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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	RNA-sequencing: After RNA extraction, RNA concentrations were obtained using nanodrop or a fluorometric Qubit RNA assay (Life Technologies, Grand Island, New York, USA). The quality of the RNA (RNA integrity number) was determined on the Agilent 2100 Bioanalyzer (Agilent Technologies, Palo Alto, CA, USA) as per the manufacturer's instructions. To construct the libraries, 250 ng of high quality total RNA sample (RIN >8) was processed using Stranded mRNA Prep kit (Illumina) according to manufacturer instructions. Briefly, after purification of poly-A containing mRNA molecules, mRNA molecules are fragmented and reverse-transcribed using random primers. Replacement of dTTP by dUTP during the second strand synthesis will permit to achieve the strand specificity. Addition of a single A base to the cDNA is followed by ligation of Illumina adapters. Libraries were quantified by Q bit and profiles were assessed using the DNA High Sensitivity LabChip kit on an Agilent Bioanalyzer. Libraries were sequenced on an Illumina Nextseq 500 instrument using 75 base-lengths read V2 chemistry in a paired-end mode.
Data analysis	1. Graphpad Prism 10 (10.2.0) 2. Image J plugin IHC profiler (1.54) 3. After sequencing, a primary analysis based on AOZAN software (ENS, Paris) was applied to demultiplex and control the quality of the raw data (based of FastQC modules / version 0.11.5). Obtained fastq files were then aligned using STAR algorithm (version 2.5.2b) and quality control of the alignment realized with Picard tools (version 2.8.1). Reads were then counted using Featurecount (version Rsubread 1.24.1) and the statistical analyses on the read counts were performed with the DESeq2 package version 1.14.1 to determine the proportion of differentially expressed genes between two conditions. The set of differentially expressed transcript was analyzed through the use of IPA version 81348237 (QIAGEN Inc., https://www.qiagenbioinformatics.com/products/ingenuitypathway-analysis).

Enrichments were also explored using GSEA (Gene Set Enrichment Analysis) 4.2.3 software (https://www.gsea-msigdb.org/gsea/). GSEA determined whether gene sets from the Molecular Signatures Database, related to Hallmarks, REACTOME pathways and GO biological processes (v2022.1), were randomly distributed throughout our ranked transcript list or if they were located at the top or bottom of it. The selected parameters were : tTest, gene_set permutation (n=1000), collapse.
Hierarchical clustering was performed using Heatmapper web server (http://www.heatmapper.ca/). Venn diagrams were designed using Funrich v3.1.3 (www.funrich.org).

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, its Supplementary information, the source data file and from the corresponding author upon request. RNA-sequencing data have been deposited in the Gene Expression Omnibus (GEO) database under accession code GSE220993 (https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE220993). Datasets used in supplementary figure 1 are available at GEO, accession number GSE13355 (https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE13355).

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	The ratio men:women was 1:1 for pustular psoriasis patients and age of patients ranged from 19 to 85 years with an average of 50 years.
Reporting on race, ethnicity, or other socially relevant groupings	Informations were not available.
Population characteristics	Diagnosis and treatments of the studied population are indicated in supplementary table 1, and mutational status in Supplementary table 2.
Recruitment	N/A
Ethics oversight	Informed written consent to the protocol was obtained for all subjects and was approved by the Ethical Review Committee for publications of the Cochin university Hospital (CLEP), Decision N°: AAA-2022-08049 and by the "Comité de Protection des Personnes" (ID-RCB: 2014-A01017-40 and 2011-A00820-41) at Saint-Louis Hospital. The collection of personal data was approved by the "Commission Nationale de l'Informatique et des Libertés".

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	For mouse experiments with IMQ and RNA, prior experience in our laboratory and in the literature suggested groups of 3-5 animals per group were sufficiently-powered to compare different genotypes. Pilot experiments with the Hamp-deficient and Hamp-overexpressed mice confirmed this. The number of mice is indicated in the figure legends. Concerning human biopsies, we analyzed lesional skin biopsies taken from 24 patients with vulgaris psoriasis, 26 patients with pustular psoriasis and 14 normal skin specimens from healthy controls matched for age and gender.
Data exclusions	All data points and animals were included in the statistical analyses, except samples where RNA/cDNA quality or tissue quality after processing was poor (below commonly accepted standards).
Replication	All attempts of replication were successful. The number of biological replicates is indicated in the figure legends.

Randomization	Animals were selected for inclusion in the study based on pre-specified criteria (genotype, littermates).
Blinding	Investigators were not blinded to the group allocation. However, data collection was performed in an unbiased manner.

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	Hepcidin-25 (ab30760, Abcam) FPN (NBP1-21502 Novus) Ki67 (ab15580, Abcam, # GR328 5096-1) Ki67 (D3B5, #9129S, Cell signaling technology) FPN (MTP11-A, Alpha Diagnostics, # 116989912.5-L) CXCL1 (ab86436 Abcam) anti-PMN (sc-71674, Santa Cruz, # K1620).
Validation	All antibodies used here have validation data available on the respective vendor's website (Abcam, Novus, Alpha Diagnostics, Santa Cruz).

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s)	Human keratinocyte cell line HaCat : DKFZ Collection (CLS Cell Lines Service, Eppelheim, Germany). Normal Human Epidermal Keratinocytes (NHEK) (PromoCell) KCP7 : human primary skin keratinocytes (KCs) derived from infant foreskin (Zhong et al., 2004). FCP7 : human primary fibroblasts (FCs) derived from infant foreskin (Zhong et al., 2004).
Authentication	The cell line has been provided by CLS. Mycoplasma contaminations are ruled out through PCR-based and luminescence-based mycoplasma assays. The absence of bacterial, fungal or yeast contamination is controlled through daily visual cell monitoring.
Mycoplasma contamination	Cell lines were negative for mycoplasma contamination.
Commonly misidentified lines (See ICLAC register)	*Name any commonly misidentified cell lines used in the study and provide a rationale for their use.*

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	To generate Hamp1KOker mice, Hamp1lox/lox mice were bred with K14-Cre transgenic mice , in which the Cre recombinase is under the control of the murine K14 promoter. Studies were performed in Hamp1KOker mice on a C57BL6J background, using 8-12 week old littermates. To generate Hamp1 KI-Ker mice, we first generated a Rosa26-pCAG-LSL-Hamp mouse line by homologous recombination Knock-in technology into Rosa26 locus. The Rosa26-pCAG-LSL-Hamp mice were bred with K14-Cre. Studies were performed in Hamp1KIker mice on a C57BL6J/N background, using 4-6 week old littermates. Mice were housed in specific-pathogen-free animal care facilities at Institut Cochin with 12- hour light-dark cycle, ambient temperature at 22+/−2 °C, humidity within 30%-70%, and received standard chow ad libitum. libitum.

Wild animals	The study did not involve wild animals.
Reporting on sex	Both male and female Hamp1 KI-Ker mice were used. For the IMQ experiments, female mice were used as 1. The skin of male mice is thicker than that of female mice (making analysis of Imiquimod-induced skin thickening more difficult) 2. The intensity of response to TLR7 (Imiquimod receptor) is sex-dependent. However, experiments can be reproduced in males.
Field-collected samples	N/A
Ethics oversight	The animal studies described here were reviewed and approved (Agreements n° APAFIS#9788-2017020314017133 and n° APAFIS#40199-2022102719322238 v8) by the Ministry of Higher Education, Research and Innovation and are in accordance with the principles and guidelines established by the European Convention for the Protection of Laboratory Animals (Council of Europe, ETS 123, 1991).

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.*