

Supplementary Material

1 **Nitrogen fertilizer amendment alter the bacterial community** 2 **structure in the rhizosphere of rice (*Oryza sativa* L.) and** 3 **improve crop yield**

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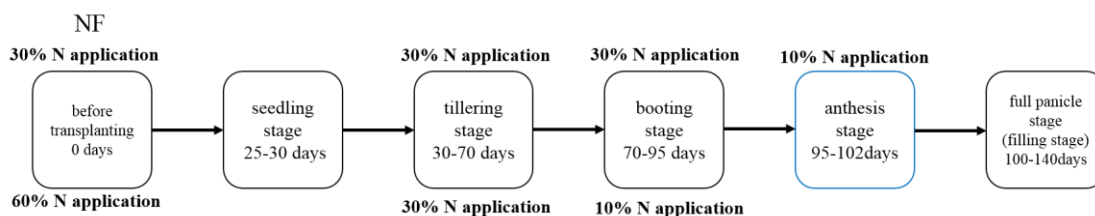
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23 **1 Supplementary Figures and Tables**

24 **1.1 Supplementary Figures**

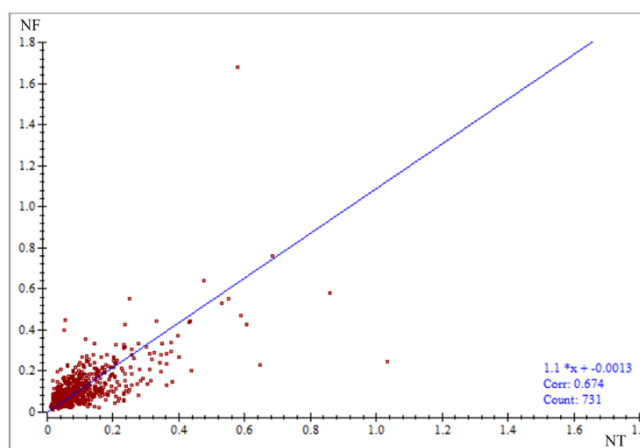
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27 Figure S1. The major stages of days after transplanting of rice (Jinhui 809) and N application.

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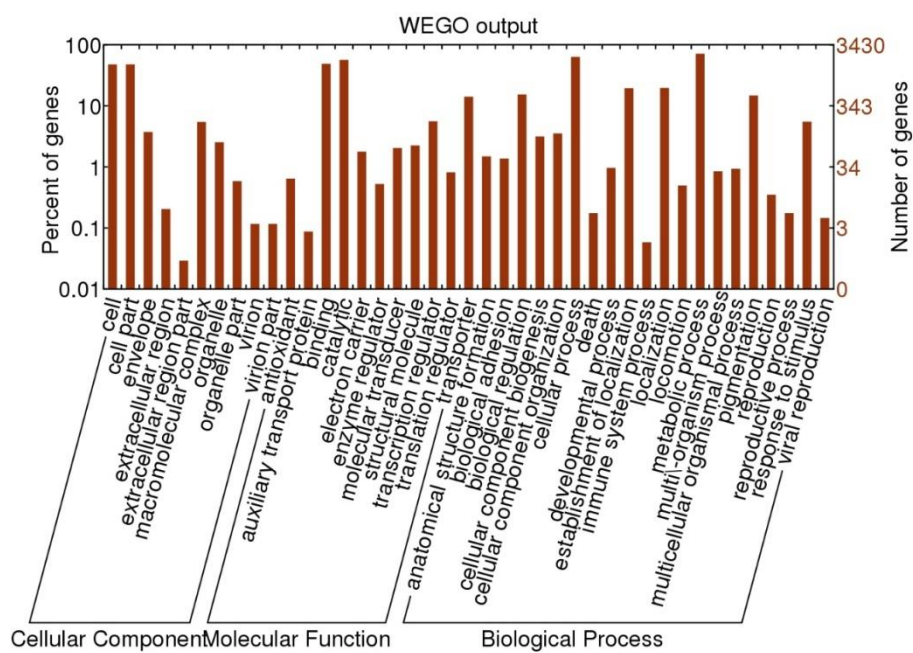


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30 **Figure S2.** The 2-DE maps from the two different soil samples with significant correlations between
31 scatter plots. NT, traditional nitrogen application; NF, efficient nitrogen application.

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35 **Figure S3.** Gene Ontology (GO) for the identified soil proteins. The right coordinate axis
 36 indicates the number of proteins for each GO annotation, and the left one represents the proportion
 37 of proteins for every GO annotation.

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1.2 Supplementary Tables

Table S1 Relative abundance (RA) and taxonomic assignment of significantly more abundant dominant bacterial T-RFs in NF treatment soil

T- RF (bp)	RE	RA (%)		Ecological functions	T-RFLP PAT assignment	Phylum
		NF	NT			
147	<i>MspI</i>	1.31	0	Cellulose degradation	<i>Aneurinibacillus aneurinilyticus</i> ATCC 12856 (T). (D78455)	<i>Firmicutes</i>
				Cellulose degradation	<i>Aneurinibacillus aneurinilyticus</i> NCIMB 156. (X6 645)	<i>Firmicutes</i>
				Cellulose degradation	<i>Aneurinibacillus migulanus</i> ATCC 9999 (T). (D78462)	<i>Firmicutes</i>
241	<i>AluI</i>	2.66	1.49	Cellulose degradation	<i>Cytophaga sp. str.</i> BD1-16. (AB 15525)	<i>Bacteroidetes</i>
250	<i>AluI</i>	1.07	0.85	C cycle	<i>Paenibacillus curdolanolyticus str.</i> YK9 IFO 15724 (T).	<i>Firmicutes</i>
228	<i>AluI</i>	1.20	0.00	N cycle	<i>Moorella thermoacetica</i> ATCC 3973. (M59121)	<i>Firmicutes</i>
331	<i>HaeIII</i>	1.64	0	Nitrification	<i>Nitrospira sp.</i> (AJ22442)	<i>Nitrospirae</i>
				Nitrification	<i>Nitrospira sp.</i> (AJ22439)	<i>Nitrospirae</i>
282	<i>AluI</i>	2.17	1.51	Uncheat	<i>Haemophilus actinomycetemcomitans</i> ATCC 33384 (T).	<i>Proteobacteria</i>
				Uncheat	<i>Haemophilus parainfluenzae str.</i> 429 (M.Pittman) ATCC 79 1.	<i>Proteobacteria</i>
				Uncheat	<i>Haemophilus paraphrophilus str.</i> Funagli (K. Zinnemann)	<i>Proteobacteria</i>
229	<i>AluI</i>	1.08	1.00	Uncheat	<i>Aquifex pyrophilus str.</i> Kol5a. (M83548)	<i>Aquificae</i>
538	<i>MspI</i>	1.74	0.00	Pathogen	<i>Spiroplasma clarkii str.</i> CN-5 ATCC 33827 (T). (M24474)	<i>Tenericutes</i>
				Pathogen	<i>Spiroplasma diabroticae str.</i> DU-1 ATCC 4321 (T).	<i>Tenericutes</i>
				Pathogen	<i>Spiroplasma monobiae str.</i> MQ-1 ATCC 33825 (T). (M24481)	<i>Tenericutes</i>
209	<i>HaeIII</i>	2.06	0.60	Pathogen	<i>Staphylococcus kloosii str.</i> SC21 ATCC 43959 (T).	<i>Firmicutes</i>

Table S2 Relative abundance (RA) and taxonomic assignment of significantly more abundant dominant bacterial T-RFs in NT treatment soil

T-RF (bp)	RE	RA (%)		Ecological functions	T-RFLP PAT assignment	Phylum
		NF	NT			
74	<i>MspI</i>	0.68	1.18	S cycle	<i>Desulfohalobium retbaense</i> str. HR1 DSM 5692 (T).	<i>Proteobacteria</i>
88	<i>MspI</i>	0.00	1.33	Denitrification	<i>Neisseria animalis</i> str. NA1 ATCC 19573. (L6172)	<i>Proteobacteria</i>
				Denitrification	<i>Neisseria denitrificans</i> str. M37 ATCC 14686 (T). (M352)	<i>Proteobacteria</i>
				Denitrification	<i>Neisseria denitrificans</i> str. M37 ATCC 14686 (T). (L6173)	<i>Proteobacteria</i>
308	<i>HaeIII</i>	0.28	1.04	mosquito eradication	<i>Bacillus sphaericus</i> NRS 1198. (L1416)	<i>Firmicutes</i>
310	<i>HaeIII</i>	0.68	2.49	Pathogen	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> ATCC 126 (T).	<i>Firmicutes</i>
				Pathogen	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> ATCC 126 (T).	<i>Firmicutes</i>
				Pathogen	<i>Staphylococcus capitis</i> subsp. <i>ureolyticus</i> ATCC 49326 (T).	<i>Firmicutes</i>
				Pathogen	<i>Staphylococcus caprae</i> ATCC 35538 (T). (AB 9935)	<i>Firmicutes</i>
				Pathogen	<i>Staphylococcus epidermidis</i> ATCC 1499 (T).	<i>Firmicutes</i>
				Pathogen	<i>Staphylococcus equorum</i> ATCC 43958 (T). (AB 9939)	<i>Firmicutes</i>
				Pathogen	<i>Staphylococcus lugdunensis</i> str. N86 297 ATCC 438 9 (T).	<i>Firmicutes</i>
				Pathogen	<i>Staphylococcus succinus</i> str. AMG-D1 ATCC 7337 (T).	<i>Firmicutes</i>
				Pathogen	<i>Staphylococcus succinus</i> str. AMG-D2. (AF 4219)	<i>Firmicutes</i>
148	<i>MspI</i>	0.00	2.49	Pathogen	<i>Aerococcus urinae</i> NCFB 2893 (T).	<i>Firmicutes</i>

					(M77819)	
				Pathogen	<i>Aerococcus urinae</i> str. 1656-92. (U64458)	<i>Firmicutes</i>
286	<i>HaeIII</i>	0.92	1.81	Pathogen	<i>Eubacterium ruminantium</i> str. GA 195 ATCC 17233 (T).	<i>Firmicutes</i>
100	<i>AfaI</i>	0.60	5.34	Pathogen	<i>Mycoplasma corogypsi</i> str. BV1 ATCC 51148 (T). (L854)	<i>Tenericutes</i>
106	<i>AfaI</i>	0.00	3.67	Pathogen	<i>Haliscomenobacter hydrossis</i> ATCC 27775 (T). (M5879)	<i>Bacteroidetes</i>
				Pathogen	<i>Mycoplasma neurolyticum</i> str. Sabin type A ATCC 19988 (T).	<i>Tenericutes</i>
110	<i>AfaI</i>	0.00	3.90	Pathogen	<i>Afipia clevelandensis</i> . (M69186)	<i>Proteobacteria</i>
243	<i>AluI</i>	0.65	2.33	Pathogen	<i>Mobiluncus curtisii</i> subsp. <i>curtisii</i> str. BV 345-16 ATCC 35241	<i>Actinobacteria</i>
338	<i>HaeIII</i>	0.00	1.37	C cycle	<i>Weissella confusus</i> ATCC 1881 (T). (M2336)	<i>Bacteroidetes</i>
				C cycle	<i>Weissella kandleri</i> DSM 2 593 (T). (M2338)	<i>Bacteroidetes</i>
				C cycle	<i>Weissella minor</i> NCDO 1973. (X52569)	<i>Bacteroidetes</i>
				C cycle	<i>Weissella viridescens</i> str. S38A ATCC 127 6 (T). (M234)	<i>Bacteroidetes</i>
				C cycle	<i>Pediococcus pentosaceus</i> str. LS 5. (AB 18215)	<i>Firmicutes</i>
232	<i>AluI</i>	0.00	1.05	C cycle	<i>Lactobacillus casei</i> subsp. <i>casei</i> ATCC 393 (T). (M23928)	<i>Firmicutes</i>
				C cycle	<i>Lactobacillus rhamnosus</i> DSM 221 (T). (M58815)	<i>Firmicutes</i>

Table S3 Soil proteins identified by MALDI TOF-TOF MS

spot no ^{a)}	GI no ^{b)}	protein name ^{c)}	MW/pI ^{d)}	match peptide ^{e)}	Score	Species	Tendence ^{f)}
Protein originate from Microbe							
Carbohydrate metabolism							
9	gi 24276190 2	triosephosphate isomerase[EC:5.3.1.1]	27058/5.58	3	138	<i>Talaromyces stipitatus</i>	None
21	gi 10702627 9	alcohol dehydrogenase GroES-like protein[EC:1.1.1.1]	36446/6.14	3	346	<i>Burkholderia cenocepacia</i>	Down
26	gi 11535268 1	aldehyde dehydrogenase[EC:1.2.1.3]	49983/5.9		101(PM F)	<i>Burkholderia ambifaria</i>	Up
30	gi 12751935 9	Enolase[EC:4.2.1.11]	46955/5.36	2	212	<i>Candida glycerinogenes</i>	Down
37	gi 120642	Glyceraldehyde-3-phosphate dehydrogenase[EC:1.2.1.9]	31516/6.02	1	59	<i>Escherichia coli</i>	Down
71	gi 10702627 9	alcohol dehydrogenase GroES-like protein[EC:1.1.1.1]	36446/6.14	3	346	<i>Burkholderia cenocepacia</i>	None
78	gi 19057369 8	phosphopyruvate hydratase[EC:4.2.1.11]	45755/5.03	3	115	<i>Stenotrophomonas maltophilia</i>	None
138	gi 15297187 3	phosphoglycerate kinase[EC:2.7.2.3]	40720/5.02	2	103	<i>Klebsiella pneumoniae</i>	None
Energy metabolism							
28	gi 21253824 5	nitroreductase family protein, putative[EC:1.13.11.79]	30703/8.67	2	166	<i>Penicillium marneffeii</i>	Up
34	gi 91178118	mitochondrial F-ATPase beta subunit	36166/5	4	332	<i>Kluyveromyces marxianus</i>	Up
54	gi 19057594 2	FOF1 ATP synthase subunit beta[EC:3.6.3.14]	50840/5.1	4	184	<i>Stenotrophomonas maltophilia</i>	Up
55	gi 33593402	putative oxidoreductase[EC:1.2.7.1]	52540/5.82	1	66	<i>Bordetella pertussis</i>	Down

72	gi 12665344 3	F0F1 ATP synthase subunit alpha[EC:3.6.3.14]	54718/5.43	4	161	<i>Bacillus</i>	None
77	gi 19057499 5	putative protein associated with polyhydroxyalkanoate inclusion	17928/5.29		95(PMF)	<i>Stenotrophomonas maltophilia</i>	None
84	gi 31940415 9	Polyphosphate kinase[EC:2.7.4.1]	81409/6		93(PMF)	<i>Bartonella rochalimae</i>	None
88	gi 31740195 1	ABC transporter	43367/7.01	3	158	<i>Achromobacter xylosoxidans</i>	None
105	gi 13429327 1	electron transfer flavoprotein, alpha subunit	31476/5.27	10	117	<i>Burkholderia vietnamiensis</i>	None
108	gi 24280650 1	ATP synthase F1, beta subunit, putative[EC:3.6.3.14]	55699/5.11		142(PMF)	<i>Talaromyces stipitatus</i>	None
109	gi 29360418 8	electron transfer flavoprotein alpha subunit	30797/4.97	3	184	<i>Achromobacter piechaudii</i>	None
124	gi 21253852 1	ATP synthase F1, beta subunit, putative[EC:3.6.3.14]	55696/5.16	4	366	<i>Penicillium marneffeii</i>	None
137	gi 31279489 5	ATP synthase beta chain[EC:3.6.3.14]	50705/5.18	5	412	<i>Burkholderia rhizoxinica</i>	None
141	gi 53719521	dihydrolipoamide dehydrogenase[EC:1.8.1.4]	50669/6.1	3	236	<i>Burkholderia pseudomallei</i>	None
158	gi 78067213	inorganic pyrophosphatase[EC:3.6.1.1]	19390/5.19	2	113	<i>Burkholderia</i>	None
Cell development and motility							
13	gi 50057090	surface layer protein	32061/4.77	1	59	<i>Bacillus fusiformis</i>	Up
20	gi 50057090	surface layer protein	32061/4.77	1	120	<i>Bacillus fusiformis</i>	Up
23	gi 11761910 3	outer membrane protein A	37973/4.94	1	68	<i>Aeromonas hydrophila subsp Candidatus Sulcia muelleri</i>	Down
24	gi 94502270	outer membrane protein A	43892/6.44	1	130		Up
27	gi 50057090	surface layer protein	32061/4.77	1	75	<i>Bacillus fusiformis</i>	Up
29	gi 24239230 4	flagellin	40089/4.8	1	178	<i>Bacillus</i>	Up

35	gi 12665385 5	putative S-layer protein/N-acetylmuramoyl-L-alanine amidase	120572/5.07	3	105	<i>Bacillus</i>	Down
36	gi 31740379 1	flagellar biosynthesis	57900/5.21	1	241	<i>Achromobacter xylosoxidans</i>	Down
41	gi 12665247 4	flagellin protein	29278/9.27	2	181	<i>Bacillus</i>	Down
49	gi 91782371	OmpC family outer membrane porin	40240/9.14	1	90	<i>Burkholderia xenovorans</i>	Down
70	gi 12665385 5	putative S-layer protein/N-acetylmuramoyl-L-alanine amidase[EC:3.5.1.28]	120572/5.07	3	176	<i>Bacillus</i>	None
87	gi 70992107	N,O-diacetyl muramidase	24795/6.02	2	224	<i>Aspergillus fumigatus</i>	None
96	gi 12665247 4	flagellin protein	29278/5.36	1	102	<i>Bacillus</i>	None
116	gi 15297074 6	oligopeptide ABC transporter periplasmic substrate- binding protein	61464/6.12	3	300	<i>Klebsiella pneumoniae</i>	None
149	gi 19057249 1	putative fatty acid transport system, membrane protein	49950/6	4	373	<i>Stenotrophomonas maltophilia</i>	None
151	gi 58422901	OmpA	24087/4.93	1	123	<i>Enterobacter cloacae</i>	None
156	gi 19910967	flagellin protein FliA(A)	29131/6.45	1	136	<i>Clostridium novyi</i>	None
Signal transduction							
58	gi 25452404 6	TonB-dependent receptor	99332/6.04	4	174	<i>Stenotrophomonas</i>	Down
62	gi 19057534 5	putative TonB dependent receptor protein	100897/5.43	4	111	<i>Stenotrophomonas maltophilia</i>	Up
69	gi 25452104 5	TonB-dependent receptor domain protein	100172/4.93	2	106	<i>Stenotrophomonas</i>	None
82	gi 13429107 8	UspA domain-containing protein	16872/5.77	4	218	<i>Burkholderia vietnamiensis</i>	None
83	gi 19057584 4	putative TonB dependent receptor protein	103730/5.2	2	74	<i>Stenotrophomonas maltophilia</i>	None

104	gi 254521045	TonB-dependent receptor domain protein	100172/4.93	2	154	<i>Stenotrophomonas</i>	None
110	gi 254521045	TonB-dependent receptor domain protein	100172/4.93	2	92	<i>Stenotrophomonas</i>	None
111	gi 254521045	TonB-dependent receptor domain protein	100172/4.93	1	71	<i>Stenotrophomonas</i>	None
113	gi 190575345	putative TonB dependent receptor protein	100897/5.43	4	240	<i>Stenotrophomonas maltophilia</i>	None
159	gi 17545619	signal peptide protein[EC:3.4.23.-]	23689/9.52	2	168	<i>Ralstonia solanacearum</i>	None
Protein metabolism							
4	gi 126652707	peptidase, M42 family protein[EC:3.4.24.-]	39409/		95(PMF)	<i>Bacillus sp. B14905</i>	Up
5	gi 194291029	elongation factor tu	43392/5.49		157(PMF)	<i>cupriavidus taiwanensis</i>	Down
8	gi 2654449	elongation factor Tu	43227/5.58	2	163	<i>Pasteurella multocida</i>	Up
19	gi 241662151	co-chaperonin GroES	10330/5.78	2	92	<i>Ralstonia pickettii</i>	Up
25	gi 311747409	putative peptidase[EC:3.4.11.1]	69227/5.73		88(PMF)	<i>Algoriphagus</i>	Down
31	gi 192360498	ATPase, AAA family domain protein[EC:3.6.3.8]	50016/5.76		89(PMF)	<i>Cellvibrio japonicus</i>	Down
32	gi 118379374	Viral A-type inclusion protein repeat containing protein	311258/6.01		91(PMF)	<i>Tetrahymena thermophila</i>	Down
39	gi 22121784	Cpn60(60kDa chaperonin)	19764/4.8	4	259	<i>Achromobacter denitrificans</i>	Down
42	gi 416939	RecName: Full=Elongation factor Tu; Short=EF-Tu	43077/5.4	1	101	<i>cupriavidus taiwanensis</i>	Up
57	gi 293604177	30S ribosomal protein S1	62900/5.09	2	70	<i>Achromobacter piechaudii</i>	Down
63	gi 17545628	30S ribosomal protein S1	61576/5.24		93(PMF)	<i>Ralstonia</i>	Down

)	<i>solanacearum</i>	
67	gi 15602972	chaperonin GroEL	57369/4.82	1	119		<i>Pasteurella multocida</i>	Up
85	gi 17545628	30S ribosomal protein S1	61576/5.24	4	267		<i>Ralstonia solanacearum</i>	None
92	gi 18792767 5	chaperonin GroEL	57424/5.08	4	377		<i>Ralstonia pickettii</i>	None
95	gi 13429602 7	elongation factor Ts	31073/5.25	4	266		<i>Burkholderia vietnamiensis</i>	None
115	gi 29360375 2	chaperone DnaK	69618/4.92	2	201		<i>Achromobacter piechaudii</i>	None
117	gi 23875016 4	Valyl-tRNA synthetase[EC:6.1.1.9]	109958/5.24		84		<i>Yersinia rohdei</i>	None
120	gi 15603222	elongation factor Tu	43440/5.39	4	308		<i>Pasteurella multocida</i>	None
131	gi 53723863	50S ribosomal protein L7/L12	12552/4.9	1	75		<i>Burkholderia mallei</i>	None
142	gi 347163	protein F	33477/5.55	8	95		<i>Pseudomonas fluorescens</i>	None
146	gi 53720125	30S ribosomal protein S1	62326/8.83	2	68		<i>Burkholderia pseudomallei</i>	None
153	gi 22121908	Cpn60	19923/4.95	2	161		<i>Ralstonia pickettii</i>	None
161	gi 24166294 4	elongation factor Ts	31185/5.39	4	266		<i>Ralstonia pickettii</i>	None
164	gi 5689240	pro-aminopeptidase protease[EC:3.4.11.2]	62924/5.9	1	56		<i>Aeromonas punctata</i>	None
167	gi 24166215 2	chaperonin GroEL	57570/5.08	4	580		<i>Ralstonia pickettii</i>	None
Amino acid metabolism								
17	gi 13429475 3	dihydroorotase[EC:3.5.2.3]	39760/6.05	4	141		<i>Burkholderia vietnamiensis</i>	Up
68	gi 311105104	3-deoxy-7-phosphoheptulonate synthase 1[EC:2.5.1.54]	39208/6.36	1	73		<i>Achromobacter xylosoxidans</i>	None

74	gi 78066808	2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase[EC:2.3.1.117]	29632/5.67	3	214	<i>Burkholderia</i>	None
79	gi 78061567	3-hydroxyisobutyrate dehydrogenase[EC:1.1.1.31]	30285/6.04	1	103	<i>Burkholderia</i>	None
121	gi 21253481 4	glutamine synthetase[EC:6.3.1.2]	37847/5.49	3	231	<i>Burkholderia</i>	None
165	gi 11761984 0	Leu/Ile/Val-binding protein	38328/6.01	2	150	<i>Aeromonas hydrophila</i>	None
Defense response							
38	gi 15640750	anti-oxidant AhpCTSA family protein[EC:1.11.1.15]	23018/5.37	2	169	<i>Vibrio cholerae</i>	Down
44	gi 78067343	superoxide dismutase(SOD)[EC:1.15.1.1]	21090/5.61	4	236	<i>Burkholderia</i>	Up
47	gi 13429173 6	heat shock protein Hsp20	15752/5.17	4	127	<i>Burkholderia vietnamiensis</i>	Down
50	gi 13429173 6	heat shock protein Hsp20	15752/5.17	1	219	<i>Burkholderia vietnamiensis</i> G4	Down
64	gi 45356863	heat shock protein 70	67300/5.28	3	134	<i>Aspergillus fumigatus</i>	Down
123	gi 62125797	heat shock protein 70	69625/5.03	5	323	<i>Penicillium marneffeii</i>	None
155	gi 1169373	Heat shock protein 70	69812/4.88	2	160	<i>Burkholderia vietnamiensis</i>	None
56	gi 10702888 1	alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal allergen[EC:1.11.1.15]	20465/5.05	5	314	<i>Burkholderia cenocepacia</i>	Up
81	gi 13429468 8	thiol peroxidase atypical 2-Cys peroxiredoxin[EC:1.11.1.5]	17386/5.3	4	665	<i>Burkholderia vietnamiensis</i>	None
98	gi 16152823 7	superoxide dismutase(SOD)[EC:1.15.1.1]	24184/5.01	1	119	<i>Nitrosopumilus maritimus</i>	None
126	gi 15640750	anti-oxidant AhpCTSA family protein[EC:1.11.1.15]	23018/5.37	3	296	<i>Vibrio cholerae</i>	None
128	gi 18747756 3	alkyl hydroperoxide reductase[EC:1.11.1.15]	20388/5.12	5	711	<i>Bordetella avium</i>	None
132	gi 13429468 8	thiol peroxidase atypical 2-Cys peroxiredoxin)[EC:1.11.1.15]	17386/5.3	5	739	<i>Burkholderia vietnamiensis</i>	None

134	gi 18793010 3	thiol peroxidase(POD)[EC:1.11.1.15]	17367/5.1	5	281	<i>Ralstonia pickettii</i>	None
150	gi 33594422	alkyl hydroperoxide reductase[EC:1.11.1.15]	20331/5.11	1	90	<i>Bordetella pertussis</i> <i>Tohama</i>	None
Transcription							
1	gi 16385924 5	DNA-directed RNA polymerase subunit alpha[EC:2.7.7.6]	36356/5.6	6	387	<i>Bordetella petrii</i>	Up
15	gi 23992808 4	transcriptional regulator	100234/7.43		91(PMF)	<i>Streptomyces</i> <i>ghanaensis</i>	Up
16	gi 17547712	DNA-directed RNA polymerase subunit alpha[EC:2.7.7.6]	35567/5.52	2	237	<i>Ralstonia</i> <i>solanacearum</i>	Up
40	gi 78066729	phage shock protein A,	24253/5.08	2	171	<i>Burkholderia</i>	Down
45	gi 29715612 8	DNA-binding protein[EC:3.6.4.12]	31246/9.6		90(PMF)	<i>Streptomyces</i> <i>bingchenggensis</i>	Up
48	gi 78064769	uroporphyrinogen decarboxylase[EC:4.1.1.37]	42525/6.38	1	56	<i>Burkholderia</i>	Down
53	gi 30087184 6	DNA-directed RNA polymerase omega subunit family protein-like protein[EC:2.7.7.6]	648473/4.41		106(PM F)	<i>Brachyspira</i> <i>pilosicoli</i>	Down
65	gi 30252520 8	ribosomal RNA large subunit methyltransferase	40041/8.73		75(PMF)	<i>Streptomyces</i>	Down
106	gi 29681430 8	spermidine synthase[EC:2.5.1.16]	853693/5.41		66	<i>Arthroderma otae</i>	None
144	gi 53720795	DNA-directed RNA polymerase subunit alpha[EC:2.7.7.6]	35777/5.76	1	139	<i>Burkholderia</i> <i>pseudomallei</i>	None
<u>Unclear Function</u>							
73	gi 13429631 6	phasin family protein	19791/5.95	2	254	<i>Burkholderia</i>	None
75	gi 90420396	DJ-1/PfpI family protein[EC:3.2.-.-]	24069/4.57	1	67	<i>Aurantimonas</i> <i>manganooxydans</i>	None
90	gi 31740496 1	hypothetical protein HMPREF0005_04545	36553/5.17	3	218	<i>Achromobacter</i> <i>xylosoxydans</i>	None
97	gi 70984685	allergen Asp F3[EC:1.11.1.15]	18555/5.36	4	390	<i>Aspergillus</i>	None

118	gi 299535068	hypothetical protein BFZC1_03563	531110/4.95	2	54	<i>Lysinibacillus fusiformis</i>	None
127	gi 70996869	conserved hypothetical protein	25537/4.82	3	273	<i>Aspergillus fumigatus</i>	None
135	gi 225387039	hypothetical protein CLOSTASPAR_00789	36953/8.05	8	91	<i>Clostridium asparagiforme</i>	None
Protein originate from plant							
Amino acid metabolism							
14	gi 115489654	Ethylene-responsive methionine synthase[EC:2.1.1.14]	84955/5.93	1	118	<i>Oryza sativa</i>	Up
89	gi 17529621	S-adenosylmethionine synthetase[EC:2.5.1.6]	43648/5.93	2	137	<i>Oryza sativa</i> Indica Group	None
Carbohydrate metabolism							
61	gi 13249140	Glucanase[EC:3.2.1.4]	34755/ 5.92		144	<i>Oryza sativa</i>	Up
112	gi 968996	Glyceraldehyde-3-phosphate dehydrogenase[EC:1.2.1.9]	36641/6.61	2	139	<i>Oryza sativa</i>	None
100	gi 75225211	Putative aconitate hydratase[E.C. 4.2.1.3]	98591/5.67	2	136	<i>Oryza sativa</i>	None
Unclear Function							
91	gi 218198489	hypothetical protein OsI_23591	33360/5.20		110	<i>Oryza sativa</i> Indica Group	None
136	gi 225430043	hypothetical protein	39471/8.89	8	87	<i>Vitis vinifera</i>	None
Protein originate from fauna							
Genetic Information Processing							
18	gi 49388033	Proteasome subunit beta type 3[EC:3.4.25.1]	23111/5.17		67	<i>Oryza sativa</i> Japonica Group	Up
130	gi 115480019	Proteasome subunit beta type 1[EC:3.4.25.1]	24608/6.43		136	<i>Oryza sativa</i>	None

Carbohydrate metabolism							
86	gi 17003239 9	malate dehydrogenase [EC:1.1.1.37]	35315/6.15	1	54	<i>Culex quinquefasciatus</i>	None
Biosynthesis of unsaturated fatty acids							
148	gi 24169108 1	short-chain alcohol dehydrogenase, putative[EC:1.1.1.100]	31511/5.06		90(PMF)	<i>Ixodes scapularis</i>	None
Unclear Function							
51	gi 24639402	female sterile (1) Yb	118746/6.58	17	91	<i>Drosophila melanogaster</i>	Down
94	gi 32147771 4	Hypothetical protein DAPPUDRAFT_206384	280287/5.05	31	89	<i>Daphnia pulex</i>	None
139	gi 14969427 4	similar to zinc finger and BTB domain containing 40 isoform 1	140502/5.69	9	86	<i>Equus caballus</i>	None
162	gi 11548238 2	Chaperonin CPN60-1	61097/5.71		204	<i>Oryza sativa</i>	None

Note: a) The numbering corresponds to the 2-DE gel in Figure 3. b) GI number in NCBI. c) Protein name. d) Theoretical molecular weight and pI e). The number of peptides. f) The tendency of proteins compared with the NT treatment