Table S4. Coding *FMN1* variants in the associated CHIR 10 region.

Genotypes of the three sequenced family members and a variable number of genotyped controls are displayed (0: reference allele; 1: variant allele).

CHIR10	*FMN1*	Effect	Family trio			Unrelated controls					
			w/w child	W/w father	W/w mother	w/w (without wattles) 0/0	0/1	1/1	W/. (with wattles) 0/0	0/1	1/1
g.25,952,169A>G	exon 2: c.1980A>G	synonymous	1/1	0/1	0/1	48	29	24		1	2
g.25,973,006T>A	exon 3: c.2076T>A	non-synonymous (p.Asp692Glu)	0/0	0/1	0/1	126			65	9	
g.26,072,689G>A	exon 7: c.4491G>A	synonymous	1/1	0/1	0/1	48	17	36	2	1	