

## Supporting Information

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DNALI1 Promotes Neurodegeneration after Traumatic Brain Injury via Inhibition of Autophagosome-Lysosome Fusion

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## Supporting Information

# **DNALI1 promotes neurodegeneration after traumatic brain injury via inhibition of autophagosome-lysosome fusion**

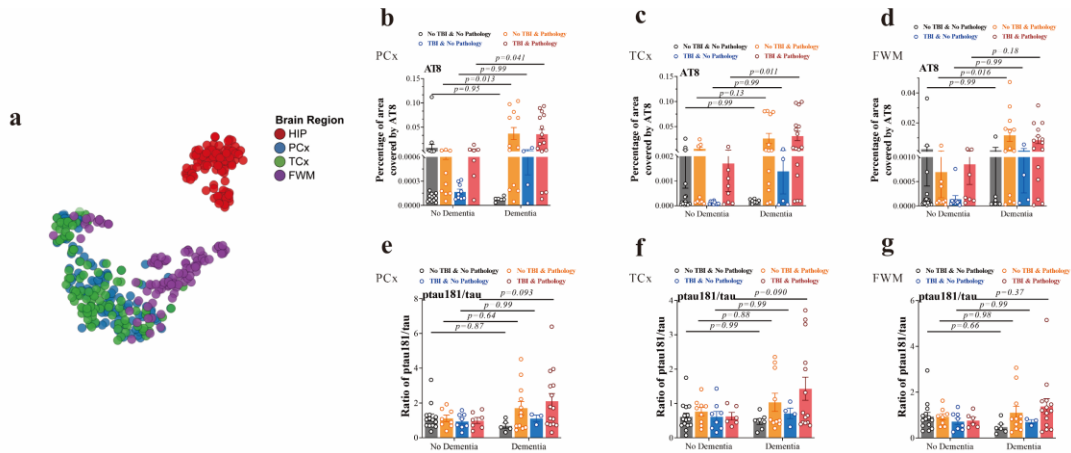
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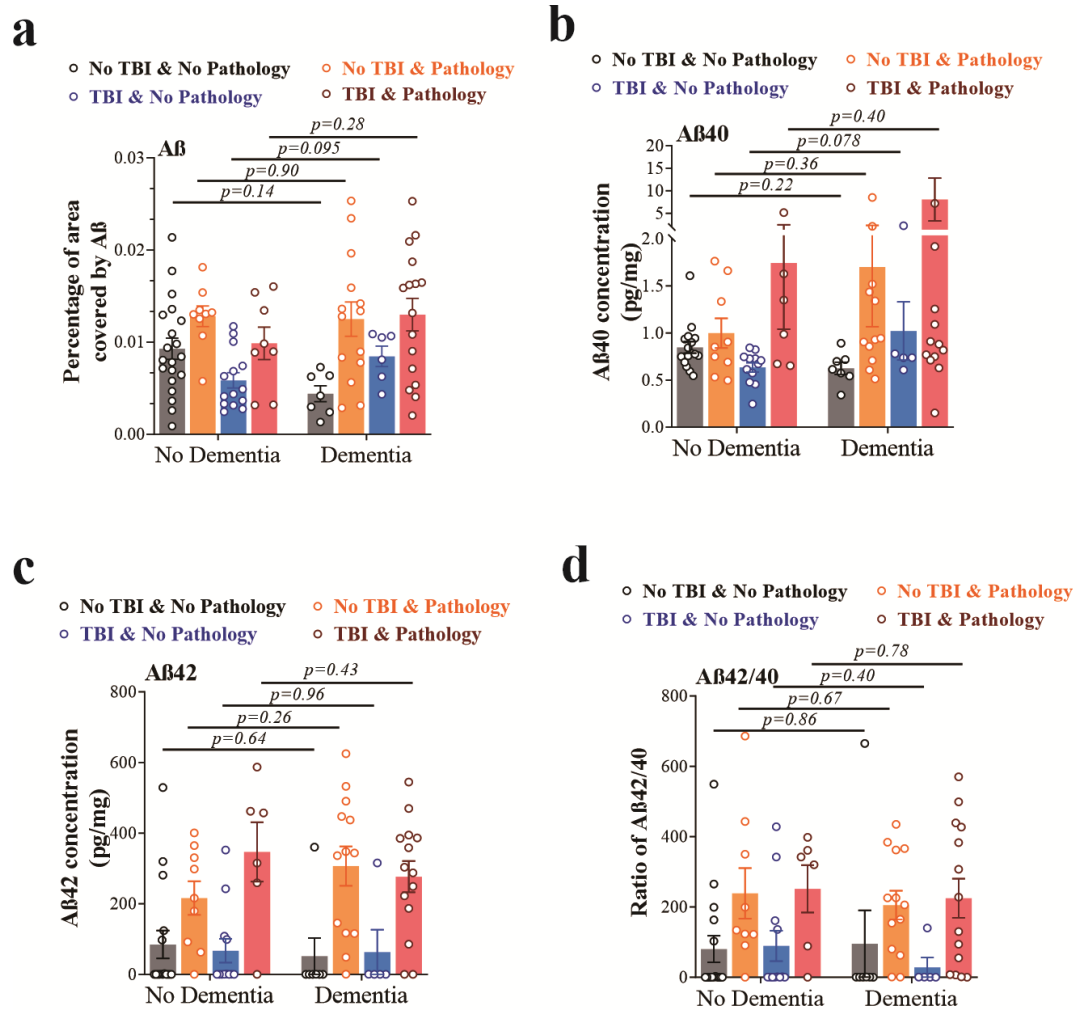
This PDF file includes:

Figures. S1 to S9

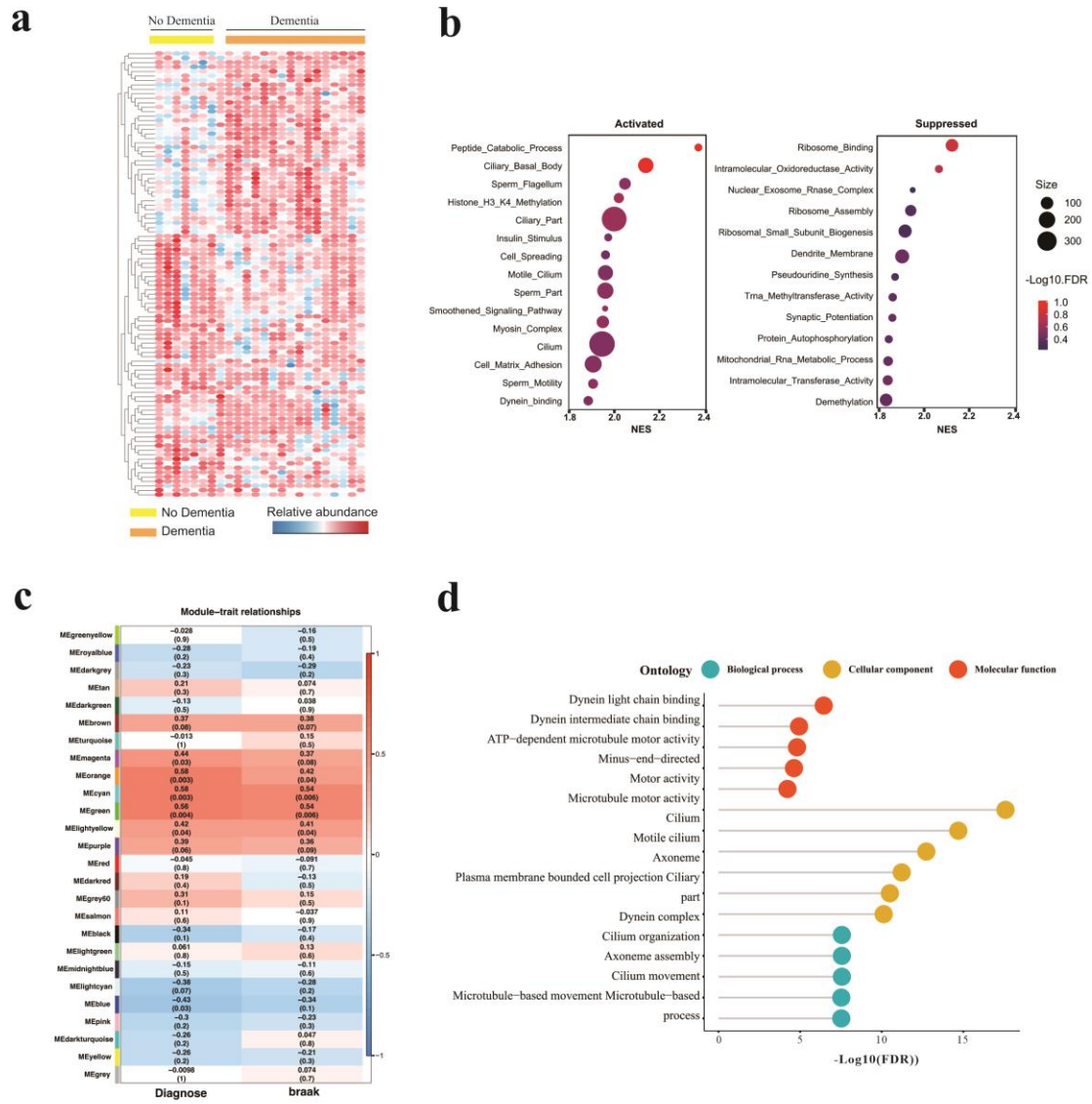
Tables S1 to S3



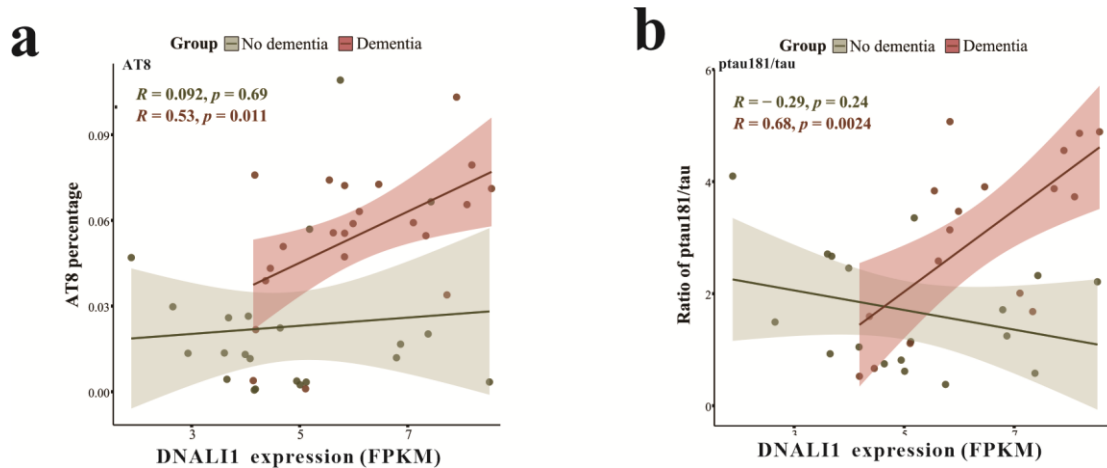
**Figure S1. The hippocampus is the most unique brain region in the study. a.** t-Distributed Stochastic Neighbor Embedding (tSNE) analysis for four brain regions of RNA-seq data in Aging, Dementia and Traumatic Brain Injury Study. **b-d.** The comparison of the percentage of area covered by AT8 detected by histology and immunohistochemistry (IHC) among different groups in the parietal cortex (PCx) (**b**), temporal cortex (TCx) (**c**) and frontal white matter (FWM) (**d**). **e-g.** The comparison of the ratio of ptau181/tau detected by Luminex assays among different groups in PCx (**e**), TCx (**f**) and FWM (**g**). Two-way ANOVA with Sidak's multiple comparisons test (**b-g**) was used. P values are indicated on the graphs.



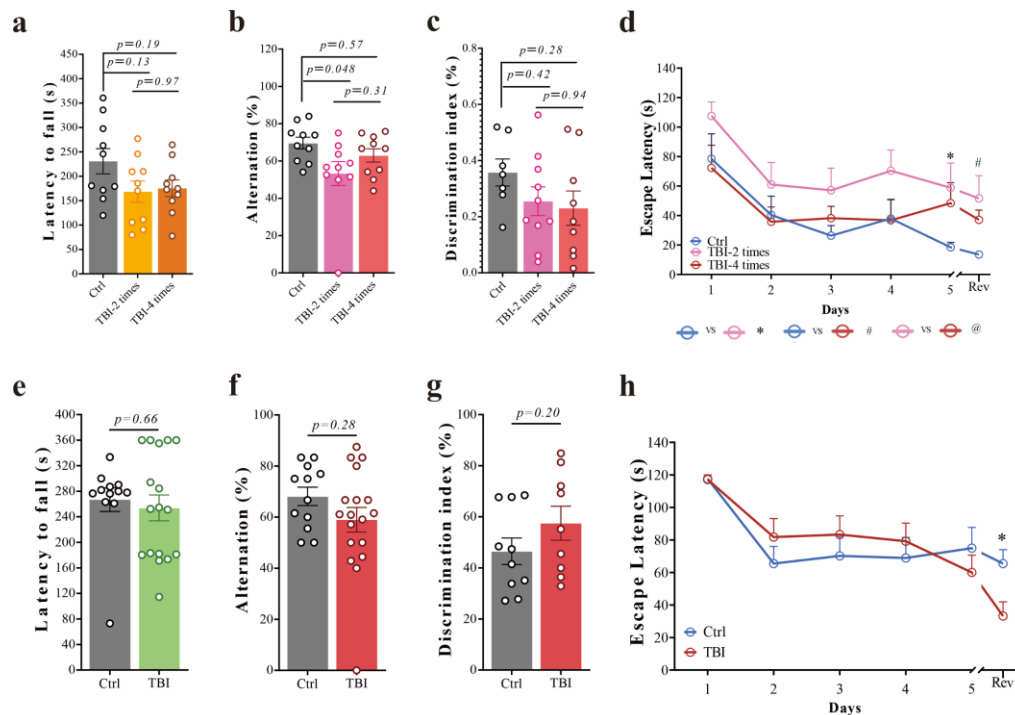
**Figure S2. A $\beta$  related indexes showed no significant differences between different groups. a.** Levels of percentage of area covered by A $\beta$  detected by IHC among different groups. **b.** Levels of A $\beta$ 40 detected by Luminex assays among different groups. **c.** Levels of A $\beta$ 42 detected by Luminex assays among different groups. **d.** Ratio of A $\beta$ 42/40 detected by Luminex assays among different groups. The data are presented as the means  $\pm$  SEM. Two-way ANOVA with Sidak's multiple comparisons test (**a-d**) was used. P values are indicated on the graphs.



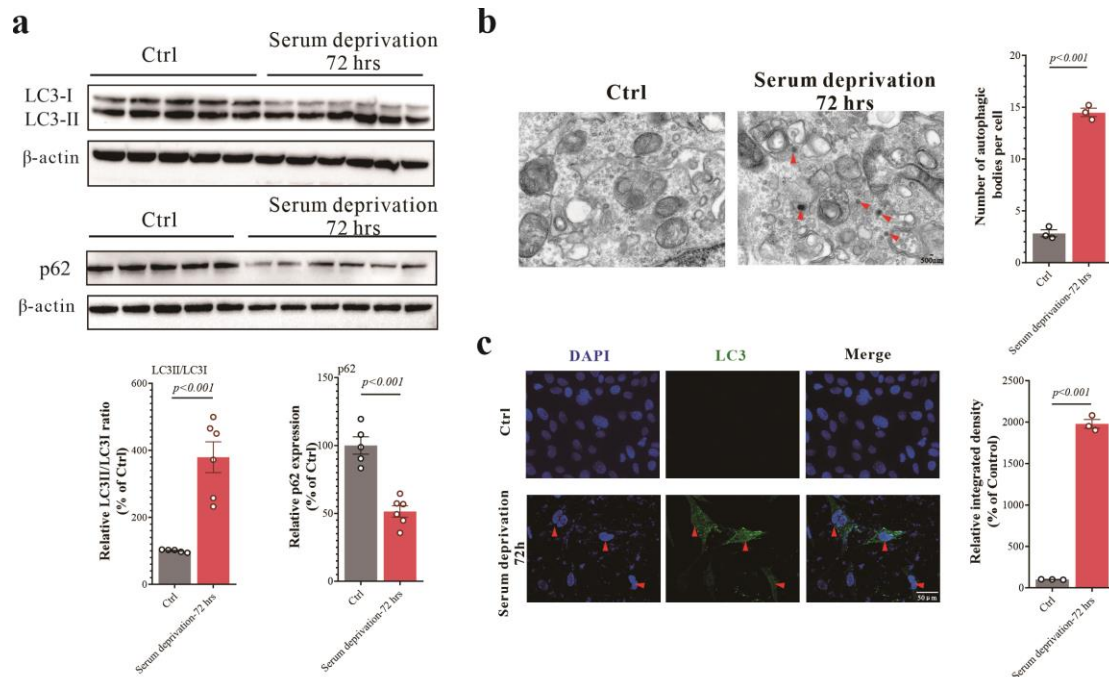
**Figure S3. Cilium and dynein pathways were related to the pathology of post-traumatic brain injury neurodegeneration. a.** Heatmap analysis of the top 200 different expression genes between the dementia group and non-demented group, which was calculated by limma package in R as described in methods. **b.** The top 10 significantly active and suppressed pathways in dementia patients, based on gene set enrichment analysis (GSEA). **c.** The correlation coefficients and p-values of gene modules with dementia diagnosis and Braak stage, and colors representing the magnitude of the correlation coefficients. **d.** The Go pathway of the gene model most relevant to dementia.



**Figure S4. *DNAL11* expression was significantly correlated with AT8, or the ratio of ptau181/tau. a.** The correlation between *DNAL11* expression fragments per kilobase per million (FPKM) and the percentage of area covered by AT8 for dementia and non-dementia groups. **b.** The correlation between *DNAL11* expression (FPKM) and the ratio of ptau181/tau for dementia and non-dementia groups. Pearson Correlation was used. P values are indicated on the graphs.

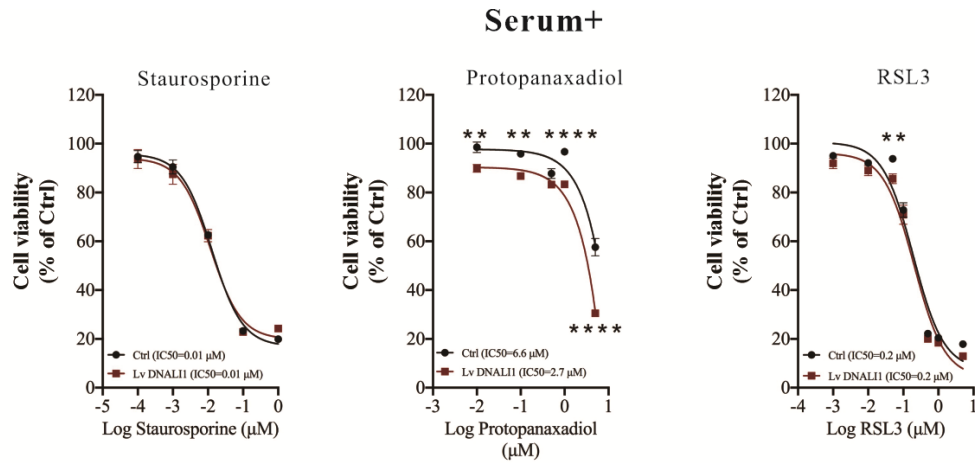
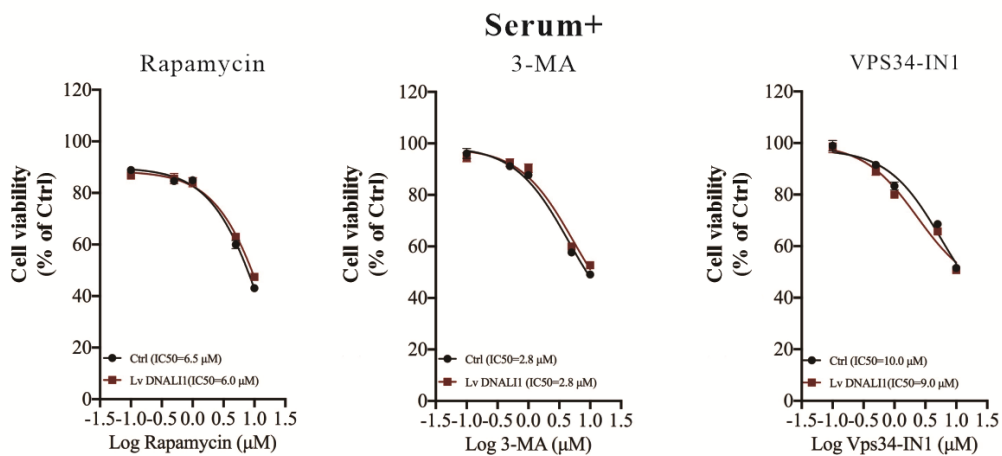


**Figure S5. Two mild replicate hits and one month after hit is optimal for experiments.** **a.** The performances on the rotarod test for different times of repetitive impact groups were analyzed one month after the brain injury (Ctrl,  $n = 10$ ; TBI-2 times,  $n = 10$ ; TBI-4 times,  $n = 10$ ). **b.** The performances on the Y-Maze spontaneous alternation test for different times of repetitive impact groups were analyzed one month after the brain injury (Ctrl,  $n = 10$ ; TBI-2 times,  $n = 10$ ; TBI-4 times,  $n = 10$ ). **c.** The performances on the Novel object recognition test for different times of repetitive impact groups were analyzed one month after the brain injury (Ctrl,  $n = 10$ ; TBI-2 times,  $n = 10$ ; TBI-4 times,  $n = 10$ ). **d.** The performances for different times of repetitive impact groups on the Morris water maze test were analyzed one month after the brain injury (Ctrl,  $n = 10$ ; TBI-2 times,  $n = 10$ ; TBI-4 times,  $n = 10$ ). **e.** The performance on the rotarod test was analyzed six months after the 2-times-hit brain injury (Ctrl,  $n = 12$ ; TBI,  $n = 12$ ). **f.** The performance on the Y-Maze spontaneous alternation test was analyzed six months after the 2-times-hit brain injury (Ctrl,  $n = 12$ ; TBI,  $n = 12$ ). **g.** The performance on the Novel object recognition test was analyzed six months after the 2-times-hit brain injury (Ctrl,  $n = 12$ ; TBI,  $n = 12$ ). **h.** The performance on the Morris water maze test was analyzed six months after the 2-times-hit brain injury (Ctrl,  $n = 12$ ; TBI,  $n = 12$ ). The data are presented as the means  $\pm$  SEM. One-way ANOVA with Tukey's multiple comparisons test (**a-d**) and T-test (**e-h**) were used. P values are indicated on the graphs, \* & #:  $p < 0.05$ .

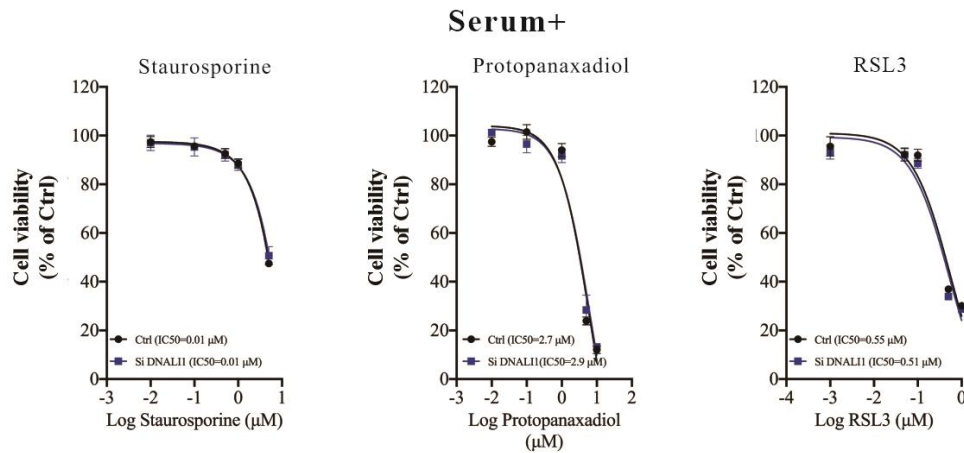
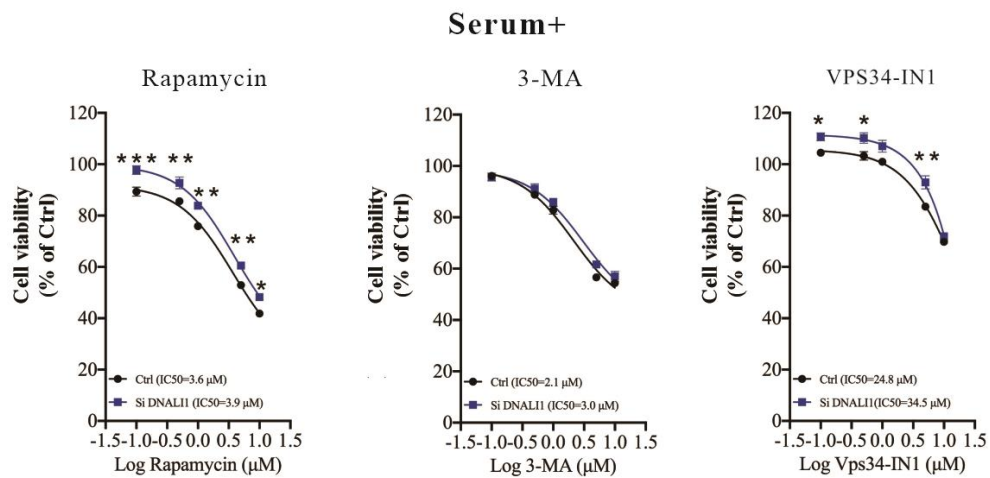


**Figure S6. Autophagy level was activated after TBI.** **a.** Western blot analysis of LC3 and p62 after 72h serum depletion (Ctrl, n = 5; TBI, n = 6). The data are normalized to  $\beta$ -actin and expressed relative to the control. **b.** Transmission electron microscopy images and quantification of the number of autophagic bodies for control and serum depletion cells, red arrowheads indicate autophagic vacuoles. Scale bars, 5000 nm, as indicated. **c.** Immunofluorescent colabeling of Lc3 (green) and nuclear (blue) and corresponding statistical results after 72h serum depletion. n = 3. Scale bar, 50  $\mu$ m, as indicated. The data are presented as the means  $\pm$  SEM. T-test (**a-c**) was used. P values are indicated on the graphs.

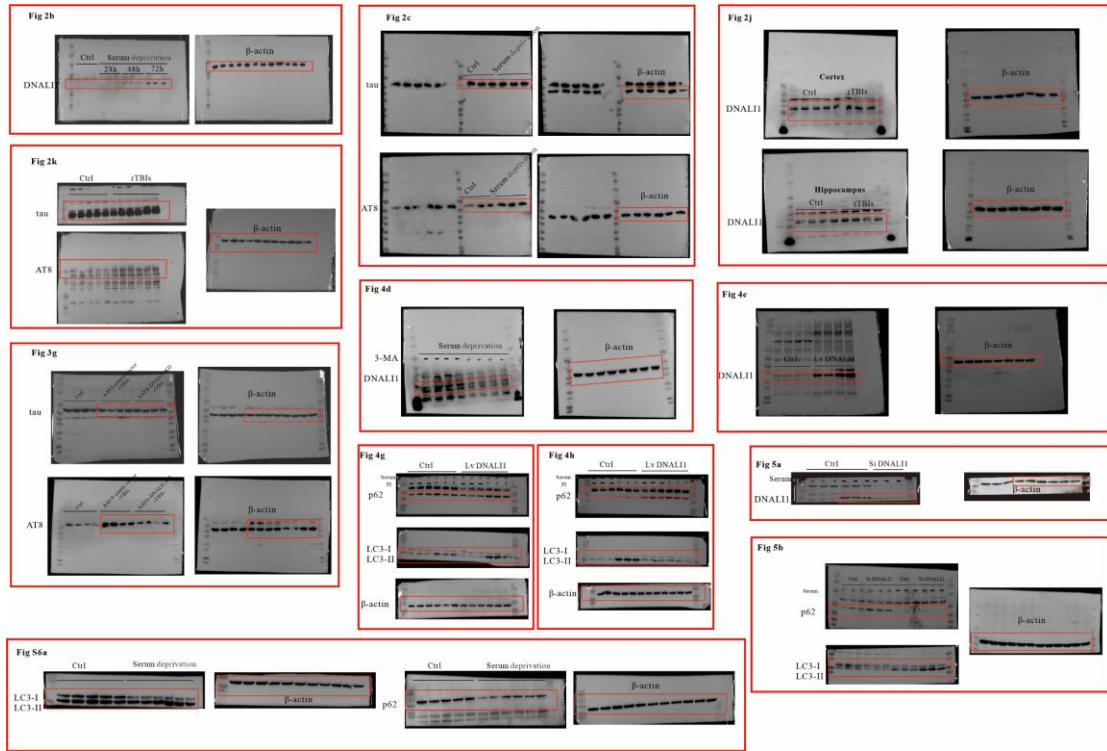


**a****b**

**Figure S7. DNALI1 overexpression did not affect the cell susceptibilities to cell death and autophagy regulators.** **a.** Cell viability of normal and DNALI1 overexpression cells after staurosporine, protopanaxadiol, and RSL3 treatment under serum normal status,  $n = 6$  wells from one representative of 3 independent experiments. **b.** Cell viability of normal and DNALI1 overexpression cells after Rapamycin, 3-MA, or VPS34-IN1 treatment under serum normal status,  $n = 6$  wells from one representative of 3 independent experiments. The data are presented as the means  $\pm$  SEM. Two-way ANOVA with Sidak's multiple comparisons test (**a-b**) was used. P values are indicated on the graphs.

**a****b**

**Figure S8. DNALI1 inhibition did not affect the cell susceptibilities to cell death regulators significantly.** **a.** Cell viability of normal and DNALI1 inhibition cells after staurosporine, protopanaxadiol and RSL3 treatment under serum normal status,  $n = 6$  wells from one representative of 3 independent experiments. **b.** Cell viability of normal and DNALI1 inhibition cells after Rapamycin, 3-MA, or VPS34-IN1 treatment under serum normal status,  $n = 6$  wells from one representative of 3 independent experiments. The data are presented as the means  $\pm$  SEM. Two-way ANOVA with Sidak's multiple comparisons test (**a-b**) was used. P values are indicated on the graphs.



**Figure S9.** All uncropped images of the western blots in the study.

**Table S1. Demographic Characteristics of Aging, Dementia and Traumatic Brain Injury Study.**

	<b>Control (n=57)</b>	<b>Dementia (n=50)</b>	<b>P value</b>
Age, mean (SD) years	88.44 (6.71)	90.18 (6.46)	0.176 <sup>a</sup>
Education, mean (SD) years	14.68 (3.22)	13.54 (3.16)	0.067 <sup>a</sup>
Braak stage	2.82 (1.49)	4.1 (1.74)	< 0.001
CERAD score	1.23 (0.91)	1.76 (1.20)	0.01 <sup>a</sup>
Presence of ApoE4 allele	7	13	0.085 <sup>b</sup>
Ever TBI with Loss of Consciousness	27	26	0.70 <sup>b</sup>
Longest duration of loss of consciousness			
< 10 sec	11	8	—
10 sec - 1 min	0	2	—
1-2 min	3	2	—
3-5 min	2	1	—
6-9 min	1	0	—
10 min - 1 h	4	4	—
> 1 h	4	4	—

Total, n = 107. Data are presented as mean (SD) or n. TBI = Traumatic brain injury; CERAD = Consortium to Establish a Registry for Alzheimer's Disease.

a: P-values from Student's T-Test test.

b: P-values from the chi-square test.

**Table S2. Short interfering RNA sequences.**

<b>Target</b>		<b>Sequences</b>
DNALI1	Forward	CCCAACMGGAAGGCAUUAUTT
	Reverse	AUAAMGCCUCCAGUMGGTT

**Table S3. DNA sequences bound by sgRNAs.**

<b>sgRNA</b>		<b>Target sequences</b>
DNALI1-mouse-sp	Forward	TGGCTGTGGGCTTGTA TAG
	Reverse	CTAGTACAAGCCCACAGCCA
Empty	Forward	GCACTACCAGAGCTAACTCA
	Reverse	TGAGTTAGCTCTGGTAGTGC
SiRNA- <i>DNALI1</i>	Forward	CCCAACMGGAAGGCAUUAUTT
	Reverse	AUAAMGCCUCCAGUMGGGTT