Model-independent reorganization of translation in TDP-43 Amyotrophic Lateral Sclerosis

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Abstract

The RNA-binding protein TDP-43 is a major contributor of Amyotrophic Lateral Sclerosis (ALS). Despite its recognized involvement in the disease, the molecular mechanisms linking TDP-43 dysregulation to ALS pathogenesis remain elusive. No clear consensus has been reached as to how it may directly or indirectly impact protein synthesis at genome-wide level. To elucidate TDP-43-associated dysfunctions in this process, we exploited *in cellulo* and *in vivo* models of TDP-43 proteinopathy integrating multiple ribosome profiling techniques, a tag-free miniaturized polysomal profiling coupled with RNA sequencing, and biochemical assays with subcellular (i.e., cell body and axon) and compartment-specific (i.e., RNA granules and polysomes) resolution. Across ALS models,

we identified a systemic dysregulation in translation, characterized by: i) widespread axonal- and polysome-specific downregulation of TDP-43 target mRNAs, ii) reorganization of mRNA distribution between ribosome-free and polysomal compartments, and iii) altered ribosome dynamics and occupancy with downstream reorganisation of ribosome engagement with mRNAs. These findings suggest that ALS pathogenesis is characterised by a systemic reorganisation of ribosomes, providing a novel mechanistic framework for understanding disease progression.

Introduction

Amyotrophic Lateral Sclerosis (ALS) is a fatal neurological disorder primarily characterised by progressive degeneration of upper and lower motor neurons and alterations in axons and presynaptic terminals in the corticobulbar/corticospinal tract and in the motor component of peripheral nerves (Ito et al., 2017). Around 90% of ALS cases are sporadic and the remaining 5% have an established genetic cause (Kim et al., 2020; Taylor et al., 2016). Even if our understanding of the genetic basis of ALS has steadily advanced, progress in developing new therapies remains hindered by our limited knowledge of the fundamental cellular and molecular events in affected cells. ALS, as many other neurodegenerative diseases, is characterised by defects in mRNA metabolism, affecting RNA granule formation and local axonal translation (Wang and Sun, 2023). RNA granules preside over RNA transport and storage (Shin and Brangwyne, 2017; Wang et al., 2018; Maharana et al., 2018; Pierron and Weil, 2018) and their formation is tightly connected with regulation of protein synthesis (Bauer et al., 2023). Protein synthesis, or mRNA translation, takes place in membrane-less compartments, called polysomes, which form a complex integrated platform of molecules such as ribosomes, mRNAs, aminoacyl-tRNAs (aa-tRNAs), RNA binding proteins (RBPs) and non-coding RNAs (Pecoraro et al., 2022). Polysomes and granules share mRNAs and RBPs (Simsek et al., 2017; Leppek et al., 2021; Anadolu et al., 2023), and ribosome concentration modulates translation efficiency (Mills and Green, 2017) and granules phase separation (Delarue et al., 2018).

The presence of axon-targeting signals in the 3' UTR of several mRNAs (Shigeoka et al., 2016) suggests that specific RNAs, and the associated translational machinery, must be precisely transported along axons and translationally regulated *in situ* by RBPs (Fusco et al., 2021; Bellon et al., 2017; Cioni et al., 2019). Mutations in RBPs such as TDP-43 (Kabashi et al.2008) and FUS (Kwiatkowski et al.2009; Vance et al. 2009) are major contributors to the development of genetic ALS, also associated to Fronto-Temporal Dementia (ALS/FTD), most likely by altering mRNA localization, maturation, and translation. TDP-43, which is encoded by the TARBDP gene (Buratti et al., 2001), plays a role in RNA transport and granule formation (Corbet et al., 2021; Maharana et al., 2018), binding several thousands of mRNAs in their 3' UTR through GU repeats (Tollervey et al., 2011; Polymenidou et al., 2011). TDP-

43 mislocalisation produces cytoplasmic aggregates, which are common hallmarks of >90% of all ALS cases (Neumann et al., 2006; Peng et al., 2020). In addition, accumulation of cytoplasmic TDP-43 is associated with broad defects in RNA metabolism, from mRNA splicing (Fiesel et al., 2012) and transport (Alami et al., 2014; Bilsland et al., 2010) to stress granule formation (Colombrita et al., 2009), mRNA degradation (Tank et al., 2018) and protein synthesis (Arai et al., 2006; Neumann et al., 2006; Geser et al., 2008; McCluskey et al., 2009; Ling et al., 2013, Arnold et al., 2013; Russo et al., 2017).

Previous studies provided evidence for a functional role of cytoplasmic TDP-43 in translation (Blokhuis et al., 2016; Sun et al., 2015), further supported by the observation of TDP-43 association with translation regulators and machinery components (Freibaum et al., 2010; Higashi et al., 2013; Coyne et al., 2015; Russo et al., 2017). Although TDP-43 dysfunction has been shown to cause translation alterations (Piol et al., 2023), either at global or mRNA-specific levels, and in several *in vitro* (Fiesel et al., 2012; Charif et al., 2020; Neelegadan et al., 2019; Russo et al., 2017; Chu et al., 2019; Altman et al., 2021; Majumder et al., 2012) and *in vivo* (Gao et al., 2021; Coyne et al., 2015; Lehmkuhl et al., 2021, Charif et al., 2020) models of ALS, no uniform conclusions as to how TDP-43 dysregulation may impact on protein synthesis in ALS has been reached. To date, the combined effect on local mRNA exchange and on the crosstalk between granules and polysomes induced by TDP-43 proteinopathy has never been simultaneously explored at subcellular resolution and genome-wide level. This understanding could help addressing unanswered questions on the global impact of TDP-43 on the disease.

To simultaneously portray the repertoires of translational defects caused by TDP-43 proteinopathy at subcellular (cell body vs axon) and compartment (RNA granules and polysomes) levels, we used a tag-free miniaturised polysomal profiling strategy coupled with RNA-Seq and biochemical assays. We exploited this method in cortical neurons cultured in microfluidic chambers as our primary model of ALS. Comparing these results with *in cellulo* (Brown et al., 2022) and *in vivo* model of the disease (Arnold et al., 2013) using active and total ribosome profiling from primary cortical neurons, and RNAseq from patients' post-mortem spinal cords (Krach et al., 2018), we potentially uncovered a disease-model independent mechanism. This mechanism involves the reorganization of

ribosome recruitment on mRNAs (Frei et al., 2020) within neurons, suggesting a broader and more systemic impact of TDP-43 dysfunction on intracellular organization. These findings introduce a novel layer of complexity to ALS pathology and provide fresh insight that could reshape how we interpret past and future studies of the disease.

Results

Ribosome reorganization into larger polysomes is a common feature in ALS models.

To build on previous qualitative findings suggesting that TDP-43 associates with polysomes (Freibaum et al., 2010; Higashi et al., 2013; Coyne et al., 2015; Russo et al., 2017; Coyne et al., 2014; Majumder et al., 2016; Neelagandan et al., 2019), we quantitatively determined the relative association of endogenous TDP-43 with the translation compartment, namely ribosomal subunits, ribosomes and polysomes, and with RNA granules by applying polysome profiling in human and mouse cell lines and mouse tissues (**Fig. 1a**). This approach enables the isolation of proteins or RNA associated with the translation machinery (i.e. ribosomes and polysomes) or not associated with ribosomes, which we will refer to as "ribonucleoprotein particles (RNPs)/granules" throughout this manuscript. Using established markers of the small (RPS6) and large (RPL26) ribosomal subunits and of RNA granules (FUS and HuD) (**Supplementary Fig. 1a-c**), we found that under physiological conditions the majority of the endogenous TDP-43 protein co-sediments with RNPs/granules. This pattern was consistent in human induced pluripotent stem cells (hiPSCs), murine motor neuron-like cell lines (NSC-34) and murine cortex and spinal cord (**Fig.1b** and **Supplementary Fig. 1a-c**). Notably, a small fraction of the total TDP-43, ranging between 2% and 5%, was found to associate with the translation machinery (**Fig. 1b**).

To understand whether the association of endogenous TDP-43 with the translation machinery is exclusively RNA-dependent, we performed a subcellular fractionation assay in hiPSCs with and without RNAse treatment (**Fig. 1c**), as described in Lauria et al., 2020. The ribosomal proteins of the small (RPS6) and large (RPL26) subunits were used as markers of ribosomes and polysomes, FUS as a marker of RNA granules, and the polyA-binding protein (PABP) as a control of mRNA-dependent association of proteins with polysomes. In agreement with what was observed in **Fig. 1b** (left donut plot) and **Supplementary Fig. 1a,** in the absence of RNAse treatment (**Fig. 1c,** left panel), the large majority of TDP-43 primarily associates with RNPs/granules (S100 lane)**.** After a step of high salt wash, the association of TDP-43 with the ribosome pellet is still visible (WR lane), suggesting that TDP-43 directly binds the translation machinery. As suggested by its binding with RACK1 (Russo et al., 2017),

after endonuclease digestion (**Fig. 1c,** right panel), TDP-43 is still associated with ribosomes (R and WR lanes) through RNA-independent interactions.

Next, we explored the hypothesis that TDP-43 proteinopathy changes the balance between TDP-43 association with RNPs/granules and the translation machinery, resulting in alterations of ribosome engagement with the mRNAs. Since mild overexpression of WT or mutant TDP-43 in neurons leads to TDP-43 proteinopathy and ALS-like neuronal phenotypes (Tsai et al., 2010), we took advantage of TDP-43 overexpression-based *in vivo* and *in cellulo* models: i) cortices and spinal cords of an *in vivo* murine model of ALS characterised by the transgenic expression in the central nervous system of the mutant human TDP-43-Q331K (hTDP-43-Q331K) (Arnold et al., 2013) (**Supplementary Fig. 1d**); ii) three murine motor neuron-like cell lines (NSC-34) stably engineered for the doxycycline-inducible expression of His-HA-tagged hTDP-43-WT or two hTDP-43 mutants (A315T and Q331K) (**Supplementary Fig. 1e**).

We first performed polysome profiling to obtain the fraction of ribosomes in polysomes (FRP) in the two models (**Fig. 1d** and **Supplementary Fig. 1f,g**) and observed no significant variation (**Supplementary Fig. 1g**), as also shown in MN1 cell lines (Neelagandan et al., 2019). Second, we investigated the co-sedimentation of hTDP-43-Q331K with ribosomal markers and additional control proteins along the polysome profiling fractions in the cortex and spinal cord of the *in vivo* model of ALS at an early symptomatic stages of the disease (**Fig. 1e-h**). We revealed that hTDP-43-Q331K significantly increases its association with ribosomes and lighter polysomes (**Fig. 1e,f**), whilst no changes were observed for FUS protein, another RBP involved in ALS. The change in hTDP-43-Q331K is accompanied by a redistribution of the ribosomal markers RPL26 (large subunit) and RPS6 (small subunit), which shifts towards polysomes with a higher number of ribosomes (**Fig. 1e,f**). In agreement with these results, changes in the co-sedimentation profiles of TDP-43 were also observed in murine motor neuron-like models of TDP-43 proteinopathy (**Fig. 1g,h**). In these cell lines, both TDP-43-WT and TDP-43-Q331K accumulated in the RNPs/granule fractions, TDP-43-Q331K showed a decrease in polysomes and TDP-43-A315T exhibited an increased association with polysomes (**Fig. 1h**). Despite these differences, in the three cellular models of TDP-43 proteinopathy, the markers of the ribosomal

subunits modestly shifted towards polysomes with a higher number of ribosomes, mirroring the redistribution of ribosomes observed *in vivo* (**Fig 1d-f**).

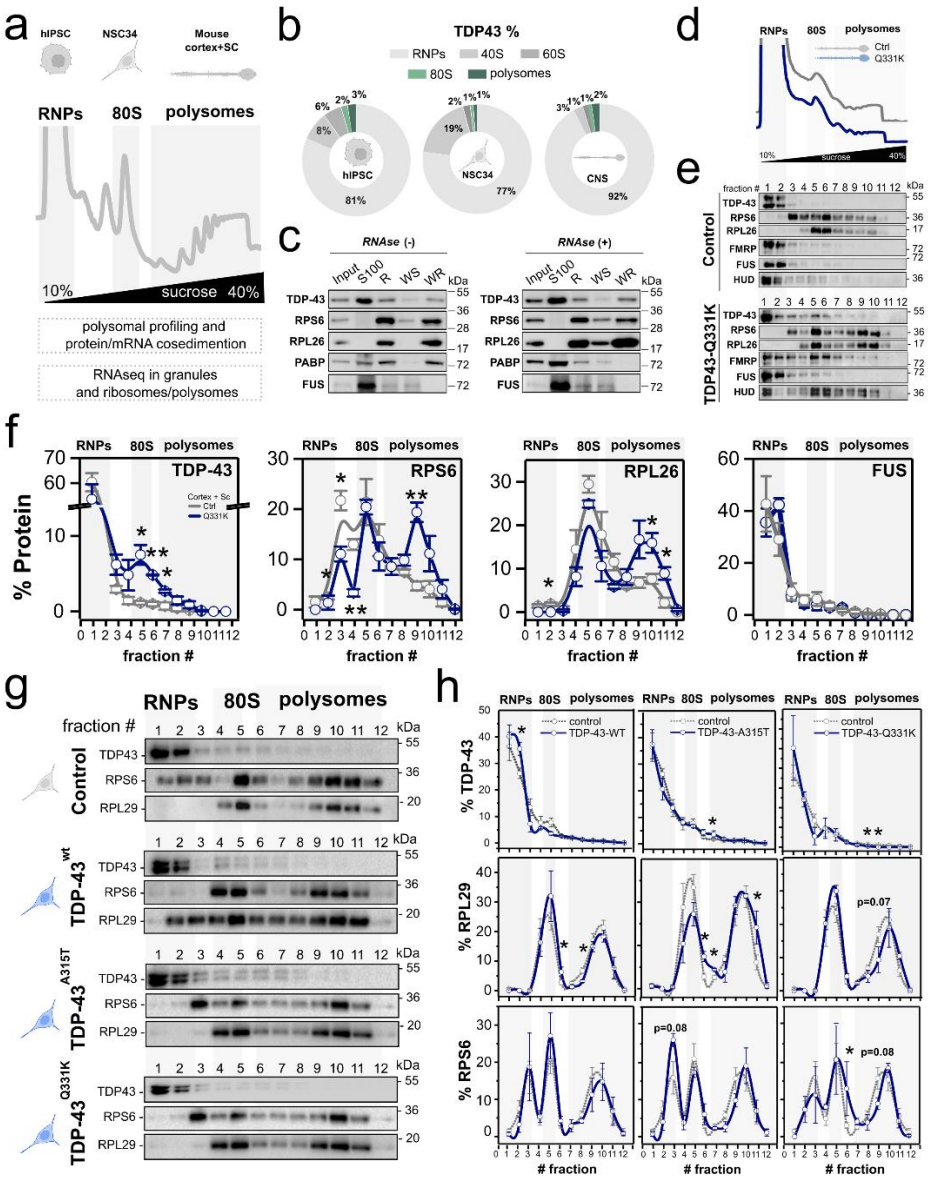

Fig. 1. TDP-43 associates with polysomes and TDP-43 proteinopathy induces alterations of ribosome engagement with mRNAs. (**a**) Schematic representation of the biological systems and approaches used in this paper to investigate TDP-43's role in translation. (**b**) Donut plots reporting the relative percentages of endogenous TDP-43 co-sedimentation with RNPs, 40S, 60S, 80S, and polysomes in polysome profiles of hiPSCs, NSC-34 cell lines, and murine central nervous system (CNS). Data are mean of n=3 biologically independent replicates. (**c**) Western blot analysis of subcellular fractions before (left) and after (right) RNAse I treatment of cytoplasmic lysates from hiPSCs (input). Labels correspond to ribosome-free cytoplasmic components (S100); ribosomes and polysomes (R); loosely ribosome-bound proteins (WS); and strongly ribosome-bound

proteins (WR). Ribosomal markers RPL26 and RPS6 were used as control of ribosome sedimentation. FUS was used as a marker of RNA granules. PABP was used as control for RNA-dependent interactions. (**d-e**) Representative polysome profiles (d) and representative co-sedimentation profiles (e) of TDP-43, ribosomal markers (RPL26, RPS6), and RNA-binding proteins (FMRP, FUS, and HUD) in the cortex and spinal cord of control and transgenic mice expressing hTDP-43-Q331K. (**f**) Relative percentage distribution along the profile of TDP-43, ribosomal markers (RPS6, RPL26), and FUS in the cortex and spinal cord of control and transgenic mice expressing hTDP-43-Q331K. Data are mean ± SEM of n=3 biologically independent replicates. Differences were assessed with two-tailed T-test (P-value: *<0.05, **<0.01). (**g**) Representative co-sedimentation profiles of TDP-43 and ribosomal markers (RPL29, RPS6) in NSC-34 expressing His-HA-tagged hTDP-43-WT or two hTDP-43 mutants (A315T and Q331K). (**h**) Relative percentage distribution along the profile of TDP-43 and ribosomal markers (RPL29, RPS6) in NSC-34 expressing His-HA-tagged hTDP-43-WT or two hTDP-43 mutants (A315T and Q331K). Data are mean ± SEM of n=3 biologically independent replicates. Differences were assessed with two-tailed T-test (P-value: *<0.05, **<0.01).

Increase in mutant TDP-43 association with polysomes in the cell body disrupts protein synthesis in the axons in a murine model of ALS

The variations in the association of TDP-43 with the translation machinery in the *in vivo* and *in vitro* models of ALS, along with the reorganization of ribosomes into larger polysomes, prompted us to investigate whether this effect is potentially restricted to the axon or the cell body of primary cortical neurons (PCNs). We used PNCs cultured in microfluidic chambers to spatially restrict the cell bodies and the axons and a miniaturised polysome profiling strategy for low input samples to obtain a sedimentation profile with a dot blot (**Fig. 2a, Supplementary Fig. 2a,b**). After demonstrating that the co-sedimentation patterns of ribosomal proteins and polysome-associated PABP1 is similar in the miniaturised and traditional sucrose gradients (Lauria et al., 2020) (**Supplementary Fig. 1c**), we applied this method to the cell body and axon of PCNs overexpressing the Turbo Red Fluorescent Protein (TRFP) as control, and overexpressing TDP-43-A315T fused to TRFP (**Figure 2b,c** and **Supplementary Fig. 2d-h**). The distribution of the ribosomal markers in control samples helped us identifying the ribosome and polysome fractions, which in the control cell body are in fraction 7-8 and 9-12, respectively (**Figure 2b**, left panels). We used this result to inform the interpretation of the axonal dot blot where the ribosomal proteins RPL26 and RPS6 are not completely incorporated in axonal

ribosomes or polysomes (**Fig. 2b**, right panels), as previously reported (Fusco et al., 2021). In agreement with what shown in whole cells and tissues, in the cell bodies the endogenous TDP-43 is primarily associated with RNPs/granules, whilst in the axons the polysome-associated endogenous TDP-43 accounts for 1/5 of the axonal TDP-43 (**Supplementary Fig. 2i**). In agreement with what was observed in NSC-34 cells expressing TDP-43-A315T (**Fig. 1g,h**), we found that the association of TDP-43-A315T with polysomes increases in the cell body (**Fig. 2d**, left panels). Conversely, in the axon, we did not observed alterations in the association of TDP-43 with ribosomes or polysomes but a slight shift of the ribosomal proteins towards RNPs/granules fractions (**Fig. 2d**, right panels), suggesting different rewiring of translation in the cell body and axon. In line with this hypothesis, using an *in situ* puromycin-based labelling approach (David et al., 2012), we found an increase in the number of axonal foci of active translation in the axons of PCNs overexpressing TRFP-TDP-43-WT and TRFP-TDP-43-A315T (**Figure 2e,f**).

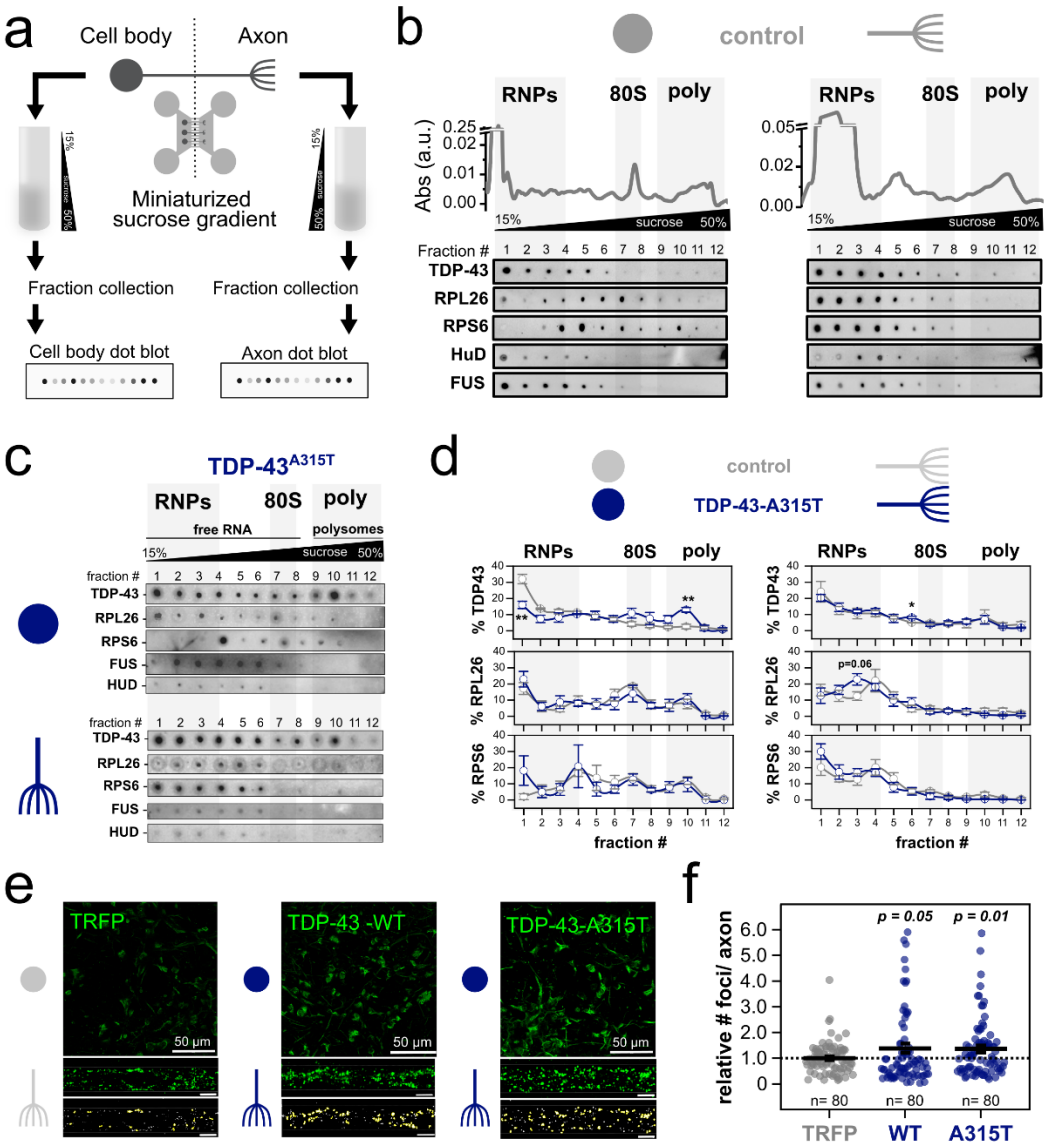

Figure 2. TDP-43 proteinopathy causes axonal protein synthesis alterations *in cellulo*. (**a**) Experimental design for the isolation of cell bodies and axon from cortical neurons cultured in microfluidic chambers. . (**b-c**) Representative polysomal profiles and dot blot co-sedimentation profiles of TDP-43, ribosomal markers (Rpl26 and Rps6), and RNA-binding proteins (FMRP, Fus and Hud) in cell body and axons from wild type PCNs (c) and PCNs upon ectopic expression of TDP-43-A315T (d) cultured in microfluidic chambers. (**d**) Quantification of co-sedimentation profiles of TDP-43 and ribosomal markers in the cell body and axons of PCNs control and expressing TRFP-TDP-43-A315T. Data are mean ± SEM of n=3-4 biologically independent replicates. Differences were assessed with two-tailed T-test (P-value: *<0.5, **<0.1). (**e**) Immunofluorescence of cell bodies and axons in microgrooves of microfluidic chambers after puromycilation assay. Neurons infected with TRFP (left panel), TDP-43-WT (middle panel), TDP-43-A315T (right panel) were treated with puromycin and sites of active translation were labelled with Alexa 488 nm (green dots). (**f**) Average number of foci of active translation per 10 µm axon length in axons

of cortical neurons expressing TDP-43-WT or TDP-43-A315T relative to TRFP controls. Differences were assessed with two-tailed T-test. P-values are reported in the figure.

TDP-43 proteinopathy alters ribosome dynamics and occupancy of TDP-43 target mRNAs

To test the hypothesis that changes in mutants TDP-43 association with the translation machinery may lead to alterations in ribosome dynamics and functionality, impacting protein synthesis, as observed here and in other models of ALS (Altman et al., 2021), we utilized two complementary approaches. First, to determine the ribosome kinetics in PCNs isolated from the mouse model of ALS expressing hTDP-43-A331K and littermate controls, we performed a ribosome run-off assay (**Fig. 3a**). Using polysome profiling, we monitored the kinetics of polysome disappearance upon treatment with harringtonine (**Fig. 3b**), which selectively blocks ribosomes at the start codon (Fresno et al., 1977). After deriving the time constants, we found a decrease in ribosome kinetics in ALS (**Fig. 3c**), further strengthening the shift of ribosomal proteins towards heavier polysomes. Second, to understand if these alterations impact the ribosome recruitment on mRNAs and their functionality, we performed traditional ribosome profiling (Ingolia et al., 2009) and, in parallel, RiboLace (Clamer et al., 2018) (**Fig. 3d**). The first method helps identify both active and inactive (or stalled) ribosomes, while the second specifically provides ribosome occupancy data for active ribosomes. Despite no differences in ribosome positioning at the beginning or end of mRNAs (**Supplementary Fig 3a**), we observed numerous significant changes in ribosome occupancy (**Fig 3e**, **Supplementary Fig. 3b,c** and **Supplementary File 1**), which are likely not driven by variations at the level of active ribosomes (**Fig. 3e,f**). To understand if the pronounced alternations in total ribosome occupancy may specifically impact TDP-43 targets, we performed an enrichment analysis for TDP-43 target mRNAs (**Fig. 3g**), showing that mRNAs with reduced ribosome occupancy are bound by TDP-43. Our results indicate that ribosome alterations in this ALS model are predominantly occurring on TDP-43 targets.

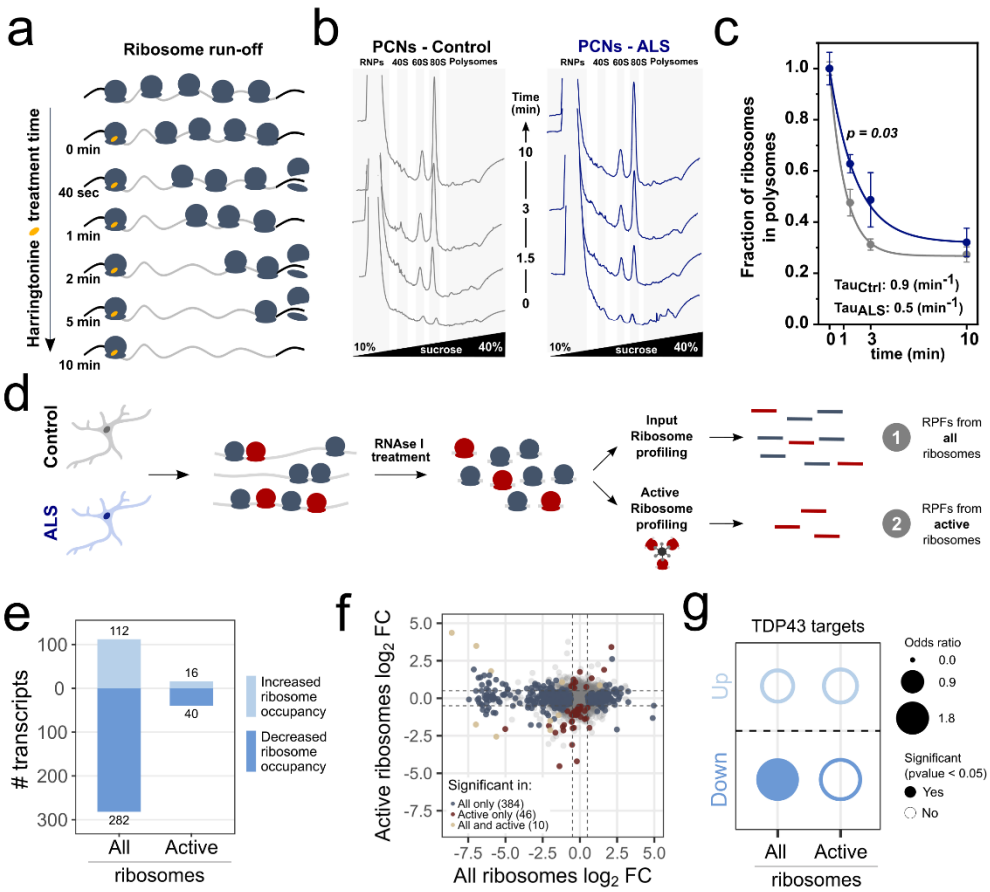

Fig 3. TDP-43 proteinopathy induces different translational alterations in TDP-43 target mRNAs and non target mRNAs. (**a**) Scheme summarising the effect of harringtonine-induced ribosome run-off. Increasing the time of harringtonine treatment results in a progressive accumulation of 80S fraction on the start codon and depletion of polysomes fraction. (**b**) The effect of harringtonine on polysome profiles from control PCNs (left panel) and PCNs expressing hTDP-43-Q331K (right panel) treated only with cycloheximide (time point 0) and after 1.5, 3, and 10 minutes of harringtonine treatment. (**c**) FRP calculated from the polysome profiles of harringtonine treated cells for each time point: data were fitted with an exponential decay curve to compute the ribosome kinetics (Tau) values, which is 1.8 times slower in ALS (tALS= 0.5 min-1) compared to control (tCTRL= 0.9 min-1) condition. Data are mean SEM of n=5-7 biologically independent replicates. Differences were assessed with two-tailed T-test (P-value: * < 0.05) (**d**) Schematic of the experimental design for studying the localization of all ribosomes (either active or inactive) and only active ribosomes. (**e**) Number of mRNAs showing decreased or increased ribosome occupancy in ALS considering both active and inactive ribosomes ("All") or only active ribosomes. (**f**) Comparison of ribosome occupancy variations based on both active and inactive ribosomes ("All", x-axis) and on active ribosomes (y-axis). The colour reports whether the variation is significant only if considering both active and inactive ribosomes ("All only"), only according to the active ribosomes ("Active only") or both populations ("All and active"). (**g**) Enrichment analysis of TDP-43 target mRNAs among transcripts showing increased and decreased ribosome occupancy in ALS. Dot size is

proportional to the enrichment measured by odds ratio and the significant enrichments are reported as filled circles (Fisher's exact test).

TDP-43 proteinopathy causes massive axonal downregulation of TDP-43 mRNA targets and alters their association with the axonal translation machinery.

To understand if these translation alterations are predominantly occurring on TDP-43 targets also at the subcellular level, we determined the catalogue of RNP/granule-associated RNAs and polysome-associated RNAs from both cell bodies and axons of PCNs cultured in microfluidic chambers by RNA-Seq (Pisciottani et al., 2023) (**Fig 4a**, **Supplementary Fig. 4a, Supplementary File 2**). The expression of Map2 and Nfl mRNAs, as markers of dendrites and neurons, respectively (Briese et al., 2016), showed no dendritic contaminations in the axonal compartment (**Fig. 4b**). Importantly, mRNAs in the control axonal RNPs/granule and polysome compartments are more likely to be bound by TDP-43 than mRNAs localised in the cell body (**Fig. 4c**).

These results suggest that mRNAs associated with axonal RNPs/granules and axonal polysomes may be more sensitive to TDP-43 proteinopathy. In fact, in our PCN models of ALS expressing TDP-43-WT or TDP-43-A315T (Pisciottani et al., 2023) used before (**Figure 2a**, **Supplementary 4b**), the differential expression analysis at the cell body level (**Fig. 4d**) revealed 1071 (TDP-43-WT) and 1018 (TDP-43-A315T) differentially expressed genes (DEGs) (**Fig. 4d**). Of these DEGs only 58 and 72 are shared across the RNPs/granules and polysomal compartment, respectively. Strikingly, in the axon the number of DEGs is almost three times larger than in the cell body (2685 for TDP-43-WT and 2744 for TDP-43-A315T), accounting for 89% of the total changes (**Fig. 4d**). The number of DEGs shared across the RNPs/granules and polysomal compartment, are ~ 1/10, i.e. 278 (TDP-43-WT) and 213 (TDP-43-A315T). Interaction network analysis of proteins encoded by axonal DEGs in both conditions revealed shared (**Fig. 4e**) or specific (**Supplementary Fig. 4c**) protein communities. Interestingly, the emerging communities are mainly associated with localization/transport, catabolic and metabolic processes, cell projection, and mitochondrion (**Fig. 4e** and **Supplementary Fig. 4c**). These communities recall several themes known to be altered in ALS

(Briese et al., 2020, Nagano et al., 2020, Lehmkul et al., 2021, Guise et el., 2024; Pisciottani et al., 2023).

As in the ribosome profiling analysis (**Fig. 3g**), we observed a significant enrichment of TDP-43 targets in the downregulated set of DEGs (**Fig. 4f**). This enrichment is axonal-specific (**Fig. 4f**, right panels), as no enrichment was associated with the cell body compartment (**Fig. 4f**, left panels) or with up-regulated genes. This robust depletion of axonal mRNA can be induced by abnormal association of mRNA with polysomes, defective axonal transport or mRNA degradation (Briese et al., 2020; Tank et al., 2018). We can exclude the abnormal association of mRNA with polysomes because the extent of mRNA alterations is the same in RNPs/granules and polysomal compartments, and the massive defective transport because the axonal downregulation is not accompanied by an upregulation in the cell body (**Fig. 4d**). We thus considered the known role played by TDP-43 in RNA destabilisation (Ayala et al., 2011; Tank et al., 2018) and found an axonal-specific enrichment of unstable RNAs among downregulated TDP-43 targets (**Fig. 4g**), whilst the up-regulated genes showed less or no enrichment. These results are in line with the previously observed decrease in ribosome dynamics (**Fig. 3c**) that can cause mRNA instability (Mills and Green, 2017; Stein, K. C. & Frydman 2019; Morris et al., 2021).

The fact that hundreds of TDP-43 targets mRNAs are unstable and particularly enriched in the axon, is likely to impact ribosome availability, potentially leading to widespread consequences in gene expression, due to systemic rewiring of ribosome engagement with available transcripts. This idea aligns with the concept of cellular resource reallocation (Mills and Green, 2017; Frei et al., 2020). To validate this hypothesis and mimic the effect of TDP-43 targets or of non-targets, we developed an assay in NSC-34 cells to observe the impact of TDP-43-WT and TDP-43-A315T overexpression (**Fig. 4h**) on fluorescent sensors. One sensor includes 3 or 4 TDP-43 binding sites (EBFP-TS, namely TDP-43 sensor), whereas the second does not (EGFP, namely capacity monitor) (**Fig. 4h,** upper panel). The idea underlying this design is that we would observe an increase in the translation of the TDP-43 independence capacity monitor and a concomitant downregulation of the TDP-43 sensor if ribosome reorganization is occurring. In keeping with our hypothesis, we observed that the higher the number of TDP-43 binding sites in the sensor, the less efficient is its translation upon overexpression of TDP-43-

WT or TDP-43-A315T compared to controls (**Fig. 4h**, bottom panel, grey). Conversely, the capacity monitor, mimicking TDP-43 non-target mRNAs, is more efficiently translated in both ALS-like models (**Fig. 4h**, bottom panel, green), supporting the hypothesis of cellular resource reallocation. Stemming from these findings, we propose a model of ALS based on slower ribosome dynamics that may cause a drop in the levels of TDP-43 target mRNAs, release of ribosomes, and their reorganization on the remaining mRNAs, mainly from those not normally regulated by TDP-43 (**Figure 4i**).

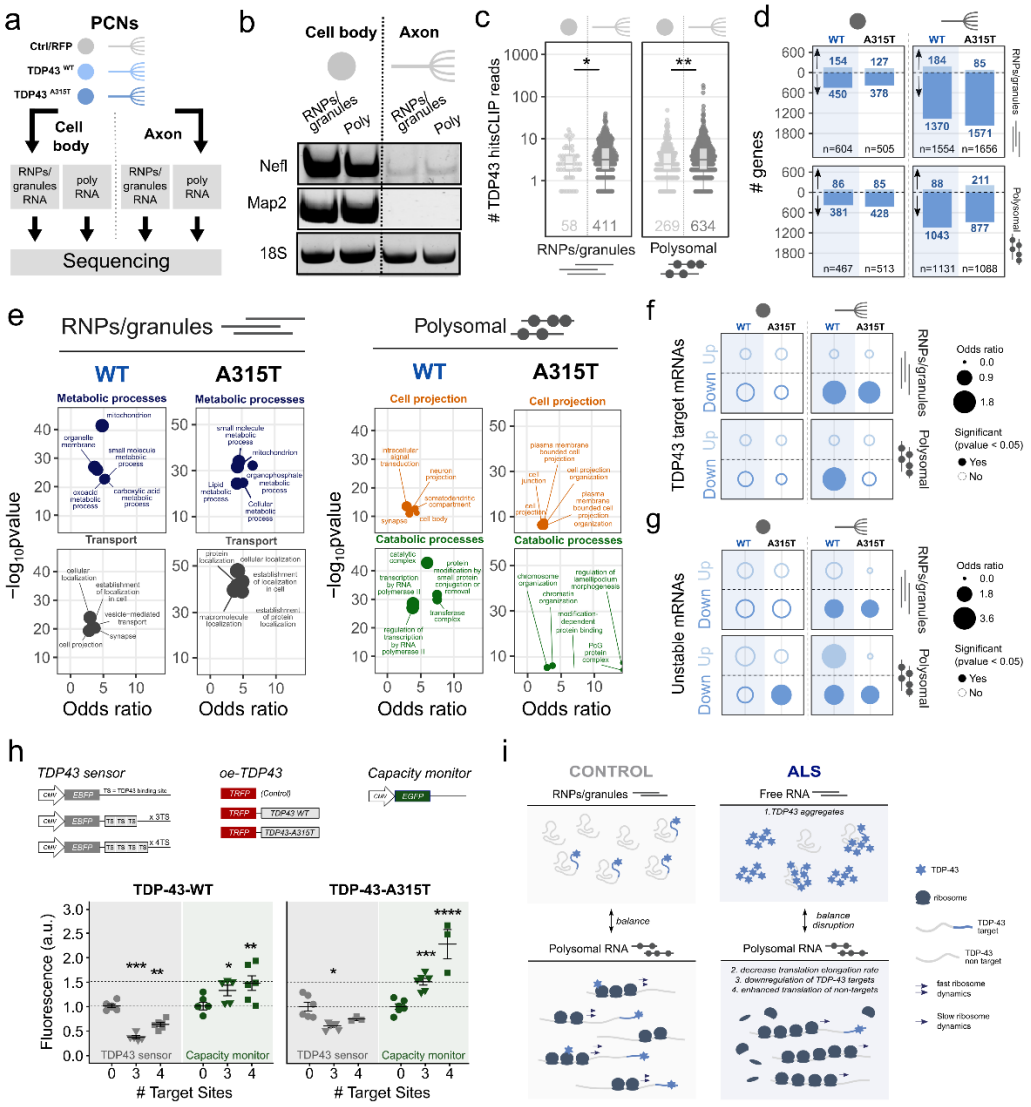

Fig 4. TDP-43 wild-type and mutants induce the downregulation of unstable TDP-43 target genes, primarily in the axon. (**a**) Experimental design for the isolation of RNAs not associated with polysomes (RNPs/granules) and associated with polysomes (polysomal RNA) in cell bodies and axons. from PCNs expressing TDP-43-WT, TDP-43-A315T, and TRFP as a control, cultured in microfluidic chambers. (**b**) RT-PCR of free and polysomal RNA for the neuronal cytoplasmatic Nfl, the

dendrite marker Map2, and the ribosome marker 18S in control PCNs expressing TRFP. (**c**) Number of TDP-43 CLIP-Seq hits (Polymenidou et al., 2011) for polysomal and RNPs/granules enriched in the cell body chamber and in axons of PCN expressing TRFP. The number of genes is shown at the bottom of the boxes. Differences were assessed with two- two-tailed T-test (P-value: * < 0.05, ** < 0.01). (**d**) Bar plot showing the number of up- and down-regulated mRNAs in the cell body and axon upon TDP-43-WT and TDP-43-A315T expression with respect to TRFP. The number of DEGs for each comparison is reported next to the bars and the total number of DEGs is shown at the bottom of the boxes. (**e**) Functional enrichment analysis of the top two communities based on the interaction network of proteins encoded by RNPs/granules (left panel) and polysomal (right panel) genes enriched in the axon, shared across PCNs upon TDP-43-WT and TDP-43-A315T expression. (**f-g**) Enrichment analysis of TDP-43 target genes (f) and of destabilised genes due to the expression of TDP-43 (Tank et al., 2018) (g) among up- and down-regulated genes identified upon TDP-43-WT or TDP-43-A315T expression. Dot size is proportional to the enrichment measured by odds ratio and the significant enrichments are reported as filled circles (Fisher's exact test). (**h**) Upper panels: schematic representation of plasmids used in the translational burden assay where NSC-34 cells were co-transfected with 3 plasmids to monitor TDP-43 target and non-target translation in control and diseased condition. Bottom panels: relative fluorescence signal of TDP-43 sensor (gray) and capacity monitor (green) upon TDP-43-WT and TDP-43-A315T expression, respectively. Data are mean ± SEM of n=3-6 biologically independent replicates. Differences were assessed with two-tailed T-test (P-value: *<0.05; **<0.01; ***<0.001; ****<0.0001). (**c**) Proposed working hypothesis of translational effects of TDP-43 overexpression.

TDP-43 target mRNAs show alterations in post-mortem spinal cords from ALS patients and alterations of ribosome *in vivo* at a very early stage of ALS.

To assess the potential clinical relevance of our findings, we retrieved a publicly available RNA-Seq dataset from post-mortem spinal cords of sporadic ALS patients (Krach et al., 2018) and a dataset based on ribosome occupancy in human motor neurons after TDP-43 silencing (Brown et al., 2022). By intersecting these datasets with ours we found eleven common DEGs (**Fig. 5a**). Nine out of these DEGs have already been associated with ALS or other neurodegenerative diseases (**Table 1**). Next. to expand our investigation into common underlying mechanisms leading to potential disease- and translation-relevant changes, we selected a set of 21 genes for further *in vivo* analysis at a very early stage of the disease. The genes were selected as follows: i) eleven common DEGs, listed in **Table 1**, ii) five DEGs shared between our results and dataset from patients (Krach et al., 2018) (Synj1, Rpl26, Rps4x, Rps6, Gapdh), and iii) five not differentially expressed genes (Gap43, Matr3, Rpl29, Rps14, Smn1). Among the selected genes, 13 genes are TDP-43 target mRNAs and the remaining 8 are not.

We used Actin-b as a housekeeping gene because it shows no variations either at mRNA and protein levels (**Supplementary Fig. 5a**). In agreement with the widespread RNA downregulation revealed by our previous analysis (**Fig. 4**), the transcriptional level of these genes in the spinal cord and cortex of ALS early symptomatic mice shows a global trend of downregulation (**Fig. 5b**). Next, we analysed the association of the 21 transcripts with polysomes using the relative distribution of the mRNAs with the translation machinery (**Fig. 5c** and **Supplementary Fig. 5b,c**). We observed that TDP-43 non-target mRNAs increase their association with the 80S/monosome fraction, while TDP-43 target mRNAs shift significantly toward the heavier polysome fraction (**Fig. 5d**). These results suggest that the downregulation of mRNA levels is accompanied by a marked reorganization of ribosomes on TDP-43 target mRNAs. Further supporting the hypothesis that target and non-target RNAs show different ribosome reorganization, in the axon of *in vitro* models of ALS we observed a robust increase in protein production for the non-target RNA *Gapdh*, whilst the TDP-43 targets Vim and Rrbp1 undergo minor or no significant changes (**Fig. 5**).

In conclusion, this study reveals TDP-43-driven widespread disruptions in RNA metabolism, which is characterised by systemic ribosome reallocation and altered mRNA translation across cellular compartments and at very early stage of disease in multiple models of ALS.

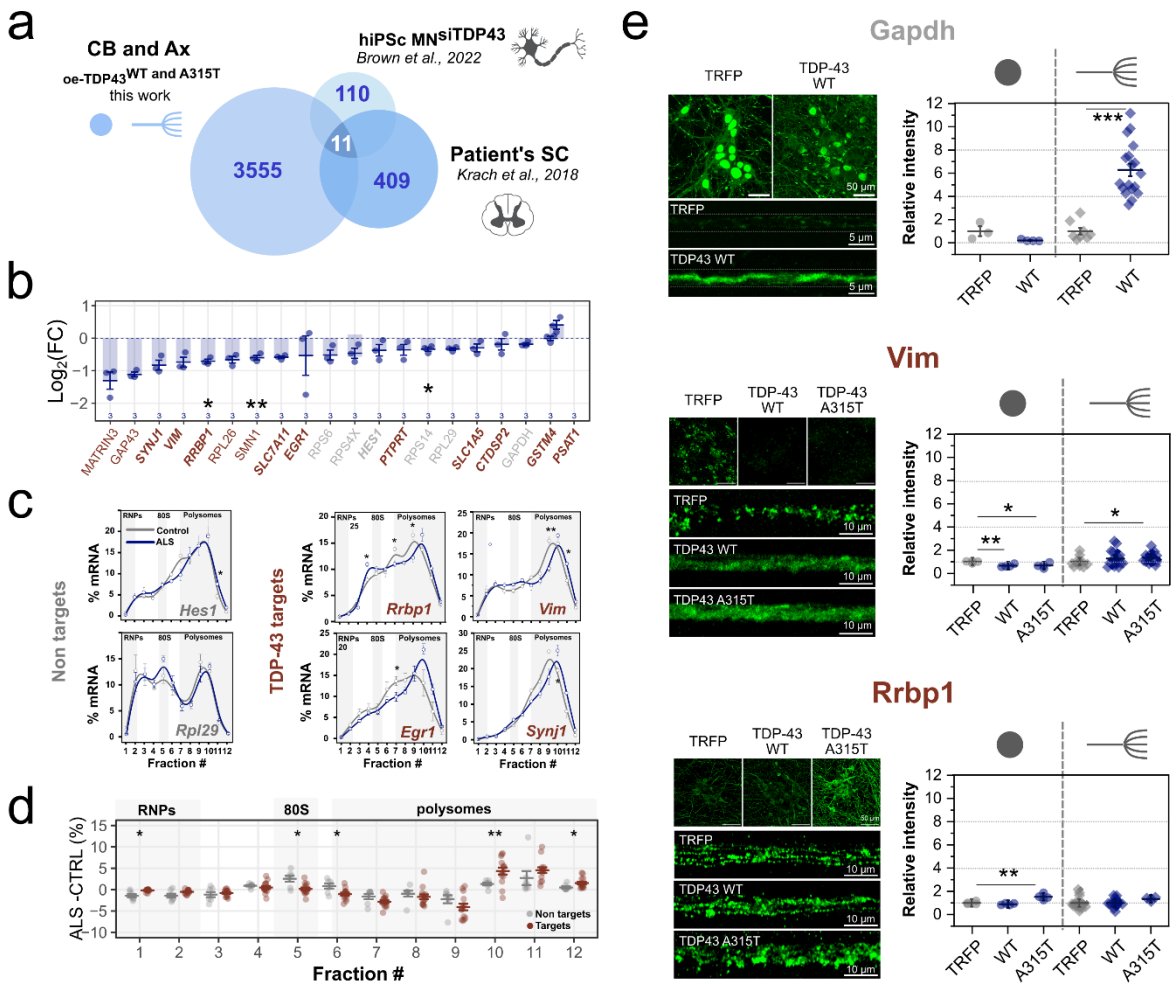

Fig. 5. TDP-43 targets show translational defects at an early symptomatic stage of the disease. (**a**) Overlap between differentially expressed genes (DEGs) identified in our *in vitro* model of ALS, in spinal cords of ALS patients (Krach et al., 2018) and hiPSc motor neurons (Brown et al., 2022), compared to the control condition. Only genes expressed in all samples were considered. The 11 shared genes are listed in Table 1. (**b**) qPCR-derived fold changes in mRNAs for selected TDP-43 targets (red text) and non-target (grey text) genes upon expression of hTDP-43-Q331K in mouse spinal cords and cortices. Data were normalised to Actin-b. The number of biologically independent replicates is reported at the bottom of the box. Data are mean ± SEM. Differences were assessed with two-tailed T-test (P-value: *<0.05, **<0.01). (**c**) Representative relative co-sedimentation profile of TDP-43 non-targets mRNAs and weak, medium and strong TDP-43 targets mRNAs along the sucrose gradient fractions of control and ALS mouse spinal cords and cortices. Data are mean ± SEM of n=3 biologically independent replicates. Differences were assessed with two-tailed T-test (P-value: *<0.05, **<0.01). (**d**) Differences between ALS and control relative percentage co-sedimentation along the sucrose gradient fractions. Data are mean ± SEM of 8 TDP-43 non-target and 12 TDP-43 target genes. Differences were assessed with two-tailed T-test (P-value: *< 0.05, **<0.01). (**e**) Representative images of immunofluorescence (left panels) and relative fluorescence intensity quantification (right panels) of one non-target (Gapdh) and two TDP-43 targets (Vim and Rrbp1) in the cell body and in axons of PCNs cultured in

microfluidic chambers and infected with TRFP control, TDP-43-WT or A315T. Differences were assessed with two-tailed T-test (P-value: *<0.05, **<0.01, ***<0.001).

Table 1.

Gene	Description	References
C1orf216	chromosome 1 open reading frame 216	
CTDSP2	CTD small phosphatase 2	
EGR1	early growth response 1	Ledener et al., 2007; Moujalled et al. 2017; Godini at al., 2018
GSTM4	glutathione S-transferase mu 4	Klim et al., 2019; Cha et al., 2020
HES1	es family bHLH transcription factor 1	von Grabowiecki et al., 2015; Yang et al., 2015
PSAT1	phosphoserine aminotransferase 1	Martins De-Sousa et al., 2012
PTPRT	protein tyrosine phosphatase receptor type T	Carter et al., 2009; Liu et al. 2020
RRBP1	ribosome binding protein 1	Tank et al., 2018
SLC1A5	solute carrier family 1 member 5	Lee et al., 2016
SLC7A11	solute carrier family 7 member 11	Vallerga et al., 2020
VIM	vimentin	Zhou et al., 2015

List of 11 DEGs in our in vitro models of TDP-43-proteinopathy (this study), in post-mortem spinal cords of sporadic ALS patients (Krach et al., 2018) and in human motor neurons with siTDP-43 (Brown et al., 2022).

Discussion

In our investigation as to how TDP-43 impact on protein synthesis in multiple cell lines, tissues, and primary cultures, we expanded on previous qualitative observations about TDP-43 interaction with polysomes (Coyne et al., 2014; Majumder et al., 2016; Russo et al., 2017; Neelagandan et al., 2019), and quantified the fraction of endogenous and cytoplasmic TDP-43 associated with ribosomes to be <5%. In line with reports showing TDP-43-positive granules containing polyribosomes and being transported to axons and dendrites (Miyashiro et al., 2003; Simsek et al., 2017; Thelen and Kye, 2020; Nagano et al., 2020), in the axons of PCNs the fraction of TDP-43 associated with polysomes is ten times higher than in other cell types, with an enrichment in TDP-43 targets. These findings represent an intriguing clue as to how neurons are likely sensitive to translational defects due to TDP-43 mislocalisation or mutations. In fact, global protein synthesis has been reported to either increase (Gao et al., 2021, Fiesel et al., 2012, Charif et al., 2020) or decrease (Gao et al., 2021, Altman et al., 2021, Russo et al., 2017) in various models of TDP-43 proteinopathy, also within the axon (Pisciottani et al., 2023, Briese et al., 2020). Similarly, defective translation was observed in single transcripts and corresponding proteins (Coyne et al., 2014, Chu et al., 2019; Majumder et al., 2016, Majumder et al., 2012), showing the complexity of alterations in protein synthesis in multiple models of ALS (Bjork et al., 2022, Wang and Sun, 2023).

As an attempt to understand whether global or local defects in RNPs/granules and polysomes may underlie common molecular mechanisms, we used a method to further improve the resolution achieved by transcriptome and translatome analyses of cell bodies and axons previously obtained *in vitro* (Nijssen et al., 2018; Briese et al., 2016; Glock et al., 2021) and *in vivo* (Shigeoka et al., 2016), also in ALS models (Nijssen et al., 2018, Rotem et al., 2017). We found robust down-regulation of both RNA/free and polysomal TDP-43 targets in the axon, confirming the widespread polysomal-specific downregulation observed in an *in vivo* model of ALS (Marques et al., 2020). In line with these results, the overexpression of TDP-43-WT and mutants causes widespread mRNA instability, which is an event shared across multiple models of ALS and not accompanied by a decrease in RNA synthesis (Barmada et al., 2015). These events may be triggered by the loss of TDP-43 function resulting in the inclusion of

cryptic exons into mRNAs and Nonsense-Mediated Decay (NMD) (Tan et al., 2016; Tziortzouda et al., 2021; Ling et al., 2015) or by a decrease in translation elongation rates (Duviau et al., 2023; Schoemaker and Green 2012, Dong et al., 2024), which we observed as decrease in ribosome dynamics in PCNs purified from an *in vivo* model of ALS.

Given the fact that TDP-43 target mRNAs represent a large proportion of cellular transcriptomes (Polimenidou et al., 2011), the lack of mRNA molecules may induce not only a worsening in protein aggregation (Maharana et al., 2018) but also the reorganization of ribosomes on available mRNAs. Indeed, we observed widespread change in ribosomes recruitment on polysomes, which is in agreement with the increase in detectable ribosomes in ALS models and in patients (Verheijen et al., 2014) and the proposed trapping of ribosomes in SGs (Anadolu et al., 2023). On the contrary, the minor changes in the relative distribution of TDP-43 in RNP/granules and polysomes RNA suggest that the observed changes are not necessarily driven by stress granules formation or TDP-43 aggregation (Colombrita et al., 2009; Khalfallah et al., 2018). This reorganisation may then lead to an increased probability for non-target transcripts to be translated due to the increased ribosome availability, (Mills & Green 2017) which we observed using capacity monitor assays.

The reallocation of cellular resources (Frei et al., 2020; Cella et al., 2023), i.e. mRNAs and ribosomes, possibly reconciles the apparent inconsistencies in global, gene or cell compartment-specific protein levels in ALS (Fiesel et al., 2012, Majumder et al., 2012; Majumder et al., 2016; Gao et al., 2021; Lehmkuhl et al., 2021; Russo et al., 2017; MacNair et al., 2016; Coyne et al., 2014; Altman et al., 2021; Chu et al., 2019; Higashi et al., 2013). Both global and specific protein levels may vary depending on the available resources, with the axons being particularly sensitive to changes in the equilibrium between ribosomes availability and TDP-43 targets and non-target mRNA levels. We supported this hypothesis at the mRNA-specific level for two transcripts (*Rrbp1*, *Vim*) that are transcriptionally dysregulated in post-mortem spinal cords of ALS patients (Krach et al., 2018) and motor neurons obtained from hiPCS upon TDP-43 silencing (Brown et al, 2022).

Our results can be summarised in a mechanistic model centered on the concept of reallocation of cellular resources (Metzl-Raz et al., 2017) – in our case mRNAs and ribosomes - that explains widespread and complex alterations in multiple TDP-43-based models of ALS. This model is supported by our results (Cella et al., 2023; Frei et al., 2020) in motor neuron-like cell lines, where TDP-43 target genes are down-regulated at the protein level in favour of the increased abundance in TDP-43 non-target reporter. According to this hypothesis, our ALS models share: i) the preferential destabilisation and downregulation of TDP-43 target RNAs (Tank et al., 2018) and the formation of TDP-43 aggregates (Chen-Plotkin et al., 2010); ii) the massive decrease in TDP-43 target mRNAs and the likely increase in ribosome availability leading to the preferred translation of TDP-43 non-target mRNAs or remaining TDP-43 targets.

In summary, we propose a unifying model of ALS pathogenesis based on the concept of disruption of the equilibrium between cellular resources, caused by a mass snowball effect in RNA metabolism resulting in the robust reorganisation of ribosomes along mRNAs and a fine balance in protein synthesis.

MATERIAL AND METHODS

Mouse model of ALS

The hTDP-43-Q331K mouse model of ALS (B6N.Cg-Tg (PrnpTARDBP*Q331K)103Dwc/J)) was purchased from The Jackson Laboratory and was generated on a C57BL6 background, as described in (Arnold et al., 2013). Non-transgenic C57BL/6N littermates were used as controls. Litters were genotyped using standard protocols. Mice were housed within the animal care facilities at the University of Trento under appropriate conditions. Animal breeding and procedures were conducted under appropriate project and personal license granted by the ethical committee of the University of Trento and were approved by the Italian Ministry of Health (D. Lgs no. 2014/26, implementation of the 2010/63/UE).

Cultures of primary cortical neurons for microfluidic chambers

Primary cortical neurons were isolated from wild type C56BL/6J mice. The pregnant female was euthanized by CO2 at 14.5 days of gestation. The cortex was isolated from the embryos and purified from meninges, cut into small pieces and incubated for 5 minutes in DMEM/F12, 0.0125 M glucose, 1% P/S, 1 mM EDTA and then digested in trypsin by incubation in DMEM/F12, 0.0125 M glucose, 1% P/S, 0.25% trypsin, for 10 minutes at 37°C. After trypsin neutralisation in DMEM/F12, 0.0125 M glucose, 1% P/S, 20% FBS, samples were mechanically dissociated into single cells in DMEM/F12, 0.0125 M glucose, 1% P/S, 10% FBS, 4 KU/mL DNAseI, using fire-polished glass pipettes. The cells suspension was then filtered with a 70 µm cell strainer nylon filter, counted and centrifuged for 5 minutes at 163 g at RT to be resuspended in complete Neurobasal medium (Neurobasal, 2% B27 supplement, 18 mM HEPES, 1% P/S, 0.5 mM L-Glutamine). Cortical neurons were seeded on poly-D-lysine (PDL) and laminin coated glasses or plates at the desired concentration. Cortical neurons were maintained in culture at 37°C and 5% CO2 and half medium was changed every two days.

Microfluidic chambers

Microfluidic chambers (SD450 Xona microfluidics) were used for cell body and axonal polysomal profiling and immunofluorescence. Glass coverslips were cleaned with 1 M HCI for 4 hours, extensively washed in milliQ water and dried in the oven. Next, the coverslips and the microfluidic chambers were sterilised in 70% ethanol and dried under a laminar flux hood at RT. The coverslips were coated overnight with 500 µg/mL poly-D-lysine and then assembled with the microfluidic device. The microfluidic chambers were equilibrated with PBS, followed by equilibration in the neurobasal medium. Cortical neurons resuspended in neurobasal medium at the concentration of 25,000 cells/µL were plated in a final amount of 250,000 cells/chamber following the SD450 Xona Microfluidics protocol. BDNF at a final concentration of 10 ng/mL was added every two days in the axonal compartment starting from DIV2.

Production, titration and infection of lentiviral particles

Lentiviral particles were prepared as described previously (Amendola et al., 2005). Briefly HEK293T cells were transient co-transfected using the calcium-phosphate precipitation method with the transfer vectors, the MDLg/pRRE plasmid, the RSV-Rev plasmid and the MDLg plasmid encoding the G glycoprotein of the vesicular stomatitis virus. Cell supernatants containing lentiviral particles were collected 72 h after transfection, filtered and subjected to ultracentrifugation. The pellets were resuspended, divided into aliquots and stored at -80°C. To calculate the titer of lentiviral particles, cortical neurons were seeded in a 24-well plate and infected at 5 DIV with a serial dilution (from 10-3 to 10-7) of lentiviral particles overexpressing TRFP-TDP-43-WT, TRFP-TDP-43-A315T and TRFP. Uninfected cortical neurons were used as control. The experiment was repeated in triplicate for each condition. Cortical neurons were fixed at 9 DIV and processed for immunofluorescence with TRFP and TuJ1 primary antibodies. ArrayScan microscope (Thermo Fisher ArrayScan XTI HCA Reader) was used to acquire 20 random fields per well. For every field the TRFP-positive infected cells (red) and the total number of cells, stained with a nuclear marker (DAPI), were counted. Then, TRFP-positive cells and DAPI-positive cells coming from all fields were summed. A ratio between the number of the total TRFP-positive cells and the total DAPI-positive cells present in each well was calculated. To calculate the titer a percentage ratio between TRFP-positive cells and total DAPI positive cells between 0.1%

and 10% (dynamic range) was chosen, and this formula was used: (Infected cells/Total cells) *Dilution factor*Number of seeded cells. In our experiments a MOI (multiplicity of infections) of 4 was used to ensure the infection of almost total cells without inducing cellular toxicity. Cortical neurons were infected at 5 DIV and treated, fixed or lysed at different DIV based on the experimental needs.

Cell line cultures

Motor-neuron like cell line NSC-34 and hiPSC cell line were maintained in culture at 37°C with 5% of CO_2. NSC-34 cells were cultured in Dulbecco's Modified Eagle's Medium (DMEM) with 4.5 g/l glucose supplemented with 2 mM glutamine, 10% FBS, 100 U/mL penicillin and 100 mg/mL streptomycin. hiPSC cells were seeded on Geltrex-coated 6-well plated and cultured in TeSR-E8 medium.

Transduction and generation of NSC-34 inducible cell lines

The full-length human TDP-43 cDNA was amplified from SK-N-BE cells with AccuPrime DNA polymerase (Thermofisher Scientific) and cloned in SgfI and MluI sites of pCMV6-AN-His-HA plasmid (OriGene) to generate the vector pCMV6-His-HA-hTDP-43-WT, expressing the hTDP-43-WT gene with an N-terminal polyhistidine (His) and HA tag. The mutants hTDP-43-A315T, hTDP-43-Q331K, and hTDP-43-M337V were obtained via PCR-directed mutagenesis. For lentiviruses preparation, the His-HA tagged genes were excised from pCMV6-His-HA plasmids and subcloned into the BamHI and XhoI sites of the vector pENTR1A (Addgene). The resulting vectors were then recombined with pLenti CMV/TO Puro DEST (Addgene) to get the lentiviral vectors expressing His-HA-tagged hTDP-43-WT and its mutants under the control of a doxycycline-inducible promoter. Lentiviruses were then prepared in accordance with the protocols detailed by Campeau et al. 2009, meeting Biosafety Level 2 (BSL-2) requirements.

To generate inducible cell lines, NSC-34 cells were transduced with the pLentiCMV_TetR_Blast vector (Addgene), constitutively expressing the tetracycline (Tet) repressor under the control of a CMV promoter and selected for 7 days using 10 µg/ml Blasticidin (Sigma-Aldrich). The stable cells were

infected with the lentiviral vectors expressing hTDP-43-WT and mutants in the presence of 4 µg/ml polybrene and selected by using 5 µg/ml puromycin.

Subcellular fractionation

hiPSC were lysed with polysomal buffer containing 10 mM NaCl, 10 mM $MgCl_2$, 10 mM Tris–HCl pH 7.5, 1% Triton X-100, 1% sodium deoxycholate, 0.005 U/µL DNAseI, 0.2 U/µL RNase inhibitor, 1 mM dithiothreitol and 10 µg/mL cycloheximide and protease-inhibitor EDTA-free. A few microlitres of lysate was retained for protein extraction (input). The sample was centrifuged for 90 min at 100,000 rpm using a TLA100.2 rotor in a Beckman Optima™ LE-80K Ultracentrifuge. The supernatant corresponds to the S100 fraction and does not contain ribosome-bound proteins. The pellet containing ribosomes (R pellet) was resuspended in high salt buffer containing 15 mM Tris-HCl pH 7.4, 500 mM KCl, 5 mM $MgCl_2$, 2 mM dithiothreitol (DTT), 290 mM sucrose. Few microliters were maintained for protein extraction while the remaining volume was loaded on a discontinuous sucrose gradient (40% (w/V) sucrose in 15 mM Tris-HCl pH 7.4, 500 mM KCl, 5 mM $MgCl_2$, 2 mM DTT (bottom layer); and 480 µl buffer 20% (w/V) sucrose, 15 mM Tris-HCl pH 7.4, 500 mM KCl, 5 mM $MgCl_2$, 2 mM DTT (top layer) and ultracentrifuged at 4°C for 17 h using a TLS-5S rotor at 33,000 rpm in Beckman Optima™ LE-80K ultracentrifuge. The supernatant (WS) contained proteins loosely associated with ribosomes and the pellet contained washed ribosomes (WR). Pellet was dissolved in sample buffer and proteins in the other fractions extracted using methanol-chloroform. For RNAse treatment, cytoplasmic lysate was treated with RNAse I (10U per unit absorbance at 260 nm of lysate) for 45 minutes at RT, before applying the same protocol. Western blot analysis was done using the primary antibodies detailed in **Supplementary Table 1.**

Ribosome profiling and active ribosome profiling

Cytoplasmic lysates from control and ALS mouse primary cortical neurons were prepared as previously described (Bernabò et al. 2017). The RNA content of each lysate was assessed by measuring the absorbance at 260 nm with the Thermo Scientific NanoDrop. The NaCl concentration was adjusted to 100 mM. If not processed immediately, samples were stored at -80 °C. Lysates were treated with RNase

I (2/3 Invitrogen and 1/3 BioResearch Technologies) using 7.5 U / a.u. Abs260 nm of the lysate and incubated at room temperature for 45 minutes. The reaction was stopped by adding 100 U of SUPERase-In RNase inhibitor (Thermo Fisher Scientific). Polysome profiling was performed as previously described (Lauria et al. 2020). Fractions corresponding to the 80S monosome were collected. For RiboSeq, the hyper-resolution RiboLace 360 Gel Free Kit (Immagina BioTechnology, catalog n. 360SQ-12) was used for the library preparation according to the manufacturer's instructions. For active RiboSeq, the RiboLace kit (Immagina BioTechnology) was used for ribosome purification and library preparation according to the manufacturer's instructions. Eventually, RiboSeq and active RiboSeq libraries were quantified using High Sensitivity DNA kit (Agilent Technologies) on the Agilent 2100 Bioanalyzer. Single read sequencing 100 cycles was performed with the Illumina NovaSeq 6000 by the Next Generation Sequencing Facility (CIBIO, University of Trento, Italy).

Miniaturised polysome profiling from cortical neurons cultured in microfluidic chambers

The compartmentalised axons and cell bodies were lysed directly in the corresponding compartments of the microfluidic chamber by fluxing several times 100 µL of polysome lysis buffer (10 mM NaCl, 10 mM $MgCl_2$, 10 mM Tris–HCl pH 7.5, 1% Triton X-100, 1% sodium deoxycholate, 0.005 U/mL DNAseI, 0.2 U/µL RNase inhibitor, 1 mM DTT and 10 µg/mL cycloheximide). The lysates were centrifuged at 14000 g for 5 minutes at 4°C to pellet membrane debris, nuclei and mitochondria. The cell body supernatant was incubated 20 minutes before storage at -80°C. For polysome profiling the lysates were loaded onto a 15–50% linear sucrose gradient formed in 2.2 mL polyallomer tubes. Sucrose buffers were prepared in 100 mM NaCl, 10 mM $MgCl_2$, 30 mM Tris–HCl, pH 7.5. Sucrose gradients were centrifuged in a Beckman Optima™ TL Ultracentrifuge for 90 minutes at 180,000 g at 4°C using a Beckman TLS-55 swinging rotor. To collect sucrose fractions and measure the absorbance at 254 nm, a Teledyne Isco model 160 gradient analyser equipped with a UA-6 UV/VIS detector was employed. The resulting 200 µl fractions were directly used to extract RNA samples or stored at -80°C.

RNA purification from polysomal profiles, library preparation

For studying both the transcriptional and the translational levels of the axons and cells, total cytosolic RNA (pool of all the fractions) and polysomal RNA (collection of fractions corresponding to the polysomal peaks) were purified from the polysomal profiles. Both total and polysomal RNA extractions were performed with Direct-zol™ RNA purification Kit (Zymo Research). For RNPs/granule transcriptome and translatome analysis at subcellular resolution, after sucrose gradient fractionation, sucrose fractions not associated to polysomes containing RNPs, ribosomal subunits and 80S were pooled in the RNPs/granule fraction. Sucrose fractions containing polysomes were pooled into the "polysome fraction". Trizol was used to extract the RNA. After purification, the RNA was resuspended in DNAse-RNAse nuclease free-water and quantified at the Agilent 2100 Bionalyzer by using the Agilent RNA 6000 Pico kit. The libraries were obtained using Ovation® Single Cell RNA-Seq System (Nugen) or Ovation® SoLo® RNA-Seq library preparation kit (Tecan) according to the manufacturer's protocol. The qualitative and quantitative control of the libraries was performed with High Sensitivity DNA Chip (Agilent Technologies) before sequencing. Single read sequencing 100 cycles was performed with the Illumina NovaSeq 6000 by the Next Generation Sequencing Facility (CIBIO, University of Trento, Italy).

RT-PCR from RNP/granule and polysomal RNA in axons and cell bodies

For PCR, reverse transcription reaction was performed on 100 pg of RNP/granule and polysomal RNA of cell body and axonal compartments, using the RevertAid First Strand cDNA synthesis kit (Thermo Fisher Scientific). The PCR reaction was performed on 1 µL cDNA for each sample, using Taq DNA Polymerase (Invitrogen), 10X PCR Buffer – Mg, 50 mM $MgCl_2$, 10 mM dNTPs and 10 µM FW and RV primers of the selected genes. PCR was performed using C1000 Touch Thermal Cycler (Biorad). The PCR program was set as follows: initial denaturation step at 94°C for 3 minutes, 35-40 cycles composed of a denaturation step at 94°C for 45 seconds, annealing step at 58-60°C for 30 seconds and extension step at 72°C for 90 second. Final extension was performed at 72°C for 10 minutes. The PCR reactions were run on 8% polyacrylamide gel in TAE and amplicons visualized at the ChemiDoc MP Imaging System (Biorad). Primers are listed in **Supplementary Table 2**.

Co-sedimentation profiles of proteins from cell bodies and axonal polysome profiling

After polysome profiling, the proteins were extracted fraction by fraction with methanol-chloroform method (Bernabò et al., 2017). After resuspension in milliQ water, 1 µL of each fraction was spotted onto a nitrocellulose membrane for dot blot analysis. Membranes were left drying for 30-45 min at room temperature and incubated in a blocking solution for 4 hours at RT in rotation. Next, membranes were incubated with primary antibody overnight at 4°C, under orbital agitation. The following day, membranes were washed twice in TBS-Tween for 30 minutes and incubated at RT with secondary antibody for 1h and 30 minutes. After antibody removal, two washes with TBS-Tween were followed by a final wash with TBS (30 minutes/wash). The reaction was developed by using SuperSignal™ West Femto Maximum Sensitivity Substrate (ThermoScientific) and the images acquired with ChemiDoc MP Imaging System (Biorad). To obtain the relative distribution of proteins along the profile, the percentage of each protein fraction by fraction was obtained as follows:

$$\%\,[Protein]_n = \frac{[Dens^{Protein}]_n}{\sum_{i=1}^{12}[Dens^{Protein}]_i}$$

where *n* is the number of a specific fraction between 1 and 12 and $\%\,[Protein]_n$ is the percentage of the protein of interest in the fraction of interest, and $Dens^{Protein}$ is the densitometry of the protein signal.

Polysome profiling from cell lines and tissues and protein extraction

Doxycycline-inducible NSC-34 cells were seeded at 1.5×10^6 cells/10 cm dish and treated with 2 µg/ml doxycycline (Clontech) for 48h to express His-HA-tagged hTDP-43 WT or mutants (hTDP-43-A315T, hTDP-43-Q331K, and hTDP-43-M337V). After reaching 80-90% of confluence, cells were treated with 10 µg/mL cycloheximide for 3 minutes at 37°C. Cytoplasmic lysates were obtained as described earlier (Bernabò et al., 2017). The lysate was then centrifuged at 20000 g for 5 min at 4°C to allow the sedimentation of membrane debris, nuclei and mitochondria. The supernatant was recovered and after 20 min on ice was stored at -80°C or directly transferred onto a 10–40% linear sucrose gradient as

described in (Lauria et al., 2020) and centrifuged in a Beckman Optima™ LE-80K Ultracentrifuge for 90 min at 180,000 g at 4°C using a swinging rotor. To collect sucrose fractions and measure the absorbance at 254 nm, a Teledyne Isco model 160 gradient analyser equipped with a UA-6 UV/VIS detector was employed. Each fraction was stored at - 80°C for protein extraction. Mouse cortex and spinal cords from the hTDP-43-Q331K mouse model of ALS and controls were dissected and pulverised in a mortar with a pestle under liquid nitrogen and the powder was lysed as described in (Lauria et al., 2020). Tissue debris were removed by centrifugation at 18.000 g for 1 min at 4°C. Nuclei were removed from the pre-cleared lysate by a second centrifugation at 13.200 g for 5 min at 4°C and incubated on ice for 30 min. The polysome-containing lysate was stored at -80°C or directly layered onto a linear sucrose gradient as previously described. Protein isolation from both cell cultures or tissues was performed fraction by fraction using classical methanol/chloroform precipitation. The protein pellet was resuspended in 60 µl Electrophoresis Sample Buffer (Santa Cruz) before immunoblotting.

Fraction of ribosomes in polysomes (FRP)

From the chromatogram of the polysome profiles the fraction of ribosomes in polysomes (FRP) was obtained as follows:

$$\%FRP = \frac{Polysomes_{Area}}{(80S_{Area} + Polysomes_{Area})} \cdot 100$$

where $Polysomes_{Area}$ is the area under the peaks of polysomes, the $80S_{Area}$ is the area under the 80S. Statistical analysis of data was carried out by using Student's T-test for identification of difference between two groups.

Total protein purification and Western blotting from cortex and spinal cords of the mouse model of ALS

Frozen spinal cord and cortex tissues from control or ALS mice were pulverised using mortar and pestle working under liquid nitrogen during the whole procedure. The powder was lysed in RIPA buffer (50 mM Tris-HCl pH 8.0, 150 mM NaCl, 1% NP40, 0.5% sodium-deoxycholate, 2% SDS) supplemented

with protease inhibitor and homogenised with a Kimble® 749540-0000 Pellet Pestle® Cordless Motor. The samples were incubated on ice for 15 min and centrifuged at 15,000 rpm in F-45-30-11 rotor at 4°C for 15 min to pellet cell debris. The supernatants were collected and stored at -80C. Protein quantification was performed by using the DC assay kit (BioRad). For total protein analysis, the same quantity of proteins (20–30μg) for each sample was used. Protein samples were diluted in 2X Electrophoresis Sample Buffer (Santa Cruz) and milliQ water to reach a final loading volume of 20 μL and loaded on polyacrylamide gels (8%, 10% or 12%). After total protein evaluation by ponceau staining, WB analysis was performed as previously described. The list of primary and secondary antibodies used is in **Supplementary Table 1**. To determine the Fold Change of protein expression between ALS and control conditions, the signals' intensities of the Western Blot bands were measured using the ImageJ software (https://imagej.nih.gov/). The signal's intensity of each protein in each replicate was normalised to the respective intensity of ActB protein (housekeeping). Thus, the Normalized Protein Expression was defined as follows:

$$NPE_{protein} = \frac{D_{protein}}{D_{housekeeping}}$$

where $D_{protein}$ is the signal's intensity relative to the protein in a replicate, $D_{housekeeping}$ is the signal's intensity of the Western Blot band corresponding to ActB in the replicate. For each protein, the mean of the NPE obtained from the three control replicates was calculated as follows:

$$Mean\left[NPE_{protein}\right]_{CTRL} = \frac{\sum_{i=1}^{3}\left[NPE_{protein_i}\right]_{CTRL}}{3}$$

Lastly, the mean NPE control, calculated for a protein, was used to compute the FC of protein expression in ALS with respect to the control condition:

$$FC_{protein} = \frac{\sum_{i=1}^{3}\frac{\left[NPE_{protein_i}\right]_{ALS}}{Mean\left[NPE_{protein}\right]_{CTRL}}}{3}$$

Statistical analysis of data was carried out by using Student's T-test for identification of difference in total protein expression between two groups.

RT-qPCR from total RNA and co-sedimentation analysis of mRNAs

Polysomal profiling from frozen spinal cord and cortex tissues, derived from (3-months old) ALS (TDP-43-Q331K) and control mice, was performed as described previously (Bernabò, et al. 2017). Total cytosolic RNA (pool of all the sucrose fractions) and RNA from each sucrose fraction were extracted using phenol-chloroform as described previously (Tebaldi et al., 2018). Before the reverse transcription reaction, all samples were treated with DNAse. Equal volumes of RNA from sucrose fractions were used for cDNA synthesis using the RevertAid First Strand cDNA synthesis kit (Thermo Fisher Scientific). For total cytoplasmic RNA 500 ng were used for cDNA synthesis using the RevertAid First Strand cDNA synthesis kit (Thermo Fisher Scientific). In both cases, cDNA synthesis reaction was performed by using OligodT. qPCR was performed using the CFX Connect Real-Time PCR Detection System (BioRad) using the qPCRBIO SyGreen Mix Separate-ROX (PCR Biosystem). The list of primers is in **Supplementary Table 2**. For qPCR data analysis to obtain the co-sedimentation profiles of the mRNAs of interest, the percentage of each transcript's distribution along the profile was obtained using the following formula in the case of qPCR:

$$\% \text{ [mRNA]}n = [\, mRNA]_n \,/\, mRNA]_n$$

where n is the number of the fraction and %[mRNA]n is the percentage of mRNA of choice in each fraction, C_t mRNA is the Ct for each RNA in each fraction. For the differential expression analysis of the mRNAs of interest, the qPCR results of gene expression were normalised to ActB expression level. Precisely, the ΔCT for each transcript was calculated as CTgene – CTActB. Then, the log2FC was calculated from ΔΔCT values obtained comparing the expression of the gene of interest between TDP-43-WT (Control) or TDP-43-Q331K (ALS) condition.

Ribosome run-off experiments and calculation of ribosome kinetics

Primary cortical neurons were extracted from mouse embryos (E15.5) and maintained in culture, as described earlier. At DIV 7, cells seeded in 10 cm Petri dishes (5 million cells/dish) were treated with Harringtonine (Abcam) in Neurobasal medium (GibcoTM) at a final concentration of 2 µg/mL. After harringtonine addition, the dishes were gently mixed and were incubated at 37°C for 0, 1.5, 3 and 10 min. Sharply, at the end of the harringtonine-incubation time, cycloheximide was added to the cell culture medium to a final concentration of 10 µg/mL to stabilise elongating ribosomes. Finally, a cytoplasmic lysate was obtained as described earlier and analysed by polysomal profiling. For each time point of harringtonine treatment (0, 1.5, 3, 10 min), the mean FRP value among the replicates was calculated. The obtained mean FRP values were fitted with the following exponential decay function, separately for control and ALS conditions:

$$y(x) = y0 + Ae^{-xt}$$

The ribosome kinetics was measured as the reciprocal of the decay constant ($\tau = 1/t$), thus expressed as minutes^{-1} (min^{-1}).

Puromycilation in PCNs cultured in microfluidic chambers, imaging and particle analysis

The puromycilation reaction was performed according to (David et al., 2012). Mouse cortical neuron (DIV10) were incubated with 100 µg/ml cycloheximide for 15 minutes at 37°C. Next, 100 µg/ml puromycin was added and kept for 5 minutes at 37°C. Cells were washed on ice with cold HBS (119 mM NaCl, 5 mM KCl, 2 mM $CaCl_2$, 2 mM $MgCl_2$, 30 mM glucose, cycloheximide 100 µg/ml and 0.0003% digitonin, 25 mM Hepes, pH 7.3) for 2 min. A second wash was performed with the same buffer without digitonin to eliminate the detergent. Cells were then fixed 15 minutes with PBS solution containing 4% paraformaldehyde, 4% sucrose and 100 µg/ml cycloheximide. After 3 washes with PBS, cells were permeabilized and blocked with 5% BSA, 0.1% Triton X-100 in PBS for 30 minutes and then incubated with primary antibodies (**Supplementary Table 1**) for 1 h. After 3 washes with PBS, the coverslips were incubated with a convenient secondary antibody for 1 hour. Cells were then washed with PBS and microfluidic chambers detached from the coverslip to be mounted with Prolong Diamond Antifade Mountant containing DAPI (Invitrogen). Images were acquired using a Leica TCS SP8

microscope. 4096 x 4096 pixel (pixel size/ voxel size: 0.284 μm) images of whole chambers were acquired using HC PL FLUORAR 10x/0.30 dry objective. 2048 x 2048 pixels (pixel size/ voxel size: 0.09 μm) images of cell bodies and axons were acquired using HC PL APO CS2 63x/1.4 NA oil objective. Samples were illuminated using Diode 405, Argon and DPSS 561 lasers, for excitation at 405 nm, 488 nm and 561 nm wavelengths, respectively. Images were acquired with PMTs detectors using the following parameters: Alexa Fluor 488: 500–540 nm, TRFP: 566-650 nm, DAPI: 410-475 nm emission wavelength ranges. Z-stack imaging was performed on cell bodies, axons in the microgrooves and distal axons. Images of Vim and Rrbp1 immunofluorescence were taken on a Leica TCS SP8 microscope with the same parameters. For Gapdh, samples were imaged on a Leica SP5 microscope. Images at 4096 x 4096 pixels (pixel size/ voxel size: 0.378 μm) were acquired from the whole chambers using HC PL FLUORAR 10x/0.30 dry objective. Images at 2048 x 2048 pixels (pixel size/ voxel size: 0.12 μm) for the cell bodies and axons in the microgrooves were acquired using HCX PL APO CS 63x/1.4 NA oil objective. Samples were excited using Argon and HeNe lasers and excitation wavelengths were set at 488 nm and 543 nm, respectively. Images were acquired with PMTs detectors using the following parameters: Alexa Fluor 488 500–540 nm and TRFP 566-650 nm. Z-stack imaging was performed in cell bodies and axons in the microgrooves. The images were analyzed with ImageJ-software (https://imagej.nih.gov/ij/). To count puromycin positive foci and measure their area and perimeter, images of axon in the microgrooves were processed to subtract the background and a threshold was set at 1% before producing a binary image. Regions of interests (ROI) for axons were captured at 112 x 2048 pixels (10 μm x 185 μm). For particle analysis a lower size threshold for particles count was set to 20 pixel units. Area and perimeter were measured for all the included particles. Particles with area < 0.3 μm^2 were excluded from the analysis.

Fluorescence intensity analysis of cortical neurons in microfluidic chambers

Puromycin, Gapdh, Vim and Rrbp1 fluorescence intensities were analysed with the ImageJ-software (https://imagej.nih.gov/ij/). Stacks of each image were Z-projected with a convenient plugin and fluorescence measured as integrated density. In the images of the cell body the fluorescence was measured relatively to the number of cells in each ROI. ROI fluorescence was normalised to the

background intensity and the results expressed as variations with respect to the TRFP control condition that was set to 1.

Translational burden analysis

NSC-34 cells were maintained in Dulbecco's modified Eagle medium (DMEM, Gibco) supplemented with 10% FBS (Atlanta BIO), 1% penicillin/streptomycin/L-glutamine (Sigma-Aldrich), and 1% non-essential amino acids (HyClone) at 37 °C and 5% CO_2. For transfection, $3.75*10^4$ cells per well were transfected in 48-well plates. The transfection solution was prepared using polyethylenimine (PEI) "MAX" (Mw 40,000, Polysciences, Inc.) in a 1:2 (µg DNA to µg PEI) ratio with a total of 150 ng of plasmid DNA per well. Both DNA and PEI were diluted in 12.5 µL of Opti-MEM I reduced serum media (Gibco) per well before being mixed and incubated for 25 min prior to addition to the cells. To determine the translational burden, cells were analysed with a BD Celesta™ cell analyzer (BD Biosciences) using 488 and 561 lasers. For each sample >30,000 events were collected and fluorescence data were acquired with the following cytometer settings: 405 nm laser and 450/40 bandpass filter for EBFP, 488 nm laser and 530/30 nm bandpass filter for EGFP, 561 nm laser and 610/20 nm filter for TRFP. Transfected cells were washed with DPBS, detached with 15 µL of Trypsin-EDTA (0.25%), and resuspended in 125 µL of DPBS + 1% FBS + 0.2 mM EDTA (Thermo Fisher). Fluorescence intensity in arbitrary units (a.u.) was used as a measure of protein expression. For each experiment a compensation matrix was created using unstained (wild type cells), and single-color controls (EBFP only, TRFP only, EGFP only). Live cell population and single cells were selected according to FCS/SSC parameters. Data analysis was performed with FlowJo V.10.

Data analysis

Preprocessing and alignment of ribosome profiling data

RiboSeq and active RiboSeq data were processed following the instructions provided by Immagina BioTechnology. Briefly, after adapter removal (TCTCCTTGCATAATCACCAACC), the UMI (first 4 and last 4 nucleotides) and then the barcode (first 8 nucleotides) were extracted, and only reads starting

with a T, which was trimmed, and longer than 15 nucleotides were retained (CutAdapt v3.7; UMI-Tools v1.1.2). Reads mapping on the collection of M. musculus rRNAs (from the SILVA rRNA database) and tRNAs (from the Genomic tRNA database) were discarded and the remaining reads were mapped on the reference genome GRCm39 with STAR (v2.7.10a), using the Gencode vM32 gene annotation.

Ribosome profiling analyses

Positional analysis were performed using the riboWaltz R package v2.0 (Lauria et al., 2018). Differential ribosome occupancy analyses are based on the number of P-sites falling in the coding sequence of each transcript, as computed by riboWaltz.

Preprocessing and alignment of RNA-Seq data

Reads were processed by removing the 3' Illumina Universal Adapter (AGATCGGAAGAG), trimming the first 8 nucleotides and discarding reads shorter than 40 nucleotides (Cutadapt v2.5). Processed reads were aligned to the mouse genome (GRCm38.p6) with STAR (v2.5.3a), using the Gencode M17 gene annotation, based on ENSEMBL release 92. A maximum of 10 multiple alignments for each read was allowed. Reads mapping at the same positions, but the one with the highest mapping quality score, were removed with Picard Tools MarkDuplicates (v2.18.9, REMOVE_DUPLICATES=true). Counts of mapped reads per gene were retrieved by HTSeq (v0.11.0, --stranded=no). All programs were used with default settings unless otherwise specified.

Differential analyses

To remove size or compositional differences between libraries, gene expression levels were normalised among replicates using the trimmed mean of M-values normalisation method (TMM) implemented in the edgeR Bioconductor package. Only genes with FPKM $\geqslant$ 10 in all replicates of at least 1 sample were kept for subsequent analysis. Differentially expressed genes, cellular and axonal enriched genes and genes with decreased and increased TE were detected with edgeR (glmQLFTest function) with a triple threshold: i) absolute value of log2 fold change, log2 fold enrichment and fold translational

efficiency ⩾ 0.75; ii) p-value representing the statistical significance ⩽ 0.05; iii) average CPM among replicates of each sample ⩾ 0.05.

Network analyses

Protein-protein interactions were downloaded from the STRING database (v 11.0, Mus Musculus dataset). Only interactions with interaction score ⩾ 0.3 were considered (this threshold includes medium and high confidence interactions). Network analysis was performed with the igraph R package and protein communities within the network were identified with the cluster_fast_greedy function.

Functional enrichment analyses

Annotation enrichment analysis with Gene Ontology terms, REACTOME and KEGG pathways were performed with the clusterProfiler Bioconductor package.

Analysis of TDP-43 CLIP data

CLIP-Seq data retrieved from Polymenidou et al., 2011 were aligned to the mouse transcriptome using the Gencode M17 annotation, based on ENSEMBL release 92.

Definition of TDP-43 targets

TDP-43 targets were defined according to the presence of TDP-43 binding motifs, retrieved from Polymenidou et al., 2011, on the 3' UTR of annotated protein codings. Genes not including any motifs were labelled as non-target RNAs.

Enrichment analyses

Enrichment of TDP-43 target genes defined in this work and destabilised genes (retrieved from Tank et al., 2018) among DEGs identified upon TDP-43-WT or TDP-43-A315T expression were performed by Fisher's exact test. The set of genes with FPKM ⩾ 10 in all replicates of at least 1 sample were used as background.

Data availability

RNA-Seq data generated by the current study have been deposited in the Gene Expression Omnibus (GEO) under the accession code GSE239419. All other data supporting the findings of this study are available from the corresponding author on reasonable request. Source data are provided with this paper.

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Author contributions

G.V. conceived and designed the study and directed the research. F.L., G.T., T.T. and E.B. processed all sequencing data and performed the analyses; F.M., M.M., I.B., M.S., C.P., L.L., R.A., A.B. and M.d'A. performed experimental work. A.P., L.C. and G.G.C. optimised and produced the viral particles for the expression of TDP-43-WT and TDP-43-A315T. D.P. and A.P. produced the cellular lysates from hiPSCs. D.P. and A.Q. developed the NSC-34 stable and inducible cell lines. L.D. and M.B. dissected all tissues from the mouse model. F.C. and V.S. produced plasmids and performed the translational burden experiments. A.Q, G.G.C. and G.V. obtained the funding. G.V., F.M., F.L. and C.P. wrote the manuscript, with input from all authors.

Competing interests

G.V. has been a scientific advisor to IMMAGINA Biotechnology until November 2022. M.C. is the CEO of IMMAGINA Biotechnology. The other authors declare no competing interests.

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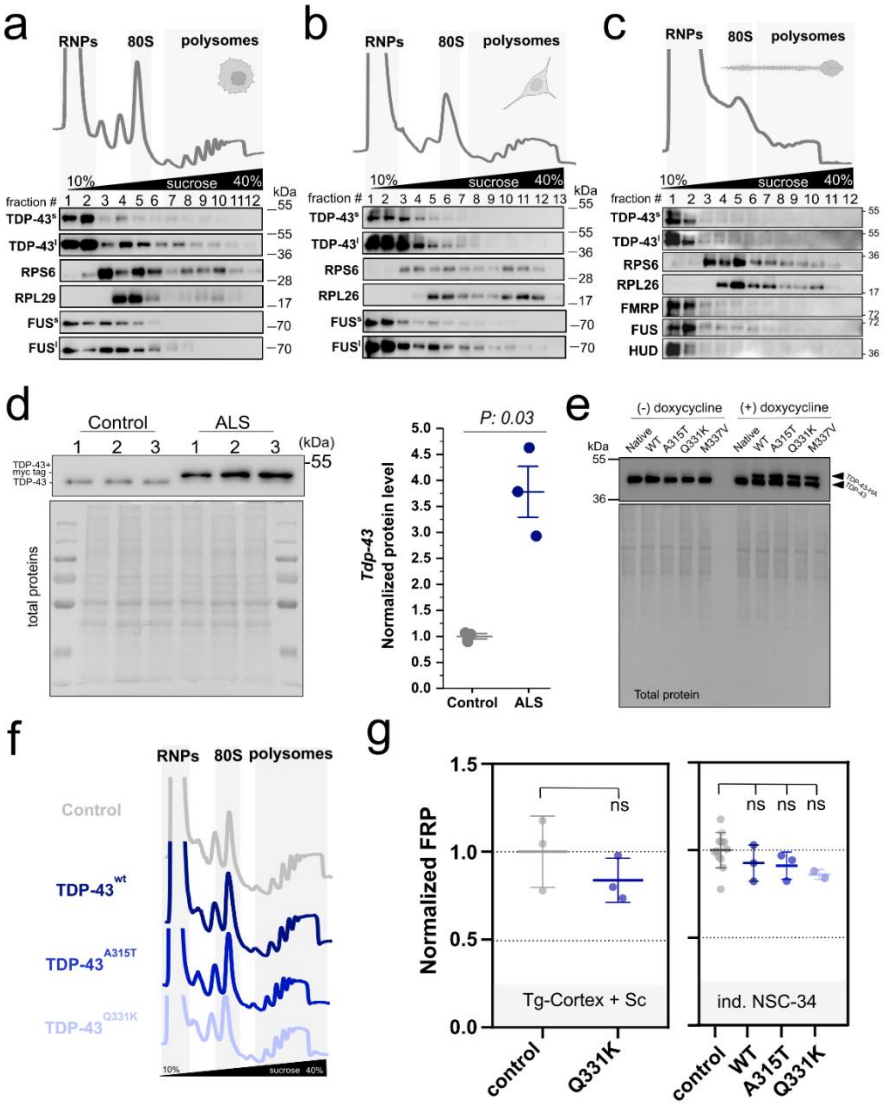
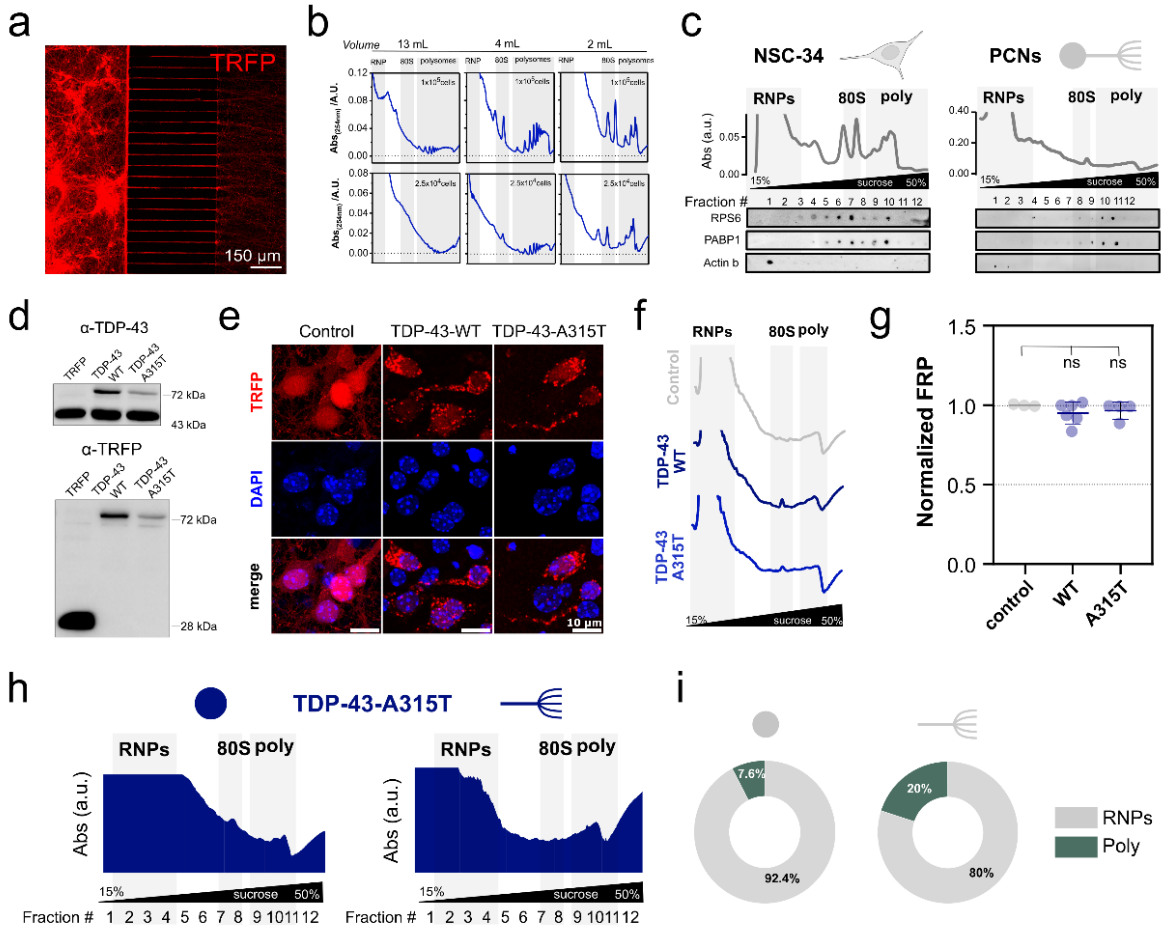
SUPPLEMEMNTARY FIGURES



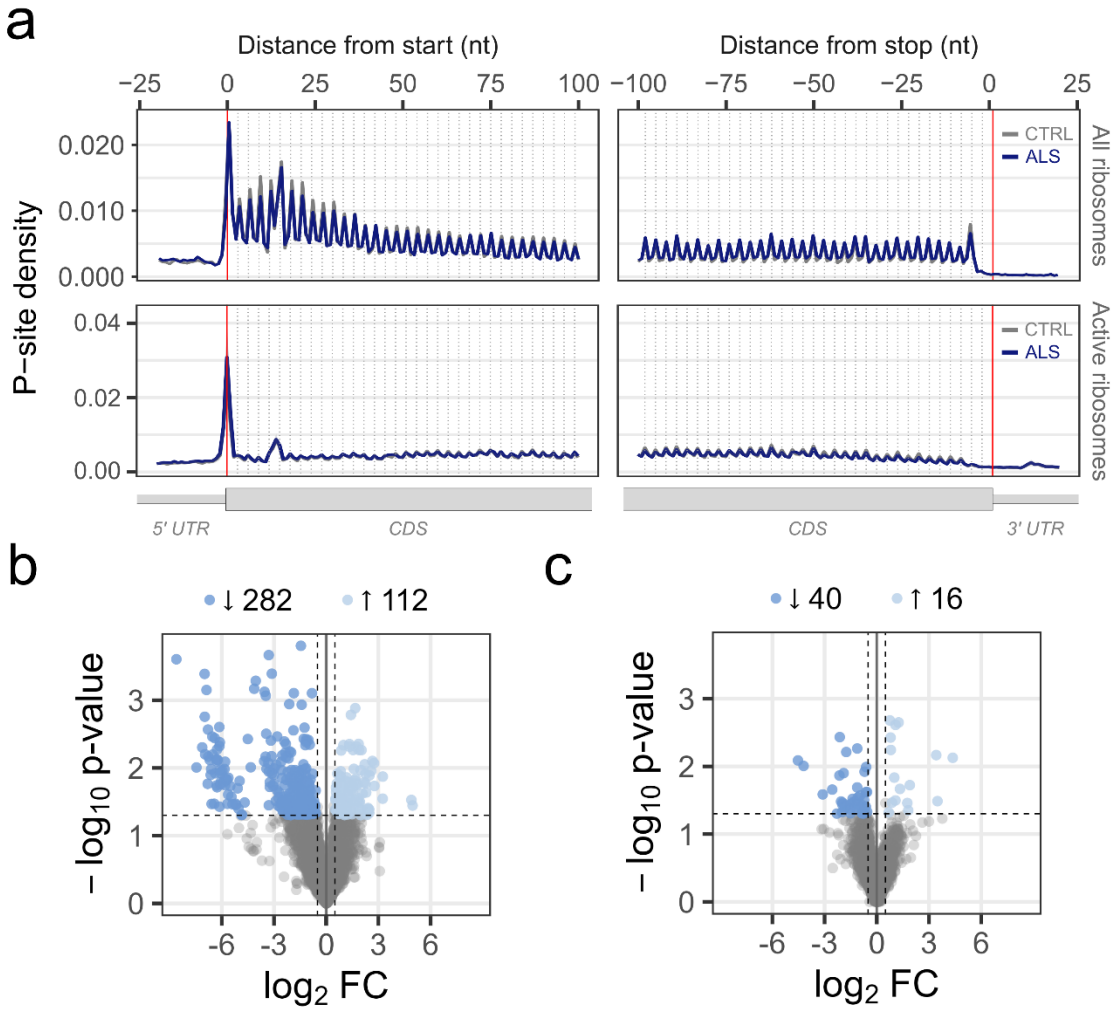
Supplementary Figure 1 (**a-c**) Representative polysome profiles (upper panels) and representative co-sedimentation profiles (lower panels) of TDP-43, ribosome markers (RPS6, RPL29 or RPL26), and RNA-binding proteins (FUS, FMRP, and HUD) performed in (a) hiPSCs, (b) NSC-34 cell lines and (c) murine central nervous system (CNS). (**d**) Left panel: western blot analysis of TDP-43 and hTDP-43-Q331K in the cortex and spinal cord from 3 months-old non-transgenic controls and hTDP-43-Q331K mouse model of ALS. Total proteins were assessed using ponceau dyeing of the membrane. Lanes 1-3 represent biologically independent replicates. Right panel: quantification of TDP-43 protein levels in 3 months-old control and hTDP-43-Q331K mouse model of ALS after normalisation for total protein abundance. Data are mean ± SEM of n=3 biologically

independent replicates. Differences were assessed with two-tailed T-test. P-value is reported in figure (**e**) Western blot analysis of transgene (human) and endogenous (murine) TDP-43 in NCS-34 cells stably transduced to express His-HA-tagged hTDP-43-WT and mutants A315T, Q331K and M337V after induction with doxycycline. (**f**) Examples of polysome profiles from NSC-34 expressing His-HA-tagged hTDP-43-WT or two hTDP-43 mutants (A315T and Q331K). (**g**) Fraction of ribosomes in polysomes (FRP) in the cortex and spinal cord of control and transgenic mice expressing hTDP-43-Q331K (left panel) and doxycycline-inducible NSC-34 cell lines expressing His-HA-tagged hTDP-43-WT, hTDP-43-A315T, and hTDP-43-Q331K (right panel). Data are mean ± SEM of n=3-9 biologically independent replicates. No significant changes according to two-tailed T-test were detected.

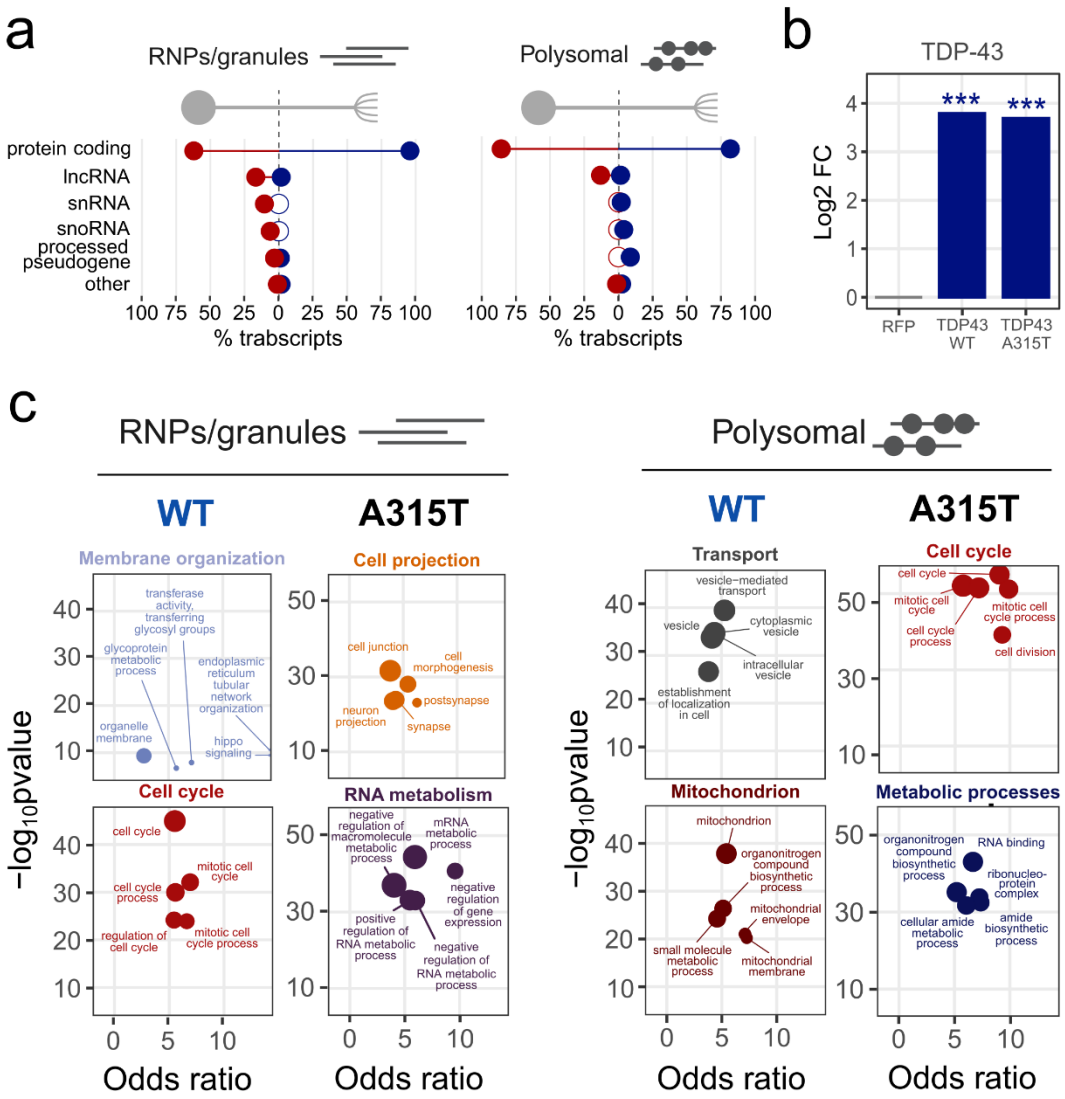


Supplementary Figure 2. (**a**) Representative immunofluorescence image of mouse PCNs expressing TRFP cultured in microfluidic chambers to compartmentalise cell bodies (left) and axons (right). (**b**) Polysomal purification optimization in 15%-50% sucrose gradients formed in different tubes and with a decreasing number of MCF7 cells. The miniaturised 2 mL sucrose gradient efficiently allows the sedimentation and isolation of polysomes. (**c**) representative polysomal profile and dot blot co-sedimentation profiles of ribosomal markers obtained with miniaturised polysome profiling in control NSC-34 (left panels) and in wild type PCNs (right panels). PABP was used as a control for RNA-dependent interactions and Actin B was used as negative control. (**d**) Western blot of total protein lysates obtained from murine PCNs infected with TRFP, TRFP-TDP-43-WT and TRFP-TDP-43-A315T to monitor the expression levels of endogenous TDP-43 and exogenous TRFP-TDP-43-WT and TRFP-TDP-43-A315T proteins. (**e**) Immunofluorescence of mouse PCNs expressing TRFP-TDP-43-WT, TRFP-TDP-43-A315T, and only TRFP as control. Antibodies against TRFP were used to evaluate TDP-43-positive inclusions in the cytoplasm, compared to nuclear marker (DAPI). (**f**) Examples of polysome profiles from PCNs infected with TRFP as control, and PCNs expressing TRFP-TDP-43-WT and TRFP-TDP-43-A315T. (**g**) Fraction of ribosomes in polysomes (FRP) in PCNs expressing TRFP-TDP-43-WT, TRFP-TDP-43-A315T and TRPF as control. Data are mean ± SEM of n=3-6 biologically independent replicates. No significant changes according to two-tailed T-test were detected. (**h**) Representative profiles obtained with miniaturised polysome profiling in axons and cell body of murine PCNs expressing TRFP-TDP-43-A315T. (**i**)

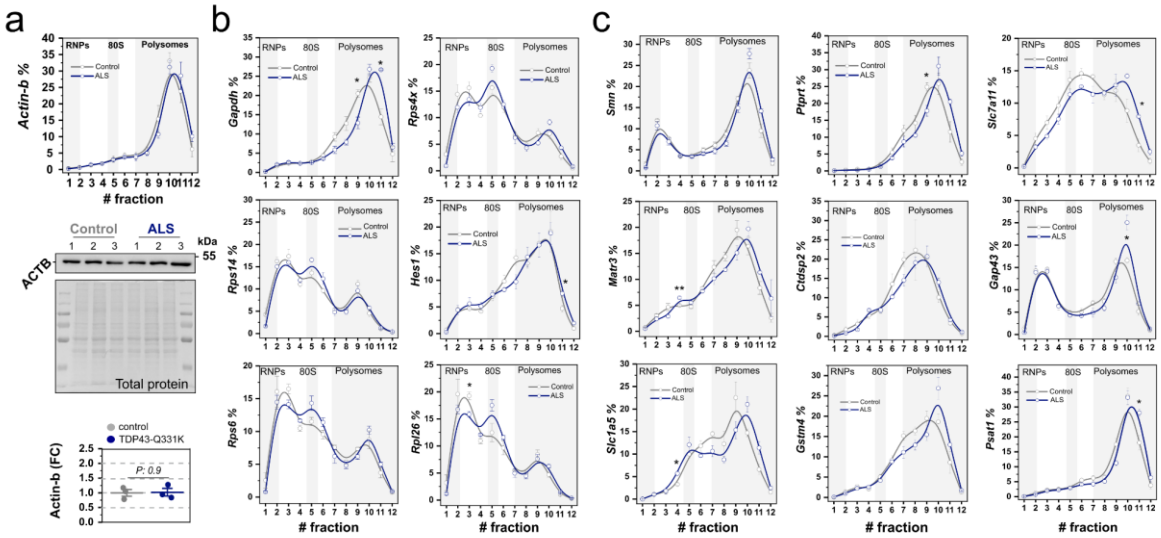
Donut plots with relative percentages of endogenous TDP-43 association in RNPs/granules and polysome compartments in the cell body and axons of wild type PCNs.



Supplementary Figure 3. (**a**) Overlay meta-profiles based on the localization of active and inactive ribosomes (top) and only active ribosomes (bottom) in ctrl (gray) and ALS (blue). Data are mean ± SEM of n=3 biologically independent replicates. (**d-e**) Volcano plot displaying variations in the ribosome occupancy according to active and inactive ribosomes (d) and only active ribosomes (e). mRNAs displaying significant variations are coloured according to the direction of the change: decreased ribosome occupancy (blue) and increased ribosome occupancy (light blue). The number of transcripts is reported above.



Supplementary Figure 4. (**a**) Percentage of biotypes of free (top panel) and polysomal (bottom panels) RNAs found to be enriched in the cell body (red) or in axonal (blue) compartment in control cortical neurons. (**b**) Level of cellular polysomal TDP-43 RNA in the cell bodies of neurons expressing TDP-43-WT and TDP-43-A315T with respect to TRFP. Differences were assessed with two-tailed T-test (P-value: *** p <0.001). (**c**) Functional enrichment analysis of the top two communities based on the interaction network of proteins encoded by RNPs/granules (left panel) and polysomal (right panel) genes enriched in the axon, not shared across PCNs upon TDP-43-WT and TDP-43-A315T expression.



Supplementary Fig. 5. (**a**) Actin-b mRNA shows no variations at mRNA or protein levels in control and ALS spinal cords and cortices. Upper panel: relative co-sedimentation profile of Actin-b mRNA along the sucrose gradient fractions. Middle panel: protein levels of ACTB obtained using western blot analysis in n=3 biologically independent replicates. Bottom panel: relative changes of ACTB protein expression. In the upper and bottom panels, data are mean ± SEM of n=3 biologically independent replicates. Differences were assessed with two-tailed T-test. The p-value is reported in the figure. (**b-c**) Relative co-sedimentation profile of TDP-43 non-targets (b) and TDP-43 target (c) mRNAs out of the 21 transcripts selected for *in vivo* analysis. Data are mean ± SEM among n=3 biologically independent replicates. Differences were assessed with two-tailed T-test (P-value: *< 0.05, **<0.01).

SUPPLEMEMNTARY TABLES

Supplementary Table 1. List of antibodies.

Protein	Company & code	Dilution
ACTB	SantaCruz sc69879	WB 1:1000 Dot blot 1:1000
ALEXA 488 anti-mouse	Invitrogen A-11001	IF 1: 1000
ATTO 594 anti-mouse	Sigma 76085	IF 1: 1000
FUS	Novus Biologicals NB 100-565	WB: 1:7000 Dot blot 1:5000
GAPDH	SantaCruz sc-166545	WB 1:1000 IF 1:200
HRP goat anti-mouse	Thermo Scientific 31430	WB 1:1000-3000 Sub fract 1:1000-3000 Dot blot 1:1000
HRP goat anti-rabbit	Thermo Scientific 31460	WB 1:1000-3000 Sub fract 1:1000-3000 Dot blot 1:1000
HUD	SantaCruz sc-2899	WB 1:1000 Dot blot 1:200
MATR3	Bethyl Laboratories A300-591A	WB 1:1000
PABP	Abcam ab21060	WB 1:2000 Sub fract 1:1000 Dot blot 1:1000
PUROMYCIN	Millipore MABE343	WB 1:5000 IF 1:4000
RPL26	Abcam	WB 1:1000

	ab59567	Sub fract 1:2000 Dot blot 1:1000
RPL29	Thermo Scientific PA5-27545	WB 1:1000
RPS6	Cell Signalling 2217	WB 1:1000 Sub fract 1:1000 Dot blot 1:1000
RRBP1	Genetek GT5610	WB 1:3000 IF 1:125
SMN	BD Transduction Laboratories 610646	WB 1:1000
TDP43	Proteintech 10782-2AP	WB 1:1000 Sub fract 1:1000 Dot blot 1:1000
VIM	Genetek GT812	WB 1:3000 IF 1:250

Supplementary Table 2. List of primers for qPCR and PCR.

Gene	Forward	Reverse
18S	ATGGCCGTTCTTAGTTGGTG	AACGCCACTTGTCCCTCTAA
Ctdsp2	ACTCTGCTACACTGTGCCTT	GTCTGATTTCCTGCTCTGCG
Egr1	ACGAGTAGAAGGACCGTTGG	CAGGCATGTGATGGAGAGGA
Gap43	CACTGATAACTCGCCGTCCT	AGCCTCGGGGTCTTCTTTAC
Gapdh	CTCCCATTCTTCCACCTTTG	ATGTAGGCCATGAGGTCCAC
Gstm4	ATCCTGGACCTGCACCTTAT	CCAAGTGGCCACCTTTGTAT
Hes1	TCACTTCGGACTCCATGTGG	CGTCAGAAGAGAGAGGTGGG
Lars2	GAGCTGGGATTAGACCGTCG	CTGCGGTTCCTCTCGTAC
Map2	GTGAACAAGAGAAGGAAGCCC	GCGAAGGTGGCAGATTAGC
Matrin3	GGACACCAAGGATGACCAGACA	TCGCCCACTGAACTACCACTTT
Nfl	CATGCAGGACACAATCAAC	AGCTGCAATCTCAATGTCCAA
Psat1	CAAGCACCTGGAACCTCAAC	CACCAGCGAAAATCACACCA
Ptprt	AAAACCCTCCGCAACAACAA	CCAGTGCCACCTCATATACAAAT
Rpl14	CAGGGCTTTAGTGGATGGACC	TGGCTGCCCATTTCGTATTGA
Rpl26	CGAGAGAAGGCTAATGGCAC	GGCTTTCCTCTCCAGGATCT
Rpl29	AATGGCACAGAAATGGCATC	GGCCTTTCTTGTTGTGCTTC
Rps14	CCAACTCCTTGCACCTCTGG	GGAAACCATCTGCCGAGTGA
Rps4x	TGGATCTCTCTTCCCAGAGG	TTCACCCACTGCTCTGTTTG
Rps6	TTTGGCCAAGAGAATGAAGG	CTCAGTGAGGACAGCCTACG
Rrbp1	GGATGGTAGCAGCTCAAAGG	CTGGAAGTTGGGCCTGGATA
Slc1a5	ACAGCATCCAGTGTCGGTG	TCCACGTTGAGGACAGTACA
Slc7a11	AGCATGGCACCTTTGTTCTG	CCCAAGGTTCAACATCGCAA
Smn1	TGCTCCGTGGACCTCATTTCTT	TGGCTTTCCTGGTCCTAATCCTGA
Synj1	AGCCCTCGGAGACATTGAAA	AGAGAAGGCTGCTGAGGAAA
Vim	GCCTCTGCCAACCTTTTCTT	CAACCGTCTTAATCAGGAGTGT
β-actin	GAGACCTTCAACACCCCAGC	GGCGTGAGGGAGAGCATA