# nature portfolio

Corresponding author(s):	Angelo Peschiaroli
Last updated by author(s):	May 17th. 2023

# **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.

<.	トつ	ıŤ١	ist	117	$\sim$
J	Lα	I L	เอเ	. 14	L

For	all st	atistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.
n/a	Cor	nfirmed
	$\boxtimes$	The exact sample size $(n)$ for each experimental group/condition, given as a discrete number and unit of measurement
	$\boxtimes$	A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
	$\boxtimes$	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.
$\boxtimes$		A description of all covariates tested
X		A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
	$\boxtimes$	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)
	$\boxtimes$	For null hypothesis testing, the test statistic (e.g. <i>F</i> , <i>t</i> , <i>r</i> ) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted <i>Give P values as exact values whenever suitable.</i>
$\boxtimes$		For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
$\boxtimes$		For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
$\boxtimes$		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

Images: Leica Stellaris 8 . NIKON A1 and Leica DM6

Western blotting: Uvitec Alliance Q9

qPCR: Applied Biosystem QuanStudio 5 Real-Time PCR system

Data analysis

Leica Application Sulte x (LASX) NIKON NIS Elements software A1 **UVITEC Nine Alliance software** Graph Pad Prism 8.0

IGV 2.11.2

Applied Biosystem QuanStudio Design and Analysis software

Image J software 1.53a

VENN (http://www.interactivenn.net)

ChIRP-seq data were analyzed with "chipseq" version 1.2.2 pipeline included into the nf-core platform (https://nf-co.re/chipseq) with default parameters (Ewels et al 2020) (doi: 10.5281/zenodo.3240506);

ShinyGO version 0.76 (Ge et al 2020);

ComplexHeatmap R package (Gu et al 2016);

DoRothEA software (Garcia-Alonso et al., 2019);

GREAT tool (Regions Enrichment of Annotations Tool) (Mclean et al., 2010);

RNA-seq data were analyzed with "rnaseq" version 3.3 pipeline included into the nf-core platform (https://nfco.re/rnaseq) with default parameters (Ewels et al., 2020) (doi:10.5281/zenodo.5550247);

DESeq2 package (Love et al., 2014);

(IPA tool (Kramer et al. 2014);
Let Bill 1 "
Limma library;
Regions Enrichment of Annotations Tool (GREAT) (McLean et al, 2010);
regions enfliciment of Annotations roof (GNEAT) (inclean et al., 2010),
MEME algorithm (Bailey et al, 2015);
EnhancedVolcano R package;
Intervene software (Khan & Mathelier, 2017);
intervene software (Khan & Mathener, 2017),
IPA tools (Kramer et al., 2014);
Three of any 2011,

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 sequencing data that support the findings of this study have been deposited in the National Center for Biotechnology Information Gene Expression Omnibus (GEO) under the Series accession number GSE205961. This Series includes the access to RNA-seq data (GSE205960) ChIRP-seq data (GSE205959) and IncRNAs microarray (GSE232654). Public ChIP-seq was downloaded from GEO database under the accession number GSM1446927. Public RNA-seq data were downloaded from GEO database under the accession numbers GSM1446880 and GSM1446883. Public lamellas Ichthyosis and psoriasis microarray data were downloaded from GEO database under the accession numbers GSE108640 and GSE13555, respectively. Public ALOX12B knock-out mice microarray data were downloaded from GEO database under the accession number (GSE127435). Source data are provided with this paper.

### Human research participants

Policy information about studies involving human research participants and Sex and Gender in Research.		
Reporting on sex and gender	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	w 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.odf		

for a reference copy of the document with all sections, see <u>nature.com/documents/nr-reporting-summary-flat.p</u>

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

# Life sciences study design

Blinding

Sample size No statistical methods were used to determine the sample size. Sample sizes were chose as large as possible to yield high statistical significance.

Data exclusions No samples were excluded.

Replication All experiments were repeated to assure reproducibility (the number of biological replicates per experiment varied and it is mentioned in the figure legends). All attempts for replication shows similar results.

Randomization For drug treatments, samples were allocated into each group randomly. In each imaging session, samples were acquired selecting randomly approximately the same number of images for each condition in order to control for any variance. There are no other experiments that require randomization and therefore no randomization was performed.

For paraspeckles and ki67 positive cells counts, and corneo thickness measurement, the researcher was single-blinded during imaging acquisition and analysis. For others experiments, no blinding was used as there are no handling steps that are realistically subject to researcher bias.

# 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	Methods
n/a Involved in the study	n/a Involved in the study
Antibodies	ChIP-seq
Eukaryotic cell lines	Flow cytometry
Palaeontology and archaeology	MRI-based neuroimaging
Animals and other organisms	
Clinical data	
Dual use research of concern	
•	
Antibodies	
Anti-p63 (mouse monoc Anti-KRT1 (Biolegend, ca Anti-KRT10 (Covance, ca Anti-ZNF750 (Sigma-Ald Anti-beta-actin (Sigma-Ald Anti-Histone H3 (acetyl Anti-Loricrin (Covance ca Anti-SFPQ (rabbit Sigma Anti-Histone H3 (tri met Anti-KLF4 (RD Systems ca Anti-PARP (rabbit polycl Anti-PARP (rabbit polycl Anti-Integrin a6b4 (mou Anti-Ki67 (rabbit Cell Sig Anti-rabbit 488 (goat Lif Anti-mouse 568 (goat Lif Anti-mouse 568 (goat Lif Anti-mouse 568 (goat Lif Anti-sedish cojugated and Horsedish cojugated and rabbit IgG and mouse Ig	2K8X, (Cell Signaling, cat. numb. mAb #13109). Specificity: Human. Validated for WB, IP, IHC, ChIP. clonal , Abcam, cat. numb. AB735). Specificity: Human. Validated for IHC at. numb. PRB-149P). Specificity: Human. Validated for WB, IHC. lrich, Prestige Antibody, cat. numb. HPA023012). Specificity: Human. Validated for IHC. lrich, Prestige Antibody, cat. numb. HPA023012). Specificity: Human. Validated for WB, IF, IF and E:lisa t. numb. ab19845). Specificity: Human, mouse, rat. Validated for WB, IHC, ChIP. K8 + K18 + K23 + K27), Abcam, cat. numb. ab47915). Specificity: Human. Validated for WB, IHC. hr. hr. hr. hr. hr. hr. hr. hr. hr. hr
Validation See manufacturer's info	ormation above. Anti-ZNF750 antibody has been validated for WB in Gatti et al., PNAS 2022.
Eukaryotic cell lines	

Policy information about <u>cell lines and Sex and Gender in Research</u>

Cell line source(s)	A253 (ATCC HTB-41), FaDu (ATCC HTP-43), HCC1954 (ATCC CRL-2338) and hMEC (ATCC PCS-600-010) were purchased by ATCC. Human primary keratinocytes (HEKn) was purcased by Life Techonologies (Cat. numb. C0015C).
Authentication	No authentication was performed.
Mycoplasma contamination	Cell lines were tested negative for mycoplasma contamination using Mycoplasma detection kit MycoAlert kit (Lonza cat no LT07-218).
Commonly misidentified lines (See <u>ICLAC</u> register)	No commonly misidentified cell lines were used.