**Supplementary Methods and Materials**

**SNP selection criteria, imputation and bioinformatic analyses**

SNPs were selected based upon: a MAF >0.05 in Europeans from the 1,000 Genomes Project, functional annotation (missense, frameshift, insertion/deletion, 5’ or 3’ UTR, 5’ or 3’ splice site, introducing a stop codon), expression quantitative trait loci (eQTL) in lymphoblastoid cell lines (SCAN database) (1), and already published variant-phenotype associations in the literature. Redundancy was minimized by excluding variants if they were in high LD (r2 ≥0.80) with other identified variants.

Using the directly genotyped SNPs, additional variants were imputed within a 5 Mb window of a gene center, and variants located within 25 kb of the gene transcription start and stop sites were retained for final analyses. Sample phasing and imputation were carried out using Impute2 version 2.30 (2, 3). Phased reference haplotypes, based on the 1000 Genomes Project, were used. Only variants with information scores >0.90 and expected MAF >0.02 were retained.

Data from ENCODE and the Roadmap Epigenomics Consortium were queried using a variety of bioinformatic resources to inform predictions regarding variant function, and to help prioritize variants for functional validation. Bioinformatic tools queried included: Regulome DB (4), HaploReg (5), Ensembl (6), and the UCSC genome browser (7). Variants in high LD (r2 ≥0.80 in Europeans from the 1000 Genomes Project) with the variant associated with OS were also analyzed (Table S2).

**References**

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