

**Electronic supplementary materials:**

**Table S1** Differences in the number of functional gene pathways of soil bacterial communities involved in the decomposition process under nitrogen with four forms. Data (means and SE;  $n = 18$ ) with different letters in a transverse column indicate statistically significant differences ( $P < 0.05$ ).

The number of functional gene pathways of soil bacterial communities of most samples that lower than one was not shown in this table.

Abbreviations: CK, control; MixN, the mixed nitrogen forms.

	CK	Nitrate	Ammonium	Urea	MixN
4-hydroxyphenylacetate degradation	1261.3±317.19b	1614.11±110.23ab	1752.99±122.94a	1896.95±118.86a	1872.02±158.81a
Superpathway of L-arginine, putrescine, and 4-aminobutanoate degradation	14.46±7.20b	11.44±1.64b	21.74±1.76ab	42.84±14.96a	18.08±4.42ab
L-arginine degradation II (AST pathway)	2044.42±417.01b	3061.43±323.89a	3147.51±221.32a	3554.06±223.35a	3165.28±329.49a
Anaerobic aromatic compound degradation (Thauera aromatica)	0.00±0.00ns	0.63±0.29ns	2.60±1.29ns	1.67±0.63ns	0.98±0.61ns
Catechol degradation to $\beta$ -ketoadipate	1388.92±318.8b	2020.09±116.23a	1942.06±116.73a	2018.77±102.81a	2009.08±114.97a

Benzoyl-coa degradation II (anaerobic)	4.83±0.41b	12.8±2.58a	11.33±1.85a	12.87±1.80a	10.68±1.29ab
Creatinine degradation I	2434.14±574.62ns	3201.86±283.56ns	3209.58±306.02ns	3750.7±459.23ns	3614.79±399.42ns
Glucose degradation (oxidative)	73.98±20.17b	352.36±22.10a	302.61±47.02ab	443.97±125.22a	373.44±92.06a
Superpathway of fucose and rhamnose degradation	241.58±51.26ns	230.19±23.08ns	305.15±36.96ns	592.62±229.43ns	318.98±63.62ns
Fucose degradation	429.63±99.15b	1020.43±83.81a	1093.46±120.43a	1337.97±202.63a	1127.91±161.43a
Superpathway of hexuronide and hexuronate degradation	5647.49±1341.55b	7058.14±453.34ab	7425.53±285.72a	8516.32±355.85a	7580.72±356.69a
D-galactarate degradation I	1370.9±291.71b	1886.36±98.20a	2040.68±120.87a	2228.95±180.27a	2107.79±147.50a
D-galacturonate degradation I	11591.56±2722.75b	13994.59±777.72ab	14979.24±343.42a	16477.43±765.26a	14763.74±614.30a
Gallate degradation II	863.06±211.03b	1180.68±71.39a	1115±55.49ab	1186.57±51.47a	1217.74±110.02a
Gallate degradation I	612.01±143.19ns	837.89±78.80ns	783.85±74.60ns	836.09±60.87ns	837.97±98.88ns

Superpathway of N-acetylglucosamine, N-acetylmannosamine and N-acetylneuraminate degradation	3397.26±775.26b	4119.57±280.05ab	4488.5±400.18ab	5688.02±787.72a	4602.94±316.46ab
D-glucarate degradation I	1160.22±256.76b	1732.93±94.62a	1908.71±113.58a	2187.86±182.10a	2040.62±180.33a
Superpathway of D-glucarate and D-galactarate degradation	1370.9±291.71b	1886.36±98.20a	2040.68±120.87a	2228.95±180.27a	2107.79±147.50a
Glucose and glucose-1-phosphate degradation	8759.32±1553.48ns	9995.21±408.44ns	11190.33±1107.21ns	11007.65±704.03ns	10058.69±389.95ns
Superpathway of β-D-glucuronide and D-glucuronate degradation	5144.32±1245.86b	6791.96±420.47a	7033.35±336.97a	8119.94±291.07a	7282.26±407.29a
Glycogen degradation I (bacterial)	26283.83±6090.88b	31412.43±1387.3ab	33839.11±1159.87a	36476.41±1680.13a	33088.96±784.14a
Superpathway of glycol metabolism and degradation	86±12.73ns	79.01±10.03ns	110.67±15.62ns	239.24±91.62ns	116.51±26.76ns

Superpathway of glycerol degradation to 1,3-propanediol	691.09±203.34ns	580.14±43.06ns	614.25±88.96ns	799.06±83.70ns	750.77±59.18ns
3-phenylpropanoate and 3-(3-hydroxyphenyl)propanoate degradation to 2-oxopent-4-enoate	203.61±46.15b	624.05±134.18ab	605.32±126.32ab	756.36±166.71a	700.00±131.52a
Superpathway of hexitol degradation (bacteria)	3583.11±1119.62ns	2797.73±150.02ns	3170.01±122.09ns	4143.47±825.55ns	3404.56±311.80ns
L-histidine degradation I	23584.65±5941.57ns	26321.15±1638.74ns	28274.87±1021.61ns	28918.69±1320.77ns	27988.83±859.18ns
Lactose and galactose degradation I	73.86±16.93ns	88.32±17.01ns	105.96±17.95ns	481.96±269.38ns	146±60.85ns
L-leucine degradation I	24503.76±6459.59ns	28814.02±2698.35ns	28949.62±1126.15ns	29165.63±1175.55ns	28268.34±986.98ns
Superpathway of methylglyoxal degradation	40.43±11.07b	82.23±9.40ab	115.64±20.48ab	178.74±49.27a	121.87±21.75ab
Methylgallate degradation	1067.92±260.61b	1457±86.19a	1379.62±67.65ab	1468.78±62.64a	1506.28±134.84a

Superpathway of L-arginine and L-ornithine degradation	14.46±7.20b	11.44±1.64b	21.74±1.76ab	42.84±14.96a	18.08±4.42ab
Superpathway of ornithine degradation	1143.68±381.70ns	1331.84±220.26ns	1292.2±259.81ns	1711.77±346.56ns	1438.87±306.41ns
Acetylene degradation	15846.07±4111.87ns	18050.91±1448.38ns	18109.39±1695.12ns	19238.77±1489.54ns	17488.41±539.02ns
L-glutamate degradation V (via hydroxyglutarate)	27.86±8.28ns	72.16±11.91ns	102.58±15.59ns	587.13±466.17ns	153.7±64ns
Purine nucleobases degradation I (anaerobic)	18800.60±4899.30b	21717.94±1061.07ab	22566.77±284.72ab	23233.82±566.72a	23424.32±630.37a
Protocatechuate degradation I (meta-cleavage pathway)	1065.1±259.99b	1443.28±89.22a	1374.51±75.21ab	1469.87±67.01a	1489.36±126.76a
3-phenylpropanoate degradation	1431.65±422.70b	2060.82±177.19ab	2219.25±200.96ab	2265.19±161.00a	2633.73±333.59a
Superpathway of N-acetylneuraminate degradation	7199.93±1523.95b	8251.18±622.34ab	9023.08±959.36ab	11271.77±1708.91a	8682.18±637.76ab

Myo-inositol degradation I	2231.36±664.51b	2866±268.71ab	3153.45±361.90ab	3253.13±258.49ab	3552.46±365.04a
Nylon-6 oligomer degradation	360.41±180.26ns	464.46±25.07ns	478.23±27.89ns	476.22±21.19ns	510.47±54.74ns
Protocatechuate degradation II (ortho-cleavage pathway)	10580.78±2708.81b	13570.41±514.44a	13657.11±600.83a	14454.33±451.92a	14748.3±723.85a
Benzoyl-coa degradation I (aerobic)	109.35±24.55b	345.01±57.66a	337.11±46.79a	315.98±31.69a	363.63±39.06a
Mandelate degradation I	29.14±14.79ns	20.11±3.17ns	21.89±3.57ns	20.26±2.38ns	27.95±4.39ns
Superpathway of taurine degradation	255.23±42.45b	371.57±36.11a	444.67±37.84a	441.97±19.34a	437.76±42.18a
Glycine betaine degradation I	2137±637.32b	2768.31±201.02ab	3338.26±406.64ab	3533.09±421.92a	3207.79±340.05ab
Sucrose degradation II (sucrose synthase)	5186.59±1350.99ns	7209.04±1306.25ns	8912.71±2126.48ns	10413.63±2158.68ns	8176.72±1259.93ns
S-methyl-5-thio- $\alpha$ -D-ribose 1-phosphate degradation	2010.8±1035.77a	811.68±81.38b	980.38±130.78b	916.21±79.18b	848.57±106.22b
Creatinine degradation II	91.66±17.40ns	99.52±13.45ns	110.46±17.56ns	106.12±8.22ns	119.96±17.83ns
4-aminobutanoate degradation V	15823.64±4222.39ns	17598±861.32ns	18396.52±551.98ns	18629.33±429.66ns	18813.06±609.07ns

L-histidine degradation II	6286.14±1618.49ns	7599.27±873.63ns	8128.39±643.05ns	7736.42±608.26ns	7609.07±679.93ns
L-glutamate degradation VIII (to propanoate)	13.94±11.03ns	41.12±6.47ns	53.02±8.62ns	150.86±94.96ns	57.18±19.05ns
Glutaryl-coa degradation	14±4.16ns	36.98±6.40ns	52.92±8.26ns	419.76±356.16ns	82.56±35.87ns
Toluene degradation IV (aerobic) (via catechol)	545.49±123.78b	1018.18±87.85a	1017.7±81.97a	1168.75±133.97a	1220.72±151.07a
Toluene degradation I (aerobic) (via o- cresol)	6250.48±1732.11ns	7188.84±373.53ns	7153.51±351.37ns	7439.68±304.3ns	7360.27±463.94ns
Toluene degradation III (aerobic) (via p- cresol)	2668.36±655.53b	3307.04±174.79ab	3268.93±212.83ab	3587.86±220.54a	3381.4±266.38ab
Toluene degradation II (aerobic) (via 4- methylcatechol)	6250.48±1732.11ns	7188.84±373.53ns	7153.51±351.37ns	7439.68±304.3ns	7360.27±463.94ns

Superpathway of aerobic toluene degradation	723.54±169.62b	1242.52±107.59a	1258.26±88.61a	1391.98±137.99a	1399.1±182.71a
Toluene degradation VI (anaerobic)	0.00±0.00a	0.46±0.22ab	2.05±0.97a	1.25±0.49ab	0.73±0.46ab
P-cymene degradation	1918.72±1918.72ns	774.4±774.40ns	911.16±419.78ns	471.79±471.79ns	819.52±518.75ns
Sucrose degradation IV (sucrose phosphorylase)	8178.29±1482.63ns	9314.72±367.8ns	10417.88±1008.88ns	10277.31±644.22ns	9367.44±332.58ns
Catechol degradation I (meta-cleavage pathway)	5668.18±1502.63ns	6378.3±351.01ns	6443.59±395.15ns	6590.04±289.85ns	6572.18±426.93ns
Catechol degradation III (ortho-cleavage pathway)	1568.42±373.09b	2093.83±132.12a	1947.5±88.58ab	2104.94±97.44a	2051.91±116.32a
Catechol degradation to 2-oxopent-4-enoate II	5412.86±1361.59ns	5887.26±348.15ns	6239.59±299.25ns	6426.45±233.78ns	6124.21±227.58ns



Catechol degradation II (meta-cleavage pathway)	5580.36±1469.63ns	6097.3±395.42ns	6165.21±280.62ns	6317.6±216.79ns	6165.14±269.36ns
Aromatic compounds degradation via β-ketoadipate	1568.42±373.09b	2093.83±132.12a	1947.5±88.58ab	2104.94±97.44a	2051.91±116.32a
Adenosine nucleotides degradation IV	247.29±121.33b	537.78±94.04ab	572.29±81.67a	473.86±11.16ab	706.15±125.31a
2-nitrobenzoate degradation I	3140.95±821.62ns	3143.16±316.9ns	3529.33±368.6ns	3345.69±270.26ns	3046.96±202.04ns
L-tryptophan degradation to 2-amino-3-carboxymuconate semialdehyde	6717.35±1620.50ns	8402.88±1066.25ns	8524.13±611.73ns	8306.27±747.80ns	7652.02±636.96ns
2-amino-3-carboxymuconate semialdehyde degradation to 2-oxopentenoate	3045.55±821.48ns	2880.51±282.30ns	3263.62±348.77ns	3088.79±238.70ns	2829.81±170.07ns
L-tryptophan degradation IX	4628.19±1230.57ns	4849.15±491.92ns	5130.94±422.11ns	4978.97±333.3ns	4635.22±255.12ns
Urate biosynthesis/inosine 5'-phosphate degradation	39218.29±10186.61b	46373.31±3571.95ab	47297.22±960.01ab	50521.87±1095.70a	46963.71±1478.57ab

Allantoin degradation to glyoxylate III	1860.97±519.40b	2475.33±197.06ab	2607.12±205.24ab	3076.76±257.50a	2906.47±348.77a
Glycogen degradation II (eukaryotic)	2035.73±598.98b	2450.95±188.26ab	2626.79±196.36ab	3181.11±158.19a	2775.07±261ab
Superpathway of phenylethylamine degradation	2501.21±648.35b	3233.08±204ab	3238.43±167.25ab	3535.64±224.52a	3564.89±230.36a
Chlorosalicylate degradation	12.57±4.98ns	18.01±3.60ns	16.28±1.14ns	22.8±6.03ns	16.78±2.56ns
Superpathway of salicylate degradation	1582.85±377.62b	2119.42±102.90a	2019.03±74.63a	2178.74±95.45a	2132.09±121.26a
4-methylcatechol degradation (ortho cleavage)	2213.76±630.65ns	2422.87±265.64ns	2170.48±173.46ns	2270.74±120.30ns	2173.23±115.19ns
Sucrose degradation III (sucrose invertase)	8178.29±1482.63ns	9314.72±367.8ns	10417.88±1008.88ns	10729.17±890.44ns	9367.44±332.58ns
2-aminophenol degradation	1136.68±281.14b	1585.57±77.25a	1693.14±103.67a	1689.38±91.46a	1669.06±137.34a
Galactose degradation I (Leloir pathway)	22998.56±5447.35b	28799.53±1532.01a	30509.89±585.32a	32329.4±1271.99a	31002.94±445.03a
Superpathway of vanillin and vanillate degradation	808.48±193.10b	1082.06±88.32a	1030.37±88.16ab	1104.54±70.92a	1093.59±114.86a

Syringate degradation	1341.44±331.87b	1840.68±128.15ab	1715.57±98.46a	1829.49±78.60a	1874.45±161.66a
Purine nucleotides degradation II (aerobic)	31421.31±7639.54b	37164.62±2051.23ab	38789.81±961.01a	40507.7±817.44a	38362.25±1060.40a
L-tryptophan degradation XII (Geobacillus)	2514.47±635.14b	3267.06±172.68a	3426.13±179.01a	3417.96±149.72a	3339.07±216.17a
4-deoxy-L-threo-hex-4-enopyranuronate degradation	9674.2±2292.87ns	10448.88±770.74ns	11244.75±463.94ns	12185.06±572.98ns	10841.42±306.79ns
Chondroitin sulfate degradation I (bacterial)	6.51±6.51b	22.22±6.43ab	29.89±9.2ab	87.22±39.43a	46.18±16.42ab
Guanosine nucleotides degradation III	32160.14±7765.9b	38815.36±2474.44ab	41103.39±817.64a	42468.22±1042.66a	40414.12±1264.47a
Superpathway of sulfolactate degradation	421.76±125.84b	790.89±52.29ab	909.85±81.81a	1005.08±63.85a	954.05±111.41a
Cinnamate and 3-hydroxycinnamate degradation to 2-oxopent-4-enoate	203.61±46.15b	624.05±134.18ab	605.32±126.32ab	756.36±166.71a	700±131.52a
L-rhamnose degradation II	6.59±1.53ns	8.10±3.15ns	14.72±4.42ns	57.97±39.68ns	16.44±7.72ns

Starch degradation III	777.68±216.82ns	563.12±72.16ns	610.07±95.48ns	597.23±91.63ns	506.34±24.44ns
Starch degradation V	25119.49±5832.99b	29996.52±1356.93ab	32192.61±1069.05a	34744.8±1623.15a	31496.47±737.02a
Superpathway of glucose and xylose degradation	18569.94±4521.97c	21764.02±803.97bc	23905.54±532.04ab	27029.16±1856.92a	24136.02±1270.87ab
Chitin derivatives degradation	72.83±23.17b	165.47±31.54ab	153.96±20.99ab	244.51±48.23a	203.69±54.11ab
Androstenedione degradation	914.43±229.17b	1406.12±122.42ab	1450.06±164.02a	1558.61±160.58a	1652.4±164.07a
Sitosterol degradation to androstenedione	76.68±16.64ns	279.1±133.47ns	263.87±138.25ns	342.78±176.5ns	318.12±116.55ns
Mandelate degradation to acetyl-coa	106.7±50.44ns	80.32±11.87ns	85.99±13.02ns	80.21±8.39ns	108.65±16.68ns
1,5-anhydrofructose degradation	768.42±200.99ns	903.72±50.31ns	1062.57±137.39ns	1099.56±108.76ns	1066.45±102.13ns
4-hydroxyacetophenone degradation	0.00±0.00ns	3.00±1.53ns	2.47±1.68ns	2.85±1.80ns	5.36±3.22ns
Glycerol degradation to butanol	2540.04±769.67ns	2084.93±151.64ns	2441.92±183.96ns	3079.04±687.48ns	2240.92±226.95ns
L-1,2-propanediol degradation	350.46±58.8ns	1129.08±485.32ns	1004.74±422.82ns	1484.25±609.80ns	1286.57±414.41ns
4-coumarate degradation (anaerobic)	20.47±3.30b	37±3.92a	37.82±2.02a	46.73±3.45a	40.06±5.16a

Vanillin and vanillate degradation I	808.48±193.10ns	1082.06±88.32ns	1030.37±88.16ns	1104.54±70.92ns	1093.59±114.86ns
Vanillin and vanillate degradation II	888.54±215.33ns	1180.64±94.70ns	1123.99±94.47ns	1204.4±74.99ns	1192.98±123.76ns
Superpathway of pyrimidine ribonucleosides degradation	19.14±3.00b	20.25±1.88b	22.61±1.52ab	19.42±2.85b	28.70±3.26a
Nicotinate degradation I	112.86±33.75b	180.91±12.50a	177.27±13.75a	212.90±12.94a	207.75±24.21a
Myo-, chiro- and scillo-inositol degradation	2883.86±896.85b	3907.32±366.80ab	4373±537.54ab	4402.92±370.89ab	4910.5±500.14a
D-fructuronate degradation	11705.8±2701.54c	14332.34±754.33bc	15547.58±283.07ab	17341.06±841.03a	15367.32±650.06ab
L-arabinose degradation IV	608.75±184.80b	763.42±57.51ab	782.87±105.73ab	921.82±39.89a	848.3±59.71ab
Aromatic biogenic amine degradation (bacteria)	10783.41±2706.83b	12482.69±621.8ab	13642.22±324.32a	14546.59±459.50a	13624.3±436.80a
Mannan degradation	1865.39±491.62ns	2294.63±379.48ns	2358.64±320.59ns	3000.89±640.22ns	3288.69±662.90ns
Heparin degradation	15.48±3.78b	70.63±25.54ab	72.59±13.92ab	136.03±35.83a	101.92±29.62ab

3-phenylpropanoate and 3-(3-hydroxyphenyl)propanoate degradation	723.8±155.40b	1835.67±311.85a	1803.37±297.03a	2114.16±366.60a	2023.78±317.23a
Purine ribonucleosides degradation	13158.19±3564.73b	14421.26±681.88ab	15442.67±265.80ab	17517.02±1160.73a	15780.39±564.33ab
Superpathway of purine deoxyribonucleosides degradation	15341.47±3744.58ns	17751.03±1090.48ns	18203.77±1194.6ns	19461.14±1101.93ns	17675.88±493.75ns
Superpathway of pyrimidine deoxyribonucleosides degradation	12846.07±3131.37ns	14568.76±963.7ns	14926.48±746.69ns	16158.63±922.79ns	14567.07±322ns
Methylphosphonate degradation I	2424.93±639.56b	3741.47±257.52a	4143.7±246.88a	4395.53±237.1a	4294.8±443.67a
Phenylacetate degradation I (aerobic)	4208.89±1050.41ns	4847.54±325.12ns	4758.23±404.49ns	5056.95±273.76ns	4699.33±351.46ns
Allantoin degradation IV (anaerobic)	134.69±22.11ns	159.57±23.93ns	205.99±30.32ns	271.37±75.46ns	257.36±65.66ns
L-rhamnose degradation I	4750.02±1314.41b	5598.71±216.68ab	6023.91±329.46ab	6527.55±254.2a	6530.93±306.48a
Adenosine nucleotides degradation II	31572.32±7758.93b	38179.46±2561.26ab	40096.47±827.73a	41443.3±906.17a	39616.13±1254.47a
L-tyrosine degradation I	12492.92±4097.10ns	14911.64±2137.62ns	14025.6±974.13ns	14146.52±646.14ns	13395.31±856.12ns

L-valine degradation I	117.75±28.15b	337.06±44.20a	383.08±48.84a	365.2±36.18a	384.52±59.04a
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**Table S2** Differences in the number of functional gene pathways of soil bacterial communities involved in the decomposition process treated with the leaves of the four invasive plants and *P. laciniata*. Data (means and SE;  $n = 15$ ) with different letters in a transverse column indicate statistically significant differences ( $P < 0.05$ ). The number of functional gene pathways of soil bacterial communities of most samples that lower than one was not shown in this table. Abbreviations: PL, *Pterocypsela laciniata* (Houtt.) Shih; BP, *Bidens pilosa* L.; CC, *Conyza canadensis* (L.) Cronq.; SC, *Solidago canadensis* L.; SS, *Symphyotrichum subulatum* (Michx.) G.L. Nesom.

	PL	BP	CC	SC	SS
4-hydroxyphenylacetate degradation	1644.6±82.04b	1954.54±64ab	2108.31±149.84a	1808.66±111.32ab	1792.92±52.55b
Superpathway of L-arginine, putrescine, and 4-aminobutanoate degradation	20.96±4.85ns	24.37±8.26ns	23.9±3.07ns	16.74±2.62ns	34.82±19.53ns
L-arginine degradation II (AST pathway)	3761.83±156.99a	3182.52±136.14b	3281.1±217.67ab	2625.31±142.61c	2616.91±197.03c
Anaerobic aromatic compound degradation (Thauera aromatica)	2.21±0.64ab	3.12±1.46a	1.63±0.37ab	0.21±0.21b	0.72±0.44ab
Catechol degradation to β-ketoadipate	2020.73±101.16ns	1897.23±82.06ns	2062.66±100.02ns	2287.87±249.08ns	1889.61±62.02ns



Benzoyl-coa degradation II (anaerobic)	10.95±0.74ab	15.23±1.07a	13.82±1.60a	13.45±2.43a	8.33±0.71b
Creatinine degradation I	3344.44±214.83b	4394.78±130.95a	4269.32±347.7a	3290.13±332.92b	2499.71±43.47c
Glucose degradation (oxidative)	421.95±99.89ab	345.69±21.67ab	508.76±145.58a	355.66±73.56ab	217.1±26.35b
Superpathway of fucose and rhamnose degradation	231.52±37.91ns	254.7±27.88ns	401.16±77.14ns	293.31±20.07ns	585.77±286.42ns
Fucose degradation	1250.33±130.53ns	1075.33±117.04ns	1180.01±163.02ns	1054.51±100.70ns	1207.49±238.09ns
Superpathway of hexuronide and hexuronate degradation	8493.1±453.96ns	7263.28±267.48ns	7673.26±377.51ns	7303.4±537.98ns	7194.11±395.29ns
D-galactarate degradation I	1905.89±76.48ns	2079.44±67.34ns	2228.96±87.39ns	2296.37±169.99ns	2237.44±197.13ns
D-galacturonate degradation I	16785.31±904.44ns	15076.16±530.7ns	14878.05±784.16ns	14348.3±933.78ns	14681.51±770.23ns
Gallate degradation II	1270.87±29.09ns	1093±17.87ns	1216.24±61.33ns	1389.82±182.34ns	1127.3±98.12ns
Gallate degradation I	965.28±51.7a	684.88±15.4bc	861.63±44.15ab	847.47±108.66a-c	655.89±51.85c

Superpathway of N-acetylglucosamine, N-acetylmannosamine and N-acetylneuraminate degradation	3787.39±361.57ns	5122.38±260.99ns	4754.35±316.13ns	5157.63±350.82ns	5197.8±1069.5ns
D-glucarate degradation I	1913.15±120.98ns	1876.6±51.25ns	2196.98±141.05ns	2184.41±102.85ns	2082.89±207.76ns
Superpathway of D-glucarate and D-galactarate degradation	1905.89±76.48ns	2079.44±67.34ns	2228.96±87.39ns	2296.37±169.99ns	2237.44±197.13ns
Glucose and glucose-1-phosphate degradation	9774.32±1231.25ns	12221.97±1169.1ns	10298.25±464.57ns	12735.1±1578.44ns	10602.42±350.94ns
Superpathway of β-D-glucuronide and D-glucuronate degradation	7840.01±415.51ns	6681.02±226.11ns	7747.61±286.06ns	7121.34±562.81ns	6667.52±391.49ns
Glycogen degradation I (bacterial)	34718.57±1669.39ns	36637.31±1071.59ns	31991.69±811.49ns	34434.41±2299.6ns	33124.61±2313.12ns
Superpathway of glycol metabolism and degradation	83.64±18.38ns	90.15±11.65ns	158.86±36.34ns	105.65±9.6ns	221.16±116.64ns

Superpathway of glycerol degradation to 1,3-propanediol	883.35±53.93a	631.04±58.95b	701.67±48.07ab	660.15±69.39ab	634.72±115.59b
3-phenylpropanoate and 3-(3-hydroxyphenyl)propanoate degradation to 2-oxopent-4-enoate	1038.81±137.04a	599.26±35.96bc	828.28±123.79ab	596.83±51.00bc	484.70±40.03c
Superpathway of hexitol degradation (bacteria)	2784.22±275.41b	3500.87±243.33ab	3346.64±312.52ab	3382.94±271.08ab	4438.48±924.09a
L-histidine degradation I	31608.02±703.72a	28613.56±592.65b	27641.89±545.13bc	25327.58±1592.15c	25396.42±638.42c
Lactose and galactose degradation I	53.4±18.89ns	214.02±89.79ns	209.22±57.99ns	145.59±49.10ns	432.81±337.67ns
L-leucine degradation I	32774.75±726.24a	28981.04±674.02b	28272.57±553.68bc	26100.72±1746.32bc	25709.12±574.08c
Superpathway of methylglyoxal degradation	172.7±29.62ns	85.95±7.04ns	134.38±23.57ns	83.77±10.74ns	152.91±55.69ns
Methylgallate degradation	1567.82±33.68ns	1354.32±22.24ns	1503.26±74.47ns	1716.5±223.26ns	1394.74±119.43ns
Superpathway of L-arginine and L-ornithine degradation	20.96±4.85ns	24.37±8.26ns	23.90±3.07ns	16.74±2.62ns	34.82±19.53ns

Superpathway of ornithine degradation	1690.78±235.32ns	1454.84±231.32ns	1999.58±289.67ns	1372.03±263.00ns	1455.42±298.79ns
Acetylene degradation	16397.17±1164.69b	18879.64±1449.87ab	17404.87±371.63ab	21180.57±1813.35a	18677.83±1644.36ab
L-glutamate degradation V (via hydroxyglutarate)	67.54±9.35ns	60.34±7.41ns	199.71±71.33ns	78.74±6.94ns	688.96±556.64ns
Purine nucleobases degradation I (anaerobic)	23676.09±870.74ns	23465.96±511.65ns	21966.85±194.11ns	22800.09±1653.41ns	22656.26±415.34ns
Protocatechuate degradation I (meta-cleavage pathway)	1594.07±40.75ns	1362.77±17.08ns	1489.3±69.86ns	1649.08±210.06ns	1357.66±121.26ns
3-phenylpropanoate degradation	1885.17±114.21c	2395.79±170.52bc	2474.94±59.08b	3081.18±338.58a	2590.27±104.56ab
Superpathway of N-acetylneuraminate degradation	7186.42±908.16ns	10367.49±623.06ns	9332.99±512.22ns	10479.04±968.00ns	10534.88±2222.96ns
Myo-inositol degradation I	2827.28±158.29c	2999.7±180.74c	3753.22±265.19ab	4053.95±310.77a	3298.25±116.75bc
Nylon-6 oligomer degradation	493.49±7.04ab	488.24±10.80ab	456.04±37.61b	589.98±75.82a	456.39±16.58b

Protocatechuate degradation II (ortho-cleavage pathway)	14520.44±244.56a	14370.49±473.7ab	15246.47±375.53a	14848.22±1005.37a	12765.43±292.64b
Benzoyl-coa degradation I (aerobic)	318.57±44.57ns	339.69±21.79ns	409.15±17.15ns	327.23±27.42ns	402.96±45.06ns
Mandelate degradation I	20.33±5.31ns	37.29±2.88ns	21.68±2.19ns	33.1±9.41ns	27.23±5.44ns
Superpathway of taurine degradation	370.28±39.11ns	459.78±15.46ns	464.02±17.39ns	457.35±42.30ns	410.18±37.49ns
Glycine betaine degradation I	3042.53±464.24bc	3075.54±33.82bc	4117.74±344.28a	3587.77±422.69ab	2409.3±141.34c
Sucrose degradation II (sucrose synthase)	5448.73±996.12b	10909.86±1702.99a	5959.01±1234.71ab	10218.03±2308.56ab	9231.82±1815.2ab
S-methyl-5-thio- $\alpha$ -D-ribose 1-phosphate degradation	891.67±106.25ab	1026.14±105.85a	849.95±133.84ab	674.68±17.26b	842.31±60.87ab
Creatinine degradation II	113.25±18.42ab	115.54±5.56ab	125.12±7.48a	80.81±14.37b	100.12±12.27ab
4-aminobutanoate degradation V	19129.64±510.93ns	18643.64±321.82ns	18885.22±374.35ns	18201.91±1195.16ns	17046.87±389.15ns
L-histidine degradation II	9042.86±305.99a	7922.38±479.94a	8048.84±332.13a	6411.11±650.54b	6147.95±357.62b
L-glutamate degradation VIII (to propanoate)	29.74±4.11ns	52.26±4.77ns	78.27±18.82ns	50.2±4.87ns	175.19±112.22ns

Glutaryl-coa degradation	34.39±4.86ns	30.59±3.77ns	107.87±40.13ns	40.14±3.61ns	495.42±426.02ns
Toluene degradation IV (aerobic) (via catechol)	1025.73±80.71b	1022.38±34.43b	1389.42±94.5a	1296.85±102.06a	1047.77±71.72b
Toluene degradation I (aerobic) (via o-cresol)	7640.92±202.87ab	7156.28±127.99bc	8208.57±202.26a	7531.59±520.76ab	6387.3±200.00c
Toluene degradation III (aerobic) (via p-cresol)	3659.9±100.03ab	3420.63±98.23a-c	3891.4±254.37a	3153.74±176.53bc	2966.17±182.89c
Toluene degradation II (aerobic) (via 4-methylcatechol)	7640.92±202.87ab	7156.28±127.99bc	8208.57±202.26a	7531.59±520.76ab	6387.3±200.00c
Superpathway of aerobic toluene degradation	1202.95±69.34c	1315.06±36.22bc	1633.75±92.13a	1549.96±120.04ab	1217.48±62.64c
Toluene degradation VI (anaerobic)	1.64±0.49ab	2.31±1.12a	1.32±0.36ab	0.15±0.15b	0.55±0.34ab
P-cymene degradation	0.00±0.00b	316.45±316.45b	508.38±508.38b	2813.16±479.92a	322.32±322.32b
Sucrose degradation IV (sucrose phosphorylase)	9221.39±1177.50ns	11395.92±1101.25ns	9587.29±398.51ns	11793.1±1463.74ns	9868.65±358.23ns
Catechol degradation I (meta-cleavage pathway)	7041.11±190.82ab	6261.00±141.72bc	7215.47±230.99a	6776.25±506.45ab	5577.52±198.96c

Catechol degradation III (ortho-cleavage pathway)	2135.41±79.06ns	1969.52±63.62ns	2138.91±120.17ns	2201.88±232.04ns	1883.24±94.88ns
Catechol degradation to 2-oxopent-4-enoate II	6694.19±150.49a	6324.71±180.48a	6360.64±235.71a	5538.63±302.83b	5586.32±173.97b
Catechol degradation II (meta-cleavage pathway)	6726.02±180.01a	6115.75±87.05a-c	6581.23±195.29ab	5929.03±364.25bc	5469.02±191.88c
Aromatic compounds degradation via β-ketoadipate	2135.41±79.06ns	1969.52±63.62ns	2138.91±120.17ns	2201.88±232.04ns	1883.24±94.88ns
Adenosine nucleotides degradation IV	471.05±44.29ns	620.14±135.41ns	591.74±99.77ns	739.37±109.96ns	535±64.67ns
2-nitrobenzoate degradation I	3926.93±131.37a	3152.76±209.53b	3178.78±128.10b	2447.55±133.40c	2685.96±122.68c
L-tryptophan degradation to 2-amino-3-carboxymuconate semialdehyde	9938.98±544.23a	8072.69±708.03b	7684.6±204.61bc	5964.14±360.04d	6584.79±81.59cd
2-amino-3-carboxymuconate semialdehyde degradation to 2-oxopentenoate	3600.6±123.40a	2911.9±170.01bc	2964.05±118.51b	2327.89±132.57d	2508.1±146.34cd

L-tryptophan degradation IX	5727.66±91.20a	4745.56±246.38b	4862.91±162.28b	3903.42±216.60c	4067.43±141.21c
Urate biosynthesis/inosine 5'-phosphate degradation	50470.61±1327.82a	48553.69±1061.44ab	47479.42±663.85ab	45755.19±3061.52ab	44147.38±2367.69b
Allantoin degradation to glyoxylate III	2480.18±156.08bc	2924.28±117.26ab	3500.24±245.26a	3111±250.84a	2323.8±109.23c
Glycogen degradation II (eukaryotic)	2459.45±151.48ns	2391.82±79.88ns	2971.3±255.58ns	2986.59±270.04ns	2628.6±242.24ns
Superpathway of phenylethylamine degradation	3749.15±113.17a	3443.38±96.21ab	3800.98±214.95a	3415.8±188.12ab	3225.01±123.09b
Chlorosalicylate degradation	13.07±0.64ns	21.11±1.55ns	18.64±3.00ns	23.36±3.25ns	22.08±7.44ns
Superpathway of salicylate degradation	2172.4±61.07ns	2054.87±59.50ns	2246.11±112.99ns	2304.46±239.24ns	1962.82±88.62ns
4-methylcatechol degradation (ortho cleavage)	2461.21±121.00ns	2151.56±75.54ns	2333.73±122.17ns	2074.82±189.67ns	2103.25±144.16ns
Sucrose degradation III (sucrose invertase)	9221.39±1177.50ns	11395.92±1101.25ns	9587.29±398.51ns	11793.1±1463.74ns	10410.89±890.88ns
2-aminophenol degradation	1812.00±41.02a	1640.75±107.65ab	1848.48±91.70a	1624.13±103.46ab	1501.69±57.82b
Galactose degradation I (Leloir pathway)	32101.82±915.23ns	32447.53±693.25ns	29893.91±746.34ns	29289.89±1633.35ns	29920.05±1704.38ns



Superpathway of vanillin and vanillate degradation	1254.07±55.10a	940.63±14.51b	1095.77±40.94ab	1130.60±133.08ab	907.45±75.30b
Syringate degradation	1994.34±59.38ns	1667.56±24.42ns	1908.58±92.47ns	2090.33±301.28ns	1725.08±162.89ns
Purine nucleotides degradation II (aerobic)	39621.29±1299.57ns	40586.42±865.65ns	38312.95±611.02ns	38826.95±2332.49ns	36201.3±1528.66ns
L-tryptophan degradation XII (Geobacillus)	3746.37±69.35a	3326.26±176.43ab	3624.35±141.31a	3170.78±183.30b	2992.14±100.59b
4-deoxy-L-threo-hex-4-enopyranuronate degradation	12711.66±888.80a	11427.27±421.63ab	10853.09±555.57ab	10084.07±733.29b	10961.43±551.11ab
Chondroitin sulfate degradation I (bacterial)	13.44±2.91b	38.75±17.78b	40.59±13.81b	37.18±9.46b	108.64±42.79a
Guanosine nucleotides degradation III	43066.28±771.74a	41790.18±1018.4ab	40279.57±876.85a-c	38447.76±2338.74bc	37096.9±1332.89c
Superpathway of sulfolactate degradation	974.83±57.84ab	843.47±41.61bc	1077.13±65.79a	1039.12±90.26a	735.45±33.18c
Cinnamate and 3-hydroxycinnamate degradation to 2-oxopent-4-enoate	1038.81±137.04a	599.26±35.96bc	828.28±123.79ab	596.83±51.00bc	484.7±40.03c
L-rhamnose degradation II	4.36±2.31ns	7.59±1.76ns	21.91±8.38ns	9.30±1.52ns	61.2±48.6ns

Starch degradation III	663.75±26.01a	627.25±71.25ab	572.78±19.96ab	348.75±28.92c	484.37±79.67bc
Starch degradation V	33017.44±1568.7ns	34793.72±983.82ns	30454.06±749.01ns	32667.85±2167.44ns	31608.66±2259.46ns
Superpathway of glucose and xylose degradation	23679.75±1104.86ns	24508.51±766.63ns	24207.99±1518.58ns	23672.07±1209.91ns	24986.36±2725.64ns
Chitin derivatives degradation	139.01±29.75ns	159.27±22.31ns	258.51±47.15ns	243.57±35.89ns	168.24±55.39ns
Androstenedione degradation	1771.16±40.08a	1452.96±21.64bc	1868.31±99.61a	1635.24±142.44ab	1334.27±91.15c
Sitosterol degradation to androstenedione	838.75±160.61a	98.33±18.84b	207.6±30.83b	198.72±33.70b	171.01±42.57b
Mandelate degradation to acetyl-coa	79.69±18.64ns	140.51±9.54ns	87.19±8.55ns	127.5±33.84ns	105.5±19.47ns
1,5-anhydrofructose degradation	1017.82±113.90ab	902.11±35.88b	1221.81±139.13a	1195.86±90.78ab	951.86±39.26ab
4-hydroxyacetophenone degradation	0.68±0.44b	3.21±0.80b	1.12±0.34b	12.21±2.35a	1.85±0.22b
Glycerol degradation to butanol	2141.45±203.82ns	2568.41±168.64ns	2430.21±236.11ns	2167.01±120.37ns	3253.91±811.82ns
L-1,2-propanediol degradation	2986.71±588.25a	411.7±62.56b	849.54±138.69b	970.39±169.75b	922.71±194.57b
4-coumarate degradation (anaerobic)	37.75±5.88ns	41.67±2.50ns	38.70±2.47ns	44.35±3.16ns	38.51±6.49ns

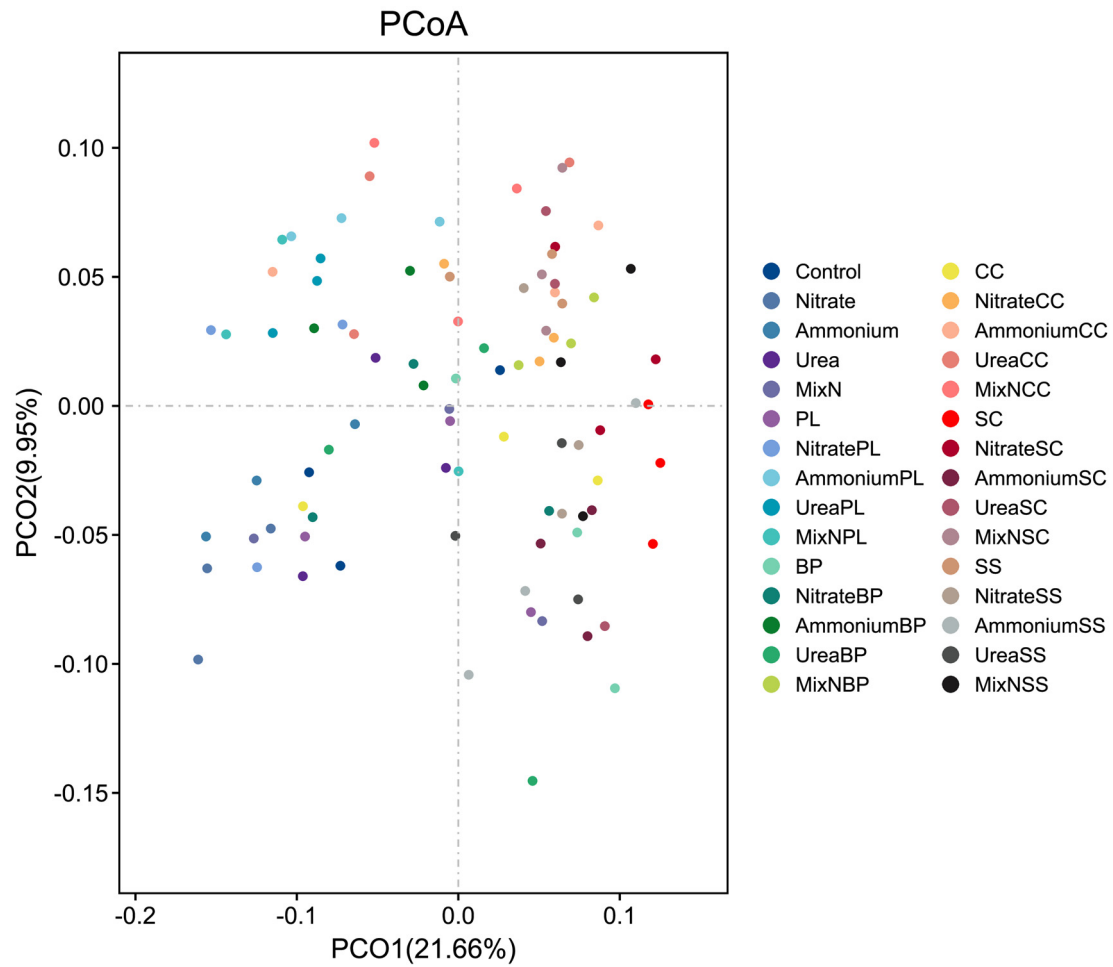
Vanillin and vanillate degradation I	1254.07±55.10a	940.63±14.51b	1095.77±40.94ab	1130.60±133.08ab	907.45±75.30b
Vanillin and vanillate degradation II	1360.78±56.79a	1028.35±15.33b	1191.45±45.21ab	1235.10±144.11ab	995.09±81.07b
Superpathway of pyrimidine ribonucleosides degradation	22.96±4.27ns	25.46±1.55ns	21.47±4.23ns	23.97±2.13ns	15.98±2.81ns
Nicotinate degradation I	183.33±8.64b	205.58±8.85ab	212.58±11.75ab	243.39±19.74a	222.51±26.04ab
Myo-, chiro- and scillo-inositol degradation	3976.91±210.06c	4000.22±281.73c	5073.31±366.2ab	5667.53±406.94a	4678.58±217.36bc
D-fructuronate degradation	17448.91±1077.93ns	15548.37±565.72ns	15400.97±724.53ns	14922.56±1007.98ns	15814.95±903.62ns
L-arabinose degradation IV	841.49±152.2ns	884.96±57.99ns	792.64±27.86ns	1022.24±71.25ns	932.39±26.27ns
Aromatic biogenic amine degradation (bacteria)	15378.71±547.86a	13591.37±245.95b	13972.15±440.21ab	13293.31±843.59b	12609.1±336.35b
Mannan degradation	2075.23±298.3b	2641.23±182.12b	2290.02±178.65b	2611.28±287.19b	4869.52±586.94a
Heparin degradation	149.55±33.24a	86.44±21.23ab	99.76±33.47ab	58.48±17.89b	99.36±27.81ab

3-phenylpropanoate and 3-(3-hydroxyphenyl)propanoate degradation	2760.32±271.43a	1838.64±75.55bc	2349.19±244.27ab	1854.4±136.27bc	1515.69±102.69c
Purine ribonucleosides degradation	16151.46±790.92ns	16412.08±336.39ns	15737.61±667.71ns	14979.45±895.95ns	16077.1±1684.63ns
Superpathway of purine deoxyribonucleosides degradation	17283.69±956.74ns	19148.78±947.98ns	17576.27±351.73ns	20139.88±1469.46ns	18256.3±1483.11ns
Superpathway of pyrimidine deoxyribonucleosides degradation	14677.38±753.98ns	15547.58±646.39ns	14370.17±341.35ns	15714.77±1050.34ns	15052.33±1302.93ns
Methylphosphonate degradation I	3623.74±261.92c	4200.87±129.95bc	4963±227.51a	4672.71±377.43ab	4008.6±98.43bc
Phenylacetate degradation I (aerobic)	5558.98±83.09a	4835.26±189.95ab	5264.52±298.51a	4110.2±223.88b	4281.85±317.15b
Allantoin degradation IV (anaerobic)	131.26±23.88ns	262.19±68.62ns	198.2±29.22ns	259.98±30.63ns	271.1±92.87ns
L-rhamnose degradation I	6356.36±335.22ns	6262.8±219.34ns	6418.05±313.56ns	6479.81±409.48ns	6191.37±357.48ns
Adenosine nucleotides degradation II	41789.49±818.4a	40989.54±733.47a	39676.38±795.98ab	38345.08±2521.85ab	36176.46±1128.57b
L-tyrosine degradation I	15619.97±595.97a	13624.28±537.4ab	14296.82±345.51a	11993.92±1028.75b	12113.84±591.59b

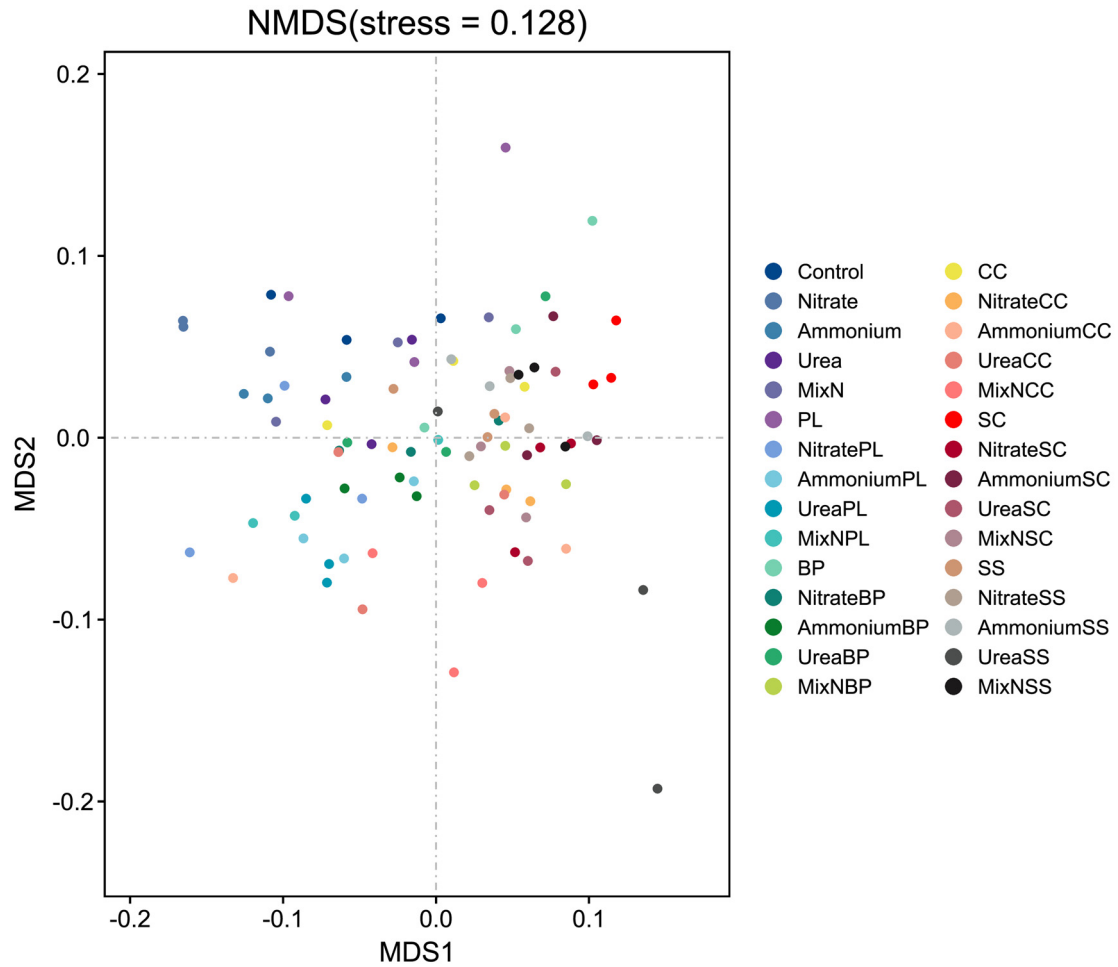
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L-valine degradation I	392.8±35.83ab	387.82±27.29ab	458.11±56.47a	350.08±23.37ab	332.46±31.70b
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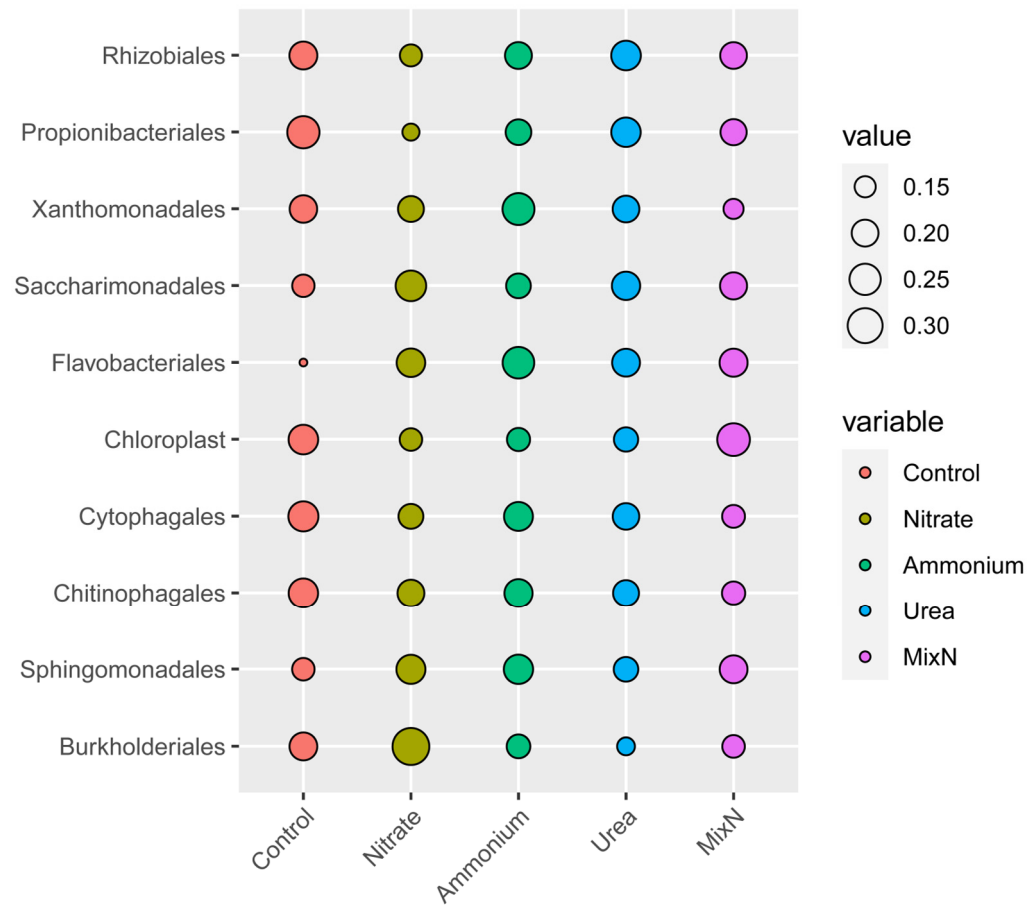
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**Figure S1** PCoA of beta diversity estimates of soil bacterial communities treated with the leaves of the four invasive plants and *P. laciniata* under nitrogen with four forms based on weighted UniFrac distance. Abbreviations: PL, *Pterocypsela laciniata* (Houtt.) Shih; BP, *Bidens pilosa* L.; CC, *Conyza canadensis* (L.) Cronq.; SC, *Solidago canadensis* L.; SS, *Symphyotrichum subulatum* (Michx.) G.L. Nesom; CK, control; MixN, the mixed nitrogen forms.

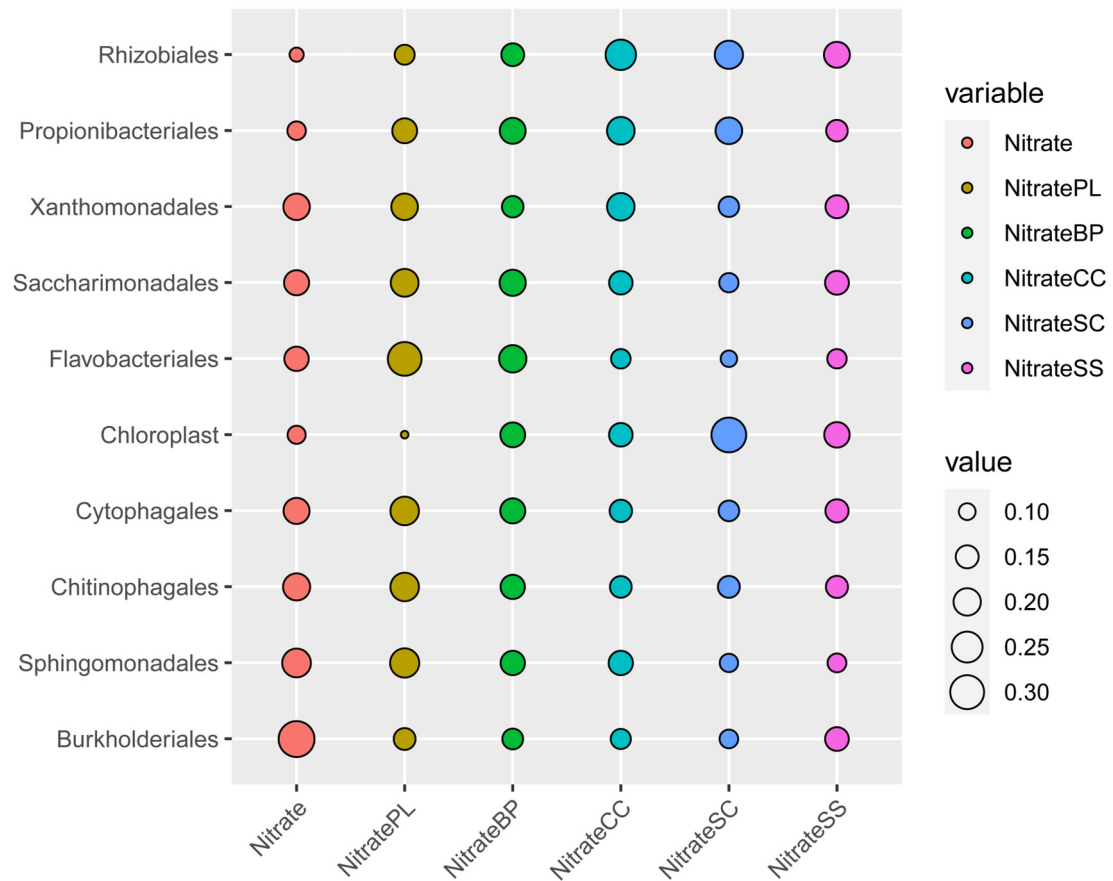


**Figure S2** NMDS of beta diversity estimates of soil bacterial communities treated with the leaves of the four invasive plants and *P. laciniata* under nitrogen with four forms based on weighted UniFrac distance. Abbreviations have the same meanings as defined in Figure S1.

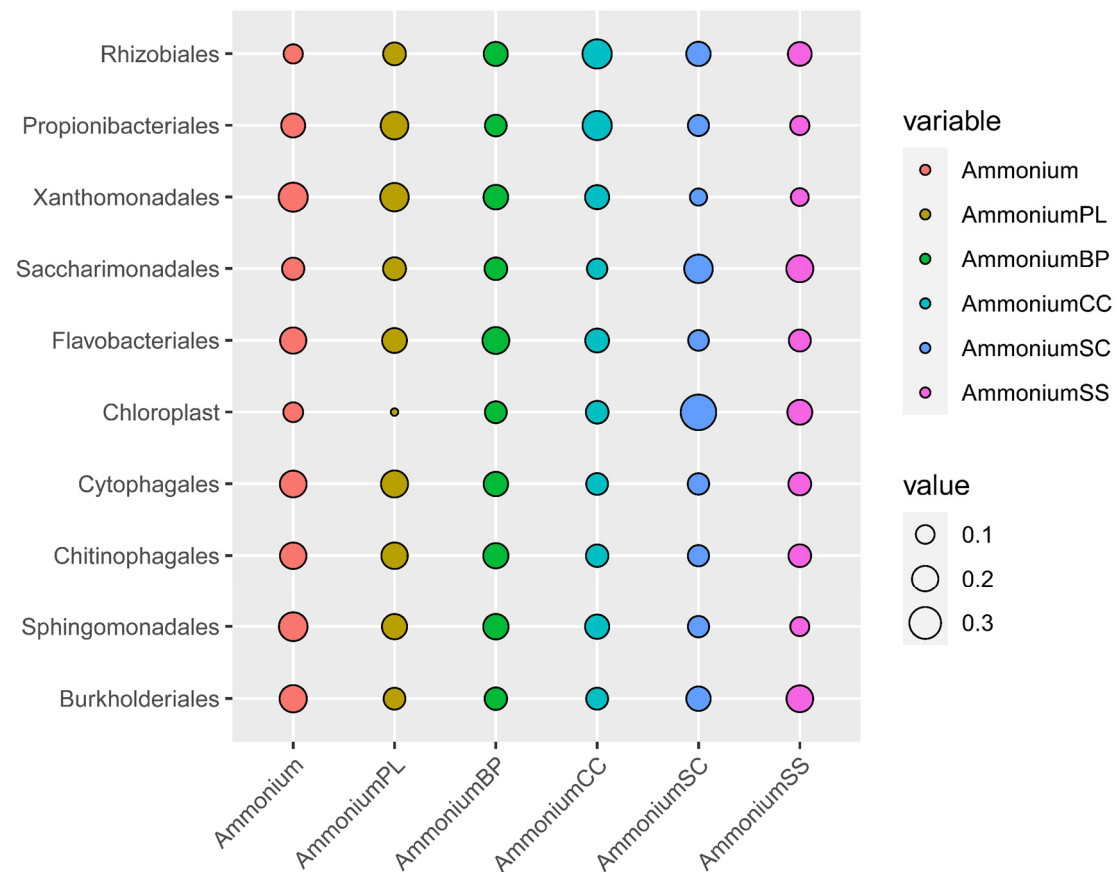


**Figure S3** Bubble chart of soil bacterial biomarkers at the order level under nitrogen with four forms. Abbreviations have the same meanings as defined in Figure S1.

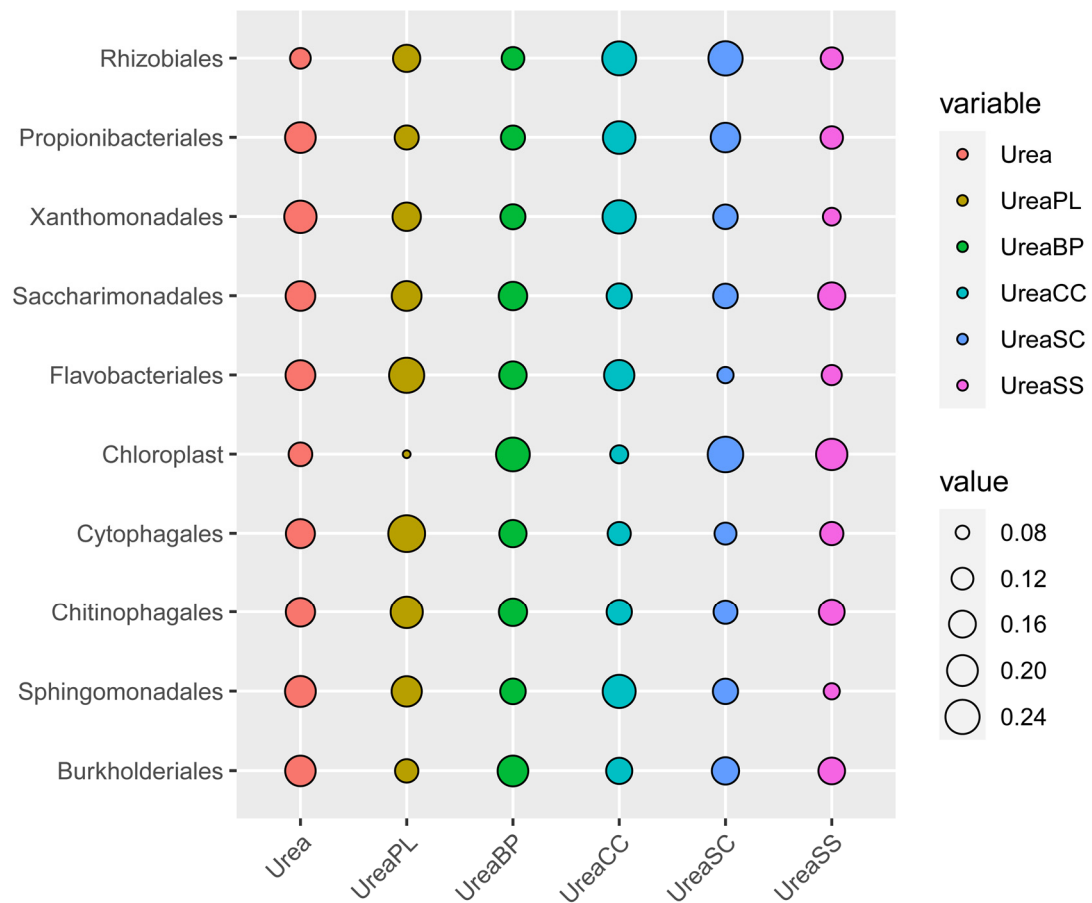




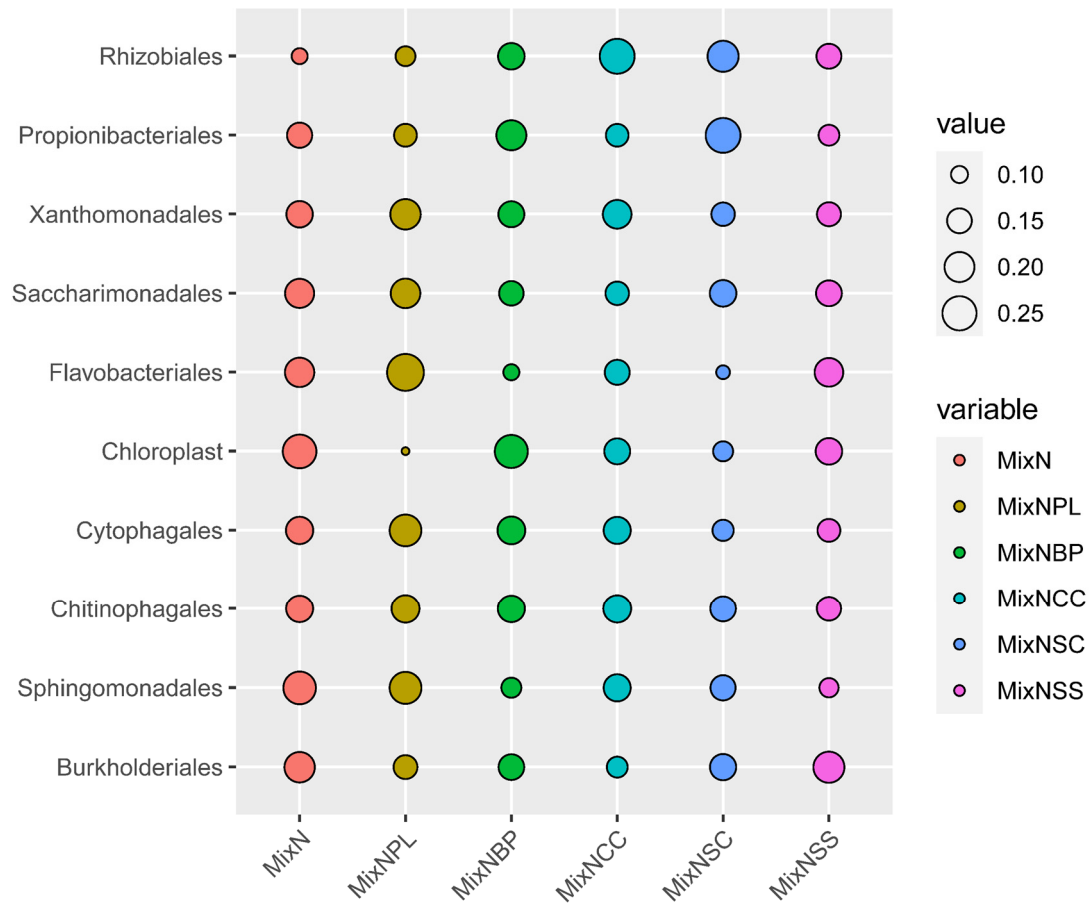
**Figure S4** Bubble chart of soil bacterial biomarkers at the order level treated with the leaves of the four invasive plants and *P. laciniata* under nitrate. Abbreviations have the same meanings as defined in Figure S1.



**Figure S5** Bubble chart of soil bacterial biomarkers at the order level treated with the leaves of the four invasive plants and *P. laciniata* under ammonium. Abbreviations have the same meanings as defined in Figure S1.



**Figure S6** Bubble chart of soil bacterial biomarkers at the order level treated with the leaves of the four invasive plants and *P. laciniata* under urea. Abbreviations have the same meanings as defined in Figure S1.



**Figure S7** Bubble chart of soil bacterial biomarkers at the order level treated with the leaves of the four invasive plants and *P. laciniata* under the mixed nitrogen forms. Abbreviations have the same meanings as defined in Figure S1.