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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	Image acquisition was performed using Olympus VS200 slide scanner and Olympus FV3000 confocal microscope. No custom software was used for data collection.
Data analysis	Image analysis and quantification were performed using ImageJ (NIH, USA; version 1.53) and GraphPad Prism 7.0 (GraphPad Software, San Diego, CA, USA). Statistical analyses were conducted using GraphPad Prism 7.0. No custom code was used for data analysis.

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

All data generated or analyzed during this study are included in the published article and its supplementary information files. The raw RNA-seq data have been deposited in the NCBI Sequence Read Archive (SRA) under BioProject accession number PRJNA1436578. The reviewer link is: https://dataview.ncbi.nlm.nih.gov/

object/PRJNA1436578?reviewer=k5jh92bbbc7f5h3p3oim1h5jn4. Additional datasets used and/or analyzed during the current study are available from the corresponding author upon reasonable request.

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	*Use the terms sex (biological attribute) and gender (shaped by social and cultural circumstances) carefully in order to avoid confusing both terms. Indicate if findings apply to only one sex or gender; describe whether sex and gender were considered in study design; whether sex and/or gender was determined based on self-reporting or assigned and methods used.* *Provide in the source data disaggregated sex and gender data, where this information has been collected, and if consent has been obtained for sharing of individual-level data; provide overall numbers in this Reporting Summary. Please state if this information has not been collected.* *Report sex- and gender-based analyses where performed, justify reasons for lack of sex- and gender-based analysis.*
Reporting on race, ethnicity, or other socially relevant groupings	*Please specify the socially constructed or socially relevant categorization variable(s) used in your manuscript and explain why they were used. Please note that such variables should not be used as proxies for other socially constructed/relevant variables (for example, race or ethnicity should not be used as a proxy for socioeconomic status).* *Provide clear definitions of the relevant terms used, how they were provided (by the participants/respondents, the researchers, or third parties), and the method(s) used to classify people into the different categories (e.g. self-report, census or administrative data, social media data, etc.)* *Please provide details about how you controlled for confounding variables in your analyses.*
Population characteristics	*Describe the covariate-relevant population characteristics of the human research participants (e.g. age, genotypic information, past and current diagnosis and treatment categories). If you filled out the behavioural & social sciences study design questions and have nothing to add here, write "See above."*
Recruitment	*Describe how participants were recruited. Outline any potential self-selection bias or other biases that may be present and how these are likely to impact results.*
Ethics oversight	*Identify the organization(s) that approved the study protocol.*

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	Sample sizes were determined based on previous studies and preliminary experiments. For wound closure assessment, n = 6 mice per group was used to ensure adequate statistical power. For histological, immunofluorescence, and Western blot analyses, n = 3 mice per group or three independent experiments were performed, which were sufficient to detect biologically meaningful differences. No formal sample size calculation was performed.
Data exclusions	No data were excluded from the analyses. All collected data points were included in the final analysis.
Replication	All experiments were performed with at least three independent biological replicates, and each experiment included at least three technical replicates. All attempts at replication were successful, and the findings were consistently reproducible.
Randomization	Mice were randomly assigned to treatment groups using a computer-generated randomization scheme. For in vitro experiments, cells were randomly allocated to different treatment conditions.
Blinding	Data collection and analysis were performed by investigators blinded to group allocation. Wound photography, histological evaluation, immunofluorescence quantification, and Western blot analysis were all conducted in a blinded manner. Surgical procedures and treatments were performed by unblinded researchers, but outcome assessments were blinded.

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

All antibodies used in this study are listed in Supplementary Table S2. Briefly, primary antibodies against iNOS (Proteintech, 18985-1-AP), ARG1 (Affinity, DF6657), Ki67 (Affinity, AF0198), p-PI3K (Affinity, AF3241), PI3K (Affinity, AF6241), p-AKT (Affinity, AF0016), AKT (Proteintech, 10176-2-AP), K10 (HUABIO, ET1609-75), IL-10 (Affinity, DF6894), TNF-α (Wanleibio, WL01581), IL-1β (Wanleibio, WL02257), IL-6 (Wanleibio, WL02841), LC3 (CST, #4108), F4/80 (Santa Cruz, sc-52664), p-mTOR (CST, #2971s), and mTOR (CST, #2983s) were used. Secondary antibodies were HRP-conjugated (Proteintech, SA00001-2) for Western blotting or CoraLite488/Cy3-conjugated for immunofluorescence. All antibodies were used at dilutions specified in Supplementary Table S2.

Validation

The specificity of each primary antibody was validated by the manufacturers as indicated on their websites. For antibodies from Cell Signaling Technology (CST), validation data are available on the CST website. For antibodies from Proteintech, Affinity, HUABIO, Wanleibio, and Santa Cruz, validation information is provided in the product datasheets. In addition, antibody specificity was confirmed by the presence of single bands at the expected molecular weights in Western blot analyses, and by appropriate positive and negative controls in immunofluorescence staining. No antibody validation was performed independently in this study beyond the manufacturer's specifications and established literature citations.

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s)

The following eukaryotic cell lines were used in this study:HaCaT (human keratinocyte cell line), obtained from the Kunming Institute of Zoology Cell Bank (KCB200442YJ); RAW264.7 (mouse monocyte/macrophage cell line), obtained from the Kunming Institute of Zoology Cell Bank (KCB200603YJ).

Authentication

Both HaCaT and RAW264.7 cell lines were authenticated by the Kunming Institute of Zoology Cell Bank using short tandem repeat (STR) profiling and morphological analysis prior to distribution. No further authentication was performed in our laboratory.

Mycoplasma contamination

All cell lines tested negative for mycoplasma contamination using a mycoplasma detection kit (Beyotime, China) before use in experiments.

Commonly misidentified lines
(See ICLAC register)

Neither HaCaT nor RAW264.7 is listed in the ICLAC Register of Misidentified Cell Lines. These cell lines are widely used in wound healing and inflammation research and are appropriate for the purposes of this study.

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

ale Kunming mice (Mus musculus), 6–8 weeks old, weighing approximately 25–30 g, were used in this study. All mice were obtained from Kunming Chushang Technology Co., Ltd. (Kunming, China). Animals were housed under controlled environmental conditions (23 ± 1 °C, 12-hour light/dark cycle) with free access to food and water.

Wild animals

This study did not involve wild animals.

Reporting on sex

Only male mice were used in this study. Sex was not considered as a variable in the study design because the primary objective was to evaluate the wound healing efficacy of OL-RA11 in a standardized model. The use of male mice minimized variability associated with estrous cycles in females. Therefore, sex-based analyses were not performed, and findings apply only to male mice. No sex-disaggregated data were collected.

Field-collected samples

This study did not involve field-collected samples.

Ethics oversight

All animal experiments were approved by the Animal Ethics Committee of the Laboratory Animal Department of Kunming Medical University (Approval No. kmmu20220069). All procedures were conducted in strict accordance with relevant ethical regulations for animal use.

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

Plants

Seed stocks	*Report on the source of all seed stocks or other plant material used. If applicable, state the seed stock centre and catalogue number. If plant specimens were collected from the field, describe the collection location, date and sampling procedures.*
Novel plant genotypes	*Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor was applied.*
Authentication	*Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosiacism, off-target gene editing) were examined.*