

## 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 no software was used

Data analysis Statistical analyses were performed under Statistical Package for Social Sciences version 22.0 (SPSS, Chicago, IL, USA) for human serum data. GraphPad Prism version 7 and Statistical Package for Social Sciences version 20.0 for Statistical analysis of all other data.

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 analysed during this study are included in this published article (and its supplementary information files).

## 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](https://www.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	We included 240 Caucasian and 186 Chinese Han subjects into our cross-sectional study of EMC10 serum concentrations. In two interventional studies, we measured circulating EMC10 before and 12 months after a combined exercise and calorie restricted diet study (n=50), before and 12 months after bariatric surgery (n=50). 240 donors of paired omental and SC adipose tissue samples were used to measure adipose tissue EMC10 mRNA expression, who underwent abdominal surgery for cholecystectomy, weight reduction surgery, abdominal injuries or explorative laparotomy.
Data exclusions	We defined the following exclusion criteria: 1) Thyroid dysfunction, 2) alcohol or drug abuse, 3) pregnancy, 4) treatment with thiazolidinediones
Replication	The CLIA system had an intra- and inter-assay coefficient of variation at 3.3-13.8% and 12-16.3%, respectively
Randomization	Patients in the experimental and control groups were divided into subgroups based on their gender and BMI.
Blinding	Investigators were blinded to group allocation during data collection and data analysis

## 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
<input type="checkbox"/>	<input checked="" type="checkbox"/> Antibodies
<input type="checkbox"/>	<input checked="" type="checkbox"/> Eukaryotic cell lines
<input checked="" type="checkbox"/>	<input type="checkbox"/> Palaeontology and archaeology
<input type="checkbox"/>	<input checked="" type="checkbox"/> Animals and other organisms
<input type="checkbox"/>	<input checked="" type="checkbox"/> Human research participants
<input checked="" type="checkbox"/>	<input type="checkbox"/> Clinical data
<input checked="" type="checkbox"/>	<input type="checkbox"/> Dual use research of concern

### Methods

n/a	Involved in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> ChIP-seq
<input checked="" type="checkbox"/>	<input type="checkbox"/> Flow cytometry
<input checked="" type="checkbox"/>	<input type="checkbox"/> MRI-based neuroimaging

## Antibodies

Antibodies used	Rabbit polyclonal antibodies to EMC10 and mouse monoclonal antibodies to EMC10 (Phrenzer Biotechnology, Shanghai, China). Anti-pCREB (#9198), anti-total CREB (#9197), anti-pP38MAPK (#4511), anti-total P38MAPK (#8690) antibodies were obtained from Cell Signaling.
Validation	Rabbit polyclonal antibodies to EMC10 and mouse monoclonal antibodies to EMC10 information were under submission for patent. Other antibodies information can be found on "https://www.cellsignal.com/" with each catalog number.

## Eukaryotic cell lines

Policy information about [cell lines](#)

Cell line source(s)	Hela cells purchased from ATCC
Authentication	Short Tandem Repeat (STR) DNA profiling were used to authenticate cell line
Mycoplasma contamination	All cell lines tested negative for mycoplasma contamination
Commonly misidentified lines (See <a href="#">ICLAC</a> register)	There were no commonly misidentified cell lines used in the study

## Animals and other organisms

Policy information about [studies involving animals](#); [ARRIVE guidelines](#) recommended for reporting animal research

Laboratory animals	C57BL/6J and ob/ob male mice were obtained from the Jackson Laboratory (USA). Emc10 knockout and transgenic male mice used in this study are on a C57BL/6 background. Age information can be found in each experiment group.
Wild animals	The study didn't involve wild animals
Field-collected samples	the study did not involve samples collected from field
Ethics oversight	The animal protocols were approved by the Institutional Animal Care and Use Committee (IACUC) of University of Illinois at Chicago.

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

## Human research participants

Policy information about [studies involving human research participants](#)

Population characteristics	For cross-sectional study, 240 Caucasian individuals which were either lean (BMI < 25 kg/m <sup>2</sup> , n=30, average age 61.53, females =18), overweight (BMI 25-30 kg/m <sup>2</sup> , n=22, average age 65.08, females =12) or obese (BMI > 30 kg/m <sup>2</sup> , n=188, average age 47.93, females = 134) and 186 Chinese subjects which were either lean (BMI < 24 kg/m <sup>2</sup> , n=32, average age 50.41, females =26), overweight (BMI 24-28 kg/m <sup>2</sup> , n=115, average age 51.25, females =58) or obese (BMI > 28 kg/m <sup>2</sup> , n=39, average age 52.64, females =27) were included. For follow-up studies, 100 overweight or obese Caucasian individuals (bariatric surgery, n=50, average age 47.86; hypocaloric diet and exercise, n=50, average age 51.44) were included.
Recruitment	For the purpose of our studies, we selected 240 Caucasian individuals from the Leipzig Obesity Biobank for whom serum and adipose tissues were available, and 100 Caucasian individuals underwent exercise and calorie restricted diet or bariatric surgery for whom serum were available at baseline and 12 months follow-up. Chinese participants were recruited through Shanghai diabetes screening program.
Ethics oversight	All studies were approved by the ethics committee of the University of Leipzig (approval numbers: 159-12-21052012 and 017-12-23012012) and all subjects gave written informed consent before taking part in the study.

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