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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	Utilizing the NEBNext® UltraTM RNA Library Prep Kit for Illumina® (NEB, USA), we established bulk RNA libraries. Each sample's attribute sequences were appended with unique index codes. The quality of these libraries was assessed using the Agilent Bioanalyzer 2100 system. Subsequently, the samples, marked with indexes, were clustered on the cBot Cluster Generation System, using the TruSeq PE Cluster Kit v3-cBot-HS (Illumina). The Illumina Novaseq platform was used to sequence the library preparation, generating 150 bp paired-end reads.

Data analysis	The raw reads of 6 samples were initially processed using fastp software to remove adapters or poor-quality sequences. Hisat2 software, version 2.0.5, was then applied to map the high-quality paired-end reads to the GRCh38 reference genome. The number of genes was counted using Feature Counts (version 1.5.0-p3). The analysis of differential gene expression between two distinct groups, each with triplicate biological replicates, using the DESeq2 R package, version 1.20.0. This package offers statistical methods for evaluating changes in gene expression within high-throughput datasets, employing a negative binomial distribution-based model. The p-values were adjusted using the Benjamini and Hochberg method to manage the false discovery rate. Genes identified by DESeq2 with a P-value < 0.05 and |log2FoldChange| > 0.5, identified by DESeq2, were categorized as differentially expressed genes (DEGs). The clusterProfiler R package was utilized to conduct Gene Ontology (GO) enrichment analysis on the DEGs, accounting for gene length bias. GO terms were deemed significantly enriched by the DEGs at a p-value < 0.05. The Gene Set Enrichment Analysis (GSEA) is a computational method developed to assess whether a particular gene set shows a notable and coherent variation between two distinct biological states. In this process, genes are sorted based on the magnitude of their differential expression levels across the two samples. GSEA is capable of detecting even minor alterations in gene expression. For our analysis, we utilized a localized version of the GSEA software tool (http://www.broadinstitute.org/gsea/index.jsp) and applied the Gene Ontology (GO) dataset to conduct the GSEA independently.

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

Data supporting the findings of this study are available in the article and its Supplementary information. Source data are provided with this paper. The RNA-sequencing data produced for this research have been submitted to the Genome Sequence Archive (GSA) and the accession code HRA009305. The transcriptome data with OA condition during the study are available in the GSA-human database (https://ngdc.cncb.ac.cn/gsub/submit/biosample/subSAM130589/finishedOverview). Furthermore, all other relevant data that substantiate the findings of study are included in the article and supplementary information file.

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	n/a
Reporting on race, ethnicity, or other socially relevant groupings	n/a
Population characteristics	n/a
Recruitment	n/a
Ethics oversight	n/a

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 both in vitro and in vivo experiments, a minimum of three randomly selected biological replicates per experimental group were analyzed each time, with sample selection guided by effect size estimation and distribution overlap. Although preliminary power calculations were not performed, sample sizes were justified by aligning with published methodologies and experimental objectives to ensure reproducibility and reliability. This approach helps to ensure statistical power while minimizing resource use.
Data exclusions	No data were excluded.
Replication	All attempts at replication were successful. The experiment was repeated three times with similar results obtained.

Randomization	The samples were randomly grouped. They were numbered and then evenly distributed into different groups through a random drawing.
Blinding	The investigators were blind.

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
[ ]	[x] Antibodies
[ ]	[x] Eukaryotic cell lines
[x]	[ ] Palaeontology and archaeology
[ ]	[x] Animals and other organisms
[x]	[ ] Clinical data
[x]	[ ] Dual use research of concern
[x]	[ ] Plants

Methods

n/a	Involved in the study
[x]	[ ] ChIP-seq
[ ]	[x] Flow cytometry
[x]	[ ] MRI-based neuroimaging

Antibodies

Antibodies used	CD86-FITC (Proteintech, FITC-65068, GL1, 21007510,1:50); CD163 (Proteintech, 16646-1-AP, 00123179,1:200); CD31 (Proteintech, 11265-1-AP, 00134709,1:500); α-SMA (Abcam, ab7817, 1A4,1:100); FITC-conjugated (Proteintech, SA00003-1, 20000824,1:1000); FITC-conjugated (Proteintech, SA00003-2, 20000747,1:1000); Cy3-conjugated (Proteintech, SA00009-2, 20000786,1:100)
Validation	All validation data for the antibodies mentioned in this manuscript are accessible via the manufacturers' websites. Each antibody has undergone internal validation by the suppliers on their respective product pages, targeting mouse antigens. To assess antibody performance, we have incorporated samples with documented positive or negative reactivity for the antigen in question, serving as positive and negative controls where applicable. Additionally, we have included isotope controls as necessary. https://www.ptgcn.com/products/CD86-Antibody-FITC-65068.htm https://www.ptgcn.com/products/CD163-Antibody-16646-1-AP.htm https://www.ptgcn.com/products/PECAM1-Antibody-11265-1-AP.htm https://www.abcam.cn/products/primary-antibodies/alpha-smooth-muscle-actin-antibody-1a4-ab7817.html https://www.ptgcn.com/products/Fluorescein-FITC-conjugated-Affinipure-Goat-Anti-Mouse-IgG-H-L-secondary-antibody.htm https://www.ptgcn.com/products/Fluorescein-FITC-conjugated-Affinipure-Goat-Anti-Rabbit-IgG-H-L-secondary-antibody.htm https://www.ptgcn.com/products/Cy3-conjugated-Affinipure-Goat-Anti-Rabbit-IgG-H-L-secondary-antibody.htm

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s)	Immortalized human umbilical vein endothelial cells (HUVEC) and RAW 264.7 cells were purchased from the Cell Bank of the Chinese Academy of Science (Shanghai, China), serial numbers GNHu39 and SCSP-5036, respectively. The RAW 264.7 cells are derived from male BALB/c mice, while the gender of the HUVEC is lot-specific.
Authentication	We submitted samples for short tandem repeat analysis to discriminate the unique DNA profiles of each cell line before experiments.
Mycoplasma contamination	All cell lines tested negative for mycoplasma contamination.
Commonly misidentified lines (See ICLAC register)	No commonly misidentified line was used.

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 mice male 8 weeks
Wild animals	No wild animals were involved.
Reporting on sex	The findings apply to all genders.
Field-collected samples	No filed-collected samples was involved.
Ethics oversight	The Animal Ethics Committee of Shanghai Jiao Tong University Affiliated Ninth People's Hospital authorized all animal studies. The experiments received approval from the Animal Ethics Committee of Shanghai Ninth People's Hospital (SH9H-2022-A75-1).

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

Plants

Seed stocks	n/a
Novel plant genotypes	n/a
Authentication	n/a

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	5×10^5 RAW 264.7 cells were seeded on each well of a six-well plate and cultured with low-glucose DMEM containing 10% fetal bovine serum (FBS), until macrophage reached almost 80%. After culturing in low-glucose DMEM without FBS for 8 hours, RAW 264.7 cells were induced to M1 polarization by 1 μg/mL lipopolysaccharide (LPS, #L2880, Sigma-Aldrich, United States) and 30 ng/mL interferon-γ (IFN-γ, #315-05-100, PeproTech, United States) for 24 hours. Cells were divided into three groups: treated with high-glucose DMEM without induction; treated with high-glucose DMEM + LPS + IFN-γ group; and treated with OSA-GEL@GC in high-glucose DMEM + LPS + IFN-γ group. For flow cytometry, 2×10^5 cells were incubated with fluorescein isothiocyanate (FITC) anti-mouse CD86 (1:50, FITC-65068, Proteintech, United States), CD163 antibody (1:200, 16646-1-AP, Proteintech, United States) and Cy3-conjugated Affinipure Goat Anti-Rabbit IgG (1:100, SA00009-2, Proteintech, United States). After being washed twice with flow cytometry staining buffer (PF00018, Proteintech, United States), polarization of RAW 264.7 cells was analyzed
Instrument	Agilent, NovoCyte 3000, 2010011W
Software	NovoExpress 1.6.2
Cell population abundance	The expression of cluster differentiation on the surface of macrophages can indicate whether a macrophage exhibits the M1 or M2 phenotype. CD86-FITC and CD163 antibodies were employed to quantitatively determine the percentage of cells undergoing M1 or M2 polarization, respectively.
Gating strategy	M1 macrophages were positively stained with CD86-FITC. And M2 macrophages were combined with CD163 antibody with positively stained for PE.

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