

Supplement

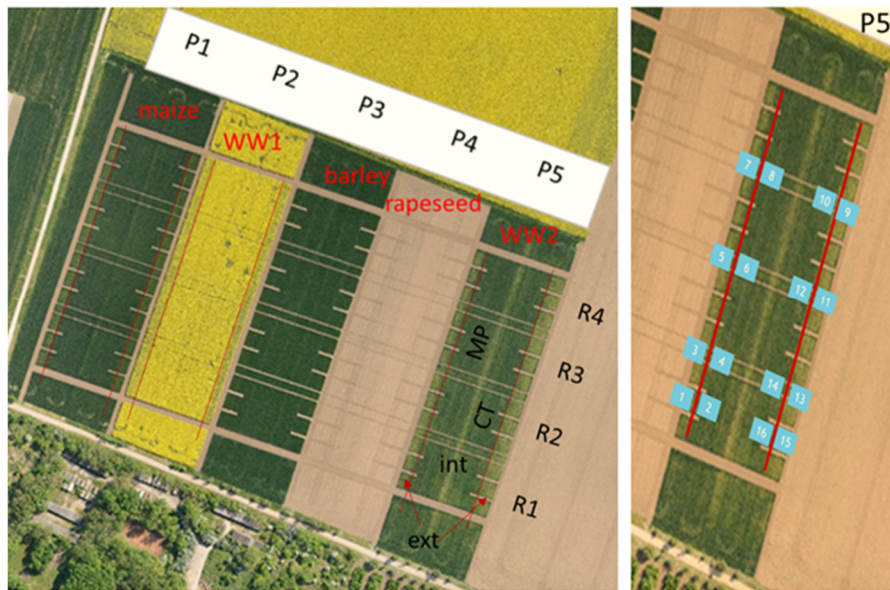
Long-term conservation tillage with reduced nitrogen fertilization intensity can improve winter wheat health via positive plant-microorganism feedback in the rhizosphere

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12 **Supplement Text 1:** Detailed field work calendar for cultivation of winter wheat after
13 rapeseed in the long-term field trial Bernburg, growing season 2018/2019. MP-
14 mouldboard plough tillage, CT- cultivator tillage, Ext- extensive N-fertilization intensity
15 without fungicides and growth regulators, Int- intensive N-fertilization intensity with
16 pesticides and growth regulators.

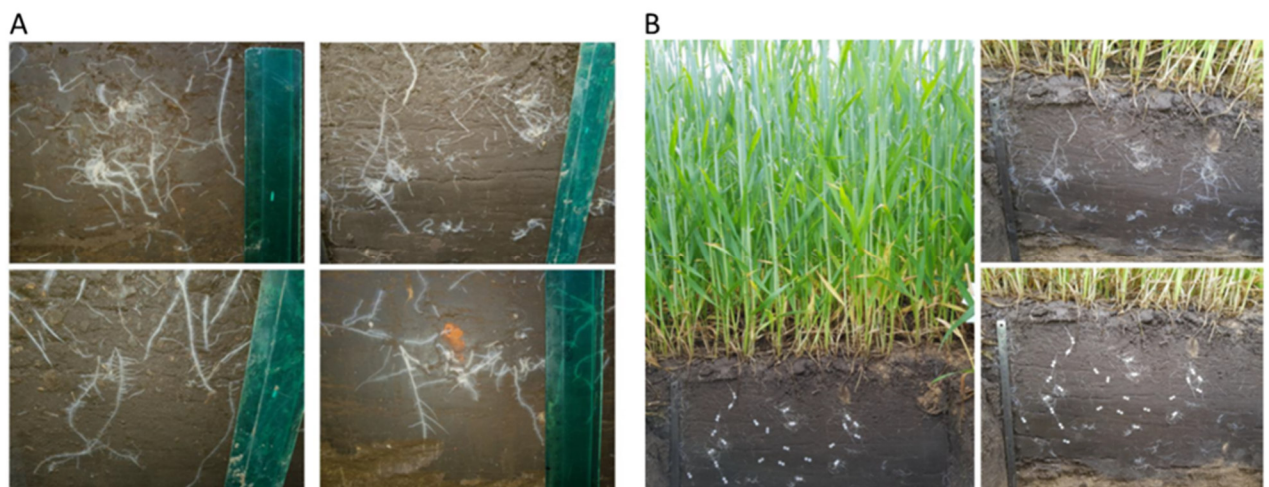
| | | |
|----|----------------------|--|
| 17 | 09 July 2018 | mulcher |
| 18 | 08 August 2018 | disc harrow |
| 19 | 16 August 2018 | basic fertilizer |
| 20 | 09 October 2018 | MP tilled |
| 21 | 09 October 2018 | CT: 2x heavy cultivator |
| 22 | 09 October 2018 | light cultivator |
| 23 | 10 October 2018 | sowing with Amazone 300 seeds m ⁻² |
| 24 | 20 October 2018 | MP: emergence of plants |
| 25 | 21 October 2018 | CT: emergence of plants |
| 26 | 26 October 2018 | milled in |
| 27 | 16 November 2018 | plants counted |
| 28 | 21 February 2019 | soil sampling for Nmin |
| 29 | 26 February 2019 | herbicide treatment 70 g ha ⁻¹ Biathlon HD + 1.0 L ha ⁻¹ Dash + |
| 30 | | 20 g ha ⁻¹ Dirigent |
| 31 | 07 March 2019 | 1 st Nitrogen fertilization: Int 60 kg N ha ⁻¹ Domogran 45, Ext 30 kg |
| 32 | | N ha ⁻¹ Domogran 45 |
| 33 | 08 April 2019 | Int: growth regulators 1.0 L ha ⁻¹ CCC ₇₂₀ |
| 34 | 09 April 2019 | Root window installation |
| 35 | 15 April 2019 | 2 nd Nitrogen fertilization: Int 70 kg N ha ⁻¹ HS, Ext 30 kg N ha ⁻¹ HS |
| 36 | 08 May 2019 | Int: fungicide treatment 1.0 L ha ⁻¹ Priaxor + 1.0 L ha ⁻¹ Osiris |
| 37 | 21 May 2019 | Root window sampling |
| 38 | 23 May 2019 | Int: 3 rd Nitrogen fertilization 40 kg N ha ⁻¹ KAS |
| 39 | 04 June 2019 | Int: 0.5 L ha ⁻¹ Taspa +0.5 L ha ⁻¹ Folicur + 0.075 L ha ⁻¹ Karate |
| 40 | | Zeon |
| 41 | 23 July 2019 | harvest |
| 42 | 26 July 2019 | soil sampling for Nmin |

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45 **Figure S1.** Aerial view on the long-term field trial Bernburg (left) and installation
 46 positions of root windows in winter wheat 2 (cv. Lemmy) grown under cultivator tillage
 47 (CT) or mouldboard plough (MP) with either intensive (Int) or extensive N-fertilization
 48 intensity (Ext), (Source: Anhalt University of Applied Sciences).



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50 **Figure S2.** A) Root development of winter wheat (cv. Lemmy) along the root window
 51 42 days after installation (EC 59). B) Sorption filter sampling.

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Table S1. List of wheat (*Triticum aestivum*) genes selected for qRT-PCR analysis, their corresponding primer pairs, amplification efficiency (AE, calculated from amplification curve) and references.

| Gene | Forward P (5' to 3') Reverse P (5' to 3') | AE (%) | Reference |
|---|--|--------|------------------------------|
| <i>TaUBI</i> Q (Ubiquitin) | CCTTCACTTGGTTCTCCGTCT AACGACCAGGACGACAGACACA | 91.64 | Cruz et al. 2015 |
| <i>TaEF1α</i> (Elongation factor 1 α) | ATGATTCCCAACCAAGCCCAT ACACCAACAGCCACAGTTTGC | 96.20 | Cruz et al. 2015 |
| <i>TaPR1</i> (β -1,3-glucanase HQ848391) | CAATAACCTCGGCGTCTTCATCAC TTATTTACTCGCTCGGTCCCTCTG | 97.87 | Casassola et al. 2015 |
| <i>TaLOX</i> (Lipoxygenase) | CGACCCGCAGCTGTTGA CCCTTGATCGGAGGTGTT | 94.75 | Cruz et al. 2015 |
| <i>Tad1</i> (AB089942 Defensin) | GCAGAGCCACAAGTTCAAGG GTCCGCTTGCACTAGCACTT | 93.49 | This study |
| <i>TaAOS</i> (Allene Oxide Synthase) | ACCGTGTTCAACAGCTACGG AGCGCCTCTATCGTCACCTT | 97.87 | Wang et al. 2017 |
| <i>TaCHI</i> (Chitinase) | CTGGACCTGGACTTCGACAC CGCTTGAGCACGGGTTAAT | 94.34 | Cruz et al. 2015 |
| <i>TaSOD</i> (JQ613154.1 Superoxide Dismutase) | CATTGTCGATAGCCAGATTCTTT AGTCTTCCACCAGCATTTCCAGTA | 98.96 | Zhang et al. 2016 |
| <i>TaCAT</i> (GU984379.1 Catalase) | TTTGATGGGAGTCTTGTGCTTGTG ACGGTGAGGGAGTTGTGCTTGTT | 94.74 | Zhang et al. 2016 |
| <i>TaPOX</i> (Peroxidase X53675.1) | CAGCCCTGTAGCCAACATAAA GCACTTCCACGACTGCTTTG | 96.28 | Zhang et al., 2016 |
| <i>TaRubiscoSSU</i> (ribulose biphosphate carboxylase/oxygenase small subunit on Chr5) | GGTGGAGGAGGTCAAGAAGGAG MGTCGTGAGTGAGCTGTTTAGGC | 92.11 | Buchner and Hawkesford, 2014 |
| <i>TaPIE1</i> (EF583940) (ERF transcription factor) | GGAGCCACCAGTCCGTATGA CACCCGGCAGAGGTATTCAA | 92.03 | Zhu et al. 2014 |
| <i>TaGSTU4</i> (Glutathione-S- transferase 4) | TTCAAGCATCCAACCTCTCC GCTGTCACATCCATCCAAAA | 97.88 | This study |
| <i>TaGSTZ</i> (Glutathione-S- transferase) | CCAAGCCCATTGTTACCAG GTGGATGAGCACGGGTATCT | 90.37 | This study |
| <i>TaPIMP2</i> - (MYB Transcription Factor) | GCATTGTACGGCCAGTTTCG CGAGGAGGCTCTGTTCTTGG | 93.72 | Wei et al. 2017b |
| <i>TaMYB80</i> (MYB Transcription Factor 80) | CAGATGCTCCTCCCTTGG GTGATCCTGGTGTAGTTGC | 91.15 | Zhao et al. 2017 |
| <i>TaODORANT1</i> (MYB Transcription Factor) | CCGAAGCCCATGTACCTCC CGGATCTATGATCGGTCTATGTG | 103.99 | Wei et al, 2017a |
| <i>TaWRKY49</i> (WRKY transcription factor) | CTTCCCTGCCGCATTCT ACGCTCTCGCCCTAGTG | 95.4 | Wang et al. 2017 |
| <i>TaWRKY62</i> (WRKY transcription factor) | TCGTTGACCACCACCAG AGCCGTCCCCAAATCCA | 91.22 | Wang et al. 2017 |
| <i>TaNIR1</i> (Nitrate Reductase) | GGCCAATTCTTCATCTCCTTCTG TACRTSCACAGATTGATGCGTCSA | 92.06 | Buchner and Hawkesford 2014 |
| <i>TaNIR</i> (Nitrite reductase) | ACGAGGAGTAGGCCGGCTASGAG ATCAGCCGCAGCCCATCTCTRC | 90.47 | Buchner and Hawkesford 2014 |

| | | | |
|--|---|--------|-----------------------------|
| <i>TaNPF7.1</i> (nitrate transporter/Peptide transporter family) | CTACAAGACCTGCGCCATCTTC GATGAGGTATAGCCGCGAGGAG | 91.60 | Buchner and Hawkesford 2014 |
| <i>TaGDH2</i> (Glutamate dehydrogenase 2) | AGGATGGGAGCATTACCTTGG GGATATAAGAACTKTCATCCACCACG | 94.56 | Buchner and Hawkesford 2014 |
| <i>TaVIT2</i> (Iron transporter) | CTCCCCCTACATGTTTCGT CCCTTGACGTAGCCGAA | 95.07 | Connorton et al. 2017 |
| <i>TaMPK3</i> (Mitogen activated Protein Kinase 3) | GGAGATCAAGCTCCTCAGGC ACTGGCAGTGTTCTTCCGAG | 90.99 | Goyal et al. 2018 |
| <i>TaMPK4</i> (Mitogen activated Protein Kinase) | TCGAGCCTGGGATTTCTTCG GTCAACAGTGATGCGTCTGC | 91.56 | Goyal et al. 2018 |
| <i>TaMPK6</i> (Mitogen activated Protein Kinase) | CAGCTTATCTCCGAGGAAAACG TTGTGCCGCACTAGTTGGA | 94.18 | Goyal et al. 2018 |
| <i>TaMKK6</i> (Mitogen activated Protein Kinase Kinase) | CAGCTTATCTCCGAGGAAAACG TTGTGCCGCACTAGTTGGA | 92.16 | Goyal et al. 2018 |
| <i>TaMKK10-1/3a</i> (Mitogen activated Protein Kinase Kinase) | CTCAAGGTCCAGCACTACGG CCACCAGCTCGAGGAGTAGA | 91.78 | Goyal et al. 2018 |
| <i>TaMKK10-1/3b</i> (Mitogen activated Protein Kinase Kinase) | CCAGGGCCCTATGATCCGTA TTGCCGAAGAAGATAGCGCA | 100.07 | Goyal et al. 2018 |

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62 patterns of members of the NITRATE TRANSPORTER 1/PEPTIDE TRANSPORTER
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89 *Trichoderma longibrachiatum* T6 enhances tolerance of wheat to salt stress through
90 improvement of antioxidative defense system and gene expression. *Frontiers in plant*
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92 Zhao, Y., Tian, X., Wang, F., Zhang, L., Xin, M., Hu, Z., Yao, Y., Ni, Z., Sun, Q. and
93 Peng, H., 2017. Characterization of wheat MYB genes responsive to high
94 temperatures. *BMC plant biology*, 17(1), pp.1-14.

95 Zhu, X., Qi, L., Liu, X., Cai, S., Xu, H., Huang, R., Li, J., Wei, X. and Zhang, Z., 2014.
96 The wheat ethylene response factor transcription factor pathogen-induced ERF1
97 mediates host responses to both the necrotrophic pathogen *Rhizoctonia cerealis* and
98 freezing stresses. *Plant physiology*, 164(3), pp.1499-1514.

99 **Table S2.** HPLC conditions for determination of phenolic compounds in rhizosphere
100 soil solutions.

| UHPLC-MS (identification) | RP-HPLC (quantitative analysis with known standards) |
|---|--|
| <p><u>HPLC System:</u> Agilent 1290 Ultra Performance Liquid Chromatography System with QExactive Plus Electrospray Mass Spectrometer (Thermo Fisher Scientific)</p> <p><u>Column:</u> Eclipse Plus C18, 1.8 μm 2.2 x 50 mm column (Agilent)</p> <p><u>Eluent:</u> 0.2% formic acid (solvent A); 0.2% formic acid in acetonitrile (solvent B)</p> <p><u>Gradient elution:</u> 0 - 1.5 min: 0% B; 1.5 - 7 min: 0 - 15% B; 7-19 min: 15 - 75% B; 19 - 22 min 75 - 100% B; 22 - 22.1 min: 100 - 0% B; 22.1 - 23.1 min: 0% B.</p> <p><u>Flow rate:</u> 0.3 mL min⁻¹</p> <p><u>Column temperature:</u> 40°C</p> <p><u>Detection:</u> MS parameters: ESI positive/negative, HESI Source, Capillary Temp 360°C, Sheath gas 60, Aux gas 20, Probe Heater 380°C, resolution 70.000, NCE 20,60,110.</p> | <p><u>HPLC System:</u> Shimadzu LC10</p> <p><u>Column:</u> GROM-SIL 120 ODS ST, 5 μm, 290 x 4.6 mm + 20 x 4.6 mm guard column (Grom, Herrenberg, Germany)</p> <p><u>Eluent:</u> 18 mM KH₂PO₄ (pH 2.49) (solvent A); methanol (solvent B)</p> <p><u>Gradient elution:</u> 0 - 32 min: 0 - 25% B; 32 - 33 min: 25 - 50% B; 33 - 45 min: 50 - 55% B; 45 - 50 min: 55 - 100% B; 50 - 60 min: 100% B; 60 - 70 min 100 - 0% B</p> <p><u>Flow rate:</u> 0.4 mL min⁻¹</p> <p><u>Column temperature:</u> 40°C</p> <p>Detection: UV 280 nm</p> |

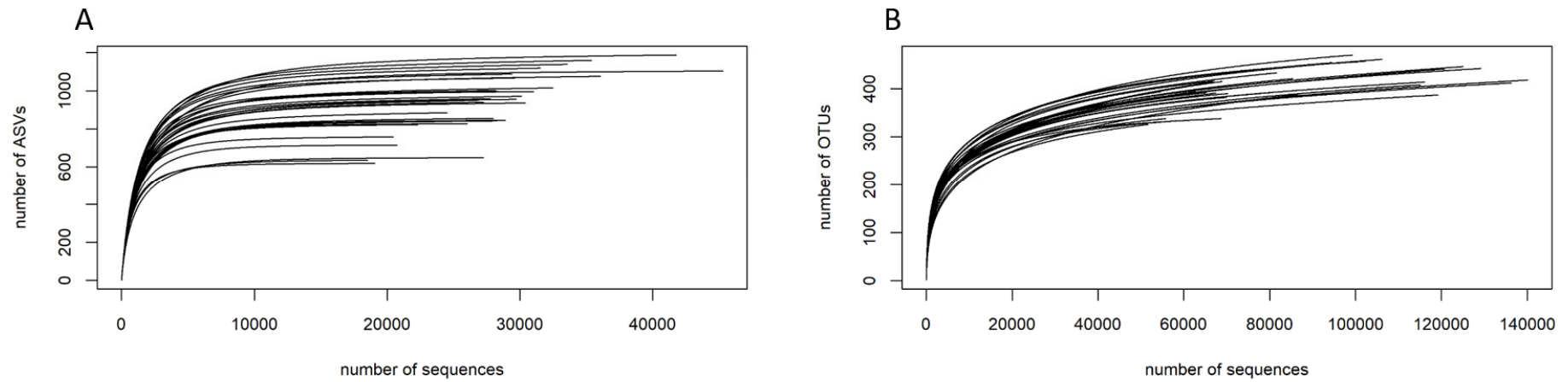
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107 **Figure S3.** Rarefaction curves for A) 16S rRNA gene and B) ITS amplicon sequencing. Since all curves reached saturation, sequencing
108 depth was sufficient to cover microbial diversity in rhizosphere and root-affected soil samples.

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Table S3. Overview of Illumina barcodes and ITS2 primer combinations for each sample in root-affected soil (RA) and the rhizosphere (RH). Data are available in the European Nucleotide Archive (ENA) under PRJEB67553. MP- mouldboard plough tillage, CT- cultivator tillage, Ext- extensive N-fertilization intensity without fungicides and growth regulators, Int- intensive N-fertilization intensity with pesticides and growth regulators.

| Run | | <u>Barcode</u> + Primer (forward) | <u>Barcode</u> + Primer (reverse) |
|--------------------------|---------------------|--|--|
| RA soil (ERR12207969) | RH (ERR12207970) | | |
| MP-Int-1 | MP-Int-1 | 5'- <u>CAGGACGT</u> GTGAATCATCGAATCTTTGAA-3' | 5'- <u>ATTACTCGT</u> CCCTCCGCTTATTGATATGC-3' |
| MP-Int-2 | MP-Int-2 | | 5'- <u>TCCGGAGAT</u> CCTCCGCTTATTGATATGC-3' |
| MP-Int-3 | MP-Int-3 | | 5'- <u>CGCTCATT</u> TCCTCCGCTTATTGATATGC-3' |
| MP-Int-4 | MP-Int-4 | | 5'- <u>GAGATTCCT</u> CCTCCGCTTATTGATATGC-3' |
| MP-Ext-1 | MP-Ext-1 | | 5'- <u>ATTCAGAA</u> TCCCTCCGCTTATTGATATGC-3' |
| MP-Ext-2 | MP-Ext-2 | | 5'- <u>GAATTCGT</u> TCCTCCGCTTATTGATATGC-3' |
| MP-Ext-3 | MP-Ext-3 | | 5'- <u>CTGAAGCT</u> TCCTCCGCTTATTGATATGC-3' |
| MP-Ext-4 | MP-Ext-4 | | 5'- <u>TAATGCGC</u> TCCTCCGCTTATTGATATGC-3' |
| CT-Int-1 | CT-Int-1 | 5'- <u>GTACTGACG</u> TGAATCATCGAATCTTTGAA-3' | 5'- <u>ATTACTCGT</u> CCCTCCGCTTATTGATATGC-3' |
| - | CT-Int-2 | | 5'- <u>TCCGGAGAT</u> CCTCCGCTTATTGATATGC-3' |
| CT-Int-3 | CT-Int-3 | | 5'- <u>CGCTCATT</u> TCCTCCGCTTATTGATATGC-3' |
| CT-Int-4 | CT-Int-4 | | 5'- <u>GAGATTCCT</u> CCTCCGCTTATTGATATGC-3' |
| CT-Ext-1 | CT-Ext-1 | | 5'- <u>ATTCAGAA</u> TCCCTCCGCTTATTGATATGC-3' |
| CT-Ext-2 | CT-Ext-2 | | 5'- <u>GAATTCGT</u> TCCTCCGCTTATTGATATGC-3' |
| CT-Ext-3 | CT-Ext-3 | | 5'- <u>CTGAAGCT</u> TCCTCCGCTTATTGATATGC-3' |
| CT-Ext-4 | CT-Ext-4 | | 5'- <u>TAATGCGC</u> TCCTCCGCTTATTGATATGC-3' |

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2 **Table S4.** List of plant-beneficial functions used to build the customized database
3 based on Kyoto Encyclopedia of Genes and Genomes (KEGG) Orthology database
4 (November 2022).

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See excel file.

Table S5. Statistical analysis of the nutrient status of winter wheat (cv. Lemmy, EC 59) grown at long-term field trial Bernburg with different tillage practices (CT, cultivator tillage; MP, mouldboard plough) and N-fertilization intensities (Int, intensive N-fertilization with pesticides and growth regulators; Ext, extensive N-fertilization without fungicides and growth regulators). *P*-values from two-way ANOVA showing the effect of tillage practice and N-fertilization intensity and their interactions on nutrient levels. For metabolites with a significant interaction effect ($p < 0.05$), the simple main effect was performed to test the effect of N-fertilization intensity (Fert.) at each tillage practice on metabolite level ($p < 0.025$).

| | Tillage | Fertilization | Tillage x Fertilization | Simple-main effect | |
|--------------------|---------|---------------|-------------------------|--------------------|----------|
| | | | | CT Fert. | MP Fert. |
| C _{total} | 0.330 | 0.065 | 0.029 | 0.008 | 0.755 |
| N _{total} | 0.100 | 0.003 | 0.028 | < 0.001 | 0.418 |
| P | 0.526 | 0.568 | 0.019 | 0.159 | 0.038 |
| K | 0.587 | 0.011 | 0.158 | - | - |
| Mg | 0.015 | < 0.001 | 0.205 | - | - |
| Ca | 0.003 | < 0.001 | 0.300 | - | - |
| S | < 0.001 | < 0.001 | 0.436 | - | - |
| Cu | 0.003 | 0.338 | 0.756 | - | - |
| Fe | 0.056 | 0.064 | 0.464 | - | - |
| Mn | 0.282 | 0.805 | 0.736 | - | - |
| Zn | 0.597 | 0.382 | 0.901 | - | - |

Table S6. Statistical analysis of metabolite levels of winter wheat (cv. Lemmy, EC 59) grown in the long-term field experiment Bernburg with different tillage practices (CT, cultivator tillage; MP, mouldboard plough) and N-fertilization intensities (Int- intensive N-fertilization with pesticides and growth regulators; Ext- extensive N-fertilization without fungicides and growth regulators). *P*-values from two-way ANOVA showing the effect of tillage practice and N-fertilization intensity and their interactions on shoot, apical and basal root exudates. For metabolites with a significant interaction effect ($p < 0.05$), the simple main effect was performed to test the effect of N-fertilization intensity (Fert.) at each tillage practice on metabolite level ($p < 0.025$).

| | | Tillage | Fertilization | Tillage x Fertilization | Simple-main effect | |
|-------------|----------------------|---------|---------------|-------------------------|--------------------|----------|
| | | | | | CT Fert. | MP Fert. |
| Shoot | Salicylic acid | < 0.001 | < 0.001 | 0.003 | < 0.001 | 0.118 |
| | Jasmonic acid | < 0.001 | < 0.001 | < 0.001 | < 0.001 | 0.173 |
| | Proline | < 0.001 | < 0.001 | 0.469 | - | - |
| | Phenol | < 0.001 | < 0.001 | < 0.001 | < 0.001 | 0.289 |
| | Ascorbate peroxidase | < 0.001 | 0.160 | 0.693 | - | - |
| | Total antioxidants | < 0.001 | 0.216 | 0.369 | - | - |
| Apical root | Tryptophan | < 0.001 | 0.431 | 0.469 | - | - |
| | Asparagin | < 0.001 | 0.899 | 0.322 | - | - |
| | Benzoic acid | < 0.001 | 0.007 | 0.026 | 0.628 | 0.002 |
| | Caffeic acid | 0.936 | 0.027 | 0.069 | - | - |
| | Catechin* | - | - | - | - | - |
| | Cinnamic acid | 0.622 | 0.043 | 0.082 | - | - |
| | MBOA | < 0.001 | 0.161 | 0.110 | - | - |
| | MeBOA | < 0.001 | 0.007 | 0.292 | - | - |
| | Morin | 0.189 | 0.017 | 0.462 | - | - |
| | Succinic acid | < 0.001 | 0.392 | 0.138 | - | - |
| | p-Coumaric acid | 0.022 | 0.543 | 0.180 | - | - |
| | Trehalose | < 0.001 | 0.015 | 0.032 | 0.003 | 0.778 |
| Basal root | Benzoic acid | 0.028 | 0.096 | 0.291 | - | - |
| | Caffeic acid | 0.020 | 0.827 | 0.064 | - | - |
| | Catechin* | - | - | - | - | - |
| | Cinnamic acid | < 0.001 | 0.380 | 0.540 | - | - |
| | MBOA | 0.048 | 0.076 | 0.368 | - | - |
| | MeBOA | 0.456 | 0.184 | 0.647 | - | - |
| | Morin | 0.814 | 0.205 | 0.088 | - | - |
| | p-Coumaric acid | < 0.001 | 0.482 | 0.482 | - | - |

*not statistically evaluable

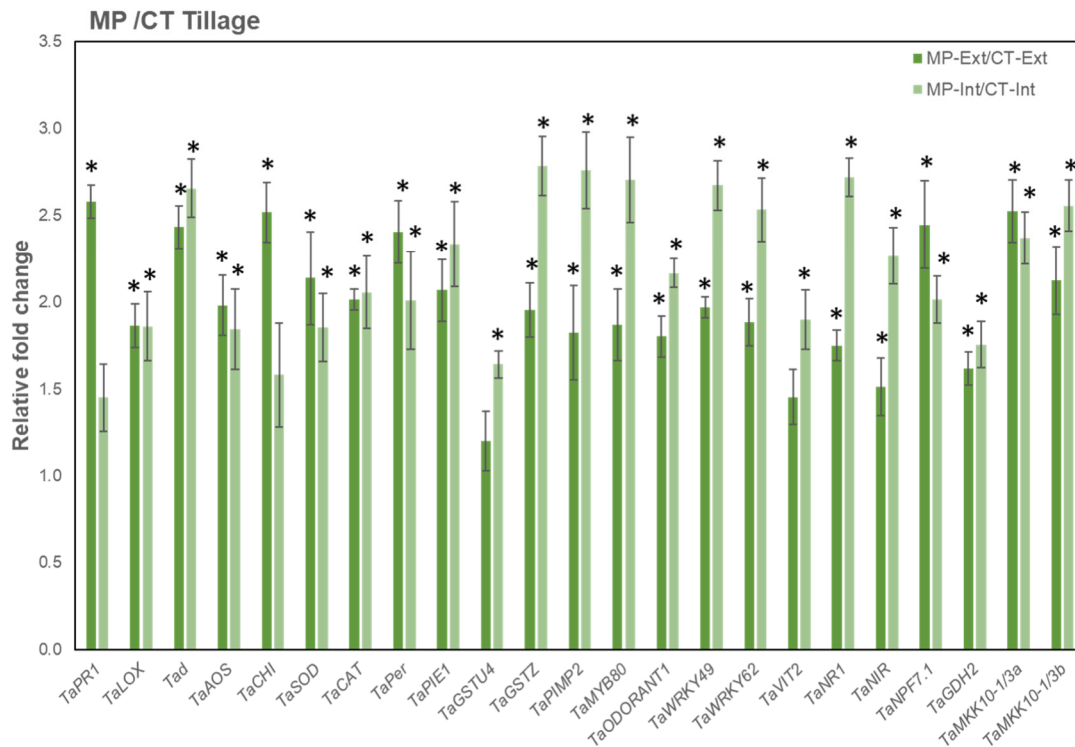


Figure S4. Log fold change in expression ($\Delta\Delta CT$) of genes (23 out of 28) showing significantly enhanced expression in winter wheat plants (cv. Lemmy, EC 59) from mouldboard plough (MP) soils compared to cultivator tillage (CT) soils. Ext- extensive N-fertilization intensity without fungicides and growth regulators, Int- intensive N-fertilization intensity with pesticides and growth regulators. Asterisk indicates significant difference in $\Delta\Delta CT$ according to pairwise Tukey HSD ($p < 0.05$). Error bars indicate standard error of mean ($n=4$).

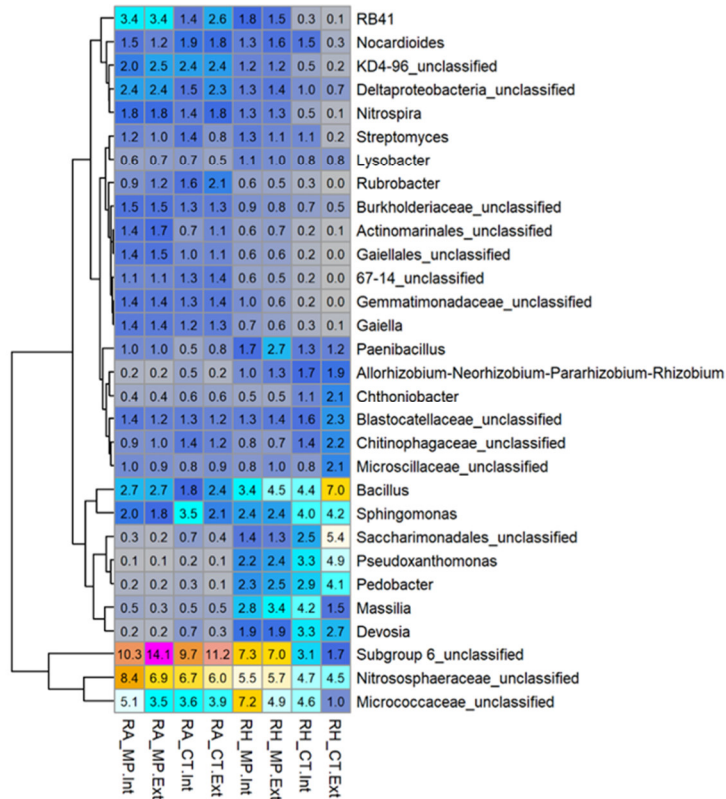
Table S7. Effects of different long-term agricultural practices on primary and secondary metabolites in rhizosphere soil solution of apical and basal roots and root-affected soil of winter wheat (cv. Lemmy; EC 59). MP- mouldboard plough tillage, CT- cultivator tillage, Ext- extensive N-fertilization intensity without fungicides and growth regulators, Int- intensive N-fertilization intensity with pesticides and growth regulators. Values of apical and basal root-soil solution are presented as means \pm standard deviation of four replicates. Root-affected soil solution values are shown as mean \pm standard deviation of two replicates. Means not sharing any letters are significantly different by the Tukey-test ($p \leq 0.05$). Metabolites below the detection threshold are not shown.

| | | Metabolites [nmol cm ⁻¹ root length] | | | | | | | |
|---|-------------|--|-------------|--------|--------------|--------|-------------|--------|--|
| | | MP-Int | | MP-Ext | | CT-Int | | CT-Ext | |
| Apical rhizosphere soil solution | | | | | | | | | |
| Asparagine | 3.74 ±0.21 | b | 3.82 ±0.13 | b | 6.31 ±0.14 | a | 6.24 ±0.08 | a | |
| Benzoic acid | 10.40 ±1.17 | a | 7.98 ±0.93 | b | 5.58 ±0.66 | c | 5.29 ±0.39 | c | |
| Caffeic acid | 6.70 ±0.37 | a | 5.78 ±0.51 | b | 6.28 ±0.40 | ab | 6.17 ±0.33 | ab | |
| Catechin* | 0.01 | - | 0.69 | - | 1.01 ±0.21 | - | 0.66 ±0.18 | - | |
| Cinnamic acid | 8.84 ±1.13 | a | 7.63 ±0.59 | b | 7.98 ±0.50 | ab | 7.86 ±0.35 | ab | |
| MBOA | 0.71 ±0.12 | b | 0.29 ±0.29 | b | 35.80 ±5.99 | a | 41.63 ±4.05 | a | |
| MeBOA | 10.66 ±0.75 | a | 9.13 ±0.62 | b | 3.43 ±1.00 | c | 2.67 ±0.04 | c | |
| Morin | 4.08 ±0.31 | ns | 3.53 ±0.31 | ns | 4.18 ±0.36 | ns | 3.87 ±0.26 | ns | |
| p-Coumaric acid | 6.17 ±0.98 | ns | 6.47 ±0.48 | ns | 7.70 ±0.97 | ns | 6.93 ±0.35 | ns | |
| Succinic acid | 1.11 ±0.14 | b | 1.33 ±0.13 | b | 1.88 ±0.22 | a | 1.82 ±0.22 | a | |
| Trehalose | 16.00 ±4.32 | c | 17.75 ±6.24 | c | 57.48 ±11.86 | b | 80.00 ±9.80 | a | |
| Tryptophan | 0.01 ±0.001 | b | 0.01 ±0.001 | b | 0.02 ±0.001 | a | 0.02 ±0.001 | a | |
| Basal rhizosphere soil solution | | | | | | | | | |
| Benzoic acid | 2.03 ±1.39 | ab | 1.63 ±1.29 | b | 4.09 ±1.02 | a | 2.42 ±0.74 | ab | |
| Caffeic acid | 0.66 ±0.45 | b | 0.97 ±0.26 | ab | 1.31 ±0.11 | a | 1.06 ±0.14 | ab | |
| Catechin* | 0.11 ±0.20 | - | 0.01 | - | 0.01 | - | 0.01 | - | |
| Cinnamic acid | 0.97 ±0.12 | bc | 0.95 ±0.08 | c | 1.24 ±0.04 | a | 1.16 ±0.11 | ab | |
| MBOA | 0.16 ±0.25 | ns | 0.44 ±0.29 | ns | 0.04 ±0.01 | ns | 0.13 ±0.10 | ns | |
| MeBOA | 1.76 ±0.45 | ns | 1.45 ±0.20 | ns | 1.81 ±0.24 | ns | 1.65 ±0.35 | ns | |
| Morin | 0.53 ±0.15 | ns | 0.83 ±0.23 | ns | 0.68 ±0.19 | ns | 0.63 ±0.19 | ns | |
| p-Coumaric acid | 0.74 ±0.10 | b | 0.74 ±0.06 | b | 0.97 ±0.04 | a | 0.91 ±0.09 | a | |
| Root affected soil solution | | | | | | | | | |
| Catechin* | 0.10 ±0.10 | - | 0.96 ±0.19 | - | 0.69 | - | 0.76 ±0.10 | - | |
| 2H-Benzoxazin* | 4.25 ±0.10 | - | 6.19 ±0.33 | - | 8.90 ±1.54 | - | 8.83 ±1.44 | - | |
| Cinnamic acid* | 1.51 ±0.27 | - | 1.88 ±0.52 | - | 1.23 ±0.17 | - | 1.59 ±0.69 | - | |

* not statistically evaluable

ns, no significant difference between treatments

A



B

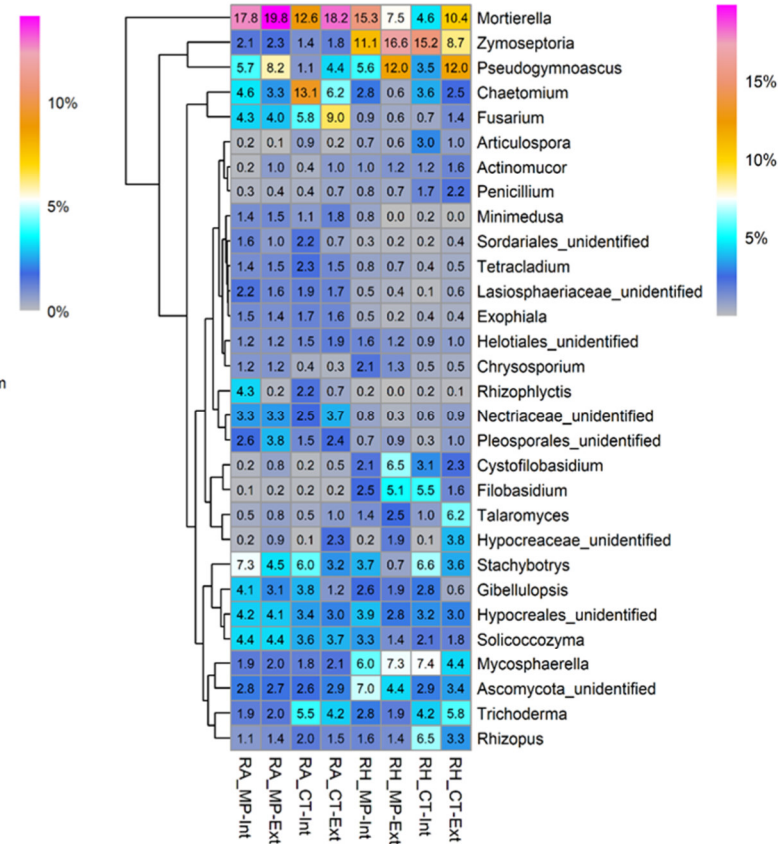


Figure S5. Heatmap showing the relative abundance distribution of the 30 most abundant A) bacterial and archaeal or B) fungal genera in root-affected soil (RA) and rhizosphere (RH) of winter wheat (cv. Lemmy, EC 59) grown in soil under different agricultural practices (MP- mouldboard plough; CT- cultivator tillage; Int- intensive N-fertilization intensity with pesticides and growth regulators; Ext- extensive N-fertilization intensity without fungicides and growth regulators). Numbers represent relative abundances.

Table S8. Bacterial and archaeal alpha-diversity in root-affected soil (RA) and rhizosphere (RH) of winter wheat (cv. Lemmy, EC 59). A) *P*-values from two-way ANOVA showing the effect of tillage practice (MP- mouldboard plough tillage, CT- cultivator tillage) and N-fertilization intensity (Ext- extensive N-fertilization without fungicides and growth regulators, Int- intensive N-fertilization with pesticides and growth regulators) and their interaction. B) Means \pm standard deviation. Different letters indicate significant differences between long-term agricultural practices according to two-way ANOVA followed by Tukey's Test. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.

| A) | | | | | | |
|---|----------------------|--------------------|-------------------|---------------------|-------------------|-------------------|
| Factors | RA | | | RH | | |
| | Richness | Shannon | Pielou | Richness | Shannon | Pielou |
| Tillage practice | 0.309 | 0.347 | <0.001*** | 0.212 | 0.159 | 0.674 |
| N-Fertilization Intensity | 0.001** | <0.001*** | 0.411 | 0.857 | 0.607 | 0.470 |
| Tillage practice \times N-Fertilization Intensity | 0.945 | 0.480 | 0.008** | 0.743 | 0.939 | 0.360 |
| B) | | | | | | |
| Treatments | RA | | | RH | | |
| | Richness | Shannon | Pielou | Richness | Shannon | Pielou |
| MP-Int | 910.1 \pm 51.8 b | 6.22 \pm 0.05 b | 0.91 \pm 0 c | 948.2 \pm 136.7 a | 6.19 \pm 0.08 a | 0.90 \pm 0.01 a |
| MP-Ext | 1073.1 \pm 79.1 a | 6.41 \pm 0.08 a | 0.92 \pm 0 bc | 904.9 \pm 184.7 a | 6.15 \pm 0.18 a | 0.91 \pm 0 a |
| CT-Int | 854.3 \pm 118.6 b | 6.27 \pm 0.09 ab | 0.93 \pm 0.01 a | 810.6 \pm 197.3 a | 6.06 \pm 0.1 a | 0.91 \pm 0.02 a |
| CT-Ext | 1022.7 \pm 44.2 ab | 6.41 \pm 0.04 a | 0.93 \pm 0 ab | 823.3 \pm 138.5 a | 6.00 \pm 0.29 a | 0.90 \pm 0.02 a |

Table S9. Fungal alpha-diversity in root-affected soil (RA) and rhizosphere (RH) of winter wheat (cv. Lemmy, EC 59). A) *P*-values from two-way-ANOVA showing the effect of tillage practice (MP- mouldboard plough tillage, CT- cultivator tillage) and N-fertilization intensity (Ext- extensive N-fertilization without fungicides and growth regulators, Int- intensive N-fertilization with pesticides and growth regulators) and their interaction. B) Means \pm standard deviation. Different letters indicate significant differences between long-term agricultural treatments by two-way ANOVA followed by Tukey's Test. If ANOVA assumptions failed, data were transformed by Tukey's Ladder of Power (\dagger). * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.

| A) Factors | RA | | | RH | | |
|--|---------------------|--------------------|--------------------|---------------------|-------------------|-------------------|
| | Richness | Shannon | Pielou | Richness | Shannon | Pielou |
| Tillage practice | 0.0096** | 0.9240 | 0.1197 | 0.0960 | 0.766 | 0.617 |
| N-Fertilization Intensity | 0.0570 | 0.0260* | 0.1785 | 0.0089** | 0.331 | 0.157 |
| Tillage practice \times N-Fertilization Intensity | 0.4540 | 0.0085** | 0.0138* | 0.1440 | 0.053 | 0.050 |
| B) Treatments | RA | | | RH | | |
| | Richness | Shannon | Pielou | Richness | Shannon | Pielou |
| MP-Int | 360.0 \pm 19.5 b | 4.18 \pm 0.06 ab | 0.71 \pm 0.01 a | 351.3 \pm 25.3 b | 4.05 \pm 0.22 a | 0.69 \pm 0.03 a |
| MP-Ext | 371.5 \pm 9.8 ab | 4.17 \pm 0.09 ab | 0.70 \pm 0.02 ab | 368.5 \pm 18.3 ab | 3.64 \pm 0.39 a | 0.62 \pm 0.06 a |
| CT-Int | 382.3 \pm 33.5 ab | 4.07 \pm 0.06 b | 0.69 \pm 0.01 b | 353.3 \pm 27.1 b | 3.74 \pm 0.17 a | 0.64 \pm 0.02 a |
| CT-Ext | 409.0 \pm 8.2 a | 4.27 \pm 0.03 a | 0.71 \pm 0 a | 391.3 \pm 5.0 a | 3.88 \pm 0.20 a | 0.65 \pm 0.03 a |

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52 **Table S10.** Bacterial/Archaeal species (ASV) with differential relative abundance in the rhizosphere of winter wheat (cv. Lemmy, EC 59)
53 grown in soil under MP- mouldboard plough tillage and CT- cultivator tillage practice (FDR<0.05). Only discriminative species with mean
54 >0.1% are displayed. Significantly enriched taxa are marked in bold. Mean \pm standard deviation is shown (n=8).

| Phylum | Class | Order | Family | Genus | ASV | MP | CT |
|----------------|-----------------------------|--|--|--|----------|---------------------------------|---------------|
| Acidobacteria | Blastocatellia (Subgroup 4) | Pyrinomonadales | <i>Pyrinomonadaceae</i> | <i>RB41</i> | ASV28818 | 0.2 \pm 0.1 | 0 \pm 0 |
| Acidobacteria | Subgroup 6 | Subgroup 6_unclassified | <i>Subgroup 6_unclassified</i> | <i>Subgroup 6_unclassified</i> | ASV31872 | 0.2 \pm 0 | 0 \pm 0 |
| Acidobacteria | Subgroup 6 | uncultivated soil bacterium clone C028 | <i>uncultivated soil bacterium clone C028_unclassified</i> | <i>uncultivated soil bacterium clone C028_unclassified</i> | ASV6835 | 0.2 \pm 0.1 | 0 \pm 0 |
| Acidobacteria | Blastocatellia (Subgroup 4) | Pyrinomonadales | <i>Pyrinomonadaceae</i> | <i>RB41</i> | ASV36824 | 0.1 \pm 0.1 | 0 \pm 0 |
| Acidobacteria | Subgroup 6 | Subgroup 6_unclassified | <i>Subgroup 6_unclassified</i> | <i>Subgroup 6_unclassified</i> | ASV17915 | 0.1 \pm 0.1 | 0 \pm 0 |
| Acidobacteria | Blastocatellia (Subgroup 4) | Pyrinomonadales | <i>Pyrinomonadaceae</i> | <i>RB41</i> | ASV4136 | 0.5 \pm 0.2 | 0 \pm 0.1 |
| Acidobacteria | Subgroup 6 | Subgroup 6_unclassified | <i>Subgroup 6_unclassified</i> | <i>Subgroup 6_unclassified</i> | ASV47414 | 0.3 \pm 0.1 | 0 \pm 0.1 |
| Acidobacteria | Subgroup 6 | uncultured bacterium gp6 | <i>uncultured bacterium gp6_unclassified</i> | <i>uncultured bacterium gp6_unclassified</i> | ASV19064 | 0.1 \pm 0 | 0 \pm 0 |
| Actinobacteria | Actinobacteria | Micrococcales | <i>Micrococcaceae</i> | <i>Micrococcaceae_unclassified</i> | ASV49496 | 2.3 \pm 0.8 | 0.9 \pm 0.7 |
| Actinobacteria | Actinobacteria | Micrococcales | <i>Microbacteriaceae</i> | <i>Agromyces</i> | ASV660 | 0.7 \pm 0.1 | 0.2 \pm 0.2 |
| Actinobacteria | Actinobacteria | Micrococcales | <i>Micrococcaceae</i> | <i>Micrococcaceae_unclassified</i> | ASV16162 | 0.5 \pm 0.2 | 0 \pm 0.1 |
| Actinobacteria | Actinobacteria | Streptomycetales | <i>Streptomycetaceae</i> | <i>Streptomyces</i> | ASV43643 | 0.1 \pm 0.1 | 0 \pm 0 |
| Actinobacteria | Actinobacteria | Frankiales | <i>Geodermatophilaceae</i> | <i>Blastococcus</i> | ASV8669 | 0.1 \pm 0.1 | 0 \pm 0 |
| Actinobacteria | Actinobacteria | Micromonosporales | <i>Micromonosporaceae</i> | <i>Catellatospora</i> | ASV46965 | 0.1 \pm 0 | 0 \pm 0 |
| Actinobacteria | Acidimicrobiia | Actinomarinales | <i>Actinomarinales_unclassified</i> | <i>Actinomarinales_unclassified</i> | ASV45546 | 0.1 \pm 0.1 | 0 \pm 0 |
| Bacteroidetes | Bacteroidia | Chitinophagales | <i>Chitinophagaceae</i> | <i>Terrimonas</i> | ASV11972 | 0.7 \pm 0.2 | 0.4 \pm 0.2 |
| Bacteroidetes | Bacteroidia | Sphingobacteriales | <i>Sphingobacteriaceae</i> | <i>Pedobacter</i> | ASV24586 | 0.3 \pm 0.2 | 0 \pm 0.1 |
| Bacteroidetes | Bacteroidia | Flavobacteriales | <i>Flavobacteriaceae</i> | <i>Flavobacterium</i> | ASV31878 | 0.1 \pm 0.1 | 0 \pm 0 |
| Chloroflexi | KD4-96 | KD4-96_unclassified | <i>KD4-96_unclassified</i> | <i>KD4-96_unclassified</i> | ASV19302 | 0.2 \pm 0 | 0 \pm 0 |
| Chloroflexi | Dehalococcoidia | S085 | <i>S085_unclassified</i> | <i>S085_unclassified</i> | ASV6612 | 0.1 \pm 0.1 | 0 \pm 0 |
| Chloroflexi | KD4-96 | KD4-96_unclassified | <i>KD4-96_unclassified</i> | <i>KD4-96_unclassified</i> | ASV34550 | 0.1 \pm 0.2 | 0 \pm 0 |
| Firmicutes | Bacilli | Bacillales | <i>Paenibacillaceae</i> | <i>Paenibacillus</i> | ASV2746 | 0.4 \pm 0.1 | 0.2 \pm 0.1 |
| Firmicutes | Bacilli | Bacillales | <i>Paenibacillaceae</i> | <i>Cohnella</i> | ASV41641 | 0.2 \pm 0.1 | 0.1 \pm 0 |
| Nitrospirae | Nitrospira | Nitrospirales | <i>Nitrospiraceae</i> | <i>Nitrospira</i> | ASV33194 | 0.6 \pm 0.1 | 0.2 \pm 0.2 |
| Nitrospirae | Nitrospira | Nitrospirales | <i>Nitrospiraceae</i> | <i>Nitrospira</i> | ASV35563 | 0.5 \pm 0.1 | 0 \pm 0.1 |

| | | | | | | | |
|-----------------|-----------------------------|-----------------------|---------------------------------------|--|----------|------------------|------------------|
| Patescibacteria | Saccharimonadia | Saccharimonadales | <i>Saccharimonadaceae</i> | <i>Saccharimonadaceae_unclassified</i> | ASV10175 | 0.3 ± 0.1 | 0 ± 0.1 |
| Patescibacteria | Saccharimonadia | Saccharimonadales | <i>Saccharimonadales_unclassified</i> | <i>Saccharimonadales_unclassified</i> | ASV9848 | 0.1 ± 0.1 | 0 ± 0 |
| Proteobacteria | Gammaproteobacteria | Betaproteobacteriales | <i>Burkholderiaceae</i> | <i>Massilia</i> | ASV41323 | 0.2 ± 0.2 | 0 ± 0 |
| Proteobacteria | Gammaproteobacteria | Xanthomonadales | <i>Xanthomonadaceae</i> | <i>Lysobacter</i> | ASV37269 | 0.1 ± 0.1 | 0 ± 0 |
| Proteobacteria | Gammaproteobacteria | Betaproteobacteriales | <i>Nitrosomonadaceae</i> | <i>MND1</i> | ASV4972 | 0.1 ± 0 | 0 ± 0 |
| Thaumarchaeota | Nitrososphaeria | Nitrososphaerales | <i>Nitrososphaeraceae</i> | <i>Nitrososphaeraceae_unclassified</i> | ASV42131 | 1.4 ± 0.5 | 1 ± 0.3 |
| Thaumarchaeota | Nitrososphaeria | Nitrososphaerales | <i>Nitrososphaeraceae</i> | <i>Nitrososphaeraceae_unclassified</i> | ASV35975 | 0.4 ± 0.1 | 0 ± 0.1 |
| Acidobacteria | Blastocatellia (Subgroup 4) | Blastocatellales | <i>Blastocatellaceae</i> | <i>Blastocatellaceae_unclassified</i> | ASV14058 | 0 ± 0 | 0.1 ± 0.1 |
| Actinobacteria | Actinobacteria | Micrococcales | <i>Microbacteriaceae</i> | <i>Microbacteriaceae_unclassified</i> | ASV37410 | 0 ± 0 | 0.2 ± 0.1 |
| Actinobacteria | Actinobacteria | Micrococcales | <i>Microbacteriaceae</i> | <i>Microbacteriaceae_unclassified</i> | ASV10235 | 0 ± 0 | 0.1 ± 0.1 |
| Bacteroidetes | Bacteroidia | Cytophagales | <i>Microscillaceae</i> | <i>Chryseolinea</i> | ASV33311 | 0 ± 0 | 0.1 ± 0.1 |
| Bacteroidetes | Bacteroidia | Cytophagales | <i>Spirosomaceae</i> | <i>Dyadobacter</i> | ASV20945 | 0 ± 0 | 0.2 ± 0.2 |
| Chloroflexi | Anaerolineae | SBR1031 | <i>A4b</i> | <i>A4b_unclassified</i> | ASV3082 | 0 ± 0 | 0.2 ± 0.1 |
| Firmicutes | Bacilli | Bacillales | <i>Bacillaceae</i> | <i>Bacillus</i> | ASV13035 | 0.2 ± 0.1 | 0.5 ± 0.2 |
| Firmicutes | Bacilli | Bacillales | <i>Bacillaceae</i> | <i>Bacillus</i> | ASV47072 | 0.2 ± 0.1 | 1 ± 0.4 |
| Firmicutes | Bacilli | Bacillales | <i>Bacillaceae</i> | <i>Bacillus</i> | ASV10264 | 0.2 ± 0.1 | 0.7 ± 0.3 |
| Patescibacteria | Saccharimonadia | Saccharimonadales | <i>Saccharimonadaceae</i> | <i>Saccharimonadaceae_unclassified</i> | ASV36575 | 0 ± 0 | 0.3 ± 0.2 |
| Patescibacteria | Saccharimonadia | Saccharimonadales | <i>Saccharimonadaceae</i> | <i>Saccharimonadaceae_unclassified</i> | ASV51676 | 0 ± 0 | 0.5 ± 0.9 |
| Patescibacteria | Saccharimonadia | Saccharimonadales | <i>Saccharimonadales_unclassified</i> | <i>Saccharimonadales_unclassified</i> | ASV37232 | 0 ± 0 | 0.1 ± 0.2 |
| Patescibacteria | Saccharimonadia | Saccharimonadales | <i>Saccharimonadales_unclassified</i> | <i>Saccharimonadales_unclassified</i> | ASV21430 | 0 ± 0 | 0.1 ± 0.1 |
| Patescibacteria | Saccharimonadia | Saccharimonadales | <i>Saccharimonadales_unclassified</i> | <i>Saccharimonadales_unclassified</i> | ASV47124 | 0 ± 0 | 0.2 ± 0.4 |
| Proteobacteria | Alphaproteobacteria | Sphingomonadales | <i>Sphingomonadaceae</i> | <i>Sphingomonas</i> | ASV40734 | 0.2 ± 0.1 | 0.6 ± 0.2 |
| Proteobacteria | Alphaproteobacteria | Sphingomonadales | <i>Sphingomonadaceae</i> | <i>Sphingomonas</i> | ASV7204 | 0 ± 0 | 0.3 ± 0.3 |
| Proteobacteria | Alphaproteobacteria | Rhizobiales | <i>Rhizobiaceae</i> | <i>Mesorhizobium</i> | ASV47384 | 0 ± 0 | 0.1 ± 0.1 |
| Proteobacteria | Alphaproteobacteria | Sphingomonadales | <i>Sphingomonadaceae</i> | <i>Sphingomonas</i> | ASV15752 | 0 ± 0 | 0.2 ± 0.3 |
| Proteobacteria | Alphaproteobacteria | Rhizobiales | <i>Devosiaceae</i> | <i>Devosia</i> | ASV30746 | 0 ± 0 | 0.1 ± 0.2 |
| Proteobacteria | Alphaproteobacteria | Rhizobiales | <i>Devosiaceae</i> | <i>Devosia</i> | ASV38130 | 0 ± 0 | 0.1 ± 0.2 |
| Proteobacteria | Alphaproteobacteria | Rhizobiales | <i>Devosiaceae</i> | <i>Devosia</i> | ASV1636 | 0.2 ± 0.1 | 0.7 ± 0.3 |
| Proteobacteria | Gammaproteobacteria | Betaproteobacteriales | <i>Methylophilaceae</i> | <i>Methylothera</i> | ASV11982 | 0.1 ± 0.1 | 0.4 ± 0.3 |
| Proteobacteria | Gammaproteobacteria | Betaproteobacteriales | <i>Burkholderiaceae</i> | <i>Caenimonas</i> | ASV21850 | 0 ± 0 | 0.2 ± 0.1 |

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|-----------------|---------------------|--------------------|----------------------------|--|----------|-----------|------------------|
| Proteobacteria | Gammaproteobacteria | Xanthomonadales | <i>Xanthomonadaceae</i> | <i>Pseudoxanthomonas</i> | ASV36003 | 0 ± 0 | 0.2 ± 0.2 |
| Proteobacteria | Gammaproteobacteria | Xanthomonadales | <i>Xanthomonadaceae</i> | <i>Pseudoxanthomonas</i> | ASV9333 | 0 ± 0 | 0.1 ± 0.1 |
| Proteobacteria | Gammaproteobacteria | Xanthomonadales | <i>Xanthomonadaceae</i> | <i>Pseudoxanthomonas</i> | ASV48785 | 1.8 ± 0.3 | 3.2 ± 1.8 |
| Thaumarchaeota | Nitrososphaeria | Nitrososphaerales | <i>Nitrososphaeraceae</i> | <i>Nitrososphaeraceae_unclassified</i> | ASV24360 | 0.1 ± 0 | 0.6 ± 0.2 |
| Verrucomicrobia | Verrucomicrobiae | Chthoniobacterales | <i>Chthoniobacteraceae</i> | <i>Chthoniobacter</i> | ASV39202 | 0.1 ± 0.1 | 0.3 ± 0.2 |

Table S11. Fungal species (ASVs) with differential relative abundance in the rhizosphere of winter wheat (cv. Lemmy, EC 59) grown in soil under MP- mouldboard plough tillage or CT- cultivator tillage practice (FDR<0.05). Only discriminative species with mean >0.1% are displayed. Significantly enriched taxa are marked in bold. Mean \pm standard deviation is shown (n=8), unident. - unidentified, inc. sed. – incertae sedis.

| Phylum | Class | Order | Family | Genus | ASV | MP | CT |
|-------------------|---------------------|-------------------------------|-------------------------------|-----------------------------------|--------------------------------------|---------------------------------|---------------------------------|
| Ascomycota | Ascomycota_unident. | Ascomycota_unident. | <i>Ascomycota_unident.</i> | <i>Ascomycota_unident.</i> | <i>Ascomycota sp</i> | 2.0 \pm 1.0 | 0.3 \pm 0.1 |
| Ascomycota | Eurotiomycetes | Euriales | <i>Trichocomaceae</i> | <i>Talaromyces</i> | <i>Talaromyces sayulitensis</i> | 0.2 \pm 0.3 | 0 \pm 0 |
| Ascomycota | Eurotiomycetes | Onygenales | <i>Onygenales_inc. sed.</i> | <i>Chrysosporium</i> | <i>Chrysosporium lobatum</i> | 1.3 \pm 0.9 | 0.5 \pm 0.3 |
| Ascomycota | Eurotiomycetes | Onygenales | <i>Onygenales_inc. sed.</i> | <i>Chrysosporium</i> | <i>Chrysosporium pseudomerdarium</i> | 0.3 \pm 0.3 | 0 \pm 0 |
| Ascomycota | Eurotiomycetes | Onygenales | <i>Onygenales_unident.</i> | <i>Onygenales_unident.</i> | <i>Onygenales sp</i> | 0.1 \pm 0.1 | 0 \pm 0 |
| Ascomycota | Leotiomycetes | Helotiales | <i>Helotiaceae</i> | <i>Scytalidium</i> | <i>Scytalidium circinatum</i> | 0.2 \pm 0.2 | 0 \pm 0 |
| Ascomycota | Leotiomycetes | Leotiomycetes_unident. | <i>Leotiomycetes_unident.</i> | <i>Leotiomycetes_unident.</i> | <i>Leotiomycetes sp</i> | 0.2 \pm 0.2 | 0 \pm 0 |
| Ascomycota | Leotiomycetes | Thelebolales | <i>Pseudeurotiaceae</i> | <i>Pseudogymnoascus</i> | <i>Pseudogymnoascus pannorum</i> | 1.4 \pm 0.7 | 0.2 \pm 0.1 |
| Ascomycota | Pezizomycetes | Pezizales | <i>Pyronemataceae</i> | <i>Pyronemataceae_unident.</i> | <i>Pyronemataceae sp</i> | 0.3 \pm 0.2 | 0.1 \pm 0.1 |
| Ascomycota | Sordariomycetes | Hypocreales | <i>Hypocreaceae</i> | <i>Trichoderma</i> | <i>Trichoderma barbatum</i> | 0.3 \pm 0.2 | 0 \pm 0 |
| Ascomycota | Sordariomycetes | Hypocreales | <i>Hypocreales_inc. sed.</i> | <i>Acremonium</i> | <i>Acremonium persicinum</i> | 0.6 \pm 0.2 | 0.1 \pm 0 |
| Ascomycota | Sordariomycetes | Sordariales | <i>Lasiosphaeriaceae</i> | <i>Lasiosphaeriaceae_unident.</i> | <i>Lasiosphaeriaceae sp</i> | 0.2 \pm 0.1 | 0 \pm 0 |
| Basidiomycota | Agaricomycetes | Agaricales | <i>Strophariaceae</i> | <i>Strophariaceae_unident.</i> | <i>Strophariaceae sp</i> | 1.2 \pm 2.1 | 0.1 \pm 0.1 |
| Basidiomycota | Agaricomycetes | Cantharellales | <i>Ceratobasidiaceae</i> | <i>Ceratobasidiaceae_unident.</i> | <i>Ceratobasidiaceae sp</i> | 0.2 \pm 0.2 | 0 \pm 0 |
| Basidiomycota | Cystobasidiomycetes | Cystobasidiomycetes_inc. sed. | <i>Symmetrosporaceae</i> | <i>Symmetrospora</i> | <i>Symmetrospora coprosmae</i> | 0.2 \pm 0.1 | 0.1 \pm 0 |
| Basidiomycota | Exobasidiomycetes | Entylomatales | <i>Entylomatales_unident.</i> | <i>Entylomatales_unident.</i> | <i>Entylomatales sp</i> | 0.2 \pm 0.3 | 0 \pm 0 |
| Basidiomycota | Microbotryomycetes | Sporidiobolales | <i>Sporidiobolaceae</i> | <i>Sporidiobolaceae_unident.</i> | <i>Sporidiobolaceae sp</i> | 1.3 \pm 0.7 | 0.4 \pm 0.3 |
| Basidiomycota | Tremellomycetes | Filobasidiales | <i>Filobasidiaceae</i> | <i>Filobasidium</i> | <i>Filobasidium magnum</i> | 0.1 \pm 0.2 | 0 \pm 0 |
| Chytridiomycota | Spizellomycetes | Spizellomycetales | <i>Powellomycetaceae</i> | <i>Powellomyces</i> | <i>Powellomyces hirtus</i> | 0.1 \pm 0.1 | 0 \pm 0 |
| Mortierellomycota | Mortierellomycetes | Mortierellales | <i>Mortierellaceae</i> | <i>Mortierella</i> | <i>Mortierella fimbricystis</i> | 0.9 \pm 0.6 | 0.1 \pm 0 |
| Mortierellomycota | Mortierellomycetes | Mortierellales | <i>Mortierellaceae</i> | <i>Mortierella</i> | <i>Mortierella antarctica</i> | 0.5 \pm 0.4 | 0.1 \pm 0 |
| Mortierellomycota | Mortierellomycetes | Mortierellales | <i>Mortierellaceae</i> | <i>Mortierella</i> | <i>Mortierella gamsii</i> | 0.4 \pm 0.5 | 0.1 \pm 0.1 |
| Mortierellomycota | Mortierellomycetes | Mortierellales | <i>Mortierellaceae</i> | <i>Mortierella</i> | <i>Mortierella amoeboides</i> | 0.1 \pm 0.3 | 0 \pm 0 |
| Olpidiomycota | Olpidiomycetes | Olpidiales | <i>Olpidiaceae</i> | <i>Olpidium</i> | <i>Olpidium brassicae</i> | 1.0 \pm 1.5 | 0 \pm 0 |
| Ascomycota | Ascomycota_unident. | Ascomycota_unident. | <i>Ascomycota_unident.</i> | <i>Ascomycota_unident.</i> | <i>Ascomycota sp</i> | 0 \pm 0 | 0.1 \pm 0.1 |

| | | | | | | | |
|-----------------|-----------------------|---------------------|------------------------------|-----------------------------------|------------------------------------|-----------|------------------|
| Ascomycota | Dothideomycetes | Pleosporales | <i>Cucurbitariaceae</i> | <i>Pyrenochaetopsis</i> | <i>Pyrenochaetopsis leptospora</i> | 0 ± 0 | 0.2 ± 0.1 |
| Ascomycota | Dothideomycetes | Pleosporales | <i>Leptosphaeriaceae</i> | <i>Leptosphaeriaceae_unident.</i> | <i>Leptosphaeriaceae sp</i> | 0.2 ± 0.2 | 1.2 ± 0.6 |
| Ascomycota | Dothideomycetes | Pleosporales | <i>Leptosphaeriaceae</i> | <i>Leptosphaeria</i> | <i>Leptosphaeria maculans</i> | 0 ± 0 | 0.2 ± 0.2 |
| Ascomycota | Dothideomycetes | Pleosporales | <i>Pleosporales_unident.</i> | <i>Pleosporales_unident.</i> | <i>Pleosporales sp</i> | 0 ± 0 | 0.2 ± 0.3 |
| Ascomycota | Eurotiomycetes | Eurotiales | <i>Aspergillaceae</i> | <i>Penicillium</i> | <i>Penicillium aethiopicum</i> | 0.6 ± 0.3 | 1.7 ± 0.5 |
| Ascomycota | Leotiomycetes | Helotiales | <i>Helotiaceae</i> | <i>Articulospora</i> | <i>Articulospora sp</i> | 0.7 ± 0.6 | 2.0 ± 1.4 |
| Ascomycota | Leotiomycetes | Helotiales | <i>Helotiaceae</i> | <i>Hymenoscyphus</i> | <i>Hymenoscyphus menthae</i> | 0 ± 0 | 0.1 ± 0.3 |
| Ascomycota | Pezizomycetes | Pezizales | <i>Pezizales_unident.</i> | <i>Pezizales_unident.</i> | <i>Pezizales sp</i> | 0 ± 0 | 0.1 ± 0.2 |
| Ascomycota | Sordariomycetes | Glomerellales | <i>Plectosphaerellaceae</i> | <i>Plectosphaerella</i> | <i>Plectosphaerella alismatis</i> | 0 ± 0 | 0.3 ± 0.2 |
| Ascomycota | Sordariomycetes | Hypocreales | <i>Hypocreaceae</i> | <i>Trichoderma</i> | <i>Trichoderma petersenii</i> | 0.4 ± 0.2 | 2.0 ± 1.8 |
| Ascomycota | Sordariomycetes | Hypocreales | <i>Hypocreaceae</i> | <i>Trichoderma</i> | <i>Trichoderma piluliferum</i> | 0.5 ± 0.4 | 1.8 ± 0.8 |
| Ascomycota | Sordariomycetes | Hypocreales | <i>Hypocreales_inc. sed.</i> | <i>Sarocladium</i> | <i>Sarocladium bactrocephalum</i> | 0 ± 0 | 0.3 ± 0.4 |
| Ascomycota | Sordariomycetes | Hypocreales | <i>Nectriaceae</i> | <i>Stephanonectria</i> | <i>Stephanonectria keithii</i> | 0 ± 0 | 0.1 ± 0.1 |
| Ascomycota | Sordariomycetes | Hypocreales | <i>Nectriaceae</i> | <i>Fusarium</i> | <i>Fusarium sp</i> | 0.2 ± 0.2 | 0.6 ± 0.4 |
| Ascomycota | Sordariomycetes | Hypocreales | <i>Nectriaceae</i> | <i>Nectriaceae_unident.</i> | <i>Nectriaceae sp</i> | 0.1 ± 0.1 | 0.4 ± 0.2 |
| Ascomycota | Sordariomycetes | Hypocreales | <i>Stachybotryaceae</i> | <i>Stachybotrys</i> | <i>Stachybotrys chartarum</i> | 2.2 ± 1.9 | 5.1 ± 2.5 |
| Ascomycota | Sordariomycetes | Hypocreales | <i>Stachybotryaceae</i> | <i>Stachybotryaceae_unident.</i> | <i>Stachybotryaceae sp</i> | 0 ± 0 | 0.3 ± 0.5 |
| Ascomycota | Sordariomycetes | Sordariales | <i>Chaetomiaceae</i> | <i>Chaetomium</i> | <i>Chaetomium sp</i> | 1.6 ± 2.3 | 3.0 ± 0.9 |
| Ascomycota | Sordariomycetes | Sordariales | <i>Lasiosphaeriaceae</i> | <i>Schizothecium</i> | <i>Schizothecium carpinicola</i> | 0 ± 0 | 0.1 ± 0.1 |
| Basidiomycota | Tremellomycetes | Cystofilobasidiales | <i>Mrakiaceae</i> | <i>Tausonia</i> | <i>Tausonia pullulans</i> | 0.3 ± 0.2 | 0.7 ± 0.4 |
| Basidiomycota | Tremellomycetes | Tremellales | <i>Bulleribasidiaceae</i> | <i>Vishniacozyma</i> | <i>Vishniacozyma dimennae</i> | 0 ± 0 | 0.1 ± 0.1 |
| Chytridiomycota | Rhizophlyctidomycetes | Rhizophlyctidales | <i>Rhizophlyctidaceae</i> | <i>Rhizophlyctis</i> | <i>Rhizophlyctis rosea</i> | 0 ± 0 | 0.1 ± 0.1 |
| Mucoromycota | Mucoromycetes | Mucorales | <i>Mucoraceae</i> | <i>Mucor</i> | <i>Mucor circinelloides</i> | 0 ± 0 | 0.1 ± 0.1 |
| Mucoromycota | Mucoromycetes | Mucorales | <i>Rhizopodaceae</i> | <i>Rhizopus</i> | <i>Rhizopus arrhizus</i> | 1.5 ± 0.8 | 4.9 ± 2.1 |

Table S12. Fungal species (ASVs) with differential relative abundance in the rhizosphere of winter wheat (cv. Lemmy, EC 59) grown in soil under intensive (Int) or extensive (Ext) N-fertilization intensity (FDR<0.05) in root window setup. Only discriminative species with mean >0.1% are displayed. Significantly enriched taxa are marked in bold. Mean \pm standard deviation is shown (n=8), unident. - unidentified, inc. sed. – incertae sedis.

| Phylum | Class | Order | Family | Genus | ASV | Int | Ext |
|-------------------|---------------------|-------------------------------|---------------------------------|-------------------------------|--|---------------------------------|----------------------------------|
| Ascomycota | Ascomycota_unident. | Ascomycota_unident. | <i>Ascomycota_unident.</i> | <i>Ascomycota_unident.</i> | <i>Ascomycota</i> sp | 1.0 \pm 0.6 | 0.2 \pm 0.1 |
| Ascomycota | Sordariomycetes | Glomerellales | <i>Plectosphaerellaceae</i> | <i>Plectosphaerella</i> | <i>Plectosphaerella cucumerina</i> | 0.4 \pm 0.3 | 0.1 \pm 0 |
| Ascomycota | Sordariomycetes | Hypocreales | <i>Clavicipitaceae</i> | <i>Metarhizium</i> | <i>Metarhizium carneum</i> | 0.4 \pm 0.5 | 0.1 \pm 0.1 |
| Ascomycota | Sordariomycetes | Hypocreales | <i>Hypocreales_inc. sed.</i> | <i>Acremonium</i> | <i>Acremonium rutilum</i> | 0.3 \pm 0.2 | 0 \pm 0 |
| Basidiomycota | Agaricomycetes | Cantharellales | <i>Cantharellales_inc. sed.</i> | <i>Minimedusa</i> | <i>Minimedusa polyspora</i> | 0.5 \pm 0.7 | 0 \pm 0 |
| Fungi_unident. | Fungi_unident. | Fungi_unident. | <i>Fungi_unident.</i> | <i>Fungi_unident.</i> | <i>Fungi</i> sp | 0.1 \pm 0.1 | 0 \pm 0 |
| Ascomycota | Dothideomycetes | Pleosporales | <i>Pleosporales_unident.</i> | <i>Pleosporales_unident.</i> | <i>Pleosporales</i> sp | 0 \pm 0 | 0.2 \pm 0.3 |
| Ascomycota | Eurotiomycetes | Eurotiales | <i>Trichocomaceae</i> | <i>Talaromyces</i> | <i>Talaromyces veerkampii</i> | 0.5 \pm 0.2 | 3.6 \pm 4.8 |
| Ascomycota | Eurotiomycetes | Eurotiales | <i>Trichocomaceae</i> | <i>Talaromyces</i> | <i>Talaromyces sayulitensis</i> | 0 \pm 0 | 0.2 \pm 0.3 |
| Ascomycota | Leotiomycetes | Thelebolales | <i>Pseudeurotiaceae</i> | <i>Pseudogymnoascus</i> | <i>Pseudogymnoascus appendiculatus</i> | 3.4 \pm 1.2 | 11.5 \pm 8.0 |
| Ascomycota | Pezizomycetes | Pezizales | <i>Pezizales_unident.</i> | <i>Pezizales_unident.</i> | <i>Pezizales</i> sp | 0 \pm 0 | 0.1 \pm 0.2 |
| Ascomycota | Sordariomycetes | Hypocreales | <i>Hypocreaceae</i> | <i>Hypocreaceae_unident.</i> | <i>Hypocreaceae</i> sp | 0.2 \pm 0.1 | 2.9 \pm 1.7 |
| Ascomycota | Sordariomycetes | Hypocreales | <i>Nectriaceae</i> | <i>Fusarium</i> | <i>Fusarium</i> sp | 0 \pm 0 | 0.4 \pm 0.3 |
| Basidiomycota | Agaricomycetes | Agaricales | <i>Bolbitiaceae</i> | <i>Conocybe</i> | <i>Conocybe cylindracea</i> | 0.1 \pm 0.1 | 0.4 \pm 0.6 |
| Basidiomycota | Cystobasidiomycetes | Cystobasidiomycetes_inc. sed. | <i>Symmetrosporaceae</i> | <i>Symmetrospora</i> | <i>Symmetrospora coprosmae</i> | 0.1 \pm 0 | 0.2 \pm 0.1 |
| Basidiomycota | Exobasidiomycetes | Entylomatales | <i>Entylomatales_unident.</i> | <i>Entylomatales_unident.</i> | <i>Entylomatales</i> sp | 0 \pm 0 | 0.2 \pm 0.4 |
| Basidiomycota | Tremellomycetes | Filobasidiales | <i>Filobasidiaceae</i> | <i>Filobasidium</i> | <i>Filobasidium oeirense</i> | 0.3 \pm 0.2 | 1.0 \pm 0.7 |
| Basidiomycota | Tremellomycetes | Filobasidiales | <i>Filobasidiaceae</i> | <i>Filobasidium</i> | <i>Filobasidium magnum</i> | 0 \pm 0 | 0.2 \pm 0.2 |
| Mortierellomycota | Mortierellomycetes | Mortierellales | <i>Mortierellaceae</i> | <i>Mortierella</i> | <i>Mortierella alpina</i> | 1.2 \pm 0.9 | 2.4 \pm 1.5 |
| Olpidiomycota | Olpidiomycetes | Olpidiales | <i>Olpidiaceae</i> | <i>Olpidium</i> | <i>Olpidium brassicae</i> | 0 \pm 0 | 1.0 \pm 1.5 |

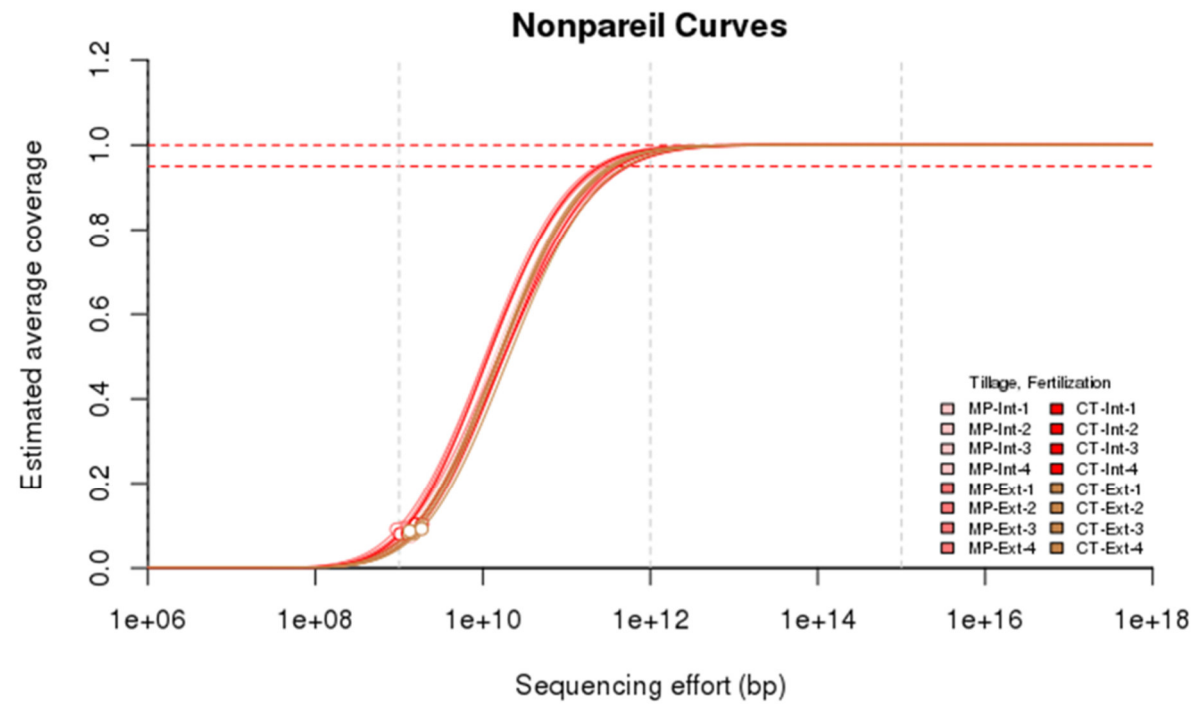


Figure S7. Nonpareil curves generated from shotgun metagenome sequencing showing the estimated coverage of the diversity per sample. Estimated average coverage is given in percent with 0.2 = 20%.

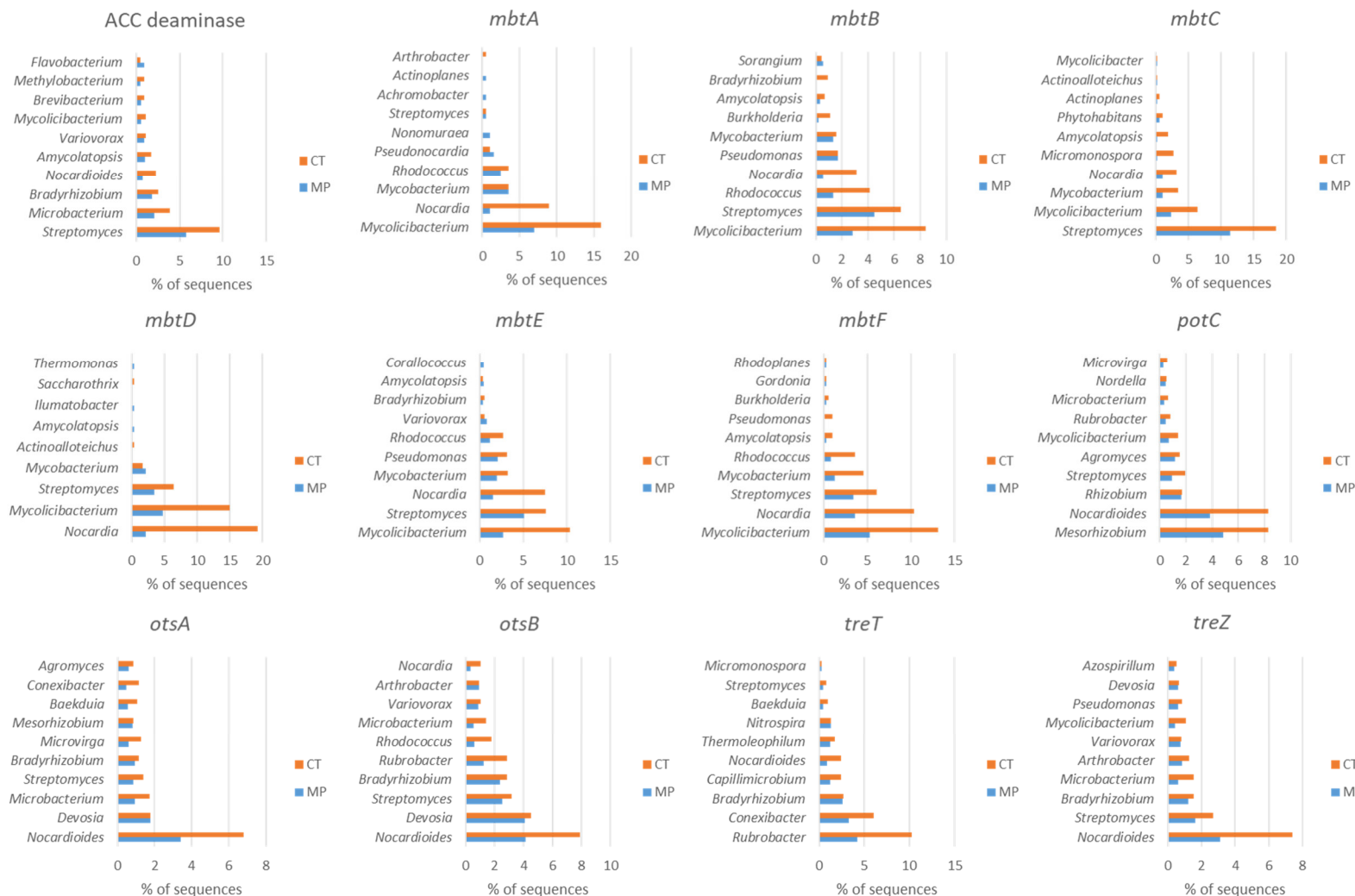


Figure S8. Taxonomic classification of functional genes, which were enriched in the rhizosphere of winter wheat (cv. Lemmy, EC 5) grown in soil under cultivator tillage (CT) compared to mouldboard plough (MP) practice, to bacterial genera. Presented are the ten most abundant genera in percent (%).

Table S13. Tentative phylogenetic affiliation of bacterial/archaeal ASVs with differential relative abundance (mean >0.5%) in the rhizosphere of winter wheat (cv. Lemmy, EC 59) grown in MP vs. CT soils (FDR < 0.05; Table 6) using BLAST-NCBI database (only type material; last access 15th Aug 2023). These responder ASVs were used for correlation analysis (Fig. 4).

| ASV | ASV_code | Closest BLAST hit | E-value | % Identity | Accession No. |
|----------|-----------------------------------|--|-----------|------------|---------------|
| ASV4136 | 154b2b2a745651308f22aa62f5588a29 | <i>Brevitalea aridisoli</i> | 1.00E-177 | 93.98% | NR_151987.1 |
| ASV49496 | f2f1d769ca62216f2e97e5d0a34fe83e | <i>Arthrobacter ulcerisalmonis</i> | 0 | 100.00% | NR_180330.1 |
| ASV660 | 03488ba0e533f5a3bdfaacf062cebbcb8 | <i>Agromyces ramosus</i> | 0 | 100.00% | NR_026165.1 |
| ASV16162 | 4fb99d087105de2a392094534160d00f | <i>Arthrobacter ulcerisalmonis</i> | 0 | 99.75% | NR_180330.1 |
| ASV11972 | 3b4d1ccea11192cfca9f57f04498cc7b | <i>Terrimonas soli</i> | 0 | 97.79% | NR_159891.1 |
| ASV33194 | a31e927c29b211c2217ceab4811ccd93 | <i>Nitrospira japonica</i> | 0 | 99.01% | NR_114396.1 |
| ASV35563 | aeb2943e3abd311274dd041ee2a7fb6e | <i>Nitrospira moscoviensis</i> | 2.00E-179 | 94.79% | NR_029287.1 |
| ASV42131 | ced92f47e90cfe4f20141ecccbe3d0bd | <i>Nitrososphaera viennensis</i> | 3.00E-158 | 93.78% | NR_134097.1 |
| ASV47072 | e7208cd1eab8e0bdd5eabbb5beb554fa | <i>Bacillus clarus</i> | 0 | 100.00% | NR_115526.1 |
| ASV10264 | 33520d147bffa680f811c4e5d7a21a1f | <i>Priestia aryabhatai</i> | 0 | 100.00% | NR_118442.1 |
| ASV51676 | fd95a692130d1f70fbfcb622f1295902 | <i>Alkaliphilus metalliredigens</i> QYMF | 7.00E-80 | 80.95% | NR_074633.1 |
| ASV40734 | c7ca0091732cdf76b704f5df3c86f0ad | <i>Sphingomonas sediminicola</i> | 0 | 99.74% | NR_132332.1 |
| ASV1636 | 086f2152fdb38513ada7b4f3dc53d3eb | <i>Devosia oryzae</i> | 0 | 100.00% | NR_181423.1 |
| ASV48785 | ef7bba86c6cd44346b4b78d369274e86 | <i>Pseudoxanthomonas sacheonensis</i> | 0 | 99.52% | NR_044293.1 |
| ASV24360 | 77dd56bf2aedeadc155e7cce44978662 | <i>Nitrososphaera viennensis</i> | 1.00E-171 | 95.95% | NR_134097.1 |

Table S14. Tentative identification of fungal ASVs with differential relative abundance (mean >0.5%) in the rhizosphere of winter wheat grown in MP vs. CT soils (FDR < 0.05; Table 7) using SH identifier from UNITE database (version 8.0) with corresponding Accession-number, taxonomy and similarity based on the output file of taxonomic assignment with GALAXY Bioinformatics Platform. These responder ASVs were used for correlation analysis (Fig. 4).

| SH No. | Accession No. | Phylum | Class | Order | Family | Genus | Species | Similarity |
|----------------|---------------|----------------------|-----------------------|------------------------|-----------------------------------|---------------------|------------------------------|------------|
| SH1610194.08FU | GU721832 | p__Ascomycota | c__Sordariomycetes | o__Hypocreales | f__Nectriaceae | g__Fusarium | s__Fusarium_sp | 100 |
| SH1615796.08FU | MF782744 | p__Ascomycota | c__Sordariomycetes | o__Sordariales | f__Chaetomiaceae | g__Chaetomium | s__Chaetomium_sp | 99.56 |
| SH2305819.08FU | FJ860810 | p__Ascomycota | c__Sordariomycetes | o__Hypocreales | f__Hypocreaceae | g__Trichoderma | s__Trichoderma_piluliferum | 100 |
| SH1608147.08FU | KC008744 | p__Mortierellomycota | c__Mortierellomycetes | o__Mortierellales | f__Mortierellaceae | g__Mortierella | s__Mortierella_fimbricystis | 98.72 |
| SH1513361.08FU | AB540575 | p__Ascomycota | c__Sordariomycetes | o__Hypocreales | f__Hypocreales_fam_Incertae_sedis | g__Acremonium | s__Acremonium_persicinum | 100 |
| SH2303584.08FU | DQ323441 | p__Ascomycota | c__Sordariomycetes | o__Hypocreales | f__Hypocreaceae | g__Trichoderma | s__Trichoderma_petersenii | 100 |
| SH2190001.08FU | AY371635 | p__Ascomycota | c__Eurotiomycetes | o__Eurotiales | f__Aspergillaceae | g__Penicillium | s__Penicillium_aethiopicum | 100 |
| SH1635388.08FU | DQ133892 | p__Ascomycota | c__Dothideomycetes | o__Pleosporales | f__Leptosphaeriaceae | g__unidentified | s__Leptosphaeriaceae_sp | 100 |
| SH1519091.08FU | AY997067 | p__Olpidiomycota | c__Olpidiomycetes | o__Olpidiales | f__Olpidiaceae | g__Olpidium | s__Olpidium_brassicae | 99.35 |
| SH2267912.08FU | DQ117444 | p__Ascomycota | c__Leotiomycetes | o__Thelebolales | f__Pseudeurotiaceae | g__Pseudogymnoascus | s__Pseudogymnoascus_pannorum | 99.55 |
| SH1650287.08FU | HQ630347 | p__Mortierellomycota | c__Mortierellomycetes | o__Mortierellales | f__Mortierellaceae | g__Mortierella | s__Mortierella_antarctica | 100 |
| SH1648789.08FU | HG936236 | p__Ascomycota | c__Leotiomycetes | o__Helotiales | f__Helotiaceae | g__Articulospora | s__Articulospora_sp | 100 |
| SH1555467.08FU | MH107898 | p__Ascomycota | c__unidentified | o__unidentified | f__unidentified | g__unidentified | s__Ascomycota_sp | 97.98 |
| SH1650607.08FU | AF444417 | p__Basidiomycota | c__Tremellomycetes | o__Cystofilobasidiales | f__Mrakiaceae | g__Tausonia | s__Tausonia_pullulans | 100 |
| SH1510152.08FU | JN206324 | p__Mucoromycota | c__Mucoromycetes | o__Mucorales | f__Rhizopodaceae | g__Rhizopus | s__Rhizopus_arrhizus | 100 |
| SH1557965.08FU | EF568081 | p__Ascomycota | c__Sordariomycetes | o__Hypocreales | f__Stachybotryaceae | g__Stachybotrys | s__Stachybotrys_chartarum | 100 |
| SH1552992.08FU | HQ914933 | p__Ascomycota | c__Eurotiomycetes | o__Onygenales | f__Onygenales_fam_Incertae_sedis | g__Chrysosporium | s__Chrysosporium_lobatum | 100 |
| SH1639424.08FU | EU144472 | p__Basidiomycota | c__Agaricomycetes | o__Agaricales | f__Strophariaceae | g__unidentified | s__Strophariaceae_sp | 99.6 |
| SH1575137.08FU | AB093521 | p__Basidiomycota | c__Microbotryomycetes | o__Sporidiobolales | f__Sporidiobolaceae | g__unidentified | s__Sporidiobolaceae_sp | 99.268 |

Table S15. Characteristics of root-associated soil from winter wheat (cv. Lemmy; EC 59) grown under different long-term agricultural practices (MP- mouldboard plough, CT- cultivator tillage, Ext- extensive fertilization without fungicides and growth regulators, Int- intensive fertilization with pesticides and growth regulators). The soil was sampled at a depth between 0 and 30 cm. Micro- and macro-nutrients were analyzed according to the certified protocols of VDLUFA by AGROLAB GmbH (Leinefelde-Worbis, Germany). Abbreviations: total carbon (TC), total nitrogen (TN), dry matter (DM), organic matter (OM). Values represent means \pm standard deviation of four replicates. Means not sharing any letter are significantly different by the Tukey's test ($p \leq 0.05$).

| | MP-Int | | | MP-Ext | | | CT-Int | | | CT-Ext | | |
|---------------------------------|--------|------------|----|--------|------------|----|--------|------------|----|--------|------------|----|
| pH | 7.3 | ± 0.2 | ns | 7.5 | ± 0.1 | ns | 7.1 | ± 0.4 | ns | 7.2 | ± 0.3 | ns |
| C/N | 11.0 | ± 0 | ns | 10.3 | ± 2.4 | ns | 10.5 | ± 1.3 | ns | 11.0 | ± 1.4 | ns |
| [%] | | | | | | | | | | | | |
| TC | 1.82 | ± 0.07 | c | 1.82 | ± 0.02 | c | 2.42 | ± 0.08 | a | 2.09 | ± 0.04 | b |
| TN | 0.15 | ± 0 | b | 0.17 | ± 0.04 | ab | 0.23 | ± 0.03 | a | 0.19 | ± 0.02 | ab |
| DM | 80.3 | ± 0.96 | ns | 80.4 | ± 0.32 | ns | 78.3 | ± 1.36 | ns | 78.7 | ± 0.99 | ns |
| OM | 2.98 | ± 0.08 | c | 2.95 | ± 0.04 | c | 4.06 | ± 0.21 | a | 3.46 | ± 0.08 | b |
| [mg 100 g ⁻¹ soil] | | | | | | | | | | | | |
| NO ₃ -N | 0.58 | ± 0.16 | a | 0.24 | ± 0.04 | b | 0.50 | ± 0.11 | a | 0.24 | ± 0.04 | b |
| NH ₄ -N [#] | 0.12 | ± 0.02 | ab | 0.06 | ± 0.01 | c | 0.19 | ± 0.07 | a | 0.10 | ± 0.01 | bc |
| K | 16.1 | ± 1.2 | b | 21.0 | ± 2.0 | b | 35.6 | ± 4.4 | a | 31.5 | ± 3.3 | a |
| Mg | 10.1 | ± 2.1 | ab | 8.4 | ± 0.8 | b | 13.1 | ± 2.6 | a | 10.5 | ± 2.8 | ab |
| P | 15.2 | ± 3.6 | b | 21.4 | ± 3.1 | a | 19.3 | ± 4.7 | ab | 18.4 | ± 4.7 | ab |
| Ca | 250 | ± 22 | ab | 254 | ± 10 | a | 226 | ± 26 | b | 237 | ± 21 | ab |
| Fe | 4.9 | ± 1.0 | ns | 4.5 | ± 0.6 | ns | 5.8 | ± 1.9 | ns | 4.9 | ± 1.9 | ns |
| [mg kg ⁻¹ soil] | | | | | | | | | | | | |
| Cu | 2.8 | ± 0.2 | ns | 2.8 | ± 0.2 | ns | 2.6 | ± 0.5 | ns | 2.6 | ± 0.5 | ns |
| Mn | 202 | ± 87 | ns | 171 | ± 69 | ns | 220 | ± 101 | ns | 195 | ± 96 | ns |
| Na | 12.0 | ± 1.1 | ns | 12.9 | ± 1.9 | ns | 12.6 | ± 1.3 | ns | 12.4 | ± 1.4 | ns |
| Zn | 3.9 | ± 0.4 | ns | 4.2 | ± 0.4 | ns | 4.1 | ± 0.5 | ns | 3.7 | ± 0.4 | ns |

ns: not significant

[#]: statistical analysis after Tukey's ladder of powers transformation