

Reporting Summary

Nature Portfolio wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Portfolio policies, see our [Editorial Policies](#) and the [Editorial Policy Checklist](#).

Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a Confirmed

- ☐ ☒ The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement
- ☐ ☒ A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
- ☐ ☒ The statistical test(s) used AND whether they are one- or two-sided
Only common tests should be described solely by name; describe more complex techniques in the Methods section.
- ☒ ☐ A description of all covariates tested
- ☒ ☐ A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
- ☐ ☒ A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
- ☐ ☒ For null hypothesis testing, the test statistic (e.g. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P value noted
Give P values as exact values whenever suitable.
- ☒ ☐ For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
- ☐ ☒ For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
- ☒ ☐ Estimates of effect sizes (e.g. Cohen's d , Pearson's r), indicating how they were calculated

Our web collection on [statistics for biologists](#) contains articles on many of the points above.

Software and code

Policy information about [availability of computer code](#)

Data collection Living Image Version 4.5.2, FLIR IR Camera software for thermal images.

Data analysis MATLAB (Mathworks, Natick), ADS simulator (Keysight), FLIR IR Camera software, OsiriX software for MRI analysis. A Python script was used to calculate the required voltage levels and communicated the information to a signal generator, using National Instruments' implementation of the Virtual Instrument Software Architecture API (NI-VISA) through a graphical user interface (GUI). 1-g SAR were calculated in a 3D full-wave simulator (CST Studio Suite, Simulia) using the finite element method and a 3D mouse model.

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio [guidelines for submitting code & software](#) for further information.

Data

Policy information about [availability of data](#)

All manuscripts must include a [data availability statement](#). This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our [policy](#)

The authors declare that the data supporting the findings of this study are available within the paper [and its supplementary information files].

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☒ Life sciences ☐ Behavioural & social sciences ☐ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see [nature.com/documents/nr-reporting-summary-flat.pdf](https://www.nature.com/documents/nr-reporting-summary-flat.pdf)

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	Sample size was not statistically predetermined but all experiments were performed in at least in duplicate with each experimental group. For In vivo survival studies 10 mice were used for each treatment or control type. These sample sizes were sufficient to obtain statistically significant differences between treated or non-treated groups.
Data exclusions	No data were excluded from the analysis.
Replication	All attempts at replication were successful. Experiments were performed in at least duplicate to confirm reproducibility.
Randomization	Experimental groups were formed based on what was being tested with random selections. The same type of animals were used for all experiments.
Blinding	Tumor measurements by BLI and MRI and survival tests were performed in a blinded format.

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involved in the study
☒	☐ Antibodies
☐	☒ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☐	☒ Animals and other organisms
☒	☐ Human research participants
☒	☐ Clinical data
☒	☐ Dual use research of concern

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Eukaryotic cell lines

Policy information about [cell lines](#)

Cell line source(s)	U87-eGFP-Fluc and GBM39-Fluc human glioblastoma cells acquired as gifts from Profs. Irina V. Balyasnikova at Northwestern University and Prof. Paul Mischel at Stanford University, respectively. GL26 cells were acquired as gift from Dr. Gerald Grant at Stanford University.
Authentication	Cell line was not independently authenticated.
Mycoplasma contamination	All cell lines tested negative for mycoplasma contamination.
Commonly misidentified lines (See ICLAC register)	No commonly misidentified cell lines were used.

Animals and other organisms

Policy information about [studies involving animals](#); [ARRIVE guidelines](#) recommended for reporting animal research

Laboratory animals	Athymic female CD-1 nude mice (n = 115, 25-30 g, 10 weeks old, Charles River Laboratories, USA) and immunocompetent C57BL/6J mice (n = 20, 20-25g, 8 weeks old, Jackson Laboratory, USA) were used.
Wild animals	The study did not involve wild animals.

Field-collected samples	The study did not involve field-collected samples.
Ethics oversight	All animal experiments were performed in accordance with a protocol (APLAC No. 31515) approved by the Stanford University Administrative Panels on Laboratory Animal Care (APLAC).

Note that full information on the approval of the study protocol must also be provided in the manuscript.