

## Appendix Figures and Tables

### HDAC6 inhibition restores TDP-43 pathology and axonal transport defects in human motor neurons with *TARDBP* mutations

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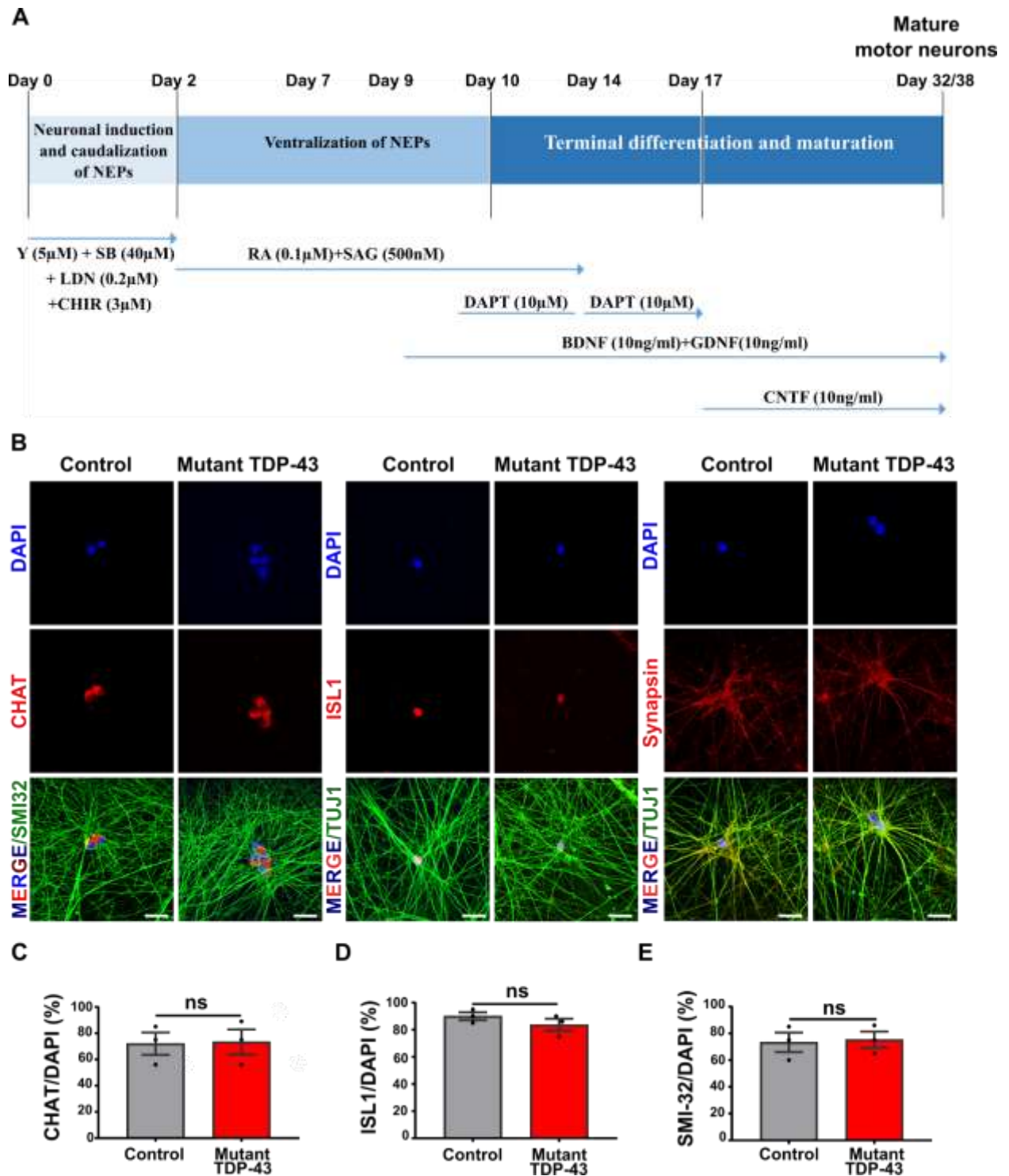
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#### KEYWORDS

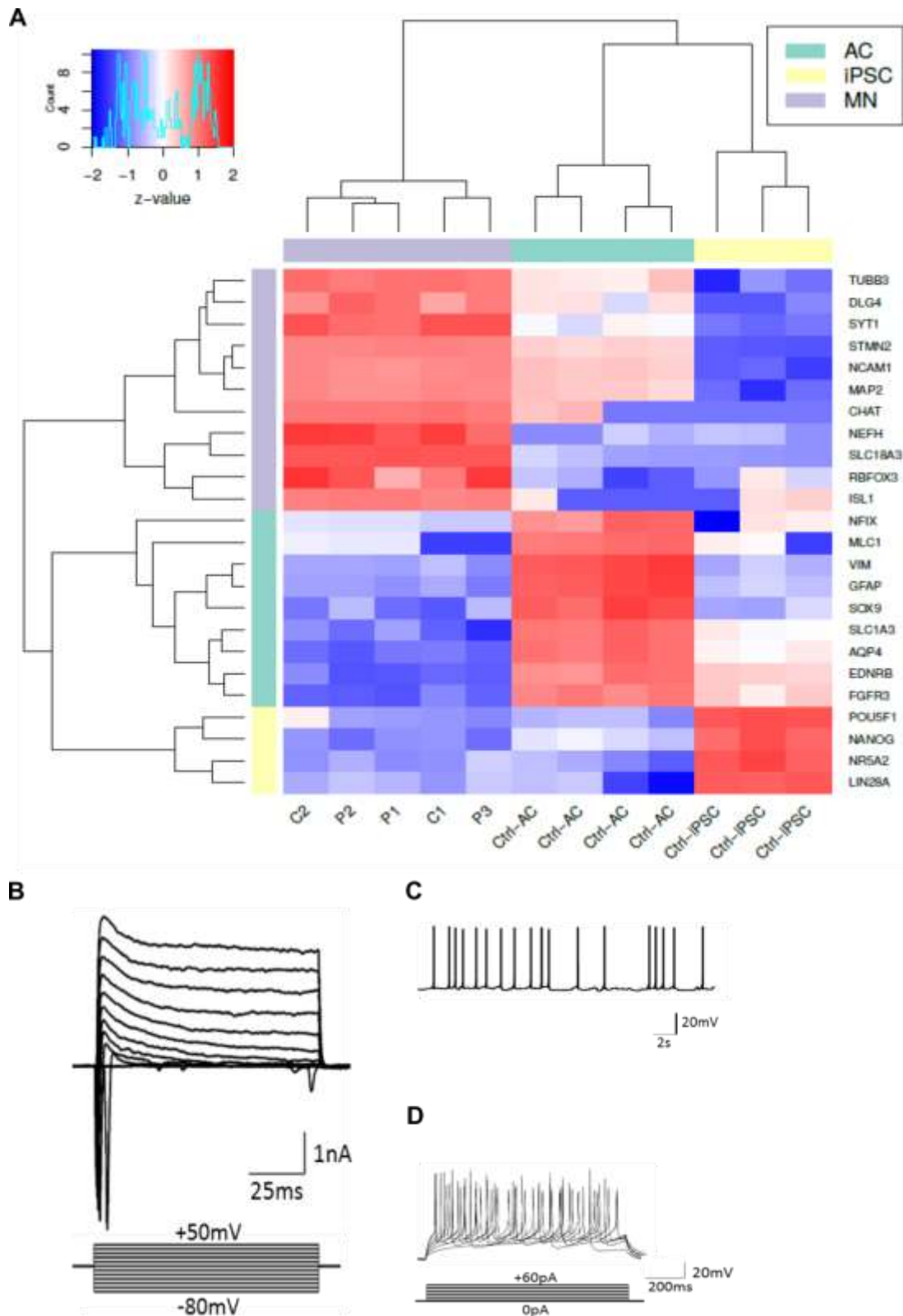
TDP-43, induced pluripotent stem cells, wild-type and mutant tagged TDP-43, axonal transport, HDAC6.

## **Table of Contents**

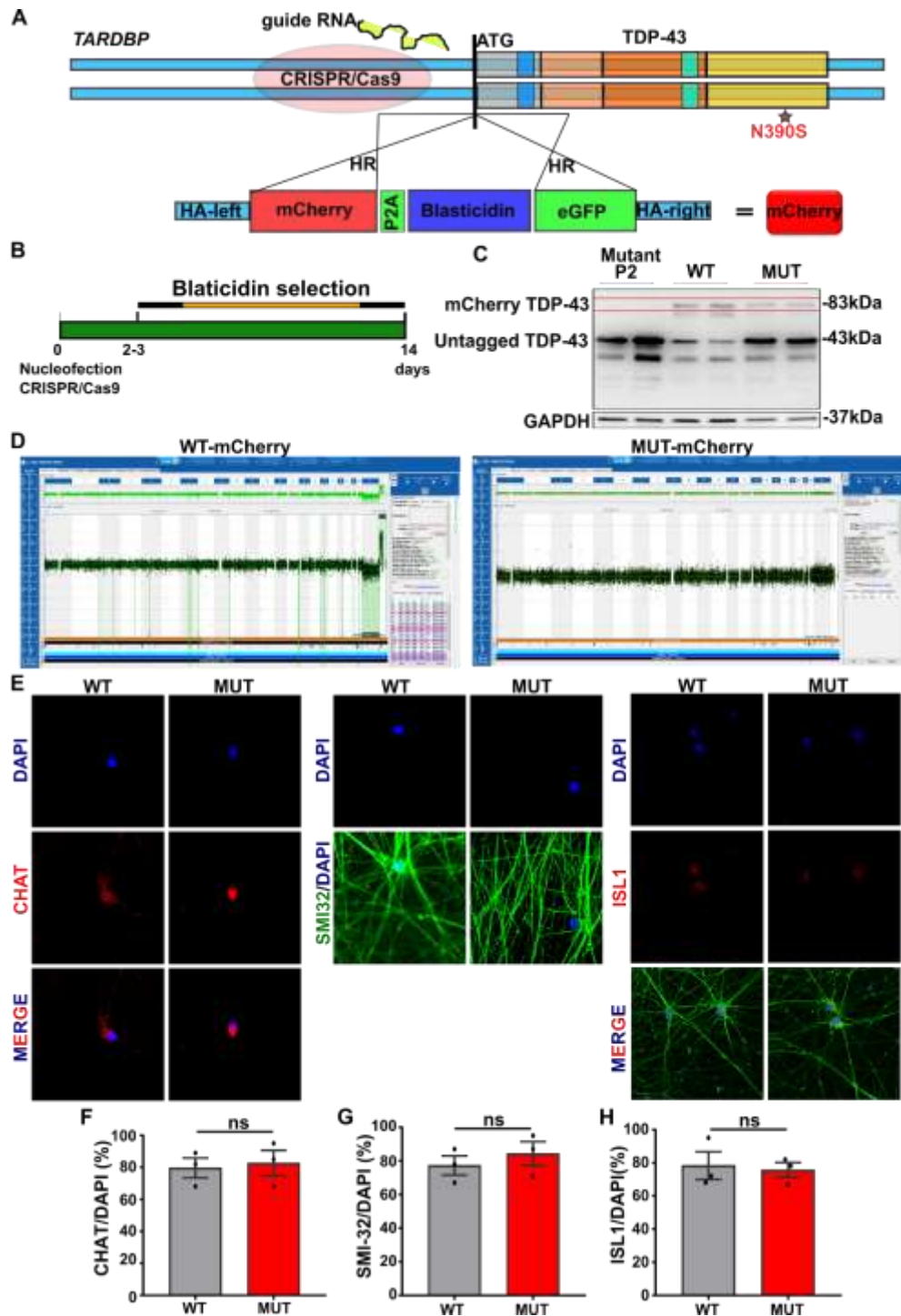
<b>Appendix Figure S1.....</b>	<b>3</b>
<b>Appendix Figure S2.....</b>	<b>4</b>
<b>Appendix Figure S3.....</b>	<b>5</b>
<b>Appendix Figure S4.....</b>	<b>6</b>
<b>Appendix Figure S5.....</b>	<b>7</b>
<b>Appendix Figure S6.....</b>	<b>8</b>
<b>Appendix Figure S7.....</b>	<b>9</b>
<b>Appendix Figure S8.....</b>	<b>10</b>
<b>Appendix Table S1.....</b>	<b>11</b>
<b>Appendix Table S2.....</b>	<b>11</b>
<b>Appendix Table S3.....</b>	<b>12</b>
<b>Appendix Table S4.....</b>	<b>13</b>



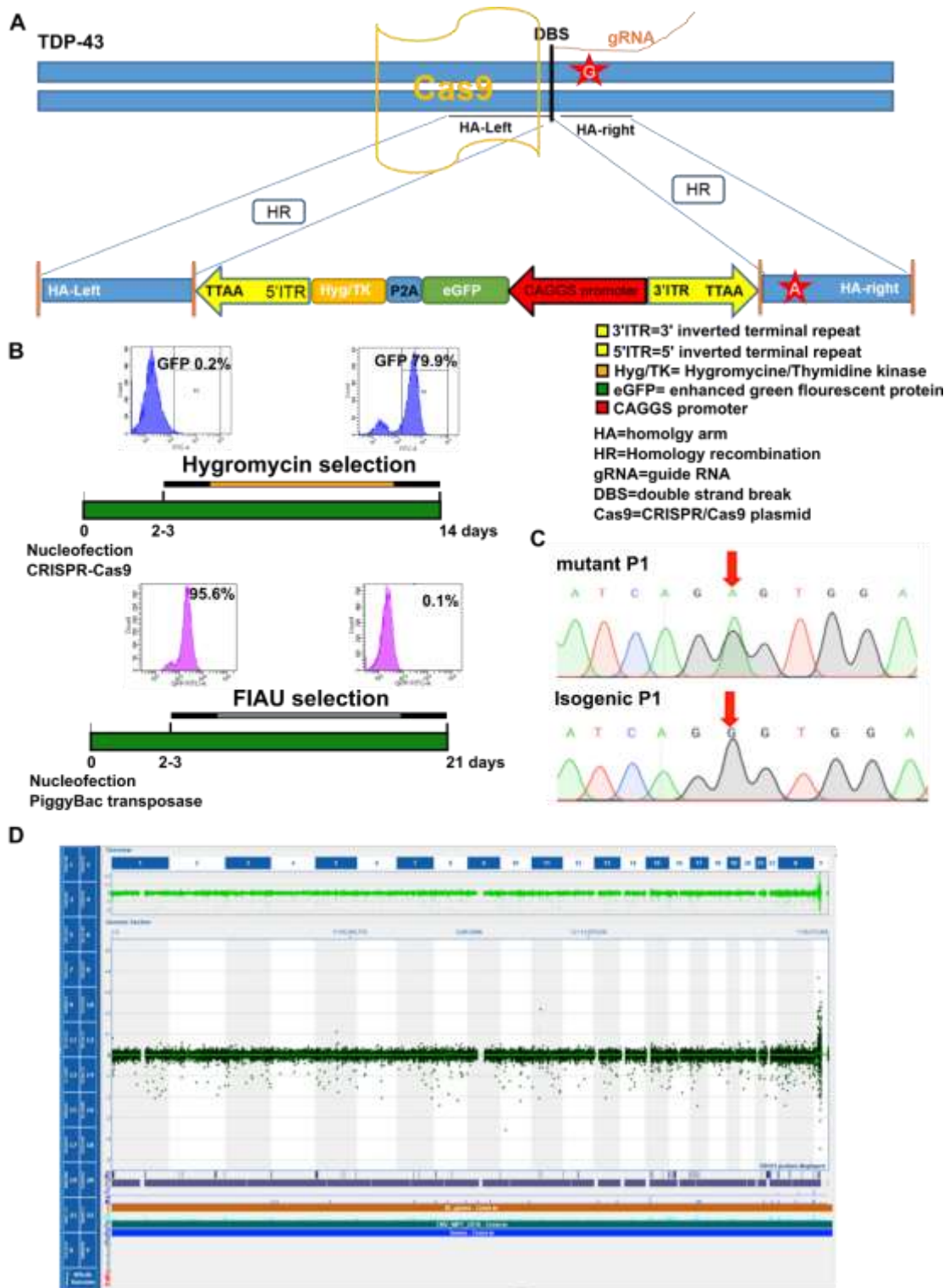
**Appendix Figure S1. Mutant TDP-43 iPSCs differentiation into functional motor neurons.** **A** Scheme representing the used protocol to differentiate iPSC to motor neurons. **B** Representative immunofluorescent staining of healthy control (C0) and mutant TDP-43 (P2) iPSC-derived motor neurons. Scale bar: 100µm. **C** Quantification of ISL1 positive cells, **D** quantification of CHAT positive cells and **E** quantification of SMI32 positive cells. Each dot represent the average of one differentiation with n=30 control (C0=10, C1=10 and C2=10) and n=30 mutant TDP-43 (P1=10, P2=10 and P3=10) cells counted per differentiation. Paired-t-test in all panels: Data was combined from three independent differentiations. Data are shown as mean ± SEM, ns: not significant.



**Appendix Figure S2. Mutant iPSC-derived motor neuron characterization.** **A** RNA sequencing analysis in iPSC-derived motor neurons indicates exclusive enrichment of motor neuron specific transcripts versus iPSC - and astrocyte specific transcripts. **B** Representative traces of in- ( $\text{Na}^+$ ) and outward ( $\text{K}^+$ ) currents (top panel) elicited by an experimental voltage pulse step protocol (lower panel). **C** Representative trace of spontaneous action potentials. **D** Representative traces of action potentials (top panel) evoked by an experimental current pulse step protocol (lower panel).

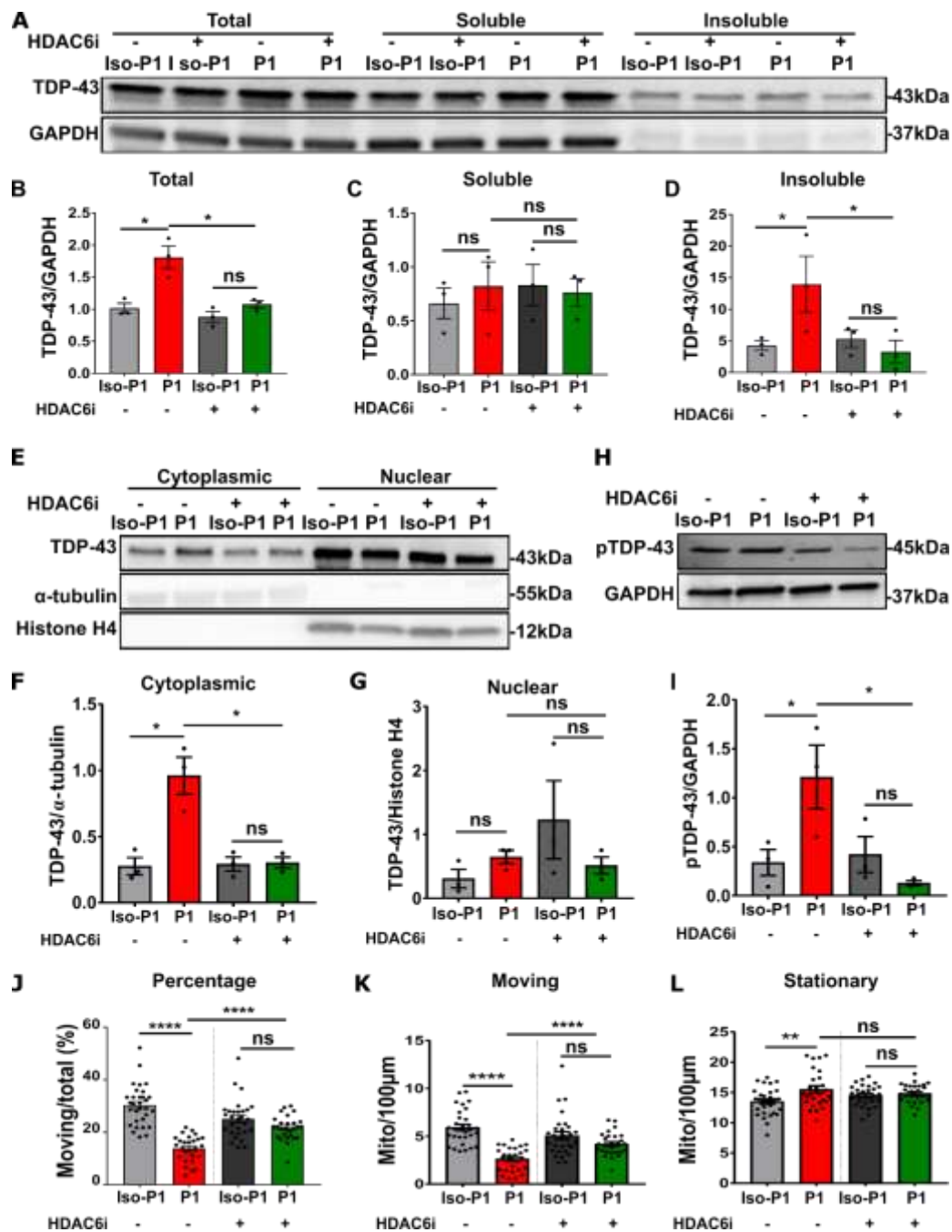


**Appendix Figure S3. Generation of mCherry tagged mutant TDP-43 patient cell lines using CRISPR-Cas9 genome technology.** **A** Overview of the used strategy to generate tagged lines with CRISPR/Cas9 genome editing. Donor template DNA with the selection cassette containing blasticidin and a highly similar sequence (homology arm-right and left), necessary for very efficient homology recombination with the target gene sequence. **B** Experimental design of blasticidin selection to select positive colonies. **C** Western blot confirming the expression of both the mCherry tagged TDP-43 as well as the untagged TDP-43 in the newly generated cell lines. **D** CGH array of WT-mCherry (left panel) and MUT-mCherry (right panel). **E** Immunofluorescence to evaluate motor neuron specific markers. **F** Quantification of CHAT+, **G** quantification SMI-32+ and **H** quantification of ISL1+ cells. Each dot represents an independent differentiation. Ratio paired-t-test. For all panels: Data combined from three independent differentiations. Data are shown as mean  $\pm$  SEM. ns: not significant.

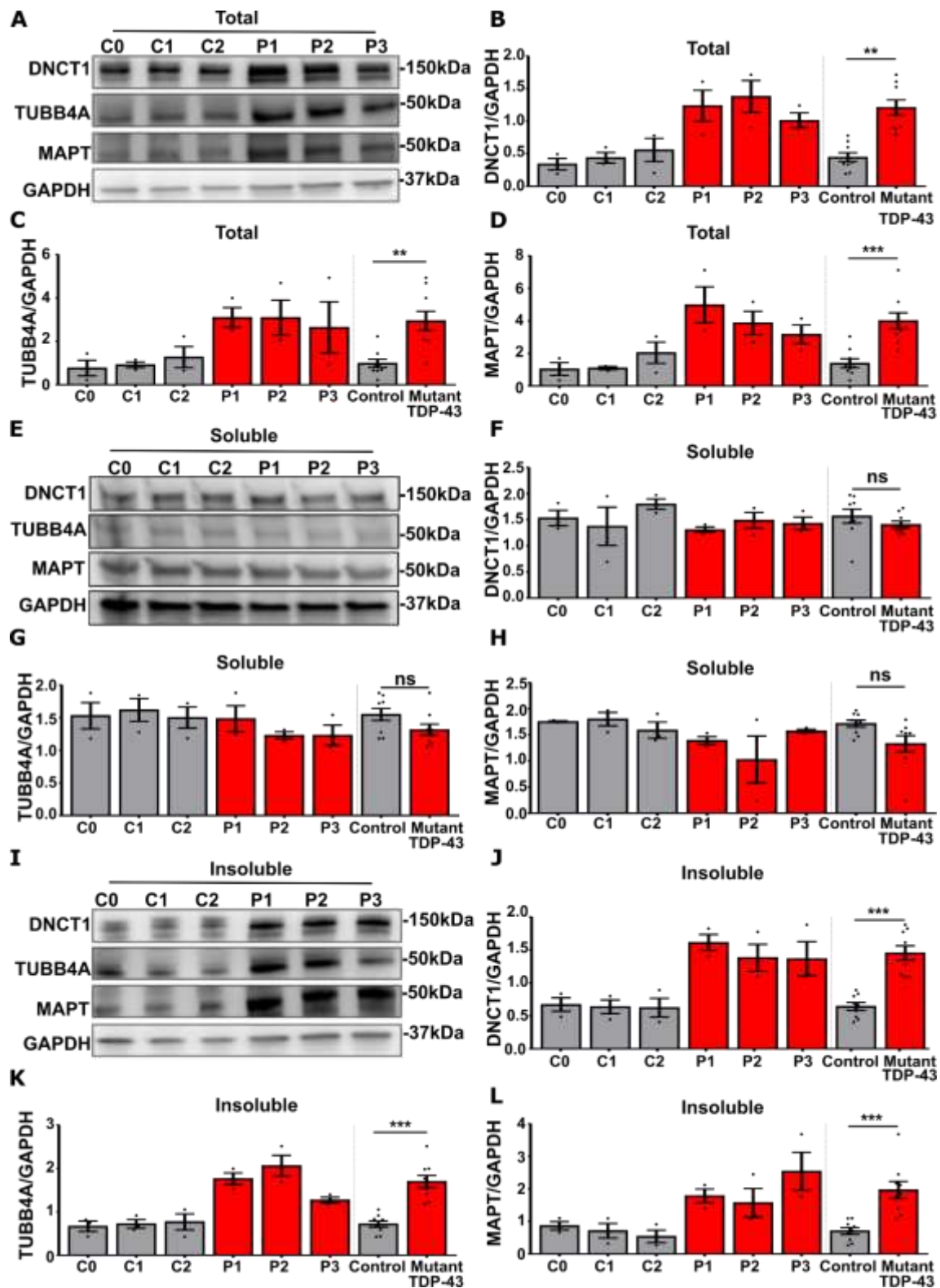


**Appendix Figure S4. Generation of an isogenic, gene-corrected control line.** **A** General overview of the experimental design and strategy used to generate isogenic control by correcting heterozygous point mutation with CRISPR/Cas9 genome editing. Donor template DNA with the selection cassette containing, hygromycin (positive selector), FIAU (negative selector) and containing highly similar sequence (homology arm-right and left), necessary for very efficient homology recombination with the target gene sequence. **B** Experimental design of hygromycin selection and piggyBac excision of the cassette from the positive clone, confirmed by fluorescence-activated cell sorting (FACS). **C** Confirming the presence of mutation by Sanger sequencing in mutant P1 (G287S) versus isogenic P1 (G287G) iPSC line. **D** CGH-array, indicating no significant genome-wide aberrations between mutant P1 and isogenic P1.



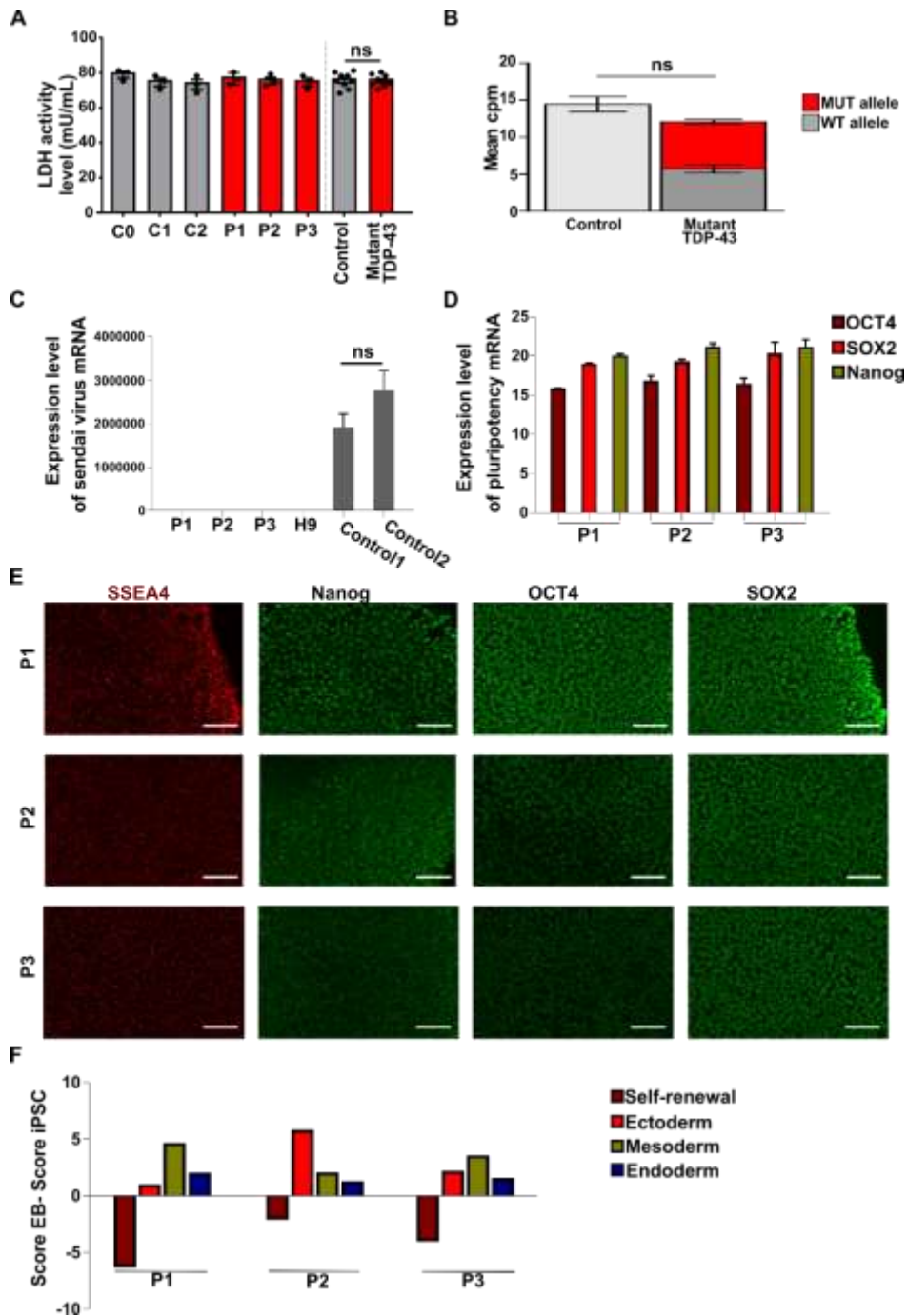


**Appendix Figure S5. HDAC6 inhibitor rescues the observed TDP-43 pathology and axonal transport defects in the mutant TDP-43.** **A, B, C** and **D** Representative Western blot of total, soluble and insoluble TDP-43 levels. **(B)** Quantification of total full-length TDP-43, **(C)** quantification of soluble full-length TDP-43, ratio paired-t-test and **(D)** quantification of insoluble full-length TDP-43 levels, ratio paired-t-test. Each dot represents an independent differentiation. **E** Representative Western blot of nucleo-cytoplasmic fractionation of mutant P1 and Iso-P1. **F** Graph shows quantification of cytoplasmic fraction. **G** Graph shows quantification of nuclear fraction, ratio paired-t-test. **H** Representative Western blot of pTDP-43 levels. **I** Graph shows quantification of pTDP-43, ratio paired-t-test. **J, K, L** Quantification of percentage of moving mitochondria **(J)**, the absolute amount of moving mitochondria **(K)** and of the amount of stationary mitochondria **(L)** normalized to neurite length 100μm. Each dot represents one neurite with for Iso-P1 (n=31) versus mutant P1 (n=27) and Iso-P1 with HDAC6 inhibitor (n=29) versus mutant P1 with HDAC6 inhibitor (n=27), unpaired Mann-Whitney test. Data was combined from three independent differentiations. Data are shown as mean ± SEM, \*p<0.05, \*\*p<0.01, \*\*\*\*p<0.0001, ns: not significant.

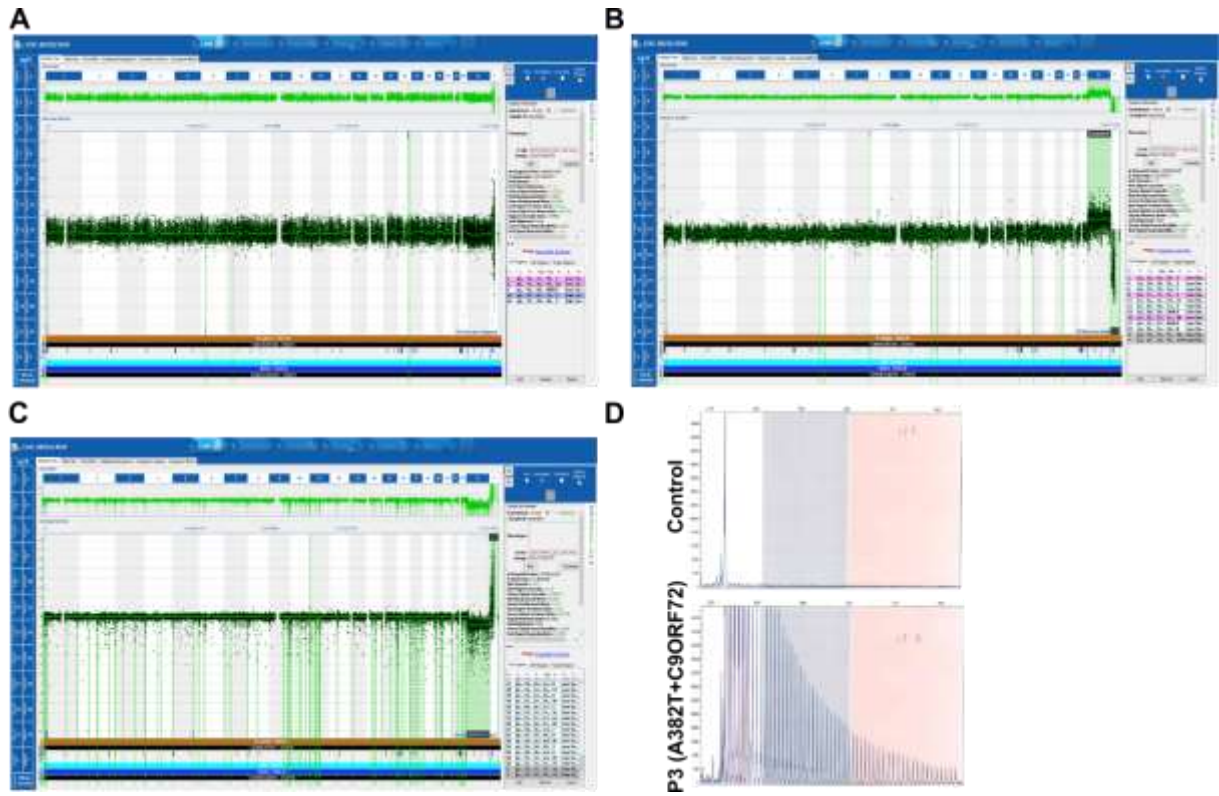


**Appendix Figure S6. Validation of the interactome data.** We studied the binding partners that favoured mutant TDP-43 in **A** total, **E** soluble and **I** insoluble fractions using Western blot of motor neurons derived from control and mutant TDP-43 iPSC lines. **B** quantification of dynactin 1 (DNCT1), **C** quantification of TUBB4A and **D** quantification MAPT in total fraction. **F** Quantification of DNCT1, **G** quantification of TUBB4A and **H** quantification MAPT in the soluble fraction. **J** Quantification DNCT1, **K** quantification of TUBB4A and **L** quantification of MAPT in the insoluble fraction. Each dot represents an independent differentiation. Ratio paired-t-test. For all panels: Data combined from three independent differentiations. Data are shown as mean  $\pm$  SEM, \*\* $p < 0.01$ , \*\*\* $p < 0.001$ , ns=not significant.





**Appendix Figure S7. LDH assay, RNA expression of motor neurons and quality control of the generated iPSC lines from patient skin fibroblasts.** **A** LDH assay, to compare cytotoxicity in control and mutant TDP-43 iPSC-derived motor neurons. Data from three independent differentiations, paired-t-test. Data are shown as mean  $\pm$  SEM, ns: not significant. **B** Evaluation of TDP-43 RNA expression in the transcriptomic data between control (C1 and C2) and mutant TDP-43 (P1, P2 and P3) iPSC-derived motor neurons, data from one individual differentiation. Mutant TDP-43 bar is divided into two red and grey, representing mutant and wild type allele respectively, chi-squared test. Data are shown as mean  $\pm$  SEM, ns: not significant. **C** Sendai virus PCR of the three mutant TDP-43 lines, a negative control (H9) and two positive controls (Control1 and Control2), unpaired Mann-Whitney test. Data from three different clones and shown as mean  $\pm$  SEM. **D** Pluripotency PCR, data from different clones and **E** represented immunofluorescence staining of iPSC pluripotency markers, *i.e.* Nanog, SOX2, OCT4 and SSEA4. Scale bar: 25 $\mu$ m. **F** qPCR of embryonic body formation experiment showing the presence of the three germ layer markers, data collected from one clone of each iPSC line.

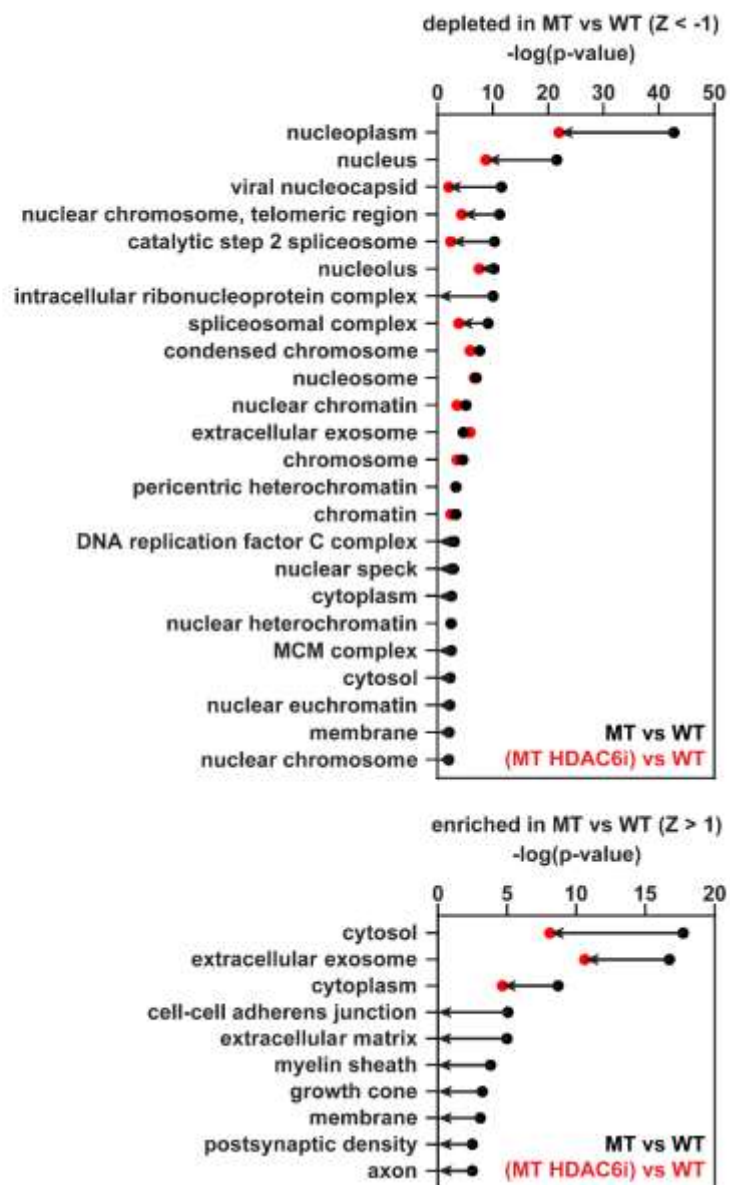


**Appendix Figure S8. CGH array of the mutant TDP-43 and tagged iPSC lines. A (P1), B (P2) and C (P3). D** Electropherograms of the PCR products of repeat-primed PCR reactions with control (upper-panel) and mutant P3 (lower-panel), evaluating the GGCCCC<sub>n</sub> repeat expansion.

**Appendix Table S1.** Overview of human iPSC lines used in this study.

Code	ALS mutation	Diagnosis	Gender	iPSC lines
C0	None	/	F	1
C1	None	/	F	1
C2	None	/	M	1
P1	G287S	TARDBP-ALS	F	2
P2	N390S	TARDBP-ALS	M	3
P3	A382T+C9ORF72 (>60 repeats)	TARDBP-ALS	F	3
Isogenic P1	G287G	TARDBP-ALS	F	1
WT-mCherry (P2)	N390S	TARDBP-ALS	M	1
MUT-mCherry (P2)	N390S	TARDBP-ALS	M	1

**Appendix Table S2.** List of depleted and enriched genes in MUT- versus WT-Cherry iPSC-derived motor neurons



**Appendix Table S3.** List of antibodies used for (1) immunohistochemistry and (2) Western blot.

Antibody	Isotype	Dilution (1)	Dilution (2)	Source
Synapsin 1	Rabbit IgG	1/2000		Merck Millipore
Tuj1	Mouse IgG	1/500		Abcam
CHAT	Rabbit IgG	1/500	1/200	Merck Millipore
ISL1	Rabbit IgG	1/200	1/100	Merck Millipore
SMI32	Rabbit IgG	1/1000	1/500	Abcam
TARDBP	Rabbit IgG	1/200	1/500	Proteintech
pTARDBP	Mouse IgG	1/200	1/500	Proteintech
$\alpha$ -tubulin	Mouse IgG		1/5000	Abcam
Histone H4	Rabbit IgG		1/500	Abcam
GAPDH	Mouse IgG		1/5000	Abcam
Acetylated $\alpha$ -tubulin	Mouse IgG		1/5000	Abcam
SSEA4	Mouse IgG	1/200		Santa Cruz
Tra1-60	Mouse IgG	1/1000		Merck Millipore
OCT4	Rabbit IgG	1/400		Santa Cruz
Nanog	Goat IgG	1/500		R&D
SOX2	Goat IgG	1/500		R&D
DNCT1	Goat IgG		1/500	Abcam
TUBB4A	Rabbit IgG		1/1000	Mybiosource
MAPT	Rabbit IgG		1/250	lsbio

**Appendix Table S4.** Primers used in making of tagged lines, isogenic control, sequencing, Semi-quantify PCR and qPCR

Name	Forward primer sequence 5'---3'	Reverse primer sequence 5'---3'
Isogenic HA-left donor template	CTGCAGAAGGTGTAGACGTTGAGAG C	ATGCGTCATTTTGACTCACGCGGT
Isogenic HA-right donor template	TATTGACGTCAATGGGCGGGG	CACAACCAGGCAACTACTCTCCCAG
Isogenic guide RNA TDP-43	CACCGAACTGCTCTGTAGTGCTGCC	AAACGGCAGCACTACAGAGCAGTT C
Isogenic TDP-43 amplification	GGGGTTTAAATGAAATGAGTGTTTC	AAACAAAAGAACCAAACACTGTGA
Isogenic TDP-43 amplification nested PCR	GCCGAACCTAAGCACAAATAGC	GAACCAAACACTGTGACACCA
Isogenic TDP-43 amplification nested PCR Sequencing	GAAGATTTGGTGGTAATCCAGG	CCAATCAGGCAAACAGCAG
Tagged lines HA-left Donor template	GATCTGGCTGGTCTTGAACCTC	CCTAAATGCACAGCGACGGA
Tagged lines HA-right Donor template	GGCGGGCCATTTACCGTAAG	CCTGTGATGCGTGATGACGA
Tagged lines cDNA amplification	AAGGGCGAGATCAAGCAGAGG	CCAATCAGGCAAACAGCAGTTCA
Tagged lines cDNA amplification sequencing	TCCACAACGAGGACTACACC	CTATACCAACCAACCACAACCC
Tagged lines guide RNA	CACCGCCGAAGATGAGAACGATGAGC	AAACGCTCATCGTTCTCATCTTCGG C
OCT4	GATGGCGTACTGTGGGCC	TGGGACTCCTCCGGGTTTTG
Nanog	CAGCCCCGATTCTTCCAGTCCC	CGGAAGATTCCCAGTCGGGTTTCC C
SOX2	GGGAAATGGGAGGGGTGCAAAAG AGG	GGGAAATGGGAGGGGTGCAAAAG AGG
Sendai	TGCCCAAGCAGACACCACCTG GCA	