

Supplementary Information

Figure 1. Linkage disequilibrium plot of HapMap SNPs in *STAT3* gene with 5' flanking 2 kb sequence. SNPs are displayed in reverse strand. Genotype data for SNPs in the region chr17:37718869..37795931 in Han Chinese in Beijing was downloaded from <http://www.hapmap.org> (Rel 27 Phase II + III, Feb09). SNPs with MAF ≥ 0.05 were analyzed to obtain the pairwise LD plot using the Tagger program in Haploview (version, 4.2). D' is indicated directly by both the brightness of red color and percentage. (a) TagSNP rs1053005 located in 3'-UTR captured the common SNPs in block 1; (b) TagSNP rs957970 located in an intron region captured the common SNPs in block 2; and (c) rs4796793 located in putative promoter region was in high linkage disequilibrium with rs957970 ($r^2 = 0.95$) and was predicted to generate a transcription factor binding site for FOXD1 by SNPInspector (version, 2.4).

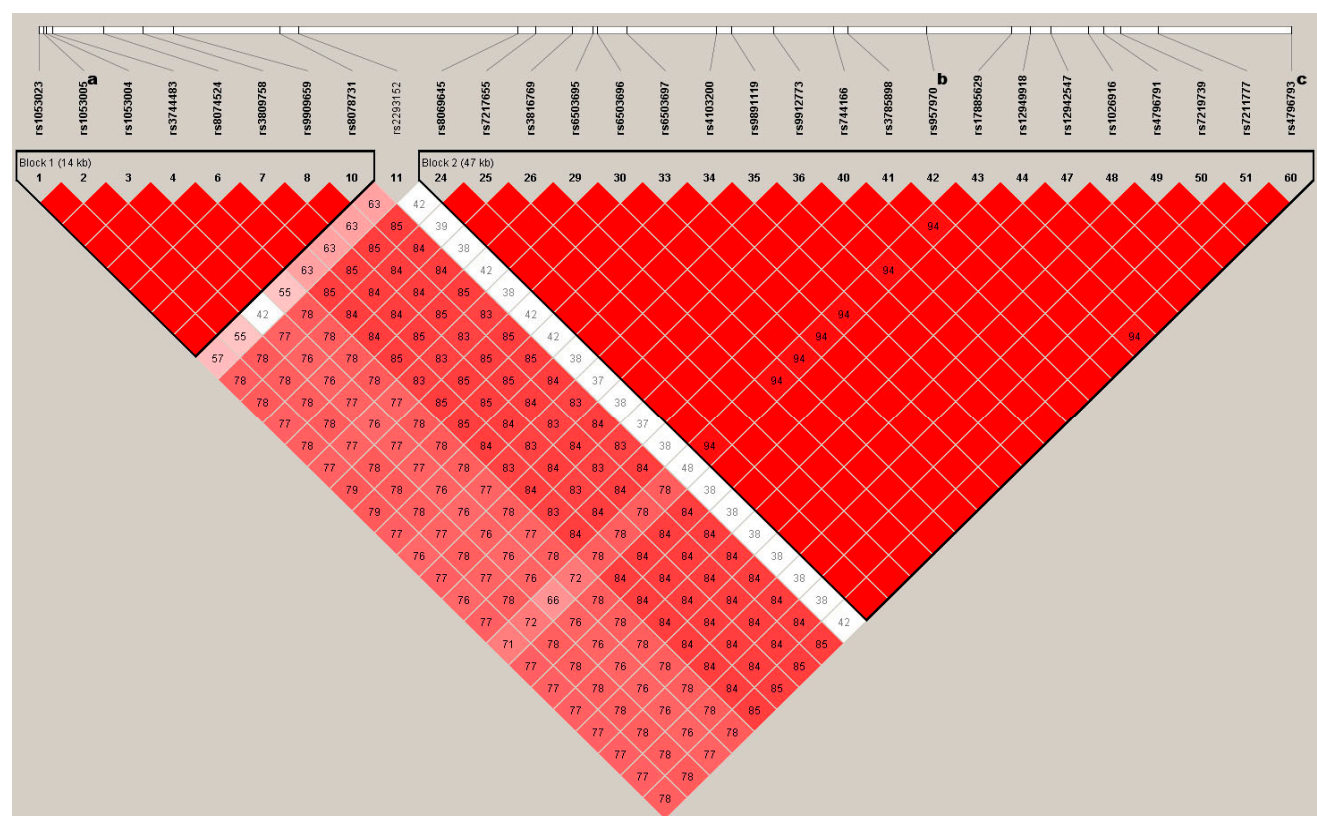


Figure 2. A>G variation of rs1053005 impairs the targeting of has-miR-1303 at STAT3 3' untranslated region. MicroRNA target prediction was performed using RNA22 program (version 1.0). STAT3 cDNA sequence is in accordance with ENST00000264657. * rs1053005 (A>G) is sited at the No. 4298 nucleotide of STAT3 cDNA. “:” represents uncomplementary base pairing.

