Description of Additional Supplementary Files

File Name: Supplementary Data 1
Description: For each of the associated signals identified in either GERA or UKB, we computed each variant's ability to explain the observed signal within a 2 Mb window (±1.0 Mb with respect to the original lead SNP) and derived the smallest set of variants that included the causal variant with 95% probability (95% credible set). The 24 credible sets include a total of 1,098 variants in 28 annotated genes. Abbreviations: CHR, chromosome, SNP, single nucleotide polymorphism; BP, base pair; A_min, minor allele; A_maj, major allele.