nature portfolio

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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	A gel image with ethidium bromide staining was obtained by Gel Doc EZ system with Image Lab software ver. 6.0.1 (Bio-Rad). Mass spectra were obtained by autoflex maX with flexControl software ver. 3.4 (Bruker). LC-MS data was obtained by Q Exactive Hybrid Quadrupole-Orbitrap Mass Spectrometer (ThermoFisher Scientific) with Xcalibur 4.1.50 (ThermoFisher Scientific). CD spectra were recorded on a J-720 circular spectrometer (JASCO). Chemiluminescence was detected using the SpectraMax M5 plate reader (Molecular Devices)
Data analysis	Gel images were analyzed using Image Lab software ver. 6.1.0 (Bio-Rad). Mass spectra were analyzed using flexAnalysis software ver. 3.4 (Bruker).

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 are included in the manuscript.

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	NA
Reporting on race, ethnicity, or other socially relevant groupings	NA
Population characteristics	NA
Recruitment	NA
Ethics oversight	NA

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	The sample sizes are described in the figure legends or the Methods section.
Data exclusions	No data was excluded.
Replication	Replication of experiments are described in figure legends.
Randomization	Randomization was not relevant to this study.
Blinding	Blinding was not relevant to this study.

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

Peroxidase AffiniPure™ Donkey Anti-Mouse IgG (H+L) (Jackson ImmunoResearch Laboratories, Inc. Catalog number 715-035-150, Lot number 162296. Antibodies provided in the PathHunter® eXpress CCR2 CHO-K1 β-Arrestin GPCR Assay (DiscoverX) was used for 4.5 MCP-1/CCR2 inhibition assay.

Carlumab (CNTO 888) was obtained from MedChemExpress (catalog number HY-P99188, lot number 241405) and was used for the cell migration assay.

Validation

The use of anti-mouse IgG for ELISA was validated by Jackson ImmunoResearch Laboratories, Inc.
https://www.jacksonimmuno.com/catalog/products/715-035-150

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s)

PathHunter® eXpress CCR2 CHO-K1
THP-1 cells

Authentication

The cells included overexpress PK-tagged CCR2 and EA-tagged β-Arrestin-2. Activation of CCR2 stimulates the recruitment of β-Arrestin-2 and produces EFC signal.

THP-1 cells were obtained from JCRB (Japanese cancer research resources bank; catalog number JCRB0112.1, lot number 07262023). Information on this cell line is available at: https://cellbank.nibiohn.go.jp/~cellbank/en/search_res_det.cgi?ID=282.

Mycoplasma contamination

THP-1 cells were tested negative for mycoplasma contamination.

Commonly misidentified lines
(See ICLAC register)

No commonly misidentified cell lines were used in the 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

BALB/c (Balb/cCrSlc) mice, aged 6 weeks, were obtained from Japan SLC, Inc. through local distributor Shimizu Laboratory Supplies Co., Ltd. (Kyoto, Japan).
Animals were housed at the animal facility of the Kyoto University under the specific pathogen-free conditions.

Wild animals

The study did not involve wild animals.

Reporting on sex

The immunogenicity test was performed using female mice.

Field-collected samples

No field collected samples were used in this study.

Ethics oversight

The animal experiments were carried out in accordance with the institutional guidelines approved by the Kyoto University Animal Care Committee.

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.*