Supporting Information

McLysaght et al. 10.1073/pnas.1309324111

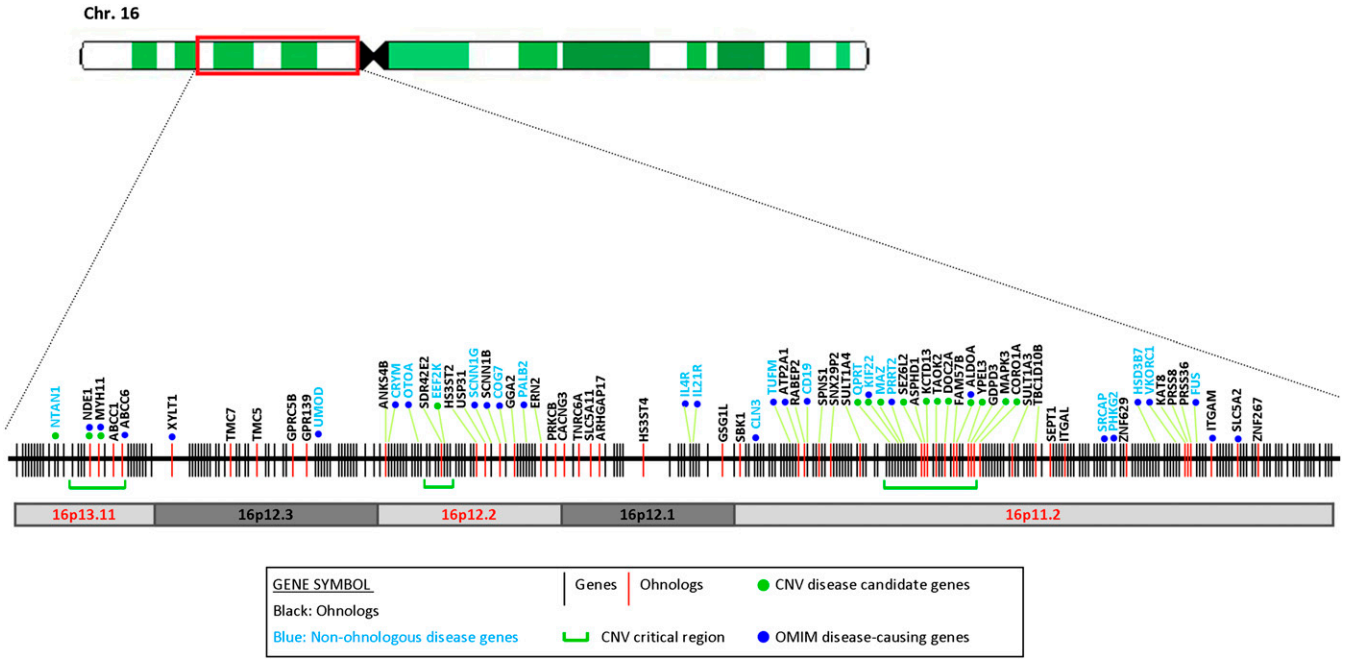

Fig. S1. Ohnologs and disease candidate genes in the highly unstable genomic region on chromosome 16p (NCBI37/hg19). The three genomic hotspots in the region (16p13.11, 16p12.2, and 16p11.2) are labeled in red. A green solid bar indicates the critical regions of the pathogenic copy number variants (CNVs) identified at each locus. Red and black vertical lines represent ohnologs and other genes respectively. Green dots mark reported disease candidate genes for the pathogenic CNVs, whereas blue dots mark the disease-causing genes from the Online Mendelian Inheritance in Man (OMIM) database. Gene symbols labeled in black and blue indicate ohnologs and nonohnologous disease candidate genes, respectively.

Other Supporting Information Files

Table S1 (DOC)
Table S2 (DOC)
Table S3 (DOC)
Table S4 (DOC)
Table S5 (DOC)
Table S6 (DOC)
Table S7 (DOC)