
Figures and figure supplements

A novel monomeric amyloid β -activated signaling pathway regulates brain development via inhibition of microglia

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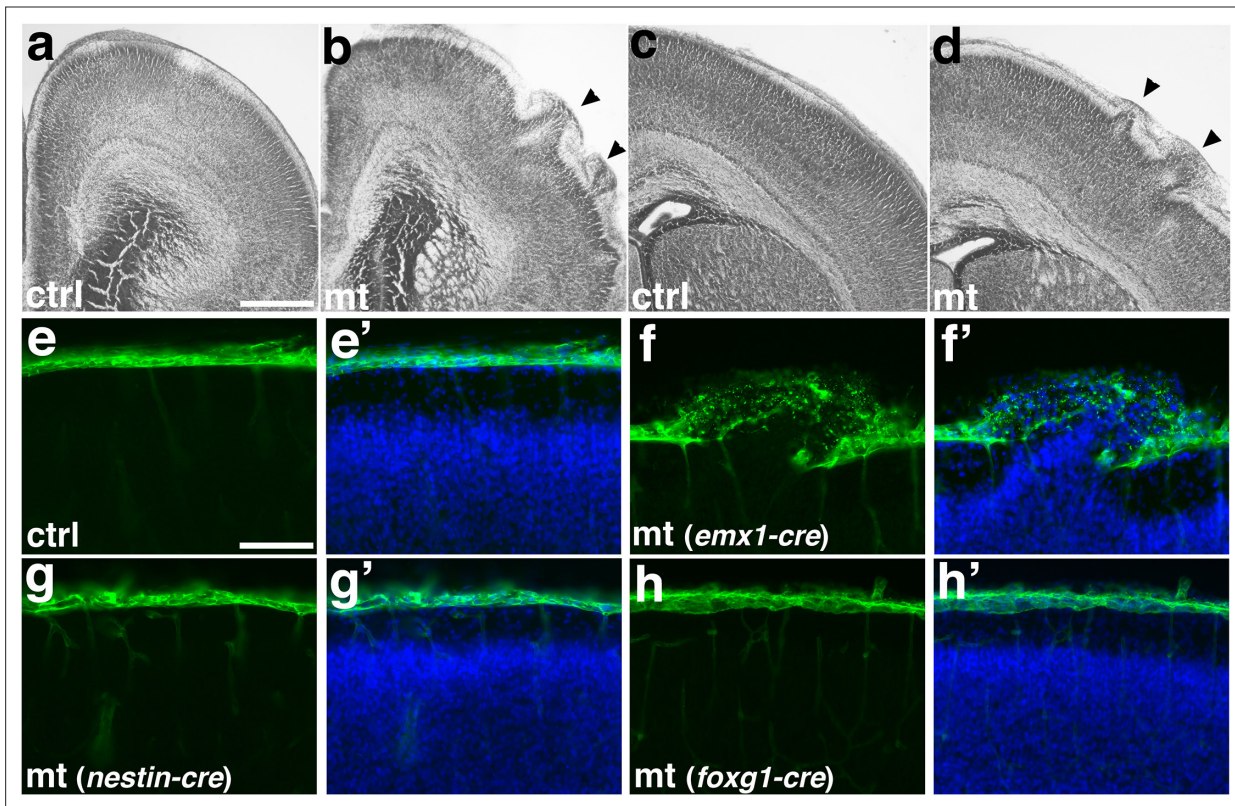


Figure 1. Deletion of *Ric8a* using *Emx1-Cre* results in cortical ectopia due to non-neural deficits. (a–d) Nissl staining of control (ctrl, (a)&(c)) and mutant mt, (b&d) anterior motor (a–b) and posterior somatosensory (c–d) cortex at P0. (e–e') Laminin (LN, in green) and nuclear (DAPI, in blue) staining of control cortices at P0. A continuous basement membrane is observed at the pia, beneath which cells are well organized in the cortical wall. (f–f') Staining of *Ric8a:Emx1-Cre* mutant cortices at P0. Basement membrane breach and neuronal ectopia are observed following *Ric8a* deletion by *Emx1-Cre*, a *Cre* line expressed in cortical radial glial progenitors beginning at E10.5. (g–g') Staining of *Ric8a:Nestin-Cre* mutant cortices at P0. No obvious basement membrane breach or neuronal ectopia is observed following *Ric8a* deletion by *Nestin-Cre*, a *Cre* line expressed in cortical progenitors beginning around E12.5. (h–h') Staining of *Ric8a:Foxg1-Cre* mutant cortices at P0. No obvious basement membrane breach or neuronal ectopia is observed following *Ric8a* deletion by *Foxg1-Cre*, a *Cre* line expressed in forebrain neural progenitors from E9.0. Scale bars, 640 μ m for (a–b), 400 μ m for (c–d), and 100 μ m for (e–h').

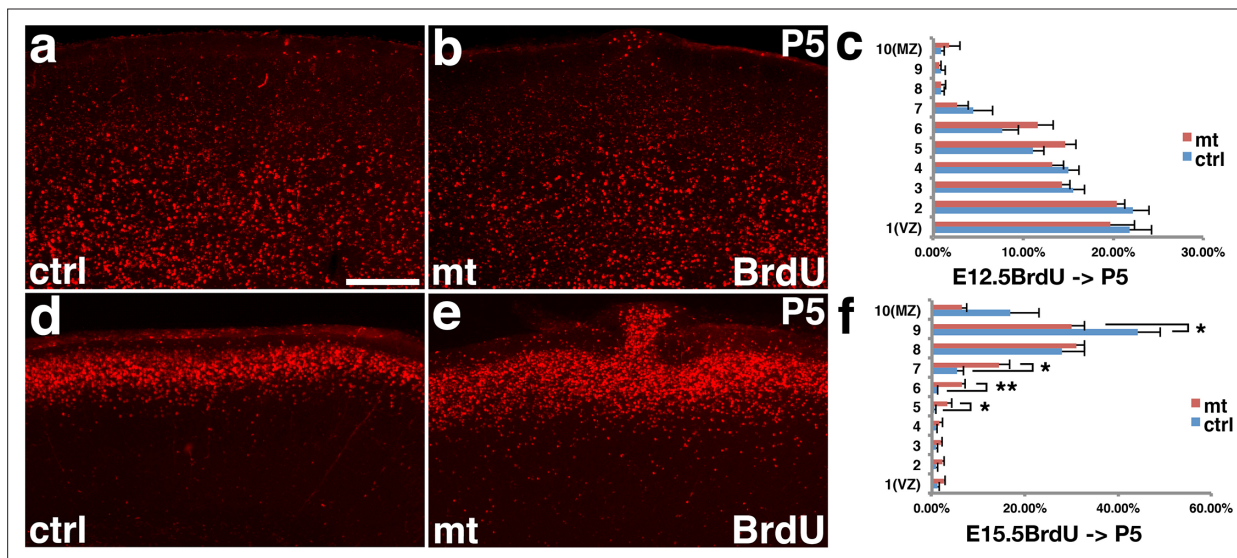


Figure 1—figure supplement 1. Birth-dating of early and late-born neurons in *Ric8a:Emx1-Cre* mutant cortices. (a–c) BrdU (in red) staining in control (a) and mutant (b) cortices at P5 after administration at E12.5. Quantification is shown in (c). No statistically significant differences were observed between control and mutant neurons in regions without ectopia. (d–f) BrdU staining in control (d) and mutant (e) cortices at P5 after administration at E15.5. Quantification is shown in (f). Neuronal migration appears slightly delayed in mutants as compared to controls. *, $P < 0.05$; **, $P < 0.01$; $n = 5$.

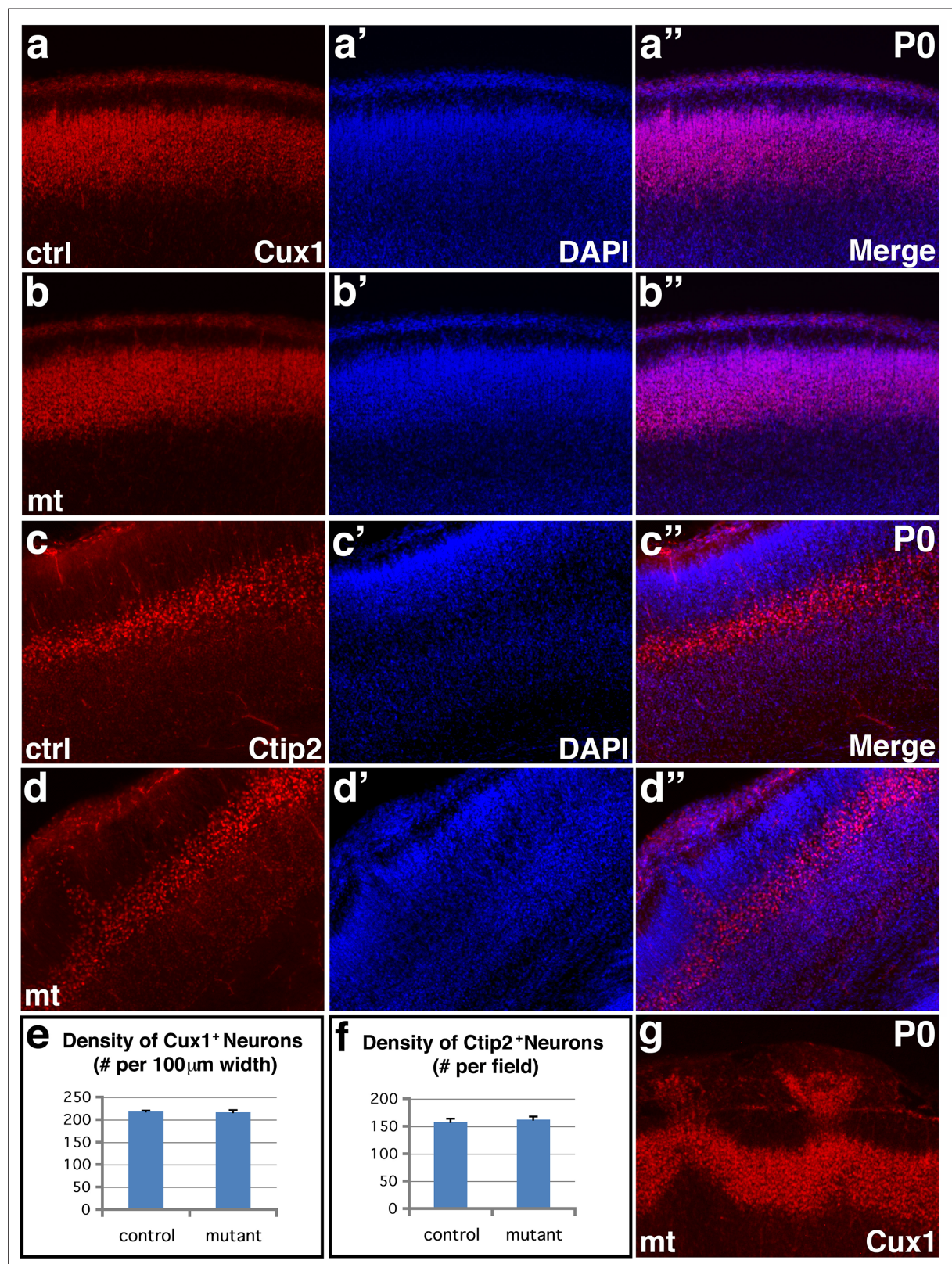


Figure 1—figure supplement 2. Lamina-specific neuronal markers are normal outside ectopia in *Ric8a:Emx1-Cre* mutant cortices. (**a–b**) (") Cux1 (in red) and nuclear (DAPI, in blue) staining of control (**a–a**") and mutant (**b–b**") cortices at P0 in a region without ectopia. No obvious changes in the expression pattern of Cux1, an upper layer neuronal marker, were observed in the mutant cortex, except in areas with ectopia (see panel (**g**)). (**c–d**") Ctip2 (in red) and nuclear (DAPI, in blue) staining of control (**c–c**") and mutant (**d–d**") cortices at P0. No obvious changes in the expression pattern of Ctip2, a deep

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layer neuronal marker, were observed in the mutant cortex, except in areas with ectopia. **(e–f)** Quantification of cortical neurons positive for Cux1 **(e)** and Ctip2 **(f)** in matching cortical regions at P0. No significant differences were observed in the density of Cux1 (control, 218.1 ± 1.7 per 100 μm cortical width; mutant, 216.4 ± 4.3 per 100 μm cortical width; $P=0.36$, $n=12$) or Ctip2 (control, 157.8 ± 5.0 per field; mutant, 161.9 ± 5.9 per field; $P=0.31$, $n=12$) positive neurons between controls and mutants. **(g)** Cux1 (in red) staining of mutant cortices at P0 in a region with ectopia. Scale bar in **(a)**, 200 μm for all panels.

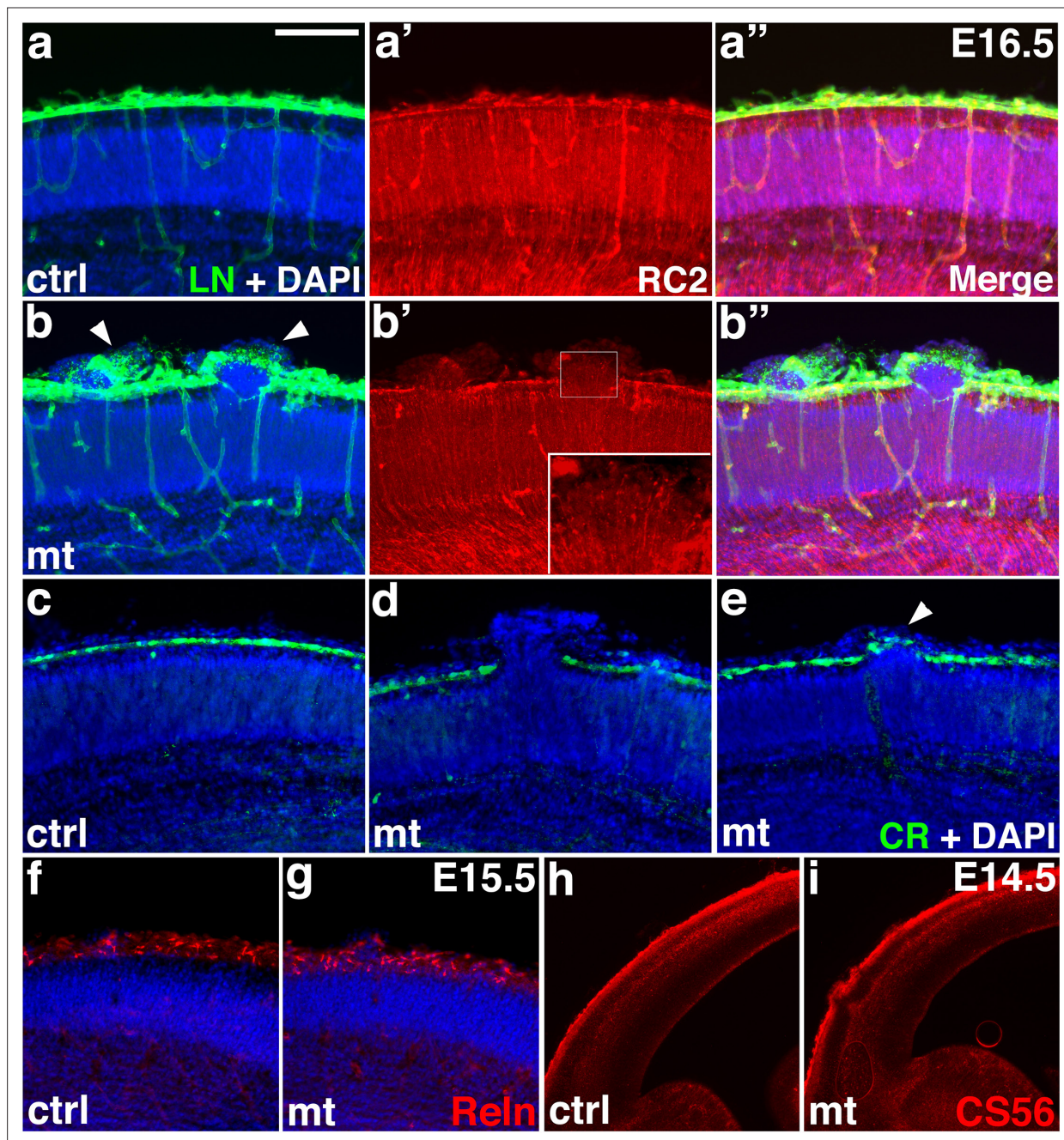


Figure 1—figure supplement 3. Neuronal ectopia in *Ric8a:Emx1-Cre* mutants result from pial basement membrane breach during embryogenesis. **(a–a'')** Laminin (LN, in green), radial glial marker RC2 (in red), and nuclear (DAPI, in blue) staining of control cortices at E16.5. A continuous basement membrane is observed at the pia, where radial glial endfeet are anchored. **(b–b'')** Laminin, RC2, and nuclear staining of *Ric8a:Emx1-Cre* mutant cortices at E16.5. Neuronal ectopias are consistently observed at sites of basement membrane breakage (arrowheads in **b**). Radial glial fibers at these sites extend beyond the pia (inset in **b'**). **(c–e)** Calretinin (CR, in green) and nuclear (DAPI, in blue) staining of control (**c**) and mutant (**d–e**) cortices at E16.5. A continuous row of Calretinin positive Cajal-Retzius cells is observed in the marginal zone of control cortices (**c**). By contrast, in mutants, Cajal-Retzius cells are absent at large ectopias (**d**). However, they appear passively displaced by over-migrating neurons at small ectopias (arrowhead in **e**). **(f–g)** Reelin (Reln, in red) and nuclear (DAPI, in blue) staining of control (**f**) and *Ric8a:Emx1-Cre* mutant (**g**) cortices at E15.5. Strong Reelin expression is observed in Cajal-Retzius cells in the marginal zone of both control and mutant cortices. **(h–i)** Chondroitin sulfate proteoglycan (CS56, in red) staining of control (**h**) and mutant (**i**) cortices at E14.5. Normal preplate splitting is observed in mutants. Scale bar in **(a)**, 200 μ m for **(a–g)** and 500 μ m for **(h–i)**.

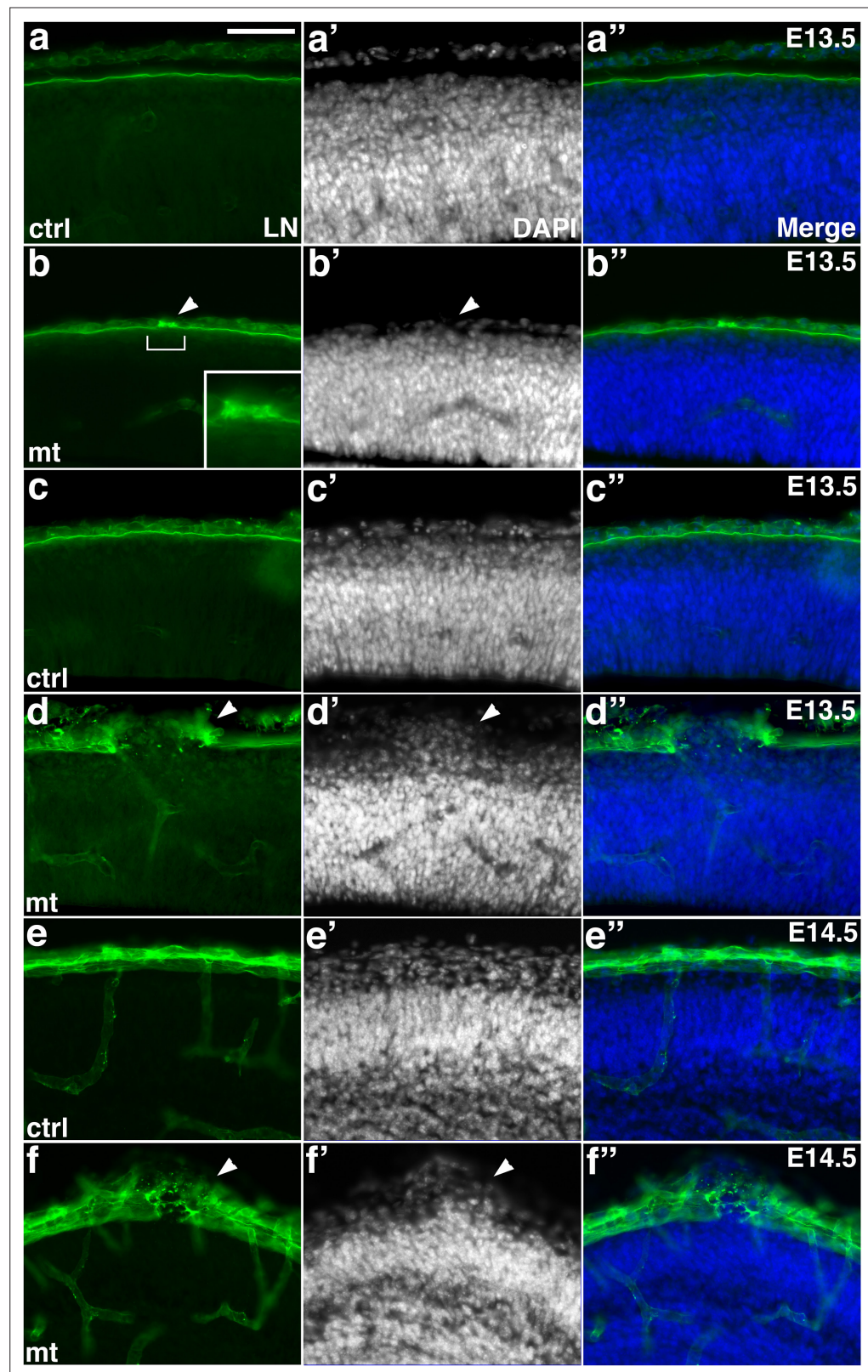


Figure 1—figure supplement 4. Basement membrane breaches precede neuronal ectopia in *Ric8a:Emx1-Cre* mutant cortice. s. (a-a'') Laminin (LN, in green) and nuclear (DAPI, in blue) staining of control cortices at E13.5. A continuous basement membrane is observed at the pia, beneath which cells are well organized in the cortical wall. (b-b'') Laminin and nuclear staining of *Ric8a:Emx1-Cre* mutant cortices at E13.5. In a subset of mutants, a

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small disruption of basement membrane is observed (bracket and inset in **b**), but not yet associated with ectopia (arrowhead in **b'**). (**c-c''**) Laminin (LN, in green) and nuclear (DAPI, in blue) staining of control cortices at E13.5. (**d-d''**) Laminin and nuclear staining of *Ric8a:Emx1-Cre* mutant cortices at E13.5. Although at E13.5 we observe basement membrane defects in the absence of neuronal ectopia (see **b-b''**), when there are neuronal ectopia, they are always associated with basement membrane breakage. (**e-e''**) Laminin and nuclear staining of control cortices at E14.5. (**f-f''**) Laminin and nuclear staining of *Ric8a:Emx1-Cre* mutant cortices at E14.5. Neuronal ectopia at E14.5 are also always associated with basement membrane breakage. Scale bar in (**a**), 100 μ m for all panels.

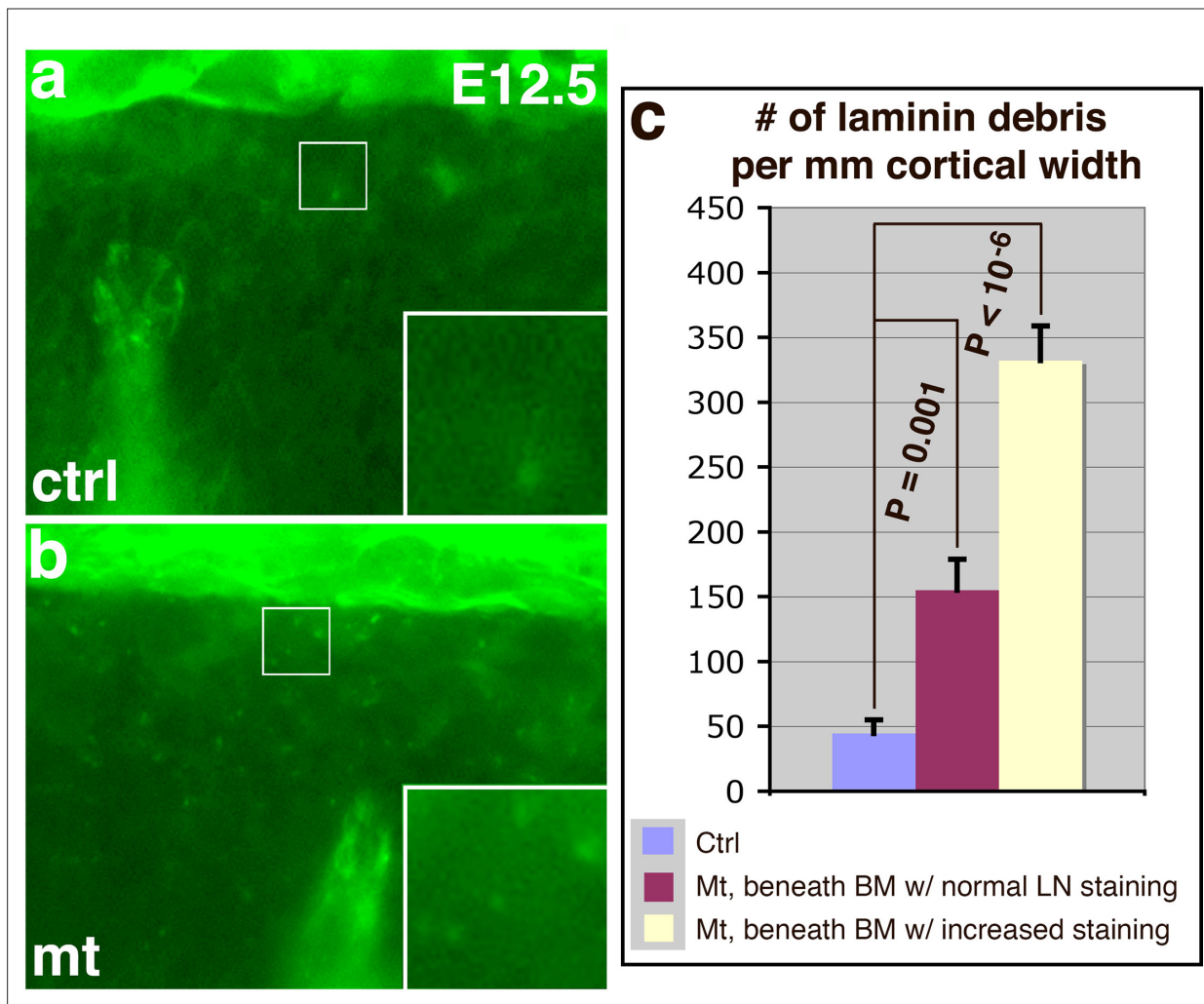


Figure 1—figure supplement 5. Signs of basement membrane degradation before breach formation at E12.5. (a–b) Laminin (in green) staining of control (a) and *Ric8a:Emx1-Cre* mutant (b) cortices at E12.5. Increased numbers of laminin positive debris were observed in mutants (compare insets), even though breaches had yet to form. (c) Quantitative analysis shows significant increases.

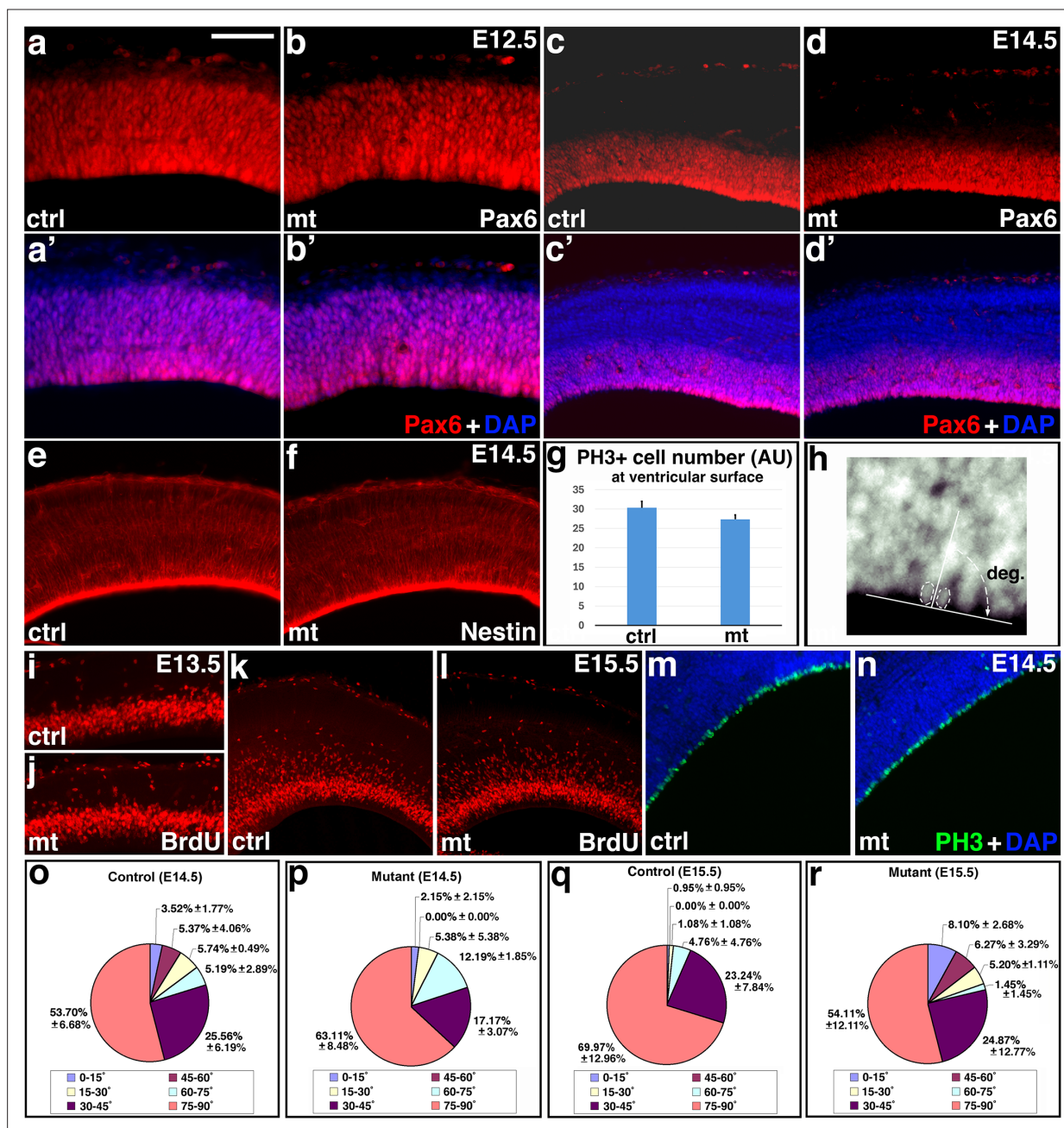


Figure 1—figure supplement 6. Cortical radial glial identity and proliferation are unaffected in *Ric8a:Emx1-Cre* mutants. (a–b') Pax6 (in red) and nuclear (DAPI, in blue) staining of control (a&a') and mutant (b&b') cortices at E12.5. (c–d') Pax6 (in red) and nuclear (DAPI, in blue) staining of control (c&c') and mutant (d&d') cortices at E14.5. No ectopic Pax6 positive cells were observed at either E12.5 or E14.5. (e–f) Nestin (in red) and nuclear (DAPI, in blue) staining of control (e) and mutant (f) cortices at E14.5. (g) Quantification showed no significant differences in the number of phospho-histone 3 (PH3) positive cells at the ventricular surface between control and mutants at E14.5 (AU, arbitrary units; $P=0.15$, $n=9$ each). See also images in (m–n). (h) Cleavage plane of neural progenitors is defined by the angle between the equatorial plate and the ventricular surface. See quantification results in (o–r). (i–j) BrdU staining (in red) in control (i) and mutant (j) cortices at E13.5. (k–l) BrdU staining (in red) in control (k) and mutant (l) cortices at E15.5. (m–n) Phospho-histone 3 (PH3, in green) and nuclear (DAPI, in blue) staining of control (m) and mutant (n) cortices at E14.5. (o–p) Cleavage plane distribution of radial glial mitosis in control (o) and mutant (p) cortices at E14.5. No significant differences were observed ($P>0.4$, $n=3$ animals each genotype; 73 cells for controls and 76 cells for mutants). (q–r) Cleavage plane distribution of radial glial mitosis in control (q) and mutant (r) cortices at E15.5. No significant differences were observed ($P>0.1$, $n=3$ animals each genotype; 70 cells for controls and 59 cells for mutants). Scale bar in (a), 100 μm for (a–b') and 200 μm for (c–n).

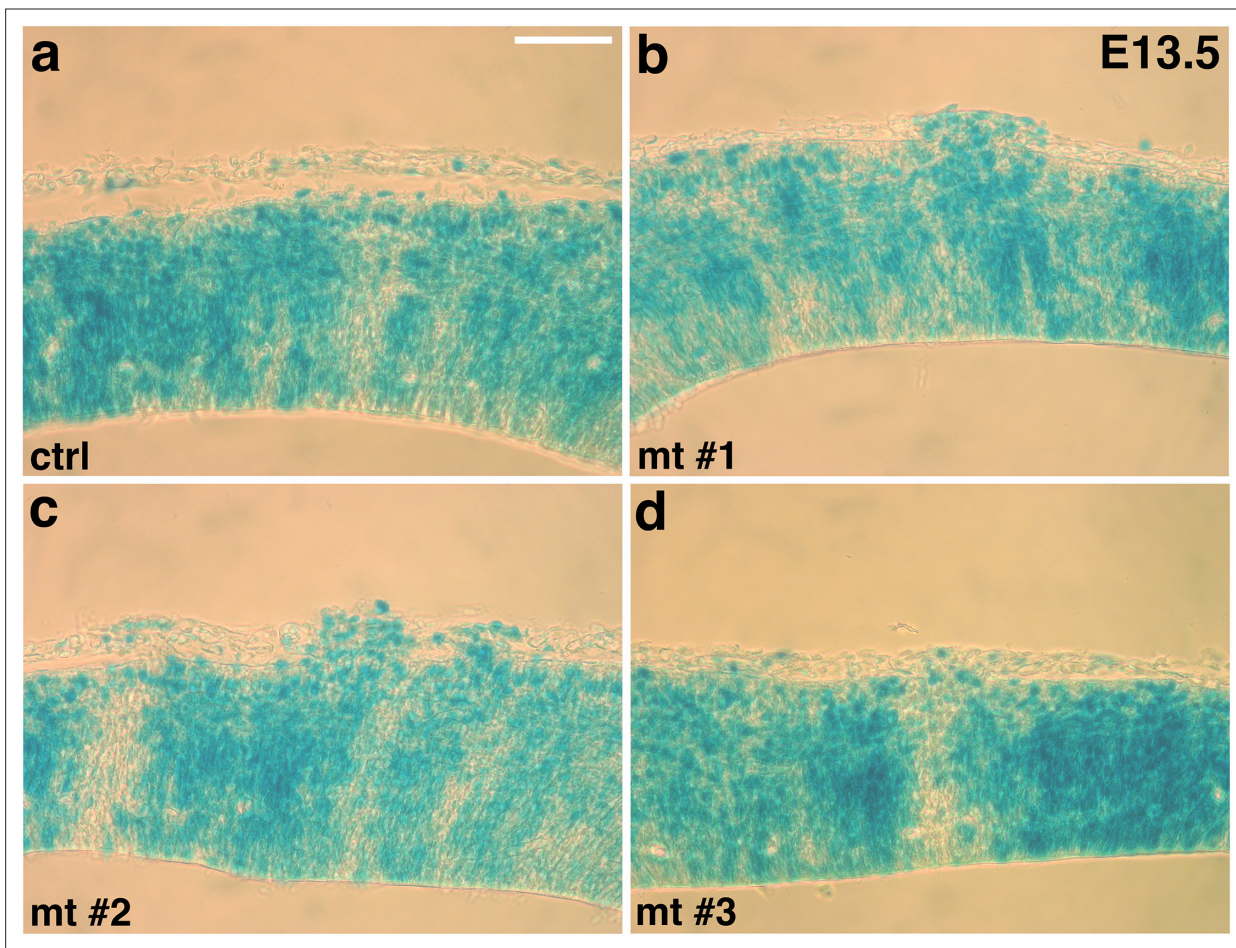


Figure 1—figure supplement 7. Wnt pathway activity is normal in *Ric8a:Emx1-Cre* mutant cortices. X-gal staining of BAT-lacZ expression in *Ric8a:Emx1-Cre* control (a) and mutant (b–d) cortices at E13.5. No obvious differences are observed between controls and three different mutants at this stage.

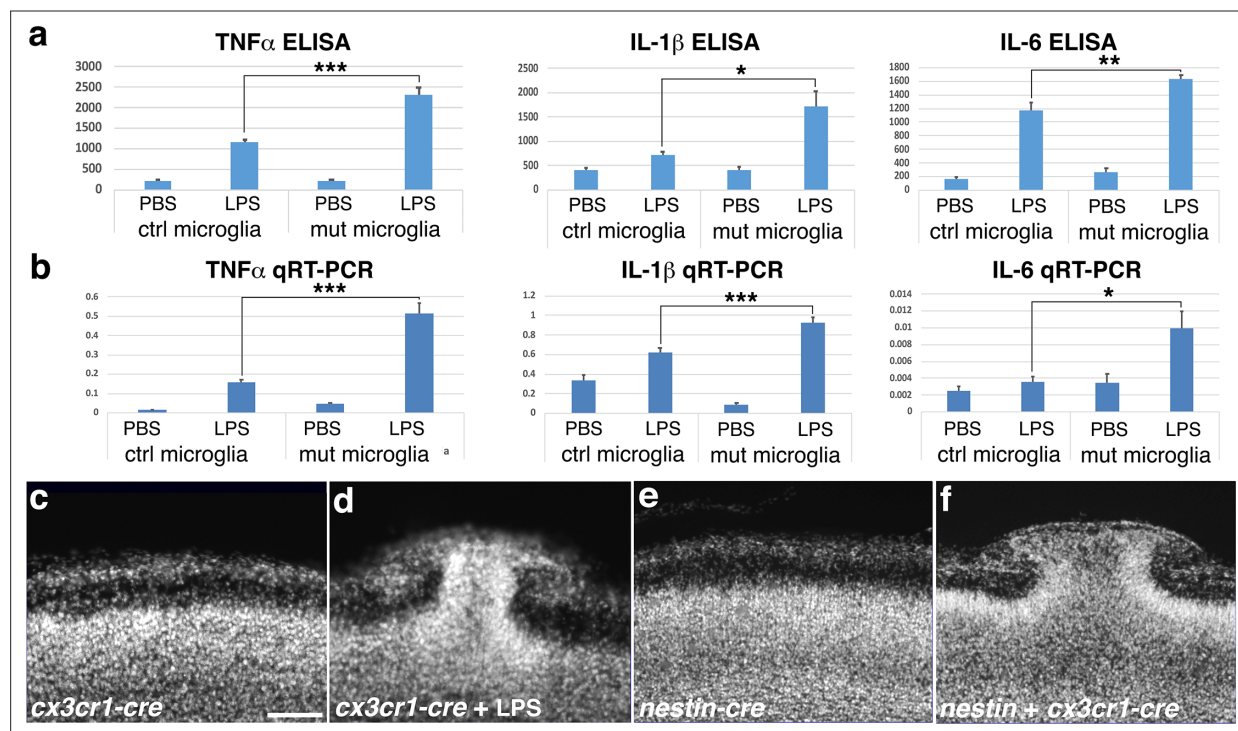


Figure 2. *Ric8a* deficiency in microglia is responsible for cortical ectopia. (a) TNF α , IL-1 β , and IL-6 secretion (pg/ml) in control and *Ric8a:Cx3cr1-Cre* mutant microglia following LPS stimulation. *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$; $n = 6-8$ each group. (b) TNF α , IL-1 β , and IL-6 mRNA expression in control and *Ric8a:Cx3cr1-Cre* mutant microglia following LPS stimulation. *, $P < 0.05$; ***, $P < 0.001$; $n = 5-6$ each group. (c-d) Nuclear (DAPI, in grey) staining of *Ric8a:Cx3cr1-Cre* mutant cortices at P0 in the absence (c) or presence (d) of LPS treatment during embryogenesis. (e-f) Nuclear (DAPI, in grey) staining of *Ric8a:Nestin-Cre* single cre (e) and *Ric8a:Nestin-Cr + Cx3cr1-Cre* double Cre (f) mutant cortices at P0. Scale bar in (c), 100 μm for (c-f).

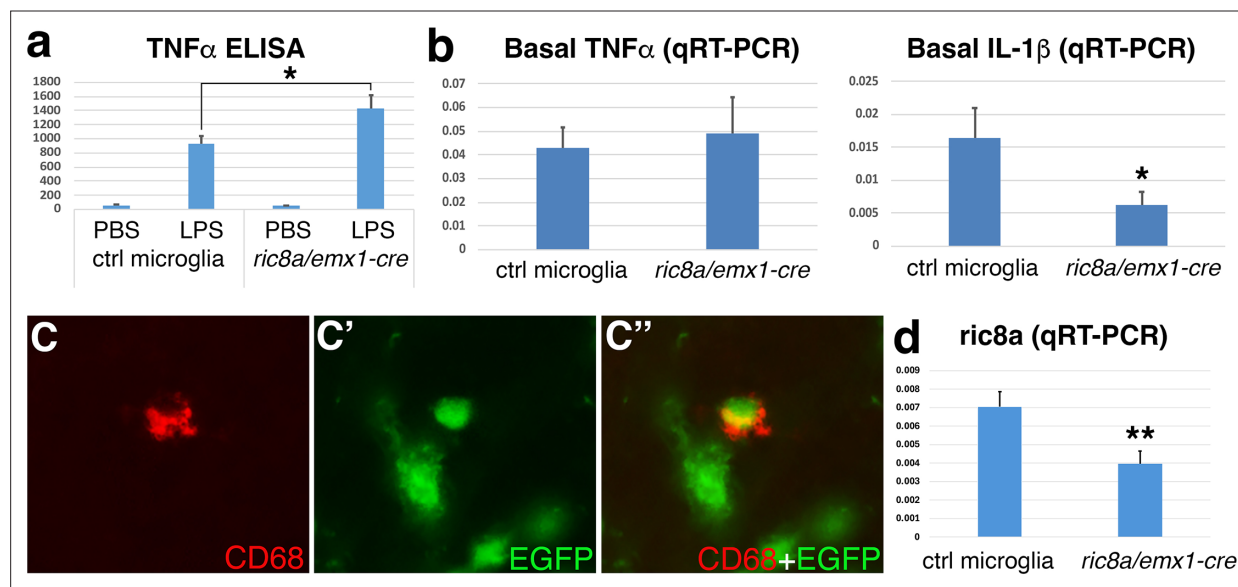


Figure 2—figure supplement 1. *Emx1-Cre* is active in microglia. (a–b) TNF α secretion (pg/ml) (a) and basal TNF α and IL-1 β mRNA expression (b) in control and *Ric8a:Emx1-Cre* mutant microglia. *, $P < 0.05$; $n = 5–8$ each group. (c–c'') The Rosa26 EGFP (green) is induced in CD68 positive (red) microglial cells by *Emx1-Cre*. (d) Quantitative RT-PCR analysis of microglia cultured from *Ric8a:Emx1-Cre* mutant cortices showed severe loss of *Ric8a* mRNA in microglial cells. **, $P < 0.01$; $n = 5–8$ each group.

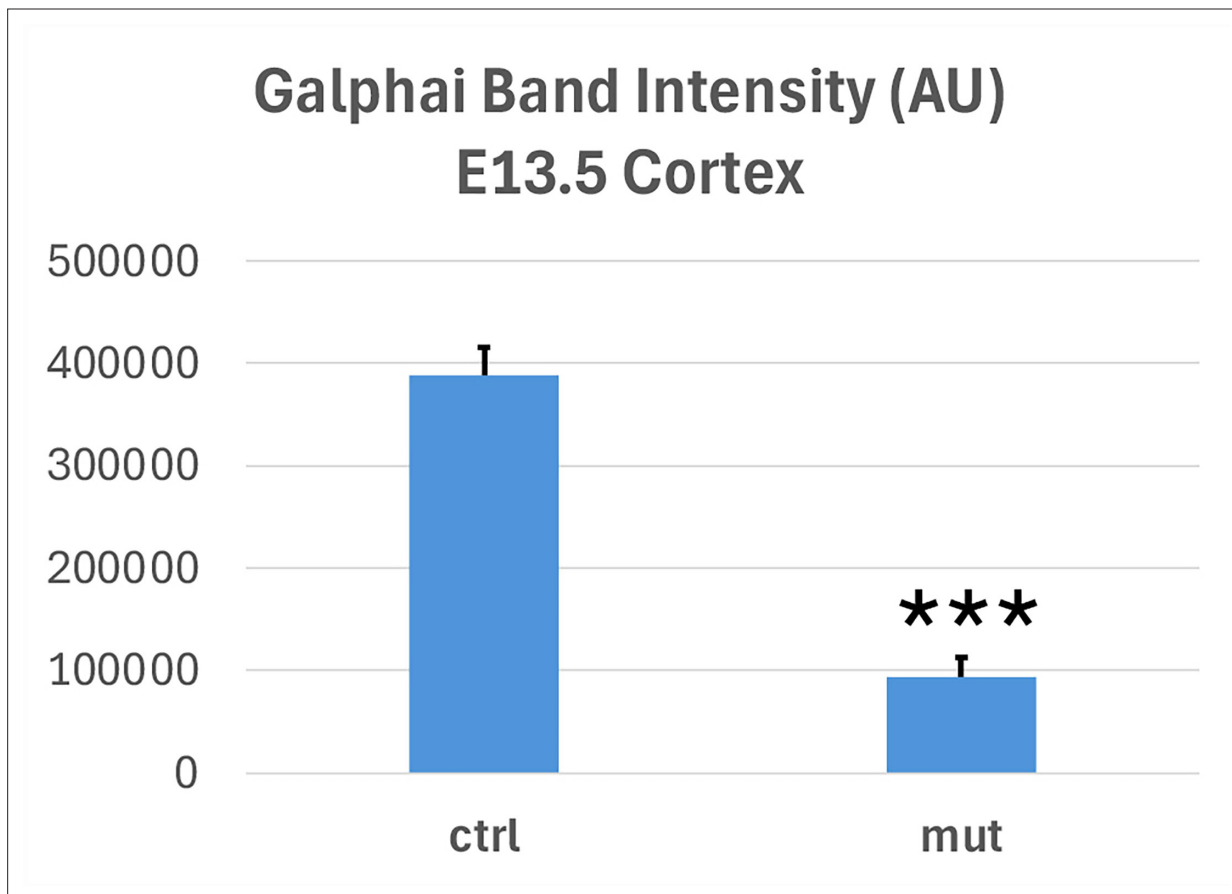


Figure 2—figure supplement 2. G α i protein is severely depleted from *Ric8a:Emx1-Cre* mutant cortices. Western blot analysis of Gai proteins in E13.5 *Ric8a:Emx1-Cre* mutant cortices showed that G α i protein levels were severely reduced (AU, arbitrary units). $P < 0.001$, $n = 3$ each.

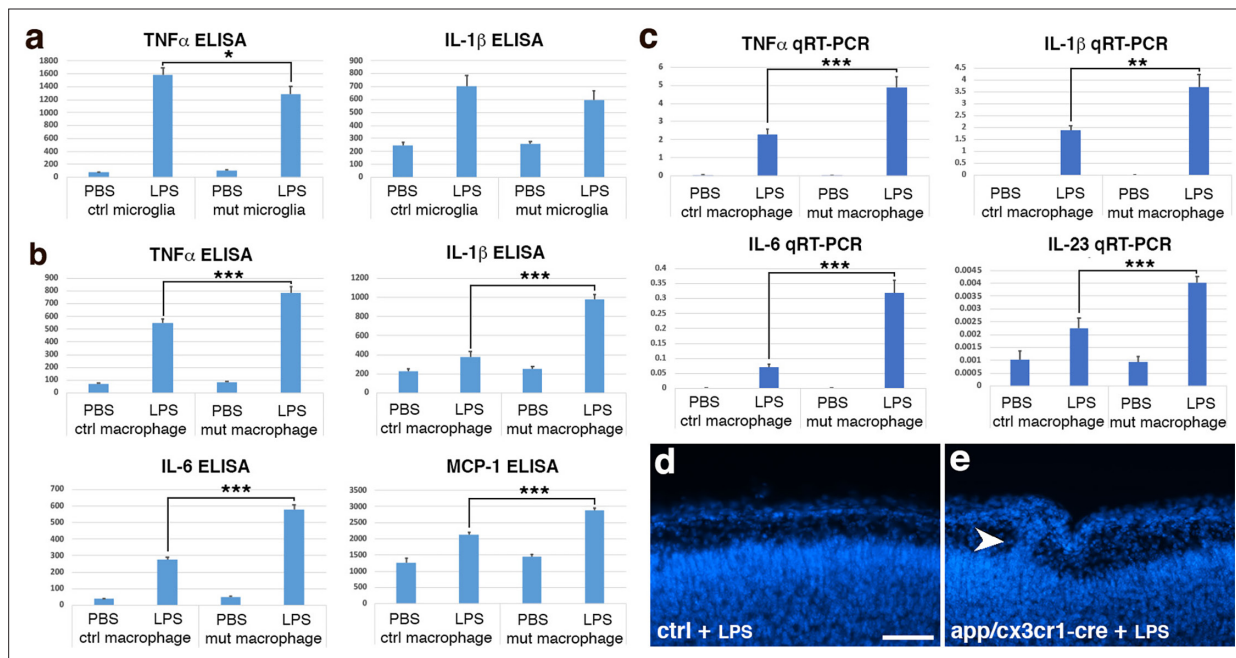


Figure 3. *App* deficiency results in hypersensitive microglia and cortical ectopia. **(a)** TNF α and IL-1 β secretion (pg/ml) in cultured control and *App:Cx3cr1-Cre* mutant microglia following LPS stimulation. *, $P < 0.05$; $n = 7-9$ each group. **(b)** TNF α , IL-1 β , IL-6, and MCP1 secretion (pg/ml) in fresh unelicited control and *App:Cx3cr1-Cre* mutant peritoneal macrophages following LPS stimulation. ***, $P < 0.001$; $n = 7-10$ each group. **(c)** TNF α , IL-1 β , IL-6, and IL-23 mRNA expression in fresh unelicited control and *App:Cx3cr1-Cre* mutant peritoneal macrophages following LPS stimulation. **, $P < 0.01$; ***, $P < 0.001$; $n = 6$ each group. **(d-e)** Nuclear (DAPI, in blue) staining of control **(D)** and LPS-treated *App:Cx3cr1-Cre* mutant **(E)** cortices at P0. Note cortical ectopia in the mutant cortex (arrowhead). Scale bar in **(d)**, 200 μ m for **(d-e)**.

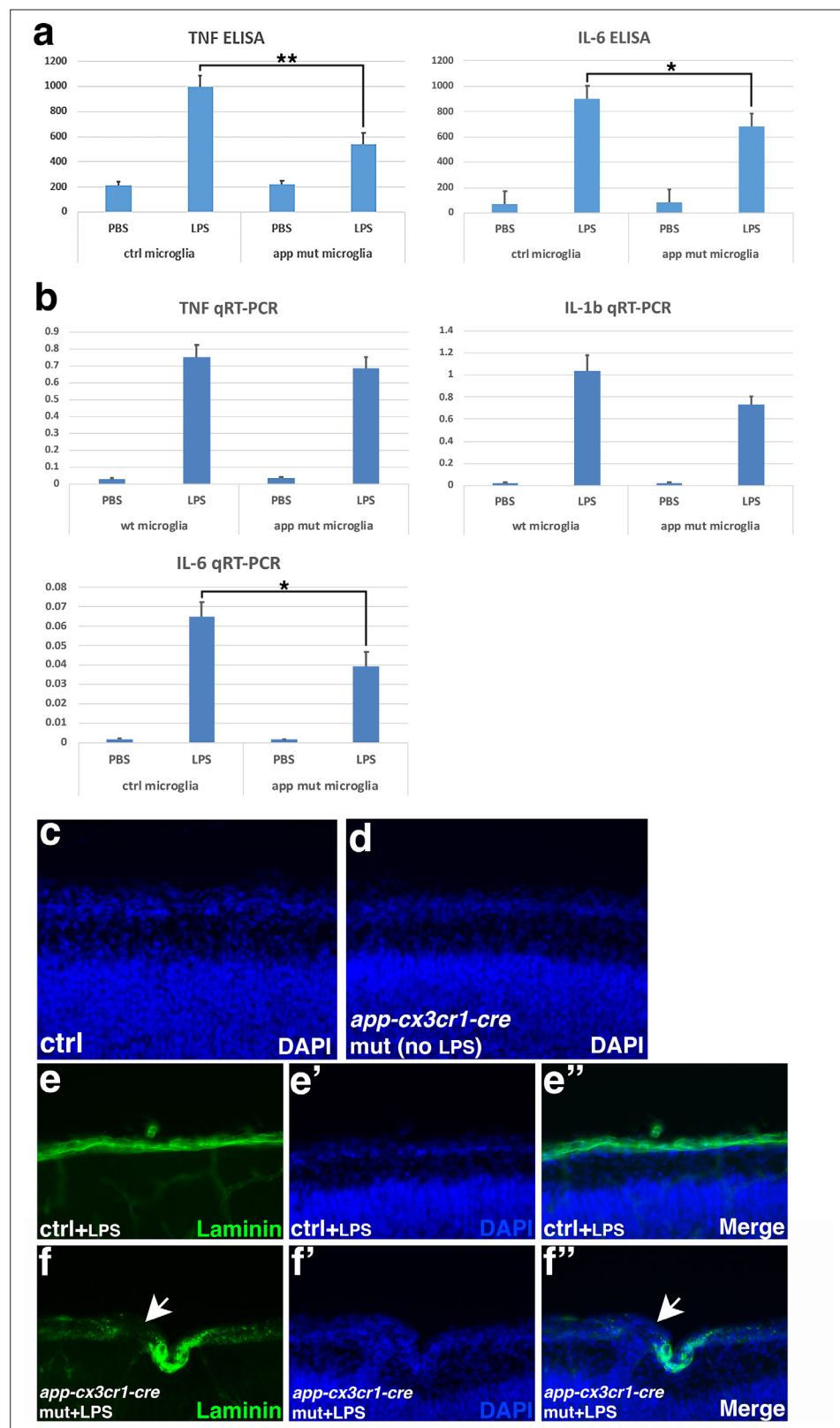


Figure 3—figure supplement 1. Cytokine secretion and transcriptional induction in *App:Cx3cr1-Cre* mutant microglia. **a.** (a) $\text{TNF}\alpha$ and IL-6 secretion (pg/ml) in control and *App:Cx3cr1-Cre* mutant microglia following overnight LPS stimulation. *, $P < 0.05$; **, $P < 0.01$; $n = 9-13$ each group. **(b)** $\text{TNF}\alpha$, IL-1 β and IL-6 mRNA expression in control and *App:Cx3cr1-Cre* mutant microglia following overnight 3 hr LPS stimulation. *, $P < 0.05$; $n = 6-7$ each group. **c-f** Immunofluorescence images of microglia. **c** and **d** show DAPI staining of control and *app-cx3cr1-cre* mutant microglia, respectively. **e** and **f** show Laminin staining of control and *app-cx3cr1-cre* mutant microglia, respectively. **e'** and **f'** show DAPI staining of control and *app-cx3cr1-cre* mutant microglia, respectively. **e''** and **f''** show merged images of Laminin and DAPI staining. White arrowheads in **f** and **f''** point to microglia. **Figure 3—figure supplement 1 continued on next page**

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group. **(c–d)** *App:Cx3cr1-Cre* mutant cortices showed no ectopia at P0 without LPS treatment at embryonic stages (DAPI, blue). **(e–f’)** *App:Cx3cr1-Cre* mutant cortices treated with LPS at embryonic stages showed perturbed basement membrane and gaps at sites of ectopia (white arrows) at P0 (Laminin, green; DAPI, blue).

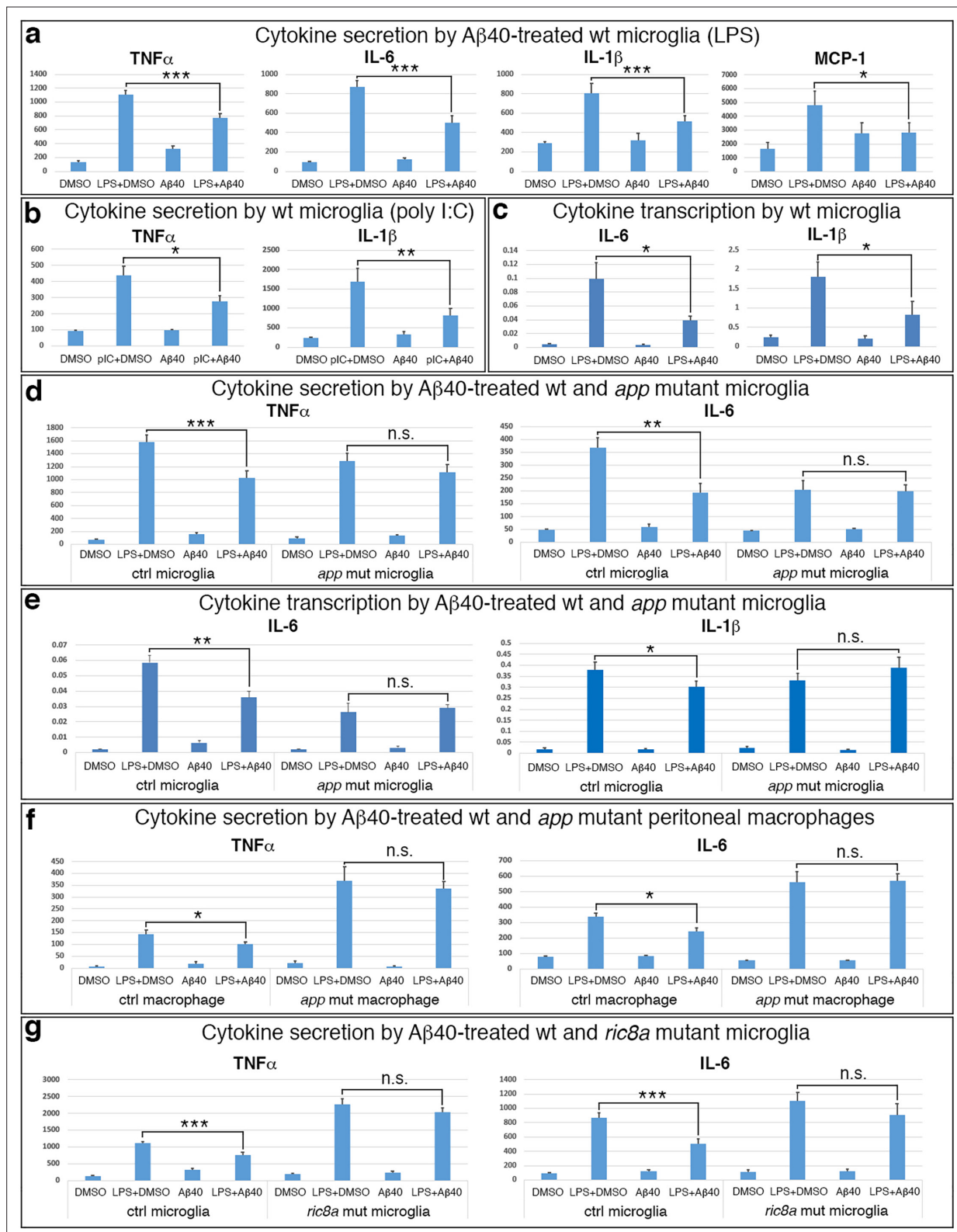


Figure 4. Monomeric Aβ40 suppresses microglia via APP and Ric8a. **(a)** TNFα, IL-6, IL-1β, and MCP1 secretion (pg/ml) by wildtype microglia following LPS stimulation in the absence or presence of Aβ40 (200 or 500 nM). *, $P < 0.05$; ***, $P < 0.001$; $n = 8-14$ each group. **(b)** TNFα and IL-1β secretion (pg/ml) by wildtype microglia following poly I:C stimulation in the absence or presence of Aβ40 (500 nM). *, $P < 0.05$; **, $P < 0.01$; $n = 6-7$ each group. **(c)** IL-6 and IL-1β mRNA induction in wildtype microglia following LPS stimulation in the absence or presence of Aβ40 (500 nM). *, $P < 0.05$; $n = 6$ each group. **(d)** TNFα

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and IL-6 secretion (pg/ml) by control and *App:Cx3cr1-Cre* mutant microglia following LPS stimulation in the absence or presence of A β 40 (200 nM). **, $P<0.01$; ***, $P<0.001$; n=8 each group. (e) IL-6 and IL-1 β mRNA induction in control and *App:Cx3cr1-Cre* mutant microglia following LPS stimulation in the absence or presence of A β 40 (200 nM). *, $P<0.05$; **, $P<0.01$; n=6 each group. (f) TNF α and IL-6 secretion (pg/ml) by control and *App:Cx3cr1-Cre* mutant peritoneal macrophages following LPS stimulation in the absence or presence of A β 40 (500 nM). *, $P<0.05$; n=6–7 each group. (g) TNF α and IL-6 secretion (pg/ml) by control and *Ric8a:Cx3cr1-Cre* mutant microglia following LPS stimulation in the absence or presence of A β 40 (200 nM). ***, $P<0.001$; n=12–14 each group.

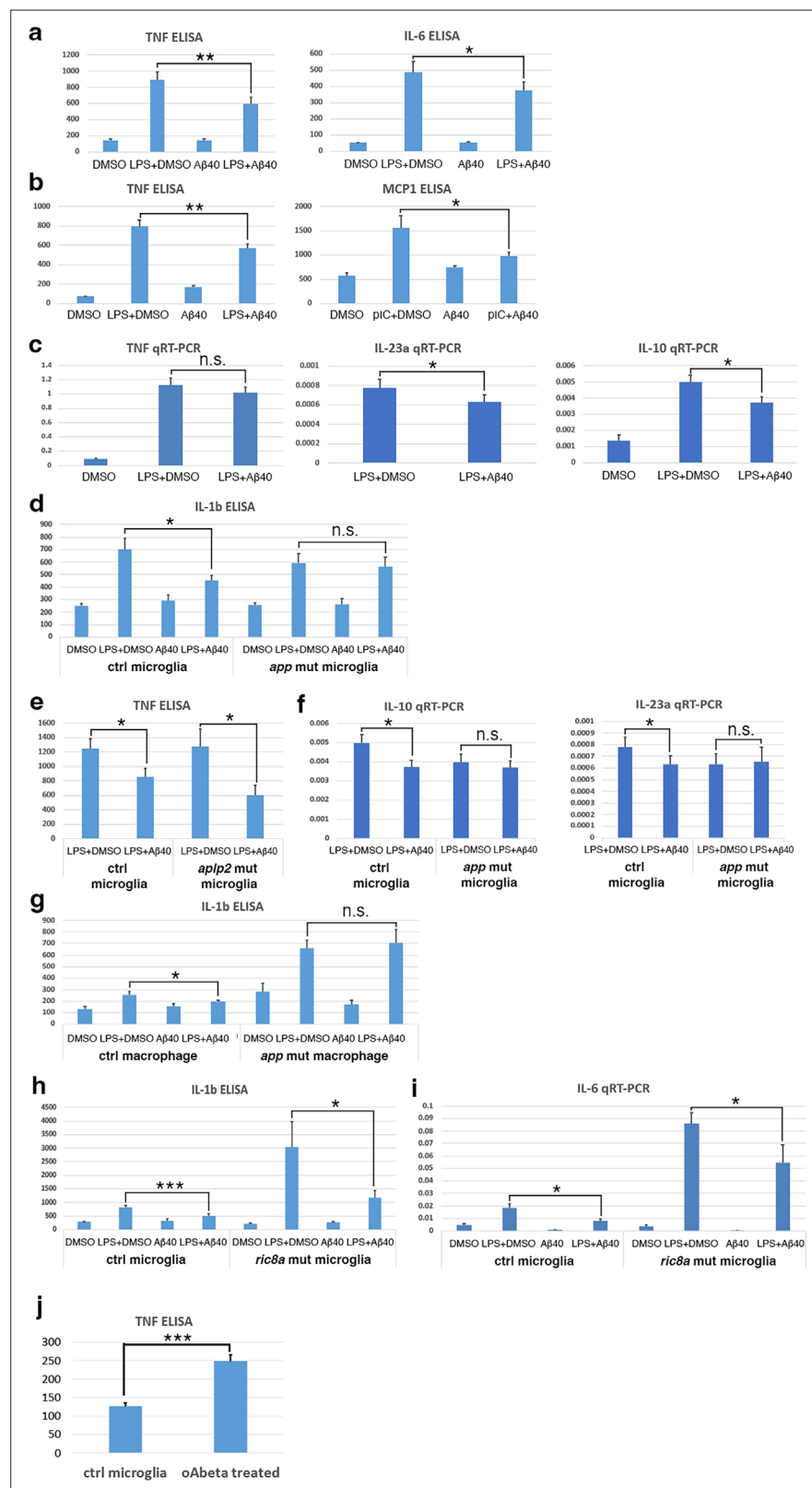


Figure 4—figure supplement 1. Effects of monomeric Aβ on cytokine secretion and transcription in control and mutant microglial lineage cells. (a) TNFα and IL-6 secretion (pg/ml) in wildtype microglia following LPS stimulation in the absence or presence of Aβ40 (50 nM). *, $P < 0.05$; **, $P < 0.01$; $n = 25$ each group for TNFα and 11 each group for IL-6. (b) TNFα and MCP1 secretion (pg/ml) in wildtype microglia following LPS stimulation in the

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absence or presence of A β 40 (500 nM) from Genscript. Effects on IL-1 β secretion in **Figure 4b** was also performed with Genscript A β 40. All other experiments in Fig. 7 were performed with ApexBio A β 40. *, $P < 0.05$; **, $P < 0.01$; n=5–7 each group. (c) TNF α , IL-23, and IL-10 mRNA expression in wildtype microglia following LPS stimulation in the absence or presence of A β 40 (400 nM). *, $P < 0.05$; n=6 each group. (d) IL-1 β secretion (pg/ml) in control and *App:Cx3cr1-Cre* mutant microglia following LPS stimulation in the absence or presence of A β 40. *, $P < 0.05$; n=8–12 each group. (e) TNF α (pg/ml) in control or *Aplp2:Cx3cr1-Cre* mutant microglia following LPS stimulation in the absence or presence of A β 40 (400 nM). *, $P < 0.05$; n=9–13 each group. (f) IL-10 and IL-23 mRNA expression in control and *App:Cx3cr1-Cre* mutant microglia following LPS stimulation in the absence or presence of A β 40 (400 nM). *, $P < 0.05$; n=6 each group. (g) IL-1 β secretion (pg/ml) in fresh unelicited control and *App:Cx3cr1-Cre* mutant peritoneal macrophages following LPS stimulation in the absence or presence of A β 40 (400 nM). *, $P < 0.05$; n=12 each group. (h) IL-1 β secretion (pg/ml) in f control and *Ric8a:Cx3cr1-Cre* mutant microglia following LPS stimulation in the absence or presence of A β 40 (500 nM). *, $P < 0.05$; ***, $P < 0.001$; n=7–8 each group. (i) IL-6 mRNA expression in control and *Ric8a:Cx3cr1-Cre* mutant microglia following LPS stimulation in the absence or presence of A β 40 (200 nM). *, $P < 0.05$; n=6 each group. (j) TNF α (pg/ml) in wildtype microglia in the absence or presence of A β 40 oligomers aggregated (at 10 μ M monomer equivalent). ***, $P < 0.001$; n=10 each group.

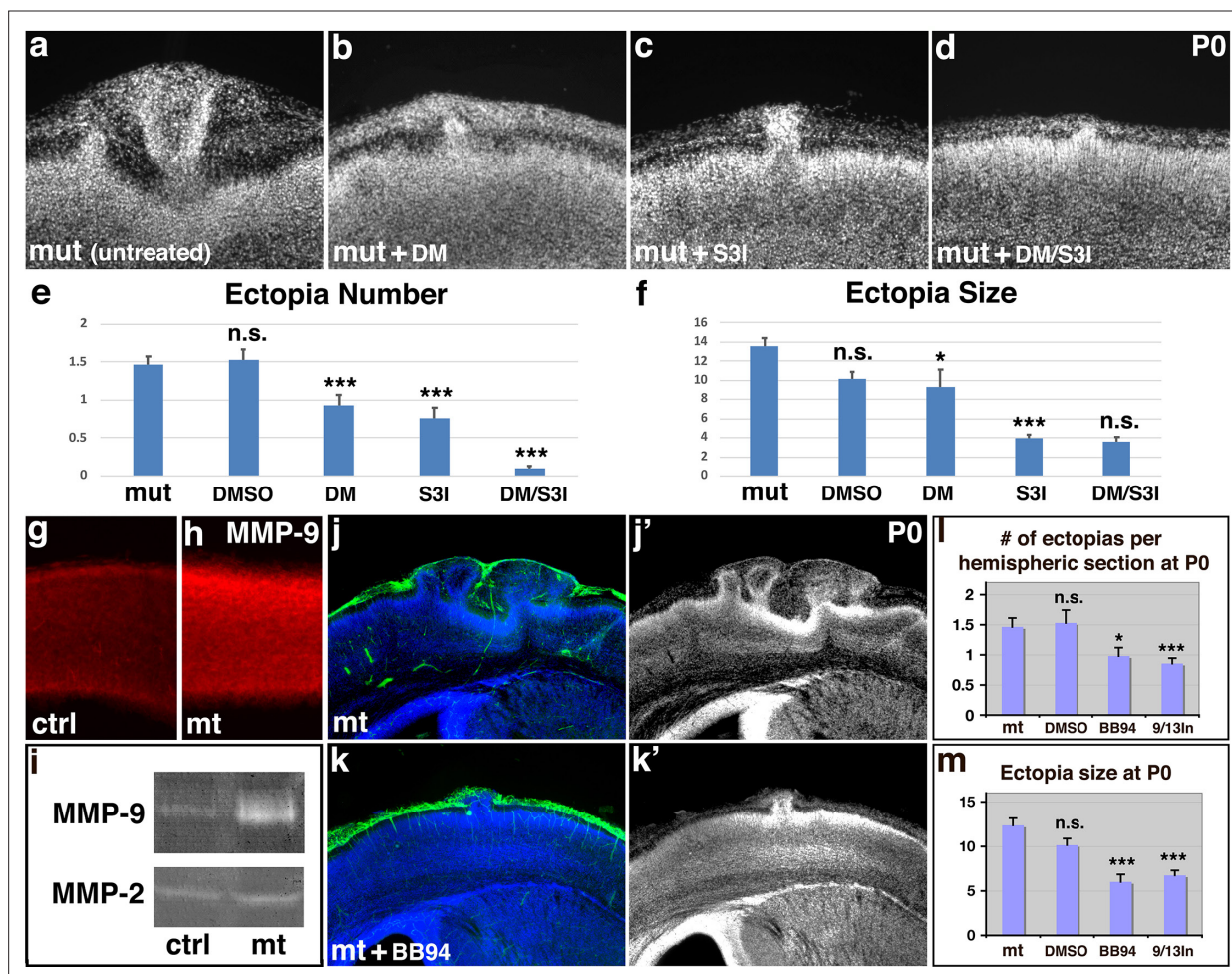


Figure 5. Inhibition of both microglial inflammatory activation and cortical MMP9 activity suppresses basement membrane breach and neuronal ectopia. (**a–d**) Nuclear (DAPI, in grey) staining of untreated (**a**), anti-inflammatory drug dorsomorphin (DM) (**b**), Stat3 inhibitor S3I-201 (S3I) (**c**), and DM/S3I (**d**) dual treated *Ric8a:Emx1-Cre* mutant cortices at P0. (**e–f**) Quantitative analysis of ectopia number (**e**) and size (**f**) in the neonatal mutant cortex after DMSO, DM, S3I, and DM/S3I dual treatment at E12.5. *, $P < 0.05$; ***, $P < 0.001$; all compared to untreated mutants. The reduction in ectopia size after dual treatment is not statistically significant, likely due to the small number of ectopias that remained. (**g–h**) MMP9 (in red) staining of control (**g**) and mutant cortices (**h**) at E13.5. Quantification shows statistically significant increases in mutants (control, 24.8 ± 0.2 AU (Arbitrary Units); mutant, 35.7 ± 1.7 AU; $P = 0.002$; $n = 6$). (**i**) Gel zymography of control and mutant cortical lysates at E13.5. Increased levels of MMP9 but not of MMP2 were observed in mutants (control, 1.00 ± 0.06 AU; mutant, 3.72 ± 1.86 AU; $P = 0.028$; $n = 4$). See further details in supplemental Fig. 13. (**j–k'**) Laminin (in green) and nuclear (DAPI, in blue) staining of mutant cortices untreated (**j**) or treated (**k'**) with BB94. (**l–m**) Quantitative analysis of ectopia number and size following MMP inhibitor BB94 or MMP9/13 inhibitor I treatment. *, $P < 0.05$; ***, $P < 0.001$; all compared to untreated mutants.

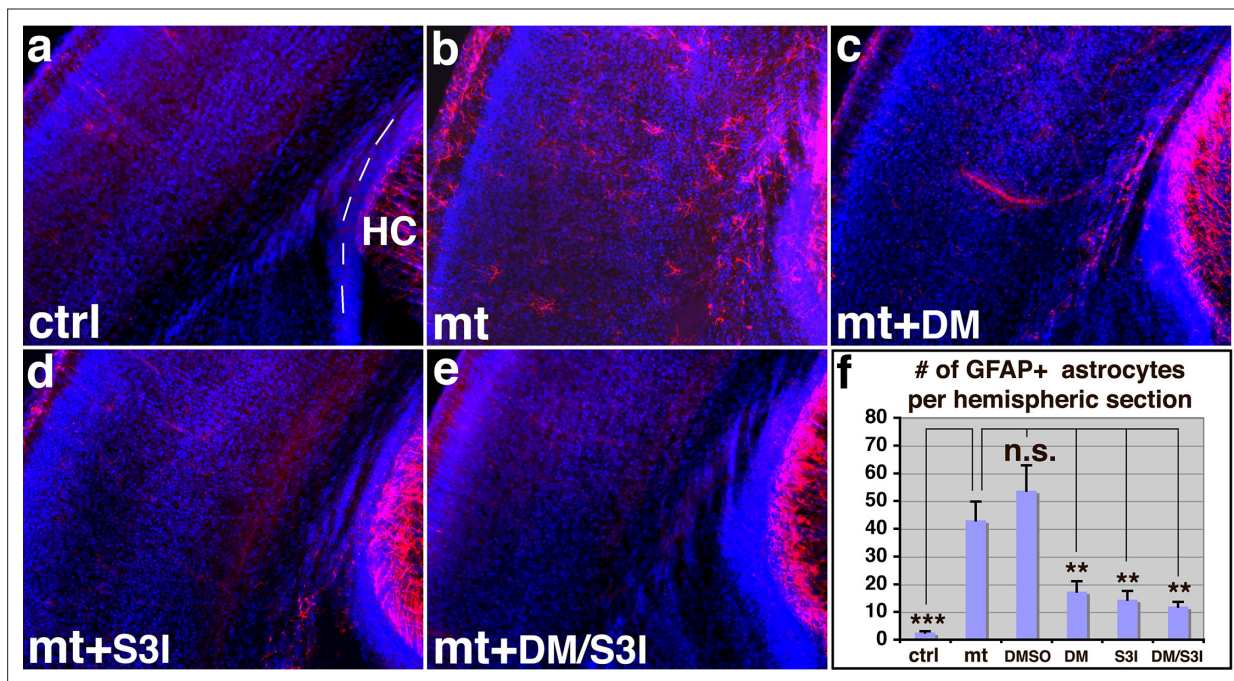


Figure 5—figure supplement 1. Suppression of astrogliosis in *Ric8a:Emx1-Cre* mutant cortices by anti-inflammatory drugs, dorsomorphin (DM) and S3I-201 (S3I). (a–e) GFAP (in red) and nuclear (DAPI, in blue) staining of neonatal control (a) and mutant cortices without treatment (b) or mutant cortices after dorsomorphin DM, (c), S3I-201 S3I, (d), or dual DM + S3I, (e) treatment at E12.5. Note, GFAP is normally expressed in the neonatal hippocampus (HC) (dashed line in a). (f) Quantitative analysis of GFAP-positive astrocyte numbers in the neonatal mutant cortex after treatment at E12.5.

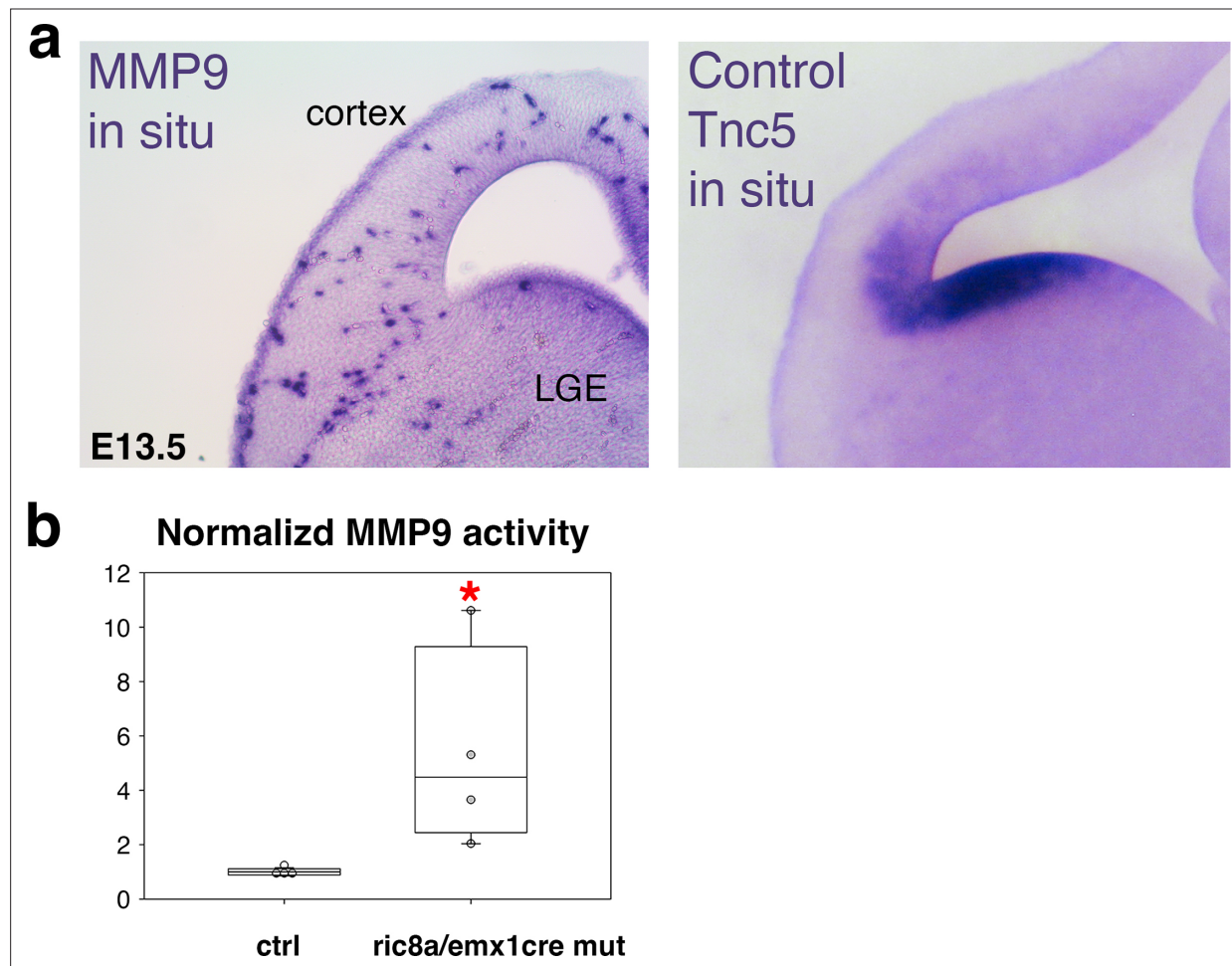


Figure 5—figure supplement 2. MMP9 in situ and activity in E13.5 *Ric8a:Emx1-Cre* mutant cortices. **(a)** Sections of E13.5 brain wholemount in situ of MMP9 showed a sparse MMP9 expressing cell population resembling microglia (LGE, lateral ganglionic eminence). Tnc5 in situ was performed as control for validating probe specificity. **(b)** Quantification showed MMP9 activity levels were significantly increased in E13.5 *, $P < 0.05$; $n = 4$ each.

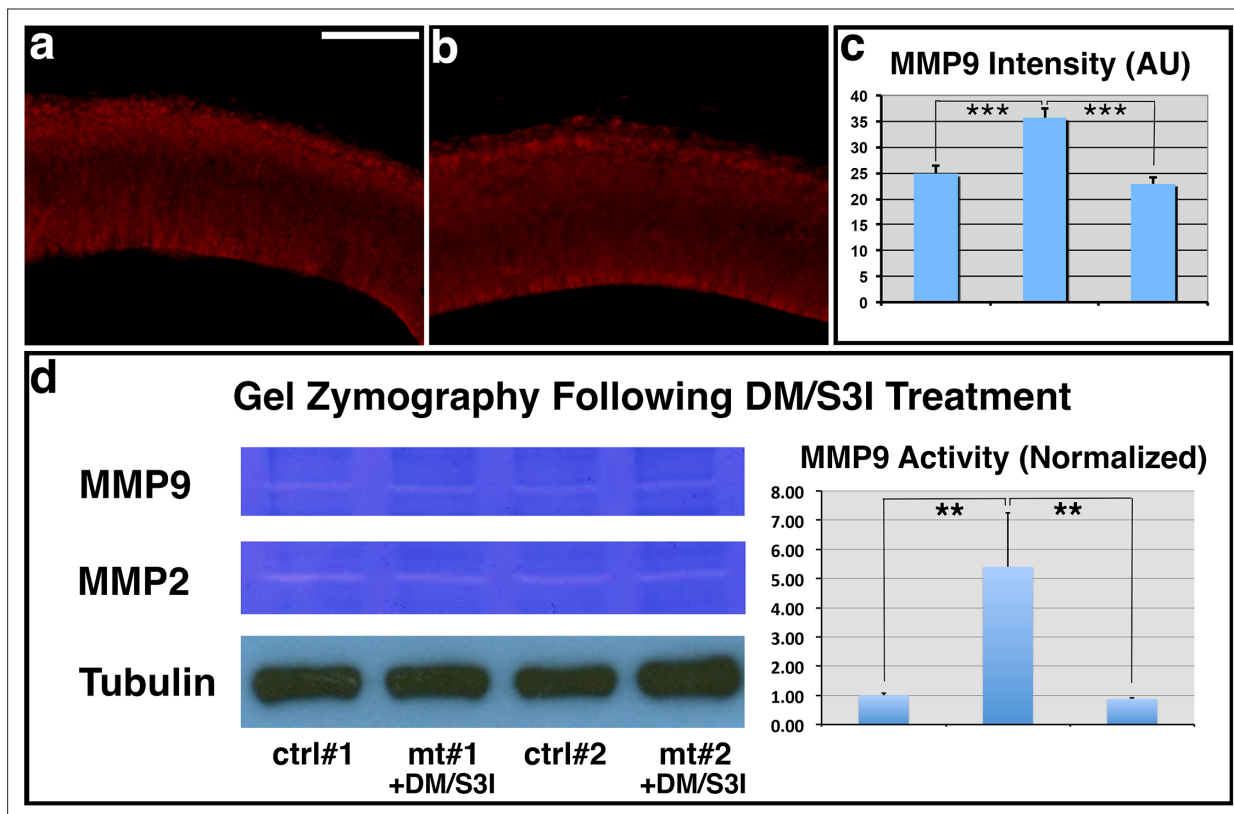


Figure 5—figure supplement 3. Suppression of MMP9 expression in *Ric8a:Emx1-Cre* mutant cortices by anti-inflammatory drugs, dorsomorphin (DM) and S3I-201 (S3I). **(a)** MMP9 (in red) staining in control cortices at E13.5. **(b)** MMP9 (in red) staining in mutant cortices at E13.5 after DM and S3I dual treatment at E12.5. **(c)** Quantitative analysis of MMP9 expression. No significant differences are observed in mutants after inhibitor treatment in comparison to controls (***, $P < 0.001$; $n = 6$ each group, ANOVA). **(d)** Gel zymography of E13.5 control and mutant cortical lysates following DM/S3I treatment at E12.5. Similar levels of MMP9 are observed between controls and mutants. Quantification also showed no significant differences in normalized MMP9 levels (**, $P < 0.01$; $n = 4-6$ each group, ANOVA).