

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

ImageJ (National Institutes of Health, <http://imagej.nih.gov/ij/>) ImageJ version: 1.52h bundled with 64-bit Java 1.8.0_172 (open source); Adobe Photoshop (CS6; Adobe systems) Adobe Photoshop version: 13.0 x64

Data analysis

Origin version: OriginPro 2016 (64-bit) b9.3.226

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 main data supporting the examples of this protocol are available within the article and its Supplementary Information files. Extra data are available from the corresponding author upon reasonable request. The source data underlying Figure 3b and Supplementary Figure 5b are provided as Source Data files.

Human research participants

Policy information about [studies involving human research participants and Sex and Gender in Research](#).

Reporting on sex and gender	<input type="text" value="The information has not been collected."/>
Population characteristics	<input type="text" value="To demonstrate the practical application of this method, we studied nine whole blood samples from breast cancer patients, one whole blood sample from healthy control and one whole blood sample from benign cancer patient. No special requirements was needed for the selection of cancer patients' samples."/>
Recruitment	<input type="text" value="All patients' samples were taken with informed consent."/>
Ethics oversight	<input type="text" value="Renji Hospital, School of Medicine, Shanghai Jiao Tong University"/>

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

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	<input type="text" value="Nine whole blood samples from breast cancer patients, one whole blood sample from healthy control and one whole blood sample from benign cancer patient."/>
Data exclusions	<input type="text" value="No data were excluded from analysis."/>
Replication	<input type="text" value="At least 3 independent experiments were conducted for the most general experiments. Quantitative analysis for CTC capture was not replicated because of the a extremely time-consuming process for cell counting under microscopy."/>
Randomization	<input type="text" value="N/A"/>
Blinding	<input type="text" value="N/A"/>

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		Methods	
n/a	Involvement in the study	n/a	Involvement in the study
<input type="checkbox"/>	<input checked="" type="checkbox"/> Antibodies	<input checked="" type="checkbox"/>	<input type="checkbox"/> ChIP-seq
<input type="checkbox"/>	<input checked="" type="checkbox"/> Eukaryotic cell lines	<input type="checkbox"/>	<input checked="" type="checkbox"/> Flow cytometry
<input checked="" type="checkbox"/>	<input type="checkbox"/> Palaeontology and archaeology	<input checked="" type="checkbox"/>	<input type="checkbox"/> MRI-based neuroimaging
<input checked="" type="checkbox"/>	<input type="checkbox"/> Animals and other organisms		
<input checked="" type="checkbox"/>	<input type="checkbox"/> Clinical data		
<input checked="" type="checkbox"/>	<input type="checkbox"/> Dual use research of concern		

Antibodies

Antibodies used	<input type="text" value="PE Mouse Anti-Human Cytokeratin and FITC Mouse Anti-Human CD45"/>
Validation	<input type="text" value="Validation statements on specificity of the antibodies and citations can be found from manufacturers validation statements."/>

Eukaryotic cell lines

Policy information about [cell lines and Sex and Gender in Research](#)

Cell line source(s)	MCF-7 (CCTCC, cat. no. GDC0055) Ramos (ATCC, cat. no. CRL-1596) MDA-MB-231 (CCTCC, cat. no. GDC0297) HepG2 (CCTCC, cat. no. GDC0024) HCT116 (CCTCC, cat. no. GDC0625)
Authentication	We purchased new cell line from CCTCC.
Mycoplasma contamination	The cell lines were not tested for mycoplasma contamination.
Commonly misidentified lines (See ICLAC register)	<i>Name any commonly misidentified cell lines used in the study and provide a rationale for their use.</i>

Flow Cytometry

Plots

Confirm that:

- The axis labels state the marker and fluorochrome used (e.g. CD4-FITC).
- The axis scales are clearly visible. Include numbers along axes only for bottom left plot of group (a 'group' is an analysis of identical markers).
- All plots are contour plots with outliers or pseudocolor plots.
- A numerical value for number of cells or percentage (with statistics) is provided.

Methodology

Sample preparation	Sample preparation described with detail as part of the protocol manuscript in the Procedure section.
Instrument	Samples were analyzed on a BD FACSAArray bioanalyzer.
Software	Flow cytometry data was analyzed with FlowJo v.10 software.
Cell population abundance	N/A
Gating strategy	N/A

- Tick this box to confirm that a figure exemplifying the gating strategy is provided in the Supplementary Information.