Supplementary table 1. Functional prediction results of selected loci in the database.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| SNP | LD | LD | Ref | Alt | Functional | Haploreg |
| (r2) | (D') | annotation |
| rs3093203 | 1 | 1 | G | A | 3'-UTR | Motifs changed,Selected eQTL hits |
| rs3093193 | 1 | 1 | C | G | intronic | Motifs changed,Selected eQTL hits |
| rs12459936 | 1 | 1 | C | T | intronic | Motifs changed,Selected eQTL hits |
| rs3093144 | 1 | 1 | C | T | intronic | Enhancer histone marks,Motifs changed,Selected eQTL hits |
| rs3093110 | 1 | 1 | A | G | intronic | Promoter histone marks,Motifs changed,Selected eQTL,GRASP QTL hits |

SNP: single-nucleotide polymorphism; LD, linkage disequilibrium; Ref, reference allele; Alt, altered allele; UTR, untranslated region; eQTL: expression quantitative trait loci;GRASP: Genome-Wide Repository of Association between SNPs and Phenotypes.