

Associated variant in *NCF2*: rs10911363

rs3845466

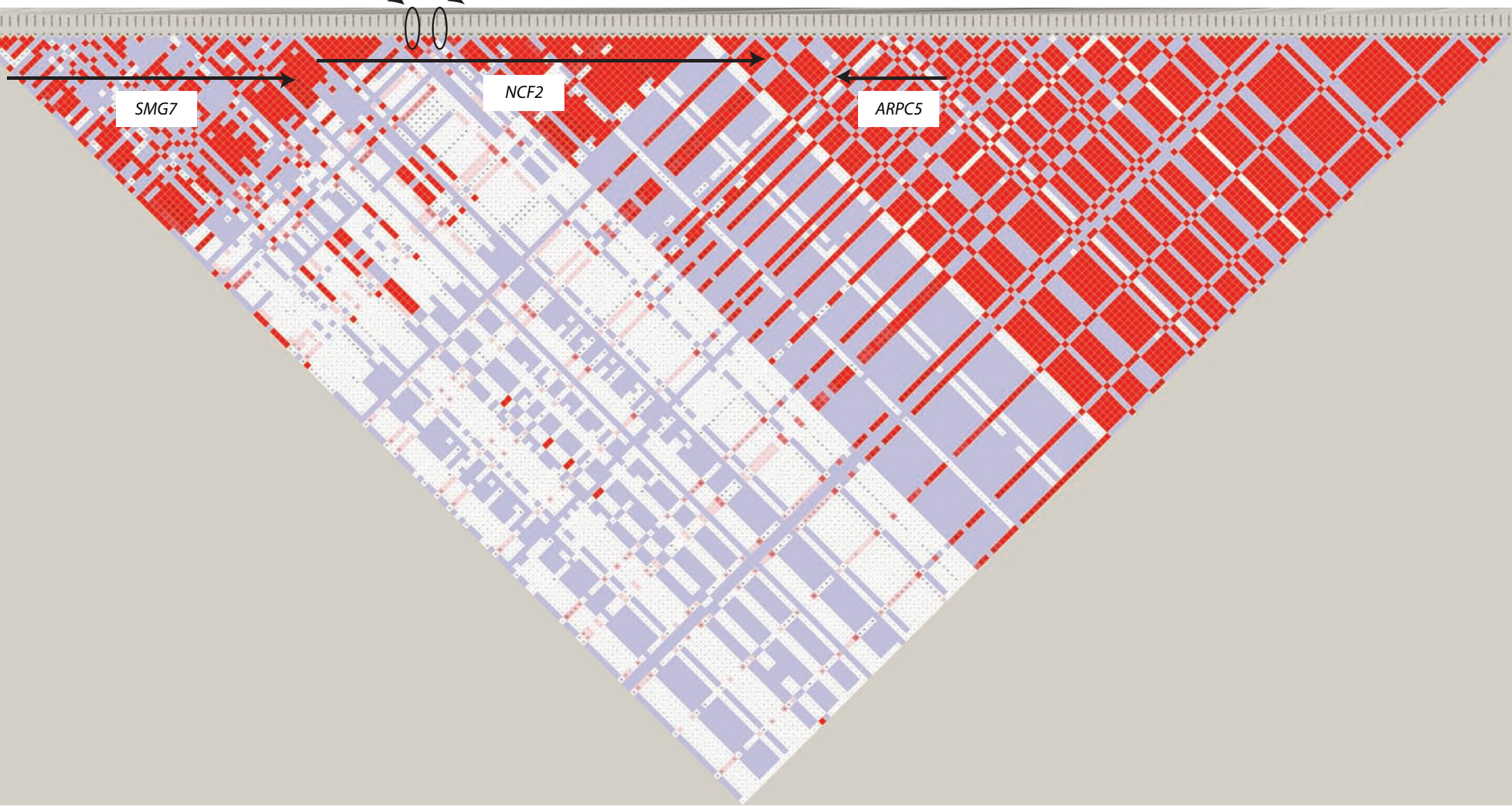
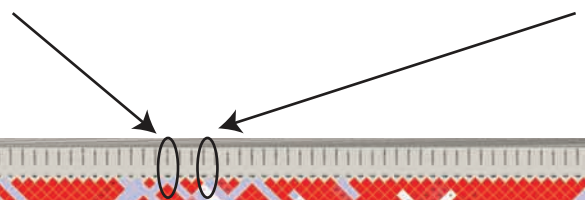


Figure S2A: LD pattern in 200 kb region around rs10911363

(Chr 1: 181,716,380-181,916,379- HAPMAP Data Rel 27 phase II+III Feb09, NCBI assembly dbSNP 126)

Published variant: rs921916

GW significant variant: rs2366293

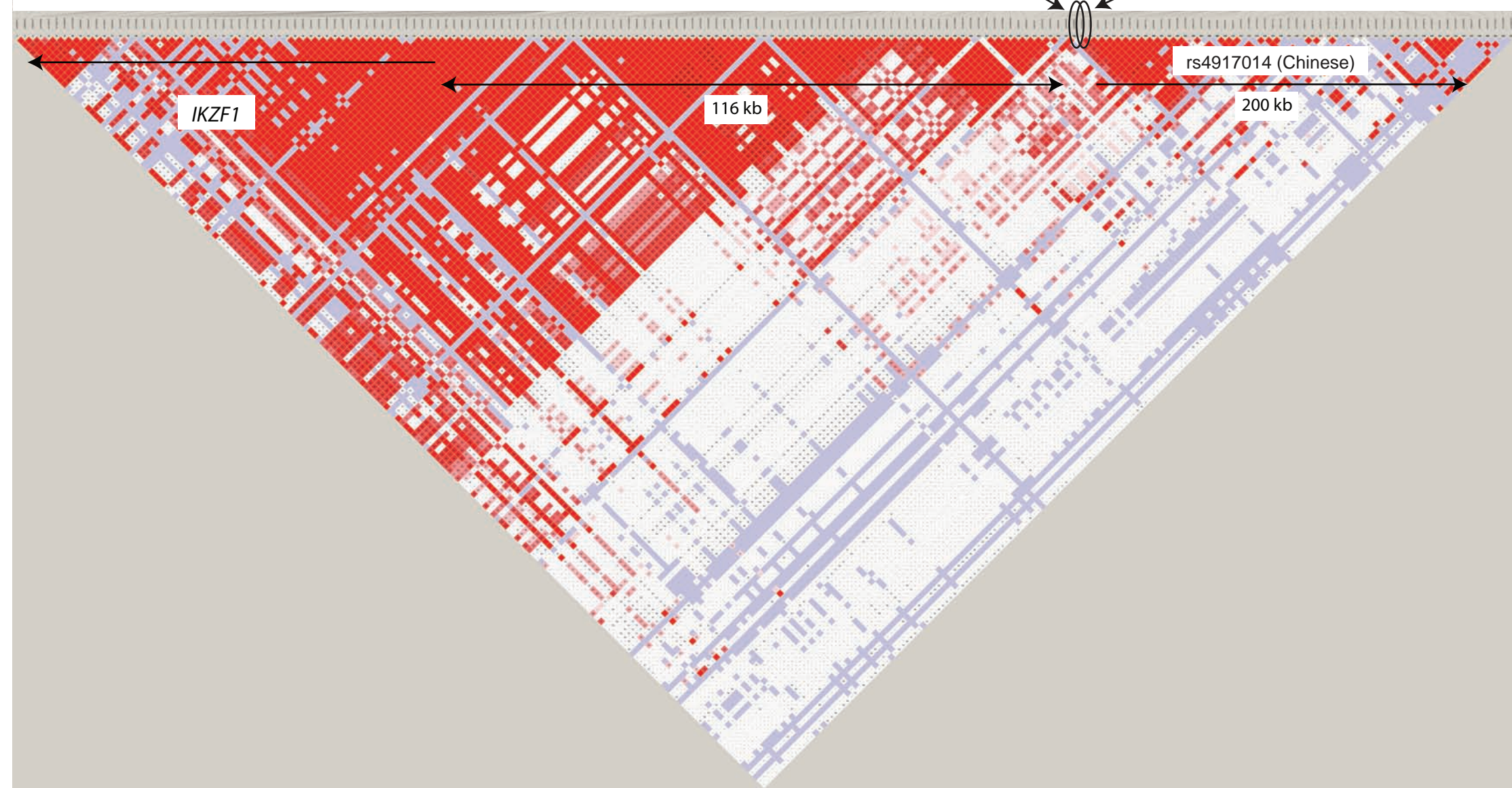


Figure S2B: LD pattern in 155.8 kb region around rs2366293

(Chr 7: 50,120,474-50,276,274 - HAPMAP Data Rel 27 phase II+III Feb09, NCBI assembly dbSNP 126)



Figure S2C: LD pattern in 100 kb region around the gap between *IRF8* and rs2280381

(Chr 16: 84500150-845600149 - HAPMAP Data Rel 27 phase II+III Feb09, NCBI assembly dbSNP 126)

Associated variant in *IFIH1*: rs1990760

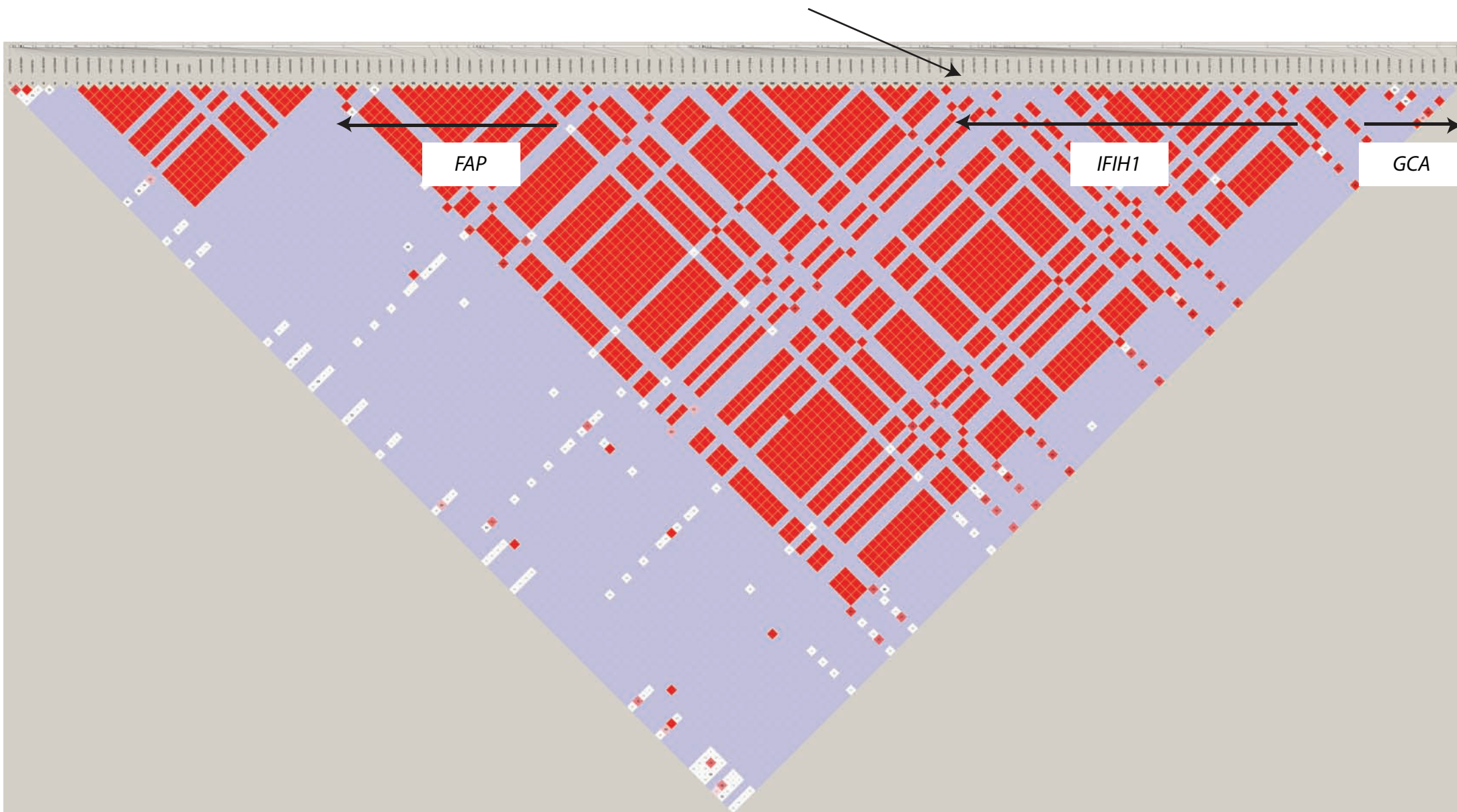


Figure S2D: LD pattern in 250kb region around rs1990760

(Chr 2: 162,700,000-162,949,999 - HAPMAP Data Rel 27 phase II+III Feb09, NCBI assembly dbSNP 126)

Associated variant in *TYK2*: rs280519

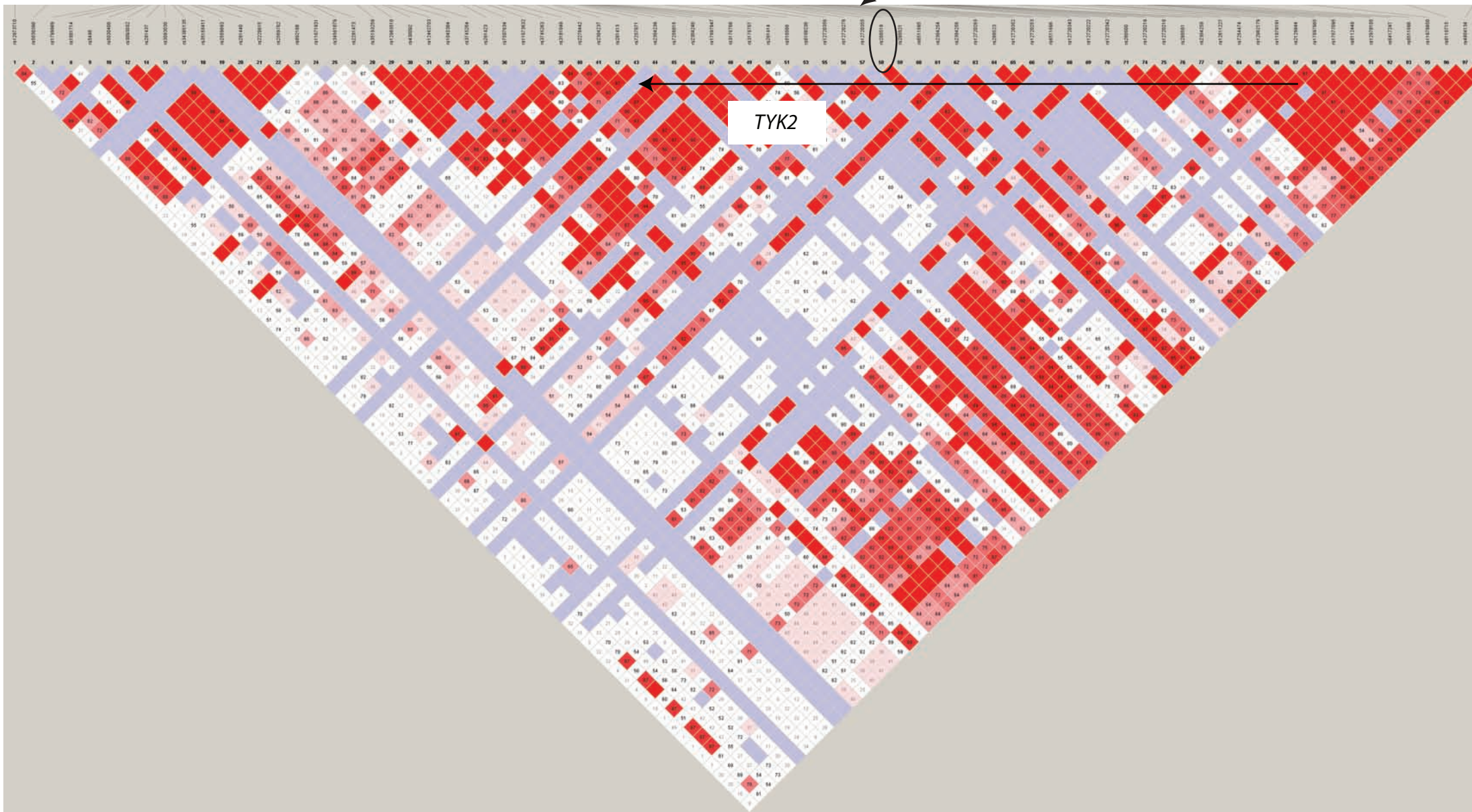


Figure S2E: LD pattern in 200 kb region around rs280519

(Chr 19: 10,233,933-10433933 - HAPMAP Data Rel 27 phase II+III Feb09, NCBI assembly dbSNP 126)