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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	Flow cytometry, FlowJo v10 (FlowJo LLC). R analyses, ggeffects (v2.2.1), betareg (v3.2-1), AUCell (v1.28.0) AME margin (v0.3.28),RUV-III (v0.9.7.1),limma (v3.60.3),fgsea (v1.30.0),Harmony (v1.2.3),Seurat (v5.2.1),confint' (v1.11.0), dplyr 1.1.2, tidyr 1.3.0, readxl 1.4.3, readr 2.1.4 and magrittr 2.0.3.Sequencing, HTSeq (v2.0.3), Microscopy,HALO v3.6.4134 and HighPlex FL v4.2.3.
Data analysis	FlowJo version 10 (FlowJo LLC), DE gene analysis performed using R limma (v3.60.3). Volcano plots with ggplot2 (v3.5.1).Statistical analysis and data presentation: Graphpad Prism 9, GSEA analysis derived from GSE112825 Santucci et al 2019.statistical analyses for human cohort were conducted using Rv4 and murine cohort data analyses using Graphpad Prism v9, General: Microsoft Excel 2010

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

Processed and raw RNA Sequencing counts for human PB-TRM signature can be accessed via publicly available GEO: GSE271307 and Data availability statement has been provided in the manuscript including accession codes.

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), and sexual orientation and race, ethnicity and racism.

Reporting on sex and gender	"Parity and lactation induce T cell mediated breast cancer protection" only apply to women.
Reporting on race, ethnicity, or other socially relevant groupings	Malaysian and Australian (European ancestry predominantly) cohorts (Figure 5) Reed et al. collated datasets in Figure 1a also including European, Hispanic , Asian, African American populations.
Population characteristics	Demographic (patients de-identified) information were provided in SI table guide from Kathleen Cuningham Foundation Consortium for Research into Familial Breast Cancer (kConFab), Australia.
Recruitment	For Breast FACS and TILs/breastfeeding analyses, patients were approached by a prospective biobanking effort prior to commencement of this study. No significant biases are expected. Human MyBrCa cohort was a large study designed to recruit broadly. Again no important biases expected.
Ethics oversight	Complete ethics information and approval numbers for human and murine studies are provided in the manuscript methods section.

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

Life sciences study design

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

Sample size	In an exploratory study of this nature it is not possible to pre-specify the sample size. Cases were acquired, data analyzed and demographic and information surrounding epidemiology were gathered retrospectively at the final endpoint post collation of full comprehensive analsysis. The final sample size was determined in an adaptive fashion based on equal representation.
Data exclusions	MyBrCa clinical cohort, 3 cases without PAM50, 20 cases contained “normal-like” classification were excluded from the analysis. Parity was defined as at least one live birth, and pregnancy-associated cancers were not excluded in this analysis.
Replication	All characterisations of breast immune infiltration were replicated in 90 patient cohort as described in respective methods sections and Bulk RNASeq was performed on T cells isolated from multiple cases and matched peripheral blood contrasts were used for comparison. Mammary infiltrating lymphocytes in murine models shown by flow cytometry, immunohistochemistry, tumour models were replicated at least twice, shown from either pooled repeats or representative of independent repeats with similar results indicated in figure legends
Randomization	Therapeutic interventions in murine studies begun prior tumour cell inoculation and continued following BC onset randomization is not relevant.
Blinding	Investigators performed prospective collections for human and murine cohorts, retrosective analyses were performed from published datasets Data was not blinded.

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
☐	☒ Antibodies
☐	☒ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☐	☒ Animals and other organisms
☒	☐ Clinical data
☒	☐ Dual use research of concern
☒	☐ Plants

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☐	☒ Flow cytometry
☒	☐ MRI-based neuroimaging

Antibodies

Antibodies used

Human antibodies:
Marker; Flurophore; Catalogue#, Supplier
CD45 BV510 Human 304036 B2411217 H130 Biolegend
CD45 FITC Human 555482 4248832 H130 BD Biosciences
CD3 APC-H7 Human 560176 7234624 SK7 BD Biosciences
CD8 BV605 Human 301040 B230656 RPA-T8 Biolegend
CD8 PE Human 555635 6095935 HIT8a BD Biosciences
CD4 BV650 Human 317436 B2300991 OKT4 Biolegend
CD197,CCR7 BV711 Human 353228 B223097 G043H7 Biolegend
CD45RA FITC Human 555488 5181589 HI100 BD Biosciences CD69 PerCP-Cy5.5 Human 310926 B234158 FN50 Biolegend HLA ABC PE-Cy5 Human 555554 5163888 G46-2.6 BD
CD69 PECY7 Human 310912 B210943 FN50 Biolegend
CD103 BV421 Human 350214 B238177 BerACT8 Biolegend pan-cytokeratin (AE1/AE3); Human ;M3515; DAKO
CD3e;(SP7); Human; Ab16669;Abcam
CD8;(4B11); Human; NCL-L-CD8-4B11;Leica Biosystems CD69; (EPR21814);Human;Ab233396; Abcam
CD103;(EPR416602);Human;Ab129202; Abcam

Murine antibodies
CD45 APCCY7;Mouse; 109824;Biolegend
TCR-β BB700 Mouse; 745846 BD Biosciences
TCR-β BV786 Mouse 742484 Biosciences
TCR-Vα2 PerCP Cy5.5 Mouse 560529 BD Pharmagen
CD8 BV711 Mouse 100748 Biolegend
CD8 BUV395 Mouse 563786 BD Pharmagen
CD4 BUV805 Mouse 741912 BD Pharmagen
CD44 BV605 Mouse 103047 Biolegend
CD62L PECY7 Mouse 104418 Biolegend
CD62L BUV737 Mouse 612833 Pharmagen
CD69 BUV395 Mouse 38290563760 BD Pharmagen
CD69 PE Mouse 12069183 Invitrogen
CD103 FITC Mouse 121420 Biolegend
CD103 PE Mouse 12103182 Invitrogen
CD11B BV711 Mouse 101242 Biolegend
CD11C BV786 Mouse 117335 Biolegend
F4/80 EF-450 Mouse 48480182 Invitrogen
MHC-II (I-A/I-E) APC Mouse 17532182 Invitrogen
CD1d tetramer biotinylated PBS-57 66233 NIH
Streptavidin PE Mouse 12-4317-87 eBioscience
Streptavidin PE Mouse 554061 BD Pharmagen
BioxCell murine depletion antibodies; Isotype control rat IgG2b catalogue #BE0090;Anti-CD4 clone GK1.5, catalogue # BE0003-1;Anti-CD8a clone YTS 169.4, catalogue # BE0117; Anti-CD8b clone 53-5.8, catalogue # BE0223.

Murine antibodies

Marker	Fluorphore	Catalogue #	Supplier
CD49a	BUV395	740262	BD
NK1.1	BUV563	741233	BD
CD8b	BUV661	741585	BD
CD8a	RB545	569278	BD
CD4	BUV805	741913	BD
Ly108	BV421	740090	BD
CD103	BV480	566118	BD
CD44	BV510	563114	BD
Ly6C	BV570	128030	Biolegend
KLRG1	BV605	564013	Biolegend
CXCR3	BV650	126531	Biolegend
CD39	BV711	567295	BD
PD-1	BV750	135263	Biolegend
CD244	BV785	740860	BD
TCRgd	BB700	745818	BD
CXCR6	PE-Dazzle54	151117	Biolegend
CD69	PE-Cy5	15-0691-82	Invitrogen
CD45.2	SparkNIR685	109864	Biolegend
CD62L	APC-R700	565159	BD
TCRb	APC-Cy7	109220	Biolegend
CD38	APC-Fire810	102746	Biolegend
Granzyme A	ef450	3029841	Invitrogen
TCF1	AF488	644S	CST
Granzyme B	APC	MHGB05	Invitrogen
Tbet	PE/Fire 810	644839	Biolegend
CD45	PerCP	103130	Biolegend
CD19	AF488	115521	Biolegend
TCRgd	PE-Cy7	118123	Biolegend
NK1.1	BV570	108733	Biolegend
CD3	SparkNIR685	100262	Biolegend
CD44	APCR700	565480	BD
CD62L	BUV737	612833	BD
CD103	BV421	121422	Biolegend
CD49a	BUV563	741306	BD
CD39	PE-Dazzle 594	143812	Biolegend
CD11b	BV711	209715	Biolegend
CD11c	BV785	117335	Biolegend
F480	APC	123115	Biolegend
Ly6G	BV650	127641	Biolegend
Ly6C	BV605	128036	Biolegend
MHC-II	SparkBlue550	107661	Biolegend
CD170	PerCP-Fire 806	155536	Biolegend
XCR1	Spark UV387	148236	Biolegend
SIRPa	APC-Fire750	144030	Biolegend
CX3CR1	Spark Blue 574	285185	Biolegend
CD64	PE-Fire 744	161010	BD
PD1	RY586	753854	BD
FOXP3	e450	48-5773-82	Thermofisher

Validation

All antibodies were validated by the supplier and validation statements are available in the manufacturer's website. Additionally, functional experiments were reported in extended figures for murine T cell depletion antibodies provided in the manuscript.

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s)	AT3-OVA and D2A1 cell lines sourced from Prof. Phil Darcy and A/Prof Kara Britt respectively from Peter MacCallum Cancer Centre laboratory stocks, Melbourne, Australia
Authentication	Both cell lines were well established and published.
Mycoplasma contamination	Cell lines in this study were repetitively tested mycoplasma negative.
Commonly misidentified lines (See ICLAC register)	Cell lines in this study are not listed in the ILAC database.

Animals and other research organisms

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

Laboratory animals	C57BL/6J wild type (wt) and BALB/c wt mice, RAG1-/-; RAG2-/-γc-/- and OT-I CD45.2 and gBT-I CD45.1/CD45.2.Mice were used between 7-8 weeks of age.
Wild animals	no wild animals were used in the study.
Reporting on sex	female mice
Field-collected samples	This study does not involve samples collected from the field
Ethics oversight	All animal experiments procedures conducted in this study were approved by the relevant Peter MacCallum Cancer Centre Animal Experimentation Ethics Committee or by The University of Melbourne Animal Ethics Committee and conducted in accordance with the National Health and Medical Research Council Australian Code of Practice for the Care and Use of Animals for Scientific Purposes.

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

Clinical data

Policy information about clinical studies

All manuscripts should comply with the ICMJE guidelines for publication of clinical research and a completed CONSORT checklist must be included with all submissions.

Clinical trial registration	We utilised immune scores and associated clinical information from the MyBrCa dataset obtained from the original publication that contain BC subtype, parity information and breastfeeding data were described Pan et al 2024. This was not a clinical trial
Study protocol	Clinical data previously reported in Pan ***et al*** 2024
Data collection	Extended MyBrCa demo table were provided in the supplemental table information in the current study and were previously described in Pan ***et al*** 2024.
Outcomes	Clinical data reported in Pan et al 2024. In this study we utilized report significantly higher tumoural immune content in “basal-like” TNBC in parous women overall, compared with the Nulliparous women who subsequently developed breast cancer and our parous (PB)-TRM gene signature was highly enriched with both parity and breastfeeding status, highlighting the specificity of the P-TRM signature to breast involution by parity, and the specific influence of lactation.

Plants

Seed stocks	not applicable
Novel plant genotypes	not applicable
Authentication	not applicable

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	Human breast and Murine tissue samples were dissociated into single cell suspension was created using a modified published protocol Savas et al 2018. Adipose content were removed briefly from the mammary glands and the connective tissues were then finely diced into smaller fragments in RPMI1640 containing, 1 mg/ml collagenase type 4 and incubated for 30 minutes at 37C. Digested tissue fragments were teased through a 70um sieve, the sieve irrigated with neat PBS prior downstream analyses (Please refer further to respective tissue processing methods and resources table)
Instrument	BD Symphony A5 or LSR Fortessa X-20 (BD Biosciences, San Diego, CA, USA); 5-laser Cytek Aurora (Cytek Biosciences)
Software	FlowJo Version 10; OMIQ were used for FACS data interpretation and data presentation
Cell population abundance	Bulk RNA Seq, a total of 5x10e3 and blood 1x10e4 T cell fractions were FACS purified. Reanalysis of isolated CD8+ T cell following FACS were assessed for >90% purity of individual samples. total immune counts per gram were presented.
Gating strategy	Gating strategies including preliminary FSC/SSC gates of the starting population were provided **in Extended Data Figure 11 legends**

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