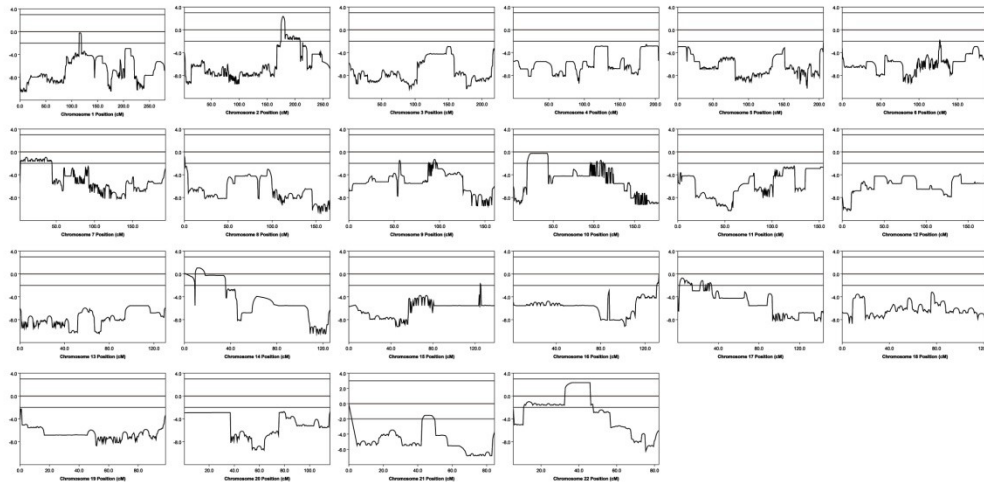


SUPPLEMENTARY MATERIALS FOR

Whole-genome linkage analysis with whole-exome sequencing identifies a novel frameshift variant in *NEFH* in a Chinese family with CMT2



Supplementary Figure S1 Linkage analysis results of all autosomes. The X-axis represents the physical location and Y-axis represents LOD scores.

Supplementary Table S1. Overview of exome capture statistics of family member III4 with CMT

Exome Capture Statistics	CMT III4
Target region (bp)	46019796
Raw reads	77603488
Raw data yield (Mb)	6984
Reads mapped to genome	68612687
Reads mapped to target region	54366397
Data mapped to target region (Mb)	4091.95
Mean depth of target region(X)	88.92
Coverage of target region(%)	98.9
Average read length(bp)	89.98
Rate of nucleotide match(%)	0.18
Fraction of target covered \geq 4X(%)	96.04
Fraction of target covered \geq 10X(%)	91.29
Fraction of target covered \geq 20X(%)	84.58
Capture specificity(%)	79.62
Reads mapped to flanking region	6470180
Mean depth of flanking region(X)	20.18
Coverage of flanking region(%)	91.04
Fraction of flanking covered \geq 4X(%)	69.7
Fraction of flanking covered \geq 10X(%)	47.93
Fraction of flanking covered \geq 20X(%)	30.94
Fraction of unique mapped bases on or near target(%)	88.64
Duplication rate(%)	9.93
Mean depth of chrX(X)	65.24
Mean depth of chrY(Y)	89.47
GC rate(%)	44.63
Gender test result	M