Supplementary file – Futterer et al 2018

Supplementary Table 1

Summary of Whole exome sequencing results for both patients.

	Patient III:3		Patient III:5	
Variant type	**known**	**novel**	**known**	**novel**
All variants	23943	583	24293	607
heterozygous	13111	506	13712	524
homozygous	10832	77	10581	83
Coding variants	21143	522	21441	540
heterozygous	11614	457	12114	471
homozygous	9529	65	9327	69
Splice variants	2800	61	2852	67
heterozygous	1497	49	1598	53
homozygous	1303	12	1254	14
Nonsynonymous SNVs	9678	277	9785	275
heterozygous	5326	246	5530	255
homozygous	4352	31	4255	20
Synonymous SNVs	10871	190	11070	194
heterozygous	6017	178	6299	176
homozygous	4854	12	4771	18
Stoploss SNVs	47	0	45	2
heterozygous	16	0	19	1
homozygous	31	0	26	1
Stopgain SNVs	82	3	82	5
heterozygous	59	3	65	5
homozygous	23	0	17	0
Deletions	204	21	203	34
heterozygous	99	11	106	21
homozygous	105	10	97	13
Insertions	220	30	221	27
heterozygous	73	18	76	12
homozygous	147	12	145	15
Frameshift deletions	69	5	69	9
heterozygous	22	2	29	5
homozygous	47	3	40	4
Frameshift insertions	112	9	119	8
heterozygous	21	5	22	0
homozygous	91	4	97	8
Transition:Transversion ratio	3.02	2.87	3	3.16
heterozygous	3.13	2.94	3.07	3.04
homozygous	2.88	2.28	2.91	5.14

Supplementary Table 2

Pathogenicity prediction and variant classification of the genetic variants. PhyloP scores vary between -14 and +6 and measure conservation at each individual base, sites predicted to be conserved are assigned a positive score, fast evolving sites are assigned a negative score. PhastCons values vary between 0 and 1 and reflect the probability that each nucleotide belongs to a conserved element. Mutationtaster uses a Beyes classifier to predict the effect of a mutation from a feed a classifiers. SIFT damaging prediction score= <0.05. Provean deleterious score = <-2.5. PolyPhen-2 predictions are appraised qualitatively as benign or damaging. The ACMG consensus guidelines, including supporting evidence, are also shown.

Gene	**Variant**	**Protein effect**	**EXaC**	**PhyloP**	**Phast Cons**	**Mutation taster**	**SIFT**	**Provean**	**PolyPh en-**	**ACMG**	**Classificati on**
ANKRD18A	c.2395_2397del^{hom}	p.E799del^{hom}	Novel	0.772	0.965	Polymorphism	NA	Deleterious	NA	PM2, PP (segregatio n), PM6	Uncertain Significance
GNE	c.G1246A^{hom}	p.G416R^{hom}	Novel	5.343	1	Disease causing	Damaging	Neutral	Damagi ng	PM2, PP (segregatio n), PM6	Uncertain Significance
FRMPD1	c.C1526T^{hom}	p.A509V^{hom}	0.000371	-1.459	0	Polymorphism	Tolerated	Neutral	Benign	PM2, PP (segregatio n), PM6	Uncertain Significance

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