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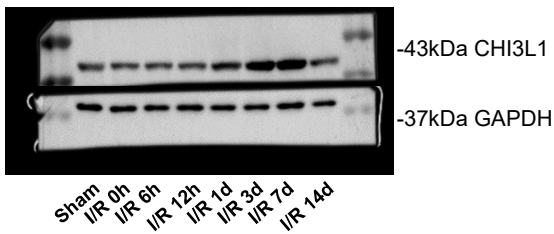


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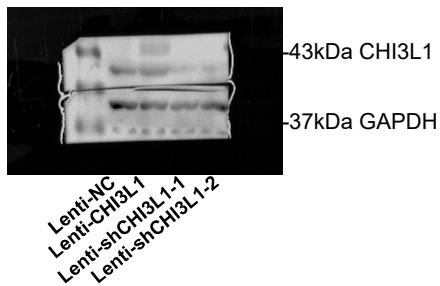


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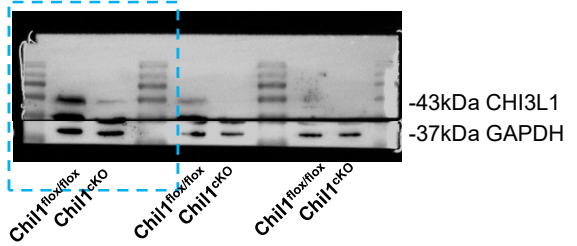


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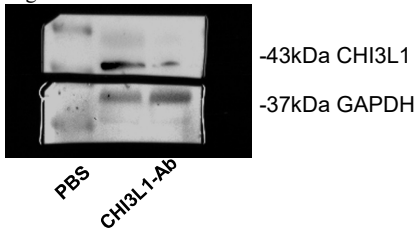


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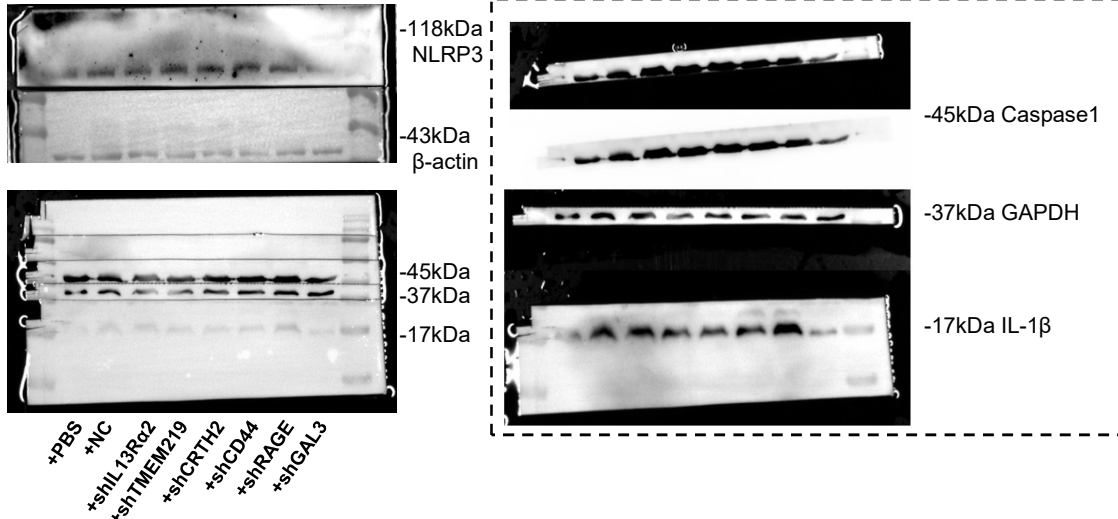


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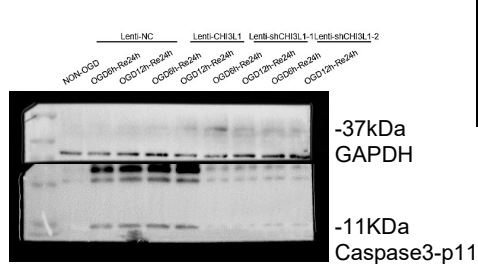


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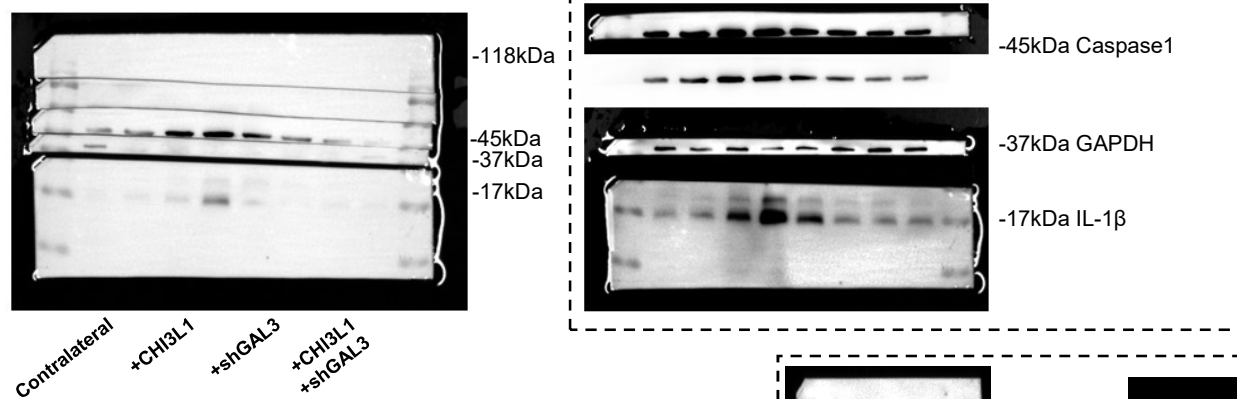


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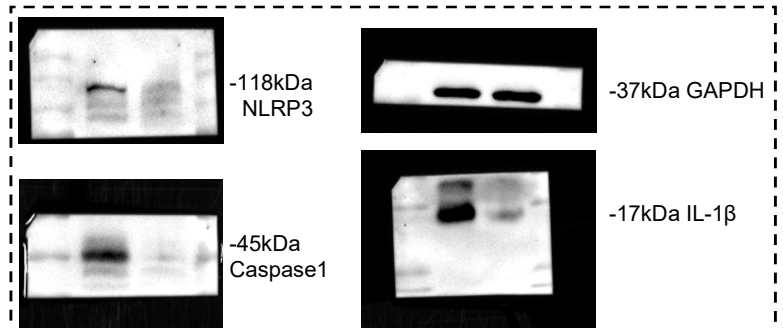
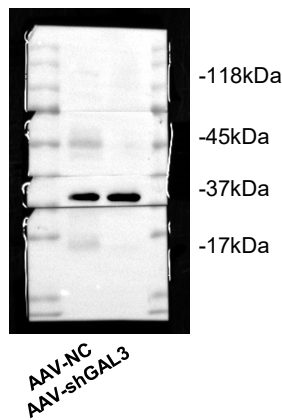
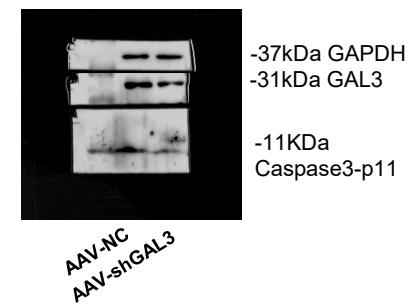


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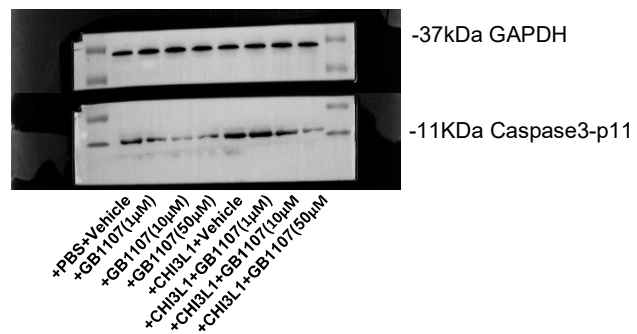


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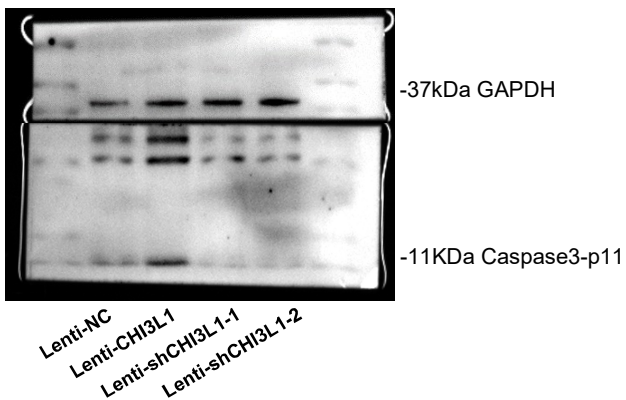


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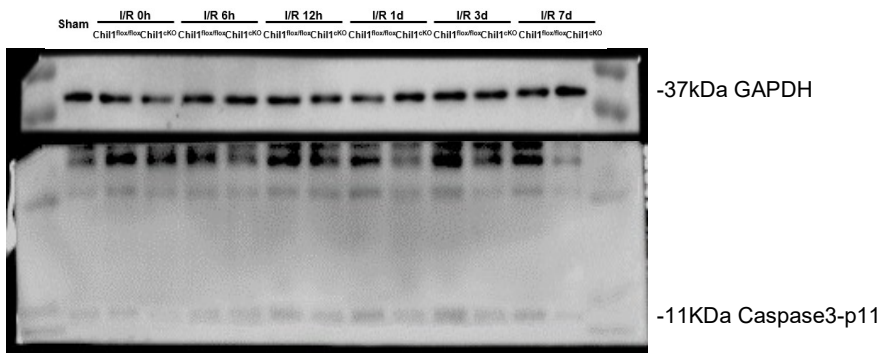


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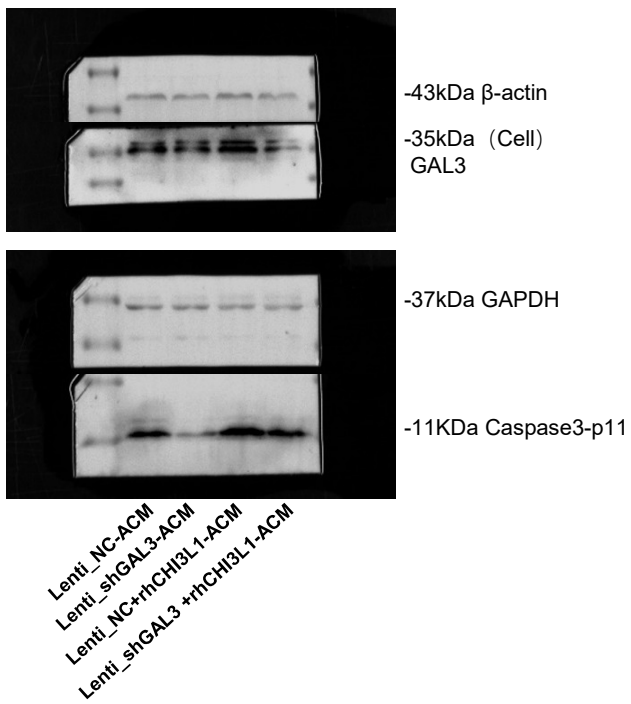


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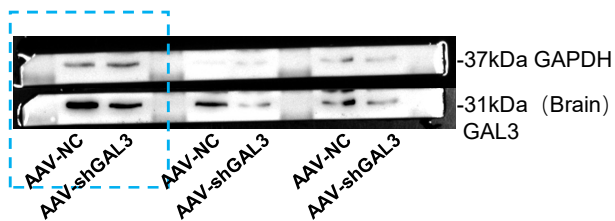
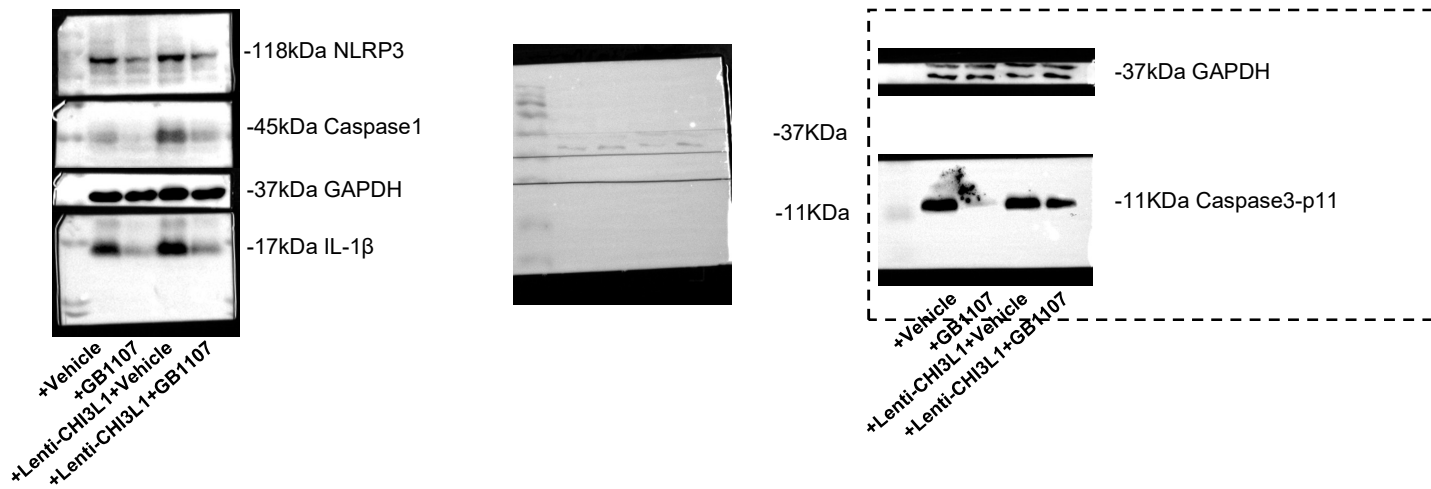


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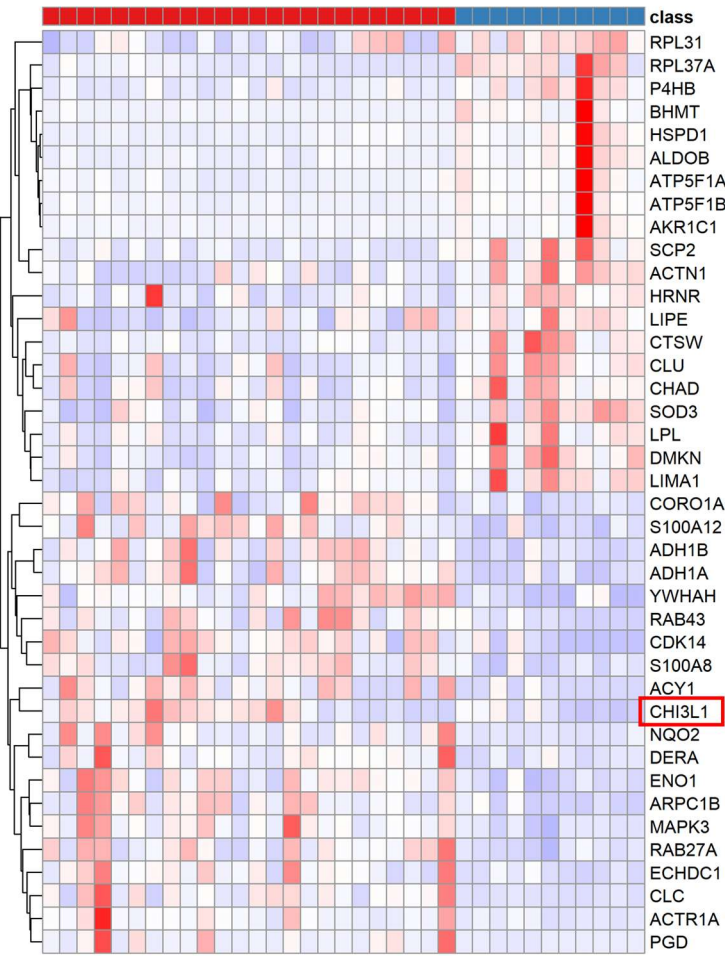
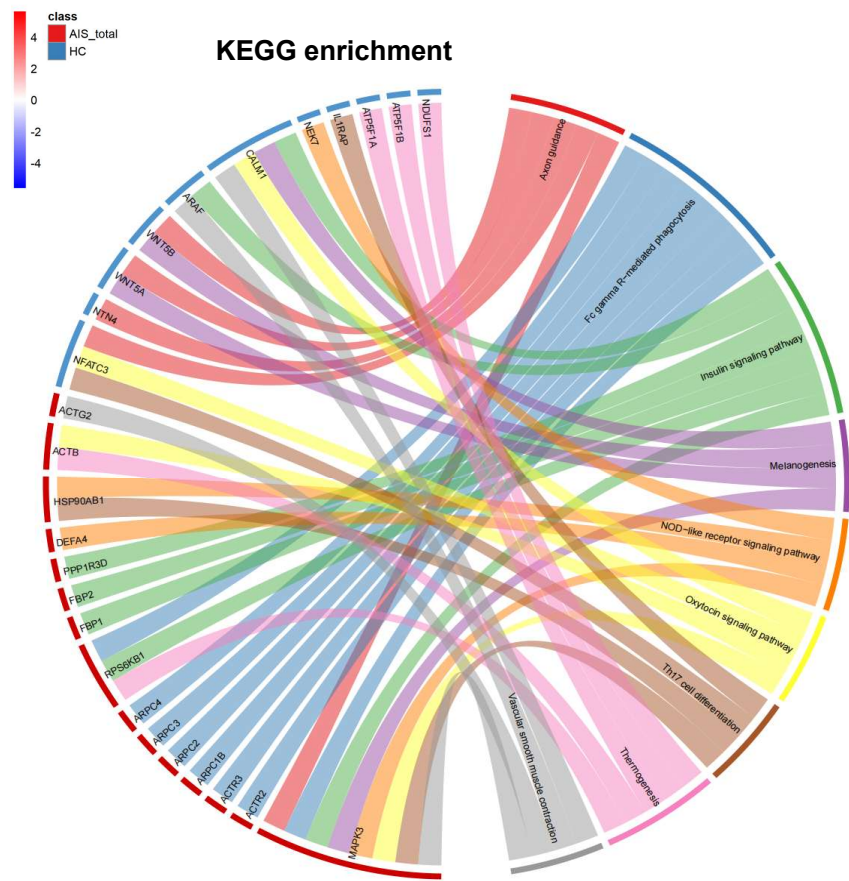
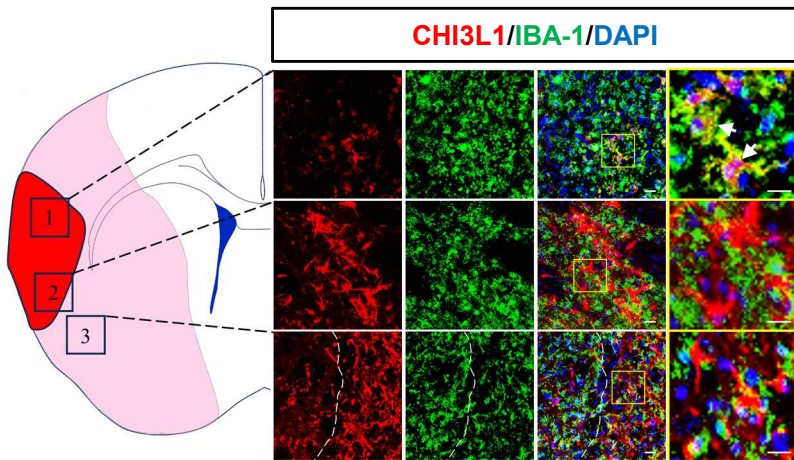
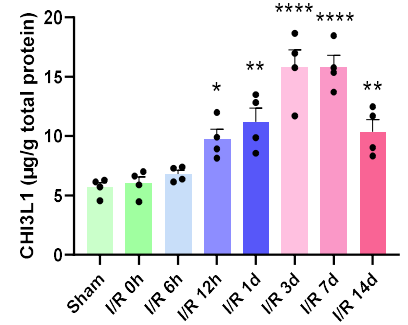
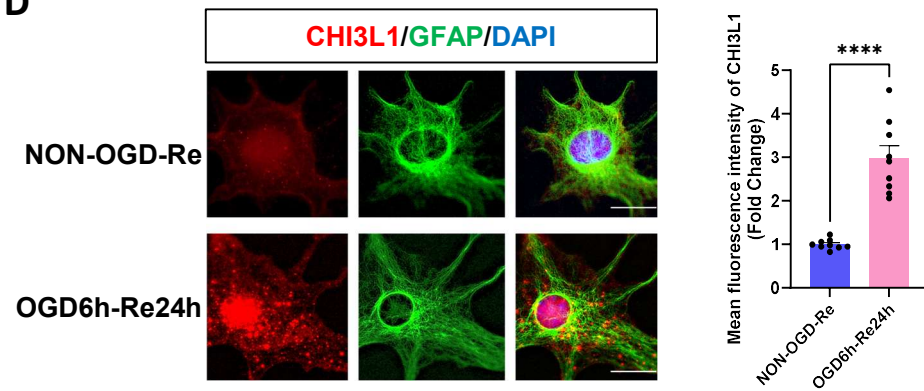
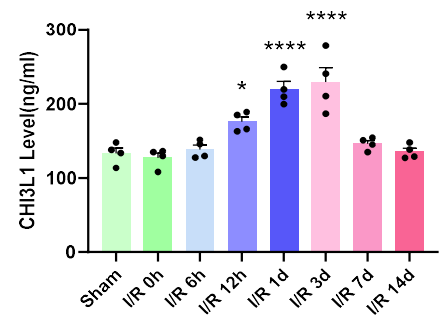
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Fig. S1 Molecular and Cellular Insights into CHI3L1 in Acute Ischemic Stroke

(A) Heatmap of differentially expressed serum proteins between acute ischemic stroke (AIS) patients (n = 24) and healthy controls (HC, n = 11), based on proteomic profiling. Red indicates upregulation; blue indicates downregulation.

(B) KEGG pathway enrichment analysis of the differentially expressed proteins. Enriched pathways are shown with lines denoting functional relationships.

(C) Representative immunofluorescence images of IBA-1 (green) and CHI3L1 (red) in various brain regions of tMCAO mice. A subset of microglia co-localized with CHI3L1 near the infarct core. Nuclei were stained with Hoechst (blue). Scale bar = 10 μ m.

(D) Immunofluorescence images of primary astrocytes stained for GFAP (green) and CHI3L1 (red) following 6 h oxygen-glucose deprivation and 24 h reoxygenation (OGD6h-Re24h). CHI3L1 expression was significantly increased compared to control. n = 9 cells from three independent cultures. Scale bar = 10 μ m.

(E) CHI3L1 protein levels in mouse brain tissue at various time points (Sham, IR 6h, IR 12h, IR 1d, IR 3d, IR 7d, IR 14d) after tMCAO, measured by ELISA.

(F) CHI3L1 protein levels in mouse serum at various time points after tMCAO, measured by ELISA.

Data analyzed by Student's t-test or one-way ANOVA, Statistical significance: *p < 0.05; **p < 0.01; ***p < 0.001; ****p < 0.0001. Data are presented as mean \pm SEM.

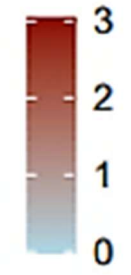
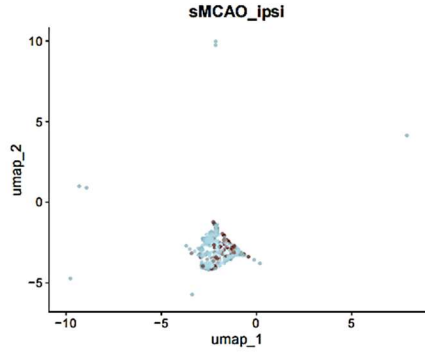
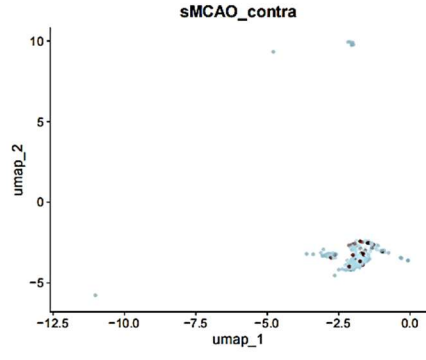
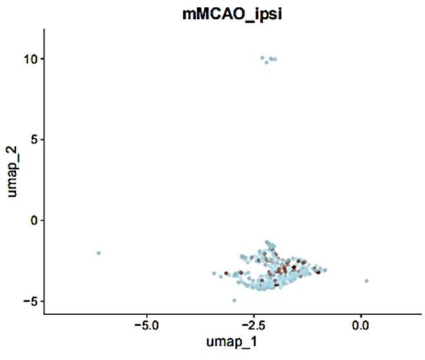
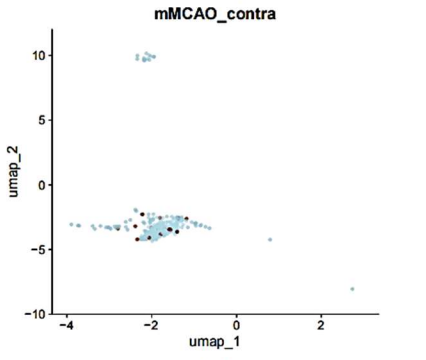
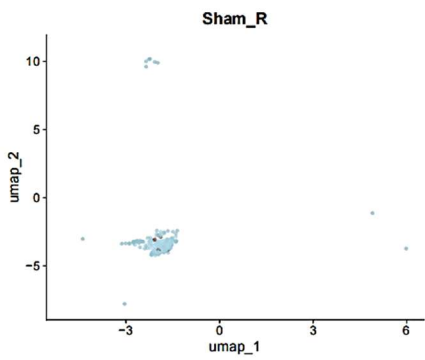
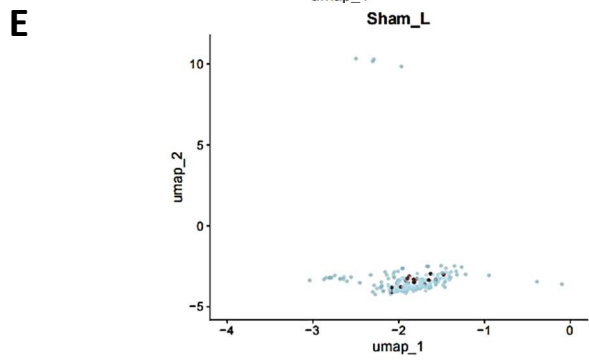
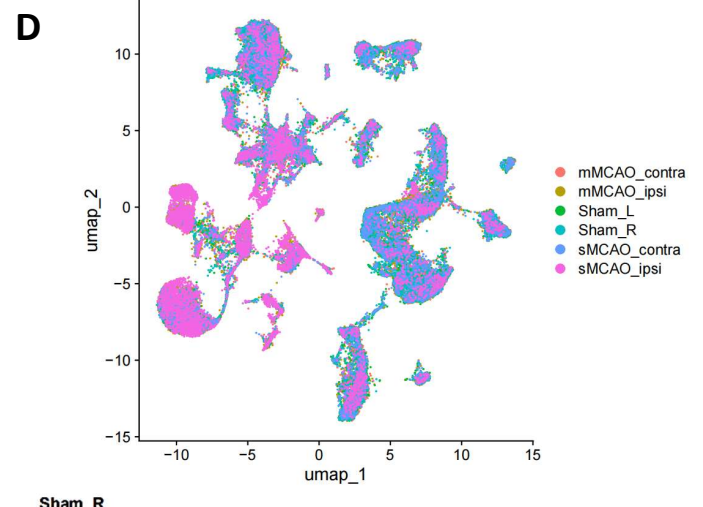
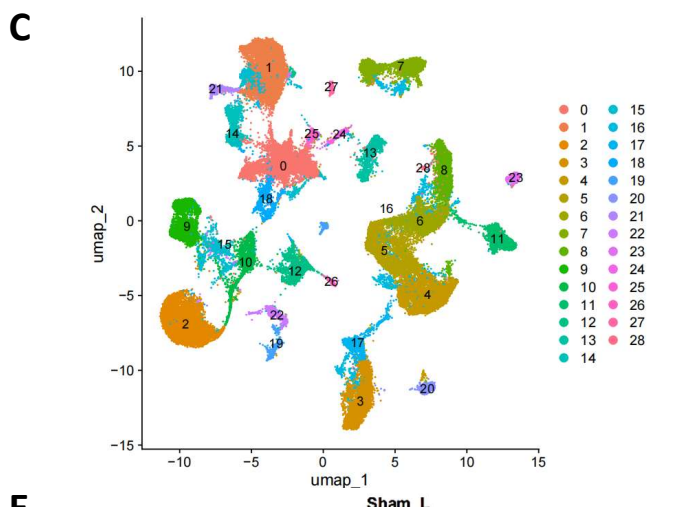
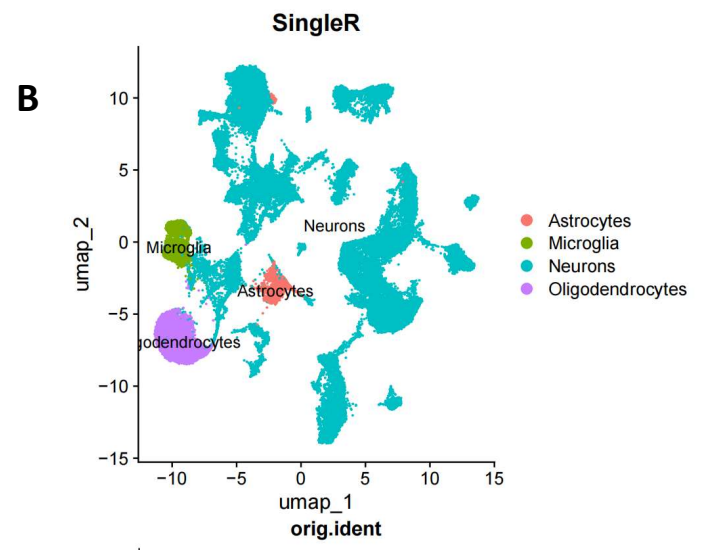
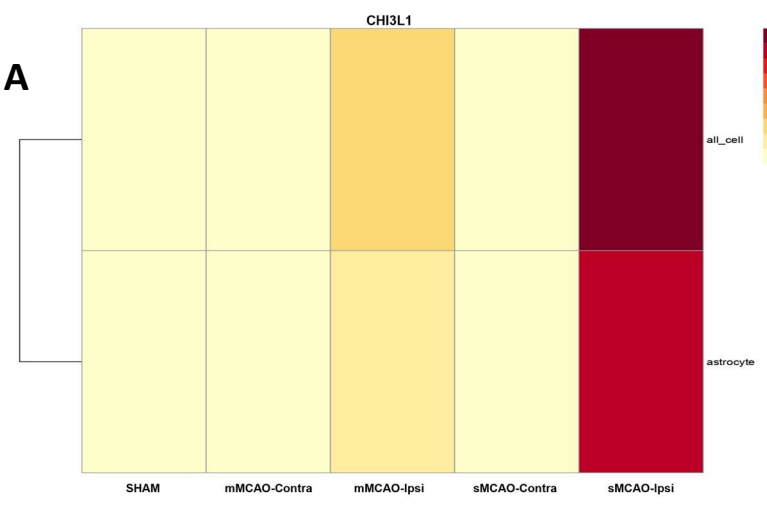


Fig. S2 Single-Cell RNA Sequencing Analysis of CHI3L1 Expression in Ischemic Brain

(A) Heatmap of CHI3L1 expression from single-cell RNA sequencing data (GEO). Experimental groups include SHAM, mMCAO-Contra, mMCAO-Ipsi, sMCAO-Contra, and sMCAO-Ipsi. CHI3L1 upregulation post-tMCAO is primarily attributed to astrocytes. Color scale represents expression intensity. (acc=GSE250245, PMID: 39043661); Sham L = left brain hemispheres of Sham operated controls; Sham R = right hemispheres of Sham operated controls; mMCAO contra: left brain hemispheres of MCAO group animals, with moderate infarction severity, hemispheres contralateral to infarction; mMCAO ipsi: right brain hemispheres of MCAO group animals, with moderate infarction severity, hemispheres ipsilateral to infarction, sMCAO contra: left brain hemispheres of MCAO group animals, with severe infarction severity, hemispheres contralateral to infarction; sMCAO ipsi: right brain hemispheres of MCAO group animals, with severe infarction severity, hemispheres ipsilateral to infarction.

(B) SingleR cell type annotation UMAP plot, identifying major cell populations: Astrocytes, Neurons, Microglia, and Oligodendrocytes.

(C) UMAP plot colored by cell clusters.

(D) UMAP plot colored by experimental groups (mMCAO_Contra, mMCAO_Ipsi, Sham_L, Sham_R, sMCAO_Contra, sMCAO_Ipsi).

(E) Feature plots showing CHI3L1 expression in Astrocytes distribution across groups: Sham_L, Sham_R, mMCAO_Contra, mMCAO_Ipsi, sMCAO_Contra, and sMCAO_Ipsi. The color scale represents CHI3L1 expression levels.

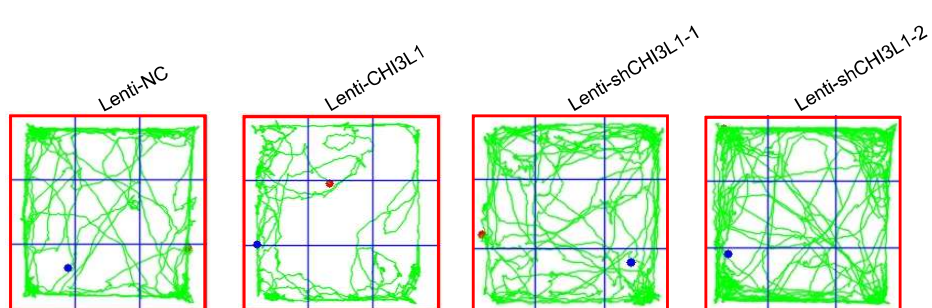
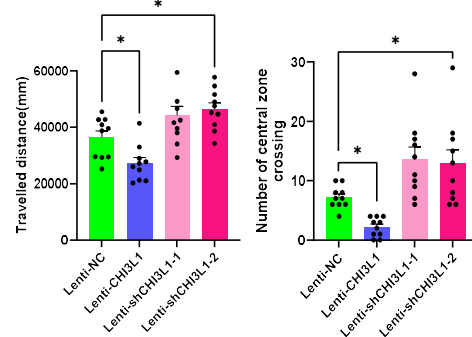
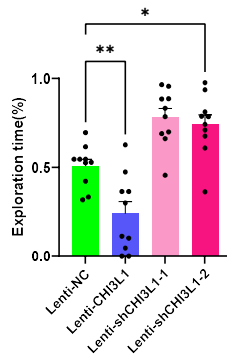
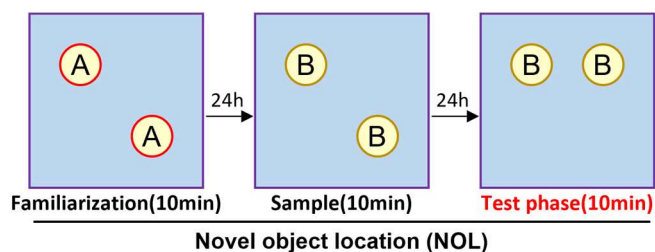
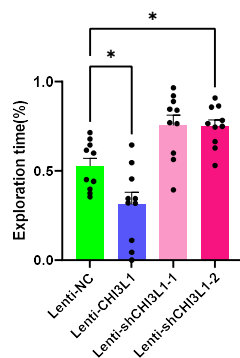
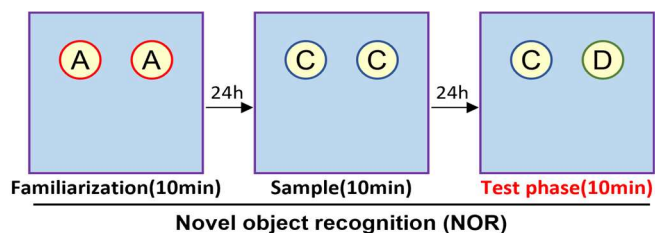
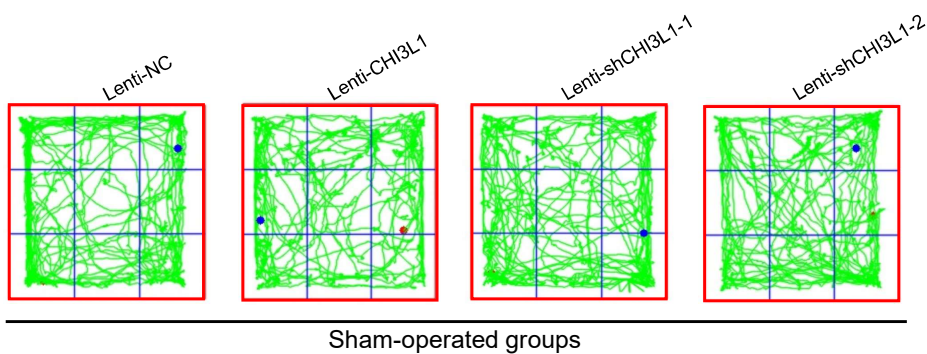
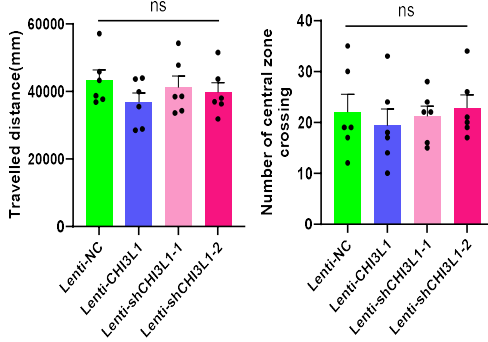
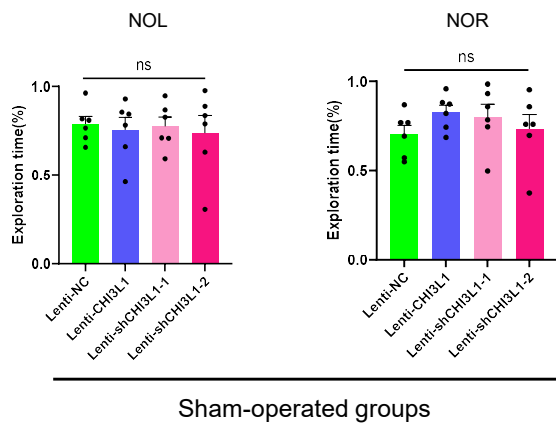
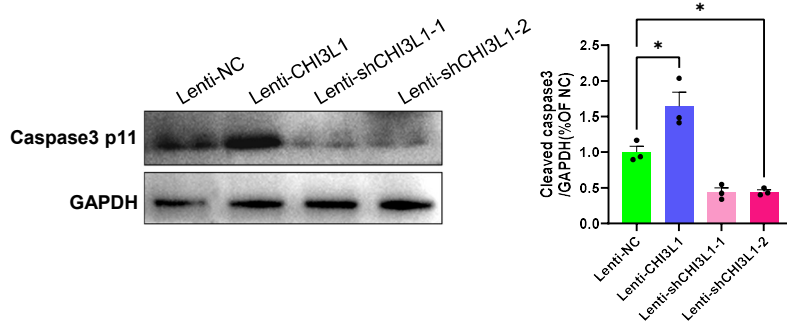
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Fig. S3 Behavioral and Apoptotic Effects of Lentivirus - mediated CHI3L1 Manipulation in a Mouse Model

(A-B) Open Field Test (OFT) in four experimental groups post tMCAO: Lent-NC, Lent-CHI3L1 (overexpression), Lent-shCHI3L1-1, and Lent-shCHI3L1-2 (knockdown). (A) Representative movement paths. (B) Quantification of total distance traveled and center area crossings. n = 10 mice per group.

(C) Novel Object Location (NOL) test post tMCAO. Schematic shows the familiarization, sample, and test phases (each 10 min). CHI3L1 knockdown mice showed increased exploratory preference for the novel location, while CHI3L1 overexpression reduced preference. n = 10 per group.

(D) Novel Object Recognition (NOR) test post tMCAO. Following the same trial structure as the NOL test, CHI3L1 knockdown enhanced, and overexpression reduced, preference for the novel object. n = 10 per group.

(E-F) OFT in four experimental groups (Sham-operated groups): Lent-NC, Lent-CHI3L1 (overexpression), Lent-shCHI3L1-1, and Lent-shCHI3L1-2 (knockdown).

(E) Representative movement paths. (F) Quantification of total distance traveled and center area crossings. n = 6 mice per group.

(G) NOL and NOR test in Sham-operated groups. n = 6 mice per group.

(H) Western blot analysis of cleaved caspase-3 (Caspase3 p11) in brain tissue from lentivirus-injected groups (Lent-NC, Lent-CHI3L1, Lent-shCHI3L1-1, Lent-shCHI3L1-2) post tMCAO to assess neuronal apoptosis. n = 3 per group.

Data are presented as mean \pm SEM. Statistical significance was evaluated using one-way ANOVA with Tukey's multiple comparisons test or Kruskal-Wallis test as appropriate. p < 0.05; *p < 0.01; **p < 0.001; ***p < 0.0001.

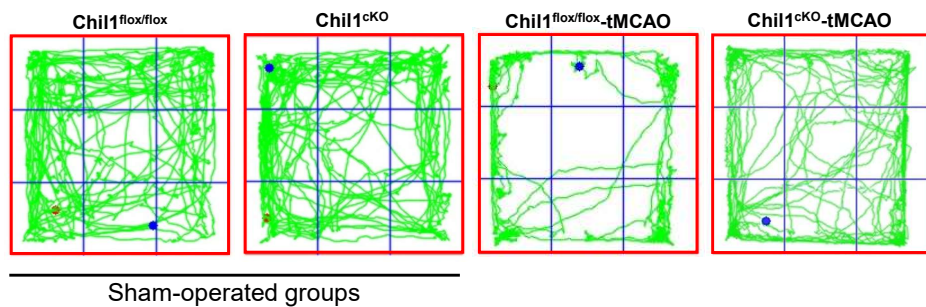
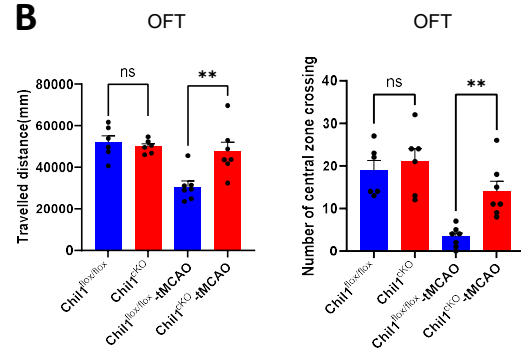
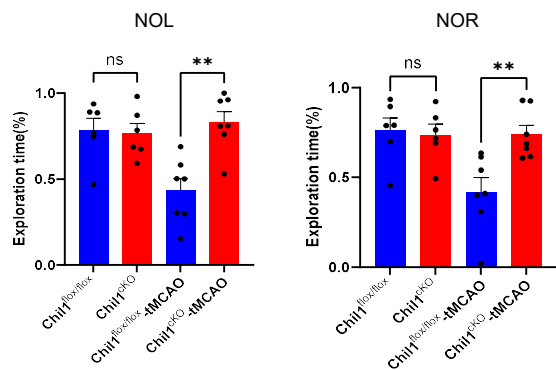
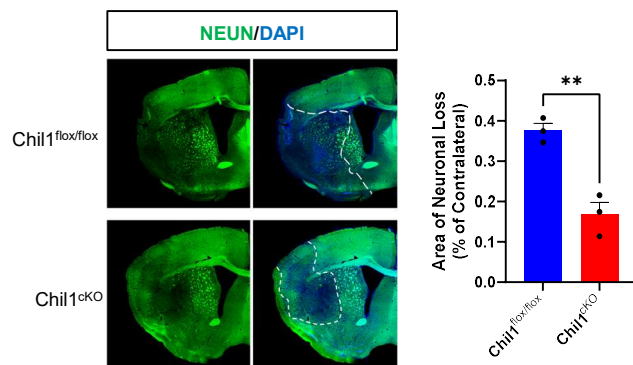
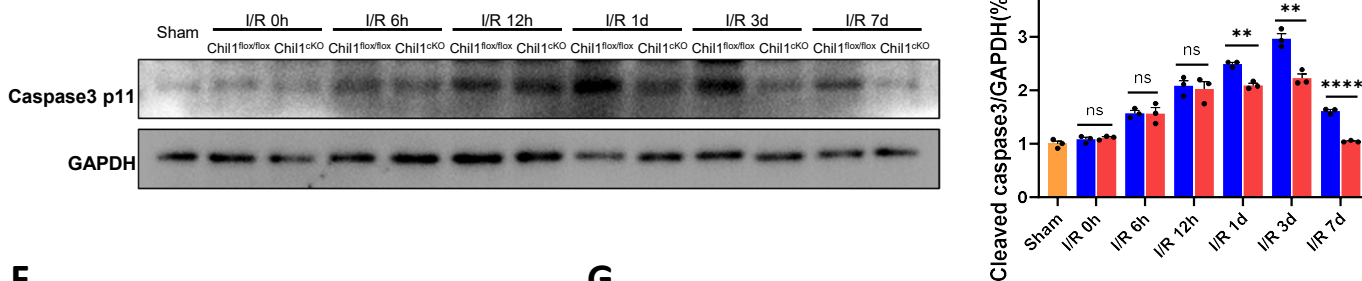
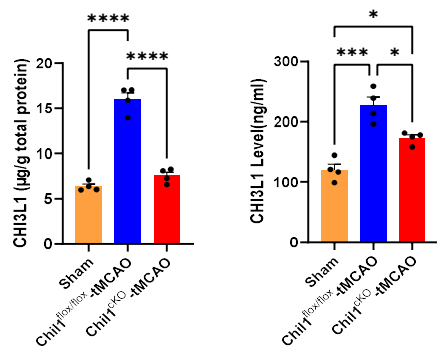
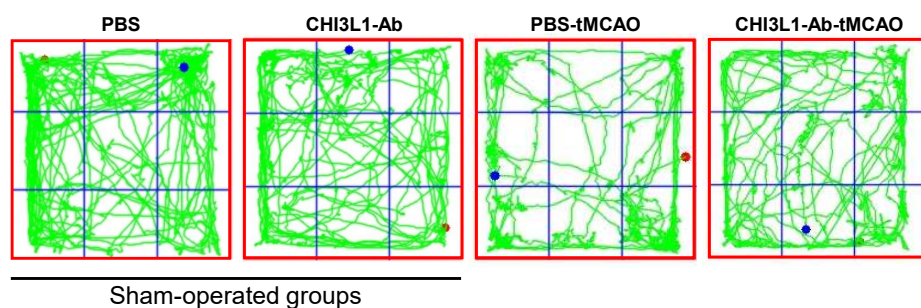
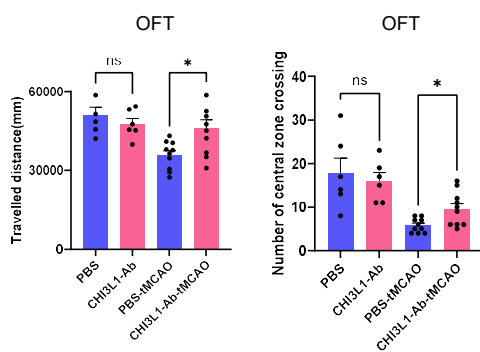
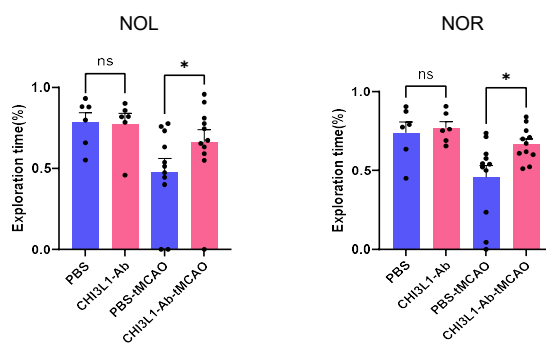
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Fig. S4 Behavioral and Neuronal Integrity Analysis in Genetically Altered and CHI3L1 - Antibody - Treated Mice

(A-B) OFT in *Chil1^{fllox/fllox}* and *Chil1^{ckO}* Mice. (A) Representative movement paths. (B) Quantification of total distance traveled and center area crossings. Non-tMCAO groups: N = 6 animals per group; tMCAO groups: N = 7 animals per group.

(C) NOL and NOR Tests in *Chil1^{fllox/fllox}* and *Chil1^{ckO}* Mice. Non-tMCAO groups: N = 6 animals per group; tMCAO groups: N = 7 animals per group.

(D) Immunofluorescence staining of NeuN (green) and DAPI (blue) in *Chil1^{fllox/fllox}* and *Chil1^{ckO}* mice at day 7 post-tMCAO. N = 3 per group.

(E) Neuronal apoptosis evaluated by Western blotting for cleaved caspase-3 (Caspase3 p11) expression at different time points post-ischemia in genetically modified mouse groups (*Chil1^{fllox/fllox}* and *Chil1^{ckO}* Mice). n = 3 per group.

(F) Left: ELISA for CHI3L1 protein levels in brain tissue of *Chil1^{fllox/fllox}* and *Chil1^{ckO}* mice at day 3 post-tMCAO. Right: ELISA for CHI3L1 levels in serum of *Chil1^{fllox/fllox}* and *Chil1^{ckO}* mice at day 3 post-tMCAO. n = 4 per group.

(G-H) OFT in PBS and anti-CHI3L1 treatment groups. (G) Representative movement paths. (H) Quantification of total distance traveled and center area crossings. Non-tMCAO groups: n = 6 animals per group; tMCAO groups: n = 11 animals per group.

(I) NOL and NOR tests in PBS and anti-CHI3L1 treatment groups. Non-tMCAO groups: n = 6 animals per group; tMCAO groups: n = 11 animals per group.

Data are presented as mean \pm SEM. statistical significance was evaluated using the Mann - Whitney test or Student's t - test. Significance levels: *p < 0.05; **p < 0.01; ***p < 0.001; ****p < 0.0001.

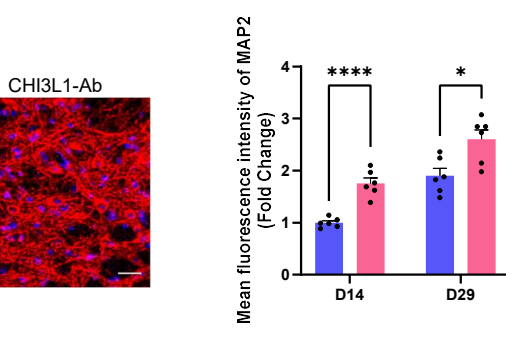
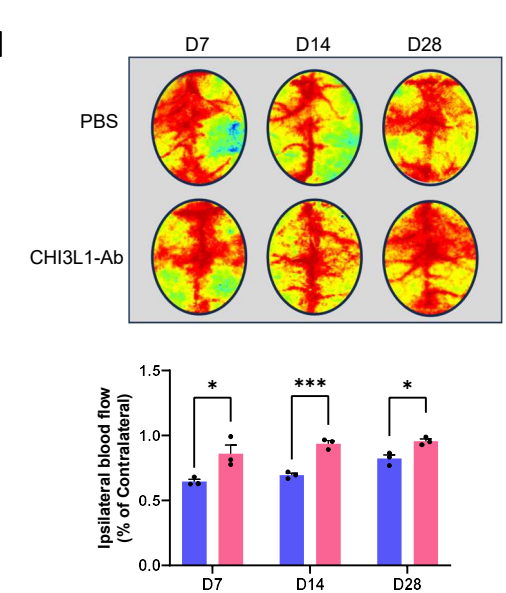
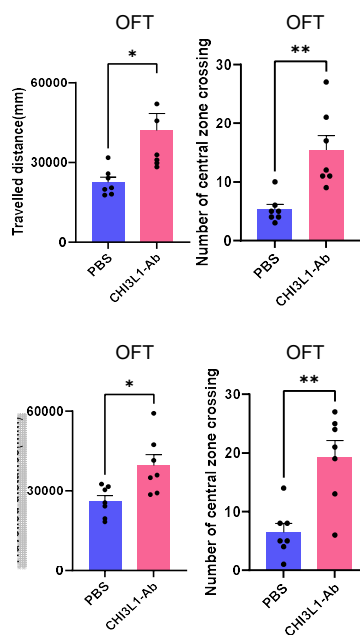
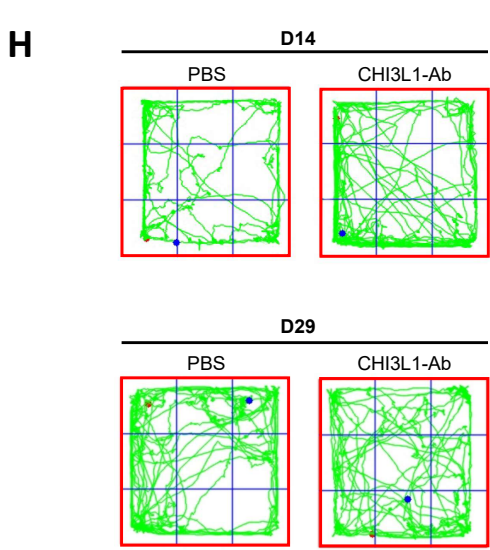
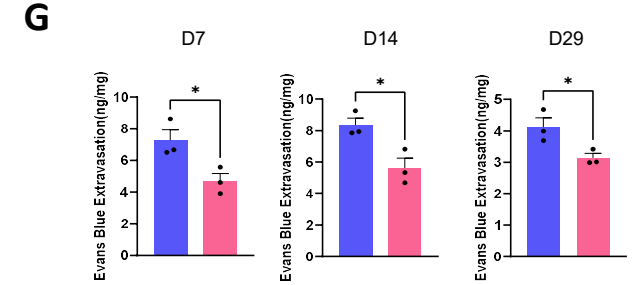
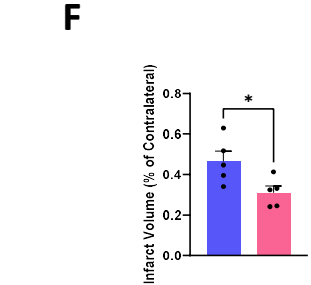
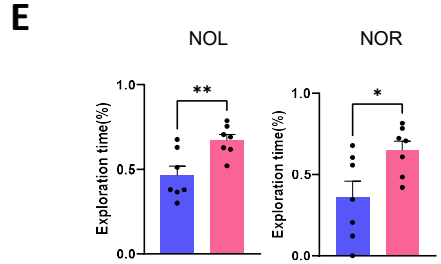
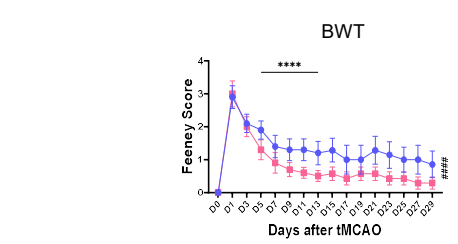
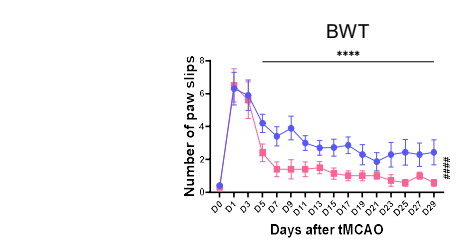
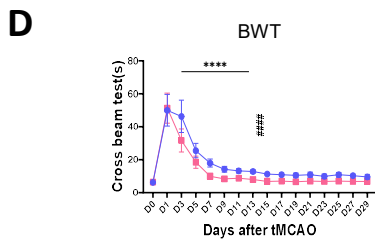
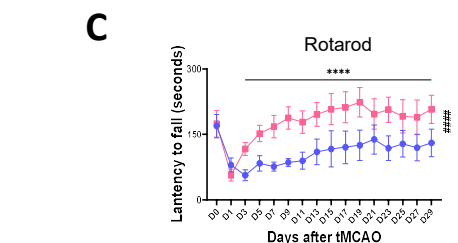
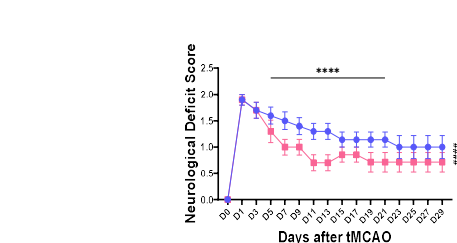
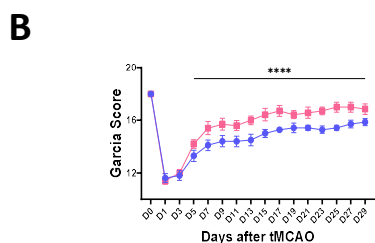
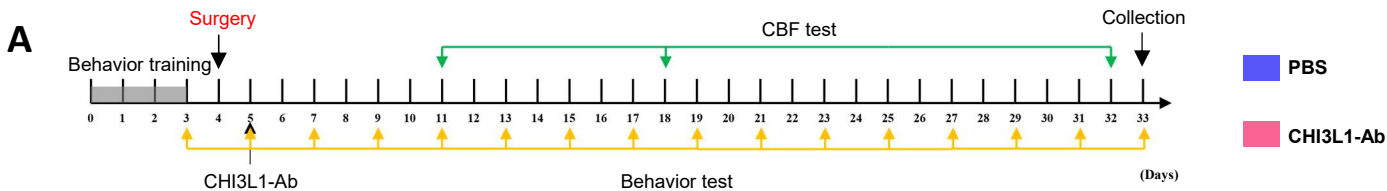


Fig. S5 Long-Term Prognostic Analysis of Post-tMCAO CHI3L1-Ab Treatment in Mice

(A) Mice received stereotaxic intracerebral injection of CHI3L1-Ab or PBS within 24 h post-tMCAO, followed by behavioral tests and sample collection up to 4 weeks.

(B-D) Motor function recovery assessed by Garcia scores, Neurological deficit scores (B), rotarod test (C), and beam-walking test (D) over 29 days post-tMCAO (n = 10 mice per group). Significance levels: *p < 0.05; **p < 0.01; ***p < 0.001; ****p < 0.0001 compared to the control mice at indicated time points; #p < 0.05; ##p < 0.01; ###p < 0.001; ####p < 0.0001 compared to the control mice across the entire experiment.

(E) NOL and NOR tests assessing cognitive function at days 7 post-tMCAO. N = 7 animals per group.

(F) Infarct volume quantification by TTC staining at days 5 post-tMCAO. N = 5 animals per group.

(G) Blood-brain barrier (BBB) permeability evaluated by Evans blue assay at days 7, 14, and 29 post-tMCAO (n = 3 per group at each time point).

(H) OFT at days 14 and 29 post-tMCAO: (left) representative movement paths; (right) quantification of total distance traveled and center area crossings N = 7 animals per group.

(I) Laser speckle imaging for CBF distribution and quantification of relative CBF at days 7, 14, and 28 post-tMCAO (n = 3 per group at each time point)

(J) Immunohistochemistry of MAP2 (red) and DAPI (blue) in peri-infarct penumbra at 14 and 29 days post-stroke (n = 6).

Data are presented as mean ± SEM. Data analyzed by two-way ANOVA or Mann - Whitney test or Student's t - test. Significance thresholds: *p < 0.05; **p < 0.01; ***p < 0.001; ****p < 0.0001.

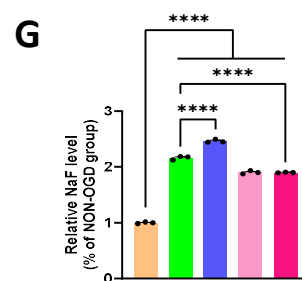
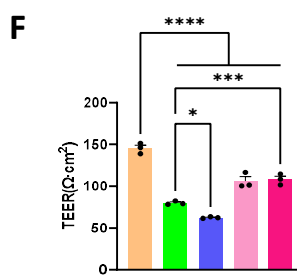
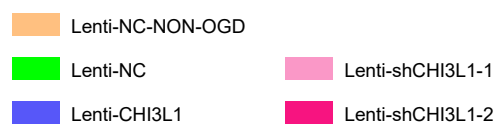
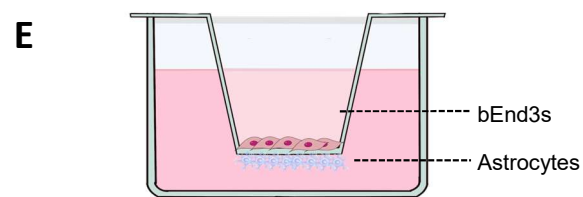
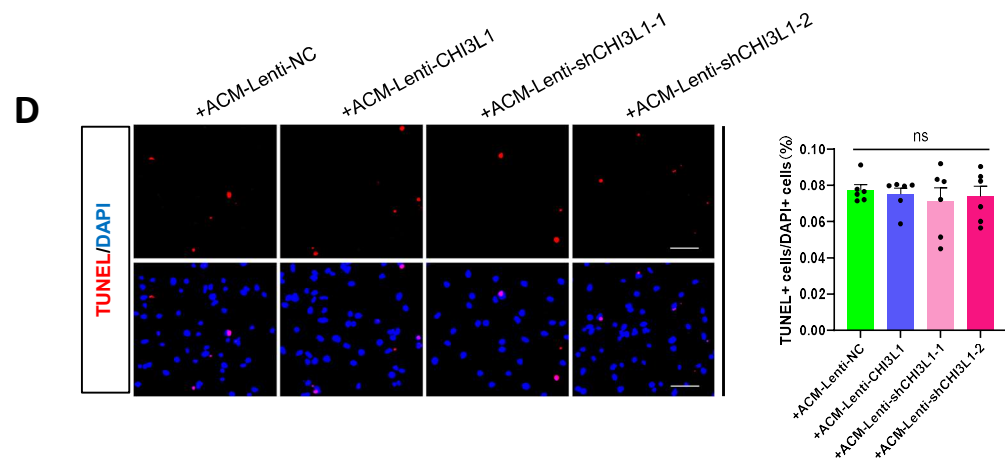
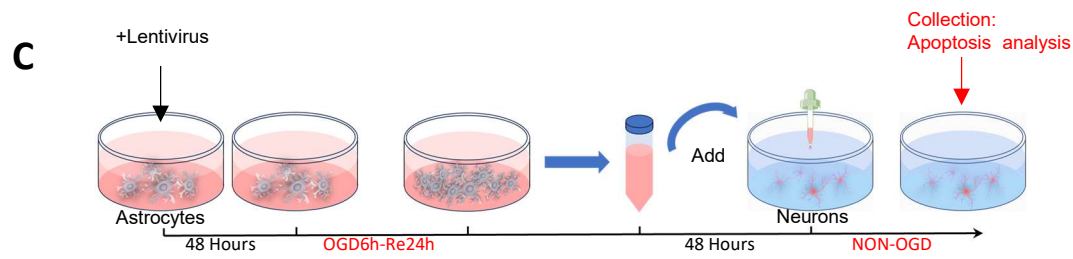
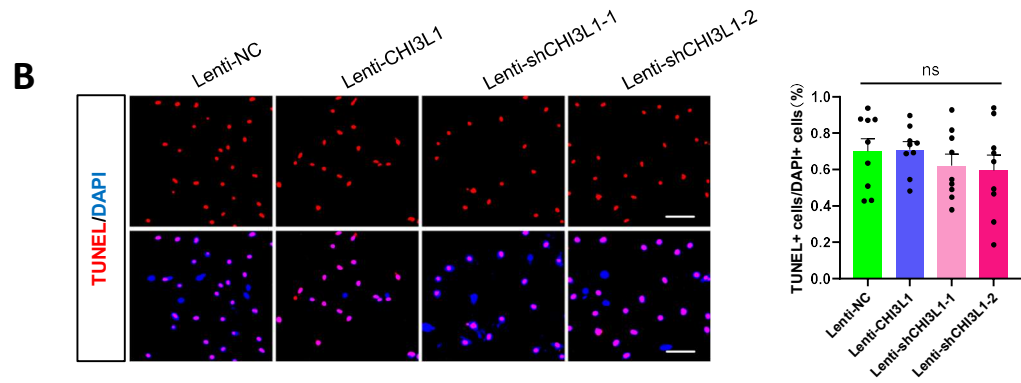
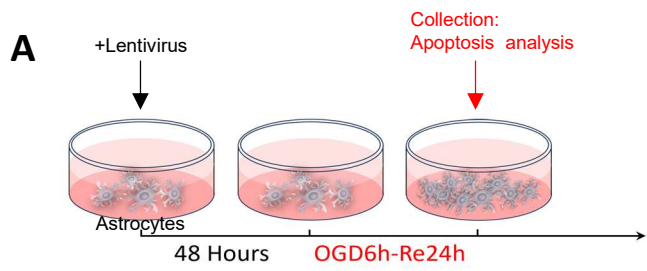


Fig. S6 Role of CHI3L1 in Astrocyte Apoptosis, Neuronal Apoptosis, and In Vitro Blood-Brain Barrier (BBB) Function Under OGD/Re Conditions

(A) Primary astrocytes were transfected with CHI3L1 - related lentiviruses (Lent - NC, Lent - CHI3L1, Lent - shCHI3L1 - 1, Lent - shCHI3L1 - 2). After 48 hours of culture, they were subjected to oxygen - glucose deprivation for 6 hours followed by reoxygenation for 24 hours (OGD6h - Re24h), and then apoptosis analysis was conducted.

(B) TUNEL assay was performed on the four groups of astrocytes. Representative images of TUNEL (red) and DAPI (blue) staining are shown. There were no significant differences in apoptosis among the four groups. N = 9 from three independent cultures per group.

(C) After the astrocytes were transfected with CHI3L1 - related lentiviruses and subjected to OGD6h - Re24h, the astrocyte - conditioned medium (ACM) was collected. This ACM was then added to primary - cultured neurons, which were not subjected to OGD treatment. Subsequently, apoptosis analysis was carried out on these neurons.

(D) TUNEL staining was performed on the neurons treated as described in (C). Representative images of TUNEL (red) and DAPI (blue) staining are presented.

(E-G) In Vitro Blood-Brain Barrier (BBB) Model Analysis of CHI3L1 Manipulation Under OGD/Re Conditions (E) Schematic of the Transwell co-culture system for the in vitro BBB model: Astrocytes were seeded on the basolateral side of Transwell inserts, subjected to lentiviral transfection (Lent-NC, Lent-CHI3L1, Lent-shCHI3L1-1, Lent-shCHI3L1-2), Mouse brain microvascular endothelial cells (bEnd.3) were subsequently seeded into the apical chamber. (F) Measurement of transendothelial electrical resistance (TEER) in the in vitro BBB model. (G) Sodium fluorescein (NAF) permeability assay to evaluate BBB permeability.

Data are presented as mean \pm SEM; statistical significance by one-way ANOVA with Tukey's multiple comparisons test or Kruskal - Wallis test. Significance levels: **p < 0.01, ***p < 0.001, ****p < 0.0001.

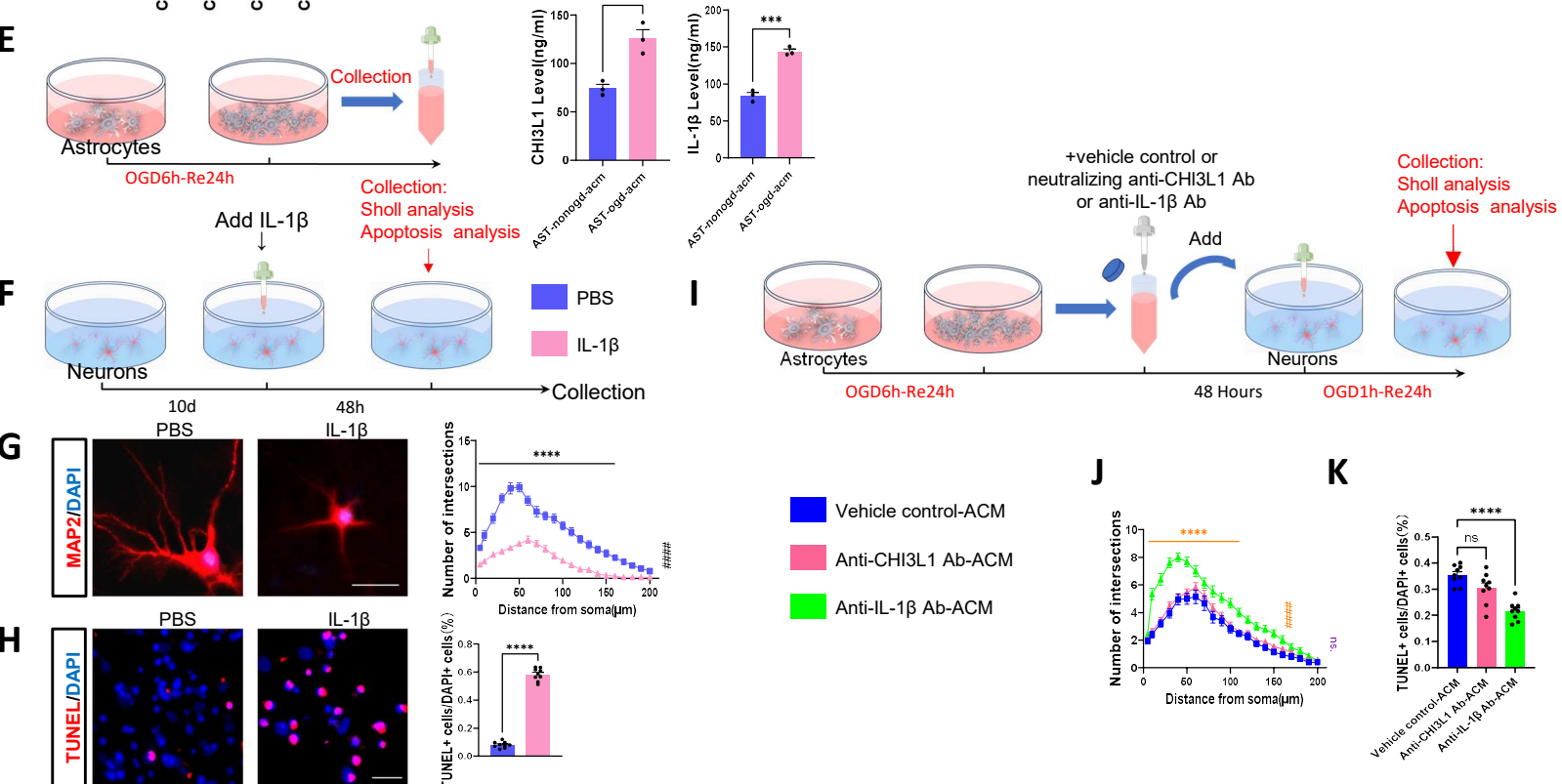
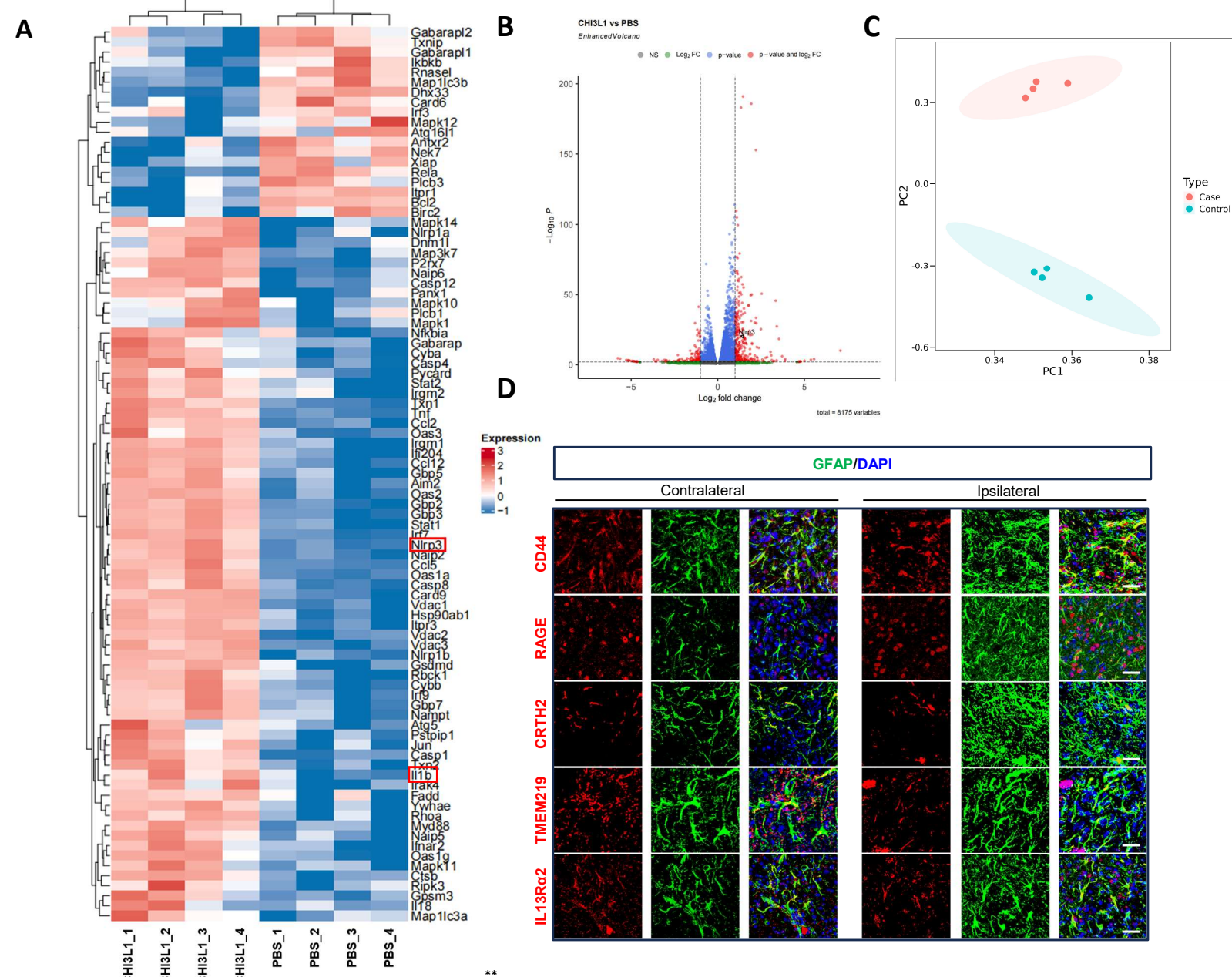


Fig. S7 Gene Expression Analysis in Astrocytes related to CHI3L1

(A) RNA - sequencing was performed on primary astrocytes treated with PBS or CHI3L1 - protein. N = 4 per group. Principal Component Analysis (PCA) was used to visualize the differences between the two groups. The PCA plot shows that the samples from the two groups (represented by different colors) are clearly separated, indicating distinct gene expression patterns.

(B) The volcano plot from the RNA - sequencing analysis of primary astrocytes treated with PBS or CHI3L1 - protein is shown. It illustrates the fold - change and statistical significance (p - value) of gene expression. Points above the horizontal dashed line represent genes with significant differential expression.

(C) Differential expression analysis of the RNA - sequencing data from primary astrocytes treated with PBS or CHI3L1 - protein identified significant changes in NLRP3 expression. The heatmap shows the expression levels of various genes, with NLRP3 highlighted. Different colors represent different expression levels, indicating the up - or down - regulation of genes in the two treatment groups.

(D) Immunofluorescence staining was conducted to visualize the expression levels of six CHI3L1 downstream receptors (IL13R α 2, TMEM219, CRTH2, CD44, RAGE, GAL3) in the peri-infarct region of the contralateral and ipsilateral hemisphere after tMCAO. For each receptor, images show staining for the receptor in red, GFAP (a marker for astrocytes) in green, and nuclei counterstained with DAPI in blue.

(E) Experimental design: Primary astrocytes were subjected to OGD6h-Re24h, and the conditioned medium was collected. ELISA was used to detect CHI3L1 and IL-1 β levels in the medium. N = 3 per group.

(F) Schematic of recombinant IL-1 β treatment on primary neurons: Neurons were cultured for 10 days, then treated with IL-1 β for 48 h, followed by Sholl analysis and apoptosis assessment.

(G) Immunofluorescence staining of MAP2 (red) in neurons treated with PBS or IL-1 β , with Sholl analysis quantification of dendritic complexity. Scale bar=10 μ m.

(H) TUNEL staining (red) of neurons treated with PBS or IL-1 β , with quantification of TUNEL-positive cells. Scale bar=50 μ m.

(I) Experimental design and outcomes of astrocyte-conditioned medium (ACM) pretreatment with CHI3L1-neutralizing antibody or IL-1 β -neutralizing antibody, followed by neuronal OGD1h-Re24h: (I) Sholl analysis of neuronal dendritic complexity, In the analysis, orange bars represent the comparison between the Vehicle control-ACM and Anti-IL-1 β Ab-ACM groups, while purple bars comparison between the Vehicle control-ACM and Anti-CHI3L1 Ab-ACM groups; (J) TUNEL staining quantification of neuronal apoptosis.

Data are presented as mean \pm SEM. Statistical significance was evaluated using Student's t-test or two-way ANOVA. Significance levels: p < 0.05, *p < 0.001, **p < 0.0001; #p < 0.05; ##p < 0.01; ###p < 0.001; ####p < 0.0001 ns, not significant.

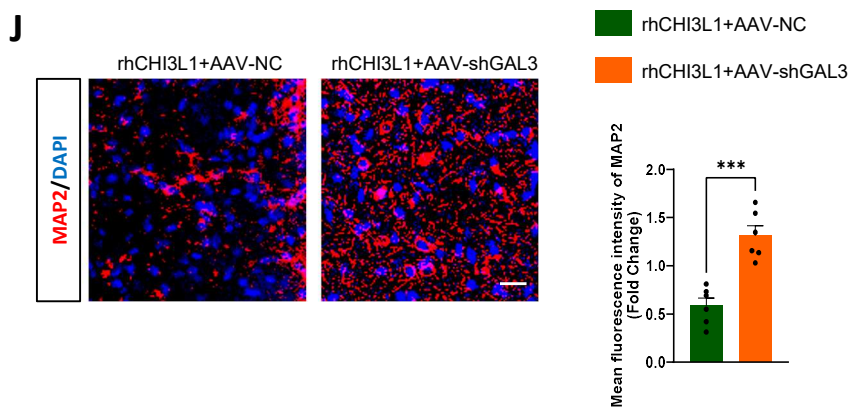
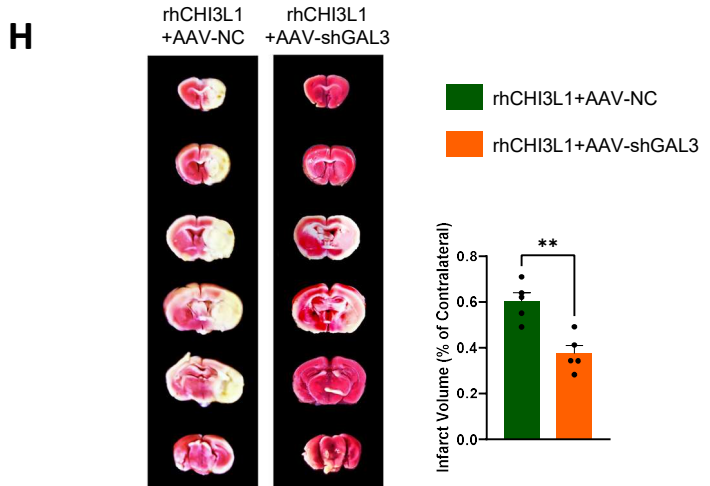
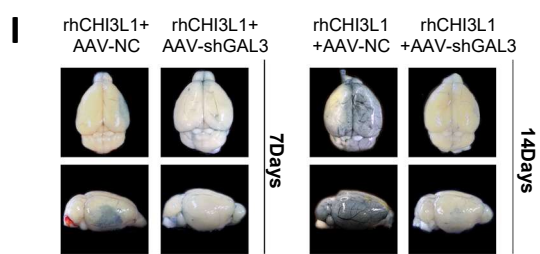
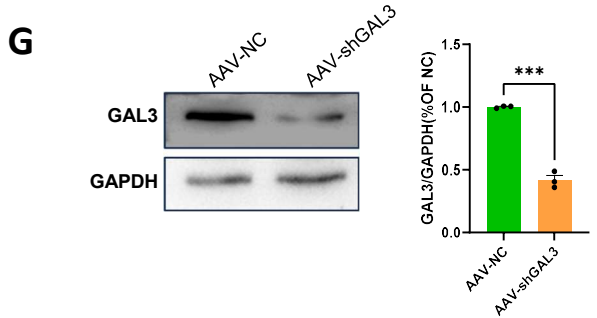
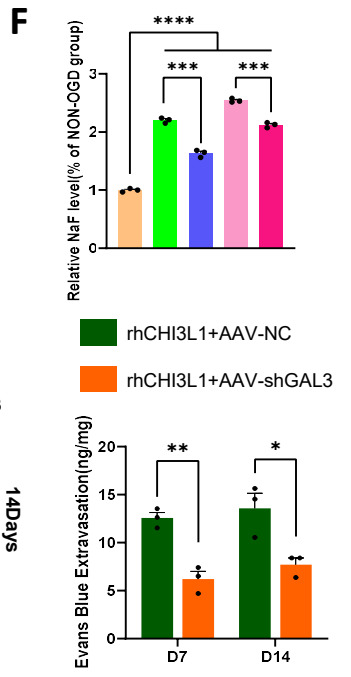
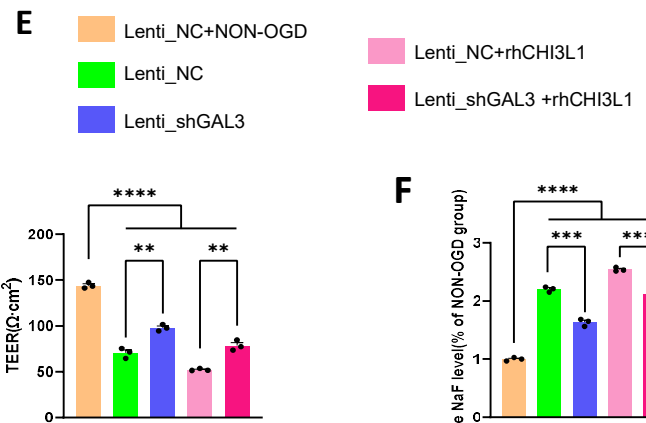
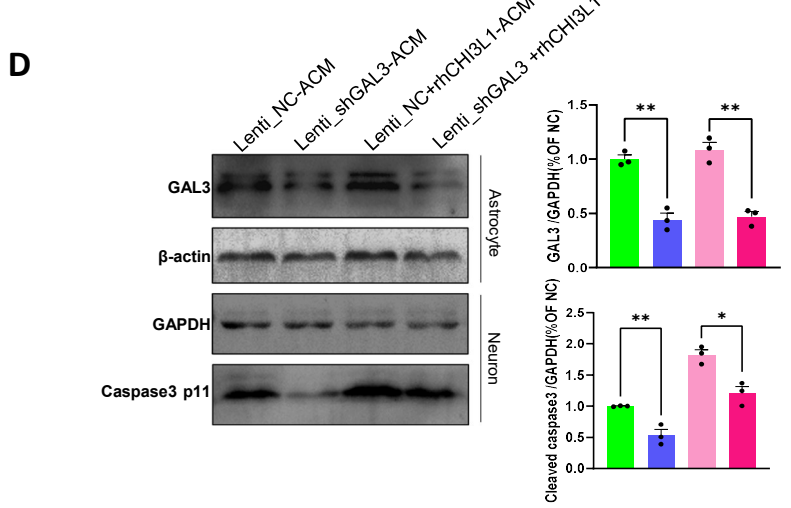
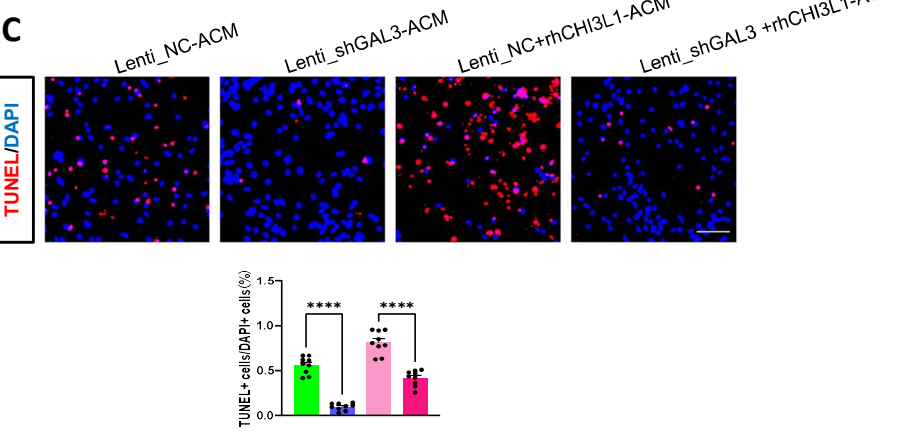
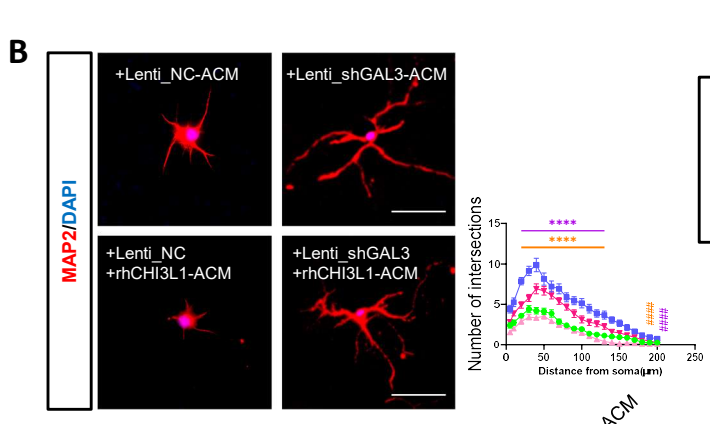
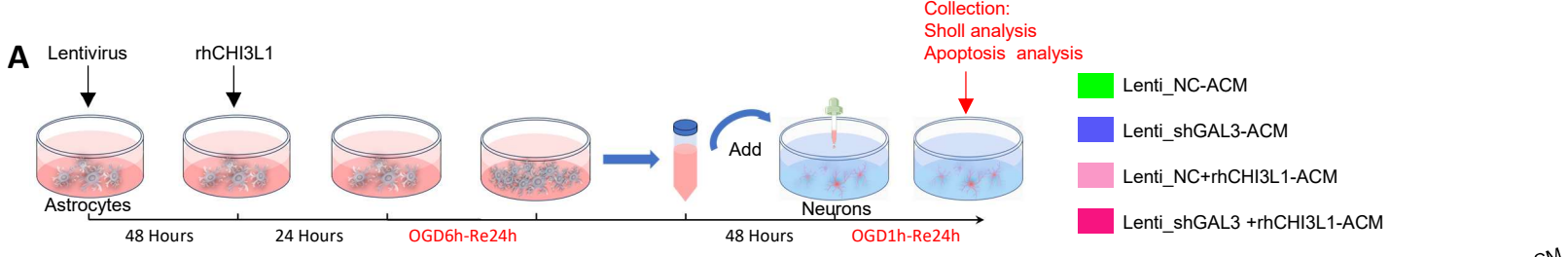


Fig. S8 GAL3 Mediates CHI3L1-Induced Neuronal Injury, BBB Dysfunction, and Infarct Expansion After Ischemic Stroke

- (A) Primary astrocytes were transfected with lentivirus (Lenti - NC or Lenti - shGAL3). After 48 hours, recombinant human CHI3L1 protein (rhCHI3L1) was either added or omitted, and the astrocytes were subsequently subjected to oxygen - glucose deprivation followed by reoxygenation (OGD - Re). The conditioned medium (ACM) from these astrocytes was collected. Primary - cultured neurons were then treated with this ACM for 48 hours. Following this, the neurons were subjected to oxygen - glucose deprivation for 6 hours (OGD6h) and reoxygenation for 24 hours (Re24h).
- (B) Morphology of neurons treated with ACM from different groups (Lenti - NC - ACM, Lenti - shGAL3 - ACM, Lenti - NC + rhCHI3L1 - ACM, Lenti - shGAL3 + rhCHI3L1 - ACM) was observed. Microscopic imaging was performed to visualize the neurons, with representative images of MAP2 (red) and DAPI (blue) staining shown. In the analysis, orange bars represent the comparison between the +Lenti_NC - ACM and +Lenti_shGAL3 - ACM groups, while purple bars represent the comparison between the +Lenti_NC + rhCHI3L1_ACM and +Lenti_shGAL3 + rhCHI3L1_ACM groups. N = 15 neurons from 3 independent experiments. Scale bar = 10 μ m. Significance levels: *p < 0.05; **p < 0.01; ***p < 0.001; ****p < 0.0001 compared to the 0 μ m group at indicated distances; #p < 0.05; ##p < 0.01; ###p < 0.001; ####p < 0.0001 compared to the 0 μ m group across the entire distance. Data were analyzed by two - way ANOVA and Sidak's multiple comparison tests (mean \pm SEM).
- (C) Neurons treated with ACM from CHI3L1 - protein - stimulated astrocytes showed increased apoptosis, as detected by TUNEL staining (red) and DAPI counterstaining (blue). ACM from shGAL3 - transfected astrocytes reduced this effect. N = 9 from 3 independent experiments. Scale bar = 100 μ m.
- (D) Western blotting was performed to confirm the transfection efficiency of shGAL3 in astrocytes and to assess cleaved caspase - 3 (Caspase3 p11) expression in neurons treated with ACM. The blots for GAL3, β - actin, GAPDH, and Caspase3 p11 are shown. N = 3 per group.
- (E) Transendothelial electrical resistance (TEER) measurement in the in vitro BBB model across groups. N = 3 per group.
- (F) Relative permeability of sodium fluorescein (NAF) in the in vitro BBB model across groups. N = 3 per group.
- (G) Mice were stereotaxically injected with AAV (AAV - NC or AAV - shGAL3). Western blotting was used to verify the knockdown efficiency of GAL3 in the ischemic brain tissue. N = 3 per group.
- (H) Infarct volume assessment by TTC staining in mice treated with rhCHI3L1 + AAV-NC or AAV-shGAL3 (n=5).
- (I) Blood-brain barrier (BBB) permeability evaluated by Evans blue assay at days 7 and 14 post-tMCAO(n=3).
- (J) Immunohistochemistry of MAP2 (red) and DAPI (blue) in peri-infarct penumbra at 14 days post-stroke (n = 6).
- Data are presented as mean \pm SEM. Statistical significance was evaluated using Student's t-test or one-way ANOVA. Significance levels: *p < 0.05; **p < 0.01; ***p < 0.001; ****p < 0.0001.

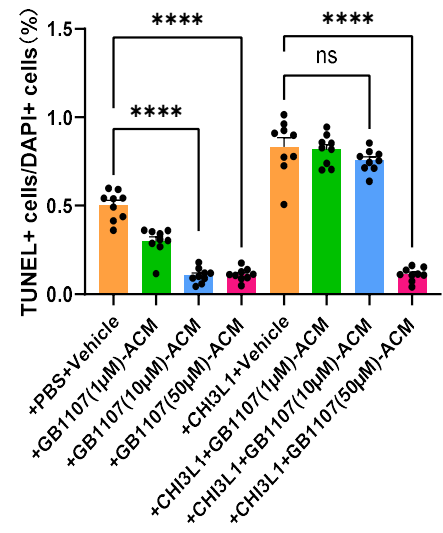
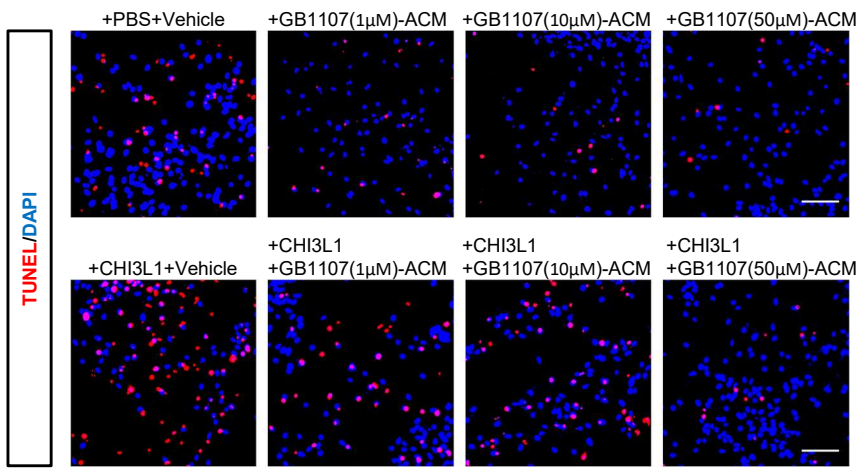
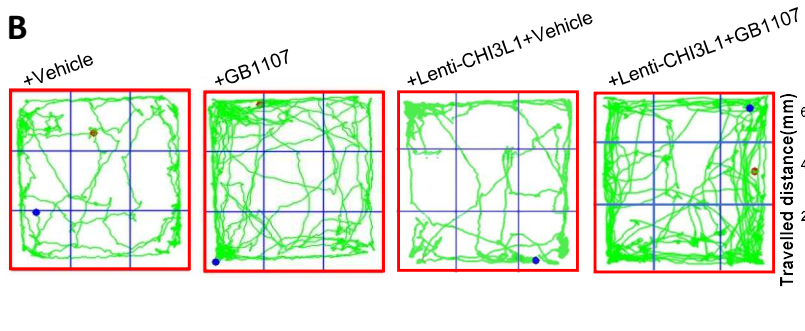
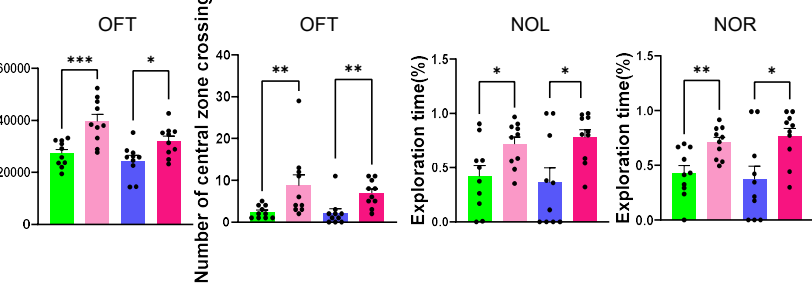
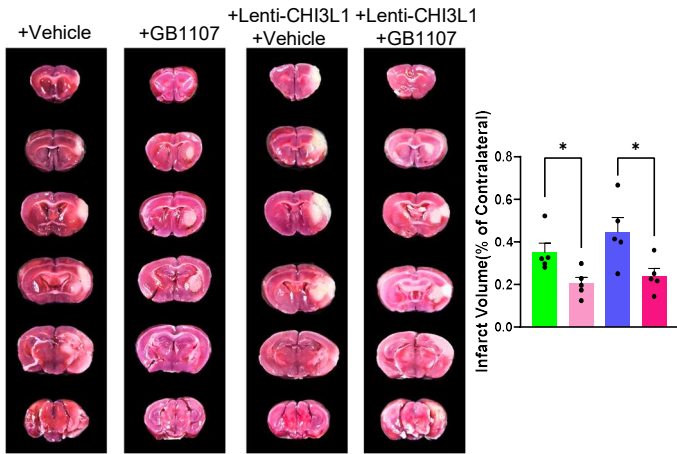
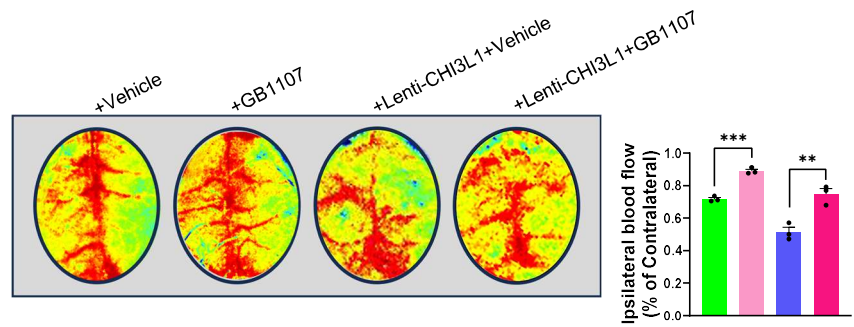
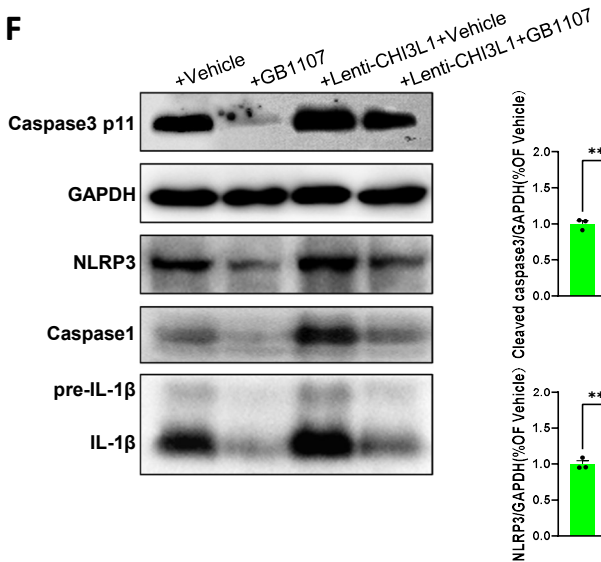
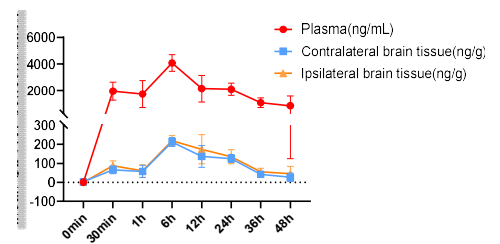
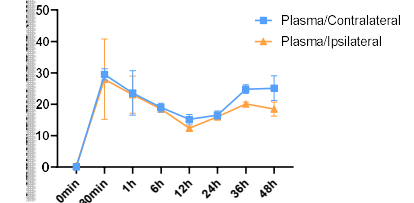
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Fig. S9 GB1107: A Potential In Vitro Therapeutic Modulator of CHI3L1 - Induced Neuronal Stress

(A) TUNEL staining (red) and DAPI counterstaining (blue) were carried out on neurons treated with ACM from astrocytes that had been treated with different combinations of rhCHI3L1 and GB1107. N = 9 from 3 independent experiments. Scale bar = 100 μ m.

(B) OFT showing improved locomotor activity in GB1107-treated mice.

(C) NOL and NOR tests evaluating cognitive outcomes (n = 10 per group).

(D) Infarct volume assessment by TTC staining (n = 5).

(E) CBF quantification on day 7 post-tMCAO (n = 3).

(F) Western blot analysis of cleaved caspase-3 levels and assessment of NLRP3 pathway (n = 3).

(G) Time-course of GB1107 concentration in mouse plasma, contralateral brain tissue, and ipsilateral (infarct-side) brain tissue at various time points post-administration.

(H) Ratio of GB1107 concentration in plasma to that in contralateral brain tissue, and plasma to ipsilateral brain tissue, at different time points post-administration. Data are presented as mean \pm SEM. Statistical significance was determined using one - way ANOVA followed by Tukey's multiple comparison test or Kruskal - Wallis test, with significance levels: *p < 0.05; **p < 0.01; ***p < 0.001; ****p < 0.0001.

Studies of CHI3L1 serum levels (by ELISA)	Controls ng/ml (n)	AIS ng/ml (n)	References
Park et al.,2012	41(34)	251-310(105)	PMID: 23272150
Shao et al.,2016	76(85)	95(141)	DOI: 10.1371/journal.pone.0051722. PMID: 27650381 DOI: 10.1111/ane.12688.

Table S1 Comparison of CHI3L1/YKL - 40 Concentrations (Measured by ELISA) in Serum Samples between Healthy Control and Stroke Cohorts in Recent Studies

This table summarizes data from recent publications reporting serum concentrations of CHI3L1/YKL-40, measured by ELISA (in ng/mL), in healthy control and stroke cohorts. For each study, the mean CHI3L1/YKL-40 concentration and corresponding sample size (n) are provided for both groups.

	HCs (n=11)	AISs (n=24)	P-value (HCs vs AISs)
Age (years)	60.2±4.5	62.7±5.1	0.1727
Gender (Female/Male)	4/7	11/13	-
Mean admission NIHSS scores	-	4.2±4.6	-
Mean discharge NIHSS scores	-	3.1±4.0	-
Smoking	4/7	7/17	-
Alcohol Abuse	1/10	4/20	-
Diabetes	5/6	8/16	-
Other Cardiovascular and Cerebrovascular Diseases	5/6	14/10	-

Table S2 Comparison of Basic Information of Protein - Sequenced Serum Samples between Healthy Control Subjects and Acute Ischemic Stroke Patients

This table summarizes the baseline characteristics of 35 serum samples, including 11 healthy control (HC) subjects and 24 acute ischemic stroke (AIS) patients. Continuous variables are presented as mean ± standard deviation (SD), and categorical variables are reported as counts or proportions. The table compares demographic and clinical parameters such as age, sex, NIHSS scores (AIS group only), and the prevalence of risk factors including smoking, alcohol use, diabetes, and cardiovascular/cerebrovascular comorbidities. P-values indicate the statistical significance of differences between the two groups.

	HCs (n=15)	AISs (n=70)	P-value (HCs vs AISs)
Age (years)	60.7±9.8	62.9±14.3	0.5725
Gender (Female/Male)	8/7	45/25	-
Mean admission NIHSS scores	-	4.7±5.1	-
Mean discharge NIHSS scores	-	2.8±4.0	-
Mean infarct volume	-	45.0±106.0	-
Smoking	4/11	33/37	-
Alcohol Abuse	2/13	13/57	-
Diabetes	3/13	26/44	-
Other Cardiovascular and Cerebrovascular Diseases	10/5	41/29	-
CHI3L1 (ng/ml)	197.6±30.8	427.1±212.5	<0.0001

Table S3 Comparison of Basic Information and CHI3L1 ELISA Results of Serum Samples between Healthy Control Subjects and Acute Ischemic Stroke Patients

This table summarizes the characteristics of 85 serum samples, comprising 15 healthy control (HC) subjects and 70 acute ischemic stroke (AIS) patients. Continuous variables are expressed as mean ± standard deviation (SD), while categorical variables are shown as frequencies or proportions. The comparison includes age, sex, NIHSS scores at admission and discharge (AIS group), infarct volume, and the prevalence of vascular risk factors such as smoking, alcohol consumption, diabetes, and other cardiovascular or cerebrovascular diseases. CHI3L1 concentrations measured by ELISA in serum are also reported. P-values indicate the statistical significance of differences between the HC and AIS groups for each parameter.

ALDH1L1::CreERT2-1	GCCTGCATTACCGGTCGATGC
ALDH1L1::CreERT2-2	CAGGGTGTATAAGCAATCCC
Chil1-1	GCTACCCAACATGTCAATAGCTCA
Chil1-2	CATATGGTGGGAATAATCTTGGA
shGal3-1	CTGGAGCTTATCCTGGCTCAA
shGal3-2	CCGCATGCTGATCACAATCAT
shL-13Ra2-1	ATATTCTGATACCAACTATAAC
shL-13Ra2-2	TTGGACTCATCAGACTATAAA
shTMEM219-1	GTCGGTACTGACCACCTTG
shTMEM219-2	CATGGTAGTCAGATAGGATTG
shCRTH2-1	GCTCAACACAATACCAATATT
shCRTH2-2	CACTGCTCTATGTGTTACAT
shCD44-1	GTGTAGTGCCTACGCCATTAA
shCD44-2	CCGAATTAGCTGGACACTCAA
shRAGE_1	GCACTTAGATGGGAACTTCT
shRAGE_2	GGGCATTAGCTGTTGGTTGA

Table S4 Target sequences of the shRNAs and genotyping primers