**ONLINE SUPPLEMENTARY RESOURCES**

**File name: Online Supplementary Resource 1**

Methods : A detailed description of library preparation, high-throughput sequencing, data analysis, variant interpretation, variant classification, multi-gene panel design and sample preparation has been provided in this section. In addition, more details have been provided for copy number variation analysis for large deletion/duplication and confirmation by second method in this study.

**Figure S1:** This supplementary file illustrates the age distribution of the 1012 patients referred for neurological disorders.

**File name:** **Online Supplementary Resource 2**

**Description of data:** This supplementary file contains 8 supplementary tables (Table S1–S8). Description of all the supplementary tables is provided below

**Table S1:** This table lists all ‘pathogenic’/‘likely pathogenic’ single-nucleotide and indel variants identified in the study along with the NGS (next-generation sequencing) quality parameters.

**Table S2:** This table lists all ‘pathogenic’/‘likely pathogenic’ structural variants identified in the study along with the NGS (next-generation sequencing) quality parameters.

**Table S3:** This table contains the list of all ‘pathogenic’/‘likely pathogenic’ single-nucleotide and indel variants detected in this study cohort.

**Table S4:** This table contains the list of all ‘pathogenic’/‘likely pathogenic’ structural variants identified in this study cohort.

**Table S5**: This table lists all ‘variant of uncertain significance with probable damaging effect’ (VUSD) variants identified in this study cohort.

**Table S6:** This table lists all ‘variant of uncertain significance’ (VUS) variants identified in this study cohort.

**Table S7:** This table lists ‘pathogenic’/‘likely pathogenic’ variants identified in the ACMG (American College of Medical Genetics and Genomics) recommended genes as secondary or incidental findings.

**Table S8:** This table contains the list of those cases that were referred with multiple phenotypes, wherein a confirmed diagnosis was arrived at with multi-gene panel testing.