A 25 Mainland Chinese cohort of patients with PURA-related neurodevelopmental disorders: clinical delineation and genotype–phenotype correlations

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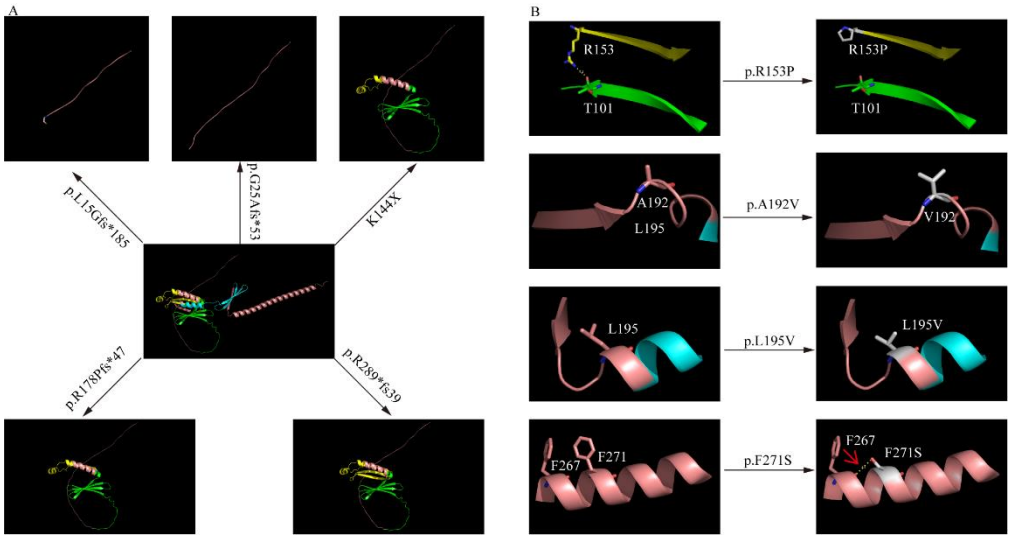
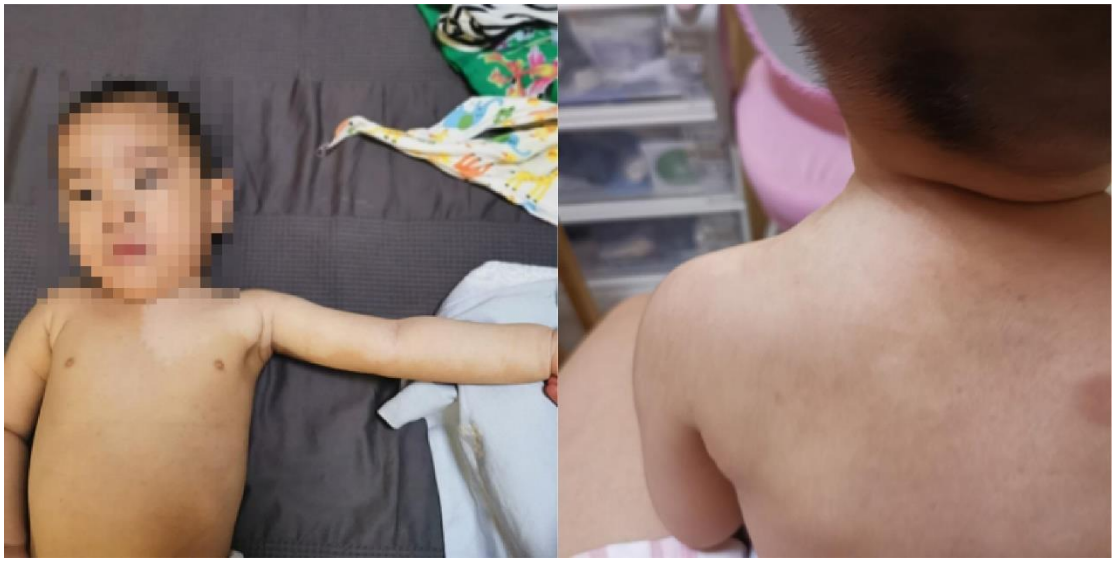


Supplementary Fig. S1: The effects of *PURA* variants on protein structure. The representation of the structure of human PURA (GenBank: NP_005850.1) was predicted by alphafold (The red arrow indicates the H-bonds). PUR-Ⅰdomain, PUR-Ⅱdomain and PUR-Ⅲ domain is respectively shown in green, yellow and cyon. (A) The effects of loss-of-function variants on protein structure. (B) The effects of missense variants on protein structure.



Supplementary Fig. S2: Large areas of lightened skin pigmentation of patient 7 was shown.

Table S3. Summarization of *PURA* gene variants in 24 patients with PURA syndrome (including detailed ACMG classification)

Patient	Variant	Protein change	ACMG classification	Pathogenicity
P1	c.159dup	p.L54Afs*147	PM2+PVS1-Strong+PS2+PS4-Supporting+PP4(P)	Pathogenic
P2	c.42_43del	p.L15Gfs*185	PM2+PVS1-Strong +PS2-Moderate+PP4(LP)	Likely pathogenic
P3	c.159dup	p.L54Afs*147	PM2+PVS1-Strong+PS2+PS4-Supporting +PP4(P)	Pathogenic
P4	c.697_699del	p.F233del	PM2+PM4+PM6-Supporting+PS4+PP4 (P)	Pathogenic
P5	c.449delG	p.R150Pfs*75	PM2+PVS1-Strong +PS2+PP4(P)	Pathogenic
P6	c.159dup	p.L54Afs*147	PM2+PVS1-Strong+PM6+PS4-Supporting+PP4(P)	Pathogenic
P7	c.697_699del	p.F233del	PM2+PM4+PM6-Supporting+PP4+PS4 (P)	Pathogenic
P8	c.159dup	p.L54Afs*147	PM2+PVS1-Strong+PM6+PS4-Supporting+PP4(P)	Pathogenic
P9	c.692T>G	p.F231C	PM2+PM5+PM6-Supporting+PP4(LP)	Likely pathogenic
P10	c.575C>T	p.A192V	PM2+PM1+PM6-Supporting+PP4(LP)	Likely pathogenic
P11	c.458G>C	p.R153P	PM2+PM6-Supporting+PP4(VUS)	Uncertain significance
P12	c.531del	p.P178Lfs*47	PM2+PVS1-Strong +PS2+PP4(P)	Pathogenic
P13	c.10C>T	p.R4X	PM2+PVS1-Strong +PS2-Moderate+PP4(LP)	Likely Pathogenic
P14	c.583C>G	p.L195V	PM2+PM6-Supporting+PP4(VUS)	Uncertain significance
P15	c.865delC	p.R289fs*39	PM2+PVS1-Strong+PS2-Supporting(LP)	Likely pathogenic
P16	c.812T>C	p.F271S	PM2+PS2-Supporting+PP3(VUS)	Uncertain significance
P17	c.72delC	p.G25Afs*53	PM2+PVS1-Strong +PS2+PP4(P)	Pathogenic
P18	c.506G>C	p.R169P	PM2+PP3+PS2+PP4(LP)	Likely pathogenic
P19	c.697_699del	p.F233del	PM2+PM4+PM6-Supporting+PS4+PP4(P)	Pathogenic
P20	c.697_699del	p.F233del	PM2+PM4+PM6-Supporting+PS4+PP4(P)	Pathogenic
P21	c.218T>G	p.F73C	PM2+ PS2+PP4(LP)	Likely pathogenic
P22	c.550C>T	p.Q184Ter	PM2+PVS1-Strong +PM6-Supporting (LP)	Likely pathogenic
P23	c.149_156dup	p.G53Pfs*28	PM2+PVS1-Strong +PM6+PP4(LP)	Likely pathogenic

P24	c.430A>T	p.K144X	PM2+PVS1-Strong +PS2-Moderate(LP)	Likely pathogenic