

Supplementary Table S1. WES data output.

	Data
Target regions coverage, 2x ¹	98.0%
Target regions coverage, 10x ¹	96.5%
Target regions coverage, 20x ¹	94.6%
Average sequencing depth on target ¹	86x
Number of variants with predicted functional effect	12,416
Novel, clinically associated, and unknown/low frequency variants ²	534
Putative disease genes (Autosomal Recessive/X-linked inheritance) ³	13 ⁴
Candidate genes (Autosomal Recessive/X-linked inheritance)	1, <i>LTBP3</i>

¹ Referred to Nimblegen SeqCap V.2 (Roche).

² MAF <1% in gnomAD v.2.1 database, and frequency <1% in our *in-house* database.

³ Filtering retained genes with functionally relevant variants by excluding variants predicted as benign by CADD (scaled score <20) and M-CAP algorithms or benign/likely benign by interVar.

⁴ *ATP10B* (c.1381G>T, p.Ala461Ser), *CLMN* (c.472C>G, p.Pro158Ala), *COL12A1* (c.1694G>A, p.Arg565Lys), *EDA* (c.1051G>A, p.Val351Ile), *ERN1* (c.1478_1486delAGCAGCAGC, p.Gln493_Gln495del), *KBTBD13* (c.376G>A, p.Ala126Thr), *LTBP3* (c.2894-2A>G), *NSD1* (c.1678G>A, p.Gly560Arg), *PSIP1* (c.1358C>T, p.Ala453Val), *RAB3GAP1* (c.1211A>T, p.Asn404Ile), *SPACA1* (c.437G>A, p.Arg146His), *TPH1* (c.1154A>T, p.Lys385Met), *XBP1* (c.85G>A, p.Gly29Arg).