

Figure S1. Top *CCR5* eQTLs SNPs in lung are not in LD in African (A) and AMR populations (B). In Asian population, our selected SNPs are in LD only in South Asian (D) while in East Asian (C), only rs35951367 and rs9845542 are in LD with ($r^2=1$). The D' and r^2 data are computed by using the web tool LD-link (<https://ldlink.nci.nih.gov/?tab=home>).

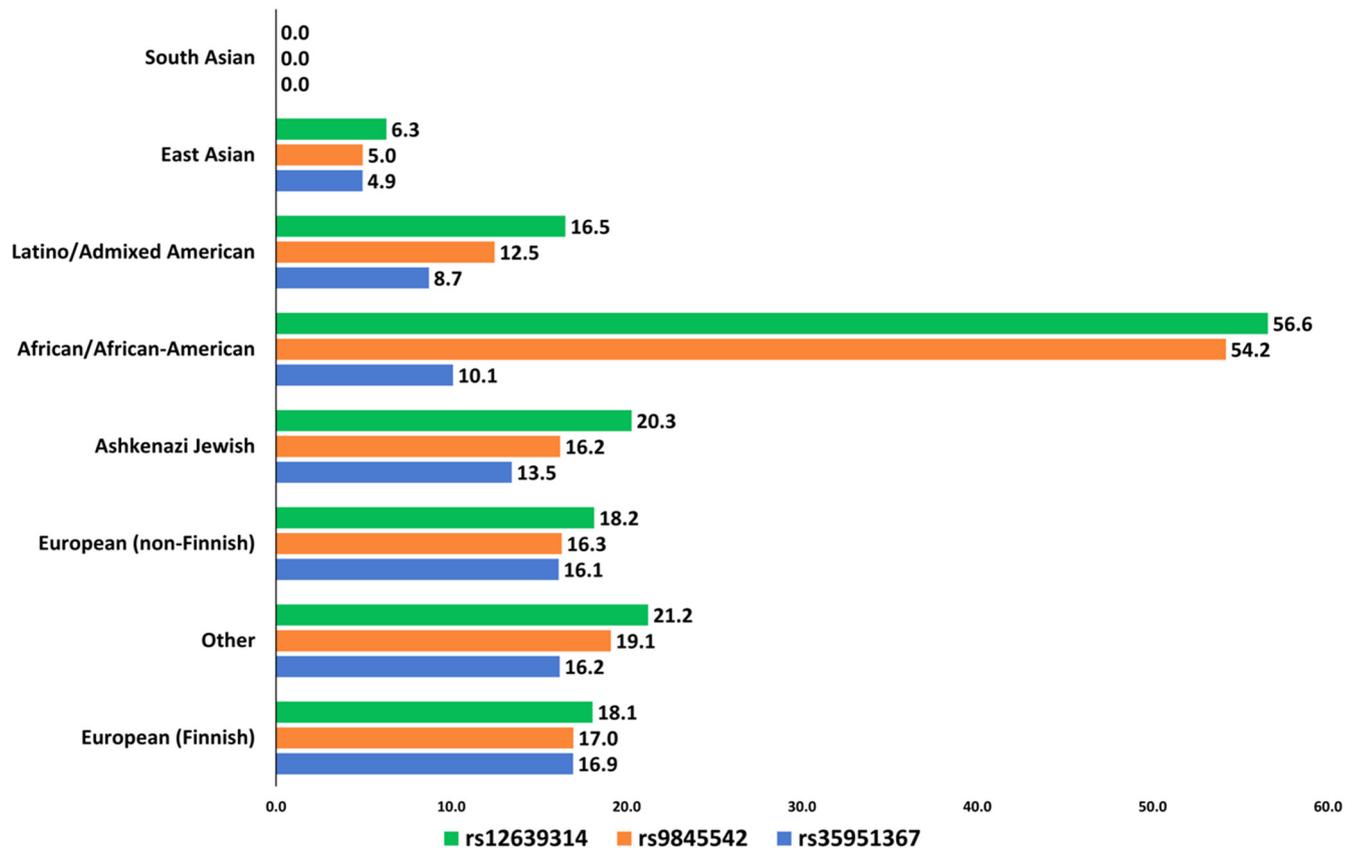
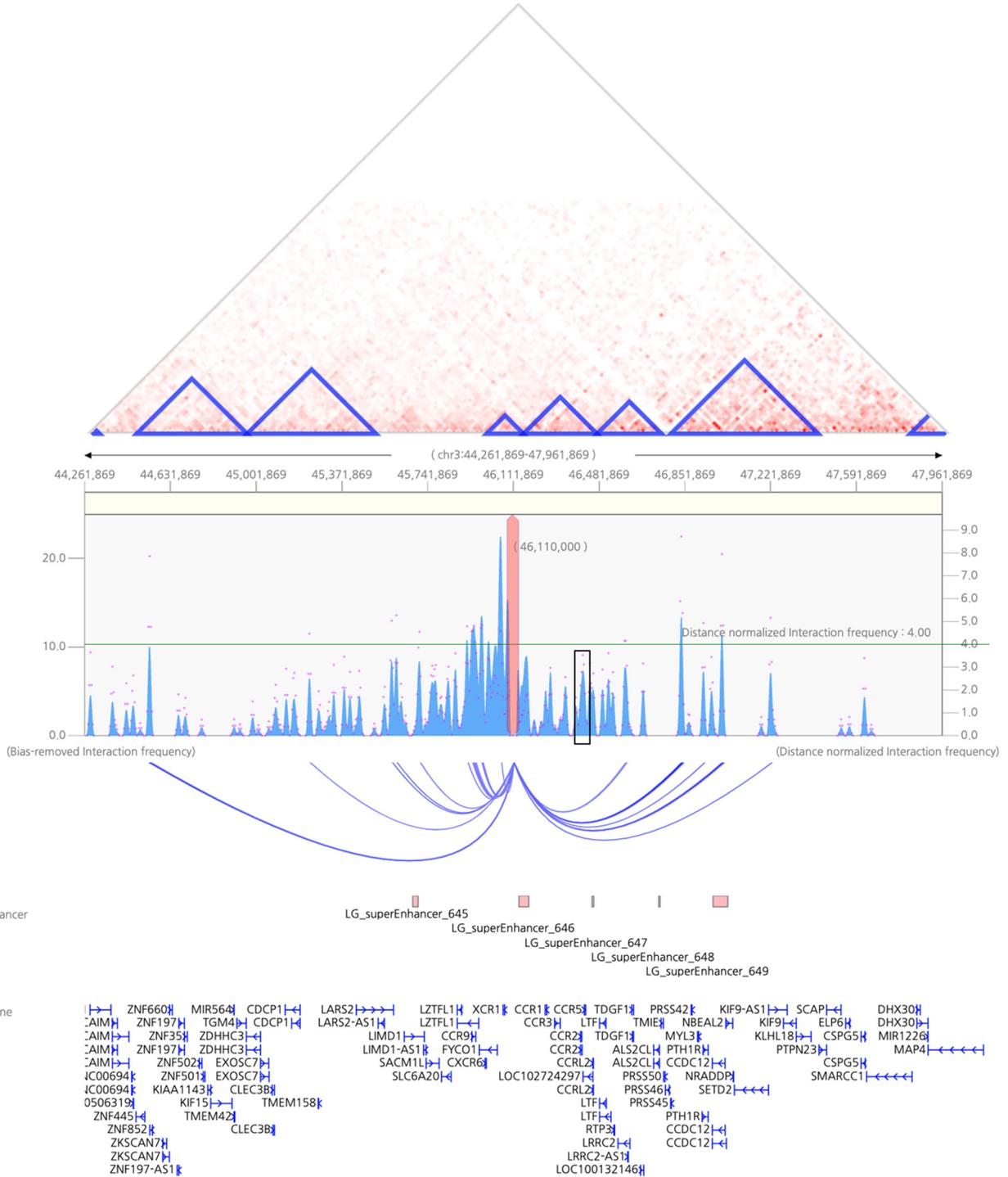


Figure S2. Minor allele frequencies of the selected SNPs in different populations. The graph shows the frequency of minor allele (expressed as percentage) of rs9845542, rs12639314 and rs35951367 in different populations. The minor allele C of rs35951367 is more frequent in European populations than in non-European ones. Frequency data was taken from gnomAD browser (<https://gnomad.broadinstitute.org/>).

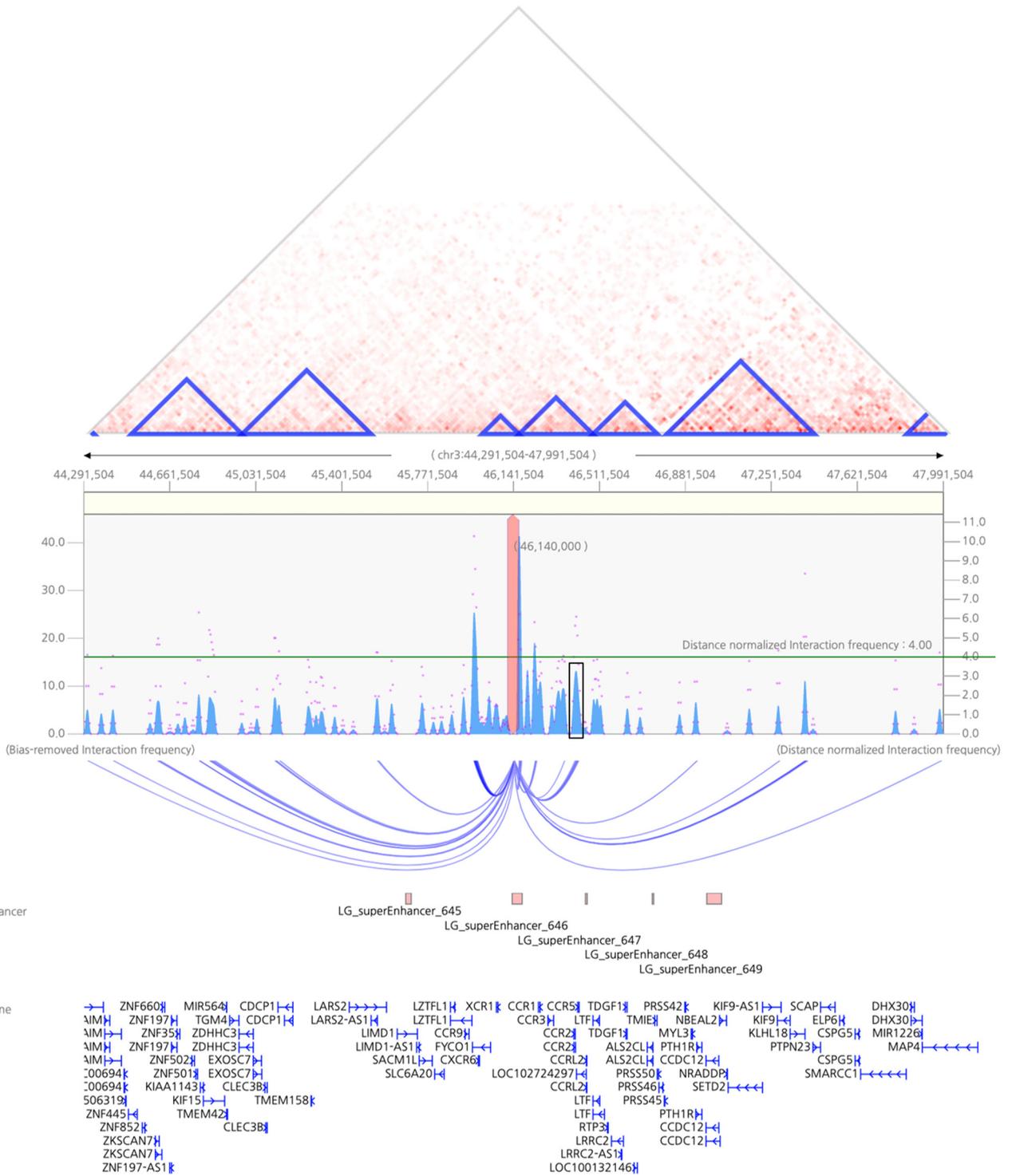
A

rs9845542



B

rs12639314



C

rs35951367

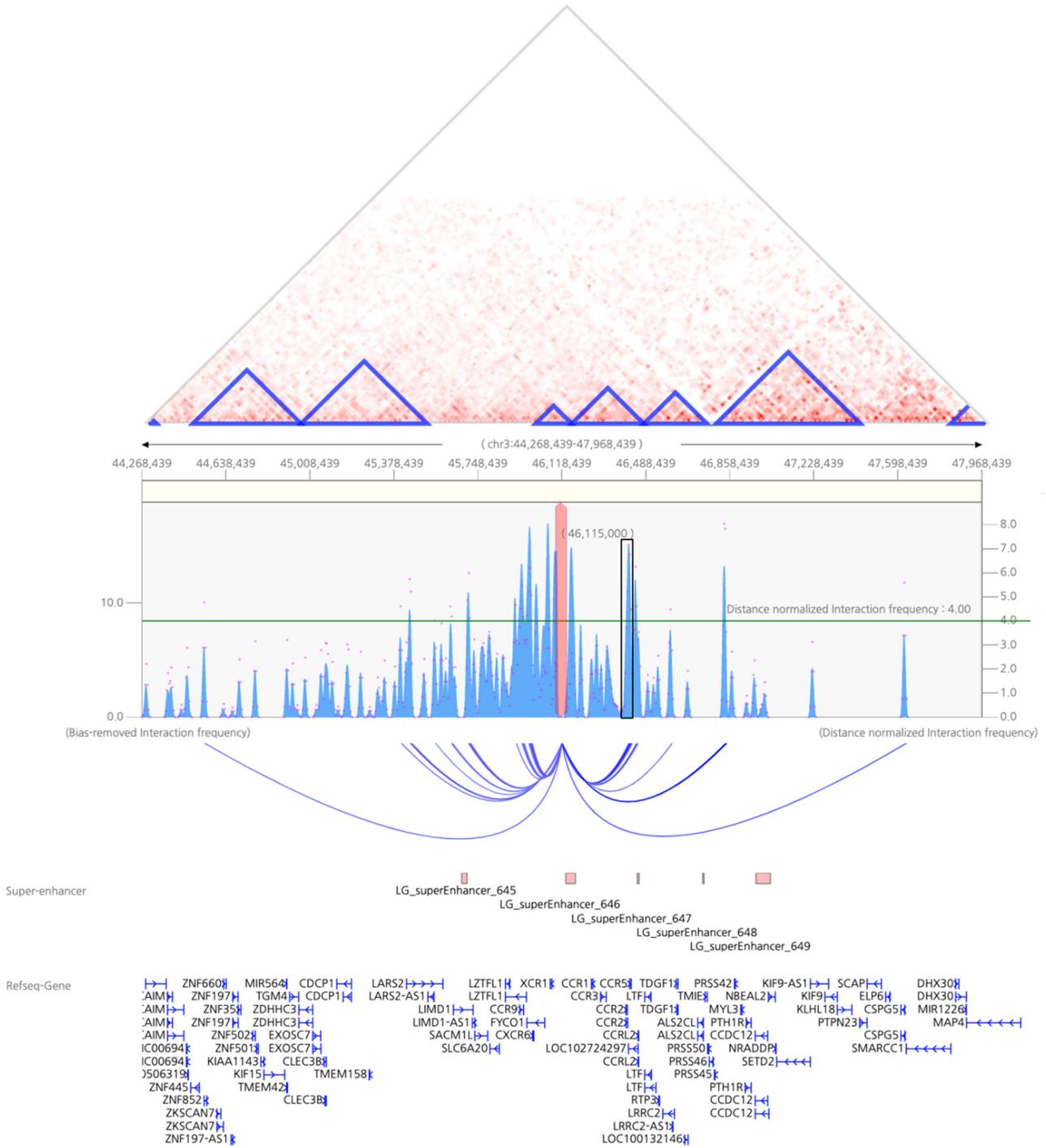


Figure S3. rs35951367 shows the highest level of interaction with *CCR5* in lung. Figures show the Hi-C data of 3 selected SNPs. Black boxes show the interaction value, expressed as Distance Normalized Interaction Frequency (DNFI), between the selected SNPs and *CCR5* in lung. The cut-off value is defined by the green line. Data were obtained from 3DIV (<http://kobic.kr/3div/>).

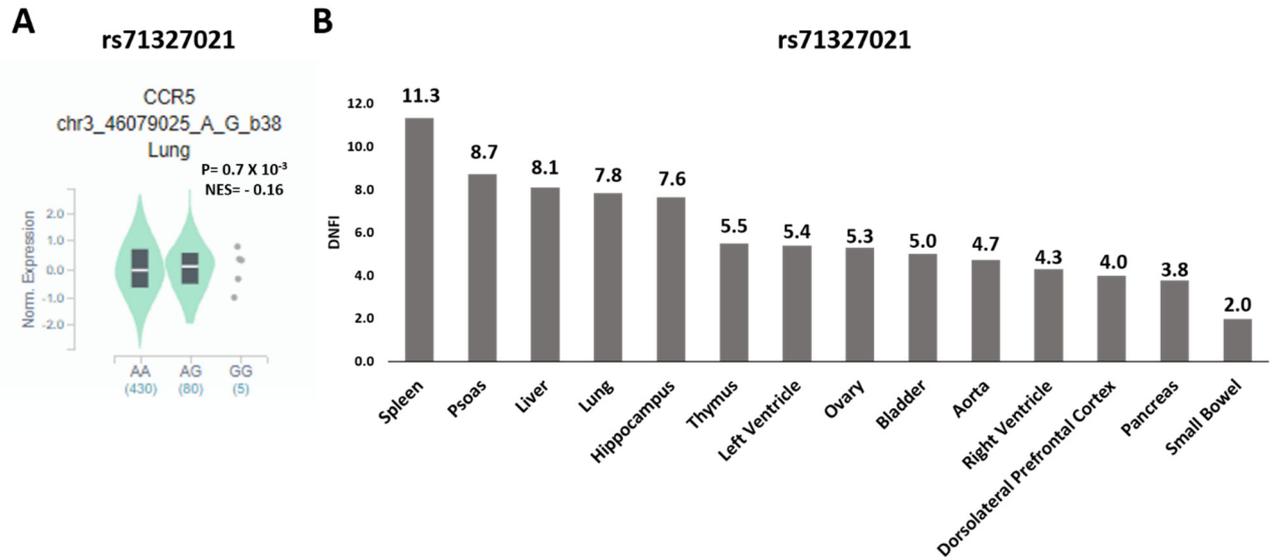


Figure S4. Minor allele of rs71327021 was associated with low expression of *CCR5* in lung but this last one is not tissue where interaction with *CCR5* is stronger. A) Violin plot shows the effect of eQTLs SNP rs71327021 on *CCR5* expression in lung. B) Hi-C data show interaction between rs71327021 and *CCR5* in all tissue. NES: normalized effect size.