**Supplemental Tables**

**Supplemental Table 1:** *In silico* analysis of variants in patients with inherited metabolic disorders and other genetic causes of pediatric movement disorders.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Gene** | **Variantsreference** | **SIFT** | **MutTaster** | **Conservation in species** | **gmAD allele count in allele number** |
| *SLC2A1* | c.624\_625delinsGT (p.Glu209Valfs\*21) | NA | NA | NA | None |
| *SURF1* | c.324-11T>G11 | NA | NA | NA | None |
| *PDHA1* | c.910C>T (p.Arg304X) 12 | NA | NA | 13/13 | None |
| *DNAJC19* | c.280+1\_280+5delGTAAG10 | NA | NA | 13/13 | 1 in 245938 |
| *DLD* | c.(1123G>A (p.Glu375Lys)14 | Deleterious | NA | 13/13 | 25 in 276968 |
| *TPP1* | c.500\_503dupTGGA (p.Phe169GlyfsX20) | NA | NA | 8/11 | None |
| c.1058C>A (p.Thr353Asn) | Tolerated | Disease causing | 8/11 | 9 in 276962 |
| c.509-1G>C | NA | NA | NA | 113 in 277058 |
| c.139C>G (p.Leu47Val) | Tolerated | Disease causing | 8/9 | None |
| *HMGCS2* | c.862C>T (p.Arg288X) | NA | NA | 7/12 | 2 in 276850 |
| *SLC52A2* | c.917G>A (p.Gly306Glu) | Deleterious | Disease causing | 10/11 | None |
| *SCN2A* | c.658A>G (p.Arg220Gly)9 | Deleterious | Disease causing | 12/12 | None |
| *SLC9A6* | c.584+5G>A9 | NA | NA | NA | None |
| *STXBP1* | partial deletion of exon 3-49 | NA | NA | NA | None |
| c.1614\_1616delCAT (p.Ile539del)9 | NA | NA | 12/13 | None |
| c.364C>T (p.Arg122X)9 | NA | NA | NA | None |
| c.1249+1G>A15 | NA | NA | NA | None |
| *CACNA1A* | c.4177G>A (p.Val1393Met) | Deleterious | Disease causing | 9/11 | None |
| *ATM* | c.590G>A (p.Gly197Glu) | Tolerated | Disease causing | 7/11 | None |
| *KCNA2* | c.890G>A (p.Arg297Gln)16 | Deleterious | Disease causing | 12/12 | None |
| *CAMTA1* | c.882\_883insCG (p.Gly295ArgfsX96) | NA | NA | NA | None |
| *ATP1A3* | c.2840G>A (p.Gly947Glu) | Deleterious | Disease causing | 9/10 | None |
| *SLC16A2* | c.605G>A (p.Gly202Glu) | Tolerated | Disease causing | 9/11 | None |
| *BCAP31* | c.533\_536dup (p.Ser180Alafs\*6)10 | NA | NA  | NA | None |
| *CTNNB1* | c.1043\_1044delCT (p.Ser348CysfsX4) | NA | NA | NA | None |
| *SLC13A5* | c.716+5G>A | NA | NA | NA | 1 in 244376 |

**Abbreviations (listed alphabetically):** gnomAD= Genome Aggregation Database (gnomAD); MutTaster= Mutation Taster; SIFT= Sorting Intolerant From Tolerant