

Reporting Summary

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Statistical parameters

When statistical analyses are reported, confirm that the following items are present in the relevant location (e.g. 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
- An indication of 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 statistics 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
- Clearly defined error bars
State explicitly what error bars represent (e.g. SD, SE, CI)

Our web collection on [statistics for biologists](#) may be useful.

Software and code

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

Data collection JPK data processing (v 6.0.42); Bruker Topspin;

Data analysis JPK data processing (v 6.0.42); Wavemetrics Igor 6.35 with custom-written protocol; Gelpro; Origin 8.0;

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/reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research [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 list of figures that have associated raw data
- A description of any restrictions on data availability

All data generated and analyzed during this study are included in this article and its Supplementary Information, and are also available from the authors upon reasonable request.

Field-specific reporting

Please select 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/authors/policies/ReportingSummary-flat.pdf](https://www.nature.com/authors/policies/ReportingSummary-flat.pdf)

Life sciences study design

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

Sample size	N/A
Data exclusions	N/A
Replication	N/A
Randomization	N/A
Blinding	N/A

Reporting for specific materials, systems and methods

Materials & experimental systems

n/a	Involvement in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> Unique biological materials
<input type="checkbox"/>	<input checked="" type="checkbox"/> Antibodies
<input checked="" type="checkbox"/>	<input type="checkbox"/> Eukaryotic cell lines
<input checked="" type="checkbox"/>	<input type="checkbox"/> Palaeontology
<input checked="" type="checkbox"/>	<input type="checkbox"/> Animals and other organisms
<input checked="" type="checkbox"/>	<input type="checkbox"/> Human research participants

Methods

n/a	Involvement in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> ChIP-seq
<input checked="" type="checkbox"/>	<input type="checkbox"/> Flow cytometry
<input checked="" type="checkbox"/>	<input type="checkbox"/> MRI-based neuroimaging

Antibodies

Antibodies used

1. Anti-Her2 positive trastuzumab was purchased from efe-bio (shanghai), CAS 180288-69-1, Lot E122375
 2. Goat anti-Human IgG antibody-HRP was purchased from Beyotime, China, Cat: A0201, diluted as 1:1000 ratio for ELISA
 3. Mouse anti-Human IgG1 Fc secondary antibody-Horse Radish Peroxidase (HRP) (Cat: A-10648, ThermoFisher, USA), anti-Human (κ -chain specific), goat F(ab')₂ fragment-HRP antibody (Cat: SAB3701414, Sigma-Aldrich, Germany) and his-tag (27E8) mouse monoclonal antibody-HRP conjugate (Cat: 9991, Cell Signaling Technology, USA) were diluted by 1:1000 ratio for western blot.

Validation

1. Trastuzumab is a humanized monoclonal antibody for patients with invasive breast cancers that overexpress HER2. Trastuzumab has been clinically used to treat Her2 positive metastatic breast cancer and HER2 positive gastric cancer.
 2. Goat anti-Human IgG antibody-HRP is the secondary antibody targeting human IgG (trastuzumab in this paper), and can be detected by catalyzing TMB (3,3',5,5'-Tetramethylbenzidine Liquid Substrate, Cat: T4444, Sigma-Aldrich, Germany) to blue product in ELISA.
 3. Mouse anti-Human IgG1 Fc secondary antibody-HRP is the secondary antibody targeting human IgG1 Fc domain (heavy chain of trastuzumab in this paper), anti-Human (κ -chain specific), goat F(ab')₂ fragment-HRP antibody is the secondary antibody targeting human κ -chain (light chain of trastuzumab in this paper), and his-tag (27E8) mouse monoclonal antibody-HRP conjugate detects recombinant proteins containing the 6xHis epitope tag (internal reference 6xhis-GB1 protein in this paper). Three of them can be detected using ECL™ Prime Western Blotting System.