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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	All QPCR results were collected with LightCycler® 480; All images with luciferase bioluminescence signal were collected with CCD camera (NightOwl); Microscope images were collected with different microscopes (Leica205FA stereo-microscopy, Leica SP5 confocal microscope, Leica DM6000 microscopy, Leica TCS SP8X confocal microscope and Zeiss Axio Imager fluorescence microscope) and specified in the manuscript. Images for root length were taken with Alphaimager. Images for X-ray film were scanned with scanner or Cannon Camera.
Data analysis	MATLAB Version: 9.5.0.944444 (R2018b), The MathWorks, Inc., Natick, Massachusetts, United States. R version 3.3.1 (2016-06-21), The R Foundation for Statistical Computing. Python 3.5.4 |Anaconda 2.4.1 (64-bit)| (default, Aug 14 2017, 13:41:13) [MSC v.1900 64 bit (AMD64)] on win32 Microsoft Excel, Office 365. Prism 8 for windows v8.04 Custom image analysis code described fully in methods section and available as supplementary file and at https://github.com/ReaAntKour/NTL8TemperatureGrowth/. (Fiji Is Just)Image J: ImageJ 1.52i, Wayne Rasband, National Institutes of Health, USA, http://imagej.nih.gov/ij, Java 1.8.0_66(64-bit)

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

Quantitative source data for figures and full scanned images of western blots are provided with the paper. Raw images that support the findings of this study are available at doi: 10.6084/m9.figshare.12283970. Code is available as a supplementary file and at https://github.com/ReaAntKour/NTL8TemperatureGrowth/

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	No statistical approach was used to predetermine sample size. Sample sizes were determined based on previous publications on similar experiments. The determined sample size was adequate as the differences between experimental groups was significant and reproducible.
Data exclusions	Following the automatic image analysis pipeline, the processed images were manually curated to exclude failed results. The exclusion criterion was based on this processing, and images where the signal appeared in the wrong part or was missed by the algorithm were excluded from further analysis. A total of 23 images out of 629 were excluded using this process. No other data exclusion was performed.
Replication	All key experimental findings were reproduced in several independent biological repeats with multiple technical replicates. The number of repeats is indicated in the figure legends. Main Conclusions were confirmed in different assays (genetic assays including forward genetics with multiple allelic mutations and confirmation by transgenics, Immunoblot assay with transgenics carrying two different tags, bioimaging with different microscopies, and computational simulation).
Randomization	Multiple, randomly selected plants from a plate were collected for each replicate. Given the small nature of the experiments, different treatments were carried out in parallel, with minimum covarying factors, and therefore further randomisation of plates was not performed
Blinding	Blinding was not necessary for the molecular biology techniques, where bias could not be introduced as samples were treated together and identically. For imaging, the same settings were used for all comparisons and the results were consistent with the automatically analysed data.

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

Antibodies

Antibodies used	anti-HA-peroxidase, Roche, catalog number 12013819001, clone number HA (3F10), dilution 1:4000 anti-GFP, Roche, catalog number11814460001, mixed clone of 7.1 and 13.1, LOT19958500, dilution 1:4000 anti-HA-TAG, cell signaling technology, catalog number 3724s, clone number c29f4, lot: 8 and 9, dilution 1:5000 ECLTM anti-mouse IgG, horsera dish peroxidase linked whole antibody (from sheep) GPR, 1ml, GE healthcare UK limited, catalog number NXA931V, lot14263051, dilution 1:40000

ECL TM anti-rabbit IgG, horsera dish peroxidase linked whole antibody (from donkey), 1ml, GE healthcare UK limited, catalog number NA934V, lot 16953209, dilution 1:40000
anti-MPK6, Sigma-Aldrich, catalog number A7104, dilution 1:6000

Validation

All antibodies are commercial. Validation statements and relevant citation of primary antibody are available from the manufacturers:
anti-HA-peroxidase, Roche, catalog number 12013819001, clone number HA (3F10): https://www.sigmaaldrich.com/catalog/product/roche/12013819001?lang=en&region=GB;
anti-GFP, Roche, catalog number11814460001: https://www.sigmaaldrich.com/catalog/product/roche/11814460001?lang=en&region=GB; also validated in Fig.2a in the manuscript, where the negative control Col-0 shows no band.
anti-HA-TAG, cell signaling technology, catalog number 3724s, clone number c29f4: https://www.cellsignal.com/products/primary-antibodies/ha-tag-c29f4-rabbit-mab/3724; also validated in the western shown in Fig.2d&e (lane excluded from main figure, shown in source data) with Col-0 negative control.
anti-MPK6, Sigma-Aldrich, catalog number A7104: https://www.sigmaaldrich.com/catalog/product/sigma/a7104?lang=en&region=GB