

# Recessive *GNE* Mutations in Korean Nonaka Distal Myopathy Patients with or without Peripheral Neuropathy

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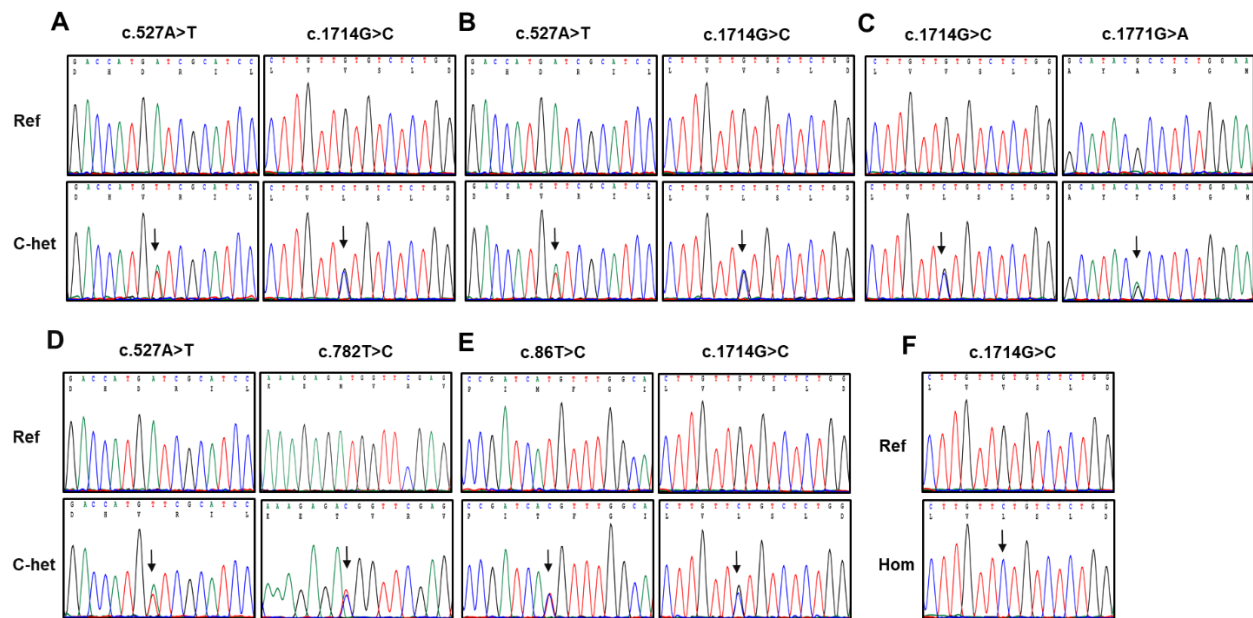
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**Figure S1.** Chromatograms of the *GNE* mutations observed in patients with myopathy. Results were derived via Sanger sequencing, and vertical arrows were employed to pinpoint the mutation sites (Ref: reference allele, C-het: compound heterozygote, Hom: homozygote). (A,B) c.527A>T and c.1714G>C mutations in families of Myo-6 and Myo-8, (C) c.1714G>C and c.1771G>A mutations in pedigree Myo24, (D) c.527A>T and c.782T>C mutations in pedigree Myo-35, (E) c.86T>C and c.1714G>C mutations in pedigree Myo-41, and (F) c.1714G>C homozygous mutation in pedigree Myo-12.

**Table S1.** Interpretation of the *GNE* gene variants according to the ACMG/AMP criteria.

Variants		Criteria	Evaluation
Nucleotides	Amino Acids		
c.86T>C	p.Met29Thr	PM1+PM2+PM3+PP1+PP3+PP4	P
c.527A>T	p.Asp176Val	PM1+PM2+PM3+PP1+PP3+PP4+PP5	P
c.782T>C	p.Met261Thr	PM1+PM2+PM3+PP1+PP3+PP4	LP
c.1714G>C	p.Val572Leu	PM1+PM2+PM3+PP1+PP3+PP4+PP5	P
c.1771G>A	p.Ala591Thr	PM1+PM2+PM3+PP1+PP3+PP4	LP

Abbreviations: ACMG-AMP: The American College of Medical Genetics and Genomics and the Association for Molecular Pathology, LP: likely pathogenic, P: pathogenic.

**Table S2.** Predicted effects of missense mutations using several bioinformatic tools.

Variants	DDG (kcal/mol) <sup>a</sup>			
	MAESTROweb	DynaMut2	PremPS	DeepDDG
p.Met29Thr	0.39	-1.28	-2.47	-2.21
p.Asp176Val	-0.15	0.06	-0.23	-0.187
p.Met261Thr	0.33	-1.72	-2.17	-0.909
p.Val572Leu	0.03	-0.34	-0.39	-1.095
p.Ala591Thr	0.22	-1.67	-1	-0.762

Abbreviations: MAESTROweb: Mutation Analysis for the Estimation of Stability Changes in Proteins Web Server; DynaMut2: Dynamic mutation 2; PremPS: Prediction of the Effects of Missense Mutations using Protein Structure; DeepDDG: Deep Learning-based  $\Delta\Delta G$  (delta delta G).

<sup>a</sup> DDG or  $\Delta\Delta G$  (kcal/mol): difference in Gibbs free energy between two states (wild-type and mutant). A negative value ( $\Delta\Delta G < 0$ ) suggests that the mutant protein destabilizes the protein structure and function compared to the wild type while a positive value ( $\Delta\Delta G > 0$ ) indicates that the mutant stabilizes the protein.