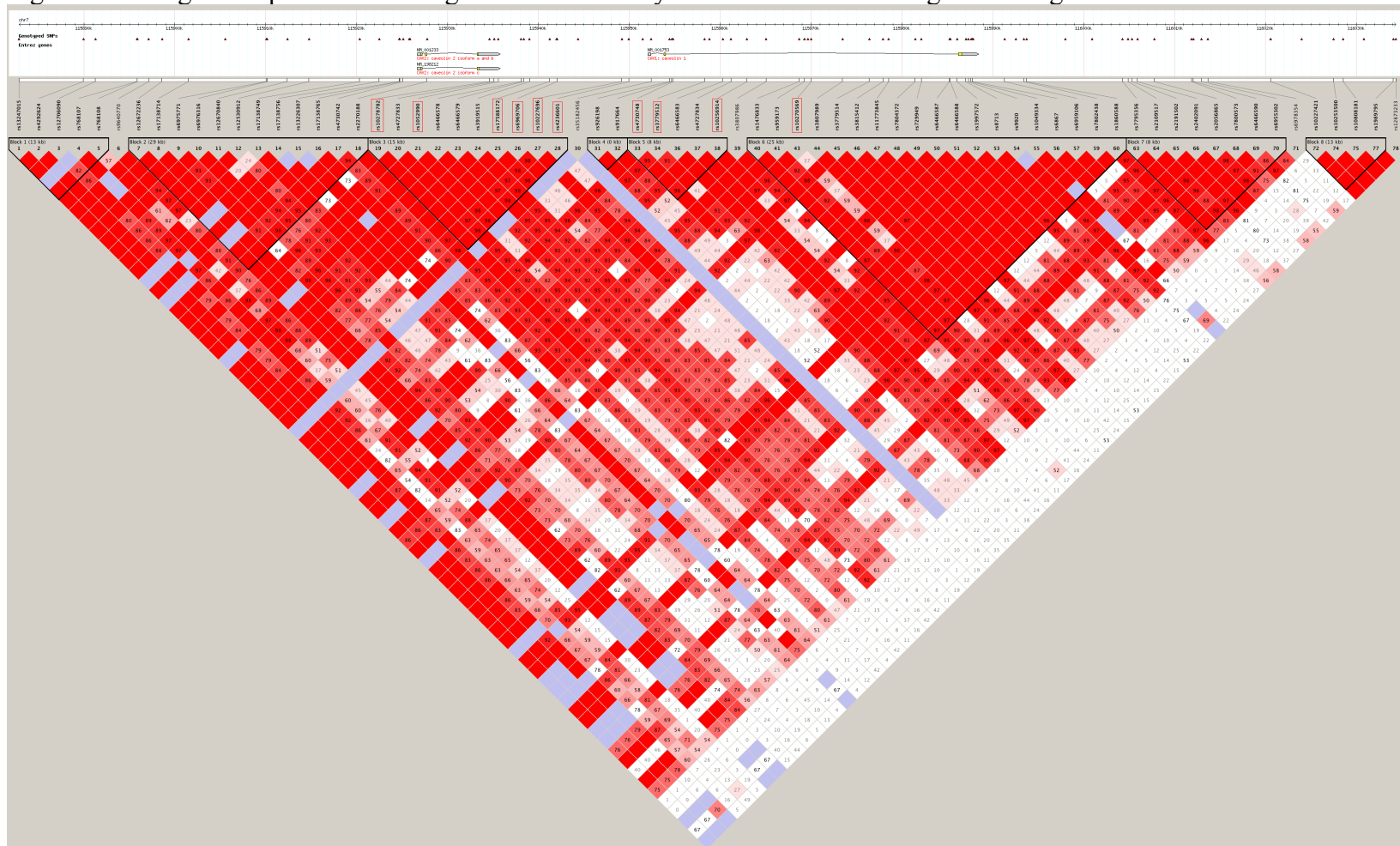


Figure 3: Linkage Disequilibrium among the 70 SNPs analyzed in the *CAVI/CAV2* genomic region.



Among the 70 SNPs in the *CAVI/CAV2* genomic region analyzed in this study, there are eight linkage disequilibrium (LD) blocks and five independent SNPs that did not fall into any LD blocks based on the Gabriel et al method as implemented in Haploview.