Table 1: Variants of unknown significance (VUS) identified in Case 1 (blue) and Case 2 (green)

Case	Chr.	Gene	OMIM phenotype	Inheritance pattern	gnomAD MAF [Highest]
Case 1	1	*CR2*	Immunodeficiency, common variable	AR	0.00416% African
	1	*WDR26*	Skraban-Deardorff syndrome	AD	0.00%
	11	*EXT2*	Exostoses, Seizures, scoliosis, and macrocephaly syndrome	AD	0.00580% East Asian
	11	*RNASEH2C*	Aicardi-Goutieres syndrome	AR	0.00%
	X	*SEPT6*	X-linked Intellectual Disability	X-linked	0.00%
	12	*POLE*	FILS syndrome IMAGE-I syndrome	AR	0.00%
	16	*HYDIN*	Ciliary dyskinesia, primary, 5	AR	0.00%
	5	*C6*	C6 deficiency; Combined C6/C7 deficiency	AR	0.000899%
	5	*C6*	C6 deficiency; Combined C6/C7 deficiency	AR	0.00416%
	9	*DNAI1*	Ciliary dyskinesia, with or without situs inversus	AR	0.000895%
	9	*C5*	C5 deficiency	AR	0.0845%
Case 2	22	*TUBA8*	Cortical dysplasia, other brain malformations	AR	0.0149%
	6	*PSMB8*	Proteasome-associated autoinflammatory syndrome 1	AR	0.00%
	9	*DOCK8*	Hyper-IgE recurrent infection syndrome	AR	0.0942%