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1 **Altered SOD1 maturation and post-translational** 2 **modification in amyotrophic lateral sclerosis spinal cord**

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15 **Running title:** SOD1 biochemistry in post-mortem ALS

16

1 **Abstract**

2 Aberrant self-assembly and toxicity of wild-type and mutant superoxide dismutase 1 (SOD1) has
3 been widely examined *in silico*, *in vitro*, and in transgenic animal models of amyotrophic lateral
4 sclerosis (ALS). Detailed examination of the protein in disease-affected tissues from ALS
5 patients, however, remains scarce.

6 We employed histological, biochemical and analytical techniques to profile alterations to SOD1
7 protein deposition, subcellular localization, maturation and post-translational modification in
8 post-mortem spinal cord tissues from ALS cases and controls. Tissues were dissected into ventral
9 and dorsal spinal cord grey matter to assess the specificity of alterations within regions of motor
10 neuron degeneration.

11 We provide evidence of the mislocalization and accumulation of structurally-disordered,
12 immature SOD1 protein conformers in spinal cord motor neurons of *SOD1*-linked and non-
13 *SOD1*-linked familial ALS cases, and sporadic ALS cases, compared with control motor
14 neurons. These changes were collectively associated with instability and mismetallation of
15 enzymatically-active SOD1 dimers, as well as alterations to SOD1 post-translational
16 modifications and molecular chaperones governing SOD1 maturation. Atypical changes to
17 SOD1 protein were largely restricted to regions of neurodegeneration in ALS cases, and clearly
18 differentiated all forms of ALS from controls. Substantial heterogeneity in the presence of these
19 changes was also observed between ALS cases.

20 Our data demonstrates that varying forms of SOD1 proteinopathy are a common feature of all
21 forms of ALS, and support the presence of one or more convergent biochemical pathways
22 leading to SOD1 proteinopathy in ALS. The majority of these alterations are specific to regions
23 of neurodegeneration, and may therefore constitute valid targets for therapeutic development.

24 **Keywords:** superoxide dismutase-1; neurodegeneration; mislocalization; amyotrophic lateral
25 sclerosis; post-translational modifications

26 **Abbreviations:** ALS = amyotrophic lateral sclerosis; CCS = copper chaperone for SOD1;
27 disSOD1 = structurally-disordered SOD1; fALS = familial amyotrophic lateral sclerosis; GSH =
28 glutathione; pI = isoelectric point; PTM = post-translational modification; sALS = sporadic
29 amyotrophic lateral sclerosis; SOD1 = superoxide dismutase-1

1 Introduction

2 Amyotrophic lateral sclerosis (ALS) is a fatal adult-onset neurodegenerative disease
3 characterized by the progressive loss of motor neurons in the cortex, brain stem and ventral horns
4 of the spinal cord. Ten percent of ALS cases are hereditary (familial; fALS), while the remaining
5 ~90% lack an overt familial history, referred to as sporadic (s)ALS.¹ The gene encoding
6 superoxide dismutase 1 (SOD1) was the first dominantly-inherited genetic risk factor identified
7 for ALS.² and over 200 *SOD1* mutations have since been documented in fALS patients
8 (<http://alsod.iop.kcl.ac.uk>). These mutations disrupt key structural or functional motifs within
9 SOD1 protein, resulting in structurally-disordered mutant proteins that are strongly implicated in
10 motor neuron death.³ A number of studies have also identified structurally-disordered wild-type
11 SOD1 proteinopathy in the spinal cord of non-*SOD1*-linked fALS and sALS patients.⁴⁻¹¹ This
12 finding, however, is not consistently reported,¹²⁻¹⁴ making it unclear whether wild-type SOD1
13 contributes to motor neuron death in ALS patients lacking *SOD1* mutations.

14 Pathways hypothesized to underlie the self-assembly and toxicity of both wild-type and mutant
15 SOD1 protein have been identified *in silico* and using *in vitro* systems, and in cellular and animal
16 models of ALS.³ Evidence of these pathways in ALS patients *in vivo* or post-mortem, however,
17 is scarce. This data is vital to ascertain whether SOD1 proteinopathy may indeed contribute to
18 motor neuron death in familial and sporadic ALS patients through similar mechanisms to those
19 identified in well-characterized disease models. Such knowledge may reveal productive
20 treatment avenues, and improve the development and choice of preclinical models for
21 therapeutic development, factors which are proposed to underlie recurrent failures to translate
22 promising interventions into the clinic.¹⁵

23 Data from transgenic mouse models, cultured cells and *in vitro* proteomic assays demonstrate
24 *SOD1* mutations disrupt copper and zinc binding, intramolecular disulfide bond formation and
25 protein dimerization (recently reviewed)³. These perturbations promote the accumulation of
26 immature structurally-disordered SOD1 conformers, which elicit mitochondrial dysfunction,¹⁶
27 bioenergetic failure,¹⁷ reactive oxygen species accumulation¹⁸ and ultimately neurodegeneration
28 in preclinical models. Non-genetic factors can also provoke structural and/or functional
29 alterations to wild-type SOD1 protein analogous to those associated with *SOD1* mutations. These

1 include post-translational modifications (PTM) to key amino acid residue side chains, as well as
2 disruptions to molecular chaperones involved in SOD1 protein maturation. These alterations
3 confer toxic properties to wild-type SOD1 mirroring those of some mutant proteins *in vitro*,⁴
4 implying convergent molecular pathways resulting in SOD1 proteinopathy, irrelevant of *SOD1*
5 mutation status.¹⁹ Despite this abundance of data from preclinical models, it is unclear whether
6 abnormal SOD1 proteinopathy is unique to *SOD1*-fALS patients, or constitutes a shared feature
7 amongst all forms of ALS.

8 In this study, we characterized SOD1 proteinopathy in post-mortem spinal cord tissues from
9 familial and sporadic ALS patients, and profiled soluble and aggregated SOD1 protein
10 biochemistry within these same tissues for evidence of non-genetic alterations to SOD1 that may
11 underlie any proteinopathy. We show that structurally-disordered, immature SOD1 conformers
12 becomes mislocalized from the ER-golgi network and nucleus to the cytoplasm in *SOD1*-linked
13 (*SOD1*-)fALS, non-*SOD1*-linked (non-*SOD1*-)fALS and sALS spinal cord motor neurons, where
14 they accumulate and often form large inclusions. These findings were associated with the de-
15 metallation and destabilization of enzymatically-active mature SOD1 protein, as well as
16 alterations to SOD1 PTMs and molecular chaperones governing SOD1 maturation.
17 Heterogeneity in the presence of these alterations between ALS cases reinforces the likelihood
18 that SOD1 proteinopathy arises from multiple biochemical pathways in ALS patients. Our data
19 suggest some of these alterations may contribute to motor neuron death in ALS patients by
20 promoting neurotoxic SOD1 proteinopathy, implying these pathways may constitute valid targets
21 for therapeutic development.

22 **Materials and methods**

23 **Human post-mortem tissues**

24 Formalin-fixed and fresh frozen human post-mortem brain and spinal cord tissues from patients
25 with *SOD1*-associated familial amyotrophic lateral sclerosis (*SOD1*-fALS; $n = 3$), non-*SOD1*-
26 associated fALS (non-*SOD1*-fALS; $n = 4$), sporadic ALS (sALS; $n = 9$) and age-matched
27 controls ($n = 10$) were obtained from the MRC London Neurodegenerative Diseases Brain Bank

1 (King's College, London, UK) and the University of Maryland Brain and Tissue Bank, a
2 biorepository of the NIH NeuroBioBank (Maryland, USA). Diagnoses of ALS were determined
3 clinically using patient histories received from the donors' physicians. Pathological identification
4 of motor neuron loss in the anterior horn of the spinal cord by brain bank neuropathologists
5 confirmed clinical findings. All ALS cases were free of other neurological or neuropathological
6 conditions. Genotyping confirmed *SOD1* and *C9ORF72* mutation status of ALS cases, as
7 described below. Age-matched control cases were free of any clinically diagnosed neurological
8 disorders and neuropathological abnormalities. Ethics approval was obtained from the University
9 of Sydney Human Research Ethics Committee (approval number 2019/309). Demographic and
10 clinical information for all cases are detailed in **Supplementary Table 1**. Diagnostic groups
11 were matched for age and post-mortem interval (Kruskal-Wallis test, $p > 0.05$; **Supplementary**
12 **Table 2**). A principal component analysis of all data collected in this study revealed neither of
13 these factors significantly impacted variables of interest in the ventral spinal cord
14 (**Supplementary Figure 1**, further details in statistical analyses). This analysis also found no
15 impact of sex on measured variables, despite differences in the ratio of males to females between
16 diagnostic groups (**Supplementary Figure 2**).

17 Fixed and fresh frozen tissues from the cervical and thoracic spinal cord represented regions of
18 severe motor neuron degeneration in ALS, samples of occipital cortex represented a non-
19 degenerating control region external to the spinal cord. Tissue availability varied between cases
20 (**Supplementary Table 1**). Formalin-fixed tissues were embedded in paraffin and 7 μ m sections
21 prepared for immunohistochemical analyses. Fresh frozen tissues were trimmed to remove most
22 of the white matter. Fresh frozen spinal cord tissues were bisected into dorsal and ventral regions
23 representing degenerating and non-degenerating spinal cord tissues in ALS respectively.
24 Paraffin-embedded formalin-fixed and fresh frozen tissue samples were randomly numbered by a
25 secondary investigator (B.G.T. or S.G.) prior to experimentation to blind primary investigators
26 (B.G.T., S.G., S.R., A.R., or J.A.F) to case diagnoses.

27 **SOD1 and C9ORF72 genotyping**

28 *SOD1* and *C9ORF72* genotyping was performed in ALS and control cases as previously
29 described.²⁰ DNA was extracted from fresh frozen human brain tissue from the occipital cortex

1 using the DNeasy DNA extraction kit (Cat. #69506; Qiagen, Hilden, Germany), according to
2 manufacturer's instructions. All five exons of SOD1, and at least 10bp of flanking sequence were
3 sequenced using PCR amplification and Sanger sequencing. The repeat primed PCR method was
4 used to amplify the *C9orf72* hexanucleotide repeat sequence and was analysed by fragment
5 analysis.²⁰ All results were independently analysed by two team members. Positive samples were
6 repeated twice to confirm results.

7 **Immunohistochemistry**

8 Fixed tissue sections used for 3,3'-Diaminobenzidine (DAB) staining and brightfield microscopy
9 were deparaffinated and antigen retrieval performed in citrate buffer (pH 6; Fronine, Australia) at
10 95°C for 30 min. Sections were then washed with 50% ethanol, incubated with 3% H₂O₂
11 (Fronine, Australia) in 50% ethanol to quench non-specific peroxidase activity, and blocked
12 (0.5% casein, 1% bovine serum albumin in PBS) for 1.5 h at room temperature. Sections were
13 then incubated overnight with appropriate primary antibodies diluted in blocking solution
14 (**Supplementary Table 3**). Primary antibodies were detected using biotinylated IgG secondary
15 antibodies (2 h, room temperature, 1:200 diluted in blocking solution) (Vector Laboratories,
16 Burlingame, CA) followed by Vector Elite Kit tertiary antibody complex (2 h, room temperature,
17 1:100 diluted in PBS) (Vector Laboratories, Burlingame, CA), and visualised using a DAB
18 (Sigma-Aldrich, St. Louis, MO, USA) solution containing cobalt and nickel ions, changing the
19 chromogen colour from brown to black to enable distinction of DAB staining from pigmented
20 neurons in the SNc. Sections were finally dehydrated and mounted with DPX, visualized and
21 imaged using an Olympus VS 120 Slide Scanner at 40x magnification (Olympus-life science,
22 Shinjuku, Tokyo, Japan), and images processed using OlyVIA (Version 3.1; Olympus-life
23 science) or Fiji (National Institute of Health (NIH)) software.

24 A lack of consistency between immunostaining protocols investigating mammalian SOD1
25 misfolding may underlie variability in misfolded SOD1 detection within ALS post-mortem
26 tissues and transgenic SOD1 mice.⁹ Accordingly, our DAB immunostaining protocol for
27 misfolded SOD1 protein adhered to guidelines proposed by Pare and colleagues⁹, except for
28 performing Hematoxylin/Eosin staining on adjacent serial tissue sections, which could not be
29 performed due to limited tissue availability. A *no primary* negative control (processed as above

1 in the absence of primary antibodies) was also included for each diagnostic group to identify
2 protocol- and tissue-related artefacts independent of primary antibody immunoreactivity.

3 **Multiplexed immunofluorescence**

4 Fixed tissue sections used for fluorescent staining and confocal microscopy were deparaffinated,
5 antigen retrieved, quenched, blocked and incubated with appropriate primary antibodies
6 (**Supplementary Table 3**) as above. Multiplexed fluorescent immunolabelling was then
7 performed using OPAL fluorophores (Akoya Biosciences, Menlo Park, CA, USA) according to
8 the manufacturer's instructions. Antibody stripping between OPAL fluorophore incubations was
9 performed at 95°C for 40 min using AR6 commercial buffer (Akoya Biosciences, USA).
10 Following incubation with the final fluorophore sections were washed with PBS and cover-
11 slipped with 80% glycerol. Images were collected at 60x magnification using a Nikon C2+
12 Confocal Microscope System (Nikon, Minato City, Tokyo, Japan) and Nikon NIS-elements
13 software (Version 5.20.02; Nikon, Japan), and were viewed and analysed using Fiji software
14 (National Institute of Health, Bethesda, Maryland, USA).

15 As above, a *no primary* negative control was included for each diagnostic group to identify non-
16 specific fluorescent signals originating from autofluorescent tissue features (e.g. lipofuscin) or
17 direct binding of secondary antibodies to tissues (**Supplementary Figure 3**). During acquisition
18 of double- or triple-immunolabelled fluorescent images a sequential protocol was used where
19 each fluorophore was excited and the corresponding channel was individually acquired, before
20 moving onto the next fluorophore and channel, to prevent any spectral cross-contamination
21 between channels. Negligible spectral overlap was identified between OPAL650, OPAL620 and
22 OPAL520 fluorophores using this protocol (**Supplementary Figure 3**), indicating an absence of
23 fluorophore cross-contamination across channels.

24 **Neuronal quantification**

25 Spinal cord motor neurons were quantified in DAB-immunostained serial 7µm fixed tissues
26 sections, whereby cells immunopositive for neuron-specific class III β-tubulin (TUJ-1) in ventral
27 horn grey matter were counted in every fifth tissue section for a total of 4 sections.

1 Quantification was completed by a single investigator (BT) blinded to sample diagnosis. Grey
2 matter area (mm^2) was recorded in Fiji software to enable conversion of neuron counts to
3 neuronal densities (counts per mm^2). Due to the absence of neuronal cell bodies in dorsal horn
4 grey matter of the spinal cord, the average area (mm^2) of grey matter in this region was used to
5 approximate alterations to neuronal tract density. An index of neuronal loss was calculated for
6 each investigated region of each case by normalizing neuronal density for each region/case to the
7 mean neuronal density of the same investigated region for the healthy control group; Sample
8 Index = $1 - (\text{sample neuronal density} / \text{healthy control mean neuronal density for sample region})$.
9 Higher index values are associated with lower neuronal densities or greater neuron death. This
10 index was used to explore correlations between neuron loss and quantified pathological features
11 within investigated regions.

12 **Quantification of pathological features of interest**

13 Immunostaining for SOD1 and CCS was performed in ventral horn grey matter of the cervical
14 and thoracic spinal cord as above, using appropriate primary antibodies (**Supplementary Table**
15 **3**). Pan and conformation-specific primary antibodies were employed for SOD1 immunostaining.
16 Pathologies of interest were SOD1 deposits, diffuse cytosolic SOD1, granular cytoplasmic
17 SOD1, CCS deposits and diffuse cytosolic CCS. Counts of each pathology were expressed as the
18 proportion of neurons exhibiting evidence of that pathology to account for differences in motor
19 neuron number between cervical and thoracic spinal cord levels. Conformation-specific SOD1
20 antibodies yielded a 10-fold improvement in the identification of motor neuron inclusions
21 compared with pan-SOD1 antibodies, supporting the strong involvement of disSOD1 conformers
22 in SOD1 aggregation. Quantification of diffuse cytosolic disordered SOD1 staining was
23 performed in sections stained with U β B conformation-specific SOD1 antibody and DAB. Using
24 Fiji software, average DAB stain intensity was measured throughout the cross section of the
25 neuron and was normalized to the average stain intensity within an area of similar size located
26 immediately adjacent to the motor neuron of interest.

1 **Fresh frozen tissue homogenization and fractionation**

2 Fresh frozen tissue samples were homogenized in 5 volumes (μL) of homogenization buffer
3 (20mM Tris-base, pH 7.6, 1:100 EDTA-free protease inhibitor (Sigma-Aldrich, USA), 1:10
4 EDTA-free phosphatase inhibitor (PhosSTOP; Roche, Basel, Switzerland)) per mg of tissue at
5 4°C using a hand-held tissue grinder with metal-free polypropylene probes (Kontes Pellet
6 Pestle[®], Sigma-Aldrich, USA). Homogenates were aliquoted and stored at -80°C , or were
7 centrifuged (16,000g, 30min, 4°C) and the supernatant and pellet collected, aliquoted and stored
8 at -80°C . Protein concentrations within homogenates and supernatants were quantified using a
9 Pierce[™] BCA Protein Assay Kit (ThermoFisher Scientific, USA). Supernatant and pellet tissue
10 fractions will subsequently be referred to as soluble and insoluble tissue extracts, respectively.
11 Measures were undertaken to prevent metal contamination of tissue extracts, including the use of
12 plastic forceps for handling tissues, and the removal of trace metal impurities from buffers and
13 glassware using Chelex resin (Bio-Rad) and a metal-chelating rinse solution (0.37% EDTA in
14 2.25mM K_3PO_4 ; Sigma-Aldrich, USA), respectively. These measures were also incorporated into
15 native isoelectric focussing experiments and SOD1 specific activity assays.

16 **SOD1 specific activity**

17 SOD1 antioxidant activity was quantified in soluble tissue extracts using a commercial SOD
18 Assay Kit (Cat. #19160, Sigma-Aldrich, USA) and potassium cyanide (KCN), as previously
19 described.²¹ KCN is a potent inhibitor of SOD1 antioxidant activity.^{22,23} Duplicate samples
20 containing 2 μg protein were incubated with 15mM KCN or 20mM Tris buffer (pH 7.6; Sigma-
21 Aldrich, USA) for 60min at room temperature, and SOD activity (U/mL) measured in both
22 samples using the SOD Assay Kit, according to manufacturers' instructions. SOD1 activity
23 (U/mL) was calculated by subtracting SOD activity measured in the KCN duplicate (non-SOD1
24 SOD activity) from the SOD activity measured in the Tris buffer duplicate (total SOD activity).
25 As validation of complete SOD1 inhibition in KCN duplicates, incubation of commercial SOD1
26 (0-200U/mL) with 15mM KCN for 60min at room temperature completely inhibited SOD1
27 activity up to $\sim 50\text{U/mL}$ (**Supplementary Figure 4**), whereas the average total SOD activity in
28 age-matched control samples was only 3.91U/mL in Tris buffer duplicates. The specific activity

1 of SOD1 (U/mL/SOD1 protein) was determined by normalising SOD1 activity to SOD1 protein
2 levels measured by immunoblotting.

3 **Immunoblotting**

4 10µg (SOD1) or 30µg (CCS, GFAP) total protein from soluble tissue extracts was incubated in
5 loading buffer (100mM dithiothreitol, 3% SDS, 10% glycerol, 0.05% bromophenol blue,
6 62.5mM Tris-base, pH 7.4; Sigma-Aldrich, USA) at 95°C for 15min. Extracts were then loaded
7 into Any kD Mini-PROTEAN TGX Precast Protein Gels (15 well, 15µL; Bio-Rad) and
8 separated using the Bio-Rad Mini-PROTEAN Tetra Cell system (180V, 40min, 4°C). Separated
9 proteins were transferred to Immun-blot PVDF membrane (0.2µm pore size; Bio-Rad) overnight
10 at 9V and 4°C, before membranes were dried for 2h at room temperature and proteins stained
11 with Sypro Ruby Protein Blot Stain (ThermoFisher Scientific, USA), according to the
12 manufacturer's instructions. Sypro Ruby-stained membranes were imaged using a Chemi-Doc
13 XRS imaging system (630BP30nm filter, Bio-Rad), and total protein in each sample quantified
14 by densitometry using ImageLab software (Version 5.2, Bio-Rad). Membranes were then
15 blocked for 2h with 5% skim milk diluted in PBS-T (PBS containing 0.1% Tween 20; Sigma-
16 Aldrich, USA) and incubated overnight at 4°C with primary antibodies against SOD1, CCS and
17 GFAP proteins (**Supplementary Table 3**) diluted in blocking solution. Primary antibodies were
18 detected using appropriate horseradish peroxidase-conjugated secondary antibodies (Bio-Rad)
19 diluted in blocking solution (1:2,000) for 2h at room temperature. Protein signals were developed
20 using ECL western blotting substrate (Bio-Rad), detected using a Chemi-Doc XRS imaging
21 system (Bio-Rad), and quantified by densitometry using ImageLab software (Version 5.2, Bio-
22 Rad), all according to manufacturers' instructions. Protein levels of SOD1, CCS and GFAP were
23 normalized to total protein levels within the same sample to correct for variations in protein
24 loading, and an internal standard (pooled from all tissue samples) was included on every gel to
25 correct for variability between gels and immunoblot runs. SOD1 protein amount was confirmed
26 to exhibit a linear correlation with SOD1 immunoblot densitometry (**Supplementary Figure 5**)
27 from 0-1µg using a recombinant human SOD1 protein standard. This encompasses the protein
28 loading amounts employed in our experiments, validating our SOD1 quantification method and
29 accuracy. SOD1 and CCS reside within neurons and glia,^{21,24} and thus quantification of SOD1

1 and CCS protein levels must take into account neuron loss and astrogliosis within degenerating
2 regions in ALS, reported herein and elsewhere.²⁵ SOD1 and CCS protein levels were therefore
3 normalized to a combined cellular index (CCI), which was generated by multiplying indices of
4 neuronal loss (quantified by immunohistochemistry, **Fig. 1i**) and astrogliosis (quantified by
5 GFAP immunoblot, **Supplementary Figure 6**).

6 **Measurement of enzymatically-active SOD1 metallation**

7 The metal content of enzymatically-active, dimeric SOD1 was quantified using size-exclusion
8 chromatography (SEC) coupled with native isoelectric focussing (nIEF), synchrotron radiation
9 X-ray fluorescence (SXRF) analyses and particle-induced X-ray emission spectroscopy (PIXE),
10 according to our published method.²⁶ Briefly, spinal cord and brain tissue homogenates were
11 subjected to SEC to purify mature SOD1 dimers from post-mortem tissues, and SOD1 identified
12 within collected fractions using nano-liquid chromatography-tandem mass spectrometry at a high
13 sequence coverage of 92%. SOD1-containing fractions were then applied along immobilized pH
14 gradient (IPG) gels in duplicate and nIEF performed to further purify dimeric SOD1 according to
15 its pI. SEC-nIEF collectively yielded a 99-fold enrichment of SOD1 protein in post-mortem
16 tissue extracts. After the pI of enzymatically-active, dimeric SOD1 was identified within the first
17 duplicate IPG gel using NBT staining and mass spectrometry, metal quantification was
18 performed on the second duplicate IPG gel at the pI of active SOD1 using SXRF and PIXE. The
19 SXRF analyses were performed in the microprobe hutch of the Hard X-ray Micro/Nano-Probe
20 beamline P06 at the synchrotron PETRA III (DESY) in Hamburg (Germany). The analyses were
21 carried out with an X-ray beam of 12 keV photon energy. The PIXE analyses were performed
22 with 3 MeV proton beam (focussed down a spot size of 2 μm) produced at the AIFIRA facility
23 of the CENBG (Gradignan, France) using a 3.5 MV singletron in-line particle accelerator (High
24 Voltage Engineering Europe). For both techniques, triplicates were recorded for each sample and
25 mean Cu/Zn ratios were calculated. Proteomic analyses using mass spectrometry identified
26 minimal other metalloproteins within IPG gels at the pI of mature SOD1,²⁶ and their extremely
27 low abundance compared with SOD1 ($\leq 0.57\%$) in protein extracts suggests negligible metal
28 contamination from these proteins. Neither SEC nor nIEF altered the pI or the copper:zinc ratio

1 of a commercially-available human SOD1 control,²⁶ indicating preservation of endogenous metal
2 binding stoichiometry in purified SOD1 protein.

3 **Native isoelectric focussing (nIEF)**

4 Soluble tissue extract aliquots (40µg total protein) were supplemented with DNase and RNase
5 (Sigma-Aldrich, USA) to a final concentration of 10µg/mL and diluted to 140µL using trace
6 metal-free 20mM Tris-base, pH 7.6. Duplicate immobilized pH gradient (IPG) gels (pH 4.5-5.5,
7 7 cm; Zoom[®] IPG Strip, ThermoFisher Scientific, USA) were rehydrated passively using 140µL
8 diluted soluble extract in an IPG re-swelling tray (Bio-Rad) for 2h at 10°C. The backing of the
9 IPG gels was covered in mineral oil (Bio-Rad) to prevent drying during rehydration. Gels were
10 then focussed in a Protean IEF Cell (Bio-Rad) for 12kVh at 10°C (50µA/gel; **Supplementary**
11 **Table 4**). Immediately following nIEF SOD1 activity was detected in IPG gels using nitroblue
12 tetrazolium, as described previously,²¹ and the isoelectric point (pI) of SOD1 in each sample
13 determined. One IPG strip rehydrated with commercially available human SOD1 (5µg, ≥2,500
14 units activity/mg protein; Sigma-Aldrich, USA) was included per sample run to control for
15 variability between runs.

16 **Tissue preparation for SOD1 aggregate metal quantification**

17 The metal content of SOD1 aggregates in the ventral spinal cord of ALS cases was quantified in
18 fresh frozen tissue sections using XFM at the Australian Synchrotron (Clayton, Victoria,
19 Australia), according to our published method.²⁷ Briefly, frozen spinal cord tissue blocks from 3
20 *SOD1*-fALS, 1 non-*SOD1*-fALS and 1 sALS case underwent serial cryosectioning (20µm) at -
21 20°C. Immunohistochemical identification of SOD1 aggregates was performed on the first of
22 two facing serial sections, using B8H10 conformation-specific SOD1 primary antibody coupled
23 with DAB staining on a Superfrost[™] microscope slide (ThermoFisher Scientific, USA), as
24 described above. The adjacent section was reversed and mounted on a Si₃N₄ window (5 & 5mm,
25 200nm film thickness, 200mm frame thickness; Australian National Fabrication Facility, QLD,
26 Australia) with the matching tissue face exposed for synchrotron radiation analyses. We used an
27 Olympus VS120 slide scanner (Olympus, Japan) to map the locations of SOD1 aggregates within

1 immunolabelled sections using brightfield microscopy, and to map unlabelled facing sections
2 mounted on Si_3N_4 windows using differential interference contrast imaging. Images of facing
3 sections were overlaid using OlyVIA 2.9 software (Olympus, Japan) and X, Y pixel coordinates
4 of SOD1 aggregates identified in unlabelled sections from their location in DAB-
5 immunolabelled sections, often using distinct tissue features (blood vessels, dorsal or ventral
6 horn boundaries) to triangulate aggregate locations in unlabelled sections. Pixel coordinates of
7 aggregates were recorded and later transferred to motor stage positions at the beamline facility.

8 **Australian Synchrotron XFM beamline operating parameters**

9 The XFM beamline at the Australian Synchrotron²⁸ is a in-vacuum undulator hard x-ray
10 microprobe with a Maia 384 detector,²⁹ which allows the rapid imaging of large samples. A
11 Kirkpatrick-Baez mirror microprobe was used to focus monochromatic 15.8keV X-rays to a $2\mu\text{m}$
12 spot. Samples were mounted on Perspex frame and scanned in fly-scan mode with $1\mu\text{m}$ step size
13 and 5ms dwell per pixel. Total x-ray fluorescence emission spectra were collected by the Maia
14 detector. Pixel coordinates from OlyVIA 2.9 were directly imported into the beamline using the
15 integrated motor control system described previously.²⁸

16 **Australian Synchrotron XFM data analysis**

17 Elemental maps were produced by fitting the x-ray fluorescence (XRF) emission energies to the
18 total XRF spectrum from each pixel. Model spectrum was produced with the assumption that
19 dried tissues was $5\mu\text{m}$ thick. This quantitative deconvolution of elemental fluorescence was
20 performed using GeoPIXE v7.2 which applies a first-order “matrix” correction to estimate the
21 reabsorption of the elemental fluorescence by the tissue.³⁰ Images were exported as 32-bit tiffs
22 for further analysis in Fiji software (National Institute of Health, USA) as previously described.³¹
23 Images were analysed as described previously.³¹ In brief, limit of detection (LOD) for each
24 element was determined and each pixel corrected for background. A threshold of the upper 1%
25 was also excluded from analysis. Aggregates were outlined by aligning brightfield microscopy
26 photomicrographs with XFM images. Images were then normalised by pixel-wise division of
27 Compton scatter emission to correct for variation in surface density and self-absorption effects,

1 and aggregate measurements extracted for stacked XFM elemental maps. Extracted, corrected
2 and normalised XFM data was imported into SPSS Statistics v26 (International Business
3 Machines, Illinois, USA) with matching subject demographic data. Outliers were defined by
4 SPSS as 'extreme values' ≥ 3 x the interquartile range (or 2 standard deviations) and excluded
5 from analysis. A two-sided T-test was used to compare elemental levels in SOD1 aggregates
6 with background tissue and active SOD1. A significant difference in Cu:Zn ratio from the
7 expected 1:1 was inferred from a 95% confidence interval that did not span 1 (Wilcoxon signed
8 rank test).

9 Immunoprecipitation

10 SOD1 protein was immunoprecipitated from post-mortem spinal cord tissue homogenates using
11 Dynabeads M-280 Tosylactivated (Invitrogen, Carlsbad, CA, USA), according to manufacturer's
12 instructions. Ten milligrams of Dynabeads M-280 Tosylactivated were conjugated to 100ug
13 polyclonal SOD1 antibody (Enzo Life Sciences, Farmingdale, NY, USA; **Supplementary Table**
14 **3**) diluted to 40mg beads/mL in coupling buffer (0.1M boric acid, pH 9.5; 1.2M ammonium
15 sulphate) overnight at 37°C. Dynabeads were blocked with 0.5% BSA in PBS (pH 7.4), washed
16 with 0.1% BSA in PBS (pH 7.4), and incubated with ventral spinal cord tissue homogenates
17 (200ug) diluted in PBS (pH 7.4) to 40mg beads/mL overnight at 4°C. Following PBS washes,
18 immunoprecipitated proteins were eluted from Dynabeads using successive 10min incubations
19 with 0.1M glycine (pH 3), eluants neutralized using an equivalent volume of ammonium
20 bicarbonate (pH 8) and extracts dried under pressure using a vacuum concentrator. We observed
21 minimal reductions in the amount of SOD1 protein captured over successive rounds of
22 immunoprecipitation upon re-use of antibody-coupled Dynabeads (**Supplementary Figure 7**),
23 and hence beads were re-used for 3 successive rounds of immunocapture. No measurable SOD1
24 protein was bound to antibody-coupled Dynabeads post elution (**Supplementary Figure 7**),
25 negating the possibility of cross-contamination between samples assigned to successive rounds
26 of immunocapture. No alterations to the antioxidant activity or metal content of a commercially-
27 available human SOD1 standard were observed following immunoprecipitation (**Supplementary**
28 **Figure 7**),³² indicating SOD1 protein was likely isolated from post-mortem tissues having
29 retained its endogenous metal occupancy and protein conformation. SOD1 protein was also not

1 identified in immunoprecipitates prepared using dynabeads that were not conjugated to our
2 capture antibody (**Supplementary Figure 7**).

3 **Sample preparation for mass spectrometry**

4 Dried SOD1 immunoprecipitates were resuspended in 50 mM ammonium bicarbonate (pH 8)
5 containing 6M urea, reduced with dithiothreitol (DTT; 10 mM final) for 30min at 56 °C,
6 alkylated with iodoacetamide (IAA; 20 mM final) for 30min at room temperature in the dark,
7 and finally quenched with a further 10 mM DTT for 30min at room temperature. Samples were
8 diluted five-fold using 50 mM ammonium bicarbonate (pH 8) to reduce the concentration of urea
9 to 1.2M and acetonitrile added (10% final), before in-solution digestion performed overnight at
10 room temperature using 0.2µg sequencing-grade modified trypsin (Promega, Madison, WI,
11 USA). Samples were then acidified using trifluoroacetic acid, desalted using Pierce C18 Tips
12 (ThermoFisher Scientific, USA) according to manufacturer's instructions, and dried under
13 pressure using a vacuum concentrator. Samples were resuspended in loading buffer (0.1% formic
14 acid, 3% ACN) and transferred to HPLC vials immediately prior to mass spectrometry analyses.

15 Cysteine residues are highly susceptible to oxidation compared with other amino acids,³³
16 therefore sample preparation for cysteine redox analysis utilized separate tissues prepared under
17 a global reductive protein preparation strategy to limit the introduction of artifactual
18 modifications during sample processing.³⁴ Samples were homogenized as described above, and
19 homogenates incubated with N-ethylmaleimide (NEM; 20 mM final) for 10min at room
20 temperature to alkylate free thiol groups. Excess NEM was quenched with DTT (25mM final)
21 for 15min at room temperature, after which sample pH was adjusted above 7 using sodium
22 hydroxide and samples reduced for 1h at room temperature. Homogenates were then incubated
23 with MMTS (60 mM final) for 1.5h at 30 °C to quench DTT and alkylate nascent thiols, and
24 proteins precipitated using chloroform/methanol precipitation. Proteins were resuspended in
25 50mM ammonium bicarbonate (pH 8) containing 6 M urea, diluted 5-fold using 50mM
26 ammonium bicarbonate (pH 8), and protein concentration quantified using a BCA assay
27 according to manufacturer's instructions. Acetonitrile was then added (10% final), and in-
28 solution digestion performed overnight at room temperature using sequencing-grade modified
29 trypsin (1:50 trypsin:protein; Promega, Madison, WI, USA). Samples were then acidified using

1 trifluoroacetic acid, dried under pressure using a vacuum concentrator, resuspended in loading
2 buffer (0.1% formic acid, 3% ACN) and transferred to HPLC vials immediately prior to mass
3 spectrometry analyses.

4 **Mass spectrometry data acquisition**

5 Label-free Fourier Transform Mass Spectrometry was employed to analyse immunoprecipitated
6 protein extracts at Sydney Mass Spectrometry (Sydney, New South Wales, Australia). Analyses
7 were performed using an UltiMate 3000 RSLCnano system (ThermoFisher Scientific, USA)
8 coupled online via a Nanospray Ion Source (ThermoFisher Scientific, USA) to an Orbitrap
9 Fusion Tribrid Mass Spectrometer (ThermoFisher Scientific, USA). Peptide digests were loaded
10 onto an in-house packed ReproSil-Pur 120 C18-AQ analytical column (75µm id x 40 cm, 1.9µm
11 particle size; Dr Maisch, Ammerbuch, Germany) regulated to 60°C using a PRSO-V2 Sonation
12 column oven (Sonation, Baden-Wuerttemberg, Germany). A binary gradient of solvent A (0.1%
13 formic acid in MilliQ water) to solvent B (0.1% formic acid in 80% ACN diluted with MilliQ
14 water) was used for peptide elution at a separation flow rate of 300-450 nL/min over 90min
15 (**Supplementary Table 5**). The mass spectrometer operated in positive ion mode at a 2.4 kV
16 needle voltage. Data were acquired using Xcalibur software (Version 4.4.16.14, ThermoFisher
17 Scientific, USA) in a data-dependent mode. MS scans (m/z 300-1650) were recorded at a
18 resolution of R = 60 000 (@ m/z 200) and a standard automatic gain control target within
19 50msec. Dynamic exclusion was set to 9s with a mass tolerance of ±10ppm and top speed
20 fragmentation in higher-energy collisional dissociation (HCD) mode was performed for the top 5
21 most abundant precursor ions. MS/MS scans with a target value of 200% were collected in the
22 ion trap with a maximum fill time of 28 msec. Additionally, only +2 to +5 charged ions were
23 selected for HCD fragmentation. Other settings were as follows: heated capillary temperature,
24 300°C; normalized HCD collision energy of 30% and an isolation width of 1.6 m/z.
25 Monoisotopic precursor selection (MIPS) was set to Peptide and an intensity threshold was set to
26 2×10^4 .

27 For cysteine redox analysis, liquid chromatography-mass spectrometry was conducted on a Q-
28 Exactive HFX mass spectrometer (ThermoFisher scientific) coupled to an UltiMate 3000
29 RSLCnano UHPLC (ThermoFisher Scientific). Peptides were separated on a home-packed

1 column (1.9 μm , 40 cm \times 75 μm 120 \AA pore size) of ReproSil Pur C₁₈ AQ beads (Dr. Maisch
2 GmbH, AmmerbuchEntringen, Germany) regulated at 60 °C with a PRSO-V2 Sonation column
3 oven. A binary gradient of Buffer A (0.1% formic acid) to Buffer B (90% ACN 0.1% formic
4 acid) from 5% to 98% buffer B was used to elute peptide over 90min at a rate of 300 nL / min.
5 The MS was coupled to a Nanospray Ion Source (ThermoFisher Scientific) and was operated in
6 positive ion data dependant acquisition mode with a needle voltage of 2.4 kV and ion transfer
7 capillary temperature of 300 °C. Precursor ions were surveyed with an AGC target of 1e6,
8 maximum fill time of 50ms and the orbitrap operating between 300-1650 m/z at a resolution of R
9 = 60000 at 200 m/z . The top 20 precursor ions with charges 2⁺ - 4⁺ were taken for higher
10 collisional energy dissociation with an isolation window of 1.4 m/z , AGC target of 3e6, maximum
11 ion fill time of 90ms and normalised collision energy of 27 (N)CE. This occurred with a dynamic
12 exclusion window of 15s. Fragment ions were detected with a resolution of R = 15000 at 200
13 $S/m/z$. For PRM experiments the MS was operated in data independent acquisition mode
14 consisting of a precursor ion scan followed by a loop of the scheduled inclusion list
15 (**Supplementary Table 6**). Peptides were monitored with 16 min acquisition windows. The
16 precursor ion scan occurred with a resolution of R = 30000 at 200 m/z and fragment ion scans
17 occurred with an isolation window of 0.7Da and a maximum fill time of 65 ms, otherwise MS
18 parameters were as stated above ($n=3$ injection replicates per sample).

19 **Mass spectrometry data analysis**

20 Raw data generated from immunoprecipitated protein extracts was processed using MaxQuant
21 software (Version 2.0.1.0, Max Planck Institute of Biochemistry, Planegg, Germany) under
22 default settings.³⁵ Spectra were screened against Uniprot entry P00441 (SODC-HUMAN),
23 corresponding to human SOD1, with peptides higher than 4600 Da or lower than 7 amino acids
24 excluded from further analyses. Search parameters were as follows: mass accuracy of the MIPS
25 precursor and peptide fragments was set to 10 ppm and 0.6 Da respectively. Only b- and y-ions
26 were considered for mass calculation. Oxidation of methionines (+16 Da) and protein N-terminal
27 acetylation (+42 Da) were considered as variable modifications for protein quantification,
28 whereas carbamidomethylation of cysteines (+57 Da) as well as carbamylation (+43 Da) of
29 lysines and residue N-termini were included as variable modifications for peptide identification

1 and quantification. Given the presence of I113T and D101G mutations in *SOD1*-fALS samples,
2 Xle->Thr and Asp->Gly were also included as variable modifications. PTMs of interest for
3 comparison between ALS subgroups and controls were analysed in separate analysis batches,
4 and included; 3-deoxyglucosone-derived hydroimidazolone (R; 144.0423), α -amino adipic acid
5 (K; +14.9633), acetylation (K; +42.0106), allysine (K; -1.0316), carboxyethyllysine (K;
6 +72.0211), carboxymethyllysine (K; 58.0055), deamidation (N/Q; +0.9840), glycation (K/R;
7 +108.0211 with neutral loss of three water molecules),³⁶ methylglyoxal-derived
8 hydroimidazolone (R; +54.0106)), nitration (W; +44.9976) oxidation (H/W; +15.9949),
9 phosphorylation (S/T; +79.9663), succinylation (K; +100.0160), ubiquitination (K; 114.0429). A
10 maximum of 5 modifications per peptide was allowed. Two missed trypsin cleavages were
11 allowed. LFQ protein abundance was calculated using the MaxLFQ algorithm embedded in
12 MaxQuant, requiring at least two ratio counts of unique peptides. Peptide validation was
13 performed using the Andromeda algorithm and peptides were excluded if they possessed an
14 andromeda score lower than 80 or a localization score lower than 0.8. The false discovery rate
15 (FDR) for both peptides and proteins was adjusted to less than 1% using a target and decoy
16 approach. The 'match between runs' option was enabled using a time window of 0.7 min. We
17 achieved an average sequence coverage of 97.2% for SOD1 protein identified in sample
18 immunoprecipitates. SOD1 protein was not identified in negative control immunoprecipitates
19 prepared using dynabeads that were not conjugated to our capture antibody, suggesting
20 negligible false discovery of SOD1 protein in ALS and control protein extracts. Modified peptide
21 intensities were normalised to SOD1 protein LFQ intensities to account for protein and/or
22 sample concentration variance. No differences in the relative levels of PTMs of interest were
23 identified between immunoprecipitated and non-immunoprecipitated commercial SOD1 protein
24 (**Supplementary Table 7**), implying our immunoprecipitation protocol did not significantly alter
25 PTMs of interest. Strong correlations between the abundance of SOD1 protein in technical
26 replicates, as well as the abundance of modified peptides in these replicates, highlights the
27 reproducibility of our experimental workflow (**Supplementary Figure 8**).

28 Raw data generated from samples prepared for cysteine redox analysis was processed using
29 Proteome Discoverer (ThermoFisher Scientific, version 2.4) and was searched against a *Homo*
30 *Sapiens* Uniprot database (release 2020_05) with an in-house Mascot server (Matrix Science,
31 London, UK) allowing for 2 missed trypsin cleavages and a minimum peptide length of 6

1 residues. Cys-*N*-ethylmaleimide (+125.05 Da) was set as a fixed modification and Cys-
2 methylthio (+45.99 Da), Met oxidation (+16.00 Da) and N/Q deamidation (+0.98 Da) as variable
3 modifications. A precursor mass tolerance of 20 ppm and fragment mass tolerance of 0.2 Da was
4 used with a strict FDR cut-off of 1% and relaxed FDR cut-off of 5%. The results from the DDA
5 experiment were then used to build a spectral library in Skyline (version 20.02). Chromatogram
6 integration was performed in Skyline and summed transition peak areas for each peptide were
7 taken for further processing. Each modified Cys peptide was normalised to two non-modified
8 SOD peptides to account for protein and/or sample concentration variance. Rather than
9 averaging these values, which would weight the normalization more towards one of the two non-
10 modified peptides, normalised peak areas for both non-modified peptides were expressed as a
11 ratio compared with the control diagnostic group, and were averaged to obtain final values.

12 **Glutathione quantification**

13 Glutathione concentrations were quantified in soluble extracts using a published Tietze
14 enzymatic recycling assay,³⁷ modified to be compatible with a microtitre plate
15 spectrophotometer. Protein was precipitated using 5% 5-sulfosalicylic acid, samples promptly
16 centrifuged (10,000g, 10min, 4°C), and supernatant collected and diluted five-fold using 20mM
17 Tris buffer (pH 8) to reduce 5-sulfosalicylic acid to 1% before assay commencement. All assay
18 steps were undertaken within an Atmosbag glove bag (Cat. # Z530212, Sigma-Aldrich, USA)
19 under anaerobic conditions (<1% O₂) using ultra-high purity nitrogen gas (99.999%, BOC
20 Healthcare), except for spectrophotometry measurements where plates were sealed with airtight
21 adhesive strips and transported to the microplate plate reader. Adhesive strips did not alter
22 sample absorption (**Supplementary Figure 9**). Anaerobic experimental conditions, together with
23 storage of post-mortem tissues and extracts at -80°C prior to analysis, greatly reduces glutathione
24 degradation, ensuring measurements are as close to endogenous glutathione levels as possible.³⁸

25 **Inductively coupled plasma-mass spectrometry (ICP-MS)**

26 Metal levels in soluble and insoluble tissue extracts were quantified using inductively coupled
27 plasma-mass spectrometry (ICP-MS), according to our group's published methods.³⁹ Soluble

1 extracts were thawed on ice and diluted with 1% nitric acid (1:10 v/v; Suprapur grade, Merk
2 Millipore) prior to analysis. Insoluble extracts were freeze-dried overnight, weighed, and
3 digested overnight using concentrated nitric acid (50 μ L, 70%, Suprapur grade, Merk Millipore)
4 at room temperature. Samples were then digested for a further 30min at 70°C, and incubated
5 with concentrated hydrogen peroxide (30%, VWH International, PA, USA) for 60min at 70°C,
6 and diluted with 1% nitric acid (1:10 v/v; Suprapur grade, Merk Millipore) prior to analysis.
7 Total metal levels in each sample were measured in triplicate using an Agilent Technologies
8 7700 ICP-MS system with a Teflon MiraMist concentric nebuliser and Scott-type double-pass
9 spray chamber (Glass Expansion, VIC, Australia). Buffer controls containing 1% nitric acid were
10 incorporated every 20 samples. Helium (3 mL/min) was used as a collision gas for removal of
11 polyatomic interferences. Measured mass-to-charge (m/z) ratios were 44 (Ca), 55 (Mn), 56 (Fe),
12 63 (Cu), 66 (Zn), 78 (Se), 111 (Cd). External calibration was performed using multi-element
13 standards (Sigma-Aldrich, USA) diluted in 1% HNO₃ and yttrium (Y; m/z = 89; Accustandard,
14 Connecticut, USA) was used as reference element via online introduction with a Teflon T-piece.
15 Measurements were background corrected to metal levels in buffer controls, adjusted for dilution
16 factors and were standardized against original wet tissue weights. Samples below the
17 instrument's limits of detection were excluded from analyses.

18 **Statistical analyses**

19 Statistical analyses were performed using IBM SPSS Statistics (Version 27, IBM, Armonk, New
20 York, United States) and GraphPad prism (Version 7.02, Graphpad, San Diego, CA, USA).
21 Parametric tests or descriptive statistics with parametric assumptions (standard two-way and one-
22 way ANOVA, Pearson's r and t-test) were used for variables meeting the associated assumptions,
23 with data normality assessed using either the D'Agostino-Pearson (omnibus K2) normality test
24 or the Shapiro-Wilk (Royston) normality test. Two- and one-way ANOVAs were paired with
25 Sidak's and Dunnet's multiple comparisons post-hoc tests, respectively, to assess pair-wise
26 comparisons between select diagnostic groups for a given variable. Non-parametric tests or
27 statistics (Kruskal-Wallis test, Spearman's r and Mann-Whitney U-test) were used for variables
28 where the observed data did not fit the assumptions of parametric tests, with Kruskal-Wallis tests
29 paired with Dunn's multiple comparisons post-hoc tests to assess pair-wise comparisons between

1 select diagnostic groups for a given variable. Where appropriate, non-parametric data were
2 transformed using $X=\text{Log}(X)$ or $X=\text{SQRT}(X)$ to meet parametric assumptions required for
3 grouped analyses using Two-way ANOVA. Outliers were identified using the combined robust
4 regression and outlier removal (ROUT) method with a maximum false discovery rate of 5%.
5 Final values were reported as mean \pm SEM. A p -value of less than 0.05 was accepted as the level
6 of significance. Details of the statistical tests employed (test statistics, sample sizes, p values) for
7 each variable of interest are included in the corresponding figure legend or results text section.
8 An n of 9 cases per diagnostic group was strongly powered to detect differences in SOD1
9 misfolding and conformational change (97.9-98.5% power, two-tailed t -test, $\alpha = 5\%$; SPSS
10 software, IBM, Armonk, NY, USA) in a preliminary power analysis of pilot data describing the
11 isoelectric point of wild-type SOD1 protein in the ventral spinal cord of a subset of sALS cases
12 ($n = 3$) and age-matched controls ($n = 3$). Difficulties in sourcing and obtaining appropriate
13 tissues from *SOD1*-fALS and non-*SOD1*-fALS cases limited the sample sizes of these diagnostic
14 groups, however retrospective power analyses reveal data from both groups were still strongly
15 powered to detect differences in many measured variables (SOD1 pI, % MNs exhibiting granular
16 disSOD1, SOD1 protein levels, SOD1 spec act.) compared with age-matched controls due to the
17 large effect sizes observed for these variables (77.2-100% power).

18 **Principal component analysis (PCA)**

19 PCA was performed, and corresponding plots constructed, using Rstudio 1.4.1717, R 4.1.0
20 (RStudio Team, RStudio: Integrated Development Environment for R, Boston, MA, USA) and
21 associated packages FactoMinerR 2.4,⁴⁰ missMDA 1.18,⁴¹ factoextra 1.0.7,⁴² and tidyverse
22 1.3.1.⁴³ The full reproducible code is available from the corresponding author upon reasonable
23 request. Active variables ($n=23$) for the principal component analysis (PCA) are : % motor
24 neurons containing granular SOD1 (MN_granular_disSOD1), SOD1 inclusions (MN_disSOD1),
25 granular CCS (MN_granular_CCS) and diffuse cytoplasmic CCS (MN_diffuse_CCS), motor
26 neuron density (neuronal_density), total (SOD1_act) and specific SOD1 activity
27 (SOD1_spec_act), SOD1 (SOD1_level) and CCS protein levels (CCS_level), Cu:Zn atomic ratio
28 within enzymatically-active soluble mature SOD1 (SOD1_CuZn_ratio), active SOD1 pI (pI),
29 glutathione levels (GSH), and copper and zinc levels in whole tissues (Total_Cu, Total_Zn), as

1 well as soluble and insoluble tissue extracts (Soluble_Cu, Soluble_Zn, Insoluble_Cu,
2 Insoluble_Zn). SOD1 PTM data was also included, although these were grouped based on
3 similarities in expected functional consequences; PTMox – oxidation His, Trp, Cys, nitration
4 Trp; PTMch – acetylation Lys, Phosphorylation Ser; PTMdeam – deamidation Asn; PTMage –
5 CEL Lys; GlyGly_Lys91. Supplementary variables (case #, clinical diagnostic, age, sex, post-
6 mortem interval (PMI), site of onset) do not influence on the PCA analysis and allow for easier
7 interpretation and visualisation of the results. The data were scaled before PCA and missing
8 values were processed with the missMDA package. Our PCA revealed no significant differences
9 in the relative levels of variables of interest between thoracic and cervical spinal cord levels
10 (**Supplementary Figure 10**). Thoracic and cervical spinal cord values were therefore averaged
11 for cases possessing data for both spinal cord levels, yielding one data point per case for grouped
12 statistical analyses.

13 **Data availability**

14 The data and materials that support the findings of this study are available from the
15 corresponding author upon reasonable request.

16 **Results**

17 **Disordered SOD1 conformers are mislocalized and accumulate in spinal cord** 18 **motor neurons of ALS cases.**

19 Nascent, unfolded human SOD1 is structurally-disordered and lacks antioxidant activity.⁴⁴
20 Maturation of these immature species to enzymatically-active, mature SOD1 dimers is
21 multifaceted, and hence SOD1 protein exists within healthy neurons as a complex mixture of
22 immature, intermediate and mature conformers.^{3,45} The accumulation of structurally-disordered
23 immature and intermediate conformers, hereon referred to as disordered (dis)SOD1, underlies
24 the self-assembly and toxicity of mutant and wild-type SOD1 *in vitro* and in transgenic SOD1
25 mice.^{46,47}

1 We employed immunohistochemistry to profile the subcellular distributions of mature and
2 disSOD1 conformers in 7 μ m fixed post-mortem ventral spinal cord tissue sections collected
3 from ALS patients and age-matched controls (**Supplementary Table 1**). Monoclonal and
4 polyclonal pan-SOD1 antibodies recognizing full-length human SOD1 (**Supplementary Table**
5 **3**) identified diffuse cytosolic SOD1 immunoreactivity in 94% of spinal cord motor neurons in
6 age-matched control cases (**Fig. 1a**), consistent with the primary subcellular localization of
7 enzymatically-active mature SOD1.⁴⁸ Faint SOD1-immunopositive cytoplasmic granules (2.5 -
8 6 μ m diameter) were observed within 10-20% of control spinal cord motor neurons (**Fig. 1a**),
9 which colocalized with cis-golgi (GM130; **Fig. 1b**) and endoplasmic reticulum (ER; calreticulin;
10 **Fig. 1b**) markers, indicating partial localization of SOD1 to these compartments in control spinal
11 cord motor neurons. Nuclear SOD1 immunostaining was also observed, consistent with a role for
12 SOD1 as a nuclear transcription factor regulating antioxidant response genes.⁴⁹ Owing to the
13 broad amino acid sequence coverage of their binding epitopes, pan-SOD1 antibodies
14 immunolabel multiple mature and immature SOD1 conformers, thus it is unclear which specific
15 conformers exist in each of these compartments.

16 Conformation-specific SOD1 antibodies can selectively detect immature disSOD1 conformers in
17 human post-mortem tissues. We probed adjacent control spinal cord sections with EDI, B8H10,
18 and U β B conformation-specific antibodies (**Supplementary Table 3**), producing strong granular
19 cytoplasmic SOD1 immunostaining within 66% of motor neurons, respectively, across all
20 control cases (**Fig. 1a**). Colocalization of granular cytoplasmic SOD1 immunostaining with
21 GM130 and calreticulin in sections probed with conformation-specific SOD1 antibodies (**Fig.**
22 **1b**) identified disSOD1 conformers within the ER-golgi network in control motor neurons,
23 constituting a physiological population of unfolded SOD1 in this compartment. A greater
24 intensity of nuclear SOD1 immunostaining in these sections compared with those probed with
25 pan SOD1 antibodies (**Fig. 1a**) suggests immature conformers may mediate the transcriptional
26 activity of SOD1, rather than the mature, enzymatically active protein. In contrast, low-intensity
27 diffuse cytosolic immunoreactivity was present within only 34% of control spinal cord motor
28 neurons in these tissue sections (**Fig. 1a**). This suggests disSOD1 conformers exist either
29 transiently, or in significantly lower abundance, within the cytosol of control motor neurons
30 under physiological conditions. Overall we show that mature SOD1 conformers likely constitute
31 the dominant SOD1 species in the cytoplasm of healthy spinal cord motor neurons, whilst

1 immature SOD1 conformers are present in relatively greater amounts in the nucleus and ER-
2 Golgi network of these neurons.

3 Using control motor neuron immunostaining as a baseline, we applied pan and conformation-
4 specific immunostaining to ventral spinal cord tissues from *SOD1*-fALS, non-*SOD1*-fALS and
5 sALS cases to evaluate mature and immature SOD1 deposition and subcellular localization. The
6 proportion of motor neurons possessing granular SOD1 immunostaining was reduced by 64-70%
7 in all ALS subgroups compared with controls (**Fig. 1d,e**), and was replaced by high-intensity
8 diffuse cytosolic disSOD1 and/or disSOD1 protein inclusions in the perikarya and neurites of
9 these neurons in all ALS cases (**Fig. 1f, Table 1**). Nuclear disSOD1 was also absent in ALS
10 spinal cord motor neurons at end-stage disease (**Fig. 1f**). Given the broad combined epitope
11 coverage of all antibodies employed, these data signify a subcellular re-distribution of disSOD1
12 conformers within vulnerable motor neurons in ALS; indeed, disordered SOD1 conformers were
13 primarily no longer localized to the ER-golgi network in these patients (**Fig. 1g**). Reductions in
14 spinal cord motor neuron density (**Fig. 1h**) were strongly correlated with lower proportions of
15 granular disSOD1 motor neurons (**Fig. 1i**), but not higher proportions of motor neurons
16 possessing disSOD1 inclusions (**Fig. 1j,k**). This is consistent with the involvement of smaller
17 disSOD1 assemblages, rather than larger insoluble SOD1 deposits, in SOD1-mediated neuronal
18 toxicity in ALS models.⁴⁷ Collectively, our findings indicate that immature disSOD1 conformers
19 are mislocalized to the cytoplasm from the nucleus and ER-Golgi network in ALS spinal cord
20 motor neurons by end-stage disease, where they accumulate and often form large inclusions.
21 These alterations are a reliable feature of all forms of ALS, which may be associated with motor
22 neuron degeneration.

23 **Enzymatically-dysfunctional SOD1 conformers are more abundant in the**
24 **ventral spinal cord of ALS cases.**

25 Efficient superoxide detoxification by SOD1 is highly dependent upon correct protein folding
26 and maturation.³ To assess whether the cytoplasmic mislocalization and accumulation of
27 immature disSOD1 conformers impacts superoxide clearance by SOD1, we quantified SOD1
28 enzymatic activity in fresh frozen tissue from the ventral and dorsal spinal cord of our post-
29 mortem cohort.²¹ Total SOD1 activity was unchanged in the ventral and dorsal spinal cord in all

1 ALS subgroups compared with controls (**Fig. 2a**), indicating similar superoxide buffering
2 capacities within these regions in ALS cases. These data are surprising considering oxidative
3 stress is widely reported within the ALS spinal cord¹⁸ an environment that would be expected
4 to result in an increased proportion of mature, enzymatically active SOD1 to increase superoxide
5 clearance.

6 Therefore, to investigate whether SOD1 protein production and/or maturation are dysregulated in
7 ALS, we quantified SOD1 protein levels using immunoblotting and calculated SOD1 enzymatic
8 activity per unit of protein (specific activity). Ventral spinal cord SOD1 protein levels were
9 moderately increased in all ALS subgroups compared with controls (2-2.9-fold; **Fig. 2b**),
10 however SOD1 specific activity was reduced by 55-75% in this region of all ALS cases (**Fig.**
11 **2c**). These data are consistent with reductions in SOD1 activity measured in red blood cells,
12 fibroblast and lymphoblast cell lines derived from *SOD1*-fALS patients.⁵⁰ Levels of total SOD1
13 protein and specific activity were unchanged within the non-degenerating (**Supplementary**
14 **Figure 11**) dorsal spinal cord (**Fig. 2b,c**) of all ALS cases, indicating these alterations are
15 restricted to regions of neuron death. Lower SOD1 specific activity was strongly correlated with
16 decreased motor neuron density and greater disSOD1 mislocalization to the cytoplasm in the
17 ventral spinal cord of ALS cases (**Fig. 2d,e**), consistent with a reduced viability of SOD1-
18 deficient neurons under conditions of redox imbalance in *Sod1*^{+/-} mice.^{18,50} Overall, these data
19 demonstrate enzymatically-dysfunctional SOD1 conformers selectively accumulate within
20 vulnerable regions of the spinal cord in ALS (**Fig. 2f**).

21 **Mature SOD1 destabilization may contribute to disordered SOD1 conformer** 22 **accumulation in ALS spinal cord.**

23 The accumulation of immature disSOD1 conformers in ALS motor neurons could result from
24 disruptions to pathways governing SOD1 protein maturation, or alternatively from the
25 destabilization of mature, enzymatically-active SOD1 dimers, hereon referred to as mature
26 SOD1. Mature SOD1 contains one zinc and copper ion per monomer, which together underlie its
27 exceptional structural stability and enzymatic activity. Immature SOD1, on the other hand,
28 exhibits a reduction in the binding of its metal cofactors, which underlies its greater structural
29 disorder and reduced enzymatic activity.³ We evaluated mature SOD1 stability and functionality

1 by quantifying metals bound to enzymatically-active SOD1 dimers (**Fig. 3a**).²⁶ Mature SOD1
2 purified from the ventral and dorsal spinal cord of control cases contained copper and zinc in an
3 exact 1:1 ratio (**Fig. 3b**),²⁶ consistent with the theoretical copper:zinc ratio bound to a mature
4 SOD1 dimer. By contrast, the copper:zinc ratio of mature SOD1 was significantly elevated in the
5 ventral spinal cord of 42% of ALS cases (5-of-12; 1 Cu : 0.6 Zn) compared with controls (**Fig.**
6 **3b**), including 2 *SOD1*-fALS (I113T and D101G *SOD1* mutants), 1 non-*SOD1*-fALS (*C9ORF*
7 hexanucleotide repeat expansion mutant) and 2 sALS cases. Mature SOD1 metallation was
8 unchanged in the non-degenerating occipital cortex of affected cases (**Supplementary Figure**
9 **12**), suggesting perturbed SOD1 zinc binding results from biochemical factors unique to the
10 ventral spinal cord. Our data provide the first evidence of alterations to the metallation of mature
11 mutant and wild-type SOD1 in a proportion of familial and sporadic ALS patients, which may
12 contribute to SOD1 pathology in these patients.

13 Alterations to SOD1 protein isoelectric point (pI) reflect conformational changes⁵¹ that can alter
14 both its aggregation propensity and the electrostatic guidance of anionic superoxide towards the
15 active site. Mature SOD1 pI was significantly elevated in the ventral spinal cord in all ALS
16 subgroups, and in the dorsal spinal cord of *SOD1*-fALS cases, compared with controls (**Fig.**
17 **3c,d**), suggestive of conformational changes to mature SOD1 in these regions. Whilst elevated
18 pIs in both spinal cord sub-regions of *SOD1*-fALS cases suggests *SOD1* mutations may
19 contribute to these alterations in *SOD1*-fALS, only one of the two mutant proteins examined in
20 this study exhibits a reduced surface charge compared with wild-type SOD1,⁵² implicating
21 alternative unknown factors. Likewise, the selectivity of this increase to the ventral spinal cord in
22 other ALS cases indicates non-genetic factors unique to this region underlie such changes in
23 these cases. Subcellular mislocalization of SOD1 to the cytoplasm within spinal cord motor
24 neurons, for example, may contribute to the reduction in mature SOD1 surface charge in this
25 region (**Fig. 3e**). Mature SOD1 pI was also increased in the ventral spinal cord of ALS cases
26 exhibiting SOD1 zinc deficiency ($n = 5$), compared with control ($n = 10$) and remaining ALS
27 cases ($n = 11$; **Fig. 3f**). Whilst conformational change in mature SOD1 was not associated with
28 reduced enzymatic activity (data not shown; Spearman's $r = -0.296$, $p = 0.13$), it was correlated
29 with greater motor neuron loss and deposition of SOD1 in the ventral spinal cord of ALS cases
30 (**Fig. 3g,h**), consistent with data demonstrating reduced surface charge of SOD1 dimers
31 promotes neurotoxic SOD1 aggregation from a native-like dimeric state *in vitro*.³ Overall, these

1 results indicate that conformational change and mismetallation of mature SOD1 may contribute
2 to the accumulation of dysfunctional, immature SOD1 conformers in the ventral spinal cord of
3 ALS patients.

4 **Zinc-deficient mature SOD1 is unlikely to undergo self-assembly from a**
5 **native-like dimeric state in ALS cases.**

6 To ascertain whether zinc-deficient mature SOD1 may indeed aggregate directly from a
7 disordered dimer-like state *in vivo*, we assessed whether the metal content of ventral spinal cord
8 disSOD1 deposits reflects the elevated copper:zinc ratio of soluble mature SOD1 in this region in
9 select ALS patients. Copper and zinc levels were quantified within 45 individual SOD1
10 aggregates, ranging from 2.5-30 μ m in diameter, and 25 areas of surrounding grey matter tissue
11 of a similar size, in frozen unstained ventral spinal cord sections from 3 *SOD1*-fALS and 1 sALS
12 case (**Fig. 4a,b**). Compton inelastic scattering was also measured simultaneously as an index of
13 tissue matter density, revealing increased density within SOD1 aggregates compared with
14 surrounding tissues (**Fig. 4c**). Normalization of metal levels to Compton scatter values ensured
15 that varying tissue matter densities between aggregates, as well as between aggregates and
16 surrounding tissues, did not confound interpretation of metal data. We identified a 70% increase
17 in zinc (**Fig. 4d**), and a 12% reduction in copper (**Fig. 4e**), within SOD1 aggregates compared
18 with surrounding grey matter tissues, constituting a significant decrease in the copper:zinc ratio
19 within SOD1 aggregates compared with surrounding tissues (**Fig. 4f**) and the copper:zinc ratio of
20 soluble mature SOD1 measured in these same cases (**Fig. 4g**). We speculate that these data
21 indicate zinc-deficient, copper-containing mature SOD1 may not form aggregates from a native-
22 like dimeric state *in vivo*. Instead, we propose that zinc-deficiency promotes mature SOD1
23 dissolution into alternative metal-deficient disSOD1 conformers, which subsequently aggregate,
24 as reported elsewhere.⁵³ We recognize that this may also involve the recruitment of additional
25 zinc-binding proteins, including CCS,²¹ which contribute to the reduced copper:zinc ratio within
26 SOD1 aggregates.

1 **SOD1 protein PTMs are altered specifically in the vulnerable ventral spinal**
2 **cord of ALS cases.**

3 The post-translational modification of key amino acid residue side chains within SOD1 protein
4 regulates its structure (**Fig. 5a,b**), maturation, metallation, subcellular localization and enzymatic
5 function.^{3,54} Recognizing that disSOD1 proteinopathy in ALS patients may result from altered
6 SOD1 PTMs, we constructed post-translational fingerprints of SOD1 protein
7 immunoprecipitated in its native state from post-mortem ventral and dorsal spinal cord of ALS
8 patients and controls, identifying 42 individual PTMs to 29 residues (19%) of SOD1 protein
9 across all diagnostic groups (**Fig. 5c, Supplementary Tables 8,9**).

10 Oxidation of SOD1 His48 and His63 was significantly increased (2-fold) in the ventral spinal
11 cord of ALS cases possessing Zn-deficient soluble SOD1, compared with controls and remaining
12 ALS cases (**Supplementary Tables 8,9**). This finding is consistent with a role for oxidation of
13 metal-coordinating His residues in inducing SOD1 mismetallation *in vitro*⁵⁵ (**Fig. 5d**).
14 Significant increases in Trp32 oxidation (1.7-fold) and nitration (3.4-fold) were also identified
15 within SOD1 protein isolated from the ventral spinal cord of three *SOD1*-fALS and five sALS
16 cases, respectively, compared with controls (**Supplementary Tables 8,9**). Considering the role
17 of this residue in redox-induced aggregation and propagation of disSOD1 in cellular and animal
18 models of ALS⁵⁶ (**Fig. 5e**), these modifications may contribute to the development of SOD1
19 proteinopathy in affected cases.

20 Whilst Lys succinylation was unchanged between ALS cases and controls (**Supplementary**
21 **Table 8**), Lys3 acetylation and Ser98 phosphorylation were significantly reduced in six and four
22 sALS cases, respectively, compared with controls (**Supplementary Tables 8,9**). Although
23 reduced Lys3 acetylation may increase the susceptibility of Lys3 to destabilizing PTMs, we did
24 not detect any increase in oxidation of this residue between diagnostic groups (**Supplementary**
25 **Table 8**). This reduction may, however, underlie the elevated active SOD1 pI in these cases (**Fig.**
26 **3**), which is proposed to promote SOD1 aggregation and intercellular propagation *in vitro*.⁵⁷
27 Functionally, neither alteration is likely to underlie reduced SOD1 specific activity within the
28 ventral spinal cord of sALS patients given their respective locations within SOD1's dimer
29 interface and β -barrel (**Fig. 5f**). Reduced Ser98 phosphorylation may, however, impede SOD1-

1 mediated transcription of protective antioxidant genes by impairing SOD1 nuclear
2 translocation.⁴⁹

3 Deamidation of Gln15, Asn26, Asn53 and Asn131 was significantly increased in mutant SOD1
4 protein isolated from the ventral spinal cord of all *SOD1*-fALS cases compared with controls
5 (**Supplementary Tables 8,9**). Comparatively mild (2-fold) increases in Asn26 deamidation may
6 destabilize local hydrogen bonding networks in loop II, with similar increases in Gln15
7 deamidation capable of disrupting hydrogen bonding across the dimer interface to diminish
8 dimer stability (**Fig. 5g**). Excessive (>10-fold) deamidation of Asn53 within the disulfide loop
9 GDNT motif, and Asn131 within the electrostatic loop, on the other hand, can significantly
10 impact coupling of SOD1 to copper chaperone for SOD1 (CCS) and greatly reduce the stability
11 of mature SOD1 dimers^{3,58} (**Fig. 5g**). This may promote SOD1 aggregation in these patients.

12 Whilst no sites of glycation were detected within SOD1 protein isolated from ALS cases and
13 controls, levels of the advanced glycation end-product carboxyethyllysine were elevated at
14 electrostatic loop residues Lys122 and Lys128 in mutant SOD1 protein isolated from ventral
15 spinal cord of all *SOD1*-fALS cases compared with controls (**Supplementary Tables 8,9**). *In*
16 *vitro* data suggest charge alterations resulting from these PTMs may disrupt superoxide diffusion
17 towards the active site⁵⁹ and alter stabilizing bonds between the electrostatic and disulfide loops,
18 promoting structural disorder and aggregation⁶⁰ (**Fig. 5h**).

19 Tryptic digestion of ubiquitin-conjugated proteins results in Gly-Gly dipeptide remnants on
20 conjugated lysine residues, which serve as indicators of protein ubiquitination.⁶¹ Consistent with
21 immunohistochemical analyses of SOD1 aggregates previously reported by our group,²¹ we
22 identified a significant 2.5-fold increase in ubiquitination of mutant SOD1 at Lys91 in all *SOD1*-
23 fALS cases compared with controls (**Supplementary Tables 8,9**), indicative of efforts by the
24 ubiquitin-proteasome system to clear mutant disSOD1 from the ventral spinal cord of these
25 cases. It is unclear why similar elevations in ubiquitination were not observed in non-SOD1-
26 fALS or sALS cases exhibiting wild-type disSOD1 deposition, which suggests wild-type
27 disSOD1 does not elicit the same proteostatic response from the UPS as mutant SOD1.

28 Analysis of free thiol groups in whole protein extracts prepared specially for cysteine redox
29 analysis³⁴ revealed 2- and 4-fold increases in reversible PTMs to Cys57 and Cys146,
30 respectively, in mutant SOD1 protein isolated from the ventral spinal cord of all *SOD1*-fALS

1 cases, and in wild-type SOD1 protein isolated from the ventral spinal cord of one sALS case,
2 compared with controls and remaining ALS cases (**Fig. 5i, Supplementary Tables 8,9**). Whilst
3 the identity of these modifications remains unclear, increases in any candidate modification –
4 sulfenic acid, S-nitrosylation, S-glutathionylation, S-palmitoylation, disulfide bonding –
5 negatively impacts the subcellular localization, structure and/or aggregation propensity of SOD1
6 protein *in vitro*.⁶²⁻⁶⁴ Indeed, all four cases exhibiting elevated reversible cysteine modifications
7 possessed significantly higher SOD1 aggregate densities compared with other ALS cases
8 examined (**Supplementary Table 9**), consistent with a role for redox-induced aggregation of
9 SOD1 in these cases.⁶⁵ It is unclear whether these modifications are upstream or downstream of
10 redox imbalance documented in this region,¹⁸ however we speculate that they likely form a cycle
11 culminating in oxidative stress and a deteriorating antioxidant capacity within ALS spinal cord
12 motor neurons. Whilst we did not identify irreversible Cys PTMs in these cases (sulfinic/sulfonic
13 acid), the greater magnitude of corresponding reductions in unmodified Cys57 (9.3-fold) and
14 Cys146 (8.8-fold) residues (**Fig. 5j, Supplementary Table 8**) compared with reversible PTMs
15 (2-to-4-fold) in these cases suggests they may be present but are undetectable in complex whole
16 protein extracts.

17 In summary, we identified significant differences in levels of 15 PTMs to 14 SOD1 protein
18 residues (9%) across 69% of ALS cases compared with controls (**Fig. 5k, Supplementary Table**
19 **8,9**). Importantly, only one of these alterations was also present in the dorsal spinal cord of
20 affected cases (**Supplementary Table 8**), suggesting that the unique biochemical environment of
21 the diseased ventral spinal cord may underlie alterations to SOD1 PTMs in these cases. Further
22 examinations into these unknown pre-disposing factors for each altered PTM are warranted.

23 **Disruptions to pathways governing SOD1 protein maturation may contribute** 24 **to SOD1 pathology in ALS cases.**

25 In addition to direct alteration of SOD1 protein biochemistry, the impairment of key molecular
26 chaperones facilitating SOD1 protein maturation promotes disSOD1 proteinopathy *in vitro*.^{66,67}
27 To evaluate whether disrupted CCS may contribute to disSOD1 pathology in our ALS cases we
28 profiled the subcellular distribution of CCS protein within spinal cord motor neurons and
29 quantified CCS protein levels. Monoclonal and polyclonal antibodies recognizing full-length

1 human CCS (**Supplementary Table 3**) identified CCS protein within cytoplasmic granules of a
2 similar size and shape to those described for immature disSOD1 in approximately 37% of control
3 spinal cord motor neurons (**Fig. 6a**), consistent with preferential binding of CCS to immature
4 SOD1 to promote metal insertion and maturation to mature SOD1.^{66,67} Low-intensity diffuse
5 cytosolic CCS immunoreactivity was virtually absent within control spinal cord motor neurons
6 (**Fig. 6a**) **Supplementary Table 10**).

7 The proportion of motor neurons possessing granular CCS immunostaining was significantly
8 reduced in all ALS subgroups compared with controls (**Fig. 6a,b**), indicating alterations to the
9 subcellular localization of CCS within these neurons. The proportions of motor neurons lacking
10 granular CCS and disSOD1 immunostaining were strongly correlated (**Fig. 6c**), suggesting CCS
11 either contributes, or responds, to disSOD1 mislocalization to the cytoplasm. Diffuse CCS
12 cytoplasmic staining was more intense and more prevalent in motor neurons of ALS cases
13 compared with controls (**Fig. 6a,d**), and was associated with strong diffuse disSOD1 pathology
14 (**Supplementary Figure 13**). CCS protein levels were significantly increased in the ventral, but
15 not dorsal, spinal cord of ALS cases compared with controls (**Fig. 6e**), and CCS and SOD1
16 protein levels were strongly correlated in the ventral spinal cord (**Fig. 6f**). CCS-immunopositive
17 protein inclusions of varying morphologies were also observed in the perikarya and neuritic
18 processes of 67-88% of *SOD1*-fALS motor neurons, as well as occasionally (<10%) in motor
19 neurons of two non-*SOD1*-fALS and three sALS cases (**Fig. 6a**, **Supplementary Table 10**).

20 Glutathione in its reduced redox state (GSH) can also facilitate SOD1 copper loading and
21 disulfide bond formation.⁶⁸ We quantified a 2.5-to-14-fold reduction in GSH concentrations
22 between all ALS subgroups compared with controls (**Fig. 6g**). Considering reductions in GSH
23 were correlated with reductions in SOD1 specific activity (**Fig. 6h**), we speculate that alterations
24 to CCS-independent SOD1 maturation pathways may contribute to immature disSOD1
25 accumulation in ALS patients by attenuating SOD1 copper loading.

26 Aside from disruptions to molecular chaperones governing SOD1 maturation, reduced copper or
27 zinc bioavailability may contribute to SOD1 mismetallation in ALS cases (**Fig. 3, 4**). We
28 identified a 47-71% increase in whole tissue zinc levels in the ventral and dorsal spinal cord of
29 all ALS subgroups except the *SOD1*-fALS dorsal spinal cord (**Fig. 6i**), suggesting mature SOD1
30 zinc-deficiency in select ALS cases is not likely to arise from a bulk reduction in zinc

1 bioavailability. Copper levels remained unchanged in these tissues (**Fig. 6h; Supplementary**
2 **Table 11**). To assess whether the compartmentalization of copper or zinc may also be altered in
3 these patients, we partitioned whole tissue extracts into cytosolic and interstitial components
4 (soluble fraction), and those encased within membranes, cellular organelles and other
5 compartments (insoluble fraction).³⁹ Whilst zinc levels remained significantly elevated in both
6 tissue fractions (**Fig. 6i**), copper was reduced 28-49% selectively in the soluble ventral spinal
7 cord tissue fraction of all ALS subgroups compared with controls (**Fig. 6i**). Our data suggest zinc
8 is elevated globally in all subcellular compartments of both spinal cord subregions, whilst copper
9 is reduced selectively within the cytosol of ALS spinal cord motor neurons and glia, and the
10 surrounding interstitium. Strong correlations between these biometal alterations and CCS protein
11 levels reinforce a regulatory role for these metals in CCS expression⁶⁹ (**Fig. 6j,k**), whilst
12 additional correlations with higher proportions of motor neurons lacking granular disSOD1 or
13 CCS immunostaining (**Fig. 6l,m**) suggests immature disSOD1 and CCS mislocalization to the
14 cytoplasm are associated with biometal dysregulation in the ventral spinal cord. Copper
15 redistribution within this region was also associated with reduced GSH (**Fig. 6n**), consistent with
16 a role for GSH in cellular copper handling,⁷⁰ which may impact SOD1 specific activity in ALS
17 patients by reducing the availability of SOD1's catalytic copper cofactor (**Fig. 6o**).

18 Collectively we provide the first post-mortem tissue-derived evidence that alterations to cellular
19 biometals and molecular chaperones facilitating SOD1 protein maturation may contribute to
20 SOD1 mismetallation, aggregation, enzymatic dysfunction and subcellular redistribution in the
21 ventral spinal cord of ALS patients.

22 **Alterations to SOD1 biochemistry clearly demarcate ALS cases from controls**

23 Alterations to SOD1 biochemistry, metallochaperones, and tissue biometal levels, were
24 identified in all ALS cases compared with controls, indicating such factors may constitute
25 biomarkers for ALS. By applying a principal component analysis (PCA) to 23 parameters
26 examined in this study we were able to accurately distinguish ALS cases from controls (**Fig 7a**).
27 The first three dimensions of this analysis accounted for the majority (64.6%) of variation
28 between cases, with the clear separation of ALS cases from controls largely a result of dimension
29 1. This suggests that variables which contributed most to this dimension should be investigated

1 further as potential biomarkers of ALS; disSOD1 and CCS subcellular localization, disSOD1
2 deposition, active SOD1 surface charge (pI) and tissue zinc levels (**Fig 7b**).

3 Importantly, we did not observe a clear separation of *SOD1*-fALS, non-*SOD1*-fALS and sALS
4 cases across the three primary PCA dimensions (**Fig 7a**). This is consistent with mounting data
5 demonstrating similarities in the biochemistry of aberrant wild-type and mutant SOD1
6 proteinopathy in familial and sporadic forms of ALS.³ When considered as a single cohort
7 however, we note substantial dispersion of ALS cases across dimensions 2 and 3 of our analysis.
8 This is indicative of substantial heterogeneity in alterations to SOD1 biochemistry between
9 individual ALS cases, in particular whole tissue copper levels, multiple SOD1 PTMs, SOD1
10 activity and soluble SOD1 metallation (**Fig 7c,d**). It is possible that such dispersion of ALS cases
11 may arise from differences in the site of disease onset (limb vs bulbar; **Fig 7e**), or from
12 differences between ALS patient subgroups (SOD1-fALS vs sALS).

13 Despite substantial heterogeneity in alterations to SOD1 biochemistry between ALS patients, our
14 data suggest SOD1 biochemistry and other variables measured in this study may be able to
15 distinguish ALS cases from controls, warranting further studies examining these factors in larger
16 patient cohorts post-mortem and in the clinic.

17 Discussion

18 Despite several decades of intensive research into ALS-associated disease mechanisms in
19 cellular and animal models of SOD1 proteinopathy, this is the first study to construct distinct
20 profiles of the subcellular localization, relative abundance and deposition of mature and
21 immature SOD1 conformers in spinal cord motor neurons of familial and sporadic ALS cases,
22 and age-matched controls. We demonstrate that while large SOD1 protein inclusions are not
23 reliable hallmarks of disease in spinal cord motor neurons of non-*SOD1*-linked fALS and sALS,
24 the mislocalization of immature, structurally-disordered SOD1 from the nucleus and ER-Golgi
25 network to the cytoplasm are characteristic of this vulnerable region in all forms of ALS. The
26 presence of soluble or insoluble disSOD1 in non-*SOD1*-fALS and sALS cases is currently
27 controversial.^{4-12,24} We and others⁹ posit this largely derives from methodological differences
28 between studies. Accordingly, our disSOD1 immunostaining protocol adhered to logical

1 guidelines recently proposed by Pare and colleagues for the use of conformation-specific SOD1
2 antibodies,⁹ which aim to minimize false-positives whilst maximizing tissue antigenicity to avoid
3 false-negatives.

4 Accompanying our profiles of mature and immature SOD1 abundance, subcellular localization
5 and deposition, we provide the first evidence that immature disSOD1 accumulation in the
6 cytoplasm of ALS spinal cord motor neurons likely arises from both the destabilization of mature
7 SOD1 and from abnormalities in SOD1 maturation in this region of ALS patients. Our novel
8 SEC-nIEF workflow is the first to ensure metallation analyses focus selectively on
9 enzymatically-active mature SOD1,²⁶ identifying reduced zinc binding and conformational
10 change within mature SOD1 dimers; a finding which has yet to be reported in any transgenic
11 ALS model. We are also the first to conduct such analyses on SOD1 protein isolated in it's
12 native state from human tissues, a factor which we propose is likely to underlie discrepancies
13 between our results and those previously reported from human SOD1-overexpressing transgenic
14 animal and cellular models of ALS. Whilst such over-expression is able to generate a robust ALS
15 phenotype in these models, even wild-type human SOD1 is frequently isolated from these
16 systems exhibiting reduced metallation,^{71,72} questioning whether changes identified accurately
17 resemble those characterizing human ALS patients. Indeed, Lelie and colleagues⁷¹ found copper
18 and zinc binding by endogenous mouse SOD1 was much closer to the expected 1:1 ratio
19 compared with wild-type (Cu:Zn – ~1:3) and mutant (Cu:Zn – ~1:2.2) human SOD1 isolated
20 from the spinal cord of transgenic mice of the same strain. These discrepancies are proposed to
21 arise from the over-saturation of endogenous metallochaperones driving SOD1 metallation, or
22 from dissimilarities between endogenous and transgenic human SOD1 proteins, warranting
23 further investigation.

24 We also provide preliminary evidence of disruptions to SOD1's molecular chaperones, CCS and
25 GSH, as well as atypical post-translational modification of structural motifs (e.g. GDNT)
26 governing the maturation of SOD1 in ALS post-mortem tissues. Whilst a previous study by
27 Watanabe and colleagues⁷³ only identified CCS-immunopositive inclusions in lumbar spinal cord
28 motor neurons of one-of-seventeen sALS cases, and neither of two *SOD1*-fALS cases, we
29 highlight substantial differences in methodology between this and our study; spinal cord sub-
30 regions examined, antibodies and dilutions employed and number of spinal cord sections

1 analyzed per patient. Perhaps most importantly for *SOD1*-fALS cases, we analyzed tissues from
2 patients carrying I113T and D101G *SOD1* mutations, which likely impact SOD1-CCS coupling
3 and metal transfer differently compared with A4V and unknown *SOD1* mutants examined by
4 Watanabe et al.⁷³ This has already been demonstrated to some extent *in vitro*,⁷⁴ whereby CCS is
5 reported to possess a reduced efficacy in promoting zinc binding to mutant disSOD1 compared
6 with wild-type SOD1.⁷⁴ We speculate that this suggests structural disorder in immature mutant or
7 wild-type proteins could subsequently result in under-metallation of mature SOD1 or SOD1
8 aggregate precursors, warranting further investigation. CCS also influences the subcellular
9 compartmentalization of disSOD1 within organelles such as mitochondria by modulating SOD1
10 disulfide status.⁷⁵ This suggests CCS mislocalization may precede and drive that of disSOD1 in
11 ALS spinal cord motor neurons, although alterations to CCS biochemistry have not been
12 thoroughly investigated in ALS post-mortem cases to date. Further profiling of chaperone-SOD1
13 interactions under physiological and pathological conditions is required to confirm the potential
14 roles of CCS and GSH in the development of atypical SOD1 proteinopathy in ALS.

15 Many of the altered SOD1 PTMs in this study promote disSOD1 accumulation,^{49,76} self-
16 assembly and mislocalization *in vitro*,^{3,54} and are thus also likely to contribute to the
17 development of disSOD1 proteinopathy in the vulnerable ventral spinal cord of ALS patients.
18 Indeed, immature disSOD1 protein is thought to exist on the precipice of aggregation, with even
19 small disturbances in charge or hydrophobicity capable of surpassing small energy barriers
20 between folding states to promote self-assembly.⁷⁷ Additionally, the absence of all but one of
21 these alterations in the dorsal spinal cord of our ALS cases suggests SOD1 proteinopathy is
22 promoted selectively within the ventral spinal cord by endogenous biochemical factors within
23 this region.

24 Importantly, whilst the majority of biochemical changes to SOD1 identified in this study are
25 specific to the ventral spinal cord, this does not necessarily equate to an aetiological contribution
26 of all of these factors in motor neuron degeneration. Using our post-mortem data alone, it is
27 difficult to establish whether alterations to SOD1 biochemistry precede, or follow, motor neuron
28 death in ALS patients. It is indeed possible that some of the observed changes are attributable to
29 cell death pathways activated by alternative aetiological factors, rather than any important
30 SOD1-dependent mechanism. This is certainly the case for factors we report herein for the first

1 time or which are seldom investigated elsewhere to date – disSOD1 and CCS subcellular
2 mislocalization, and alterations to SOD1 phosphorylation, deamidation, acetylation. Whilst
3 reported structural and/or functional consequences of such changes for SOD1 may often imply
4 associations with neuronal damage,^{49,58,75} direct examination of the cytotoxicity of these
5 perturbations is required to examine any causal relationships. For other alterations, however,
6 there is ample data from cellular and animal models of ALS to suggest an aetiological link with
7 ALS; hence the inclusion of these variables for investigation in this study. Soluble disSOD1
8 conformers are widely linked to the protein's toxicity in cellular and animal models of
9 ALS,^{46,47,80} especially those that are metal-deficient^{53,81} or are atypically oxidized⁸² or glycated.⁸³
10 Taken together, we posit that our data implicate mechanisms of SOD1-dependent toxicity in the
11 death of spinal cord motor neurons in ALS patients.

12 Interestingly, substantial heterogeneity in the post-translational profile of SOD1 protein between
13 ALS cases (**Supplementary Table 9**) suggests molecular mechanisms resulting in SOD1
14 proteinopathy and toxicity are variable between individual ALS patients, which may contribute
15 to variability in disease progression in affected individuals. A similar concept was proposed by
16 Wang and colleagues,⁸⁴ who reported biochemical differences between mutant SOD1 proteins
17 accounted for 69% of variability in *SOD1*-fALS patient survival times. Heterogeneity in
18 additional disease-linked mechanisms between our ALS cases may combine with disSOD1
19 proteinopathy to influence rates of disease progression, including TDP-43 mislocalization and
20 deposition, reported in a related study. The presence of multiple PTM alterations to SOD1 in
21 63% of cases examined (**Supplementary Table 9**) also indicates several pathways resulting in
22 SOD1 self-assembly may be present in many patients. Mechanistically, we speculate that
23 structural disorder induced by *SOD1* mutations, or early-stage alterations to SOD1 PTMs, may
24 promote subsequent alterations by increasing the solvent accessibility of new PTM sites. This
25 may explain the greater number of alterations to mutant SOD1 in our *SOD1*-fALS cases
26 compared with wild-type SOD1 in other ALS cases, although this may differ for other mutations
27 not examined herein. Considering the similar disSOD1 conformations identified between cases
28 using conformation-specific disSOD1 antibodies, we posit that these distinct pathways often
29 culminate in common structural endpoints, reinforcing existing studies demonstrating similar
30 disordered motifs within mutant and wild-type SOD1 proteins in ALS patients.⁴

1 Heterogeneity in ALS-linked pathologies has no doubt contributed to the limited success of past
2 clinical trials in this disorder, suggesting multimodal or personalized treatment approaches may
3 be required to meaningfully attenuate disease progression. For example, we reason that the
4 cysteine-reactive compound Ebselen is unlikely to improve SOD1 folding and maturation in
5 patients exhibiting redox modification of SOD1's cysteine residues,⁸⁵ and cases exhibiting
6 increased oxidation of key proteins such as SOD1 are likely to respond better to antioxidant
7 therapies. Similar categorization of *SOD1*-fALS patients into metal-binding-region and wild-
8 type-like *SOD1* mutants has already been proposed to identify those most likely to respond to
9 copper supplementation using diacetylbis(4-methylthiosemicarbazonato)copper^{II} (Cu^{II}(atsm)),
10 given the negligible protection reported in cultured cells expressing metal-binding-region SOD1
11 mutants compared with wild-type-like mutants.⁸⁶ A notable caveat of this proposal is the current
12 lack of clinical diagnostic assays capable of differentiating these patient subgroups, which will
13 be key to the successful implementation of such personalized approaches. Whilst our study
14 provides preliminary evidence that heterogenous SOD1 biochemistry between ALS patients may
15 enable such stratification of these patients into subgroups that are more amenable to specific
16 therapeutic approaches, difficulties in sourcing greater numbers of familial (SOD1, C9ORF)
17 ALS cases prevents any concrete conclusions being drawn. Further studies examining these
18 factors in larger patient cohorts are warranted.

19 Overall, we provide post-mortem evidence of pathways of SOD1 neurotoxicity in the spinal cord
20 of ALS patients, which have previously only been characterized in cellular and animal models of
21 ALS. Altered SOD1 biochemistry clearly differentiates all forms of ALS from controls,
22 indicating SOD1 likely constitutes a valuable therapeutic target in all patient groups, irrelevant of
23 *SOD1* gene status.

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1 **Author contributions**

2 B.G.T. and K.L.D. designed the study and obtained human research ethics approval, and together
3 with S.G. obtained and processed human tissues for subsequent analyses. B.G.T., S.G., V.C. and
4 A.A. performed immunostaining and quantification. B.G.T. performed immunoblotting and
5 immunoprecipitation, and quantified SOD1 activity and GSH levels. B.G.T. and S.R. conducted
6 nIEF experiments for measuring SOD1 pI, whilst S.R., F.P., A.C., R.O., Y.R., S.C., S.V.M. and
7 G.F. conducted SEC-nIEF, mass spectrometry, PIXE and SXRF experiments to assess active
8 SOD1 metallation. S.G. and D.J.P. performed XFM to measure SOD1 aggregate metal content.
9 B.G.T., A.A. and J.A. conducted mass spectrometry for quantification of SOD1 PTMs. A.R.,
10 M.W. and S.C. conducted cysteine redox mass spectrometry analyses. B.G.T. and D.H.
11 performed ICP-MS experiments to quantify tissue metal levels. K.K. and P.J.C. performed
12 analyses of commercial SOD1 metallation before and after immunoprecipitation. J.A.F., A.H.,
13 N.G. and I.P.B. performed *SOD1* and *C9ORF72* genotyping experiments. B.S., C.T., C.V., C.S.
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16 manuscript with input from all authors.

17 **Competing interests**

18 All authors report no conflicts of interest.

19 **Supplementary material**

20 Supplementary material is available at *Brain* online.

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1 **Figure Legends**

2 **Figure 1. DisSOD1 accumulation, aggregation and mislocalization in the vulnerable ventral**
3 **spinal cord of ALS cases. a,** Pan-SOD1 antibodies, as well as conformation-specific antibodies
4 raised against disordered mutant SOD1 (B8H10), disordered SOD1 with an exposed dimer
5 interface (EDI) and disordered SOD1 with an unfolded β -barrel (UBB) were employed to profile
6 the distribution of mature SOD1 and disSOD1 conformers within control ($n = 10$) ventral spinal
7 cord tissues. These SOD1 antibodies (**Supplementary Table 3**) detected granular cytoplasmic
8 staining (arrowheads) and diffuse cytosolic staining (arrows) within control motor neurons. **b,**
9 Visualization of granular SOD1 immunostaining within control spinal cord motor neurons using
10 the UBB conformation-specific SOD1 antibody and DAB chromogen. Granular SOD1
11 immunostaining strongly colocalized with the ER-golgi markers Calreticulin and GM130 in
12 control motor neurons. DAPI was also employed to visualize cell nuclei. **c,** No immunostaining
13 was observed in spinal cord tissue sections processed as above in the absence of primary
14 antibodies. **d,** Motor neurons possessing granular SOD1 immunostaining were less abundant in
15 all ALS subgroups compared with controls (One-way ANOVA: $p < 0.0001$, $F = 55.82$; Dunnet's
16 multiple comparisons post-hoc tests: $p < 0.0001$ for all comparisons). **e,** Granule numbers within
17 surviving ALS motor neurons exhibiting granular SOD1 immunostaining were equivalent to
18 those within control motor neurons (Kruskal-Wallis H test, $p = 0.073$, $H = 6.975$). **f,** In addition
19 to granular and diffuse cytosolic immunostaining, conformation-specific antibodies labelled a
20 variety of disSOD1 inclusions in ventral spinal cord motor neurons of *SOD1*-fALS ($n = 3$), non-
21 *SOD1*-fALS ($n = 4$) and sALS ($n = 9$) cases; punctate inclusions (dotted arrowheads), globular
22 inclusions (single downwards arrowheads) and fibrillar skein-like inclusions (double downwards
23 arrowheads). Case numbers (**Supplementary Table 1**) are listed in the top left corner of each
24 panel of **a** and **f**. **g,** Disordered SOD1 conformers immunolabelled by the UBB SOD1 antibody
25 were not colocalized with the ER-golgi markers Calreticulin and GM130 in motor neurons of
26 ALS cases. DAPI was also employed to visualize cell nuclei. Scale bars in **a**, **b**, **c**, **f** and **g**
27 represent $25\mu\text{m}$. **h,** Significant reductions in motor neuron density were observed in all ALS
28 subgroups compared with controls (One-way ANOVA: $p < 0.0001$, $F = 30.65$; Dunnet's multiple
29 comparisons post-hoc tests: $p < 0.0001$ for all comparisons). **i,** The proportion of granular spinal

1 cord motor neurons was correlated with great indices of motor neuronal loss in the ventral spinal
 2 cord. **j**, The proportion of motor neurons (MNs) with punctate, globular and skein-like disSOD1
 3 inclusions was higher in *SOD1*-fALS cases compared with non-*SOD1*-fALS and sALS cases
 4 (One-way ANOVA: $p = 0.0011$, $F = 13.39$; Dunnet's multiple comparisons post-hoc tests: non-
 5 *SOD1*-fALS: $p = 0.0008$; sALS: $p = 0.002$). Data in **d**, **e**, **h**, and **j** represent mean \pm SEM.
 6 * $p < 0.05$, *** $p < 0.001$, **** $p < 0.0001$. **k**, The proportion of spinal cord motor neurons with
 7 disSOD1 inclusion pathology was not correlated with neuronal loss in the ventral spinal cord.
 8 Spearman's r coefficient, the p value and the number of XY pairs analysed (n) are stated within
 9 panels **i** and **k**. A correlation is strong if Spearman's $r = 0.5$ or higher.

10 **Figure 2. Alterations to SOD1 protein levels and SOD1 specific activity, but not total SOD1**
 11 **activity, in the vulnerable ventral spinal cord of all ALS cases.** **a**, Total SOD1 antioxidant
 12 activity was unchanged in the ventral and dorsal spinal cord of ALS cases compared with
 13 controls (Two-way ANOVA; $F(3, 36) = 1.888$, $p = 0.1491$). **b**, SOD1 protein levels were
 14 significantly increased in the VSpC (Two-way ANOVA with Sidak's multiple comparisons post-
 15 hoc test; *SOD1*-fALS: $p = 0.0035$; non-*SOD1*-fALS: $p = 0.03$; sALS: $p = 0.0065$), but not DSpC
 16 (*SOD1*-fALS: $p = 0.677$; non-*SOD1*-fALS: $p = 0.974$; sALS: $p = 0.999$), of all ALS subgroups
 17 compared with controls. Representative SOD1 immunoblots (SOD1₂ antibody, **Supplementary**
 18 **Table 3**) and Sypro Ruby blot staining for total protein in the VSpC are shown. **c**, SOD1 specific
 19 activity (antioxidant activity per unit of SOD1 protein) was significantly decreased in the VSpC
 20 (Two-way ANOVA with Sidak's multiple comparisons post-hoc test; *SOD1*-fALS: $p = 0.0488$;
 21 non-*SOD1*-fALS: $p = 0.0011$; sALS: $p = 0.0002$), but not DSpC (Two-way ANOVA with
 22 Sidak's multiple comparisons post-hoc test; *SOD1*-fALS: $p = 0.495$; non-*SOD1*-fALS: $p =$
 23 0.661 ; sALS: $p = 0.724$), of all ALS subgroups compared with controls. Data in a-c represent
 24 mean \pm SEM. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$. **d,e** Reductions in SOD1 specific activity were
 25 strongly correlated with higher indices of neuron loss (**d**) and greater proportions of motor
 26 neurons lacking granular staining with UBB conformation-specific SOD1 antibody (**e**).
 27 Spearman's r coefficient, p values and the number of XY pairs analysed (n) are stated within
 28 panels **d** and **e**. A correlation is strong if Spearman's $r = 0.5$ or higher.

29 **Figure 3. Mature SOD1 metallation and surface charge are altered in the vulnerable**
 30 **ventral spinal cord of ALS cases.** **a**. Experimental workflow for measuring mature SOD1 metal

1 content after purification of SOD1 from post-mortem tissue protein extracts.²⁶ Size exclusion
2 chromatography (SEC) and native isoelectric focussing (nIEF) yielded over 99-fold enrichment
3 of enzymatically-active, SOD1 protein dimers by separating protein extracts according to
4 molecular weight (MW) and isoelectric point (pI), respectively. The absence of purple nitroblue-
5 tetrazolium (NBT) staining identified enzymatically-active SOD1 in the first of two duplicate
6 immobilized pH-gradient (IPG) gels, which informed on the location of mature SOD1 in the
7 second unstained IPG gel for synchrotron X-ray fluorescence (SXRF) analysis of metal content.
8 **b.** Mature SOD1 exhibited an increased copper:zinc atomic ratio (Cu:Zn) in 5-of-12 ALS cases
9 compared with controls (Kruskal-Wallis H Test: $p = 0.0014$, $H = 10.59$; Dunn's multiple
10 comparisons post-hoc tests: Zn-def ALS: $p = 0.0118$; remaining ALS: $p = 0.9999$). Control $n =$
11 7, remaining ALS $n = 7$. For ALS cases to be included in the Zn-deficient (Zn-def) group, their
12 soluble mature SOD1 Cu:Zn ratio had to lie outside of 2 standard deviations from the mean
13 control Cu:Zn ratio. This range is commonly used to statistically delineate outliers and is
14 represented by the red shaded band in this panel. **c.** Mature SOD1 isoelectric point (pI) was
15 significantly elevated in the ventral spinal cord (VSpC) of all ALS subgroups (Two-way
16 ANOVA with Sidak's multiple comparisons post-hoc test; *SOD1*-fALS: $p < 0.0001$; non-*SOD1*-
17 fALS: $p = 0.0002$; sALS: $p = 0.0002$), as well as in the dorsal spinal cord (DSpC) of *SOD1*-fALS
18 cases (Two-way ANOVA with Sidak's multiple comparisons post-hoc test; *SOD1*-fALS: $p =$
19 0.0036; non-*SOD1*-fALS: $p = 0.65$; sALS: $p = 0.163$), compared with controls. **d.** Representative
20 nitroblue tetrazolium-stained IEF gel, with enzymatically-active SOD1 clearly visible by an
21 achromatic gel band (red arrow). **e.** The pI of mature SOD1 in cases exhibiting an increased
22 Cu:Zn ratio of enzymatically-active SOD1 dimers was significantly elevated compared with both
23 controls, and ALS cases in which alterations to mature SOD1 metal content were absent (One-
24 way ANOVA: $p < 0.0001$, $F = 29.13$; Holm-Sidak's multiple comparisons post-hoc test: control:
25 $p < 0.0001$; remaining ALS: $p = 0.009$). Data in **b**, **c**, and **e** represent mean \pm SEM. * $p < 0.05$,
26 ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$. **f.** Increases in mature SOD1 pI were significantly
27 correlated with lower proportions of spinal cord motor neuron possessing granular SOD1
28 staining. **g**, **h.** Increases in mature SOD1 pI were significantly correlated with greater loss of
29 spinal cord motor neurons (**g**) and more disSOD1 deposition (**h**) in these same post-mortem
30 tissues cases. Spearman's r coefficient, the p value and the number of XY pairs analysed (n) is
31 stated within panels **f**, **g** and **h**. A correlation is strong if Spearman's $r = 0.5$ or higher.

1 **Figure 4. Cu:Zn ratios within individual SOD1 aggregates are distinct from purified**
 2 **soluble mature SOD1. a.** Experimental workflow for identifying and analysing SOD1 aggregate
 3 metal content in post-mortem spinal cord tissues from ALS patients. Following serial sectioning
 4 of frozen post-mortem spinal cord tissues onto alternating superfrost slides and Si₃N₄
 5 synchrotron grids (1), SOD1 aggregates were immunostained on superfrost slides using B8H10
 6 conformation-specific SOD1 antibody (2) and their locations mapped as regions of interest (ROI)
 7 using an Olympus Slide Scanner (3). Tissue maps containing ROIs were superimposed over
 8 differential interference contrast images of facing, serial, unstained frozen tissue sections
 9 mounted on Si₃N₄ grids (4). Synchrotron radiation was directed at ROIs within unstained tissues
 10 mounted on Si₃N₄ grids using the X-ray fluorescence microscopy (XFM) beamline of the
 11 Australian Synchrotron (5), and X-ray fluorescence emission spectra and Compton scatter
 12 spectra collected by the Maia detector (6). **b,c.** Compton scatter and XFM images of
 13 representative SOD1 aggregates in the ventral spinal cord of 3 *SOD1*-fALS and 1 sALS case (**b**).
 14 Scale bars represent 10µm, regions of interest are marked by white dashed circles. Case numbers
 15 and *SOD1* mutations are listed in the top left hand corner of each panel. Higher Compton scatter
 16 values, represented by darker pixels, signify greater tissue matter densities in SOD1 aggregates
 17 compared with surrounding ventral horn grey matter tissue (Surr. Tissue; **c**; Unpaired *t*-test; $p <$
 18 0.0001 , $t = 4.731$, $df = 66$). **d-g**, Zinc was increased by 70% (**d**; Unpaired *t*-test; $p <$ 0.0001 , $t =$
 19 9.339 , $df = 67$), and copper reduced by 12% (**e**; Unpaired *t*-test; $p <$ 0.0001 , $t = 5.012$, $df = 62$),
 20 within SOD1 aggregates compared with surrounding grey matter tissues, resulting in a
 21 significant decrease in the atomic ratio of copper:zinc within SOD1 aggregates compared with
 22 surrounding tissues (**f**; Mann-Whitney U test; $p <$ 0.0001 , $U = 8.5$) and the copper:zinc ratio of
 23 soluble mature SOD1 measured in these cases (**g**; Mann-Whitney U test; $p <$ 0.0001 , $U = 0$).
 24 Data in **c-g** represent mean±SEM. **** $p <$ 0.0001 .

25 **Figure 5. SOD1 protein structure and locations of PTMs which are significantly altered in**
 26 **the ventral spinal cord of fALS and sALS cases. a,b.** Mature SOD1 is dimeric, with each
 27 monomer comprising an eight-stranded β-barrel (grey) with one bound Cu (orange) and Zn
 28 (cyan) ion. The electrostatic loop (blue) contains charged and polar residues important for
 29 guiding anionic superoxide towards Cu in the active site. Three histidine residues and one
 30 aspartic acid residue (cyan) within the metal-binding loop (green) facilitate Zn coordination,
 31 whilst four histidine residues (orange) mediate Cu coordination. The disulfide loop (yellow) is a

1 substructure within the metal-binding loop, containing one of two cysteine residues that form an
2 intramolecular disulfide bond within SOD1 protein (yellow). The Greek key loop (pink) forms a
3 plug at one pole of the β -barrel and contributes to dimer interface stability. **c.** Distribution of all
4 residues identified as sites of PTMs in SOD1 protein isolated from the ventral spinal cord of
5 ALS cases and controls. Significant differences in the oxidation of His48 and His63 (**d**),
6 oxidation and nitration of Trp32 (**e**), acetylation of Lys3 (**f**), phosphorylation of Ser98 (**f**),
7 deamidation of Gln15, Asn26, Asn53 and Asn131 (**g**), and in the levels of carboxyethyllysine at
8 Lys122 and Lys128 (**h**), were identified between a proportion of ALS cases and controls.
9 Residues are labelled in wild-type SOD1 using three letter amino acid codes and the side chains
10 (**d-h**) of altered residues are highlighted in red. Details of specific ALS cases exhibiting
11 alterations to each PTM are presented in **Supplementary Table 9**. Reversible PTMs to Cys57
12 and Cys146 (**i**) were significantly increased in SOD1 protein isolated from three *SOD1*-fALS
13 cases and one sALS case (cluster), compared with controls and remaining ALS cases (One-way
14 ANOVA: Cys 57, $p < 0.0001$, $F = 36.72$; Cys146, $p < 0.0001$, $F = 120.2$; Dunnett's multiple
15 comparisons post-hoc tests: $p < 0.0001$ when comparing both Cys57 and Cys146 to controls and
16 remaining ALS cases). Corresponding significant reductions in unmodified Cys57 and Cys146
17 (**j**) residues were also identified in these cases compared with controls and remaining ALS cases
18 (Kruskal-Wallis H Test with Dunn's multiple comparisons post-hoc tests for both residues; Cys
19 57 - cluster vs control: $p = 0.03$; Cys146 - cluster vs control: $p = 0.04$). Complete details of
20 statistical analyses presented in **i** and **j** are presented in **Supplementary Table 8**. Data in **i** and **j**
21 represent mean \pm SEM. * $p < 0.05$, **** $p < 0.0001$. **k.** Distribution of all residues whose post-
22 translational modification is significantly altered in ALS cases.

23 **Figure 6. Alterations to the subcellular localization and levels of CCS protein, as well as in**
24 **the levels of reduced glutathione, copper and zinc, in the vulnerable ventral spinal cord of**
25 **ALS cases. a,** Pan-CCS antibodies were employed to profile the distribution of CCS within
26 ventral spinal cord motor neurons from *SOD1*-fALS ($n = 3$), non-*SOD1*-fALS ($n = 4$) and sALS
27 ($n = 9$) cases, and controls ($n = 10$). CCS antibodies (**Supplementary Table 3**) detected granular
28 cytoplasmic staining (arrowheads) and diffuse cytosolic staining (arrows) within ALS and
29 control motor neurons. In addition to granular and diffuse cytosolic immunostaining, CCS
30 antibodies labelled motor neuron inclusions of punctate (dotted arrowheads), globular (single
31 downwards arrowheads) and fibrillar skein-like morphologies (double downwards arrowheads).

1 Case numbers (**Supplementary Table 1**) are listed in the top left corner of each panel. Scale
2 bars represent 25 μ m. **b**, Motor neurons lacking granular CCS immunostaining were more
3 abundant in all ALS cases compared with controls (Kruskal-Wallis H test: $p = 0.0005$, $H =$
4 17.71 ; Dunn's post-hoc tests: *SOD1*-fALS: $p = 0.0008$; non-*SOD1*-fALS: $p = 0.036$; sALS: $p =$
5 0.011 compared with controls). **c**, The proportion of spinal cord motor neurons lacking granular
6 CCS and SOD1 immunostaining were strongly correlated. **d**, The proportion of motor neurons
7 possessing diffuse cytosolic CCS immunoreactivity was significantly higher in *SOD1*-fALS and
8 non-*SOD1*-fALS cases compared with controls (Kruskal-Wallis H test: $p = 0.0014$, $H = 11.33$;
9 Dunn's post-hoc tests: *SOD1*-fALS: $p = 0.006$; non-*SOD1*-fALS: $p = 0.05$), with a strong trend
10 for a similar increase in sALS cases compared with controls (sALS: $p = 0.07$). **e**, CCS protein
11 levels were significantly increased in the ventral, but not dorsal, spinal cord of all ALS
12 subgroups (Two-way ANOVA: $F(3, 58) = 11.89$, $p < 0.0001$; Sidak's multiple comparisons
13 post-hoc tests: VSpC – *SOD1*-fALS: $p = 0.002$; non-*SOD1*-fALS: $p = 0.0011$; sALS: $p < 0.0001$;
14 DSpC – *SOD1*-fALS: $p = 0.931$; non-*SOD1*-fALS: $p = 0.995$; sALS: $p = 0.163$). **f**, CCS and
15 SOD1 protein levels were significantly correlated within the ventral spinal cord. **g**, Glutathione
16 (GSH) concentrations were significantly reduced in the ventral and dorsal spinal cord of *SOD1*-
17 fALS cases, and in the ventral spinal cord of non-*SOD1*-fALS and sALS cases (Two-way
18 ANOVA: $F(3, 42) = 10.52$, $p < 0.0001$; Sidak's multiple comparisons post-hoc tests: VSpC –
19 *SOD1*-fALS: $p = 0.0007$; non-*SOD1*-fALS: $p = 0.0127$; sALS: $p = 0.002$; DSpC – *SOD1*-fALS:
20 $p = 0.022$; non-*SOD1*-fALS: $p = 0.291$; sALS: $p = 0.231$). **h**, Reduced cellular glutathione (GSH)
21 concentrations are correlated with reduced SOD1 specific activity in the ventral spinal cord. **i**,
22 Levels of zinc and copper were measured in whole tissue homogenates, as well as in Tris-buffer-
23 soluble and Tris-buffer-insoluble tissue extracts, prepared from fresh frozen ventral and dorsal
24 spinal cord tissues of ALS cases and controls. Tissues were homogenized in Tris-buffer and
25 homogenates centrifuged at 16,000g for 30 min at 4°C to separate soluble and insoluble tissue
26 fractions. Metal data is given as ug Cu or Zn per gram wet weight tissue. Complete details of
27 statistical tests performed and test statistics are reported in **Supplementary Table 11**. Data in **b**,
28 **d**, **e**, **g** and **i** represent mean \pm SEM. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$. Strong
29 correlations were identified between biometal level changes and alterations to CCS protein levels
30 (**j**, **k**), as well as increases in the proportions of motor neurons lacking granular disSOD1 or CCS
31 immunostaining (**l**, **m**) in the ventral spinal cord. Reductions in the proportion of copper in the

1 soluble tissue fraction were also associated with reduced GSH concentrations (**n**) and SOD1
2 specific activity (**o**) in the ventral spinal cord. Spearman's r coefficient, the p value and the
3 number of XY pairs analysed (n) are stated within panels **c**, **f**, **h** and **j – o**. A correlation is strong
4 if Spearman's $r = 0.5$ or higher.

5 **Figure 7. Principal component analysis of variables measured in this study.** Active variables
6 for this principal component analysis (PCA) were: % motor neurons containing granular SOD1
7 (MN_granular_disSOD1), SOD1 inclusions (MN_disSOD1), granular CCS (MN_granular_CCS)
8 and diffuse cytoplasmic CCS (MN_diffuse_CCS), motor neuron density (neuronal_density),
9 total (SOD1_act) and specific SOD1 activity (SOD1_spec_act), SOD1 (SOD1 level) and CCS
10 protein levels (CCS level), Cu:Zn atomic ratio within enzymatically-active soluble mature SOD1
11 (SOD1_CuZn_ratio), active SOD1 pI (pI), glutathione levels (GSH), and copper and zinc levels
12 in whole tissues (Total_Cu, Total_Zn), as well as soluble (Soluble_Cu, Soluble_Zn) and
13 insoluble tissue extracts (Insoluble_Cu, Insoluble_Zn). SOD1 PTM data was also included,
14 although these were grouped based on similarities in expected functional consequences; PTMox
15 – oxidation His, Trp, Cys, nitration Trp; PTMch – acetylation Lys, Phosphorylation Ser;
16 PTMdeam – deamidation Asn; PTMage – CEL Lys; GlyGly_Lys91. Each point represents a
17 sample of ventral spinal cord sample in this study – that is, each dot expresses every
18 measurement obtained for that particular sample as a single value in two-dimensional space.
19 Large dots with coloured ellipses represent the centroid for that category or grouping and its 95%
20 confidence interval. **a**, PCA plot of *SOD1*-fALS (green), non-*SOD1*-fALS (orange), sALS (red)
21 and control (blue) cases across dimension 1 (x axis), dimension 2 (z axis) and dimension 3 (y
22 axis). **b-d**, The % contribution of the top 10 most influential variables comprising dimensions 1 -
23 3. The mean % contribution of all variables to each dimension is indicated by a red dotted line. **e**,
24 PCA plot of ALS cases grouped according to site of onset; bulbar (blue) or limb (red).

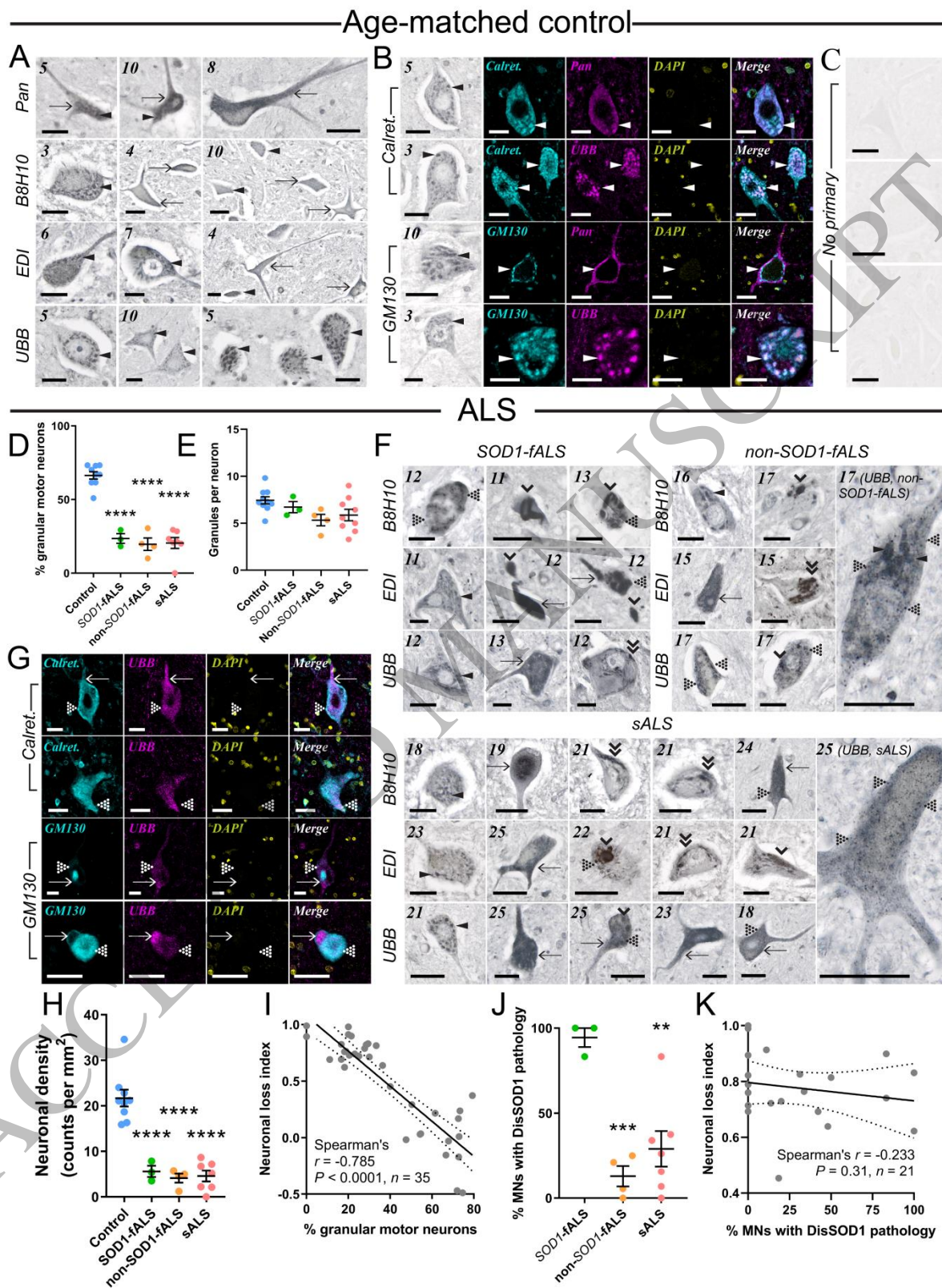
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1 **Table 1** Characterization and quantification of SOD1 inclusions, as well as diffuse cytosolic and granular cytoplasmic
 2 disordered SOD1 staining, in ventral spinal cord tissue sections from all post-mortem tissue cases

Case #	Diagnostic Group	Disordered SOD1 Inclusions			Intense diffuse staining	Quantification (%MNs)	
		Globular	Skein-like	Punctate		Inclusions + diffuse staining	Granular
1	Age-matched Control	-	-	-	✓	+	+++
2	Age-matched Control	NA	NA	NA	NA	NA	NA
3	Age-matched Control	-	-	-	-	-	+++
4	Age-matched Control	-	-	-	✓	+	+++
5	Age-matched Control	-	-	-	✓	+	+++
6	Age-matched Control	-	-	-	-	-	+++
7	Age-matched Control	-	-	-	✓	++	+++
8	Age-matched Control	-	-	-	✓	++	+++
9	Age-matched Control	-	-	-	-	-	+++
10	Age-matched Control	-	-	-	✓	+	+++
11	fALS (SOD1, II I3T)	✓	✓	✓	✓	++++	++
12	fALS (SOD1, II I3T)	✓	-	✓	✓	++++	+
13	fALS (SOD1, DI I01G)	✓	✓	✓	✓	++++	+
14	fALS (C9ORF72)	-	-	✓	✓	+	+
15	fALS (unknown)	✓	-	✓	✓	++	++
16	fALS (C9ORF72)	✓	-	-	✓	+	+
17	fALS (C9ORF72)	✓	-	✓	✓	+	+
18	sALS	-	-	✓	-	++++	+
19	sALS	-	-	-	✓	+	-
20	sALS	-	-	-	✓	++	+
21	sALS	✓	✓	-	✓	+	+
22	sALS	✓	-	✓	✓	+	+
23	sALS	-	-	-	✓	++	++
24	sALS	-	-	✓	✓	+	+
25	sALS	-	-	✓	✓	++	++
26	sALS	NA	NA	NA	NA	NA	NA

3 Staining was performed using 7 µm paraffin-embedded formalin-fixed tissue sections and B8H10, ED1 and UBB conformation-specific SOD1
 4 primary antibodies. Fixed tissues were not available (NA) for some cases. The four morphologies of disordered SOD1 pathology were noted as
 5 present (✓) or absent (-), and the proportion of motor neurons exhibiting any of the four morphologies quantified. The number of motor
 6 neurons exhibiting granular disordered SOD1 immunostaining was also quantified within each spinal cord ventral horn, expressed as a
 7 proportion of the total number of motor neurons in that ventral horn. Quantification classifications: - = 0%, + = >0–25%, ++ = 26–50%, +++ =
 8 51–75%, +++++ = 76–100%. fALS = familial amyotrophic lateral sclerosis; MN = motor neuron; NA = tissue not available; sALS = sporadic
 9 amyotrophic lateral sclerosis.

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Figure 1
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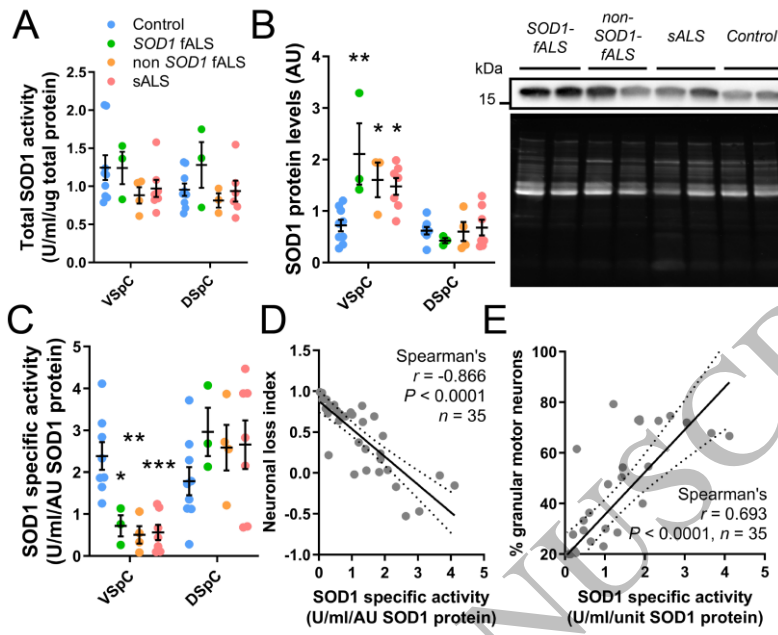


Figure 2
107x85 mm (.66 x DPI)

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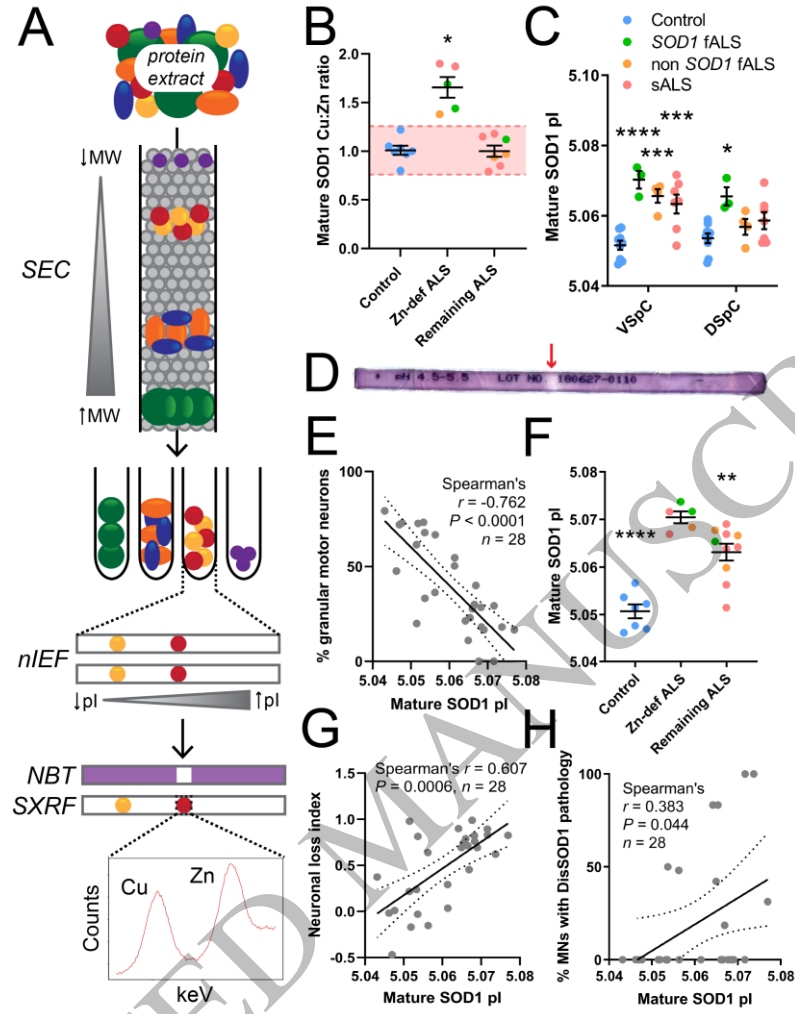


Figure 3
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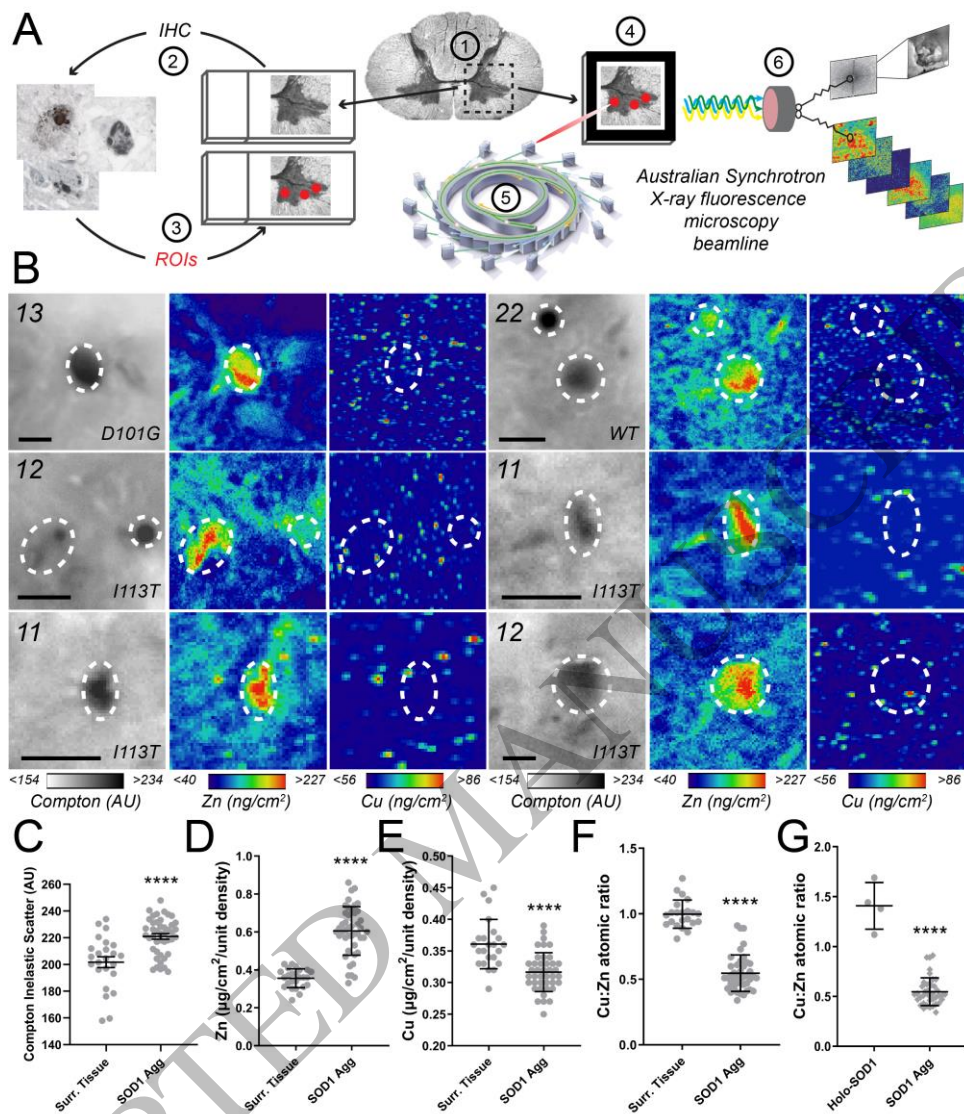


Figure 4
128x148 mm (.66 x DPI)

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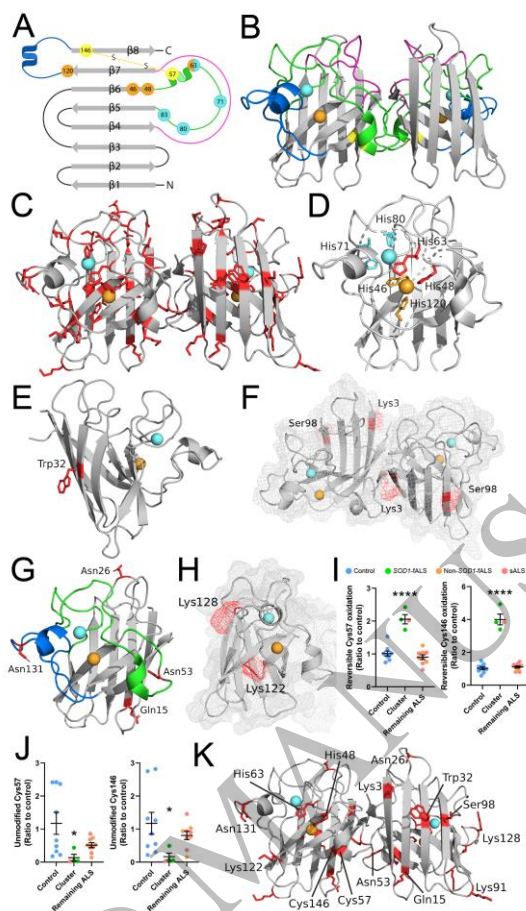


Figure 5
73x120 mm (.66 x DPI)

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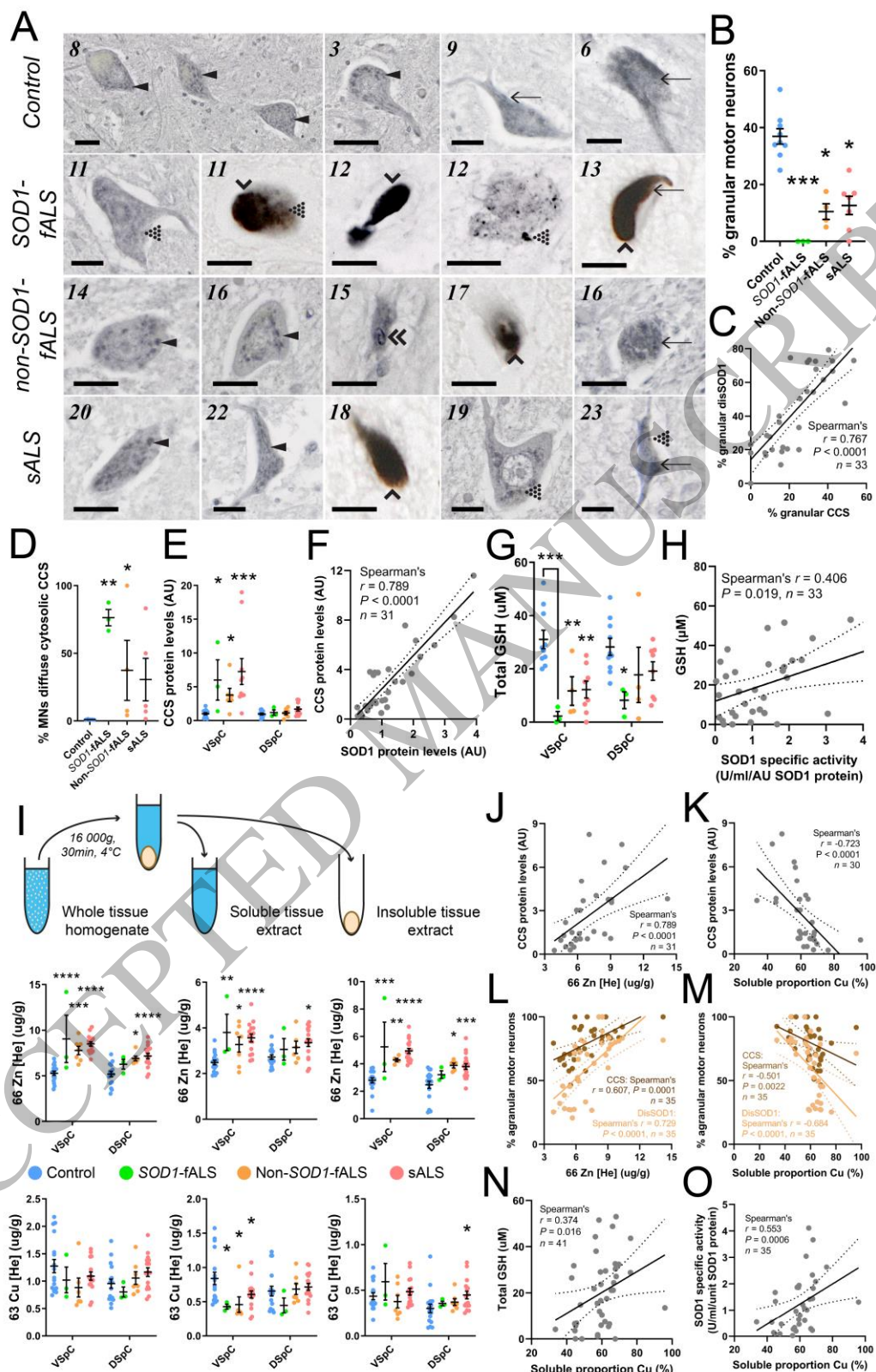


Figure 6
139x213 mm (.66 x DPI)

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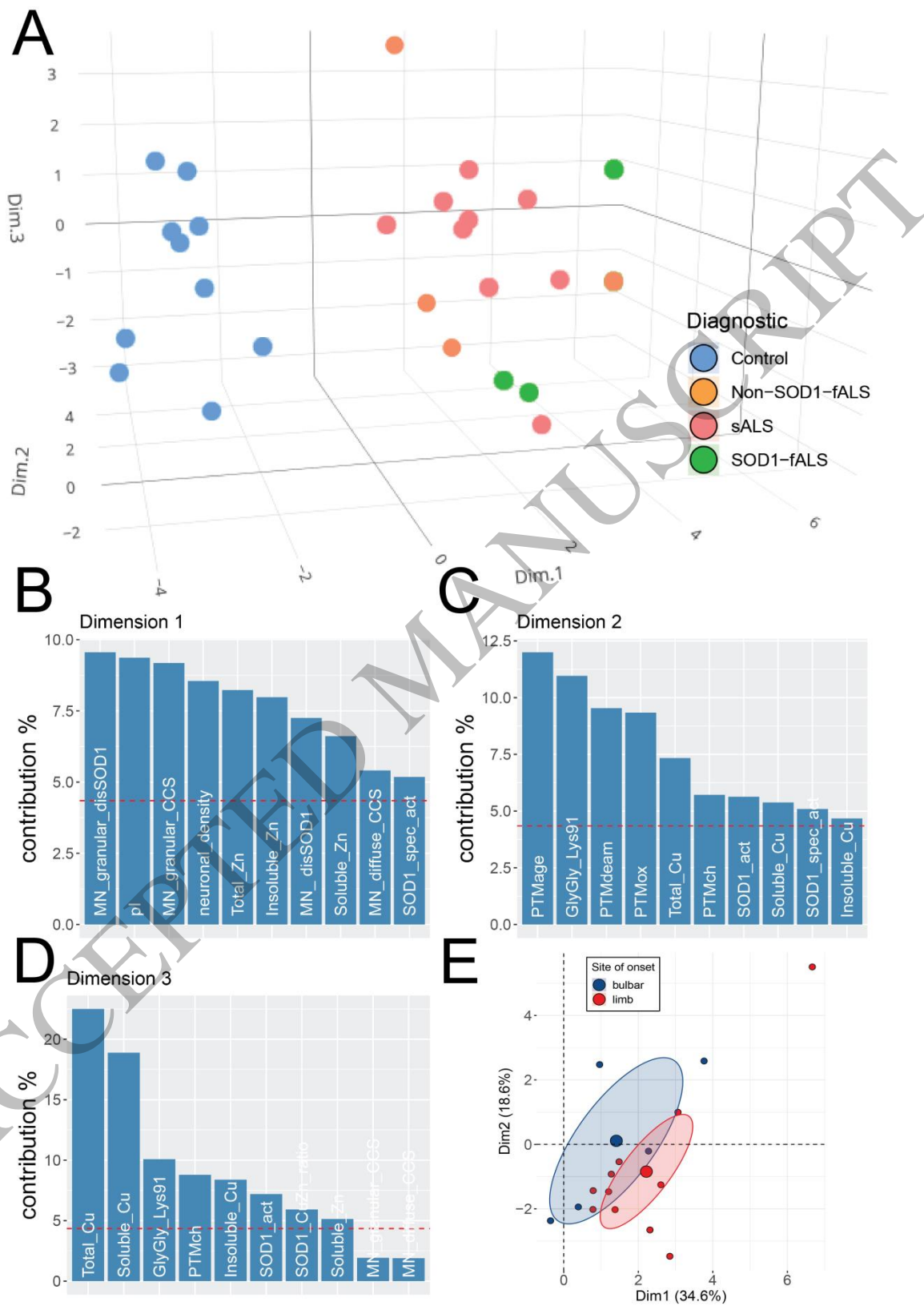


Figure 7
159x232 mm (.66 x DPI)

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