

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 [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

ODA raw files were processed in the MaxQuant environment (1.6.3.4). DIA raw files were analyzed using Spectronaut Pulsar X software (Biognosys, version 12.0.20491.17)

Data analysis

Perseus, the R framework (<https://www.r-project.org/>) and CKG's analytics core module (<https://github.com/MannLabs/CKG>)

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 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 mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium via the PRIDE partner repository with the dataset identifier PXD019909 (username: reviewer26347@ebi.ac.uk, password: gC4bRv4h during the review process)60.

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	No sample size calculation was performed. We have included samples from 32 donors enabling us to analyse at least triplicates for all samples. Most data on skin layer and cellular subsets are on N=5.
Data exclusions	We haven't excluded data.
Replication	The mass spectrometry experiments described in this study were performed independently on the same mass spectrometer
Randomization	Donors were anonymous and the project included one group. No randomization took place during processing or analyses of tissue and cells. The analyses performed were complex and took months to perform and there was a need to keep a strict overview of all samples, passages, fractions and LC MS/MS runs.
Blinding	Investigators were not blinded during processing or analyses in this study to keep a strict overview of samples, passages, fractions and LC MS/MS runs.

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	Involvement
<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 and archaeology
<input checked="" type="checkbox"/>	<input type="checkbox"/> Animals and other organisms
<input type="checkbox"/>	<input checked="" type="checkbox"/> Human research participants
<input type="checkbox"/>	<input checked="" type="checkbox"/> Clinical data
<input checked="" type="checkbox"/>	<input type="checkbox"/> Dual use research of concern

Methods

n/a	Involvement
<input checked="" type="checkbox"/>	<input type="checkbox"/> ChIP-seq
<input type="checkbox"/>	<input checked="" type="checkbox"/> Flow cytometry
<input checked="" type="checkbox"/>	<input type="checkbox"/> MRI-based neuroimaging

Antibodies

Antibodies used

Flowcytometry
 CD1a-FITC BD Pharmingen #555806 1:100
 CD1a-BV421 BioLegend #300128 1:100
 CD3-PE-Cy7 BioLegend #344816 1:100
 CD3-PE-CF594 BD Biosciences #562280 1:200
 CD3-BV605 BioLegend #317322 1:100
 CD4-Dazzle594 BioLegend #317448 1:200
 CD8-PE-Cy7 BD Pharmingen #557746 1:100
 CD11b-PE Immunotech #PN IM2581 1:100
 CD11c-APC BD Biosciences #333144 1:100
 CD14-FITC BD Biosciences #345784 1:100
 CD14-Dazzle594 BioLegend #325634 1:200
 CD31-FITC BioLegend #303104 1:100
 CD34-PE-Cy7 BioLegend #343516 1:100
 CD45-APC-Cy7 BD Biosciences #348815 1:200
 CD94-FITC BD Pharmingen #555888 1:100
 CD94-APC BioLegend #305508 1:100
 CD117-PE-Cy5.5 Beckman Coulter #A66333 1:100
 FcERI-BV421 BioLegend #334624 1:100

	In order to sort epidermal T cells and melanocytes by flow cytometry, the cell surface of freshly-prepared epidermal cells were stained with antibodies.
Instrument	FACSAria cell-sorting equipment (BD Biosciences)
Software	BD FACSDiva v8, FlowJo v10.4
Cell population abundance	The purity of the cells isolated by flow cytometry was determined in the same gate used for sorting and expressed as percentage of total lymphocytes in post-sort samples.
Gating strategy	Following CD45 positive gating, epidermal T cells were gated as CD3 positive and HLA-DR, CD1a, and CD94 negative, whereas dermal T cells were gated as CD3 positive and HLA-DR, FcERI, CD11c, CD14 and CD94 negative, being either CD4 or CD8 positive. Following CD45 positive gating and selection of HLA-DR positive cells, dermal CD1a+ dendritic cells were gated as CD11c positive and CD3, CD14 and CD94 negative, whereas dermal CD14+ dendritic cells were gated as CD11c and CD14 positive and CD3, CD1a and auto-fluorescent negative. Dermal macrophages were gated as auto-fluorescent and CD14 positive, following CD45 and HLA-DR positive gating. Dermal mast cells were gated as FcERI and CD117 positive and HLA-DR, CD3, CD14 and CD94 negative, following CD45 positive gating. Following CD45 negative gating, epidermal melanocytes were gated as CD117 positive and CD1a, and CD3 negative, whereas dermal endothelial cells were gated as CD31 and CD34 positive and CD3, CD11b and CD11c negative. Details of the gating strategy are shown in Supplementary Figures 2a-d.

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