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General Article

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GENERAL ARTICLE

Characterization of molecular mechanisms underlying the axonal Charcot–Marie–Tooth neuropathy caused by *MORC2* mutations

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Abstract

Mutations in *MORC2* lead to an axonal form of Charcot–Marie–Tooth (CMT) neuropathy type 2Z. To date, 31 families have been described with mutations in *MORC2*, indicating that this gene is frequently involved in axonal CMT cases. While the genetic data clearly establish the causative role of *MORC2* in CMT2Z, the impact of its mutations on neuronal biology and

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their phenotypic consequences in patients remains to be clarified. We show that the full-length form of MORC2 is highly expressed in both embryonic and adult human neural tissues and that Morc2 expression is dynamically regulated in both the developing and the maturing murine nervous system. To determine the effect of the most common MORC2 mutations, p.S87L and p.R252W, we used several *in vitro* cell culture paradigms. Both mutations induced transcriptional changes in patient-derived fibroblasts and when expressed in rodent sensory neurons. These changes were more pronounced and accompanied by abnormal axonal morphology, in neurons expressing the MORC2 p.S87L mutation, which is associated with a more severe clinical phenotype. These data provide insight into the neuronal specificity of the mutated MORC2-mediated phenotype and highlight the importance of neuronal cell models to study the pathophysiology of CMT2Z.

Introduction

The Charcot–Marie–Tooth (CMT) disease is the most frequently inherited neurological disease with a prevalence of 28/100000 and refers to a clinically heterogeneous demyelinating or axonal neuropathy that affects peripheral nerves (1–3). More than 80 genes have been linked to different forms of CMT (Neuromuscular Disease Center; http://neuromuscular.wustl.edu/time/hmsn.html). As a part of our ongoing effort to identify new genes implicated in CMT, we recently detected a novel variant c.568C>T (p.R190W) in *MORC2* in an axonal CMT family [4]. The mutational screening of *MORC2* in available clinical cohorts allowed the diagnosis of two additional sporadic cases: one with the same mutation and the other with a novel missense mutation c.74C>T (p.S25L) (4). The c.568C>T (p.R190W) and the c.74C>T (p.S25L) mutations are also named c.754C>T (p.R252W) and c.260C>T (p.S87L), based on the isoform encoding the NM_001303256 MORC2 transcript (5).

Currently, 31 families have been identified with mutations in *MORC2*, showing its frequent implication in CMT in various populations (4–13). This new form of axonal CMT (CMT2Z; MIM 616688) presents with a number of both early and late onset heterogeneous clinical features, including a spinal muscular atrophy (SMA) phenotype, axonal neuropathy with pyramidal signs, distal and proximal weakness in an asymmetric and random manner associated with important sensory loss and the appearance of cerebellar atrophy and diaphragmatic paralysis. The most frequent mutation is the p.R252W that represents more than 50% of cases (4–13).

Microrchidia (MORC) family CW-type zinc finger 2 (MORC2) is a member of the MORC protein family (14,15) conserved in higher eukaryotes. Four MORC proteins have been predicted in humans that share multiple conserved domains: a GHL (Gyrase B, Hsp90 and MutL)-ATPase domain at the amino-terminus, a CW-type zinc finger domain and three predicted coiled-coil domains. The following several functions have been attributed to MORC2: gene transcriptional repression in gastric cancer cells (16); promotion of breast cancer invasion and metastasis (17); interaction with ATP-citrate lyase (ACLY), involvement in lipogenesis and adipogenesis (18); transcriptional regulation of ArgBP2, which is part of the actin-dependent processes such as cell adhesion and migration (19); and as substrate of PAK1 (p21-activated kinase 1), an integrator of extracellular signals and nuclear processes (20). Importantly, MORC2 also functions as an effector of epigenetic silencing by the human silencing hub (HUSH) complex (21). Dimerization and DNA binding of the MORC2 ATPase module was shown to be implicated in HUSH-mediated repression (22).

In this study, the characterization of MORC2 expression reveals its dynamic regulation in the developing and mature peripheral and central nervous systems. To investigate the pathophysiological mechanism underlying neurodegeneration caused by *MORC2* mutations, various cellular models, including HeLa cells, patient-derived fibroblasts and primary neuronal cultures, have been used. Our data indicate that while *MORC2* mutations result in transcriptional changes in non-neuronal cells, the pathogenic phenotype is more pronounced in neurons, where detectable axonal alterations were observed. These data provide insight into the neuronal specificity of the MORC2-mediated disease phenotype and highlights the importance of neuronal-based cellular models to study the pathophysiology of CMT2Z.

Results

Analysis of the expression of MORC2 isoforms in human nervous tissues

The human *MORC2* gene is transcribed as two transcripts NM_001303256 (5657 bp) encoding a 1032 aa protein (NP_001290185) and the NM_014941 (6052 bp) encoding a protein of 970 aa (NP_055756). Due to the presence of an additional exon containing several STOP codons, the translation of the longer transcript (NM_014941) is initiated at an in-frame downstream start codon resulting in the shorter 970 aa protein (NP_055756; Fig. 1A). The two mutations presented in this manuscript can therefore be named p.S25L and p.R190W based on the short protein isoform (NP_055756, 970 aa) or p.S87L and p.R252W based on the long protein isoform (NP_001290185, 1032 aa; Fig. 1A).

To establish which MORC2 isoform is present in human nervous tissues, we used a real time-PCR (RT-PCR)-based approach. Three specific primer pairs were designed to amplify cDNA templates prepared from human dorsal root ganglia (DRG) collected at different developmental stages and from adult spinal cord. Using primer pairs hMORC2_1F/R and hMORC2_2F/R, we detected a 155 bp and a 114 bp amplicons, which both correspond to NM_001303256 encoding the longer (1032 aa) MORC2 protein (Fig. 1A and B). The lack of amplification of the 1021 bp amplicon with the hMORC2_1F/R primers indicates that the NM_001303256 transcript is predominantly expressed in the first trimester embryonic and adult human neural tissues. This observation was confirmed by using hMORC2_3F/R primers specific for the NM_014941 transcript encoding the 970 aa protein isoform. PCR amplification did not detect the expected 131 bp amplicon in spinal cord samples and only a very weak expression of this amplicon was observed in the DRG tissue (Fig. 1A and B). Similar results were obtained using the human neuronal and non-neuronal cell lines SH-SY5Y and HeLa, respectively (Supplementary Material, Fig. S1). Together, these data demonstrate that the transcript NM_001303256 encoding the long (1032 aa) isoform of the MORC2 protein is the predominant form expressed in neural tissues.

Spatiotemporal expression profile of *Morc2* in mice

Quantitative PCR (qPCR)-based profiling revealed that *Morc2* is dynamically regulated in brain with a peak in expression at E17.5 to P2 followed by lower levels of expression at P10 and during

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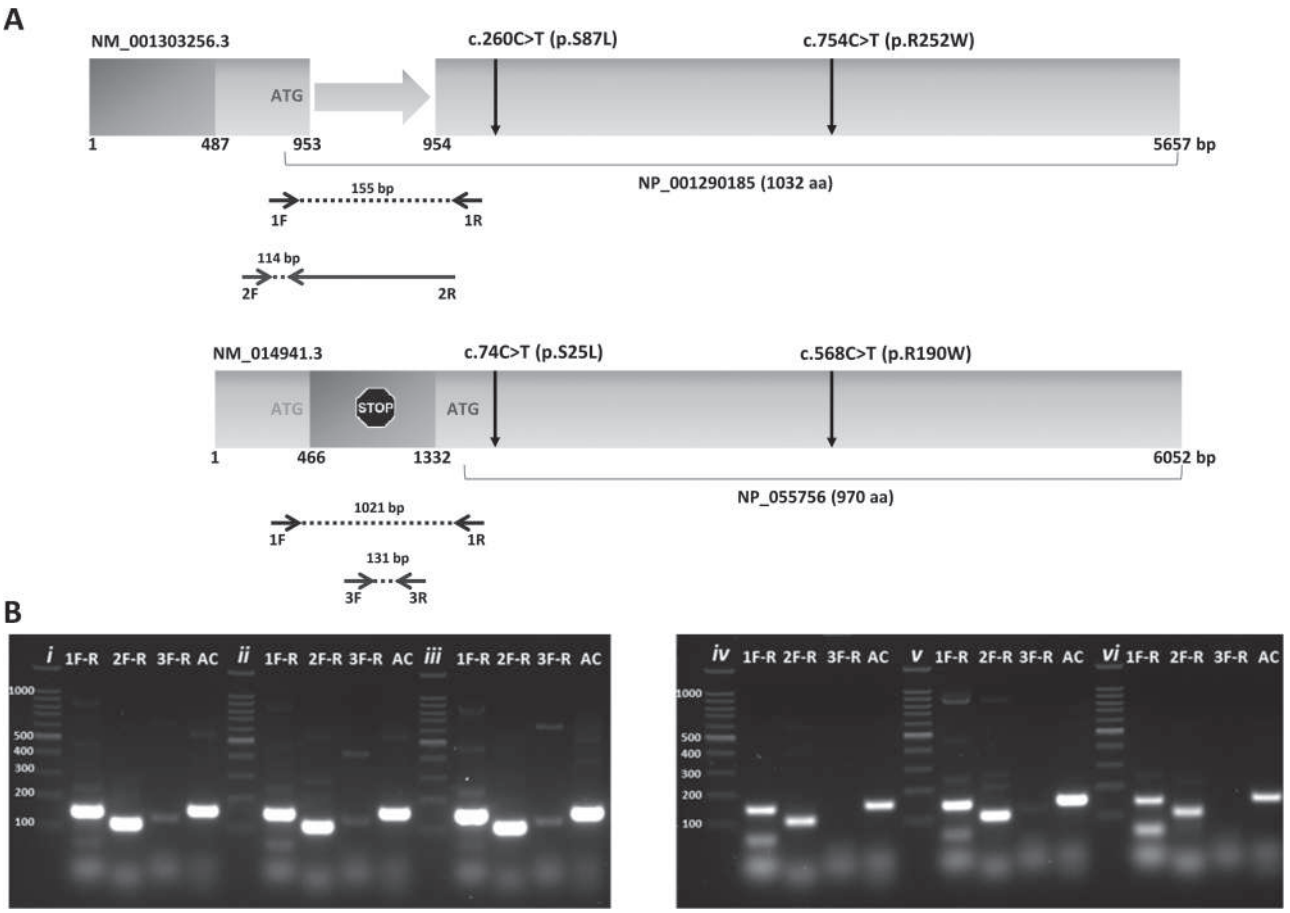

Figure 1. Characterization of the expression of MORC2 isoforms in nervous system. **(A)** Schematic representation of the two MORC2 transcripts showing the position of designed primers and amplicon sizes. Primer pair 1F-1R was designed to amplify the two isoforms with different amplicon sizes (155 bp for NM_001303256 and 1021 bp for NM_014941); primer pair 2F-2R was designed to amplify only the NM_001303256 isoform with an amplicon size of 114 bp. Primer pair 3F-3R was designed internally to the absent fragment in NM_001303256, to specifically amplify the NM_014941 with an amplicon of size of 131 bp. **(B)** RT-PCR characterization of MORC2 expression using the aforementioned primers and cDNA template prepared from DRGs isolated from aborted human embryos of different ages (i: 7.5 weeks, ii: 8–8.5 weeks, iii: 9 weeks) and neurons isolated from adult spinal cord (iv and v: cervical region, vi: lumbar region). Human *actin* was used as a control (AC).

adulthood (Fig. 2A and B). A substantial developmental decrease was also observed in the spinal cord and in the sciatic nerve. Additionally, *Morc2* was expressed in E17.5 DRG as well as in primary cultures of Schwann cells and DRG sensory neurons (Fig. 2A and B). Western blot analysis using samples from brain and sciatic nerves revealed a similar protein expression profile to the mRNA analysis. Morc2 protein showed peak expression at the earlier stages with a progressive decrease during aging (Fig. 2C and D).

Molecular pathomechanism of the *MORC2* mutations

Since we identified the first two *MORC2* mutations in three unrelated CMT2Z families (4), a total of 31 families have now been reported (5–13). Our ongoing characterization of CMT patients identified two additional CMT2Z families, one carrying the p.R252W mutation and another one with a novel missense variant c.1217C>T (p.A406V) (23). Taking into account the known 33 CMT2Z families, the most frequent mutation is p.R252W (17 cases; 51.5% of CMT2Z cases; Fig. 3A). In 15 out of the 17 families with the p.R252W mutation, the mutational event occurred *de novo*. The cytosine nucleotide (c.754C) involved with the p.R252W mutation is located in a CpG dinucleotide. Using sodium bisulphite sequencing of control DNA, 5mC cytosine nucleotides were identified in genomic DNA surrounding the c.C754T change. Primers were designed to amplify a 278 bp amplicon containing the c.754C nucleotide. A total of 15 cytosines were identified and analyzed in the amplicon with >99% of the non-CpG dinucleotide cytosines being converted to thymidine reflecting their unmethylated status (Fig. 3B). In contrast, the cytosines located in CpG dinucleotides were mostly unconverted (Fig. 3B). In particular, the cytosine nucleotide giving rise to the p.R252W was unconverted to thymidine in 12 of the 19 bisulphite-treated DNA clones assessed indicating the predominantly methylated status of c.754C potentially contributing to its behavior as a mutational hotspot (Fig. 3B).

To date, the 10 different MORC2 mutations are known to be located in the ATPase domain (p.S87L, p.R132L, p.E236G and p.R252W), or next to this domain, in a transition position between the first coiled-coil and the CW-type finger domain (p.Q400R, p.C407Y, p.A431V, p.T424R, p.D466N and p.A406V) with relative homology with the ribosomal S5 domain (21) (Fig. 4A). A more detailed analysis was undertaken on p.R252W, which is the most frequent mutation, and on p.S87L, which is reported to be associated with the most severe CMT2Z phenotype (4). Since both mutations are located in the ATPase domain of the

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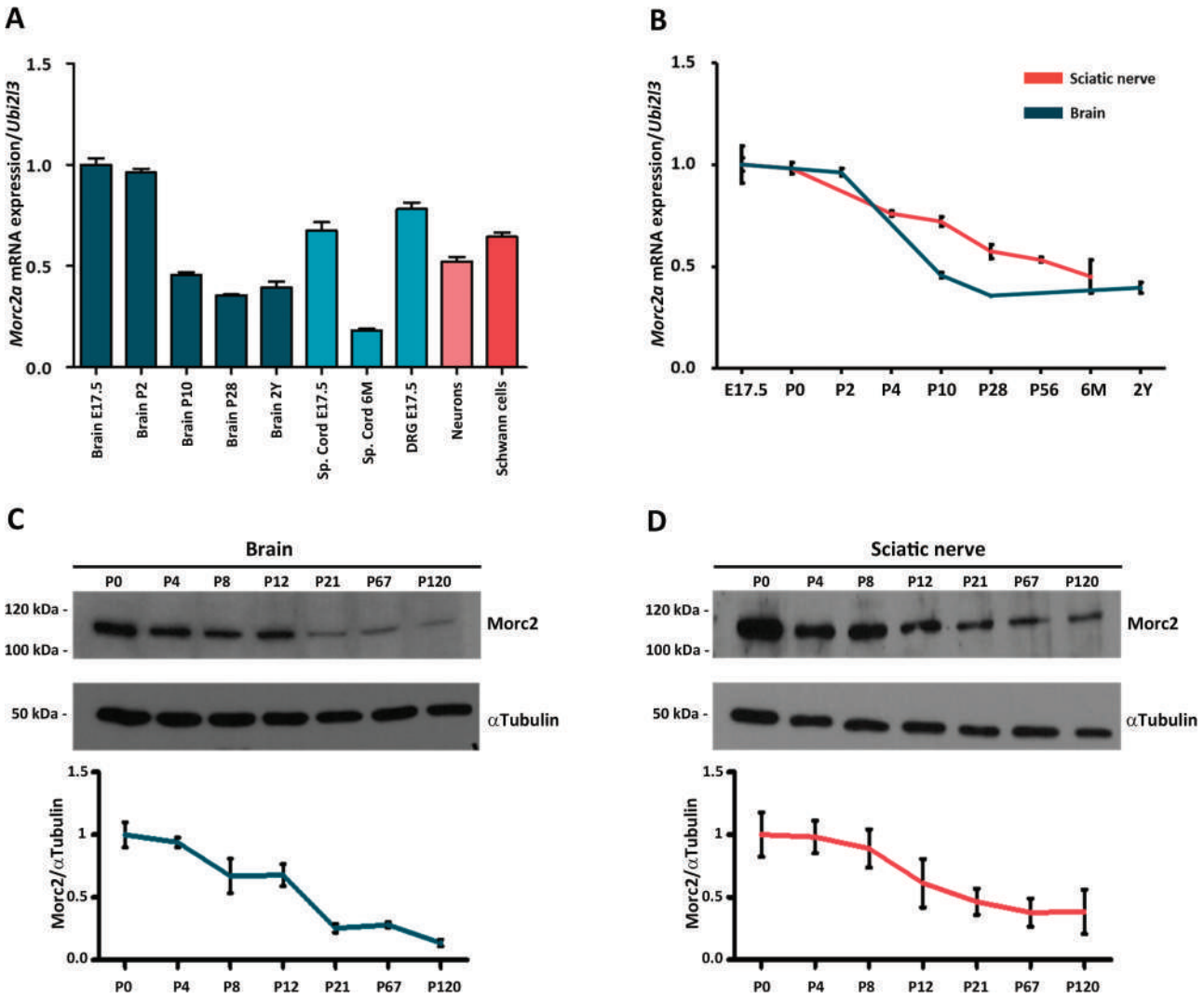

Figure 2. Characterization of the Morc2 expression profiles during neuronal development. **(A and B)** qPCR of the *Morc2a* expression in several mice nervous tissues and cells. The relative expression levels of *Morc2a* at the different time points were normalized using Ubiquitin (*Ubi2l3*) with the brain expression at E17.5 being set to 1. **(C and D)** Western blot-based quantification of Morc2 protein in mice brain (C) and sciatic nerve (D) samples isolated at selected time points. α Tubulin was used to normalize the amount of loaded protein. The relative protein levels for each time point were obtained using the brain at P0 set as +1. E = Embryonic stage, P = Post-natal day, M = Months, Y = Years.

MORC2 protein, we first evaluated if these mutations altered ATPase activity. Western blot analysis was used to confirm the stability of overexpressed wild-type (WT) and mutated MORC2 in HeLa cells (Fig. 4B). A colorimetric ATPase assay performed in transiently transfected HeLa cells showed that the p.S87L caused a significant reduction of the ATPase activity when compared with WT activity, while the p.R252W mutation did not (Fig. 4C).

MORC2 is known to promote the phosphorylation and activity of ACLY, an enzyme involved in the formation of acetyl-coA in the cytoplasm (18). Acetyl-coA is a substrate for choline acetyl transferase, an enzyme involved in the production of acetylcholine that is a key molecule for neuronal function and survival (24). As the ATPase activity was not affected by the p.R252W mutation we evaluated if the most common mutation could affect ACLY activity, by using a previously described malate dehydrogenase (MDH) enzyme activity assay to indirectly assess ACLY activity (25). However, the assay showed that there was no difference in MDH enzyme activity between patient p.R252W and control fibroblasts (Supplementary Material, Fig. S2).

Characterization of human fibroblasts derived from CMT2Z patients

To date, expression of MORC2 has been described mainly in the nucleus, where the majority of the MORC2 functions have been reported, and to a lesser extent, in the cytoplasm (18). By immunofluorescence analysis of control and CMT2Z patient skin biopsy-derived fibroblasts, we confirmed the previously described location for MORC2 in the nucleus and cytoplasm (Fig. 5A). Neither the p.R252W or p.S87L mutations showed an altered pattern of cellular localization. Similar findings were obtained using transfected HeLa cells (Supplementary Material, Fig. S3).

Since MORC2 was previously characterized as a transcriptional regulator (21), transcriptome analysis was used to evaluate changes in the mRNA profile of fibroblasts derived from patients carrying CMT2Z mutations. We observed a high number of genes with altered expression for both mutations compared with control, but in particular for the fibroblast

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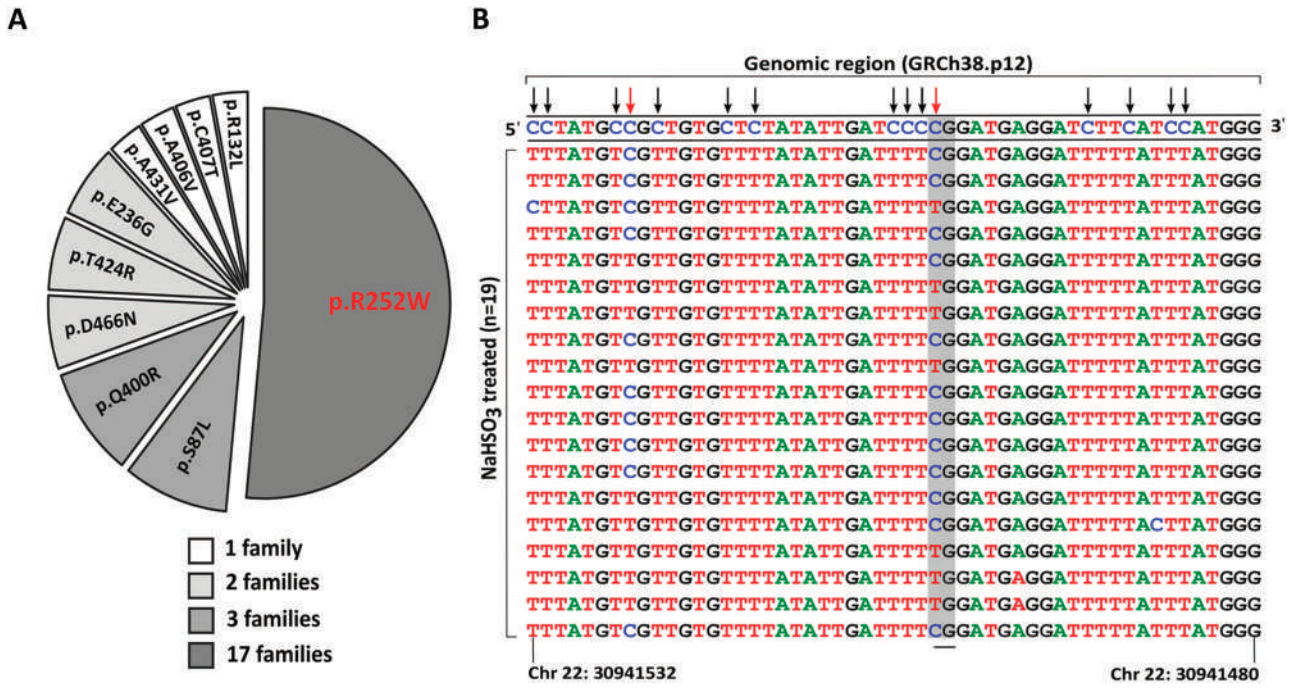

Figure 3. Genetics of CMT2Z. **(A)** Distribution of MORC2 mutations identified in CMT2Z patients, using protein nomenclature (NP_001290185). **(B)** Characterization of the methylation status of CpG dinucleotides in exon 10 of the *MORC2* gene (NM_001303256) using bisulphite sequencing analysis. Sequence from n = 19 clones of bisulphite-treated DNA containing the c.754C nucleotide are aligned to the genomic consensus sequence (underlined sequence on the top of the panel). Converted (black arrows) and non-converted (red arrows) cytosines are shown. Non-CpG cytosines are converted to thymidine and most of the CpG cytosines for each clone remain unchanged, which indicates that nucleotide position c.754 can have 5-methylcytosine nucleotides. The CpG dinucleotide containing c.754C is remarked in gray.

transcriptome of the p.R252W mutation in which we noted more than 800 dysregulated genes when compared with the control fibroblast transcriptome (Fig. 5B). The clustering by functional groups for the genes with altered expression resulted in four different enrichment categories: zinc finger (*ZNF*), homeobox, helicases and metallothionein genes (Fig. 5C). Importantly, the transcriptomics approach showed a high percentage of repressed *ZNF*-family genes in both mutants (Fig. 5D), matching the data generated using other cellular models (21).

Neuronal features induced by overexpression of mutated MORC2 in rodent sensory neurons

Although transcriptome analysis identified evidence of an altered expression profile in patients' fibroblasts, the staining of cells with MORC2 did not show abnormal localization of the protein. Studies were therefore undertaken to evaluate the impact of MORC2 mutations in neuronal cells, which represent a relevant tissue likely to be contributing to the neurological phenotype of CMT2Z. Purified DRG sensory neurons from E15.5 rat embryos were transduced with lentivirus particles inducing expression of green fluorescent protein (GFP), WT-MORC2 or mutant (p.S87L and p.R252W) MORC2. Transduction efficiency was similar for different viral constructs (Supplementary Material, Fig. S4). Moreover, the three forms of MORC2 showed substantial overexpression of both RNA and protein in infected neurons, while MORC2 expression was undetectable in non-transduced neurons and neurons overexpressing the lentiviral GFP alone (Supplementary Material, Fig. S5). The morphology of the somas of infected neurons was unaltered by overexpression of WT or mutated forms of MORC2 (Fig. 6). The expression of endogenous Morc2 and overexpressed forms of MORC2 were predominantly detected in the nuclei of the cells. However, all forms of MORC2 were also detected in the axons (Fig. 6). Strikingly, detailed analysis of axons using SMI32 staining revealed the presence of axonal swellings in neurons expressing the p.S87L mutation (Fig. 7A). Further quantification confirmed this observation for the p.S87L mutation while the p.R252W-expressing neurons had an axonal morphology similar to the neurons expressing WT-MORC2 (Fig. 7B). As observed in sensory neurons, all forms of MORC2 also predominantly localized to the nuclei of the Schwann cells whereas the expression was undetectable in Schwann cells transfected with the plasmid containing GFP as a control (Fig. S6).

Transcriptional analysis of rat sensory neurons expressing mutated forms of MORC2

In order to perform an in-depth characterization of the consequences of the MORC2 mutated isoforms, a gene expression microarray analysis was performed. This approach was conducted on rat DRG sensory neurons expressing the WT-MORC2, the two mutated forms of MORC2 or GFP. The overexpression of the human WT-*MORC2* gene slightly altered the transcriptome profile of rat sensory neurons when compared with GFP-expressing neurons; 37 genes were upregulated and 14 showed reduced expression (Supplementary Material, Table S1). However, there was a substantial difference in the expression profiles for the two clinical variants (Fig. 8A). The analysis of the p.S87L mutation revealed that 209 genes were upregulated and 77 genes downregulated (Supplementary Material, Table S2). For the p.R252W mutation, 99 genes were found to be upregulated and 56 genes downregulated (Supplementary Material, Table S3) when compared with the GFP control.

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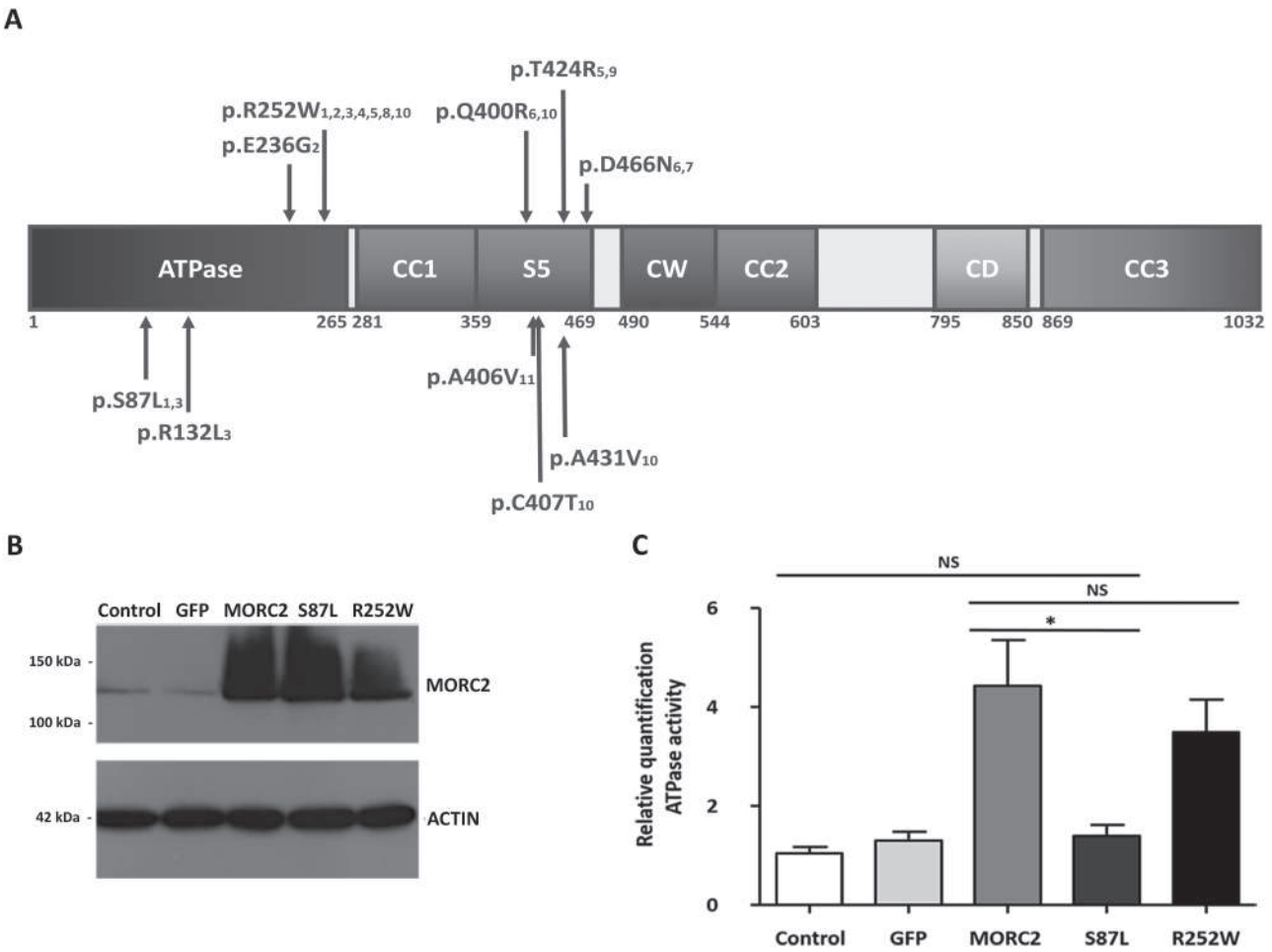

Figure 4. The level of ATPase activity in HeLa cells expressing WT and mutated forms of MORC2. **(A)** Schematic representation of MORC2 protein structure with the localization of mutations identified in CMT2Z patients. CC1, 2 and 3: coiled-coil domains; S5: ribosomal protein S5 domain; CW: CW-type finger domain; CD: Chromo-like domain. $_1$Sevilla *et al.* (4); $_2$Albulym *et al.* (5); $_3$Hyun *et al.* (8); $_4$Lassuthova *et al.* (6); $_5$Schottmann *et al.* (10); $_6$Zhao *et al.* (7); $_7$Semplicini *et al.* (11); $_8$Bansagi *et al.* (9); $_9$Zanni *et al.* (12); $_{10}$Ando *et al.* (13); $_{11}$Frasquet *et al.* (23). **(B)** Western blot demonstrating the relative level of MORC2 protein expression in HeLa cells transfected with the different isoforms of MORC2 and transduction controls. **(C)** ATPase assay in HeLa cells transduced with expression constructs for GFP and the different isoforms of MORC2. The enzymatic activity (U/mL) was normalized to the control (Activity ATPase Control = 1). *$P < 0.05$, NS = Not significant.

By investigating the transcriptome-wide changes and integrating diverse types of biological data to determine pathways and networks of interest, three families of enriched genes were identified in samples expressing both mutations: *ZNF* genes, homeobox genes and neurotransmitter receptors. In addition, the kinesin family was exclusively altered in transcriptome data from the p.S87L mutant (Fig. 8B).

To investigate a possible interaction between *MORC2* and genes causing other forms of CMT, the expression of 118 rat orthologous genes associated with inherited peripheral neuropathies in humans was analyzed (Supplementary Material, Table S4). Interestingly, both mutations were associated with a strong decrease in expression of *Hspb1* ($P < 0.05$; Fig. 8C), a gene known to cause CMT type 2F (CMT2F; MIM 606595) and distal hereditary motor neuropathy (dHMN) type IIB (dHMN2B; MIM 608634) (26). The reduced *Hspb1* expression was also confirmed by qPCR (Fig. 8D).

The *ZNF* genes represent the largest family of primate transcription factors. Thirteen *ZNF* genes were differentially expressed when comparing p.S87L and control expression profiles, with three genes significantly upregulated and ten genes downregulated ($P < 0.05$). Five dysregulated *ZNF* genes were identified when comparing p.R252W with control expression profiles, with one gene upregulated and four downregulated ($P < 0.05$; Supplementary Material, Table S5). Altered expression levels in *ZNF* genes as repressed targets of p.R252W have previously been reported (21), and similar findings were observed using human fibroblasts (Fig. 5C).

A total of four homeobox genes were significantly dysregulated ($P < 0.01$; Fig. 8B; Supplementary Material, Table S6), which is similar to the patient fibroblast data (Fig. 5C). Both mutations showed upregulation of the *Gsc*, *Hoxb13* and *Hoxc10* genes. Additionally, *Hoxc6* was upregulated in p.S87L and *Hoxb8* in p.R252W (Supplementary Material, Table S6). Strikingly, changes in expression of the *Hoxb13* represent one of the highest log fold changes observed in the transcriptome analysis.

The observed expression changes in neurotransmitter receptors and kinesins are most likely relevant for the pathophysiology of the human disease, since these families of genes may reflect pathological changes and/or compensatory mechanisms in neurons affected by CMT2Z. Within the group of neurotransmitter receptors, five genes were differentially expressed in p.S87L versus the control, with four genes upregulated and one gene significantly downregulated. Comparison of expression

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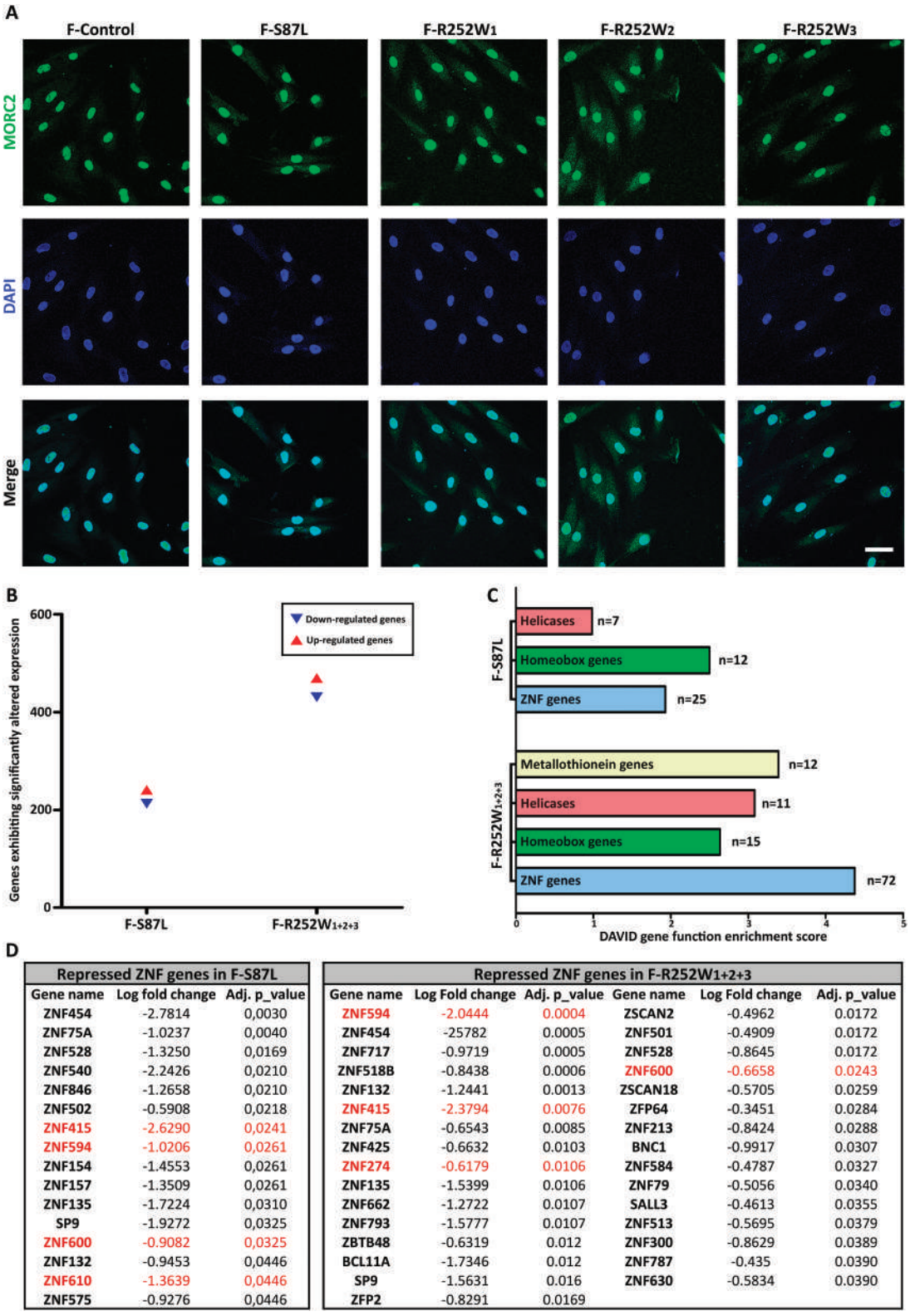

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Repressed ZNF genes in F-S87L		
Gene name	Log fold change	Adj. p_value
ZNF454	-2.7814	0,0030
ZNF75A	-1.0237	0,0040
ZNF528	-1.3250	0,0169
ZNF540	-2.2426	0,0210
ZNF846	-1.2658	0,0210
ZNF502	-0.5908	0,0218
ZNF415	-2.6290	0,0241
ZNF594	-1.0206	0,0261
ZNF154	-1.4553	0,0261
ZNF157	-1.3509	0,0261
ZNF135	-1.7224	0,0310
SP9	-1.9272	0,0325
ZNF600	-0.9082	0,0325
ZNF132	-0.9453	0,0446
ZNF610	-1.3639	0,0446
ZNF575	-0.9276	0,0446

Repressed ZNF genes in F-R252W1+2+3					
Gene name	Log Fold change	Adj. p_value	Gene name	Log Fold change	Adj. p_value
ZNF594	-2.0444	0.0004	ZSCAN2	-0.4962	0.0172
ZNF454	-25782	0.0005	ZNF501	-0.4909	0.0172
ZNF717	-0.9719	0.0005	ZNF528	-0.8645	0.0172
ZNF518B	-0.8438	0.0006	ZNF600	-0.6658	0.0243
ZNF132	-1.2441	0.0013	ZSCAN18	-0.5705	0.0259
ZNF415	-2.3794	0.0076	ZFP64	-0.3451	0.0284
ZNF75A	-0.6543	0.0085	ZNF213	-0.8424	0.0288
ZNF425	-0.6632	0.0103	BNC1	-0.9917	0.0307
ZNF274	-0.6179	0.0106	ZNF584	-0.4787	0.0327
ZNF135	-1.5399	0.0106	ZNF79	-0.5056	0.0340
ZNF662	-1.2722	0.0107	SALL3	-0.4613	0.0355
ZNF793	-1.5777	0.0107	ZNF513	-0.5695	0.0379
ZBTB48	-0.6319	0.012	ZNF300	-0.8629	0.0389
BCL11A	-1.7346	0.012	ZNF787	-0.435	0.0390
SP9	-1.5631	0.016	ZNF630	-0.5834	0.0390
ZFP2	-0.8291	0.0169			

Figure 5. Characterization of human fibroblasts derived from CMT2Z patients carrying mutations S87L and R252W. **(A)** Immunofluorescence-based analysis of MORC2 subcellular localization in fibroblast cultures. Scale bar = 50 µm. **(B)** Number of genes exhibiting significantly altered expression using a human fibroblast line derived from a healthy subject as a control. Blue triangles are showing repressed genes and the red ones indicate the overexpressed genes. **(C)** DAVID gene function enrichment score for the patient fibroblast lines. **(D)** List of repressed *ZNF* genes for the patient fibroblast lines. Genes in red were previously described to be regulated by MORC2 (21). F-Control = Fibroblast line derived from healthy control, F-S87L = Fibroblast line derived from a patient carrying the p.S87L mutation, F-R252W = Fibroblast line derived from patients carrying the p.R252W mutation (1, 2 or 3), F-R252W$_{1+2+3}$ = average of transcriptomic results obtained in three patients with MORC2 p.R252W mutation.

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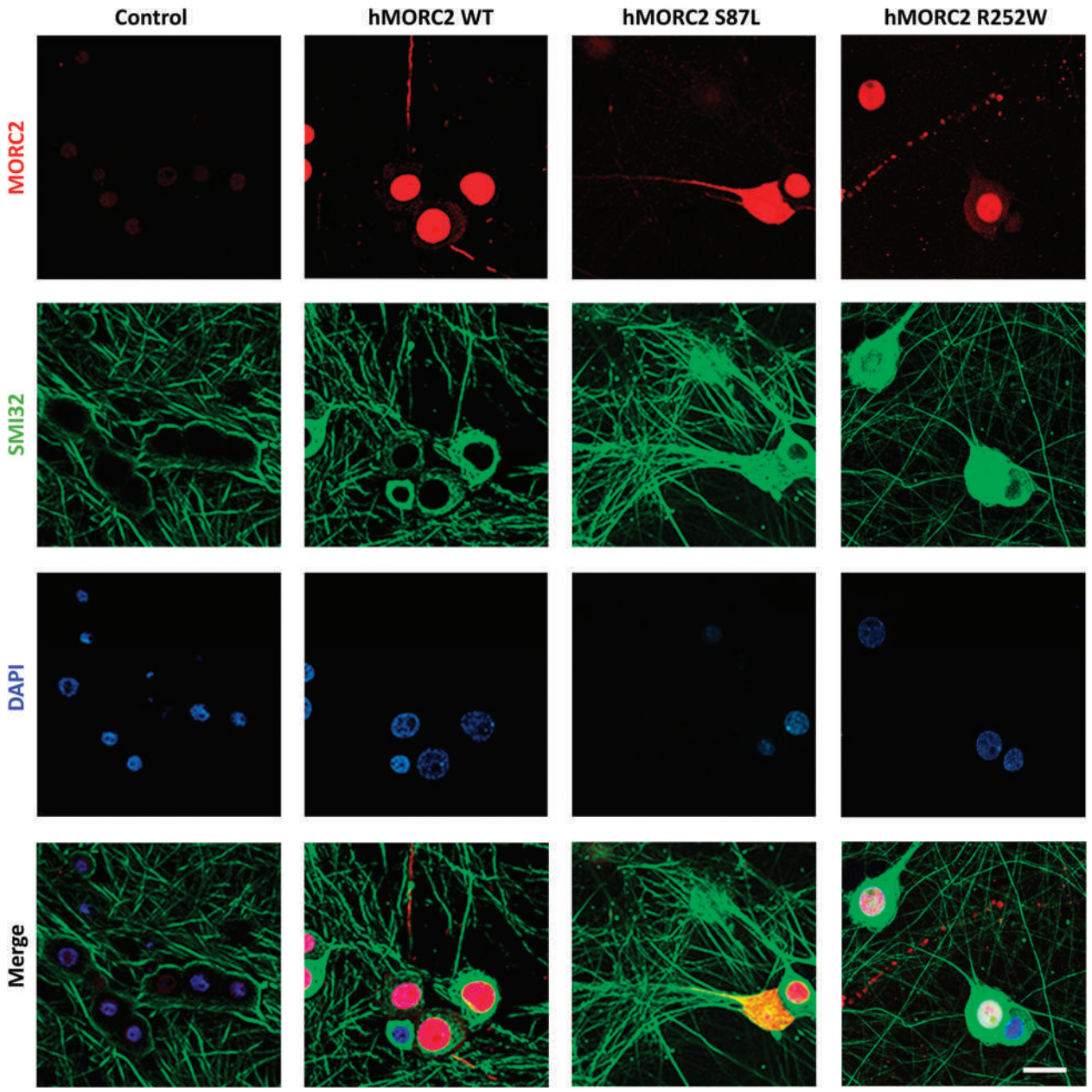

Figure 6. MORC2 expression in purified rat sensory neurons. Analysis of MORC2 subcellular localization in neuronal cultures infected with viruses carrying depicted constructs. Virally mediated gene expression was induced for 4 days with doxycycline. Scale bar = 20 μm.

between p.R252W and the control identified seven upregulated and two downregulated genes (Fig. 8C). Finally, five kinesin transcripts specifically upregulated in p.S87L were detected (Fig. 8C). The latter could highlight a possible defect in anterograde axonal transport that could contribute to the observed axonal swelling phenotype, which was induced by this mutation in sensory neuron cultures. Validation of gene expression changes in various neurotransmitter receptors was carried out by qPCR including GABA (gamma-aminobutyric acid) receptors (*Gabra1*, *Gabra5* and *Gabrb1*) implicated in GABAergic neurotransmission in the mammalian central nervous system, and the *Grik3* encoding a glutamate receptor (Fig. 8D). Overexpression of *Kif18b*, *Kifc1* and *Kif11*, which was exclusively found with the p.S87L mutation, was confirmed by qPCR (Fig. 8D).

Discussion

Including this work, 33 CMT2Z cases have been reported so far (4–13). In this study, we provide insight into the phenotypic variation of two different MORC2 mutations leading to clinical presentations ranging from axonal CMT to severe SMA.

In humans, two MORC2 transcripts have been annotated and we have shown that the transcript NM_001303256, encoding the MORC2 1032 aa protein, is the predominant isoform expressed in neural tissues and occurs in a controlled, spatiotemporal manner. Both the Morc2 transcript and protein show peak expression at the earlier stages with a progressive decrease during aging suggesting distinct roles in developing and mature nervous systems. Interestingly, the complete loss-of-function murine model

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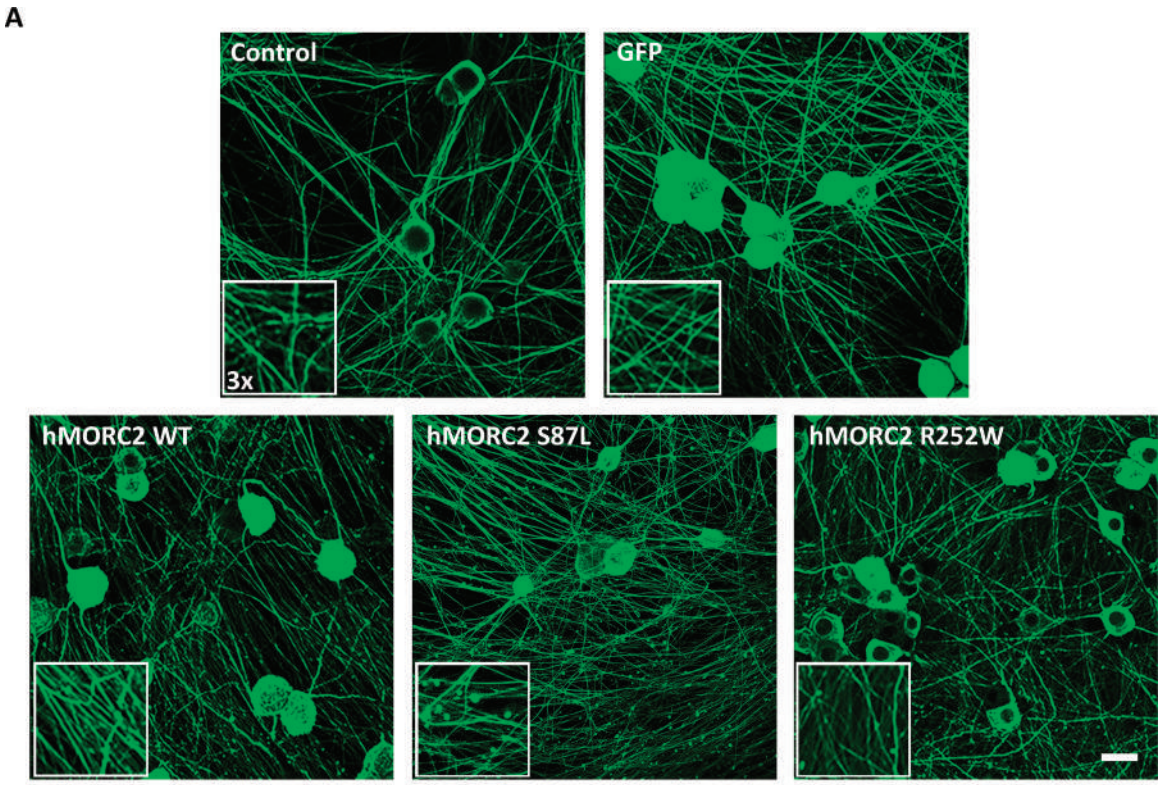

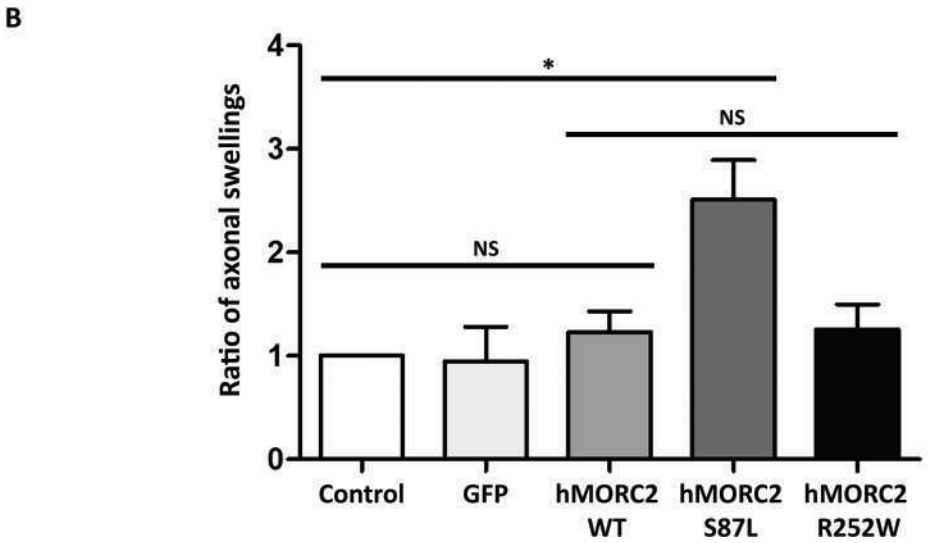

Figure 7. Analysis of axonal swellings induced by MORC2 expression in neuronal cultures. **(A)** Neurofilament (SMI32) staining of infected neurons in which virally mediated gene expression was induced for 4 days with doxycycline. Enlarged insets (magnification 3×) are shown on bottom left of each image. Scale bar = 20 µm. **(B)** Quantification of axonal swellings. Number for uninfected (control) neuronal cultures was set to 1 and all other values were appropriately normalized. *$P < 0.05$, NS = Not significant.

for *Morc2a* is lethal, showing growth retardation and abnormalities in neural system development (https://dmdd.org.uk/mutants/Morc2a) further supporting a developmental role for MORC2.

The *MORC2* neuropathy (CMT2Z) is the second most frequent form of axonal CMT, after CMT type 2A2 (CMT2A2; MIM 609260) that is a consequence of *MFN2* mutations (13,27). More than half of the CMT2Z cases (17 families) are due to the c.754C>T (p.R252W) mutation, which is *de novo* in at least 15 cases, suggesting this is a recurrent substitution because of a mutational hot spot (4–6,8,9,13). It is widely established that the CpG islands are mutational hot spots due to instability of the 5-methylcytosines in DNA, and the cytosine nucleotide c.754C is located in a CpG dinucleotide. Bisulphite sequencing revealed that the c.754C remains in a predominantly methylated status favoring the mutational event, underpinning that the common

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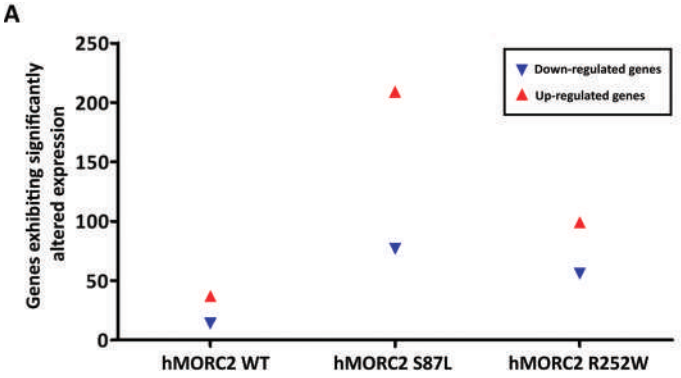

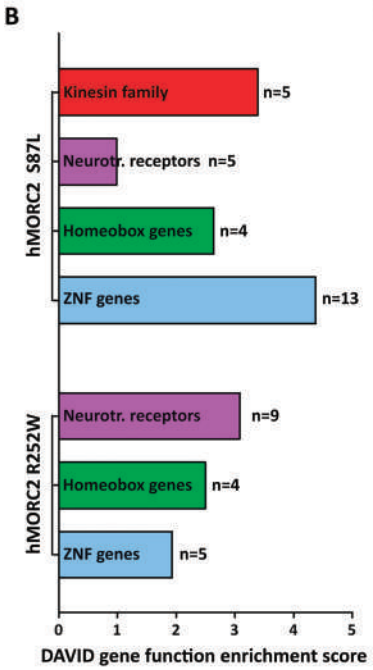

C

Altered neuronal-related genes in hMORC2 S87L			
Gene family	Gene name	Log fold change	Adj. p_value
AChE dinamycs-related	*Prima1*	-0.8107	0.0225
Chaperone-mediated protein folding	*Hspb1*	-2.0045	0.0138
Gaba receptors	*Gabra1*	1.8839	0.0102
	Gabra5	2.1599	0.0402
Glutamate receptors	*Grik3*	0.9542	0.0318
SLCs	*Slco3a1*	1.1453	0.0118
Kinesin family	*Kif18b*	2.6480	0.0012
	Kif20b	2.5508	0.0138
	Kifc1	1.4901	0.0103
	Kif20a	1.6522	0.0179
	Kif11	2.1956	0.0018

Altered neuronal-related genes in hMORC2 R252W			
Gene family	Gene name	Log fold change	Adj. p_value
Chaperone-mediated protein folding	*Hspb1*	-2.1645	0.0161
Gaba receptors	*Gabra1*	1.4898	0.0439
	Gabra5	2.4493	0.0306
	Gabrb1	2.4636	0.0322
Glutamate receptors	*Grik3*	1.0610	0.0292
nAChRs superfamily	*Chrnb4*	1.3944	0.0322
SLCs	*Slco3a1*	1.1645	0.0161
	Slc39a6	-0.6013	0.0475
TMEM proteins	*Tmem178a*	1.1397	0.0322
	Tmem81	-1.3848	0.0292

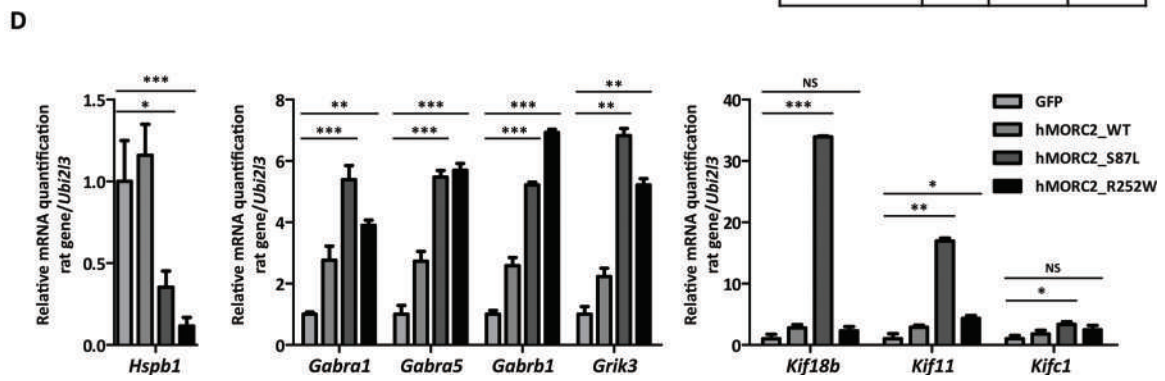

Figure 8. Transcriptional changes in sensory neurons expressing mutated forms of MORC2. **(A)** Number of genes exhibiting significantly altered expression using GFP as a control. Blue triangles are showing repressed genes and the red ones indicate the overexpressed genes. **(B)** DAVID gene function enrichment score for the rat sensory neurons expressing hMORC2 S87L and R252W. **(C)** Changes in genes encoding proteins with recognized neuronal functions. **(D)** qPCR based confirmation of alterations found in the rat transcriptomic analysis. Ubiquitin (*Ubi2l3*) was used as the normalizer for the amount of RNA used. The measurements obtained for GFP were set as 1 and all other samples were appropriately normalized. $^{*}P < 0.05$, $^{**}P < 0.001$, $^{***}P < 0.0001$, NS = Not significant.

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p.R252W mutation is the result of spontaneous deamination of a 5-methylcytosine to yield thymine.

Both the p.R252W and the p.S87L mutations are located in the ATPase domain of MORC2. We therefore evaluated the ATPase activity for both full-length MORC2 mutations in HeLa cells and observed that only p.S87L led to a significant decrease in ATPase activity. Douse *et al.* (22) recently reported a reduced rate of ATP hydrolysis for both neuropathy-associated mutations using a construct that included the first 603 amino acids of MORC2. Together with our findings, these results demonstrate that the ATPase activity plays a role in the MORC2 function. Interestingly, both increased and decreased biochemical MORC2 activity can cause a gain-of-function phenotype (22). It is therefore possible that haploinsufficiency caused by certain MORC2 mutations leads to decreased MORC2 activity manifested genetically as a dominant effect.

The observed differences in the ATPase activity for different mutations suggest that alteration of other molecular functions of MORC2 might also be contributing to the CMT2Z phenotype. Since MORC2 is known to promote the phosphorylation and activity of ACLY, an enzyme involved in the formation of acetyl-coA in the cytoplasm (18), we measured its activity in fibroblasts derived from a patient carrying p.R252W mutation as compared with a control fibroblasts. No changes in ACLY activity were observed with the p.R252W indicating that this mutation does not impact this particular role of MORC2 in fibroblasts.

MORC2 was previously described to play a role as a transcriptional regulator. We used both the patient derived fibroblasts and rodent sensory neuron cultures to evaluate any potential morphological difference and transcriptional changes caused by an altered MORC2 function. We observed that, structurally, mutant MORC2 fibroblasts did not present any morphological abnormalities compared with control cells. Interestingly, we however observed that in neurons, the p.S87L form of MORC2 led to an increase in axonal swellings, a hallmark of axonal injury. Axonal swellings have been previously described in neurodegenerative diseases, such as CMT type 2E (CMT2E; MIM 607684) caused by *NEFL* mutations (28). The axonal swelling, which represents abnormal accumulation of axonal cargos and cytoskeletal proteins, directly affects the axonal transport systems through microtubules and motor proteins (29,30). Regarding the p.S87L mutation, a defective axonal transport could therefore underlie the pathogenesis of the neuropathy and contribute to disease severity and progression.

At the transcriptional level, our microarray data indicated enrichment of sets of genes related to *ZNF*, helicases and homeobox genes in the human fibroblast lines carrying both investigated mutations. In addition, p.R252W fibroblasts also show altered expression in metallothionein genes. These findings were partly confirmed using rat DRG sensory neurons, since for the two used cellular models, homeobox and *ZNF* genes showed altered expression. The overexpression of homeobox genes is of interest as *Hox* genes encode conserved transcription factors regulating development and maintenance of different cellular populations (31,32), which is compatible with the observed spatiotemporal expression pattern of *Morc2* and its suggested role in the development and maintenance of the nervous system. *ZNF* genes were previously observed to be regulated by MORC2 (22). The *ZNF* genes are classically defined as a large family of transcription factors that can bind to DNA, RNA, lipids and proteins (33). Thus, ZNF-encoded proteins are implicated in transcriptional regulation, DNA recognition, RNA packaging, signal transduction, actin targeting, telomere maintenance, DNA repair, cell migration and many other processes (34). In addition to the well-established involvement of the *ZNF* genes in a variety of developmental processes (35,36), they are also implicated in diseases, including SMA (37) and Parkinson's disease (38). Collectively, these data indicate that impaired MORC2 function alters the expression of multiple transcripts involved in neuronal development.

Neurons infected with p.R252W or p.S87L showed altered expression of different neurotransmitter receptors, which are critical for basic functioning of the nervous system. In addition, expression of the kinesin gene group was altered in neurons expressing the p.S87L form. Within the group of neurotransmitter receptors, we observed that the genes differentially expressed included GABA receptors, a family of proteins involved in the GABAergic neurotransmission of the mammalian central nervous system (*Gabra1, Gabra5* and *Gabrb1*) and a glutamate receptor (*Grik3*), which is the predominant excitatory neurotransmitter found at synapses in the mammalian brain. The altered expression of the genes *Kif18b*, *Kifc1* and *Kif11* detected in neurons expressing the p.S87L mutation encode kinesin proteins that are abundant in the axoplasm and are required for both fast anterograde and fast retrograde transport (29,30). In *Drosophila* the functional disruption of kinesins leads to posterior paralysis and axonal swellings (39,40) and deficiency in kinesins can cause neurological disorders, e.g. KIF5A dysregulation is involved in an axonal form of CMT and spastic paraplegia (41).

We also detected that the motor protein *Hspb1*, in which mutations in the human orthologue cause CMT2F, is strongly repressed in both p.R252W and p.S87L expressing neurons. It was previously shown that the expression of S135F-mutant HSPB1 in cultured mouse motor neurons led to progressive degeneration of motor neurons with disruption of the neurofilament network and aggregation of the NFL (neurofilament light) protein, encoded by the *NEFL* gene that is involved in CMT2E (42).

In conclusion, our data provide a new insight into the physiological and pathophysiological roles of MORC2 within the neural system. Both enzymatic and regulatory functions were previously linked to MORC2 (16–20). We confirmed the reported link between *MORC2* and *ZNF* genes (21), which, together with observed altered expression of homeobox genes, indicates that MORC2 can play a role in the development of the nervous system. In the *in vitro* neuronal model used in our study, we also detected a dysregulated expression of neurotransmitter receptors, and kinesin genes, which encodes for proteins involved in axonal transport. Strikingly, the only altered CMT-related gene was *Hspb1*, which plays a role in the architecture of cytoskeleton. Together, the structural and transcriptional changes in neuronal cultures expressing the mutated forms of MORC2 indicate that at least part of the induced defects lead to altered axonal homeostasis. Our results, therefore, contribute and support the emerging concept that alterations in axonal transport, neurofilament homeostasis and architecture of cytoskeleton are common mechanisms contributing to the CMT phenotype (43–45). Our observations warrant further exploration in particular using a human neuronal model, such as human motor neurons (MNs) derived from fibroblasts of CMT2Z patients via hiPSCs. In addition, the observed MORC2 expression in Schwann cells indicates its possible role in glia. Integration of transcriptomic, proteomic and functional data generated from characterization of both neuronal and glial models will provide additional insight into the pathophysiology of the CMT2Z and may also help to generate suitable cellular model of the disease allowing for evaluation of relevant therapeutic strategies.

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Materials and Methods

Ethics statement

Skin biopsies from CMT2Z patients were obtained under approved by the ethics board of the corresponding hospitals where patients are supervised and written informed consents were signed.

Human first trimester tissue was collected after elective surgical abortions with maternal oral and written informed consent. Midwives informing the patients (>18 years old and Swedish-speaking) and responsible for the procedure of obtaining oral and written informed consent were not involved in the research study. The Regional Human Ethics Committee, Stockholm, Sweden approved the collection. The post-conceptional age of the tissue was determined by examination of anatomical landmarks in addition to clinical ultrasound. For adult stages, the RNA was isolated from the cervical and lumbar samples of spinal cord of post-mortem subjects. Ethical approval for the use of adult human *post mortem* specimens was granted from the regional ethical review board in Stockholm, Sweden (Regionala Etikprövnings nämnden, Stockholm, EPN). All adult human spinal cord samples were obtained from the Netherlands Brain Bank (http://www.brainbank.nl) and the National Disease Research Interchange (http://www.ndriresource.org) with the written informed consent from the donors or next of kin.

Rat and mice were sacrificed by exposure to CO_2. All animal work was performed in accordance with the Swedish regulations and approved by the regional ethics review committee Stockholm, Stockholms norra djurförsöksetiska nämnd (N79/15).

Expression of MORC2 isoforms in human nervous tissues

Total RNA was isolated from DRGs dissected from human first trimester tissues collected at 7.5, 8–8.5 and 9 weeks post-conception.

Total RNA was extracted using Direct-zol™ RNA MiniPrep Plus (Zymo Research, Irvine, CA, USA) and the reverse transcribed template was prepared from 0.5 µg of total RNA using PrimeScript Reverse Transcriptase (Takara, Noji-higashi, Japan). Expression of MORC2 isoforms was measured after PCR amplification with the primer pairs hMORC2_1, hMORC2_2 and hMORC2_3 (Supplementary Material, Table S7). Normalization and amplification efficiency was confirmed using human actin primers.

Spatiotemporal analysis of Morc2 expression in mice peripheral nervous system

Total RNA from brain, spinal cord, DRG and sciatic nerve at different development stages was isolated using RNeasy Plus Mini Kit (Qiagen, Hilden, Germany). Direct-zol™ RNA MiniPrep Plus (Zymo Research, Irvine, CA, USA) was used to extract RNA from cultured neurons and Schwann cells. The reverse-transcribed template was prepared from 1 µg of total RNA using the QuantiTect Reverse Transcription Kit (Qiagen, Hilden, Germany). Morc2 was amplified by RT-PCR using the primer pairs mMorc2a-1 and mMorc2a-2 (Supplementary Material, Table S7). The expression was normalized using the endogenous mouse gene *Ubiquitin2l3* (primers Ubi2l3).

Brain and sciatic nerve protein extracts were obtained from mice at selected time points using a polytron homogenizer and RIPA lysis buffer (50 mM Tris–HCl pH 7.4, 5 mM DL-Dithiothreitol, 150 mM NaCl, 1% NP-40, 0.5% deoxycolate). A rabbit polyclonal Morc2 antibody (Santa Cruz Biotechnology, Dallas, TX, USA) and a mouse monoclonal α-Tubulin antibody (Sigma-Aldrich, St. Louis, MI, USA) were used to perform immunoblotting studies.

Bisulphite sequencing

Genomic DNA (2 µg) was treated with sodium bisulphite using the EpiTect Bisulphite Kit (Qiagen, Hilden, Germany). Nested PCR was used to amplify a 278 bp fragment encompassing the MORC2 R252 residue. The first round of PCR was performed in a total volume of 25 µl using 2 µg of purified bi-sulphite treated DNA, 0.4 µM of each primer compatible with bisulphite-converted sequence and MyTaq HS Red Mix (Bioline, London, UK). Nested PCR was performed using the same primers and reagent concentration with template (1.5 µl) from the first round of PCR. The PCR amplicon was gel purified using the ISOLATE II PCR and Gel Kit and cloned into the pCR4-TOPO TA vector (Thermo Fisher Scientific, Waltham, MA, USA). Nineteen clones were sequenced using BigDye Terminator v3.1 Cycle Sequencing protocols at the Australian Cancer Research Foundation facility (Garvan Institute of Medical Research, Darlinghurst, Australia).

MORC2 immunofluorescence in human fibroblasts derived from CMT2Z patients

Fibroblast cell lines grown in Dulbecco's Modified Eagle's Medium (DMEM) without glucose [DMEM, 10% heat-inactivated fetal bovine serum (FBS), 1% L-glutamine, 1% Penicillin/Streptomycin (P/S) and 1% Sodium Pyruvate] were fixed in 4% paraformaldehyde, permeabilized with Triton 0.25% in phosphate-buffered saline (PBS) and incubated in blocking buffer (5% Horse Serum in PBS) for 1 h at room temperature (RT). The primary antibody anti-MORC2 (Santa Cruz Biotechnology, Dallas, TX, USA) was incubated in blocking buffer overnight (o/n) at 4°C. The next day, samples were incubated with the appropriate secondary antibody (Alexa-488, Thermo Fisher Scientific, Waltham, MA, USA) in blocking buffer during 1 h at RT and mounted with Vectashied including DAPI (Vector laboratories, Burlingame, CA, USA). Slides were examined with LSM880 confocal microscope (Zeiss, Oberkochen, Germany).

Generation of lentiviral vectors

For the overexpression experiment, lentiviral particles were produced by co-transfecting 293T cells with the lentiviral vector pSlik-Hygro (Addgene, Cambridge, MA, USA) containing GFP as a control, human WT-MORC2, MORC2 p.R252W, MORC2 p.S87L (under an inducible Doxycycline promoter) and the co-vectors PLP1, PLP2 and PLP/VSVG (Invitrogen, Carlsbad, CA, USA). Cells were incubated at 37°C and 5% CO_2 and 12 h after transduction the medium (DMEM) supplemented with 10% (v/v) FBS and 1% (v/v) P/S was replaced. The conditioned medium was harvested after 48 h. The viruses were concentrated by 4 h centrifugation at 24000 rcf at 4°C, aliquoted and stored at −80°C.

Generation of continuous cell lines overexpressing MORC2 and ATPase assay

HeLa cells grown in DMEM plus [DMEM, 10% (v/v) heat-inactivated FBS, 5 g/L D-glucose, 1% (v/v) L-glutamine and 1% (v/v) P/S] were exposed to lentiviruses containing GFP, WT-MORC2 or MORC2 mutants (p.S87L and p.R252W) for 12 h

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and were selected with 4 cycles of DMEM supplemented with 200 µg/mL of Hygromycin, changing the medium every 2 days post-infection. The transgene expression was induced by exposure to DMEM with 2 µg/mL of Doxycycline for 4 days. The nuclear extracts were prepared using an extraction method by high salt concentration as described previously (20) and kept on ice while the protein was quantified with BCA kit (Thermo Fisher Scientific, Waltham, MA, USA). For the ATPase assay, 50 µg of nuclear protein was used in the High Throughput Colorimetric ATPase Assays (Innova Bioscience, San Diego, CA, USA). The data were presented as the average ± the standard deviation for three independent assays and the results were normalized with the uninfected control set to 1. Statistical significance was determined by two-tailed Student's t test and considered statistically significant when P was <0.05. In order to confirm an equal MORC2 overexpression for all the samples, 30 µg of protein was loaded on a 10% (v/v) polyacrylamide gel under reducing conditions. Membranes were blocked by incubation with 5% w/v milk powder in TBST (25 mm Tris–HCl, 150 mm NaCl, 0.05% v/v Tween 20, pH 7.4) for 1 h at RT. For immunodetection, the polyvinylidene difluoride membranes were incubated o/n with anti-MORC2 1:250 (v/v) (Santa Cruz Biotechnology, Dallas, TX, USA) and anti-Actin 1:2000 (v/v) (Sigma-Aldrich, St. Louis, MI, USA) diluted in 3% w/v bovine serum albumin (BSA) in TBST. The day after, the appropriate secondary horseradish peroxidase (HRP)-conjugated antibodies were incubated for 1 h at RT using a dilution of 1:10000 (v/v), followed by exposure to a film (Fujifilm, Tilburg, The Netherlands).

ACLY activity enzyme assay

ACLY enzyme activity was indirectly assayed using the commercial MDH Colorimetric Kit (Biovision, Milpitas, CA, USA) according to the manufacturer's instructions. Absorbance readings at 450 nm were taken at 1 min interval for 20 min at 37°C using an EnSpire Multimode Plate Reader (Perkin Elmer, Waltham, MA, USA) to monitor NADH production. Cell extracts from the patient (p.R252W) and control fibroblasts were used for the assay. The assay was performed for three independent experiments and the mean ± standard error of the mean (SEM) MDH activity was calculated.

Preparation of rat sensory neuron cultures

DRGs were dissected from rat Sprague–Dawley embryos at embryonic day 15.5 (E15.5). Dissected DRGs were triturated in 0.25% (v/v) trypsin containing 0.25% (v/v) EDTA for 1 h at 37°C, harvested by soft centrifugation (100 rcf for 15 min) and resuspended in C-medium [DMEM with 10% (v/v) Fetal Calf Serum (FCS), 1% (v/v) P/S, 200 mM L-glutamine, 50 µg/mL 2.5S Nerve Growth Factor (NGF)]. Cells were plated at a concentration of 1.5 DRG per 12 mm glass covers coated by growth factor reduced Matrigel (Clontech, Fremont, CA, USA) or Poly-L-Lysine (Sigma-Aldrich, St. Louis, MI, USA) o/n at 37°C and 5% CO_2. The day after, the medium was replaced by Neurobasal (NB)-supplemented medium (NB medium with 2 g/L D-glucose, 1X B27 supplement, 1% P/S (v/v), 200 mM L-glutamine and 50 µg/mL 2.5S NGF) and cultured for 1 week replacing the medium every 2 days. To archive pure neuron cultures, dissociated DRG cultures were cycled for 3 weeks between NB-supplemented medium and NB-supplemented medium with 10 µM Fluorodeoxyuridine (Sigma-Aldrich, St. Louis, MI, USA).

Overexpression of mutated forms of MORC2 in rat sensory neurons

Neuronal cultures were infected with lentivirus containing GFP, WT-MORC2, MORC2 p.S87L and MORC2 p.R252W in NB-supplemented medium for 12 h and were selected using 200 µg/mL of Hygromycin for 1 week. The overexpression of the transgene was induced with 2 µg/mL of Doxycycline for 4 days.

Immunofluorescence assays, RNA and protein extraction of neuronal cultures

For the immunofluorescence assays, dissociated DRG neurons were fixed in 4% (v/v) paraformaldehyde and incubated in blocking buffer [1% (v/v) Normal Goat Serum, 5% BSA (v/v) and 0.3% (v/v) Triton X-100 in PBS] for 1 h at RT and washed in PBS. The primary antibodies anti-MORC2 (Santa Cruz Biotechnology, Dallas, TX, USA) and anti-SMI32 (Millipore, Burlington, MA, USA) were incubated in blocking buffer + PBS in a dilution 1:1 o/n at 4°C. The next day, samples were incubated with the appropriate secondary antibodies conjugated with fluorophores (Alexa-488 or Alexa-594, Thermo Fisher Scientific, Waltham, MA, USA) in PBS for 1 h at RT, stained with DAPI, dried and mounted with Vectashied (Vector laboratories, Burlingame, CA, USA). Slides were examined with LSM880 confocal microscope (Zeiss, Oberkochen, Germany). To confirm the overexpression, total RNA was extracted using Direct-zol™ RNA MiniPrep Plus (Zymo Research, Irvine, CA, USA) and 0.150 µg was employed to prepare reverse transcribed template using 'PrimeScript Reverse Transcriptase' (Takara, Noji-higashi, Japan). *MORC2* expression was examined through RT-PCR with the primer pair hMORC2_4 (S7 Table). Equal cDNA loading was established using primers against actin. For western blot analysis, the neurons were kept on ice with ice-cold lysis buffer [25 mm Tris–HCl pH 7.5, 95 mm NaCl, 10 mm EDTA, 2% (v/v) sodium dodecyl sulfate (SDS), 1 mm NaF and 1 mm $NaVO_4$ in PBS] for 30 min and were homogenized with tissue-lyser. Proteins lysates were obtained through centrifugation at 4°C and 16,000 rcf for 10 min with protein concentration determined using the BCA kit (Thermo Fisher Scientific, Waltham, MA, USA). Finally, the tubes were boiled during 5 min and stored at −80°C. For SDS-PAGE (polyacrylamide gel electrophoresis), 30 µg of proteins from each sample were separated on a 10% (v/v) polyacrylamide gel under reducing conditions. After the blocking with 5% w/v milk powder in TBST during 1 h at RT, the membranes were incubated o/n with anti-MORC2 (Santa Cruz Biotechnology, Dallas, TX, USA) and anti-Actin (Sigma-Aldrich, St. Louis, MI, USA) diluted in 3% w/v BSA in TBST and the next day, the appropriate secondary HRP-conjugated antibodies were incubated for 1 h at RT, followed by developing on a film (Fujifilm, Tilburg, The Netherlands).

Generation of primary rat Schwann cells transiently overexpressing MORC2

Primary rat Schwann cells have been cultured as previously described (46). Briefly, sciatic nerves of P3 Sprague–Dawley rats were collected and dissociated in 1 mL DMEM plus 300 µl of 10 mg/mL collagenase (Worthington, Columbus, OH, USA). The tissue was subsequently incubated with 0.25% trypsin (Gibco, Thermo Fisher Scientific, Waltham, MA, USA) and plated in DMEM with 10% FCS (Gibco, Thermo Fisher Scientific, Waltham, MA, USA). The purity of culture was achieved by depletion of fibroblast using anti–Thy 1.1 antibody (Millipore, Burlington, MA, USA) and rabbit complement (Sigma-Aldrich, St. Louis, MI, USA).

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Pure rat Schwann cells were expanded in DMEM supplemented with 10% FCS, 4 mM forskolin (Sigma-Aldrich, St. Louis, MI, USA) and 10 ng/mL of human recombinant NRG1-beta 1 (R&D System, Minneapolis, MN, USA).

The transient overexpression of the MORC2 isoforms was achieved by transfecting the Schwann cells with pcDNA3.1 containing GFP as a control, human WT-MORC2, MORC2 p.R252W and MORC2 p.S87L (under CMV promoter). Forty eight h after the transfection the cells were fixed with 4%PFA in PBS and the immunofluorescence has been performed as described for the DRG neurons.

Analysis of axonal swellings in infected rat sensory neurons

The average number of axonal swellings was calculated based on 15 pictures from each sample immunostained with SMI32 (Millipore, Burlington, MA, USA) per infection. All the data were reported as the sample mean ± SEM for three independent lentiviral infections of the neuronal cultures and the results were normalized with the control sample. Pairwise comparisons between means of different groups were performed using a Student t-test (two tailed, unpaired) and considered statistically significant when $P < 0.05$.

Transcriptome analysis in human fibroblast and rat sensory neurons

The quality and quantity of RNA was evaluated by spectrometry (NanoDrop ND1000, NanoDrop Technologies, Wilminton, Delaware USA) and by RNA 6000 Nano Bioanalyzer (Agilent Technologies, Palo Alto, CA, USA) assays (Supplementary Material, Table S8). Two hundred ng of total RNA were used to produce Cyanine 3-CTP-labeled cRNA using the One-Color Low Input Quick Amp Labeling Kit (Agilent p/n 5190–2305) according to the manufacturer's instructions. Following One-Color Microarray-Based Gene Expression Analysis protocol Version 6.7 (Agilent p/n G4140–90040), 600 ng of labeled cRNA was hybridized with the SurePrint G3 Rat Gene Expression v2 8x60K Microarray (Agilent p/n G4858A-074036) containing 30,584 Entrez Genes (unique) and SurePrint G3 Human Gene Expression v3 8×60K Microarray (Agilent p/n G4858A-072363) containing 26,083 Entrez Genes (unique) + 30,606 lncRNAs (unique). Arrays were scanned in an Agilent Microarray Scanner (Agilent G2565C) according to the manufacturer's protocol and data extracted using Agilent Feature Extraction Software 11.5.1.1 following the Agilent protocol GE1_1105_Oct12, grid templates 072363_D_F_20150612 and 074036_D_F_20150914 and the QC Metric Set GE1_QCMT_Oct12. Agilent Processed Signal (Agilent Feature Extraction Software) was standardized using quantile normalization (47). Differential gene expression was carried out using the *limma* (48) package from Bioconductor. Multiple testing adjustments of *P* were performed according to the False Discovery Rate method (49,50). Gene enrichment analysis was carried out with DAVID Bioinformatics Resources, version 6.8 (51).

Supplementary Material

Supplementary Material is available at *HMG* online.

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