated for genotype imputation.

For Illumina 1M chips, SNP genotypes were generated from normalized bead intensity data using Genome Studio. Samples with a call rate < 97% were excluded (n = 35). Regular sample QC procedures, including sex, relatedness, heterozygosity rate and PCA outlier checking, were performed as described above (n = 231). SNPs with call rates < 97% (n = 35,743), MAF < 1% (n = 89,032) or HWE $P \leq 1 \times 10^{-6}$ (n

= 954) were excluded. After applying quality control criteria, a set of 716,466 SNPs for 1,823 individuals was generated for genotype imputation.

For each GWAS dataset, the entire set was imputed together as follows: the genotypes were phased using SHAPEIT (see **URLs**)[57,58] for each chromosome, and imputation was performed for each 5-Mb chromosome interval using IMPUTE2 (see **URLs**)[59]. The haplotypes derived from the 1000 Genomes Project Phase 1 (release v3, see **URLs**) were used as reference data[60]. Because two genotyping platforms were adopted for GWAS set 3, we used two phased reference panels in this special case as proposed by Howie *et al.*[59]. For each platform, the pre-phased data from the other platform were used as the second reference panel. The variants with INFO > 0.8, MAF > 0.01, a call rate ≥ 97% and HWE $P \geq 1 \times 10^{-6}$ in the controls were saved for further analysis. Those present in at least two datasets were saved for the meta-analysis. A set of 5,107,227 genetic variants for 7,699 cases and 18,327 controls remained in the final analysis.

PGC2 GWAS dataset

The PGC2 GWAS dataset[7] comprised 49 case-control samples (34,241 cases and 45,604 controls) and 3 family-based samples (1,235 parent affected-offspring trios). All of the samples were of European ancestry, excluding three case-control samples that were of East Asian ancestry (1,836 cases and 3,383 controls). The summary results for the PGC2 dataset and European only dataset (EUR49) were downloaded from the PGC website (see **URLs**).

Replication dataset

The replication sample consisted of 4,384 cases and 5,770 controls of Chinese Han ancestry. More details of the general characteristics and genotyping were presented in our previous research[19]. For the Chinese-only analyses, the independent SNPs with $P < 1 \times 10^{-5}$ in the Chinese GWAS analysis of pre- or post-correction with the inflation factor were selected. For the trans-ancestry analysis, the independent SNPs with $P < 5 \times 10^{-7}$ in the Chinese (pre- or post-correction) and PGC2 GWAS meta-analyses were selected. The pre-correction datasets were used only for including more candidate SNPs for replication. All the association results present in this article were based on the post-correction datasets where the global inflations were controlled. A total of 295 SNPs were analyzed in the Chinese replication analysis.

Power calculations

Power calculations were performed using the GAS Power Calculator[61] with a range of genotype relative risks and disease allele frequencies, assuming a population prevalence of 0.01 and a significance level of 5×10^{-8}. For the Chinese-only (n = 36,180) and trans-ancestry (n = 118,495) analyses, we had adequate power (>80%) to detect variants of low risk allele frequencies (RAF) of 0.03 with genotypic relative risks (GRR) of 1.318 and 1.161, respectively. This sample size in Chinese-only analyses was large enough to achieve adequate power for risk variants with GRR of

1.150 and RAF of 0.14 to 0.85, and the trans-ancestry analyses achieved adequate power for risk variants with 1.075 and RAF of 0.15 to 0.84.

Statistical methods and bioinformatics analysis

Population substructure was evaluated using a PCA with EIGENSTRAT software (see **URLs**) based on LD-pruned autosomal SNPs genotypes[62,63]. Two rounds PCA were performed. One round with samples from the HapMap Project phase 3 (HapMap3) was performed to help identify any admixed samples, and the other one was performed for each subset of cases and controls, where individual outliers (> 6 standard deviations from mean on any one of the top 10 PCs) were identified and removed for five iterations and final PCs reflecting subtle ancestry information for each sample were generated for further correction. In the Chinese GWAS stage, the association was analyzed for subsets using a logistic regression model involving covariates for PCs to adjust for possible population stratification. We evaluated the impact on genome-wide test statistics for the 20 PCs to determine the PC inclusion in the final association analysis for each dataset. In the Chinese replication stage, the associations between SNPs and schizophrenia risk were evaluated based on the logistic regression using SNPTEST[64]. The Higgins and Thompson I^2 index was used for assessing heterogeneity across datasets[65]. Both fixed-effect and random-effects models meta-analyses were adopted in this study. The variants with pronounced heterogeneity (I^2 >75%) were combined in a random-effects model in the trans-ancestry meta-analysis[17].

We assessed the genome-wide congruence of risk alleles across samples using binomial sign tests that, compared the direction of the effect sizes of independent SNPs between PGC2 and Chinese GWAS results. P-values were generated under the null hypothesis (H0: P = 0.50). The proportion of variance in liability to schizophrenia explained by the common SNPs was estimated using Genome-wide Complex Trait Analysis (GCTA)[66], and the PCs were included in the analysis as covariates. For each of the associated loci (except the eMHC region due to the complexity of this region[7]), we calculated an approximate Bayes factor of Wakefield and the posterior probability of driving the association for each SNP within a 2-Mb window, and then created 99% credibility sets[38,39,67]. We created credibility sets using the Chinese, PGC2 (European), and combined datasets separately. We conducted the trans-ancestry fine mapping in the presence of functional information using PAINTOR according to the suggested pipeline, as well as PGC2 only and Chinese only analyses for comparison. The primary functional annotations for SNPs proposed by Gusev *et al.*[41] were obtained from the Price lab web (see **URLs**). The reference epigenomes of 127 human tissues and cell types[45] were obtained from the NIH Roadmap Epigenomics Mapping Consortium (see **URLs**). We included the seven highlighted epigenomic marks (H3K4me3, H3K4me1, H3K36me3, H3K27me3, H3K9me3, H3K27ac and H3K9ac)[45] in our analyses. Enrichment analyses of the schizophrenia associations in the current and PGC2 analyses with the epigenomic features were performed using GREGOR (Genomic Regulatory Elements and Gwas Overlap algoRithm)[68], and the top 100 enriched annotations were selected for further PAINTOR analyses. The online tool HaploReg[23] (v4.1, see **URLs**) was used to explore the genes nearest to the index SNPs and genes containing a missense mutation in high LD ($r^2 > 0.8$, based on the 1000G Phase 1 CEU or ASI population for the LD calculation) with the GWS SNPs. The effect of GWS SNPs on expression in eQTL studies of different tissues (including blood and brain tissues[25-27]) were extracted from the query results of HaploReg[23] and CommonMind Consortium Knowledge Portal[28]. A significant eQTL was declared as having an FDR of 0.05 in the original reports[25-28] and located in the credible interval covered by the 99% credible set for the regulated gene for the datasets where detailed results were available for establishing the credible sets[25,27]. We used DEPICT[24] to identify the most likely causal genes for the schizophrenia-associated loci based on the functional similarity among genes from associated regions. We carried out SMR analysis[29] for the blood and brain tissues eQTL datasets [25,27] using the 1000 Genomes Project data as reference files. For the gene prioritization analysis at the GWS loci (excluding the eMHC region due to the complexity of this region[29]), only probes with at least one *cis*-eQTL at P value $< 5.0 \times 10^{-8}$ were considered for SMR analysis and a significant threshold was set as $P_{SMR} < 5.20 \times 10^{-5}$ corresponding to a Bonferroni correction for 960 tests (960 probes with *cis*-eQTL at P value $< 5.0 \times 10^{-8}$ across the GWS loci)[29]. The HEIDI (heterogeneity in dependent instruments) test was performed as well and P value <0.05 was considered to indicate significant heterogeneity. The genes prioritized by the GWS index SNP or its high LD ($r^2 > 0.8$) proxies were listed. In addition, the SMR analysis was also performed for some specific SNPs and genes. In this situation, the *P* value threshold for selecting eQTL was not applicable and the details were shown in the results. We searched the published literature for these genes with respect to schizophrenia in PubMed (see **URLs**) and the NHGRI-EBI GWAS Catalog (see **URLs**), and we obtained additional functional evidence for these SNPs and genes from the published literature, the UCSC genome database (see **URLs**) and GeneCards (see **URLs**).

LD score regression for Chinese GWAS data

We estimated Chinese LD Scores from the Chinese samples in the 1000 Genomes Project Phase 3 using the LD Score (LDSC, see **URLs**) software package[14]. We used a window size of 1 centiMorgan (cM) to estimate LD scores, excluded singletons and did not set an r^2 cutoff. The LD score regression intercept from the Chinese GWAS data was estimated according to application notes for real data from the LDSC developers[14]. As Bulik-Sullivan BK *et al.* proposed[14], correcting test statistics with the LD Score regression intercept is a robust way for controlling the confounding bias from inflation. Correction was applied to Chinese GWAS meta-analysis results by multiplying standard errors by the square root of the correction factor[16].

Polygenic scoring analysis

Approximately 1,000 cases and 1,000 controls from the Chinese sample were randomly selected as the target sample. Risk-profile SNPs ($P_T = 5 \times 10^{-8}$, 1×10^{-6}, 0.0001, 0.001, 0.01, 0.05, 0.1, 0.2, 0.5 and 1) from the training GWAS datasets (the PGC2 dataset, the Chinese GWAS dataset excluding the target sample and the two datasets combined) were selected using the PLINK "--clumped" function, and SNPs within 500 kb or with $r^2 \geq 0.1$ were discarded. The risk-profile SNPs were then used to generate scores for the target samples using the PLINK "--score" function. The case-control status was then predicted by logistic regression analysis of polygenic scores plus PC covariates. Nagelkerke's R^2 was used for the full model using the polygenic score plus the covariates minus R^2 for the covariates alone, yielding an estimate of the explained variance. The R^2 was then transformed into a liability scale[48], assuming a population prevalence of 1% for schizophrenia[7].

Pathway analysis

MAGMA[46] was used to explore pathway-based associations in the genome-wide meta-analysis dataset. An F-test was used to compute the gene *P* value, and the gene *P* values and gene correlation matrix are then used for the gene-set analysis with a regression model[46]. We defined gene boundaries 35 kb upstream and 10 kb downstream for assigning SNPs to a gene, which was adopted in a recent psychiatric disorder pathway analysis[47]. Each gene was then assigned pathways in the Gene Ontology (GO), PANTHER, Ingenuity, Kyoto Encyclopedia of Genes and Genomes (KEGG), Reactome and BioCarta gene set databases[69]. A total of 2,981 pathways or gene sets were used in this analysis.

Data availability

Summary statistics for the meta-analyses will be made available at http://gwas.bio-x.cn/.

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65. Higgins, J.P.T., Thompson, S.G., Deeks, J.J. & Altman, D.G. Measuring inconsistency in meta-analyses. *British Medical Journal* **327**, 557-560 (2003).
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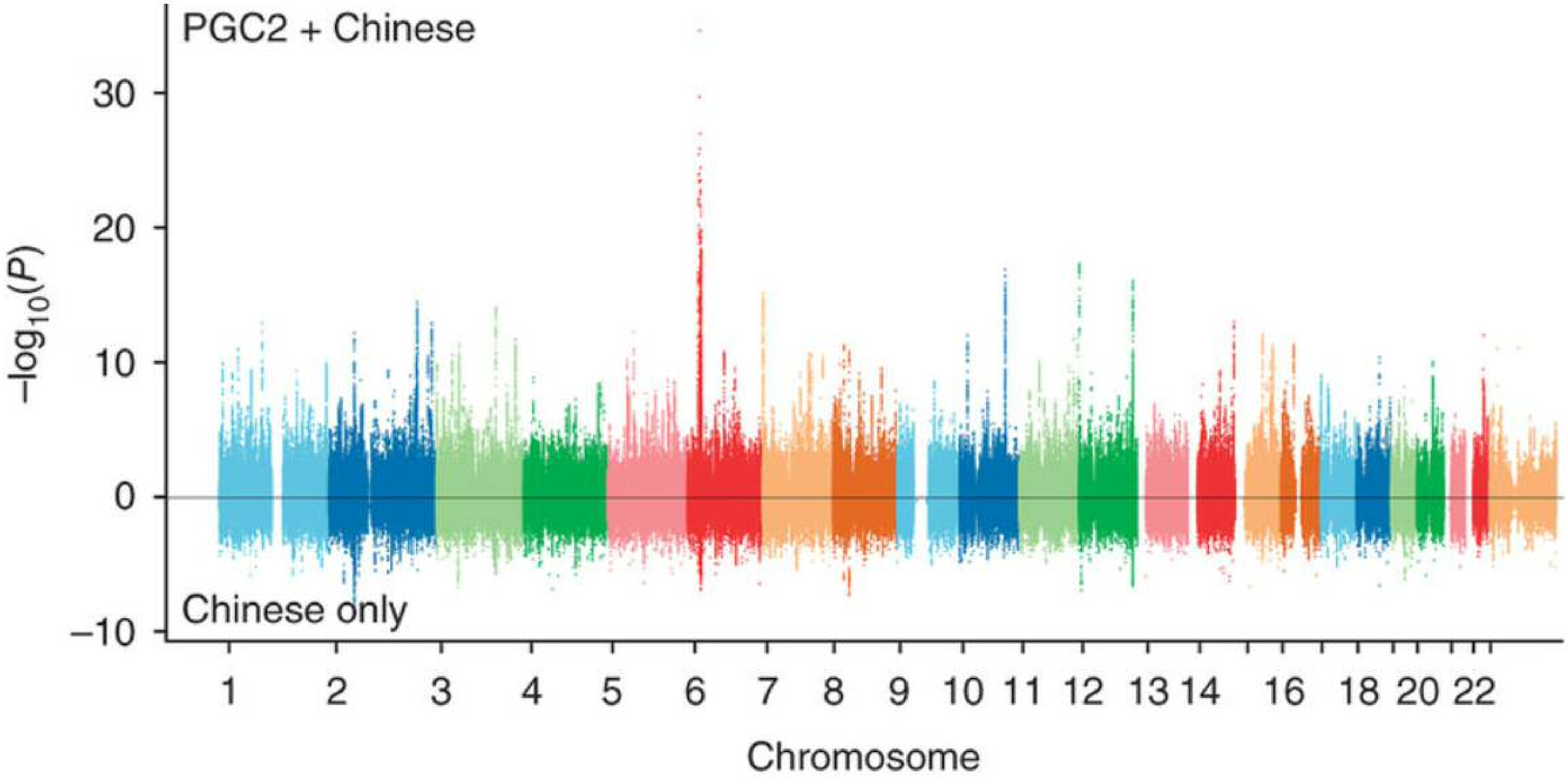
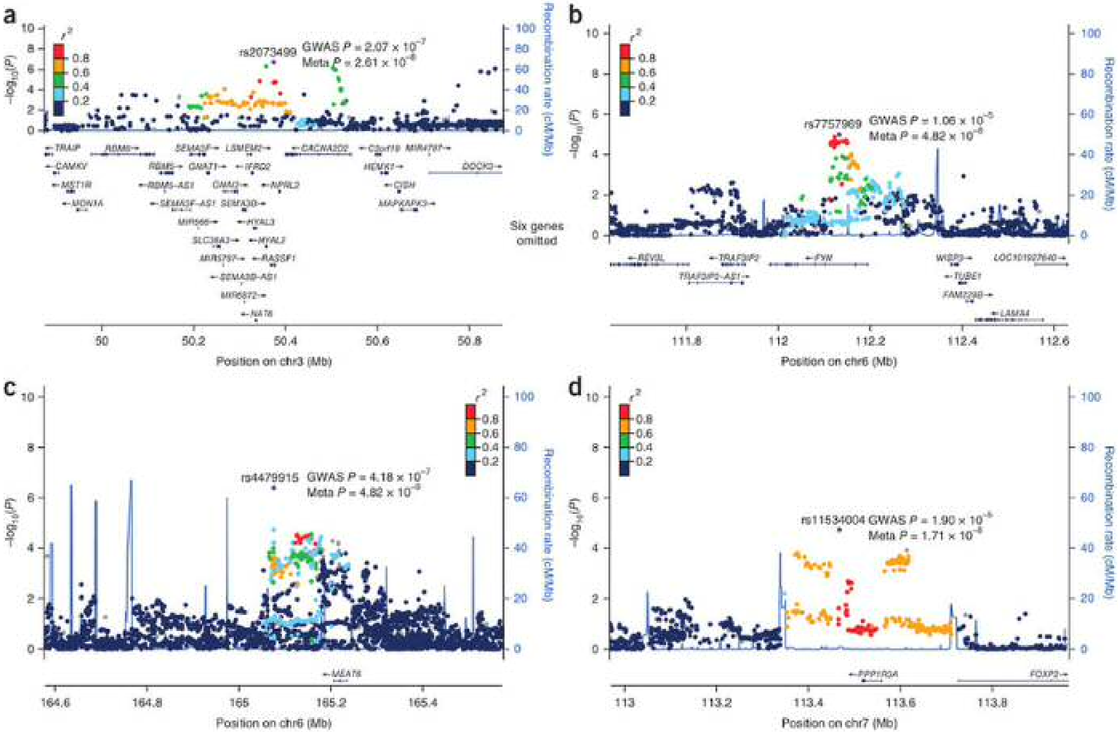

PGC2 + Chinese
Chinese only
30
20
10
0
−10
−log10(P)
1
2
3
4
5
6
7
8
9
10
11
12
13
14
16
18
20
22
Chromosome

Figure 2 : Regional plots for novel GWS loci in Chinese people.

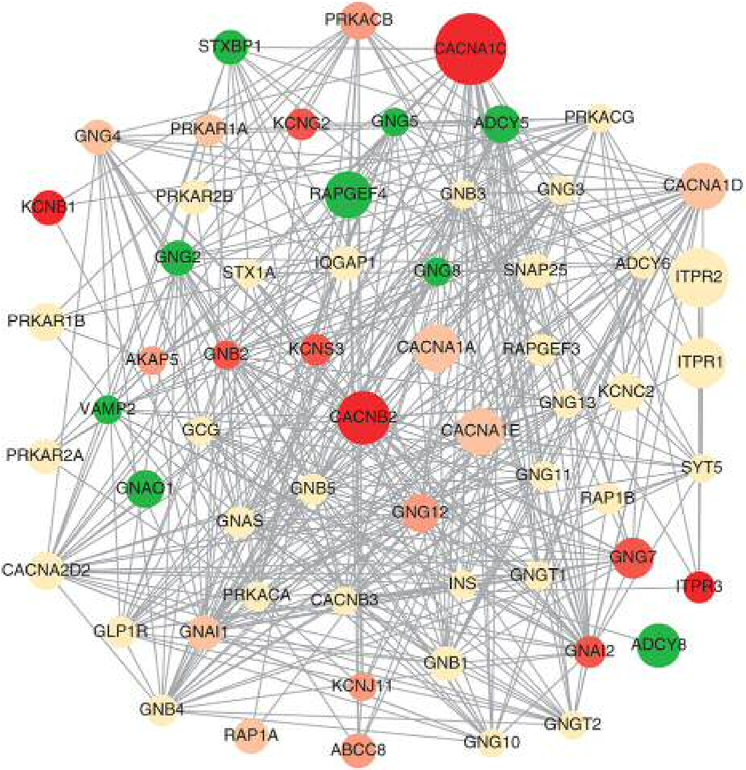
From: Genome-wide association analysis identifies 30 new susceptibility loci for schizophrenia



(**a**) rs2073499 at 3p21.31. (**b**) rs7757969 at 6q21. (**c**) rs4479915 at 6q27. (**d**) rs11534004 at 7q31.1. Meta, meta-analysis; chr, chromosome. $-\log_{10}P$ values are shown for SNPs for the region 500 kb on either side of the marker SNPs. The index SNP is shown in purple, and the r^2 values of the other SNPs are indicated by color. The r^2 values were established on the basis of 1000 Genomes data (November 2014). P values for the GWAS stage are shown with circles, and P values for the meta-analysis combining all data sets are shown with text. The genes within the relevant regions are annotated and shown as arrows.

Figure 3 : Interaction network of the schizophrenia-associated pathway 'glucagon-like peptide-1 regulates insulin secretion'.

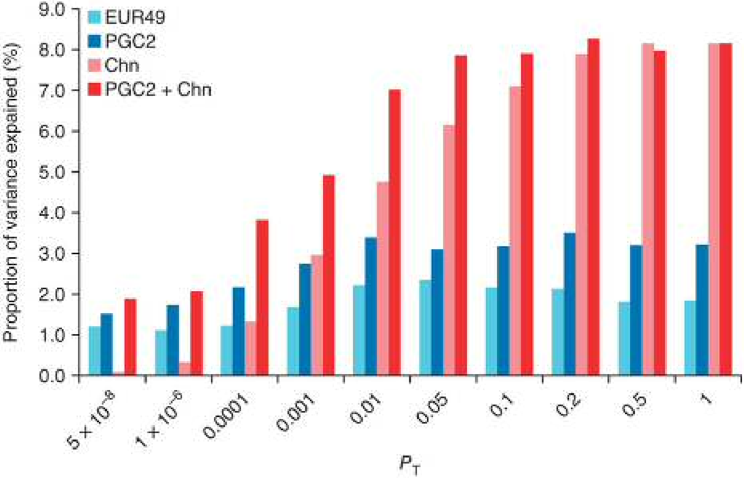
From: Genome-wide association analysis identifies 30 new susceptibility loci for schizophrenia



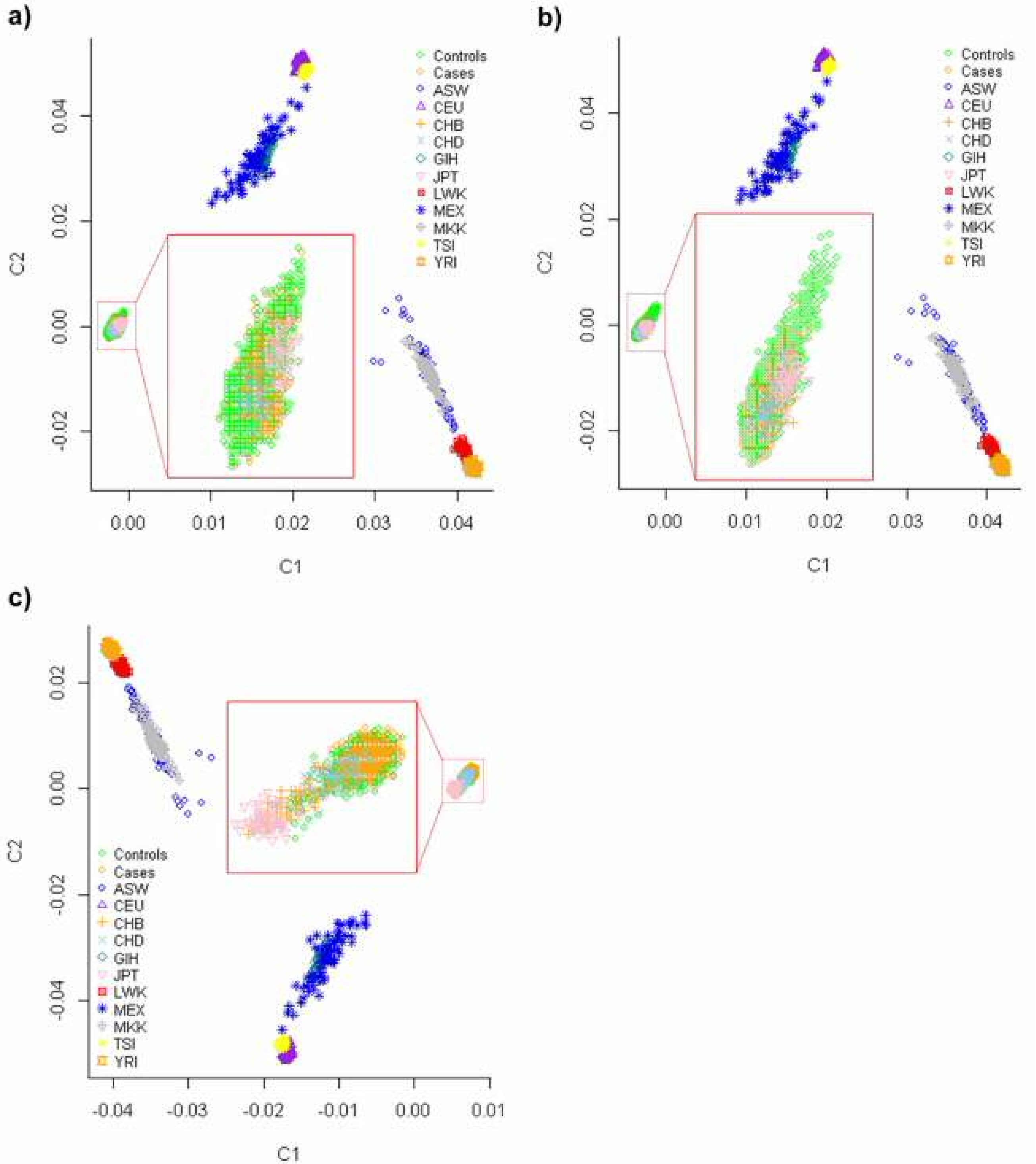
The network shows functional interactions for the genes in the pathway 'glucagon-like peptide-1 regulates insulin secretion' from the Reactome database. Each node represents a gene, and each edge represents a functional interaction. The node size corresponds to the gene size. The node color corresponds to the significance of the gene on the basis of the MAGMA analysis, and the green-to-red gradient corresponds to nonsignificance to high significance.

Figure 4 : Polygenic risk-score profiling analysis.

From: Genome-wide association analysis identifies 30 new susceptibility loci for schizophrenia



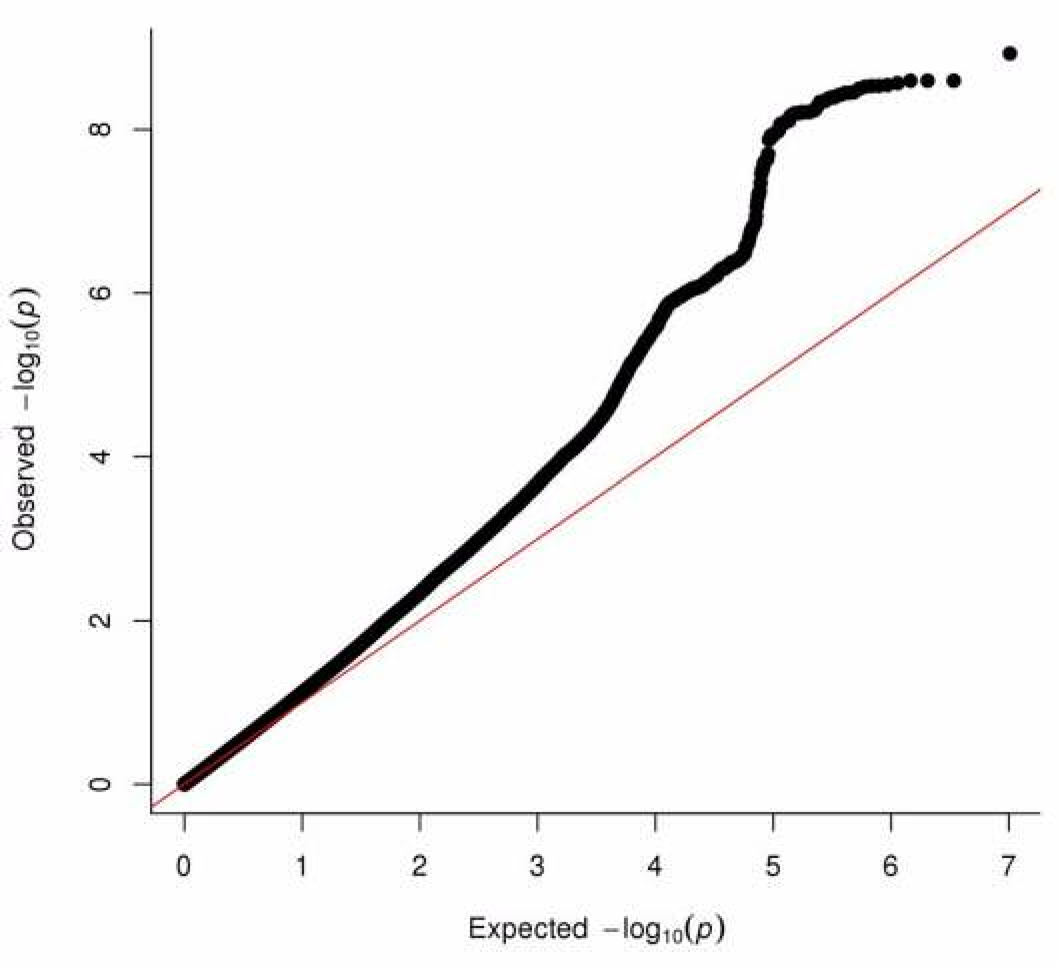
Polygenic risk-score profiling analysis using approximately 1,000 randomly selected schizophrenia cases and 1,000 controls from the Chinese sample as a target and deriving risk alleles from three training data sets: the PGC2 European-only (EUR49) data set (light blue); the full PGC2 data set (blue); the Chinese (Chn) sample excluding the target sample (light red); and the Chinese and PGC2 data sets combined (red). The x axis shows ten P-value thresholds ($P_T = 5 \times 10^{-8}$, 1×10^{-6}, 0.0001, 0.001, 0.01, 0.05, 0.1, 0.2, 0.5 and 1). The y axis is the estimate of the proportion of variance explained on the liability scale, which is converted from Nagelkerke's pseudo R^2 (computed by comparison of a full model including covariates and polygenic risk scores to a reduced model including covariates only).



Supplementary Figure 1

Principal components analysis (PCA) of Chinese GWAS sample with HapMap3 sample

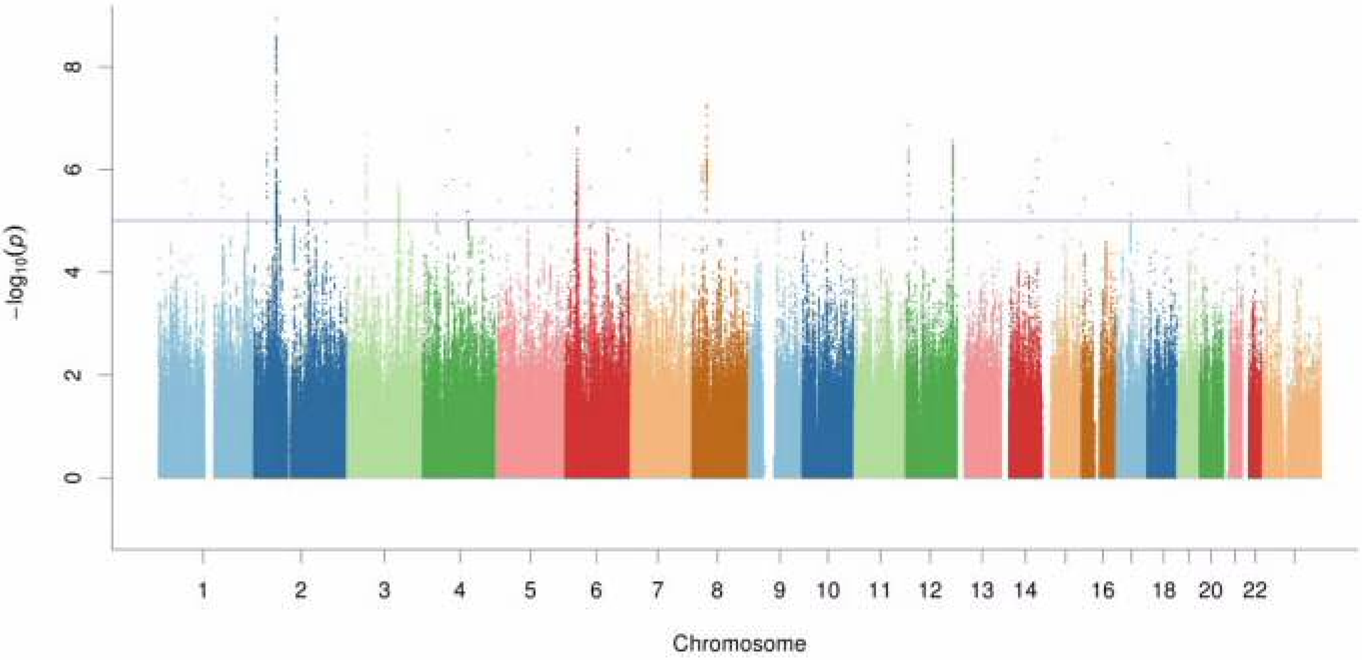
a) GWAS Set 1, **b**) GWAS Set 2, **c**) GWAS Set 3. Plot of the first two principal components (C1 and C2) from principal components analysis (PCA) of Chinese GWAS sample with HapMap3 sample. The enlarged area is for the Aisan sample, including our cases and controls.



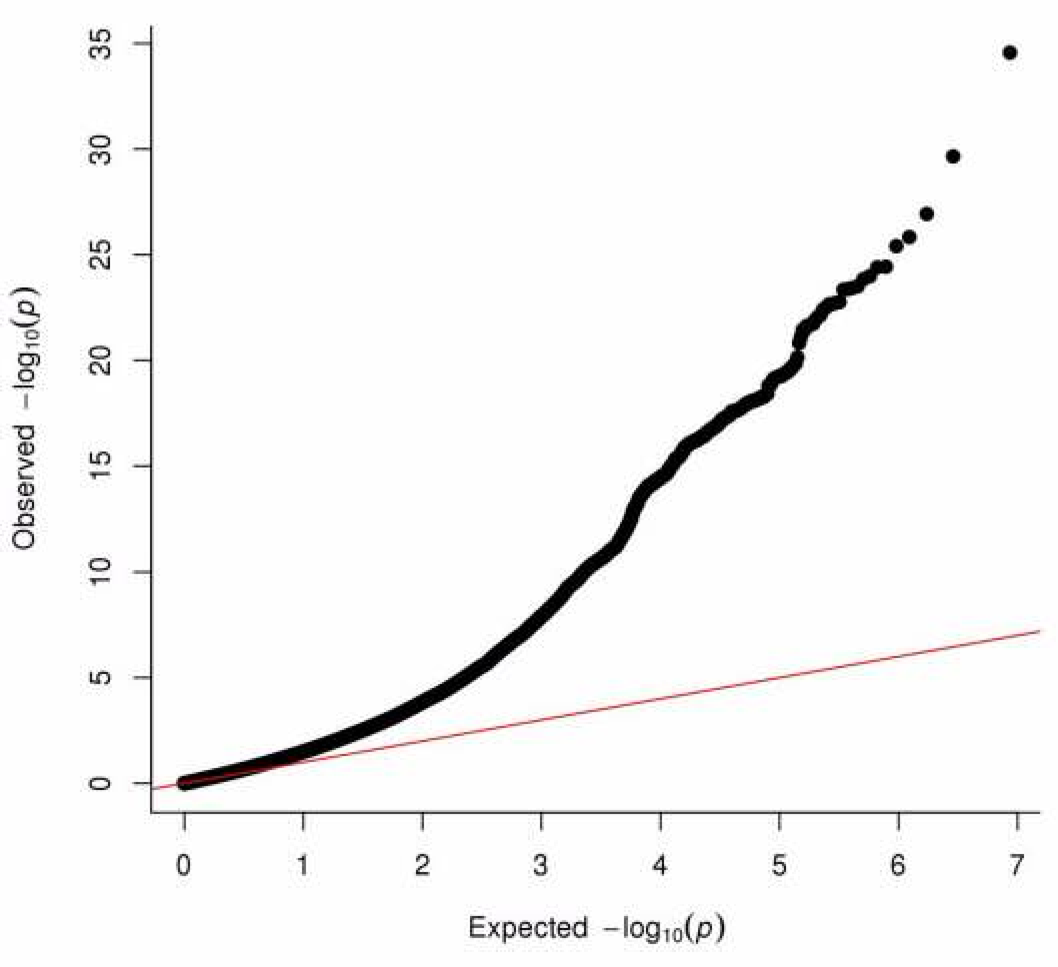
Supplementary Figure 2

Quantile-quantile (Q-Q) plot of Chinese GWAS analysis

The Q-Q plot representative of observed (y axis) vs. expected (x axis) SNP *P* values distribution. Expected *P* values are those expected under the null hypothesis, and the uniform null distribution is marked with a red line.



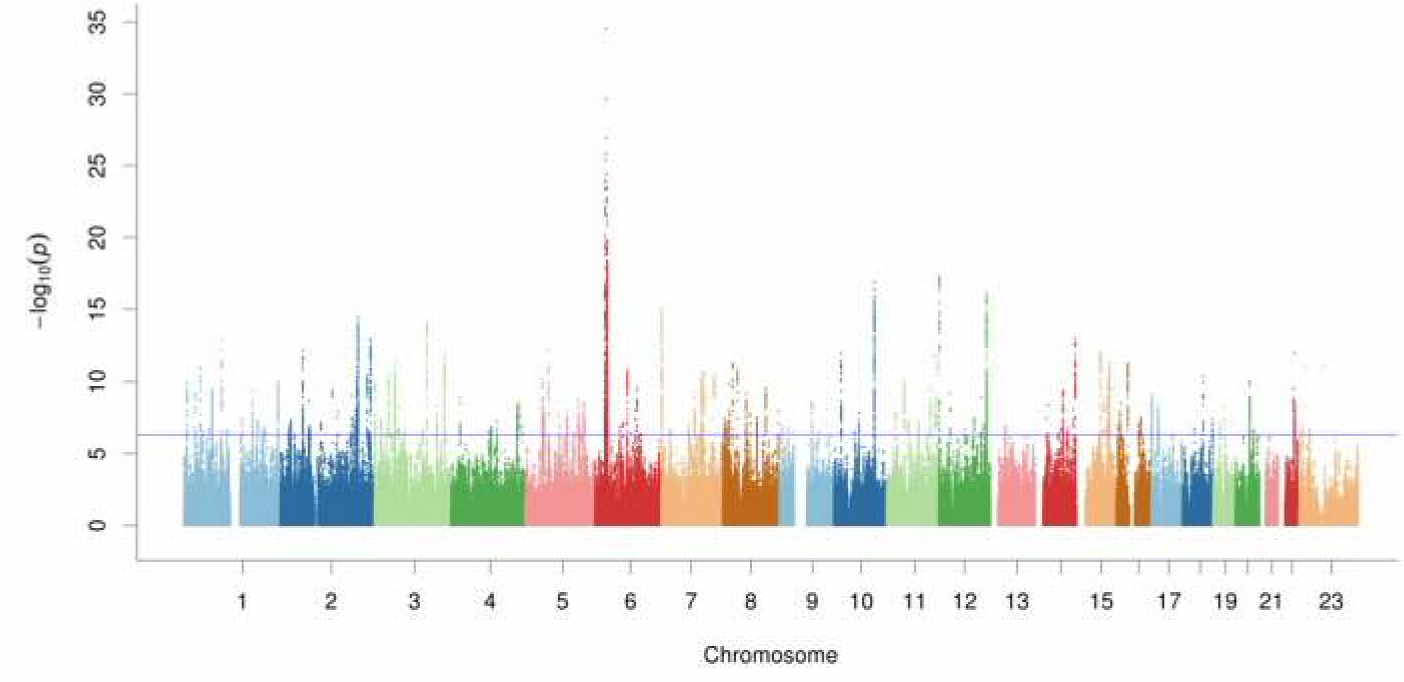
Supplementary Figure 3
Manhattan plot of Chinese GWAS analysis
Genome-wide P-values (–$\log_{10}$ *P*, y axis) plotted against their respective chromosomal positions (x axis). The blue line is the suggestive significance level (1×10^{-5}).



Supplementary Figure 4

Quantile-quantile (Q-Q) plot of Chinese and PGC2 GWAS meta-analysis

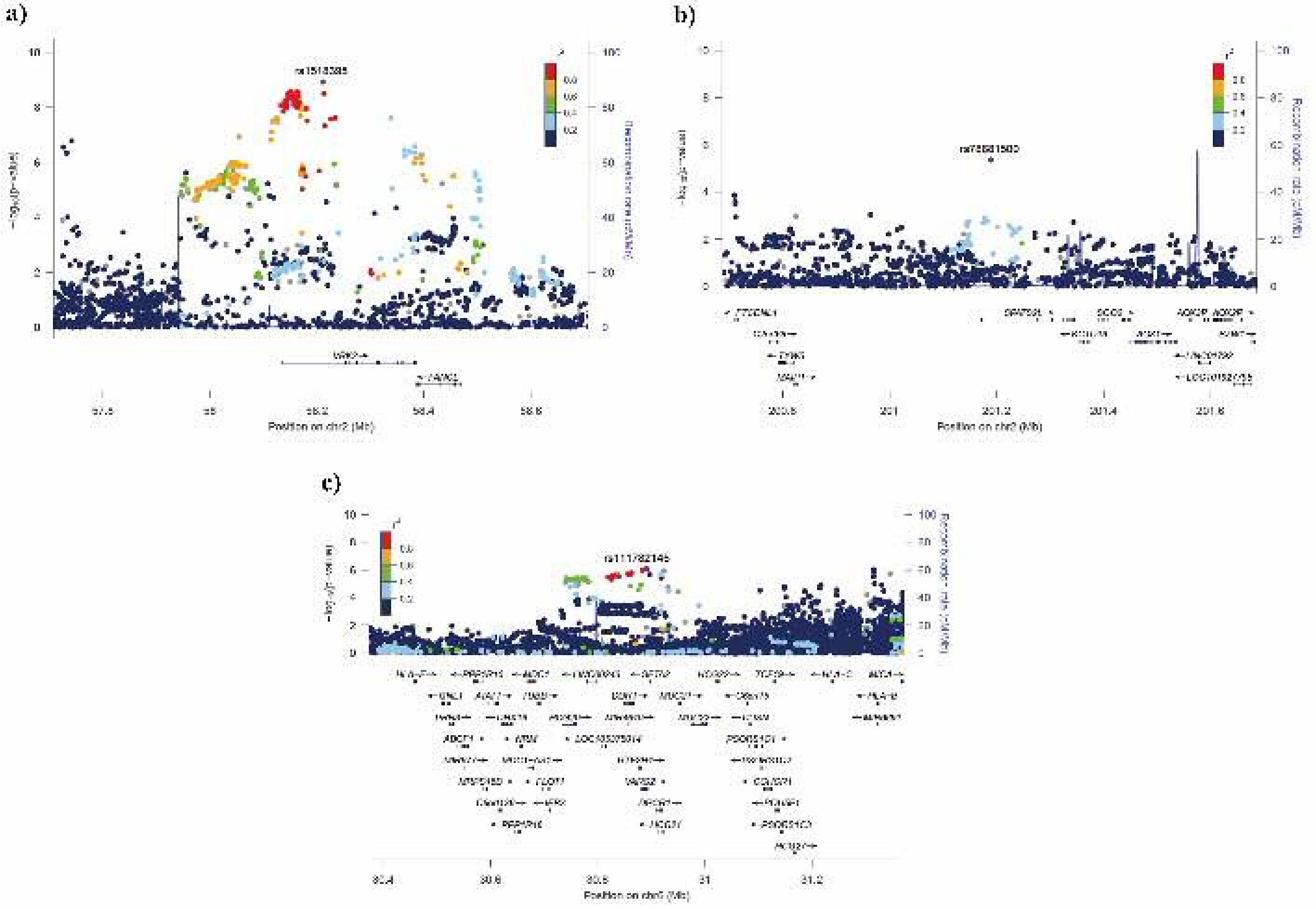
The Q-Q plot representative of observed (y axis) vs. expected (x axis) SNP *P* values distribution. Expected *P* values are those expected under the null hypothesis, and the uniform null distribution is marked with a red line.



Supplementary Figure 5

Manhattan plot of Chinese and PGC2 GWAS meta-analysis

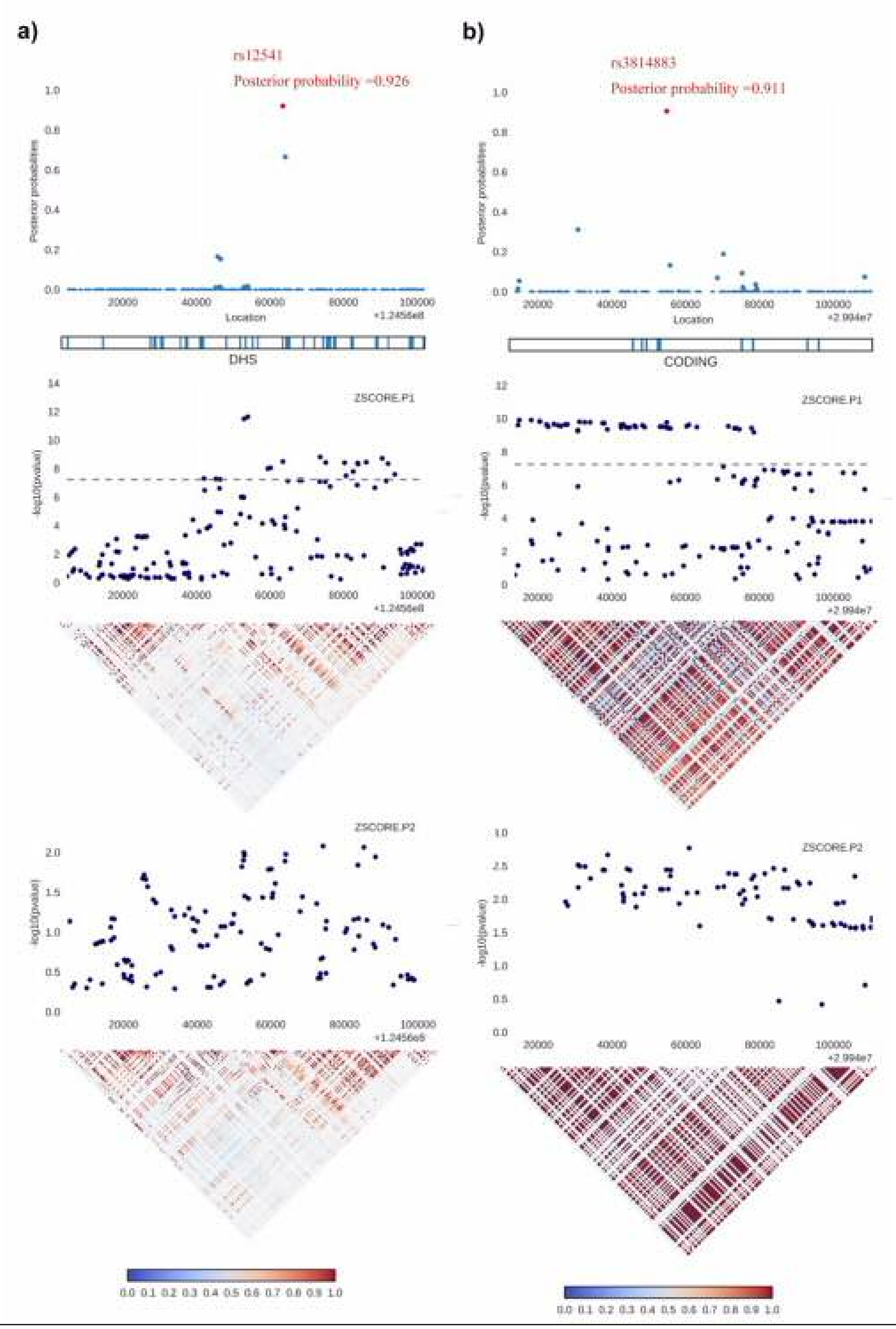
Genome-wide P-values ($-\log_{10} P$, y axis) plotted against their respective chromosomal positions (x axis). The blue line is the suggestive significance level (5×10^{-7}).



Supplementary Figure 6

Regional plots of the GWS loci from the Chinese GWAS and replication meta-analysis

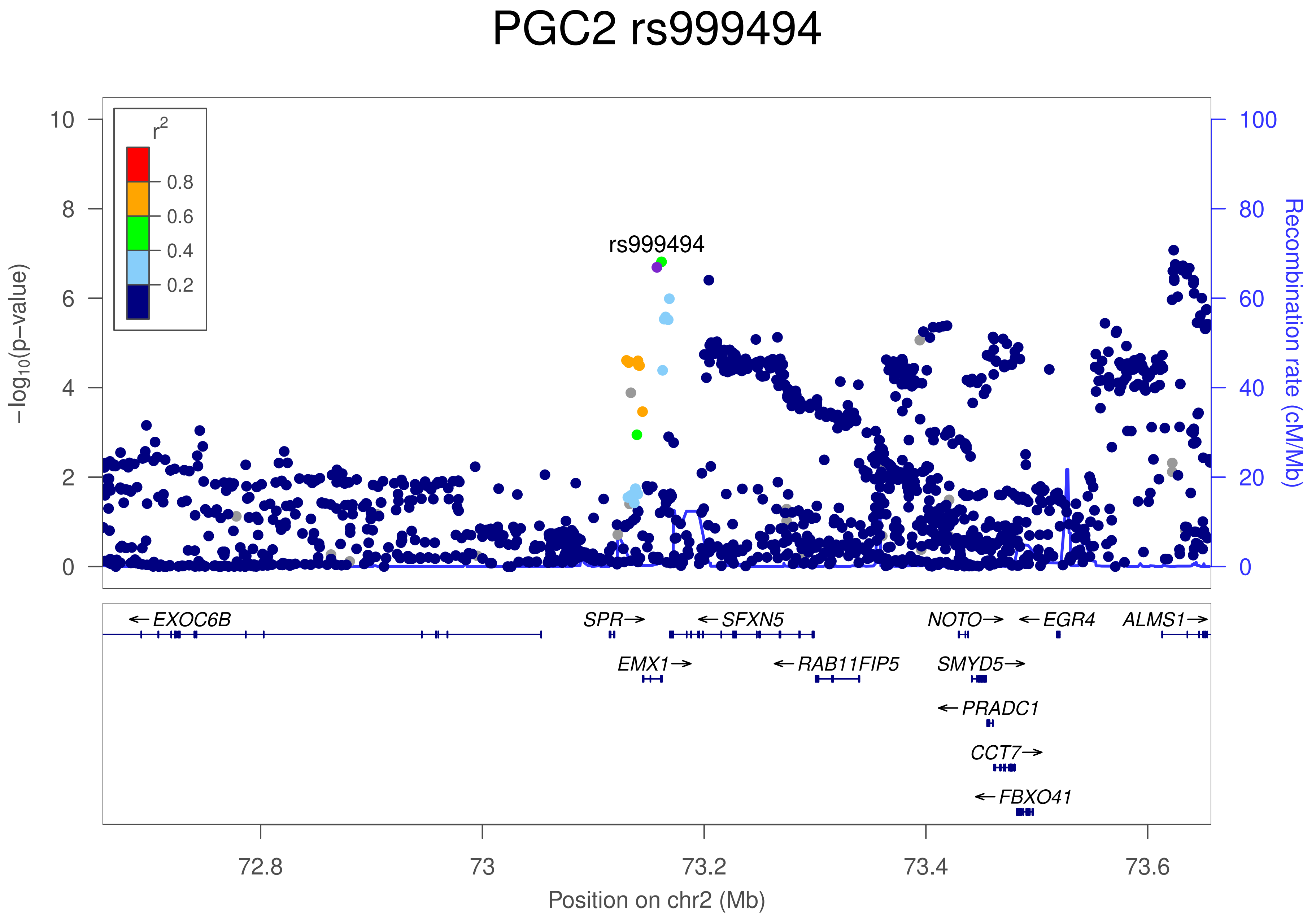
a) rs1518395 at 2p16.1, **b**) rs78681500 at 2q33.1, **c**) rs111782145 at eMHC. $-\log_{10} P$ values are shown for SNPs for the region 500 kb on either side of the marker SNPs. The index SNP is shown in purple, and the r2 values of the other SNPs are indicated by color. The r2 values are established based on the 1000 Genome data. The genes within the relevant regions are annotated and shown as arrows.



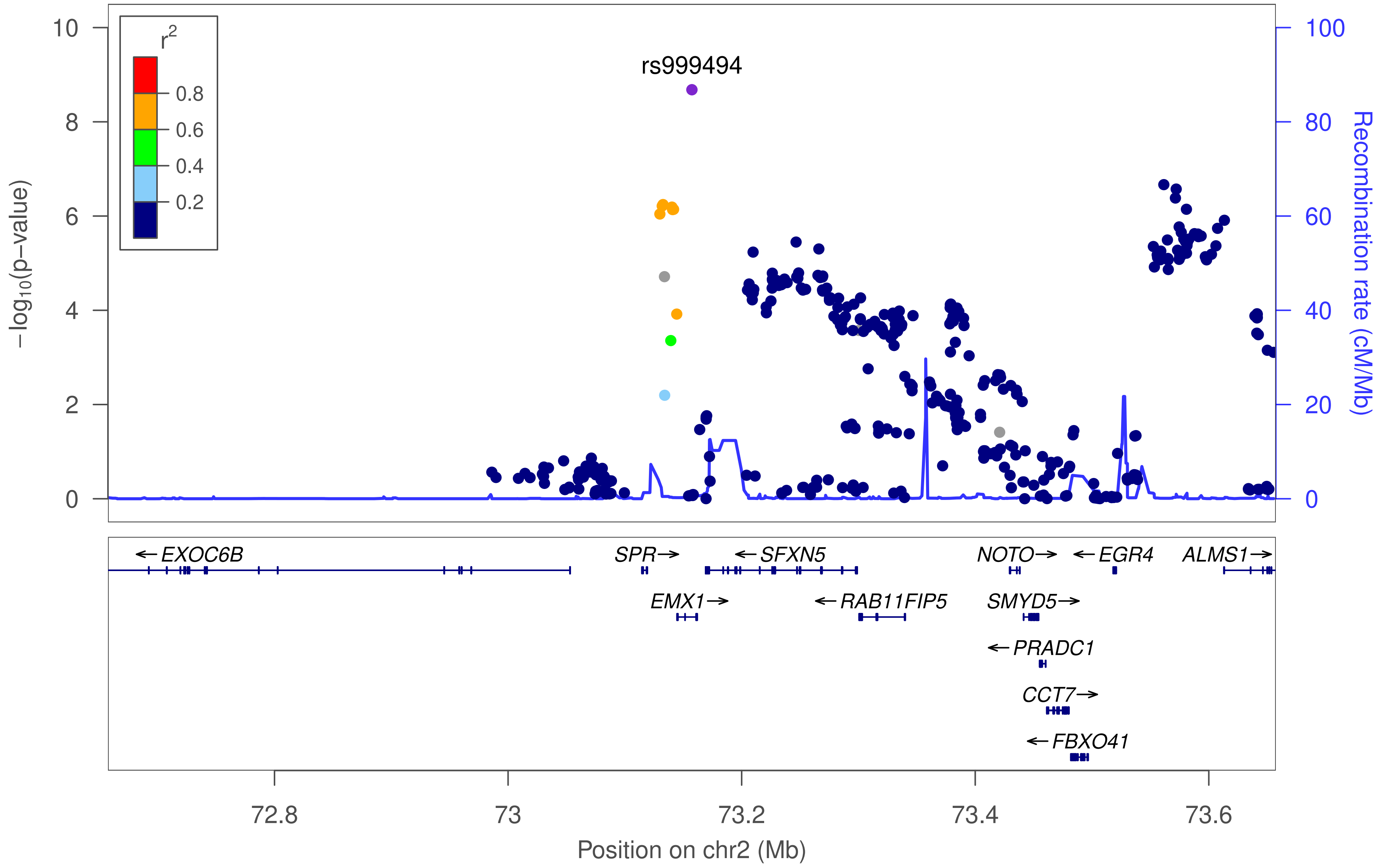
Supplementary Figure 7

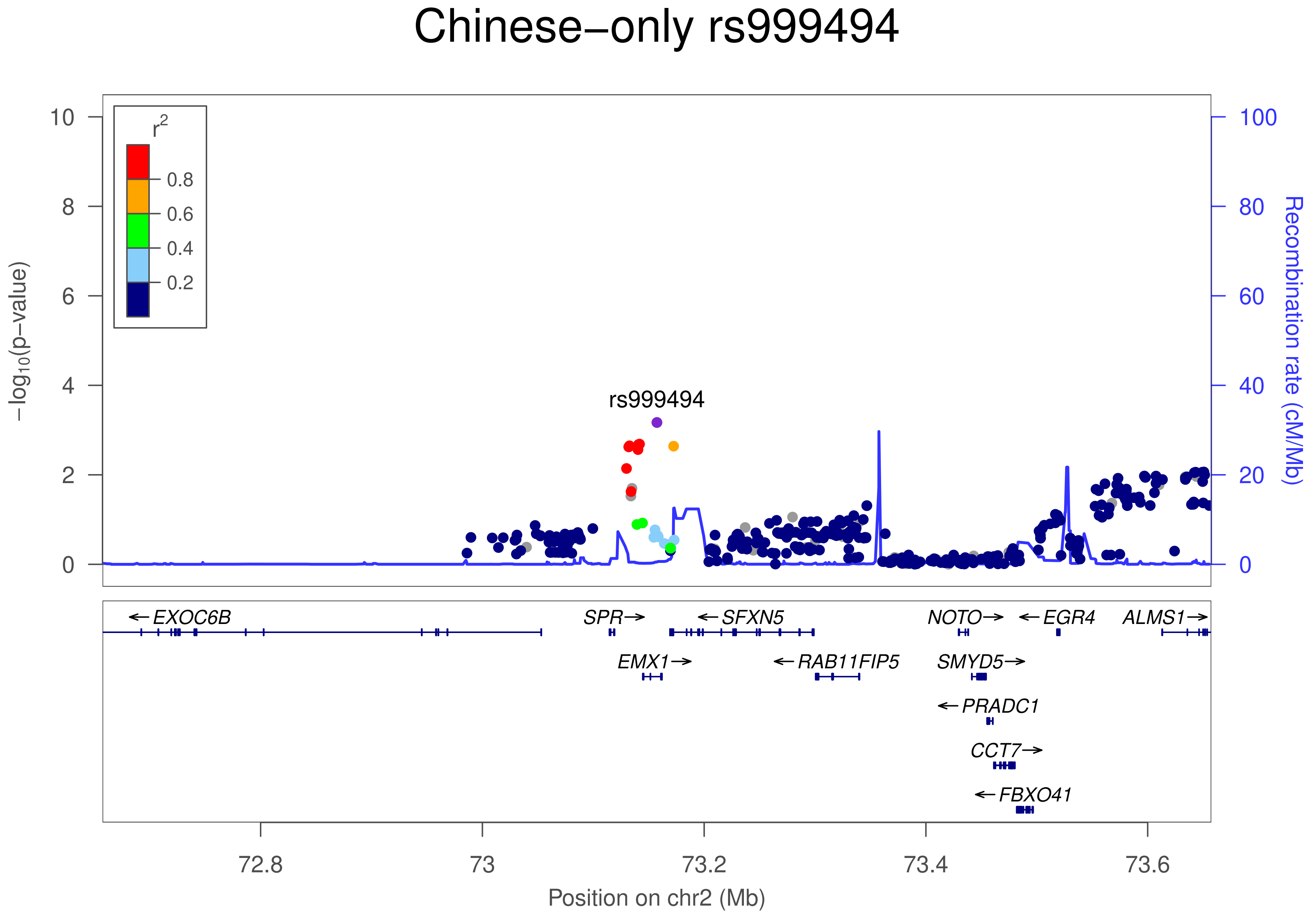
Fine-mapping analyses for No. 80 and 103 GWS loci using PAINTOR

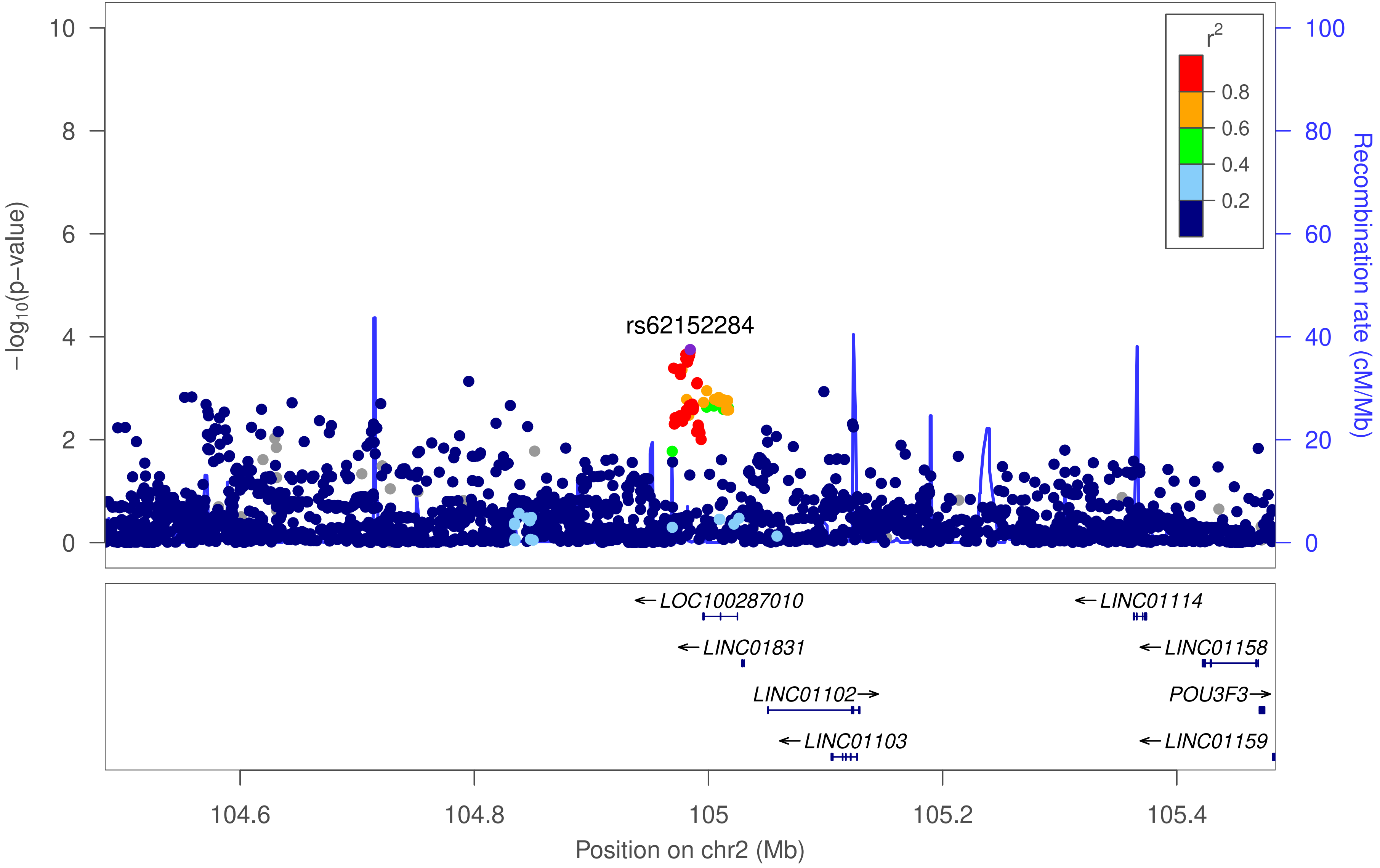
Novel Loci

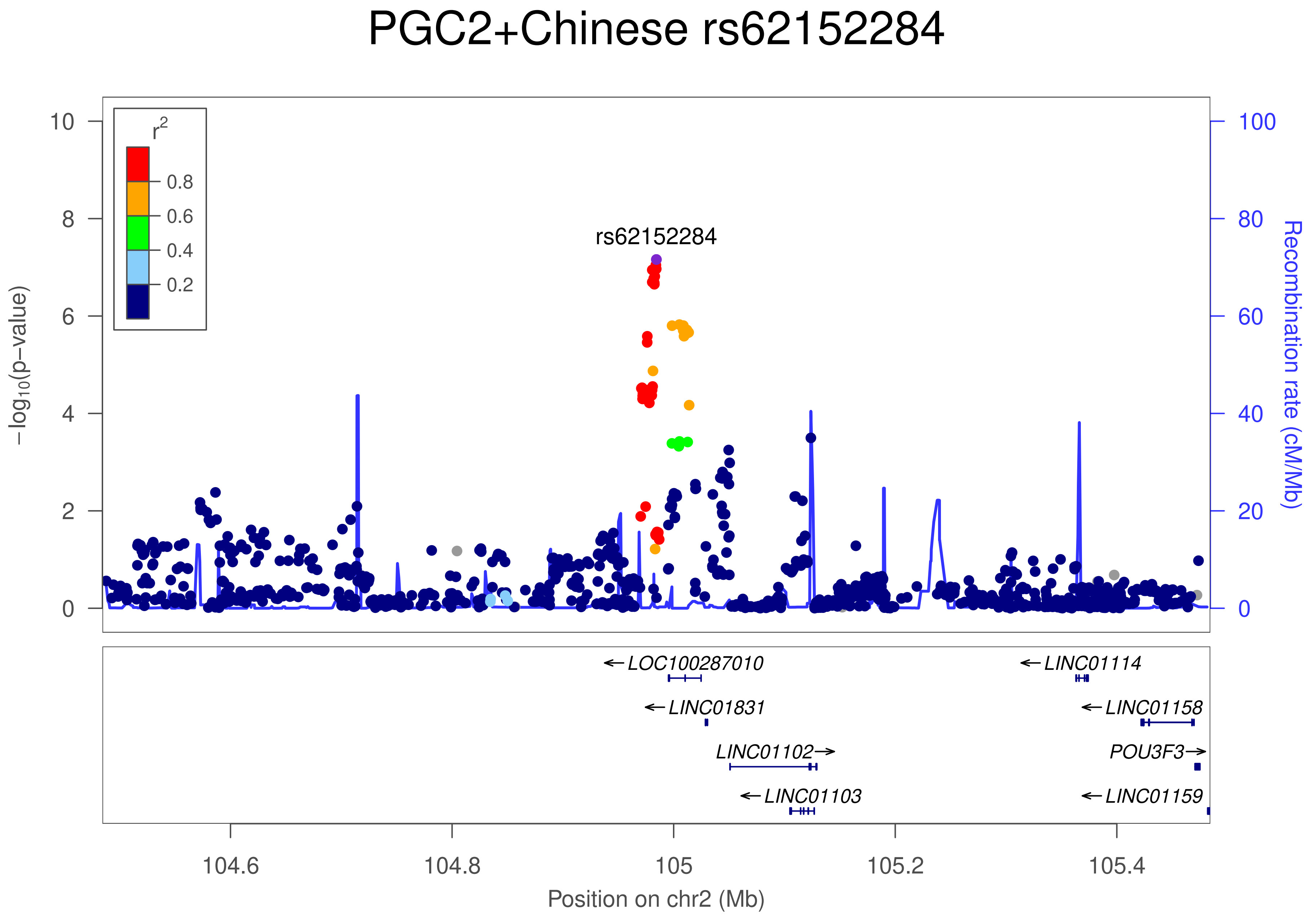

PGC2 rs999494
r^2
0.8
0.6
0.4
0.2
rs999494
$-\log_{10}$(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
← EXOC6B
SPR →
← SFXN5
NOTO →
← EGR4
ALMS1 →
EMX1 →
← RAB11FIP5
SMYD5 →
← PRADC1
CCT7 →
← FBXO41
72.8
73
73.2
73.4
73.6
Position on chr2 (Mb)

PGC2+Chinese rs999494

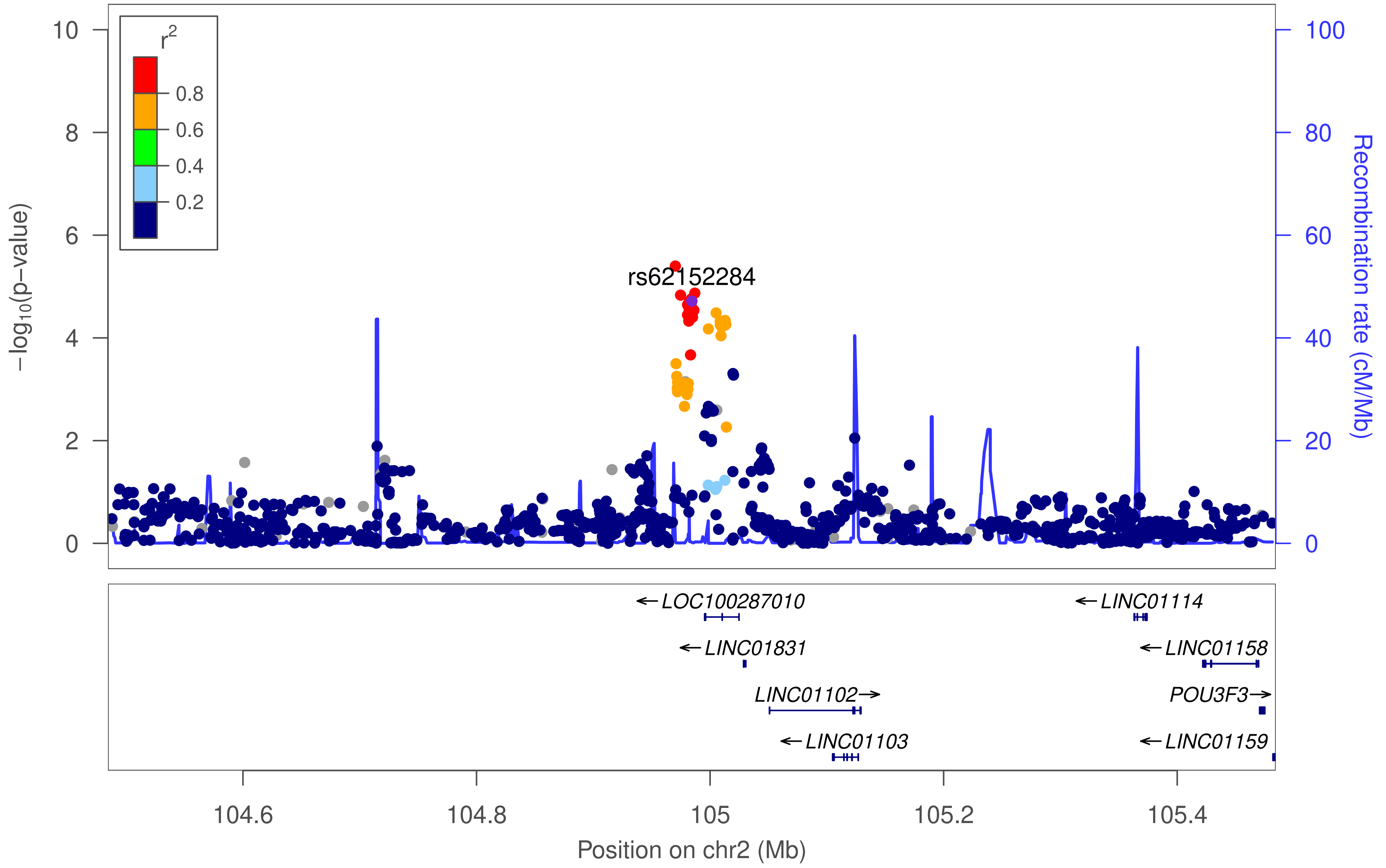


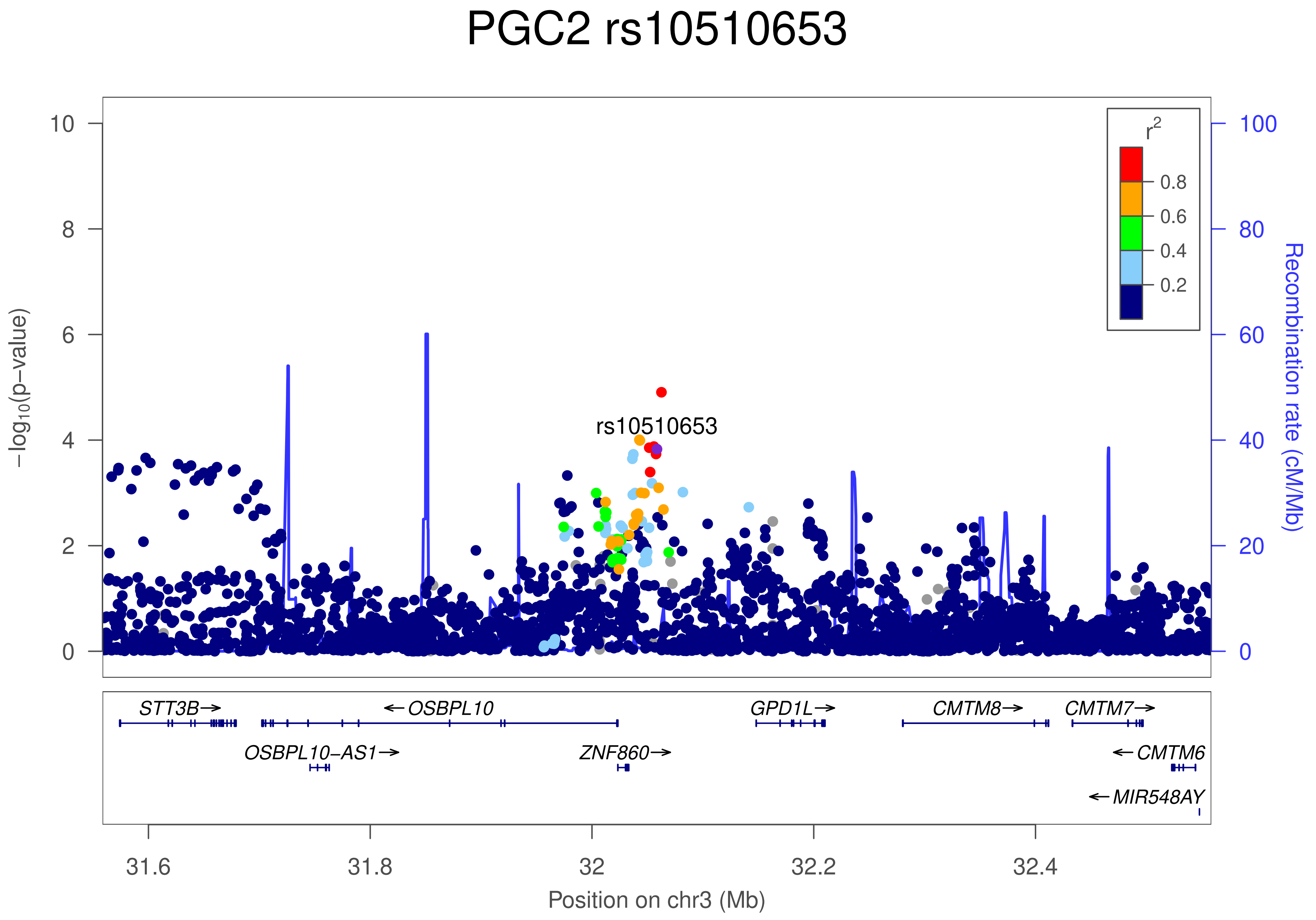

Chinese–only rs999494
r²
0.8
0.6
0.4
0.2
rs999494
−log₁₀(p−value)
10
8
6
4
2
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
← EXOC6B
SPR →
← SFXN5
NOTO →
← EGR4
ALMS1 →
EMX1 →
← RAB11FIP5
SMYD5 →
← PRADC1
CCT7 →
← FBXO41
72.8
73
73.2
73.4
73.6
Position on chr2 (Mb)

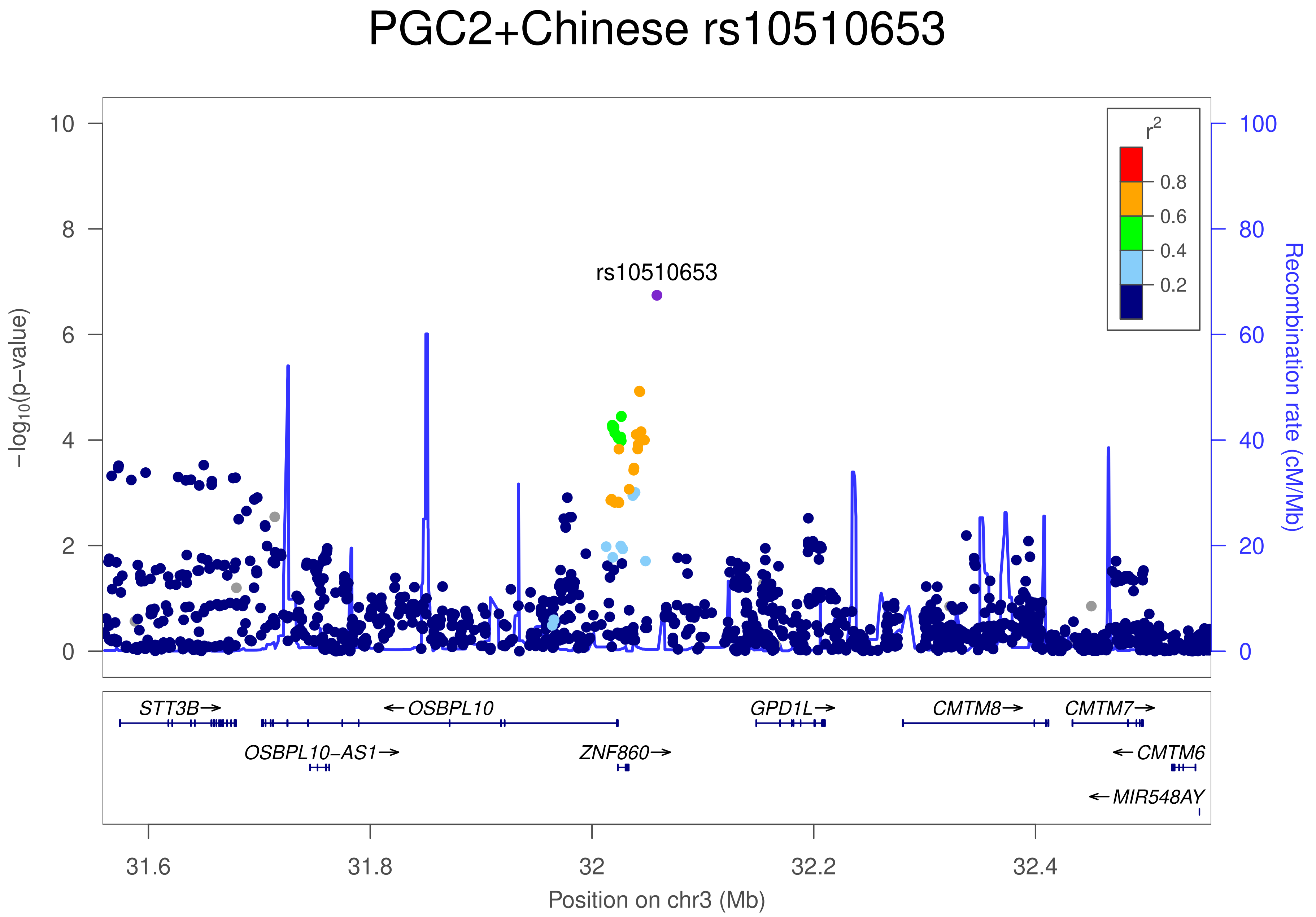

PGC2 rs62152284


PGC2+Chinese rs62152284
r²
0.8
0.6
0.4
0.2
rs62152284
10
8
6
4
2
0
−log₁₀(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
← LOC100287010
← LINC01831
LINC01102 →
← LINC01103
← LINC01114
← LINC01158
POU3F3 →
← LINC01159
104.6
104.8
105
105.2
105.4
Position on chr2 (Mb)

Chinese–only rs62152284

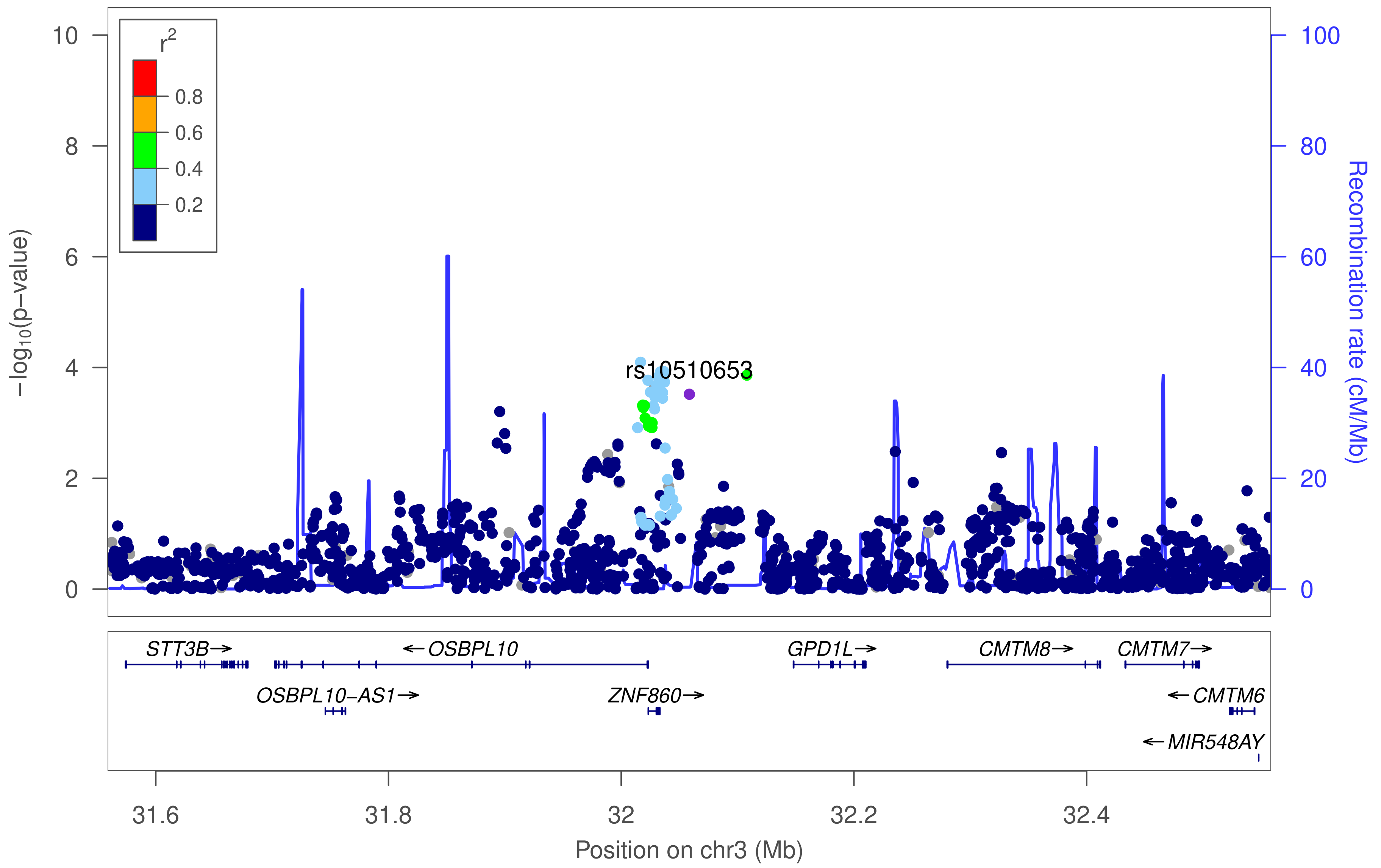



PGC2 rs10510653
rs10510653
−log10(p−value)
10
8
6
4
2
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
r2
0.8
0.6
0.4
0.2
STT3B→
←OSBPL10
GPD1L→
CMTM8→
CMTM7→
OSBPL10−AS1→
ZNF860→
←CMTM6
←MIR548AY
31.6
31.8
32
32.2
32.4
Position on chr3 (Mb)

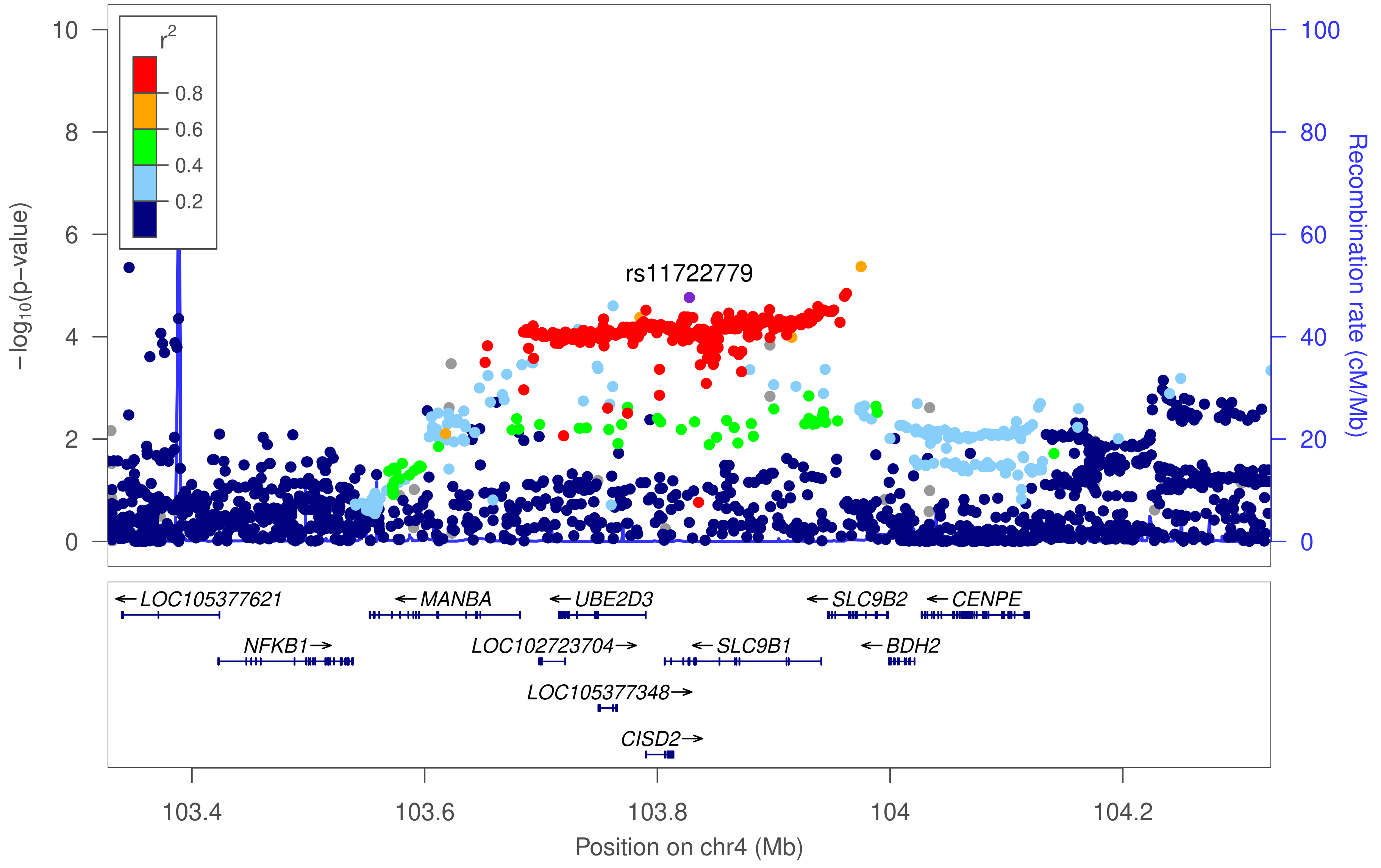


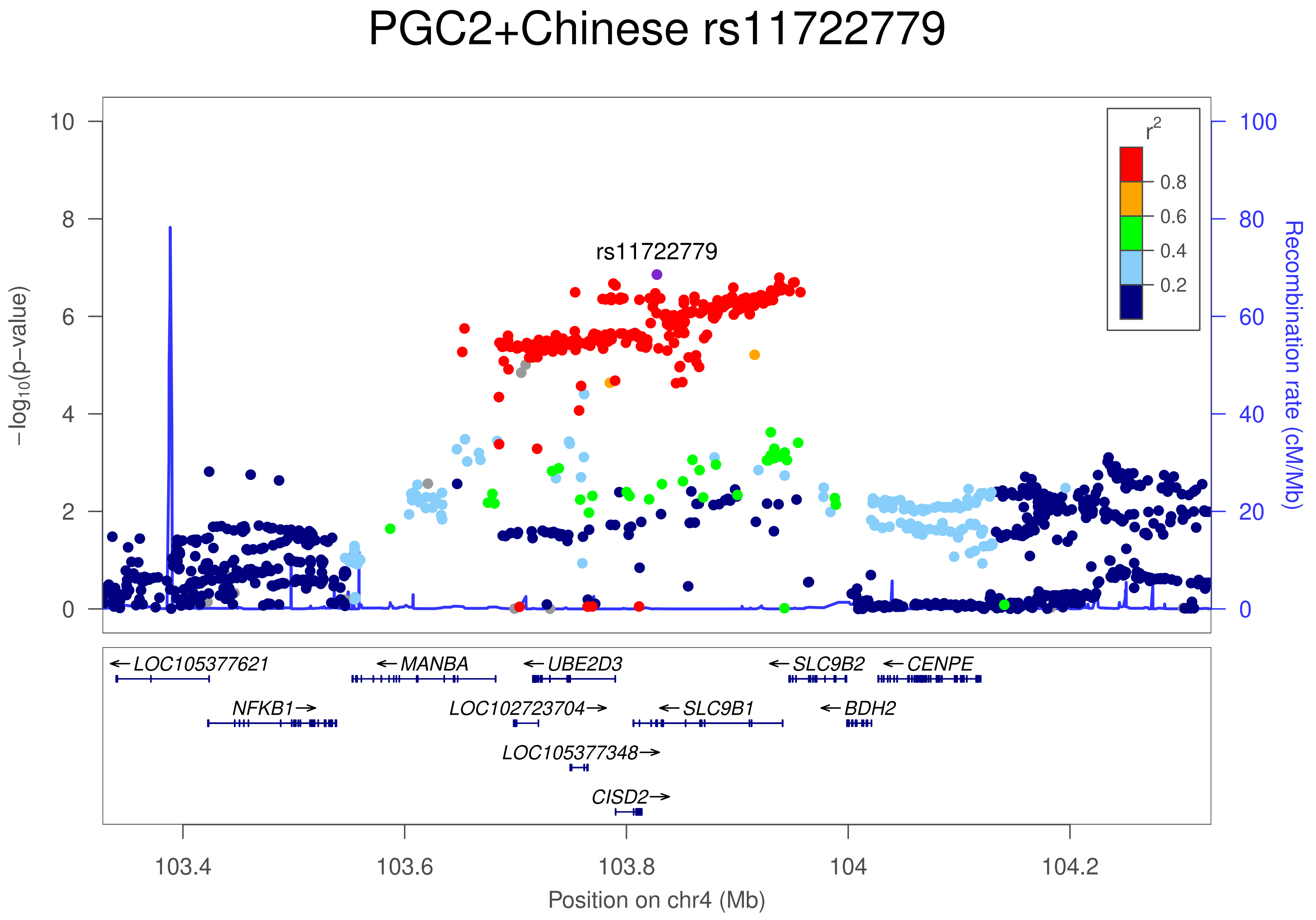
PGC2+Chinese rs10510653

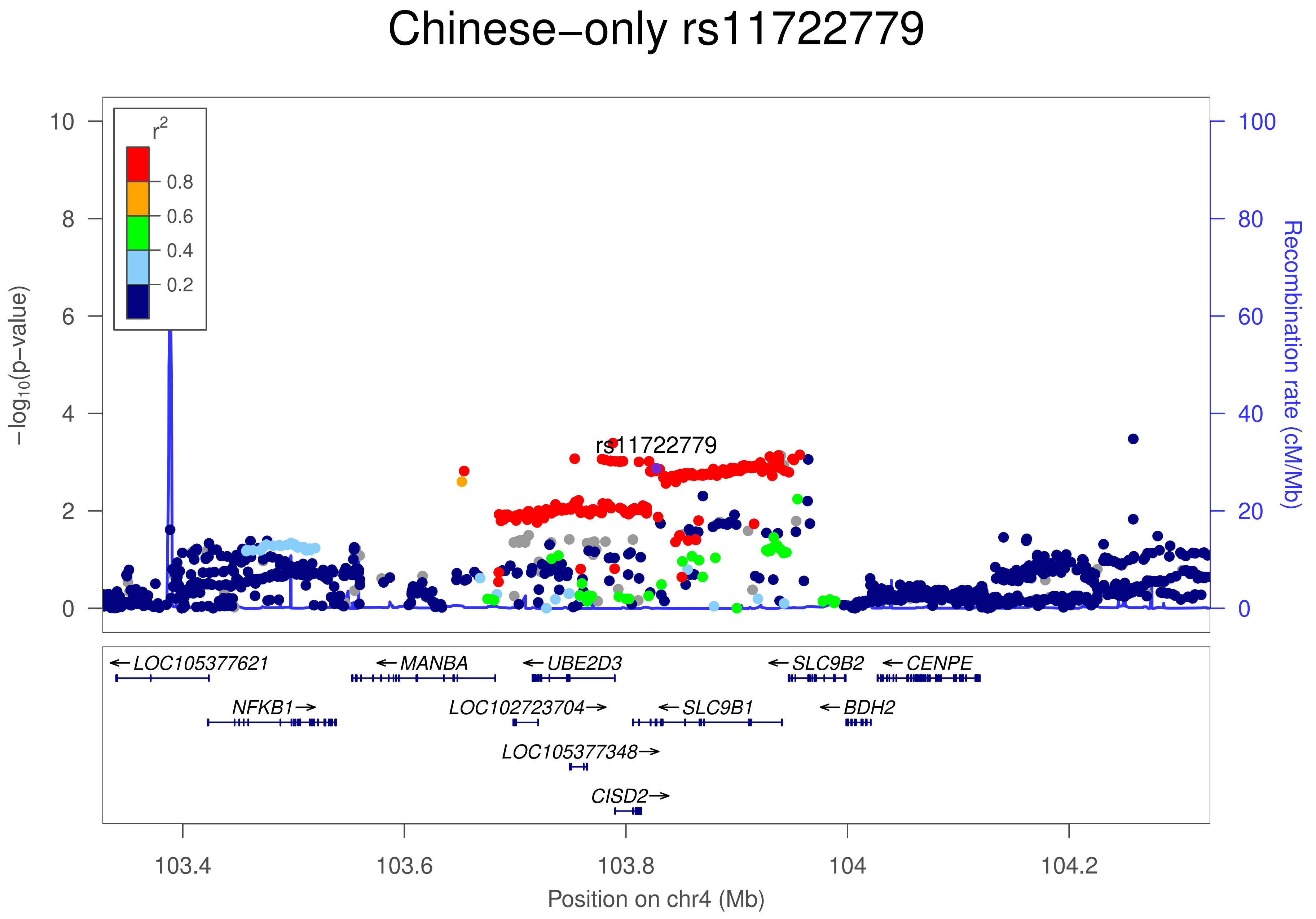
Chinese−only rs10510653

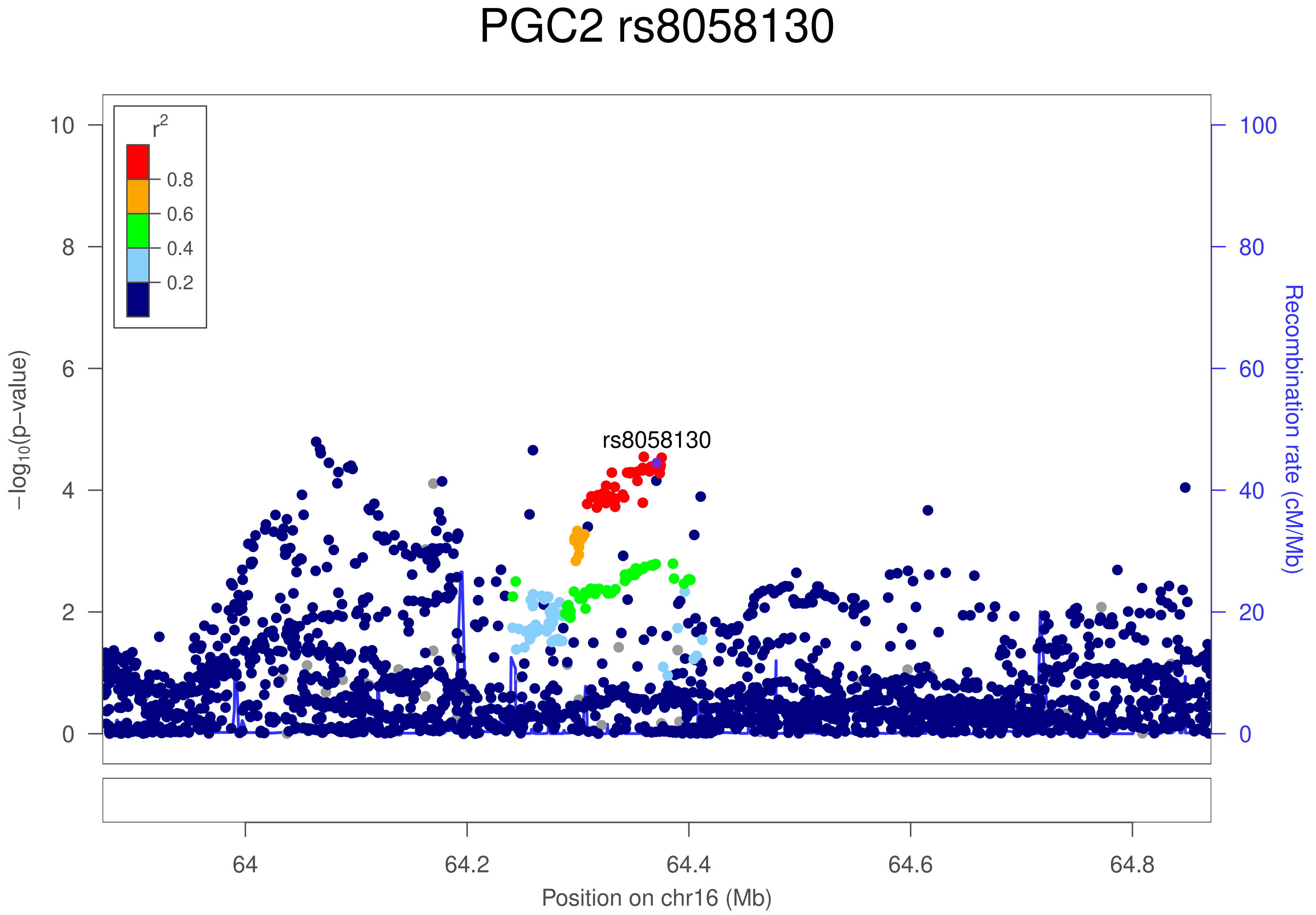


PGC2 rs11722779




PGC2+Chinese rs11722779
rs11722779
−log10(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
r2
0.8
0.6
0.4
0.2
←LOC105377621
←MANBA
←UBE2D3
←SLC9B2
←CENPE
NFKB1→
LOC102723704→
←SLC9B1
←BDH2
LOC105377348→
CISD2→
103.4
103.6
103.8
104
104.2
Position on chr4 (Mb)


Chinese–only rs11722779
r^2
0.8
0.6
0.4
0.2
rs11722779
−log$_{10}$(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
←LOC105377621
←MANBA
←UBE2D3
←SLC9B2
←CENPE
NFKB1→
LOC102723704→
←SLC9B1
←BDH2
LOC105377348→
CISD2→
103.4
103.6
103.8
104
104.2
Position on chr4 (Mb)


PGC2 rs8058130
r2
0.8
0.6
0.4
0.2
rs8058130
−log10(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
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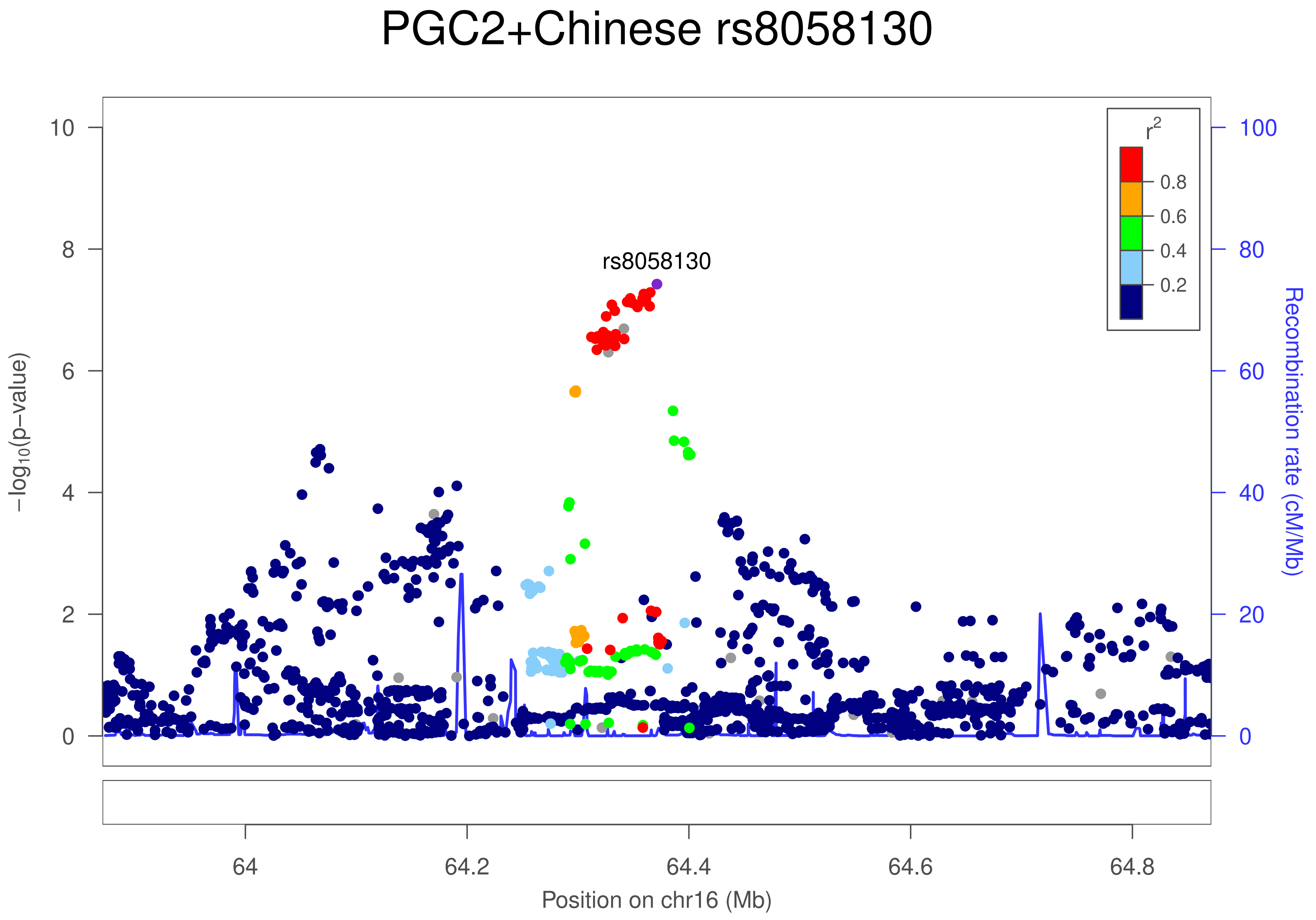
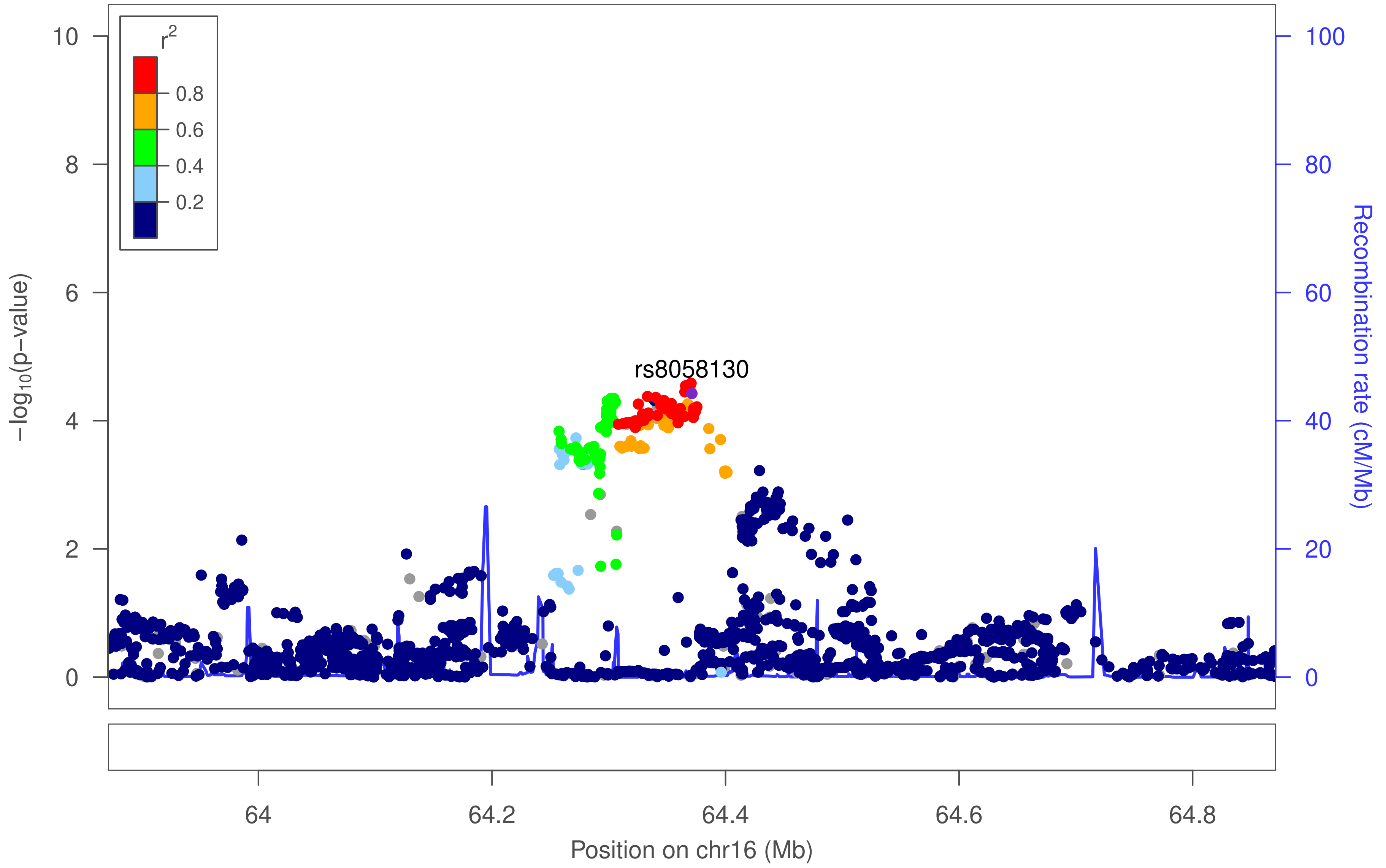
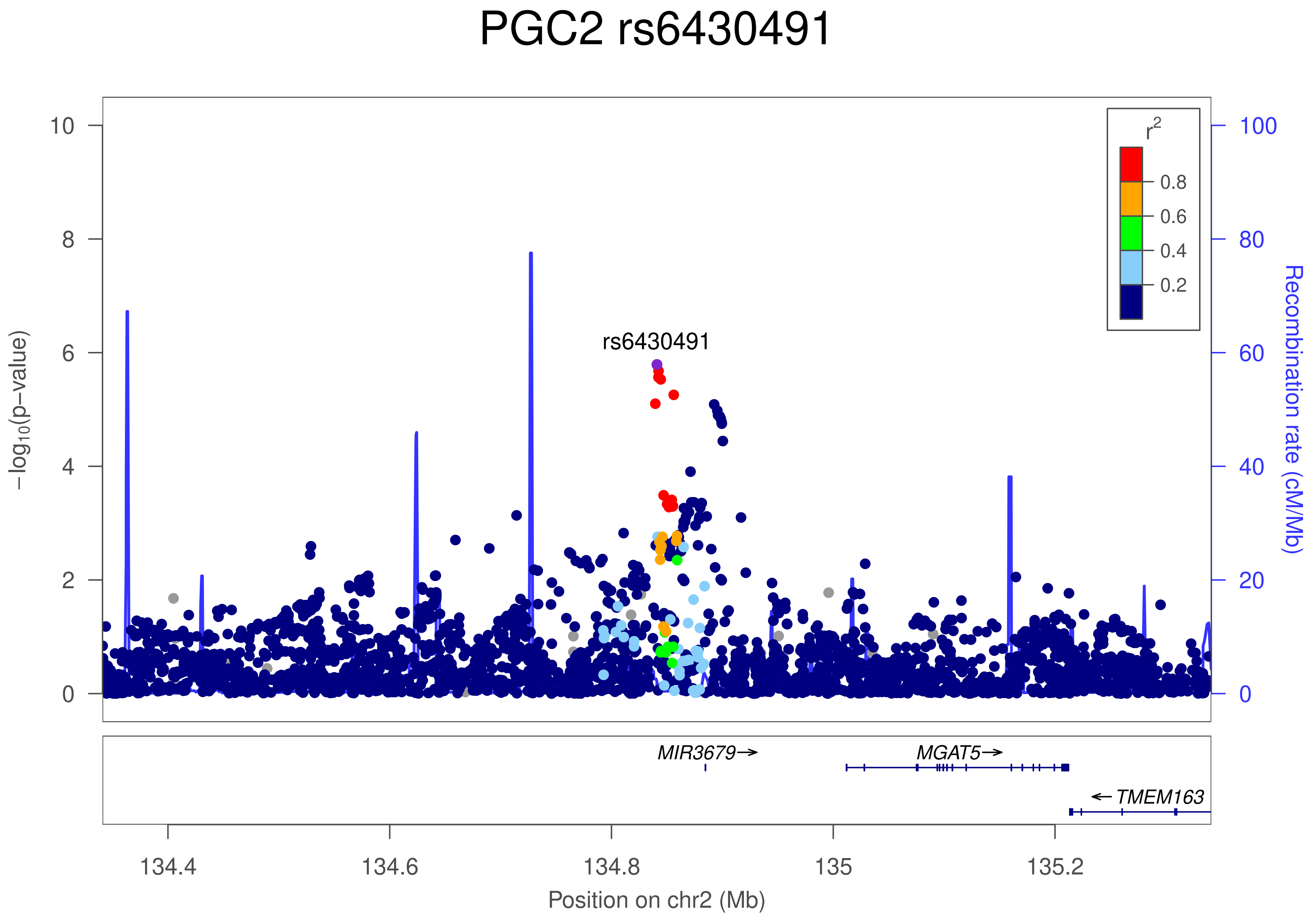
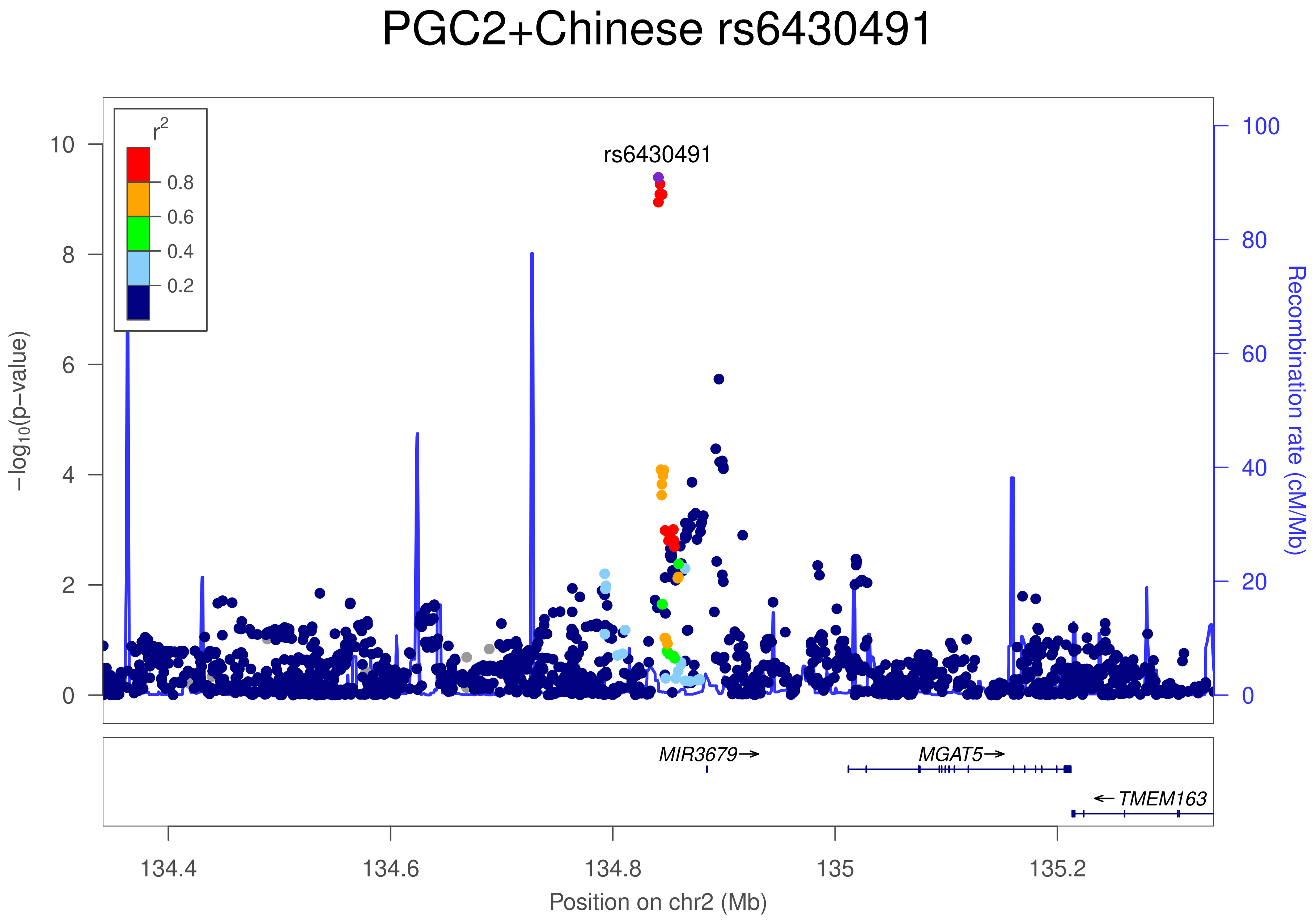
20
40
60
80
100
64
64.2
64.4
64.6
64.8
Position on chr16 (Mb)

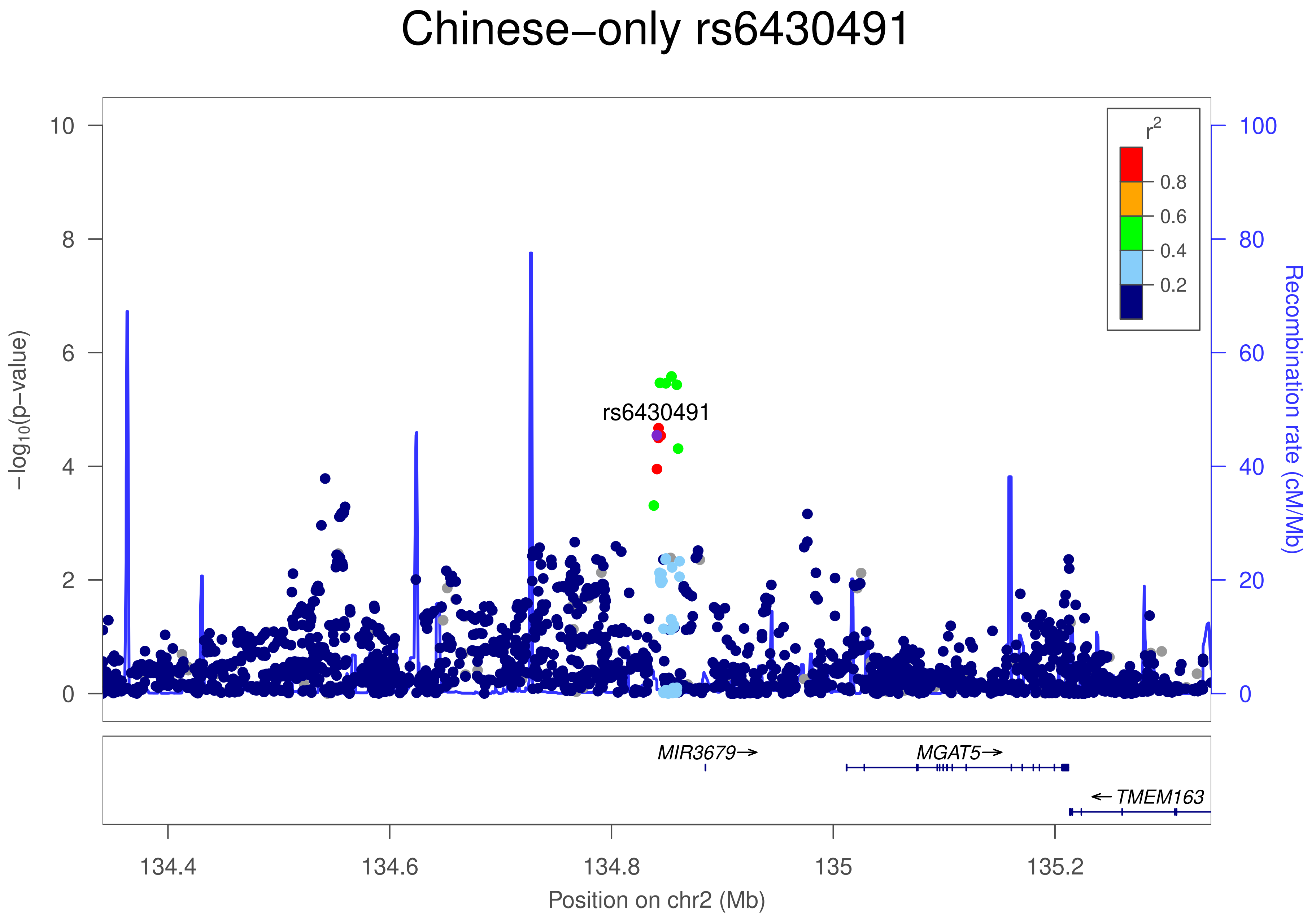

PGC2+Chinese rs8058130
rs8058130
r2
0.8
0.6
0.4
0.2
−log10(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
64
64.2
64.4
64.6
64.8
Position on chr16 (Mb)

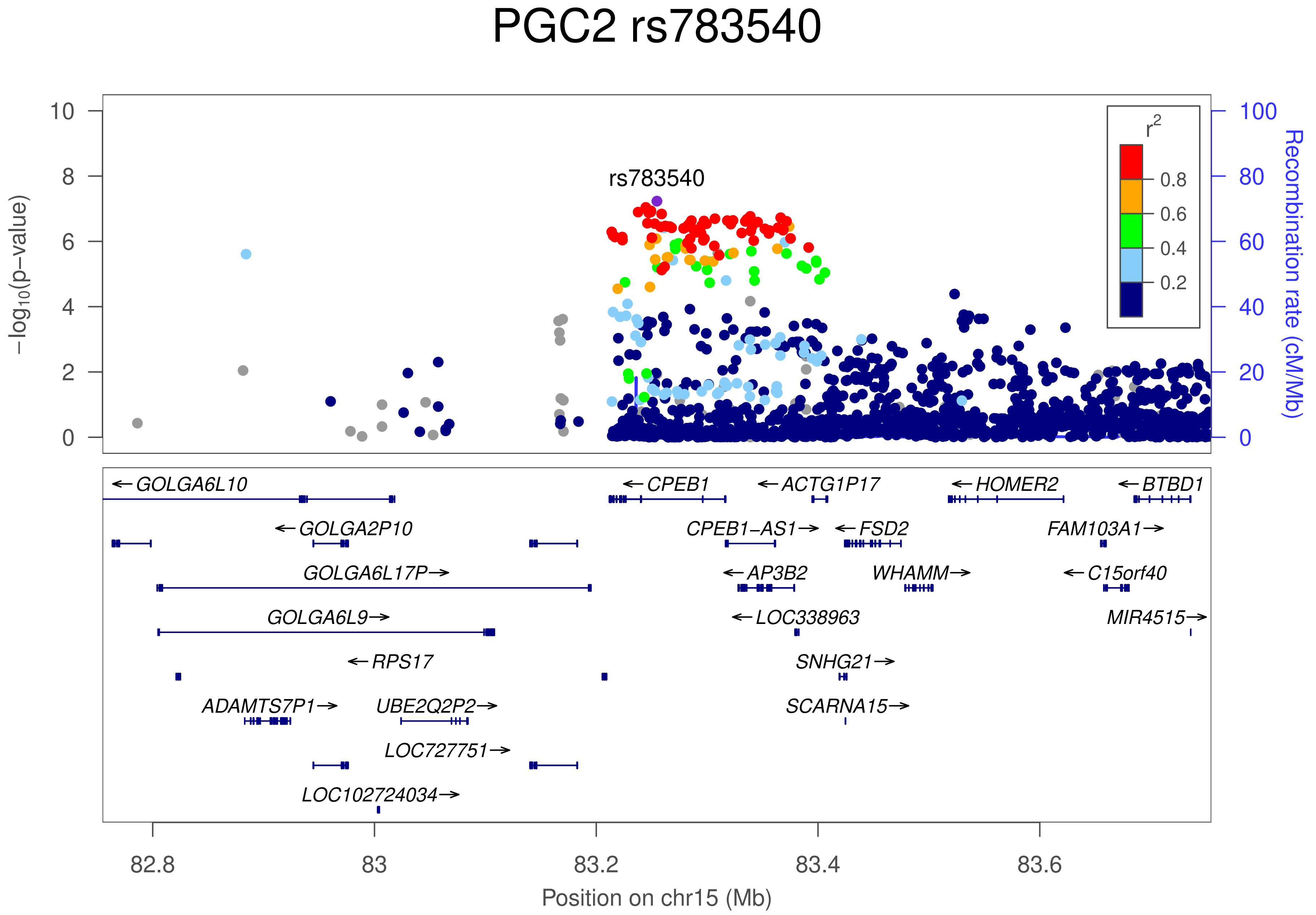
Chinese−only rs8058130



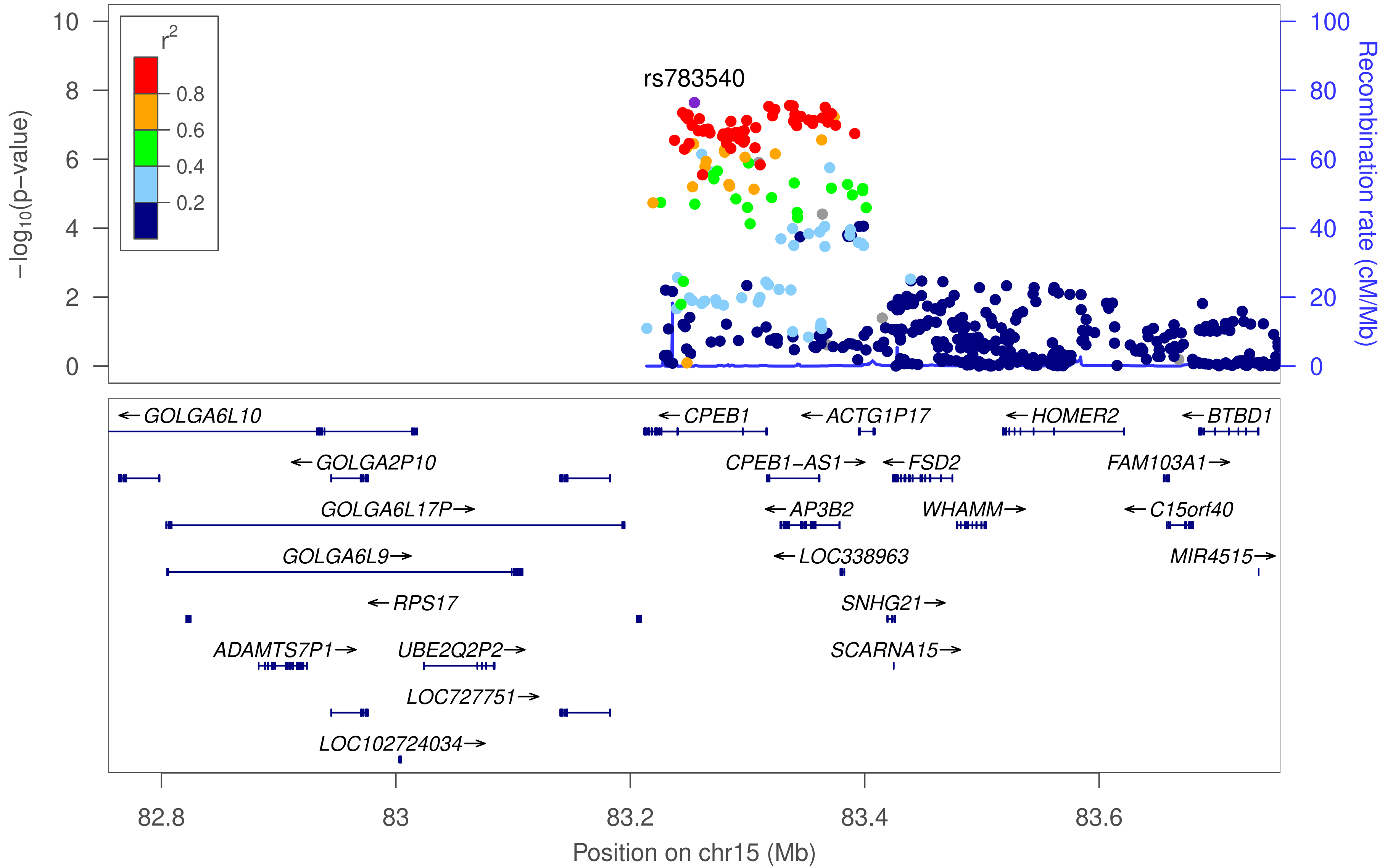

PGC2 rs6430491
rs6430491
r²
0.8
0.6
0.4
0.2
−log₁₀(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
MIR3679→
MGAT5→
←TMEM163
134.4
134.6
134.8
135
135.2
Position on chr2 (Mb)

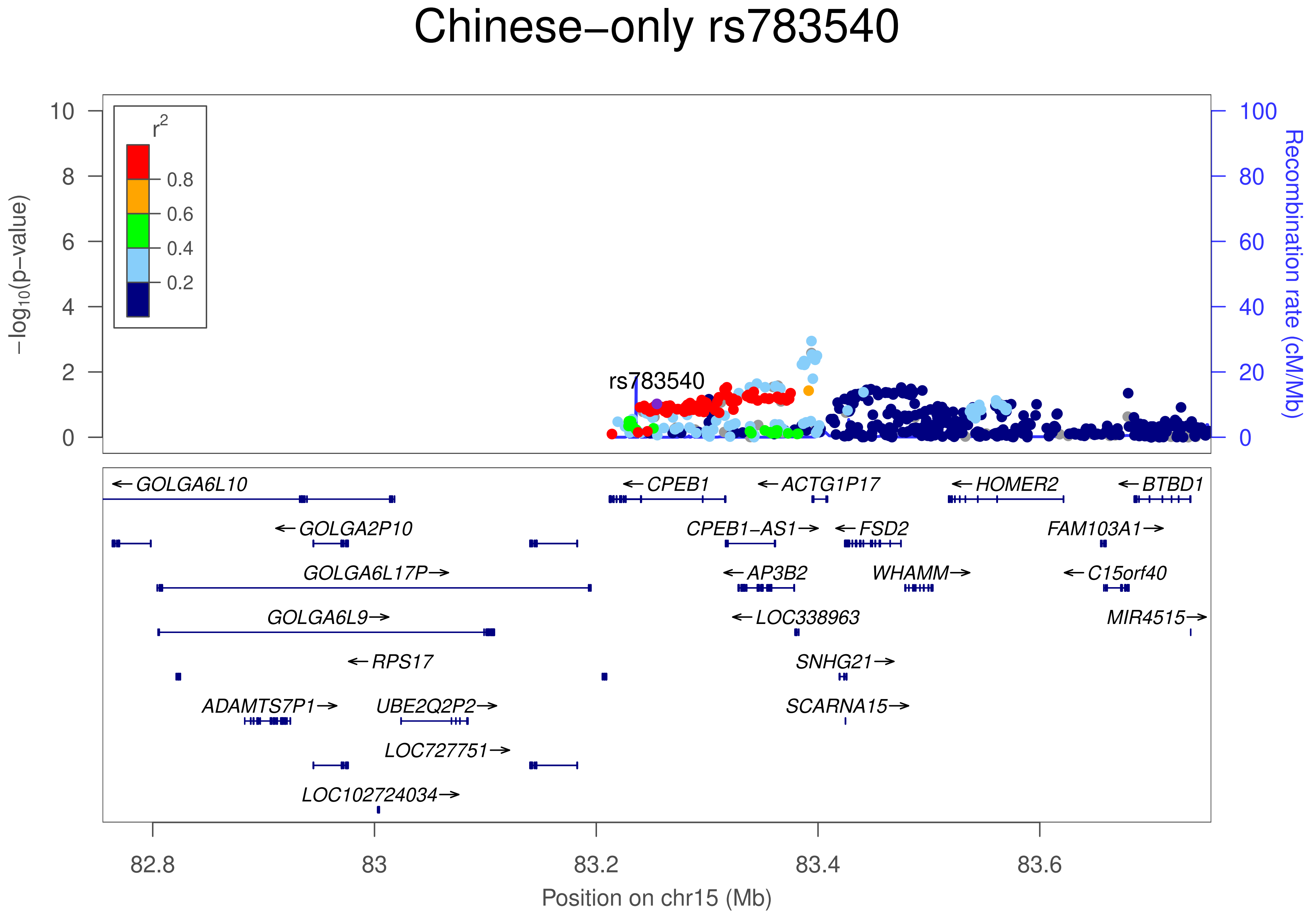

PGC2+Chinese rs6430491
r2
0.8
0.6
0.4
0.2
rs6430491
−log10(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
MIR3679→
MGAT5→
←TMEM163
134.4
134.6
134.8
135
135.2
Position on chr2 (Mb)

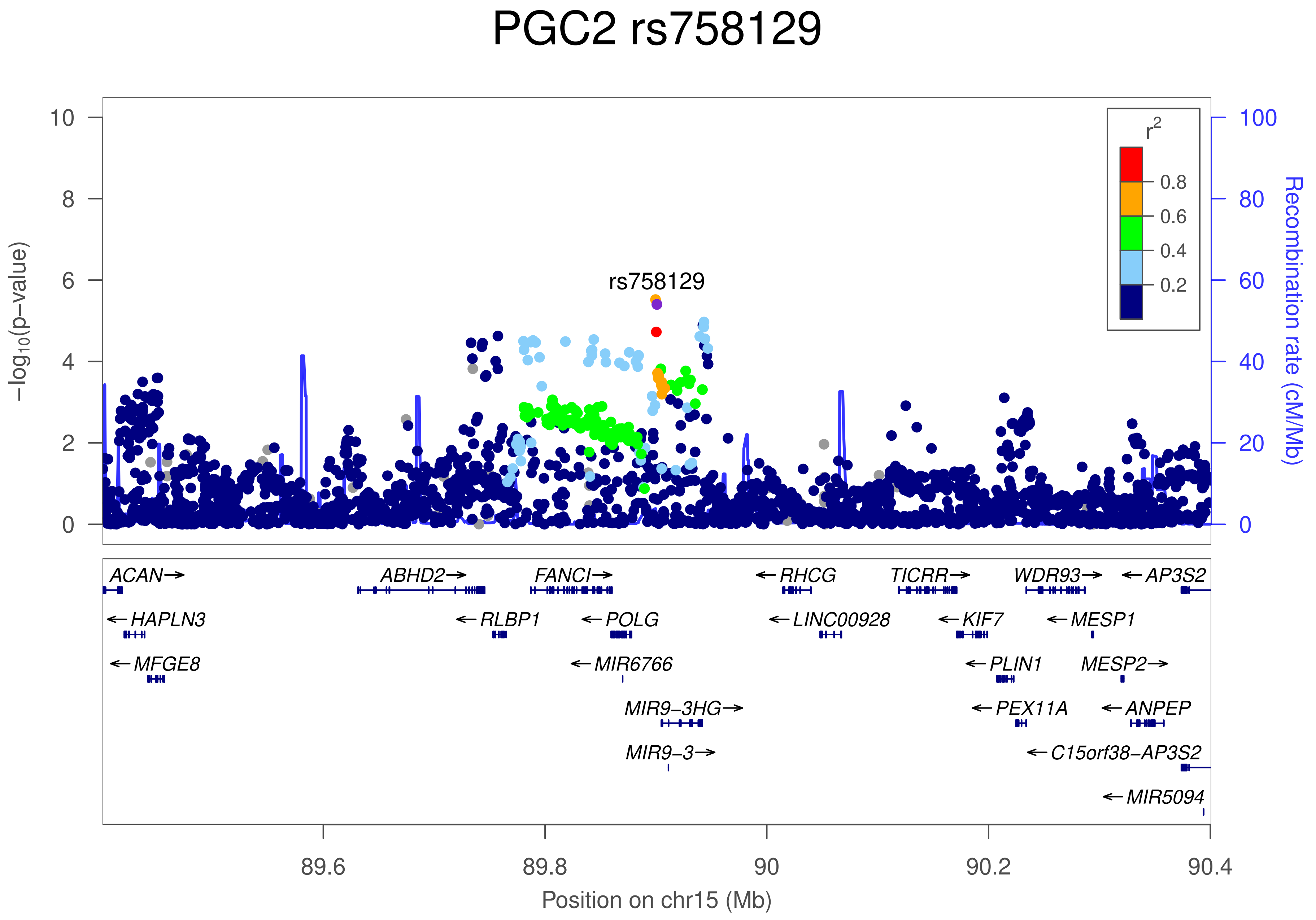

Chinese−only rs6430491
r²
0.8
0.6
0.4
0.2
rs6430491
−log₁₀(p−value)
10
8
6
4
2
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
MIR3679→
MGAT5→
←TMEM163
134.4
134.6
134.8
135
135.2
Position on chr2 (Mb)

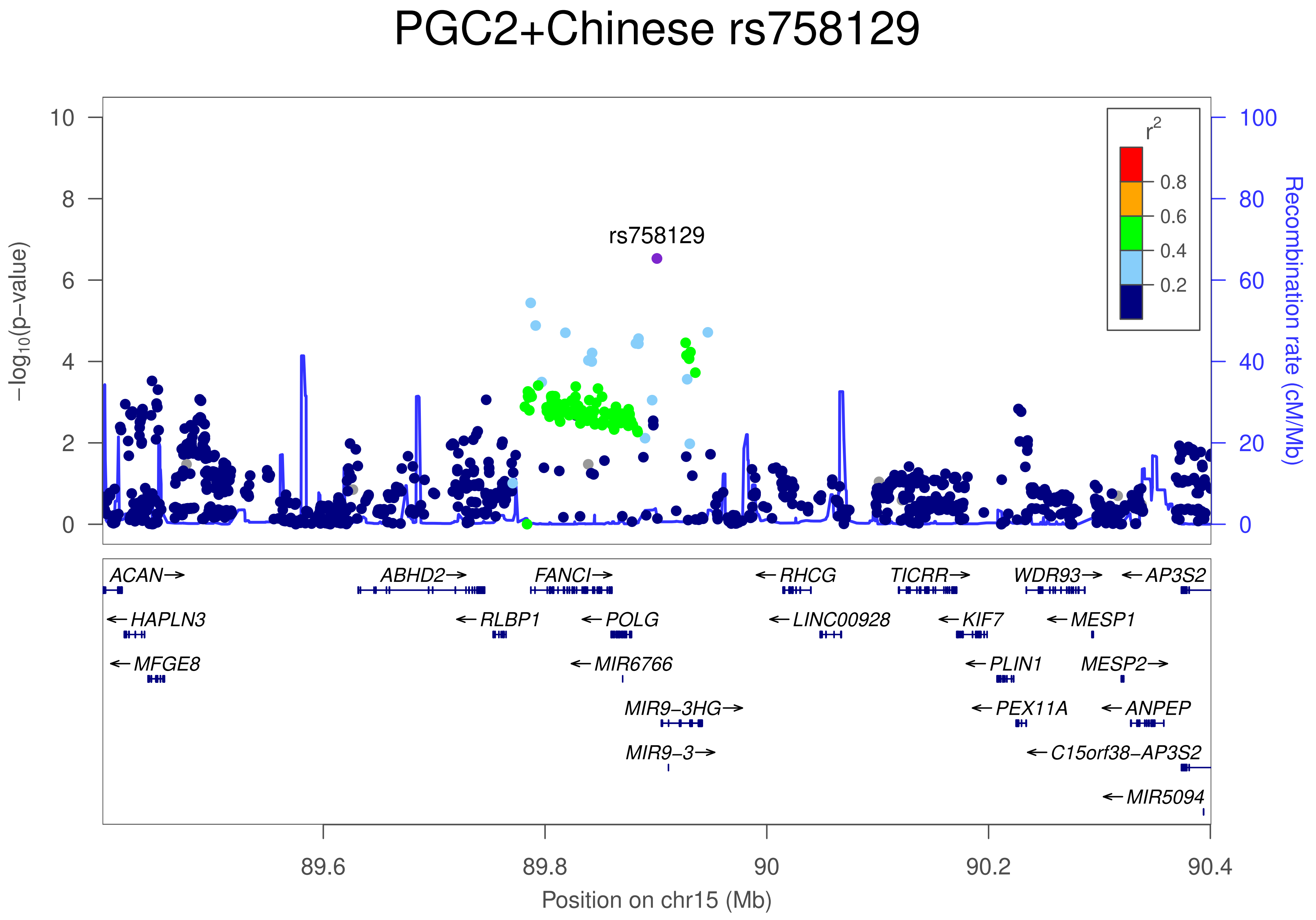

PGC2 rs783540
rs783540
−log10(p−value)
10
8
6
4
2
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
r2
0.8
0.6
0.4
0.2
←GOLGA6L10
←CPEB1
←ACTG1P17
←HOMER2
←BTBD1
←GOLGA2P10
CPEB1−AS1→
←FSD2
FAM103A1→
GOLGA6L17P→
←AP3B2
WHAMM→
←C15orf40
GOLGA6L9→
←LOC338963
MIR4515→
←RPS17
SNHG21→
ADAMTS7P1→
UBE2Q2P2→
SCARNA15→
LOC727751→
LOC102724034→
82.8
83
83.2
83.4
83.6
Position on chr15 (Mb)

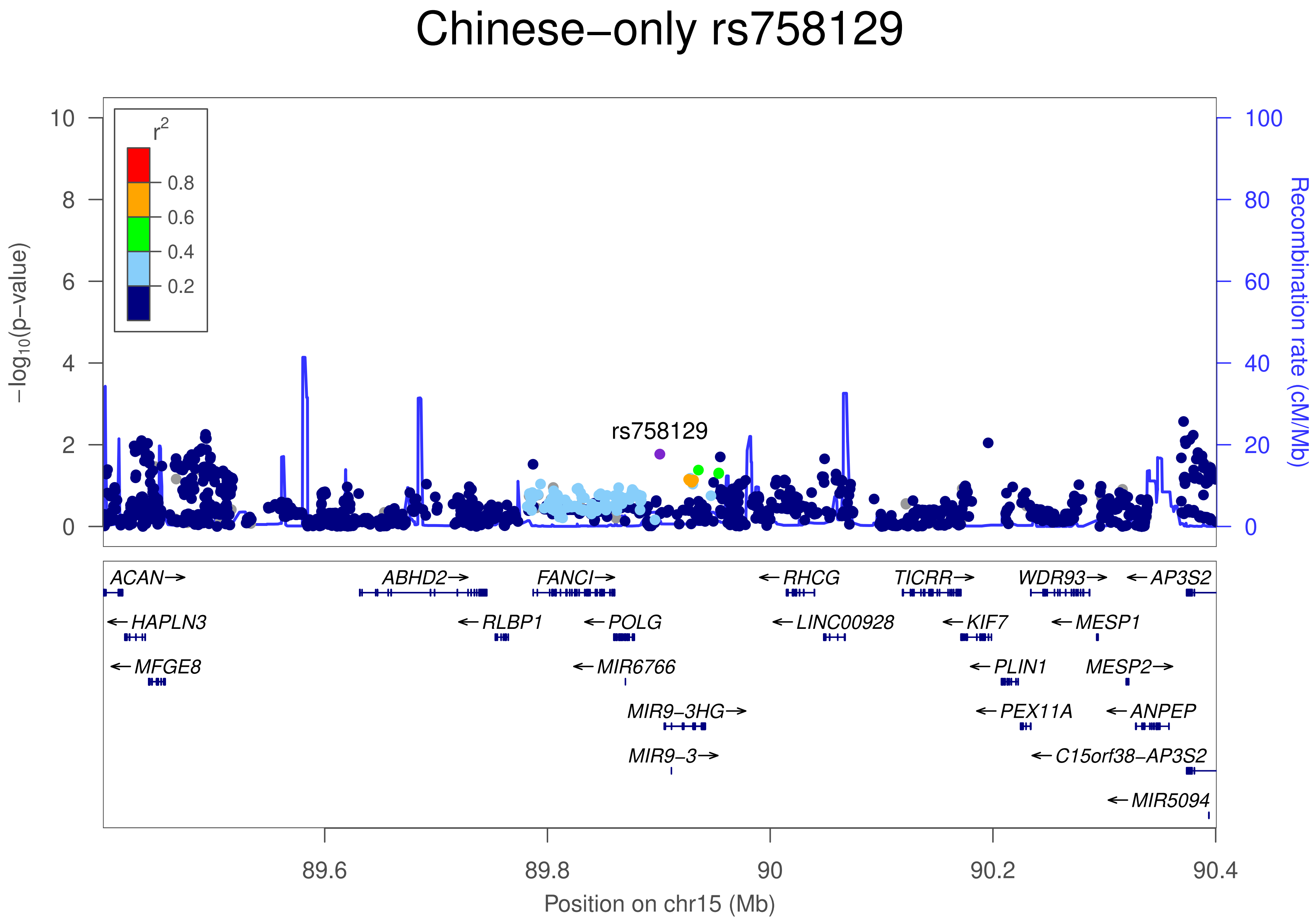
PGC2+Chinese rs783540




Chinese−only rs783540
r2
0.8
0.6
0.4
0.2
10
8
6
4
2
0
−log10(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
rs783540
←GOLGA6L10
←CPEB1
←ACTG1P17
←HOMER2
←BTBD1
←GOLGA2P10
CPEB1−AS1→
←FSD2
FAM103A1→
GOLGA6L17P→
←AP3B2
WHAMM→
←C15orf40
GOLGA6L9→
←LOC338963
MIR4515→
←RPS17
SNHG21→
ADAMTS7P1→
UBE2Q2P2→
SCARNA15→
LOC727751→
LOC102724034→
82.8
83
83.2
83.4
83.6
Position on chr15 (Mb)

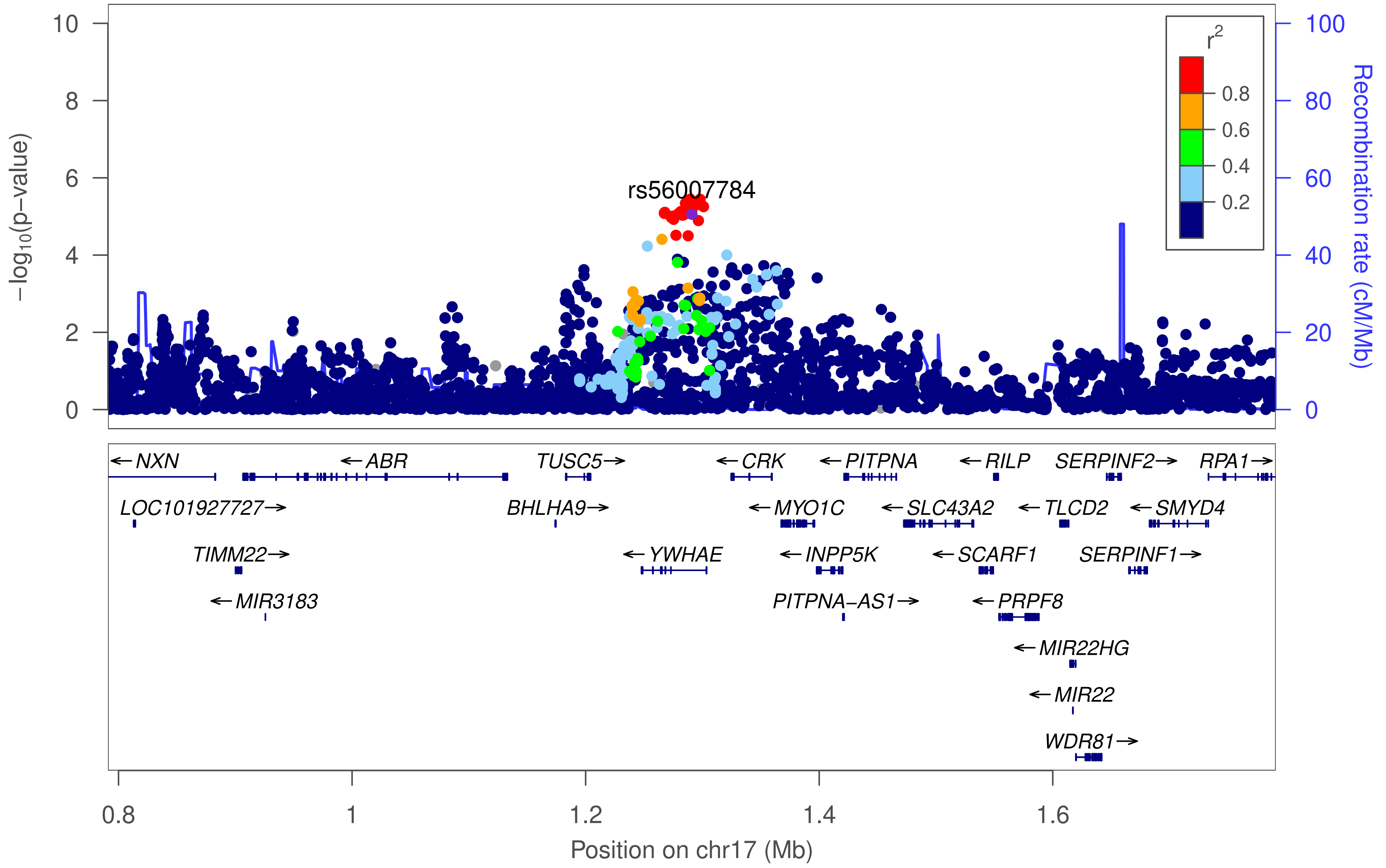

PGC2 rs758129
rs758129
−log10(p−value)
10
8
6
4
2
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
r2
0.8
0.6
0.4
0.2
ACAN→
ABHD2→
FANCI→
←RHCG
TICRR→
WDR93→
←AP3S2
←HAPLN3
←RLBP1
←POLG
←LINC00928
←KIF7
←MESP1
←MFGE8
←MIR6766
←PLIN1
MESP2→
MIR9−3HG→
←PEX11A
←ANPEP
MIR9−3→
←C15orf38−AP3S2
←MIR5094
89.6
89.8
90
90.2
90.4
Position on chr15 (Mb)

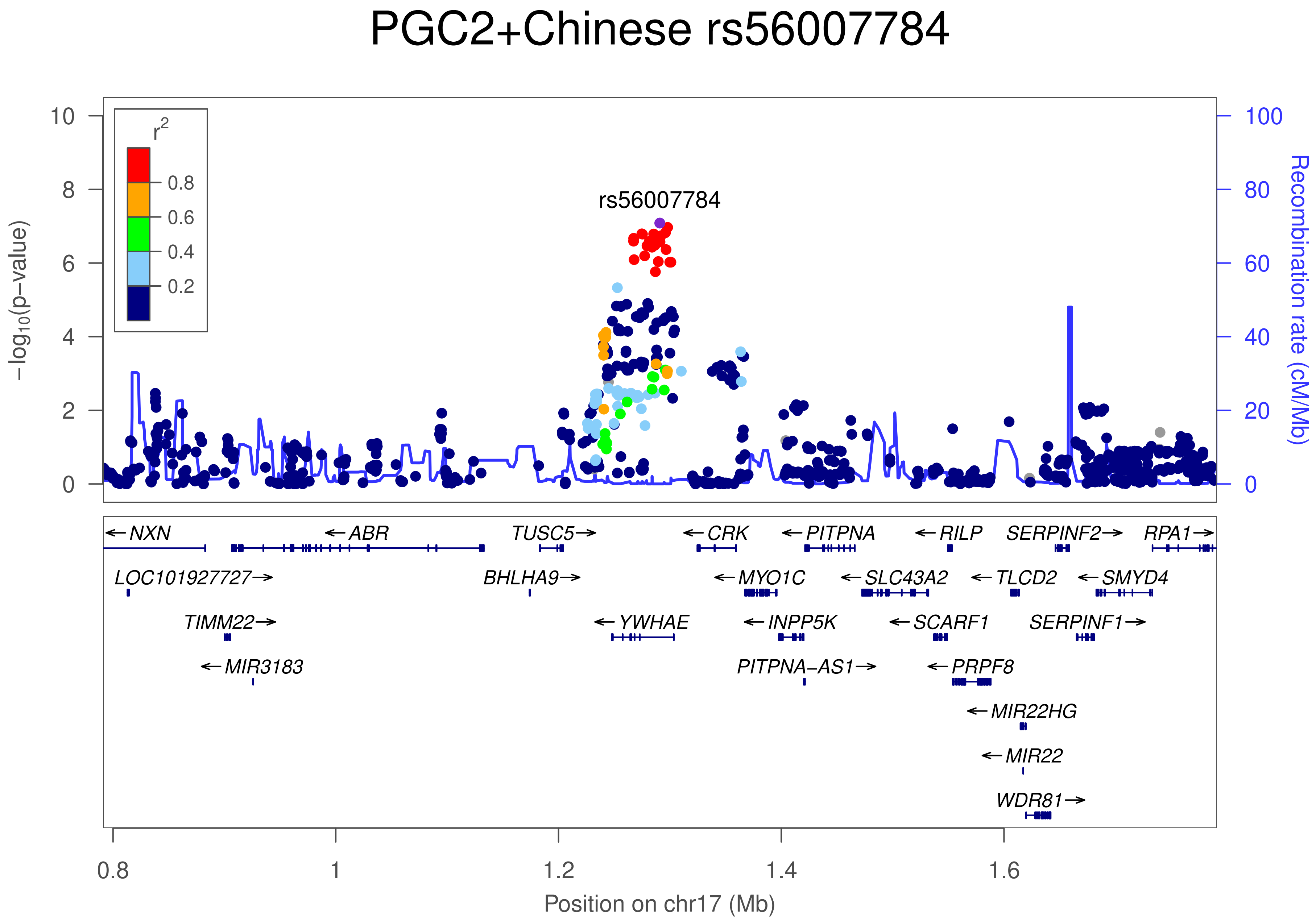

PGC2+Chinese rs758129
rs758129
−log10(p−value)
Recombination rate (cM/Mb)
r2
0.8
0.6
0.4
0.2
0
2
4
6
8
10
0
20
40
60
80
100
ACAN→
HAPLN3
MFGE8
ABHD2→
RLBP1
FANCI→
POLG
MIR6766
MIR9−3HG→
MIR9−3→
RHCG
LINC00928
TICRR→
KIF7
PLIN1
PEX11A
WDR93→
MESP1
MESP2→
ANPEP
C15orf38−AP3S2
MIR5094
AP3S2
89.6
89.8
90
90.2
90.4
Position on chr15 (Mb)

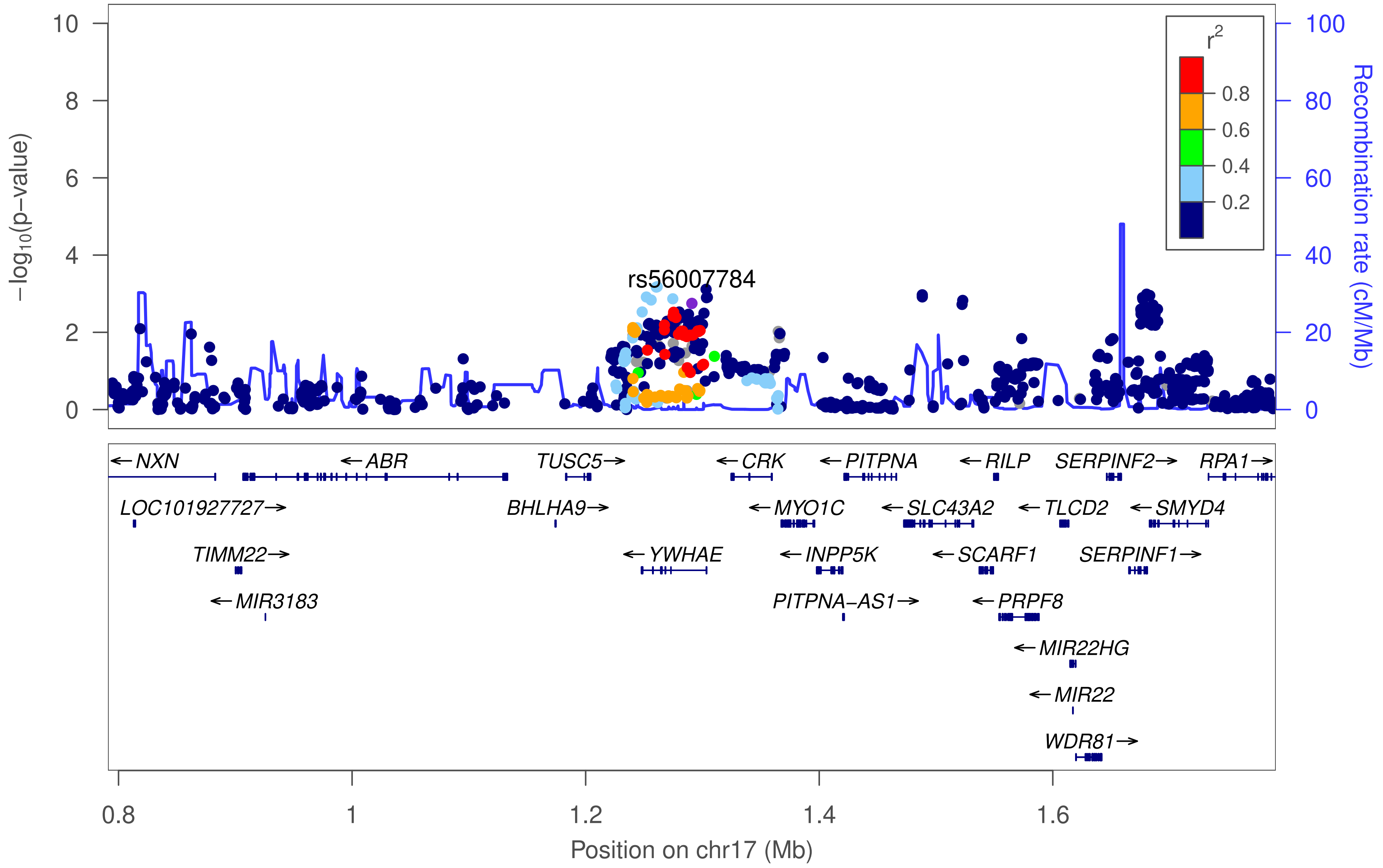


Chinese−only rs758129
r2
0.8
0.6
0.4
0.2
−log10(p−value)
10
8
6
4
2
0
rs758129
100
80
60
40
20
0
Recombination rate (cM/Mb)
ACAN→
ABHD2→
FANCI→
←RHCG
TICRR→
WDR93→
←AP3S2
←HAPLN3
←RLBP1
←POLG
←LINC00928
←KIF7
←MESP1
←MFGE8
←MIR6766
←PLIN1
MESP2→
MIR9−3HG→
←PEX11A
←ANPEP
MIR9−3→
←C15orf38−AP3S2
←MIR5094
89.6
89.8
90
90.2
90.4
Position on chr15 (Mb)

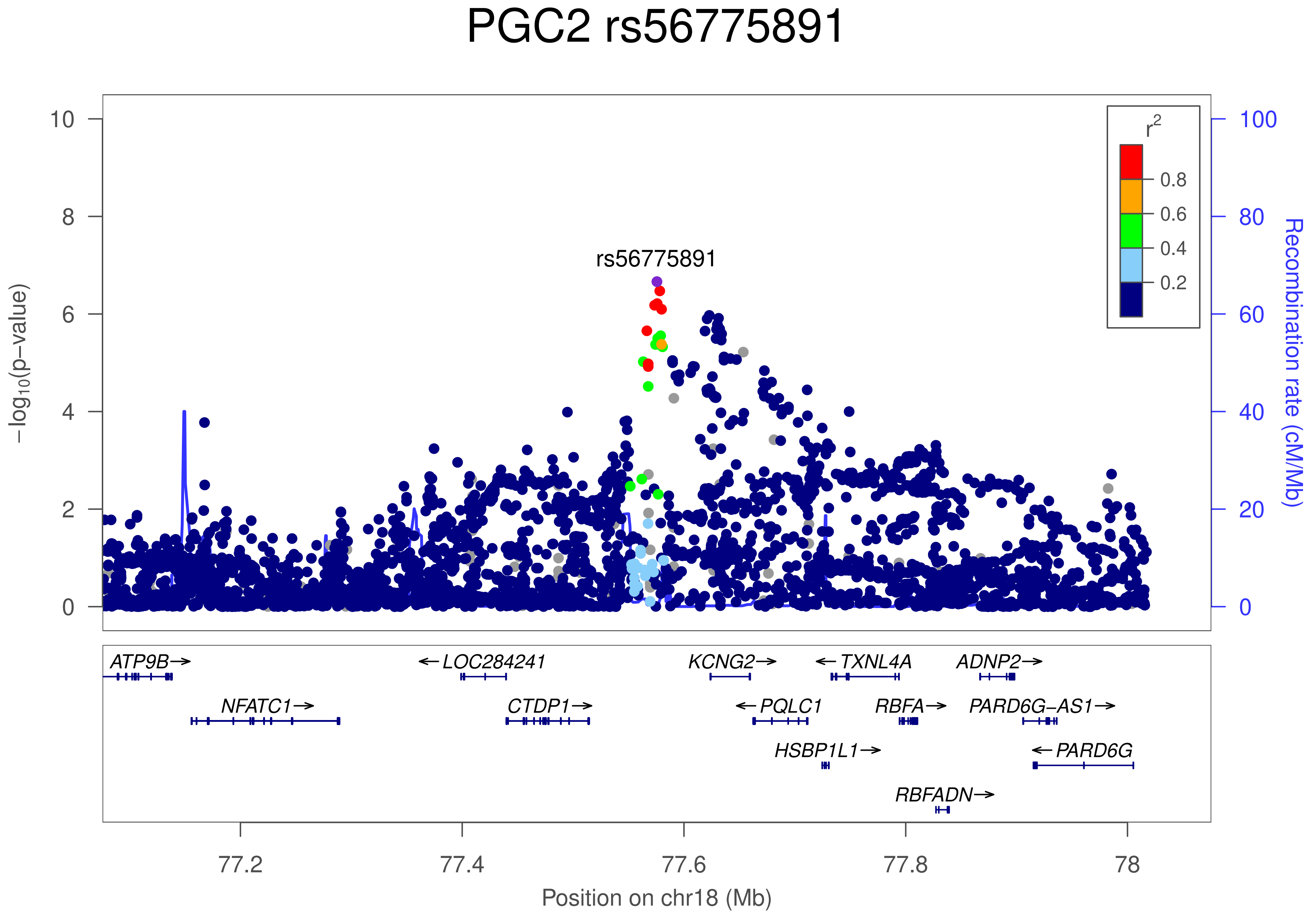
PGC2 rs56007784



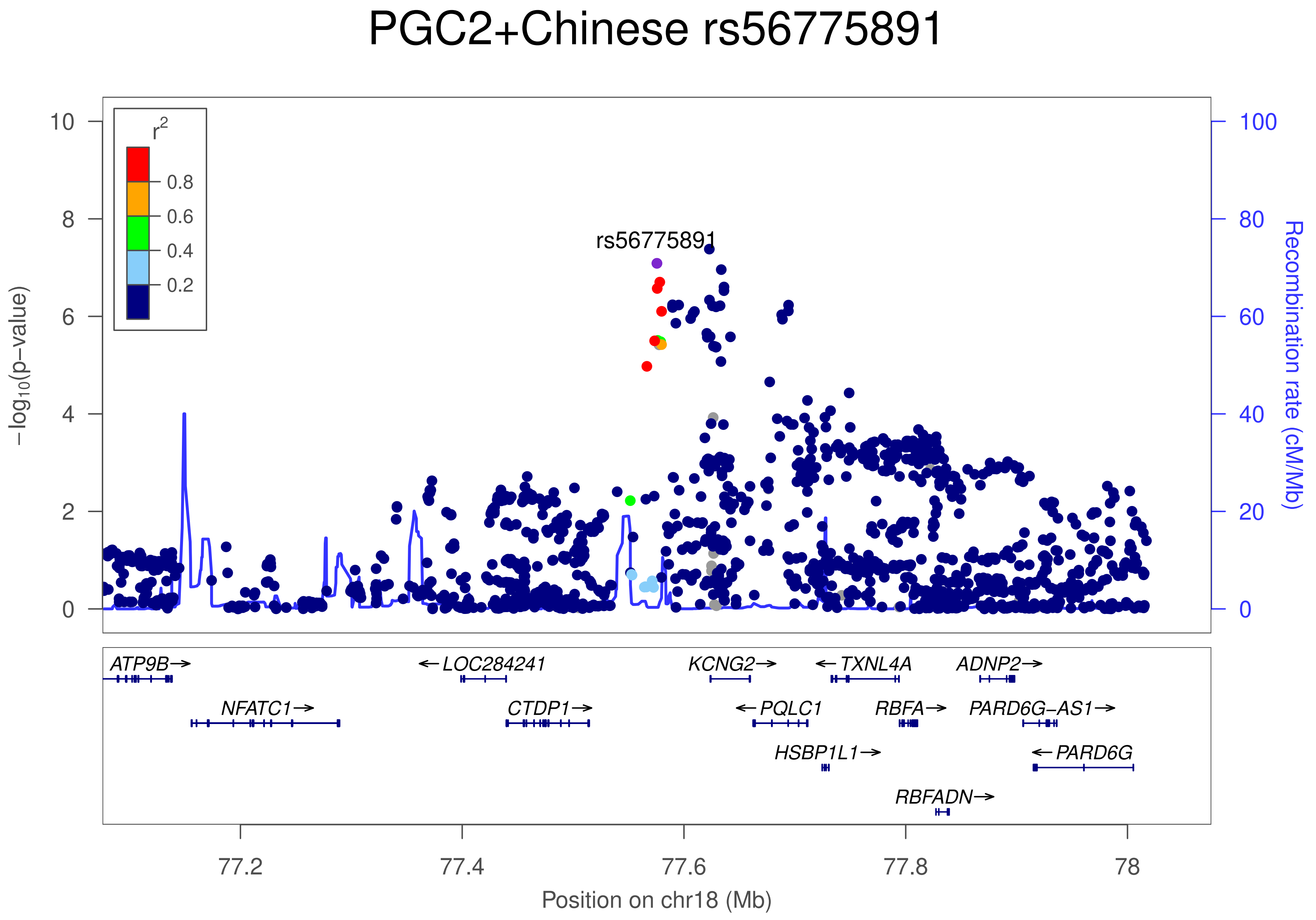

PGC2+Chinese rs56007784
rs56007784
r²
0.8
0.6
0.4
0.2
−log10(p−value)
10
8
6
4
2
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
←NXN
←ABR
TUSC5→
←CRK
←PITPNA
←RILP
SERPINF2→
RPA1→
LOC101927727→
BHLHA9→
←MYO1C
←SLC43A2
←TLCD2
←SMYD4
TIMM22→
←YWHAE
←INPP5K
←SCARF1
SERPINF1→
←MIR3183
PITPNA−AS1→
←PRPF8
←MIR22HG
←MIR22
WDR81→
0.8
1
1.2
1.4
1.6
Position on chr17 (Mb)



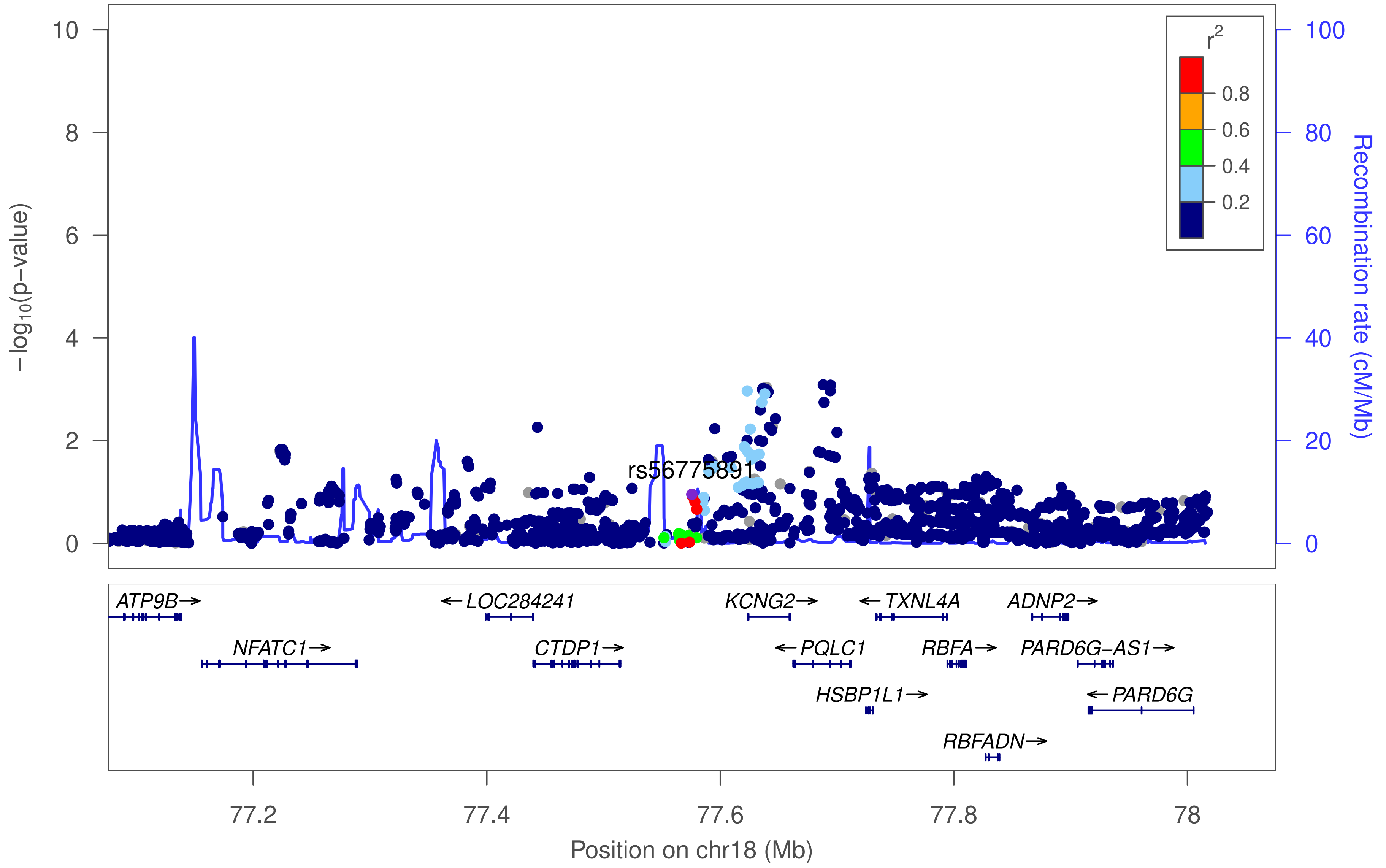
Chinese–only rs56007784

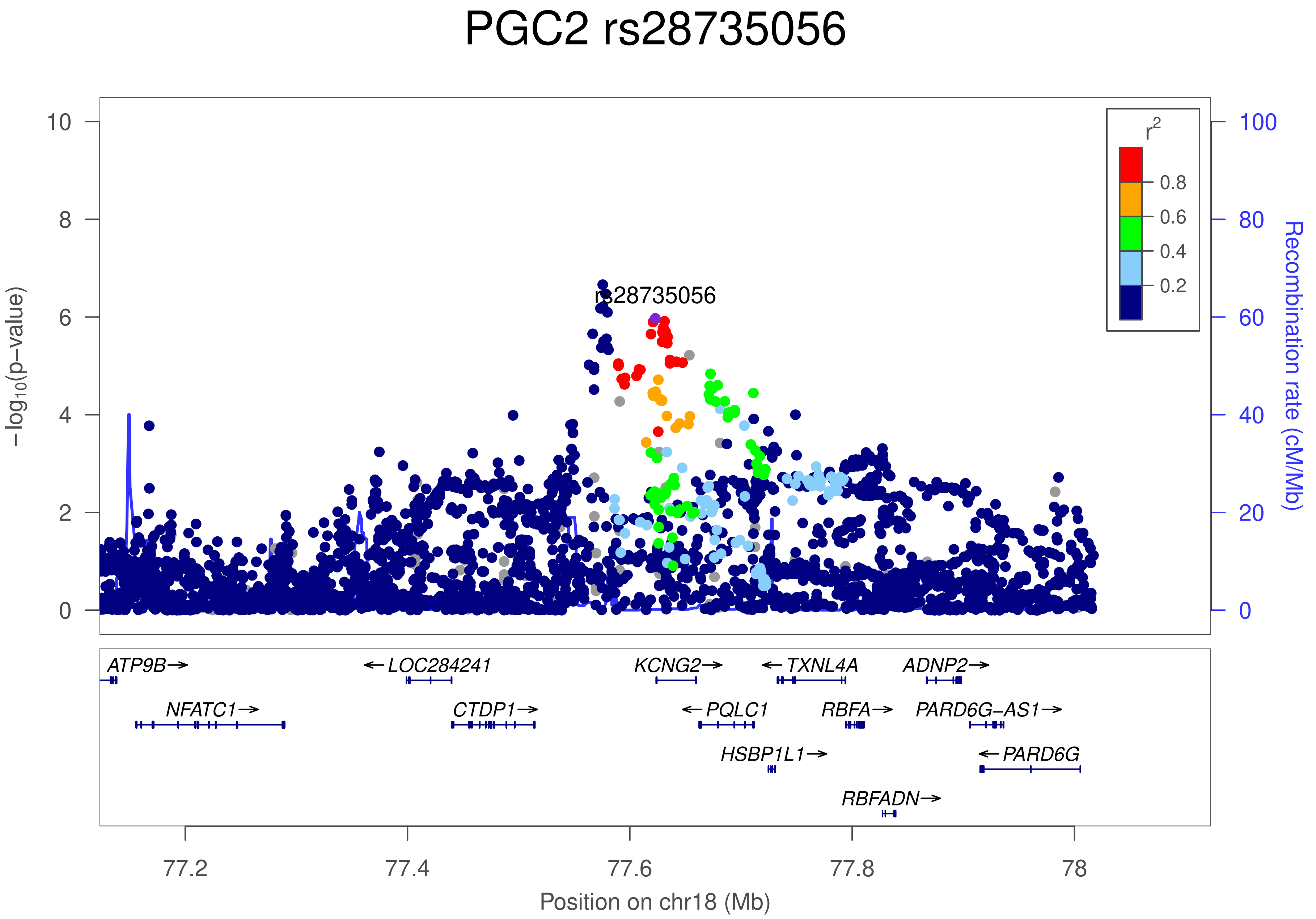


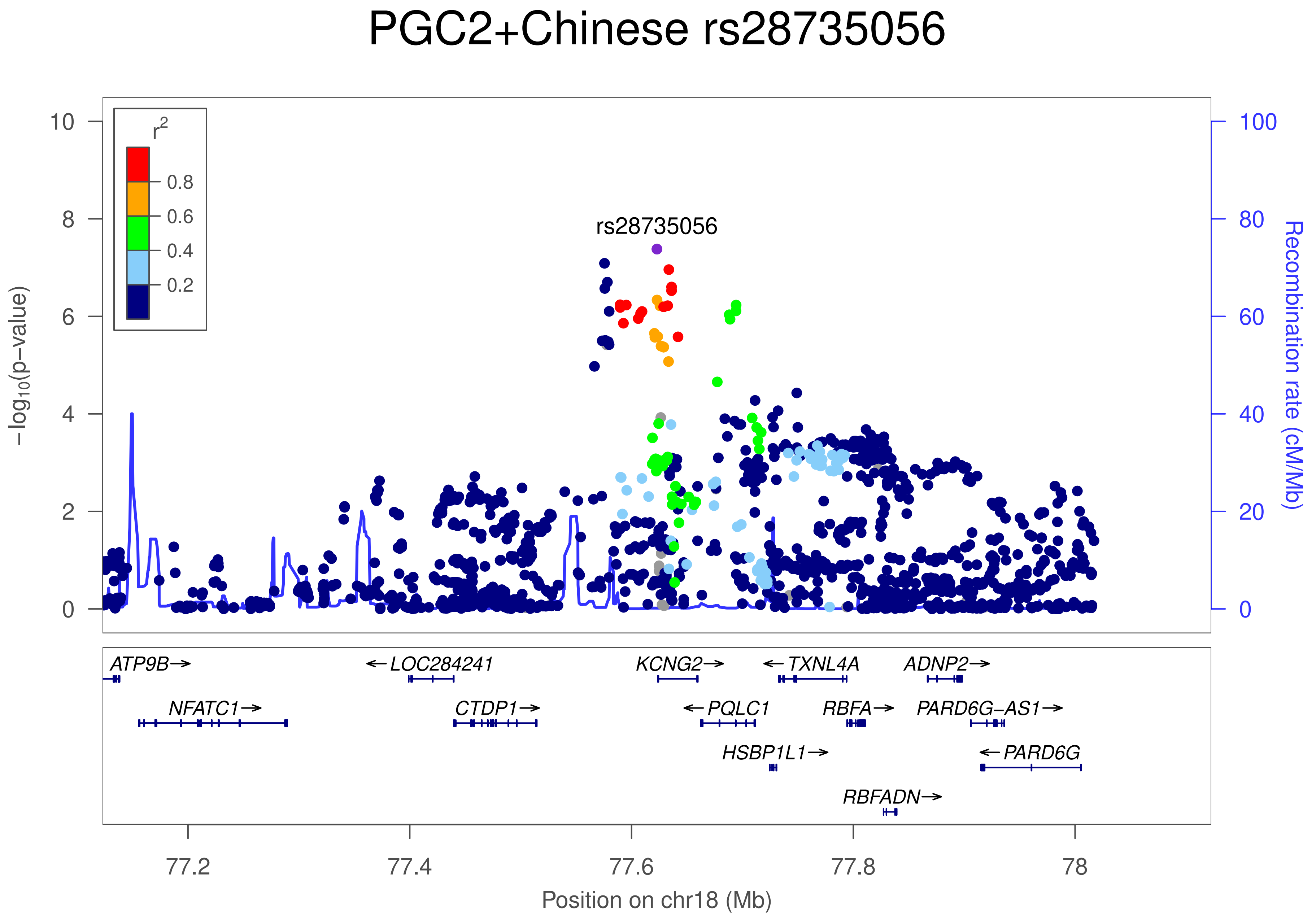
PGC2 rs56775891
rs56775891
−log10(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
r2
0.2
0.4
0.6
0.8
ATP9B→
←LOC284241
KCNG2→
←TXNL4A
ADNP2→
NFATC1→
CTDP1→
←PQLC1
RBFA→
PARD6G−AS1→
HSBP1L1→
←PARD6G
RBFADN→
77.2
77.4
77.6
77.8
78
Position on chr18 (Mb)

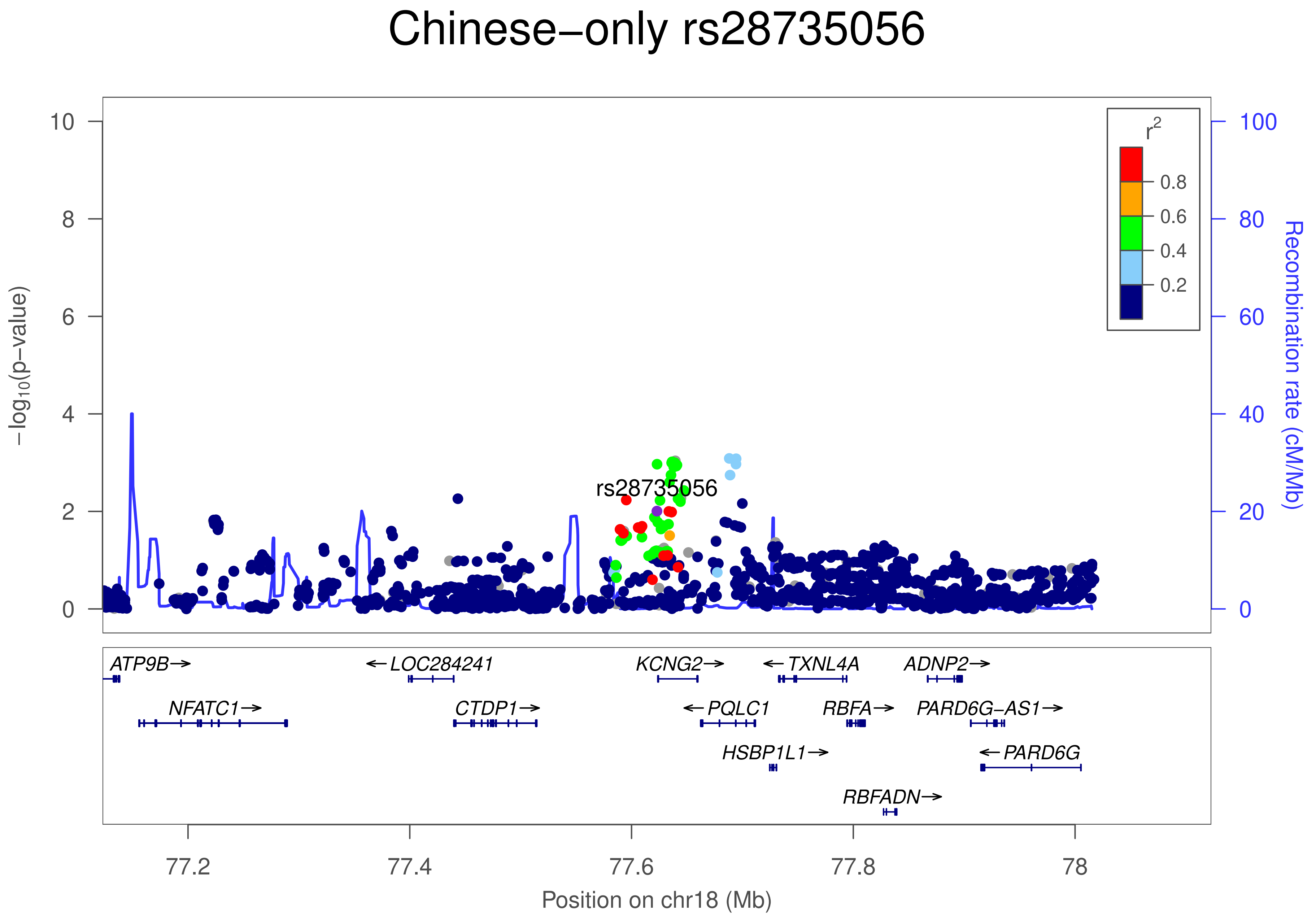

PGC2+Chinese rs56775891
r2
0.8
0.6
0.4
0.2
rs56775891
−log10(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
ATP9B→
NFATC1→
←LOC284241
CTDP1→
KCNG2→
←PQLC1
HSBP1L1→
←TXNL4A
RBFA→
RBFADN→
ADNP2→
PARD6G−AS1→
←PARD6G
77.2
77.4
77.6
77.8
78
Position on chr18 (Mb)

Chinese–only rs56775891

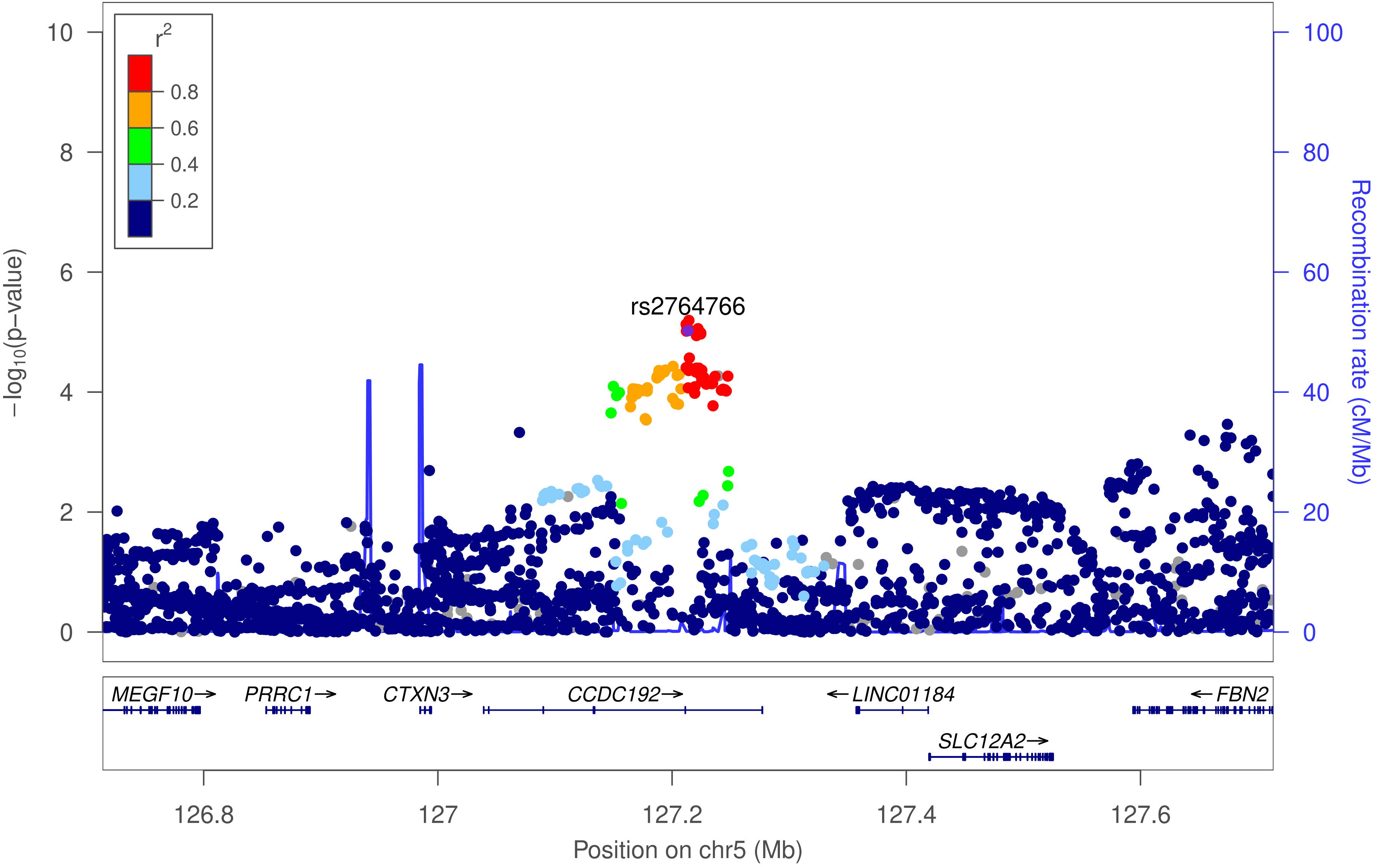



PGC2 rs28735056
rs28735056
−log10(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
r2
0.8
0.6
0.4
0.2
ATP9B→
NFATC1→
←LOC284241
CTDP1→
KCNG2→
←PQLC1
←TXNL4A
HSBP1L1→
RBFA→
RBFADN→
ADNP2→
PARD6G−AS1→
←PARD6G
77.2
77.4
77.6
77.8
78
Position on chr18 (Mb)

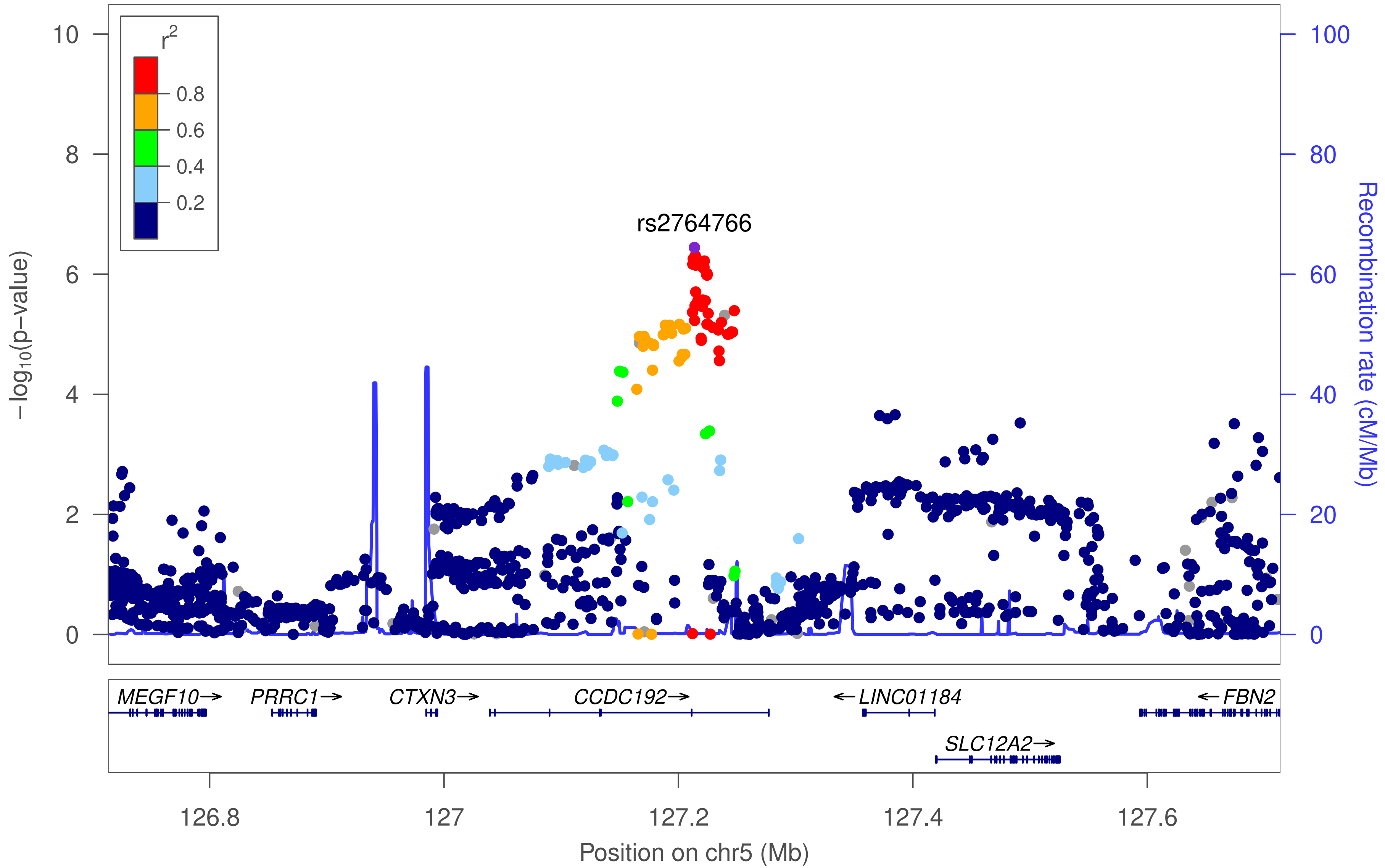

PGC2+Chinese rs28735056
r2
0.8
0.6
0.4
0.2
rs28735056
−log10(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
ATP9B→
←LOC284241
KCNG2→
←TXNL4A
ADNP2→
NFATC1→
CTDP1→
←PQLC1
RBFA→
PARD6G−AS1→
HSBP1L1→
←PARD6G
RBFADN→
77.2
77.4
77.6
77.8
78
Position on chr18 (Mb)

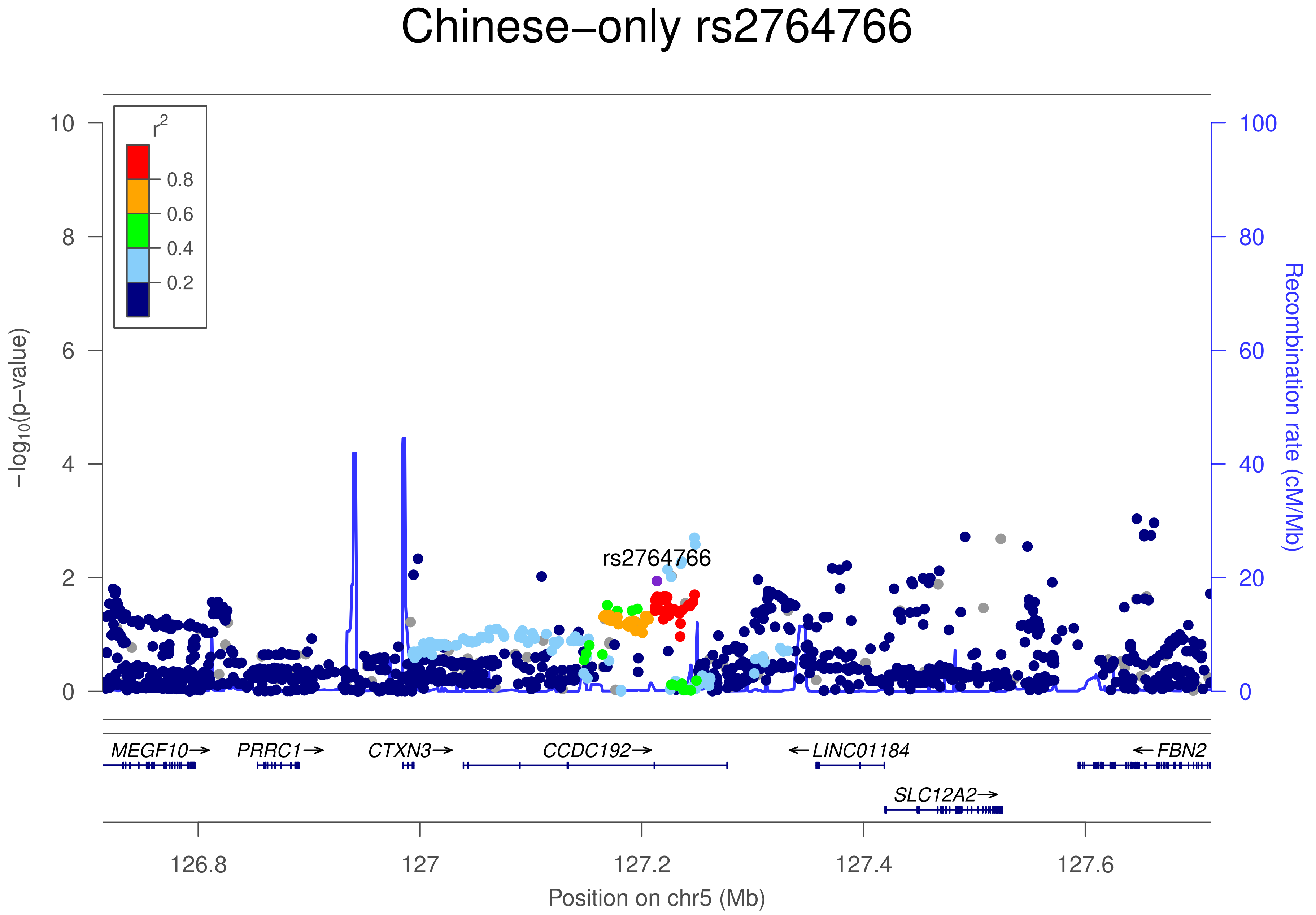

Chinese–only rs28735056
−log₁₀(p−value)
10
8
6
4
2
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
r²
0.8
0.6
0.4
0.2
rs28735056
ATP9B→
←LOC284241
KCNG2→
←TXNL4A
ADNP2→
NFATC1→
CTDP1→
←PQLC1
RBFA→
PARD6G−AS1→
HSBP1L1→
←PARD6G
RBFADN→
77.2
77.4
77.6
77.8
78
Position on chr18 (Mb)

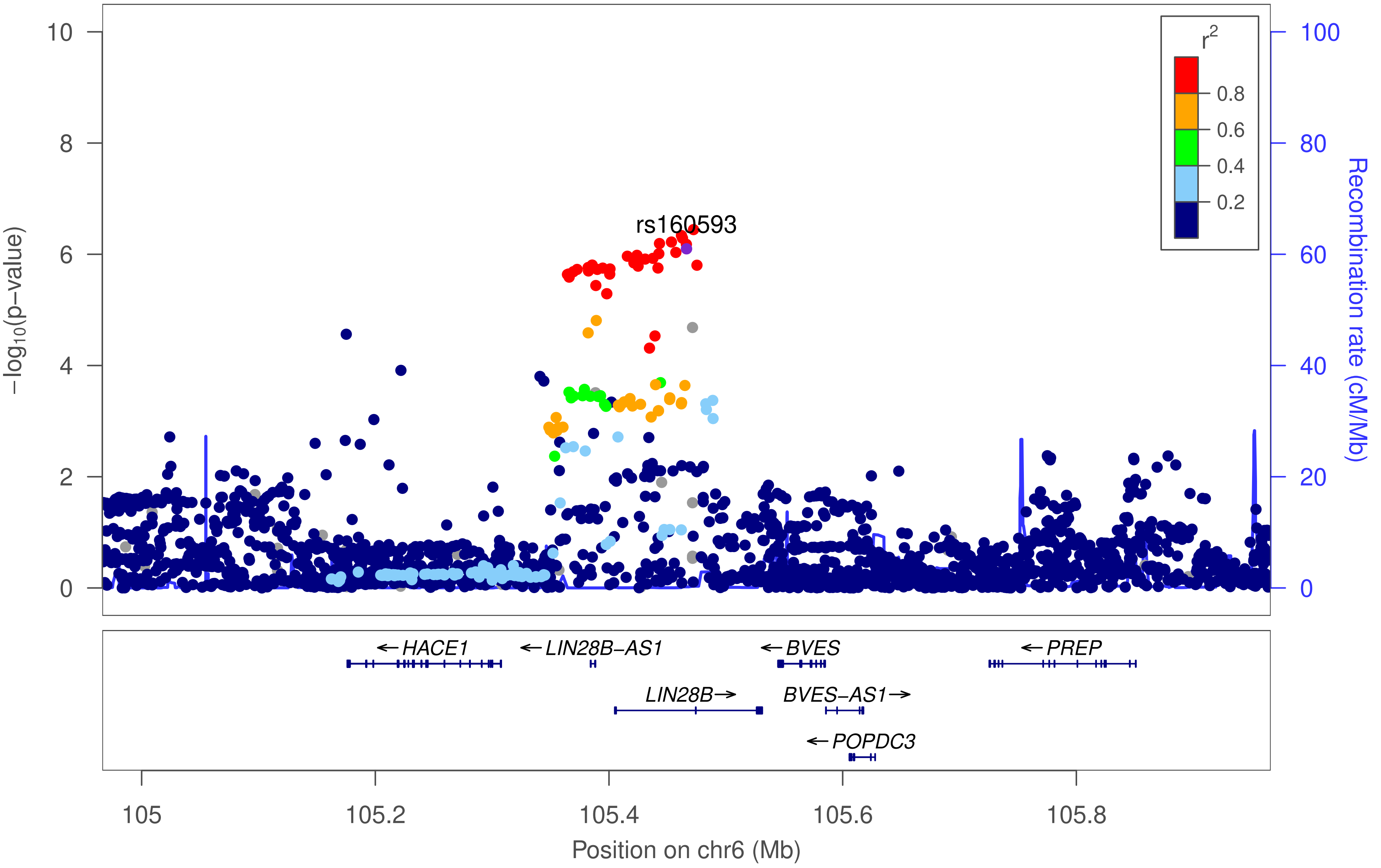
PGC2 rs2764766



PGC2+Chinese rs2764766

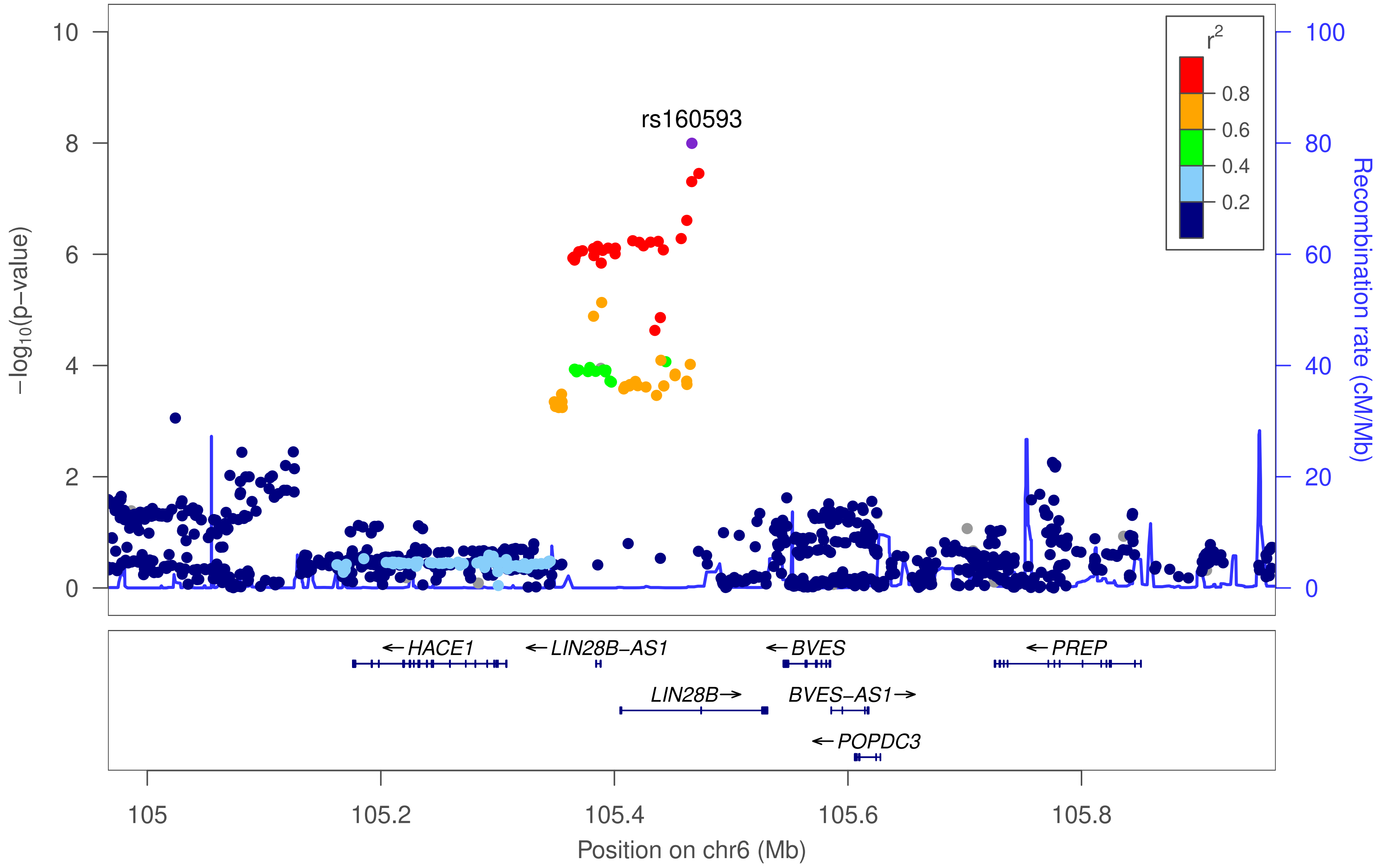



Chinese−only rs2764766
−log10(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
r2
0.8
0.6
0.4
0.2
rs2764766
MEGF10→
PRRC1→
CTXN3→
CCDC192→
←LINC01184
SLC12A2→
←FBN2
126.8
127
127.2
127.4
127.6
Position on chr5 (Mb)

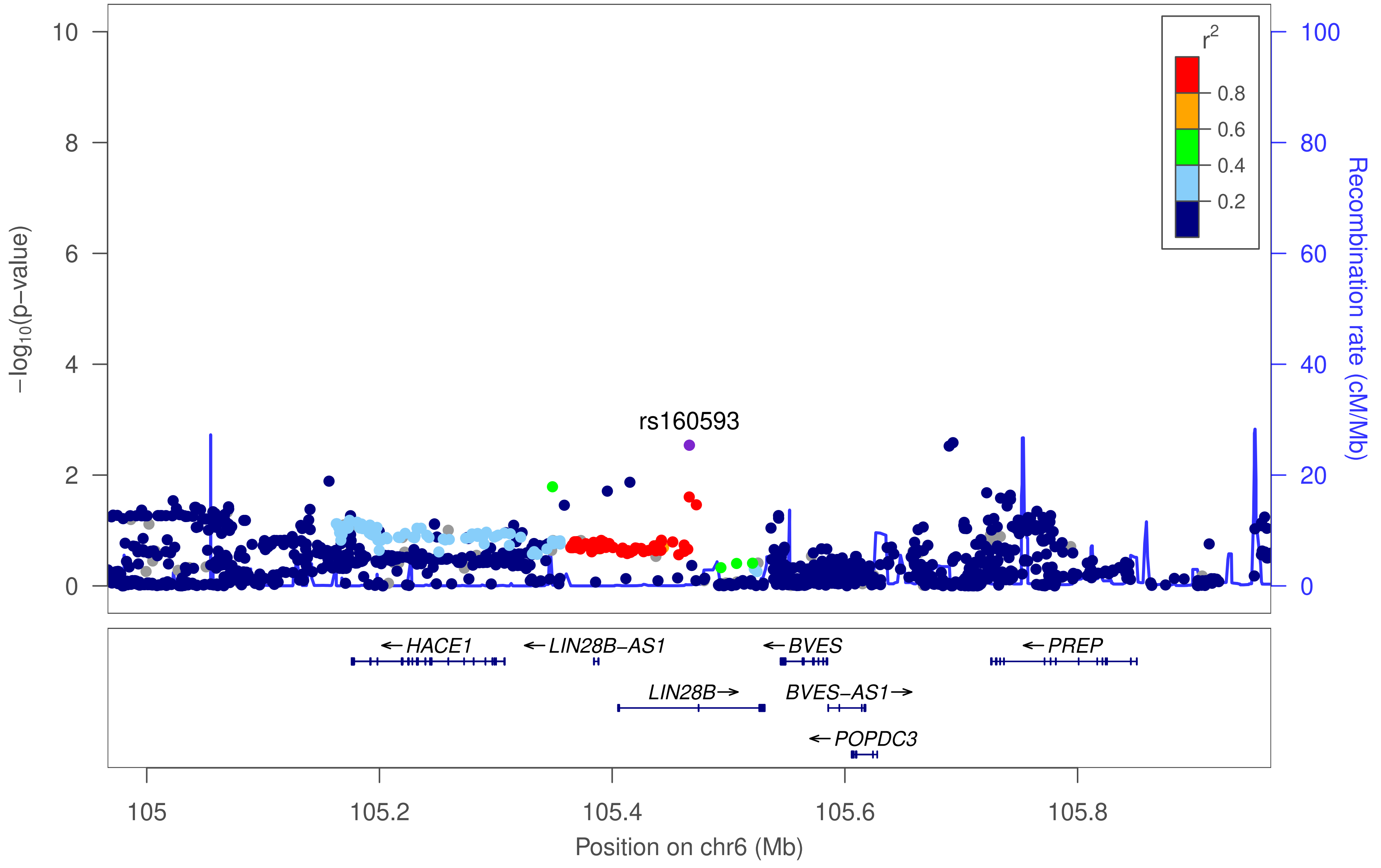


PGC2 rs160593

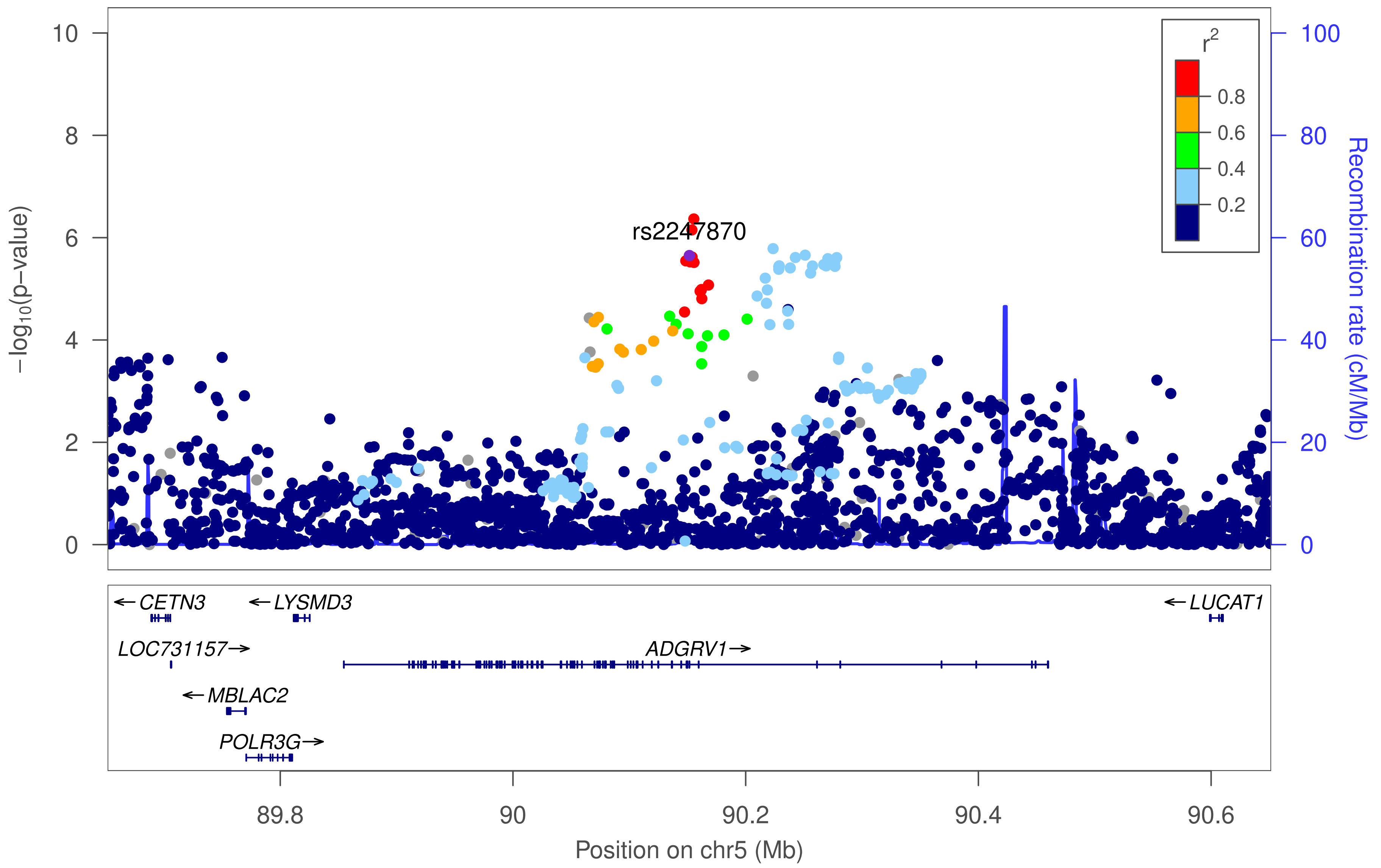
PGC2+Chinese rs160593

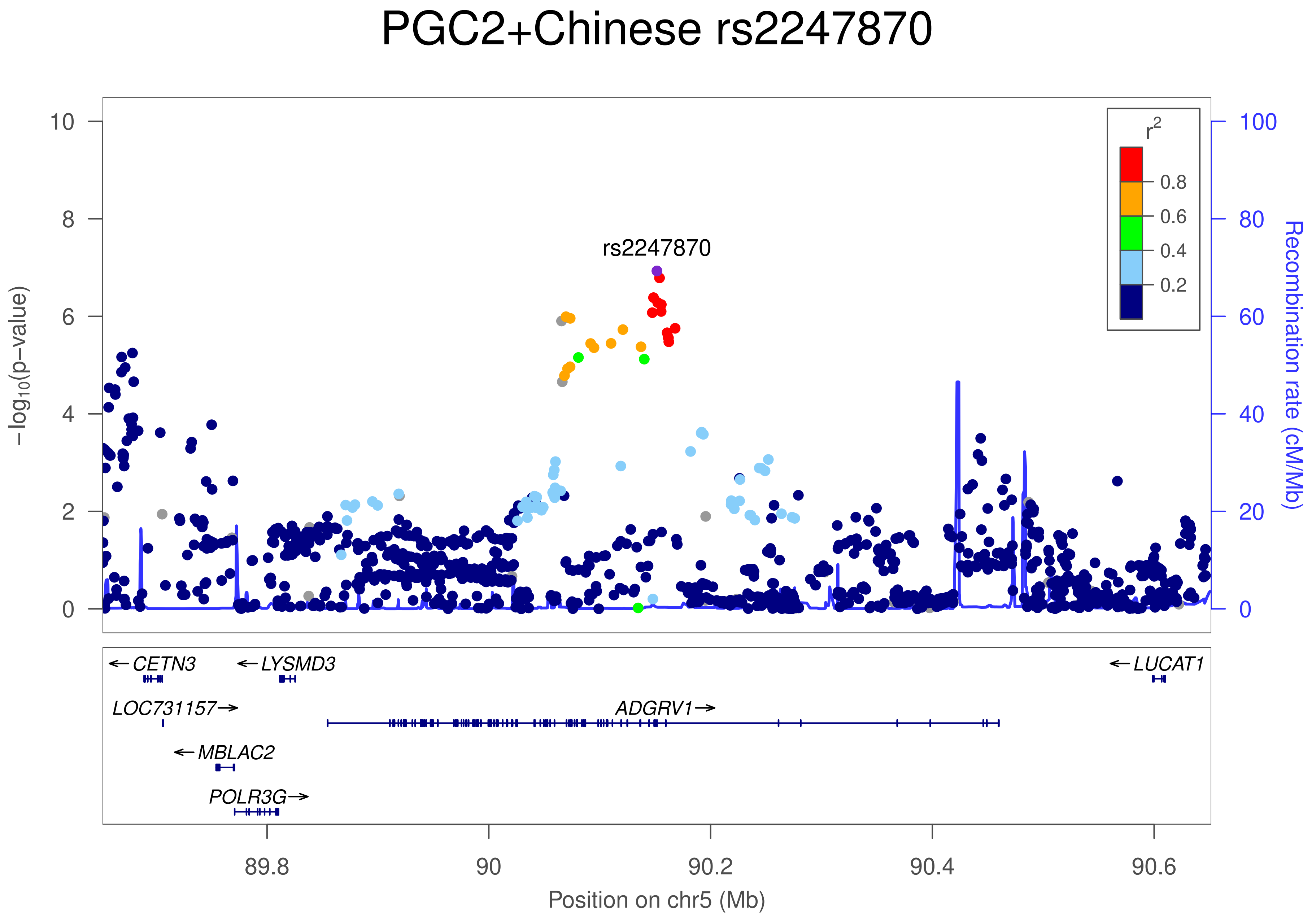


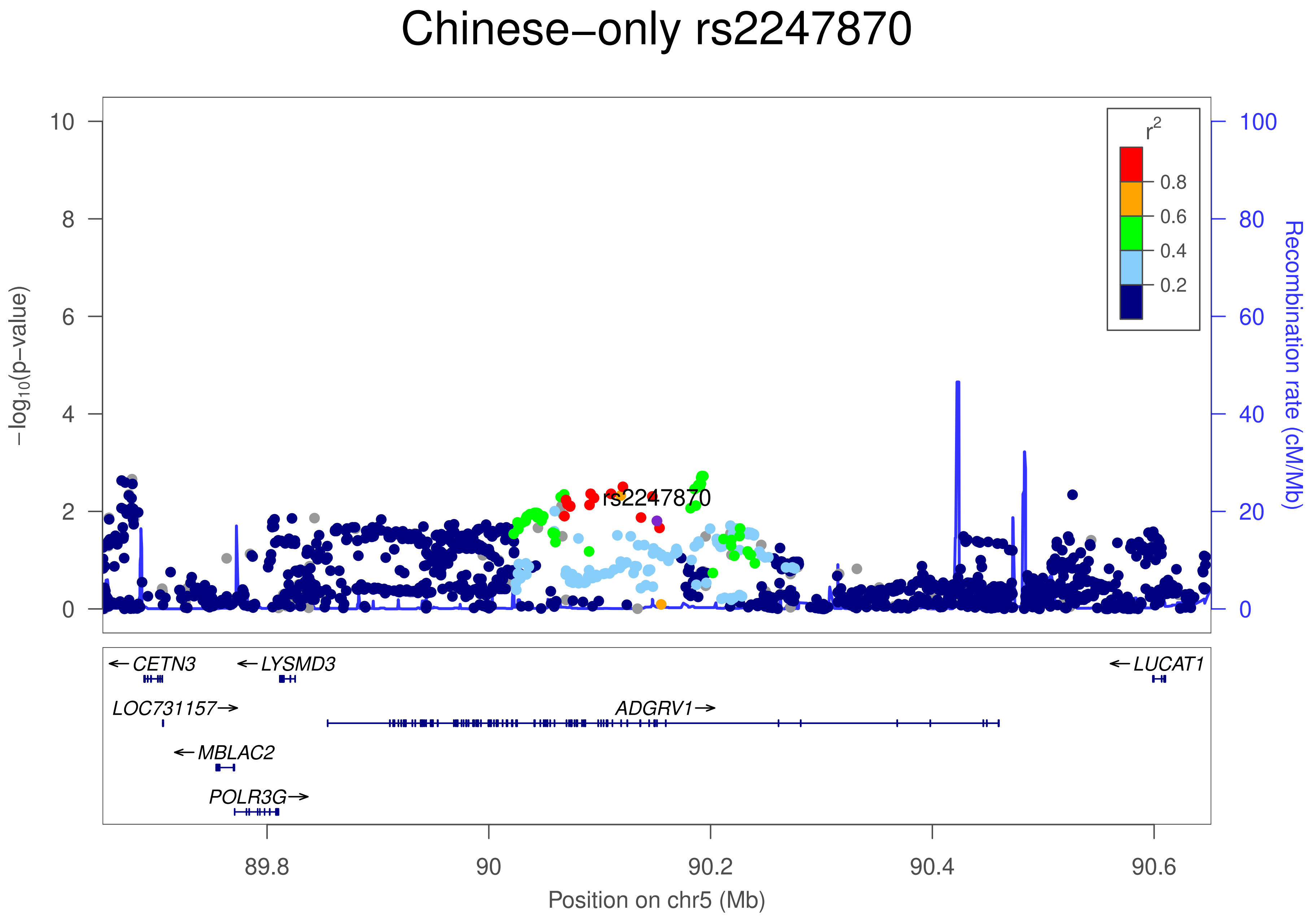
Chinese−only rs160593

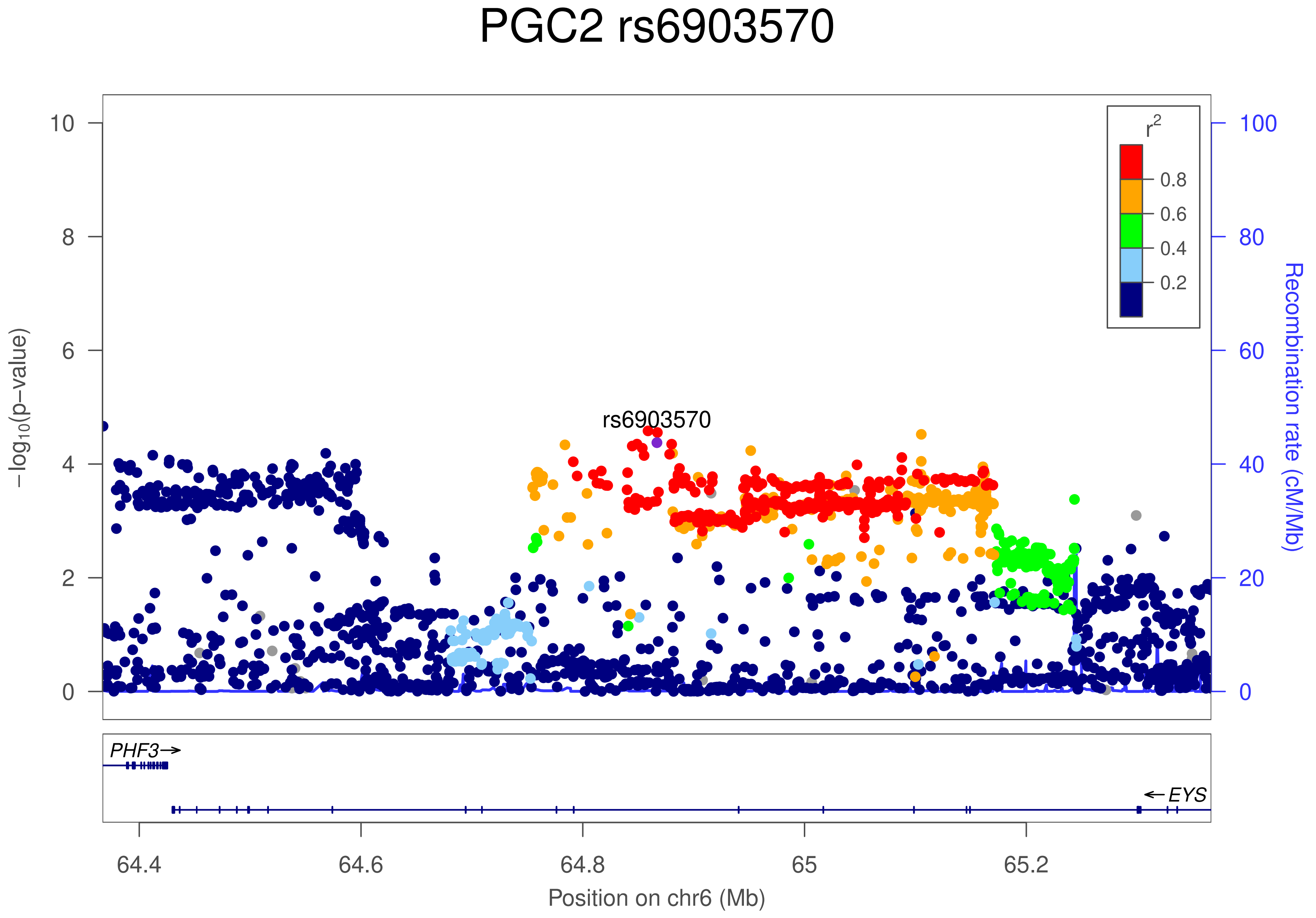


PGC2 rs2247870

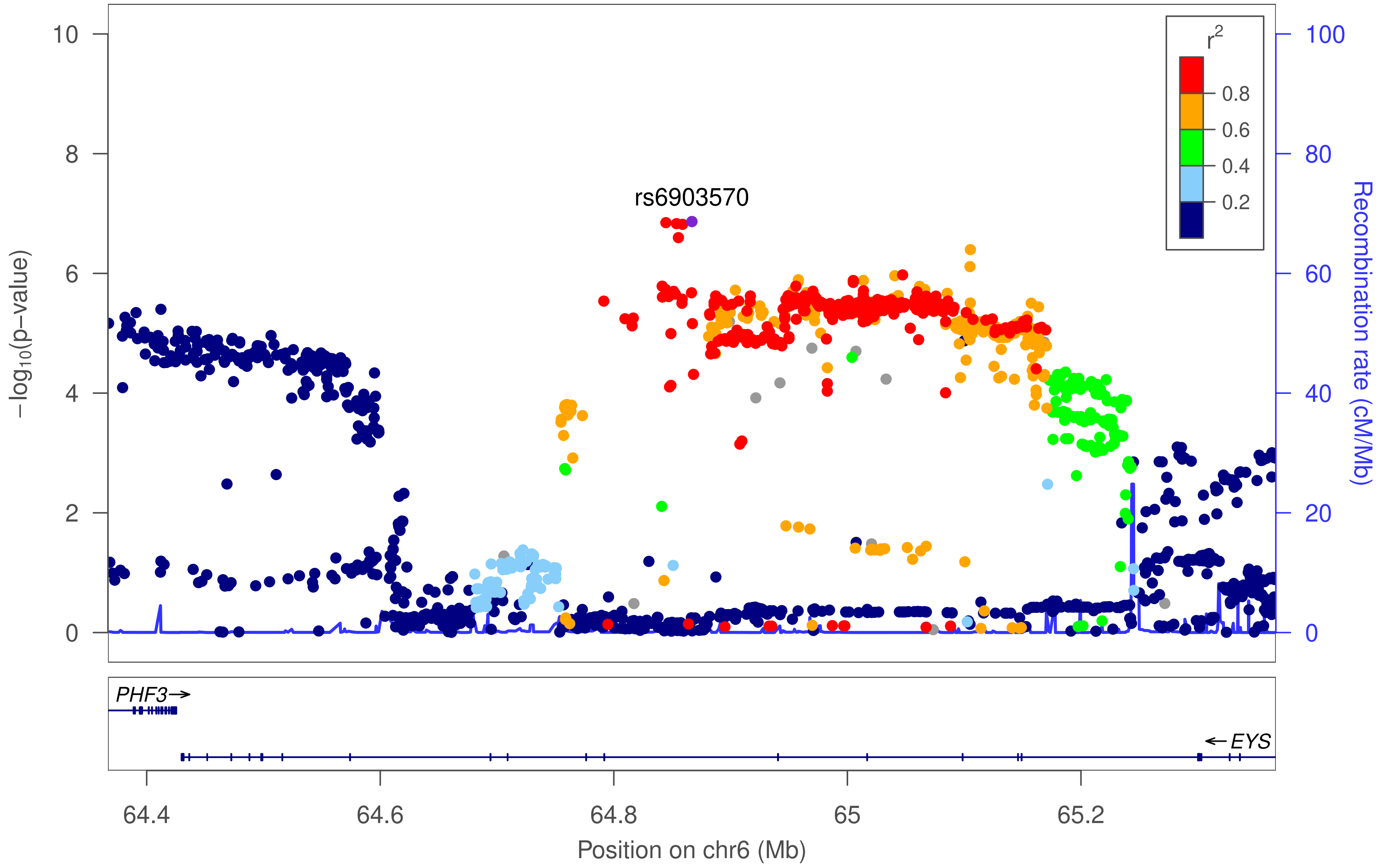



PGC2+Chinese rs2247870
rs2247870
r²
0.8
0.6
0.4
0.2
10
8
6
4
2
0
−log₁₀(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
← CETN3
← LYSMD3
← LUCAT1
LOC731157 →
ADGRV1 →
← MBLAC2
POLR3G →
89.8
90
90.2
90.4
90.6
Position on chr5 (Mb)

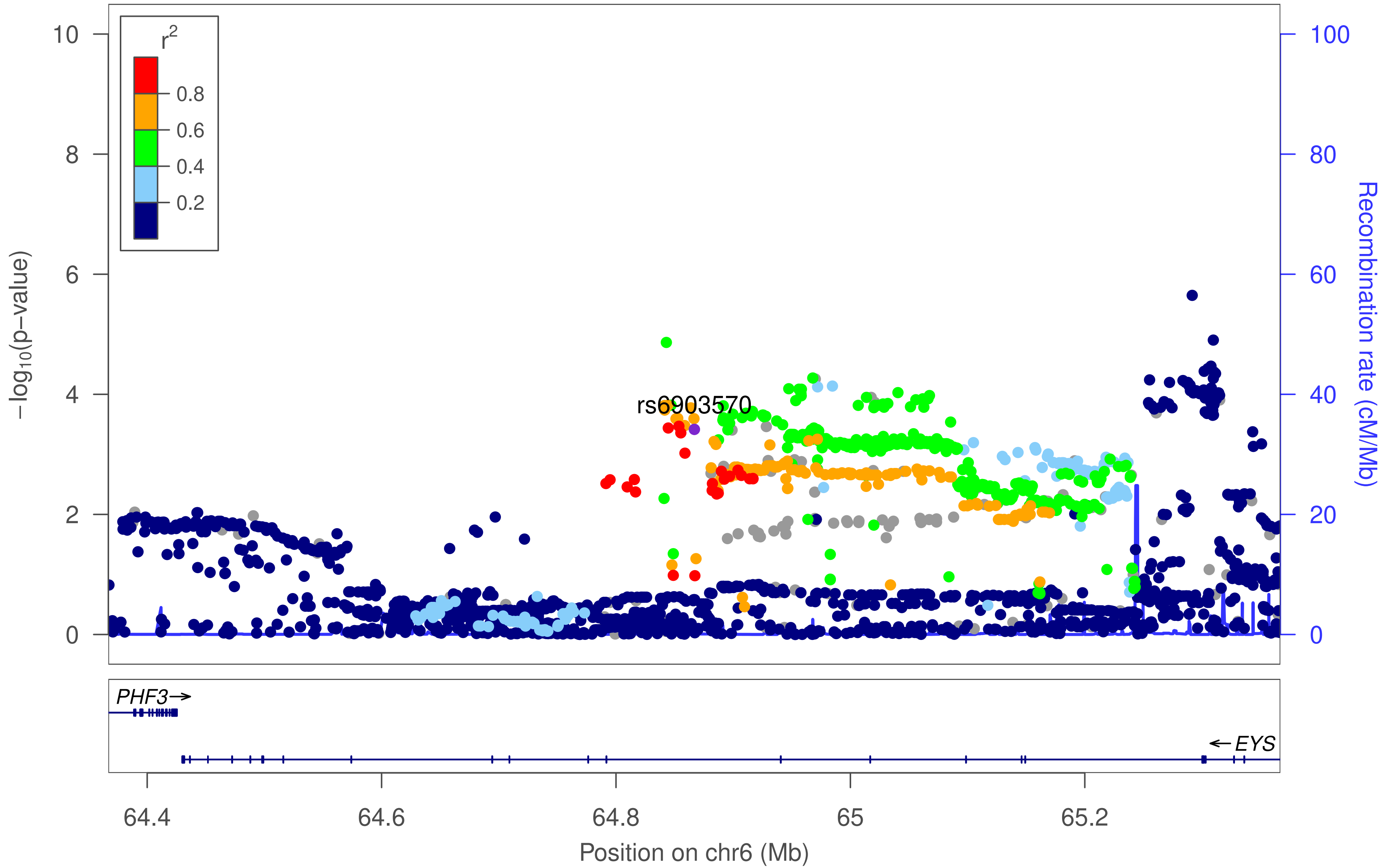

Chinese–only rs2247870
r²
0.8
0.6
0.4
0.2
−log₁₀(p−value)
10
8
6
4
2
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
rs2247870
← CETN3
← LYSMD3
← LUCAT1
LOC731157 →
ADGRV1 →
← MBLAC2
POLR3G →
89.8
90
90.2
90.4
90.6
Position on chr5 (Mb)

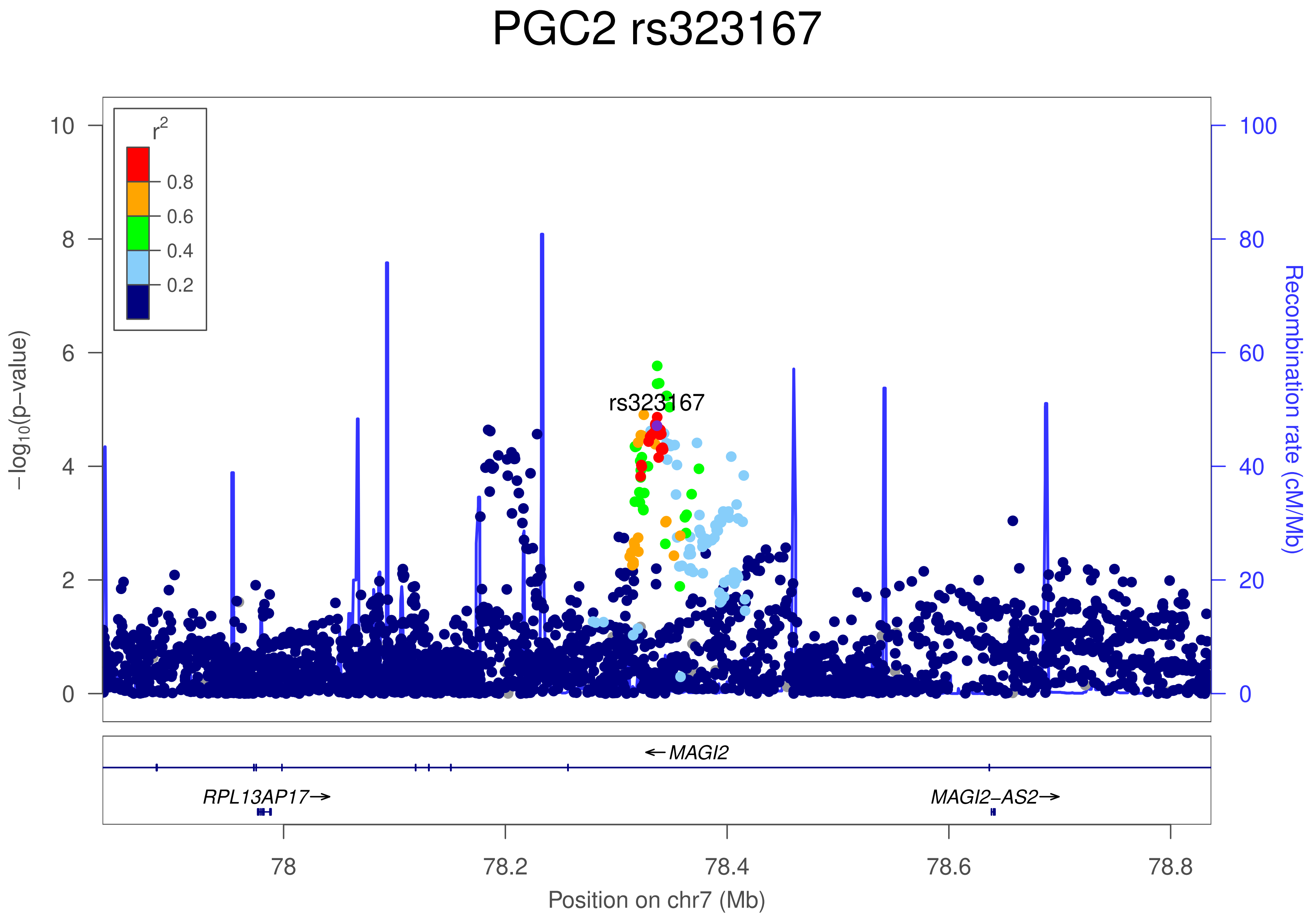

PGC2 rs6903570
rs6903570
−log10(p−value)
10
8
6
4
2
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
r2
0.8
0.6
0.4
0.2
PHF3→
←EYS
64.4
64.6
64.8
65
65.2
Position on chr6 (Mb)

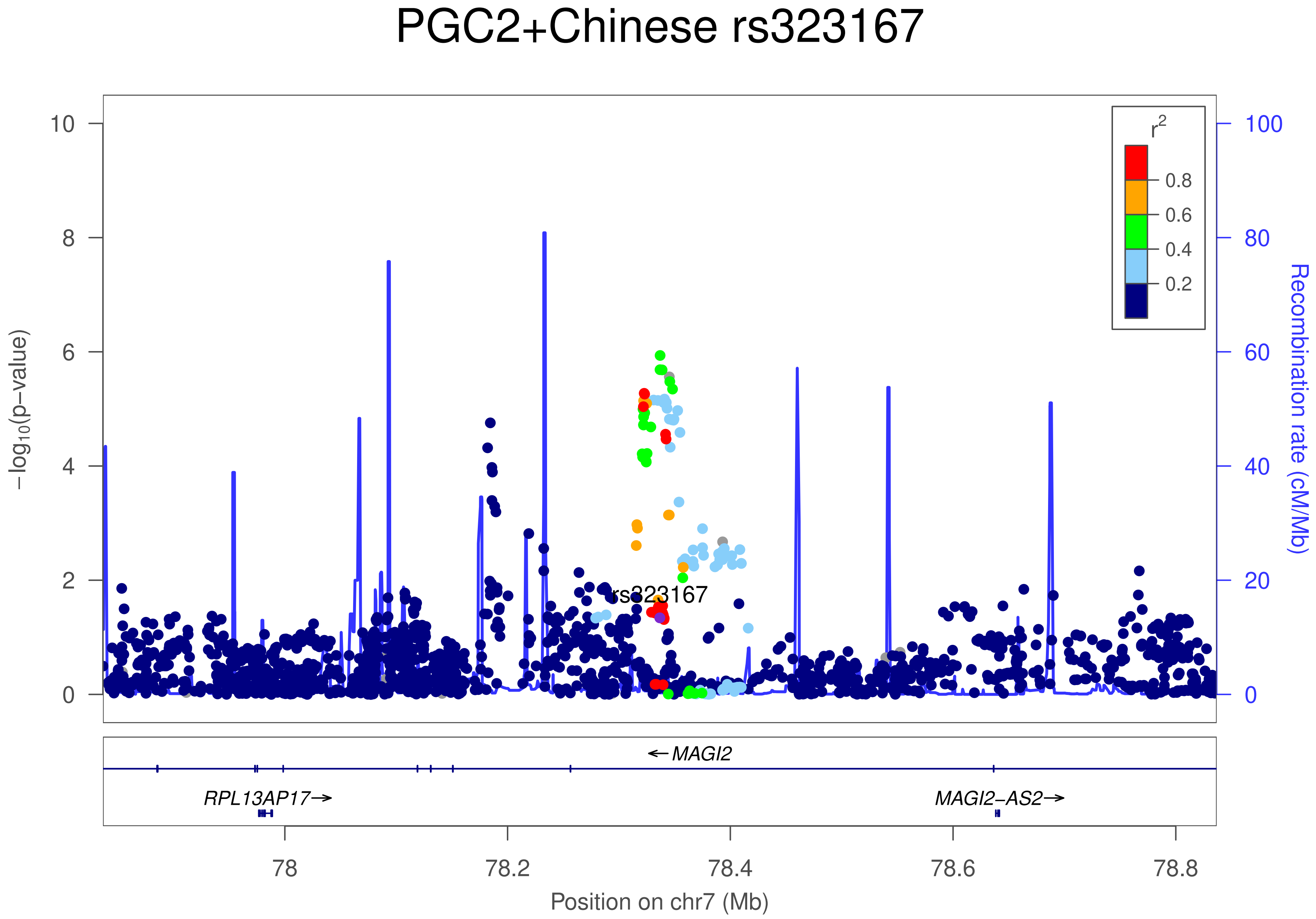
PGC2+Chinese rs6903570

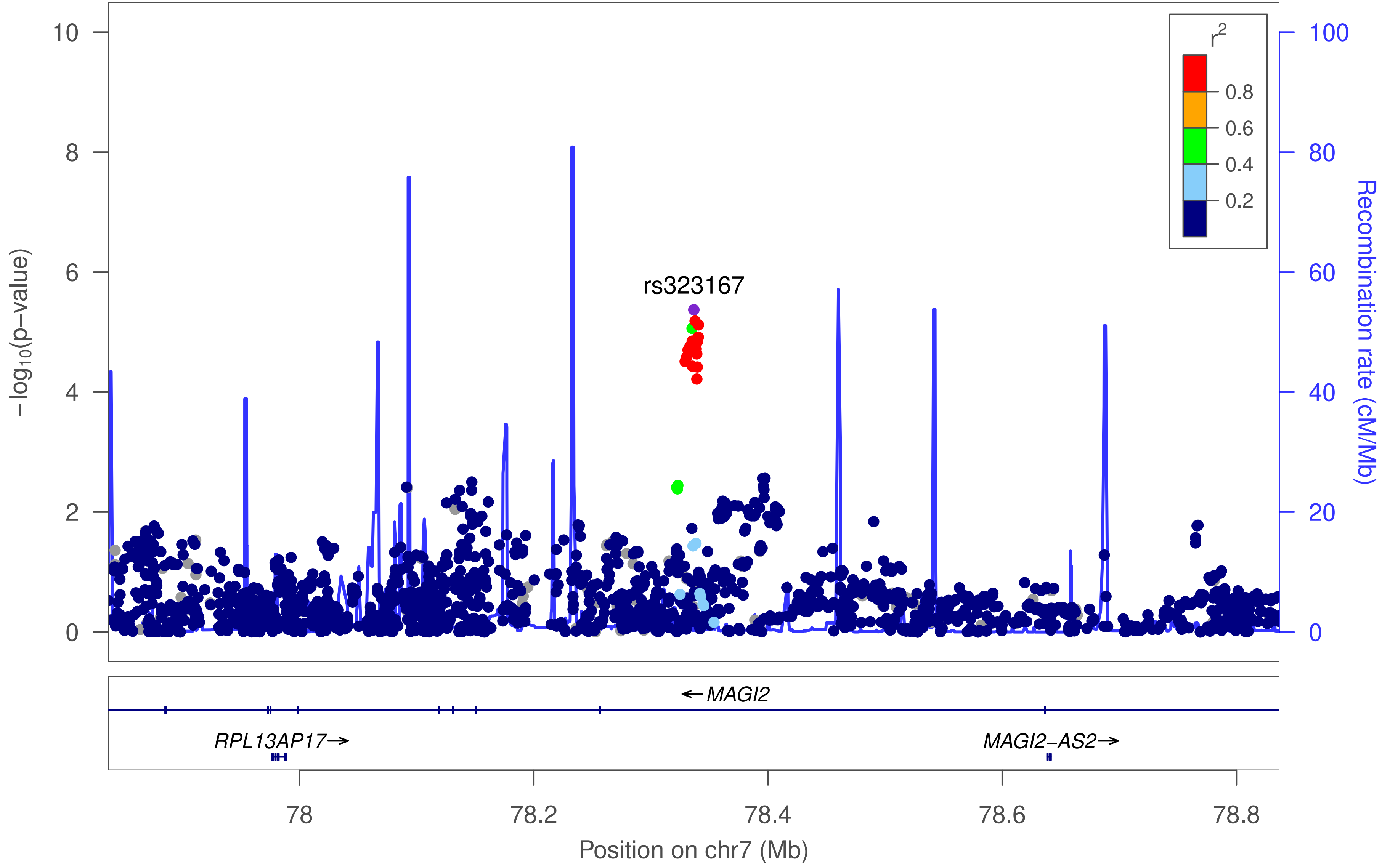


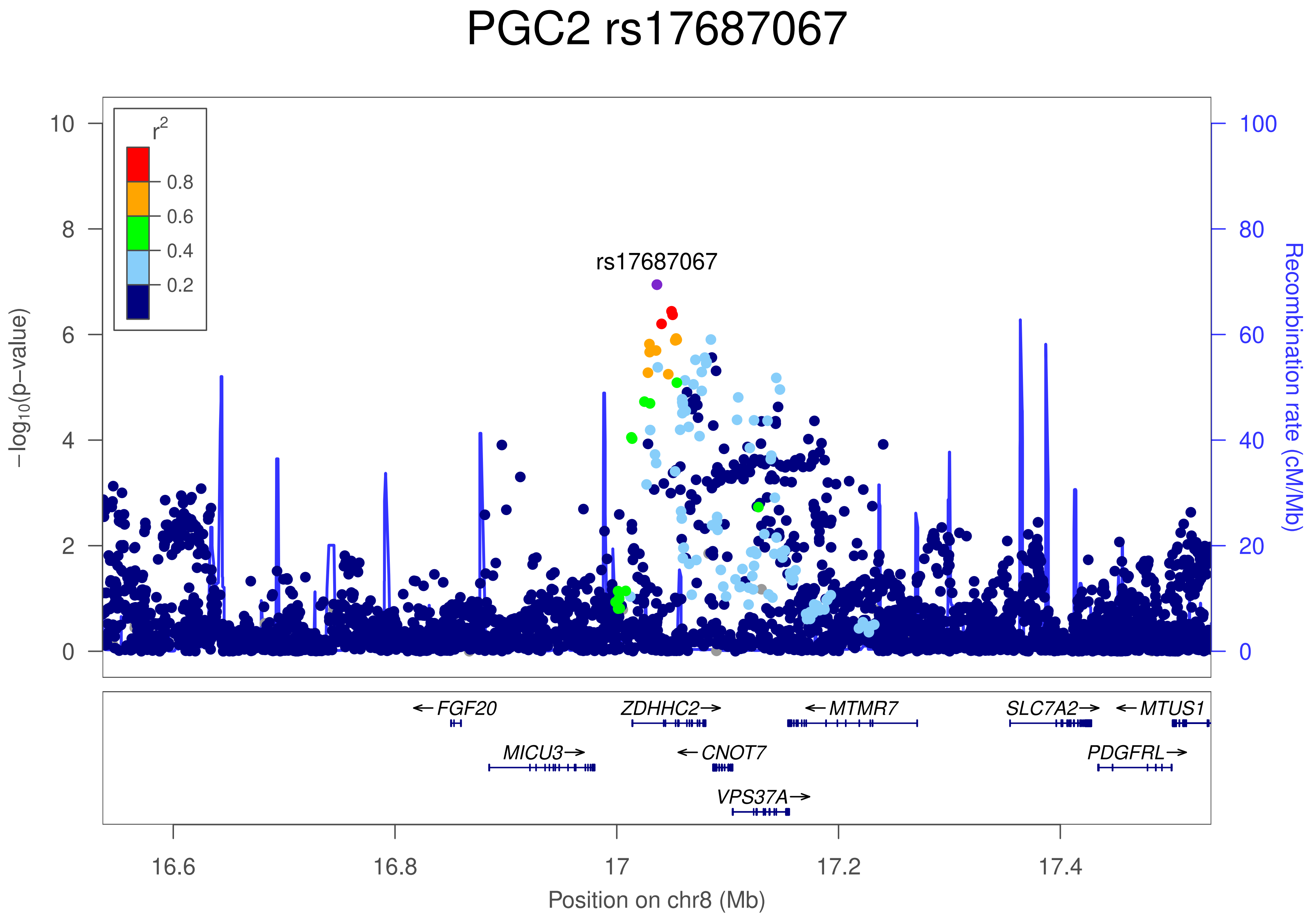
Chinese−only rs6903570

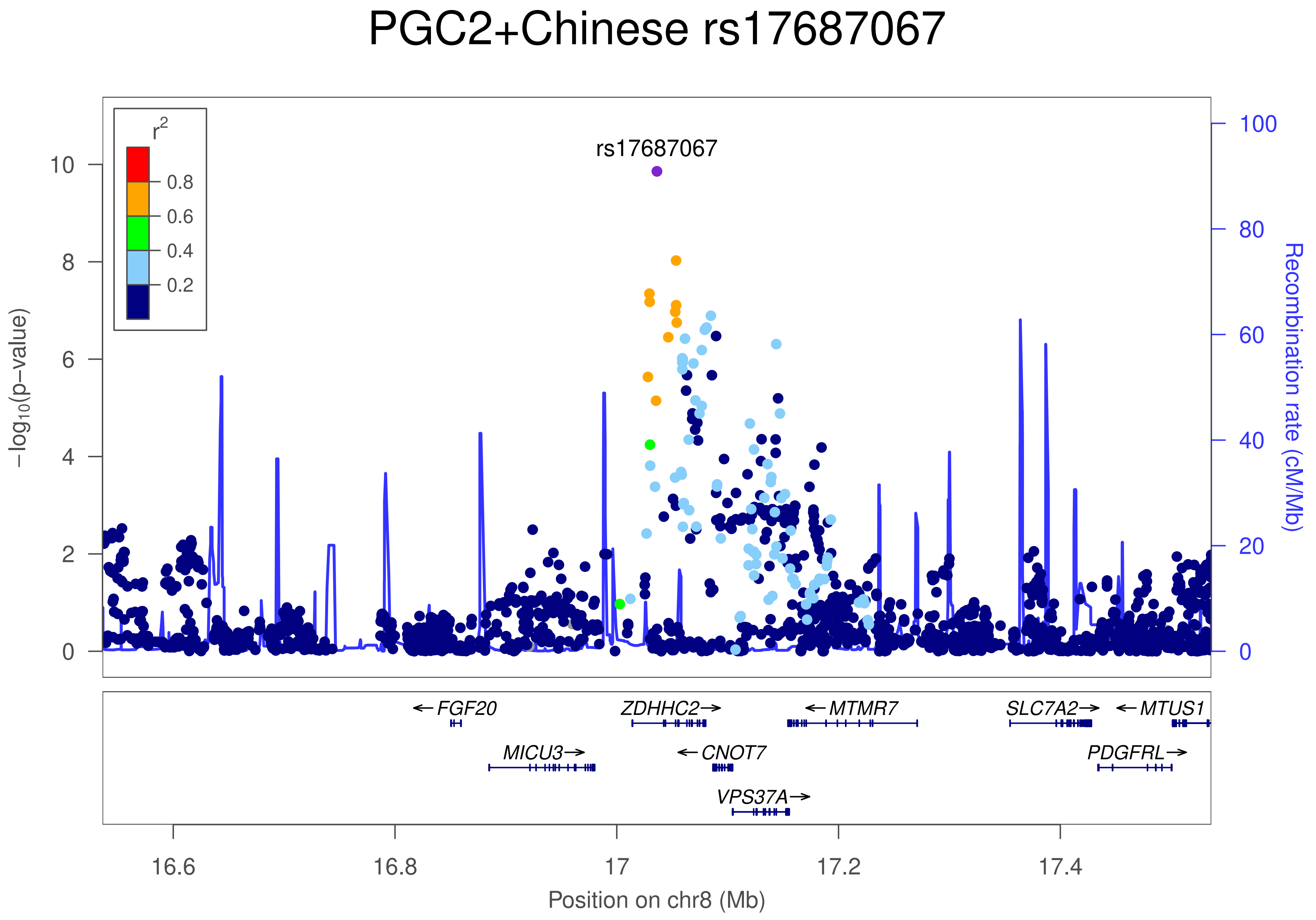



PGC2 rs323167
r2
0.8
0.6
0.4
0.2
10
8
6
4
2
0
−log10(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
rs323167
← MAGI2
RPL13AP17→
MAGI2−AS2→
78
78.2
78.4
78.6
78.8
Position on chr7 (Mb)

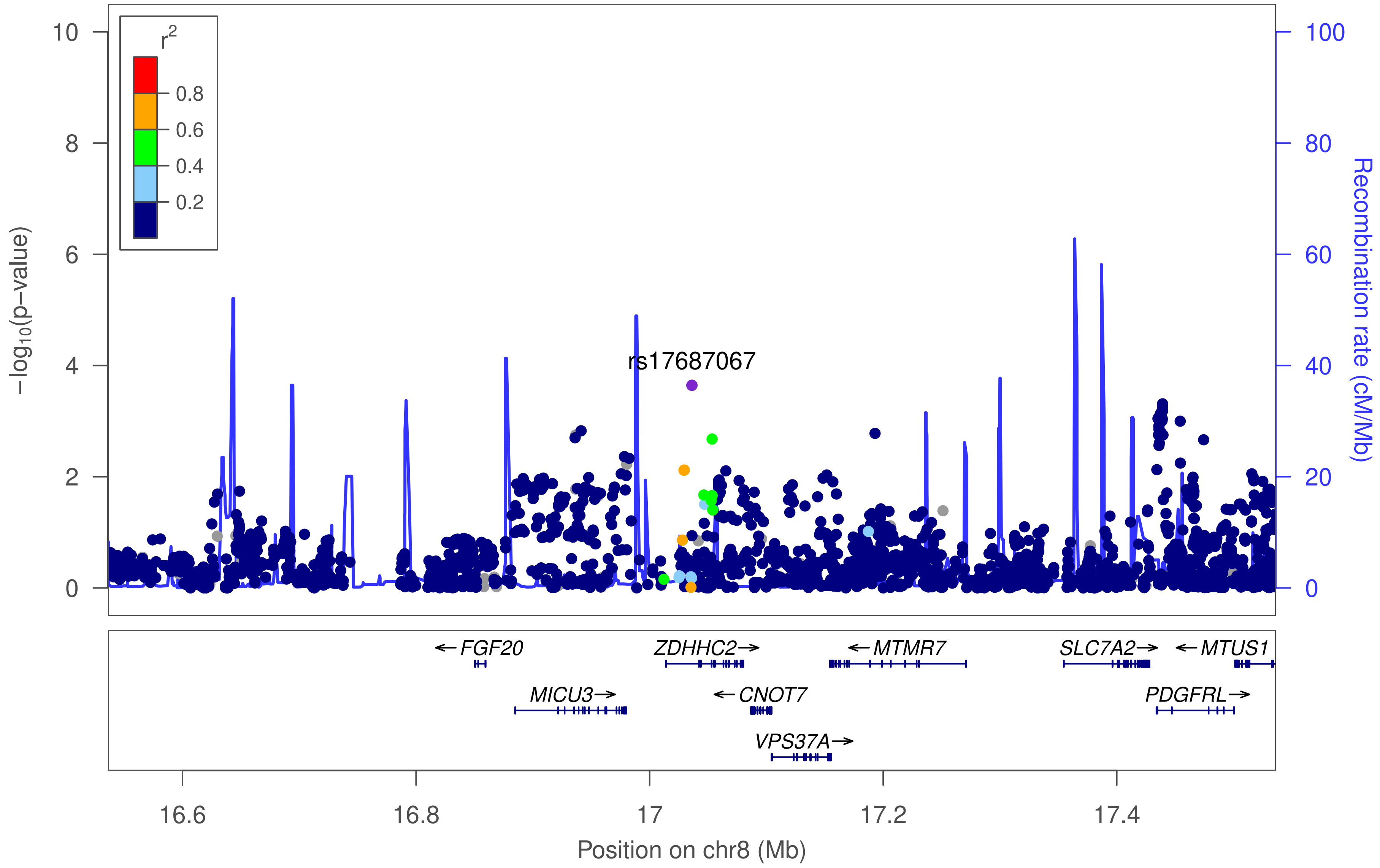

PGC2+Chinese rs323167
−log10(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
r2
0.8
0.6
0.4
0.2
rs323167
← MAGI2
RPL13AP17→
MAGI2−AS2→
78
78.2
78.4
78.6
78.8
Position on chr7 (Mb)

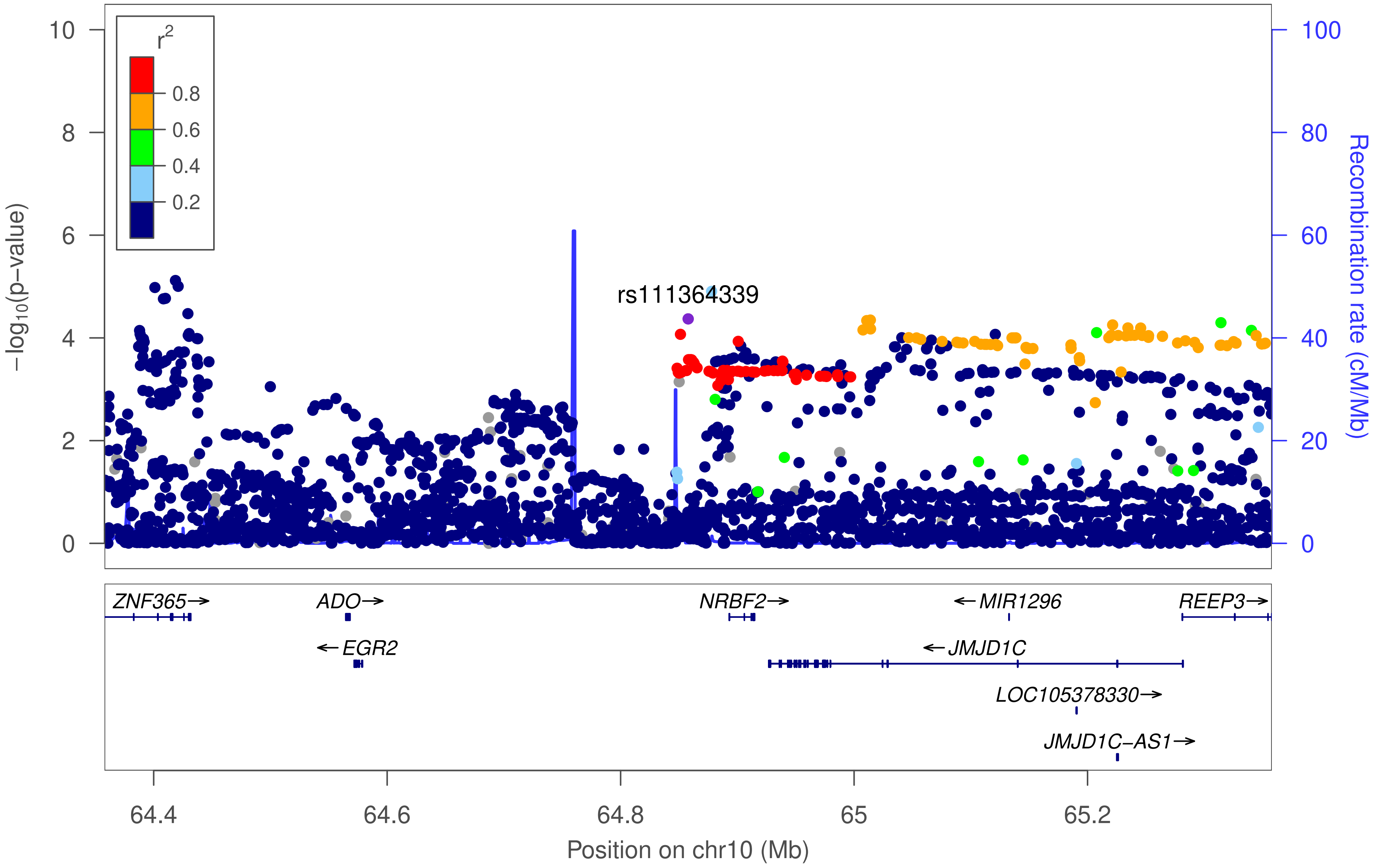

Chinese–only rs323167


PGC2 rs17687067
r²
0.8
0.6
0.4
0.2
rs17687067
−log₁₀(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
← FGF20
ZDHHC2 →
← MTMR7
SLC7A2 →
← MTUS1
MICU3 →
← CNOT7
PDGFRL →
VPS37A →
16.6
16.8
17
17.2
17.4
Position on chr8 (Mb)

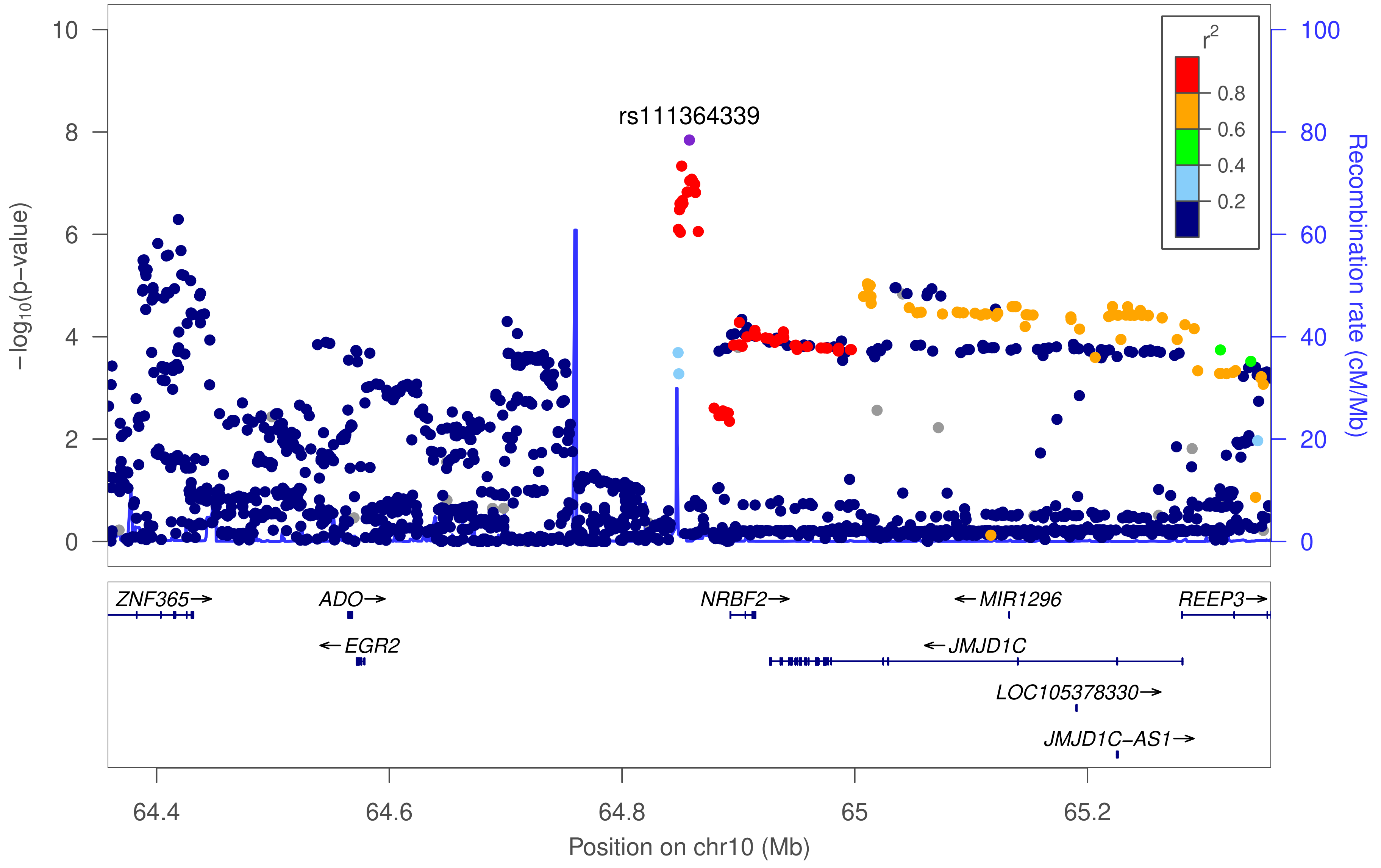

PGC2+Chinese rs17687067
r²
0.8
0.6
0.4
0.2
rs17687067
−log₁₀(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
←FGF20
ZDHHC2→
←MTMR7
SLC7A2→
←MTUS1
MICU3→
←CNOT7
PDGFRL→
VPS37A→
16.6
16.8
17
17.2
17.4
Position on chr8 (Mb)

Chinese–only rs17687067

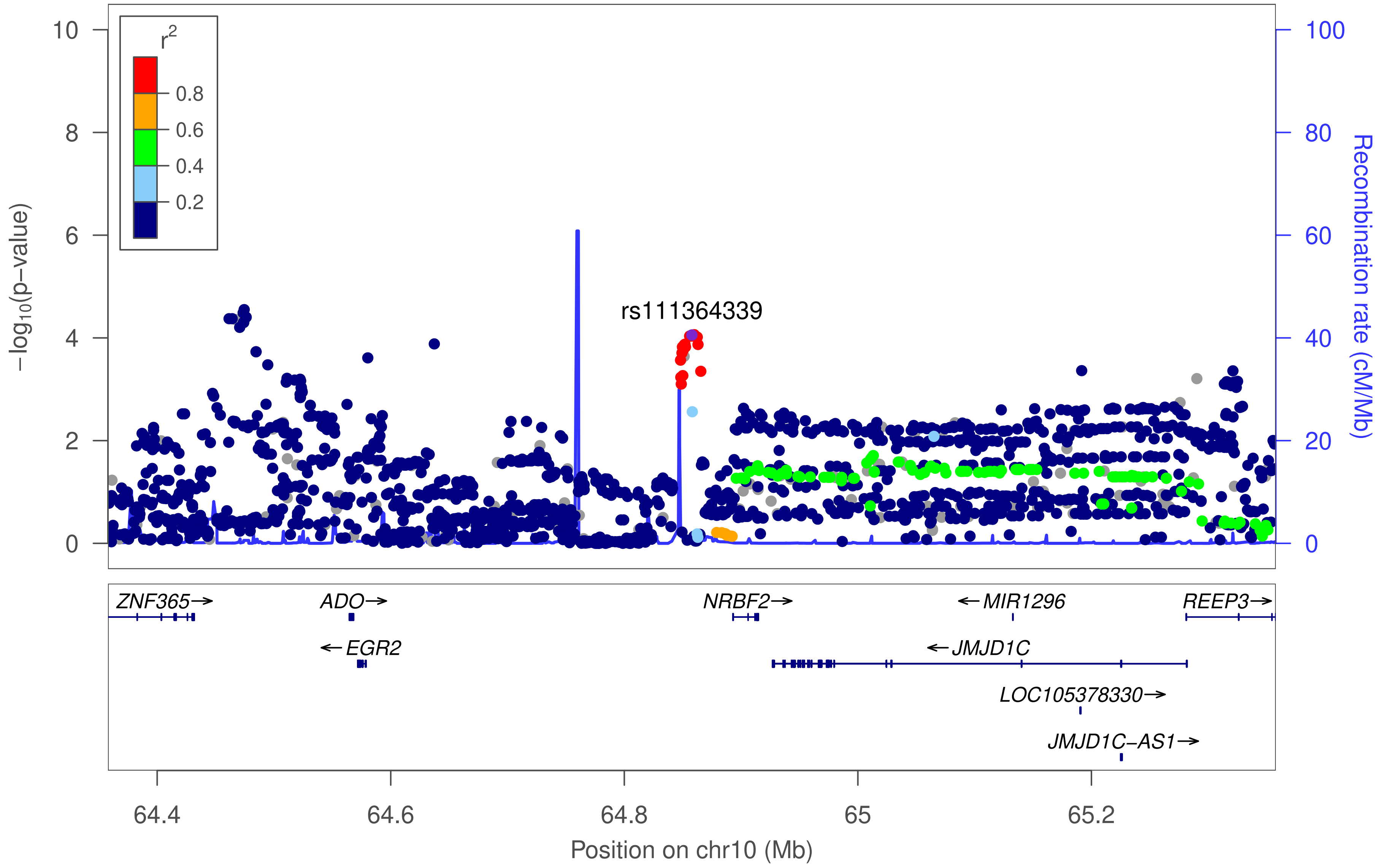


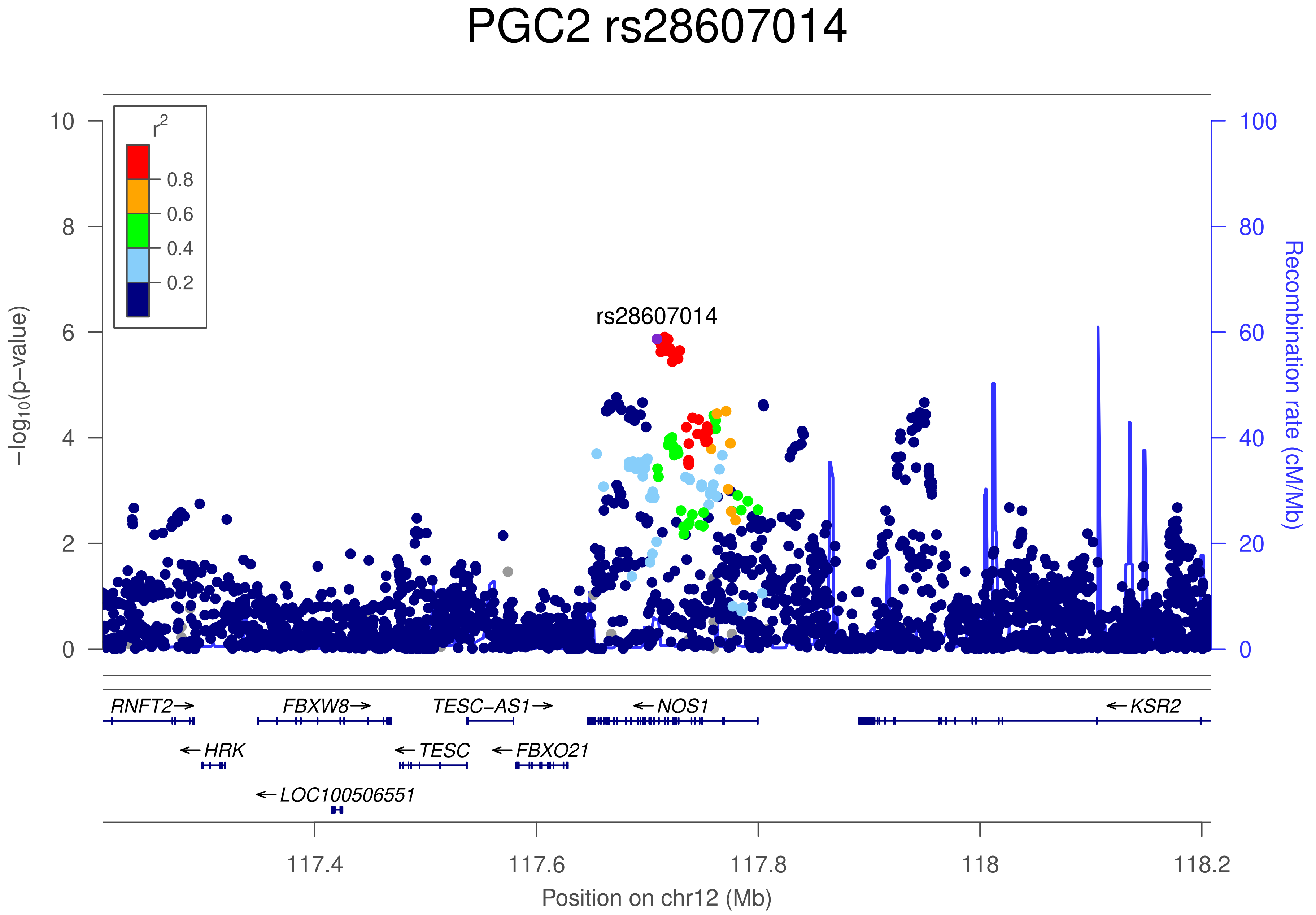

PGC2 rs111364339

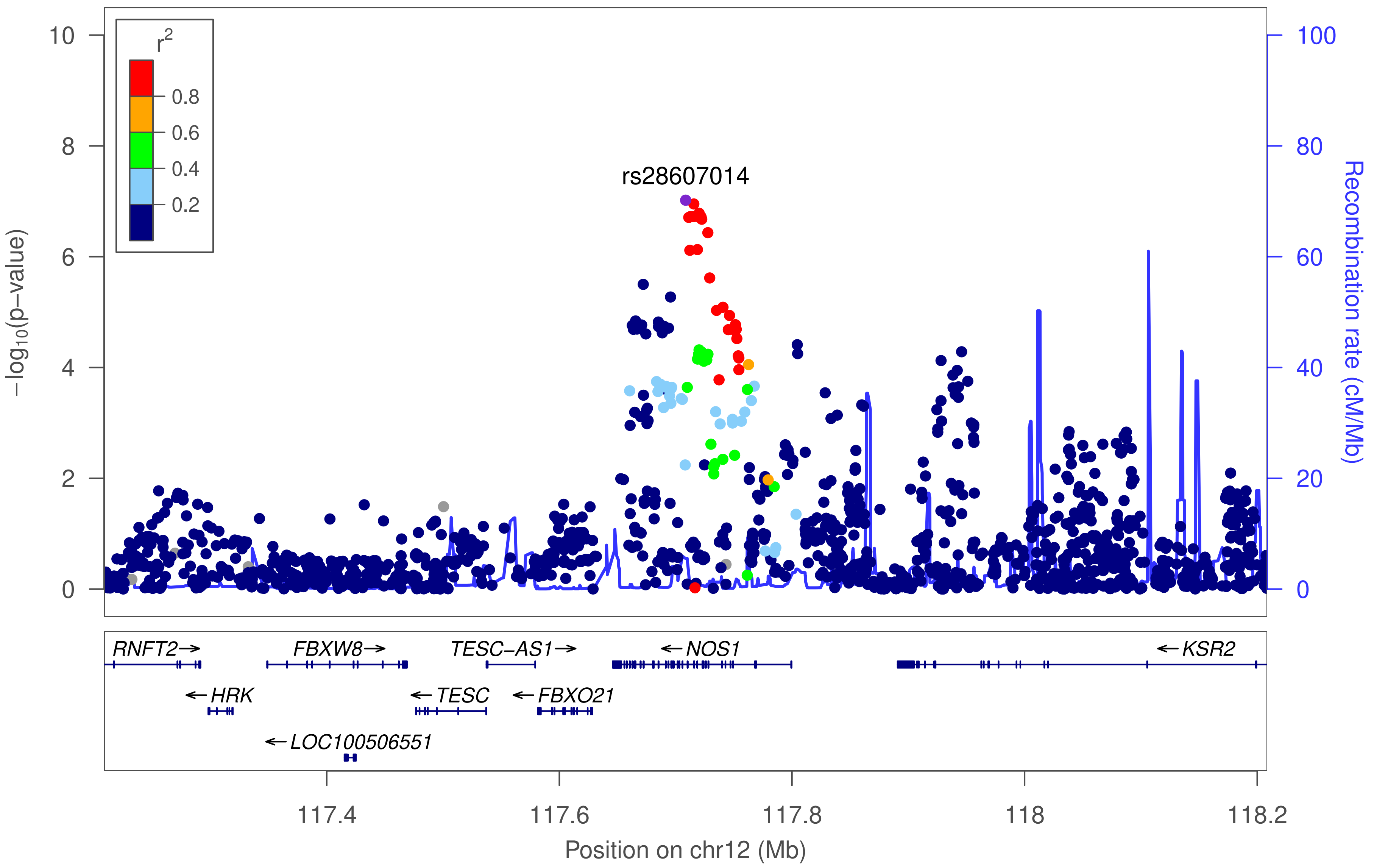
PGC2+Chinese rs111364339



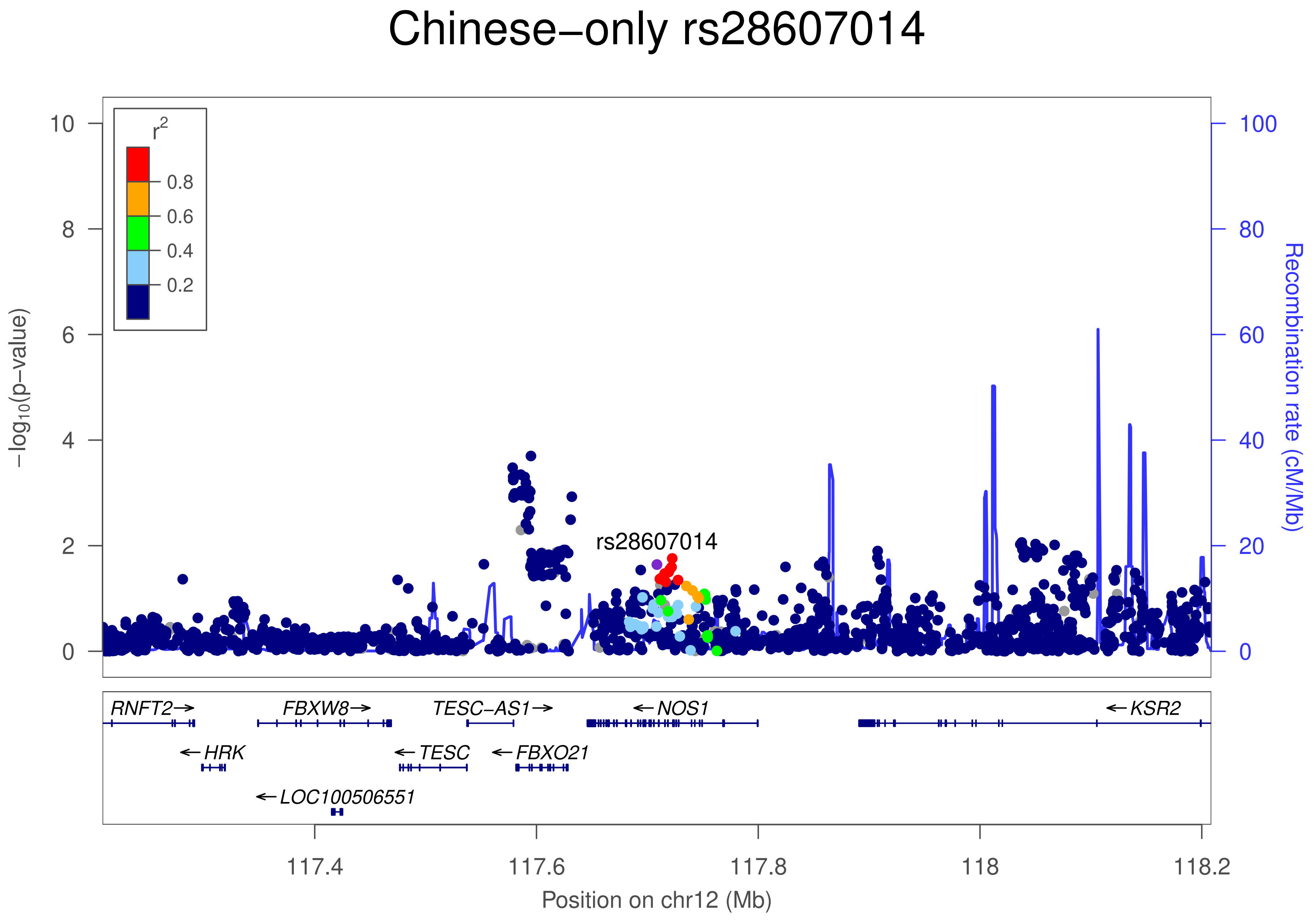
Chinese−only rs111364339

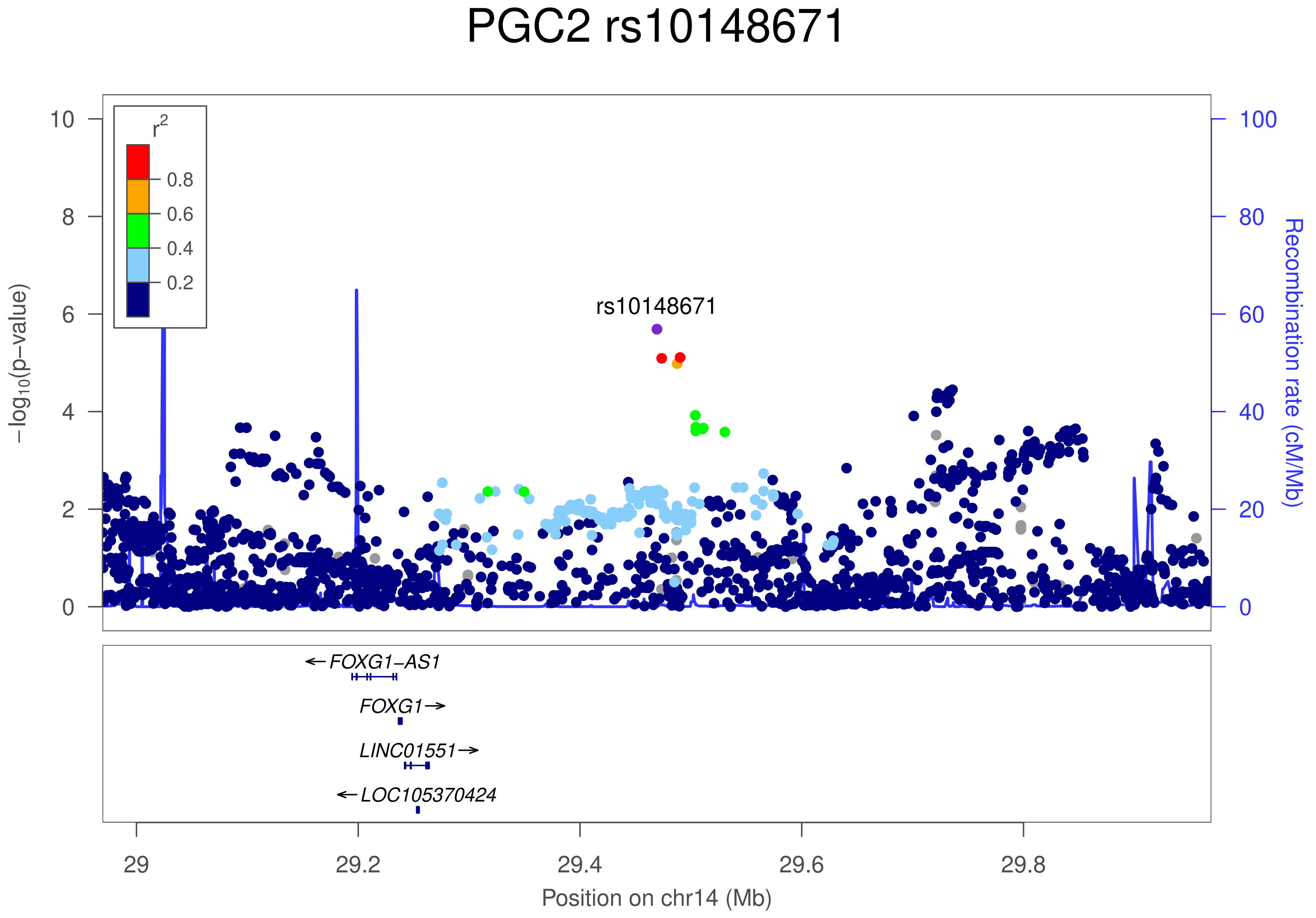



PGC2 rs28607014
r2
0.8
0.6
0.4
0.2
rs28607014
−log10(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
RNFT2→
FBXW8→
TESC−AS1→
←NOS1
←KSR2
←HRK
←TESC
←FBXO21
←LOC100506551
117.4
117.6
117.8
118
118.2
Position on chr12 (Mb)

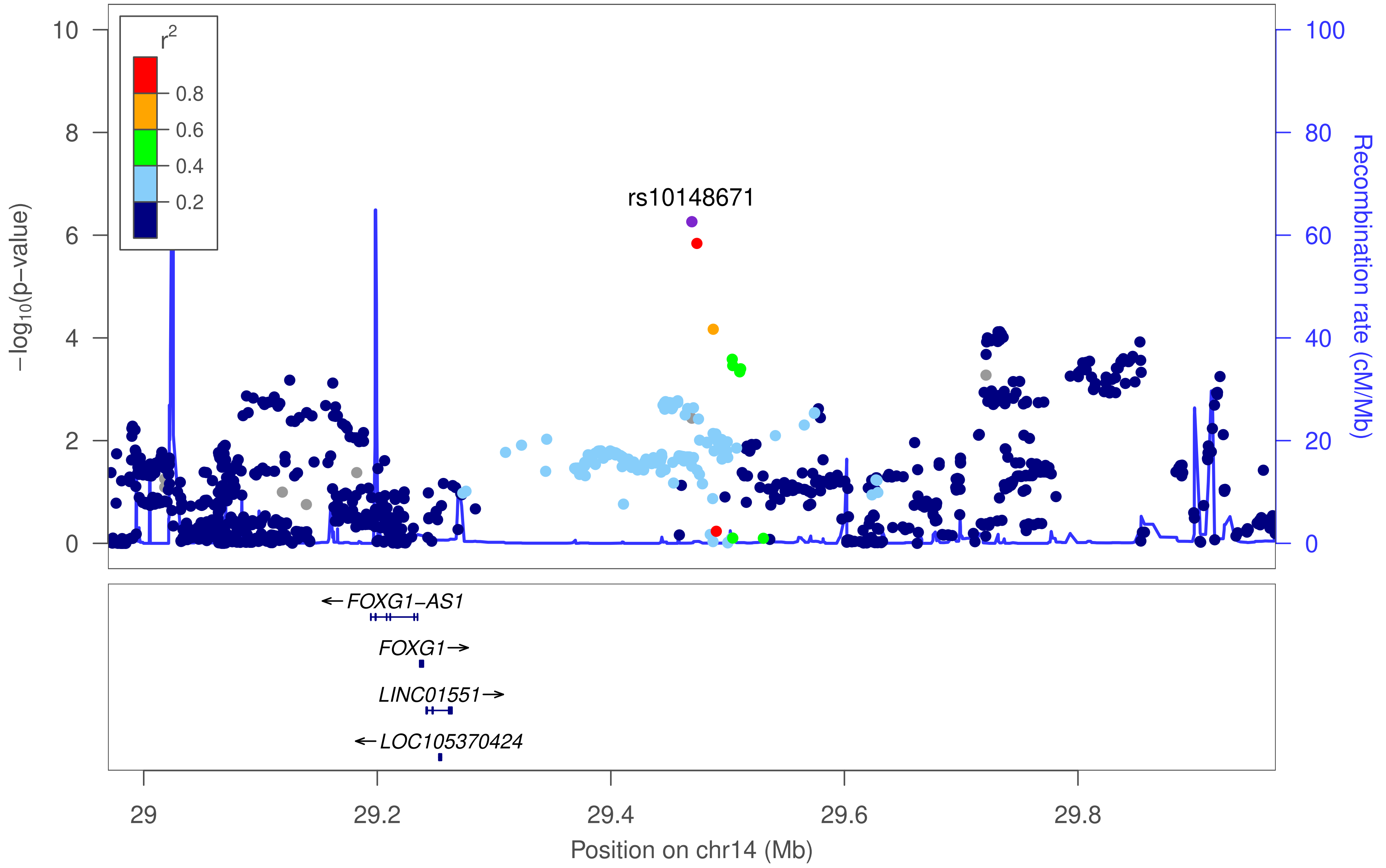


PGC2+Chinese rs28607014

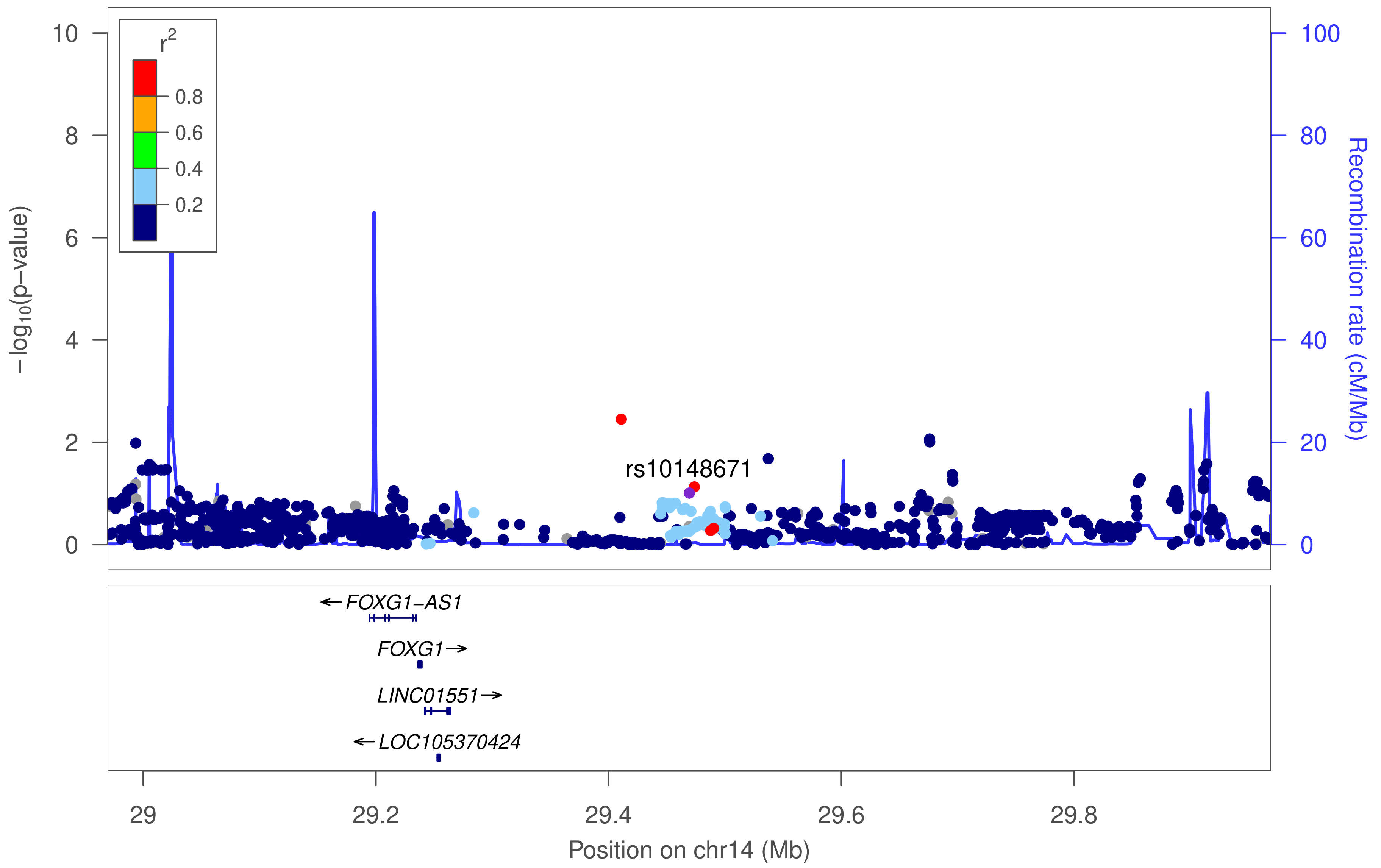

Chinese–only rs28607014
r^2
0.8
0.6
0.4
0.2
rs28607014
−log$_{10}$(p−value)
10
8
6
4
2
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
RNFT2→
FBXW8→
TESC−AS1→
←NOS1
←KSR2
←HRK
←TESC
←FBXO21
←LOC100506551
117.4
117.6
117.8
118
118.2
Position on chr12 (Mb)


PGC2 rs10148671
r²
0.8
0.6
0.4
0.2
rs10148671
10
8
6
4
2
0
−log₁₀(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
←FOXG1−AS1
FOXG1→
LINC01551→
←LOC105370424
29
29.2
29.4
29.6
29.8
Position on chr14 (Mb)

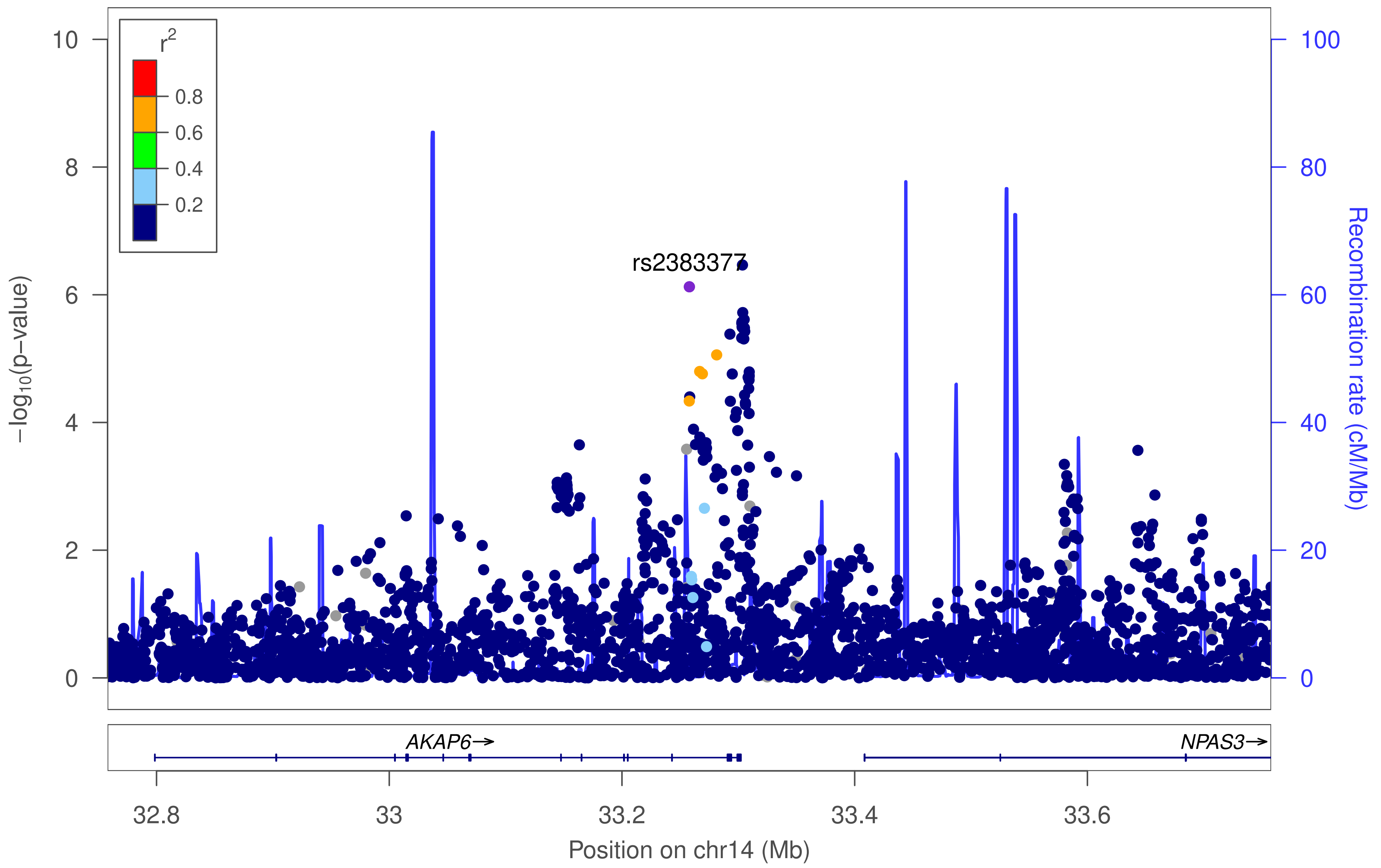
PGC2+Chinese rs10148671

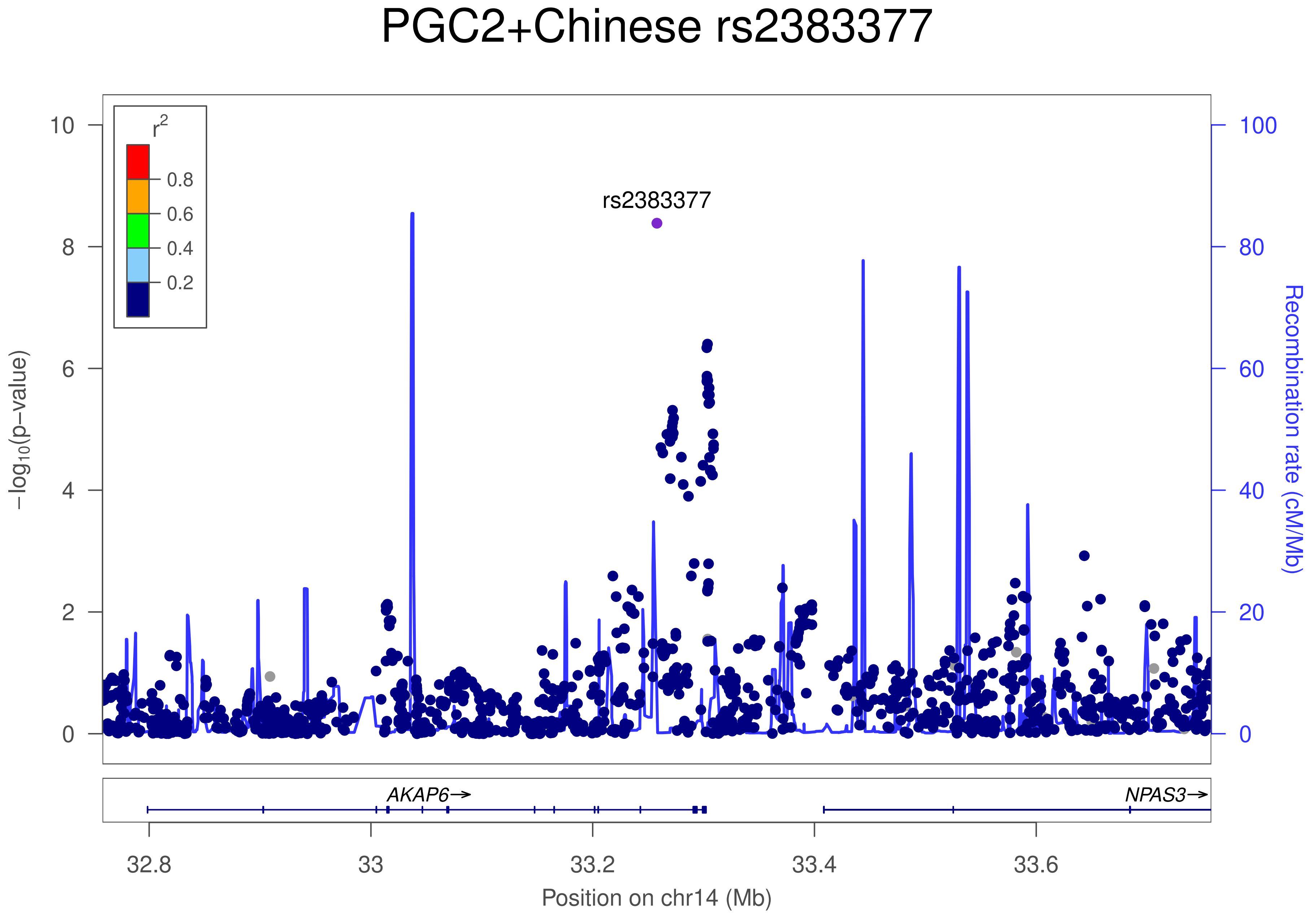


Chinese−only rs10148671

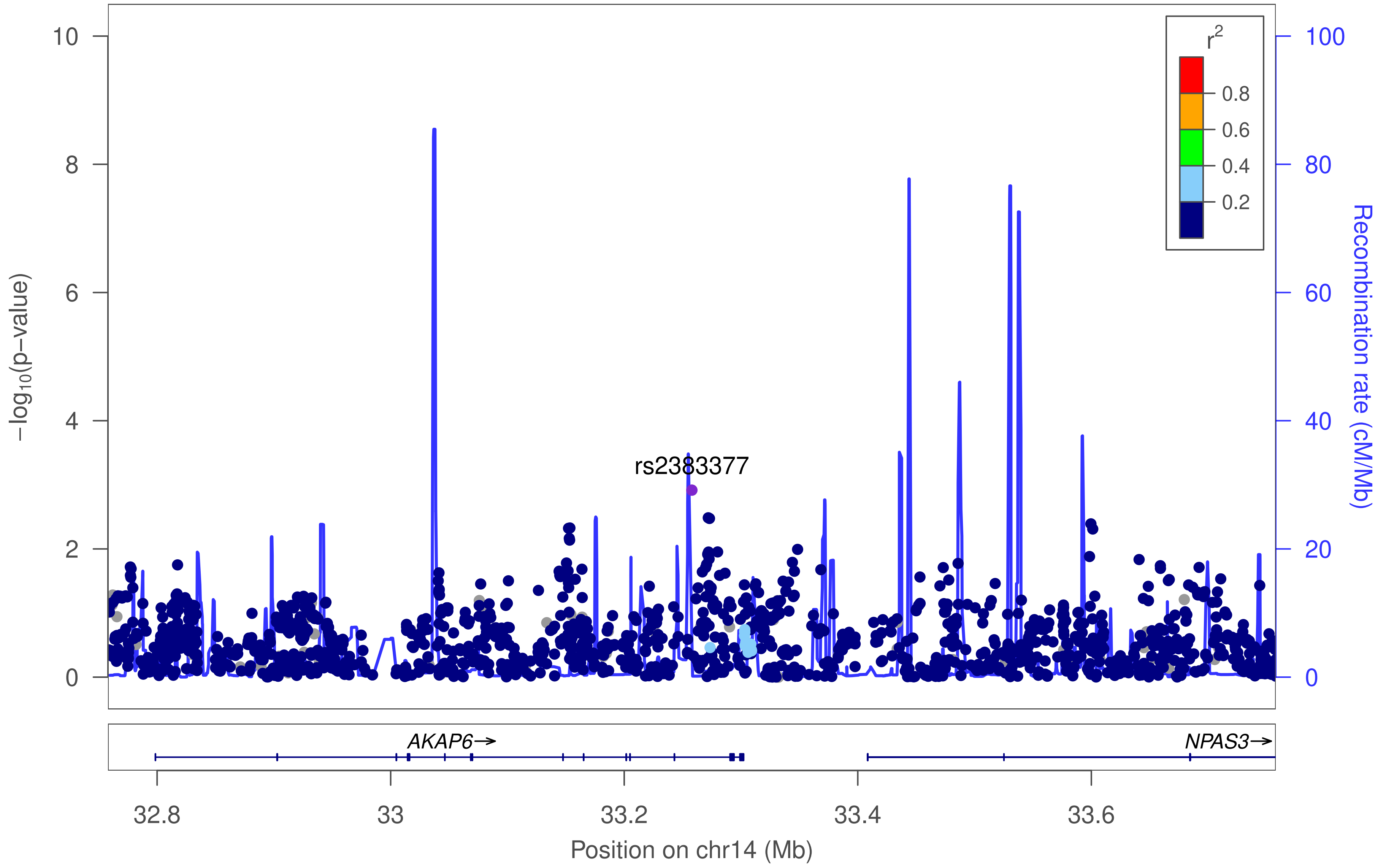


PGC2 rs2383377

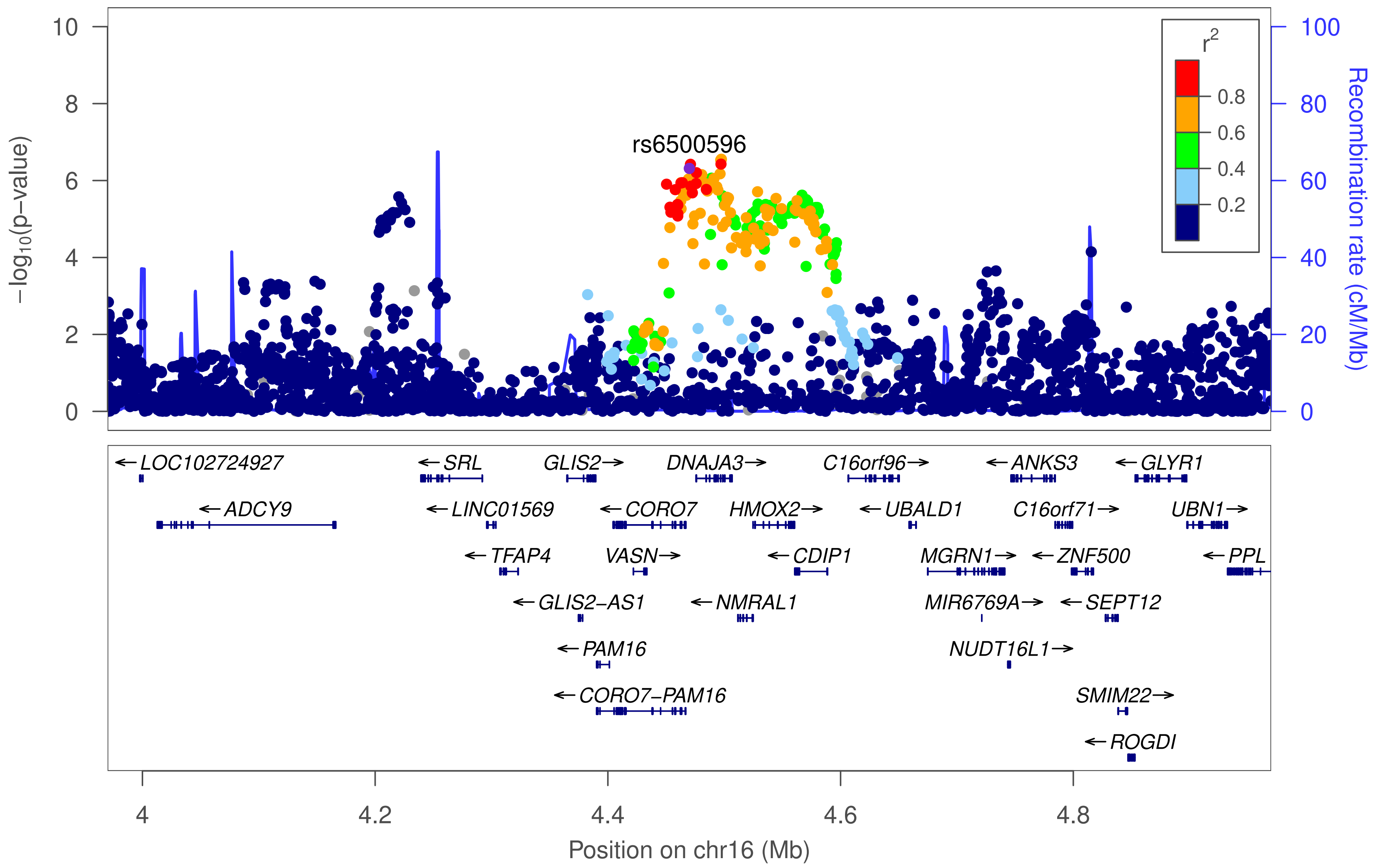



PGC2+Chinese rs2383377
r2
0.8
0.6
0.4
0.2
rs2383377
−log10(p−value)
10
8
6
4
2
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
AKAP6→
NPAS3→
32.8
33
33.2
33.4
33.6
Position on chr14 (Mb)

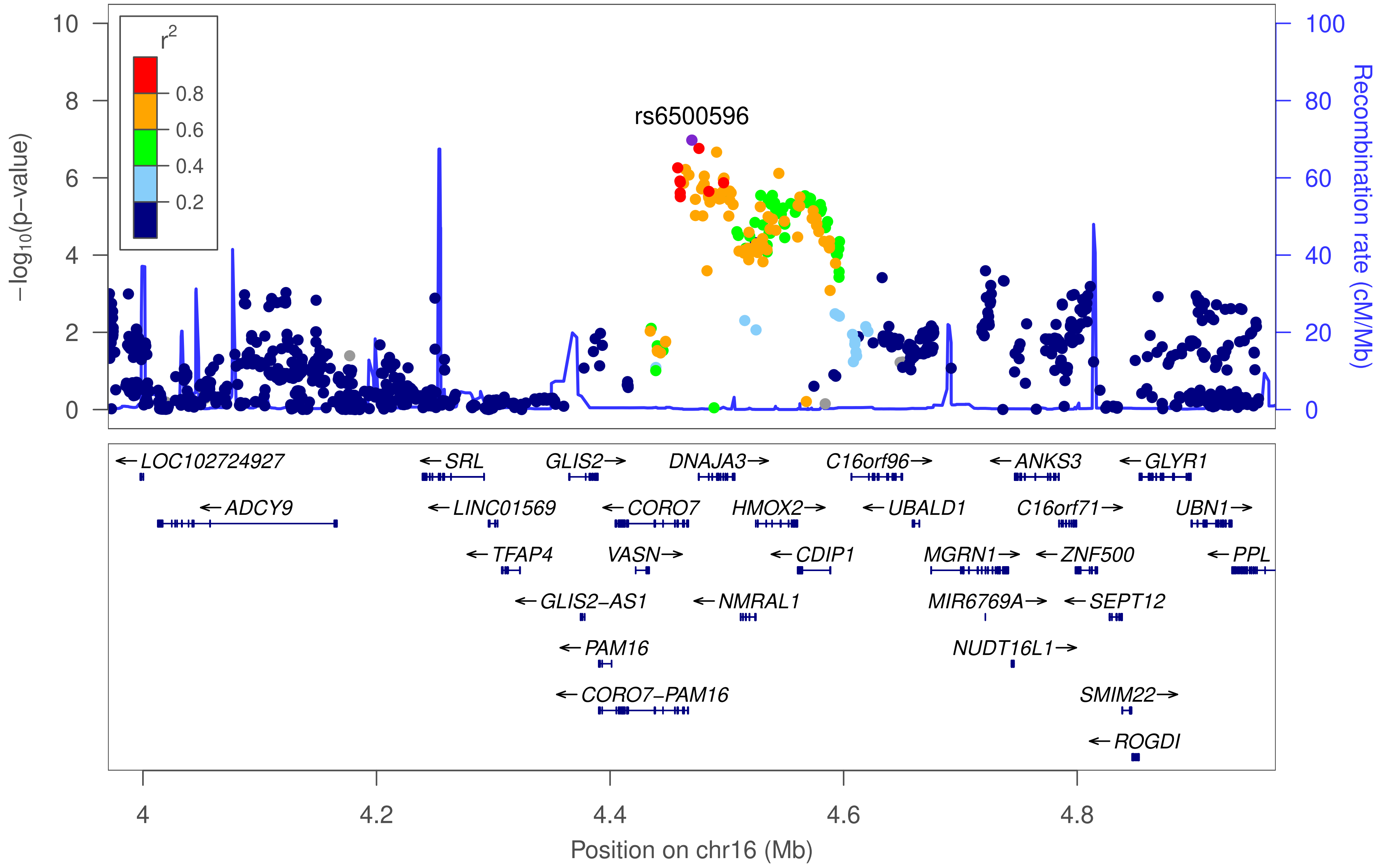
Chinese−only rs2383377



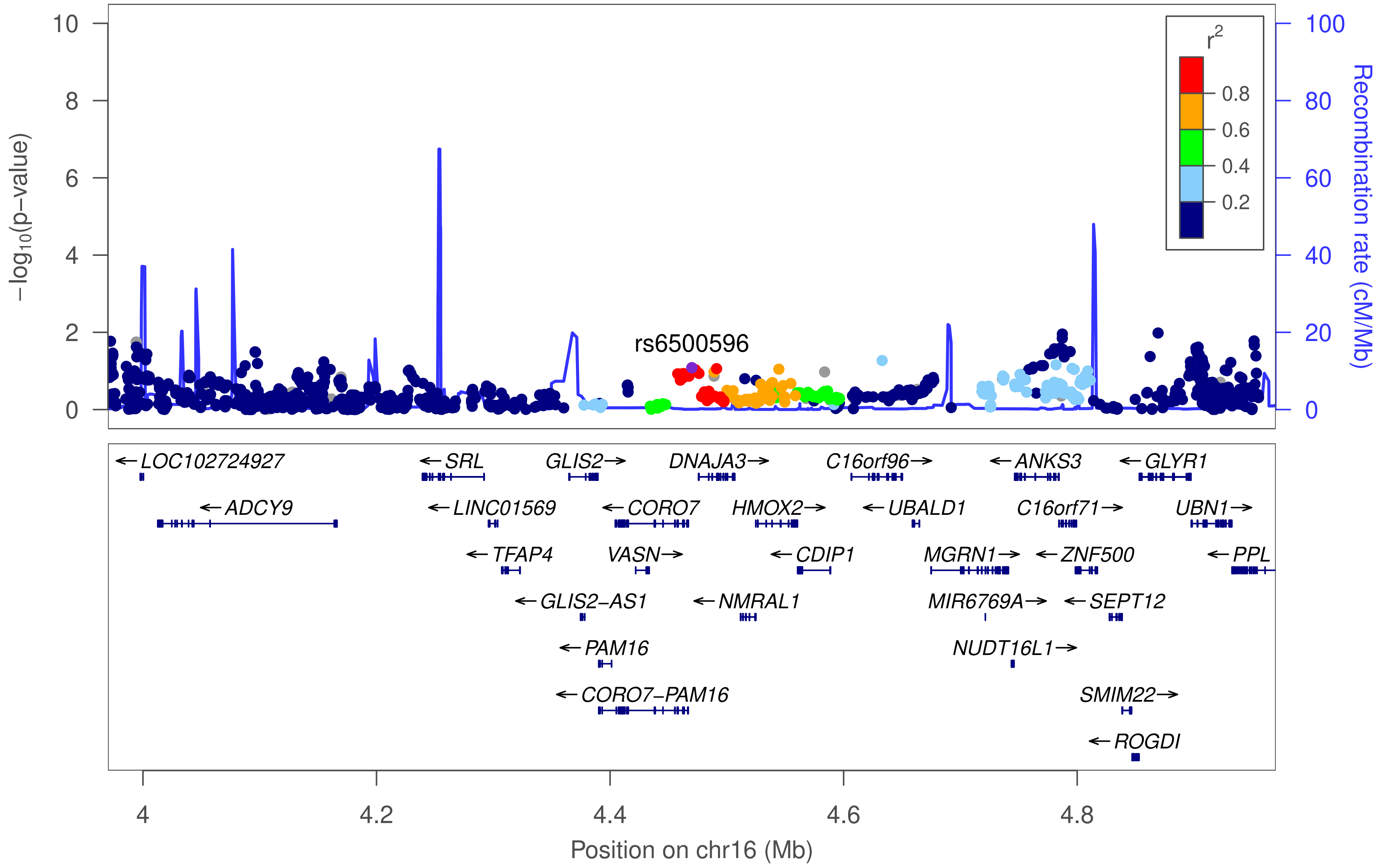
PGC2 rs6500596



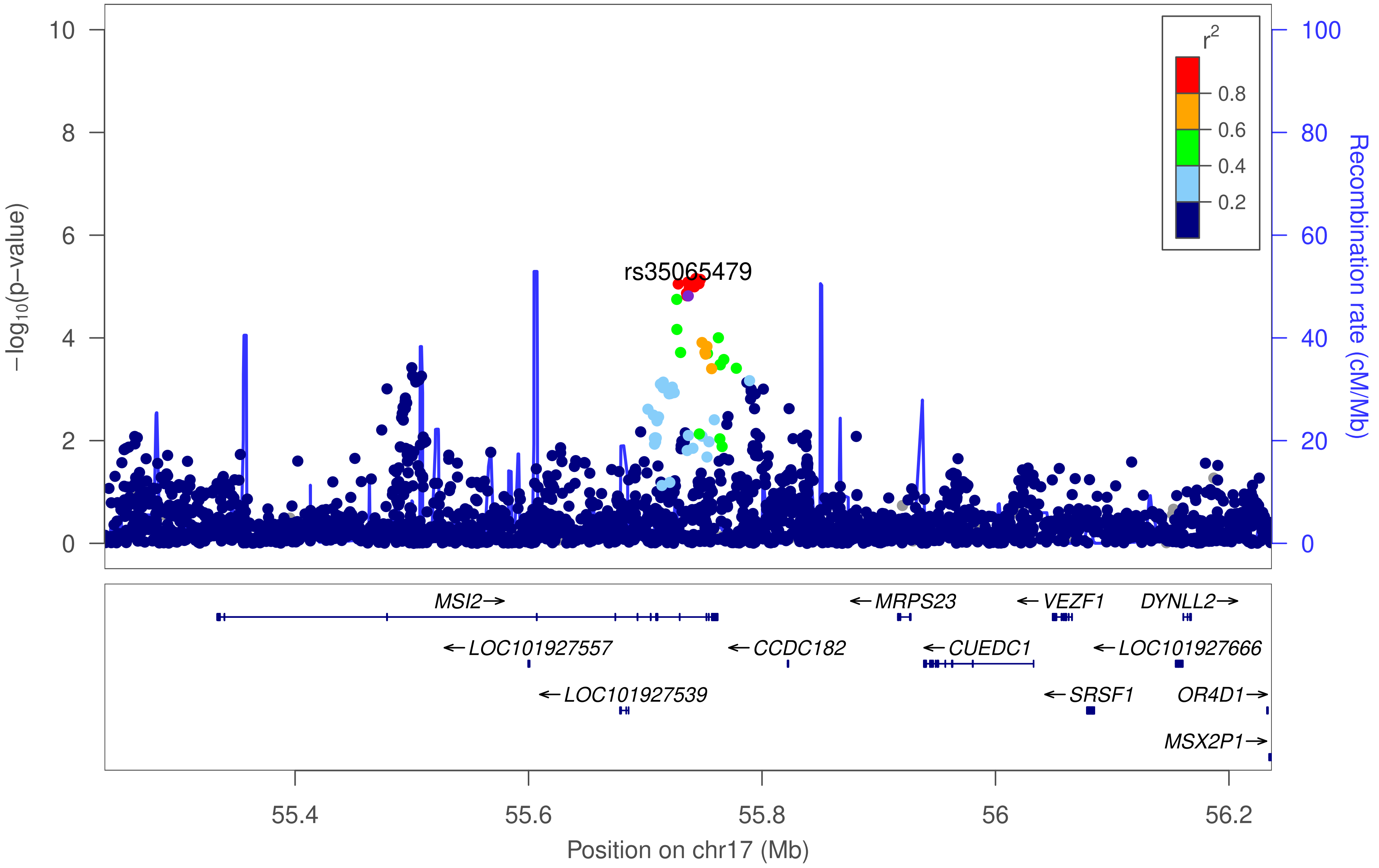
PGC2+Chinese rs6500596



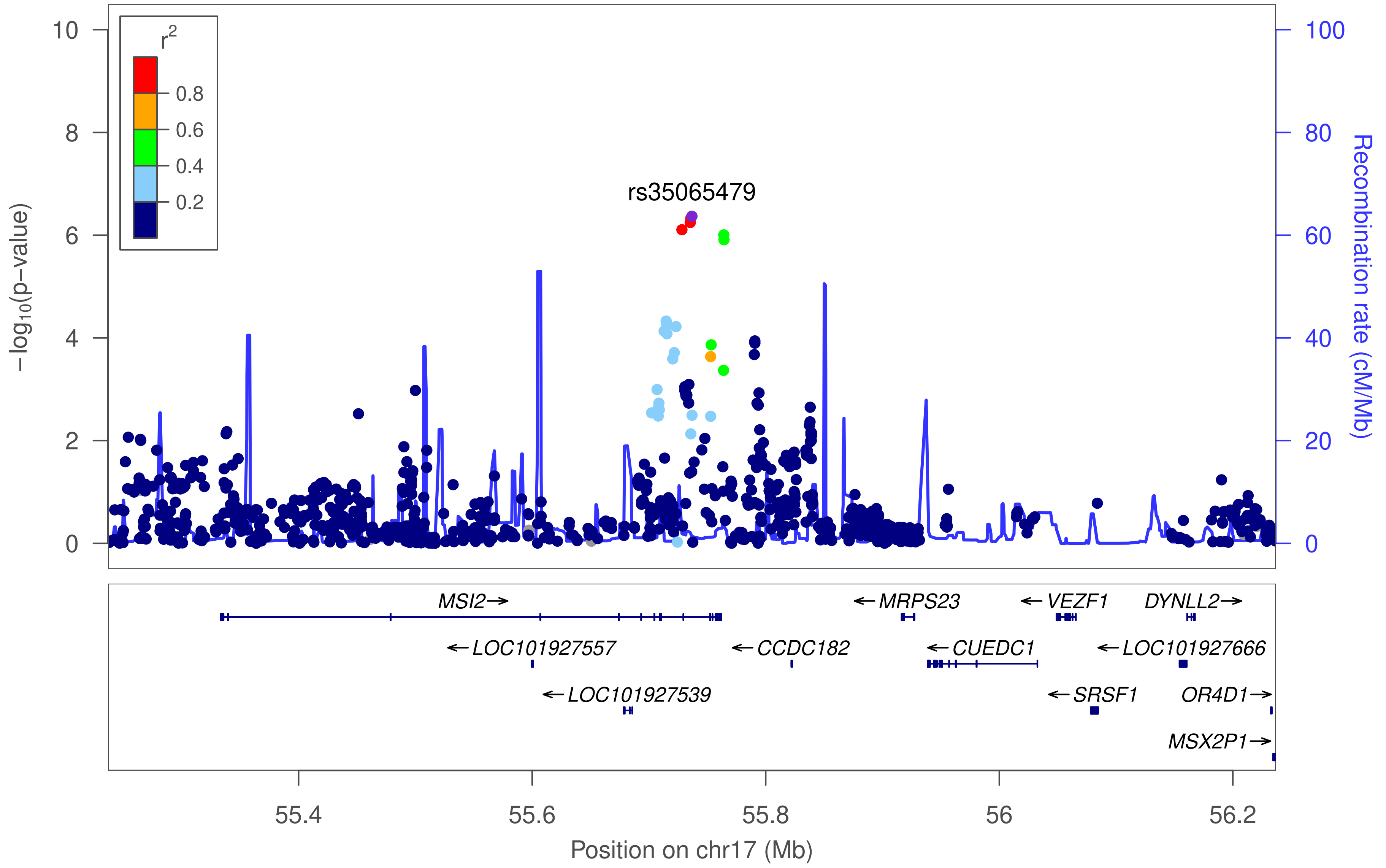
Chinese−only rs6500596

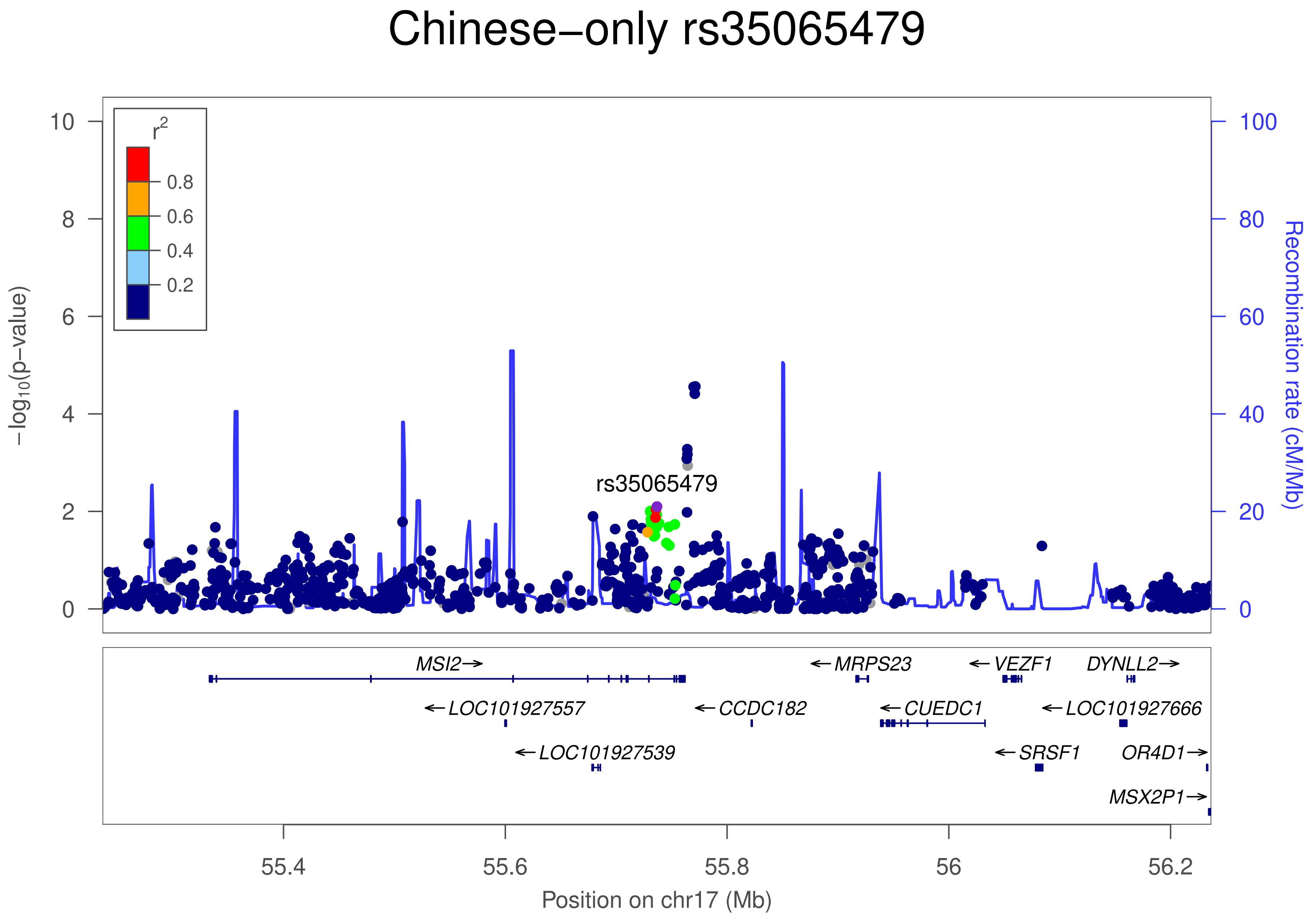


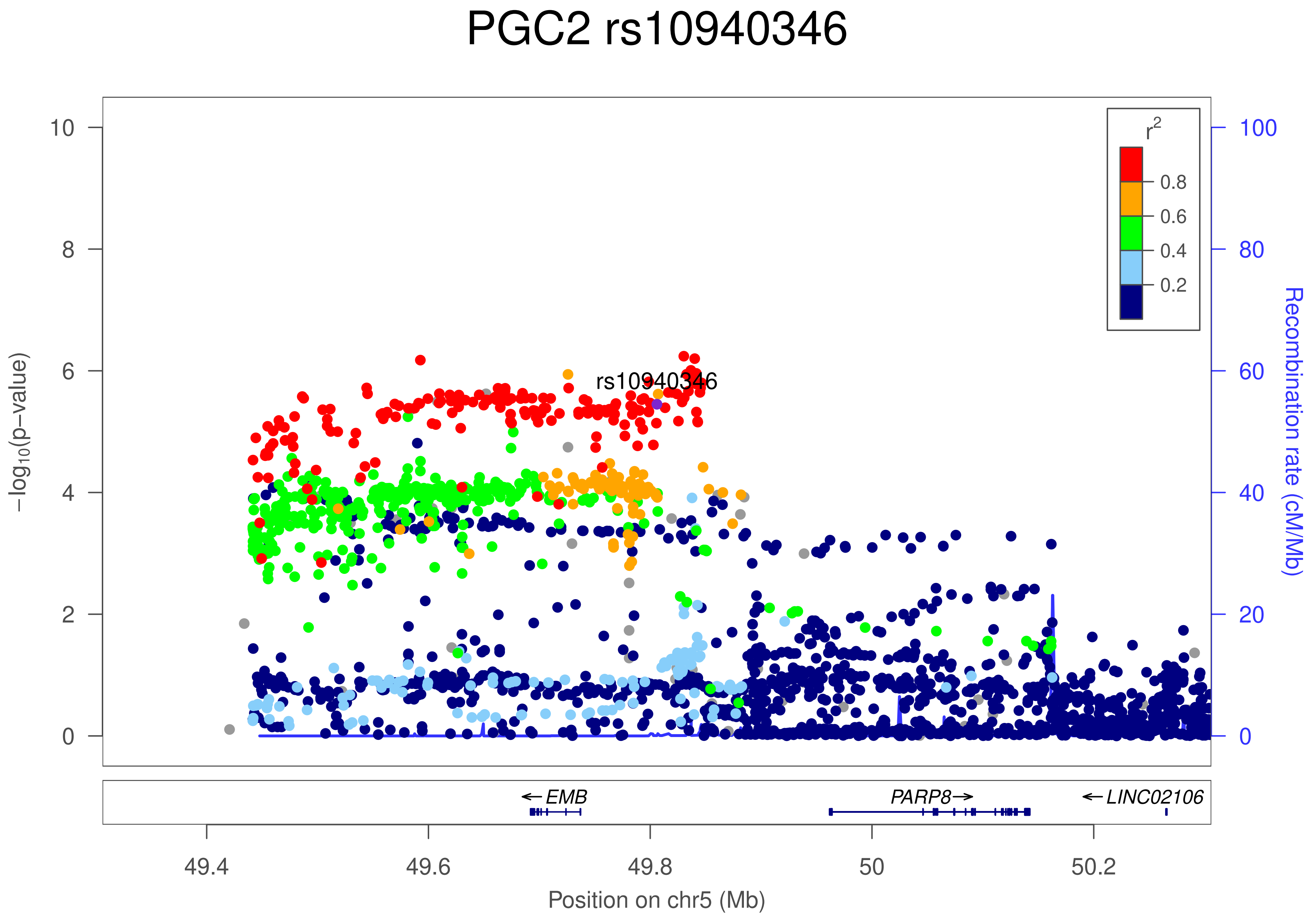
PGC2 rs35065479



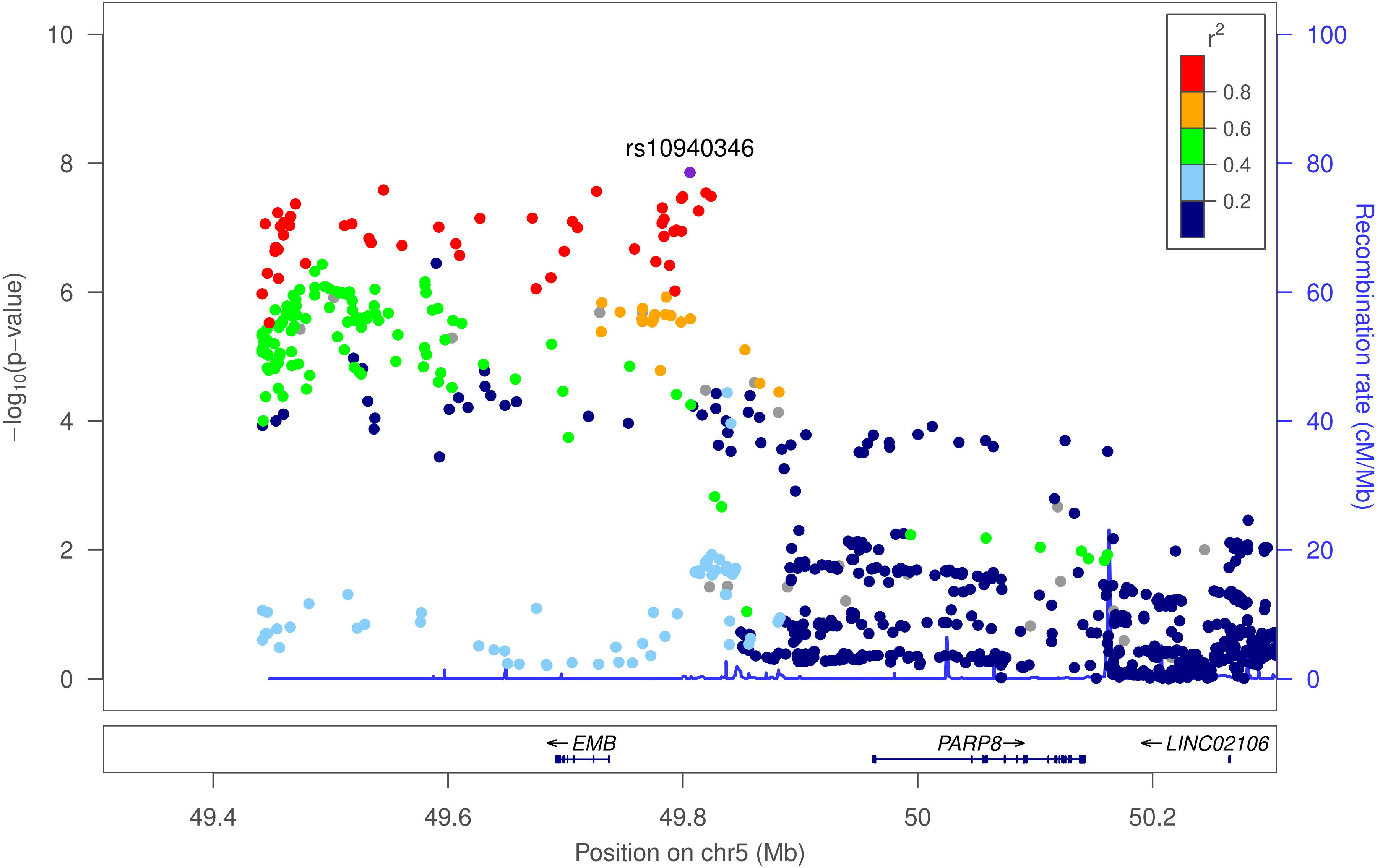
PGC2+Chinese rs35065479



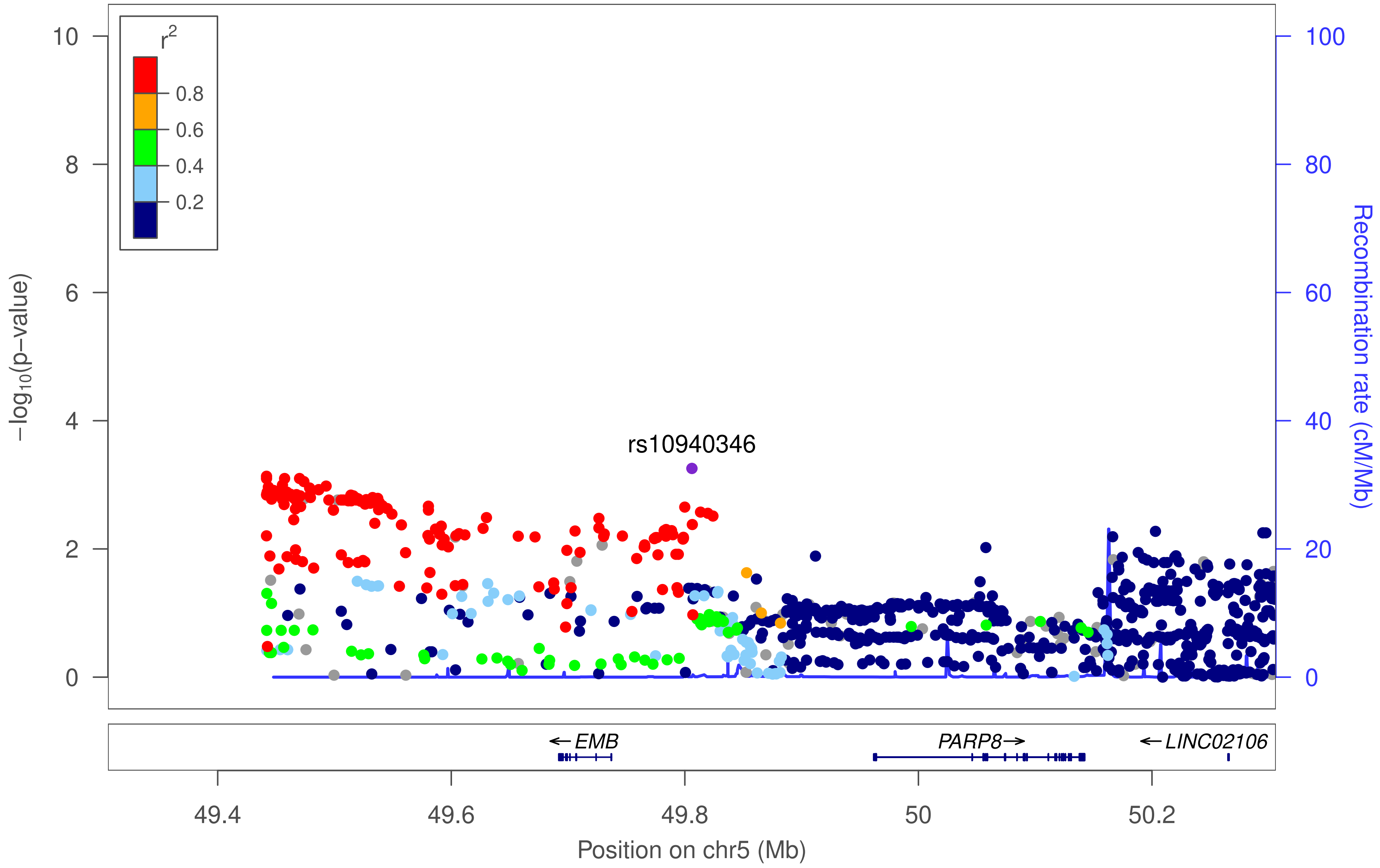

Chinese–only rs35065479
r²
0.8
0.6
0.4
0.2
10
8
6
4
2
0
$-\log_{10}$(p–value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
rs35065479
MSI2→
←MRPS23
←VEZF1
DYNLL2→
←LOC101927557
←CCDC182
←CUEDC1
←LOC101927666
←LOC101927539
←SRSF1
OR4D1→
MSX2P1→
55.4
55.6
55.8
56
56.2
Position on chr17 (Mb)


PGC2 rs10940346
−log10(p−value)
10
8
6
4
2
0
rs10940346
r2
0.8
0.6
0.4
0.2
100
80
60
40
20
0
Recombination rate (cM/Mb)
←EMB
PARP8→
←LINC02106
49.4
49.6
49.8
50
50.2
Position on chr5 (Mb)

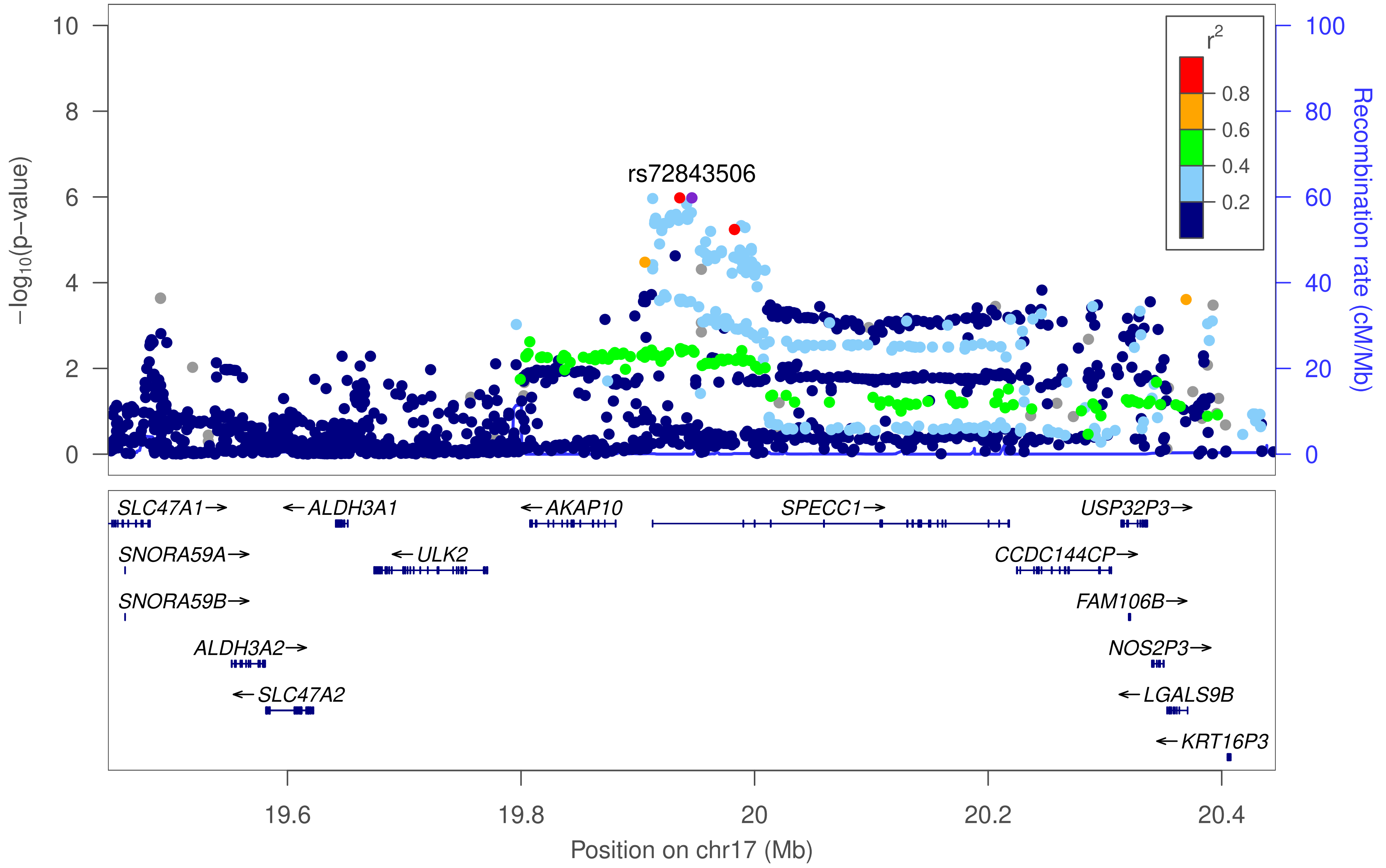
PGC2+Chinese rs10940346

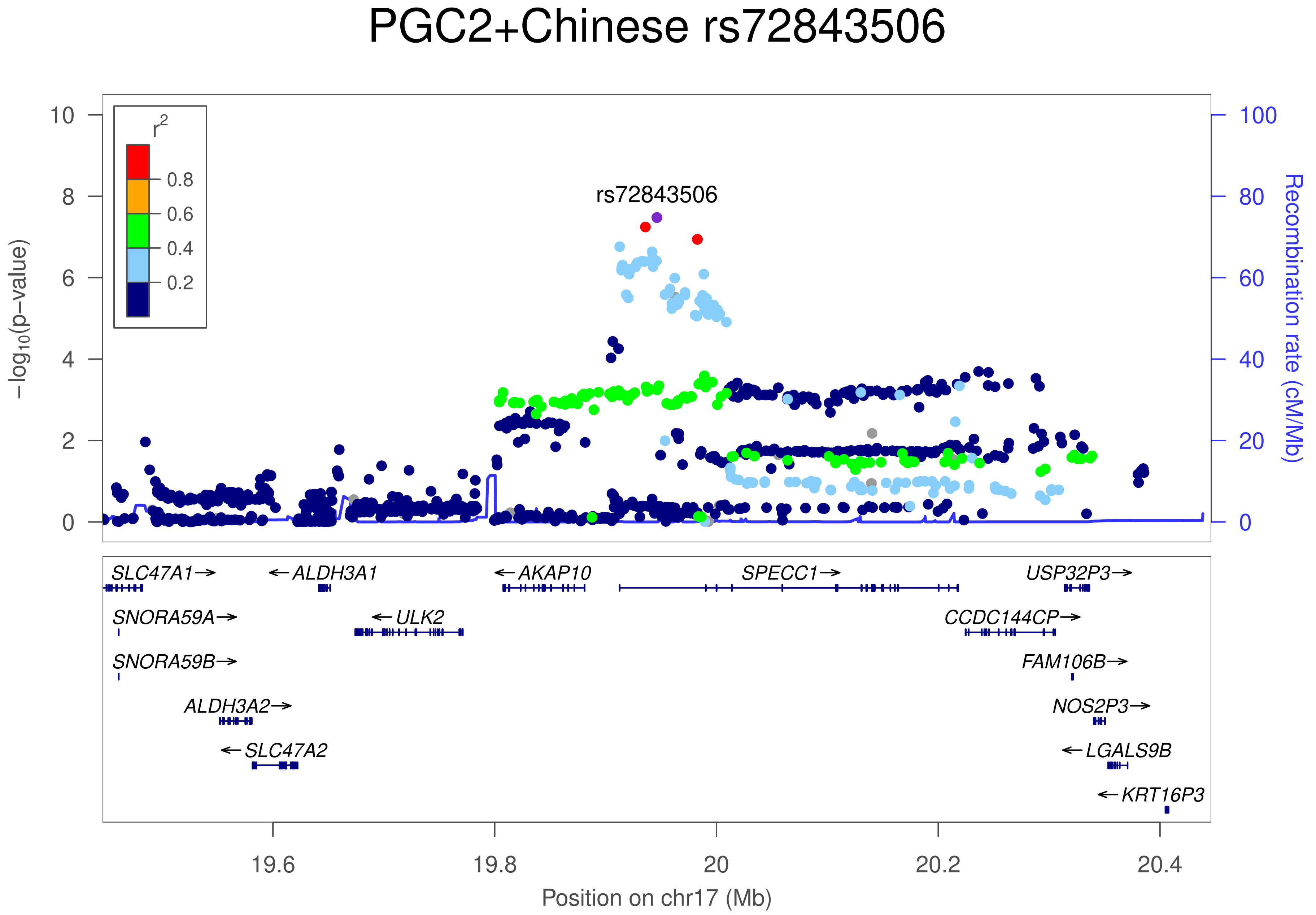


Chinese−only rs10940346

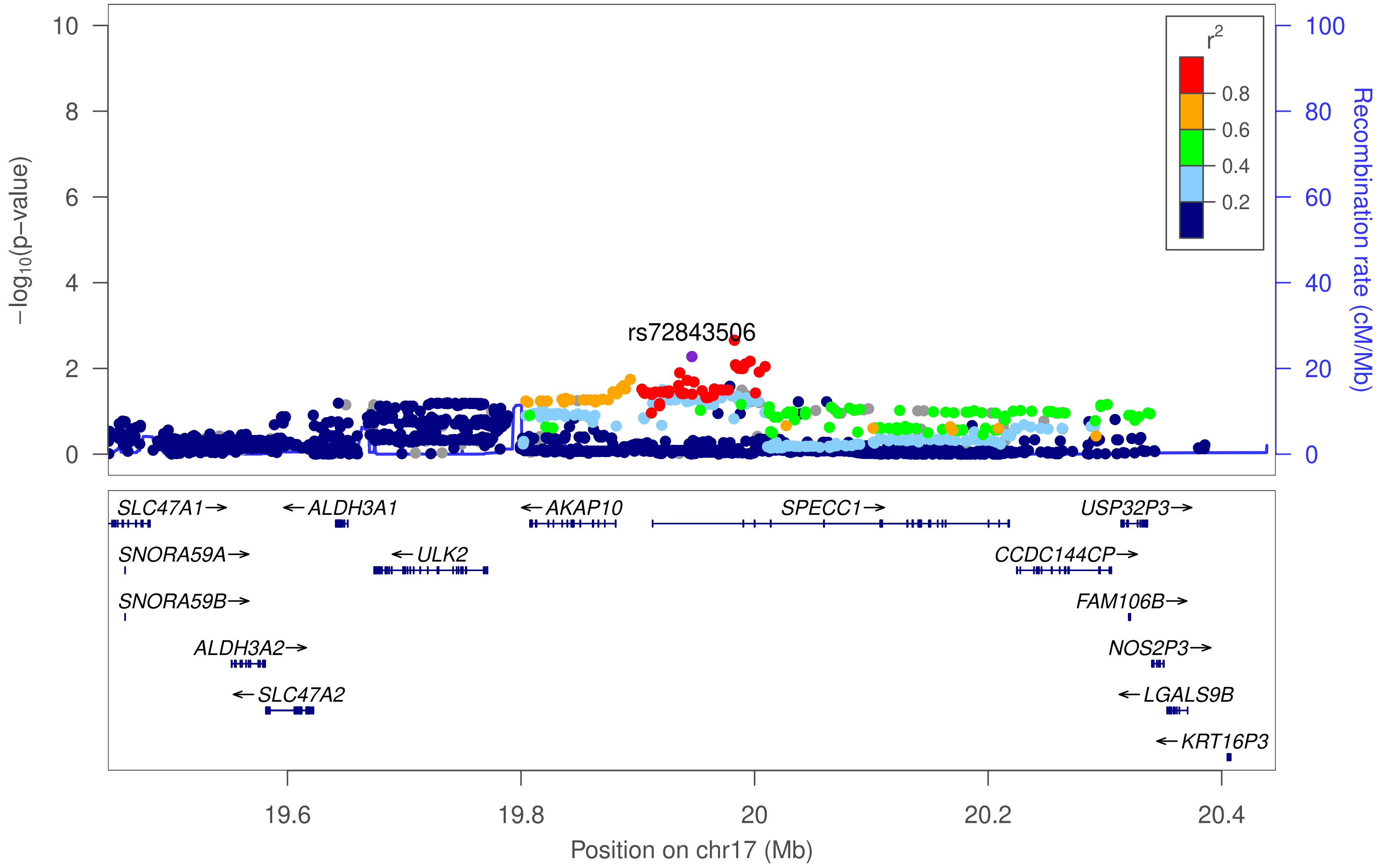


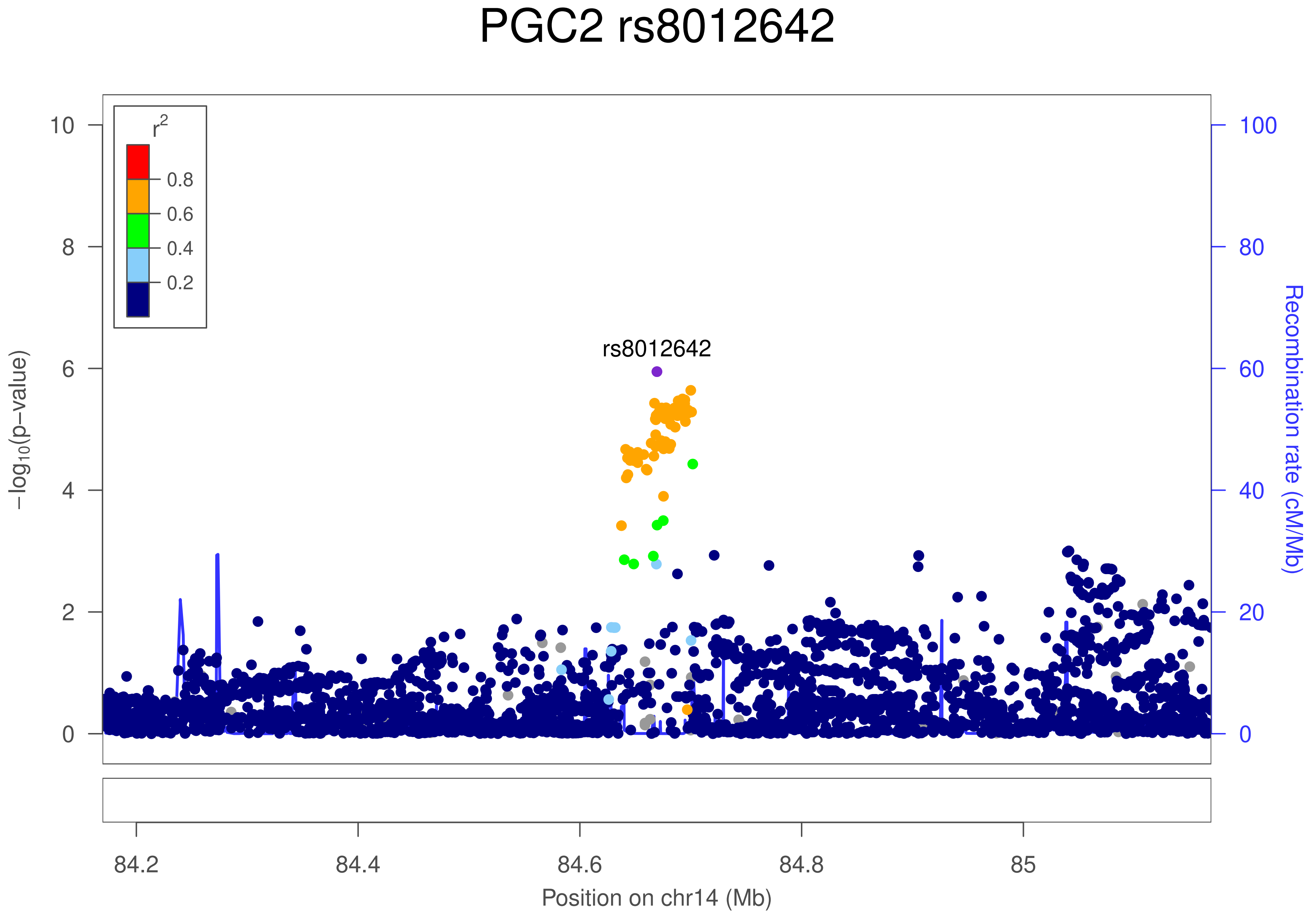
PGC2 rs72843506



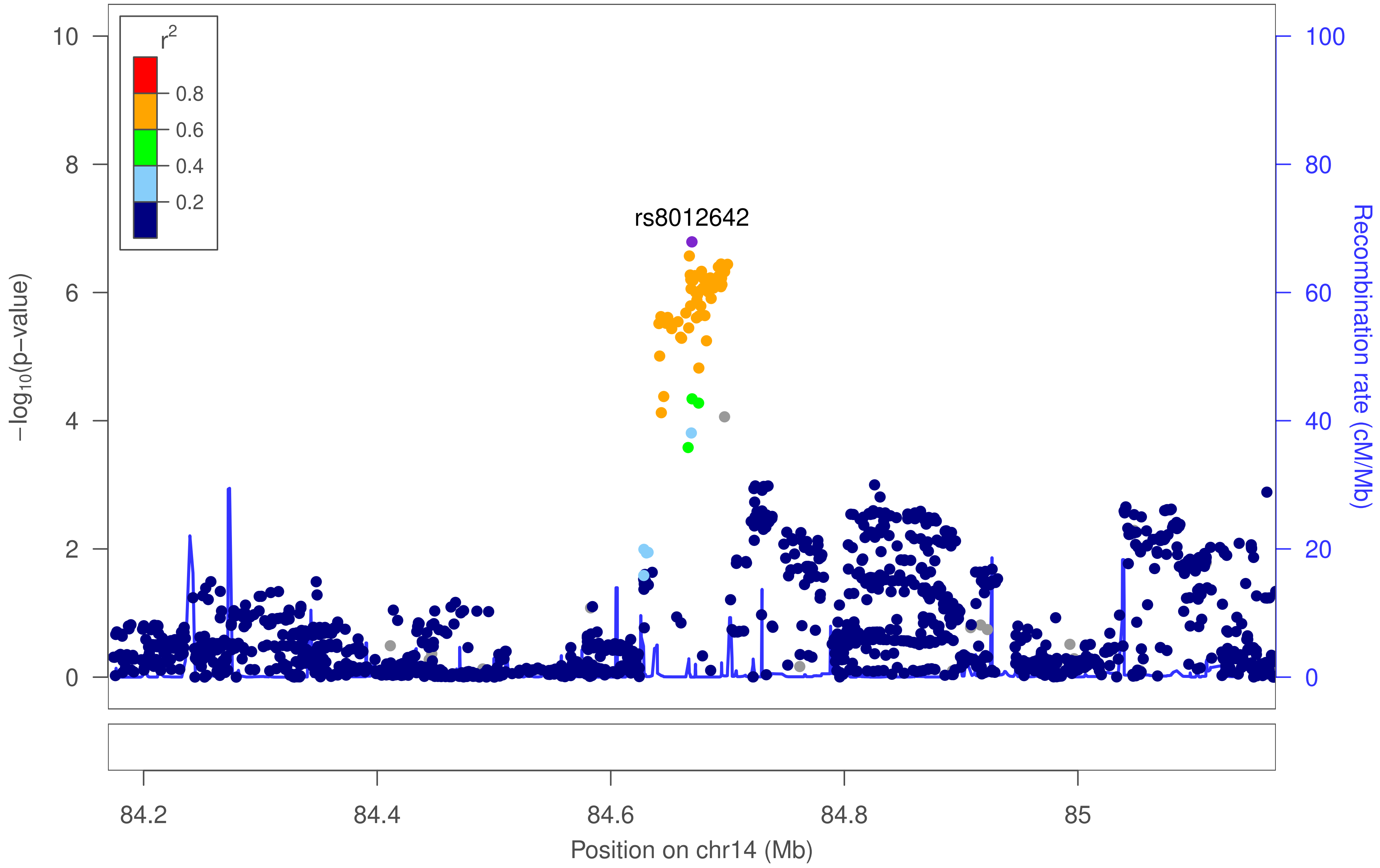

PGC2+Chinese rs72843506
rs72843506
r2
0.8
0.6
0.4
0.2
10
8
6
4
2
0
−log10(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
SLC47A1→
←ALDH3A1
←AKAP10
SPECC1→
USP32P3→
SNORA59A→
←ULK2
CCDC144CP→
SNORA59B→
FAM106B→
ALDH3A2→
NOS2P3→
←SLC47A2
←LGALS9B
←KRT16P3
19.6
19.8
20
20.2
20.4
Position on chr17 (Mb)

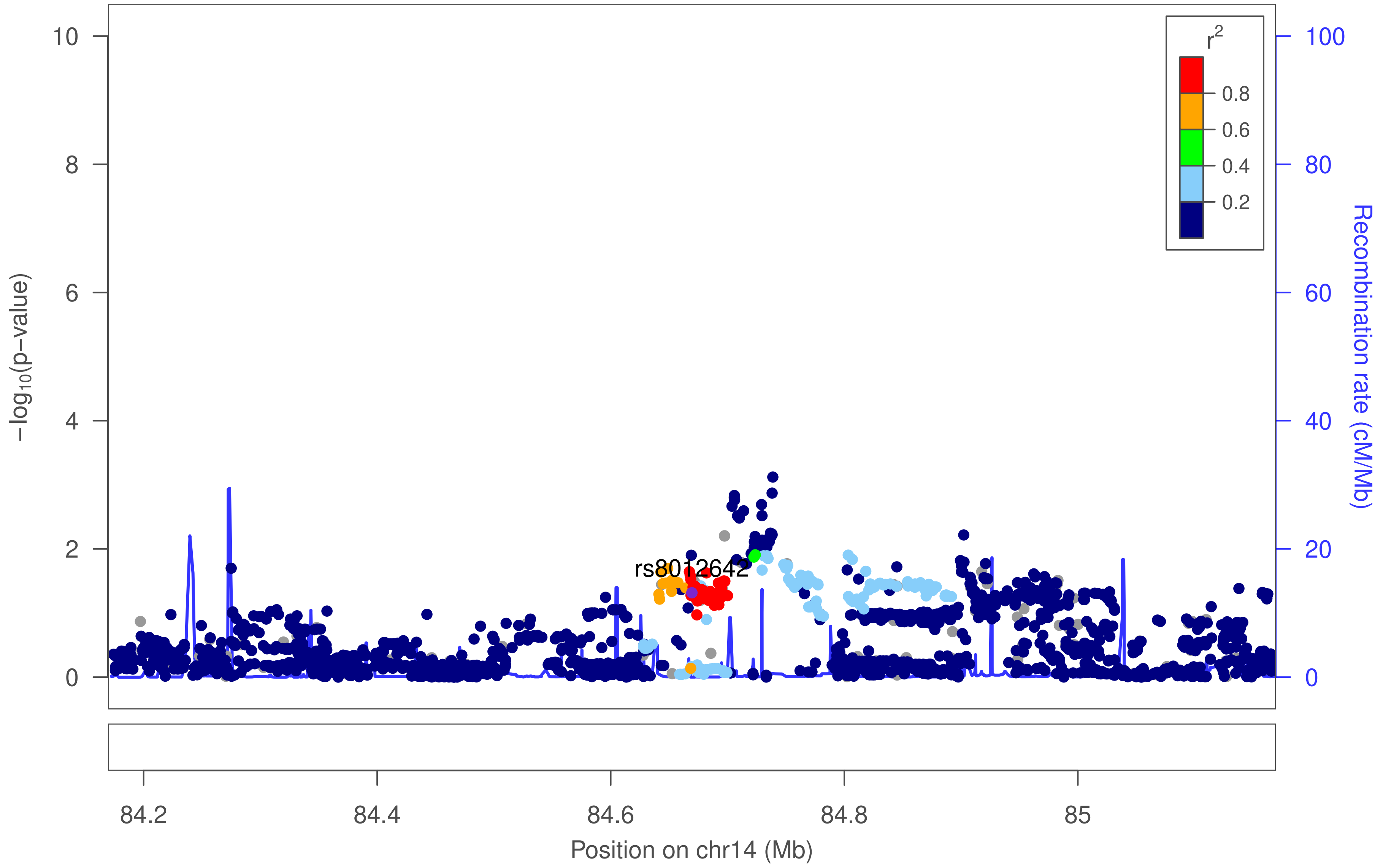
Chinese–only rs72843506



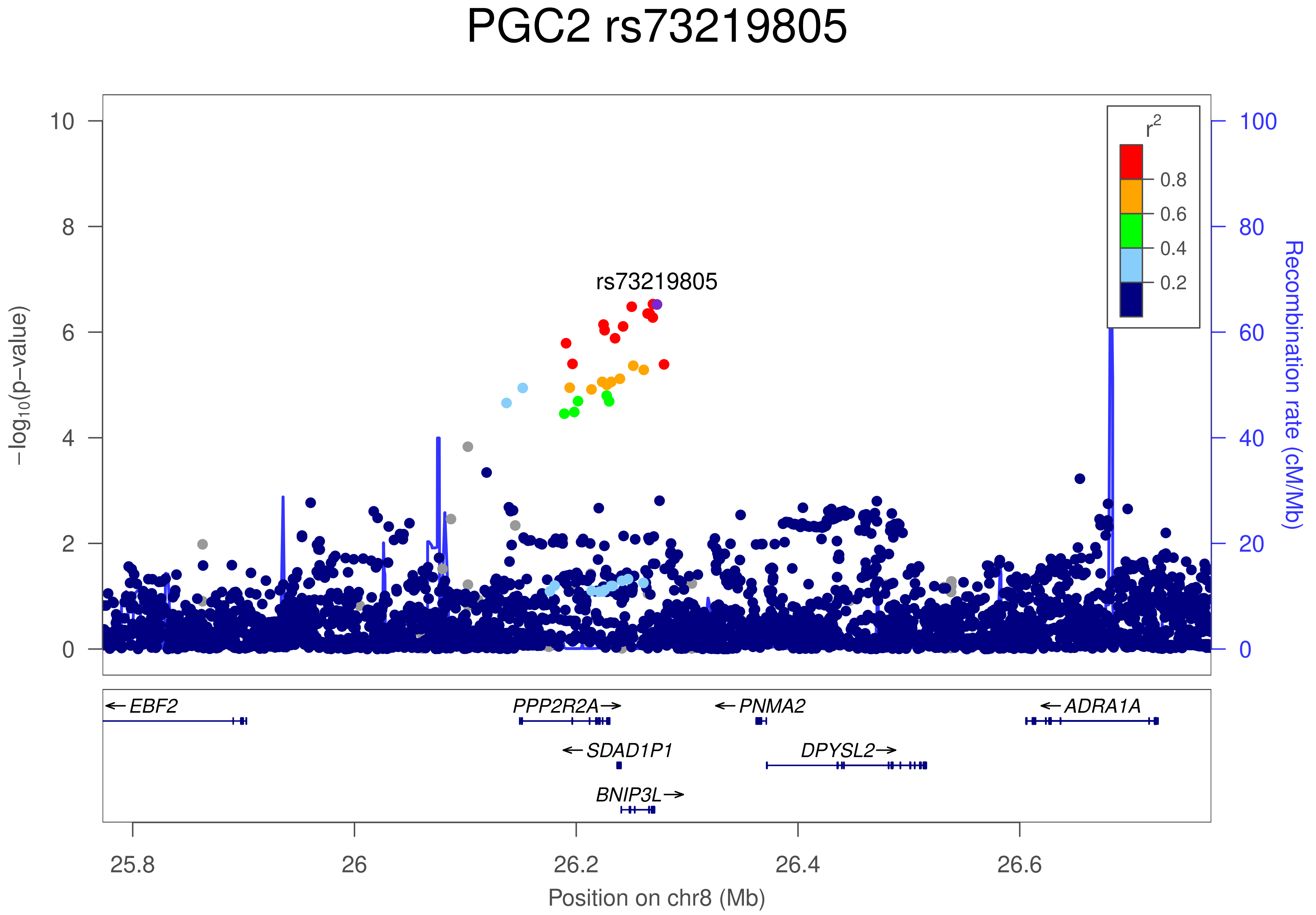

PGC2 rs8012642
r^2
0.8
0.6
0.4
0.2
rs8012642
−log10(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
84.2
84.4
84.6
84.8
85
Position on chr14 (Mb)

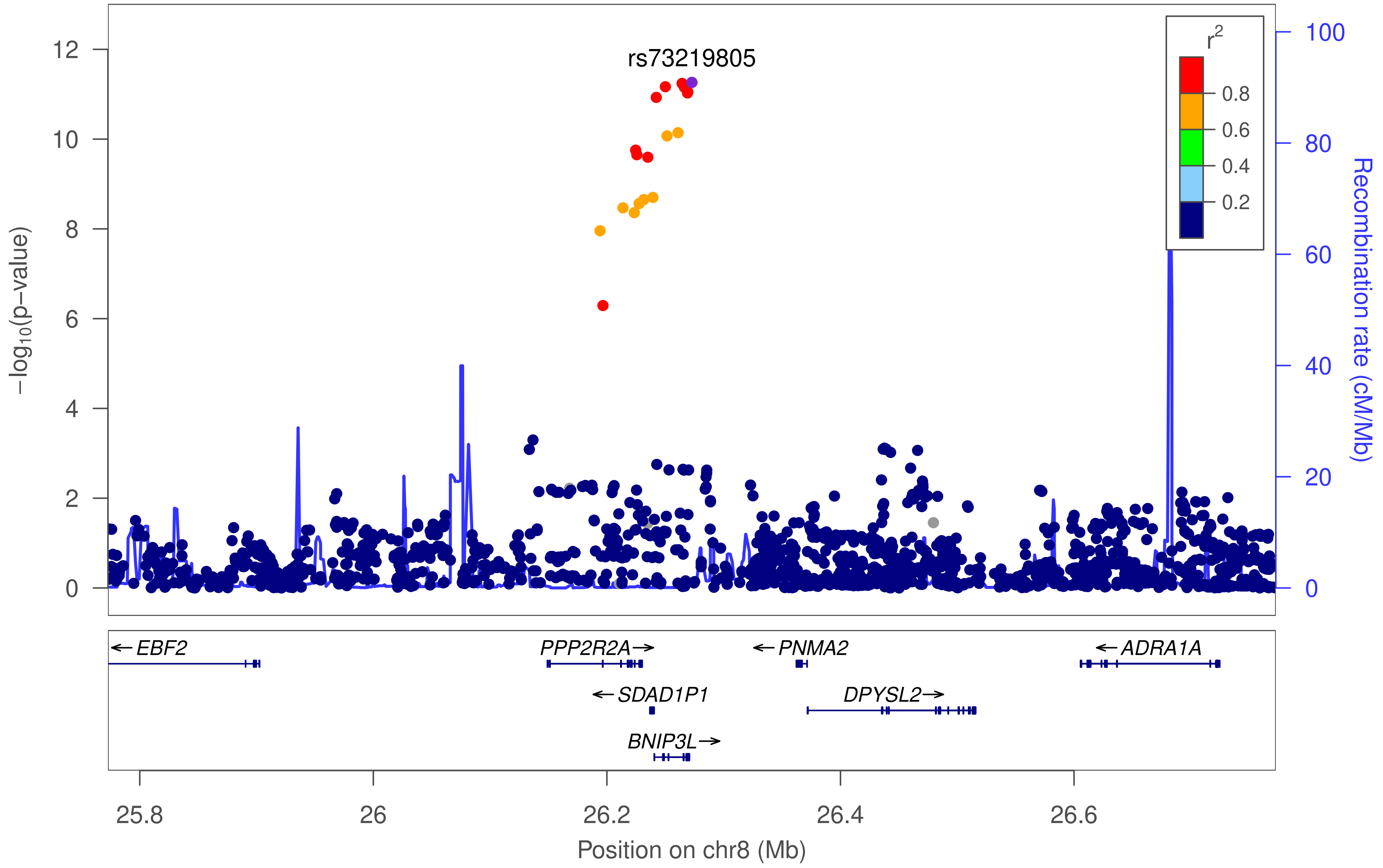
PGC2+Chinese rs8012642





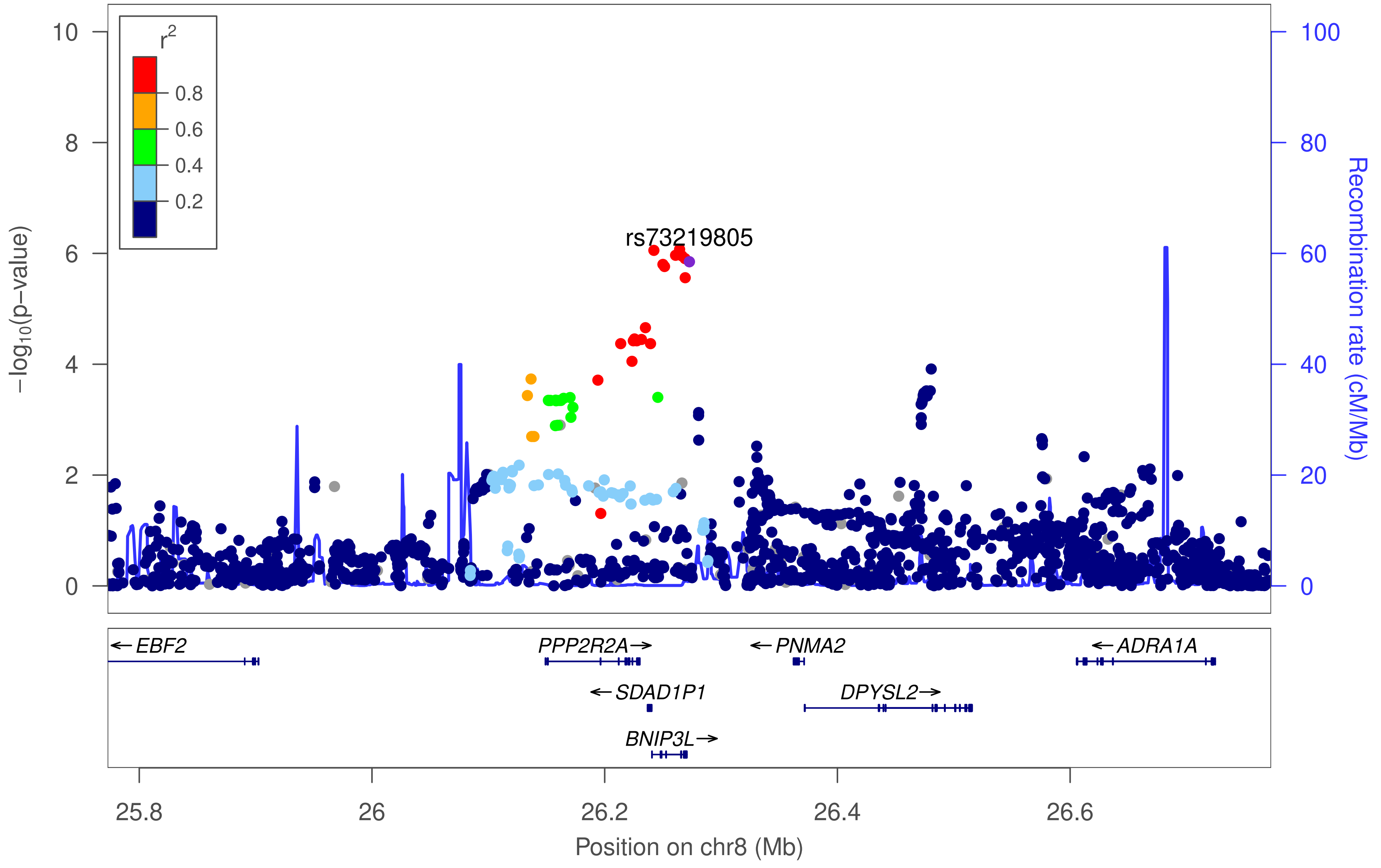
Chinese–only rs8012642


PGC2 rs73219805
rs73219805
r2
0.8
0.6
0.4
0.2
−log10(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
EBF2
PPP2R2A
SDAD1P1
BNIP3L
PNMA2
DPYSL2
ADRA1A
25.8
26
26.2
26.4
26.6
Position on chr8 (Mb)

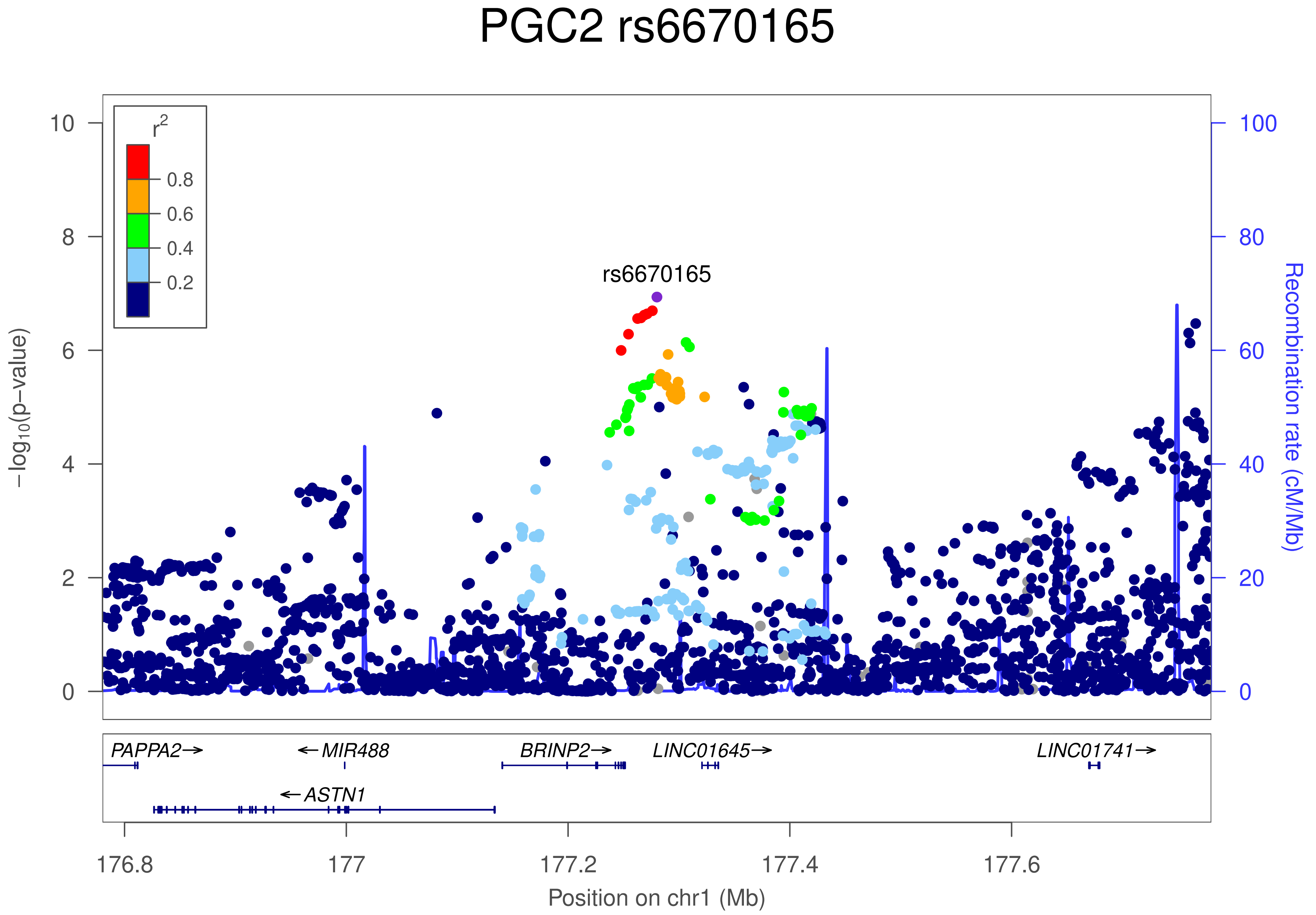


PGC2+Chinese rs73219805

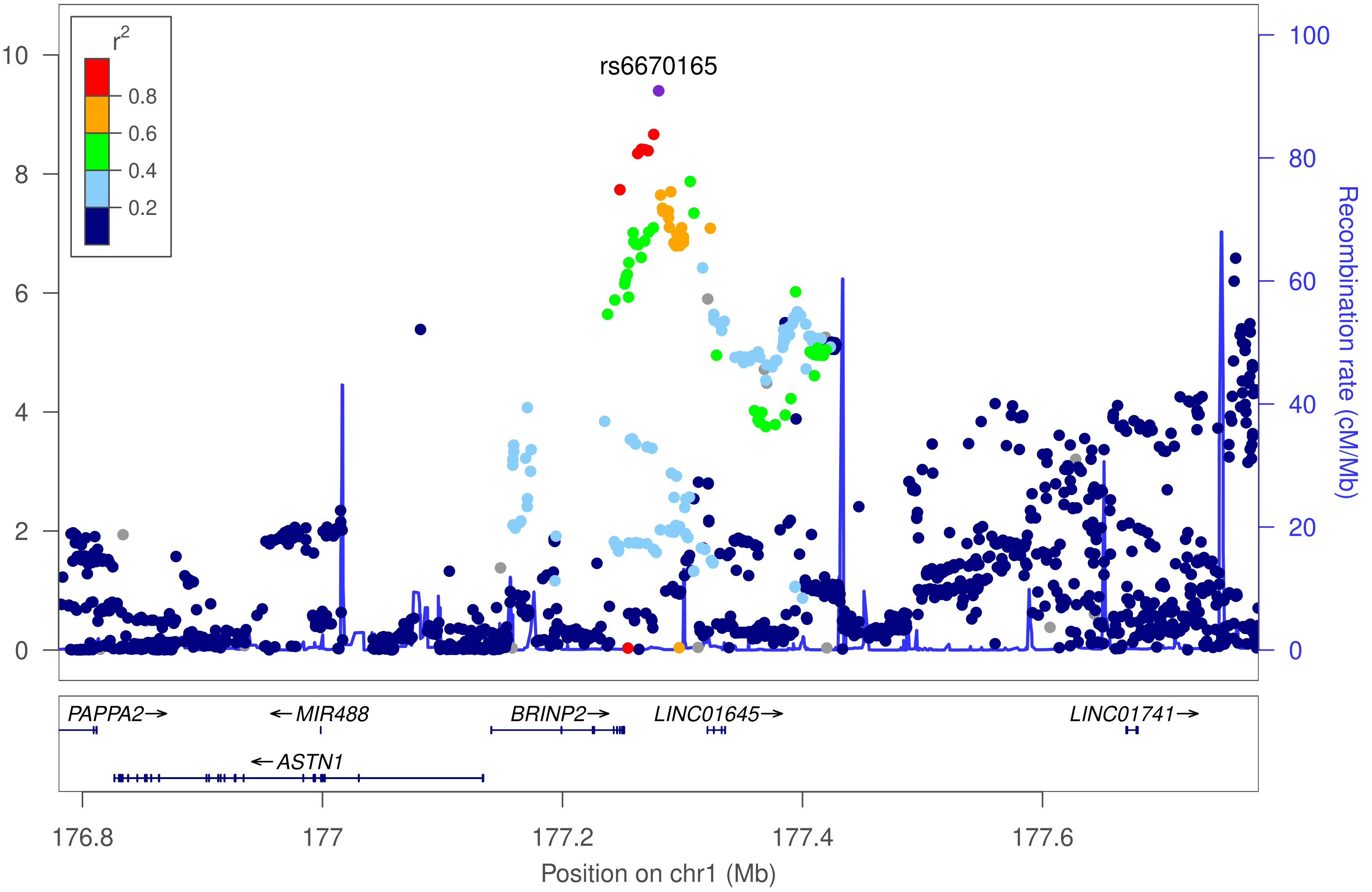
Chinese–only rs73219805

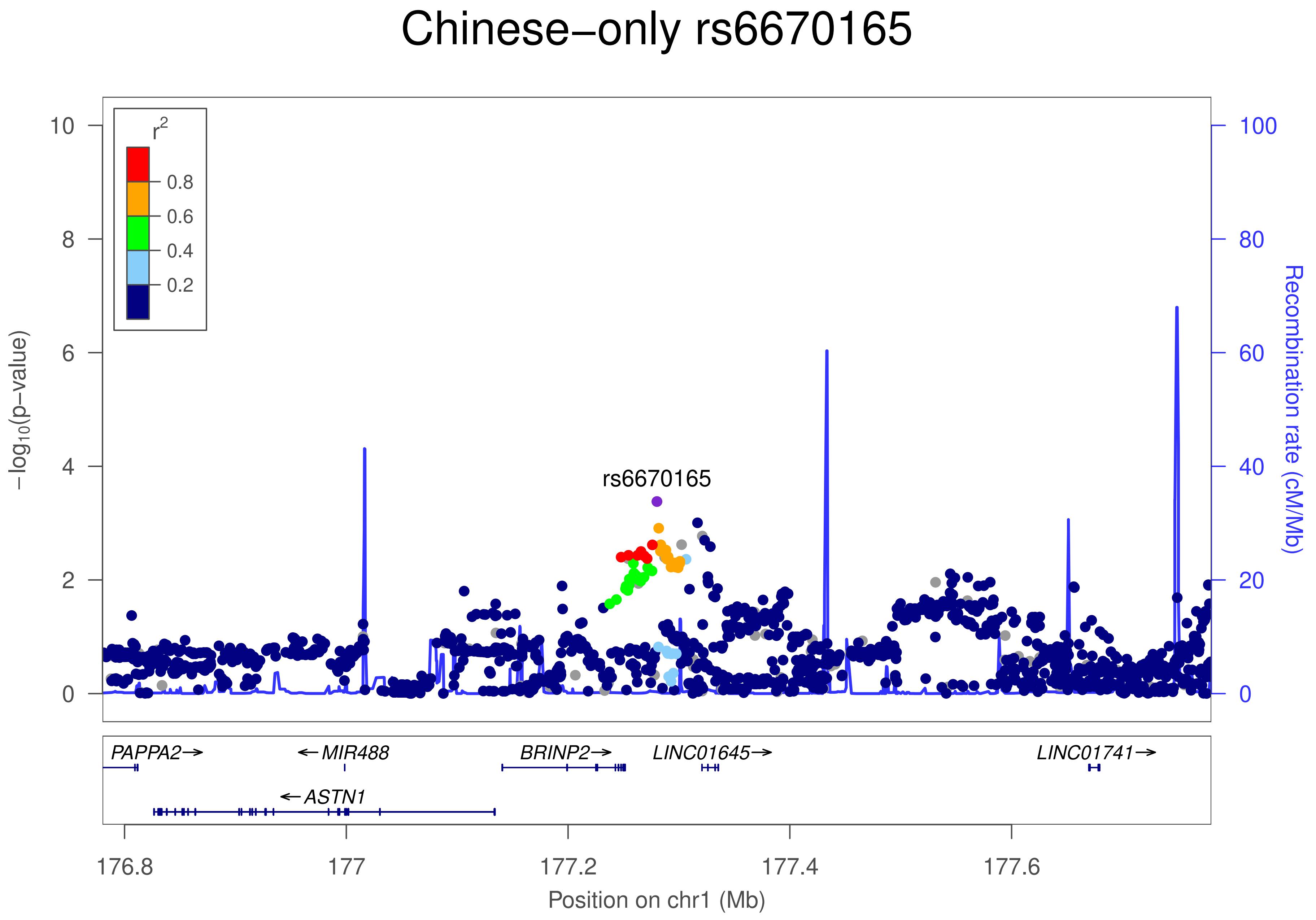


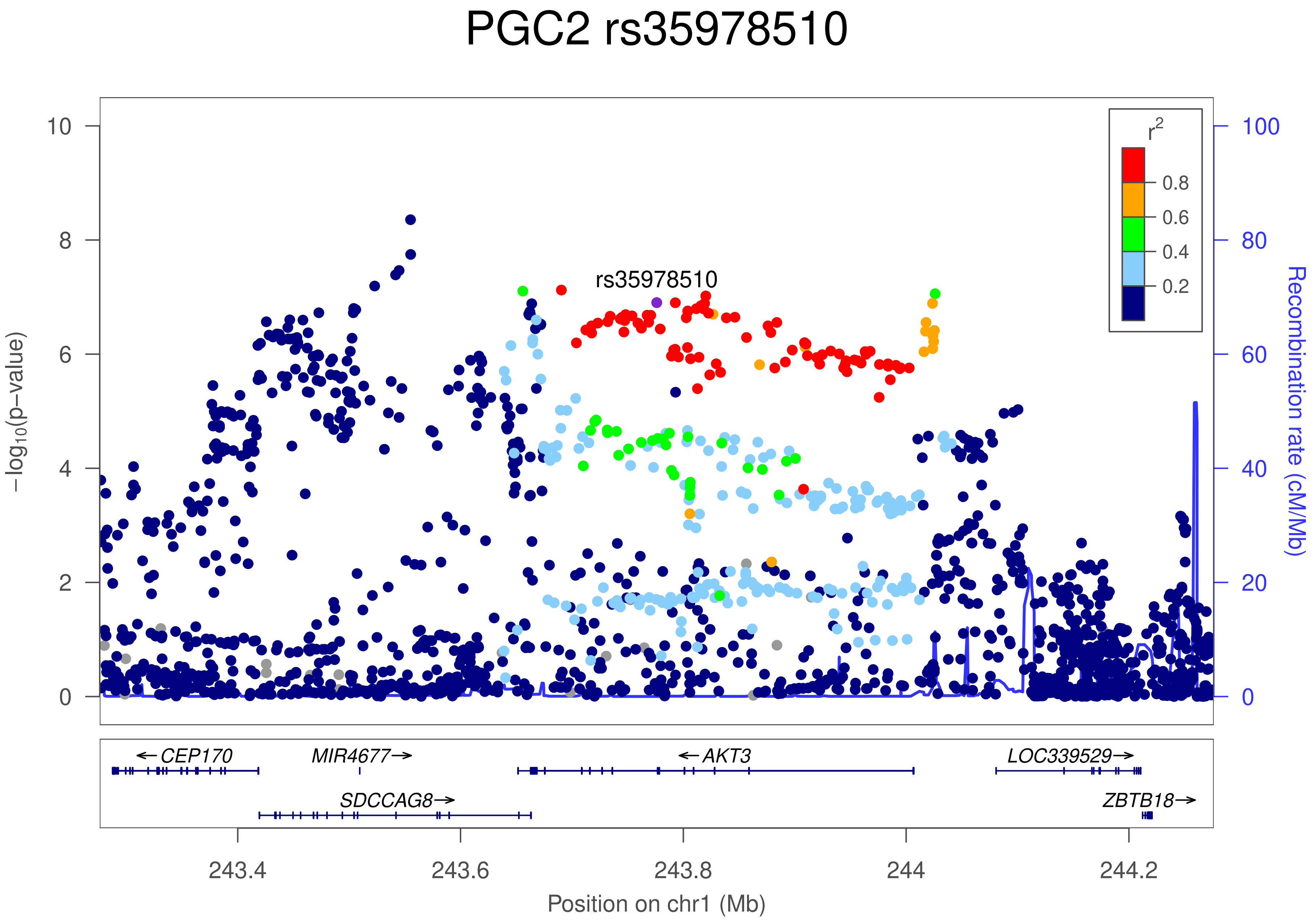
Known Loci


PGC2 rs6670165
r^2
0.8
0.6
0.4
0.2
rs6670165
10
8
6
4
2
0
−log$_{10}$(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
PAPPA2→
←MIR488
BRINP2→
LINC01645→
LINC01741→
←ASTN1
176.8
177
177.2
177.4
177.6
Position on chr1 (Mb)

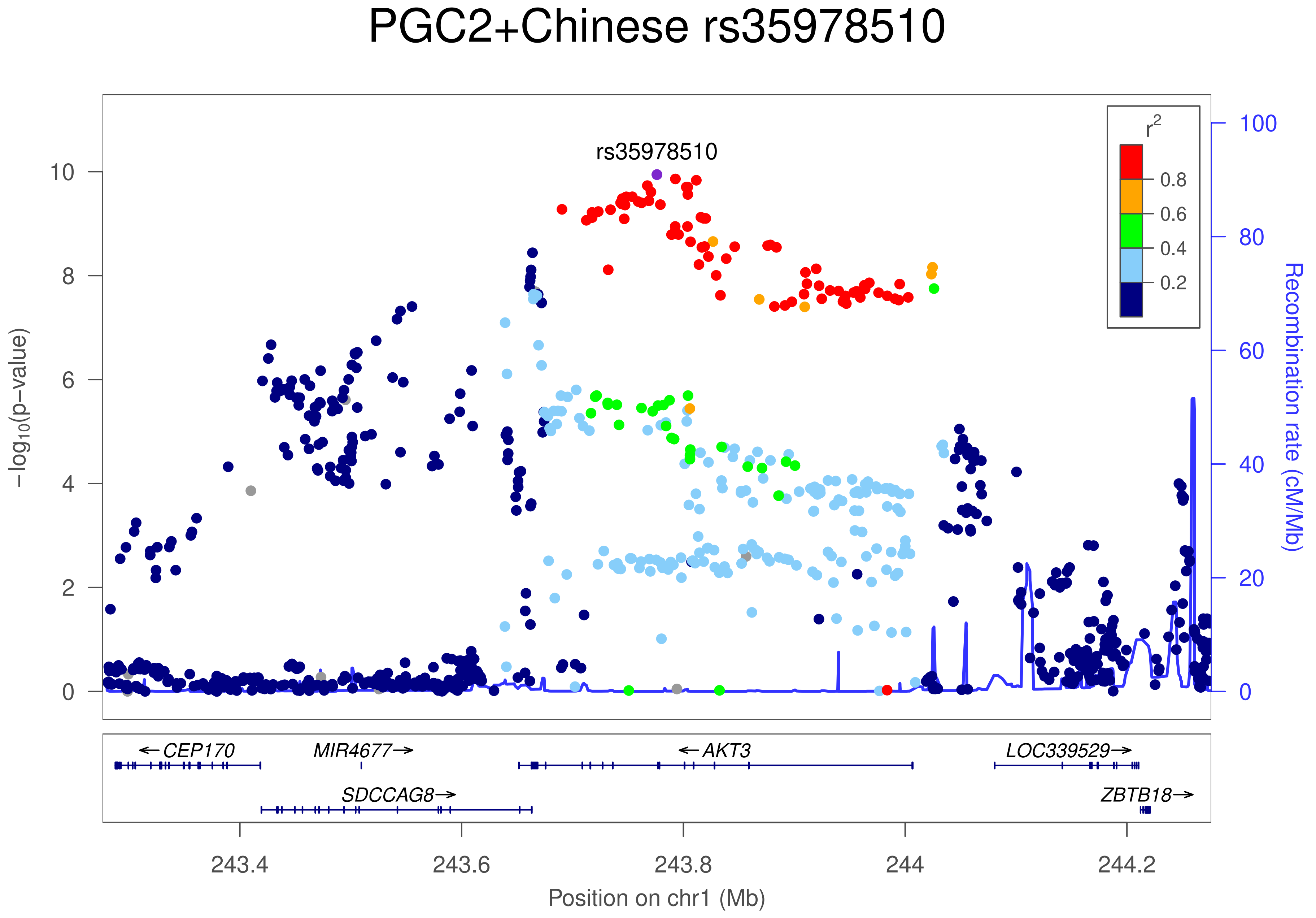
PGC2+Chinese rs6670165

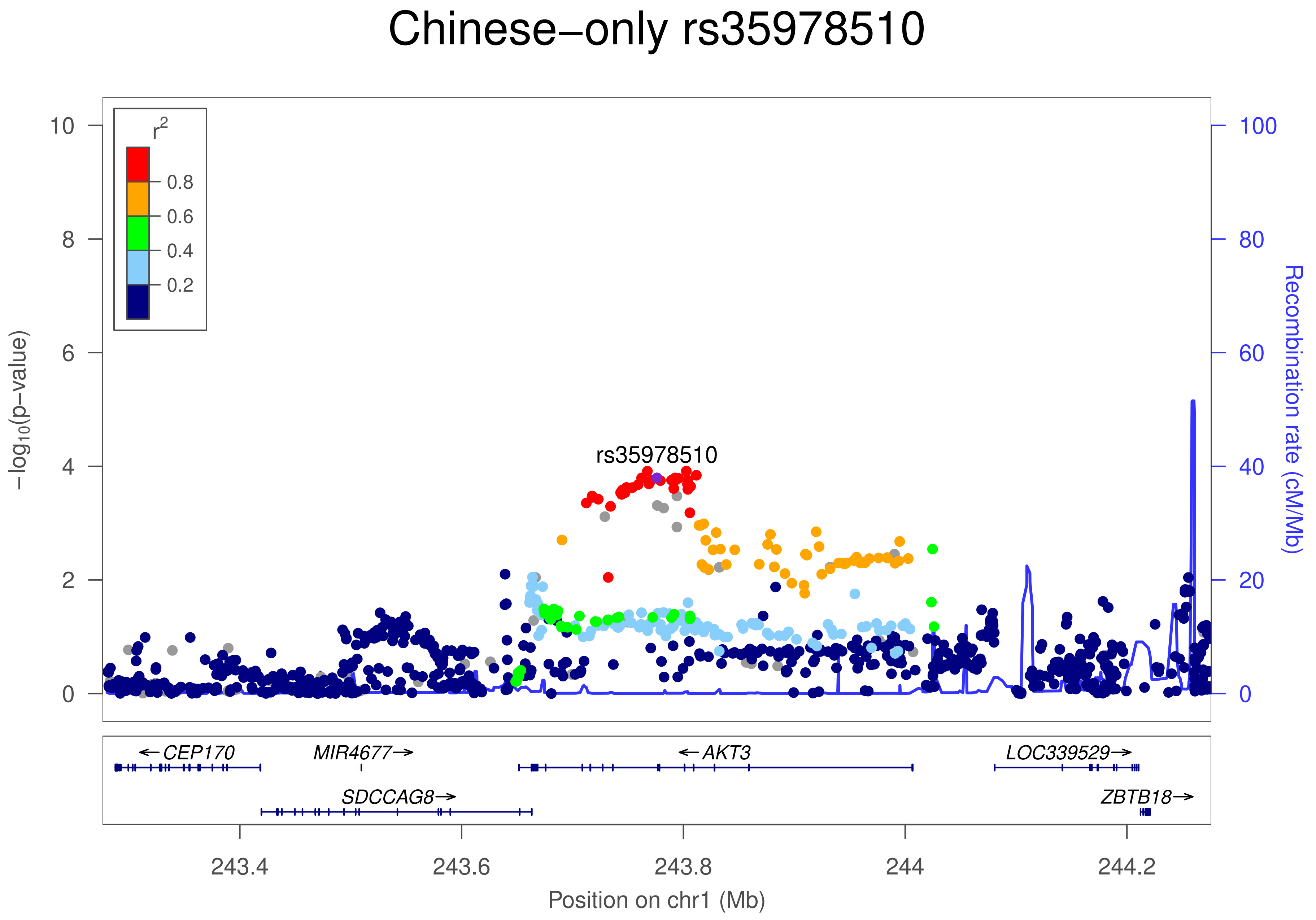



Chinese−only rs6670165
r2
0.8
0.6
0.4
0.2
−log10(p−value)
10
8
6
4
2
0
rs6670165
100
80
60
40
20
0
Recombination rate (cM/Mb)
PAPPA2→
←MIR488
BRINP2→
LINC01645→
LINC01741→
←ASTN1
176.8
177
177.2
177.4
177.6
Position on chr1 (Mb)

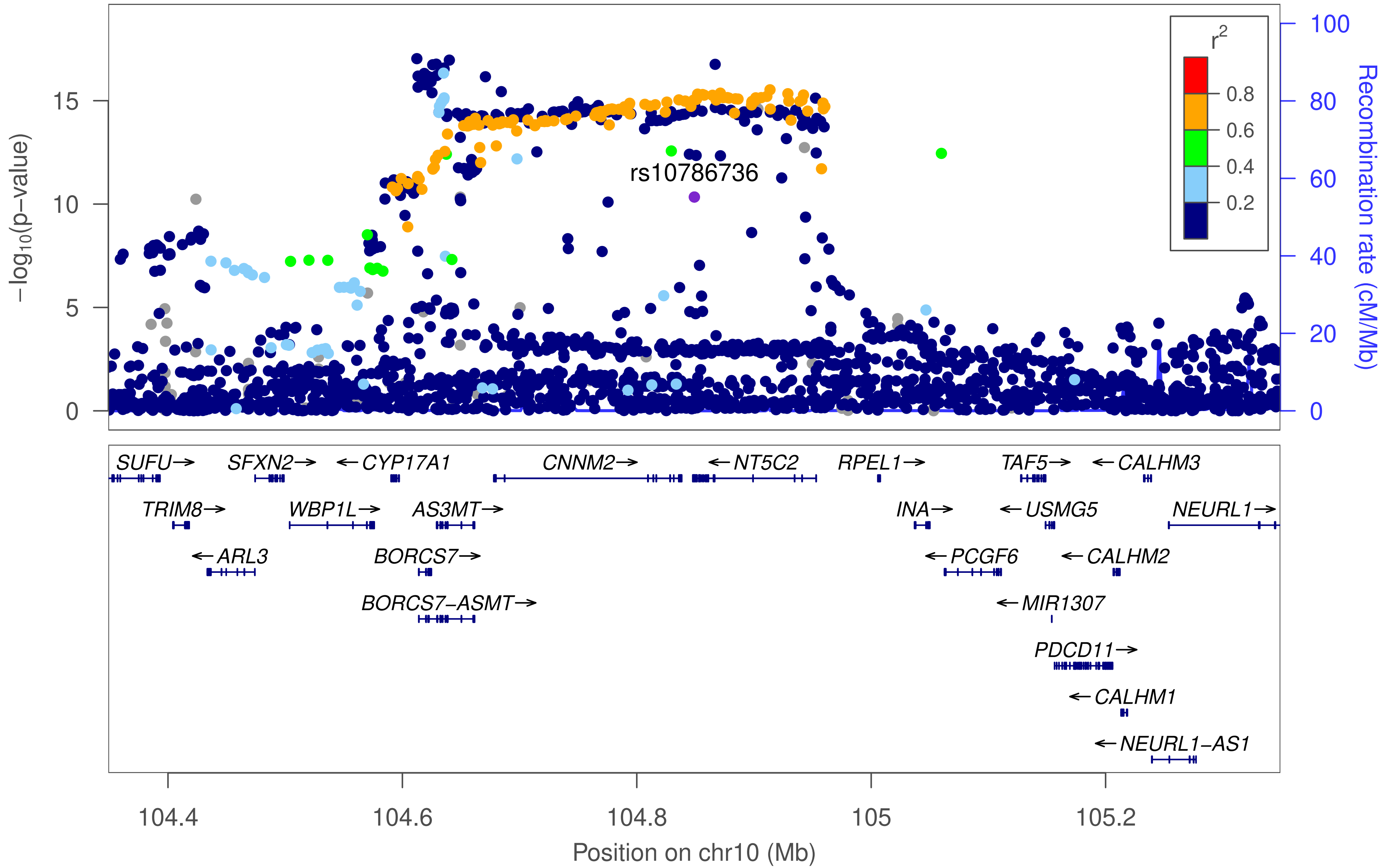


PGC2 rs35978510

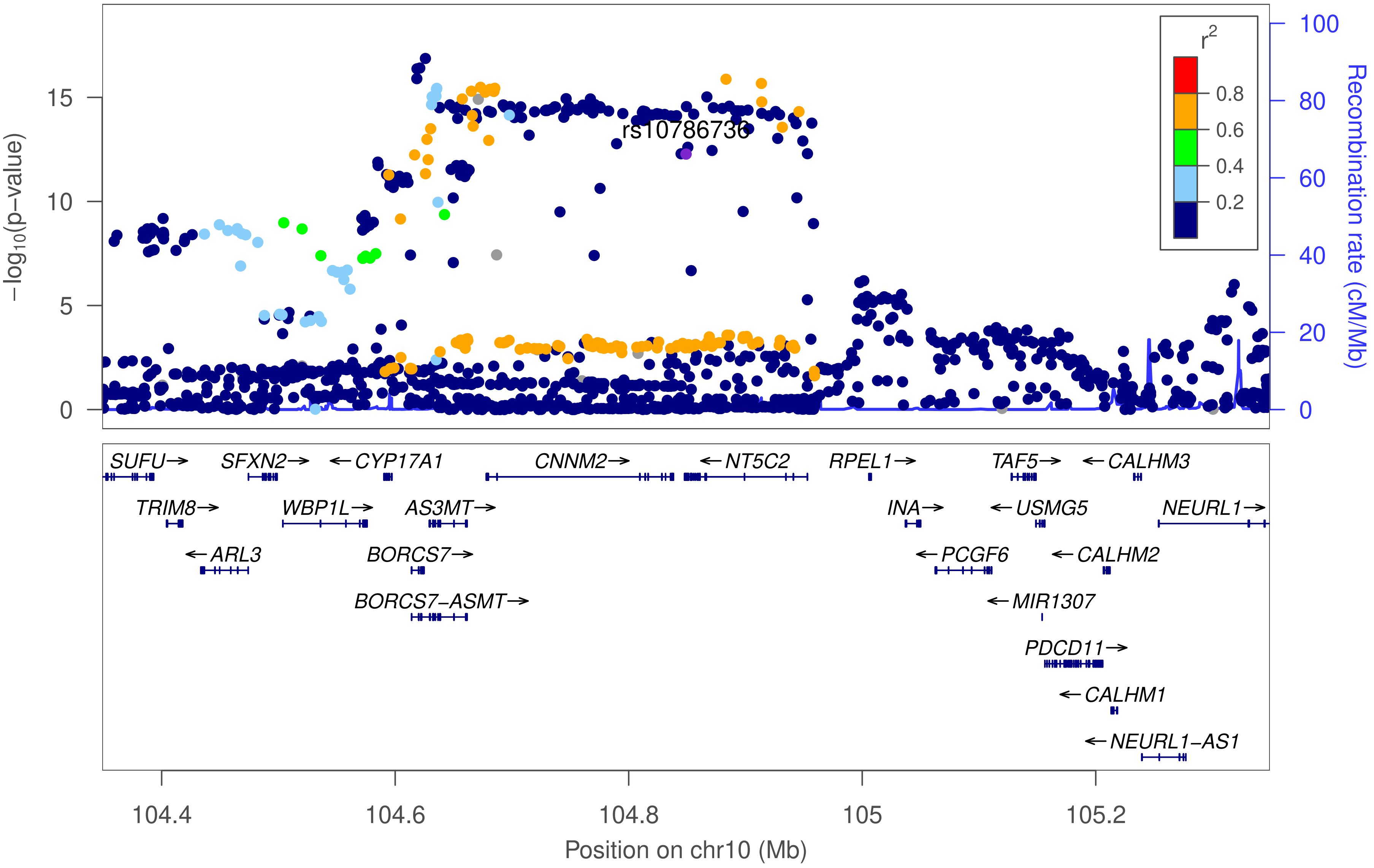

PGC2+Chinese rs35978510
rs35978510
r2
0.8
0.6
0.4
0.2
−log10(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
←CEP170
MIR4677→
←AKT3
LOC339529→
SDCCAG8→
ZBTB18→
243.4
243.6
243.8
244
244.2
Position on chr1 (Mb)

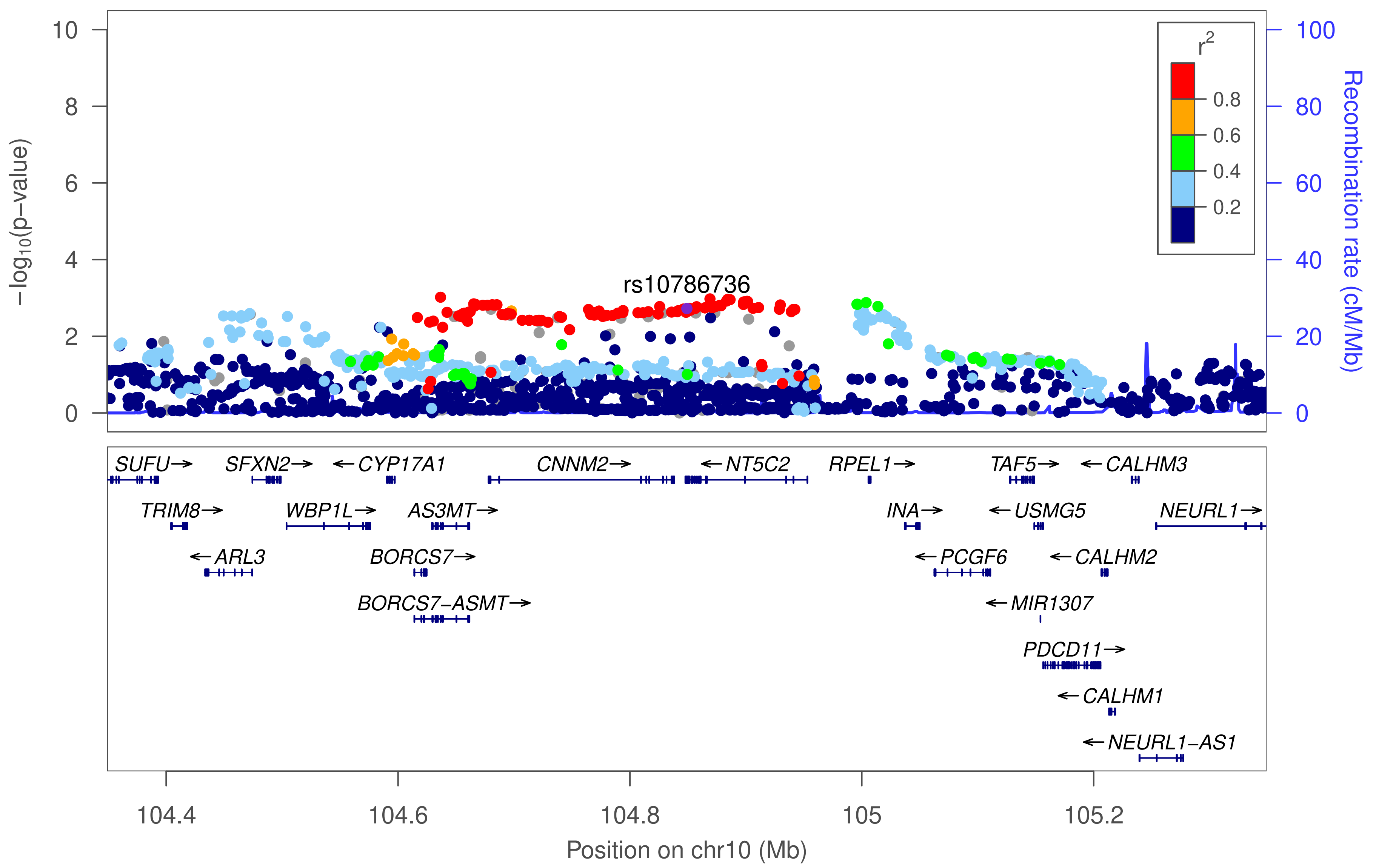

Chinese–only rs35978510
rs35978510
r²
0.8
0.6
0.4
0.2
−log₁₀(p−value)
10
8
6
4
2
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
←CEP170
MIR4677→
←AKT3
LOC339529→
SDCCAG8→
ZBTB18→
243.4
243.6
243.8
244
244.2
Position on chr1 (Mb)

PGC2 rs10786736

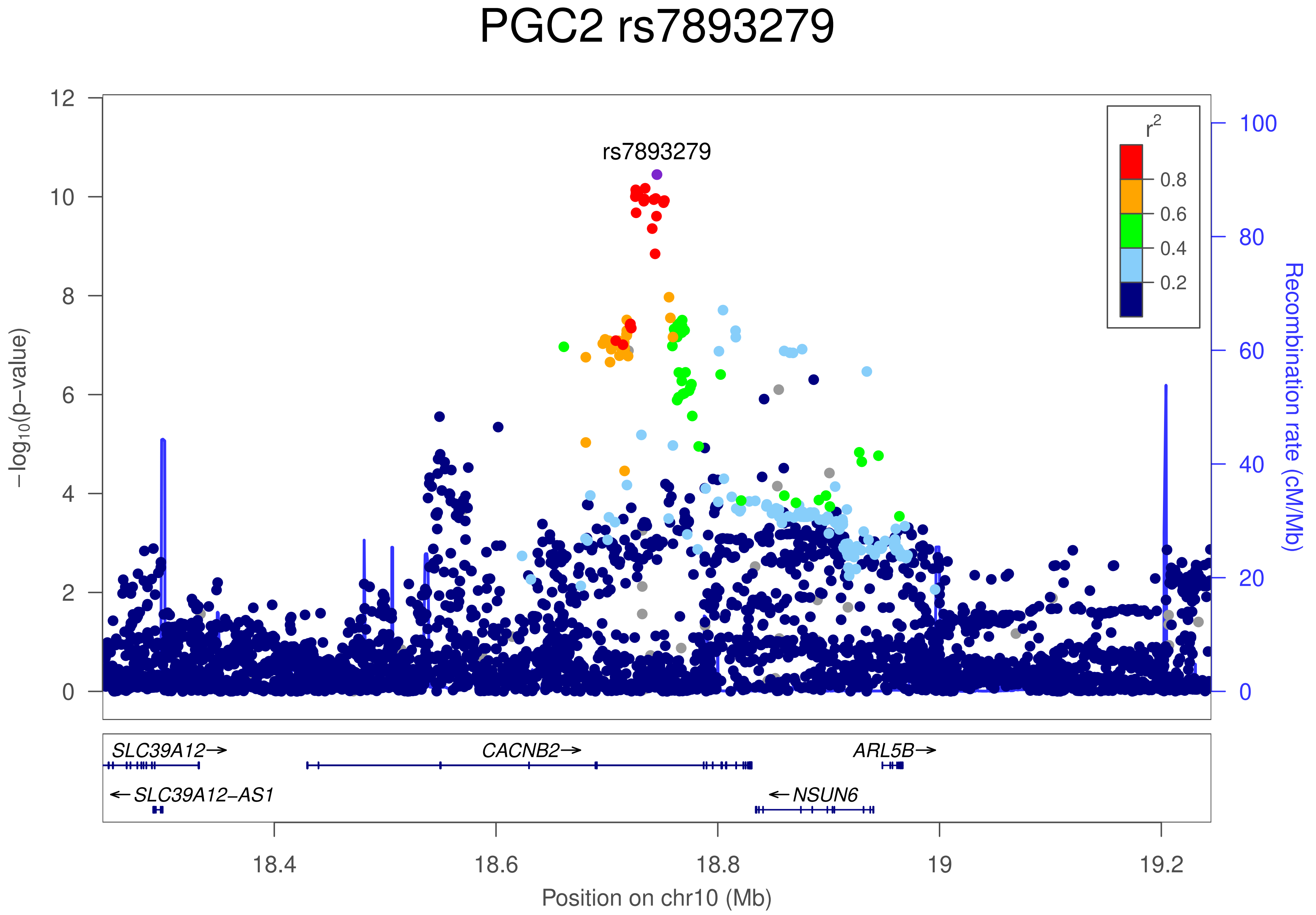


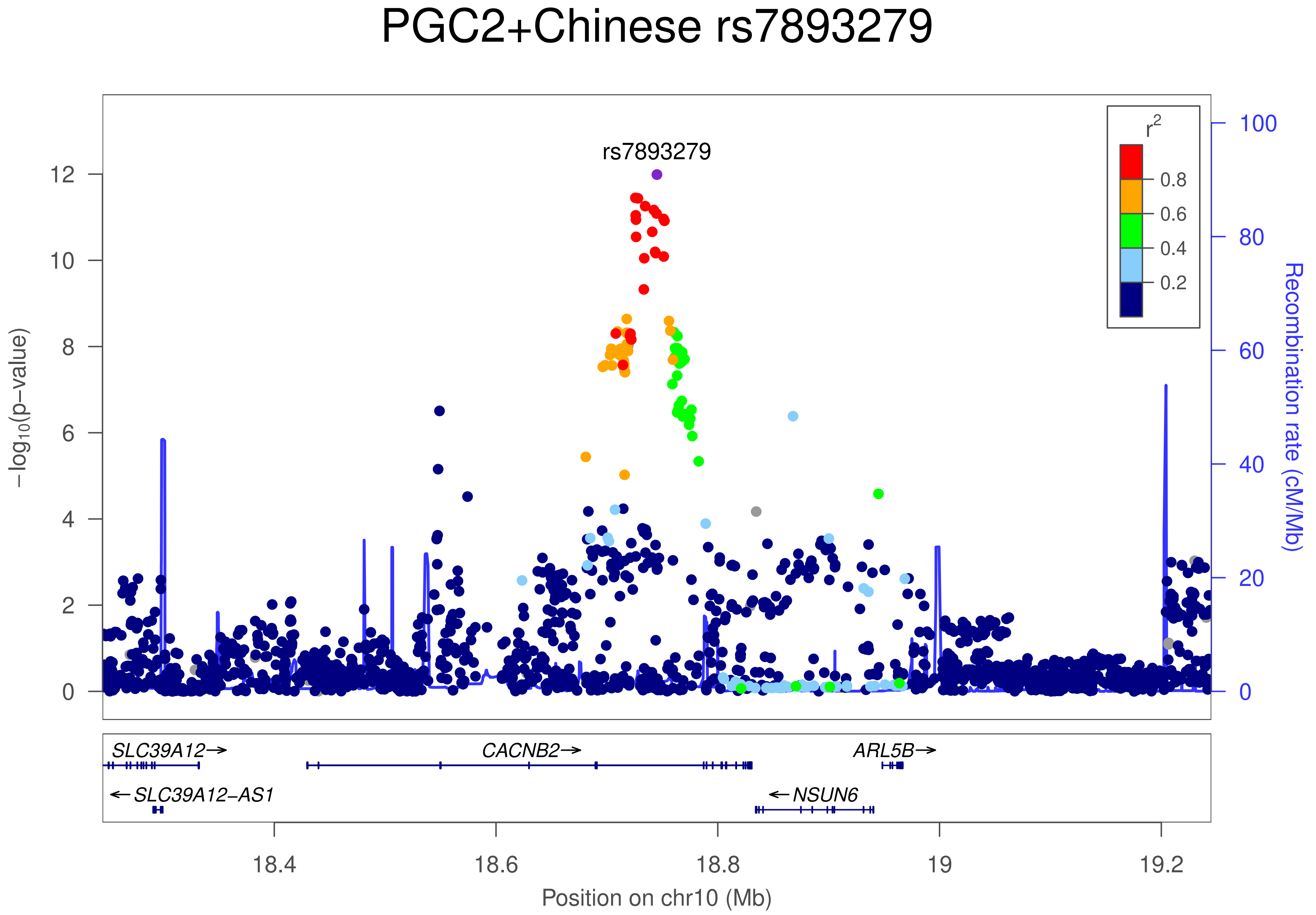
PGC2+Chinese rs10786736

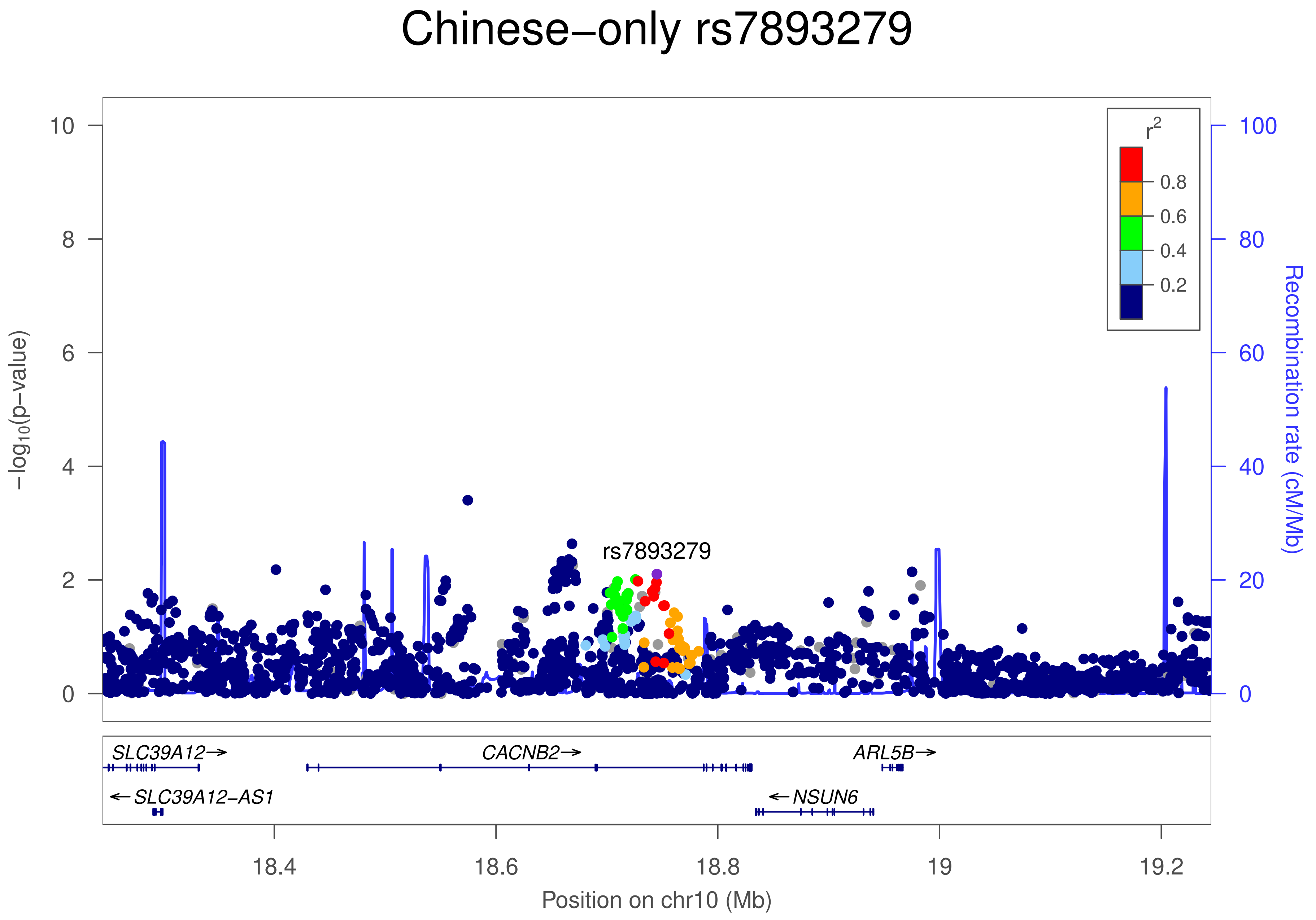




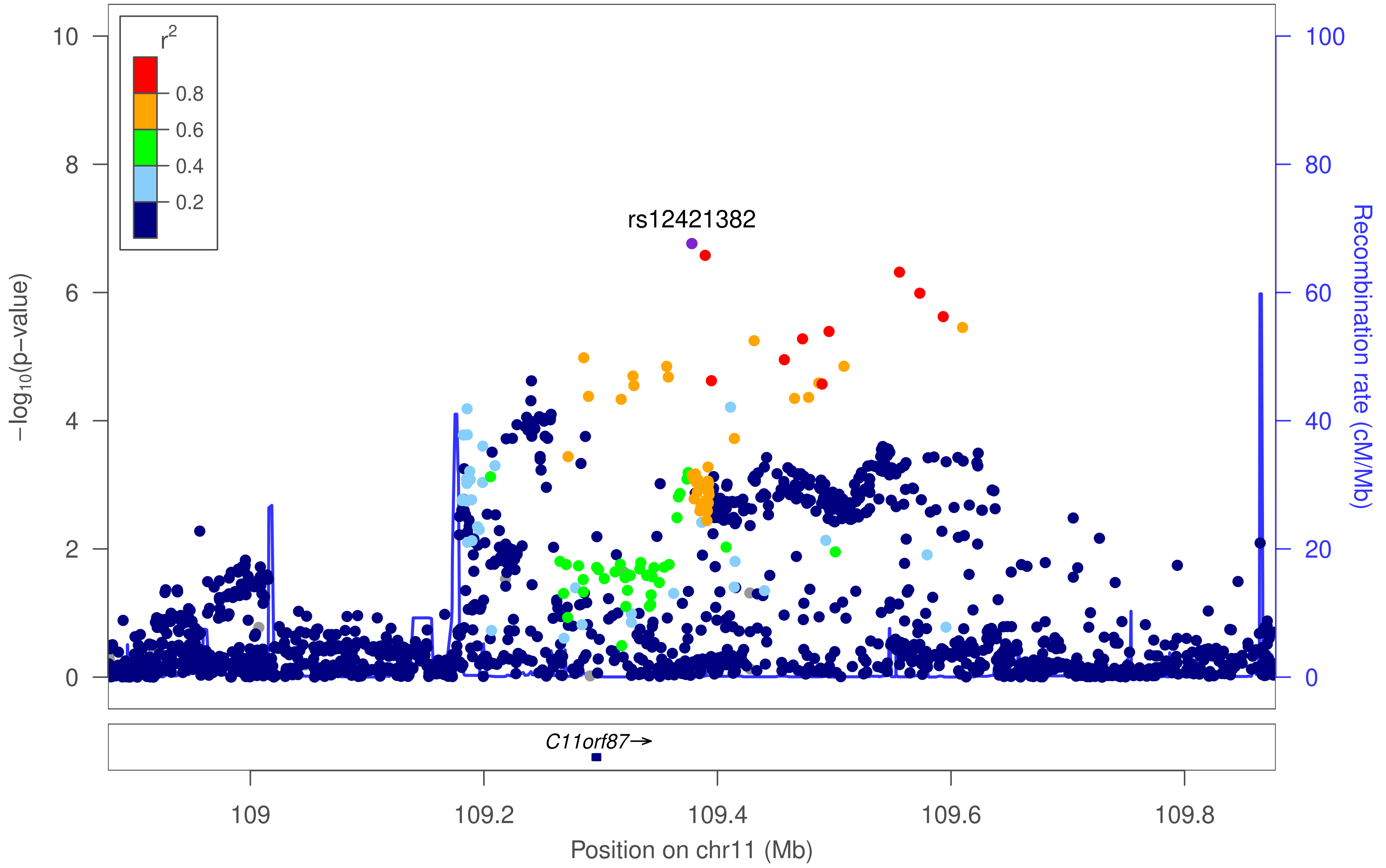
Chinese−only rs10786736


PGC2 rs7893279
rs7893279
−log10(p−value)
0
2
4
6
8
10
12
Recombination rate (cM/Mb)
0
20
40
60
80
100
r2
0.8
0.6
0.4
0.2
SLC39A12→
CACNB2→
ARL5B→
←SLC39A12−AS1
←NSUN6
18.4
18.6
18.8
19
19.2
Position on chr10 (Mb)

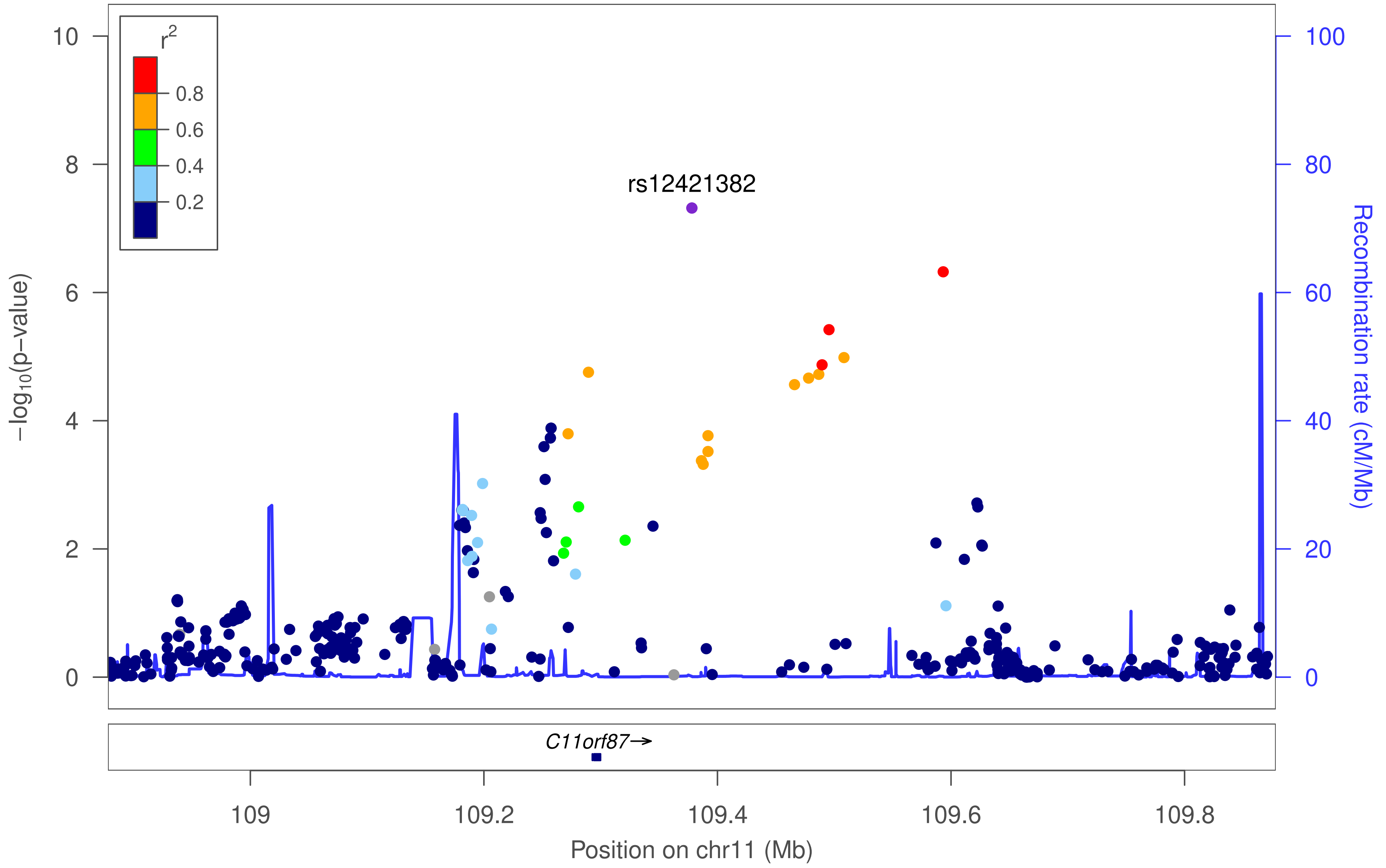

PGC2+Chinese rs7893279
rs7893279
−log10(p−value)
0
2
4
6
8
10
12
Recombination rate (cM/Mb)
0
20
40
60
80
100
r²
0.8
0.6
0.4
0.2
SLC39A12→
CACNB2→
ARL5B→
←SLC39A12−AS1
←NSUN6
18.4
18.6
18.8
19
19.2
Position on chr10 (Mb)

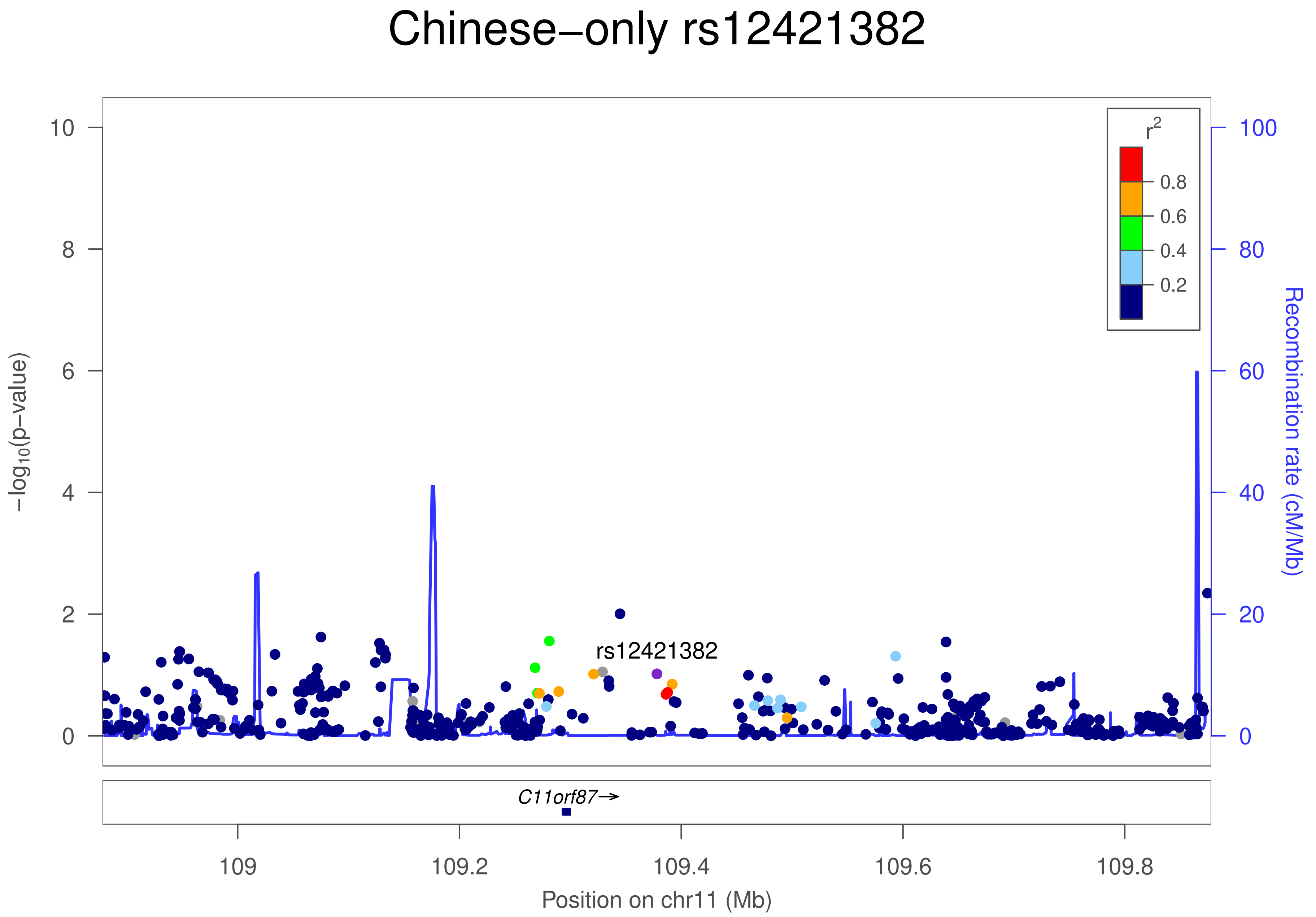

Chinese−only rs7893279
−log10(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
r2
0.8
0.6
0.4
0.2
rs7893279
SLC39A12→
CACNB2→
ARL5B→
←SLC39A12−AS1
←NSUN6
18.4
18.6
18.8
19
19.2
Position on chr10 (Mb)

PGC2 rs12421382

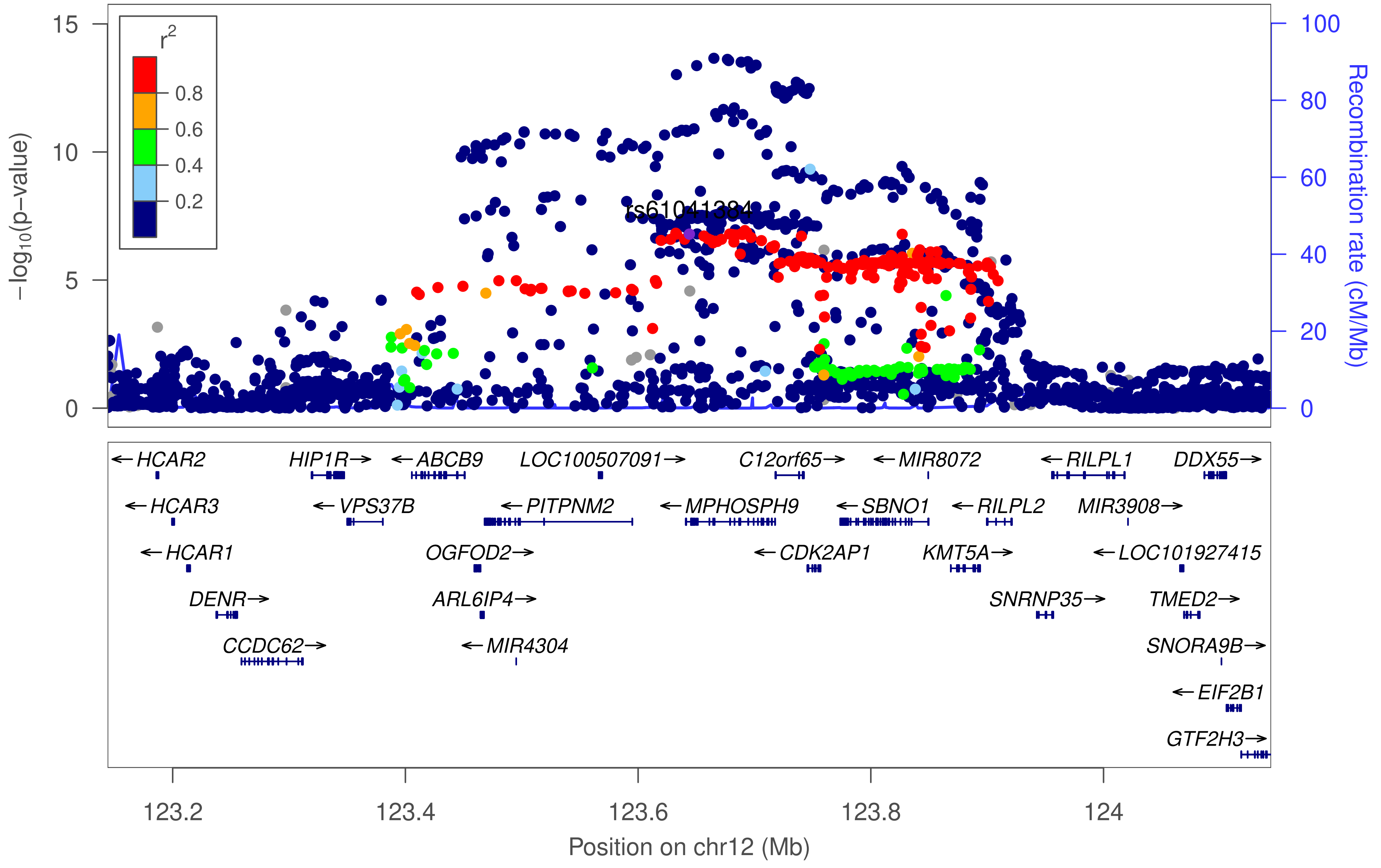


PGC2+Chinese rs12421382



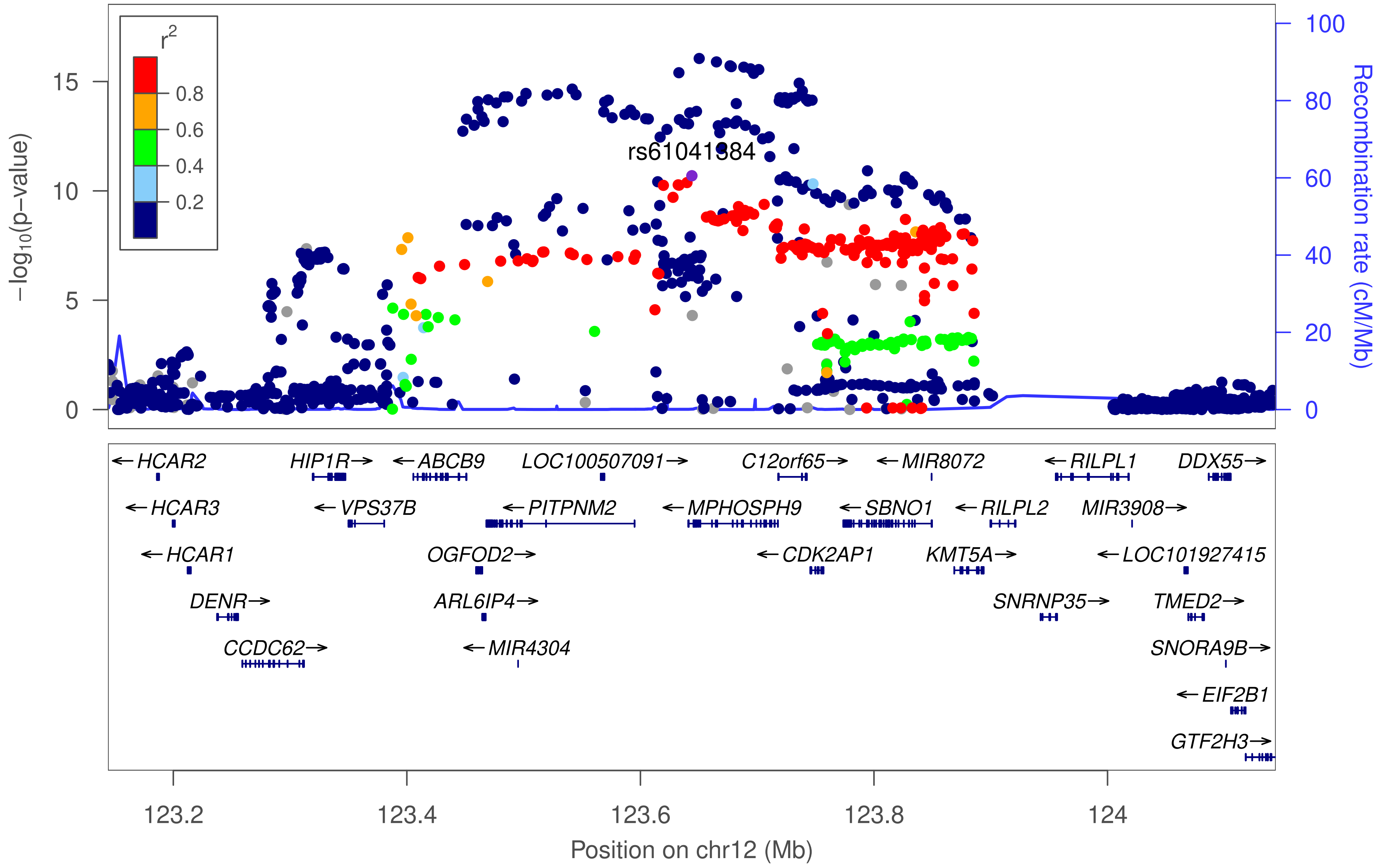


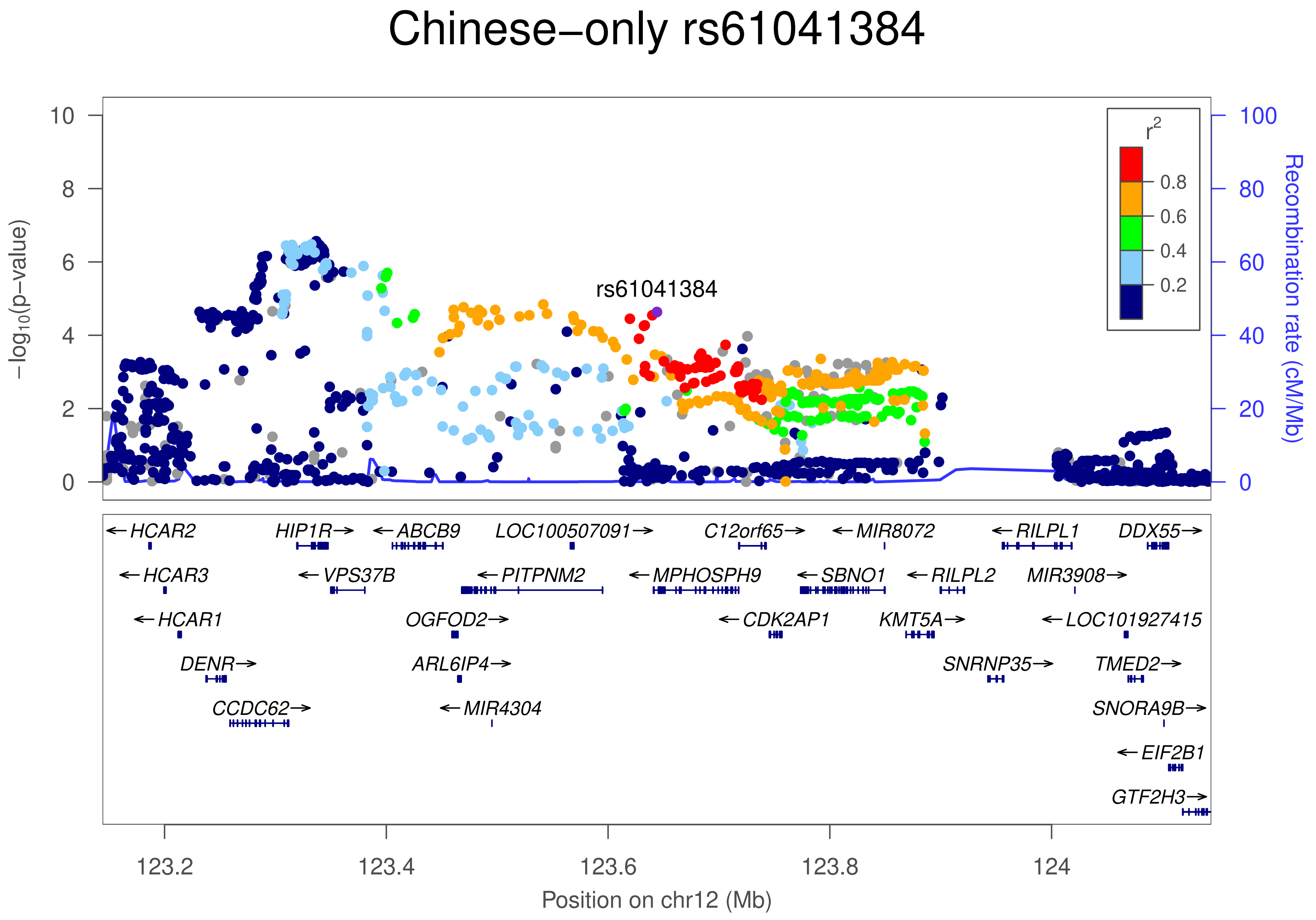
Chinese–only rs12421382
−log10(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
r2
0.8
0.6
0.4
0.2
rs12421382
C11orf87→
109
109.2
109.4
109.6
109.8
Position on chr11 (Mb)

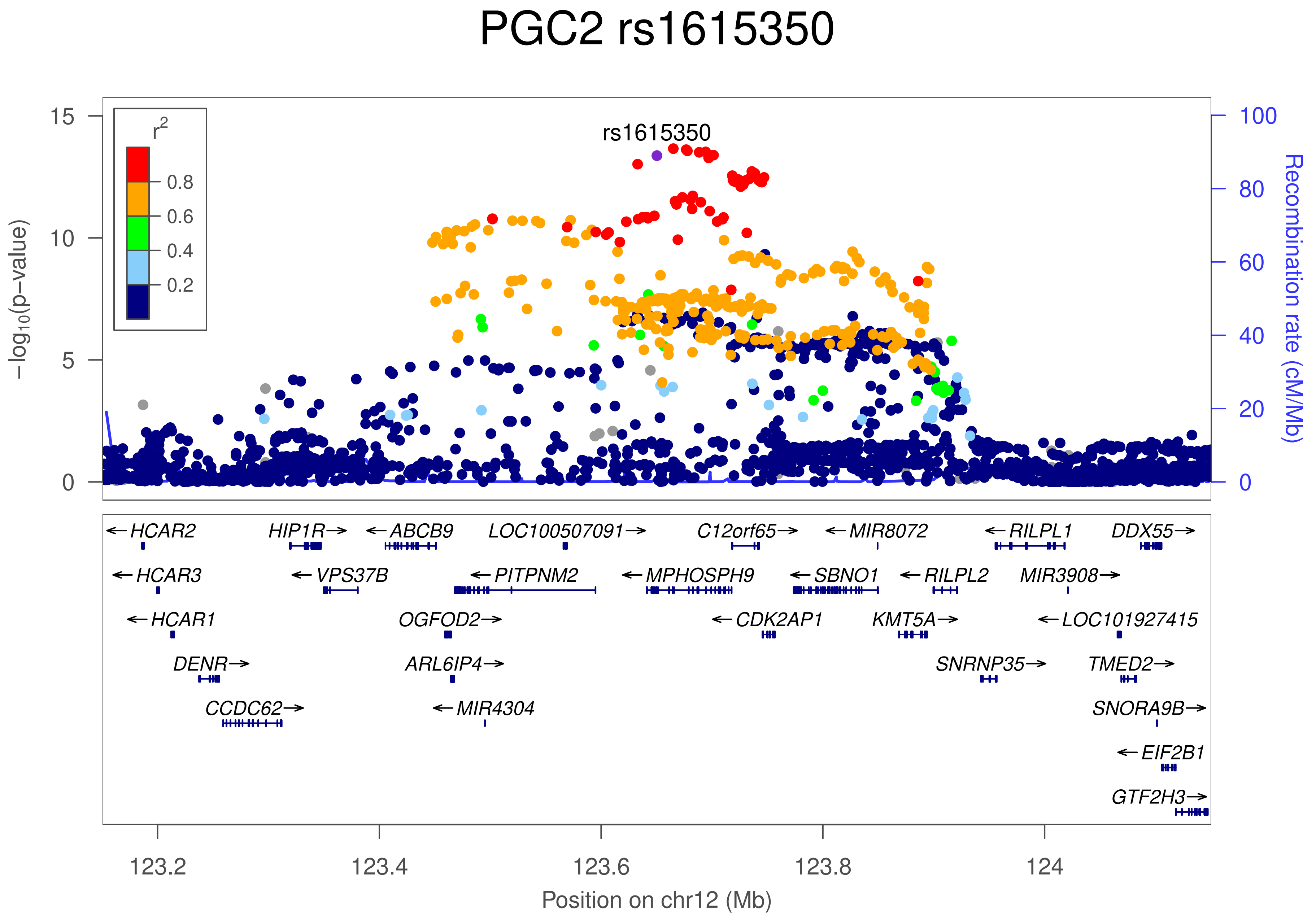


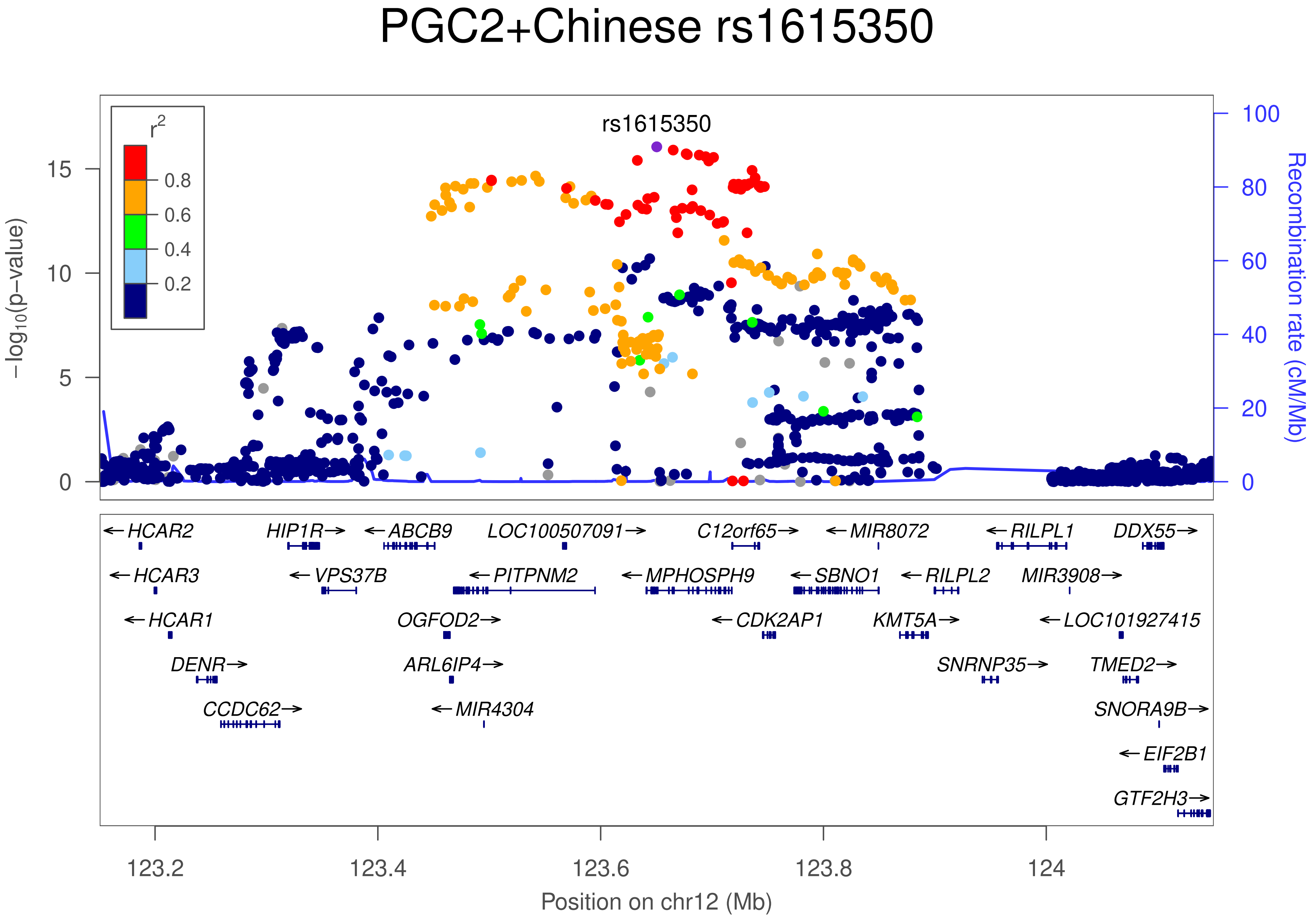
PGC2 rs61041384

PGC2+Chinese rs61041384

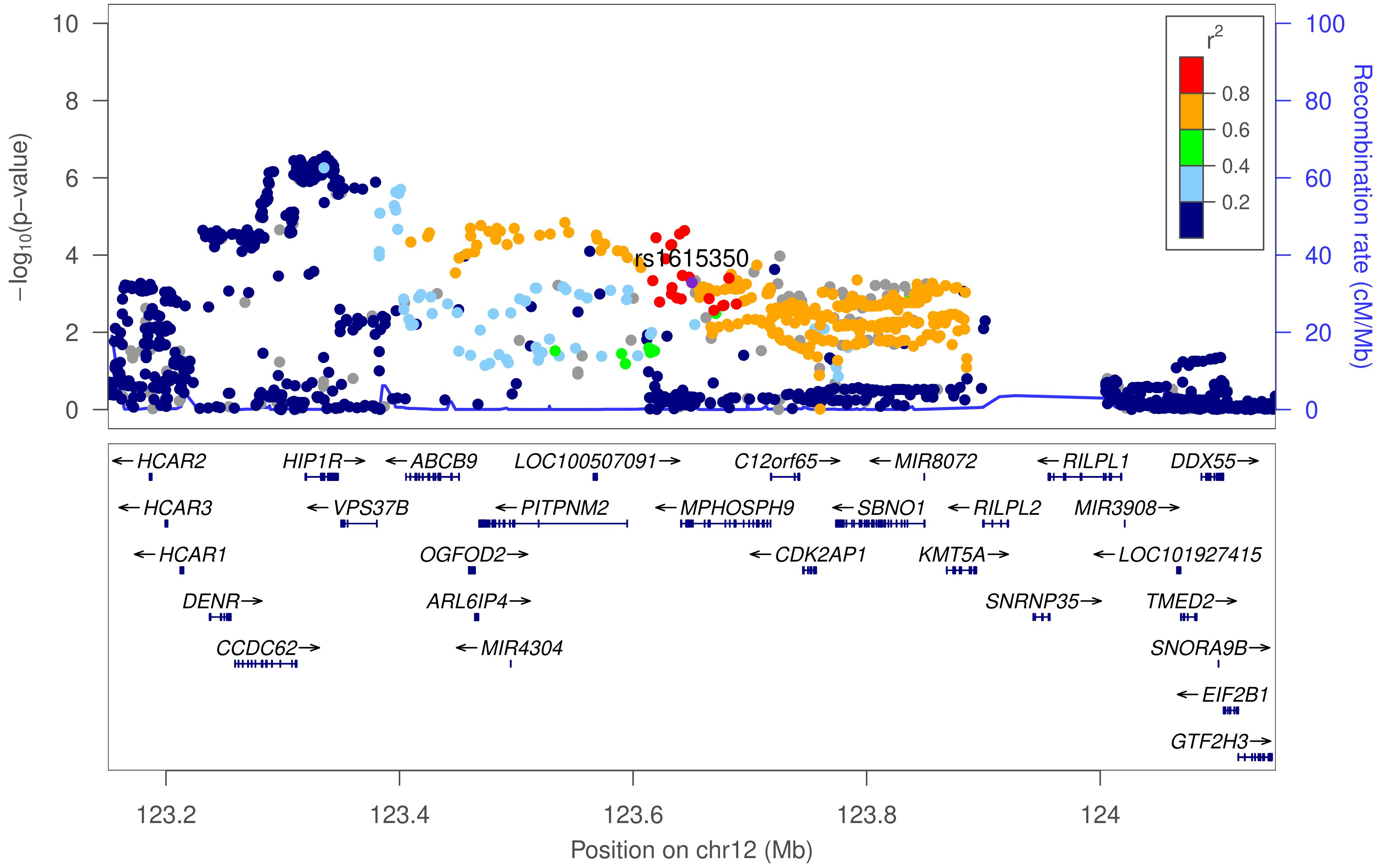



Chinese−only rs61041384
rs61041384
−log10(p−value)
10
8
6
4
2
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
r²
0.8
0.6
0.4
0.2
←HCAR2
HIP1R→
←ABCB9
LOC100507091→
C12orf65→
←MIR8072
←RILPL1
DDX55→
←HCAR3
←VPS37B
←PITPNM2
←MPHOSPH9
←SBNO1
←RILPL2
MIR3908→
←HCAR1
OGFOD2→
←CDK2AP1
KMT5A→
←LOC101927415
DENR→
ARL6IP4→
SNRNP35→
TMED2→
CCDC62→
←MIR4304
SNORA9B→
←EIF2B1
GTF2H3→
123.2
123.4
123.6
123.8
124
Position on chr12 (Mb)

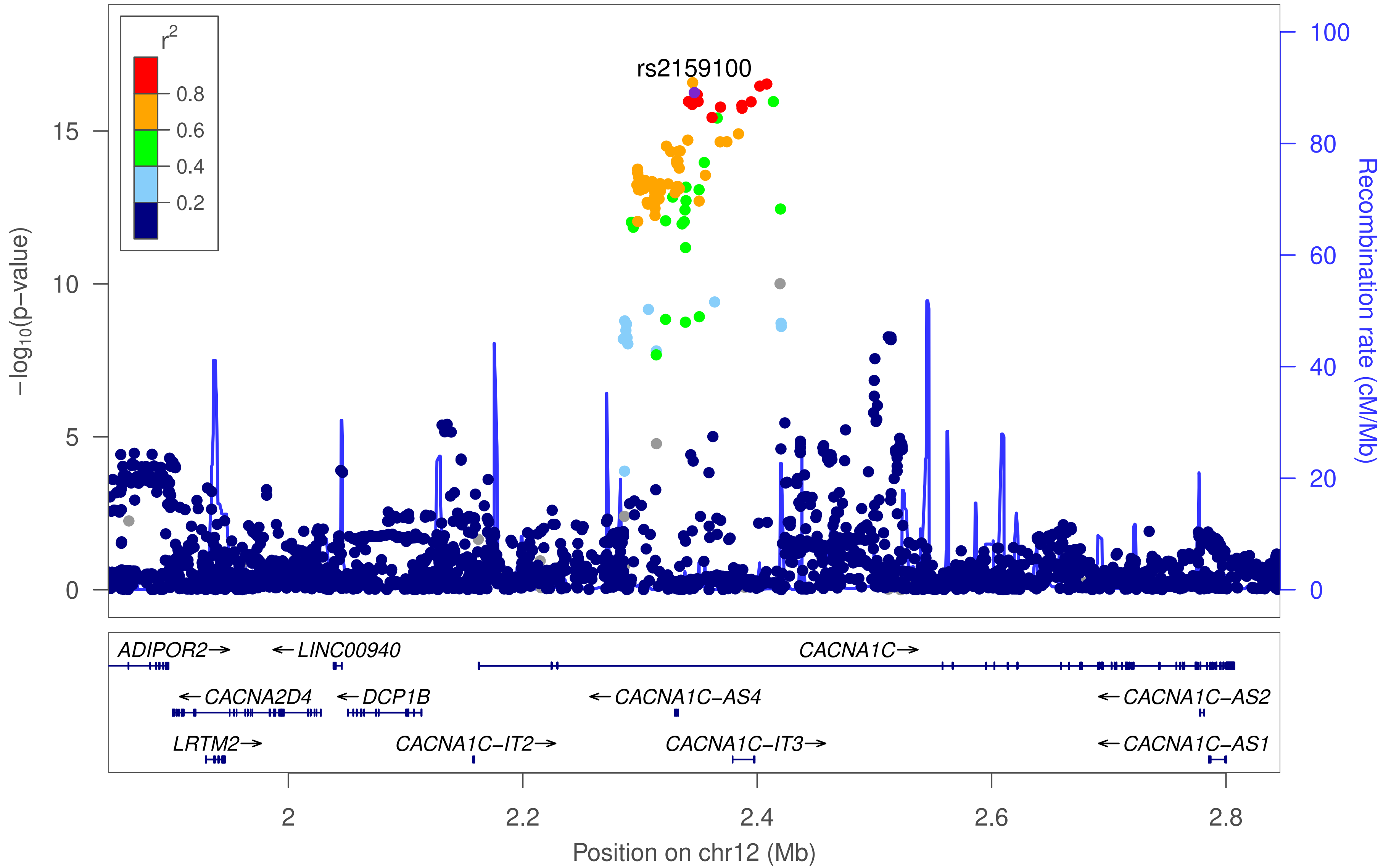

PGC2 rs1615350
rs1615350
r2
0.8
0.6
0.4
0.2
−log10(p−value)
15
10
5
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
←HCAR2
HIP1R→
←ABCB9
LOC100507091→
C12orf65→
←MIR8072
←RILPL1
DDX55→
←HCAR3
←VPS37B
←PITPNM2
←MPHOSPH9
←SBNO1
←RILPL2
MIR3908→
←HCAR1
OGFOD2→
←CDK2AP1
KMT5A→
←LOC101927415
DENR→
ARL6IP4→
SNRNP35→
TMED2→
CCDC62→
←MIR4304
SNORA9B→
←EIF2B1
GTF2H3→
123.2
123.4
123.6
123.8
124
Position on chr12 (Mb)

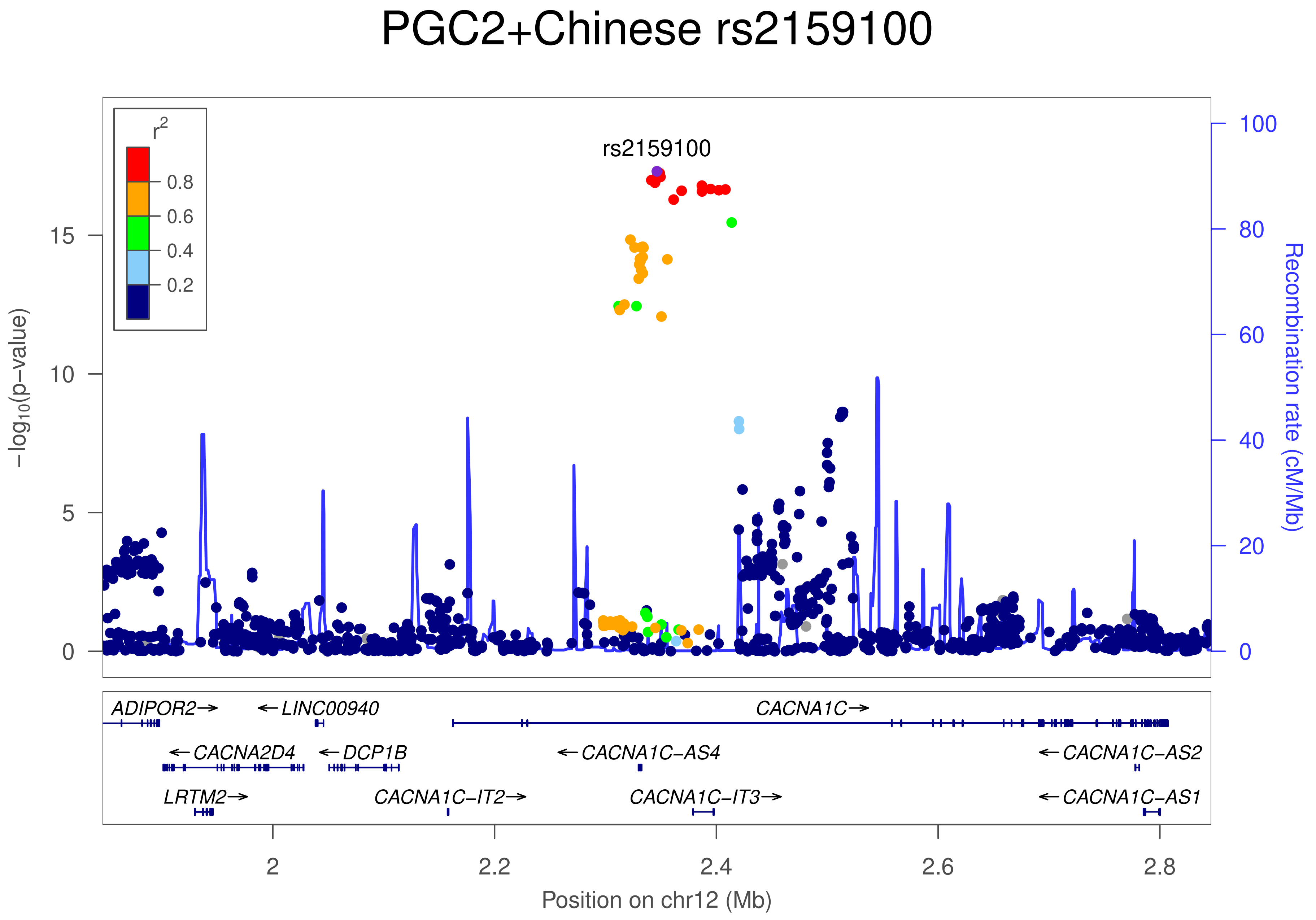

PGC2+Chinese rs1615350
rs1615350
r2
0.8
0.6
0.4
0.2
−log10(p−value)
0
5
10
15
Recombination rate (cM/Mb)
0
20
40
60
80
100
←HCAR2
HIP1R→
←ABCB9
LOC100507091→
C12orf65→
←MIR8072
←RILPL1
DDX55→
←HCAR3
←VPS37B
←PITPNM2
←MPHOSPH9
←SBNO1
←RILPL2
MIR3908→
←HCAR1
OGFOD2→
←CDK2AP1
KMT5A→
←LOC101927415
DENR→
ARL6IP4→
SNRNP35→
TMED2→
CCDC62→
←MIR4304
SNORA9B→
←EIF2B1
GTF2H3→
123.2
123.4
123.6
123.8
124
Position on chr12 (Mb)

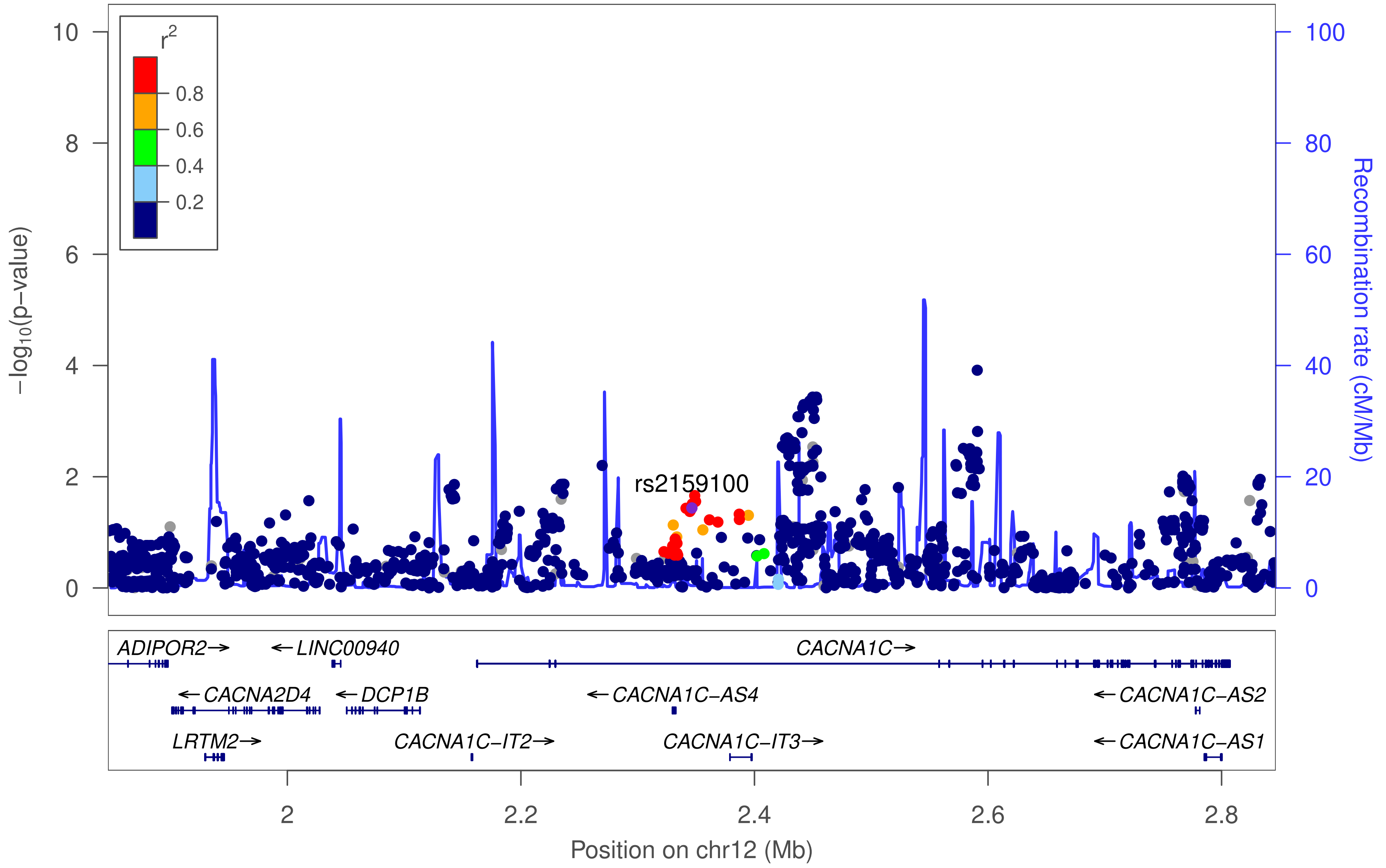
Chinese−only rs1615350



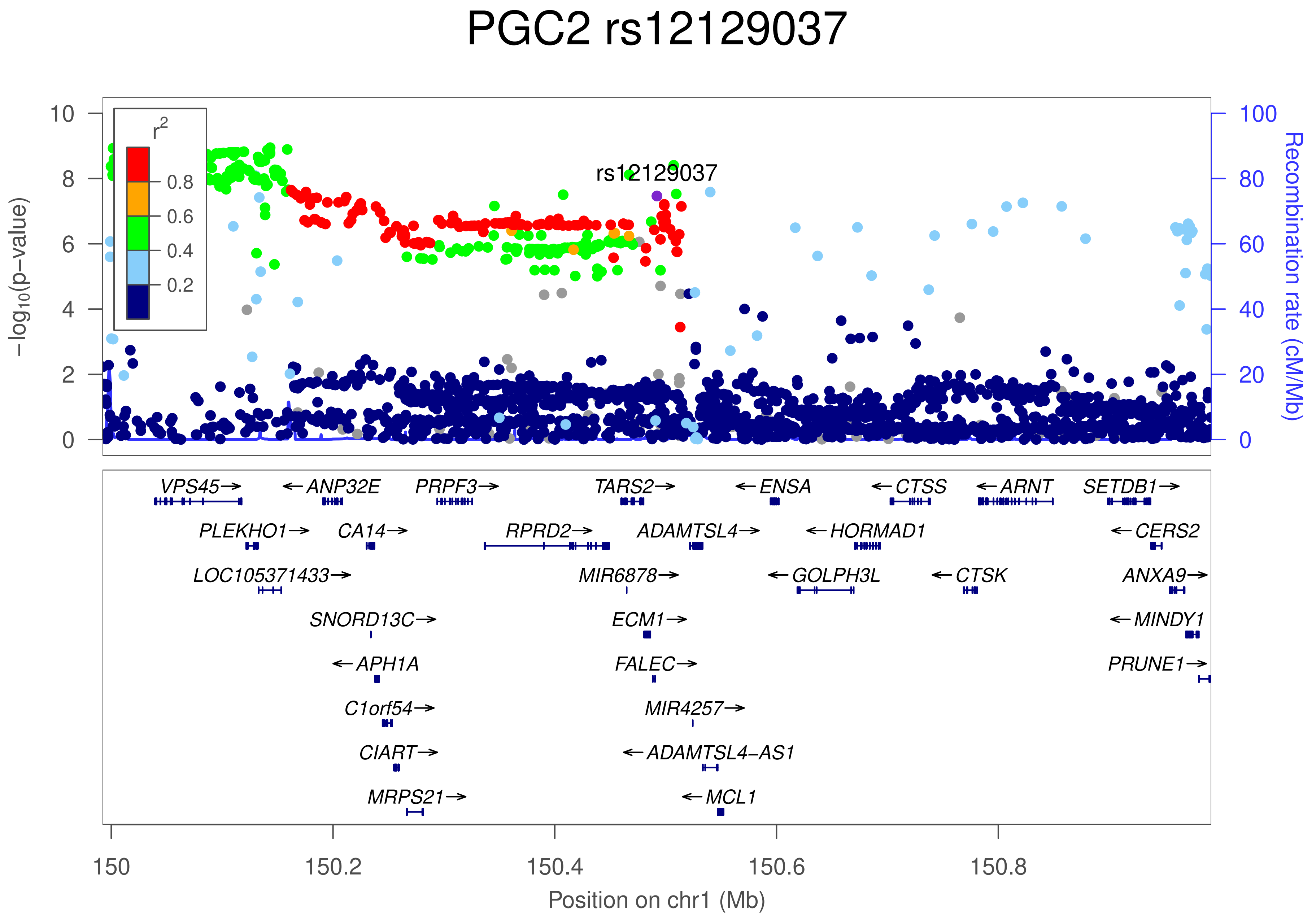
PGC2 rs2159100

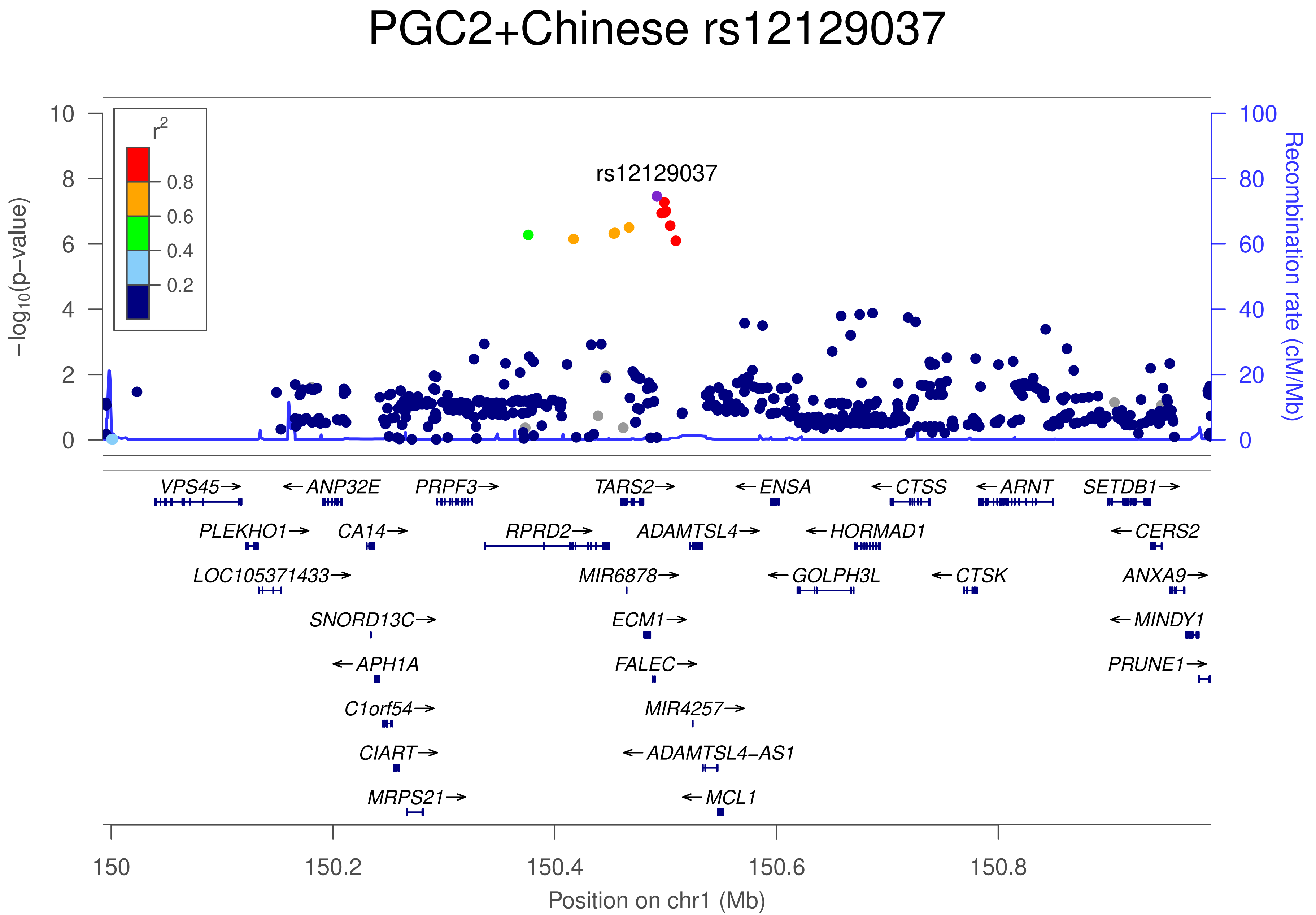



PGC2+Chinese rs2159100
r²
0.8
0.6
0.4
0.2
rs2159100
−log₁₀(p−value)
0
5
10
15
Recombination rate (cM/Mb)
0
20
40
60
80
100
ADIPOR2→
←LINC00940
CACNA1C→
←CACNA2D4
←DCP1B
←CACNA1C−AS4
←CACNA1C−AS2
LRTM2→
CACNA1C−IT2→
CACNA1C−IT3→
←CACNA1C−AS1
2
2.2
2.4
2.6
2.8
Position on chr12 (Mb)



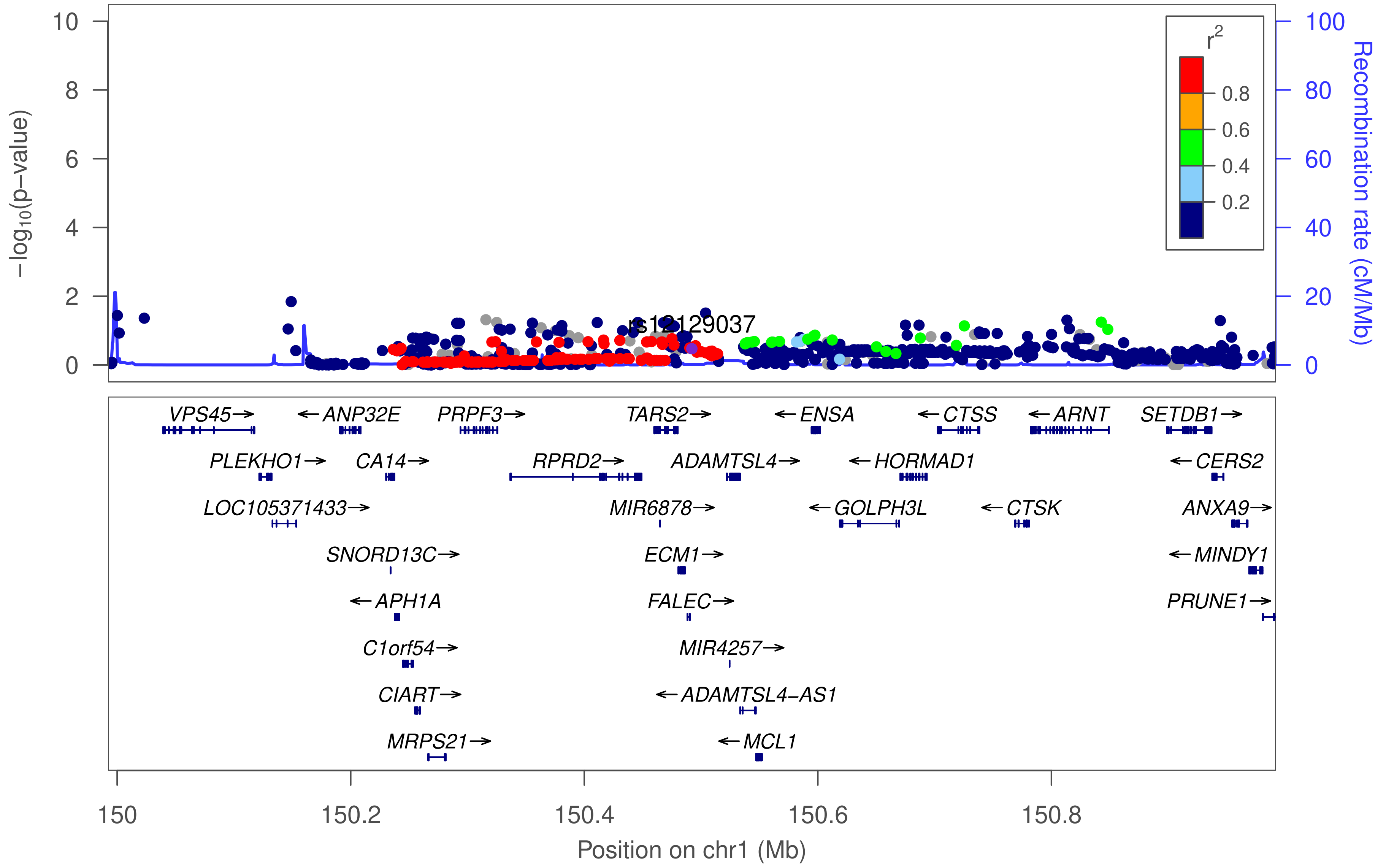
Chinese−only rs2159100


PGC2 rs12129037
rs12129037
r2
0.8
0.6
0.4
0.2
−log10(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
VPS45→
←ANP32E
PRPF3→
TARS2→
←ENSA
←CTSS
←ARNT
SETDB1→
PLEKHO1→
CA14→
RPRD2→
ADAMTSL4→
←HORMAD1
←CERS2
LOC105371433→
MIR6878→
←GOLPH3L
←CTSK
ANXA9→
SNORD13C→
ECM1→
←MINDY1
←APH1A
FALEC→
PRUNE1→
C1orf54→
MIR4257→
CIART→
←ADAMTSL4−AS1
MRPS21→
←MCL1
150
150.2
150.4
150.6
150.8
Position on chr1 (Mb)

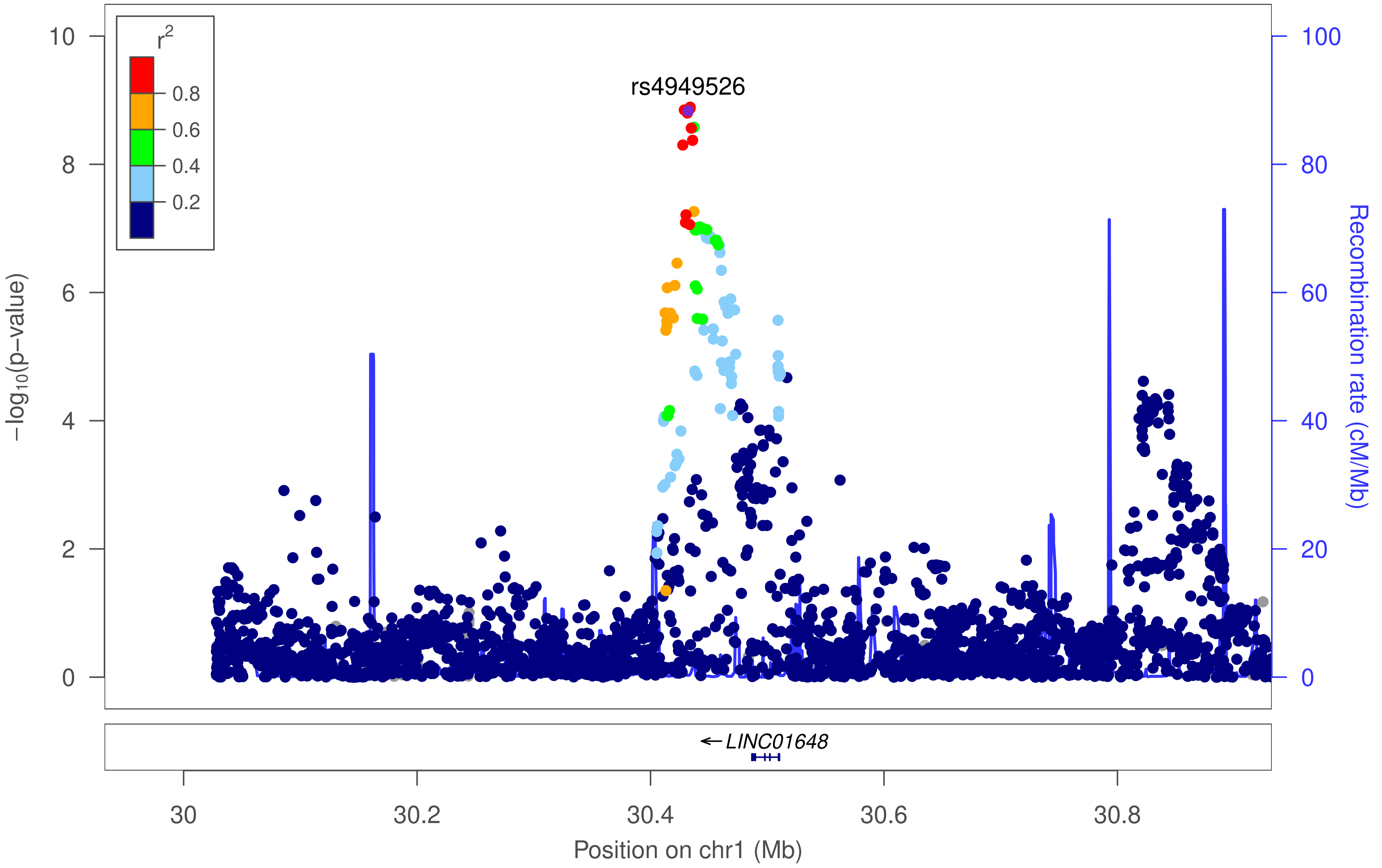


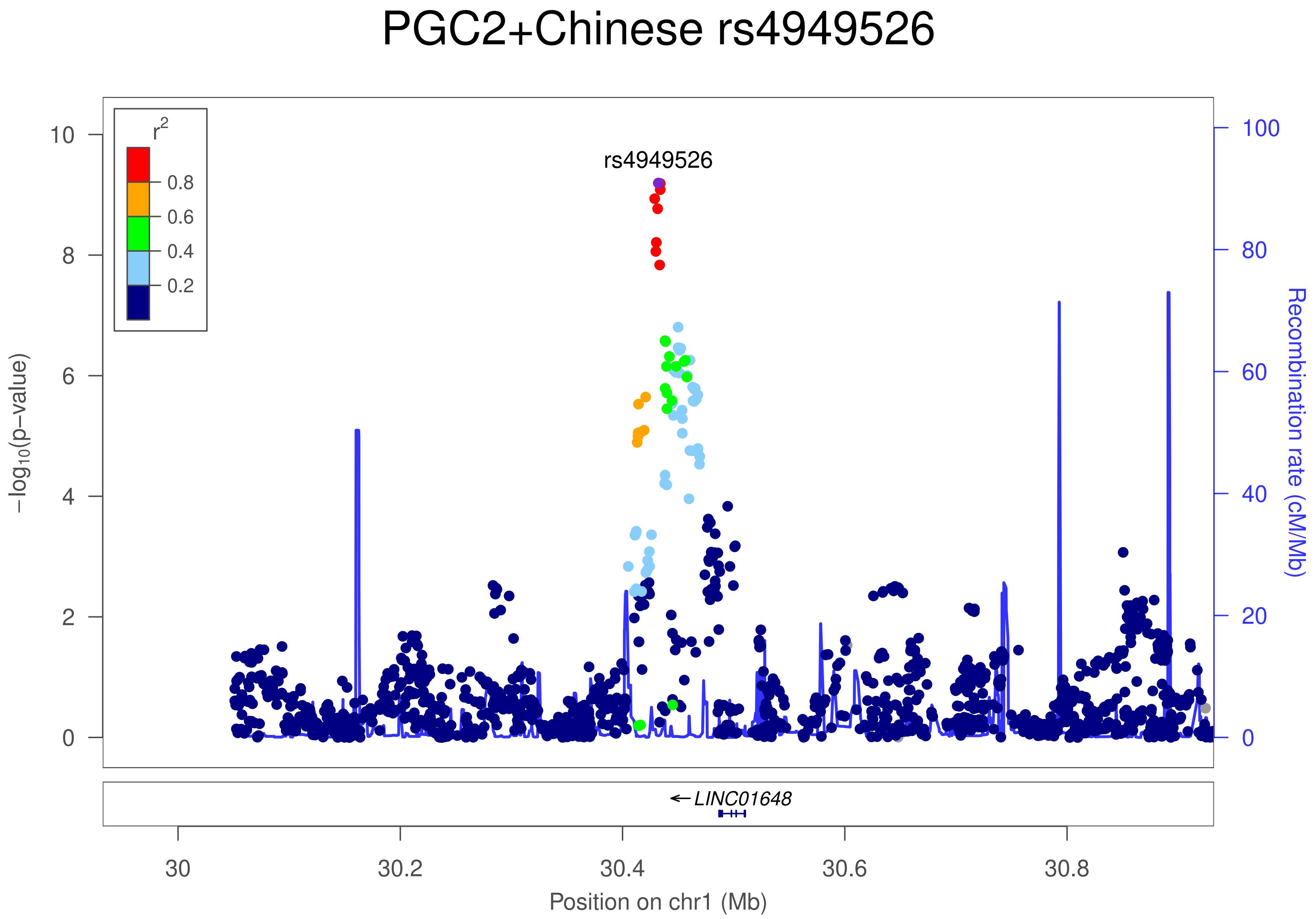
PGC2+Chinese rs12129037
rs12129037
r²
0.8
0.6
0.4
0.2
−log₁₀(p−value)
10
8
6
4
2
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
VPS45→
←ANP32E
PRPF3→
TARS2→
←ENSA
←CTSS
←ARNT
SETDB1→
PLEKHO1→
CA14→
RPRD2→
ADAMTSL4→
←HORMAD1
←CERS2
LOC105371433→
MIR6878→
←GOLPH3L
←CTSK
ANXA9→
SNORD13C→
ECM1→
←MINDY1
←APH1A
FALEC→
PRUNE1→
C1orf54→
MIR4257→
CIART→
←ADAMTSL4−AS1
MRPS21→
←MCL1
150
150.2
150.4
150.6
150.8
Position on chr1 (Mb)

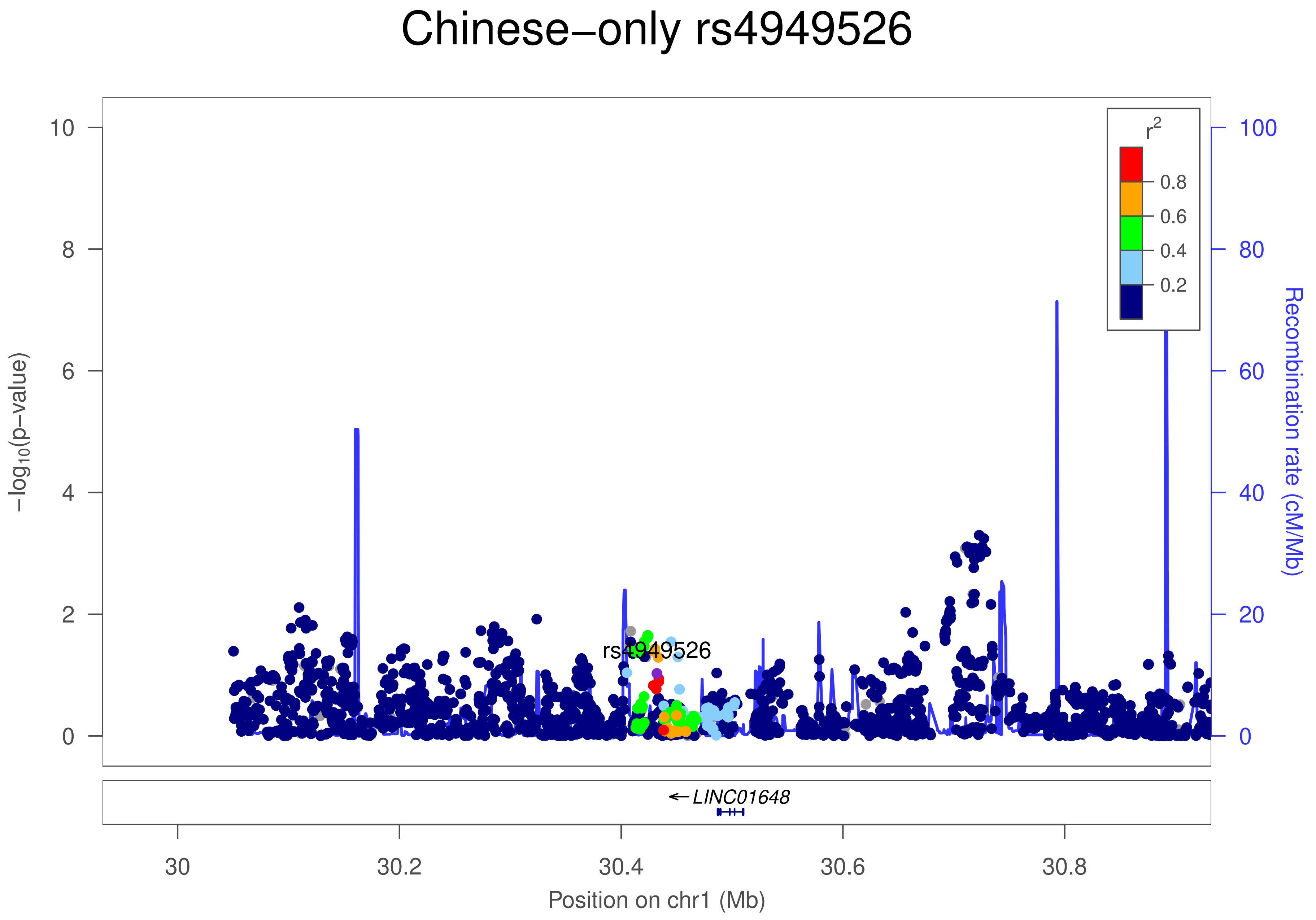
Chinese−only rs12129037

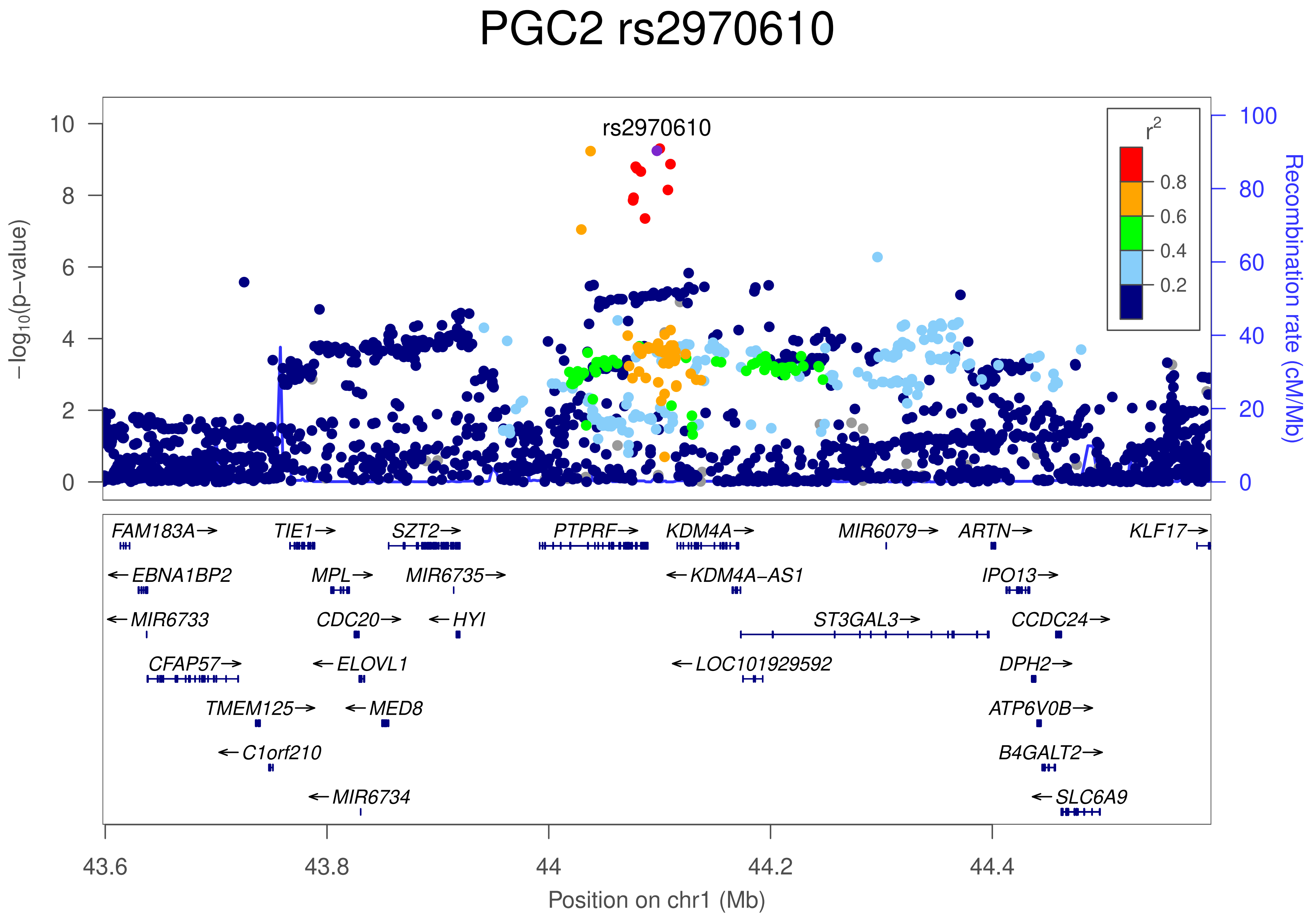


PGC2 rs4949526

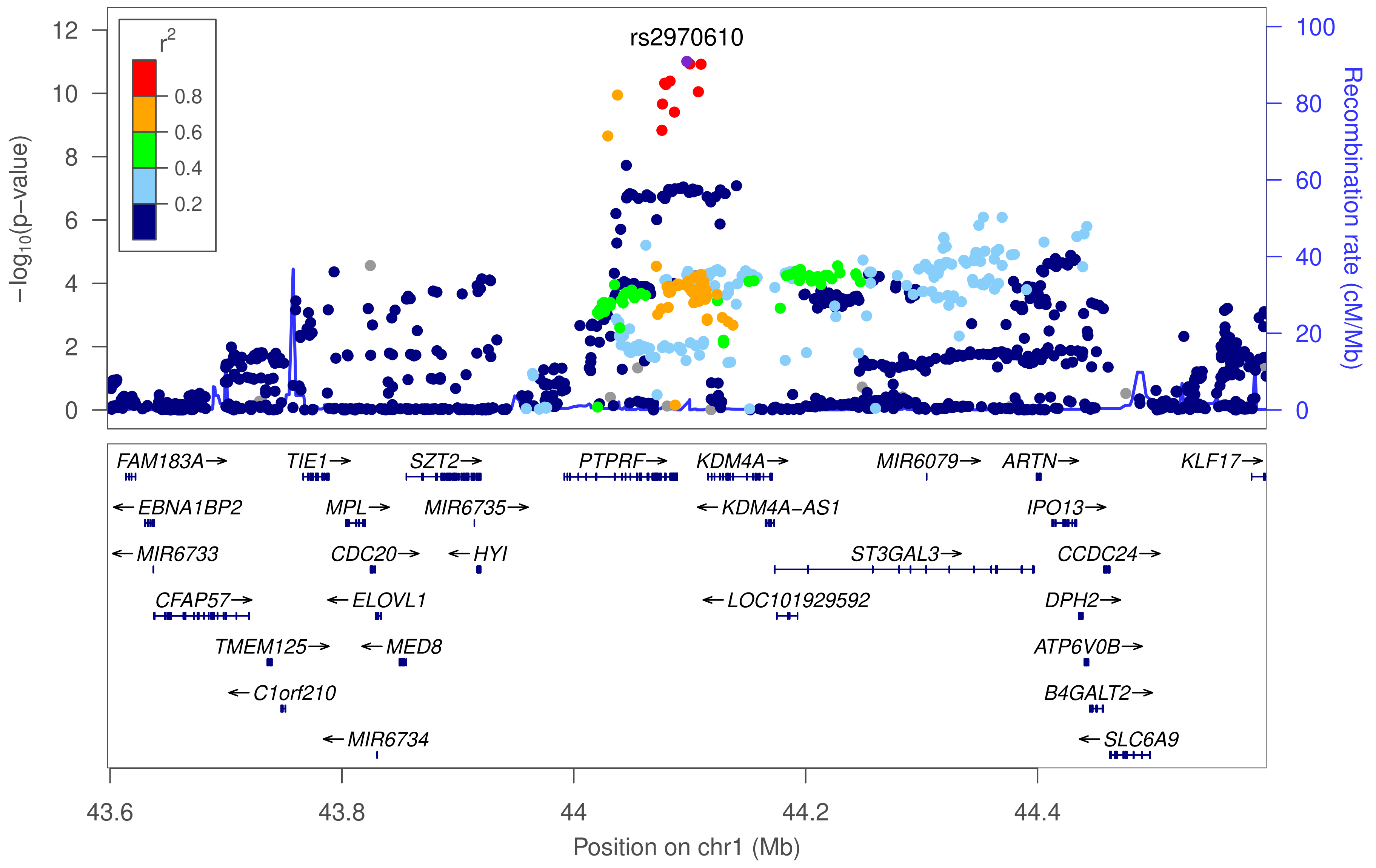


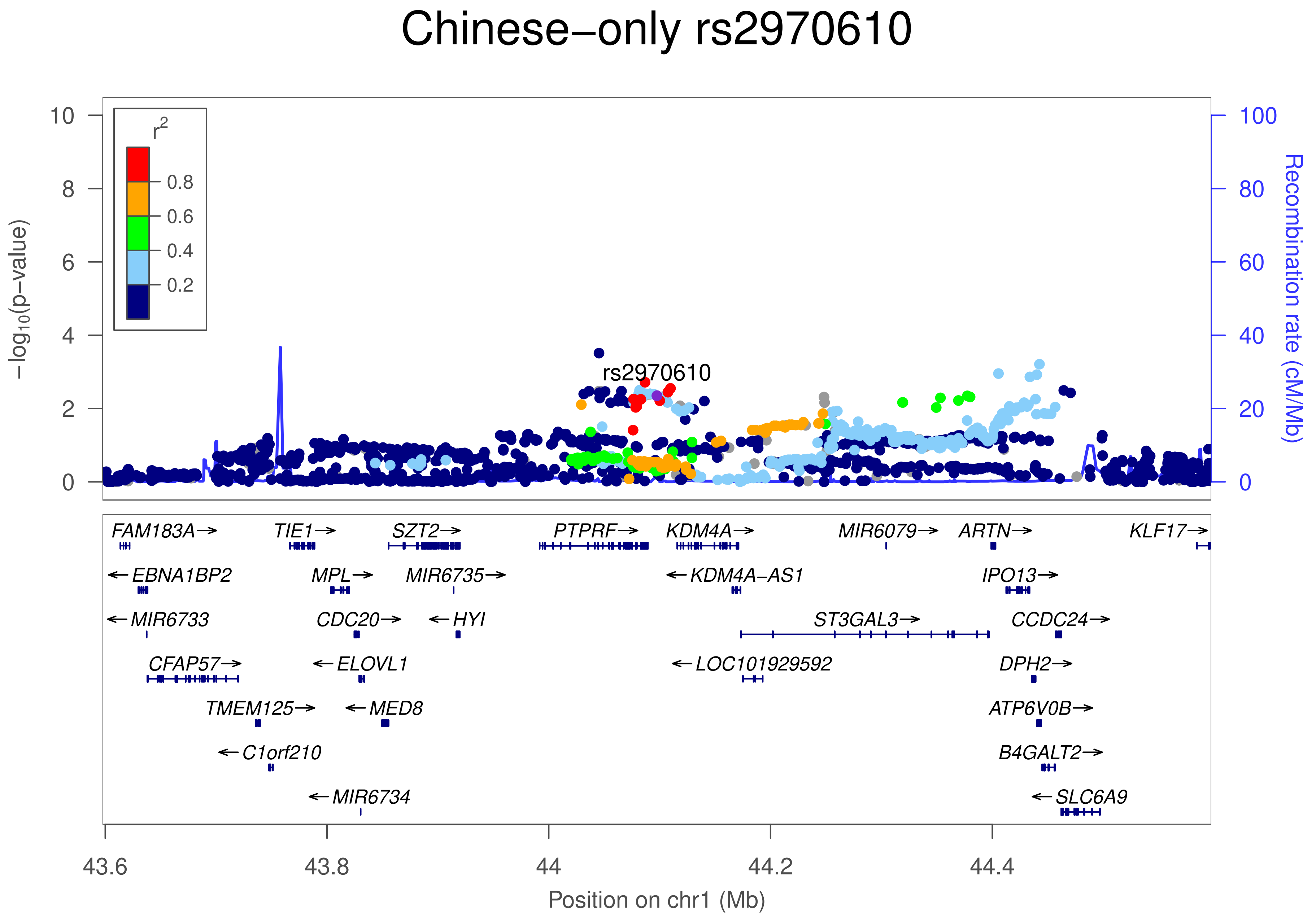

PGC2+Chinese rs4949526
r²
0.8
0.6
0.4
0.2
rs4949526
−log₁₀(p−value)
10
8
6
4
2
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
LINC01648
30
30.2
30.4
30.6
30.8
Position on chr1 (Mb)

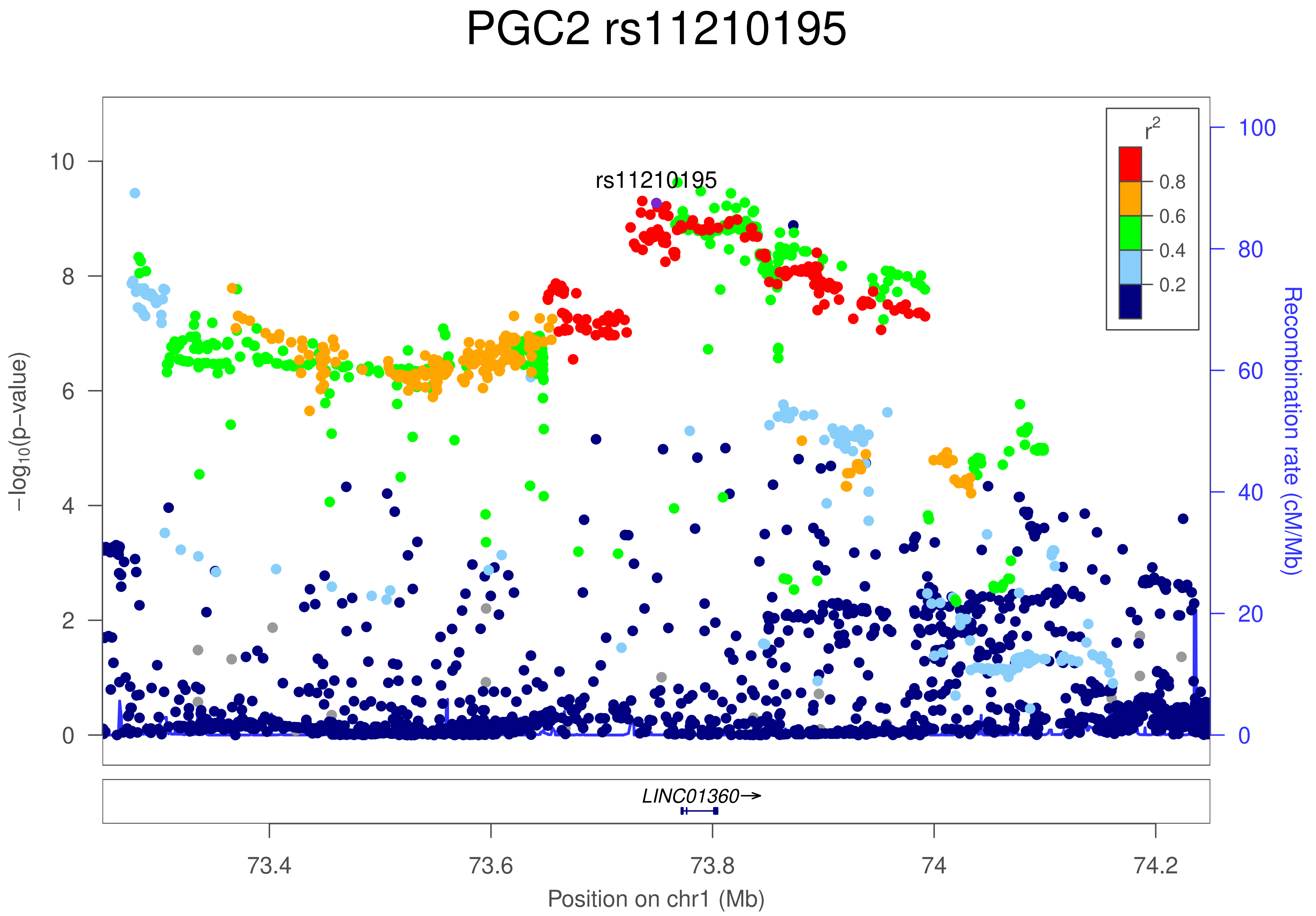

Chinese−only rs4949526
−log10(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
r²
0.8
0.6
0.4
0.2
rs4949526
← LINC01648
30
30.2
30.4
30.6
30.8
Position on chr1 (Mb)

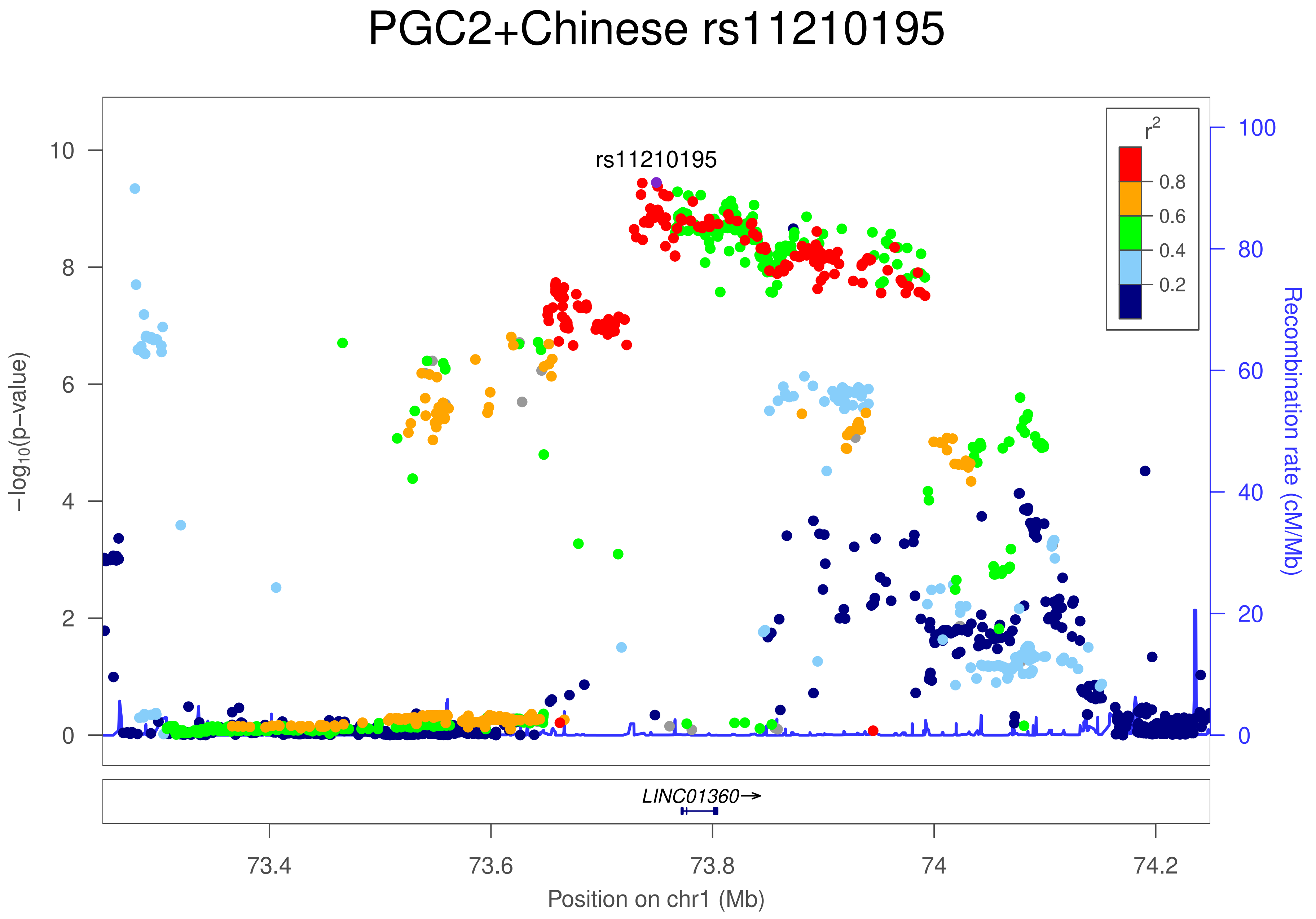

PGC2 rs2970610
rs2970610
r^2
0.8
0.6
0.4
0.2
−log$_{10}$(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
FAM183A→
TIE1→
SZT2→
PTPRF→
KDM4A→
MIR6079→
ARTN→
KLF17→
←EBNA1BP2
MPL→
MIR6735→
←KDM4A−AS1
IPO13→
←MIR6733
CDC20→
←HYI
ST3GAL3→
CCDC24→
CFAP57→
←ELOVL1
←LOC101929592
DPH2→
TMEM125→
←MED8
ATP6V0B→
←C1orf210
B4GALT2→
←MIR6734
←SLC6A9
43.6
43.8
44
44.2
44.4
Position on chr1 (Mb)

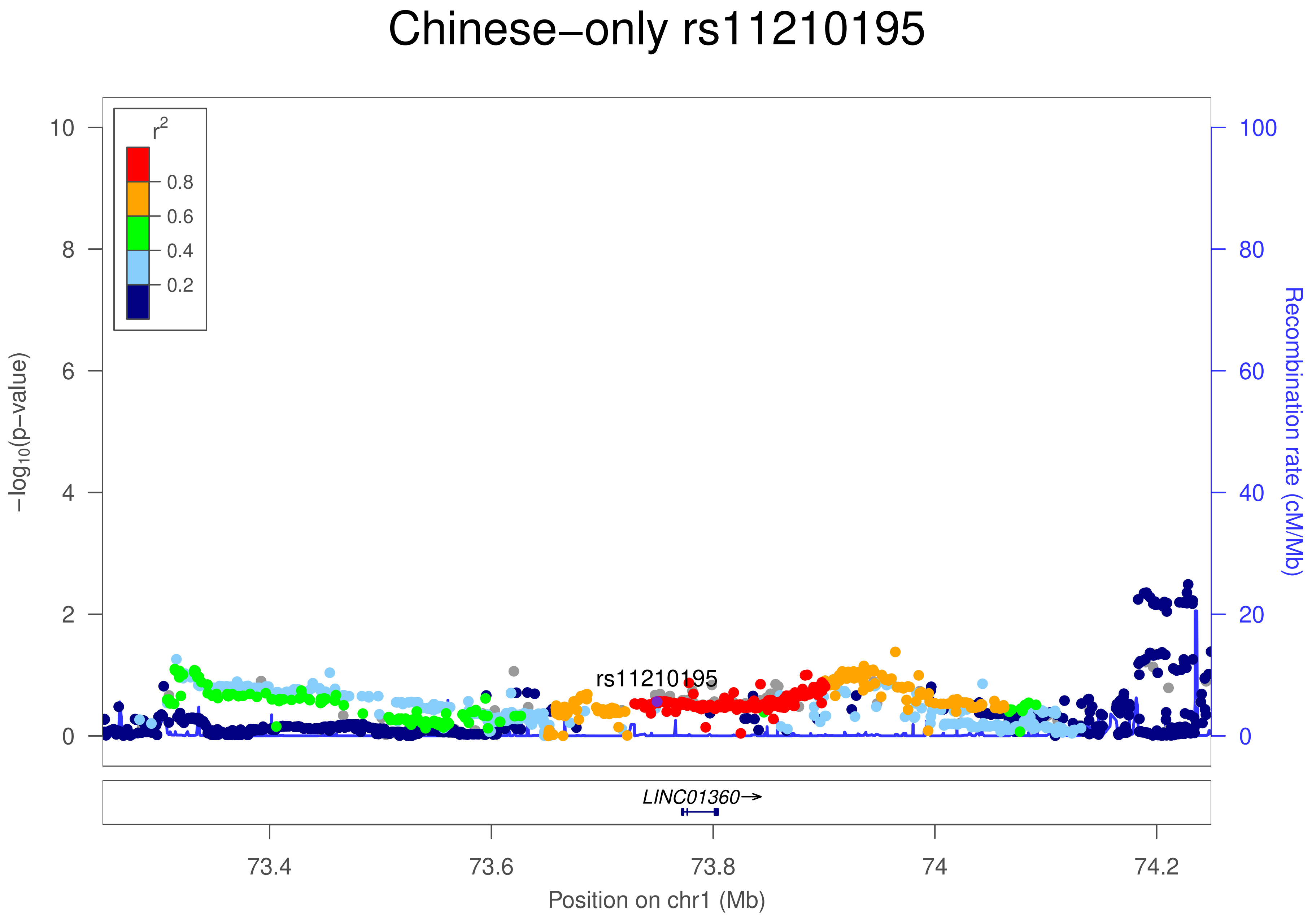
PGC2+Chinese rs2970610

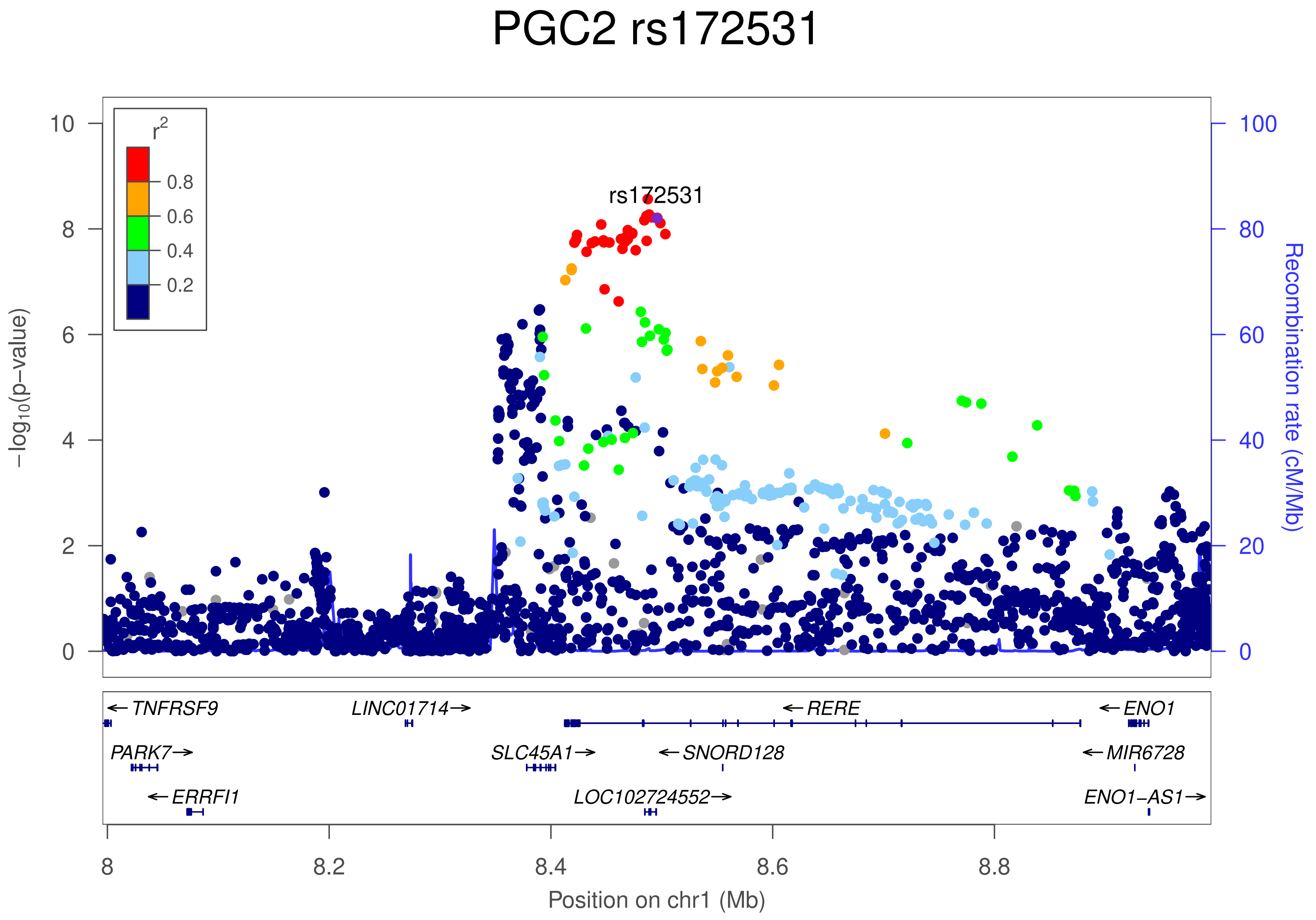


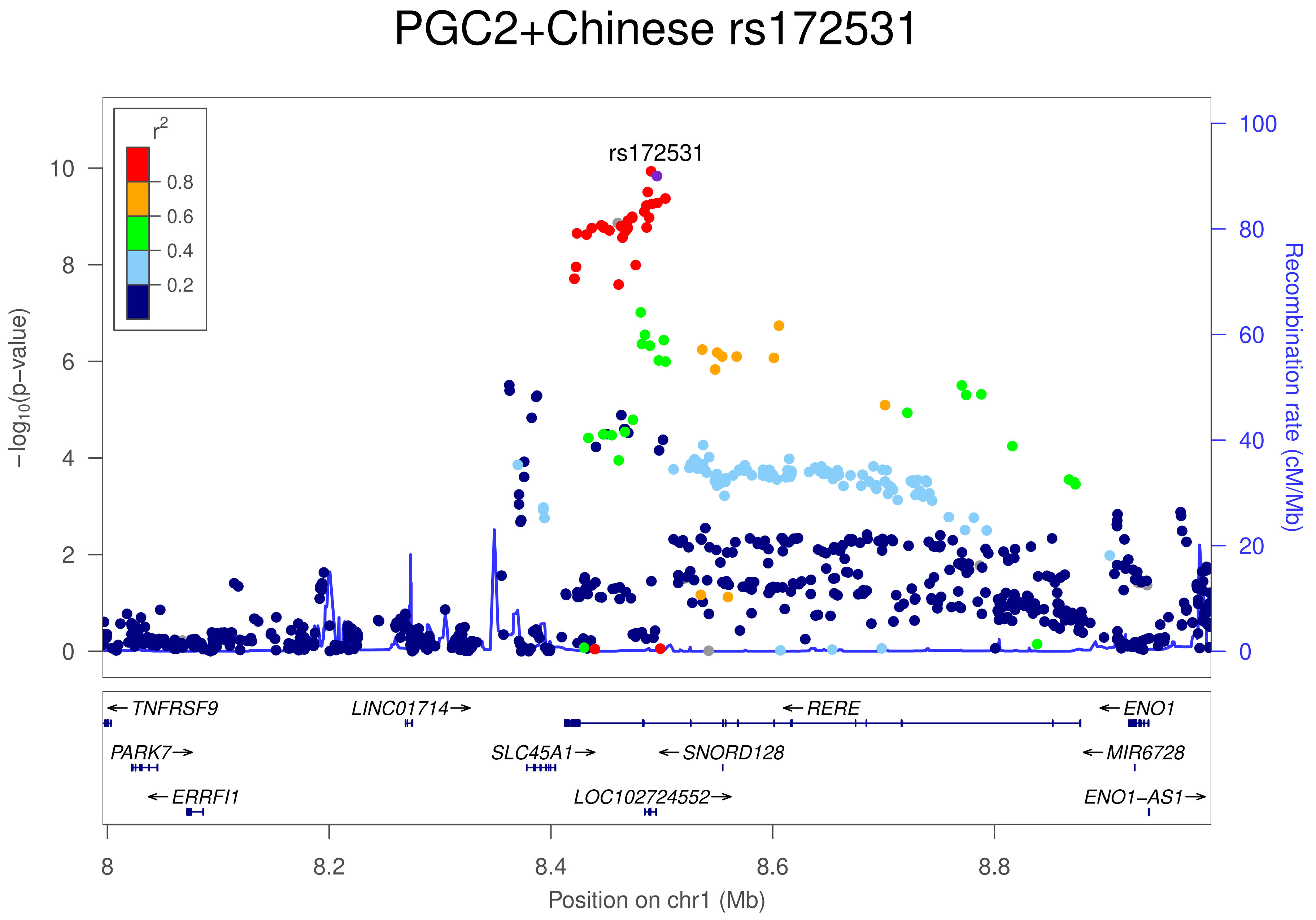

Chinese−only rs2970610
10
8
6
4
2
0
$-\log_{10}$(p−value)
r^2
0.8
0.6
0.4
0.2
rs2970610
100
80
60
40
20
0
Recombination rate (cM/Mb)
FAM183A→
TIE1→
SZT2→
PTPRF→
KDM4A→
MIR6079→
ARTN→
KLF17→
←EBNA1BP2
MPL→
MIR6735→
←KDM4A−AS1
IPO13→
←MIR6733
CDC20→
←HYI
ST3GAL3→
CCDC24→
CFAP57→
←ELOVL1
←LOC101929592
DPH2→
TMEM125→
←MED8
ATP6V0B→
←C1orf210
B4GALT2→
←MIR6734
←SLC6A9
43.6
43.8
44
44.2
44.4
Position on chr1 (Mb)


PGC2 rs11210195
rs11210195
r²
0.8
0.6
0.4
0.2
−log10(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
LINC01360→
73.4
73.6
73.8
74
74.2
Position on chr1 (Mb)

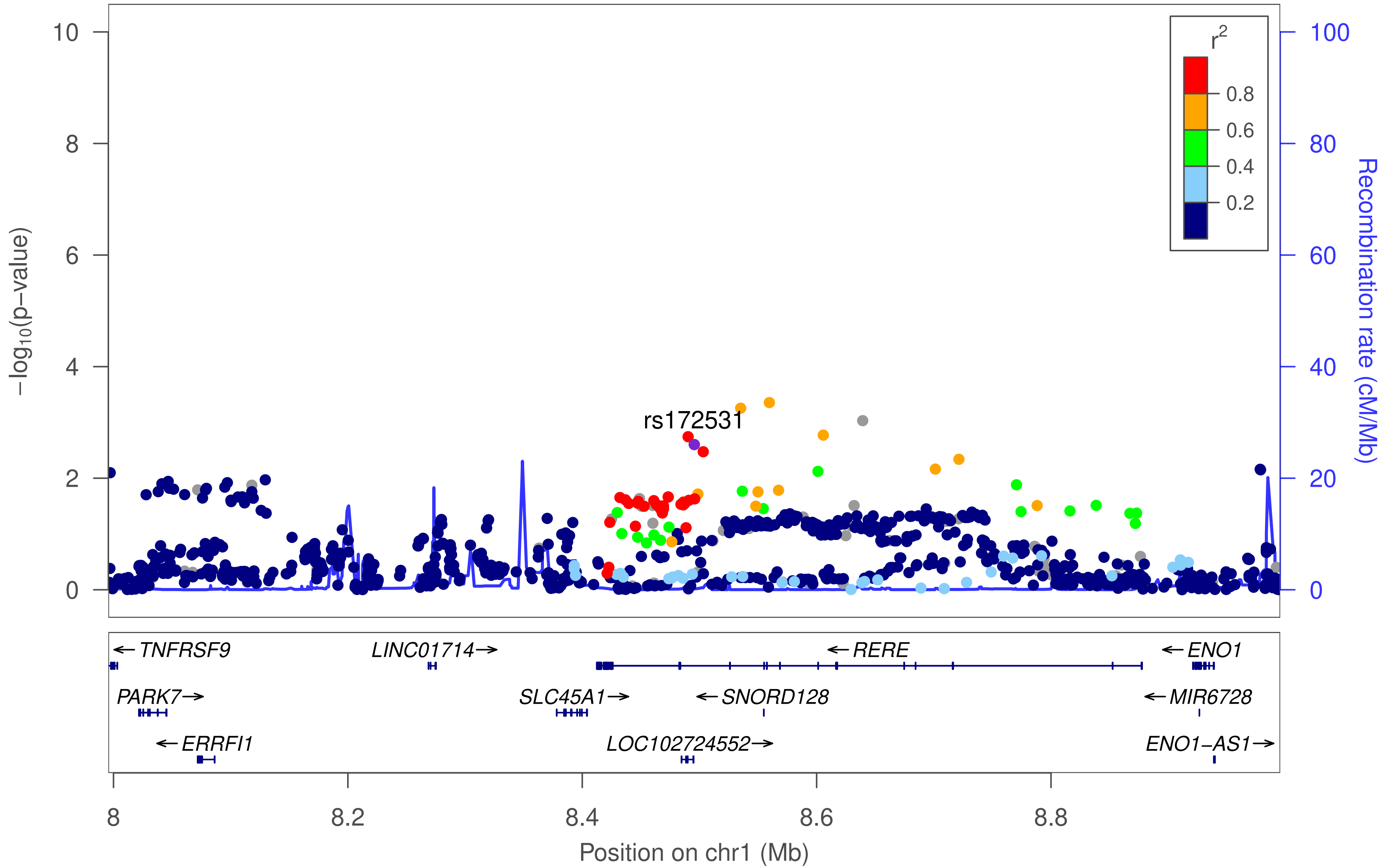

PGC2+Chinese rs11210195
rs11210195
−log10(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
r2
0.8
0.6
0.4
0.2
LINC01360→
73.4
73.6
73.8
74
74.2
Position on chr1 (Mb)


Chinese−only rs11210195
r2
0.8
0.6
0.4
0.2
−log10(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
rs11210195
LINC01360→
73.4
73.6
73.8
74
74.2
Position on chr1 (Mb)

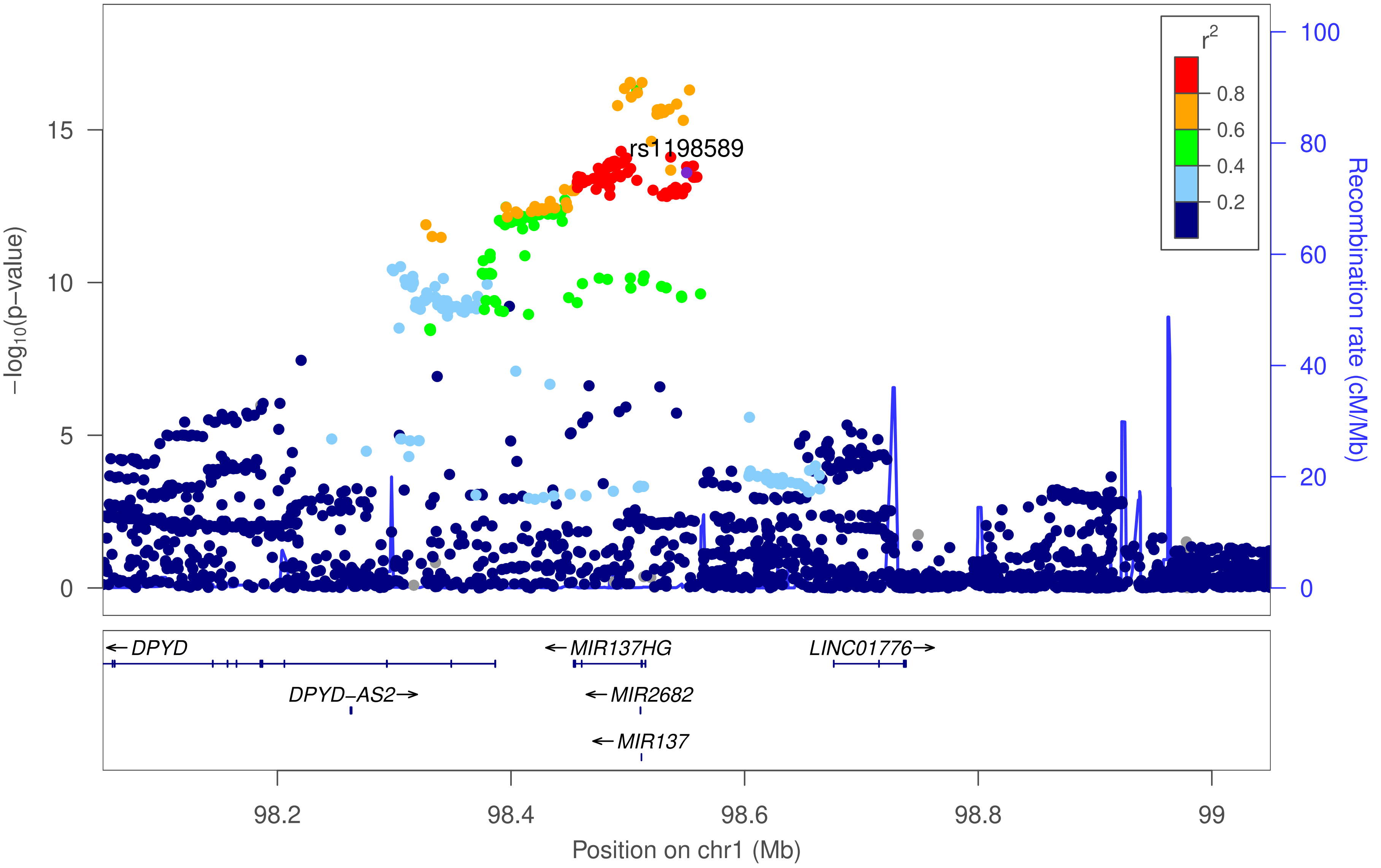

PGC2 rs172531
r²
0.8
0.6
0.4
0.2
rs172531
10
8
6
4
2
0
−log₁₀(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
← TNFRSF9
LINC01714 →
← RERE
← ENO1
PARK7 →
SLC45A1 →
← SNORD128
← MIR6728
← ERRFI1
LOC102724552 →
ENO1−AS1 →
8
8.2
8.4
8.6
8.8
Position on chr1 (Mb)

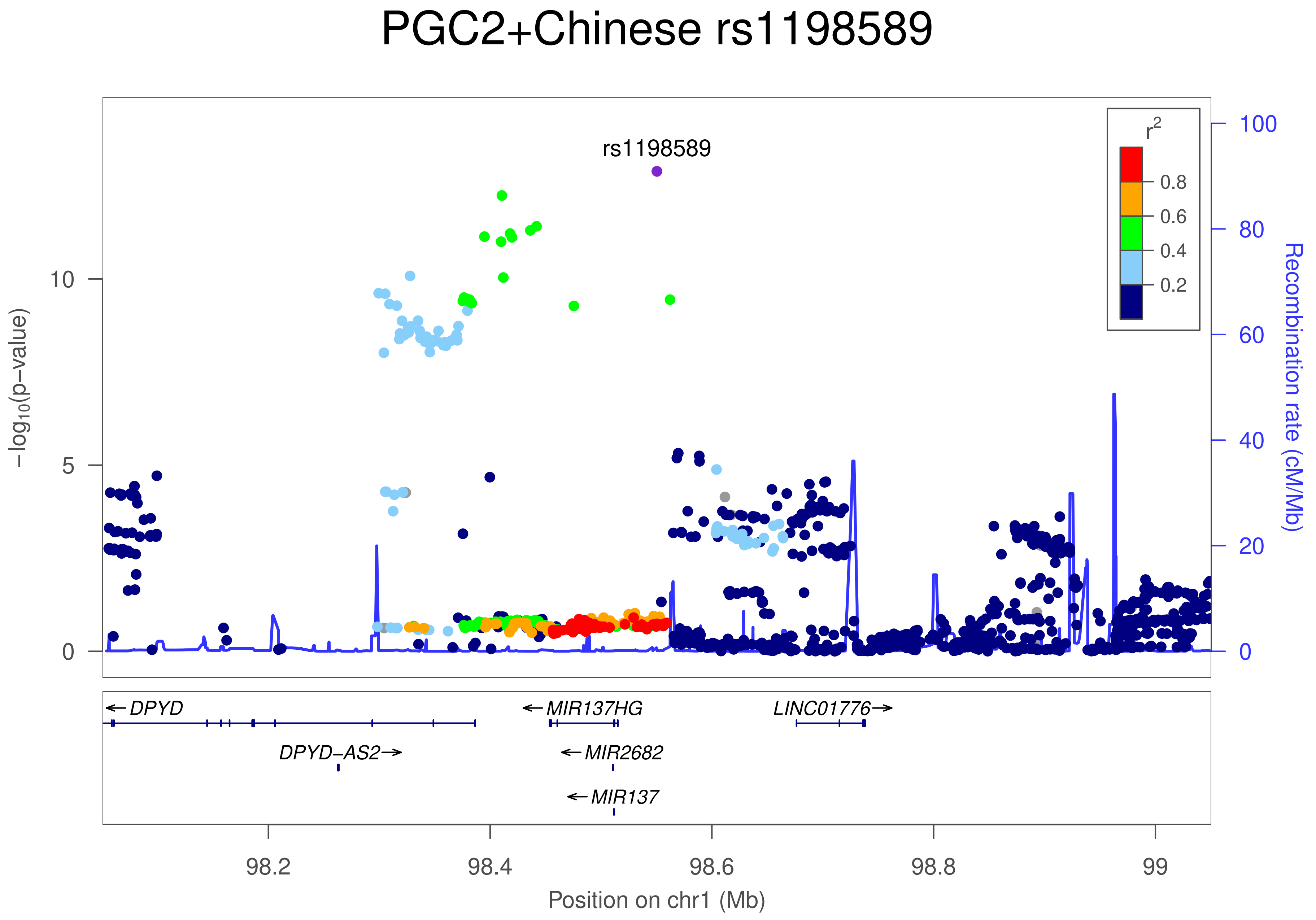

PGC2+Chinese rs172531
r²
0.8
0.6
0.4
0.2
rs172531
−log10(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
TNFRSF9
LINC01714
RERE
ENO1
PARK7
SLC45A1
SNORD128
MIR6728
ERRFI1
LOC102724552
ENO1−AS1
8
8.2
8.4
8.6
8.8
Position on chr1 (Mb)

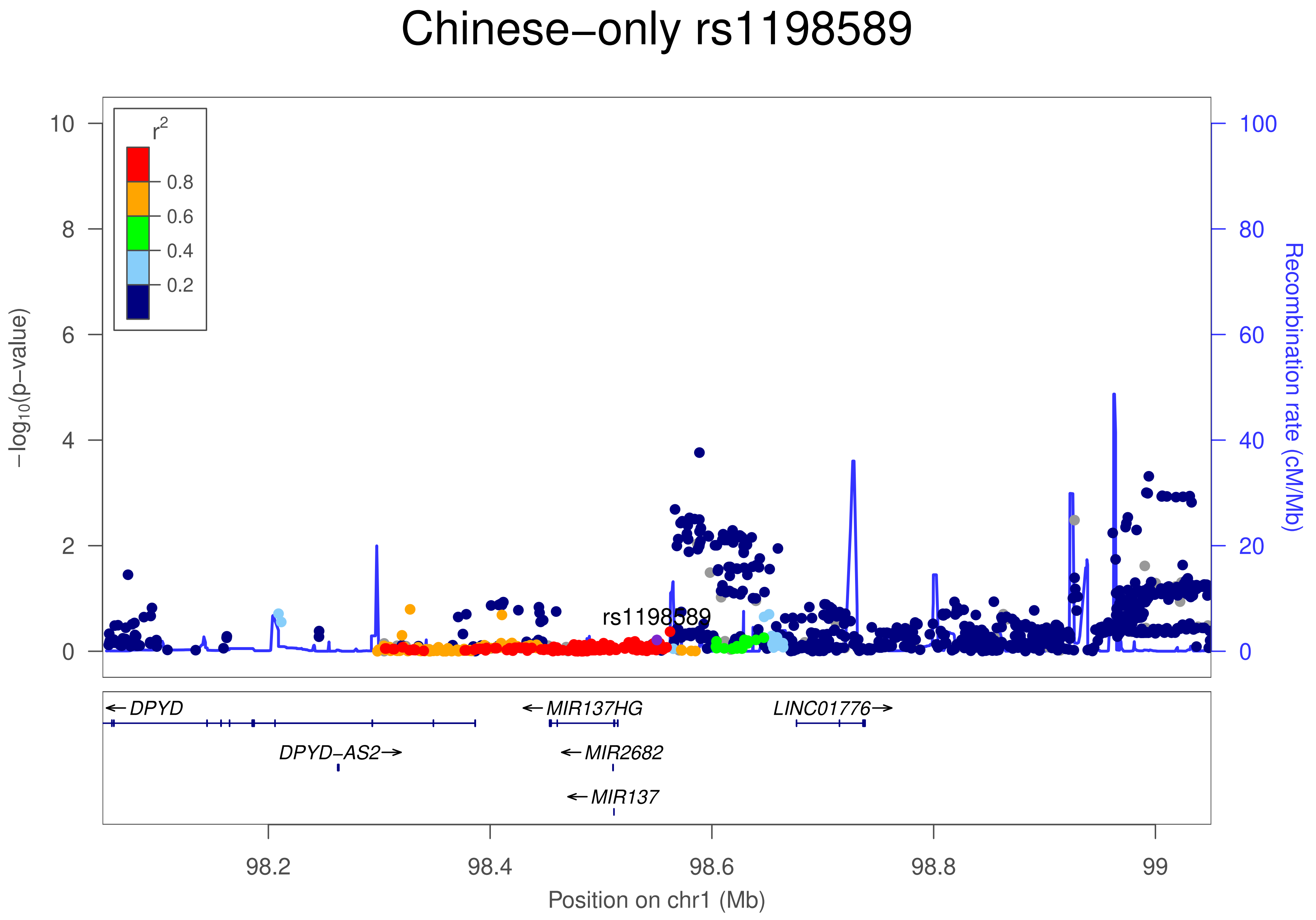
Chinese–only rs172531



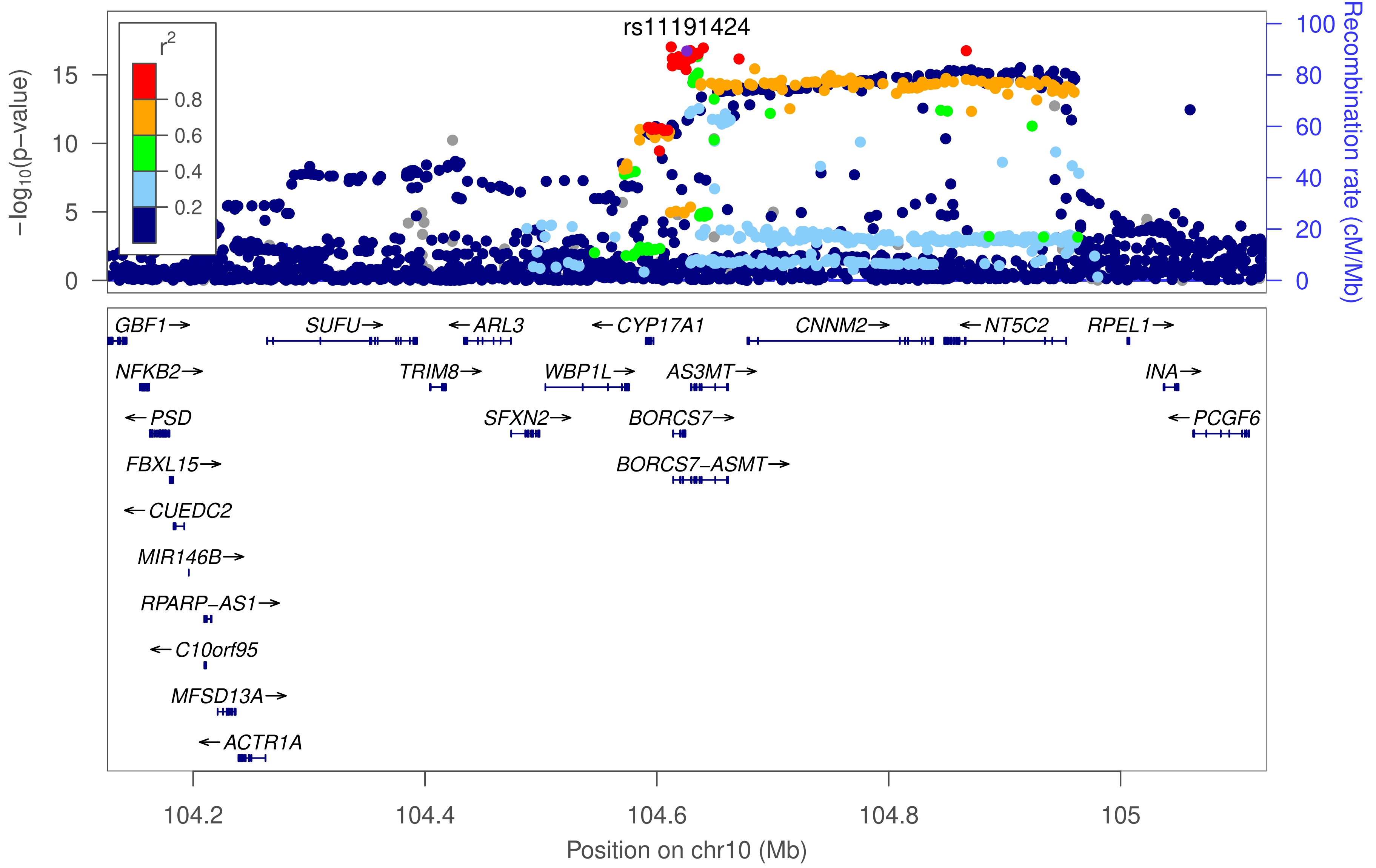
PGC2 rs1198589



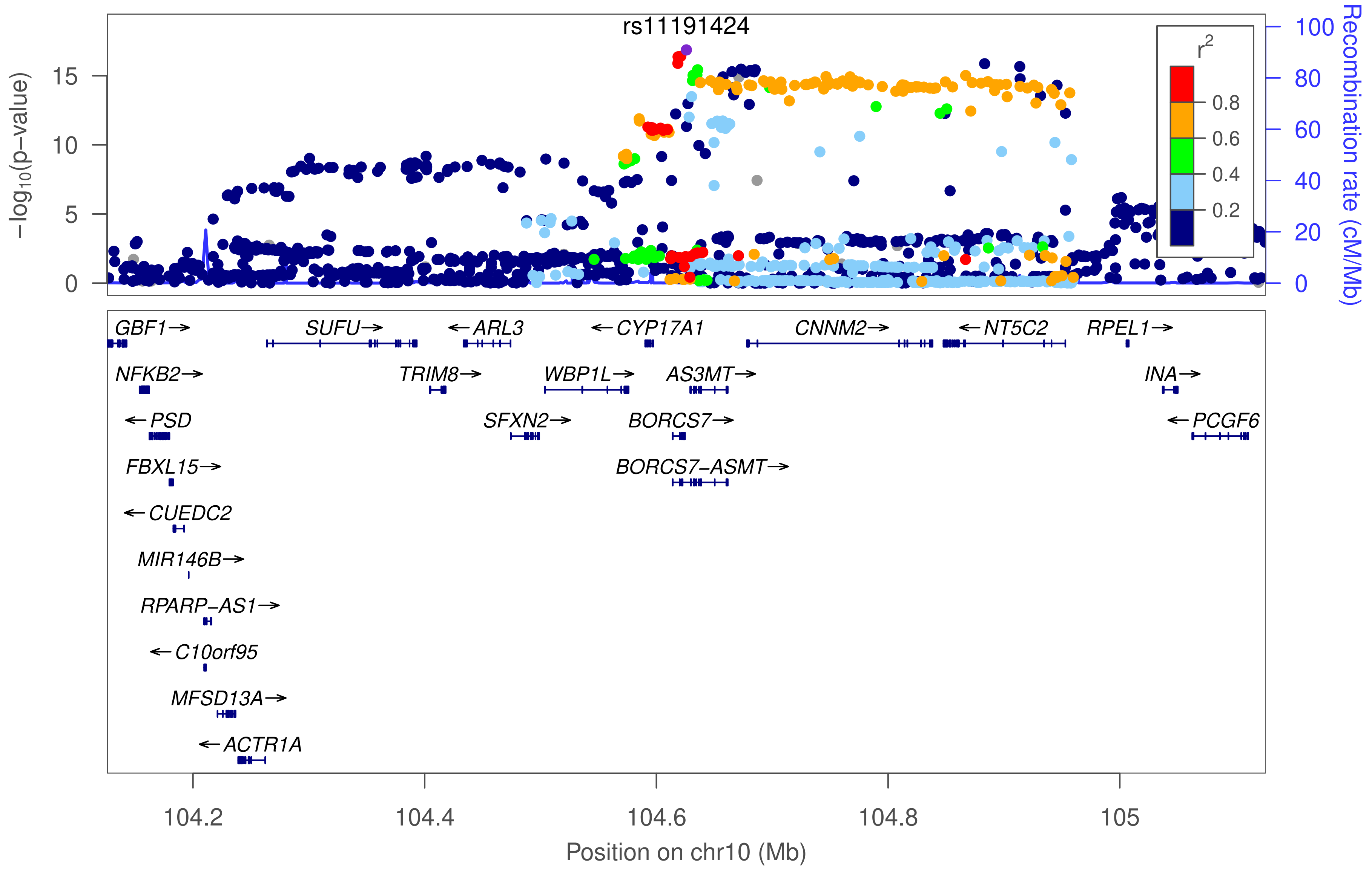

PGC2+Chinese rs1198589
rs1198589
r²
0.8
0.6
0.4
0.2
−log10(p−value)
0
5
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
← DPYD
← MIR137HG
LINC01776 →
DPYD−AS2 →
← MIR2682
← MIR137
98.2
98.4
98.6
98.8
99
Position on chr1 (Mb)


Chinese−only rs1198589
r2
0.8
0.6
0.4
0.2
10
8
6
4
2
0
−log10(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
rs1198589
← DPYD
← MIR137HG
LINC01776 →
DPYD−AS2 →
← MIR2682
← MIR137
98.2
98.4
98.6
98.8
99
Position on chr1 (Mb)

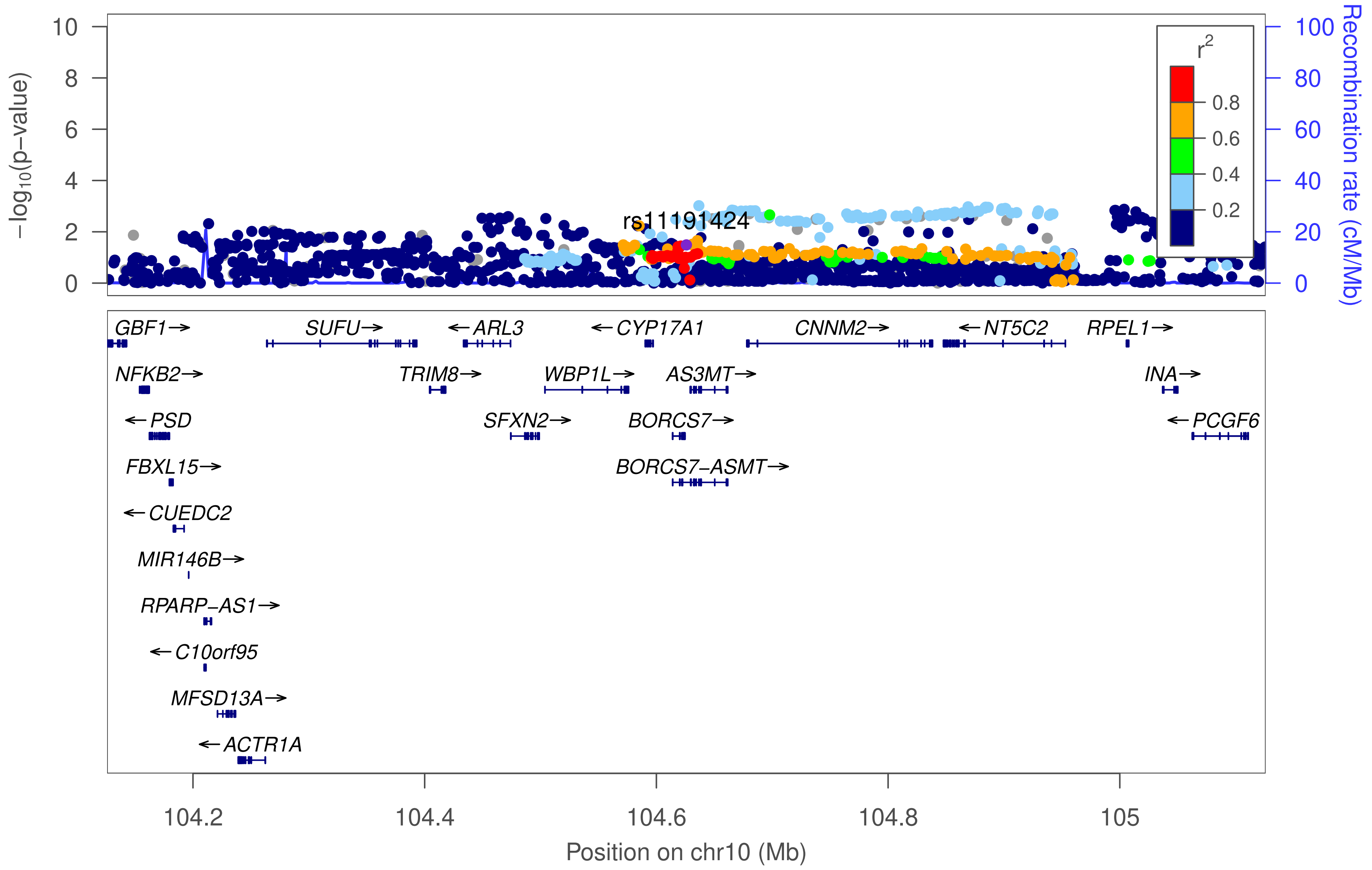
PGC2 rs11191424



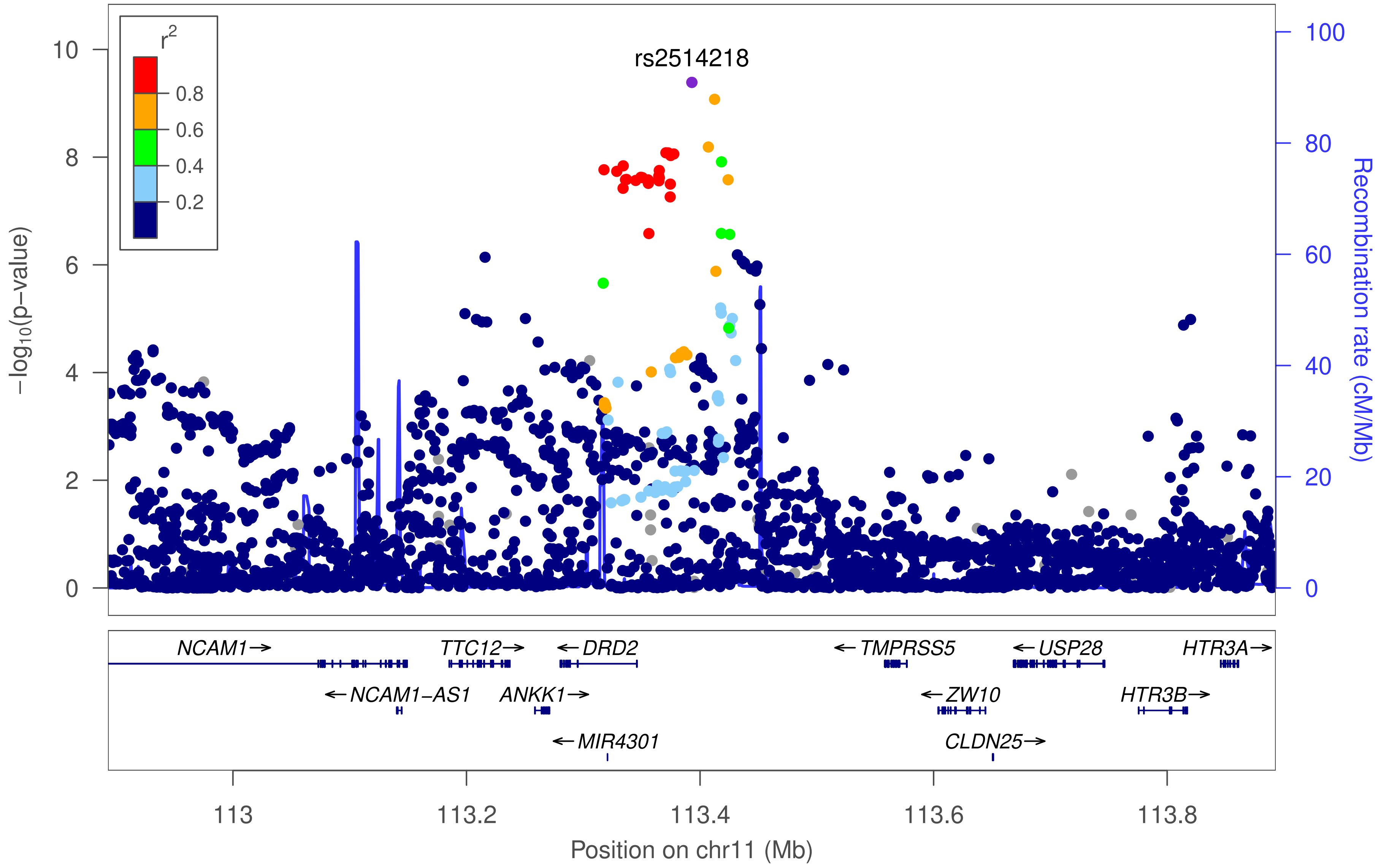
PGC2+Chinese rs11191424

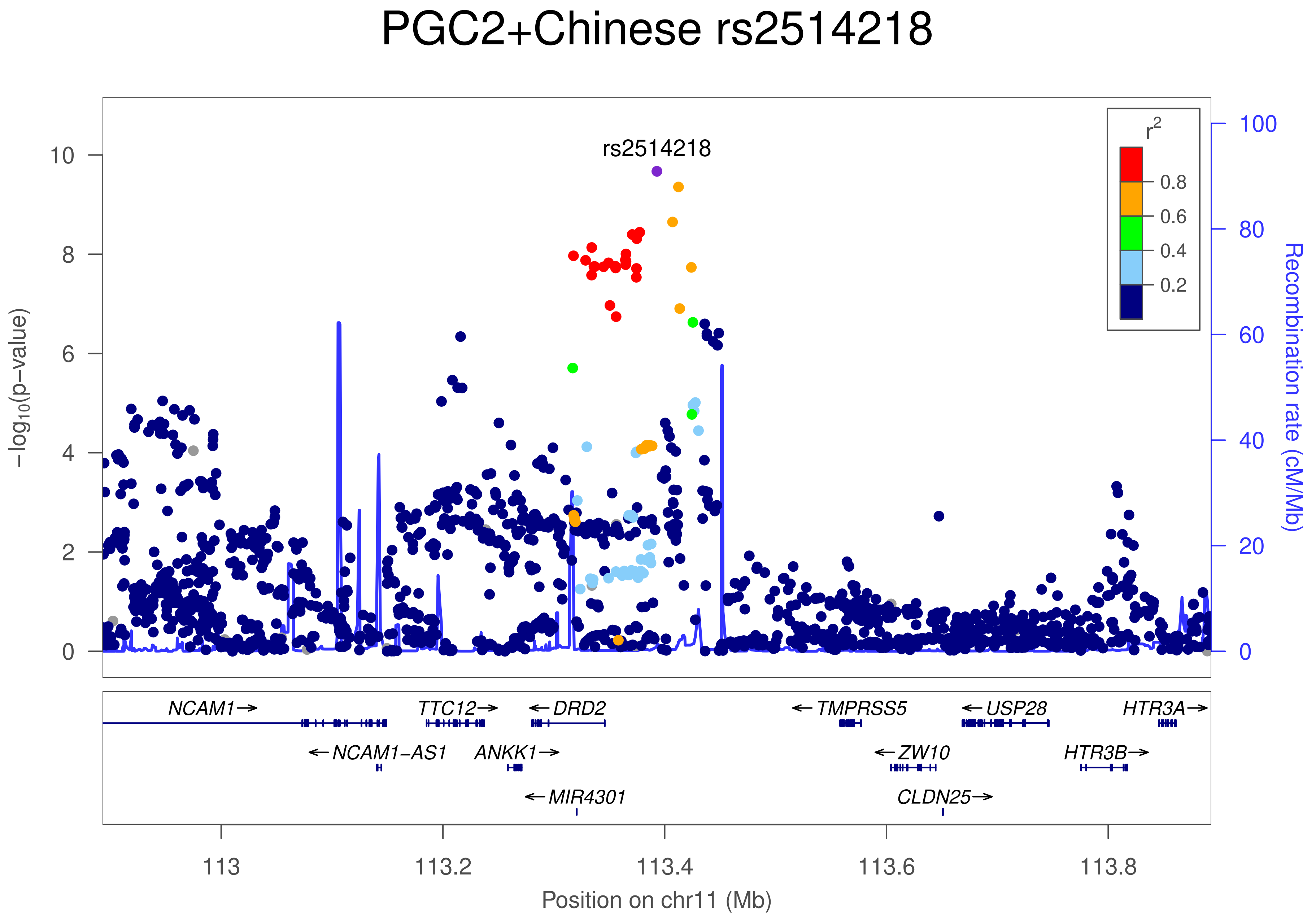


Chinese−only rs11191424

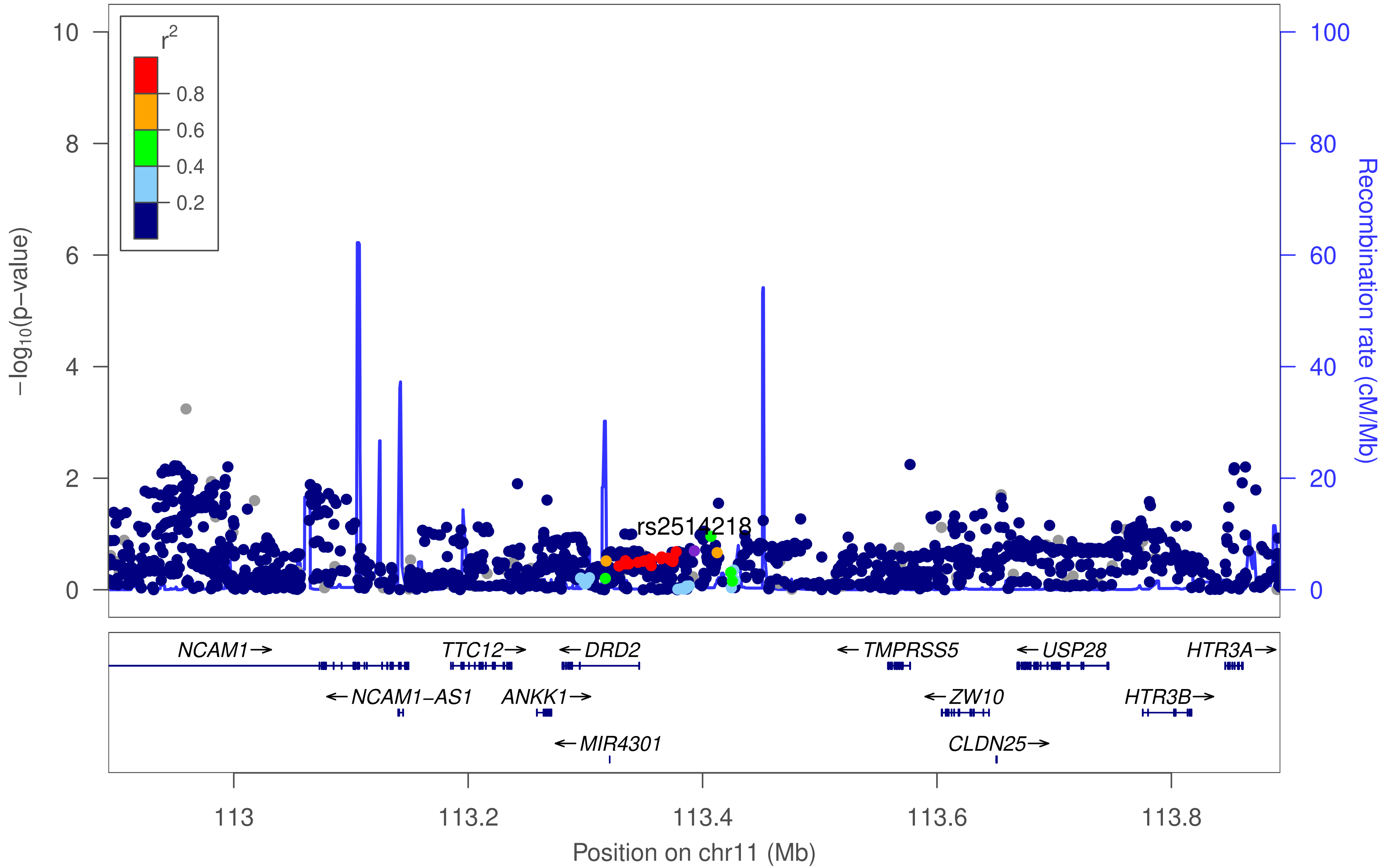


PGC2 rs2514218

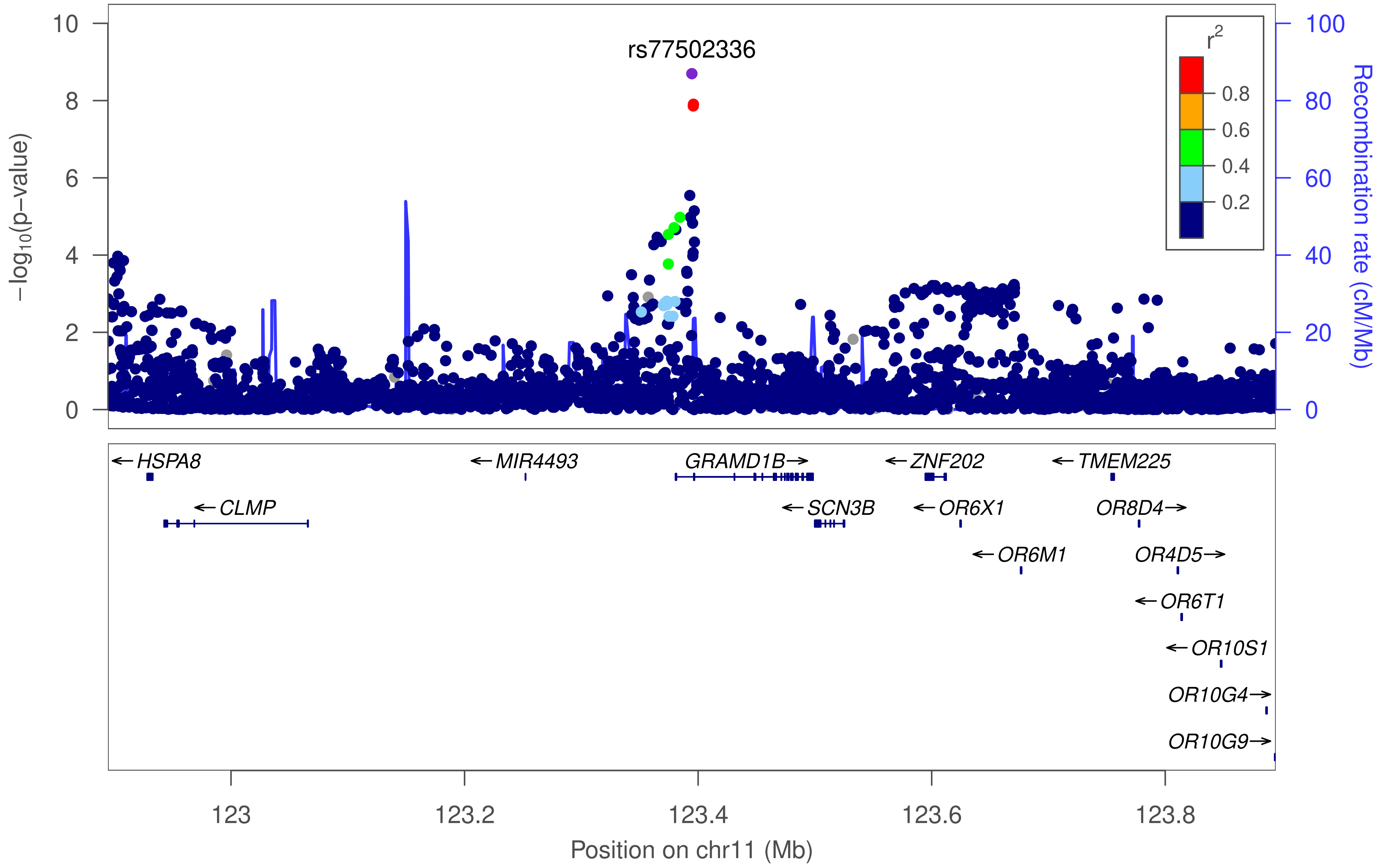


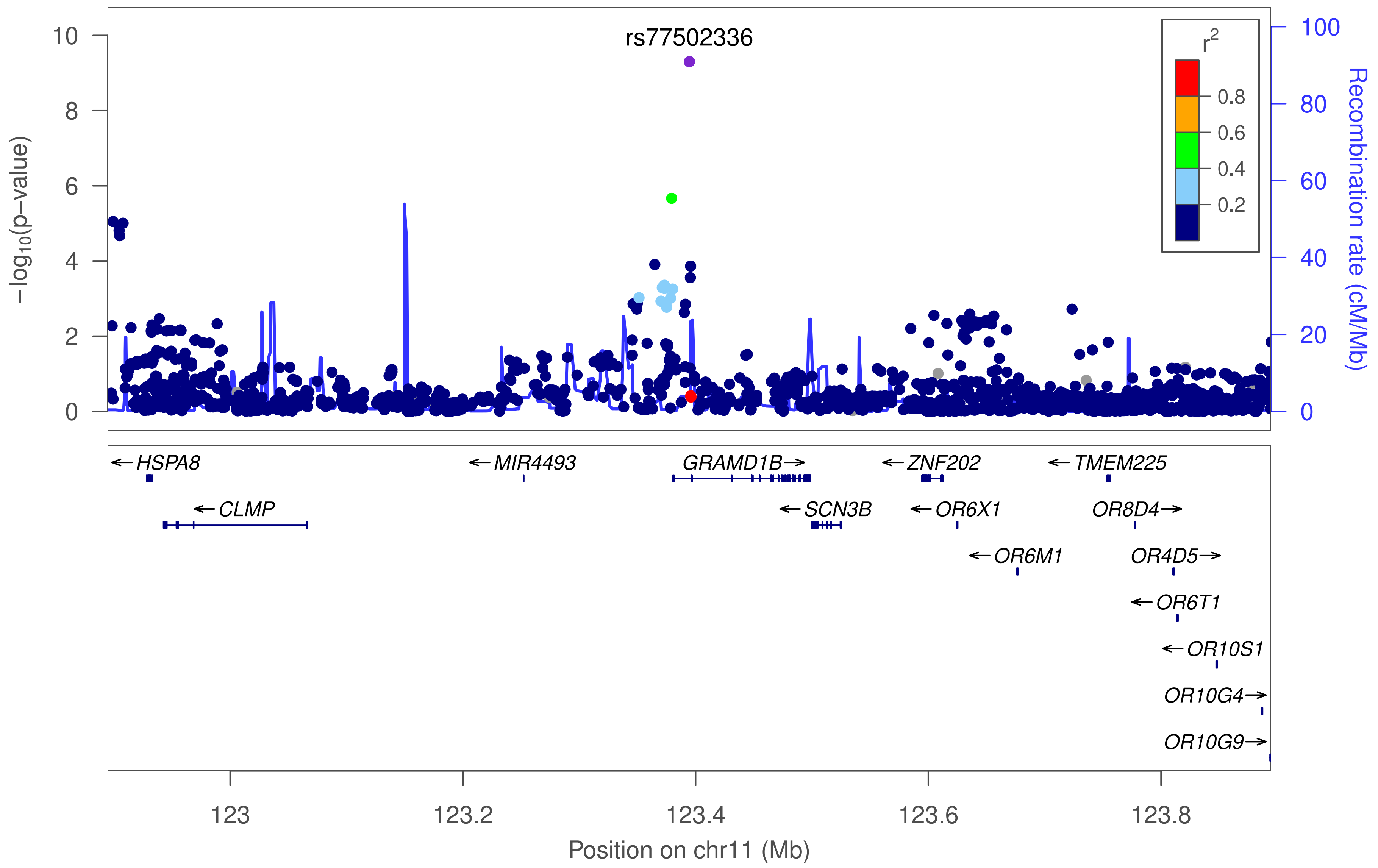

PGC2+Chinese rs2514218
rs2514218
r²
0.8
0.6
0.4
0.2
−log10(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
NCAM1→
TTC12→
←DRD2
←TMPRSS5
←USP28
HTR3A→
←NCAM1−AS1
ANKK1→
←ZW10
HTR3B→
←MIR4301
CLDN25→
113
113.2
113.4
113.6
113.8
Position on chr11 (Mb)

Chinese−only rs2514218



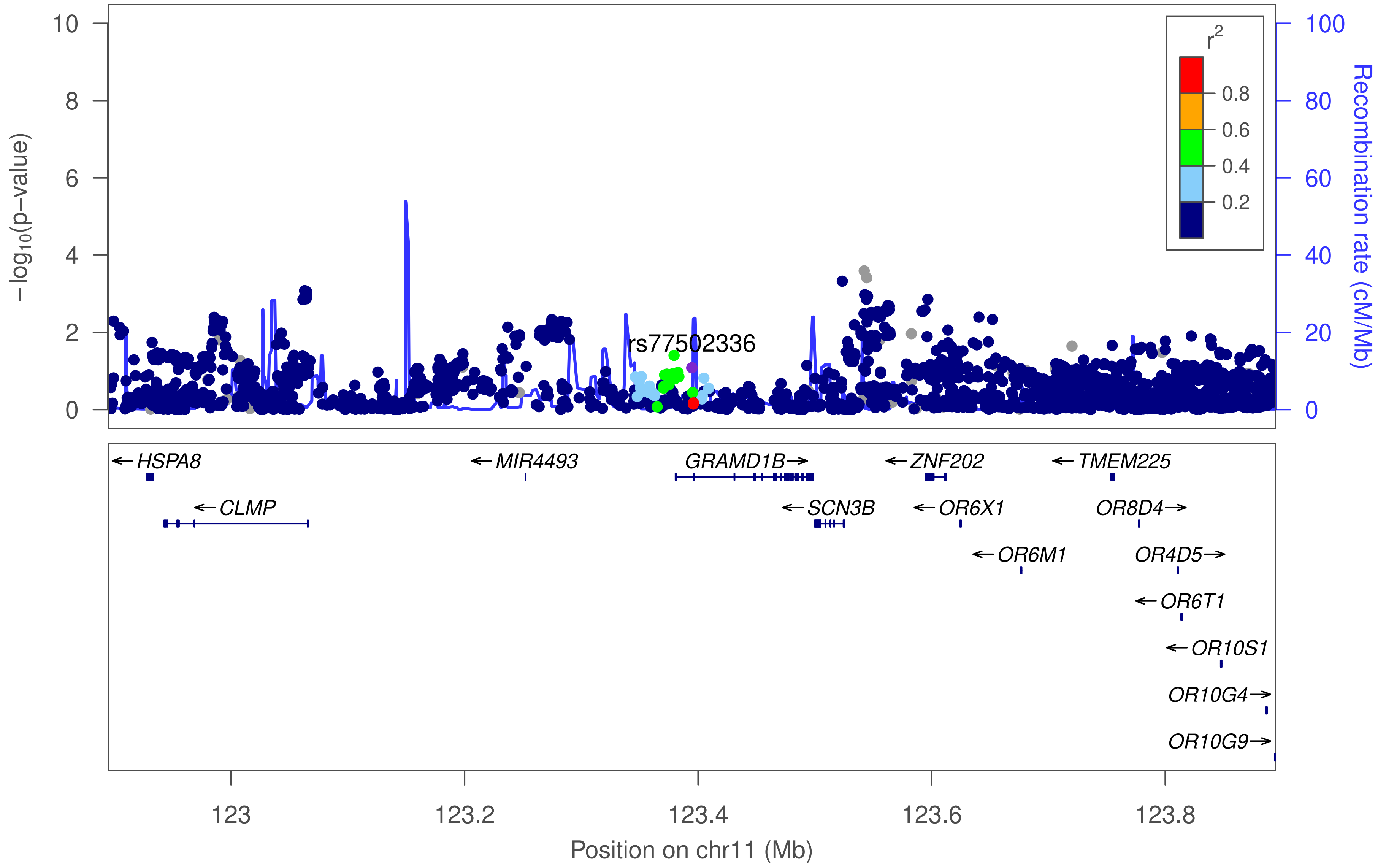
PGC2 rs77502336



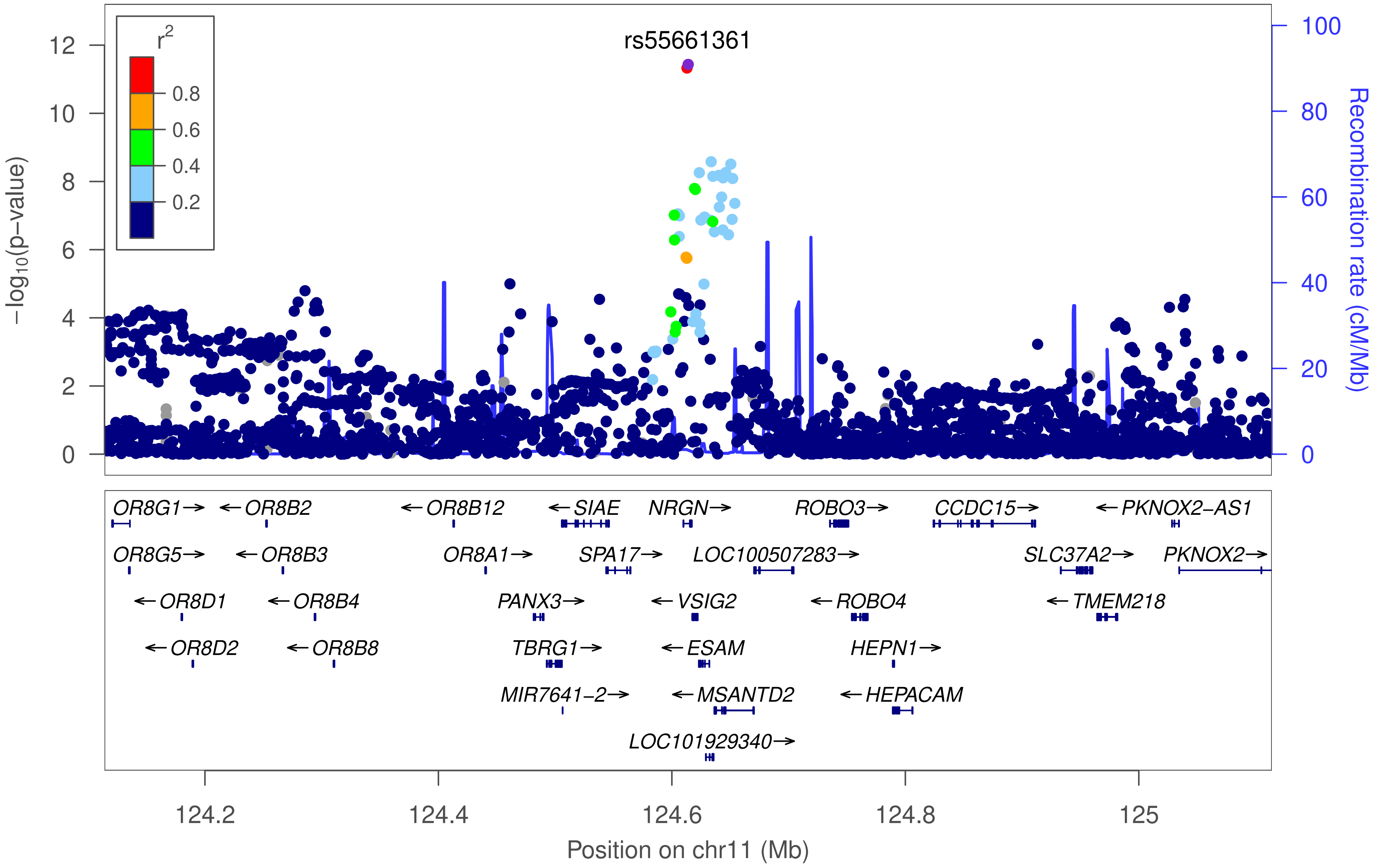


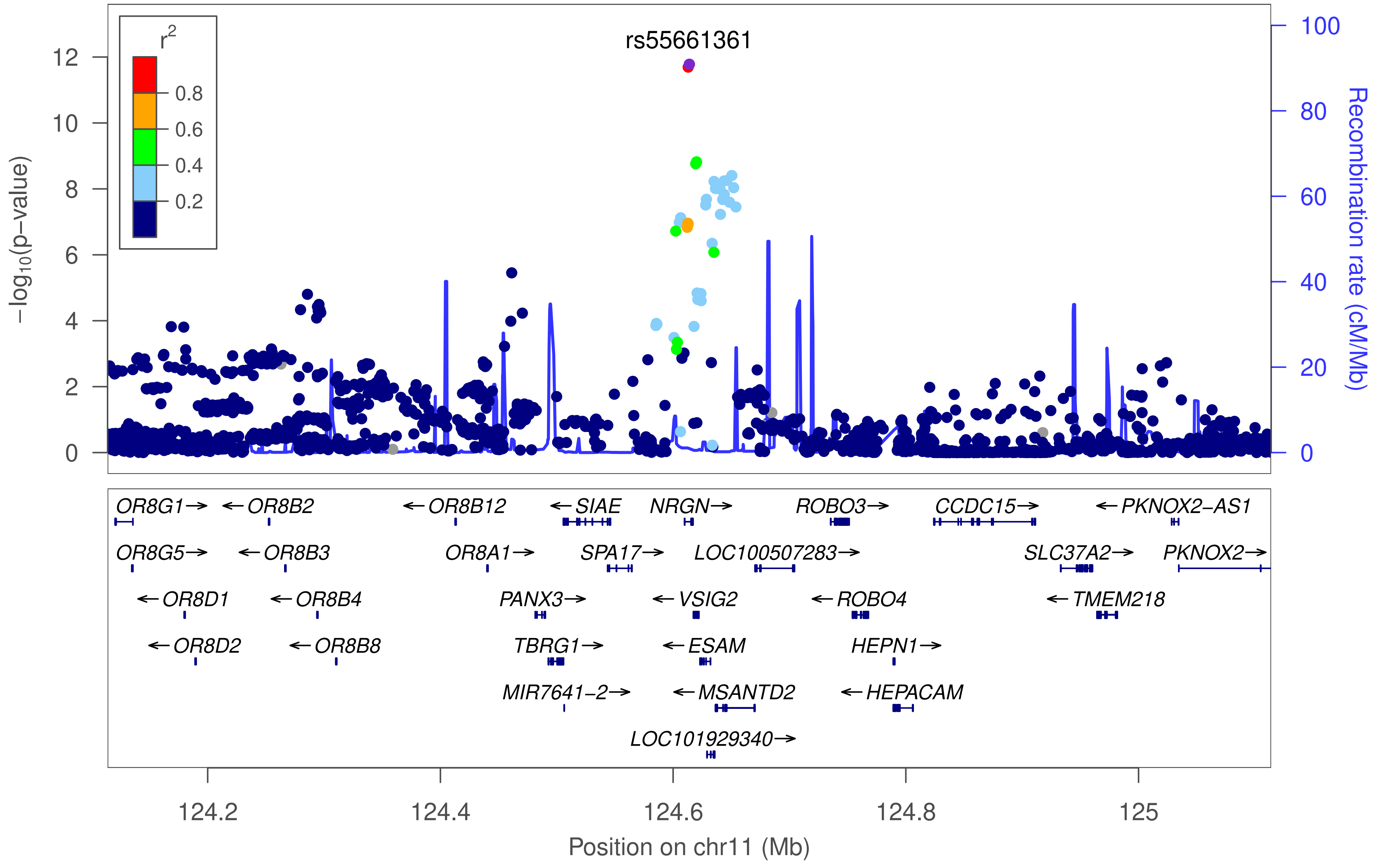
PGC2+Chinese rs77502336

Chinese−only rs77502336

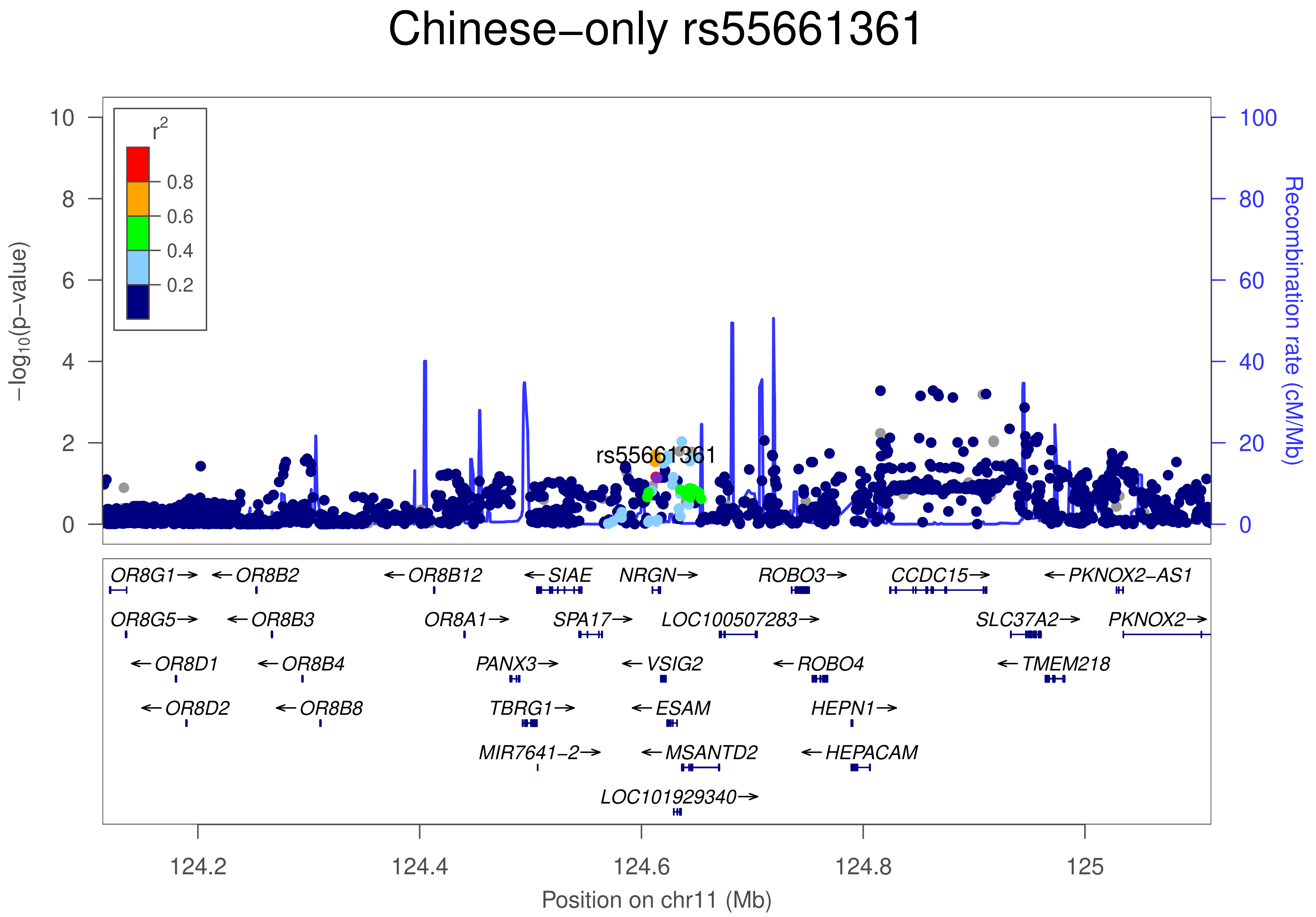


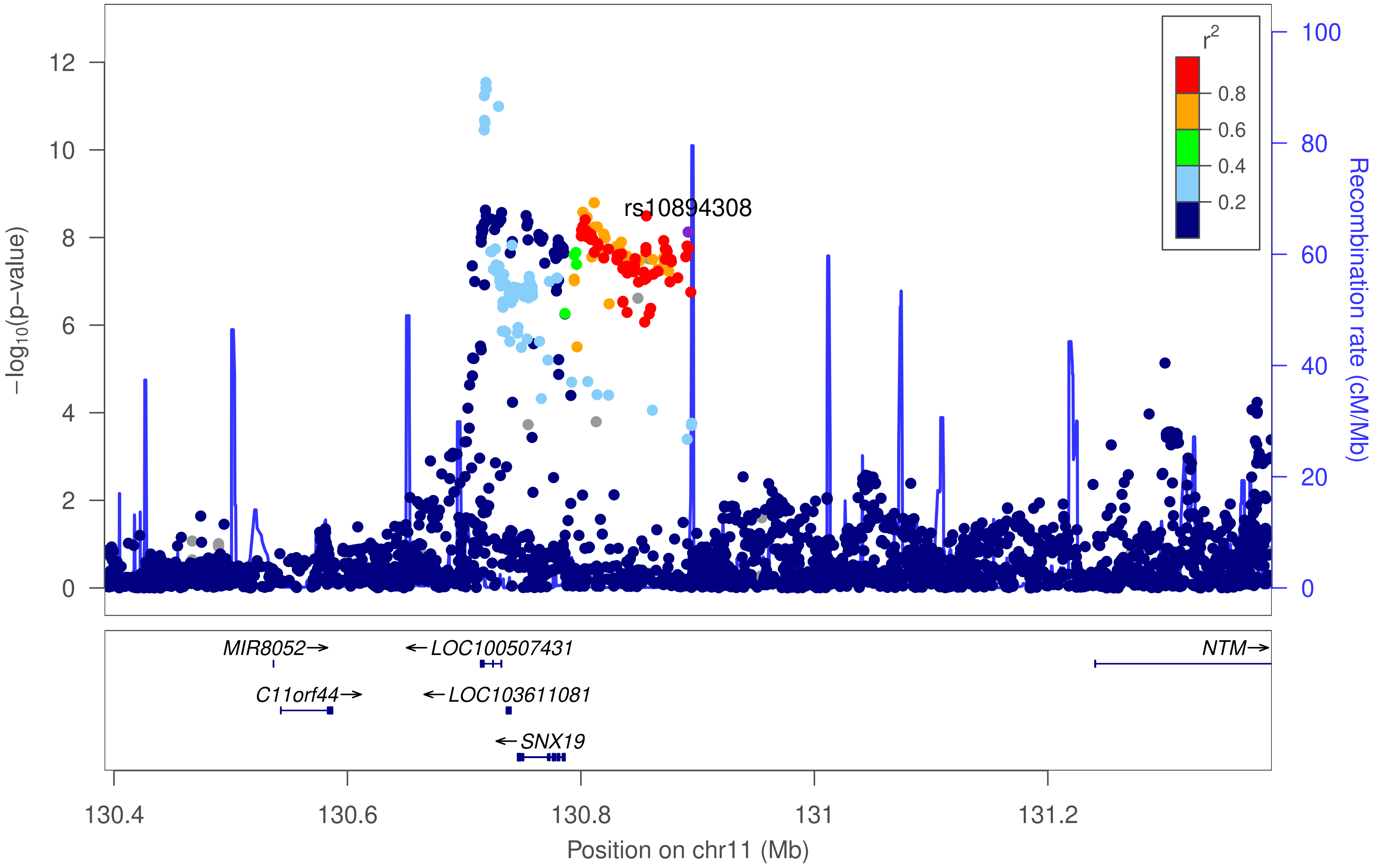
PGC2 rs55661361



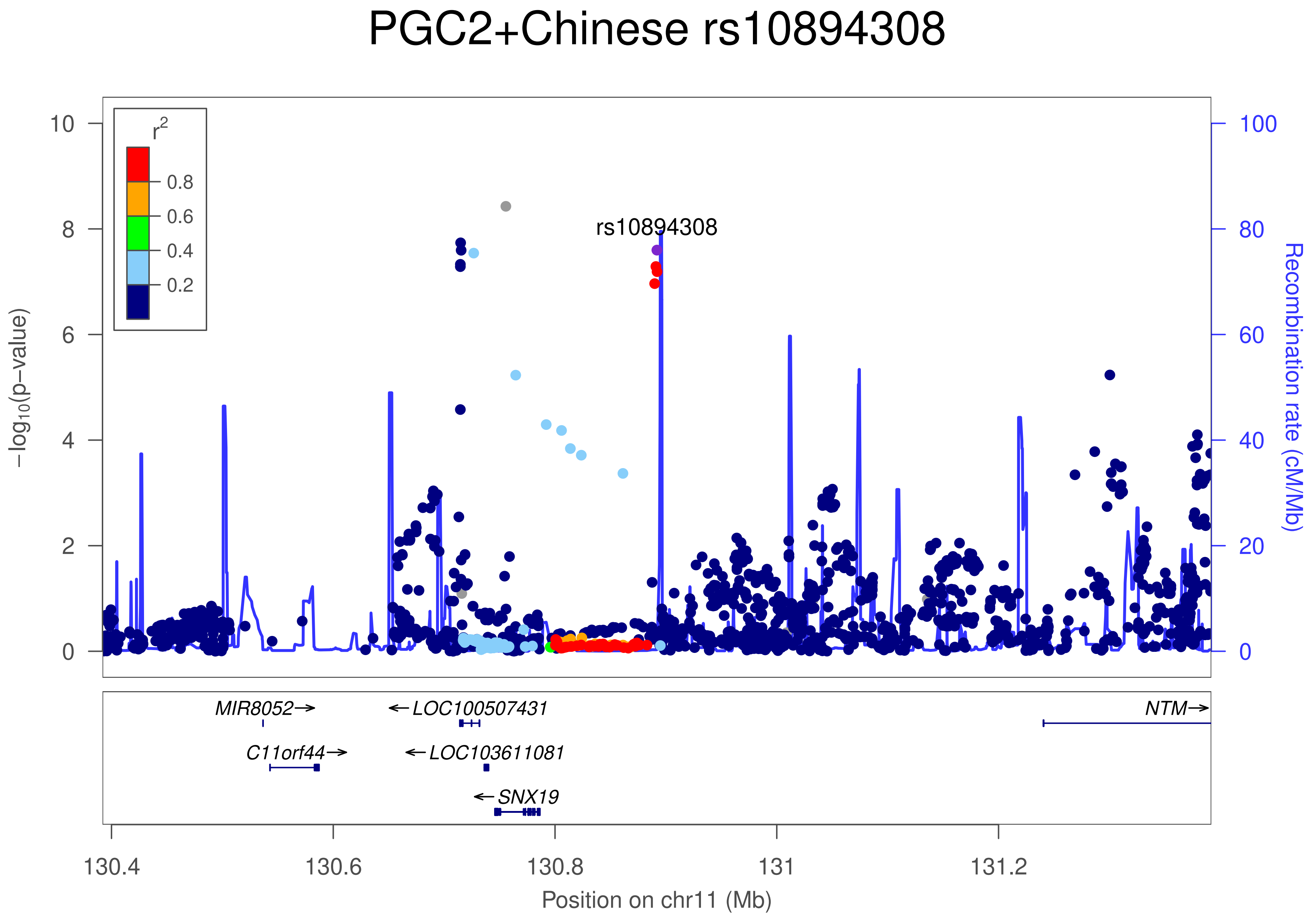


PGC2+Chinese rs55661361

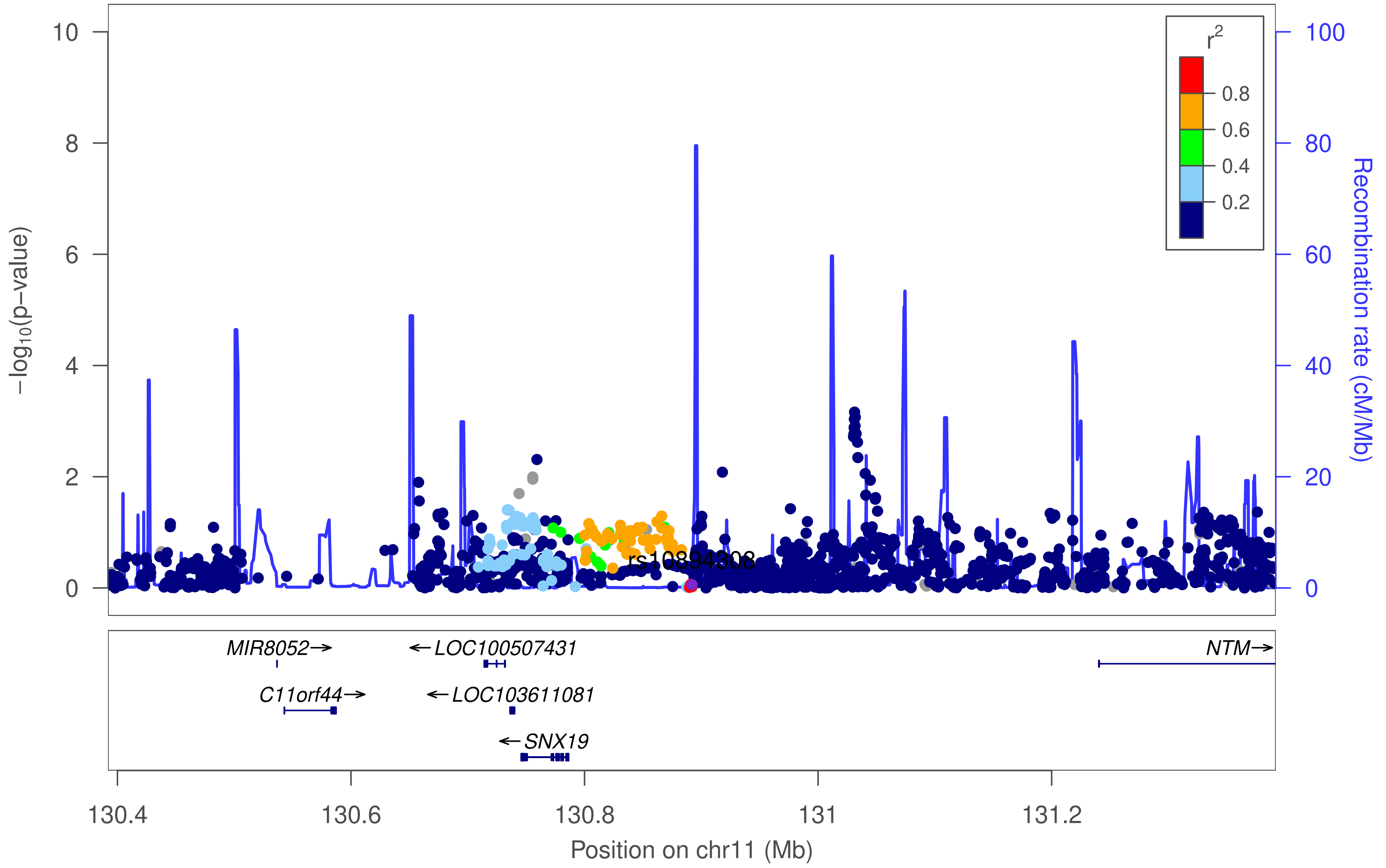

Chinese−only rs55661361
r^2
0.8
0.6
0.4
0.2
rs55661361
−log$_{10}$(p−value)
10
8
6
4
2
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
OR8G1→
←OR8B2
←OR8B12
←SIAE
NRGN→
ROBO3→
CCDC15→
←PKNOX2−AS1
OR8G5→
←OR8B3
OR8A1→
SPA17→
LOC100507283→
SLC37A2→
PKNOX2→
←OR8D1
←OR8B4
PANX3→
←VSIG2
←ROBO4
←TMEM218
←OR8D2
←OR8B8
TBRG1→
←ESAM
HEPN1→
MIR7641−2→
←MSANTD2
←HEPACAM
LOC101929340→
124.2
124.4
124.6
124.8
125
Position on chr11 (Mb)

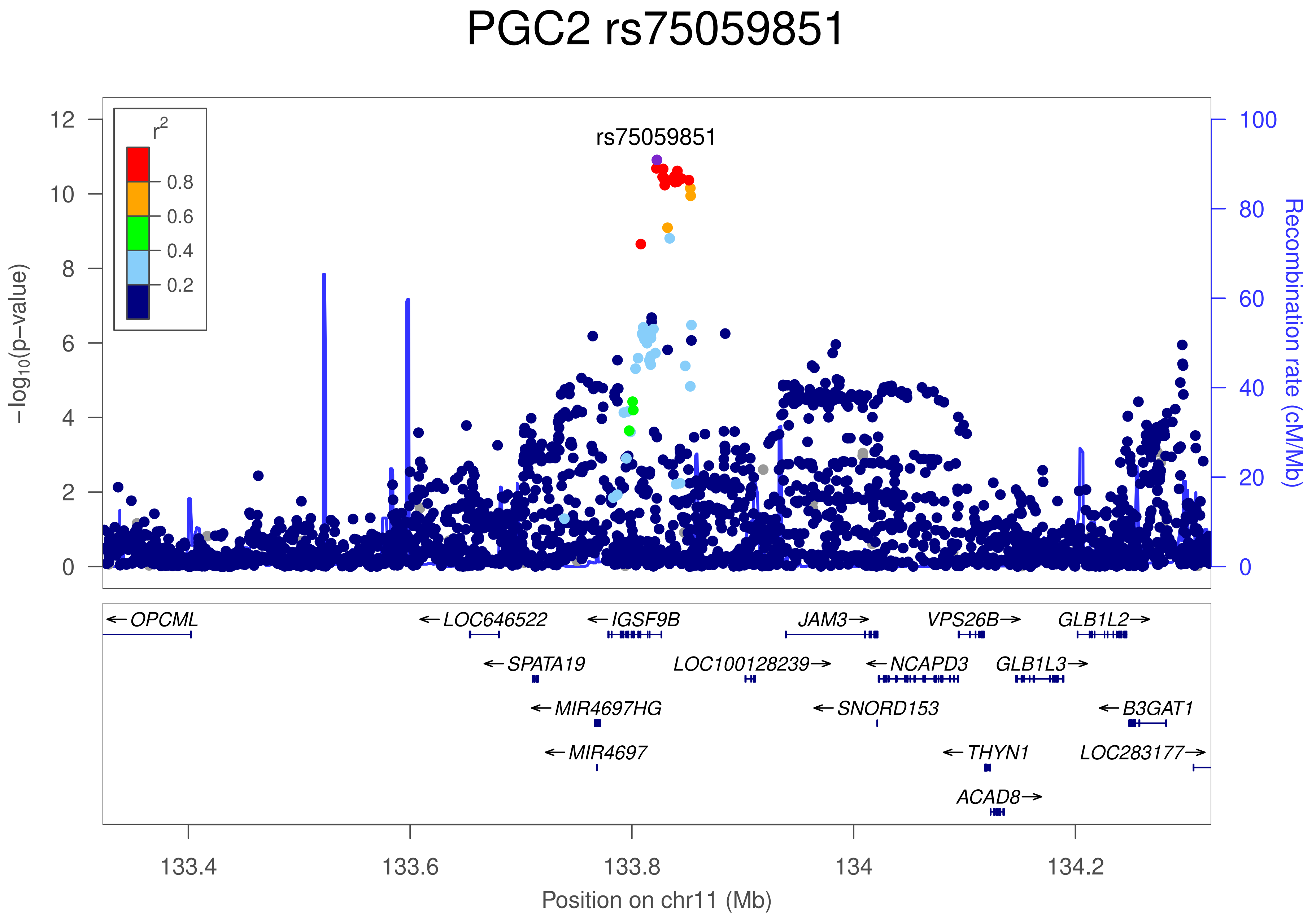


PGC2 rs10894308

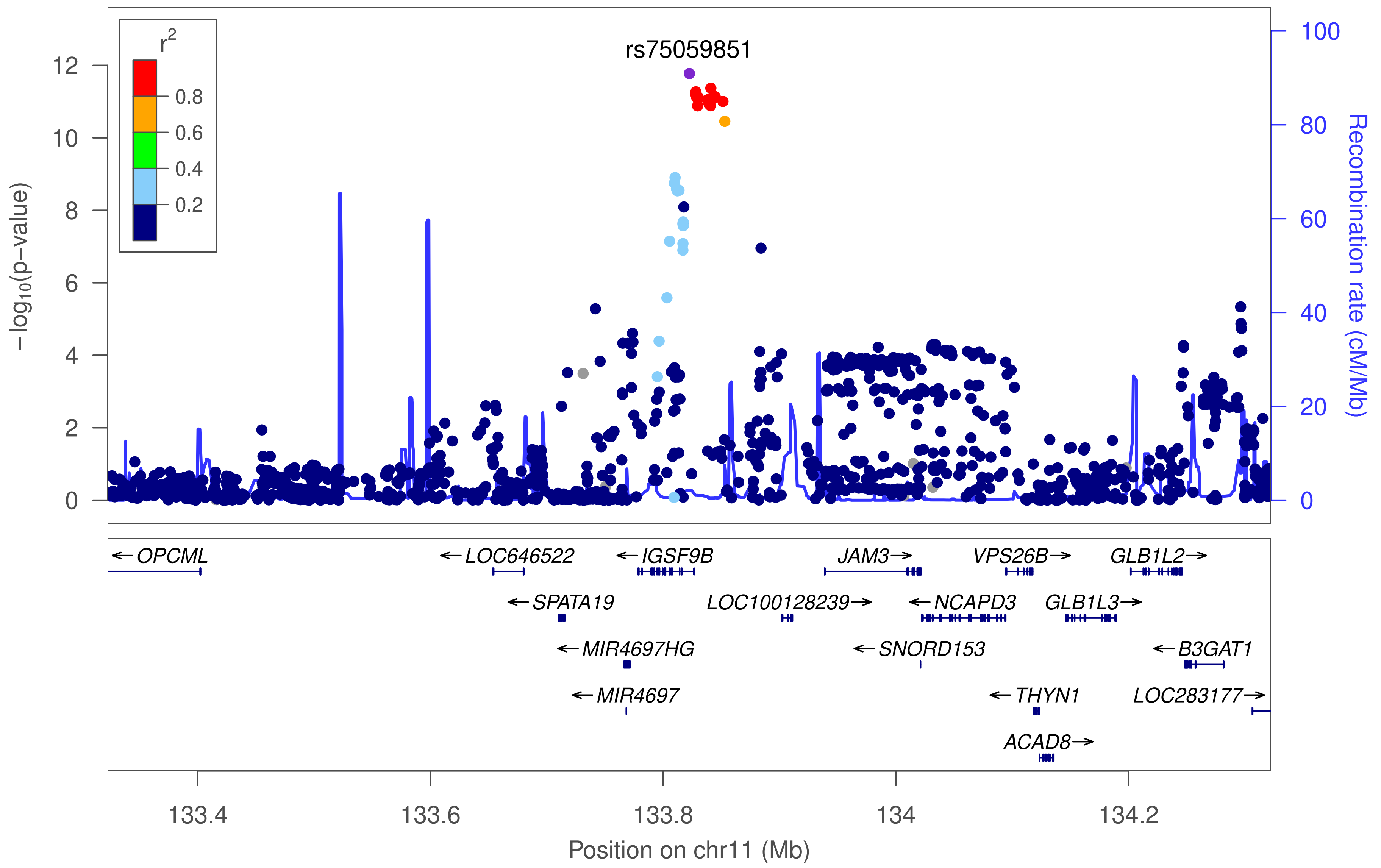

PGC2+Chinese rs10894308
r2
0.8
0.6
0.4
0.2
rs10894308
−log10(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
MIR8052→
←LOC100507431
C11orf44→
←LOC103611081
←SNX19
NTM→
130.4
130.6
130.8
131
131.2
Position on chr11 (Mb)

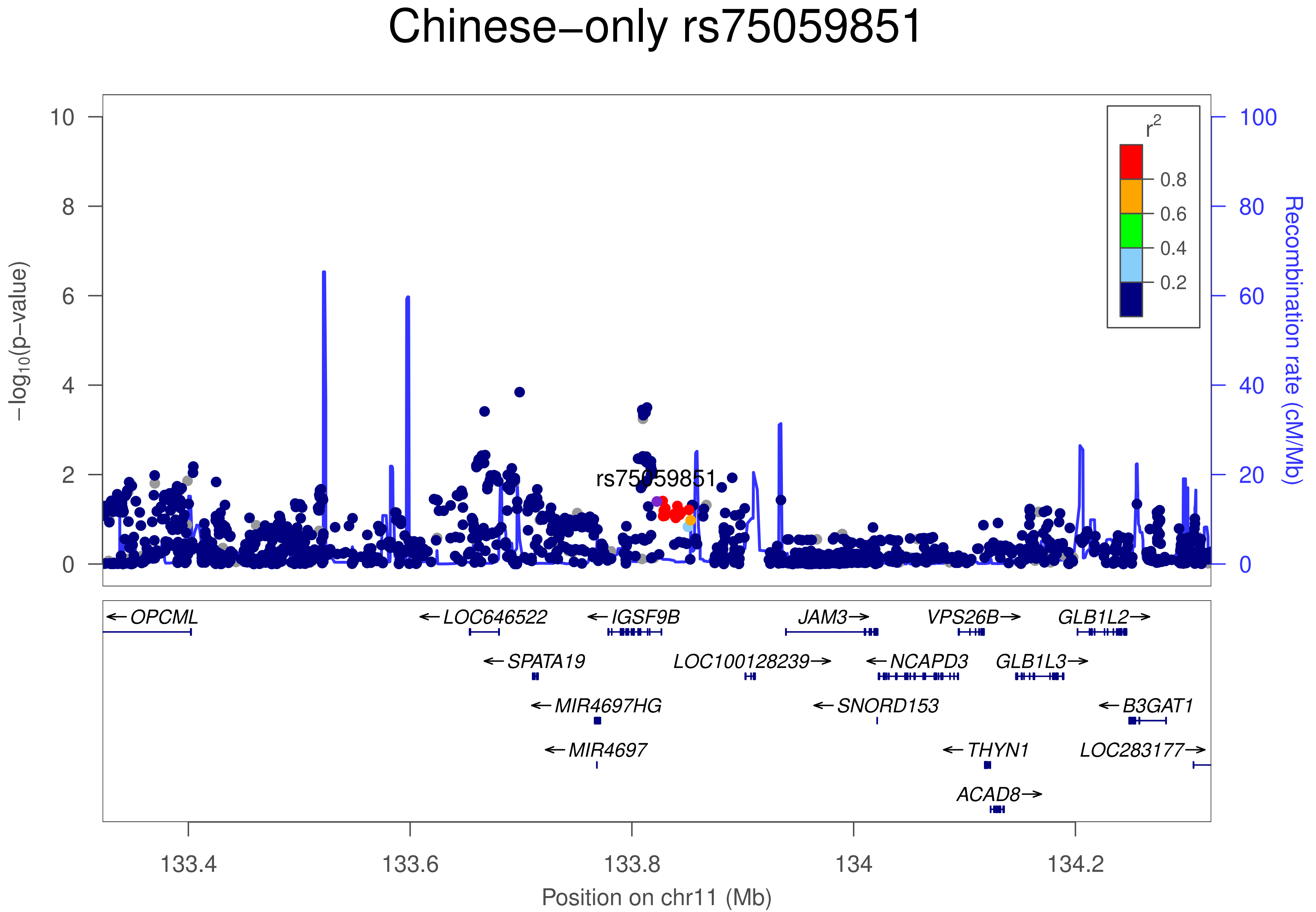
Chinese–only rs10894308



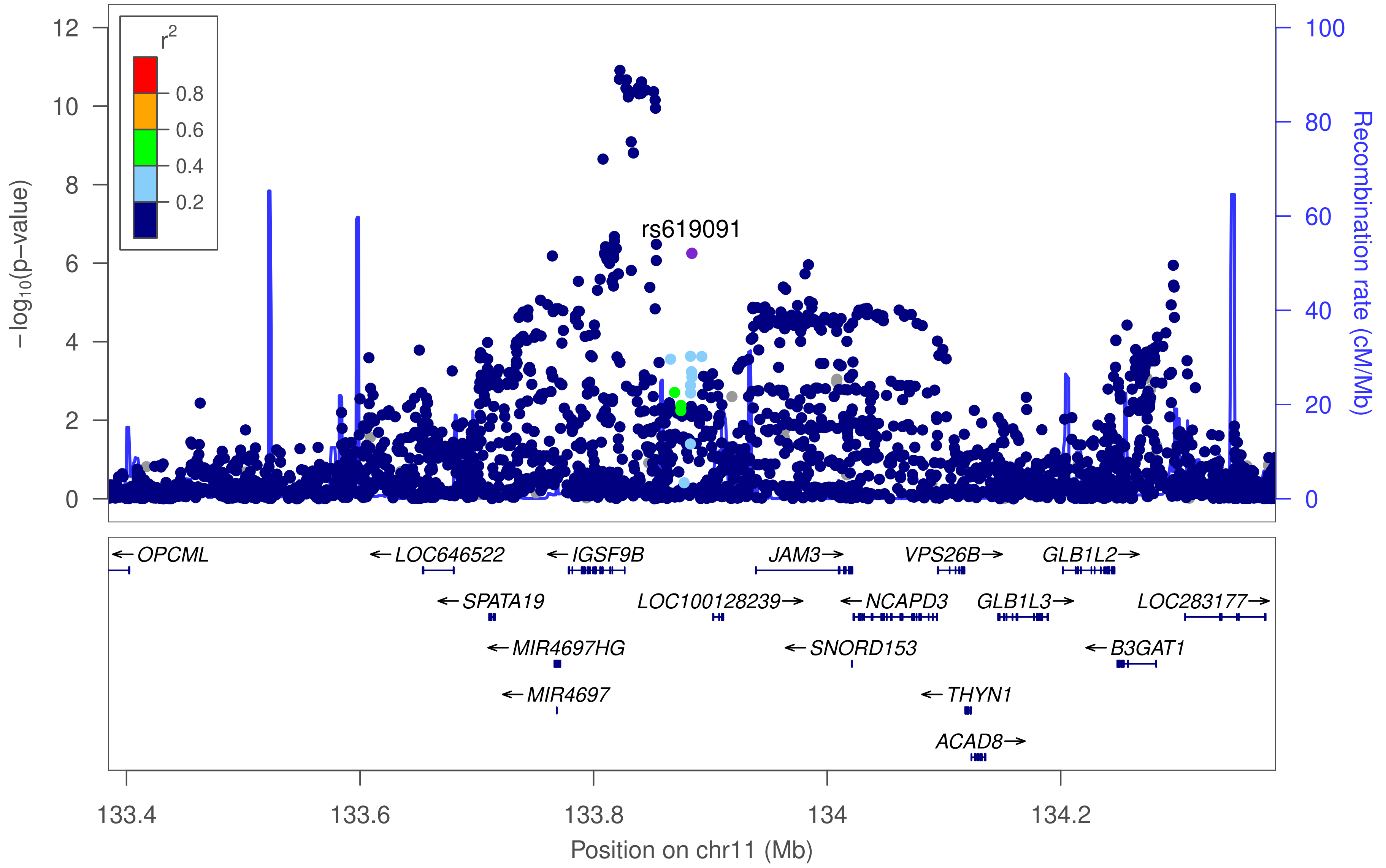

PGC2 rs75059851
rs75059851
r2
0.8
0.6
0.4
0.2
12
10
8
6
4
2
0
−log10(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
← OPCML
← LOC646522
← IGSF9B
JAM3 →
VPS26B →
GLB1L2 →
← SPATA19
LOC100128239 →
← NCAPD3
GLB1L3 →
← MIR4697HG
← SNORD153
← B3GAT1
← MIR4697
← THYN1
LOC283177 →
ACAD8 →
133.4
133.6
133.8
134
134.2
Position on chr11 (Mb)

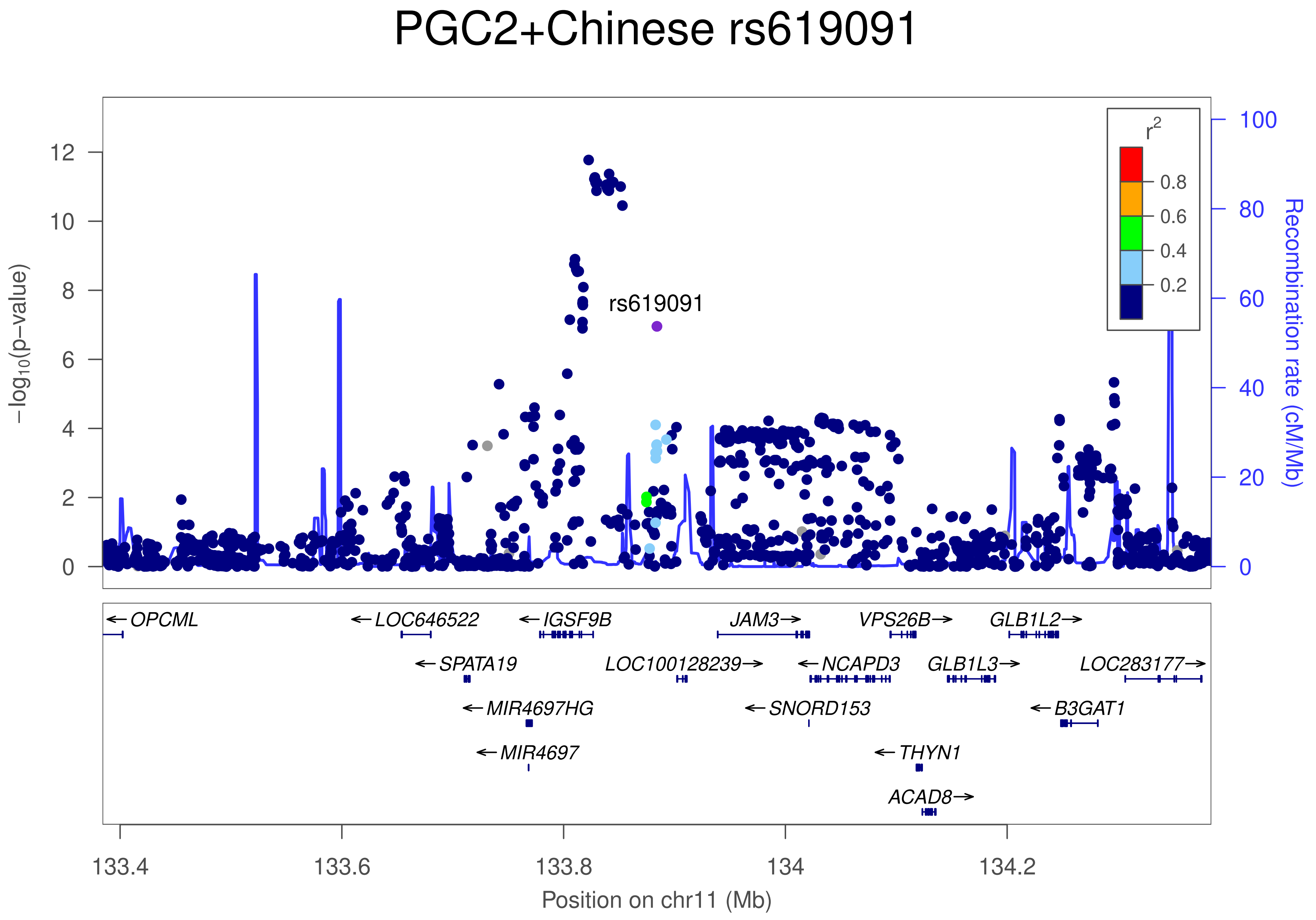
PGC2+Chinese rs75059851

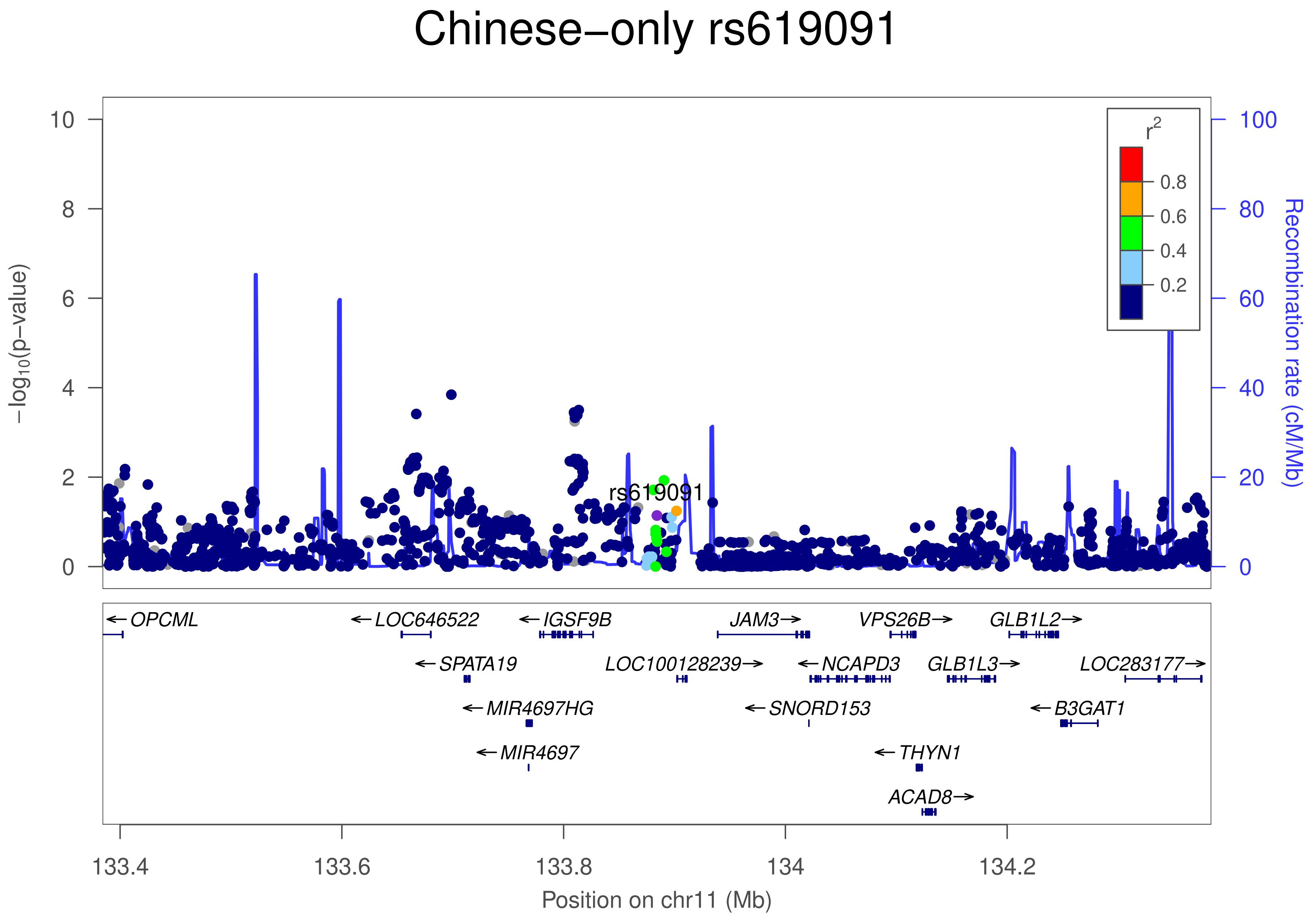


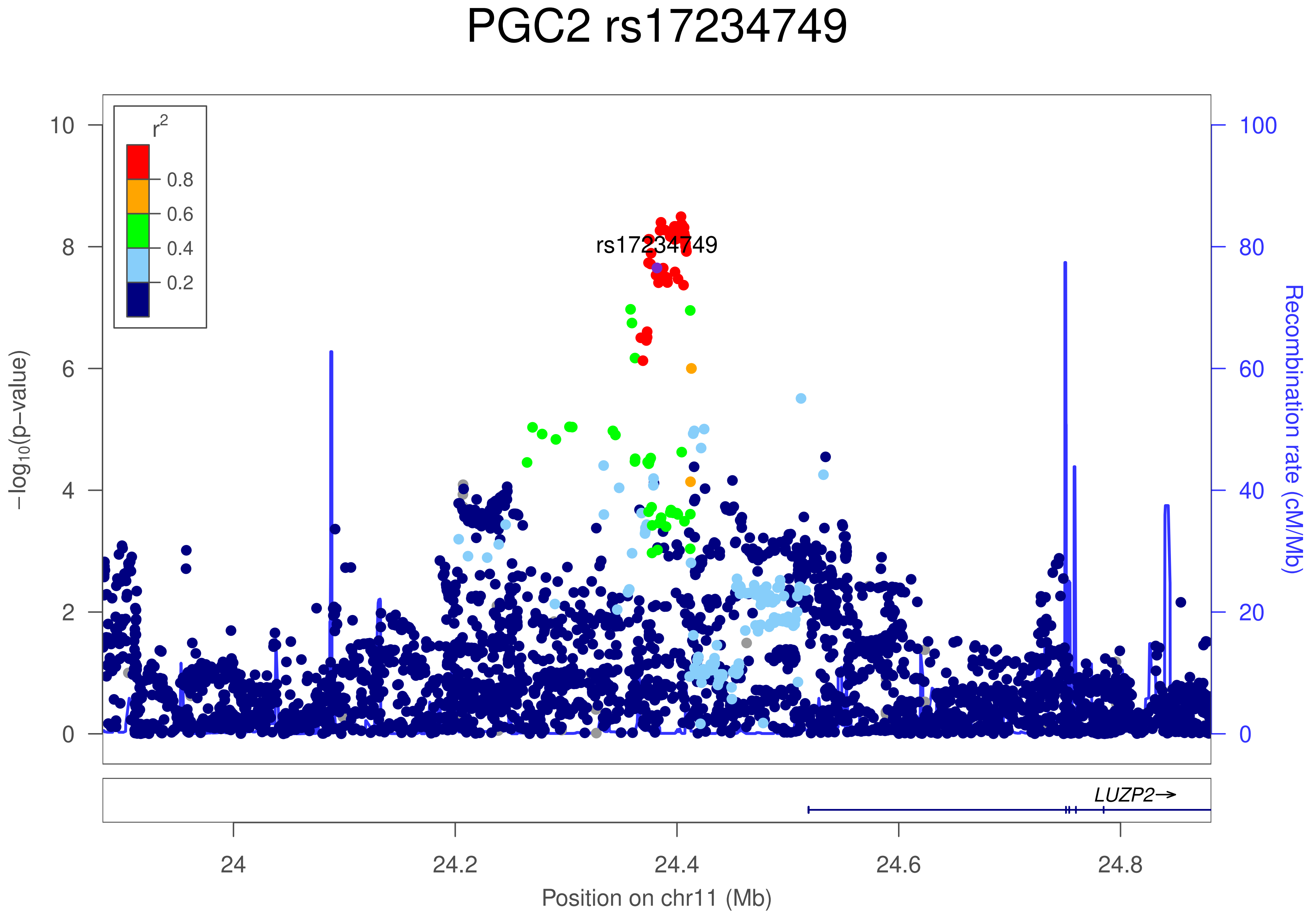

Chinese–only rs75059851
−log10(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
r²
0.8
0.6
0.4
0.2
rs75059851
←OPCML
←LOC646522
←IGSF9B
JAM3→
VPS26B→
GLB1L2→
←SPATA19
LOC100128239→
←NCAPD3
GLB1L3→
←MIR4697HG
←SNORD153
←B3GAT1
←MIR4697
←THYN1
LOC283177→
ACAD8→
133.4
133.6
133.8
134
134.2
Position on chr11 (Mb)

PGC2 rs619091

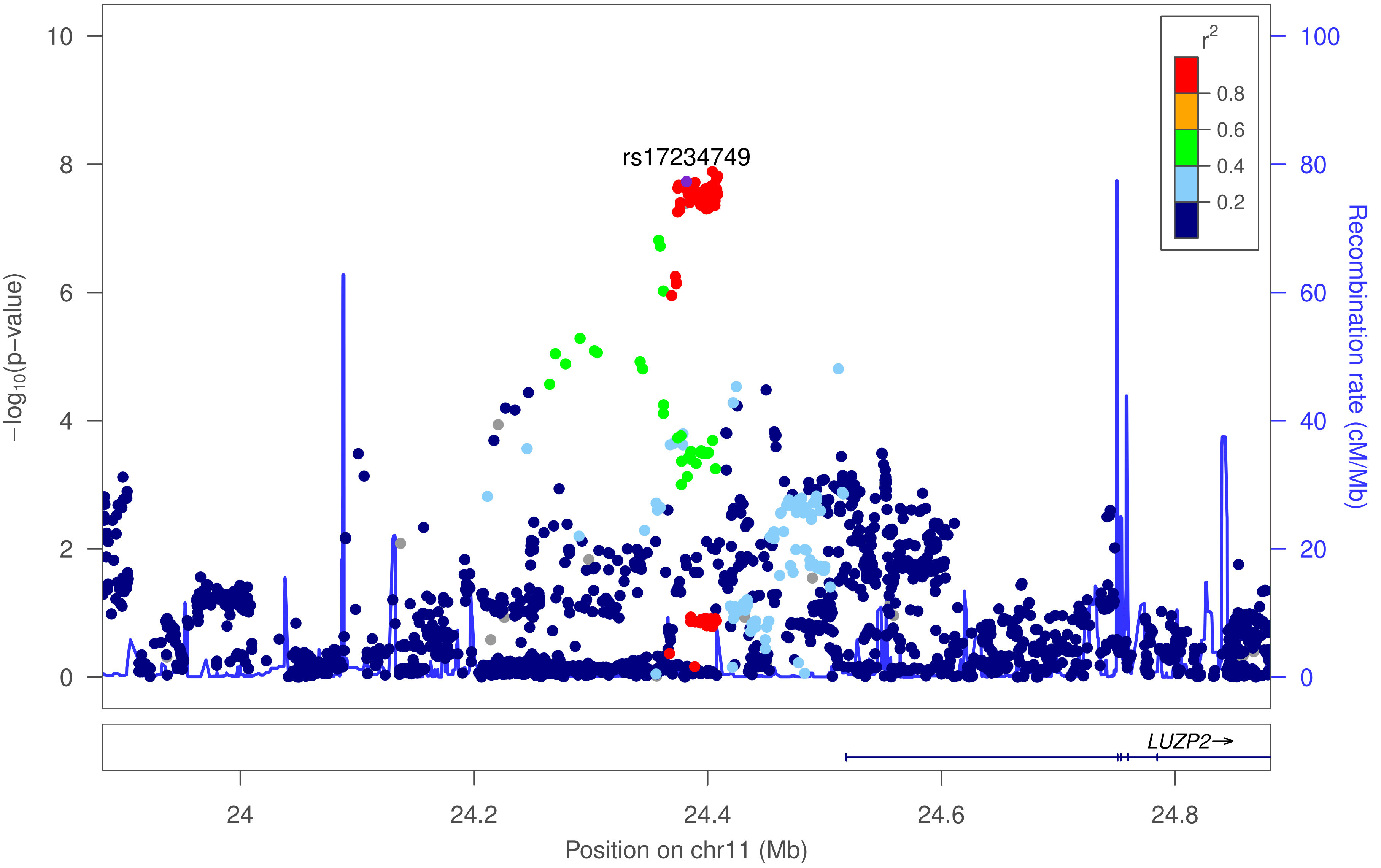



PGC2+Chinese rs619091
−log10(p−value)
0
2
4
6
8
10
12
Recombination rate (cM/Mb)
0
20
40
60
80
100
rs619091
r2
0.2
0.4
0.6
0.8
← OPCML
← LOC646522
← IGSF9B
JAM3 →
VPS26B →
GLB1L2 →
← SPATA19
LOC100128239 →
← NCAPD3
GLB1L3 →
LOC283177 →
← MIR4697HG
← SNORD153
← B3GAT1
← MIR4697
← THYN1
ACAD8 →
133.4
133.6
133.8
134
134.2
Position on chr11 (Mb)

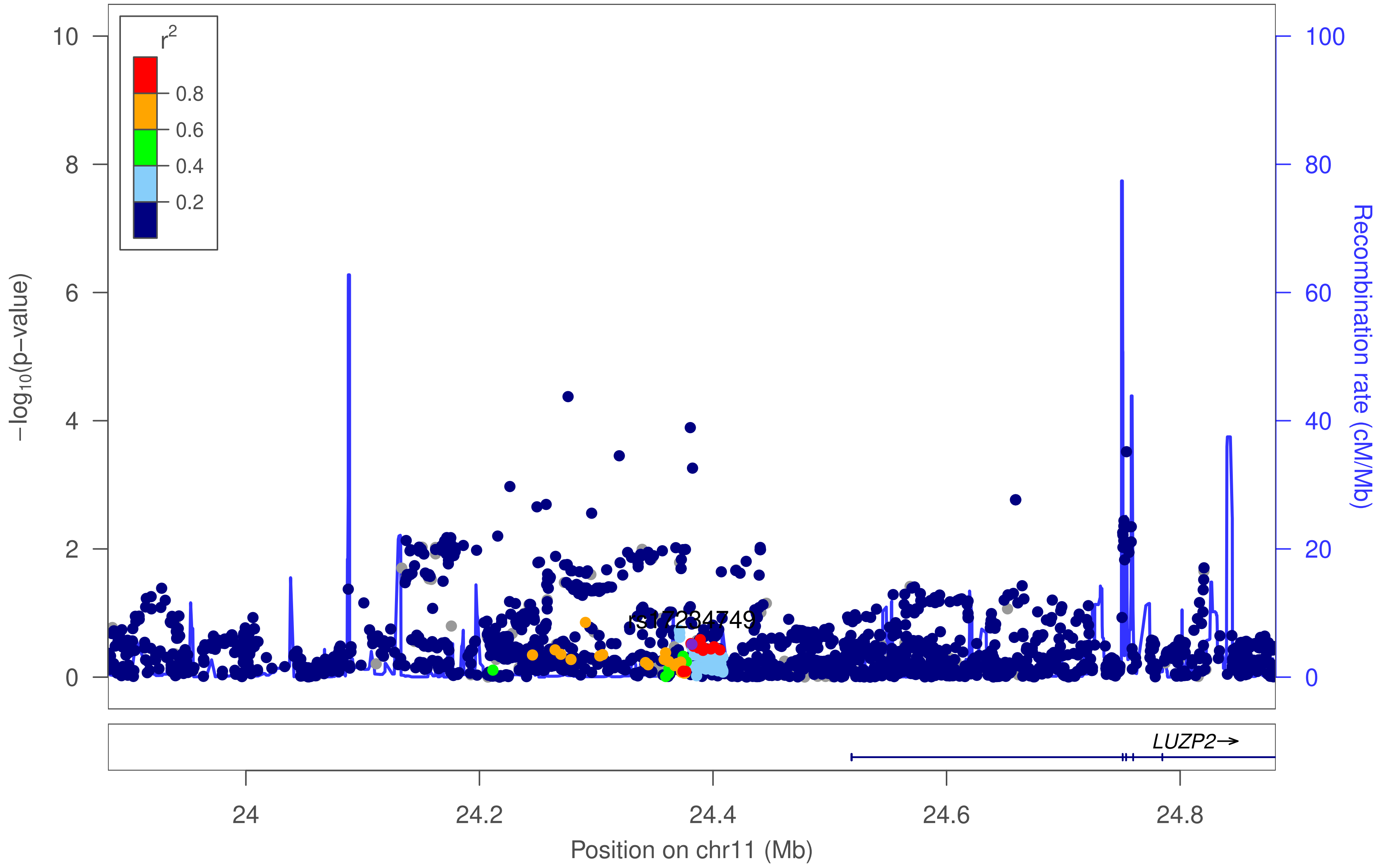

Chinese−only rs619091

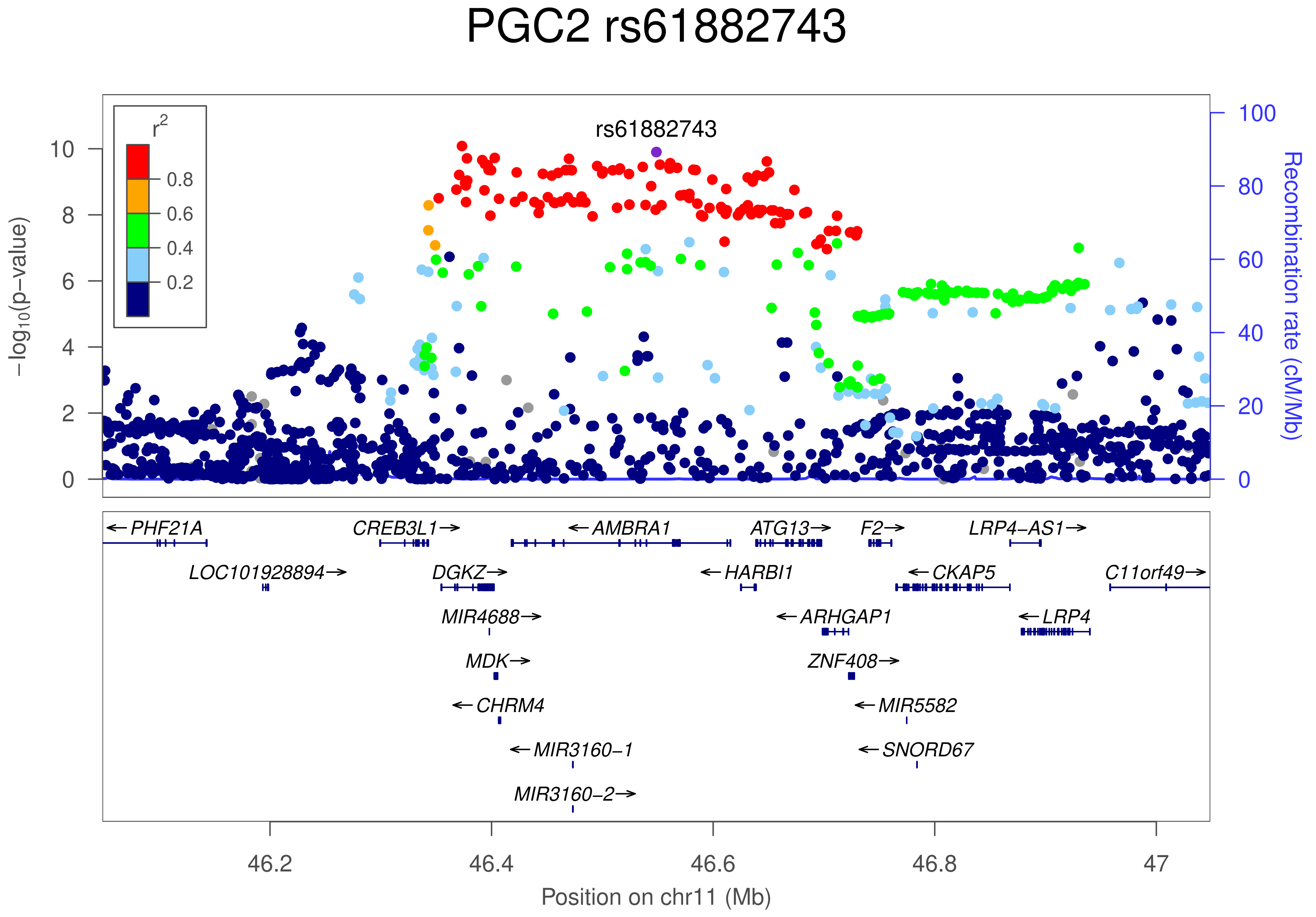

PGC2 rs17234749
r2
0.8
0.6
0.4
0.2
rs17234749
−log10(p−value)
10
8
6
4
2
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
LUZP2→
24
24.2
24.4
24.6
24.8
Position on chr11 (Mb)

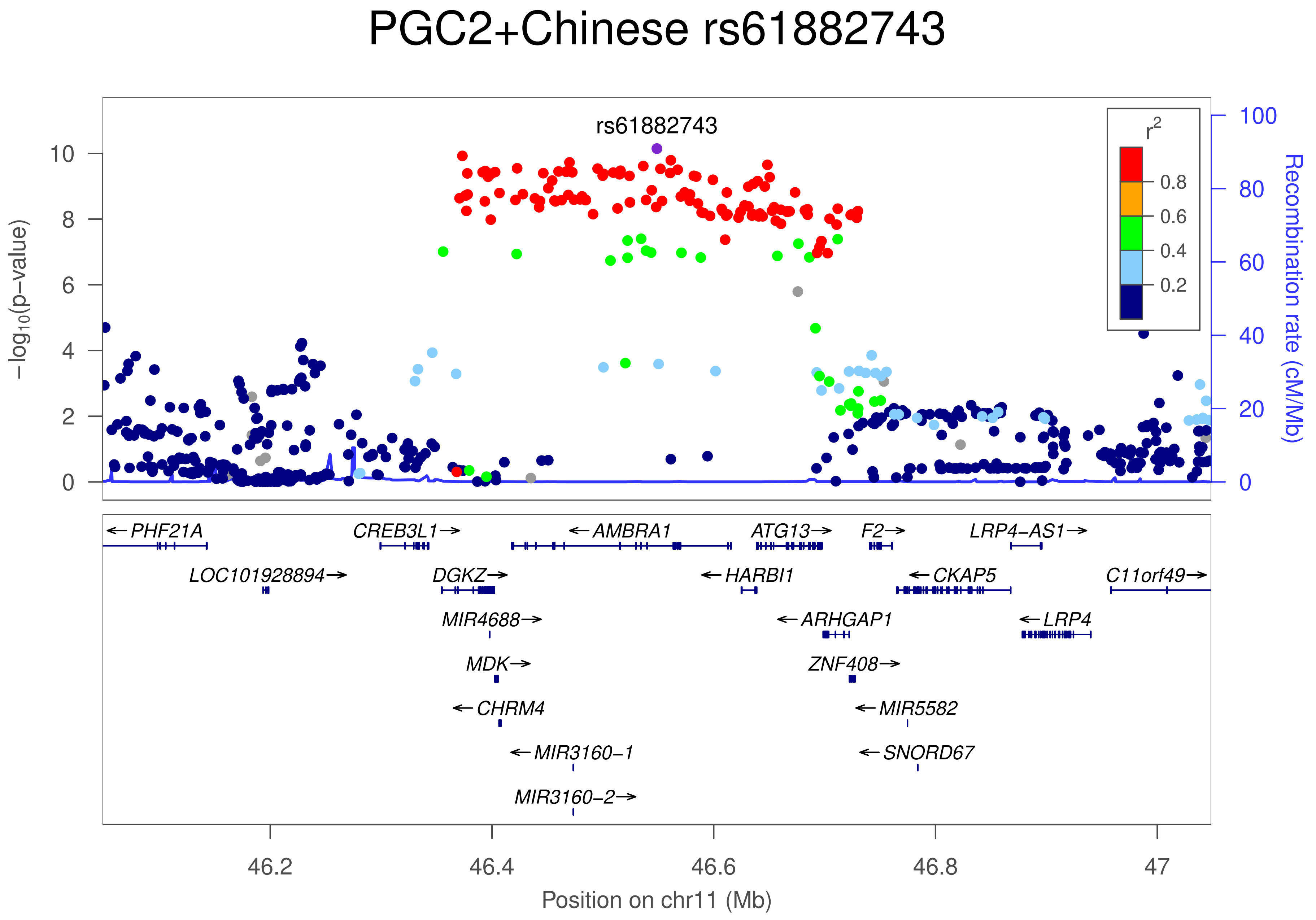
PGC2+Chinese rs17234749



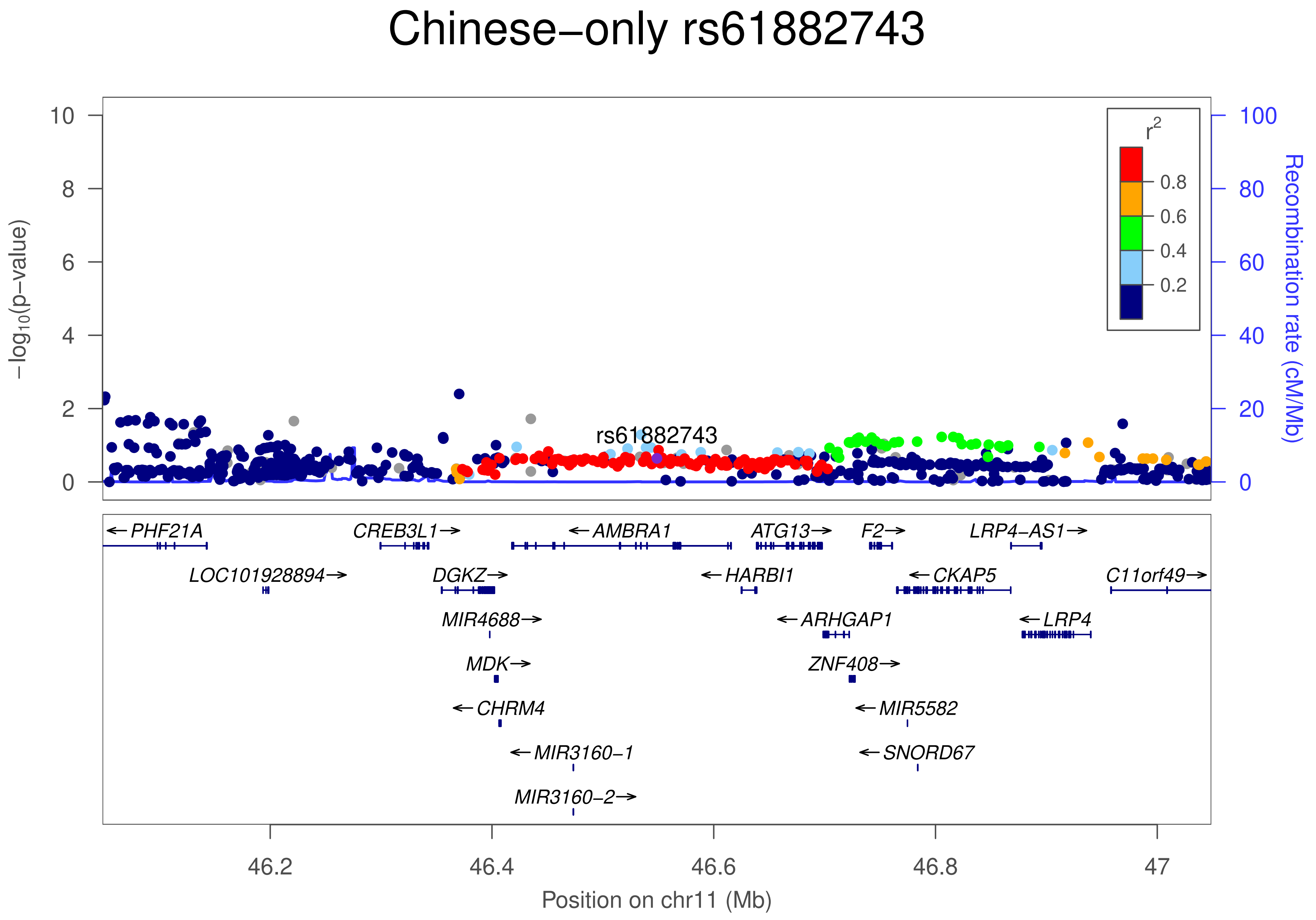
Chinese−only rs17234749



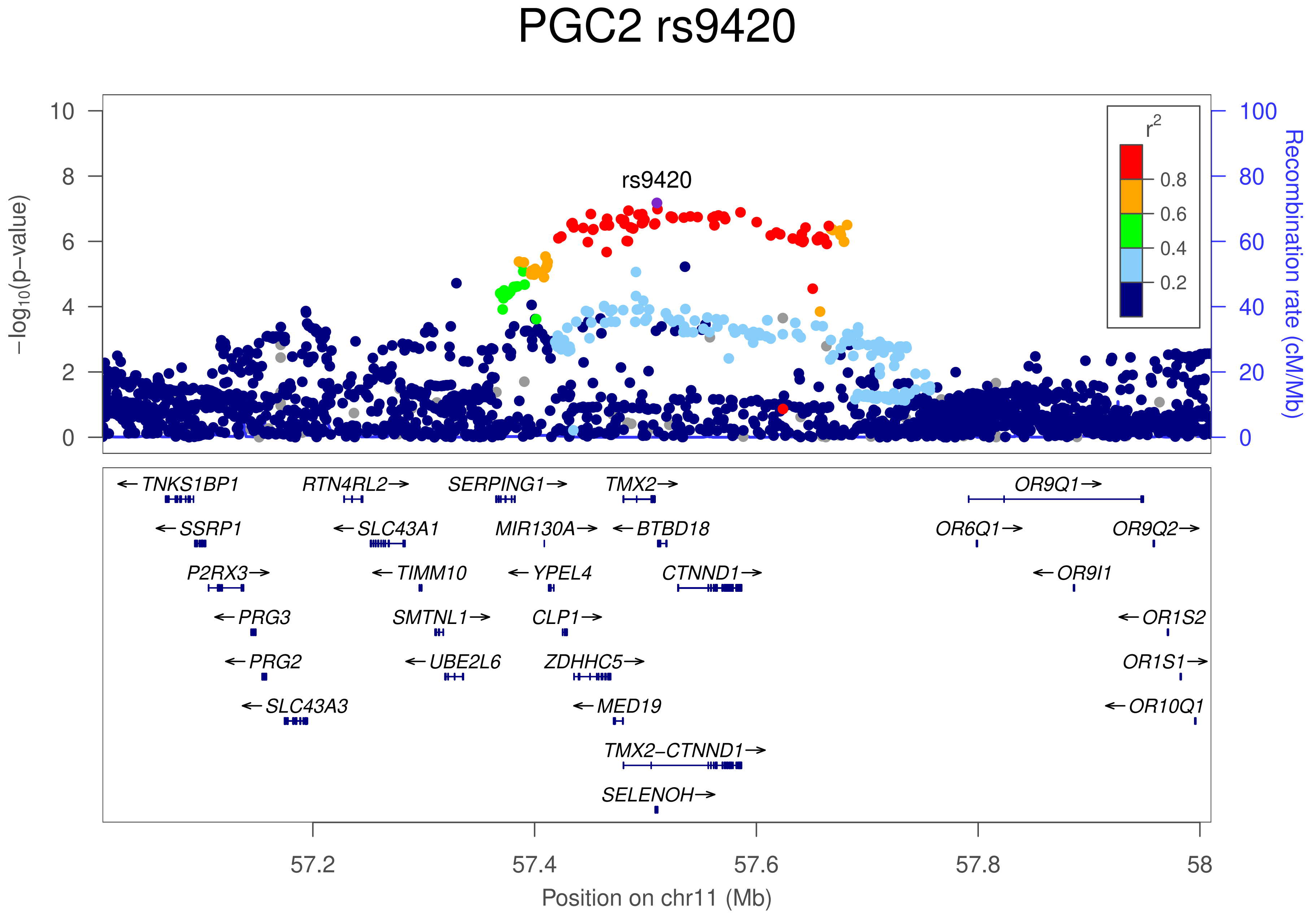

PGC2 rs61882743
rs61882743
r2
0.8
0.6
0.4
0.2
−log10(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
← PHF21A
CREB3L1 →
← AMBRA1
ATG13 →
F2 →
LRP4−AS1 →
LOC101928894 →
DGKZ →
← HARBI1
← CKAP5
C11orf49 →
MIR4688 →
← ARHGAP1
← LRP4
MDK →
ZNF408 →
← CHRM4
← MIR5582
← MIR3160−1
← SNORD67
MIR3160−2 →
46.2
46.4
46.6
46.8
47
Position on chr11 (Mb)

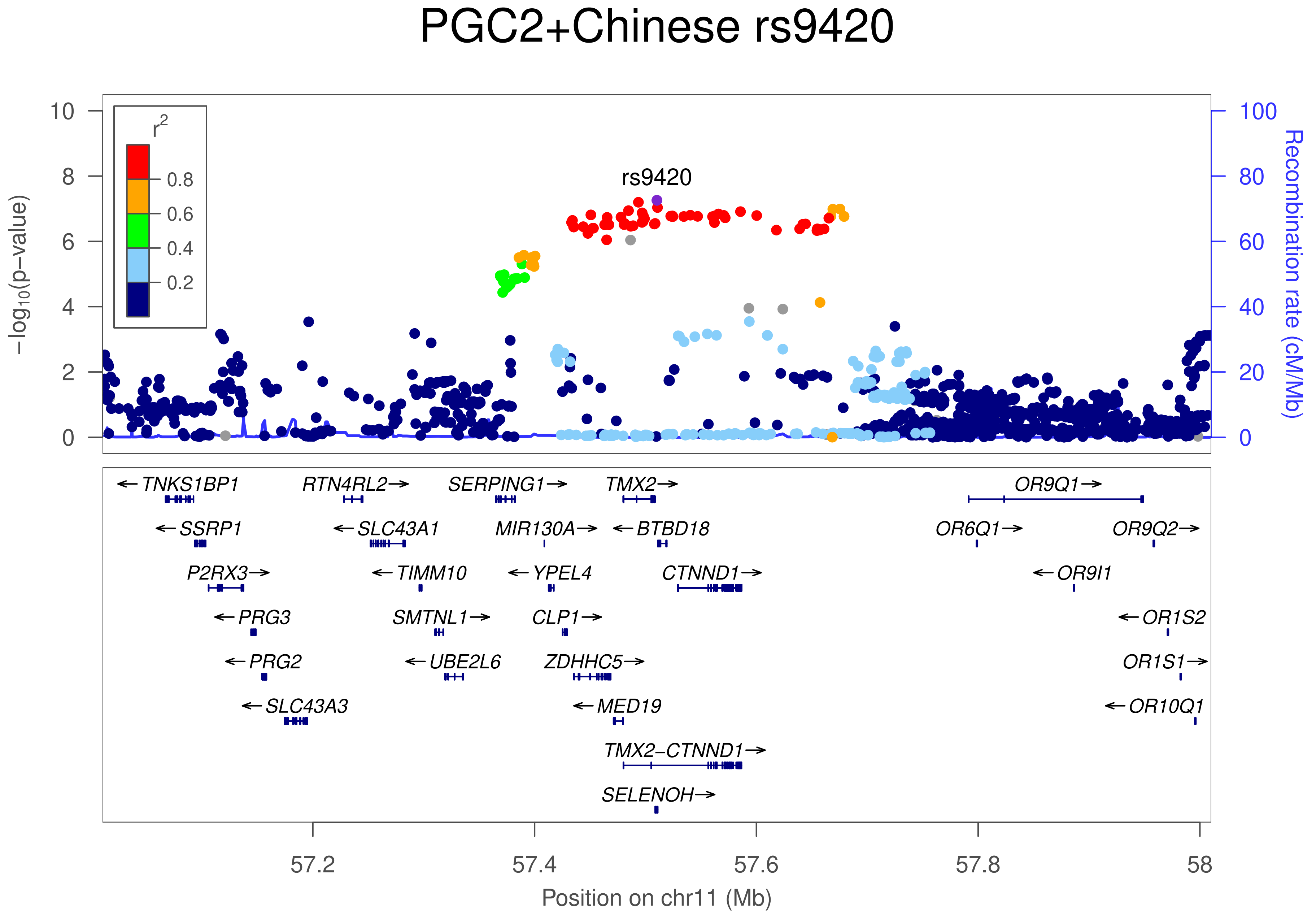


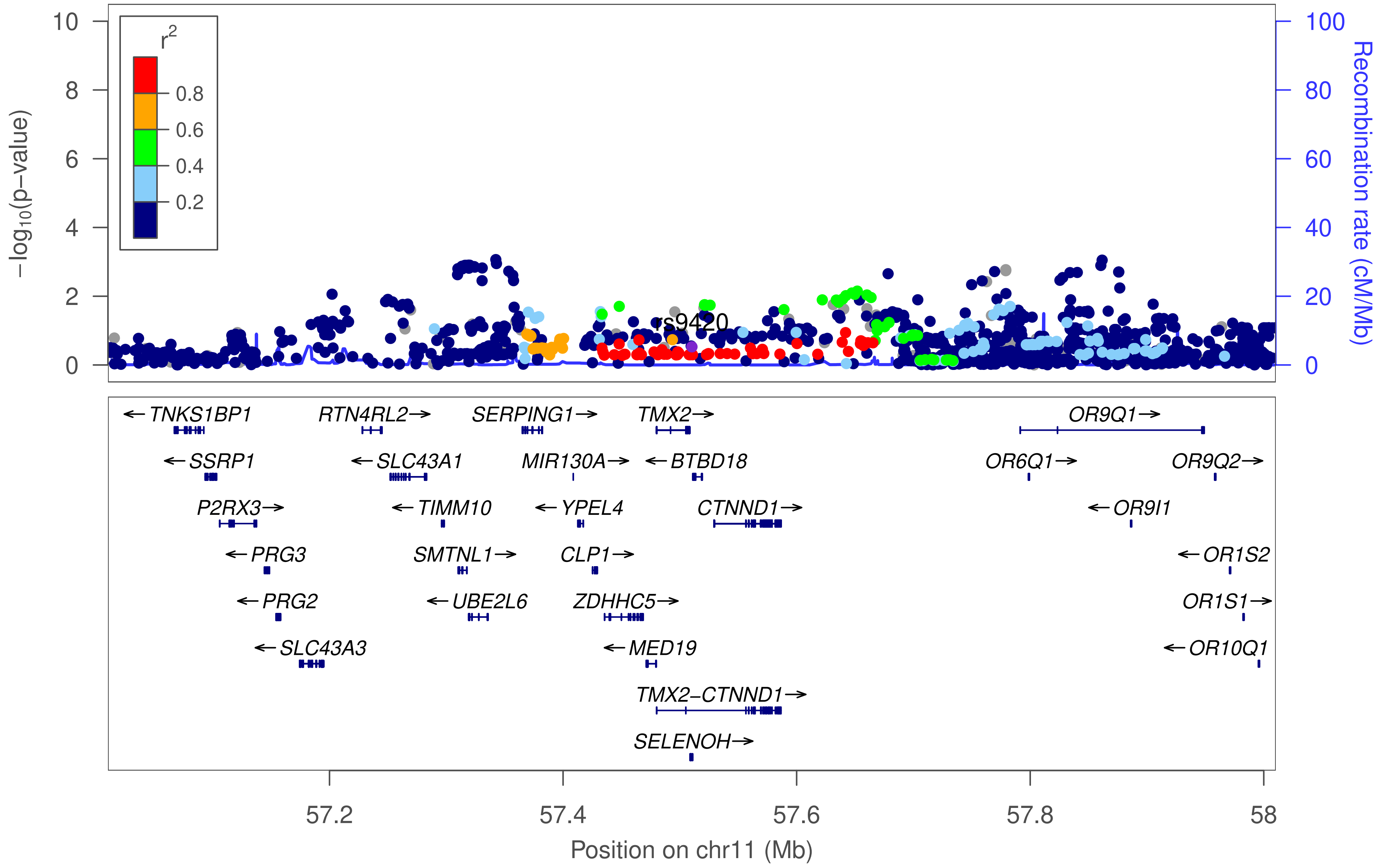
PGC2+Chinese rs61882743



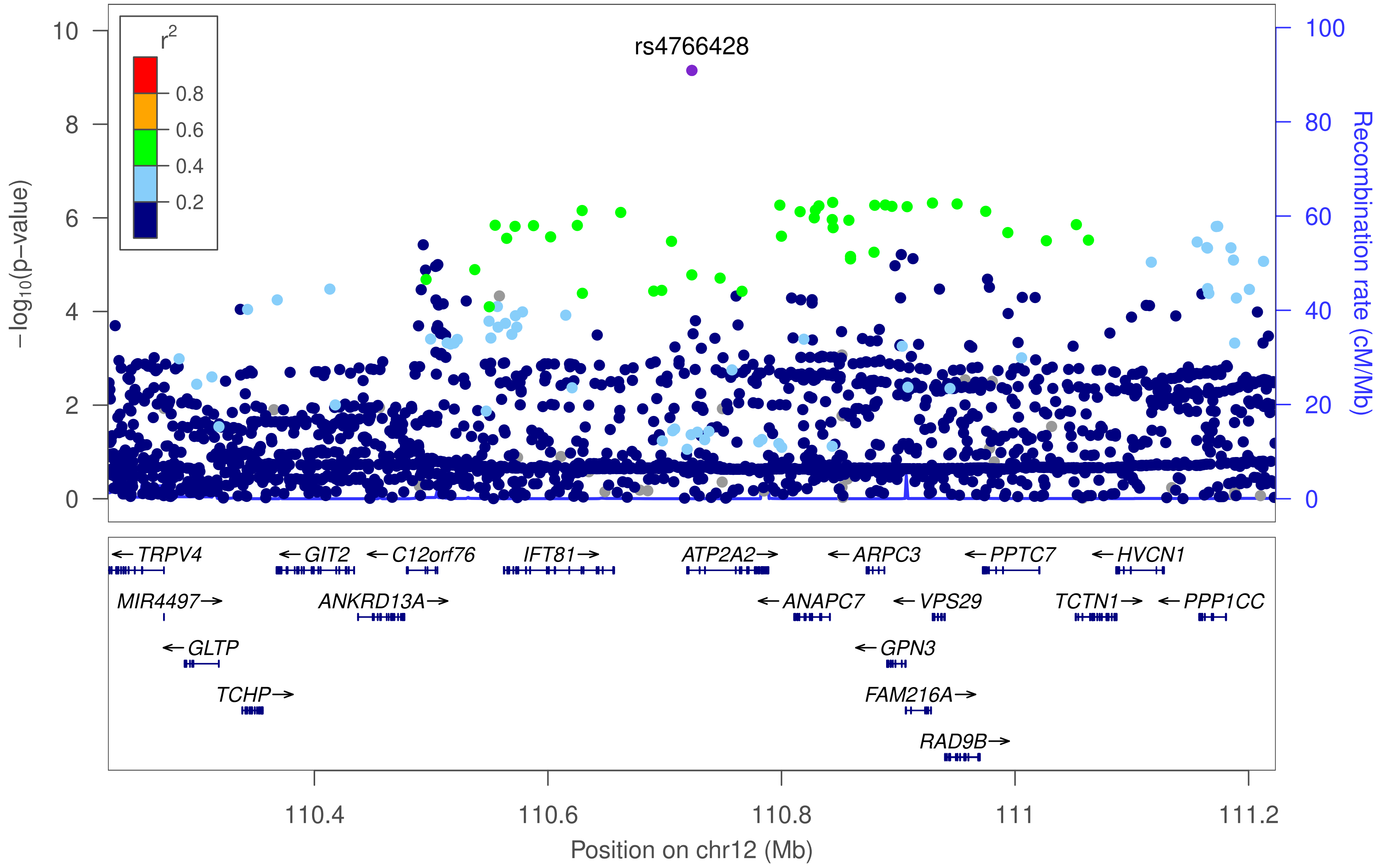
Chinese–only rs61882743

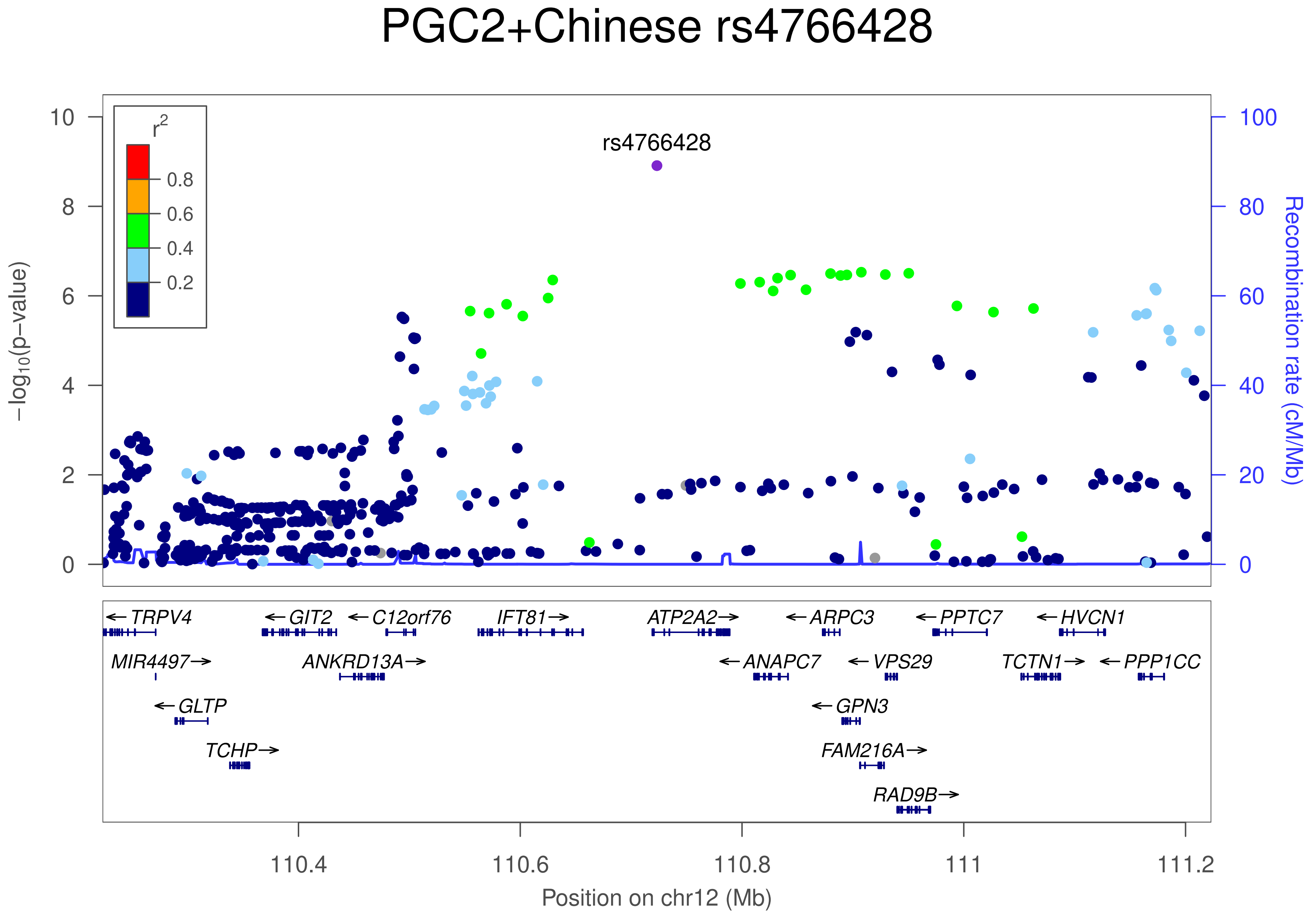

PGC2 rs9420
rs9420
−log10(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
r2
0.2
0.4
0.6
0.8
←TNKS1BP1
RTN4RL2→
SERPING1→
TMX2→
OR9Q1→
←SSRP1
←SLC43A1
MIR130A→
←BTBD18
OR6Q1→
OR9Q2→
P2RX3→
←TIMM10
←YPEL4
CTNND1→
←OR9I1
←PRG3
SMTNL1→
CLP1→
←OR1S2
←PRG2
←UBE2L6
ZDHHC5→
OR1S1→
←SLC43A3
←MED19
←OR10Q1
TMX2−CTNND1→
SELENOH→
57.2
57.4
57.6
57.8
58
Position on chr11 (Mb)


PGC2+Chinese rs9420
r2
0.8
0.6
0.4
0.2
rs9420
−log10(p−value)
10
8
6
4
2
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
←TNKS1BP1
RTN4RL2→
SERPING1→
TMX2→
OR9Q1→
←SSRP1
←SLC43A1
MIR130A→
←BTBD18
OR6Q1→
OR9Q2→
P2RX3→
←TIMM10
←YPEL4
CTNND1→
←OR9I1
←PRG3
SMTNL1→
CLP1→
←OR1S2
←PRG2
←UBE2L6
ZDHHC5→
OR1S1→
←SLC43A3
←MED19
←OR10Q1
TMX2−CTNND1→
SELENOH→
57.2
57.4
57.6
57.8
58
Position on chr11 (Mb)

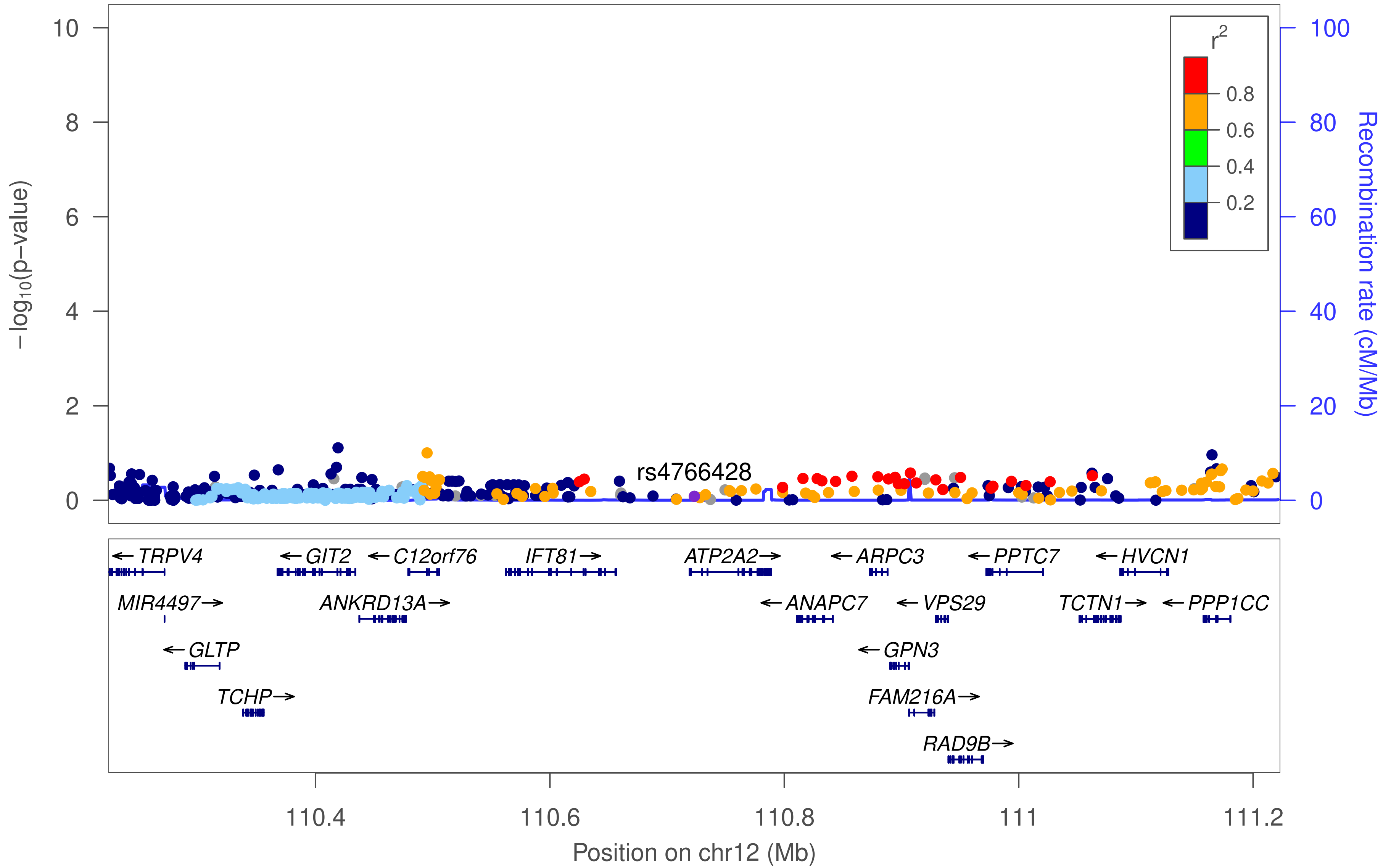

Chinese–only rs9420

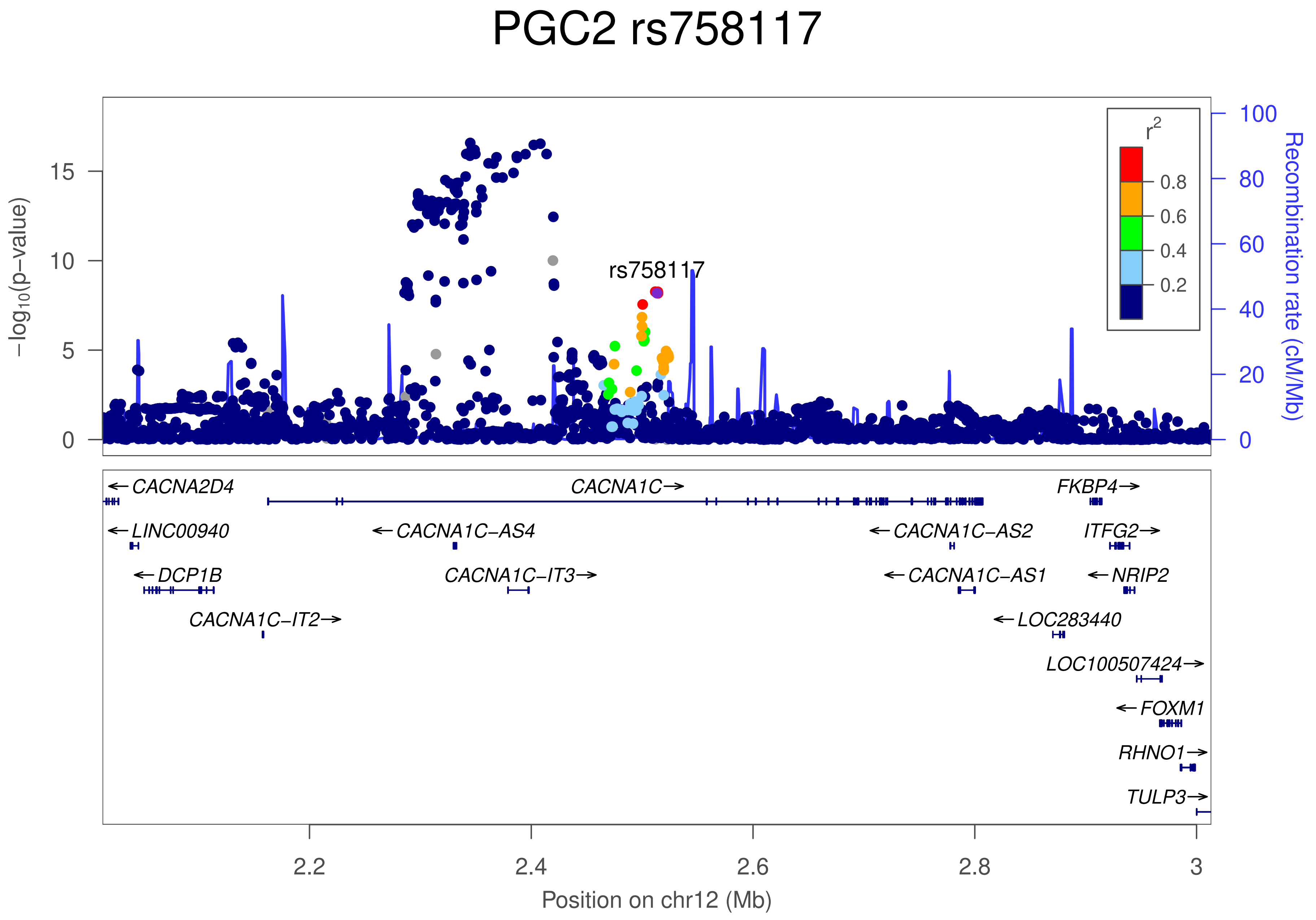
PGC2 rs4766428



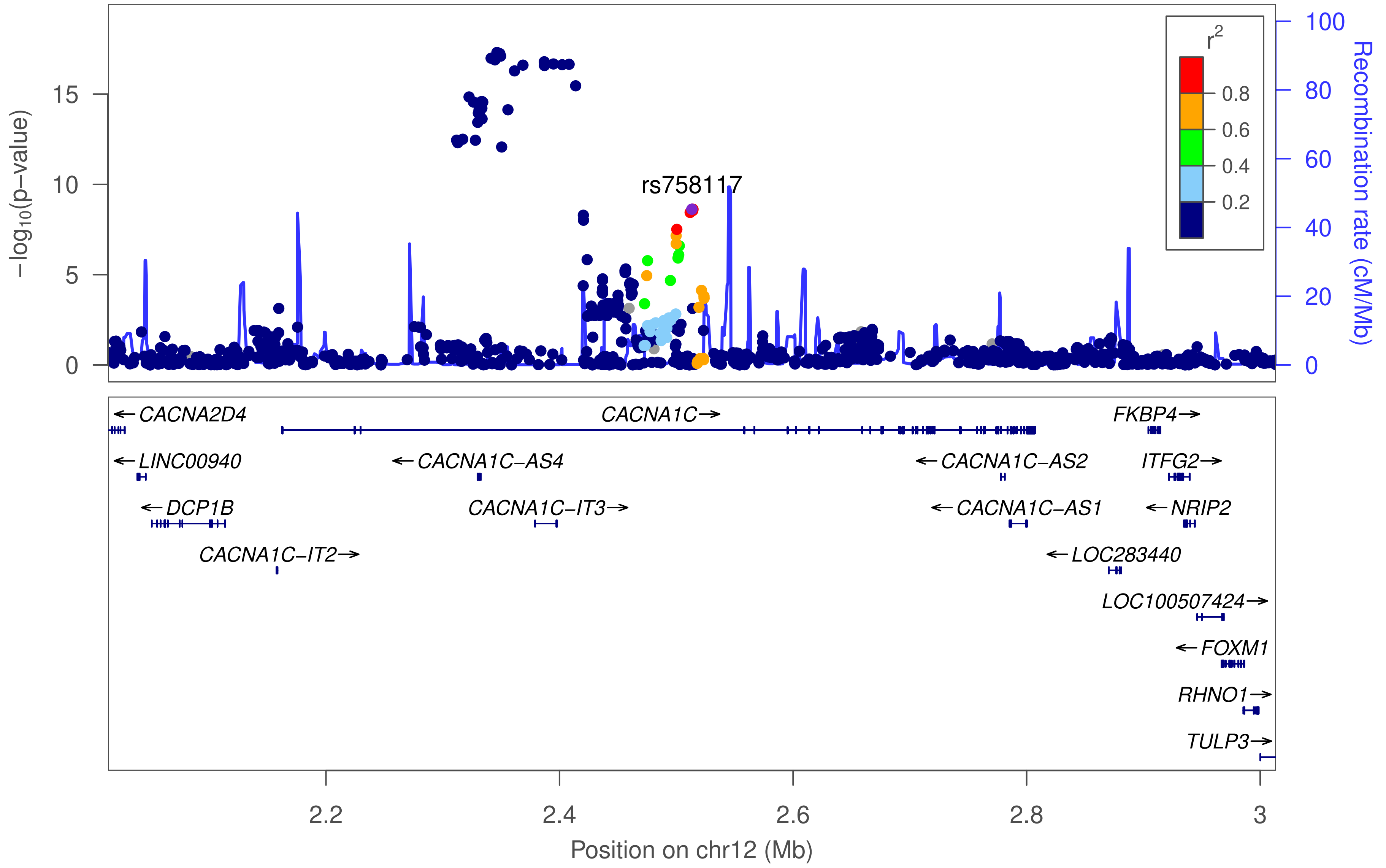

PGC2+Chinese rs4766428
rs4766428
r2
0.8
0.6
0.4
0.2
−log10(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
TRPV4
GIT2
C12orf76
IFT81
ATP2A2
ARPC3
PPTC7
HVCN1
MIR4497
ANKRD13A
ANAPC7
VPS29
TCTN1
PPP1CC
GLTP
GPN3
TCHP
FAM216A
RAD9B
110.4
110.6
110.8
111
111.2
Position on chr12 (Mb)

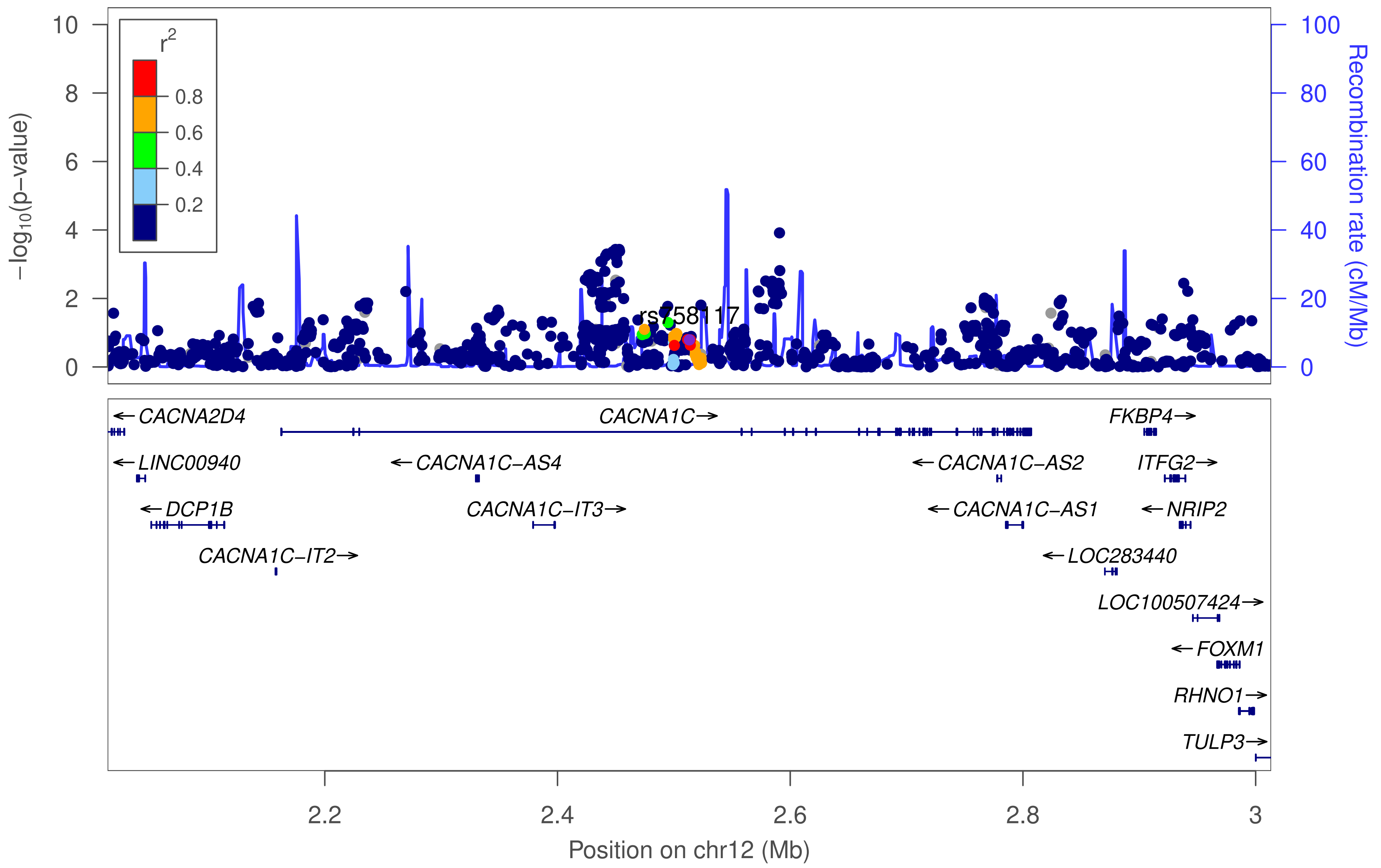
Chinese–only rs4766428



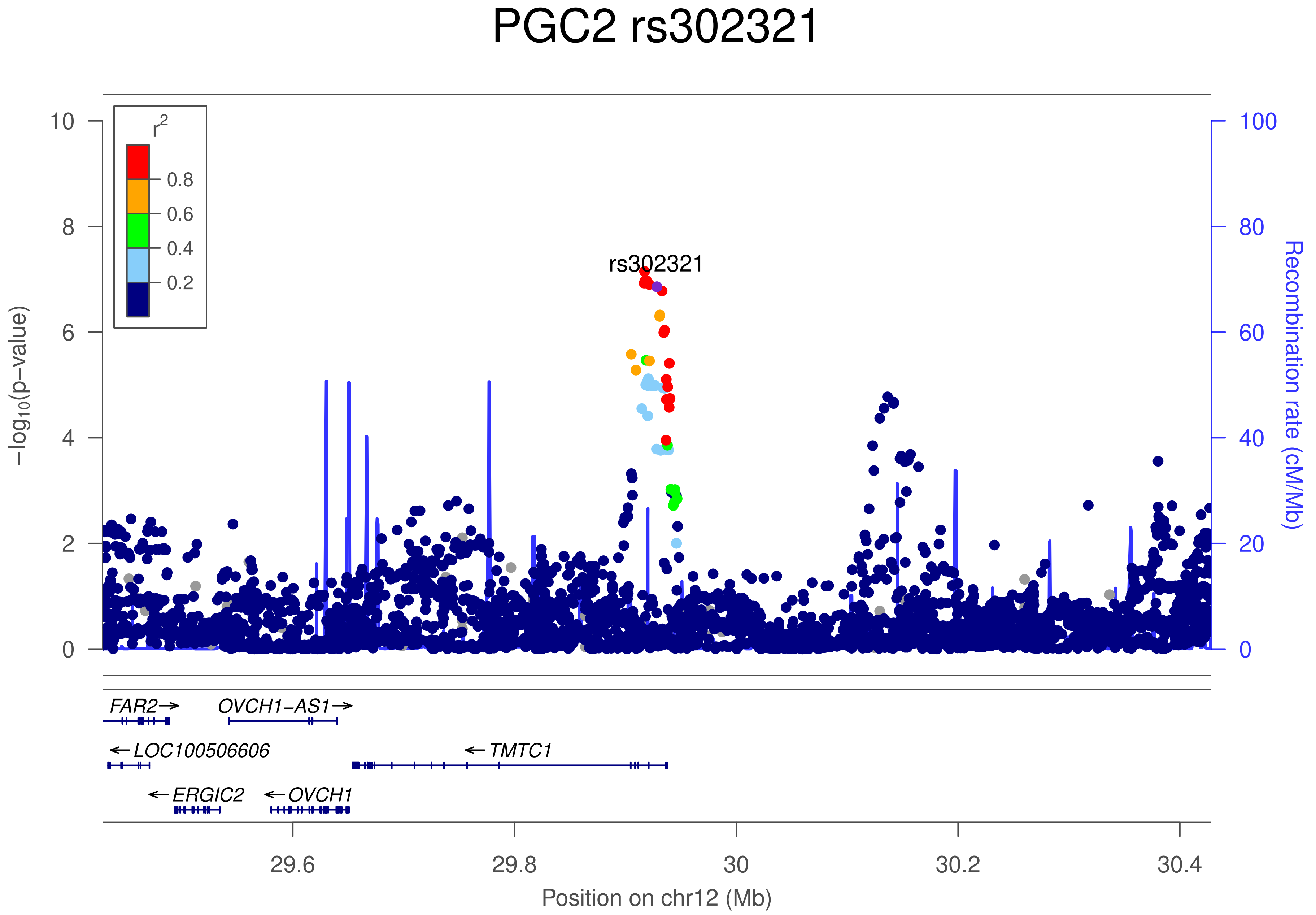

PGC2 rs758117
−log10(p−value)
0
5
10
15
rs758117
r2
0.8
0.6
0.4
0.2
100
80
60
40
20
0
Recombination rate (cM/Mb)
← CACNA2D4
CACNA1C→
FKBP4→
← LINC00940
← CACNA1C−AS4
← CACNA1C−AS2
ITFG2→
← DCP1B
CACNA1C−IT3→
← CACNA1C−AS1
← NRIP2
CACNA1C−IT2→
← LOC283440
LOC100507424→
← FOXM1
RHNO1→
TULP3→
2.2
2.4
2.6
2.8
3
Position on chr12 (Mb)

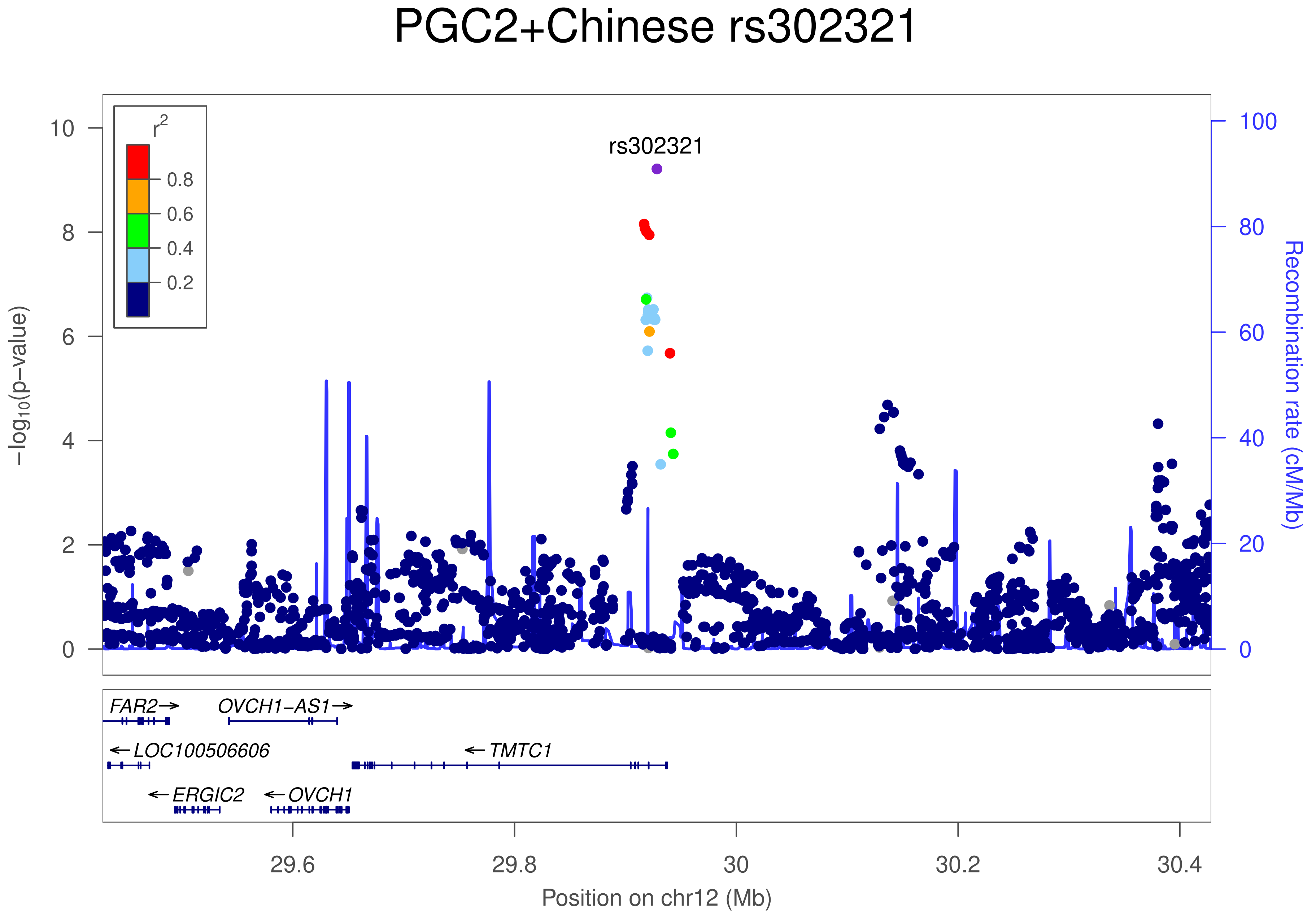
PGC2+Chinese rs758117

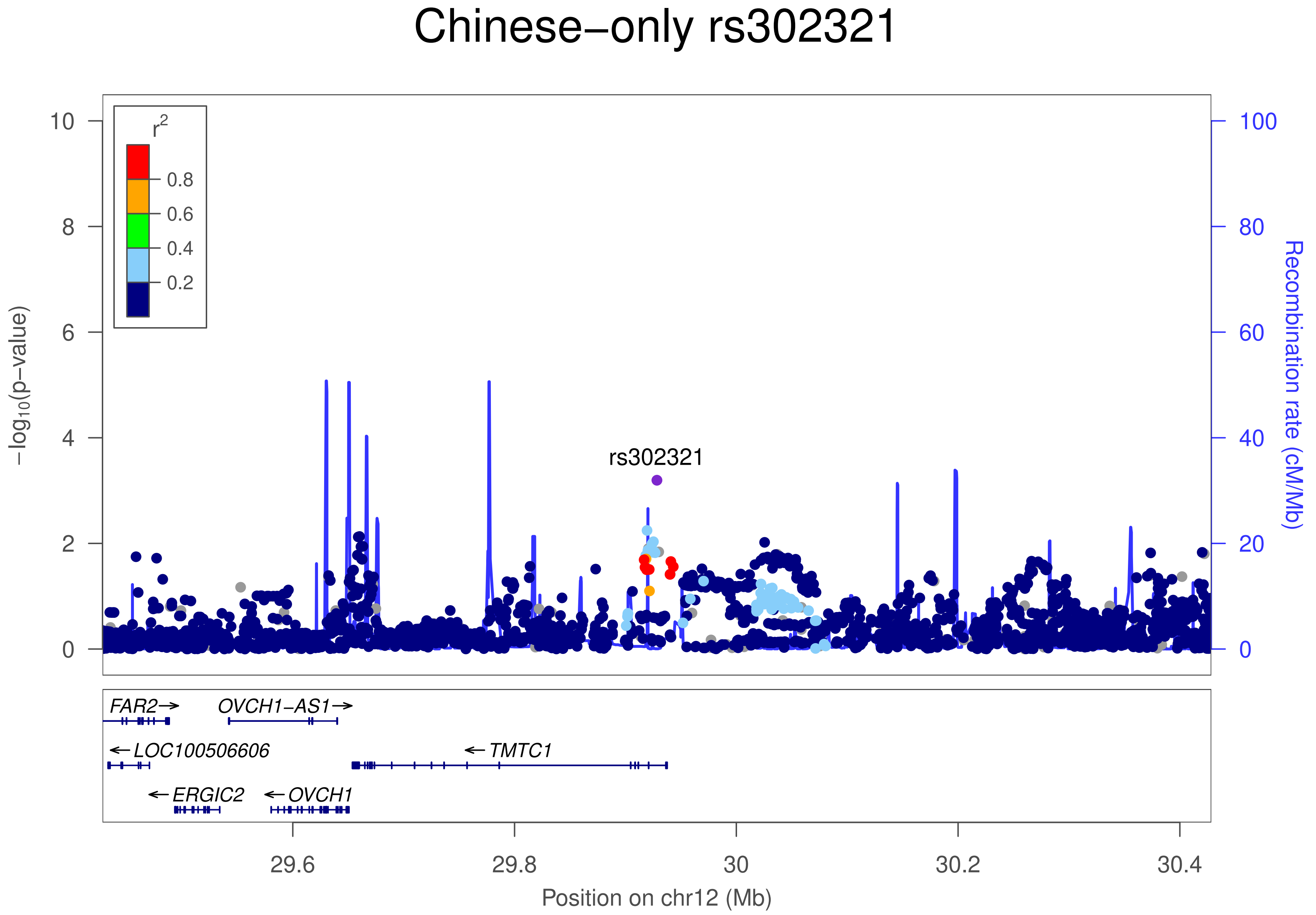


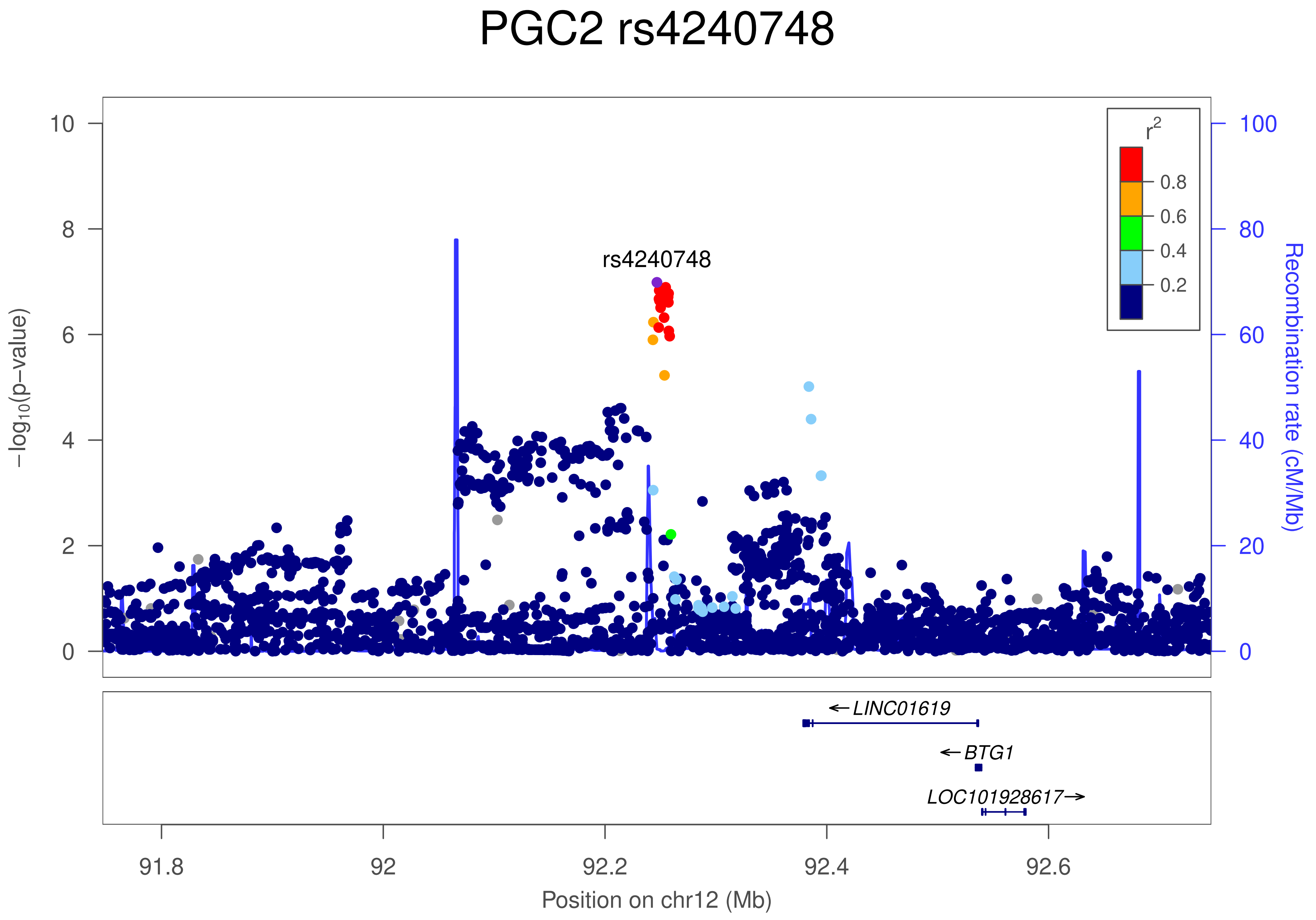


Chinese–only rs758117

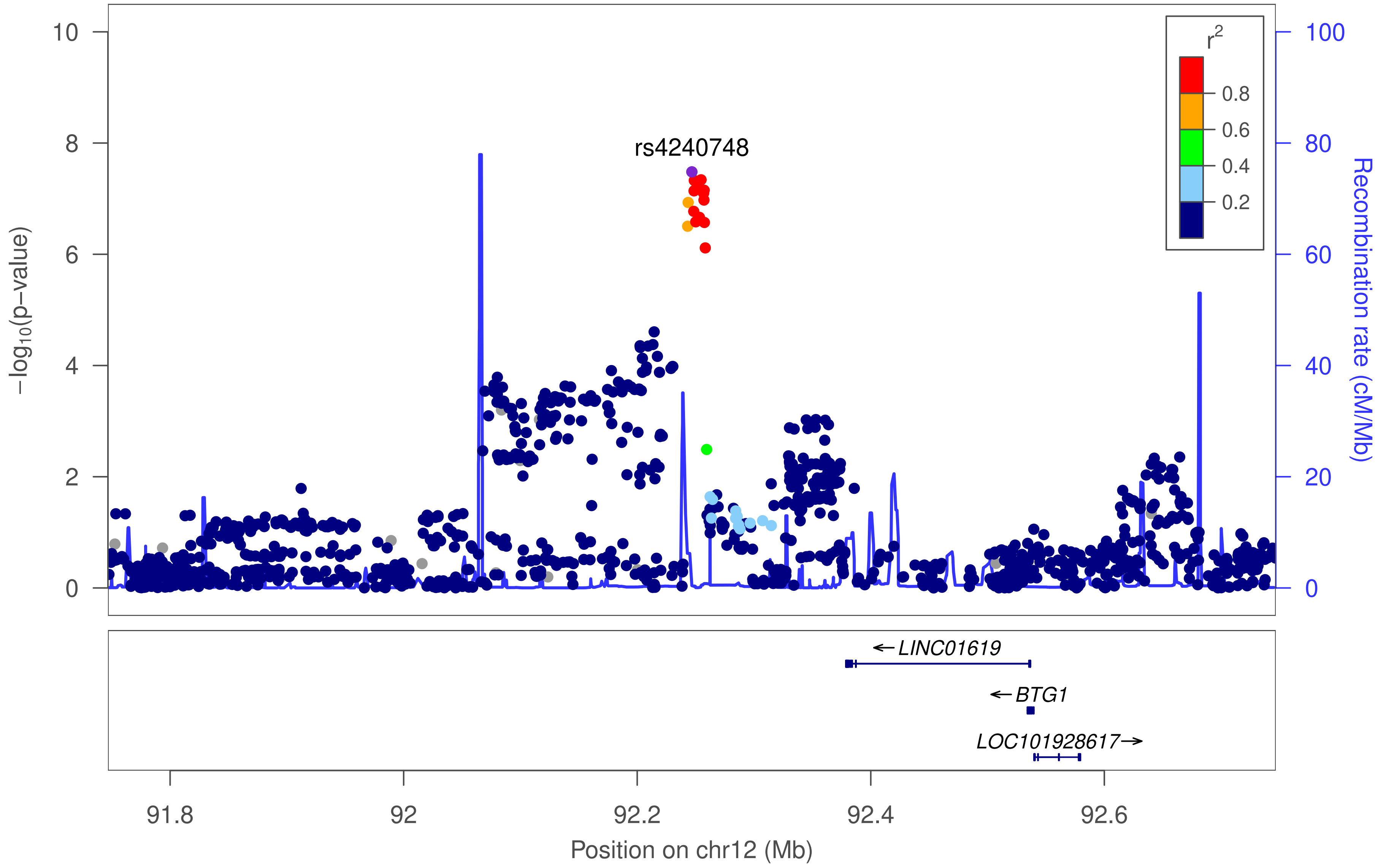

PGC2 rs302321
rs302321
r^2
0.8
0.6
0.4
0.2
10
8
6
4
2
0
$-\log_{10}$(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
FAR2→
OVCH1−AS1→
←LOC100506606
←TMTC1
←ERGIC2
←OVCH1
29.6
29.8
30
30.2
30.4
Position on chr12 (Mb)


PGC2+Chinese rs302321
r2
0.8
0.6
0.4
0.2
rs302321
−log10(p−value)
10
8
6
4
2
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
FAR2→
OVCH1−AS1→
←LOC100506606
←TMTC1
←ERGIC2
←OVCH1
29.6
29.8
30
30.2
30.4
Position on chr12 (Mb)

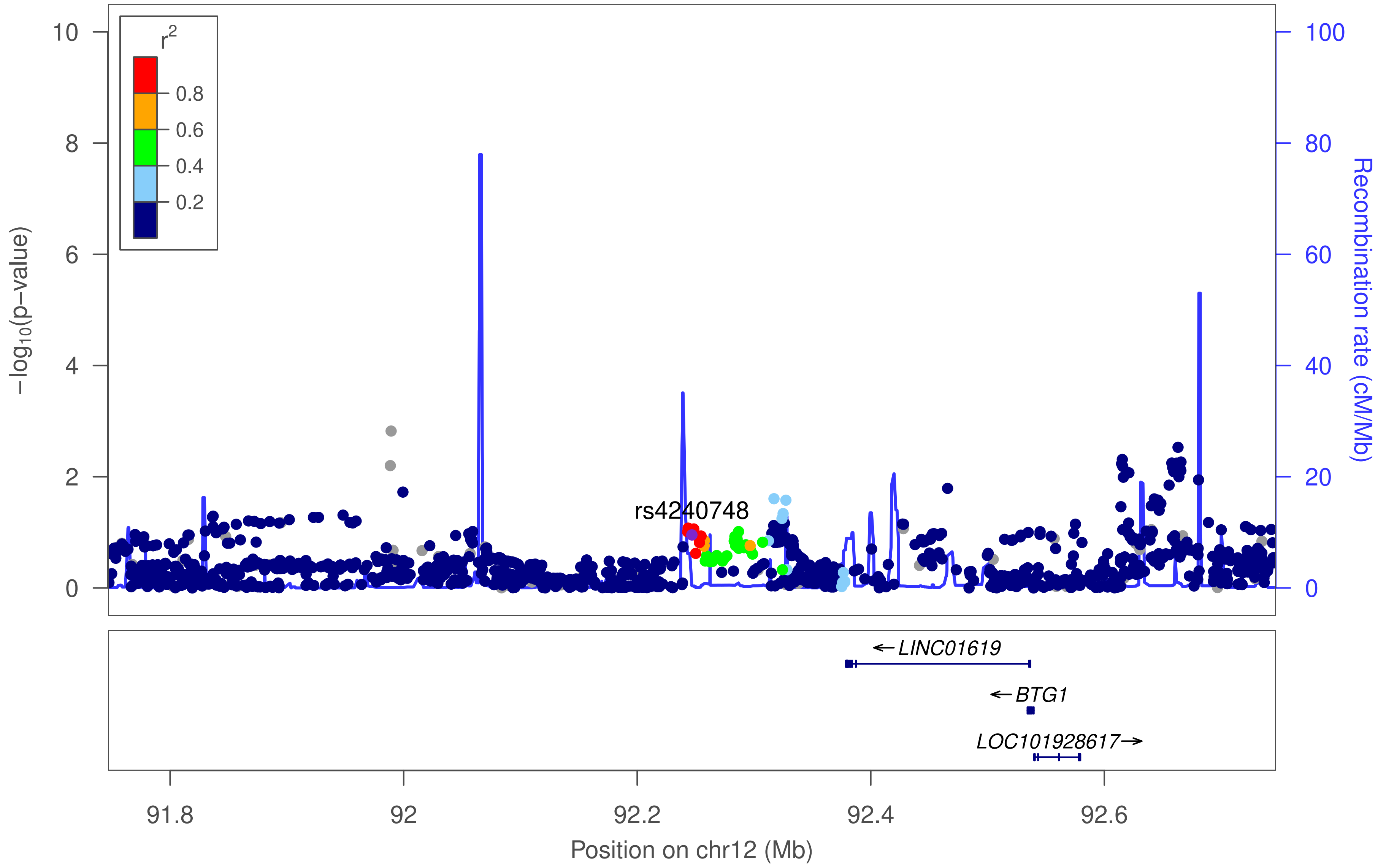

Chinese−only rs302321
r2
0.8
0.6
0.4
0.2
rs302321
−log10(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
FAR2→
OVCH1−AS1→
←LOC100506606
←TMTC1
←ERGIC2
←OVCH1
29.6
29.8
30
30.2
30.4
Position on chr12 (Mb)


PGC2 rs4240748
rs4240748
r^2
0.8
0.6
0.4
0.2
−log10(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
LINC01619
BTG1
LOC101928617
91.8
92
92.2
92.4
92.6
Position on chr12 (Mb)

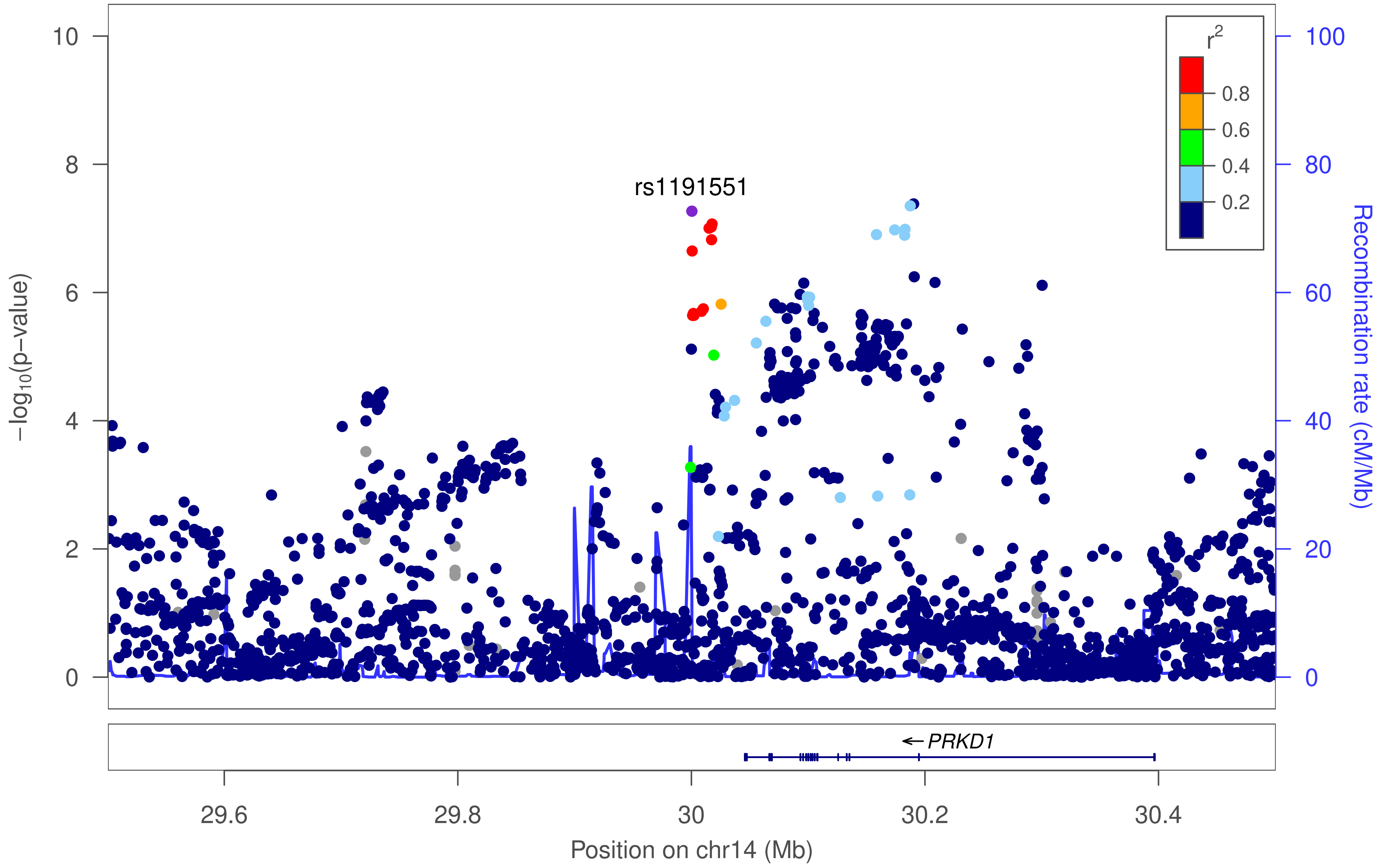
PGC2+Chinese rs4240748

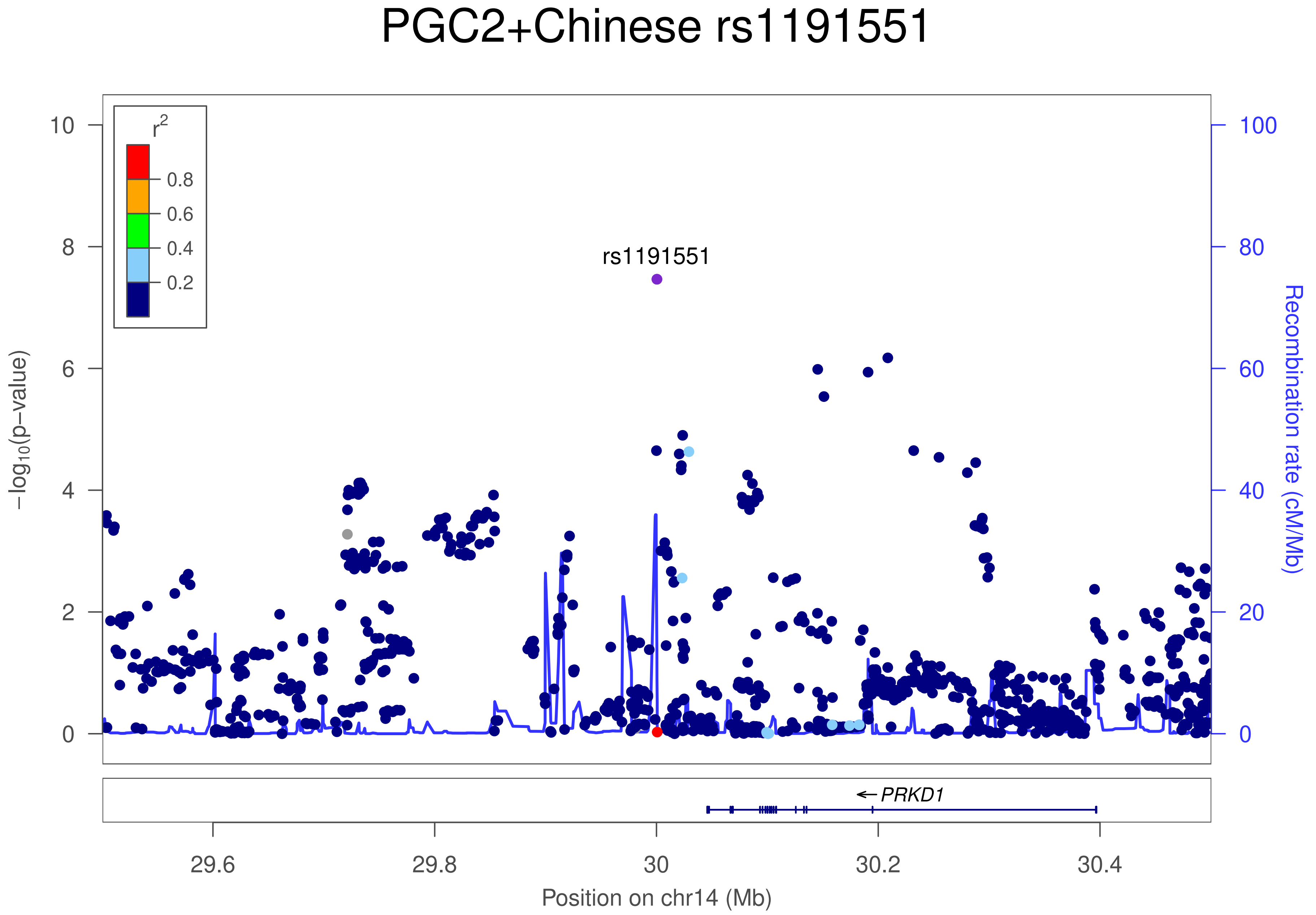


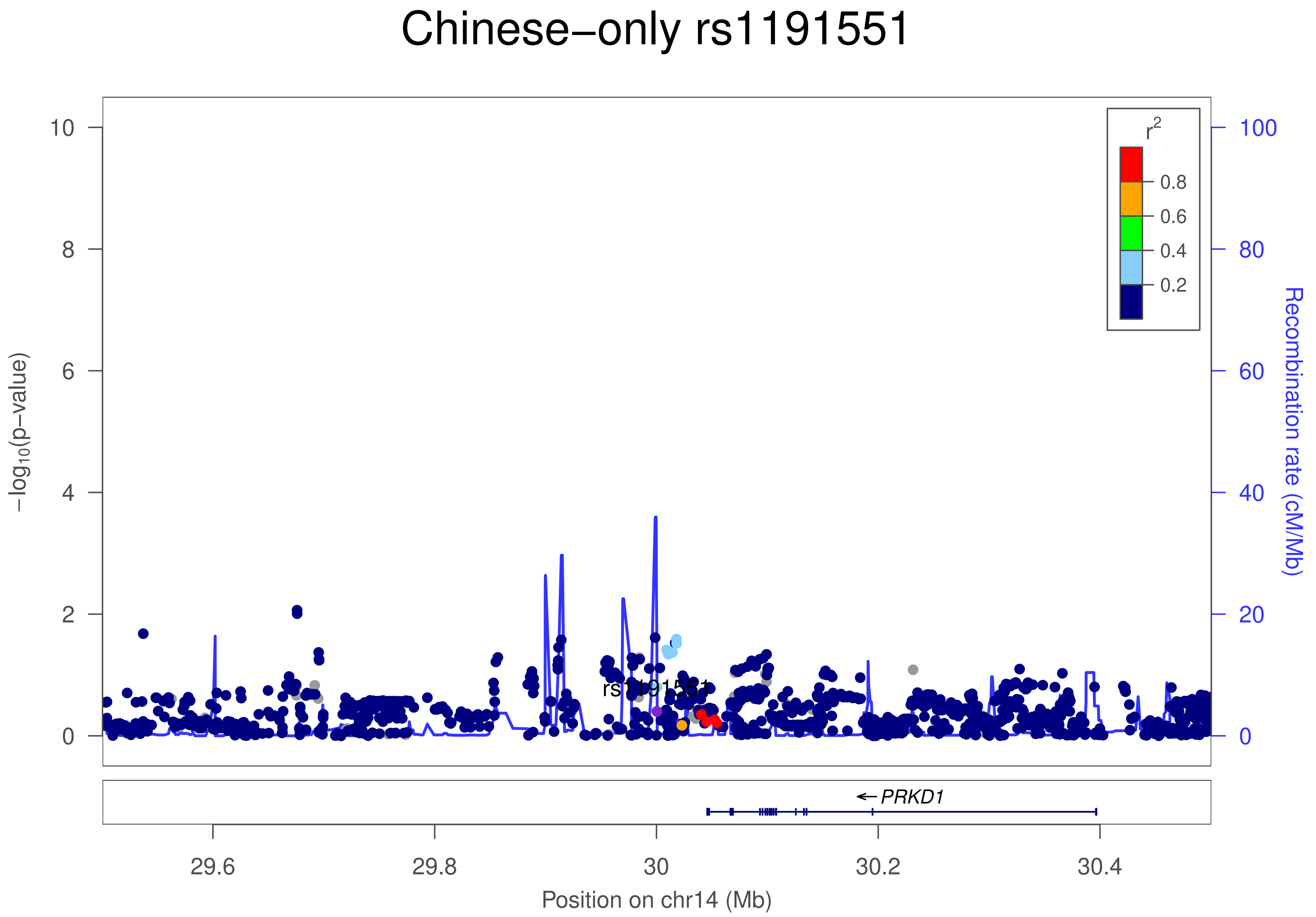
Chinese−only rs4240748

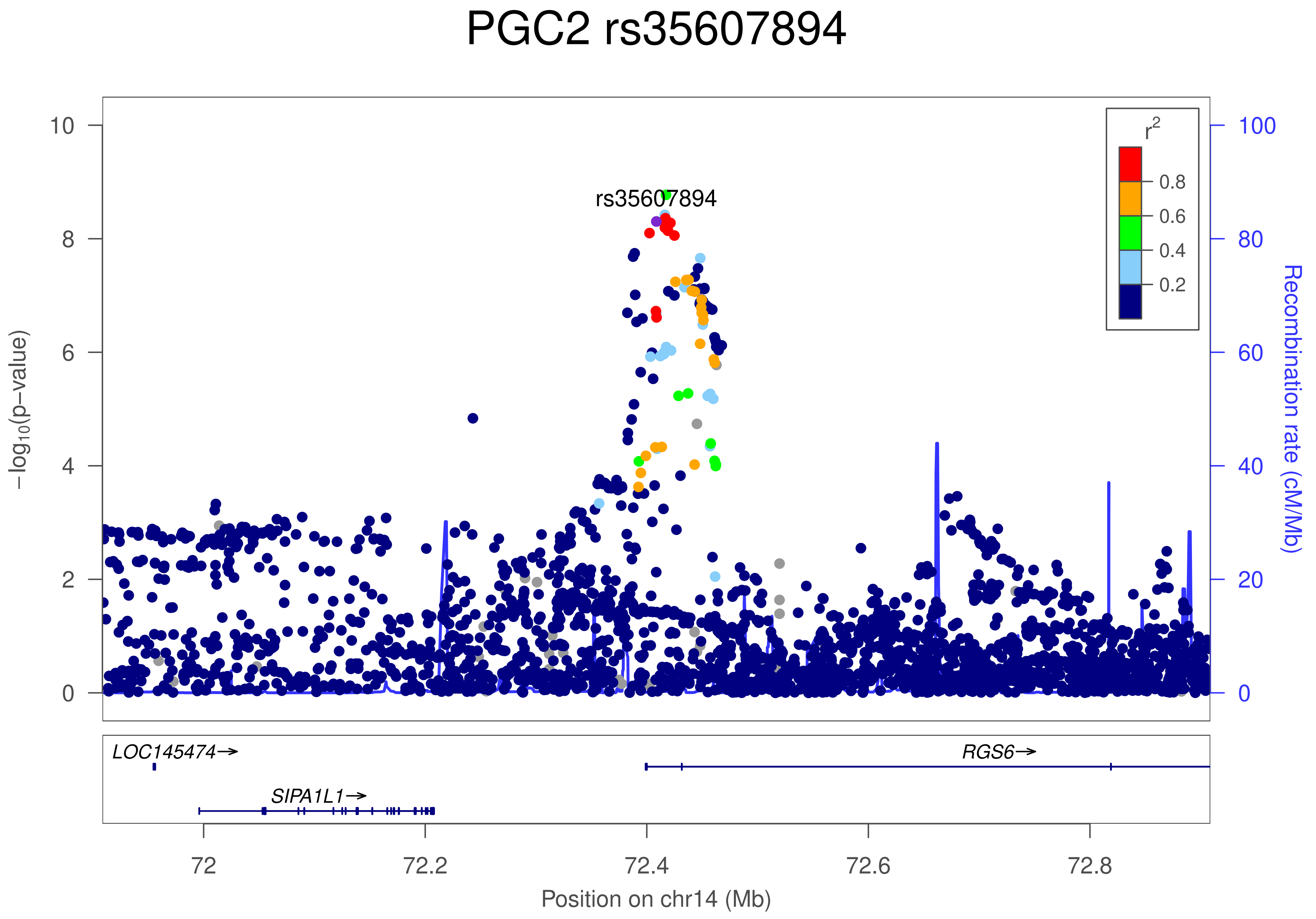


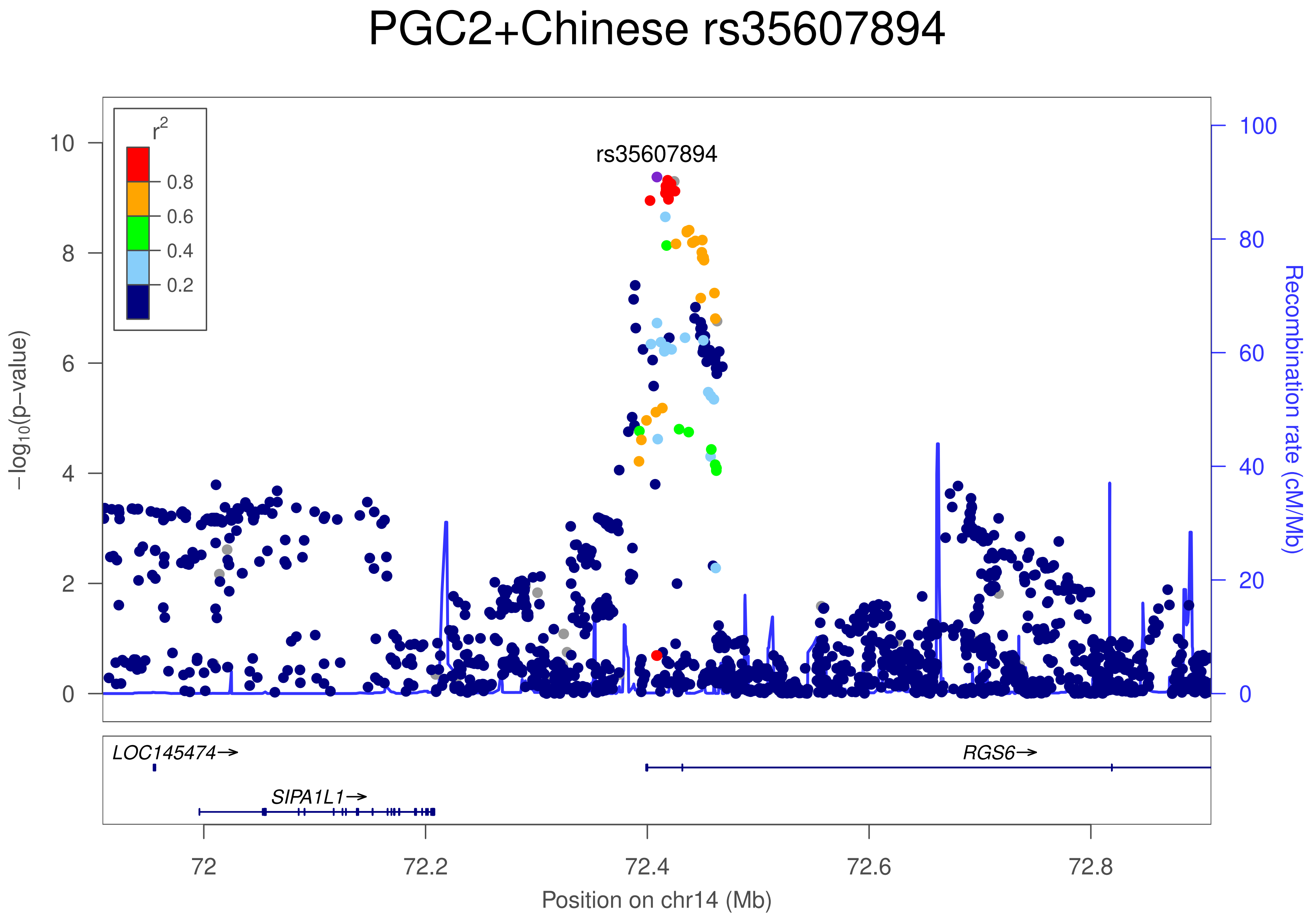
PGC2 rs1191551

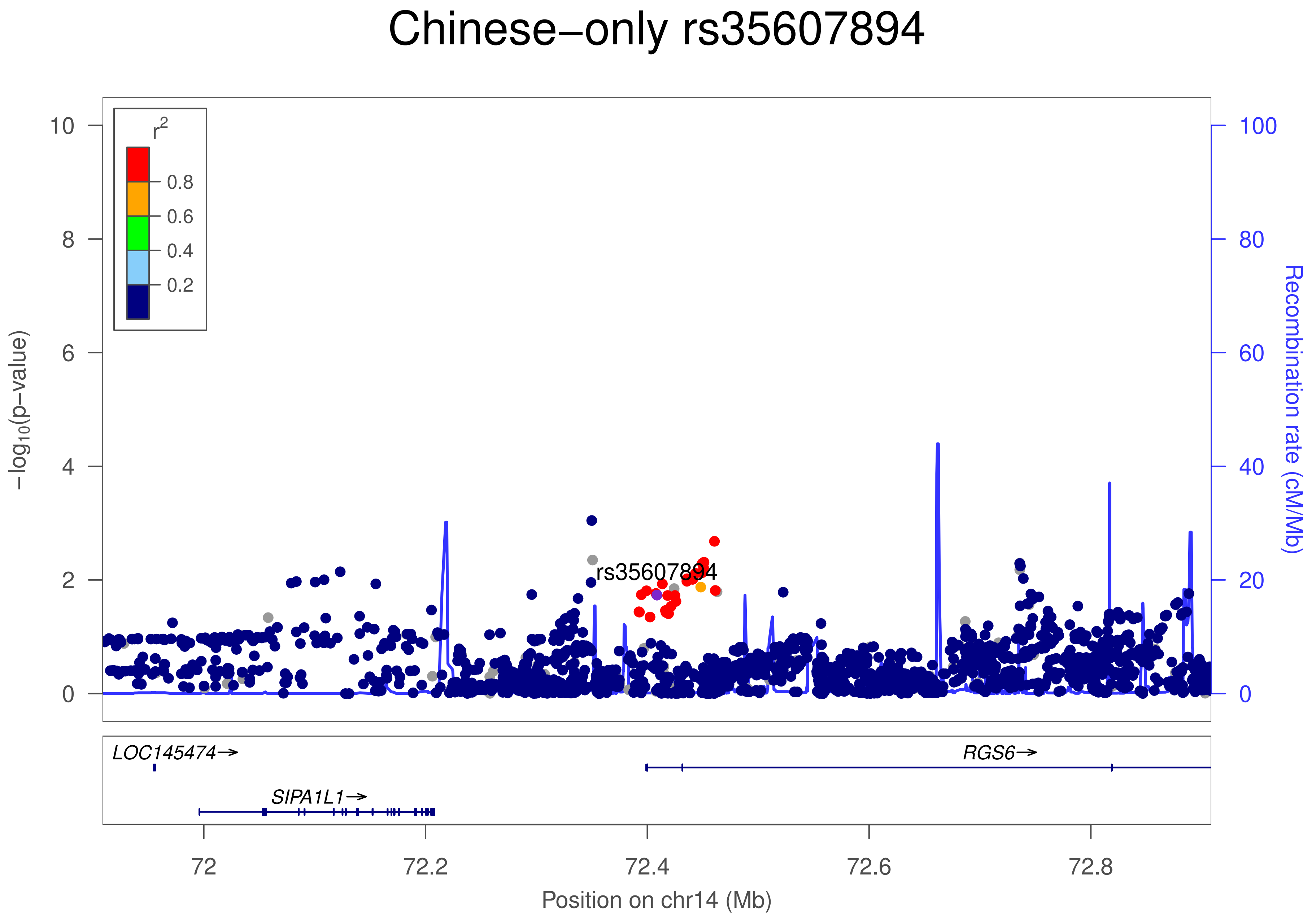



PGC2+Chinese rs1191551
r²
0.8
0.6
0.4
0.2
rs1191551
−log₁₀(p−value)
10
8
6
4
2
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
← PRKD1
29.6
29.8
30
30.2
30.4
Position on chr14 (Mb)

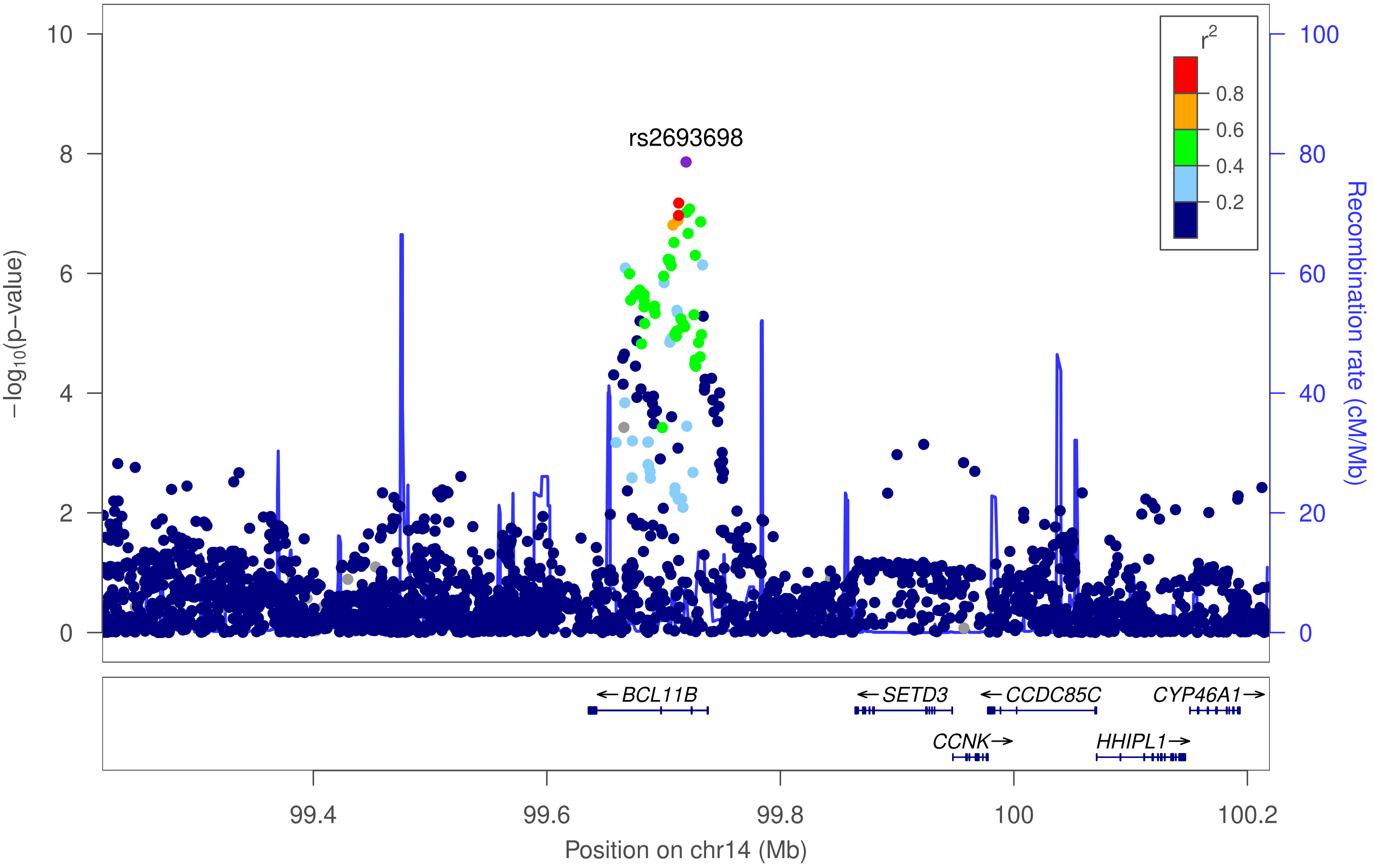

Chinese–only rs1191551
r²
0.8
0.6
0.4
0.2
−log₁₀(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
rs1191551
← PRKD1
29.6
29.8
30
30.2
30.4
Position on chr14 (Mb)


PGC2 rs35607894
rs35607894
r²
0.8
0.6
0.4
0.2
−log₁₀(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
LOC145474→
SIPA1L1→
RGS6→
72
72.2
72.4
72.6
72.8
Position on chr14 (Mb)

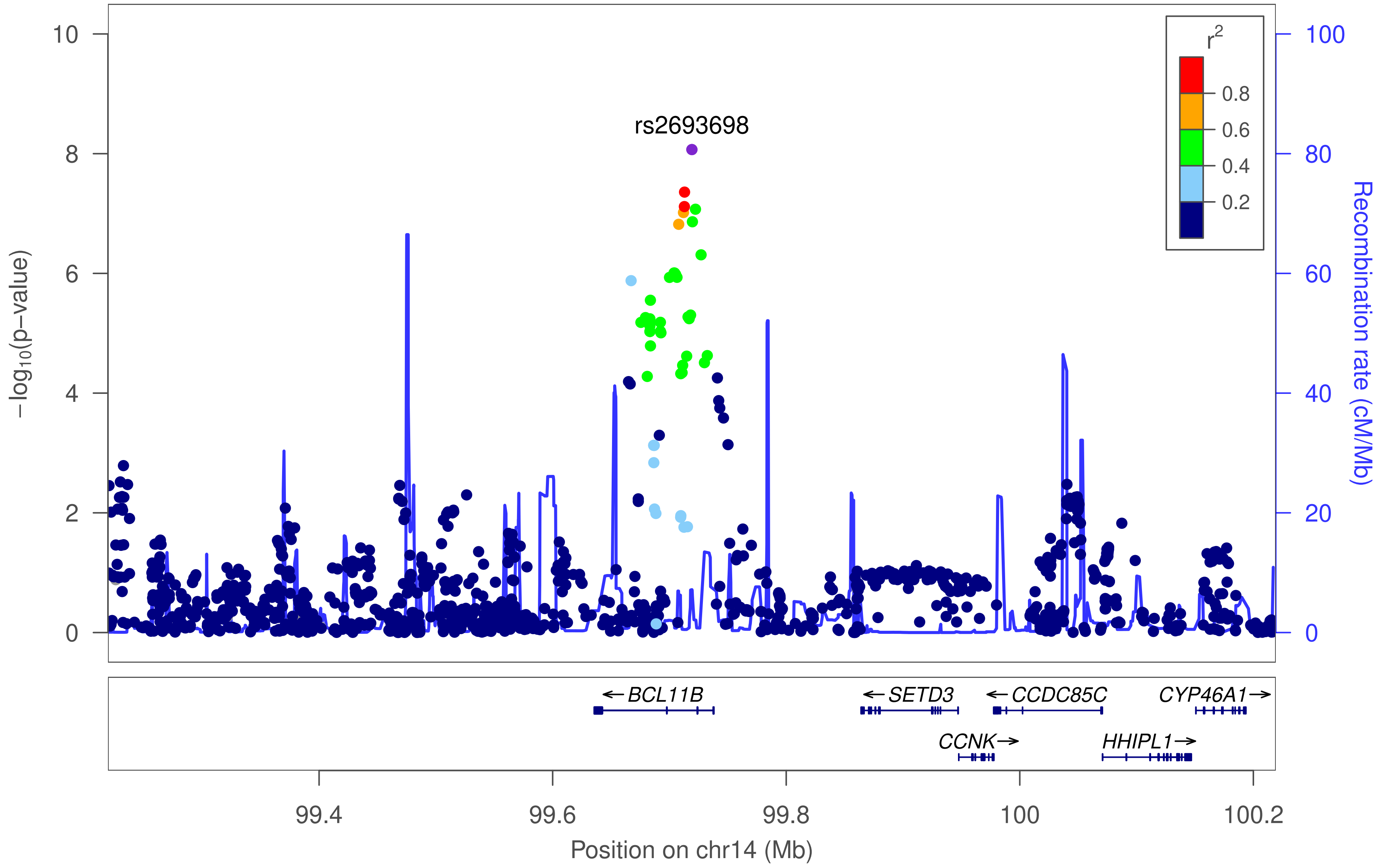

PGC2+Chinese rs35607894
r²
0.8
0.6
0.4
0.2
rs35607894
10
8
6
4
2
0
−log₁₀(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
LOC145474→
RGS6→
SIPA1L1→
72
72.2
72.4
72.6
72.8
Position on chr14 (Mb)


Chinese−only rs35607894
r2
0.8
0.6
0.4
0.2
−log10(p−value)
10
8
6
4
2
0
100
80
60
40
20
0
Recombination rate (cM/Mb)
rs35607894
LOC145474→
RGS6→
SIPA1L1→
72
72.2
72.4
72.6
72.8
Position on chr14 (Mb)

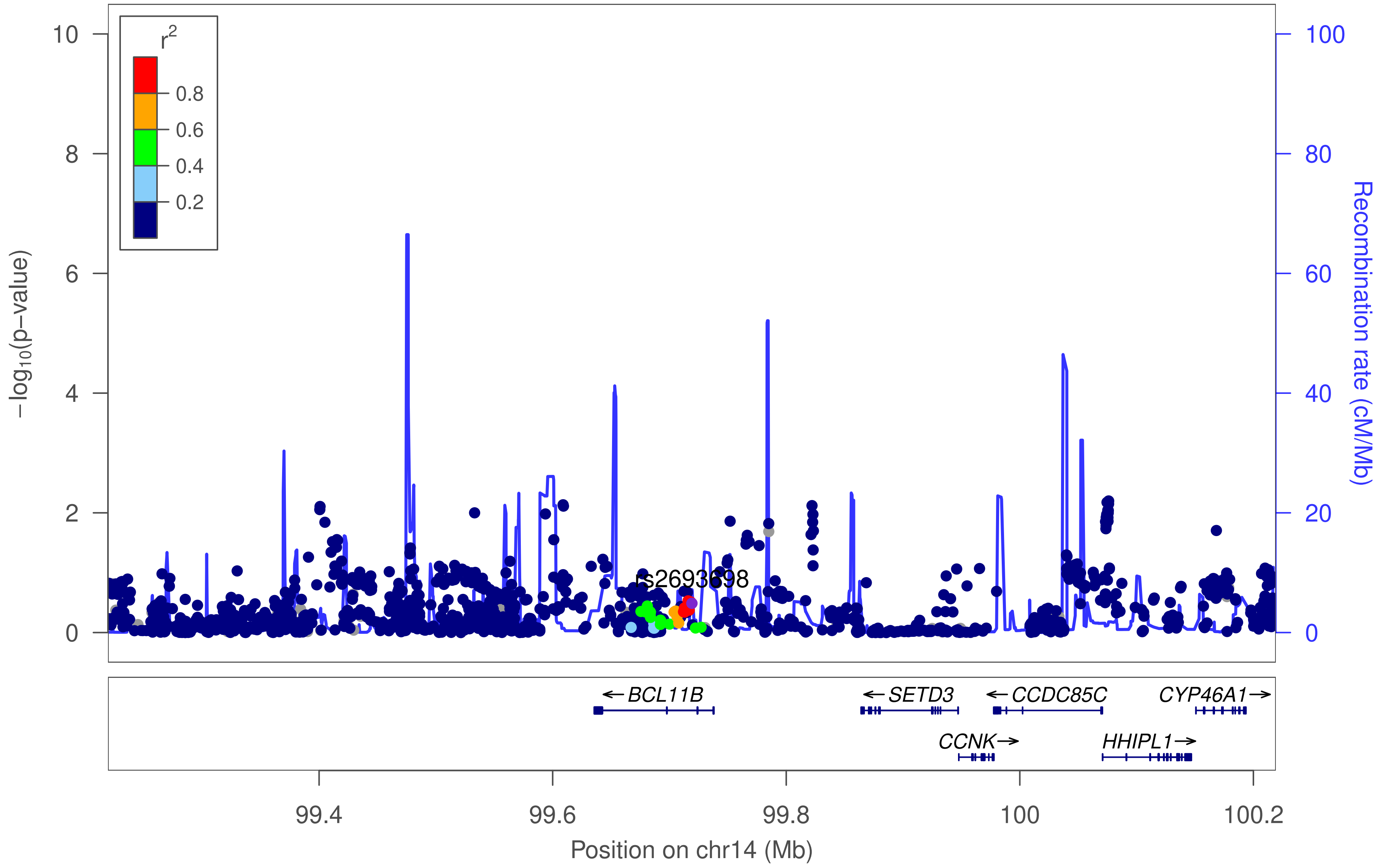
PGC2 rs2693698



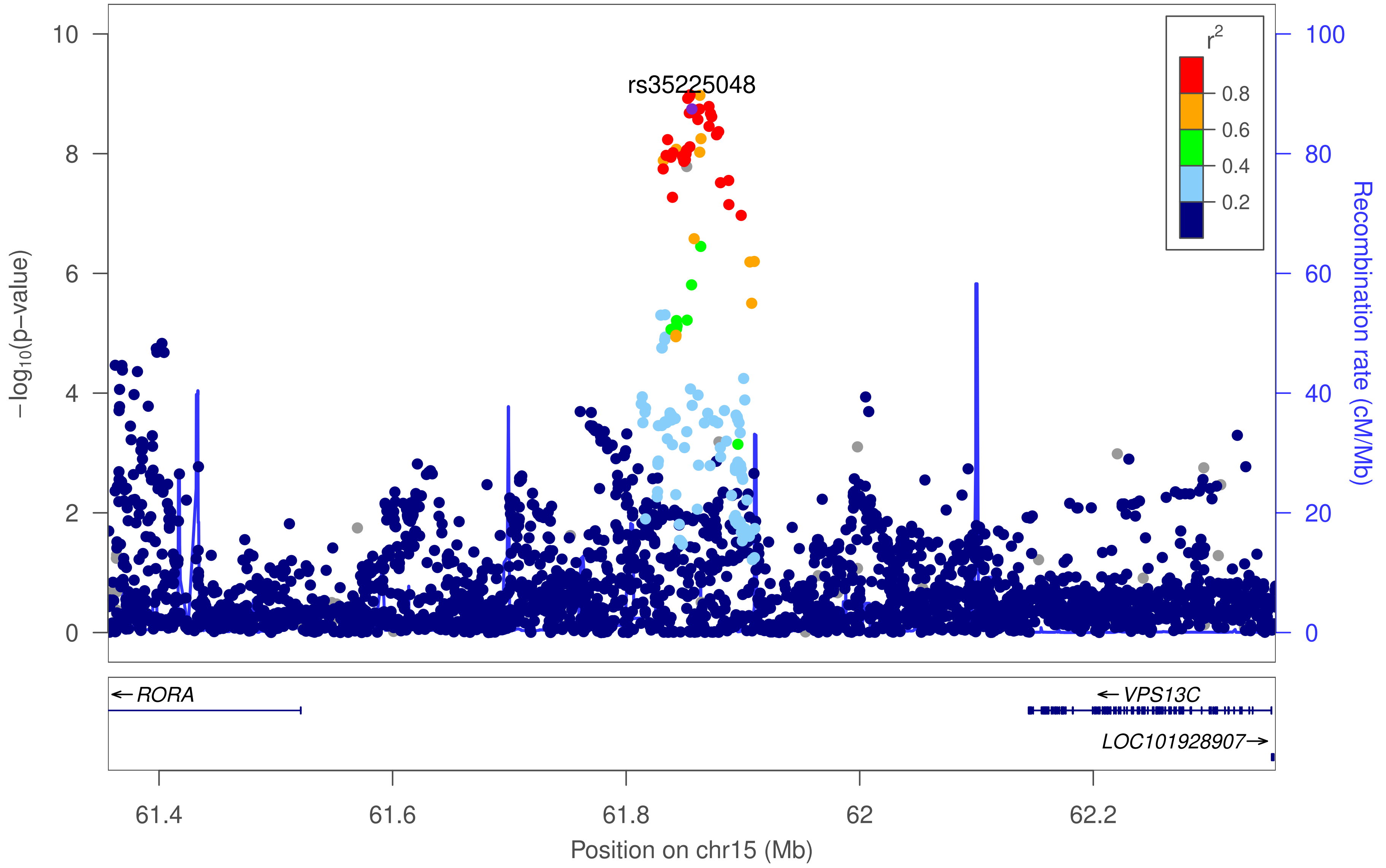
PGC2+Chinese rs2693698

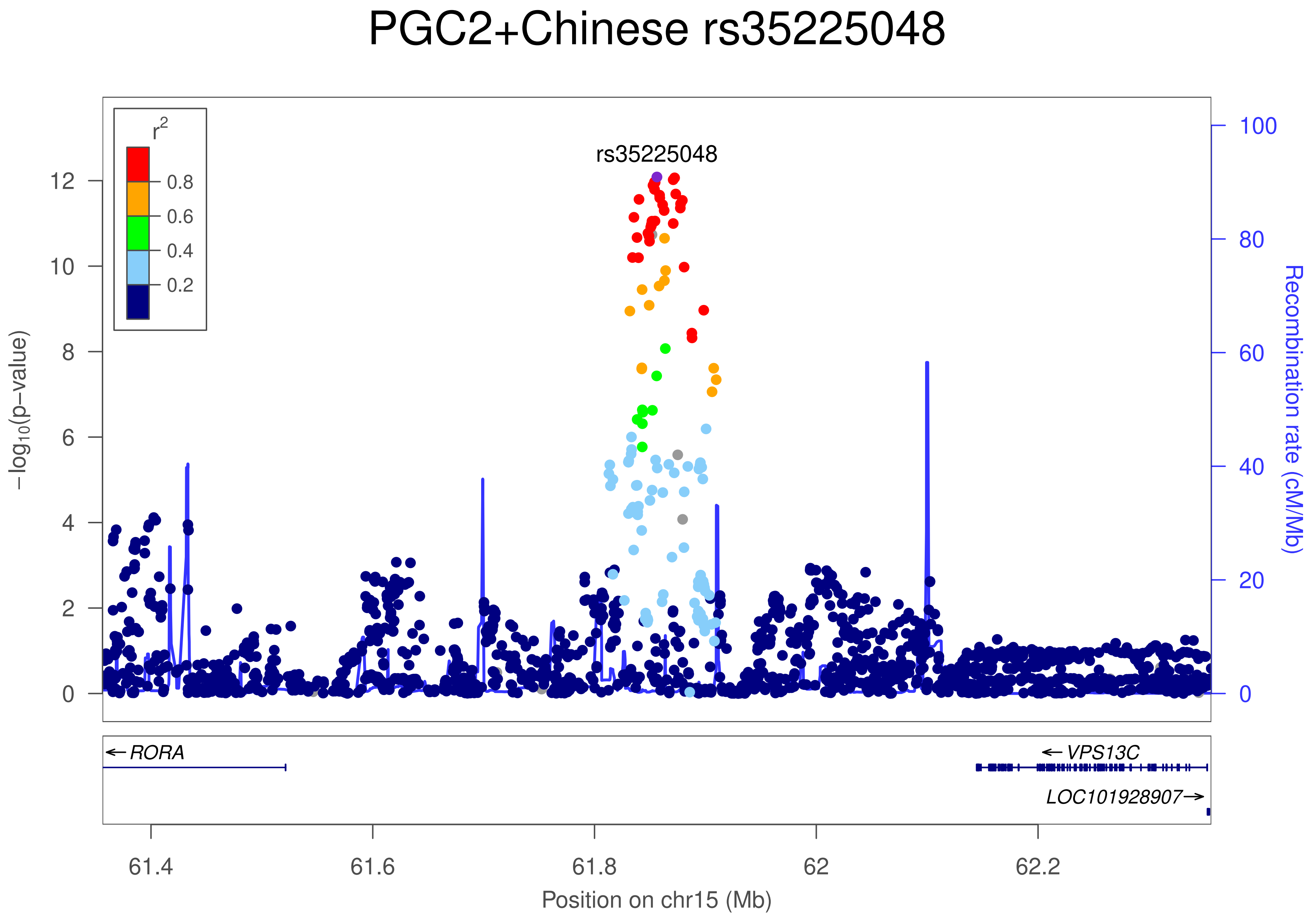


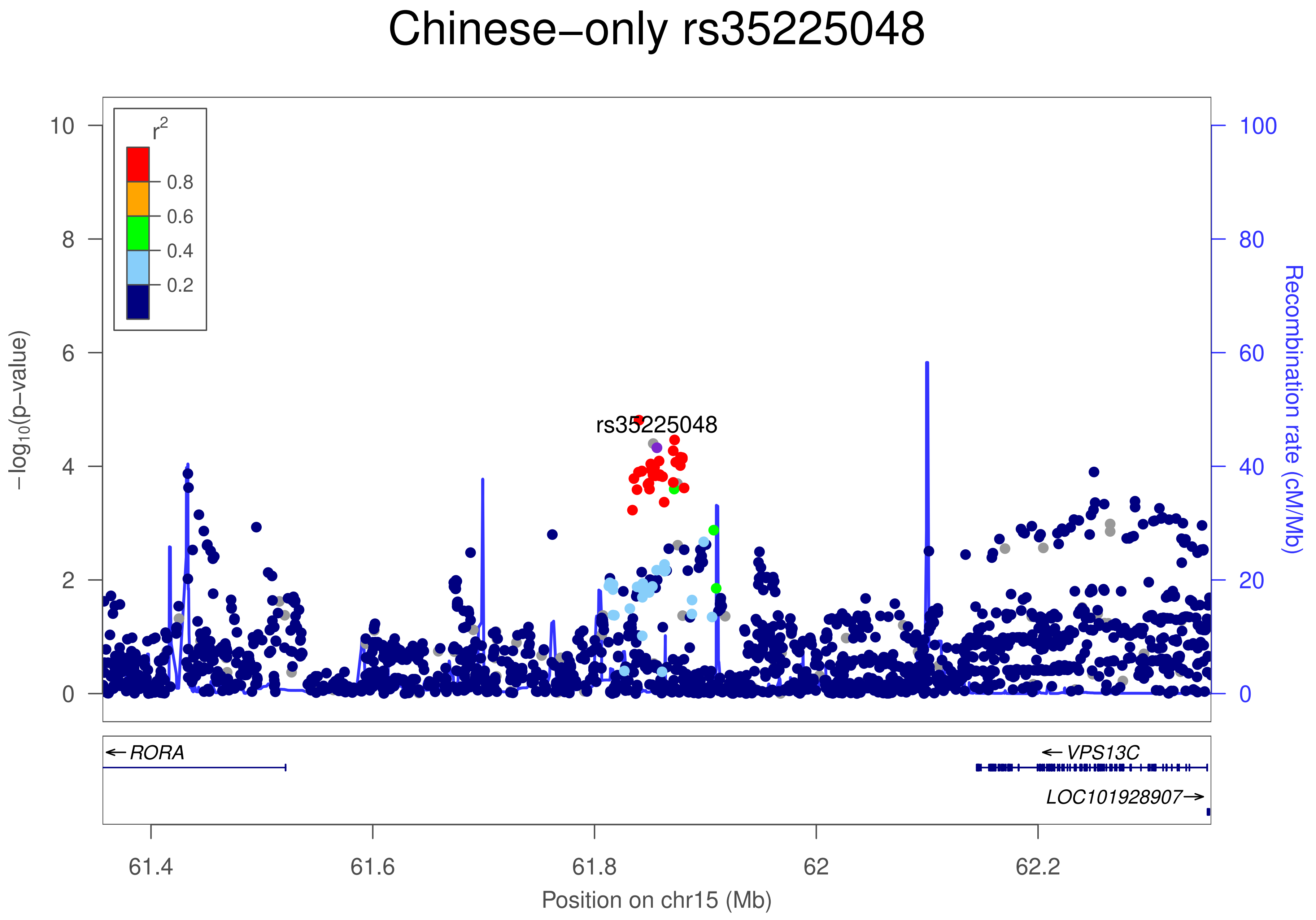
Chinese−only rs2693698



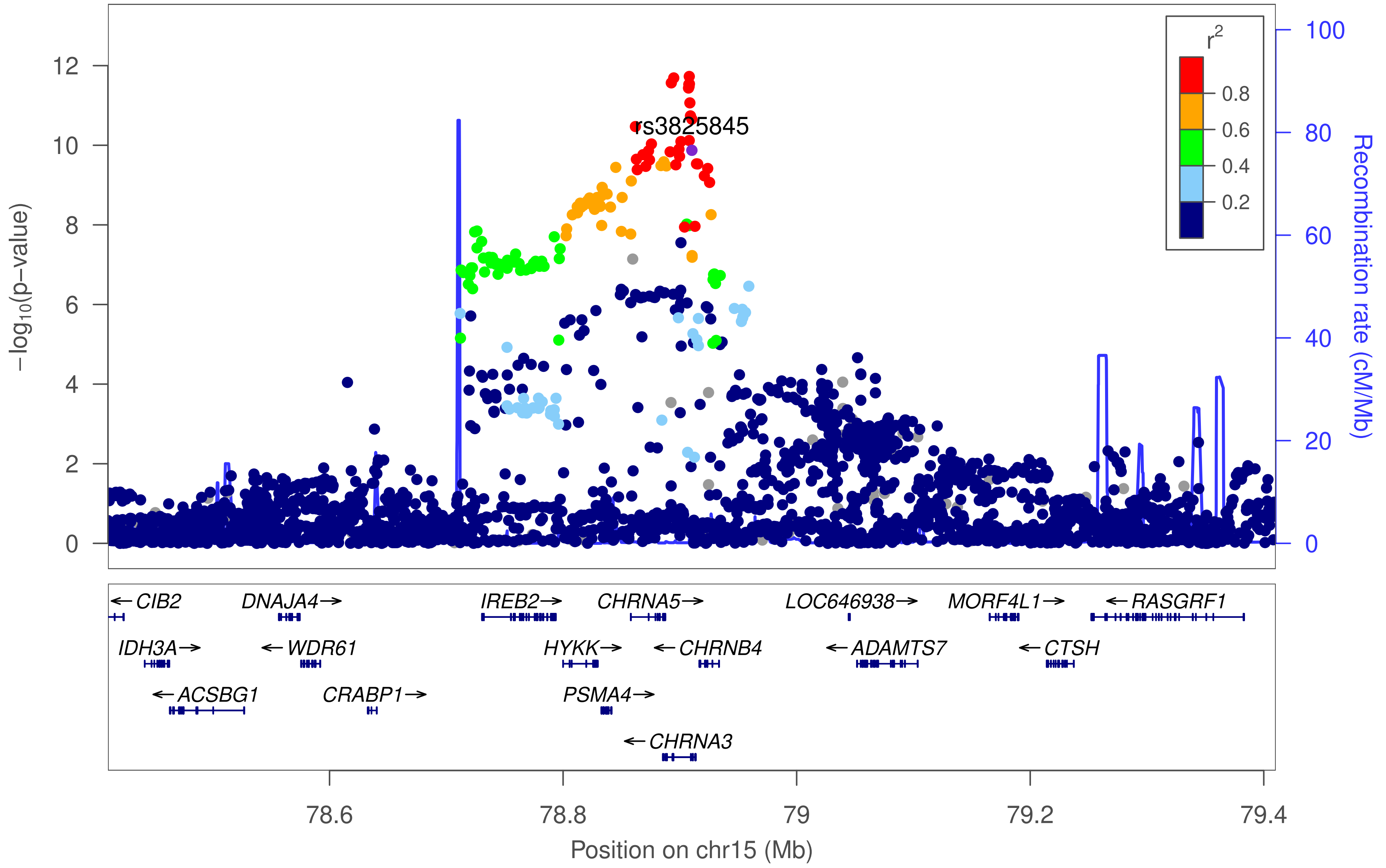
PGC2 rs35225048

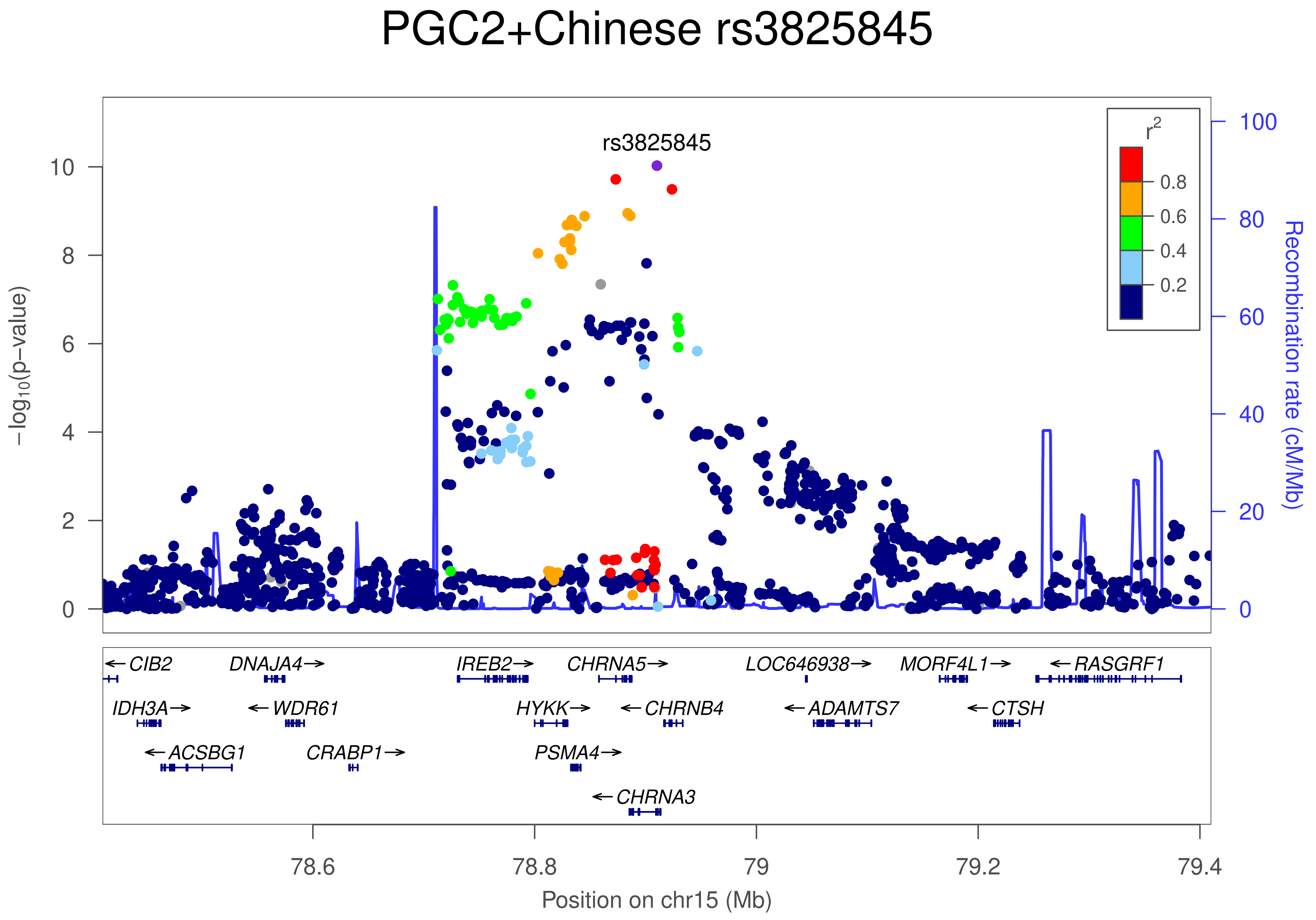



PGC2+Chinese rs35225048
rs35225048
r²
0.8
0.6
0.4
0.2
−log10(p−value)
0
2
4
6
8
10
12
Recombination rate (cM/Mb)
0
20
40
60
80
100
← RORA
← VPS13C
LOC101928907→
61.4
61.6
61.8
62
62.2
Position on chr15 (Mb)

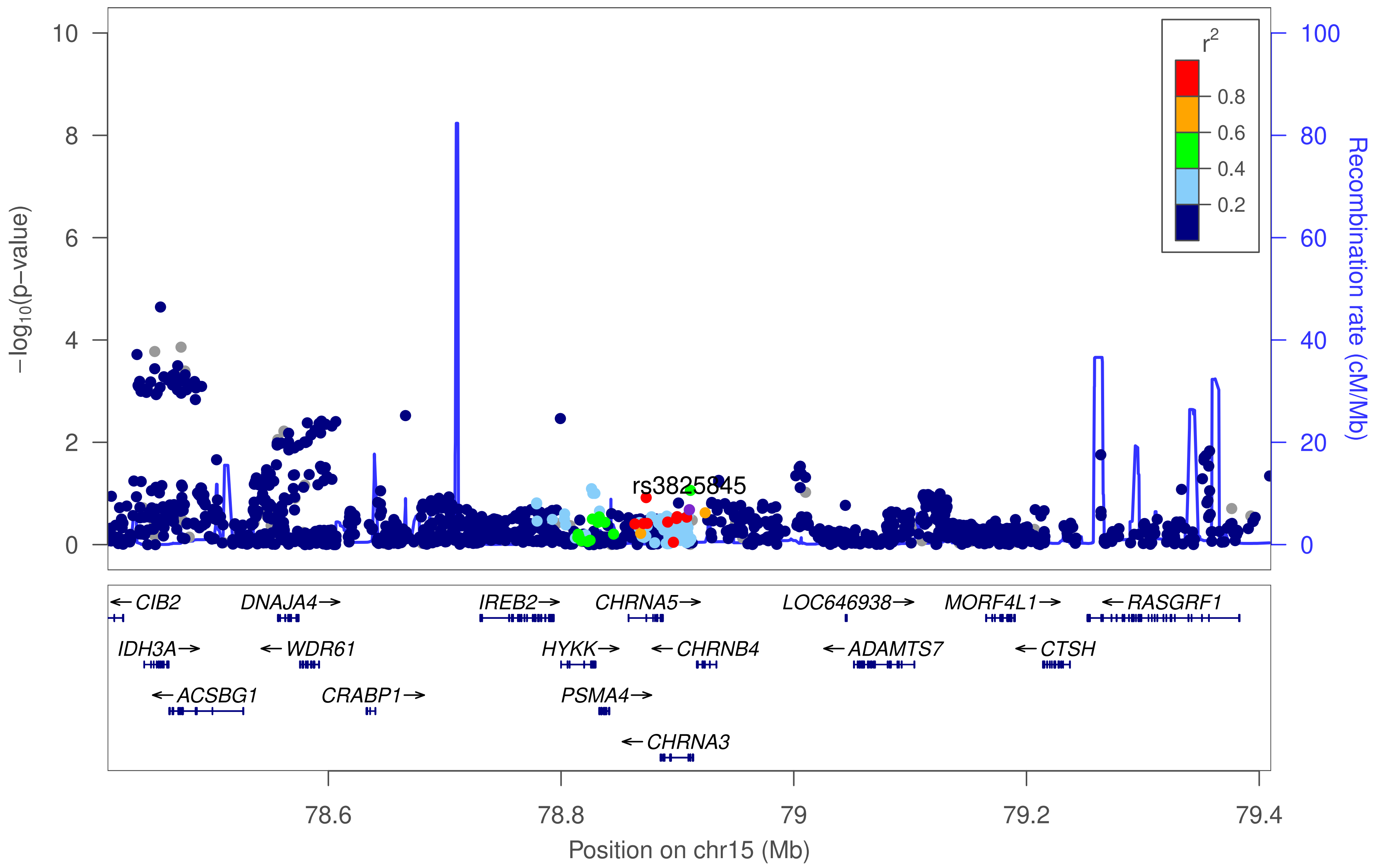

Chinese–only rs35225048
r^2
0.8
0.6
0.4
0.2
rs35225048
$-\log_{10}$(p–value)
10
8
6
4
2
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
← RORA
← VPS13C
LOC101928907→
61.4
61.6
61.8
62
62.2
Position on chr15 (Mb)

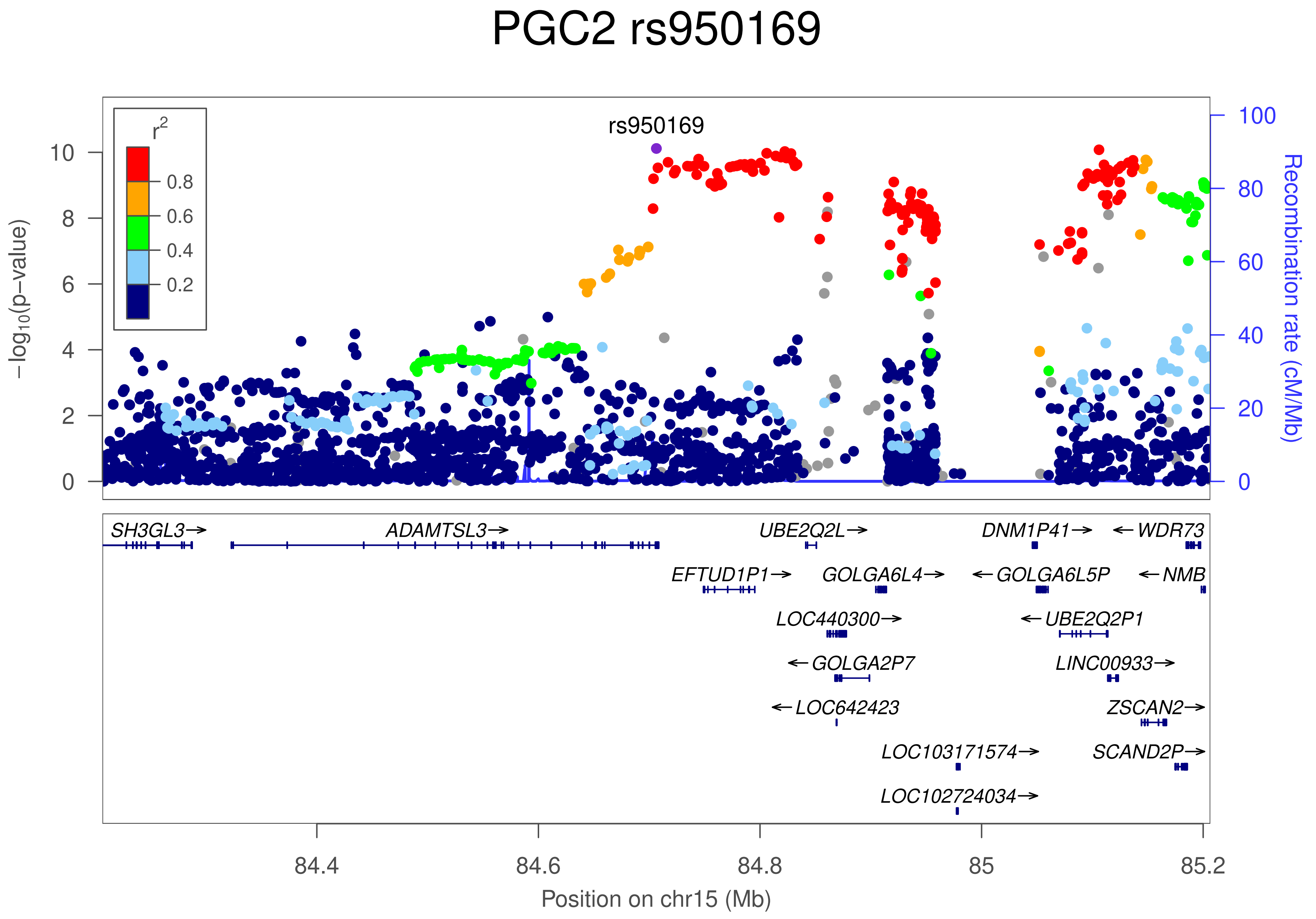
PGC2 rs3825845

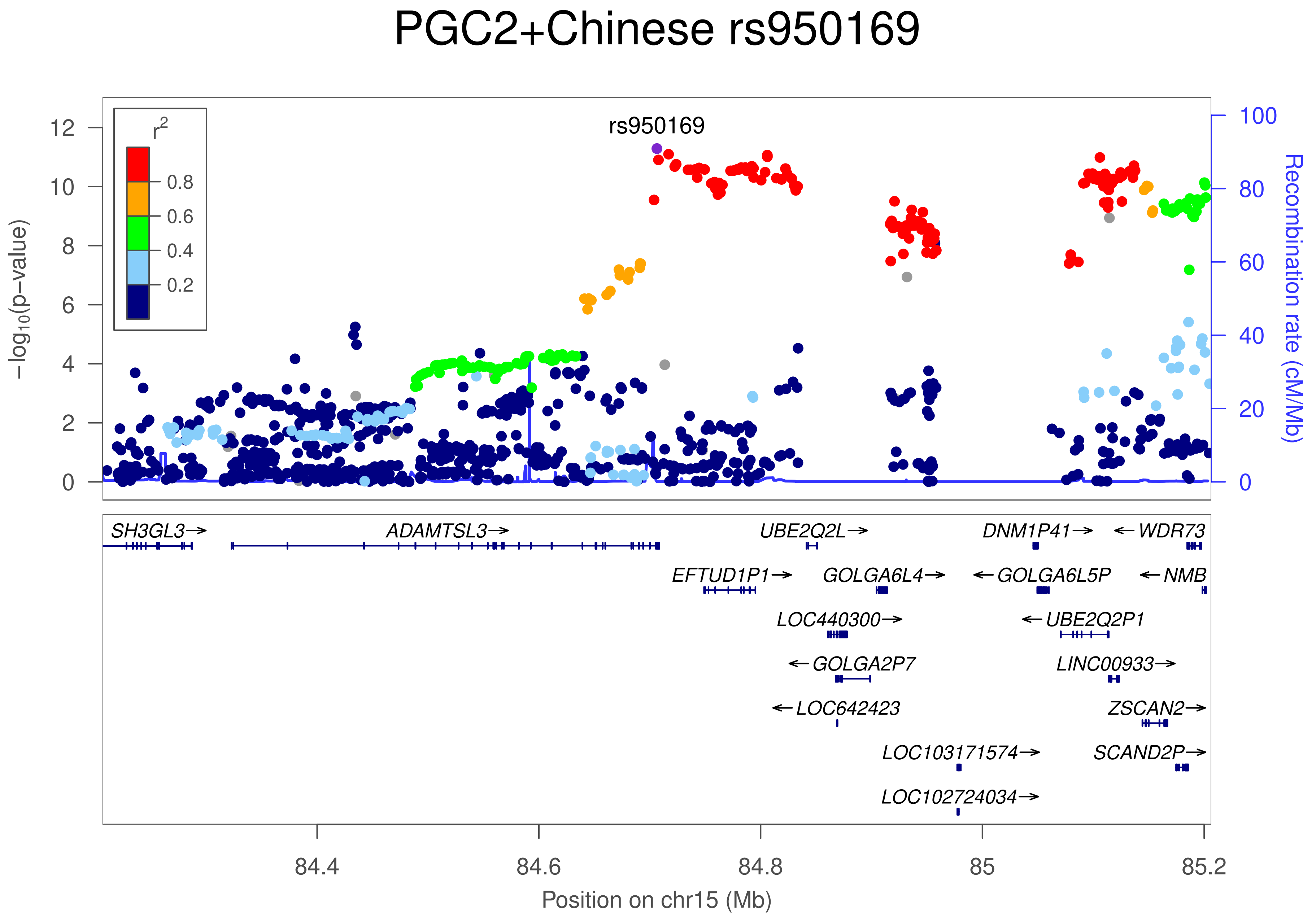


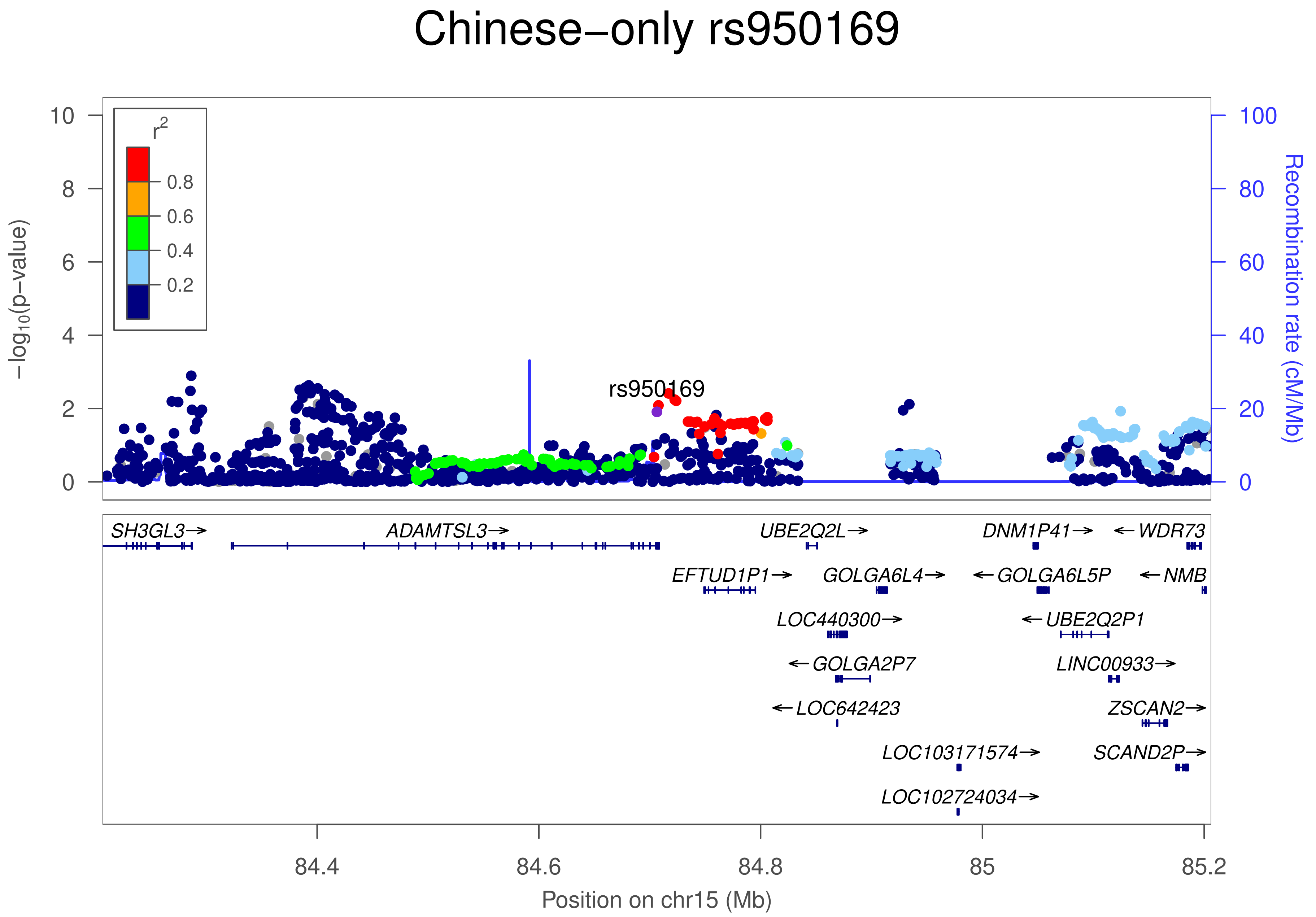

PGC2+Chinese rs3825845
rs3825845
−log10(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
r2
0.8
0.6
0.4
0.2
← CIB2
DNAJA4→
IREB2→
CHRNA5→
LOC646938→
MORF4L1→
← RASGRF1
IDH3A→
← WDR61
HYKK→
← CHRNB4
← ADAMTS7
← CTSH
← ACSBG1
CRABP1→
PSMA4→
← CHRNA3
78.6
78.8
79
79.2
79.4
Position on chr15 (Mb)

Chinese−only rs3825845

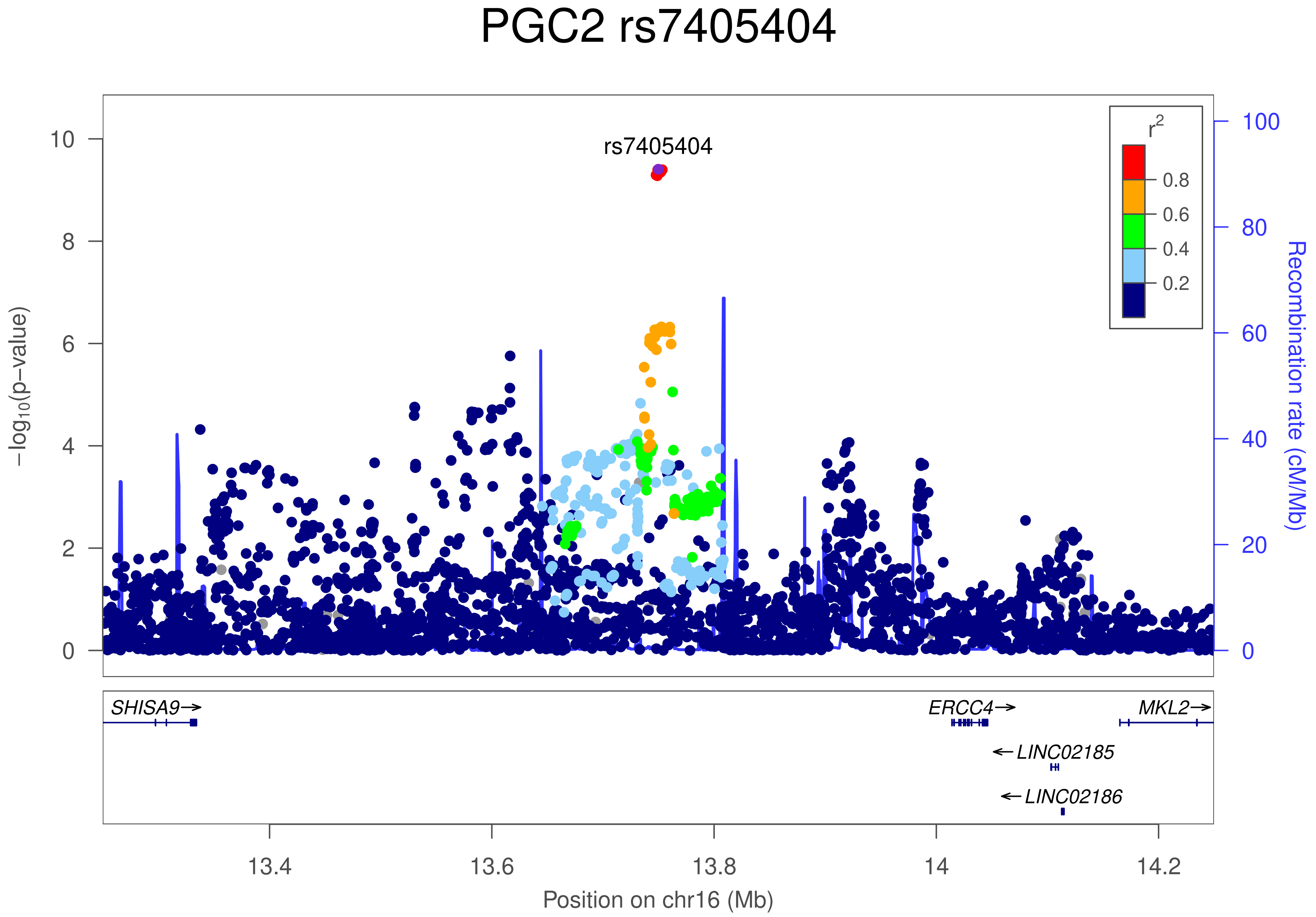



PGC2 rs950169
rs950169
r2
0.8
0.6
0.4
0.2
10
8
6
4
2
0
−log10(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
SH3GL3→
ADAMTSL3→
UBE2Q2L→
DNM1P41→
←WDR73
EFTUD1P1→
GOLGA6L4→
←GOLGA6L5P
←NMB
LOC440300→
←UBE2Q2P1
←GOLGA2P7
LINC00933→
←LOC642423
ZSCAN2→
LOC103171574→
SCAND2P→
LOC102724034→
84.4
84.6
84.8
85
85.2
Position on chr15 (Mb)

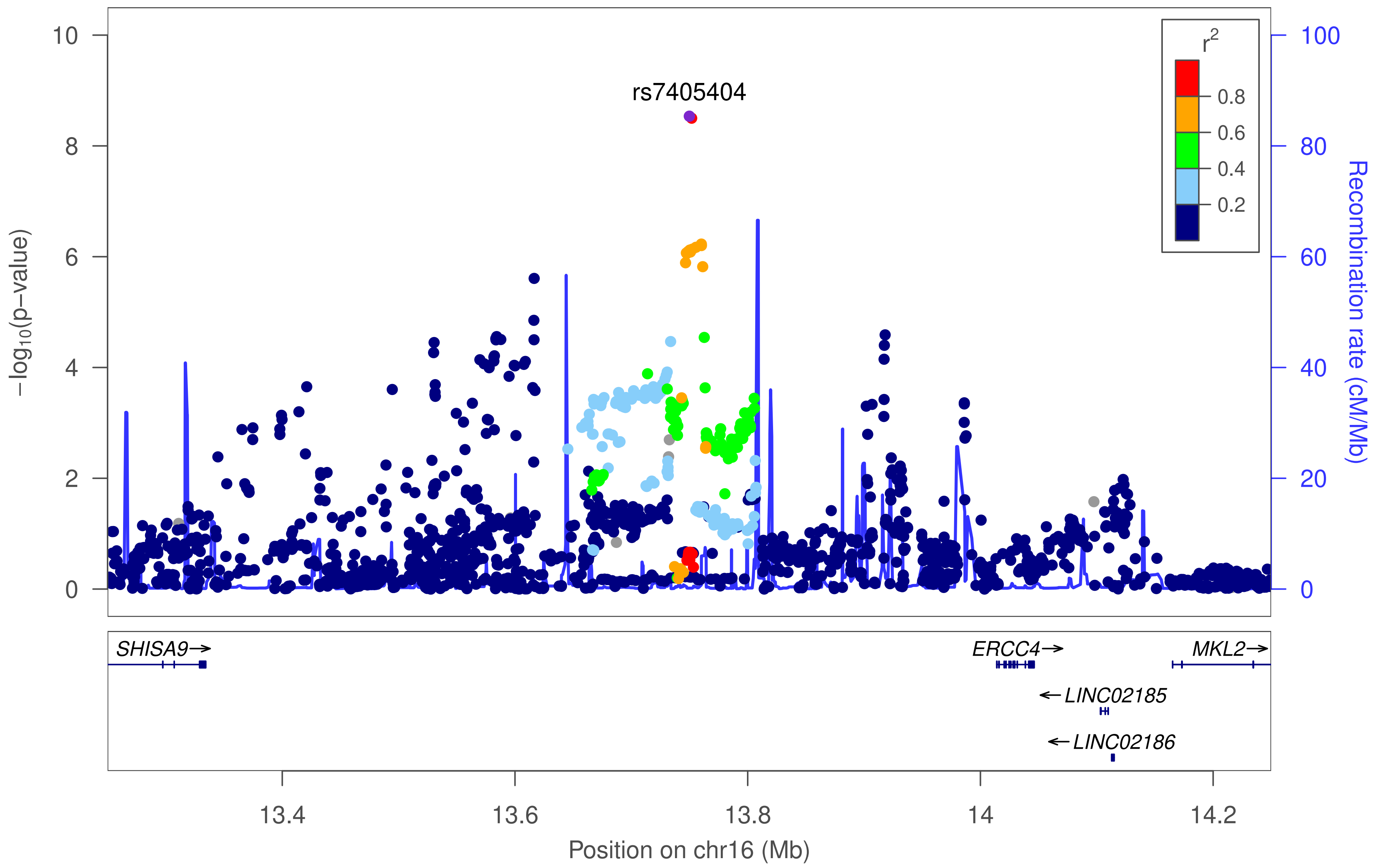

PGC2+Chinese rs950169
rs950169
r2
0.8
0.6
0.4
0.2
−log10(p−value)
0
2
4
6
8
10
12
Recombination rate (cM/Mb)
0
20
40
60
80
100
SH3GL3→
ADAMTSL3→
UBE2Q2L→
DNM1P41→
←WDR73
EFTUD1P1→
GOLGA6L4→
←GOLGA6L5P
←NMB
LOC440300→
←UBE2Q2P1
←GOLGA2P7
LINC00933→
←LOC642423
ZSCAN2→
LOC103171574→
SCAND2P→
LOC102724034→
84.4
84.6
84.8
85
85.2
Position on chr15 (Mb)



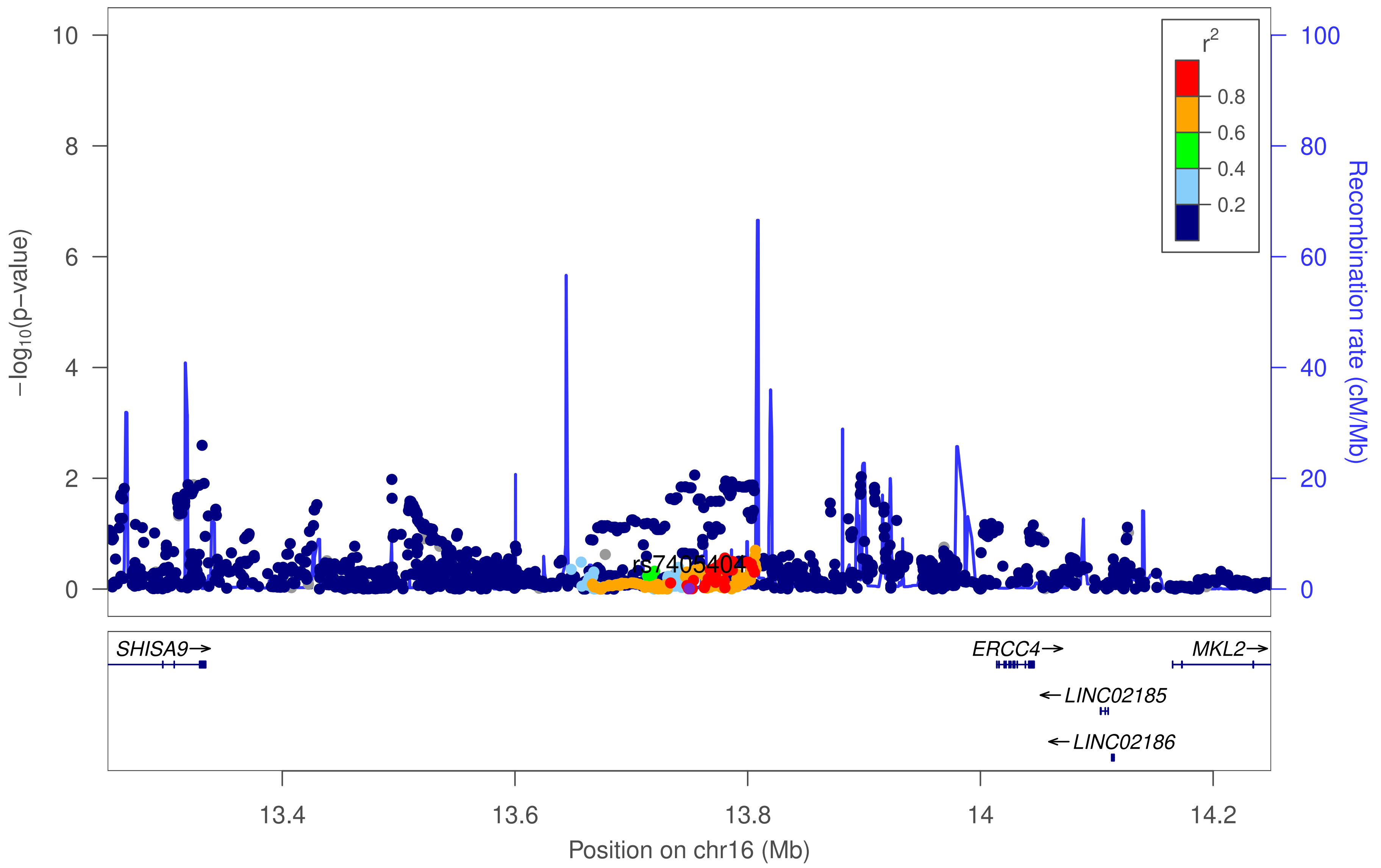
Chinese–only rs950169


PGC2 rs7405404
rs7405404
−log10(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
r2
0.8
0.6
0.4
0.2
SHISA9→
ERCC4→
MKL2→
←LINC02185
←LINC02186
13.4
13.6
13.8
14
14.2
Position on chr16 (Mb)

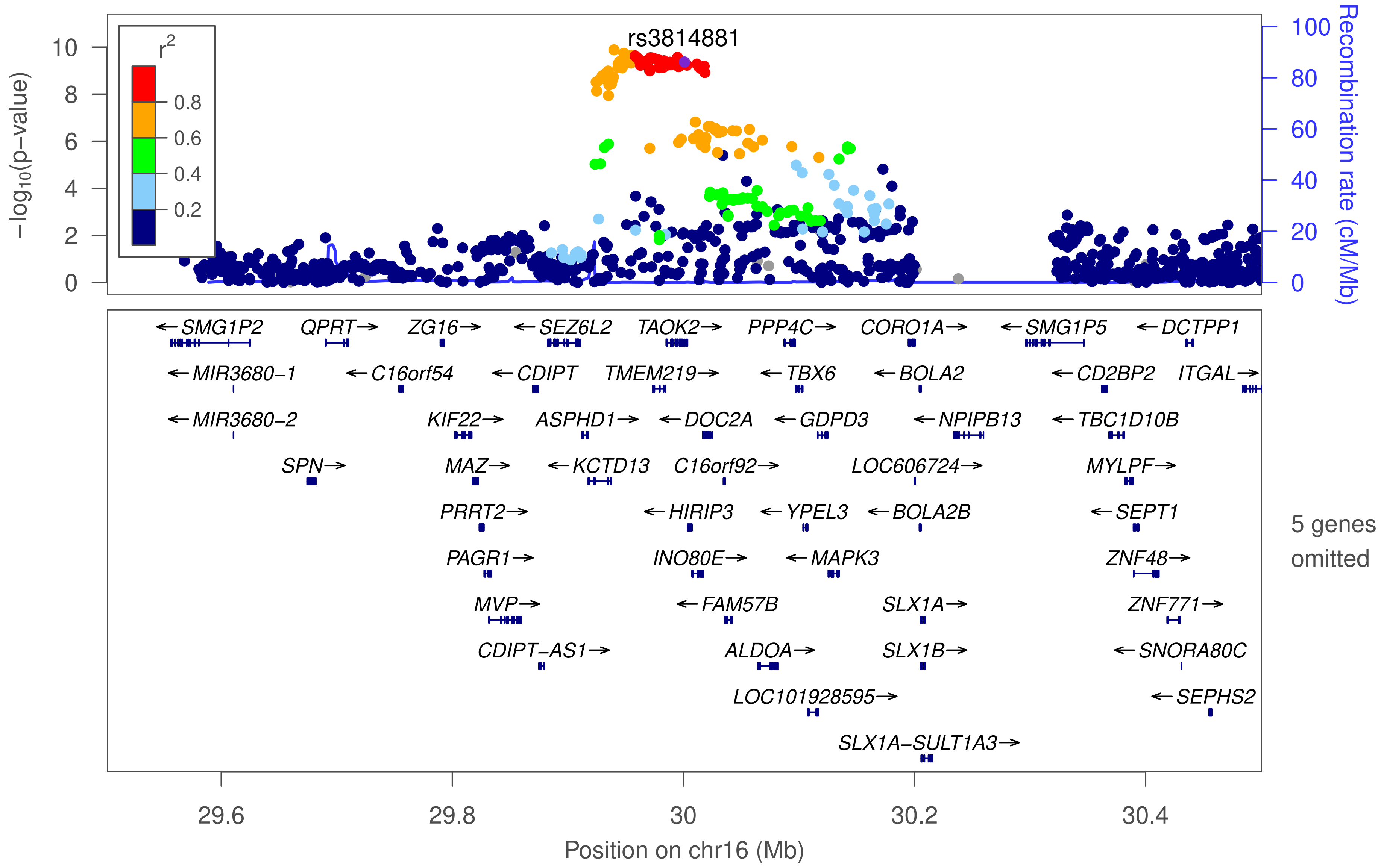
PGC2+Chinese rs7405404

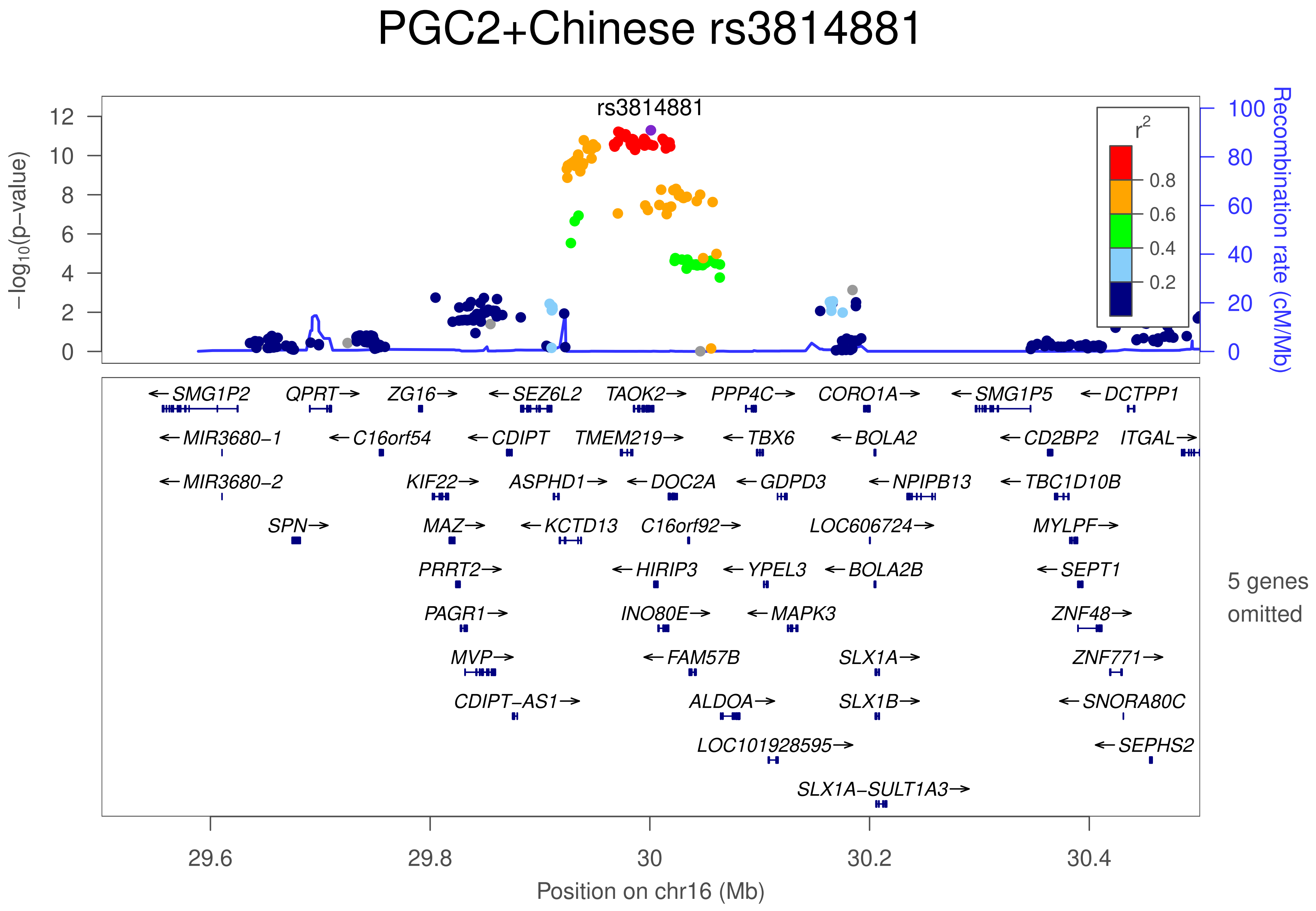


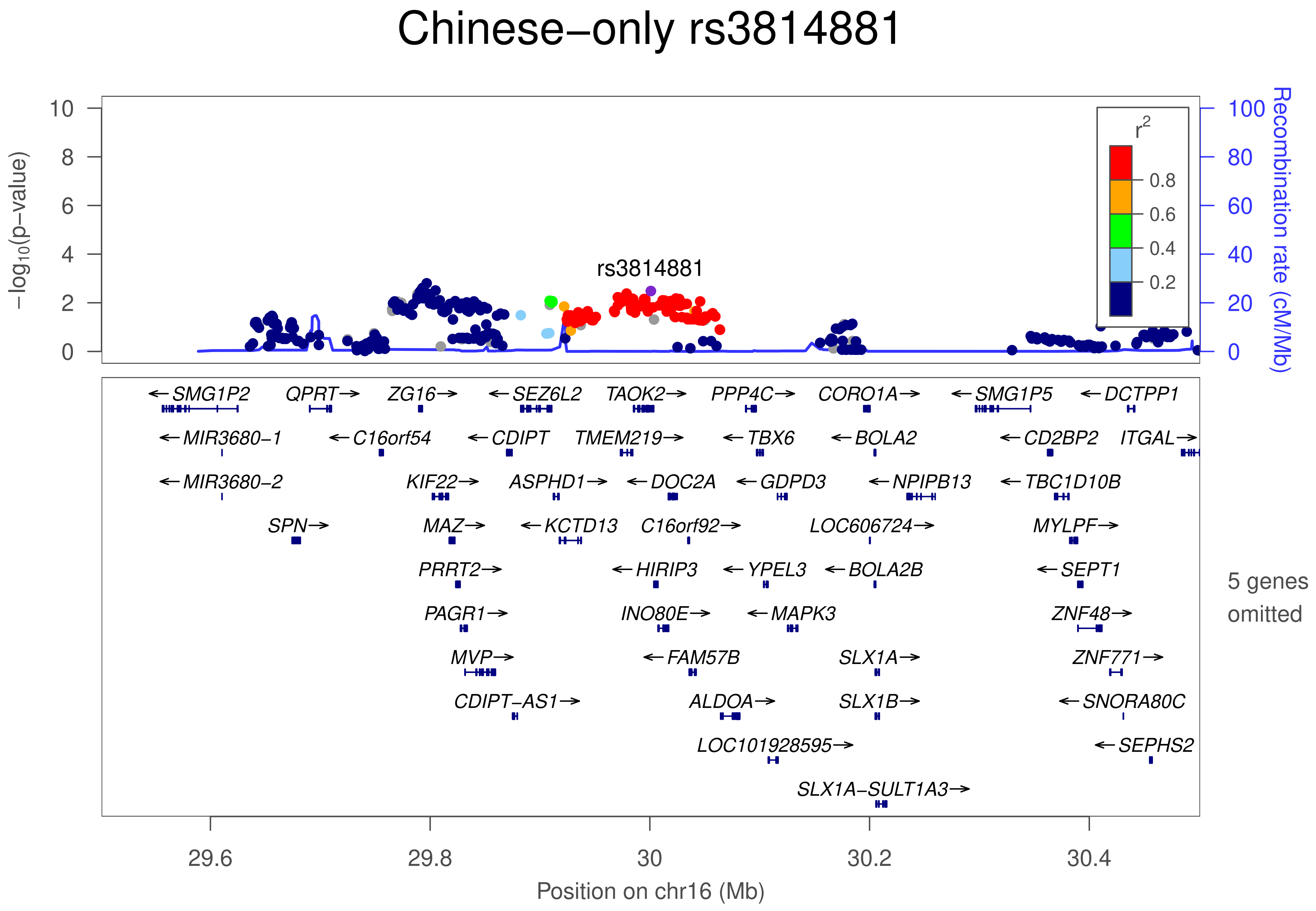
Chinese−only rs7405404



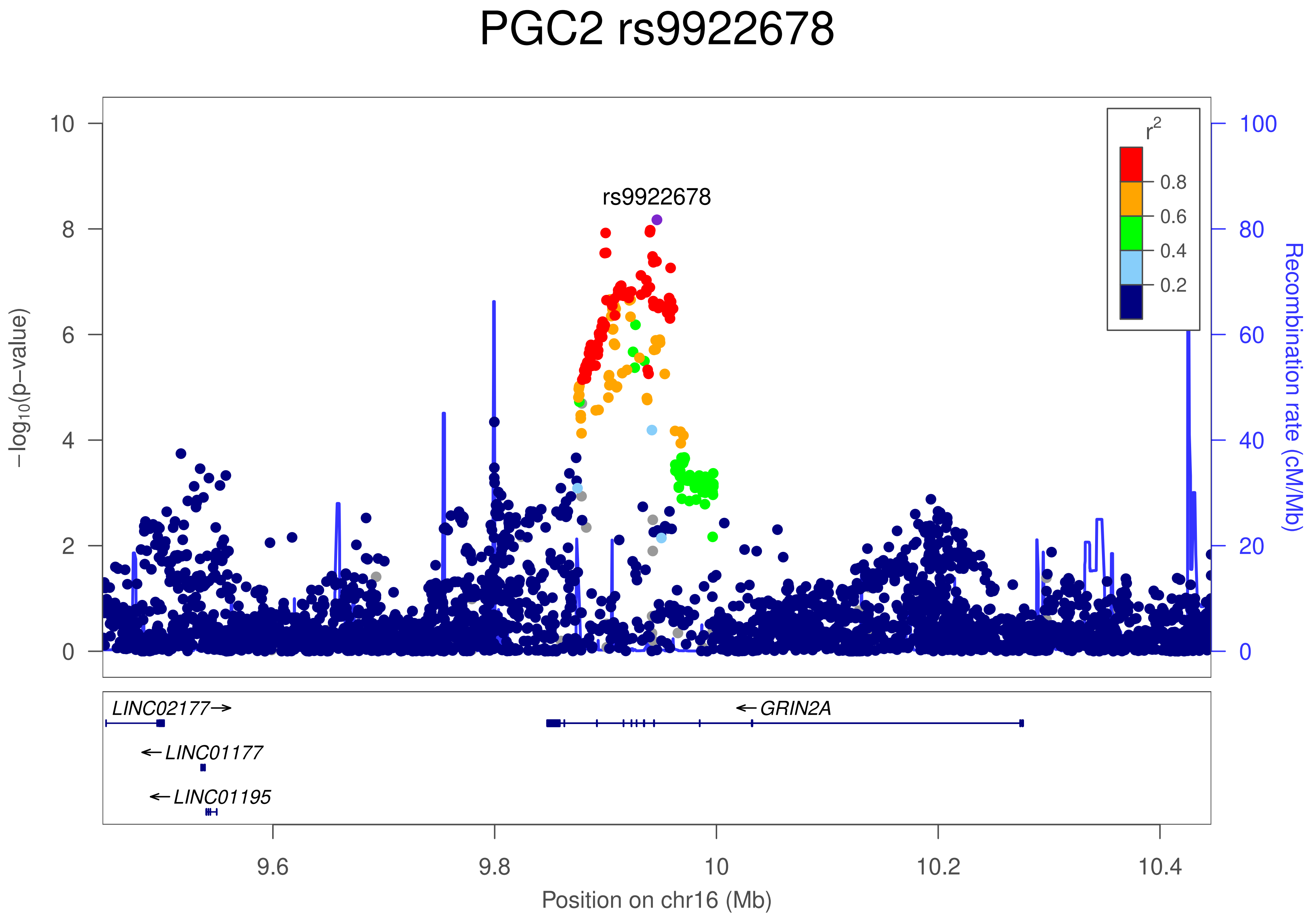
PGC2 rs3814881

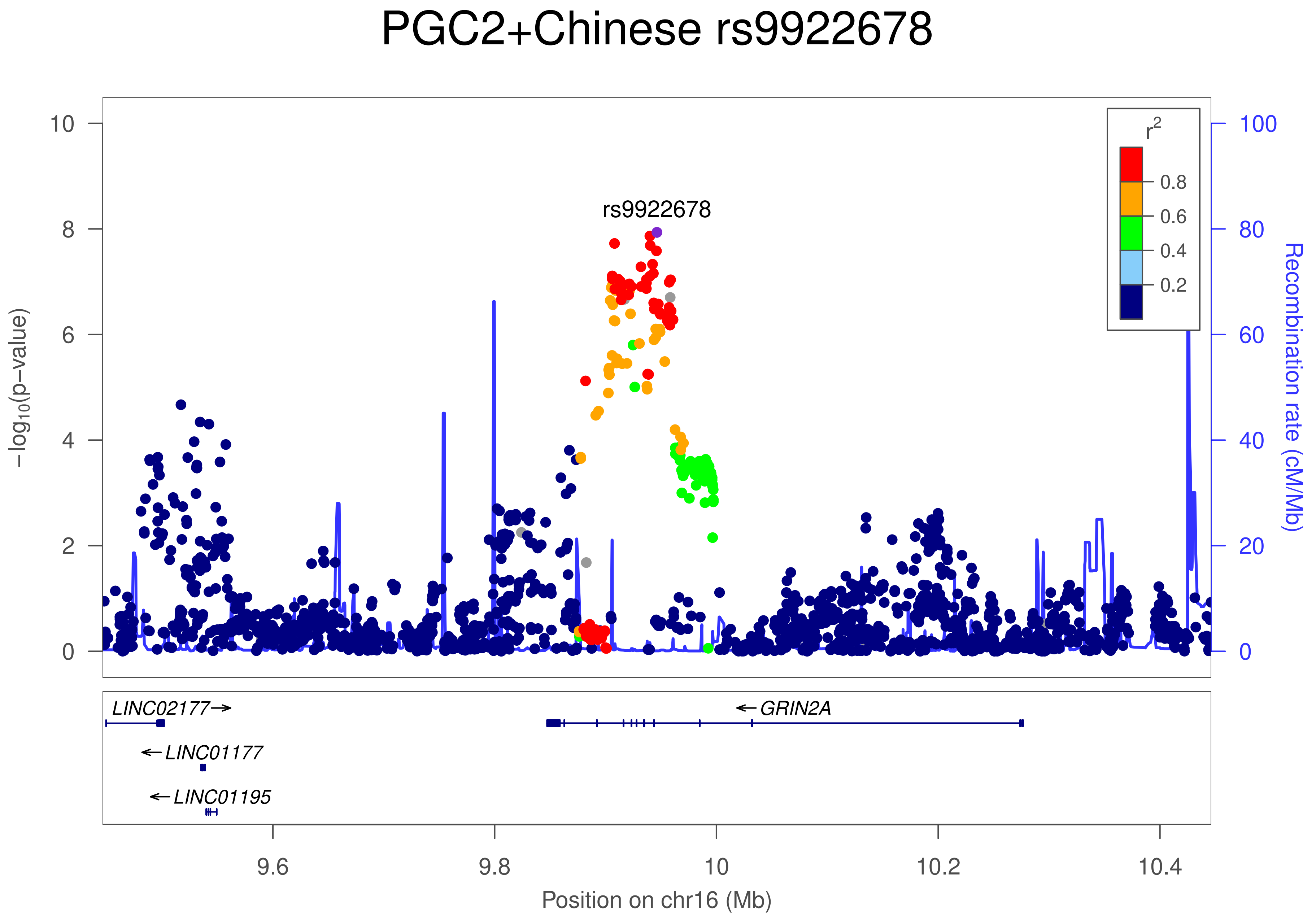



PGC2+Chinese rs3814881
rs3814881
−log10(p−value)
12
10
8
6
4
2
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
r2
0.8
0.6
0.4
0.2
←SMG1P2
QPRT→
ZG16→
←SEZ6L2
TAOK2→
PPP4C→
CORO1A→
←SMG1P5
←DCTPP1
←MIR3680−1
←C16orf54
←CDIPT
TMEM219→
←TBX6
←BOLA2
←CD2BP2
ITGAL→
←MIR3680−2
KIF22→
ASPHD1→
←DOC2A
←GDPD3
←NPIPB13
←TBC1D10B
SPN→
MAZ→
←KCTD13
C16orf92→
LOC606724→
MYLPF→
PRRT2→
←HIRIP3
←YPEL3
←BOLA2B
←SEPT1
PAGR1→
INO80E→
←MAPK3
ZNF48→
MVP→
←FAM57B
SLX1A→
ZNF771→
CDIPT−AS1→
ALDOA→
SLX1B→
←SNORA80C
LOC101928595→
←SEPHS2
SLX1A−SULT1A3→
5 genes omitted
29.6
29.8
30
30.2
30.4
Position on chr16 (Mb)

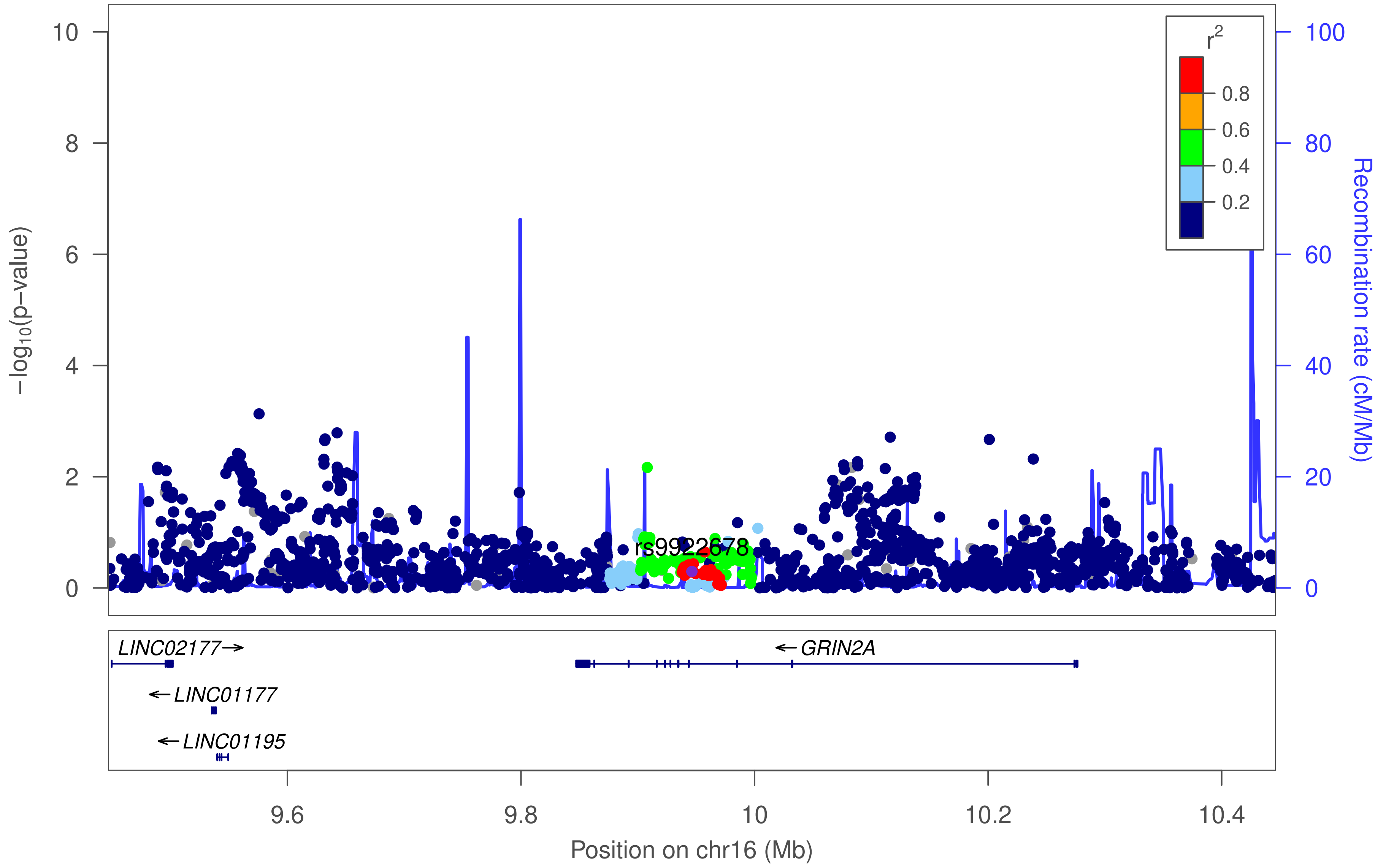


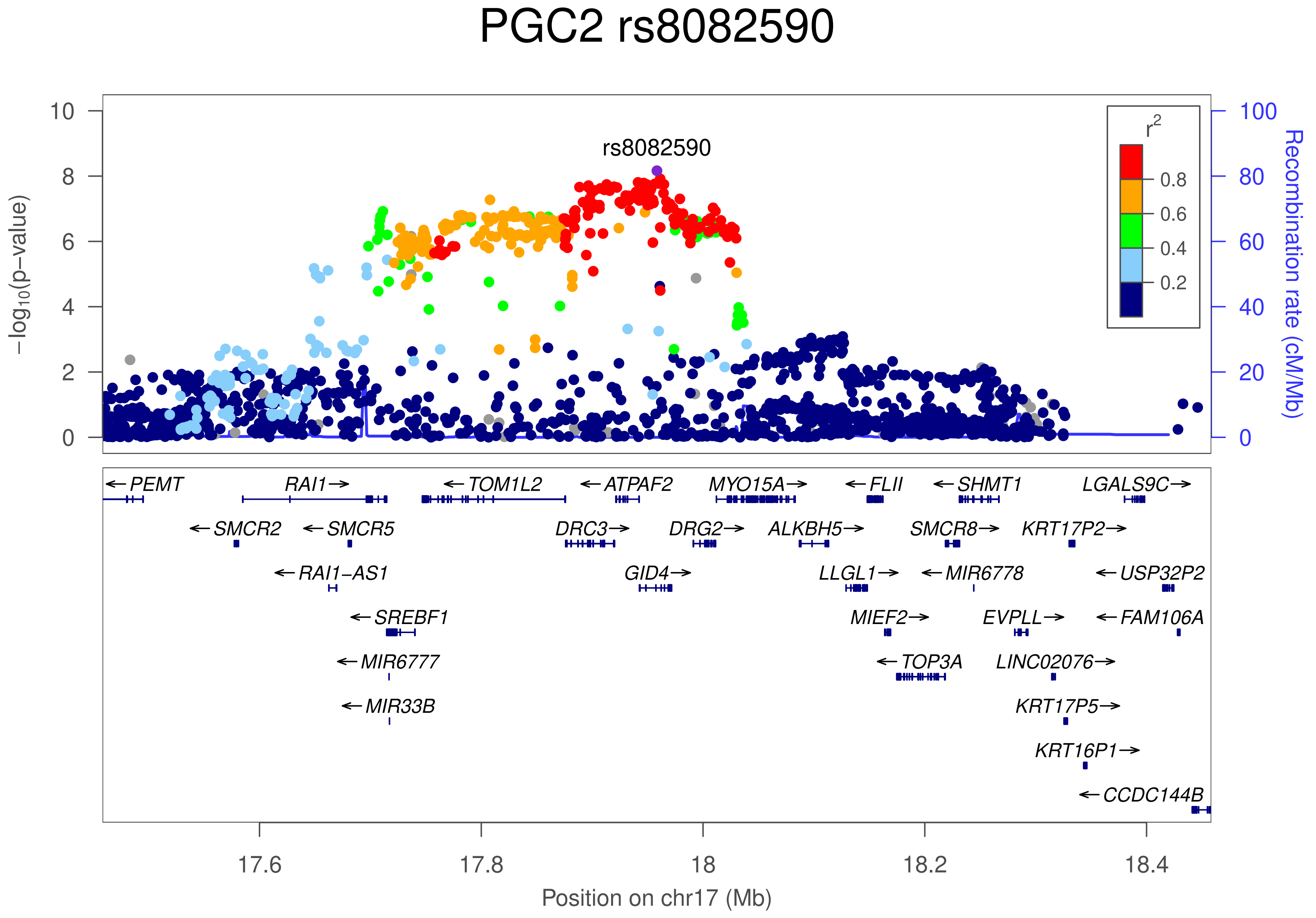
Chinese−only rs3814881
rs3814881
−log10(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
r2
0.2
0.4
0.6
0.8
←SMG1P2
QPRT→
ZG16→
←SEZ6L2
TAOK2→
PPP4C→
CORO1A→
←SMG1P5
←DCTPP1
←MIR3680−1
←C16orf54
←CDIPT
TMEM219→
←TBX6
←BOLA2
←CD2BP2
ITGAL→
←MIR3680−2
KIF22→
ASPHD1→
←DOC2A
←GDPD3
←NPIPB13
←TBC1D10B
SPN→
MAZ→
←KCTD13
C16orf92→
LOC606724→
MYLPF→
PRRT2→
←HIRIP3
←YPEL3
←BOLA2B
←SEPT1
PAGR1→
INO80E→
←MAPK3
ZNF48→
MVP→
←FAM57B
SLX1A→
ZNF771→
CDIPT−AS1→
ALDOA→
SLX1B→
←SNORA80C
LOC101928595→
←SEPHS2
SLX1A−SULT1A3→
5 genes omitted
29.6
29.8
30
30.2
30.4
Position on chr16 (Mb)

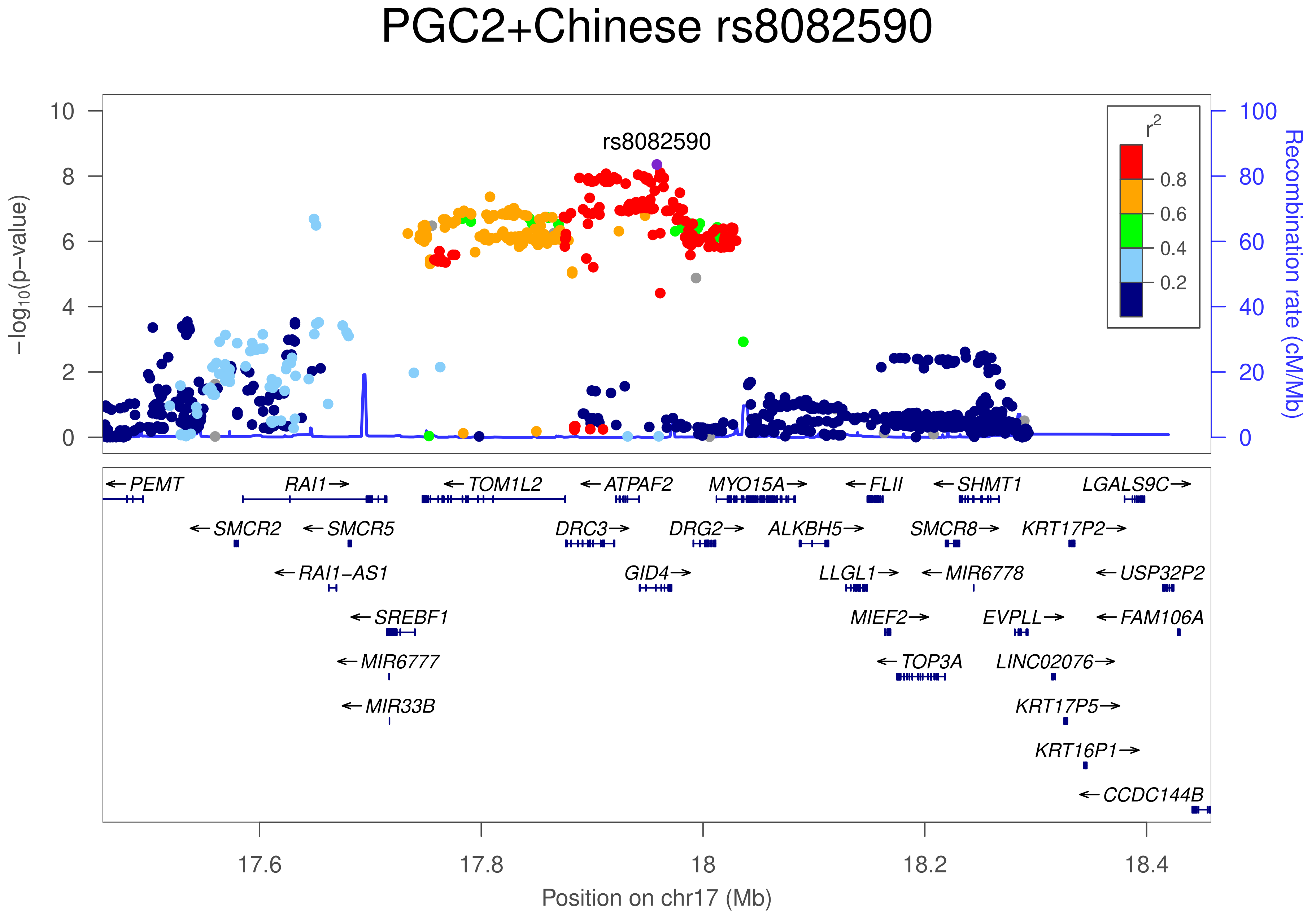

PGC2 rs9922678
rs9922678
−log10(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
r2
0.8
0.6
0.4
0.2
LINC02177→
←GRIN2A
←LINC01177
←LINC01195
9.6
9.8
10
10.2
10.4
Position on chr16 (Mb)


PGC2+Chinese rs9922678
rs9922678
r2
0.8
0.6
0.4
0.2
10
8
6
4
2
0
$-\log_{10}$(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
LINC02177→
←GRIN2A
←LINC01177
←LINC01195
9.6
9.8
10
10.2
10.4
Position on chr16 (Mb)

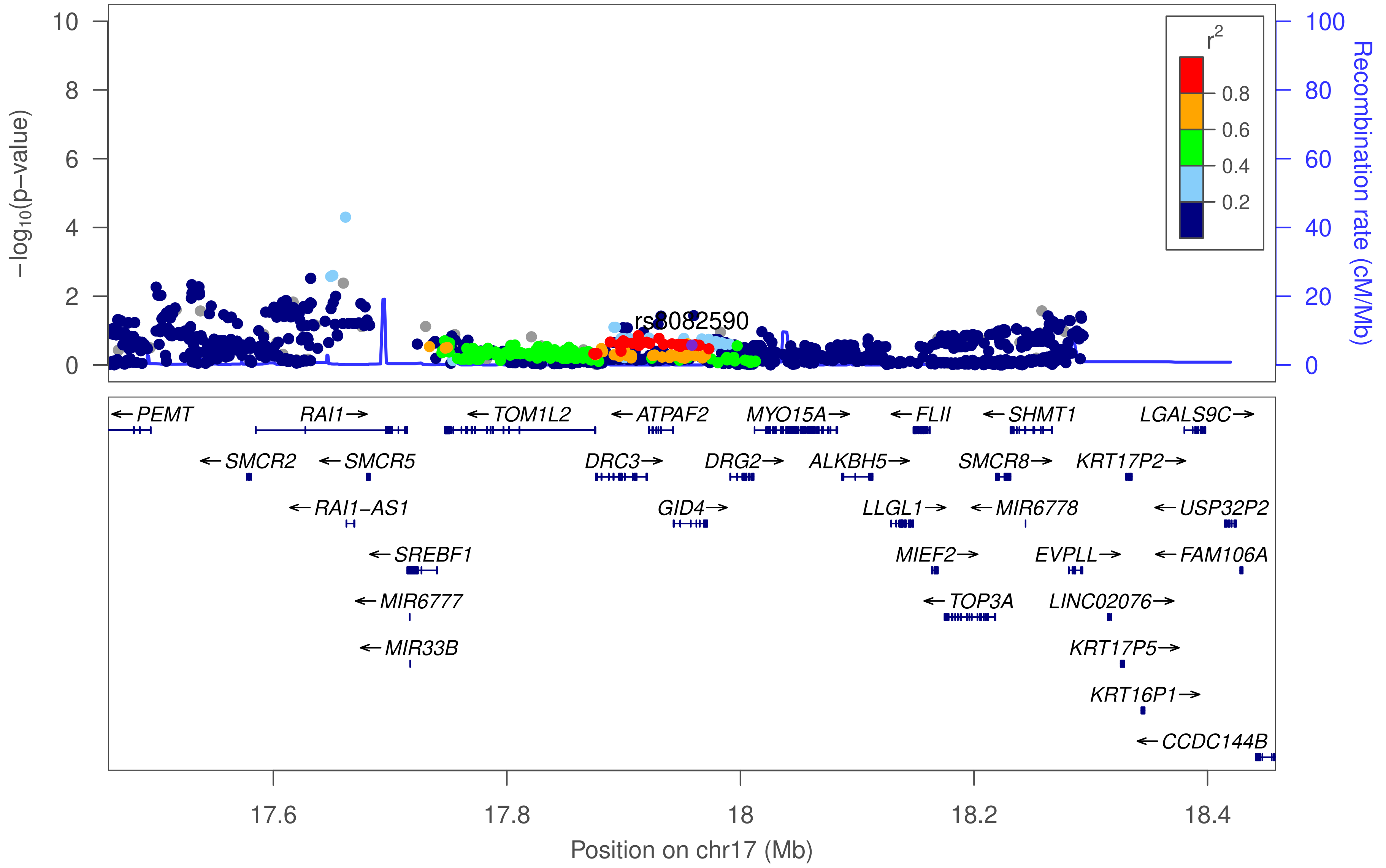
Chinese−only rs9922678



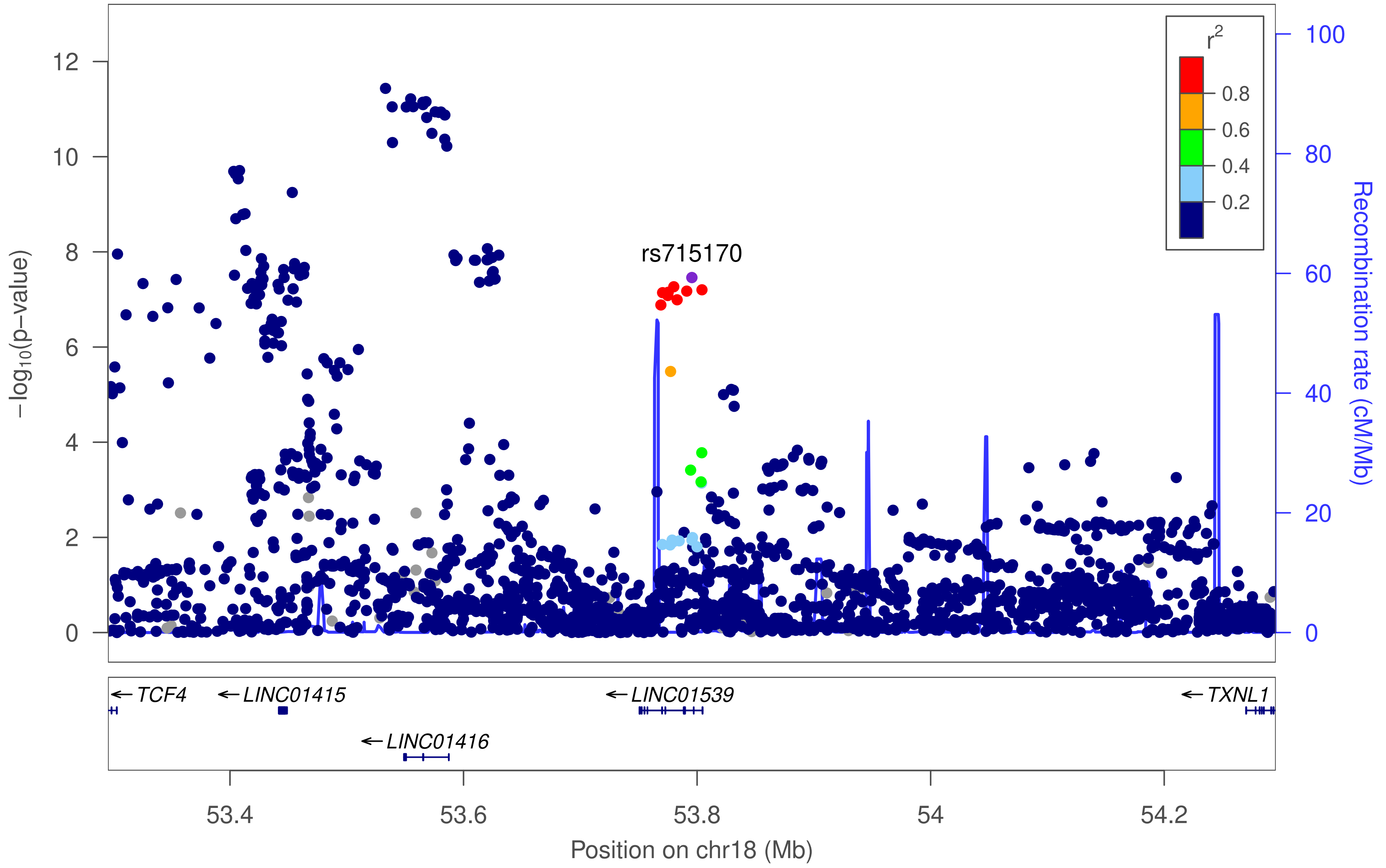

PGC2 rs8082590
rs8082590
−log10(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
r2
0.8
0.6
0.4
0.2
←PEMT
RAI1→
←TOM1L2
←ATPAF2
MYO15A→
←FLII
←SHMT1
LGALS9C→
←SMCR2
←SMCR5
DRC3→
DRG2→
ALKBH5→
SMCR8→
KRT17P2→
←RAI1−AS1
GID4→
LLGL1→
←MIR6778
←USP32P2
←SREBF1
MIEF2→
EVPLL→
←FAM106A
←MIR6777
←TOP3A
LINC02076→
←MIR33B
KRT17P5→
KRT16P1→
←CCDC144B
17.6
17.8
18
18.2
18.4
Position on chr17 (Mb)


PGC2+Chinese rs8082590
rs8082590
−log10(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
r2
0.8
0.6
0.4
0.2
PEMT
RAI1
TOM1L2
ATPAF2
MYO15A
FLII
SHMT1
LGALS9C
SMCR2
SMCR5
DRC3
DRG2
ALKBH5
SMCR8
KRT17P2
RAI1−AS1
GID4
LLGL1
MIR6778
USP32P2
SREBF1
MIEF2
EVPLL
FAM106A
MIR6777
TOP3A
LINC02076
MIR33B
KRT17P5
KRT16P1
CCDC144B
17.6
17.8
18
18.2
18.4
Position on chr17 (Mb)

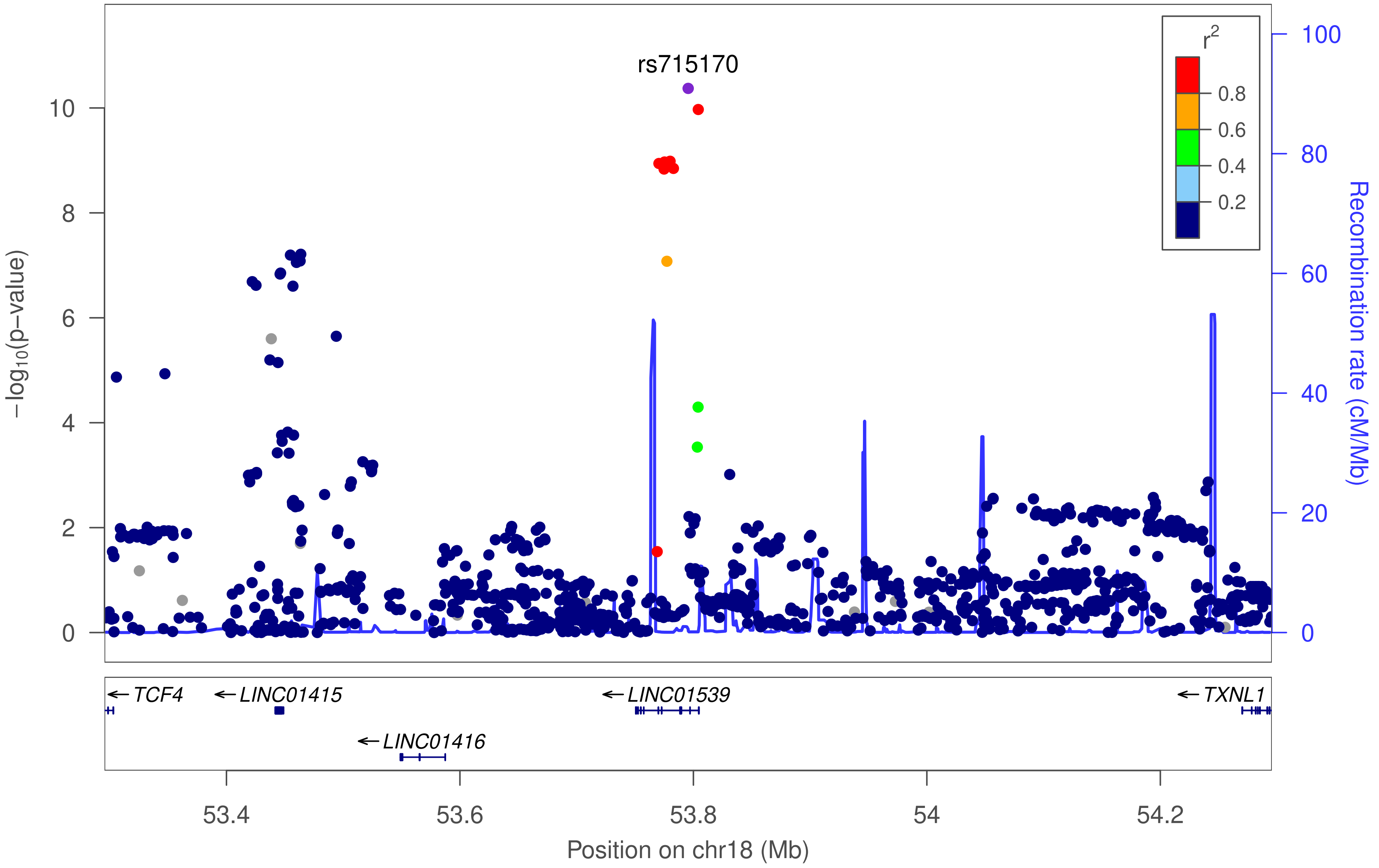
Chinese−only rs8082590



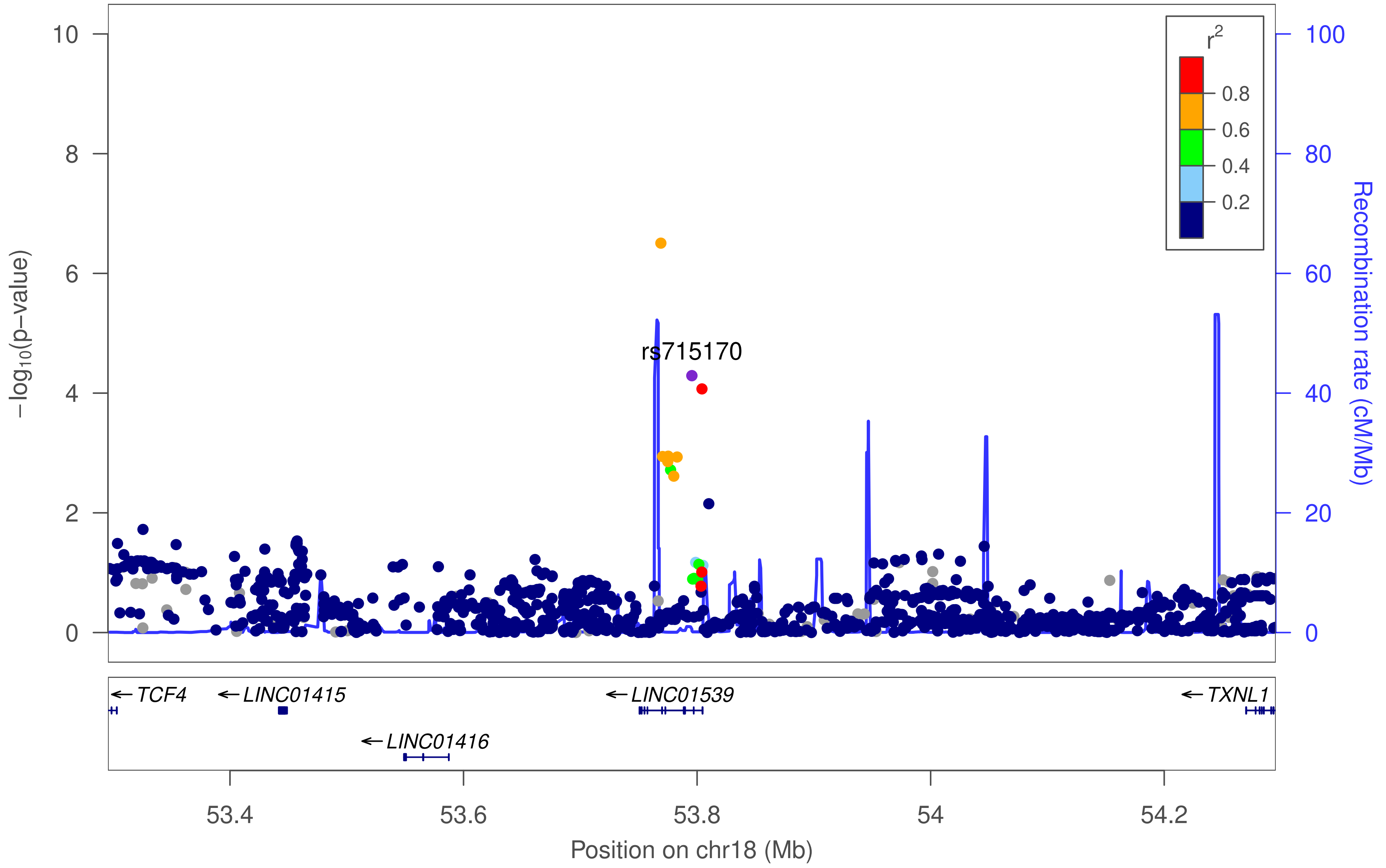
PGC2 rs715170



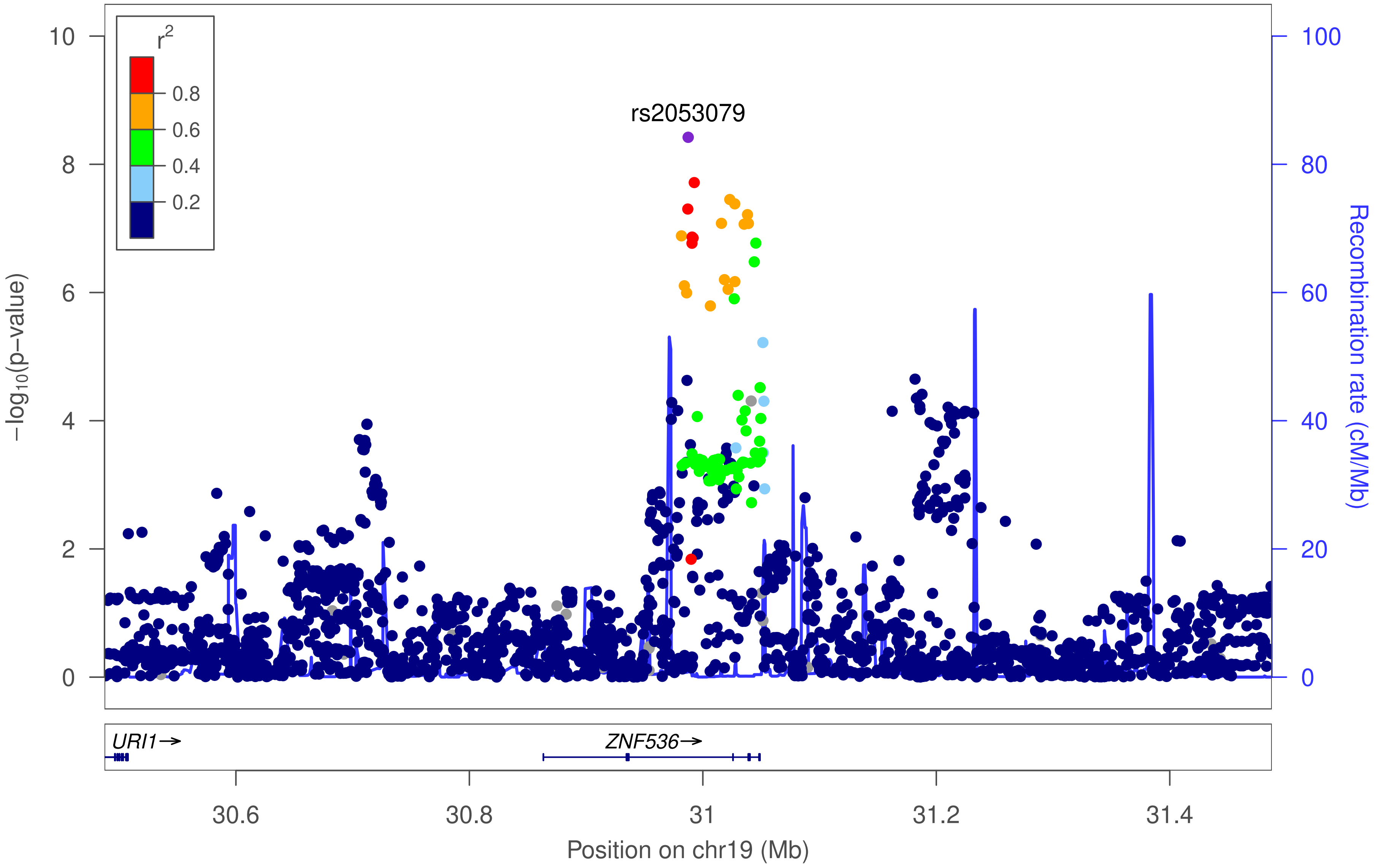
PGC2+Chinese rs715170

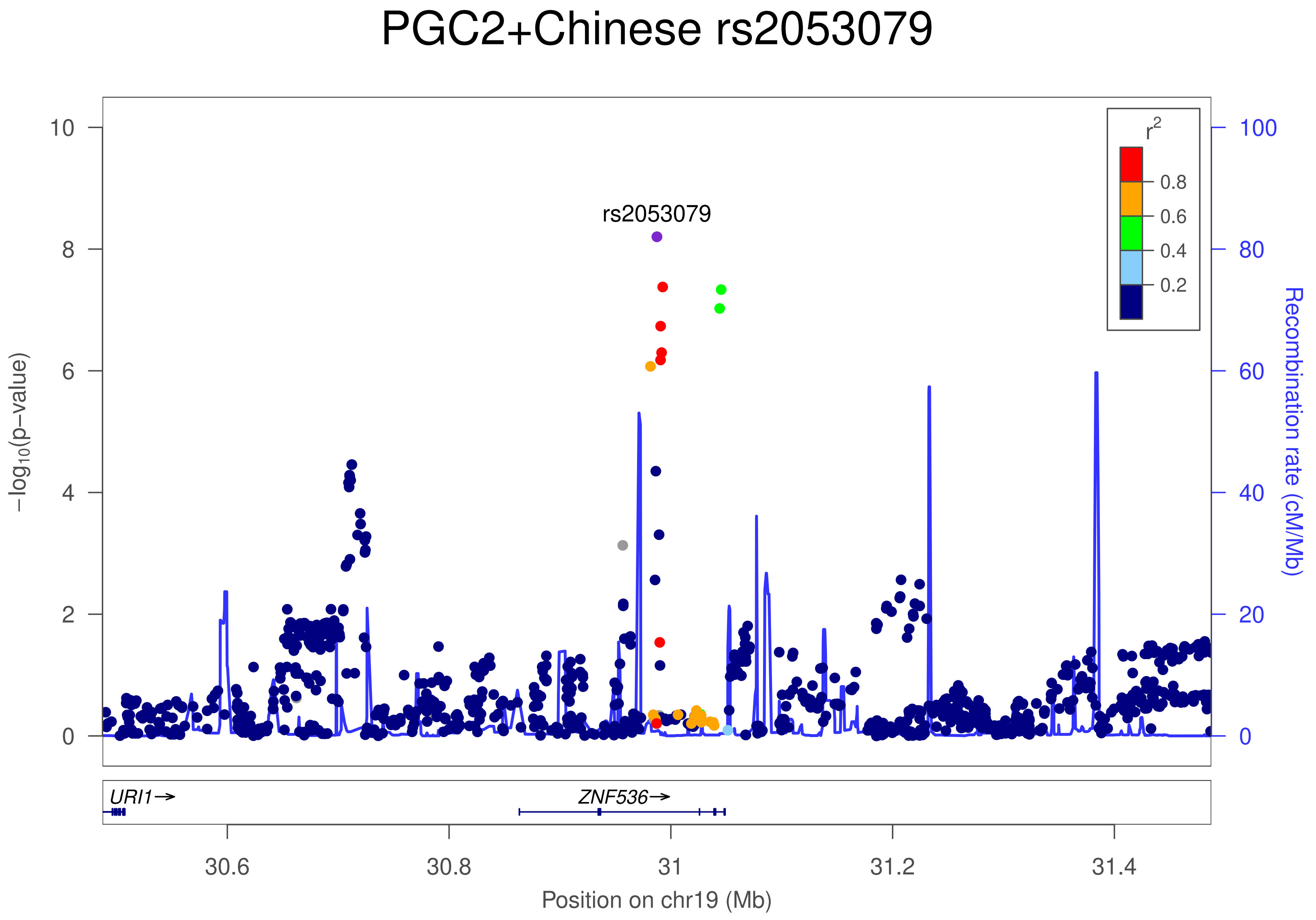


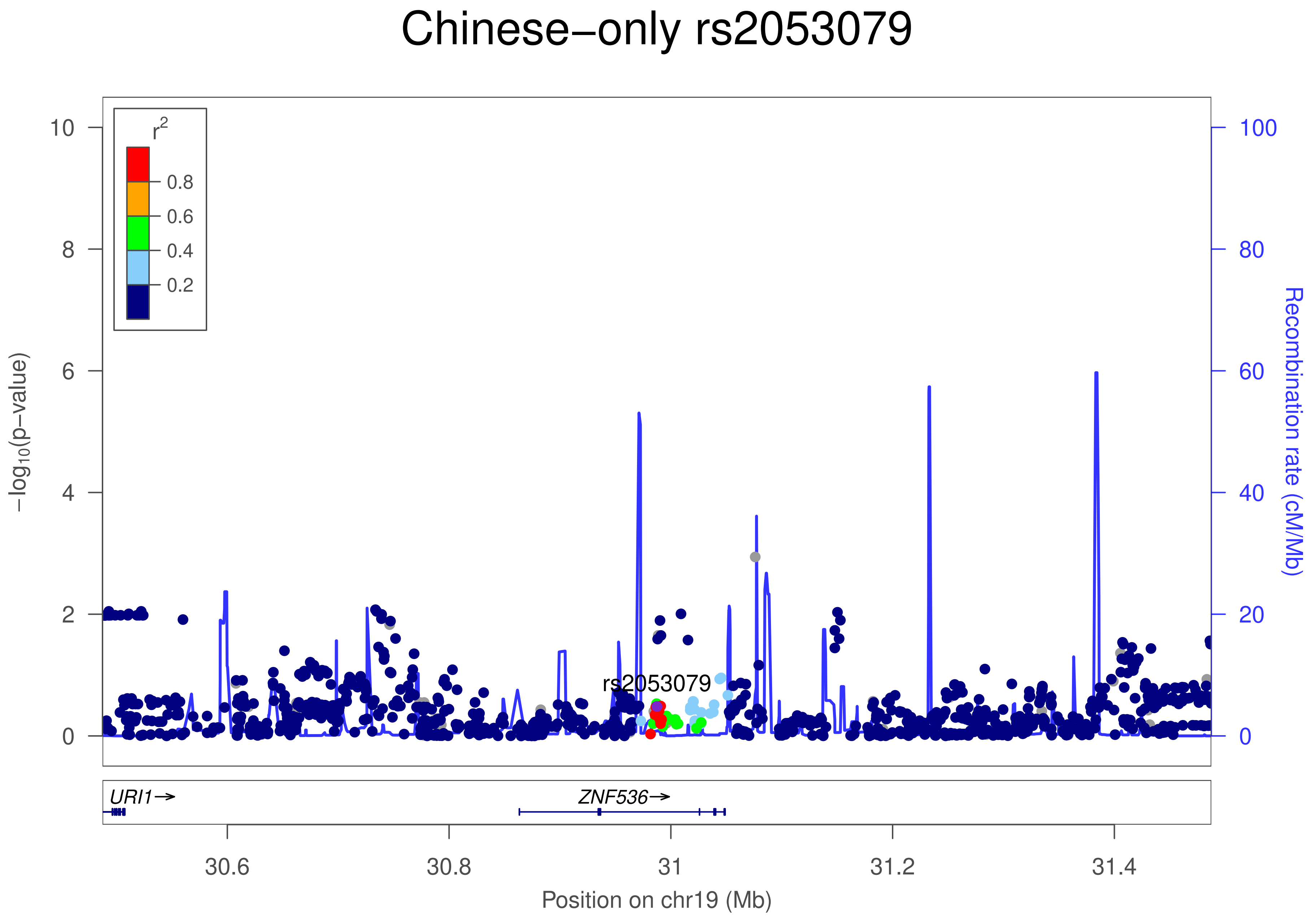
Chinese−only rs715170



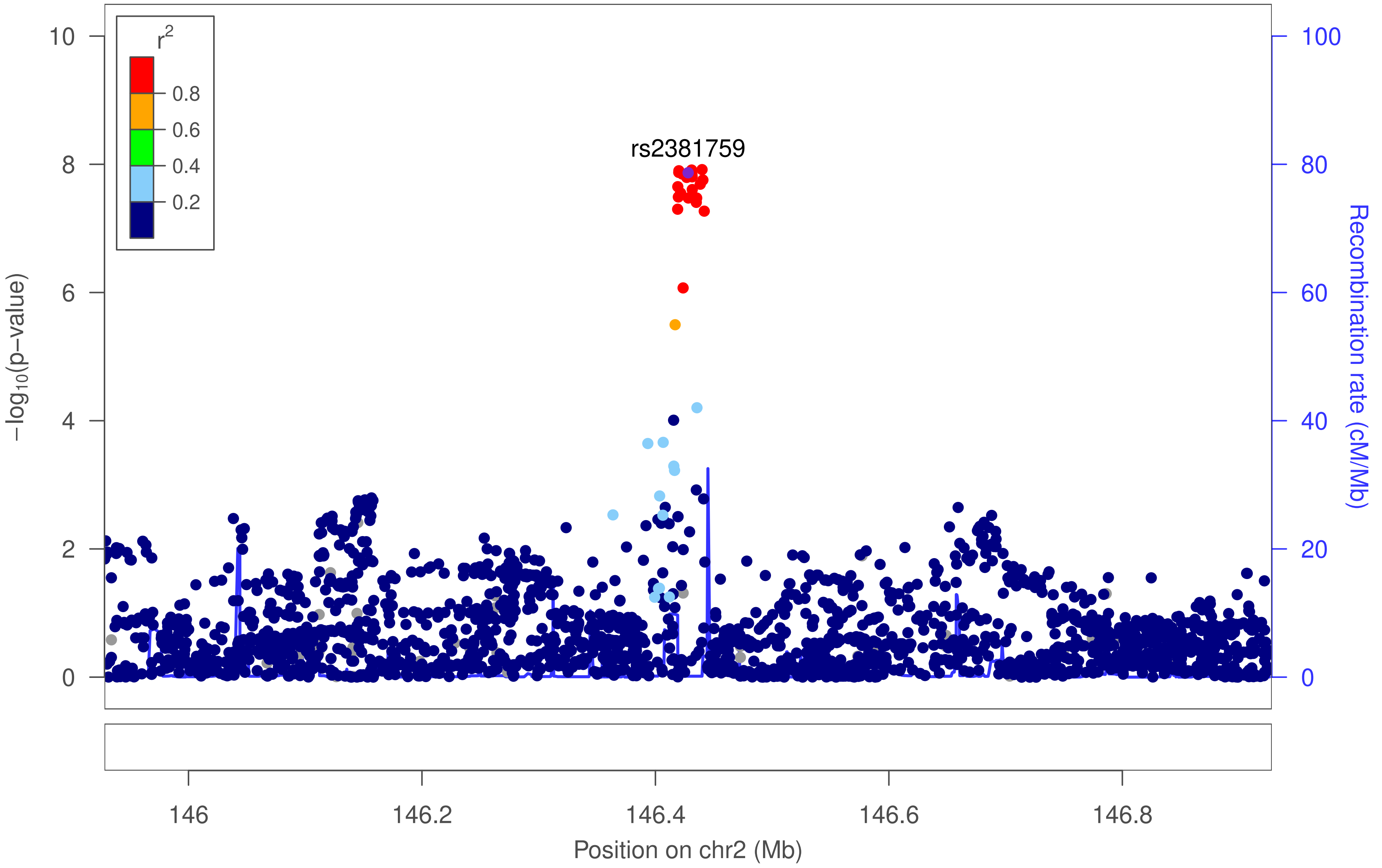
PGC2 rs2053079

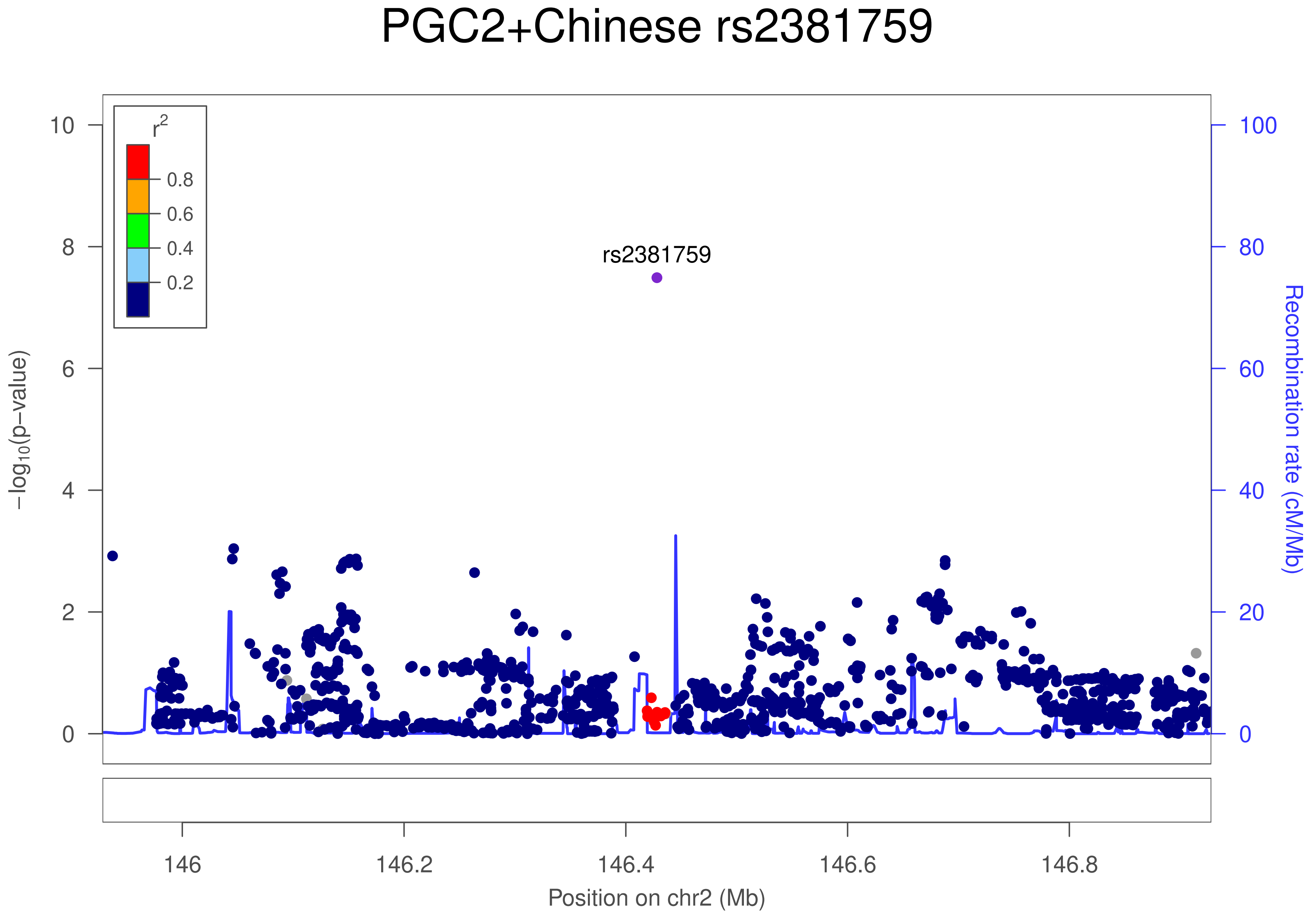



PGC2+Chinese rs2053079
rs2053079
r²
0.8
0.6
0.4
0.2
−log₁₀(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
URI1→
ZNF536→
30.6
30.8
31
31.2
31.4
Position on chr19 (Mb)

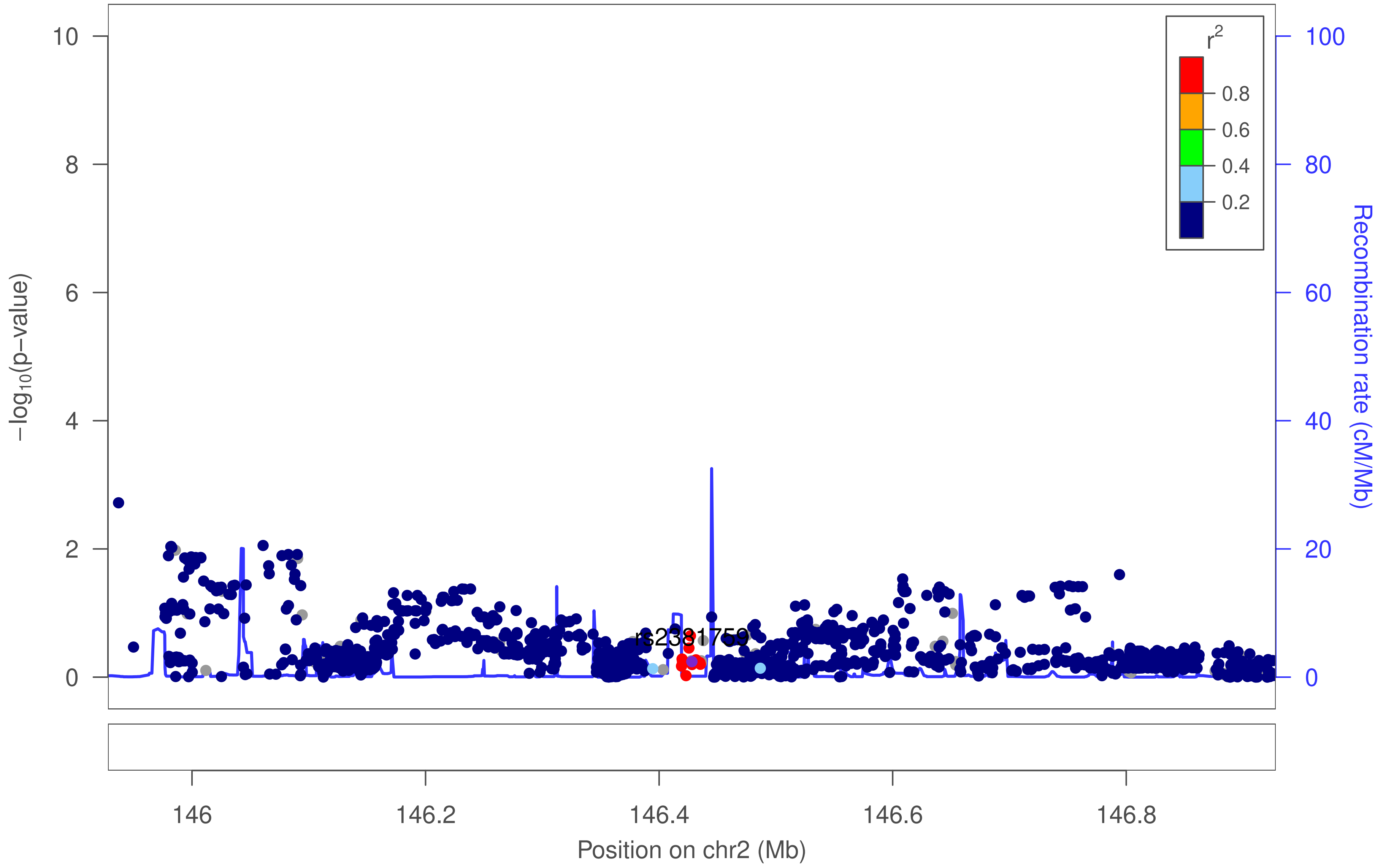

Chinese−only rs2053079
r²
0.8
0.6
0.4
0.2
−log₁₀(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
rs2053079
URI1→
ZNF536→
30.6
30.8
31
31.2
31.4
Position on chr19 (Mb)

PGC2 rs2381759

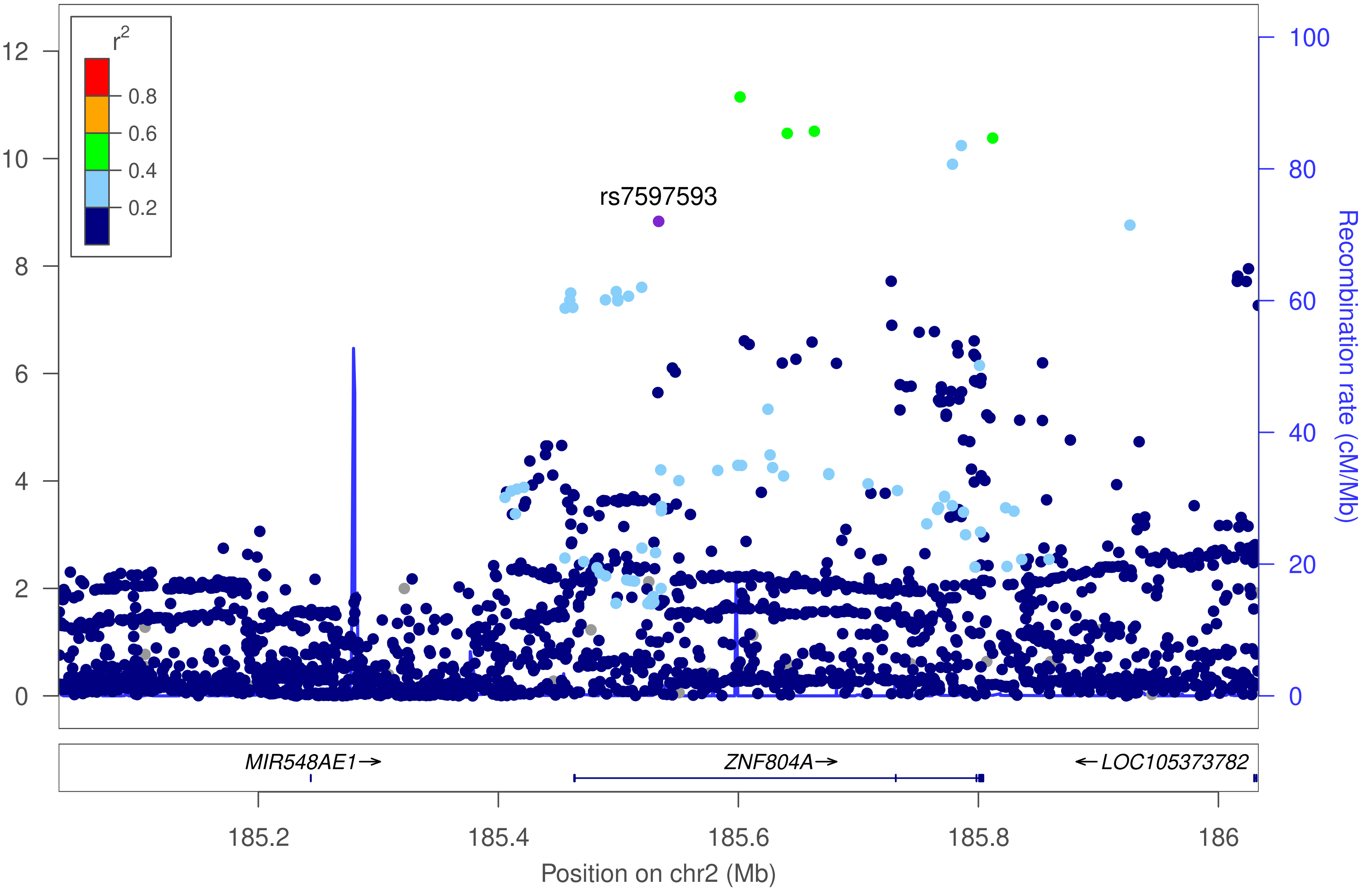


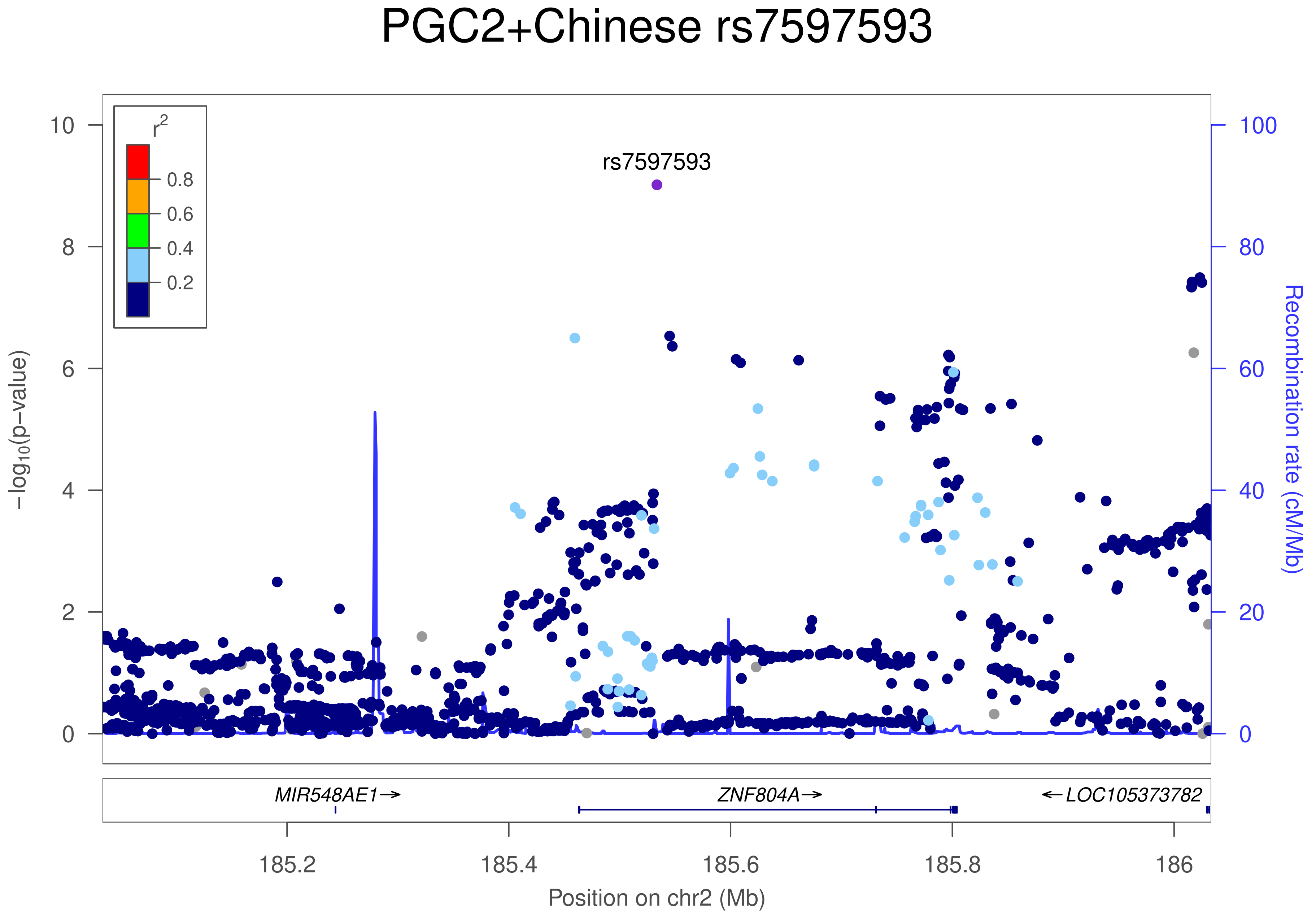

PGC2+Chinese rs2381759
r²
0.8
0.6
0.4
0.2
rs2381759
−log₁₀(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
146
146.2
146.4
146.6
146.8
Position on chr2 (Mb)

Chinese−only rs2381759

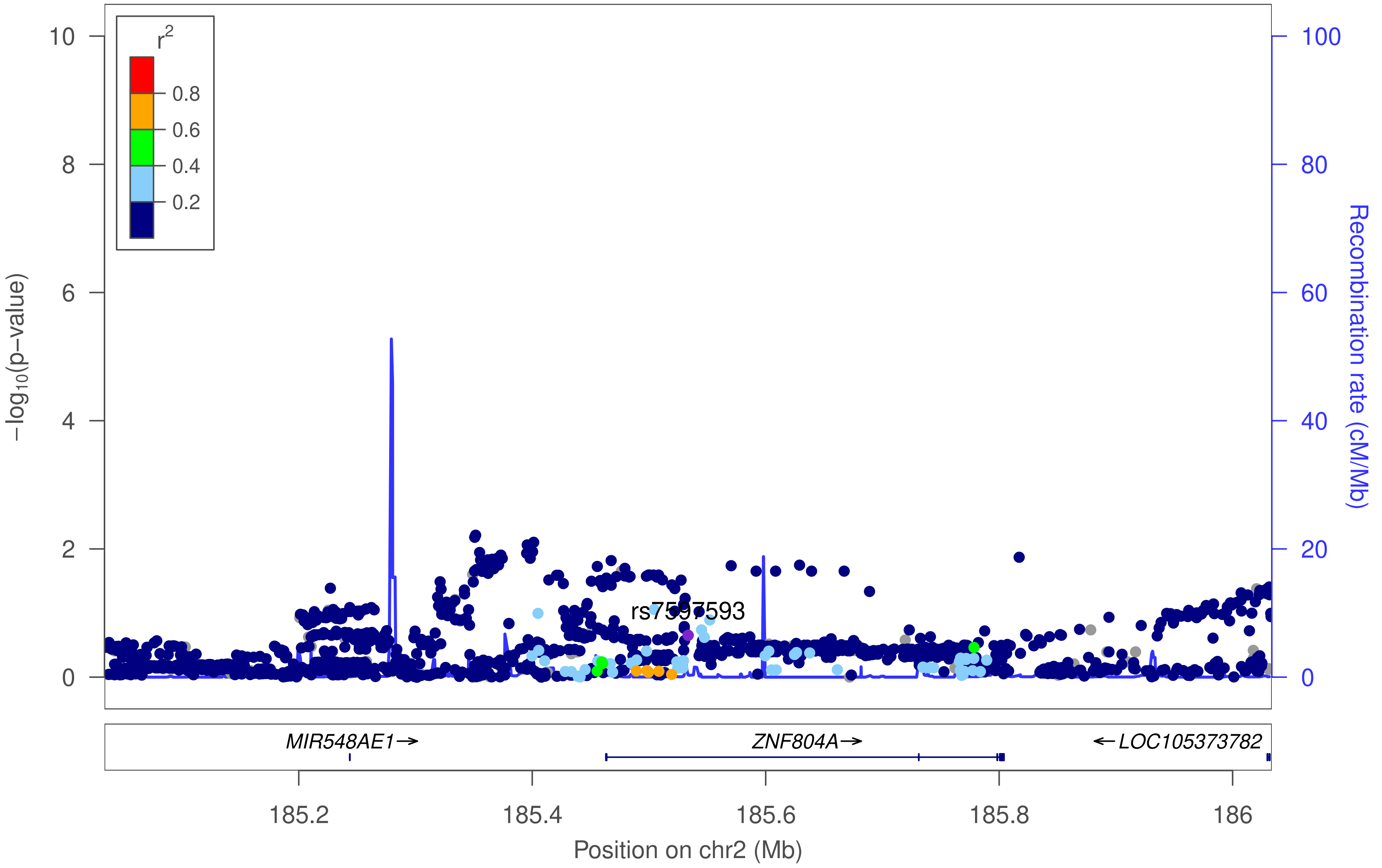


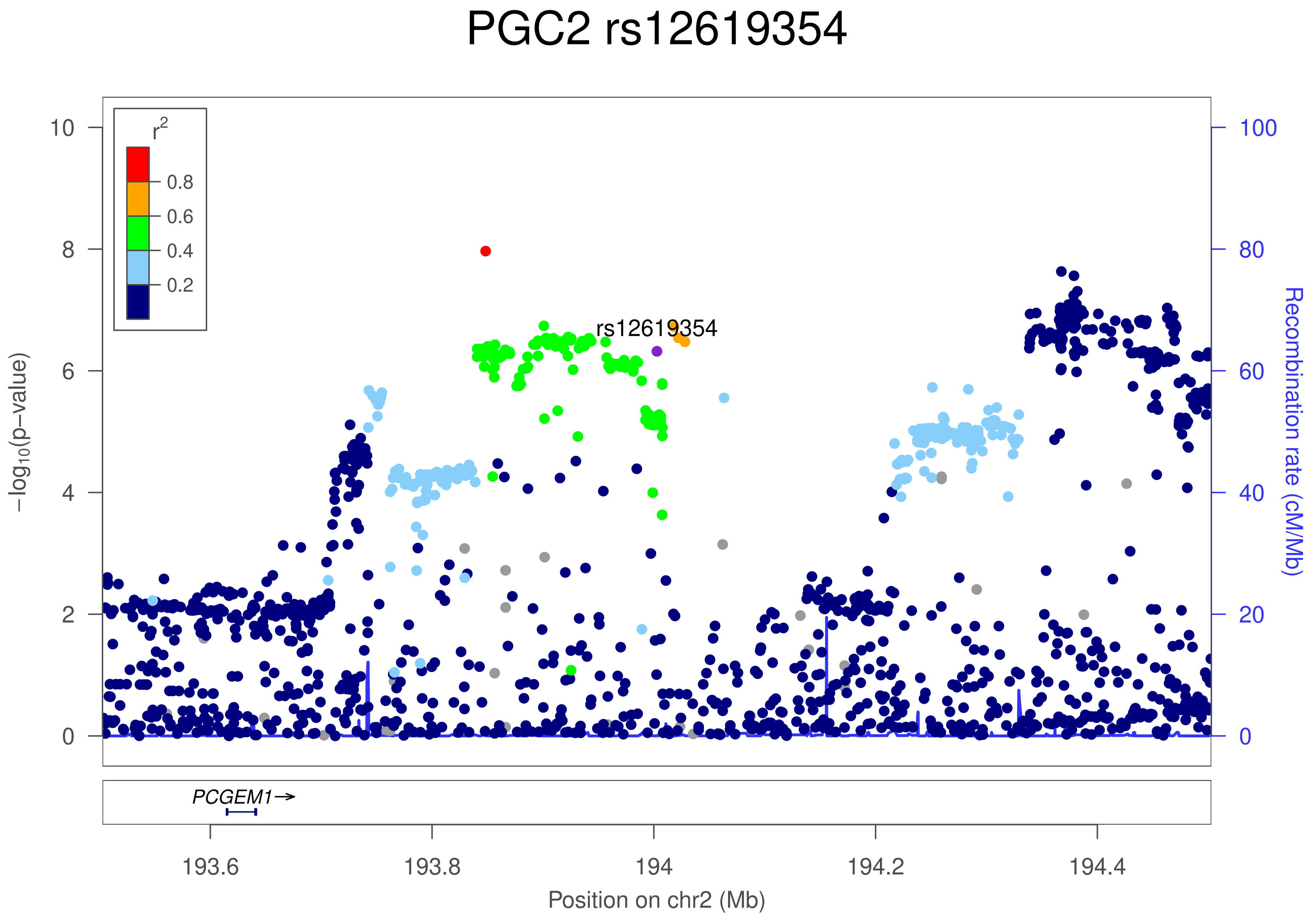
PGC2 rs7597593

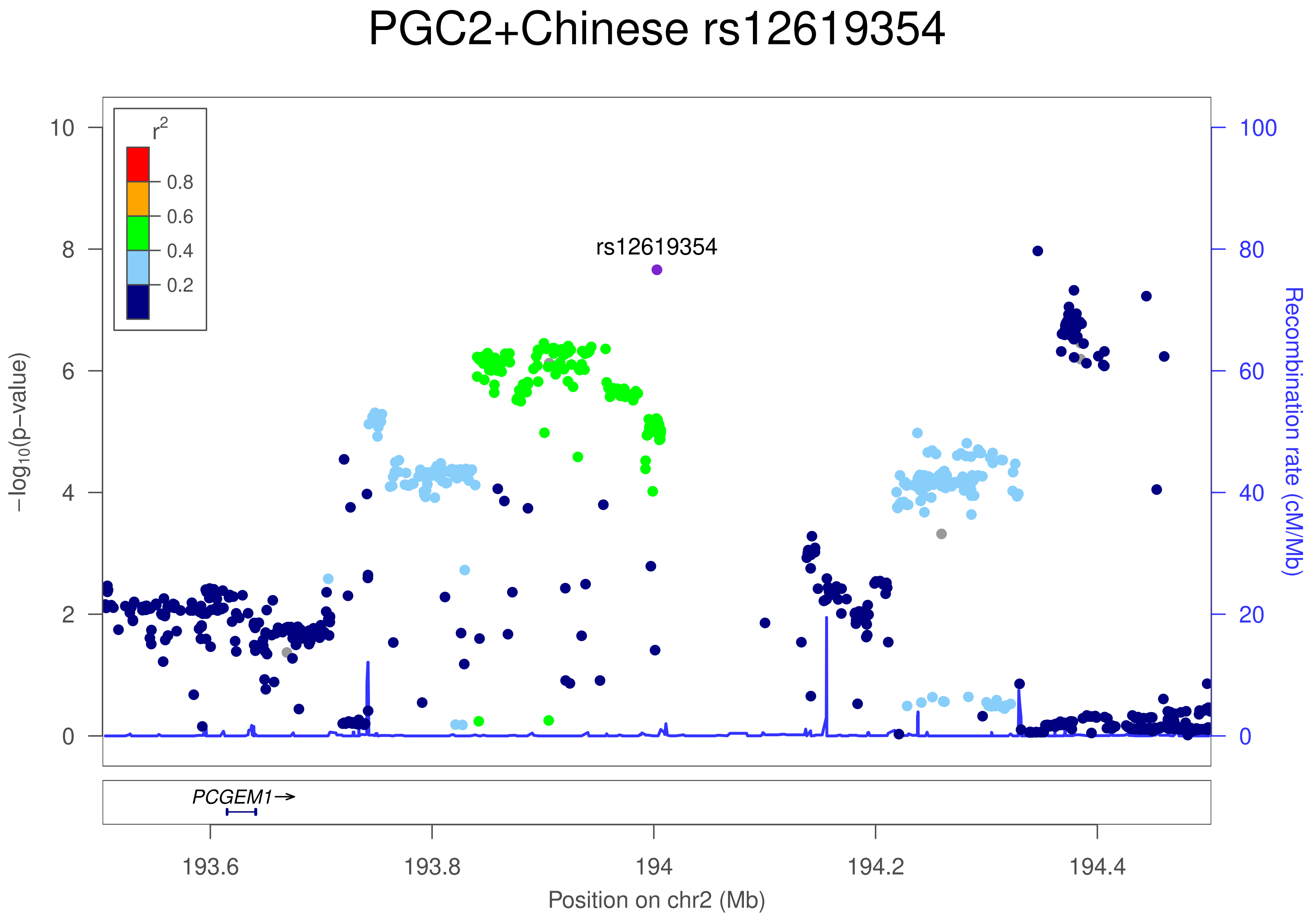


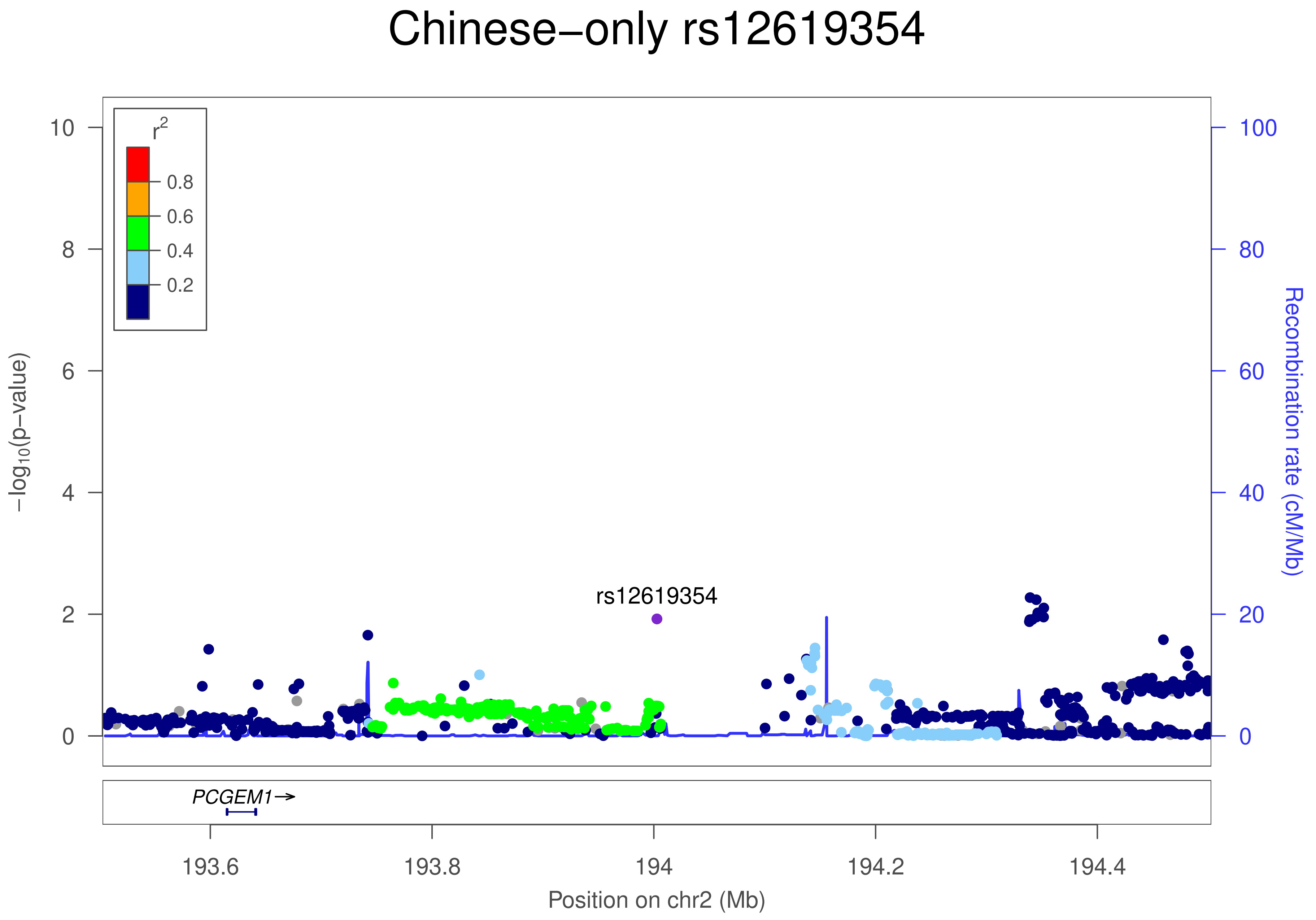

PGC2+Chinese rs7597593
rs7597593
r2
0.8
0.6
0.4
0.2
−log10(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
MIR548AE1→
ZNF804A→
←LOC105373782
185.2
185.4
185.6
185.8
186
Position on chr2 (Mb)

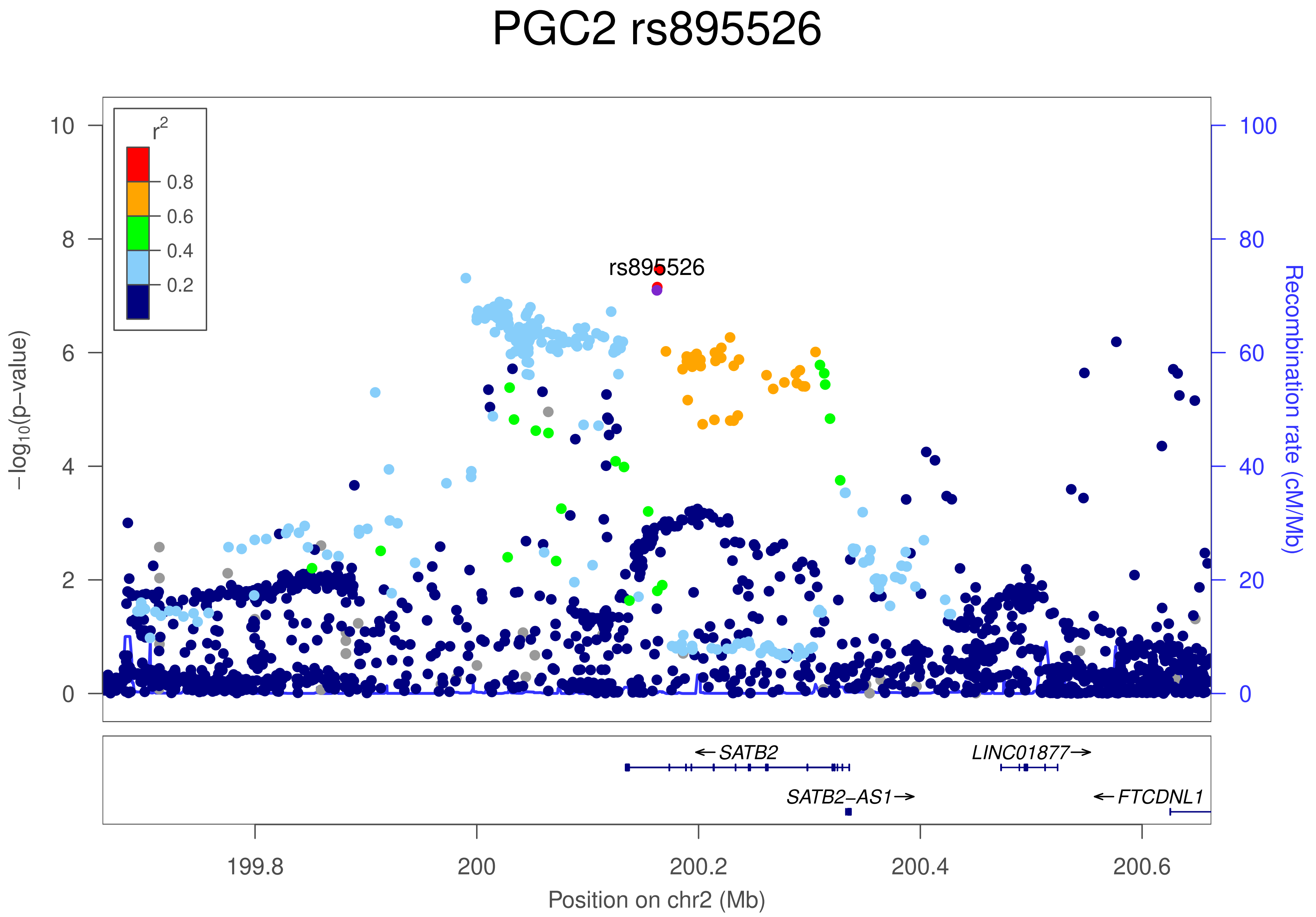
Chinese−only rs7597593

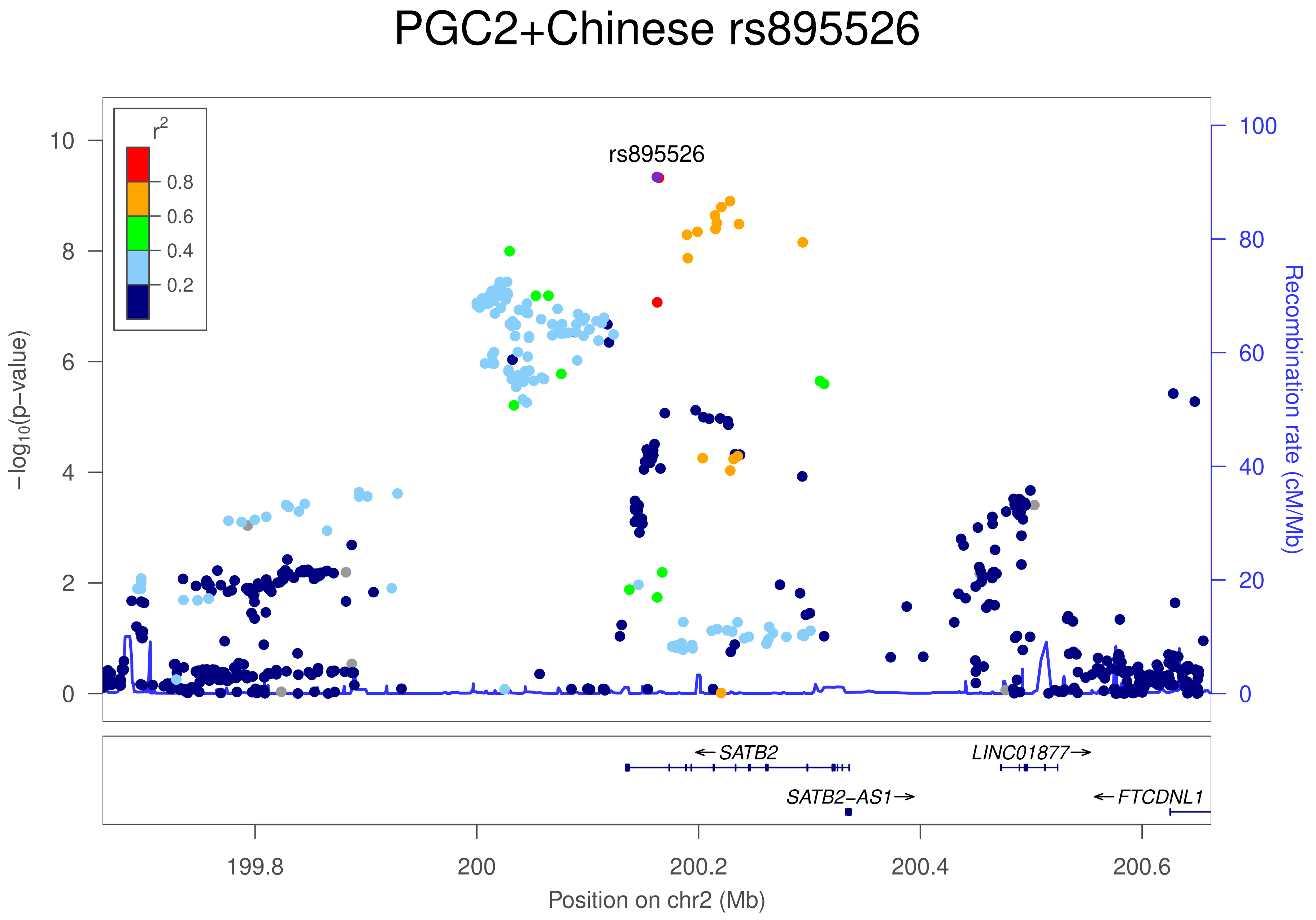



PGC2 rs12619354
r2
0.8
0.6
0.4
0.2
rs12619354
−log10(p−value)
10
8
6
4
2
0
100
80
60
40
20
0
Recombination rate (cM/Mb)
PCGEM1→
193.6
193.8
194
194.2
194.4
Position on chr2 (Mb)

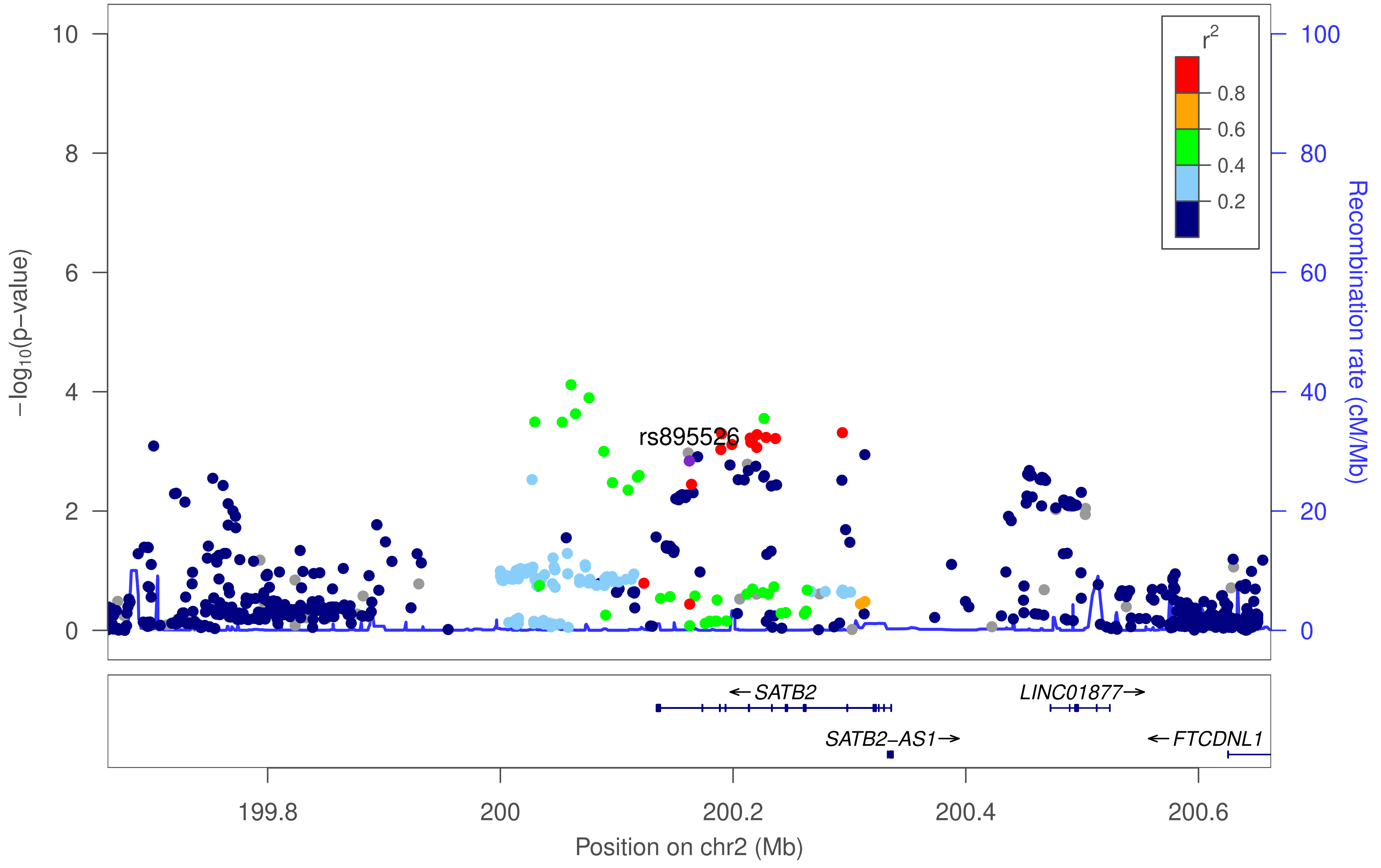

PGC2+Chinese rs12619354
r^2
0.8
0.6
0.4
0.2
rs12619354
−log$_{10}$(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
PCGEM1→
193.6
193.8
194
194.2
194.4
Position on chr2 (Mb)

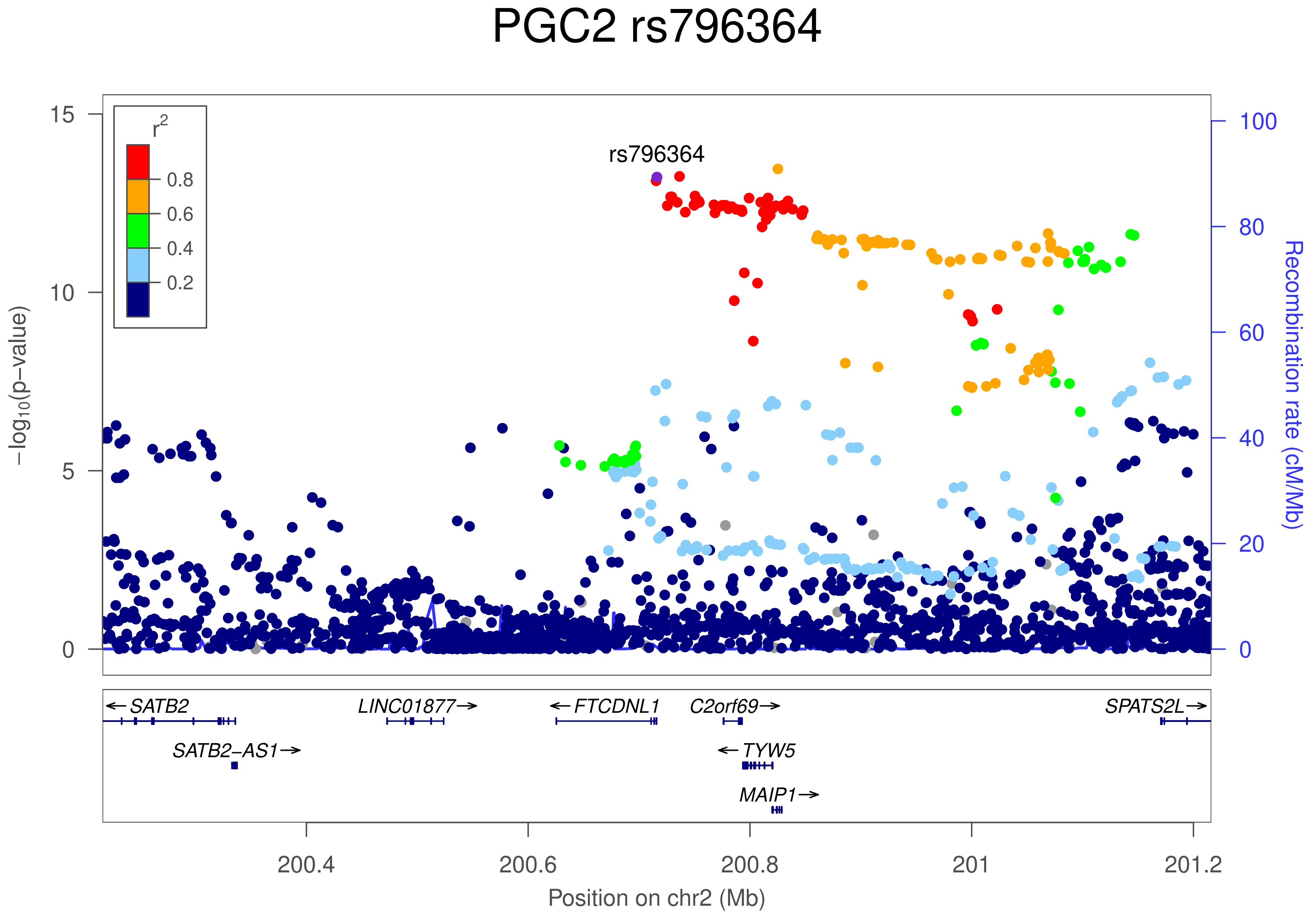

Chinese−only rs12619354
r²
0.8
0.6
0.4
0.2
10
8
6
4
2
0
−log₁₀(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
rs12619354
PCGEM1→
193.6
193.8
194
194.2
194.4
Position on chr2 (Mb)

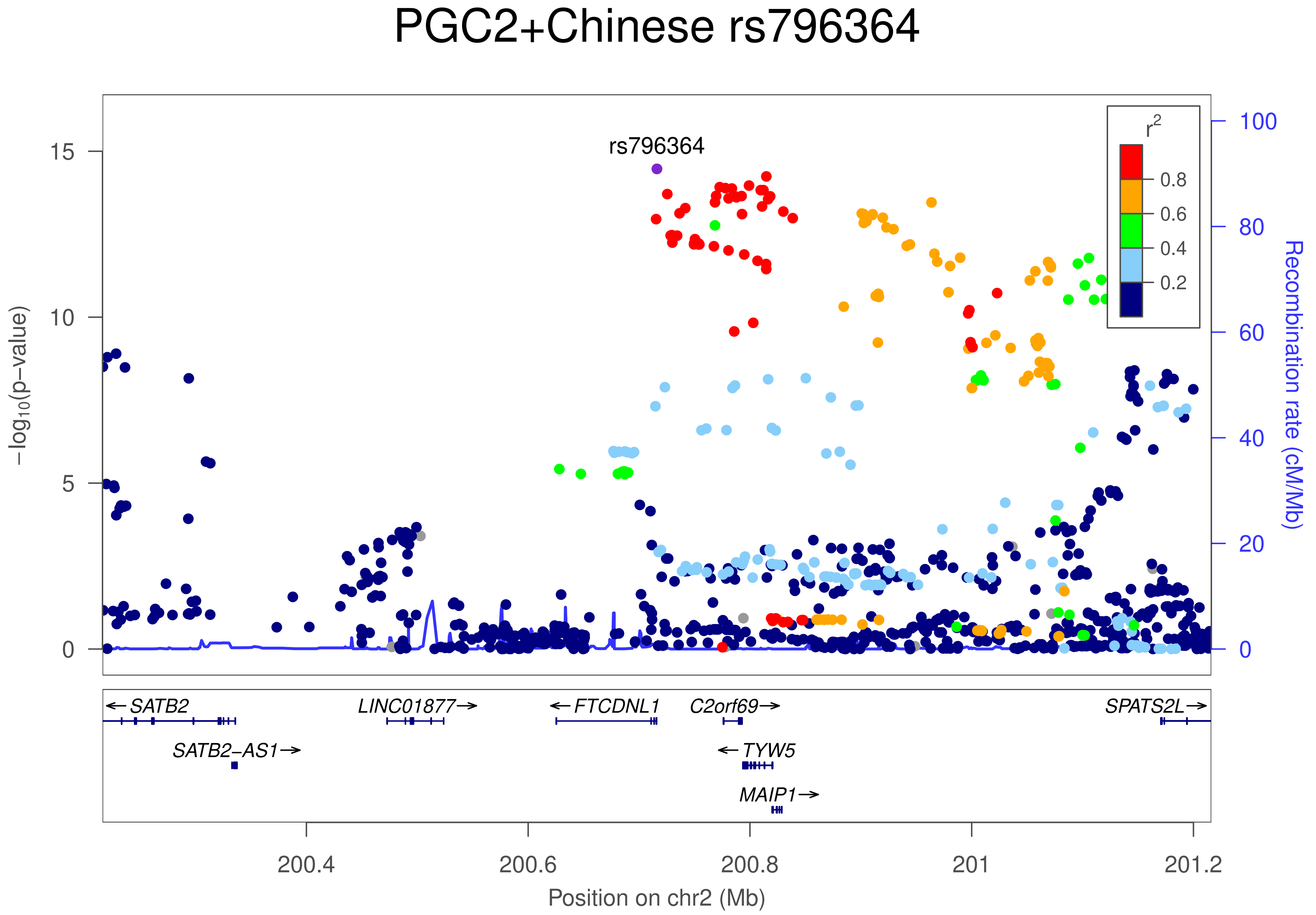

PGC2 rs895526
r^2
0.8
0.6
0.4
0.2
rs895526
10
8
6
4
2
0
−log10(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
←SATB2
LINC01877→
SATB2−AS1→
←FTCDNL1
199.8
200
200.2
200.4
200.6
Position on chr2 (Mb)


PGC2+Chinese rs895526
r²
0.8
0.6
0.4
0.2
rs895526
−log₁₀(p−value)
10
8
6
4
2
0
100
80
60
40
20
0
Recombination rate (cM/Mb)
←SATB2
LINC01877→
SATB2−AS1→
←FTCDNL1
199.8
200
200.2
200.4
200.6
Position on chr2 (Mb)

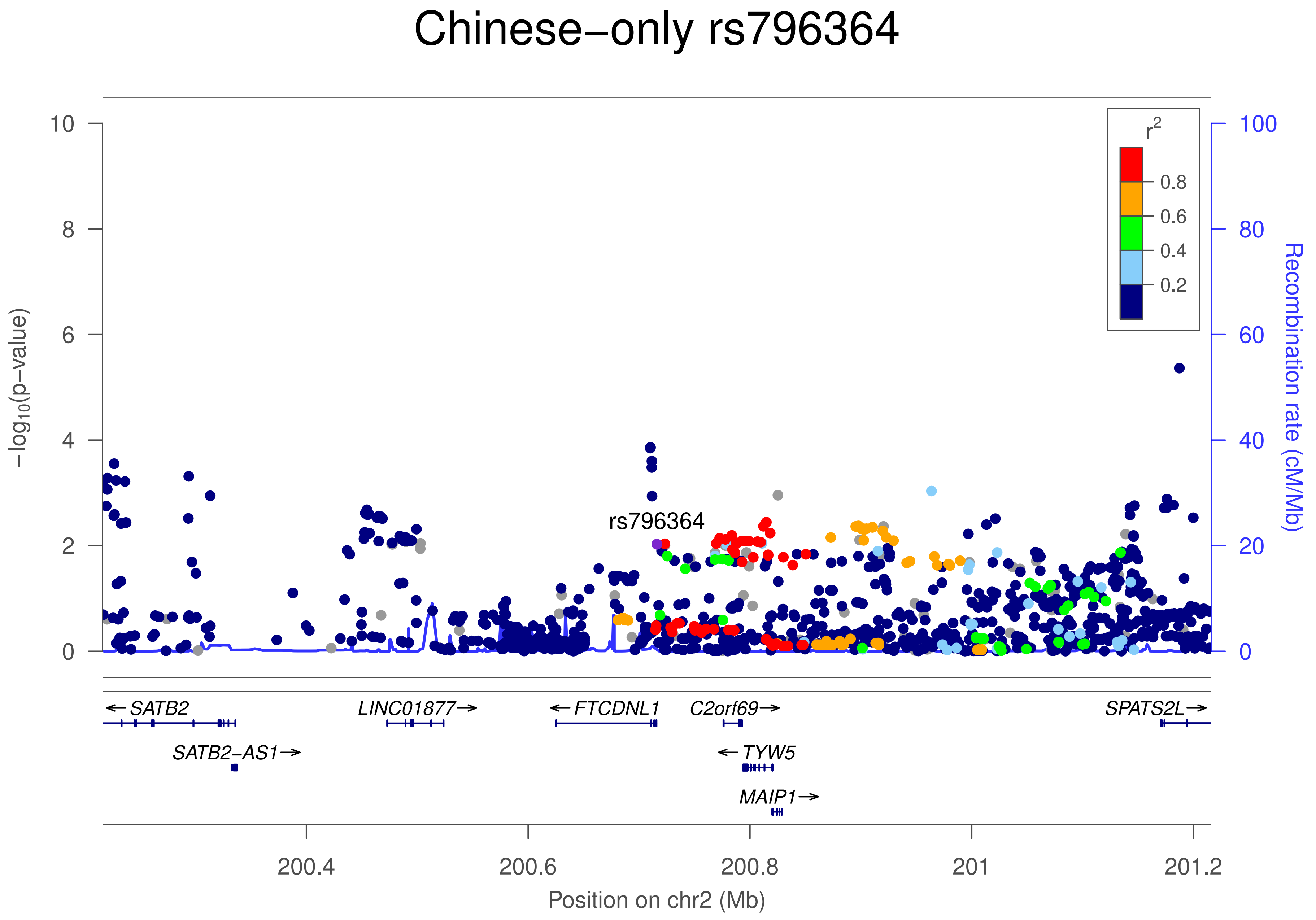
Chinese−only rs895526




PGC2 rs796364

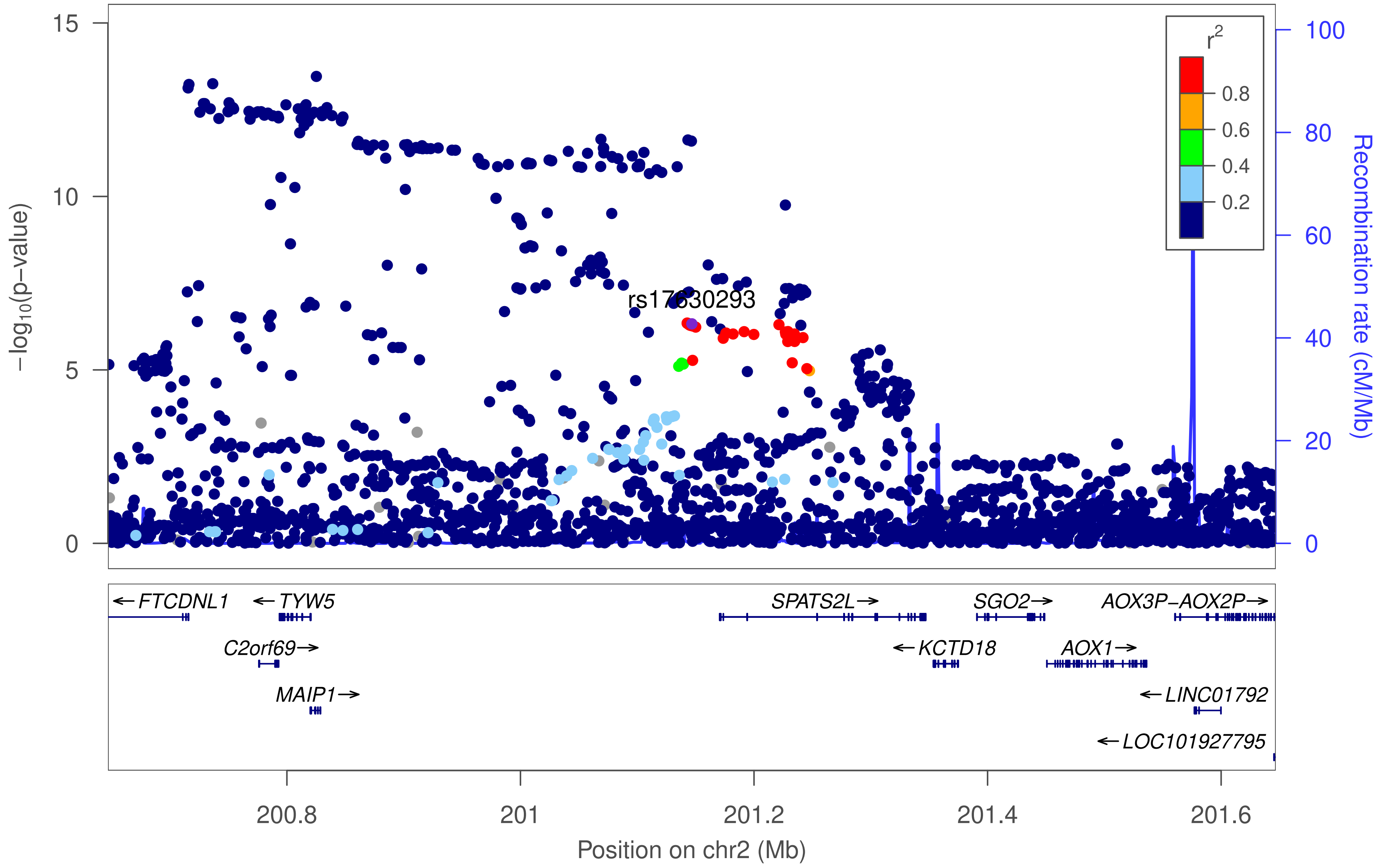


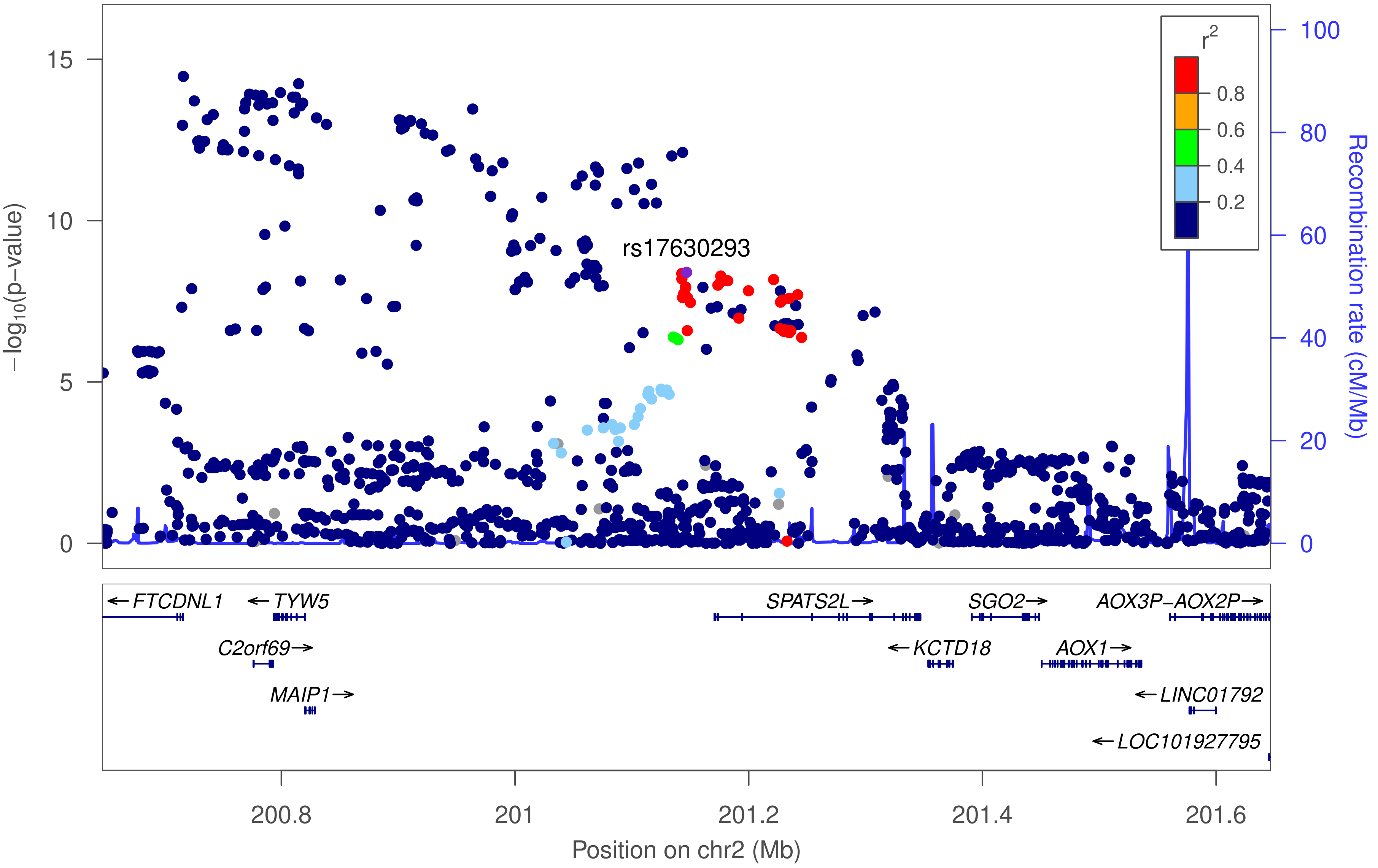
PGC2+Chinese rs796364
rs796364
r²
0.8
0.6
0.4
0.2
15
10
5
0
−log10(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
← SATB2
LINC01877→
← FTCDNL1
C2orf69→
SPATS2L→
SATB2−AS1→
← TYW5
MAIP1→
200.4
200.6
200.8
201
201.2
Position on chr2 (Mb)



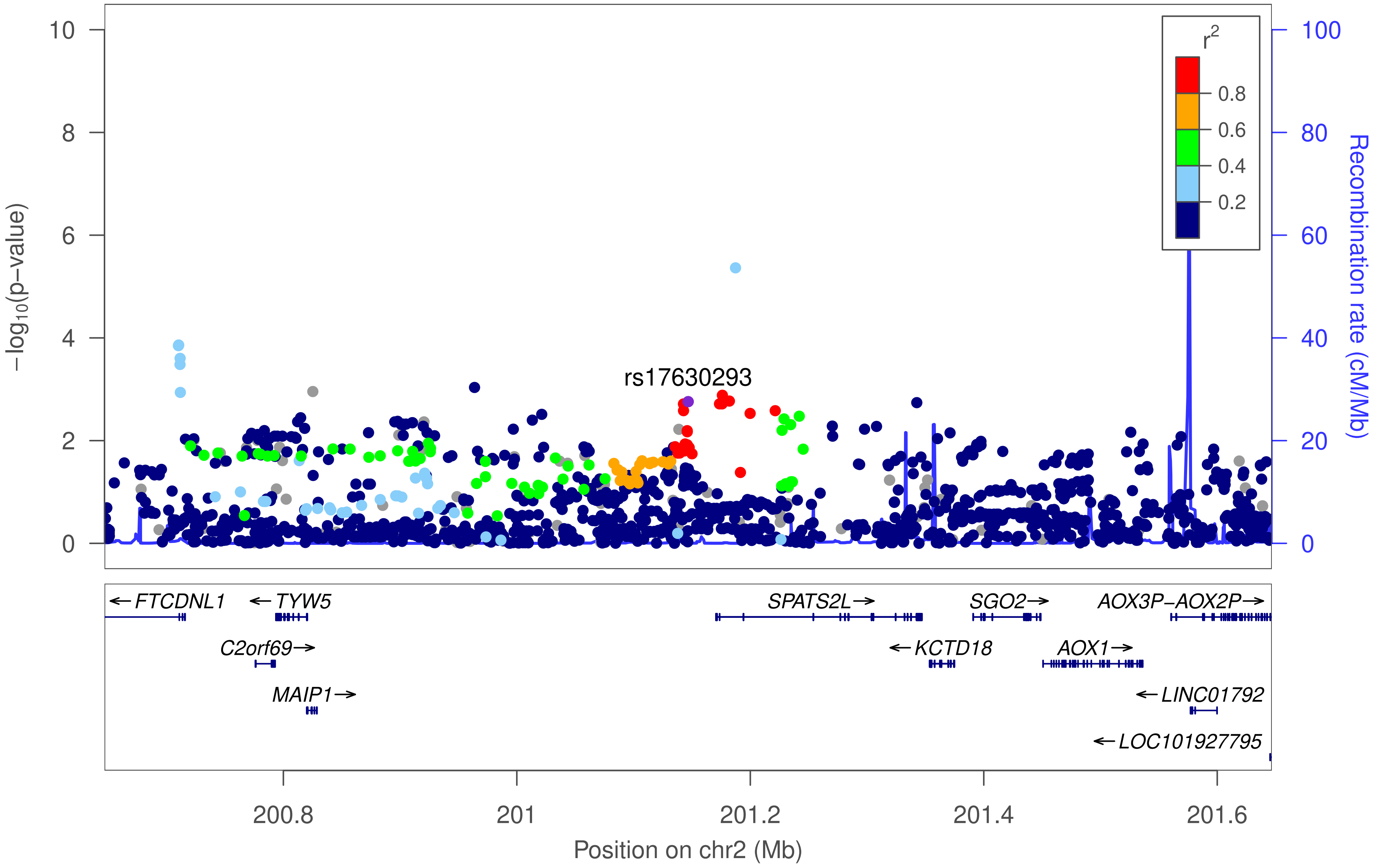
Chinese−only rs796364
−log10(p−value)
10
8
6
4
2
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
r2
0.8
0.6
0.4
0.2
rs796364
← SATB2
SATB2−AS1 →
LINC01877 →
← FTCDNL1
C2orf69 →
← TYW5
MAIP1 →
SPATS2L →
200.4
200.6
200.8
201
201.2
Position on chr2 (Mb)

PGC2 rs17630293

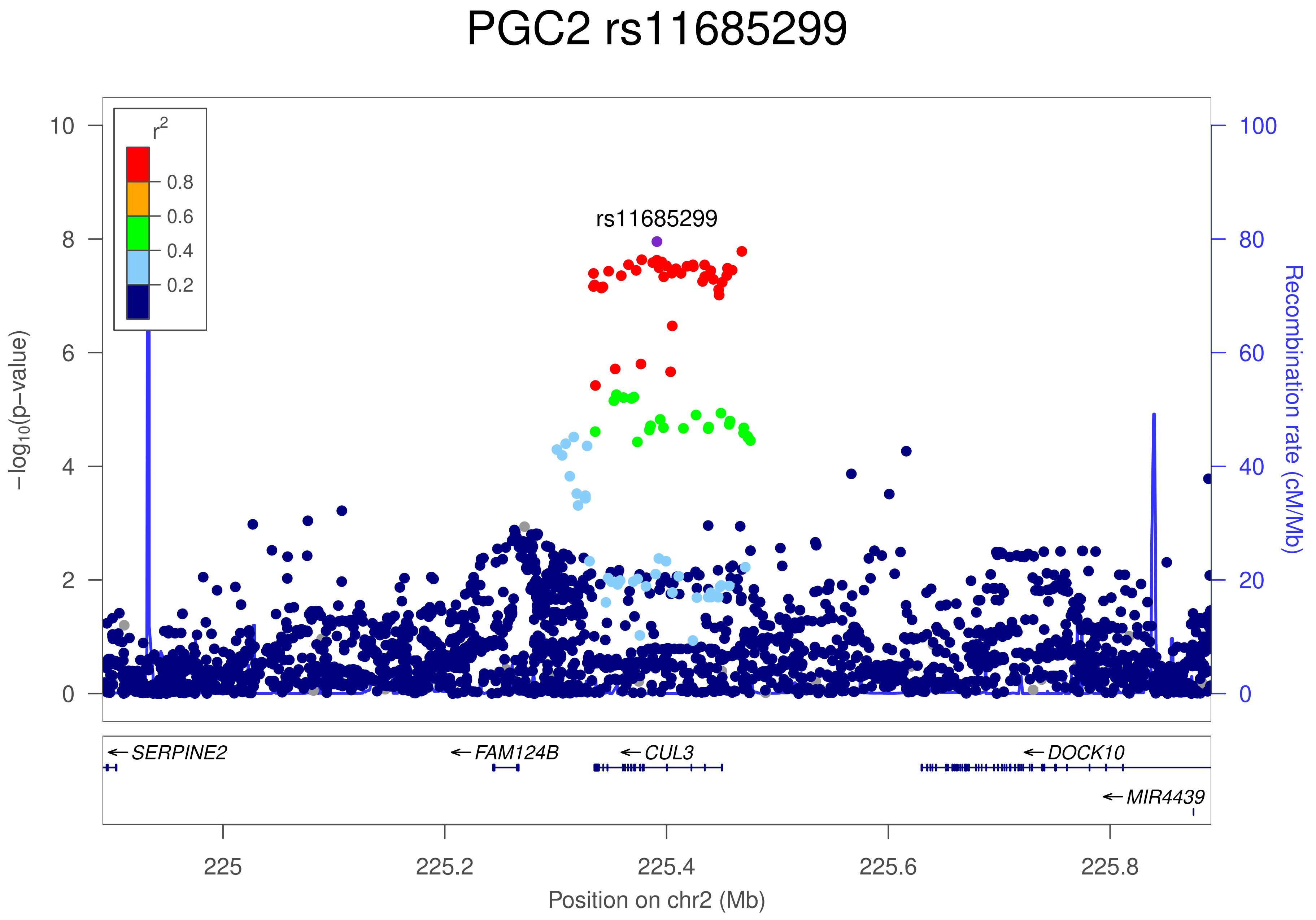


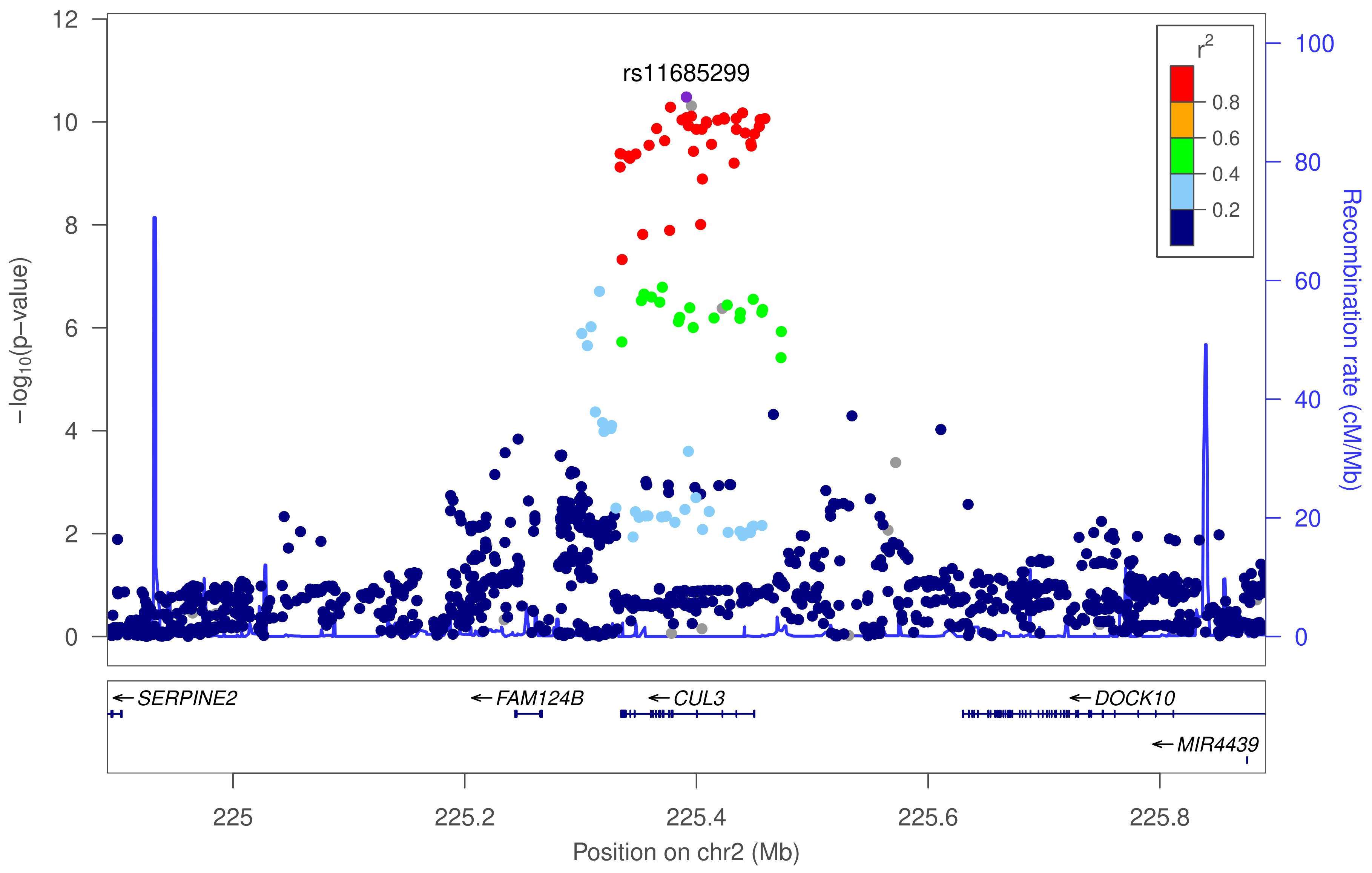


PGC2+Chinese rs17630293



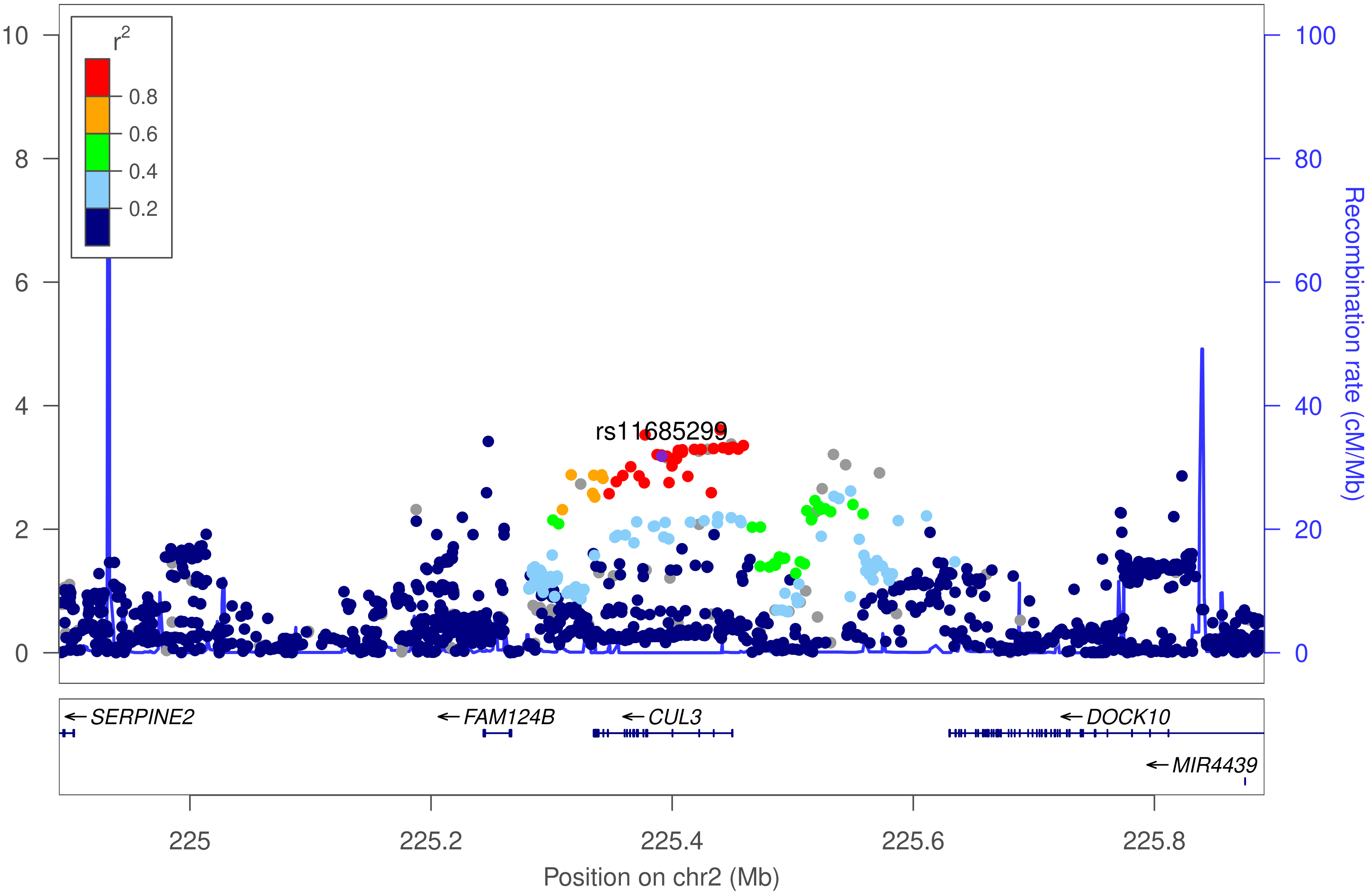
Chinese–only rs17630293


PGC2 rs11685299
r2
0.8
0.6
0.4
0.2
rs11685299
10
8
6
4
2
0
−log10(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
SERPINE2
FAM124B
CUL3
DOCK10
MIR4439
225
225.2
225.4
225.6
225.8
Position on chr2 (Mb)

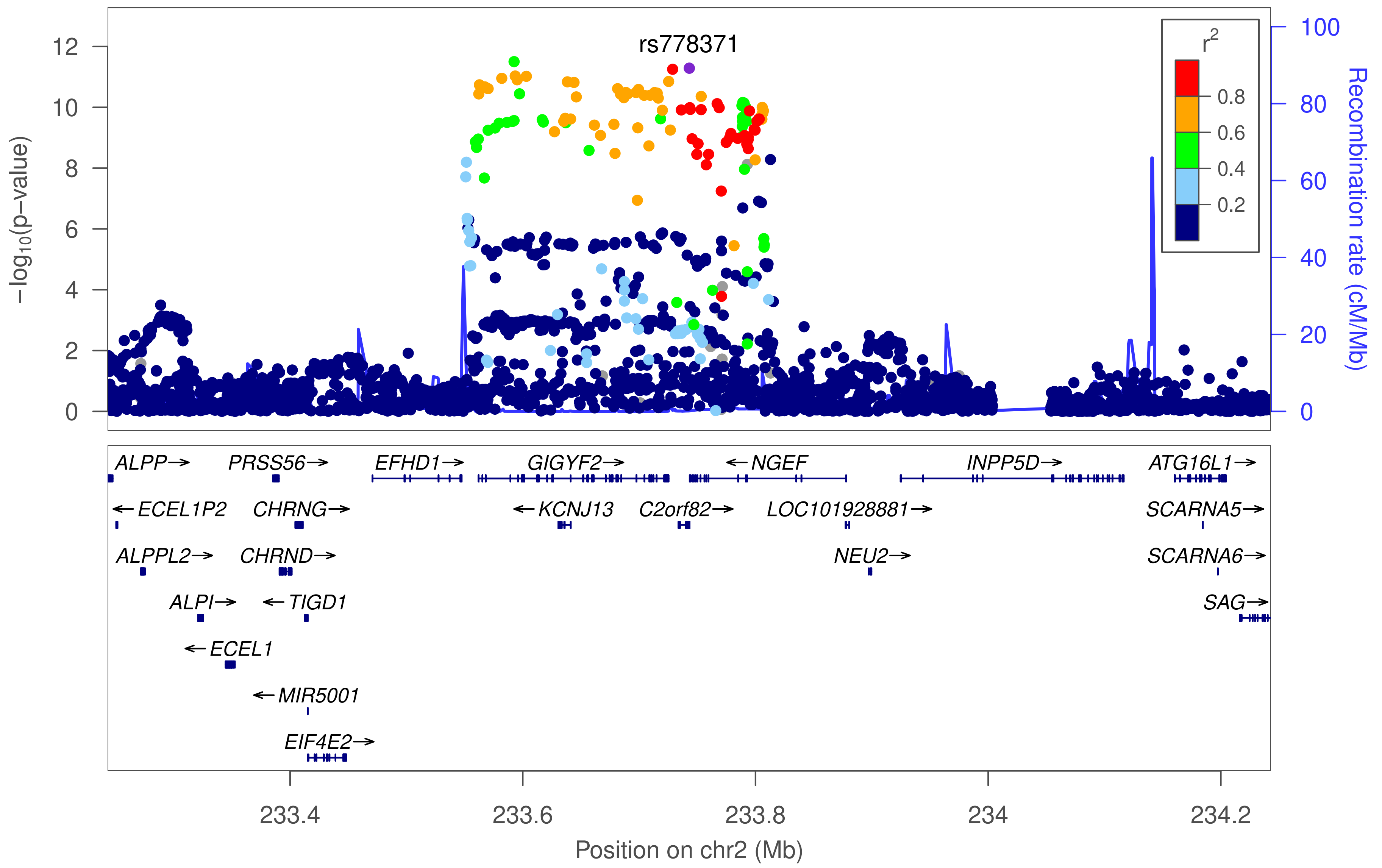


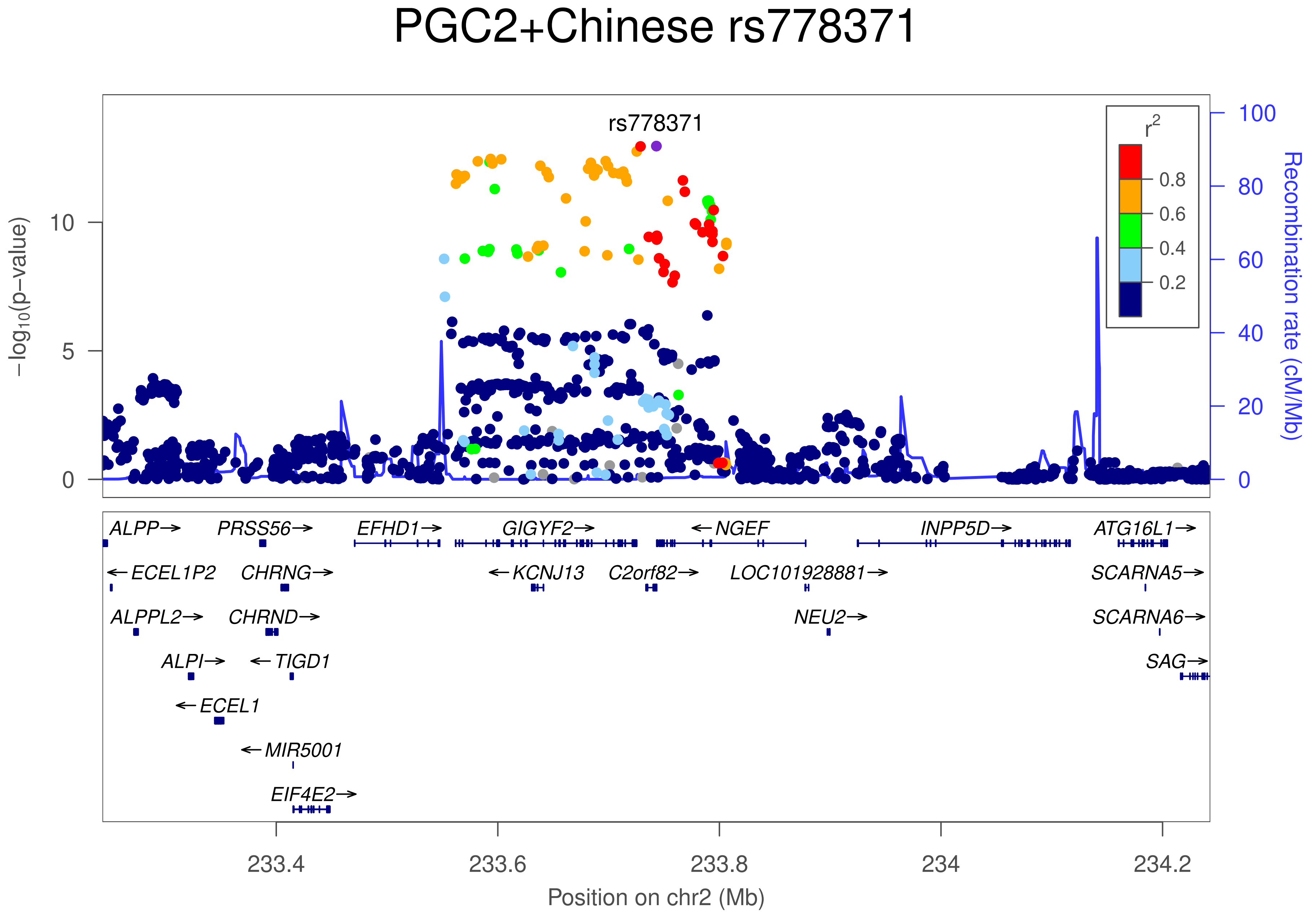
PGC2+Chinese rs11685299

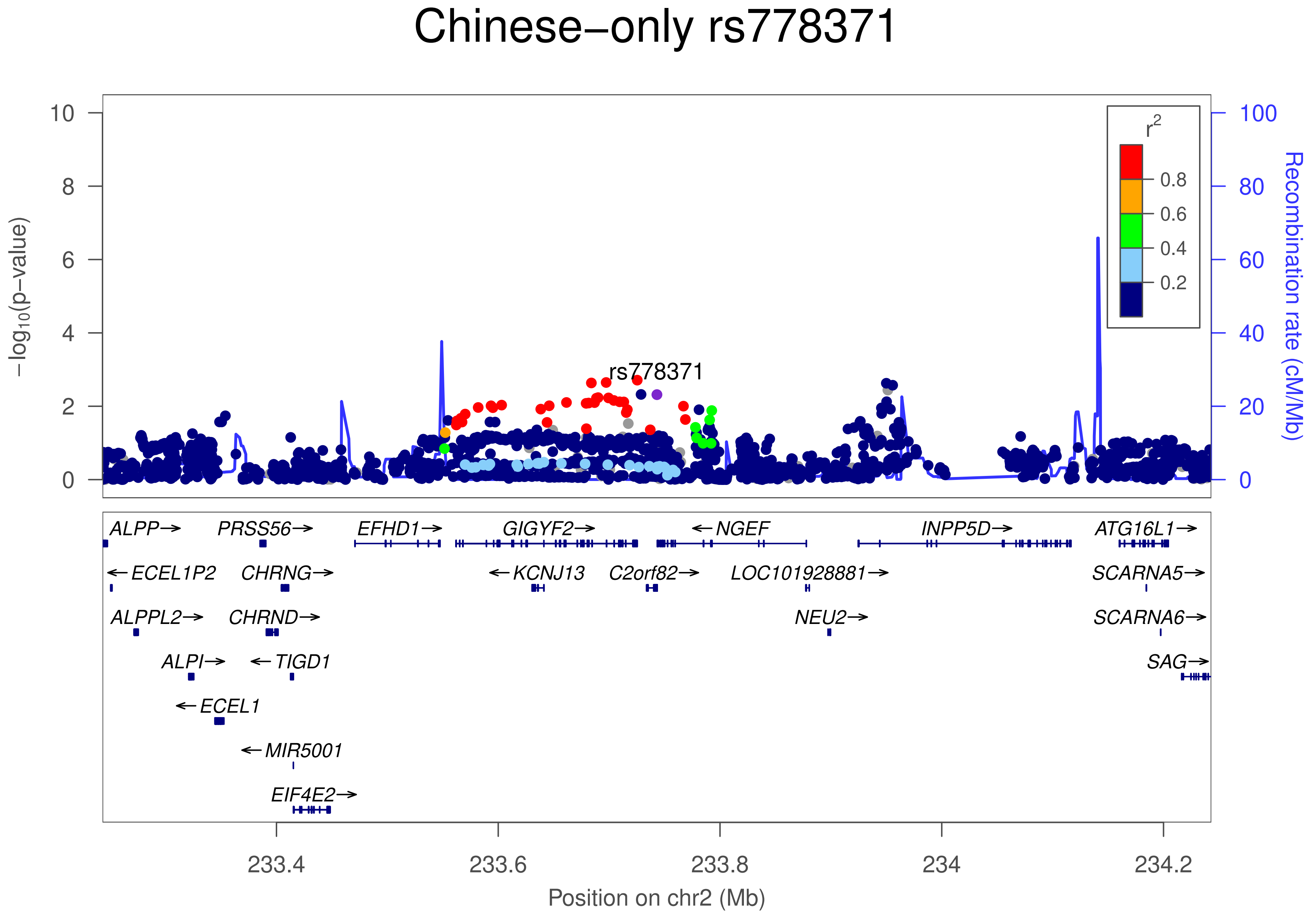
Chinese–only rs11685299



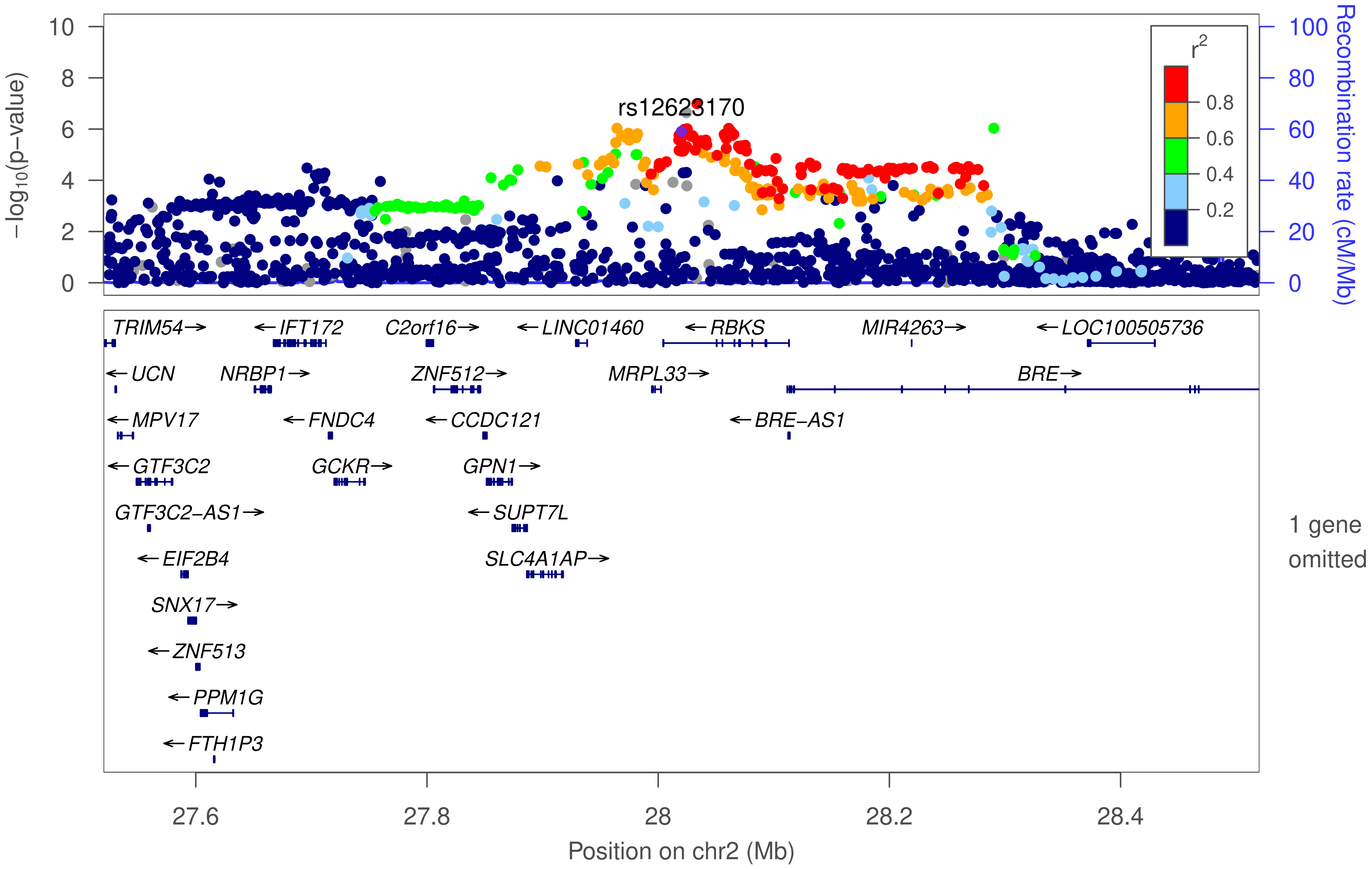
PGC2 rs778371

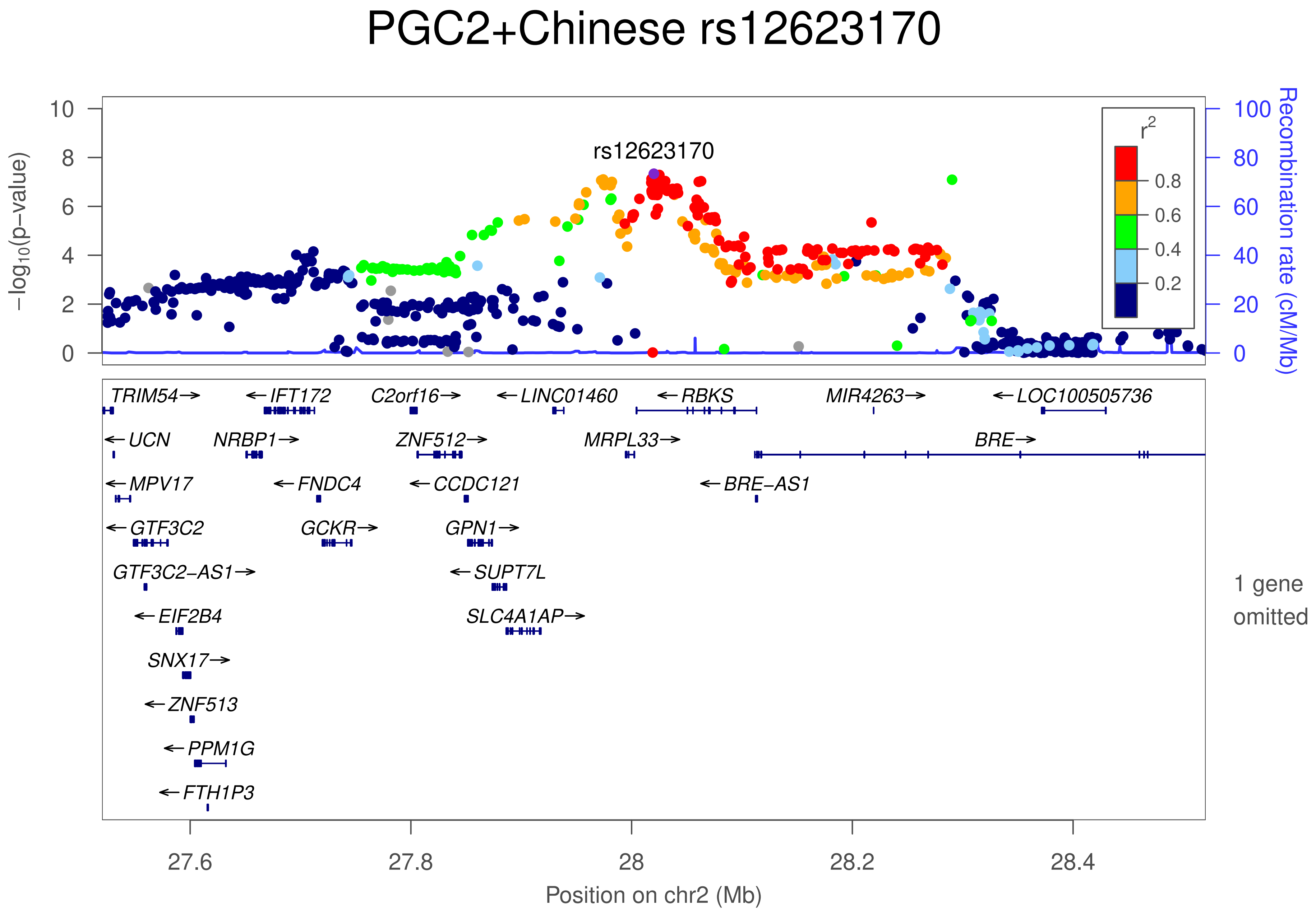



PGC2+Chinese rs778371
rs778371
r2
0.8
0.6
0.4
0.2
−log10(p−value)
10
5
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
ALPP→
PRSS56→
EFHD1→
GIGYF2→
←NGEF
INPP5D→
ATG16L1→
←ECEL1P2
CHRNG→
←KCNJ13
C2orf82→
LOC101928881→
SCARNA5→
ALPPL2→
CHRND→
NEU2→
SCARNA6→
ALPI→
←TIGD1
SAG→
←ECEL1
←MIR5001
EIF4E2→
233.4
233.6
233.8
234
234.2
Position on chr2 (Mb)

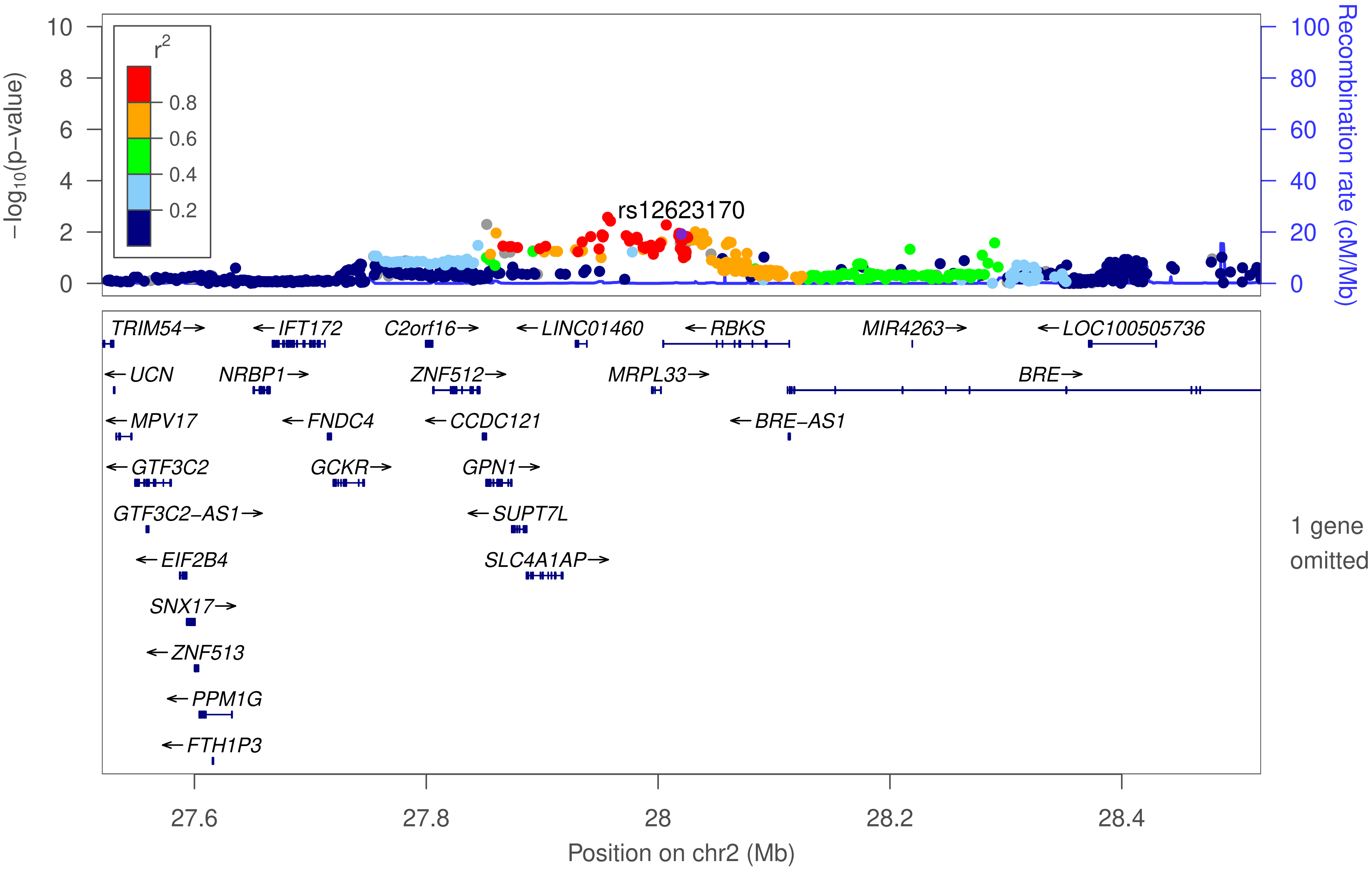

Chinese–only rs778371
rs778371
$-\log_{10}$(p–value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
r^2
0.8
0.6
0.4
0.2
ALPP→
PRSS56→
EFHD1→
GIGYF2→
←NGEF
INPP5D→
ATG16L1→
←ECEL1P2
CHRNG→
←KCNJ13
C2orf82→
LOC101928881→
SCARNA5→
ALPPL2→
CHRND→
NEU2→
SCARNA6→
ALPI→
←TIGD1
SAG→
←ECEL1
←MIR5001
EIF4E2→
233.4
233.6
233.8
234
234.2
Position on chr2 (Mb)

PGC2 rs12623170

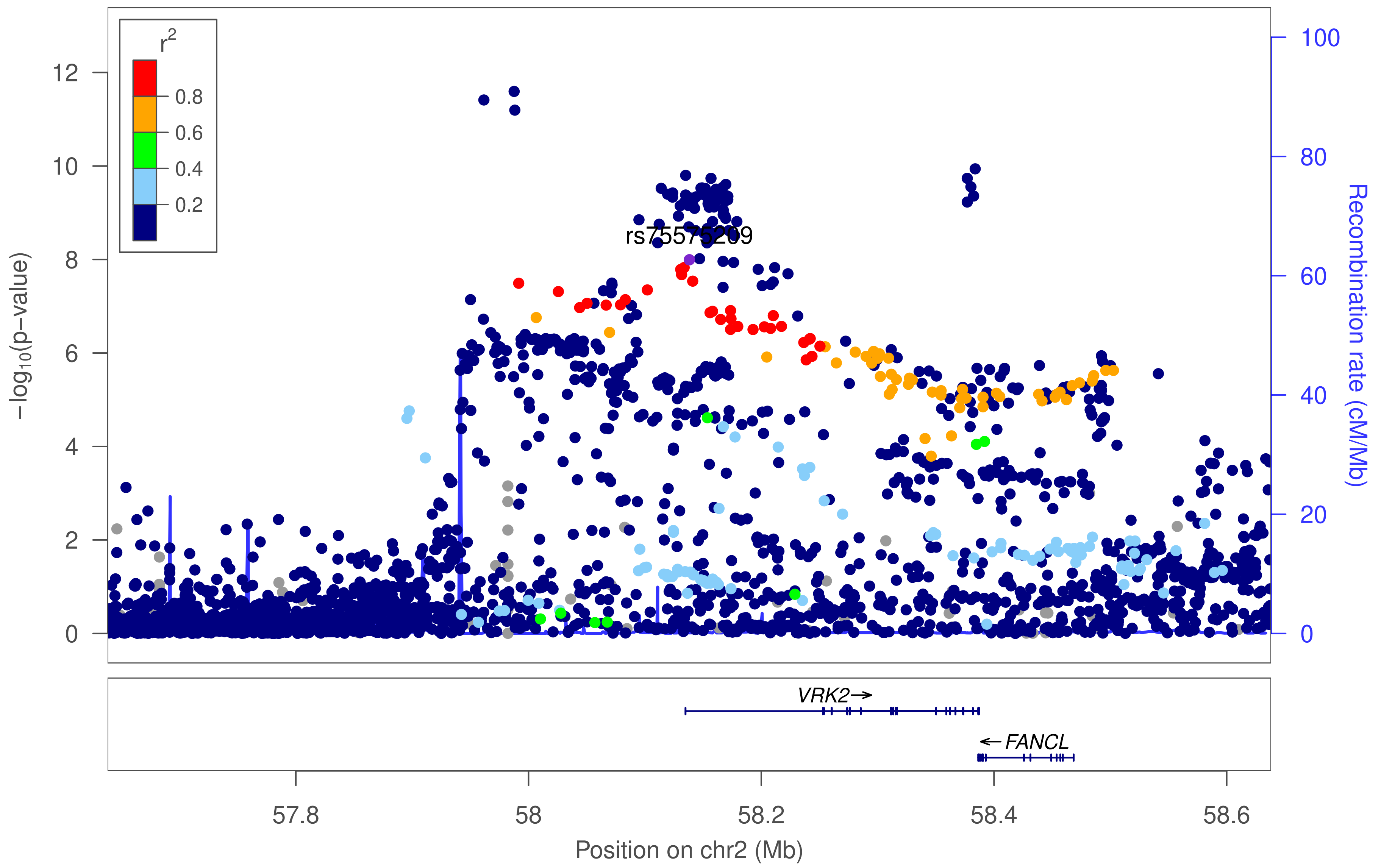


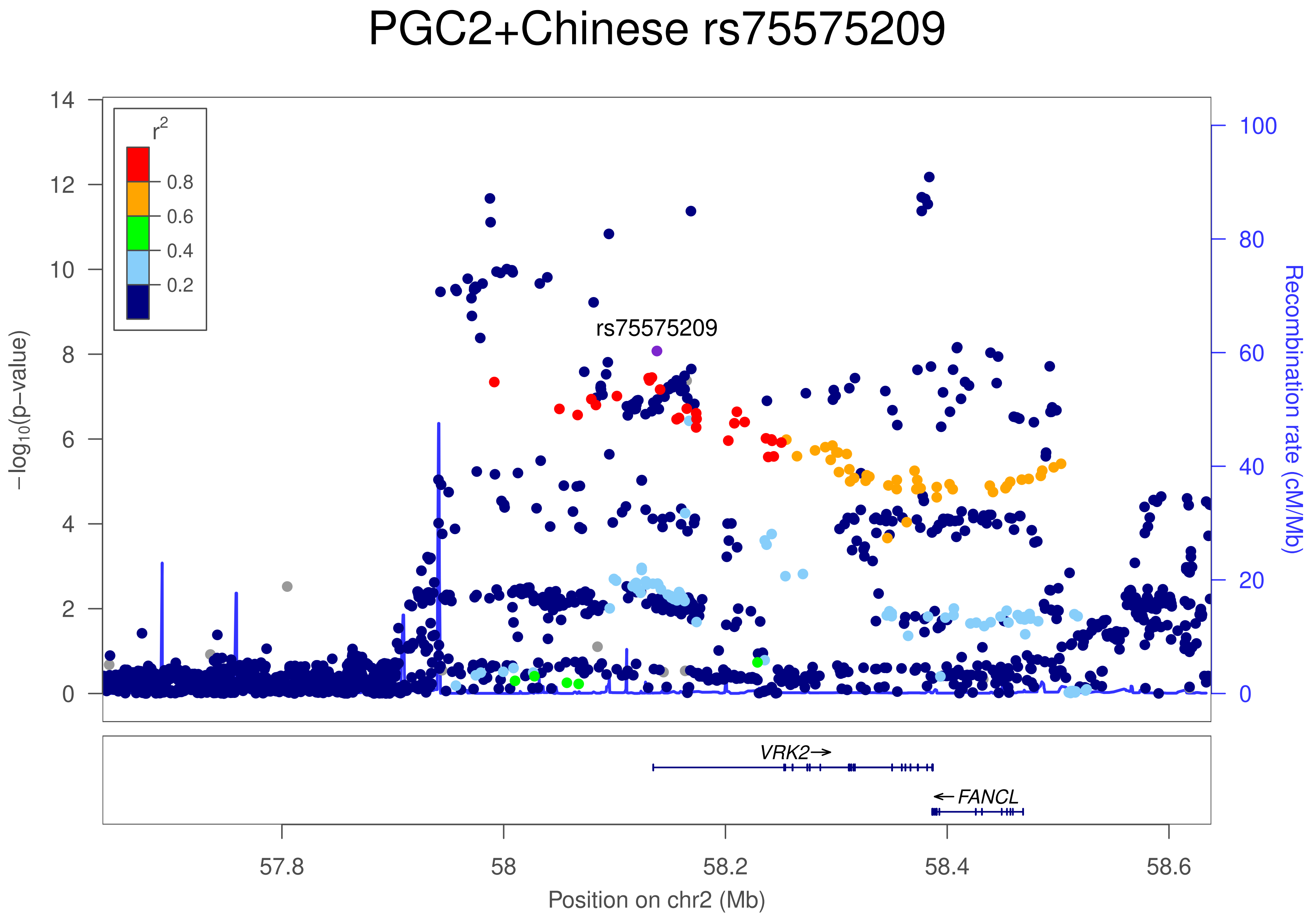

PGC2+Chinese rs12623170
rs12623170
−log10(p−value)
10
8
6
4
2
0
100
80
60
40
20
0
Recombination rate (cM/Mb)
r2
0.8
0.6
0.4
0.2
TRIM54→
←IFT172
C2orf16→
←LINC01460
←RBKS
MIR4263→
←LOC100505736
←UCN
NRBP1→
ZNF512→
MRPL33→
BRE→
←MPV17
←FNDC4
←CCDC121
←BRE−AS1
←GTF3C2
GCKR→
GPN1→
GTF3C2−AS1→
←SUPT7L
←EIF2B4
SLC4A1AP→
SNX17→
←ZNF513
←PPM1G
←FTH1P3
1 gene omitted
27.6
27.8
28
28.2
28.4
Position on chr2 (Mb)

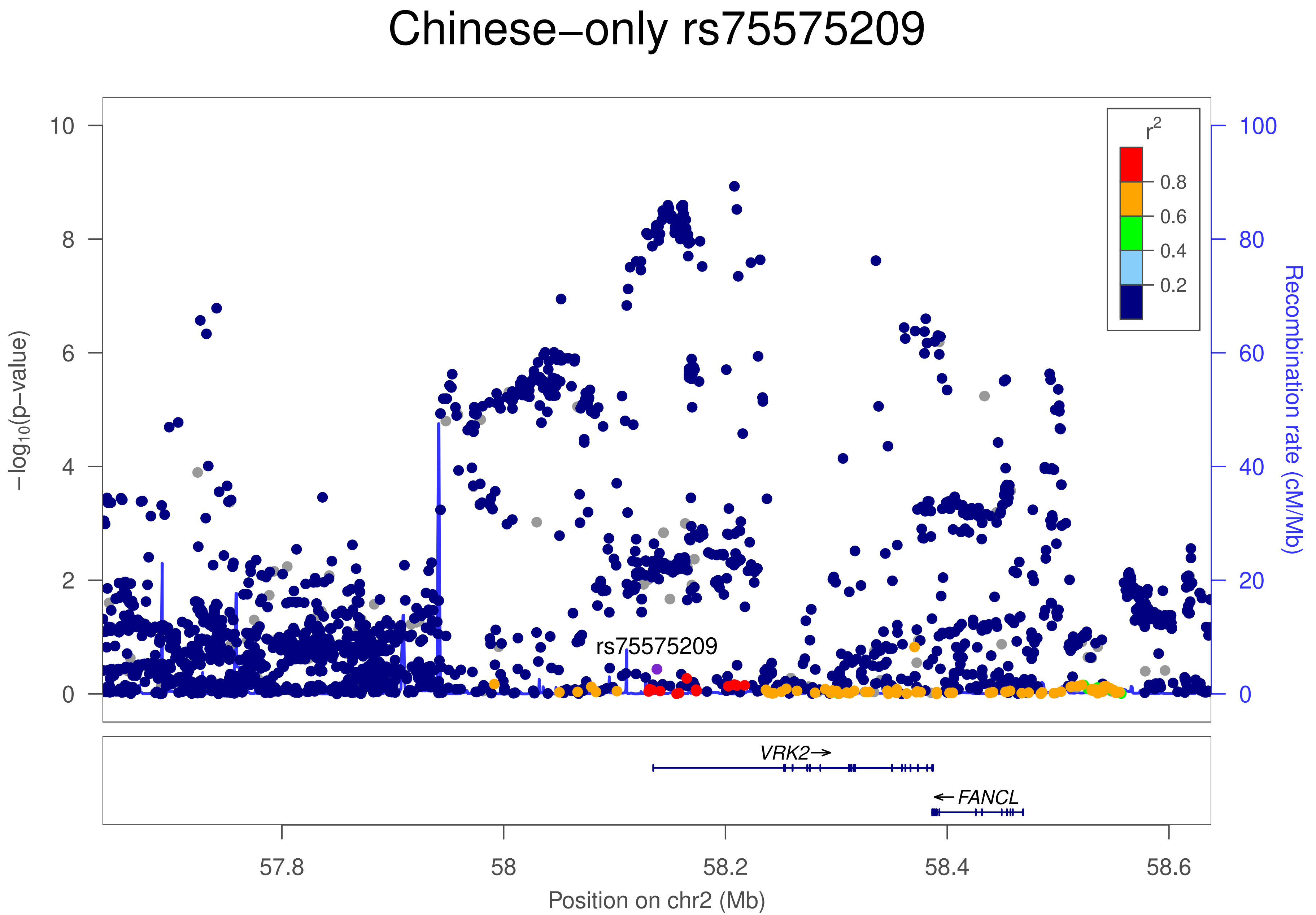
Chinese–only rs12623170



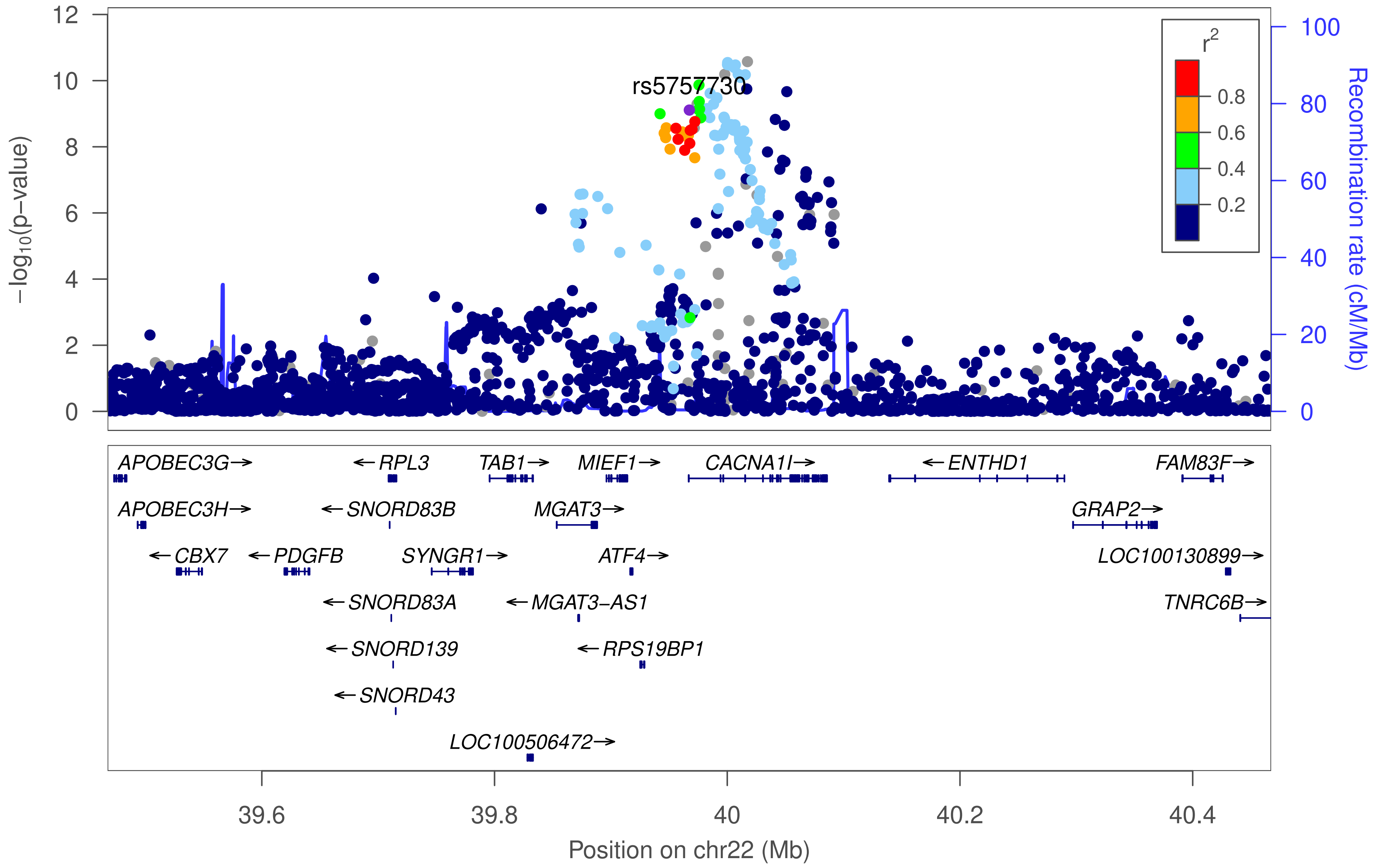
PGC2 rs75575209



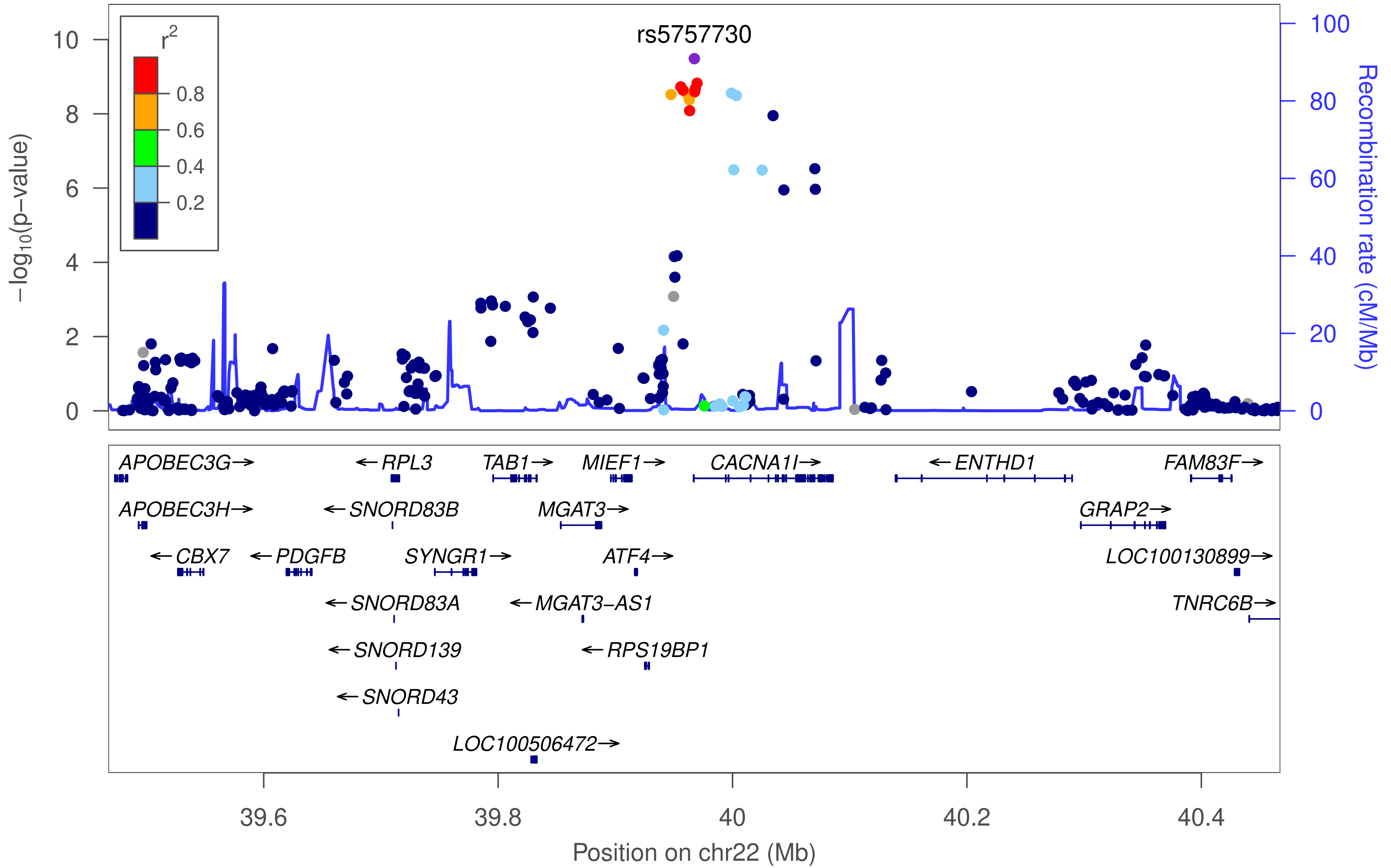

PGC2+Chinese rs75575209
r²
0.8
0.6
0.4
0.2
rs75575209
−log₁₀(p−value)
0
2
4
6
8
10
12
14
Recombination rate (cM/Mb)
0
20
40
60
80
100
VRK2→
←FANCL
57.8
58
58.2
58.4
58.6
Position on chr2 (Mb)

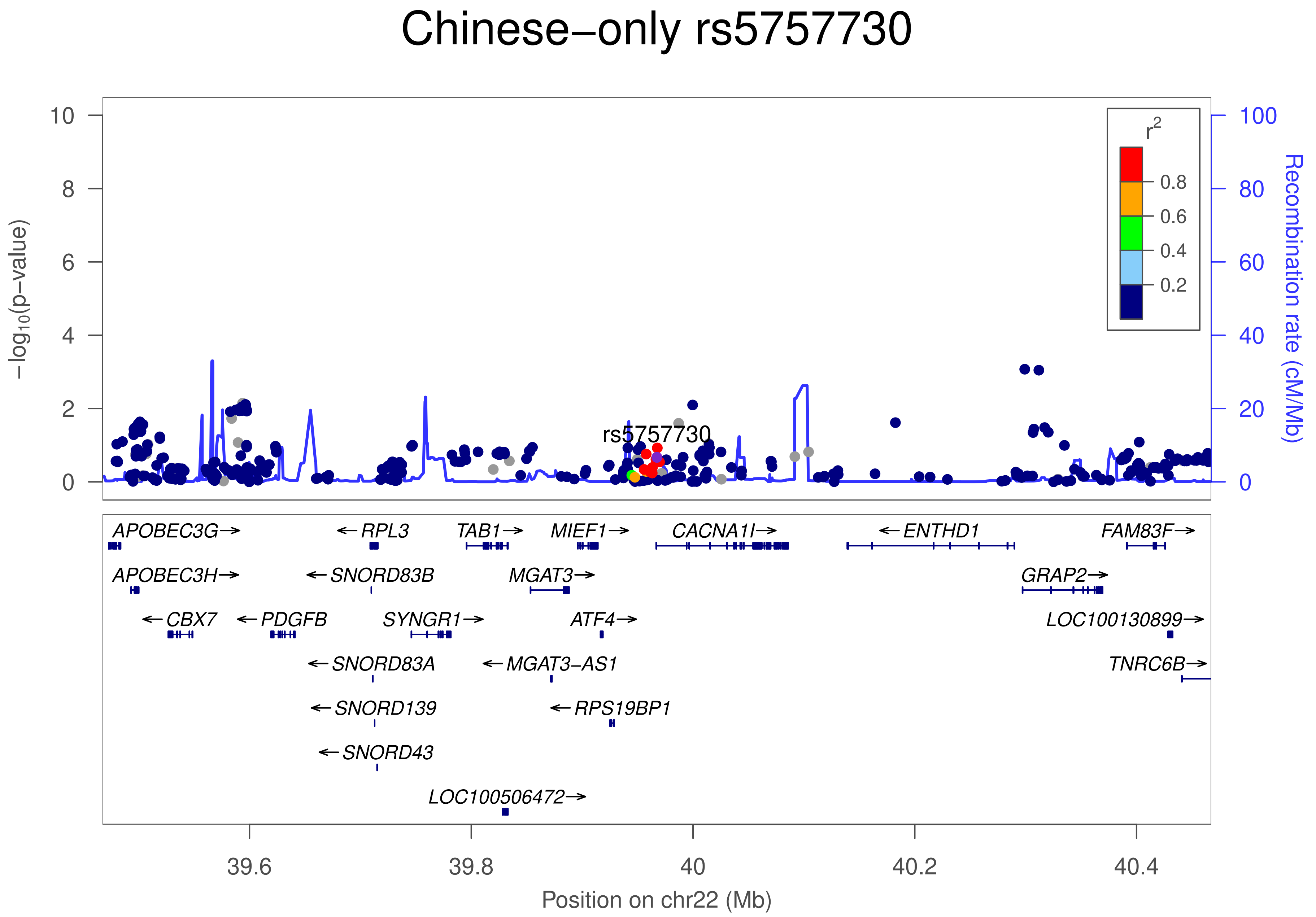

Chinese−only rs75575209
−log10(p−value)
10
8
6
4
2
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
r2
0.8
0.6
0.4
0.2
rs75575209
VRK2→
←FANCL
57.8
58
58.2
58.4
58.6
Position on chr2 (Mb)

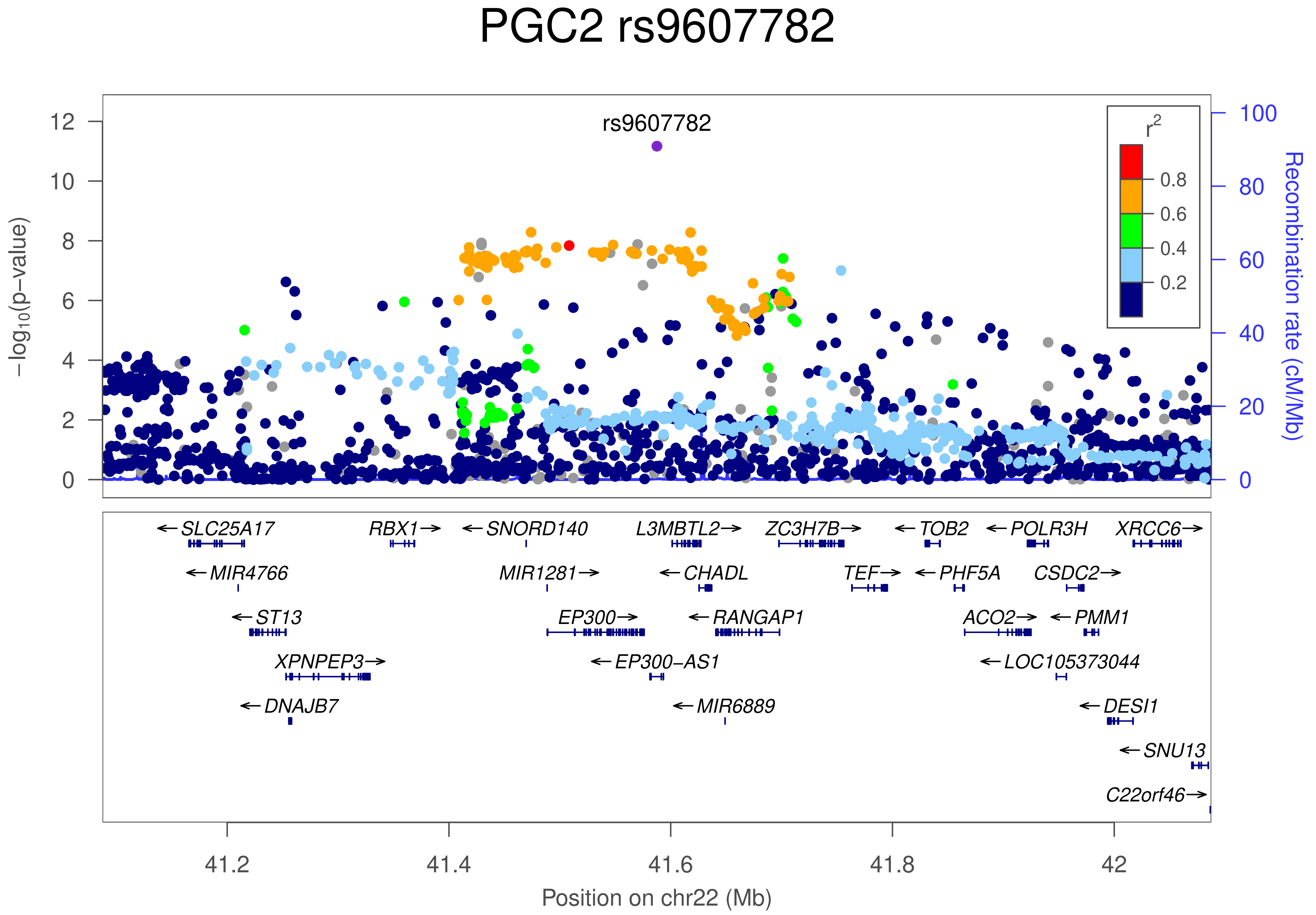
PGC2 rs5757730

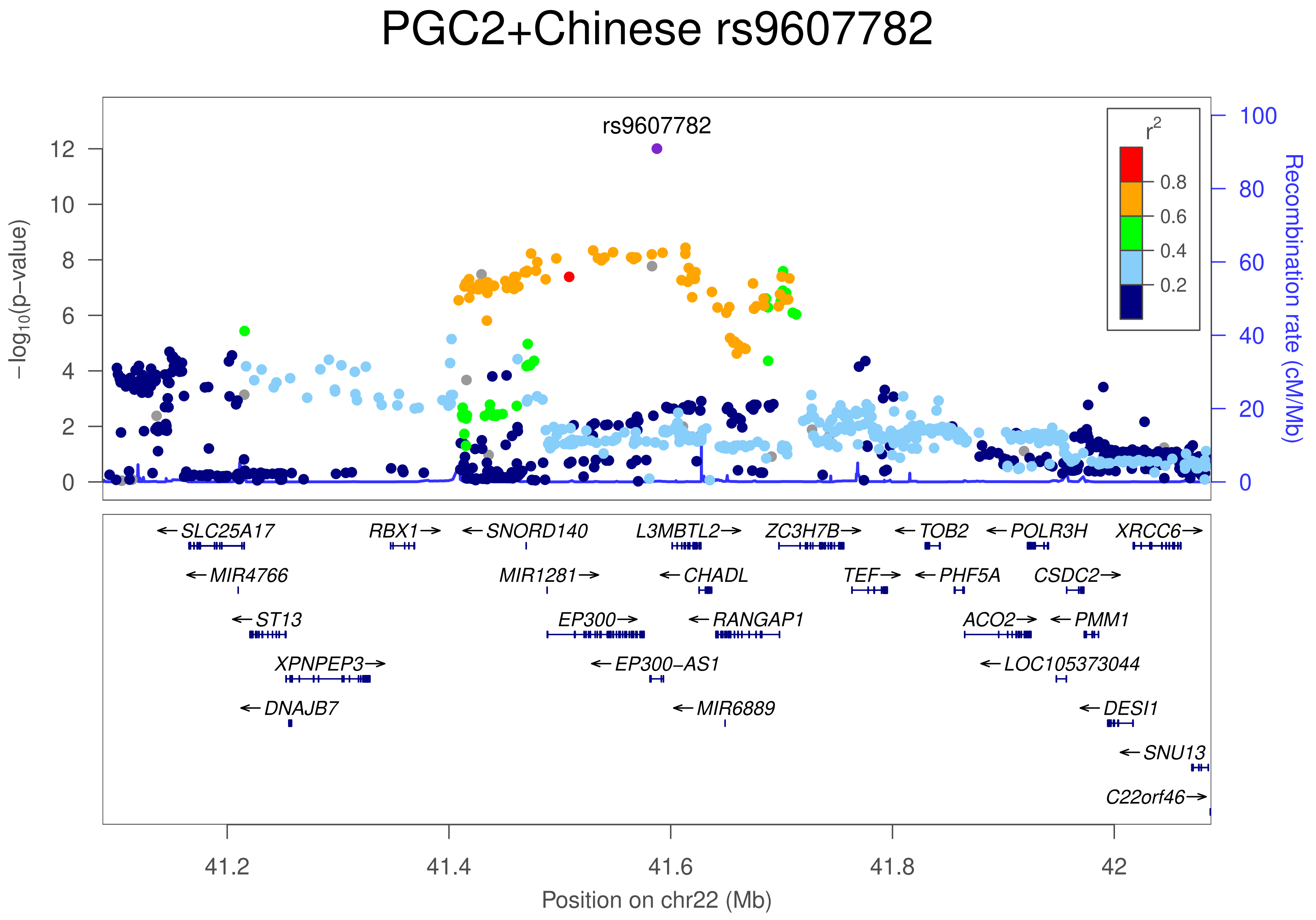


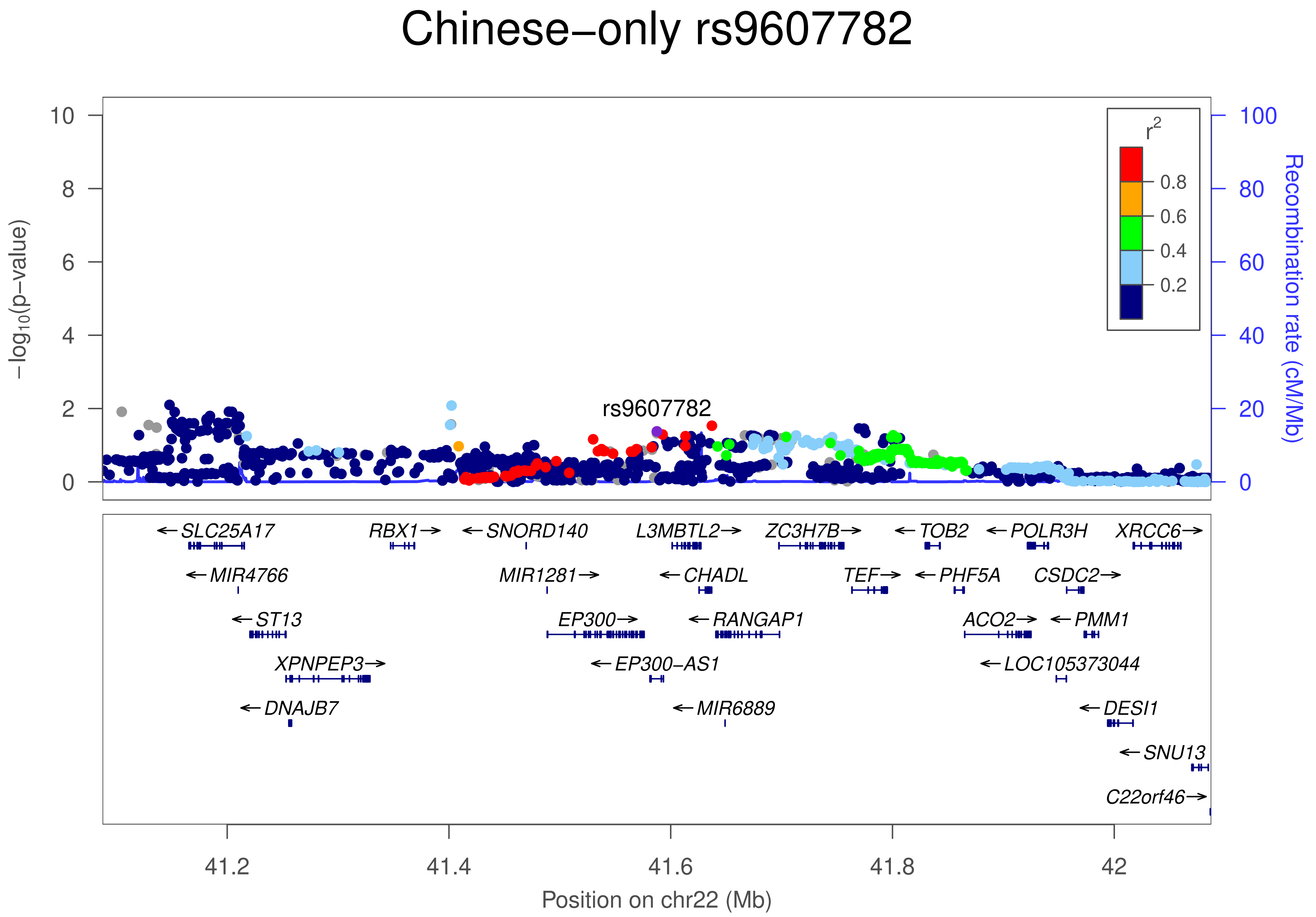
PGC2+Chinese rs5757730




Chinese−only rs5757730
−log10(p−value)
10
8
6
4
2
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
r2
0.8
0.6
0.4
0.2
rs5757730
APOBEC3G→
APOBEC3H→
←CBX7
←PDGFB
←RPL3
←SNORD83B
SYNGR1→
←SNORD83A
←SNORD139
←SNORD43
TAB1→
MGAT3→
←MGAT3−AS1
LOC100506472→
MIEF1→
ATF4→
←RPS19BP1
CACNA1I→
←ENTHD1
GRAP2→
FAM83F→
LOC100130899→
TNRC6B→
39.6
39.8
40
40.2
40.4
Position on chr22 (Mb)

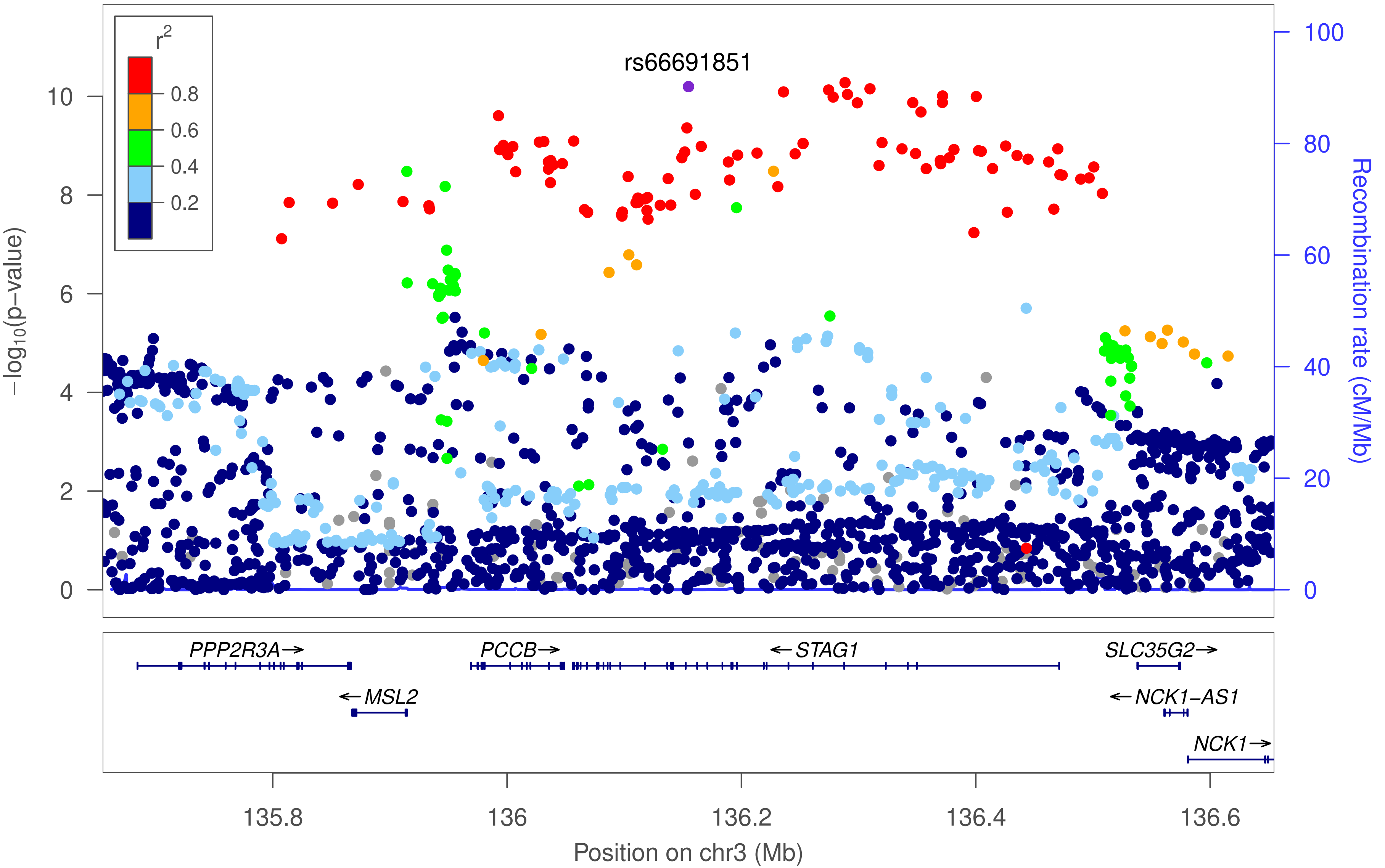

PGC2 rs9607782
rs9607782
r2
0.8
0.6
0.4
0.2
−log10(p−value)
0
2
4
6
8
10
12
Recombination rate (cM/Mb)
0
20
40
60
80
100
SLC25A17
RBX1
SNORD140
L3MBTL2
ZC3H7B
TOB2
POLR3H
XRCC6
MIR4766
MIR1281
CHADL
TEF
PHF5A
CSDC2
ST13
EP300
RANGAP1
ACO2
PMM1
XPNPEP3
EP300−AS1
LOC105373044
DNAJB7
MIR6889
DESI1
SNU13
C22orf46
41.2
41.4
41.6
41.8
42
Position on chr22 (Mb)

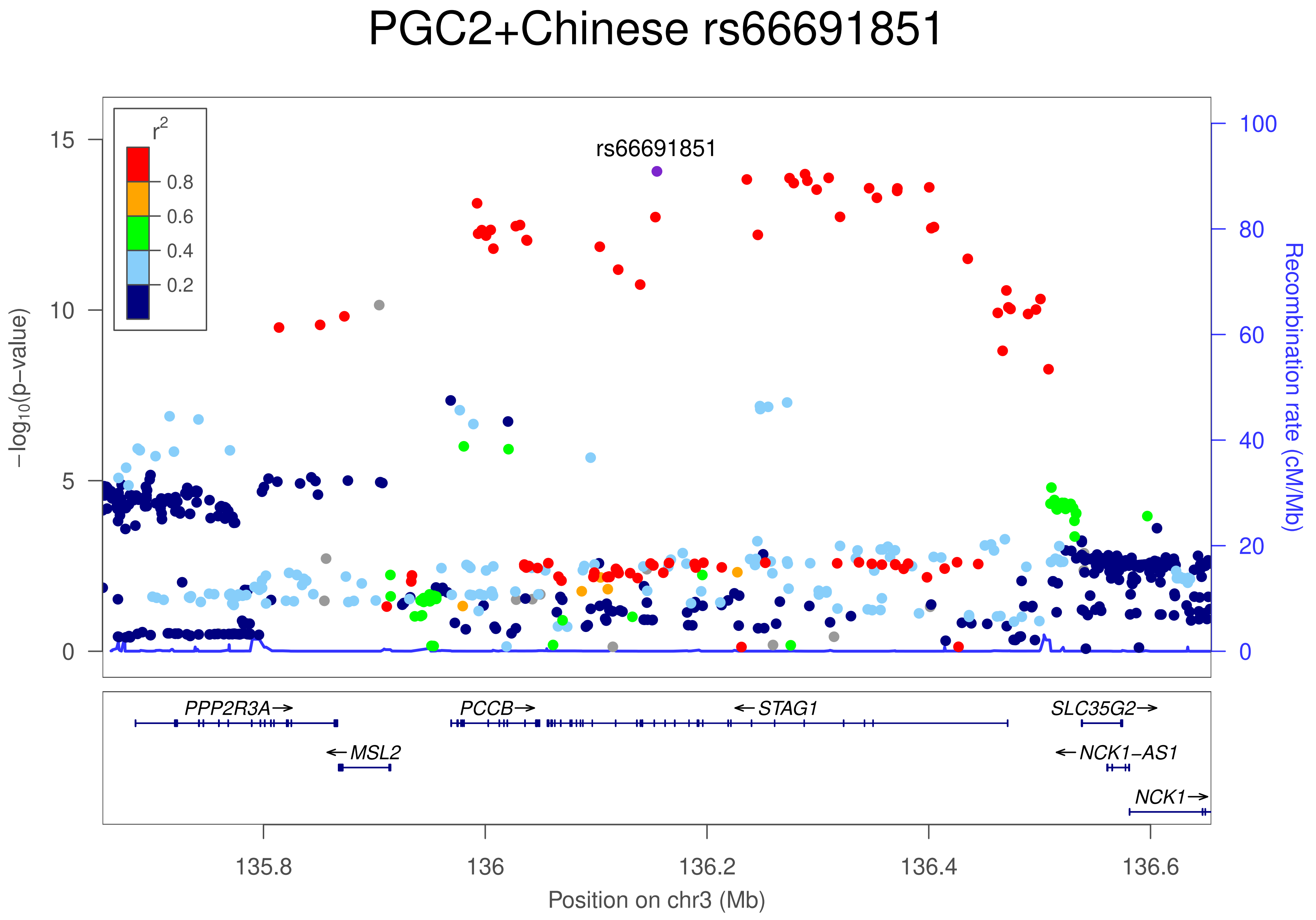

PGC2+Chinese rs9607782
rs9607782
−log10(p−value)
0
2
4
6
8
10
12
Recombination rate (cM/Mb)
0
20
40
60
80
100
r2
0.2
0.4
0.6
0.8
← SLC25A17
RBX1 →
← SNORD140
L3MBTL2 →
ZC3H7B →
← TOB2
← POLR3H
XRCC6 →
← MIR4766
MIR1281 →
← CHADL
TEF →
← PHF5A
CSDC2 →
← ST13
EP300 →
← RANGAP1
ACO2 →
← PMM1
XPNPEP3 →
← EP300−AS1
← LOC105373044
← DNAJB7
← MIR6889
← DESI1
← SNU13
C22orf46 →
41.2
41.4
41.6
41.8
42
Position on chr22 (Mb)



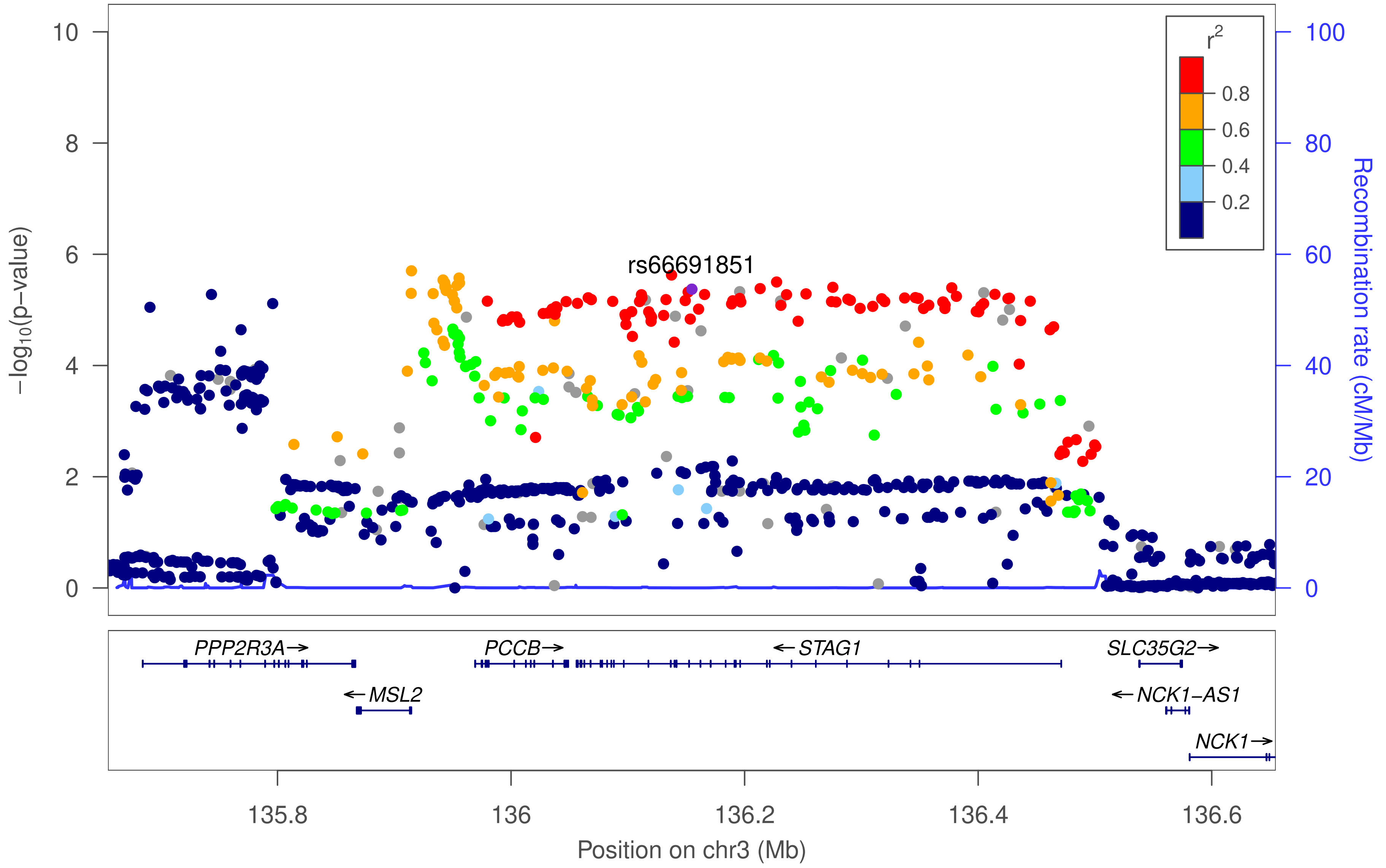
Chinese−only rs9607782
−log10(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
r2
0.8
0.6
0.4
0.2
rs9607782
SLC25A17
MIR4766
ST13
XPNPEP3
DNAJB7
RBX1
SNORD140
MIR1281
EP300
EP300−AS1
L3MBTL2
CHADL
RANGAP1
MIR6889
ZC3H7B
TEF
TOB2
PHF5A
ACO2
LOC105373044
POLR3H
CSDC2
PMM1
DESI1
XRCC6
SNU13
C22orf46
41.2
41.4
41.6
41.8
42
Position on chr22 (Mb)

PGC2 rs66691851

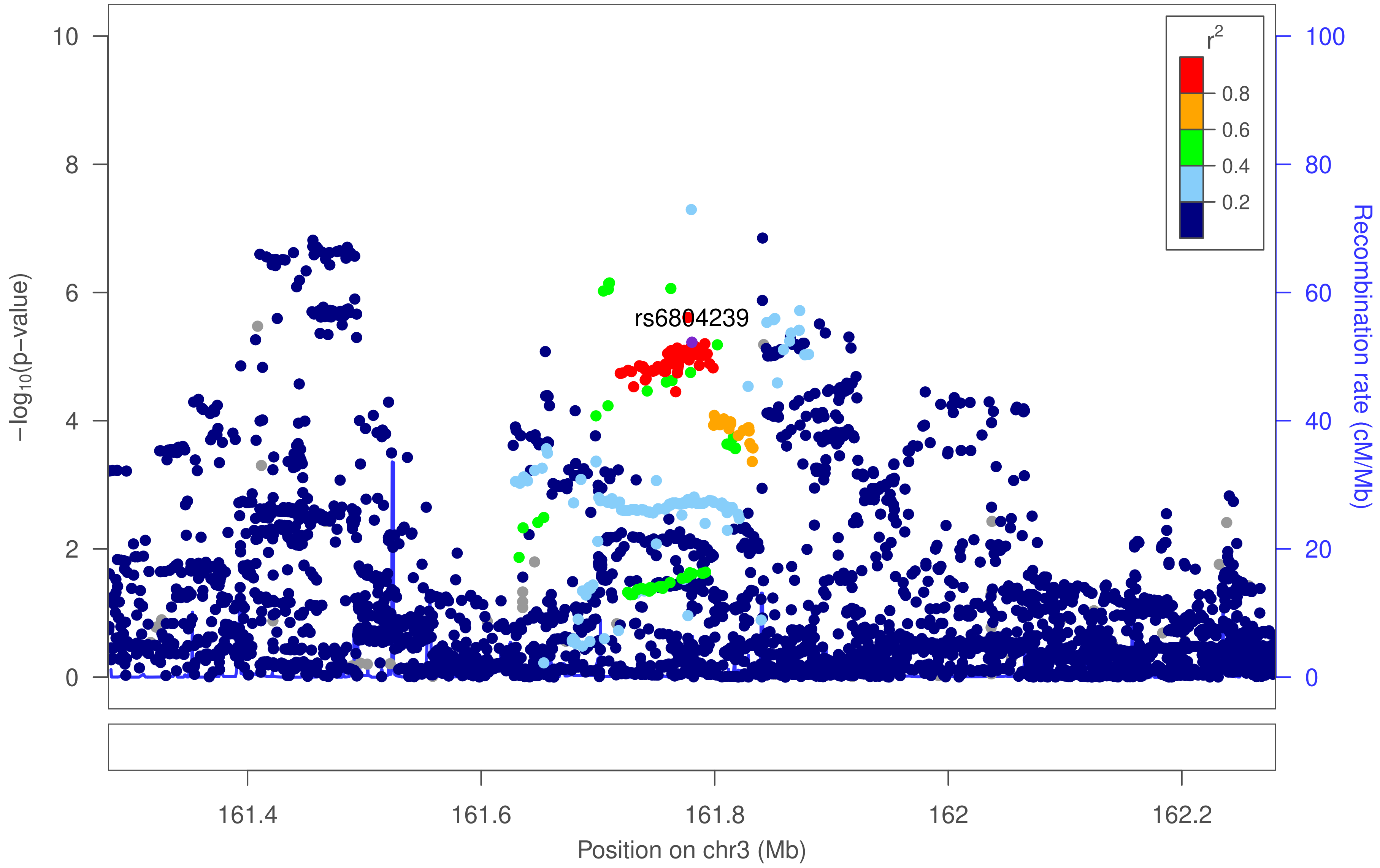



PGC2+Chinese rs66691851
r²
0.8
0.6
0.4
0.2
rs66691851
−log₁₀(p−value)
15
10
5
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
PPP2R3A→
←MSL2
PCCB→
←STAG1
SLC35G2→
←NCK1−AS1
NCK1→
135.8
136
136.2
136.4
136.6
Position on chr3 (Mb)

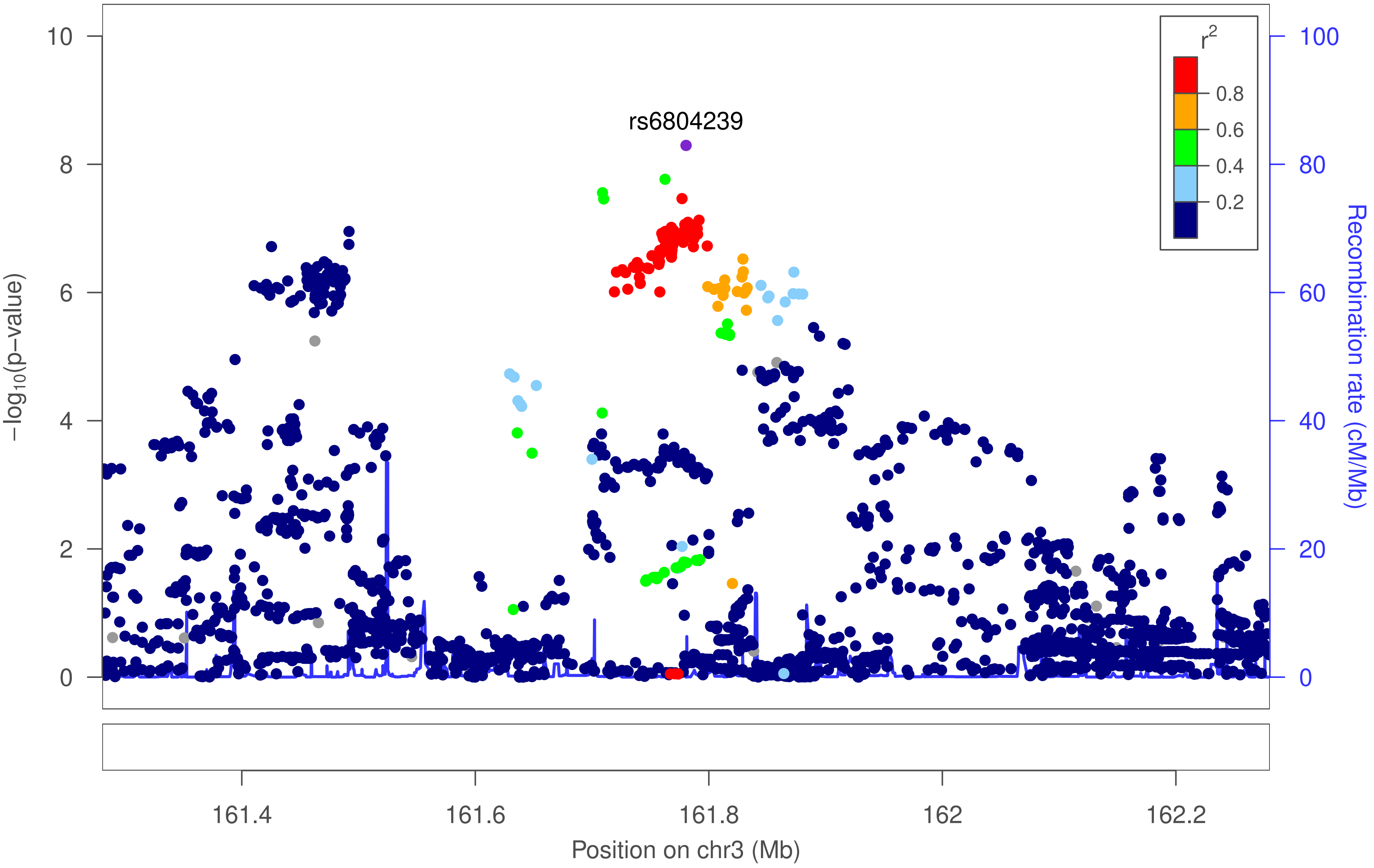
Chinese–only rs66691851

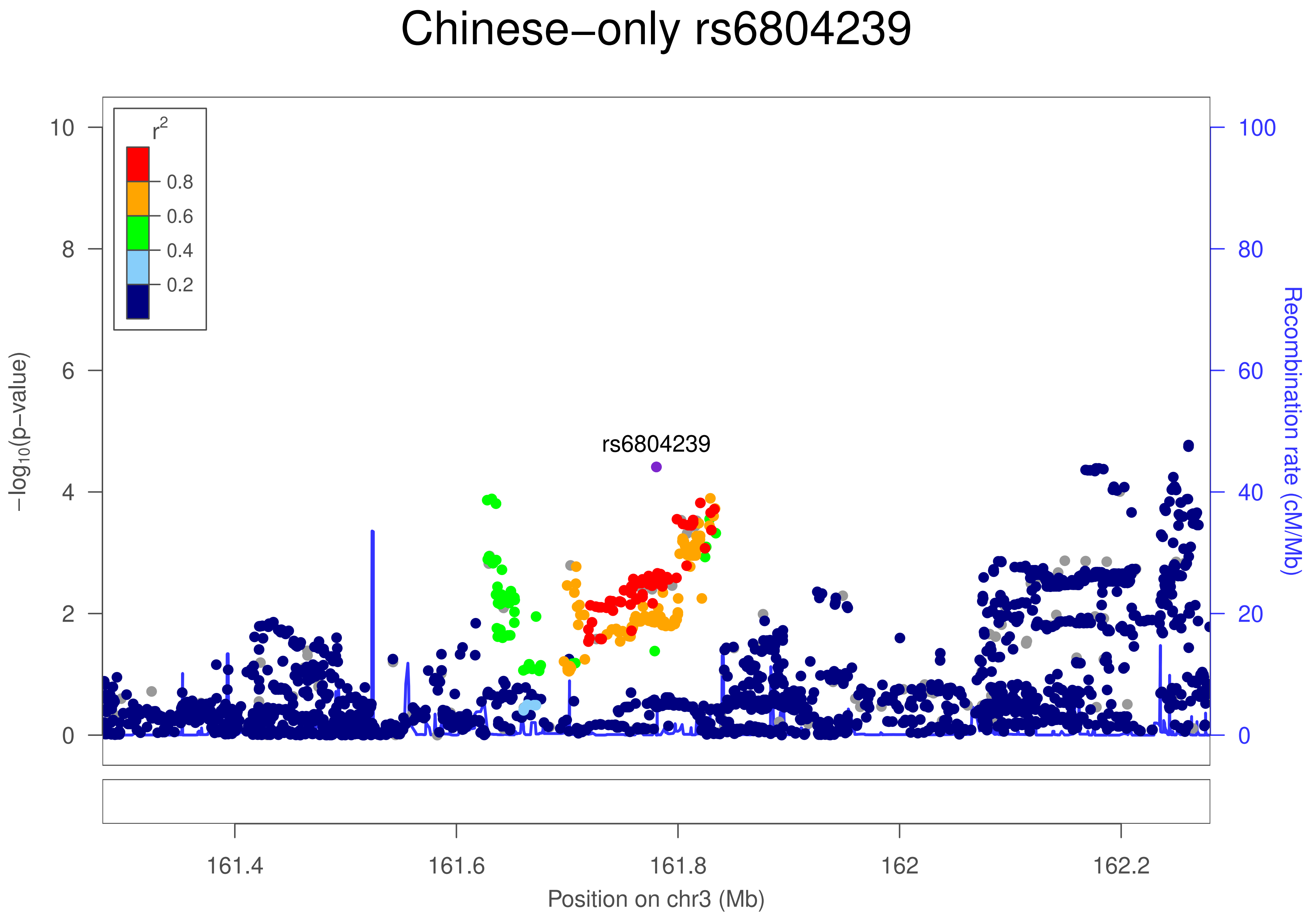


PGC2 rs6804239

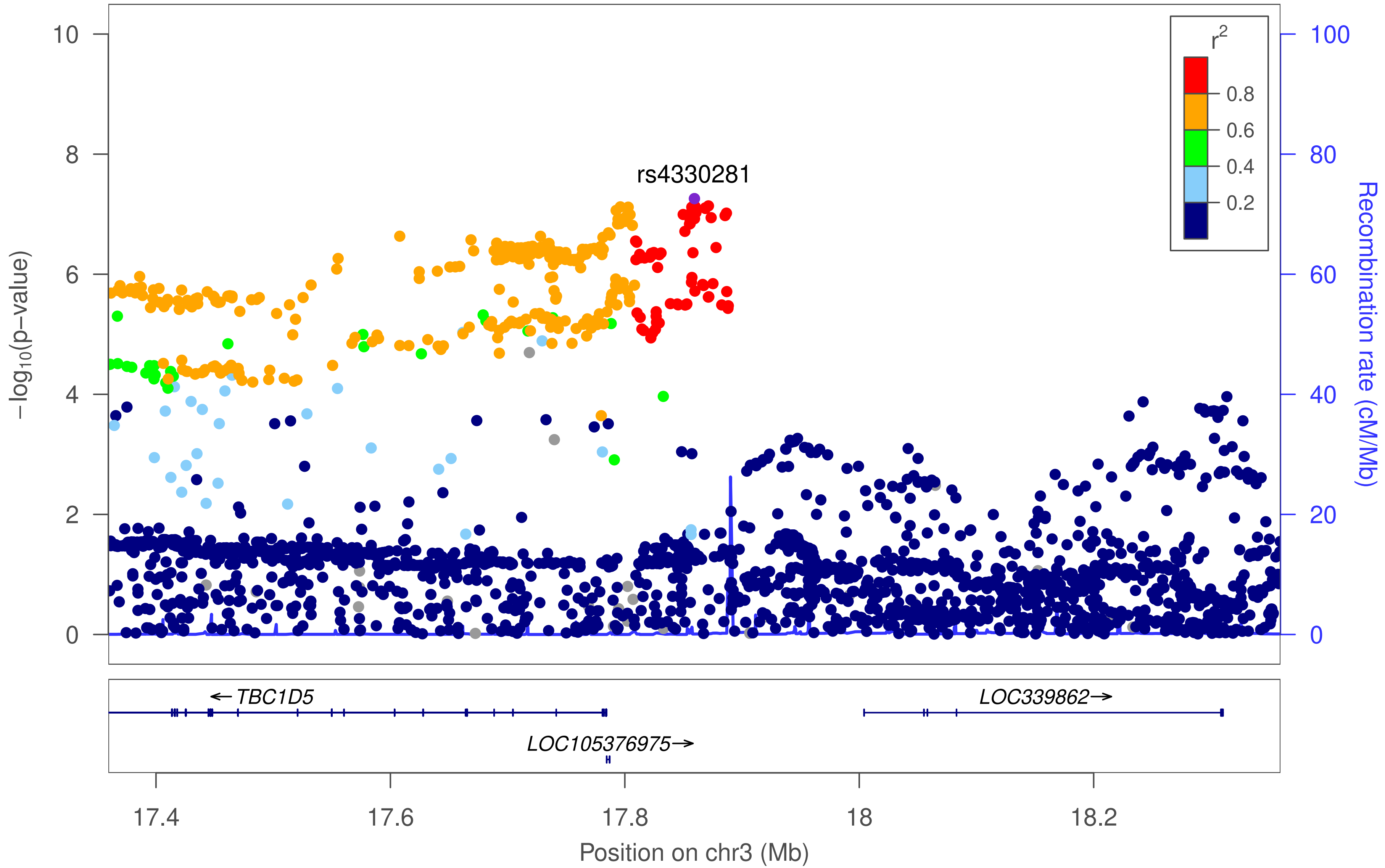


PGC2+Chinese rs6804239

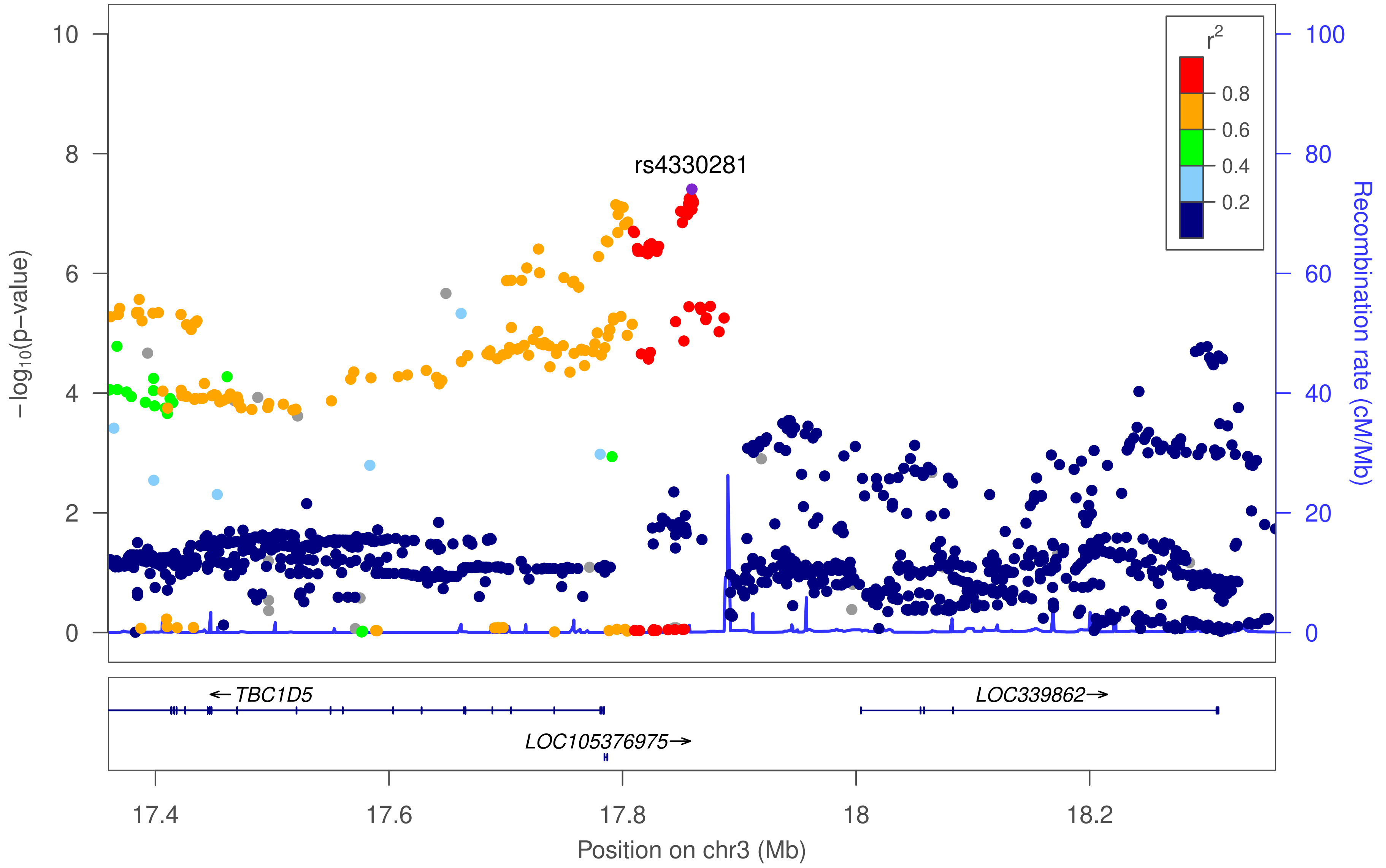


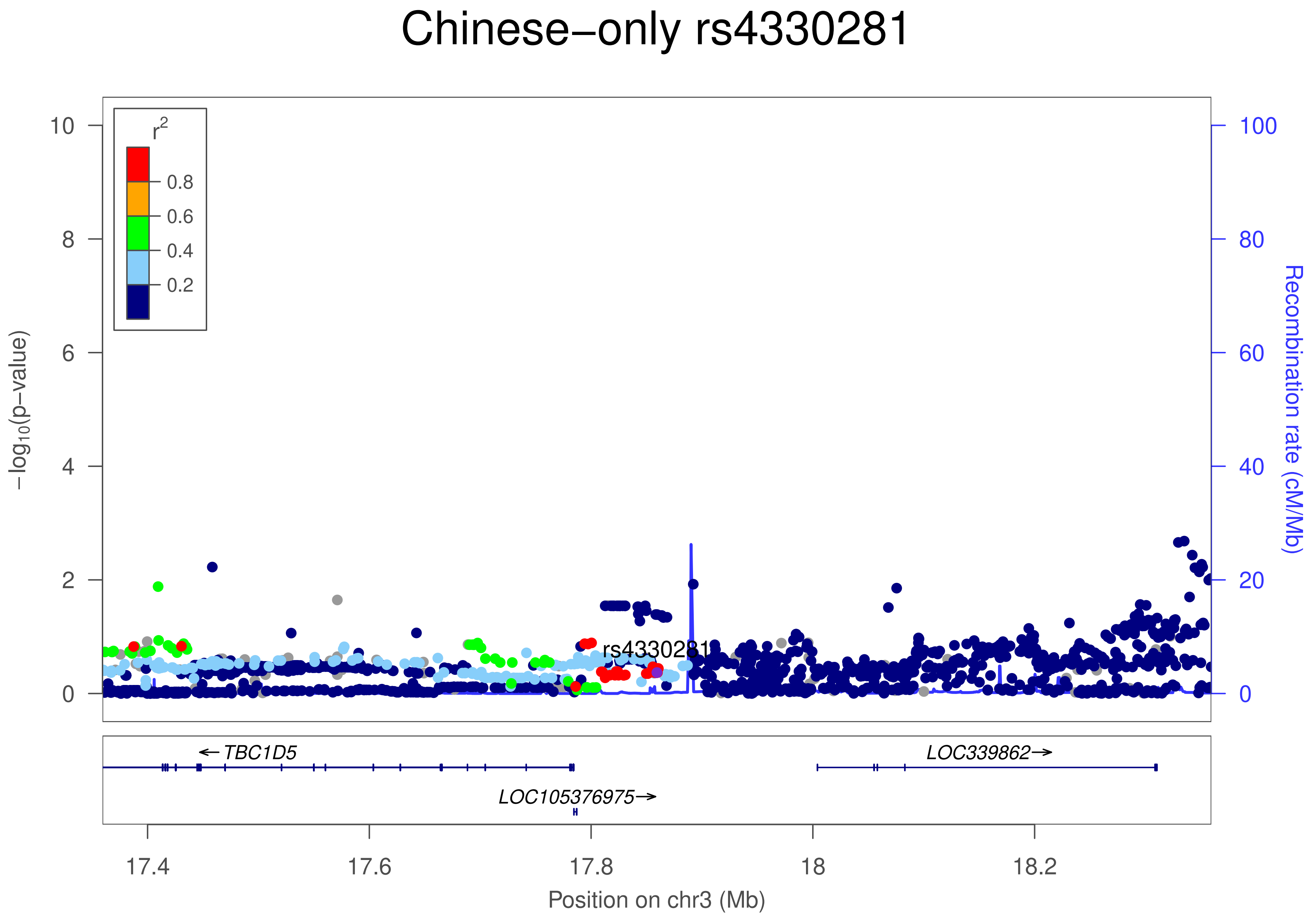

Chinese−only rs6804239
r²
0.8
0.6
0.4
0.2
rs6804239
−log₁₀(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
161.4
161.6
161.8
162
162.2
Position on chr3 (Mb)

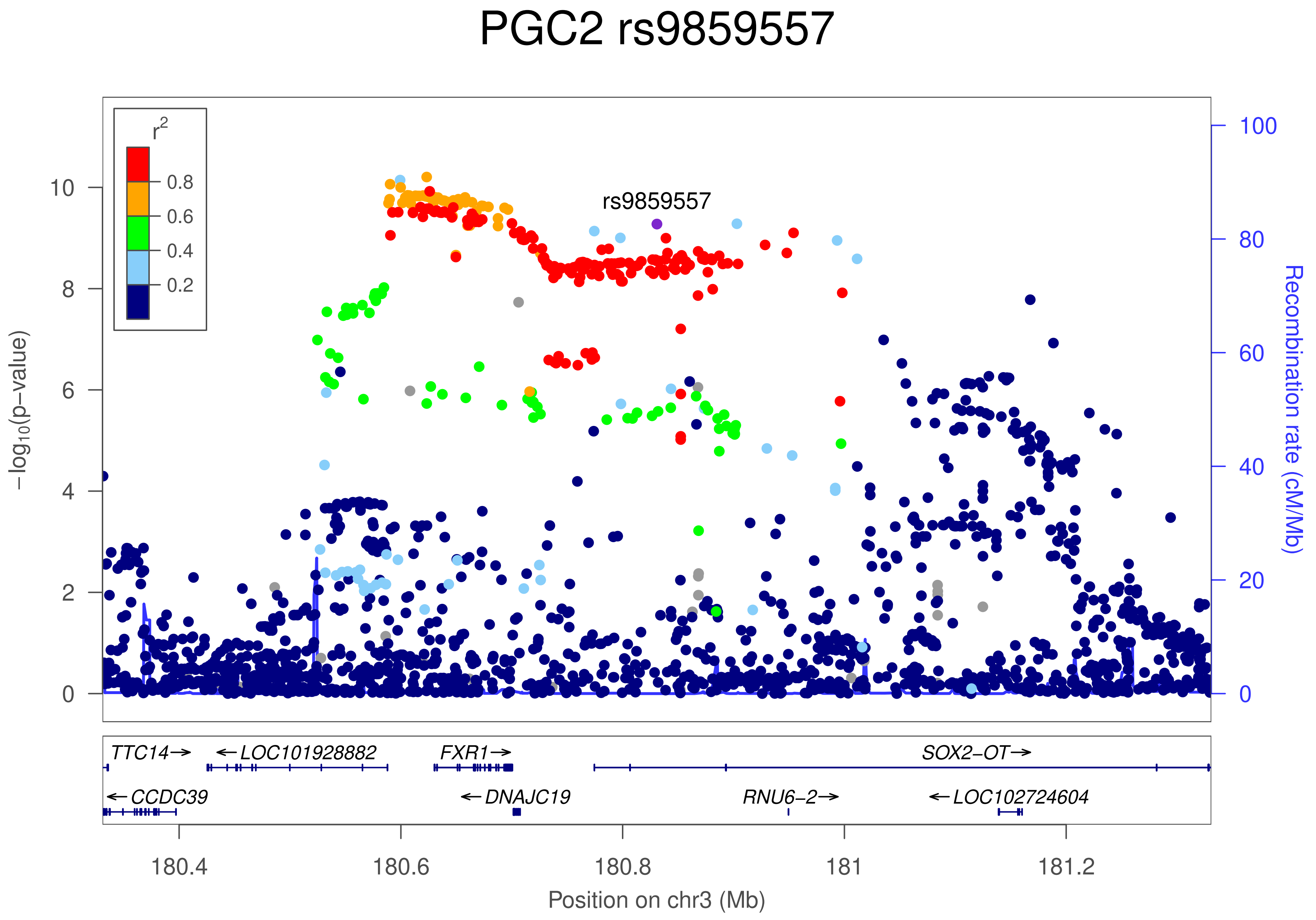
PGC2 rs4330281

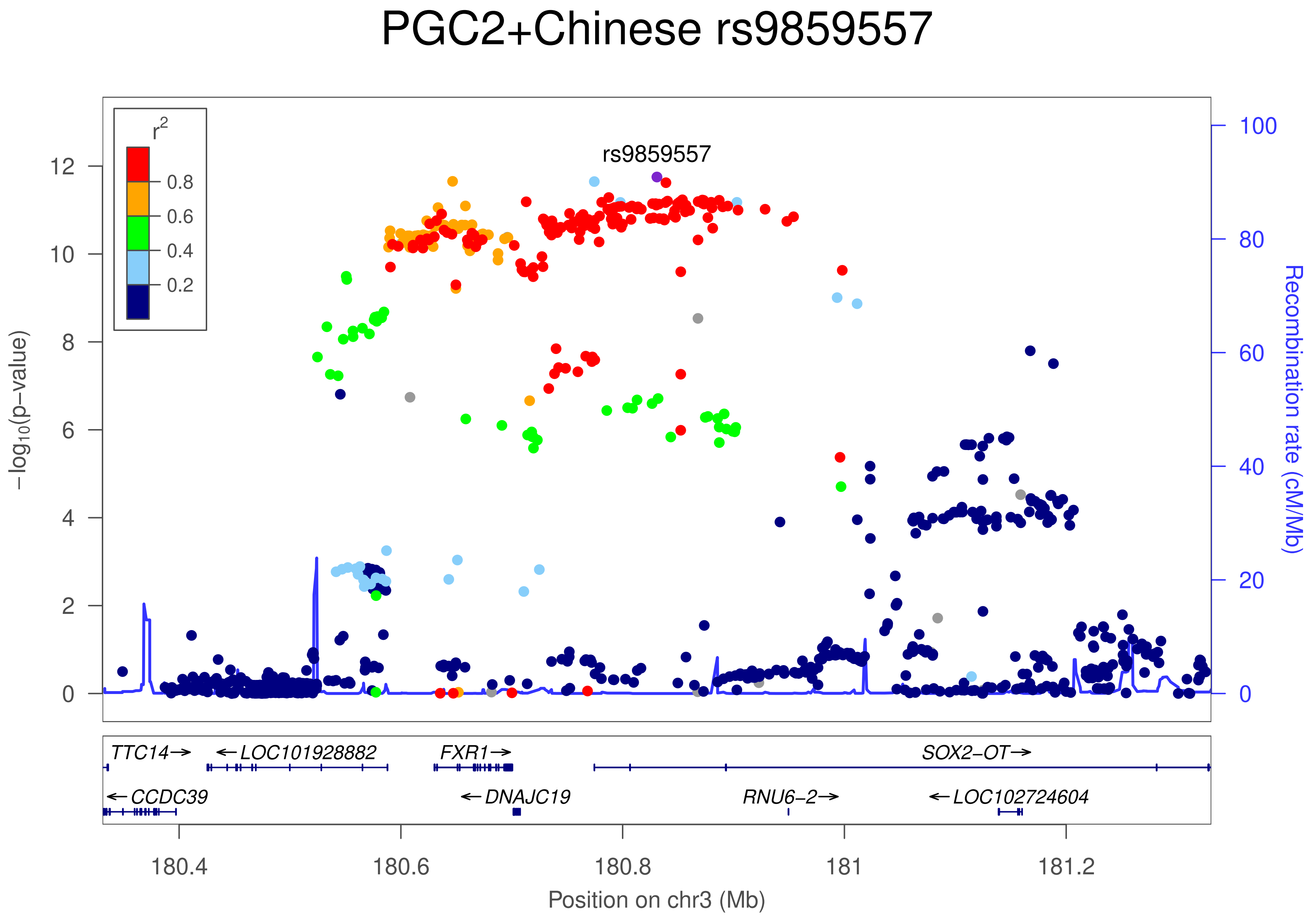


PGC2+Chinese rs4330281

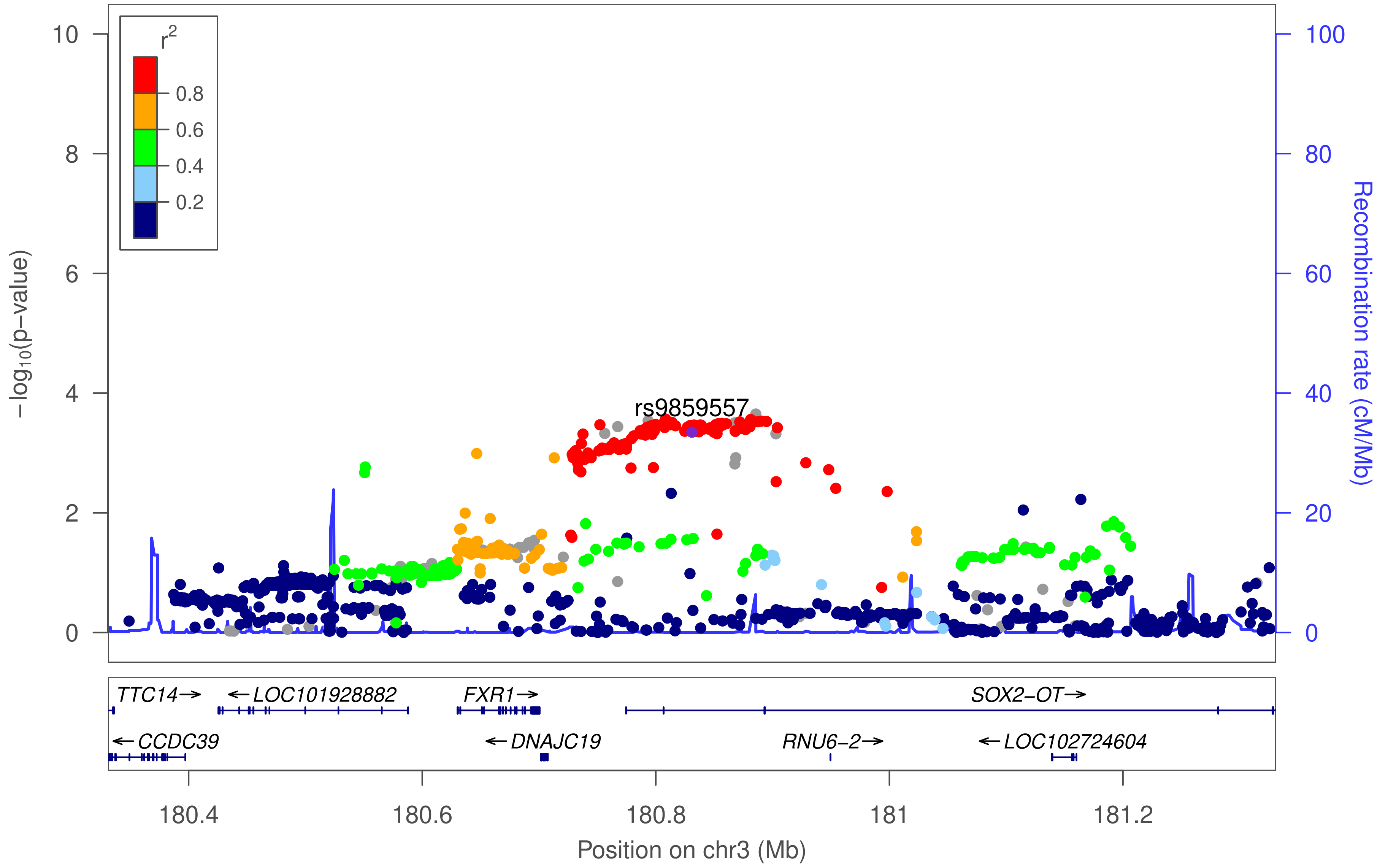


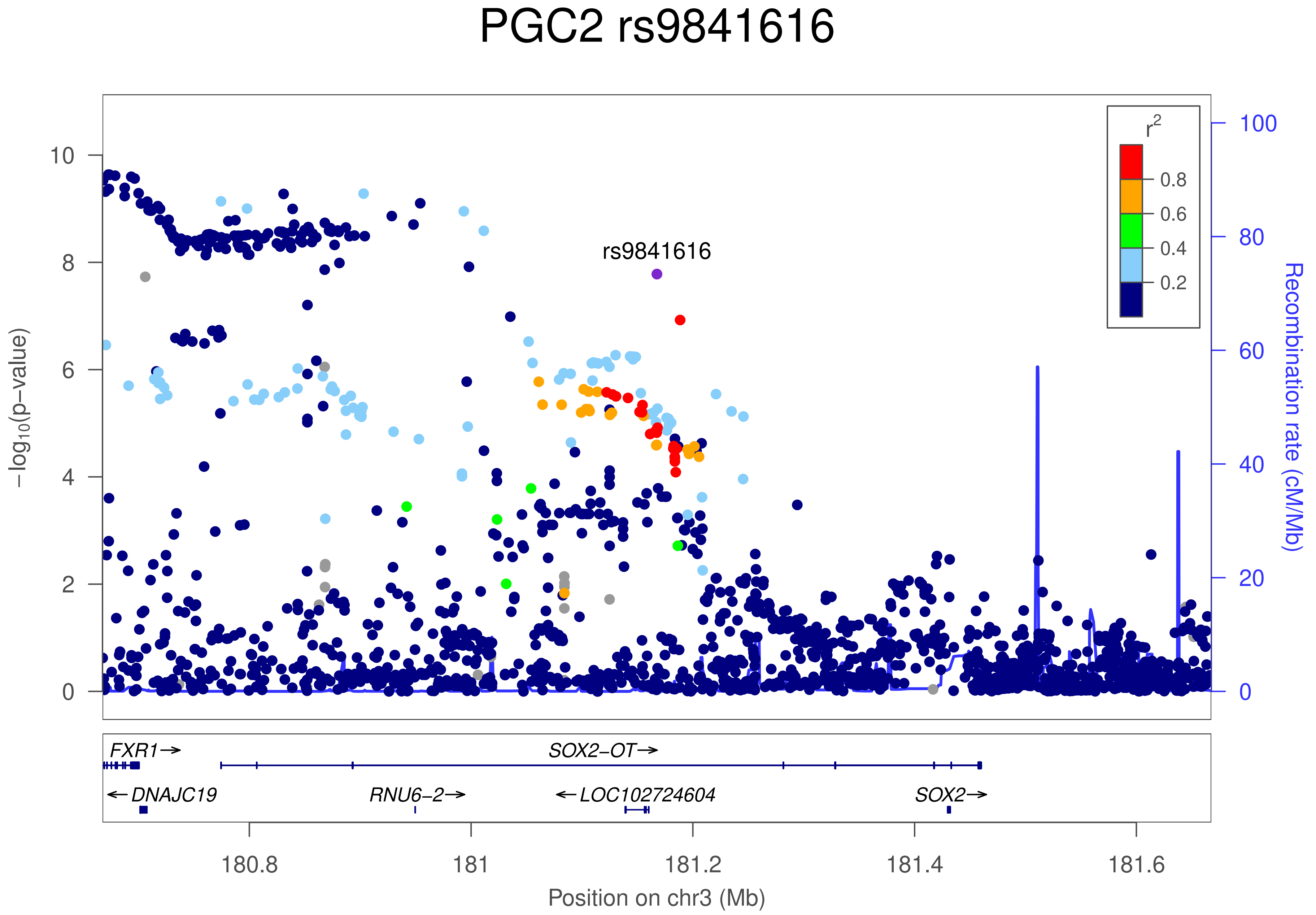

Chinese–only rs4330281
r^2
0.8
0.6
0.4
0.2
$-\log_{10}$(p–value)
10
8
6
4
2
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
rs4330281
← TBC1D5
LOC339862→
LOC105376975→
17.4
17.6
17.8
18
18.2
Position on chr3 (Mb)

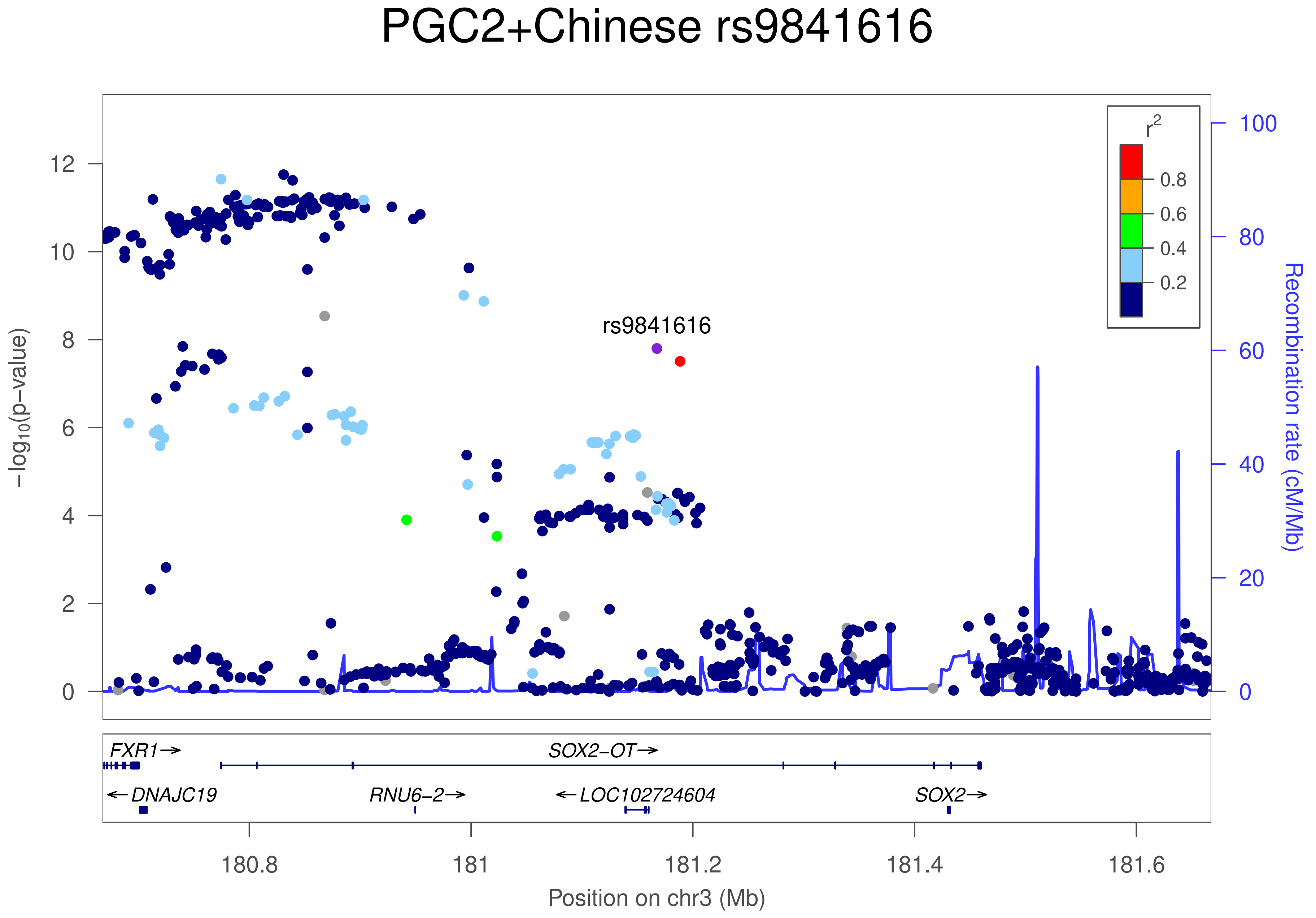

PGC2 rs9859557
r²
0.8
0.6
0.4
0.2
rs9859557
−log₁₀(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
TTC14→
←LOC101928882
FXR1→
SOX2−OT→
←CCDC39
←DNAJC19
RNU6−2→
←LOC102724604
180.4
180.6
180.8
181
181.2
Position on chr3 (Mb)

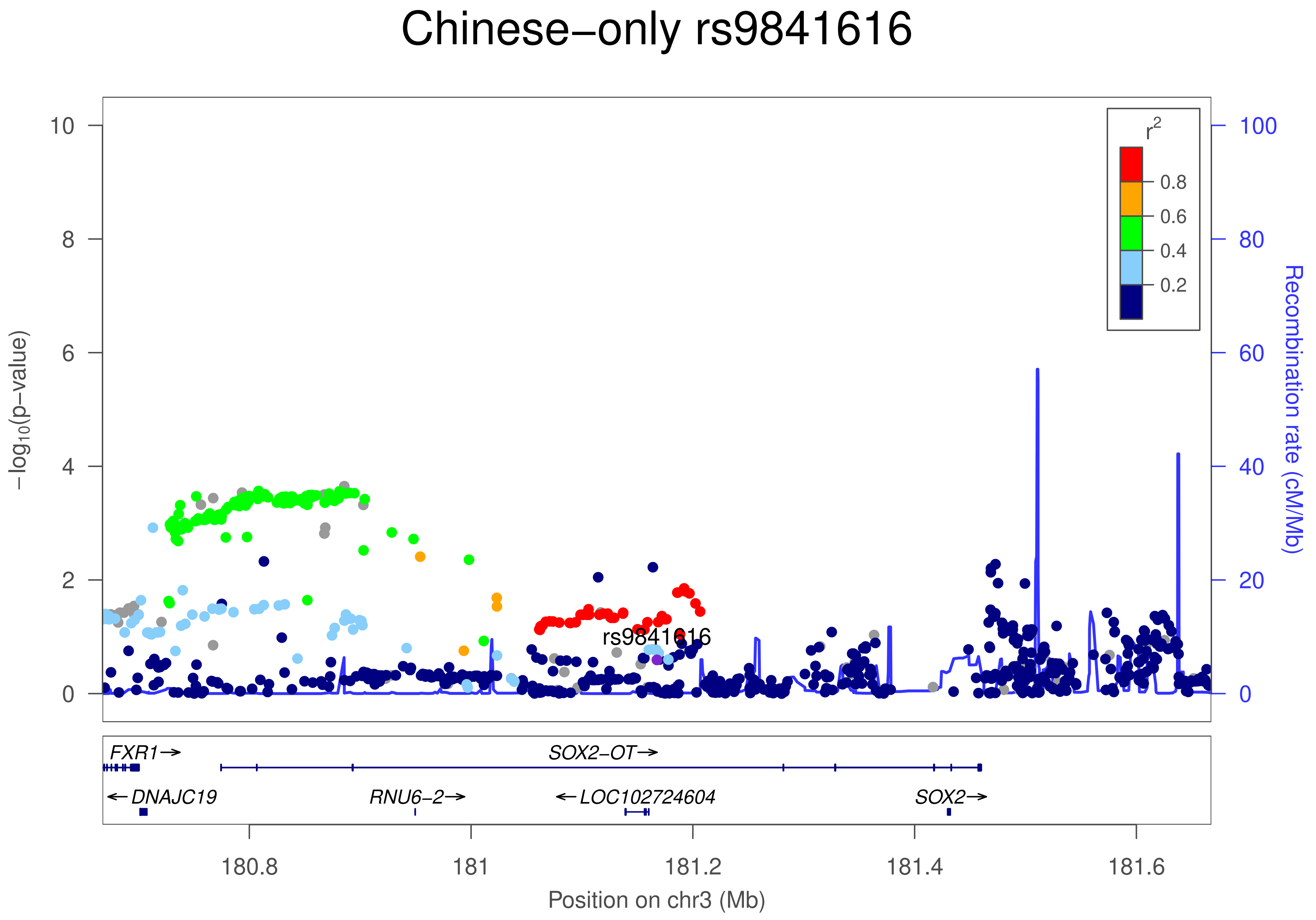

PGC2+Chinese rs9859557
r²
0.8
0.6
0.4
0.2
rs9859557
−log₁₀(p−value)
0
2
4
6
8
10
12
Recombination rate (cM/Mb)
0
20
40
60
80
100
TTC14→
←LOC101928882
FXR1→
SOX2−OT→
←CCDC39
←DNAJC19
RNU6−2→
←LOC102724604
180.4
180.6
180.8
181
181.2
Position on chr3 (Mb)

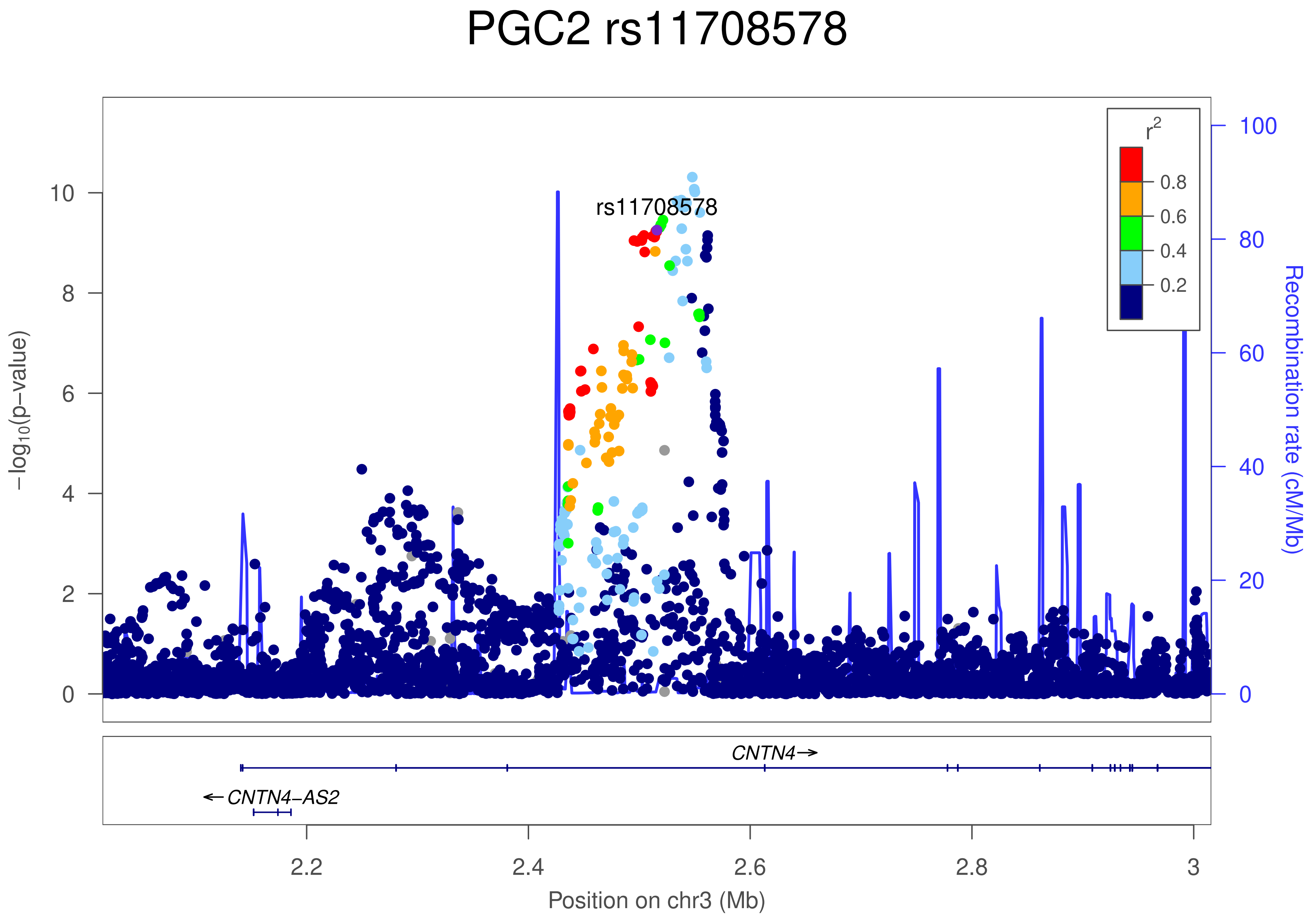
Chinese−only rs9859557

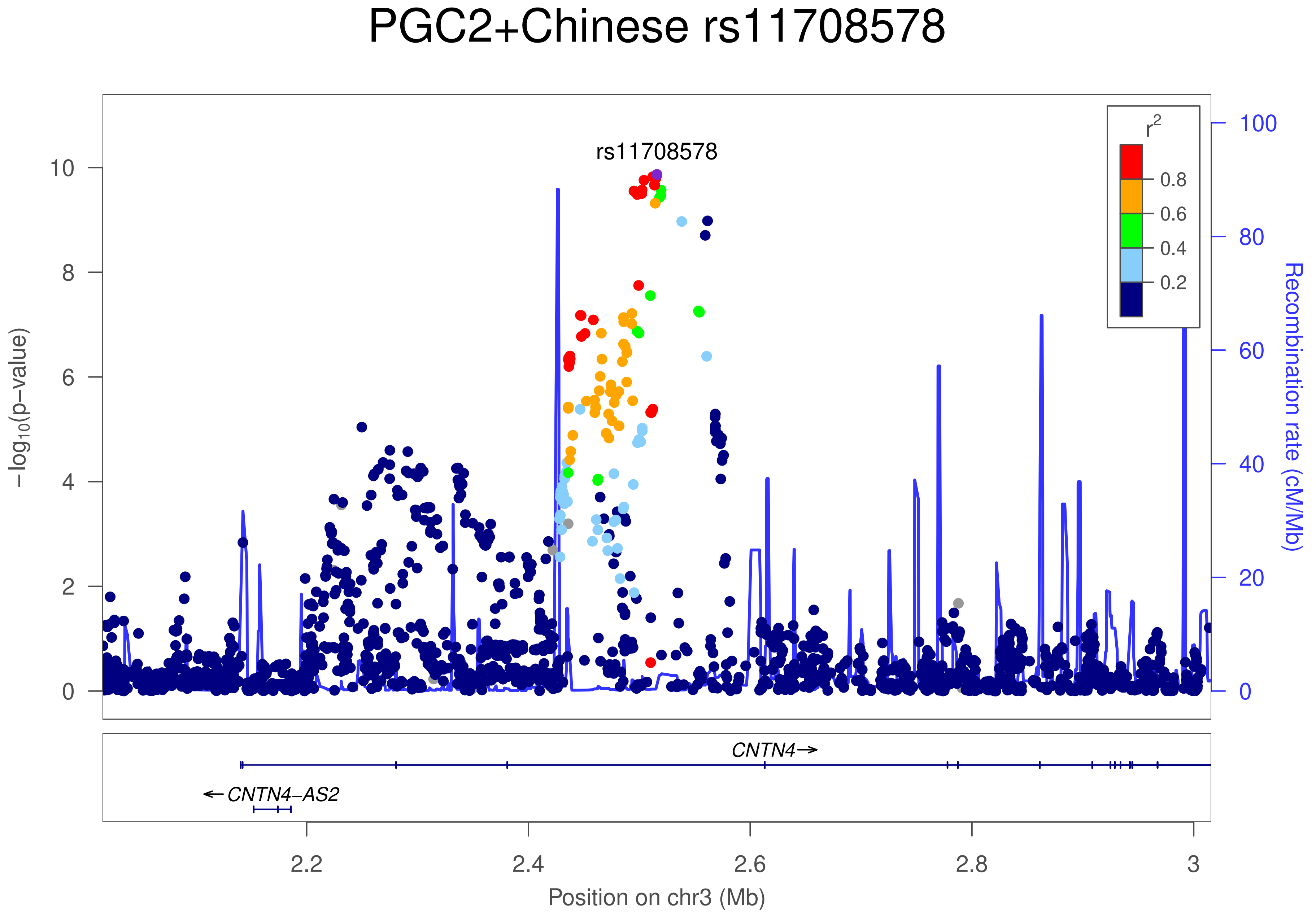



PGC2 rs9841616
rs9841616
−log10(p−value)
0
2
4
6
8
10
r2
0.8
0.6
0.4
0.2
100
80
60
40
20
0
Recombination rate (cM/Mb)
FXR1→
SOX2−OT→
←DNAJC19
RNU6−2→
←LOC102724604
SOX2→
180.8
181
181.2
181.4
181.6
Position on chr3 (Mb)

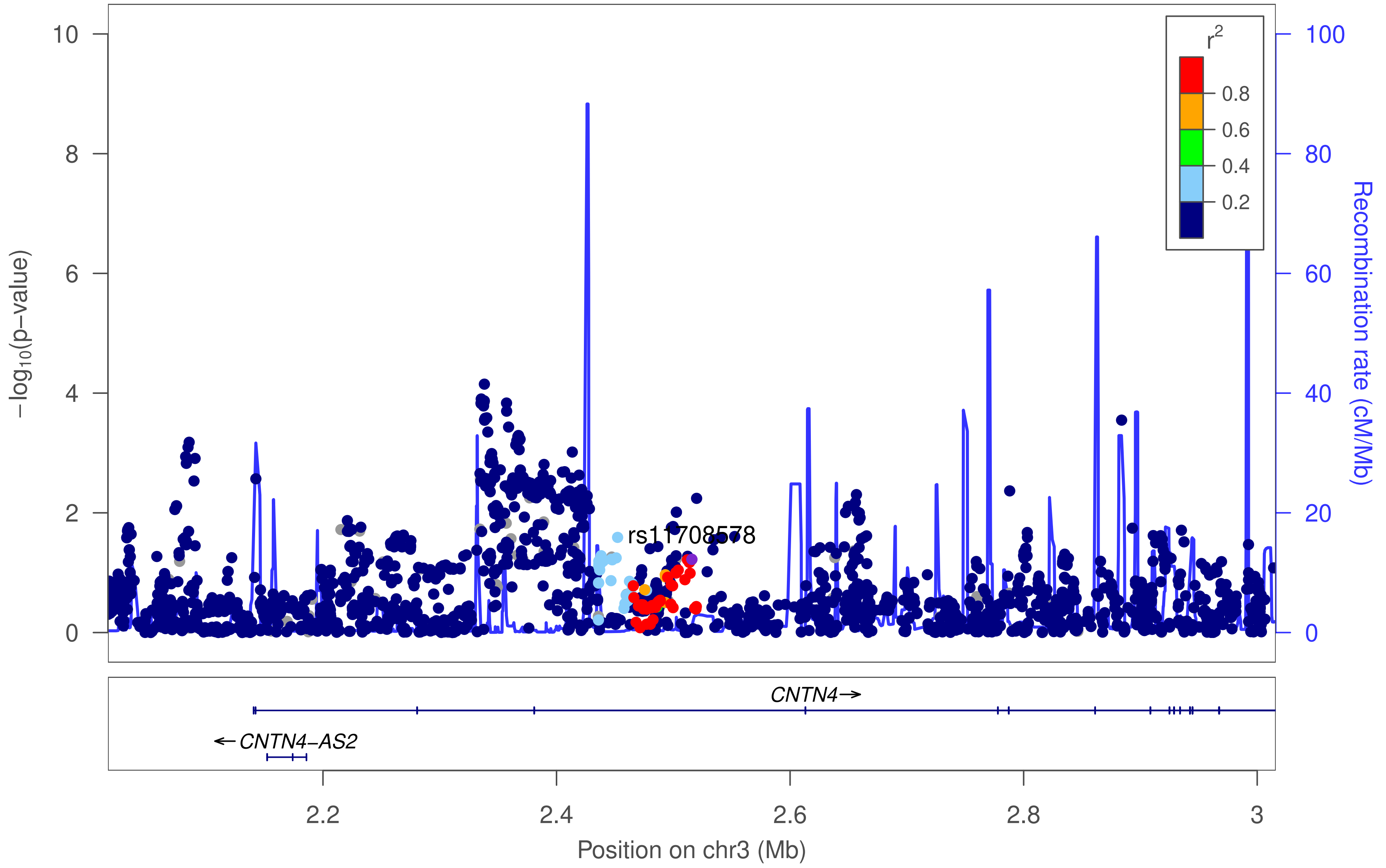

PGC2+Chinese rs9841616
rs9841616
−log10(p−value)
0
2
4
6
8
10
12
Recombination rate (cM/Mb)
0
20
40
60
80
100
r2
0.8
0.6
0.4
0.2
FXR1→
SOX2−OT→
←DNAJC19
RNU6−2→
←LOC102724604
SOX2→
180.8
181
181.2
181.4
181.6
Position on chr3 (Mb)


Chinese−only rs9841616
r²
0.8
0.6
0.4
0.2
−log₁₀(p−value)
10
8
6
4
2
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
rs9841616
FXR1→
SOX2−OT→
←DNAJC19
RNU6−2→
←LOC102724604
SOX2→
180.8
181
181.2
181.4
181.6
Position on chr3 (Mb)

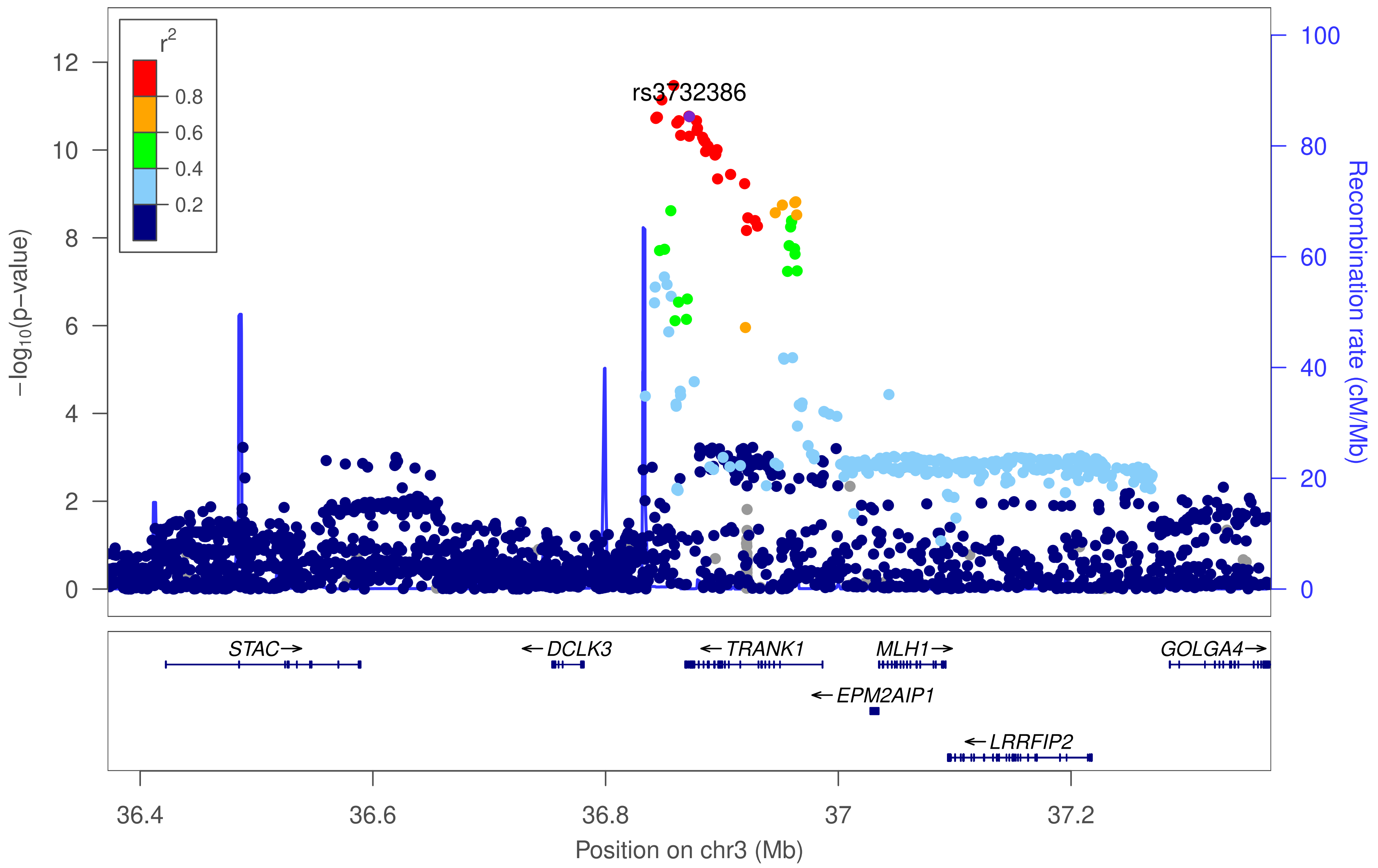

PGC2 rs11708578
rs11708578
r2
0.8
0.6
0.4
0.2
−log10(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
CNTN4→
←CNTN4−AS2
2.2
2.4
2.6
2.8
3
Position on chr3 (Mb)

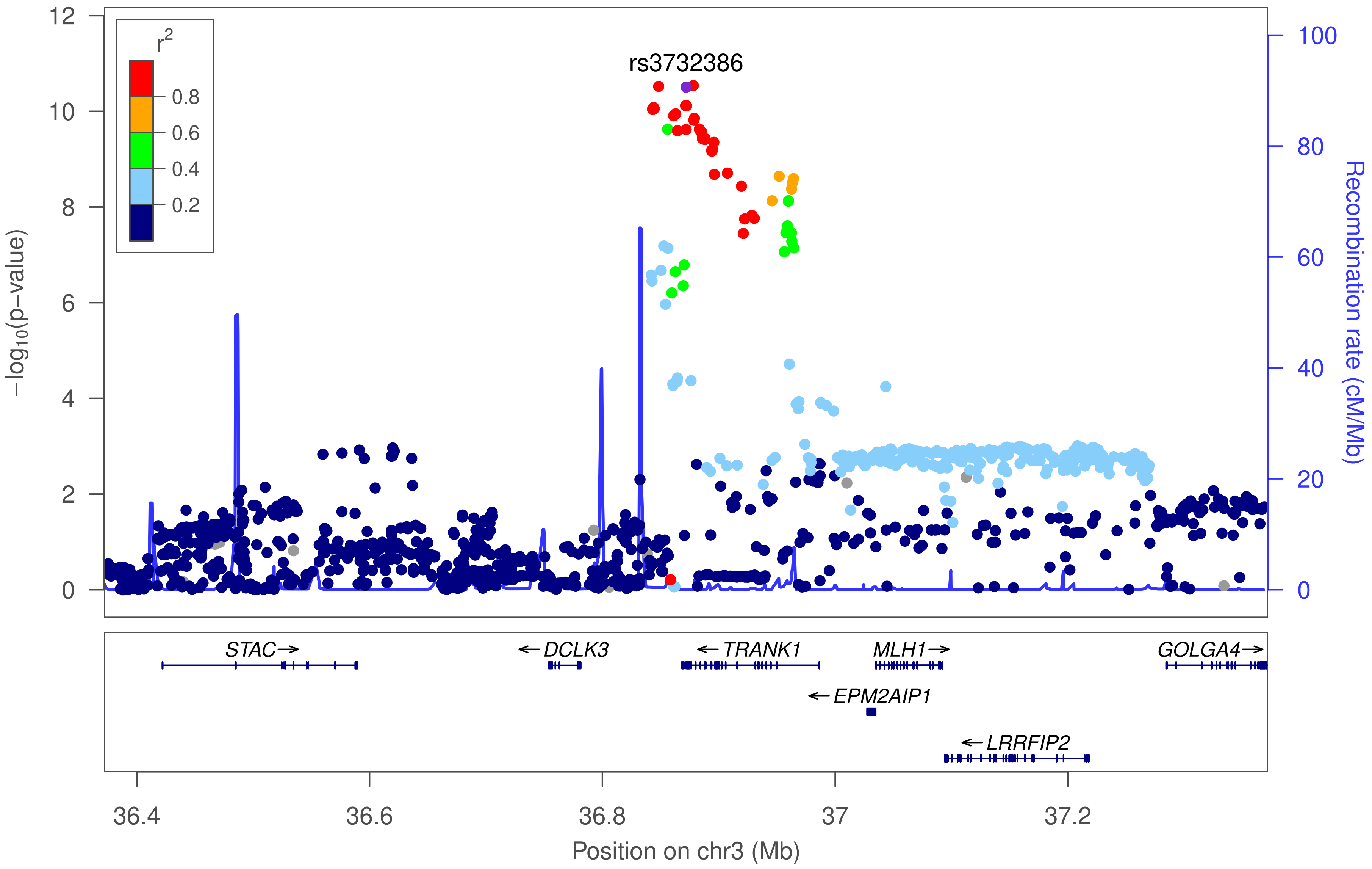

PGC2+Chinese rs11708578
rs11708578
r^2
0.8
0.6
0.4
0.2
−log$_{10}$(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
CNTN4→
←CNTN4−AS2
2.2
2.4
2.6
2.8
3
Position on chr3 (Mb)

Chinese−only rs11708578

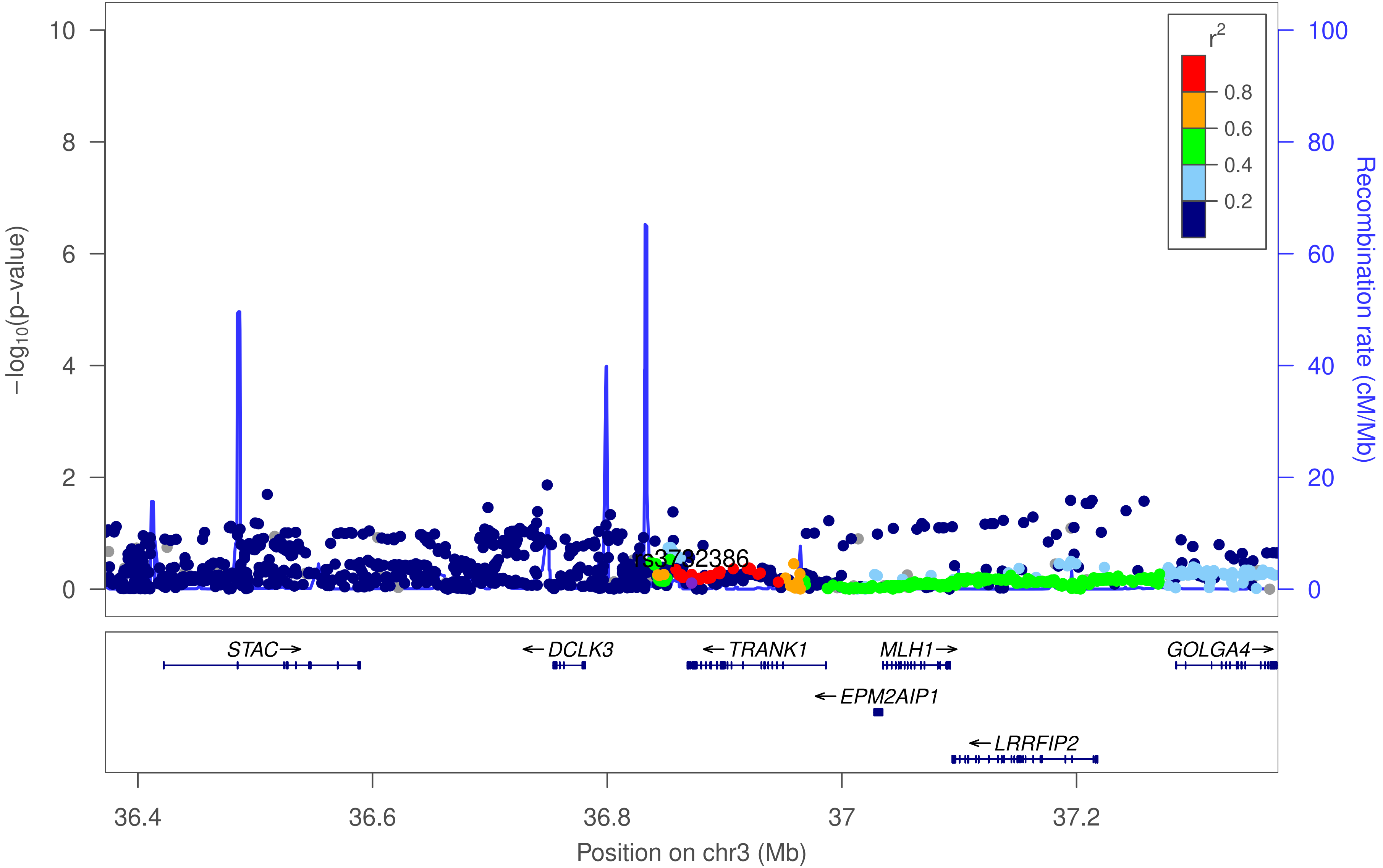


PGC2 rs3732386

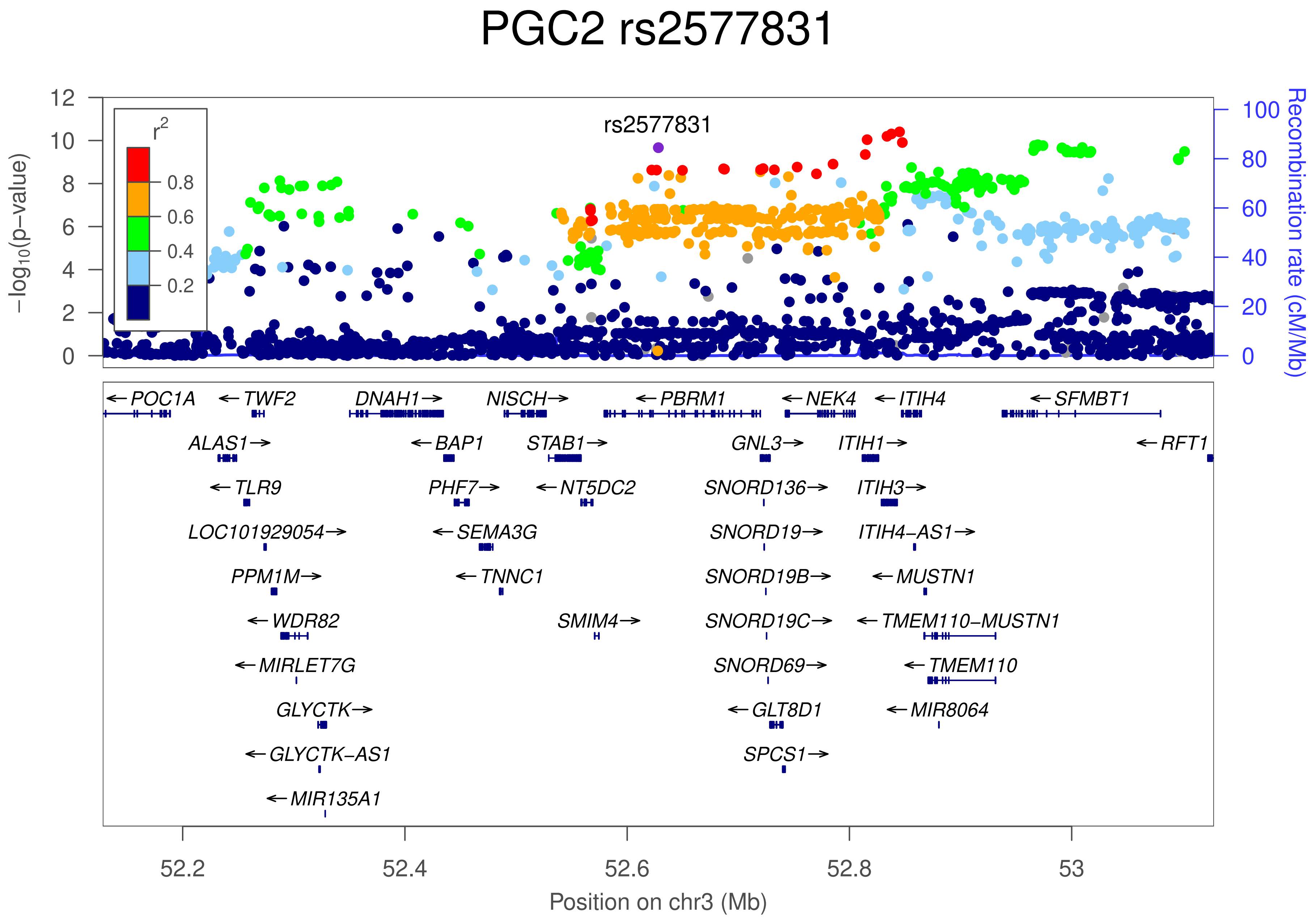


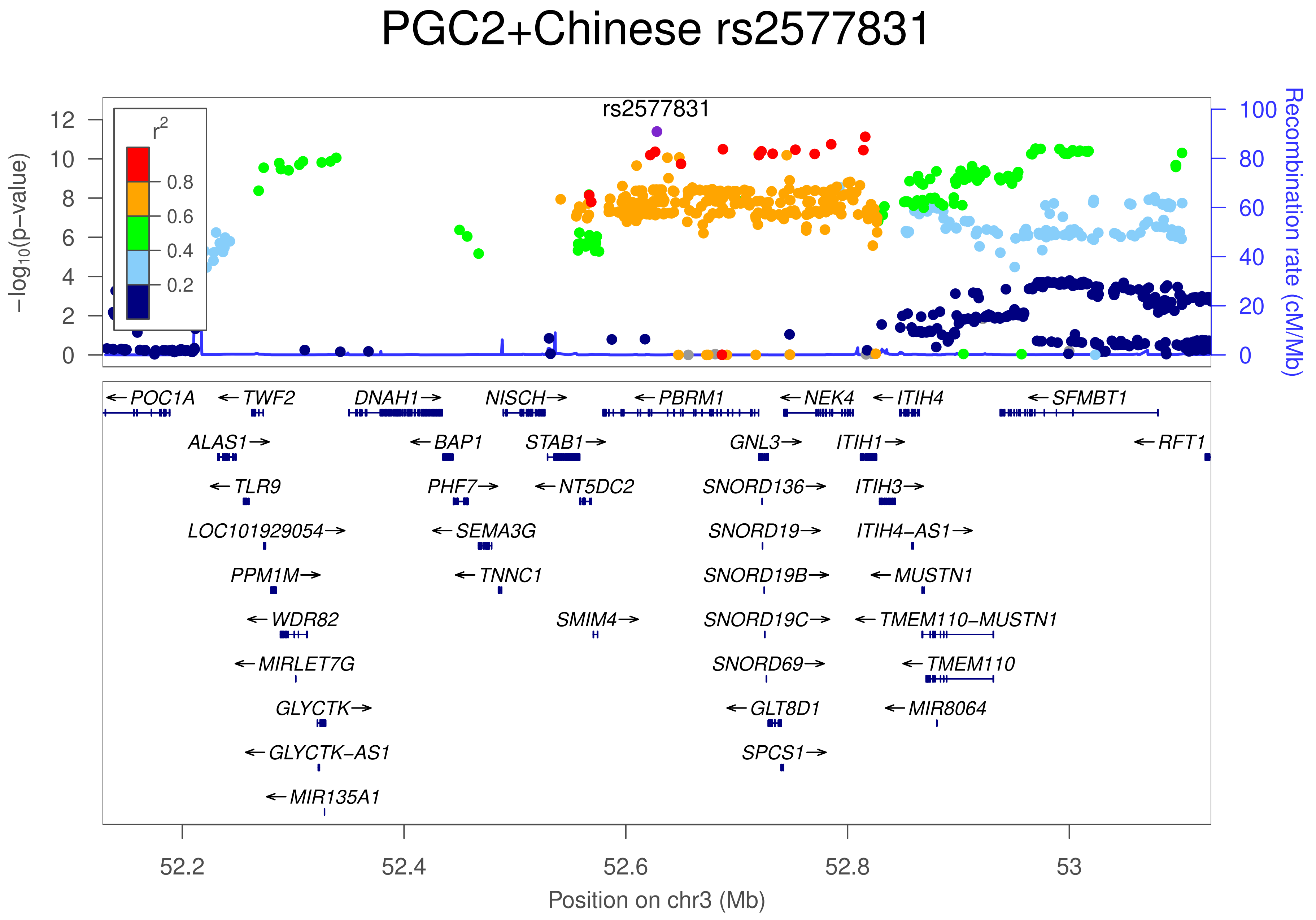


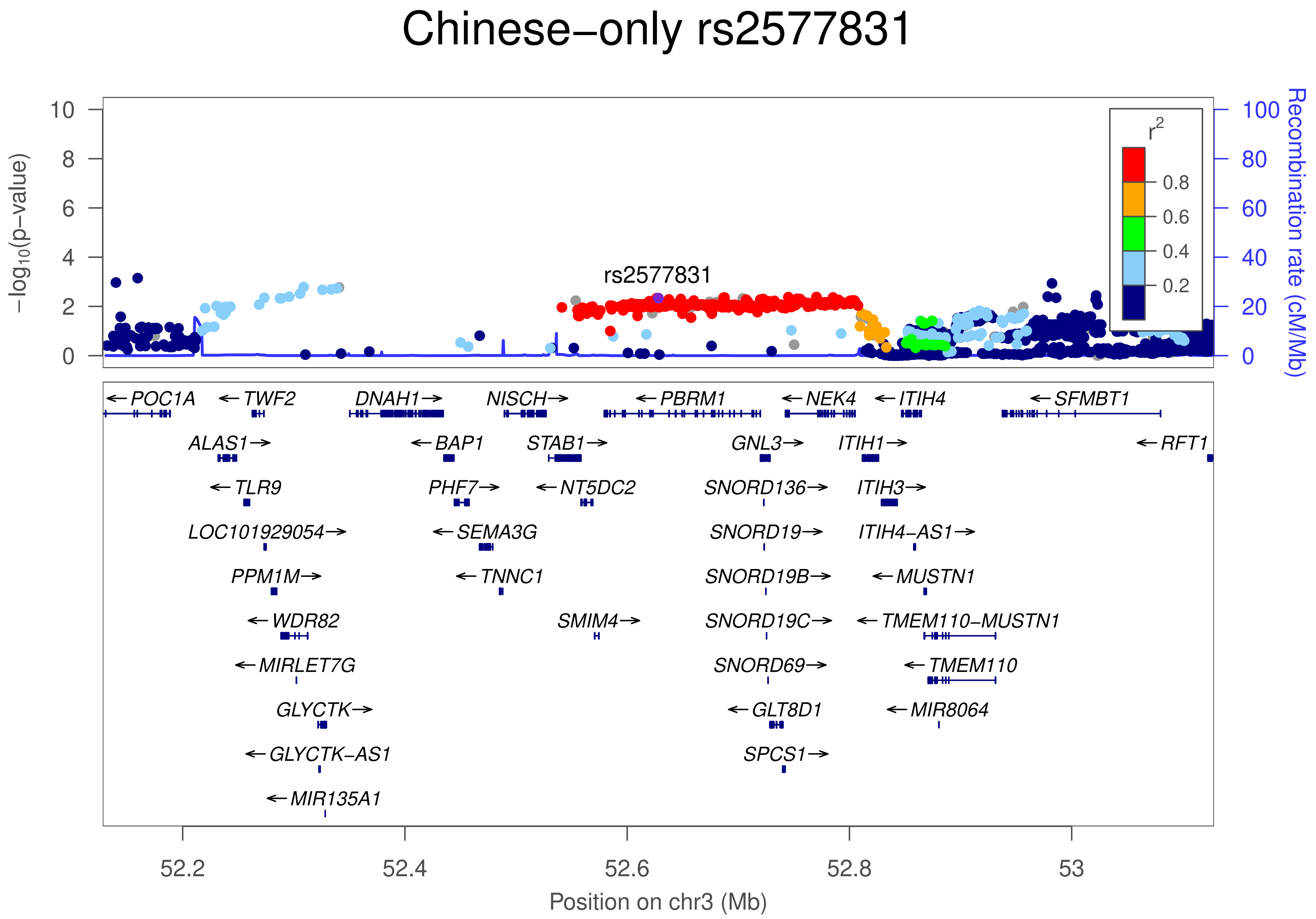
PGC2+Chinese rs3732386

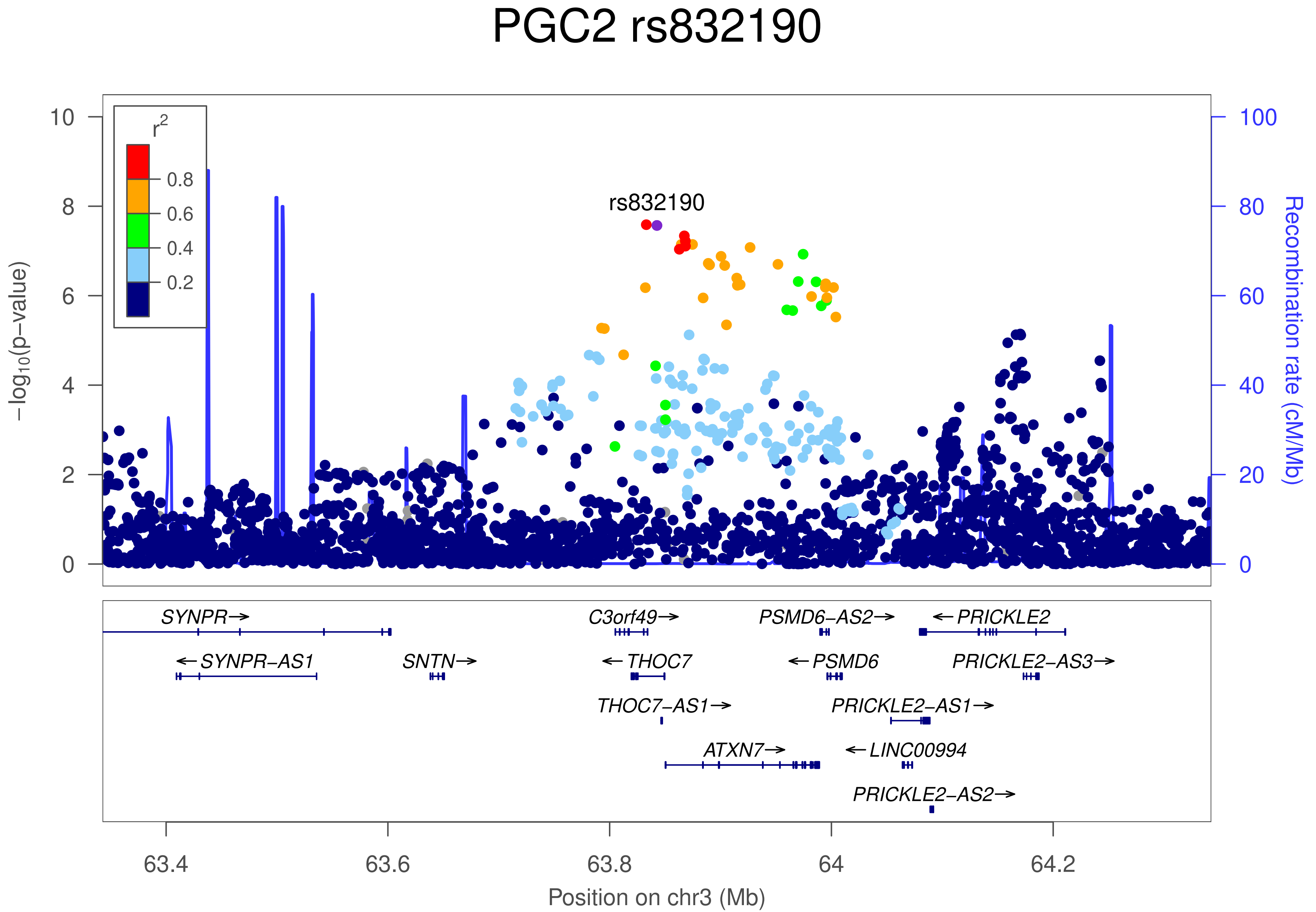


Chinese–only rs3732386

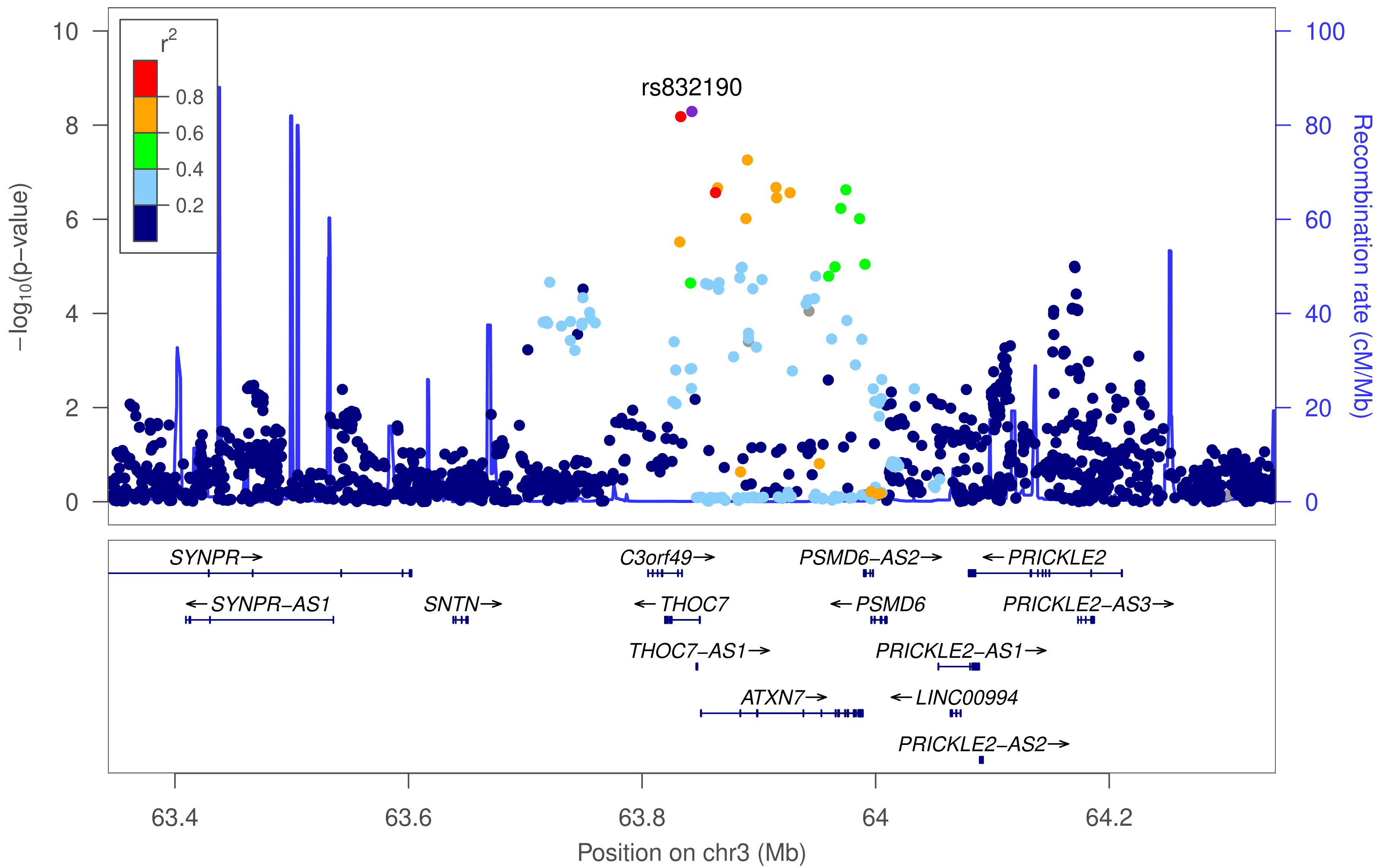

PGC2 rs2577831
rs2577831
−log10(p−value)
0
2
4
6
8
10
12
r2
0.2
0.4
0.6
0.8
Recombination rate (cM/Mb)
0
20
40
60
80
100
←POC1A
←TWF2
DNAH1→
NISCH→
←PBRM1
←NEK4
←ITIH4
←SFMBT1
ALAS1→
←BAP1
STAB1→
GNL3→
ITIH1→
←RFT1
←TLR9
PHF7→
←NT5DC2
SNORD136→
ITIH3→
LOC101929054→
←SEMA3G
SNORD19→
ITIH4−AS1→
PPM1M→
←TNNC1
SNORD19B→
←MUSTN1
←WDR82
SMIM4→
SNORD19C→
←TMEM110−MUSTN1
←MIRLET7G
SNORD69→
←TMEM110
GLYCTK→
←GLT8D1
←MIR8064
←GLYCTK−AS1
SPCS1→
←MIR135A1
52.2
52.4
52.6
52.8
53
Position on chr3 (Mb)

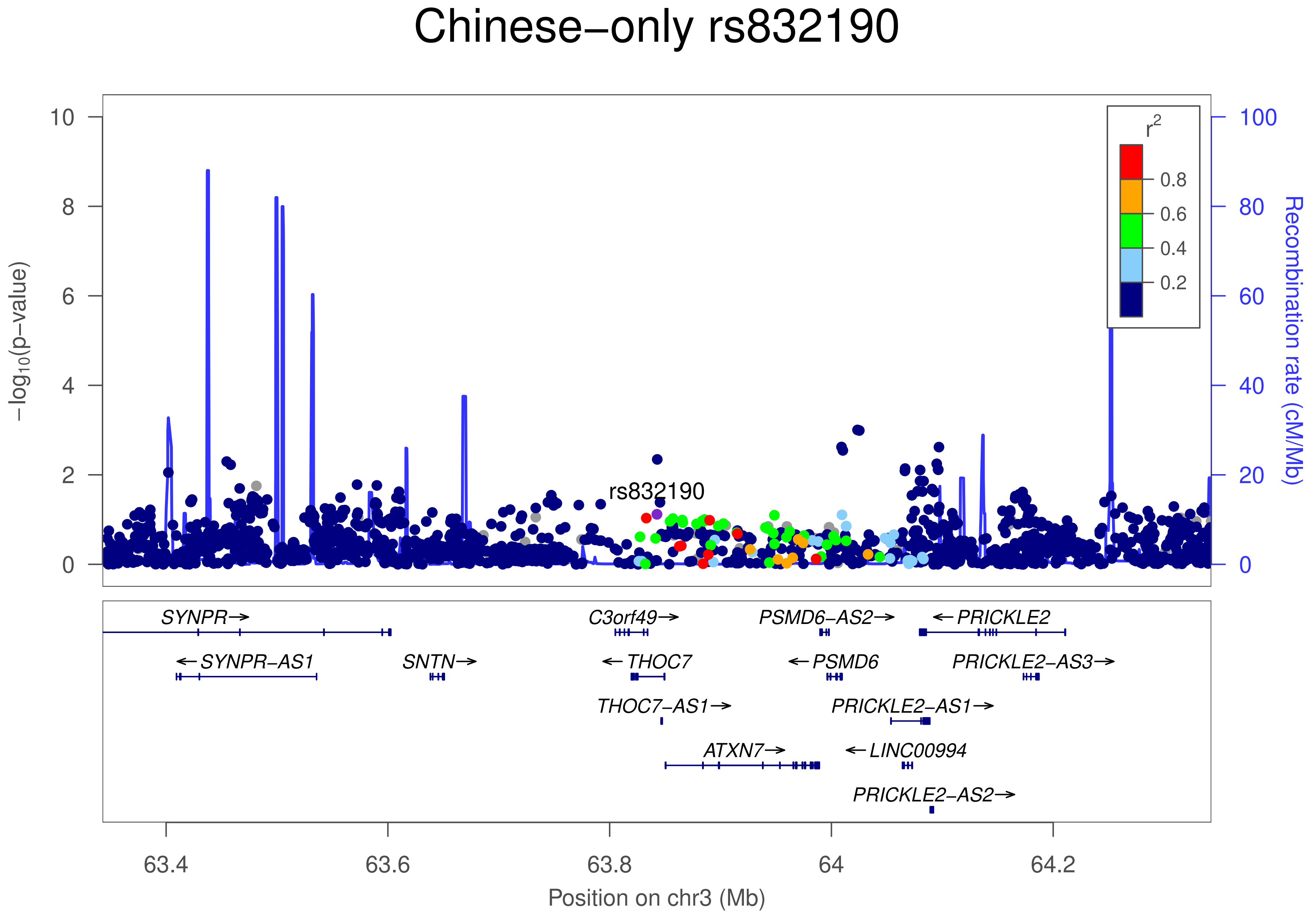

PGC2+Chinese rs2577831
rs2577831
r2
0.8
0.6
0.4
0.2
−log10(p−value)
0
2
4
6
8
10
12
Recombination rate (cM/Mb)
0
20
40
60
80
100
← POC1A
← TWF2
DNAH1 →
NISCH →
← PBRM1
← NEK4
← ITIH4
← SFMBT1
ALAS1 →
← BAP1
STAB1 →
GNL3 →
ITIH1 →
← RFT1
← TLR9
PHF7 →
← NT5DC2
SNORD136 →
ITIH3 →
LOC101929054 →
← SEMA3G
SNORD19 →
ITIH4−AS1 →
PPM1M →
← TNNC1
SNORD19B →
← MUSTN1
← WDR82
SMIM4 →
SNORD19C →
← TMEM110−MUSTN1
← MIRLET7G
SNORD69 →
← TMEM110
GLYCTK →
← GLT8D1
← MIR8064
← GLYCTK−AS1
SPCS1 →
← MIR135A1
52.2
52.4
52.6
52.8
53
Position on chr3 (Mb)

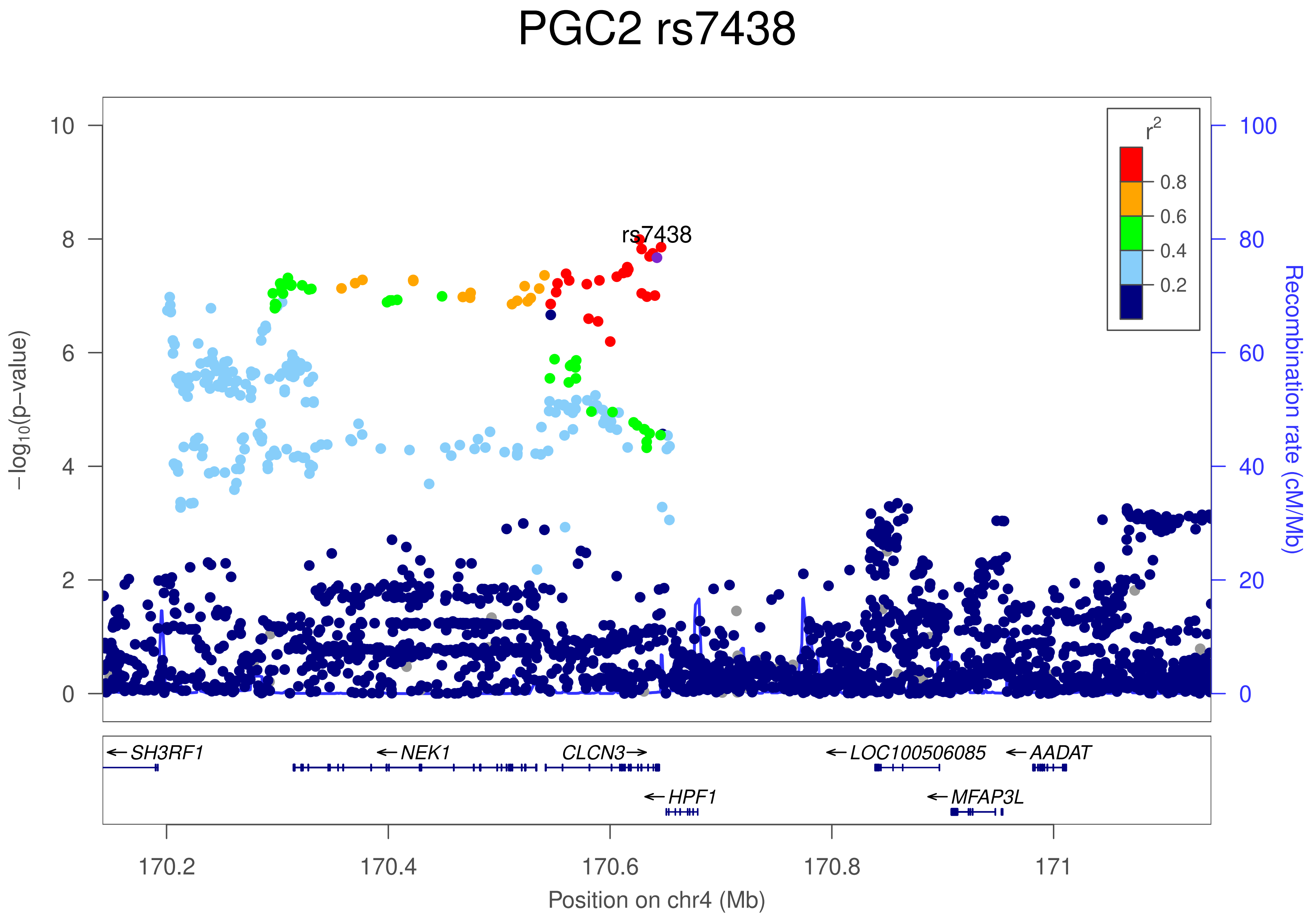

Chinese−only rs2577831
−log10(p−value)
10
8
6
4
2
0
rs2577831
r2
0.8
0.6
0.4
0.2
100
80
60
40
20
0
Recombination rate (cM/Mb)
← POC1A
← TWF2
DNAH1 →
NISCH →
← PBRM1
← NEK4
← ITIH4
← SFMBT1
ALAS1 →
← BAP1
STAB1 →
GNL3 →
ITIH1 →
← RFT1
← TLR9
PHF7 →
← NT5DC2
SNORD136 →
ITIH3 →
LOC101929054 →
← SEMA3G
SNORD19 →
ITIH4−AS1 →
PPM1M →
← TNNC1
SNORD19B →
← MUSTN1
← WDR82
SMIM4 →
SNORD19C →
← TMEM110−MUSTN1
← MIRLET7G
SNORD69 →
← TMEM110
GLYCTK →
← GLT8D1
← MIR8064
← GLYCTK−AS1
SPCS1 →
← MIR135A1
52.2
52.4
52.6
52.8
53
Position on chr3 (Mb)


PGC2 rs832190
rs832190
r^2
0.8
0.6
0.4
0.2
$-\log_{10}$(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
SYNPR→
←SYNPR−AS1
SNTN→
C3orf49→
←THOC7
THOC7−AS1→
ATXN7→
PSMD6−AS2→
←PSMD6
←LINC00994
PRICKLE2−AS1→
PRICKLE2−AS2→
←PRICKLE2
PRICKLE2−AS3→
63.4
63.6
63.8
64
64.2
Position on chr3 (Mb)

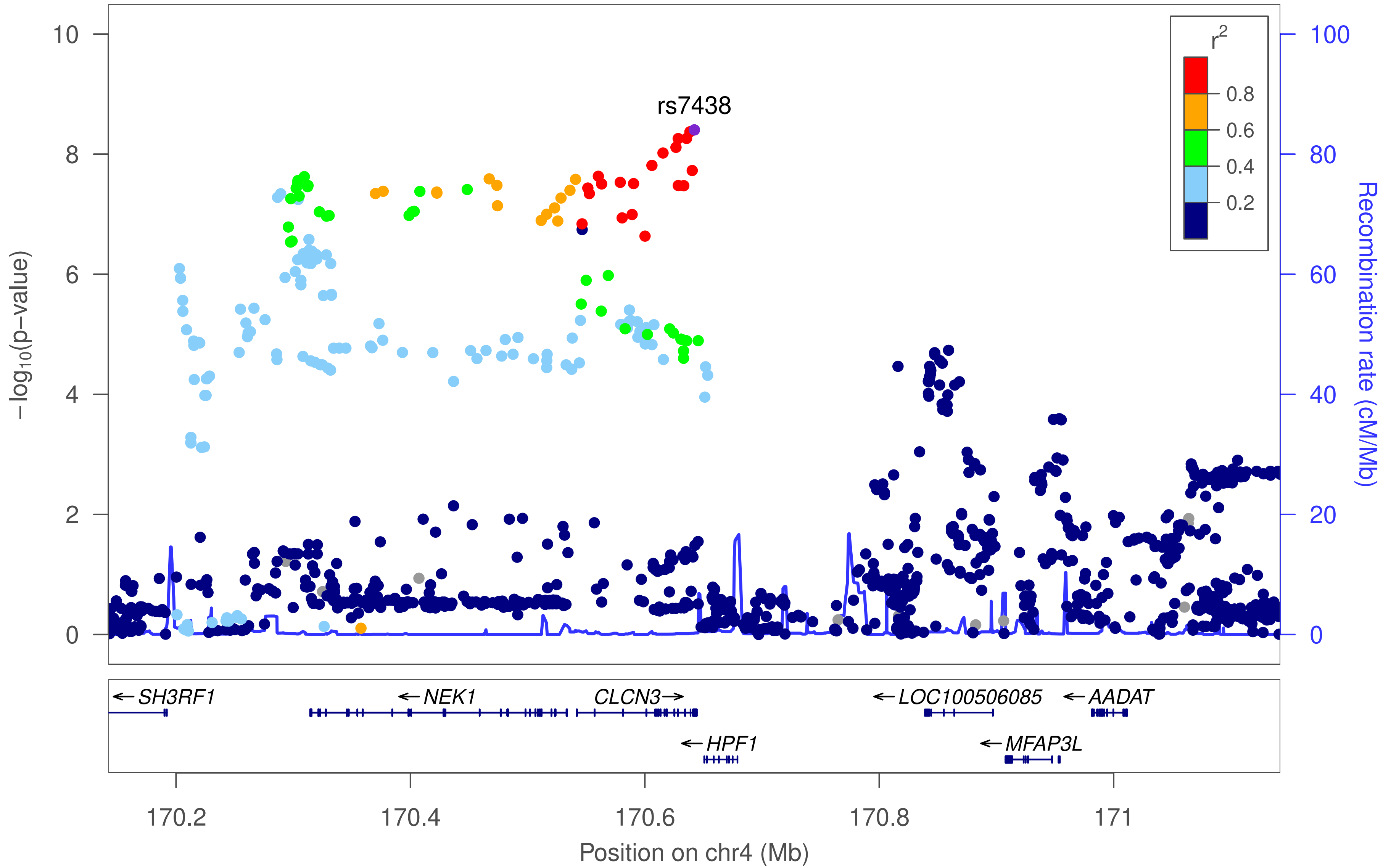
PGC2+Chinese rs832190



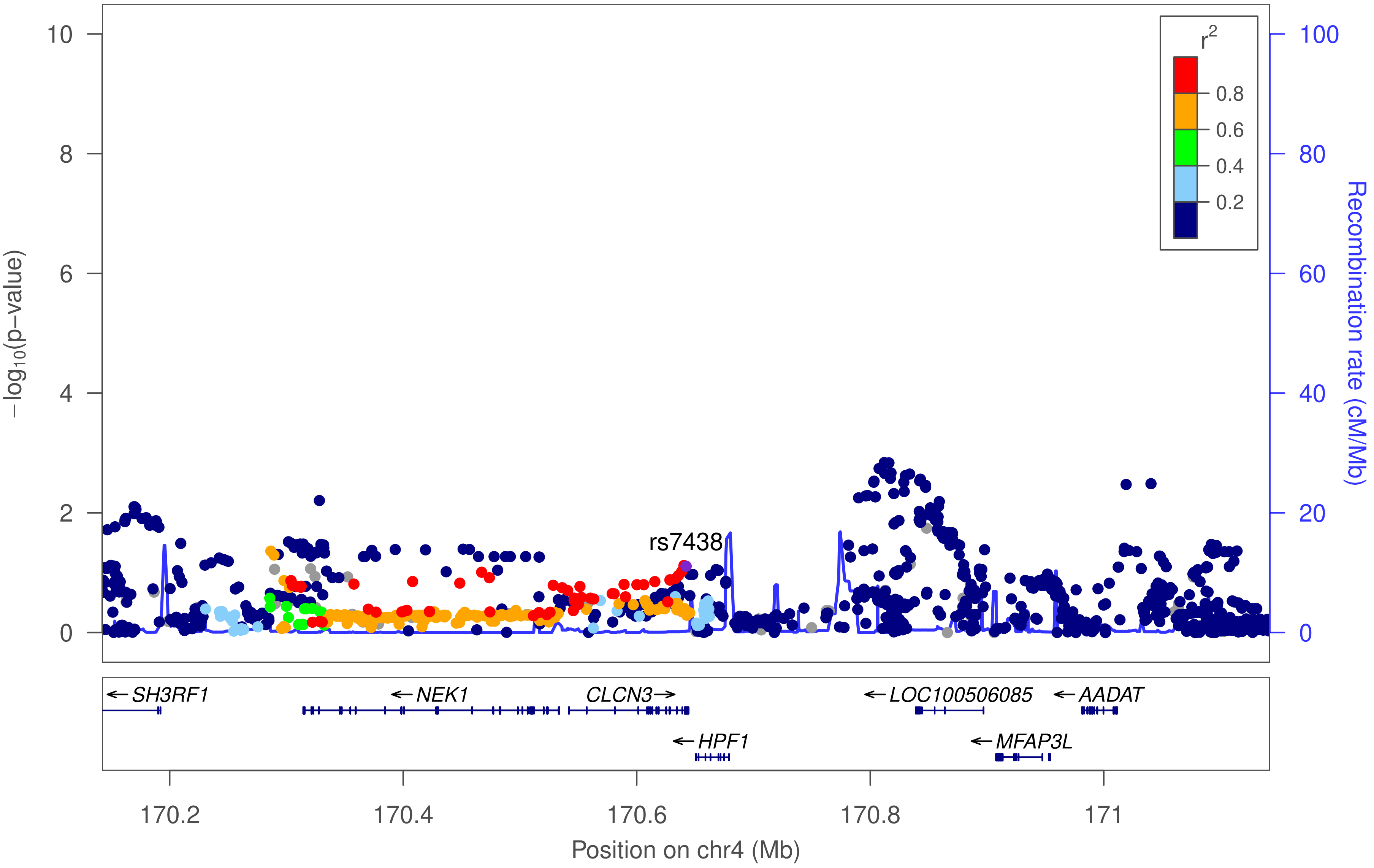

Chinese–only rs832190
−log10(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
r2
0.2
0.4
0.6
0.8
rs832190
SYNPR→
←SYNPR−AS1
SNTN→
C3orf49→
←THOC7
THOC7−AS1→
ATXN7→
PSMD6−AS2→
←PSMD6
←PRICKLE2
PRICKLE2−AS3→
PRICKLE2−AS1→
←LINC00994
PRICKLE2−AS2→
63.4
63.6
63.8
64
64.2
Position on chr3 (Mb)

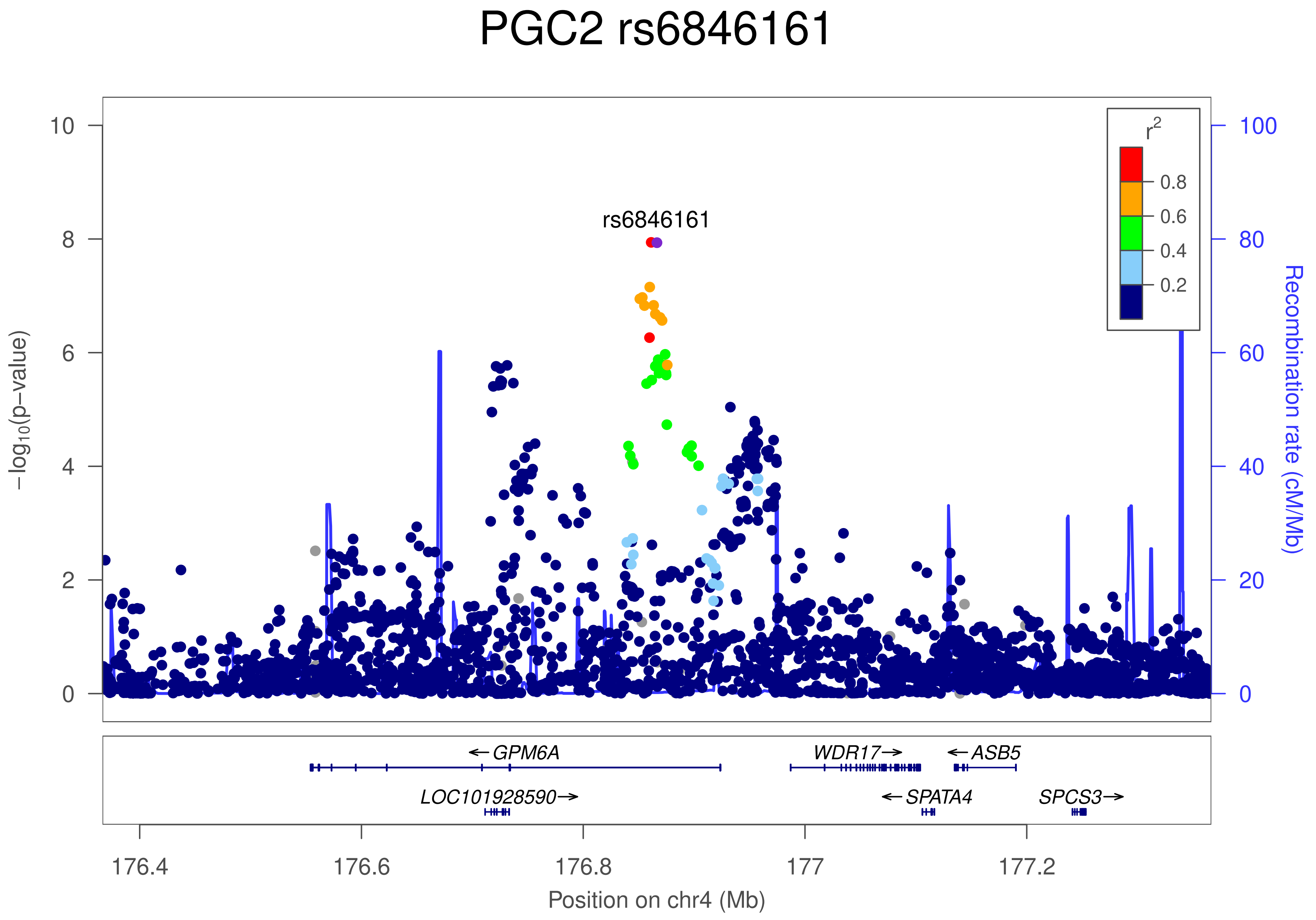

PGC2 rs7438
rs7438
r²
0.8
0.6
0.4
0.2
−log10(p−value)
10
8
6
4
2
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
← SH3RF1
← NEK1
CLCN3→
← HPF1
← LOC100506085
← AADAT
← MFAP3L
170.2
170.4
170.6
170.8
171
Position on chr4 (Mb)

PGC2+Chinese rs7438

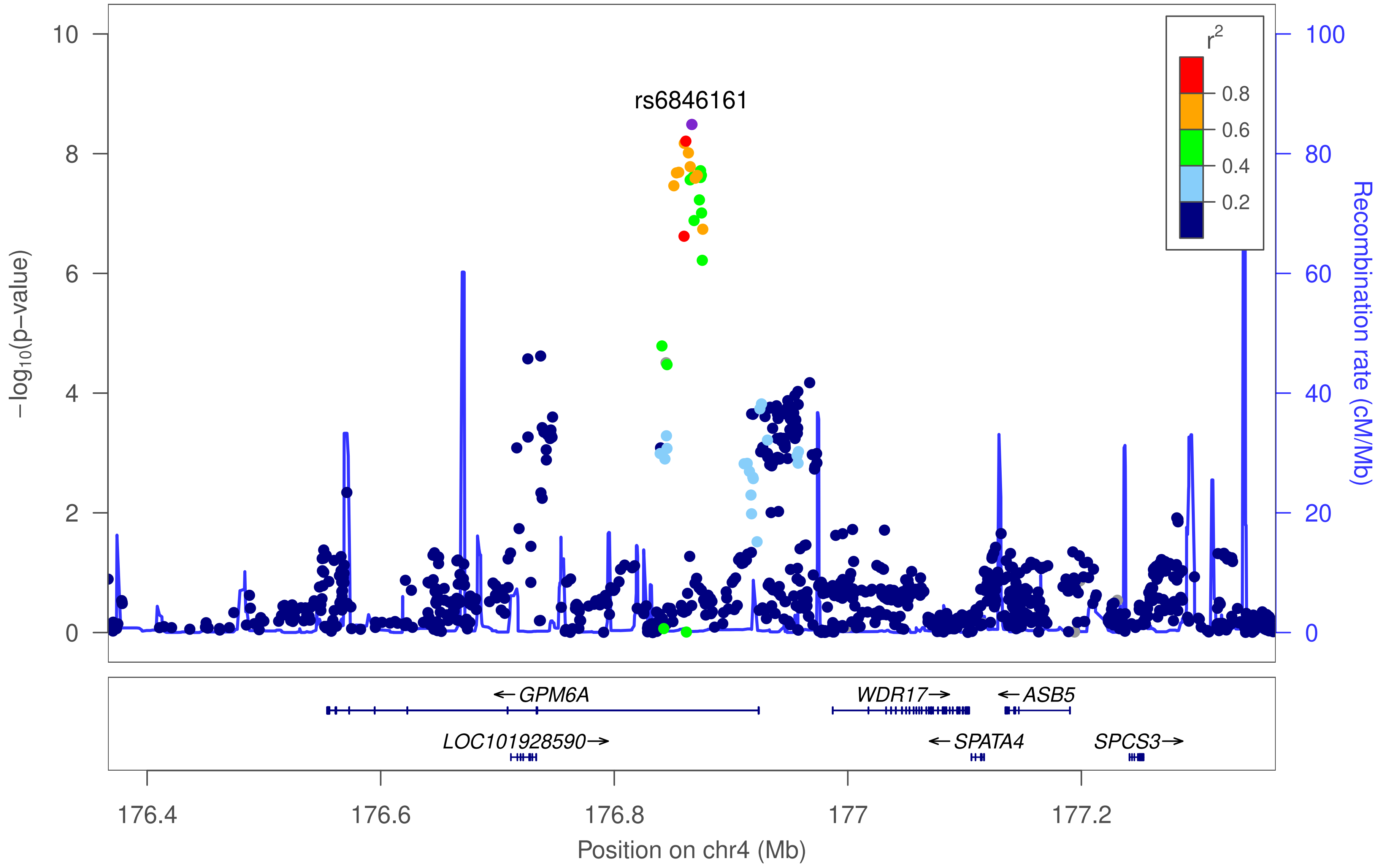


Chinese–only rs7438

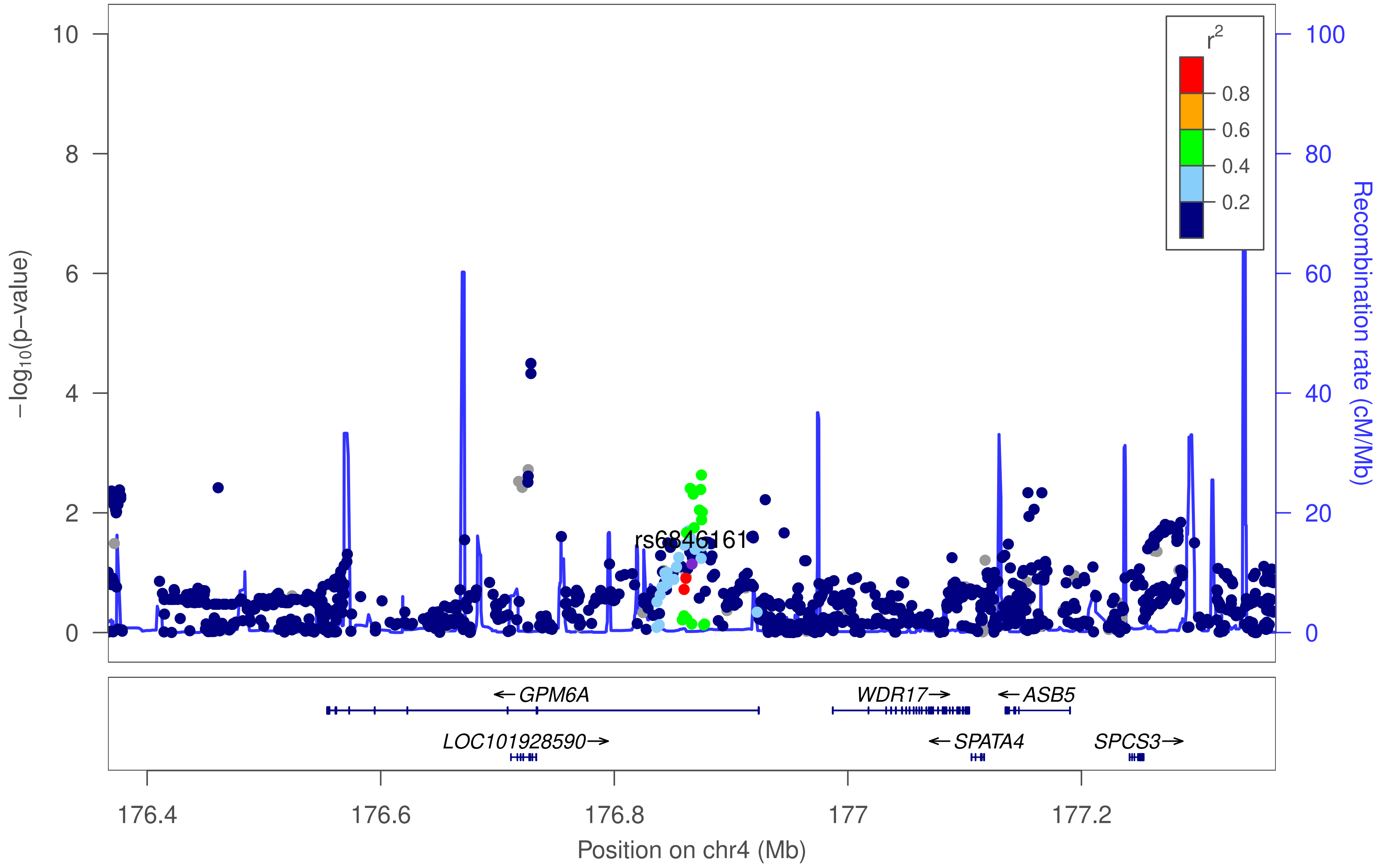



PGC2 rs6846161
rs6846161
r²
0.8
0.6
0.4
0.2
−log₁₀(p−value)
10
8
6
4
2
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
← GPM6A
WDR17 →
← ASB5
LOC101928590 →
← SPATA4
SPCS3 →
176.4
176.6
176.8
177
177.2
Position on chr4 (Mb)

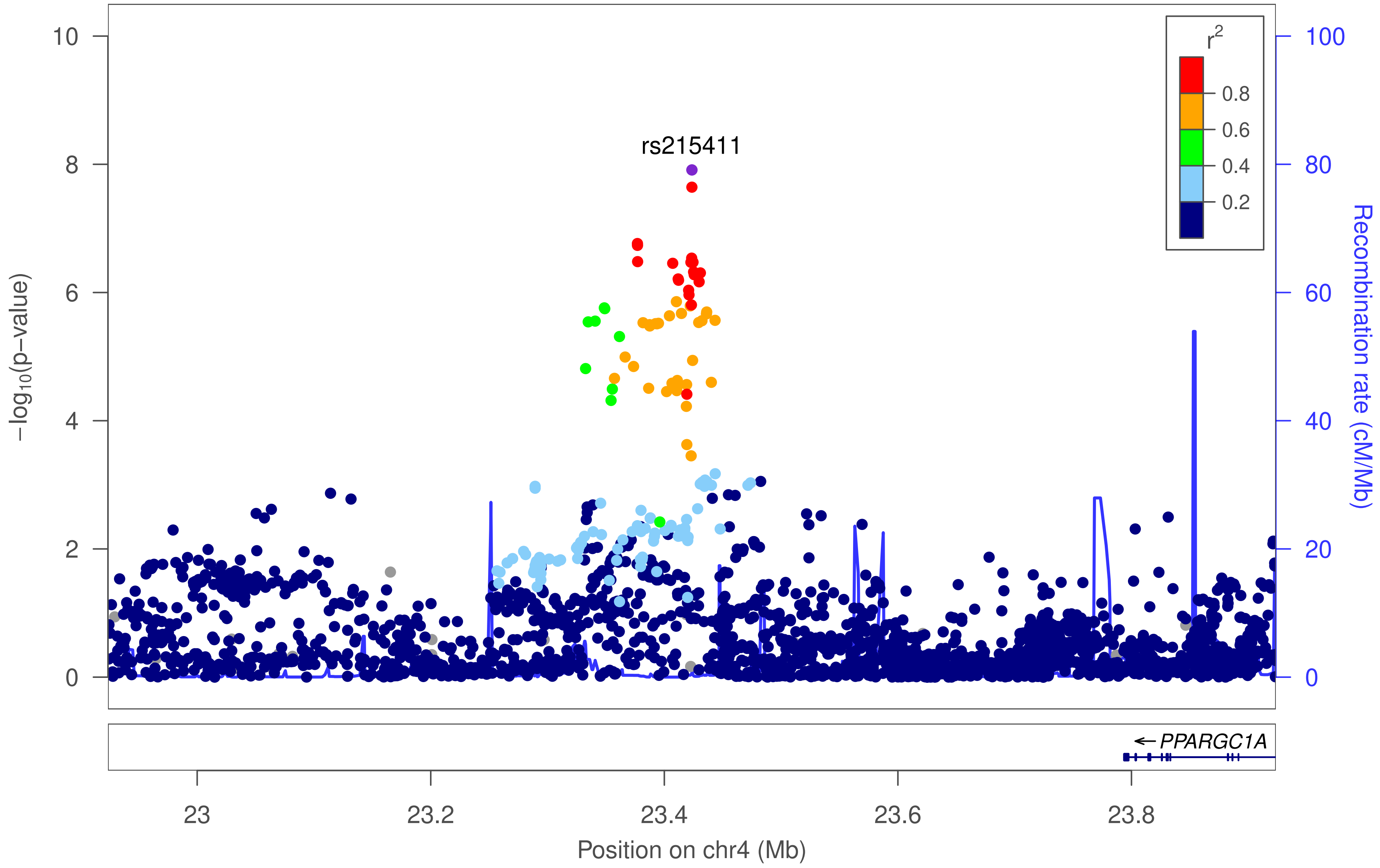
PGC2+Chinese rs6846161



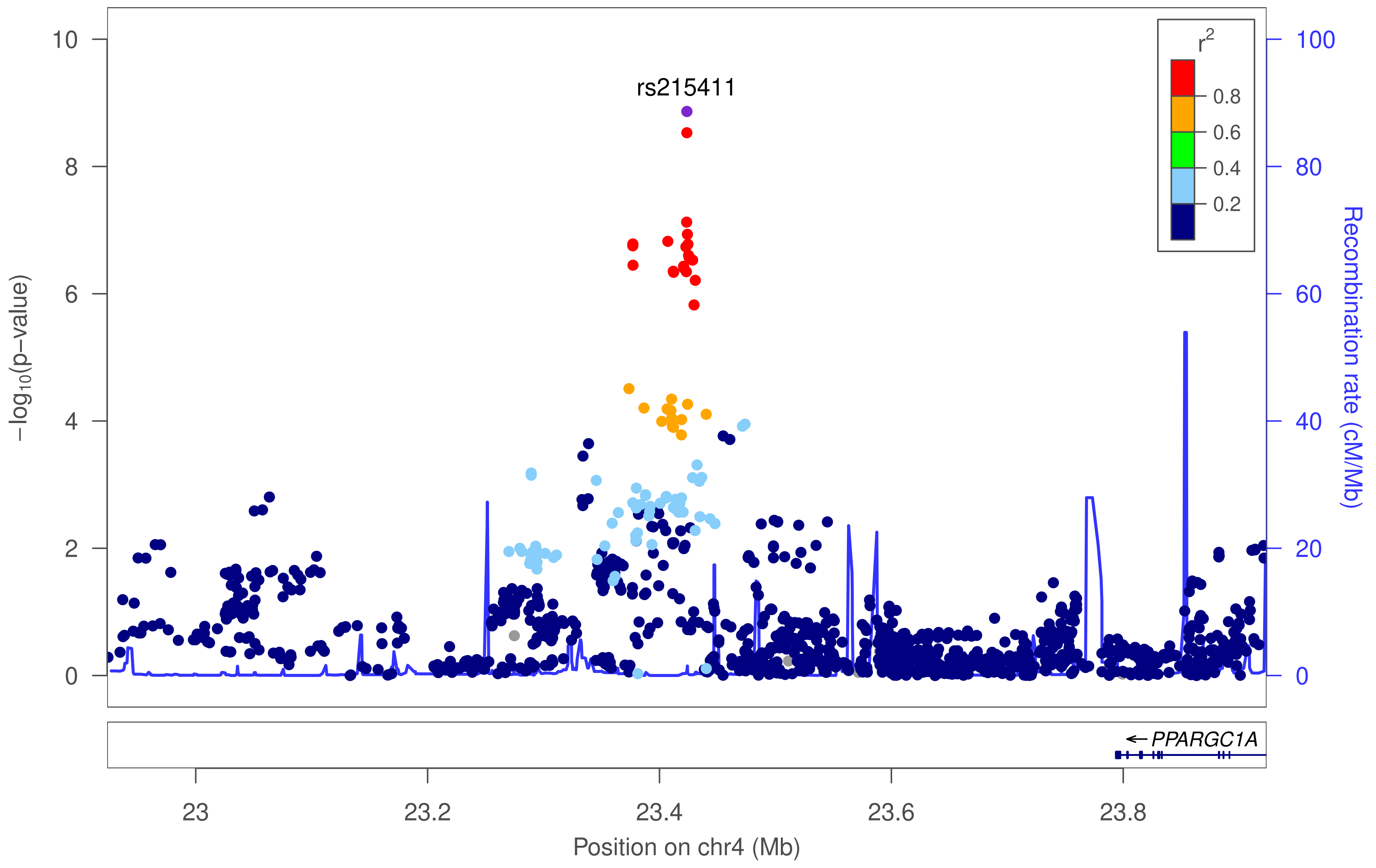
Chinese−only rs6846161

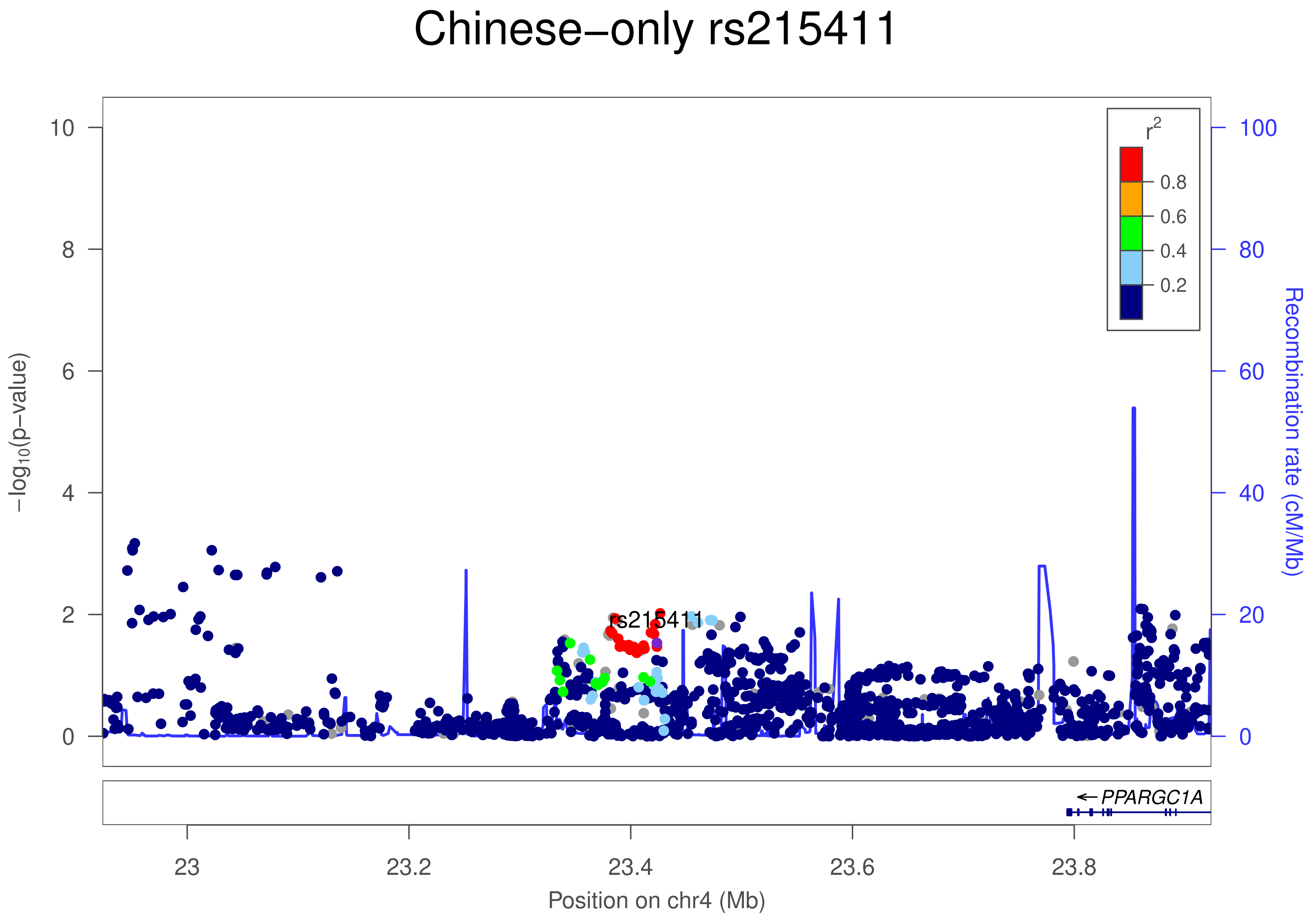


PGC2 rs215411

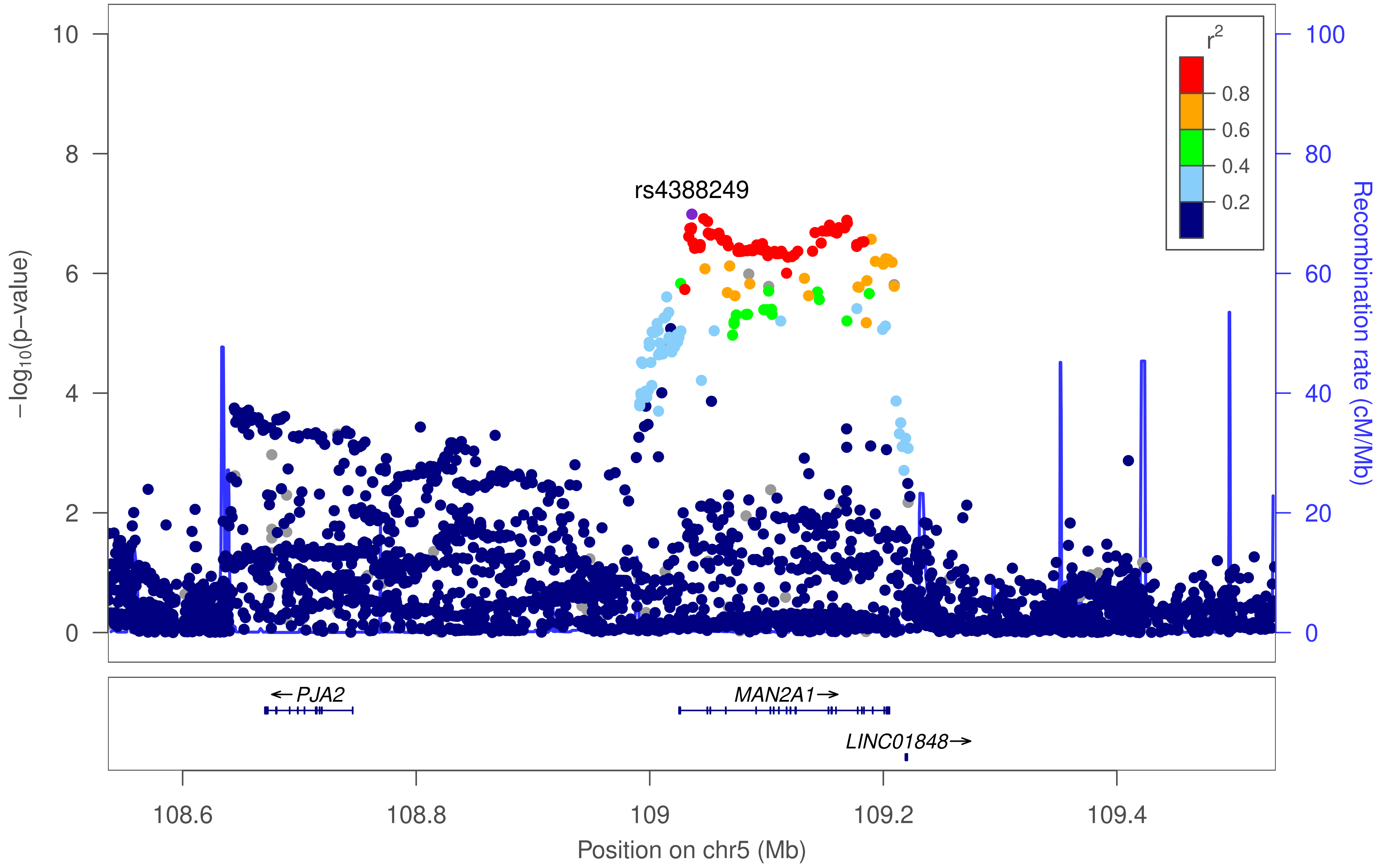


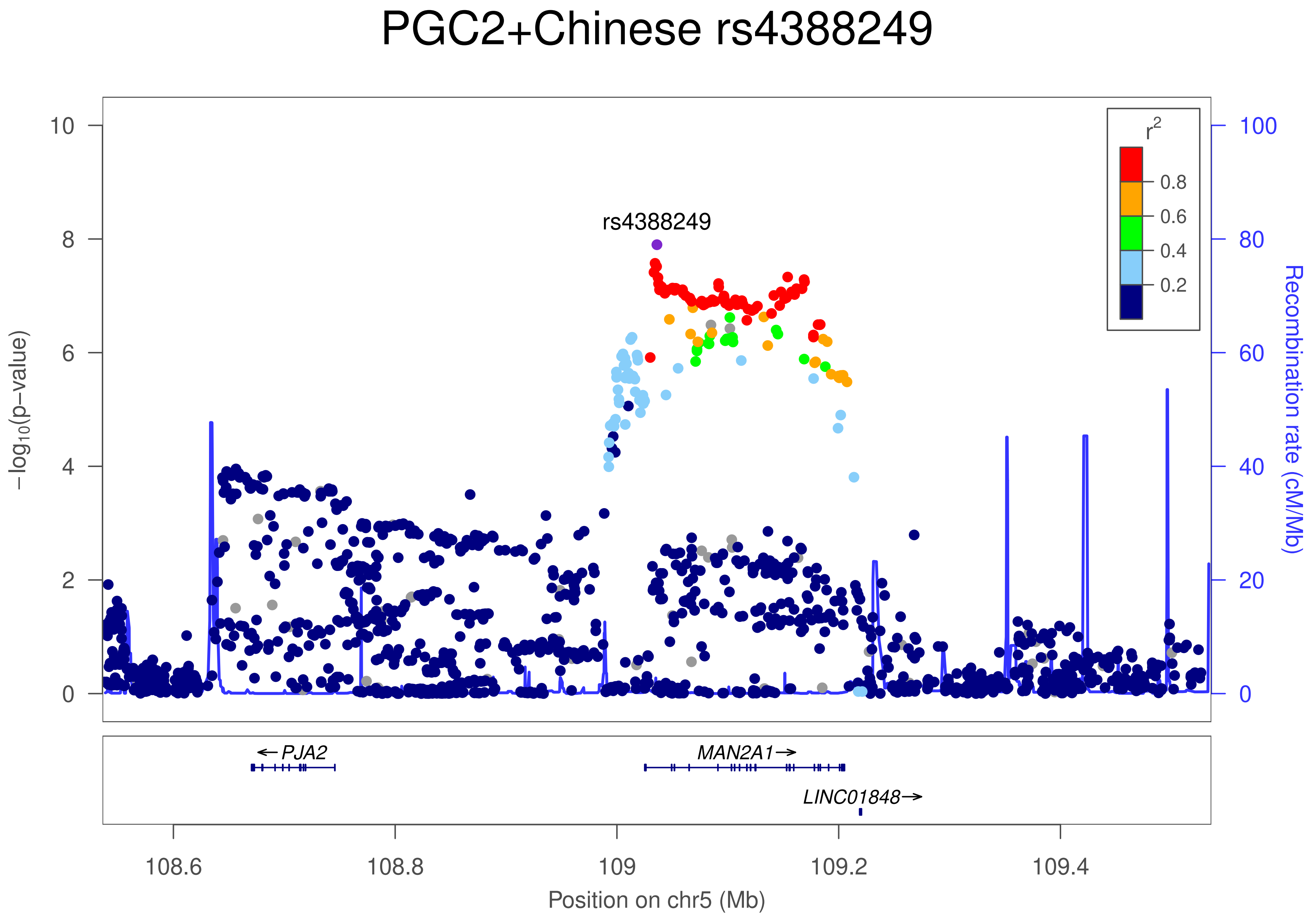
PGC2+Chinese rs215411



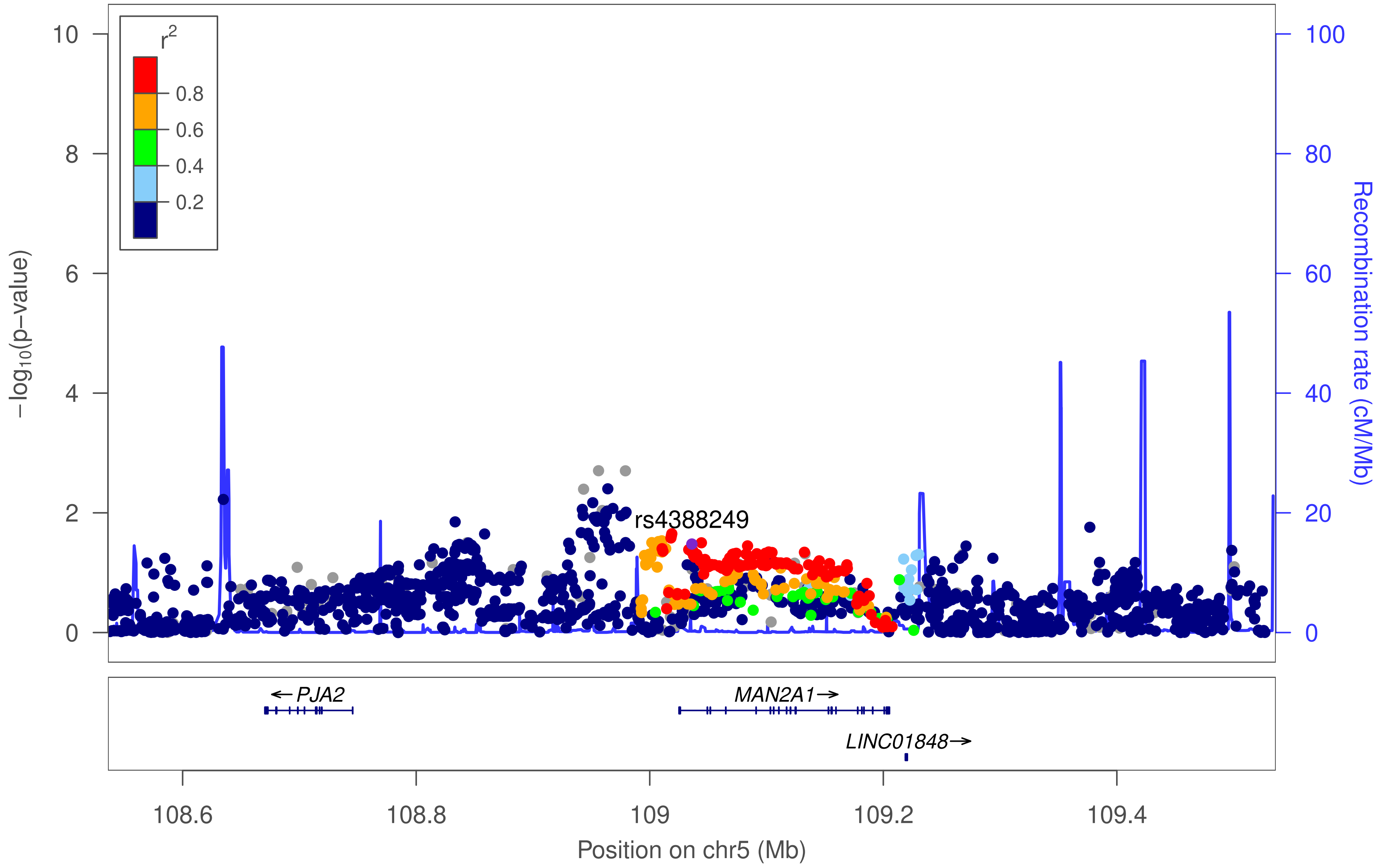

Chinese−only rs215411
r²
0.8
0.6
0.4
0.2
10
8
6
4
2
0
−log₁₀(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
rs215411
← PPARGC1A
23
23.2
23.4
23.6
23.8
Position on chr4 (Mb)

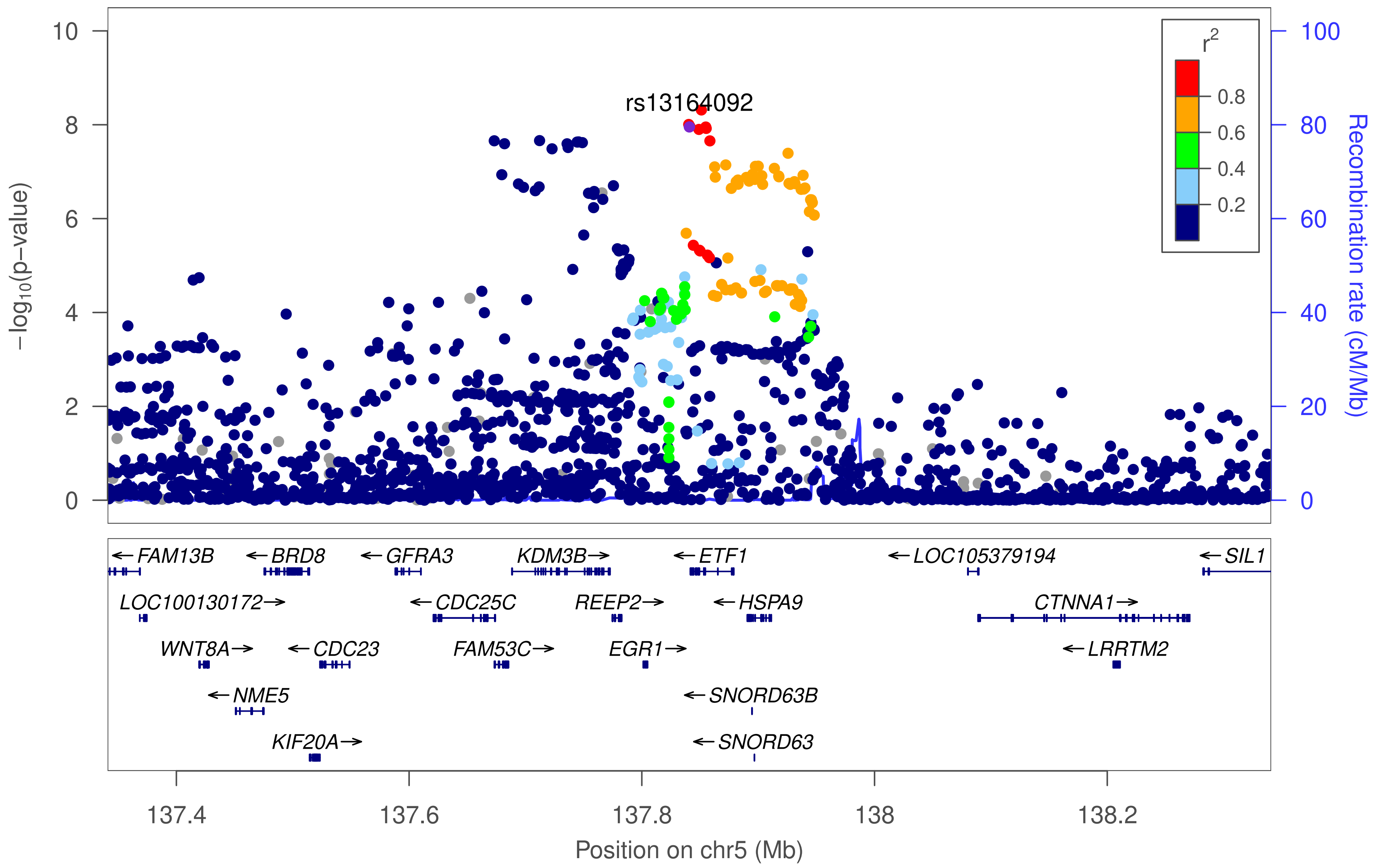
PGC2 rs4388249



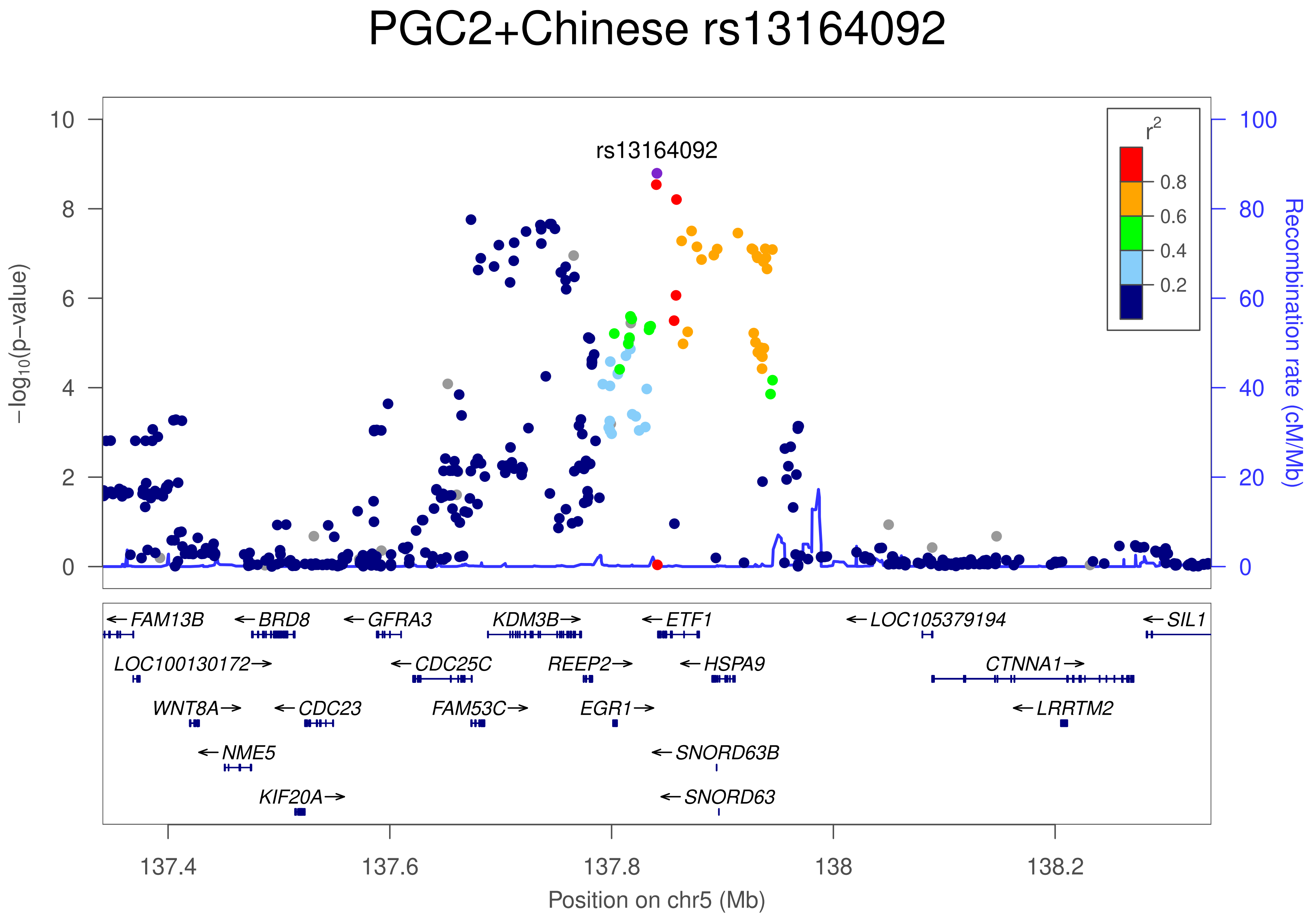

PGC2+Chinese rs4388249
rs4388249
r2
0.8
0.6
0.4
0.2
−log10(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
← PJA2
MAN2A1→
LINC01848→
108.6
108.8
109
109.2
109.4
Position on chr5 (Mb)

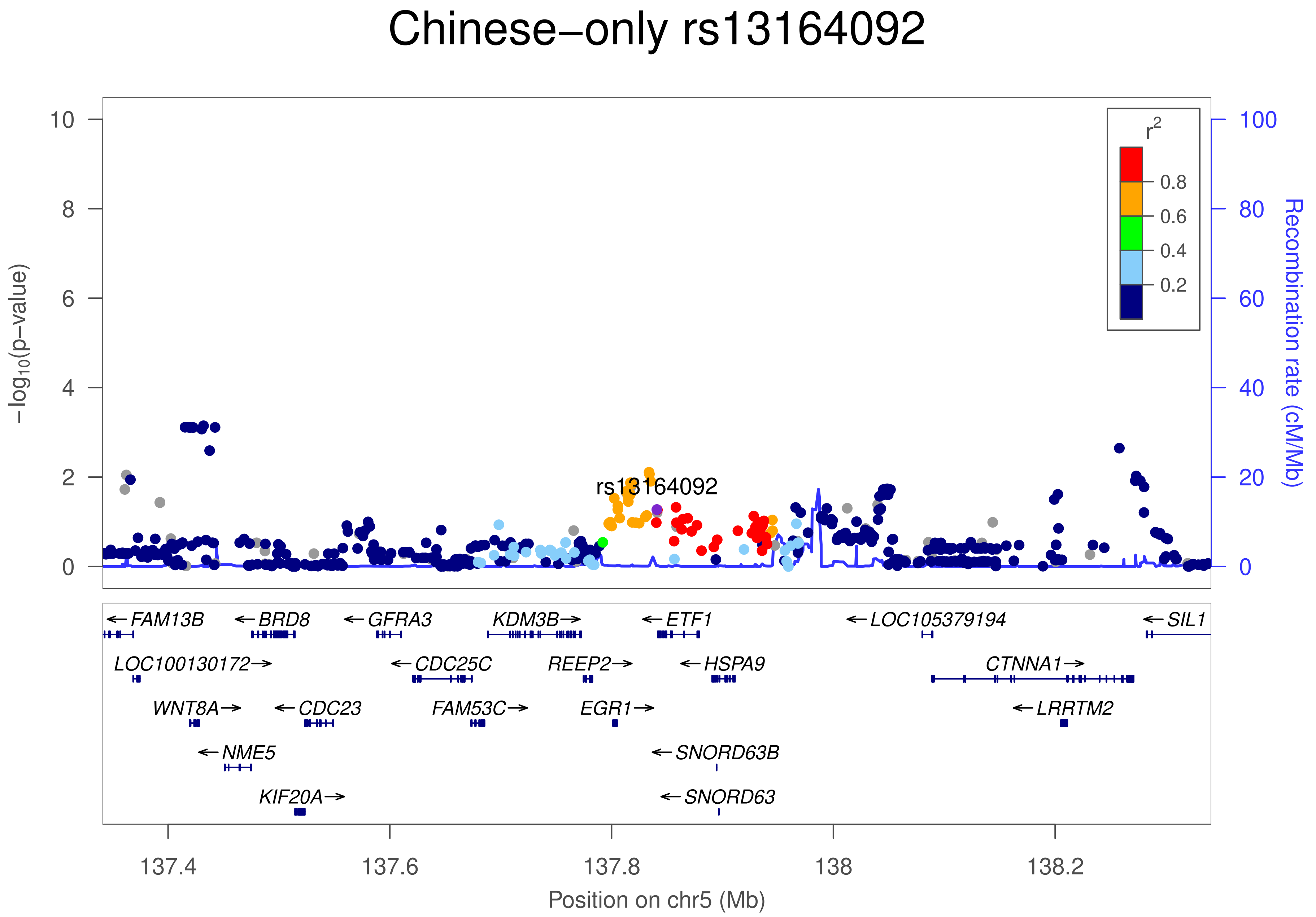
Chinese−only rs4388249

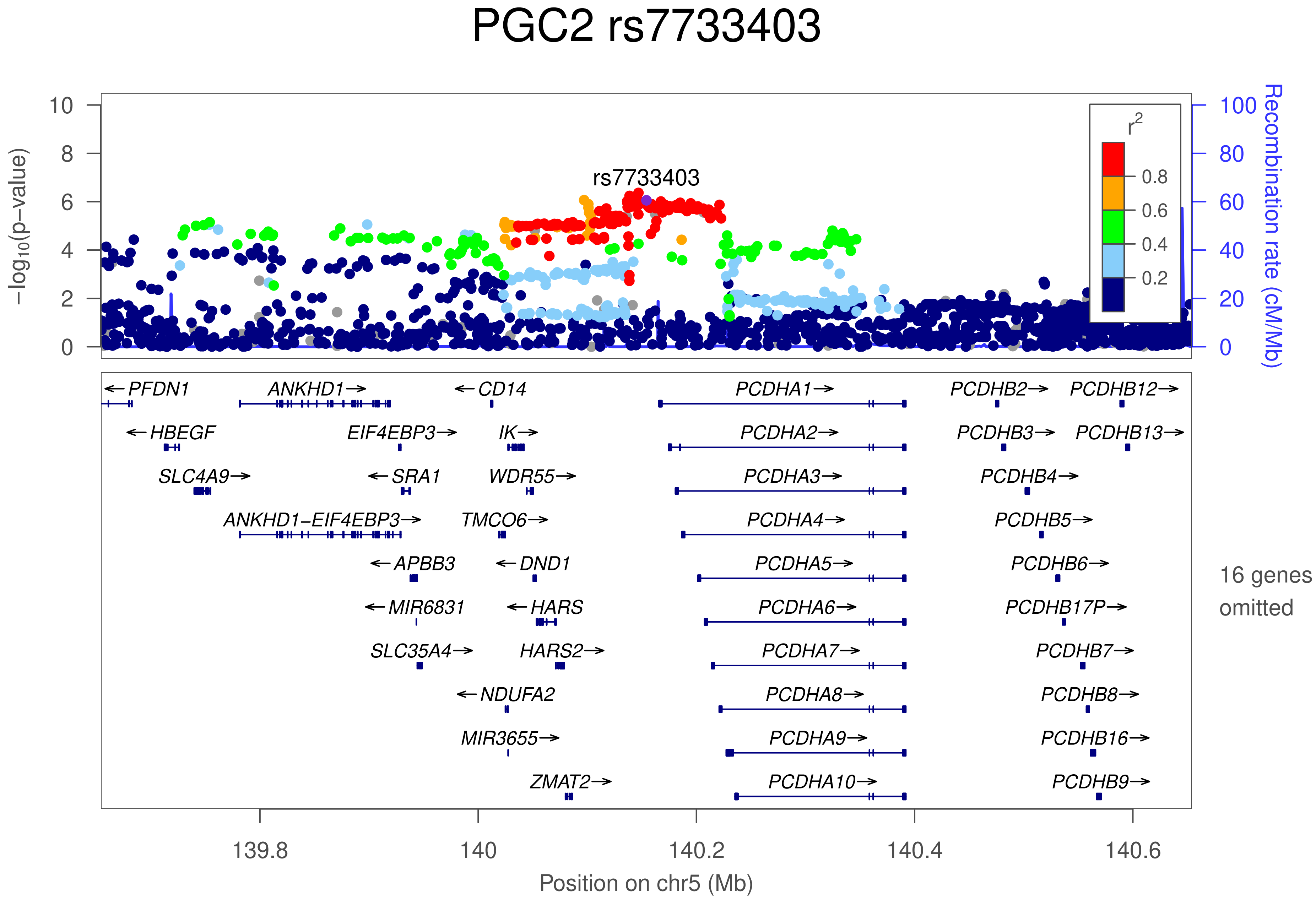


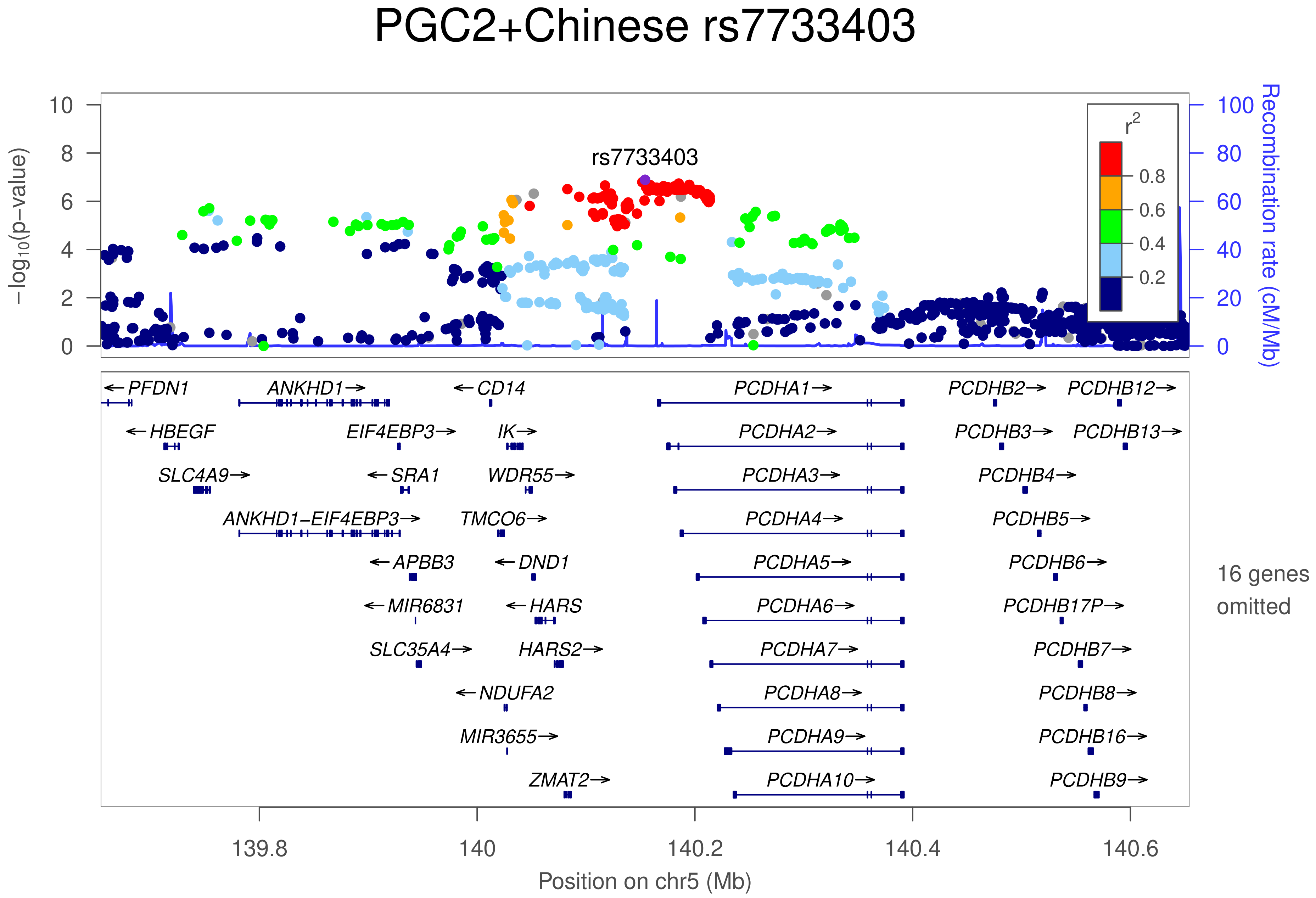


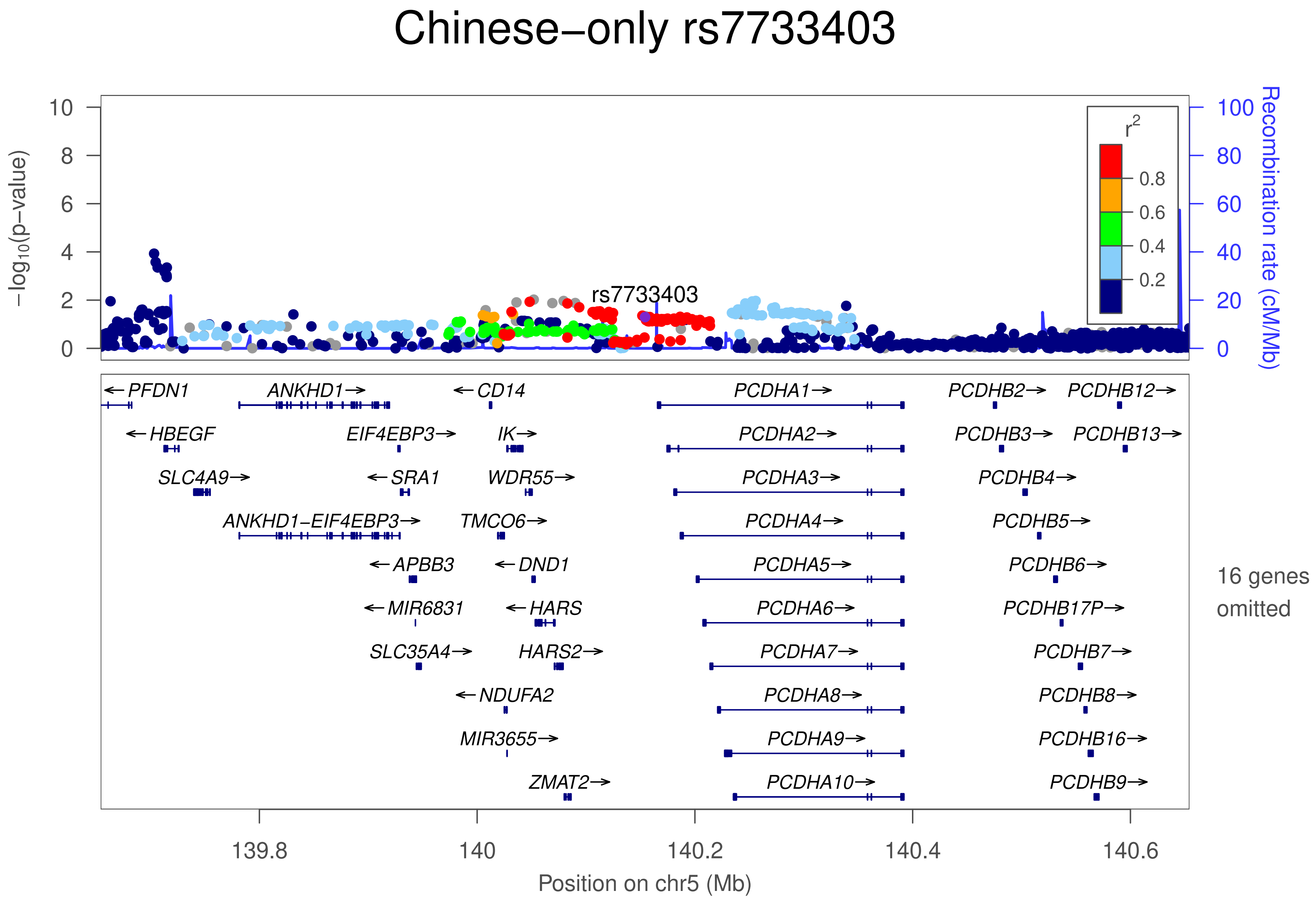
PGC2 rs13164092


PGC2+Chinese rs13164092
rs13164092
−log10(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
r2
0.8
0.6
0.4
0.2
FAM13B
BRD8
GFRA3
KDM3B
ETF1
LOC105379194
SIL1
LOC100130172
CDC25C
REEP2
HSPA9
CTNNA1
WNT8A
CDC23
FAM53C
EGR1
LRRTM2
NME5
SNORD63B
KIF20A
SNORD63
137.4
137.6
137.8
138
138.2
Position on chr5 (Mb)


Chinese–only rs13164092
−log$_{10}$(p−value)
10
8
6
4
2
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
r^2
0.8
0.6
0.4
0.2
rs13164092
←FAM13B
←BRD8
←GFRA3
KDM3B→
←ETF1
←LOC105379194
←SIL1
LOC100130172→
←CDC25C
REEP2→
←HSPA9
CTNNA1→
WNT8A→
←CDC23
FAM53C→
EGR1→
←LRRTM2
←NME5
←SNORD63B
KIF20A→
←SNORD63
137.4
137.6
137.8
138
138.2
Position on chr5 (Mb)

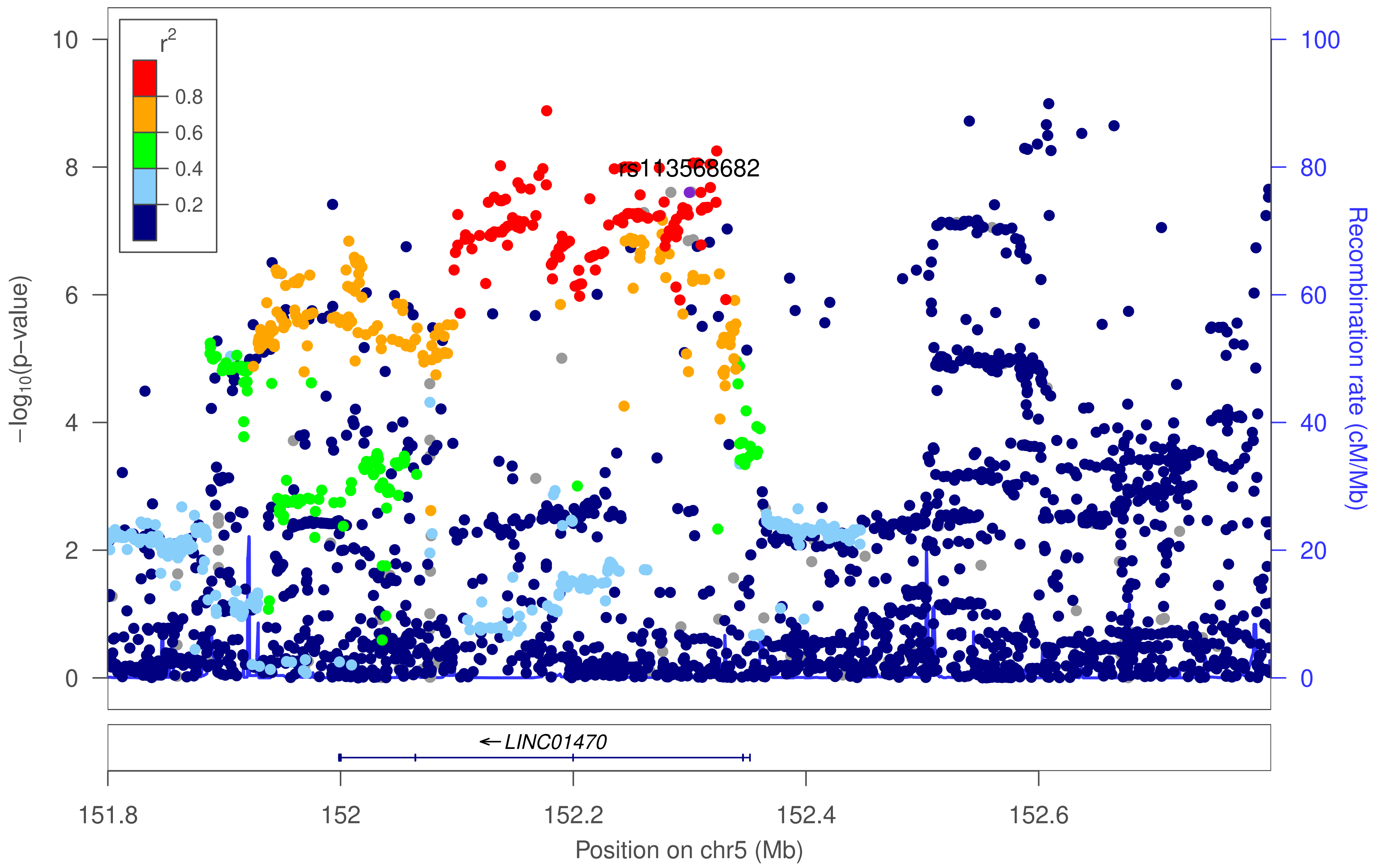

PGC2 rs7733403
rs7733403
−log10(p−value)
10
8
6
4
2
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
r2
0.8
0.6
0.4
0.2
← PFDN1
ANKHD1 →
← CD14
PCDHA1 →
PCDHB2 →
PCDHB12 →
← HBEGF
EIF4EBP3 →
IK →
PCDHA2 →
PCDHB3 →
PCDHB13 →
SLC4A9 →
← SRA1
WDR55 →
PCDHA3 →
PCDHB4 →
ANKHD1−EIF4EBP3 →
TMCO6 →
PCDHA4 →
PCDHB5 →
← APBB3
← DND1
PCDHA5 →
PCDHB6 →
16 genes omitted
← MIR6831
← HARS
PCDHA6 →
PCDHB17P →
SLC35A4 →
HARS2 →
PCDHA7 →
PCDHB7 →
← NDUFA2
PCDHA8 →
PCDHB8 →
MIR3655 →
PCDHA9 →
PCDHB16 →
ZMAT2 →
PCDHA10 →
PCDHB9 →
139.8
140
140.2
140.4
140.6
Position on chr5 (Mb)


PGC2+Chinese rs7733403
rs7733403
−log10(p−value)
10
8
6
4
2
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
r2
0.8
0.6
0.4
0.2
← PFDN1
ANKHD1 →
← CD14
PCDHA1 →
PCDHB2 →
PCDHB12 →
← HBEGF
EIF4EBP3 →
IK →
PCDHA2 →
PCDHB3 →
PCDHB13 →
SLC4A9 →
← SRA1
WDR55 →
PCDHA3 →
PCDHB4 →
ANKHD1−EIF4EBP3 →
TMCO6 →
PCDHA4 →
PCDHB5 →
← APBB3
← DND1
PCDHA5 →
PCDHB6 →
16 genes omitted
← MIR6831
← HARS
PCDHA6 →
PCDHB17P →
SLC35A4 →
HARS2 →
PCDHA7 →
PCDHB7 →
← NDUFA2
PCDHA8 →
PCDHB8 →
MIR3655 →
PCDHA9 →
PCDHB16 →
ZMAT2 →
PCDHA10 →
PCDHB9 →
139.8
140
140.2
140.4
140.6
Position on chr5 (Mb)

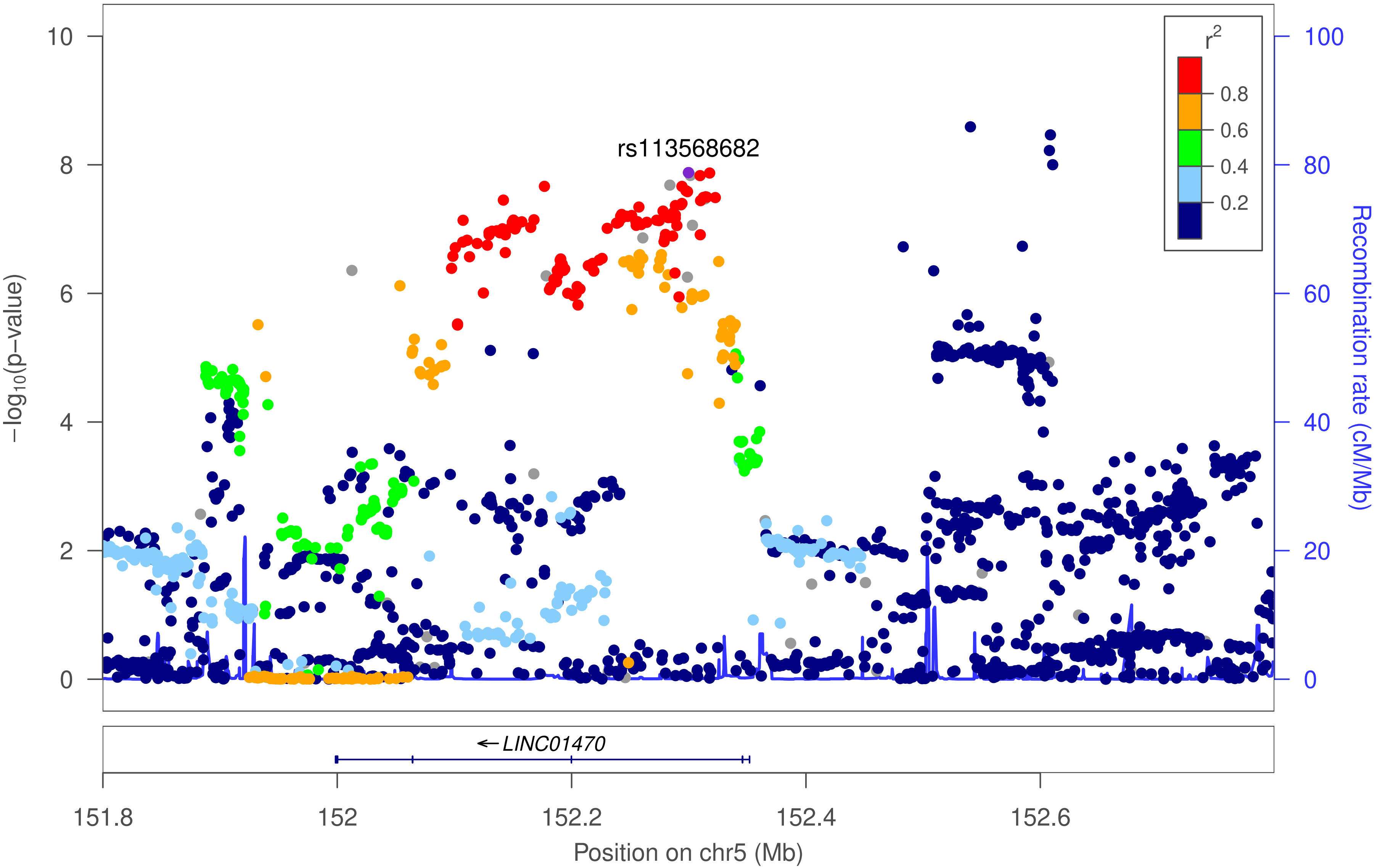


Chinese–only rs7733403

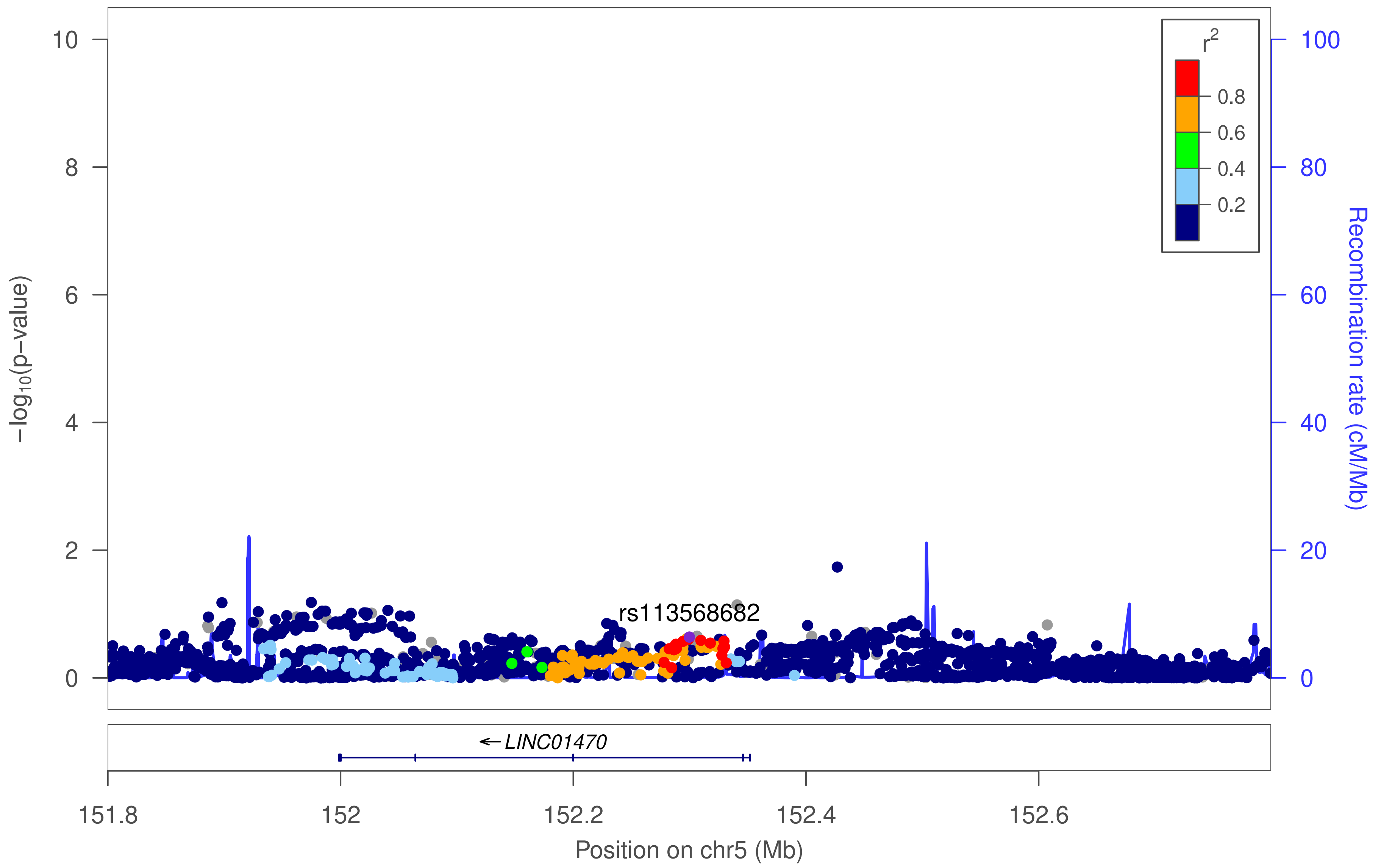
PGC2 rs113568682



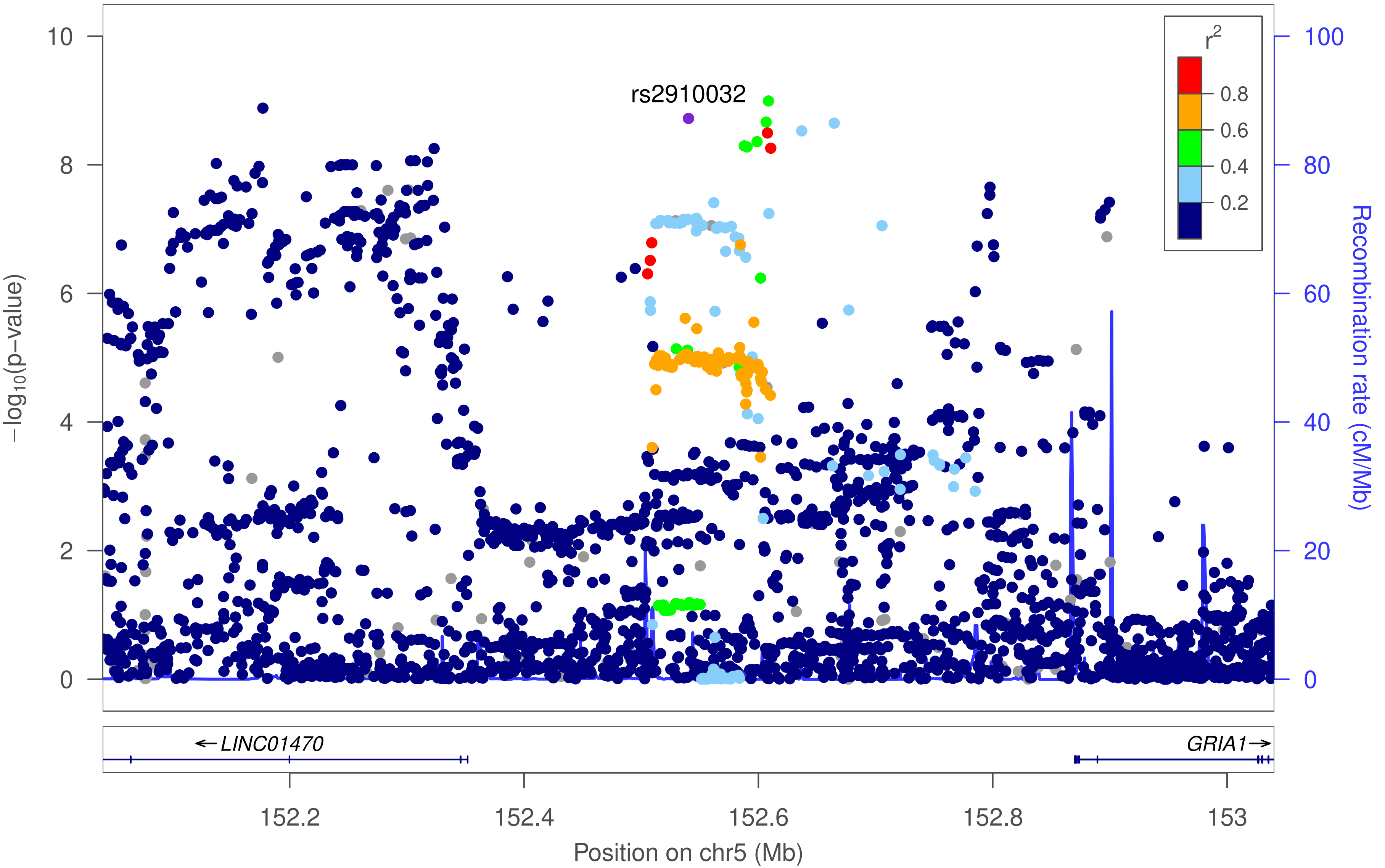
PGC2+Chinese rs113568682

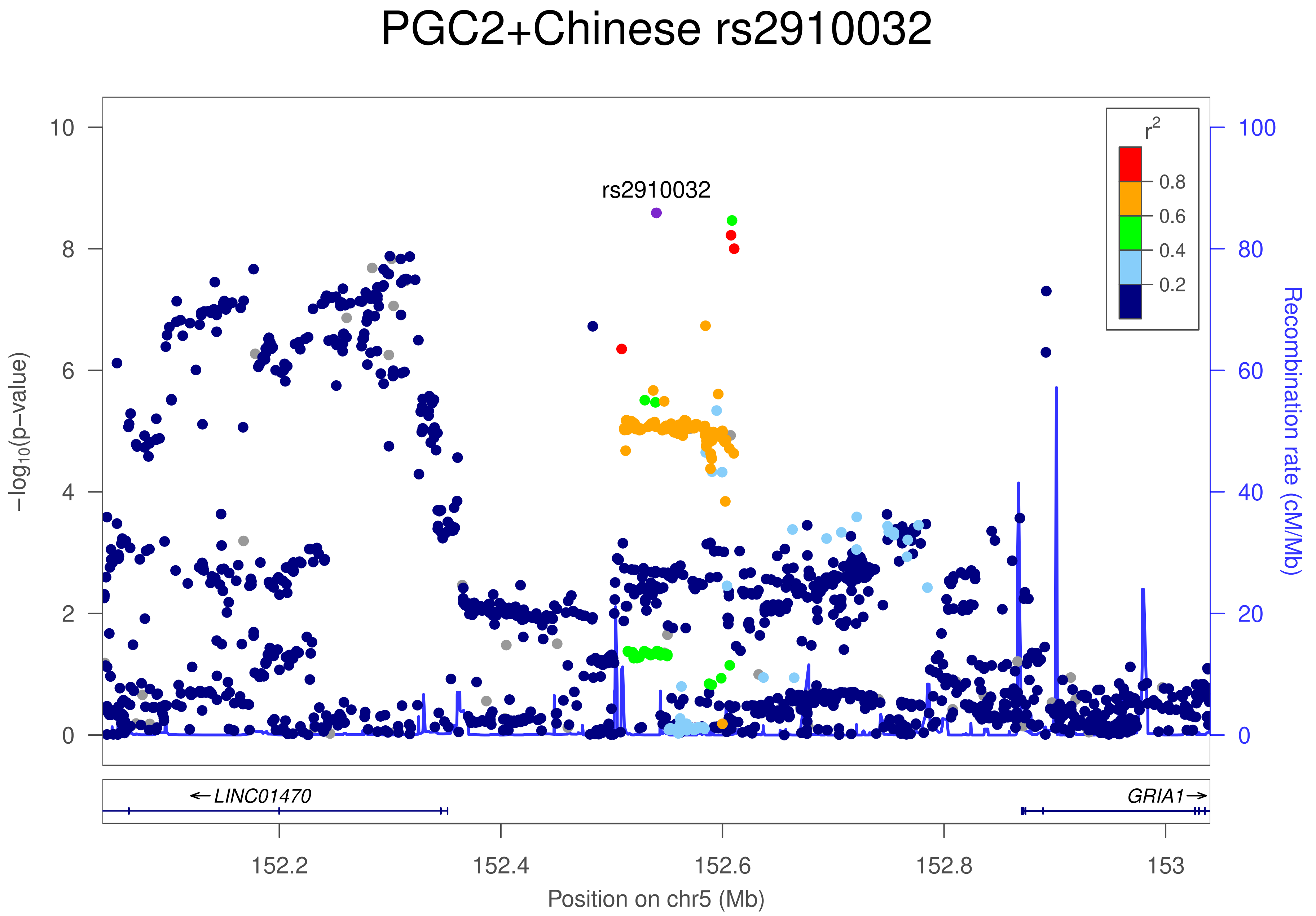


Chinese−only rs113568682

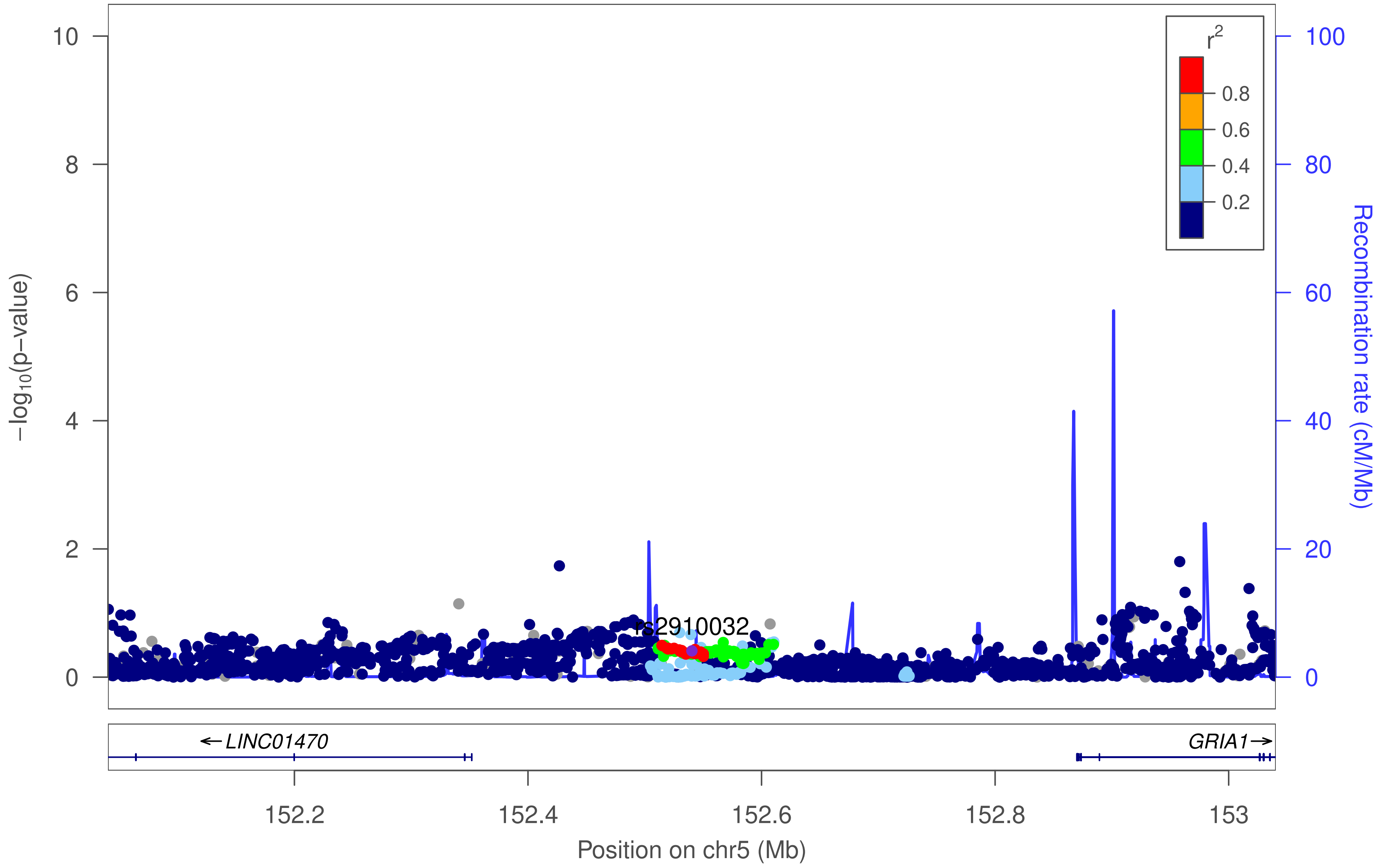


PGC2 rs2910032

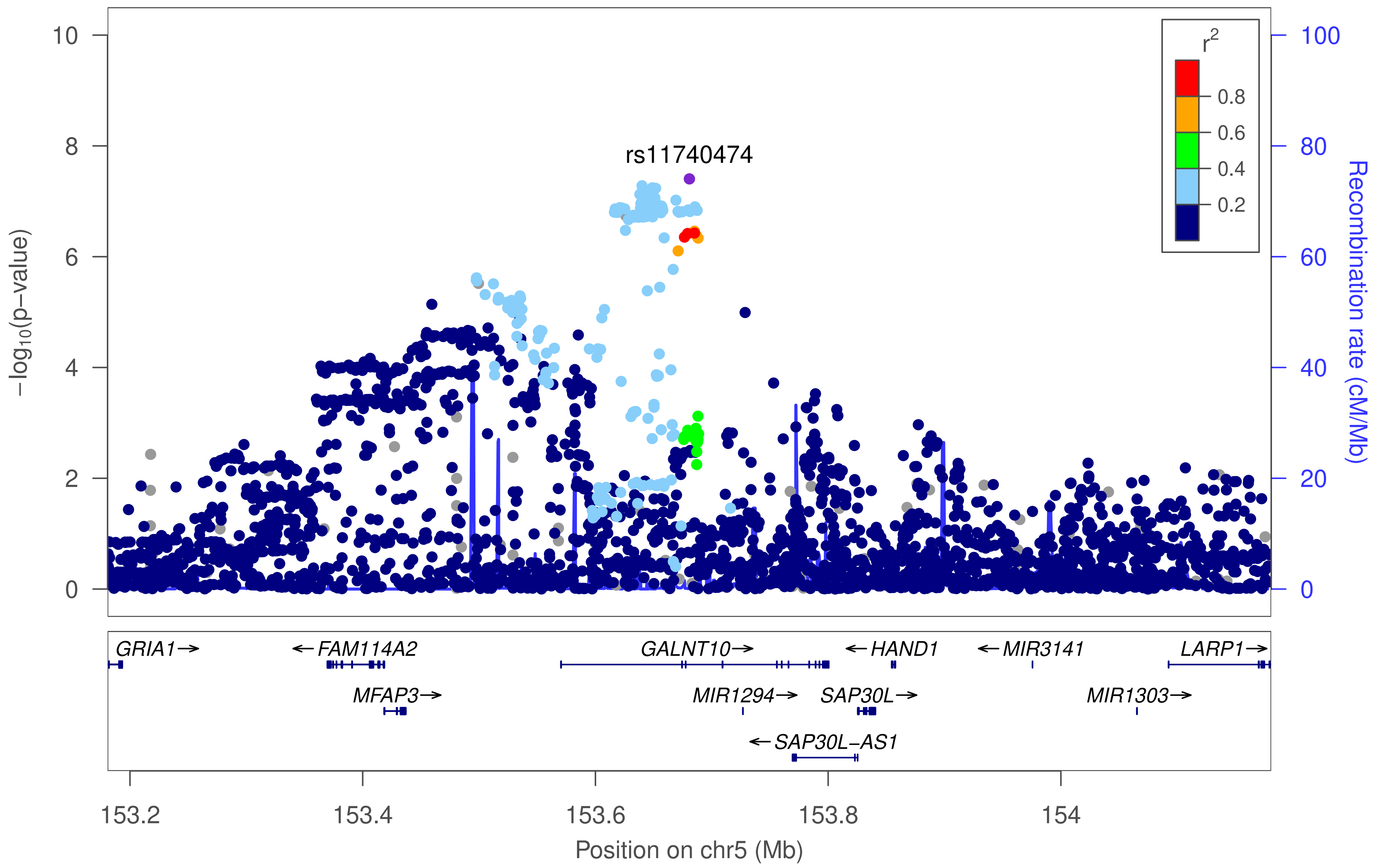



PGC2+Chinese rs2910032
rs2910032
−log10(p−value)
10
8
6
4
2
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
r2
0.8
0.6
0.4
0.2
←LINC01470
GRIA1→
152.2
152.4
152.6
152.8
153
Position on chr5 (Mb)

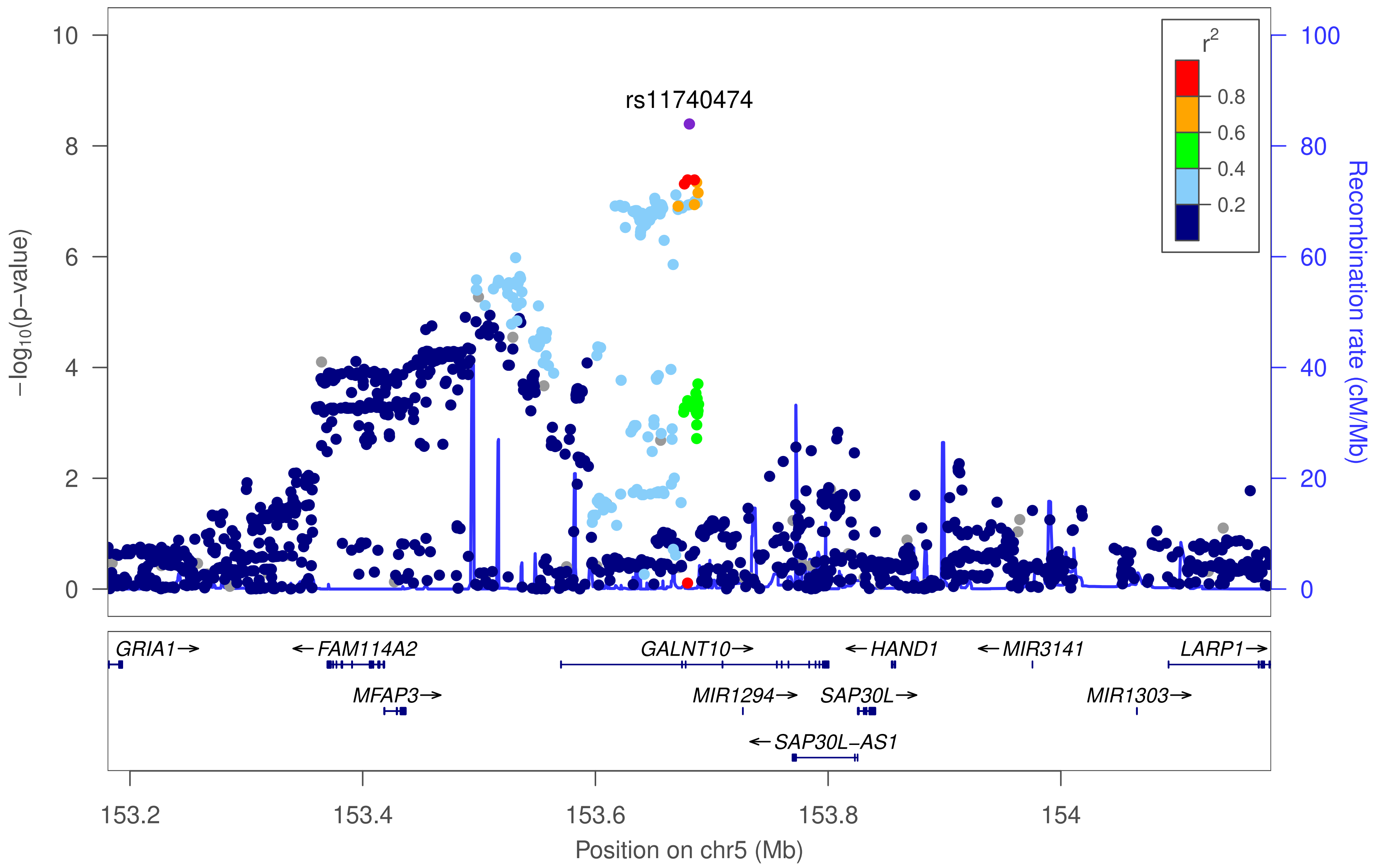
Chinese−only rs2910032

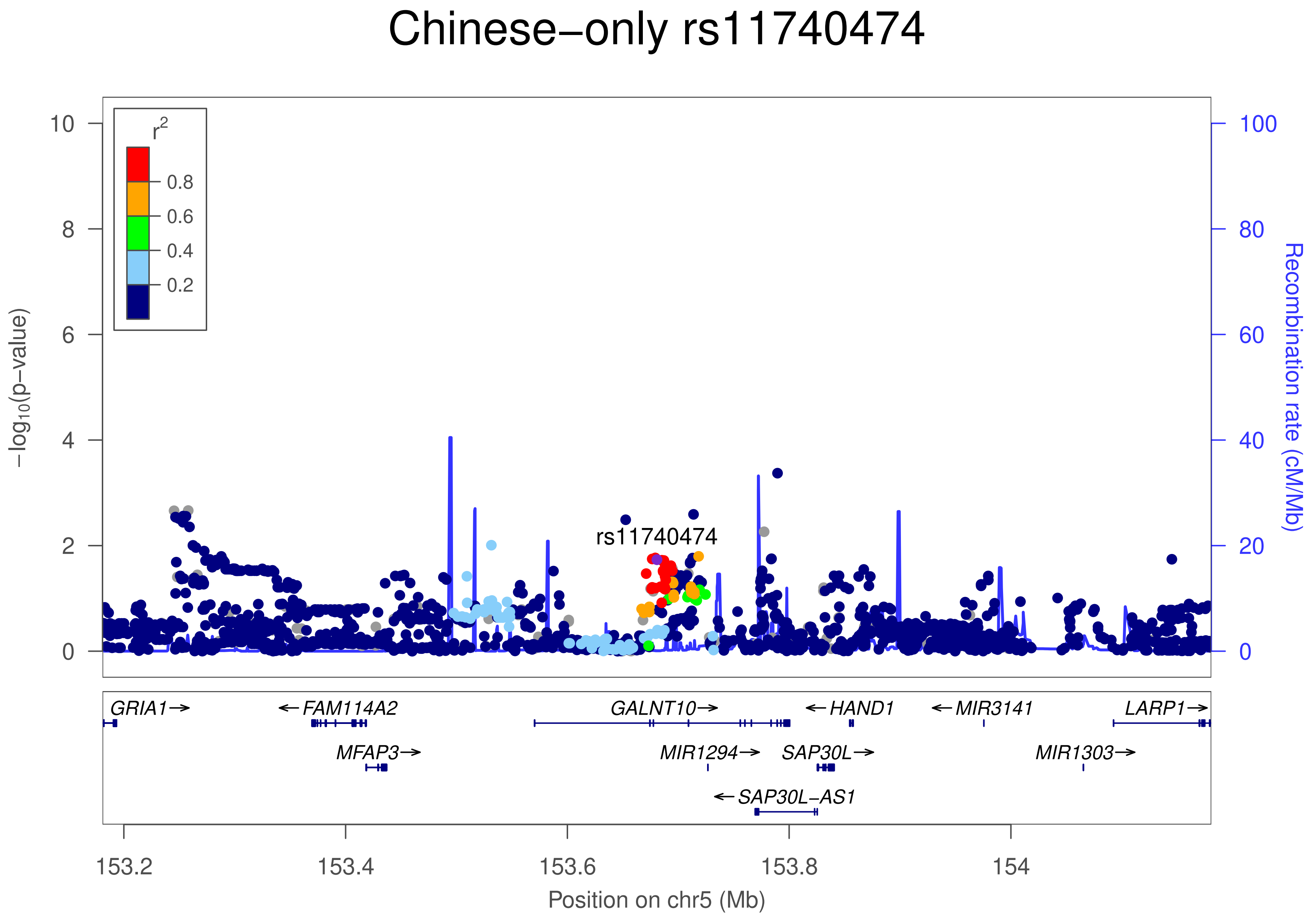


PGC2 rs11740474

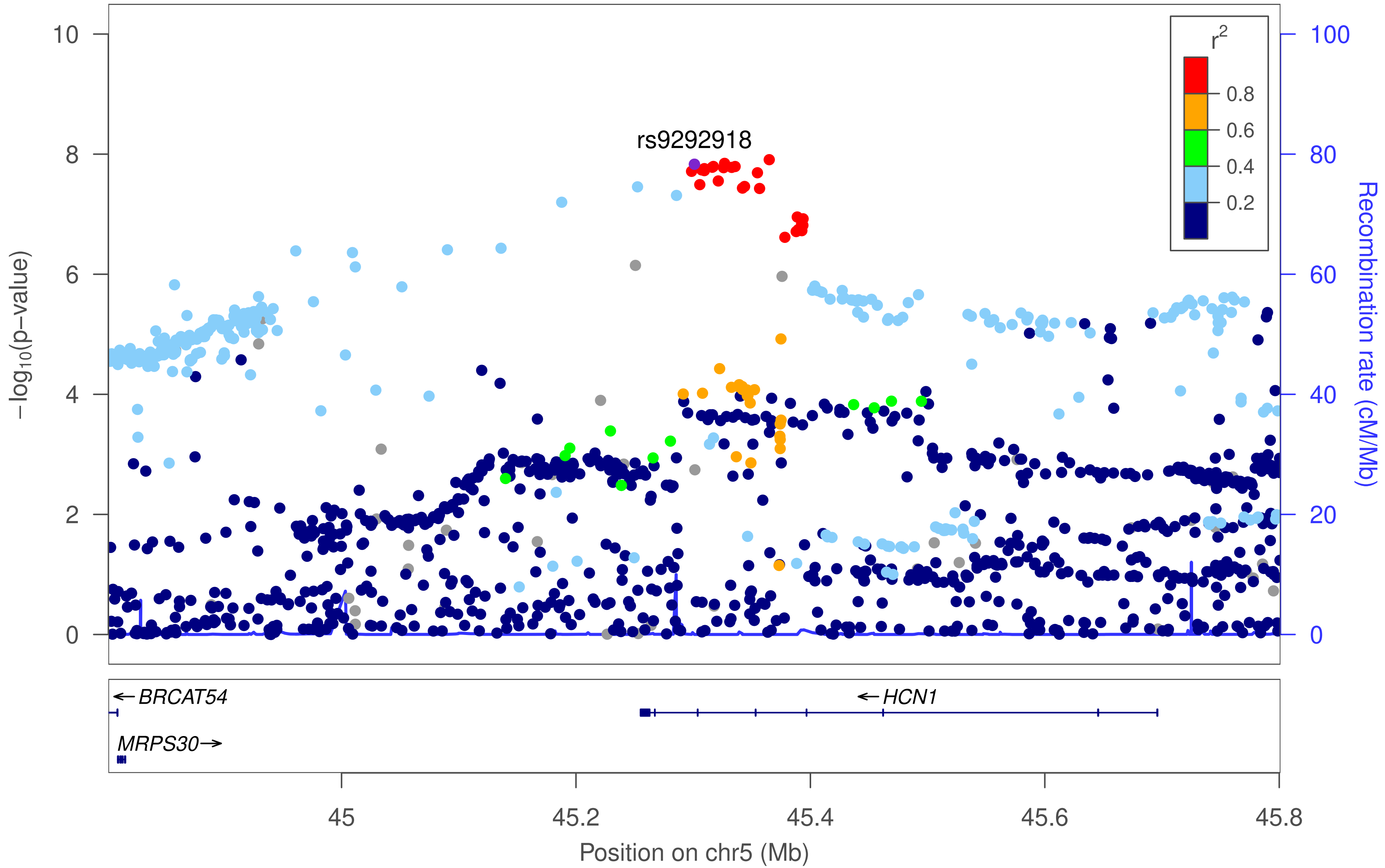


PGC2+Chinese rs11740474

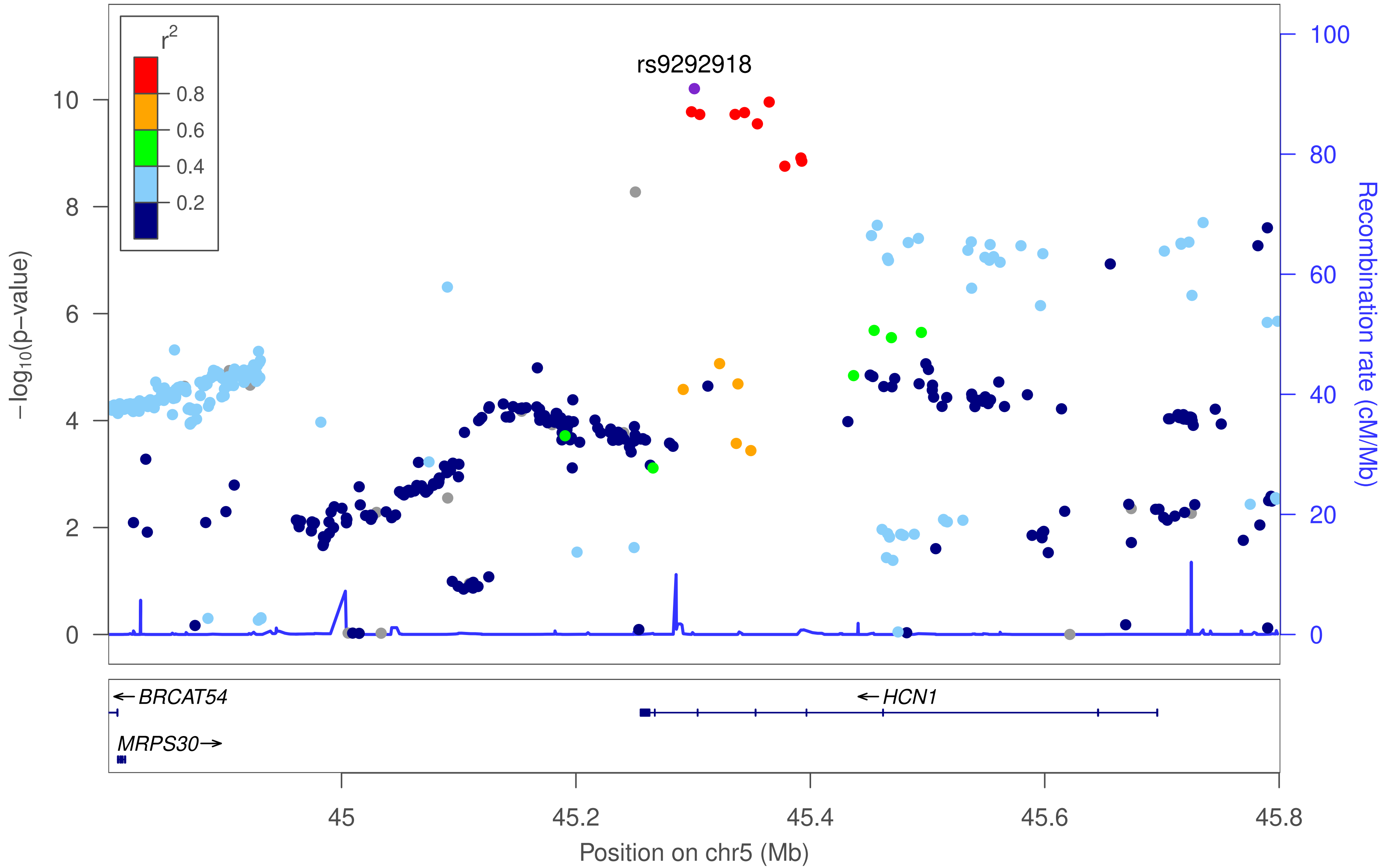



Chinese−only rs11740474
r²
0.8
0.6
0.4
0.2
rs11740474
−log10(p−value)
10
8
6
4
2
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
GRIA1→
←FAM114A2
GALNT10→
←HAND1
←MIR3141
LARP1→
MFAP3→
MIR1294→
SAP30L→
MIR1303→
←SAP30L−AS1
153.2
153.4
153.6
153.8
154
Position on chr5 (Mb)

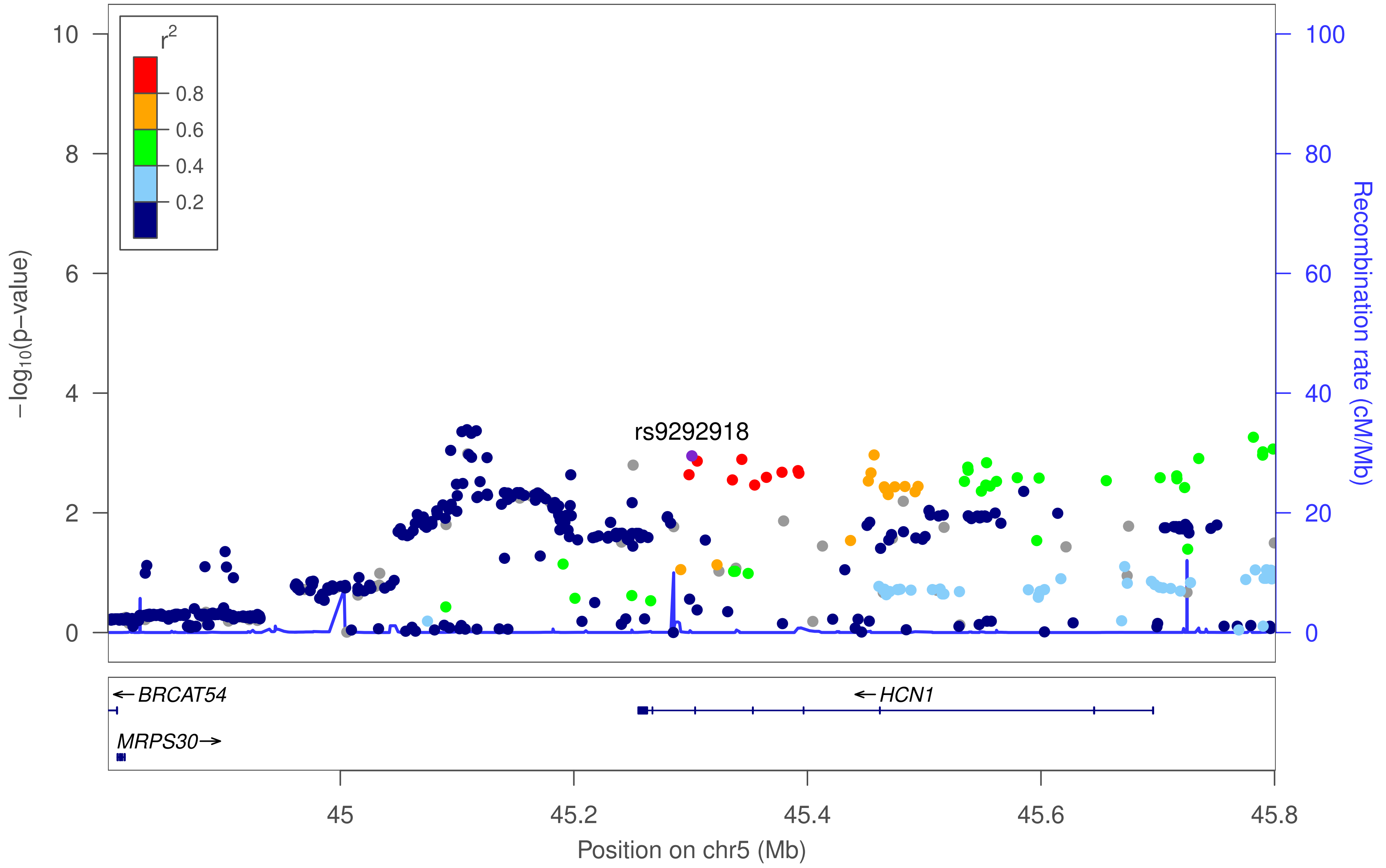
PGC2 rs9292918



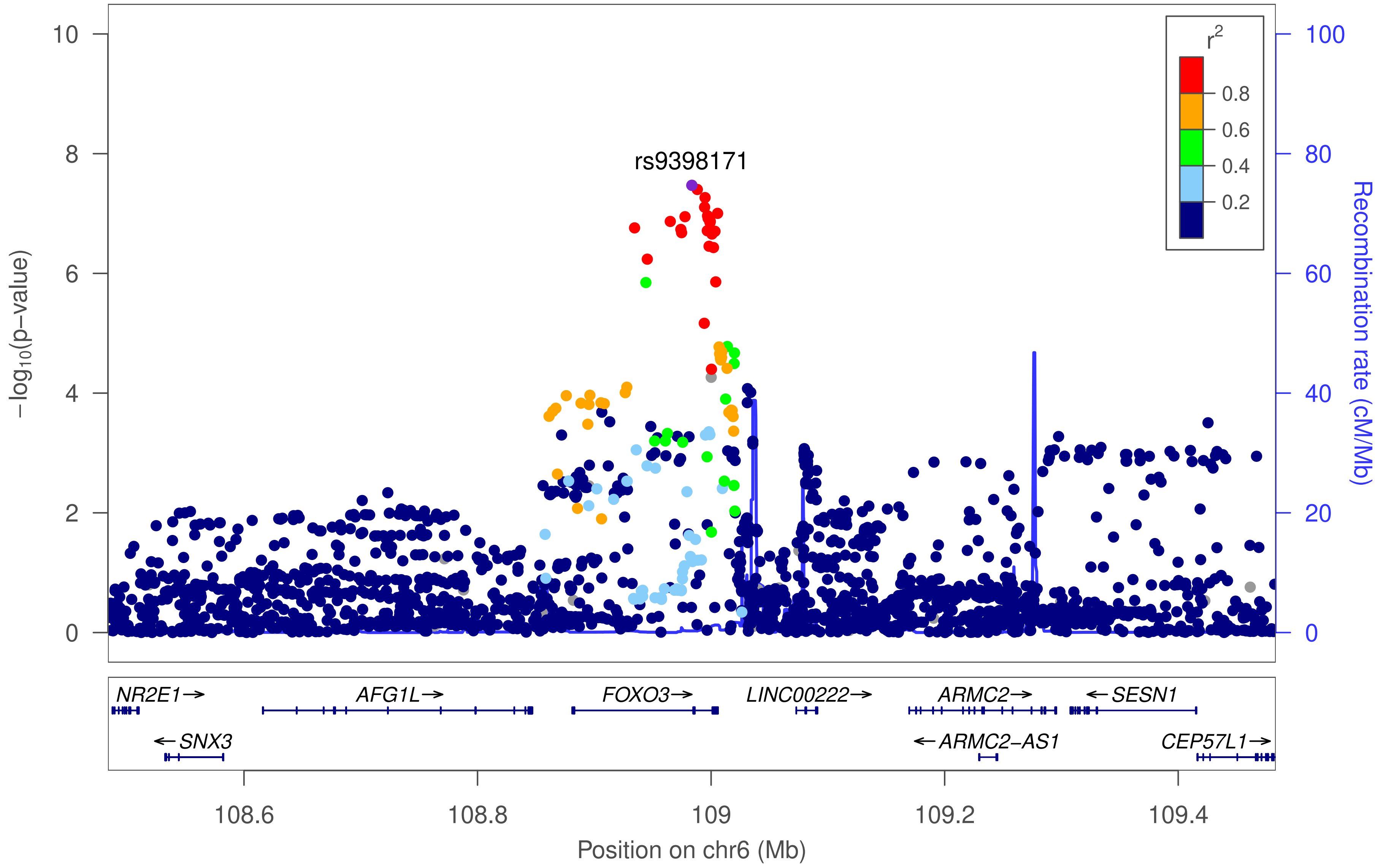
PGC2+Chinese rs9292918

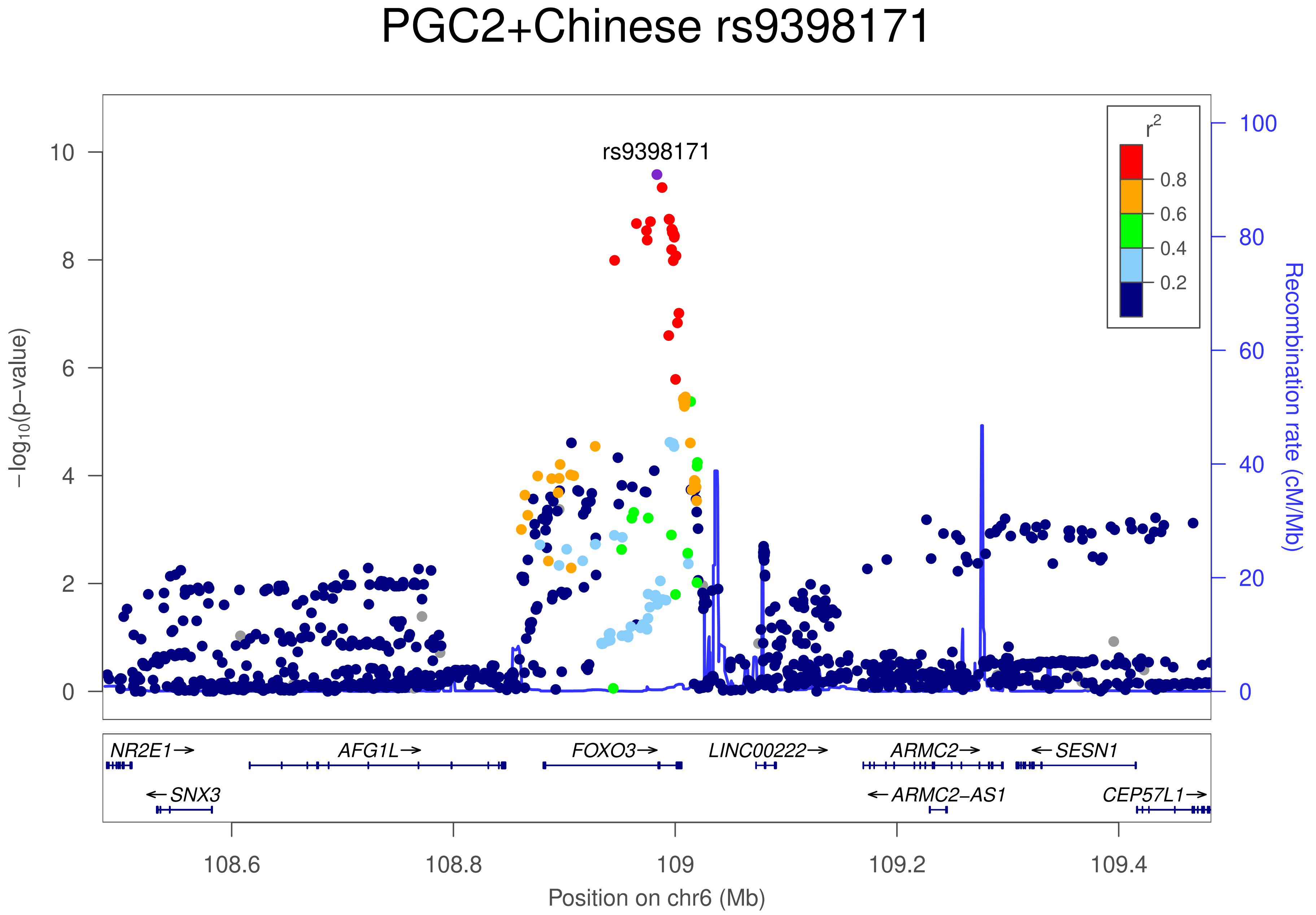


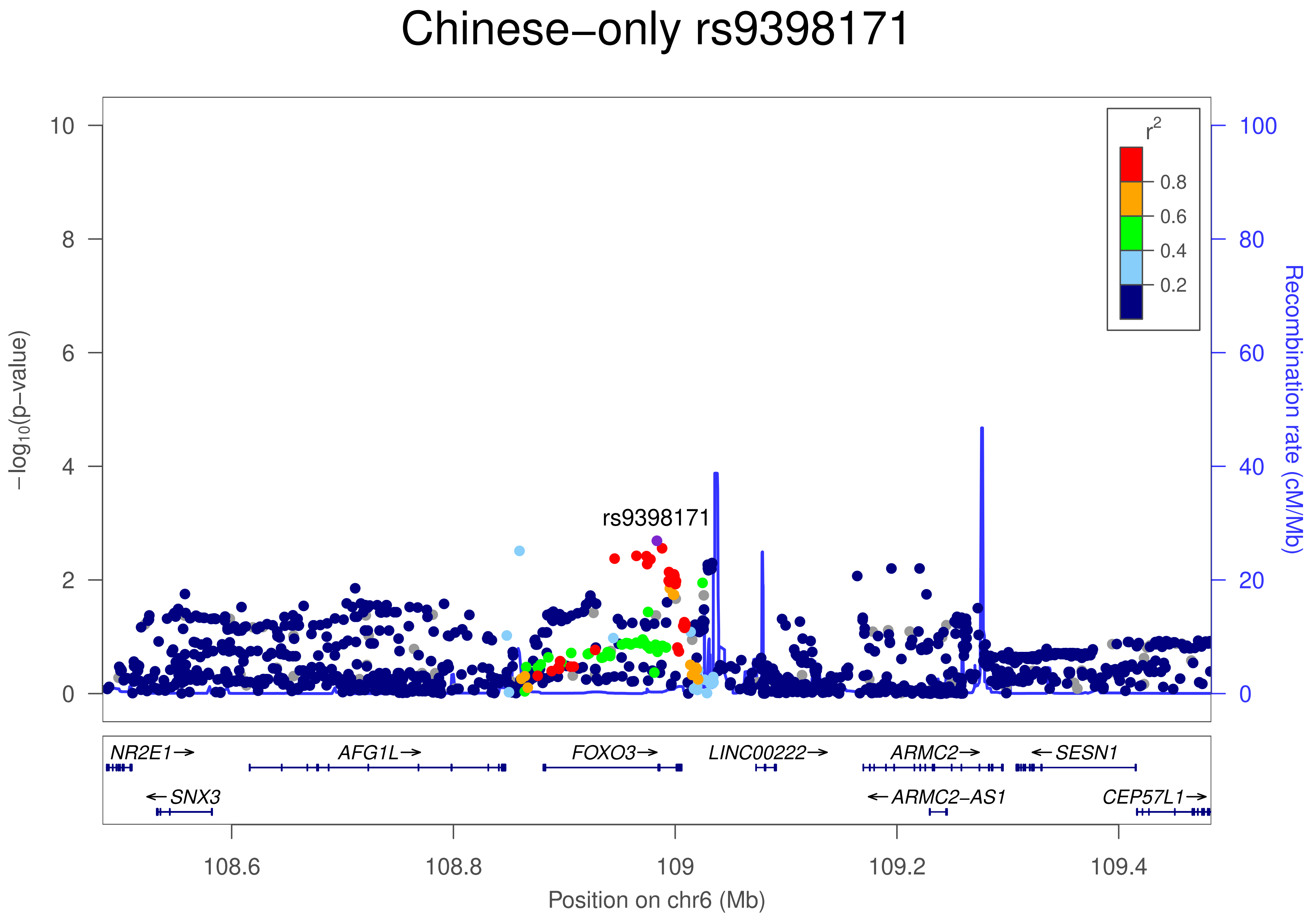
Chinese−only rs9292918

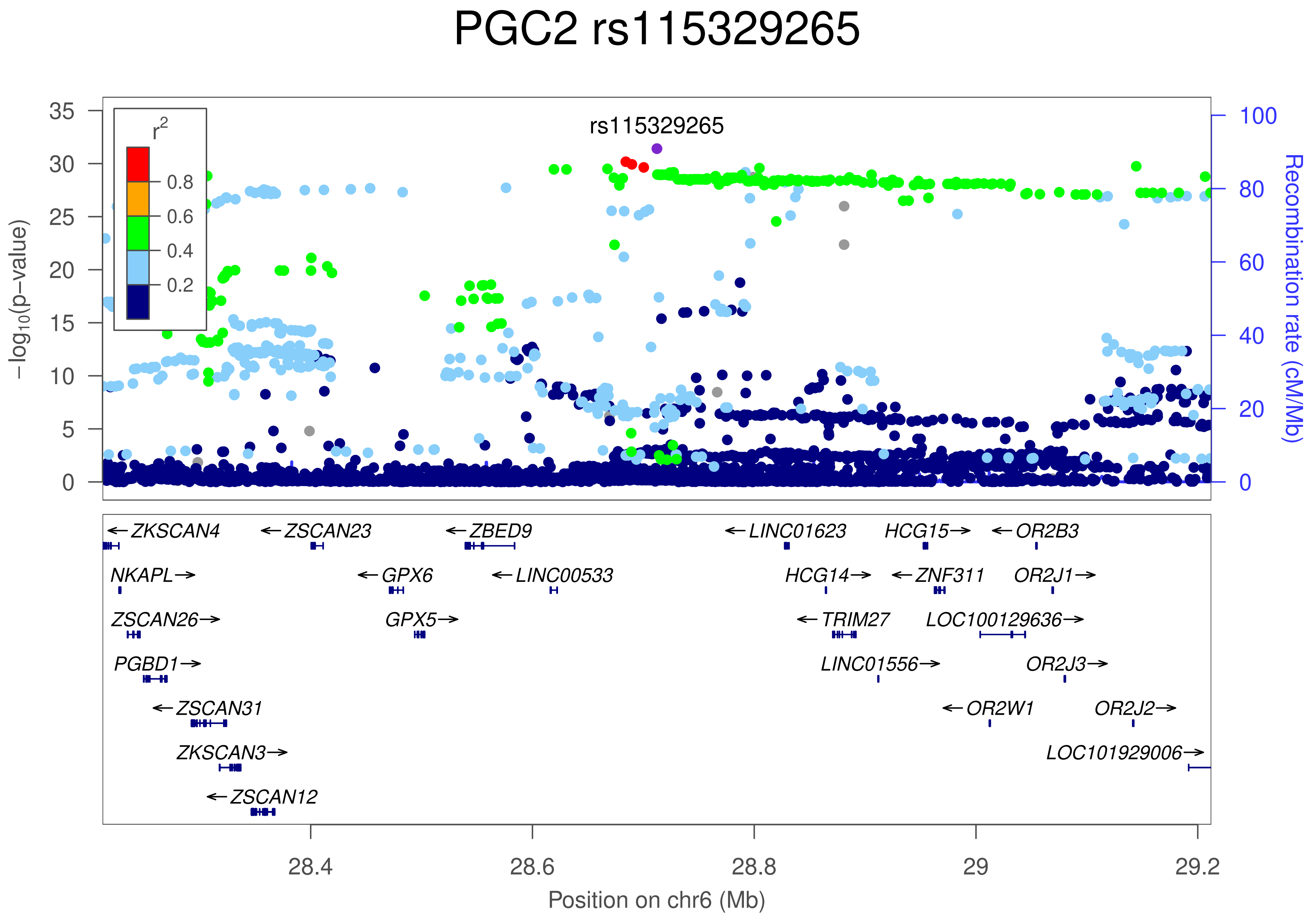


PGC2 rs9398171

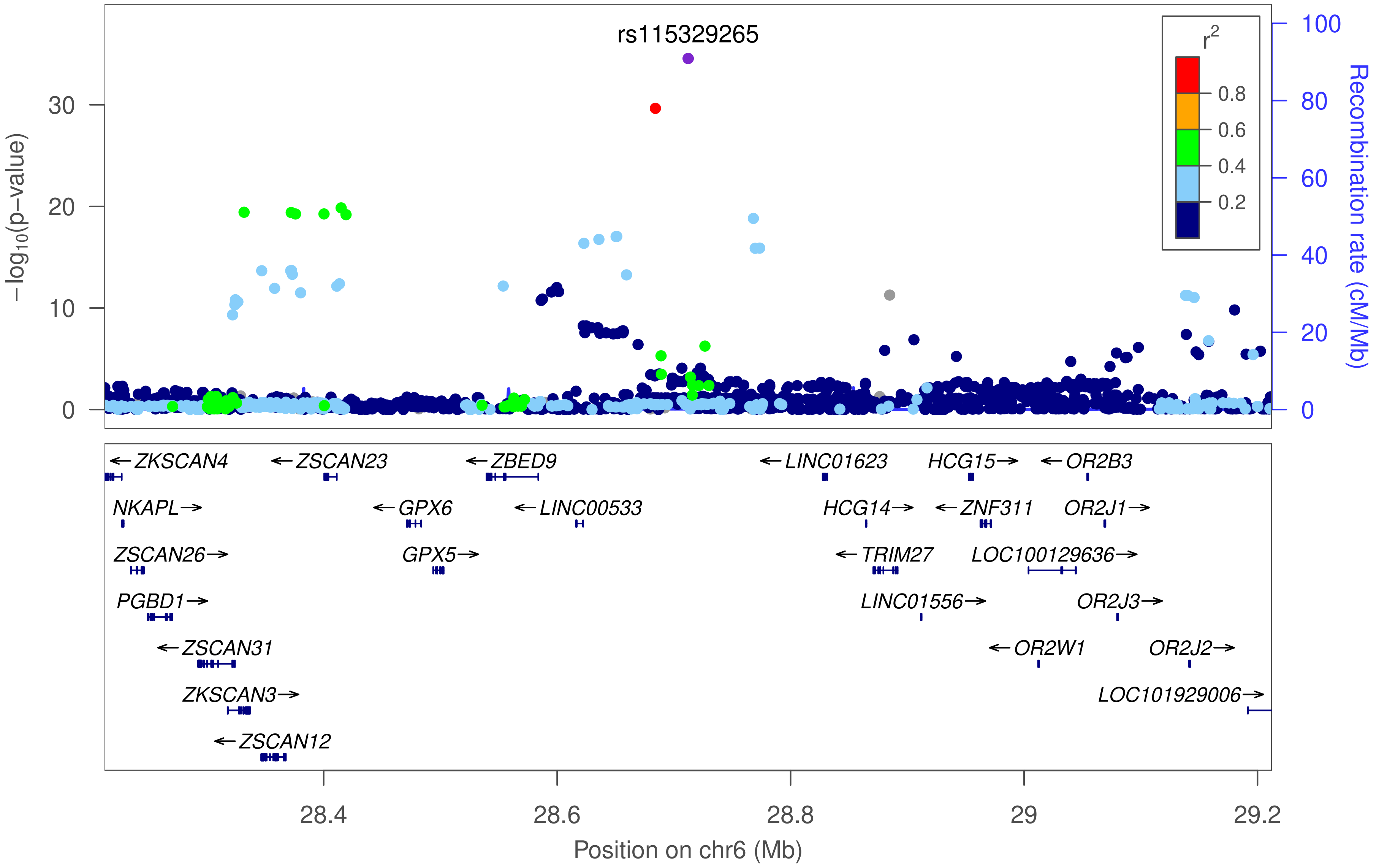



PGC2+Chinese rs9398171
rs9398171
−log10(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
r2
0.8
0.6
0.4
0.2
NR2E1→
AFG1L→
FOXO3→
LINC00222→
ARMC2→
←SESN1
←SNX3
←ARMC2−AS1
CEP57L1→
108.6
108.8
109
109.2
109.4
Position on chr6 (Mb)

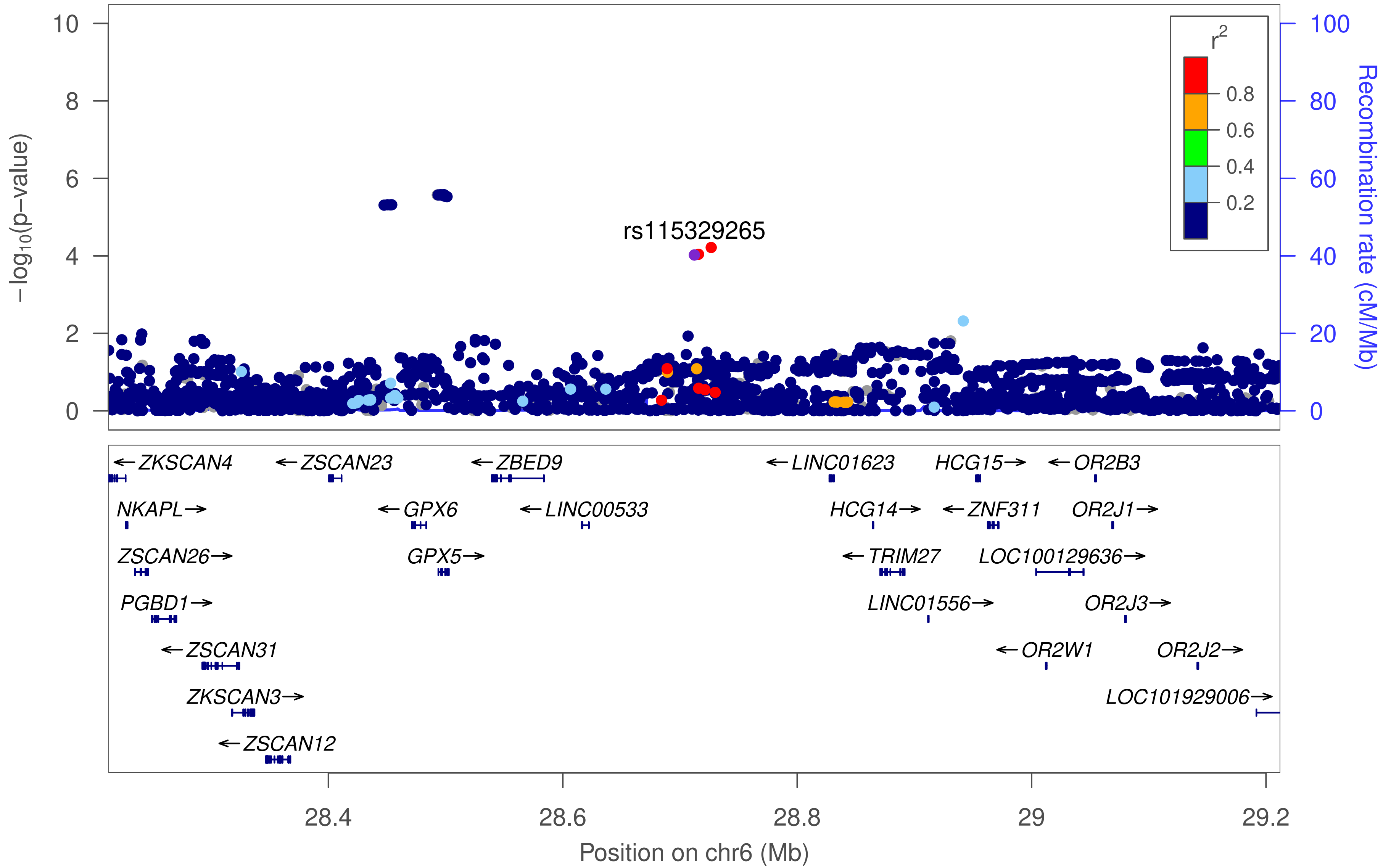

Chinese−only rs9398171
−log10(p−value)
10
8
6
4
2
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
r2
0.8
0.6
0.4
0.2
rs9398171
NR2E1→
←SNX3
AFG1L→
FOXO3→
LINC00222→
ARMC2→
←ARMC2−AS1
←SESN1
CEP57L1→
108.6
108.8
109
109.2
109.4
Position on chr6 (Mb)

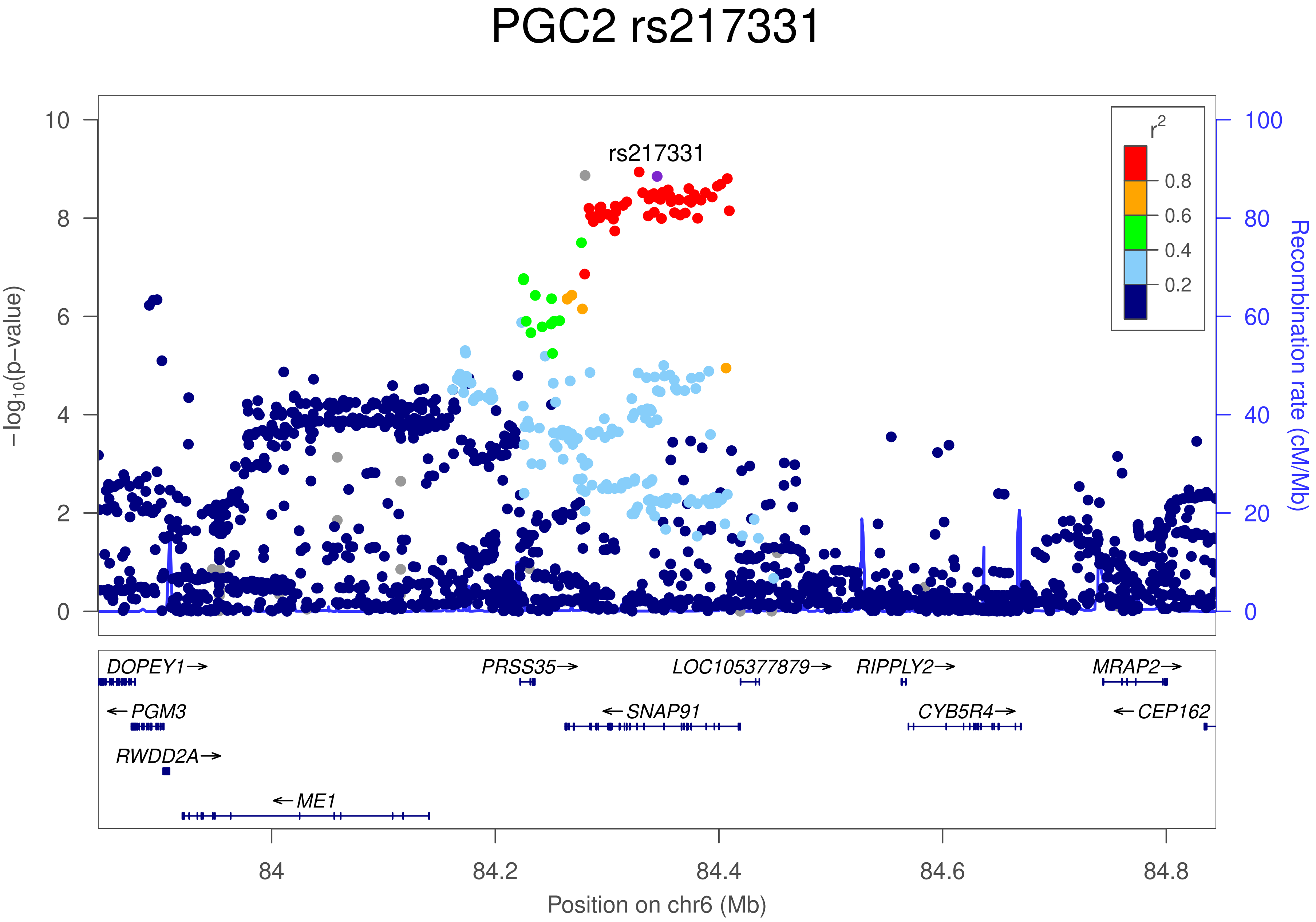

PGC2 rs115329265
rs115329265
r^2
0.8
0.6
0.4
0.2
−log10(p−value)
35
30
25
20
15
10
5
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
←ZKSCAN4
←ZSCAN23
←ZBED9
←LINC01623
HCG15→
←OR2B3
NKAPL→
←GPX6
←LINC00533
HCG14→
←ZNF311
OR2J1→
ZSCAN26→
GPX5→
←TRIM27
LOC100129636→
PGBD1→
LINC01556→
OR2J3→
←ZSCAN31
←OR2W1
OR2J2→
ZKSCAN3→
LOC101929006→
←ZSCAN12
28.4
28.6
28.8
29
29.2
Position on chr6 (Mb)

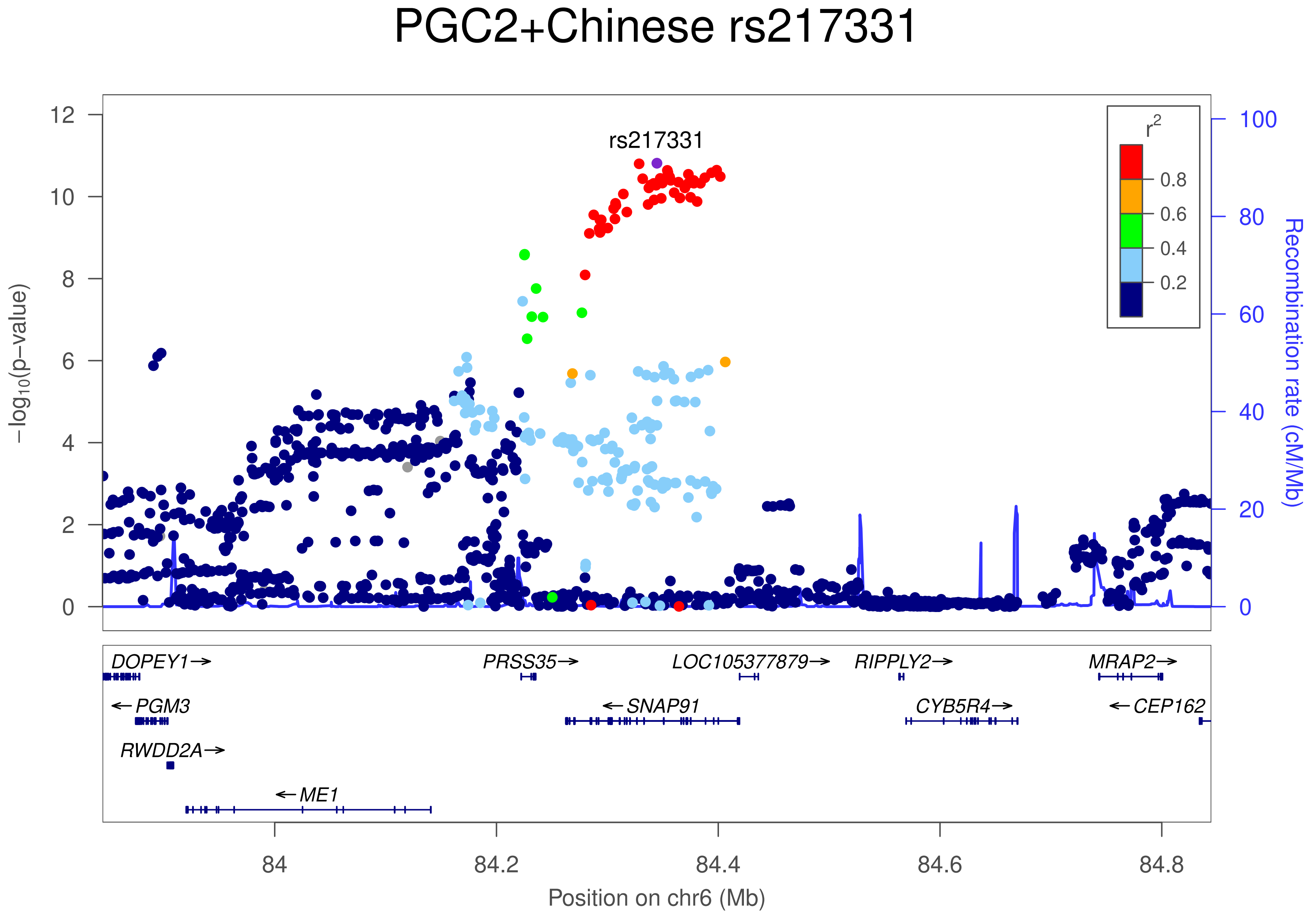
PGC2+Chinese rs115329265

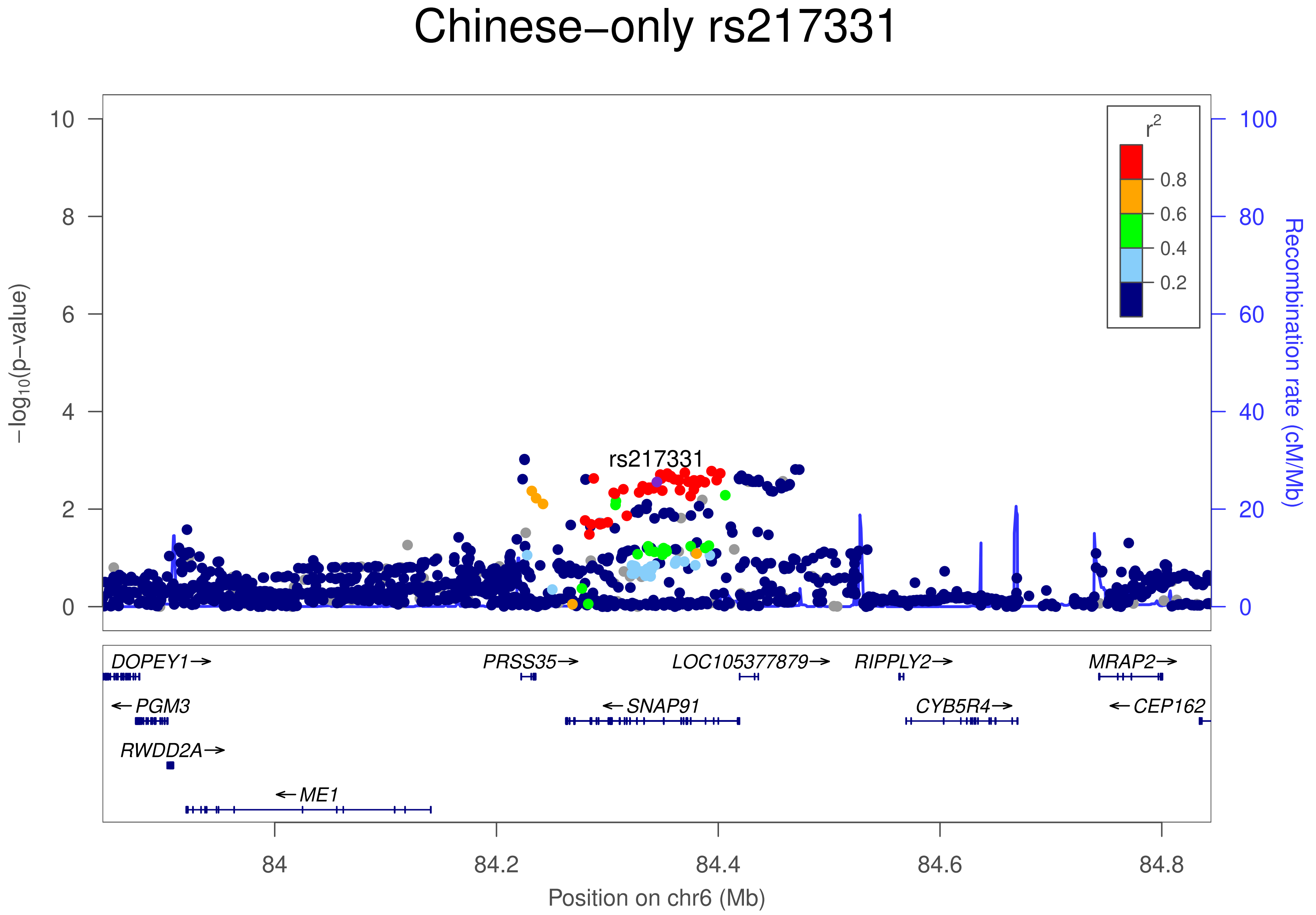


Chinese–only rs115329265

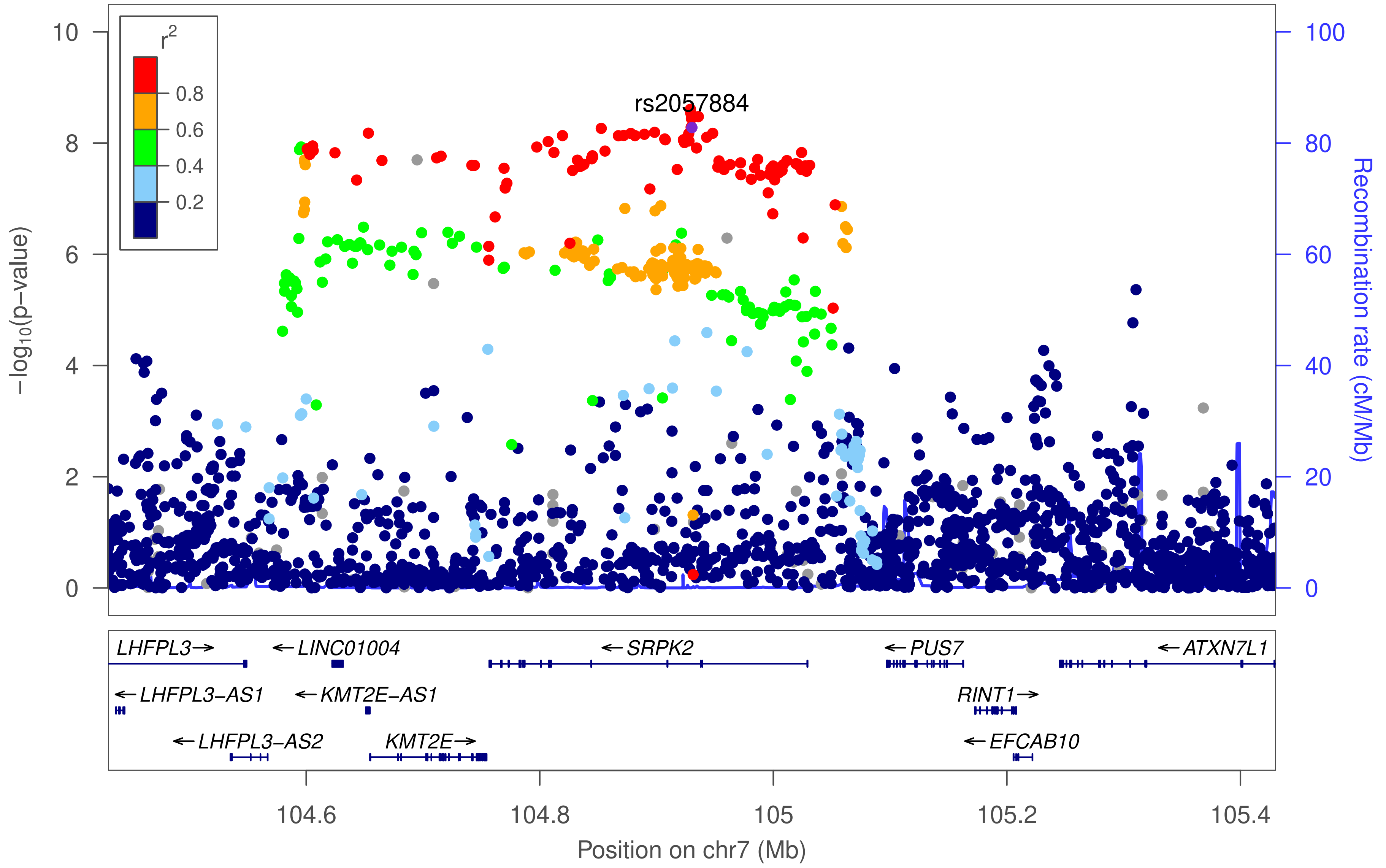



PGC2 rs217331
rs217331
−log10(p−value)
10
8
6
4
2
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
r2
0.8
0.6
0.4
0.2
DOPEY1→
PRSS35→
LOC105377879→
RIPPLY2→
MRAP2→
←PGM3
←SNAP91
CYB5R4→
←CEP162
RWDD2A→
←ME1
84
84.2
84.4
84.6
84.8
Position on chr6 (Mb)

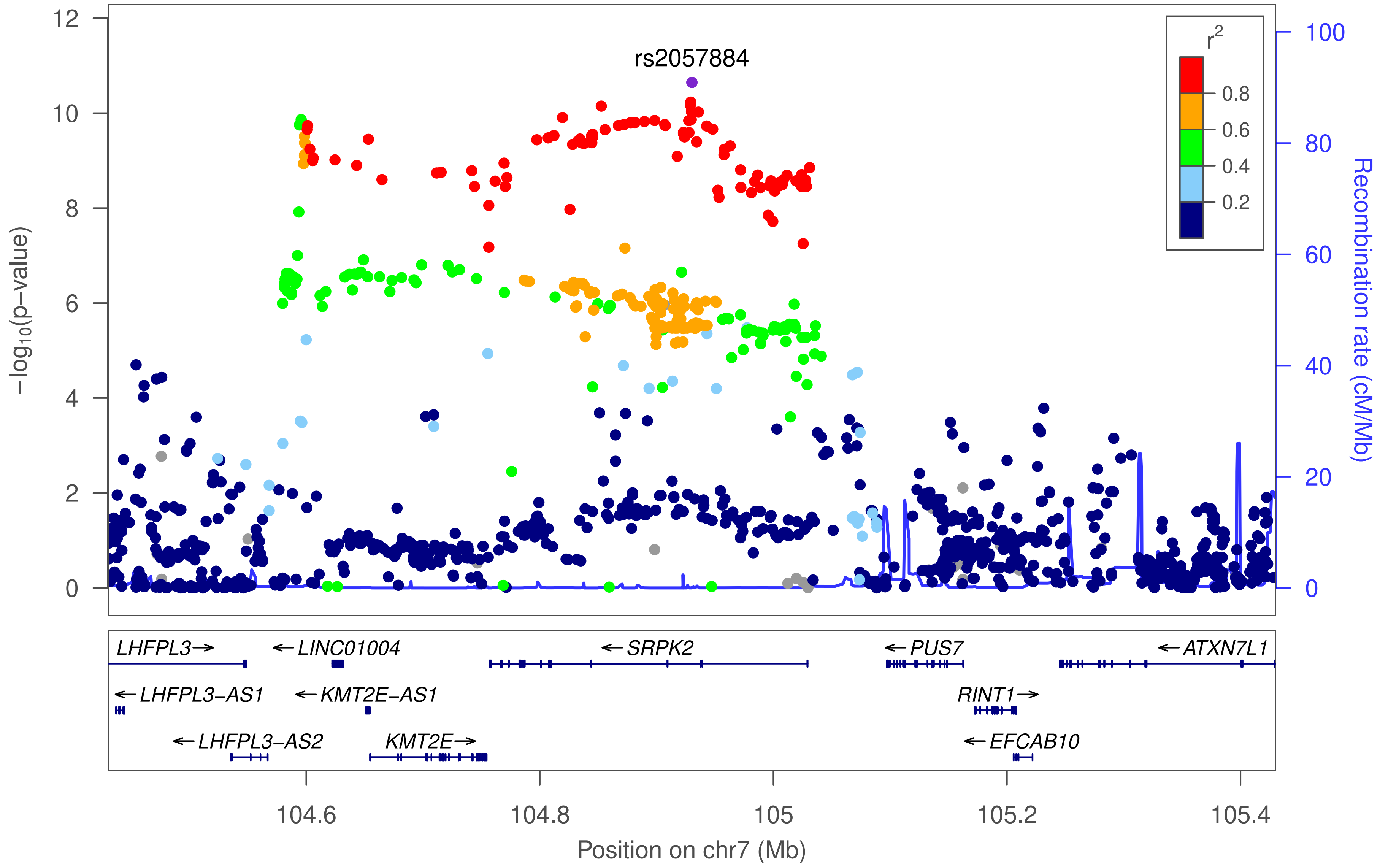

PGC2+Chinese rs217331
rs217331
−log10(p−value)
12
10
8
6
4
2
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
r2
0.8
0.6
0.4
0.2
DOPEY1→
←PGM3
RWDD2A→
←ME1
PRSS35→
←SNAP91
LOC105377879→
RIPPLY2→
CYB5R4→
MRAP2→
←CEP162
84
84.2
84.4
84.6
84.8
Position on chr6 (Mb)

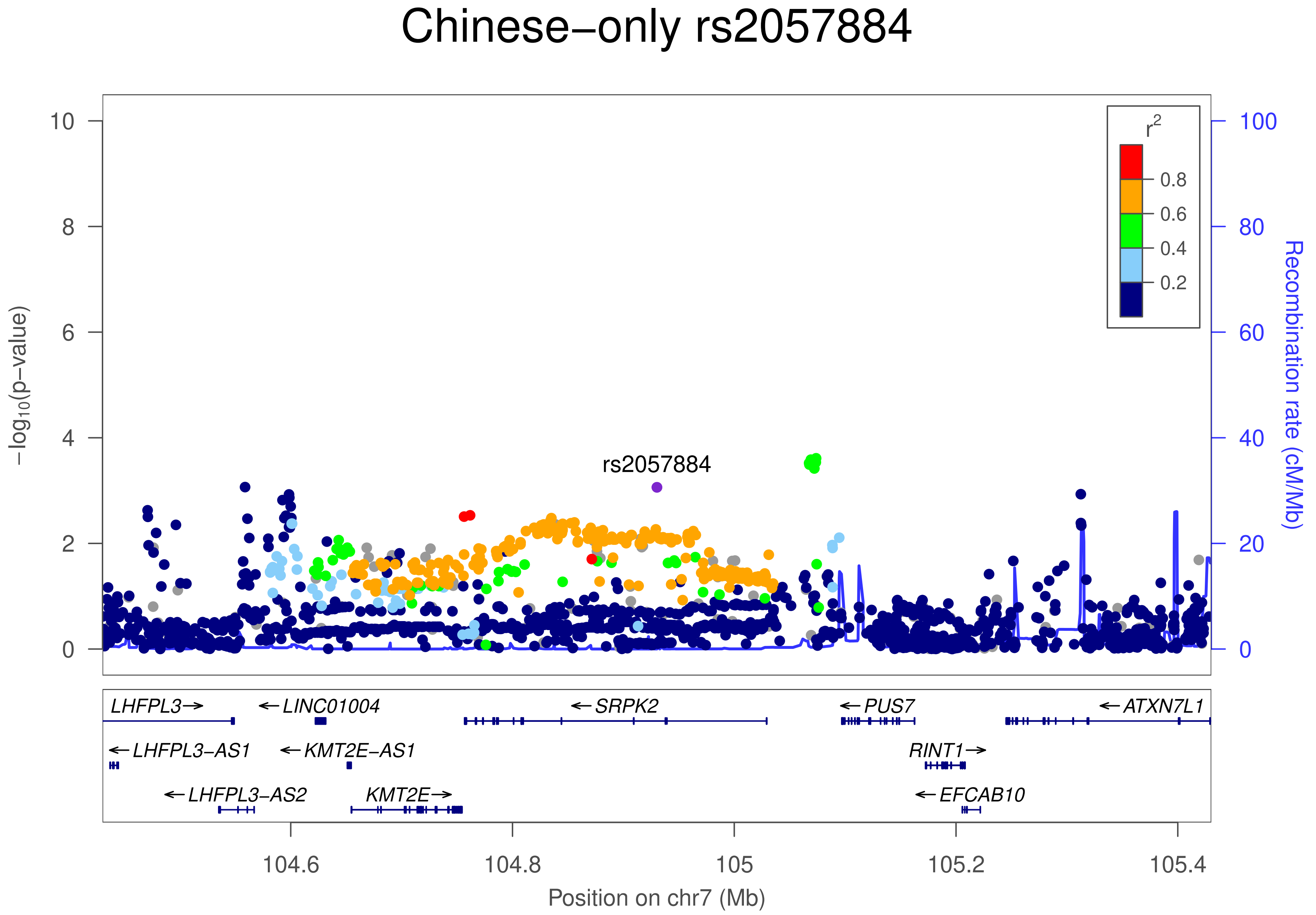

Chinese–only rs217331
rs217331
−log₁₀(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
r²
0.8
0.6
0.4
0.2
DOPEY1→
PRSS35→
LOC105377879→
RIPPLY2→
MRAP2→
←PGM3
←SNAP91
CYB5R4→
←CEP162
RWDD2A→
←ME1
84
84.2
84.4
84.6
84.8
Position on chr6 (Mb)

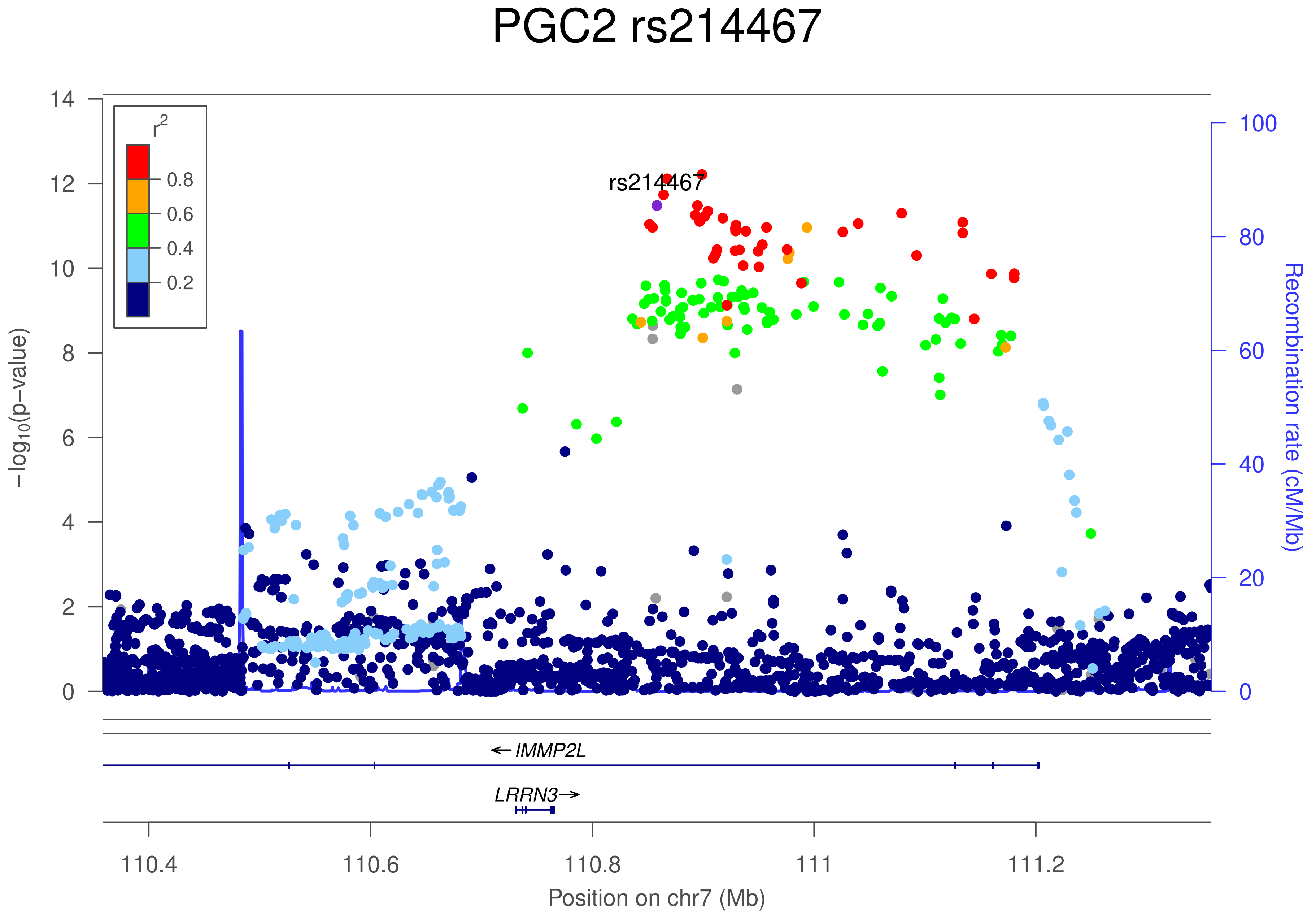
PGC2 rs2057884



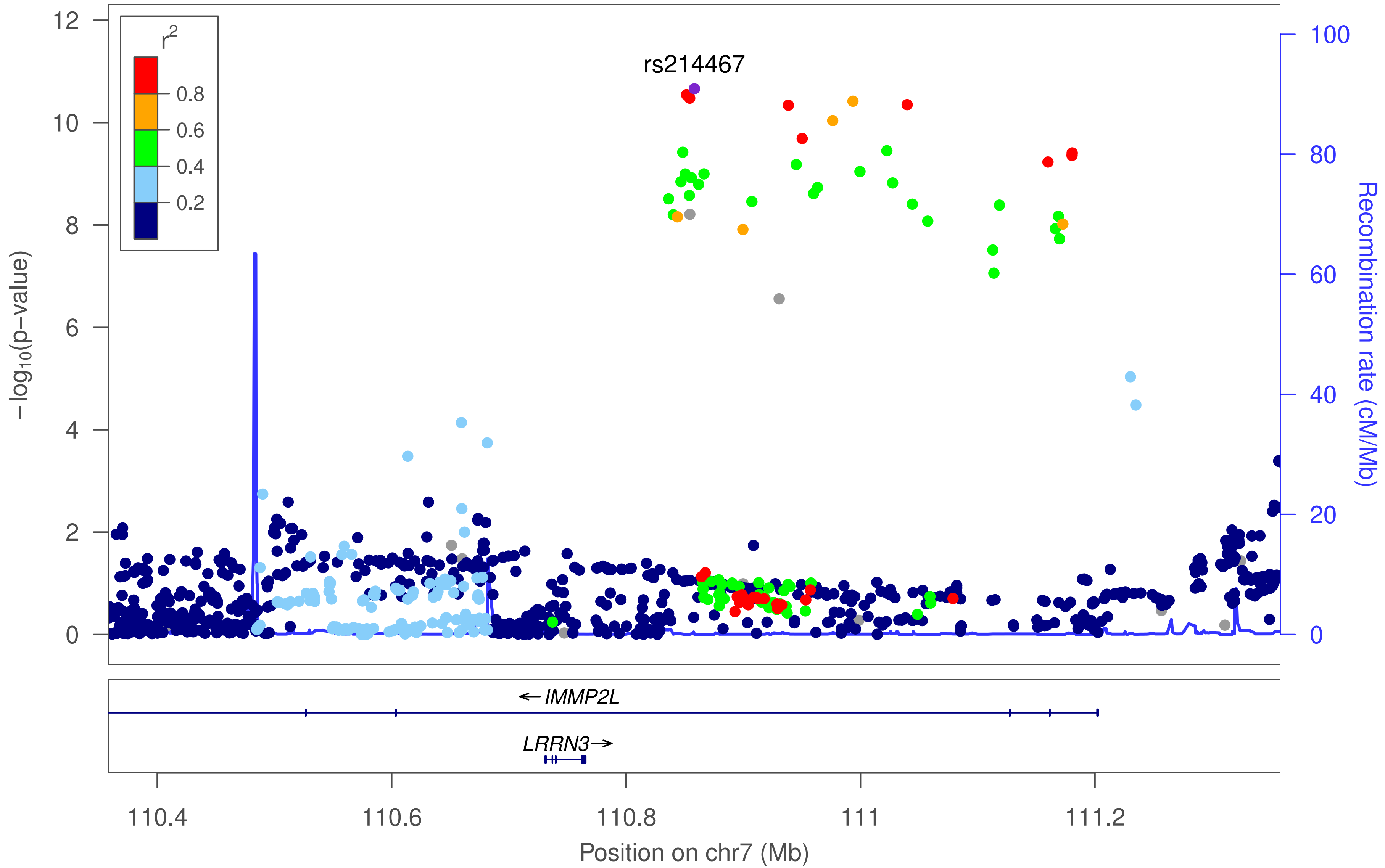
PGC2+Chinese rs2057884

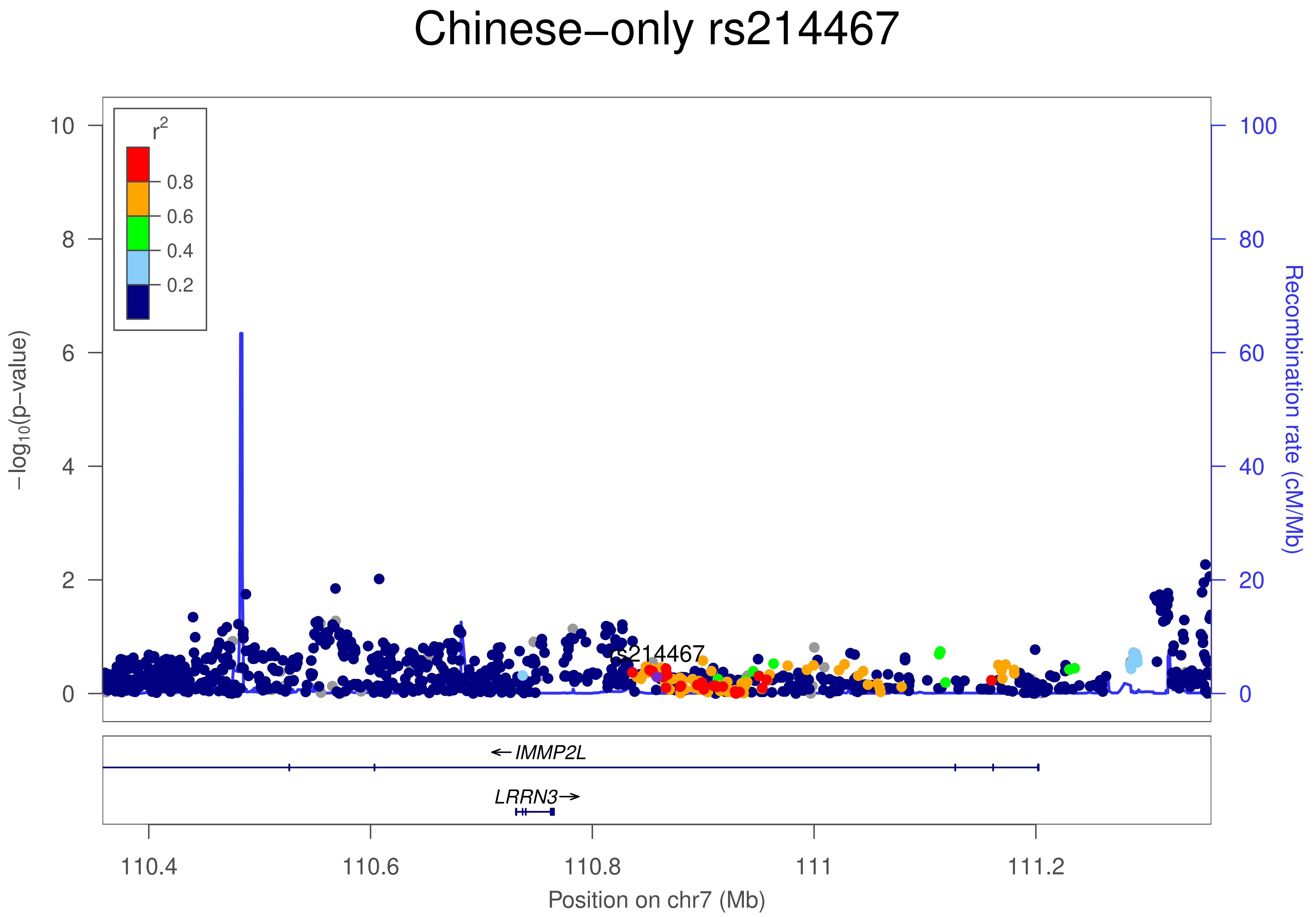


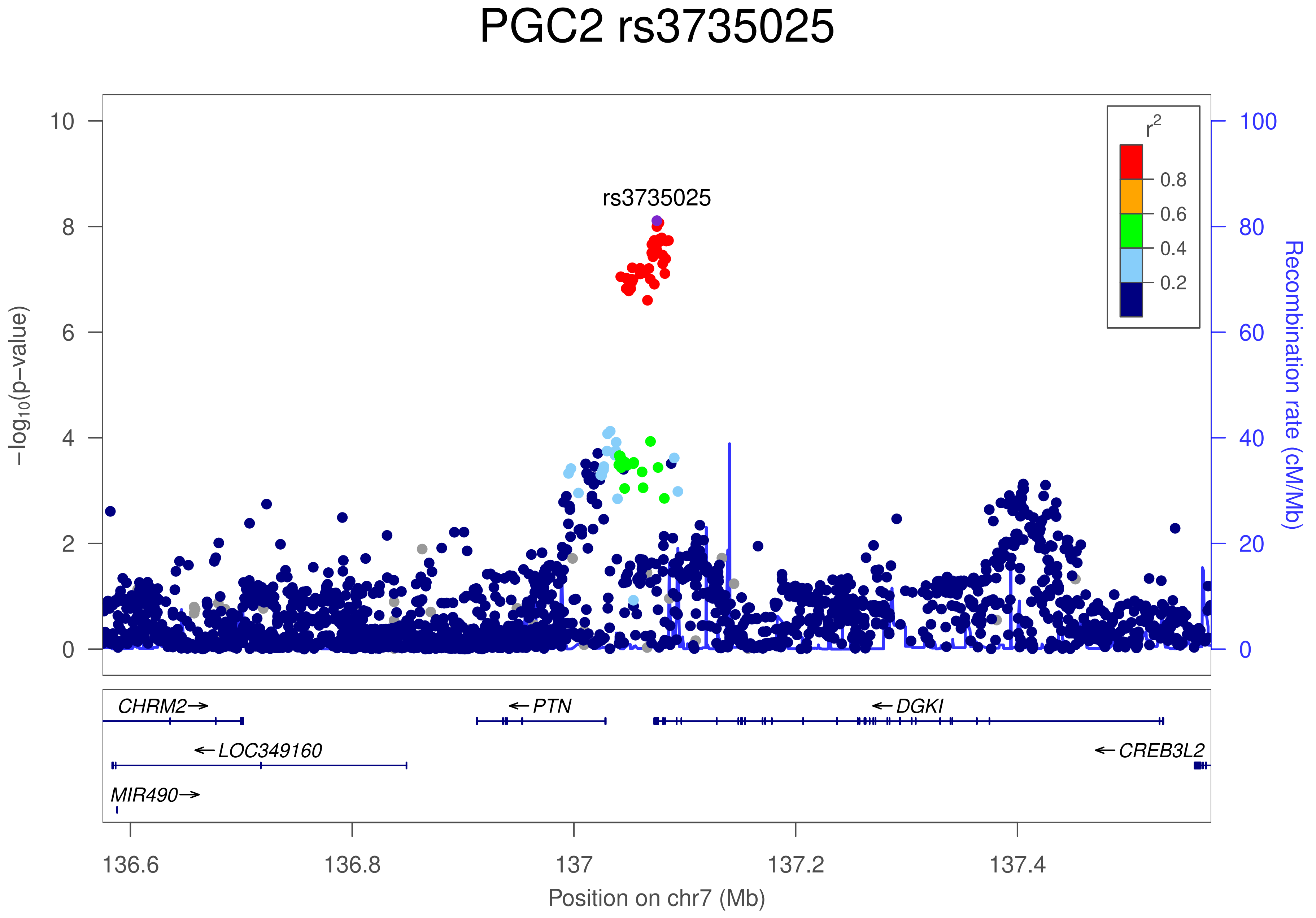

Chinese−only rs2057884
r^2
0.8
0.6
0.4
0.2
10
8
6
4
2
0
−log$_{10}$(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
rs2057884
LHFPL3→
←LINC01004
←SRPK2
←PUS7
←ATXN7L1
←LHFPL3−AS1
←KMT2E−AS1
RINT1→
←LHFPL3−AS2
KMT2E→
←EFCAB10
104.6
104.8
105
105.2
105.4
Position on chr7 (Mb)

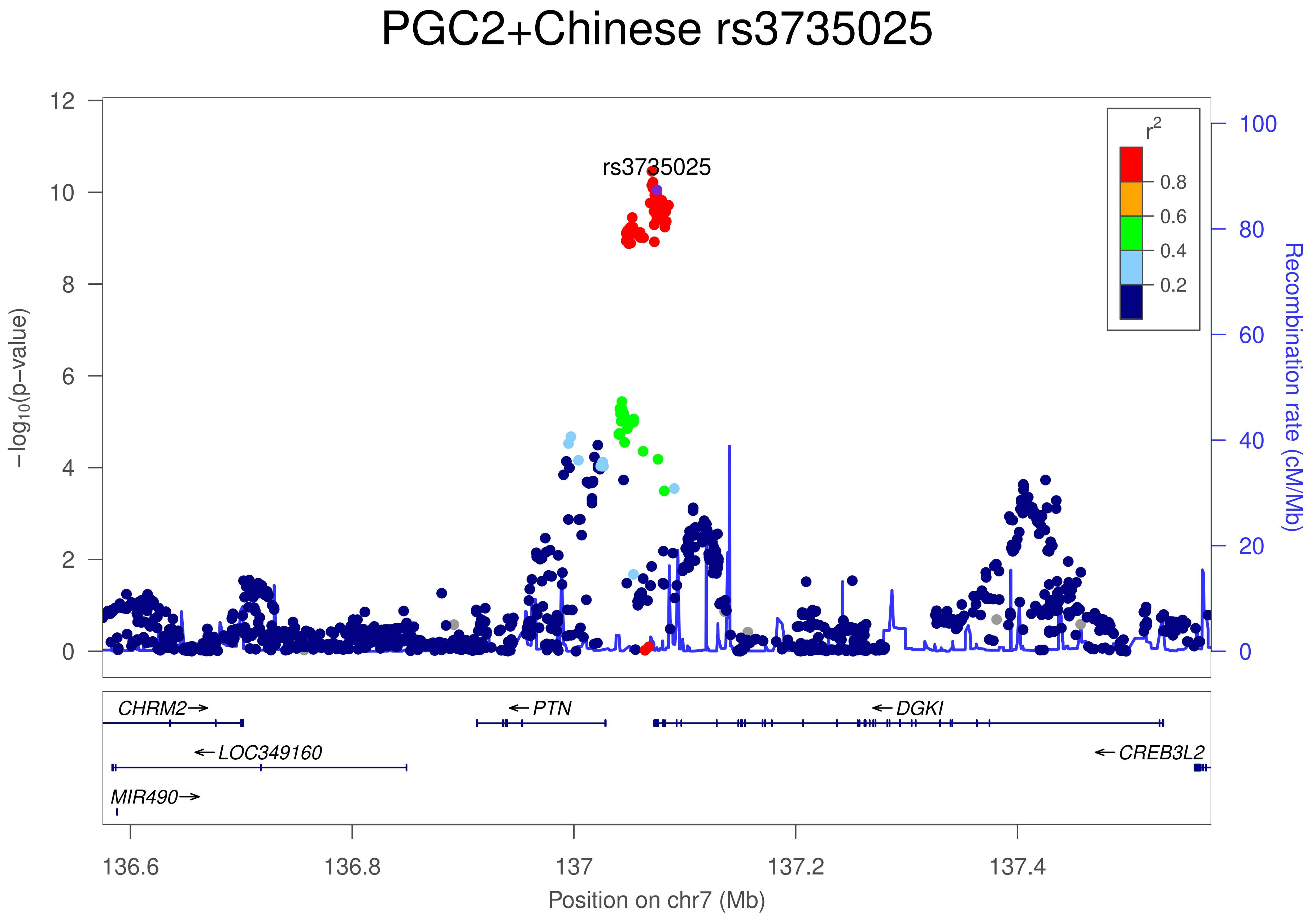

PGC2 rs214467
r2
0.8
0.6
0.4
0.2
rs214467
−log10(p−value)
14
12
10
8
6
4
2
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
← IMMP2L
LRRN3→
110.4
110.6
110.8
111
111.2
Position on chr7 (Mb)

PGC2+Chinese rs214467

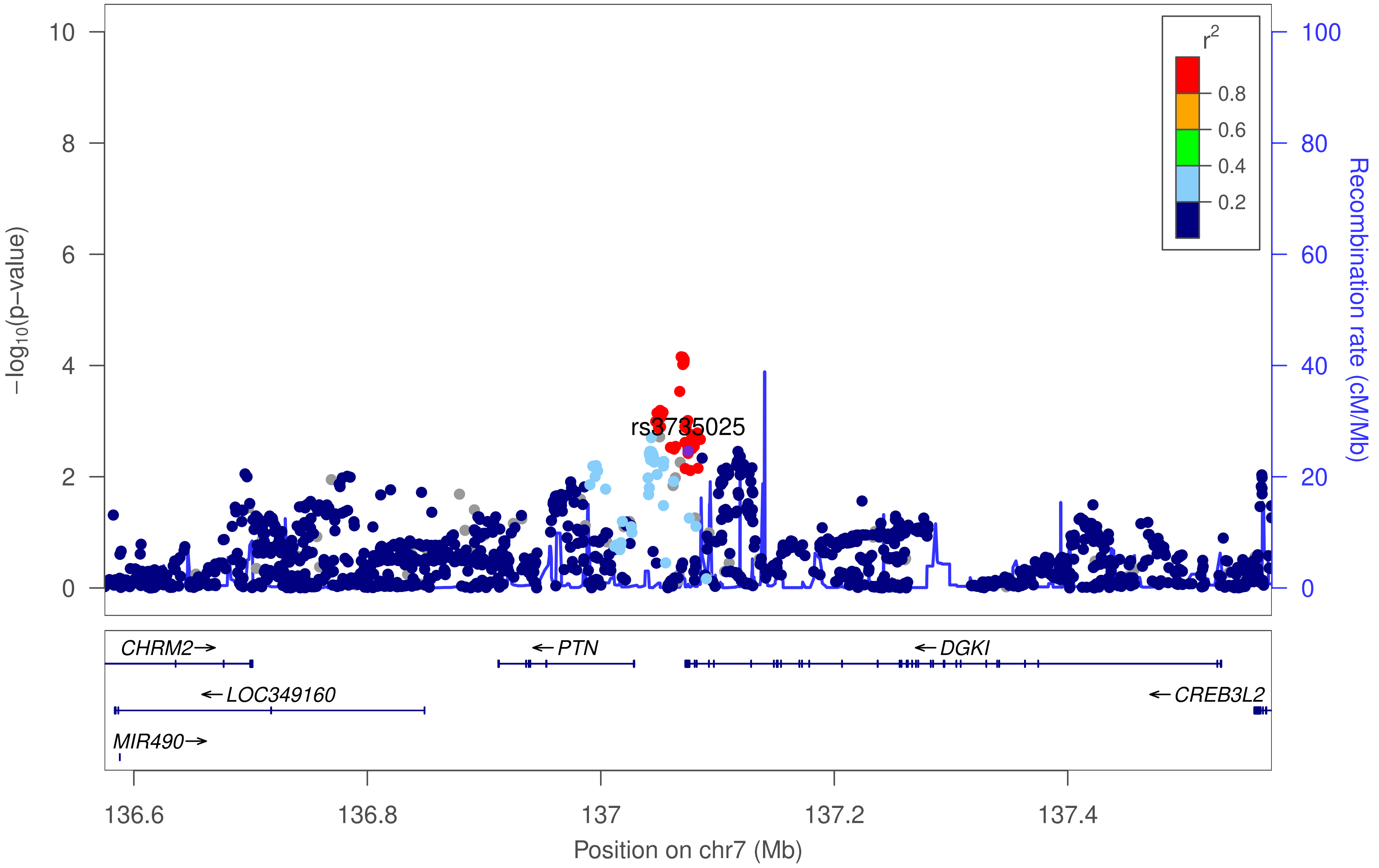


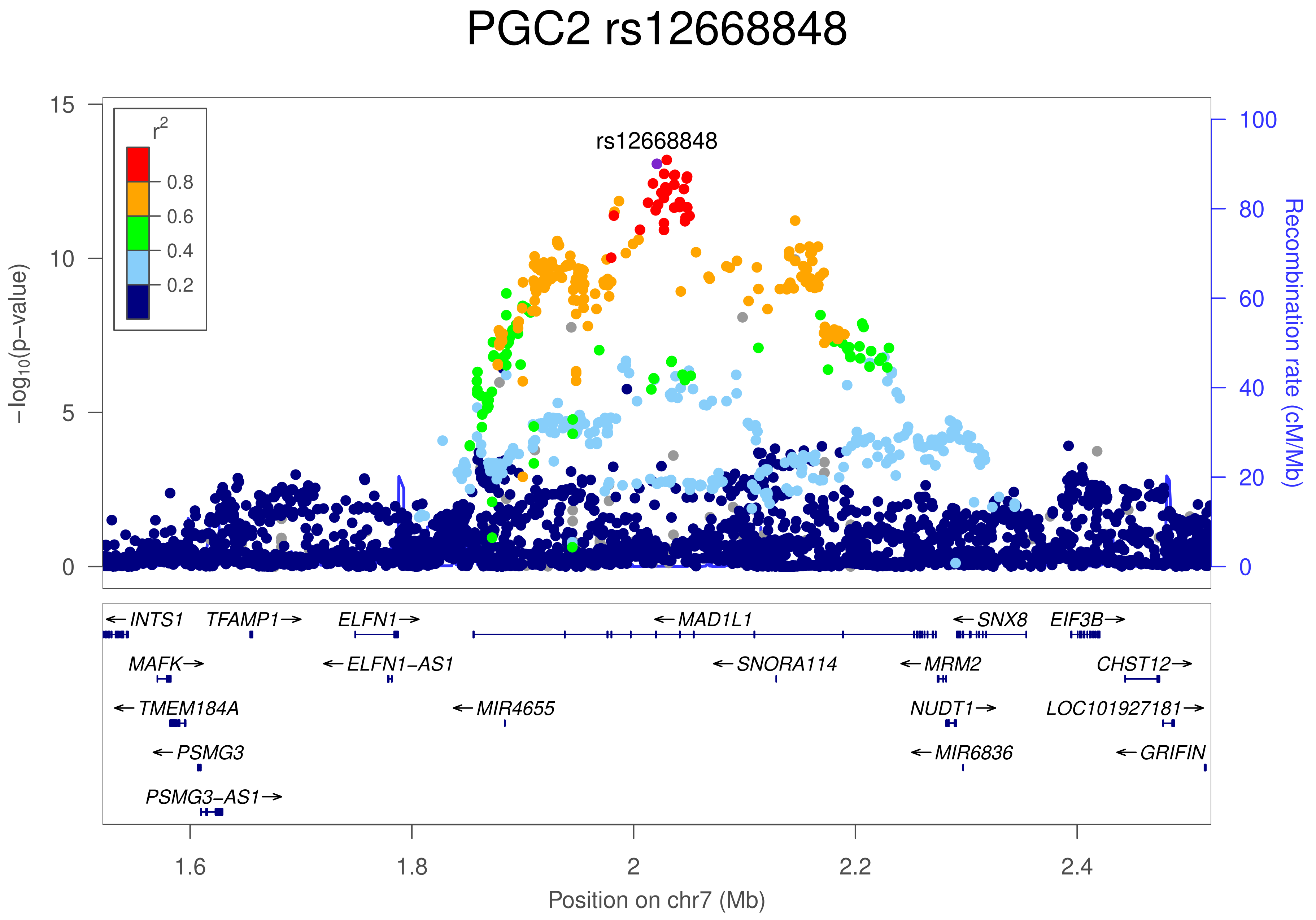

Chinese−only rs214467
r^2
0.8
0.6
0.4
0.2
10
8
6
4
2
0
−log$_{10}$(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
rs214467
← IMMP2L
LRRN3 →
110.4
110.6
110.8
111
111.2
Position on chr7 (Mb)

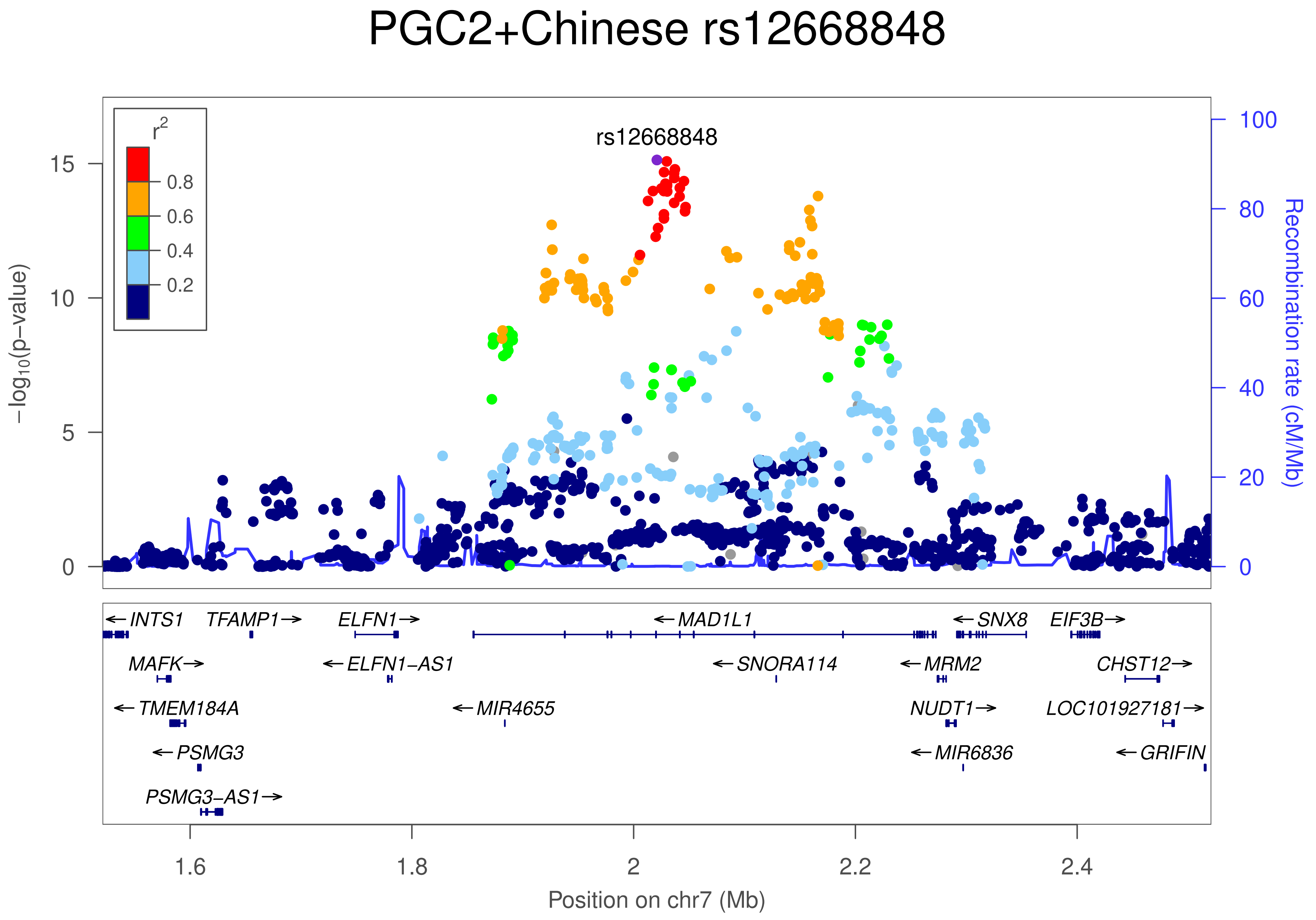

PGC2 rs3735025
rs3735025
−log10(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
r2
0.8
0.6
0.4
0.2
CHRM2→
←PTN
←DGKI
←LOC349160
←CREB3L2
MIR490→
136.6
136.8
137
137.2
137.4
Position on chr7 (Mb)

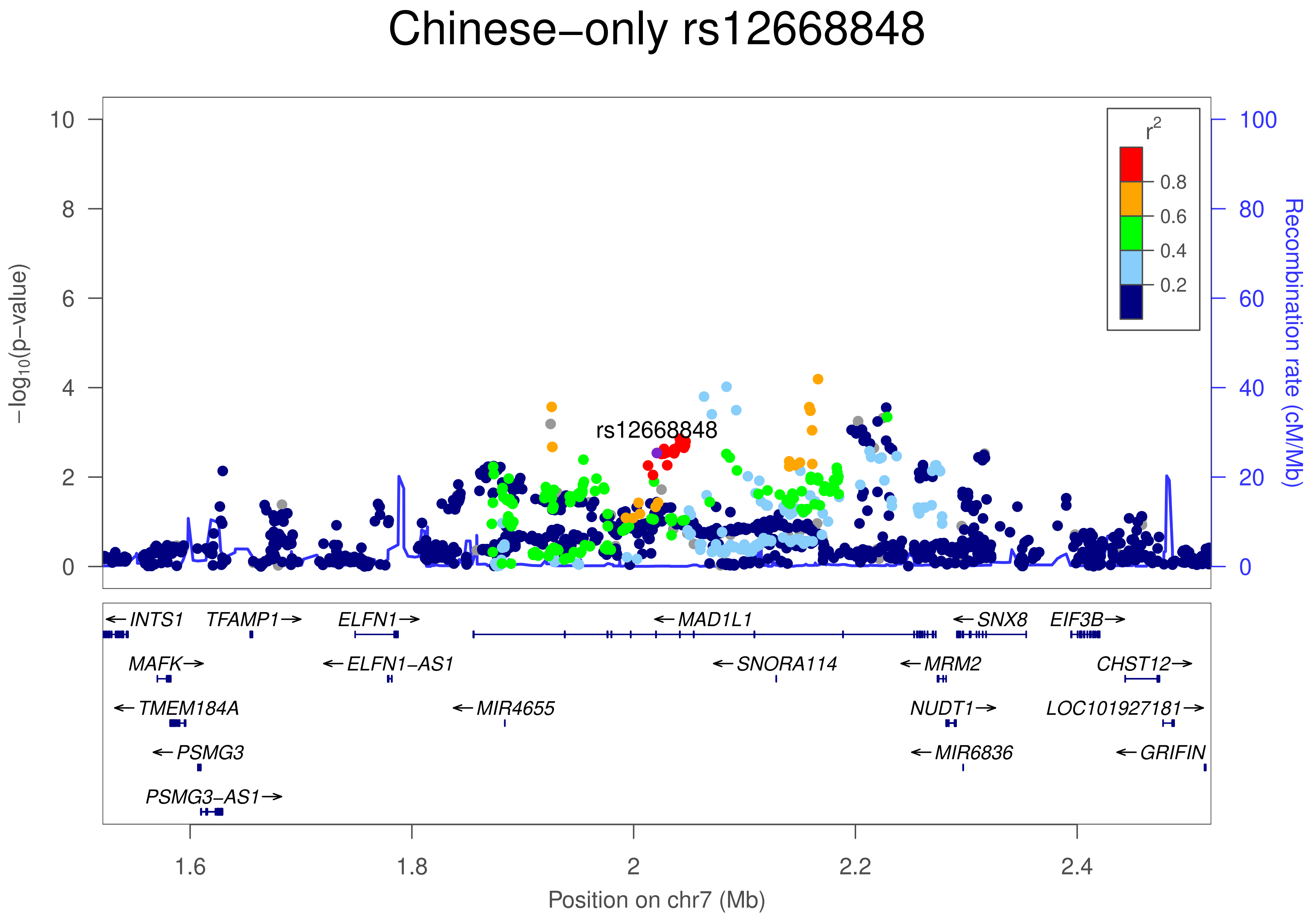

PGC2+Chinese rs3735025
rs3735025
−log10(p−value)
0
2
4
6
8
10
12
Recombination rate (cM/Mb)
0
20
40
60
80
100
r²
0.8
0.6
0.4
0.2
CHRM2→
←PTN
←DGKI
←LOC349160
←CREB3L2
MIR490→
136.6
136.8
137
137.2
137.4
Position on chr7 (Mb)

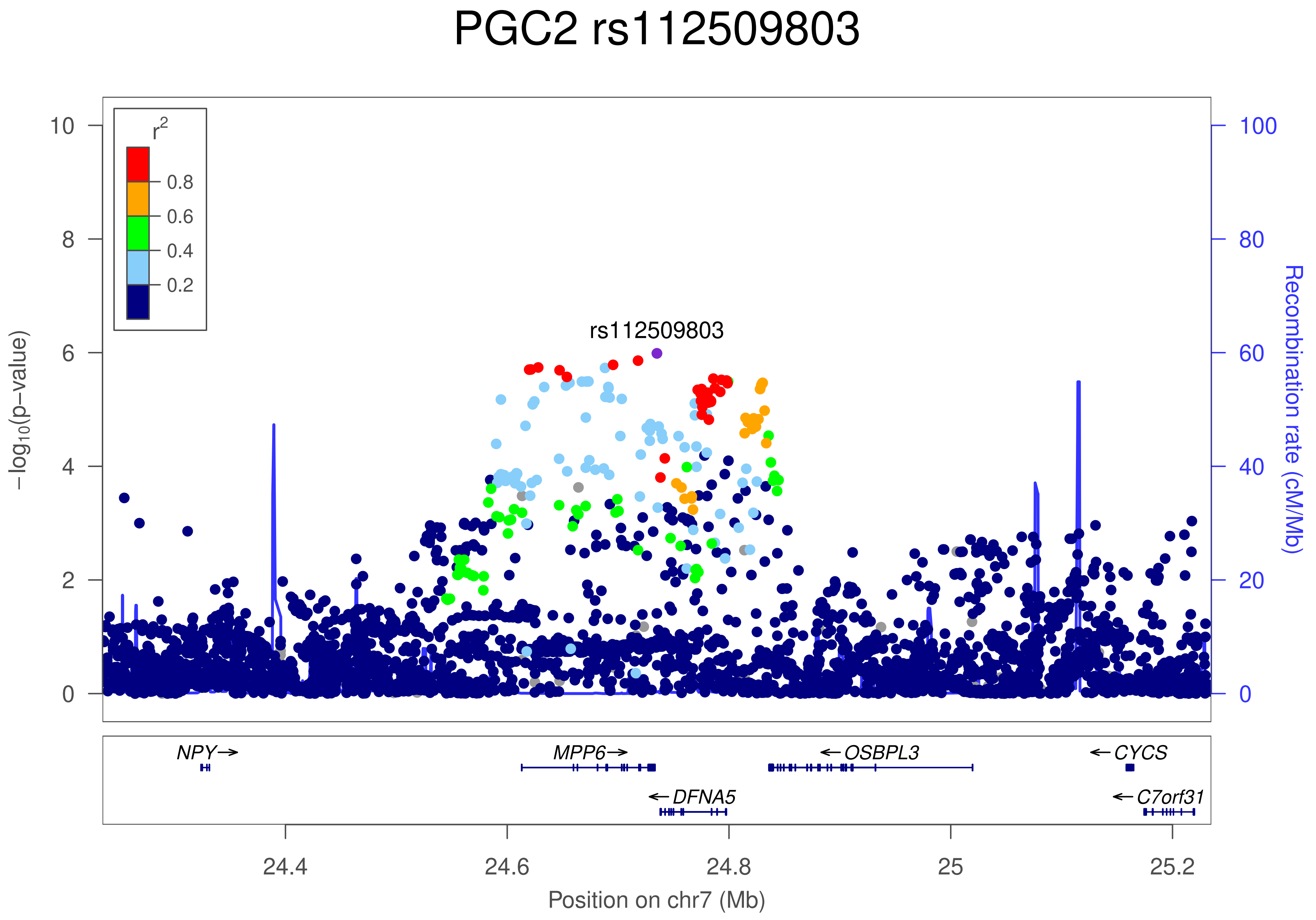
Chinese−only rs3735025

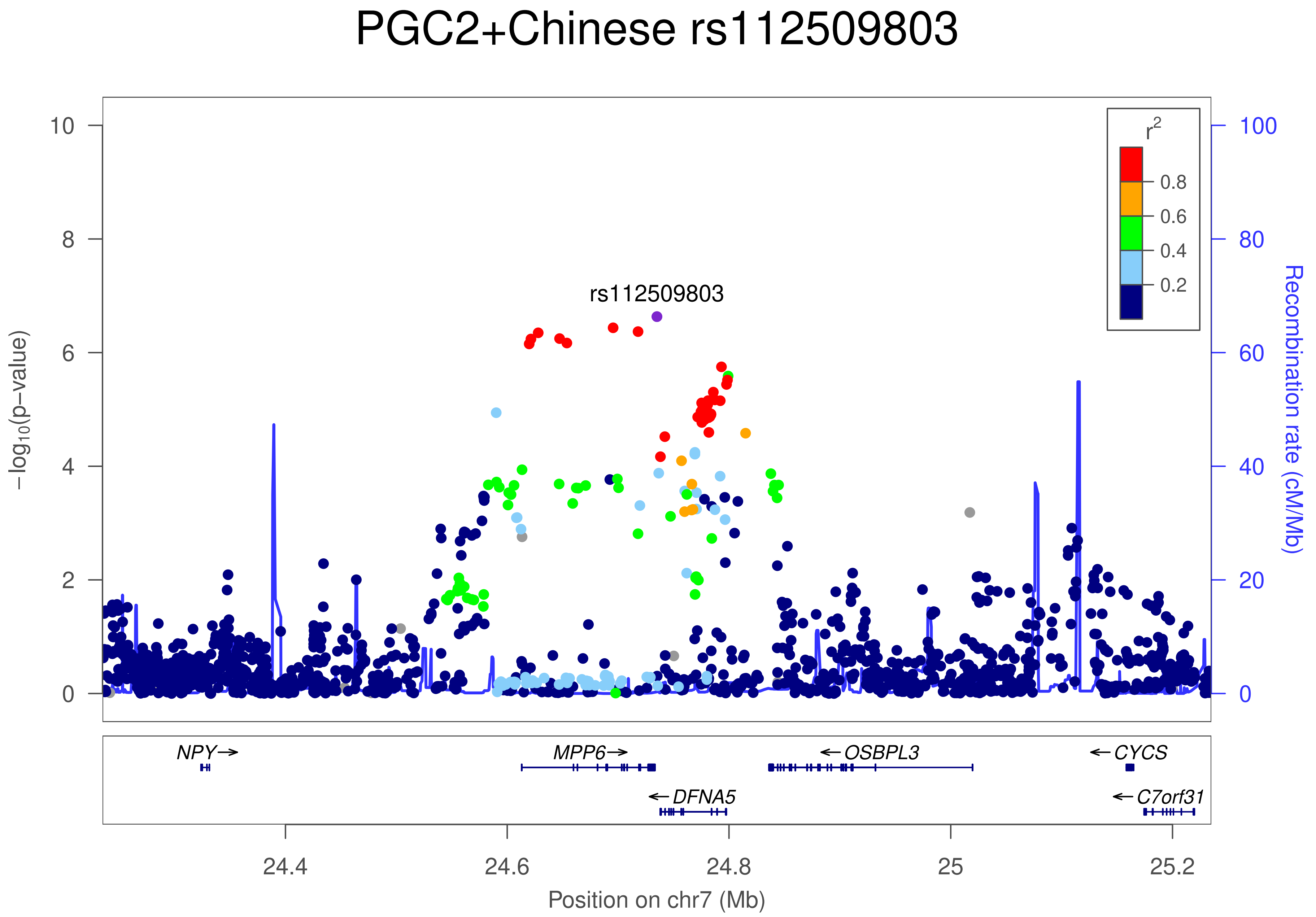


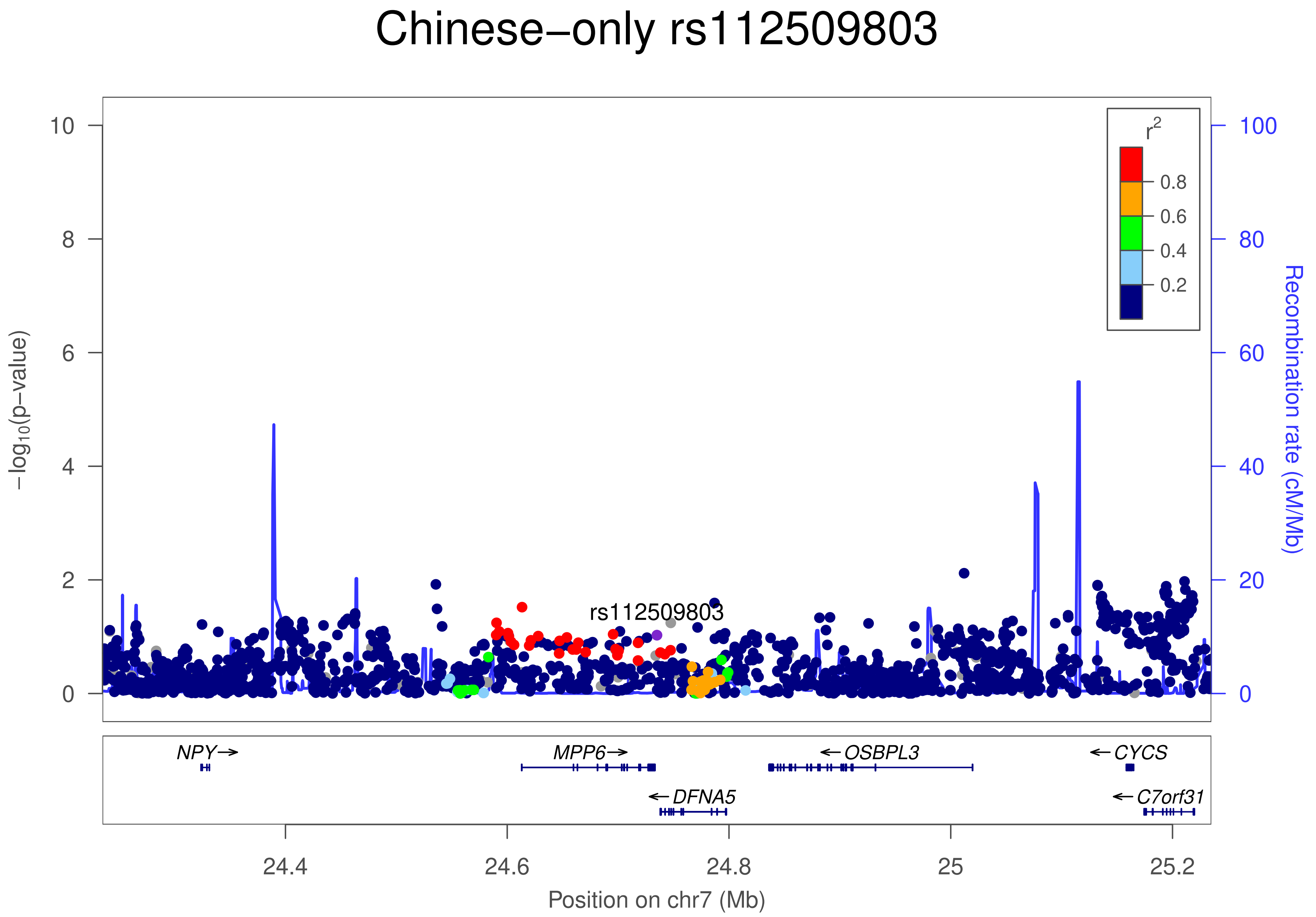

PGC2 rs12668848
r²
0.8
0.6
0.4
0.2
rs12668848
15
10
5
0
−log₁₀(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
← INTS1
TFAMP1 →
ELFN1 →
← MAD1L1
← SNX8
EIF3B →
MAFK →
← ELFN1−AS1
← SNORA114
← MRM2
CHST12 →
← TMEM184A
← MIR4655
NUDT1 →
LOC101927181 →
← PSMG3
← MIR6836
← GRIFIN
PSMG3−AS1 →
1.6
1.8
2
2.2
2.4
Position on chr7 (Mb)

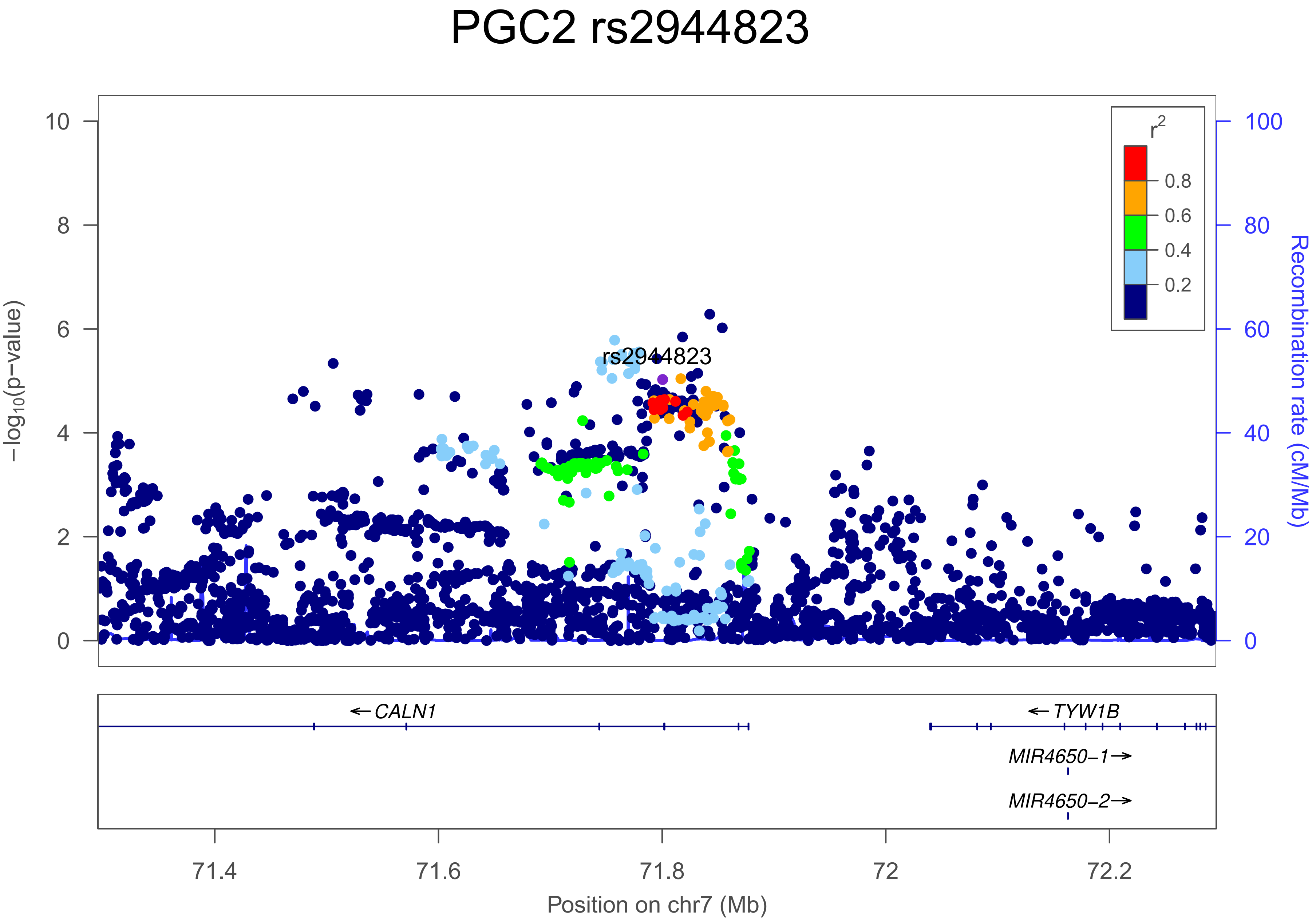

PGC2+Chinese rs12668848
rs12668848
r2
0.8
0.6
0.4
0.2
−log10(p−value)
0
5
10
15
Recombination rate (cM/Mb)
0
20
40
60
80
100
←INTS1
TFAMP1→
ELFN1→
←MAD1L1
←SNX8
EIF3B→
MAFK→
←ELFN1−AS1
←SNORA114
←MRM2
CHST12→
←TMEM184A
←MIR4655
NUDT1→
LOC101927181→
←PSMG3
←MIR6836
←GRIFIN
PSMG3−AS1→
1.6
1.8
2
2.2
2.4
Position on chr7 (Mb)

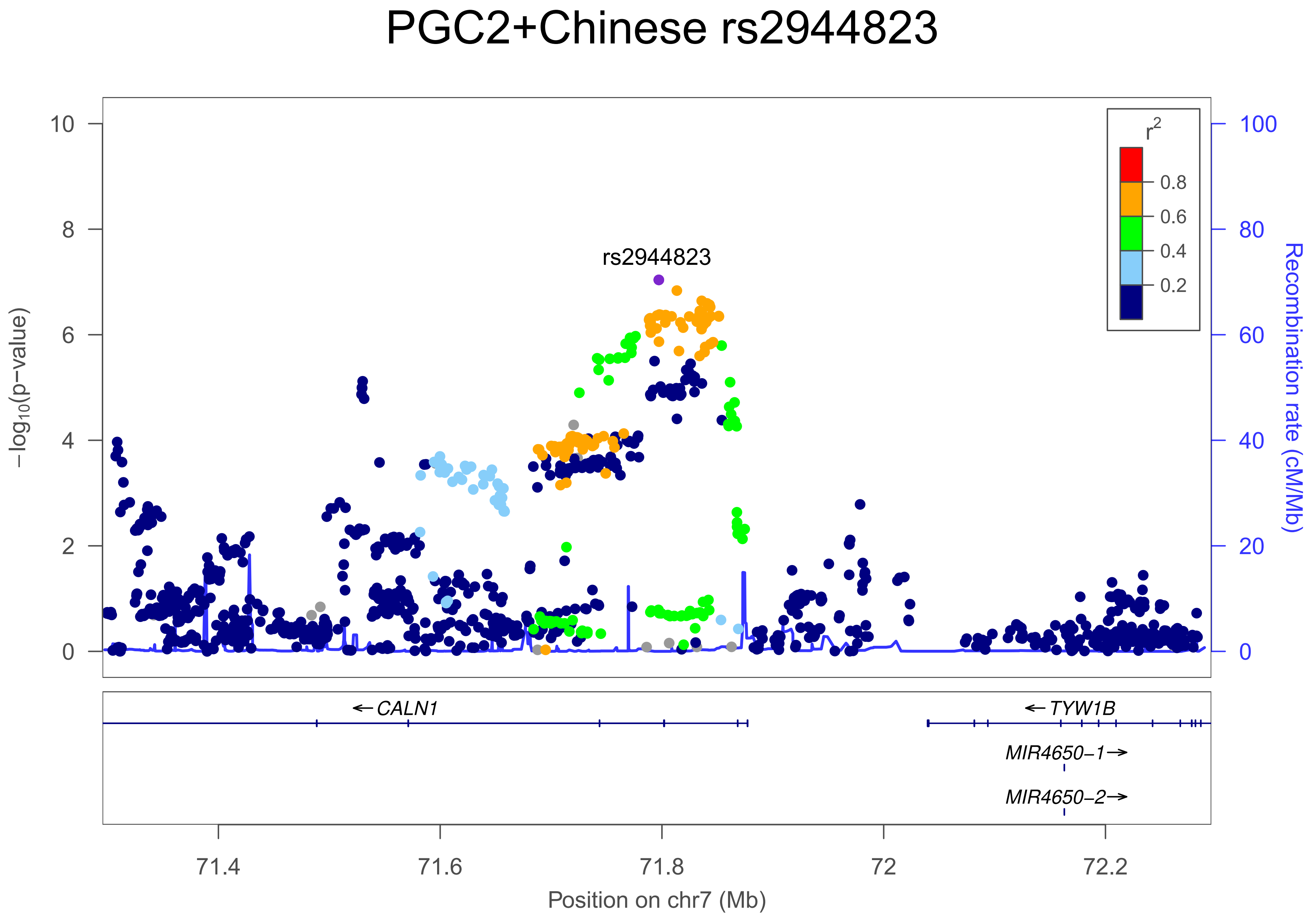

Chinese−only rs12668848
10
8
6
4
2
0
$-\log_{10}$(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
r^2
0.8
0.6
0.4
0.2
rs12668848
← INTS1
TFAMP1 →
ELFN1 →
← MAD1L1
← SNX8
EIF3B →
MAFK →
← ELFN1−AS1
← SNORA114
← MRM2
CHST12 →
← TMEM184A
← MIR4655
NUDT1 →
LOC101927181 →
← PSMG3
← MIR6836
← GRIFIN
PSMG3−AS1 →
1.6
1.8
2
2.2
2.4
Position on chr7 (Mb)

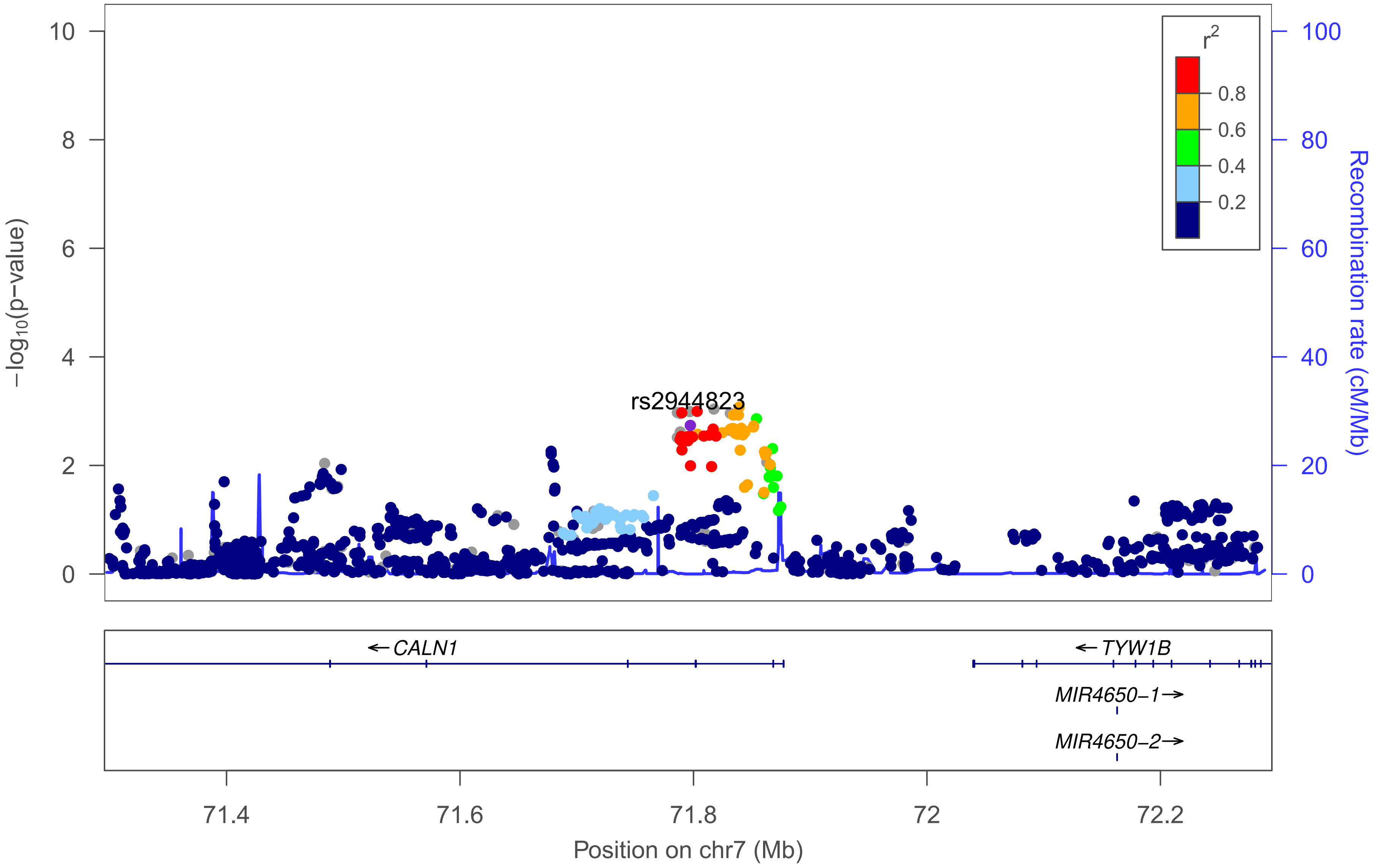

PGC2 rs112509803
r^2
0.8
0.6
0.4
0.2
rs112509803
10
8
6
4
2
0
−log10(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
NPY→
MPP6→
←OSBPL3
←CYCS
←DFNA5
←C7orf31
24.4
24.6
24.8
25
25.2
Position on chr7 (Mb)


PGC2+Chinese rs112509803
rs112509803
r²
0.8
0.6
0.4
0.2
−log₁₀(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
NPY→
MPP6→
←OSBPL3
←CYCS
←DFNA5
←C7orf31
24.4
24.6
24.8
25
25.2
Position on chr7 (Mb)

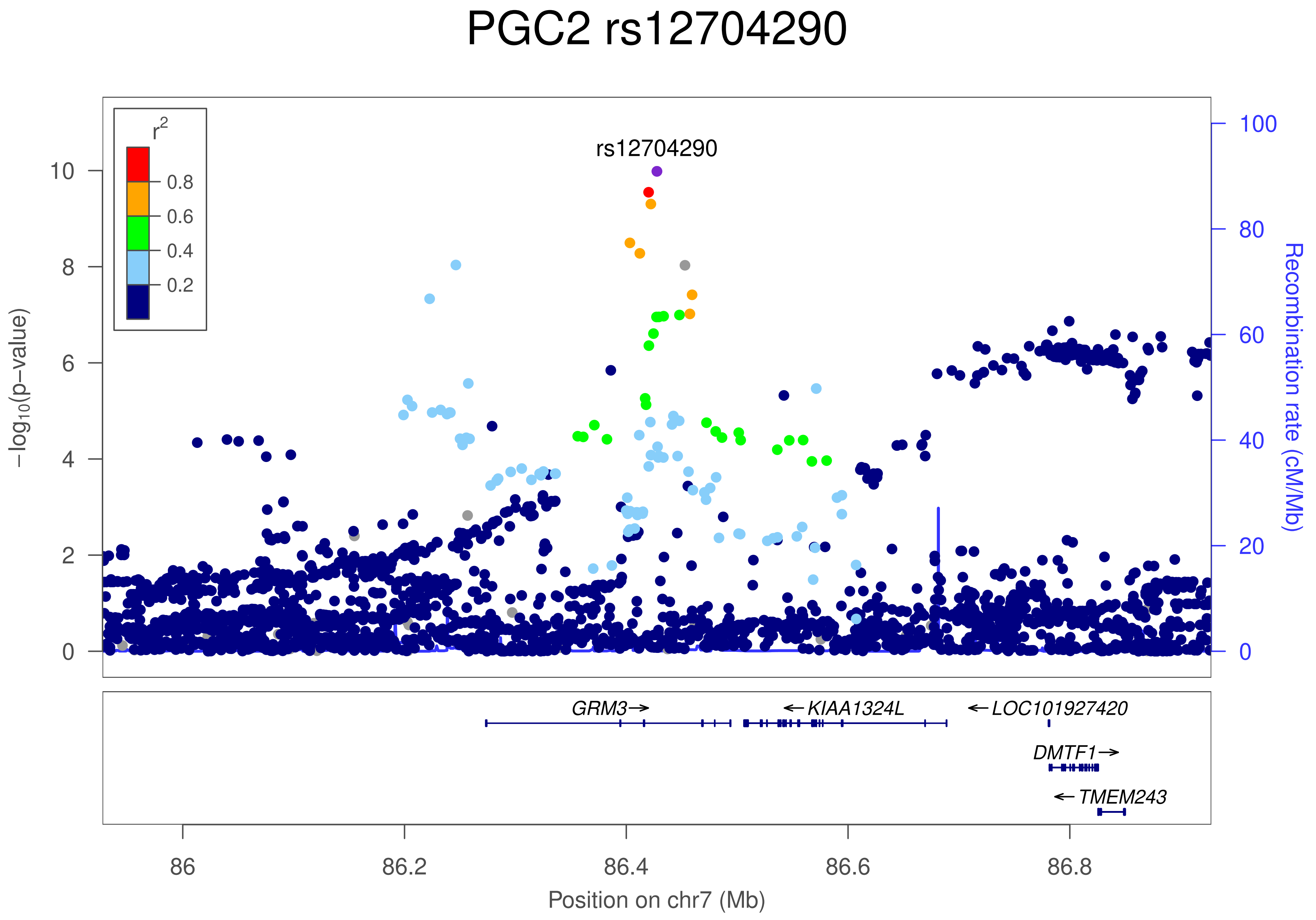

Chinese−only rs112509803
−log10(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
r2
0.8
0.6
0.4
0.2
rs112509803
NPY→
MPP6→
←OSBPL3
←CYCS
←DFNA5
←C7orf31
24.4
24.6
24.8
25
25.2
Position on chr7 (Mb)


PGC2 rs2944823
rs2944823
r²
0.8
0.6
0.4
0.2
−log10(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
← CALN1
← TYW1B
MIR4650−1 →
MIR4650−2 →
71.4
71.6
71.8
72
72.2
Position on chr7 (Mb)

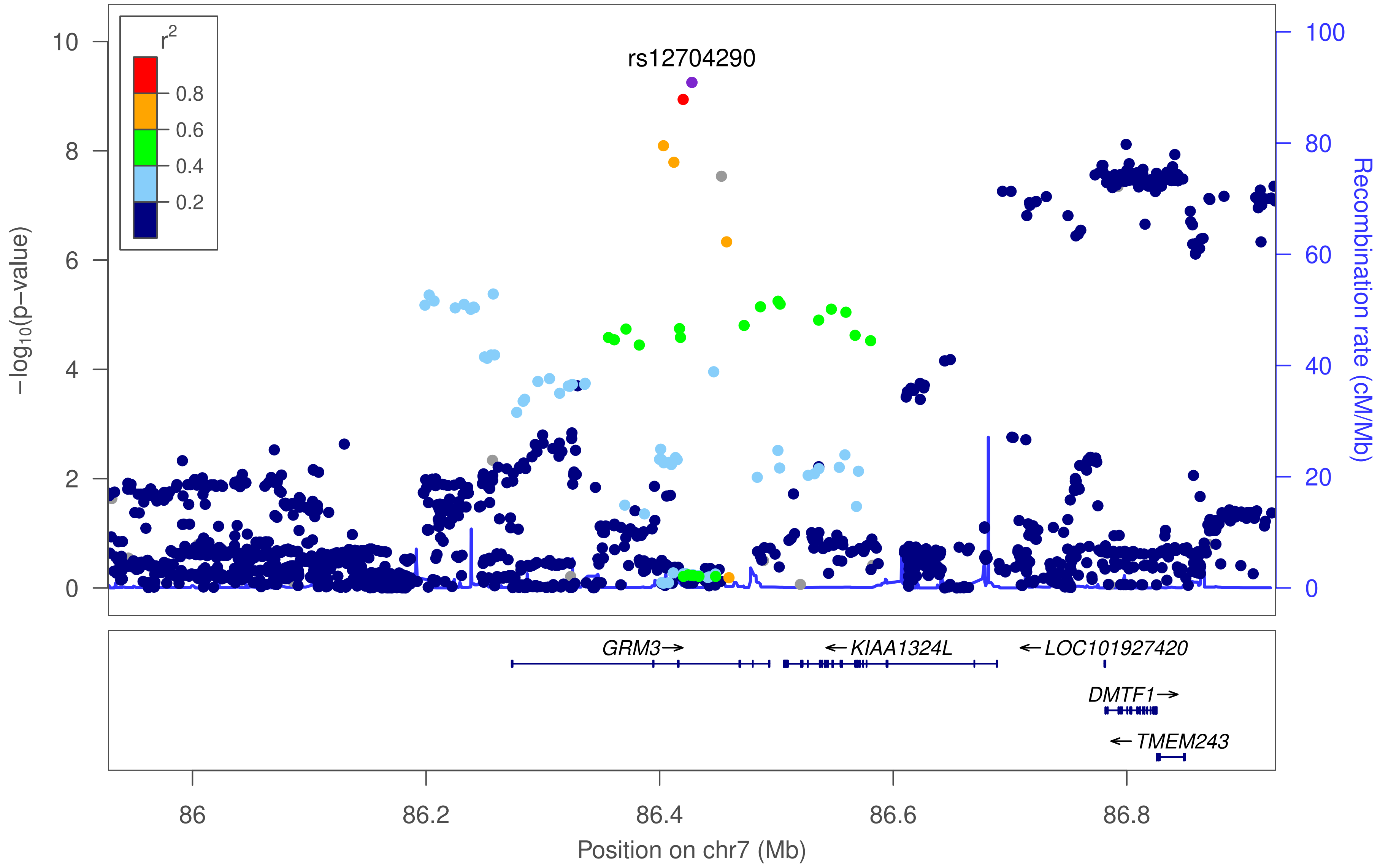

PGC2+Chinese rs2944823
rs2944823
−log10(p−value)
10
8
6
4
2
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
r2
0.8
0.6
0.4
0.2
← CALN1
← TYW1B
MIR4650−1 →
MIR4650−2 →
71.4
71.6
71.8
72
72.2
Position on chr7 (Mb)

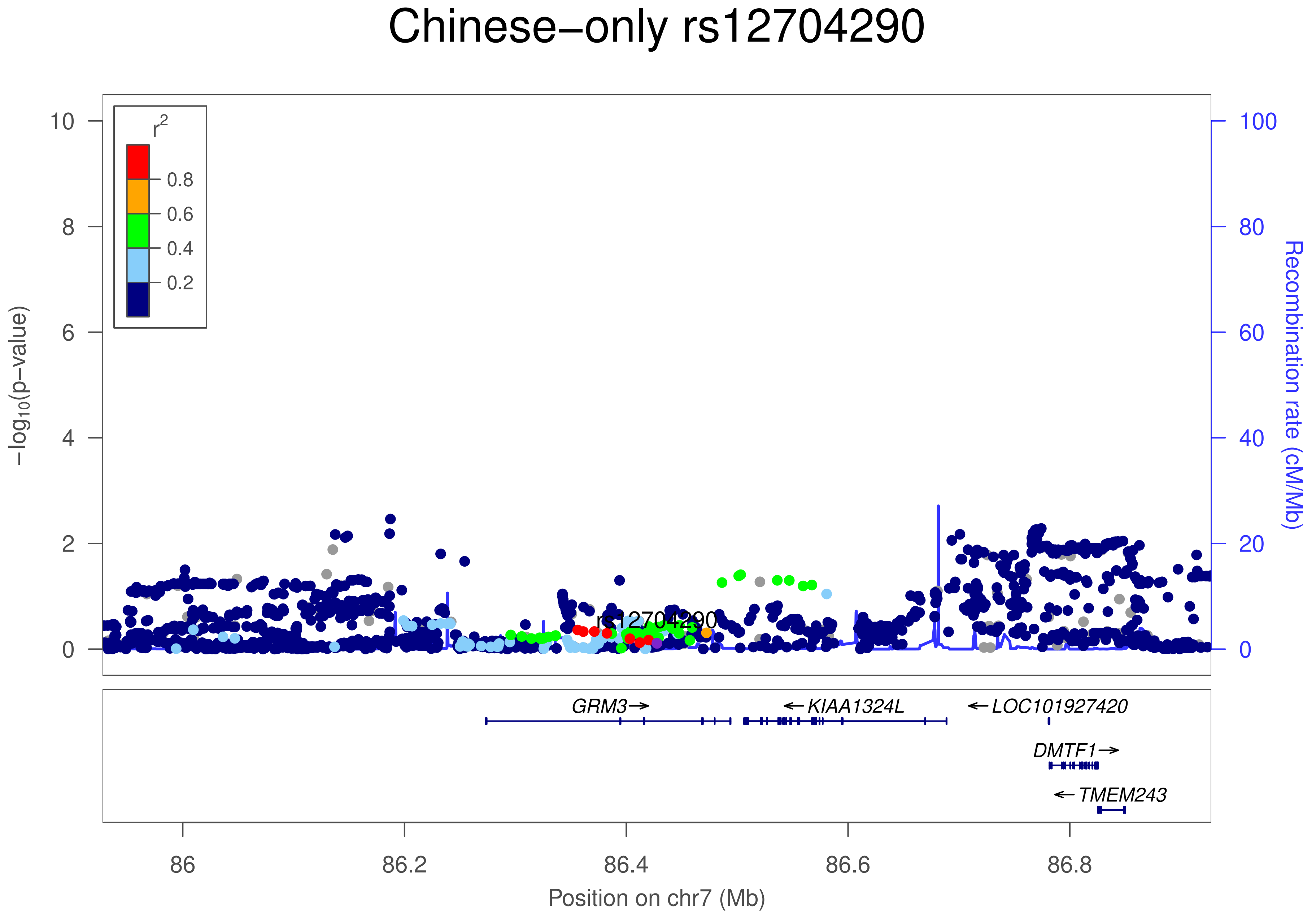


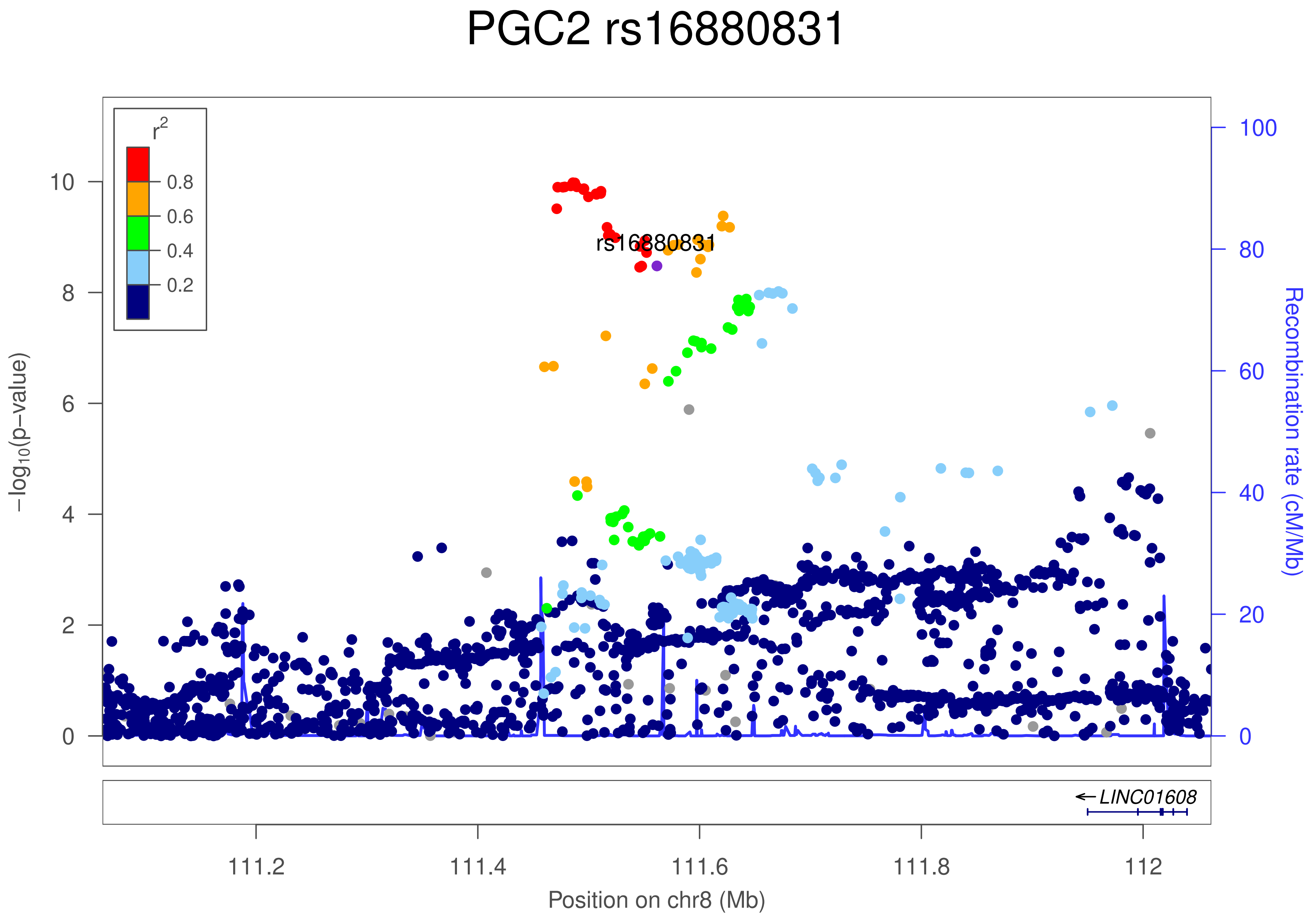
Chinese-only rs2944823


PGC2 rs12704290
rs12704290
r^2
0.8
0.6
0.4
0.2
−log$_{10}$(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
GRM3→
←KIAA1324L
←LOC101927420
DMTF1→
←TMEM243
86
86.2
86.4
86.6
86.8
Position on chr7 (Mb)

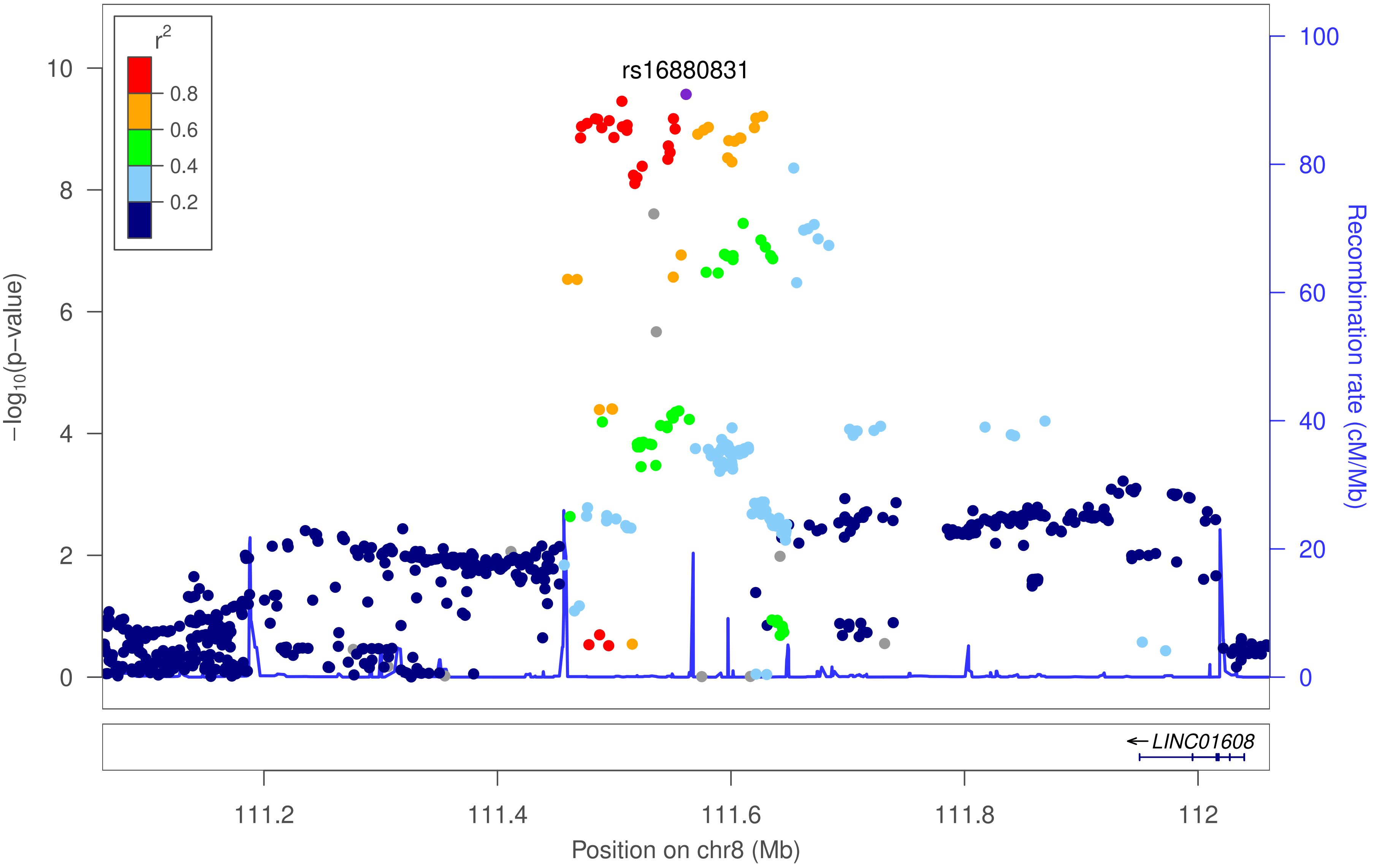
PGC2+Chinese rs12704290

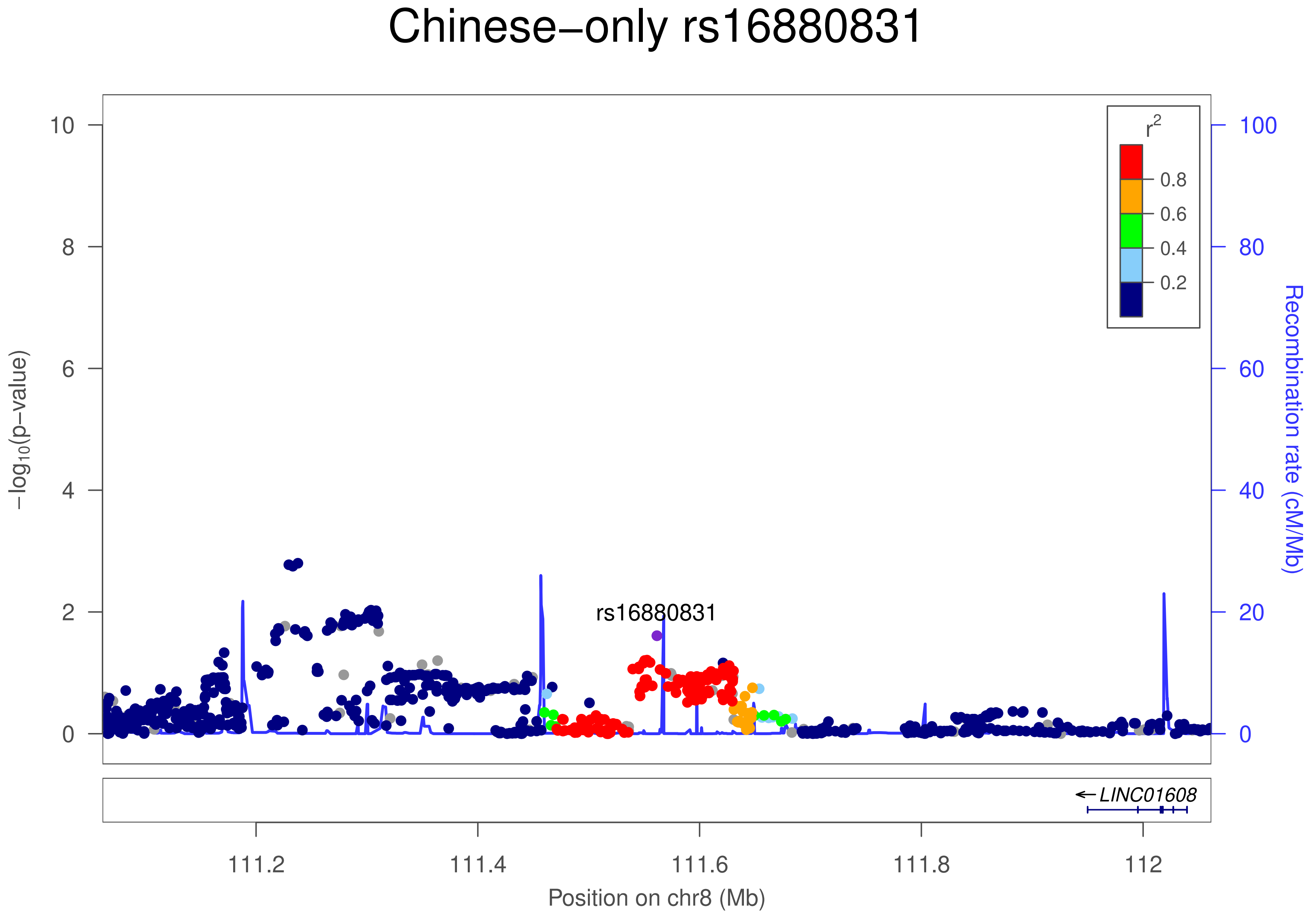



Chinese–only rs12704290
r²
0.8
0.6
0.4
0.2
$-\log_{10}$(p–value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
rs12704290
GRM3→
←KIAA1324L
←LOC101927420
DMTF1→
←TMEM243
86
86.2
86.4
86.6
86.8
Position on chr7 (Mb)

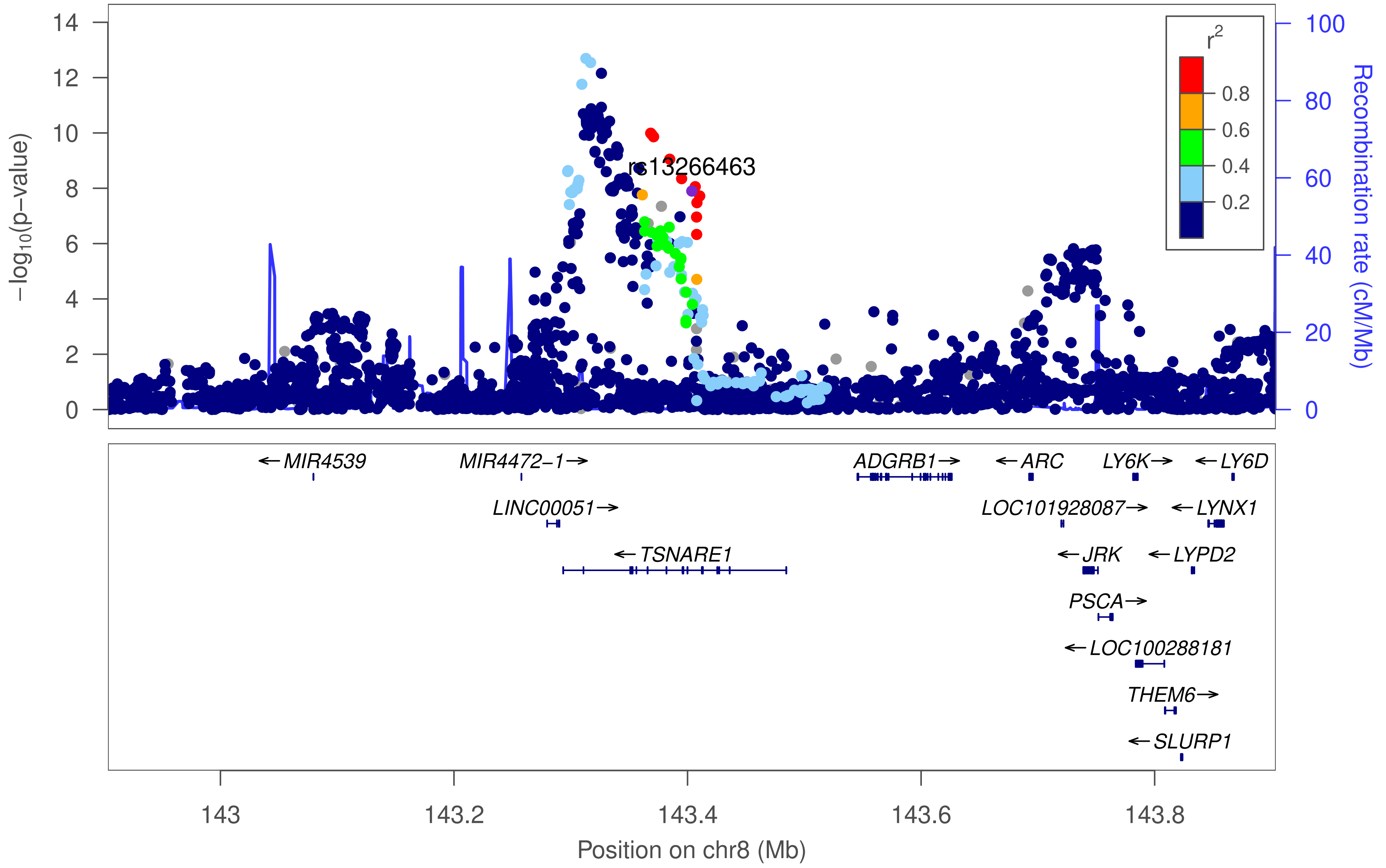

PGC2 rs16880831
r²
0.8
0.6
0.4
0.2
rs16880831
10
8
6
4
2
0
−log10(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
LINC01608
111.2
111.4
111.6
111.8
112
Position on chr8 (Mb)

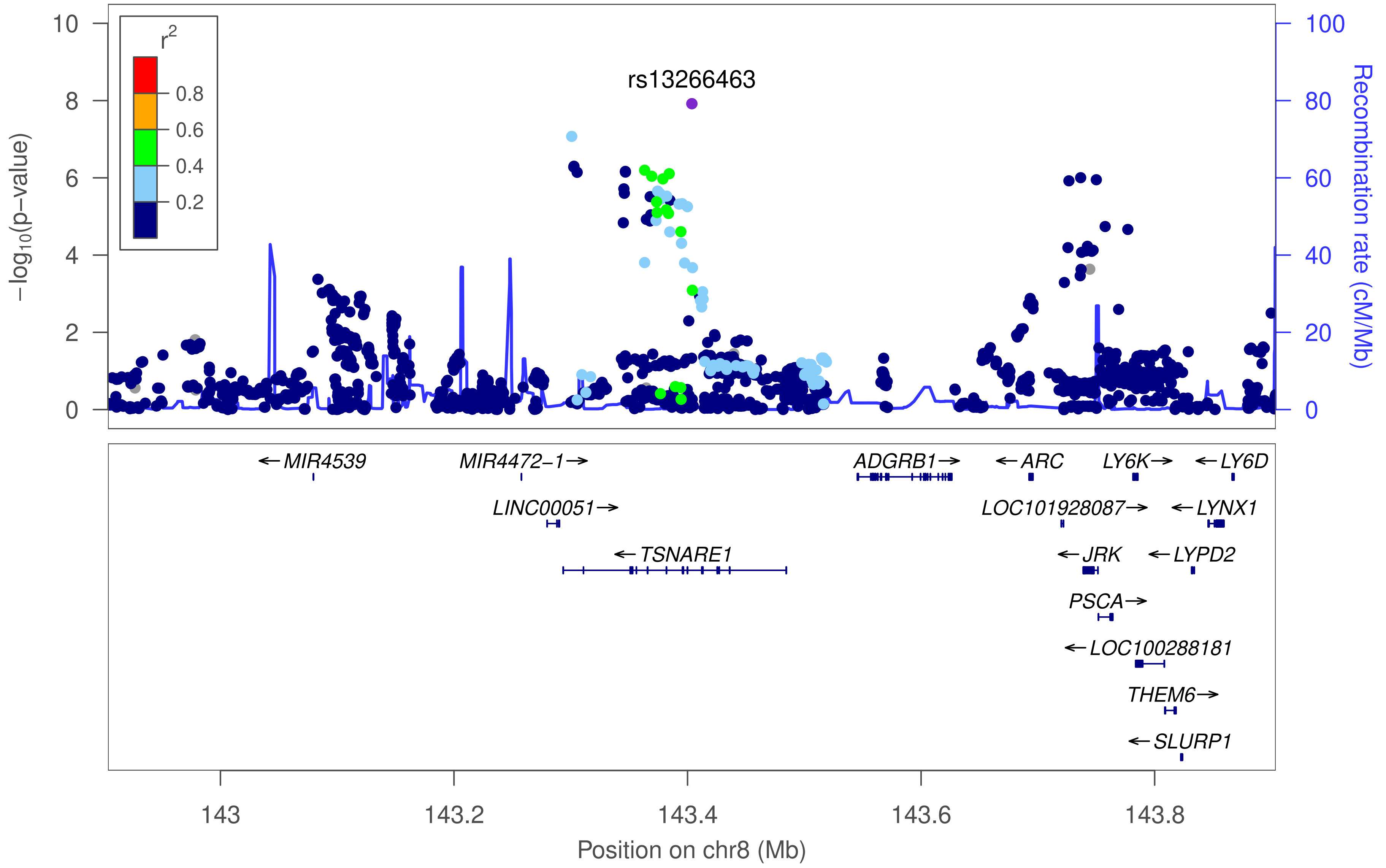
PGC2+Chinese rs16880831



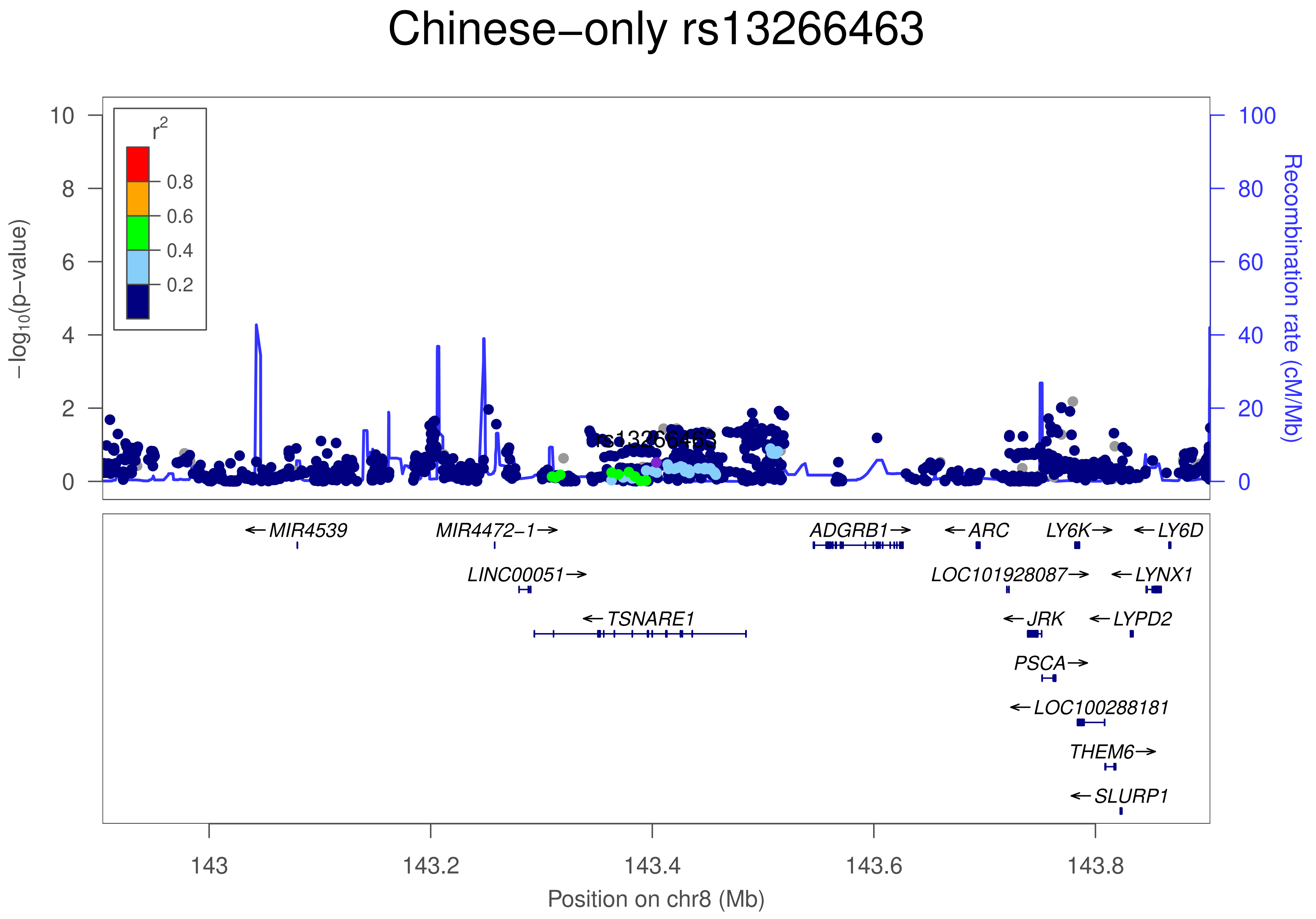

Chinese–only rs16880831
r2
0.8
0.6
0.4
0.2
10
8
6
4
2
0
−log10(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
rs16880831
← LINC01608
111.2
111.4
111.6
111.8
112
Position on chr8 (Mb)

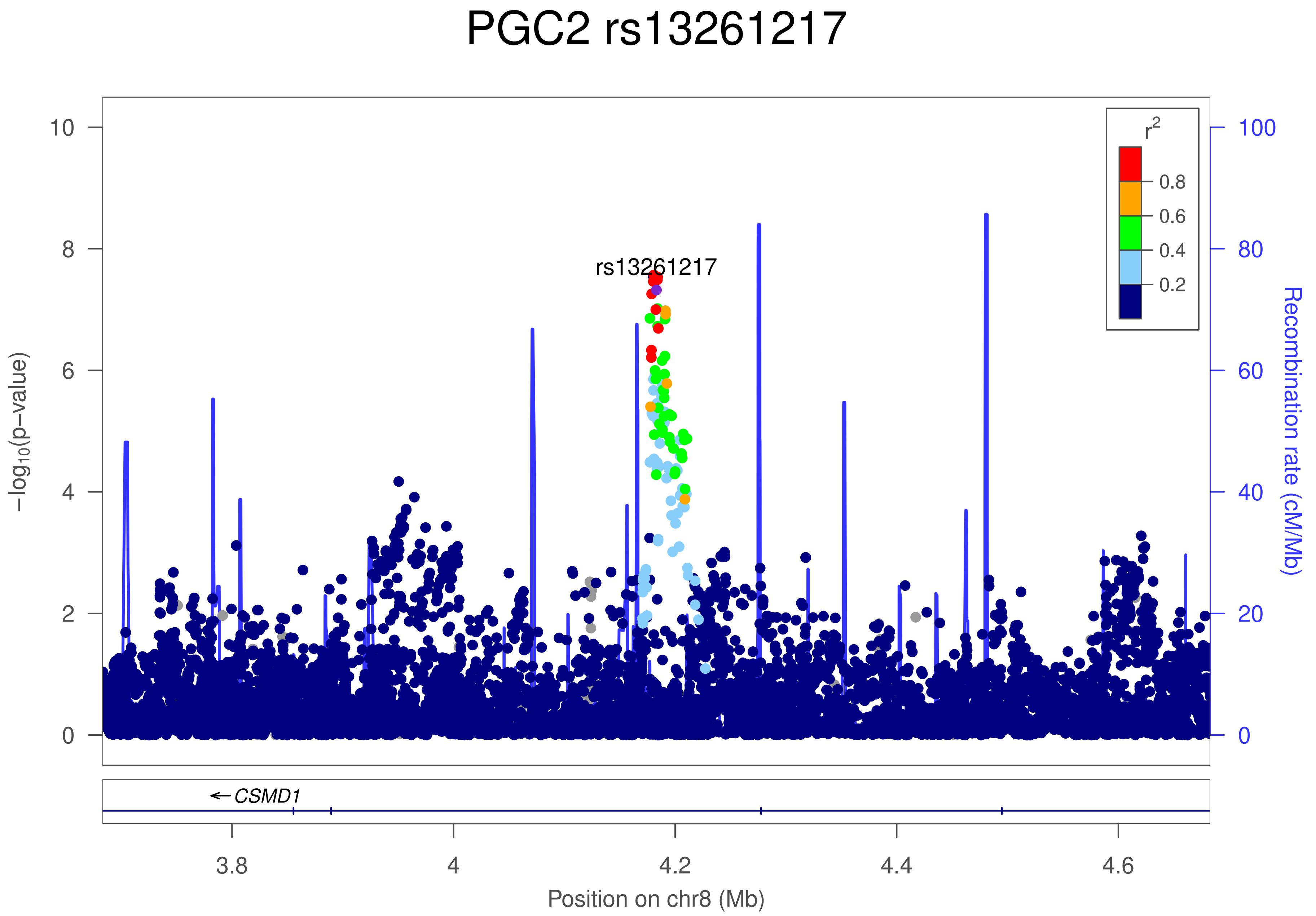
PGC2 rs13266463

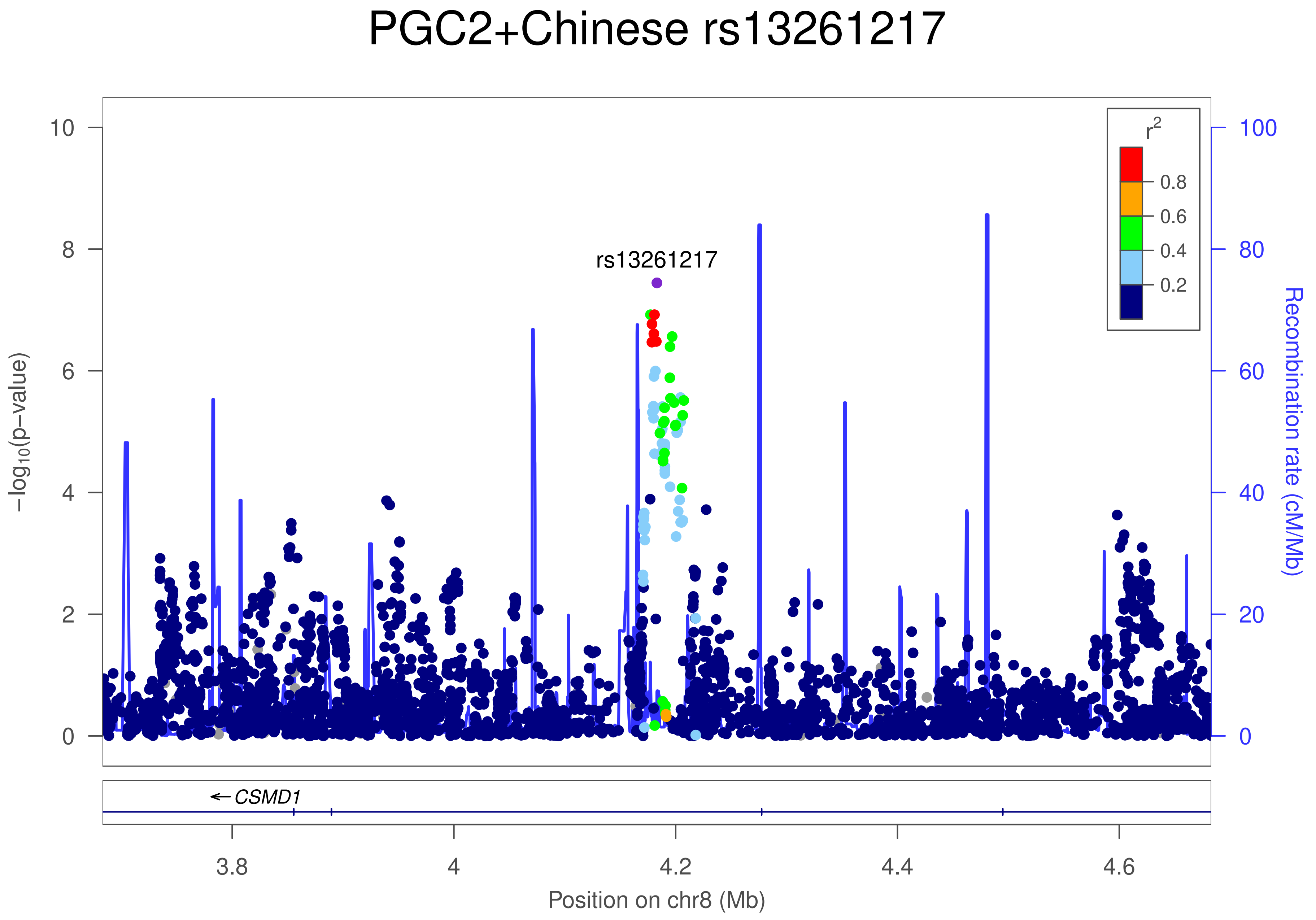


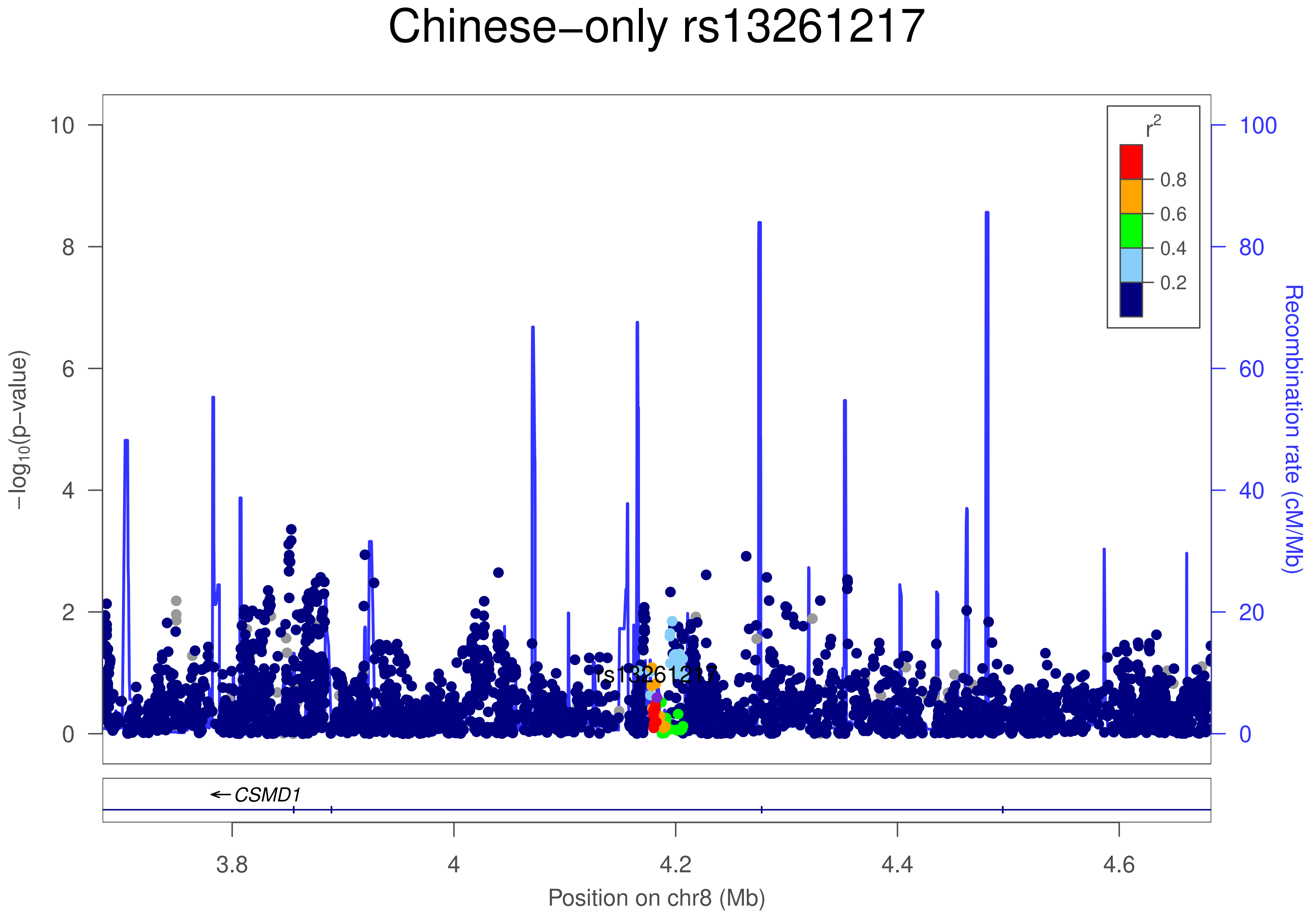


PGC2+Chinese rs13266463

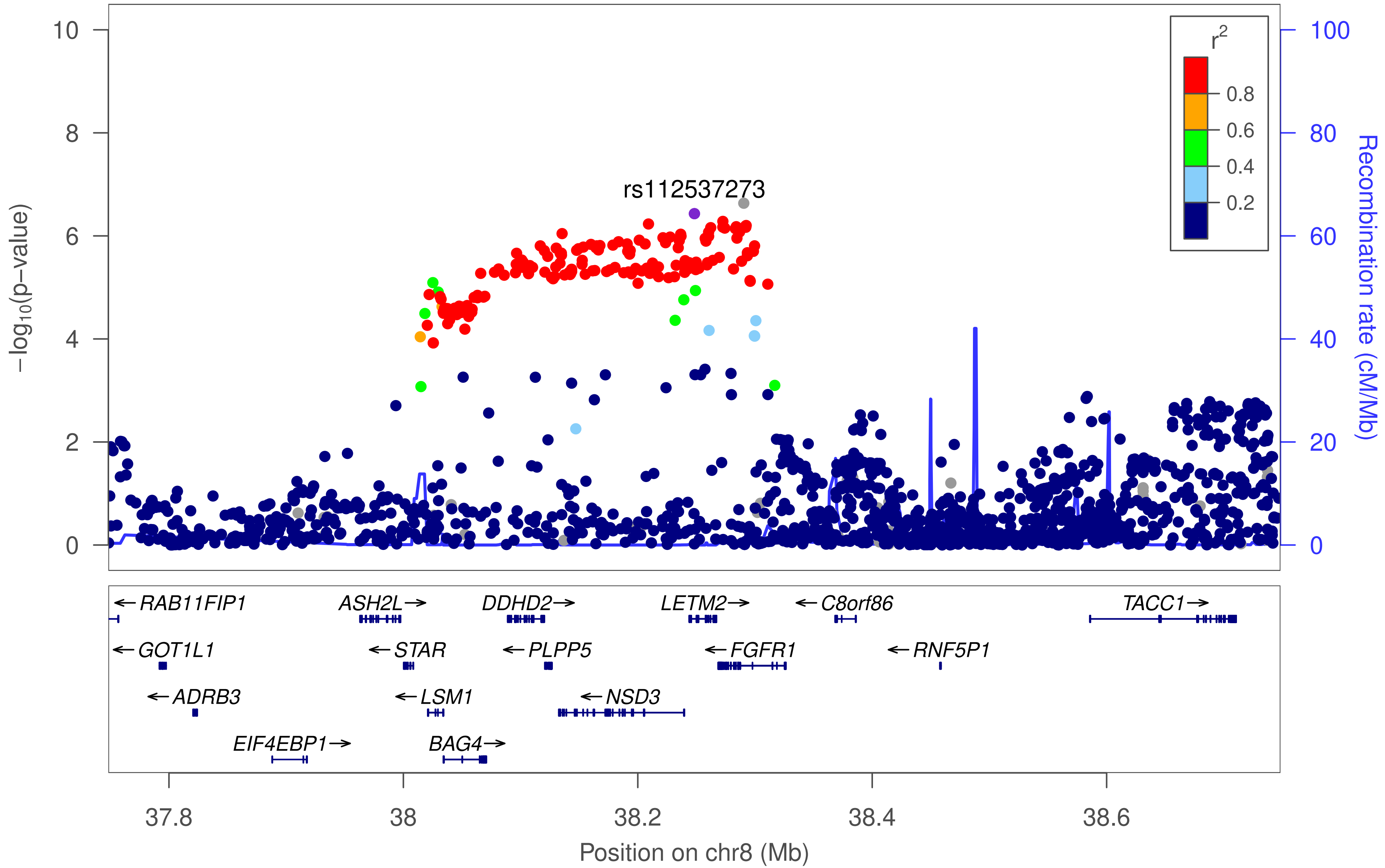

Chinese−only rs13266463
−log10(p−value)
10
8
6
4
2
0
r2
0.8
0.6
0.4
0.2
rs13266463
Recombination rate (cM/Mb)
100
80
60
40
20
0
←MIR4539
MIR4472−1→
ADGRB1→
←ARC
LY6K→
←LY6D
LINC00051→
LOC101928087→
←LYNX1
←TSNARE1
←JRK
←LYPD2
PSCA→
←LOC100288181
THEM6→
←SLURP1
143
143.2
143.4
143.6
143.8
Position on chr8 (Mb)

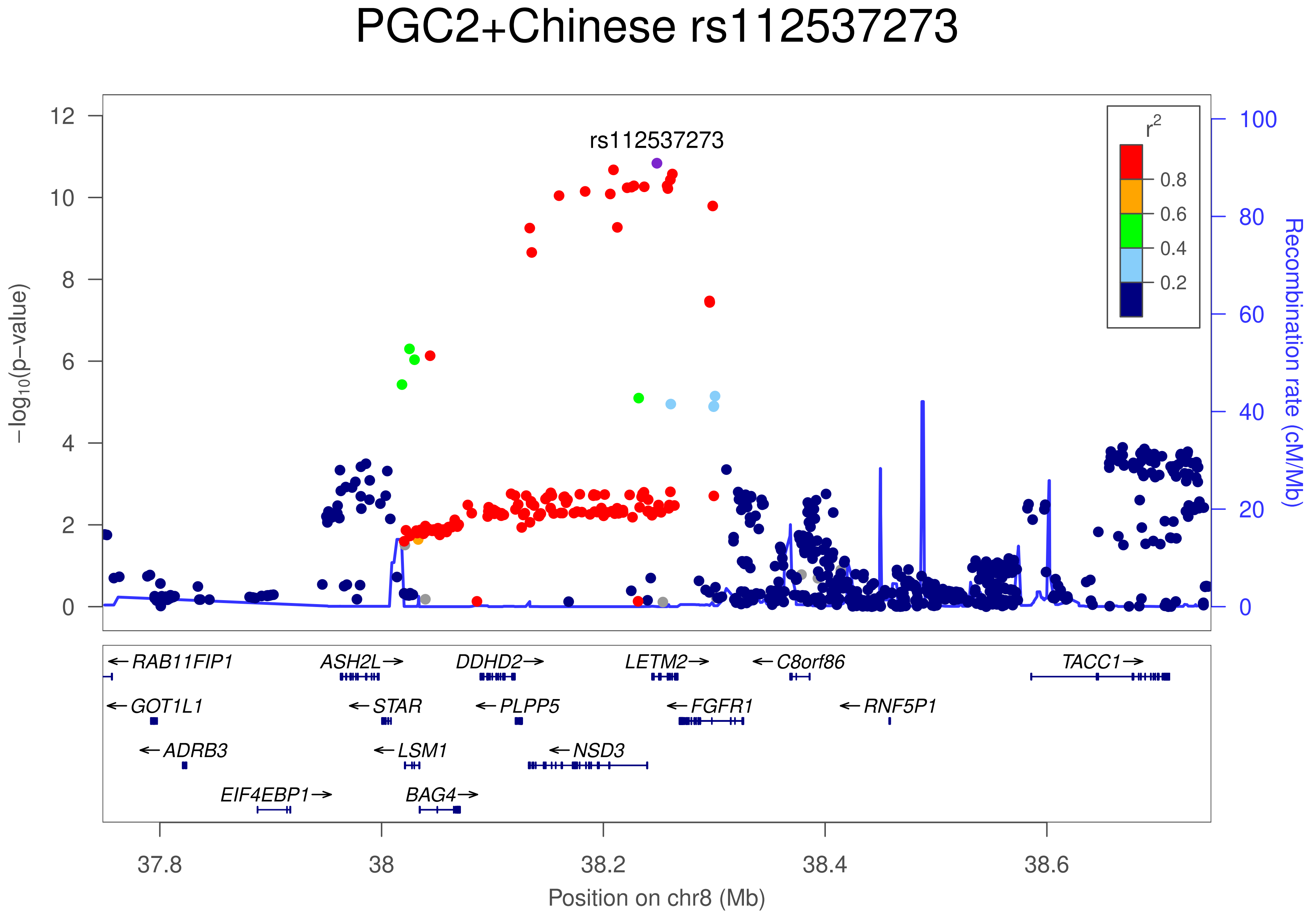

PGC2 rs13261217
rs13261217
r^2
0.8
0.6
0.4
0.2
10
8
6
4
2
0
−log10(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
← CSMD1
3.8
4
4.2
4.4
4.6
Position on chr8 (Mb)

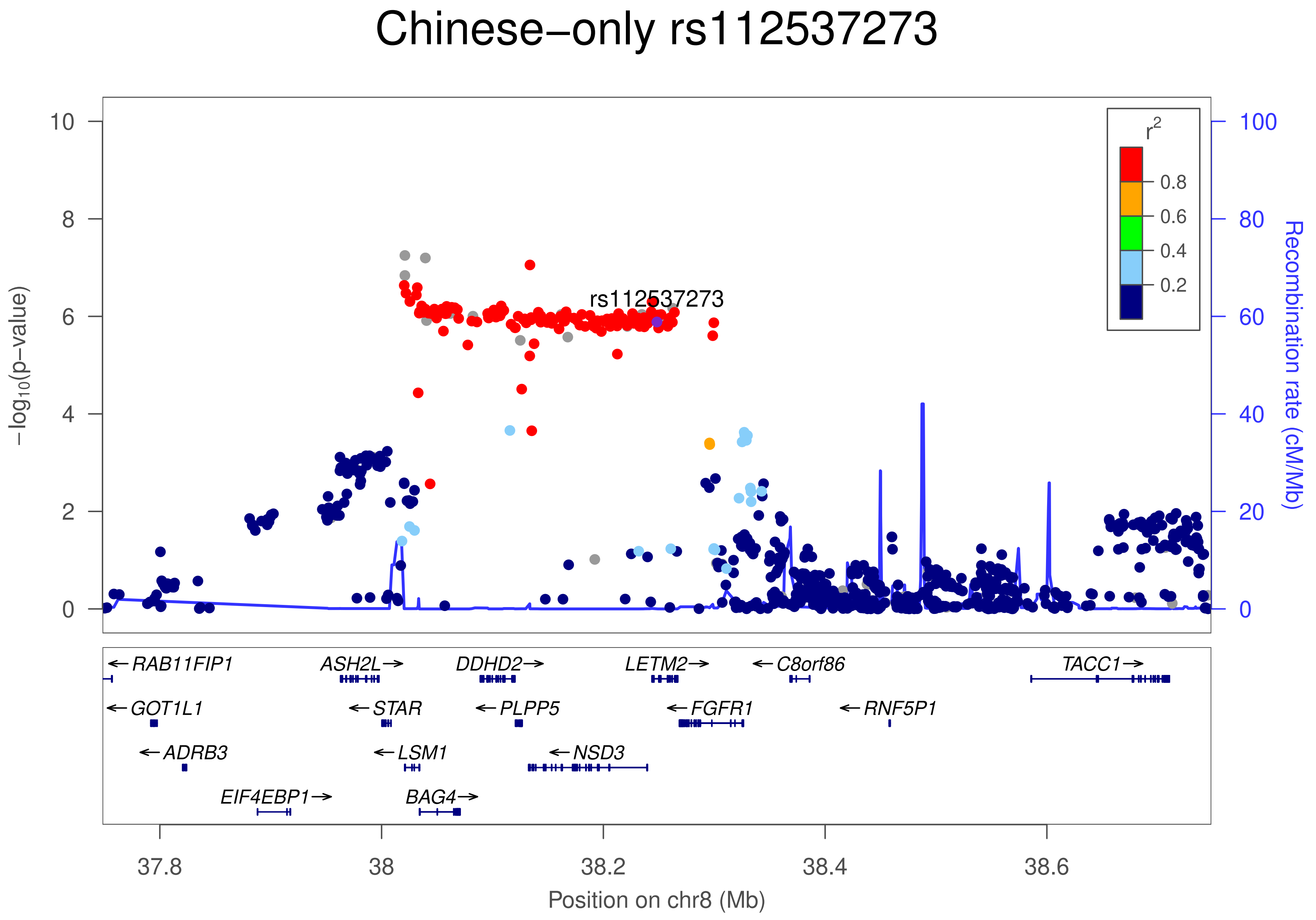

PGC2+Chinese rs13261217
rs13261217
−log10(p−value)
10
8
6
4
2
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
r2
0.8
0.6
0.4
0.2
← CSMD1
3.8
4
4.2
4.4
4.6
Position on chr8 (Mb)

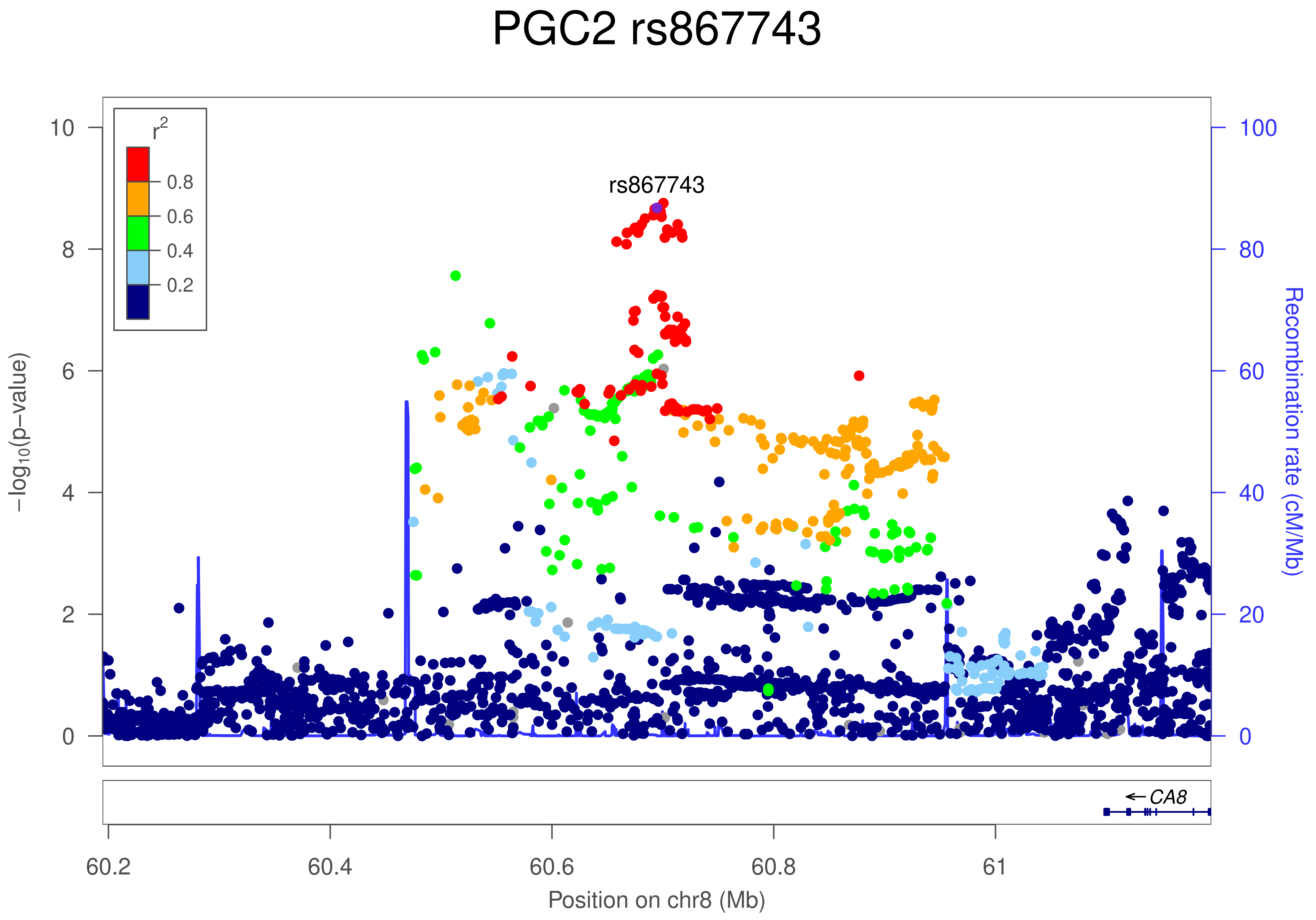

Chinese−only rs13261217
−log10(p−value)
10
8
6
4
2
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
r2
0.8
0.6
0.4
0.2
rs13261217
← CSMD1
3.8
4
4.2
4.4
4.6
Position on chr8 (Mb)

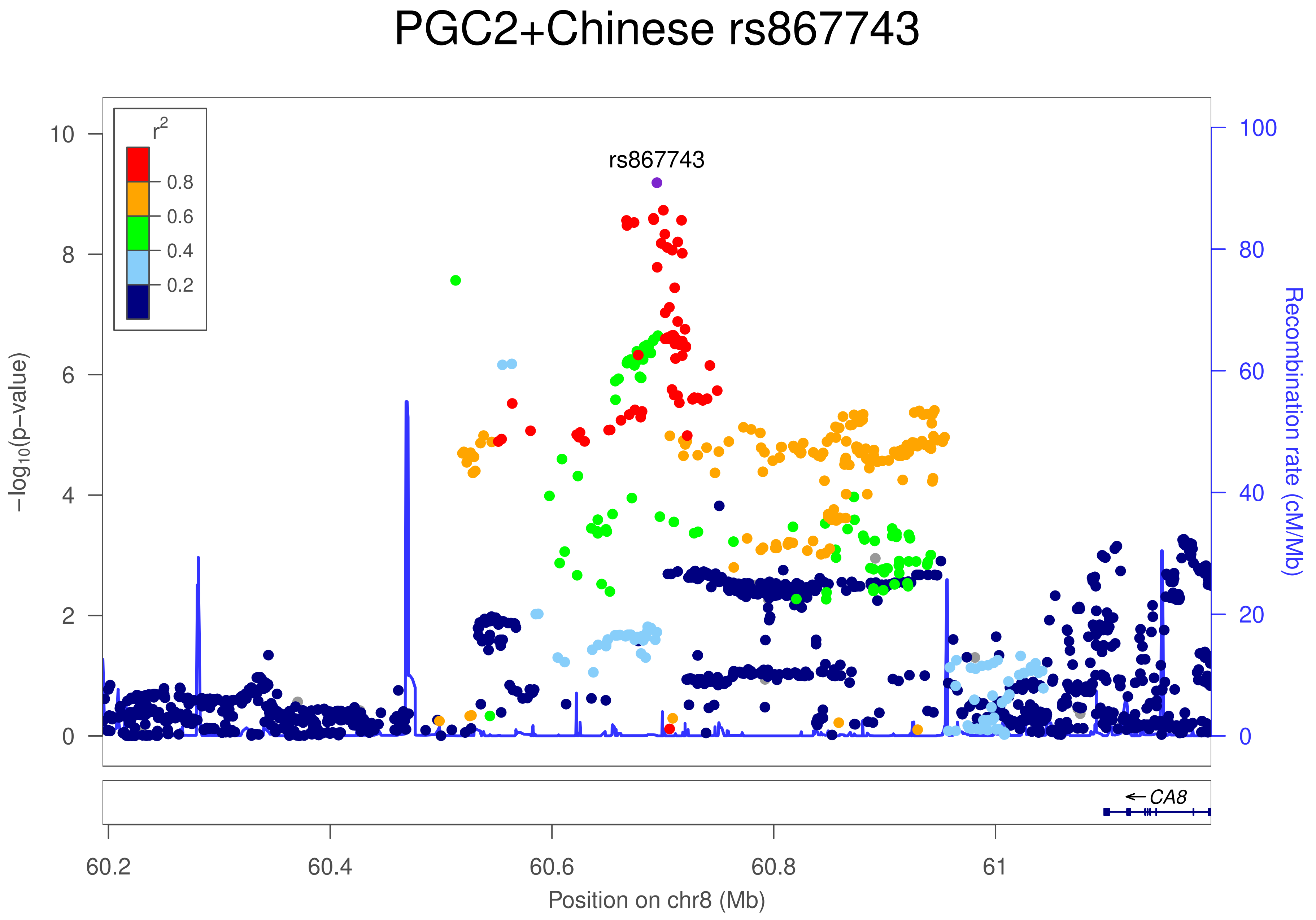
PGC2 rs112537273



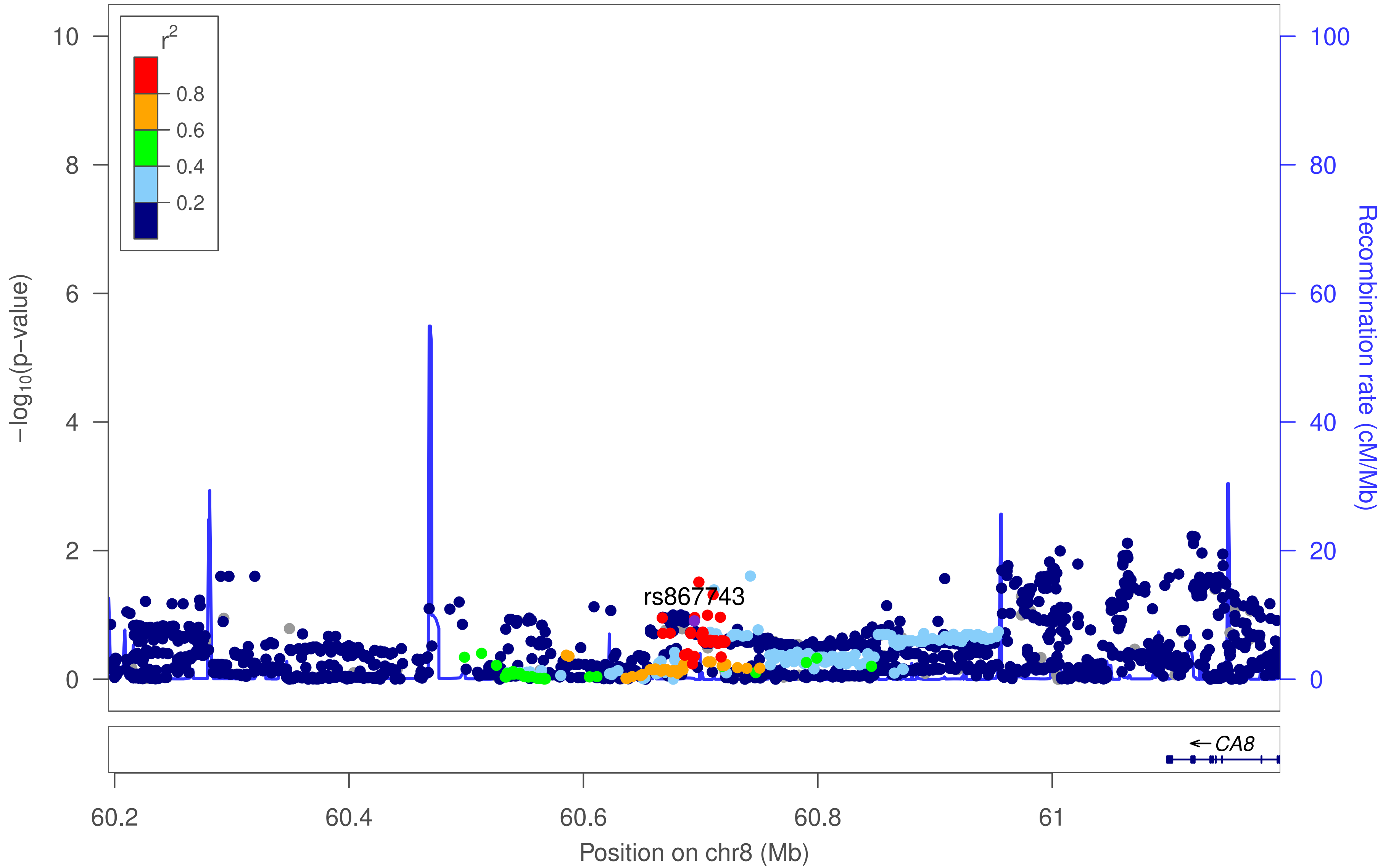

PGC2+Chinese rs112537273
rs112537273
$-\log_{10}$(p−value)
0
2
4
6
8
10
12
Recombination rate (cM/Mb)
0
20
40
60
80
100
r^2
0.8
0.6
0.4
0.2
RAB11FIP1
ASH2L
DDHD2
LETM2
C8orf86
TACC1
GOT1L1
STAR
PLPP5
FGFR1
RNF5P1
ADRB3
LSM1
NSD3
EIF4EBP1
BAG4
37.8
38
38.2
38.4
38.6
Position on chr8 (Mb)


Chinese–only rs112537273
rs112537273
−log10(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
r2
0.8
0.6
0.4
0.2
← RAB11FIP1
ASH2L →
DDHD2 →
LETM2 →
← C8orf86
TACC1 →
← GOT1L1
← STAR
← PLPP5
← FGFR1
← RNF5P1
← ADRB3
← LSM1
← NSD3
EIF4EBP1 →
BAG4 →
37.8
38
38.2
38.4
38.6
Position on chr8 (Mb)

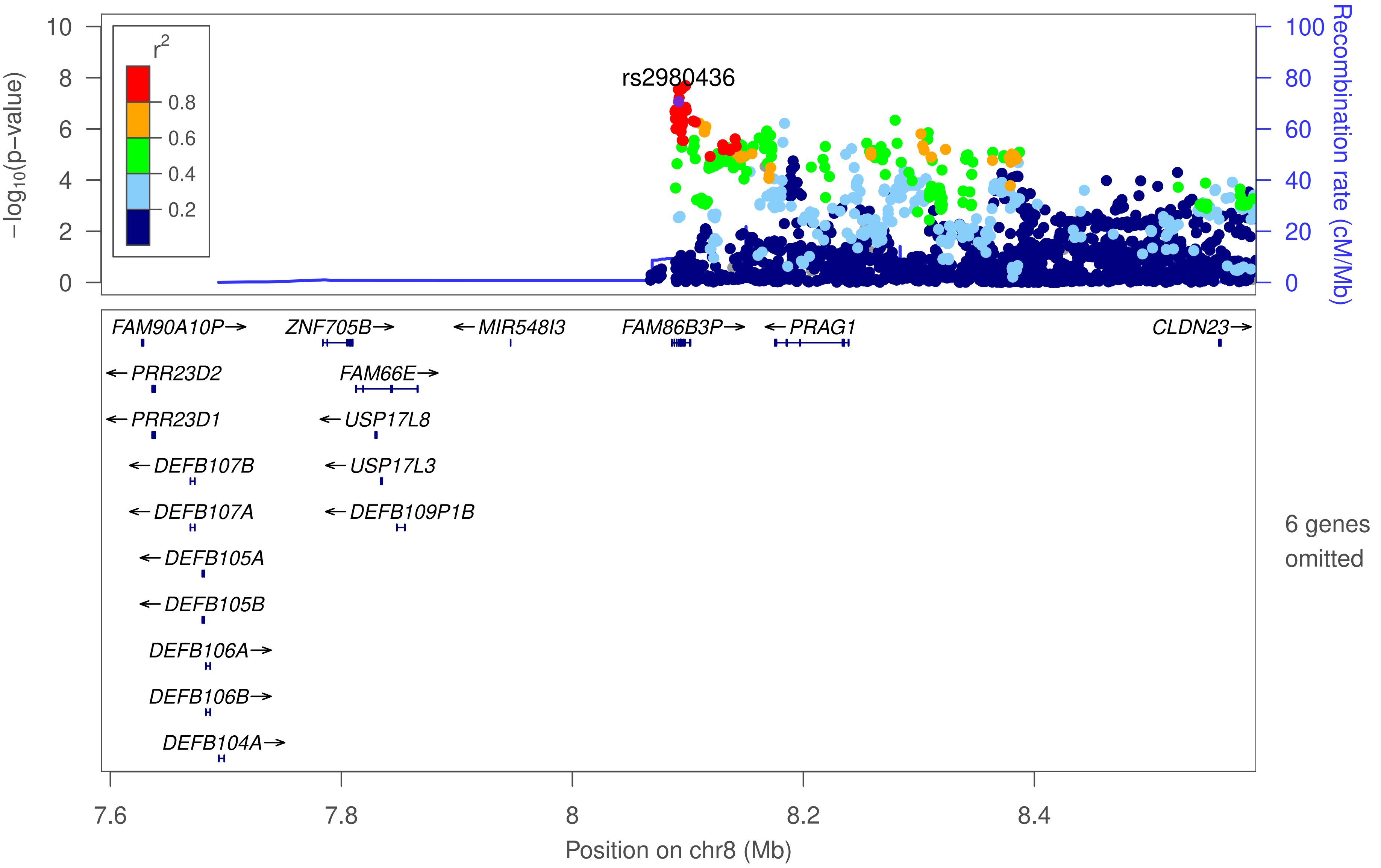

PGC2 rs867743
r2
0.8
0.6
0.4
0.2
rs867743
−log10(p−value)
10
8
6
4
2
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
← CA8
60.2
60.4
60.6
60.8
61
Position on chr8 (Mb)

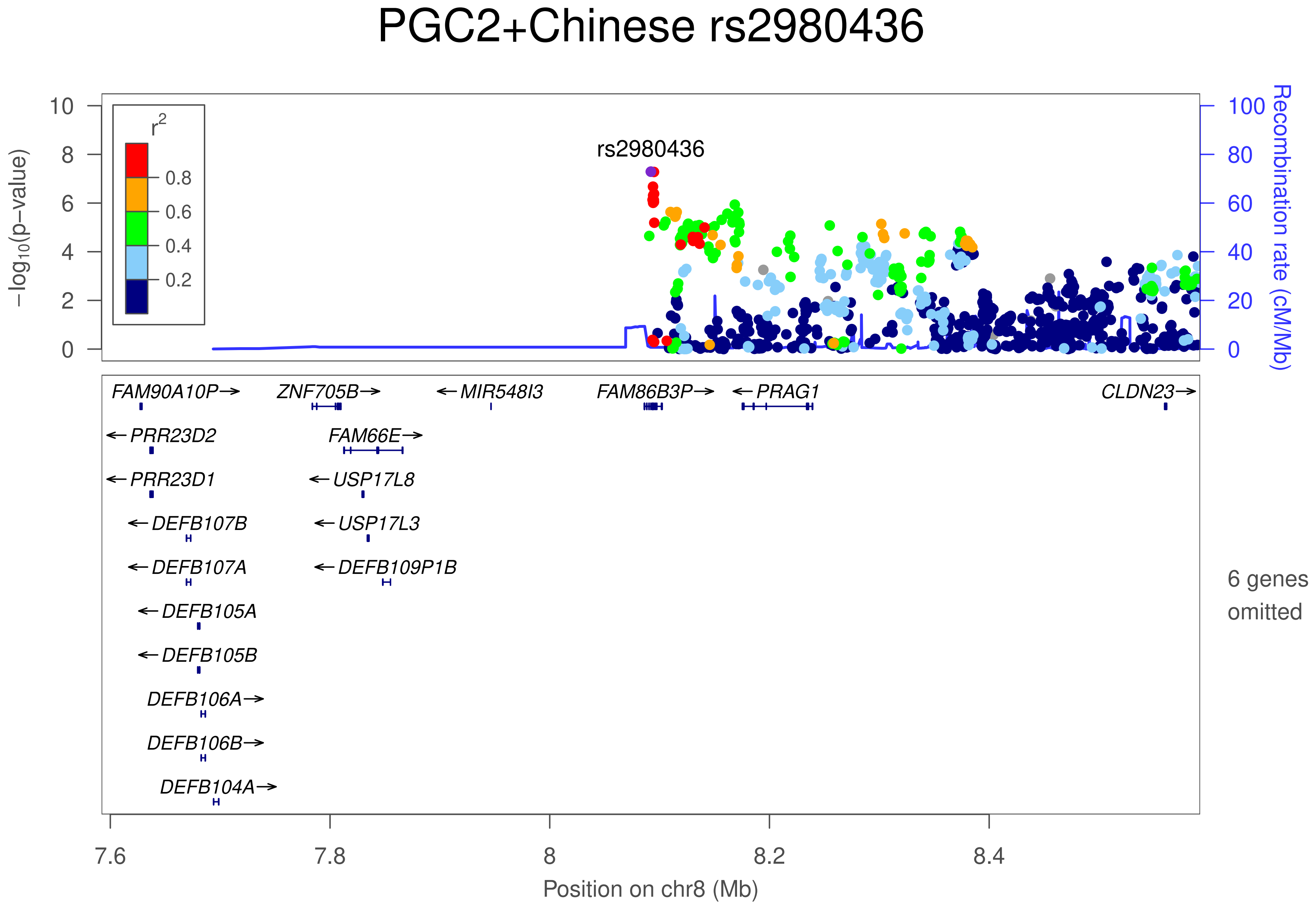

PGC2+Chinese rs867743
r²
0.8
0.6
0.4
0.2
rs867743
−log₁₀(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
← CA8
60.2
60.4
60.6
60.8
61
Position on chr8 (Mb)

Chinese−only rs867743

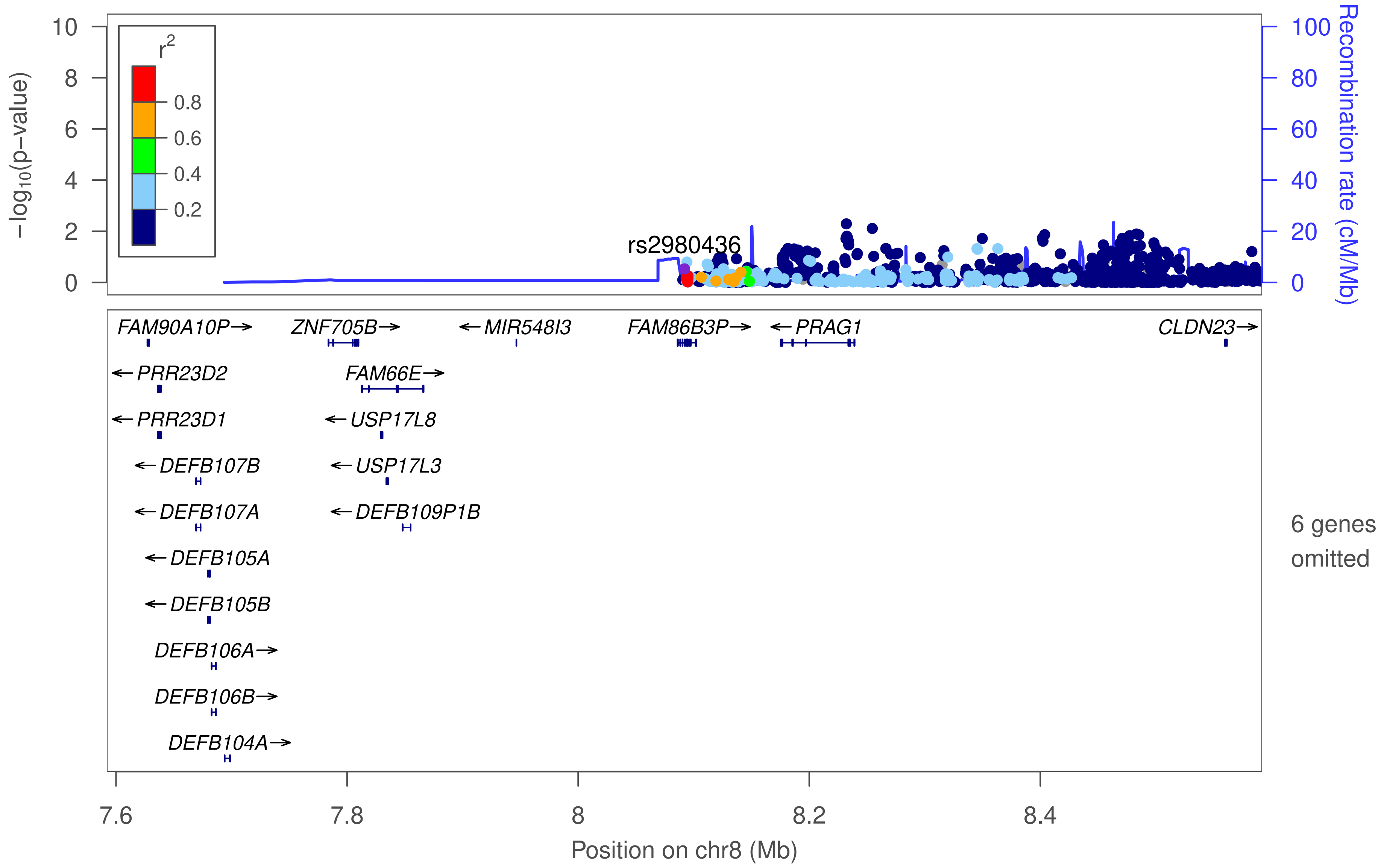


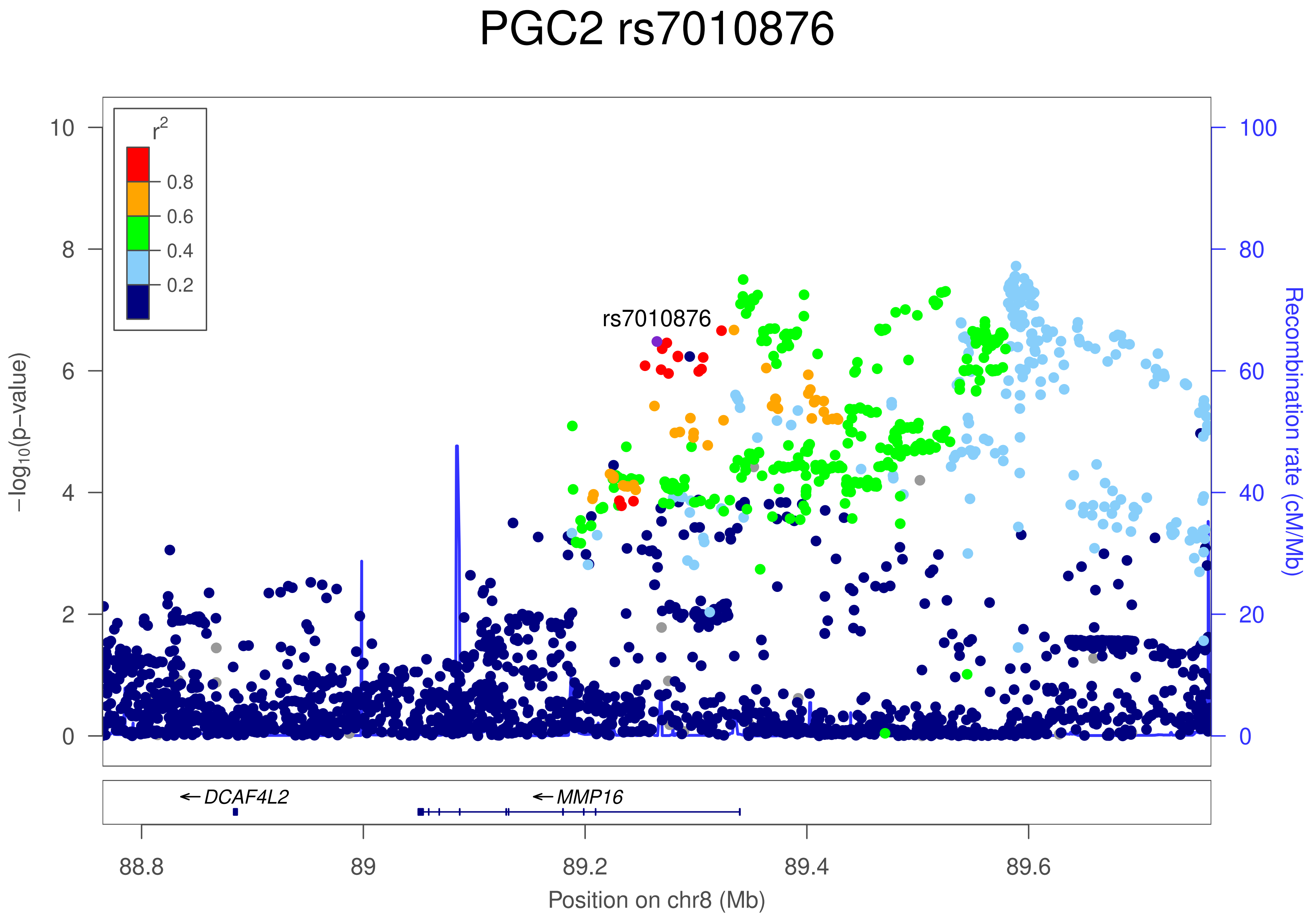
PGC2 rs2980436



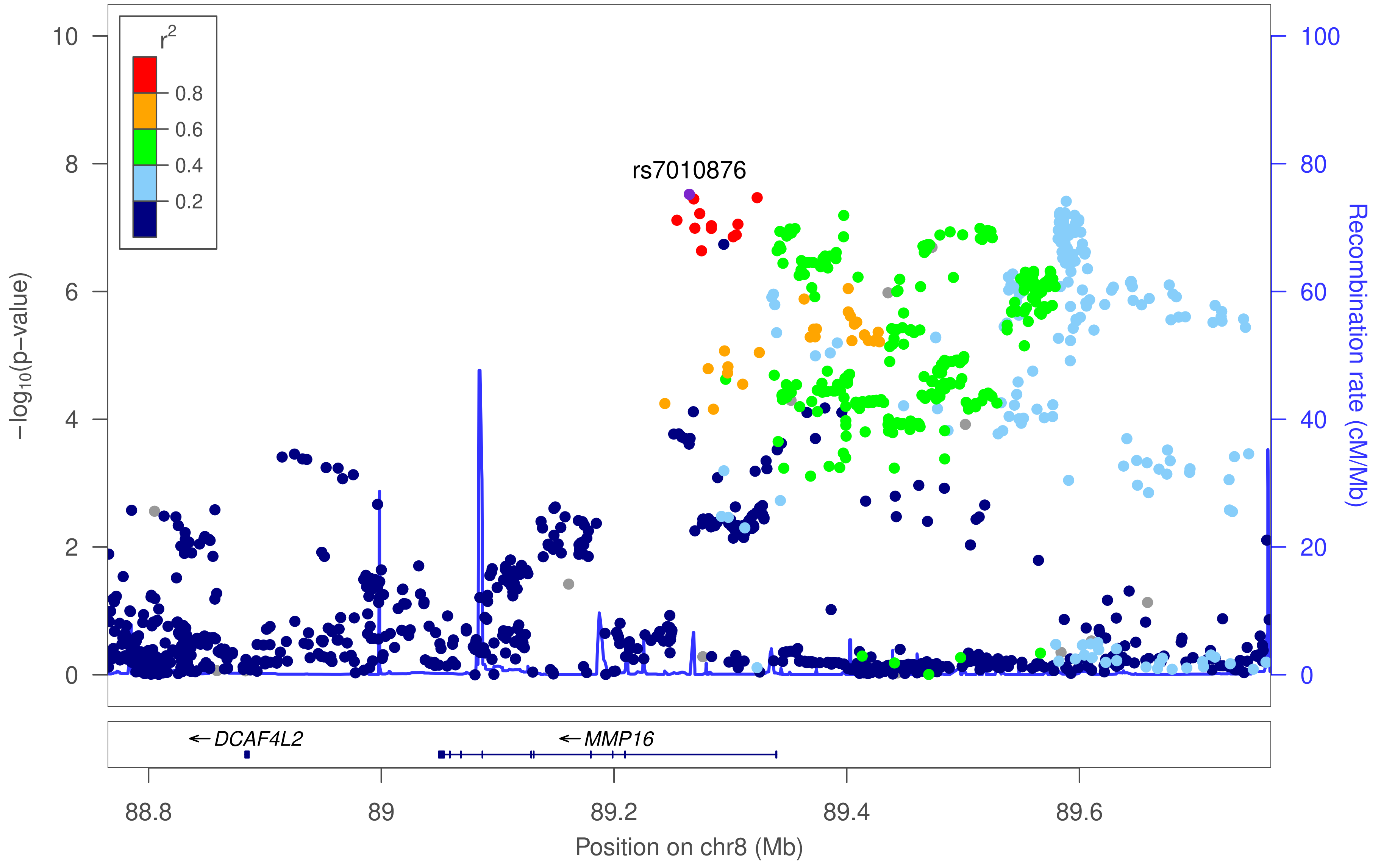

PGC2+Chinese rs2980436
−log10(p−value)
0
2
4
6
8
10
r2
0.8
0.6
0.4
0.2
rs2980436
Recombination rate (cM/Mb)
0
20
40
60
80
100
FAM90A10P→
ZNF705B→
←MIR548I3
FAM86B3P→
←PRAG1
CLDN23→
←PRR23D2
FAM66E→
←PRR23D1
←USP17L8
←DEFB107B
←USP17L3
←DEFB107A
←DEFB109P1B
←DEFB105A
←DEFB105B
DEFB106A→
DEFB106B→
DEFB104A→
6 genes omitted
7.6
7.8
8
8.2
8.4
Position on chr8 (Mb)

Chinese−only rs2980436

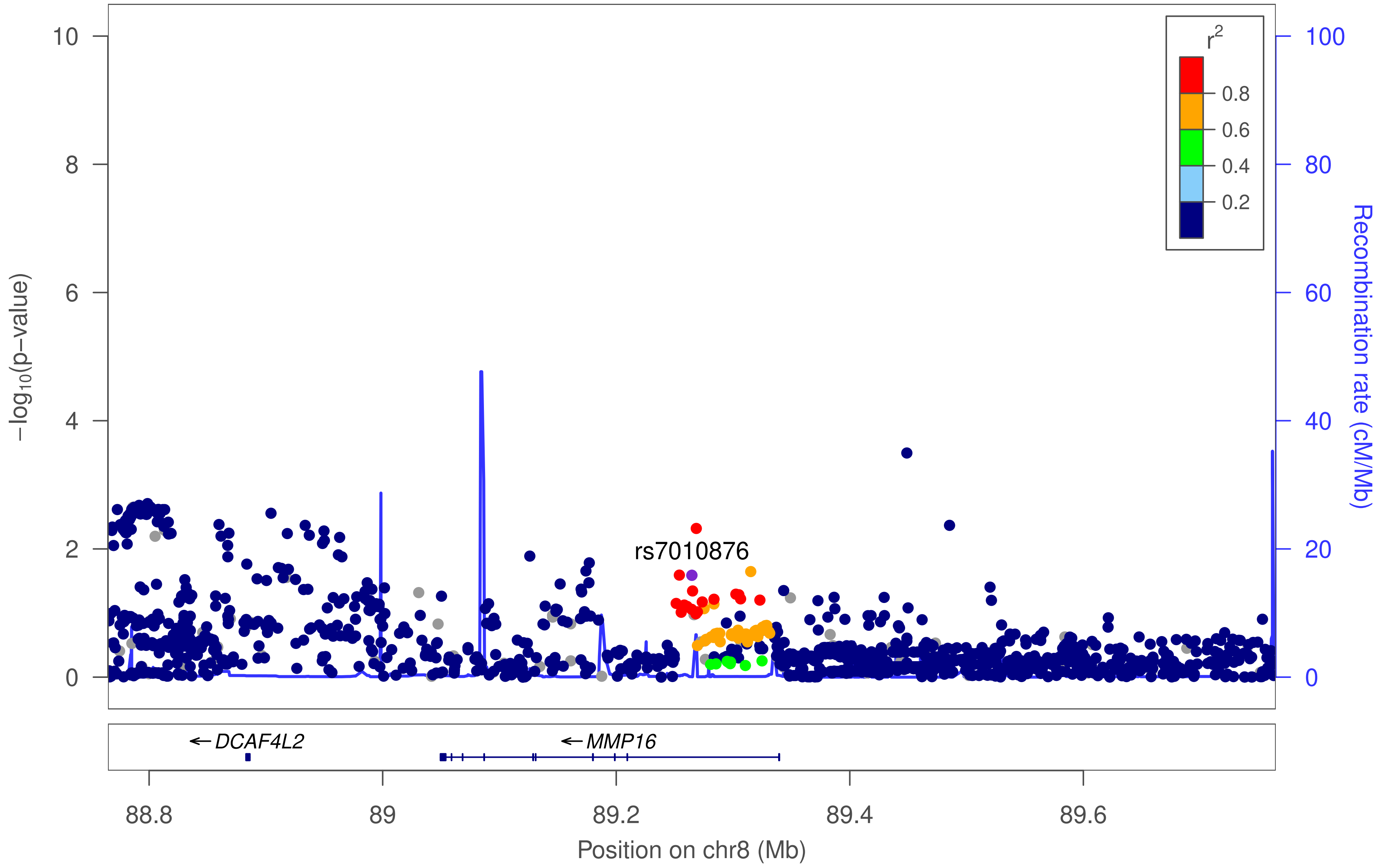



PGC2 rs7010876
r²
0.8
0.6
0.4
0.2
rs7010876
10
8
6
4
2
0
−log₁₀(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
DCAF4L2
MMP16
88.8
89
89.2
89.4
89.6
Position on chr8 (Mb)

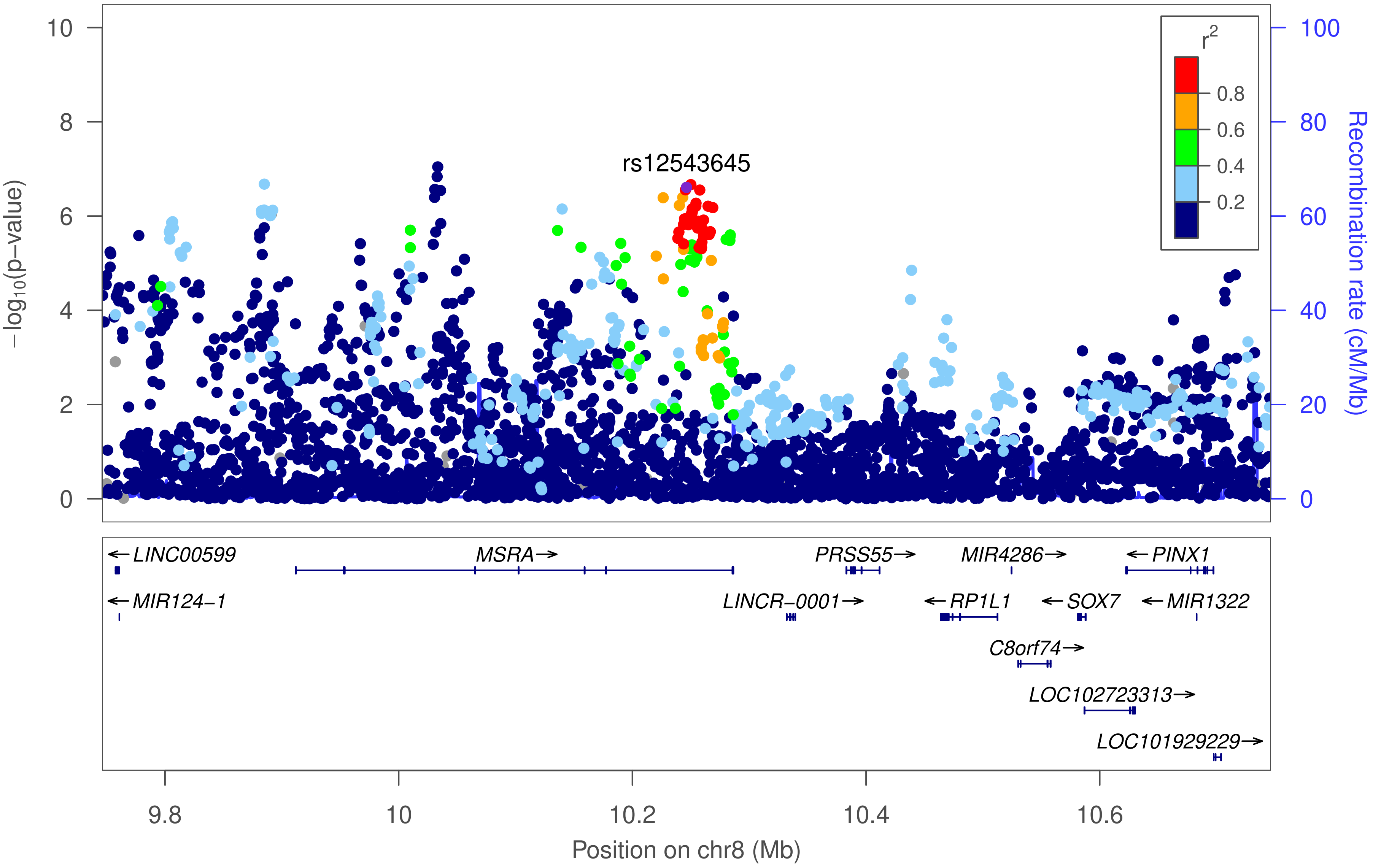
PGC2+Chinese rs7010876



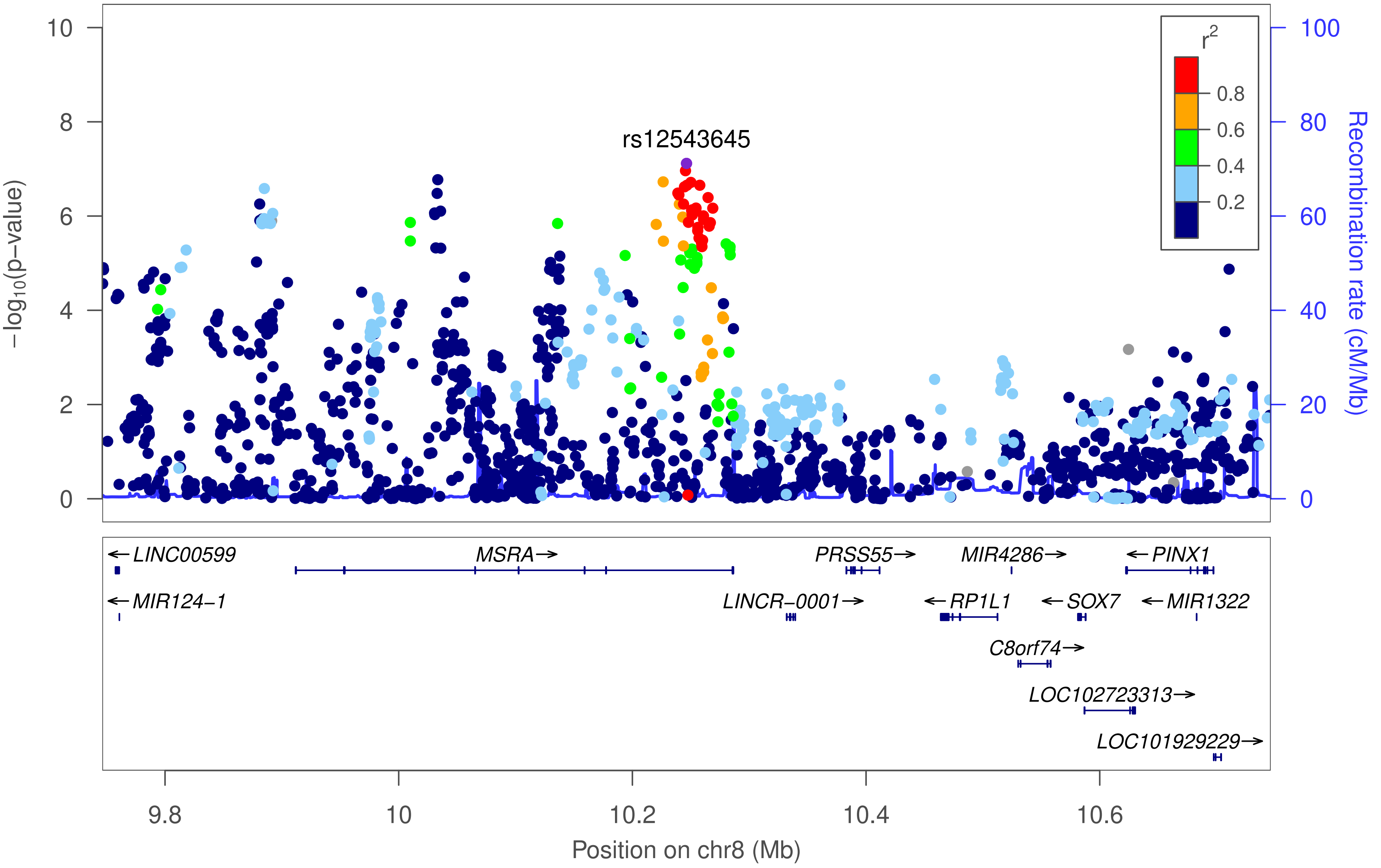
Chinese−only rs7010876

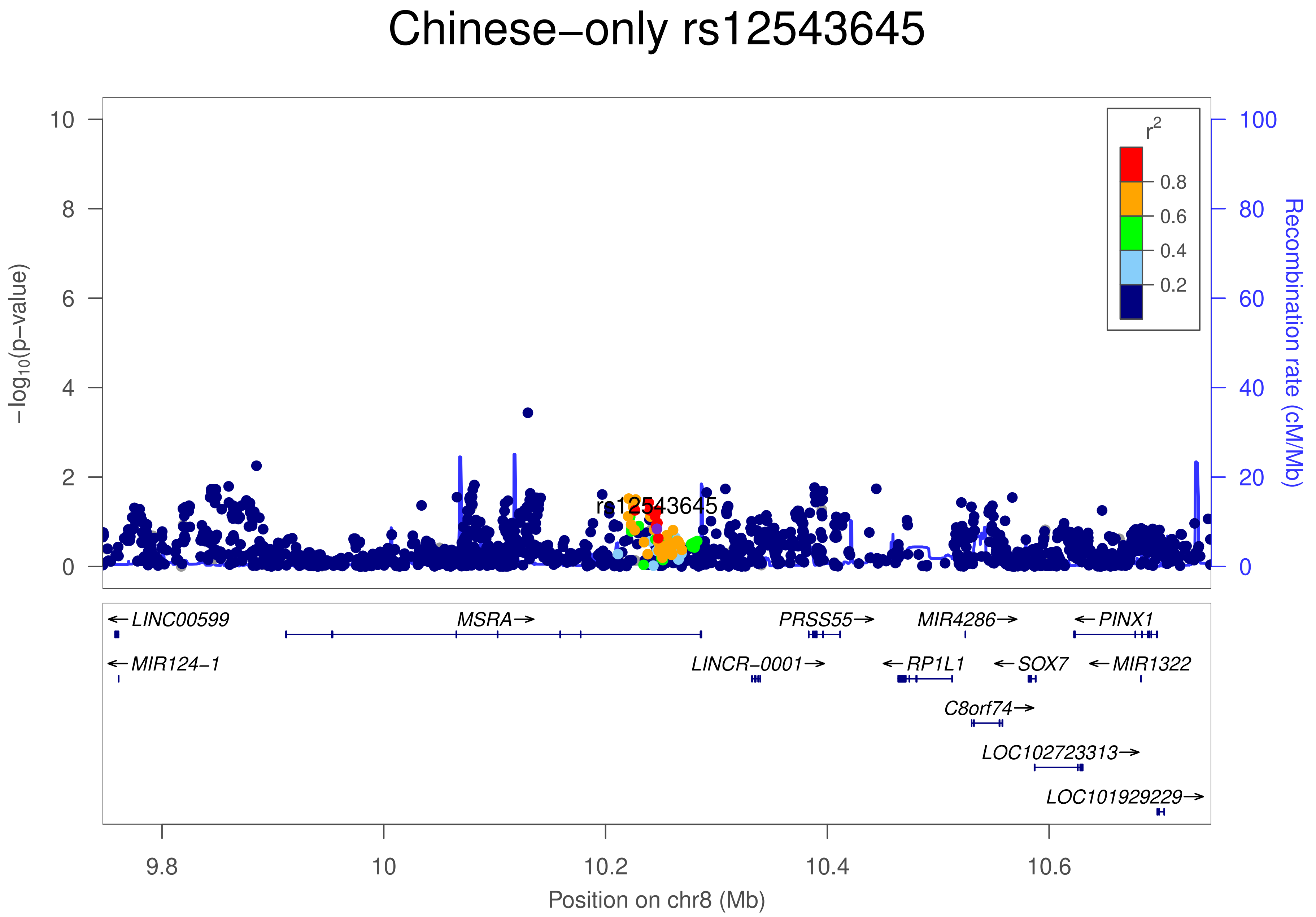


PGC2 rs12543645



PGC2+Chinese rs12543645




Chinese−only rs12543645
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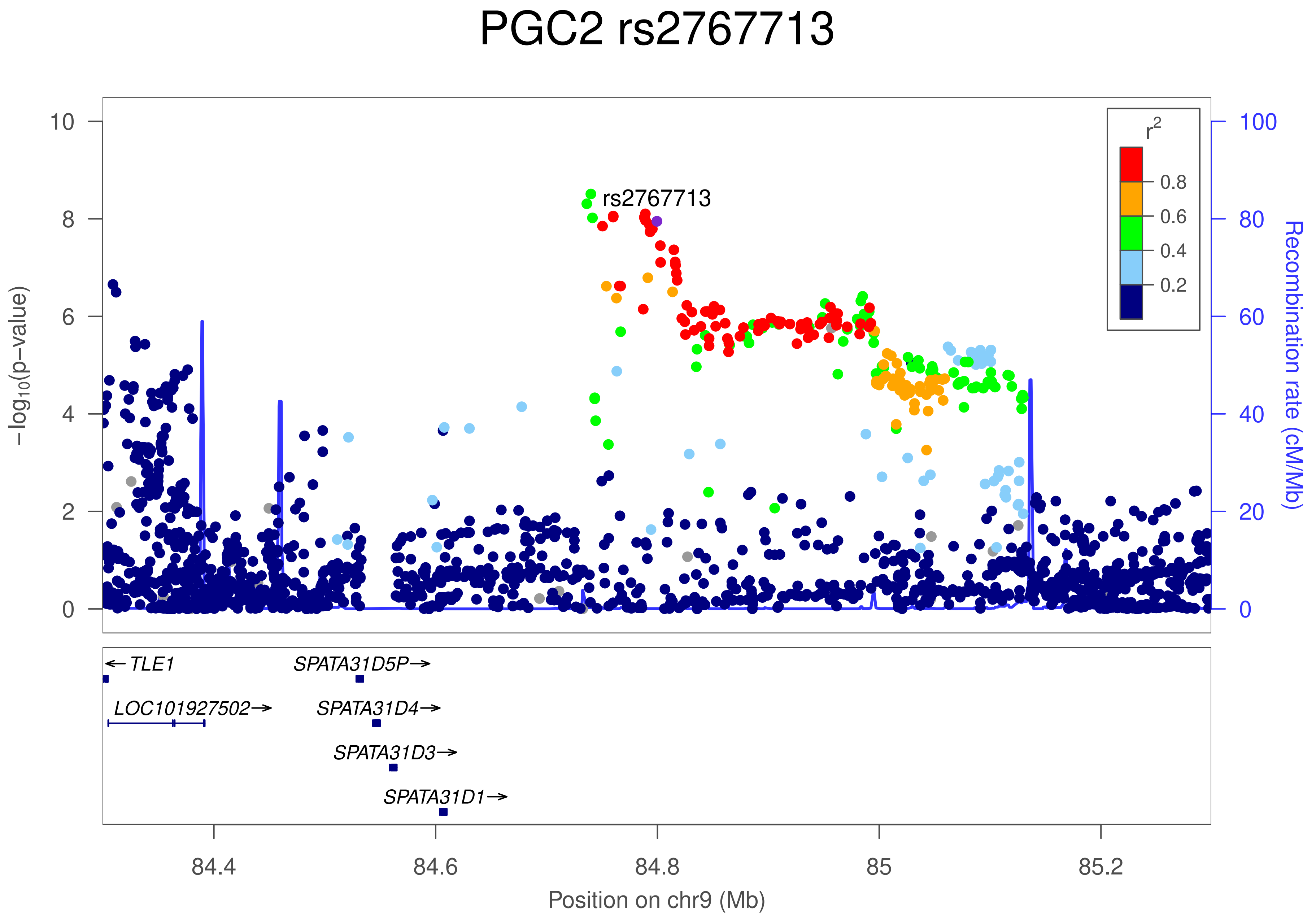
8
6
4
2
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
r2
0.8
0.6
0.4
0.2
rs12543645
←LINC00599
MSRA→
PRSS55→
MIR4286→
←PINX1
←MIR124−1
LINCR−0001→
←RP1L1
←SOX7
←MIR1322
C8orf74→
LOC102723313→
LOC101929229→
9.8
10
10.2
10.4
10.6
Position on chr8 (Mb)


PGC2 rs2767713
rs2767713
−log10(p−value)
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8
6
4
2
0
Recombination rate (cM/Mb)
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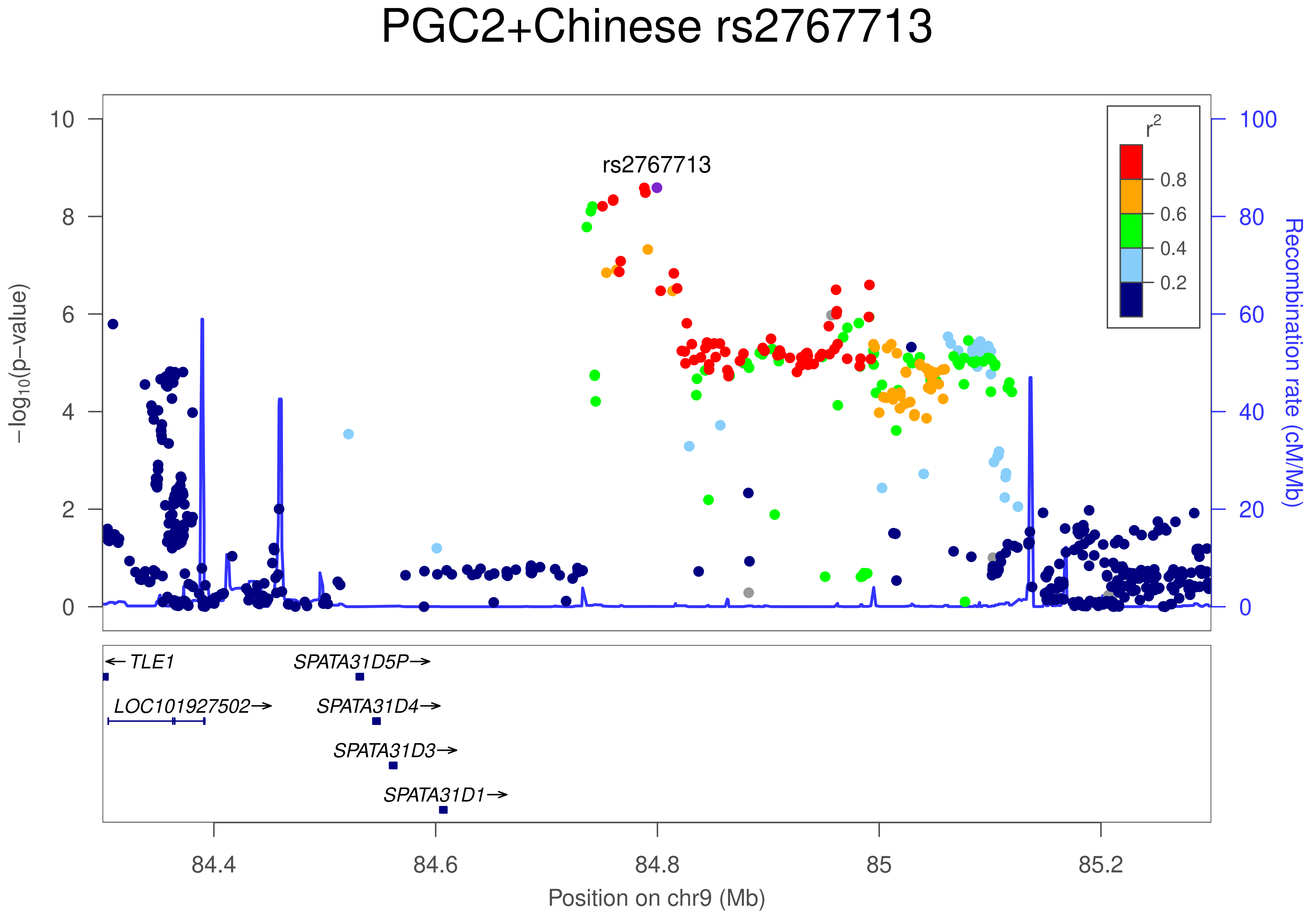
80
60
40
20
0
r2
0.8
0.6
0.4
0.2
← TLE1
SPATA31D5P→
LOC101927502→
SPATA31D4→
SPATA31D3→
SPATA31D1→
84.4
84.6
84.8
85
85.2
Position on chr9 (Mb)


PGC2+Chinese rs2767713
rs2767713
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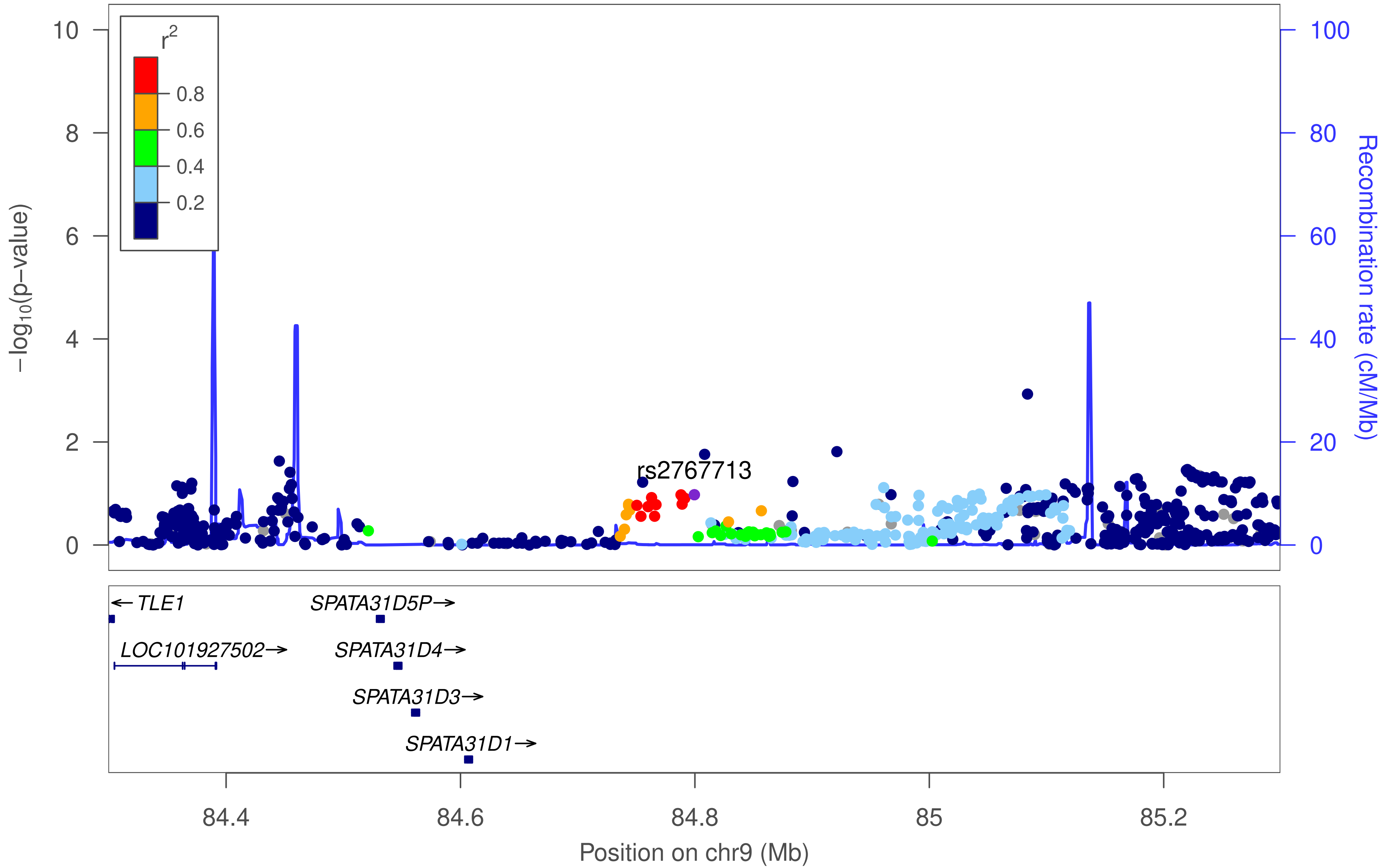
Recombination rate (cM/Mb)
r2
0.8
0.6
0.4
0.2
0
2
4
6
8
10
0
20
40
60
80
100
← TLE1
SPATA31D5P→
LOC101927502→
SPATA31D4→
SPATA31D3→
SPATA31D1→
84.4
84.6
84.8
85
85.2
Position on chr9 (Mb)

Chinese−only rs2767713



Supplementary Table 1. Description of Chinese samples

Stage	Platform[a]	Regions	Cases, N (BIOX1)	Controls, N (BIOX1)
GWAS set 1	SNP6.0	Northern China	1,623 (1,517)	3,690 (1,567)
GWAS set 1	SNP6.0	Central China	1,606 (1,226)	5,732 (2,832)
GWAS set 1	SNP6.0	Southern China	946 (905)	1,048 (970)
GWAS set 2	CHB1	Central China	1,734	2,391
GWAS set 2	CHB1	Northern China	738	3,537
GWAS set 3	CHB1 or 1M	Southern China	1,052	1,929
GWAS			**7,699**	**18,327**
Replication	Illumina+	Central & Northern China	4,384	5,770
GWAS & Replication			**12,083**	**24,097**

[a] SNP6.0 = Affymetrix Genome-Wide Human SNP Array 6.0; CHB1 = Affymetrix Axiom^{TM} Genome-Wide CHB1 Array Plate; 1M = illumina 1M Array; Illumina+ = Illumina HumanHap610-Quad, Human660W-Quad and Human OmniZhongHua BeadChips; Exome = Affymetrix Axiom myDesign Human Genotyping Array (based on Axiom® Exome 319 Array). For the GWAS set 1, BIOX1 indicates the number of sample in the discovery phase of our prior GWAS analysis (Shi *et al*, Nat Genet, 2011).

Supplementary Table 7. Concordance in the direction of effect of schizophrenia risk alleles

***P* value threshold**	**CHN into PGC2**	**PGC2 into CHN**

	Concordant SNPs/total SNPs	**%**	**Binomial test *P***	**Concordant SNPs/total SNPs**	**%**	**Binomial test *P***
P ⩽0.0001	136/201	67.7%	3.06E-07	684/1022	66.9%	5.90E-28
0.0001 < *P* ⩽0.001	513/898	57.1%	1.09E-05	1044/1747	59.8%	1.67E-16
0.001 < *P* ⩽0.01	2776/4769	58.2%	3.74E-30	3498/6191	56.5%	7.09E-25
0.01 < *P* ⩽0.05	6960/12578	55.3%	2.60E-33	6970/13034	53.5%	1.09E-15
0.05 < *P* ⩽0.5	23961/45916	52.2%	4.05E-21	25726/49695	51.8%	1.66E-15
0.5 < *P* ⩽1	24687/49125	50.3%	1.32E-01	23892/47710	50.1%	3.69E-01

The Chinese (CHN) data set was comprised of 7,699 cases and 18,327 controls. The PGC2 data set was comprised of 35,476 cases and 46,839 controls. For each comparison, we first identified independent SNPs with evidence of association for schizophrenia from the discovery data set, and then aligned the effect of the schizophrenia risk allele into the other data set.

Supplementary Table 2. Results for the independent variants in 104 GWS regions in the PGC2 and C

Region ID	Chr.	SNP	Position	A1/A2	OR (SE)	P value	I^2
1	1	rs172531	8,495,590	G/A	1.073 (0.011)	1.46E-10	47
2	1	rs4949526	30,432,219	T/C	1.067 (0.010)	6.39E-10	2
3	1	rs2970610	44,097,530	T/C	1.072 (0.010)	9.77E-12	0
4	1	rs11210195	73,749,283	C/T	1.065 (0.010)	3.57E-10	0
5	1	rs1198589	98,550,411	T/C	0.905 (0.013)	1.29E-13	72
6	1	rs12129037	150,492,114	C/T	0.914 (0.016)	3.49E-08	0
7	1	rs6670165	177,280,121	T/C	1.080 (0.012)	4.01E-10	19
8	1	rs10803138	243,555,219	A/G	0.934 (0.012)	3.93E-08	28
8	1	rs35978510	243,776,117	C/T	1.069 (0.010)	1.14E-10	0
9	2	rs12623170	28,020,157	C/T	1.063 (0.011)	4.62E-08	0
10	2	rs75575209	58,138,192	T/A	1.112 (0.018)	8.39E-09	0
10	2	rs7596038	58,383,820	T/C	0.929 (0.010)	6.64E-13	54
11	2	rs999494	73,157,395	T/C	0.926 (0.013)	2.08E-09	64
12	2	rs6430491	134,840,967	A/G	0.930 (0.012)	4.02E-10	27
13	2	rs2381759	146,428,031	T/A	0.930 (0.013)	3.23E-08	50
14	2	rs12622667	149,520,186	C/T	1.090 (0.015)	1.24E-08	0
15	2	rs7597593	185,533,580	T/C	1.066 (0.010)	9.63E-10	0
16	2	rs12619354	194,002,782	C/T	0.943 (0.010)	2.19E-08	0
16	2	rs10204454	194,346,284	C/T	0.943 (0.010)	1.07E-08	0
17	2	rs6434928	198,304,577	G/A	1.074 (0.010)	9.62E-12	17
18	2	rs895526	200,162,425	T/C	0.930 (0.012)	4.60E-10	0
18	2	rs796364	200,716,119	C/A	1.098 (0.012)	3.00E-15	21
18	2	rs17630293	201,146,776	G/T	0.897 (0.018)	4.01E-09	0
19	2	rs11685299	225,391,296	A/C	0.934 (0.010)	3.28E-11	0
20	2	rs778371	233,743,109	G/A	1.087 (0.011)	1.10E-13	0
21	3	rs11708578	2,515,894	G/A	1.080 (0.012)	1.35E-10	0
22	3	rs4330281	17,859,366	T/C	0.943 (0.011)	3.91E-08	0
23	3	rs3732386	36,871,993	T/C	1.076 (0.011)	3.12E-11	6
24	3	rs2577831	52,628,056	A/C	0.936 (0.010)	4.06E-12	0
25	3	rs832190	63,842,629	T/C	0.942 (0.010)	5.13E-09	0
26	3	rs66691851	136,154,828	C/T	1.081 (0.010)	9.00E-15	74

27	3	rs6804239	161,780,488	C/T	1.060 (0.010)	5.07E-09	69
28	3	rs9859557	180,830,910	T/A	0.917 (0.012)	1.77E-12	9
28	3	rs9841616	181,167,585	A/T	0.928 (0.013)	1.59E-08	17
29	4	rs215411	23,423,603	A/T	1.069 (0.011)	1.37E-09	0
30	4	rs7438	170,642,246	A/G	1.062 (0.010)	3.94E-09	0
31	4	rs6846161	176,866,459	A/G	1.068 (0.011)	3.25E-09	0
32	5	rs9292918	45,301,035	G/T	1.078 (0.011)	6.21E-11	0
33	5	rs10940346	49,806,042	A/G	0.947 (0.010)	1.39E-08	21
34	5	rs4391122	60,598,543	G/A	0.930 (0.010)	5.71E-13	68
35	5	rs1065861	88,091,950	A/T	0.894 (0.020)	2.03E-08	0
36	5	rs4388249	109,036,066	C/T	0.935 (0.012)	1.26E-08	0
37	5	rs3756766	137,673,167	A/C	1.068 (0.012)	1.75E-08	0
37	5	rs13164092	137,840,860	G/A	1.062 (0.010)	1.61E-09	0
38	5	rs113568682	152,299,754	T/A	0.937 (0.011)	1.32E-08	0
38	5	rs2910032	152,540,354	C/T	1.061 (0.010)	2.57E-09	33
38	5	rs7727515	152,892,304	A/G	0.915 (0.016)	4.97E-08	0
39	5	rs11740474	153,680,747	T/A	1.066 (0.011)	4.02E-09	19
40	6	rs115329265	28,712,247	G/A	0.824 (0.016)	0.00E-16	0
41	6	rs217331	84,344,689	C/G	0.937 (0.010)	1.53E-11	0
42	6	rs160593	105,466,332	G/A	1.058 (0.010)	1.01E-08	0
43	6	rs9398171	108,983,527	C/T	1.068 (0.010)	2.62E-10	0
44	7	rs12668848	2,020,995	G/A	1.084 (0.010)	0.00E-16	0
45	7	rs12704290	86,427,626	A/G	0.908 (0.016)	5.60E-10	70
45	7	rs11982256	86,799,441	A/T	0.869 (0.024)	7.63E-09	0
46	7	rs2057884	104,930,250	T/C	1.069 (0.010)	2.25E-11	0
47	7	rs214467	110,858,268	A/G	1.072 (0.010)	2.17E-11	75
48	7	rs7801375	131,567,263	A/G	0.924 (0.014)	4.26E-08	30
49	7	rs3735025	137,074,844	C/T	0.937 (0.010)	8.93E-11	0
50	8	rs13261217	4,183,057	G/A	1.069 (0.012)	3.59E-08	0
51	8	rs17687067	17,036,201	C/A	1.078 (0.012)	1.39E-10	0
52	8	rs13259407	18,422,923	T/C	0.947 (0.010)	1.73E-08	0
53	8	rs73219805	26,272,768	A/G	1.086 (0.012)	5.45E-12	49
54	8	rs112537273	38,248,306	C/T	0.926 (0.011)	1.45E-11	72
55	8	rs867743	60,694,647	G/A	1.065 (0.010)	6.48E-10	0
56	8	rs7012816	70,964,743	A/G	1.076 (0.013)	1.60E-08	6

57	8	rs7010876	89,264,751	T/A	1.065 (0.011)	3.01E-08	0
58	8	rs16880831	111,561,505	G/T	1.079 (0.012)	2.70E-10	0
59	8	rs13266463	143,403,693	G/A	1.060 (0.010)	1.20E-08	0
60	9	rs2767713	84,799,537	A/C	0.934 (0.012)	2.58E-09	0
61	10	rs7893279	18,745,105	G/T	0.893 (0.016)	1.02E-12	0
62	10	rs111364339	64,857,872	C/T	1.113 (0.019)	1.44E-08	0
63	10	rs11191424	104,625,886	A/G	0.919 (0.010)	0.00E-16	72
63	10	rs10786736	104,849,116	C/G	0.904 (0.014)	5.30E-13	10
64	11	rs17234749	24,381,898	G/A	1.059 (0.010)	1.86E-08	0
65	11	rs61882743	46,548,754	G/C	1.092 (0.013)	7.16E-11	0
66	11	rs12421382	109,378,071	T/C	0.945 (0.010)	4.81E-08	0
67	11	rs2514218	113,392,994	T/C	0.930 (0.011)	2.14E-10	0
68	11	rs77502336	123,394,636	C/G	1.068 (0.011)	4.99E-10	0
69	11	rs55661361	124,613,957	A/G	0.930 (0.010)	1.65E-12	33
70	11	rs10894308	130,891,895	A/G	0.945 (0.010)	2.52E-08	59
71	11	rs75059851	133,822,569	G/A	0.911 (0.013)	1.68E-12	0
72	12	rs2159100	2,346,393	T/C	1.100 (0.011)	0.00E-16	0
72	12	rs758117	2,513,309	T/C	0.935 (0.011)	2.37E-09	0
73	12	rs302321	29,928,388	A/C	0.939 (0.010)	6.11E-10	6
74	12	rs4240748	92,246,786	C/G	0.945 (0.010)	3.29E-08	0
75	12	rs4766428	110,723,245	C/T	0.936 (0.011)	1.23E-09	17
76	12	rs61041384	123,644,043	C/T	1.129 (0.018)	2.03E-11	0
76	12	rs1615350	123,650,335	C/T	1.093 (0.011)	0.00E-16	0
77	14	rs1191551	30,000,405	T/G	1.074 (0.013)	3.42E-08	0
78	14	rs2383377	33,257,914	A/G	1.089 (0.015)	4.12E-09	0
79	14	rs35607894	72,408,638	A/G	1.091 (0.014)	4.19E-10	0
80	14	rs2693698	99,719,219	A/G	0.939 (0.011)	8.54E-09	0
81	14	rs12887734	104,046,834	T/G	1.084 (0.011)	9.80E-14	53
82	15	rs35225048	61,856,263	C/T	1.072 (0.010)	8.20E-13	44
83	15	rs12148337	70,589,272	C/T	0.945 (0.010)	3.04E-09	0
84	15	rs3825845	78,910,258	T/C	0.926 (0.012)	9.40E-11	0
85	15	rs783540	83,254,708	G/A	1.055 (0.010)	2.28E-08	0
86	15	rs950169	84,706,461	T/C	0.921 (0.012)	5.17E-12	0
87	15	rs11539637	91,428,290	C/T	0.936 (0.011)	3.10E-10	16
88	16	rs9922678	9,946,319	A/G	1.065 (0.011)	1.16E-08	36

89	16	rs7405404	13,749,859	T/C	1.073 (0.012)	2.91E-09	75
90	16	rs3814881	30,000,901	A/G	0.936 (0.010)	5.11E-12	0
91	16	rs7193419	63,697,134	C/T	0.948 (0.010)	3.15E-08	52
92	16	rs8058130	64,371,163	A/G	0.945 (0.010)	3.77E-08	74
93	17	rs4523957	2,208,899	G/T	0.937 (0.011)	8.83E-10	0
94	17	rs8082590	17,958,402	A/G	0.937 (0.011)	4.43E-09	0
95	17	rs72843506	19,946,287	A/T	1.072 (0.013)	3.33E-08	18
96	18	rs17598729	53,251,562	C/T	1.088 (0.014)	7.76E-10	0
96	18	rs715170	53,795,514	T/C	0.929 (0.011)	4.23E-11	70
97	18	rs28735056	77,622,879	G/A	1.058 (0.010)	4.17E-08	0
98	19	rs2053079	30,987,423	G/A	1.068 (0.011)	6.27E-09	54
99	20	rs2103655	37,425,958	G/A	0.935 (0.010)	8.61E-11	57
100	22	rs5757730	39,967,430	A/G	0.933 (0.011)	3.26E-10	0
101	22	rs9607782	41,587,556	A/T	1.092 (0.012)	9.86E-13	0
102	22	rs6002655	42,603,814	C/T	0.942 (0.010)	6.16E-09	66
103	23	rs1378559	21,380,266	C/T	0.925 (0.011)	1.03E-11	37
104	23	rs5937157	68,377,126	G/T	1.072 (0.010)	8.56E-12	0

Genomic position was based on the UCSC hg19/NCBI Build 37.

OR=odds ratio for A1 and SE=standard error.

I^2 index represents the degree of heterogeneity.

The previously reported schizophrenia associated variants were extracted from the NHGRI-EBI GWAS Ca

The r2 values between the index SNPs and previously reported associated variants were calculated based on

hinese GWAS meta-analysis

Previously reported schizoprhenia associated variant	r2 with previously reported variant
chr1_8424984_D	0.768
rs1498232	1
rs11210892	1
rs12129573	0.553
rs1702294	0.629
rs140505938	0.573
rs6670165	same
rs10803138	same
chr1_243881945_I	0.685
rs12474906	0.839
rs75575209	same
rs11682175	0.306
/	/
/	/
chr2_146436222_I	1
chr2_149429178_D	/
rs11693094	0.411
rs59979824	0.873
rs59979824	0.087
rs6434928	same
rs6704641	0.962
chr2_200825237_I	/
chr2_200825237_I	/
rs11685299	same
rs6704768	0.471
rs17194490	0.276
rs4330281	same
rs75968099	0.91
rs2535627	0.882
rs832187	0.967
rs7432375	0.995

rs28730912	0.387
chr3_180594593_I	0.688
rs9841616	same
rs215411	same
rs10520163	0.989
rs1106568	1
rs1501357	0.982
/	/
rs4391122	same
/	/
rs4388249	same
rs10043984	0.993
rs3849046	0.979
rs111294930	0.683
rs2973155	0.446
rs12522290	0.178
rs11740474	same
rs115329265	same
chr6_84280274_D	/
/	/
rs9398171	same
chr7_2025096_I	1
rs12704290	same
rs12704290	0.058
rs6466055	1
rs13240464	0.978
rs7801375	same
rs3735025	same
rs10503253	0.985
/	/
/	/
/	/
rs16887244	0.89
rs6984242	1
/	/

rs7819570	0.425
rs36068923	0.958
rs4129585	0.284
rs11139497	0.56
rs7893279	same
/	/
rs11191419	0.988
rs7907645	0.159
rs11027857	0.887
chr11_46350213_D	0.465
rs12421382	same
rs2514218	same
rs77502336	same
rs55661361	same
rs10791097	0.299
rs75059851	same
rs2007044	0.806
rs2239063	1
rs679087	0.96
rs4240748	same
rs4766428	same
rs2851447	0.091
rs2851447	0.987
rs2068012	0.062
/	/
rs2332700	0.521
rs2693698	same
rs12887734	same
rs12903146	0.963
rs12148337	same
rs8042374	0.985
/	/
rs950169	same
rs4702	0.657
rs9922678	same

rs7405404	same
rs12691307	0.698
rs2018916	0.964
/	/
rs4523957	same
rs8082590	same
/	/
rs9636107	0.19
rs715170	same
/	/
rs2053079	same
rs6065094	0.915
chr22_39987017_D	/
rs9607782	same
rs6002655	same
rs1378559	same
rs5937157	same

talog (https://www.ebi.ac.uk/gwas, as to Jan. 2017).
1000 Genome Project dataset .

Supplementary Table 3. Results for the Chinese GWAS and replication

Chr.	SNP	Position	A1/A2	Chinese Meta-analysis		Chinese GWAS Stage
				OR (SE)	P value	OR (SE)
1	rs12029971	70,923,260	G/A	1.196 (0.055)	1.22E-03	1.404 (0.071)
1	rs17109458	83,416,943	G/A	1.096 (0.027)	7.30E-04	1.163 (0.034)
1	rs6427113	167,845,787	C/T	1.112 (0.026)	3.73E-05	1.146 (0.032)
1	rs56413107	188,596,106	C/T	1.084 (0.023)	4.82E-04	1.141 (0.029)
1	rs12134906	233,547,030	T/C	0.863 (0.048)	1.98E-03	0.765 (0.060)
2	rs146300688	34,287,284	T/C	0.612 (0.100)	8.09E-07	0.528 (0.127)
2	rs4671990	55,129,821	G/C	1.107 (0.025)	4.87E-05	1.154 (0.033)
2	rs820970	57,741,088	G/T	1.156 (0.032)	6.28E-06	1.216 (0.037)
2	rs58218705	57,953,600	T/C	1.119 (0.028)	6.98E-05	1.175 (0.034)
2	**rs1518395**	**58,208,074**	**A/G**	**0.862 (0.020)**	**3.79E-13**	**0.858 (0.025)**
2	rs359260	60,486,936	G/T	1.120 (0.023)	6.60E-07	1.153 (0.028)
2	rs12052801	68,423,218	G/A	0.908 (0.020)	9.27E-07	0.890 (0.024)
2	rs950394	104,970,247	A/G	1.096 (0.019)	1.11E-06	1.113 (0.023)
2	rs12619999	107,135,634	C/T	1.106 (0.029)	5.62E-04	1.220 (0.043)
2	rs12620761	134,854,131	T/C	0.910 (0.021)	5.51E-06	0.884 (0.026)
2	rs10928112	142,330,969	C/A	0.912 (0.019)	2.07E-06	0.895 (0.024)
2	rs77373077	155,321,956	D/I	0.943 (0.023)	1.19E-02	0.880 (0.030)
2	rs10193506	189,174,910	G/T	1.102 (0.029)	8.58E-04	1.172 (0.036)
2	**rs78681500**	**201,187,316**	**T/C**	**0.751 (0.045)**	**3.08E-10**	**0.736 (0.067)**
3	rs13326300	49,905,300	A/G	0.774 (0.074)	5.48E-04	0.657 (0.096)
3	**rs2073499**	**50,374,293**	**A/G**	**0.899 (0.019)**	**2.61E-08**	**0.884 (0.024)**
3	rs14192	132,076,551	C/T	0.912 (0.030)	1.89E-03	0.849 (0.037)
3	rs9845788	135,914,715	G/A	1.113 (0.024)	9.92E-06	1.150 (0.029)
3	rs966851	162,260,833	C/G	0.933 (0.026)	6.62E-03	0.871 (0.032)
4	rs1531327	36,919,306	A/G	0.946 (0.030)	6.28E-02	0.829 (0.042)
4	rs17608026	38,195,269	C/T	1.074 (0.018)	9.71E-05	1.102 (0.023)
4	rs6848386	42,146,657	C/T	0.883 (0.051)	1.45E-02	0.736 (0.071)
4	rs1021487	59,457,085	C/T	1.105 (0.019)	1.49E-07	1.121 (0.024)
4	rs41464545	65,818,407	G/A	1.150 (0.029)	1.28E-06	1.201 (0.035)
4	rs77243265	79,071,628	A/G	1.127 (0.035)	7.32E-04	1.246 (0.046)
4	rs7677022	113,576,108	G/A	1.137 (0.048)	7.83E-03	1.361 (0.069)
4	rs28419375	118,827,751	C/T	1.061 (0.020)	3.28E-03	1.127 (0.025)
4	rs12512463	126,899,057	T/C	0.920 (0.021)	8.90E-05	0.890 (0.026)
5	rs36214230	8,215,447	D/I	1.069 (0.018)	2.90E-04	1.113 (0.023)
5	rs2962250	50,389,991	G/A	1.178 (0.032)	2.14E-07	1.183 (0.038)
5	rs187568	83,315,623	A/C	0.907 (0.021)	2.87E-06	0.878 (0.026)
5	rs722714	145,226,615	T/C	1.108 (0.031)	9.07E-04	1.211 (0.042)

5	rs7715082	148,345,628	G/A	1.080 (0.023)	6.32E-04	1.140 (0.028)
5	rs998864	167,785,204	T/G	1.174 (0.057)	4.77E-03	1.348 (0.068)
6	**rs111782145**	**30,873,508**	**C/T**	**0.813 (0.037)**	**1.80E-08**	**0.798 (0.046)**
6	rs3013169	64,842,960	T/G	0.916 (0.019)	3.16E-06	0.904 (0.023)
6	rs12660387	65,291,644	G/A	1.106 (0.023)	9.37E-06	1.144 (0.029)
6	rs9354996	72,035,192	C/T	1.096 (0.022)	2.85E-05	1.124 (0.027)
6	rs6568650	110,898,948	G/A	0.939 (0.018)	6.40E-04	0.907 (0.023)
6	rs940539	110,977,458	G/A	1.119 (0.029)	1.25E-04	1.172 (0.037)
6	**rs7757969**	**112,132,032**	**C/T**	**1.110 (0.019)**	**4.82E-08**	**1.110 (0.024)**
6	rs557186	124,943,240	C/A	0.896 (0.031)	4.24E-04	0.849 (0.038)
6	**rs4479915**	**165,075,601**	**G/C**	**0.876 (0.023)**	**4.82E-09**	**0.860 (0.030)**
7	rs2961033	75,964,343	C/T	1.065 (0.019)	7.77E-04	1.108 (0.023)
7	rs323167	78,336,677	C/T	1.095 (0.024)	1.65E-04	1.145 (0.029)
7	**rs11534004**	**113,467,444**	**G/A**	**0.890 (0.021)**	**1.71E-08**	**0.897 (0.025)**
7	rs116834142	152,303,332	G/A	1.249 (0.063)	4.46E-04	1.463 (0.086)
8	rs117325001	26,242,272	T/G	1.083 (0.019)	1.71E-05	1.118 (0.023)
8	rs5891007	38,021,010	I/D	0.902 (0.020)	1.39E-07	0.876 (0.024)
8	rs3812429	71,101,719	C/T	1.077 (0.020)	1.58E-04	1.112 (0.024)
9	rs7022128	1,876,048	C/A	0.876 (0.031)	1.45E-05	0.838 (0.041)
9	rs76028754	78,778,388	C/T	1.079 (0.020)	1.76E-04	1.117 (0.025)
10	rs6560760	1,725,157	T/C	1.104 (0.031)	1.43E-03	1.179 (0.039)
10	rs2388393	2,686,848	T/C	1.082 (0.021)	1.81E-04	1.118 (0.026)
10	rs117900362	24,150,317	C/T	1.199 (0.041)	1.01E-05	1.210 (0.044)
11	rs7928792	61,698,488	G/C	1.068 (0.022)	3.10E-03	1.125 (0.027)
12	rs3759413	7,291,206	T/C	1.127 (0.023)	2.44E-07	1.162 (0.029)
12	rs3803070	94,688,688	C/A	1.082 (0.023)	4.87E-04	1.138 (0.028)
12	rs144026710	106,998,088	T/C	1.266 (0.080)	3.24E-03	1.667 (0.118)
12	rs10744422	123,336,789	T/C	1.092 (0.019)	4.76E-06	1.131 (0.024)
13	rs7989524	19,631,157	A/C	0.860 (0.032)	3.11E-06	0.811 (0.044)
14	rs2806049	73,526,613	A/G	0.897 (0.025)	1.51E-05	0.868 (0.031)
14	rs61990820	80,366,270	A/G	1.133 (0.025)	7.41E-07	1.165 (0.033)
14	rs4277287	94,417,541	A/G	0.887 (0.040)	2.67E-03	0.760 (0.055)
15	rs76528668	33,757,740	T/C	1.175 (0.046)	3.98E-04	1.390 (0.064)
15	rs4775413	61,840,103	T/C	1.084 (0.020)	5.20E-05	1.113 (0.025)
15	rs12916327	97,729,447	C/A	1.050 (0.026)	5.46E-02	1.184 (0.038)
16	rs11077311	8,539,285	C/T	1.059 (0.019)	1.99E-03	1.112 (0.023)
16	rs72833348	81,325,469	T/C	1.070 (0.036)	5.77E-02	1.268 (0.050)
17	rs11078930	38,141,955	T/C	0.934 (0.018)	1.49E-04	0.904 (0.023)
18	rs1792709	53,768,975	A/G	0.870 (0.026)	6.33E-08	0.849 (0.032)
18	rs13381974	71,344,330	T/C	0.874 (0.043)	1.59E-03	0.745 (0.068)
19	rs259282	33,163,043	T/C	0.912 (0.020)	5.04E-06	0.885 (0.025)

19	rs10995	46,030,154	G/A	0.918 (0.025)	7.94E-04	0.858 (0.034)
20	rs75206192	21,558,073	G/A	1.233 (0.061)	6.11E-04	1.430 (0.075)
21	rs1075704	36,063,474	T/G	0.897 (0.027)	4.61E-05	0.850 (0.036)

The genome-wide significant SNPs in the meta-analysis were indicated as bold.
Genomic position was based on the UCSC hg19/NCBI Build 37.
OR=odds ratio for A1 and SE=standard error.

nese GWAS Stage	Chinese Replication Stage	
P value	OR (SE)	P value
1.76E-06	0.934 (0.088)	4.40E-01
7.49E-06	0.982 (0.046)	6.91E-01
1.96E-05	1.051 (0.044)	2.52E-01
3.75E-06	0.981 (0.040)	6.28E-01
6.99E-06	1.068 (0.079)	4.06E-01
5.01E-07	0.774 (0.160)	1.10E-01
1.48E-05	1.047 (0.038)	2.36E-01
1.64E-07	1.002 (0.063)	9.72E-01
2.38E-06	1.005 (0.051)	9.15E-01
1.18E-09	**0.871 (0.035)**	**6.78E-05**
3.88E-07	1.059 (0.039)	1.46E-01
1.70E-06	0.943 (0.033)	7.63E-02
3.99E-06	1.064 (0.032)	4.95E-02
3.98E-06	1.017 (0.040)	6.65E-01
2.62E-06	0.955 (0.034)	1.72E-01
4.16E-06	0.945 (0.032)	7.56E-02
1.46E-05	1.058 (0.038)	1.37E-01
1.14E-05	0.984 (0.049)	7.41E-01
4.32E-06	**0.765 (0.062)**	**1.71E-05**
1.29E-05	0.981 (0.116)	8.68E-01
2.07E-07	**0.928 (0.032)**	**1.98E-02**
9.74E-06	1.039 (0.050)	4.49E-01
1.98E-06	1.038 (0.043)	3.78E-01
1.69E-05	1.051 (0.042)	2.37E-01
7.31E-06	1.089 (0.043)	4.84E-02
1.53E-05	1.021 (0.031)	4.99E-01
1.79E-05	1.067 (0.073)	3.72E-01
2.08E-06	1.079 (0.031)	1.46E-02
1.71E-07	1.049 (0.051)	3.48E-01
1.58E-06	0.970 (0.056)	5.93E-01
6.77E-06	0.952 (0.068)	4.67E-01
2.03E-06	0.951 (0.034)	1.40E-01
9.34E-06	0.979 (0.036)	5.58E-01
4.07E-06	0.997 (0.031)	9.34E-01
1.13E-05	1.168 (0.056)	5.56E-03
5.09E-07	0.963 (0.035)	2.78E-01
5.30E-06	0.997 (0.046)	9.54E-01

2.49E-06	0.972 (0.039)	4.72E-01
1.26E-05	0.864 (0.102)	1.50E-01
8.79E-07	**0.840 (0.062)**	**4.77E-03**
1.37E-05	0.940 (0.032)	5.16E-02
2.25E-06	1.042 (0.038)	2.87E-01
1.17E-05	1.040 (0.039)	3.11E-01
1.72E-05	1.003 (0.031)	9.34E-01
1.39E-05	1.029 (0.049)	5.53E-01
1.06E-05	**1.111 (0.033)**	**1.62E-03**
1.47E-05	1.002 (0.054)	9.65E-01
4.18E-07	**0.898 (0.035)**	**2.04E-03**
1.04E-05	0.989 (0.032)	7.34E-01
4.25E-06	1.000 (0.042)	9.94E-01
1.90E-05	**0.875 (0.036)**	**2.42E-04**
8.95E-06	1.033 (0.094)	7.31E-01
8.82E-07	1.016 (0.032)	6.10E-01
5.63E-08	0.951 (0.033)	1.32E-01
1.07E-05	1.011 (0.034)	7.40E-01
1.73E-05	0.925 (0.046)	9.33E-02
1.07E-05	1.011 (0.035)	7.62E-01
1.84E-05	0.976 (0.053)	6.48E-01
1.61E-05	1.015 (0.036)	6.80E-01
1.82E-05	1.138 (0.109)	2.37E-01
1.46E-05	0.964 (0.038)	3.40E-01
1.36E-07	1.062 (0.040)	1.33E-01
5.57E-06	0.993 (0.037)	8.50E-01
1.58E-05	1.003 (0.109)	9.81E-01
2.71E-07	1.024 (0.033)	4.70E-01
1.43E-06	0.925 (0.048)	1.06E-01
5.21E-06	0.954 (0.042)	2.69E-01
2.70E-06	1.087 (0.040)	3.66E-02
6.66E-07	1.051 (0.058)	3.89E-01
2.49E-07	0.987 (0.065)	8.45E-01
1.54E-05	1.032 (0.034)	3.48E-01
7.60E-06	0.950 (0.035)	1.35E-01
3.68E-06	0.964 (0.032)	2.48E-01
1.88E-06	0.896 (0.051)	3.19E-02
7.46E-06	0.991 (0.031)	7.59E-01
3.12E-07	0.909 (0.044)	3.23E-02
1.53E-05	0.969 (0.055)	5.77E-01
8.49E-07	0.967 (0.034)	3.12E-01

7.33E-06	0.999 (0.038)	9.87E-01
1.79E-06	0.917 (0.106)	4.11E-01
6.84E-06	0.957 (0.040)	2.70E-01

Supplementary Table 4. Results for meta-analysis of the Chinese and PGC2 samples

Chr.	SNP	Position	A1/A2	Meta-analysis of the Chinese and PGC2 samples			PGC2	
				OR (SE)	P value	I^2	OR (SE)	P value
1	**rs172531**	**8,495,590**	**A/G**	**0.931 (0.011)**	**5.05E-11**	**39**	**0.936 (0.011)**	**6.29E-09**
1	**rs4949526**	**30,432,219**	**T/C**	**1.065 (0.010)**	**2.81E-10**	**20**	**1.072 (0.012)**	**1.46E-09**
1	**rs2970610**	**44,097,530**	**T/C**	**1.072 (0.010)**	**1.24E-12**	**0**	**1.072 (0.011)**	**5.69E-10**
1	rs12138061	50,572,096	A/C	1.057 (0.011)	1.21E-07	0	1.059 (0.013)	6.04E-06
1	rs4347184	66,313,994	T/G	1.049 (0.009)	2.18E-07	0	1.055 (0.011)	6.92E-07
1	**rs11210195**	**73,749,283**	**T/C**	**0.943 (0.010)**	**1.76E-09**	**69**	**0.936 (0.011)**	**5.36E-10**
1	rs36025579	97,802,624	A/G	0.951 (0.010)	5.31E-07	0	0.948 (0.012)	8.20E-06
1	**rs1198589**	**98,550,411**	**T/C**	**0.907 (0.013)**	**1.20E-13**	**75**	**0.897 (0.014)**	**2.60E-14**
1	rs11102159	111,324,727	T/C	1.048 (0.010)	3.19E-06	10	1.055 (0.012)	8.16E-06
1	rs7523654	115,861,265	T/C	1.049 (0.010)	1.53E-06	0	1.047 (0.012)	5.54E-05
1	**rs12129037**	**150,492,114**	**T/C**	**1.096 (0.016)**	**4.51E-09**	**0**	**1.100 (0.017)**	**3.43E-08**
1	**rs6670165**	**177,280,121**	**T/C**	**1.073 (0.012)**	**3.37E-09**	**0**	**1.074 (0.014)**	**1.16E-07**
1	rs9970077	177,760,918	A/G	1.058 (0.012)	2.00E-06	66	1.071 (0.014)	7.43E-07
1	rs12139672	190,940,627	A/G	0.946 (0.011)	3.21E-07	48	0.936 (0.013)	4.49E-07
1	rs11240341	205,015,284	T/C	1.049 (0.010)	2.81E-06	36	1.055 (0.011)	1.74E-06
1	rs7523273	207,977,083	A/G	1.055 (0.011)	6.26E-07	62	1.062 (0.012)	1.61E-07
1	rs7529073	214,147,889	T/C	0.954 (0.009)	2.59E-07	0	0.950 (0.011)	9.69E-07
1	rs10803138	243,555,219	A/G	0.937 (0.012)	8.31E-08	66	0.932 (0.013)	1.79E-08
1	**rs35978510**	**243,776,117**	**T/C**	**0.941 (0.010)**	**6.50E-10**	**0**	**0.940 (0.012)**	**1.25E-07**
2	rs10199182	22,747,124	A/T	1.052 (0.010)	6.71E-07	70	1.059 (0.011)	1.31E-07
2	**rs12623170**	**28,020,157**	**T/C**	**0.943 (0.010)**	**2.52E-08**	**0**	**0.940 (0.013)**	**1.24E-06**
2	rs2372993	37,561,929	T/C	0.953 (0.010)	7.42E-07	0	0.955 (0.011)	2.45E-05
2	rs80256351	58,071,593	A/C	0.898 (0.020)	5.36E-08	64	0.881 (0.023)	3.20E-08
2	**rs75575209**	**58,138,192**	**A/T**	**0.902 (0.018)**	**1.24E-08**	**16**	**0.896 (0.019)**	**1.01E-08**
2	rs7596038	58,383,820	T/C	0.895 (0.045)	1.29E-02	92	0.934 (0.011)	1.15E-10
2	**rs999494**	**73,157,395**	**T/C**	**0.924 (0.012)**	**2.40E-10**	**58**	**0.932 (0.014)**	**2.04E-07**
2	rs7560272	73,561,485	A/T	0.949 (0.010)	5.67E-07	0	0.948 (0.012)	3.63E-06
2	rs35430959	76,465,288	T/C	0.932 (0.013)	5.68E-08	0	0.933 (0.013)	2.08E-07
2	rs61712019	77,704,889	T/C	1.056 (0.011)	1.18E-06	0	1.059 (0.012)	1.96E-06
2	**rs62152284**	**104,984,387**	**T/C**	**1.065 (0.011)**	**5.86E-09**	**65**	**1.051 (0.013)**	**1.78E-04**
2	**rs6430491**	**134,840,967**	**A/G**	**0.936 (0.011)**	**9.55E-10**	**0**	**0.938 (0.013)**	**1.61E-06**
2	**rs2381759**	**146,428,031**	**A/T**	**0.929 (0.013)**	**8.63E-09**	**11**	**0.924 (0.014)**	**1.36E-08**
2	rs35662245	147,583,187	A/T	1.050 (0.010)	4.62E-07	0	1.052 (0.011)	4.22E-06
2	rs12622667	149,520,186	T/C	0.935 (0.014)	1.14E-06	27	0.920 (0.019)	1.69E-05
2	rs3845702	180,848,488	A/C	1.063 (0.011)	5.96E-08	57	1.051 (0.014)	2.41E-04
2	**rs7597593**	**185,533,580**	**T/C**	**1.066 (0.010)**	**9.30E-11**	**0**	**1.068 (0.011)**	**1.47E-09**

2	**rs12619354**	**194,002,782**	**T/C**	**1.056 (0.010)**	**3.81E-08**	**0**	**1.058 (0.011)**	**4.78E-07**
2	rs10204454	194,346,284	T/C	0.971 (0.030)	3.27E-01	82	0.946 (0.011)	2.09E-07
2	rs6434928	198,304,577	A/G	0.958 (0.035)	2.21E-01	89	0.927 (0.011)	1.48E-11
2	**rs895526**	**200,162,425**	**T/C**	**0.936 (0.011)**	**9.27E-10**	**0**	**0.929 (0.014)**	**8.00E-08**
2	**rs796364**	**200,716,119**	**A/C**	**0.912 (0.011)**	**0.00E-16**	**21**	**0.905 (0.013)**	**5.90E-14**
2	**rs17630293**	**201,146,776**	**T/G**	**1.124 (0.017)**	**3.32E-12**	**0**	**1.129 (0.024)**	**4.69E-07**
2	**rs11685299**	**225,391,296**	**A/C**	**0.934 (0.010)**	**4.70E-12**	**0**	**0.937 (0.011)**	**1.11E-08**
2	rs2194545	229,283,211	A/G	0.954 (0.010)	1.67E-06	69	0.947 (0.011)	3.25E-07
2	**rs778371**	**233,743,109**	**A/G**	**0.923 (0.011)**	**2.18E-13**	**0**	**0.922 (0.012)**	**5.17E-12**
3	**rs11708578**	**2,515,894**	**A/G**	**0.925 (0.012)**	**7.28E-11**	**0**	**0.927 (0.012)**	**5.56E-10**
3	**rs4330281**	**17,859,366**	**T/C**	**0.942 (0.011)**	**3.04E-08**	**0**	**0.943 (0.011)**	**5.51E-08**
3	rs1506297	30,072,307	T/C	1.058 (0.011)	7.69E-07	57	1.061 (0.012)	2.66E-07
3	**rs10510653**	**32,058,559**	**A/T**	**1.074 (0.013)**	**2.54E-08**	**0**	**1.070 (0.018)**	**1.48E-04**
3	**rs3732386**	**36,871,993**	**T/C**	**1.075 (0.011)**	**2.88E-11**	**11**	**1.078 (0.011)**	**1.73E-11**
3	rs7619427	44,077,041	A/G	0.921 (0.016)	1.85E-07	0	0.922 (0.017)	1.67E-06
3	rs9882618	50,237,545	T/C	1.095 (0.019)	9.66E-07	61	1.158 (0.039)	2.04E-04
3	**rs2577831**	**52,628,056**	**A/C**	**0.936 (0.009)**	**4.53E-13**	**0**	**0.935 (0.011)**	**2.15E-10**
3	rs2358740	53,455,569	T/G	0.949 (0.010)	7.01E-08	0	0.945 (0.011)	5.14E-07
3	rs1353545	60,287,845	C/G	1.057 (0.011)	1.72E-07	63	1.064 (0.011)	4.26E-08
3	rs13074132	60,321,082	T/C	1.052 (0.011)	2.37E-06	59	1.058 (0.011)	6.94E-07
3	**rs832190**	**63,842,629**	**T/C**	**0.948 (0.010)**	**3.93E-08**	**57**	**0.941 (0.011)**	**2.69E-08**
3	rs7372960	71,254,751	T/C	1.064 (0.012)	3.15E-07	48	1.070 (0.013)	1.25E-07
3	rs11127668	79,915,770	T/C	0.952 (0.010)	5.18E-07	0	0.951 (0.011)	6.25E-06
3	rs1838472	124,051,661	T/C	0.948 (0.010)	1.86E-07	7	0.952 (0.011)	6.83E-06
3	**rs66691851**	**136,154,828**	**T/C**	**0.926 (0.010)**	**4.00E-15**	**45**	**0.932 (0.011)**	**6.35E-11**
3	rs192812	161,491,831	T/C	0.949 (0.010)	8.82E-08	0	0.949 (0.011)	1.26E-06
3	**rs6804239**	**161,780,488**	**T/C**	**0.943 (0.009)**	**8.41E-10**	**56**	**0.951 (0.011)**	**5.97E-06**
3	**rs9859557**	**180,830,910**	**A/T**	**1.094 (0.012)**	**6.00E-14**	**52**	**1.085 (0.013)**	**5.30E-10**
3	**rs9841616**	**181,167,585**	**A/T**	**0.928 (0.013)**	**5.35E-09**	**0**	**0.922 (0.014)**	**1.65E-08**
4	**rs215411**	**23,423,603**	**A/T**	**1.069 (0.011)**	**6.37E-10**	**0**	**1.067 (0.011)**	**1.22E-08**
4	rs4626214	97,727,069	A/G	0.952 (0.010)	4.76E-07	0	0.947 (0.011)	6.07E-07
4	**rs11722779**	**103,827,488**	**T/G**	**0.951 (0.009)**	**3.40E-08**	**0**	**0.955 (0.011)**	**1.71E-05**
4	rs2905627	105,450,085	T/C	1.050 (0.010)	2.84E-06	69	1.059 (0.012)	5.17E-07
4	rs4833558	118,919,497	T/C	0.955 (0.010)	2.71E-06	0	0.953 (0.011)	2.59E-05
4	**rs7438**	**170,642,246**	**A/G**	**1.066 (0.010)**	**7.46E-11**	**0**	**1.062 (0.011)**	**2.13E-08**
4	**rs6846161**	**176,866,459**	**A/G**	**1.067 (0.011)**	**9.96E-10**	**0**	**1.072 (0.012)**	**1.16E-08**
4	rs35751669	183,637,657	A/G	0.957 (0.032)	1.64E-01	85	0.928 (0.014)	1.64E-07
5	**rs9292918**	**45,301,035**	**T/G**	**0.932 (0.011)**	**4.47E-11**	**0**	**0.927 (0.013)**	**1.47E-08**
5	**rs10940346**	**49,806,042**	**A/G**	**0.949 (0.009)**	**1.11E-08**	**0**	**0.952 (0.011)**	**3.54E-06**
5	rs4391122	60,598,543	A/G	0.953 (0.034)	1.53E-01	85	0.924 (0.011)	1.73E-13
5	rs1065861	88,091,950	A/T	0.921 (0.040)	3.90E-02	75	0.888 (0.023)	1.39E-07

5	**rs2247870**	**90,151,589**	**A/G**	**1.052 (0.009)**	**2.54E-08**	**0**	**1.051 (0.011)**	**2.24E-06**
5	**rs4388249**	**109,036,066**	**T/C**	**1.066 (0.011)**	**8.38E-09**	**12**	**1.075 (0.014)**	**1.03E-07**
5	rs248083	126,510,168	A/G	1.055 (0.010)	5.97E-08	0	1.052 (0.011)	6.06E-06
5	**rs2764766**	**127,213,625**	**C/G**	**1.055 (0.009)**	**1.94E-08**	**0**	**1.050 (0.011)**	**9.47E-06**
5	rs3756766	137,673,167	A/C	1.062 (0.011)	7.84E-08	61	1.069 (0.012)	2.19E-08
5	**rs13164092**	**137,840,860**	**A/G**	**0.943 (0.010)**	**9.79E-10**	**0**	**0.941 (0.011)**	**1.11E-08**
5	**rs7733403**	**140,154,215**	**A/G**	**1.052 (0.009)**	**2.06E-08**	**0**	**1.053 (0.011)**	**8.76E-07**
5	rs319204	146,262,489	T/C	1.051 (0.010)	4.35E-07	0	1.046 (0.011)	4.20E-05
5	**rs113568682**	**152,299,754**	**A/T**	**1.064 (0.011)**	**3.77E-08**	**15**	**1.068 (0.012)**	**2.50E-08**
5	rs76091702	152,482,963	T/C	1.124 (0.022)	1.20E-07	0	1.123 (0.023)	5.60E-07
5	**rs2910032**	**152,540,354**	**T/C**	**0.943 (0.010)**	**1.04E-09**	**14**	**0.938 (0.011)**	**1.90E-09**
5	rs7727515	152,892,304	A/G	0.945 (0.042)	1.84E-01	81	0.910 (0.017)	5.84E-08
5	**rs11740474**	**153,680,747**	**A/T**	**0.941 (0.011)**	**1.81E-08**	**0**	**0.941 (0.011)**	**3.94E-08**
6	**rs115329265**	**28,712,247**	**A/G**	**1.210 (0.015)**	**0.00E-16**	**0**	**1.213 (0.016)**	**0.00E-16**
6	**rs6903570**	**64,866,857**	**T/C**	**0.947 (0.010)**	**2.70E-08**	**13**	**0.953 (0.012)**	**4.20E-05**
6	rs34321714	73,164,144	C/G	0.952 (0.010)	3.12E-07	55	0.946 (0.011)	1.45E-07
6	**rs217331**	**84,344,689**	**C/G**	**0.934 (0.009)**	**1.63E-13**	**0**	**0.937 (0.011)**	**1.42E-09**
6	rs12190758	93,148,341	A/G	0.939 (0.012)	4.03E-07	0	0.939 (0.013)	4.73E-07
6	**rs160593**	**105,466,332**	**A/G**	**0.947 (0.009)**	**7.69E-09**	**0**	**0.948 (0.011)**	**7.97E-07**
6	**rs9398171**	**108,983,527**	**T/C**	**0.935 (0.010)**	**1.85E-11**	**0**	**0.938 (0.012)**	**3.37E-08**
6	rs9384900	114,711,095	T/C	1.055 (0.011)	1.04E-06	0	1.059 (0.012)	1.49E-06
6	rs12664251	119,344,546	A/C	1.049 (0.010)	7.14E-07	0	1.044 (0.011)	8.27E-05
7	**rs12668848**	**2,020,995**	**A/G**	**0.923 (0.010)**	**0.00E-16**	**0**	**0.923 (0.011)**	**8.70E-14**
7	rs7811417	21,534,152	T/C	1.050 (0.009)	2.05E-07	0	1.051 (0.011)	7.45E-06
7	**rs112509803**	**24,735,004**	**C/G**	**1.090 (0.016)**	**4.80E-08**	**0**	**1.086 (0.017)**	**1.03E-06**
7	**rs2944823**	**71,795,470**	**A/G**	**1.059 (0.010)**	**3.21E-08**	**0**	**1.054 (0.012)**	**9.45E-06**
7	**rs323167**	**78,336,677**	**T/C**	**0.946 (0.010)**	**4.47E-08**	**62**	**0.954 (0.011)**	**1.93E-05**
7	**rs12704290**	**86,427,626**	**A/G**	**0.908 (0.015)**	**2.61E-10**	**62**	**0.899 (0.017)**	**1.04E-10**
7	rs11982256	86,799,441	A/T	0.899 (0.049)	3.13E-02	79	0.857 (0.029)	1.36E-07
7	rs221780	100,297,035	C/G	0.933 (0.013)	3.11E-07	0	0.937 (0.015)	8.43E-06
7	**rs2057884**	**104,930,250**	**T/C**	**1.069 (0.010)**	**2.02E-12**	**0**	**1.067 (0.011)**	**5.26E-09**
7	rs7807720	110,073,755	A/G	1.054 (0.010)	1.36E-07	0	1.055 (0.011)	8.97E-07
7	**rs214467**	**110,858,268**	**A/G**	**1.073 (0.010)**	**7.69E-13**	**48**	**1.081 (0.011)**	**3.32E-12**
7	rs7801375	131,567,263	A/G	0.926 (0.014)	6.03E-08	53	0.920 (0.015)	2.26E-08
7	**rs3735025**	**137,074,844**	**T/C**	**1.068 (0.010)**	**3.60E-12**	**0**	**1.066 (0.011)**	**7.75E-09**
8	**rs13261217**	**4,183,057**	**A/G**	**0.934 (0.011)**	**2.12E-09**	**0**	**0.933 (0.013)**	**4.77E-08**
8	rs12541020	4,817,592	T/C	1.052 (0.010)	3.60E-07	0	1.052 (0.012)	2.67E-05
8	**rs2980436**	**8,092,025**	**A/G**	**1.057 (0.010)**	**2.31E-08**	**0**	**1.060 (0.011)**	**8.54E-08**
8	**rs12543645**	**10,246,325**	**C/G**	**1.058 (0.010)**	**3.32E-08**	**0**	**1.059 (0.011)**	**2.46E-07**
8	**rs17687067**	**17,036,201**	**A/C**	**0.925 (0.011)**	**3.39E-12**	**0**	**0.931 (0.014)**	**1.14E-07**
8	rs13259407	18,422,923	T/C	0.957 (0.009)	1.65E-06	45	0.950 (0.011)	1.41E-06

8	**rs73219805**	**26,272,768**	**A/G**	**1.078 (0.011)**	**1.94E-11**	**0**	**1.074 (0.014)**	**2.99E-07**
8	rs11778040	27,419,807	T/C	0.939 (0.013)	8.31E-07	64	0.931 (0.014)	1.94E-07
8	**rs112537273**	**38,248,306**	**T/C**	**1.077 (0.011)**	**1.06E-11**	**22**	**1.068 (0.013)**	**3.70E-07**
8	**rs867743**	**60,694,647**	**A/G**	**0.945 (0.010)**	**4.97E-09**	**62**	**0.938 (0.011)**	**2.11E-09**
8	rs7012816	70,964,743	A/G	1.064 (0.012)	4.08E-07	0	1.068 (0.015)	8.38E-06
8	**rs7010876**	**89,264,751**	**A/T**	**0.939 (0.011)**	**1.48E-08**	**0**	**0.941 (0.012)**	**3.30E-07**
8	rs1460583	106,108,593	T/C	0.957 (0.010)	3.68E-06	0	0.955 (0.011)	4.72E-05
8	**rs16880831**	**111,561,505**	**T/G**	**0.930 (0.012)**	**4.34E-10**	**0**	**0.926 (0.013)**	**3.31E-09**
8	**rs13266463**	**143,403,693**	**A/G**	**0.947 (0.010)**	**2.25E-08**	**52**	**0.941 (0.011)**	**1.26E-08**
9	rs7022054	7,173,500	A/G	0.951 (0.010)	1.37E-07	0	0.949 (0.011)	1.02E-06
9	rs9695226	22,759,396	A/G	0.945 (0.011)	1.63E-07	0	0.942 (0.012)	2.52E-07
9	rs10124101	36,308,827	A/G	0.952 (0.009)	2.00E-07	0	0.951 (0.011)	2.20E-06
9	**rs2767713**	**84,799,537**	**A/C**	**0.941 (0.011)**	**2.02E-08**	**60**	**0.933 (0.012)**	**1.12E-08**
9	rs3824451	101,071,522	T/C	0.943 (0.012)	2.01E-06	66	0.931 (0.015)	7.88E-07
9	rs11790388	129,740,283	A/G	0.934 (0.013)	7.93E-08	0	0.935 (0.015)	4.58E-06
10	rs7099380	18,549,016	A/G	1.054 (0.010)	7.38E-08	0	1.051 (0.011)	2.79E-06
10	**rs7893279**	**18,745,105**	**T/G**	**1.117 (0.015)**	**3.29E-13**	**0**	**1.120 (0.017)**	**3.56E-11**
10	rs61847307	53,944,442	T/C	0.943 (0.012)	3.78E-07	24	0.939 (0.012)	2.08E-07
10	rs7915131	64,418,656	T/C	0.954 (0.010)	6.23E-07	0	0.954 (0.011)	7.62E-06
10	**rs111364339**	**64,857,872**	**T/C**	**0.906 (0.017)**	**5.37E-09**	**0**	**0.897 (0.027)**	**4.26E-05**
10	**rs11191424**	**104,625,886**	**A/G**	**0.917 (0.009)**	**0.00E-16**	**37**	**0.910 (0.011)**	**0.00E-16**
10	**rs10786736**	**104,849,116**	**C/G**	**0.897 (0.013)**	**0.00E-16**	**0**	**0.896 (0.017)**	**4.56E-11**
11	**rs17234749**	**24,381,898**	**A/G**	**0.943 (0.010)**	**5.39E-09**	**0**	**0.941 (0.011)**	**2.23E-08**
11	**rs61882743**	**46,548,754**	**C/G**	**0.914 (0.013)**	**6.99E-12**	**0**	**0.913 (0.014)**	**1.26E-10**
11	**rs9420**	**57,510,294**	**A/G**	**1.061 (0.010)**	**8.52E-09**	**0**	**1.063 (0.011)**	**6.65E-08**
11	rs7934083	81,203,521	T/C	0.948 (0.010)	1.61E-07	0	0.945 (0.011)	2.42E-07
11	rs1864774	83,199,276	T/C	0.953 (0.009)	1.87E-07	2	0.948 (0.011)	5.48E-07
11	**rs12421382**	**109,378,071**	**T/C**	**0.945 (0.010)**	**1.51E-08**	**0**	**0.943 (0.011)**	**1.72E-07**
11	rs4987094	113,215,923	A/G	1.058 (0.026)	3.03E-02	78	1.085 (0.017)	7.23E-07
11	**rs2514218**	**113,392,994**	**T/C**	**0.928 (0.011)**	**5.01E-11**	**0**	**0.930 (0.012)**	**4.09E-10**
11	**rs77502336**	**123,394,636**	**C/G**	**1.063 (0.010)**	**1.35E-09**	**48**	**1.071 (0.011)**	**2.01E-09**
11	**rs55661361**	**124,613,957**	**A/G**	**0.932 (0.010)**	**1.16E-12**	**55**	**0.925 (0.011)**	**3.68E-12**
11	**rs10894308**	**130,891,895**	**A/G**	**0.947 (0.010)**	**2.09E-08**	**64**	**0.940 (0.011)**	**7.52E-09**
11	**rs75059851**	**133,822,569**	**A/G**	**1.098 (0.013)**	**8.78E-13**	**0**	**1.096 (0.014)**	**1.23E-11**
11	**rs619091**	**133,884,137**	**A/T**	**0.947 (0.009)**	**5.85E-09**	**0**	**0.947 (0.011)**	**5.60E-07**
12	**rs2159100**	**2,346,393**	**T/C**	**1.102 (0.011)**	**0.00E-16**	**0**	**1.100 (0.011)**	**0.00E-16**
12	**rs758117**	**2,513,309**	**T/C**	**0.941 (0.011)**	**1.68E-08**	**62**	**0.934 (0.012)**	**6.46E-09**
12	**rs302321**	**29,928,388**	**A/C**	**0.937 (0.010)**	**2.07E-11**	**46**	**0.943 (0.011)**	**1.38E-07**
12	rs10878577	67,593,841	A/C	1.059 (0.012)	9.33E-07	0	1.060 (0.012)	2.69E-06
12	**rs4240748**	**92,246,786**	**C/G**	**0.948 (0.010)**	**4.55E-08**	**5**	**0.943 (0.011)**	**1.03E-07**
12	**rs4766428**	**110,723,245**	**T/C**	**1.065 (0.011)**	**2.60E-09**	**62**	**1.071 (0.011)**	**7.09E-10**

12	**rs28607014**	**117,708,611**	**T/C**	**0.946 (0.010)**	**1.75E-08**	**0**	**0.948 (0.011)**	**1.36E-06**
12	**rs61041384**	**123,644,043**	**T/C**	**0.891 (0.016)**	**5.50E-13**	**0**	**0.875 (0.025)**	**1.61E-07**
12	**rs1615350**	**123,650,335**	**T/C**	**0.916 (0.010)**	**0.00E-16**	**0**	**0.914 (0.012)**	**4.20E-14**
12	rs34102591	124,480,801	A/G	0.934 (0.012)	5.05E-08	0	0.933 (0.014)	4.07E-07
13	rs1411740	38,830,142	A/G	1.053 (0.010)	1.55E-07	0	1.054 (0.011)	1.87E-06
14	**rs10148671**	**29,469,373**	**T/C**	**0.947 (0.010)**	**4.46E-08**	**0**	**0.948 (0.011)**	**2.04E-06**
14	**rs1191551**	**30,000,405**	**T/G**	**1.074 (0.013)**	**2.28E-08**	**0**	**1.073 (0.013)**	**5.39E-08**
14	**rs2383377**	**33,257,914**	**A/G**	**1.081 (0.014)**	**2.36E-08**	**0**	**1.084 (0.016)**	**7.50E-07**
14	rs12431410	60,166,022	T/C	0.952 (0.010)	5.15E-07	38	0.946 (0.011)	4.22E-07
14	rs11625793	66,315,883	A/G	0.950 (0.010)	1.91E-07	0	0.948 (0.011)	8.95E-07
14	rs2526882	71,374,702	A/G	0.954 (0.010)	1.32E-06	70	0.945 (0.011)	3.17E-07
14	**rs35607894**	**72,408,638**	**A/G**	**1.094 (0.014)**	**5.37E-11**	**38**	**1.088 (0.014)**	**4.96E-09**
14	**rs8012642**	**84,669,481**	**C/G**	**1.055 (0.010)**	**4.66E-08**	**0**	**1.057 (0.011)**	**1.13E-06**
14	**rs2693698**	**99,719,219**	**A/G**	**0.941 (0.011)**	**2.20E-08**	**0**	**0.939 (0.011)**	**1.38E-08**
14	rs12887734	104,046,834	T/G	1.059 (0.032)	7.75E-02	86	1.091 (0.012)	1.18E-13
15	rs12911832	58,985,904	A/T	1.059 (0.011)	7.88E-08	0	1.056 (0.012)	4.65E-06
15	**rs35225048**	**61,856,263**	**T/C**	**0.935 (0.009)**	**7.77E-13**	**0**	**0.938 (0.011)**	**1.79E-09**
15	rs12148337	70,589,272	T/C	1.050 (0.009)	6.29E-08	59	1.059 (0.011)	5.33E-08
15	**rs3825845**	**78,910,258**	**T/C**	**0.932 (0.011)**	**2.47E-10**	**70**	**0.922 (0.013)**	**1.34E-10**
15	**rs783540**	**83,254,708**	**A/G**	**0.950 (0.009)**	**3.05E-08**	**37**	**0.944 (0.011)**	**5.86E-08**
15	**rs950169**	**84,706,461**	**T/C**	**0.923 (0.012)**	**5.17E-12**	**0**	**0.924 (0.012)**	**7.62E-11**
15	**rs758129**	**89,900,887**	**A/G**	**0.945 (0.010)**	**2.87E-08**	**12**	**0.950 (0.011)**	**3.96E-06**
15	rs11539637	91,428,290	T/C	1.096 (0.033)	5.92E-03	80	1.065 (0.011)	8.60E-09
16	**rs6500596**	**4,470,027**	**T/G**	**0.939 (0.011)**	**5.24E-09**	**0**	**0.940 (0.012)**	**4.84E-07**
16	**rs9922678**	**9,946,319**	**A/G**	**1.065 (0.011)**	**3.36E-09**	**0**	**1.070 (0.012)**	**6.72E-09**
16	**rs7405404**	**13,749,859**	**T/C**	**1.073 (0.012)**	**8.06E-10**	**58**	**1.081 (0.013)**	**3.93E-10**
16	**rs3814881**	**30,000,901**	**A/G**	**0.936 (0.009)**	**8.41E-13**	**0**	**0.936 (0.011)**	**4.27E-10**
16	rs12325245	58,681,393	A/T	0.943 (0.033)	7.51E-02	76	0.916 (0.015)	1.15E-08
16	rs7193419	63,697,134	T/C	1.037 (0.026)	1.61E-01	83	1.062 (0.011)	1.59E-08
16	**rs8058130**	**64,371,163**	**A/G**	**0.948 (0.010)**	**4.77E-08**	**21**	**0.954 (0.011)**	**3.57E-05**
16	rs55757091	68,323,654	A/G	1.071 (0.013)	1.70E-07	0	1.073 (0.014)	5.72E-07
17	**rs56007784**	**1,290,950**	**C/G**	**1.059 (0.009)**	**1.16E-09**	**62**	**1.050 (0.011)**	**8.77E-06**
17	rs4523957	2,208,899	T/G	1.040 (0.032)	2.25E-01	84	1.071 (0.011)	1.04E-09
17	**rs8082590**	**17,958,402**	**A/G**	**0.936 (0.011)**	**7.40E-10**	**0**	**0.936 (0.012)**	**6.84E-09**
17	**rs72843506**	**19,946,287**	**A/T**	**1.070 (0.012)**	**3.73E-08**	**0**	**1.067 (0.013)**	**1.05E-06**
17	**rs35065479**	**55,736,735**	**A/G**	**1.066 (0.011)**	**2.31E-08**	**0**	**1.061 (0.014)**	**1.52E-05**
18	rs12327082	31,591,459	A/T	0.946 (0.010)	7.47E-08	0	0.947 (0.011)	3.91E-07
18	rs4632195	50,746,748	T/C	1.051 (0.010)	1.50E-06	0	1.051 (0.011)	4.19E-06
18	rs7233277	52,741,518	A/G	1.032 (0.023)	1.82E-01	77	1.053 (0.011)	1.10E-06
18	rs17598729	53,251,562	T/C	1.009 (0.079)	9.10E-01	94	1.088 (0.014)	4.03E-09
18	**rs715170**	**53,795,514**	**T/C**	**0.928 (0.011)**	**5.21E-12**	**64**	**0.936 (0.012)**	**3.47E-08**

18	**rs56775891**	**77,575,613**	**T/C**	**1.058 (0.010)**	**1.85E-08**	**0**	**1.063 (0.012)**	**2.17E-07**
18	**rs28735056**	**77,622,879**	**A/G**	**0.941 (0.010)**	**4.60E-10**	**42**	**0.948 (0.011)**	**1.07E-06**
19	rs3764567	19,440,066	T/C	0.982 (0.041)	6.59E-01	92	0.944 (0.011)	1.63E-07
19	**rs2053079**	**30,987,423**	**A/G**	**0.938 (0.011)**	**4.64E-09**	**61**	**0.929 (0.012)**	**3.79E-09**
19	rs56873913	50,091,199	T/G	1.061 (0.012)	4.15E-07	53	1.069 (0.013)	2.19E-07
20	rs1075195	37,346,751	T/C	1.062 (0.012)	9.24E-07	45	1.079 (0.017)	6.66E-06
20	rs2103655	37,425,958	A/G	1.047 (0.031)	1.43E-01	87	1.078 (0.012)	8.86E-11
20	rs7267348	48,131,036	T/C	0.947 (0.011)	2.99E-07	66	0.938 (0.012)	1.18E-07
20	rs7273691	58,253,504	T/C	1.069 (0.012)	7.75E-08	45	1.062 (0.013)	5.99E-06
22	**rs5757730**	**39,967,430**	**A/G**	**0.933 (0.011)**	**1.84E-10**	**0**	**0.934 (0.011)**	**7.75E-10**
22	rs714031	40,070,234	T/C	0.944 (0.011)	8.04E-08	33	0.947 (0.011)	5.58E-07
22	rs17002069	41,050,986	C/G	1.062 (0.012)	2.05E-07	0	1.064 (0.013)	3.05E-06
22	**rs9607782**	**41,587,556**	**A/T**	**1.090 (0.012)**	**1.01E-12**	**0**	**1.091 (0.013)**	**6.76E-12**
22	rs6002655	42,603,814	T/C	1.041 (0.029)	1.61E-01	83	1.068 (0.011)	1.48E-09

The genome-wide significant SNPs in the meta-analysis were indicated as bold.
Genomic position was based on the UCSC hg19/NCBI Build 37.
OR=odds ratio for A1 and SE=standard error.
I^2 index represents the degree of heterogeneity.

Chinese GWAS and Replication	
OR (SE)	**P value**
0.894 (0.034)	**9.26E-04**
1.044 (0.020)	**3.11E-02**
1.071 (0.020)	**4.94E-04**
1.053 (0.019)	6.38E-03
1.033 (0.019)	8.82E-02
0.982 (0.025)	**4.64E-01**
0.958 (0.018)	1.92E-02
0.968 (0.036)	**3.67E-01**
1.031 (0.018)	8.69E-02
1.052 (0.019)	8.12E-03
1.079 (0.037)	**4.06E-02**
1.068 (0.025)	**7.71E-03**
1.022 (0.023)	3.37E-01
0.968 (0.020)	9.73E-02
1.020 (0.025)	4.11E-01
1.010 (0.029)	7.16E-01
0.968 (0.018)	7.24E-02
1.016 (0.049)	7.44E-01
0.944 (0.018)	**1.49E-03**
0.992 (0.034)	8.15E-01
0.950 (0.018)	**5.63E-03**
0.946 (0.021)	8.47E-03
0.950 (0.039)	1.92E-01
0.953 (0.054)	**3.74E-01**
0.853 (0.023)	1.13E-11
0.884 (0.031)	**8.88E-05**
0.956 (0.024)	5.96E-02
0.924 (0.048)	1.02E-01
1.035 (0.029)	2.38E-01
1.093 (0.019)	**2.01E-06**
0.933 (0.018)	**1.38E-04**
0.957 (0.031)	**1.57E-01**
1.042 (0.019)	3.52E-02
0.950 (0.020)	1.05E-02
1.091 (0.020)	2.05E-05
1.057 (0.023)	**1.61E-02**

1.050 (0.022)	**2.43E-02**
1.004 (0.023)	8.56E-01
0.994 (0.021)	7.88E-01
0.946 (0.018)	**2.14E-03**
0.930 (0.021)	**5.48E-04**
1.119 (0.023)	**1.54E-06**
0.925 (0.020)	**9.36E-05**
0.993 (0.024)	7.58E-01
0.931 (0.028)	**1.09E-02**
0.878 (0.059)	**2.75E-02**
0.894 (0.102)	**2.72E-01**
0.962 (0.063)	5.40E-01
1.077 (0.018)	**4.37E-05**
1.026 (0.046)	**5.81E-01**
0.908 (0.046)	3.80E-02
1.078 (0.021)	3.62E-04
0.938 (0.018)	**4.40E-04**
0.960 (0.019)	3.44E-02
1.010 (0.029)	7.21E-01
1.002 (0.032)	9.39E-01
0.976 (0.021)	**2.35E-01**
1.004 (0.044)	9.28E-01
0.956 (0.021)	2.91E-02
0.922 (0.029)	4.79E-03
0.900 (0.023)	**5.70E-06**
0.948 (0.023)	2.30E-02
0.921 (0.019)	**1.04E-05**
1.135 (0.028)	**8.04E-06**
0.951 (0.029)	**7.89E-02**
1.089 (0.034)	**1.27E-02**
0.971 (0.023)	1.96E-01
0.938 (0.018)	**3.56E-04**
1.008 (0.025)	7.43E-01
0.959 (0.020)	3.92E-02
1.088 (0.025)	**6.36E-04**
1.052 (0.021)	**1.83E-02**
0.989 (0.021)	6.06E-01
0.940 (0.018)	**6.45E-04**
0.941 (0.018)	**7.33E-04**
0.989 (0.024)	6.40E-01
0.962 (0.033)	2.37E-01

1.055 (0.018)	**2.99E-03**
1.048 (0.019)	**1.54E-02**
1.064 (0.020)	2.40E-03
1.067 (0.018)	**4.21E-04**
1.012 (0.033)	7.21E-01
0.951 (0.023)	**2.76E-02**
1.051 (0.018)	**6.90E-03**
1.072 (0.022)	1.70E-03
1.025 (0.036)	**4.84E-01**
1.134 (0.073)	8.81E-02
0.965 (0.024)	**1.39E-01**
0.991 (0.033)	7.89E-01
0.952 (0.041)	**2.25E-01**
1.195 (0.041)	**1.56E-05**
0.931 (0.018)	**9.14E-05**
0.982 (0.023)	4.14E-01
0.924 (0.018)	**1.92E-05**
0.944 (0.096)	5.46E-01
0.943 (0.020)	**2.74E-03**
0.924 (0.020)	**1.16E-04**
1.033 (0.028)	2.48E-01
1.063 (0.020)	2.03E-03
0.924 (0.021)	**1.32E-04**
1.048 (0.018)	9.16E-03
1.117 (0.045)	**1.28E-02**
1.073 (0.021)	**7.49E-04**
0.913 (0.024)	**1.65E-04**
0.964 (0.040)	**3.56E-01**
0.946 (0.035)	1.14E-01
0.913 (0.035)	9.62E-03
1.077 (0.019)	**7.09E-05**
1.047 (0.023)	5.13E-02
1.047 (0.021)	**2.67E-02**
0.994 (0.051)	9.02E-01
1.076 (0.019)	**1.08E-04**
0.941 (0.024)	**1.20E-02**
1.054 (0.018)	3.87E-03
1.043 (0.026)	**1.05E-01**
1.053 (0.026)	**5.15E-02**
0.912 (0.020)	**4.16E-06**
0.977 (0.018)	2.16E-01

1.083 (0.018)	**1.35E-05**
0.990 (0.034)	7.59E-01
1.097 (0.020)	**3.03E-06**
0.978 (0.023)	**3.32E-01**
1.055 (0.022)	1.32E-02
0.926 (0.031)	**1.28E-02**
0.960 (0.019)	2.69E-02
0.947 (0.025)	**2.95E-02**
0.976 (0.023)	**2.84E-01**
0.957 (0.022)	4.82E-02
0.965 (0.031)	2.50E-01
0.957 (0.021)	3.10E-02
0.975 (0.025)	**2.96E-01**
0.976 (0.023)	2.95E-01
0.932 (0.025)	4.83E-03
1.072 (0.025)	5.71E-03
1.108 (0.034)	**2.21E-03**
0.984 (0.039)	6.75E-01
0.954 (0.022)	2.91E-02
0.912 (0.022)	**2.84E-05**
0.935 (0.018)	**1.81E-04**
0.900 (0.020)	**1.96E-07**
0.954 (0.027)	**7.98E-02**
0.917 (0.037)	**1.92E-02**
1.052 (0.025)	**4.17E-02**
0.966 (0.029)	2.32E-01
0.968 (0.018)	7.43E-02
0.955 (0.021)	**2.57E-02**
1.030 (0.018)	9.93E-02
0.881 (0.055)	**2.02E-02**
1.035 (0.021)	**1.02E-01**
0.957 (0.020)	**3.16E-02**
0.981 (0.023)	**3.98E-01**
1.128 (0.053)	**2.34E-02**
0.948 (0.018)	**3.35E-03**
1.134 (0.039)	**1.40E-03**
0.979 (0.026)	**4.08E-01**
0.914 (0.021)	**1.26E-05**
1.049 (0.033)	1.52E-01
0.966 (0.021)	**1.07E-01**
1.005 (0.037)	**8.86E-01**

0.940 (0.021)	**3.45E-03**
0.902 (0.020)	**4.65E-07**
0.921 (0.020)	**2.72E-05**
0.940 (0.031)	4.54E-02
1.050 (0.022)	2.65E-02
0.944 (0.021)	**6.14E-03**
1.095 (0.073)	**2.10E-01**
1.071 (0.026)	**8.68E-03**
0.976 (0.022)	2.58E-01
0.958 (0.024)	7.04E-02
0.986 (0.021)	5.13E-01
1.154 (0.044)	**1.22E-03**
1.051 (0.020)	**1.21E-02**
0.992 (0.057)	**8.93E-01**
1.022 (0.022)	3.09E-01
1.069 (0.024)	4.46E-03
0.925 (0.020)	**9.44E-05**
1.025 (0.018)	1.77E-01
0.968 (0.023)	**1.54E-01**
0.969 (0.018)	**7.88E-02**
0.911 (0.040)	**1.79E-02**
0.923 (0.024)	**1.09E-03**
1.140 (0.029)	4.37E-06
0.936 (0.022)	**2.99E-03**
1.041 (0.028)	**1.46E-01**
1.029 (0.030)	**3.46E-01**
0.936 (0.019)	**4.84E-04**
0.979 (0.029)	4.62E-01
1.008 (0.019)	6.66E-01
0.931 (0.019)	**1.84E-04**
1.056 (0.034)	1.06E-01
1.087 (0.019)	**8.78E-06**
1.004 (0.023)	8.81E-01
0.936 (0.032)	**3.65E-02**
1.088 (0.033)	**9.98E-03**
1.077 (0.021)	**3.42E-04**
0.938 (0.036)	7.60E-02
1.051 (0.036)	1.61E-01
1.005 (0.020)	8.15E-01
0.929 (0.036)	4.31E-02
0.893 (0.025)	**7.86E-06**

1.044 (0.019)	**2.19E-02**
0.919 (0.021)	**4.12E-05**
1.025 (0.021)	2.31E-01
0.969 (0.023)	**1.64E-01**
1.024 (0.027)	3.80E-01
1.044 (0.018)	1.78E-02
1.013 (0.019)	5.20E-01
0.978 (0.022)	3.09E-01
1.117 (0.035)	1.52E-03
0.915 (0.054)	**1.02E-01**
0.885 (0.054)	2.39E-02
1.055 (0.024)	2.31E-02
1.083 (0.040)	**4.78E-02**
1.008 (0.021)	6.97E-01

Supplementary Table 5. GWS schizophrenia loci in this study

Locus ID	Chr.	SNP	Position	A1/A2	OR (SE)	P value
1	1	rs172531	8,495,590	A/G	0.931 (0.011)	5.05E-11
2	1	rs4949526	30,432,219	T/C	1.065 (0.010)	2.81E-10
3	1	rs2970610	44,097,530	T/C	1.072 (0.010)	1.24E-12
4	1	rs11210195	73,749,283	T/C	0.943 (0.010)	1.76E-09
5	1	rs1198589	98,550,411	T/C	0.907 (0.013)	1.20E-13
6	1	rs12129037	150,492,114	T/C	1.096 (0.016)	4.51E-09
7	1	rs6670165	177,280,121	T/C	1.073 (0.012)	3.37E-09
8	1	rs35978510	243,776,117	T/C	0.941 (0.010)	6.50E-10
9	2	rs12623170	28,020,157	T/C	0.943 (0.010)	2.52E-08
10	2	rs75575209	58,138,192	A/T	0.902 (0.018)	1.24E-08
10	2	rs1518395	58,208,074	A/G	0.862 (0.020)	3.79E-13
11	2	rs999494	73,157,395	T/C	0.924 (0.012)	2.40E-10
12	2	rs62152284	104,984,387	T/C	1.065 (0.011)	5.86E-09
13	2	rs6430491	134,840,967	A/G	0.936 (0.011)	9.55E-10
14	2	rs2381759	146,428,031	A/T	0.929 (0.013)	8.63E-09
15	2	rs7597593	185,533,580	T/C	1.066 (0.010)	9.30E-11
16	2	rs12619354	194,002,782	T/C	1.056 (0.010)	3.81E-08
17	2	rs895526	200,162,425	T/C	0.936 (0.011)	9.27E-10
18	2	rs796364	200,716,119	A/C	0.912 (0.011)	0.00E-16
18	2	rs17630293	201,146,776	T/G	1.124 (0.017)	3.32E-12
18	2	rs78681500	201,187,316	T/C	0.751 (0.045)	3.08E-10
19	2	rs11685299	225,391,296	A/C	0.934 (0.010)	4.70E-12
20	2	rs778371	233,743,109	A/G	0.923 (0.011)	2.18E-13
21	3	rs11708578	2,515,894	A/G	0.925 (0.012)	7.28E-11
22	3	rs4330281	17,859,366	T/C	0.942 (0.011)	3.04E-08
23	3	rs10510653	32,058,559	A/T	1.074 (0.013)	2.54E-08
24	3	rs3732386	36,871,993	T/C	1.075 (0.011)	2.88E-11
25	3	rs2073499	50,374,293	A/G	0.899 (0.019)	2.61E-08
26	3	rs2577831	52,628,056	A/C	0.936 (0.009)	4.53E-13
27	3	rs832190	63,842,629	T/C	0.948 (0.010)	3.93E-08
28	3	rs66691851	136,154,828	T/C	0.926 (0.010)	4.00E-15
29	3	rs6804239	161,780,488	T/C	0.943 (0.009)	8.41E-10
30	3	rs9859557	180,830,910	A/T	1.094 (0.012)	6.00E-14
30	3	rs9841616	181,167,585	A/T	0.928 (0.013)	5.35E-09
31	4	rs215411	23,423,603	A/T	1.069 (0.011)	6.37E-10
32	4	rs11722779	103,827,488	T/G	0.951 (0.009)	3.40E-08
33	4	rs7438	170,642,246	A/G	1.066 (0.010)	7.46E-11
34	4	rs6846161	176,866,459	A/G	1.067 (0.011)	9.96E-10

35	5	rs9292918	45,301,035	T/G	0.932 (0.011)	4.47E-11
36	5	rs10940346	49,806,042	A/G	0.949 (0.009)	1.11E-08
37	5	rs2247870	90,151,589	A/G	1.052 (0.009)	2.54E-08
38	5	rs4388249	109,036,066	T/C	1.066 (0.011)	8.38E-09
39	5	rs2764766	127,213,625	C/G	1.055 (0.009)	1.94E-08
40	5	rs13164092	137,840,860	A/G	0.943 (0.010)	9.79E-10
41	5	rs7733403	140,154,215	A/G	1.052 (0.009)	2.06E-08
42	5	rs113568682	152,299,754	A/T	1.064 (0.011)	3.77E-08
42	5	rs2910032	152,540,354	T/C	0.943 (0.010)	1.04E-09
43	5	rs11740474	153,680,747	A/T	0.941 (0.011)	1.81E-08
44	6	rs115329265	28,712,247	A/G	1.210 (0.015)	0.00E-16
44	6	rs111782145	30,873,508	C/T	0.813 (0.037)	1.80E-08
45	6	rs6903570	64,866,857	T/C	0.947 (0.010)	2.70E-08
46	6	rs217331	84,344,689	C/G	0.934 (0.009)	1.63E-13
47	6	rs160593	105,466,332	A/G	0.947 (0.009)	7.69E-09
48	6	rs9398171	108,983,527	T/C	0.935 (0.010)	1.85E-11
49	6	rs7757969	112,132,032	C/T	1.110 (0.019)	4.82E-08
50	6	rs4479915	165,075,601	G/C	0.876 (0.023)	4.82E-09
51	7	rs12668848	2,020,995	A/G	0.923 (0.010)	0.00E-16
52	7	rs112509803	24,735,004	C/G	1.090 (0.016)	4.80E-08
53	7	rs2944823	71,795,470	A/G	1.059 (0.010)	3.21E-08
54	7	rs323167	78,336,677	T/C	0.946 (0.010)	4.47E-08
55	7	rs12704290	86,427,626	A/G	0.908 (0.015)	2.61E-10
56	7	rs2057884	104,930,250	T/C	1.069 (0.010)	2.02E-12
57	7	rs214467	110,858,268	A/G	1.073 (0.010)	7.69E-13
58	7	rs11534004	113,467,444	G/A	0.890 (0.021)	1.71E-08
59	7	rs3735025	137,074,844	T/C	1.068 (0.010)	3.60E-12
60	8	rs13261217	4,183,057	A/G	0.934 (0.011)	2.12E-09
61	8	rs2980436	8,092,025	A/G	1.057 (0.010)	2.31E-08
62	8	rs12543645	10,246,325	C/G	1.058 (0.010)	3.32E-08
63	8	rs17687067	17,036,201	A/C	0.925 (0.011)	3.39E-12
64	8	rs73219805	26,272,768	A/G	1.078 (0.011)	1.94E-11
65	8	rs112537273	38,248,306	T/C	1.077 (0.011)	1.06E-11
66	8	rs867743	60,694,647	A/G	0.945 (0.010)	4.97E-09
67	8	rs7010876	89,264,751	A/T	0.939 (0.011)	1.48E-08
68	8	rs16880831	111,561,505	T/G	0.930 (0.012)	4.34E-10
69	8	rs13266463	143,403,693	A/G	0.947 (0.010)	2.25E-08
70	9	rs2767713	84,799,537	A/C	0.941 (0.011)	2.02E-08
71	10	rs7893279	18,745,105	T/G	1.117 (0.015)	3.29E-13
72	10	rs111364339	64,857,872	T/C	0.906 (0.017)	5.37E-09
73	10	rs11191424	104,625,886	A/G	0.917 (0.009)	0.00E-16

73	10	rs10786736	104,849,116	C/G	0.897 (0.013)	0.00E-16
74	11	rs17234749	24,381,898	A/G	0.943 (0.010)	5.39E-09
75	11	rs61882743	46,548,754	C/G	0.914 (0.013)	6.99E-12
76	11	rs9420	57,510,294	A/G	1.061 (0.010)	8.52E-09
77	11	rs12421382	109,378,071	T/C	0.945 (0.010)	1.51E-08
78	11	rs2514218	113,392,994	T/C	0.928 (0.011)	5.01E-11
79	11	rs77502336	123,394,636	C/G	1.063 (0.010)	1.35E-09
80	11	rs55661361	124,613,957	A/G	0.932 (0.010)	1.16E-12
81	11	rs10894308	130,891,895	A/G	0.947 (0.010)	2.09E-08
82	11	rs75059851	133,822,569	A/G	1.098 (0.013)	8.78E-13
82	11	rs619091	133,884,137	A/T	0.947 (0.009)	5.85E-09
83	12	rs2159100	2,346,393	T/C	1.102 (0.011)	0.00E-16
83	12	rs758117	2,513,309	T/C	0.941 (0.011)	1.68E-08
84	12	rs302321	29,928,388	A/C	0.937 (0.010)	2.07E-11
85	12	rs4240748	92,246,786	C/G	0.948 (0.010)	4.55E-08
86	12	rs4766428	110,723,245	T/C	1.065 (0.011)	2.60E-09
87	12	rs28607014	117,708,611	T/C	0.946 (0.010)	1.75E-08
88	12	rs61041384	123,644,043	T/C	0.891 (0.016)	5.50E-13
88	12	rs1615350	123,650,335	T/C	0.916 (0.010)	0.00E-16
89	14	rs10148671	29,469,373	T/C	0.947 (0.010)	4.46E-08
90	14	rs1191551	30,000,405	T/G	1.074 (0.013)	2.28E-08
91	14	rs2383377	33,257,914	A/G	1.081 (0.014)	2.36E-08
92	14	rs35607894	72,408,638	A/G	1.094 (0.014)	5.37E-11
93	14	rs8012642	84,669,481	C/G	1.055 (0.010)	4.66E-08
94	14	rs2693698	99,719,219	A/G	0.941 (0.011)	2.20E-08
95	15	rs35225048	61,856,263	T/C	0.935 (0.009)	7.77E-13
96	15	rs3825845	78,910,258	T/C	0.932 (0.011)	2.47E-10
97	15	rs783540	83,254,708	A/G	0.950 (0.009)	3.05E-08
98	15	rs950169	84,706,461	T/C	0.923 (0.012)	5.17E-12
99	15	rs758129	89,900,887	A/G	0.945 (0.010)	2.87E-08
100	16	rs6500596	4,470,027	T/G	0.939 (0.011)	5.24E-09
101	16	rs9922678	9,946,319	A/G	1.065 (0.011)	3.36E-09
102	16	rs7405404	13,749,859	T/C	1.073 (0.012)	8.06E-10
103	16	rs3814881	30,000,901	A/G	0.936 (0.009)	8.41E-13
104	16	rs8058130	64,371,163	A/G	0.948 (0.010)	4.77E-08
105	17	rs56007784	1,290,950	C/G	1.059 (0.009)	1.16E-09
106	17	rs8082590	17,958,402	A/G	0.936 (0.011)	7.40E-10
107	17	rs72843506	19,946,287	A/T	1.070 (0.012)	3.73E-08
108	17	rs35065479	55,736,735	A/G	1.066 (0.011)	2.31E-08
109	18	rs715170	53,795,514	T/C	0.928 (0.011)	5.21E-12
110	18	rs56775891	77,575,613	T/C	1.058 (0.010)	1.85E-08

110	18	rs28735056	77,622,879	A/G	0.941 (0.010)	4.60E-10
111	19	rs2053079	30,987,423	A/G	0.938 (0.011)	4.64E-09
112	22	rs5757730	39,967,430	A/G	0.933 (0.011)	1.84E-10
113	22	rs9607782	41,587,556	A/T	1.090 (0.012)	1.01E-12

Genomic position was based on the UCSC hg19/NCBI Build 37.

OR=odds ratio for A1 and SE=standard error.

The results are based on the meta-analysis of Chinese GWAS and replication samples (CHN) or all sample

[a] The SNPs also reached GWS in the meta-analysis of Chinese GWAS and replication samples.

[b] The LD results were based on the 1000Genome Project (European or Chinese samples).

[c] eMHC, the extended major histocompatibility complex region.

Reported SNP (LD)	Analysis
rs301797 (0.982; 0.869)	ALL
rs1498232 (1.000; 0.984)	ALL
rs11210892 (1.000; 1.000)	ALL
rs12129573 (0.553; 0.922)	ALL
rs1625579 (0.623; 1.000)	ALL
rs140505938 (0.573; 0.001)	ALL
rs6670165 (same)	ALL
rs14403 (0.122; 0.350)	ALL
rs12474906 (0.839; 0.716)	ALL
rs75575209 (same)	ALL
rs11682175 (0.351; 0.167)	CHN
Novel	ALL
Novel	ALL
Novel	ALL
rs2381759 (same)	ALL
rs11693094 (0.411; 0.662)	ALL
rs59979824 (0.873; 0.805)	ALL
rs6704641 (0.963; 1.000)	ALL
rs2949006 (0.973; 1.000)	ALL
rs1367858 (0.019; 0.110)	ALL
rs1367858 (NA; 0.054)	CHN
rs11685299 (same)	ALL
rs778371 (same)	ALL
rs17194490 (0.276; NA)	ALL
rs4330281 (same)	ALL
Novel	ALL
rs75968099 (0.910; 0.894)	ALL
Novel	CHN
rs2710323 (0.964; 0.736)	ALL
rs832190 (same)	ALL
rs66691851 (same)	ALL
rs28730912 (0.387; NA)	ALL
rs13096210 (0.265; 0.692)	ALL
rs9841616 (same)	ALL
rs215411 (same)	ALL
Novel	ALL
rs10520163 (0.989; 0.991)	ALL
rs1106568 (1.000; 0.959)	ALL

rs1501357 (0.982; 0.961)	ALL
Novel	ALL
Novel	ALL
rs4388249 (same)	ALL
Novel	ALL
rs3849046 (0.979; 0.991)	ALL
r5_140143664_I (NA; 1.00	ALL
rs111294930 (0.683; NA)	ALL
rs2910032 (same)	ALL
rs11740474 (same)	ALL
MHC[c], rs115329265 (same)	ALL
eMHC[c] (NA; NA)	CHN
Novel	ALL
rs3798869 (0.995; 0.993)	ALL
Novel	ALL
rs9398171 (same)	ALL
Novel	CHN
Novel	CHN
rs12668848 (same)	ALL
r7_24747494_D (NA; 0.99	ALL
rs2944829 (0.826; 0.996)	ALL
Novel	ALL
rs12704290 (same)	ALL
rs6466055 (1.000; 0.723)	ALL
rs13240464 (0.978; 0.829)	ALL
Novel	CHN
rs3735025 (same)	ALL
rs10503253 (0.985; 0.972)	ALL
rs2945232 (0.948; 0.832)	ALL
rs73191547 (0.158; 0.007)	ALL
Novel	ALL
Novel	ALL
rs16887244 (0.890; 0.950)	ALL
rs6984242 (1.000; 1.000)	ALL
rs7819570 (0.425; 0.027)	ALL
rs4642619 (0.958; 0.856)	ALL
rs4129585 (0.284; 0.476)	ALL
rs11139497 (0.560; 0.736)	ALL
rs7893279 (same)	ALL
Novel	ALL
rs7085104 (1.000; 0.993)	ALL

rs10883832 (0.714; 0.983)	ALL
rs12360997 (0.912; 0.362)	ALL
rs7951870 (0.981; 0.820)	ALL
rs9420 (same)	ALL
rs12421382 (same)	ALL
rs2514218 (same)	ALL
rs77502336 (same)	ALL
rs55661361 (same)	ALL
rs10791097 (0.299; 0.270)	ALL
rs75059851 (same)	ALL
rs75059851 (0.034; 0.001)	ALL
rs1006737 (1.000; 1.000)	ALL
rs12823424 (1.000; 1.000)	ALL
rs679087 (0.960; 0.992)	ALL
rs4240748 (same)	ALL
rs4766428 (same)	ALL
Novel	ALL
rs2851447 (0.091; 0.918)	ALL
rs2851447 (0.987; 0.813)	ALL
Novel	ALL
rs2068012 (0.062; 0.003)	ALL
Novel	ALL
rs2332700 (0.521; 0.104)	ALL
Novel	ALL
rs2693698 (same)	ALL
rs12903146 (0.963; 0.958)	ALL
rs8042374 (0.985; 0.315)	ALL
Novel	ALL
rs950169 (same)	ALL
Novel	ALL
Novel	ALL
rs9922678 (same)	ALL
rs7405404 (same)	ALL
rs12691307 (0.698; 0.857)	ALL
Novel	ALL
Novel	ALL
rs8082590 (same)	ALL
Novel	ALL
Novel	ALL
rs715170 (same)	ALL
Novel	ALL

Novel	ALL
rs2053079 (same)	ALL
rs5757717 (0.479; 0.004)	ALL
rs9607782 (same)	ALL

s (ALL), which were shown in the ‘Analysis’ column.

Supplementary Table 6. Results of the meta-analysis of the Chinese and PGC2 samples for the index S

ID in PGC2		Index SNP/Proxy	Chr.	Position	Alleles	PGC2		Chinese
Locus	SNP					OR (SE)	P value	OR (SE)
1	1	rs4648845	1	2,387,101	T/C	1.071 (0.012)	4.03E-09	NA
2	2	rs172531 (P)	1	8,495,590	A/G	0.936 (0.011)	6.29E-09	0.894 (0.034)
3	3	rs4949526 (P)	1	30,432,219	T/C	1.072 (0.012)	1.46E-09	1.044 (0.020)
4	4	rs11210892	1	44,100,084	G/A	1.072 (0.011)	4.97E-10	1.069 (0.024)
5	5	rs12129573	1	73,768,366	A/C	1.072 (0.011)	2.35E-10	1.027 (0.027)
6	6	rs36025579 (P)	1	97,802,624	A/G	0.948 (0.012)	8.20E-06	0.958 (0.018)
6	7	rs1198589 (P)	1	98,550,411	T/C	0.897 (0.014)	2.60E-14	0.968 (0.036)
7	8	rs12129037 (P)	1	150,492,114	T/C	1.100 (0.017)	3.43E-08	1.079 (0.037)
8	9	rs6670165	1	177,280,121	T/C	1.074 (0.014)	1.16E-07	1.068 (0.025)
9	10	rs7523273	1	207,977,083	A/G	1.062 (0.012)	1.61E-07	1.010 (0.029)
10	11	rs10803138	1	243,555,219	A/G	0.932 (0.013)	1.79E-08	1.016 (0.049)
10	12	rs77149735	1	243,555,105	A/G	1.329 (0.049)	4.40E-09	NA
10	13	rs14403	1	243,663,893	T/C	0.935 (0.013)	1.31E-07	0.937 (0.025)
10	14	rs35978510 (P)	1	243,776,117	T/C	0.940 (0.012)	1.25E-07	0.944 (0.018)
11	15	rs11682175	2	57,987,593	T/C	0.928 (0.011)	2.54E-12	0.949 (0.018)
11	16	rs75575209	2	58,138,192	A/T	0.896 (0.019)	1.01E-08	0.953 (0.054)
12	17	rs3768644	2	72,361,505	A/G	0.910 (0.018)	1.30E-07	NA
13	18	rs2381759 (P)	2	146,428,031	A/T	0.924 (0.014)	1.36E-08	0.957 (0.031)
14	19	rs12622667 (P)	2	149,520,186	T/C	0.920 (0.019)	1.69E-05	0.950 (0.020)
15	20	rs2909457	2	162,845,855	G/A	1.061 (0.011)	4.38E-08	0.949 (0.039)
16	21	rs7597593 (P)	2	185,533,580	T/C	1.068 (0.011)	1.47E-09	1.057 (0.023)
17	22	rs12619354 (P)	2	194,002,782	T/C	1.058 (0.011)	4.78E-07	1.050 (0.022)
18	23	rs6434928	2	198,304,577	A/G	0.927 (0.011)	1.48E-11	0.994 (0.021)
19	24	rs6704641	2	200,164,252	G/A	0.927 (0.014)	3.40E-08	0.938 (0.022)
20	25	rs796364 (P)	2	200,716,119	A/C	0.905 (0.013)	5.90E-14	0.930 (0.021)
21	26	rs11685299	2	225,391,296	A/C	0.937 (0.011)	1.11E-08	0.925 (0.020)
22	27	rs6704768	2	233,592,501	A/G	0.929 (0.011)	3.15E-12	0.952 (0.022)
23	28	rs11708578 (P)	3	2,515,894	A/G	0.927 (0.012)	5.56E-10	0.878 (0.059)
24	29	rs4330281	3	17,859,366	T/C	0.943 (0.011)	5.51E-08	0.894 (0.102)
25	30	rs3732386 (P)	3	36,871,993	T/C	1.078 (0.011)	1.73E-11	1.026 (0.046)
26	31	rs2577831 (P)	3	52,628,056	A/C	0.935 (0.011)	2.15E-10	0.938 (0.018)
27	32	rs832187	3	63,833,050	T/C	0.941 (0.011)	2.58E-08	0.954 (0.028)
28	33	rs7432375	3	136,288,405	G/A	1.074 (0.011)	5.27E-11	1.136 (0.028)
29	34	rs9859557 (P)	3	180,830,910	A/T	1.085 (0.013)	5.30E-10	1.135 (0.028)
29	35	rs9841616	3	181,167,585	A/T	0.922 (0.014)	1.65E-08	0.951 (0.029)
30	36	rs215411	4	23,423,603	A/T	1.067 (0.011)	1.22E-08	1.089 (0.034)
31	37	rs35518360	4	103,146,890	A/T	0.865 (0.020)	9.57E-13	NA

32	38	rs7438 (P)	4	170,642,246	A/G	1.062 (0.011)	2.13E-08	1.088 (0.025)
33	39	rs6846161 (P)	4	176,866,459	A/G	1.072 (0.012)	1.16E-08	1.052 (0.021)
34	40	rs1501357	5	45,364,875	C/T	1.080 (0.013)	1.24E-08	1.072 (0.023)
35	41	rs4391122	5	60,598,543	A/G	0.924 (0.011)	1.73E-13	0.989 (0.024)
36	42	rs16867576	5	88,746,331	A/G	1.101 (0.017)	1.36E-08	NA
37	43	rs4388249	5	109,036,066	T/C	1.075 (0.014)	1.03E-07	1.048 (0.019)
38	44	rs10043984	5	137,712,121	T/C	1.069 (0.012)	2.18E-08	1.018 (0.032)
38	45	rs13164092 (P)	5	137,840,860	A/G	0.941 (0.011)	1.11E-08	0.951 (0.023)
39	46	rs7733403 (P)	5	140,154,215	A/G	1.053 (0.011)	8.76E-07	1.051 (0.018)
40	47	rs79212538	5	151,993,104	T/G	1.152 (0.026)	3.84E-08	NA
40	48	rs113568682 (P)	5	152,299,754	A/T	1.068 (0.012)	2.50E-08	1.025 (0.036)
40	49	rs2973155	5	152,608,619	C/T	1.070 (0.011)	1.02E-09	1.022 (0.022)
40	50	rs7727515 (P)	5	152,892,304	A/G	0.910 (0.017)	5.84E-08	0.991 (0.033)
41	51	rs11740474	5	153,680,747	A/T	0.941 (0.011)	3.94E-08	0.952 (0.041)
42	52	rs115329265	6	28,712,247	A/G	1.213 (0.016)	0.00E-16	1.195 (0.041)
43	53	rs34321714 (P)	6	73,164,144	C/G	0.946 (0.011)	1.45E-07	0.982 (0.023)
44	54	rs217331 (P)	6	84,344,689	C/G	0.937 (0.011)	1.42E-09	0.924 (0.018)
45	55	rs117074560	6	96,459,651	T/C	0.855 (0.028)	1.66E-08	NA
46	56	rs12668848 (P)	7	2,020,995	A/G	0.923 (0.011)	8.70E-14	0.924 (0.021)
47	57	rs112509803 (P)	7	24,735,004	C/G	1.086 (0.017)	1.03E-06	1.117 (0.045)
48	58	rs12704290	7	86,427,626	A/G	0.899 (0.017)	1.04E-10	0.964 (0.040)
49	59	rs6466055	7	104,929,064	A/C	1.068 (0.011)	2.46E-09	1.066 (0.024)
50	60	rs7807720 (P)	7	110,073,755	A/G	1.055 (0.011)	8.97E-07	1.047 (0.023)
51	61	rs214467 (P)	7	110,858,268	A/G	1.081 (0.011)	3.32E-12	1.047 (0.021)
52	62	rs7801375	7	131,567,263	A/G	0.920 (0.015)	2.26E-08	0.994 (0.051)
53	63	rs3735025	7	137,074,844	T/C	1.066 (0.011)	7.75E-09	1.076 (0.019)
54	64	rs13261217 (P)	8	4,183,057	A/G	0.933 (0.013)	4.77E-08	0.941 (0.024)
55	65	rs11778040 (P)	8	27,419,807	T/C	0.931 (0.014)	1.94E-07	0.990 (0.034)
56	66	rs6984242	8	60,700,469	G/A	1.067 (0.011)	1.76E-09	1.031 (0.024)
57	67	rs7010876 (P)	8	89,264,751	A/T	0.941 (0.012)	3.30E-07	0.926 (0.031)
58	68	rs16880831 (P)	8	111,561,505	T/G	0.926 (0.013)	3.31E-09	0.947 (0.025)
59	69	rs13266463 (P)	8	143,403,693	A/G	0.941 (0.011)	1.26E-08	0.976 (0.023)
60	70	rs11139497	9	84,739,941	T/A	0.934 (0.012)	3.09E-09	0.979 (0.030)
61	71	rs7893279	10	18,745,105	T/G	1.120 (0.017)	3.56E-11	1.108 (0.034)
62	72	rs10786736 (P)	10	104,849,116	C/G	0.896 (0.017)	4.56E-11	0.900 (0.020)
62	73	rs11191424 (P)	10	104,625,886	A/G	0.910 (0.011)	0.00E-16	0.935 (0.018)
62	74	rs55833108	10	104,741,583	T/G	1.078 (0.013)	1.42E-08	0.988 (0.041)
62	75	r10_104957618_	10	104,957,618	I2/D	0.842 (0.023)	1.04E-13	NA
63	76	rs11027857	11	24,403,620	A/G	1.065 (0.011)	3.21E-09	1.012 (0.024)
64	77	rs61882743 (P)	11	46,548,754	C/G	0.913 (0.014)	1.26E-10	0.917 (0.037)
65	78	rs9420	11	57,510,294	A/G	1.063 (0.011)	6.65E-08	1.052 (0.025)

66	79	rs12421382	11	109,378,071	T/C	0.943 (0.011)	1.72E-07	0.955 (0.021)
67	80	rs2514218	11	113,392,994	T/C	0.930 (0.012)	4.09E-10	0.881 (0.055)
68	81	rs77502336	11	123,394,636	C/G	1.071 (0.011)	2.01E-09	1.035 (0.021)
69	82	rs55661361	11	124,613,957	A/G	0.925 (0.011)	3.68E-12	0.957 (0.020)
70	83	rs10894308 (P)	11	130,891,895	A/G	0.940 (0.011)	7.52E-09	0.981 (0.023)
71	84	rs75059851	11	133,822,569	A/G	1.096 (0.014)	1.23E-11	1.128 (0.053)
72	85	rs2159100 (P)	12	2,346,393	T/C	1.100 (0.011)	0.00E-16	1.134 (0.039)
72	86	rs2239063	12	2,511,831	A/C	1.071 (0.012)	5.39E-09	1.023 (0.021)
73	87	rs302321 (P)	12	29,928,388	A/C	0.943 (0.011)	1.38E-07	0.914 (0.021)
74	88	rs324017	12	57,487,814	A/C	0.941 (0.012)	2.13E-07	1.014 (0.030)
74	89	rs12826178	12	57,622,371	T/G	0.846 (0.024)	5.30E-12	NA
75	90	rs4240748	12	92,246,786	C/G	0.943 (0.011)	1.03E-07	0.966 (0.021)
76	91	rs10860964	12	103,596,455	C/T	0.943 (0.011)	9.92E-08	1.058 (0.038)
77	92	rs4766428	12	110,723,245	T/C	1.071 (0.011)	7.09E-10	1.005 (0.037)
78	93	rs2851447	12	123,665,113	G/C	1.095 (0.012)	2.10E-14	1.081 (0.024)
79	94	rs1191551 (P)	14	30,000,405	T/G	1.073 (0.013)	5.39E-08	1.095 (0.073)
80	95	rs35607894 (P)	14	72,408,638	A/G	1.088 (0.014)	4.96E-09	1.154 (0.044)
81	96	rs2693698	14	99,719,219	A/G	0.939 (0.011)	1.38E-08	0.992 (0.057)
82	97	rs12887734	14	104,046,834	T/G	1.091 (0.012)	1.18E-13	1.022 (0.022)
83	98	rs56205728	15	40,567,237	A/G	1.070 (0.012)	4.92E-08	0.875 (0.062)
84	99	rs12903146	15	61,854,663	A/G	1.067 (0.011)	1.04E-09	1.097 (0.025)
85	100	rs12148337	15	70,589,272	T/C	1.059 (0.011)	5.33E-08	1.025 (0.018)
86	101	rs3825845 (P)	15	78,910,258	T/C	0.922 (0.013)	1.34E-10	0.968 (0.023)
86	102	rs190065944	15	78,859,610	A/G	1.078 (0.014)	7.22E-08	1.089 (0.101)
87	103	rs950169	15	84,706,461	T/C	0.924 (0.012)	7.62E-11	0.911 (0.040)
88	104	rs11539637 (P)	15	91,428,290	T/C	1.065 (0.011)	8.60E-09	1.140 (0.029)
89	105	rs9922678	16	9,946,319	A/G	1.070 (0.012)	6.72E-09	1.041 (0.028)
90	106	rs7405404	16	13,749,859	T/C	1.081 (0.013)	3.93E-10	1.029 (0.030)
91	107	rs12691307	16	29,939,877	G/A	0.932 (0.011)	1.30E-10	0.942 (0.029)
92	108	rs12325245	16	58,681,393	A/T	0.916 (0.015)	1.15E-08	0.979 (0.029)
93	109	rs8044995	16	68,189,340	A/G	1.081 (0.014)	3.27E-08	1.003 (0.034)
94	110	rs4523957	17	2,208,899	T/G	1.071 (0.011)	1.04E-09	1.004 (0.023)
95	111	rs8082590	17	17,958,402	A/G	0.936 (0.012)	6.84E-09	0.936 (0.032)
96	112	rs7233277 (P)	18	52,741,518	A/G	1.053 (0.011)	1.10E-06	1.005 (0.020)
96	113	rs78322266	18	53,063,676	T/G	1.194 (0.031)	1.10E-08	NA
96	114	rs9636107	18	53,200,117	A/G	0.927 (0.011)	9.10E-13	1.028 (0.032)
97	115	rs72934570	18	53,533,189	T/C	0.865 (0.021)	3.67E-12	NA
97	116	rs715170	18	53,795,514	T/C	0.936 (0.012)	3.47E-08	0.893 (0.025)
98	117	rs3764567 (P)	19	19,440,066	T/C	0.944 (0.011)	1.63E-07	1.025 (0.021)
99	118	rs2053079	19	30,987,423	A/G	0.929 (0.012)	3.79E-09	0.969 (0.023)
100	119	rs56873913	19	50,091,199	T/G	1.069 (0.013)	2.19E-07	1.024 (0.027)

101	120	rs6065094	20	37,453,194	A/G	0.928 (0.011)	5.52E-11	0.981 (0.024)
102	121	rs7267348	20	48,131,036	T/C	0.938 (0.012)	1.18E-07	0.978 (0.022)
103	122	rs5757730 (P)	22	39,967,430	A/G	0.934 (0.011)	7.75E-10	0.915 (0.054)
104	123	rs9607782	22	41,587,556	A/T	1.091 (0.013)	6.76E-12	1.083 (0.040)
105	124	rs1023500	22	42,340,844	T/C	1.076 (0.014)	5.04E-08	1.006 (0.027)
105	125	rs6002655	22	42,603,814	T/C	1.068 (0.011)	1.48E-09	1.008 (0.021)
106	126	rs12845396	23	6,029,533	T/A	1.052 (0.010)	3.14E-07	1.003 (0.031)
107	127	rs1378559	23	21,380,266	C/T	0.919 (0.013)	1.68E-11	0.957 (0.029)
108	128	rs5937157	23	68,377,126	G/T	1.071 (0.010)	5.74E-11	1.117 (0.055)

The ID for Loci and SNP is from the PGC2 report (***Nature*** 511, 421–427, 2014).

The SNP followed by (P) indicated a proxy of the index SNP.

Genomic position was based on the UCSC hg19/NCBI Build 37.

OR=odds ratio for A1 and SE=standard error.

I^2 index represents the degree of heterogeneity.

PGC2+Chinese (Fixed) are the results under a fixed-effects model meta-analysis.

NPs or their proxies identified in the PGC2 report

Chinese	PGC2+Chinese			PGC2+Chinese (Fixed)	
P value	OR (SE)	P value	I2	OR (SE)	P value
NA	NA	NA	NA	NA	NA
9.26E-04	0.931 (0.011)	5.05E-11	39	0.931 (0.011)	5.05E-11
3.11E-02	1.065 (0.010)	2.81E-10	20	1.065 (0.010)	2.81E-10
6.11E-03	1.071 (0.010)	1.17E-11	0	1.071 (0.010)	1.17E-11
3.26E-01	1.065 (0.010)	5.14E-10	53	1.065 (0.010)	5.14E-10
1.92E-02	0.951 (0.010)	5.31E-07	0	0.951 (0.010)	5.31E-07
3.67E-01	0.907 (0.013)	1.20E-13	75	0.907 (0.013)	1.20E-13
4.06E-02	1.096 (0.016)	4.51E-09	0	1.096 (0.016)	4.51E-09
7.71E-03	1.073 (0.012)	3.37E-09	0	1.073 (0.012)	3.37E-09
7.16E-01	1.055 (0.011)	6.26E-07	62	1.055 (0.011)	6.26E-07
7.44E-01	0.937 (0.012)	8.31E-08	66	0.937 (0.012)	8.31E-08
NA	NA	NA	NA	NA	NA
8.90E-03	0.935 (0.011)	3.63E-09	0	0.935 (0.011)	3.63E-09
1.49E-03	0.941 (0.010)	6.50E-10	0	0.941 (0.010)	6.50E-10
4.46E-03	0.934 (0.009)	7.30E-14	10	0.934 (0.009)	7.30E-14
3.74E-01	0.902 (0.018)	1.24E-08	16	0.902 (0.018)	1.24E-08
NA	NA	NA	NA	NA	NA
1.57E-01	0.929 (0.013)	8.63E-09	11	0.929 (0.013)	8.63E-09
1.05E-02	0.935 (0.014)	1.14E-06	27	0.935 (0.014)	1.14E-06
1.79E-01	1.010 (0.055)	8.62E-01	87	1.052 (0.010)	9.30E-07
1.61E-02	1.066 (0.010)	9.30E-11	0	1.066 (0.010)	9.30E-11
2.43E-02	1.056 (0.010)	3.81E-08	0	1.056 (0.010)	3.81E-08
7.88E-01	0.958 (0.035)	2.21E-01	89	0.942 (0.010)	1.50E-09
3.57E-03	0.930 (0.012)	4.75E-10	0	0.930 (0.012)	4.75E-10
5.48E-04	0.912 (0.011)	0.00E-16	21	0.912 (0.011)	0.00E-16
9.36E-05	0.934 (0.010)	4.70E-12	0	0.934 (0.010)	4.70E-12
2.68E-02	0.933 (0.010)	4.49E-13	0	0.933 (0.010)	4.49E-13
2.75E-02	0.925 (0.012)	7.28E-11	0	0.925 (0.012)	7.28E-11
2.72E-01	0.942 (0.011)	3.04E-08	0	0.942 (0.011)	3.04E-08
5.81E-01	1.075 (0.011)	2.88E-11	11	1.075 (0.011)	2.88E-11
4.40E-04	0.936 (0.009)	4.53E-13	0	0.936 (0.009)	4.53E-13
9.26E-02	0.943 (0.010)	6.60E-09	0	0.943 (0.010)	6.60E-09
6.41E-06	1.082 (0.010)	1.00E-14	71	1.082 (0.010)	1.00E-14
8.04E-06	1.094 (0.012)	6.00E-14	52	1.094 (0.012)	6.00E-14
7.89E-02	0.928 (0.013)	5.35E-09	0	0.928 (0.013)	5.35E-09
1.27E-02	1.069 (0.011)	6.37E-10	0	1.069 (0.011)	6.37E-10
NA	NA	NA	NA	NA	NA

6.36E-04	1.066 (0.010)	7.46E-11	0	1.066 (0.010)	7.46E-11
1.83E-02	1.067 (0.011)	9.96E-10	0	1.067 (0.011)	9.96E-10
2.55E-03	1.078 (0.012)	1.10E-10	0	1.078 (0.012)	1.10E-10
6.40E-01	0.953 (0.034)	1.53E-01	85	0.935 (0.010)	4.77E-12
NA	NA	NA	NA	NA	NA
1.54E-02	1.066 (0.011)	8.38E-09	12	1.066 (0.011)	8.38E-09
5.77E-01	1.063 (0.011)	5.73E-08	53	1.063 (0.011)	5.73E-08
2.76E-02	0.943 (0.010)	9.79E-10	0	0.943 (0.010)	9.79E-10
6.90E-03	1.052 (0.009)	2.06E-08	0	1.052 (0.009)	2.06E-08
NA	NA	NA	NA	NA	NA
4.84E-01	1.064 (0.011)	3.77E-08	15	1.064 (0.011)	3.77E-08
3.39E-01	1.060 (0.010)	3.42E-09	71	1.060 (0.010)	3.42E-09
7.89E-01	0.945 (0.042)	1.84E-01	81	0.927 (0.015)	8.47E-07
2.25E-01	0.941 (0.011)	1.81E-08	0	0.941 (0.011)	1.81E-08
1.56E-05	1.210 (0.015)	0.00E-16	0	1.210 (0.015)	0.00E-16
4.14E-01	0.952 (0.010)	3.12E-07	55	0.952 (0.010)	3.12E-07
1.92E-05	0.934 (0.009)	1.63E-13	0	0.934 (0.009)	1.63E-13
NA	NA	NA	NA	NA	NA
1.32E-04	0.923 (0.010)	0.00E-16	0	0.923 (0.010)	0.00E-16
1.28E-02	1.090 (0.016)	4.80E-08	0	1.090 (0.016)	4.80E-08
3.56E-01	0.908 (0.015)	2.61E-10	62	0.908 (0.015)	2.61E-10
7.10E-03	1.068 (0.010)	6.39E-11	0	1.068 (0.010)	6.39E-11
5.13E-02	1.054 (0.010)	1.36E-07	0	1.054 (0.010)	1.36E-07
2.67E-02	1.073 (0.010)	7.69E-13	48	1.073 (0.010)	7.69E-13
9.02E-01	0.926 (0.014)	6.03E-08	53	0.926 (0.014)	6.03E-08
1.08E-04	1.068 (0.010)	3.60E-12	0	1.068 (0.010)	3.60E-12
1.20E-02	0.934 (0.011)	2.12E-09	0	0.934 (0.011)	2.12E-09
7.59E-01	0.939 (0.013)	8.31E-07	64	0.939 (0.013)	8.31E-07
2.04E-01	1.060 (0.010)	1.86E-09	42	1.060 (0.010)	1.86E-09
1.28E-02	0.939 (0.011)	1.48E-08	0	0.939 (0.011)	1.48E-08
2.95E-02	0.930 (0.012)	4.34E-10	0	0.930 (0.012)	4.34E-10
2.84E-01	0.947 (0.010)	2.25E-08	52	0.947 (0.010)	2.25E-08
4.92E-01	0.940 (0.011)	7.82E-09	53	0.940 (0.011)	7.82E-09
2.21E-03	1.117 (0.015)	3.29E-13	0	1.117 (0.015)	3.29E-13
1.96E-07	0.897 (0.013)	0.00E-16	0	0.897 (0.013)	0.00E-16
1.81E-04	0.917 (0.009)	0.00E-16	37	0.917 (0.009)	0.00E-16
7.73E-01	1.041 (0.043)	3.45E-01	76	1.069 (0.013)	1.10E-07
NA	NA	NA	NA	NA	NA
6.26E-01	1.056 (0.010)	2.15E-08	73	1.056 (0.010)	2.15E-08
1.92E-02	0.914 (0.013)	6.99E-12	0	0.914 (0.013)	6.99E-12
4.17E-02	1.061 (0.010)	8.52E-09	0	1.061 (0.010)	8.52E-09

2.57E-02	0.945 (0.010)	1.51E-08	0	0.945 (0.010)	1.51E-08
2.02E-02	0.928 (0.011)	5.01E-11	0	0.928 (0.011)	5.01E-11
1.02E-01	1.063 (0.010)	1.35E-09	48	1.063 (0.010)	1.35E-09
3.16E-02	0.932 (0.010)	1.16E-12	55	0.932 (0.010)	1.16E-12
3.98E-01	0.947 (0.010)	2.09E-08	64	0.947 (0.010)	2.09E-08
2.34E-02	1.098 (0.013)	8.78E-13	0	1.098 (0.013)	8.78E-13
1.40E-03	1.102 (0.011)	0.00E-16	0	1.102 (0.011)	0.00E-16
2.67E-01	1.060 (0.010)	1.77E-08	73	1.060 (0.010)	1.77E-08
1.26E-05	0.937 (0.010)	2.07E-11	46	0.937 (0.010)	2.07E-11
6.41E-01	0.972 (0.037)	4.42E-01	82	0.950 (0.011)	2.87E-06
NA	NA	NA	NA	NA	NA
1.07E-01	0.948 (0.010)	4.55E-08	5	0.948 (0.010)	4.55E-08
1.31E-01	0.993 (0.058)	9.09E-01	89	0.952 (0.011)	2.53E-06
8.86E-01	1.065 (0.011)	2.60E-09	62	1.065 (0.011)	2.60E-09
1.34E-03	1.092 (0.011)	0.00E-16	0	1.092 (0.011)	0.00E-16
2.10E-01	1.074 (0.013)	2.28E-08	0	1.074 (0.013)	2.28E-08
1.22E-03	1.094 (0.014)	5.37E-11	38	1.094 (0.014)	5.37E-11
8.93E-01	0.941 (0.011)	2.20E-08	0	0.941 (0.011)	2.20E-08
3.09E-01	1.059 (0.032)	7.75E-02	86	1.075 (0.010)	1.95E-12
3.24E-02	0.977 (0.100)	8.13E-01	90	1.062 (0.012)	8.21E-07
1.47E-04	1.072 (0.010)	1.09E-12	10	1.072 (0.010)	1.09E-12
1.77E-01	1.050 (0.009)	6.29E-08	59	1.050 (0.009)	6.29E-08
1.54E-01	0.932 (0.011)	2.47E-10	70	0.932 (0.011)	2.47E-10
3.94E-01	1.078 (0.014)	4.54E-08	0	1.078 (0.014)	4.54E-08
1.79E-02	0.923 (0.012)	5.17E-12	0	0.923 (0.012)	5.17E-12
4.37E-06	1.096 (0.033)	5.92E-03	80	1.075 (0.010)	2.18E-12
1.46E-01	1.065 (0.011)	3.36E-09	0	1.065 (0.011)	3.36E-09
3.46E-01	1.073 (0.012)	8.06E-10	58	1.073 (0.012)	8.06E-10
3.85E-02	0.933 (0.010)	1.65E-11	0	0.933 (0.010)	1.65E-11
4.62E-01	0.943 (0.033)	7.51E-02	76	0.930 (0.013)	7.36E-08
9.24E-01	1.048 (0.037)	1.98E-01	75	1.069 (0.013)	2.82E-07
8.81E-01	1.040 (0.032)	2.25E-01	84	1.058 (0.010)	2.68E-08
3.65E-02	0.936 (0.011)	7.40E-10	0	0.936 (0.011)	7.40E-10
8.15E-01	1.032 (0.023)	1.82E-01	77	1.042 (0.009)	9.38E-06
NA	NA	NA	NA	NA	NA
3.78E-01	0.972 (0.052)	5.85E-01	90	0.936 (0.010)	9.69E-11
NA	NA	NA	NA	NA	NA
7.86E-06	0.928 (0.011)	5.21E-12	64	0.928 (0.011)	5.21E-12
2.31E-01	0.982 (0.041)	6.59E-01	92	0.961 (0.010)	5.17E-05
1.64E-01	0.938 (0.011)	4.64E-09	61	0.938 (0.011)	4.64E-09
3.80E-01	1.061 (0.012)	4.15E-07	53	1.061 (0.012)	4.15E-07

4.12E-01	0.950 (0.027)	5.91E-02	77	0.938 (0.010)	3.25E-10
3.09E-01	0.947 (0.011)	2.99E-07	66	0.947 (0.011)	2.99E-07
1.02E-01	0.933 (0.011)	1.84E-10	0	0.933 (0.011)	1.84E-10
4.78E-02	1.090 (0.012)	1.01E-12	0	1.090 (0.012)	1.01E-12
8.15E-01	1.045 (0.033)	1.89E-01	80	1.062 (0.012)	6.52E-07
6.97E-01	1.041 (0.029)	1.61E-01	83	1.056 (0.010)	2.60E-08
9.15E-01	1.047 (0.009)	8.75E-07	54	1.047 (0.009)	8.75E-07
1.31E-01	0.925 (0.011)	1.03E-11	37	0.925 (0.011)	1.03E-11
4.32E-02	1.072 (0.010)	8.56E-12	0	1.072 (0.010)	8.56E-12

Supplementary Table 8. GWS schizophrenia loci and notable genes

Locus ID	Chr.	SNP	Position	P value
1	1	rs172531	8495590	5.05E-11
2	1	rs4949526	30432219	2.81E-10
3	1	rs2970610	44097530	1.24E-12
4	1	rs11210195	73749283	1.76E-09
5	1	rs1198589	98550411	1.20E-13
6	1	rs12129037	150492114	4.51E-09
7	1	rs6670165	177280121	3.37E-09
8	1	rs35978510	243776117	6.50E-10
9	2	rs12623170	28020157	2.52E-08
10	2	rs75575209	58138192	1.24E-08
10	2	rs1518395	58208074	3.79E-13
11	2	rs999494	73157395	2.40E-10
12	2	rs62152284	104984387	5.86E-09
13	2	rs6430491	134840967	9.55E-10
14	2	rs2381759	146428031	8.63E-09
15	2	rs7597593	185533580	9.30E-11
16	2	rs12619354	194002782	3.81E-08
17	2	rs895526	200162425	9.27E-10
18	2	rs796364	200716119	0.00E-16
18	2	rs17630293	201146776	3.32E-12
18	2	rs78681500	201187316	3.08E-10
19	2	rs11685299	225391296	4.70E-12
20	2	rs778371	233743109	2.18E-13
21	3	rs11708578	2515894	7.28E-11
22	3	rs4330281	17859366	3.04E-08
23	3	rs10510653	32058559	2.54E-08
24	3	rs3732386	36871993	2.88E-11
25	3	rs2073499	50374293	2.61E-08
26	3	rs2577831	52628056	4.53E-13
27	3	rs832190	63842629	3.93E-08
28	3	rs66691851	136154828	4.00E-15
29	3	rs6804239	161780488	8.41E-10
30	3	rs9859557	180830910	6.00E-14
30	3	rs9841616	181167585	5.35E-09
31	4	rs215411	23423603	6.37E-10
32	4	rs11722779	103827488	3.40E-08

33	4	rs7438	170642246	7.46E-11
34	4	rs6846161	176866459	9.96E-10
35	5	rs9292918	45301035	4.47E-11
36	5	rs10940346	49806042	1.11E-08
37	5	rs2247870	90151589	2.54E-08
38	5	rs4388249	109036066	8.38E-09
39	5	rs2764766	127213625	1.94E-08
40	5	rs13164092	137840860	9.79E-10
41	5	rs7733403	140154215	2.06E-08
42	5	rs113568682	152299754	3.77E-08
42	5	rs2910032	152540354	1.04E-09
43	5	rs11740474	153680747	1.81E-08
44	6	rs115329265	28712247	0.00E-16
44	6	rs111782145	30873508	1.80E-08
45	6	rs6903570	64866857	2.70E-08
46	6	rs217331	84344689	1.63E-13
47	6	rs160593	105466332	7.69E-09
48	6	rs9398171	108983527	1.85E-11
49	6	rs7757969	112132032	4.82E-08
50	6	rs4479915	165075601	4.82E-09
51	7	rs12668848	2020995	0.00E-16
52	7	rs112509803	24735004	4.80E-08
53	7	rs2944823	71795470	3.21E-08
54	7	rs323167	78336677	4.47E-08
55	7	rs12704290	86427626	2.61E-10
56	7	rs2057884	104930250	2.02E-12
57	7	rs214467	110858268	7.69E-13
58	7	rs11534004	113467444	1.71E-08
59	7	rs3735025	137074844	3.60E-12
60	8	rs13261217	4183057	2.12E-09
61	8	rs2980436	8092025	2.31E-08
62	8	rs12543645	10246325	3.32E-08
63	8	rs17687067	17036201	3.39E-12
64	8	rs73219805	26272768	1.94E-11
65	8	rs112537273	38248306	1.06E-11
66	8	rs867743	60694647	4.97E-09
67	8	rs7010876	89264751	1.48E-08
68	8	rs16880831	111561505	4.34E-10

69	8	rs13266463	143403693	2.25E-08
70	9	rs2767713	84799537	2.02E-08
71	10	rs7893279	18745105	3.29E-13
72	10	rs111364339	64857872	5.37E-09
73	10	rs11191424	104625886	0.00E-16
73	10	rs10786736	104849116	0.00E-16
74	11	rs17234749	24381898	5.39E-09
75	11	rs61882743	46548754	6.99E-12
76	11	rs9420	57510294	8.52E-09
77	11	rs12421382	109378071	1.51E-08
78	11	rs2514218	113392994	5.01E-11
79	11	rs77502336	123394636	1.35E-09
80	11	rs55661361	124613957	1.16E-12
81	11	rs10894308	130891895	2.09E-08
82	11	rs75059851	133822569	8.78E-13
82	11	rs619091	133884137	5.85E-09
83	12	rs2159100	2346393	0.00E-16
83	12	rs758117	2513309	1.68E-08
84	12	rs302321	29928388	2.07E-11
85	12	rs4240748	92246786	4.55E-08
86	12	rs4766428	110723245	2.60E-09
87	12	rs28607014	117708611	1.75E-08
88	12	rs61041384	123644043	5.50E-13
88	12	rs1615350	123650335	0.00E-16
89	14	rs10148671	29469373	4.46E-08
90	14	rs1191551	30000405	2.28E-08
91	14	rs2383377	33257914	2.36E-08
92	14	rs35607894	72408638	5.37E-11
93	14	rs8012642	84669481	4.66E-08
94	14	rs2693698	99719219	2.20E-08
95	15	rs35225048	61856263	7.77E-13
96	15	rs3825845	78910258	2.47E-10
97	15	rs783540	83254708	3.05E-08
98	15	rs950169	84706461	5.17E-12
99	15	rs758129	89900887	2.87E-08
100	16	rs6500596	4470027	5.24E-09
101	16	rs9922678	9946319	3.36E-09
102	16	rs7405404	13749859	8.06E-10

103	16	rs3814881	30000901	8.41E-13
104	16	rs8058130	64371163	4.77E-08
105	17	rs56007784	1290950	1.16E-09
106	17	rs8082590	17958402	7.40E-10
107	17	rs72843506	19946287	3.73E-08
108	17	rs35065479	55736735	2.31E-08
109	18	rs715170	53795514	5.21E-12
110	18	rs56775891	77575613	1.85E-08
110	18	rs28735056	77622879	4.60E-10
111	19	rs2053079	30987423	4.64E-09
112	22	rs5757730	39967430	1.84E-10
113	22	rs9607782	41587556	1.01E-12

Genomic position was based on the UCSC hg19/NCBI Build 37.

[a]Notable genes from gene nearest to the index SNP (N); Schizophrenia-associated variant is in strong LD (r2 ⩾0.8) w

Notable gene(s)[a]
RERE (N, Q), *SLC45A1* (Q)
MATN1 (N), *PTPRU* (Q)
KDM4A (D), *MED8* (Q), *PTPRF* (N), *ST3GAL3* (D)
LRRIQ3 (N)
MIR137 (N)
ECM1 (N), *MRPS21* (S), *RPRD2* (M, D)
FAM5B (N, M, D)
AKT3 (N, D, Q)
RBKS (N)
VRK2 (N)
VRK2 (N)
EMX1 (N, D)
LOC100287010 (N)
MIR3679 (N)
TEX41 (N)
ZNF804A (N, D)
PCGEM1 (N)
SATB2 (N, D)
ERGIC3 (Q), *FONG* (N), *TYW5* (Q)
SPATS2L (N)
SPATS2L (N)
CUL3 (N)
C2orf82 (Q), *NGEF* (N, D)
CNTN4 (N, Q)
TBC1D5 (N, D)
GPD1L (Q), *ZNF860* (N)
DCLK3 (Q), *MLH1* (Q), *TRANK1* (N)
HYAL3 (Q), *RASSF1* (N)
GLT8D1 (Q), *GLYCTK* (Q), *GNL3* (M, Q, S), *NEK4* (Q), *PBRM1* (N, D), *SFMBT1* (Q), *SPCS1* (M)
ATXN7 (D), *THOC7* (N, Q)
MSL2 (D), *PCCB* (Q, S), *STAG1* (N, D), *TMEM22* (D)
OTOL1 (N)
DNAJC19 (N), *SOX2OT* (D)
SOX2OT (N)
MIR548AJ2 (N)
BDH2 (Q), *CENPE* (Q), *CISD2* (Q), *KRT8P46* (Q), *LRRC37A15P* (Q), *NHEDC1* (N), *SLC9B1* (Q)

CLCN3 (N, D, Q), *NEK1* (D)
GPM6A (N, D)
HCN1 (N, D)
EMB (N, Q)
ADGRV1 (N, M, D)
MAN2A1 (N, Q)
LINC01184 (N)
EGR1 (D), *ETF1* (N, S)
NDUFA2 (Q), *PCDHA1* (N, M, Q, S), *PCDHA10* (Q), *PCDHA13* (Q), *PCDHA2* (M, Q), *PCDHA3* (M, D, Q), *PCDHA4* (M, Q), *PCDHA5* (M, D), *PCDHA7* (Q), *PCDHA8* (M, Q), *PCDHAC2* (D, Q), *PCDHB3* (Q), *SRA1* (Q), *TMCO6* (Q), *WDR55* (Q, S), *ZMAT2* (Q)
GRIA1 (D), *NMUR2* (N)
GRIA1 (N, D)
GALNT10 (N)
ZKSCAN3 (Q), *ZNF323* (Q), *ZSCAN23* (Q)
CDSN (M), *DPCR1* (M), *GTF2H4* (N)
EYS (N), *PHF3* (D), *PTP4A1* (D)
MRAP2 (Q), *SNAP91* (N, D, Q)
HACE1 (Q), *LIN28B* (N, Q)
FOXO3 (N), *ZNF259P1* (Q)
FYN (N, Q)
C6orf118 (N)
FTSJ2 (Q), *MAD1L1* (N)
DFNA5 (N)
CALN1 (N, Q)
MAGI2 (N, D)
DMTF1 (D), *GRM3* (N, D), *KIAA1324L* (D)
MLL5 (D), *SRPK2* (N, D)
IMMP2L (N, Q), *LRRN3* (D)
PPP1R3A (N, M)
DGKI (N)
CSMD1 (N, D)
ERI1 (Q), *FAM85B* (Q, S), *FAM86B3P* (Q, S), *FAM86C1* (N)
MSRA (N, D)
MTMR7 (Q), *VPS37A* (Q), *ZDHHC2* (N, D, Q)
BNIP3L (N, D), *PPP2R2A* (D), *SDAD1P1* (Q)
BAG4 (Q), *DDHD2* (Q), *LETM2* (N), *LSM1* (S), *WHSC1L1* (D, Q)
CA8 (N)
MMP16 (N, D)
KCNV1 (N, D)

TSNARE1 (N)
FAM75D1 (N)
CACNB2 (N, D)
JMJD1C (D), *NRBF2* (N)
ARL3 (Q), *AS3MT* (Q), *C10orf32* (Q), *C10orf32-AS3MT* (N), *CNNM2* (Q), *WBP1L* (Q)
C10orf32 (Q), *INA* (Q), *NT5C2* (N, Q)
LUZP2 (N)
AMBRA1 (N, D), *CHRM4* (D), *DGKZ* (D), *MDK* (Q)
C11orf31 (N), *MED19* (Q), *YPEL4* (D), *ZDHHC5* (Q, S)
C11orf87 (N, D)
DRD2 (N, D)
GRAMD1B (N, D)
NRGN (N, D)
SNX19 (N, Q)
IGSF9B (N, D)
LOC100128239 (N)
CACNA1C (N)
CACNA1C (N)
TMTC1 (N, Q)
BTG1 (N)
ANAPC7 (Q), *ATP2A2* (N, D)
NOS1 (N)
MPHOSPH9 (N, M)
ABCB9 (D, Q), *MPHOSPH9* (N), *OGFOD2* (Q), *PITPNM2* (D), *SETD8* (D, Q)
LINC01551 (N)
MIR548AI (N)
AKAP6 (N, D), *NPAS3* (D)
RGS6 (N, D, Q)
FLRT2 (N)
BCL11B (N, D)
VPS13C (N)
CHRNA3 (N), *PSMA4* (Q)
AP3B2 (D, Q), *CPEB1* (N, Q)
ADAMTSL3 (N, M), *CSPG4P11* (Q, S), *CSPG4P5* (Q), *EFTUD1P1* (Q), *ZSCAN2* (Q)
MIR9-3 (N), *POLG* (D), *RLBP1* (Q)
CDIP1 (Q), *CORO7* (N, D, Q), *DNAJA3* (M, Q), *NMRAL1* (Q, S)
GRIN2A (N, D)
ERCC4 (N)

ASPHD1 (D), *DOC2A* (M, D, Q), *FAM57B* (D), *INO80E* (D, Q, S), *KCTD13* (D), *MAPK3* (Q), *SEZ6L2* (Q), *TAOK2* (N, D), *TMEM219* (Q), *YPEL3* (D, Q)
CDH11 (N)
YWHAE (N)
ATPAF2 (Q), *C17ORF39* (N, S), *DRG2* (Q), *LRRC48* (M), *RAI1* (D), *SREBF1* (Q), *TOM1L2* (D, Q)
AKAP10 (D), *CCDC144CP* (Q), *SPECC1* (N, D, Q), *USP32P3* (Q)
TSPOAP1-AS1 (Q), *MSI2* (N)
LINC01539 (N), *TCF4* (D)
KCNG2 (N, Q, S)
KCNG2 (N)
ZNF536 (N, D)
CACNA1I (N)
CSDC2 (Q), *EP300* (N, D), *MCHR1* (Q), *POLR3H* (Q), *RANGAP1* (Q), *XPNPEP3* (Q), *ZC3H7B* (D)

Supplementary Table 9. The fine-mapping regions for schizophrenia GWS loci in different data sets.

Locus ID	Chr.	99% credible set: Starting co-ordinate ,Interval; (number of overlapped genes)	
		PGC2	**CHN**
1	1	8390054, 113189; (2)	7497299, 1997802; (20)
2	1	30427639, 31388; 0	29433064, 1998113; (15)
3	1	44037685, 72065; (1)	43097894, 1998867; (46)
4	1	73275828, 715965; (1)	72749726, 1999474; (5)
5	1	98470051, 86109; (3)	97550864, 1998978; (10)
6	1	149999764, 857412; (24)	149815323, 1671375; (65)
7	1	176957925, 1313556; (8)	176281402, 1998252; (9)
8	1	243376757, 723646; (5)	242777164, 1998893; (10)
9	2	27020321, 1997154; (49)	27021417, 1997640; (49)
10	2	57961602, 422219; (1)	57741088, 752173; (2)
11	2	72361439, 1547720; (16)	72160993, 1992339; (22)
12	2	103984489, 1998265; (14)	103984489, 1997277; (14)
13	2	133841029, 1998777; (11)	133841008, 1998798; (11)
14	2	146419047, 22782; 0	145431068, 1996682; (2)
15	2	185601420, 285869; (1)	184534475, 1999022; (1)
16	2	193726047, 1264488; 0	193005232, 1996841; (2)
17	2	200715388, 431012; (4)	199162457, 1999808; (8)
18	2	200715388, 431012; (4)	200189480, 1997507; (26)

19	2	225334070, 133771; (1)	224391301, 1996805; (10)
20	2	233562197, 244575; (4)	232749825, 1993197; (39)
21	3	2495202, 66490; (1)	1515988, 1999847; (5)
22	3	17220098, 668159; (1)	16859710, 1999180; (5)
23	3	31058620, 1999878; (13)	31058620, 1998976; (13)
24	3	36843149, 52593; (1)	35872376, 1999364; (10)
25	3	49375349, 1998359; (54)	49377710, 1991149; (53)
26	3	52273421, 901597; (31)	51633843, 1992975; (60)
27	3	63792668, 377623; (10)	62842652, 1999378; (20)
28	3	135872958, 635051; (3)	135270611, 1795252; (8)
29	3	160903774, 1161513; (4)	160780968, 1997348; (6)
30	3	180588841, 404584; (3)	179832076, 1963726; (8)
31	4	23332578, 799976; (2)	22423933, 1998764; (4)
32	4	103146888, 41822; (1)	73278615, 709534; ()
33	4	170198392, 447612; (2)	169642615, 1999456; (9)
34	4	176717618, 254085; (1)	175866860, 1966322; (7)
35	5	44751956, 1547795; (3)	44301390, 1998361; (5)
36	5	49441779, 442981; (1)	49441779, 1363819; (5)
37	5	89252602, 1838413; (10)	89153327, 1997254; (10)
38	5	108288903, 920440; (3)	108036442, 1999315; (6)
39	5	126214489, 1997064; (8)	126213705, 1999698; (8)

40	5	137673167, 273334; (8)	136841167, 1943480; (34)
41	5	139348915, 997554; (43)	139173238, 1980395; (95)
42	5	151936546, 962987; (2)	151299988, 1999279; (5)
43	5	152705483, 984528; (4)	152681292, 1998332; (14)
45	6	63886188, 1979278; (4)	63867068, 1999491; (4)
46	6	84280274, 128982; (1)	83347332, 1996594; (11)
47	6	104852424, 1604405; (7)	104466881, 1995554; (7)
48	6	108934461, 85572; (1)	107983816, 1999638; (20)
49	6	111135020, 1980433; (16)	111133776, 1997782; (16)
50	6	164075611, 1999150; (2)	164075988, 1995828; (2)
51	7	1982181, 163449; (1)	1021259, 1991997; (34)
52	7	23735881, 1807173; (9)	23735096, 1999463; (9)
53	7	70796475, 1481574; (5)	70796055, 1997650; (22)
54	7	77337436, 1999180; (8)	77337436, 1999065; (8)
55	7	86222651, 1022310; (8)	85427738, 1999308; (9)
56	7	104593713, 469660; (4)	103930969, 1999051; (14)
57	7	110848329, 332216; (1)	109859343, 1997336; (5)
58	7	112468072, 1998473; (7)	112469673, 1992985; (7)
59	7	137039670, 45581; (1)	136075224, 1998829; (9)
60	8	4177231, 641994; (1)	3183064, 1999145; (1)
61	8	8088877, 1002026; (7)	8090584, 1000319; (7)

62	8	9255004, 1923090; (14)	9246431, 1998873; (17)
63	8	16036469, 1998029; (14)	16036260, 1999890; (14)
64	8	25465390, 1807196; (9)	25273907, 1998679; (12)
65	8	38021982, 288929; (7)	38020408, 279217; (7)
66	8	60482795, 394183; 0	59694660, 1998797; (5)
67	8	89188454, 572710; (1)	88265473, 1999263; (3)
68	8	111471166, 200025; 0	110563924, 1996107; (3)
69	8	143309504, 23728; (1)	142404555, 1998931; (29)
70	9	84293453, 807478; (6)	83800037, 1999320; (7)
71	10	18717884, 98124; (1)	17745124, 1999375; (10)
72	10	63858387, 1998678; (10)	63858726, 1998989; (10)
73	10	104612335, 349677; (5)	103888934, 1959060; (42)
74	11	24374339, 34145; 0	23382183, 1999380; (2)
75	11	46343189, 368666; (10)	45549453, 1997594; (43)
76	11	57385856, 295973; (10)	56510623, 1998535; (47)
77	11	108430237, 1946771; (6)	108378207, 1999805; (6)
78	11	113317745, 106298; (2)	112394430, 1993527; (18)
79	11	123364917, 937249; (23)	122394829, 1999776; (32)
80	11	124613957, 1; (1)	123614033, 1999540; (45)
81	11	130717153, 138947; (1)	129903279, 1988236; (10)
82	11	133822133, 30552; (1)	132885767, 1998300; (16)

83	12	2322513, 91291; (3)	1514912, 1998075; (27)
84	12	29905251, 236548; (1)	28929407, 1998727; (8)
85	12	92067323, 318494; (1)	91246989, 1998394; (13)
86	12	110554818, 618705; (12)	109723411, 1998846; (32)
87	12	116721603, 1985864; (18)	116708829, 1997390; (19)
88	12	123632930, 114032; (3)	123164062, 713251; (19)
89	14	29469373, 830989; (2)	28475766, 1993317; (4)
90	14	29469373, 830989; (2)	29000427, 1999466; (4)
91	14	32260547, 1995597; (5)	32258270, 1996987; (5)
92	14	71409614, 1058018; (5)	71409614, 1999003; (8)
93	14	83670415, 1983907; 0	83670415, 1998900; 0
94	14	99667179, 66776; (1)	98719335, 1999322; (12)
95	15	61831680, 49121; 0	60859615, 1993162; (8)
96	15	78845110, 70136; (2)	77912725, 1997462; (30)
97	15	82884151, 1321118; (27)	82254896, 1999367; (31)
98	15	84703470, 654388; (19)	83707015, 1999280; (28)
99	15	88901385, 1998005; (42)	88901171, 1999600; (42)
100	16	4220264, 771127; (27)	3470161, 1999571; (45)
101	16	9881953, 78927; (1)	8947036, 1998319; (11)
102	16	13748916, 4469; 0	12750936, 1991465; (11)
103	16	84736303, 80683; ()	29003109, 1996354; (81)

104	16	63636945, 1240845; 0	63372373, 1996782; (3)
105	17	2024854, 195961; (3)	293138, 1985255; (44)
106	17	17698254, 331604; (10)	16959955, 1958304; (45)
107	17	18951783, 1890049; (27)	19113214, 1832674; (27)
108	17	54737958, 1998683; (38)	54738257, 1998403; (38)
109	18	53160491, 425174; (2)	52796053, 1997972; (7)
110	18	77031213, 880400; (11)	76622938, 1394136; (13)
111	19	30981639, 63722; (1)	29987454, 1999762; (9)
112	22	39942234, 108933; (1)	38970439, 1994898; (42)
113	22	41027819, 1547012; (46)	40589869, 1996205; (50)

-ordinate ,Interval; ped genes)	Overlapped gene(s) for the interval in PGC2+CHN analysis
PGC2+CHN	
8423510, 79733; (1)	*RERE;*
30428943, 21040; 0	/
44037685, 72065; (1)	*PTPRF;*
73278615, 713037; (1)	*LOC101927295;*
98327831, 222581; (4)	*DPYD; MIR137; MIR137HG; MIR2682;*
150376141, 127915; (5)	*ECM1; LINC00568; MIR6878; RPRD2; TARS2;*
177247854, 513065; (2)	*BRINP2; LOC101928778;*
243661222, 364778; (2)	*AKT3; SDCCAG8;*
27036181, 1254167; (44)	*GTF3C2; GTF3C2-AS1; IFT172; KHK; KRTCAP3; MAPRE3; MIR4263;*
57967563, 416258; (1)	*VRK2;*
73129974, 483368; (10)	*EMX1; FBXO41; NOTO; PRADC1; RAB11FIP5;*
104976198, 37308; (1)	*LOC100287010;*
134840967, 3441; 0	/
146428031, 1; 0	/
185459544, 598173; (1)	*ZNF804A;*
193720640, 936126; 0	/
200715388, 248365; (4)	*C2orf47; C2orf69; FTCDNL1; TYW5;*
200715388, 248365; (4)	*C2orf47; C2orf69; FTCDNL1; TYW5;*

225334070, 125011; (1)	*CUL3;*
233562197, 228286; (4)	*C2orf82; GIGYF2; KCNJ13; NGEF;*
2495202, 66355; (1)	*CNTN4;*
17232635, 1067986; (2)	*LOC339862; TBC1D5;*
31059727, 1997869; (13)	*CMTM8; CNOT10; DYNC1LI1; GLB1; GPD1L; OSBPL10; OSBPL10-AS1;*
36843149, 108750; (1)	*TRANK1;*
49406080, 1962779; (52)	*MIR4787; MIR5193; MIR5787; MIR6872;*
52268866, 832715; (31)	*NT5DC2; PBRM1; PHF7; PPM1M; SEMA3G; SEMBT1; SMIM4;*
63833050, 141428; (4)	*ATXN7; C3orf49; THOC7; THOC7-AS1;*
135992645, 412039; (2)	*PCCB; STAG1;*
161410557, 469845; 0	/
180588841, 365278; (3)	*DNAJC19; FXR1; SOX2-OT;*
23376954, 51626; (1)	*MIR548AJ2;*
103653976, 302981; (5)	*CISD2; MANBA; SLC9B1; SLC9B2; UBE2D3;*
170202862, 439385; (2)	*CLCN3; NEK1;*
176851045, 23742; (1)	*GPM6A;*
45250730, 1049021; (1)	*HCN1;*
49441779, 382265; (1)	*EMB;*
89253181, 1762683; (10)	*CETN3; ADGRV1; LOC731157; LUCAT1; LYSMD3; MBLAC2;*
108999512, 204410; (1)	*MAN2A1;*
126214489, 1170373; (6)	*C5orf63; CTXN3; LINC01184; MARCH3; MEGF10; PRRC1;*

137673167, 271871; (8)	*CDC25C; EGR1; ETF1; FAM53C; HSPA9; KDM3B; REEP2; SNORD63;*
139514964, 821672; (38)	*PCDHA5; PCDHA6; PCDHA7; PCDHA8;*
151932354, 959951; (2)	*GRIA1; LOC101927134;*
152891951, 796265; (4)	*FAM114A2; GALNT10; GRIA1; MFAP3;*
64131810, 1089800; (3)	*EYS; PHF3; PTP4A1;*
84287712, 114096; (1)	*SNAP91;*
105364421, 107900; (2)	*LIN28B; LINC00577;*
108945370, 55373; (1)	*FOXO3;*
111134735, 1991157; (16)	*KIAA1919; LAMA4; REV3L; RFPL4B; RPF2; SLC16A10; TRAF3IP2;*
164141649, 1930167; (2)	*C6orf118; PDE10A;*
2012997, 153323; (1)	*MAD1L1;*
23737795, 1279391; (6)	*DFNA5; FAM221A; MPP6; NPY; OSBPL3; STK31;*
71308684, 557034; (1)	*CALN1;*
77385325, 1936272; (8)	*MAGI2-AS3; MIR548AU; PHTF2; RPL13AP17;*
86403263, 537390; (4)	*DMTF1; GRM3; KIAA1324L; TMEM243;*
104594253, 436856; (4)	*KMT2E; KMT2E-AS1; LINC01004; SRPK2;*
110836200, 344345; (1)	*IMMP2L;*
112483091, 1979567; (7)	*LINC00998; LOC101928036; MIR3666;*
137047137, 38114; (1)	*DGKI;*
3614683, 1205495; (1)	*CSMD1;*
8090584, 1000319; (7)	*FAM86B3P; MFHAS1; MIR4660; PPP1R3B;*

9370559, 1340157; (11)	*MIR124-1; MIR597;* *MIR1322; MSRA; PINX1;* *PRSS55; RP1L1; SOX7;*
17029436, 24080; (1)	*ZDHHC2;*
26224593, 48176; (2)	*BNIP3L; PPP2R2A;*
38160043, 138605; (3)	*FGFR1; LETM2;* *WHSC1L1;*
60513088, 207672; 0	/
89254045, 488613; (1)	*MMP16;*
111471166, 182548; 0	/
143300814, 449215; (4)	*ARC; BAI1; JRK;* *TSNARE1;*
84308948, 789472; (5)	*SPATA31D1; SPATA31D3;* *SPATA31D4;*
18725659, 26233; (1)	*CACNB2;*
64100181, 1214094; (9)	*JMJD1C-AS1; LOC283045;* *MIR1296; NRBF2; REEP3;*
104618524, 310668; (5)	*AS3MT; C10orf32;* *C10orf32-ASMT; CNNM2;* *NT5C2;*
24358141, 50343; 0	/
46370767, 359277; (11)	*ATG13; CHRM4; DGKZ;* *HARBI1; MDK; MIR3160-* *1; MIR3160-2; MIR4688;*
57385856, 293225; (10)	*CTNND1; MED19;* *MIR130A; TMX2; TMX2-* *CTNND1; YPEL4;*
109289538, 303768; (1)	*C11orf87;*
113317745, 106298; (2)	*DRD2; MIR4301;*
123394636, 1; 0	/
124613957, 1; (1)	*NRGN;*
130714613, 177417; (1)	*SNX19;*
133822569, 28844; (1)	*IGSF9B;*

2341385, 66810; (2)	*CACNA1C; CACNA1C-IT3;*
29916839, 11550; (1)	*TMTC1;*
92243186, 14324; 0	/
109884367, 1328396; (26)	*GIT2; GLTP; GPN3; HVCN1; IFT81; KCTD10;*
117662712, 283134; (2)	*KSR2; NOS1;*
123460719, 286243; (8)	*CDK2AP1; LOC100507091; MIR4304; MPHOSPH9;*
29469373, 825430; (2)	*MIR548AI; PRKD1;*
29125021, 1169782; (4)	*C14orf23; FOXG1; MIR548AI; PRKD1;*
33257914, 980040; (2)	*AKAP6; NPAS3;*
72387640, 75248; (1)	*RGS6;*
84641244, 58769; 0	/
99667179, 59908; (1)	*BCL11B;*
61835519, 43661; 0	/
78712699, 211147; (6)	*CHRNA3; CHRNA5; CHRNB4; HYKK; IREB2; PSMA4;*
83237769, 153769; (4)	*AP3B2; CPEB1; LOC283692; LOC338963;*
84703874, 653776; (19)	*LOC642423; LOC102724034;*
88901912, 1986262; (40)	*LOC101929743; MESP1; MESP2; MFGE8; MIR7-2;*
4457907, 138541; (6)	*CDIP1; CORO7; CORO7-PAM16; DNAJA3; HMOX2; NMRAL1;*
9904150, 56730; (1)	*GRIN2A;*
13747292, 12926; 0	/
29929728, 88773; (6)	*DOC2A; HIRIP3; INO80E; KCTD13; TAOK2; TMEM219;*

63696480, 689169; 0	/
1267395, 941505; (27)	*OVCA2; PITPNA; PITPNA-AS1; PRPF8; RILP; RPA1; RTN4RL1; SCARF1;*
17649172, 380686; (11)	*LRRC48; MIR33B; MIR6777; MYO15A; RAI1; SMCR5; SREBF1;*
19141582, 861380; (17)	*MAPK7; MFAP4; MIR1180; RNF112; SLC47A1;*
55712975, 1023666; (27)	*LOC101927688; LPO; MIR142; MIR4736; MKS1; MPO; MRPS23; MSI2;*
53251562, 552595; (3)	*LOC100505474; LOC101927273; TCF4;*
77566535, 127760; (2)	*KCNG2; PQLC1;*
30987423, 57938; (1)	*ZNF536;*
39947574, 55694; (1)	*CACNA1I;*
41587556, 25748; (2)	*EP300-AS1; L3MBTL2;*

Supplementary Table 10. Results for fine-mapping analysis using PAINTOR

Index SNP (Locus)	Chr.	Position	SNP	Posterior probability
				PGC2+CHN
1_rs172531_8495590	1	8448404	rs11121178	1.000
1_rs172531_8495590	1	8535164	rs4995074	1.000
1_rs11210195_73749283	1	73725998	rs12136984	1.000
1_rs11210195_73749283	1	73796006	rs12022895	0.997
1_rs1198589_98550411	1	98541677	rs4950142	0.837
1_rs6670165_177280121	1	177282235	rs17315346	0.985
1_rs35978510_243776117	1	243804577	rs144763434	1.000
2_rs12623170_28020157	2	27980616	rs183183485	0.746
2_rs75575209_58138192	2	58179795	rs79005319	0.942
2_rs1518395_58208074	2	58215594	rs61452738	0.027
2_rs999494_73157395	2	73134895	rs71404794	0.000
2_rs999494_73157395	2	73157395	rs999494	0.000
2_rs999494_73157395	2	73161551	rs2077586	1.000
2_rs999494_73157395	2	73162541	rs12470805	0.998
2_rs2381759_146428031	2	146423720	rs187057723	0.999
2_rs2381759_146428031	2	146441828	rs72857442	0.994
2_rs12619354_194002782	2	194002782	rs12619354	1.000
2_rs12619354_194002782	2	194022118	rs35752752	0.869
2_rs78681500_201187316	2	201143409	rs11688415	0.876
3_rs3732386_36871993	3	36856030	rs9834970	0.857
3_rs2073499_50374293	3	50374293	rs2073499	1.000
3_rs2577831_52628056	3	52624387	rs73078824	0.634
3_rs832190_63842629	3	63871648	rs704366	0.872
3_rs66691851_136154828	3	136147771	rs9867368	0.000
3_rs66691851_136154828	3	136162622	rs11306711	0.999
3_rs9859557_180830910	3	180797921	rs12635178	1.000
3_rs9859557_180830910	3	180843625	rs13072578	0.871
4_rs11722779_103827488	4	103802165	rs78640361	0.589
4_rs7438_170642246	4	170647421	rs72621983	0.919
5_rs9292918_45301035	5	45285752	rs16902086	0.000
5_rs9292918_45301035	5	45301035	rs9292918	0.958
5_rs13164092_137840860	5	137863991	rs72805822	0.788
5_rs113568682_152299754	5	152332252	rs75668976	0.918
6_rs160593_105466332	6	105471467	rs187150974	1.000
6_rs9398171_108983527	6	109012460	rs6937254	0.159
7_rs12704290_86427626	7	86422141	rs12704289	0.996
7_rs12704290_86427626	7	86427626	rs12704290	0.002

7_rs2057884_104930250	7	104915608	rs6975268	0.818
7_rs214467_110858268	7	110821730	rs4730483	1.000
7_rs11534004_113467444	7	113467444	rs11534004	0.998
8_rs17687067_17036201	8	17036201	rs17687067	0.954
8_rs112537273_38248306	8	38231874	rs2932005	0.000
8_rs16880831_111561505	8	111571834	rs113501829	0.817
10_rs11191424_104625886	10	104636276	rs77335224	0.872
10_rs10786736_104849116	10	104829469	rs1926032	0.189
11_rs61882743_46548754	11	46531807	rs61882716	1.000
11_rs61882743_46548754	11	46537370	rs141181296	1.000
11_rs9420_57510294	11	57483039	rs543725	1.000
11_rs9420_57510294	11	57484130	rs71460549	1.000
11_rs77502336_123394636	11	123394636	rs77502336	0.960
11_rs55661361_124613957	11	124623492	rs12541	0.926
11_rs619091_133884137	11	133853665	rs12366213	0.912
12_rs4766428_110723245	12	110723245	rs4766428	0.979
12_rs61041384_123644043	12	123600280	rs145510454	0.521
14_rs2383377_33257914	14	33257914	rs2383377	0.896
15_rs950169_84706461	15	84657643	rs11629550	0.993
16_rs3814881_30000901	16	29994922	rs3814883	0.911
17_rs8082590_17958402	17	17947710	rs2955382	0.800
17_rs8082590_17958402	17	17990671	rs9890563	0.987
18_rs715170_53795514	18	53768975	rs1792709	0.867
19_rs2053079_30987423	19	31015906	rs10415509	0.881
22_rs9607782_41587556	22	41587556	rs9607782	0.968

Posterior probability	
PGC2	CHN
1.000	0.011
0.998	0.336
1.000	0.003
0.000	0.003
0.890	0.002
0.989	0.002
1.000	0.009
0.850	0.002
0.266	0.000
0.000	0.806
0.000	1.000
0.000	1.000
1.000	0.000
0.998	0.000
0.999	0.003
0.994	0.003
1.000	0.026
0.862	0.003
0.467	0.001
0.150	0.001
0.000	1.000
0.893	0.001
0.183	0.003
0.877	0.000
0.000	0.973
1.000	0.000
0.871	0.000
0.958	0.002
0.353	0.003
0.000	0.977
0.230	0.798
0.801	0.002
0.229	0.003
0.996	0.003
0.873	0.002
0.008	0.003
0.818	0.000

0.856	0.002
1.000	0.003
0.000	1.000
0.164	0.293
0.954	0.000
0.999	0.003
0.993	0.002
0.994	0.001
1.000	0.003
1.000	0.003
0.002	0.003
1.000	0.003
0.633	0.000
0.734	0.001
0.918	0.002
1.000	0.000
0.000	0.978
0.270	0.040
0.993	0.003
0.000	0.000
0.861	0.000
0.970	0.001
0.085	0.859
0.289	0.002
0.958	0.001

Supplementary Table 11. Annotations for the 16 SNPs with a posterior probability of greater than 0.

SNP	Promoter histone marks	Enhancer histone marks	DNAse	Proteins bound	Motifs changed	Selected eQTL hits
rs10415509					FXR,Foxc1,Pax-8	
rs11688415		4 tissues	4 tissues	STAT3		17 hits
rs12022895					AIRE,CIZ,Pou2f2	1 hit
rs12541	GI	13 tissues	MUS,BLD		5 altered motifs	1 hit
rs12704289		BRN, ADRL				1 hit
rs17687067			BLD		4 altered motifs	7 hits
rs2383377						
rs3814883		FAT, STRM, SKIN			14 altered motifs	62 hits
rs543725					7 altered motifs	18 hits
rs704366		4 tissues			5 altered motifs	
rs72621983					4 altered motifs	1 hit

rs75668976					DMRT3,DMRT5	
rs77502336		ESDR, ADRL, OVRY				
rs79005319					Foxp1	1 hit
rs9292918					Evi-1,Irf,Pou1f1	1 hit
rs9834970		9 tissues	8 tissues			2 hits

80 only in the trans-ethnic analysis

RefSeq genes	dbSNP
ZNF536	intronic
27kb 5' of *SPATS2L*	
696kb 3' of *LRRIQ3*	
ESAM	3'-UTR
GRM3	intronic
ZDHHC2	intronic
AKAP6	intronic
TAOK2	synonymous
TMX2	intronic
ATXN7	intronic
3.2kb 3' of *C4orf27*	

538kb 5' of *GRIA1*	
1.9kb 5' of *GRAMD1B*	
94kb 5' of *VRK2*	
HCN1	intronic
12kb 3' of *TRANK1*	

Supplementary Table 12. eQTL analysis of rs3814883

Data set	Tissue
Gibbs2010	Cerbellum
Gibbs2010	FrontalCortex
GTEx2015_v6	Adipose_Subcutaneous
GTEx2015_v6	Adipose_Subcutaneous
GTEx2015_v6	Adipose_Subcutaneous
GTEx2015_v6	Adipose_Subcutaneous
GTEx2015_v6	Adipose_Visceral_Omentum
GTEx2015_v6	Artery_Aorta
GTEx2015_v6	Artery_Aorta
GTEx2015_v6	Artery_Tibial
GTEx2015_v6	Artery_Tibial
GTEx2015_v6	Brain_Cerebellum
GTEx2015_v6	Breast_Mammary_Tissue
GTEx2015_v6	Breast_Mammary_Tissue
GTEx2015_v6	Cells_EBV-transformed_lymphocyte
GTEx2015_v6	Cells_Transformed_fibroblasts
GTEx2015_v6	Colon_Transverse
GTEx2015_v6	Colon_Transverse
GTEx2015_v6	Esophagus_Mucosa
GTEx2015_v6	Esophagus_Mucosa
GTEx2015_v6	Esophagus_Muscularis
GTEx2015_v6	Esophagus_Muscularis
GTEx2015_v6	Heart_Atrial_Appendage
GTEx2015_v6	Heart_Left_Ventricle
GTEx2015_v6	Lung
GTEx2015_v6	Lung
GTEx2015_v6	Lung
GTEx2015_v6	Muscle_Skeletal
GTEx2015_v6	Muscle_Skeletal
GTEx2015_v6	Muscle_Skeletal
GTEx2015_v6	Nerve_Tibial
GTEx2015_v6	Nerve_Tibial
GTEx2015_v6	Nerve_Tibial
GTEx2015_v6	Nerve_Tibial
GTEx2015_v6	Pituitary
GTEx2015_v6	Skin_Not_Sun_Exposed_Suprapubic
GTEx2015_v6	Skin_Not_Sun_Exposed_Suprapubic
GTEx2015_v6	Skin_Sun_Exposed_Lower_leg

GTEx2015_v6	Skin_Sun_Exposed_Lower_leg
GTEx2015_v6	Skin_Sun_Exposed_Lower_leg
GTEx2015_v6	Skin_Sun_Exposed_Lower_leg
GTEx2015_v6	Spleen
GTEx2015_v6	Testis
GTEx2015_v6	Thyroid
GTEx2015_v6	Thyroid
GTEx2015_v6	Thyroid
GTEx2015_v6	Thyroid
GTEx2015_v6	Whole_Blood
Lappalainen2013	Lymphoblastoid_EUR_exonlevel
Lappalainen2013	Lymphoblastoid_EUR_exonlevel
Lappalainen2013	Lymphoblastoid_EUR_exonlevel
Lappalainen2013	Lymphoblastoid_EUR_exonlevel
Lappalainen2013	Lymphoblastoid_EUR_exonlevel
Lappalainen2013	Lymphoblastoid_EUR_exonlevel
Lappalainen2013	Lymphoblastoid_EUR_exonlevel
Lappalainen2013	Lymphoblastoid_EUR_exonlevel
Lappalainen2013	Lymphoblastoid_EUR_exonlevel
Lappalainen2013	Lymphoblastoid_EUR_exonlevel
Lappalainen2013	Lymphoblastoid_EUR_genelevel
Westra2013	Whole_Blood
Westra2013	Whole_Blood
Westra2013	Whole_Blood

Gene or Exon	**P value**
SEZ6L2	2.37E-08
SEZ6L2	5.03E-08
YPEL3	1.15E-12
INO80E	9.97E-11
RP11-347C12.1	2.78E-10
RP11-231C14.4	3.35E-07
INO80E	1.11E-11
INO80E	6.51E-11
YPEL3	1.20E-07
INO80E	8.00E-15
YPEL3	4.62E-10
YPEL3	5.36E-07
INO80E	2.30E-08
YPEL3	4.86E-07
MAPK3	4.20E-06
TMEM219	2.22E-05
INO80E	2.95E-09
DOC2A	6.92E-09
INO80E	3.87E-12
YPEL3	1.82E-06
YPEL3	4.33E-07
INO80E	1.69E-05
INO80E	3.58E-10
INO80E	8.23E-08
INO80E	2.50E-13
YPEL3	1.60E-08
RP11-347C12.1	2.31E-05
FAM57B	1.32E-10
RP11-347C12.1	1.52E-07
TBX6	1.33E-06
INO80E	0.00E-16
YPEL3	6.06E-12
TBX6	7.19E-08
RP11-347C12.1	4.99E-06
INO80E	2.13E-08
INO80E	3.34E-07
YPEL3	1.84E-05
YPEL3	1.56E-11

INO80E	6.26E-09
RP11-347C12.1	6.81E-08
RP11-455F5.3	7.06E-06
INO80E	2.63E-07
INO80E	1.98E-08
INO80E	5.80E-14
YPEL3	3.68E-09
RP11-347C12.1	2.02E-06
RP11-347C12.2	2.63E-05
MAPK3	4.00E-15
ENSG00000149925.12_30078206_30078359	4.00E-11
ENSG00000102882.7_30128991_30129105	5.89E-09
ENSG00000102882.7_30127956_30128324	1.82E-08
ENSG00000102882.7_30129670_30129859	6.66E-08
ENSG00000102882.7_30128475_30128606	2.87E-07
ENSG00000102882.7_30129368_30129484	2.89E-07
ENSG00000102882.7_30133145_30134311	4.61E-07
ENSG00000149922.6_30100014_30100160	8.50E-07
ENSG00000102882.7_30125426_30126029	6.31E-06
ENSG00000149922.6_30097114_30097759	1.18E-05
TBX6	2.65E-07
KCTD13	3.07E-09
INO80E	1.34E-08
ZNF688|*BOLA2B*|*CORO1A*	3.22E-06

In the 99% credible set interval?
-
-
No
Yes
Yes
No
Yes
Yes
No
Yes
No
Yes
Yes
No
Yes
Yes
Yes
Yes
Yes
No
No
Yes
Yes
Yes
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Yes
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No
Yes
-

Supplementary Table 13. The top 100 enriched cell-type specific epigenomic annotations for schizoph

EID	Tissue/Cell Type	Group
E072	Brain Inferior Temporal Lobe	Brain
E067	Brain Angular Gyrus	Brain
E012	hESC Derived CD56+ Ectoderm Cultured Cells	ES-deriv
E082	Fetal Brain Female	Brain
E073	Brain Mid Frontal Lobe	Brain
E072	Brain Inferior Temporal Lobe	Brain
E045	CD4+ CD25int CD127+ Tmem Primary Cells	Blood & T-cell
E003	H1 Cell Line	ESC
E082	Fetal Brain Female	Brain
E053	Neurosphere Cultured Cells Cortex Derived	Neurosph
E068	Brain Anterior Caudate	Brain
E072	Brain Inferior Temporal Lobe	Brain
E067	Brain Angular Gyrus	Brain
E073	Brain Mid Frontal Lobe	Brain
E009	H9 Derived Neuronal Progenitor Cultured Cells	ES-deriv
E020	iPS-20b Cell Line	iPSC
E127	NHEK-Epidermal Keratinocytes	ENCODE2012
E024	4star	ESC
E073	Brain Mid Frontal Lobe	Brain
E048	CD8 Memory Primary Cells	Blood & T-cell
E033	CD3 Primary Cells Cord BI	Blood & T-cell
E081	Fetal Brain Male	Brain
E074	Brain Substantia Nigra	Brain
E074	Brain Substantia Nigra	Brain
E016	HUES64 Cell Line	ESC
E069	Brain Cingulate Gyrus	Brain
E058	Penis Foreskin Keratinocyte Primary Cells skin03	Epithelial
E020	iPS-20b Cell Line	iPSC
E070	Brain Germinal Matrix	Brain
E070	Brain Germinal Matrix	Brain
E018	iPS-15b Cell Line	iPSC
E068	Brain Anterior Caudate	Brain
E112	Thymus	Thymus
E010	H9 Derived Neuron Cultured Cells	ES-deriv
E020	iPS-20b Cell Line	iPSC
E071	Brain Hippocampus Middle	Brain
E068	Brain Anterior Caudate	Brain
E054	urosphere Cultured Cells Ganglionic Eminence Deri	Neurosph

E011	hESC Derived CD184+ Endoderm Cultured Cells	ES-deriv
E070	Brain Germinal Matrix	Brain
E022	iPS DF 19.11 Cell Line	iPSC
E024	4star	ESC
E071	Brain Hippocampus Middle	Brain
E082	Fetal Brain Female	Brain
E057	Penis Foreskin Keratinocyte Primary Cells skin02	Epithelial
E093	Fetal Thymus	Thymus
E069	Brain Cingulate Gyrus	Brain
E012	hESC Derived CD56+ Ectoderm Cultured Cells	ES-deriv
E038	CD4 Naive Primary Cells	Blood & T-cell
E082	Fetal Brain Female	Brain
E007	H1 Derived Neuronal Progenitor Cultured Cells	ES-deriv
E009	H9 Derived Neuronal Progenitor Cultured Cells	ES-deriv
E071	Brain Hippocampus Middle	Brain
E119	HMEC Mammary Epithelial	ENCODE2012
E003	H1 Cell Line	ESC
E037	CD4 Memory Primary Cells	Blood & T-cell
E010	H9 Derived Neuron Cultured Cells	ES-deriv
E053	Neurosphere Cultured Cells Cortex Derived	Neurosph
E015	HUES6 Cell Line	ESC
E004	H1 BMP4 Derived Mesendoderm Cultured Cells	ES-deriv
E003	H1 Cell Line	ESC
E002	ES-WA7 Cell Line	ESC
E028	Breast vHMEC	Epithelial
E019	iPS-18 Cell Line	iPSC
E125	NH-A Astrocytes	ENCODE2012
E067	Brain Angular Gyrus	Brain
E018	iPS-15b Cell Line	iPSC
E081	Fetal Brain Male	Brain
E010	H9 Derived Neuron Cultured Cells	ES-deriv
E057	Penis Foreskin Keratinocyte Primary Cells skin02	Epithelial
E099	Placenta Amnion	Other
E116	GM12878 Lymphoblastoid	ENCODE2012
E056	Penis Foreskin Fibroblast Primary Cells skin02	Epithelial
E004	H1 BMP4 Derived Mesendoderm Cultured Cells	ES-deriv
E125	NH-A Astrocytes	ENCODE2012
E012	hESC Derived CD56+ Ectoderm Cultured Cells	ES-deriv
E026	Marrow Derived Mesenchymal Stem Cell Cultured	Mesench
E001	ES-I3 Cell Line	ESC
E039	CD4+ CD25- CD45RA+ Naive Primary Cells	Blood & T-cell

E022	iPS DF 19.11 Cell Line	iPSC
E002	ES-WA7 Cell Line	ESC
E008	H9 Cell Line	ESC
E112	Thymus	Thymus
E016	HUES64 Cell Line	ESC
E081	Fetal Brain Male	Brain
E024	4star	ESC
E087	Pancreatic Islets	Other
E087	Pancreatic Islets	Other
E069	Brain Cingulate Gyrus	Brain
E009	H9 Derived Neuronal Progenitor Cultured Cells	ES-deriv
E021	iPS DF 6.9 Cell Line	iPSC
E062	Peripheral Blood Mononuclear Primary Cells	Blood & T-cell
E070	Brain Germinal Matrix	Brain
E067	Brain Angular Gyrus	Brain
E054	urosphere Cultured Cells Ganglionic Eminence Deri	Neurosph
E129	Osteoblasts	ENCODE2012
E044	CD4+ CD25+ CD127- Treg Primary Cells	Blood & T-cell
E074	Brain Substantia Nigra	Brain
E058	Penis Foreskin Keratinocyte Primary Cells skin03	Epithelial
E018	iPS-15b Cell Line	iPSC

EID, the epigenome identifier in the Roadmap Epigenomics Project.

Descriptions for cell and tissue types, related groups, and marks at the Roadmap Epigenomics Project webs

P value, enrichment P for schizophrenia associations derived from GREGOR.

renia associations in the current and PGC2 analyses

Mark	P value
H3K27ac	1.84E-07
H3K27ac	3.01E-07
H3K27ac	3.19E-07
H3K4me1	9.31E-07
H3K9ac	1.22E-06
H3K9ac	1.50E-06
H3K36me3	2.00E-06
H3K4me1	2.14E-06
H3K27ac	2.30E-06
H3K27ac	2.46E-06
H3K27ac	2.54E-06
H3K4me3	3.16E-06
H3K4me3	3.19E-06
H3K27ac	3.57E-06
H3K27ac	4.45E-06
H3K9ac	4.87E-06
H3K4me1	4.91E-06
H3K4me1	5.65E-06
H3K4me3	5.94E-06
H3K36me3	6.00E-06
H3K36me3	6.70E-06
H3K9ac	6.76E-06
H3K27ac	7.07E-06
H3K4me3	8.08E-06
H3K27ac	8.31E-06
H3K4me3	8.84E-06
H3K4me1	9.08E-06
H3K27ac	9.41E-06
H3K27ac	9.98E-06
H3K9ac	1.01E-05
H3K4me1	1.09E-05
H3K4me3	1.10E-05
H3K36me3	1.30E-05
H3K9ac	1.33E-05
H3K4me3	1.42E-05
H3K27ac	1.45E-05
H3K9ac	1.47E-05
H3K27ac	1.51E-05

H3K4me3	1.55E-05
H3K4me1	1.58E-05
H3K27ac	1.59E-05
H3K4me3	1.61E-05
H3K4me3	1.85E-05
H3K4me3	1.96E-05
H3K27ac	2.17E-05
H3K36me3	2.41E-05
H3K27ac	2.45E-05
H3K4me3	2.47E-05
H3K36me3	2.53E-05
H3K9ac	2.53E-05
H3K27ac	2.70E-05
H3K9ac	2.70E-05
H3K9ac	2.70E-05
H3K4me1	2.84E-05
H3K27ac	3.00E-05
H3K36me3	3.11E-05
H3K27ac	3.31E-05
H3K4me1	3.40E-05
H3K4me1	3.47E-05
H3K27ac	3.59E-05
H3K4me3	3.69E-05
H3K4me3	3.87E-05
H3K4me1	4.15E-05
H3K4me3	4.42E-05
H3K9ac	4.65E-05
H3K9ac	4.89E-05
H3K27ac	5.36E-05
H3K4me1	5.55E-05
H3K4me3	5.56E-05
H3K9ac	5.72E-05
H3K9ac	5.98E-05
H3K36me3	5.99E-05
H3K9ac	6.03E-05
H3K4me3	6.27E-05
H3K36me3	6.44E-05
H3K9ac	6.58E-05
H3K36me3	6.58E-05
H3K9ac	6.63E-05
H3K36me3	6.99E-05

H3K4me3	7.39E-05
H3K4me1	7.47E-05
H3K4me3	7.69E-05
H3K9ac	7.90E-05
H3K4me3	8.02E-05
H3K4me3	8.04E-05
H3K27ac	8.05E-05
H3K27ac	8.40E-05
H3K9ac	8.40E-05
H3K9ac	8.40E-05
H3K4me3	8.51E-05
H3K27ac	8.54E-05
H3K36me3	8.70E-05
H3K4me3	9.07E-05
H3K4me1	9.17E-05
H3K4me3	9.21E-05
H3K9ac	9.70E-05
H3K36me3	1.01E-04
H3K4me1	1.02E-04
H3K9ac	1.04E-04
H3K4me3	1.05E-04

ite (http://www.roadmapepigenomics.org).

Supplementary Table 14. The top ranked SNPs with higher posterior probability in the further PAIN

Index SNP (Locus)	Chr.	Position	SNP	Posterior probability
5_rs13164092_137840860	5	137863991	rs72805822	0.851
5_rs13164092_137840860	5	137863991	rs72805822	0.841
5_rs13164092_137840860	5	137863991	rs72805822	0.835
1_rs6670165_177280121	1	177280121	rs6670165	0.808
5_rs13164092_137840860	5	137863991	rs72805822	0.812
1_rs6670165_177280121	1	177280121	rs6670165	0.845
1_rs6670165_177280121	1	177280121	rs6670165	0.838
1_rs6670165_177280121	1	177280121	rs6670165	0.829
1_rs6670165_177280121	1	177280121	rs6670165	0.822
1_rs6670165_177280121	1	177280121	rs6670165	0.817
1_rs6670165_177280121	1	177280121	rs6670165	0.845
1_rs6670165_177280121	1	177280121	rs6670165	0.829
1_rs6670165_177280121	1	177280121	rs6670165	0.827
1_rs6670165_177280121	1	177280121	rs6670165	0.814
5_rs13164092_137840860	5	137863991	rs72805822	0.863
5_rs13164092_137840860	5	137863991	rs72805822	0.824
2_rs78681500_201187316	2	201143409	rs11688415	0.947
2_rs78681500_201187316	2	201143409	rs11688415	0.943
5_rs13164092_137840860	5	137863991	rs72805822	0.908
5_rs13164092_137840860	5	137863991	rs72805822	0.901
8_rs112537273_38248306	8	38262493	rs144330574	0.841
8_rs112537273_38248306	8	38262493	rs144330574	0.825
2_rs78681500_201187316	2	201143409	rs11688415	0.926
5_rs13164092_137840860	5	137863991	rs72805822	0.818
2_rs78681500_201187316	2	201143409	rs11688415	0.950
2_rs78681500_201187316	2	201143409	rs11688415	0.947
5_rs13164092_137840860	5	137863991	rs72805822	0.915
8_rs112537273_38248306	8	38262493	rs144330574	0.846
8_rs112537273_38248306	8	38262493	rs144330574	0.837

5_rs13164092_137840860	5	137863991	rs72805822	0.831
5_rs13164092_137840860	5	137863991	rs72805822	0.806
14_rs2383377_33257914	14	33257914	rs2383377	0.915
2_rs78681500_201187316	2	201143409	rs11688415	0.894
5_rs13164092_137840860	5	137863991	rs72805822	0.837
1_rs6670165_177280121	1	177280121	rs6670165	0.820
7_rs2057884_104930250	7	104915608	rs6975268	0.838
5_rs13164092_137840860	5	137863991	rs72805822	0.810
5_rs13164092_137840860	5	137863991	rs72805822	0.812
1_rs6670165_177280121	1	177280121	rs6670165	0.834
17_rs8082590_17958402	17	17947710	rs2955382	0.835

[a]EID, the epigenome identifier in the Roadmap Epigenomics Project.

Descriptions for cell and tissue types, related groups, and marks at the Roadmap Epigenomics Project webs

TOR analyses with the cell-type specific epigenomic annotations

RoadMap cell-type specific epigenomic annotations[a]			
EID	**Mark**	**Tissue/Cell Type**	**Group**
E038	H3K36me3	CD4 Naive Primary Cells	Blood & T-cell
E033	H3K36me3	CD3 Primary Cells Cord Bl	Blood & T-cell
E039	H3K36me3	CD4+ CD25- CD45RA+ Naive Primary Cells	Blood & T-cell
E070	H3K27ac	Brain Germinal Matrix	Brain
E082	H3K27ac	Fetal Brain Female	Brain
E069	H3K4me3	Brain Cingulate Gyrus	Brain
E072	H3K4me3	Brain Inferior Temporal Lobe	Brain
E068	H3K4me3	Brain Anterior Caudate	Brain
E074	H3K4me3	Brain Substantia Nigra	Brain
E071	H3K4me3	Brain Hippocampus Middle	Brain
E067	H3K9ac	Brain Angular Gyrus	Brain
E068	H3K9ac	Brain Anterior Caudate	Brain
E073	H3K9ac	Brain Mid Frontal Lobe	Brain
E072	H3K9ac	Brain Inferior Temporal Lobe	Brain
E125	H3K36me3	NH-A Astrocytes	ENCODE2012
E116	H3K36me3	GM12878 Lymphoblastoid	ENCODE2012
E127	H3K4me1	NHEK-Epidermal Keratinocytes	ENCODE2012
E119	H3K4me1	HMEC Mammary Epithelial	ENCODE2012
E127	H3K4me1	NHEK-Epidermal Keratinocytes	ENCODE2012
E119	H3K4me1	HMEC Mammary Epithelial	ENCODE2012
E127	H3K4me1	NHEK-Epidermal Keratinocytes	ENCODE2012
E119	H3K4me1	HMEC Mammary Epithelial	ENCODE2012
E057	H3K27ac	Penis Foreskin Keratinocyte Primary Cells skin02	Epithelial
E057	H3K27ac	Penis Foreskin Keratinocyte Primary Cells skin02	Epithelial
E028	H3K4me1	Breast vHMEC	Epithelial
E058	H3K4me1	Penis Foreskin Keratinocyte Primary Cells skin03	Epithelial
E028	H3K4me1	Breast vHMEC	Epithelial
E028	H3K4me1	Breast vHMEC	Epithelial
E058	H3K4me1	Penis Foreskin Keratinocyte Primary Cells skin03	Epithelial

E058	H3K9ac	Penis Foreskin Keratinocyte Primary Cells skin03	Epithelial
E057	H3K9ac	Penis Foreskin Keratinocyte Primary Cells skin02	Epithelial
E002	H3K4me1	ES-WA7 Cell Line	ESC
E003	H3K4me1	H1 Cell Line	ESC
E024	H3K4me1	4star	ESC
E010	H3K27ac	H9 Derived Neuron Cultured Cells	ES-deriv
E009	H3K27ac	H9 Derived Neuronal Progenitor Cultured Cells	ES-deriv
E026	H3K36me3	Bone Marrow Derived Mesenchymal Stem Cell Cultured Cells	Mesench
E054	H3K27ac	Neurosphere Cultured Cells Ganglionic Eminence Derived	Neurosph
E087	H3K27ac	Pancreatic Islets	Other
E093	H3K36me3	Fetal Thymus	Thymus

ite (http://www.roadmapepigenomics.org).

Supplementary Table 15. Top 30 significantly enriched pathways and gene sets in the cross-ethnic me

DATABASE	GENE SET
REACTOME	REGULATION_OF_INSULIN_SECRETION_BY_GLUCAGON_LIKE_PEPTIDE_1
REACTOME	INHIBITION_OF_INSULIN_SECRETION_BY_ADRENALINE_NORADRENALINE
KEGG	KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION
GOTERM	AXONAL_FASCICULATION
PANTHER_BIOLOGICAL_PROCESS	PHOSPHATE_TRANSPORT
REACTOME	PI3K_AKT_SIGNALLING
PANTHER_MOLECULAR_FUNCTION	MAJOR_HISTOCOMPATIBILITY_COMPLEX_ANTIGEN
PANTHER_BIOLOGICAL_PROCESS	DETERMINATION_OF_DORSAL/VENTRAL_AXIS
GOTERM	GLUCOSE_HOMEOSTASIS
GOTERM	NEURON_MIGRATION
GOTERM	POSTSYNAPTIC_DENSITY
REACTOME	SIGNALING_BY_NOTCH
REACTOME	NRIF_SIGNALS_CELL_DEATH_FROM_THE_NUCLEUS
GOTERM	ANTIGEN_PROCESSING_AND_PRESENTATION
GOTERM	CELLULAR_RESPIRATION
GOTERM	CELL_FATE_DETERMINATION
GOTERM	VOLTAGE-GATED_CALCIUM_CHANNEL_COMPLEX
GOTERM	MITOCHONDRIAL_NUCLEOID
GOTERM	MITOTIC_CELL_CYCLE_CHECKPOINT
KEGG	KEGG_ALLOGRAFT_REJECTION
PANTHER_MOLECULAR_FUNCTION	G-PROTEIN
GOTERM	VISUAL_LEARNING
GOTERM	VOLTAGE-GATED_ION_CHANNEL_ACTIVITY
KEGG	KEGG_GRAFT_VERSUS_HOST_DISEASE
GOTERM	SODIUM_CHANNEL_ACTIVITY
GOTERM	ANTIGEN_PROCESSING_AND_PRESENTATION_OF_PEPTIDE_OR_POLYSACCHARIDE_ANTIGEN_VIA_MHC_CLASS_II
GOTERM	MHC_CLASS_II_PROTEIN_COMPLEX
GOTERM	HISTONE_METHYLTRANSFERASE_ACTIVITY_(H3-K4_SPECIFIC)
Ingenuity	NEUREGULIN.SIGNALING
GOTERM	PEPTIDYL-TYROSINE_PHOSPHORYLATION

NGENES denotes the number of genes in pathway (number of genes successfully mapped by MAGMA).

ta-analysis

NGENES	BETA	BETA_STD	SE	P
61	0.713	0.041	0.146	5.14E-07
30	0.888	0.035	0.224	3.81E-05
78	0.571	0.037	0.158	1.49E-04
10	1.25	0.029	0.354	2.01E-04
16	1.19	0.035	0.336	2.08E-04
37	0.646	0.029	0.193	4.14E-04
30	0.738	0.03	0.227	5.68E-04
16	0.905	0.026	0.28	6.03E-04
45	0.515	0.025	0.16	6.51E-04
53	0.475	0.025	0.15	7.68E-04
71	0.406	0.025	0.13	9.01E-04
16	0.877	0.026	0.281	9.12E-04
13	1.13	0.03	0.369	1.12E-03
29	0.642	0.025	0.21	1.15E-03
9	1.42	0.031	0.467	1.22E-03
12	1.02	0.026	0.338	1.31E-03
22	0.747	0.026	0.248	1.32E-03
30	0.631	0.025	0.21	1.34E-03
12	1.07	0.027	0.363	1.55E-03
34	0.61	0.026	0.208	1.67E-03
19	0.763	0.024	0.26	1.69E-03
25	0.693	0.025	0.236	1.71E-03
148	0.278	0.025	0.095	1.71E-03
35	0.594	0.026	0.208	2.17E-03
11	1.13	0.027	0.401	2.38E-03
12	1.23	0.031	0.439	2.49E-03
12	1.23	0.031	0.439	2.49E-03
10	1.21	0.028	0.435	2.63E-03
26	0.614	0.023	0.224	3.08E-03
32	0.555	0.023	0.204	3.29E-03