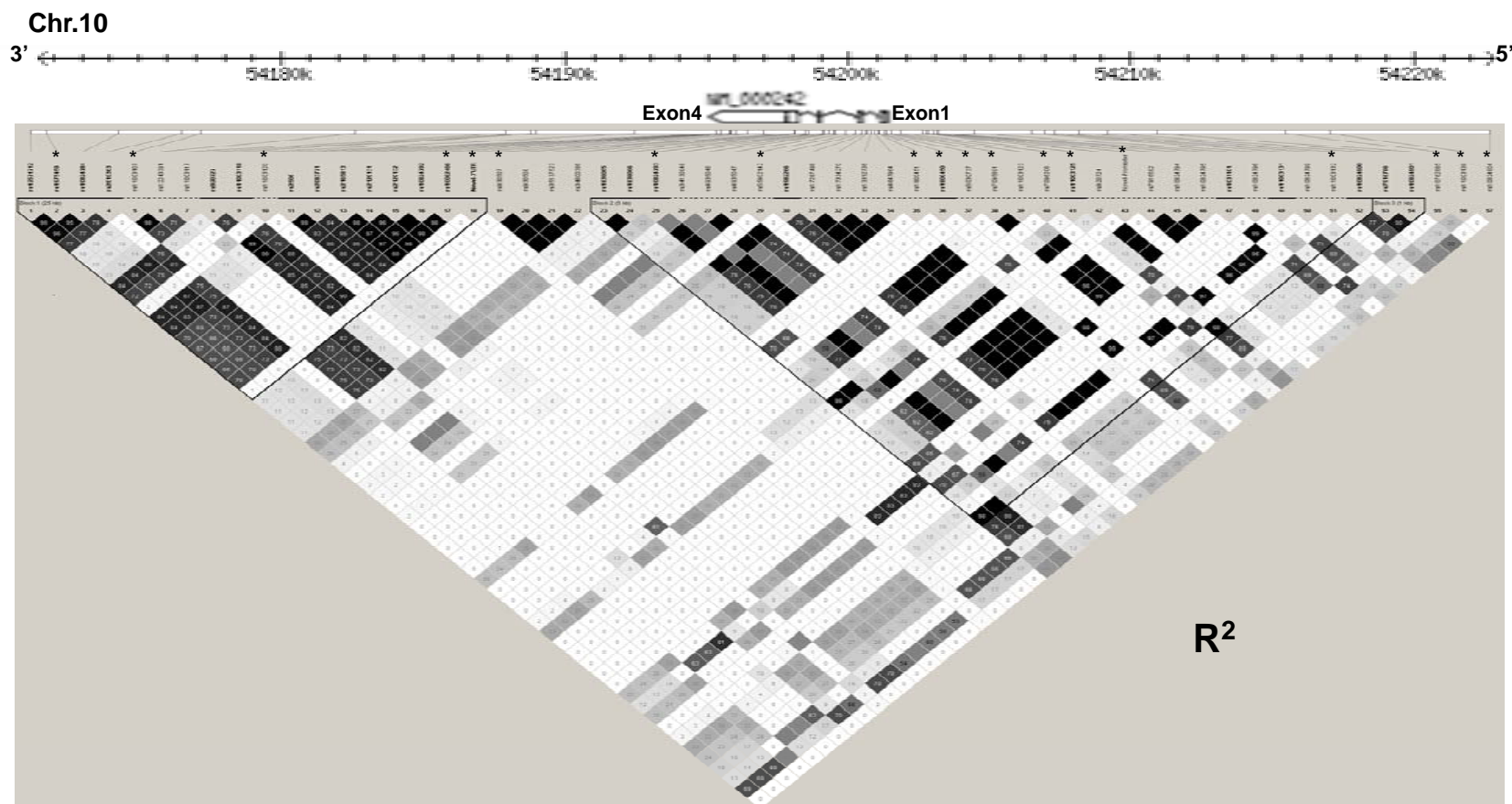


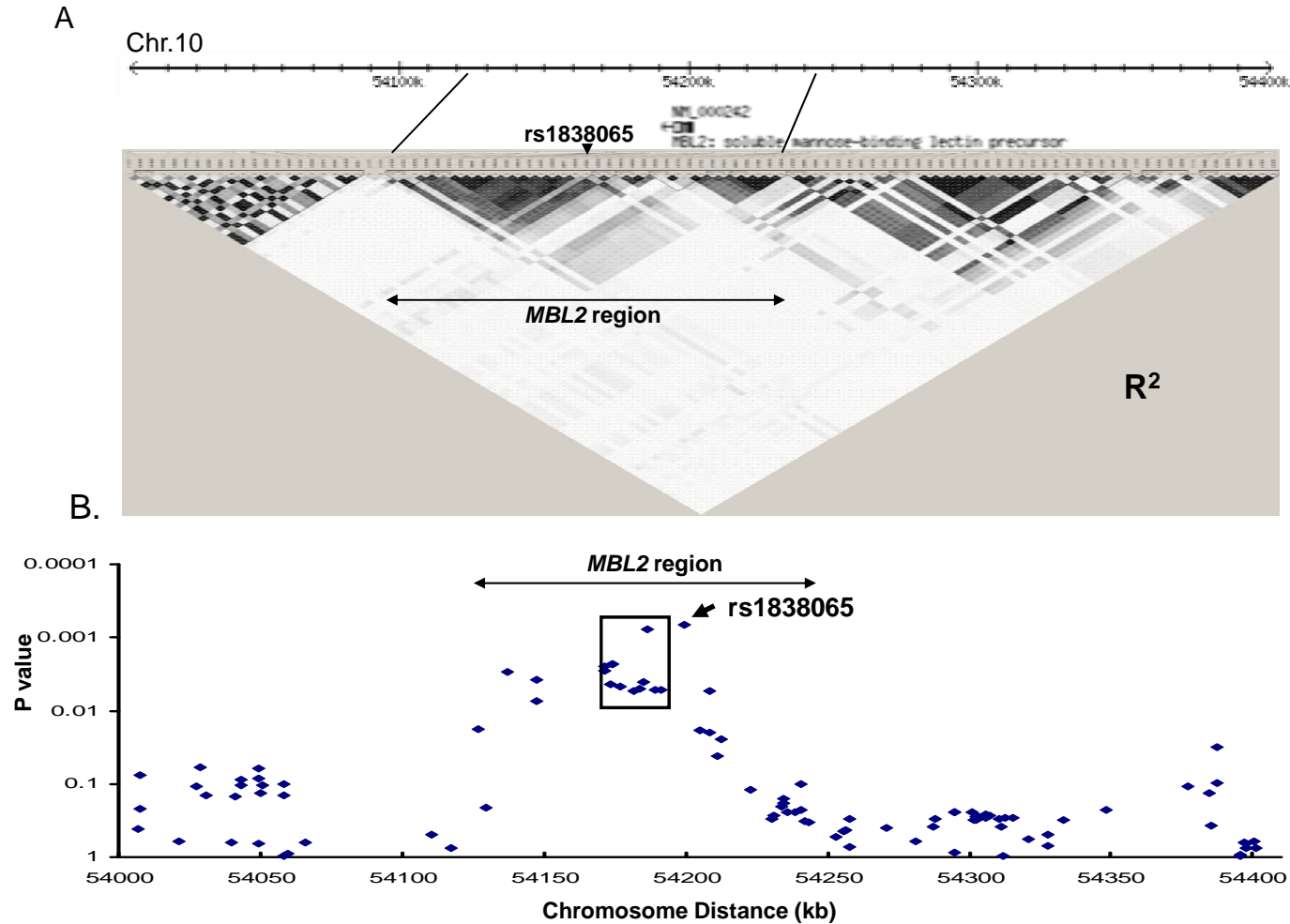
ONLINE APPENDIX

Supplemental Figure 1. Pair-wise linkage disequilibrium of 57 SNPs in and near *MBL2* in Pima Indians.



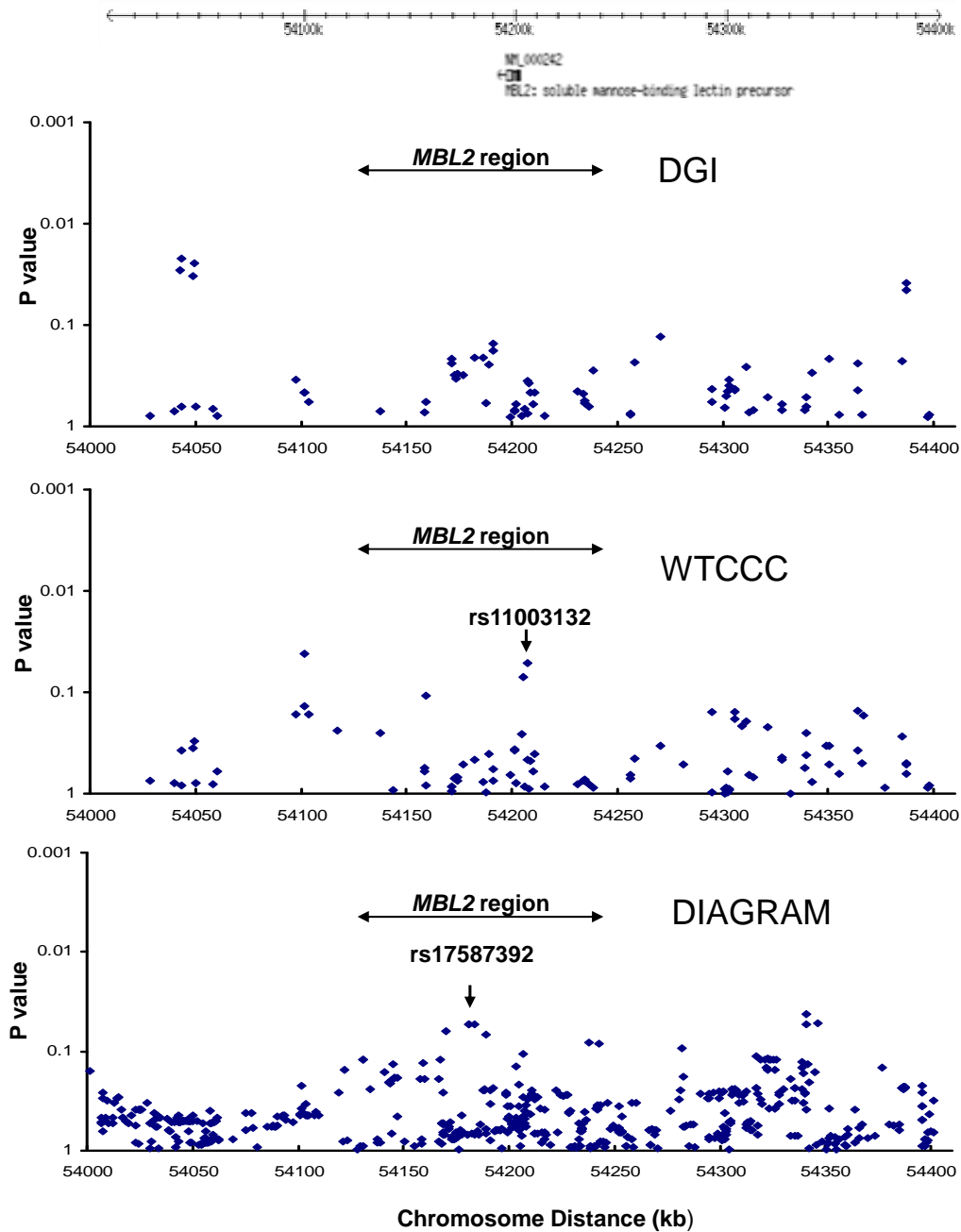
37 SNPs were identified by sequencing *MBL2* in Pima Indians (all exons, introns and 2 kb promoter) and 20 additional database SNPs that flank *MBL2* (~25kb flanking each side of the gene) were selected from the Chinese HapMap (SNPs tagged these regions in the Chinese where $R^2 \geq 0.8$, minor allele frequency ≥ 0.1). Genotyping all these variants in Pima Indians identified 19 tag SNPs ($R^2 \geq 0.8$) indicated by *. Significant SNP rs1800450 captured rs11003131 and rs1031101; whereas significant SNP rs11003125 captured rs1838065, rs1838066, rs10824801, rs10824800 and rs7916786.

Supplemental Figure 2. Pair-wise linkage disequilibrium of 101 SNP across the expanded region encompassing *MBL2* (A) and associations of these SNPs with early-onset type 2 diabetes (B) in Pima Indians.



A 1 M SNP GWAS for early-onset type 2 diabetes has previously been done in Pima Indians. Subjects with diabetes (N=300) had an age of onset <25 years and subjects without diabetes (N=334) had an age \geq 45 years. 101 SNPs cover a genomic region spanning ~400kb (chr.10: 54007027-54401287). The arrow indicates *MBL2* region which is in a high LD block (spanning ~116.5 kb). Additive P values were adjusted for sex, birth-year and family membership.

Supplemental Figure 3. Associations of SNPs across the expanded region encompassing *MBL2* with type 2 diabetes in DGI, WTCCC and DIAGRAM.



DGI and WTCCC data were obtained from public databases. DIAGRAM meta-analysis was derived from DGI, WTCCC and FUSION. SNPs (82 for DGI, 96 for WTCCC and 573 for DIAGRAM) cover the genomic region spanning ~400kb (chr.10: 54001161-54401432). The arrow indicates *MBL2* region which is in a high LD block (spanning ~116.5 kb).