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Article

Metabolic Landscape of a Genetically Engineered Mouse Model of IDH1 Mutant Glioma

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Supplementary Material

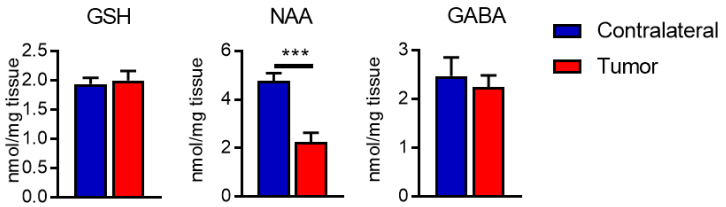

Figure S1: Quantification of metabolites directly involved with glutamate in the contralateral and tumor regions of the GEMM employed herein. Metabolic levels were computed through integration of specific regions of ^{1}H NMR spectra and the assessment of significance difference between regions was conducted using a t-test followed by Welch correction; ***, $p < 0.001$ (data displayed as mean ± SD, n = 5–6 mice).

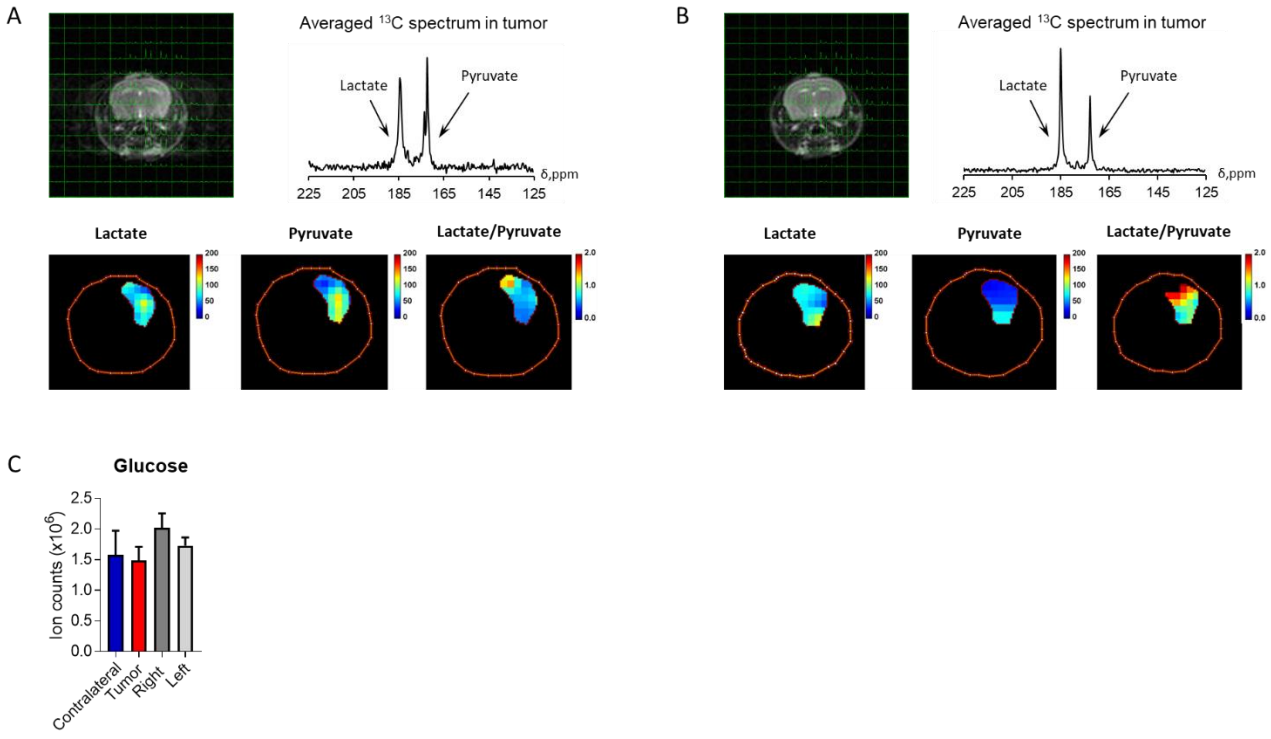

Figure S2: Glycolytic activity in the GEEMs: (**A**) and (**B**) MRI of the mouse brain with overlaid ^{13}C NMR spectra for each voxel and the averaged spectrum for the tumor region. (**C**) Glucose levels computed by LC-MS for those regions (data displayed as mean ± SD, n = 3–6 mice).

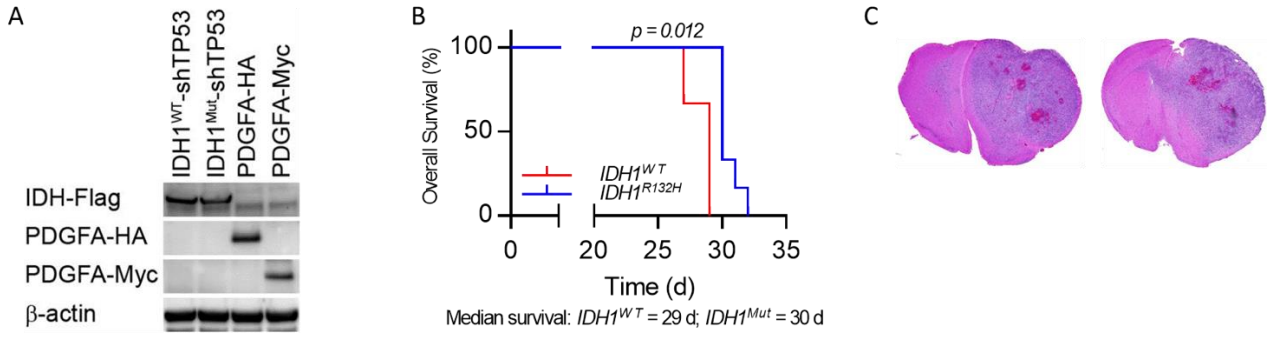

Figure S3: Molecular description and performance of the GEMM. **(A)** Immunoblotting of the transfected DF-1 cells confirms the successful expression of the transgenes. **(B)** Kaplan-Meier analysis shows the disease outcome of mouse glioma model. (**C**) Histology illustration of IDH1^{mut} mouse glioma models.

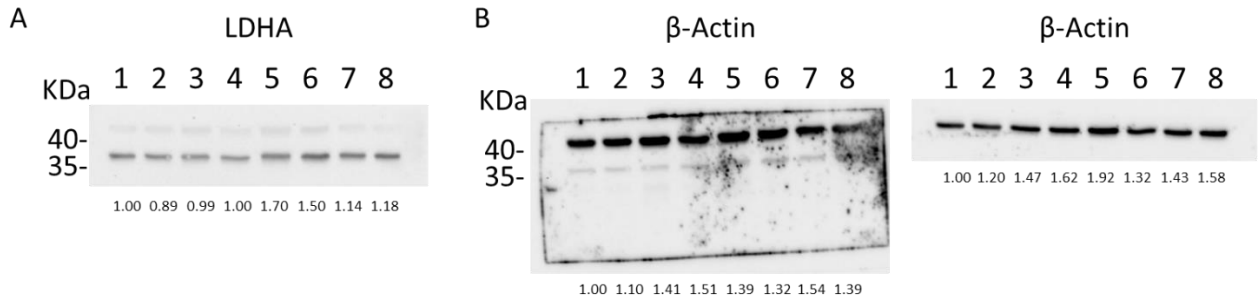

Figure S4: Lactate dehydrogenase expression in GEEM mice. (**A**) Western blot images for Figure 2D. Lanes 1–3: Contralateral region of 3 transfected mice; lanes 4–6: Tumor region of 3 transfected mice; line 7: right hemisphere from a control mouse and line 8: left hemisphere from a control mouse. (**B**) Lines as in (**A**) from two experiments.