
Supplementary information

Myelin dysfunction drives amyloid- β deposition in models of Alzheimer's disease

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Supplementary Information Figure Guide

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Tab 4. Gprofiler biological pathways enrichment analysis for DEGs between Cnp^{-/-} 5xFAD vs 5xFAD

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Supplementary Information Figure legends

SI Figure 1. Source data for western blot analysis

(a-j) Uncropped Western blot raw data. Molecular weight marker is indicated

on the left (given in kDa). Red boxes indicate cropped regions as presented in the figures and the extended data figures. For normalisation, fast green total protein staining was performed on the same blot. Corresponding figure/extended data figure is indicated above each blot.

SI Figure 2. Myelination and gliosis in myelin mutant and aged mice (SI for Extended Data Figures 1d).

(a) Raw data shown as heatmap in Extended Data Figure 1 d. The percentage area positive for immunostaining (MBP for myelin profiles, GFAP for astrogliosis and IBA1 for microgliosis) was quantified in the indicated ROIs. m: months. Bars represent means; dots represent individual mice/biological replicate/n (n=3 per group). Statistical analysis: ordinary one-way ANOVA (p-value is given in graphs).

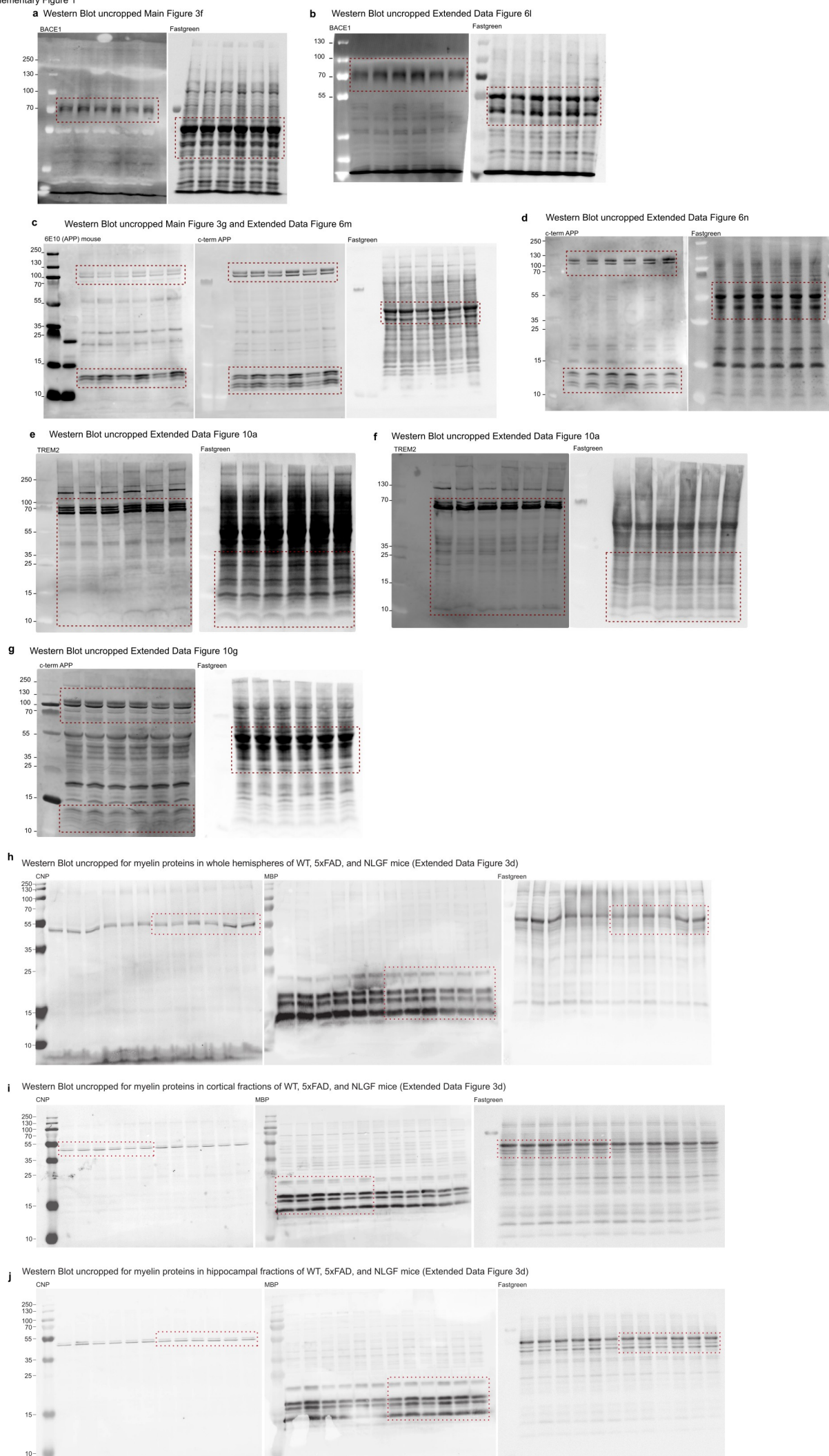
(b) Results of Tukey's posthoc test for all comparisons after ordinary one-way ANOVA on data shown in (a).

SI Figure 3. Assessment of *in toto* amyloid burden by light sheet microscopy

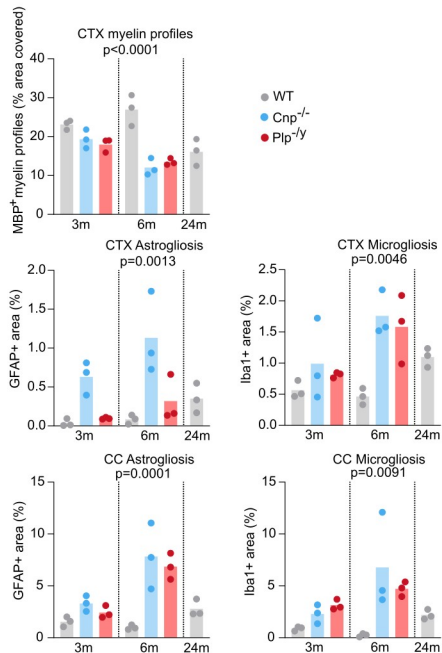
(I) Brains were subjected to *in toto* staining with the β -sheet dye Congo Red according to a modified iDisco protocol (see Material and Methods) followed by clearing in Ethylcinnamate (Eci).

(II) Cleared brains were imaged on an Ultramicroscope II (LaVision-Biotech) light sheet setup to obtain sagittal optical slices.

(III) Raw data were visualised and analysed in Arivis Vision 4D using manual region of interest annotation for hippocampus and cortex and automated plaque segmentation (intensity-thresholding: 3-month-old *5xFAD*, blobfinder algorithm: 6-month-old *5xFAD*, machine learning: 6-month-old *App^{NLGF}*).



a Quantification of gliosis and myelin content in myelin mutants



b

Statistical analysis

Comparisons	CTX			CC	
	Myelin	GFAP	Iba1	GFAP	Iba1
WT 6m vs. Cnp ^{-/-} 6m	<0.0001	0.0027	0.0092	0.0005	0.0087
WT 6m vs. Plp ^{-/-} 6m	0.0002	0.9075	0.0274	0.0021	0.1031
WT 6m vs. WT 24m	0.0016	0.8504	0.3925	0.6962	0.8357
WT 6m vs. WT 3m	0.5245	>0.9999	0.9998	0.9986	0.9994
WT 6m vs. Cnp ^{-/-} 3m	0.0291	0.1898	0.5856	0.4384	0.8052
WT 6m vs. Plp ^{-/-} 3m	0.0083	>0.9999	0.8965	0.8561	0.4881
Cnp ^{-/-} 6m vs. Plp ^{-/-} 6m	0.9903	0.0211	0.9959	0.9728	0.8021
Cnp ^{-/-} 6m vs. WT 24m	0.4646	0.0275	0.3413	0.0077	0.0914
Cnp ^{-/-} 6m vs. WT 3m	0.0013	0.0018	0.0171	0.0011	0.0188
Cnp ^{-/-} 6m vs. Cnp ^{-/-} 3m	0.0369	0.2675	0.2054	0.0175	0.102
Cnp ^{-/-} 6m vs. Plp ^{-/-} 3m	0.1227	0.003	0.0753	0.0044	0.2516
Plp ^{-/-} 6m vs. WT 24m	0.8497	>0.9999	0.6681	0.0368	0.6343
Plp ^{-/-} 6m vs. WT 3m	0.0047	0.8163	0.0504	0.0051	0.2057
Plp ^{-/-} 6m vs. Cnp ^{-/-} 3m	0.1255	0.7439	0.467	0.0818	0.6716
Plp ^{-/-} 6m vs. Plp ^{-/-} 3m	0.3564	0.928	0.2024	0.0208	0.9303
WT 24m vs. WT 3m	0.0476	0.7404	0.579	0.9203	0.9687
WT 24m vs. Cnp ^{-/-} 3m	0.6839	0.8193	0.9998	0.9991	>0.9999
WT 24m vs. Plp ^{-/-} 3m	0.9642	0.8776	0.9557	0.9999	0.9946
WT 3m vs. Cnp ^{-/-} 3m	0.5447	0.1329	0.777	0.7164	0.9566
WT 3m vs. Plp ^{-/-} 3m	0.2205	>0.9999	0.978	0.9835	0.7322
Cnp ^{-/-} 3m vs. Plp ^{-/-} 3m	0.9912	0.2101	0.9955	0.9849	0.997

Protocol *in toto* amyloid plaque burden

