**Supplementary Table 1. Predicted stability, duplex formation, and functional effect of 3′-UTR polymorphisms in miRNA-binding sites of selected genes**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Gene** | **SNP ID** | **Allele** | **Predicted miRNA** | **△ (kcal/mol)** | **miRNA/SNP target duplexes** | **Effect** |
| TNFAIP2 | rs710100 | G | [hsa-miR-155](http://www.mirbase.org/cgi-bin/query.pl?terms=hsa-miR-155-5p) | -18.00 |

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| 3' | u | g | g | g | g | a | U | A | G | U | G | C | U | A | A | U | C | G | U | A | A | U | u | 5′ |
|  |  |  |  |  |  |  | | |  | | | | | | |  | : |  |  | | | | | | | **|** | | | | | | |  |  |
| 5' | g | c | t | g | t | g | A | G | C | A | C | C | G | C | C | A | G | C | [**A**](http://www.ncbi.nlm.nih.gov/projects/SNP/snp_ref.cgi?rs=rs710100) | T | T | A | g | 3′ |

 | Gain |
| A | -18.40 |

SNP: single nucleotide polymorphism. Predictions made with the [miRNASNP\_v2](file:///C%3A%5CUsers%5Cslinnell%5CAppData%5CLocal%5CTemp%5CmiRNASNP_v2) database: <http://bioinfo.life.hust.edu.cn/miRNASNP2/index.php>

Supplementary **Table 2. Primers sequence of PCR and UEP used in this study**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Gene** | **SNP** | **First Primer(5'-3')** | **Second Primer (5'-3')** | **UEP\_DIR** | **UEP SEQ (5'-3')** |
| PGF | rs8019391 | ACGTTGGATGAAACACTTACCCATGTGCCC | ACGTTGGATGCACAAGAATAATCAGGGTGC | R | CCTCAACAACCTTCCA |
| PGF | rs2268615 | ACGTTGGATGTCCTTTCCTCACCCCACATC | ACGTTGGATGGGGAAAGTGGCAGATTCCAG | F | caccTCCCACCATGCAGGTTC |
| TNFAIP2 | rs710100 | ACGTTGGATGATTGCAGGGCCAGCCTGTAG | ACGTTGGATGTTTTAGGGTCCTGTGGCGAG | F | ggCCTGGATGTGACGTCTAA |

SNP: single nucleotide polymorphism; UEP: unextended mini sequencing primer; DIR: direction; SEQ, sequence.

Supplementary **Table 3. The information and HWE about the candidate SNPs**

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Gene** | **SNP ID** | **Chr:Position** | **Role** | **Alleles****(A/B)** | **MAF** | ***p*-value for HWE** | **OR (95%CI)** | ***p*** | **Haploreg** |
| **Cases** | **Controls** |
| PGF | rs8019391 | 14:74942979 | intronic | T/C | 0.22 | 0.20 | 0.067 | 1.13 (0.89-1.44) | 0.318 | Promoter histone marks, Enhancer histone marks, DNAse, Motifs changed, Selected eQTL hits |
| PGF | rs2268615 | 14:74951714 | intronic | A/C | 0.30 | 0.26 | 0.814 | **1.27 (1.03-1.58)** | **0.029** | Promoter histone marks, Enhancer histone marks, DNAse, Motifs changed, Selected eQTL hits |
| TNFAIP2 | rs710100 | 14:103135941 | 3′UTR | A/G | 0.40 | 0.36 | 0.200 | **1.23 (1.01-1.50)** | **0.043** | Enhancer histone marks, DNAse, Motifs changed, Selected eQTL hits |

HWE, Hardy-Weinberg equilibrium; SNP, single nucleotide polymorphism; MAF, minor allele frequency; eQTL, expression quantitative trait loci.