



**S1 Fig. Results of Bioinformatics Analysis of SNP rs4773144: Data from the ENCODE Project.**

A bioinformatics analysis with the use of the UCSC Genome Browser showed that SNP rs4773144, and 3 other SNPs (rs4773143, rs7986871 and rs3809346) in strong linkage disequilibrium ( $r^2 > 0.8$ ) with it, are located in a genomic region that has important transcriptional regulatory features including DNase I hypersensitivity and H3k27Ac marks, identified by the ENCODE project.