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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	1) Bacterial DNA was extracted from rhizosphere soil with an E.Z.N.A.® Soil DNA Kit (Omega Bio-tek, Norcross, GA, United States) and was analyzed using the MiSeq platform (Illumina, San Diego, United States) to sequence the V3-V4 region of the 16S rRNA gene. 2) Root exudate solution mentioned in Section 4.3.1 were freeze-dried, weighed, redissolved in 2.5 mL of an aqueous solution of 80% methanol, vortexed 15 min, and centrifuged at 12,000 × g for 15 min17. The final supernatant was analyzed by LC-QTOF/MS (Shimadzu LC-20A HPLC coupled with a Sciex TripleTOF 5600+). Mass spectrometry was performed using electrospray in both positive and negative ionization modes. An XSelect HSS T3 column (4.6 × 150 mm, 3.5 μm; Waters Corporation) was used for chromatographic separation. 3) Plant tissues and rhizosphere soil was extracted with 4 mL of an aqueous solution of 80% methanol, vortexed 15 min, and centrifuged at 12,000 × g for 15 min. The final supernatant was analyzed by LC-QTOF/MS and the equipment conditions are described in Section 4.3.3. 4) Quantitative Reverse Transcription-Polymerase Chain Reaction (qRT-PCR) was used to determine the relative expression of BrRBOH genes, including BrRBOH01 and BrRBOH03 ~ BrRBOH14, in plant tissues. The GeneJET Plant RNA Purification Kit (Thermo Fisher Scientific) was used to extract total RNA from plant roots. Reverse transcription was performed using SynScript® Ⅲ RT SuperMix (Tsingke Biotechnology, Beijing, China) to obtain cDNA. Then the cDNA was used as templates to perform PCR analysis using a QuantStudio stepone Plus (ABI, Thermo, United States) and the ArtiCanCEO SYBR qPCR Mix (Tsingke Biotechnology, Beijing, China) under the following conditions: initial denaturation at 95°C for 5 min, followed by 40 cycles of 95°C for 15 s, 60°C for 20 s, and 72°C for 20 s. The relative expression of each gene was normalized based on the abundance of internal standard gene BrActin. The primer sequences are listed in Table S5.
Data analysis	1) The operational taxonomic units (OTUs) were then clustered using UPARSE software, with a cutoff value of 97% similarity. Taxonomy assignment of OTUs was analyzed with the RDP classifier (http://rdp.cme.msu.edu/) against the Silva (SSU123) 16S rRNA database using a confidence threshold of 70%. Shannon diversity and PCoA based on Bray–Curtis distances were calculated at the OTU level. Linear discriminant analysis effect size (LEfSe) with Wilcoxon rank-sum test was used to compare genera between the organic pollutants and control groups, with taxa considered significantly different only when $P < 0.05$ and LDA effect size > |2.5|.

2) For metabolomics, the information about MS peaks, MS matrix, MS/MS spectra, and retention times was collected from the raw LC-QTOF/MS data using MS-DIAL software. Peak identification was performed by calculating the similarity of the retention time, mass accuracy and MS/MS profile against publicly available databases, and confirmed with chemical standards where applicable. PCA was performed based on MS matrix. Metabolites with significant changes were confirmed by Student's t test with a P-value < 0.05 and partial least squares discriminant analysis with a VIP value > 1.
3) The MS-FINDER software was used to identify pollutant intermediates based on MS and MS/MS spectra68.

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

The 16S rRNA gene sequencing data are available in the NCBI SRA under BioProject PRJNA1290846 [https://www.ncbi.nlm.nih.gov/bioproject/PRJNA1290846]. The metabonomics raw data are available in the figshare database [https://doi.org/10.6084/m9.figshare.30000316.v1]. Source data are provided with this paper.

Research involving human participants, their data, or biological material

Policy information about studies with human participants or human data. See also policy information about sex, gender (identity/presentation), and sexual orientation and race, ethnicity and racism.

Reporting on sex and gender	N/A
Reporting on race, ethnicity, or other socially relevant groupings	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 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 specific statistical methods were used to determine sample size for the experiments. Minimum of 3 biological experiment were performed.
Data exclusions	No data were excluded from the analyses.
Replication	qRT-PCR contained 3 replicates and other pot experiment contained 5 replicates.
Randomization	Randomization was not relevant in this study.
Blinding	Blinding was not relevant in this study.

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
☒	☐ Clinical data
☒	☐ Dual use research of concern
☐	☒ Plants

Methods

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

Dual use research of concern

Policy information about dual use research of concern

Hazards

Could the accidental, deliberate or reckless misuse of agents or technologies generated in the work, or the application of information presented in the manuscript, pose a threat to:

No	Yes
☒	☐ Public health
☒	☐ National security
☒	☐ Crops and/or livestock
☒	☐ Ecosystems
☒	☐ Any other significant area

Experiments of concern

Does the work involve any of these experiments of concern:

No	Yes
☒	☐ Demonstrate how to render a vaccine ineffective
☒	☐ Confer resistance to therapeutically useful antibiotics or antiviral agents
☒	☐ Enhance the virulence of a pathogen or render a nonpathogen virulent
☒	☐ Increase transmissibility of a pathogen
☒	☐ Alter the host range of a pathogen
☒	☐ Enable evasion of diagnostic/detection modalities
☒	☐ Enable the weaponization of a biological agent or toxin
☒	☐ Any other potentially harmful combination of experiments and agents

Plants

Seed stocks	The seeds of Brassica rapa were provided by Jiangsu Academy of Agricultural Sciences.
Novel plant genotypes	N/A
Authentication	N/A