

Supplemental Information

Allelic strengths of encephalopathy-associated *UBA5* variants correlate between *in vivo* and *in vitro* assays

Xueyang Pan^{1,2}, Albert N. Alvarez³, Mengqi Ma^{1,2}, Shenzhao Lu^{1,2}, Michael W. Crawford³, Lauren C. Briere⁴, Oguz Kanca^{1,2}, Shinya Yamamoto^{1,2,5}, David A. Sweetser^{4,6}, Jenny L. Wilson⁷, Ruth J. Napier^{3,8,9}, Jonathan N. Pruneda^{3,#}, Hugo J. Bellen^{1,2,5,#}

1 Department of Molecular and Human Genetics, Baylor College of Medicine, Houston, TX 77030, USA

2 Jan & Dan Duncan Neurological Research Institute, Texas Children's Hospital, Houston, TX 77030, USA

3 Department of Molecular Microbiology & Immunology, Oregon Health & Science University, Portland, OR 97239, USA

4 Center for Genomic Medicine, Massachusetts General Hospital, Boston, MA 02114, USA

5 Department of Neuroscience, Baylor College of Medicine, Houston, TX 77030, USA

6 Division of Medical Genetics & Metabolism, Massachusetts General Hospital for Children, Boston, MA 02114, USA

7 Division of Pediatric Neurology, Department of Pediatrics, Oregon Health & Science University, Portland, OR 97239, USA

8 VA Portland Health Care System, Portland, OR 97239, USA

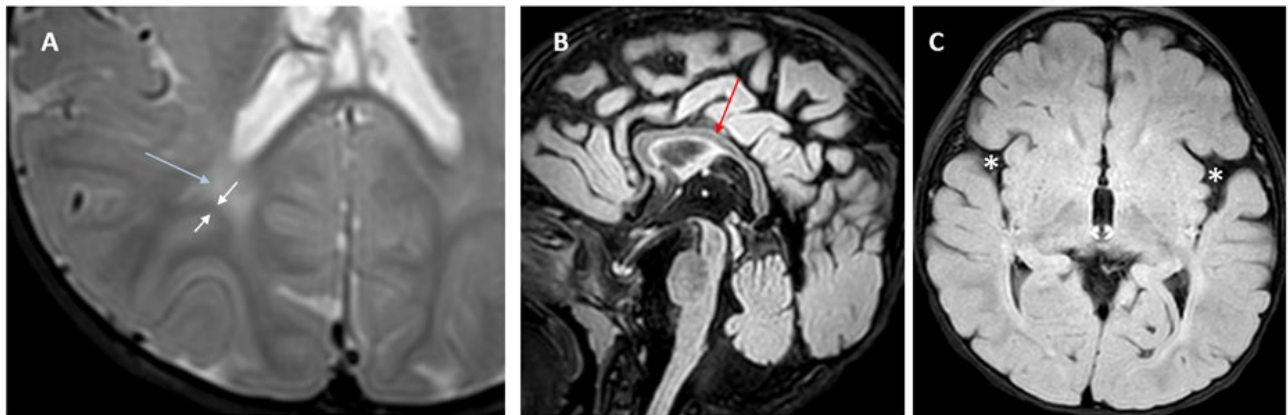
9 Division of Arthritis & Rheumatic Diseases, Oregon Health & Science University, Portland, OR 97239, USA

Correspondence: hbellens@bcm.edu, pruneda@ohsu.edu

1 Case report

2 The reported proband is a boy with axial hypotonia, generalized dystonia, lower extremity spasticity,
3 global developmental delay, esotropia and failure to thrive. An electroencephalogram (EEG) showed
4 multifocal epileptiform discharges in drowsiness and sleep. However, he has not had seizures. Two
5 magnetic resonance imaging (MRI) studies at different ages were read as normal, although on review
6 show a slightly thin corpus callosum, posterior periventricular white matter T2 hyperintensity resulting
7 in increased conspicuity of the subcortical U-fibers and widening of the Sylvian fissures (Figure S1). He
8 is not microcephalic. For more information about the clinical record of the proband please contact the
9 corresponding author.

10 On trio exome sequencing, the proband was found to have compound heterozygous variants in *UBA5*,
11 NM_024818.6:c.169A>G (p.Met57Val) and c.935A>T (p.Gln312Leu). The two variants are in *trans*
12 phase. The p.Met57Val variant has been reported in one individual with DEE44 (Colin *et al*, 2016). The
13 p.Gln312Leu variant has not been previously reported. Neither variant is reported in the gnomAD
14 database v.2.1.1 (<https://gnomad.broadinstitute.org>). Both variants are predicted to be damaging or
15 probably damaging by multiple pathogenicity prediction tools (Table S3).



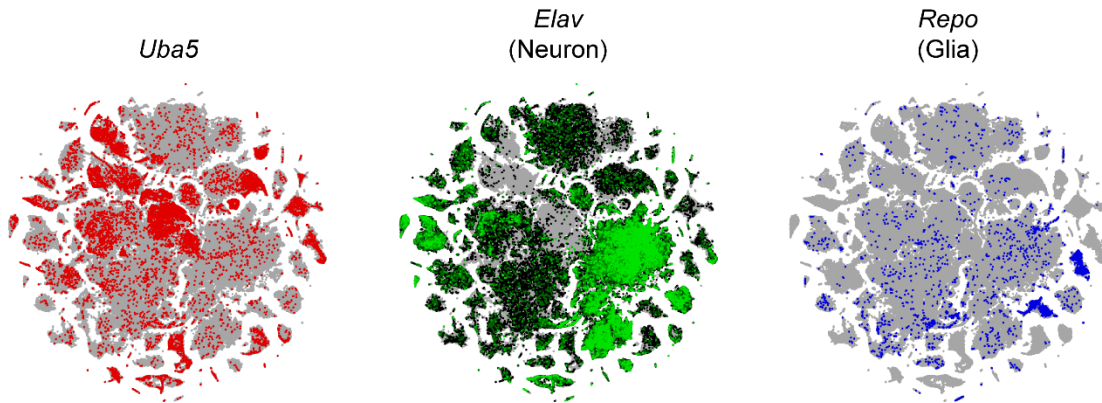
18
19 **Figure S1. Brain magnetic resonance imaging (MRI) images**

20 (A) Axial T2 image showing periventricular T2 hyperintensity (blue arrow) resulting in of
21 the subcortical U-fibers (white arrows).

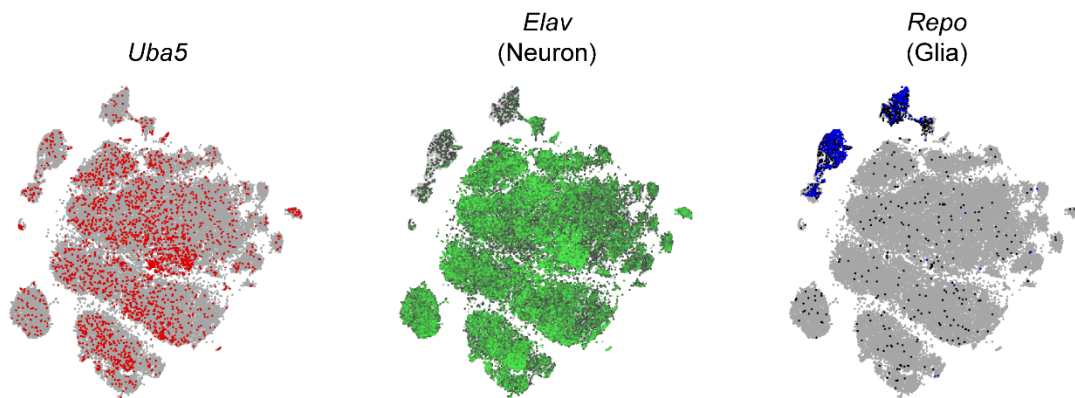
22 (B) Sagittal flair showing mild thinning of the corpus callosum (red arrow).

23 (C) Axial flair image demonstrating widening of the sylvian fissures (white asterisks).

A Adult fly - whole body



B Adult fly - brain



C

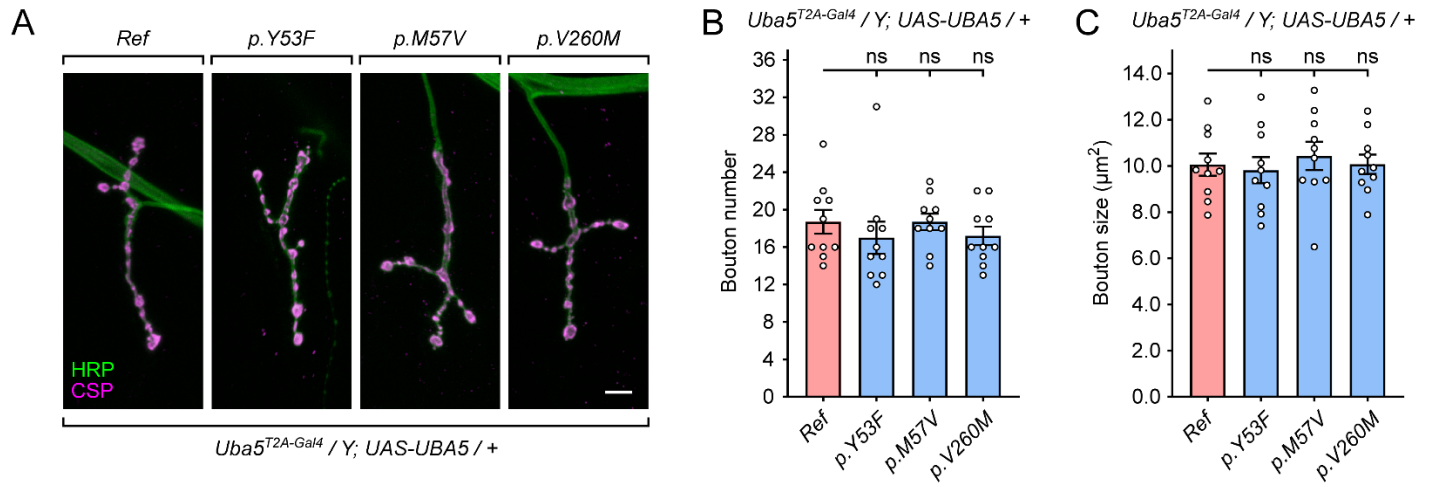
	<i>Uba5</i> ^{KO} /Y; UAS- <i>UBA5</i> ^{Ref}	<i>Uba5</i> ^{KO} /+; UAS- <i>UBA5</i> ^{Ref}
No driver	Embryonic / L1 lethal	Viable, NOP
<i>Da-Gal4</i>	Viable, NOP	Viable, NOP
<i>Act-Gal4</i>	Viable, NOP	Viable, NOP
<i>Lpp-Gal4</i>	Embryonic / L1 lethal	Viable, NOP
<i>Mef2-Gal4</i>	Embryonic / L1 lethal	Viable, NOP
<i>Elav-Gal4</i>	Embryonic / L1 lethal	Viable, NOP
<i>Repo-Gal4</i>	Embryonic / L1 lethal	Viable, NOP
<i>Elav-Gal4, Repo-Gal4</i>	Embryonic / L1 lethal	Viable, NOP

1

2 **Figure S2. Single-cell gene expression pattern of *Uba5* and the rescue of *Uba5* mutants by**
 3 **tissue-specific *UBA5* expression**

4 (A and B) The expression pattern of *Uba5* in whole adult fly (Li *et al*, 2022) (A) and adult brain tissue
 5 (Davie *et al*, 2018) (B) revealed by single-cell RNA sequencing profiles. The expression patterns of
 6 neuronal marker *Elav* and glial marker *Repo* are also shown.

7 (C) The lethality of *Uba5* hemizygous mutants is rescued by ubiquitous expression, but not by any
 8 tissue-specific expression of human *UBA5* cDNA. Overexpression of *UBA5* in *Uba5* heterozygous
 9 mutants does not cause any obvious phenotype.



1

2 **Figure S3. The Group II *UBA5* variants do not cause obvious synaptic growth defects**

3 (A) Images of NMJ4 in segments A2-A4 stained with anti-horseradish peroxidase (HRP) and anti-
 4 cysteine string protein (CSP) in humanized flies expressing reference *UBA5* or Group II variants. Scale
 5 bar, 10 µm.

6 (B and C) Quantification of the bouton number (B) and bouton size (C) of NMJs. Results are presented
 7 as means ± SEM. Statistical analyses were performed via two-sided, unpaired Student's t-test. ns, not
 8 significant.

9

1 **Table S1. Summary of genotypes of the reported cases**

References	Family	Allele #1	Allele #2
Colin, <i>et al.</i> , 2016 (Colin <i>et al.</i> , 2016)	A	p.Ala371Thr (IA [†])	p.Gln302*
	B	p.Ala371Thr (IA)	p.Lys324Asnfs*14
	C	p.Asp389Tyr (IA)	p.Val260Met (II)
	D	p.Met57Val (II)	p.Gly168Glu (III)
Muona, <i>et al.</i> , 2016 (Muona <i>et al.</i> , 2016)	A	p.Ala371Thr (IA)	p.Arg55His (III)
	B	p.Ala371Thr (IA)	p.Tyr285*
	C, E	p.Ala371Thr (IA)	p.Arg188*
	D	p.Ala371Thr (IA)	p.Arg61*
Arnadottir, <i>et al.</i> , 2017 (Arnadottir <i>et al.</i> , 2017)		p.Ala371Thr (IA)	p.Ala288= (splicing variant)
Daida, <i>et al.</i> , 2018 (Daida <i>et al.</i> , 2018)		p.Tyr72Cys (IB)	Deletion
Mignon-Ravix, <i>et al.</i> , 2018 (Mignon-Ravix <i>et al.</i> , 2018)		p.Tyr53Phe (II) ^{††}	p.Tyr53Phe (II)
Low, <i>et al.</i> , 2019 (Low <i>et al.</i> , 2019)		p.Asp389Gly (IA)	Deletion
Briere, <i>et al.</i> , 2021 (Briere <i>et al.</i> , 2021)	A	p.Ala371Thr (IA)	p.Cys303Arg (III)
	B	p.Ala371Thr (IA)	p.Arg188*
	C	p.Ala371Thr (IA)	p.Leu254Pro (III)
	D	p.Ala371Thr (IA)	p.Cys303Arg (III)
This study		p.Met57Val (II)	p.Gln312Leu (IB)

2 [†] The variant classification using fly phenotypic assays (results shown in Figure 3)

3 ^{††} Consanguineous family

4

5 **Table S2. Clinical features of individuals with *UBA5*-associated DEE44**

6 (See separate Excel table)

7

8 **Table S3. Bioinformatic predictions of the pathogenicity of reported *UBA5* variants**

	Variant 1	Variant 2
Genomic position (GRCh38)	3:132665830A>G	3:132394214A>T
Amino acid change	p.Met57Val	p.Gln312Leu
Allele frequency in gnomAD	Absent	Absent
CADD score	25.3	29.1
SIFT	Damaging	Damaging
PolyPhen2	1.000 (probably damaging)	0.999 (probably damaging)
MutationTaster	Disease causing	Disease causing
PROVEAN	-3.18 (deleterious)	-6.59 (deleterious)

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1 References

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