Description of Additional Supplementary Files

Supplementary Data 1

Curated developmental disorder genes and annotations from DDD study (DDG2P database) considered as known genes for cognitive phenotype (probable and confirmed with cognitive phenotype annotation). A gene can appear multiple times with different annotation by DDD study. Columns 13-6 are de novo meta-analysis results from MCRae et al, Nature 2017).

Supplementary Data 2

Patients for which likely pathogenic variant was identified in exome sequencing.

Supplementary Data 3

Detailed clinical information for each patient.

Supplementary Data 4

Identified likely pathogenic deletions and other deletions deleting high pLI gene.

Supplementary Data 5

Nominally significant dominant variants enriched in Finland.

Supplementary Data 6

Nominally significant recessive variants enriched in Finland.