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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	1.KEGG: KEGG.db 1.0 KEGGREST 1.34.0 2.GO: GO.db 3.14.0 org.Hs.eg.db 3.14.0 clusterProfiler v4.0.0 3.The GSEA-enriched pathway used KEGG, Msigdb v7.5.1
Data analysis	This article contains no original code. Any additional information required to reanalyze the data reported in this paper is available from the lead contact upon 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

The raw sequence data reported in this paper have been deposited in the Genome Sequence Archive (Genomics, Proteomics & Bioinformatics 2021) in National

Genomics Data Center (Nucleic Acids Res 2022), China National Center for Bioinformation / Beijing Institute of Genomics, Chinese Academy of Sciences (GSA-Human: HRA008316) that are publicly accessible at https://ngdc.cncb.ac.cn/gsa-human.

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	sex and gender were considered in this study,the details were shown as below; Written consents were obtained from each participant for sharing individual-level data. Sample ID Sex Age State HA1 male 55 healthy HA2 male 60 healthy HA3 male 49 healthy HP1 male 61 herpes zoster HP2 male 66 herpes zoster HP3 female 28 herpes zoster RP1 female 61 recoevered from herpes zoster RP2 male 66 recoevered from herpes zoster RP3 female 58 recoevered from herpes zoster
Reporting on race, ethnicity, or other socially relevant groupings	the socially constructed or socially relevant categorization variable(s)were not used in this manuscript, all participants were enrolled based on their disease progression and other physical Indicators including age, gender, with/without other chronic basic disease.
Population characteristics	Sample ID Sex Age State HA1 male 55 healthy HA2 male 60 healthy HA3 male 49 healthy HP1 male 61 herpes zoster HP2 male 66 herpes zoster HP3 female 28 herpes zoster RP1 female 61 recoevered from herpes zoster RP2 male 66 recoevered from herpes zoster RP3 female 58 recoevered from herpes zoster
Recruitment	Participants were patients who came to the Affiliated Hospital of Jiaxing University for treatment and were enrolled in the study program after obtaining informed consent
Ethics oversight	Affiliated Hospital of Jiaxing University

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	three healthy controls, three blood sample were collected during the onset of herpes zoster (HP group) and the blood sample after recovery were collected 90 days after first negative diagnose date (RP group).
Data exclusions	no data exclusion
Replication	the experiments were replicated using different individual samples (n≥10) to ensure the experimental results.
Randomization	the participants were allocated according to their disease progression and physical condition.
Blinding	the collection and analysis were performed by different researchers to avoid bias.

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

Antibody Specificity Clone Vendor Fluorochrome Cat# Usage
CD45RO human UCHL1 BD APC-Cy7 304227 flow
CD33 human P67.6 BioLegend APC 366605 flow
CD56 human HCD56 BioLegend APC 318309 flow
KLRG1 human SA231A2 ThermoFisher PerCP-Cy5.5 367707 flow
CD25 human M-A251 BioLegend APC 356109 flow
CD138 human DL101 BioLegend APC 352307 flow
CD3 human OKT3 BioLegend FITC 317305 flow
CD8 human SK1 BioLegend BV510 344731 flow
CD4 human RPA-T4 BioLegend PerCP-Cy5.5 300529 flow
CD62L human DREG-56 BioLegend PE 304805 flow
CD66b human 6/40C BioLegend BV421 392915 flow
CD192 human KO36C2 BioLegend PE 357205 flow
CD11b human ICRF44 BioLegend FITC 301329 flow
CD244 human 2-69 BioLegend PE 393507 flow
CD122 human TU27 BioLegend PE-Cy7 339013 flow
CD14 human 63D3 BioLegend PerCP-Cy5.5 367109 flow
CD196 human G034E3 BioLegend PE 353409 flow
CD16 human EPR22409-124 ABCAM AV488 AB270139 flow
CD27 human 323 EBOSCIENCE FITC 11-0279-42 flow
CD19 human 6D5 ABCAM APC AB25484 flow

Validation

Antibody Specificity Clone Vendor Fluorochrome Cat# Usage
CD45RO human UCHL1 BD APC-Cy7 304227 flow
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CD27 human 323 EBOSCIENCE FITC 11-0279-42 flow
CD19 human 6D5 ABCAM APC AB25484 flow

Plants

Seed stocks	Not applicable, this study did not involve plants.
Novel plant genotypes	Not applicable, this study did not involve plants.
Authentication	Not applicable, this study did not involve plants.

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	The whole blood underwent PBMC isolation through density gradient centrifugation using Histopaque-1077 in accordance with the manufacturer's guidelines. Specifically, the blood was mixed in a 1:1 ratio with D-PBS (Absin, abs970) containing 2mM EDTA(Corning, 46-034-CI), the diluted blood were overlaid on Lymphocytes separation medium (Absin, abs930), and centrifuged at 2000 rpm for 30 minutes at 4 degrees Celsius. PBMC were then extracted from the plasma-Histopaque interface. After washed in D-PBS(Absin, abs970) with 2mM EDTA(Corning, 46-034-CI), extracted PBMCs were cryopreserved in Cell freezing solution(Absin, abs9417).
Instrument	FACSCanto II (BD Biosciences)
Software	FlowJo v10.6 software (Tree Star)
Cell population abundance	The sequencing sample used in this study were human peripheral blood samples, therefore the sample of flow analysis were also human peripheral blood immune cells isolated by ficoll centrifugation. After centrifugation, a cell counter was used to determine the cell number contained in each sample, and the same number of cells was used for each set of analyses. Positive cells were strictly determined by flow analysis of fluorescence intensity compared to a negative control (no antibody added).
Gating strategy	monocytes: fsc/ssc gates-cd14/cd16 gates; t cell: fsc/ssc gates-cd3 gates-cd4/cd8 gates; CD8 effector tcell: t cell: fsc/ssc gates-CD3/CD8 gates-klrg1-CD122 gates; CD8 effector memory t cell: fsc/ssc gates-CD3/CD8 gates-CD45RO gates-KLRG1 gates; B cell: fsc/ssc gates-CD19 gates; neutriphils: fsc/ssc gates-CD11b gates-CD62L -CD14-CD66B gates. the gating strategy is provided in the main figures.

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