Single cell RNA sequencing in isogenic *FUS* and *TARDBP* mutant ALS lines reveals early mitochondrial dysfunction as a common pathway in motor neurons

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Abstract

Mutations in the RNA/DNA-binding proteins FUS and TDP-43 cause amyotrophic lateral sclerosis (ALS) with distinct neuropathological features. It is currently unclear how these gene mutations lead to selective motor neuron death and if there are common mechanisms across disease causations. Using single cell RNA sequencing of neurons derived from isogenic induced pluripotent stem cell lines, we show that motor neurons harbouring FUS P525L or FUS R495X mutations show a 4.9- to 15.5-fold larger transcriptional response than interneurons. About 20% (737 DEGs) of transcripts were coregulated across FUS R495X and P525L motor neurons and by comparing to a FUS knockout line we could discern that 48% (355 DEGs) were part of gain-of-function of FUS. Cross-comparing with isogenic TDP-43 M337V motor neurons, identified common mitochondrial dysfunction across FUS gain-of-function and *TARDBP* gene mutations, as did comparison with published RNA-Seq data from C9orf72-ALS motor neurons. Metabolic assessment confirmed a decrease in mitochondrial

respiration and ATP turnover in mutant *FUS* and *TARDBP* lines and live cell microscopy showed a decrease in mitochondrial motility across ALS motor axons. Thus, we have identified early mitochondrial dysfunction in motor neurons shared across ALS-causative mutations, that could have major implications for their survival and which could be targeted therapeutically.

Introduction

Amyotrophic lateral sclerosis (ALS) is a devastating disease with no cure or effective treatments which is defined by the selective loss of corticospinal motor neurons and somatic motor neurons in the brain stem and spinal cord, that innervate skeletal muscles, with resulting spasticity, muscle atrophy and paralysis *(Nijssen et al., 2017; Schweingruber and Hedlund, 2022; Swinnen and Robberecht, 2014)*. The majority of ALS cases appear sporadic with unknown etiology, but the disease can also be inherited and caused by mutations in e.g. superoxide dismutase 1 (SOD1), the DNA/RNA-binding proteins TDP-43 (encoded by the *TARDBP* gene) or FUS and C9orf72 *(DeJesus-Hernandez et al., 2011; Kwiatkowski et al., 2009; Rosen et al., 1993; Sreedharan et al., 2008; Vance et al., 2009)*. Irrespective of the disease causation, selective degeneration of somatic motor neurons is seen, which has been attributed to their high firing rate, long axons and hyperbranching with up to 2,000 muscle fibers and high energy demand and vulnerability to ER stress *(Filézac de L'Etang et al., 2015; Nijssen et al., 2017; Vandoorne et al., 2018)*. Mutations in *FUS* cause about 1-5% of familial ALS cases and are present in a number of sporadic ALS cases *(Kwiatkowski et al., 2009; Renton et al., 2014; Vance et al., 2009)*. FUS is a nucleocytoplasmic shuttling DNA- and RNA-binding hnRNP (heterogeneous ribonucleoprotein) and partakes in a broad range of cellular functions. Most FUS-linked ALS mutations destroy the protein's nuclear localization signal, resulting in cytoplasmic mis-localization, accumulation and formation of large cytoplasmic inclusions that sequester many other proteins and RNA species in neurons and glial cells *(Jutzi et al., 2020; Kwiatkowski et al., 2009; Vance et al., 2009)*. Several studies point to toxic gain-of-function (GOF) of FUS in the cytoplasm. Cytoplasmic expression of FUS in mice causes motor neuron degeneration while FUS knockout or wild-type FUS expressed at physiological levels, and localized mainly nuclear, leave motor neurons unharmed *(Dormann, 2016; Scekic-Zahirovic et al., 2016; Sharma et al., 2016)*. FUS in the cytoplasm may drive phase transition and thus

solidify RNA granules that contain FUS over time *(Patel et al., 2015; Scekic-Zahirovic et al., 2016)* or it may augment the cytosolic functions of FUS in mRNA stabilization, transport and local translation *(Bowden and Dormann, 2016)*. Mutations in another RNA-binding protein, TDP-43, cause ALS in 3% of familial and 2% of sporadic cases, in which TDP-43 is mis-localized from the nucleus to the cytoplasm of neuronal and glial cells *(Van Deerlin et al., 2008; Gitcho et al., 2008; Kabashi et al., 2008; Sreedharan et al., 2008; Yokoseki et al., 2008)*. Misexpression or overexpression of wild-type or ALS-mutant *TARDBP* in mice results in neuronal toxicity and motor neurons loss in the absence of cytoplasmic inclusions, which indicates that cytoplasmic aggregation is not a prerequisite for a neurodegenerative phenotype (Igaz et al., 2011; Wegorzewska et al., 2009). Depletion of TDP-43 from cells causes massive effects on RNA metabolism, as it maintains faithful gene expression by repressing the splicing of non-conserved cryptic exons *(Ling et al., 2015)*. TDP-43 mis-localization to the cytoplasm is seen in the majority (>95%) of all ALS patients *(Arai et al., 2006; Mackenzie et al., 2007; Neumann et al., 2006),* and may indicate loss-of-function of TDP-43*,* which thus expands the relevance of RNA metabolism to most ALS cases. It is currently unclear how mutations in FUS and TDP-43 lead to selective motor neuron death and if there are common mechanisms across these gene mutations that cause harm to motor neurons. We therefore aimed to unravel if there were any common pathways linking these different genetic etiologies of ALS and if these uniquely affected motor neurons. Towards this purpose we used induced pluripotent stem cells (iPSCs), which can model disease phenotypes in ALS and intracellular dysfunctions, including protein aggregation and axonal transport defects *(Fujimori et al., 2018; Guo et al., 2017; Mehta et al., 2021)*. Cross-comparison of patient-derived iPSC lines can be complicated by differences in genetic backgrounds, which may obscure subtle changes when several lines are compared across mutations. We therefore used isogenic CRISPR/Cas9 edited lines where each ALS-causative mutation was introduced onto the same control iPSC line. Here we report the single cell RNA sequencing across neuron types derived from isogenic lines harboring FUS P525L or R495X point mutations, knockout (KO) of FUS or the TDP-43 M337V mutation followed by metabolic assessment. Collectively our findings reveal early mitochondrial dysfunctions exacerbated in motor neurons across *FUS* mutant lines that were related to a GOF and shared with the mutant *TARDBP* line in addition to being present in iPSC lines from individuals with *C9orf72*-linked ALS. The impairment in mitochondrial respiration and ATP turnover across several mutant *FUS* and *TARDBP* lines and the decrease in mitochondrial

motility seen across ALS motor axons support a convergence of motor neuron intrinsic dysfunction and provide a foundation for therapeutically improving mitochondrial activity in ALS.

Results

Isogenic mutant ALS-FUS lines reveal early cell-type specific transcriptional dysregulation

To understand how FUS-ALS affects human motor neurons and interneurons differentially and discern gain-of-function (GOF) versus loss-of-function (LOF) mechanisms, we aimed to introduce aggressive mutations in human iPSCs and compare these lines to a *FUS* KO. To select *FUS* mutations for this purpose, we aggregated clinical features from 502 published ALS cases with *FUS* mutations in order to conduct a meta-analysis (Extended Data Fig. 1a). The results affirmed that the FUS P525L mutation results in the earliest onset (at age of 21±8 years, mean±sd) followed by FUS R495X (at age of 31±11 years) and both mutations progress rapidly to respiratory failure or death within 17±10 and 20±18 months, respectively (Extended Data Fig. 1b,c) and were selected for our studies. In contrast, most other *FUS* mutations lead to disease in midlife or later (age of 41±18 years). CRISPR/Cas9-mediated genome editing was used to introduce a homozygous *FUS* R495X mutation into the DF6-9-9T.B control line (WiCell) (Extended Data Fig. 2a, b) and compared to a FUS P525L mutation (heterozygous or homozygous) *(Jutzi et al., 2020)* which were generated on the same background. Introduction of the mutations was confirmed by dye terminator sequencing following PCR amplification of the edited loci. We also used a *FUS* KO line which had been generated on the same background that employs a gene trap in the first intron of *FUS* (Fig. 1a) *(Reber et al., 2018)*. The pluripotency of the generated iPSC lines was established by immunofluorescence microscopy using antibodies against POU5F1 (OCT-3/4) and NANOG (Extended Data Fig. 2c). Immunofluorescent staining against FUS in iPSCs confirmed the loss of FUS in the KO line, and the redistribution of FUS from nucleus to cytoplasm in the R495X and P525L lines. The homozygous lines showed a complete redistribution of FUS from nucleus to cytoplasm, while the heterozygous P525L line showed expression in both nucleus and cytoplasm, as expected (Extended Data Fig. 1d). To dissect the role of FUS' LOF and GOF in lower motor neuron vulnerability, isogenic iPSC lines were specified to spinal motor neurons and interneurons

using two distinct protocols. The first protocol generates 30-40% of interneurons *(Nijssen et al., 2018)*, here termed the heterogeneous protocol (Extended Data Fig. 3a, f), while the second protocol generates 60-80% of motor neurons *(Guo et al., 2017; Maury et al., 2015; Nijssen et al., 2019),* here termed the homogeneous protocol (Extended Data Fig. 3c, g). Differentiation of iPSC lines showed that motor neurons (ISL1/2$^+$) and interneurons were readily generated (Extended Data Fig. 3b, d) and that the proportions of specific neuronal populations and progenitors were consistent across lines, with no marked effect of the mutations on cell type specification (Extended Data Fig. 3f, g). Most ALS-associated *FUS* mutations result in a change in subcellular distribution and cytoplasmic accumulation of the mutant protein, which is thought to be toxic *(Mackenzie et al., 2011)*. Therefore, we validated mutant FUS mis-localization in motor neurons derived from the genome edited lines by immunofluorescence, which showed cytoplasmic accumulation of FUS P525L in ISL1/2$^+$ neurons, unlike for the control line. The P525L motor neurons also retained some signal in the nucleus, similar to what has been seen for other *FUS* mutations that interfere with the nuclear localization signal *(Chen et al., 2020; Ichiyanagi et al., 2016).* We also confirmed the ablation of FUS in the FUS KO motor neurons (Fig. 2a, Extended Data Fig. 4a). We used antibodies with specific epitopes spanning the FUS P525 position (wildtype P525P and mutant P525L) to delineate heteroallelic mutant and wild-type FUS in immunofluorescence staining (Extended Data Fig. 4b, d). The specificity of the antibodies was confirmed by western blots of whole cell lysates from iPSCs (Extended Data Fig. 4c). We found that in FUS P525L heterozygous motor neurons, wildtype FUS localized mainly to the nucleus, while mutant FUS P525L localized to both cytoplasm and nucleus. In homozygous FUS P525L and in FUS R495X motor neurons, we found a clear mis-localization of mutant FUS. Thus, we have generated isogenic iPSC lines in which FUS LOF and GOF in ALS can be studied across mutations and neuron types to reveal why motor neurons are particularly vulnerable and if there are common pathways that are dysregulated across mutations.

Following characterization of the isogenic FUS mutant and KO lines, we subjected differentiated cultures to FACS to isolate individual live cells and conducted Smart-seq2 single cell RNA sequencing *(Schweingruber et al., 2023)* (Fig. 1a). After quality control (see methods section), 1,415 cells remained, which were classified according to a decision tree into motor neurons, interneurons and neuronal progenitor cells (Extended Data Fig. 3e). Cells were

plotted using UMAP (uniform manifold approximation and projection), which demonstrated clustering of motor neurons, interneurons and neuronal progenitors (Fig. 1b). Cells originating from the different isogenic lines distributed across all clusters (Fig. 1c) consistent with the observation that all lines generate neurons at similar proportions (Extended Data Fig. 3f,g). UMAP projection of neurons only, after removal of progenitors, showed a clear separation of motor neurons and interneurons with clustering of V2a interneurons across lines (Fig. 1d,e). V2a excitatory interneurons are also prone to degeneration in ALS as shown in SOD1^{G93A} mice *(Romer et al., 2017)* and appear more vulnerable than V1 inhibitory interneurons to early disease processes *(Salamatina et al., 2020)*. Thus, we separated these from other interneuron types in cross-comparisons with motor neurons to delineate potential gradients in vulnerability. General neuronal markers (*MAPT*, *NEFM*, *SNAP25*) were highly expressed across neuron types while markers of proliferating cells (*SOX2*, *MKI67*, *CDK1*) were absent (Fig. 1f). Motor neurons showed expression of *ISL1*, *ISL2*, *MNX1*, *UTS2*, *SLC18A3*, and *SLC5A7* (Fig. 1f), while the presence of glutamatergic markers combined with *SOX14* and *VSX2* (*Chx10*) demarks V2a interneurons (Fig. 1g). In conclusion, we find that single cell RNA sequencing can readily identify motor neurons and interneuron subpopulations derived from the isogenic iPSC lines and that neither FUS-ALS mutations (heterozygous or homozygous) nor FUS KO impair the generation of these cell types. Thus, we proceeded to investigate if the *FUS* mutations and FUS KO affect different neurons in a cell-type specific manner. We first performed differential gene expression analysis in motor neurons, V2a interneurons and other interneurons between FUS mutations and the control line in our single cell data. In each cell line, we found that motor neurons displayed unique transcriptional changes associated with the individual mutations and little overlap with V2a and other interneurons, which suggests that the majority of transcriptional adaptation and dysregulation events are specific to motor neurons (Fig. 1h). Furthermore, motor neurons demonstrated much larger transcriptional responses to the *FUS* mutations and loss of FUS than the interneuron groups. V2a interneurons showed a surprisingly small response to the FUS mutations compared to the other, presumably more resilient, interneuron group. This analysis demonstrated that introducing the R495X or the P525L mutations resulted in a stronger transcriptional response than knocking out FUS. This is clearly indicative of both LOF and GOF being altered in mutant FUS lines. Furthermore, homozygous introduction of the FUS P525L mutation resulted in 2,365 DEGs unique to motor neurons, while the same heterozygous mutation induced

1,075 DEGs, showing a dose response to this gene mutation (Fig. 1h, Extended Data Table 1). The homozygous FUS R495X mutation induced 1,064 DEGs, which is less than half of that elicited by the more aggressive FUS P525L mutation, indicating that the transcriptional dysregulation is correlated to the severity of the mutation (Fig. 1h). In conclusion, our analysis demonstrates that each neuron type exhibits unique transcriptional responses to *FUS* mutations and FUS KO. It also shows that *FUS* mutations elicit the largest transcriptional response in motor neurons and that this appears correlated with the aggressiveness of the mutation, gene dosage as well as FUS mis-localization, and may underlie the cell-type specific vulnerabilities to FUS-ALS.

Single cell RNA sequencing points to shared gain-of-function pathways in motor neurons across FUS mutations

To clarify if motor neuron-specific DEGs were unique to the individual *FUS* mutations or shared across lines and the FUS KO we interrogated the transcriptomes across the lines (Fig. 2a). We found 471 DEGs that were commonly altered among FUS R495X and the P525L heterozygous as well as homozygous lines, indicative of a shared transcriptional response. Of those, 116 DEGs were further shared with the FUS KO motor neurons and are thus associated with a LOF in FUS-ALS (Fig. 2b, red). Thus, 355 DEG were unique to mutant FUS motor neurons and can therefore be classified as *bona fide* FUS-ALS associated GOF changes (Fig. 2b, green). The pathways that are associated with these changes were assessed by gene set enrichment analyses, leading to the identification of 655 biological processes changed in response to any of the investigated FUS mutations. Comparison of gene ontologies between the lines (Fig. 2c) identified 81 shared biological processes across mutant FUS-ALS motor neurons, eleven that were associated with a FUS-ALS LOF (Fig. 2c, red) and 70 that were not and thus represent FUS-ALS GOF (Fig. 2c, green). We found only nine biological processes that were unique to the FUS KO line and do not reflect changes found in the FUS-ALS motor neurons (Fig. 2d). Altogether, this comparative analysis suggests that the majority of FUS-ALS dysregulated processes are due to FUS GOF. The few biological processes unique to LOF in FUS-ALS motor neurons included RNA splicing, establishment of RNA localization and nuclear export together with a number of processes related to synapse organisation and activity, dendritic spine development and neuronal projections (Fig. 2e). The gene ontologies for biological processes

unique to FUS-ALS GOF included metabolic pathways e.g. downregulation of aerobic respiration, oxidative phosphorylation, and mitochondrial respiratory chain complex assembly, regulation of RNA metabolism e.g. upregulation of mRNA 3' end processing, regulation of RNA splicing, regulation of mRNA processing, RNA localization, and RNA export from nucleus and the upregulation of processes involved in organelle and vesicle turn-over e.g. endoplasmatic reticulum tubular network organisation, establishment of organelle organisation, and Golgi vesicle transport among others. We also employed commercially curated gene ontology sets to independently identify dysregulated pathways in our data. Using Qiagen's Ingenuity pathway analysis *(Krämer et al., 2014)* with DEGs between mutant FUS and control motor neurons, we identified 59 pathways that were significantly altered in FUS-ALS motor neurons (at an FDR cut-off at <0.1), and not at all in V2a interneurons and to a very low extent in the other interneurons (Fig. 2g, Extended Data Table 2). Among the top ten pathways identified in this analysis were mitochondrial dysfunction and oxidative phosphorylation, synaptogenesis signalling pathway, as well as pathways regulating translation and protein stability (EIF2 signalling, regulation of eIF4 and p70S6K signalling, mTOR signalling, and protein ubiquitination pathway). Altogether our single cell transcriptome analysis in FUS motor neurons points to shared pathways that might underly FUS-ALS pathological mechanisms, most of which are associated with FUS GOF.

Transcriptional changes shared across ALS-causative mutations in *FUS*, *TARDBP* and *C9orf72* implicate mitochondrial dysfunction within motor neurons

Disease histopathology appears unique with *FUS (Kwiatkowski et al., 2009; Vance et al., 2009)* and *TARDBP (Van Deerlin et al., 2008; Mackenzie et al., 2010)* mutations, but the selective motor neuron degeneration, glial activation and clinical presentation is similar, suggesting a convergence of pathomechanisms *(Ling et al., 2013)*. Furthermore, similar to FUS, TDP-43 is an RNA/DNA-binding protein and ALS-causative mutations in the *TARDBP* gene give rise to broad effects on RNA metabolism *(Arnold et al., 2013; Klim et al., 2019; Ling et al., 2015; Melamed et al., 2019).* We reasoned that the comparison across *FUS* and *TARDBP* gene mutations could reveal if there are pathways and DEGs central to motor neurons irrespective of the composition of aggregated proteins and disease etiology. Furthermore, as TDP-43 inclusions represent a pathological hallmark of the majority (>95%) of ALS cases *(Arai et al.,*

2006; Mackenzie et al., 2007; Neumann et al., 2006), implicating RNA dysregulation irrespective of causation *(Lagier-Tourenne and Cleveland, 2009)* and we reasoned that an analysis of *TARDBP*-ALS may give clues to downstream disease mechanisms across ALS cases more broadly. We thus generated another isogenic iPSC line (on the DF6-9-9T.B control background) that harboured the ALS-causing TDP-43 M337V mutation using CRISPR/Cas9-mediated genome editing. After verification of successful genome editing and that the mutation did not result in altered cellular TDP-43 protein levels in the iPSCs (Extended Data Fig. 5a,b), we conducted Smart-seq2 single cell RNA sequencing on motor neurons and interneurons (Fig. 3a) and cross-compared to our FUS data set (Fig. 3b-e). Following the same cell type classification (Extended Data Fig. 3e), we found that TDP-43 M337V cells from both protocols integrated in our single cell dataset (Fig. 3b,c). Differential gene expression analysis with DESeq2 demonstrated that the TDP-43 M337V mutation induced a massive transcriptional response in motor neurons with 2,284 DEGs, of which 2,143 were unique to motor neurons. V2a and the other interneuron population on the other hand, showed only moderate responses with 145 DEGs for V2a and 196 DEGs for other interneurons, of which a minority (17 DEGs) were shared between the two interneuron groups (Extended Data Fig. 5e). Differential gene expression analysis between TDP-43 M337V, *FUS* mutations and FUS KO showed that 1,088 DEGs were uniquely regulated in the TDP-43 M337V motor neurons (Fig. 3d, Extended Data Table 1). There was considerable overlap between DEGs in TDP-43 M337V and FUS P525L homozygous motor neurons, with 578 DEGs shared uniquely between the two lines (Fig. 3d, blue). Furthermore, TDP-43 M337V motor neurons shared 160 DEGs with FUS-ALS GOF (Fig. 3d, yellow) and 64 DEGs with FUS-ALS LOF (Fig. 3d, red). The GSEA between the TDP-43 M337V and control motor neurons revealed 423 biological processes that were altered in the mutant motor neurons (Extended Data Fig 5f, Extended Data Table 2). Comparing mutant TDP-43 M337V dysregulated processes with those found in *FUS* motor neurons (Fig. 2c-g) shows that the majority (370 biological processes) are unique to the *TARDBP* mutation (Fig. 3e). However, the majority of FUS dysregulated processes were also affected in TDP-43 M337V motor neurons, with eight out of 11 FUS LOF processes and 44 out of 69 FUS GOF overlapping with GO terms in the mutant *TARDBP* motor neurons (Fig. 3e). This indicates that there is shared transcriptional dysregulation across the isogenic ALS lines that relate to early and common dysfunctions in motor neurons. Upon closer inspection, we find that the biological processes that were shared across mutant *TARDBP* and *FUS* LOF mostly

relate to RNA metabolism (RNA splicing, mRNA processing, establishment of RNA localization), nuclear export and neuronal specific functions (dendritic spine development and neuron projection organization). The biological processes that were shared between mutant *TARDBP* and *FUS* GOF were upregulation of a number of RNA metabolic processes, e.g. RNA 3' end processing, regulation of splicing, RNA localization, RNA export from nucleus, mRNA transport as well as downregulation of energy metabolic processes, e.g. oxidative phosphorylation and aerobic respiration.

Collectively, we find that similarly to *FUS* mutations, the TDP-43 M337V mutation mainly triggered a response in motor neurons, while interneurons remained rather unaffected in their gene expression patterns. By comparing the motor neuron response across *FUS* and *TARDBP* mutations, we identified a shared and intrinsic signature of potentially early cellular dysfunction across ALS-causative mutations, which is characterized by changes in RNA metabolism, neuronal organization, and mitochondrial energy metabolism, and may explain their particularly susceptibility in ALS. To investigate if our findings were relevant more broadly across ALS, we compared our dataset with published bulk RNA sequencing from iPSC-derived cultures containing mostly motor neurons that harbour ALS-causative *C9orf72* hexanucleotide repeat expansions (HRE) *(Mehta et al., 2021)*. This dataset contained two C9orf72-ALS patient lines and corresponding corrected control lines, in which the HRE were excised. Following DEA and GSEA, we identified 609 biological processes that were regulated with the C9orf72 HRE. Comparison with the FUS-ALS sets defined above revealed that 601 of these biological processes were uniquely regulated in the C9orf72 dataset. The FUS-ALS LOF set did not overlap with this dataset at all and thus it could not support a role of these processes in C9orf72-ALS. However, the FUS-ALS GOF set shared eight biological processes with the *C9orf72* mutant motor neurons, including the downregulation of oxidative phosphorylation, upregulation of nuclear transport, establishment of organelle localization and negative regulation of execution phase of apoptosis (Extended Data Fig. 6). In conclusion, we find that *FUS* and *TARDBP* mutations trigger the dysregulation of many shared processes in motor neurons, several of which implicate dysfunctional mitochondrial energy metabolism. Comparison of our findings to motor neurons derived from C9orf72-ALS patient iPSCs on non-isogenic backgrounds, which can limit detectability, revealed early mitochondrial metabolic dysfunction as broadly shared pathway, strengthening the importance of our finding for ALS in general.

The downregulation of key mitochondrial pathways across isogenic ALS lines points to metabolic impairment

Our transcriptomic analysis consistently identified biological processes associated mitochondrial energy metabolism across *in vitro*-derived ALS mutant motor neurons. Notably, 14 downregulated biological processes of the 45 shared among the *FUS*-ALS GOF and *TARDBP*-ALS motor neurons were processes linked to mitochondria. Mitochondrial dysfunctions have also been recognized as hallmarks of ALS pathology in patients as well as animal and cellular models*(Ho et al., 2016; Mehta et al., 2021; Singh et al., 2021; Smith et al., 2019; Wang et al., 2016; Yu et al., 2020)*. We therefore decided to assess mitochondrial processes and pathways in more detail. In gene set enrichment analysis (GSEA), we closely investigated three pathways that were specifically downregulated in ALS motor neurons (Fig. 4a, c, e) and the expression of selected genes within these biological pathways (Fig. 4b, d, f). For the GO term "ATP synthesis-coupled electron transport" the associated genes were mostly downregulated across ALS mutations (Fig. 4a), which is illustrated by its members *COX6A1*, *NDUFS6*, and *NDUFA12* (Fig. 4b). For "Oxidative phosphorylation" (Fig. 4c), *ATP5MF*, *COX7C*, and *NDUFB9* were clearly downregulated (Fig. 4d). Among the 37 mitochondrially encoded genes, the majority was downregulated across ALS mutations (Fig. 4e), exemplified by *MT-CO3*, *MT-ND3*, and *MT-ATP6* (Fig. 4f). This analysis highlights the various mitochondrial changes that occur in ALS mutant motor neurons, across *FUS* and *TARDBP* mutations. Altogether the downregulation of these mitochondrial genes suggests that oxidative respiration is compromised early on in *in vitro*-derived ALS motor neurons.

Mitochondrial energy metabolism is disturbed in motor neurons across ALS-causative mutations

In order to assess mitochondrial activity and energy metabolism in ALS motor neurons, we performed *in vitro* differentiation according to the homogenous protocol that yields mostly spinal motor neurons. We used all the lines subjected to single cell RNA sequencing (Fig. 1-3). In addition, we included an isogenic FUS R244C line to investigate if mitochondrial dysfunction correlates with cytoplasmic mis-localization, because this mutation causes later onset of ALS than the FUS P525L mutation *(Kwiatkowski et al., 2009)* and does not show cytoplasmic mis-localization, but remains nuclear in motor neurons (Extended Data Fig. 4a,b). The

bioenergetic profile of motor neurons was assessed using a Seahorse XF96 extracellular flux analyzer on day 21 after seeding, a time-point at which motor neurons have become metabolically active and separate well into small clusters (Fig. 5a). A series of specific mitochondrial drugs (Extended Data Fig. 7a) was administered to dissect mitochondrial mechanisms in real-time, measured as oxygen consumption rate (OCR) and extracellular acidification rate (ECAR) (Extended Data Fig. 7b,c). The aggregated runs of three independent differentiations with isogenic control and mutant motor neurons are presented in Extended Data Fig. 7d. Basal cellular respiration was significantly reduced in FUS R495X, FUS P525L homozygous and TDP-43 M337V motor neurons (Extended Data Fig. 7e), mainly due to a strong reduction in mitochondrial respiration (Fig. 5b), but not non-mitochondrial respiration (Extended Data Fig. 7f). Notably neither the *FUS* knockout, nor the nuclear FUS R244C line (Extended Data Fig. 4a,b), showed significant reduction in mitochondrial respiration (Fig. 5b). Basal mitochondrial respiration was dissected into ATP-linked (Fig. 5c) and proton leak respiration (Extended Data Fig. 7g), revealing a similar pattern with significant reductions in FUS R495X, FUS P525L homozygous, and TDP-43 M337V motor neurons. To assess the bioenergetic capacity of motor neurons to respond to acutely high energy drains similar to what is seen during electric excitation, maximum substrate oxidation was induced using a mitochondrial uncoupler. Importantly, the pattern of reduced respiration was observed in FUS R495X, FUS P525L homozygous, and TDP-43 M337V motor neurons (Fig. 5d), demonstrating limited ability of these neurons to respond to high energy demands. Glycolytic acidification rates, after correction for non-glycolytic rates (Extended Data Fig. 7i), were determined to estimate glycolytic ATP production across motor neuron lines. These measurements revealed comparable basal rates, except for a significant reduction in FUS R495X motor neurons (Fig. 5e, Extended Data Fig. 7h). Upon induction of glycolysis by blocking mitochondrial ATP production with oligomycin, glycolytic capacity remained lower in FUS R495X motor neurons (Fig. 5f). OCR and ECAR were used to calculate the contribution of oxidative phosphorylation and glycolysis to the total ATP turnover. These analyses showed that the glycolytic contribution remains stable across lines, but significant reductions in mitochondrial ATP production were invoked in the FUS R495X, FUS P525L homozygous, and TDP-43 M337V motor neurons (Fig. 5g). Thus, ATP homeostasis is compromised due to defects in oxidative phosphorylation in these ALS motor neurons, which is not compensated for by glycolysis. Collectively, ALS-causative impairment in oxidative phosphorylation disables

motor neurons to meet high energetic demands in FUS R495X, FUS P525L homozygous, and TDP-43 M337V mutant lines, while FUS P525L heterozygous and FUS R244C homozygous lines that show less and no mis-localization of FUS, respectively do not display such phenotypes, providing compelling evidence that cytoplasmic protein mis-localization gives rise to this phenotype in *FUS*-ALS and *TARDBP*-ALS lines.

Impaired mitochondrial motility is seen across ALS mutant motor axons

Because mitochondrial metabolism in several ALS motor neurons was reduced at basal rates, we wondered if part of these differences may be explained by dysfunction in the subcellular distribution of mitochondria. The main subcellular compartment in motor neurons is the axon, that encompasses an estimated 98% of the neuronal cytoplasm in adult humans, and the axonal transcriptome of motor neurons is highly enriched in genes involved in the mitochondrial respiratory chain compared to the soma *(Nijssen et al., 2019)*. Furthermore, frequently spaced mitochondria are required for normal axonal function, especially electrical signal transduction. In our *in vitro* derived motor neurons using the homogenous protocol, axons can grow to more than 2 mm by day 28 if we seed embryoid bodies with motor neuron progenitors, followed by terminal differentiation and maturation during which motor axons grow radially and continuously outwards (Extended Data Fig. 7k-m). In order to assess mitochondrial motility in these axons, we imaged live neurons following a staining with a mitochondrial tracking dye (Fig. 5h, Extended Data Fig. 7k-m). This allowed us to assess the movement of mitochondria along the anterograde-retrograde axonal axis in live cell time lapse microscopy (Fig. 5i). We recorded axons during six min time lapses at 0.5 Hz and tracked mitochondria using TrackMate 7 *(Ershov et al., 2022)*. Across motor neuron lines, we tracked 14,855,019 spots (total number of mitochondria in all frames) in this manner and assembled 459,479 individual track branches (total mitochondria over the time-lapses). Based on their movement, we classified mitochondria into stationary/oscillating mitochondria, mitochondria that move in anterograde or retrograde direction, while we discarded stray movements orthogonal to the axons. Thus, we found that FUS R244C, FUS R495X, FUS P525L (heterozygous and homozygous), as well as TDP-43 M337V motor neurons displayed an increased number of stationary mitochondria compared to control motor neurons, unlike the FUS KO line (Fig. 5j), which was also reflected in a decrease of motile mitochondria in the

anterograde and retrograde direction (Fig. 5k). The change in mitochondrial motility was significantly associated with the mutations (Pearson's χ^2 test, $\chi^2 = 88192$, df = 12, $p < 2.2e-16$). We found that stationary mitochondria were strongly overrepresented in ALS motor neurons, while they were underrepresented among control and *FUS* KO motor neurons (Fig. 5l). This analysis of mitochondrial motility indicates further disturbance of mitochondria across ALS lines, which are linked to GOF toxicity. As we see the dysfunction in mitochondrial motility also in FUS R244C motor neurons this defect does not seem directly linked to protein mis-localization. Collectively, we identify early defects in mitochondrial respiration, ATP turnover and mitochondrial motility in ALS motor neurons across *FUS* and *TARBP* mutants which could put these cells at particular risk.

Discussion

Motor neurons are primarily affected in ALS, with early degeneration of the synapses between skeletal muscle and distal axon *(Fischer et al., 2004)*. In order to understand the intrinsic mechanisms that could lead to their early demise across disease etiologies, we compared the impact of ALS mutations in *FUS* and *TARDBP* on the transcriptomes of *in vitro*-derived spinal motor neurons and interneurons at single cell resolution. Isogenic lines allowed us to detect subtle transcriptomic changes that could easily have been masked in lines with diverse genetic backgrounds, even if compared with corrected controls for each non-isogenic line. Motor neurons responded to *FUS* and *TARDBP* mutations with a much greater transcriptional dysregulation than interneurons, which mirrors their higher susceptibility to intrinsic pathological mechanisms in ALS. Our findings in FUS and *TARDBP* lines are complemented and corroborated by similar results in neurons specified from familial C9orf72 and sporadic ALS patient iPSCs that demonstrated a lesser transcriptional response in V2a and V1 Renshaw interneurons compared to susceptible motor neurons *(Ho et al., 2021).* While interneurons are more resilient to ALS than most motor neurons *in vivo* only at late stages in the disease glutamatergic V2a interneurons in the brainstem and spinal cord degenerate, which facilitates respiratory failure *(Romer et al., 2017)*. It is therefore likely that our analysis detects an early dysfunction in motor neurons specifically that could be at the heart of why they display higher intrinsic vulnerability in response to ALS mutations.

In motor neurons, we observed that individual *FUS* mutations elicit distinct, but also shared transcriptomic signatures. Cross comparison of FUS R495X and P525L with FUS KO motor neurons allowed us to dissect the contribution of LOF and GOF in FUS to this shared transcriptional signature, the majority of which is associated with a potentially toxic GOF. The shared GOF might arise due to the mis-localization of FUS, given that the R495X and P525L mutations ablate FUS' nuclear localization signal, resulting in its accumulation in the cytoplasm, as we also observe in our motor neurons. Cytoplasmic mutant FUS displays toxic GOF properties across cellular models, including the sequestration of various RNA species and proteins *(Jutzi et al., 2020; Kwiatkowski et al., 2009; Vance et al., 2009).* Although we only detect few ALS-FUS linked LOF pathways, they mirror defects in dendrites in rodents with FUS depletion or overexpression of ALS mutations *(Groen et al., 2013; Orozco et al., 2012; Sephton et al., 2014)* and potentially compensatory changes in splicing regulation because FUS is a non-essential factor in neurogenesis after all *(Kino et al., 2015)*. While the loss of FUS does not elicit motor neuron disease on its own *(Kino et al., 2015)* the interplay of GOF and LOF associated changes in FUS-ALS might exacerbate the course of the disease as in late stages the abundant cytoplasmic FUS aggregates also sequester nuclear FUS (two-hit hypothesis) *(Dormann et al., 2010; Vance et al., 2009, 2013).* So far little is known about the contribution of these processes across different cell types, let alone spinal motor neurons. Our analysis of mutant FUS motor neurons affirms that LOF changes are indeed less pronounced than GOF changes, potentially due to the fact that the FUS protein belongs to the FET family of proteins that share similar functions and hence EWS and TAF15 might partially compensate for the loss of FUS in the context of nuclear depletion *(Kapeli et al., 2016; Svetoni et al., 2016)* while the shared dysfunctions across *TARDBP* and *C9orf72* datasets belong only to the latter. However, as we compared our GOF set to *C9orf72* patient data with different genetic background it is possible that we missed subtle converging dysfunctions that could have been detected in isogenicity.

Our cross-comparison with the bulk sequencing data from C9orf72 ALS patient derived motor neurons reveals unique responses but also further narrowed the signature of dysregulated genes that we detected in mutant *FUS* and *TARDBP* motor neurons. This signature contains transcriptional changes that are broadly shared among familial ALS motor neurons derived *in vitro* and might contain early converging pathological pathways. In this group, we identified

the ablation of mitochondrial respiration as an early and broad pathological stage across disease causations. Mitochondria are central organelles for oxidative phosphorylation, lipid biogenesis, calcium homeostasis, and apoptosis. Their proper function and spacing is crucial in motor neurons with their exceptionally high demands for local energy supply and calcium buffering during electric signal transduction. Dysfunctional mitochondria are a hallmark of ALS found in end stage patient tissues *(Borthwick et al., 1999; Wiedemann et al., 2002).* Perturbations found across ALS model systems encompass changes in energy metabolism, mitochondrial motility and morphology *(Smith et al., 2019)*. In ALS motor neurons derived from familial ALS iPSC lines with *SOD1*, *TARDBP* and *C9orf72* mutations or sporadic ALS iPSCs mitochondrial respiration was impaired, but not in FUS patient lines investigated so far *(Fujimori et al., 2018; Hor et al., 2021; Mehta et al., 2021; Vandoorne et al., 2019)*. In our motor neurons, the cellular respiration was compromised only with specific *FUS*-ALS mutations. Using the aggressive homozygous FUS R495X and P525L mutations, we find a lower mitochondrial respiration of motor neurons already at an early stage. Furthermore, in our isogenic ALS motor neurons we found a pattern of metabolic dysfunction that is suggestive of a causal link with the dosage of cytoplasmic FUS as exemplified by the different mitochondrial respiratory rates in FUS P525L heterozygous and homozygous lines. Indeed, the homozygous mutant motor neurons with higher amounts of cytoplasmic FUS (R495X, P525L) were impaired in contrast to nuclear FUS R244C, FUS KO, and control motor neurons. Cytoplasmic FUS dosage might also explain why previously assessed patient derived heterozygous FUS P525L motor neurons neither had metabolic reduction nor mitochondrial deformations at similar experimental time-points following careful characterisation *(Vandoorne et al., 2019)*.

Thus, our metabolic characterization of the *FUS* and *TARDBP* lines uncovers altogether a deeper link across ALS causation than was previously missing and demonstrates that cytoplasmic FUS levels encumber mitochondrial respiration early on. In a longitudinal study of the FUS Δ14 mouse model, mitochondrial dysregulation was detected at onset of symptoms at age of 12 month but not earlier in bulk spinal cord samples *(Devoy et al., 2017)*. Given the young biological age of iPSC-derived neurons *(Ho et al., 2021; Steg et al., 2021)* in our transcriptomic analysis at single cell resolution, one could infer that mitochondrial dysfunction might begin much earlier before onset of symptoms.

There is some evidence that *FUS* and *TARDBP* can both directly modulate mitochondria in ALS. Cytoplasmic FUS condensates were highly enriched for mitochondrial proteins *(Reber et al., 2021)*, but FUS mis-localization can also indirectly interfere with mitochondria by sequestering crucial mitochondrial components e.g. such as DHX30 required for translation of mitochondrial mRNAs, which hampered the renewal of the respiratory complexes *(Hikiami et al., 2022)*. A small fraction of cellular TDP-43 localizes to mitochondria and the prevention of the mitochondrial localization of TDP-43 M337V in mice ablated mitochondrial dysfunction *(Wang et al., 2013a)*. Due to its partial mitochondrial localization, TDP-43 protein can interact with multiple crucial mitochondrial proteins and mRNAs, including prohibitin-2 (PHB2), VDAC1 *(Davis et al., 2018)*, and *MT-ND3* and *MT-ND6* mRNAs *(Wang et al., 2016)*. PHB2 is important for mitochondria in neurons and its loss caused mitochondrial instability and neurodegeneration *(Merkwirth et al., 2012; Wei et al., 2017)*.

Among ALS mutations in *FUS* and *TARDBP*, we found a significant and early reduction in motile mitochondria in distal axons, in agreement with previous findings *(Guo et al., 2017; Kreiter et al., 2018; Mehta et al., 2021; Naumann et al., 2018)*. We also observed impaired trafficking of mitochondria in FUS R244C motor neurons, which indicates that mis-localization of FUS might not underly the motility defect alone. The R244C mutation is defective in DNA repair function of FUS *(Lenzken et al., 2019; Wang et al., 2013b)*, and earlier work in iPSC-derived motor neurons suggested nuclear genomic stress can act upstream of FUS aggregation and exacerbate axonal mitochondrial dysfunction *(Naumann et al., 2018)* and represent mitochondrial replication defects found also in ALS patients *(Stoccoro et al., 2018)*. The FUS mutations that we used also differ in their RNA binding ability due to their disposition of RGG domains which also modulate their ability for liquid-liquid phase transition *(Murakami et al., 2015)*. There is still ambiguity how mitochondrial respiration and motility relate to each other in neurons. Our data suggests that different mechanisms could direct defects in mitochondrial motility and metabolism. The mis-localized proteins in ALS can also have a direct impact on axonal transport by binding to motor proteins and the axonal cytoskeleton that could explain part of the motility phenotype. For example, cytoplasmic FUS associates directly with both myosin Va *(Yoshimura et al., 2006)* and KIF5 *(Kanai et al., 2004)* but also regulates the mRNA of several motor proteins, including KIF5C, KIF1B, KIF3A *(Hoell et al., 2011).* Likewise, TDP-43 binds to various cytoskeletal proteins and regulates the *MAP1B* and *NEFL* mRNAs *(Oberstadt*

et al., 2018), important components of the neuronal cytoskeleton. Furthermore *C9orf72*-derived dipeptides can road-block transport on microtubules resulting in arrested mitochondria *(Fumagalli et al., 2021)*.

Altogether the combined mitochondrial dysfunction we observe could become detrimental to motor neurons over time. Motor neurons are exceptionally vulnerable to energy depletion. One of the main reasons for this is that motor neurons are highly dependent on transport along their long axons, which can span over a meter to reach muscle targets in arms, legs, feet and hands. Furthermore, synapses such as the neuromuscular junction are major sites of neuronal energy consumption and the trafficking of mitochondria to the synapses is thus critical to meet energy requirements of signaling *(Fumagalli et al., 2021; Sheng, 2017)*. Indeed, it has been estimated that 400-800 × 10^6 ATP molecules are required just to restore the electrochemical gradient of a neuron after a single action potential via Na+/K+ pumping *(Attwell and Laughlin, 2001; Chamberlain and Sheng, 2019; Hallermann et al., 2012; Lennie, 2003)*. Mitochondria have been estimated to generate 93% of the ATP in presynaptic terminals *(Harris and Attwell, 2012)* and synapse physiology is clearly affected by local mitochondrial ATP production as local inhibition of oxidative phosphorylation or depletion of mitochondria here results in defective mobilization of synaptic vesicles, and failed neurotransmission *(Ivannikov et al., 2013; Ma et al., 2009; Verstreken et al., 2005)*. Thus, the defects we find in mitochondrial respiration and ATP production could quickly lead to severe dysfunction and miscommunication with muscles and weakening of synapses. Concomitantly, it was recently shown that targeting mitochondria with a small molecule could improve upper motor neuron health in a TDP-43 mouse model *(Gautam et al., 2023)*. The inability of ALS motor neurons to respond to high energy drains and the lack of compensatory glycolysis could render the motor neurons intrinsically more vulnerable as well as more dependent on glial support *(Joseph Bloom et al.; Lee et al., 2012)*.

Our data implicate mitochondria as important early targets in lower motor neurons. It has been shown that mitochondrial transport along axons is defective in iPSCs models of familial ALS *(Guo et al., 2017; Kreiter et al., 2018; Mehta et al., 2021)*, but it has not been investigated what regulates this disturbance and how it affects the neuromuscular junction and communication between motor neurons and muscle. ATP is also thought to be used as a hydrotrope to help solubilize hydrophobic proteins. Thus, ATP concentrations could influence

processes such as protein aggregation or liquid-liquid phase separation *(Patel et al., 2017)*, events that both occur in ALS and are thought to be detrimental to late stage motor neurons. In conclusion, we find an intrinsic and early transcriptomic signature of dysfunction across ALS motor neurons derived from human iPSCs along with defective mitochondrial metabolism affecting the capability of motor neurons to respond to high energy drains. In addition, mitochondria are less motile implicating exhaustion of axonal energy supply and decline of proper function over time. Our study points out mitochondria as an early and pivotal target to modulate in ALS.

Methods

Antibodies

Custom mouse monoclonal antibodies against the FUS C-termini were generated at Boster Bio (Pleasanton, CA, USA) with antigens of wild-type P525 (N-DSRGEHRQDRRERPY-C; clone P3-A6C4) or mutant P525L (N-CGKMDSRGEHRQDRRERLY-C; clone P1-E7B6). The custom rabbit anti-FUS (N-terminus) antibody was described *(Raczynska et al., 2015)*. The custom rabbit anti-CPSF2 (CPSF-100) in *(Reber et al., 2018)*. Other antibodies used in this study were: mouse monoclonal anti-FUS 4H11 [Santa Cruz Biotechnology, sc-47711], mouse anti-GAPDH 6C5 [Santa Cruz Biotechnology, sc-32233], rabbit anti-TARDBP [Proteintech Group, 12892-1-AP], mouse anti-OCT3/4 [Santa Cruz Biotechnology, sc-5279], rabbit anti-NANOG H155 [Santa Cruz Biotechnology, sc-33759]. Donkey anti-Rabbit IRDye 800CW [Li-Cor, 926-32213], Donkey anti-mouse IRDye 800CW [Li-Cor, 926-32212], Donkey anti-Rabbit IRDye 680LT [Li-Cor, 926-68023], Donkey anti-mouse IRDye 680LT [Li-Cor, 926-68022], Donkey anti-mouse AlexaFluor 488 [Invitrogen, A-21202], Donkey anti-rabbit AlexaFluor 546 [Invitrogen, A10040].

Plasmids

pCRISPR-EF1a-eSpCas9(1.1) was described in *(Reber et al., 2018)*. To generate the pCRISPR-EF1a-eSpCas9(1.1)-R495 plasmids two complementary oligonucleotides (sre326: 5’-CAC CGG GAC CGT GGA GGC TTC CGA-3’, sre327: 5’-AAA CTC GGA AGC CTC CAC GGT CCC-3’) or (sre324: 5’-CAC CGG ACC GTG GAG GCT TCC GAG-3’, sre325: 5’-AAA CCT CGG AAG CCT CCA CGG TCC-

3') and for M337 (JBA1: 5'-CAC CGC AGC ACT ACA GAG CAG TTG-3', and JBA2: 5'-AAA CCA ACT GCT CTG TAG TGC TGC-3') were subsequently phosphorylated using T4 polynucleotide kinase (PNK), annealed by heating to 95 °C and cooling to room temperature creating 5'-overhangs on both ends that were used to ligate into the BbsI sites of pCRISPR-EF1a-eSpCas9(1.1). Both, the FUS R495X and TDP-43 M337V donor plasmids containing disease-linked and silent mutations were ordered by gene synthesis in pUC57 [General Biosystems] and encompass homology arms of 800 bp upstream and 800 bp downstream and 808 bp upstream and 815 bp downstream of the cleavage site, respectively. The pRR-EF1a-Puro FUS R495 plasmid was ordered by gene synthesis [General Biosystems]. To generate pRR-Puro TARDBP M337 two oligos containing the CRISPR/Cas9 target site (mdr789: 5'-CGC AGC ACT ACA GAG CAG TTG GGG GAC GT-3' and mdr790: 5'-CCC CCA ACT GCT CTG TAG TGC TGC GAG CT-3') were phosphorylated using T4 PNK, annealed by heating to 95 °C and cooling to room temperature creating 5' overhangs on both ends which were used to ligate the annealed oligos into the SacI, AatII sites of pRR-Puro *(Flemr and Bühler, 2015; Reber et al., 2018)*. All plasmid sequences were confirmed by Sanger Sequencing.

Human induced pluripotent stem cell (iPSC) culture

Human iPSC lines were maintained with daily media changes in mTeSR1 or mTeSR-Plus medium (Stem cell Technologies, 85870 or 05825) as adherent cultures on plates coated with Matrigel (Corning, 354277) in a humid 5% CO_2 atmosphere at 37 °C. For passaging, they were treated with 10 µM Y-27632 (Tocris, 1254) for 1 hour and detached in DPBS (ThermoFisher, 14190250) with 0.5 mM EDTA (ThermoFisher, 15575020). The Y-27632 treatment was maintained until the next media change.

Genome editing

The generation of FUS knockout (KO) and FUS P525L iPSC lines has been described in *(Jutzi et al., 2020; Reber et al., 2018)* and genome editing was essentially performed as described therein. In short, to introduce the R495X mutation in exon 14 of the FUS gene two pCRISPR-EF1a-eSpCas9(1.1)-R495 plasmids coding for the sgRNAs targeting the sequences 5'-GGG ACC GTG GAG GCT TCC GAG GG-3' and 5'-GGA CCG TGG AGG CTT CCG AGG GG-3' were used. To introduce the M337V mutation in exon 6 of the TARDBP gene a pCRISPR-EF1a-eSpCas9(1.1)-

M337 plasmid coding for the sgRNA targeting the sequence 5'-GCA GCA CTA CAG AGC AGT TGG GG-3' was used. One day before transfection, 10 µM Y-27632 [Stemcell Technologies] and 2 µM Pyrintegrin [Stemcell Technologies] were added to the stem cell media. On the day of transfection, 6 wells of a 6-well plate with 90% confluent parental control hiPSC in mTeSR1 containing Y-27632 and Pyrintegrin were transfected with TransIT-LT1 Transfection Reagent [Mirus] for the FUS R495X and Lipofectamine 3000 for TDP-43 M337V [Life Technologies] according to the manufacturer's instructions. For the FUS R495X editing, each well was transfected with a total amount of 4.67 µg of DNA, transfecting 190 ng of pRR-EF1a-Puro-R495 and 4480 ng of a mix of pCRISPR-EF1a-SpCas9-R495 (both targets mixed 1:1) and the R495X donor plasmid for HDR. For each well a different molar ratio of pCRISPREF1a-SpCas9 R945 and donor plasmid was used (1:1, 1:3, 1:6, 4:1, 3:1, 2:1).

24 hours post transfection, the medium was changed to mTeSR1 supplemented with the 5 µl of the HDR-enhancer L755507 [Sigma], 10 µM Y-27632, and 2 µM Pyrintegrin. 48 hours post transfection, a single cell suspension was generated using Accutase [Thermo Fisher] and cells from the individual wells were pooled on a 15-cm plate in mTeSR1 containing 10 µM Y-27632 and 2 µM Pyrintegrin supplemented with 0.5 µg/ml Puromycin. Selection was maintained for one more day and Y-27632 and Pyrintegrin were maintained for four more days. Thereafter, colonies growing from single cells were picked and gDNA was isolated for clone screening using TRIzol (source) according to the manufacturer's instructions. The R495 and M337 genomic loci were amplified from the genomic DNA using the KAPA Taq ReadyMix PCR Kit according to the manufacturer's instructions using primers sre10: 5'-GTG GCT CTC ACA TGG GTA AG-3', and sre11: 5'-AAA GAC CCA GAG TGG CTA AG-3' for the R495 as well as P525L locus, and sre328: 5'-GAA TCA GGG TGG ATT TGG TAA TAG C-3' and sre331: 5'-AAT TCC CAC CAT TCT ATA CC-3'. The PCR products were purified over a preparative agarose gel using the Wizard SV Gel and PCR Clean-Up System [Promega]. Purified PCR products were sequenced at Eurofins genomics with sre125: 5'-GGG TGA TCA GGA ATT GGA AGG-3' for FUS P525L, sre11: 5'-AAA GAC CCA GAG TGG CTA AG-3' for FUS R495X, and sre270: 5'-TGG GTG GTG GGA TGA ACT TTG-3', respectively. PSC genomic stability was assessed by screening with the hPSC Genetic Analysis Kit (StemCell Technologies; #07550) which did not indicate the presence of any genomic abnormalities. Subsequent assessment with digital karyotyping (KaryoStat, ThermoFisher) highlighted the presence of a partial duplication of chromosome 14 in all cell lines, confirming comparable karyotypes across the isogenic lines.

In vitro differentiation to heterogenous spinal neurons

Adherent human iPSCs were grown to near confluence before the differentiation to heterogenous spinal/hindbrain neurons was initiated by changing the media for two days to media d1-2 (200 nM LDN193189 [Tocris, 6053], 10 µM SB431542 [Tocris, 1614], 25 ng/mL SHH-C25II [R&D Systems, 464-SH-025], 250 nM Purmorphamine [Tocris, 4551], 1 µM retinoic acid [Sigma-Aldrich, R2625]), followed by seven days medium d3–9 (Medium d1-2 with 3 µM CHIR99021 [Tocris, 4423]), one day of medium d10 (Medium d3–9 with 200 µM ascorbic acid [Sigma-Aldrich, A4403], 125 µM db-cAMP [Tocris, 1141], 2.5 µM DAPT [Tocris, 2634], 10 ng/mL each of BDNF [R&D Systems, 248-BD-025], GDNF [R&D Systems, 212-GD-010], NT-3 [R&D Systems, 267-N3-025], and CNTF [R&D Systems, 257-NT-010]), and three days of medium d11–13 (3 µM CHIR99021, 25 ng/mL SHH-C25II, 250 nM Purmorphamine, 1 µM retinoic acid, with 200 µM ascorbic acid, 125 µM db-cAMP, 2.5 µM DAPT, 10 ng/mL each of BDNF, GDNF, NT-3, and CNTF). From day 14 onwards, the neuronal culture was maintained in medium d14+ (200 µM ascorbic acid, 125 µM db-cAMP, 2.5 µM DAPT, 10 ng/mL each of BDNF, GDNF, NT3, and CNTF) until the experimental time-points or harvest.

In vitro differentiation to spinal motor neurons (homogenous protocol)

Specification of iPSC lines into spinal motor neurons was done as previously described in *(Nijssen et al., 2019)*, adapted from *(Guo et al., 2017; Maury et al., 2015)* and detailed also here. Specifically, embryoid bodies were formed and neural induction initiated (days 1-2) by resuspending iPSCs at 0.5-0.75 M cells/ml media in 50% v/v Neurobasal, 50% v/v DMEM/F12, 0.5% v/v N2 supplement, 1% v/v B-27 supplement, 5 µM Y-27632, 40 µM SB431542, 200 nM LDN193189, 3 µM CHIR99021, 200 µM ascorbic acid, followed by seven days (days 3-9) of ventralizing and caudalizing patterning in medium consisting of 50% v/v Neurobasal, 50% v/v DMEM/F12, 0.5% v/v N2 supplement, 1% v/v B-27 supplement, 200 µM ascorbic acid, 200 nM retinoic acid, 500 nM SAG [Tocris, 6390]. At day 10, the embryoid bodies were treated with 5 µM Y-27632 for 1 hour, washed with DPBS [ThermoFisher, 14190250], and then dissociated for 5-10 min with gentle titration in warm TrypLE Express [ThermoFisher, 12604021], supplemented with 5 µM Y-27632. After the embryoid bodies disband into single cells, they were collected by centrifugation at 200 g for 4 min, and resuspended in maturation medium

consisting of Neurobasal, B-27 supplement, 200 µM ascorbic acid, 10 µM DAPT, 10 ng/mL of each GDNF [Peprotech, 450-10] and BDNF [Peprotech, 450-02] and 5 µM Y-27632. The cell suspension was filtered through cell strainer caps and motor neuron progenitors were seeded at >15,000 cells/cm^2 on plates coated with fibronectin [ThermoFisher, 33016015], poly-L-ornithine (Sigma-Aldrich, P4957), and laminin A (Sigma-Aldrich, L2020). The next day, the maturation media was replaced but Y-27632 was omitted. On day 12, remaining proliferative cells were eliminated with a 48 hours pulse of 2 µM 5-fluorodeoxyuridine [Sigma-Aldrich, F0503]. From day 14 onwards, the neuron culture was maintained in medium d14+ consisting of Neurobasal, B27 supplement, 200 µM ascorbic acid, 10 ng/mL each of BDNF and GDNF with media changes every other day.

Dissociation of neuronal cultures and single cell capture by FACS

Single cells from neuronal cultures were isolated as described *(Schweingruber et al., 2023)*. Briefly, the adherent neuron cultures were treated with 5 µM Y-27632 (Tocris, 1254) for 1 hour. After washing carefully with HBSS (ThermoFisher, 14025050), the cultures were dissociated in TrypLE Express (ThermoFisher, 12604021), supplemented with 5 µM Y-27632 for 20-30 min under gentle agitation and with pipetting at 5 min intervals to break cell clumps apart. The dissociated neurons were then collected by centrifugation at 200 g for 5 min and resuspended in 500 µL HBSS supplemented with 2% v/v B-27 supplement [ThermoFisher, 0080085SA], 2% v/v KnockOut Serum Replacement [ThermoFisher, 10828028], 2% w/v bovine serum albumin [Sigma-Aldrich, A9418-10G], 25 mM D-glucose [Sigma-Aldrich, G7021-100G], 5 µM Y-27632, 10 ng/mL BDNF [Peprotech, 450-02], 10 ng/mL GDNF [Peprotech, 450-10]. The cell suspension was then filtered through cell strainer caps into FACS tubes (BD Biosciences) and was kept on ice. The single cell suspensions were index sorted within an hour of harvest on a FACSAria III or FACSAria Fusion (BD Biosciences) at 4 °C and 20 psi through a 100 µm ceramic nozzle under sterile conditions. Based on TOPRO-3 iodide staining, dead cells were excluded and neurite fragments were removed by gates based on unstained live and stained dead-cell control samples. Single cells were collected into 96 multiwell plates (ThermoFisher, 11355960 and 10036339) by dispensing individual cells in 5 nL drops directly into 3 µL ice-cold single cell lysis buffer (scLB, 0.134% Triton X-100 [Sigma], 0.5 U/µL recombinant RNase inhibitor [Takara, 2313B], 3.33 mM each dNTP [ThermoFisher, R1121],

1 mM dithiothreitol [DTT, ThermoFisher], 1.67 µM Smarter-oligo-dTVN [Biomers.net], 6.7e-7 diluted ERCC Spike-In [ThermoFisher, 4456740]). After collection the plates were immediately sealed with adhesive sheets (ThermoFisher, AB0558) and snap frozen on dry ice.

Single cell RNA sequencing (Smart-Seq2)

We prepared single-cell cDNA libraries using Smart-Seq2 *(Picelli et al., 2014)* with adaptations as described *(Schweingruber et al., 2023)*. Cell lysates were thawed on ice before denaturation at 72 °C for 3 min. Following primer annealing for 2 min on ice, 2.76 µL master mix 1 (1 µL 5x Superscript II reaction buffer [ThermoFisher], 1 µL 5 M betaine [Sigma-Aldrich], 0.25 µL 100 mM dithiothreitol (DTT), 0.035 µL 1 M magnesium chloride [ThermoFisher], 0.1 µL 100 µM Smarter-TSO [Biomers.net], 50 U SuperScript II reverse transcriptase, 5 U recombinant RNase inhibitor) was added per lysate. On a thermocycler, the first strand synthesis was carried out as follows: 90 min at 42 °C; 10 cycles of 2 min at 50 °C, 2 min at 42 °C; and 15 min at 70 °C before cooling to 4 °C. Then 7.5 µL master mix 2 (1.15 µL) was added per sample. On a thermocycler, the second strand synthesis and amplification were carried out as follows: 3 min at 98 °C; 21 cycles of 20 sec at 98 °C, 15 sec at 67 °C, 6 min at 72 °C; and 5 min at 72 °C before cooling to 12 °C. The single-cell cDNA libraries were purified with SPRI beads (SeraMag beads, in 19.5% w/v PEG 8000, 1 M sodium chloride, 10 mM Tris-HCl pH 8.0, 1 mM disodium EDTA, 0.01% v/v Igepal CA630, 0.25% w/v sodium azide). The samples were barcoded with unique Illumina Nextera Indexes using reagents from the Nextera Sample Preparation Kit. The final libraries were then combined at equimolar concentrations before purification of the pools with SPRI beads. Sequencing was performed on HiSeq 2000 (Illumina) and NovaSeq 6000 (Illumina) at NGI Sweden, Stockholm.

Single-cell RNA-Seq mapping and cell type classification

Raw sequencing reads were mapped to the hg38 human reference genome using STAR version 2.7.0e *(Dobin et al., 2013)* with parameters "-outSAMstrandField" set to "intronMotif". Aligned reads were assigned to genomic locations with the 'rpkmforgenes.py' script *(Ramsköld et al., 2009)*, using an annotation GTF file from Ensembl version 95 (GRCh38.95). In 'rpkmforgenes.py', the parameters "-fulltranscript" and "-rmnameoverlap" were used. After obtaining the raw counts, cells with < 100,000 uniquely mapped reads

and/or < 5,000 detected genes were excluded. Genes with an RPKM value of > 1 were considered detected. Cells were classified as neurons based on expression of NEFM (neurofilament-medium) at > 100 RPKM and SNAP25 at > 10 RPKM. Neurons were further classified as motor neurons if they showed expression of at least one of the transcription factors *ISL1*, *ISL2* or *MNX1* at > 1 RPKM, combined with either *SLC18A3* (VAChT) or *SLC5A7* (ChT) at > 5 RPKM, but lacked expression of the interneuron markers VSX2 (< 1 RPKM) and SIM1(< 1 RPKM). All neuronal cells that were not classified as motor neurons were generically termed interneurons. V2a interneurons were neuronal cells that were positive for both *VSX2* (CHX10) and *SOX14* at > 1 RPKM.

Identification of differentially expressed genes and pathways

Differential expression analysis between groups was conducted in R (version 3.6.1) *(R Core Team, 2021)* using the *DESeq2* package version 1.24.0 (Love et al., 2014)). Fit type was set to "local". An FDR-adjusted p-value of < 0.05 was considered significant. Gene set enrichment analysis was performed using the *fgsea* package version 1.8.0. DESeq2 outputs were ranked by test statistic to be used as input. These gene lists were compared to GO biological process pathways obtained from the human MsigDB collection (C5, GO-bp). Only pathways containing between 10-500 genes were considered in the analysis. UMAP plots, heatmaps and Venn diagrams were all generated in R. UMAP plots were generated using *Seurat* version 4.2.0 *(Butler et al., 2018)* using all cells or all neuronal cells that passed QC as input. The top 2,000 most variable gene features were used. Heatmaps were generated using the *pheatmap* package version 1.0.12. Venn diagrams were generated using the *Vennerable* package version 3.1.0 or the *venn* package version 1.11. For the QIAGEN's Ingenuity Pathway Analysis (IPA) *(Krämer et al., 2014)* the list of differentially expressed genes between mutant motor neurons and control was used as input. Genes with FDR < 0.1 were considered significantly differentially expressed for the pathway analysis and were compared to the Ingenuity Knowledge Base reference set (version Q4 2022, accessed on February 7, 2023). Canonical pathways across the different sample sets were ranked according to the FDR value aggregate of pathway enrichment across the FUS-ALS MN datasets (internally calculated by IPA). Heatmaps of significance (FDR value) and activation scores (z-score) for the 12 highest ranking

canonical pathways were generated. Pathways with an FDR of < 0.1 were considered significantly enriched.

Immunofluorescence microscopy

For imaging of iPSCs, they were grown on 12-well chamber microscope slides [ibidi, 81201] and fixed with 4% paraformaldehyde for 20 min at room temperature. The cells were then washed three times for 5 min each with PBS and then permeabilized in TBS supplemented with 0.5% v/v Triton X-100 [AppliChem], 6% bovine serum albumin (BSA) [Sigma-Aldrich], in TBS for 30 min at room temperature. Primary antibody incubation was performed in antibody diluent (0.1% v/v Triton X-100, 6% w/v BSA, in TBS) overnight at 4 °C. The cells were washed three time for 5 min with antibody diluent before being incubated with secondary antibodies in antibody diluent for 2 hours at room temperature. Subsequently, the cells were counterstained with 100 ng/ml DAPI in PBS for 10 minutes at room temperature and then washed twice for 5 min with PBS. Coverslips were then mounted using hard set antifade mounting medium [Vectashield, H-1400]. Images were acquired using an Eclipse Ti-2 epifluorescence microscope [Nikon] with a 20×/dry lens.

Neurons were grown on glass coverslips or in imaging grade 96-well plates (ibidi, 89626; IBL Austria, 220.230.042) coated with fibronectin [ThermoFisher, 33016015], poly-L-ornithine (Sigma-Aldrich, P4957), and laminin A (Sigma-Aldrich, L2020) for immunofluorescence microscopy. At indicated time-points, the neurons were washed with warm HBSS (containing magnesium and calcium chloride, ThermoFisher Scientific, 14025100), fixed in 4% w/v paraformaldehyde for 15 min, and washes three times with HBSS to end the fixation. Then, the neurons were permeabilized in blocking solution [0.5% w/v Triton X-100 (Sigma-Aldrich, X100-1L), 10% v/v normal donkey serum (Jackson ImmunoResearch, 017-000-121), in PBS (ThermoFisher Scientific, 70011044)] for 30 min. Primary antibodies were applied in fresh blocking solution over night at 4 °C. Following three washes with blocking solution over 30 min, secondary antibodies diluted in blocking solution were applied for 1.5 hours at room temperature in the dark. The neurons were washes twice with PBS (ThermoFisher Scientific, 70011044), followed by a single wash in ultrapure water (ThermoFisher Scientific, 10977049). The cells were mounted in Fluoromount G (ThermoFisher Scientific, 00-4958-02) and

subjected to inverted confocal microscopy on an LSM700 (Zeiss) or LSM800-Airy microscope (Zeiss).

Western blotting

One 10-cm dish of iPSCs was harvested by incubation with DPBS-EDTA and pelleted by centrifugation at 200 g. Cell pellets were resuspended in 400 µl RIPA buffer [Sigma Aldrich, R0278-50ML] supplemented with 2x Halt protease and phosphatase inhibitor cocktail [Thermo Fisher Scientific, 78441], 2 mM manganese sulfate, and 25 U/ml Cyanase nuclease [Serva, 18542.02] followed by incubation on ice for 30 min with vortexing in 5-min intervals. 400 µl of 2x LDS loading buffer (ThermoFisher Scientific, NP0007) supplemented with 250 mM DL-dithiothreitol (Sigma-Aldrich, 43816-50ML) were added and samples were boiled 10 min at 70 °C. Samples were loaded on 4-12% Bolt Tris-Bis gels and ran with 1x MOPS buffer, followed by blotting on nitrocellulose membranes using the iBlot2 transfer device. Membranes were blocked for 1 hour in TBS-Tween (0.1%) supplemented with 5% w/v non-fat dry milk, followed by incubation with primary antibodies over night at 4 °C. After five subsequent washes with TBS-Tween (0.1%), secondary antibodies were added in TBS-Tween (0.1%) supplemented with 5% non-fat dry milk, incubated for 1.5 hours at room temperature, followed by five consecutive 5-minute washes with TBS-Tween (0.1%) and scanning of the membranes on an Odyssey CLx scanner [Li-Cor].

Extracellular flux XF96 Seahorse measurements

Human iPSC-derived motor neurons were differentiated according to the homogenous protocol and seeded at day 10 into Seahorse XF96-well plates (Seahorse Bioscience, Agilent Technologies). At day 21 the plates were washed and incubated for 60 min in an air incubator at 37 °C with Seahorse DMEM-based assay medium, supplemented with 25 mM glucose and 2 mM glutamine (pH adjusted to 7.5). The XF96 plate was then transferred to a temperature-controlled (37 °C) Seahorse extracellular flux analyzer (Agilent Technologies) and allowed a temperature equilibration period before assay cycles (consisting of 1-min mix, 2-min wait, and 3-min measure period). Oxygen consumption rates (OCR) and extracellular acidification rates (ECAR) were dissected into different functional modules as described in detail previously *(Divakaruni and Jastroch, 2022; Keuper et al., 2014)*. In brief, after four basal assay cycles

oligomycin (5 µg/ml) was injected to inhibit the ATP synthase to determine OCR related to ATP synthesis for 3-6 cycles (lowest value of 3-6 cycles was used for calculation). 2,4-Dinitrophenol (DNP; 100 µM) was injected to stimulate maximal respiration, revealing maximal substrate oxidation capacity (3 cycles, highest value used for calculation). Next, rotenone (R, 4 µM) and antimycin A (AA, 2 µM) were added, followed by 3 assay cycles to determine the non-mitochondrial OCR (lowest of 3 values). Finally, 2-deoxy-glucose (2-DG, 100 mM) was added to determine glycolytic extracellular acidification rates (ECARs), subtracting the lowest of 6 ECAR measurements after 2-DG injection. ECAR values were transformed to PPR values using the machine settings. PPR values after 2-DG injection were subtracted to correct for non-glycolytic acidification. After the measurement, the cells were lysed and total dsDNA amount per well was determined using Quant-iT PicoGreen dsDNA Assay Kit (ThermoFisher). All OCR and PPR values were normalized to 230 ng dsDNA (mean DNA content/well of all measurements).

Live cell imaging for tracking mitochondria

Motor neurons were derived using the homogenous protocol, but the embryoid bodies were attached at day 10 to imaging grade 24-well plates (ibidi, 82406) coated with fibronectin (ThermoFisher, 33016015), poly-L-ornithine (Sigma-Aldrich, P4957), and laminin A (Sigma-Aldrich, L2020) to promote axons outgrowth. The neurons were matured until at least day 27. For tracking mitochondria, motor neurons were cultured in Imaging Optimized BrainPhys medium (Stemcell Technologies, 05796) with SM1 NeuroCult supplement (Stemcell Technologies, 05711), 200 nM L-ascorbic acid (Sigma-Aldrich, A4403), and 10 ng/mL BDNF (Peprotech, 450-02) and 10 ng/mL GDNF (Peprotech, 450-10). After addition of 50 nM TMRM (ThermoFisher Scientific, I34361) mitochondria were labelled for 30 min before the medium was replaced. Live cell microscopy was performed in an Axio Observer 7 (Zeiss) equipped with a Plan Apo 40x/0.95 Ph3 objective and under a 5% CO_2 atmosphere at 37 °C. Four regions across distal axons were selected to record 5-min long time-lapses. For analysis of mitochondrial movement, individual mitochondria were traced in Fiji *(Schindelin et al., 2012)* using the TrackMate 7 extension with the StarDist detector *(Ershov et al., 2022)* and a Sparse LAP tracker (as in 'mitotracker.py'). The mitochondrial traces were then annotated and

analysed in R (version 4.2.0) *(R Core Team, 2021)* using our custom package 'mitotrackR' (https://github.com/schwi24/mitotrackR).

Data Availability

We have deposited all raw and processed sequencing data generated in this study on the NCBI Gene Expression Omnibus (GEO) under the accession number GSE226482. The C9orf72 bulk RNA sequencing data was retrieved directly from the authors of the study *(Mehta et al., 2021)*.

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Figure legends

Figure 1. Single cell RNA sequencing identifies motor neurons and interneuron types across isogenic mutant ALS-FUS and FUS KO iPSC lines. a, Schematic showing generation of the different iPSC-lines using CRISPR-Cas9 gene editing, subsequent differentiation into motor neurons and interneurons, sorting and single-cell RNA sequencing. **b**-**e**, UMAP projections of all cells of the included cell lines that passed quality control. The top two UMAPs are colored by assigned **b**, cell type or **c**, cell line, the bottom two only contain all neuronal cells, again colored by assigned **d**, cell type or **e**, cell line. **f**, Gene expression heatmaps of all neuronal cells, showing expression data of several (motor-)neuronal marker genes, progenitor markers and housekeeping genes. **g**, Gene expression heatmaps of specific motor- and interneuron subtype marker genes. **h**, Venn diagrams showing the overlap between differentially expressed genes in motor neurons, V2a interneurons and other interneurons between the FUS mutant lines versus the control cell line. The top and bottom number in each compartment represents upregulated and downregulated genes, respectively. Genes with an adjusted p-value of < 0.05 were considered differentially expressed.

Figure 2. Identification of shared gain-of-function pathways unique to motor neurons across FUS mutations. a, Schematics showing representative patterns of different nuclear and cytoplasmic FUS protein localization in the cell lines used in this study. Confocal fluorescence microscopy with immunostaining of N-terminal FUS in motor neurons (TUBB3+, ISL1/2+) at day 28 reveals cytoplasmic accumulation of FUS R495X as well as P525L and ablation in the FUS KO line. Scale bars are 10 µm. **b**, Venn diagram showing overlap between differentially expressed genes in the different FUS mutant and control motor neurons. Genes with an adjusted p-value of < 0.05 were considered differentially expressed. GO (biological process) pathways enriched or depleted in the different FUS mutant compared to the control motor neurons (using Gene Set Enrichment Analysis, GSEA). For **b-c**, in each Venn compartment, the top number represents upregulated genes/processes, while the bottom number represents downregulated genes/processes. Pathways with an adjusted p-value of < 0.05 were considered significantly up- or downregulated. **d-f**, Heatmaps display the normalized enrichment scores (from GSEA) of selected groups of pathways from the Venn diagram in **c**. Motor neurons are compared to V2a or other interneurons to show specific or stronger

regulation of these pathways in motor neurons. **g**, Top dysregulated pathways across FUS mutant motor neurons using the Ingenuity Pathways Analysis.

Figure 3. Cross-comparisons between isogenic TDP-43 M337V and FUS ALS lines uncovers shared dysfunctions. Schematic of the generation of the TDP-43 M337V mutant iPSC line, differentiation into motor neurons and subsequent single-cell sorting and RNA-sequencing. **b**, UMAP projections of all single cells in the study that passed quality control. The two UMAPs are colored by assigned cell type (left) or cell line (right). **c**, UMAP projections of all neuronal cells in the study that passed quality control, again colored by assigned cell type (left) or cell line (right). **d**, Venn diagram showing overlap of differentially expressed genes between all FUS mutant motor neurons, as well as the TARDBP mutant motor neurons, as compared to control. Genes with an adjusted p-value of < 0.05 were considered differentially expressed. **e**, Venn diagram showing overlap in dysregulated pathways between FUS LOF lines (all FUS lines), FUS GOF lines (excluding the FUS KO), and the TDP-43 M337V line. For **d, e**, in each compartment, the top number represents upregulated genes/pathways, while the bottom number represents downregulated genes/pathways. Pathways with an adjusted p-value of < 0.05 were considered significantly up- or downregulated. **f**, Heatmaps displaying normalized enrichment scores (from GSEA) of selected groups of pathways from the Venn diagram in **e**. Motor neurons are compared to V2a interneurons to show specific or stronger regulation of these pathways in motor neurons.

Figure 4. Dysregulation in key mitochondrial pathways and genes points to metabolic impairment in motor neurons across isogenic ALS lines. a,c,e Modified GSEA plots showing the rank of all genes within this specific GO-term for all mutant motor neurons generated using the homogeneous protocol, according to the GSEA test statistic. The most significantly upregulated gene is on the top and the most significantly downregulated gene on the bottom. **b**,**d,f** Violin plots showing normalized expression values (RPKM) of three example genes of the pathway from **a** in motor neurons generated with the homogeneous protocol. * p<0.05, ** p<0.01, *** p<0.001 vs. control, derived from DESeq2 differential gene expression.

Figure 5. **Bioenergetic profiling and mitochondrial motility analysis of ALS mutant motor neurons. a**, Scheme depicting time-course of the metabolic assay. Following differentiation

with the homogenous protocol, motor neurons were assessed at day 21 using a XF96 extracellular flux analyzer. to measure oxygen consumption rates (OCR) and extracellular acidification rates (ECAR). Aggregated OCR and ECAR traces and their dissection into functional modules are shown in Extended Data Fig. 7. **b**, Mitochondrial respiration, **c**, ATP-linked respiration after subtracting proton leak respiration (Extended Data Fig. 7), **d**, Maximal substrate oxidation upon addition of uncoupler DNP, 100 µM, **e**, glycolytic ECAR at baseline and **f**, induced glycolysis after inhibition of mitochondrial ATP synthase; **f,** Calculation of cellular ATP turnover from glycolysis and oxidative phosphorylation. Glycolytic proton production rates were converted to glycolytic ATP output assuming a P/H+ ratio of 1:1 (black part of bars) and ATP-linked OCR was converted to mitochondrial ATP output assuming a P/O ratio of 2.3 (top part of bars). Data are the mean + SEM of 16-19 wells measured for three independent differentiations. * $p<0.05$, ** $p<0.01$, *** $p<0.001$, **** $p< 0.0001$ vs. control, One-way ANOVA (posthoc: Dunnett's). **h**, Schematic of the mitochondrial motility assays using live fluorescence microscopy. Motor neuron progenitors were attached as neurospheres, followed by terminal differentiation and axon outgrowth. **i,** Mitochondria were labelled using TMRM in peripheral axons and 6-min long timelapses were recorded at 0.5 Hz in 3-4 locations in at least 3 independent differentiations per line. Traces were identified using TrackMate 7 with StarDist detector and simple LAP tracer and directional movement was analyzed in R using our package 'mitotrackR'. The proportions of stationary (**j**) and motile mitochondria (**k**) were calculated. Each bubble represents the number of mitochondria in individual recordings. **l**, The influence of the mutation in isogenic motor neurons on the mitochondrial motility (as proporation of stationary, anterograde and retrograde mobile mitochondria) was assessed by Pearson's χ^2 test ($\chi^2 = 88192$, $df = 12$, $p <2.2e-16$). The association between isogenic mutants and mitochondrial motility is plotted. The sign of the residuals indicates the direction of the association, with attraction and repulsion colored as red and blue, respectively. The bubble size represents the contribution to the total χ^2 score (squared residuals over χ^2 statistic).

Abbreviations

ALS	amyotrophic lateral sclerosis
ANOVA	analysis of variance
ATP	adenosine triphosphate
2-DG	2-deoxyglucose
DEA	differential (gene) expression analysis
DEG	differentially expressed genes
DNP	2,4-dinitrophenol
DTT	dithiothreitol
ECAR	extracellular acidification rate
GO	gene ontology
GOF	gain of function
GSEA	gene set enrichment analysis
HRE	hexanucleotide repeat expansion (in C9orf72)
iPSC	induced pluripotent stem cells
KO	knockout
LOF	loss of function
NGS	next generation sequencing
OCR	oxygen consumption rate
PCR	polymerase chain reaction
RPKM	reads per kilobase of exon per million reads mapped
UMAP	uniform manifold approximation and projection

Author contributions

E.H., M.-D.R.: conceptualization of study, supervision and project administration. E.H., M.-D.R., M.J.: funding acquisition. E.H., M.-D.R.: supervision. E.H., M.-D.R., C.S., J.N., J.A.B., S.R.: methodology and study design. S.R., C.S.: literature review and meta-analysis of clinical features. S.R., J.M., N.O'B., J.A.B., M.-D.R.: genome editing and characterization of iPSC lines. C.S., J.N., J.A.B.: experimental work on neuronal culture and single-cell sorting. C.S., J.A.B.: single cell library preparation. C.S., MK: experimental work on metabolic assays (Seahorse). M.K.: metabolic analysis. C.S.: experimental work and analysis of mitochondrial motility. J.N., I.M.: RNA-sequencing data processing, differential gene expression analysis, and gene set enrichment analysis. J.N., J.M., C.S.: Ingenuity pathway analysis. J.N., C.S.: preparation of figures. C.S., E.H.: writing of original draft. All authors contributed to editing of the article and approved the manuscript.

Figure 1

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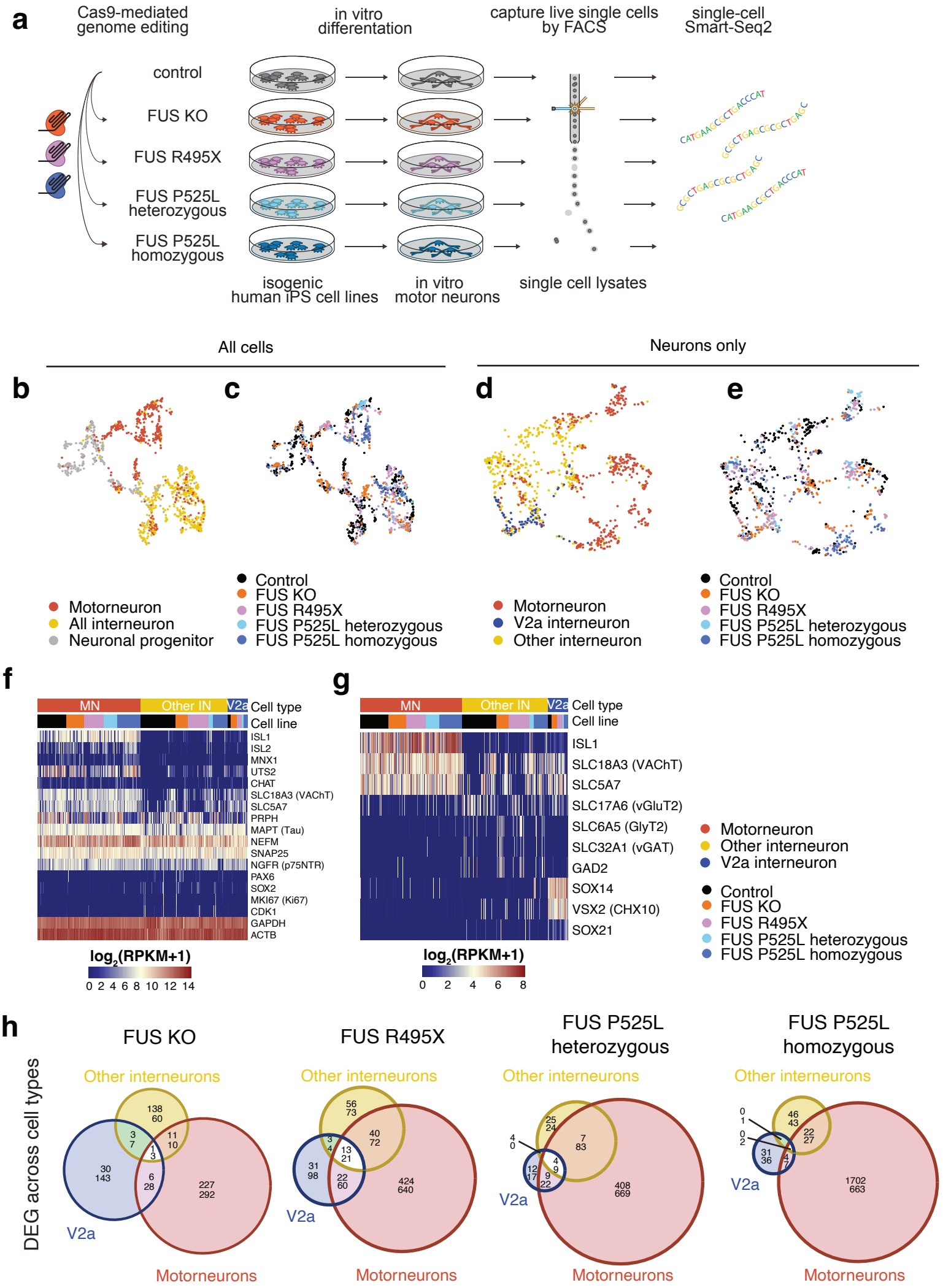

Figure 2

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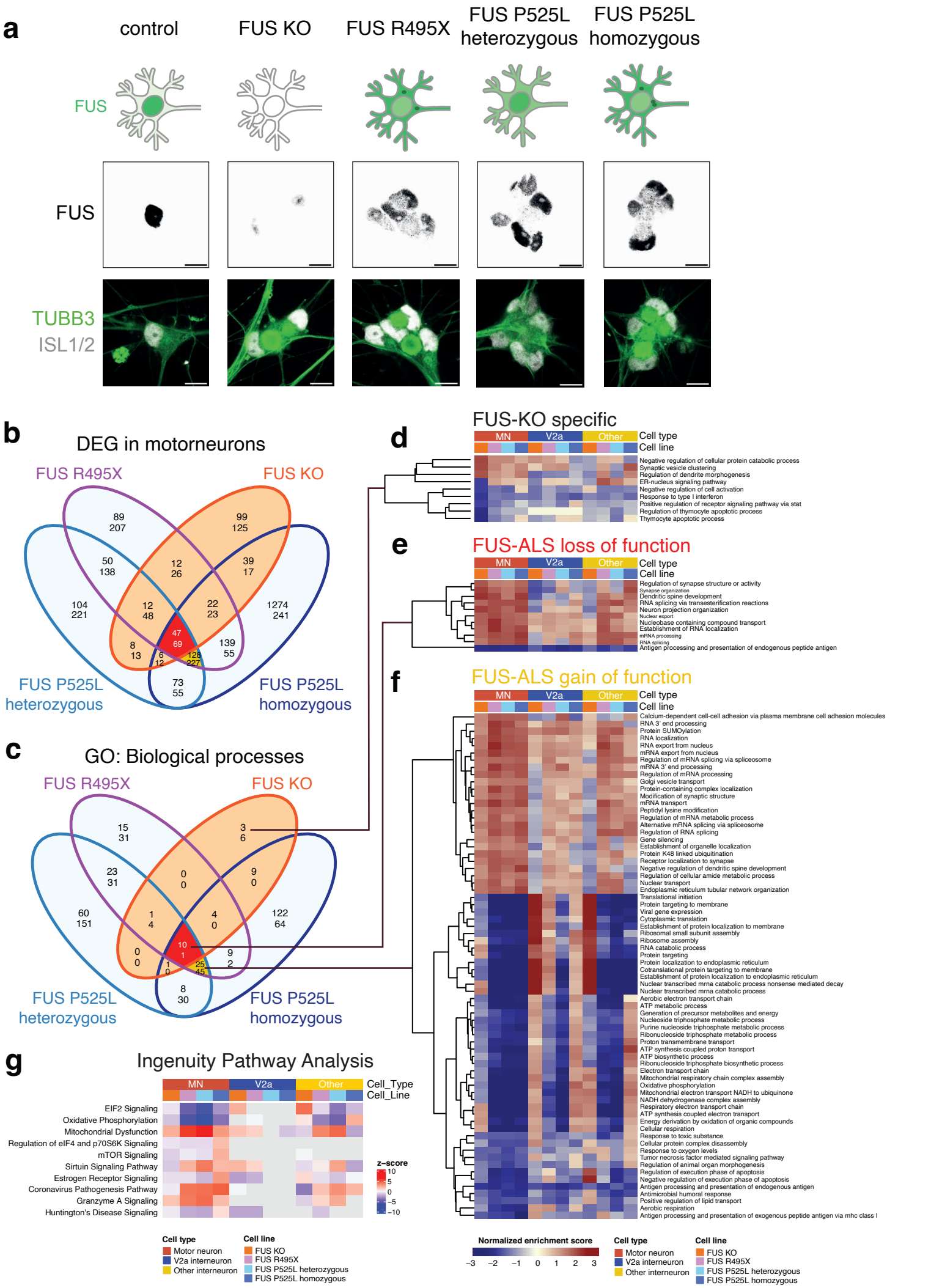

Figure 3

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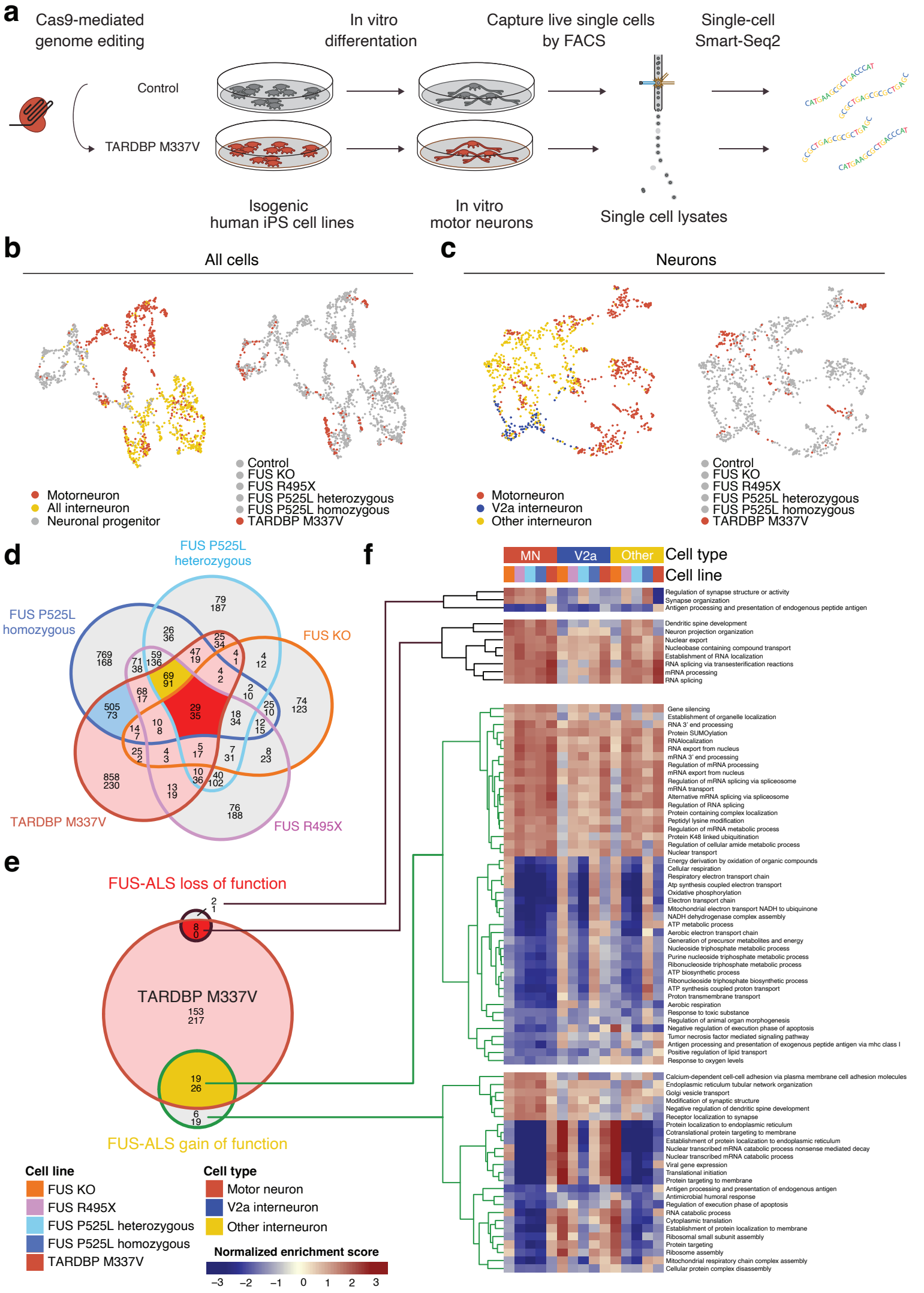

Figure 4

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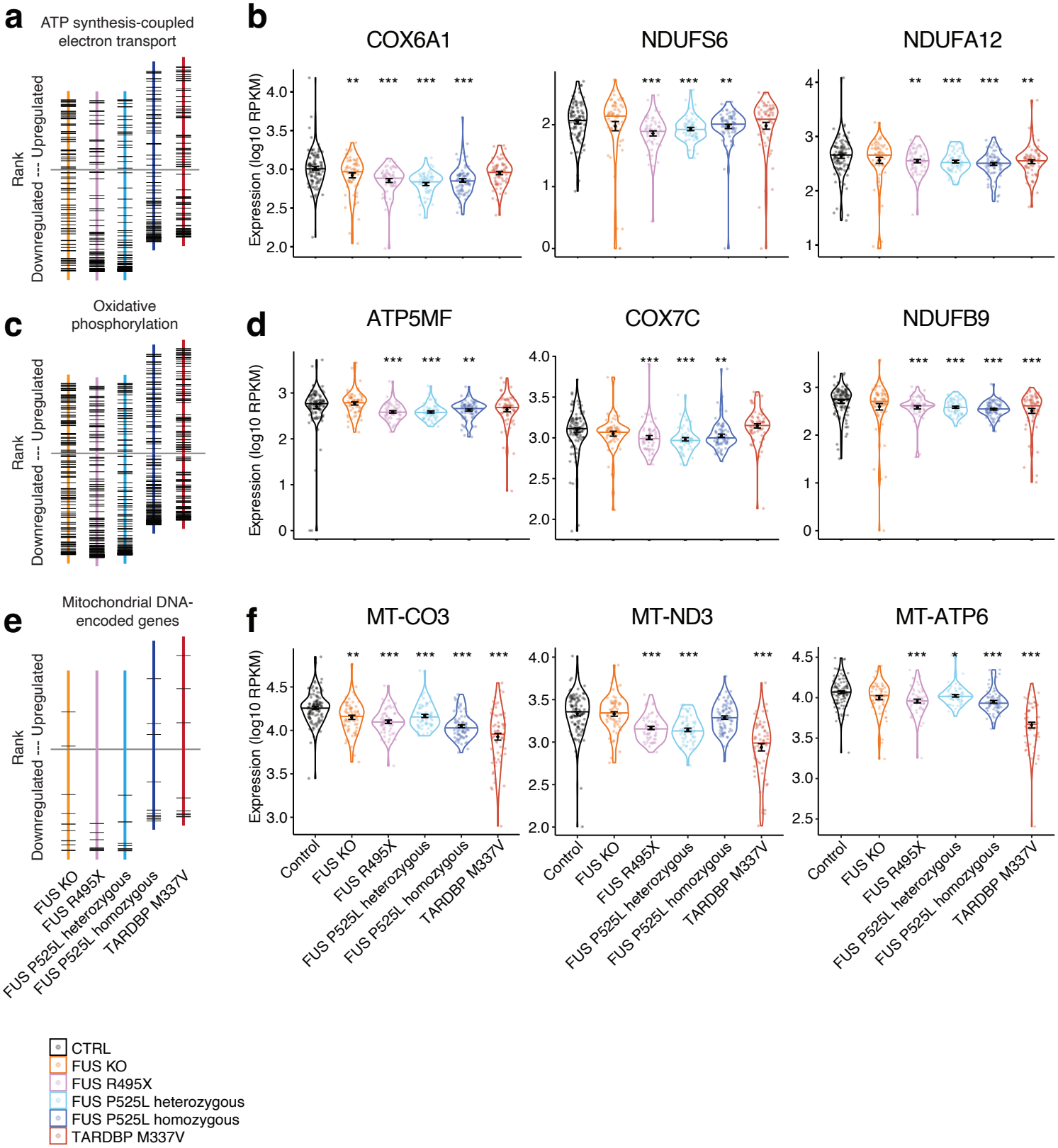
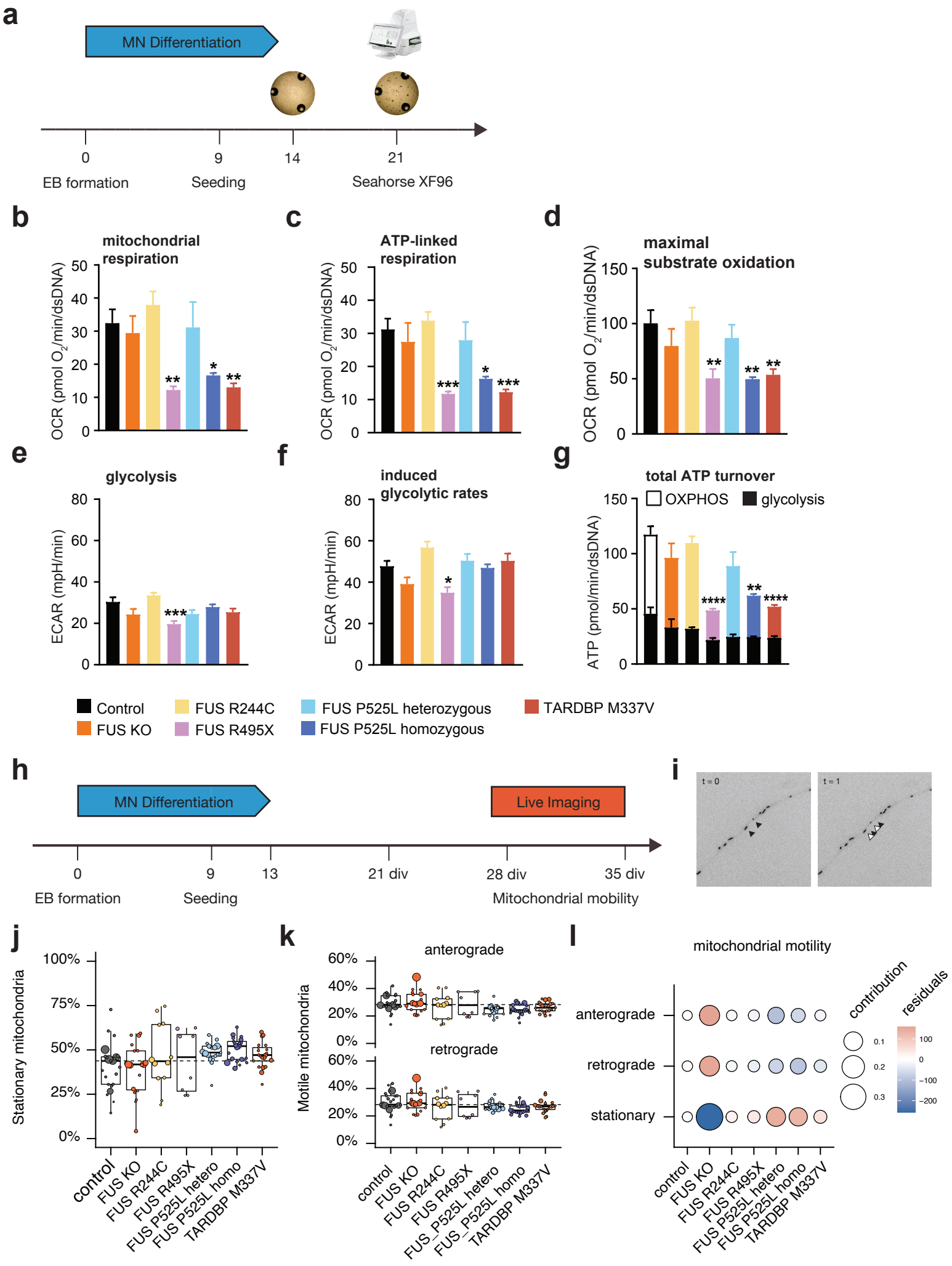


Figure 5

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