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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 Authors & Referees and the Editorial Policy Checklist.

Statistical parameters

When statistical analyses are reported, confirm that the following items are present in the relevant location (e.g. 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
☐	☒	An indication of 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 statistics 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
☐	☒	Clearly defined error bars *State explicitly what error bars represent (e.g. SD, SE, CI)*

Our web collection on statistics for biologists may be useful.

Software and code

Policy information about availability of computer code

Data collection	BD FACS Diva v6.1.3 software and Zeiss ZEN 2012 (blue edition) were used for cytofluorimetric data and image collection, respectively.
Data analysis	FlowJo version 9.3.2 GraphPad prism version 5 and version 7 Image J version 1.46r

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/reviewers upon request. 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 data that support the findings of this study are available from the corresponding authors upon request.

Field-specific reporting

Please select 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/authors/policies/ReportingSummary-flat.pdf

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	No statistical methods were used to predetermine sample size. An estimate of three to seven (or more) mice per group were used in individual experiments and assumed this sample size would be required to recognize differences between genotypes and treatments.
Data exclusions	No data excluded.
Replication	Experiments were reliably reproduced; in particular, most of the experiments were repeated yielding similar results.
Randomization	For experiments comparing transgenic or knockout mice vs. wild-type controls, the groups were set up based on genotype. In the experiments where mice were treated with Fc or Del-1-Fc or in the experiments where mice were treated with RvD1 or PBS, groups were randomly assigned to the two different treatments.
Blinding	The investigators were not blinded to the identities of the samples. Compared samples were collected and analyzed under the same conditions.

Reporting for specific materials, systems and methods

Materials & experimental systems

n/a	Involved in the study
☐	☒ Unique biological materials
☐	☒ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology
☐	☒ Animals and other organisms
☐	☒ Human research participants

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☐	☒ Flow cytometry
☒	☐ MRI-based neuroimaging

Unique biological materials

Policy information about availability of materials

Obtaining unique materials	DEL-1-Fc, DEL-1[E1-E3]-Fc and DEL-1[RGE]-Fc proteins are available by the corresponding authors upon request.

Antibodies

Antibodies used	Antibodies against CD11b (clone M1/70, 1/100 dilution, catalog number: 552850, BD Biosciences), Ly-6G (clone 1A8, 1/100 dilution, catalog number: 551461, BD Biosciences), CD115 (clone AFS98, 1/100 dilution, catalog number: 12-1152-81, eBioscience), ICAM2 (CD102, clone 3C4 (mIC2/4), 1/100 dilution, catalog number: 557444, BD Biosciences) and F4/80 (clone BM8, 1/100 dilution, catalog number: 17-48-01-80, eBioscience) were used for flow cytometry. Antibody against mouse CD16/32 was used to block Fcγ receptors (clone 2.4G2, 1/100 dilution, catalog number: 553141, BD Biosciences). For in vivo functional inhibition assays a blocking antibody against CD11b (clone M1/70, 50µg/mouse, catalog number: 101214, Biolegend) was used. For in vitro intervention assays, a blocking antibody against CD11b (clone M1/70, final concentration 10µg/ml, catalog number: 101214, Biolegend), antibody against ICAM-1 (clone YN1/1.7.4, final concentration 10µg/ml, catalog number: 116110, Biolegend) or antibody against LFA-1 integrin (clone 17/4, final concentration 10µg/ml, catalog number: 101109, Biolegend) were used. An antibody against Ly6G (clone RB6-8C5, final concentration 5µg/ml, catalog number: 14-5931-81, eBioscience) and a secondary antibody (1/500 dilution, catalog number: A-11006, Invitrogen) were used for immunostaining of gingival tissues.
Validation	The antibodies are from commercial sources and have been validated by the vendors.

Animals and other organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research

Laboratory animals	Mice were housed under specific pathogen-free conditions on a standard 12/12h light/dark cycle. 8-10 weeks old sex-matched mice were used. Food and water were provided ad libitum. In experiments where only wild-type C57BL/6 mice were used, these were purchased from Janvier Labs or the Jackson Laboratory. Del1KO mice and mice overexpressing DEL-1 in the endothelium (EC-Del1) have been previously described. Mice overexpressing in macrophages full-length DEL-1 (CD68-Del1) or the truncated version of DEL-1 that lacks the discoidin I-like domains (CD68-Del1-[E1-E3]) were generated in C57BL/6N background, using the human CD68 promoter. Mice deficient in both LXR isoforms (Nr1h3KONr1h2KO; here referred to as Lxra-LxrbDKO) in a C57BL/6 background were originally provided from D. Mangelsdorf (University Texas Southwestern). Mice deficient in αL integrin (ItgalKO) or αM integrin (ItgamKO) were previously described. Mice deficient in beta3 integrin (Itgb3KO) and their respective wild-type control mice were from the Jackson Laboratory.
Wild animals	N/A
Field-collected samples	N/A

Human research participants

Policy information about studies involving human research participants

Population characteristics	All subjects were 28 years of age or older with no serious medical illness contraindicative of periodontal treatment. Gingival crevicular fluid was collected from 7 patients (3 males and 4 females) prior to initiation of scaling and root planing and at a reevaluation appointment 6 weeks later.
Recruitment	The inclusion criteria for chronic periodontitis were diseased sites with probing pocket depth ≥ 5 mm associated with clinical attachment loss ≥ 4 mm, presence of bleeding on probing, and radiographic evidence of bone loss.

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	Single cell suspensions were prepared from peritoneal exudates from mice. Erythrocytes were removed with RBC lysis buffer and then cells were used for staining.
Instrument	FACS Canto II, FACS Aria cell sorter
Software	FlowJo version 9.3.2
Cell population abundance	Purity of FACS-sorted samples was >95%.
Gating strategy	MSU-inflammation model: After gating on the singlets, peritoneal neutrophils were identified as Ly-6G+CD11b+ cells. Apoptotic neutrophils were detected based on their positivity for Annexin V. Peritoneal monocytes/macrophages from MSU crystal-treated mice were defined as Ly-6G-CD11b+ cells after excluding the SSC high eosinophil population. Macrophages were identified and sorted as CD11b+F4/80+ cells from peritoneal fluids of untreated mice. Resident macrophages in peritoneal fluids of untreated mice were identified and sorted as CD115+ICAM2+ cells.

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