

Marked overlap of four genetic syndromes with dyskeratosis congenita confounds clinical diagnosis

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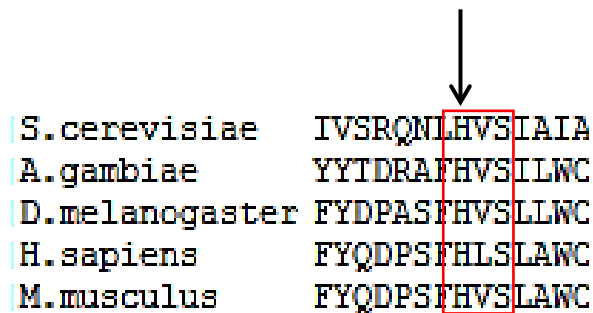
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Supplemental information:

Marked overlap of four other genetic syndromes with dyskeratosis congenita confounds clinical diagnosis

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Supplementary Figure 1



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↓
|S.cerevisiae  IVSRQNLHVSIAIA
|A.gambiae    YYTDRAFHVSIILWC
|D.melanogaster FYDPASFHVSLLLWC
|H.sapiens    FYQDPSFHLSLAWC
|M.musculus   FYQDPSFHVSLAWC
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The p.His208Arg homozygous USB1 mutation identified in Family 7 and Family 8 causes disease. Clustal alignment (<http://www.ebi.ac.uk/Tools/msa/clustalo/>) identifies the highly conserved HxS motif (red box). The arrow indicates the amino acid of interest. The accession numbers used are NP_013233, XP_307963, NP_649911, NP_078874 and NP_598715 respectively.

Supplementary Figure 2

		
H.sapiens	SNKPIHR	QPVLEIIPDVHI
R.norvegicus	SNKPIHR	QPVLEIIPDVHI
G.gallus	SNKPIHR	QPVLEIIPDVHI
X.tropicalis	SNKPIHR	QPVLEIIPDVHI
C.elegans	DKVPFHR	PAALFIAPEEI
D.rerio	SNKPLHR	QPVLEIIPDVHI

Clustal alignment for GRHL2 demonstrated that the amino acids in the red boxes are highly conserved. The red arrow highlights the p.Pro405Thr substitution identified in Family 10 and the green arrow highlights the p.Ile482Lys substitution seen in Family 9. The accession numbers used are NP_079191, NP_001127999, XP_004940038, NP_001011338, NP_490837 and NP_001076541 respectively

Supplementary Table 1: List of genes included in the targeted sequencing assay

Gene	Approved HGNC name	MIM
<i>ACD</i>	Adrenocortical dysplasia homolog	609377
<i>ANKRD26</i>	Ankyrin repeat domain 26	610855
<i>CEPBA</i>	CCAAT/enhancer binding protein alpha	116897
<i>CTC1</i>	CTS telomere maintenance complex component 1	613129
<i>DDX41</i>	DEAD-box helicase 41	608170
<i>DKC1</i>	Dyskerin pseudouridine synthase 1	300126
<i>DNAJC3</i>	DnaJ heat shock protein family (Hsp40) member C3	601184
<i>DNAJC21</i>	DnaJ heat shock protein family (Hsp40) member C21	NA
<i>ERCC6L2</i>	Excision repair cross-complementation group 6 like 2	615667
<i>ETV6</i>	ETS variant 6	600618
<i>FANCA</i>	Fanconi anemia complementation group A	607139
<i>FANCC</i>	Fanconi anemia complementation group C	613899
<i>FANCG</i>	Fanconi anemia complementation group G	602956
<i>GATA2</i>	GATA binding protein 2	137295
<i>GRHL2</i>	Grainyhead like transcription factor 2	608576
<i>LIG4</i>	Ligase IV, DNA, ATP-dependent	601837
<i>NHP2</i>	NHP2 ribonucleoprotein	606470
<i>NOP10</i>	NOP10 ribonucleoprotein	606471
<i>PARN</i>	Poly(A)-specific ribonuclease	604212
<i>PAX5</i>	Paired box 5	167414
<i>RECQL4</i>	RecQ like helicase 4	603780
<i>RMRP</i>	Mitochondrial RNA-processing endoribonuclease, RNA component	157660
<i>RTEL1</i>	Regulator of telomere length 1	608833
<i>RUNX1</i>	Runt related transcription factor 1	151385
<i>SBDS</i>	SBDS ribosome assembly guanine nucleotide exchange factor	607444
<i>SRP72</i>	Signal recognition particle 72kDa	602122
<i>TERC</i>	Telomerase RNA component	602322
<i>TERT</i>	Telomerase reverse transcriptase	187270
<i>TINF2</i>	TERF1 (TRF1)-interacting nuclear factor 2	604319
<i>TP53</i>	Tumor protein p53	191170
<i>USB1</i>	U6 snRNA biogenesis phosphodiesterase 1	613276
<i>WRAP53</i>	WD repeat containing, antisense to TP53	612661

NA – not available

Supplementary Table 2: Biallelic calls identified in Families 9-12 that underwent WES, after filtering for possible causal variants

Family	Gene	Gene name	MIM	Variant	Status	Biallelic variants in the same gene in additional families
9	<i>GRHL2</i>	Grainyhead-like 2 (Drosophila)	608576	c.T1445A:p.I482K	Homozygous	Family 10
9	<i>PAM</i>	Peptidylglycine alpha-amidating monooxygenase	170270	c.2585_2590del: p.862_864del	Homozygous	No
9	<i>TENC1</i>	Tensin like C1 domain containing phosphatase (tensin 2)	607717	c.A3563G:p.Q1188R	Homozygous	No
10	<i>FREMI1</i>	FRAS1 related extracellular matrix 1	608944	c.5845-2A>G	Homozygous	No
10	<i>GRHL2</i>	Grainyhead-like 2 (Drosophila)	608576	c.C1213A:p.P405T	Homozygous	Family 9
10	<i>INPP5F</i>	Inositol polyphosphate-5-phosphatase F	609389	c.A2884G:p.R962G	Homozygous	No
10	<i>NKRF</i>	NFKB repressing factor	300440	c.A83G:p.K28R	Homozygous	No
10	<i>SHROOM2</i>	Shroom family member 2	300103	c.G227A:p.G76E	Homozygous	No
10	<i>SSC5D</i>	Scavenger receptor cysteine rich domain containing (5 domains)	NA	c.G5A:p.R2K, c.A493G:p.N165D	Compound heterozygous	No
11	<i>C5orf60</i>	Chromosome 5 open reading frame 60	NA	c.T167C:p.L56P, c.C163T:p.R55C	Compound heterozygous	No
11	<i>GSE1</i>	Gse1 coiled-coil protein	616886	c.C3202G:p.L1068V, c.A3233G:p.Q1078R	Compound heterozygous	No
11	<i>LIG4</i>	Ligase IV, DNA, ATP-dependent	601837	c.1271_1275del:p.424_425del, c.C2440T:p.R814X	Compound heterozygous	Family 12
12	<i>LIG4</i>	Ligase IV, DNA, ATP-dependent	601837	c.1271_1275del:p.424_425del, c.C2440T:p.R814X	Compound heterozygous	Family 11