Supplemental data:

Methods used for Molecular Analyses

Patients A and B

Genomic DNA was extracted from leukocytes from both siblings and whole human exome enrichment was performed by Nimblegen SeqCAP EZ Exome and UTR Library kit, followed by paired-end 125 bp sequencing on an HiSeq 2500 (Illumina). Variants were analysed using the Broad seqr platform. Identified mutations in GNAO1 were subsequently validated by Sanger sequencing.

Patient C

WES was performed in the affected patient and her parents. The exons were captured using Agilent SureSelect Human All Exon V4 (without UTR). Analysis of the sequence data was performed using the previously described exome data analysis bioinformatics pipeline. Sanger-Sequencing of GNAO1 was performed in the patient and her parents.

Patient D

Genomic DNA was extracted from leukocytes and whole human exome enrichment was performed by SureSelect Human All Exon Kit (Agilent, 50 Mb, V5), followed by paired-end 100bp sequencing on a HiSeq2500 (Illumina). Sanger-Sequencing of GNAO1 was performed in the patient and her parents.