Description of Additional Supplementary Files

File Name: Supplementary Data 1
Description: We selected 87 loci of interest from GWAS hits with genome-wide significance (P value < 5 x 10^{-8}) from five studies. We identified all common variants in LD with these SNPs from 1000 Genomes Phase 3 (European population), filtering for minor allele frequency [MAF] >1%, LD R^2>0.8, and location within 1 Mb of the tagging SNP. This approach yielded 2180 candidate SNPs.

File Name: Supplementary Data 2
Description: The SNP-seq library contained 4363 dsDNA constructs.

File Name: Supplementary Data 3
Description: The list of 248 candidate functional SNPs was derived from the analysis of SNP-seq sequencing data.

File Name: Supplementary Data 4
Description: The list of 91 candidate functional SNPs was selected by calculating the H3K4me3 chromatin score from five chromatin ChIP-seq studies in human B cells.

File Name: Supplementary Data 5
Description: 2180 SNPs were ranked using the Combined Annotation-Dependent Depletion (CADD) score.

File Name: Supplementary Data 6
Description: Electrophoretic mobility shift assay (EMSA) blots for 52 candidate SNPs**.** Biotinylated 31 bp DNA probes centered on each allele of the 52 SNPs were incubated with nuclear extracts from either BL2 B cells or PBMCs for the EMSA. Non-biotinylated DNA fragment served as competitor.

File Name: Supplementary Data 7
Description: Five SNPs (rs2297550, rs13213604, rs276461, rs9907966, rs7302634) were evaluated by mass spectrometry to identify binding nuclear proteins, resulting in a set of candidate proteins for each allele of the SNP.

File Name: Supplementary Data 8
Description: Bioinformatic analysis predicted that transcription factors are likely to recognize each of the five high-probability variants using published ChIP-seq data.

File Name: Supplementary Data 9
Description: The sequences of primers and oligos used for SNP-seq, EMSA, and pulldown assays are listed.