Supplementary Information

Targeted sequencing
Genomic DNA from blood from patient was extracted with Qiagen DNeasy blood & tissue kits (Qiagen, Valencia, CA, USA). For mutation analysis, the coding exons and flanking introns of 69 myopathy-causative genes were enriched by hybridization capture. The captured library was sequenced by an Illumina Hiseq2000 platform with the 2X150 bp paired-end read module. The sample was pooled into a part of a single lane on a single flow cell and sequenced together. A 6 bp index sequence (Illumina) and 6 bp in-house barcode sequence were used to differentiate between samples. Total sequencing yield was 528.54 Mbp. The coverage of target region (≥10X) was 98.7%.

Variant analysis
From HiSeq2000 raw data, sequencing data of all samples were sorted by index and barcode sequences. Sorted fastq files were aligned to the hg19 reference genome with Burrows-Wheeler Aligner (BWA) (ver. 0.7.5a) algorithm. Output SAM files were converted to BAM files and sorted with SAMtools (ver. 0.1.18). Duplicate removal was performed with Picard tools (ver. 1.95) mark-duplicates. Realignment around known indel sites and base quality score recalibration (BQSR) were performed with the genome analysis toolkit (GATK) (ver. 2.6-5) to create final BAM files.

Variants were called with GATK v2.6 Unified Genotyper algorithm. Called variants were filtered by the following criteria: 1) loci depth ≥10, variant frequency ≥0.5, 2) loci depth ≥20, variant frequency ≥0.25. Filtered variants were annotated with Annovar (ver. 2013-06-21) using RefGene, dbSNP 138, and the 1000 Genomes Project SNP (2014 Sep release) of Asian population and all-population databases. Among called variants, only nonsynonymous single nucleotide variant (SNV), frameshift indel and splicing site variants were chosen. Polymorphisms in Korean populations (n=352) were filtered out. Variants with low functional score in Polyphen2 (ver. 2.2.2) were considered benign mutations and discarded. Pathogenic and likely pathogenic variants were validated by Sanger sequencing.