**Variant filtration methodology:**

**1.)** **Likely pathogenic and pathogenic variants in the ClinVar** database were screened. We found three known pathogenic variants, which associate with a neurological phenotype, however all of them is associated with a recessive inheritance and none of them is compatible with the phenotype of the cases (*TPP1* variant, neuronal lipofuscinosis; *GCDH* variant, glutaric aciduria type I., *PRODH* variant, hyperpolinemia). As the **TPP1** variant is a stop gain mutation (NM\_000391.4:c.622C>T; **p.Arg208Ter**), we segregated this in the family.

**2.)** We filtered for the known **NBIA genes** *PANK2*, *PLA2G6*, *C19orf12*, *WDR45*, *FA2H*, *ATP13A2*, *FTL*, *CP*, *DCAF17*, *COASY*. Here, we applied a 5% MAF cutoff in the GnomAD, EXaC, 1000G European databases, but no other filtration was done. Intronic variants were also included. We found no other damaging variant, compatible with the pedigree only the already known heterozygous *C19Orf12* nonsense variant, and *CP* frameshift deletion.

**3.)** We filtered for a **second variant in the intronic region of the 10 NBIA genes**, which is inherited from the mother, but not present in the father. The purpose was to filter for a potential compound heterozygous variant, which was missed during the above filtrations. We found total 245 intronic variants with MAF<5%. There were 38 variants, which was compatible with an inheritance from the mother, or a de novo status. All variant had a CADD score below 15, and there was no predicted splice site, miRNA, or small RNA binding site. There was one predicted transcription factor site (*DCAF17* gene ENST00000375255.3:c.1183-484G>T V$POU6F1\_01), however with a low GWaVa score (0.29), and minimal conservation score. Specifically, there was no predicted splice site, miRNA, small RNA, transcription factor binding site in the *CP* or *C19Orf12* gene. All variants identified in this two genes had minor conservation, low GWAVA and CADD scores.

**4.)** We performed a moderately stringent filtration in an **autosomal dominant model** on the trio with the Genesis application. Filter criteria were as follows: ExAC: < 0.001; Genesis Allele count HET/HOM <6/6; GnomAD <0.001; Inheritance: AD; Quality: DP>8, GQ>50, QUAL >35, Variant class: Lof (transcript ablation, splice acceptor, splice donor, stop gain, frameshift, stop lost, start lost); transcript amplification, inframe INDEL, missense, splice region, inclopete terminal codon, stop retained.

This filtration resulted in total 243 variants in 218 genes. From these, 38 genes were previously linked to a Mendelian disorder. Only the above mentioned *C19Orf12* and *CP* variants emerged, which are compatible with an NBIA phenotype. Other rare, damaging variants were identified in further eight genes, however none of them is compatible with the phenotype [*ERLIN2* - spastic paraplegia 18 (AR); *ATXN2* -spinocerebellar ataxia 2 (AD trinucleotide repeat disease); *DNMT1* - autosomal dominant cerebellar ataxia, deafness, and narcolepsy; *LOR* - Vohwinkel syndrome with ichthyosis (AD); *PTPRQ* - deafness 73 (AD), deafness 84A (AR); *SEC23B* -Cowden syndrome 7 (AD), Dyserythropoietic anemia, congenital, type II (AR); *SLC3A1* - cystinuria (AD, AR); *UNC45B* - cataract 43 (AD)].

**5.)** We filtered for rare, possibly damaging **de novo variants** in the index case. (ExAc < 0.001; Genesis allele count <6; GnomAd < 0.001; Inheritance pattern: de novo; DP >8; GQ > 50; QUAL > 35; Loss of function/missense/transcript amplification/ inframe indel/splice region/incomplete terminal codon/stop retained). Total 99 variant was identified compatible with a possible de novo inheritence. The high number of potential de novo variants is the result of the filtration method (filtration was not performed on genomic VCFs), but this way we do not look over a potential true positive de novo variant. From these, variants in 10 genes were found to associate with a Mendelian disorder. None of the genes were compatible with a disorder similar to the NBIA phenotype [*LOR* - Vohwinkel syndrome (AD), *ANTXR2* - Hyaline fibromatosis syndrome (AR), *LARP7-* Alazami syndrome (AR), *C2CD3* - orofaciodigital syndrome XIV (AR), *ALG8* - congenital disorder of glycosylation type Ih (AR), *MMAB* - methylmalonic aciduria (AR), *EDC3* - mental retardation 50 (AR), *MPO* - myeloperoxydase deficiency (AR), *DNMT1* - autosomal dominant cerebellar ataxia, deafness and narcolepsy (AD), *HLCS* - holocarboxylase synthetase deficiency (AR)].

**6.)** We called **CNVs** from the WGS data, and looked also at BAM files for possible structural variants in the ten NBIA gene. We used the WGS method of CNVkit. With the obtained coverage a possible binsize was 1500bp (i.e that means that larger than 1500basepair INDELs can be theoretically detected). NBIA genes were not affected by any detected CNV. Specifically, we did not detect a CNV in the C19Orf12 or CP genes. The exonic duplication in the *PLA2G6* gene, detected by the MLPA, was probably not seen with the WES because this size of CNV was not large enough for the given mean coverage.

**7**.) The artificial intelligence software **Moon diploid** (<http://www.diploid.com/moon>), and the **TGEx** (http://tgex.genecards.org/) was also used as a control for our filtering strategy with the following symptoms: generalized dystonia, neurodegeneration, iron accumulation in brain, Parkinsonism. No further relevant variant was identified by this way.