Figure S9. Linkage disequilibrium patterns in the 1000 Genomes EUR reference panel for the GWAS-implicated region spanning from PAX5 to FRMPDI on chromosome 9. The patterns, according to (A) D’ and (B) r² values, are shown for the 15 GWAS-implicated SNPs tested for replication on chromosome 9. Darker shading from pink to red indicates higher D’ values, and darker shading from grey to black indicates higher r² values. Purple coloring indicates high D’ values but lower levels of statistical significance.