

Supplementary Table 2. Prediction of the impact of the c.64G>T (p.G22C) *NR5A1* variant.

Prediction software	Score/Grade	Harmful	Definition of "harmful"
Scale-invariant feature transform (SIFT)	0.03	yes	Score <0.05
Protein Variation Effect Analyzer (PROVEAN)	-5.652	yes	≤ threshold (-2.5)
Polymorphism Phenotyping v2 (PolyPhen-2)	1.000	yes	Score ~0.447-0.909: potentially harmful Score ~0.910-1.000: very likely to be harmful
Align-Grantham Variation/Grantham Deviation (Align-GVGD)	C65	yes	~C0-C65: predicted pathogenicity grade from low to high