

Table S5. RNA and protein expression data obtained from the Human Protein Atlas for genes and respective proteins identified in this study.

Genes	RNA levels				Protein levels	
	Brain enriched	Cortex	Cerebellum	Spinal cord	Cortical neuronal cells	Cerebellar Purkinje cells
<i>KIF1A</i>	Yes	109.0	18.5	20.2	-	-
<i>POLG</i>	No	6.0	4.5	5.8	Low	High
<i>SETX</i>	No	6.8	9.8	8.1	Medium	Medium
<i>PNKP</i>	No	16.4	11.0	10.5	High	Medium
<i>ANO10</i>	No	21.0	23.8	20.0	High	Medium
<i>CACNA1A</i>	Yes	25.7	91.8	6.7	High	ND
<i>SACS</i>	No	17.2	8.8	4.1	Medium	Medium
<i>SPG11</i>	No	21.4	23.3	18.8	Medium	Low
<i>KIF1C</i>	Yes	211.6	203.0	225.5	Low	Medium
<i>SYNE1</i>	Yes	72.3	150.2	40.6	High	High
<i>HEXB</i>	No	32.8	23.3	25.3	ND	ND
<i>ATP1A3</i>	Yes	634.7	84.4	10	ND	ND
<i>FA2H</i>	Yes	61.7	67.1	75.5	ND	ND

Data was obtained from the The Human Protein Atlas [1]. The RNA values are expressed as the normalized transcripts per Kb million (nTPM) expression levels from the consensus dataset (combines the HPA and GTEx transcriptomics datasets using the internal normalization pipeline). Protein levels are qualitative, achieved by evaluation of antibody staining, RNA-seq data, and annotated protein expression data. ND, not detected.

Reference

1. Uhlen, M.; Fagerberg, L.; Hallstrom, B.M.; Lindskog, C.; Oksvold, P.; Mardinoglu, A.; Sivertsson, A.; Kampf, C.; Sjostedt, E.; Asplund, A.; et al. Proteomics. Tissue-based map of the human proteome. *Science* **2015**, *347*, 1260419, doi:10.1126/science.1260419.