nature portfolio

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Reporting Summary

Statistics

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>.

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
	\square 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. <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
\boxtimes	For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
\boxtimes	Estimates of effect sizes (e.g. Cohen's <i>d</i> , Pearson's <i>r</i>), indicating how they were calculated
	Our web collection on <u>statistics for biologists</u> contains articles on many of the points above.

Software and code

Policy information about availability of computer code

Data collection GSE180286, TCGA, METABRIC, GSE176307, GSE194040, PRJNA558949, GSE34138, GSE147322, GSE209998, GSE193103, GSE168846

Data analysis R, Graphpad Prism, HALO

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 are willing to provide any data upon reasonable request.

Research involving human participants, their data, or biological material Policy information about studies with human participants or human data. See also policy information about sex, gender (identity/presentation),

expatients enrolled are female. Exp. All the patients are Chinese from four clinical center of China. The microarrays (TMAs) of non-TNBC (Cat. HBreD090Bc03) and TNBC (Cat. HBreD090Bc01) were Shanghai, China). Outdo BioTech provided detailed clinic-pathological features. Samples that unohistochemistry (IHC), Hematoxylin and Eosin (HE), and masson staining were removed. A total C and 80 TNBC) were included in this study. The HE staining was reviewed by two pathologists, are confirmed to include paired para-tumor samples. In addition, 30 TNBC patients receiving nemotherapy (NAT) were recruited from four independent medical units. In addition, the night he RECIST1.1 criterion after receiving 8 cycles of NAT. The paraffin-embedded samples of night NAT were obtained. Table S1 lists the specific clinic-pathological characteristics. Committee of Outdo Biotech granted ethical approval for the use of TMAs. Ethical approval was tutions and informed consent was obtained. Est also be provided in the manuscript. Ecological, evolutionary & environmental sciences ments/nr-reporting-summary-flat.pdf losure is negative.
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nods
nvolved in the study
ChIP-seq
Flow cytometry
MRI-based neuroimaging

Antibodies

Antibodies used
Anti-B7-H3 (Cat. ab219648, Abcam, Cambridge, UK), anti-PD-L1 (Cat. GT2280, GeneTech, Shanghai, China), anti-CD8 (Cat. PA067, Abcarta, Suzhou, China), anti-CD8 antibody (Cat. ab217344, Abcam)

Validation The validation of antibodies are detailed and documented on Abcam, GeneTech, and Abcarta's websites.

Eukaryotic cell lines

Policy information about <u>cell lines and Sex and Gender in Research</u>

Cell line source(s) 4T1 (Cat. KG338, KeyGENE)

Authentication

Mycoplasma contamination Cel lines were routinely tested for mycoplasma

Commonly misidentified lines (See <u>ICLAC</u> register)

Animals and other research organisms

Policy information about <u>studies involving animals</u>; <u>ARRIVE guidelines</u> recommended for reporting animal research, and <u>Sex and Gender in Research</u>

Laboratory animals

female BALB/C mice

Wild animals

Five to six week old, animals were euthanized using an extra 0.5% sodium pentobarbital solution

Reporting on sex

female

Field-collected samples

NA

Ethics oversight

All animal experiments were approved by the Laboratory Animal Ethics Committee at Nanjing Medical University.

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