<u>Supplemental</u>

Supplemental Figure Legends

Figure S1. Immunoblots of HeLa cell lysates transfected with Myc-tagged Serpin A1, B1, C1 and I1 expression cDNAs to validate the specificity of serpin antibodies used in this study. All antibodies detect only their cognate recombinant protein and the correct size endogenous protein.

Figure S2. Age-dependent alteration of UBQLN2 and serpin staining in P497S mutant mice. (*A and B*) Immunofluorescence staining of UBQLN2 and Serpin A1, B1, C1, or I1 in the hippocampal region of sagittal brain sections from 8-week-old (A) and 52-week-old (B) P497S animals. Scale bars shown = $100 \mu m$ for all images.

Figure S3. Colocalization of serpin and UBQLN2 proteins in different brain regions of P497S animals. Confocal microscopy images of 52-week-old P497S animals similar to Fig 2, but showing the UBQLN2 and Serpin A1, C1, and I1 protein staining in the CA1 (top panel), CA3 (middle panel), and cortex (bottom panel) of the brain. Scale bars shown = 20 μm for all images.

Figure S4. Line scan analysis showing colocalization of serpins with UBQLN2 staining in the dentate gyrus and spinal cord sections of P497S animals. Line scans were performed through representative regions of the magnified images shown in Figs 2 and 3. Plots depict pixel intensity of the individual UBQLN2 (red) and serpin (green) image channels for the lines analyzed in the images shown to the right of each plot. Lines are

drawn through the same region of interest in each image to determine the extent of overlap between the UBQLN2 and serpin staining.

Figure S5. Colocalization of UBQLN2 and serpins proteins in puncta within spinal MN. Confocal microscopy images of 32-week-old P497S animals similar to Fig 3, but showing higher magnification images of MN, identified by ChAT-positive staining, in the SC of age-matched P497S (top panel), WT356 (middle panel), and Non-Tg (bottom panel) animals. Scale bars shown = 20 μm for all images.

Figure S6. Line scans showing the degree of overlap between UBQLN2, serpin, and LC3 staining in P497S and Non-Tg SC sections shown in Fig 4. Plots depict pixel intensity for UBQLN2 (red), serpin (green), and the autophagosome marker LC3 (magenta) for the lines shown in images below each plot. Lines are drawn through the same region of interest containing representative puncta for either the larger, extracellular puncta in P497S animals (left column) or the smaller puncta within motor neurons of P497S and Non-Tg animals (middle and right columns, respectively).

Figure S7. Line scans showing the degree of overlap between UBQLN2, serpins and LAMP1 in P497S and Non-Tg spinal cord sections shown in Fig 5. Similar to Fig S6, but measuring colocalization between UBQLN2 (red), serpins (green), the LAMP1 lysosomal marker (magenta).

Figure S8. The UBQLN2 and serpin double-positive puncta in the SC are more closely juxtaposed with microglia than with astrocytes. Confocal microscopy images of the staining of UBQLN2, Serpin A1 or C1 proteins with either GFAP (top panels) or IBA1 (bottom panels) in the SC of 32-week-old P497S animals. Scale bars shown = 100 μ m and 20 μ m for 1X and 5X zoom images, respectively.

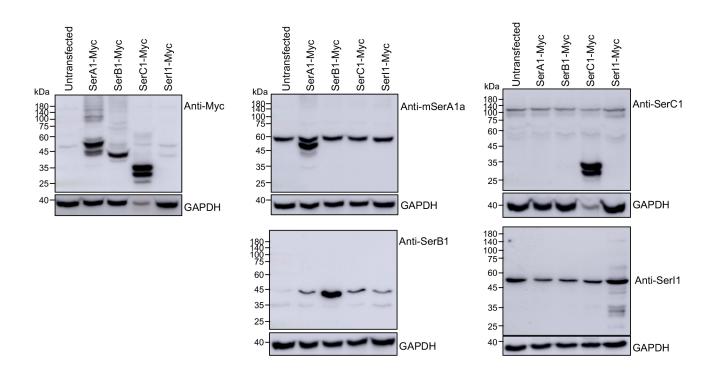
Figure S9. Comparison of the UBQLN2, Serpin A1 and C1 staining patterns in the dentate gyrus of P497S, WT 356 and Non-Tg animals. Similar to Fig 6, but showing staining for all three genotypes, as indicated. The P497S staining panels are the same as Fig 6. Scale bars shown = 100 μ m and 20 μ m for 1X and 5X zoom images, respectively.

Figure S10. Comparison of the UBQLN2, Serpin A1 and C1 staining patterns in the SC of P497S, WT 356 and Non-Tg animals. Similar to Fig S8, but showing staining in the SC for all three genotypes, as indicated. The P497S staining panels are the same as Fig 6. Scale bars shown = 100 μ m and 20 μ m for 1X and 5X zoom images, respectively. Scale bars shown = 100 μ m and 20 μ m for 1X and 5X zoom images, respectively.

Figure S11. Decreased solubility of UBQLN2 and Serpin A1 in P497S mutant animals. (A) Immunoblots of equal portions of low salt (LS), Triton-X100 (TX-100) sarkosyl (SARK) and urea fractions following sequential biochemical extraction of equal weight of cortical brain tissue from 32-week-old Non-Tg, WT356, and P497S mice. The fractions analyzed were obtained by progressive extraction of the tissues with low salt, Triton X-

100, sarkosyl, and urea buffers. The Triton X-100 fraction was not included because of aberrant migration of proteins extracted with the buffer. (*B*) Quantification of penultimate SARK fractions for UBQLN2 and serpin proteins. (*C*) Quantification of ultimate urea fractions for each serpin protein. (*D*) Ubiquitin (UBQTN) immunoblots of urea fractions from 8- and 32-week-old animals. (*E*) Quantification of 32 week urea fractions for UBQLN2 and UBQTN.

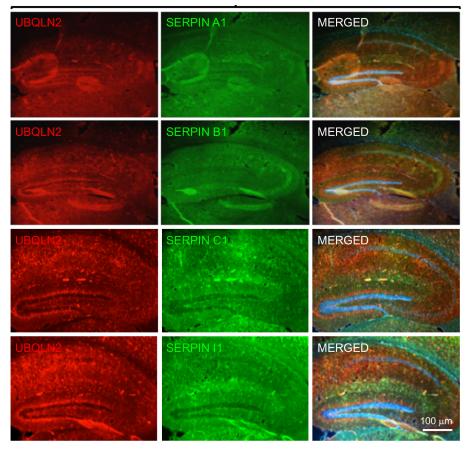
Figure S12. Quantification of serpin protein levels in mouse tissues by SDS-PAGE analysis. (A) Immunoblots of hippocampus (left) and lumbar SC tissue (right) of 3 WT356, Non-Tg, and P497S animals per genotype analyzed after separation by SDS-PAGE. (B) Quantification of immunoblots in A shows a significant decrease in Serpin I1 in the hippocampus and a significant decrease in Serpin C1 in the spinal cord of 32-week-old P497S animals. Other serpins trended toward a decrease in P497S animals though not to a level of significance. As expected, levels of the UBQLN2 transgene in both the hippocampus and spinal cord were significantly increased in P497S animals.





В

P497S: 8-week-old-mice



P497S: 52-week-old-mice

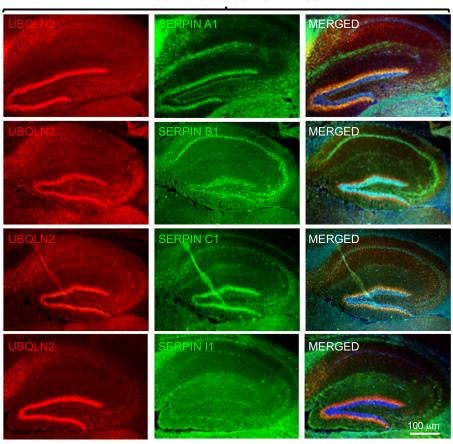
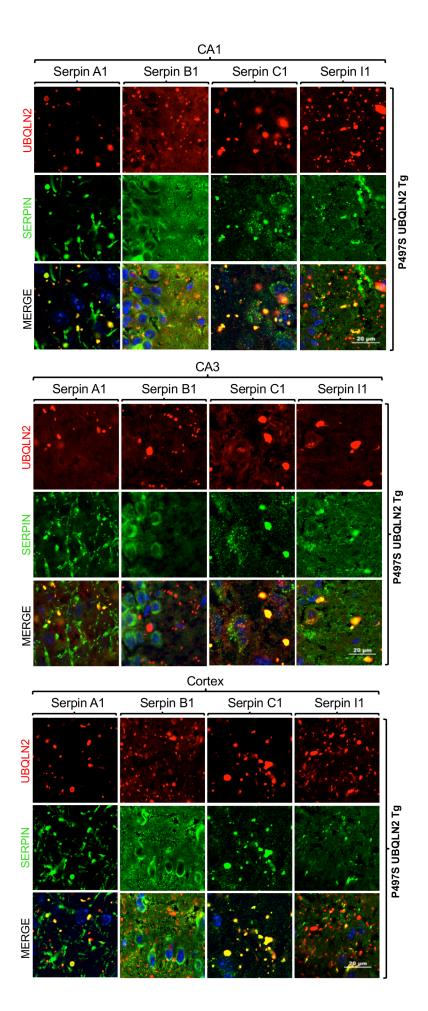
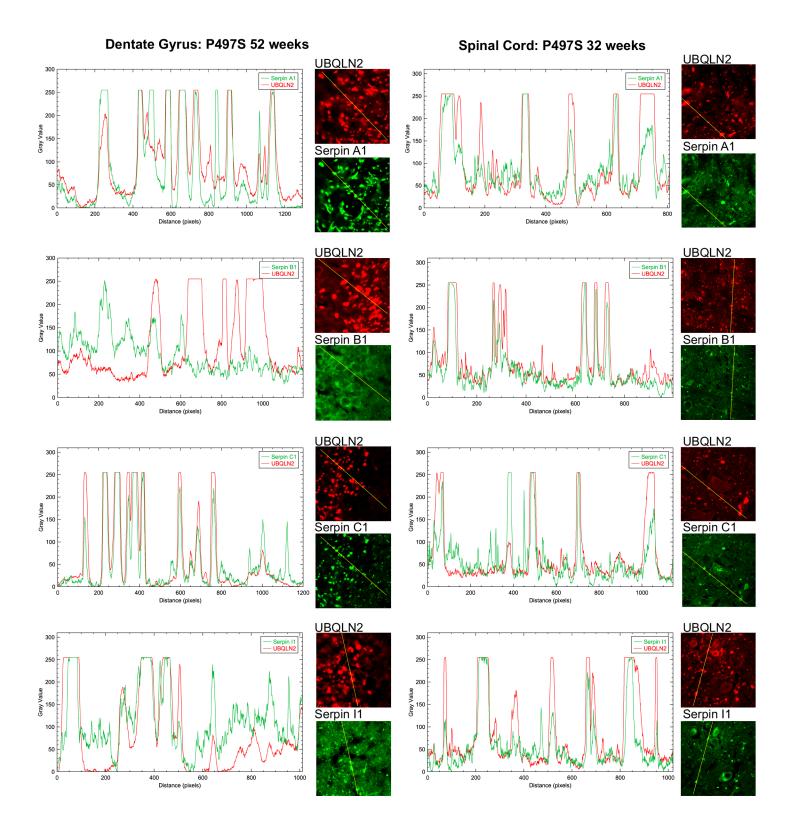
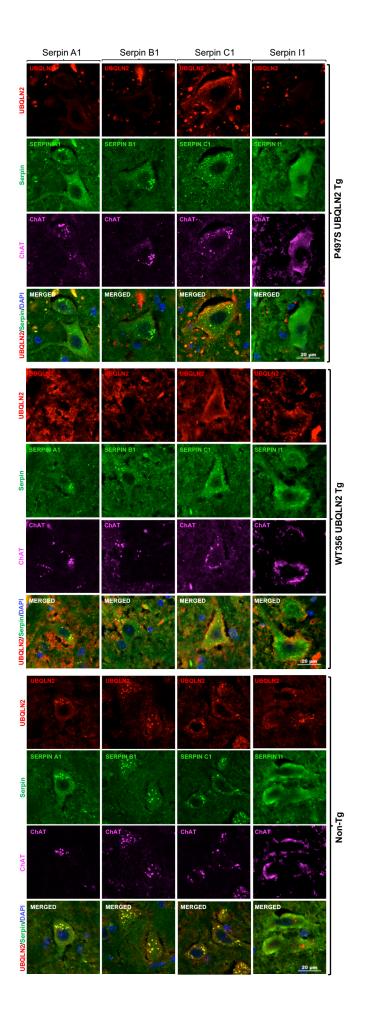
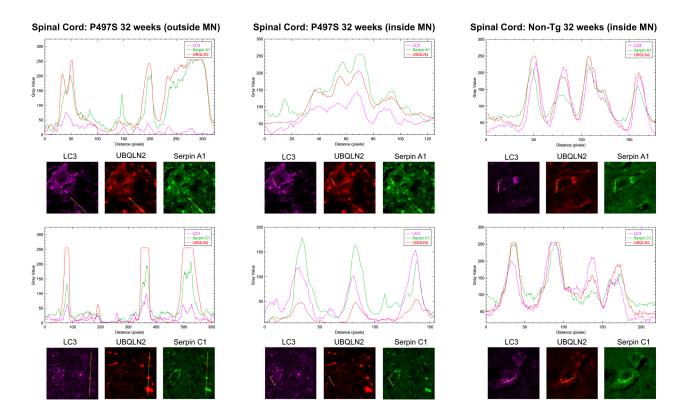


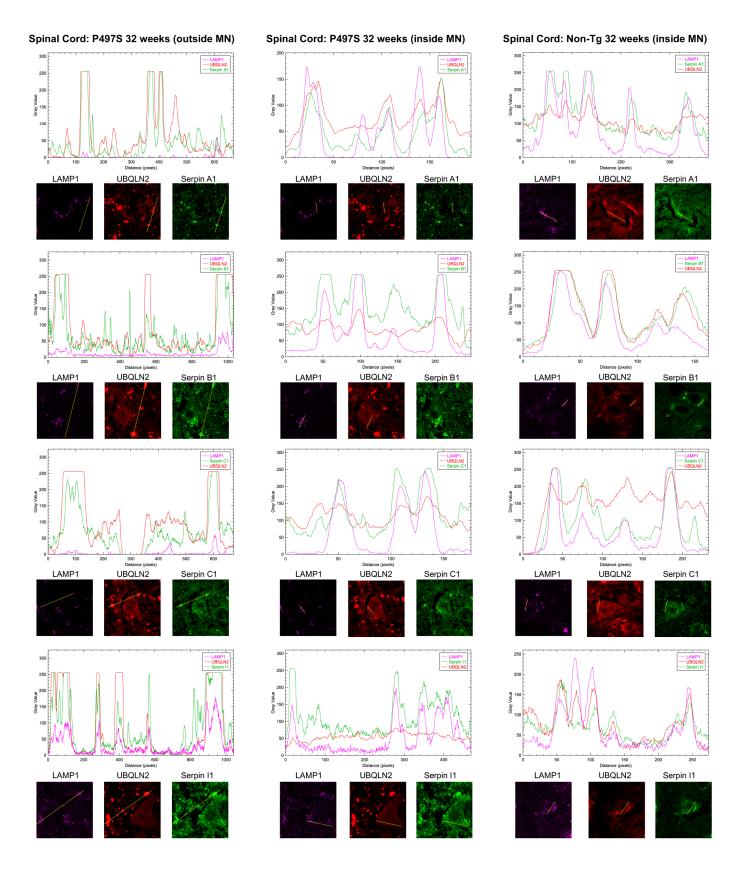
Fig S2











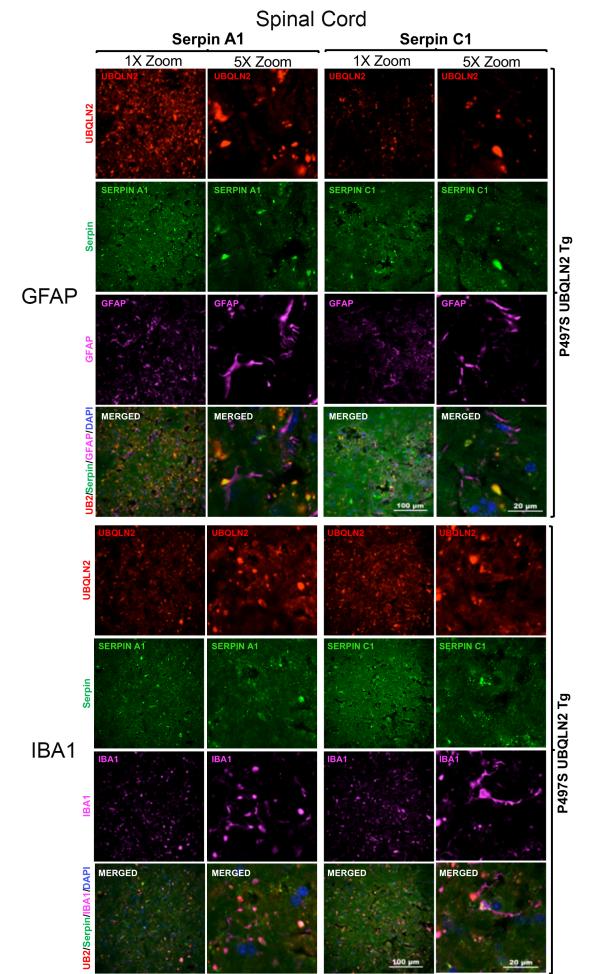


Fig S8

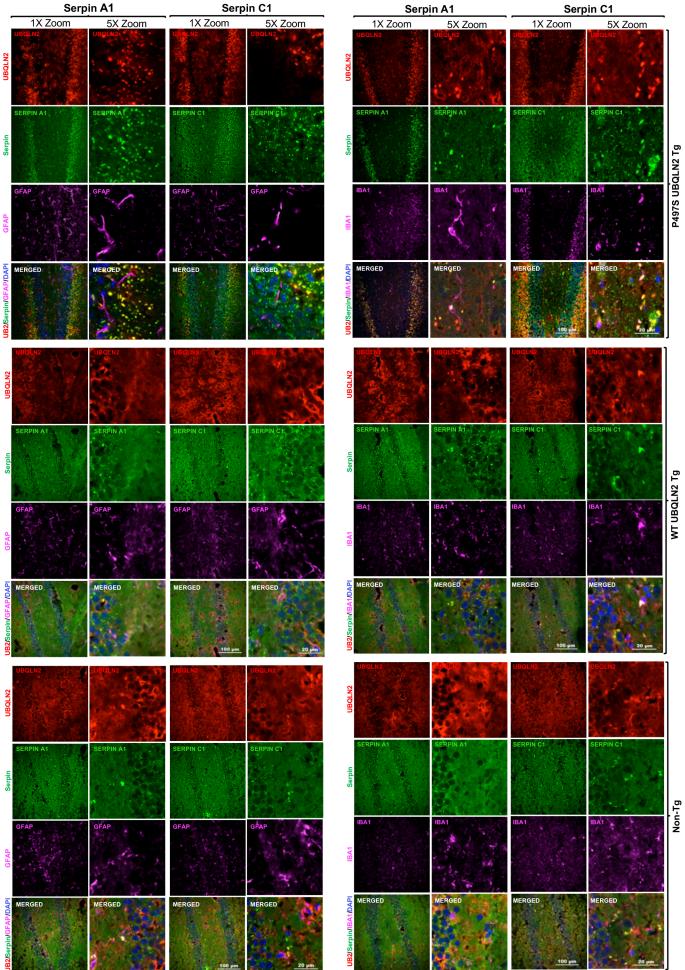


Fig S9

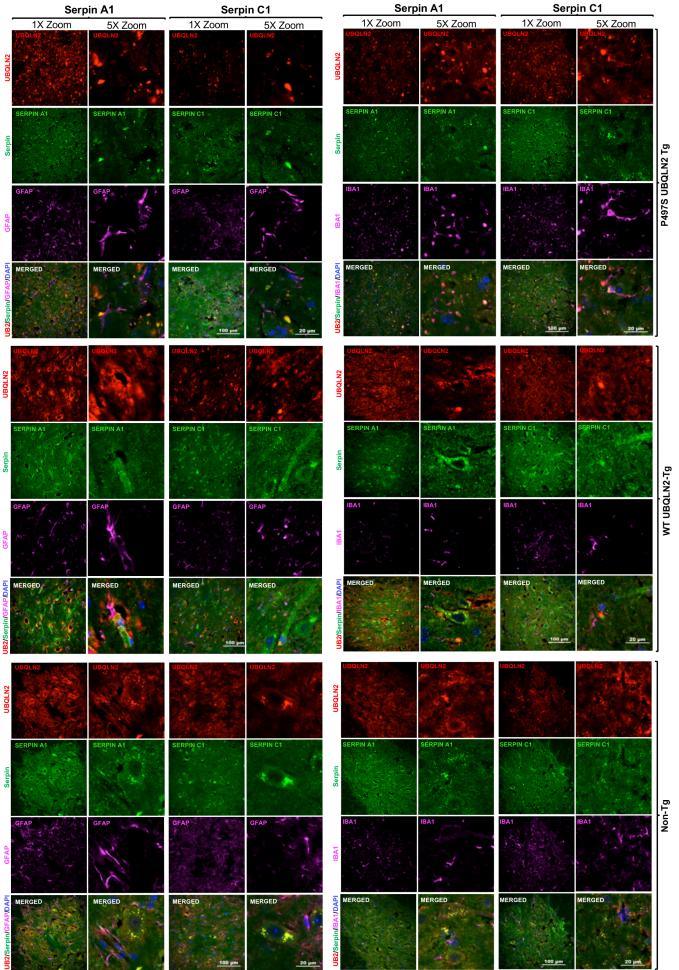


Fig S10

