Table S1. Primers and PCR conditions used in this paper

Primers	Sequence (5' – 3')	Thermal conditions	Reference
Rhizobacteria			
27F	AAC MGG ATT AGA TAC CCK G	94°C, 5 min, 1 cycle	
1492R	GGY TAC CTT GTT ACG ACT T	94°C for 1 min, 48-58°C (gradient = 48.0, 48.3, 48.9, 49.7, 113 50.8, 52.3, 54.0, 55.4, 56.5, 57.3, 57.8, 58.0°C) for 45 s, 72°C for 1 min, 30 cycles 72°C for 8 min, 1 cycle	Lane, 1990
Detection of '*Candidatus* Liberibacter asiaticus'			
Conventional PCR			Hocquellet et al, 1999
A2	TAT AAA GGT TGA CCT TTC GAG TTT	94°C for 2 min, 1 cycle,	
J5	ACA AAA GCA GAA ATA GCA CGA ACA A	94°C for 10 s, 65°C for 10s, 72°C for 1 min, 35 cycles 72°C for 4 min, 1 cycle	
qPCR			Wang *et al*., 2006
CQULA04F	TGG AGG TGT AAA AGT TGC CAA A	50°C for 2 min, 1 cycle	
CQULAP10P	ATC GTC TCG TCA AGA TTG CTA TCC GTG ATA CTA G	95°C for 15 min, 1 cycle 94°C for 15 s and 60°C for 1 min, 45 cycles	
CQULA04R	CCA ACG AAA AGA TCA GAT ATT CCT CTA		
Taxon/Group specific qPCR			
Total bacteria		95°C, 15 min, 1 cycle	Fierer *et al*., 2005
Eub338	ACT CCT ACG GGA GGC AGC AG	95°C for 1 min, 53°C for 30 s, 72°C for 1 min, 40 cycles	
Eub518	ATT ACC GCG GCT GCT GG		
Acidobacteria		95°C, 15 min, 1 cycle	Fierer *et al*., 2005
Acid31	GAT CCT GGC TCA GAA TC	95°C for 1 min, 50°C for 30 s, 72°C for 1 min, 40 cycles	
Eub518	ATT ACC GCG GCT GCT GG		
Actinobacteria		95°C, 15 min, 1 cycle	Fierer *et al*., 2005
Actino235	CGC GGC CTA TCA GCT TGT TG	95°C for 1 min, 60°C for 30 s, 72°C for 1 min, 40 cycles	
Eub518	ATT ACC GCG GCT GCT GG		
Alphaproteobacteria		95°C, 15 min, 1 cycle	Fierer *et al*., 2005
Eub338	ACT CCT ACG GGA GGC AGC AG	95°C for 1 min, 60°C for 30 s, 72°C for 1 min, 40 cycles	
Alfa685	TCT ACG RAT TTC ACC YC TAC		

Bacteroidetes		95°C, 15 min, 1 cycle 95°C for 1 min, 65°C for 30 s, 72°C for 1 min, 40 cycles	Fierer *et al*., 2005
Cfb319	GTA CTG AGA CAC GGA CCA		
Eub518	ATT ACC GCG GCT GCT GG		
Betaproteobacteria		95°C, 15 min, 1 cycle 95°C for 1 min, 60°C for 30 s, 72°C for 1 min, 40 cycles	Fierer *et al*., 2005
Eub338	ACT CCT ACG GGA GGC AGC AG		
Bet680	TCA CTG CTA CAC GYG		
Firmicutes		95°C, 15 min, 1 cycle 95°C for 1 min, 60°C for 30 s, 72°C for 1 min, 40 cycles	Fierer *et al*., 2005
Lgc353	GCA GTA GGG AAT CTT CCG		
Eub518	ATT ACC GCG GCT GCT GG		
***Pseudomonas* spp.**		95°C, 15 min, 1 cycle 95°C for 1 min, 64°C for 30 s, 72°C for 1 min, 40 cycles	Drigo *et al*., 2009
PsF	TTA GCT CCA CCT CGC GGC		
PsR	GGT CTG AGA GGA TGA TCA GT		
***Burkholderia* spp.**		95°C, 15 min, 1 cycle 95°C for 1 min, 64°C for 30 s, 72°C for 1 min, 40 cycles	Drigo *et al*., 2009
Burk3	CTG CGA AAG CCG GAT		
BurkR	TGC CAT ACT CTA GCY YGC		
***Bacillus* spp.**		95°C, 15 min, 1 cycle 95°C for 1 min, 63°C for 30 s, 72°C for 1 min, 40 cycles	Drigo *et al*., 2009
BacF	GGG AAA CCG GGG CTA ATA CCG GAT		
1378	CGG TGT GTA CAA GGC CCG GGA ACG		
qPCR of genes involved in nitrogen cycling			
narG		95°C, 15 min, 1 cycle 95°C for 15 s, 65 to 60°C for 30 s (-1°C by cycle), 72°C for 30 s, 80°C for 15 s, 6 cycles 95°C for 15 s, 60°C for 30 s, 72°C for 30 s, 80°C for 15 s, 40 cycles 95°C for 15 s, 60 to 95°C, 1 cycle	Hallin *et al*., 2009
narG1960m2F	TAY GTS GGG CAG GAR AAA CTG		
narG2050m2R	CGT AGA AGA AGC TGG TGC TGT T		
nirK		95°C, 15 min, 1 cycle 95°C for 15 s, 63 to 58°C for 30 s (-1°C by cycle), 72°C for 30 s, 80°C for 15 s, 6 cycles	Hallin *et al*., 2009
nirK876	ATY GGC GGV CAY GGC GA		
nirK1040	GCC TCG ATC AGR TTR TGG TT		

		95°C for 15 s, 60°C for 30 s, 72°C for 30 s, 80°C for 15 s, 40 cycles	
nirS		95°C for 15 s, 60 to 95°C, 1 cycle 95°C, 15 min, 1 cycle	Hallin *et al*., 2009
nirSCd3aFm	AAC GYS AAG GAR ACS GG	95°C for 15 s, 65 to 60°C for 30 s (-1°C by cycle), 72°C for 30 s, 80°C for 15 s, 6 cycles	
nirSR3cdm	GAS TTC GGR TGS GTC TTS AYG AA	95°C for 15 s, 60°C for 30 s, 72°C for 30 s, 80°C for 15 s, 40 cycles	
nosZ		95°C for 15 s, 60 to 95°C, 1 cycle 95°C, 15 min, 1 cycle	Hallin *et al*., 2009
nosZ2F	CGC RAC GGC AAS AAG GTS MSS GT	95°C for 15 s, 65 to 60°C for 30 s (-1°C by cycle), 72°C for 30 s, 80°C for 15 s, 6 cycles	
nosZ2R´	CAK RTG CAK SGC RTG GCA GAA	95°C for 15 s, 60°C for 30 s, 72°C for 30 s, 80°C for 15 s, 40 cycles	
***amoA*(AOB)**		95°C for 15 s, 60 to 95°C, 1 cycle 95°C, 10 min, 1 cycle	Hallin *et al*., 2009
amoA-1F	GGG GTT TCT ACT GGT GGT	94°C for 45 s, 58°C for 45 s, 72°C for 45 s, 39 cycles	
amoA-2R	CCC CTC KGS AAA GCC TTC TTC	95°C for 15 s, 60°C for 30 s, to 95°C for 15 s, 1 cycle	
***amoA*(AOA)**		95°C, 10 min, 1 cycle	Hallin *et al*., 2009
19F	ATG GTC TGG CTW AGA CG	94°C for 45 s, 55°C for 45 s, 72°C for 45 s, 39 cycles	
CrenamoA616r48x	GCC ATC CAB CKR TAN GTC CA	95°C for 15 s, 60°C for 30 s, to 95°C for 15 s, 1 cycle	

References:

Drigo B, van Veen JA, Kowalchuk GA. (2009). Specific rhizosphere bacterial and fungal groups respond to elevated atmospheric CO_2. *ISME J* **3:** 1204–1217.

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Hallin S, Jones CJ, Schloter M, Philippot L. (2009). Relationship between N-cycling communities and ecosystem functioning in a 50-year-old fertilization experiment. *ISME J.* **3:** 597–605

Hocquellet A, Bové JM, Garnier M. (1999). Isolation of DNA from the uncultured "*Candidatus* Liberobacter" species associated with citrus huanglongbing by RAPD. Curr Microbiol **38:** 176-182.

Lane DJ. (1990). 16S/23S rRNA sequencing In: Stackebrandt E, Goodfellow M (eds.) Nucleic *acid techniques in bacterial systematics*. John Wiley & Sons-New York, 115-147pp.

Wang Z, Yin Y, Hu H, Yuan Q, Peng G, Xia Y. (2006). Development and application of molecular-based diagnosis for '*Candidatus* Liberibacter asiaticus',the causal pathogen of citrus huanglongbing. *Plant Pathol* **55:** 630–638.

Figure S1. Rarefaction curves of 16S rRNA gene clone libraries from the rhizosphere of healthy citrus (HT1, HT2, and HT3); '*Ca.* Liberibacter asiaticus' infected citrus (IT1, IT2, and IT3); and bulk soil samples.

Figure S2. Relative abundances of the different bacterial phyla/genus in the rhizosphere of healthy (HT1, HT2, HT3); '*Ca.* Liberibacter asiaticus' infected citrus (IT1, IT2, and IT3); and bulk soil samples, as estimated using the qPCR assays. Error bars represent the standard errors of the means for three replicates. Statistical significance is represented by letters above each bar, with different letters signifying differences at $P \leq 0.01$ for each bacterial phyla/genus.

Figure S3. Hierarchical cluster analysis of (A) ribulose-l, 5-bisphosphate carboxylase ⁄ oxygenase (Rubisco); (B) carbon monoxide dehydrogenase (CODH); and (C) propionyl-CoA ⁄ acetyl-CoA carboxylase (PCC ⁄ ACC) genes in rhizosphere of '*Ca*. L. asiaticus' infected (IT1-IT3) or healthy (HT1-HT3) citrus. Genes that were present in at least three samples were used for cluster analysis. Results were generated in CLUSTER and visualized using TREEVIEW. Red indicates signal intensities above background while black indicates signal intensities below background. Brighter red colouring indicates higher signal intensities.

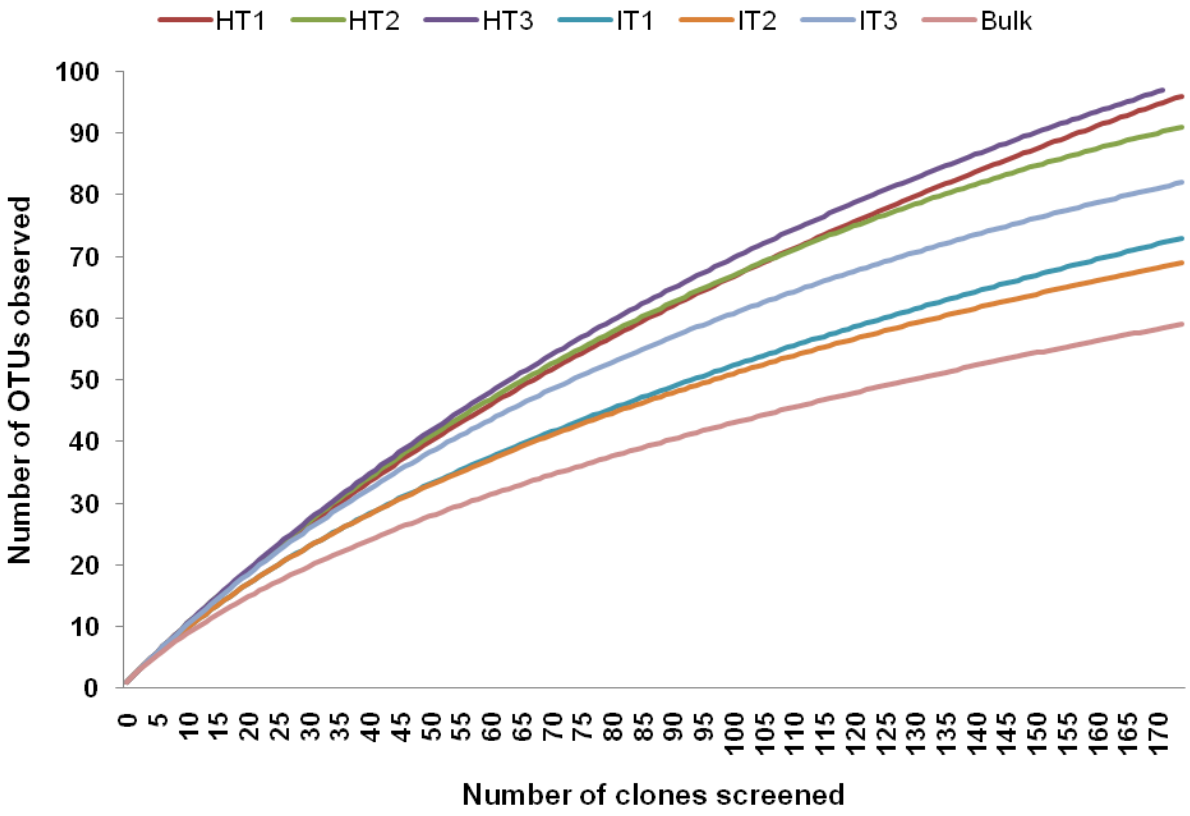

HT1
HT2
HT3
IT1
IT2
IT3
Bulk
Number of OTUs observed
0
10
20
30
40
50
60
70
80
90
100
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
105
110
115
120
125
130
135
140
145
150
155
160
165
170
Number of clones screened

Fig. S1

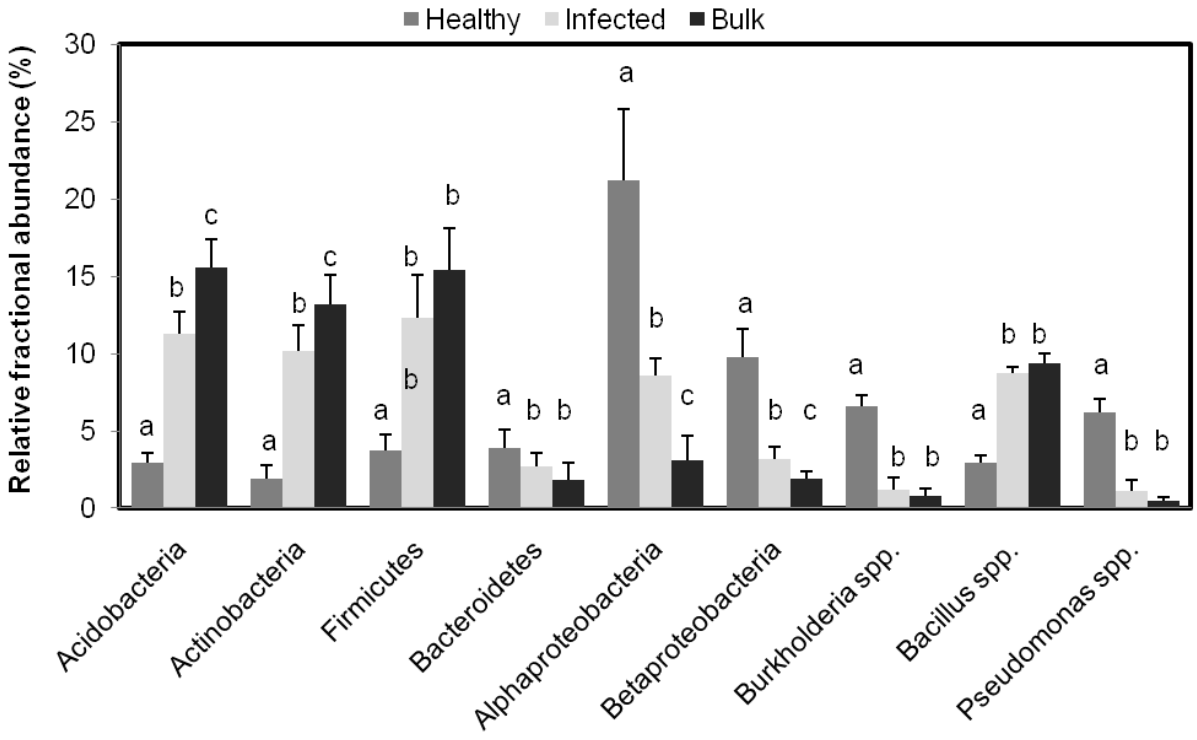

Healthy
Infected
Bulk
Relative fractional abundance (%)
30
25
20
15
10
5
0
a
b
c
a
b
c
a
b
b
a
b
b
a
b
c
a
b
c
a
b
b
a
b
b
a
b
b
Acidobacteria
Actinobacteria
Firmicutes
Bacteroidetes
Alphaproteobacteria
Betaproteobacteria
Burkholderia spp.
Bacillus spp.
Pseudomonas spp.

Fig. S2

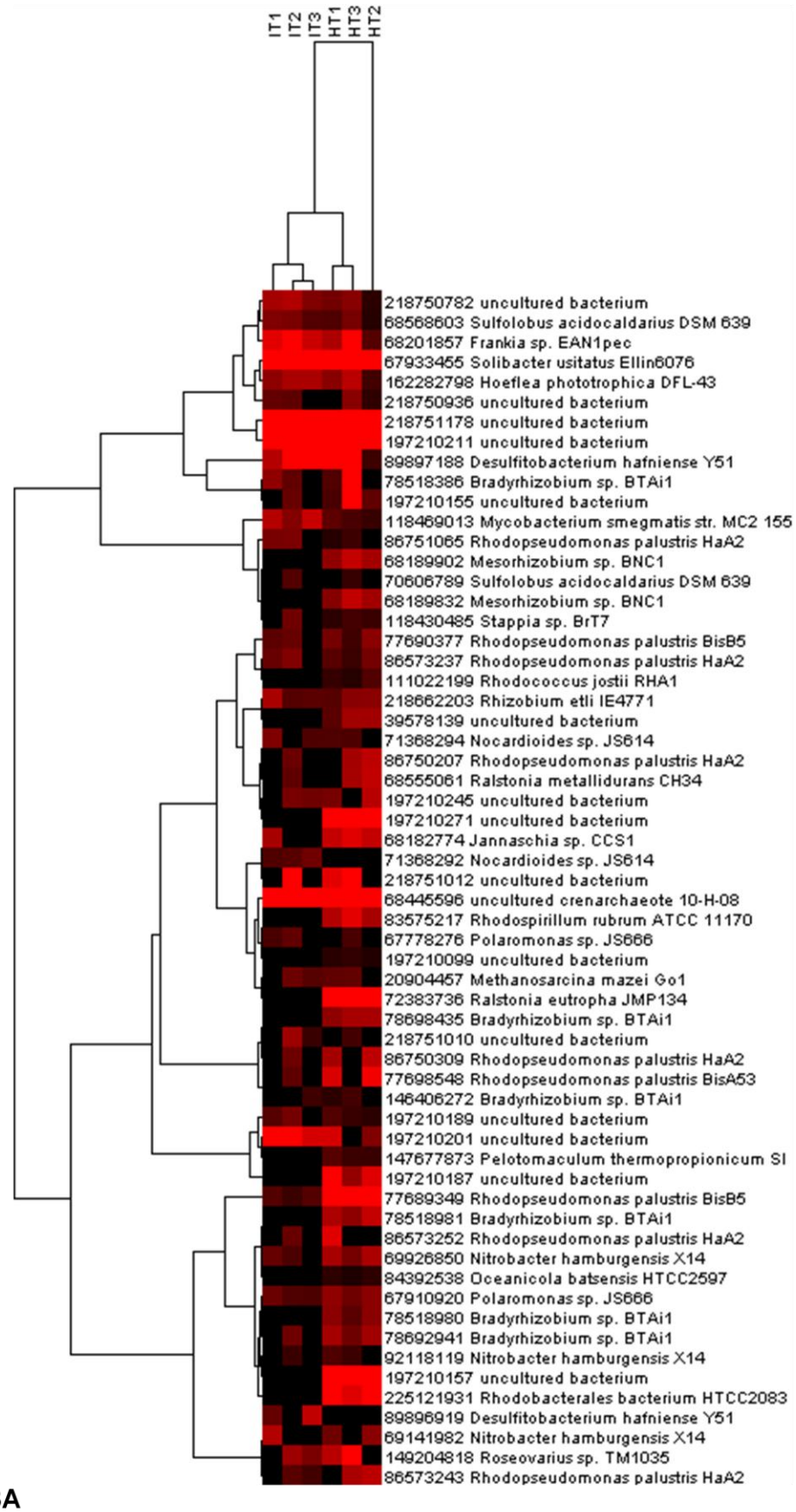
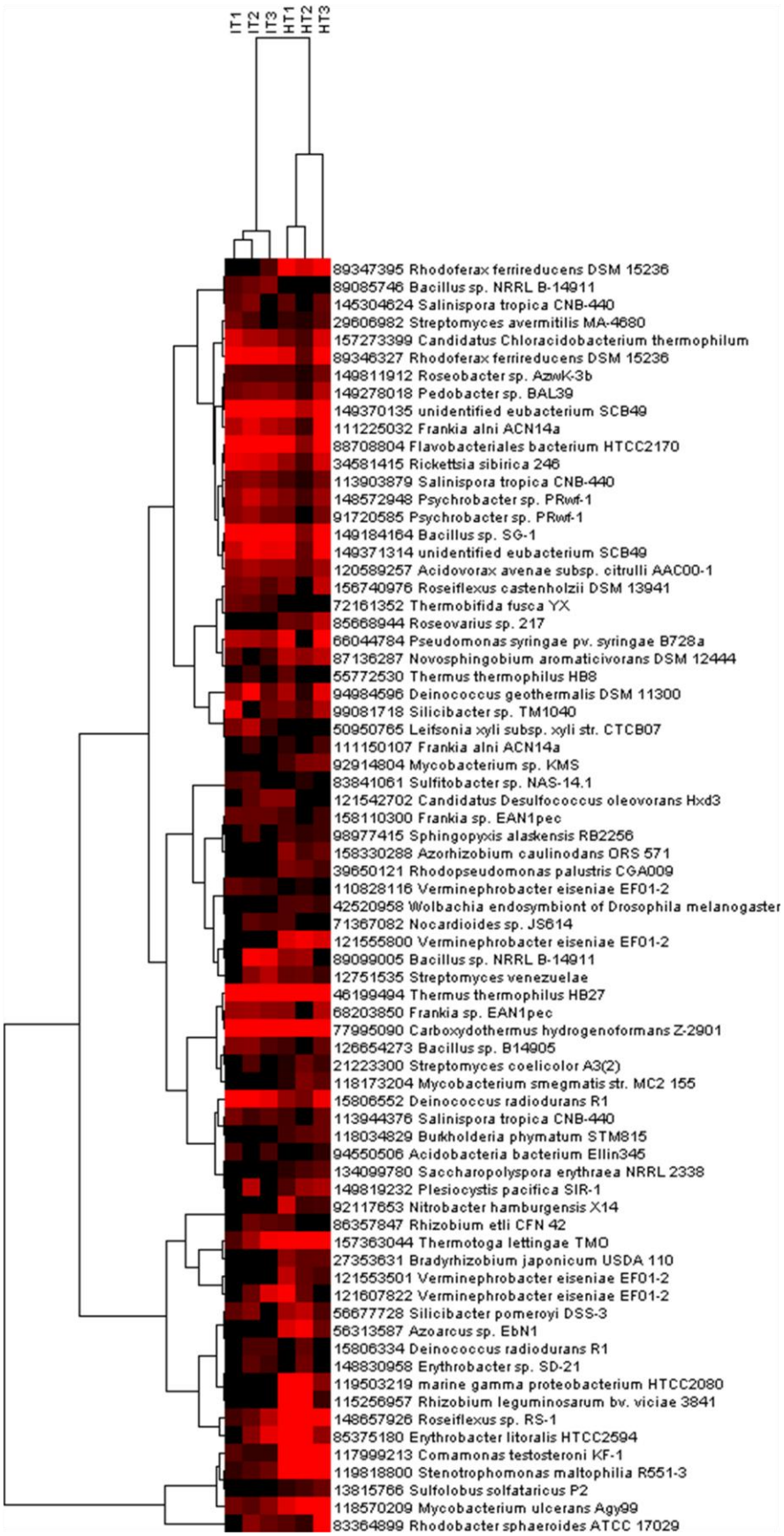

IT1
IT2
IT3
HT1
HT3
HT2
218750782 uncultured bacterium
68568603 Sulfolobus acidocaldarius DSM 639
68201857 Frankia sp. EAN1pec
67933455 Solibacter usitatus Ellin6076
162282798 Hoeflea phototrophica DFL-43
218750936 uncultured bacterium
218751178 uncultured bacterium
197210211 uncultured bacterium
89897188 Desulfitobacterium hafniense Y51
78518386 Bradyrhizobium sp. BTAi1
197210155 uncultured bacterium
118469013 Mycobacterium smegmatis str. MC2 155
86751065 Rhodopseudomonas palustris HaA2
68189902 Mesorhizobium sp. BNC1
70606789 Sulfolobus acidocaldarius DSM 639
68189832 Mesorhizobium sp. BNC1
118430485 Stappia sp. BrT7
77690377 Rhodopseudomonas palustris BisB5
86573237 Rhodopseudomonas palustris HaA2
111022199 Rhodococcus jostii RHA1
218662203 Rhizobium etli IE4771
39578139 uncultured bacterium
71368294 Nocardioides sp. JS614
86750207 Rhodopseudomonas palustris HaA2
68555061 Ralstonia metallidurans CH34
197210245 uncultured bacterium
197210271 uncultured bacterium
68182774 Jannaschia sp. CCS1
71368292 Nocardioides sp. JS614
218751012 uncultured bacterium
68445596 uncultured crenarchaeote 10-H-08
83575217 Rhodospirillum rubrum ATCC 11170
67778276 Polaromonas sp. JS666
197210099 uncultured bacterium
20904457 Methanosarcina mazei Go1
72383736 Ralstonia eutropha JMP134
78698435 Bradyrhizobium sp. BTAi1
218751010 uncultured bacterium
86750309 Rhodopseudomonas palustris HaA2
77698548 Rhodopseudomonas palustris BisA53
146406272 Bradyrhizobium sp. BTAi1
197210189 uncultured bacterium
197210201 uncultured bacterium
147677873 Pelotomaculum thermopropionicum SI
197210187 uncultured bacterium
77689349 Rhodopseudomonas palustris BisB5
78518981 Bradyrhizobium sp. BTAi1
86573252 Rhodopseudomonas palustris HaA2
69926850 Nitrobacter hamburgensis X14
84392538 Oceanicola batsensis HTCC2597
67910920 Polaromonas sp. JS666
78518980 Bradyrhizobium sp. BTAi1
78692941 Bradyrhizobium sp. BTAi1
92118119 Nitrobacter hamburgensis X14
197210157 uncultured bacterium
225121931 Rhodobacterales bacterium HTCC2083
89896919 Desulfitobacterium hafniense Y51
69141982 Nitrobacter hamburgensis X14
149204818 Roseovarius sp. TM1035
86573243 Rhodopseudomonas palustris HaA2

Fig. S3A


IT1
IT2
IT3
HT1
HT2
HT3
89347395 Rhodoferax ferrireducens DSM 15236
89085746 Bacillus sp. NRRL B-14911
145304624 Salinispora tropica CNB-440
29606982 Streptomyces avermitilis MA-4680
157273399 Candidatus Chloracidobacterium thermophilum
89346327 Rhodoferax ferrireducens DSM 15236
149811912 Roseobacter sp. AzwK-3b
149278018 Pedobacter sp. BAL39
149370135 unidentified eubacterium SCB49
111225032 Frankia alni ACN14a
88708804 Flavobacteriales bacterium HTCC2170
34581415 Rickettsia sibirica 246
113903879 Salinispora tropica CNB-440
148572948 Psychrobacter sp. PRwf-1
91720585 Psychrobacter sp. PRwf-1
149184164 Bacillus sp. SG-1
149371314 unidentified eubacterium SCB49
120589257 Acidovorax avenae subsp. citrulli AAC00-1
156740976 Roseiflexus castenholzii DSM 13941
72161352 Thermobifida fusca YX
85668944 Roseovarius sp. 217
66044784 Pseudomonas syringae pv. syringae B728a
87136287 Novosphingobium aromaticivorans DSM 12444
55772530 Thermus thermophilus HB8
94984596 Deinococcus geothermalis DSM 11300
99081718 Silicibacter sp. TM1040
50950765 Leifsonia xyli subsp. xyli str. CTCB07
111150107 Frankia alni ACN14a
92914804 Mycobacterium sp. KMS
83841061 Sulfitobacter sp. NAS-14.1
121542702 Candidatus Desulfococcus oleovorans Hxd3
158110300 Frankia sp. EAN1pec
98977415 Sphingopyxis alaskensis RB2256
158330288 Azorhizobium caulinodans ORS 571
39650121 Rhodopseudomonas palustris CGA009
110828116 Verminephrobacter eiseniae EF01-2
42520958 Wolbachia endosymbiont of Drosophila melanogaster
71367082 Nocardioides sp. JS614
121555800 Verminephrobacter eiseniae EF01-2
89099005 Bacillus sp. NRRL B-14911
12751535 Streptomyces venezuelae
46199494 Thermus thermophilus HB27
68203850 Frankia sp. EAN1pec
77995090 Carboxydothermus hydrogenoformans Z-2901
126654273 Bacillus sp. B14905
21223300 Streptomyces coelicolor A3(2)
118173204 Mycobacterium smegmatis str. MC2 155
15806552 Deinococcus radiodurans R1
113944376 Salinispora tropica CNB-440
118034829 Burkholderia phymatum STM815
94550506 Acidobacteria bacterium Ellin345
134099780 Saccharopolyspora erythraea NRRL 2338
149819232 Plesiocystis pacifica SIR-1
92117653 Nitrobacter hamburgensis X14
86357847 Rhizobium etli CFN 42
157363044 Thermotoga lettingae TMO
27353631 Bradyrhizobium japonicum USDA 110
121553501 Verminephrobacter eiseniae EF01-2
121607822 Verminephrobacter eiseniae EF01-2
56677728 Silicibacter pomeroyi DSS-3
56313587 Azoarcus sp. EbN1
15806334 Deinococcus radiodurans R1
148830958 Erythrobacter sp. SD-21
119503219 marine gamma proteobacterium HTCC2080
115256957 Rhizobium leguminosarum bv. viciae 3841
148657926 Roseiflexus sp. RS-1
85375180 Erythrobacter litoralis HTCC2594
117999213 Comamonas testosteroni KF-1
119818800 Stenotrophomonas maltophilia R551-3
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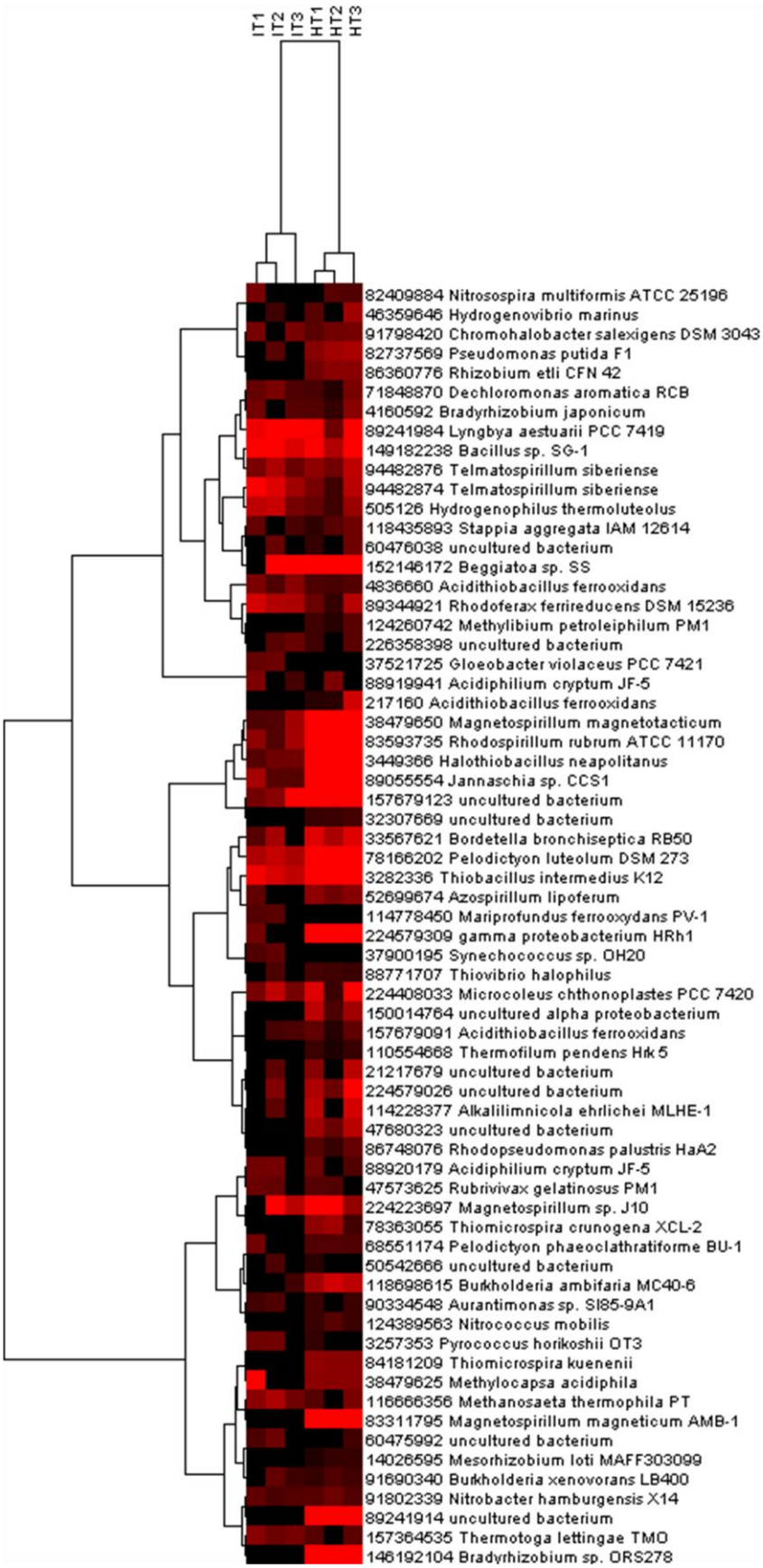
118570209 Mycobacterium ulcerans Agy99
83364899 Rhodobacter sphaeroides ATCC 17029

Fig. S3B


IT1
IT2
IT3
HT1
HT2
HT3
82409884 Nitrosospira multiformis ATCC 25196
46359646 Hydrogenovibrio marinus
91798420 Chromohalobacter salexigens DSM 3043
82737569 Pseudomonas putida F1
86360776 Rhizobium etli CFN 42
71848870 Dechloromonas aromatica RCB
4160592 Bradyrhizobium japonicum
89241984 Lyngbya aestuarii PCC 7419
149182238 Bacillus sp. SG-1
94482876 Telmatospirillum siberiense
94482874 Telmatospirillum siberiense
505126 Hydrogenophilus thermoluteolus
118435893 Stappia aggregata IAM 12614
60476038 uncultured bacterium
152146172 Beggiatoa sp. SS
4836660 Acidithiobacillus ferrooxidans
89344921 Rhodoferax ferrireducens DSM 15236
124260742 Methylibium petroleiphilum PM1
226358398 uncultured bacterium
37521725 Gloeobacter violaceus PCC 7421
88919941 Acidiphilium cryptum JF-5
217160 Acidithiobacillus ferrooxidans
38479650 Magnetospirillum magnetotacticum
83593735 Rhodospirillum rubrum ATCC 11170
3449366 Halothiobacillus neapolitanus
89055554 Jannaschia sp. CCS1
157679123 uncultured bacterium
32307669 uncultured bacterium
33567621 Bordetella bronchiseptica RB50
78166202 Pelodictyon luteolum DSM 273
3282336 Thiobacillus intermedius K12
52699674 Azospirillum lipoferum
114778450 Mariprofundus ferrooxydans PV-1
224579309 gamma proteobacterium HRh1
37900195 Synechococcus sp. OH20
88771707 Thiovibrio halophilus
224408033 Microcoleus chthonoplastes PCC 7420
150014764 uncultured alpha proteobacterium
157679091 Acidithiobacillus ferrooxidans
110554668 Thermofilum pendens Hrk 5
21217679 uncultured bacterium
224579026 uncultured bacterium
114228377 Alkalilimnicola ehrlichei MLHE-1
47680323 uncultured bacterium
86748076 Rhodopseudomonas palustris HaA2
88920179 Acidiphilium cryptum JF-5
47573625 Rubrivivax gelatinosus PM1
224223697 Magnetospirillum sp. J10
78363055 Thiomicrospira crunogena XCL-2
68551174 Pelodictyon phaeoclathratiforme BU-1
50542666 uncultured bacterium
118698615 Burkholderia ambifaria MC40-6
90334548 Aurantimonas sp. SI85-9A1
124389563 Nitrococcus mobilis
3257353 Pyrococcus horikoshii OT3
84181209 Thiomicrospira kuenenii
38479625 Methylocapsa acidiphila
116666356 Methanosaeta thermophila PT
83311795 Magnetospirillum magneticum AMB-1
60475992 uncultured bacterium
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91690340 Burkholderia xenovorans LB400
91802339 Nitrobacter hamburgensis X14
89241914 uncultured bacterium
157364535 Thermotoga lettingae TMO
146192104 Bradyrhizobium sp. ORS278

Fig. S3C