nature portfolio

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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	Sample processing and data generation are described in the method section. RNA-seq data was generated at UCLA TCGB sequencing core. Mass cytometry data was generated at UCLA JCCC Flow Cytometry core
Data analysis	The analysis is included in the method section. The source code of the analysis is available upon reasonable request

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

RNAseq data was uploaded to GEO under accession GSE237581 and CyTOF data was uploaded to FlowRepository under accession FR-FCM-Z6LY

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	Information about patient biological sex and gender is Included in Supp Table 1
Reporting on race, ethnicity, or other socially relevant groupings	Not applicable here.
Population characteristics	Disease relevant clinical characteristics of the patient population are included in Supp Table 1
Recruitment	Participants were recruited by co-investigators at UCLA Medical Center based on protocol eligibility criteria and verified by the study coordinator.
Ethics oversight	Patients signed an Informed Consent. This trial was approved by the UCLA Institutional Review Board

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	The size of treatment groups are included in the main text and Supp. Table 1. Group sizes were purely based on samples that we have collected from patients.
Data exclusions	CyTOF and RNA-seq samples passing QC are listed in Supp. Table 1
Replication	Data collected on individual patient samples could not be replicated due to the limited quantity of available specimens.
Randomization	Subjects were randomized at enrollment into 3 groups (placebo, Resiquimod, and Poly ICLC).
Blinding	Neither investigators nor patients were blinded to allocated treatment arm in this single site randomized study. Clinical equipoise was presumed maintained as both treatment arms received ATL-DC vaccination.

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	The list of antibodies for CyTOF is listed in Suppl. Table 3A

Validation	For metal conjugated antibodies used for CyTOF, validation was performed as described by the manufacturer (Fluidigm) or by the UCLA Jonsson Comprehensive Cancer Center (JCCC) Flow Cytometry Core Facility using the appropriate positive and negative cell staining and/or activation controls.

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	NCT01204684
Study protocol	The clinical protocol is attached as a supplement with the manuscript submission.
Data collection	Patients were recruited and completed treatment between 2010 and 2014. Survival follow-up continued until the present date.
Outcomes	The primary endpoint was the most effective combination of DC vaccine components. This was assessed by the immune monitoring described in the manuscript. The secondary outcomes were time to tumor progression and overall survival. These were assessed by Cox Regression and graphed by Kaplan-Meier plots.

Magnetic resonance imaging

Experimental design

Design type	N/A - The current study did not involve "functional" MRI, only anatomic MRI for visualizing and quantifying treatment response.
Design specifications	N/A - The current study involved acquisition of structural (anatomic) MRI at screening, prior to surgery, after surgery, and every treatment cycle until tumor progression, plus subsequent "off treatment" MRI scans until patient death.
Behavioral performance measures	N/A

Acquisition

Imaging type(s)	Structural/Anatomic
Field strength	3.0 T
Sequence & imaging parameters	Anatomic MR images were acquired prior to DC + adjuvant treatment and at 2-month intervals for all patients using the standardized brain tumor imaging protocol (BTIP), including three dimensional pre- and post-contrast T1-weighted images at 1-1.5mm isotropic resolution, two-dimensional T2-weighted and T2-weighted fluid attenuated inversion recovery (FLAIR) images with 3-4mm slice thickness and no interslice gap, and diffusion-weighted images with b=0, 500, and 1000 s/mm2, 3-4mm slice thickness and no interslice gap.
Area of acquisition	Whole brain

Diffusion MRI ☐ Used ☒ Not used

Preprocessing

Preprocessing software

Linear registration was performed between all images (T2, FLAIR, pre-contrast T1, post-contrast T1) to post-contrast T1-weighted images at screening using a 12–degree-of-freedom linear transformation and a correlation coefficient cost function in FSL (FLIRT; FMRIB Soft- ware Library, Oxford, England; http:// www.fmrib.ox.ac.uk/fsl/).

Estimates of tumor volume were performed using contrast-enhanced T1-weighted digital subtraction maps to exclude areas of post-surgical blood products or other sources of T1 shortening. T1 subtraction maps were created by first performing linear registration as described above. Next, Gaussian normalization of image intensity was performed for both nonenhanced and contrast enhanced T1-weighted images using custom c-code courtesy of the National Institutes of Health Magnetoencaphalography Core Facility (3dNormalize; NIMH MEG Core, Bethesda, MD; kurage.nimh.nih.gov/ meglab/ Med/3dNormalize), which normalizes image intensity by dividing each voxel by the standard deviation of the image intensity from the whole brain [SNor(x,y,z) = S (x,y,z)/stdWB], where S is raw image signal intensity, Nor is normalized, x,y,z are voxel coordinates, and stdWB is whole brain standard deviation. Next, voxel-by-voxel subtraction between normalized nonenhanced and contrast-enhanced T1-weighted images was performed using the Analysis of Functional NeuroImages software package (AFNI; 3dcalc; https://afni.nimh.nih.gov/). Image voxels with a positive (greater than zero) before-to-after change in normalized contrast enhancement signal intensity (ie, voxels increasing in MR signal after contrast agent administration) within T2-weighted FLAIR hyperintense regions were isolated to create the final T1 subtraction maps in order to exclude large vessels and other hyperintense regions outside the primary tumor area. Estimates of tumor volume included areas of contrast enhancement on T1 subtraction maps. Initial segmentation was performed automatically and final segmented volumes were edited by by an experienced independent observer with more than 10 years of experience to exclude large vessels and any obvious non-tumor regions.

Normalization

Intensity normalization was performed using custom c-code courtesy of the National Institutes of Health Magnetoencaphalography Core Facility (3dNormalize; NIMH MEG Core, Bethesda, MD; kurage.nimh.nih.gov/ meglab/ Med/3dNormalize), which normalizes image intensity by dividing each voxel by the standard deviation of the image intensity from the whole brain [SNor(x,y,z) = S (x,y,z)/stdWB], where S is raw image signal intensity, Nor is normalized, x,y,z are voxel coordinates, and stdWB is whole brain standard deviation.

Normalization template

Images were not normalized/registered to a standard template space. All images were registered to the patient-specific screening MRI exam as mentioned above.

Noise and artifact removal

No noise or artifact removal was performed.

Volume censoring

N/A

Statistical modeling & inference

Model type and settings

Specify type (mass univariate, multivariate, RSA, predictive, etc.) and describe essential details of the model at the first and second levels (e.g. fixed, random or mixed effects; drift or auto-correlation).

Effect(s) tested

Define precise effect in terms of the task or stimulus conditions instead of psychological concepts and indicate whether ANOVA or factorial designs were used.

Specify type of analysis: ☐ Whole brain ☐ ROI-based ☐ Both

Statistic type for inference

Specify voxel-wise or cluster-wise and report all relevant parameters for cluster-wise methods.

(See Eklund et al. 2016)

Correction

Describe the type of correction and how it is obtained for multiple comparisons (e.g. FWE, FDR, permutation or Monte Carlo).

Models & analysis

n/a	Involved in the study
☐	☐ Functional and/or effective connectivity
☐	☐ Graph analysis
☐	☐ Multivariate modeling or predictive analysis

Functional and/or effective connectivity

Report the measures of dependence used and the model details (e.g. Pearson correlation, partial correlation, mutual information).

Graph analysis

Report the dependent variable and connectivity measure, specifying weighted graph or binarized graph, subject- or group-level, and the global and/or node summaries used (e.g. clustering coefficient, efficiency, etc.).

Multivariate modeling and predictive analysis

Specify independent variables, features extraction and dimension reduction, model, training and evaluation metrics.