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Supplemental Data

Mutations in *TBCK*, Encoding TBC1-Domain-Containing Kinase, Lead to a Recognizable Syndrome of Intellectual Disability and Hypotonia

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	Individual 1-1*	**Individual 1-2***	**Individual 2-1**	**Individual 3-1**	**Individual 4-1**	**Individual 4-2**	**Individual 5-1**	**Individual 6-1**	**Individual 6-2**	**Individual 7-1**	**Individual 8-1**	**Individual 9-1**	**Individual 9-2**
Variants (NM_001163435.2)	Hom c.1897+1G>A	Hom c.1897+1G>A	Hom c.831_832insTA;p.Pro278Tyrfs*18	Hom c.1652T>C;p.Leu551Pro	Het [c.2060-2A>G];[c.803_806delTGAA;p.Met268fsArg*26]	Het [c.2060-2A>G];[c.803_806delTGAA;p.Met268fsArg*26]	Hom c.376C>T; p.Arg126*	Hom c.1370delA;p.Asn457Thrfs*15	Hom c.1370delA;p.Asn457Thrfs*15	Hom c.455+4 C>G	Hom c.376C>T; p.Arg126*	Het [c.(658+1_659-1)_(2059+1_2060-1)del];[c.376C>T; p.Arg126*]	Het [c.(658+1_659-1)_(2059+1_2060-1)del];[c.376C>T; p.Arg126*] *
Mutation Type	Splice Site/Frameshift	Splice Site/Frameshift	Insertion / Frameshift	Missense	Splice Site/Frameshift and Frameshift	Splice Site/Frameshift and Frameshift	Nonsense	Frameshift	Frameshift	Splice	Nonsense	Nonsense	Nonsense
ExAC Frequencies (Variant 1//Variant 2)	**Same Locus:** c.1897+1G>T 1/120206 = 0.000008319	**Same Locus:** c.1897+1G>T 1/120206 = 0.000008319	0	0	**Same Variant:** 2/120744 = 0.00001656 0 homozygotes European Non-Finnish and 0	**Same Variant:** 2/120744 =0.00001656 0 homozygotes European Non-Finnish and 0	**Same Variant:** 3/21032 = 0.00014260 homozygotes 2 Latino, 1 African	**Same Locus:** p.Asn457LysfsTer10: 11/100172=0.0001098 0 homozygotes	**Same Locus:** p.Asn457LysfsTer10: 11/100172=0.0001098 0 homozygotes	0	**Same Variant:** 3/21032= 0.00014260 homozygotes 2 Latino, 1 African	**Same Variant:** 3/21032= 0.00014260 homozygotes 2 Latino, 1 African	**Same Variant:** 3/21032= 0.00014260 homozygotes 2 Latino, 1 African
Total reads/ Total Sequence	82748773	**N/A**	106302548	129453070	117181868	143465174	**120488546**	289855072	N/A	55300000	202000000	N/A	Not available

Total aligned reads	71472572	**N/A**	105467940	128219154	116723990	142952449	**120006591**	Not available	N/A	54968200	19897000	N/A	Not available
Mean Coverage	134X	**N/A**	91X	133X	125X	143X	132X	98% at >30x	N/A	85X	202X	N/A	56X

Table S1 – Variants with ExAC database frequencies, both for the exact variant and, where noted, other variants of the same type at the same locus demonstrating allele frequencies consistent with an autosomal recessive disease, and sequencing metrics of the individuals identified by whole exome sequencing (Hom: Homozygous, Het: Heterozygous) *These patients previously reported by Alazami et al, 2015