

# Reassessment of Rare *TUBA4A* Variants in Patients with Myopathy and Neurodevelopmental Features

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## INTRODUCTION & METHODS

*TUBA4A* variants are recognized in ClinGen and gene panels for adult-onset amyotrophic lateral sclerosis (ALS) & thrombocytopenia. However, recent publications have reported variants present in children with wider phenotypes. Review of internal genome and exome sequencing (WGS/WES) data for patients with unsolved phenotypes overlapping with myopathy or neurodevelopmental features uncovered 4 rare (AF<0.0001) *de novo* variants in *TUBA4A* for deeper review and reconsideration of pathogenicity. We present the evidence supporting these variant associations with pediatric myopathy and discuss the *in silico* data supporting future investigations of their putative pathogenic mechanisms.

### Review & Reclassification of Cases

Querying all rare (AF<0.0001) *TUBA4A* variant carriers with phenotypes overlapping with myopathy or neurodevelopmental disorder (NDD)

Filtering out variants known to be benign and/or highly present in "normal" populations

Identifying existing publications and/or publicly available submissions of variant-disease relationship

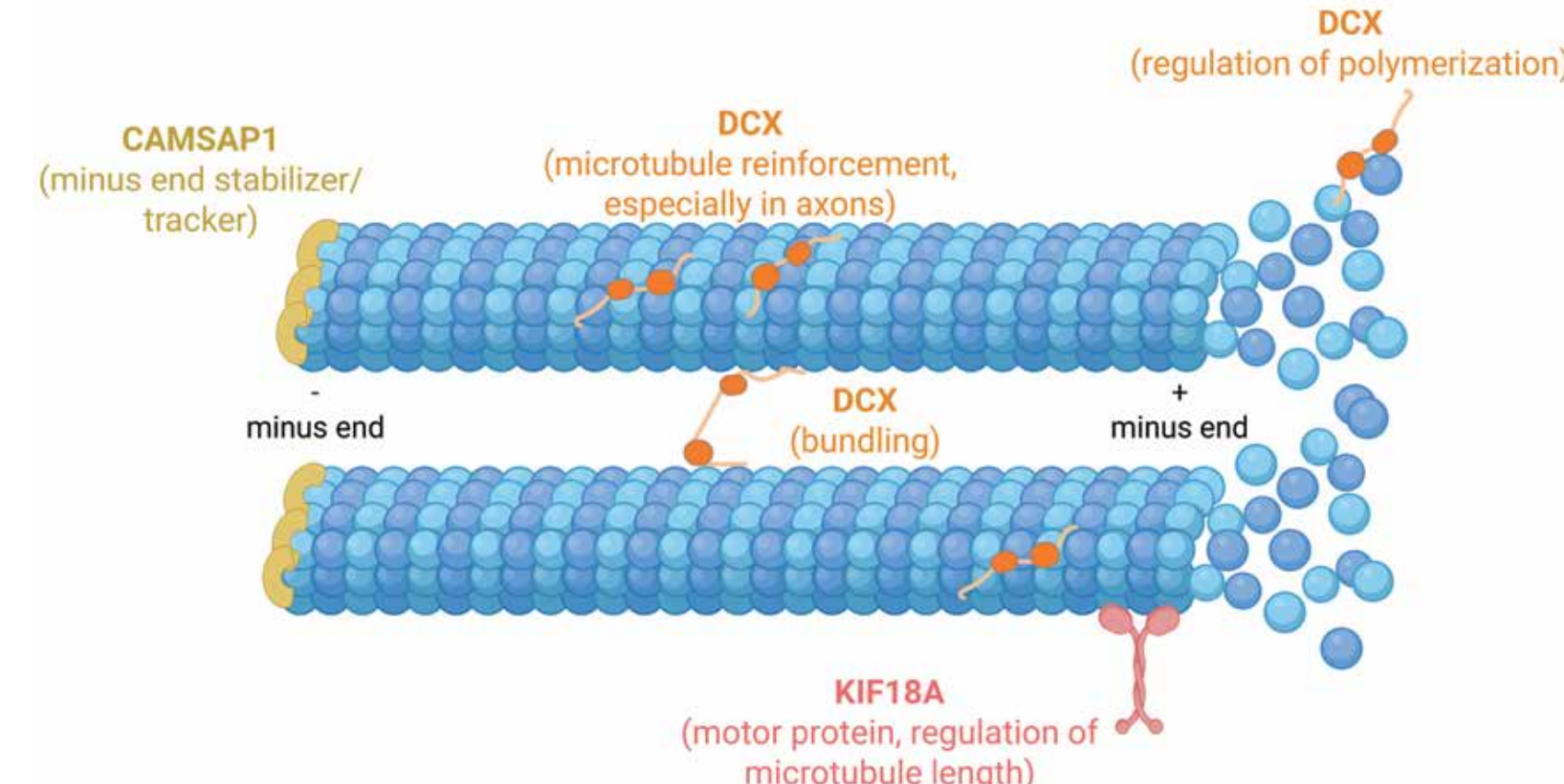
Generating computational and/or predictive evidence of:

- Conservation of the molecular alterations/residue
- Predicted  $\Delta$  in splicing (SpliceAI, Pangolin)
- Predicted missense impact (AlphaMissense, REVEL, SIFT, PolyPhen)
- Predicted  $\Delta$  in post-translational modifications (DeepMVP)
- Predicted  $\Delta$  in tertiary/quaternary protein structure (AlphaFold3)

Proposing reclassification for top variants based on ACMG/AMP guidelines

Population	not in healthy pop (PP → PM2)	--
Segregation	co-segregation with disease in multiple affected family members (PP1+)	--
De novo	--	unconfirmed (PM6) confirmed (PS2)
Functional	↓ benign missense % (PP1) hotspot/domain (PM1) functional studies (PS3)	--
Computational	multiple predictions (PP3) residue known as P (PM5) exact $\Delta$ known as P (PS1)	--
Other	supporting to moderate evidence	--

Figure 1. *TUBA4A* is a key tubulin whose molecular interactions and post-translational modifications regulate microtubule (MT) dynamics



*TUBA4A* interaction partners prioritized based on report in the Tubulin Database; Figure created with BioRender

Figure 2. Expression of *TUBA4A* and *CAMPSAP1* is enriched in skeletal muscle compared to other  $\alpha$ -tubulin and MT associated protein (MAP) genes (Human Protein Atlas)

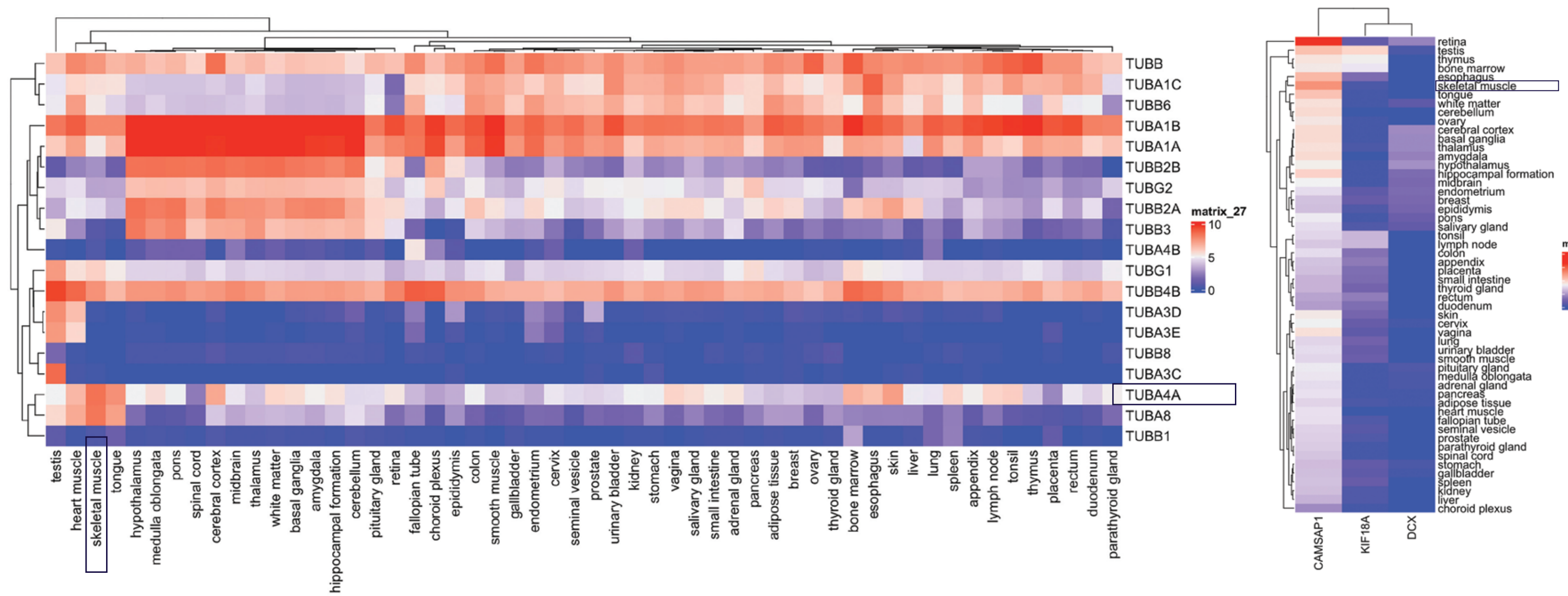


Figure 3. Internally identified myopathy & NDD patients carrying *TUBA4A* variants do not demonstrate a visually differentiable distribution pattern along the gene versus previously reported ALS variants

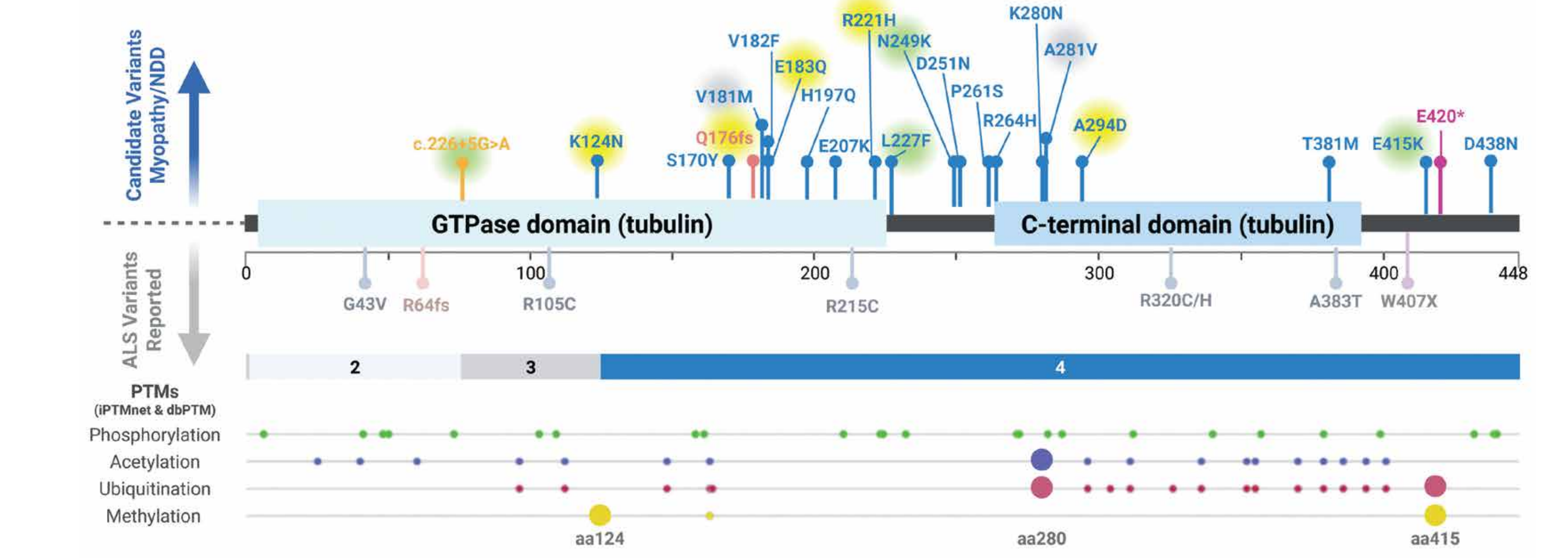


Figure 4. Variant prioritization surfaces top 4 variant candidates for reclassification

	Cases	Unsolved Myo/NDD	Age (y)	Mutation Taster	Other Predictors	PTM	Predicted change in: Structure	Interactions	Literature/Other Support
Prioritized Variants									
N249K	1	✓	18	Deleterious	AM: Strong Pathogenic	↑ acetyl ↑ methyl	None	Altered MAP interactions	No publications but ✓ Biopsy immunopositive
L227F	1	✓	2	Deleterious	AM: Strong Pathogenic	None	None	N/A	✓ Direct
c.226+5G>A	1	✓	10	Deleterious	SpliceAI: Splice Loss	N/A	N/A	N/A	✓ Indirect
E415K	1	✓	32	Deleterious	AM: Strong Pathogenic	↑ methyl ↑ sumo	None	Altered MAP interactions	✓ Direct
R221H & A281V (also carries p.K280N)	2	✓	3	Deleterious	PrimateAI: Deleterious	None	N/A	N/A	✓ Direct in Other Tissue
E183Q & A281V	1	✓	11	Deleterious	AM: Pathogenic	None	N/A	N/A	✓ Direct
K124N	1	✓	24	Benign	AM: Pathogenic	↑ glycosyl ↓ methyl ↓ ubiquitin	None	N/A	✓ Indirect
A294D	1	✓	10.5	Benign	AM: Support Pathogenic	None	N/A	N/A	None
Q176fs	1	✓	3	Deleterious	NMD due to >10%	None	N/A	N/A	None
A281V	12	3 (75% solved)	0-33	Deleterious	AM: Support Pathogenic	N/A	N/A	N/A	None
V181M	5	2 (60% solved)	2-44	Deleterious	AM: Support Pathogenic	None	N/A	N/A	✓ Indirect
Other									

AM: AlphaMissense; DD: developmental delay; ID: intellectual disability; MT: microtubule; PTM: post-translational modification; \*R: age at report (age of onset not available)

## KEY CONCLUSIONS AND DISCUSSION POINTS

- We report earlier age of onset associated with *TUBA4A* myopathy compared to later age of onset, on average, in ALS & spastic ataxias
- Though sample sizes are small, we note relatively consistent phenotypic profiles in patients carrying predicted damaging missense variants
- Our results support the inclusion of *TUBA4A* as a gene of interest for neonatal or juvenile patients presenting with hypotonia and/or progressive weakness
- In silico* analysis provide hypotheses for future investigations of the pathogenic mechanisms underlying *TUBA4A* variants and to lay a foundation for considering the potential complexity likely underlying related genotype-phenotype relationships

Figure 5. Review 4 prioritized cases provided rationale for follow-up and potential gene/variant reclassification

<b>N249K</b> Not reported c.747T>G	<b>Onset:</b> Neonate (M 0) (hypotonia; metatarsus adductus) <b>Severe, progressive</b> mobility loss (wheelchair dependence: 9yo)	<b>L227F</b> Publications Only c.679C>T	<b>Onset:</b> Infancy/neonate (F 0) (hypotonia) <b>Moderate-to-severe</b> weakness (lower limbs)
Delayed language/cognition/motor development, intellectual disability, & abnormal attention/emotional state	Diffuse bilateral weakness (upper/lower limbs), broad-based gait then wheelchair dependence, elbow/feet contractures	No ptosis/swallowing defect; mild dysarthria/slurred speech; autophagic vacuoles & TUBA4A+ aggregates in muscle biopsy	<i>In silico</i> mechanistic investigation (AlphaFold3)
249N near the regulatory residue 40K & binding interface for $\alpha$ 8-tubulin	Acetylation (Ac) at 40K increases MT stability	249K-Ac predicted to alter interaction of $\alpha$ 8-dimers with CAMSAP1 (muscle-associated MAP)	249N & 40K-Ac 249K-Ac & 40K-Ac
Current Classification: N/A (missense at same residue is VUS) Proposed Classification: <b>Likely Pathogenic</b>	Population: not in ExAC/gnomAD Segregation: N/A De novo: confirmed	Functional: TUBA4A+ aggregates Computational: multiple predictions Other: same residue variant not benign	
<b>E415K</b> Publications Only c.1243G>A	<b>Onset:</b> Childhood (M 7) (Motor problems; trouble riding bike) <b>Progressive spastic</b> disease (wheelchair dependence: 28yo)	<b>c.226+5G&gt;A</b> Not reported	<b>Onset:</b> Teenage (M 18) (exact age unconfirmed) <b>Very mild</b> severity (NMDAS SII = 2/45; total = 2/145)
Normal development; onset of progressive leg weakness, spasms, falls in teens plateauing in 20s & progressing in 30s	Hyperreflexia; dystonia; spastic/short gait then wheelchair; activity-induced hand tremors; type 2B fiber atrophy	Nystagmus; depression, ADHD, hallucinations, and insomnia; bladder abnormalities; medical history of neuropathy	<i>In silico</i> investigation (AlphaFold3) & prior reports
415E: methyl/ubiquitin site	E415K predicted to destabilize $\alpha$ -tubulin & $\uparrow$ probability of methyl/SUMO addition	Other pts (AAO 10-30yr): weak lower limbs, gait & bladder defects, nystagmus <sup>4,14</sup>	E415K & 40K-Ac E415K-me & 40K-Ac
E415K-me predicted to alter interaction with CAMSAP1			
Current Classification: N/A (missense at same residue is VUS) Proposed Classification: <b>Pathogenic</b>	Population: absent in ExAC/gnomAD Segregation: Multigeneration ancestry De novo: confirmed in 4/5 pts	Functional: N/A Computational: multiple predictions Other: --	
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