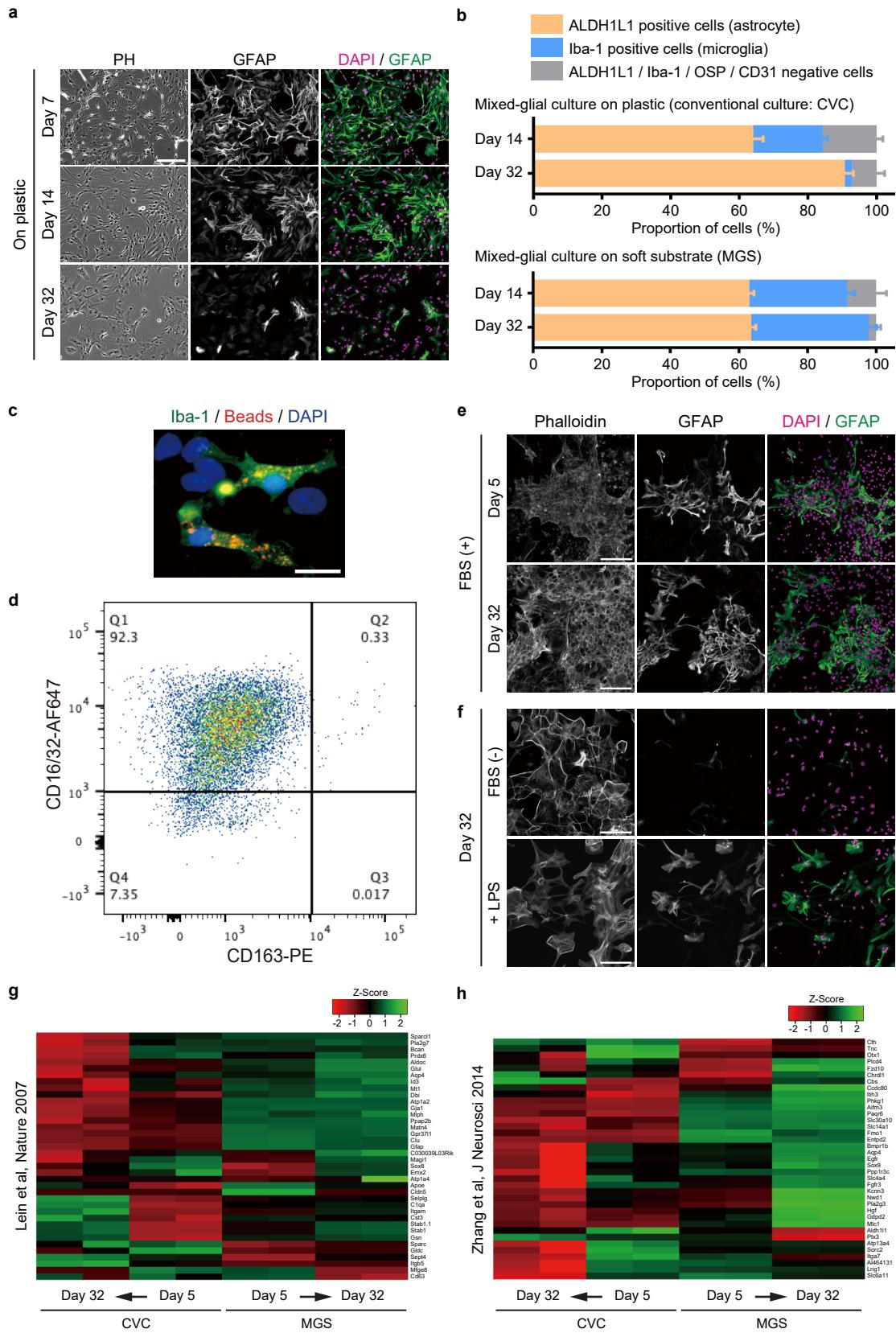


## **Extended Data**

### **Brain mimetic co-culture experiments identify mGluR1 dependence as a vulnerability of lung cancer brain metastasis**

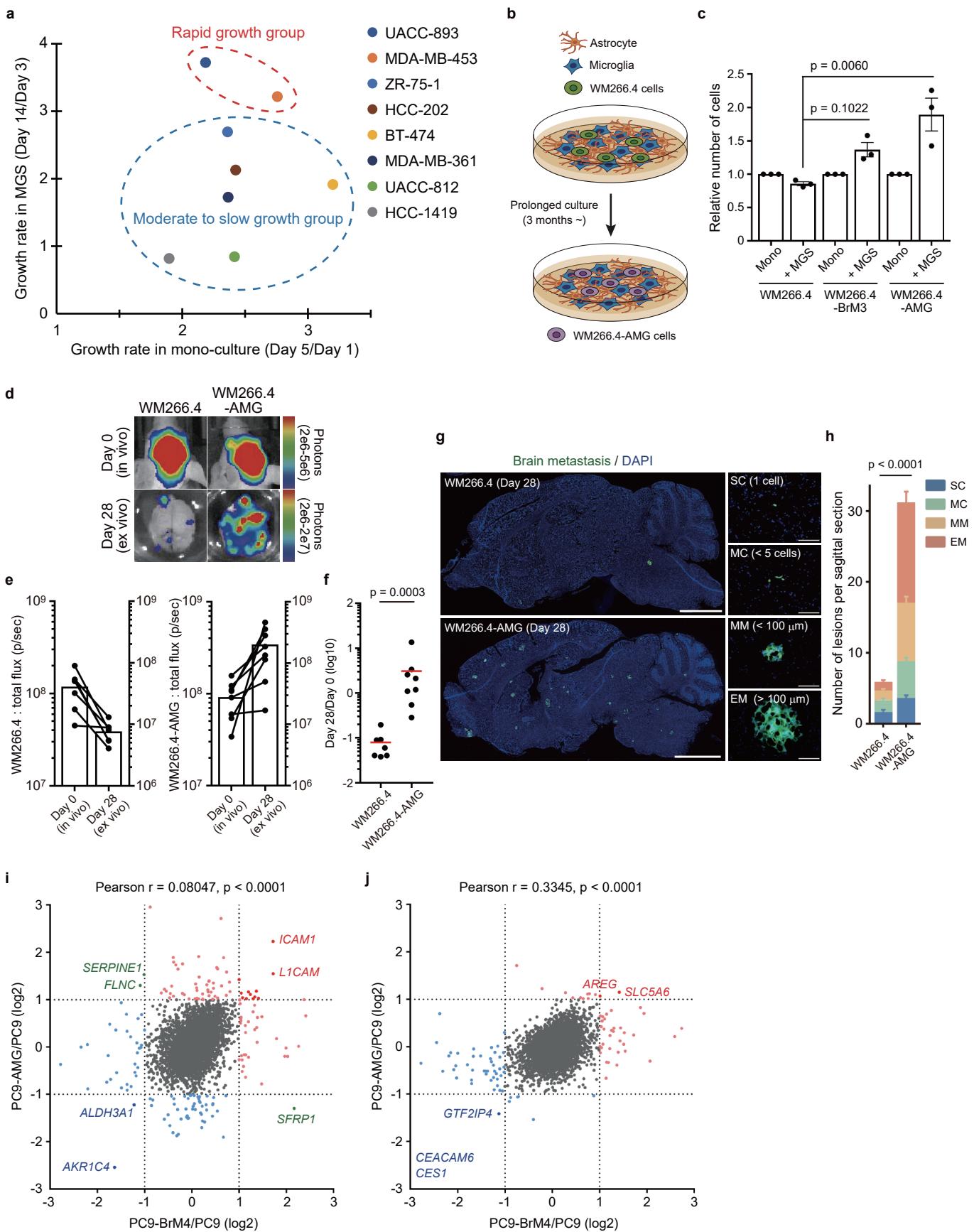
Kojiro Ishibashi, Toshiya Ichinose, Riki Kadokawa, Ryo Mizutani, Sadahiro Iwabuchi, Sumihito Togi, Hiroki Ura, Keiko Shinjo, Jun Nakayama, Shigeki Nanjo, Yo Niida, Yutaka Kondo, Shinichi Hashimoto, Erik Sahai, Seiji Yano, Mitsutoshi Nakada and Eishu Hirata

- **Extended Data Figures and Legends 1-9**
- **Supplementary Files S1-S5**



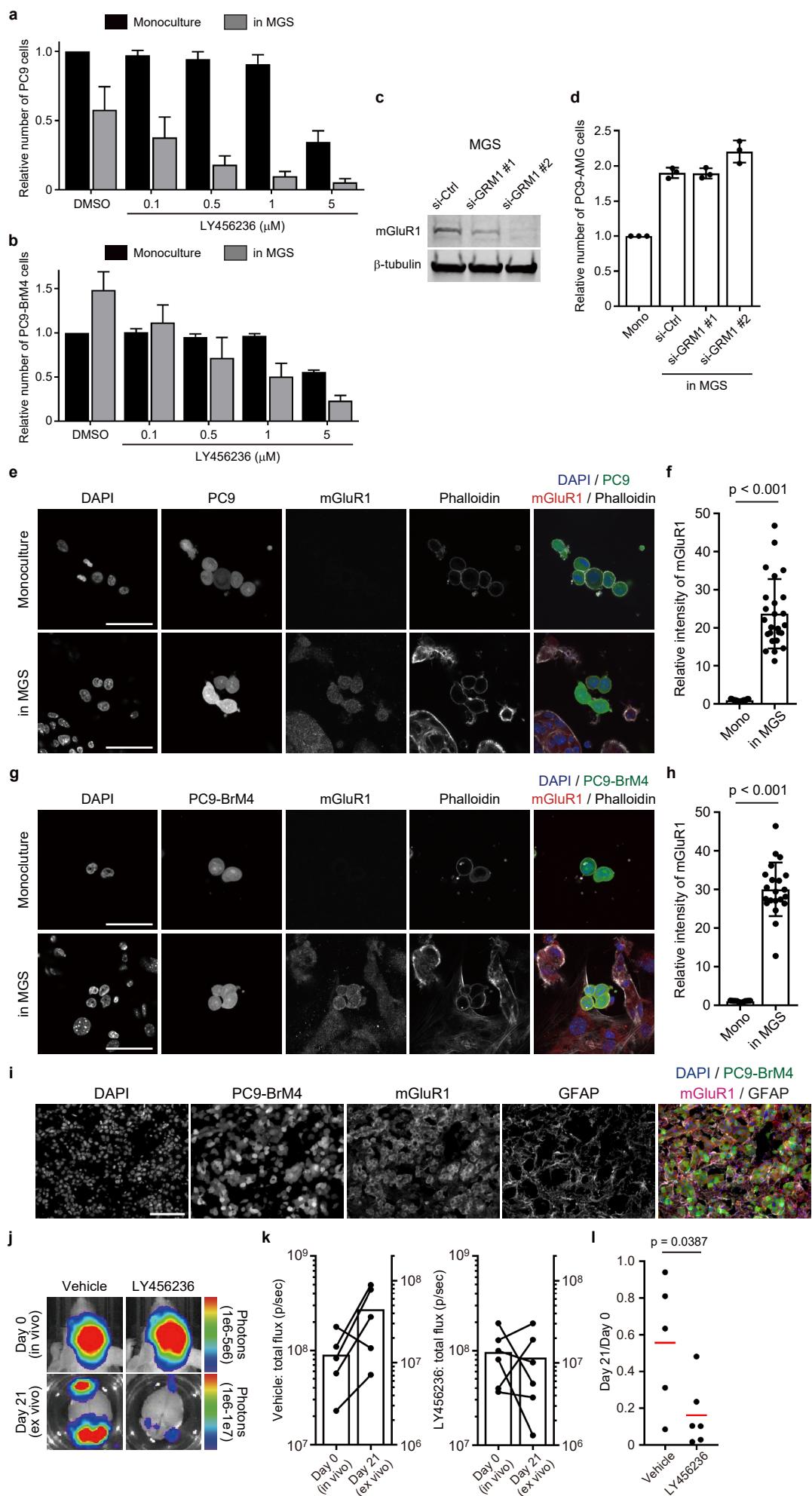
Extended Data Fig. 1 Ishibashi et al.

**Extended Data Fig. 1: MGS stably maintains astrocytes and microglia.** **a**, Astrocytes derived from C57BL/6 neonatal mouse brains were cultured on a plastic dish in DMEM supplemented with 10% FBS. Cells were fixed and stained with GFAP and DAPI at days 7, 14 and 32. Scale = 100  $\mu$ m. **b**, The proportion of astrocyte and microglia cultured on a plastic dish (upper graphs) or in MGS (lower graphs). Mixed-glial cells were fixed stained with the indicated antibodies at days 14 and 32 (n = 3, independent experiments). The bar indicates mean  $\pm$  SEM. **c**, A representative image of Iba-1-positive microglia that phagocytize carboxylate-modified polystyrene fluorescent latex beads. Green; Iba-1, Red, carboxylate-modified polystyrene fluorescent latex beads, Blue; DAPI. **d**, CD11b-positive microglia in MGS were fractionated with CD163 (x-axis) and CD16/32 (y-axis) expression. **e**, Representative images of MGS stained with phalloidin, GFAP, and DAPI at days 5 (upper panels) and 32 (lower panels). Scale = 100  $\mu$ m. **f**, Representative images of MGS stained with an anti-GFAP antibody, phalloidin and DAPI after serum removal (upper panels) and re-stimulation with LPS (lower panels) at day 32. Scale = 100  $\mu$ m. **g** and **h**, Comparative gene expression analysis of astrocytes cultured with the conventional method (CVC) or in MGS. RNAs were extracted at days 5 and 32. The astrocyte gene sets are from Lein et al., Nature 2007 (**g**), and Zhang et al., J Neurosci 2014 (**h**). Please also see Supplementary File S1.



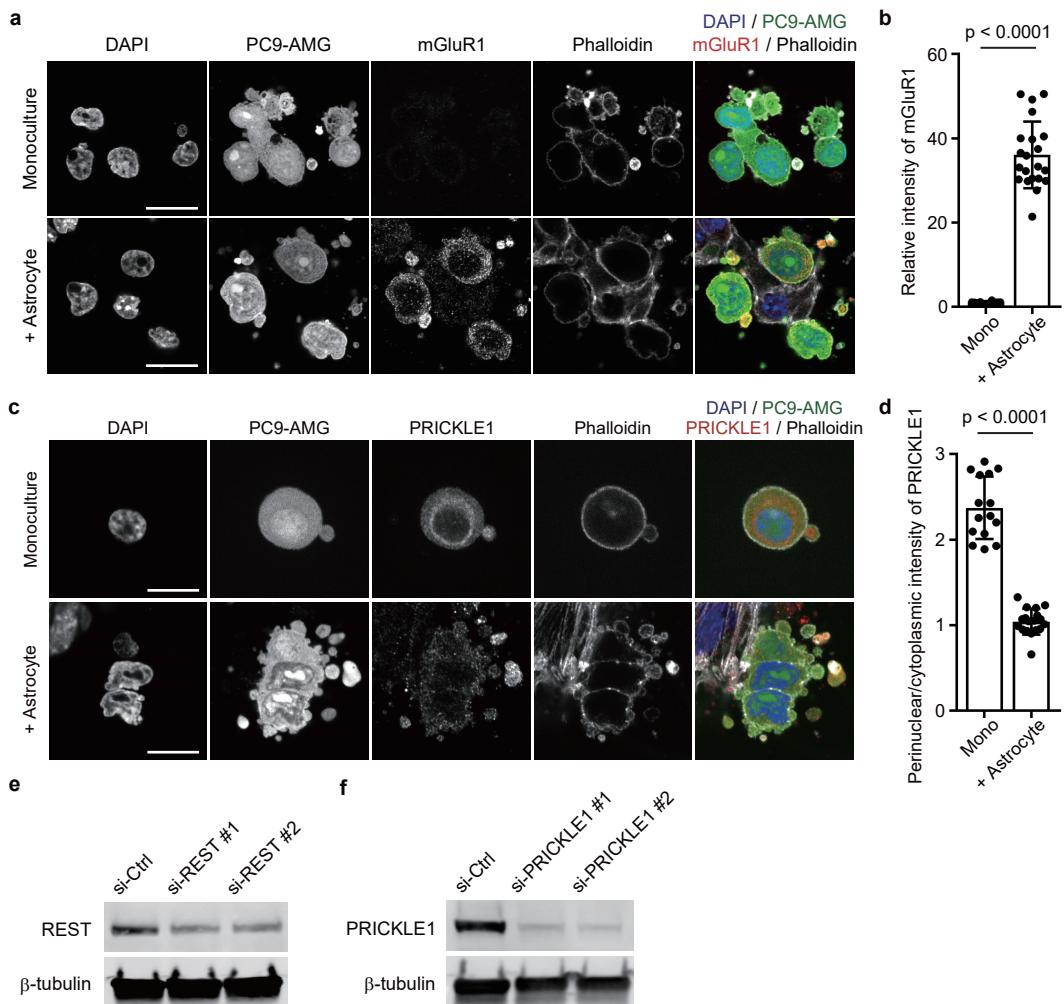
Extended Data Fig. 2 Ishibashi et al.

**Extended Data Fig. 2: Cancer cells cultured in MGS acquire brain metastatic capabilities.** **a**, A panel of HER2-positive breast cancer cell lines were subjected to in vitro proliferation assay. The x-axis indicates the growth rate in monoculture on soft collagen gels (Day 5/Day 1) and the y-axis in MGS (Day 14/Day 3). **b**, An illustration of prolonged culture of WM266.4 cells in MGS to establish WM266.4-AMG cells. **c**, Relative growth of WM266.4, WM266.4-BrM3 and WM266.4-AMG cells cultured on soft collagen gels (mono) or in MGS for 72 hours (n = 3). The bars indicate mean  $\pm$  SD. **d-f**, Representative images of bioluminescence detection from mouse brains with WM266.4 or WM266.4-AMG brain metastases (day 0, in vivo and day 28, ex vivo). **(d)** The total photon flux at day 0 (left y-axis) and day 28 (right y-axis) **(e)** and the ratio of the total photon flux (Day 28/Day 0) **(f)** are shown (n = 7 for WM266.4 and n = 8 for WM266.4-AMG). The bars indicate the mean. **g**, Representative images of sagittal brain sections with WM266.4 or WM266.4-AMG brain metastases. The four stages of brain metastasis progression are shown in the small panels. SC: single-cell, MC: micro-cluster, MM: micro-metastasis, EM: established metastasis. Scale = 2.5 mm (large panels), 100  $\mu$ m (small panels). **h**, The number of metastatic lesions per a sagittal brain section at day 28 is shown. 28 slices from 7 mice (WM266.4) and 32 slices from 8 mice (WM266.4-AMG) were used for the quantification. The bars indicate mean  $\pm$  SEM. **i, j**, A scatter plot showing the fold change of gene expression in PC9-BrM4 (x-axis) and PC9-AMG (y-axis) compared with parental PC9 cells. RNAs were extracted from the cells cultured in a conventional manner **(i)** or co-cultured in MGS **(j)**. Genes upregulated  $>$  2-fold in PC9-BrM4 or PC9-AMG are represented with red spots and downregulated  $<$  0.5-fold are represented with blue spots. Bright-red and bright-blue spots indicate genes upregulated  $>$  2-fold or downregulated  $<$  0.5-fold on one side, respectively. Green spots indicate genes upregulated  $>$  2-fold on one side and downregulated  $<$  0.5-fold on the other side. Genes with the highest expression levels, in the top 20% (average of PC9, PC9-BrM4, and PC9-AMG), were used for analysis. Please also see Supplementary Files S2 and S3.



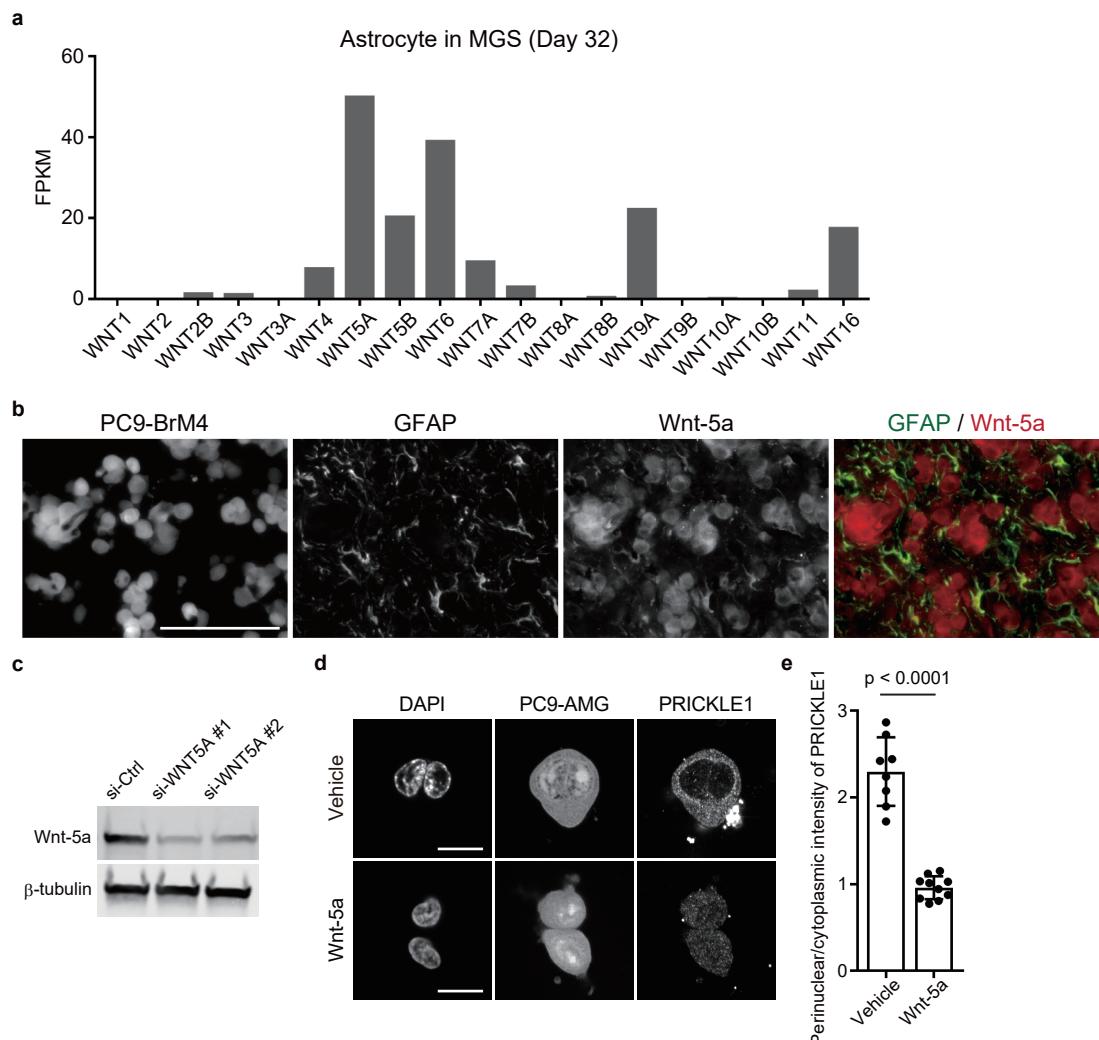
Extended Data Fig. 3 Ishibashi et al.

**Extended Data Fig. 3: LY456236 suppresses the growth of PC9 and PC9-BrM4 cells cultured in MGS.** **a, b**, PC9 (**a**) or PC9-BrM4 (**b**) cells cultured in 3D collagen gels (monoculture) or in MGS were treated with DMSO (0.01%) or LY456236 (0.1-5  $\mu$ M) for 48 hours. The relative number of viable PC9 or PC9-BrM4 cells was quantified ( $n = 3$ ). The bars indicate mean  $\pm$  SD. **c, d**, Mixed-glial cells were treated with control siRNA or siRNA targeting *GRM1* (**c**), and PC9-AMG cells were monocultured or co-cultured with these mixed-glial cells in 3D collagen gels. The relative number of viable PC9-AMG cells was quantified ( $n = 3$ ) (**d**). The bars indicate mean  $\pm$  SD. **e, f**, Representative images of PC9 cells cultured in 3D collagen gels (monoculture) or co-cultured in MGS, stained with an anti-mGluR1 antibody, DAPI and phalloidin (**e**). The relative intensity of mGluR1 was quantified ( $n = 19$  for monoculture condition and  $n = 25$  for MGS co-culture condition) (**f**). Scale = 50  $\mu$ m. **g, h**, Representative images of PC9-BrM4 cells cultured in 3D collagen gels (monoculture) or co-cultured in MGS, stained with an anti-mGluR1 antibody, DAPI and phalloidin (**g**). The relative intensity of mGluR1 was quantified ( $n = 13$  for monoculture condition and  $n = 22$  for MGS co-culture condition) (**h**). Scale = 50  $\mu$ m. **i**, Representative images of PC9-BrM4 cells in the mouse brain (day 28), stained with an anti-mGluR1 antibody, anti-GFAP antibody and DAPI. Scale = 100  $\mu$ m. **j-l**, PC9-BrM4 cells metastasized to the mouse brain were treated with vehicle or LY456236 (50 mg/kg/day) for 14 days. Representative images of bioluminescence detection (day 0, *in vivo* and day 21, *ex vivo*) (**j**), the total photon flux from the brain at day 0 (left y-axis) and day 21 (right y-axis) (**k**), and the ratio of the total photon flux (Day 21/Day 0) (**l**) are shown ( $n = 5$  for vehicle and  $n = 6$  for LY456236). The bars indicate the mean.



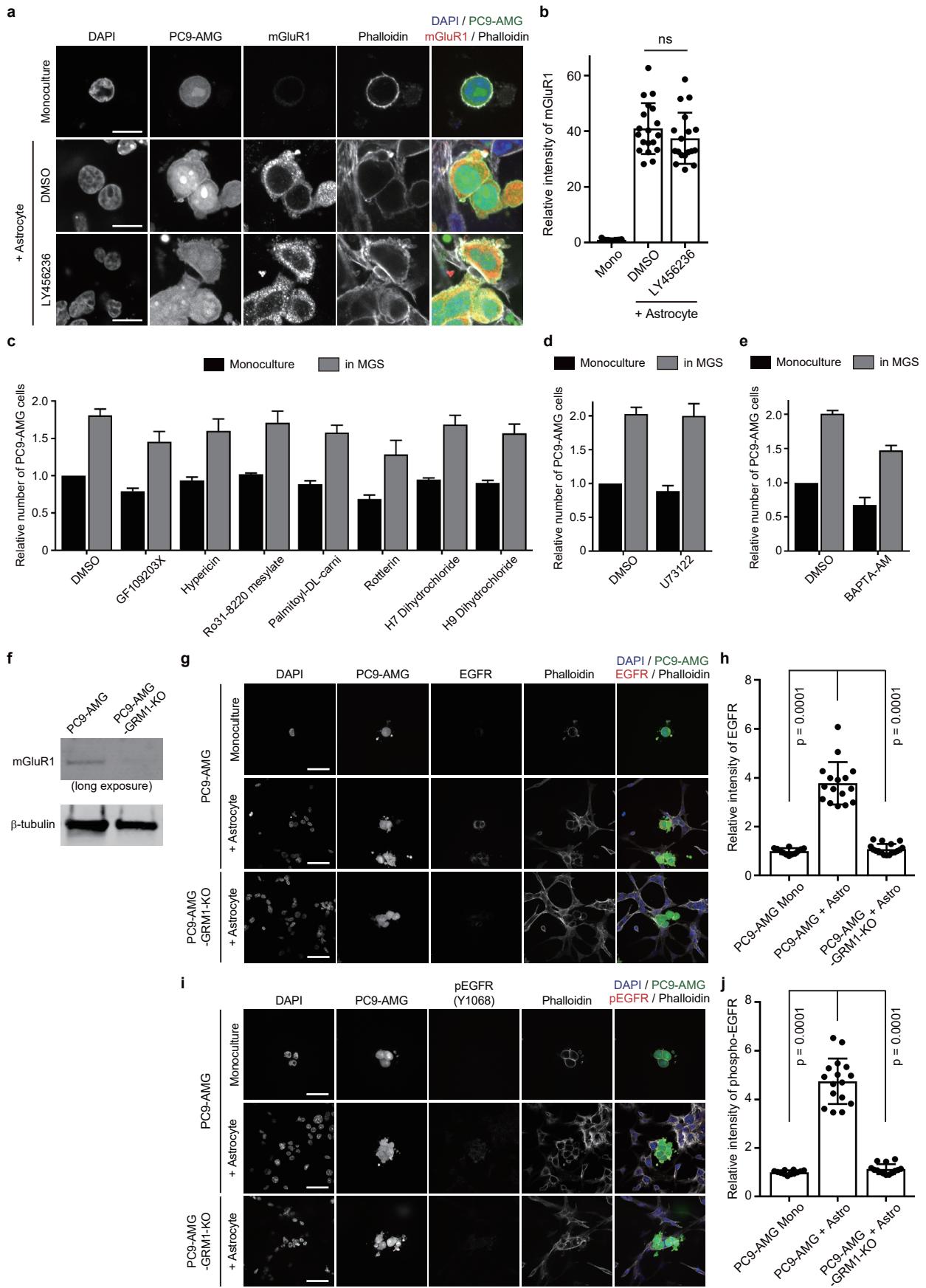
Extended Data Fig. 4 Ishibashi et al.

**Extended Data Fig. 4: Astrocytes induce mGluR1 expression in PC9-AMG cells through PRICKLE1 translocation.** **a, b,** Representative images of PC9-AMG cells cultured with or without astrocytes in 3D collagen gels, stained with an anti-mGluR1 antibody, DAPI and phalloidin (**a**). The relative intensity of mGluR1 was quantified (n = 14 for monoculture condition and n = 21 for astrocyte co-culture condition) (**b**). Scale = 20  $\mu$ m. **c, d,** Representative images of PC9-AMG cells cultured with or without astrocytes in 3D collagen gels, stained with an anti-PRICKLE1 antibody, DAPI and phalloidin (**c**). The ratio of perinuclear and cytoplasmic intensity of PRICKLE1 was quantified (n = 15 for monoculture condition and n = 18 for astrocyte co-culture condition) (**d**). Scale = 20  $\mu$ m. **e, f,** PC9-AMG cells treated with control siRNA or siRNAs targeting *REST* (**e**) or *PRICKLE1* (**f**) were immunoblotted with the indicated antibodies.



Extended Data Fig. 5 Ishibashi et al.

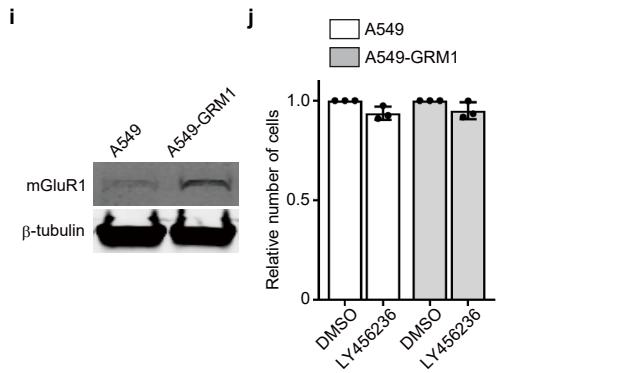
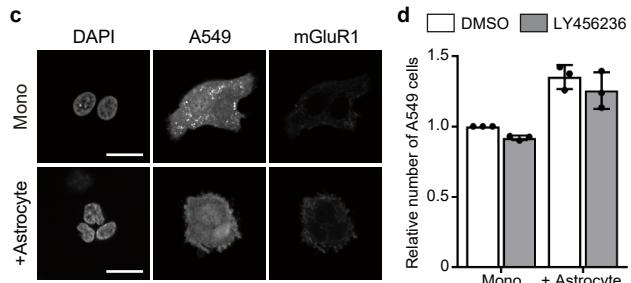
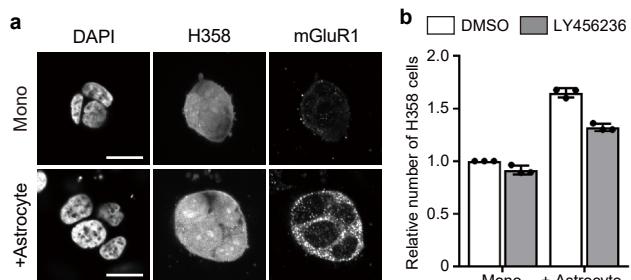
**Extended Data Fig. 5: Wnt-5a translocate PRICKLE1 and REST in cancer cells.** **a**, mRNA expression (FPKM) of *WNT* family genes in astrocytes in MGS at day 32. Please also see Supplementary File S1. **b**, Representative images of PC9-BrM4 cells in the mouse brain (day 28), stained with an anti-GFAP antibody, anti-Wnt-5a antibody and DAPI. Scale = 100  $\mu$ m. **c**, Immunoblotting of astrocytes treated with control siRNA or siRNA targeting *WNT5A*. **d, e**, Representative images of PC9-AMG cells cultured in 3D collagen gels and treated with vehicle (PBS with 0.01% BSA) or Wnt-5a (500 ng/ml) for 24 hours. Cells were fixed and stained with an anti-PRICKLE1 antibody, counterstained with DAPI (**d**). The ratio of perinuclear and cytoplasmic intensity of PRICKLE1 was quantified (n = 8 for monoculture condition and n = 10 for astrocyte co-culture condition) (**e**). Scale = 20  $\mu$ m.



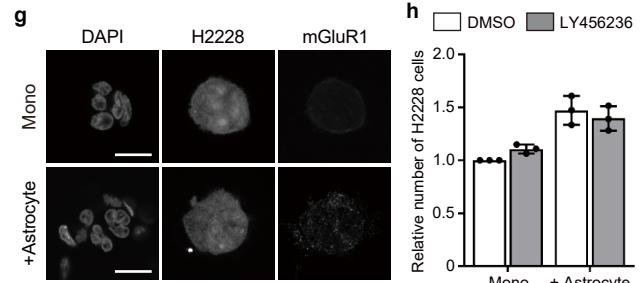
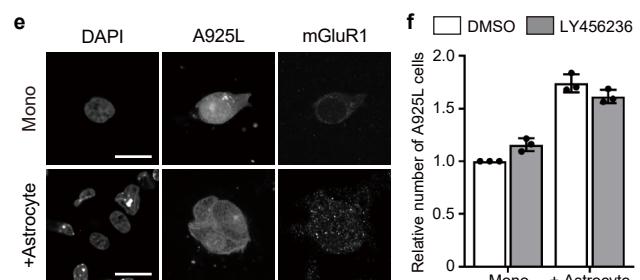
Extended Data Fig. 6 Ishibashi et al.

**Extended Data Fig. 6: Loss of mGluR1 signalling attenuates EGFR expression and phosphorylation in PC9 cells.** **a, b**, PC9-AMG cells monocultured or co-cultured with astrocytes in 3D collagen gels were treated with DMSO (0.01%) or LY456236 (1  $\mu$ M). The cells were stained with an anti-mGluR1 antibody, DAPI and phalloidin (**a**). The relative intensity of mGluR1 was quantified (from left to right, n = 13, 19, 18). Scale = 20  $\mu$ m. **c**, PC9-AMG cells cultured in 3D collagen gels (monoculture) or co-cultured in MGS were treated with DMSO (0.01%) or the indicated drug (1  $\mu$ M) for 48 hours and the relative number of viable PC9-AMG cells was quantified (n = 3). The bars indicate mean  $\pm$  SD. **d**, PC9-AMG cells cultured in 3D collagen gels (monoculture) or co-cultured in MGS were treated with DMSO (0.01%) or U73122 (5  $\mu$ M) for 48 hours. The relative number of viable PC9-AMG cells was quantified (n = 2). The bars indicate mean  $\pm$  SD. **e**, PC9-AMG cells cultured in 3D collagen gels (monoculture) or co-cultured in MGS were treated with DMSO (0.01%) or BAPTA-AM (10  $\mu$ M) for 48 hours. The relative number of viable PC9-AMG cells was quantified (n = 2). The bars indicate mean  $\pm$  SD. **f-j**, PC9-AMG and PC9-AMG-GRM1-KO cells (**f**) were monocultured or co-cultured with astrocytes in 3D collagen gels. The cells were fixed and stained with an anti-EGFR antibody (**g**) or anti-phospho-EGFR antibody (**i**), counterstained with DAPI and phalloidin. The relative intensities of EGFR (from left to right, n = 12, 16, 17) (**h**) and phospho-EGFR (from left to right, n = 12, 16, 14) (**j**) were quantified. Scale = 50  $\mu$ m.

### RAS mutant

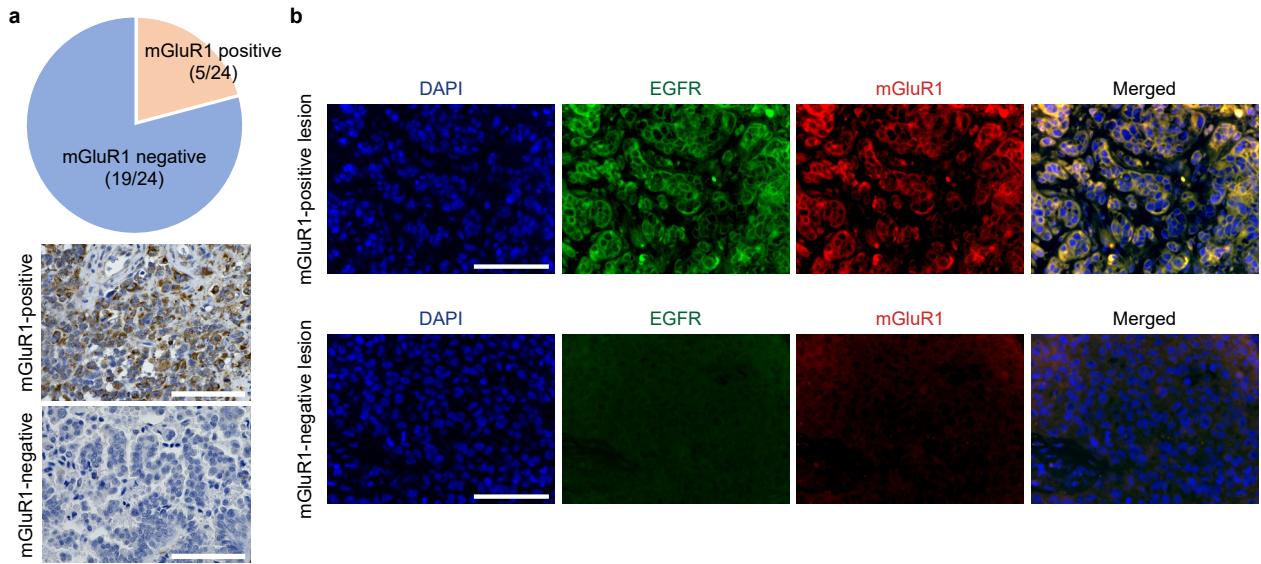


### EML4-ALK



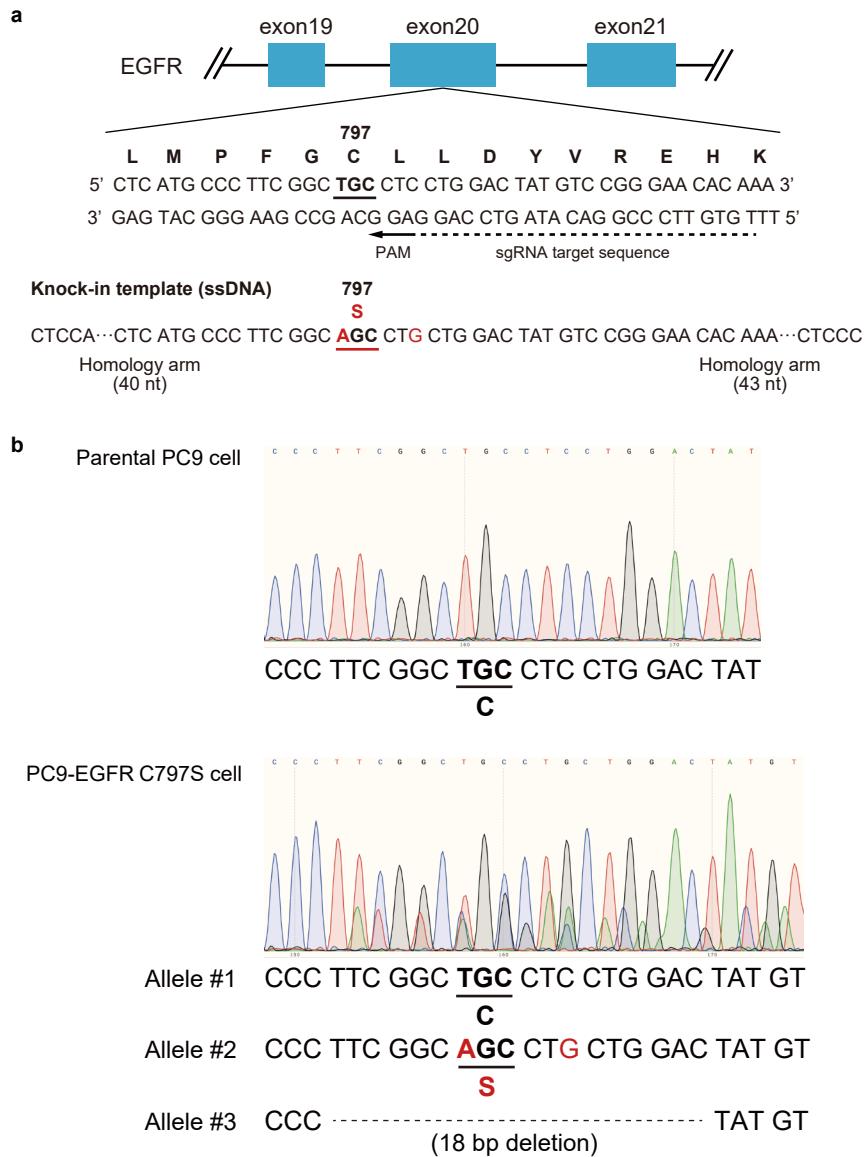
Extended Data Fig. 7 Ishibashi et al.

**Extended Data Fig. 7: EGFR-wt lung cancer cells do not become mGluR1 signalling dependent.** **a, c, e, g**, Ras-mutant human lung cancer cells, H358 (**a**) and A549 (**c**), and EML4-ALK fusion human lung cancer cells, A925L (**e**) and H2228 (**g**) were monocultured or co-cultured with astrocytes in 3D collagen gels. The cells were fixed and stained with an anti-mGluR1 antibody and DAPI. Scale = 20  $\mu$ m. **b, d, f, h**, H358 (**b**), A549 (**d**), A925L (**f**) and H2228 (**h**) cells were monocultured or co-cultured with astrocytes in 3D collagen gels and treated with DMSO (0.01%) or LY456236 (1  $\mu$ M) for 48 hours. The relative number of viable cancer cells was quantified ( $n = 3$  in each group). The bars indicate mean  $\pm$  SD. **i, j**, Parental or mGluR1-overexpressing A549 cells (**i**) were cultured in 3D collagen gels with DMSO (0.01%) or LY456236 (1  $\mu$ M) for 48 hours. The relative number of viable cells was quantified (**j**). The bars indicate mean  $\pm$  SD.



Extended Data Fig. 8 Ishibashi et al.

**Extended Data Fig. 8: Expression of mGluR1 and EGFR in human lung cancer brain metastasis.** **a**, A pie chart showing the mGluR1 positivity rates of brain metastatic lung cancer surgical specimens and representative images of mGluR1 positive and negative immunostaining. **b**, Representative images of brain metastatic lung cancer co-stained with an anti-EGFR and anti-mGluR1 antibodies, counterstained with DAPI. The upper panels show the mGluR1-positive lesion from case #3 and the lower panels show the mGluR1-negative lesion from case #5. Scale = 200  $\mu$ m. Please also see Supplementary File S4.



Extended Data Fig. 9 Ishibashi et al.

**Extended Data Fig. 9: Generation of PC9 cells with EGFR C797S mutation.** **a**, A blueprint for CRISPR/Cas9-mediated gene editing of EGFR. The sequences of sgRNA and knock-in template are shown. The base mutation to place the C797S amino acid mutation (AGC) and a silent mutation to ensure template knock-in (CTG) are highlighted in red. **b**, Results of EGFR sequencing of parental PC9 cells (top panel) and established PC9-EGFR-C797S cells (bottom panel). At least three types of EGFR alleles were detected in the PC9-EGFR-C797S cells.

**Supplementary File S1.** Gene expression data of astrocytes cultured with a conventional method or in MGS (at days 5 and 32).

**Supplementary File S2.** Gene expression data of PC9-Luc-mEGFP, PC9-Luc-mEGFP-BrM4 and PC9-Luc-mEGFP-AMG cells cultured in a conventional manner.

**Supplementary File S3.** Gene expression data of PC9-Luc-mEGFP, PC9-Luc-mEGFP-BrM4 and PC9-Luc-mEGFP-AMG cells cultured in MGS.

**Supplementary File S4.** Twenty-four clinical cases of lung cancer brain metastasis assessed for mGluR1 and EGFR expression.

**Supplementary File S5.** Primers, siRNAs, CRISPR/Cas9-related DNA/RNA templates, antibodies, and reagents.