**Figure S3: Heat map of linkage disequilibrium between *STAT6* variants interrogated in this study**



Linkage disequilibrium (LD), reported as r2, was determined for variants interrogated in this study using the *r2fast* function of R package *GenABEL*25 (above the diagonal). For comparison, LD for the same variants was determined using *rAggr*26 (http://raggr.usc.edu/) within the all European cohort (CEU+FIN+GBR+IBS+TSI) of the1000 Genomes27 and HapMap28 databases (below the diagonal).