nature research

Corresponding author(s): FRIML

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 Authors & Referees and the Editorial Policy Checklist.

Statistical parameters

When statistical analyses are reported, confirm that the following items are present in the relevant location (e.g. 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
☒	☐ An indication of 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 statistics 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
☐	☒ Clearly defined error bars *State explicitly what error bars represent (e.g. SD, SE, CI)*

Our web collection on statistics for biologists may be useful.

Software and code

Policy information about availability of computer code

Data collection	Image data was collected using the Zeiss Zen (version 2010) software, the root chip was controlled via the Arduino (Uno rev3)and AutoIt (v 3.3) programs. For preparation of the photomasks, CorelDraw (X8) and Linkcad (9) were used.
Data analysis	Images were analyzed using Fiji (2017 release) and MATLAB (R2014 and R2015a). Data was processed in MATLAB (R2015a) and MS Excel (2010 and 2013). Model was created in Comsol Multiphysics (5.2a). Boxplots were created using BoxPlotR (http://shiny.chemgrid.org/boxplotr/). Figures and movies were prepared using Fiji and Inkscape (0.92).

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/reviewers upon request. 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 source data for the results in the manuscript are provided in the Supplementary Data 1 file

Field-specific reporting

Please select 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/authors/policies/ReportingSummary-flat.pdf

Life sciences study design

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

Sample size	This study analyzes growth of individual roots inside the microfluidic device that has 8 channels for 8 independent treatments of individual roots. Therefore the sample size was physically limited by the number of roots that entered the microfluidic channel and could be successfully flown by the treatment media. In case of comparing genotypes, control was included on the same chip - further the maximum sample size for the experiment. For the other growth experiments, we used approximately 7 roots per treatment and genotype, because this number still fits one one treatment plate.
Data exclusions	The individual roots were excluded from analysis if 1) the root did not grow or grew extremely slowly 2) if the respective microfluidic channel was blocked and therefore had no flow in it.
Replication	The results were replicated in technically independent replications.
Randomization	In case of comparing two genotypes, these were grown alongside on the same microfluidic chip. In case of studying the treatment effect, the pre-treatment state was takes as a baseline.
Blinding	Blinding was not relevant for this study because the growthrates of roots were determined using image analysis, not manually.

Reporting for specific materials, systems and methods

Materials & experimental systems

n/a	Involved in the study
☐	☒ Unique biological materials
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology
☒	☐ Animals and other organisms
☒	☐ Human research participants

Methods

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

Unique biological materials

Policy information about availability of materials

Obtaining unique materials	The origin of the biological material used in the study is described in the Methods; there are no restrictions on the availability of the materials used.