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☐ Initial submission ☐ Revised version ☒ Final submission

Life Sciences Reporting Summary

Nature Research wishes to improve the reproducibility of the work that we publish. This form is intended for publication with all accepted life science papers and provides structure for consistency and transparency in reporting. Every life science submission will use this form; some list items might not apply to an individual manuscript, but all fields must be completed for clarity.

For further information on the points included in this form, see Reporting Life Sciences Research. For further information on Nature Research policies, including our data availability policy, see Authors & Referees and the Editorial Policy Checklist.

Experimental design

1. Sample size

Describe how sample size was determined.

No statistical method was used to predetermine sample size. On the basis of previous studies, we determined that we required at least 3 replicates in a sample size to derive an appropriate statistical test.

2. Data exclusions

Describe any data exclusions.

Data exclusions were only allowed for animals that died before experimental termination.

3. Replication

Describe whether the experimental findings were reliably reproduced.

The studies were replicated at least 3 different times, and were reproducible.

4. Randomization

Describe how samples/organisms/participants were allocated into experimental groups.

For animal studies, once tumors were established in mice, they were randomized into groups. This was performed in a blinded fashion, typically by a third party. For details, see Methods.

5. Blinding

Describe whether the investigators were blinded to group allocation during data collection and/or analysis.

A third party who was unaware of the treatment conditions was chosen to assess tumor size/volume.

Note: all studies involving animals and/or human research participants must disclose whether blinding and randomization were used.

6. Statistical parameters

For all figures and tables that use statistical methods, confirm that the following items are present in relevant figure legends (or in the Methods section if additional space is needed).

n/a	Confirmed	
☐	☒	The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement (animals, litters, cultures, etc.)
☐	☒	A description of how samples were collected, noting whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☐	☒	A statement indicating how many times each experiment was replicated
☐	☒	The statistical test(s) used and whether they are one- or two-sided (note: only common tests should be described solely by name; more complex techniques should be described in the Methods section)
☐	☒	A description of any assumptions or corrections, such as an adjustment for multiple comparisons
☐	☒	The test results (e.g. *P* values) given as exact values whenever possible and with confidence intervals noted
☐	☒	A clear description of statistics including central tendency (e.g. median, mean) and variation (e.g. standard deviation, interquartile range)
☐	☒	Clearly defined error bars

See the web collection on statistics for biologists for further resources and guidance.

Software

Policy information about availability of computer code

7. Software

Describe the software used to analyze the data in this study.	General statistical data was analyzed using GraphPad Prism software Version 7. ImageJ (Version 1.52j8) was used for Microscopy analysis. Flow-cytometry analysis was performed using FlowJo version 10. All the MD simulations were performed using GROMACS-4.6.1 package. NMR analysis was performed using Mnova NMR Software Version 11.0.0 (Mestrelab Research).

For manuscripts utilizing custom algorithms or software that are central to the paper but not yet described in the published literature, software must be made available to editors and reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). *Nature Methods* guidance for providing algorithms and software for publication provides further information on this topic.

Materials and reagents

Policy information about availability of materials

8. Materials availability

Indicate whether there are restrictions on availability of unique materials or if these materials are only available for distribution by a for-profit company.	All the materials are available from the authors or from standard commercial sources.

9. Antibodies

Describe the antibodies used and how they were validated for use in the system under study (i.e. assay and species).	See Tables 1 and 2 in the Supplementary Information.

10. Eukaryotic cell lines

a. State the source of each eukaryotic cell line used.	B16F10 Melanoma (ATCC), 4T1 Breast Cancer (ATCC) and RAW264.7 (ATCC) macrophage cell lines were used in this study.
b. Describe the method of cell line authentication used.	Cells were purchased from ATCC. The cells lines were authenticated by the supplier by using mycoplasma analysis, sterility analysis, species discrimination using CO1 barcode assay, and visual analysis for growth determination, morphology and viability.
c. Report whether the cell lines were tested for mycoplasma contamination.	Mycoplasma testing was performed by the supplier as a part of the authentication method. No further testing for mycoplasma contamination was performed.
d. If any of the cell lines used are listed in the database of commonly misidentified cell lines maintained by ICLAC, provide a scientific rationale for their use.	No commonly misidentified cell lines as listed in ICLAC were used.

Animals and human research participants

Policy information about studies involving animals; when reporting animal research, follow the ARRIVE guidelines

11. Description of research animals

Provide details on animals and/or animal-derived materials used in the study.	Balb/C syngeneic mouse models (4T1), female, 4–6 weeks, and C57BL/6 syngeneic mouse models (B16F10), male, 4–6 weeks.

Policy information about studies involving human research participants

12. Description of human research participants

Describe the covariate-relevant population characteristics of the human research participants.	The study did not involve human research participants.

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Flow Cytometry Reporting Summary

Form fields will expand as needed. Please do not leave fields blank.

Data presentation

For all flow cytometry data, confirm that:

☐ 1. The axis labels state the marker and fluorochrome used (e.g. CD4-FITC).

☒ 2. 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).

☒ 3. All plots are contour plots with outliers or pseudocolor plots.

☒ 4. A numerical value for number of cells or percentage (with statistics) is provided.

Methodological details

5. Describe the sample preparation.	After the required treatments and incubation, the cells were washed with PBS before collection followed by fixation/permeabilization. The cells were stained with appropriate antibodies, as described in Methods. Unstained cells and isotype controls were used. Flow cytometry was performed on BD Accuri C6 flow cytometer (BD Biosciences,USA) and the data was analyzed using FlowJo (FLowJo LLC)
6. Identify the instrument used for data collection.	BD Accuri C6
7. Describe the software used to collect and analyze the flow cytometry data.	Data was collected using BD Accuri C6 software and analyzed using FLowJo Version 10.
8. Describe the abundance of the relevant cell populations within post-sort fractions.	Sorting of cells was not performed.
9. Describe the gating strategy used.	Cells were initially on a dot plot, SSC-A vs. FSC-A. The negative population was determined by using unstained cells and isotype controls. All the cells outside the negative population were considered as positive cell population.

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