

Figure S1

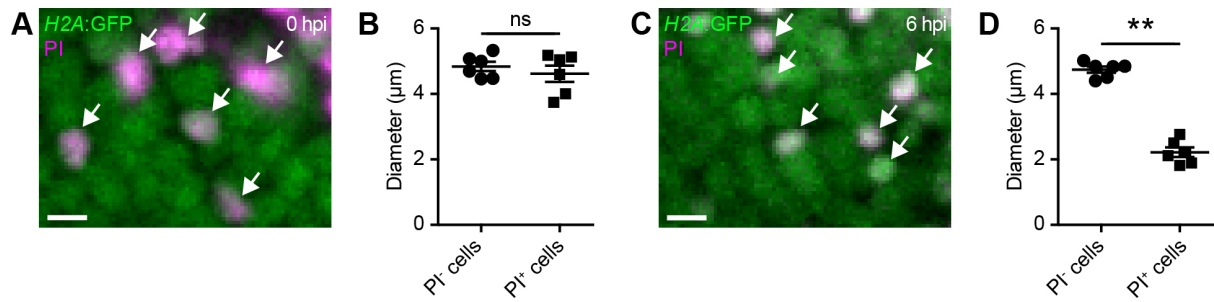


Figure S1. PI⁺ cells are pyknotic at 6 hpi but not at 0 hpi. (A,C) Confocal images of PI⁺ cells (white arrows) in H2A:GFP animals at 0 hpi (A) and 6 hpi (C). Scale bars, 5 μm. (B,D) Quantification of the size of PI⁻ and PI⁺ cells at 0 hpi (B) and 6 hpi (D). n = 6 animals per experimental group. ns, not significant and **, p < 0.01 in Mann-Whitney test.

Figure S2

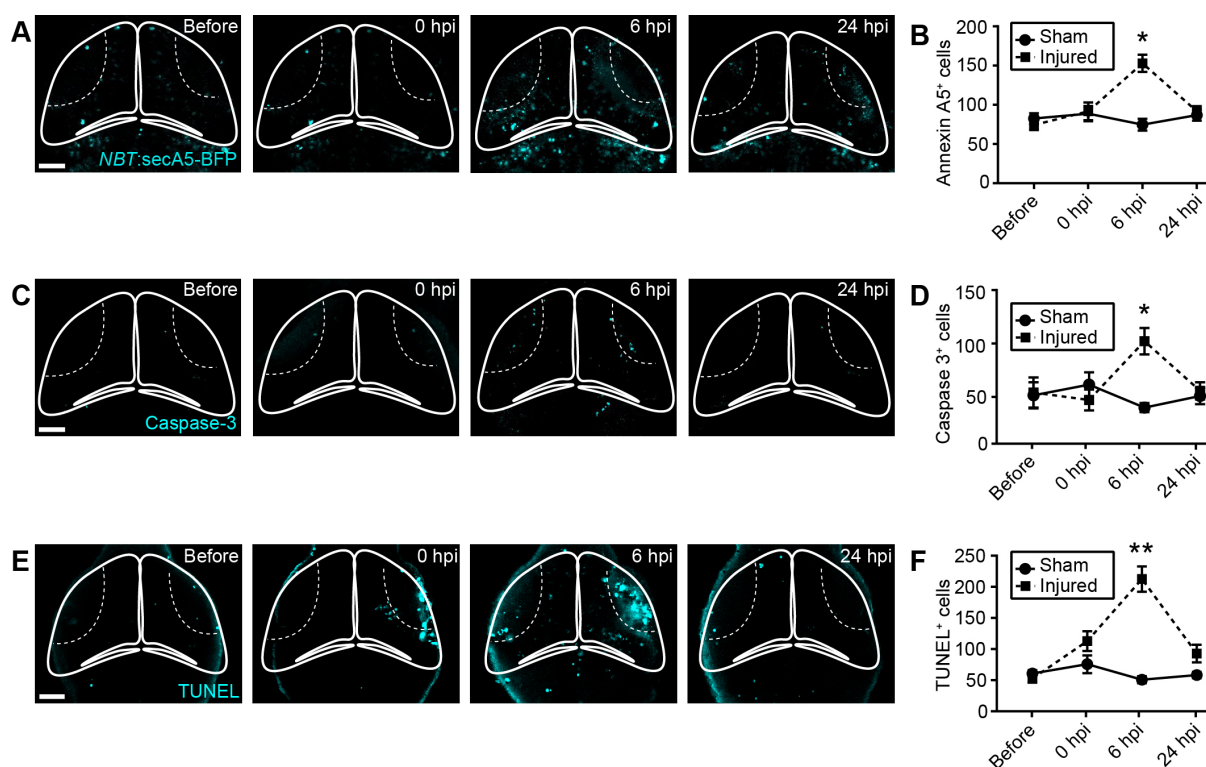


Fig. S2. Cell death after brain injury can be detected through Annexin A5 live imaging, caspase 3 immunohistochemistry, and TUNEL staining. (A,C,E) Confocal images of the tectum of a *NBT:secA5-BFP* animal (A), and animals after cleaved caspase 3 immunohistochemistry (B) or TUNEL staining (C), at different time points after injury. Scale bars, 50 μ m. (B,D,F) Quantification of Annexin A5⁺ cells (B), cleaved caspase 3⁺ cells (D) or TUNEL⁺ cells (F). $n \geq 6$ animals per experimental group. *, $p < 0.05$ and **, $p < 0.01$ in two-way ANOVA.

Figure S3

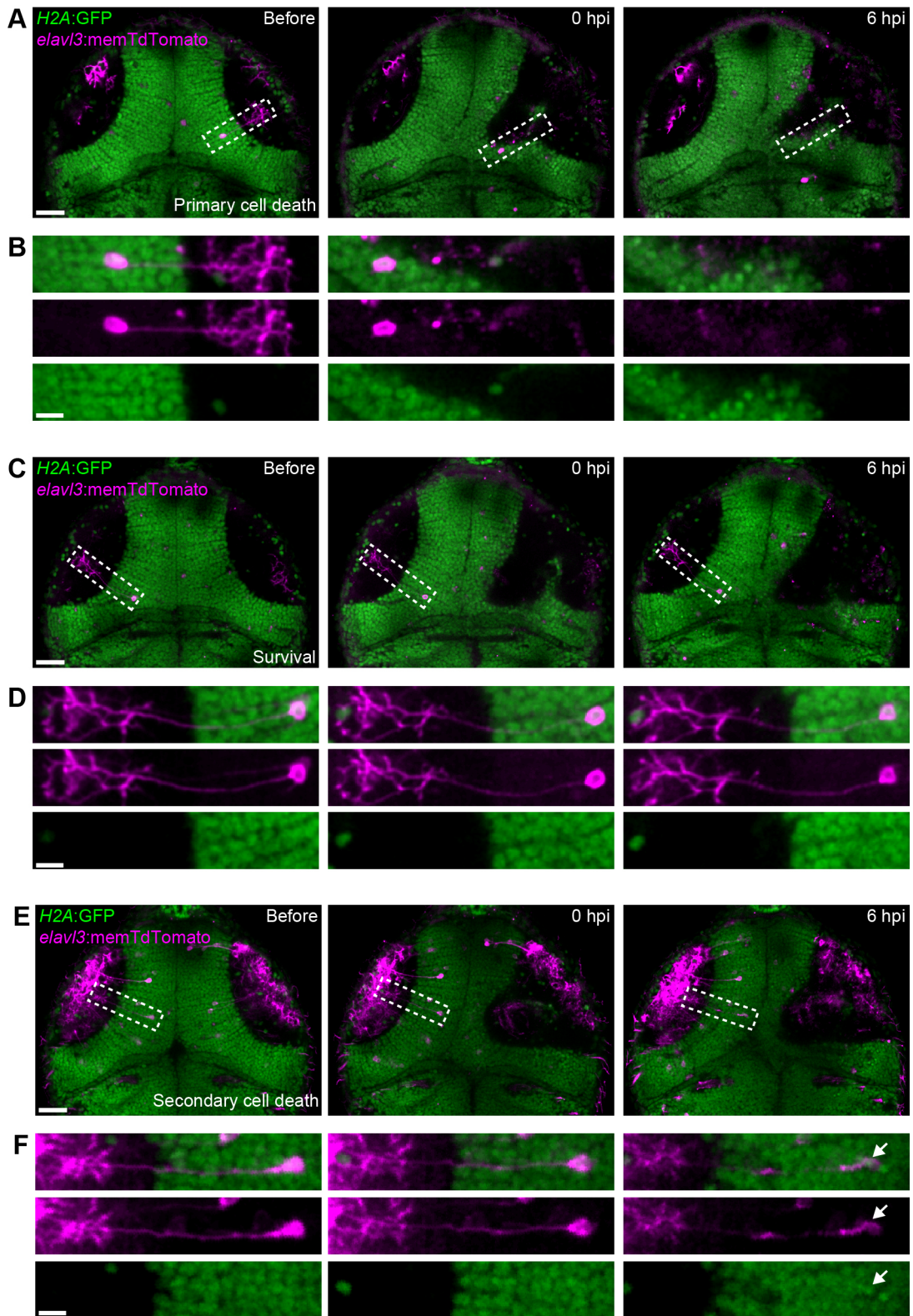


Fig. S3. *In vivo* imaging of individual tectal neurons shows that both primary and secondary cell death occur after brain injury. (A,C,E) Confocal images of the optic tectum of *H2A:GFP* transgenic animals, where tectal neurons labelled through injection of *elav/3:memTdtomato* plasmid DNA die through primary cell death (A), survive (C), or die through secondary cell death (E) after mechanical injury. Scale bars, 50 μm . (B,D,F) Close-up of neurons indicated in (A), (C) and (E). White arrow indicates pyknotic nucleus. Scale bars, 10 μm .

Figure S4

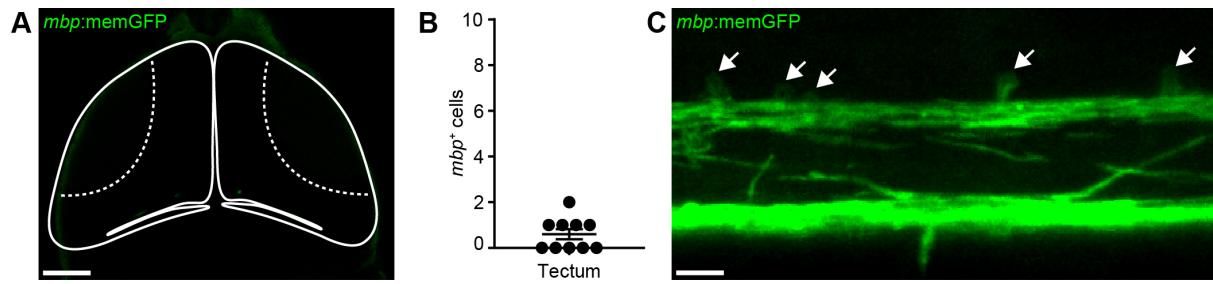


Figure S4. Very few oligodendrocytes reside in the optic tectum at 4 dpf. (A) Confocal image of the optic tectum of a *mbp:memGFP* animal. Scale bar, 50 μm . (B) Quantification of *mbp*⁺ oligodendrocytes in the optic tectum. $n = 10$ animals. (C) Confocal image of the trunk region of a *mbp:memGFP* animal. White arrows indicate cell bodies of individual oligodendrocytes. Scale bar, 10 μm .

Figure S5

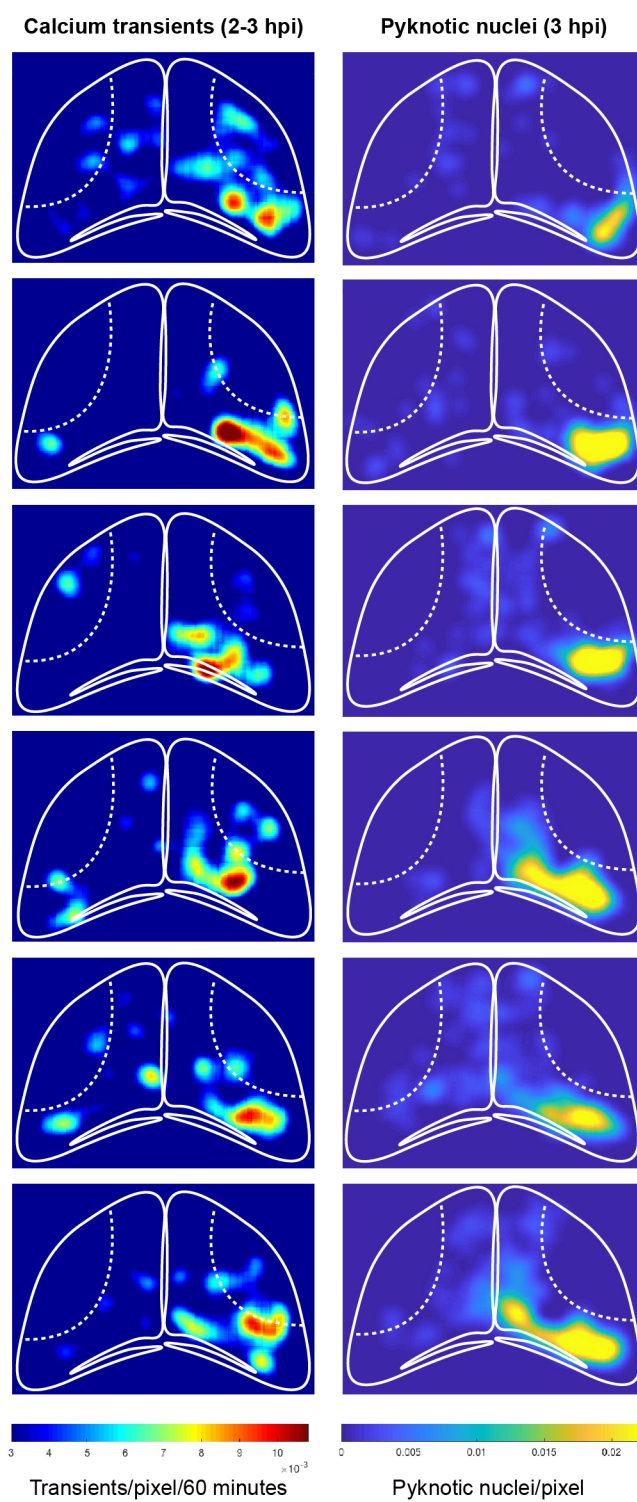


Fig. S5. The spatial pattern of calcium transients correlates with regions of cell death. Heat maps illustrating the spatial distribution of calcium transients occurring between 2 and 3 hpi (left), and of pyknotic nuclei at 3 hpi (right), in the same animals.

Figure S6

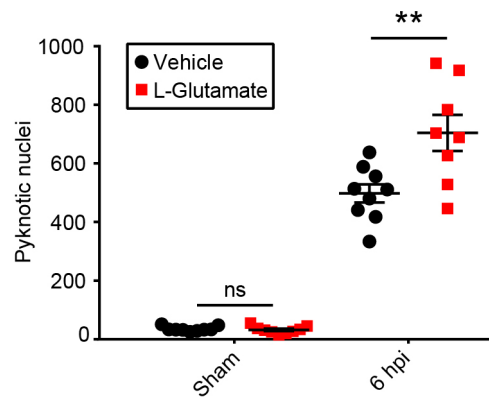


Fig. S6. L-Glutamate exacerbates secondary cell death after brain injury. Quantification of pyknotic nuclei in control animals or animals treated with L-Glutamate. $n \geq 8$ animals per experimental group. ns, not significant and **, $p < 0.01$ in two-way ANOVA.

Figure S7

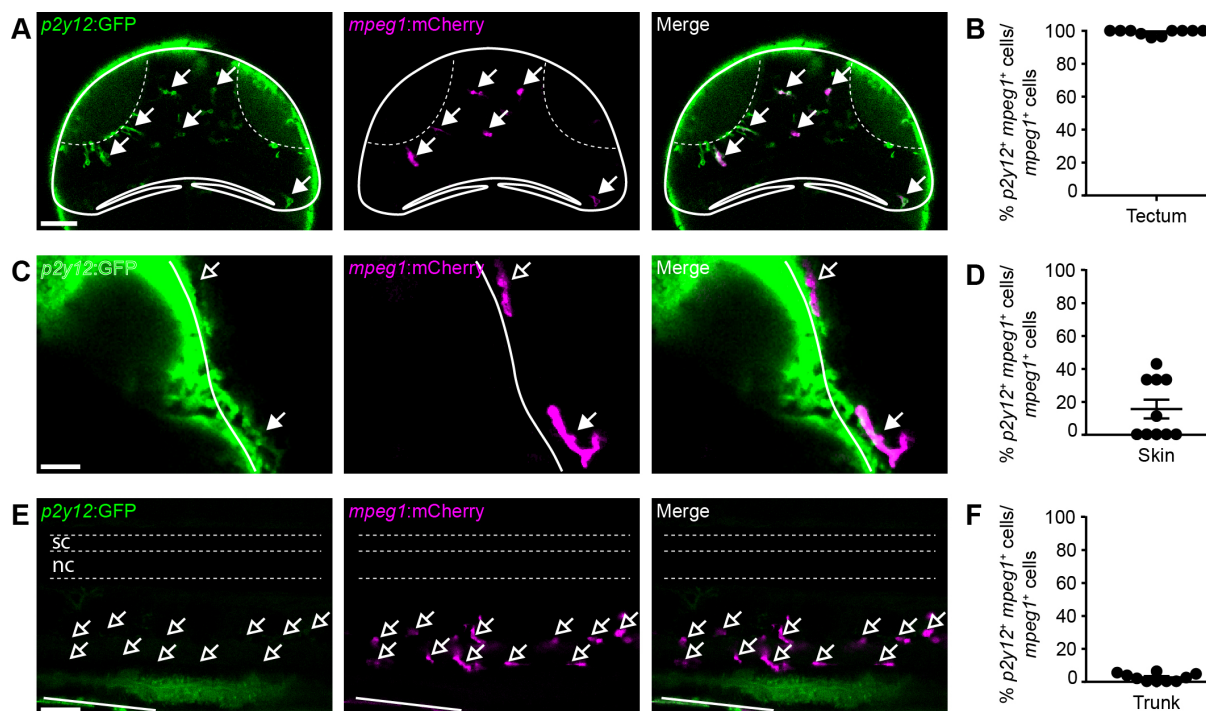


Figure S7. P2Y12 is expressed in virtually all *mpeg1*⁺ tectal cells and some *mpeg1*⁺ skin cells, but not in *mpeg1*⁺ cells in the trunk. (A,C,E) Confocal images of the optic tectum (A), skin (C), and trunk (E) of a *p2y12*:GFP;*mpeg1*:mCherry animal. Filled or empty arrows indicate colocalisation, or lack thereof, between *p2y12* and *mpeg1*. Scale bars, 50 μ m (A,E) and 20 μ m (C). (B,D,F) Quantification of the proportion of *p2y12*⁺/*mpeg1*⁺ cells among all *mpeg1*⁺ cells in the tectum (B), skin (D) and trunk (F). n = 10 animals per experimental group.

Figure S8

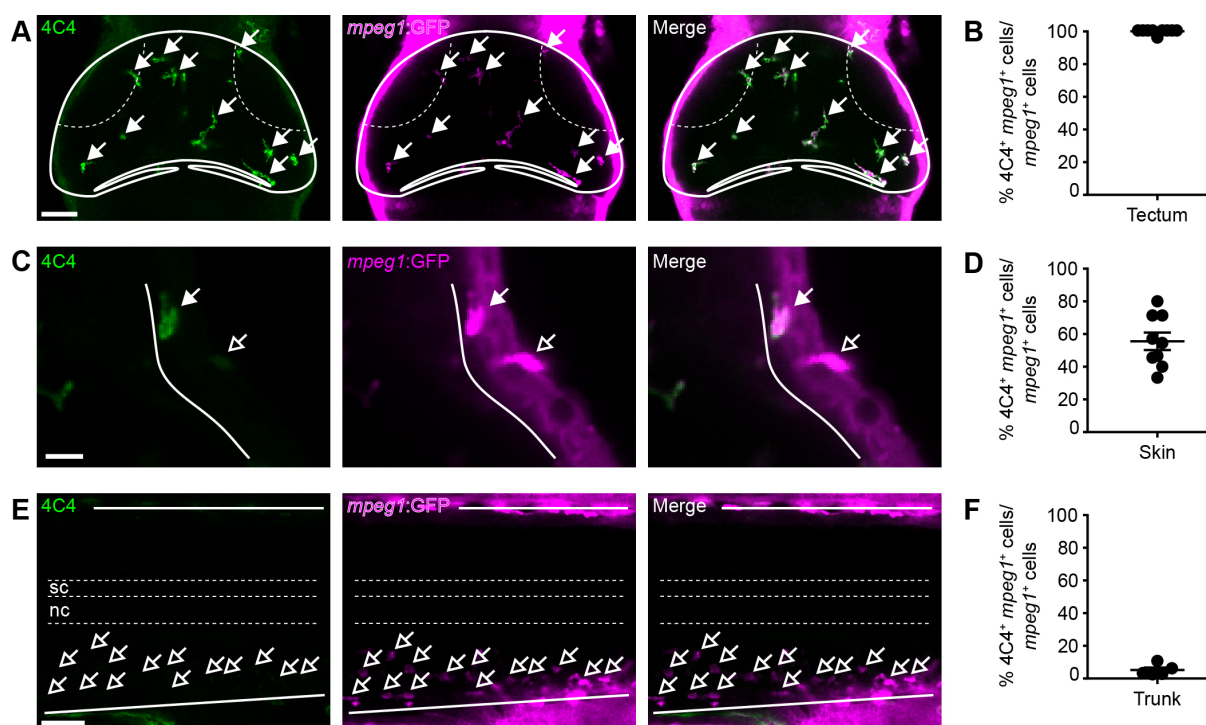


Figure S8. 4C4 immunohistochemistry labels virtually all *mpeg1*⁺ tectal cells and some *mpeg1*⁺ skin cells, but not *mpeg1*⁺ cells in the trunk. (A,C,E) Confocal images of the optic tectum (A), skin (C) and trunk (E) of a *mpeg1*:GFP animal after 4C4 and GFP immunohistochemistry. Filled or empty arrows indicate colocalisation, or lack thereof, between 4C4 and *mpeg1*. Scale bars, 50 μ m (A,E) and 20 μ m (C). (B,D,F) Quantification of the proportion of 4C4⁺/*mpeg1*⁺ cells among all *mpeg1*⁺ cells in the tectum (B), skin (D) and trunk (F). $n \geq 5$ animals per experimental group.

Figure S9



Fig. S9. The majority of *mpeg1*⁺ cells at the injury site within the brain are also labelled by 4C4 immunohistochemistry. (A) Confocal images of the optic tectum at 6 hpi in *mpeg1*:GFP animals after 4C4 and GFP immunohistochemistry. Yellow arrows indicate 4C4⁺/*mpeg1*⁺ cells. Light blue arrow indicates a 4C4⁻/*mpeg1*⁺ cell. Scale bar, 40 μm. (B,C) Quantification of 4C4⁺/*mpeg1*⁺ and 4C4⁻/*mpeg1*⁺ cells at the entire injury site (B) or within the brain (C) at 6 hpi. n = 12 animals.

Figure S10

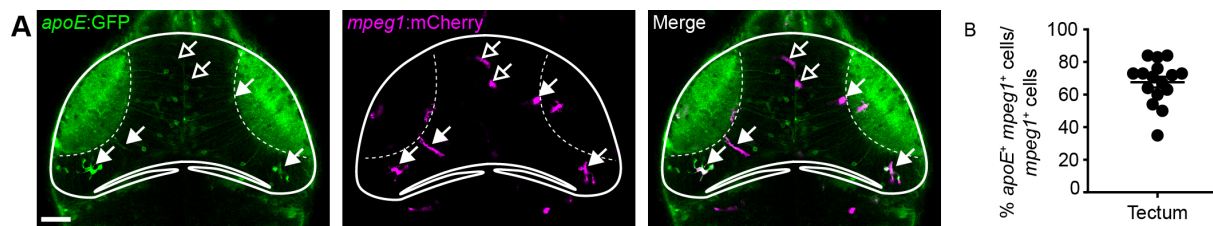


Figure S10. ApoE is expressed in a subset of *mpeg1*⁺ tectal cells. (A) Confocal images of the optic tectum of an *apoE:GFP;mpeg1:mCherry* animal. Filled or empty arrows indicate colocalisation, or lack thereof, between *apoE* and *mpeg1*. Scale bar, 50 μ m. (B) Quantification of the proportion of *apoE*⁺/*mpeg1*⁺ cells among all *mpeg1*⁺ cells in the tectum. n = 16 animals.

Figure S11

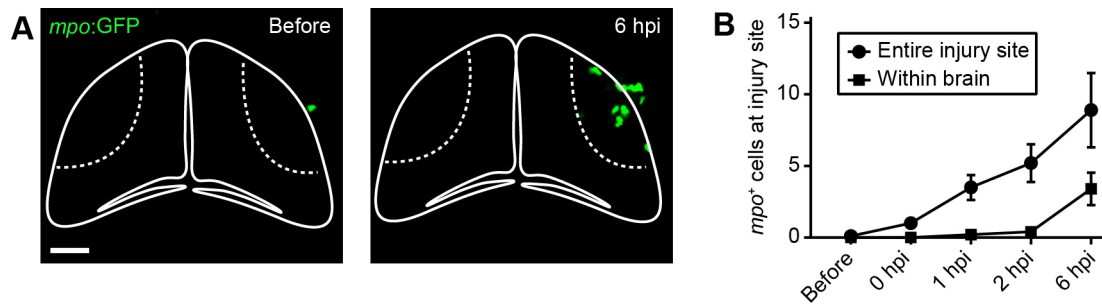


Fig. S11. Neutrophils are recruited to the injury site, but only a few are found within the brain. (A) Live imaging of the neutrophil reporter line *mpo:GFP* before injury and at 6 hpi. Scale bar, 50 μm . (B) Quantification of *mpo*⁺ cells at the entire injury site and within the brain. n = 10 animals per experimental group.

Figure S12

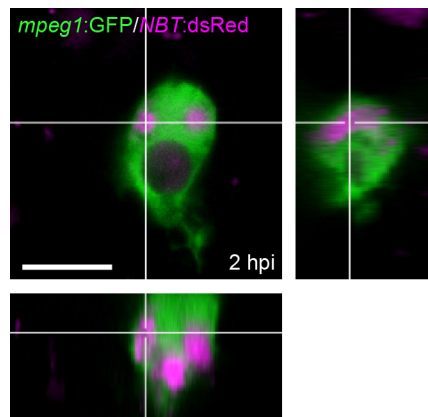


Fig. S12. Microglia take up substantial amounts of neuronal debris after brain injury. Orthogonal view of a microglial cell at 2 hpi in a *mpeg1:GFP;NBT:dsRed* animal. Scale bar, 10 μm .

Figure S13

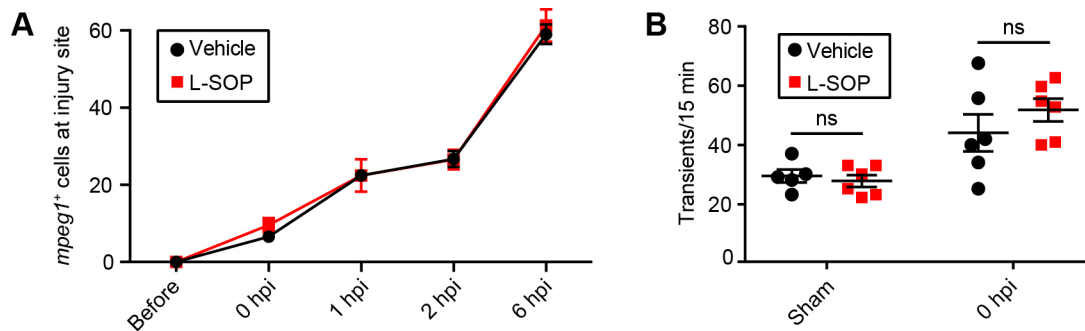


Fig. S13. L-SOP does not change microglial recruitment or tectal calcium dynamics. (A) Quantification of *mpeg1*⁺ cells at the injury site within the brain in *mpeg1*:GFP animals treated with vehicle or L-SOP. *n* = 7 animals per experimental group. (B) Quantification of calcium transients by time-lapse imaging of *β-actin*:GCaMP6f larvae treated with vehicle or L-SOP. *n* ≥ 5 animals per experimental group. ns, not significant in two-way ANOVA.

Figure S14

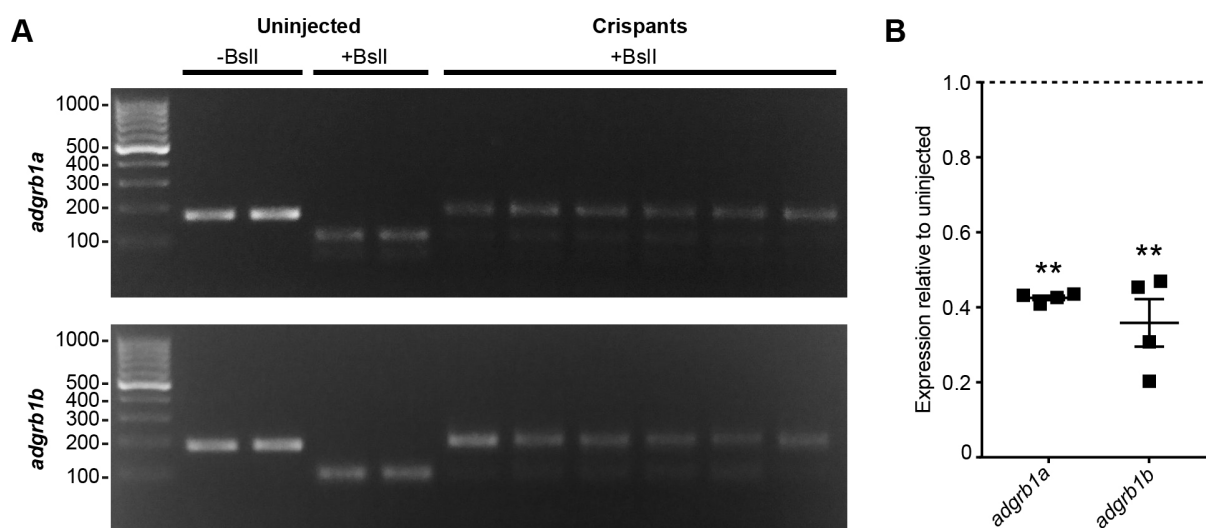


Fig. S14. CRISPR/Cas9-mediated gene editing reduces expression of the phosphatidylserine receptors *adgrb1a* and *adgrb1b*. (A) Restriction fragment length polymorphism analysis of the efficiency of CRISPR/Cas9-mediated gene editing of *adgrb1a* and *adgrb1b* in gRNA-injected F0 embryos. This demonstrates efficient somatic mutation of the gRNA target site, which becomes resistant to BslI restriction endonuclease digestion. One embryo was analysed per well. (B) RT-qPCR for *adgrb1a* and *adgrb1b* in gRNA-injected F0 embryos. Each data point represents one biological replicate, with mRNA from 10 animals pooled for each replicate. **, $p < 0.01$ in two-way ANOVA.

Figure S15

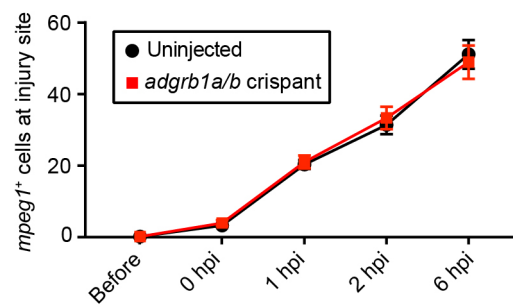


Fig. S15. Microglial recruitment is unchanged in *adgrb1a/b* crispants. Quantification of *mpeg1*⁺ cells at the injury site within the brain in *adgrb1a/b* crispants as compared to uninjected *mpeg1*:GFP animals. $n \geq 9$ animals per experimental group.

Figure S16

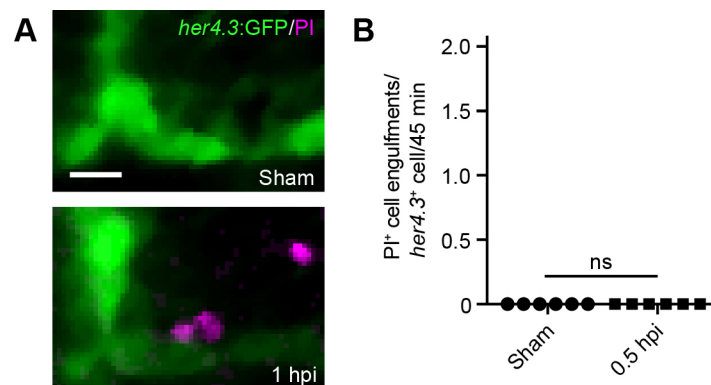


Fig. S16. *Her4.3*⁺ radial glial cells do not make a major contribution to debris clearance after brain injury. (A) Confocal images of radial glial cells in *her4.3:GFP* animals before injury or at 1 hpi. Scale bar, 20 μ m. (B) Quantification of phagocytosis of PI⁺ cells per radial glial cell from 30 to 75 min after injury. n = 6 animals per experimental group. ns, not significant in Mann-Whitney test.

Table S1. List of mutations after CRISPR/Cas9 editing of *adgrb1a*

Mutations in 37 out of 68 sequenced alleles (54% mutation rate)

GTGACCCACGCAATGCTGTTGCTCCACAAGGGGGGGCTGCTGGATATATGCTTTAGTGCCCGACTGCCTG	Wild type		x31
GTGACCCACGCAATGCTGTTGCTCCACAAtaccacagcattaaatgctacaatactctagccaag[...]	+341	(-2, +343)	
[...]cagctgcctgggagactggagctcagttatgataagcaccacgacctgctcgaatga[...]	+114	(-125, +239)	
GTGACCCACGCAATGCTGTTGCTCCACAacataaaacattgggatataatGGGGCTGCTGGATATAT	+20	(-3, +23)	
GTGACCCACGCAATGCTGTTGCTCCACAagatataatgcttagtcccgaCTGCTGGATATATGCTTTAG	+14	(-8, +22)	
GTGACCCACGCAATGCTGTTGCTCCACgcaatgctgttgcctGGGGGGGCTGCTGGATATATGCTTTAGT	+13	(-2, +15)	
GTGACCCACGCAATGCTGTTGCTCCACAAGGGGGGcatatatccaCTGCTGGATATATGCTTTAGTGCCC	+9	(-1, +10)	
GTGACCCACGCAATGCTGTTGCTCCACAgtccacagggGGCTGCTGGATATATGCTTTAGTGCCCGAC	+6	(-6, +12)	
GTGACCCACGCAATGCTGTTGCTCCACAactgctGGGGGGGCTGCTGGATATATGCTTTAGTGCCCGACT	+5		
GTGACCCACGCAATGCTGTTGCTCCACAactggatatactGCTGCTGGATATATGCTTTAGTGCCCGACTG	+4	(-7, +11)	
GTGACCCACGCAATGCTGTTGCTCCACgcaatgctGGGGCTGCTGGATATATGCTTTAGTGCCCGACTGC	+3	(-5, +8)	
GTGACCCACGCAATGCTGTTGCTCCACAacgtatGGGGCTGCTGGATATATGCTTTAGTGCCCGACTGC	+3	(-3, +6)	
GTGACCCACGCAATGCTGTTGCTcccacagcaGGGGGGGCTGCTGGATATATGCTTTAGTGCCCGACTGCCT	+1	(-8, +9)	
GTGACCCACGCAATGCTGTTGCTCCACAacagcatGGCTGCTGGATATATGCTTTAGTGCCCGACTGCCT	+1	(-5, +6)	
GTGACCCACGCAATGCTGTTGCTCCACAAGGGGGGCTGCTGGATATATGCTTTAGTGCCCGACTGCCTG	*2		x3
GTGACCCACGCAATGCTGTTGCTCCACAAGGGGGGCTGCTGGATATATGCTTTAGTGCCCGACTGCCTG	*1		
GTGACCCACGCAATGCTGTTGCTCCACA-tatatGCTGCTGGATATATGCTTTAGTGCCCGACTGCCTG	-1	(-7, +6)	
GTGACCCACGCAATGCTGTTGCTCCACA-atgctGGGGCTGCTGGATATATGCTTTAGTGCCCGACTGCCTG	-1	(-6, +5)	
GTGACCCACGCAATGCTGTTGCTCCACA-gggggGGCTGCTGGATATATGCTTTAGTGCCCGACTGCCTG	-1		
GTGACCCACGCAATGCTGTTGCTCCACA-tatatGCTGCTGGATATATGCTTTAGTGCCCGACTGCCTG	-2	(-2, +5)	
GTGACCCACGCAATGCTGTTGCTCCACA-gggggGGCTGCTGGATATATGCTTTAGTGCCCGACTGCCTG	-2		
GTGACCCACGCAATGCTGTTGCTCCACA-gggggTCTGCTGGATATATGCTTTAGTGCCCGACTGCCTG	-3	(-9, +6)	
GTGACCCACGCAATGCTGTTGCTCCCA-gggggGGCTGCTGGATATATGCTTTAGTGCCCGACTGCCTG	-3	(-5, +2)	x2
GTGACCCACGCAATGCTGTTGCTCCACA-gggggGGCTGCTGGATATATGCTTTAGTGCCCGACTGCCTG	-3		
GTGACCCACGCAATGCTGTTGCTCCA-tatatGCTGCTGGATATATGCTTTAGTGCCCGACTGCCTG	-4	(-10, +6)	
GTGACCCACGCAATGCTGTTGCTCCACA-gggggGGCTGCTGGATATATGCTTTAGTGCCCGACTGCCTG	-4	(-5, +1)	
GTGACCCACGCAATGCTGTTGCTG-gatatgctGGGGGGCTGCTGGATATATGCTTTAGTGCCCGACTGCCTG	-5	(-13, +8)	
GTGACCCACGCAATGCTGTTGCTCC-gcaatGCTGCTGGATATATGCTTTAGTGCCCGACTGCCTG	-5	(-10, +5)	x3
GTGACCCACGCAATGCTGTTGCTCCACA-gctGCTGGATATATGCTTTAGTGCCCGACTGCCTG	-5	(-6, +1)	
GTGACCCACGCAATGCTGTT-----GGGGGGGCTGCTGGATATATGCTTTAGTGCCCGACTGCCTG	-9		
GTGACCCACGCAATGCTGTTGCTCCAC-----GCTGGATATATGCTTTAGTGCCCGACTGCCTG	-11		
GTGACCCACGCAATGCTG-----GGGCTGCTGGATATATGCTTTAGTGCCCGACTGCCTG	-15		
GTGACCCACGCAAT-----GGGGGGCTGCTGGATATATGCTTTAGTGCCCGACTGCCTG	-16		
GTGACCCACGCAATGCTG-----CTGCTGGATATATGCTTTAGTGCCCGACTGCCTG	-18		
GTGACCCACGCAATGCT-----accGGATATATGCTTTAGTGCCCGACTGCCTG	-21	(-24, +3)	

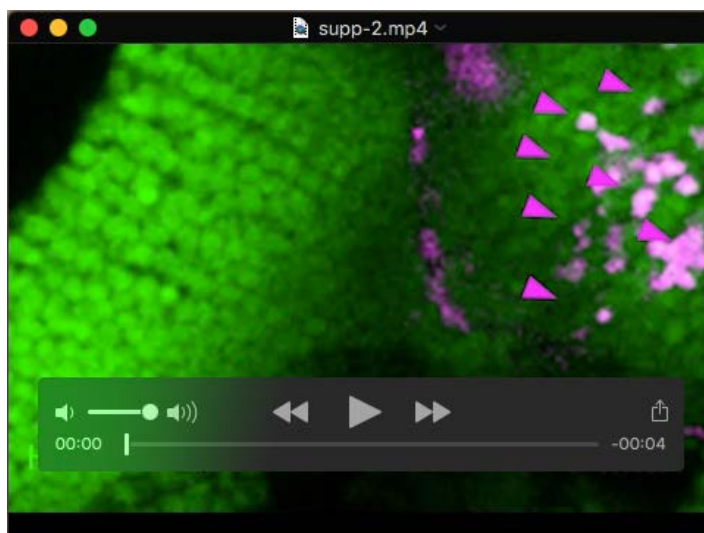
The gRNA target site is underlined. Inserted bases are highlighted in grey, and changed bases are highlighted in green.

Table S2. List of mutations after CRISPR/Cas9 editing of *adgrb1b*

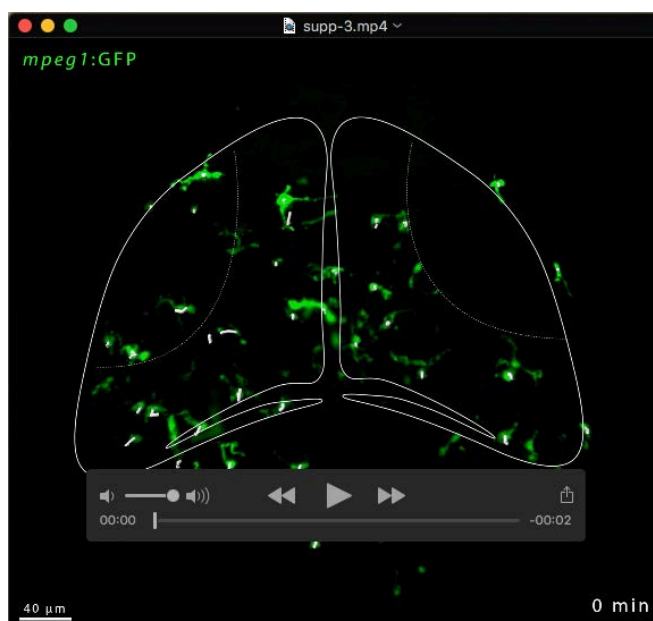
Mutations in 42 out of 45 sequenced alleles (93% mutation rate)

CGACTCAGAGAACCCGCGAGTGTAAACGGACCCTCATACGGCGGCTCCGAGTGCAGAGGGGAATGGCTGGA	wild type		x3
CGACTCAGAGAACCCGCGAGTGTAAACGGACCCT <u>aaccctaaccctaaccctaaccctaacc[...]</u>	+88	(-3, +91)	
CGACTCAGAGAACCCGCGAGTGTAAACGGACCCTC <u>Ag</u> tggggaatggctggagCGGCGGCTCCGAGTGCAG	+15	(-2, +17)	
CGACTCAGAGAACCCGCGAGTGTAAACGGACCCTC <u>tg</u> ccntggTACGGCGGCTCCGAGTGCAGAGGGGAAT	+7	(-1, +8)	
CGACTCAGAGAAC <u>ctegggg</u> gtaacggatctcattcaccCGGCGGCTCCGAGTGCAGAGGGGAATGGC	+4	(-24, +28)	
CGACTCAGAGAACCCGCGAGTGTAAACGGACCCTCAT <u>tc</u> accCGGCGGCTCCGAGTGCAGAGGGGAATGGC	+4	(-1, +5)	x2
CGACTCAGAGAACCCGCGAGTGTAAACGGACC <u>Cg</u> agtcagagGGCGGCTCCGAGTGCAGAGGGGAATGGCT	+3	(-7, +10)	
CGACTCAGAGAACCCGCGAGTGTAAACGGACCCTCATACGGCGGCTCCGAGTGCAGAGGGGAATGGCTGG	+1		x2
CGACTCAGAGAACCCGCGAGTGTAAACGGACCCTCA <u>gt</u> GGCGGCTCCGAGTGCAGAGGGGAATGGCTGGA	-1	(-3, +2)	
CGACTCAGAGAACCCGCGAGTGTAAACGGACCCTC <u>g</u> ggaccccTACGGCGGCTCCGAGTGCAGAGGGGAATGGCTGGA	-2	(-11, +9)	
CGACTCAGAGAACCCGCGAGTGTAAACGGACCCTC <u>AC</u> GGCGGCTCCGAGTGCAGAGGGGAATGGCTGGA	-2		
CGACTCAGAGAACCCGCGAGTGTAAACGG <u>g</u> ccgTACGGCGGCTCCGAGTGCAGAGGGGAATGGCTGGA	-3	(-7, +4)	
CGACTCAGAGAACCCGCGAGTGTAAACGGACC <u>CC</u> TACGGCGGCTCCGAGTGCAGAGGGGAATGGCTGGA	-3		
CGACTCAGAGAACCCGCGAGTGTAAACGGACCCTCA <u>ga</u> CTCCGAGTGCAGAGGGGAATGGCTGGA	-6	(-8, +2)	
CGACTCAGAGAACCCGCGAGTGTAAACGGACCCTCA <u>at</u> catTCCGAGTGCAGAGGGGAATGGCTGGA	-4	(-9, +5)	x2
CGACTCAGAGAACCCGCGAGTGTAAACGGACCCT <u>CG</u> GGCGGCTCCGAGTGCAGAGGGGAATGGCTGGA	-4		x5
CGACTCAGAGAACCCGCGAGTGTAAACGGACC <u>ga</u> GGCTCCGAGTGCAGAGGGGAATGGCTGGA	-8	(-10, +2)	
CGACTCAGAGAACCCGCGAGTGTAAACGGACC <u>GG</u> CTCCGAGTGCAGAGGGGAATGGCTGGA	-10		
CGACTCAGAGAACCCGCGAGTGTAAAC <u>ta</u> GGCGGCTCCGAGTGCAGAGGGGAATGGCTGGA	-11	(-13, +2)	
CGACTCAGAGAACCCGCGAGTGTAAACGGACC <u>T</u> CCGAGTGCAGAGGGGAATGGCTGGA	-12		x5
CGACTCAGAGAACCCGCGAGTGTAA <u>gggga</u> CTCCGAGTGCAGAGGGGAATGGCTGGA	-13	(-19, +6)	
CGACTCAGAGAACCCGCGAGTGT <u>AC</u> GGCGGCTCCGAGTGCAGAGGGGAATGGCTGGA	-13		
CGACTCAGAGAACCCGCGAGTGTAAACGGAC <u>CC</u> GAGTGCAGAGGGGAATGGCTGGA	-15		x4
CGACTCAGAGAACCCG <u>ag</u> TACGGCGGCTCCGAGTGCAGAGGGGAATGGCTGGA	-17	(-19, +2)	x2
CGA <u>CT</u> CCGAGTGCAGAGGGGAATGGCTGGA	-40		
C <u>CT</u> CCGAGTGCAGAGGGGAATGGCTGGA	-42		
[...]-----[...]	-98	(-135, +37)	

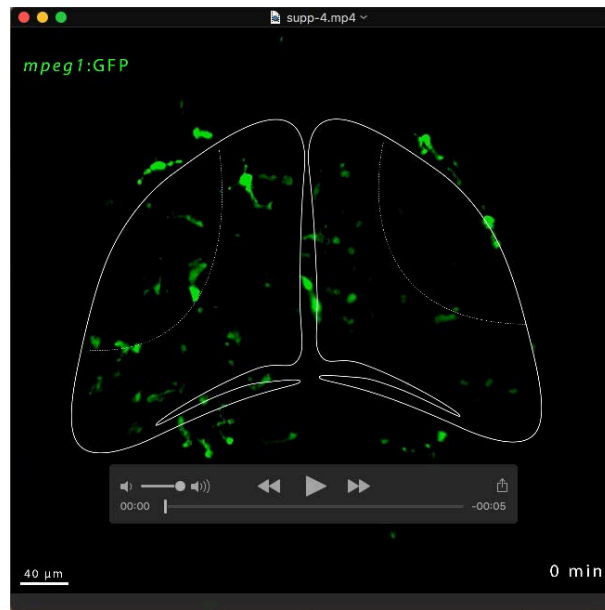
The gRNA target site is underlined. Inserted bases are highlighted in grey.



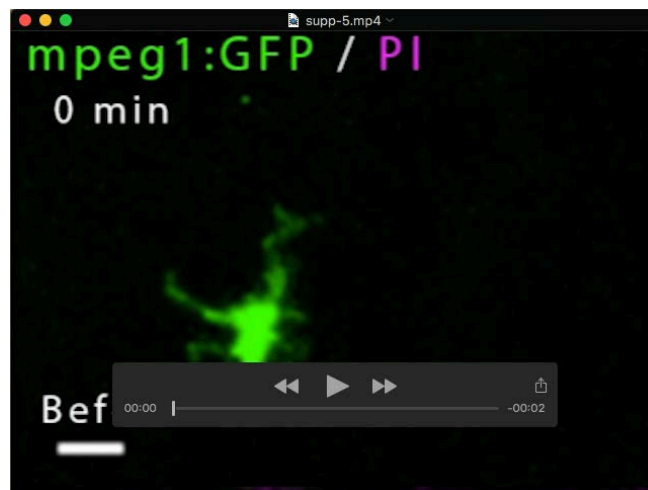
Movie 1. *In vivo* time-lapse imaging shows clearance of PI⁺ cells and appearance of pyknotic nuclei after brain injury. The movie was recorded in an *H2A:GFP* animal in the presence of PI from 120 to 230 min after injury. PI⁺ cells (magenta arrows) are removed, while pyknotic nuclei (white arrows) progressively appear within this time window. Scale bar, 15 μ m.



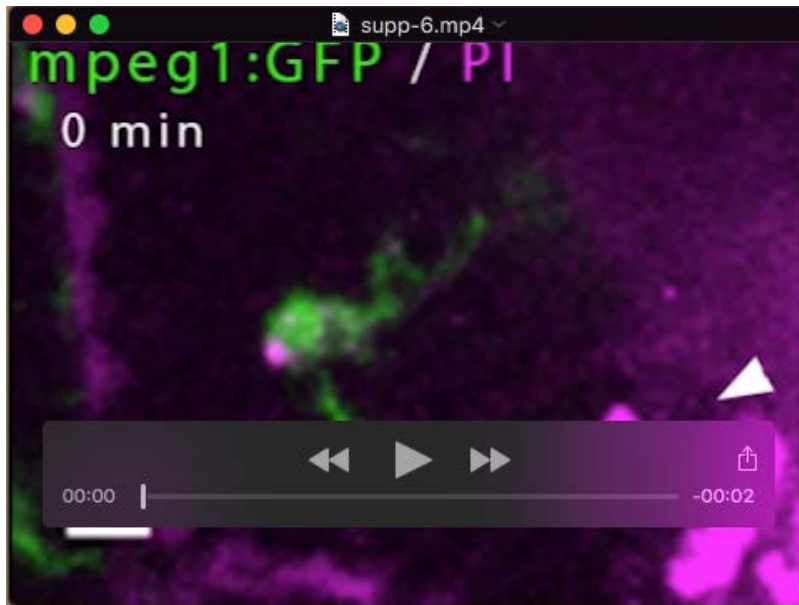
Movie 2. Macrophage-lineage cells display limited baseline motility in sham animals. The movie shows maximum intensity projections of z-stacks of the optic tectum in a sham *mpeg1:GFP* animal, indicating limited movement of the cell bodies of macrophage-lineage cells. The traces indicate cell body displacement of individual cells over 25 min. Scale bar, 40 μ m.



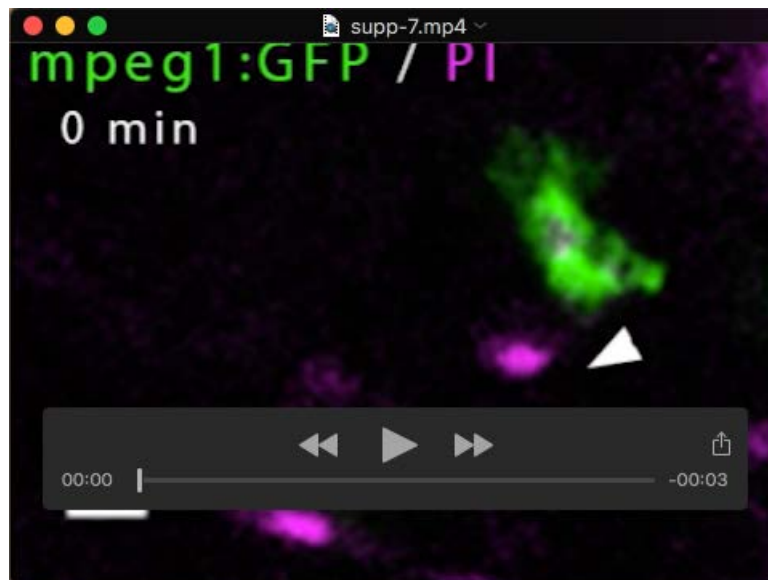
Movie 3. After injury, macrophage-lineage cells rapidly migrate towards the site of brain injury. The movie shows maximum intensity projections of z-stacks of the optic tectum in an injured *mpeg1:GFP* animal, revealing rapid directional movement of macrophage-lineage cells towards the lesion site after brain injury. The traces indicate cell body displacement of individual cells in the 140 min following injury. Scale bar, 40 μm .



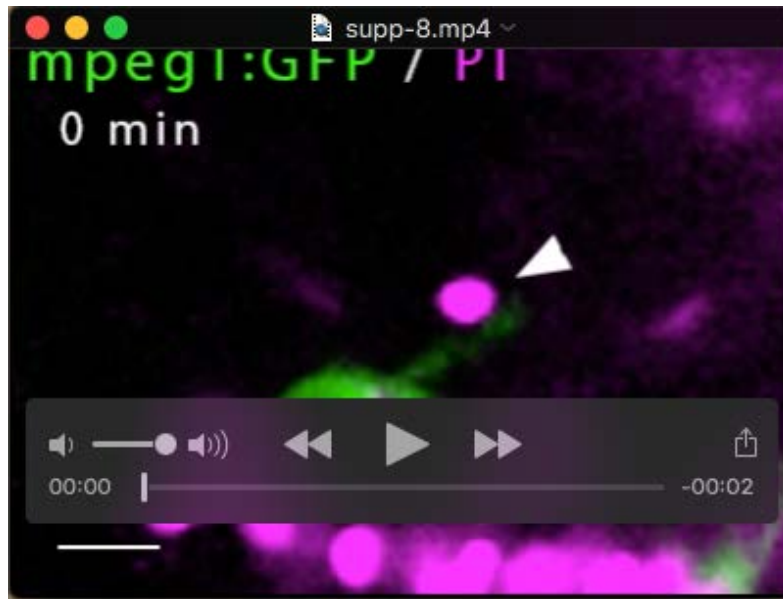
Movie 4. Microglia actively survey their environment in sham animals. Time-lapse imaging of a microglial cell reveals the highly dynamic processes with which it monitors its environment over 30 min in a sham *mpeg1:GFP* animal. Scale bar, 15 μm .



Movie 5. Microglia rapidly engulf PI⁺ cells after brain injury. Time-lapse imaging shows a microglial cell as it approaches and engulfs a PI⁺ cell after tectal injury in a *mpeg1:GFP* animal. The movie was recorded from 30 to 66 min following injury. Scale bar, 15 μ m.



Movie 6. Microglial phagocytosis is reduced in animals treated with L-SOP. Time-lapse imaging of a microglial cell in a *mpeg1:GFP* animal treated with L-SOP. The microglial cell approaches a PI⁺ cell, but does not engulf it. The movie was recorded from 30 to 72 min following injury. Scale bar, 15 μ m.



Movie 7. Microglial uptake of cellular debris is reduced in *adgrb1a/b* crispants.

In a *mpeg1:GFP* animal injected with *adgrb1a/b* gRNAs, a microglial cell extends a process towards a PI⁺ cell but does not proceed to phagocytose it. The movie was recorded from 30 to 66 min following injury. Scale bar, 15 μ m.