Supplementary Table 15. Rare germline variants (CADD> 15) in genes previously published as abnormally expressed in skin fibroblasts from vEDS patients (31), list of genes in supplementary methods.

Patient ID	Clinical Diagnosis	Rs ID	CADD/ DANN	Current Gene annotation	Gene	Exon or Intron / Total no. exons	HGVSc	HGVSp	gnomAD allele frequency	ACMG classification (See footnote)
65	hEDS	rs149479865	26.2 0.999	b)	HSPG2	21/97	ENST00000374695.3 c.2633G>A	ENSP00000363827.3 p.Arg878His	0.0002409	VUS PM2
536	hEDS	rs145474376	22.9 0.996	b)	HSPG2	46/97	ENST00000374695.3 c.5815G>A	ENSP00000363827.3 p.Ala1939Thr	0.00007685	VUS
650	hEDS	rs201421233	18.55 0.988	a)	P4HA3	7/13	ENST00000331597.4 c.934C>T	ENSP00000332170.4 p.Pro312Ser, ?	0.00007753	
1002	cEDS	rs150109595	19.84 0.989	b)	HSPG2	74/97	ENST00000374695.3 c.9908C>T	ENSP00000363827.3 p.Thr3303Met	0.00005578	VUS PM2 BP4 (Supp)
1263	hEDS	rs773364995	28.5 0.997	b)	HSPG2	61/97	ENST00000374695.3 c.7903G>A	ENSP00000363827.3 p.Glu2635Lys	0.00001221	VUS PM2
1438	hEDS	rs771862177	26.7 0.985	b)	HSPG2	88/97	ENST00000374695.3 c.12040C>A	ENSP00000363827.3 p.His4014Asn	0	VUS PM2
1439	hEDS	rs771862177	26.7 0.985	b)	HSPG2	88/97	ENST00000374695.3 c.12040C>A	ENSP00000363827.3 p.His4014Asn	0	VUS PM2
1580	hEDS	–	20.8 0.98	c)	TMEM130	5/8	ENST00000416379.2 c.722C>A	ENSP00000413163.2 p.Thr241Asn	0	VUS PM2 BP4 (Supp)
1607	hEDS	–	34 0.998	a)	HIST1H4L	1/1	NM_003546.3 c.259G>A	ENSP00000348258.2 p.Val87Met	0.000004061	
1629	hEDS	rs747291083	18.56 0.996	b)	HSPG2	16/97	ENST00000374695.3 c.2110A>G	ENSP00000363827.3 p.Ser704Gly	0.00002442	VUS PM2
1641	hEDS	rs773796176	22.1 0.998	b)	HSPG2	4/97	ENST00000374695.3 c.326G>A	ENSP00000363827.3 p.Arg109Gln	0.000004061	VUS PM2 BP4 (Supp)
1688	HDCT	rs770843975	33 0.999	a)	MMP24	4/9	ENST00000246186.6 c.794C>T	ENSP00000246186.6 p.Thr265Met	0.00004088	
1695	hEDS	rs774712031	28.6 0.998	a)	LRRFIP1	2/11	ENST00000392000.4 c.112C>T	ENSP00000375857.4 p.Arg38Cys	0.00001741	
1714	hEDS	rs75564013	21.8 0.990	a)	MMP24	9/9	ENST00000246186.6 c.1730G>C	ENSP00000246186.6 p.Arg577Pro	0.00008123	

ACMG criteria as per Richards *et al.* (9): P = pathogenic, LP = likely pathogenic, VUS/LP = variant of uncertain significance close to criteria for LP classification, VUS = variant of uncertain significance, LB = likely benign, B = benign. Individual criteria ((9), Table 3)

VUS* are defined here as including VUS that according to ACGS criteria are "hot", "warm" or "tepid" Variants of Uncertain Significance (Figure 6 of https://www.acgs.uk.com/media/11631/uk-practice-guidelines-for-variant-classification-v4-01-2020.pdf).

Segregation analysis, re-evaluation for specific phenotypic features and/or further functional analysis may enable variant reclassification, using ACMG criteria.