eSupplementary table 1. Electrophysiologic study results

	Patient 1/III-3		Patient 1/IV-7		Patient 2/III-1		Patient 2/IV-1		Patient 2/III-2		Normal value*
	Left side	Right side	Left side	Right side	Left side	Right side	Left side	Right side	Left side	Right side	
Median nerve											
MNCVs, m/s	nt	38.1	48.7	nt	nt	45.4	45.7	48.3	nt	43.9	≥49
CMAPs, mV	nt	5.8	4.2	nt	nt	4.0	9.0	5.6	nt	3.1	≥4.0
SNCVs, m/s	nt	46.5	50.7	nt	nt	41.0	48.4	44.7	36.7	34.3	≥50
SNAPs, μV	nt	2.8	14.7	nt	nt	3.5	19.1	12.8	6.1	5.8	≥20
Ulnar nerve											
MNCVs, m/s	nt	52.1	51.2	nt	nt	50.7	47.6	52.4	nt	46.6	≥49
CMAPs, mV	nt	6.7	6.6	nt	nt	4.7	6.8	8.9	nt	4.5	≥6.0
SNCVs, m/s	nt	42.6	46.9	nt	nt	52.9	43.1	47.4	44.6	44.6	≥50
SNAPs, μV	nt	4.2	13.9	nt	nt	7.9	12.3	13.2	11.2	11.3	≥17
Sural nerve											
SNCVs, m/s	40.5	37.2	39.6	33.1	NR	NR	39.8	33.5	40.3	NR	≥40
SNAPs, μV	7.3	5.6	10.3	18.5	NR	NR	10.4	10.1	10.8	NR	≥6
Tibial nerve											
MNCVs, m/s	39.2	nt	31.4	34.9	29.1	33.5	39.4	37.6	nt	NR	≥41
CMAPs, mV	0.55	nt	1.6	1.93	1.42	0.81	5.7	11.8	nt	NR	≥4.0
Peroneal nerve											
MNCVs, m/s	38.4	NR	25.6	nt	27.6	33.4	34.5	36.6	NR	NR	≥44
CMAPs, mV	0.16	NR	1.5	nt	0.18	0.42	5.7	4.5	NR	NR	≥2.0

*David C. Preston, Barbara E. Shapiro. Electromyography and neuromuscular disorders. Clinical-electrophysiologic correlations, 3rd edition. 2013

MNCVs – motor nerve conduction velocities; CMAPs – compound muscle action potentials; SNCVs – sensory nerve conduction velocities; SNAPs – sensory nerve action potentials; m/s – meters per second; mV – millivolt; μV – microvolt.

eSupplementary table 2. Summary of variants and variant reclassification

AARS1 variants	Author, year of publication	gnomAD frequency (v2.1.1. Exomes + Genomes - hg19)	Number of families observed	Number of affected individuals	Cosegregation	Domain location	REVEL score (dbNSFP version 4.1) (0-0.7 = Path, <0.3 = B)	SIFT (dbNSFP version 4.1) (0-0.05= Path)	(DANN / version 2014)	Aminoacid Conservation (vertebrates) = 100 Vert. Cons / human, rhesus, mouse, dog	Splice Ai
c.211A>T p.(Asn71Tyr)	Kon-Ping Lin et al, 2011; Hsu YH et al, 2019	0x	2	8	≤1/32	N-terminal catalytic domain	0.859	0	0.9951	yes, up to lamprey	NA
c.986G>A p.(Arg329His)	Latour et al, 2010; McLaughlin et al, 2012; Bansagi et al 2015; Lasshutova et al, 2016; Bacquet et al, 2018; Lousa et al, 2018; Lee et al, 2020; Volodarsky et al, 2021	0x	19	50	≤1/32	N-terminal catalytic domain	0.9629	0	0.9996	yes, up to lamprey	NA
c.2063A>G p.(Glu688Gly)	Bansagi et el, 2015	0x	1	3	1/4	Editing domain	0.874	0	0.9993	yes, up to lamprey	NA
c.1880>T p.(Ser627Leu)	Waterman et al, 2018	0x	1	2	1/4	Editing domain	0.8619	0	0.9994	yes, up to lamprey	NA
c.904G>A p.(Ala302Thr)	Khadilkar et al, 2017	169x	1	1	0	N-terminal catalytic domain	0.4889	0.168	0.9992	yes, up to lamprey	NA
c.1009G>A p.(Glu337Lys)	Waterman et al, 2018	0x	1	6	≤1/32	N-terminal catalytic domain	0.5189	1	0.9961	yes, up to lamprey	NA
c.976C>T p.(Arg326Trp)	Waterman et al, 2018	0x	1	7	≤1/32	N-terminal catalytic domain	0.7969	0	0.9992	yes, up to lamprey	NA
c.2564A>G p.(Gln855Arg)	Lee et al, 2020	0x	1	1	0	C-Ala domain	0.2109	0.266	0.9926	yes, till the zebrafish	NA
c.2333A>C p.(Glu778Ala)	McLaughlin et al, 2012	0x	1	1	0	C-Ala domain	0.2829	0.114	0.9858	yes, till the chicken	NA
c.2677G>A p.(Asp893Asn)	Zhao et al, 2012	0x	1	4	1/16	C-Ala domain	0.483	0.223	0.9948	yes, up to lamprey	NA
c.304G>C p.(Gly102Arg)	Motley et al, 2015	0x	1	5	≤1/32	N-terminal catalytic domain	/0.9419/ 0.9419	0/0	0.9994/0.9994	yes, up to lamprey	NA
c.525C>G p.(Phe175Leu)	Bacquet et al, 2018	2+1x	1	1	0	N-terminal catalytic domain	0.7929	0.001	0.9988	yes, up to lamprey	NA
c.1019A>G p.(Asn340Ser)	Volodarsky et al, 2021	32+2x	1	1	0	N-terminal catalytic domain	0.1589	0.032	0.9927	No	NA
c.1043C>T p.(Thr348Met)	Volodarsky et al, 2021	4x	1	1	0	N-terminal catalytic domain	0.3849	0.007	0.9989	yes, till the X_tropicalis	NA
c.1108A>G p.(Met370Val)	Volodarsky et al, 2021	48+2x	1	1	0	N-terminal catalytic domain	0.1439	0.304	0.9511	yes, till the zebrafish	NA
c.1208G>C p.(Ser403Thr)	Volodarsky et al, 2021	4x	1	1	0	N-terminal catalytic domain	0.03599	0.396	0.8265	No	NA
c.1222G>A p.(Gly408Arg)	Volodarsky et al, 2021	3x	1	1	0	N-terminal catalytic domain	0.8109	0	0.9991	yes, up to lamprey	0.72 donor gain
c.1253A>G p.(Tyr418Cys)	Volodarsky et al, 2021	6x	1	1	0	N-terminal catalytic domain	0.8069	0	0.9943	yes, up to lamprey	NA
c.1388T>C p.(Ile463Thr)	Volodarsky et al, 2021	0x	2	2	0	N-terminal catalytic domain	0.6409	0.008	0.9954	yes, till the chicken	NA
c.1409T>A p.(Ile470Asn)	Volodarsky et al, 2021	0x	1	1	0	N-terminal catalytic domain	0.656	0	0.9878	yes, up to lamprey	NA
c.1420C>T p.(Arg474Trp)	Volodarsky et al, 2021	17x	1	1	0	N-terminal catalytic domain	0.671	0.002	0.9993	yes, up to lamprey	NA
c.1429G>A p.(Gly477Ser)	Volodarsky et al, 2021	1x	1	1	0	N-terminal catalytic domain	0.112	0.133	0.9823	No	NA
c.1811A>G p.(Asn604Ser)	Volodarsky et al, 2021	44+3x	1	1	0	Editing domain	0.68	0	0.9988	yes, up to lamprey	NA
c.1823C>T p.(Thr608Met)	Schabhuttl et al, 2014; Volodarsky et al, 2021	0x	2	2	0	Editing domain	0.804	0	0.9993	yes, up to lamprey	NA
c.2185C>T p.(Arg729Trp)	Volodarsky et al, 2021	161+18x	2	2	0	Editing domain	0.324	0.008	0.9984	No	NA
c.2192C>T p.(Ser731Leu)	Volodarsky et al, 2021	11+4x	1	1	0	Editing domain	0.488	0.001	0.9987	yes, up to lamprey	NA
c.2222C>T p.(Thr741Met)	Volodarsky et al, 2021	36+15x	1	1	0	Editing domain	0.2189	0.005	0.9987	No	NA
c.2580G>A p.(Leu860=)	Volodarsky et al, 2021	172+13x	2	2	0	C-Ala domain	NA	NA	0.9055	No	0
c.2732A>G p.(Asn911Ser)	Volodarsky et al, 2021	26x	1	1	0	C-Ala domain	0.221	1	0.8541	No	NA
c.503C>T p.(Pro168Leu)	Volodarsky et al, 2021	6+1x	1	1	0	N-terminal catalytic domain	0. 744	0	0.9987	yes, up to lamprey	NA
c.72G>A p.(Thr24=)	Volodarsky et al, 2021	3+1x	1	1	0	N-terminal catalytic domain	NA	NA	0.4439	yes, till the X_tropicalis	0
c.781C>G p.(Asp261Glu)	Volodarsky et al, 2021	3x	1	1	0	N-terminal catalytic domain	0.5519	0	0.9977	yes, up to lamprey	NA
c.958C>T (p.Arg320Cys)	Volodarsky et al, 2021	8+1x	1	1	0	N-terminal catalytic domain	0.813	0	0.9993	yes, up to lamprey	NA
c.2251A>G p.(Arg751Gly)	Volodarsky et al, 2021	12+1x	2	2	0	Editing domain	0.9649	0	0.9984	yes, up to lamprey	N/A
c.1823C>A p.(Thr608Lys)	This study	0x	1	2	1/16	Editing domain	0.8259	0	0.9951	yes, up to lamprey	N/A
c.385C>G p.(Pro129Ala)	Volodarsky et al, 2021	14x	1	1	0	N-terminal catalytic domain	0.3899	0.014	0.9846	yes, till the X_tropicalis	N/A
c.1815C>G p.(His605Gln)	This study	0x	1	3	1/4	Editing domain	0,883	0	0.9937	yes, up to lamprey	N/A

AARS1 variants	MetaDome tolerance (AARS)	PS2	PS3	PS4	PM1	PM2	PM5	PP1	PP2	PP3	BS1	BS3	BS4	BP4	BP7	All criteria	ACMG Classfication (LB if BS1)	Original classification
c.211A>T p.(Asn71Tyr)	0.64 (slightly intolerant)	0	Strong (https://pubmed.ncbi.nlm.nih.gov/30261202/)	Supporting	Moderate	Moderate	0	Strong	0	Supporting	0	0	0	0	0	PS4_Supporting, PS3, PM1, PM2, PP1_Moderate, PP3	**Pathogenic**	(Likely) Pathogenic
c.986G>A p.(Arg329His)	0.7 (slightly intolerant)	0	Strong	Strong	Moderate	Moderate	0	Strong	0	Supporting	0	0	0	0	0	PS3, PS4_Strong, PM1, PM2, PP1_Strong, PP3	**Pathogenic**	(Likely) Pathogenic
c.2063A>G p.(Glu688Gly)	0.47 (intolerant)	0	0	0	Moderate	Moderate	0	Supporting	Supporting	Supporting	0	Supporting	0	0	0	PM1, PM2, PP1, PP2, PP3, BS3_Supporting	**Likely Pathogenic**	(Likely) Pathogenic
c.1880C>T p.(Ser627Leu)	1.07 (tolerant)	0	Strong	0	Moderate	Moderate	0	Supporting	0	Supporting	0	0	0	0	0	PS3, PM1, PM2, PP1, PP3	**Pathogenic**	(Likely) Pathogenic
c.904G>A p.(Ala302Thr)	0.72 (neutral)	0	0	0	Moderate	0	0	0	0	0	Strong	0	0	0	0	PM1, BS1	**Likely Benign**	(Likely) Pathogenic
c.1009G>A p.(Glu337Lys)	0.84 (neutral)	0	Strong (4-fold increase/Zebrafish dominant-negative effect)	0	Moderate	Moderate	0	Strong	0	0	0	0	0	0	0	PS3, PM1, PM2, PP1_Strong	**Pathogenic**	(Likely) Pathogenic
c.976C>T p.(Arg326Trp)	0.95 (slightly tolerant)	0	Strong	0	Moderate	Moderate	0	Strong	0	Supporting	0	0	0	0	0	PS3, PM1, PM2, PP1_Strong, PP3	**Pathogenic**	(Likely) Pathogenic
c.2564A>G p.(Gln855Arg)	0.43 (intolerant)	0	0	0	Moderate	Moderate	0	0	Supporting	0	0	0	0	Suppporting	0	PM1, PM2, PP2, BP4	**VUS**	(Likely) Pathogenic
c.2333A>C p.(Glu778Ala)	1.22 (tolerant)	0	0 (the AARSE778A variant in the C-Ala domain shows WT-like catalytic activity (McLaughlin et al., 2012), implying that nonenzymatic gain-of-function mechanisms underlie the pathogenesis of CMT2N)	0	Moderate	Moderate	0	0 (variant does not segregate with CMT phenotype in the only family reported)	0	0	0	Strong	0	Suppporting	0	PM1, PM2, PP1, BS3_Strong, BP4	**VUS**	(Likely) Pathogenic
c.2677G>A p.(Asp893Asn)	0.53 (slightly intolerant)	0	0	0	Moderate	Moderate	0	Moderate	0	0	0	Supporting	0	0	0	PM1, PM2, PP1_Moderate, BP4, BS3_Supporting	**VUS**	(Likely) Pathogenic
c.304G>C p.(Gly102Arg)	0.36 (intolerant)	0	Strong	0	Moderate	Moderate	0	Strong	Supporting	Supporting	0	0	0	0	0	PS3, PM1, PM2, PP1_Strong, PP2, PP3	**Pathogenic**	(Likely) Pathogenic
c.525C>G p.(Phe175Leu)	0.6 (slightly intolerant)	0	0	0	Moderate	0	0	0	0	Supporting	Strong	0	0	0	0	PM1, PP3, BS1	**Likely Benign**	(Likely) Pathogenic
c.1019A>G p.(Asn340Ser)	0.81 (neutral)	0	0	0	Moderate	0	0	0	0	0	Strong	0	0	0	0	PM1, BS1, BP4	**Likely Benign**	VUS
c.1043C>T p.(Thr348Met)	1.22 (tolerant)	0	0	0	Moderate	0	0	0	0	Supporting	Strong	0	0	0	0	PM1, BS1	**Likely Benign**	VUS
c.1108A>G p.(Met370Val)	0.85 (neutral)	0	0	0	Moderate	0	0	0	0	0	Strong	0	Strong	Supporting	0	PM1, BS1, BS4, BP4	**Benign**	VUS
c.1208G>C p.(Ser403Thr)	1.36 (tolerant)	0	0	0	Moderate	0	0	0	0	0	Strong	0	0	Supporting	0	PM1, BS1, BP4	**Likely Benign**	VUS
c.1222G>A p.(Gly408Arg)	0.75 (neutral)	0	0	0	Moderate	0	0	0	0	Supporting	Strong	0	0	0	0	PM1, PP3, BS1	**Likely benign for CMT2N, because predicted to result in loss of function which is not a mechanism for CMT2N**	VUS
c.1253A>G p.(Tyr418Cys)	0.33 (intolerant)	0	0	0	Moderate	0	0	0	Supporting	Supporting	Strong	0	0	0	0	PM1, PP2, PP3, BS1	**Likely Benign**	VUS
c.1388T>C p.(Ile463Thr)	0.37 (intolerant)	0	0	Supporting	Moderate	Moderate	0	0	Supporting	0	0	0	0	0	0	PS4_Supporting, PM1, PM2, PP2	**Likely pathogenic**	VUS
c.1409T>A p.(Ile470Asn)	0.46 (intolerant)	0	0	0	Moderate	Moderate	0	0	Supporting	0	0	0	0	0	0	PM1, PP2, PP2	**VUS**	VUS
c.1420C>T p.(Arg474Trp)	0.27 (intolerant)	0	0	0	Moderate	0	0	0	Supporting	Supporting	Strong	0	0	0	0	PM1, PP2, PP3, BS1	**Likely Benign**	VUS
c.1429G>A p.(Gly477Ser)	0.78 (neutral)	0	0	0	Moderate	0	0	0	0	0	0	0	0	Supporting	0	PM1, BP4	**VUS**	VUS
c.1811A>G p.(Asn604Ser)	0.68 (slightly intolerant)	0	0	0	Moderate	0	0	0	0	Supporting	Strong	0	0	0	0	PM1, PP3, BS1	**Likely Benign**	VUS
c.1823C>T p.(Thr608Met)	0.83 (neutral)	0	0	Supporting	Moderate	Moderate	Supporting	0	0	Supporting	0	0	0	0	0	PM1, PM2, PM5_Supporting, PS4_Supporting, PP3	**Likely pathogenic**	VUS
c.2185C>T p.(Arg729Trp)	0.57 (slightly intolerant)	0	0	Supporting	Moderate	0	0	0	0	0	Strong	0	0	0	0	PS4_Supporting, PM1, BS1	**Likely Benign**	VUS
c.2192C>T p.(Ser731Leu)	0.55 (slightly intolerant)	0	0	0	Moderate	0	0	0	0	Supporting	Strong	0	0	0	0	PM1, PP3, BS1	**Likely Benign**	VUS
c.2222C>T p.(Thr741Met)	0.48 (intolerant)	0	0	0	Moderate	0	0	0	Supporting	0	Strong	0	0	0	0	PM1, PP2, BS1, BP4	**Likely Benign**	VUS
c.2580G>A p.(Leu860=)	0.74 (neutral)	0	0	Supporting	Moderate	0	0	0	0	0	Strong	0	0	Supporting	Supporting	PS4_Supporting, PM1, BS1, BP4, BP7	**Likely Benign**	VUS
c.2732A>G p.(Asn911Ser)	0.42 (intolerant)	0	0	0	Moderate	0	0	0	Supporting	0	Strong	0	0	Supporting	0	PP2, PM1, BS1, BP4	**Likely Benign**	VUS
c.503C>T p.(Pro168Leu)	0.75 (neutral)	0	0	0	Moderate	0	0	0	0	Supporting	Strong	0	0	0	0	PM1, PP3, BS1	**Likely Benign**	VUS
c.72G>A p.(Thr24=)	0.59 (slightly intolerant)	0	0	0	Moderate	0	0	0	0	0	Strong	0	0	Supporting	Supporting	PM1, BS1, BP4, BP7	**Likely Benign**	VUS
c.781C>G p.(Asp261Glu)	0.46 (intolerant)	0	0	0	Moderate	0	0	0	Supporting	Supporting	Strong	0	0	0	0	PM1,PP2,PP3, BS1	**Likely Benign**	VUS
c.958C>T (p.Arg320Cys)	1.05 (tolerant)	0	0	0	Moderate	0	0	0	0	Supporting	Strong	0	0	0	0	PM1, PP3, BS1	**Likely Benign**	VUS
c.2251A>G p.(Arg751Gly)	0.6 (slightly intolerant)	0	Strong (the p.Arg751Gly mutant was more severely defective, showing both a 2-fold increase in Km (tRNA) and a 5-fold decrease in kcat, leading to an overall 10-fold decrease in kcat/Km.) we also investigated the impact of this variant on editing activity; however, there was no detectable effect of the mutation on editing function. Yeast expressing p.Arg751Gly ALA1 showed survival comparable to those expressing wild-type ALA1.	0	Moderate	0	0	0	0	Supporting	Strong	0	0	0	0	PS3, PM1, PP3, BS1 (likely path?)	**Likely Benign**	VUS
c.1823C>A p.(Thr608Lys)	0.83 (neutral)	0	0	0	Moderate	Moderate	Supporting	Moderate	0	Supporting	0	0	0	0	0	PM1, PM2, PM5_Supporting, PP1_Moderate, PP3	**Likely pathogenic**	NA
c.385C>G p.(Pro129Ala)	0.68 (slightly intolerant)	0	0	0	Moderate	0	0	0	0	0	Strong	0	0	0	0	PM1, BS1	**Likely Benign**	VUS
c.1815C>G p.(His605Gln)	0.65 (slightly intolerant)	0	0	0	Moderate	Moderate	0	Supporting	0	Supporting	0	0	0	0	0	PM1, PM2, PP1, PP2	**Likely pathogenic**	NA

eSupplementary table 3. Genotypic and clinical characteristics in CMT patients with *AARS1* variants

Author, year of publication	Family	Individual	Variant	Segregation in family	Phenotype	Age at clinical exam	Age at onset of first signs	First presenting features	Motor weakness	Sensory loss	Reflex loss	Motor NCV median nerve (m/s)	Deformity	Asymmetry	CMTNS	6MWT
Latour et al, 2010	1	III.1	c.986G>A p.(Arg329His)	+	CMT2	77	>50	Repeated ankle sprains	LL	LL	LL	32.4				
		III.3				71	50	LL weakness	LL	LL	LL+UL	35				
		III.5				67	15	Repeated ankle sprains	LL+UL	LL+UL	LL+UL	35.7				
		III.6				61	17	Walking difficulties	LL+UL	LL	LL	NA				
		IV.1				50	AS	AS	AS	AS	AS	normal				
		IV.2				54	54	Mild distal LL amyotrophy	NA	NA	NA	45.7		LL		
		IV.3				47	45	Foot deformation	NA	NA	NA	40.8	LL			
		IV.4				49	45	Repeated ankle sprains	LL+UL	LL	LL+UL	50				
		IV.5				54	6	repeated ankle sprains	LL	LL	LL	45		LL		
		IV.7				38	26	Pain and LL weakness	LL	-	LL+UL	44.5				
		IV.8				30	AS	AS	AS	AS	AS	normal				
		IV.9				32	18	LL and hand weakness	LL+UL	LL+UL	LL+UL	36.5				
		IV.10				30	10	REpeated ankle sprains	LL	LL	LL	NA				
		IV.11				41	25	Repeated ankle sprains	LL	LL	LL+UL	40.5				
		IV.12				41	NA	LL weakness	LL	LL	LL	NA				
		IV.13				32	25	LL weakness	LL+UL	-	LL	42.4				
		IV.16				34	22	Cramps in LL	LL	LL	LL	43.5				
		V.1				9	AS	AS	AS	AS	AS	46				
		V.2				28	15	Repeated ankle sprains	LL	LL	LL+UL	NA				
	2	II.1	c.986G>A p.(Arg329His)	+	CMT2	32	14	Walking difficulties	LL	LL	LL	35-39				
Lin et al, 2011	3	II.1	c.211A>T p.(Asn71Tyr)	+	CMT2	51	30	LL weakness	LL+UL	LL+UL	LL+UL	38.1			9	
		I.2				NA	45	LL weakness	LL+UL	LL+UL	LL+UL	NA				
		II.4				NA	40	LL weakness	LL+UL	LL+UL	LL+UL	NA				
		III.2				NA	11	LL weakness	LL+UL	LL+UL	LL+UL	NA				
		II.3				NA	NA	NA	LL	AS	LL+UL	NA				
		II.6				NA	NA	NA	LL	AS	LL+UL	NA				
		III.2				NA	NA	NA	LL	AS	LL+UL	NA				
McLaughlin et al, 2012	4	1	c.986G>A p.(Arg329His)	+	CMT2	NA	NA	LL weakness	LL+NA	NA	NA	NA	LL			
Schabhuttl et al, 2014	5	1	c.1823C>T p.(Thr608Met)	not tested	dHMN	30	20	NA	UL	LL+UL	AS	NA				
Motley et al, 2015	6	II-5	c.304G>C p.(Gly102Arg)	+	CMT2	22	NA adolescence	ankle sprains	LL	LL	LL	49			14	
		II-2				45	22	Gait difficulty, numbness of calves	LL	LL	LL+UL	37			11	
		II-3				46	AS	AS	LL	LL	LL+UL	46			5	
		II-4				44	AS	AS	AS	LL	AS	39			1	
		II-1				48	NA	Numbness in toes	AS	LL	AS	59			7	
Bansagi et al, 2015	7	III.1	c.986G>A p.(Arg329His)	+		50	30	UL weakness	LL+UL	LL+UL	NA	38-50	LL	UL		
		II.4				77	<10	LL weakness	LL+UL	LL+UL	NA	intermed.	LL			
		II.6				70	53	LL weakness	LL	LL	NA	intermed.				
	8	III.1	c.986G>A p.(Arg329His)	+		20	12	LL weakness	LL	LL	NA	40	LL			
	9	III.1	c.986G>A p.(Arg329His)	+		32	28	UL and LL weakness	LL+UL	LL+UL	NA	43	LL	LL+UL		
		II.1				59	0	LL weakness	LL	LL	NA	NA				
	10	II.2	c.986G>A p.(Arg329His)	+		55	30	LL weakness	LL+UL	LL+UL	NA	26				
		II.5				49	18	LL weakness	LL+UL	LL	NA	intermed.	LL	LL+UL		
	11	IV.5	c.986G>A p.(Arg329His)	+		46	<10	LL weakness	LL+UL	LL	NA	39				
		V.1				10	<10	LL weakness	LL	LL	NA	47.6				
	12	II.3	c.2063A>G p.(Glu688Gly)	+		37	<10	LL weakness	LL+UL	LL+UL	NA	NA				
		III.1				6	<1	LL weakness	LL+NA	LL+NA	NA	36.8				
		III.2				5	<1	LL weakness	LL+NA	LL+NA	NA	29.3				
Lasshuthova et al, 2016	13	3/III	c.986G>A p.(Arg329His)	+	CMT2	NA	NA	NA	NA	NA	NA	NA				
		3/IV				NA	NA	NA	NA	NA	NA	NA				
		4/VI				NA	NA	NA	NA	NA	NA	NA				
		4/V				31	10	Difficulties running, jumping	LL	LL+AL	LL+AL	NA				
	14	3/I	c.986G>A p.(Arg329His)	+	NA	NA	NA	NA	NA	NA	NA	NA				
		4/I				NA	NA	NA	NA	NA	NA	NA				
	15	1/I	c.986G>A p.(Arg329His)	+	NA	NA	NA	NA	NA	NA	NA	NA				
		2/I				NA	NA	NA	NA	NA	NA	NA				
Weterman et al, 2018	16	III-1	c.1880C>T p.(Ser627Leu)	+	CMT2	50	30	NA	LL+UL	LL+UL	LL+UL	NA				
		IV				26	NA	NA	LL	LL	LL	39	LL			
	17	III-3	c.1009G>A p.(Glu337Lys)	+	CMT2	62	7	NA	LL	LL	LL	34				
		III-4				65	17	NA	LL+NA	LL+NA	LL+NA	11				
		IV-1				30	NA	NA	LL	LL	LL	38	LL			
		IV-2				26	NA	NA	LL+UL	AS	LL	40				
		IV-3				23	NA	NA	NA	NA	NA	37				
		IV-5				38	35	NA	LL	LL	LL	39	LL			
	18	II.7	c.976C>T p.(Arg326Trp)	+	CMT2	65	60	NA	LL	LL	LL	AS	LL			
		II.10				62	NA	NA	LL+UL	AS	LL	NA				
		II.13				62	29	NA	LL+UL	AS	LL	NA				
		II.4				70	10	NA	LL	AS	LL	NA				
		III.48				50	30-40	NA	AS	AS	AS	NA				
		III.46				42	35-40	NA	LL+UL	AS	LL+UL	NA	LL			
		III.35				49	44	NA	LL	LL	LL	NA	LL			
Bacquet et al, 2018	19	18	c.986G>A p.(Arg329His)	NA	CMT1	NA	43	NA	LL+UL	LL+UL	LL+UL	25	LL			
	20	60	c.986G>A p.(Arg329His)	NA	CMT2	NA	20	NA	LL+UL	LL+UL	NA	NA				
Lousa et al, 2018	21	1	c.986G>A p.(Arg329His)	+	CMT2	NA	NA	NA	NA	NA	NA	NA				
		2				NA	NA	NA	NA	NA	NA	NA				
		3				NA	NA	NA	NA	NA	NA	NA				
Hsu et al, 2019	22	1	c.211A>T p.(Asn71Tyr)	NA	CMT2	NA	30	NA	NA	NA	NA	NA				
Lee et al, 2020	23	IV-1	c.986G>A p.(Arg329His)	+	CMT2	15	7	LL weakness	LL+UL	LL+UL	LL+UL	28.4	LL		7	
		III-8				46	8	LL weakness	LL	LL	LL+UL	36.8	LL		9	
Volodarsky et al, 2021	24	1	c.1823C>T p.(Thr608Met)	nt	CMT	NA	NA	NA	NA	NA	NA	NA				
	25	1	c.1388T>C p.(Ile463Thr)	nt	CMT	NA	NA	NA	NA	NA	NA	NA				
	26	1	c.1388T>C p.(Ile463Thr)	nt	CMT	NA	NA	NA	NA	NA	NA	NA				
	27	1	c.986G>A p.(Arg329His)	nt	CMT	NA	NA	NA	NA	NA	NA	NA				
	28	1		nt	CMT	NA	NA	NA	NA	NA	NA	NA				
	29	1		nt	CMT	NA	NA	NA	NA	NA	NA	NA				
	30	1		nt	CMT	NA	NA	NA	NA	NA	NA	NA				
This study	31	1/III-3	c.1823C>A p.(Thr608Lys)	+	CMT2	36	15	LL weakness	LL	LL	LL+UL	38,1	LL	LL	5	500
		1/IV-7			CMT2	16	10	Excersise intolerance	AS	AS	LL+UL	48,7			1	
	32	2/III-1	c.1815C>G p.(His605Gln)	+	CMT2	57	10	Exercise intolerance	LL	LL	LL	45.4	LL	LL	13	340
		2/IV-1				17	4	Exercise intolerance	AS	LL	LL	45.7			3	
		2/III-2				59	11	LL weakness	LL	LL	LL	43.9	LL	LL	14	370

CMT - Charcot-Marie-Tooth disease; LL - lower limbs; UL - upper limbs, AS - asymptomatic; NA - not available; NCV - nerve conduction velocity; CMTNS - CMT Neuropathy Score; 6MWT - 6 minute walk test