TABLE S1. Primers used in this study

Specificity	Primer	Sequence (5’–3’)	T_a °C	Reference
Bacteria	F984GC R1378	GC-clamp[a]-AACGCGAAGAACCTTAC CGGTGTGTACAAGGCCCGGGAACG	53	(1)
Bacteria	F27 R1494	AGAGTTTGATCMTGGCTCAG CTACGGYTACCTTGTTACGAC	56	(2) (3)
Bacteria	R1492	TACGGYTACCTTGTTACGACT	56	(2)
Bacteria	V3F V4R	ACTCCTACGGGAGGCAG TACNVRRGTHTCTAATYC	44	(4)
Alpha-proteobacteria	F203α	CCGCATACGCCCTACGGGGGAAAGATTTAT	56	(5)
Beta-proteobacteria	F948β	CGCACAAGCGGTGGATGA	64	(6)
Actinobacteriales	$F243_{HGC}$	GGATGAGCCCGCGGCCTA	63	(1)
Enterobacteriaceae	F234 R1423	GATGWRCCCRKATGGGA AKCTAMCTRCTTCTTTTGCAA	57	(7)
Pseudomonas	F311Ps R1459Ps	CTGGTCTGAGAGGATGATCAGT AATCACTCCGTGGTAACCGT	63	(8)
Bacillus and related taxa	BacF	GGGAAACCGGGGCTAATACCGGAT	65	(9)
Fungi	ITS1FGC ITS4 ITS2	GC-clamp-CTTGGTCATTTAGAGGAAGTAA TCCTCCGCTTATTGATATGC GCTGCGTTCTTCATCGATGC	55	(10)

[a] 5’ GC-clamp CGCCCGGGGCGCGCCCCGGGCGGGGCGGGGGCACGGGGGG

TABLE S2. Statistical analysis of the effect of soil biota on fertility of *M. hapla* feeding on tomato planted in infested soils

Dependent variable	Significance of fixed effects [a]		
	soil	sterilized	soil*sterilized
logGalls	*P*=0.015	*P*<0.001	*P*=0.070
logEggmasses	*P*=0.055	*P*<0.001	*P*=0.096
logEggs	*P*<0.001	*P*<0.001	*P*<0.001
logEggs	*P*<0.001 with sterilized=0 *P*=0.044 with sterilized=1	*P*<0.002 with soil=Kw, Go, or Gb	not applicable
fecundity	*P*=0.003	*P*<0.001	*P*=0.097

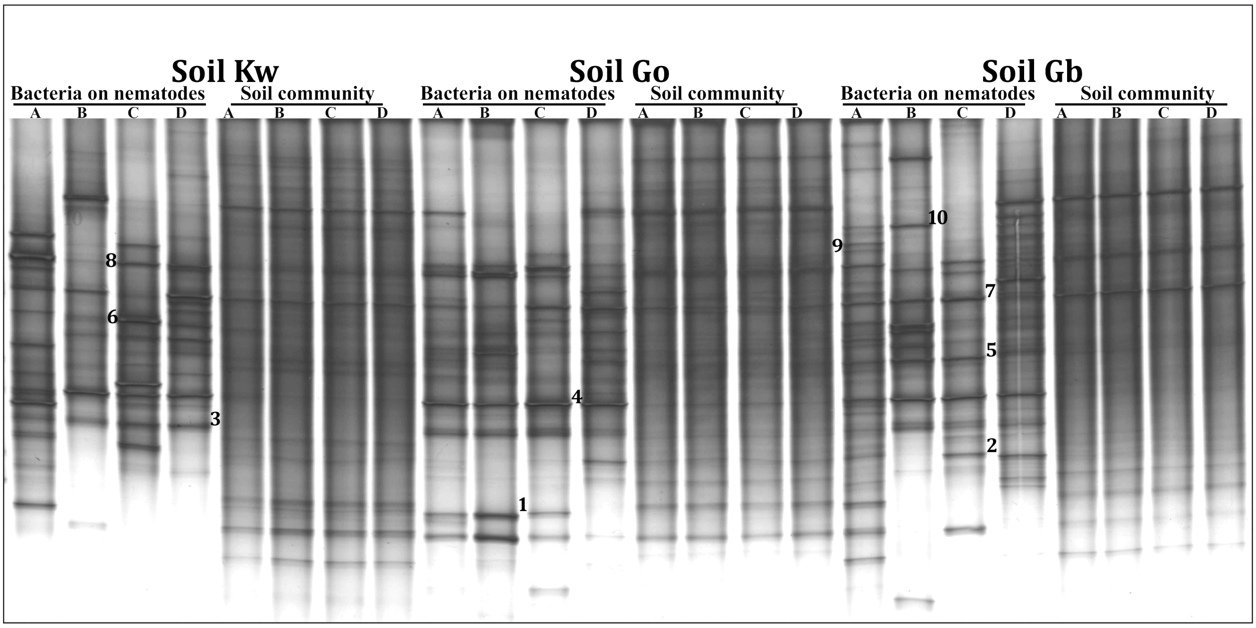
[a] Data and statistical analysis by SAS package 9.3:

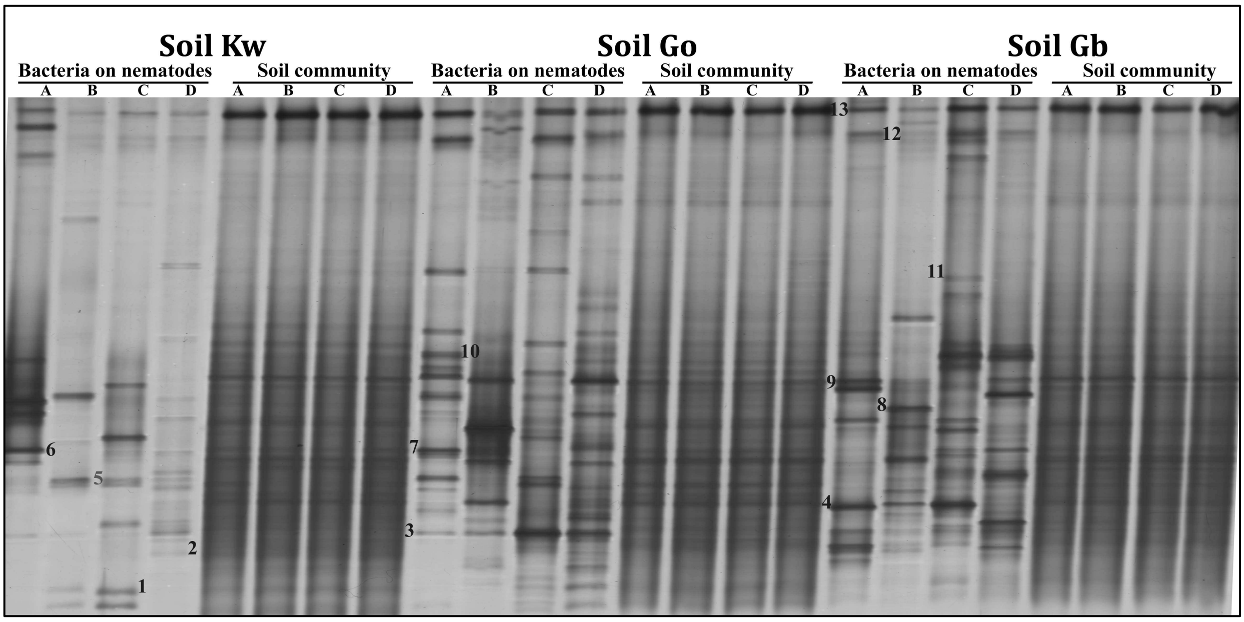
```
data M_hapla;
input block soil$ sterilized galls eggmasses eggs; /* per gram root freshweight*/
datalines;
1 Kw   0      26.1   19.9   3569.7
2 Kw   0       6.2    4.0   1968.7
3 Kw   0      14.3   10.1   1204.5
4 Kw   0      18.7   14.1   2145.9
5 Kw   0       3.8    1.0   1085.6
6 Kw   0      23.3    8.6   3506.5
7 Kw   0       5.7    3.7   1824.8
8 Kw   0      23.9   20.5   2424.2
1 Kw   1      45.6   38.6   32362.2
2 Kw   1      37.1   32.8   32861.9
3 Kw   1      37.8   32.4   25784.0
4 Kw   1      37.8   30.1   29014.1
5 Kw   1      31.2   25.9   26210.2
6 Kw   1      49.9   48.1   44296.4
7 Kw   1      32.5   31.8   30723.2
8 Kw   1      13.4   12.5   26215.0
1 Go   0      23.6   14.2   4829.7
2 Go   0      34.6   28.7   20323.7
3 Go   0      24.5   11.0   7300.6
4 Go   0      27.9   18.5   7541.0
5 Go   0      27.8   17.9   15363.6
6 Go   0      31.5   21.5   17770.4
7 Go   0      25.2   20.7   3952.9
8 Go   0      34.2   24.3   6818.2
1 Go   1      28.3   25.8   25055.9
2 Go   1      43.6   35.1   32651.0
3 Go   1      40.9   31.1   27985.5
4 Go   1      13.8   11.9   13071.9
5 Go   1      39.0   33.5   33246.5
6 Go   1      34.3   27.4   28133.0
7 Go   1      63.9   50.0   37230.2
8 Go   1      65.0   50.6   35150.5
1 Gb   0       9.1    8.1   2673.9
2 Gb   0      17.0   17.9   9242.2
3 Gb   0       7.8    2.0   6736.8
4 Gb   0      15.7    8.1   7037.0
5 Gb   0      12.5    2.3   10242.8
6 Gb   0      19.4   12.7   7870.0
7 Gb   0      17.5   12.6   5909.5
8 Gb   0      29.9   24.0   14403.0
1 Gb   1      21.3   17.2   29278.6
2 Gb   1      40.4   35.1   43593.3
3 Gb   1      48.6   35.1   38557.2
4 Gb   1      33.0   22.1   23832.9
5 Gb   1      35.2   31.9   45328.3
```

```
6 Gb   1      42.2   30.8   31615.6
7 Gb   1      31.6   27.8   50319.1
8 Gb   1      34.6   30.3   53750.7
;
data M_hapla; set M_hapla; /* log transformation */
fecundity = log(eggs / eggmasses);
logGalls= log(galls); logEggmasses= log(eggmasses); logEggs=log(eggs);

/* General tests */
proc mixed data=M_hapla; /* Effect of soil and soil sterilization on gall no. */
class block soil sterilized;
model logGalls = soil sterilized soil*sterilized / ddfm=kr; random block;
proc mixed data=M_hapla; /* Effect of soil and soil sterilization on eggmass no. */
class block soil sterilized;
model logEggmasses = soil sterilized soil*sterilized / ddfm=kr; random block;
proc mixed data=M_hapla; /* Effect of soil and soil sterilization on eggs no. */
class block soil sterilized;
model logEggs = soil sterilized soil*sterilized / ddfm=kr; random block;
proc mixed data=M_hapla; /* Effect of soil and sterilization on eggs per eggmass */
class block soil sterilized;
model fecundity = soil sterilized soil*sterilized / ddfm=kr; random block;

/* Tukey-Kramer tests for sterilized and native soils separately: */
proc sort data=M_hapla; by sterilized soil block;
proc mixed data=M_hapla; by sterilized; /* difference between soils in gall no. */
class block soil;
model logGalls = soil / ddfm=kr; random block;
lsmeans soil / ADJUST=TUKEY;
proc mixed data=M_hapla; by sterilized; /* egg masses compared between soils */
class block soil;
model logEggmasses= soil / ddfm=kr; random block;
lsmeans soil / ADJUST=TUKEY;
proc mixed data=M_hapla; by sterilized;/* no. of eggs compared between soils */
class block soil;
model logEggs = soil / ddfm=kr; random block;
lsmeans soil / ADJUST=TUKEY;
proc mixed data=M_hapla; by sterilized; /* fecundity compared between soils */
class block soil;
model fecundity = soil / ddfm=kr; random block;
lsmeans soil / ADJUST=TUKEY;
proc sort data=M_hapla; by soil sterilized block;
proc mixed data=M_hapla; by soil;  /* For verification of general effects after */
class block sterilized;            /* a significant interaction soil*sterilized */
model logEggs = sterilized / ddfm=kr; random block;
run;
```

Fig. S1. PCR-DGGE profiles of 16S rRNA genes of bacterial subgroups amplified in nested PCR from DNA of *M. hapla* juveniles from three arable soils (Kw, Go, Gb), and from total soil DNA. Ribotypes are marked that were enriched in nematode samples and characterized by sequencing (Table 2).

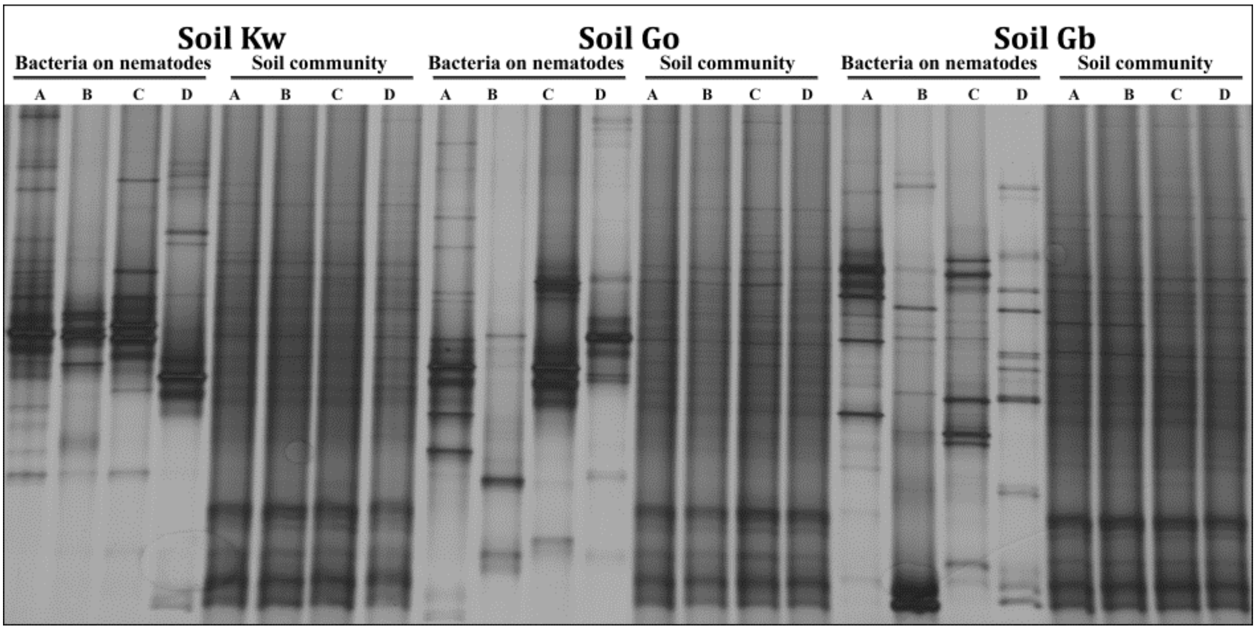
A) PCR-DGGE for “Bacillus” (based on specificity of primer BacF):



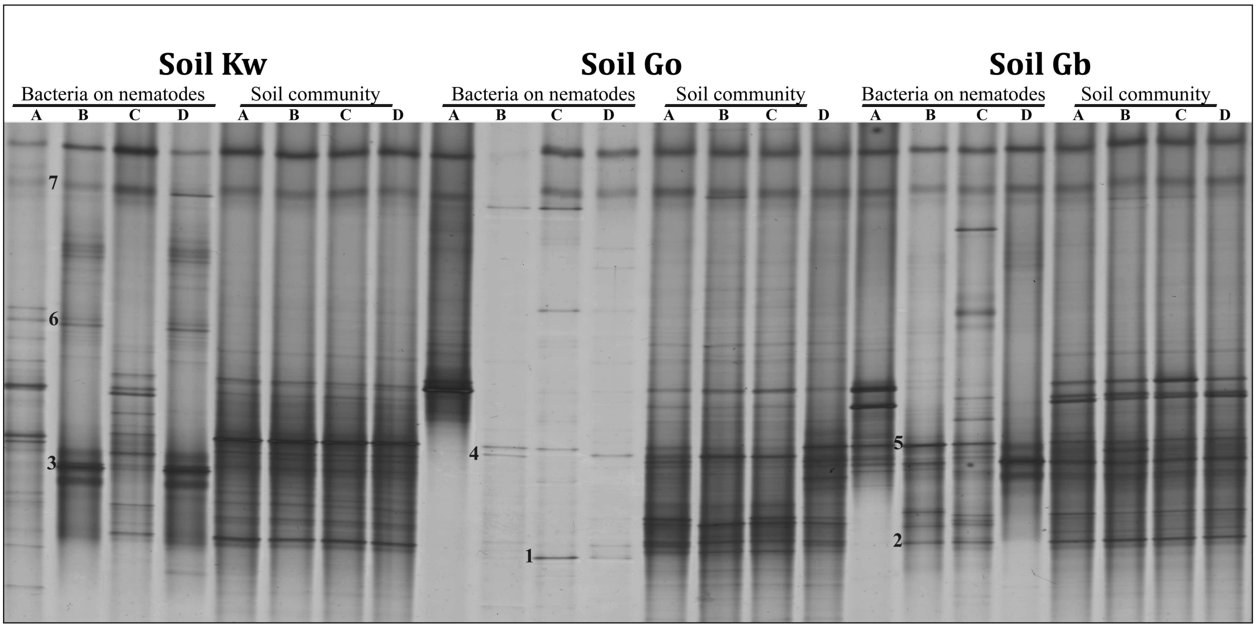


B) PCR-DGGE for *Alphaproteobacteria* (based on specificity of primer F203α):

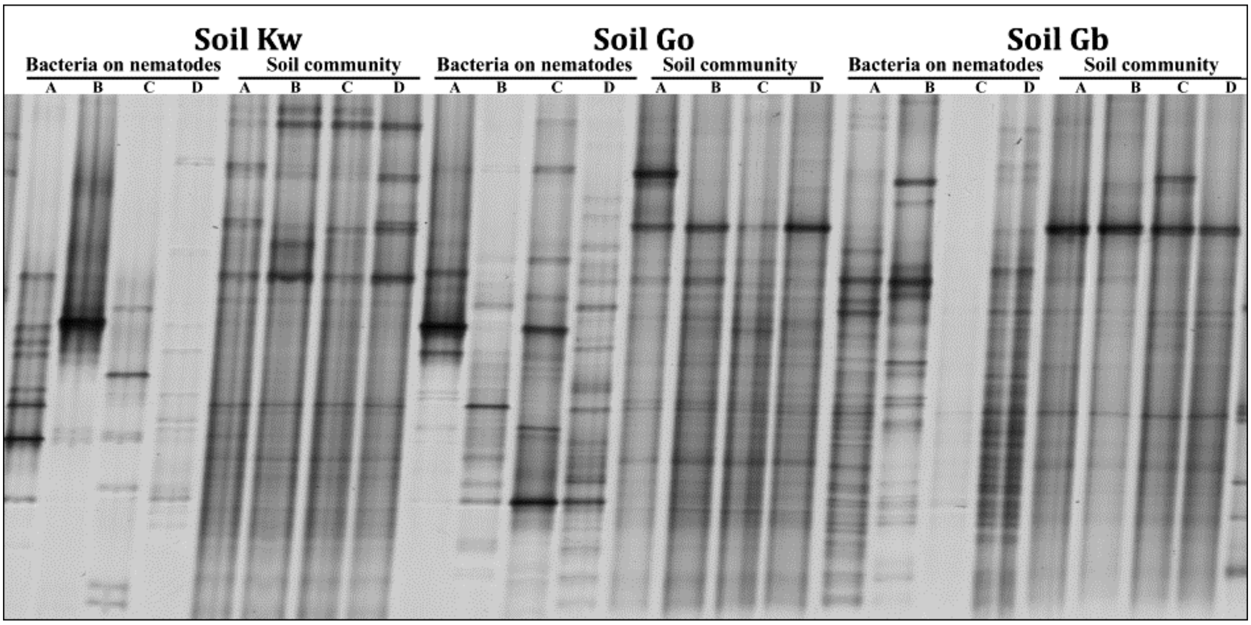
C) PCR-DGGE for *Betaproteobacteria* (based on specificity of primer F948β):



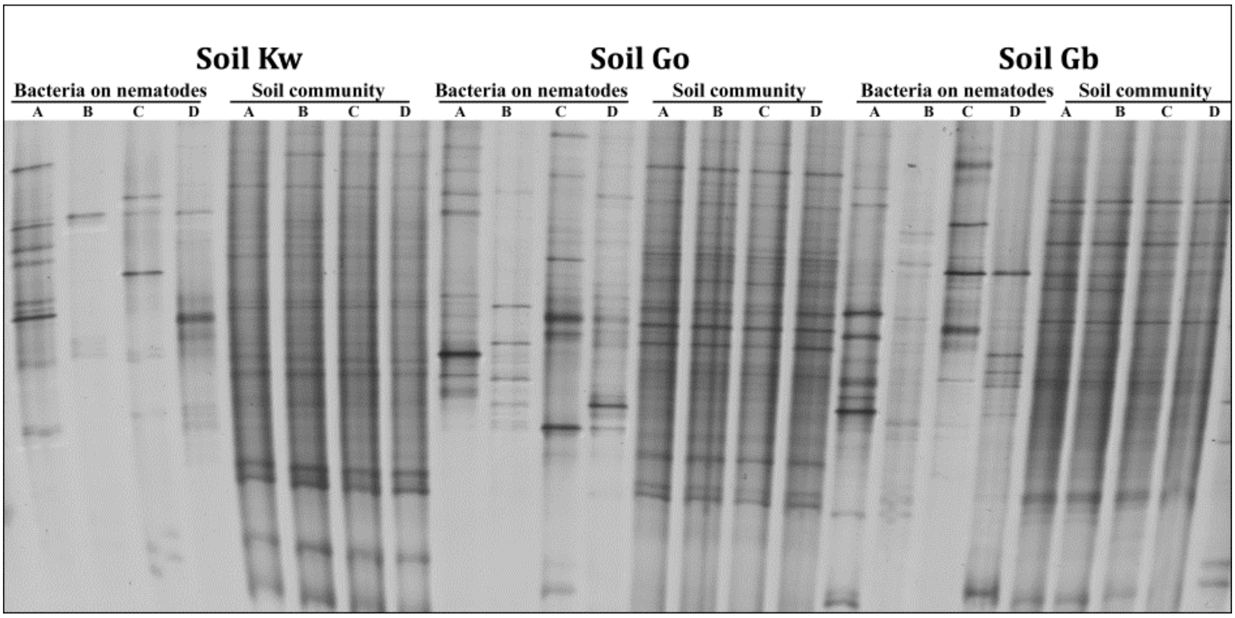
D) PCR-DGGE for *Pseudomonas* (based on specificity of primers F311Ps / R1459Ps):



E) PCR-DGGE for *Enterobacteriaceae* (based on specificity of primers F234 / R1423):



F) PCR-DGGE for *Actinobacteriales* (based on specificity of primer F243HGC):



BlastN hits with NCBI GenBank and UNITE species hypothesis (SH) database of representative (RepS) and reference ITS sequences (RefS), v.6 2014/1/15

>Fungi DGGE band no. 1
EU400587 Malassezia restricta isolate HA414, Basidiomycota, Ustilaginomycotina, Exobasidiomycetes, Malasseziales, Malasseziaceae, score 582 bits(315), e-value 4e-163, identities 324/328(99%), gaps 1

RepS SH206219.06FU, % identity 99.22, e-value 6e-127, bit score 452, Malassezia restricta

>Fungi DGGE band no. 2
GU017496 Aspergillus penicillioides isolate KH00256, Ascomycota, Pezizomycotina, Eurotiomycetes, Eurotiomycetidae, Eurotiales, Trichocomaceae, score 544 bits(294), e-value 2e-151, identities 297/298(99%), gaps 1

RepS SH213198.06FU, % identity 100.00, e-value 7e-132, bit score 468, Aspergillus penicillioides

>Fungi DGGE band no. 3
AB105353 Cryptococcus pseudolongus, Basidiomycota, Agaricomycotina, Tremellomycetes, Tremellales, score 320 bits(173), e-value 2e-84, identities 173/173(100%), gaps 0

RepS SH198505.06FU, % identity 100.0, e-value 5e-68, bit score 255, uncultured Basidiomycota

>Fungi DGGE band no. 4
JX501299 Chaetomium globosum strain ATCC6205, Ascomycota, Sordariomycetes, Sordariomycetidae, Sordariales, Chaetomiaceae, Score 503 bits(272), e-value 3e-139, identities 283/288(98%), gaps 2

HM537056 Fungal endophyte sp. g79, score 503 bits(272), e-value 3e-139, identities 283/288(98%), gaps 2

RepS SH234979.06FU, % identity 97.8, e-value 3e-105, bit score 379, Chaetomium globosum

>Fungi DGGE band no. 5
FJ439584 Arthopyreniaceae sp. GMG_P1, Ascomycota, Pezizomycotina, Dothideomycetes, Pleosporomycetidae, Pleosporales, Arthopyreniaceae, score 508 bits(275), e-value 6e-141, identities 275/275(100%), gaps 0

RepS SH011458.06FU, % identity 99.5, e-value 1e-103, bit score 374, Arthopyreniaceae

>Fungi DGGE band no. 6
AM901702 Eurotium sp. BF106, Ascomycota, Pezizomycotina, Eurotiomycetes, Eurotiomycetidae, Eurotiales, Trichocomaceae, score 475 bits(257), e-value 6e-131, identities 257/257(100%), gaps 0

RepS SH236882.06FU, % identity 100.0, e-value 1e-95, bit score 347, Eurotium repens
RepS SH236881.06FU, % identity 100.0, e-value 1e-95, bit score 347, Paecilomyces
>Fungi DGGE band no. 7
JX501311 Ganoderma applanatum strain BL26, Basidiomycota, Agaricomycetes, Polyporales, Ganodermataceae, score 582 bits(315), e-value 4e-163, identities 318/319(99%), gaps 1

RepS SH203388.06FU, % identity 100.0, e-value 3e-130, bit score 462, uncultured Ganoderma

>Fungi DGGE band no. 8
AJ300335 Cladosporium cladosporioides strain CBS 169.54 (identical to GU594746 Cladosporium cucumerinum strain 870381), Ascomycota, Pezizomycotina, Dothideomycetes, Dothideomycetidae, Capnodiales, Davidiellaceae, mitosporic Davidiellaceae, score 501 bits(271), e-value 1e-138, identities 271/271(100%), gaps 0

RepS SH005140.06FU, % identity 97.7, e-value 4e-103, bit score 372, uncultured soil fungus

>Fungi DGGE band no. 9
JX164064 Davidiella sp. FA-7B, Ascomycota, Dothideomycetes, Dothideomycetidae, Capnodiales, Davidiellaceae, score 497 bits(269), e-value 1e-137, identities 271/272(99%), gaps 0

RepS SH005107.06FU, % identity 100.0, e-value 6e-107, bit score 385, Cladosporium

>Fungi DGGE band no. 10
JX164076 Cryptococcus sp. FM-D1, Basidiomycota, Agaricomycotina, Tremellomycetes, Filobasidiales, mitosporic Filobasidiales, score 472 bits(255), e-value 7e-130, identities 255/255(100%), gaps 0

RepS SH005107.06FU, % identity 100.0, e-value 7e-93, bit score 338, Cryptococcus magnus
RepS SH019036.06FU, % identity 100.0, e-value 7e-93, bit score 338, Cryptococcus

>Fungi DGGE band no. 11
EF060720 Trichosporonales strain LM408, Basidiomycota, Agaricomycotina, Tremellomycetes, Tremellales, unclassified Trichosporonales, score 424 bits(229), e-value 2e-115, identities 237/241(98%), gaps 0

RepS SH195353.06FU, % identity 97.8, e-value 9e-85, bit score 311, Trichosporon asahii

>Fungi DGGE band no. 12
JF439489 Mortierella sp. T6, Fungi incertae sedis, Early diverging fungal lineages, Mortierellomycotina, Mortierellales, Mortierellaceae, score 499 bits(270), e-value 4e-138, identities 272/273(99%), gaps 0

JF439486 Mortierella humilis isolate F13, score 455 bits(246), e-value 8e-125, identities 266/275(97%), gaps 3

RepS SH218050.06FU, % identity 100.0, e-value 1e-102, bit score 370, Mortierella

>Fungi DGGE band no. 13
GU198183 Cylindrocarpon olidum isolate FI 2037, Ascomycota, Pezizomycotina, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, mitosporic Nectriaceae, mitosporic Neonectria, score 375 bits(203), e-value 7e-101, identities 208/210(99%), gaps 1

RepS SH232146.06FU, % identity 99.6, e-value 1e-108, bit score 390, Cylindrocarpon olidum

>Fungi DGGE band no. 14
AM410609 Ascomycete sp. VTT D-041032, Ascomycota, 697 bp, 460 bits(249), e-value=2e-126, identities 254/256(99%), gaps 1

HE972037 Gibellulopsis nigrescens, Ascomycota, Pezizomycotina, Sordariomycetes, Hypocreomycetidae, Glomerellales, Plectosphaerellaceae, score 457 bits(247), e-value 2e-125, identities 253/256(99%), gaps 0

RepS SH219633.06FU, % identity 100.0, e-value 2e-99, bit score 360, Verticillium nigrescens

>Fungi DGGE band no. 15
DQ485617 Rhizophydium sp. JEL-223, Chytridiomycota, Chytridiomycetes, Rhizophydiales, Rhizophydiaceae, score 558 bits(302), e-value 7e-156, identities 308/311(99%), gaps 0

RepS SH208245.06FU, % identity 98.1, e-value 8e-125, bit score 444, uncultured ectomycorrhizal fungus

>Bacillus DGGE band no. 1
NR_043037 Bradyrhizobium pachyrhizi strain PAC48, Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae, score 1323 bits(716), e-value 0.0, identities 748/764(98%), gaps 0

>Bacillus DGGE band no. 2

NR_044187 Sphingomonas insulae strain DS-28, Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae, score 1982 bits(1073), e-value 0.0, identities 1087/1094(99%), gaps 0

> Bacillus DGGE band no. 3
NR_036904 Staphylococcus epidermidis strain Fussel, Firmicutes; Bacilli; Bacillales; Staphylococcaceae, score 869 bits(470), e-value 0.0, identities 470/470(100%), gaps 0

> Bacillus DGGE band no. 4
NR_036904 Staphylococcus epidermidis strain Fussel, Firmicutes; Bacilli; Bacillales; Staphylococcaceae, score 2071 bits(1121), e-value 0.0, identities 1130/1134(99%), gaps 1

> Bacillus DGGE band no. 5
NR_044365 Micrococcus endophyticus strain YIM 56238, Actinobacteria; Actinomycetales; Micrococcaceae, score 1655 bits(896), e-value 0.0, identities 924/937(99%), gaps 4

> Bacillus DGGE band no. 6
NR_024691 Bacillus flexus strain IFO15715 / NR_043401 Bacillus megaterium strain IAM 13418, Firmicutes; Bacilli; Bacillales; Bacillaceae, score 1967 bits(1065), e-value 0.0, identities 1072/1075(99%), gaps 1/1075(0%)

> Bacillus DGGE band no. 7
NR_037113 Micrococcus luteus strain DSM 20030, Actinobacteria; Actinomycetales; Micrococcaceae, score 2043 bits(1106), e-value 0.0, identities 1124/1133(99%), gaps 0

>Bacillus DGGE band no. 8
NR_040847 Propionibacterium acnes, Actinobacteria; Actinomycetales; Propionibacteriaceae, score 2111 bits(1143), e-value 0.0, identities 1143/1143(100%), gaps 0

>Bacillus DGGE band no. 9
NR_041028 Methylobacterium rhodesianum strain DSM 5687, Alphaproteobacteria; Rhizobiales; Methylobacteriaceae, score 1956 bits(1059), e-value 0.0, identities 1124/1156(97%), gaps 1

> Bacillus DGGE band no. 10
NR_042778 Streptococcus thermophilus strain ATCC 19258, Firmicutes; Bacilli; Lactobacillales; Streptococcaceae, score 800 bits(433), e-value 0.0, identities 433/433(100%), gaps 0

>Alphaproteobacteria DGGE band no. 1
NR_041365 Solirubrobacter soli strain Gsoil 355, Actinobacteria, Solirubrobacterales, Solirubrobacteraceae, score 793 bits(429), identities 431/432(99.8%), gaps 0

>Alphaproteobacteria DGGE band no. 2
NR_026365 Janthinobacterium lividum strain DSM 1522, Betaproteobacteria, Burkholderiales, Oxalobacteraceae, score 747 bits(404), identities 406/407(99.8%), gaps 0

>Alphaproteobacteria DGGE band no. 3
NR_044112 Rhizobium phaseoli strain ATCC 14482, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, score 782 bits(423), identities 425/426(99.8%), gaps 0

>Alphaproteobacteria DGGE band no. 4
NR_026337 Pedomicrobium australicum strain IFAM ST1306, Alphaproteobacteria, Rhizobiales, Hyphomicrobiaceae, score 584 bits(316), identities 344/358(96.1%), gaps 0

>Alphaproteobacteria DGGE band no. 5
NR_074243 Ochrobactrum anthropi ATCC 49188 / NR_043184 O. cytisi strain ESC1, Alphaproteobacteria, Rhizobiales, Brucellaceae, score 793 bits(429), identities 433/435(99.5%), gaps 0

>Alphaproteobacteria DGGE band no. 6

NR_041967 Maricaulis maris strain ATCC 15268, Alphaproteobacteria, Rhodobacterales, Hyphomonadaceae, score 551 bits(298), identities 374/411(91.0%), gaps 4

>Alphaproteobacteria DGGE band no. 7
NR_029287 Nitrospira moscoviensis strain NSP M-1, Nitrospira, Nitrospirales, Nitrospiraceae, score 721 bits(390), identities 422/438(96.3%), gaps 0

>Alphaproteobacteria DGGE band no. 8
NR_042626 Anderseniella baltica strain BA141, Alphaproteobacteria, Rhizobiales, Rhodobiaceae, score 621 bits(336), identities 400/431(92.8%), gaps 4

>Alphaproteobacteria DGGE band no. 9
NR_044214 Devosia chinhatensis strain IPL18, Alphaproteobacteria, Rhizobiales, Hyphomicrobiaceae, score 719 bits(389), identities 420/435(96.6%), gaps 2

>Alphaproteobacteria DGGE band no. 10
NR_044302 Kaistia soli strain 5YN9-8, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, score 453 bits(245), identities 268/279(96.1%), gaps 1

>Alphaproteobacteria DGGE band no. 11
NR_027605 Magnetospirillum gryphiswaldense strain MSR-1, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae, score 702 bits(380), identities 414/430(96.3%), gaps 4

>Alphaproteobacteria DGGE band no. 12
NR_028798 Bosea eneae strain 34614, Alphaproteobacteria, Rhizobiales, Bradyrhizobiaceae, score 680 bits(368), identities 407/426(95.5%), gaps 1

>Alphaproteobacteria DGGE band no. 13
NR_043735 Rhodobacter blasticus strain ATCC 33485, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, score 667 bits(361), identities 392/407(96.3%), gaps 2

>Pseudomonas DGGE band no. 1
NR_040802.1 Pseudomonas asplenii strain ATCC 23835 / Pseudomonas monteilii strain CIP 104883, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, score 793 bits(429) , identities 433/435(99.5%), gaps 0

>Pseudomonas DGGE band no. 2
NR_043990 Pseudomonas tuomuerensis strain 78-123 / NR_024734 Pseudomonas alcaliphila strain AL15-21, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, score 782 bits(423), identities 431/435(99.1%), gaps 0/435(0%)

>Pseudomonas DGGE band no. 3
NR_025228 Pseudomonas koreensis strain Ps 9-14 / Pseudomonas brassicacearum subsp. brassicacearum NFM421 / Pseudomonas cedrina strain CFML 96-198 / Pseudomonas chlororaphis subsp. chlororaphis strain DSM 50083T / Pseudomonas kilonensis strain 520-20 / Pseudomonas thivervalensis strain SBK26, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, score 804 bits(435) , identities 435/435(100.0%), gaps 0

>Pseudomonas DGGE band no. 4
NR_024918 Pseudomonas jessenii strain CIP 105274 / NR_025227 Pseudomonas umsongensis strain Ps 3-10 / NR_043314 Pseudomonas moraviensis strain CCM 7280, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, score 776 bits(420) , identities 426/429(99.3%), gaps 0

>Pseudomonas DGGE band no. 5
NR_024918 Pseudomonas jessenii strain CIP 105274 / NR_025227 Pseudomonas umsongensis strain Ps 3-10, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, score 782 bits(423) , identities 431/435(99.1%), gaps 0

>Pseudomonas DGGE band no. 6

NR_025228 Pseudomonas koreensis strain Ps 9-14 / Pseudomonas brassicacearum subsp. brassicacearum NFM421 / Pseudomonas cedrina strain CFML 96-198 / Pseudomonas chlororaphis subsp. chlororaphis strain DSM 50083T / Pseudomonas kilonensis strain 520-20 / Pseudomonas thivervalensis strain SBK26, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, score 798 bits(432) , identities 434/435(99.8%), gaps 0

>Pseudomonas DGGE band no. 7
NR_036909 Pseudomonas taetrolens strain I11 / NR_024704 Pseudomonas lundensis strain ATCC 49968, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, score 776 bits(420) , identities 430/435(98.9%), gaps 0

>J2 specific bacterium (Table 3), row 1
KC469953, Micrococcus yunnanensis, Actinobacteria, Micrococcales, Micrococcaceae, score 595 bits(322), e-value 7e-167, identities 322/322(100%), gaps 0
> J2 specific bacterium (Table 3), row 2
AY043359 Rothia amarae, Actinobacteria, Micrococcales, Micrococcaceae, score 595 bits(322), e-value 7e-167, identities 322/322(100%), gaps 0
> J2 specific bacterium (Table 3), row 3
AJ554207 Geobacillus stearothermophilus, Firmicutes, Bacillales, Bacillaceae, score 481 bits(260), e-value 2e-132, identities 262/263(99%), gaps 0
> J2 specific bacterium (Table 3), row 4
AY188352 Streptococcus salivarius, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae, score 828 bits(448), e-value 0.0, identities 448/448(100%), gaps 0
> J2 specific bacterium (Table 3), row 5
Y07841 Anaerococcus octavius, Firmicutes, Clostridia, Clostridiales, Clostridiales, Family XI. Incertae Sedis, score 424 bits(229), e-value 2e-115, identities 234/236(99%), gaps 1
> J2 specific bacterium (Table 3), row 6
DQ911241 Peptoniphilus gorbachii, Firmicutes, Clostridia, Clostridiales, Clostridiales, Family XI. Incertae Sedis, score 634 bits(343), e-value 2e-178, identities 343/343(100%), gaps 0
> J2 specific bacterium (Table 3), row 7
Y18176 Clostridium disporicum, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, score 433 bits(234), e-value 4e-118, identities 236/237(99%), gaps 0
> J2 specific bacterium (Table 3), row 8
CP003703 Mycoplasma wenyonii, Tenericutes, Mollicutes, Mycoplasmataceae, score 619 bits(335), e-value 4e-174, identities 337/338(99%), gaps 0
> J2 specific bacterium (Table 3), row 9
EU159980 Uncultured Gemmatimonas in rhizosphere, Gemmatimonadetes, Gemmatimonadales, Gemmatimonadaceae, score 776 bits(420), e-value 0.0, identities 430/435(99%), gaps 0
> J2 specific bacterium (Table 3), row 10
HE613616 Uncultured delta proteobacterium, score 592 bits(320), e-value 9e-166, identities 320/320(100%), gaps 0
> J2 specific bacterium (Table 3), row 11
AJ242584 Ochrobactrum sp., AY594216 Brucella sp., Alphaproteobacteria, Rhizobiales, Brucellaceae, score 547 bits(296), e-value 2e-152, identities 296/296(100%), gaps 0
> J2 specific bacterium (Table 3), row 12
FM202386 Hirschia maritima, Alphaproteobacteria, Rhodobacterales, Hyphomonadaceae, score 368 bits(199), e-value 1e-98, identities 217/226(96%), gaps 0
> J2 specific bacterium (Table 3), row 13
DQ342315 Haematobacter missouriensis, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, score 486 bits(263), e-value 3e-134, identities 263/263(100%), gaps 0
> J2 specific bacterium (Table 3), row 14

AY014173 Paracoccus yeei, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, score 756 bits(409), e-value 0.0, identities 409/409(100%), gaps 0
> J2 specific bacterium (Table 3), row 15
GQ263062 Uncultured Rhodospirillaceae, Alphaproteobacteria, Rhodospirillales, score 708 bits(383), e-value 0.0, identities 383/383(100%), gaps 0
> J2 specific bacterium (Table 3), row 16
AB077038 Malikia spinosa, Betaproteobacteria, Burkholderiales, Comamonadaceae, score 577 bits(312), e-value 2e-161, identities 322/327(98%), gaps 0
> J2 specific bacterium (Table 3), row 17
Y08846 Janthinobacterium lividum, Betaproteobacteria, Burkholderiales, Oxalobacteraceae, score 479 bits(259), e-value 6e-132, identities 261/262(99%), gaps 0
> J2 specific bacterium (Table 3), row 18
HG005351 Neisseria mucosa, Betaproteobacteria, Neisseriales, Neisseriaceae, score 501 bits(271), e-value 1e-138, identities 273/274(99%), gaps 0
> J2 specific bacterium (Table 3), row 19
AB021385 Vogesella indigofera, Betaproteobacteria, Neisseriales, Neisseriaceae, score 473 bits(256), e-value 3e-130, identities 260/262(99%), gaps 0
> J2 specific bacterium (Table 3), row 20
X96963 Shigella flexneri / AF530475 S. fergusonii, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, score 813 bits(440), e-value 0.0, identities 440/440(100%), gaps 0
> J2 specific bacterium (Table 3), row 21
AJ278311 Acinetobacter schindleri, Gammaproteobacteria, Pseudomonadales, Moraxellaceae, score 481 bits(260), e-value 2e-138, identities 262/263(99%), gaps 0
> J2 specific bacterium (Table 3), row 22
X81663 Acinetobacter johnsonii, Gammaproteobacteria, Pseudomonadales, Moraxellaceae, score 486 bits(263), e-value 3e-134, identities 263/263(100%), gaps 0
> J2 specific bacterium (Table 3), row 23
AJ550856 Enhydrobacter aerosaccus, Gammaproteobacteria, Pseudomonadales, Moraxellaceae, score 826 bits(447), e-value 0.0, identities 447/447(100%), gaps 0
> J2 specific bacterium (Table 3), row 24
AJ292426 Pseudomonas kilonensis, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, score 821 bits(444), e-value 0.0, identities 444/444(100%), gaps 0

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