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Supplemental Data

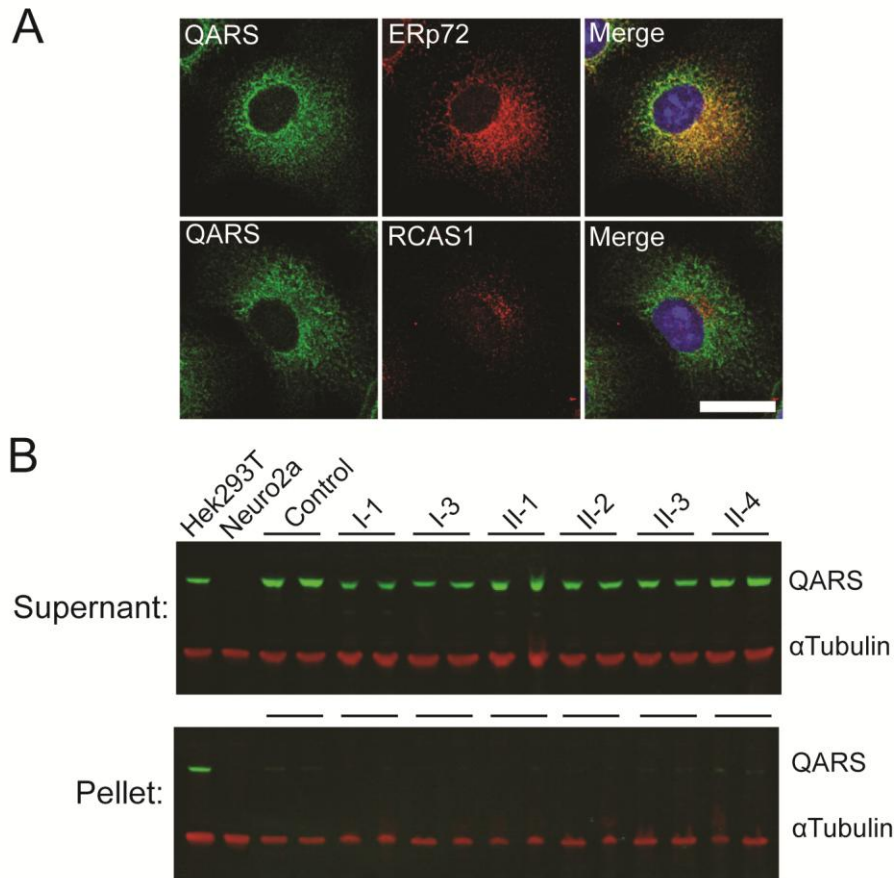
**Mutations in *QARS*, Encoding Glutaminyl-tRNA Synthetase, Cause Progressive Microcephaly, Cerebral-Cerebellar Atrophy, and Intractable Seizures**

Xiaochang Zhang, Jiqiang Ling, Giulia Barcia, Lili Jing, Jiang Wu, Brenda J. Barry, Ganeshwaran H. Mochida, R. Sean Hill, Jill M. Weimer, Quinn Stein, Annapurna Poduri, Jennifer N. Partlow, Dorothée Ville, Olivier Dulac, Tim W. Yu, Anh-Thu N. Lam, Sarah Servattalab, Jacqueline Rodriguez, Nathalie Boddaert, Arnold Munnich, Laurence Colleaux, Leonard I. Zon, Dieter Söll, Christopher A. Walsh, and Rima Nababout

	p.Gly45Val	p.Tyr57His	p.Arg403Trp	p.Arg515Trp
Consensus	TLGST	LLYGL	TLRMK	DPRLF
Identity				
H. sapiens   NP_005042	TLGST	LLYGL	TLRMK	DPRLF
P. troglodytes   XP_001147632	TLGST	LLYGL	TLRMK	DPRLF
M. mulatta   XP_001110256	TLGST	LLYGL	TLRMK	DPRLF
B. taurus   NP_001029640	TLGSS	LLYGL	TLRMK	DPRLF
C. lupus   XP_533833	TLGST	LLYGL	TLRMK	DPRLF
R. norvegicus   NP_001007625	TLGST	LLYGL	TLRMK	DPRLF
M. musculus   NP_598555	ILGST	LLYDL	TLRMK	DPRLF
G. gallus   NP_001012800	ALGSG	LLYNA	TLRMK	DPRLF
D. rerio   ENSDARP60918.4	QLGSS	LLYSM	TLRMK	DPRLF
D. melanogaster   NP_524841	--GSA	LIYHM	TLRMK	DPRLF
C. elegans   NP_502812	--SG	LLYQL	TLRLK	DPRLF
A. gambiae   XP_319458	--PGV	LIFQA	TLRMK	DPRLF
S. cerevisiae   NP_014811	--SDY	LVHNL	ILRMK	DPRLF
S. pombe   NP_596745	-VGS	LLFTL	ILRMK	DPRLY
O. sativa   NP_001054822	--GVS	LLYTV	TLRMK	DPRLL
A. thaliana   NP_001185094	TDC--	LLYSV	TLRMK	DPRLL
E. coli   AAC73774			CLRAK	DPRMP

**Figure S1. Amino acids affected by *QARS* mutations are highly conserved.**

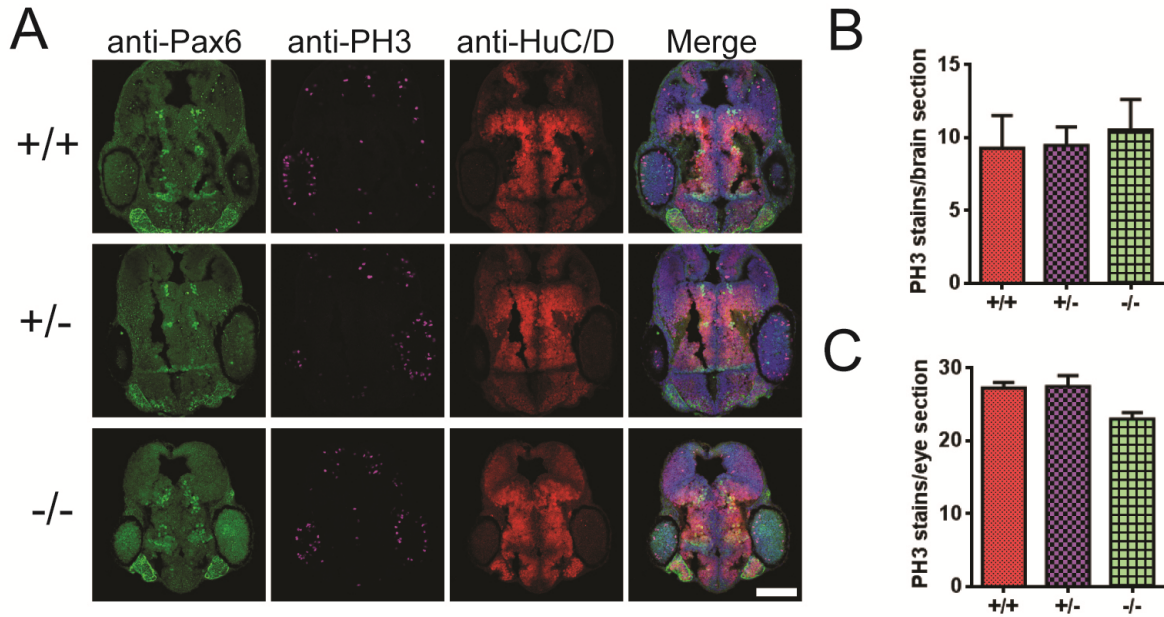
All four amino acids affected by human mutations are conserved in vertebrates and plants and two of them (Arg403 and Arg515) are conserved in all species examined.



**Figure S2. QARS subcellular localization, and protein levels in individual cell lines.**

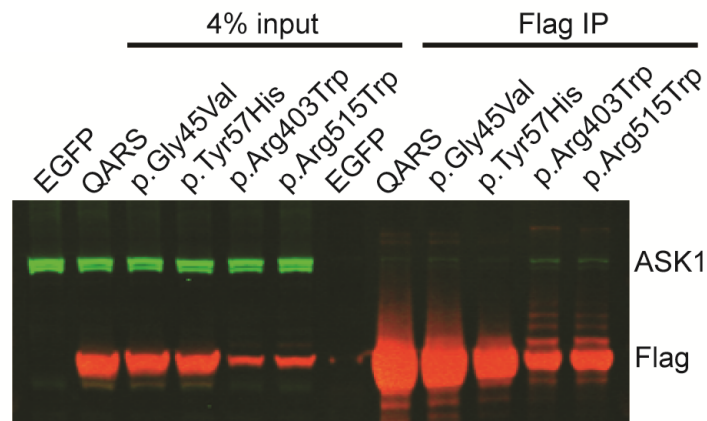
(A) Double labeling of endogenous QARS proteins with ER (ERp72) and Golgi (RCAS1) markers in Cos7 cells (monkey). Scale bar, 20  $\mu$ m.

(B) (Top) Western-blot showing that anti-QARS antibody recognizes QARS protein (green) in human cell lines but not Qars protein in a mouse cell line (Neuro2a), and that QARS protein level is similar among tested control and individual lymphoblastoid cell lines in the supernatant. (Bottom) Western-blot showing QARS protein level is low in the insoluble fraction of each lymphoblastoid cell lysate. Total protein lysates from HEK293T (human) and Neuro2a (mouse) represent positive and negative controls. Loading control, anti- $\alpha$ Tubulin (red).



**Figure S3. Neurogenesis in the brains and eyes are preserved in 2 dpf *qars* mutants.**

(A-C) Immunostaining results of fish brain sections (A) showing neural progenitors (anti-Pax6), mitotic cells (anti-PH3) and postmitotic neurons (anti-HuC/D) display similar patterns in 2 dpf *qars* mutants when compared to their (+/+) and (+/-) siblings. Scale bar, 300  $\mu$ m. Bar diagrams (B, C) showing that numbers of mitotic cells (anti-PH3 positive) are largely preserved in the brains and eyes of *qars* mutants when compared to their (+/+) and (+/-) siblings, mean  $\pm$  SEM values are presented.



**Figure S4. Effects of human variants on QARS-ASK1 interaction.**

Individual recombinant QARS variant as well as wild-type protein were expressed and immunoprecipitated (mouse anti-Flag, clone M2) from a human cell line (HEK293T). Enrichment of recombinant proteins was confirmed by blotting with a rabbit anti-Flag antibody (red). Weak interactions with endogenous ASK1 (green) are detected for all recombinant QARS proteins.

**Table S1. Oligo names and sequences.**

Name	Sequence
CH87	5'-CCATTCTACACCCACCATTTG-3'
CH90	5'-GGGCTCAGTGTGGATCTTCTT-3'
CH91	5'-GACTCCCTGTCGCTCTTCAC-3'
CH92	5'-TGCCTGTGCAGAACTAGGTG-3'
CH93	5'-CACTGCTGCTCTTTGAGGTG-3'
CH94	5'-GTGCTCGATGGAGTCACAGA-3'
CH184	5'-CGGACGTGGTGTCTTCTTTC-3'
CH185	5'-CCAGTGATCTTGTCAATGGCAG -3'
CH186	5'-GCTAGCTTGCCAAACCTACAGGT -3'
CH188	5'-CAGCAGACCCTGGTTTCCACCATTGAC-3'
CH189	5'-GTCAATGGTGGAAACCAGGGTCTGCTG-3'
CH190	5'-CGAGGCCACACTATGGATGAAGCTGG-3'
CH191	5'-CCAGCTTCATCCATAGTGTGGCCTCG-3'
CH379	5'- ACGGTACCATGGAGCAGAAGCTGATCTCAGAAGAGGACCTG GACTACAAAGACGATGACGACAAGATGGCGGCTCTAGACTCC C-3'
CH380	5'-ATCTCGAGAGCTCACACCTTTCCTGGGTC-3'
CH381	5'-CGGGATCCTGTTACATGGCTTGGCCTC-3'
CH382	5'-GAGGCCAAGCCATGTAACAGGATCCCG-3'
CH383	5'-CTGGGATGACCCATGGCTCTTTACACTC-3'
CH384	5'-GAGTGTAAGAGCCATGGGTCATCCCAG-3'
KCNT1-Ex1/2 F	5'-CATTGGTCAGCGAGTGAA-3'
KCNT1-Ex1/2 R	5'-GAACTGGCAGGACAGGTA-3'
KCNT1-Ex16/17 F	5'-TGGCTCCTGCCTGGTTCC-3'
KCNT1-Ex16/17 R	5'-AAAGTTCAGCATCAGTCA-3'

**Table S2. Additional clinical findings and developmental measurements.**

<b>Individual</b>	<b>I-1</b>	<b>I-2</b>	<b>II-1</b>	<b>II-2</b>
<b>Gender</b>	Male	Male	Male	Female
<b>Year of birth</b>	2008	2009	2008	2009
<b>Age at most recent assessment</b>	4 years	3 years	4.5 yrs	15 months
<b>Delivery</b>	Term (38wk)	Term	Term (41wk)	Term
<b>Birth Weight</b>	6.2lb (12%)	6.8lb (22%)	6lb (9%)	6.2lb (12%)
<b>Birth Height</b>	19.75" (50%)	19.5" (41%)	20.18" (66%)	19.29" (42%)
<b>Birth Head Circumference</b>	11" (-3.9SD)	12.25" (-2.1SD)	13.2" (-1.0SD)	13.2" (-1.0SD)
<b>Seizure Onset</b>	One hour after birth	First day of life	One hour after birth	One month old
<b>Developmental Features</b>	Profound delays, cortical visual impairment, normal hearing, chronic constipation, tracheomalacia, possible tapetoretinal degeneration as seen in Leber's congenital amaurosis, no meaningful visual response in either eye, nutrition by Gtube.	Profound delays, no constipation, can bubble, nystagmus, nutrition by Gtube.	Lack of visual contact from birth. Profound psychmotor delay at 4.5 years.	Normal tone and eye contact until onset of seizures, then profound delays by 15 months.
<b>Muscle tone</b>	Mixed hypotonia and hypertonia	High tone with brisk reflexes	Severe hypotonia	Severe hypotonia
<b>Dysmorphisms</b>	Sloping forehead, bitemporal narrowing, hypotelorism, bilateral epicanthal folds, broad flat nasal bridge, high arched palate. At age 5 months skin exam with slightly raised red rash across his chest and abdomen.	Less of sloping forehead than brother, has bitemporal narrowing, epicanthal folds, hypotelorism, low set and posteriorly rotated ears, broad nasal bridge, high palate. Unremarkable skin exam.	Coarse facies, hypoplastic helix of ear and prominent upper lip.	N/A
<b>Microcephaly</b>	-4.8SD at 1.5 months; -10.4SD at 21months	-5.8SD at 3 months; -7.8SD at 7 months	-3SD at 4.5 years	-2.5SD at 15 months

**Table S3. *SCTU* mutations are rare and predicted to cause deleterious amino acid substitutions.**

Person	Position (hg19)	Allele Frequency (6503 samples in EVS)	Amino acid change	SIFT	PolyPhen-2
I-3	chr3: 49141888 C>A	0	p.G45V	0.01	1
II-4	chr3: 49141853 A>G	0	p.Y57H	0.14	1
I-4	chr3: 49137482 G>A	0	p.R403W	0	1
II-3	chr3: 49136848 G>A	0	p.R515W	0	1

*QARS* mutations identified in both families were not seen in Exome Variant Server (EVS), and the amino acid substitutions are predicted to be damaging to protein functions by SIFT and PolyPhen-2.