**Supplementary data**

Whole-Exome-Sequencing:

Whole-Exome-Sequencing (WES) was performed on the genomic DNA samples extracted from blood with GenElute Blood Genomic DNA Kit (Sigma-Aldrich). Sequencing libraries were prepared using the SureSelect Human All Exon Kit V7 reagents (Agilent) following the manufactured protocol and sequenced using the Illumina NextSeq500 system (Illumina). Exome reads were aligned using BWA for sequence alignment to the GRCh37 reference, Broad Institute GATK for variant calling, ANNOVAR for variant annotation and ExomeDepth for CNV detection. In addition to this standard bioinformatics pipeline, the resulting variants’ approved gene symbol were then annotated matching related phenotypes known in OMIM, by using the “genemap2.txt” data-frame kindly provided by OMIM website. Only variants with the following criteria were further considered: exonic and splicing (passing filter) variants, non-synonymous and with a minor-allele frequency of less than 1% in ExAC. Moreover a segregation analysis was performed selecting: 1) homozygous variants present only in the proband or present in heterozygous condition in the healthy sister; 2) heterozygous variants present in the proband and absent in the healthy sister. After that, we prioritized variants related to patient phenotype, and a filter for a ‘’spasticity symptoms” gene panel was applied. This panel consists of 400 genes implicated in various forms of HSP, ataxias and spastic-ataxias syndromes, neuropathies, mitochondrial disorders, dystonias, leukodystrophies and other movement disorders (list of genes available upon requests). Prediction of pathogenicity was made by using different software publicly available, such as DANN, DEOGEN2, EIGEN, FATHMM-MKL, M-CAP, MVP, MutationAssessor, MutationTaster, PrimateAI, REVEL Poliphen2 and SIFT. Variant in *MSTO1* (freq. 0,04% in ExAC) has contradictory prediction of pathogenicity. Beside *TACO1* and *MSTO1*, no additional variants with pathogenic prediction were found. The selected variants were tested in the proband’ relatives (figure 1B) by Sanger sequencing by using an ABI 3500Dx automated sequencer.