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Reporting Summary

Nature Research 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 Research policies, see our <u>Editorial Policies</u> and the <u>Editorial Policy Checklist</u>.

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For all sta	tistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.				
n/a Con	firmed				
	The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement				
$\boxtimes \square$	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.				
$\boxtimes \square$	A description of all covariates tested				
$\boxtimes \square$	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. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted Give <i>P</i> values as exact values whenever suitable.					
$\boxtimes \square$	For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings				
$\boxtimes \square$	For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes				
\square Estimates of effect sizes (e.g. Cohen's d , Pearson's r), indicating how they were calculated					
,	Our web collection on <u>statistics for biologists</u> contains articles on many of the points above.				
Softw	are and code				
Policy inf	ormation about <u>availability of computer code</u>				
Data co	ta collection Seurat V3.2, ST Pipeline v1.7.2 , The PhenoCycler System, CITE-seq-Count 1.4.2				
Data ar	alysis The main R (Version 4.2.1) scripts used in this paper was deposited to Github: https://github.com/edicliuyang/Hiplex_proteome.				
	ripts 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 Ve 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 sequencing data reported in this paper are available at GEO: GSE213264. The high-resolution microscope images were uploaded to https://doi.org/10.6084/m9.figshare.20723680

Field-spe	ecific re	porting		
		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		
		h all sections, see <u>nature.com/documents/nr-reporting-summary-flat.pdf</u>		
Life scier	nces st	udy design		
		e points even when the disclosure is negative.		
Sample size		nainly focused on demonstrating a new spatial technique; the best way to demonstrate it is to test various tissue types. The sample us not determined in this study.		
Data exclusions	No data was e	data was excluded from the analyses.		
Replication	There are no retechnique.	ere are no replicates in this study, mainly due to the fact there are enough data collected, which can support the feasibility of the current hnique.		
Randomization	There are no o	re are no defined sample groups in this research, so randomization is not relevant to this study.		
Blinding	There are no	defined sample groups in this research, so Blinding is not relevant to this study.		
Materials & ex n/a Involved in th Antibodies Eukaryotic Palaeontol Animals ar Human res	perimental ne study cell lines logy and archaed d other organis	n/a Involved in the study ChIP-seq Flow cytometry MRI-based neuroimaging ms nts		
Antibodies used	Huma	an antibody cocktail, Biolegend. Cat No. 99502: Mouse antibody cocktail, Biolegend, Cat No. 99833		
Validation	Inese	e two antibody cocktails are pre-titrated, lyophilized TotalSeq™ panels.		
Human rese	arch part	icipants		
Policy information	about <u>studies</u>	involving human research participants		
Population chara	octeristics	A 68-year-old male with a history of bullous pemphigoid in clinical remission, off systemic immunosuppressive or immunomodulatory therapy, was immunized for COVID-19 with the Moderna mRNA vaccine under FDA EUA as standard of care. Biopsies were performed on the immunized and unimmunized skin of the upper arms just below the vaccination site 2 days post the second and third vaccine doses.		
Recruitment		Recruitment was performed through public announcements and through oral dissemination within the research arena and in		

the dermatology clinic setting which could result is self selection bias for individuals highly motivated to participate in research. This bias could result in participants with a disease background, as in our subject with autoimmune skin disease in remission off therapy. The participant was informed of potential risks and provided written and oral consent prior to participation.

Ethics oversight

This study was approved by the Institutional Review Board at the Yale School of Medicine (Protocol ID#; 2000027055).

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