# nature portfolio

Corresponding author(s): Zr	nibo Liu
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## **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 <u>Editorial Policies</u> and the <u>Editorial Policy Checklist</u>.

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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
	$oxed{oxed}$ 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.
$\boxtimes$	A description of all covariates tested
$\boxtimes$	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. <i>F</i> , <i>t</i> , <i>r</i> ) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted <i>Give P values as exact values whenever suitable.</i>
$\boxtimes$	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
$\boxtimes$	$\square$ 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

Characterization of boronsome: Zetasizer Nano ZS system (Malvern Instruments Ltd), TEM operated at 200 kV (JEM-2100, JEOL); Radio-TLC: Scan-RAM (LabLogic); 3D structures modeling and MD simulation: Spartan 14, Gromacs 2018, ATB 3.0; The Monte Carlo computation-based dose calculation: SERA 1C1; ICP-OES: microwave accelerated reaction system (Mars, CEM), Optima 7000 DV (PerkinElmer); Microscope: laser scanning confocal microscope (Nikon); PET/CT imaging: Nanoscan PET-CT 122s (Mediso Medical Imaging Systems); H&E staining: 3Dhistech (3DHISTECH)

Data analysis

3D structures modeling and MD simulation: VMD v1.9.3; Immunofluorescence staining: ImageJ v1.53a; Statistical analysis: GraphPad Prism v8; PET/CT imaging: InterViewTM FUSION v3.09 (Mediso Medical Imaging Systems); H&E staining: CaseViewer v2.4

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

All data generated or analysed during this study are included in this published article (and its supplementary information files).

Field-specific reporting				
Please select the o	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	document with all sections, see <u>nature.com/documents/nr-reporting-summary-flat.pdf</u>			
1				
Life scier	ces study design			
All studies must dis	ose on these points even when the disclosure is negative.			
Sample size	exact sample size is stated in the figure legend. In the animal experiments to detect tumour growth, for individual analyses n is 9 in each group. For all other experiment, for individual analyses n is 3, 4, or 6, selected on the basis that the variability between estimates is sufficiently small to provide significant differences between test samples in these studies.			
Data exclusions	No data were excluded from the analyses			
Replication	All results were repeated at least three times independently with similar results.			
Randomization	Randomization was applied following these two criteria: the probability of assignment to any of the experimental groups is equal for each subject and the assignment of one subject to a group does not affect the assignment of any other subject to that same group			
Blinding	Proper blinding was applied during the data collection and analysis			
We require informatis system or method liss  Materials & ex  n/a Involved in th  Antibodies  Eukaryotic  Palaeontol  Animals ar  Human res  Clinical dat	☐ ChIP-seq			
Antibodies used	anti-γH2AX antibody (1:200, abcam, ab81299, EP854(2)Y, ); goat anti-rabbit IgG H&L (1:1000, Alexa Fluor® 488, abcam, ab150077, Polyclonal)			
Validation	anti-yH2AX antibody: Rabbit anti-mouse antibody, Immunofluorescence. IgG H&L: goat anti-rabbit, Immunofluorescence.			
Eukaryotic c	Il lines			
Policy information	out <u>cell lines</u>			
Cell line source(s	The 4T1 cell lines (3101MOUSCSP5056) were obtained from National Infrastructure of Cell Line Resource (Beijing, China).			
Authentication	Identity of the cell lines were frequently checked by their morphological features but have not been authenticated by short tandem repeat (STR) profiling.			

All cell lines tested negative for mycoplasma contamination.

No commonly misidentified cell line was used in the study

Mycoplasma contamination

(See <u>ICLAC</u> register)

Commonly misidentified lines

### Animals and other organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research

Laboratory animals

6-8-weeks female BALB/c mice were obtained from Beijing Vital River Laboratory Animal Technology Co, Ltd. and maintained under specific pathogen-free facility (SPF) conditions with a 12 light/12 dark cycle, and free access to food and water. Mice were housed under temperature of  $24 \pm 2$  °C, and humidity of  $50 \pm 10$ %.

Wild animals

The study did not involve wild animals

Field-collected samples

The study did not involve samples collected from the field

Ethics oversight

All animal care and experimental procedure were performed by following the animal protocols (CCME-LiuZB-2) approved by the ethics committee of Peking University

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