

Reporting Summary

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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

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|-------------------------------------|-------------------------------------|--|
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | The statistical test(s) used AND whether they are one- or two-sided
<i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i> |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | A description of all covariates tested |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | 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) |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | For null hypothesis testing, the test statistic (e.g. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P value noted
<i>Give P values as exact values whenever suitable.</i> |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | 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

Immunohistochemistry images were analysed with HALO 10 software (IndicaLab). Immunofluorescence data were obtained with AxioScan (Zeiss)

Data analysis

Data was analysed with R software (version 3.4.4) and packages gplots, survival and FactoMineR. Custom code was produced in R for the analysis.

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. 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

The transcriptomic datasets analysed in this study can be accessed on the GDC Portal (TCGA SARC) and the Gene Expression Omnibus repository (accession numbers GSE21050, GSE21122, GSE30929). Immunohistochemistry, gene expression and clinical-related to NTUH cohorts (Fig. 3, Extended Data Figs. 7 and 8) are available from the corresponding author on reasonable request. The data that support the findings related to Fig. 4 are available from SARC but restrictions apply to the availability of these data, which were used under license for the study. Data are however available upon reasonable request to HAT (HTawbi@mdanderson.org) and with permission of SARC. All code used in this study is available from the authors upon reasonable request.

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	TCGA SARC: n=213, GSE21050: n=283, GSE21122: n=72, GSE30929: n=40, FSG: n=168, NTUH n=93, SARC028: n=47. Total: n=916.
Data exclusions	20 tumours from the NTUH cohort were excluded from gene expression (end SIC) analysis due to low quality of the extracted RNA.
Replication	No replication was done, but validation cohorts were analysed.
Randomization	Randomization is only relevant to the SARC028 cohort, which was previously published.
Blinding	All image and data analysis were performed blindly, independently of sample knowledge.

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

n/a	Involved in the study
<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 type="checkbox"/>	<input checked="" type="checkbox"/> Human research participants
<input checked="" type="checkbox"/>	<input type="checkbox"/> Clinical data

Methods

n/a	Involved 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	CD3: 2GV6, Roche ; DC-Lamp: 1010E1.01, Dendritics ; CD20: L26, Agilent ; CD8: C8/144B, Agilent ; CD21 : 1F8, Agilent ; CD23 : SP23, Abcam; CD34: Qbend-10, Agilent ; PD-L1: E1L3N, Cell Signaling ; PD-1: EH33, CoStim Pharmaceuticals ; .
Validation	The specificity of anti-CD3, anti-CD4, anti-CD8, anti-CD20, anti-CD21, anti-CD23, anti-CD34, anti-CXCR5 and anti-DC-Lamp antibodies, and MECA-79 (PNAd) was validated on FFPE tonsil sections as positive control. For anti-CD20, certified manufacturing facilities from the company guarantee full quality control including western blot and studies using COS-1 cells transfected with cDNA encoding the CD20 molecule indicate that the antibody labels an intracytoplasmic epitope localized on the CD20 molecule. For anti-CD8, certified manufacturing facilities from the company guarantee full quality control including western blot and indicate that the antibody recognizes the cd8alpha chain. For anti-CD34, certified manufacturing facilities from the company guarantee full quality control. For anti-CD21, certified manufacturing facilities from the company guarantee full quality control including western blotting of the immunogen, and that the antibody labels cells or cell lines known to express CD21 (Raji, NC 37, tonsil cells), whereas no labeling is observed in the CD21-negative Jurkat cells (T-cell line) and human erythrocytes. For anti-CD23, certified manufacturing facilities from the company guarantee full quality control including western blotting, IHC on human tonsils and flow cytometry on Raji cells. For anti-CXCR5, certified manufacturing facilities from the company guarantee full quality control using human CXCR5 transfectants by flow cytometry and lack of cross reactivity with human CXCR2, CXCR3, or CXCR4 transfectants. For PNAd, certified manufacturing facilities from the company guarantee full quality control including western blotting, IHC and flow cytometry. For anti-PD-L1, specificity was validated by the company using immunohistochemical analysis of paraffin-embedded human placenta using PD-L1 (E1L3N®) XP® Rabbit mAb in the presence of control peptide or antigen-specific peptide. Specificity was verified by using FPE sections from placenta as positive control and cerebral cortex tissue as negative control. Anti-PD-1 (Freeman GJ and col.) was obtained from CoStim Pharmaceuticals and validated as described in Fig. S1 of Giraldo et al., Clinical Cancer Research, 2015. Tonsil, placenta and cerebral cortex slides were obtained from Geneticist Inc.

Human research participants

Policy information about [studies involving human research participants](#)

Population characteristics	All available characteristics are reported in Extended Data Table 1.
Recruitment	Patients were recruited prior to the study and were not selected on specific criteria other than their pathology.
Ethics oversight	The research was approved by the Research Ethics Committee of NTUH (201605061RINA).

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