Supplementary Table 1. Genetic findings of pediatric study cohort with telomere biology disorders

Patient No.	Gene	Nucleotide change	Amino acid change	ACMG classification	Evidence of pathogenicity	References
1	*TERC*	n.514A>G		B	BA1	-
	TCAB1/WRAP53	c.202C>G	p.Arg68Gly	B	BA1	Zhong et al. Genes Dev. 2011[1]
2	*TERT*	c.3046G>A	p.Val1016Met	VUS	PM2_Supporting, PP2	-
3	*TERT*	c.2146G>A	p.Ala716Thr	P	PS4, PM5_Strong, PP3_Moderate, PM2_Sup., PP2	Zheng et al. J Int Med Res 2018[2]
4	*TERT*	c.618C>A	p.Ser206Arg	VUS	PM2_Supporting, PP2, BP4	-
5	*DKC1*	c.1346G>A	p.Arg449Gln	VUS	PS4_Mod., PP2, PM2_Supp.	Kirschner M et al. Leukemia. 2018[3]
6	*PARN*	c.1262+2_1262+3dupTA		VUS	PS1_Moder., PM2_Supp., PP3_Mod	Nurelegne HT et al. Mol Genet Genomic Med 2025[4]
7	*RTEL1*	c.3262C>T	p.Gln1088Ter	LP	PS4, PVS1, PM2_Sup.	Ballew et al, Hum Genet 2013[5] Cogan et al. Am J Respir Crit Care Med 2015[6]
8	*RTEL1*	c.439del	p.His147IlefsTer4	LP	PVS1, PM2_Sup., PM3_Sup.	Ballew et al, Hum Genet 2013[7]
	RTEL1	c.3791G>A	p.Arg1264His	P/LP	PS4, PM2_Sup., PM3_Sup., PP3_Sup.	Thompson et al. Am J Med Genet A 2025[8]
9	*TERC*	n.50C>A	-	VUS	PS4_Mod., PM1, PM2_Sup	Hinchie et al. Nat Commun 2024[9]
	RTEL1	c.3532C>T	p.Gln1178Ter	LP	PVS1, PM2_Sup.	-
10	*DKC1*	c.1058C>T	p.Ala353Val	P	PS4, PS3, PM2_Sup., PP2, PP3	-

This table summarizes genetic variants found in patients with suspected telomeropathy. Variants were evaluated using publicly available population and clinical variant databases, including Genome Aggregation Database for allele frequency assessment and ClinVar for previously reported clinical significance.
ACMG classification follows the American College of Medical Genetics and Genomics guidelines: P, pathogenic; LP, likely pathogenic; VUS, variant of uncertain significance; LB, likely benign; B, benign.
Evidence of pathogenicity is based on ACMG/AMP scoring criteria, including: PVS1, Pathogenic Very Strong – e.g., null variant (nonsense, frameshift, canonical +/-1 or 2 splice sites); PS4, Pathogenic Strong - same variant was already identified in affected individuals, its prevalence is significantly increased compared with the prevalence in controls; PM2, Pathogenic Moderate – absent or extremely rare if recessive in population databases; PS3, Pathogenic Strong – well-established functional studies supportive of a damaging effect; PP2, Missense variant in a gene that has a low rate of benign missense variation and in which missense variants are a common mechanism of disease; PP3, Multiple lines of computational evidence support a deleterious effect on the gene or gene product (conservation, evolutionary, splicing impact, etc.); PP4, Pathogenic Supporting – patient's phenotype or family history highly specific for a disease with a single genetic etiology; BP4, Benign Supporting – multiple lines of computational evidence suggest no impact; BA1, Allele frequency is >5% in Exome Sequencing Project, 1000 Genomes Project, or Exome Aggregation Consortium.

Supplementary References

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2. Zheng CM, Zhan X, Yang YH, Jiang T, Ye Q, Lu Y. A rare missense variant in telomerase reverse transcriptase is associated with idiopathic pulmonary fibrosis in a chinese han family. Chin Med J (Engl) 2018;131:2205-9.
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