

Supplementary Information: Association analyses identify 31 new risk loci for colorectal cancer susceptibility

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SUPPLEMENTARY METHODS

Colorectal cancer studies

Genome-wide association studies (GWAS) of colorectal cancer (CRC) have thus far reported 43 SNPs mapping to 40 risk loci in European populations¹⁻¹⁶ (**Supplementary Table 1**). In Asians, 18 SNPs mapping to 16 risk loci have been identified¹⁷⁻²³.

Supplementary tools

Gene expression was normalised using the TMM algorithm, implemented in edgeR²⁴. *cis*-eQTL mapping was performed separately for proximal colon, distal colon and rectum samples using FastQTL²⁵. Principal components for the SNP data and additional covariate factors were identified using Probabilistic Estimation of Expression Residuals (PEER)²⁶. Beta distribution-adjusted empirical *P*-values from FastQTL were used to calculate *Q*-values²⁷. MetaTissue²⁸ was used to generate a “pan-colonic” eQTL measure from the three individual RNA-seq datasets per patient.

Hi-C and CHi-C libraries were sequenced using HiSeq 2000 (Illumina). Reads were aligned to the GRCh37 build using bowtie2 v2.2.6²⁹ and identification of valid di-tags was performed using HiCUP v0.5.9³⁰.

ChIP libraries were sequenced using HiSeq 2000 (Illumina) with 100bp single-ended reads. Generated raw reads were filtered for quality (Phred33 $\geq$ 30) and length ($n \geq 32$), and adapter sequences were removed using Trimmomatic v0.22³¹. Reads passing filters were then aligned to the human reference (hg19) using BWA v0.6.1. Peak calls are obtained using MACS2 v 2.0.10.07132012³².

Chromatin data were obtained from HaploReg v4³³.

Supplementary datasets

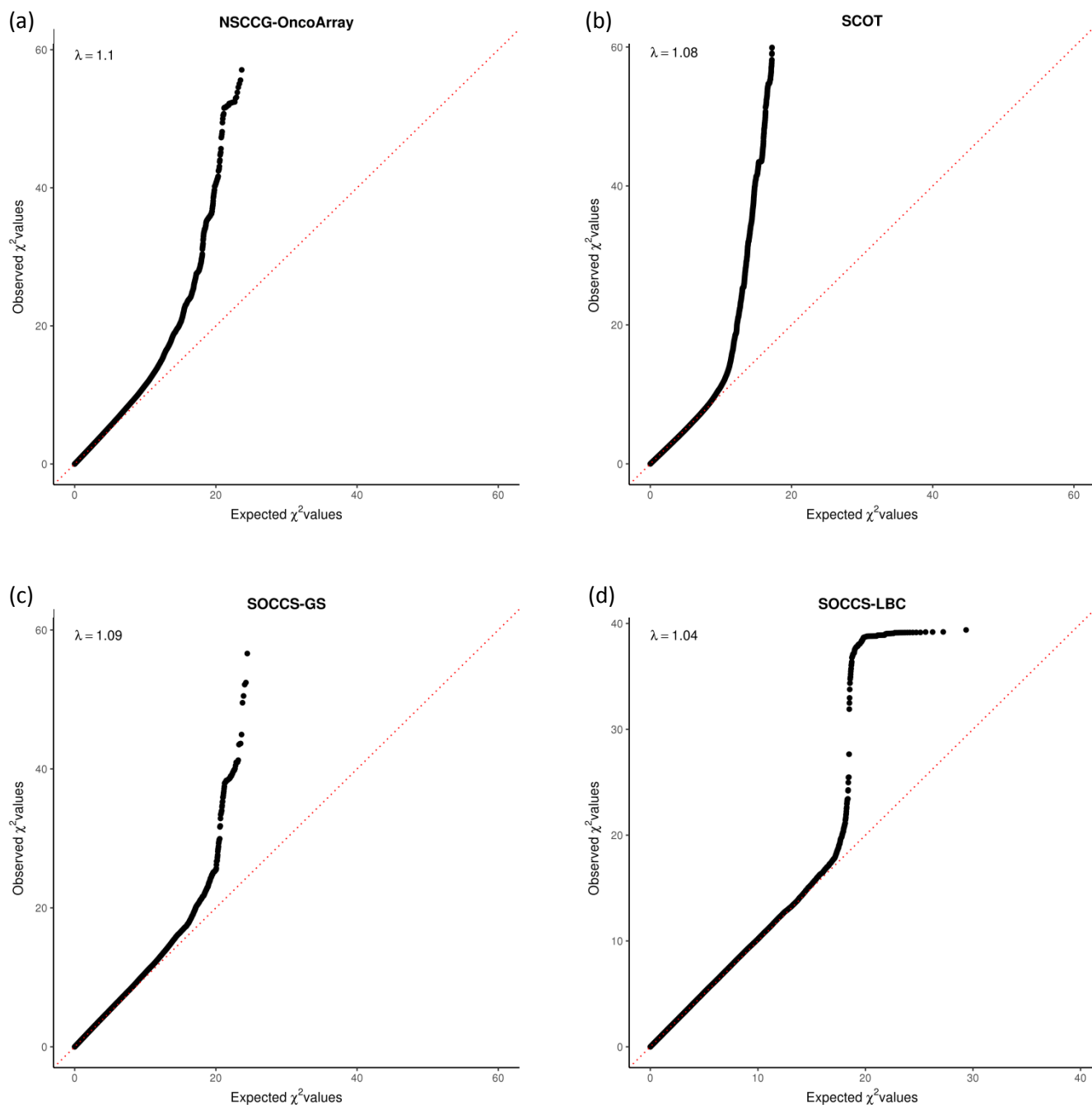
Transcription factor binding disruption was performed by testing the SNPs by estimating their effects on over 2,800 binding motifs as characterised by ENCODE³⁴, FactorBook³⁵, HOCOMOCO³⁶ and HOMER³⁷.

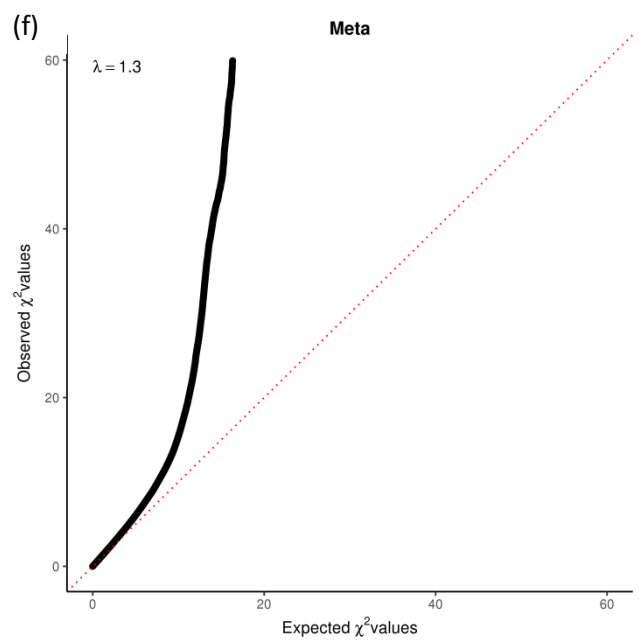
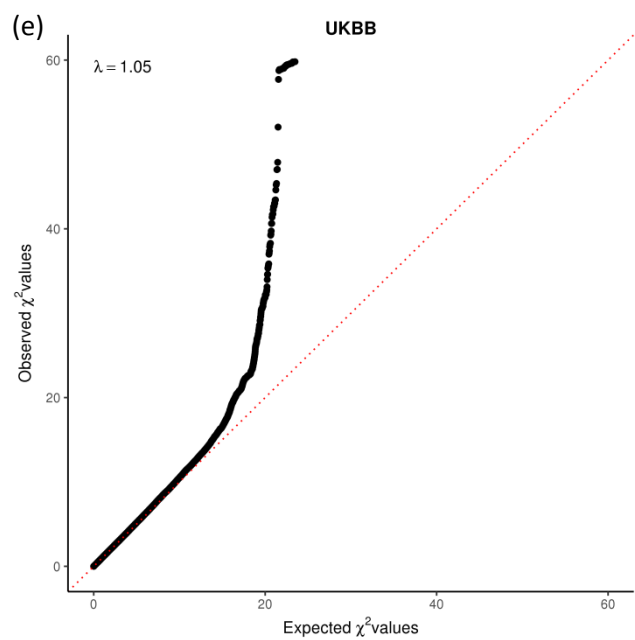
LD score regression was used to determine if any traits were correlated with CRC risk. GWAS summary data was obtained for allergy³⁸, asthma³⁸, coronary artery disease³⁹, fatty acids⁴⁰⁻⁴⁵, lipids (total cholesterol, high density lipoprotein, low density lipoprotein, triglycerides)⁴⁶, auto-immune diseases

(Crohn's disease⁴⁷, rheumatoid arthritis⁴⁸, atopic dermatitis⁴⁹, celiac disease⁵⁰, multiple sclerosis⁵¹, primary biliary cirrhosis⁵², inflammatory bowel disease⁴⁷, ulcerative colitis⁴⁷, systemic lupus erythematosus⁵³), anthropometric measures (BMI, height, body fat)^{54,55}, glucose sensitivity (fasting glucose, fasting insulin, HbA1c)^{56,57}, childhood measures (birth weight⁵⁸, birth length⁵⁹, childhood obesity⁶⁰, childhood BMI⁶¹), eGFR⁶², and type 2 diabetes⁶³.

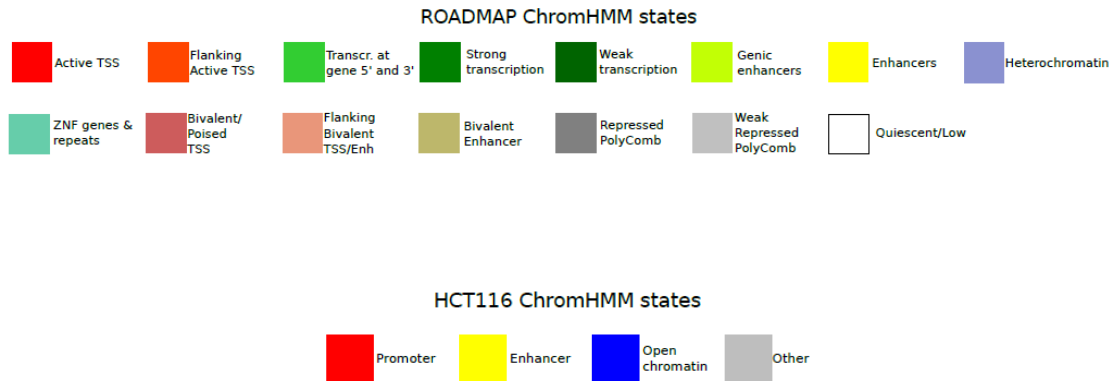
SUPPLEMENTARY FIGURES

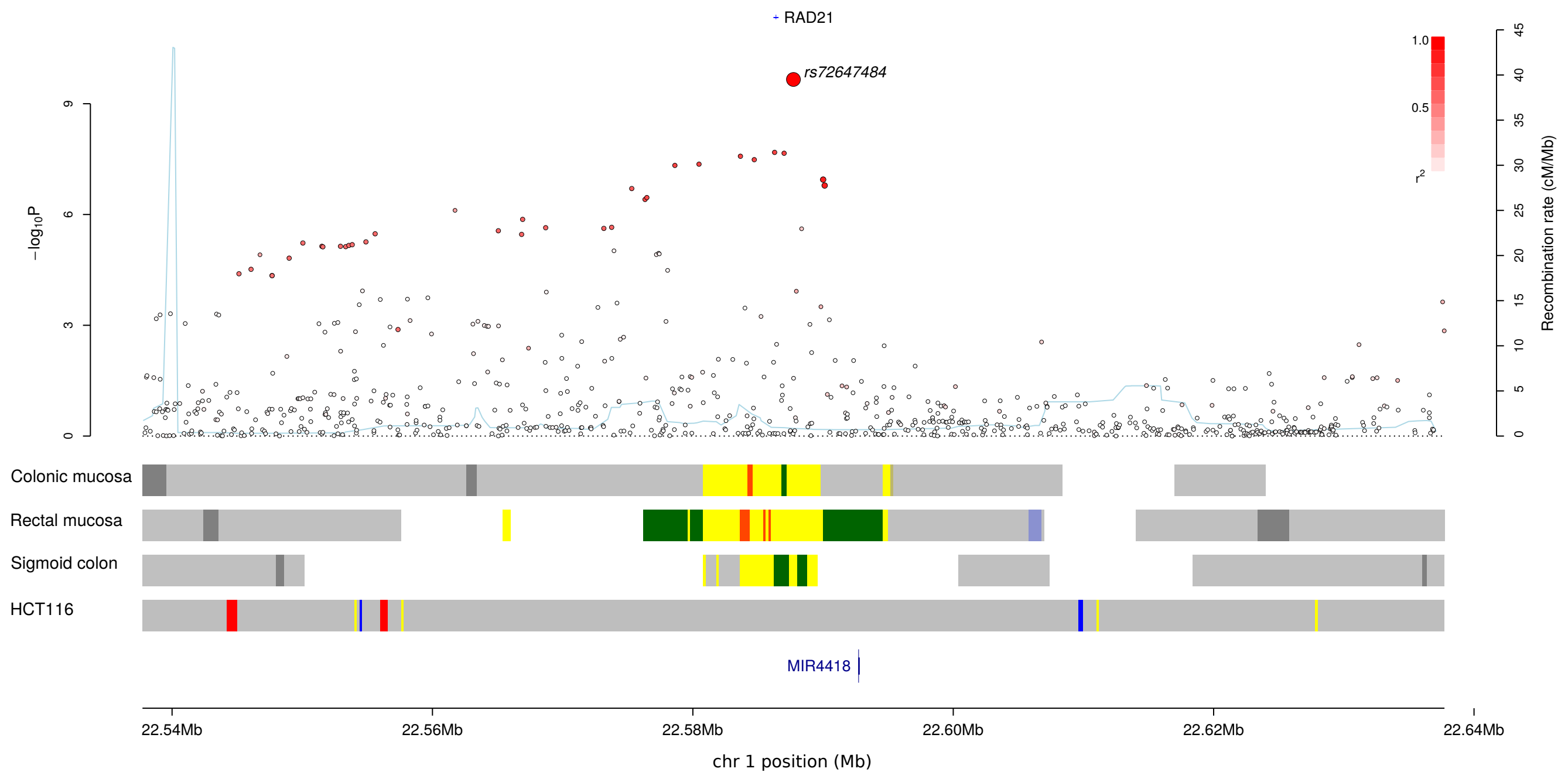
Supplementary Figure 1: Quantile-Quantile plots of observed and expected χ^2 values of association between SNP genotype and CRC after imputation for (a) NSCCG-OncoArray, (b) SCOT, (c) SOCCS/GS, (d) SOCCS/LBC, (e) UK Biobank, and (f) overall meta-analysis. Meta $\lambda_{GC} = 1.10$, $\lambda_{1000} = 1.00$. The red line represents the null hypothesis of no true association.

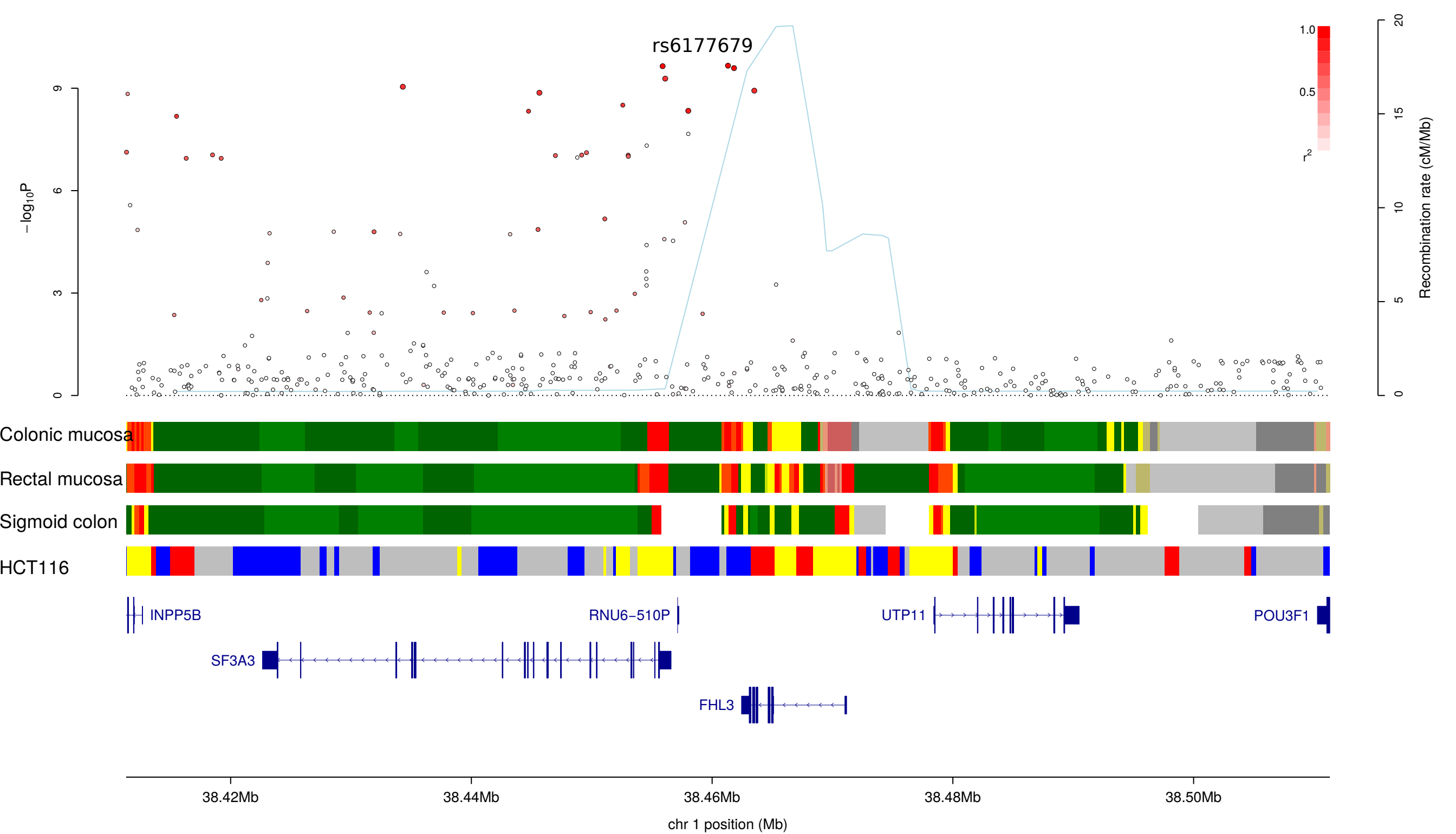


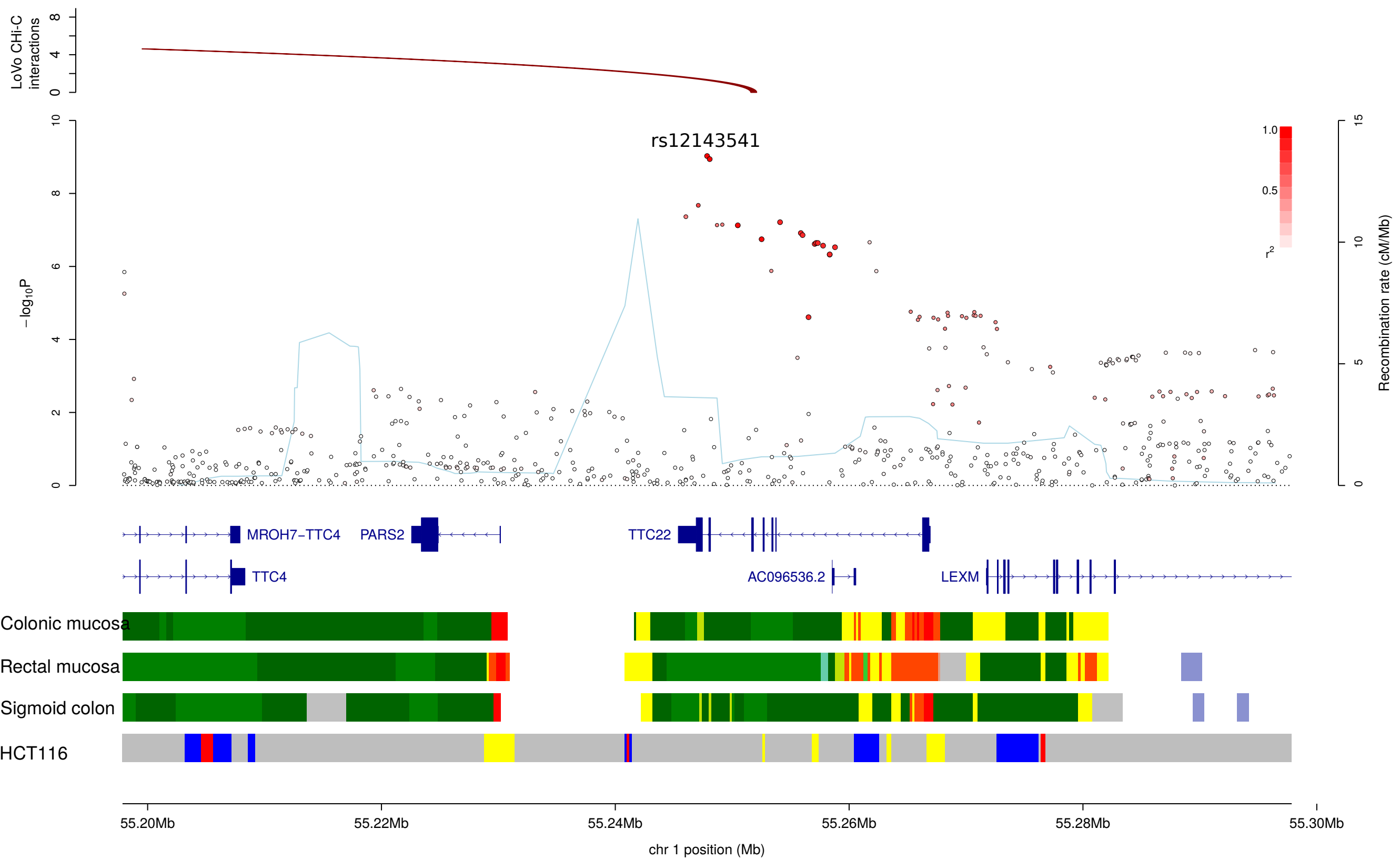


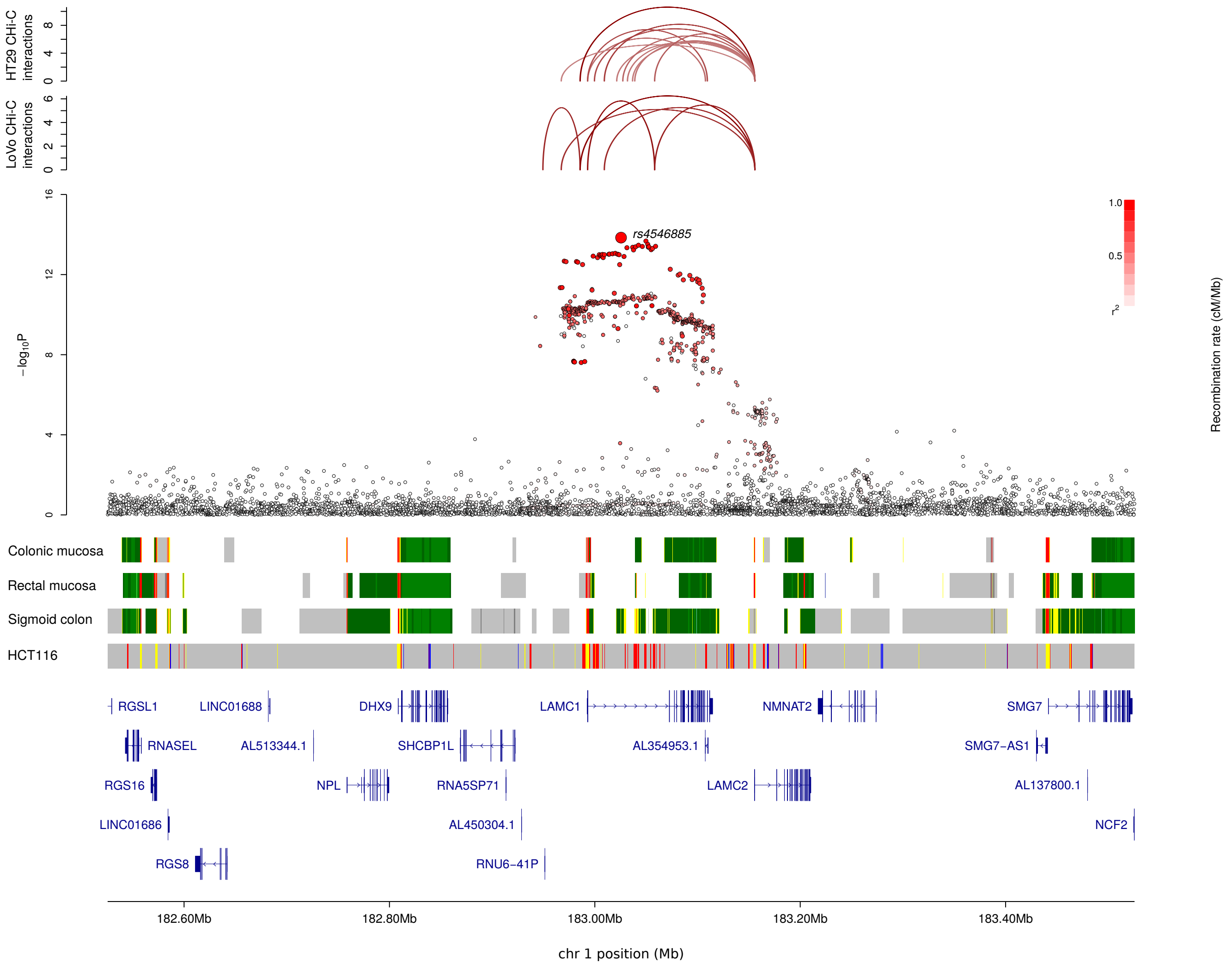
Supplementary Figure 2: Regional plots of the new colorectal cancer risk loci. In the main panel, $-\log_{10}$ P -values (y-axis) of the SNPs are shown according to their chromosomal positions (x-axis). The colour intensity of each symbol reflects the extent of LD with the top SNP: white ($r^2 = 0$) through to dark red ($r^2 = 1.0$), with r^2 estimated from EUR 1000 Genomes data. Genetic recombination rates (cM/Mb), are shown with a light blue line. Physical positions are based on GRCh37 of the human genome. Where available, the upper panel shows Hi-C contacts from HT29 or LoVo. The lower panel shows the chromatin state segmentation track from the Roadmap epigenomics project (colonic mucosa, rectal mucosa, sigmoid colon), and HCT116. Also shown are the relative positions of genes and transcripts mapping to each region of association.

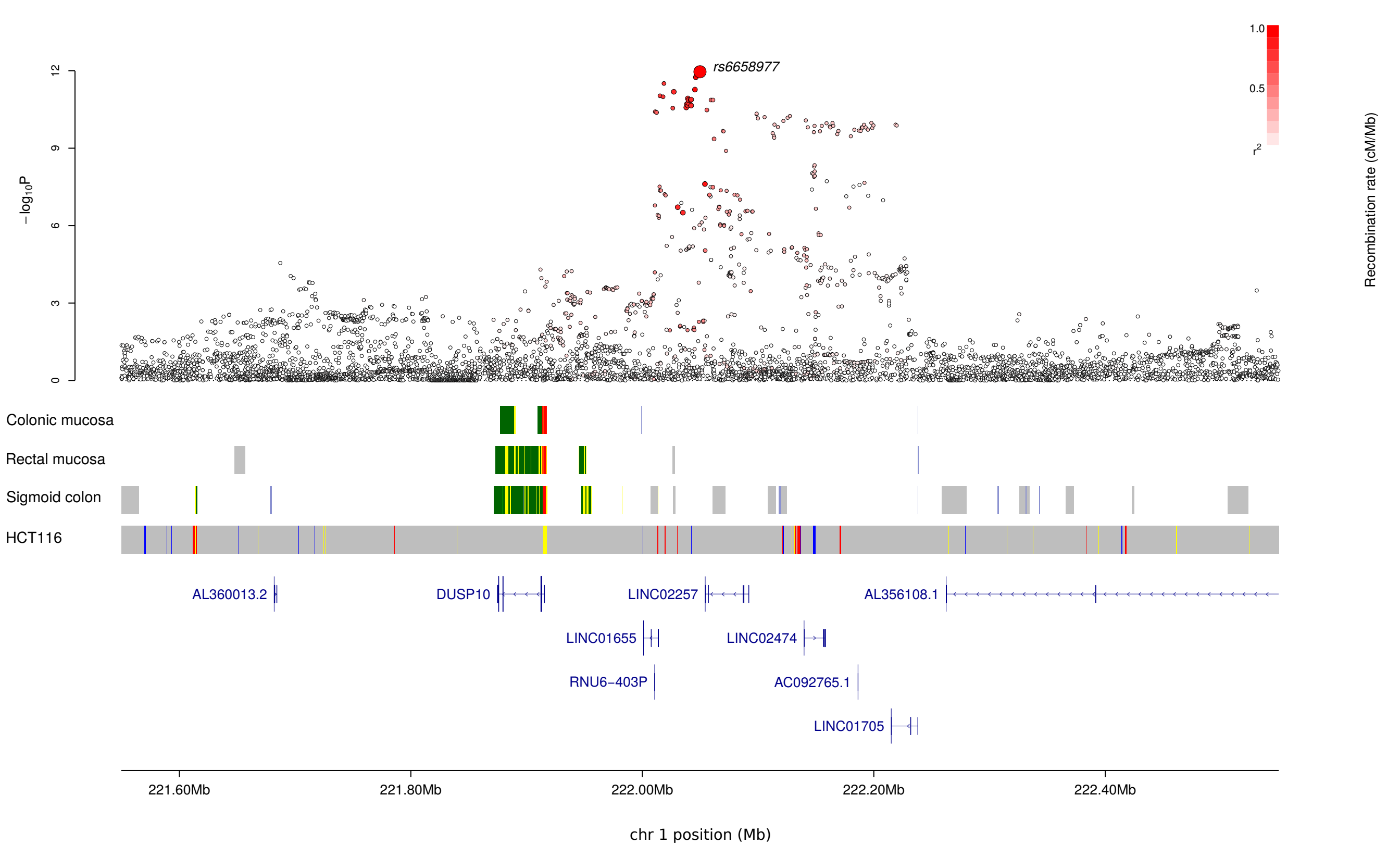


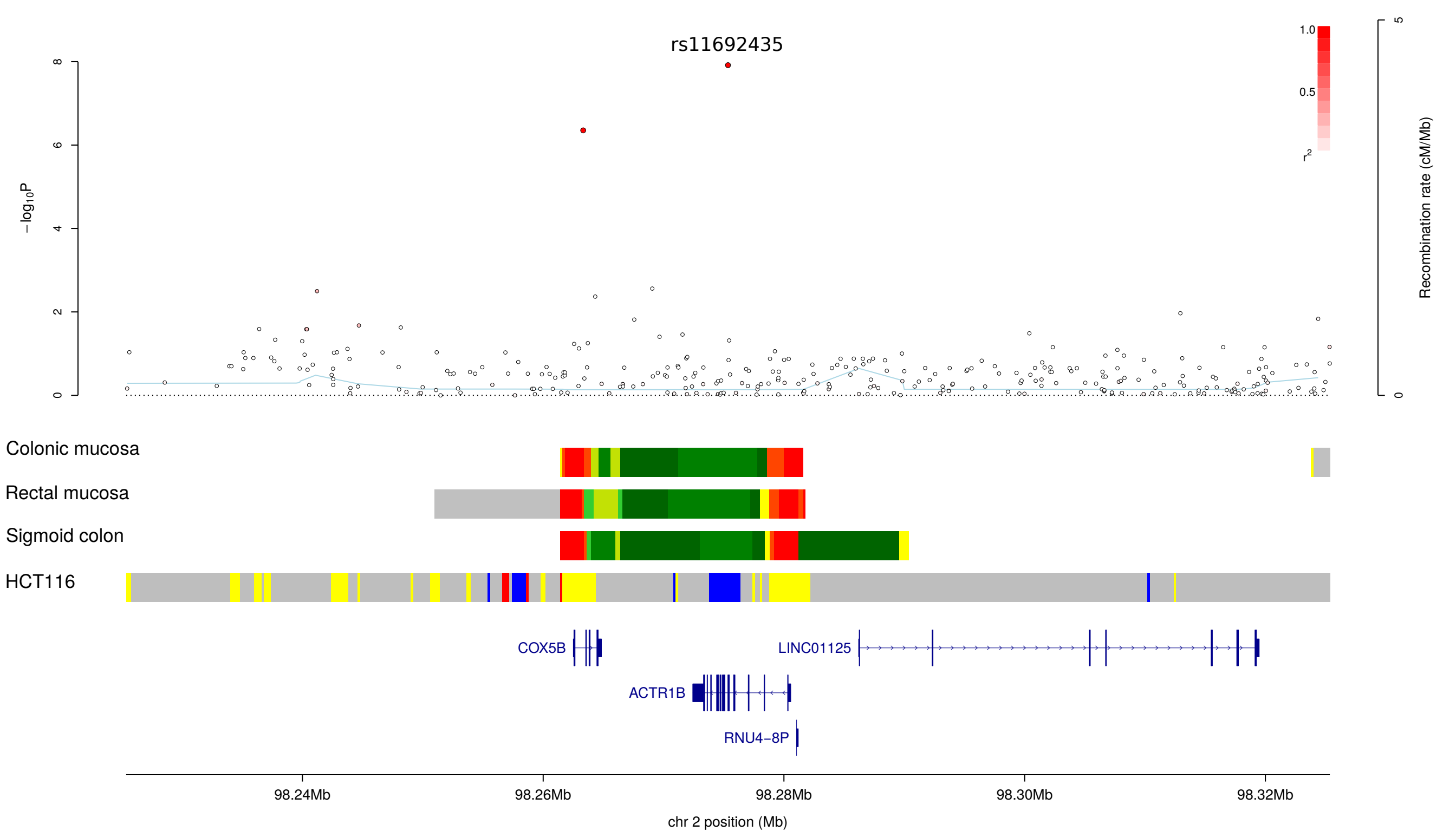


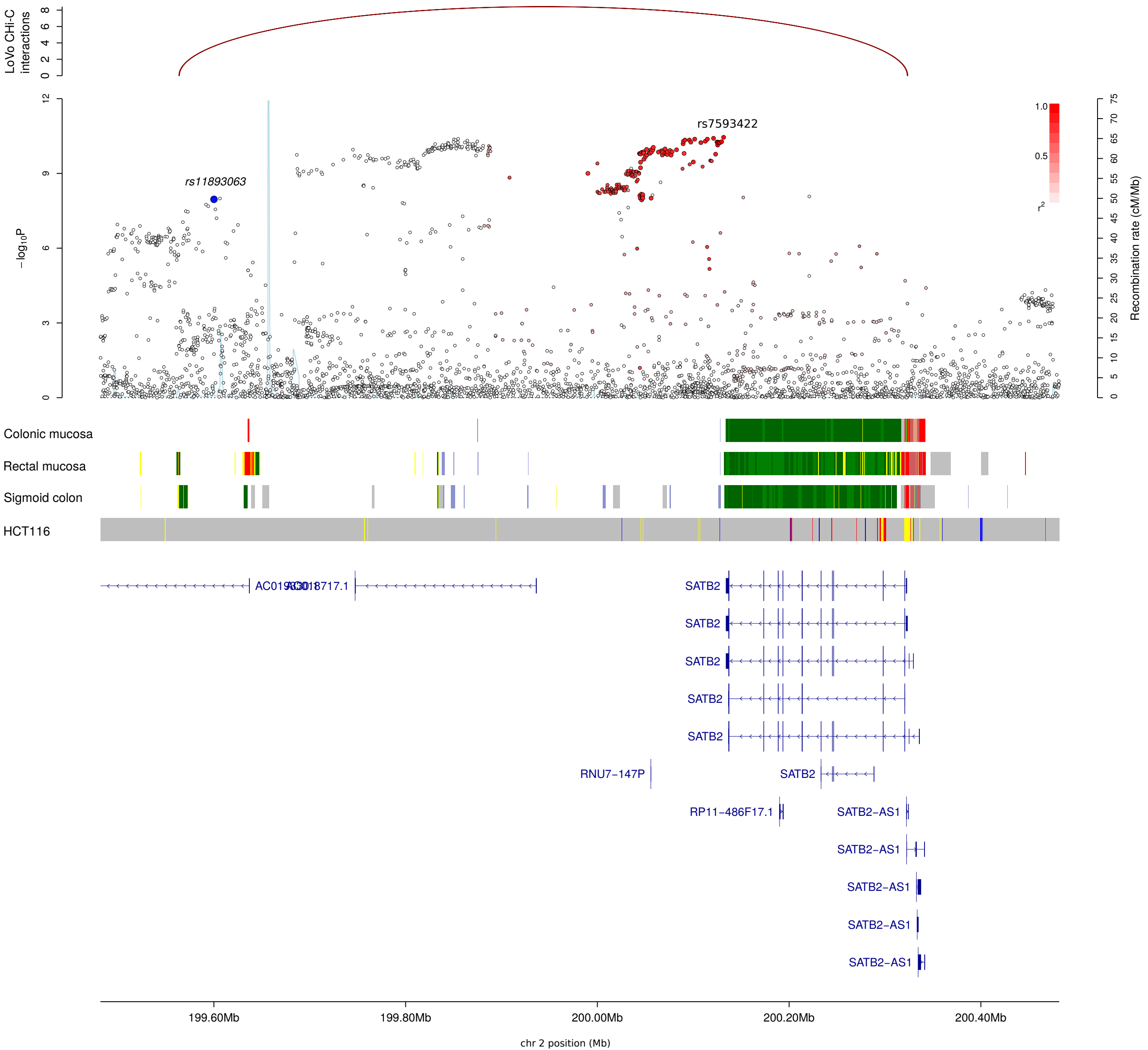


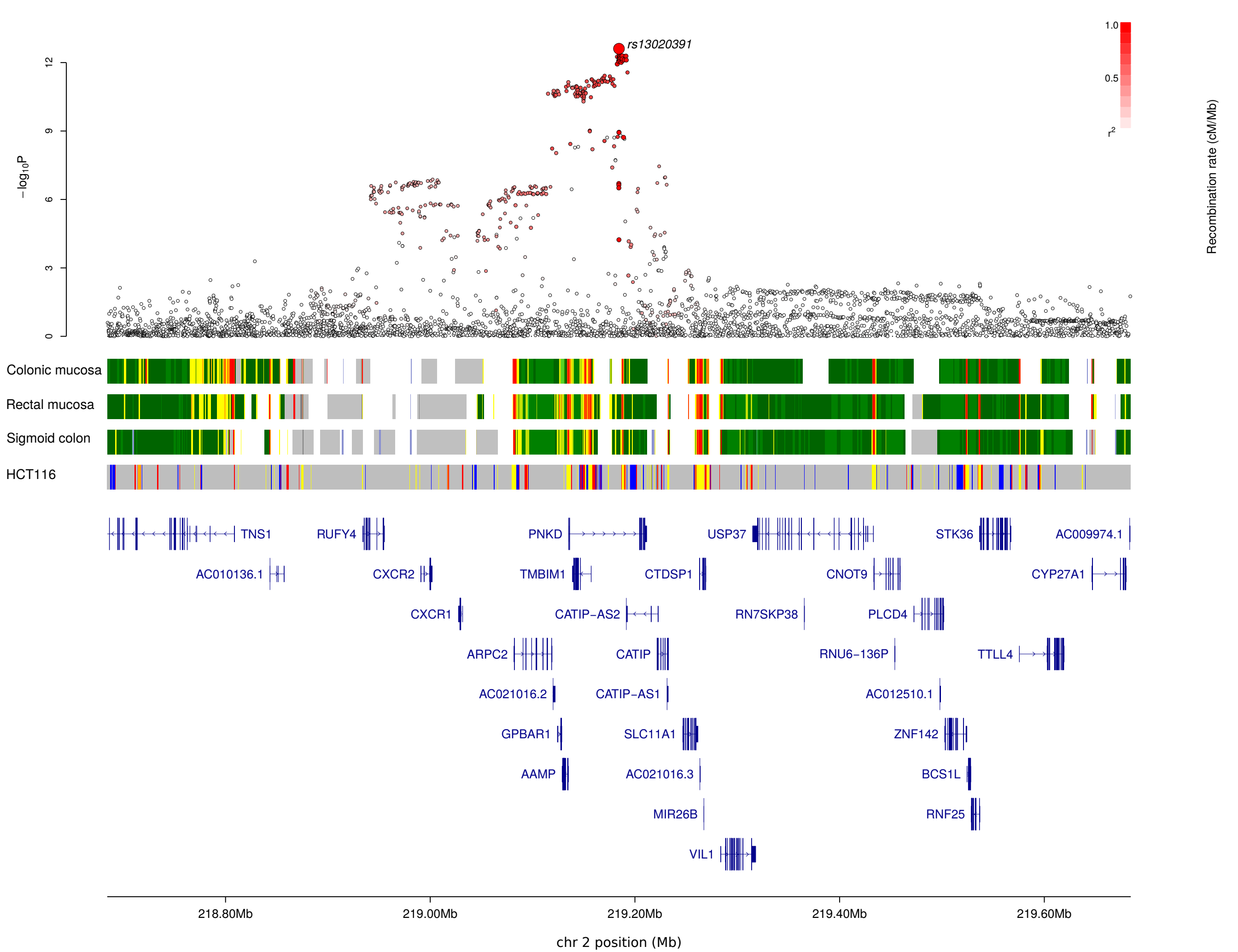


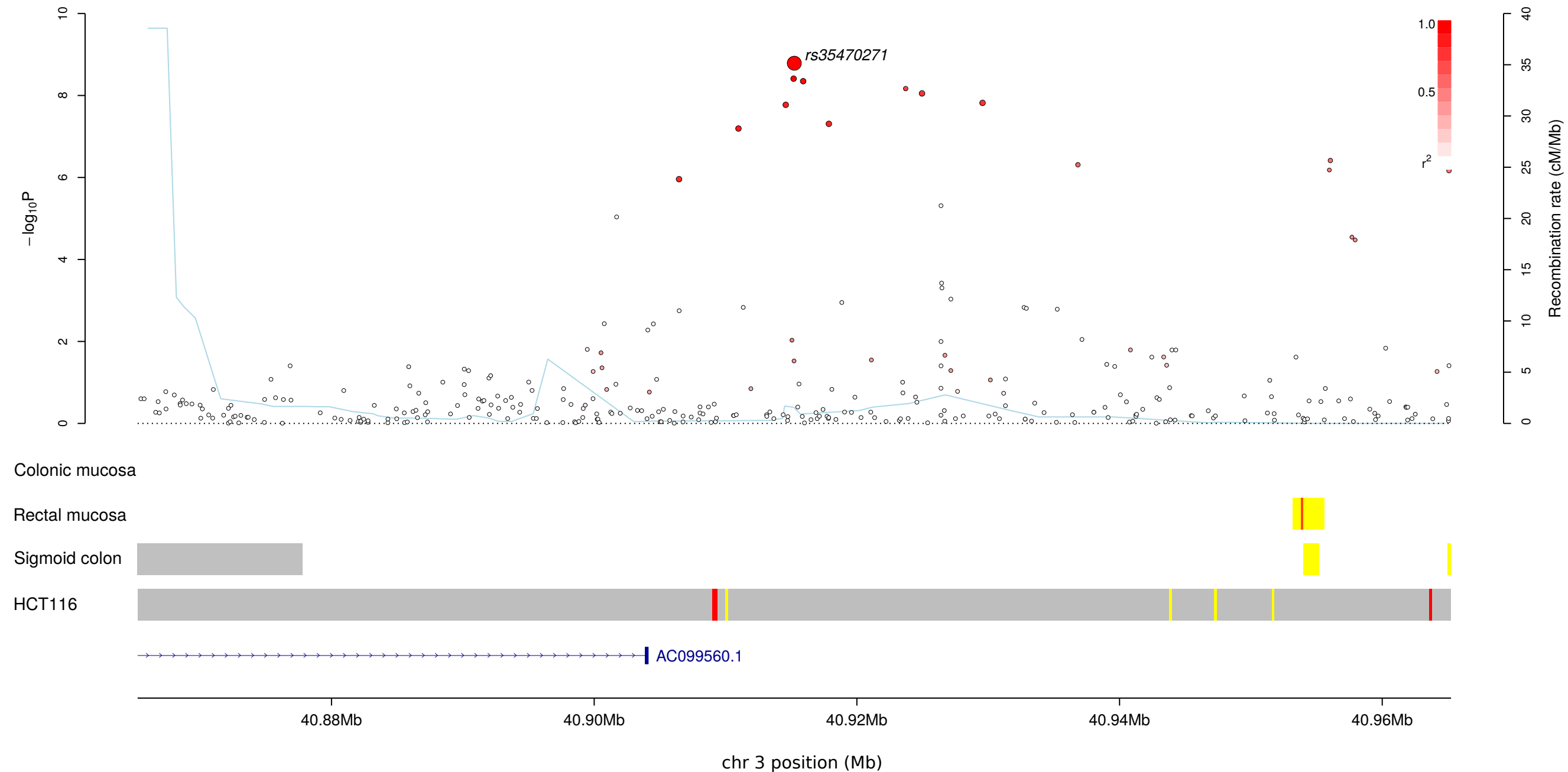


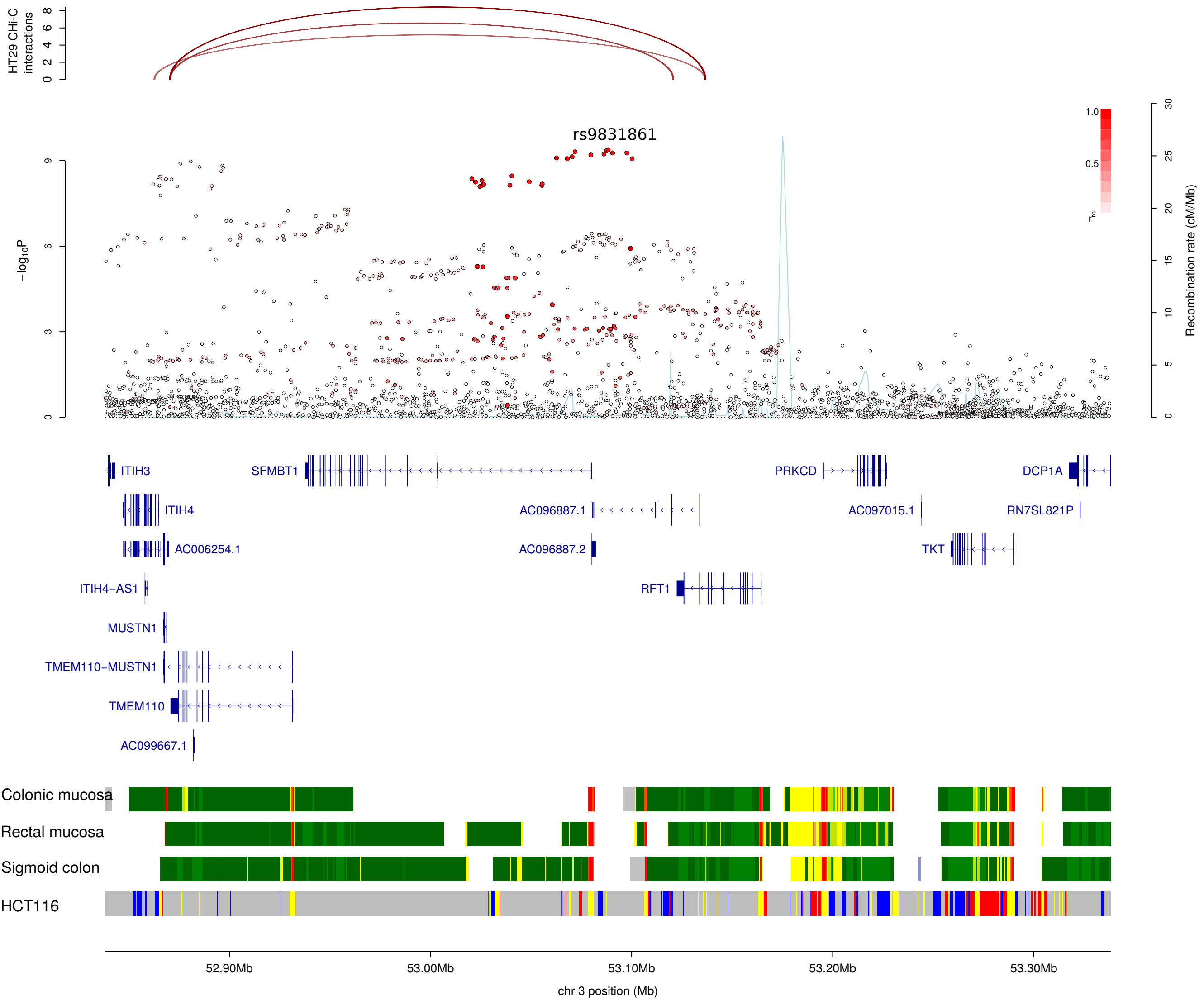


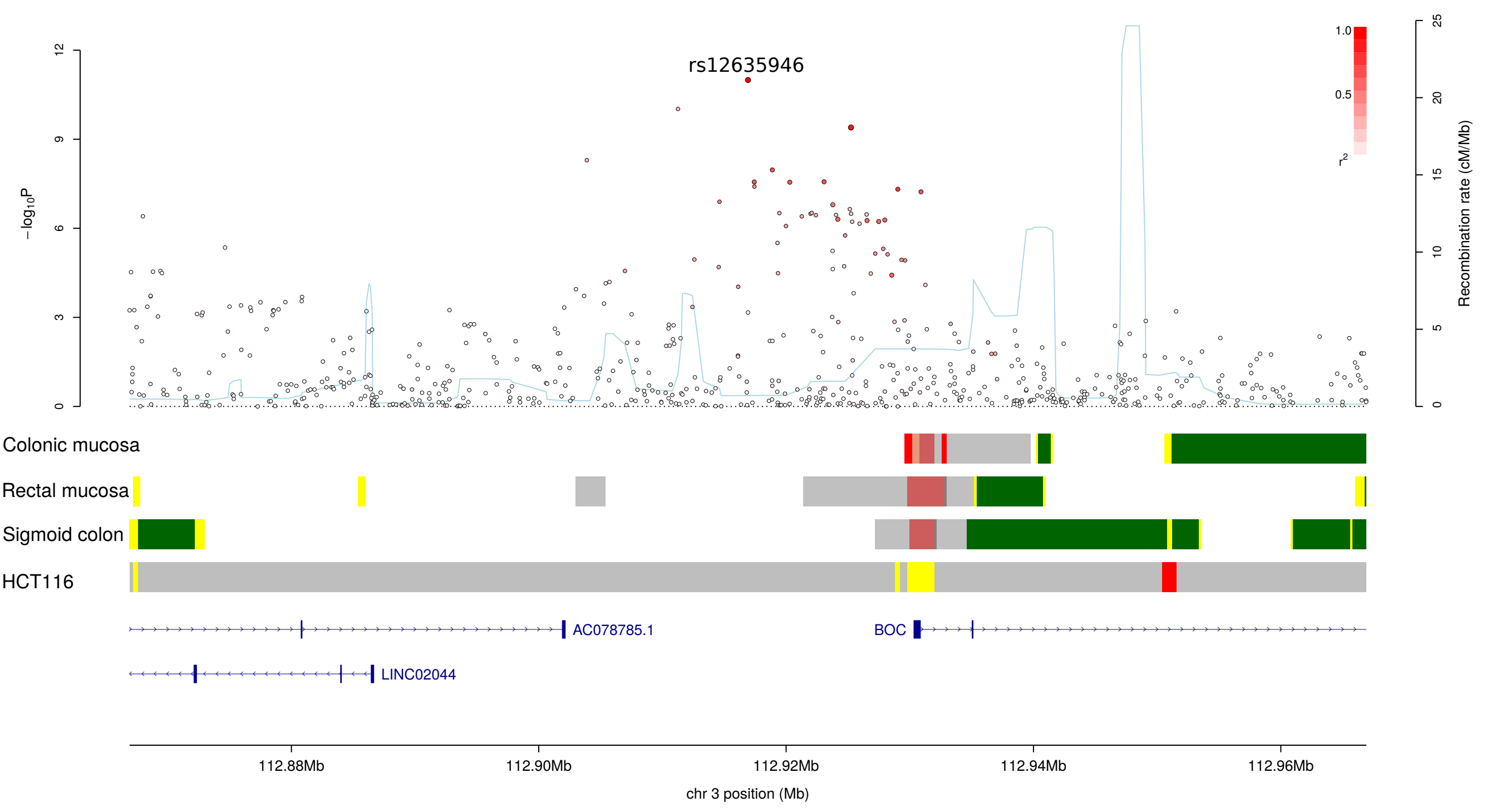


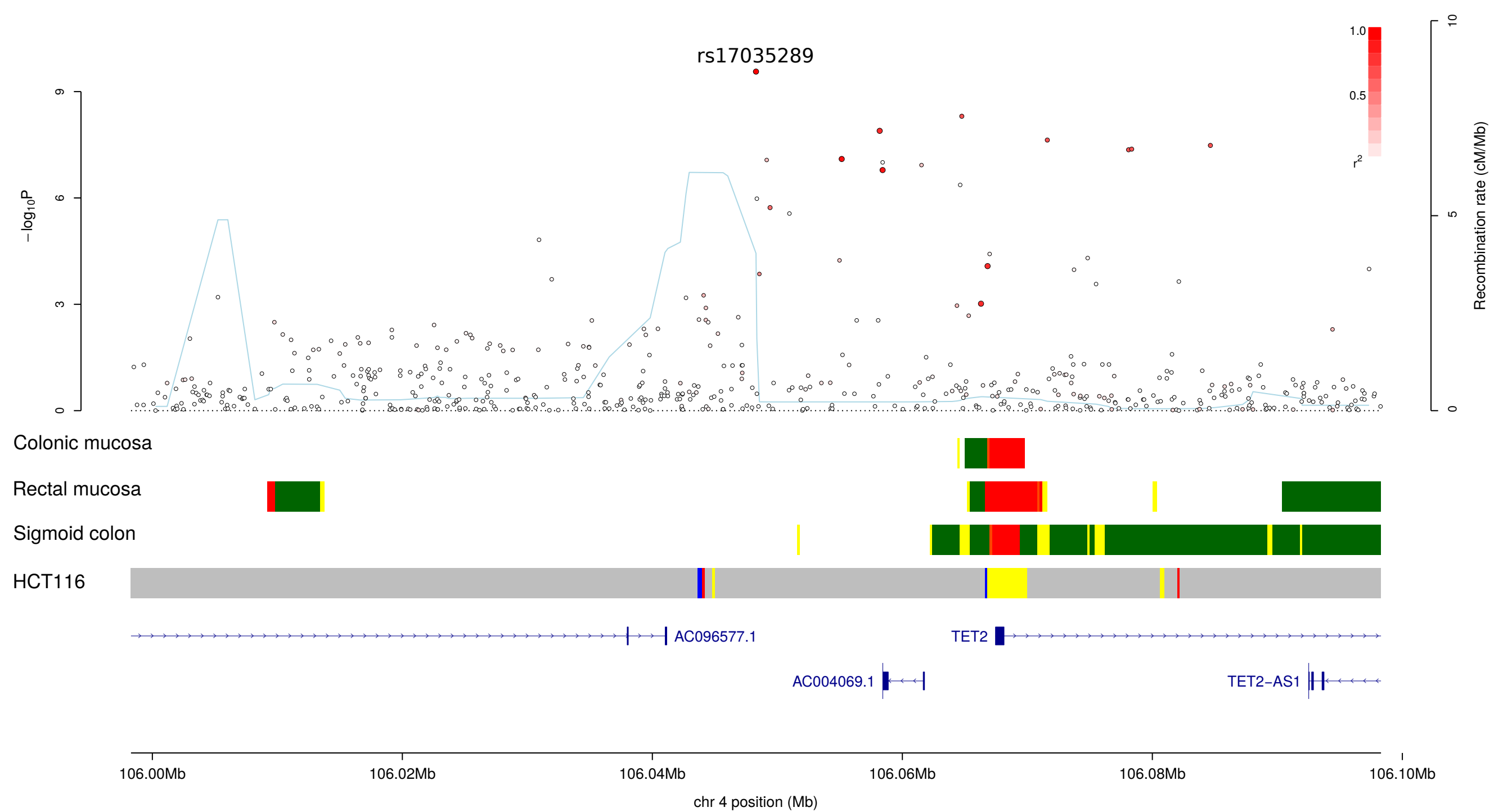


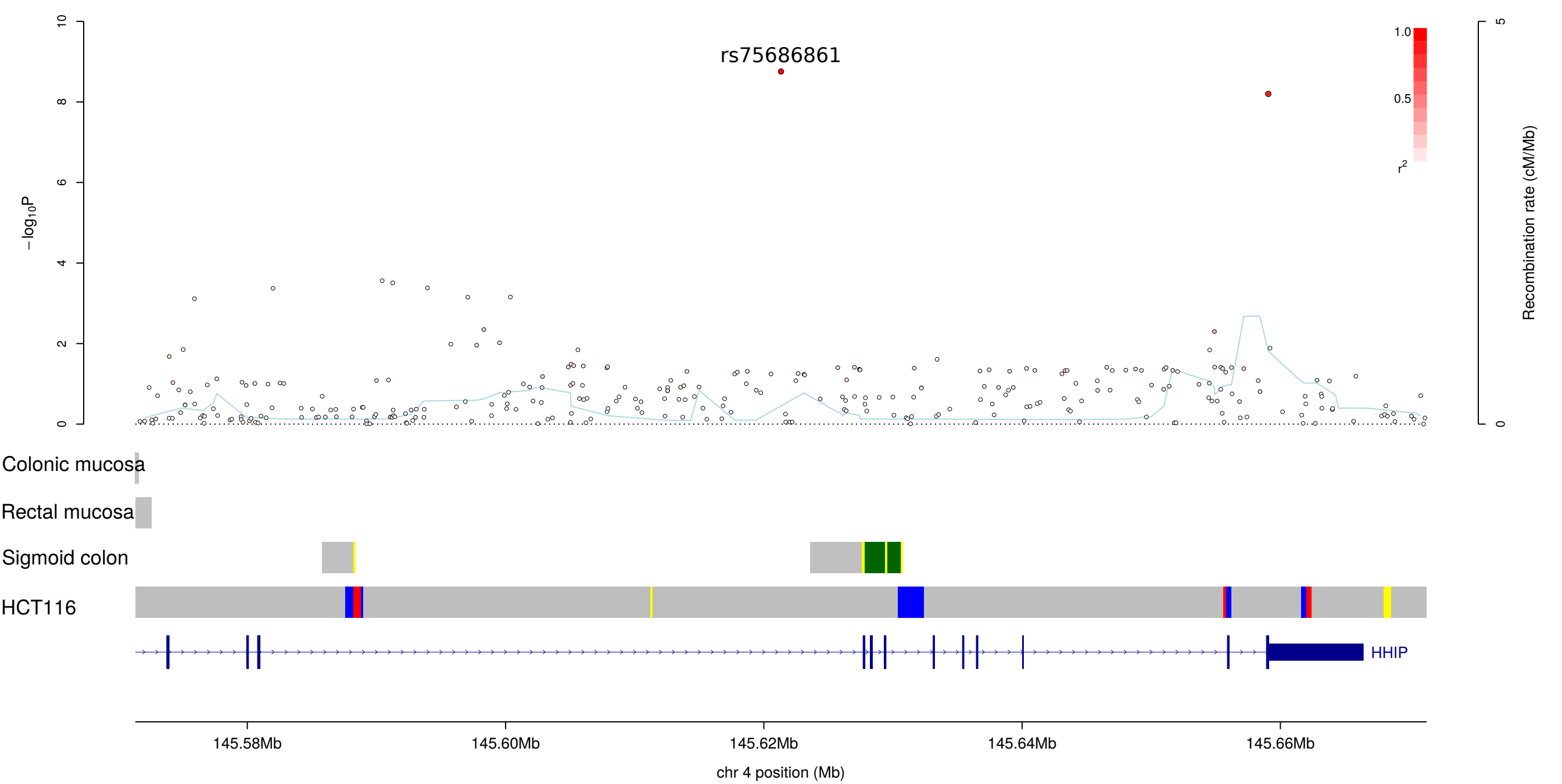


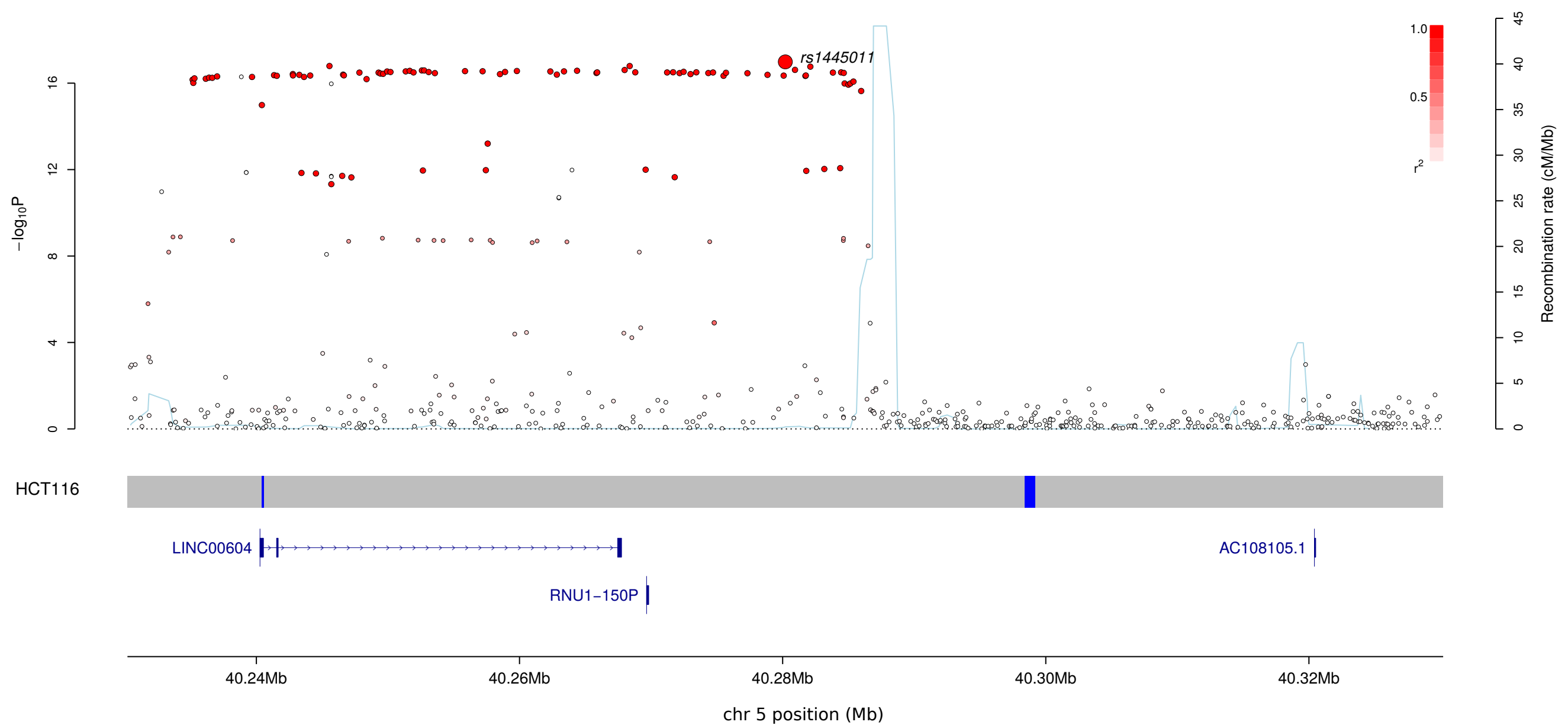


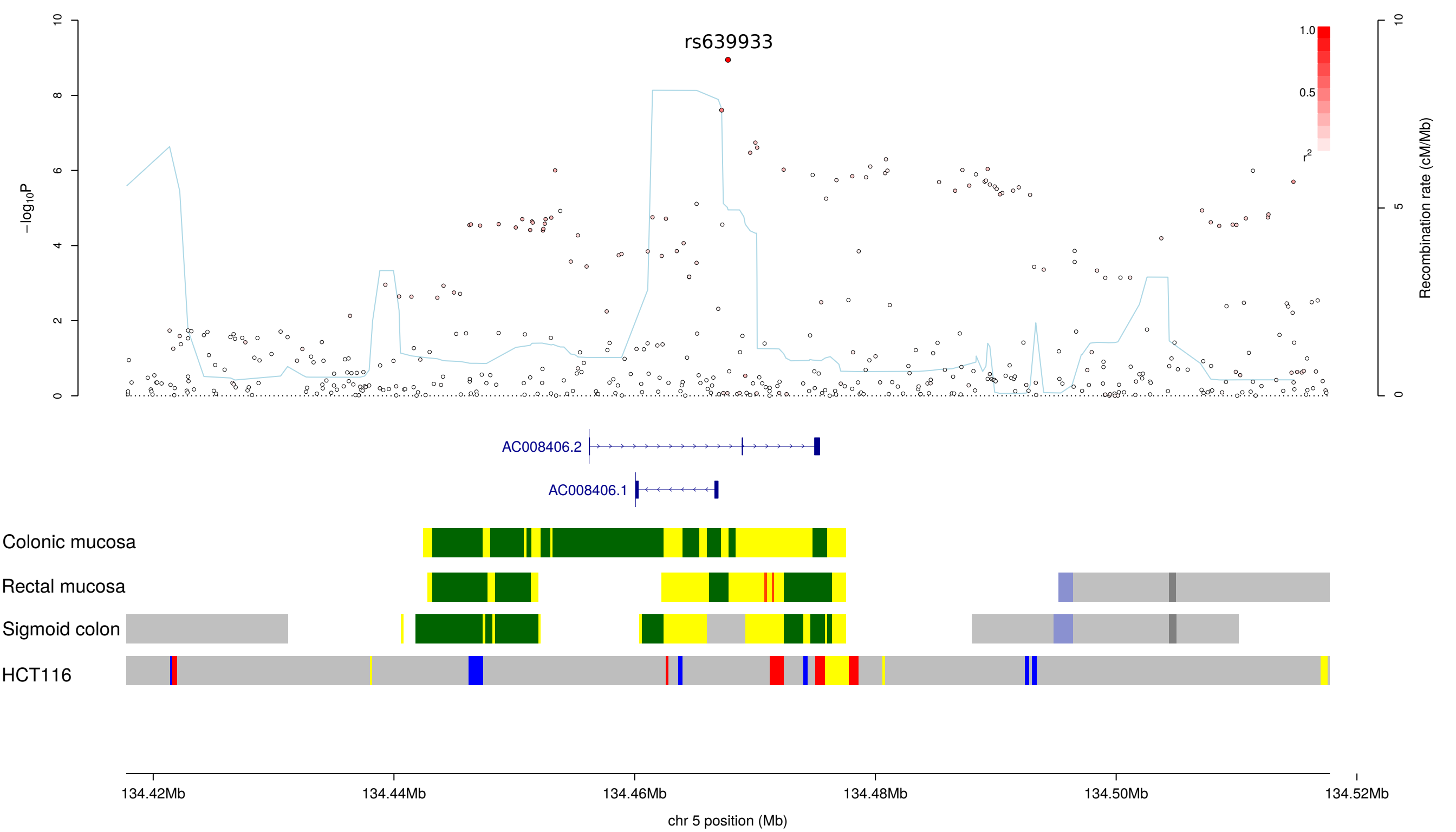


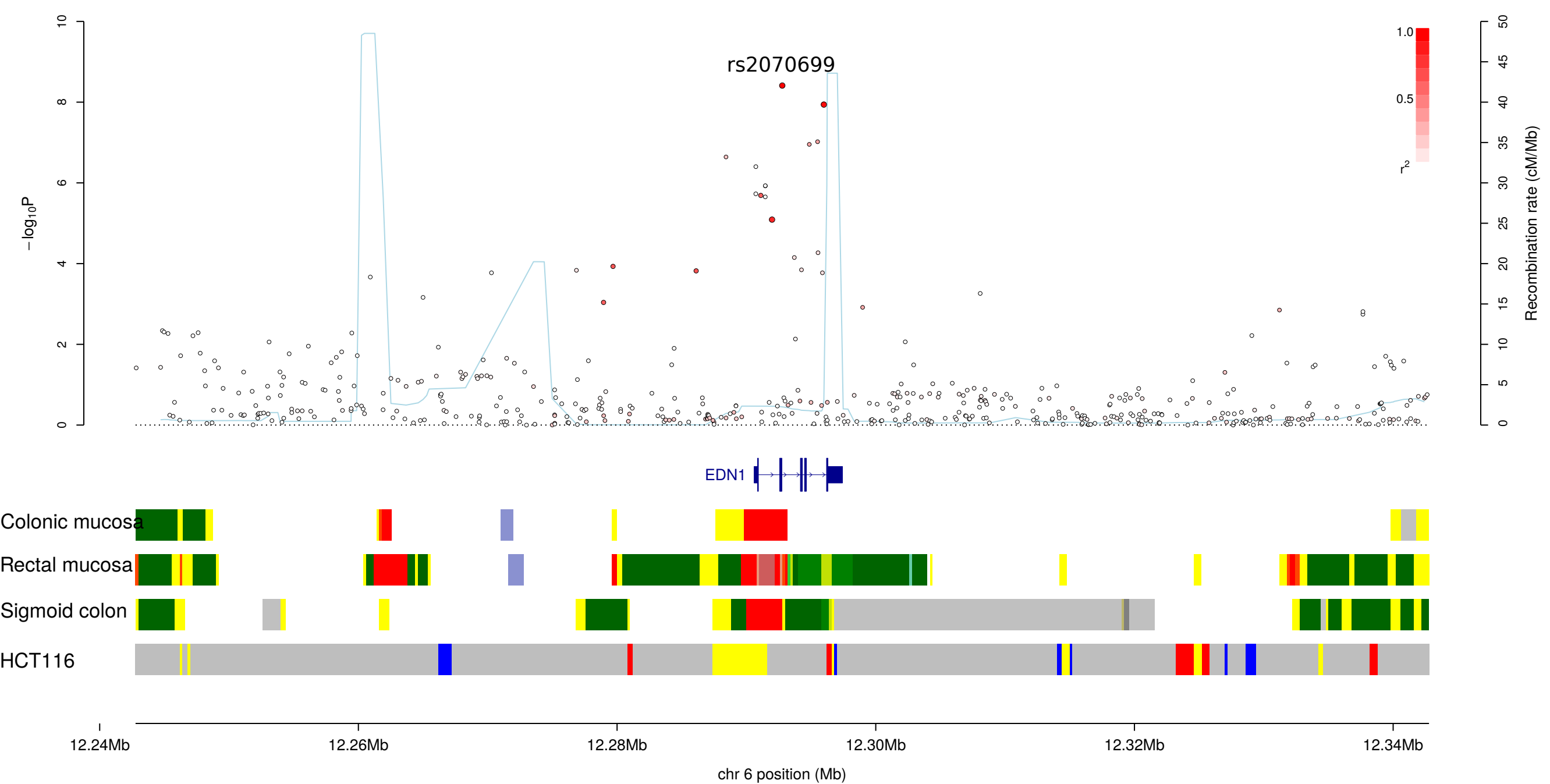


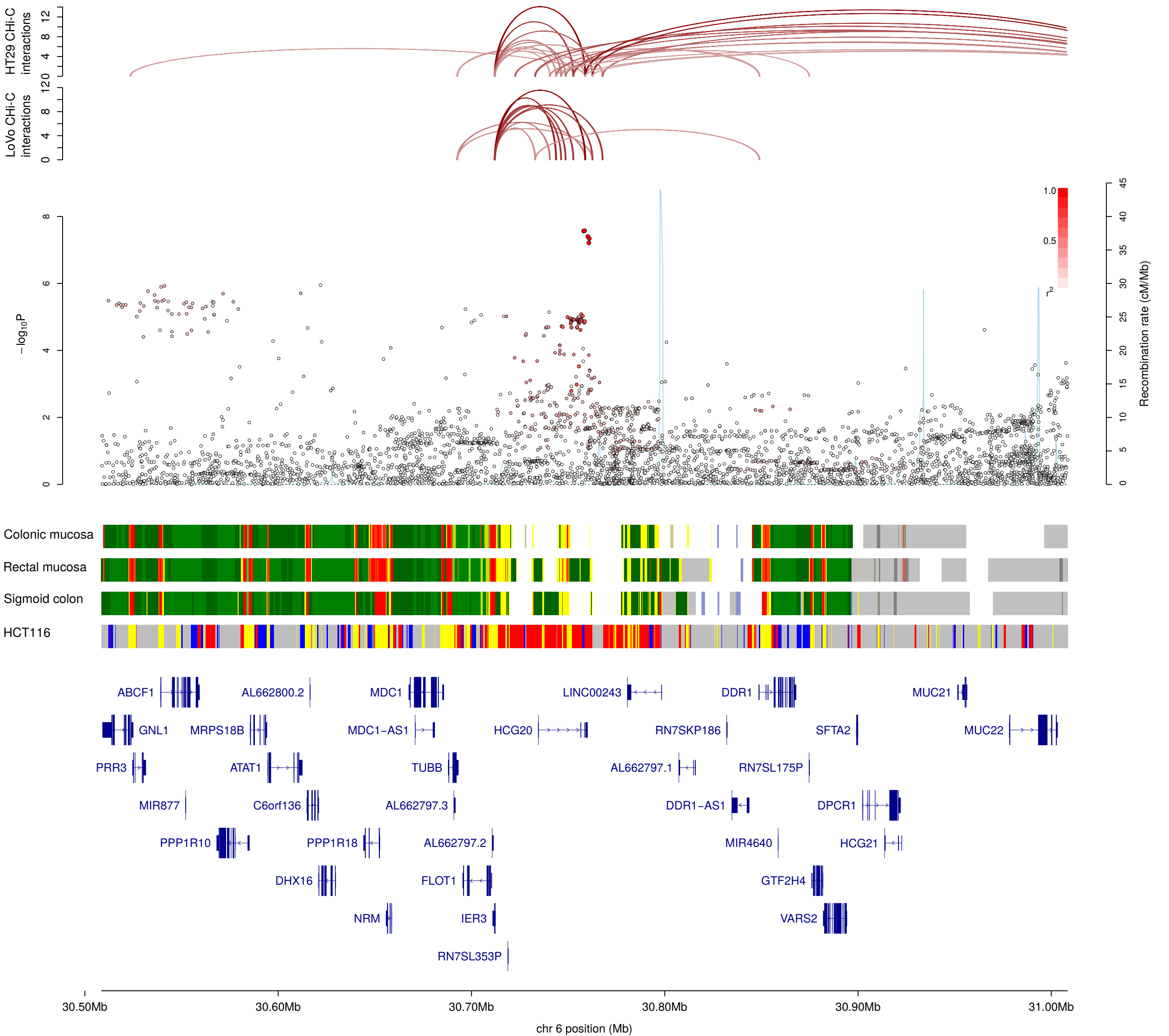


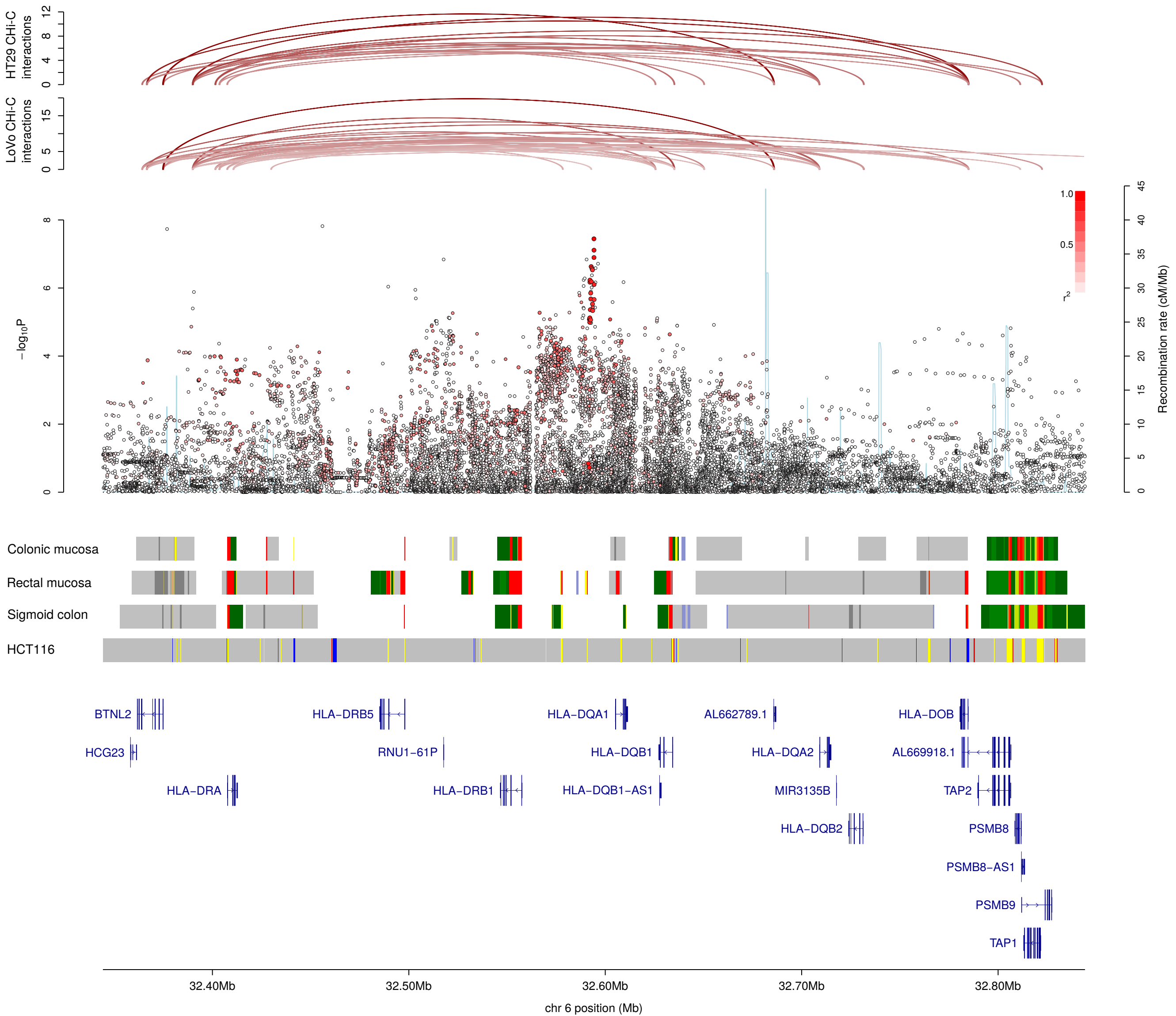


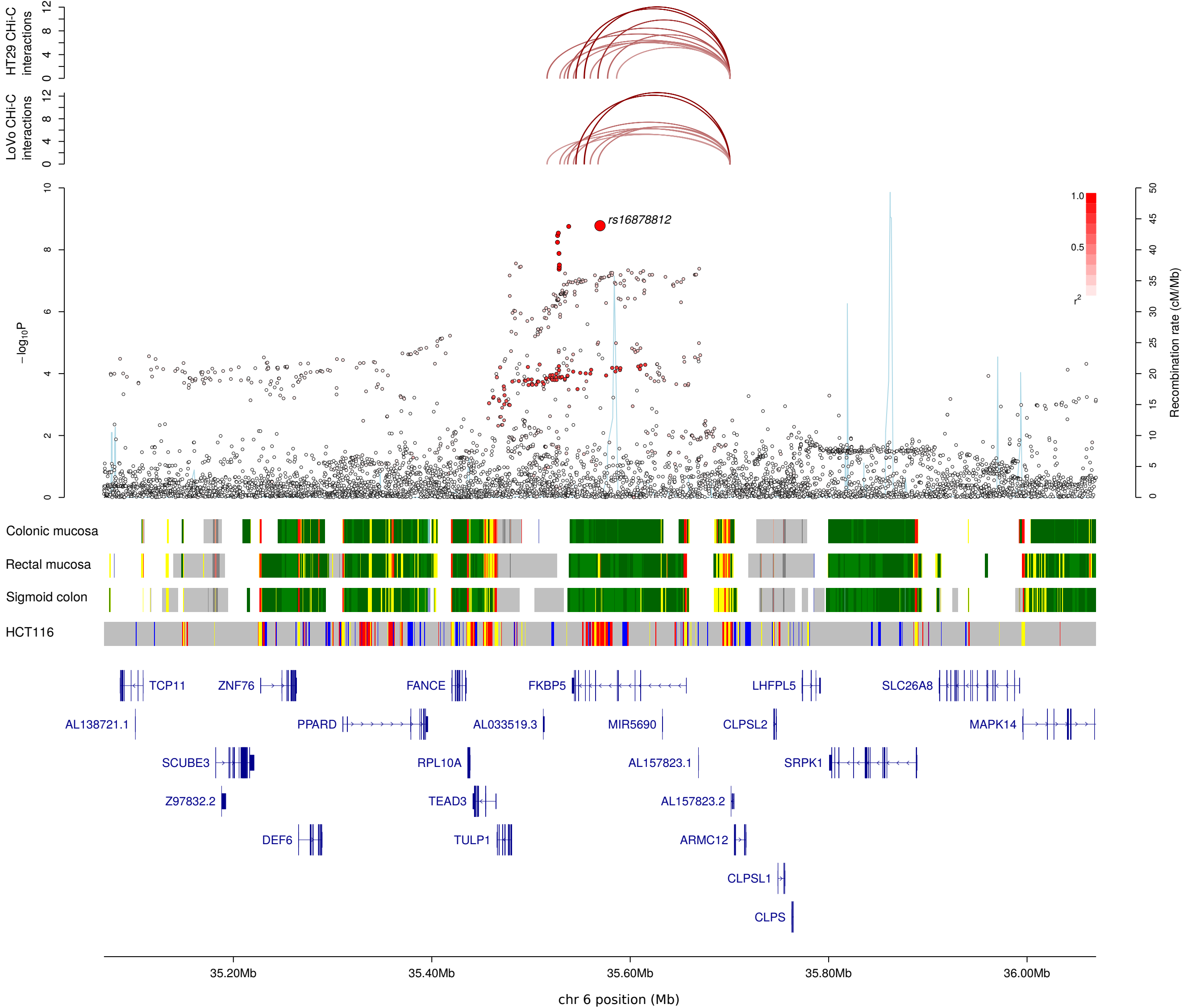


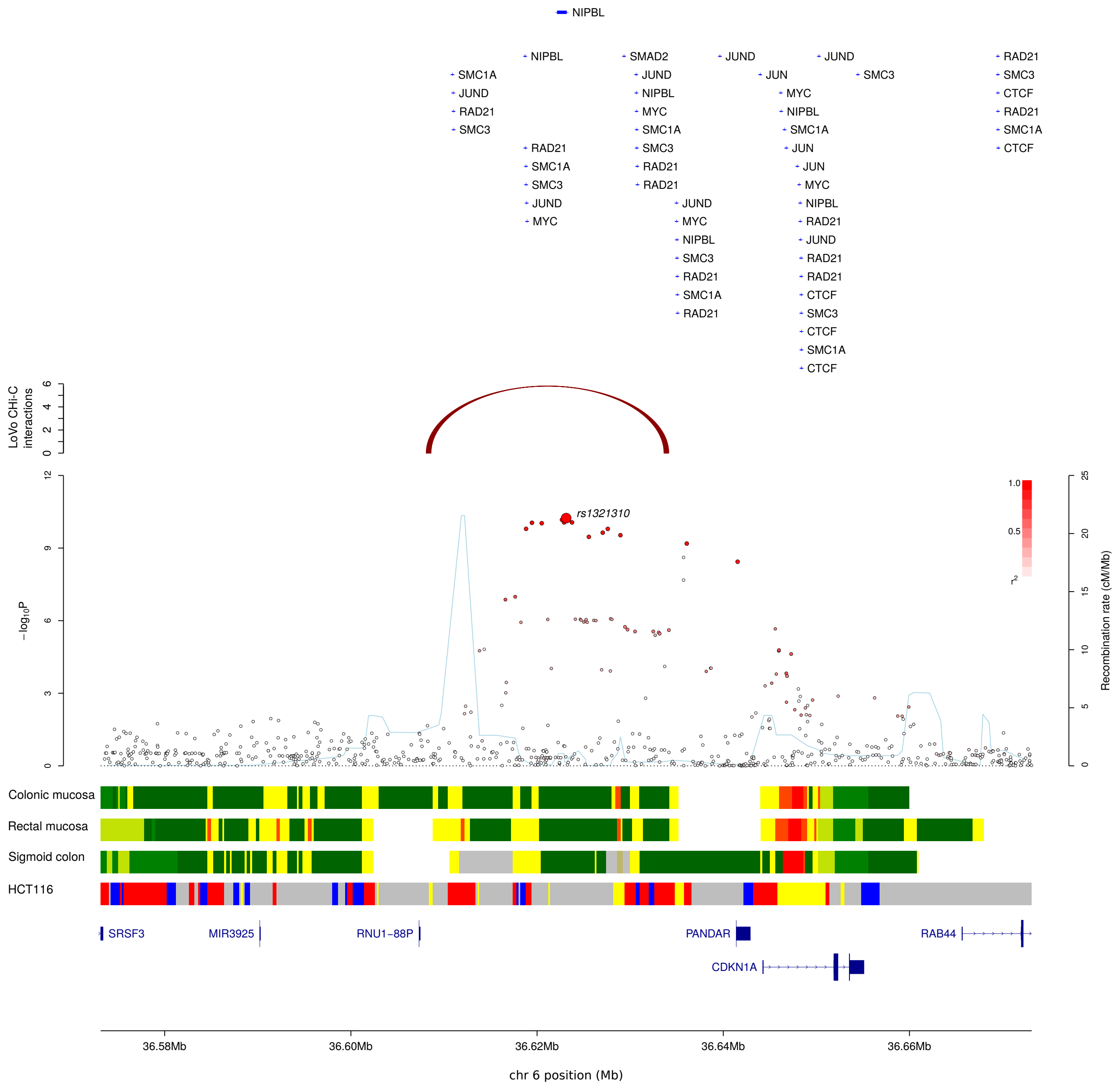


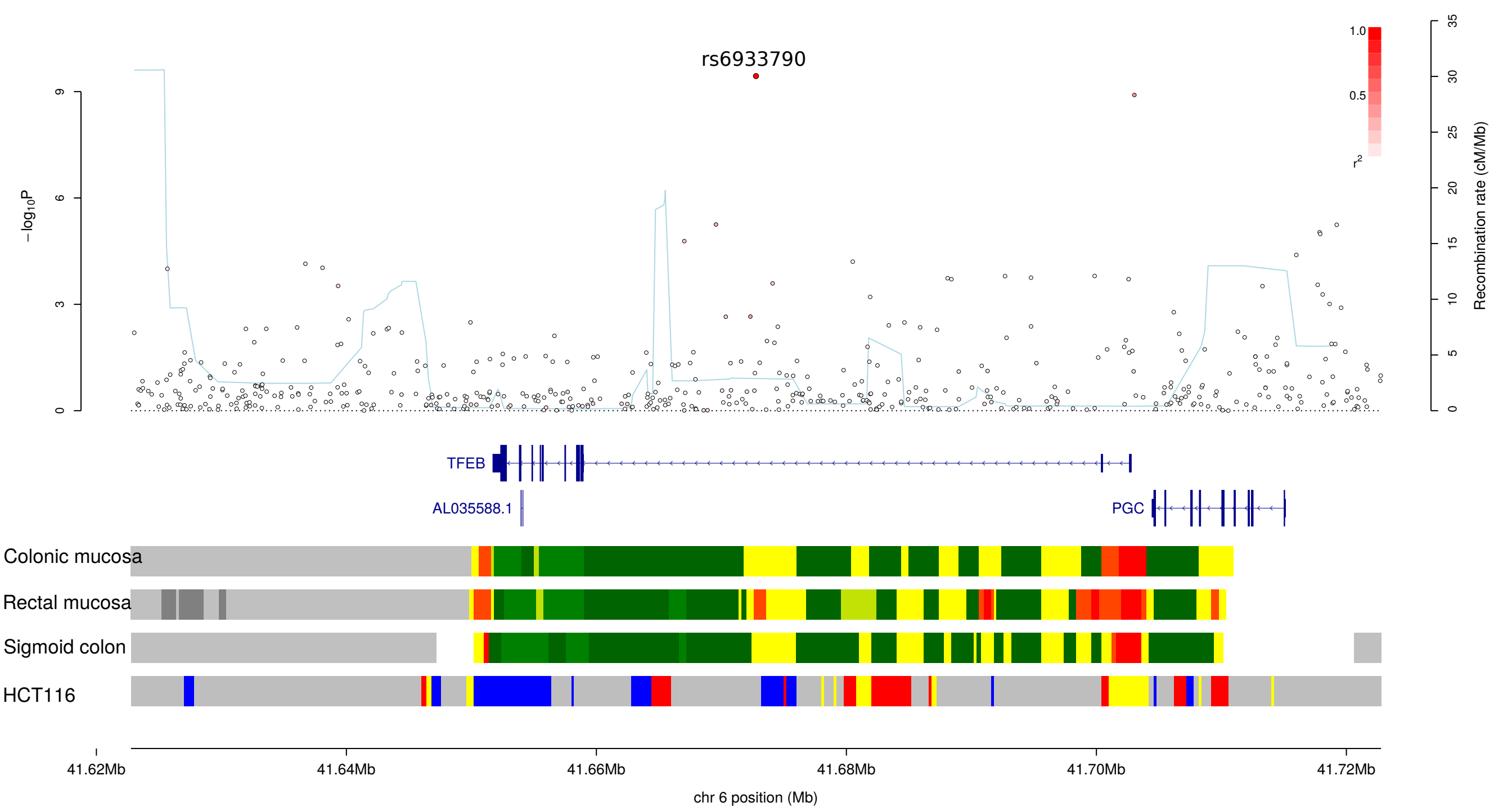


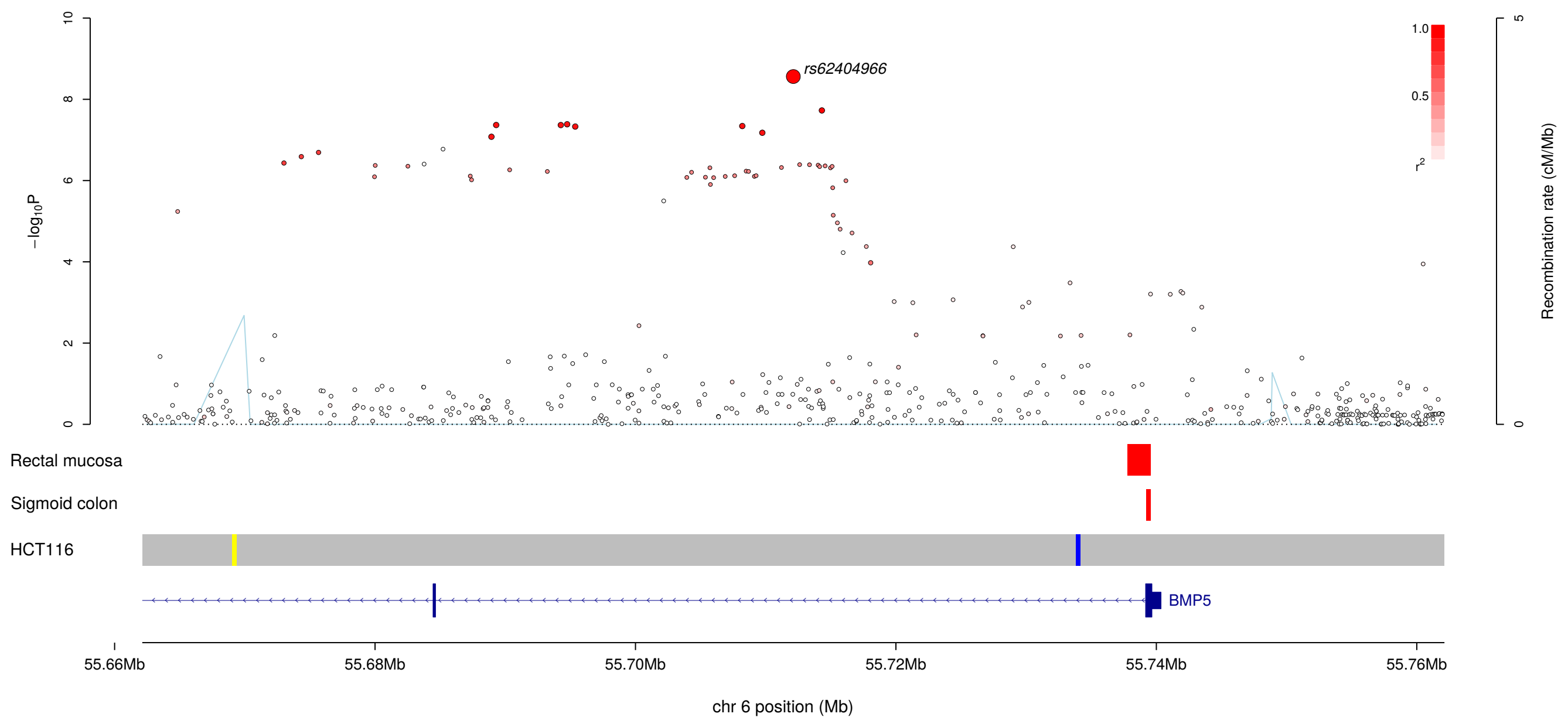


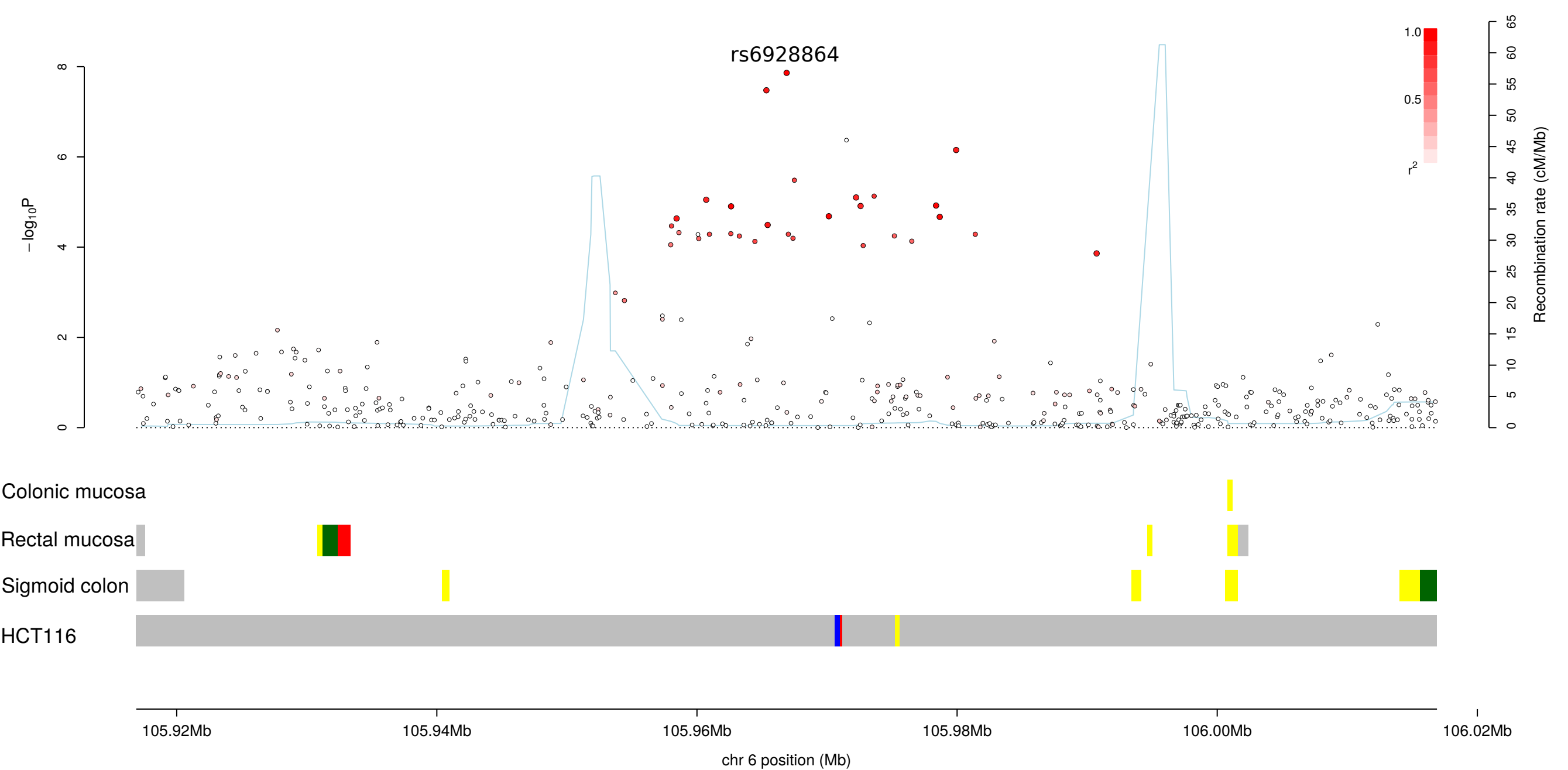


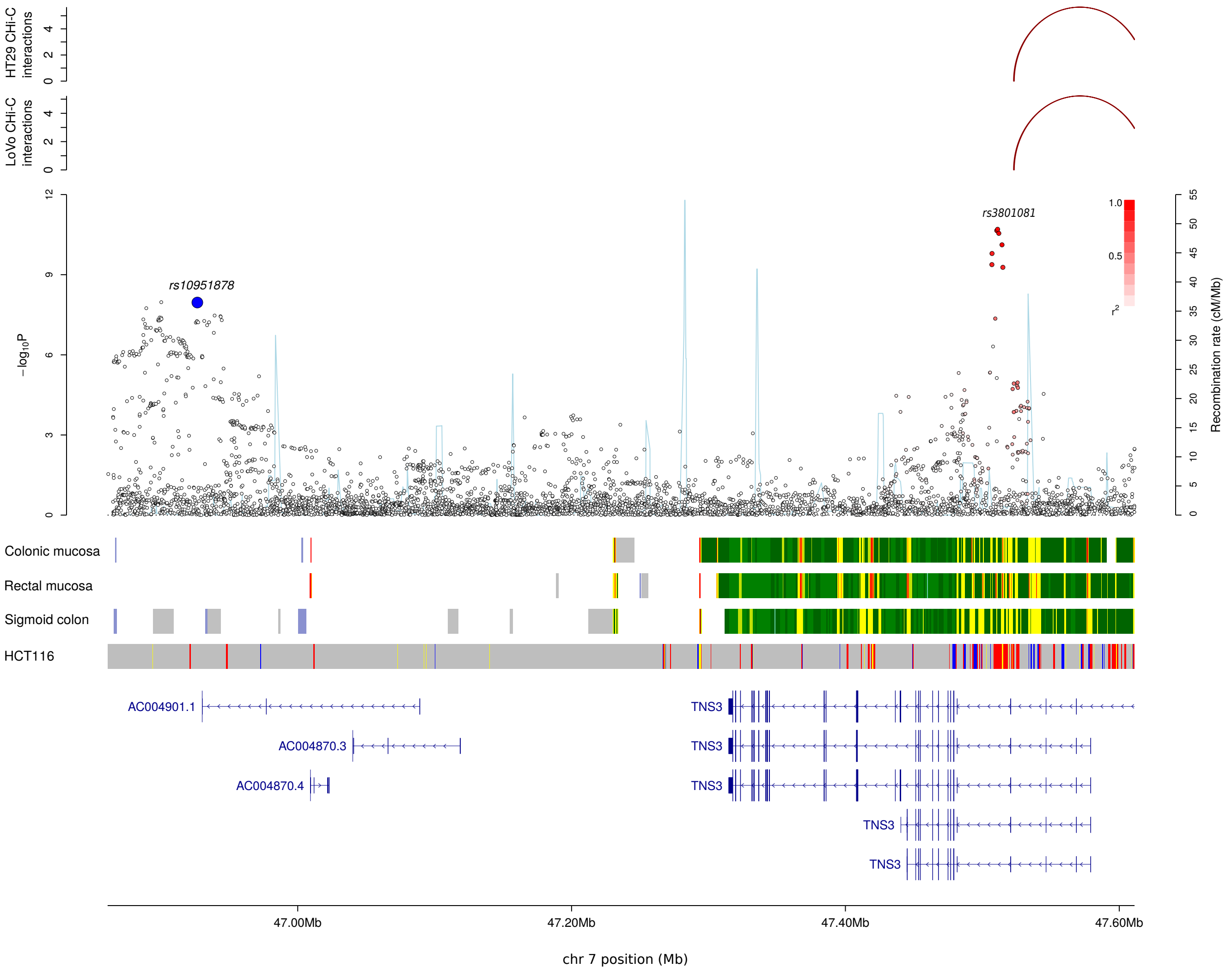


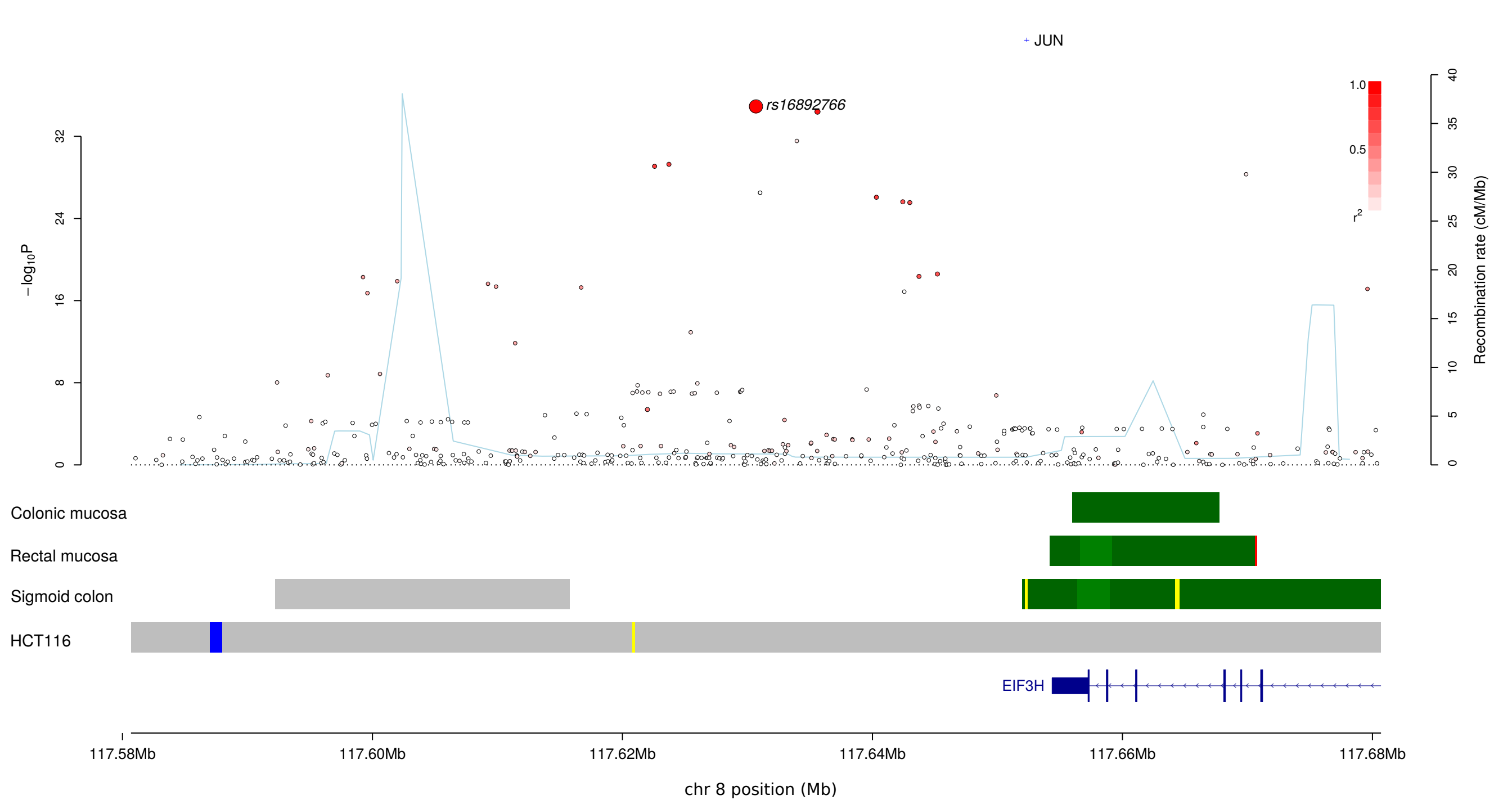


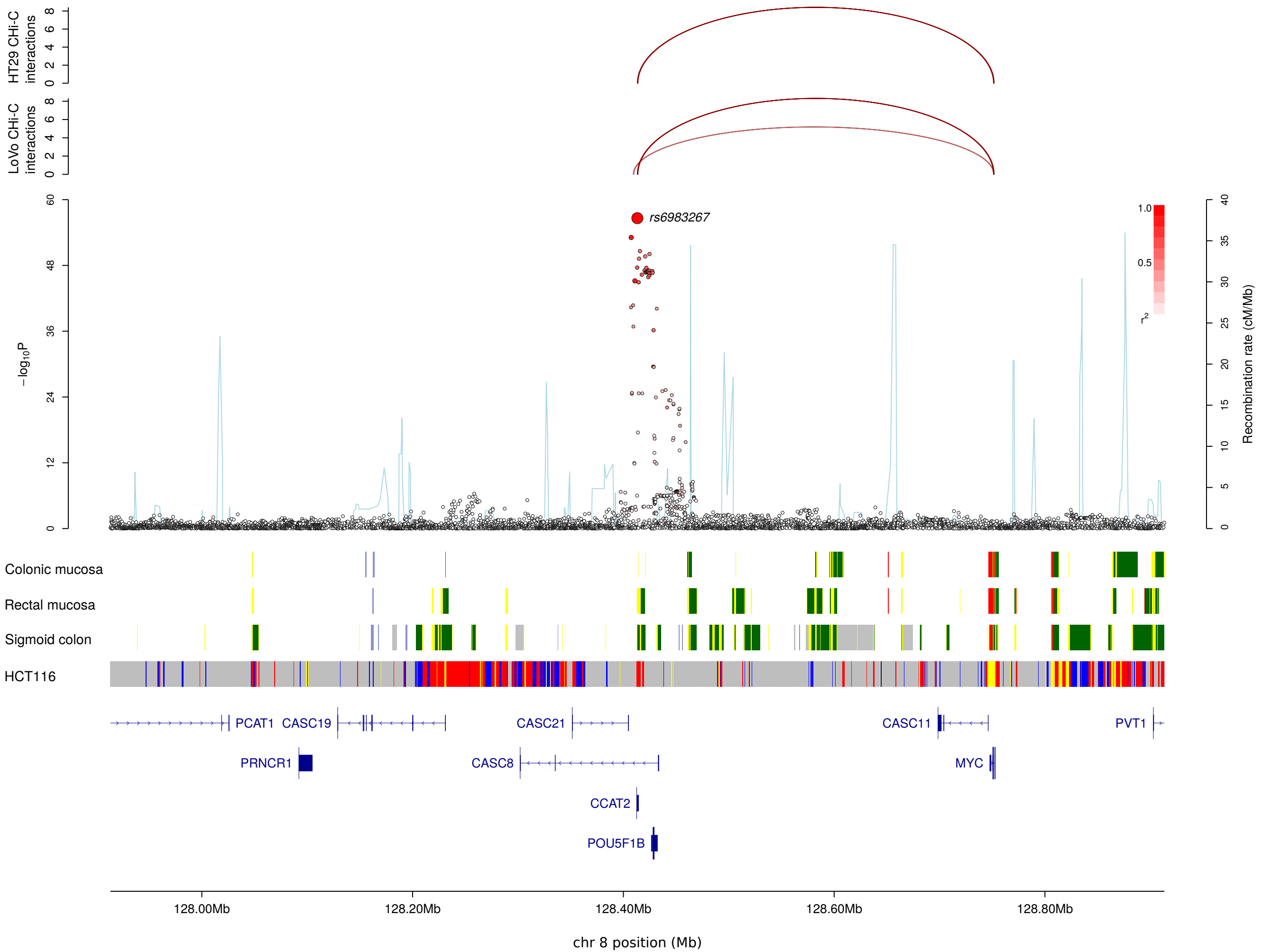


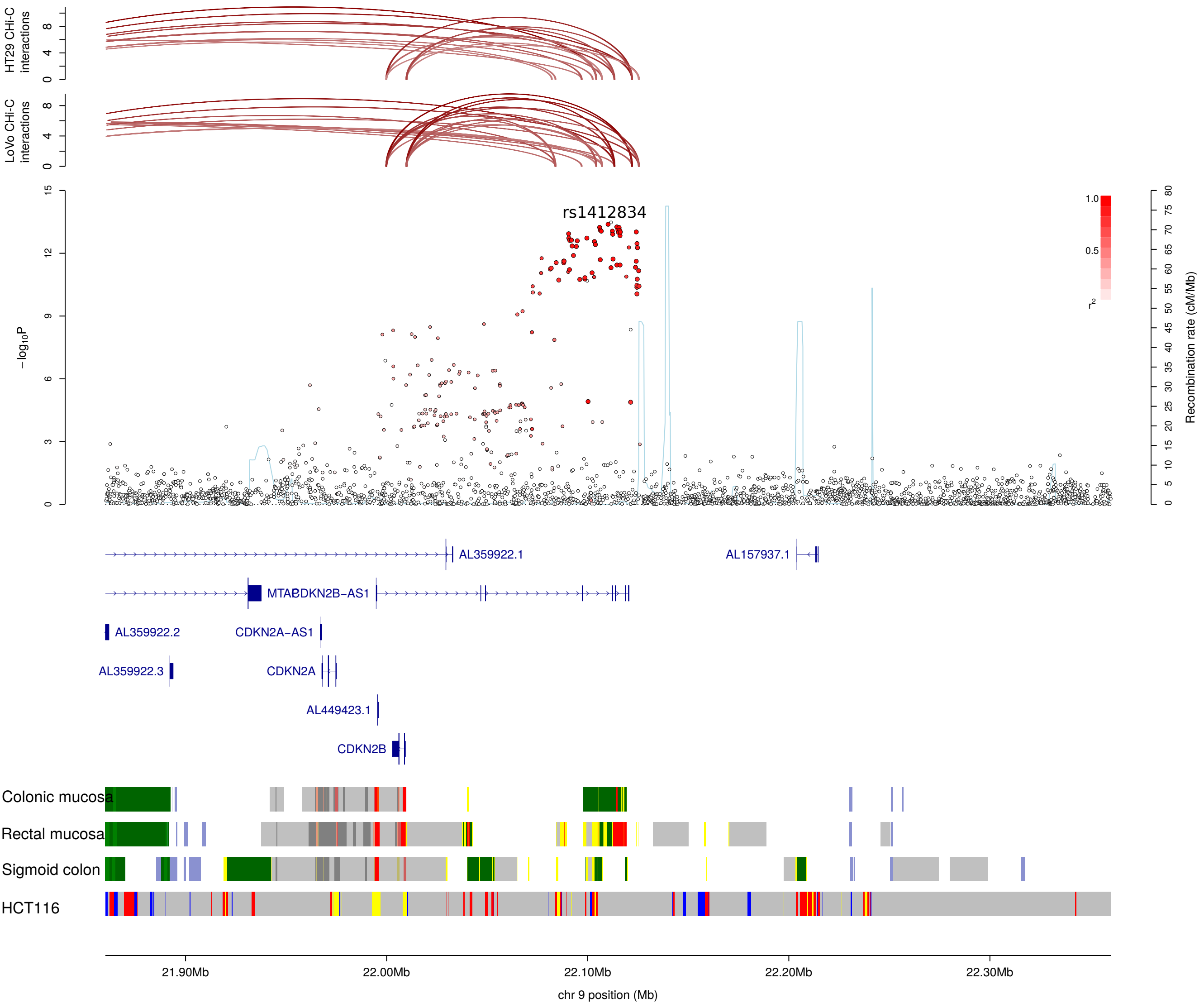


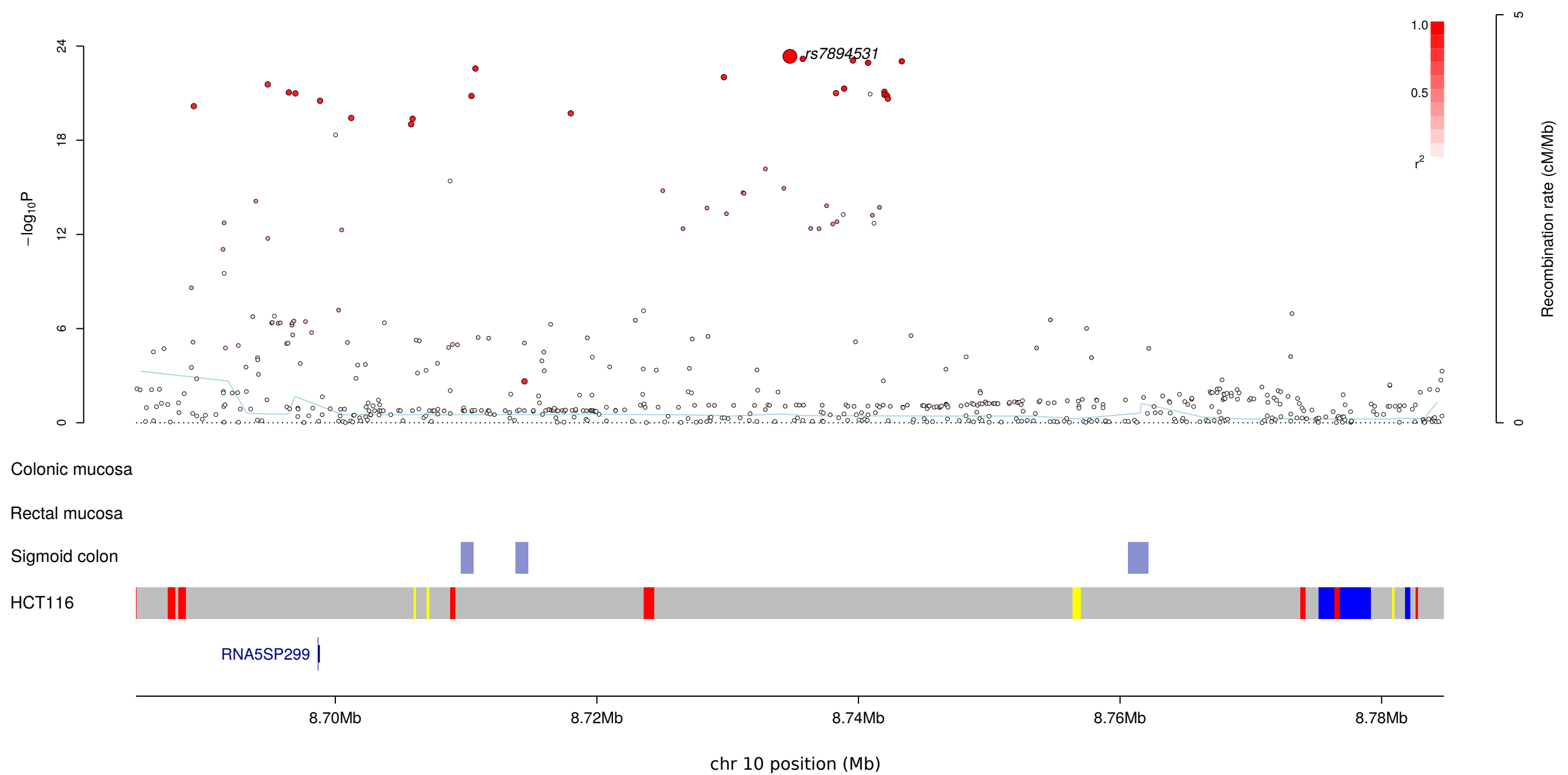


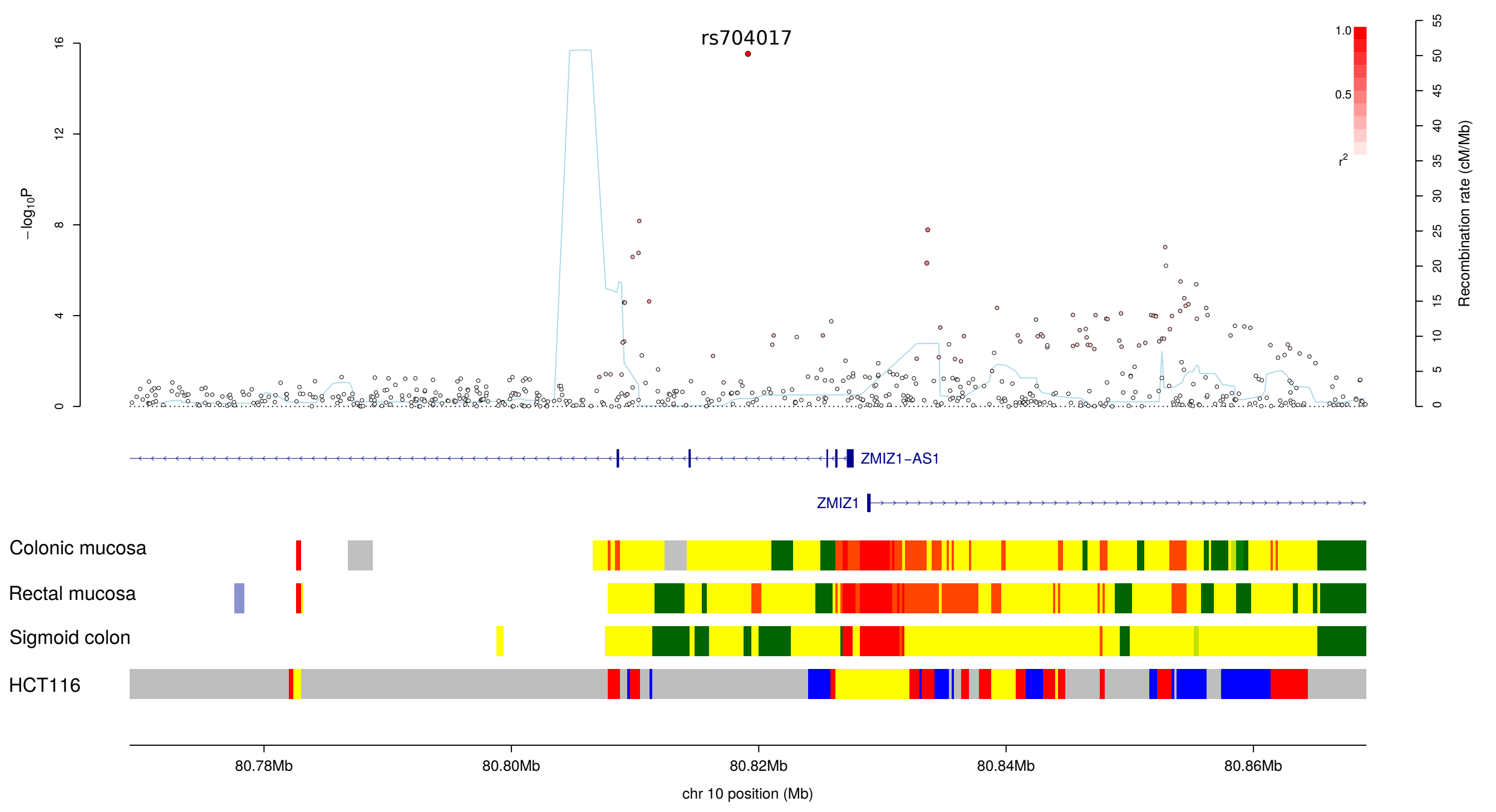


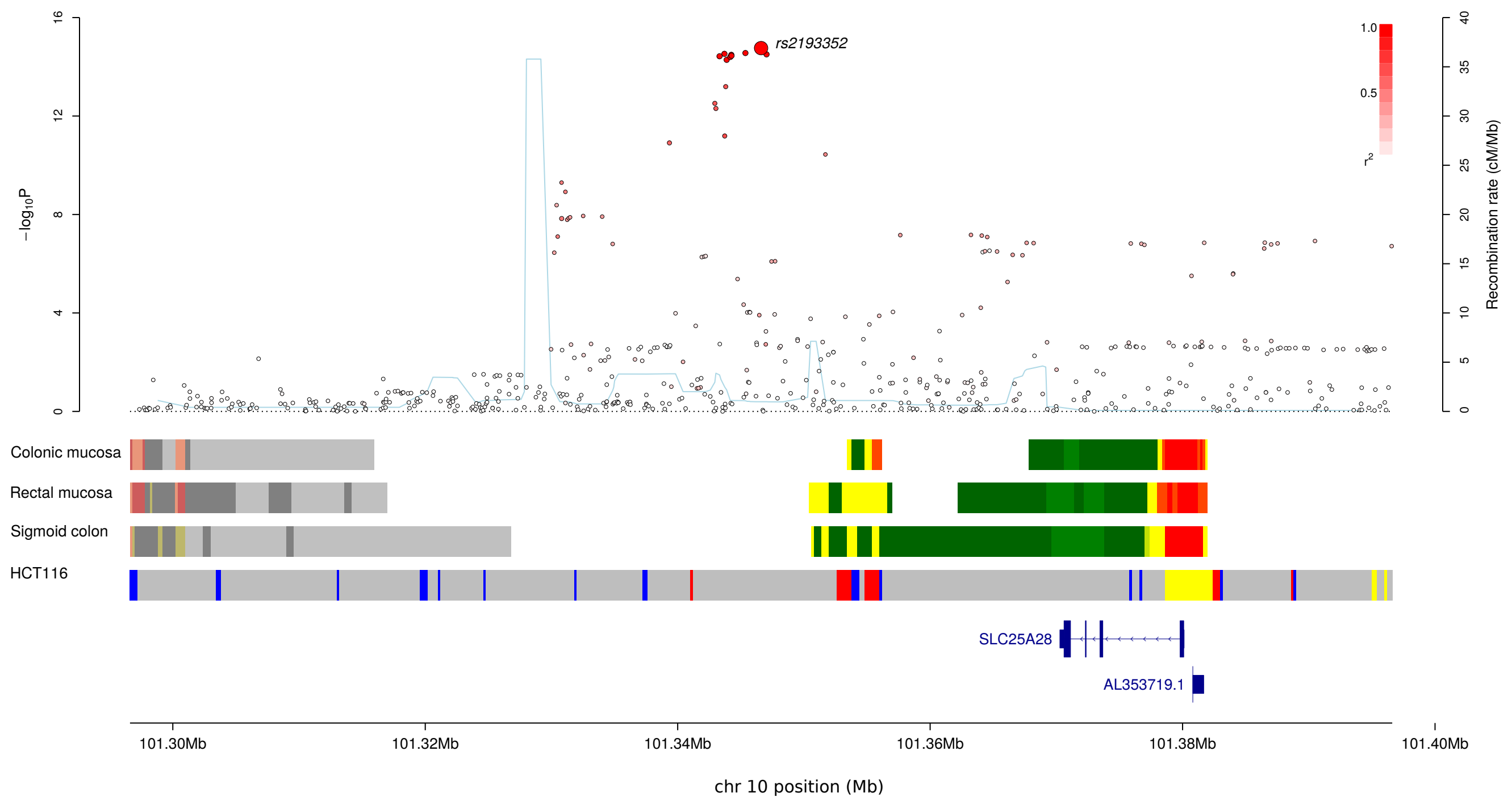


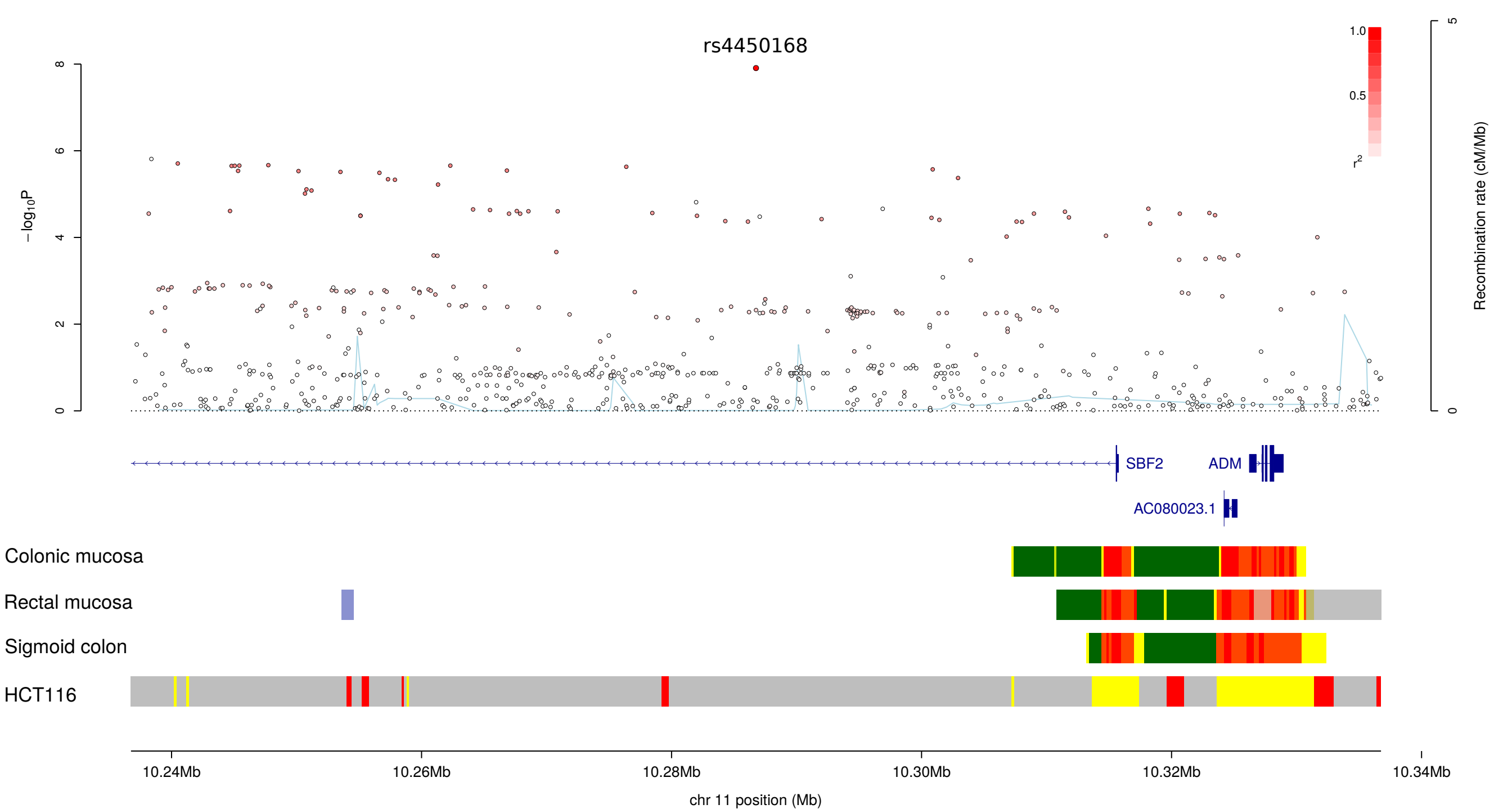


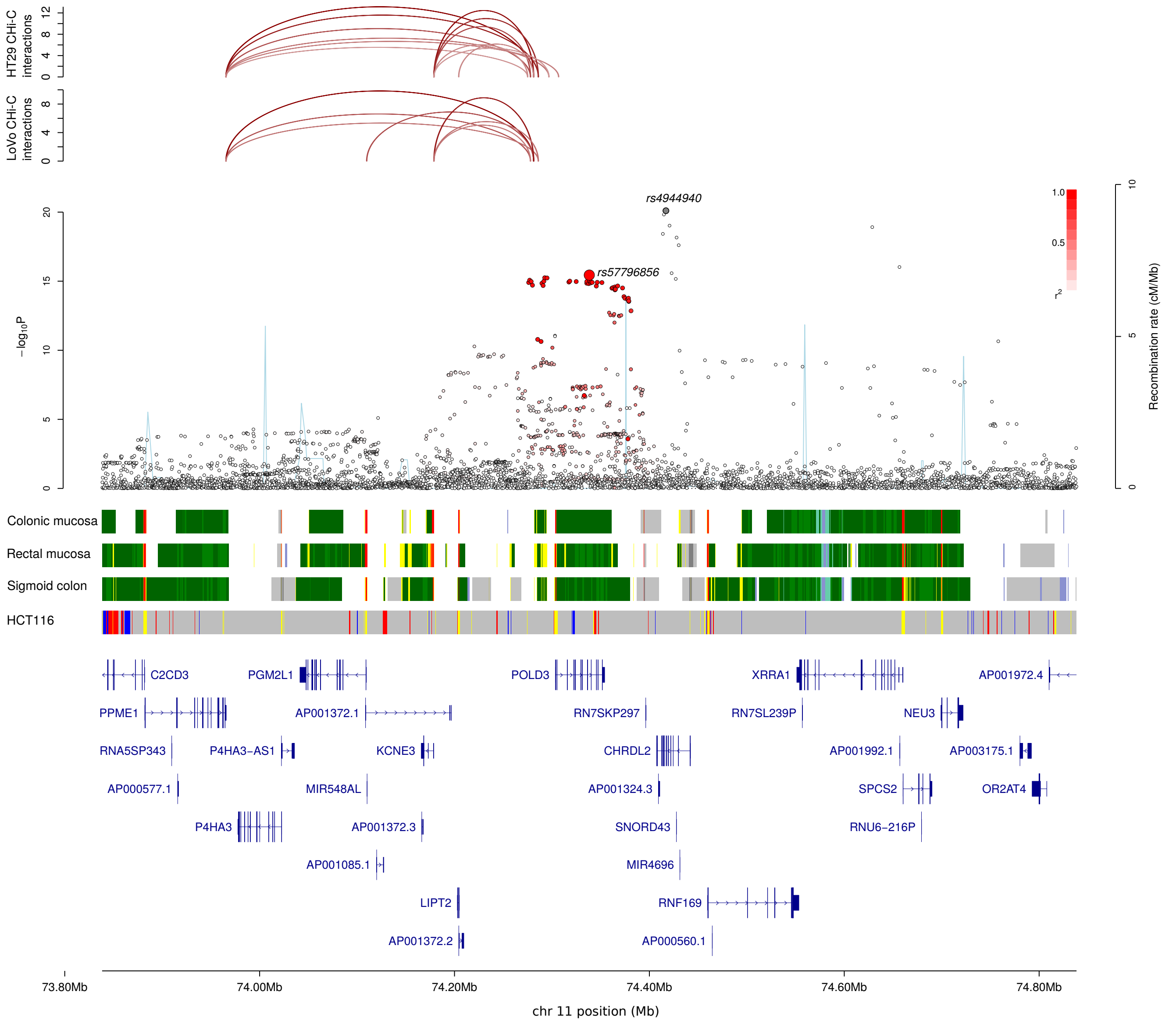


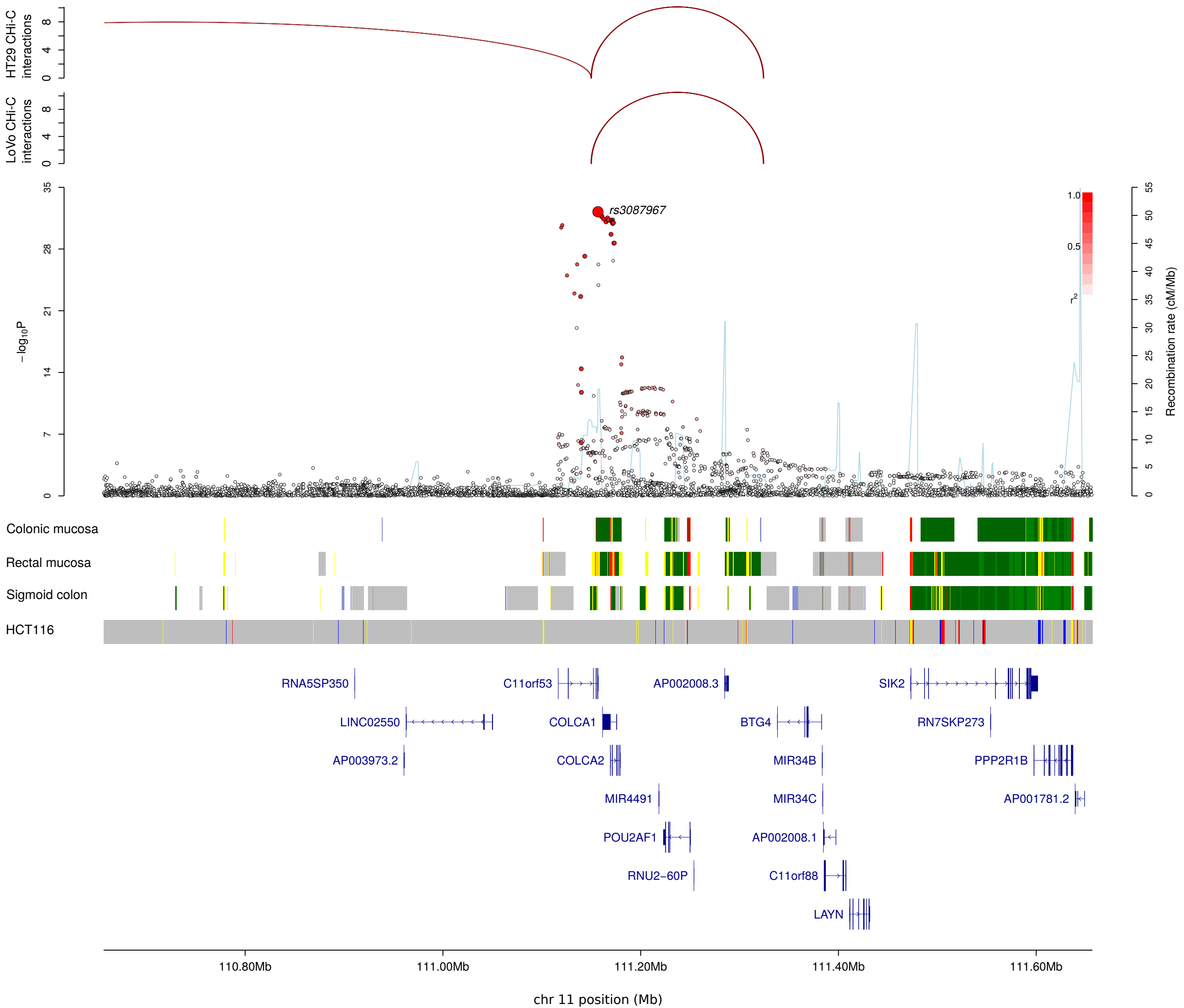


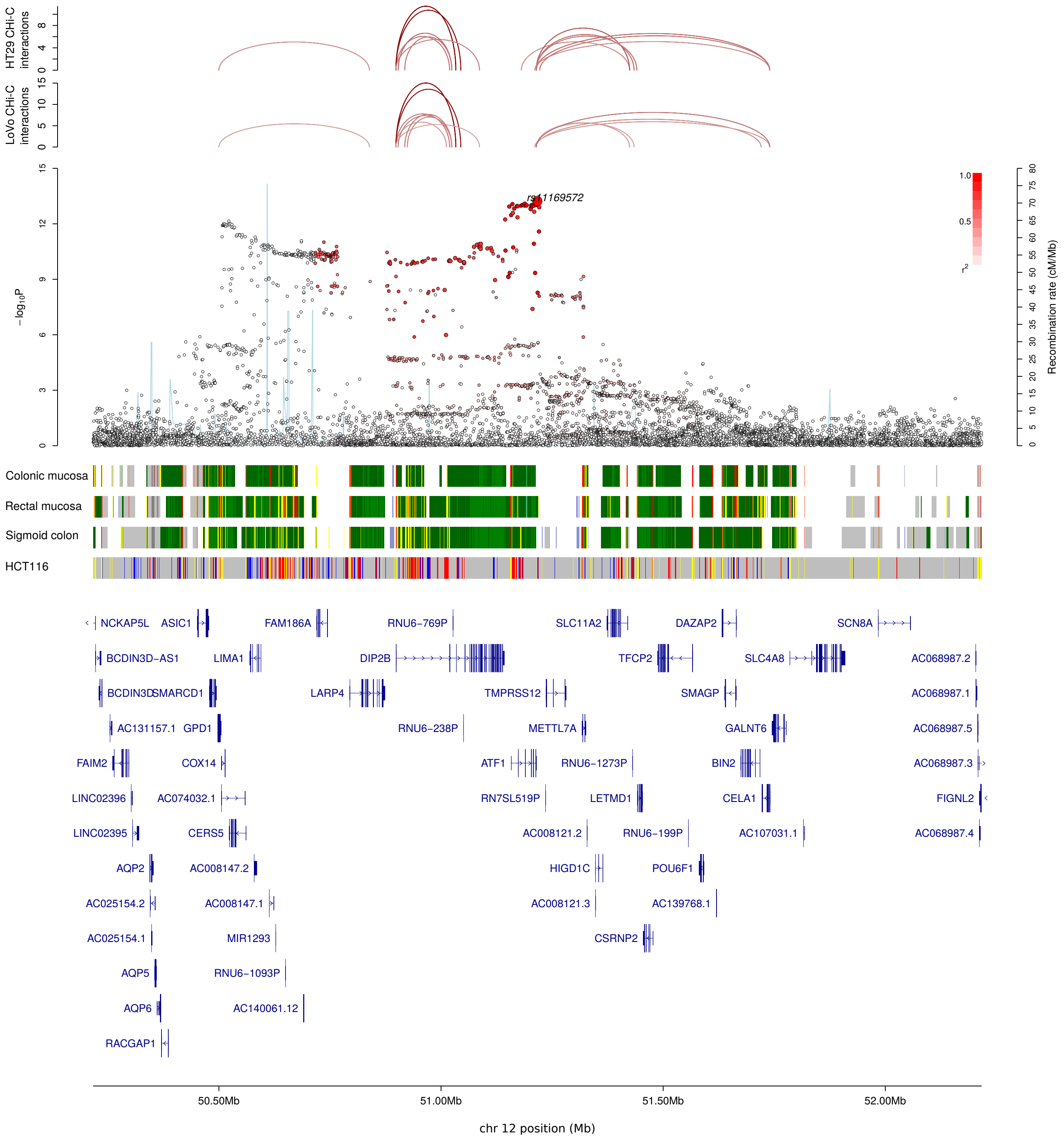


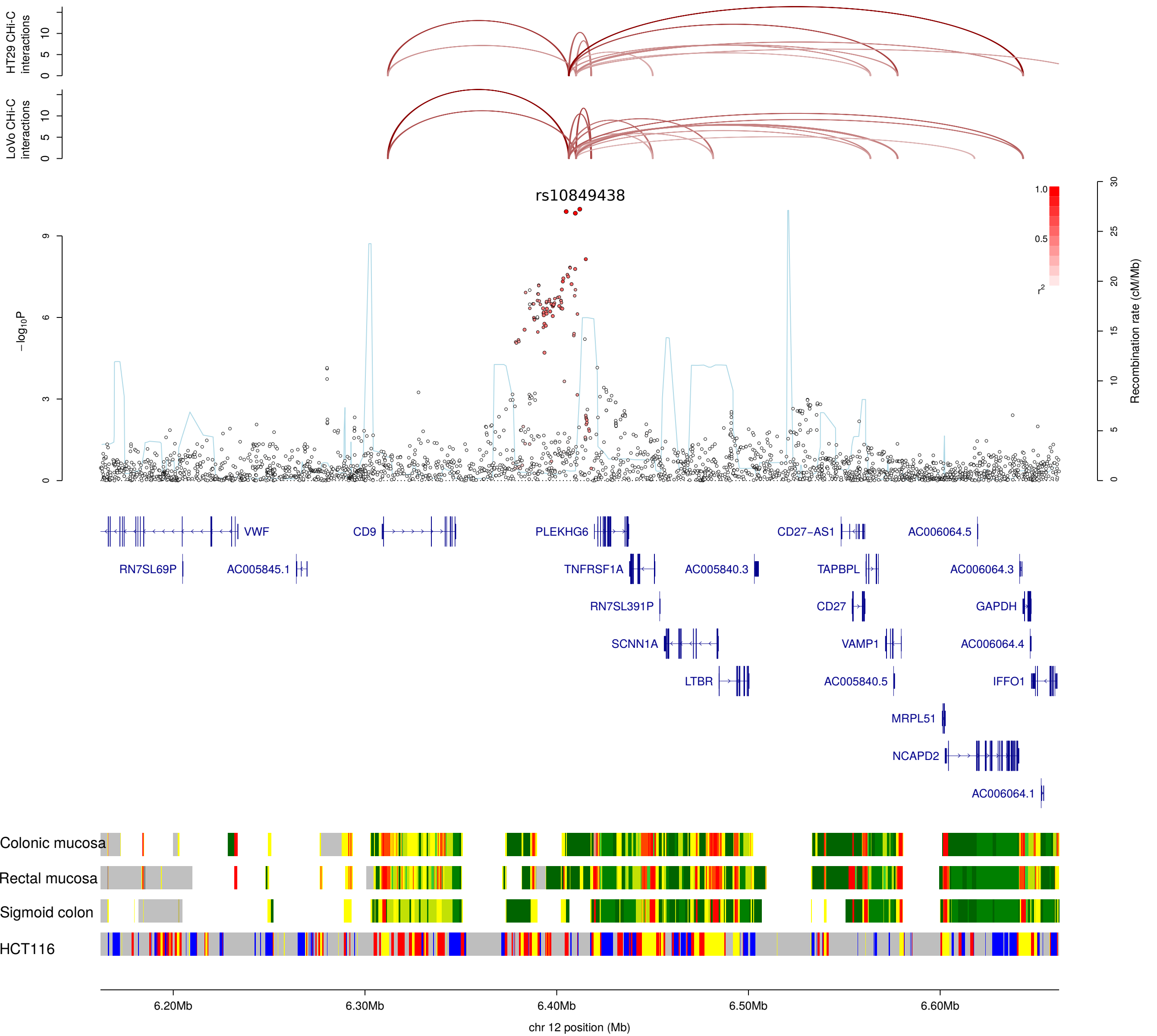


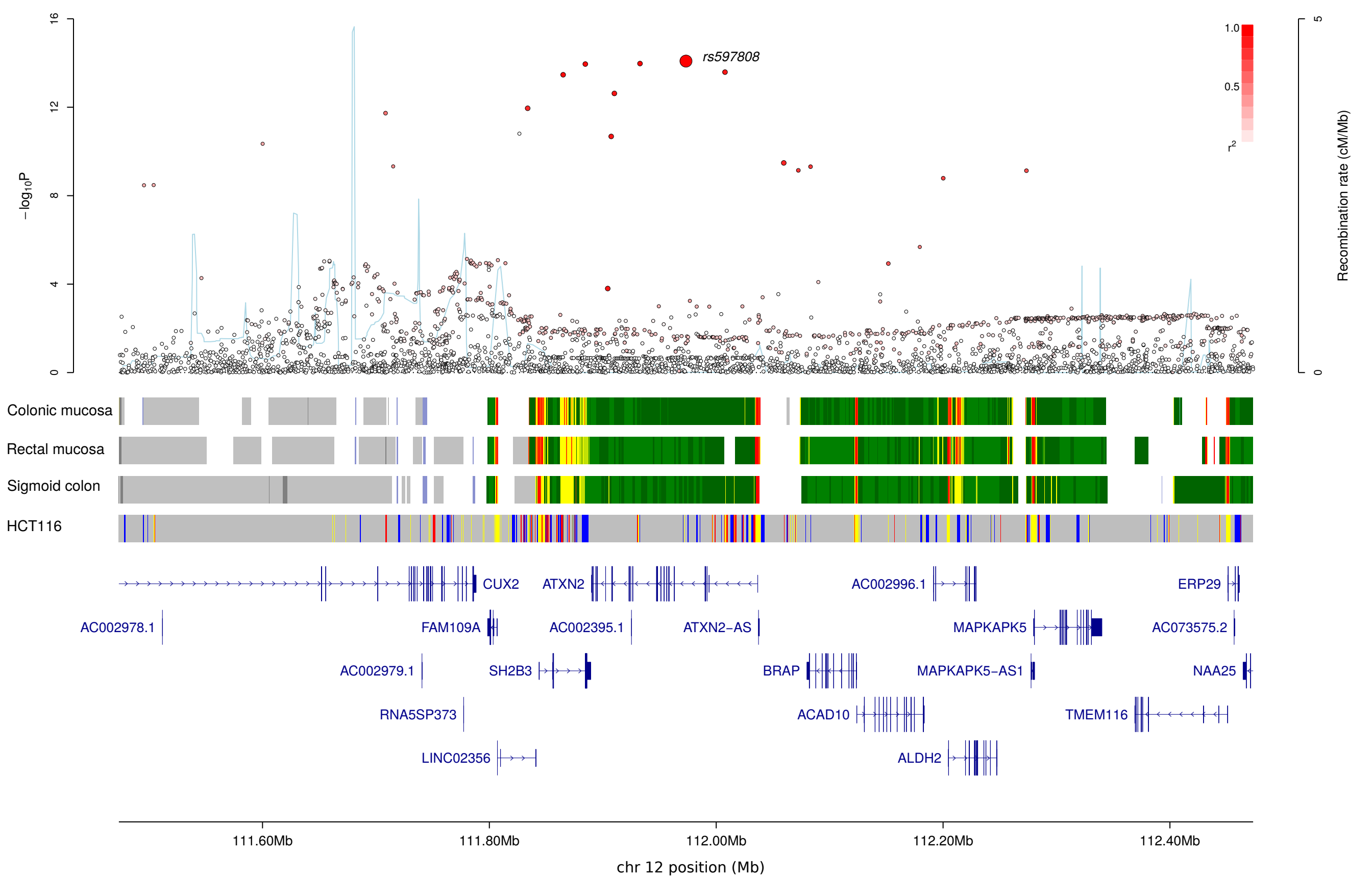


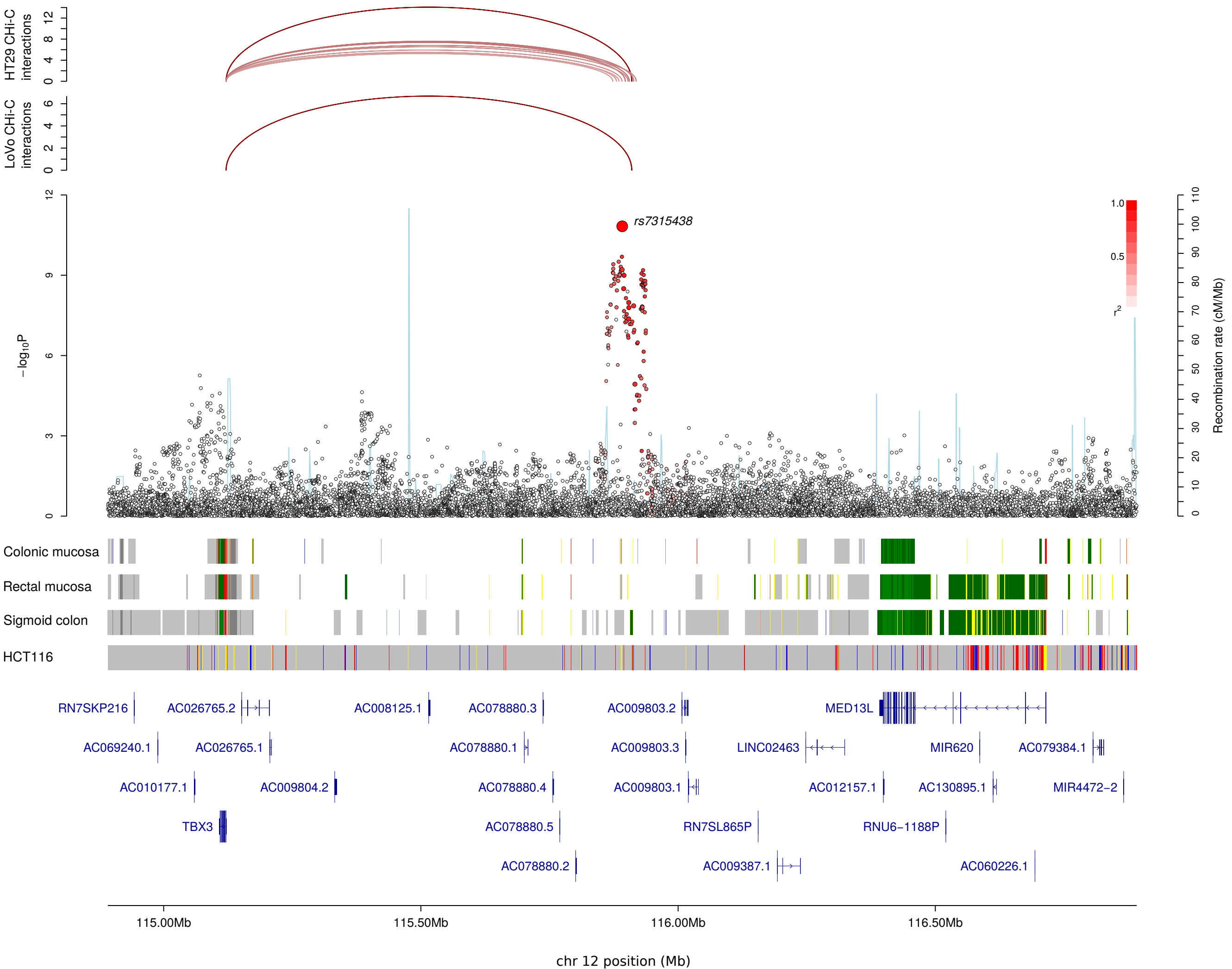


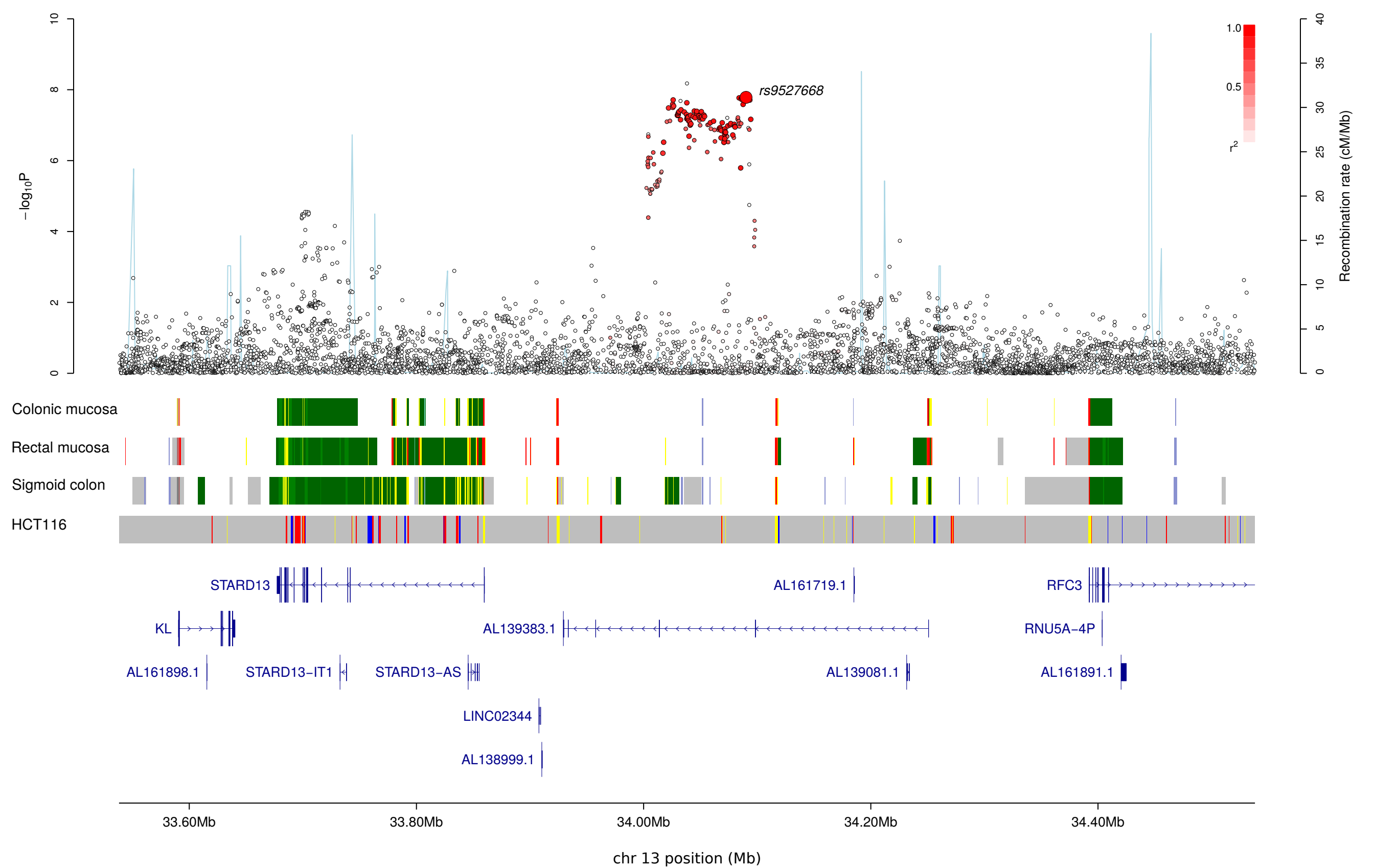


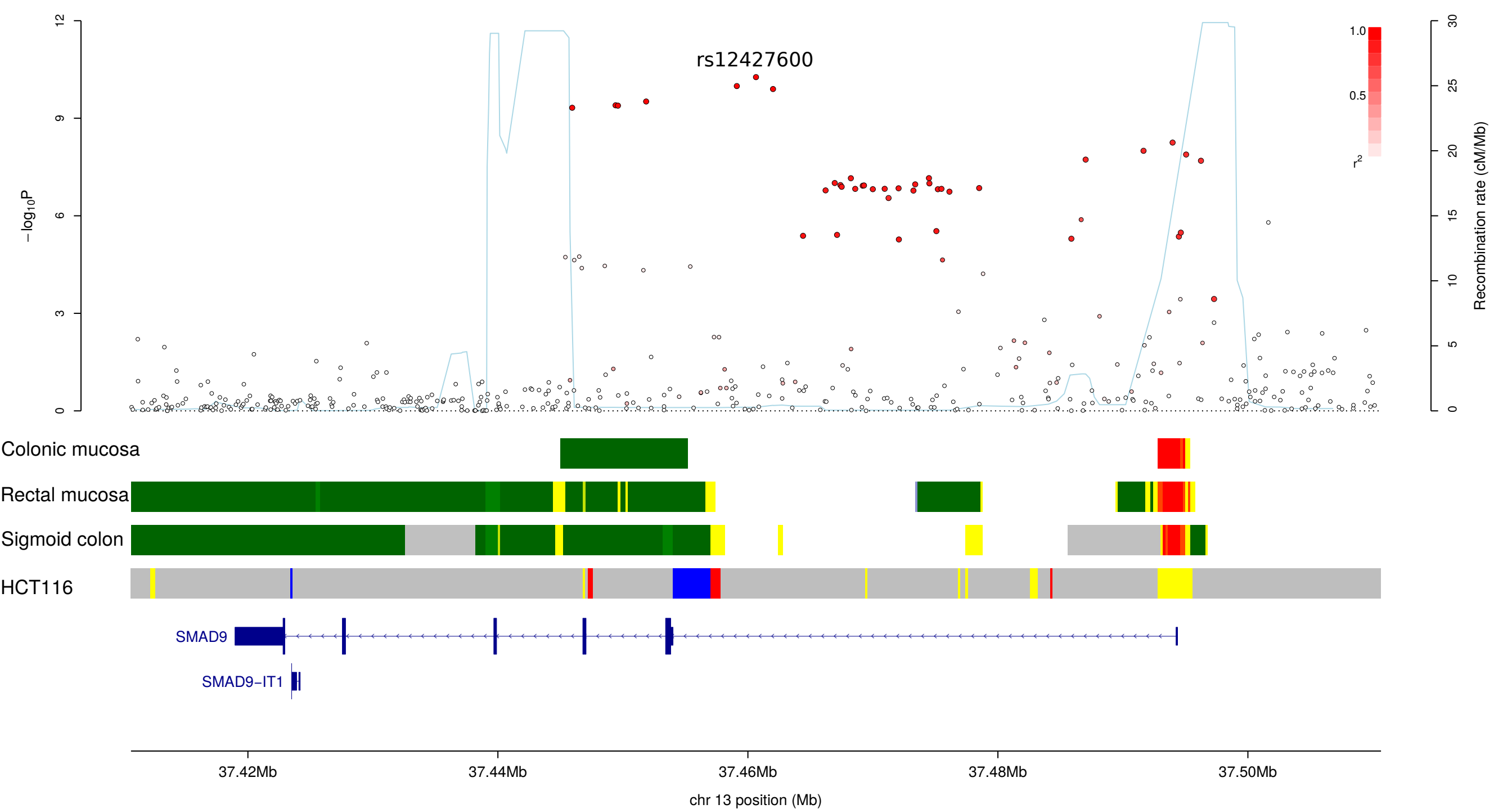


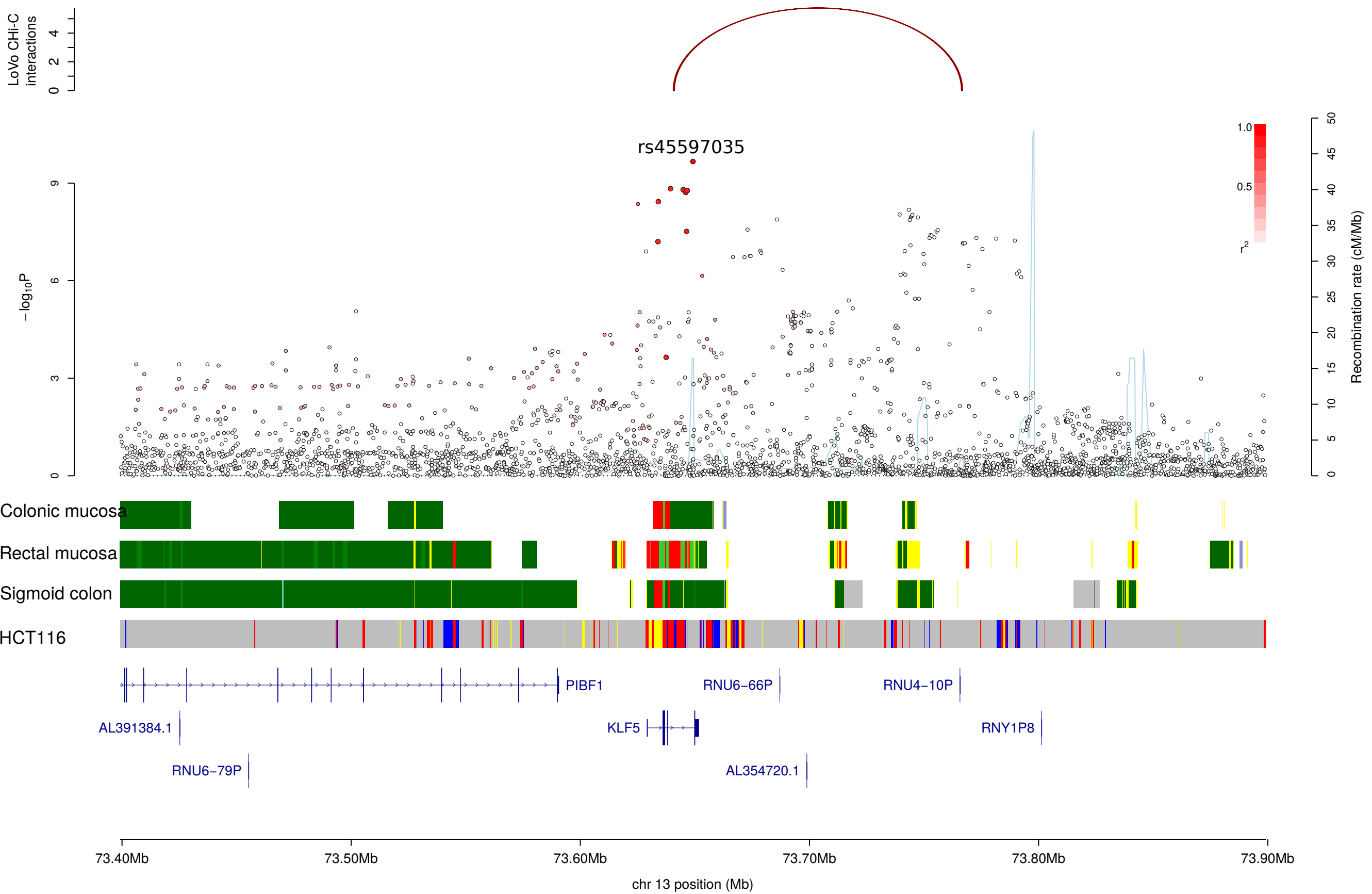


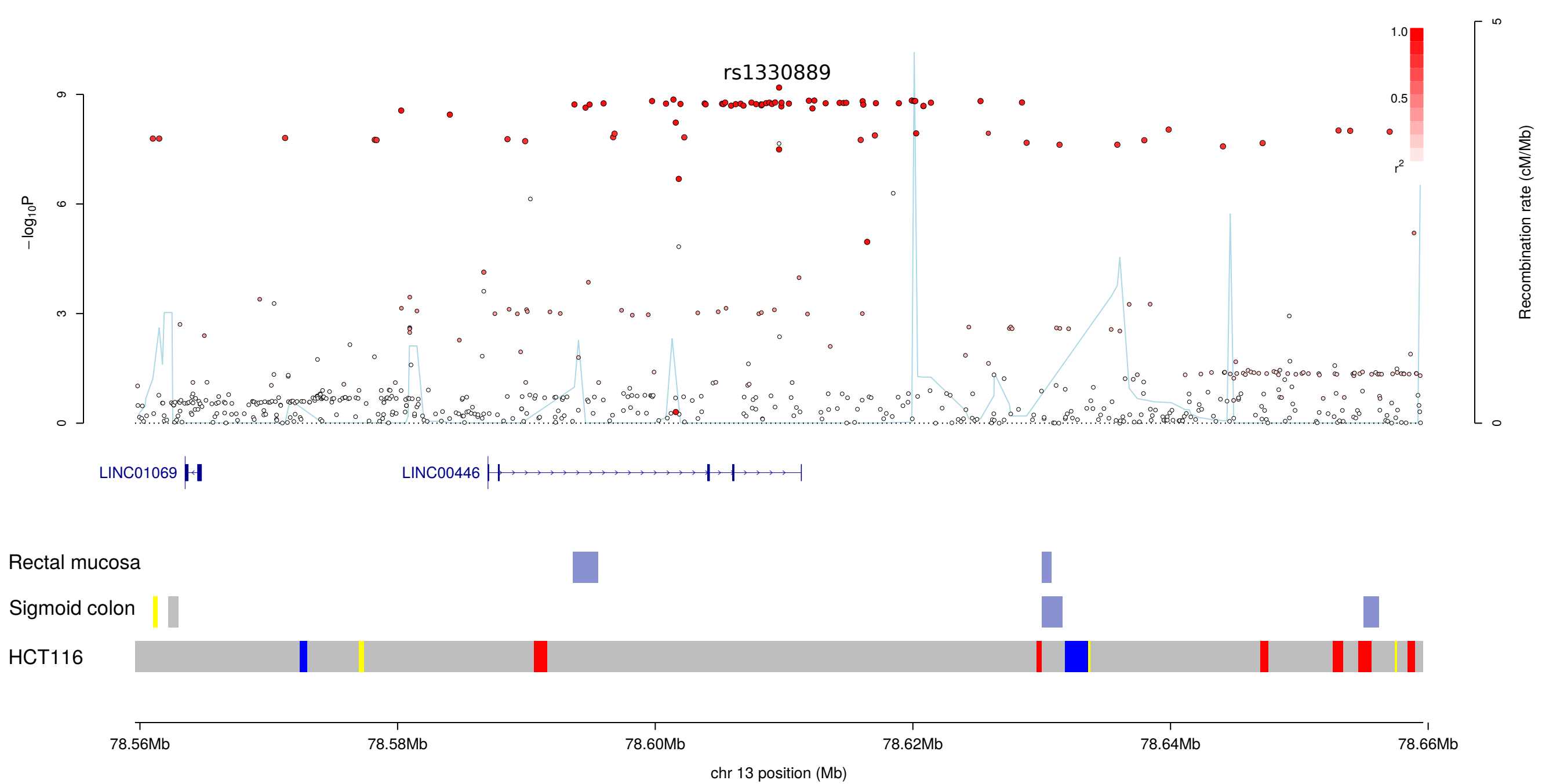


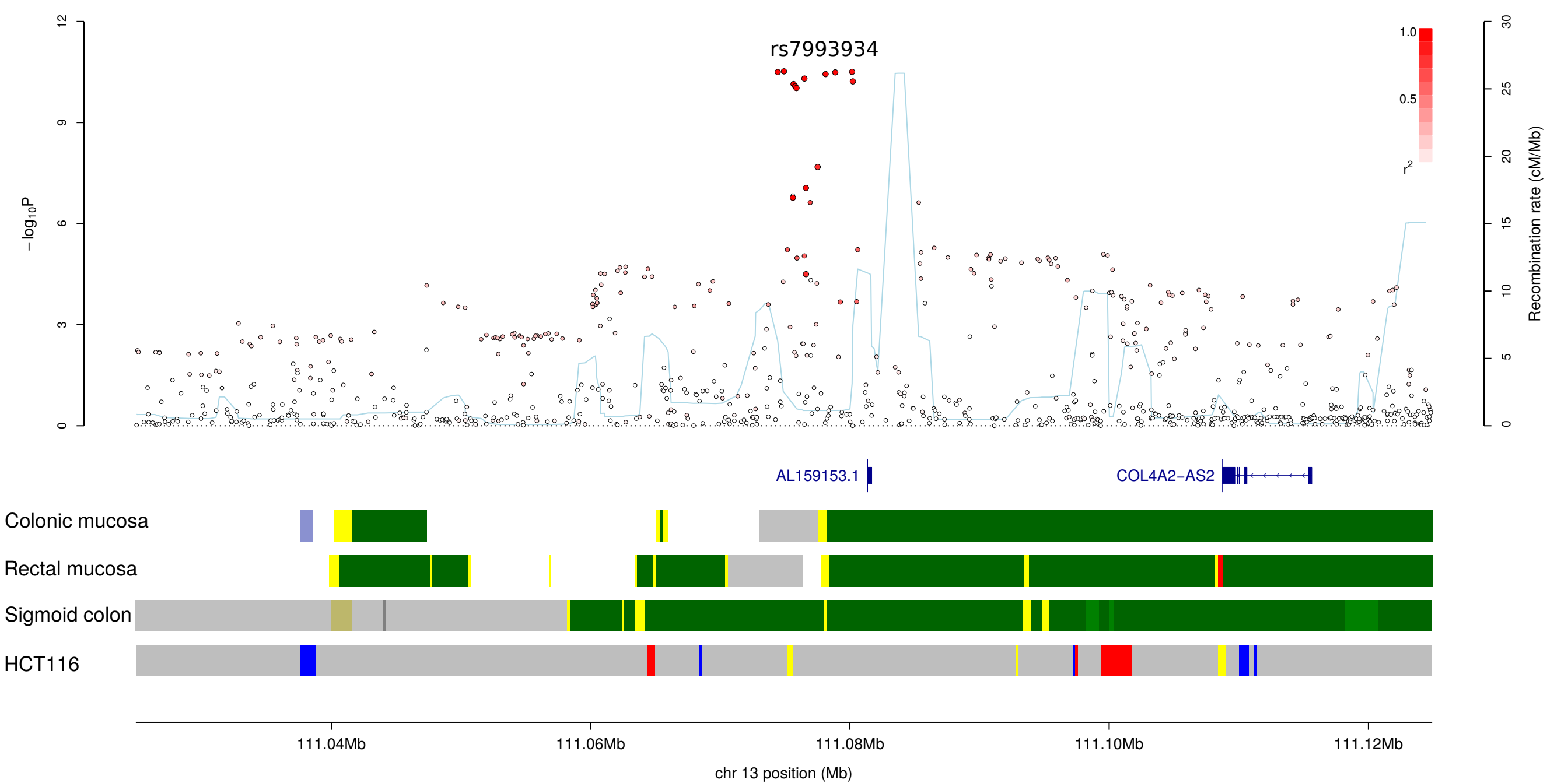


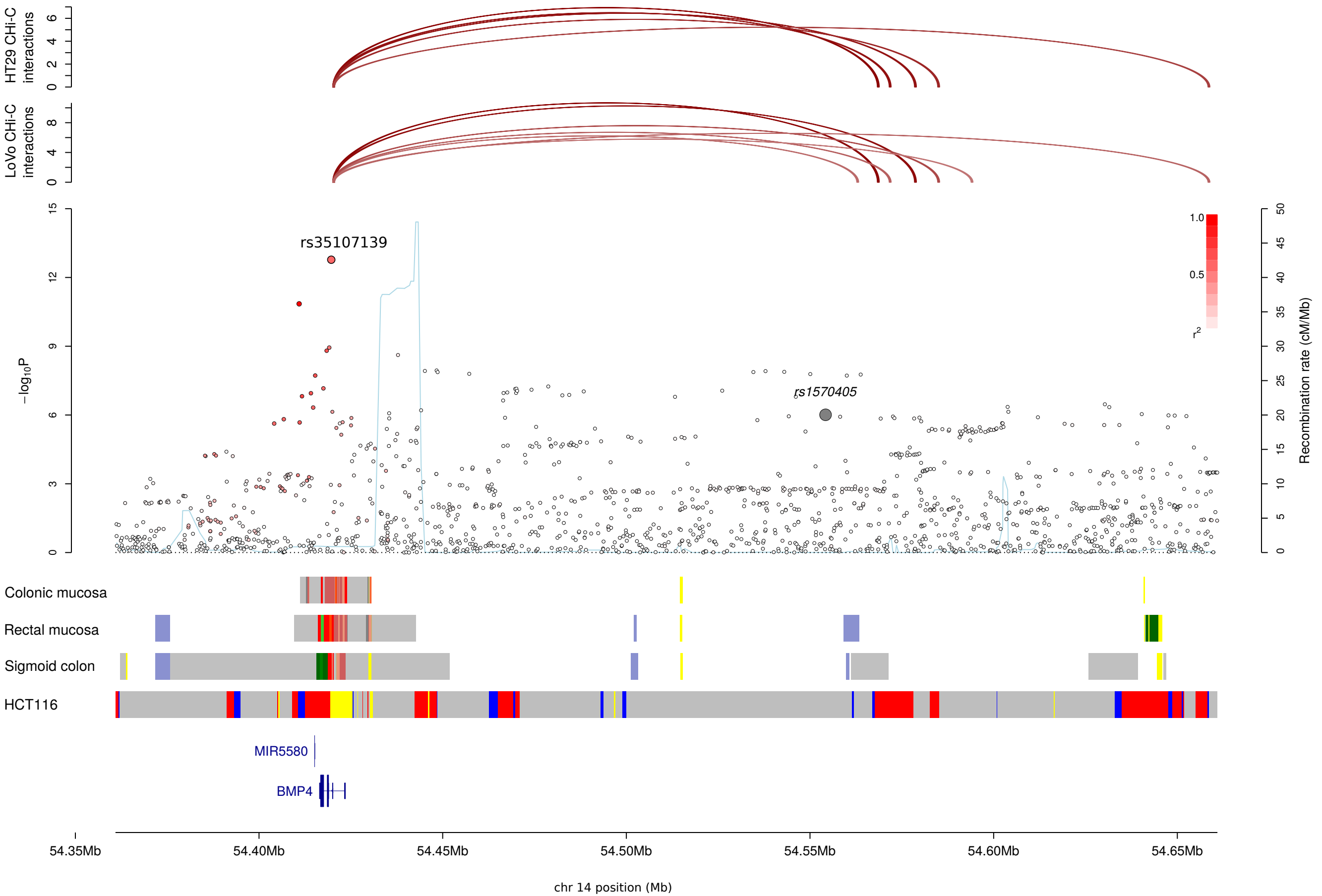


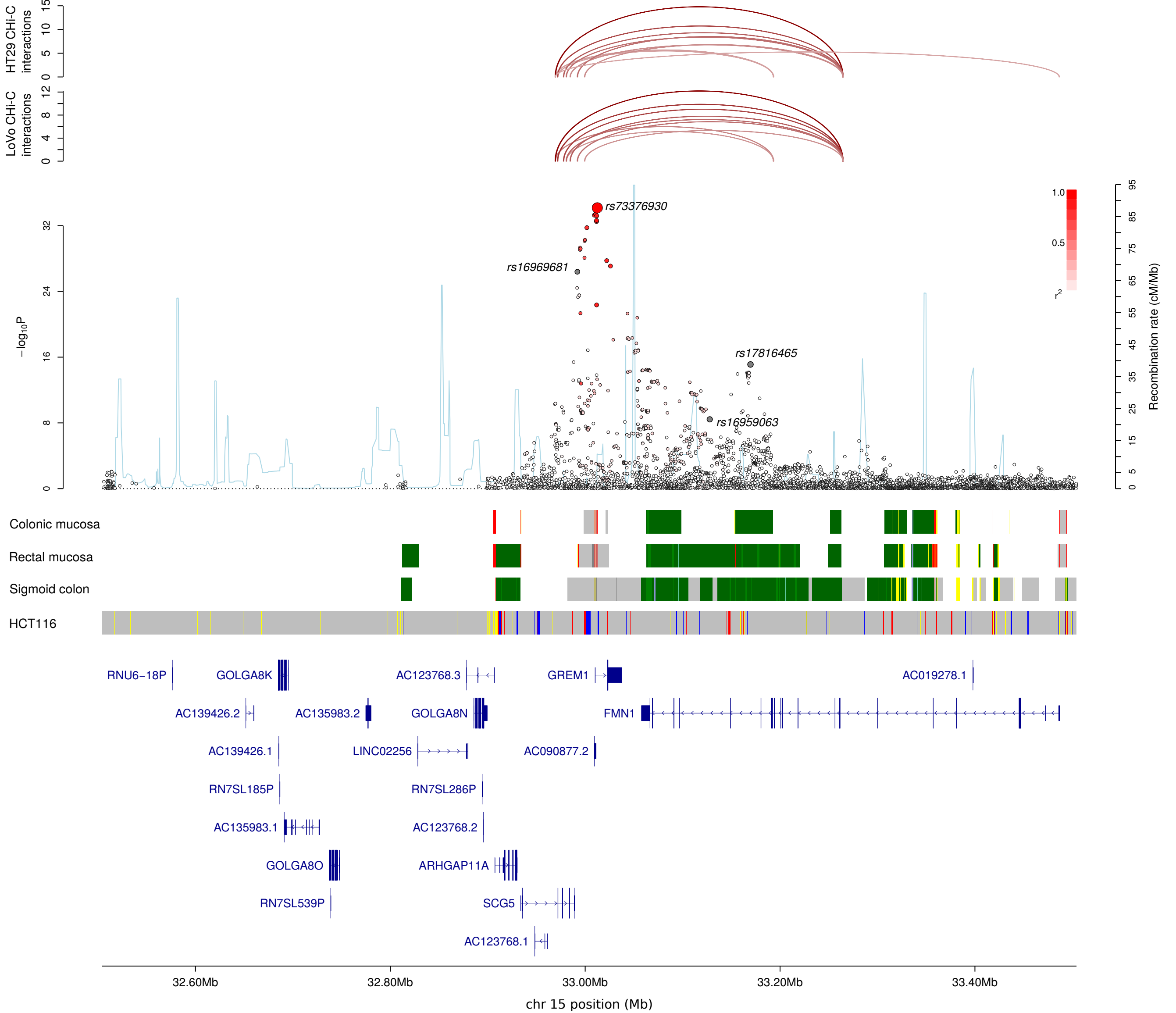


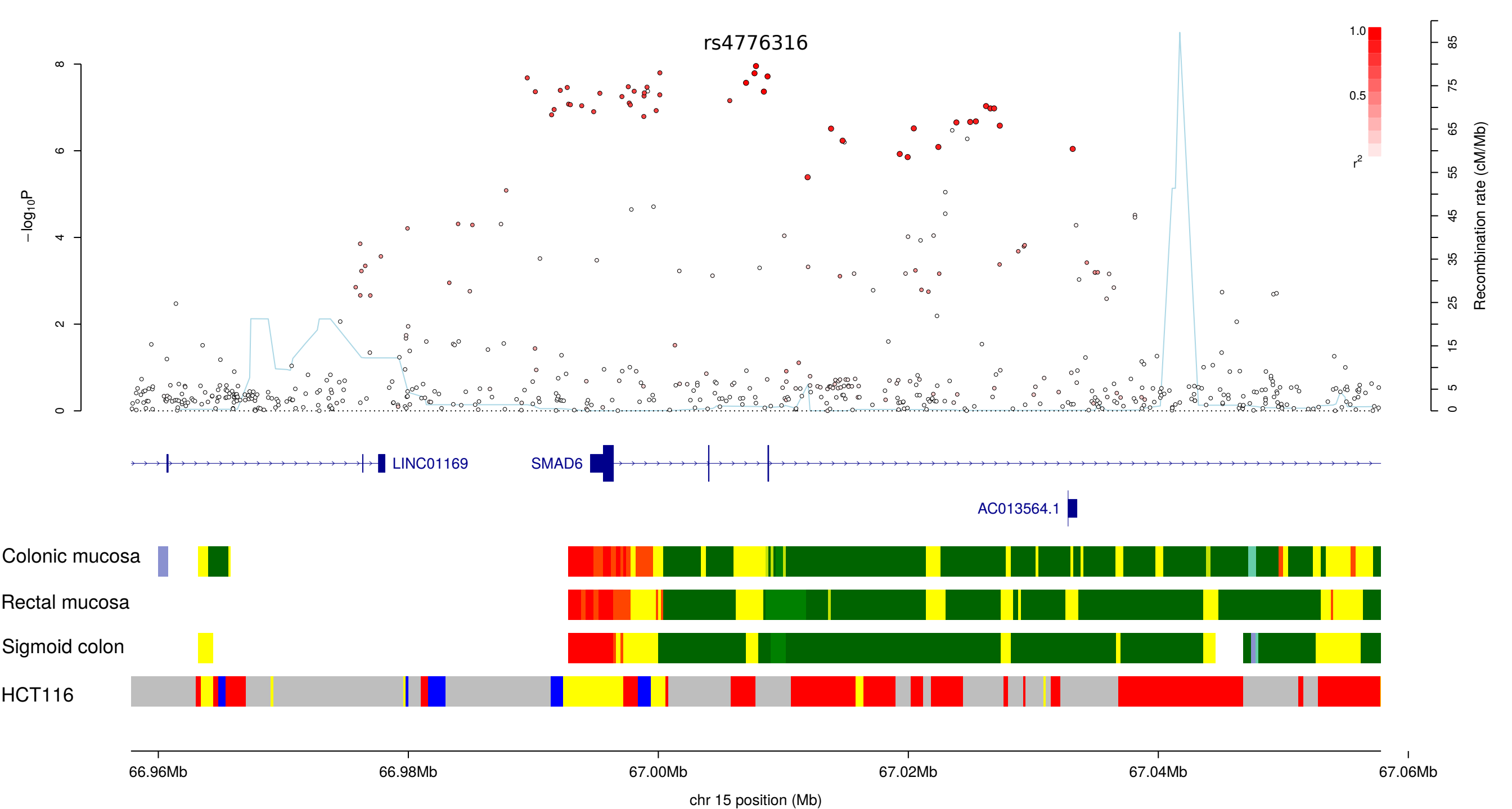


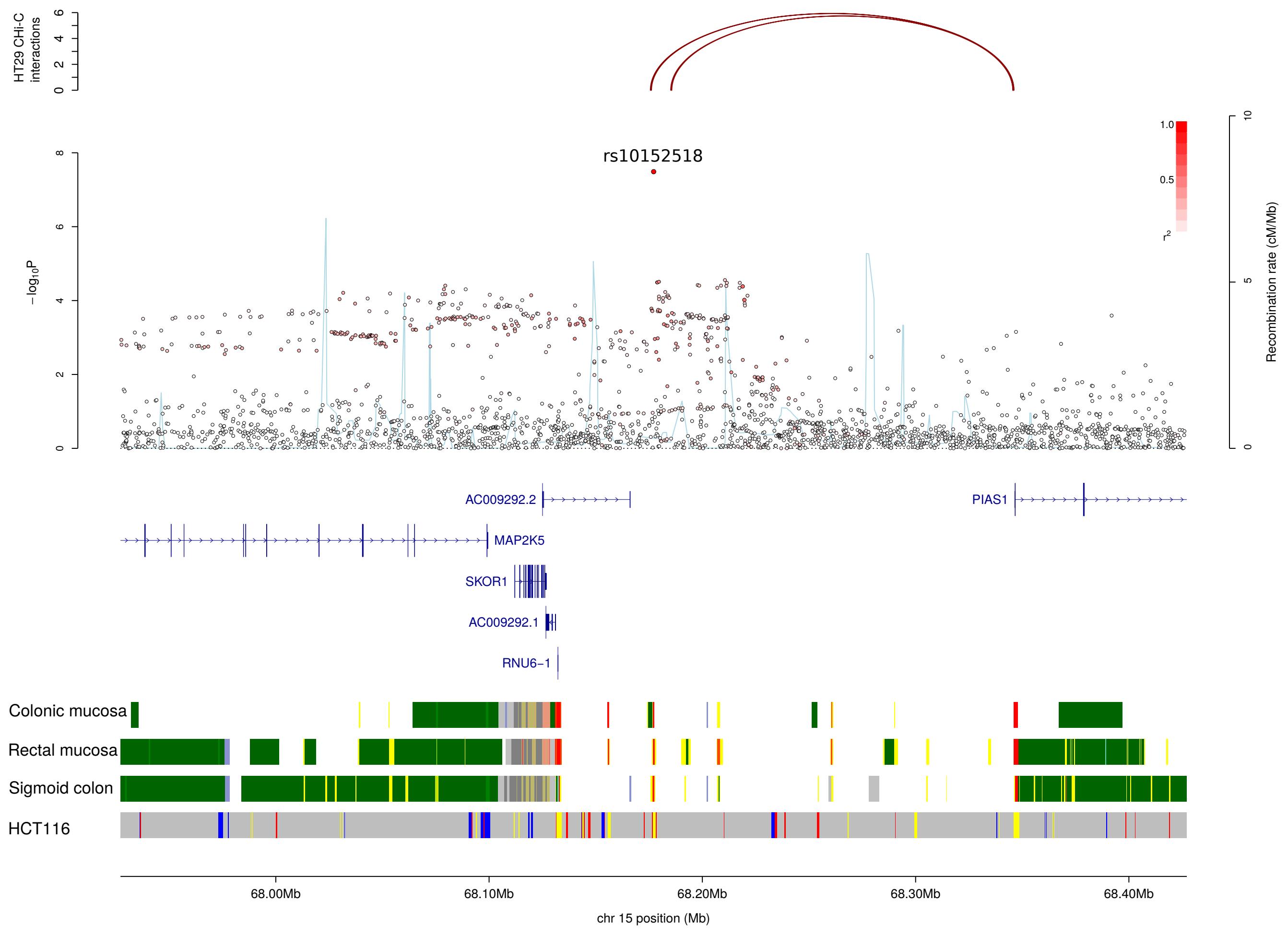


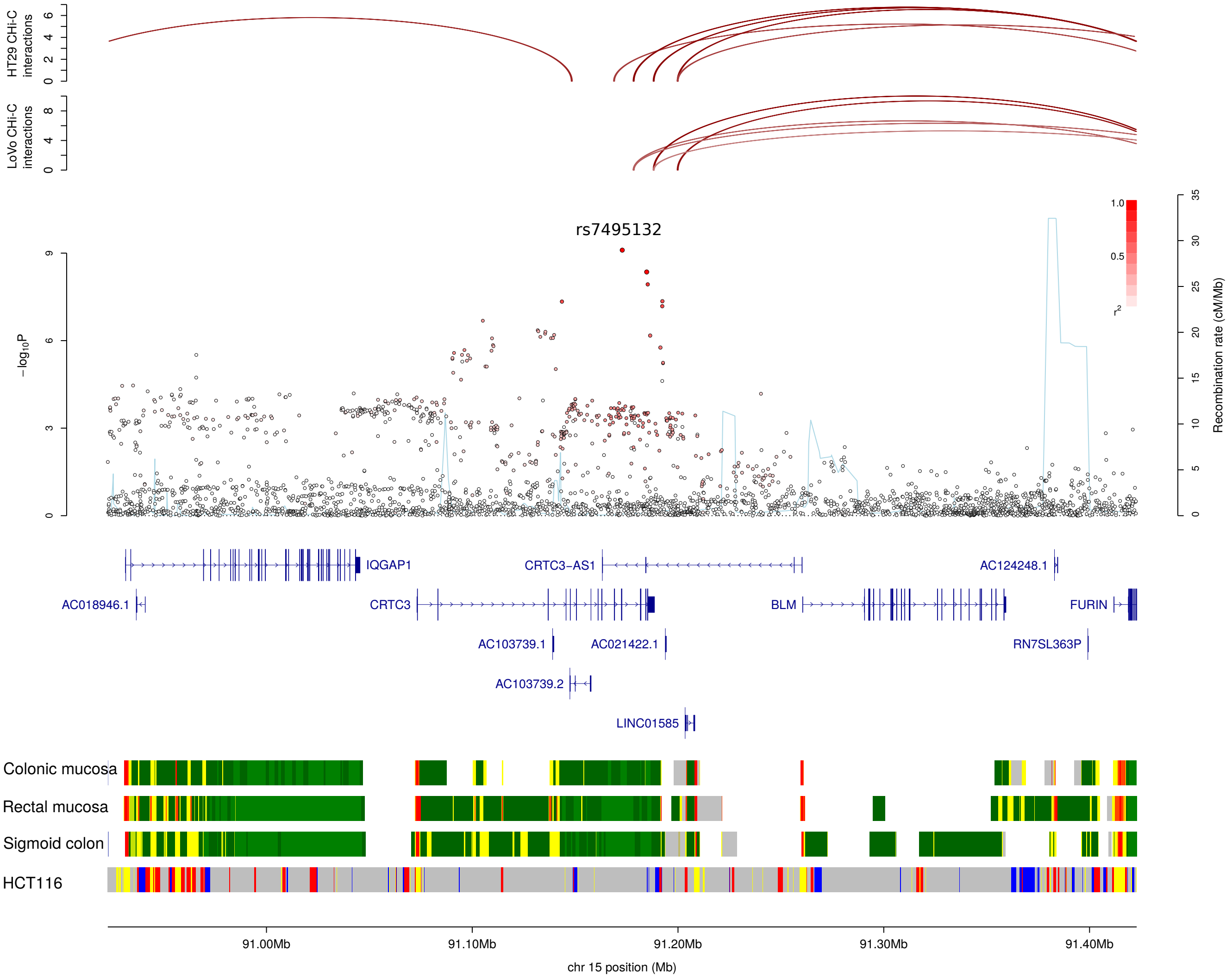


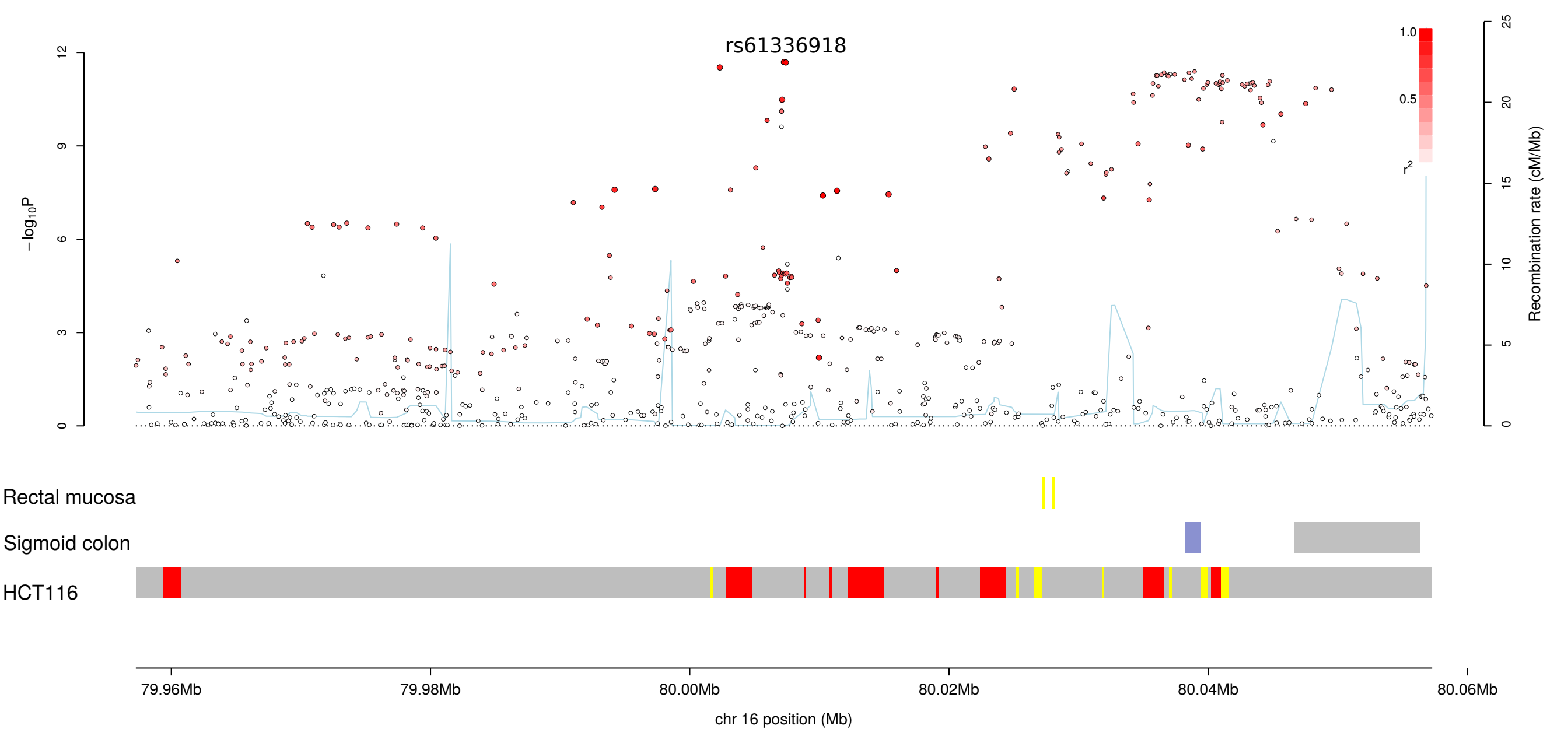


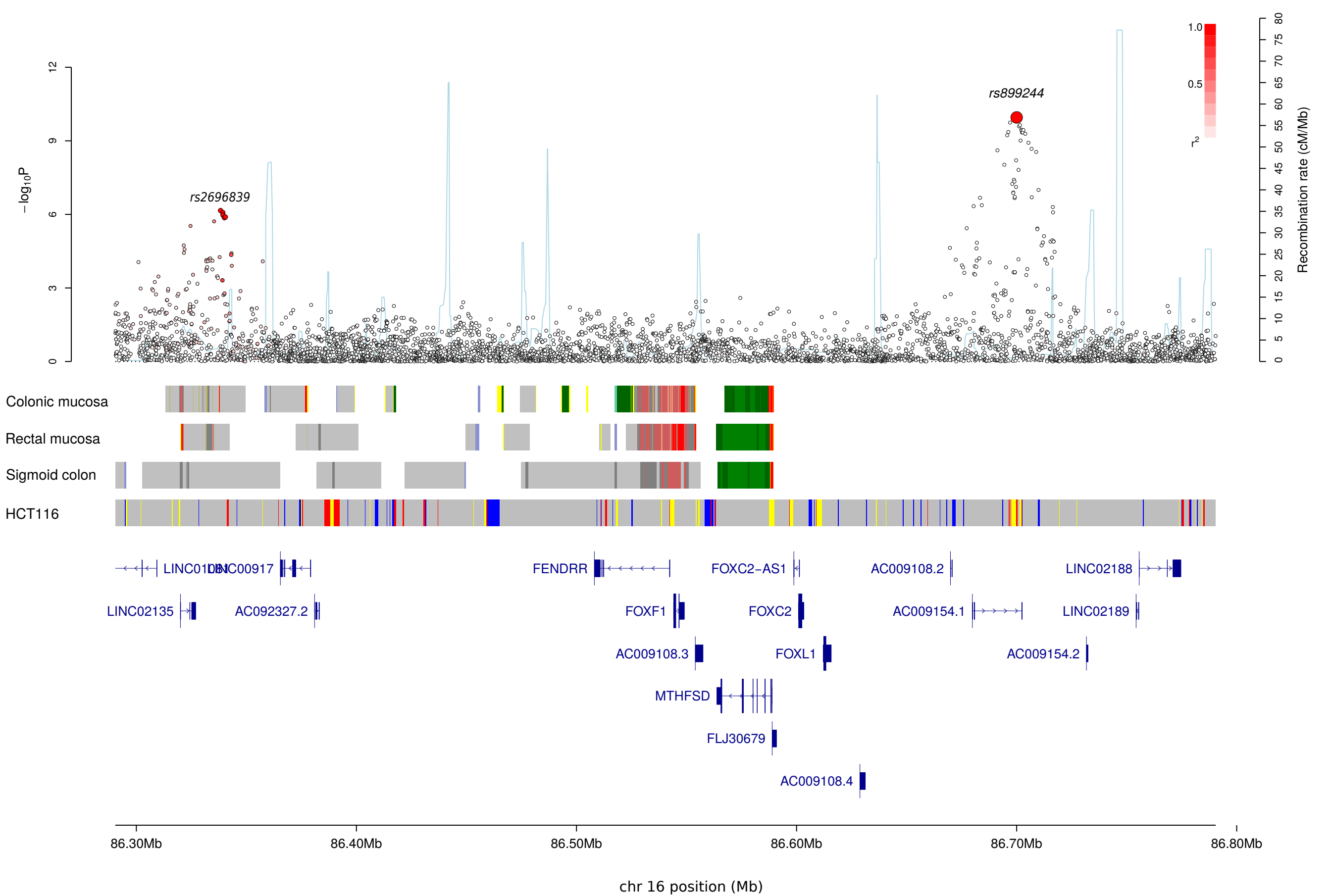


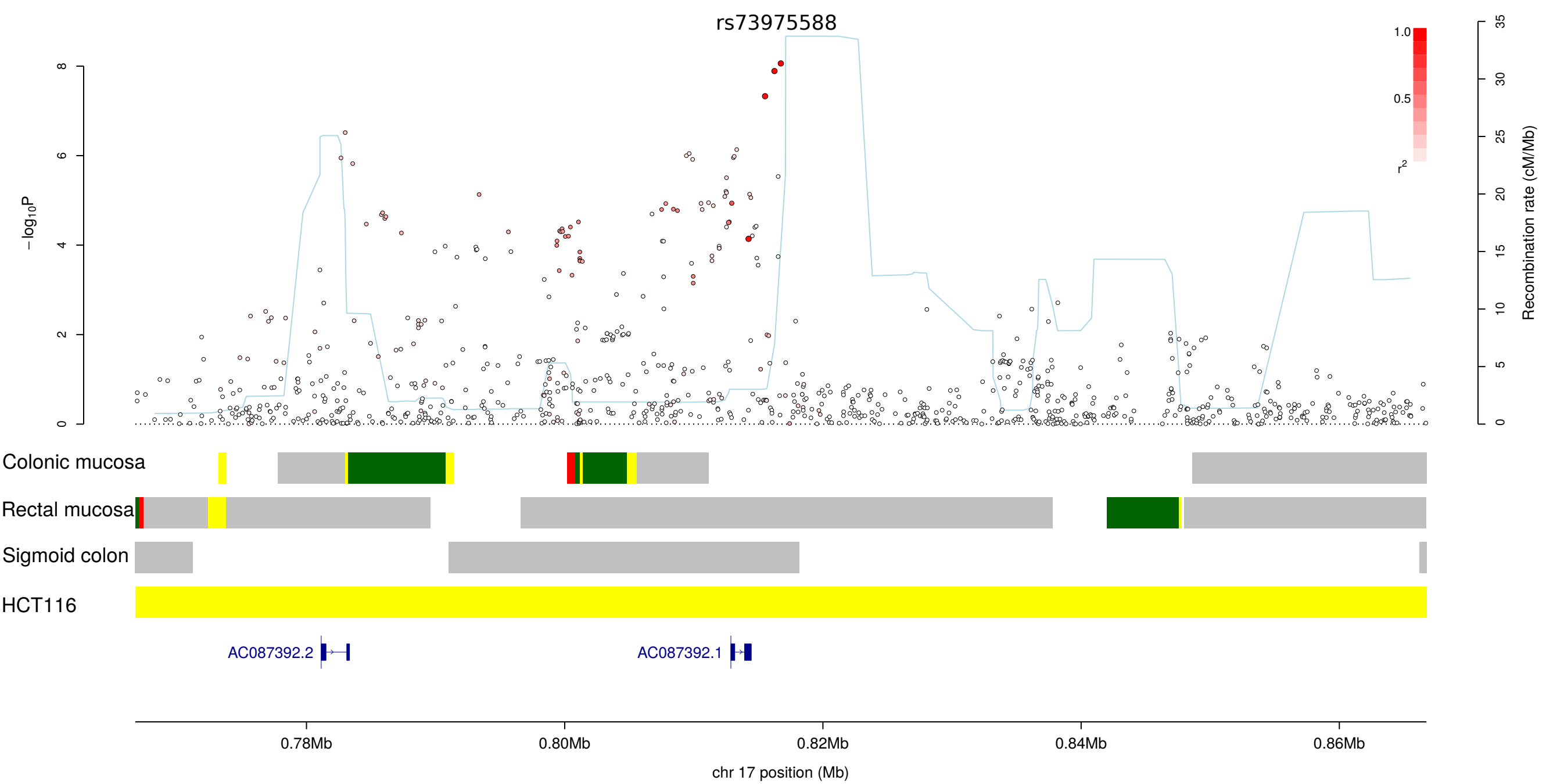


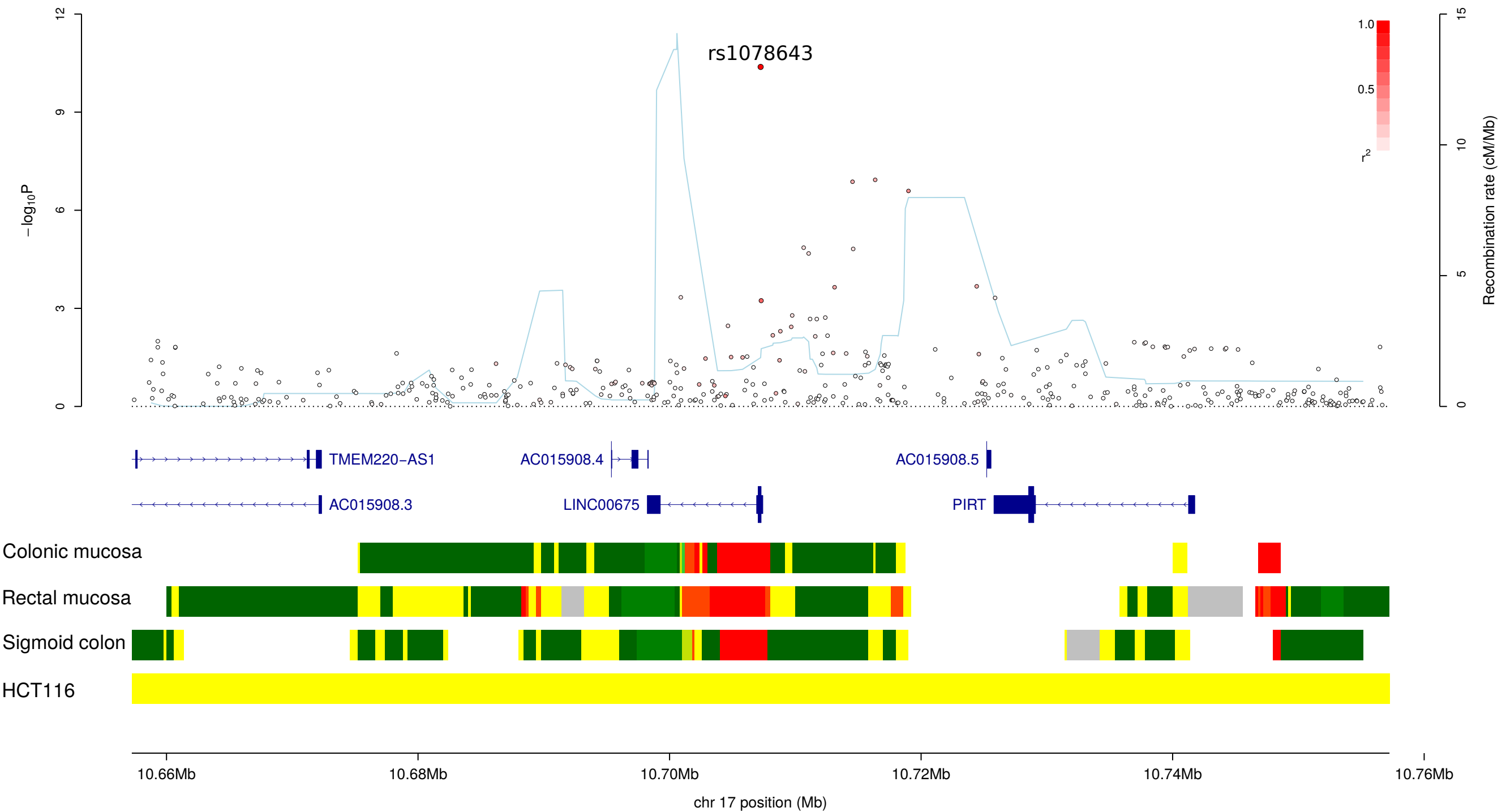


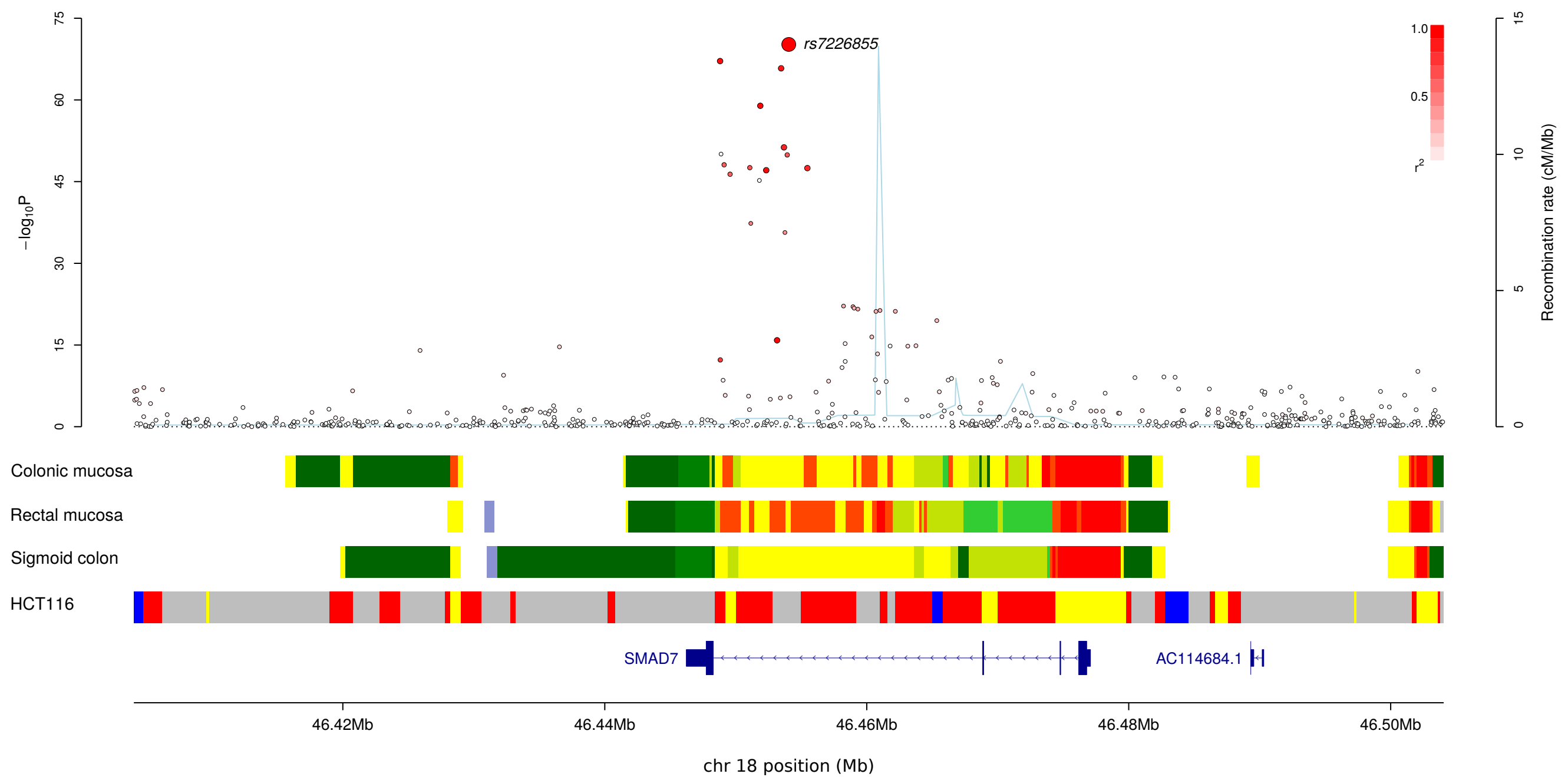


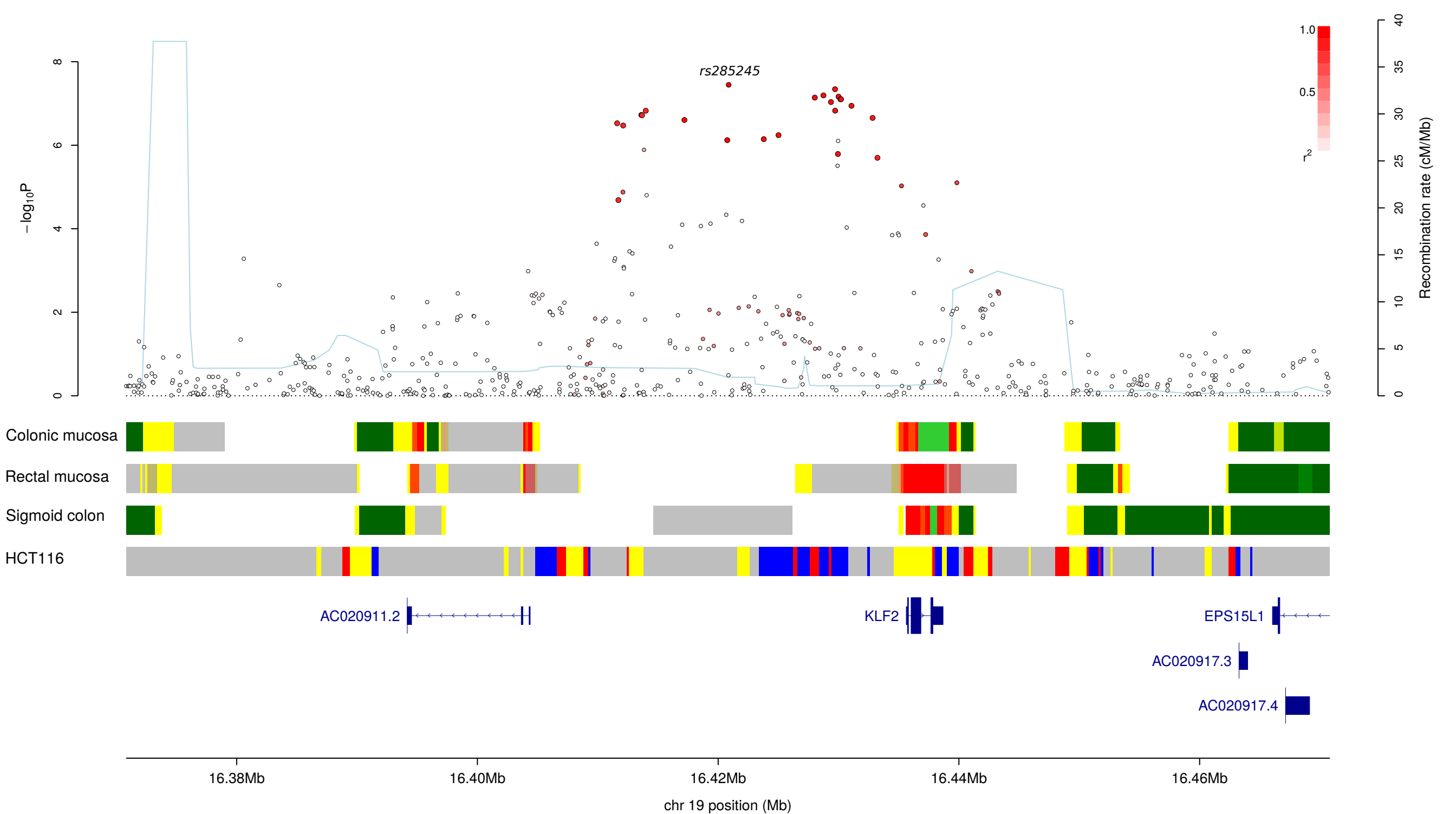


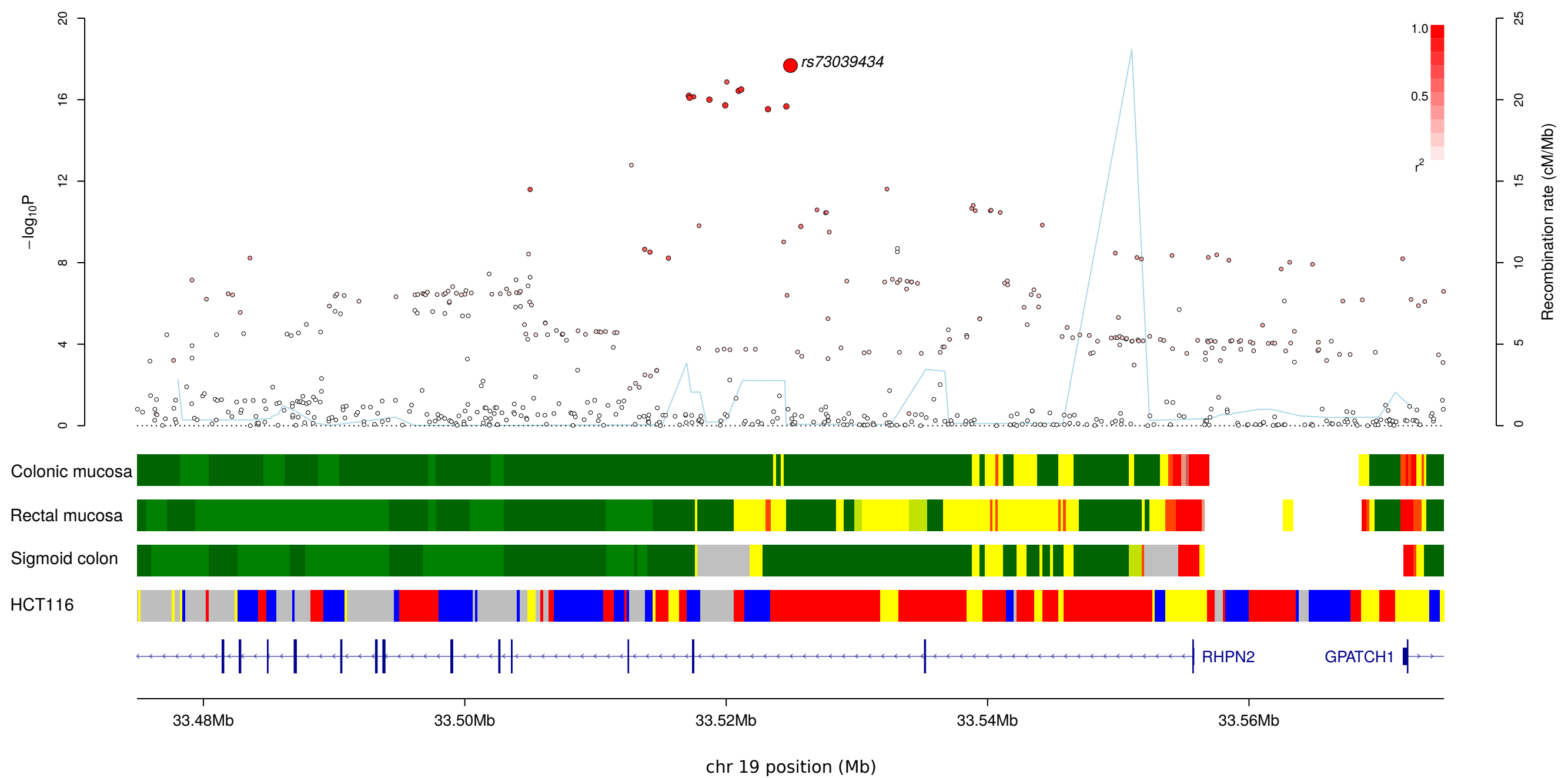


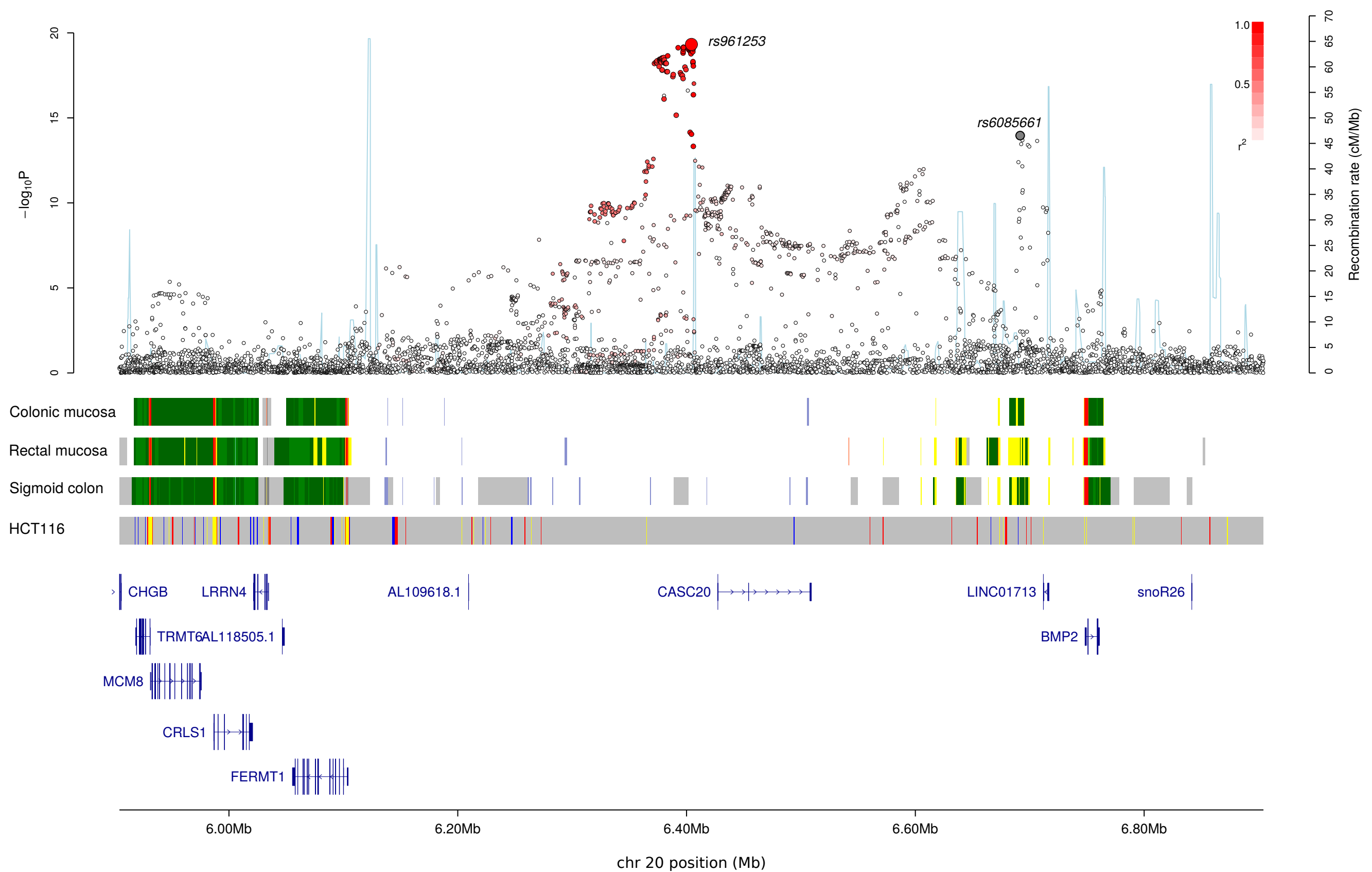


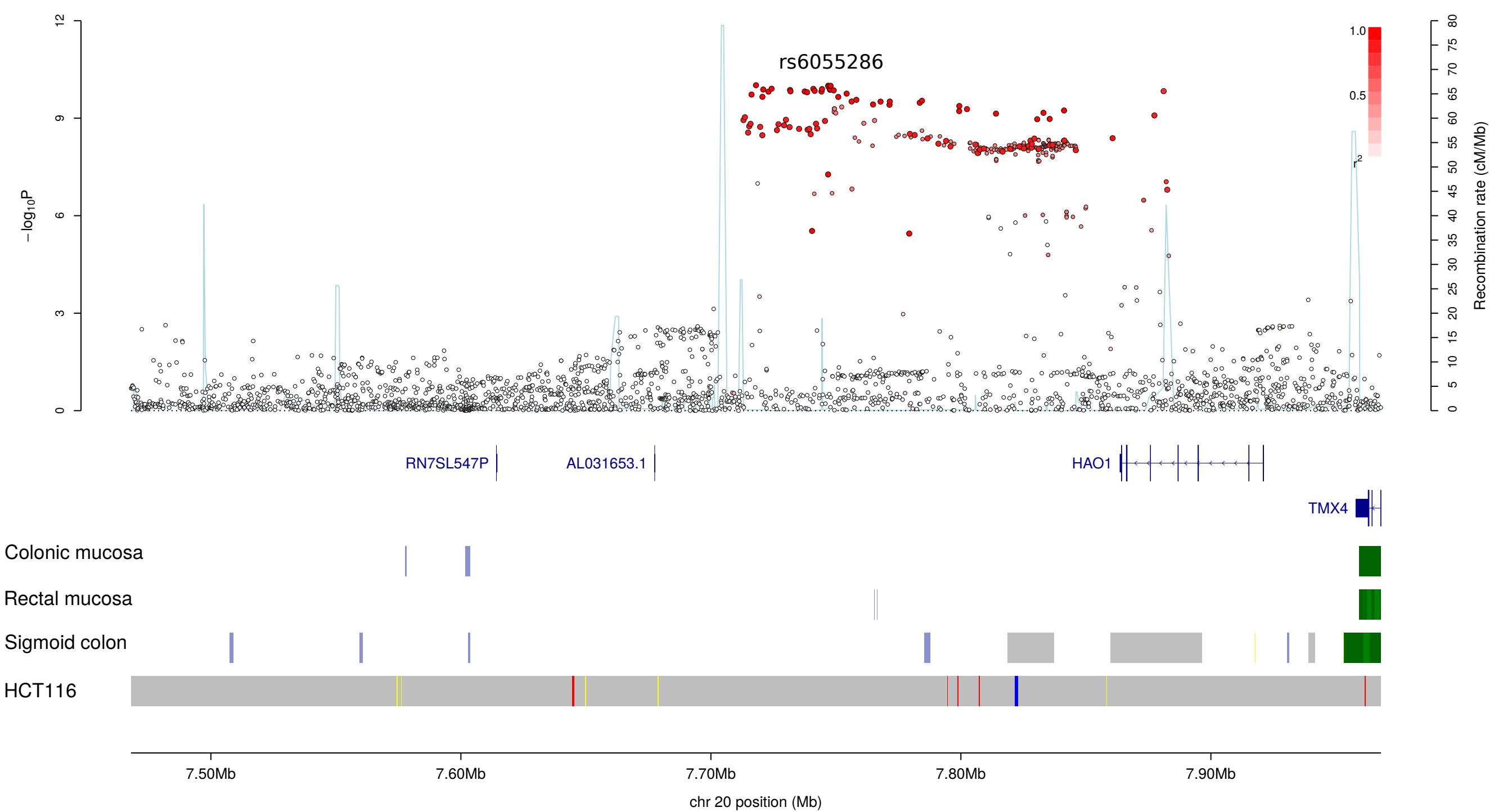


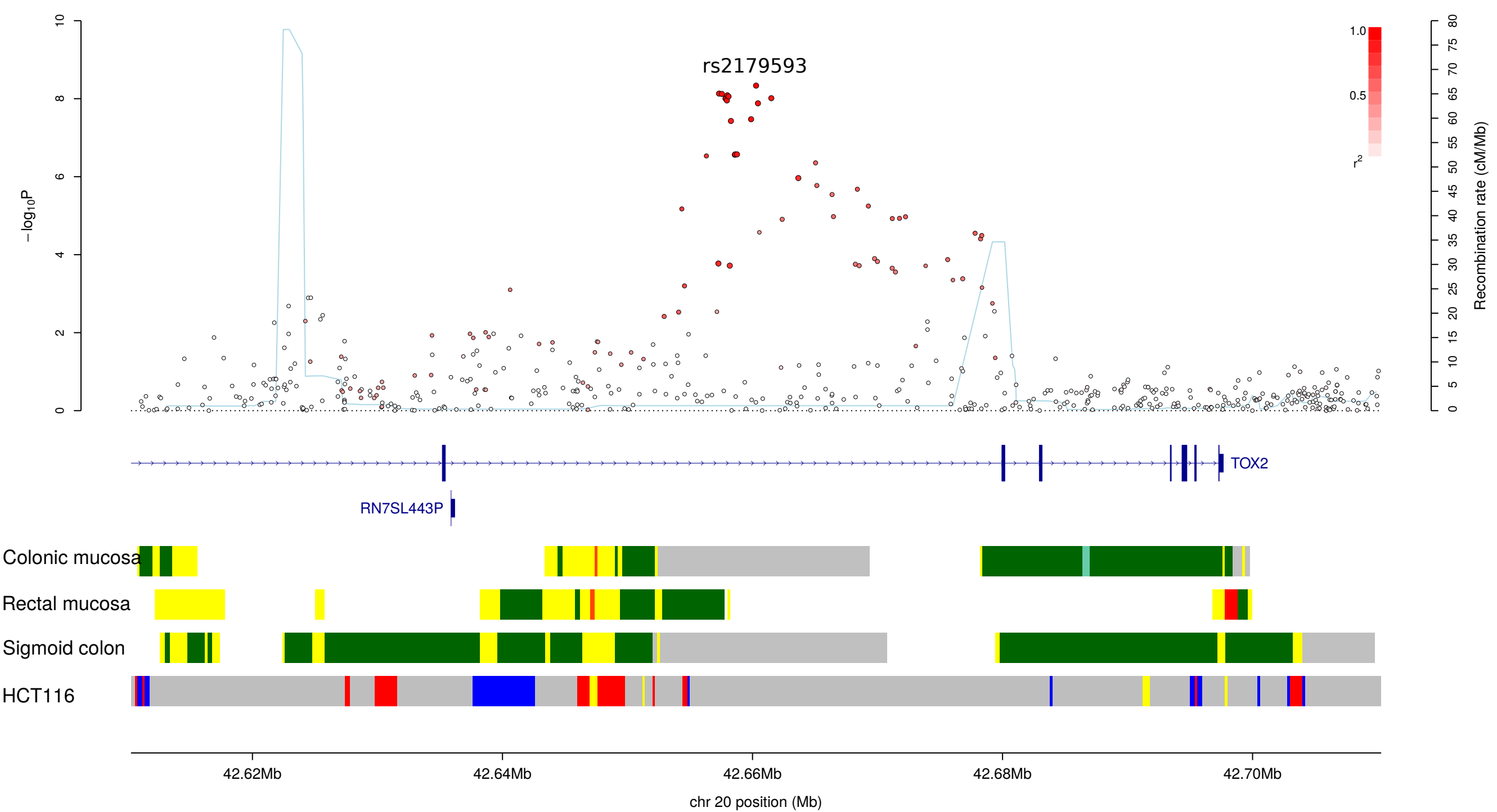


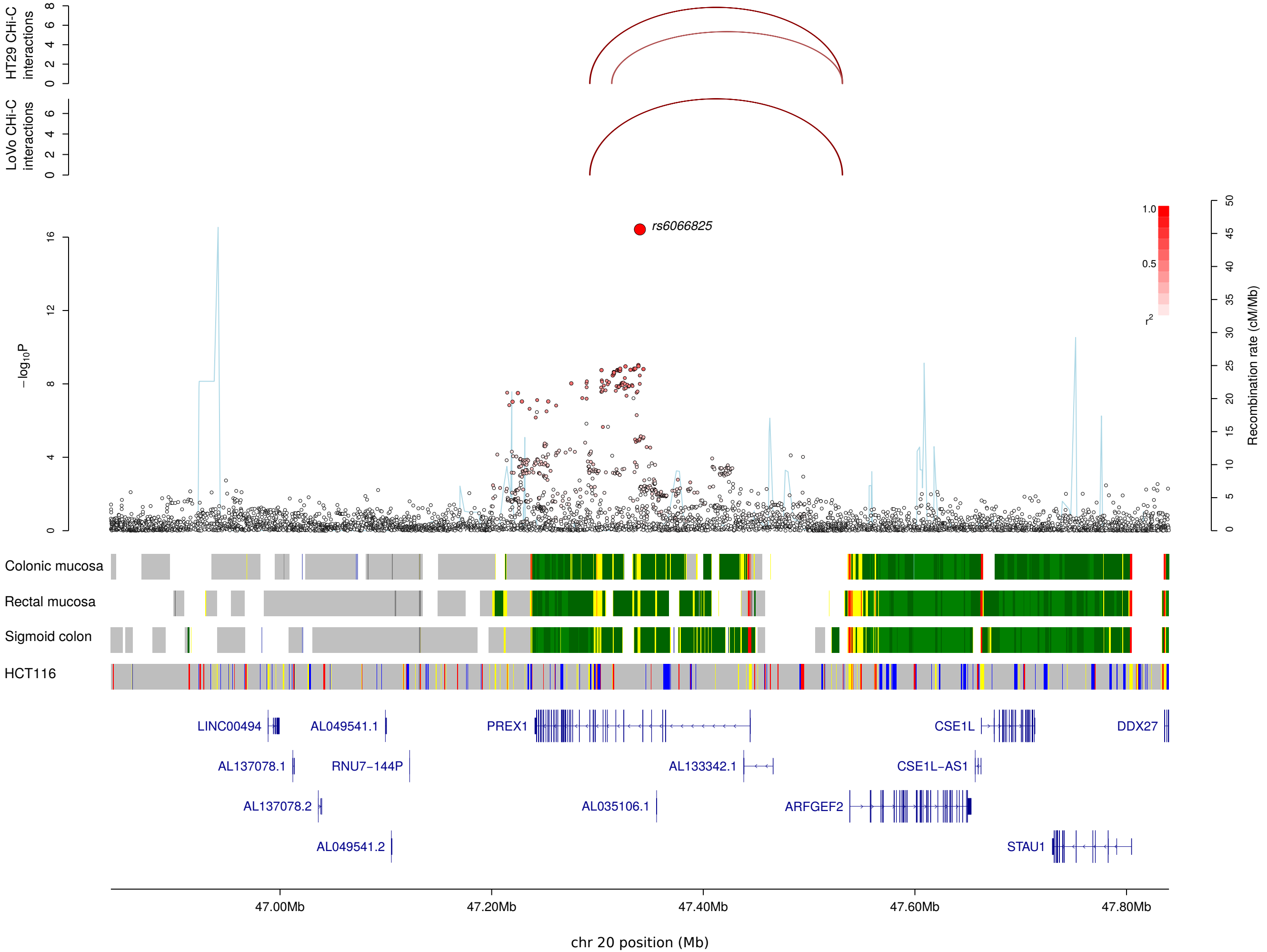


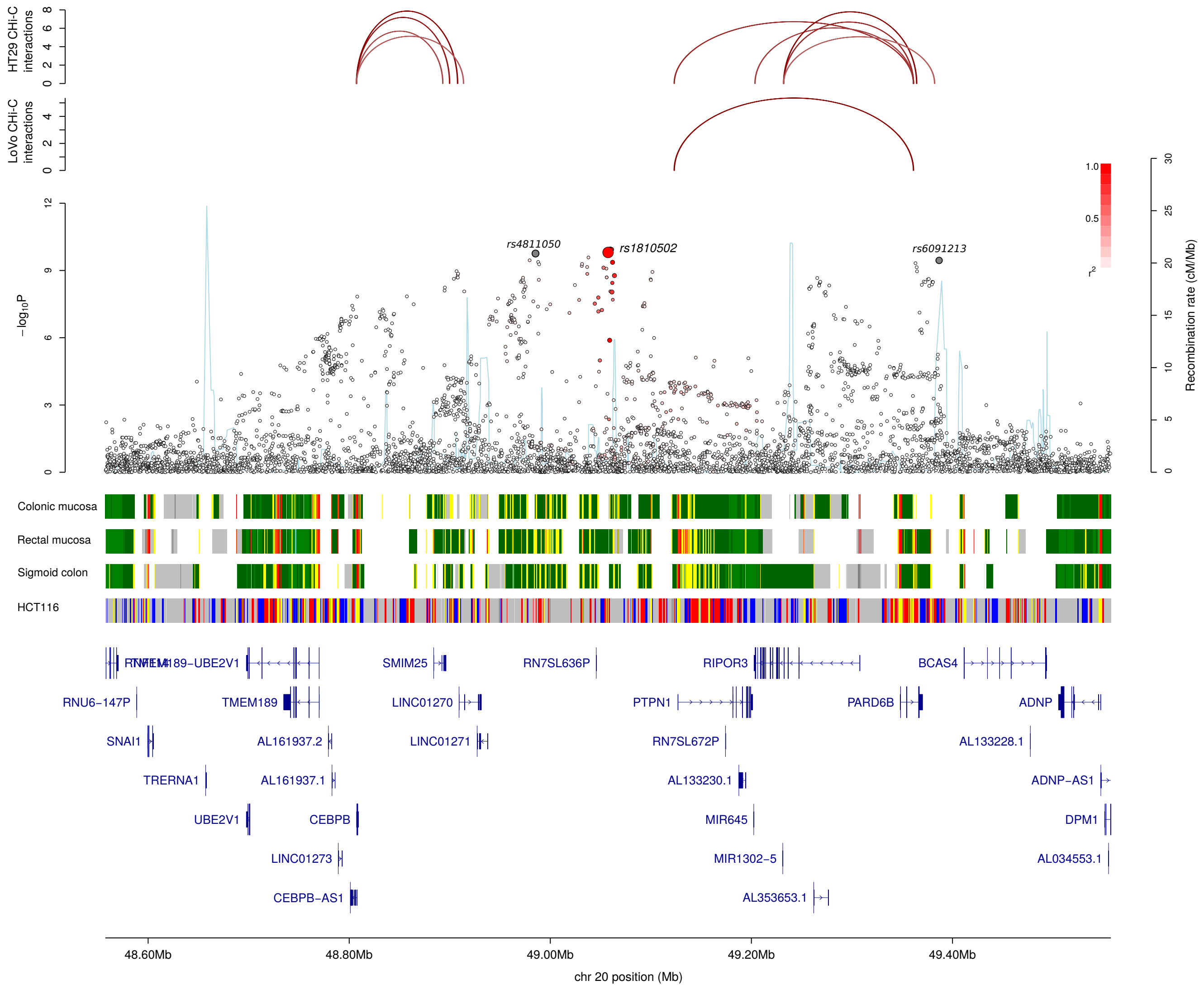


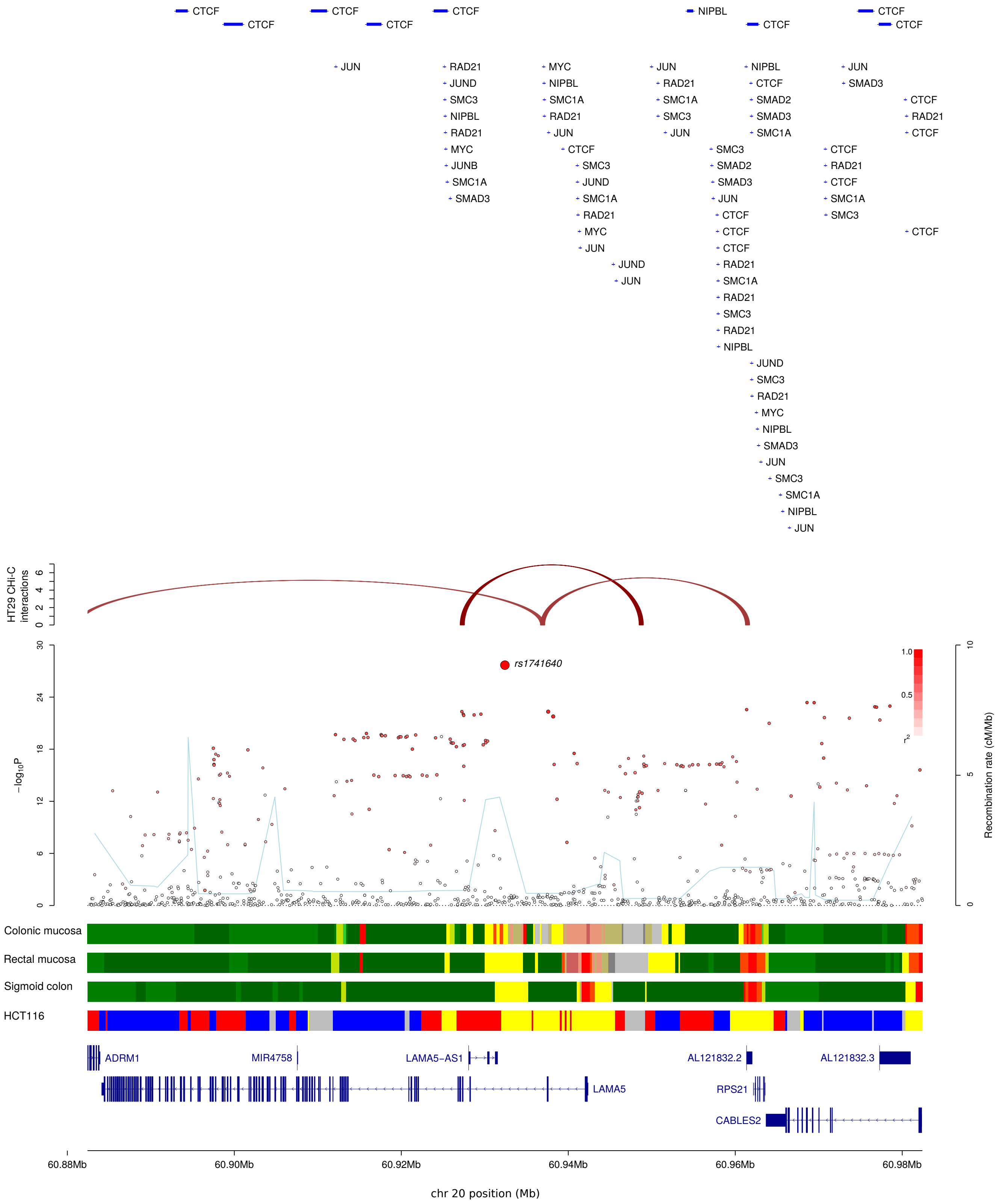


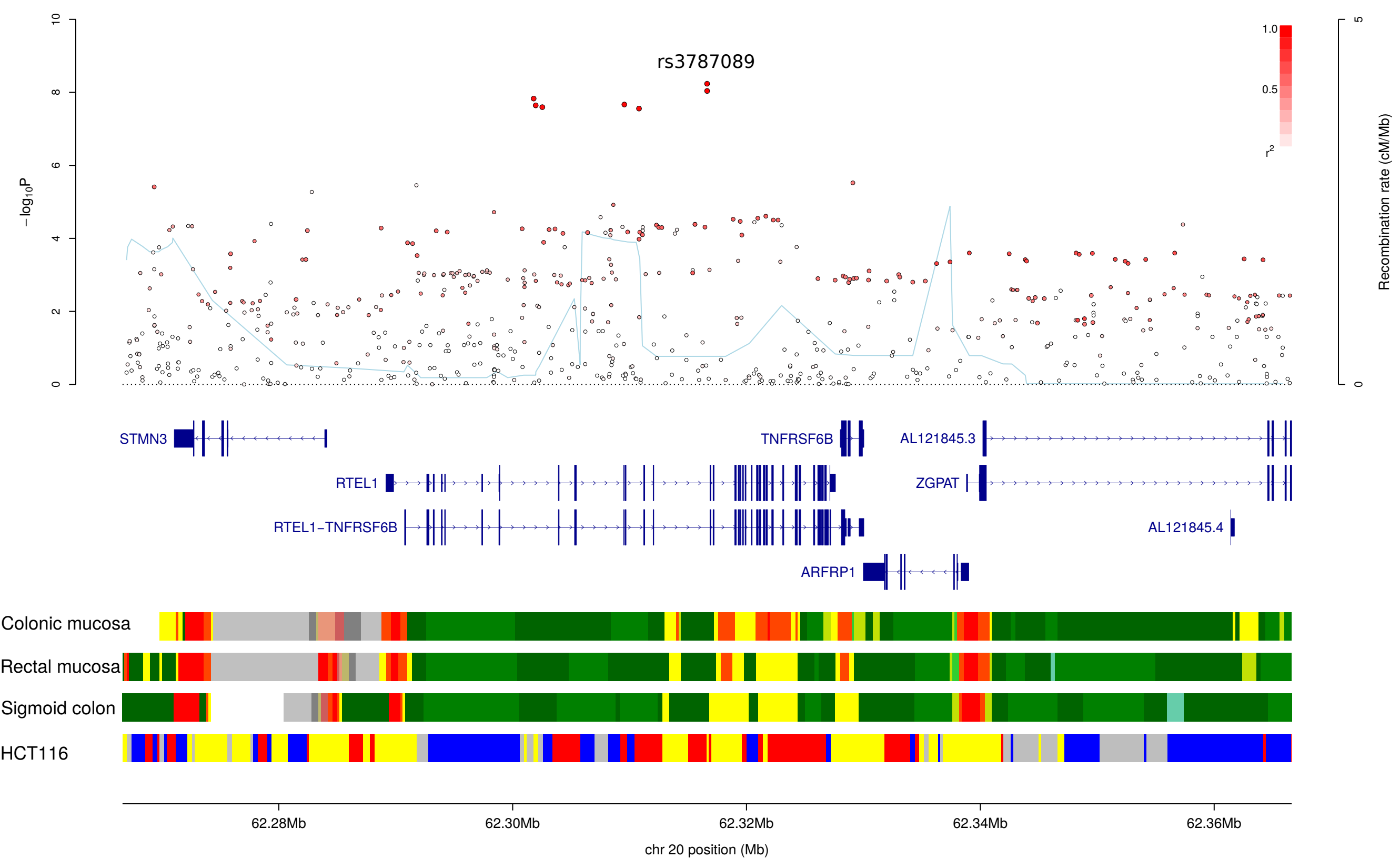


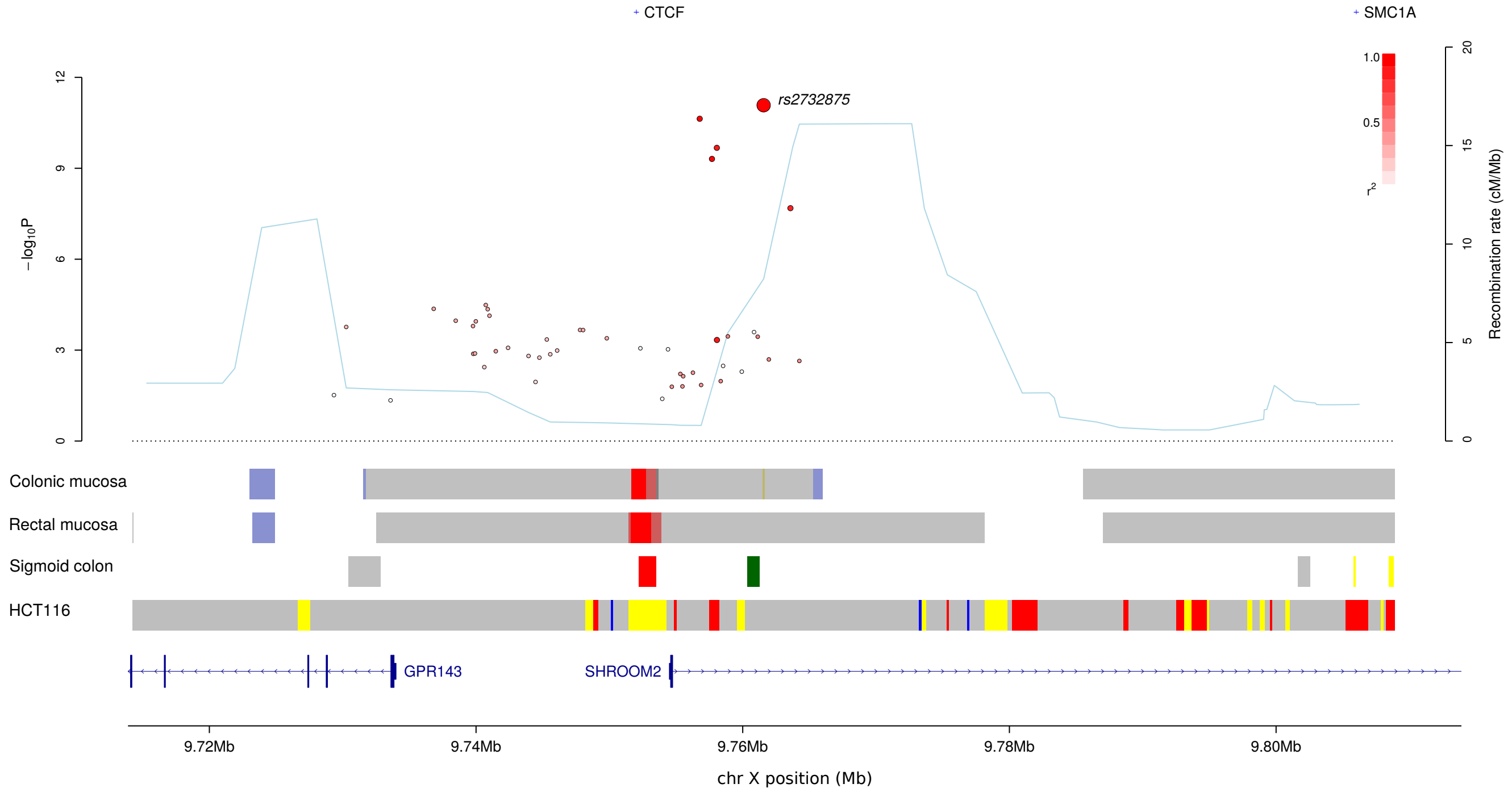




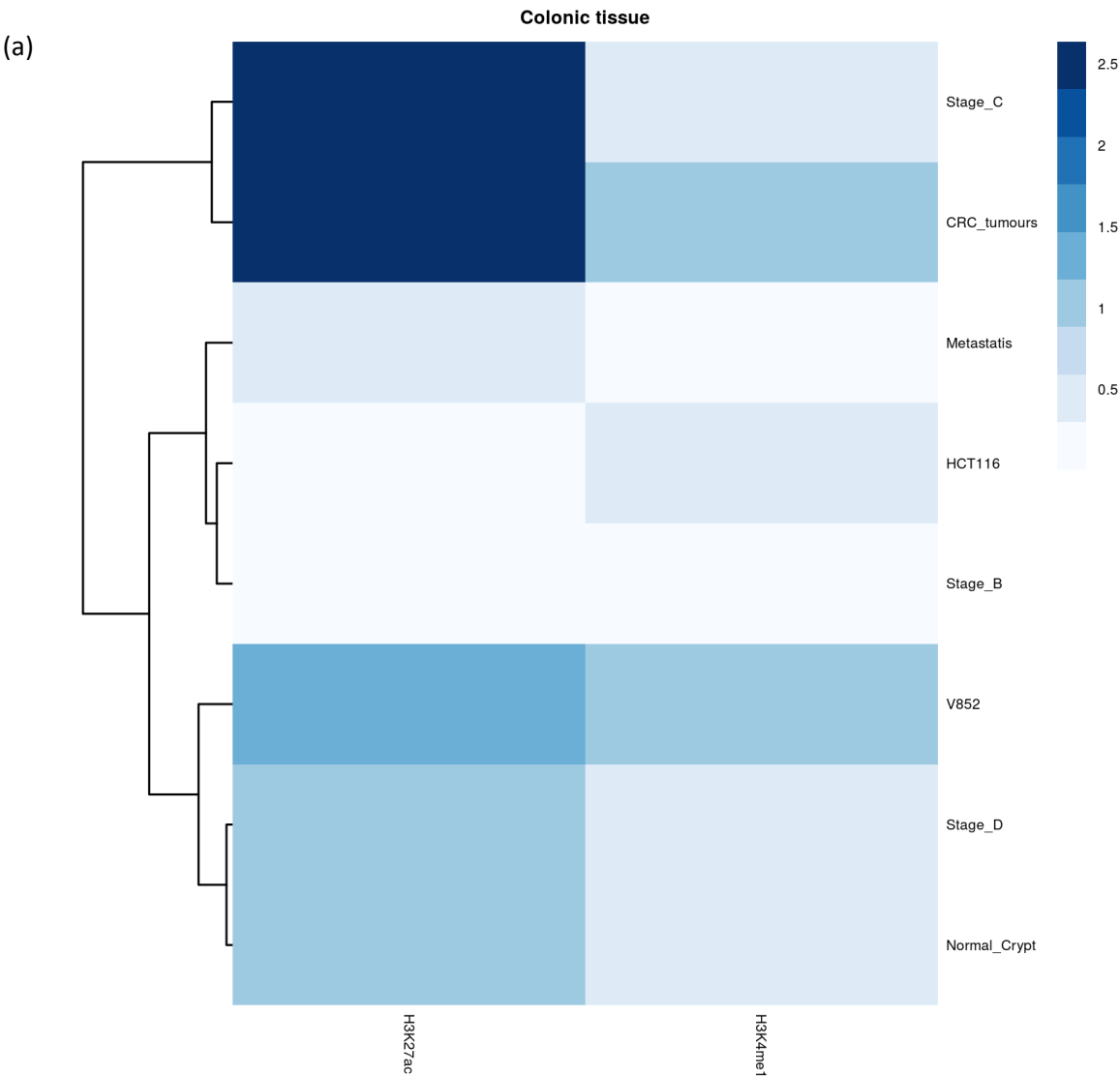








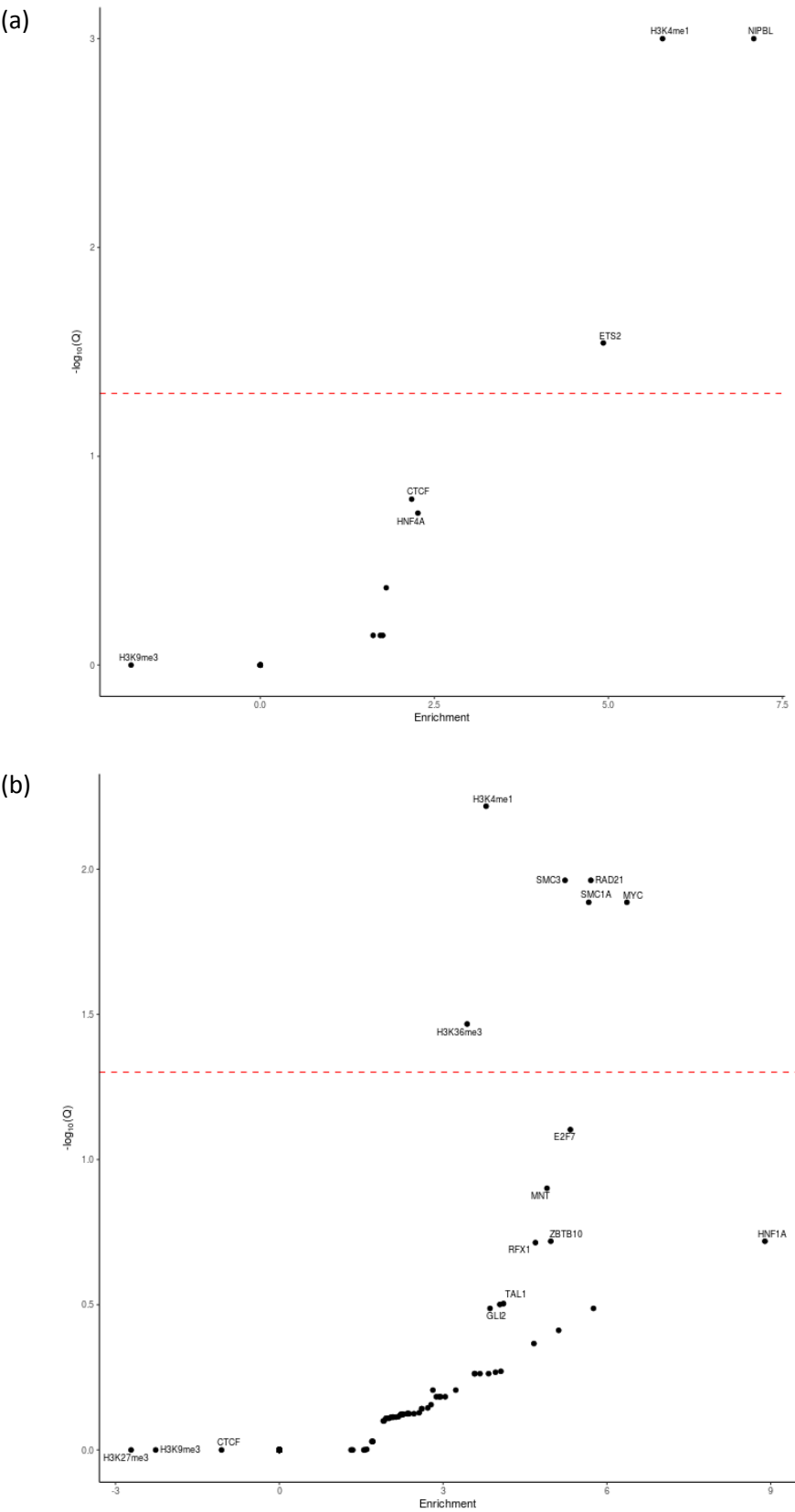
Supplementary Figure 3: Heatmap of enrichment of histone marks at colorectal cancer risk locus across (a) different colonic tissues, and (b) multiple cell types. SNP score calculated using EPIGWAS.



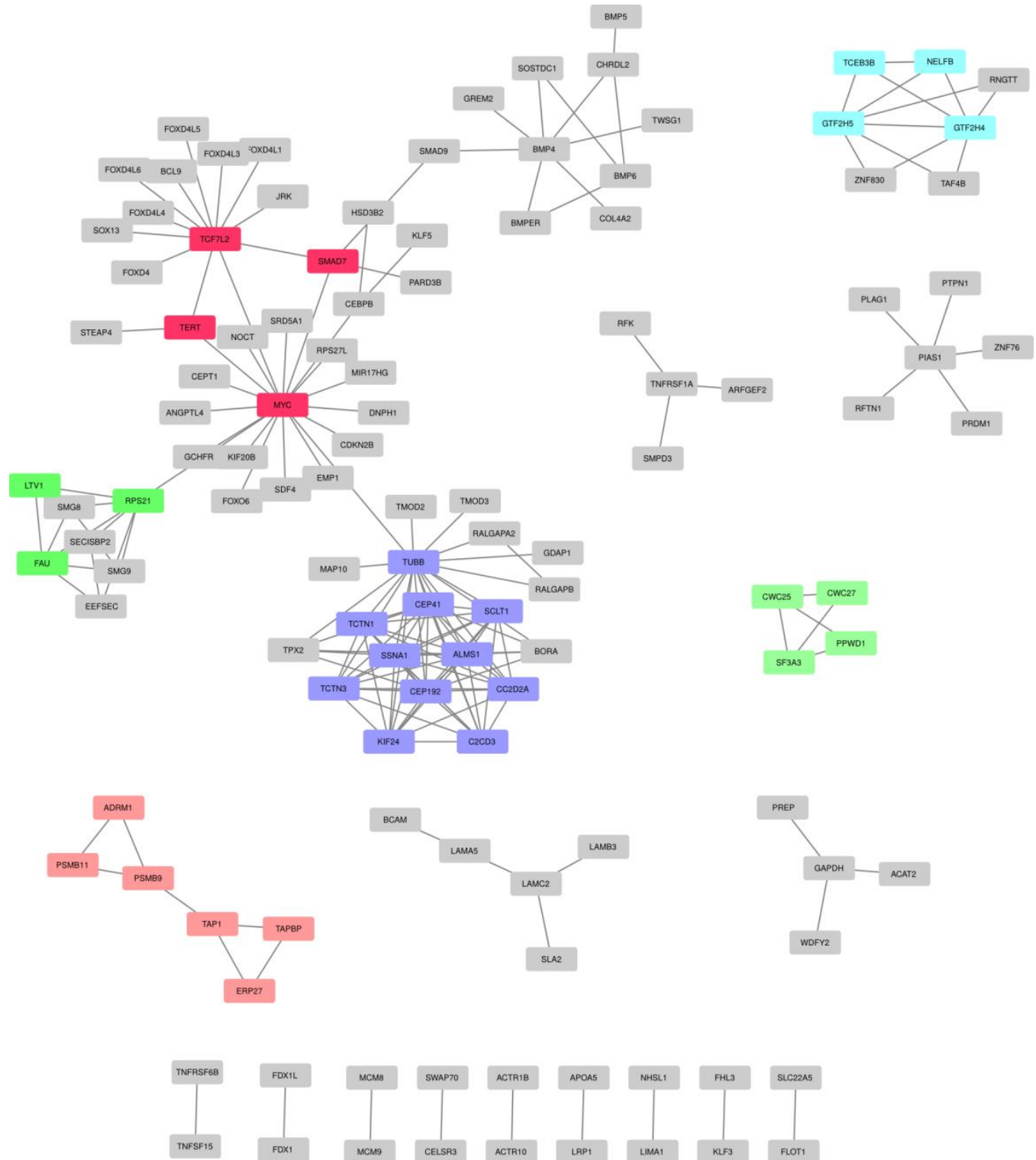
(b)



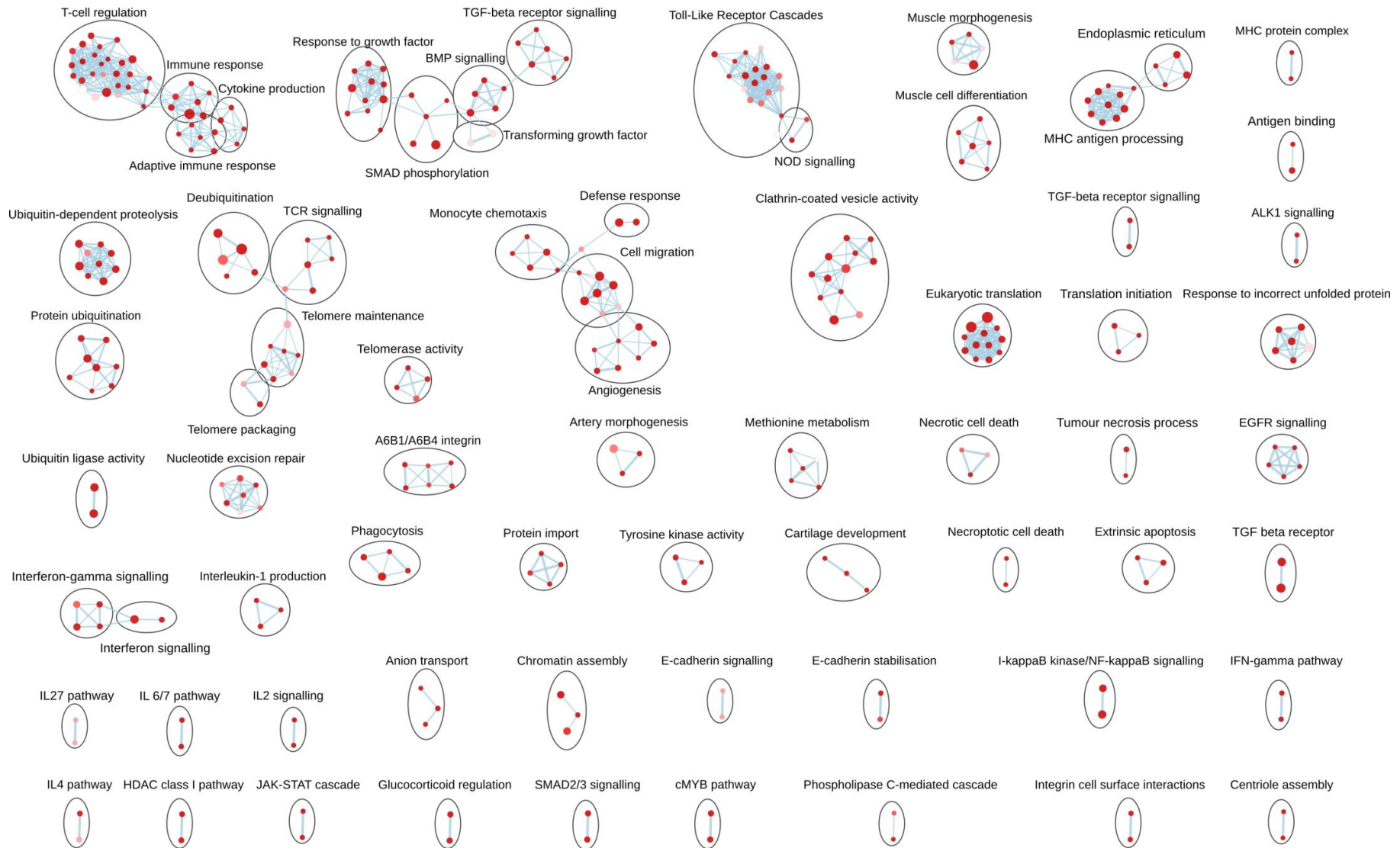
Supplementary Figure 4: Enrichment of transcription factors and histone marks in (a) LoVo and (b) HT29 cells at risk SNPs demonstrates that risk SNPs. The red line denotes the FDR Q-value of 0.05.



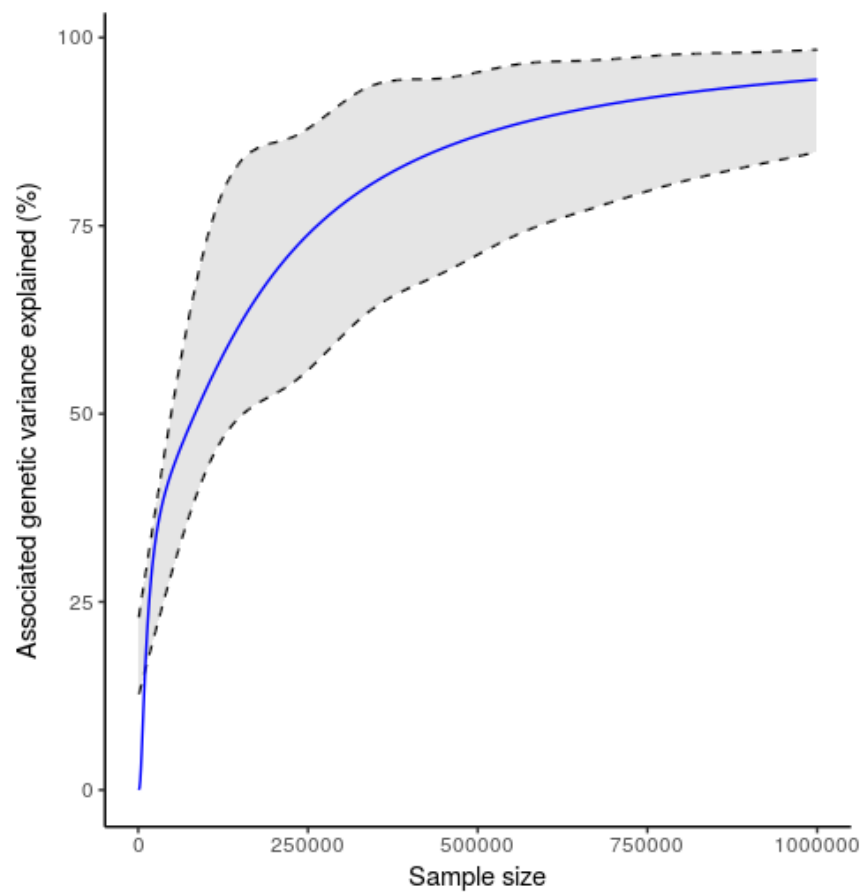
Supplementary Figure 5: Protein-protein interaction networks for colorectal cancer risk loci. Risk variants were mapped to candidate target genes, and interactions between the gene products were identified. Nodes represent credible gene products and edges represent protein-protein interactions. Nodes are coloured based on their community, i.e. genes that clustered together.



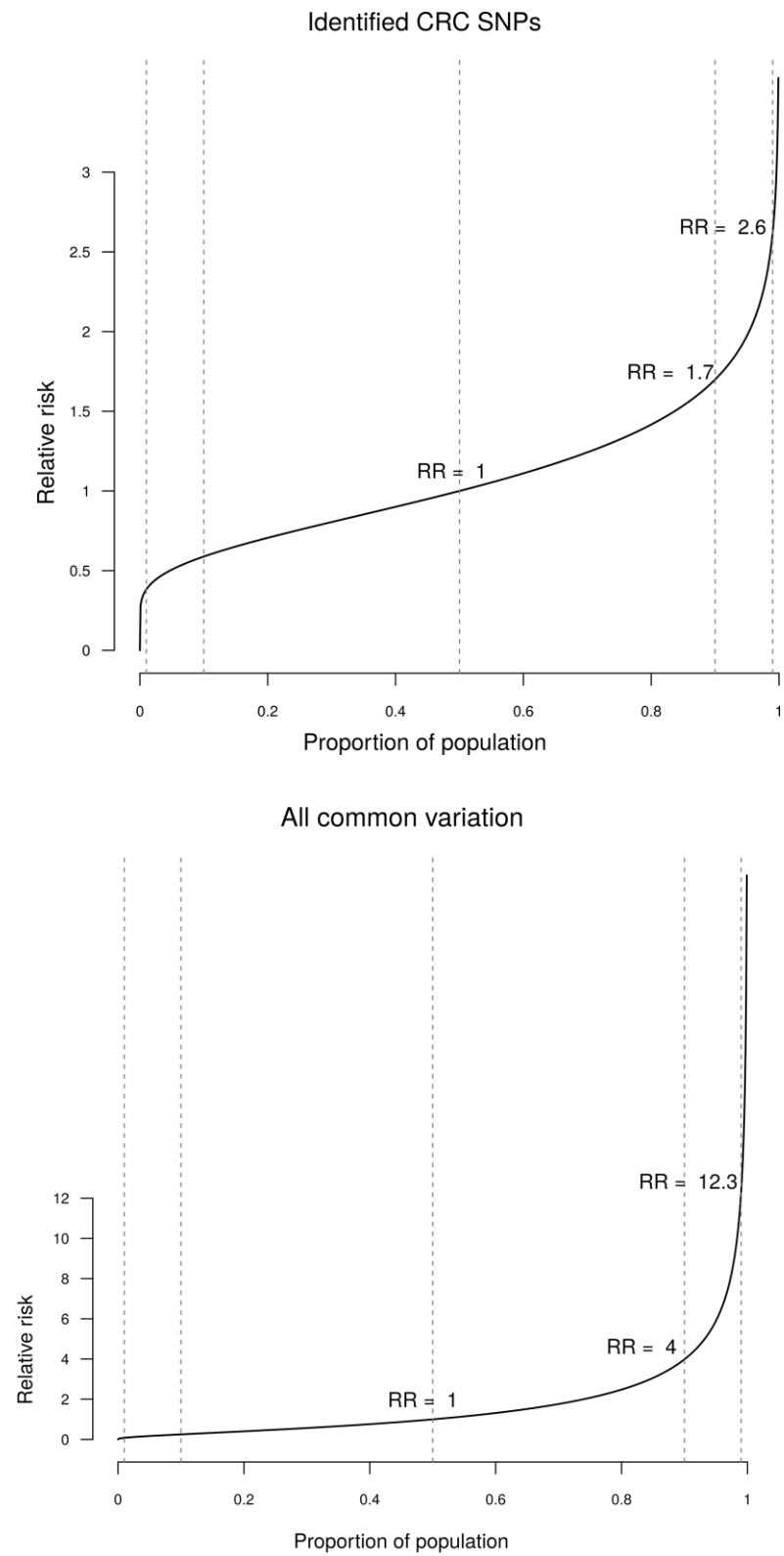
Supplementary Figure 6: Pathway enrichment using summary association statistics. Nodes represent pathways (sets of genes) and edges represent overlaps of genes within the pathways (correlation coefficient). Node size is representative of the number of genes in the pathway, and node colour represents the FDR Q-value from the enrichment analysis (deeper red indicates more significant). Only pathways with $Q < 0.05$ and connections with correlation coefficient > 0.55 are shown.



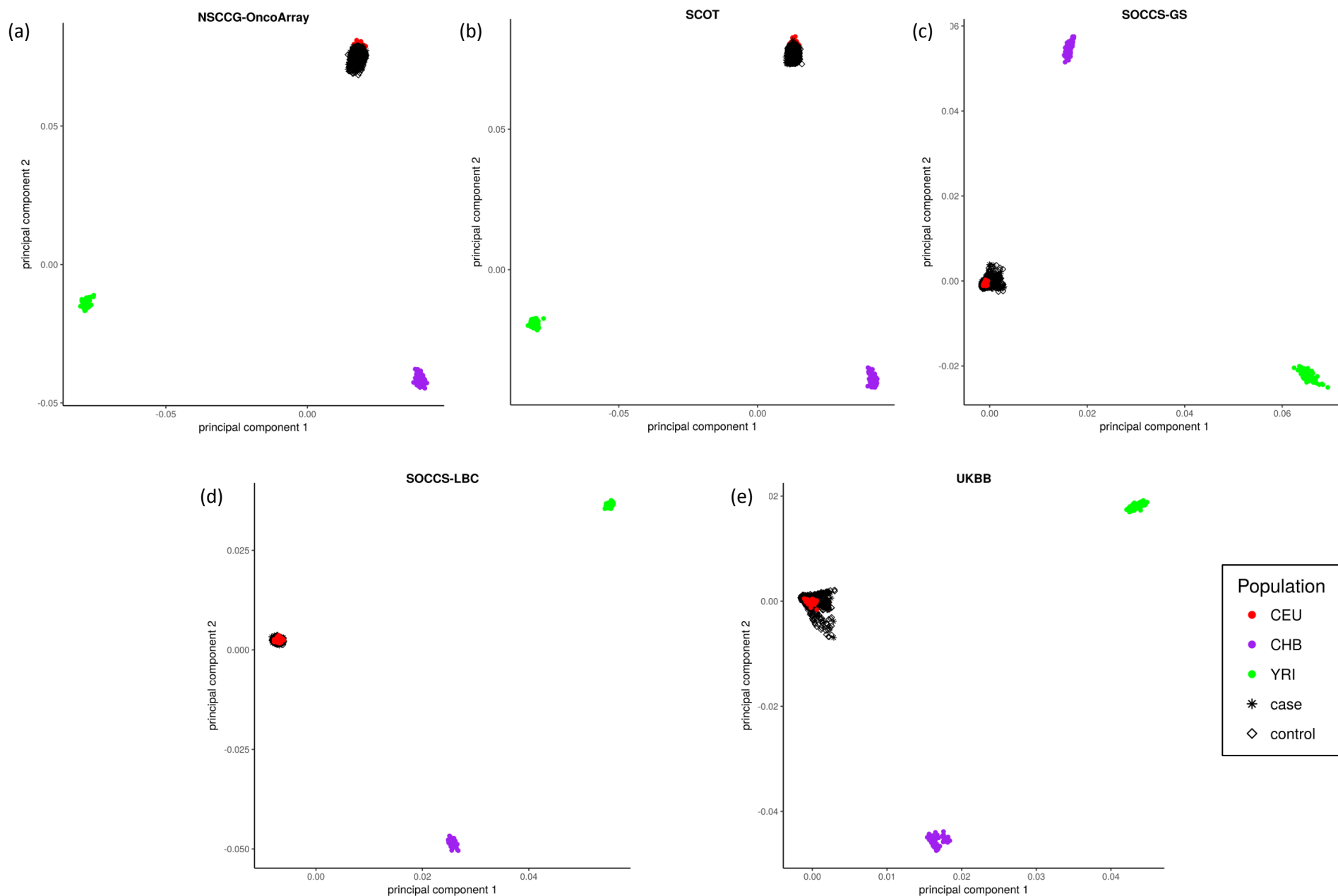
Supplementary Figure 7: Projected percentage of GWAS heritability explained for a given sample size. Results were obtained using a three-component model to estimate distribution of effect sizes. Grey shaded area represents the 95% confidence interval of the heritability estimate. The sample size indicates the total number of cases and controls, assuming a 1:1 ratio.



Supplementary Figure 8: Population risk distribution ordered by relative risk (RR), compared to the population average. Vertical dotted lines (left to right) correspond to 1%, 10%, 50%, 90%, and 99% centile, respectively. The RR distribution in the top figure was based on the 79 identified CRC risk SNPs, and the RR distribution in the bottom figure is based on assuming all common variation.



Supplementary Figure 9: Identification of individuals of non-European ancestry in cases and controls in the new GWAS. (a) NSCCG-OncoArray, (b) SCOT, (c) SOCCS/GS, (d) SOCCS/LBC, (e) UK Biobank. The first two principal components of the analysis are plotted. HapMap CEU individuals are plotted in red, JPT individuals are plotted in indigo, YRI are plotted in green. Cases and controls are plotted in black.



SUPPLEMENTARY REFERENCES

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