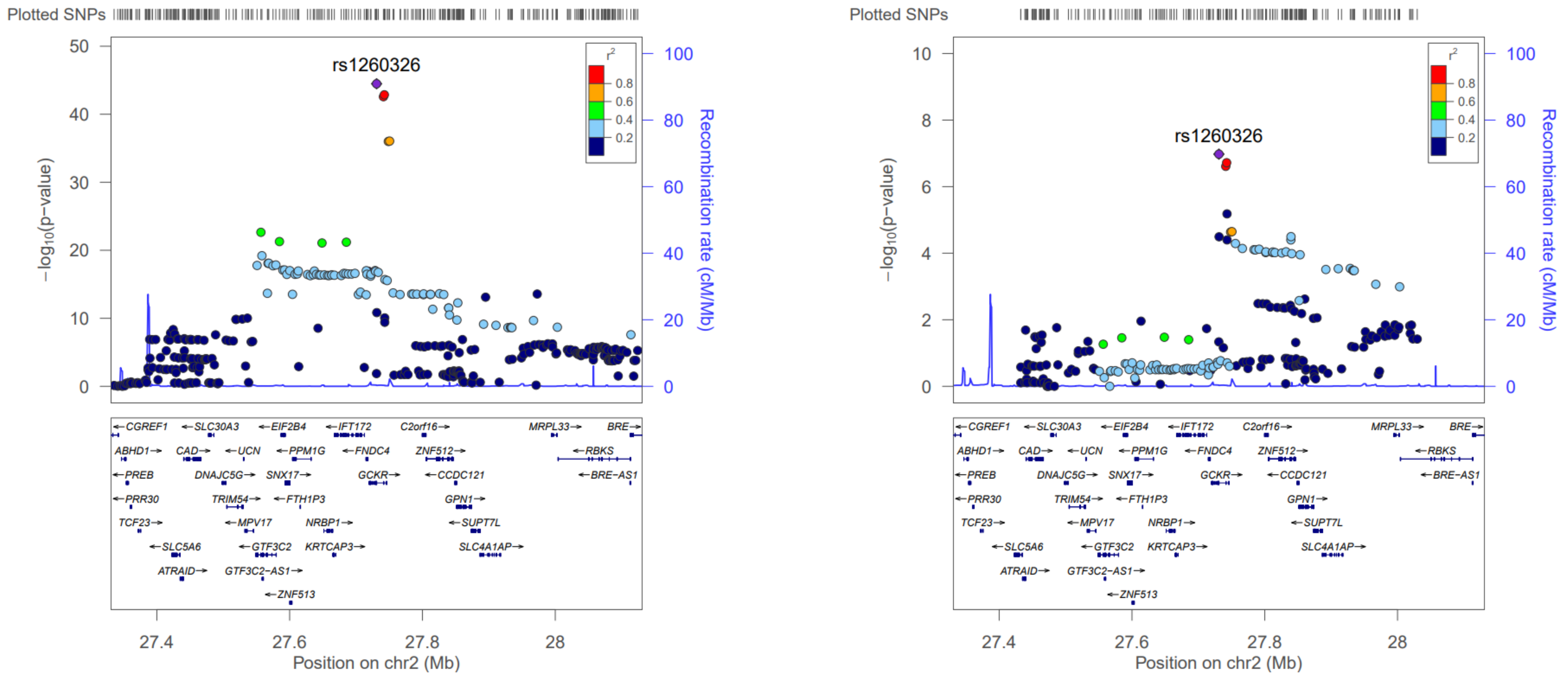
Figure S1. Regional association plots of genome-wide significant urate and habitual coffee loci. In each panel, SNPs identified as associated with both urate [2] and coffee intake [22] are plotted with their -$\log_{10}$ (p-values) as a function of genomic position using HG build 19 and 1000 genomes European reference for LD (November 2014). Each SNP is coloured according to its correlation with the index SNP (demonstrating the lowest p-value within the region, labelled in purple) according to a scale from r^2=0 to r^2=1. Urate-raising alleles are displayed on the left and coffee-associated alleles are on the right. LocusZoom plots were drawn from publicly available data ex ref [2] and taken from ref [22]. *GCKR rs2911711* is in complete linkage disequilibrium with *rs1260326.*

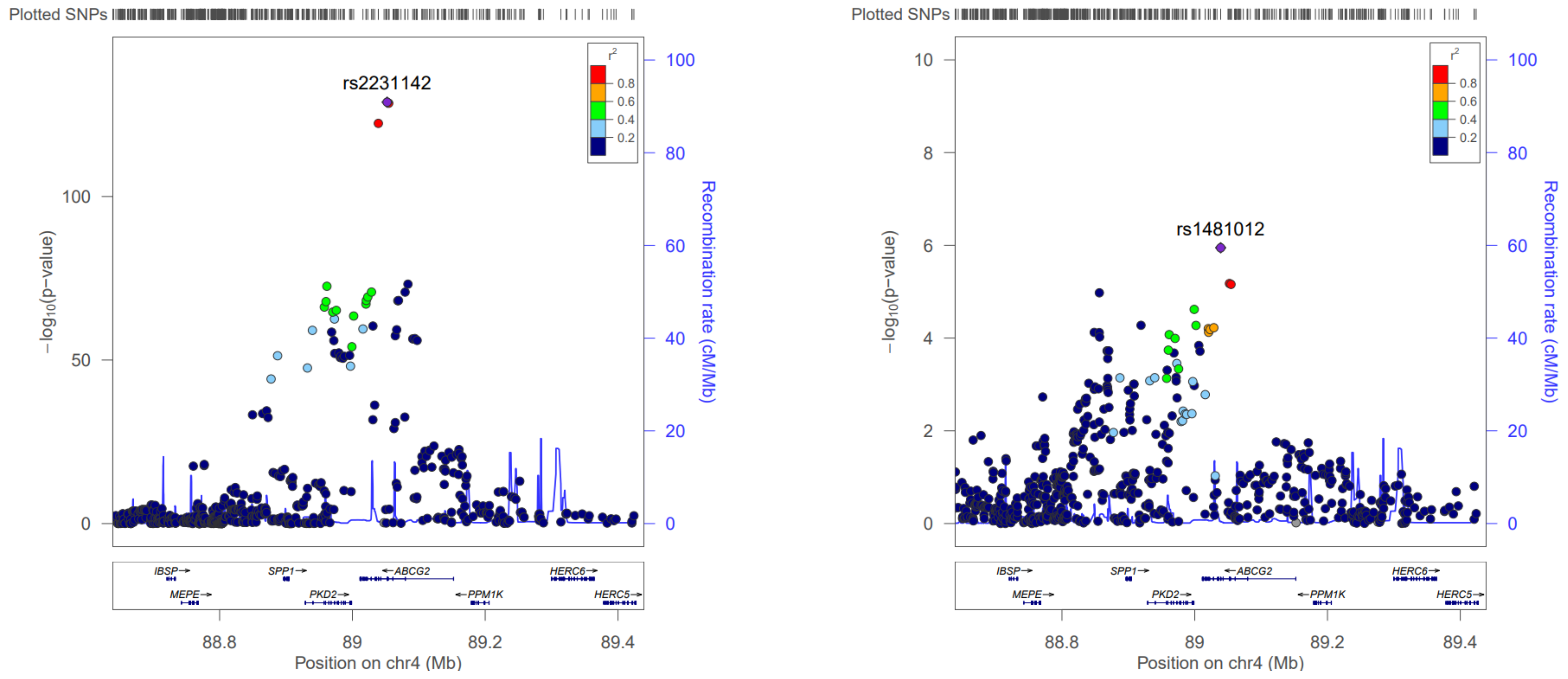
GCKR

Urate (2) Coffee (22)



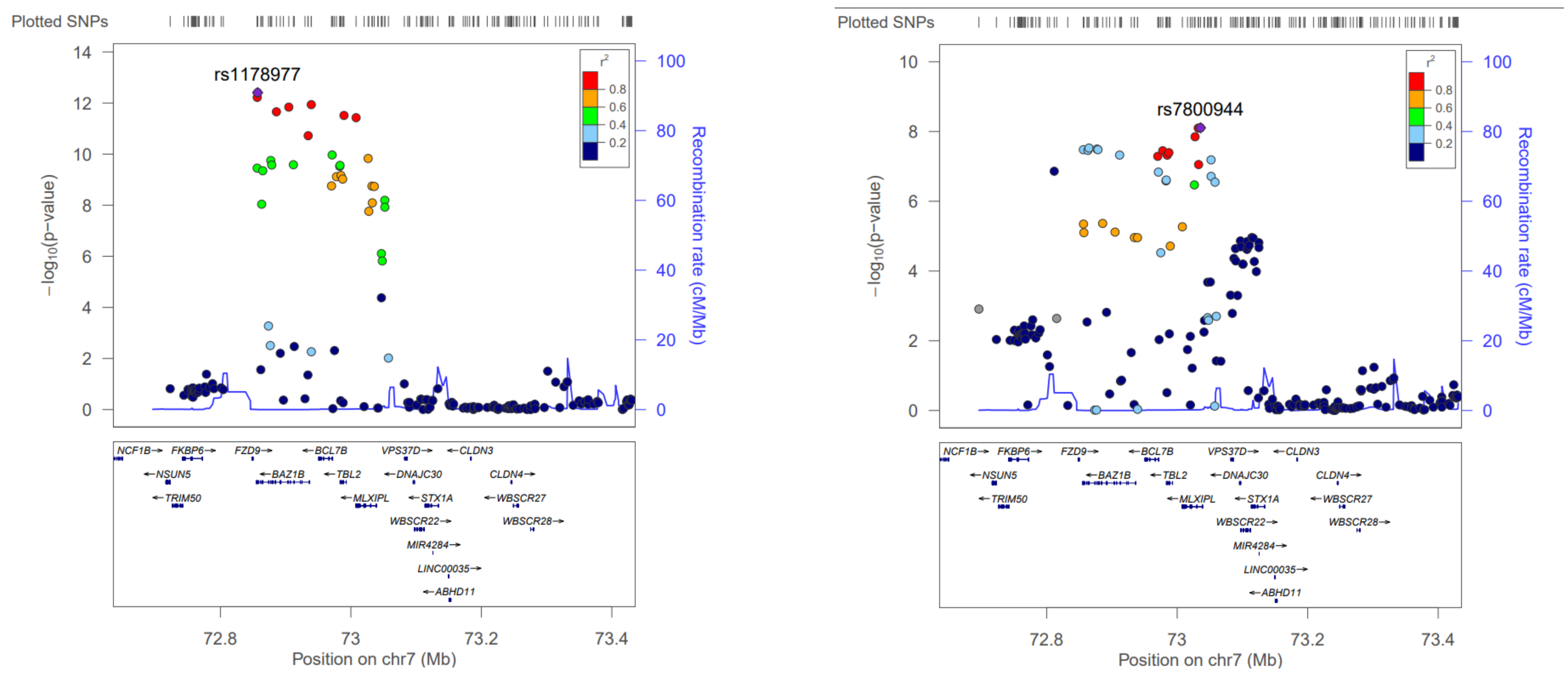
ABCG2

Urate (2) Coffee (22)



MLXIPL

Urate (2) Coffee (22)



CYP1A2

Urate (2) Coffee (22)