**eTable 1:** Extended details for the genes in Table 1 as well as several more genes that have proposed implication in ALS. In each row, the first column lists the gene abbreviation followed by the gene description, broad biological process type, and gene function. The next columns include details on the method discovery type, year and first author of representative publication, the reference(s) number in the bibliography, whether the gene’s association with ALS has been independently validated, and the gene’s relevance to disease. Listed among the final columns are brief descriptions of each gene’s pathogenic variant characteristics, a list of world ethnic populations in which associated pathogenic variants have been identified, and a list of other diseases of which the gene is also associated. GWAS = genome wide association study, WES = whole exome sequencing, eQTL = expressive quantitative trait locus, LoF = loss of function, SNP = single nucleotide polymorphism.

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