

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 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 Living Imaging, v. 4.3.1.0.16427 (PerkinElmer); LabVIEW, v.2019 (National Instruments); LumiCycle software, v. 3.002 (Actimetrics Inc., Evanston, IL); Prism v.7.0a (GraphPad).

Data analysis KEGG pathway and Gene Ontology databases were accessed via ClueGO v. 2.5.4, and visualized within Cytoscape v. 3.5.1 or as a bar plot in MATLAB R2020b (The Mathworks, Inc). Other plots were performed in MATLAB2020b.
Our LABVIEW code is publicly available (<https://github.com/Onelia-G/CAVRO-PUMPS-FOR-MICROFLUIDICS>).
Our Matlab code is publicly available (<https://github.com/Onelia-G/heap-map>) and freely available for data processing.

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 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

All data supporting the findings of this study are available within the article, its Supplementary Information, attached files, and online deposited data (RNA-seq data: GSE167763, <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE167763>, or from the authors upon reasonable request.

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	For each experimental condition at least three independent biological experiments were performed. Statistical significance was assessed by the Student's t-test and one-way ANOVA with Tukey's multiple comparisons test, and presented as the mean $\pm$ s.d, determined from at least three independent experiments. For all analysis: *: P<0.05; **: P<0.01; ***: P<0.001; ****: P<0.0001. All N values defined in the legends refer to biological replicates unless otherwise indicated.
Data exclusions	No data were excluded
Replication	For each experiments at least three independent and successful replicates were provided.
Randomization	The allocation was random.
Blinding	Blinding was performed in a first stage of the data analysis, then it was not possible due to participants involvement in data discussion.

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
☒	☐ Human research participants
☒	☐ Clinical data
☒	☐ Dual use research of concern

Methods

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

Eukaryotic cell lines

Policy information about [cell lines](#)

Cell line source(s)	Mouse fibroblasts isolated from hearings in Takahashi's Lab (UTSW). Human Foreskin Fibroblasts, HFF (ATCC, Cat. SCRC-1041).
Authentication	None of the cell line was authenticated.
Mycoplasma contamination	Absence of mycoplasma contamination was periodically checked.
Commonly misidentified lines (See ICLAC register)	Name any commonly misidentified cell lines used in the study and provide a rationale for their use.