**Table S5.** Venn’s table showing shared and unique bacterial OTUs, from the 100 most abundant taxa, between vegetation density classes (A) and plant species (B). The letter in front of the taxon represents the maximum depth of taxonomy (g: genus, f: family, c: class, o: order, p: phylum, k: kingdom).

**A**

**Vegetation density**

**classes**

**Number**

**of OTUs**

**OTUs**

\_1 \_2 \_3 \_4 \_5 \_6

77

f

\_\_

MSB

-

4B10; o\_\_

Ktedonobacterales

; p\_\_

Latescibacteria

; g\_\_

uncultured

-

S

imkaniaceae; g\_\_*Haliangium*;

c\_\_

Subgroup

6; o\_\_X35; f\_\_SM2D12; p\_\_Proteobacteria; g\_\_

*Edaphobacter*;g*\_*\_

*Acidicapsa*;f*\_*

\_cvE6;

f\_\_

Xanthomonadales

Incertae

sedis; p\_\_

TM6

(Dependentiae

); g\_\_

*Gemmatimonas*

; g\_\_

*Acidibacter*

;

f\_\_DA111; o\_\_Acidimicrobiales; c\_\_

OPB35

soil

group; g\_\_

*Rhizomicrobium*

; f\_\_

Acidobacteriaceae (Subgroup

1

); g\_\_

*Legionella*

; g\_\_

*Aciditerrimonas*

; f\_\_Tepidisphaeraceae; g\_\_SM1A02; g\_\_

*Bdellovibrio*

; c\_\_

Candidatus

Azambacteria; g\_\_

*Gaiella*

; g\_\_

*Coxiella*;g*\_*

\_

*Acidobacterium*

; f\_\_Fimbriimonadaceae; g\_\_

*Opitutus*

; c\_\_TK10;

g\_\_

*Gemmata*

; o\_\_Obscuribacterales; g\_\_

uncultured

-

Acidobacteriaceae (Subgroup 1

); p\_\_Parcubacteria;

g\_\_

*Chthoniobacter*

; g\_\_

*Aquicella*;f*\_*

\_ODP1230B8.23; g\_\_

*Pirellula*

; g\_\_H16; g\_\_

Pir4

lineage; o\_\_

SAR324

clade(Marine group B

); g\_\_uncultured

-

Planctomycetaceae; c\_\_Alphaproteobacteria; o\_\_Armatimonadales;

g\_\_

*Singulisphaera*

; g\_\_

*Planctomyces*

; g\_\_

*Candidatus*

*protochlamydia*

; g\_\_

*Candidatus*

*solibacter*;

f*\_*

\_

Acidobacteriaceae

(Subgroup 1

); g\_\_BD7

-

11CL; f\_\_Planctomycetaceae; p\_\_Chloroflexi;

f\_\_Oligoflexaceae; c\_\_Gammaproteobacteria; g\_\_

*Telmatobacter*

; p\_\_Saccharibacteria; f\_\_P3OB

-

42;

c\_\_OM190; c\_\_KD4

-

96; g\_\_

*Neochlamydia*

; g\_\_

*Acidothermus*

; g\_\_

*Bryobacter*;g*\_*

\_

*Sorangium*

; f\_\_BIrii41;

p\_\_Omnitrophica; k\_\_Bacteria; f\_\_Planctomycetaceae; f\_\_

env.OPS

17; c\_\_JG37

-

AG

-

4; c\_\_

Subgroup

2;

g\_\_

*Granulicella*

; o\_\_HTA4; o\_\_Ktedonobacterales; f\_\_

0319

-

6G20

\_1 \_2 \_3 \_4 \_5

4

c

\_\_Pla4

lineage; c\_\_vadinHA49; o\_\_C0119; p\_\_

Woesearchaeota

(DHVEG

-

6

)

\_1 \_2 \_3 \_4 \_6

1

g\_\_

*Jatrophihabitans*

\_1 \_2 \_4 \_5 \_6

2

g\_\_

*Pseudomonas*

; g\_\_

*Flavobacterium*

\_2 \_3 \_4 \_5 \_6

6

g

\_\_

uncultured

-

Cy

tophagaceae; g\_\_

*Nocardioides*

; g\_\_uncultured

-

Chitinophagaceae; f\_\_Bradyrhizobiaceae;

g\_\_

*Mucilaginibacter*

; g\_\_

*Phenylobacterium*

\_1 \_2 \_3 \_4

2

g\_\_

*Bryocella*

; g\_\_

*Anaeromyxobacter*

\_2 \_3 \_4 \_6

1

g\_\_

*Burkholderia*

*-*

*Paraburkholderia*

\_3 \_4 \_5 \_6

1

f

\_\_Elev

-

16S

-

1332

\_1 \_2 \_3

1

f

\_\_mle1

-

27

\_2 \_5 \_6

1

g\_\_

*Phaselicystis*

\_4 \_5 \_6

2

g\_\_

*Ferruginibacter*

;g*\_*

\_

*Candidatus*

*xiphinematobacter*

\_1 \_2

2

g\_\_

*Isosphaera*

; p\_\_

FCPU426

\_2 \_4

1

f\_\_Chitinophagaceae

\_3 \_5

1

g\_\_

*Geobacter*

\_4 \_6

1

g\_\_

*Parafilimonas*

\_1

11

g\_\_

*Leptospirillum*

;

c\_\_uncultured

; o\_\_

CPla

-

3 termite

group; g\_\_

*Metallibacterium*

;o*\_*

\_

Acidimicrobiales

;

g\_\_

uncultured

-

Xanth

omonadaceae; g\_\_

*Ferrithrix*

; c\_\_ML635J

-

21; p\_\_

Candidatus

Berkelbacteria;

g\_\_

*Acidiphilium*

; g\_\_

*Acidiferrobacter*

\_2

2

g\_\_

*Terracidiphilus*

; f\_\_

G12

-

WMSP1

\_3

6

g\_\_

PAUC26f; g\_\_

*Chryseolinea*

;

c\_\_Cyanobacteria

; c\_\_

Betaproteobacteria

; g\_\_

*Sphingomonas*

; g\_\_

AMGG11

\_4

2

f\_\_

Sandaracinaceae

; g\_\_

uncultured

-

Caulo

bacteraceae

\_5

6

c\_\_

UA11; g\_\_

uncultured

-

Sand

aracinaceae; g\_\_RB41; c\_\_

Subgroup

17; c\_\_

Subgroup

5; g\_\_

11

-

24

\_6

8

g\_\_

*Dokdonella*

; f\_\_

DA101

soil

group; g\_\_

uncultured

-

Gemmat

imonadaceae; g\_\_

*Rhodoplanes*

; g\_\_

*Rhizobium*

;

g\_\_uncultured

-

Bradyrhizobiaceae; o\_\_Gaiellales; g\_\_

*Arenimonas*

**B**

**Plant species**

**Number**

**of OTUs**

**OTUs**

*Betula*

*papyrifera*

*Alnus*

*rugosa*

*Picea*

sp.

93

g\_\_

uncultured

-

Acidob

acteriaceae (Subgroup 1

); p\_\_Parcubacteria; f\_\_MSB

-

4B10; o\_\_Ktedonobacterales;

g\_\_uncultured

-

Simkaniaceae; p\_\_Latescibacteria; g\_\_

*Chthoniobacter*

; g\_\_

*Aquicella*

; g\_\_uncultured

-

Cytophagaceae; f\_\_ODP1230B8.23; g\_\_

*Pirellula*

; g\_\_

*Haliangium*

; c\_\_

Subgroup

6; o\_\_X35; c\_\_

Pla4

lineage; f\_\_Chitinophagaceae; f\_\_SM2D12; g\_\_H16; g\_\_

Pir4

lineage; g\_\_

*Nocardioides*

; p\_\_Proteobacteria;

o\_\_

SAR324

clade(Marine group B

); g\_\_

*Edaphobacter*

; g\_\_

*Acidicapsa*

; g\_\_uncultured

-

Planctomycetaceae;

o\_\_Armatimonadales; c\_\_Alphaproteobacteria; f\_\_cvE6; f\_\_

Xanthomonadales

*Incertae*

*sedis*;

g\_\_

*Singulisphaera*

; g\_\_

*Bryocella*

; p\_\_

TM6

(Dependentiae

); g\_\_

*Planctomyces*

; g\_\_

*Candidatus*

*protochlamydia*; g*\_*

\_

*Gemmatimonas*

; g\_\_

*Acidibacter*; f*\_*

\_DA111; f\_\_

Acidobacteriaceae

(Subgroup 1

);

g\_\_

*Candidatus*

*solibacter*; o*\_*

Acidimicrobiales; c\_\_BD7

-

11; f\_\_Planctomycetaceae; p\_\_Chloroflexi;

c\_\_

OPB35

soil

group; f\_\_Oligoflexaceae; g\_\_

uncultured

*-*

*Chitinophagaceae*; f*\_*

\_Bradyrhizobiaceae;

g\_\_

*Rhizomicrobium*

; c\_\_Gammaproteobacteria; f\_\_

Acidobacteriaceae (Subgroup 1

); g\_\_

*Telmatobacter*

;

g\_\_

*Legionella*

; p\_\_Saccharibacteria; f\_\_P3OB

-

42; g\_\_

*Mucilaginibacter*

; g\_\_

*Aciditerrimonas*

; c\_\_OM190;

g\_\_

*Phenylobacterium*

; f\_\_Tepidisphaeraceae; g\_\_

*Geobacter*

; g\_\_

*Bdellovibrio*

; g\_\_SM1A02; c\_\_

KD4

-

96

c

\_\_Candidatus

Azambacteria; c\_\_vadinHA49; g\_\_

*Neochlamydia*

; g\_\_

*Gaiella*

; g\_\_

*Anaeromyxobacter*

;

g\_\_

*Bryobacter*

; g\_\_

*Acidothermus*

; g\_\_

*Coxiella*

; g\_\_

*Burkholderia*

*-*

*Paraburkholderia; g\_*

\_

*Sorangium*

;

f\_\_BIrii41; p\_\_Omnitrophica; g\_\_

*Flavobacterium*

; k\_\_Bacteria; g\_\_

*Acidobacterium*

; f\_\_Planctomycetaceae;

f\_\_

env.OPS

17; f\_\_Fimbriimonadaceae; c\_\_JG37

-

AG

-

4; c\_\_

Subgroup

2; g\_\_

*Opitutus*

; g\_\_

*Granulicella*

;

c\_\_TK10; o\_\_HTA4; o\_\_Ktedonobacterales; o\_\_C0119; g\_\_

*Gemmata*

; o\_\_Obscuribacterales;

g\_\_

*Jatrophihabitans*; f*\_*

\_

0319

-

6G20

*Betula*

*papyrifera*

*Picea*

sp.

3

g\_\_

*Isosphaera*

; p\_\_

Woesearchaeota

(DHVEG

-

6

); g\_\_

AMGG11

*Alnus*

*rugosa*

*Picea*

sp.

3

f

\_\_

Elev

-

16S

-

1332; f\_\_mle1

-

27; g\_\_

*Ferruginibacter*

*Betula*

*papyrifera*

4

g\_\_

*Pseudomonas*

; p\_\_FCPU426; g\_\_

*Terracidiphilus*

; f\_\_

G12

-

WMSP1

*Alnus*

*rugosa*

4

g\_\_

*Candidatus*

*xiphinematobacter*

; g\_\_

*Chryseolinea*

; g\_\_

*Phaselicystis*

;

c\_\_

Cyanobacteria

*Picea*

sp.

1

c\_\_

Betaproteobacteria