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2	Frontotemporal dementia-like disease progression elicited by
3	seeded aggregation and spread of FUS
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30	(ALS), Frontotemporal Lobar Degeneration (FTLD)
31 32	
33 34	Abstract
35	RNA binding proteins have emerged as central players in the mechanisms of many
36	neurodegenerative diseases. In particular, a proteinopathy of <u>fu</u> sed in <u>s</u> arcoma (FUS) is
37	present in some instances of familial Amyotrophic lateral sclerosis (ALS) and about 10%
38	of sporadic FTLD. Here we establish that focal injection of sonicated human FUS fibrils

39 into brains of mice in which ALS-linked mutant or wild-type human FUS replaces 40 endogenous mouse FUS is sufficient to induce focal cytoplasmic mislocalization and 41 aggregation of mutant and wild-type FUS which with time spreads to distal regions of the 42 brain. Human FUS fibril-induced FUS aggregation in the mouse brain of humanized FUS 43 mice is accelerated by an ALS-causing FUS mutant relative to wild-type human FUS. 44 Injection of sonicated human FUS fibrils does not induce FUS aggregation and 45 subsequent spreading after injection into naïve mouse brains containing only mouse FUS, 46 indicating a species barrier to human FUS aggregation and its prion-like spread. Fibril-47 induced human FUS aggregates recapitulate pathological features of FTLD including 48 increased detergent insolubility of FUS and TAF15 and amyloid-like, cytoplasmic deposits 49 of FUS that accumulate ubiquitin and p62, but not TDP-43. Finally, injection of sonicated 50 FUS fibrils is shown to exacerbate age-dependent cognitive and behavioral deficits from 51 mutant human FUS expression. Thus, focal seeded aggregation of FUS and further 52 propagation through prion-like spread elicits FUS-proteinopathy and FTLD-like disease 53 progression.

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56 Background

Fused in sarcoma (FUS) is an RNA binding protein that normally localizes 57 58 predominantly in the nucleus, however it mislocalizes and aggregates in the cytoplasm in 59 some instances of familiar amyotrophic lateral sclerosis (ALS) and in 10% of 60 frontotemporal lobar degeneration (FTLD), one of the most frequent forms of early-onset 61 dementia (1-3). The 526-amino-acid FUS protein includes a C-terminal non-classical PY 62 nuclear localization signal (NLS) which contains most of the ALS-linked mutations and a 63 N-terminal low complexity, glycine-rich, prion-like domain (4). Although an important 64 difference from transmissible spongiform encephalopathies (TSEs) is that prions behave like infectious agents, prion-like diseases belong to a group of protein misfolding neurodegenerative diseases that are characterized by the abnormal aggregation of defined host proteins (e.g., Amyloid β (A β) and tau in Alzheimer's disease, α -synuclein in Parkinson's disease, mutant polyglutamine repeats in Huntington's disease, and TDP-43 in ALS and FTLD). A β , tau, α -synuclein, and TDP-43 inclusions have been shown to develop in a stereotypical, age-dependent manner in particular brain regions from which they appear to spread (5-7).

72 Increasing evidence supports a model whereby misfolded proteins released from 73 a cell harboring pathological inclusions act on recipient cells to form *de novo* pathology by 74 corrupting endogenous normal proteins to adopt pathological conformations. Injection of 75 sonicated fibrils from either disease-associated α -synuclein, tau, or A β peptides 76 unilaterally into mouse brains expressing the respective mutant protein (8-10), induces the 77 spread of aggregates far from the site of injection, accelerating disease and enhancing 78 neuronal loss. The repetition of this process has been proposed to underlie cell-to-cell 79 propagation of pathological proteins throughout the brain (11, 12). Accumulating evidence 80 supports cell-to-cell templated propagation of A β , tau, α -synuclein, and huntingtin (13-81 18). For ALS, evidence from cell culture has suggested spread from cell-to-cell from the 82 dipeptide repeat (DPR) proteins encoded by hexanucleotide expansion in C9orf72 (19, 83 20) and seeding and spread of SOD1 have also been reported with mutant SOD1 84 transgenic mice (21-24). Additionally, TDP-43 aggregates from FTLD patients and 85 recombinant TDP-43 preformed fibrils have been proposed to induce prion-like spread 86 pathology of the protein both in cultured cells and transgenic mice expressing cytoplasmic 87 TDP-43 (25-29).

88 Neuropathological evidence from a small number of patients is consistent with the 89 hypothesis of FUS pathology spreading within the central nervous system (CNS), 90 including *1*) clinical symptoms often start focally and spread as disease progresses (30-

91 32) and 2) FUS cytoplasmic inclusions have been observed in several regions of the CNS 92 of ALS and FTLD-FUS patients with similar spatial patterns as in FTLD-Tau or FTLD-TDP-43 forms (2, 33-35). That said, FUS inclusions vary markedly, presenting distinct density 93 94 and shapes between cases (3, 35-39). Initial in vitro evidence for FUS seeding potency 95 was provided by Nomura et al. who described that FUS-LCD fibrils carrying the G156E 96 mutation seed wild-type FUS in vitro and in cell culture (40). Here we show that focal 97 injection of pre-assembled human FUS fibrils in adult mouse brains induces de novo 98 aggregation of endogenous human ALS-associated mutant FUS or human wild-type FUS 99 and seeding of a spreading pathology through the nervous system that initiates 100 neurodegeneration and compromises cognition.

103 Methods

105 Animals

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106 The generation of the humanized FUS animals was described before (41). All the mice 107 used in this report were maintained on a pure C57BL/6 background. For this study, we 108 used 16 months old males and females with the mFUS^{KO}/hFUS^{R521H or WT} genotype. All 109 experimental procedures were approved by the Institutional Animal Care and Use 110 Committee of the University of California, San Diego.

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112 **Protein purification**

113 Protein purifications were performed as described before (42). Briefly, HA-tagged 114 FUSR495X expression construct was generated using a pGST-Duet construct which 115 contains a TEV-cleavable site, resulting in a GST-TEV-HA-FUSR495X protein (43). All 116 proteins were expressed and purified from *E. coli* BL21 CodonPlus (DE3)-RIL cells under 117 native conditions. Protein expression was induced adding 1 mM IPTG for 16h at 16°C. E. 118 coli bacterial cells were lysed on ice by sonication in Phosphate-Buffered Saline (PBS) 119 supplemented with protease inhibitors (cOmplete, EDTA-free, Roche Applied Science). 120 The protein was purified over pre-packed Glutathione Sepharose High Performance resin 121 column (GSTrap HP columns, Cytiva). One-step purification of glutathione S-Transferase 122 (GST) tagged FUS protein was performed using Akta Pure fast protein liquid 123 chromatography (FPLC) system (Cytiva) at 4°C. GST-HA-FUS^{R495X} protein was eluted in 124 50 mM Tris-HCl, pH 8, 200 mM Trehalose, and 20 mM L-glutathione reduced. His-SOD1 125 protein was purified over pre-packed Ni Sepharose High Performance HisTrap HP (GE) 126 using an AKTA pure chromatography system at 4°C and eluted with 50 mM Tris pH 7.4. 127 100 mM NaCl and 400 mM Imidazole. The following Molecular Weight Markers were used: 128 Carbonic Anhydrase from bovine erythrocytes (29 KDa, Sigma), Albumin, bovine serum 129 (66KDa, Sigma) and b-Amylase from sweet potato, (200KDa, Sigma). Eluted proteins (GST-HA-FUS^{R495X}, and His-SOD1) with the expected size were collected and concentrated to final concentration of 12 mM using Amico Ultra centrifugal filter units (10 kDa molecular weight cut-off; Millipore). All proteins after purification were centrifuged for 15 min at 14,000 rpm at 4°C to remove any aggregated material. Protein concentration was calculated by Coomassie Blue with BSA protein as standard, and by colorimetric Bradford assay (Bio-Rad). For protein storage at -80°C glycerol (30%) was added.

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Protein fibrilization

139 FUS fibrilization was induced as described by Gasset-Rosa et al. (42). GST-HA-FUSR495X 140 protein was thawed and buffer exchanged into FUS assembly buffer at 4°C (50 mM Tris-141 HCl, pH 8, 200 mM trehalose, 1 mM DTT, 20 mM glutathione). TEV protease was added 142 to GST-TEV-HA-FUS^{R495X} (4 µM) in FUS assembly buffer for 3 hours to induce seed 143 formation. Next, high salt storage buffer (40 mM HEPES pH7.4, 500 mM KCI, 20 mM 144 MgCl2, 10% glycerol, 1 mM DTT) was added for 3 hours to separate the seeds (43). FUS 145 fibrilization was initiated by adding 5% of FUS seeds to GST-TEV-HA-FUS^{R495X} (4 µM) 146 and TEV protease in FUS assembly buffer for 24 hours at 22°C. His-SOD1 fibrilization 147 was induced as described in (42, 43). Finally, fibrils were dialyzed using slide-A-Lyzer 148 MINWE Dialysis Units (10 kDa molecular weight cut-off; Thermo Fisher Scientific) in PBS 149 for 3 hours and sonicated at 45% 45s just before injecting them into the animals.

150 Transmission Electron Microscope

300-mesh Formvar/carbon coated copper grids (Ted Pella) were glow-discharged and loaded with fibril protein samples (10 μl). Next, grids were stained with 2% (w/v) aqueous uranyl acetate (Ladd Research Industries, Williston, VT). Excessive liquid was removed and grids were air dried. Grids were examined using a Tecnawe G2 Spirit BioTWIN transmission electron microscope equipped with an Eagle 4k HS digital camera (FEI, Hilsboro, OR).

157 Stereotactic injections

All surgical procedures were performed using aseptic techniques. Injections were performed using 33-gauge needles and a 10 µl Hamilton syringe (Hamilton, Switzerland). 160 16-month-old mFUS^{KO}/hFUS^{R521H}, mFUS^{KO}/hFUS^{WT} or non-transgenic mice were injected 161 with 10 µg of sonicated HA-FUS^{R495X} fibrils, 10 µg of sonicated SOD1 fibrils, 10 µg HA-162 FUS^{R495X} monomer or PBS as control, following the stereotactic coordinates using bregma 163 as a reference: anteroposterior – 2.5 mm, mediolateral – 2.0 mm and dorsoventral at -1.8 164 mm (hippocampus) and -0.8 (cortex).

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166 Behavioral tests167

For each behavioral assay, a cohort of n=5-6 animals per group for the non-transgenic genotype (FUS fibrils or PBS-injected) and n=11-12 animals per group for the mFUS^{KO}/hFUS^{R521H} genotype (FUS fibrils or PBS-injected) was assessed where experimentalist was blinded to genotypes. No increased mortality was observed in any of the groups.

173 Open field test

The open field area consisted out of a square white Plexiglas (50 × 50 cm2) open field illuminated to 600 lx in the center and mice were placed in the center. The mice were allowed to explore the area for 10 mins. An overhead Noldus camera was used to monitor their movement with Ethovision XT software. Mice were tracked for multiple parameters, including distance traveled, velocity, center time, frequency in center as described in (44). *Rotarod* The rotarod test was performed as described in (45). A Rota-rod Series 8 apparatus (Ugo

Basile) was used. Before the trial was initiated, the mice were placed on the stationaryrotarod for 30s for training. Each mouse was given three trials per day, with a 60s inter-

trial interval on the accelerating rotarod (4–40 r.p.m. over 5 min) for five consecutive days.

185 The latencies to fall were automatically recorded by a computer.

186 Novel object recognition test

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188 This behavioral assay was performed as described in (41). Mice were individually 189 habituated to a 51cm x 51cm x 39cm open field for 5 min and then tested with two identical 190 objects placed in the field. Each mouse was allowed to explore the objects for 5 min. After 191 three such trials (each separated by 1 min in a holding cage), the mouse was tested in the 192 object novelty recognition test in which a novel object replaced one of the familiar objects. 193 Behavior was video recorded and then scored for contacts (touching with nose or nose 194 pointing at object and within 0.5 cm of object). Habituation to the objects across the 195 familiarization trials (decreased contacts) is an initial measure of learning and then 196 renewed interest (increased contacts) in the new object indicated successful object 197 memory. Recognition indexes were calculated using the following formula: # contacts 198 during test/(# contacts in last familiarization trial + # contacts during test). Values greater 199 than 0.5 indicate increased interest, whereas values less than 0.5 indicate decreased 200 interest in the object during the test relative to the final familiarization trial.

201 Immunofluorescence

202 Mice were intracardially perfused with 4% paraformaldehyde (PFA) in PBS and the full 203 brain was post-fixed in the same 4% PFA for 2 hours and transferred to 30% sucrose in 204 PBS for at least 2 days. Brain was embedded in HistoPrep (Fisher Chemical) and snap 205 frozen in isopentane (2-methylbutane) cooled at - 40°C on dry ice. 35 µm brain 206 cryosections were cut using a Leica 2800E Frigocut cryostat at -20°C and stored as free-207 floating sections in 1X PBS + 0.02% Sodium Azide at 4°C. The free-floating brain sections 208 were washed 3 times, 10 min in 1X PBS and then incubated in blocking solution (0.5% 209 Tween-20, 1.5% BSA in 1X PBS) for 1 hour at room temperature (RT) followed by

210 overnight incubation at RT in antibody diluent (0.3% Triton X-100 in 1X PBS) containing 211 the primary antibodies. The next day, sections were washed again 3 times, 10 min in 1X 212 PBS and incubated with secondary antibody (Jackson Immunoresearch, diluted in 0.3% 213 Triton X-100 in 1X PBS), washed again 3 times with 1X PBS and then incubated 10 min 214 with DAPI diluted in 1X PBS (Thermo Fisher Scientific, 100 ng/ml). Sections were mounted 215 on Fisherbrand Superfrost Plus Microscope Slides (Thermo Fisher Scientific) with Prolong 216 Gold antifade reagent (Thermo Fisher Scientific). Full brain images were acquired with the 217 Nanozoomer Slide Scanner (Hamamatsu©) and visualized in NDP.view2 software. Close-218 up images of brain sections displaying individual neurons were acquired with the FV1000 219 Spectral Confocal (Olympus) at 60X magnification or the spinning disk confocal Yokogawa 220 X1 confocal scanhead mounted to a Nikon Ti2 microscope with a Plan apo lamda 100x oil 221 NA 1.45 objective and Plan apo lamda 60x oil na 1.4 objective.

To quantify of FUS aggregates, brain coronal sections were carefully matched to compare similar anatomical regions, keeping track of the injected and non-injected side and immunostained with FUS, A11, OC and LOC antibodies as well DAPI. The percentage of DAPI positive cells with mislocalized aggregated FUS from similar area sizes within the cortex and hippocampus was counted.

To quantify the levels of nuclear and cytoplasmic FUS in neurons, brain coronal sections were matched to compare similar anatomical regions and immunostained with FUS, NeuN and DAPI. Images from the cortex were segmented using NeuN to identify neurons, as well as the outline of the Neuron itself. DAPI was used to segment the nucleus and record nuclear FUS intensity in neurons. Substracting the DAPI mask to the NeuN mask was used to define the cytoplasm of neurons and record FUS cytoplasmic intensity.

To quantify the number of neurons in the mouse brains, coronal brain OCT sections were immunostained with NeuN and nuclei were stained with DAPI. The hippocampal dentate gyrus region contained mostly NeuN-positive cells. For its quantitation, DAPI-positive cells were counted manually in 3–5 consecutive sections per animal using Fiji software. For the

237 motor cortex region, NeuN-positive cells were counted to exclude glia cell nuclei. Careful

- 238 matching of the sections to compare similar anatomical regions was performed for
- each set of mice.
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244 Antibody list

Antibody	Supplier	Catalog #	Dilution
Anti-FUS	Bethyl	A303-839A	IF 1:500
Anti-NeuN	Genetex	GTX133127	IF 1:500
Anti-p62	Progen	GP62-C	IF 1:500
Anti-TDP-43	Proteintech	10782-2-AP	IF 1:500 WB 1:1000
Oligomer A11	Invitrogen	AHB0052	IF 1:500
Anti-P-Ubiquitin (Pser65)	Millipore	MAB1510	IF 1:500
Anti-amyloid fibrils LOC	Millipore	AB2287	IF 1:500
Anti-Amyloid Fibrils OC	Millipore	AB2286	IF 1:500
Anti-Glial Fibrillary Acidic Protein (GFAP)	Millipore	MAB360	IF 1:1000
Anti-Hsp90 (C45G5)	Cell Signaling Technology	4877S	WB 1:5000
Anti-Iba1	Wako	019-19741	IF 1:500
Anti-FUS	Bethyl	A300-294A	WB 1:1000
Anti-TAF15	Bethyl	A300-309A	WB 1:1000
Anti-GAPDH	Millipore	CB1001	WB 1:5000

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247 Serial fractionation and Western Blot

248 249 Mouse brains were homogenized in high-salt (HS) buffer (4 ml/g; 50 mM Tris pH 7.5, 750 250 mM NaCl, 5 mM EDTA and protease and phosphatase inhibitor mix). Then the sample 251 was diluted 1:10 with Pierce™ IP Lysis Buffer [25 mM HEPES (pH7.4), 150 mM NaCl, 1 252 mM EDTA, 1% NP40, 5% V/V glycerol, protease and phosphatase inhibitor, and 1/100 253 V/V benzonase (endonuclease)]. The sample was incubated on ice for 30 min, sonicated 254 and centrifugated for 1hour at 10 000 x g at 4°C. The supernatant was used as the soluble 255 fraction and the pellet was resuspended in Laemmli SDS-loading buffer and used as the 256 insoluble fraction. 10% Bis-Tris gels were used for immunoblotting and equal volumes of 257 samples were loaded. For antibodies, see antibody list.

258 Serial fractionation and dot blot

259 Serial fractionation was performed as in (41). Mouse cortices were homogenized in high-260 salt (HS) buffer (4 ml/g; 50 mM Tris pH 7.5, 750 mM NaCl, 5 mM EDTA and protease 261 inhibitor mix), then centrifuged for 30min at 45 000 x g at 4°C resulting in the HS fraction. 262 Next, the pellet was homogenized in 500 ml of HS buffer + 1% Triton X-100 and 1M 263 sucrose and centrifuged 30min, 4°C at 45 000 x g (HS + Tx fraction). Then the remaining 264 pellet is suspended in urea buffer (2 ml/g; 7M urea, 2M thiourea, 4% CHAPS, 30 mM Tris 265 pH 8.5), centrifuged at 45 000 x g and for the remaining pellet 2 ml/g of SDS loading buffer 266 was added. Equal volumes were spotted onto a nitrocellulose membrane. For antibodies, 267 see antibody list.

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269270 Statistical analysis

Statistical analysis was performed using GraphPad Prism. All data is shown as mean ±
standard error of the mean (SEM). The Kolmogorov-Smirnov normality test was used to

evaluate the distribution of the data. If comparing two normal distributed groups, t-test was used. In case of comparing more than two normally distributed groups, data were compared by one-way analysis of variance (ANOVA) with Dunnets post-hoc tests. When data were not normality distributed and homoscedastic, the Kruskal-Wallis test was used with Dunn's multiple test as post-hoc. When P-values were lower than 0.05, significance was noted in the figure as: *P<0.05, **P<0.01, ***P<0.001, ****P<0.0001. Detailed information is shown in each figure legend.

283 Results

Amyloid-like fibrils of FUS induce aggregation and time-dependent spread of human mutant FUS^{R521H}

286 FUS pathology is present in rare sporadic ALS and familial ALS (46), but is a 287 hallmark of nearly 10% of the sporadic FTLD patients, known as FTLD-FUS (37). FUS 288 aggregation is almost universally found in sporadic FTLD-FUS patients with inclusions that 289 are tau- and TDP-43-negative (38, 46, 47). While we (41) and others (48-51) 290 demonstrated that FUS aggregation is not required for disease initiation in mice 291 expressing ALS-linked FUS mutations, but rather for its misaccumulation in axons and 292 cytoplasm, respectively, here we devised to test whether FUS aggregation contributes to 293 disease progression. To do this, we exploited our humanized FUS mice in which mouse 294 FUS is replaced by the human full-length FUS gene encoding either wild-type FUS 295 (mFUS^{KO}/hFUS^{WT}) or ALS-linked FUS^{R521H} (mFUS^{KO}/hFUS^{R521H}), the latter of which 296 develops late onset progressive motor and cognitive deficits without detectable 297 cytoplasmic FUS aggregation (41). We expressed and purified full-length recombinant 298 human FUSR495X protein HA-tagged on its amino terminus (Fig.1A), incubated with FUSR495X seeds at 22°C for 24 hours to generate spontaneously assembled, amyloid-like 299 300 fibrils *in vitro* (Fig. 1B). We selected FUS^{R495X} fibrils as the initial seeds as they would be 301 predicted to evade rapid disaggregation by endogenous Karyopherin- β 2 since FUS^{R495X} 302 lacks the PY-NLS region recognized by Karyopherin- β 2 (52) and allow to distinguish 303 between the endogenous FUS and the exogenous fibrils by immunostaining using an 304 antibody against the 500-526 amino acid peptide sequence of FUS protein that is missing 305 in the FUS^{R495X} fibrils. Those fibrils were then sonicated (Fig. 1B) and injected unilaterally 306 after disease initiation into the cortex and hippocampus of 16-month-old humanized FUS 307 mice (mFUS^{KO}/hFUS^{R521H}, Fig. 1C).

308 The fate of the sonicated fibrils was followed over time using immunodetection of 309 the HA-epitope tag to mark the pre-formed FUS fibrils. Three hour-post-injection 310 exogenously produced HA-tagged FUS fibrils were immunodetected using the HA-epitope 311 tag against the pre-formed FUS fibrils and were found to focally distribute into the cortex 312 and hippocampus within a 150 µm-area anterior-posterior from the injected coordinates 313 (Fig. S1A, left panel and Fig. S1B). Fibrils persisted for the following 3 days and were 314 predominantly immunodetected in the cytoplasm, suggesting their uptake from the cells 315 (Fig. S1A, middle panel). However, one week after injection no pre-formed FUS fibrils 316 were detected, consistent with clearance of the sonicated FUS fibrils (Fig. S1A, right 317 panel). Focal injection provoked activation of microglia and astrocytes in hippocampus 318 and cortex (Fig. S2) at 3 days post-injection on the site of injection, which was absent in 319 the contralateral side. This astrocytic/microglial activation was only transient as it was not 320 detected at 3 hours and was mitigated by 1-week post-injection (Fig. S2). Since astrocytes 321 and microglia can internalize and degrade added external aggregates in vitro (53, 54), glia 322 cells may contribute to the clearance of the injected fibril material.

323 To test whether focal injection of sonicated FUS fibrils into cortex and 324 hippocampus of humanized mutant FUS^{R521H} mice recapitulates FUS pathology and if so 325 whether it propagates with time beyond the injection site, we further analyzed brain 326 sections one, two, and six months post-injection (Fig. 1C). FUS protein partially 327 redistributed to the cytoplasm and was recruited into ~1-5 FUS immunopositive inclusions, 328 while FUS remained almost entirely in the nucleus in PBS-injected mice (Fig. 1C-E). FUS 329 cytoplasmic inclusions were observed in brain regions that were in contact with exogenous 330 FUS seeds, but also in adjacent regions without any apparent contact with the injected 331 amyloid-like fibrils, including the contralateral side of the cortex and hippocampus which 332 also exhibited cytoplasmic inclusions of FUS (Fig. 1D-I). FUS aggregates progressively 333 spread into superficial layers found beyond the brain areas that were directly connected to the cortex and hippocampus regions of the injection site (Fig. 1E,H).

335 Over time, FUS aggregation was immunodetected throughout the whole 336 hemisphere at the level of injection and in wider areas of the opposite hemisphere (Fig. 337 S3), indicating a time-dependent spread of FUS aggregates to distal regions rostrally and 338 caudally from the focal injection of FUS fibrils. At the site of injection (ipsilateral side), 19, 339 31, and 39% of the cortical and 16, 22, and 49% of hippocampal cells harbored FUS 340 inclusions at 1-, 2-, and 6-months post-injection, respectively, versus 3, 7, and >30% on 341 the contralateral side at both brain regions (Fig. 1F,I) while none were observed in PBS 342 injected mice (Fig. 1D,G). Overall, these data demonstrate that 1) exogenous FUS fibrils 343 seed *de novo* aggregation of endogenous human FUSR521H in a spatial-, temporal-344 dependent manner and 2) FUS pathology spreads to distal sites, including within the non-345 injected hemisphere (albeit cells within the contralateral side of the injected hemisphere 346 exhibited a reduced number of FUS inclusions relative to the site of injection).

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348 Neither monomers of FUS nor sonicated fibrils of SOD1 produce cytoplasmic 349 aggregation of human mutant FUS^{R521H}

350 In contrast to cytoplasmic aggregate induction and spreading of endogenously 351 expressed FUS when mice were unilaterally injected with sonicated FUS fibrils in the 352 cortex and hippocampus, FUS remained almost exclusively nuclear without detectable 353 cytoplasmic aggregates in animals injected with FUS monomers (Fig. 2A,B). Additionally, 354 we generated fibrils (Fig. 2C-E) of recombinant wild-type superoxide dismutase (SOD1) 355 (43) and focal injection of the sonicated SOD1 fibrils into mFUSKO/FUSR521H brains did not 356 provoke aggregation or mislocalization of FUS locally or distally to the injection sites (Fig. 2E). Therefore, the recruitment of endogenous mutant FUS to sonicated fibril-induced 357 358 FUS mislocalization and aggregation was unique to the injection of sonicated FUS fibrils.

359

360 Mutant FUS accelerates FUS aggregation induced by injected FUS fibrils

361 To test if human wild-type FUS can be seeded to aggregate (as is seen in 362 examples of sporadic ALS and FTLD (46)), FUSR495X fibrils were focally injected at single 363 sites within the cortex or hippocampus of 16-month-old humanized mFUS^{KO}/FUS^{WT} mice 364 in which both endogenous mouse FUS alleles had been inactivated (Fig. 2F). While de 365 novo aggregation of endogenous human wild-type FUS was induced to a level comparable 366 to that generated in humanized mutant FUS^{R521H} mice similarly injected, aggregation was 367 accelerated by two months in the mutant FUS animals (Fig. 1 and 2F-I). Specifically, after 368 injection of FUS^{R495X} fibrils, aggregation of endogenous human wild-type FUS was not 369 observed until 3 months, while aggregation of endogenous mutant FUS was observed the 370 first month post-injection. By 3 months post-injection, cytoplasmic wild-type FUS 371 aggregates were found in 25% and 32%, respectively, of cells in the ipsilateral cortex and 372 hippocampus, with spreading producing aggregates in 12% and 7%, respectively, of cells 373 in the contralateral hemisphere (Fig. 2I). By eight months post-injection, wild-type FUS-374 containing aggregates were immunodetected throughout the brain in areas outside the 375 injection site and the percentage of cells with cytoplasmic FUS aggregates rose to 46% in 376 the ipsilateral side (in cortex and hippocampus), and 20% in cortex and 32% in 377 hippocampus of the contralateral side (Fig. 21). Overall, these findings support that 1) 378 focally injected FUS^{R495X} fibrils seed aggregation of wild-type endogenous human FUS 379 and 2) the induced wild-type FUS-containing inclusions propagate beyond the injection 380 site to the opposite hemisphere, with the kinetics of spreading slower than for mutant FUS 381 (Fig. 1 and 2F-I).

382 A species barrier to FUS aggregate seeding

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Sequence variations between species have been well established to create a

384 species barrier for prion seeding and spread (55). To test for the presence of a similar 385 species barrier for FUS seeding, human FUS^{R495X} fibrils were assembled, sonicated, and 386 injected unilaterally into cortex and hippocampus of C57BL/6J mice exclusively expressing 387 mouse FUS (Fig. 2J). Examinations at timepoints up to 9 months post-injection revealed 388 that mouse FUS continued to be almost exclusively nuclear (Fig. 2J,K), with no aggregates 389 detectable at any time point, consistent with an interspecies transmission barrier that limits 390 the capability of sonicated human FUS fibrils to seed aggregation of mouse FUS.

391

392 Injected FUS fibrils increase insolubility of endogenous FUS

393 To determine whether cytoplasmic FUS inclusions revealed by immunostaining 394 acquire the characteristics of FUS inclusions found in postmortem patient material, we 395 used a combination of immunocytochemistry and biochemistry at multiple time points post-396 fibril injection (Fig. 3A). Within 1 month post-fibril injection aggregated endogenous FUS 397 (Fig. 3B) acquired pre-amyloid properties as determined by immunodetection with the A11 398 antibody that has been established to recognize a peptide backbone epitope common to 399 pre-amyloid oligomers (56). By 6 months post-injection, an overwhelming majority of FUS 400 aggregates (79.7%± 5.4) were A11-positive (Fig. S5), while as expected no such signals 401 were present either in age-matched PBS control injected mice or within 3 hours after FUS 402 fibril injection (Fig. 3B,C). Injection-induced human FUS inclusions in brains of FUS 403 humanized mice were also immunopositive (Fig. S5) using antibodies previously reported 404 to recognize mature, in vivo β -amyloid structures (51). Similarly, fibril-induced FUS 405 aggregates co-localized with p62 and ubiquitin (as described in human FUS 406 proteinopathies (2, 35, 57, 58)), but did not contain detectable levels of TDP-43 (Fig. 407 3D,E).

408 Analysis of brain homogenates from FUS-injected mice showed a marked increase 409 in detergent-insoluble FUS compared with PBS-injected mice (Fig. 3F,G and Fig. S5E,F).

While in humanized FUS mutant mice (mFUS^{KO}/hFUS^{R521H}) most FUS remained soluble 410 411 as we previously reported (41), an increase (compared to PBS injected brains) in insoluble 412 FUS was detected in extracts from brains that were FUS fibril-injected (Fig. 3F,G). The 413 FUS homologue TATA-binding protein-associated factor 15 (TAF15) (also known as 414 TATA-binding protein-associated factor 2N), but not the RNA binding protein TDP-43, was 415 also present in a detergent insoluble fraction, consistent with increased FUS and TAF15 416 insolubility reported in ALS/FTLD-FUS patients (57, 59) and extraction and imaging of 417 filaments of TAF15 from such patient samples (59).

418 After 6 months of sonicated FUS fibril injection, the vast majority (90.9%±4.2) of 419 cytoplasmic human endogenous FUS inclusions was present within neurons, with the 420 remaining 10% in glia (Fig. S6A,B). Although the overall levels of nuclear and cytoplasmic 421 FUS did not change 6 months post-injection of HA-FUS^{R495X} fibrils (Fig. S6C-E), the 422 neurons bearing FUS cytoplasmic inclusions displayed a trend towards a decrease in the 423 FUS nuclear/cytoplasmic ratio (Fig. S6F-H). Furthermore, formation of cytoplasmic FUS 424 inclusions was accompanied by increased astrocytosis and microgliosis in fibril-injected 425 mice (as revealed by increased immunoreactivity with GFAP and IBA1 antibodies, 426 respectively) at 6 months, but not at 2 months post-injection (Fig. S7).

427 Seeded aggregation of FUS provokes neurodegeneration

428 Single-dose injections of sonicated FUS fibrils (HA-FUS^{R495X}) or PBS in the cortex 429 and hippocampus were administered to cohorts of either non-transgenic mice or humanized FUS mutant mice (mFUS^{KO}/hFUS^{R521H}) and their behaviors were monitored 430 431 using novel object recognition, rotarod and open field assays at timepoints prior to 432 injection, and at 2 months and 6 months post-injection (Fig. 4A-B, Fig. S7). Cognitive 433 impairments associated with mutant FUS expression (as we previously reported (41)) 434 were significantly aggravated 6 months post-injection (Fig. 4A). While no exacerbation of 435 disease was observed in humanized mutant FUS mice within the first two months after

fibril-injection, rotarod performance was modestly decreased in fibril-injected humanized mutant mice 6 months post-injection (Fig. S8). In an open field assay, focal injection of mutant FUS fibrils also induced age-dependent deficits in the humanized FUS mice (Fig. 439 4B). Moreover, analysis of cortical and hippocampal sections revealed a significant neuronal loss in both hippocampus and cortex after FUS fibril injection compared to their PBS and non-injected controls (Fig. 4C-E), indicating exacerbation of behavioral deficits and neurodegeneration that correlate with seeded, prion-like spread of aggregated FUS.

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445 Discussion446

447 We have developed a model of FTLD disease in mice through the dissemination 448 of FUS pathology within the brain, affecting cognitive and motor functions. Focal injections 449 of human FUS aggregates in the brain of humanized FUS mice induce *de novo* pathology 450 of endogenous mutant or wild-type human FUS spreading within the brain in a spatio-451 temporal manner consistent with a model of transmission of pathology (in a prion-like 452 fashion) throughout the brain. Endogenous FUS aggregation was observed at 1 month 453 post-injection around the site of injection in the hippocampus region, a region associated 454 with pathology in both ALS and FTLD patients (2, 60) and in the cortical region, where 455 basophilic and FUS positive inclusions are found in neurons and glia cells of ALS cases, 456 and are numerous in the middle and deep layers of the neocortex in FTLD (46, 61). 457 Pathology after injection was found as well in brain areas distant from the injection sites, 458 including in the contralateral hemisphere where FUS cytoplasmic aggregates were 459 observed in a pattern mirroring the injected hemisphere similar as α -synuclein, tau and 460 TDP-43 spreading in mice (9, 29, 62, 63). Our data contribute to the mounting evidence 461 that prion-like transmission of misfolded proteins represents a common process in the 462 pathogenesis of several neurodegenerative diseases, including α-synuclein in Parkinson's 463 disease (9, 17, 64), Aβ and Tau in AD (18, 65, 66), and SOD1 or TDP-43 in ALS (21, 25,
464 26, 28).

Injection of sonicated fibrils of hFUSR495X induced aggregation and time-dependent 465 466 spread of endogenous human mutant and wild-type FUS albeit the spreading mechanism 467 remains unknown. FUS pathology may spread through adjacent cell-to-cell seed transfer, 468 through anatomical neuronal connections, possibly in a diffusion-like manner, or (most 469 likely) a combination of several mechanisms. The fact that FUS aggregates are found in 470 the contralateral hemisphere suggests spread between hemispheres through brain 471 commissures possibly the corpus callosum, but also through smaller anterior, posterior 472 and hippocampal commissures (67). Injecting sonicated FUS fibrils in an area with known 473 distal projections, such as the lateral geniculate nucleus, and evaluating the presence of 474 FUS cytoplasmic aggregation in the synaptically connected visual cortex (68), would be 475 valuable to determine if neuronal connectivity facilitates the spreading of FUS cytoplasmic 476 aggregates. The time-dependent increasing accumulation of FUS cytoplasmic aggregates 477 in the more distant brain areas after FUS-fibril injection further points to prion-like 478 spreading mechanisms in the formation of FUS pathology. One cannot completely exclude 479 that the injected sonicated FUS fibrils spread in a diffusion-like manner and seeded 480 neurons in distal regions from the injection site, where they were undetectable right after 481 injection. However, after the initial seeding event, a plausible route for FUS aggregates 482 to appear in distal regions with time is spreading of human endogenous FUS seeds 483 through the extracellular space via its release from dying cells, and/or through secretion 484 (freely or through extracellular vesicles) and uptake into recipient cells, again via 485 endocytosis and endosomal membrane rupture as it has been proposed for spreading of 486 other prion-like proteins such as tau (69-71).

487 Great heterogeneity in the morphology of FUS cytoplasmic inclusions has been 488 reported in human disease, at least some of which has been correlated with disease

489 severity and FUS mutation in ALS cases (36). Moreover, FTLD-FUS pathology is divided 490 into 3 different groups based on the morphology of the cytoplasmic inclusions and their 491 deposition pattern (37). We observed round shaped cytoplasmic inclusions of FUS mostly 492 in neurons that were ubiquitinated, p62 positive and TDP-43 negative. Moreover, 493 cytoplasmic FUS aggregates and non-pathogenic nuclear FUS are detected in the same 494 cell as reported before (61, 72). After 6 months of fibril injection, human mutant FUS further 495 display enhanced insolubility together with enhanced TAF15 insolubility but not TDP-43. 496 Both FUS and TAF15 were also detected in the detergent-insoluble fraction of the 497 Huntington's disease mice R6/2, indicating that TAF15 insolubility seems a secondary 498 effect of FUS aggregation and is not due to exposure to injected FUS fibrils. However, it 499 is possible that focal injection of amyloid-like FUS fibrils caused endogenous mouse 500 TAF15 to form fibrils which also spread throughout the brain. It would thus be of interest 501 to test if TAF15 depletion can prevent the spreading of cytoplasmic FUS aggregation in 502 mice and whether injection of recombinant TAF15 fibrils can induce endogenous human 503 FUS cytoplasmic aggregation Altogether, our model recapitulates the FUS and TAF15 504 shift in solubility and immunoreactivity for ubiquitin and p62 positive (but TDP-43 negative) 505 that has been reported in human FTLD-FUS (3, 35-39, 59, 73).

506 Proteins with prion-like domains form pathological inclusions in many 507 neurodegenerative diseases. The core region of the low complexity domain (LCD) of FUS 508 is essential to form parallel β -sheet structures reminiscent of the amyloid-like proteins (74). 509 Seeding is an important feature of amyloid-like aggregates, in which a piece of protein 510 fibril can function as a structural template for facilitating the fibrillation of soluble protein molecules (75). Fibril-induced FUS cytoplasmic inclusions exhibit enhanced insolubility, 511 512 supporting the idea that FUS inclusions could effectively transform soluble FUS into 513 insoluble aggregates, resulting in the progressive dysfunction of FUS and cytotoxicity. 514 Indeed, a seeded fibrillation of proteins and their intercellular transmission have been

515 increasingly noticed as a molecular pathomechanism that describes the progression of 516 several neurodegenerative diseases (76, 77).

517 Permissive prion transmission frequently depends on overcoming a species 518 barrier, which is determined by a range of possible conformers of a particular prion, its 519 sequence, as well as its interaction with cellular co-factors (78, 79). Here, we show the 520 existence of a seeding barrier between human and mouse FUS. One such endogenous 521 'barrier' relevant to FUS proteinopathy may be the sequence differences between mouse 522 and human FUS (which differ in 26 out of 526 amino acids), fifteen of which are located in 523 the G-rich, prion-like domain believed to be a major factor in driving aggregation (Fig. S8) 524 (80). Another plausible explanation is that mouse FUS is intrinsically less aggregation 525 prone and cannot be seeded and/or spread. A future experiment that would decipher 526 between these possibilities would be the injection of recombinant mouse FUS fibrils in 527 non-transgenic wild-type mice to test if this will induce endogenous murine FUS 528 aggregation and spreading, further supporting the idea of a species barrier.

529 FTLD patients with FUS inclusions only rarely harbour genetic alterations in FUS 530 (81) and the majority of cases are sporadic (14). Most of the ALS-linked FUS mutations 531 reported to date are localized in the NLS domain resulting in impaired nuclear transport of 532 FUS and chaperoning by Karyopherin- β 2. This is consistent with the finding that mutant 533 FUS^{R521H} exhibit accelerated initial seeding and aggregation capacity compared to wild-534 type FUS, due to a reduced transport efficiency to the nucleus and increased retention in 535 the cytoplasm.

536 Seeded aggregation of FUS provoked neurodegeneration and impaired mouse behaviour 537 but the underlying molecular mechanisms mediating cell toxicity remain to be elucidated. 538 ALS-linked mutations in FUS induce a gain of toxicity that includes stress-mediated 539 suppression in intra-axonal translation, and synaptic dysfunction (41). With FUS fibril-540 injection we observed a portion of FUS mislocalized to the cytoplasm, clustering in visible

541 inclusions that are widespread within the brain. Deletion of the NES in FUS strongly 542 suppressed toxicity of mutant FUS in Drosophila (82), suggesting that the cytoplasmic 543 localization of mutant FUS confers toxicity which is supported by the neurodegeneration 544 we observed in both the hippocampus and cortex of fibril injected mice. In parallel, we 545 observed gliosis at late time points of FUS pathology that might contribute to the damage 546 of the tissue and translated in behaviour deficits since inflammation and astrocyte-547 mediated toxicity have been identified as part of the pathogenic process of ALS/FTLD 548 (83). A natural follow up of this work is to characterize the composition of the cytoplasmic 549 FUS inclusions and define the spatial transcriptomic changes provoked by FUS 550 aggregation at different time points and brain regions as this may provide insights into the 551 pathways of seeding, spreading and vulnerability or resistance. Deciphering such 552 molecular mechanisms that underlie the spreading of FUS proteinopathy may offer 553 avenues for therapeutic interventions by blocking spreading and thereby disease 554 progression.

555 **Conclusion**

Here we show that single focal injection of sonicated human FUS fibrils into aged brains of humanized FUS mice (in which ALS-linked mutant or wild-type human FUS replaces endogenous mouse FUS) induces FUS cytoplasmic aggregation, which recapitulates features of human FUS inclusions found in ALS/FTLD patients. Importantly, spread of FUS aggregates is shown to exacerbate FTLD-like disease induced by a disease-causing mutation and ultimately initiates neurodegeneration, thus providing the first *in vivo* evidence of spreading of templated FUS aggregation in an adult central nervous system.

563

564 **Abbreviations**

565 A β Amyloid β

- 566 ALS Amyotrophic lateral sclerosis
- 567 DPR dipeptide repeat
- 568 FTLD Frontotemporal Lobar Degeneration
- 569 FUS Fused in sarcoma
- 570 LCD low complexity domain
- 571 NLS Nuclear Localization Signal
- 572 PBS Phosphate-Buffered Saline
- 573 SOD1 superoxide dismutase
- 574 TAF15 FUS homologue TATA-binding protein-associated factor 15
- 575 TSEs transmissible spongiform encephalopathies
- 576

577 **Declarations**

- 578 *Ethics approval and consent to participate*
- 579 All animal experimental procedures were approved by the Institutional Animal Care and
- 580 Use Committee of the University of California, San Diego, USA.
- 581 **Consent for publication**
- 582 Not applicable for this study.
- 583 Data availability
- 584 All data generated or analyzed during this study are included in this published article and
- available from the corresponding author on reasonable request.
- 586 Competing interests
- 587 The authors declare that they have no competing interests, except for JS. JS is a
- 588 consultant for Dewpoint Therapeutics, ADRx, and Neumora. J.S. a shareholder and
- 589 advisor at Confluence Therapeutics.
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603 Authors' contributions

FGR and SDC conceptualized and designed the study. SVS, BT, FGR, SZ, DP, MMD, JA,
YV and NGP performed experiments and analyzed the data. LG and JS provided key
reagents. SVS, BT, FGR, DWC and SDC wrote the manuscript, which was reviewed by
all authors.

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616 Figure legends

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620 Figure 1: HA-FUS^{R495X} fibrils induce human FUS mislocalization and aggregation in

621 aged humanized mutantFUS (mFUS^{KO}/hFUS^{R521H}) mice

622 A. Coomassie blue staining of recombinant HA-FUS protein. B. Electron micrograph of 623 fibrils of HA-FUS^{R495X} recombinant protein purified from bacteria (Left panel). HA-FUS^{R495X} 624 fibrils after sonication before inoculating them into mice (Right panel). Scale bars: 1 µm 625 (before sonication), 0.2 µm (after sonication). C. Sonicated HA-tagged FUSR495X fibrils 626 were injected unilaterally into the cortex and hippocampus of 16 months old humanized, 627 mutant FUS mice (mFUS^{KO}/hFUS^{R521H}). **D,E.** Immunostaining of FUS (green) and DAPI 628 (blue) of the side of the mouse brain hemisphere (ipsilateral side) injected either with PBS 629 (D) or with HA-FUS^{R495X} fibrils (E) after 1 month and 6 months post-injection. Scale bars: 630 10 µm, inset: 5 µm. The top panel illustrates the regions of the brain that were analyzed 631 and the site of injection (pink box). Yellow arrows indicate cytoplasmic FUS aggregates at 632 1- and 6-months post-injection (p.i.). F. Quantification of the percentage of cells containing 633 endogenous cytoplasmic FUS aggregates in the cortex and hippocampus at the injection 634 (ipsilateral) side 1-, 2- and 6-months post-injection. N=3 animals. Kruskal-Wallis test with 635 Dunn's multiple test post-hoc p-values: cortex p = 0.0429 and hippocampus p = 0.0219. 636 Data is presented as mean ± SEM. G,H. Immunostaining of FUS (green) and DAPI (blue) 637 of the opposite side of the mouse hemisphere (contralateral side) that was injected either 638 with PBS (G) or with HA-FUS^{R495X} fibrils (H) after 1 month and 6 months post-injection. 639 Yellow arrows indicate FUS cytoplasmic inclusions after 1- and 6-months post-injection. 640 Scale bars: 10 µm, inset: 5 µm. I. Quantification of the percentage of cells containing 641 endogenous FUS aggregates in the cortex and hippocampus at the contralateral side over 642 1-, 2- and 6-months post-fibril injection. N=3 animals. Kruskal-Wallis test with Dunn's 643 multiple test post-hoc p-values: p = 0.0225.

644 Figure 2: HA-FUS^{R495X} fibrils induce aggregation and spreading of human FUS WT

645 **but not of mouse FUS**

646 A. Electron micrograph of FUS monomeric protein (scale bar: 1 µm) which was injected 647 into 16-month old mFUS^{KO}/hFUS^{R521H} mice. **B.** Immunostaining of FUS (green) and DAPI 648 (blue) of the side of the mouse brain in which FUS monomers were injected after 2 months 649 post-injection. Scale bars: 10 µm. C. Coomassie blue staining of recombinant His-SOD1 650 protein. D. Electron micrograph of His-SOD1 fibrils obtained from recombinant protein 651 purified from bacteria (left panel) and sonicated His-SOD1 fibrils before inoculating them 652 into 16 months old humanized, mutant FUS mice (mFUS^{KO}/hFUS^{R521H}). Scale bar: 200 653 nm. E. Immunostaining of FUS (green) and DAPI (blue) of the side of the mouse brain in 654 which FUS monomers were injected after 2 months post-injection. Scale bars: 10 µm. F. 655 Sonicated HA-tagged FUSR495X fibrils were injected unilaterally into the cortex and 656 hippocampus of 16 months old humanized, FUS wild-type mice (mFUS^{KO}/hFUS^{WT}). G. 657 Immunostaining of a PBS-injected mFUS^{KO}/hFUS^{WT} mouse brain, 8 months post-injection 658 using a FUS (green) antibody. H. Immunostaining of FUS (green) and DAPI (blue) of the 659 side of the mouse brain hemisphere (ipsilateral side) injected with HA-FUS^{R495X} fibrils. 660 Yellow arrows indicate FUS cytoplasmic aggregates after 1-, 3- and 8-months post-661 injection. Scale bars: 10 µm, inset: 5 µm. I. Quantification of the percentage of cells with 662 endogenous human FUS aggregates in the cortex and hippocampus at the ipsilateral and 663 contralateral side, 1-, 3- and 8-months post-injection. N=3 animals. Kruskal-Wallis test 664 with Dunn's multiple test post-hoc p-values: cortex ipsilateral p = 0.0190, cortex 665 contralateral p = 0.0312, hippocampus ipsilateral p = 0.0299 and hippocampus 666 contralateral p = 0.0190. Data is presented as mean ± SEM. J.K. Immunostaining of FUS 667 (green) and DAPI (blue) of the side of injection (ipsilateral side) in non-transgenic 668 C57BL/6J mice (mouse FUS) brains injected with HA-FUSR495X after 6- and 9-months post-669 injection. Scale bars: 10 µm, inset: 5 µm.

670 Figure 3: Human FUS aggregates are insoluble, display pre-amyloid properties and

671 recapitulate features of human FUS pathology

672 **A.** Schematic overview of the timepoints at which FUS aggregation was analyzed using 673 immunofluorescence-based assays and biochemical insolubility assays at 3 hours, 1 674 months and 6 months post-injection. B,C. Representative confocal images of 675 mFUS^{KO}/hFUS^{R521H} mouse brains injected either with HA-FUS^{R495X} fibrils at 3 hours, 1 676 months and 6 months post-injection (B) or with PBS at 6 months post-injection (C) 677 immunolabelled using antibodies against the pre-amyloid oligomer marker A11 (red), HA 678 after 3 hours post-injection (green) and FUS after 1 month and 6 months post-injection 679 (green). Yellow arrows indicate co-localization between A11 and FUS cytoplasmic 680 inclusions detected in fibril-injected mice. DAPI (blue) as nuclear counterstaining. Scale 681 bars: 10 µm, inset: 5 µm. **D,E.** Representative confocal micrographs of mFUS^{KO}/hFUS^{R521H} 682 mouse brains injected with HA-FUSR495X fibrils using ubiquitin/p62/TDP-43 (red) and FUS 683 (green) antibodies after 1 month (D) and 6 months (E) post-injection. Yellow arrows 684 indicate co-localization between either ubiquitin/p62/TDP-43 and FUS cytoplasmic 685 aggregates. Scale bar: 10 µm, inset: 5 µm. F. Experimental outline of the serial fractionation of brain homogenates derived from mFUS^{KO}/hFUS^{R521H} mice either PBS- or 686 687 HA-FUS^{R495X} fibril-injected and R6/2 Huntington's model mice as a positive control for FUS 688 insolubility (59). G. Immunoblotting of the sequential biochemical fractions from mouse 689 brains using anti-FUS, anti-TAF15 and anti-TDP-43 antibodies. Anti-GAPDH was used as 690 loading control.

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Figure 4: Human FUS aggregates exacerbate cognitive impairments and provoke behavioral deficits and neurodegeneration in ALS-FUS mice

A. Novel object recognition test was performed in 16 months (before injection) and 22
 months old HA-FUS^{R495X} fibril-injected mFUS^{KO}/hFUS^{R521H} animals (6 months post-

696 injection) compared to PBS-injected controls and non-transgenic HA-FUSR495X fibrils or 697 PBS injected controls. N=5–12 animals per group. Unpaired t-test p-value = 0.0293. Data 698 is presented as mean ± SEM. B. Open field test was performed in 22 months old HA-699 FUS^{R495X} fibril injected mFUS^{KO}/hFUS^{R521H} animals (6 months post-injection) compared to 700 PBS-injected controls and non-transgenic HA-FUS^{R495X} fibrils or PBS injected controls. 701 N=5–12 animals per group. Unpaired t-test p-value = 0.0498. Data is presented as mean 702 ± SEM. C. Representative immunofluorescence labelling for the neuronal marker NeuN 703 (green) and DAPI in the hippocampus (upper panel) and cortex (lower panel) of 704 humanized mutant mice mFUS^{KO}/hFUS^{R521H} non-injected, and injected either with PBS or 705 HA-FUS^{R495X} fibrils. Scale bar: 25 µm. **D,E.** Quantification of neurons in hippocampus (D) 706 and cortex (E) in HA-FUSR495X fibril-injected mice compared to PBS and non-injected 707 controls. N=4 animals per condition. Data is presented as mean ± SEM. Kruskal-Wallis test with Dunn's multiple test post-hoc p-values: hippocampus (D) p* = 0.0112 and cortex 708 709 (E) $p^* = 0.0455$ and $p^{**} = 0.0053$.

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Figure 1



Figure 2



Figure 3

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Figure 4

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Figure S1: Distribution of focally-injected HA-tagged FUS^{R495X} fibrils in the mouse brain at 3 hours, 3 days and 1-week post-injection

A. Immunostaining of cortex and hippocampus of mFUS^{KO}/hFUS^{R521H} mouse brain sections 3 hours, 3 days and 1-week post-injection with HA-FUS^{R495X} fibrils using an anti-HA antibody to detect the HA-tagged FUS^{R495X} fibrils. Number 1-2 correspond to the side of injection, number 3 corresponds with the contralateral side. DAPI as nuclear counterstaining. Scale bar: 10 μm. **B.** Immunostaining of mFUS^{KO}/hFUS^{R521H} mouse brain sections 3 hours post-injection with PBS using an anti-HA antibody. **C.** Illustration summarizing the distribution of HA-FUS^{R495X} fibrils throughout the 3-day post-injection. Red dots indicate the sites where FUS aggregates are immunodetected.

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post-injection immunolabeled for GFAP (astrocytes) and Iba1 (microglia). DAPI as nuclear counterstaining. Representative confocal images of the site of injection in hippocampus (**C**) and cortex (**D**) of mFUS^{KO}/hFUS^{R521H} mice injected with PBS, 3 days post-injection immunolabeled for GFAP (astrocytes) and Iba1 (microglia). DAPI is used as nuclear counterstaining. Scale bar: 100 μm.



Figure S3: Distribution of FUS cytoplasmic aggregates in mFUS^{KO}/hFUS^{R521H} mice induced by HA-FUS^{R495X} fibrils

Illustration summarizing the distribution of FUS cytoplasmic aggregates throughout the brain, 1- and 6-months post-injection. Red dots indicate the sites where FUS aggregates are immunodetected.



Figure S4: Distribution of FUS cytoplasmic aggregates in mFUS^{KO}/hFUS^{WT} mice induced by HA-FUS^{R495X} fibrils

Illustration summarizing the distribution of FUS cytoplasmic aggregates throughout the brain, 3- and 8-months post-injection. Red dots indicate the sites where FUS aggregates are immunodetected.



Figure S5: FUS aggregates display amyloid properties

A,B. Representative confocal micrographs of mFUS^{KO}/hFUS^{R521H} mouse brains injected with HA-FUS^{R495X} fibrils, at 6 months post-injection (panel A) immunolabelled with amyloid fibril markers LOC and OC (red) and FUS (green). Yellow arrows indicate co-localization between LOC/OC and FUS cytoplasmic inclusions in fibril-injected mice but not in PBS-injected controls (panel B). **C**. Co-localization between LOC (red) and HA-FUS^{R495X} fibrils (green) 3 days post-injection. DAPI (blue) as nuclear counterstaining. Scale bars: 10 μm, inset: 2 μm. **D**. Quantification of the percentage of FUS aggregates that are A11-positive in HA-FUS^{R495X} fibril injected mFUS^{KO}/hFUS^{R521H} mice 6 months post-injection. N=3 animals. **E**. Dot-blot analysis of FUS protein levels in urea insoluble fractions of PBS and HA-FUS^{R495X} fibril injected mFUS^{KO}/hFUS^{R521H} mouse homogenates using FUS antibody. **F**. Quantification of FUS protein levels in urea insoluble fractions shown in E.

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Figure S6: FUS aggregation accumulates predominantly in neurons of fibril-injected mFUS^{KO}/hFUS^{R521H} mice

A. Immunostaining of mFUS^{KO}/hFUS^{R521H} mouse brains injected with HA-FUS^{R495X} fibrils for neuronal marker NeuN (red) and FUS (green) 6 months post-injection. Scale bars: 10 µm. B. Quantification of the percentage of NeuN-positive cells and NeuN-negative cells that contain FUS cytoplasmic aggregation. DAPI as nuclear counterstaining. N = 5. C. Quantification of the FUS nuclear intensity signal in neurons of both ipsi- and contra-lateral side mice injected either with PBS or with HA-FUS^{R495X} fibrils 6 months post-injection. N = 3 mice per group. D. Quantification of the FUS cytoplasmic intensity signal in neurons of both ipsi- and contra-lateral side mice injected either with PBS or with HA-FUS^{R495X} fibrils 6 months post-injection. N = 3 mice per group. E. Quantification of the FUS nuclear/cytoplasmic ratio in neurons of both ipsi- and contra-lateral side mice injected either with PBS or with HA-FUS^{R495X} fibrils 6 months post-injection. N = 3mice per group. F. Quantification of nuclear FUS, G. cytoplasmic FUS and H. FUS nuclear/cytoplasmic ratio in neurons with and without FUS cytoplasmic inclusions of mice injected with HA-FUS^{R495X} fibrils 6 months post-injection. N = 3 mice.

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Figure S7: FUS aggregation is accompanied by increased gliosis in fibril-injected mFUS^{KO}/hFUS^{R521H} mice

Immunostaining for astrocyte marker GFAP (green) and microglial marker Iba1 (red) of cortex of mFUS^{KO}/hFUS^{R521H} mice at 2 (**A**) and 6 months (**B**) post-injection either with PBS or with HA-FUS^{R495X} fibrils. Scale bars: 30 and 10 μ m.



Figure S8: Rotarod performance in non-transgenic and humanized mutant FUS mice injected either with PBS or sonicated FUS fibrils

Rotarod test was performed in 22 months old HA-FUS^{R495X} fibril injected mFUS^{KO}/hFUS^{R521H} animals (2 and 6 months post-injection) compared to PBS-injected controls and non-transgenic HA-FUS^{R495X} fibrils or PBS injected controls. N=5–12 animals per group. Data is presented as mean \pm SEM.

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Prion domain G-rich region

	-	
UserSeq1_H UserSeq2_m	1 1	MASNDYTQQATQSYGAYPTQPGQGYSQQSSQPYGQQSYSGYSQSTDTSGYGQSSY-SSYG MASNDYTQQATQSYGAYPTQPGQGYSQQSSQPYGQQSYSGYGQSADTSGYGQSSYGSSYG ***********
UserSeq1_H UserSeq2_m	60 61	QSQNTGYGTQSTPQGYGSTGGYGSSQSSQSSYGQQSSYPGYGQQPAPSSTSGSYGSSSQS QTQNTGYGTQSAPQGYGSTGGYGSSQSSQSSYGQQSSYPGYGQQPAPSSTSGSYGGSSQS * ******** ************************
UserSeq1_H UserSeq2_m	120 121	SSYGQPQSGSYSQQPSYGGQQQSYGQQQS-YNPPQGYGQQNQYNSSSGGGGGGGGGGGGGGAYG SSYGQPQSGGYGQQSGYGGQQQSYGQQQSSYNPPQGYGQQNQYNSSSGGGGGGGGGGG-NYG ******** * * * **********************
UserSeq1_H UserSeq2_m	179 180	QDQSSMSSGGGSGGGGGGGQQDQSGGGGGGGGGGGGGGGG
UserSeq1_H UserSeq2_m	238 230	GYEPRGRGGGRGGRGGMGGSDRGGFNKFGGPRDQGSRHDSEQDNSDNNTIFVQGLGENVT GYEPRGRGGGRGGRGGMGGSDRGGFNKFGGPRDQGSRHDSEQDNSDNNTIFVQGLGENVT ************************************

UserSeq1_H	298	IESVADYFKQIGIIKTNKKTGQPMINLYTDRETGKLKGEATVSFDDPPSAKAAIDWFDGK
UserSeq2_m	290	${\tt iesvadyfkqigiiktnkktgqpminlytdretgklkgeatvsfddppsakaaidwfdgk}$

UserSeq2_m 469 GYDRGGYRGRGGDRGGFRGGRGGGDRGGFGPGKMDSRGEHRQDRRERPY

Figure S9: Comparison of human and mouse FUS protein sequences

Supplementary Tables:

Supplementary Table S1: Statistical summary corresponding to Figure 1

Figure	Mouse genotype	Fibrils injected	Measured variable	Brain region	Kruskal-Wallis test	Dunn's multiple comparisons test	n-value
Igure	mouse generype	i ibilio ilijeoteu	measured variable	Brain region		1 month vs. 2 months	0.4116
				Cortex ipsilateral	p = 0.0203	1 month vs. 6 months	0.0429
1F			9/ of collo with outoplacmic aggregates			2 months vs. 6 months	>0.9999
	MFUS //NFUS	HA-FUS TIDRIS	7601 Cells with Cytoplasmic aggregates		p = 0.0036	1 month vs. 2 months	0.5391
				Hippocampus ipsilateral		1 month vs. 6 months	0.0219
						2 months vs. 6 months	0.5391
			%of cells with cytoplasmic aggregates	Cortex contralateral	p = 0.0750	1 month vs. 2 months	0.5934
						1 month vs. 6 months	0.0225
1	mELICKO/hELICR521H					2 months vs. 6 months	0.091
1 "	11FUS /11FUS	HA-FUS IIDHIS			p = 0.0107	not compared	
				Hippocampus contralateral		not compared	
1						not compared	

Supplementary Table S2: Statistical summary corresponding to Figure 2

Figure	Mouse genotype	Fibrils injected	Measured variable	Brain region	Kruskal-Wallis test	Dunn's multiple comparisons test	p-value
						1 month vs. 3 months	0.5172
				Cortex ipsilateral	p = 0.0036	1 month vs. 8 months	0.019
						3 months vs. 8 months	0.5172
						1 month vs. 3 months	0.7558
	mFUS ^{K0} /hFUS ^{R521H}	HA-FUS ^{R495X} fibrils	%of cells with cytoplasmic aggregates	Cortex contralateral	p = 0.0071	1 month vs. 8 months	0.0312
21						3 months vs. 8 months	0.7558
21				Hippocampus ipsilateral	p = 0.0071	1 month vs. 3 months	0.3884
						1 month vs. 8 months	0.0299
						3 months vs. 8 months	0.8656
						1 month vs. 3 months	0.5172
				Hippocampus contralateral	p = 0.0036	1 month vs. 8 months	0.019
						3 months vs. 8 months	0.5172

Supplementary Table S3: Statistical summary corresponding to Figure 4A and 4B

Figure	Measured variable	Mouse genotype	Material injected	Unpaired t-test p-value	
4A		non transgonia	PBS	0 7058	
	Pecognition index	non-transgenic	HA-FUSR ^{495X fibrils}	0.7058	
	Recognition index		PBS	0.0202	
		mFUS"/nFUS	HA-FUSR ^{495X fibrils}	0.0293	
	Time (s)	non transgonia	PBS	0.9501	
4B		non-transgenic	HA-FUSR ^{495X fibrils}	0.0591	
			PBS	0.0408	
		mrus /nrus	HA-FUSR ^{495X fibrils}	0.0498	

Supplementary Table S4: Statistical summary corresponding to Figure 4D and 4E

Figure	Measured variable	Mouse genotype	Material injected	one-way ANOVA p-value	Tukey's multiple comparisons test	p-value		
		mFUS ^{KO} /hFUS ^{R521H}	Non		Non injected vs PBS	0.3281		
4D	Neurons per mm ² in hippocampus		PBS	p = 0.0019	Non injected vs HA-FUS ^{R495X fibrils}	0.0013		
			HA-FUSR ^{495X fibrils}		PBS vs HA-FUS ^{R495X fibrils}	0.0631		
	Neurons per mm ² in cortex mFUS ^{KO} /hFUS ^{R521}			Non			Non injected vs PBS	0.315
4E		mFUS ^{KO} /hFUS ^{R521H}	PBS	p = 0.0026	Non injected vs HA-FUS ^{R495X fibrils}	0.0019		
			HA-FUSR ^{495X fibrils}		PBS vs HA-FUS ^{R495X fibrils}	0.0574		

Supplementary Table S5: Statistical summary corresponding to Supplementary S5

[Figure	Measured variable	Mouse genotype	Material injected	Compared groups	Unpaired t-test p-value
	SEE	ELIS intensity (a.u.) in urea fraction		LLA ELIOD495X fibrils	PBS	0.0024
	30F	FUS intensity (a.u.) in urea fraction	mFUS**/hFUS*****	HA-FUSR	Fibril injected	0.0024

Supplementary Table S6: Statistical summary corresponding to Supplementary S6

Figure	Measured variable	Mouse genotype	Material injected	Compared groups	Unpaired t-test p-value
SED	% of colls with EUS aggregates		LLA FLIGR495X fibrils	NeuN -	<0.0001
300	% of cells with POS aggregates	mrus /nrus	HA-FUS	NeuN +	<0.0001
SEC	ELIS puckear intensity (a.u.)	mELIOKO/hELIOR521H	LLA ELLOR495X fibrils	PBS	0.7603
300	FOS fluciear intensity (a.u.)	mFUS /nFUS	HA-FUS	Fibril injected	0.7805
SED	ELIS exteniosmic intensity (2.11)		LLA FLICR495X fibrils	PBS	0.0303
300	POS cytoplasmic intensity (a.u.)	mrus /nrus	HA-FUS	Fibril injected	0.9303
SEE	ELIS puelear/autoplaamia ratio	mFUS ^{KO} /hFUS ^{R521H}	LLA ELLOB495X fibrils	PBS	0.5429
SUE	FOS hucieancytopiasifiic fatio		HA-FUS	Fibril injected	0.5428
SEE	ELIS puelear intensity (a.u.)		LLA FLICR495X fibrils	without inclusions	0.7592
301	FOS fluciear intensity (a.u.)	mrus /nrus	HA-FUS	with inclusions	0.7592
860	ELIS exteniosmic intensity (2.11)		LLA ELLOR495X fibrils	without inclusions	0.5010
300	F05 cytoplasmic intensity (a.u.)	mrus /nrus	HA-FUS	with inclusions	0.5919
SEL	ELIS nuclear/outonlasmic ratio		LLA ELLOR495X fibrils	without inclusions	0 1695
301	F03 hucleancytoplasmic ratio	mFUS /nFUS	HA-FUS	with inclusions	0.1095

Supplementary Table S7: Statistical summary corresponding to Supplementary S8

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Figure	Measured variable	Mouse genotype	Material injected	Unpaired t-test p-value	
		non transgonia	PBS	0 5050	
S8	Time (s)	non-transgenic	HA-FUSR ^{495X fibrils}	0.5656	
			PBS	0 7252	
		mFUS"/nFUS	HA-FUSR ^{495X fibrils}	0.7252	