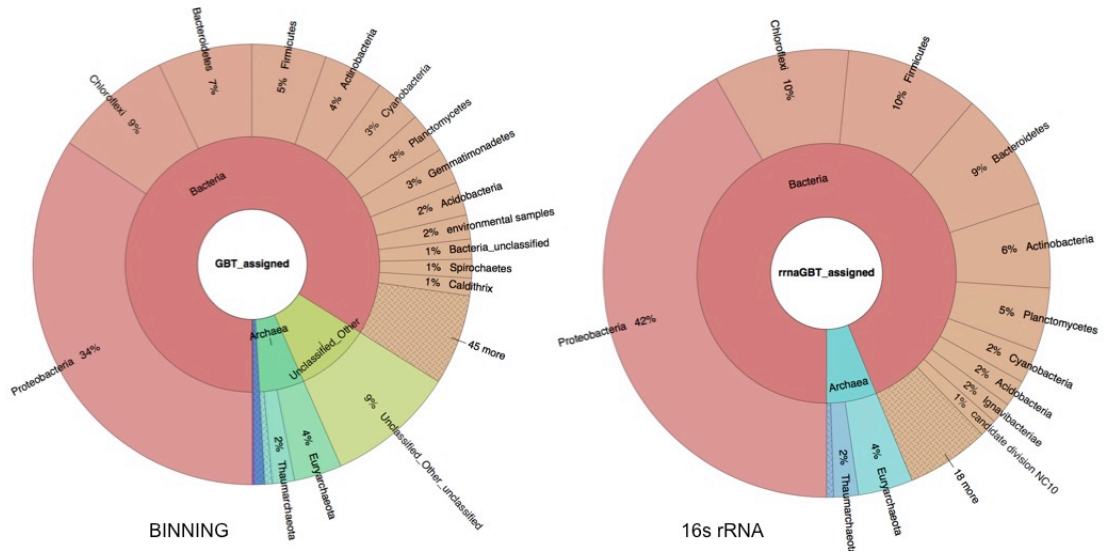
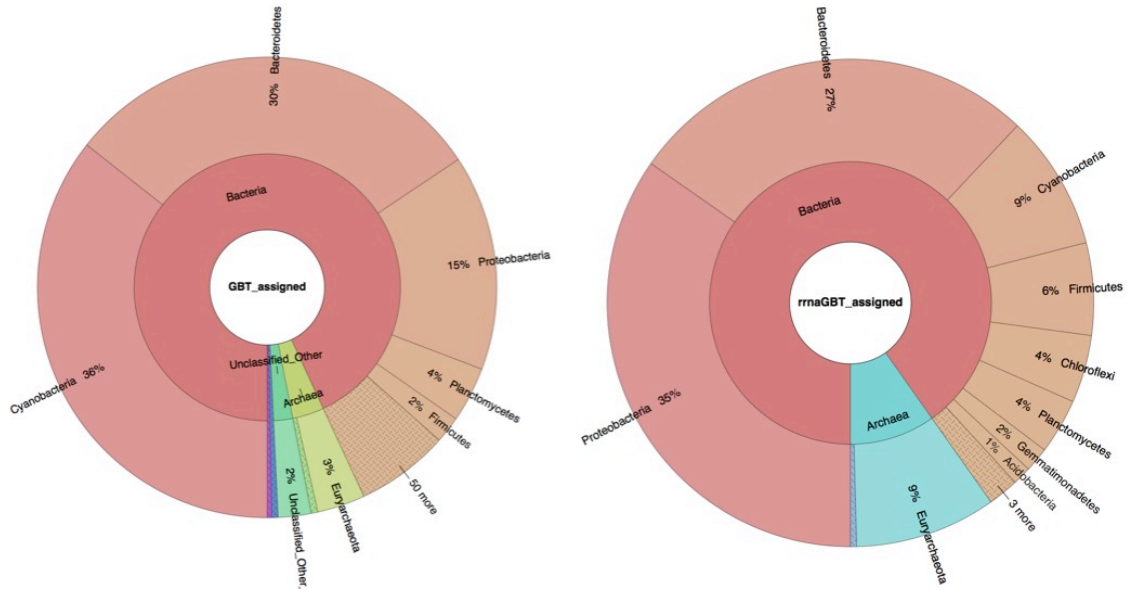


Figure S2.1. Comparison between binning of predicted genes and 16s rRNA genes for taxonomic assignment.

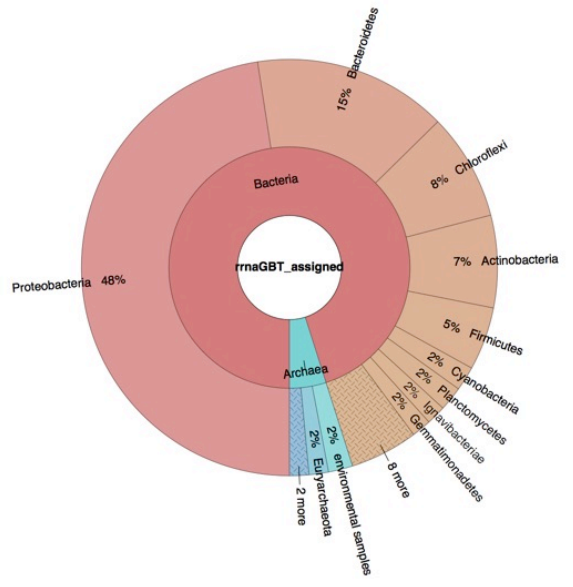
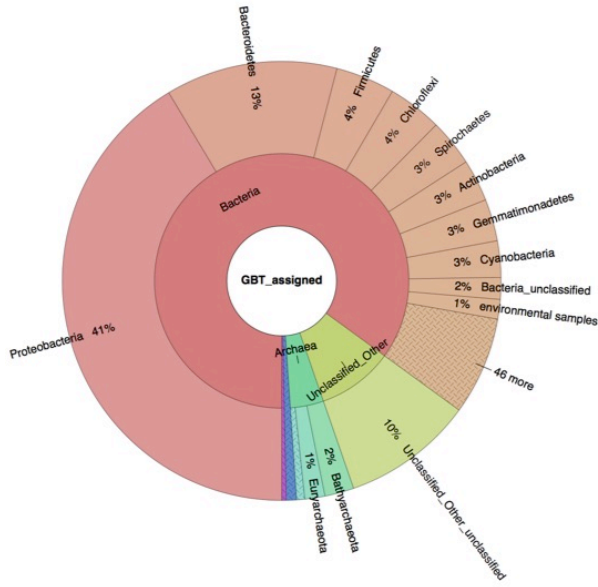
MMK



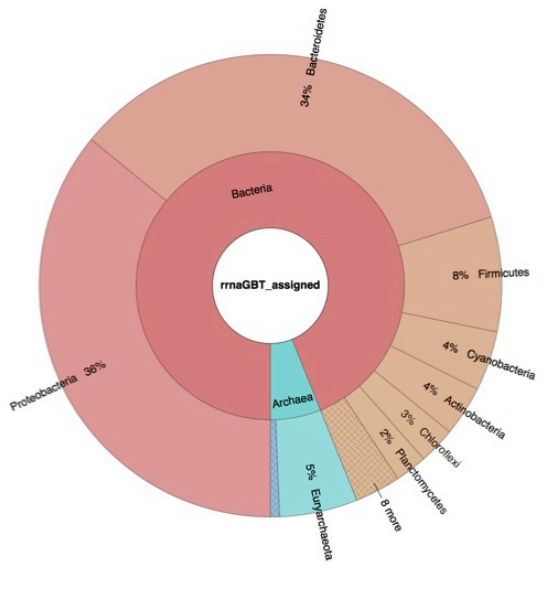
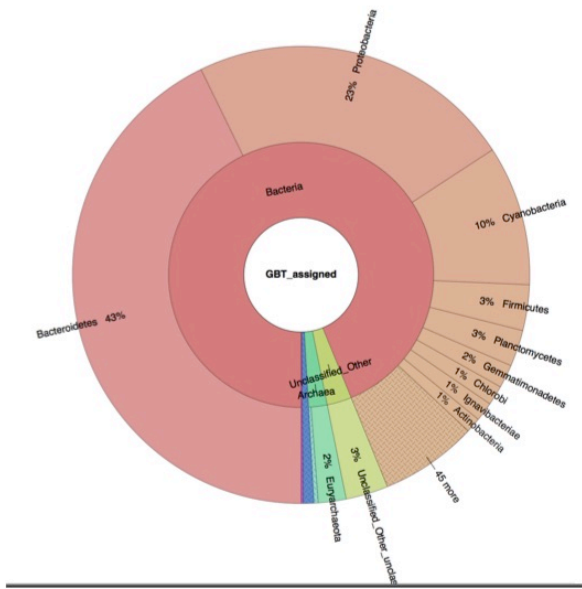
MMR

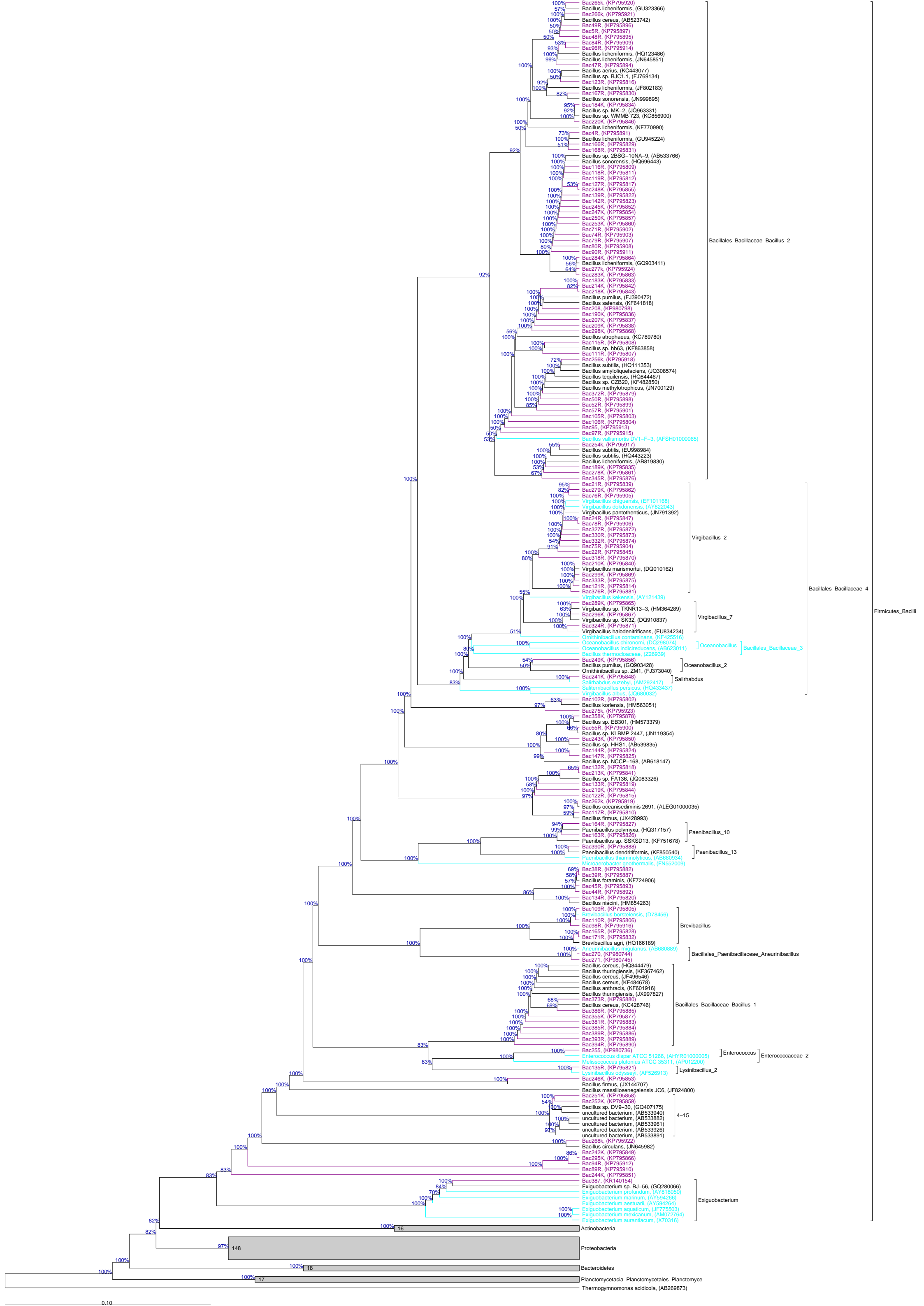


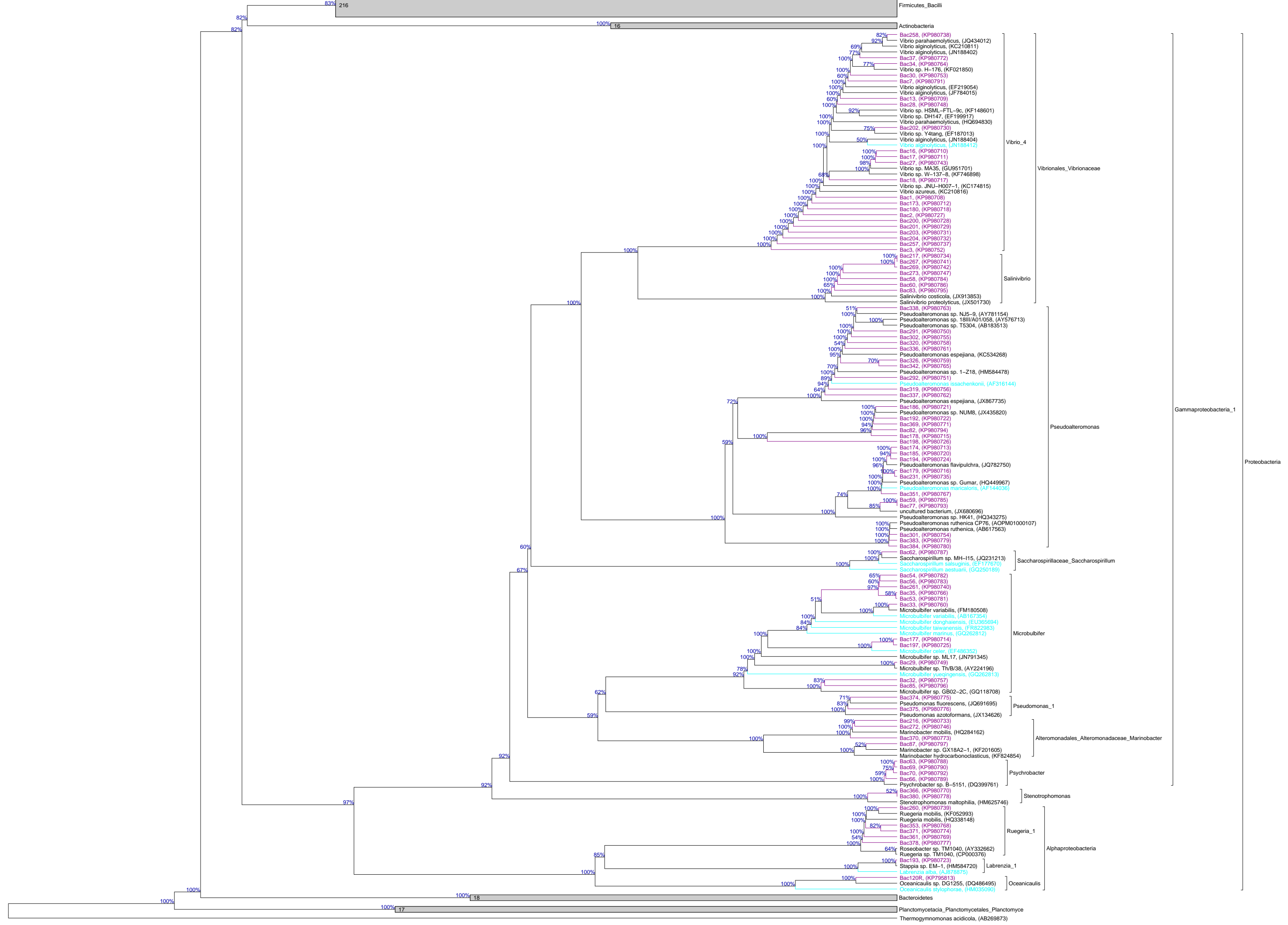
MNK

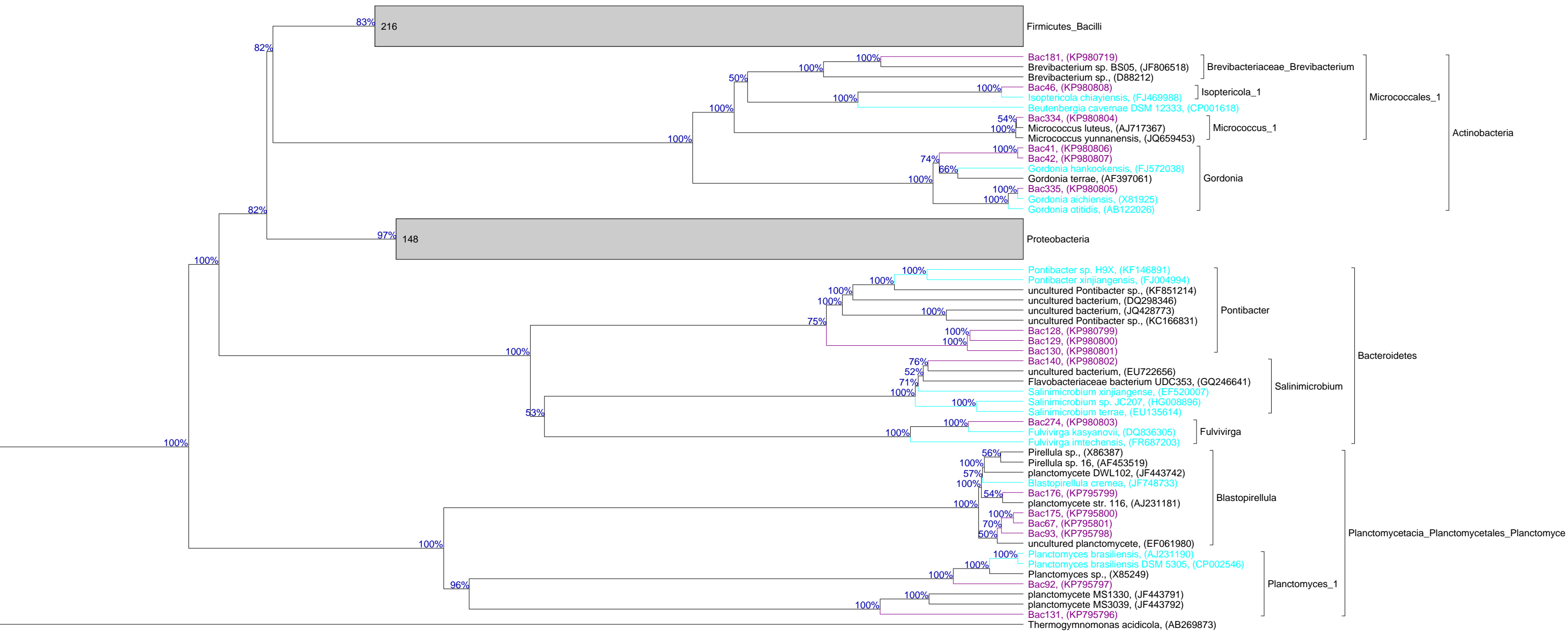


MNR









0.10

Table S2.2. Functions related to.

COMPARISON GROUP **Log Odds Ratio | Relative risk | p-value**

Aromatic Compound Degradation

MMK vs MMR	0.333 1.3696 p < 0.05
MMK vs MNR	0.138 1.1387 p < 0.05
MMR vs MNK	-0.274 0.7715 p < 0.05
MNK vs MNR	0.080 1.0777 p < 0.05
MMK vs MNK	0.059 1.0566 p < 0.05
MMR vs MNR	-0.195 0.8314 p < 0.05

Xenobiotics biodegradation

MMK vs MMR	0.448 1.5541 p < 0.05
MMK vs MNR	0.193 1.2086 p < 0.05
MMR vs MNK	-0.415 0.6649 p < 0.05
MNK vs MNR	0.16 1.1697 p < 0.05
MMK vs MNK	0.033 1.0333 p=0.0715
MMR vs MNR	-0.255 0.7777 p < 0.05

Styrene degradation

MMK vs MMR	0.523 1.6864 p < 0.05
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anaerobic aromatic compound degradation (Thauera aromatica)

MMK vs MMR	0.344 1.3916 p < 0.05
MMK vs MNR	0.14 1.1432 p < 0.05
MMR vs MNK	-0.278 0.7648 p < 0.05
MNK vs MNR	0.074 1.0741 p < 0.05

Benzoate degradation

MMK vs MMR	0.886 2.4174 p < 0.05
MMK vs MNR	0.442 1.5522 p < 0.05
MMR vs MNK	-0.968 0.3816 p < 0.05
MNK vs MNR	0.523 1.6828 p < 0.05

Toluene degradation

MMK vs MMR	0.557 1.743 p < 0.05
MMK vs MNR	0.234 1.2634 p < 0.05
MMR vs MNK	-0.465 0.6287 p < 0.05
MNK vs MNR	0.142 1.1528 p < 0.05

Ethylbenzene degradation

MMK vs MMR	0.451 1.5683 p < 0.05
MMK vs MNR	0.244 1.2755 p < 0.05

MMR vs MNK	-0.377 0.6863 p < 0.05
MNK vs MNR	0.170 1.185 p < 0.05

Xylene degradation

MMK vs MMR	0.434 1.5433 p < 0.05
MMK vs MNR	0.544 1.7224 p < 0.05
MMR vs MNK	-0.455 0.6344 p < 0.05
MNK vs MNR	0.565 1.7593 p < 0.05

Table S2.3. Bioactive compounds.

Identity	Class	Protein	Phylum	Genus
High Identities >=45%	PKS	Polyketide synthase	Cyanobacteria	Nostoc_unclassified
High Identities >=45%	PKS	Polyketide synthase family protein	Cyanobacteria	Nostoc_unclassified
High Identities >=45%	PKS	Polyketide synthase	Thaumarchaeota	Nitrosopumilus_unclassified
High Identities >=45%	NRPS	Dimodular nonribosomal peptide synthase Dhbf	Thaumarchaeota	environmental samples_unclassified
High Identities >=45%	antibiotic resistance	ABC transporter superfamily	Chloroflexi	Chloroflexaceae
High Identities >=45%	antibiotic resistance	aminoglycoside-4'-adenyltransferase	Bacteroidetes	Rhodothermus_unclassified
High Identities >=45%	antibiotic resistance	BaeR family transcriptional regulator	Proteobacteria	Syntrophobacter
High Identities >=45%	antibiotic resistance	chloramphenicol acetyltransferase	Thaumarchaeota	Nitrosopumilus_unclassified
High Identities >=45%	antibiotic resistance	Dihydrofolate reductase family	environmental samples	environmental samples_unclassified
High Identities >=45%	antibiotic resistance	DNA gyrase subunit A	Proteobacteria	Geobacter
High Identities >=45%	antibiotic resistance	macrolide export ATP-binding/permease protein MacB	Proteobacteria	Anaeromyxobacteraceae
High Identities >=45%	antibiotic resistance	putative cation efflux system protein	Bacteroidetes	Algoriphagus
High Identities >=45%	antibiotic resistance	Response regulator protein VraR	candidate division NC10	Candidatus Methyloirabilis_unclassified
High Identities >=45%	antibiotic resistance	Ribosomal protein L11P family	Synergistetes	Anaerobaculum
High Identities >=45%	antibiotic resistance	Ribosomal protein L16P family	Caldithrix	Caldithrix_unclassified
High Identities >=45%	antibiotic resistance	Ribosomal protein L22P family	Proteobacteria	Deltaproteobacteria_unclassified
High Identities >=45%	antibiotic resistance	Ribosomal protein L4P family	Acidobacteria	Thermoanaerobaculum_unclassified
High Identities >=45%	antibiotic resistance	Ribosomal protein S12P family	Chloroflexi	Anaerolinea
High Identities >=45%	antibiotic resistance	Ribosomal protein S17P family	Firmicutes	Thermosinus
High Identities >=45%	antibiotic resistance	Ribosomal protein S4P family	Acidobacteria	Thermoanaerobaculum_unclassified
High Identities >=45%	antibiotic resistance	Ribosomal protein S5P family	Acidobacteria	Thermoanaerobaculum_unclassified
High Identities >=45%	antibiotic resistance	RNA polymerase beta' chain family	Acidobacteria	Candidatus Koribacter_unclassified
High Identities >=45%	antibiotic resistance	RNA polymerase beta chain family	Acidobacteria	Candidatus Solibacter
High Identities >=45%	antibiotic resistance	RNA polymerase beta chain family	Chloroflexi	Anaerolinea
High Identities >=45%	antibiotic resistance	RND efflux transporter permease	Acidobacteria	Thermoanaerobaculum_unclassified
High Identities >=45%	antibiotic resistance	TRAFAC class translation factor GTPase superfamily, Classic translation factor GTPase family, EF-Tu/E	Chloroflexi	Anaerolinea
High Identities >=45%	antibiotic resistance	TRAFAC class translation factor GTPase superfamily, Classic translation factor GTPase family, EF-Tu/E	Nitrospirae	Thermodesulfovibrio_unclassified
High Identities >=45%	antibiotic resistance	TRAFAC class translation factor GTPase superfamily, Classic translation factor GTPase family, EF-Tu/E	Nitrospirae	Thermodesulfovibrio_unclassified
High Identities >=45%	antibiotic resistance	Type II topoisomerase family	Acidobacteria	Thermoanaerobaculum_unclassified
High Identities >=45%	antibiotic biosynthesis	Isocitrate lyase/PEP mutase superfamily	Thaumarchaeota	Nitrosopumilus_unclassified
Low Identities <45%	PKS,NRPS	Mixed trans-AT type I polyketide synthase/nonribosomal peptide synthetase	Caldithrix	Caldithrix_unclassified
Low Identities <45%	PKS	ABC transporter superfamily	Proteobacteria	Polyangiaceae
Low Identities <45%	PKS	Aldehyde dehydrogenase family	Bacteroidetes	Fulvivirga
Low Identities <45%	PKS	Beta-ketoacyl-ACP synthases family	Acidobacteria	Thermoanaerobaculum_unclassified
Low Identities <45%	PKS	Beta-ketoacyl-ACP synthases family	Chloroflexi	Herpetosiphon
Low Identities <45%	PKS	Class-II pyridoxal-phosphate-dependent aminotransferase family	Synergistetes	Dethiosulfovibrio
Low Identities <45%	PKS	Enoyl-CoA hydratase/isomerase family	environmental samples	environmental samples_unclassified
Low Identities <45%	PKS	Modular polyketide synthase	Proteobacteria	Cystobacteraceae
Low Identities <45%	PKS	Monensin polyketide synthase modules 7 and 8	Acidobacteria	Thermoanaerobaculum_unclassified
Low Identities <45%	PKS	Polyketide synthase	Acidobacteria	Granulicella_unclassified
Low Identities <45%	PKS	Polyketide synthase	Acidobacteria	Thermoanaerobaculum_unclassified

Low Identities <45%	PKS	Polyketide synthase	Actinobacteria	Geodermatophilaceae
Low Identities <45%	PKS	Polyketide synthase	Actinobacteria	Streptomycetaceae
Low Identities <45%	PKS	Polyketide synthase	Armatimonadetes	Chthonomonas
Low Identities <45%	PKS	Polyketide synthase	Chloroflexi	Anaerolinea
Low Identities <45%	PKS	Polyketide synthase	Chloroflexi	Ktedonobacter
Low Identities <45%	PKS	Polyketide synthase	Cyanobacteria	Pleurocapsa_unclassified
Low Identities <45%	PKS	Polyketide synthase	Deferribacteres	Denitrovibrio_unclassified
Low Identities <45%	PKS	Polyketide synthase	Deinococcus-Thermus	Marinithermus
Low Identities <45%	PKS	Polyketide synthase, enoylreductase	Chloroflexi	Ktedonobacter
Low Identities <45%	PKS	Polyketide synthase, enoylreductase	Cyanobacteria	Pleurocapsa_unclassified
Low Identities <45%	PKS	Polyketide synthase	environmental samples	environmental samples_unclassified
Low Identities <45%	PKS	Polyketide synthase	environmental samples	environmental samples_unclassified
Low Identities <45%	PKS	Polyketide synthase family protein	Actinobacteria	Geodermatophilaceae
Low Identities <45%	PKS	Polyketide synthase	Firmicutes	Exiguobacterium
Low Identities <45%	PKS	Polyketide synthase	Proteobacteria	Geobacter
Low Identities <45%	PKS	Polyketide synthase	Proteobacteria	Magnetospirillum
Low Identities <45%	PKS	Polyketide synthase	Proteobacteria	Myxococcaceae
Low Identities <45%	PKS	Polyketide synthase	Thaumarchaeota	Nitrosopumilus_unclassified
Low Identities <45%	PKS	Polyketide synthase subunit	Thaumarchaeota	Nitrosopumilus_unclassified
Low Identities <45%	PKS	Polyketide synthase	Thaumarchaeota	Nitrosopumilus_unclassified
Low Identities <45%	PKS	Polyketide synthase	Deinococcus-Thermus	Marinithermus
Low Identities <45%	PKS	Polyketide synthase, type I	Acidobacteria	Candidatus Chloracidobacterium_unclassified
Low Identities <45%	PKS	Putative Phthiocerol/phenolphthiocerol synthesis polyketide synthase type I PpsD	Cyanobacteria	Oscillatoriales_unclassified
Low Identities <45%	PKS	Putative polyketide synthase	Thaumarchaeota	Nitrosopumilus_unclassified
Low Identities <45%	PKS	Putative polyketide synthase PKS	Proteobacteria	Bdellovibrio
Low Identities <45%	PKS	Putative polyketide synthase	Thaumarchaeota	Candidatus Nitrosoarchaeum_unclassified
Low Identities <45%	PKS	Putative polyketide synthase	Thaumarchaeota	Nitrosopumilus_unclassified
Low Identities <45%	PKS	Putative type I polyketide synthase component	Proteobacteria	Polyangiaceae
Low Identities <45%	PKS	Putative type I polyketide synthase component	Verrucomicrobia	Verrucomicrobium
Low Identities <45%	PKS	Regulator of polyketide synthase expression	Acidobacteria	Thermoanaerobaculum_unclassified
Low Identities <45%	PKS	Regulator of polyketide synthase expression	Chloroflexi	Anaerolinea
Low Identities <45%	PKS	Rifamycin polyketide synthase	Cyanobacteria	Nostoc_unclassified
Low Identities <45%	PKS	Type I polyketide synthase	Cyanobacteria	Acaryochloris_unclassified
Low Identities <45%	PKS	Type I polyketide synthase	Cyanobacteria	Chroococciopsis_unclassified
Low Identities <45%	PKS	Type I polyketide synthase	Cyanobacteria	Lyngbya_unclassified
Low Identities <45%	PKS	Type I polyketide synthase	Proteobacteria	Azoarcus
Low Identities <45%	PKS	Type I polyketide synthase	Proteobacteria	Myxococcaceae
Low Identities <45%	NRPS	Class-III pyridoxal-phosphate-dependent aminotransferase family	Acidobacteria	Thermoanaerobaculum_unclassified
Low Identities <45%	NRPS	Non-ribosomal peptide synthase	Bacteroidetes	Rhodothermus_unclassified
Low Identities <45%	NRPS	Non-ribosomal peptide synthase	Proteobacteria	Pseudomonas
Low Identities <45%	NRPS	Non-ribosomal peptide synthetase	Acetothermia	Candidatus Acetothermum_unclassified
Low Identities <45%	NRPS	Non-ribosomal peptide synthetase	Acidobacteria	Candidatus Chloracidobacterium_unclassified
Low Identities <45%	NRPS	Non-ribosomal peptide synthetase	Acidobacteria	Candidatus Koribacter_unclassified
Low Identities <45%	NRPS	Non-ribosomal peptide synthetase	Acidobacteria	Candidatus Solibacter

Low Identities <45%	NRPS	Non-ribosomal peptide synthetase	Acidobacteria	Thermoanaerobaculum_unclassified
Low Identities <45%	NRPS	Non-ribosomal peptide synthetase	Actinobacteria	Streptomycetaceae
Low Identities <45%	NRPS	Non-ribosomal peptide synthetase	Bacteria_unclassified	Bacteria_unclassified
Low Identities <45%	NRPS	Non-ribosomal peptide synthetase	Chloroflexi	Roseiflexaceae
Low Identities <45%	NRPS	Nonribosomal peptide synthetase	environmental samples	environmental samples_unclassified
Low Identities <45%	NRPS	Non-ribosomal peptide synthetase modules and related protein	Chloroflexi	Roseiflexaceae
Low Identities <45%	NRPS	Non-ribosomal peptide synthetase modules, siderophore biosynthesis	Proteobacteria	Nannocystaceae
Low Identities <45%	NRPS	Non-ribosomal peptide synthetase	Planctomycetes	Singulisphaera
Low Identities <45%	NRPS	Non-ribosomal peptide synthetase protein	Bacteria_unclassified	Bacteria_unclassified
Low Identities <45%	NRPS	Non-ribosomal peptide synthetase	Proteobacteria	Cystobacteraceae
Low Identities <45%	NRPS	Non-ribosomal peptide synthetase	Proteobacteria	Nannocystaceae
Low Identities <45%	NRPS	Non-ribosomal peptide synthetase	Proteobacteria	Polyangiaceae
Low Identities <45%	NRPS	Non-ribosomal peptide synthetase	Planctomycetes	Singulisphaera
Low Identities <45%	NRPS	Non-ribosomal peptide synthetase ThaC1	Acidobacteria	Thermoanaerobaculum_unclassified
Low Identities <45%	NRPS	Putative non-ribosomal peptide synthetase	candidate division NC10	Candidatus Methylomirabilis_unclassified
Low Identities <45%	NRPS	Putative non-ribosomal peptide synthetase	Chloroflexi	Chloroflexaceae
Low Identities <45%	NRPS	Putative non-ribosomal peptide synthetase	Chloroflexi	Ktedonobacter
Low Identities <45%	NRPS	Putative non-ribosomal peptide synthetase	Cyanobacteria	Microcystis_unclassified
Low Identities <45%	NRPS	Putative non-ribosomal peptide synthetase	Euryarchaeota	Halalkalicoccus
Low Identities <45%	NRPS	Putative non-ribosomal peptide synthetase	Firmicutes	Clostridium
Low Identities <45%	NRPS	Putative non-ribosomal peptide synthetase	Firmicutes	Oscillibacter
Low Identities <45%	NRPS	Putative Non-ribosomal peptide synthetase	Proteobacteria	Ralstonia
Low Identities <45%	NRPS	Yersiniabactin non-ribosomal peptide synthetase	Gemmatimonadetes	Gemmatimonas_unclassified
Low Identities <45%	antibiotic resistance	ABC transporter ATP-binding protein	Acidobacteria	Candidatus Koribacter_unclassified
Low Identities <45%	antibiotic resistance	ABC transporter permease	Chloroflexi	Herpetosiphon
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Low Identities <45%	antibiotic resistance	ABC transporter superfamily	Acidobacteria	Candidatus Koribacter_unclassified
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Low Identities <45%	antibiotic resistance	ABC transporter superfamily	Acidobacteria	Thermoanaerobaculum_unclassified
Low Identities <45%	antibiotic resistance	ABC transporter superfamily	Bacteroidetes	Parabacteroides
Low Identities <45%	antibiotic resistance	ABC transporter superfamily	Chloroflexi	Roseiflexaceae
Low Identities <45%	antibiotic resistance	ABC transporter superfamily	Cyanobacteria	Gloeobacter_unclassified
Low Identities <45%	antibiotic resistance	ABC transporter superfamily	Cyanobacteria	Gloeobacter_unclassified
Low Identities <45%	antibiotic resistance	ABC transporter superfamily	Deinococcus-Thermus	Marinithermus
Low Identities <45%	antibiotic resistance	ABC transporter superfamily	environmental samples	environmental samples_unclassified
Low Identities <45%	antibiotic resistance	ABC transporter superfamily	environmental samples	environmental samples_unclassified
Low Identities <45%	antibiotic resistance	ABC transporter superfamily	Firmicutes	Clostridium
Low Identities <45%	antibiotic resistance	ABC transporter superfamily	Gemmatimonadetes	Gemmatimonadetes_unclassified
Low Identities <45%	antibiotic resistance	ABC transporter superfamily	Proteobacteria	Escherichia
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Low Identities <45%	antibiotic resistance	ABC transporter superfamily	Thaumarchaeota	Candidatus Nitrosoarchaeum_unclassified
Low Identities <45%	antibiotic resistance	ABC transporter superfamily	Thaumarchaeota	Nitrosopumilus_unclassified

Low Identities <45%	antibiotic resistance	ABC transporter superfamily	Thaumarchaeota	Nitrosopumilus_unclassified
Low Identities <45%	antibiotic resistance	ABC transporter superfamily	Thaumarchaeota	Nitrosopumilus_unclassified
Low Identities <45%	antibiotic resistance	ABC transporter superfamily	Thaumarchaeota	Nitrosopumilus_unclassified
Low Identities <45%	antibiotic resistance	ABC transporter superfamily	Verrucomicrobia	Opitutus
Low Identities <45%	antibiotic resistance	AccA family	Firmicutes	Bacillus
Low Identities <45%	antibiotic resistance	AdeR	Proteobacteria	Thiohalocapsa
Low Identities <45%	antibiotic resistance	BcrC/YbjG family	Deinococcus-Thermus	Meiothermus
Low Identities <45%	antibiotic resistance	beta-lactamase	Thaumarchaeota	Candidatus Nitrosoarchaeum_unclassified
Low Identities <45%	antibiotic resistance	Blal transcriptional regulatory family	Proteobacteria	Polyangiaceae
Low Identities <45%	antibiotic resistance	Blal transcriptional regulatory family	Verrucomicrobia	Verrucomicrobiales_unclassified
Low Identities <45%	antibiotic resistance	Cft2	Actinobacteria	Rubrobacteraceae
Low Identities <45%	antibiotic resistance	Cft2	Firmicutes	Symbiobacterium
Low Identities <45%	antibiotic resistance	Chloramphenicol acetyltransferase	Bacteroidetes	Solitalea
Low Identities <45%	antibiotic resistance	Chloramphenicol acetyltransferase	Chloroflexi	Anaerolinea
Low Identities <45%	antibiotic resistance	Chloramphenicol acetyltransferase family	Bacteroidetes	Solitalea
Low Identities <45%	antibiotic resistance	Class-C beta-lactamase family	Planctomycetes	Planctomyces
Low Identities <45%	antibiotic resistance	Class-C beta-lactamase family	Proteobacteria	Variovorax
Low Identities <45%	antibiotic resistance	Class-D beta-lactamase family	Proteobacteria	Deltaproteobacteria_unclassified
Low Identities <45%	antibiotic resistance	Class-I aminoacyl-tRNA synthetase family, IleS type 1 subfamily	Thaumarchaeota	Nitrosopumilus_unclassified
Low Identities <45%	antibiotic resistance	Class-I aminoacyl-tRNA synthetase family, IleS type 2 subfamily	Acidobacteria	Thermoanaerobaculum_unclassified
Low Identities <45%	antibiotic resistance	Class-I aminoacyl-tRNA synthetase family, IleS type 2 subfamily	Firmicutes	Eubacterium
Low Identities <45%	antibiotic resistance	DegT/DnrJ/EryC1 family, ArnB subfamily	Acetothermia	environmental samples_unclassified
Low Identities <45%	antibiotic resistance	DHPS family	Aquificae	Desulfurobacterium_unclassified
Low Identities <45%	antibiotic resistance	Drug ABC exporter, ATP-binding and membrane-spanning/permease subunit	Cyanobacteria	Cyanothece_unclassified
Low Identities <45%	antibiotic resistance	Glycosyltransferase 2 family	Acidobacteria	Thermoanaerobaculum_unclassified
Low Identities <45%	antibiotic resistance	Glycosyltransferase 2 family	Bacteroidetes	Flexibacter
Low Identities <45%	antibiotic resistance	Glycosyltransferase 2 family	Chloroflexi	Herpetosiphon
Low Identities <45%	antibiotic resistance	Glycosyltransferase 2 family	Chloroflexi	Sphaerobacteraceae
Low Identities <45%	antibiotic resistance	Glycosyltransferase 2 family	Cyanobacteria	Crinalium_unclassified
Low Identities <45%	antibiotic resistance	Glycosyltransferase 2 family	environmental samples	environmental samples_unclassified
Low Identities <45%	antibiotic resistance	Glycosyltransferase 2 family	Proteobacteria	Pelobacter
Low Identities <45%	antibiotic resistance	Glycosyltransferase 2 family	Thaumarchaeota	Candidatus Nitrosoarchaeum_unclassified
Low Identities <45%	antibiotic resistance	Glycosyltransferase 2 family	Verrucomicrobia	Chthoniobacter_unclassified
Low Identities <45%	antibiotic resistance	Isoniazid-induced protein IniA	Chloroflexi	Caldilinea
Low Identities <45%	antibiotic resistance	lipid A export ATP-binding/permease	Proteobacteria	Candidatus Entotheonella_unclassified
Low Identities <45%	antibiotic resistance	lipid A export ATP-binding/permease	Proteobacteria	Myxococcaceae
Low Identities <45%	antibiotic resistance	Metallo-beta-lactamase superfamily, Class-B beta-lactamase family	Proteobacteria	Simiduia_unclassified
Low Identities <45%	antibiotic resistance	Multiple antibiotic resistance protein MarR	Gemmatimonadetes	Gemmatimonas_unclassified
Low Identities <45%	antibiotic resistance	OmpR family transcriptional regulator	Firmicutes	Clostridium
Low Identities <45%	antibiotic resistance	OmpR family transcriptional regulator	Proteobacteria	sulfur-oxidizing symbionts_unclassified
Low Identities <45%	antibiotic resistance	OmpR family transcriptional regulator	Thaumarchaeota	Nitrosopumilus_unclassified
Low Identities <45%	antibiotic resistance	outer membrane efflux protein	Proteobacteria	Sphingomonas
Low Identities <45%	antibiotic resistance	Peptidase S45 family	Deinococcus-Thermus	Truepera
Low Identities <45%	antibiotic resistance	periplasmic multidrug efflux lipoprotein	Acidobacteria	Thermoanaerobaculum_unclassified

Low Identities <45%	antibiotic resistance	putative cation efflux system protein	Proteobacteria	Myxococcaceae
Low Identities <45%	antibiotic resistance	RecName: Full=Transcriptional activator RamA	Bacteroidetes	Bacteroides
Low Identities <45%	antibiotic resistance	Regulatory protein VanR	Acidobacteria	Thermoanaerobaculum_unclassified
Low Identities <45%	antibiotic resistance	Response regulator protein VraR	Acidobacteria	Thermoanaerobaculum_unclassified
Low Identities <45%	antibiotic resistance	Response regulator protein VraR	Chloroflexi	Ktedonobacter
Low Identities <45%	antibiotic resistance	Response regulator protein VraR	Chloroflexi	Sphaerobacteraceae
Low Identities <45%	antibiotic resistance	Response regulator protein VraR	Chloroflexi	Thermomicrobium_unclassified
Low Identities <45%	antibiotic resistance	Response regulator protein VraR	Firmicutes	Ruminiclostridium
Low Identities <45%	antibiotic resistance	Response regulator protein VraR	Gemmatimonadetes	Gemmatimonadetes_unclassified
Low Identities <45%	antibiotic resistance	response regulator	Proteobacteria	Polyangiaceae
Low Identities <45%	antibiotic resistance	Ribosomal protein L11P family	Thaumarchaeota	Nitrosopumilus_unclassified
Low Identities <45%	antibiotic resistance	Ribosomal protein L6P family	candidate division NC10	Candidatus Methyloirabilis_unclassified
Low Identities <45%	antibiotic resistance	Ribosomal protein S4P family	Thaumarchaeota	Nitrosopumilus_unclassified
Low Identities <45%	antibiotic resistance	RNA methyltransferase TsnR/AvirB family	Firmicutes	Acetohalobium
Low Identities <45%	antibiotic resistance	RNA polymerase beta chain family	Thaumarchaeota	Candidatus Nitrosoarchaeum_unclassified
Low Identities <45%	antibiotic resistance	RND efflux membrane fusion protein	Proteobacteria	Myxococcaceae
Low Identities <45%	antibiotic resistance	RND efflux transporter permease	Proteobacteria	Hydrocarboniphaga
Low Identities <45%	antibiotic resistance	TcaA family	Spirochaetes	Treponema_unclassified
Low Identities <45%	antibiotic resistance	TehB family	Planctomycetes	Rhodopirellula
Low Identities <45%	antibiotic resistance	TRAFAC class translation factor GTPase superfamily, Classic translation factor GTPase family, EF-Tu/E	Acidobacteria	Thermoanaerobaculum_unclassified
Low Identities <45%	antibiotic resistance	TRAFAC class translation factor GTPase superfamily, Classic translation factor GTPase family, TetM/T	Planctomycetes	Rhodopirellula
Low Identities <45%	antibiotic resistance	TRAFAC class translation factor GTPase superfamily, Classic translation factor GTPase family, TetM/T	Thermodesulfobacteria	Thermodesulfatator_unclassified
Low Identities <45%	antibiotic resistance	Transferase hexapeptide repeat family, LpxD subfamily	Acidobacteria	Thermoanaerobaculum_unclassified
Low Identities <45%	antibiotic resistance	Transmembrane ATP-binding ABC transporter protein	Acidobacteria	Thermoanaerobaculum_unclassified
Low Identities <45%	antibiotic resistance	Transpeptidase family	Proteobacteria	Geobacter
Low Identities <45%	antibiotic resistance	two-component response regulator	Proteobacteria	Gammaproteobacteria_unclassified
Low Identities <45%	antibiotic resistance	Type III pantothenate kinase family	Firmicutes	Thermacetogenium
Low Identities <45%	antibiotic resistance	VanRG	Thaumarchaeota	unclassified Thaumarchaeota_unclassified
Low Identities <45%	antibiotic resistance	VanRM	Chloroflexi	Anaerolinea
Low Identities <45%	antibiotic resistance	VanSM	Proteobacteria	Gammaproteobacteria_unclassified
Low Identities <45%	antibiotic resistance	VanSst	Verrucomicrobia	Opitutus
Low Identities <45%	antibiotic resistance	VanTG	Firmicutes	Caldicellulosiruptor
Low Identities <45%	antibiotic resistance	Vgb family	Proteobacteria	Myxococcaceae
Low Identities <45%	antibiotic biosynthesis,PKS	SchB/CurC family	Actinobacteria	Streptomycetaceae
Low Identities <45%	antibiotic biosynthesis	Anthranilate synthase component I family	Thaumarchaeota	Candidatus Nitrosoarchaeum_unclassified
Low Identities <45%	antibiotic biosynthesis	Bacterial non-heme bromo- and chloro-peroxidases family	Chloroflexi	Anaerolinea
Low Identities <45%	antibiotic biosynthesis	Class-II pyridoxal-phosphate-dependent aminotransferase family	Acidobacteria	Candidatus Chloracidobacterium_unclassified
Low Identities <45%	antibiotic biosynthesis	Class-V pyridoxal-phosphate-dependent aminotransferase family	Proteobacteria	Desulfomonile
Low Identities <45%	antibiotic biosynthesis	Cysteine synthase/cystathionine beta-synthase family	Bacteroidetes	Sphingobacterium
Low Identities <45%	antibiotic biosynthesis	Cysteine synthase/cystathionine beta-synthase family	Thaumarchaeota	Nitrosopumilus_unclassified
Low Identities <45%	antibiotic biosynthesis	Cytochrome P450 family	Planctomycetes	Singulisphaera
Low Identities <45%	antibiotic biosynthesis	DegT/dnrJ/eryC1 family	Thaumarchaeota	Nitrosopumilus_unclassified
Low Identities <45%	antibiotic biosynthesis	Dehydroquinase synthase family, DOI synthase subfamily	Acidobacteria	Terriglobus_unclassified
Low Identities <45%	antibiotic biosynthesis	DTDP-4-dehydrorhamnose reductase family	Euryarchaeota	Methanoculleus

Low Identities <45%	antibiotic biosynthesis	DTDP-4-dehydrorhamnose reductase family	Firmicutes	Clostridiaceae_unclassified
Low Identities <45%	antibiotic biosynthesis	Glucose-1-phosphate thymidyltransferase family	Actinobacteria	Micromonosporaceae
Low Identities <45%	antibiotic biosynthesis	Glycosyltransferase group 1 family	Bacteroidetes	Microscilla
Low Identities <45%	antibiotic biosynthesis	Glycosyltransferase group 1 family	Proteobacteria	Ectothiorhodospira
Low Identities <45%	antibiotic biosynthesis	Glycosyltransferase group 1 family	Proteobacteria	Halorhodospira
Low Identities <45%	antibiotic biosynthesis	Lincomycin biosynthesis protein LmbN	Chloroflexi	Anaerolinea
Low Identities <45%	antibiotic biosynthesis	Methyltransferase superfamily, DnrC family	Firmicutes	Sporolactobacillus
Low Identities <45%	antibiotic biosynthesis	Methyltransferase superfamily, DnrC family	Proteobacteria	Chelativorans
Low Identities <45%	antibiotic biosynthesis	Methyltransferase superfamily, DnrC family	Proteobacteria	Halomonas
Low Identities <45%	antibiotic biosynthesis	Methyltransferase superfamily, DnrC family	Thaumarchaeota	Candidatus Nitrosoarchaeum_unclassified
Low Identities <45%	antibiotic biosynthesis	Methyltransferase superfamily	Firmicutes	Desmospora
Low Identities <45%	antibiotic biosynthesis	Methyltransferase superfamily	Firmicutes	Sporolactobacillus
Low Identities <45%	antibiotic biosynthesis	Methyltransferase superfamily	Proteobacteria	Chelativorans
Low Identities <45%	antibiotic biosynthesis	Methyltransferase superfamily	Proteobacteria	Halomonas
Low Identities <45%	antibiotic biosynthesis	Methyltransferase superfamily	Proteobacteria	Thioalkalivibrio
Low Identities <45%	antibiotic biosynthesis	Methyltransferase superfamily	Thaumarchaeota	Candidatus Nitrosoarchaeum_unclassified
Low Identities <45%	antibiotic biosynthesis	Methyltransferase TylM1/DesVI family	Thaumarchaeota	Nitrosopumilus_unclassified
Low Identities <45%	antibiotic biosynthesis	NodU/Cmch family	Proteobacteria	Desulfocapsa
Low Identities <45%	antibiotic biosynthesis	Peptidase M16 family	Acidobacteria	Candidatus Chloracidobacterium_unclassified
Low Identities <45%	antibiotic biosynthesis	RelA/SpoT family	Acidobacteria	Candidatus Koribacter_unclassified
Low Identities <45%	antibiotic biosynthesis	RelA/SpoT family	Chloroflexi	Anaerolinea
Low Identities <45%	antibiotic biosynthesis	TAL/TAM family	Acidobacteria	Thermoanaerobaculum_unclassified
Low Identities <45%	antibiotic biosynthesis	Terpene synthase family	Armatimonadetes	Chthonomonas
Low Identities <45%	antibiotic biosynthesis	TrpC family	Proteobacteria	Comamonadaceae_unclassified
Low Identities <45%	antibiotic biosynthesis	TrpC family	Thaumarchaeota	Nitrosopumilus_unclassified
Low Identities <45%	antibiotic biosynthesis	Zinc-containing alcohol dehydrogenase family, DOIA dehydrogenase subfamily	Proteobacteria	Methylomonas

Table S2.4. Metagenomic contigs associated with enzymes involved in antibiotic synthesis and resistance and the species from which they are derived.

	MMK	MNR	MMR	MNK
Proteobacteria	31	113	32	310
Bacteroidetes	6	85	79	77
Acidobacteria	5	2	1	10
Firmicutes	13	29	12	81
Cyanobacteria	4	28	24	20
Chloroflexi	9	4	1	17
Gemmatimonadetes	2	3	2	3
Actinobacteria	1	7	1	33
Planctomycetes	3	7	2	8

Table S2.4i. Metagenomic contigs associated with enzymes involved in antibiotic resistance and the species from which they are derived.

	MMK	MNR	MMR	MNK
Proteobacteria	14	39	19	155
Bacteroidetes	2	31	31	40
Acidobacteria	4	0	1	4
Firmicutes	3	7	4	45
Cyanobacteria	0	16	10	25
Chloroflexi	1	3	2	12
Gemmatimonadetes	0	2	0	2
Actinobacteria	2	2	2	22
Planctomycetes	1	2	3	6

Table S2.4ii. Metagenomic contigs associated with enzymes involved in antibiotic and the species from which they are derived.

Table S2.5. Metagenomic contigs associated with PKS and NRPS enzymes and the species from which they are derived

	MMK	MNR	MMR	MNK
Proteobacteria	9	42	14	205
Bacteroidetes	2	43	37	38
Acidobacteria	3	4	2	6
Firmicutes	1	17	2	36
Cyanobacteria	7	13	13	14
Chloroflexi	3	4	1	12
Gemmatimonadetes	0	1	0	3
Actinobacteria	2	5	1	26
Planctomycetes	0	4	4	5

Table S2.5i. Metagenomic contigs associated with PKS enzymes and the species from which they are derived

	MMK	MNR	MMR	MNK
Proteobacteria	7	32	11	107
Bacteroidetes	1	39	32	28
Acidobacteria	4	2	0	2
Firmicutes	2	7	0	19
Cyanobacteria	1	13	8	14
Chloroflexi	3	1	1	8
Gemmatimonadetes	1	1	1	2
Actinobacteria	1	1	1	15
Planctomycetes	1	1	1	4

Table S2.5ii. Metagenomic contigs associated with NRPS enzymes and the species from which they are derived

Table S3.1. Morphological distinctiveness- SPSS

Sample ID	Description								
	Color	Shape	Size	Surface	Elevation	Texture	Location	type of sediments	Media
Bac 1	Creamy	irregular	small	smooth	flat	moist	R	MN	1
Bac2	Beige	irregular	small	smooth	convex	moist	R	MN	1
Bac 3	Brown	circular	micro	smooth	flat	moist	R	MN	1
Bac4	Creamy	irregular	small	rough	convrx	moist	R	MN	3
Bac5	Creamy	circular	small	smooth	convex	moist	R	MN	3
Bac7	Creamy	circular	small	smooth	convex	moist	R	MN	1
Bac9	Creamy	circular	small	smooth	convex	moist	R	MN	1
Bac13	Creamy	circular	small	smooth	convex	moist	R	MN	1
Bac16	Peach	circular	small	smooth	convex	moist	R	MN	5
Bac17	Beige	circular	small	smooth	convex	moist	R	MN	5
Bac18	Pink	circular	large	smooth	convex	moist	R	MN	5
Bac21	White	circular	small	smooth	convex	moist	R	MN	5
Bac22	Ligh Pink	irregular	small	rough	convex	moist	R	MN	5
Bac24	Peach	circular	large	smooth	convex	moist	R	MN	5
Bac26	Creamy	rhizoid	small	rough	flat	moist	R	MN	5
Bac27	Peach	irregular	small	smooth	convex	moist	R	MN	5
Bac28	Clear	circular	large	smooth	raised	moist	R	MN	5
Bac29	Brown	circular	small	smooth	convex	moist	R	MN	2
Bac32	Beige	circular	small	smooth	convex	moist	R	MN	2
Bac34	Creamy	circular	small	smooth	convex	moist	R	MN	2
Bac35	Beige	irregular	small	smooth	flat	moist	R	MN	2
Bac37	Beige	circular	small	smooth	flat	moist	R	MN	2
Bac41	Yellow	circular	large	smooth	convex	moist	R	MN	3
Bac42	Yellow	circular	micro	smooth	convex	moist	R	MN	3
Bac46	Creamy	circular	small	smooth	convex	moist	R	MN	3
Bac49	Creamy	circular	large	rough	flat	moist	R	MN	3
Bac53	Beige	circular	small	smooth	flat	moist	R	MN	3
Bac54	Brown	circular	small	smooth	flat	moist	R	MN	1
Bac56	Beige	circular	large	smooth	flat	moist	R	MN	2
Bac57	Beige	circular	small	smooth	convex	moist	R	MN	5
Bac58	Peach	circular	small	smooth	convex	moist	R	MM	1
Bac59	White	circular	small	rough	flat	dry	R	MM	1

Medium	#
MA 2216	1
10% MA 2216	2
AIA	3
Anti- MA 2216	4
MA-GM	5

Location	
Rabigh	R
Al-Kharrar	K

Bac60	Creamy	circular	small	smooth	convex	moist	R	MM	1
Bac61	Creamy	circular	small	smooth	convex	moist	R	MM	1
Bac62	Light Pink	circular	small	rough	flat	dry	R	MM	5
Bac63	Pink	circular	small	smooth	convex	moist	R	MM	5
Bac66	Creamy	irregular	small	smooth	convex	moist	R	MM	3
Bac67	Creamy	circular	micro	smooth	convex	moist	R	MM	4
Bac69	Creamy	irregular	small	rough	flat	dry	R	MM	3
Bac71	Pink	circular	large	rough	flat	dry	R	MM	1
Bac74	Pink	irregular	small	rough	flat	moist	R	MM	1
Bac75	Light Pink	circular	small	rough	flat	moist	R	MM	5
Bac76	Creamy	circular	large	rough	flat	dry	R	MM	5
Bac77	Creamy	circular	small	smooth	flat	moist	R	MM	1
Bac78	Creamy	irregular	largee	wrinkled	flat	moist	R	MM	5
Bac79	Creamy	circular	small	smooth	convex	viscous	R	MM	5
Bac80	Creamy	rhizoid	small	rough	convex	moist	R	MM	5
Bac81	Clear	circular	large	smooth	flat	moist	R	MM	2
Bac82	Creamy	circular	small	smooth	convex	moist	R	MM	2
Bac83	Creamy	circular	small	smooth	convex	moist	R	MM	2
Bac84	White	circular	small	rough	flat	dry	R	MM	5
Bac85	Creamy	circular	large	rough	flat	dry	R	MM	1
Bac87	Beige	circular	small	rough	stick on media	dry	R	MM	1
Bac90	Creamy	irregular	small	Rough	raised	moist	R	MM	2
Bac92	Orange	circular	small	smooth	flat	moist	R	MM	4
Bac93	Creamy	circular	small	smooth	convex	moist	R	MM	4
Bac94	Orange	circular	small	smooth	convex	moist	R	MM	1
Bac95	Clear	circular	small	smooth	convex	moist	R	MM	5
Bac96	Creamy	circular	small	smooth	flat	moist	R	MM	5
Bac97	White	circular	micro	smooth	flat	moist	R	MM	3
Bac98	Clear	circular	small	smooth	convex	viscous	R	MM	3
Bac105	Pink	irregular	small	rough	convex	dry	R	MM	5
Bac106	Peach	irregular	small	smooth	convex	moist	R	MM	3
Bac109	Creamy	circular	small	smooth	convex	moist	R	MM	3
Bac110	White	circular	micro	smooth	flat	moist	R	MM	3
Bac111	Pink	filamentous	small	smooth	convex	moist	R	MM	5
Bac115	Pink	circular	small	smooth	convex	moist	R	MM	5
Bac116	Peach	circular	micro	smooth	flat	moist	R	BS	1
Bac117	Creamy	circular	micro	smooth	flat	moist	R	BS	1

Bac118	Orange	circular	micro	smooth	flat	moist	R	BS	1
Bac119	Light pink	circular	micro	smooth	flat	moist	R	BS	1
Bac120	White	circular	small	smooth	convex	moist	R	BS	1
Bac121	Creamy	circular	small	smooth	flat	moist	R	BS	5
Bac122	Peach	circular	small	smooth	convex	moist	R	BS	5
Bac123	Orange	circular	small	smooth	convex	moist	R	BS	3
Bac127	Pink	circular	small	rough	convex	dry	R	BS	1
Bac128	Peach	circular	micro	smooth	convex	moist	R	BS	2
Bac129	Yellow	circular	micro	smooth	convex	moist	R	BS	2
Bac130	Orange	circular	micro	smooth	convex	moist	R	BS	2
Bac131	Peach	circular	small	smooth	convex	moist	R	BS	4
Bac132	Clear	circular	micro	smooth	flat	moist	R	BS	3
Bac133	Pech	circular	small	smooth	flat	moist	R	BS	3
Bac134	Creamy	circular	small	smooth	flat	moist	R	BS	3
Bac135	Creamy	circular	mico	smooth	flat	moist	R	BS	3
Bac139	Creamy	circular	small	rough	flat	dry	R	BS	2
Bac140	Yellow	circular	small	smooth	convex	moist	R	BS	2
Bac142	Pink	irrgular	small	rough	flat	dry	R	BS	5
Bac143	Creamy	circular	mico	smooth	convex	moist	R	BS	5
Bac144	Beige	irrgular	mico	smooth	flat	moist	R	BS	5
Bac145	Clear	circular	mico	smooth	flat	moist	R	BS	5
Bac147	Creamy	circular	mico	smooth	flat	moist	R	BS	5
Bac151	Yellow	circular	small	smooth	convex	moist	R	BS	1
Bac155	White	circular	small	smooth	flat	moist	R	BS	1
Bac156	White	circular	micro	smooth	flat	moist	R	BS	2
Bac162	Creamy	circular	mico	smooth	convex	moist	R	BS	5
Bac163	Peach	filamentous	small	smooth	convex	moist	R	BS	5
Bac164	Peach	filamentous	small	smooth	convex	moist	R	BS	5
Bac165	White	circulsr	micro	smooth	flat	moist	R	BS	2
Bac166	Pink	rhizod	small	rough	convex	moist	R	BS	5
Bac167	White	circular	small	smooth	flat	moist	R	BS	3
Bac168	Beige	circular	small	smooth	flat	moist	R	BS	3
Bac171	White	circular	small	smooth	flat	moist	R	BS	2
Bac173	Creamy	circular	small	smooth	convex	moist	K	MN	1
Bac174	Orange	circular	small	smooth	convex	moist	K	MN	1
Bac175	Black	circular	small	smooth	convex	moist	K	MN	4
Bac176	Creamy	circular	small	smooth	convex	moist	K	MN	4

Bac177	Light Yellow	irrgular	micro	smooth	flat	moist	K	MN	2
Bac178	White	circular	small	smooth	convex	moist	K	MN	2
Bac179	Yellow	circular	small	smooth	convex	moist	K	MN	2
Bac183	Creamy	circular	small	smooth	flat	moist	K	MN	3
Bac185	Yellow	circular	small	smooth	convex	moist	K	MN	2
Bac189	Pink	irrgular	small	rough	flat	moist	K	MN	5
Bac190	White	circular	small	smooth	flat	moist	K	MN	5
Bac194	Orange	circular	small	smooth	convex	moist	K	MN	2
Bac197	Yellow	circular	small	smooth	flat	moist	K	MN	2
Bac198	Yellow	circular	small	smooth	convex	moist	K	MN	1
Bac200	Creamy	circular	small	smooth	flat	moist	K	MN	5
Bac201	Clear	circular	small	smooth	convex	moist	K	MN	5
Bac202	Pink	circular	small	smooth	convex	moist	K	MN	1
Bac203	Yellow	circular	small	smooth	convex	moist	K	MN	1
Bac204	Creamy	circular	small	smooth	flat	moist	K	MN	1
Bac208	Creamy	circular	small	smooth	flat	moist	K	MN	3
Bac209	Peach	circular	small	smooth	flat	moist	K	MN	5
Bac210	Pink	irregular	small	rough	flat	dry	K	MN	5
Bac213	Orange	circular	small	smooth	flat	moist	K	MM	5
Bac214	Clear	irregular	small	smooth	flat	viscous	K	MM	5
Bac216	Yellow	circular	small	smooth	convex	moist	K	MM	2
Bac217	Creamy	circular	small	smooth	convex	moist	K	MM	2
Bac218	Creamy	circular	large	smooth	flat	moist	K	MM	5
Bac219	Orange	circular	large	smooth	flat	moist	K	MM	5
Bac220	Creamy	rhizoid	small	rough	flat	dry	K	MM	3
Bac231	Orange	circular	small	smooth	convex	moist	K	MM	1
Bac241	Creamy	circular	small	smooth	flat	moist	K	BS	1
Bac242	Brown	circular	small	smooth	flat	moist	K	BS	1
Bac243	Peach	circular	small	smooth	convex	moist	K	BS	1
Bac244	Creamy	circular	small	smooth	convex	moist	K	BS	1
Bac245	Creamy	circular	micro	smooth	flat	moist	K	BS	2
Bac246	White	circular	lage	smooth	flat lage	moist	K	BS	2
Bac247	Light Pink	circular	small	rough	stick on media	dry	K	BS	3
Bac248	Light Pink	Irregular	small	smooth	stick on media	moist	K	BS	3
Bac249	Creamy	circular	micro	smooth	convex	moist	K	BS	1
Bac250	Pink Irrgular	Irrgular	wrinkle	smooth	flat	moist	K	BS	1
Bac251	White	circular	small	smooth	convex	moist	K	BS	2

Bac252	Beige	circular	small	smooth	convex	moist	K	BS	2
Bac253	White	wrinkled	large	smooth	flat	moist	K	BS	2
Bac254	Peach	rhizoid	small	rough	convex	viscus	K	MN	5
Bac255	White	circular	small	smooth	flat	moist	K	MN	5
Bac256	Peach	circular	large	smooth	flat	moist	K	MN	5
Bac257	Peach	circular	large media	smooth	flat	viscus	K	MN	1
Bac260	Creamy	circular	micro	smooth	flat	moist	K	MN	1
Bac261	Brown	circular	micro	smooth	flat	moist	K	MN	2
Bac265	Pink	circular	small	rough	flat	moist	K	MM	3
Bac267	Peach	circular	small	smooth	convex	moist	K	MM	5
Bac268	Clear	irrgular	large	smooth	flat	moist	K	MM	5
Bac269	Peach	irrgular	large	smooth	flat	moist	K	MM	5
Bac270	White	circular	small	smooth	convex	moist	K	MM	2
Bac271	Orange	circular	micro	smooth	convex	moist	K	MM	2
Bac272	Creamy	circular	small	rough	stick on media	dry	K	MM	1
Bac273	Clear	circular	large	smooth	convex	moist	K	MM	1
Bac274	White	circular	microcolny	smooth	flat	moist	K	BS	2
Bac275	White	circular	microcolny	smooth	flat	moist	K	BS	2
Bac277	White	circular	microcolny	smooth	flat	moist	K	BS	3
Bac278	Pink	circular	small	smooth	convex	moist	K	BS	3
Bac279	white	circular	small	smooth	convex	moist	K	BS	1
Bac280	Beige	circular	small	smooth	convex	moist	K	BS	1
Bac282	Clear	filamitous	small	smooth	convex	moist	K	BS	5
Bac283	Pink	rhizoid	small	rough	convex	moist	K	BS	5
Bac284	White	circular	small	rough	stick on media	moist	K	BS	3
Bac287	White	circular	micro	smooth	flat	moist	K	BS	2
Bac288	White	circular	micro	smooth	flat	moist	K	BS	2
Bac289	Pink	irrgular	large	rough	convex	moist	K	BS	5
Bac291	Pink	irrgular	large	smooth	flat	moist	K	BS	2
Bac292	Creamy	circular	micro	smooth	convex	moist	K	BS	2
Bac295	White	circular	small	smooth	flat	moist	K	BS	5
Bac296	Pink	circular	small	smooth	convex	moist	K	BS	5
Bac298	Creamy	circular	small	smooth	convex	moist	K	MM	5
Bac299	Orange	circular	small	smooth	convex	moist	K	MM	5
Bac301	Creamy	circular	small	smooth	flat	moist	K	MM	1
Bac302	Creamy	rhizod	small	rough	flat	moist	K	MM	2
Bac306	Creamy	circular	small	smooth	convex	moist	K	MN	1

Bac318	Creamy	circular	small	smooth	convex	moist	R	MM	1
Bac320	Clear	Irrgular	micro	smooth	flat	moist	R	MM	5
Bac323	White	irrgular	small	smooth	flat	moist	R	MN	5
Bac324	Orange	circular	small	smooth	convex	moist	R	MN	5
Bac325	Orange	circular	small	smooth	convex	moist	R	MN	5
Bac327	White	circular	small	smooth	flat	moist	R	MN	5
Bac330	Light	circular	small	smooth	convex	moist	R	MN	1
Bac334	Yellow	circular	small	smooth	convex	moist	R	BS	3
Bac335	Creamy	circular	small	smooth	convex	moist	R	BS	3
Bac336	White	circular	small	smooth	convex	moist	R	BS	1
Bac337	White	circular	small	smooth	convex	moist	R	BS	1
Bac338	White	circular	small	smooth	convex	moist	R	BS	2
Bac342	White	circular	small	smooth	convex	moist	K	BS	2
Bac344	Creamy	circular	small	smooth	convex	moist	R	BS	5
Bac345	Clear	Irrgular	small	smooth	flat	moist	R	BS	5
Bac351	Yellow	circular	small	smooth	flat	moist	K	MN	5
Bac353	Creamy	circular	small	smooth	flat	moist	K	MN	3
Bac355	Light Pink	Irrgular	small	smooth	flat	moist	K	BS	5
Bac358	White	circular	micro	smooth	convex	moist	K	BS	2
Bac361	Creamy	circular	small	smooth	convex	moist	K	BS	1
Bac363	Clear	circular	micro	smooth	convex	moist	K	MM	5
Bac366	Creamy	circular	small	smooth	flat	moist	K	MM	3
Bac371	Creamy	circular	small	smooth	convex	moist	K	MM	1
Bac372	Clear	circular	small	smooth	convex	moist	R	BS	5
Bac373	White	circular	small	smooth	flat	moist	R	BS	5
Bac374	Creamy	circular	small	smooth	convex	moist	R	BS	3
Bac375	Creamy	circular	small	smooth	flat	moist	R	BS	3
Bac376	Creamy	circular	small	smooth	convex	moist	R	BS	1
Bac378	Clear	circular	small	smooth	convex	moist	R	BS	2
Bac381	Light Pink	circular	small	smooth	convex	moist	R	MM	5
Bac383	Creamy	circular	small	smooth	flat	moist	R	MM	1
Bac384	Creamy	circular	small	smooth	convex	moist	R	MM	1
Bac387	Creamy	circular	small	smooth	flat	moist	R	MN	1
Bac389	Light Pink	circular	small	smooth	convex	moist	R	MN	5
Bac390	Light Pink	circular	small	smooth	convex	moist	R	MN	5
Bac391	Creamy	circular	micro	smooth	convex	moist	R	MN	2

Table S5.1. Detailed information about all bacterial isolates.

Sample ID	Type of samples	Isolation media	Description	16S rRNA seq. (from NCBI)			PKS/NRPS			Coculturing (Annular radius) mm			
				Closest Relative by BLAST and %Sequence Similarity	Accession	Phylum	NRPS(A7R/A3F) 700-800bp	PKS1(K1F/M6R)1250-1400bp	PKS2(KS α , KS β) 800-900bp	<i>Staphylococcus aureus</i> (ATCC25923)	<i>Salmonella typhimurium</i> (dt2)	<i>Pseudomonas syringae</i> (dc3000)	<i>Escherichia coli</i> (dh5 α)
Bac 1	MN/R	1	creamy ,flat, smooth, irregular, moist	99% <i>Vibrio parahaemolyticus</i>	KC210812.1	Proteobacteria	+	-	+	-	-	-	-
Bac2	MN/R	1	Beige, convex, smooth, irregular, moist	99% <i>Vibrio parahaemolyticus</i>	KC884652.1	Proteobacteria	+	-	+	-	-	-	-
Bac 3	MN/R	1	Brown, microcolony, smooth, circular flat , moist	99% <i>Vibrio harveyi</i>	AB617569.1	Proteobacteria	+	-	-	-	-	-	-
Bac4	MN/R	3	creamy,irregular,rough, convrx, moist	99% <i>Bacillus licheniformis</i>	KC514131.1	Firmicutes	+	+	-	1	-	-	-
Bac5	MN/R	3	creamy,smooth, convex, circular, moist	99% <i>Bacillus licheniformis</i>	HE995760.1	Firmicutes	+	-	-	0.5	-	2.5	1
Bac7	MN/R	1	creamy, circular,smooth, convex, moist	99% <i>Vibrio alginolyticus</i>	JF784015.1	Proteobacteria	-	-	-	-	-	-	-
Bac9	MN/R	1	creamy,smooth, convex, circular, moist	99% <i>Vibrio harveyi</i>	AB617569.1	Proteobacteria	-	-	-	-	-	-	-
Bac13	MN/R	1	creamy, circular,smooth, convex, moist	99% <i>Vibrio alginolyticus</i>	KF443081.1	Proteobacteria	-	-	-	-	-	-	-
							47% hypothetical protein [Marinobacter manganoxydans] WP_008171913.1	+	+	-	-	-	-
Bac16	MN/R	5	Peach,circular smooth, convex, moist	99% <i>Vibrio furnissii</i>	FJ906812.1	Proteobacteria	-	+	-	-	-	-	-
Bac17	MN/R	5	Clear Beige,circular smooth, convex, moist	99% <i>Vibrio furnissii</i>	FJ906812.1	Proteobacteria	-	-	-	-	-	-	-
Bac18	MN/R	5	Clear Pink, smooth, larg colony, convex, circular, moist	99% <i>Vibrio alginolyticus</i>	JN188411.1	Proteobacteria	-	-	-	-	-	-	-
Bac21	MN/R	5	white, circular smooth, convex, moist	99% <i>Virgibacillus pantothenicus</i>	JN791392.1	Firmicutes	-	-	-	-	-	-	-
Bac22	MN/R	5	Ligh Pink, irregular,rough,convex, moist	99% <i>Virgibacillus pantothenicus</i>	JN791392.2	Firmicutes	-	-	-	-	-	-	-
Bac24	MN/R	5	Peach, huge colony, smooth, convex, circular , moist	99% <i>Virgibacillus dokdonensis</i>	JN903905.1	Firmicutes	-	-	-	-	-	-	-
Bac26	MN/R	5	creamy,rhizoid, rough, circular, moist	99% <i>Bacillus subtilis</i>	JX994100.1	Firmicutes	+	99% polyketide synthase [Bacillus] WP_029973687.1	+	-	-	-	-
Bac27	MN/R	5	Peach, smooth, convex, irregular, moist	99% <i>Vibrio furnissii</i>	FJ906812.1	Proteobacteria	-	-	-	-	-	-	-
Bac28	MN/R	5	Clear,smooth, large colony, moist, raised	99% <i>Vibrio alginolyticus</i>	JF784015.1	Proteobacteria	-	-	-	-	-	-	-
Bac29	MN/R	2	Brown, smooth, circular convex, moist	99% <i>Microbulbifer salipaludis</i>	NR_025232.1	Proteobacteria	-	-	-	-	-	-	-
Bac30	MN/R	2	white, circular smooth, convex, moist	99% <i>Vibrio alginolyticus</i>	JF784015.1	Proteobacteria	-	-	-	-	-	-	-
Bac32	MN/R	2	light brown, circular smooth, convex , moist	99% <i>Microbulbifer gwangyangensis</i>	JX628583.1	Proteobacteria	-	-	-	-	-	-	-
Bac33	MN/R	2	white, microcolony, circular, smooth, flat, moist	99% <i>Microbulbifer variabilis</i>	JN128259.1	Proteobacteria	-	-	-	-	-	-	-
Bac34	MN/R	2	creamy, circular,smooth, convex, moist	98% <i>Vibrio alginolyticus</i>	JF784015.1	Proteobacteria	-	-	-	-	-	-	-
Bac35	MN/R	2	light brown, flat, smooth, irregular , moist	99% <i>Microbulbifer maritimus</i>	JQ824943.1	Proteobacteria	-	-	-	-	-	-	-
Bac37	MN/R	2	Beige, flat, smooth, circular, moist	99% <i>Vibrio alginolyticus</i>	CP006718.1	Proteobacteria	-	-	-	-	-	-	-
Bac38	MN/R	3	white,irregular, flat, rough, moist	99% <i>Bacillus foraminis</i>	NR_042274.1	Firmicutes	-	-	-	-	-	-	-
Bac39	MN/R	3	white, circular smooth, convex, moist	99% <i>Bacillus foraminis</i>	NR_042274.1	Firmicutes	-	-	-	-	-	-	-
Bac41	MN/R	3	creamy Yellowish, large colony, circular smooth, convex, moist	99% <i>Gordonia terrae</i>	EU333873.1	Actinobacteria	-	-	-	-	-	-	-
Bac42	MN/R	3	Yellow, microcolony, circular convex, smooth, moist	99% <i>Gordonia terrae</i>	EU333873.1	Actinobacteria	-	-	-	-	-	-	-
Bac44	MN/R	3	Clear, microcolony, smooth, circular, moist	99% <i>Bacillus foraminis</i>	NR_042274.1	Firmicutes	+	-	+	-	-	-	-
Bac45	MN/R	3	white, microcolony, circular smooth , cluster, moist	99% <i>Bacillus foraminis</i>	NR_042274.1	Firmicutes	-	-	+	-	-	-	-
Bac46	MN/R	3	creamy, circular,smooth, convex, moist	99% <i>Isosphaera chiayiensis</i>	FJ469988.1	Actinobacteria	-	-	-	-	-	-	-
Bac47	MN/R	3	white, microcolony, circular, smooth, convex, moist	99% <i>Bacillus licheniformis</i>	JQ236634.1	Firmicutes	-	-	-	-	-	-	-
Bac48	MN/R	3	Clear,smooth, circular, convex, moist	99% <i>Bacillus aerius</i>	KC443101.1	Firmicutes	-	-	-	-	-	-	-
Bac49	MN/R	3	creamy, flat, rough, large colony, moist	99% <i>Bacillus licheniformis</i>	HE995760.1	Firmicutes	-	-	-	-	-	-	-
Bac50	MN/R	3	white,large colony, smooth, flat, moist	99% <i>Bacillus subtilis</i>	HF563562.1	Firmicutes	-	-	-	-	-	-	-

Bac52	MN/R	3	white,filamontous, rough, circular, moist	99% Bacillus vallismortis	KC441761.1	Firmicutes	-	-	-	-	-	-	-	
Bac53	MN/R	3	Beige,flat , smooth ,circular, moist	99% Microbulbifer maritimus	NR_025772.1	Proteobacteria	-	-	-	-	-	-	-	
Bac54	MN/R	1	Brown,flat , smooth ,circular, moist	99% Microbulbifer maritimus	NR_025772.1	Proteobacteria	-	-	-	-	-	-	-	
Bac55	MN/R	2	white, irrular , flat , moist	99% Bacillus aquimaris	GQ927174.1	Firmicutes	-	-	-	-	-	-	-	
Bac56	MN/R	2	Beige, flat , large colony, moist	98% Microbulbifer maritimus	NR_025772.1	Proteobacteria	-	-	-	-	-	-	-	
Bac57	MN/R	5	Beige, circular, convex, smooth, moist	99% Bacillus amyloliquefaciens	JQ693000.1	Firmicutes	-	-	-	-	-	5	-	
Bac58	MM/R	1	Peach,circular, smooth, convex, moist	99% Salinivibrio costicola	JX913853.1	Proteobacteria	-	-	-	-	-	-	-	
Bac59	MM/R	1	white, circular, flat, rough,dry	99% Pseudoalteromonas piscicida	AF081498.1	Proteobacteria	-	-	-	-	-	-	-	
Bac60	MM/R	1	Creacmy,circular, smooth, convex, moist	99% Salinivibrio costicola	JX913853.1	Proteobacteria	-	-	-	-	-	-	-	
Bac61	MM/R	1	Creacmy,circular, smooth, convex, moist	99% Virgibacillus pantotheticus	AB617570.1	Firmicutes	-	-	-	-	-	-	-	
Bac62	MM/R	5	ight Pink, circular, rough, flat, dry	99% Saccharospirillum salsuginis	NR_044132.1	Proteobacteria	-	-	-	-	-	-	-	
Bac63	MM/R	5	Pink,smooth, convex, circular, moist	99% Psychrobacter celer	JQ799068.1	Proteobacteria	-	-	-	-	-	-	-	
Bac66	MM/R	3	creamy,Irregular, smooth, convex, moist	99% Psychrobacter celer	JQ799068.1	Proteobacteria	-	-	-	-	-	-	-	
Bac67	MM/R	4	creamy, microcolony,circular, smooth, convex, moist	99%Blastopirellula cremea	JF443747.1	Planctomycete	-	-	-	-	-	-	-	
Bac69	MM/R	3	creamy,Irregular, circular, rough, flat, dry	99% Psychrobacter celer	JQ799068.1	Proteobacteria	-	-	-	-	-	-	-	
Bac70	MM/R	3	white, circular, smooth, convex, moist	99% Psychrobacter celer	JQ799068.1	Proteobacteria	-	-	-	-	-	-	-	
Bac71	MM/R	1	Pink, rough, flat, large colony, dry	99% Bacillus sonorensis KTT-24	HQ696443.1	Firmicutes	-	-	-	-	-	-	-	
							95% non-ribosomal peptide synthase [Bacillus subtilis] KIN39535.1	+	-	-	-	-	-	
Bac74	MM/R	1	Pink, rough, flat,irregular	99% Bacillus licheniformis	HM629383.1	Firmicutes	-	-	-	-	-	-	-	
Bac75	MM/R	5	ight Pink, circular, rough, flat	99% Virgibacillus dokdonensis	EU368764.1	Firmicutes	-	-	-	1	-	1	-	
Bac76	MM/R	5	creamy, rough, flat, large colony, dry	99% Virgibacillus dokdonensis	EU368764.1	Firmicutes	-	-	-	-	-	-	-	
Bac77	MM/R	1	creamy, circular, smooth, flat, moist	99% Pseudoalteromonas flavipulchra	NR_025126.1	Proteobacteria	-	-	-	-	-	-	-	
Bac78	MM/R	5	creamy, wrinkled, flat, large colony, smooth	99% Virgibacillus dokdonensis	JN903905.1	Firmicutes	-	-	-	-	-	-	-	
Bac79	MM/R	5	creamy, smooth, convex, circular, viscous	99% Bacillus sonorensis	HQ696443.1	Firmicutes	-	-	-	-	-	-	-	
Bac80	MM/R	5	creamy, , rough, rhizoid, convex	99% Bacillus sonorensis	HQ696443.1	Firmicutes	-	-	-	-	-	-	-	
Bac81	MM/R	2	Clear, smooth,large colony, flat, moist	99% Vibrio harveyi	FJ154796.1	Proteobacteria	-	-	-	-	-	-	-	
Bac82	MM/R	2	creamy,circular,smooth, convex, moist	99%Pseudoalteromonas shioyasakiensis.	NR_125458.1	Proteobacteria	+	-	+	-	-	-	-	
Bac83	MM/R	2	creamy,circular,smooth, convex, moist	99% Salinivibrio costicola	JX913853.1	Proteobacteria	+	-	-	-	-	-	-	
Bac84	MM/R	5	white ,circular, rough, dry,flat	99% Bacillus licheniformis	HQ143636.1	Firmicutes	95% non-ribosomal peptide synthetase [Bacillus sp. MSP5.4]WP_039073180.1	-	74% hypothetical protein [Bacillus subtilis] WP_015252614.1	+	4.5	3	3	3
Bac85	MM/R	1	creamy, large colony, flat, rough, dry	95%Microbulbifer gwangyangensis	JX628583.1	Proteobacteria	+	-	+	-	-	-	-	
Bac87	MM/R	1	Beige,circular , flat, under media	99% Marinobacter hydrocarbonoclasticus	JN160753.1	Proteobacteria	-	-	-	-	-	-	-	
Bac90	MM/R	2	Pink, circular, smooth, convex, moist	99% Bacillus sonorensis	JN700092.1	Firmicutes	-	-	-	3.75	2.75	3	3	
Bac92	MM/R	4	Orange, circular, smooth, flat, moist	97% Planctomyces brasiliensis	NR_074297.1	Planctomycetes	50% hypothetical protein [Blastopirellula marina] WP_040351748.1	+	86% hypothetical protein [Rubinisphaera brasiliensis] WP_013627469.1	-	-	-	-	
Bac93	MM/R	4	creamy, circular, smooth, convex, moist	99% Blastopirellula cremea	NR_118153.1	Planctomycetes	-	+	+	-	-	-	-	
Bac94	MM/R	1	Orange, circular,smooth, convex, moist	98% Bacillus simplex	EU221357.1	Firmicutes	-	+	-	-	-	-	-	
Bac95	MM/R	5	Clear, smooth, circular, convex, moist	99% Bacillus vallismortis	NR_024696.1	Firmicutes	-	-	-	-	-	-	-	

Bac96	MM/R	5	creamy, flat, smooth, , moist, circular	99% Bacillus licheniformis	HQ143566.1	Firmicutes	-	-	-	-	-	-	
Bac97	MM/R	3	white, microcolony, circular, flat , moist	99% Bacillus vallismortis	HQ992817.1	Firmicutes	-	-	-	-	-	-	
Bac98	MM/R	3	Clear, circular, smooth, convex, viscous	99% Brevibacillus borstelensis	KC503891.1	Firmicutes	-	-	-	5	0.5	4.25	4
Bac105	MM/R	5	Dark pink, irregular, rough, convex	99% Bacillus vallismortis	NR_024696.1	Firmicutes	-	-	-	-	-	-	-
Bac106	MM/R	3	Peach,irregular, smooth, convex, moist	99% Bacillus vallismortis	NR_024696.1	Firmicutes	+	-	-	-	-	-	-
Bac109	MM/R	3	creamy, circular, smooth, convex, moist	99% Brevibacillus borstelensis	AB680943.1	Firmicutes	+	-	-	-	-	-	-
Bac110	MM/R	3	white, flat, microcolony, moist, smooth	99% Brevibacillus borstelensis	KC503891.1	Firmicutes	-	-	-	-	-	-	-
Bac111	MM/R	5	Clear Pink, convex, filamentous, moist, smooth	99% Bacillus vallismortis	NR_024696.1	Firmicutes	-	-	-	-	-	-	-
							78% non-ribosomal peptide synthetase [Paenibacillus elgii] WP_050900668.1	89% hypothetical protein [Bacillus thuringiensis] KKB27200.1	99%hypothetical protein [Paenibacillus dendritiformis] WP_006677536.1	2	4	0.5	5
Bac115	MM/R	5	Clear Pink, circular, smooth, convex , moist	99% Bacillus axarquiensis	JF414764.1	Firmicutes	-	-	-	-	-	-	-
Bac116	BS/R	1	Peach, microcolony, circular, smooth, flat, moist	99% Bacillus sonorensis	HM854235.1	Firmicutes	-	-	-	-	-	-	-
Bac117	BS/R	1	Creamy, microcolony, circular, smooth, flat, moist	99% Bacillus oceanisediminis	JF411237.1	Firmicutes	-	-	-	-	-	-	-
Bac118	BS/R	1	Orange, microcolony, circular, smooth, flat, moist	99% Bacillus sonorensis - KTT-24	HQ696443.1	Firmicutes	-	-	-	-	-	-	-
Bac119	BS/R	1	Light pink, microcolony, circular, smooth, flat, moist	99% Bacillus sonorensis - R23	JN700092.1	Firmicutes	+	-	-	2.5	-	1	-
Bac120	BS/R	1	white, circular, smooth, convex, moist	98% Oceanicaulis sp.	JN501387.1	Protobacteria	-	-	-	-	-	-	-
Bac121	BS/R	5	creamy, circular ,smooth , flat , , moist	99% Virgibacillus olivae	HM179177.1	Firmicutes	-	-	-	-	-	-	-
Bac122	BS/R	5	Clear Peach, circular, smooth, convex, moist	99% Bacillus infantis	KC184157.1	Firmicutes	-	-	-	-	-	-	-
Bac123	BS/R	3	Orange, circular, smooth, convex	99% Bacillus licheniformis	EU870503.1	Firmicutes	-	-	-	-	-	-	-
							83% non-ribosomal synthetase [Bacillus licheniformis] WP_025805844.1	+	-	-	-	-	-
Bac127	BS/R	1	Pink, rough, flat, moist, circular, convex, dry	99% Bacillus sonorensis	HQ696443.1	Firmicutes	-	-	-	-	-	-	-
Bac128	BS/R	2	Peach,circular,smooth,convex, microcolony, moist	99% Pontibacter korlensis	AB682651.1	Bacteroidetes	-	-	-	-	-	-	-
Bac129	BS/R	2	Yellow, microcolony, circular, smooth, convex, moist	99% Pontibacter korlensis	NR_044004.1	Bacteroidetes	+	-	-	1	-	-	-
Bac130	BS/R	2	Orange, circular, smooth, convex, microcolony, moist	99% Pontibacter korlensis	NR_044004.1	Bacteroidetes	-	-	-	-	-	-	-
Bac131	BS/R	4	Peach,circular,smooth,convex, moist	98% Planctomycete sp.	JF443792.1	Planctomycetes	-	-	-	-	-	-	-
Bac132	BS/R	3	Clear, microcolony, smooth , flat, circular, moist	99% Bacillus infantis	JF411305.1	Firmicutes	-	-	-	-	-	-	-
Bac133	BS/R	3	Pech, circular, flat, smooth, moist	99% Bacillus infantis	JF411305.1	Firmicutes	+	-	-	-	-	-	-
Bac134	BS/R	3	creamy,circular, smooth, flat, moist	99% Bacillus niacini	EU221359.1	Firmicutes	-	-	-	-	-	-	-
Bac135	BS/R	3	creamy, micocolony, smooth , flat, circular, moist	99% Bacillus odysseyi	NR_025258.1	Firmicutes	-	-	-	-	-	-	-
Bac139	BS/R	2	creamy, flat, rough, dry , circular	99% Bacillus sonorensis	HQ696443.1	Firmicutes	-	-	-	1	-	-	-
Bac140	BS/R	2	Yellow, circular,smooth, convex, moist	97% Flavobacteriaceae bacterium	GQ246641.1	Bacteroidetes	-	-	-	-	-	-	-
Bac142	BS/R	5	Pink,rough, flat, irrular,	99% Bacillus sonorensis	JN700092.1	Firmicutes	-	-	-	-	-	-	-
Bac143	BS/R	5	creamy, micocolony, smooth , convex, circular, moist	99% Oceanobacillus picturae	HM179167.1	Firmicutes	-	-	-	-	-	-	-
Bac144	BS/R	5	Beige,micocolony, smooth ,irrular	99% Bacillus aquimaris	GQ927174.1	Firmicutes	-	-	-	3	-	4	3
Bac145	BS/R	5	Clear, smooth , flat, moist, circular	99% Terribacillus aidingensis	GQ304894.1	Firmicutes	-	-	-	-	-	-	-
Bac147	BS/R	5	Clear creamy, micocolony, smooth , flat, moist	99% Bacillus aquimaris	GQ927174.1	Firmicutes	-	-	-	-	-	-	-
Bac151	BS/R	1	Yellow, circular,smooth, convex, moist	99% Pseudoalteromonas viridis	EU240534.1	Proteobacteria	-	-	-	-	-	-	-
Bac155	BS/R	1	white, circular, smooth, flat, moist	99% Labrenzia marina	HQ908720.1	Proteobacteria	-	-	-	-	-	-	-
Bac156	BS/R	2	white, microcolony, circular, smooth, flat, moist	99% Vibrio corallilyticus	HF549288.1	Proteobacteria	+	+	-	-	-	-	-
Bac162	BS/R	5	Creamy, micocolony, smooth , convex, circular, moist	99% Vibrio harveyi	HQ449971.1	Proteobacteria	+	-	-	-	-	-	-
Bac163	BS/R	5	Clear Peach, filamentous, smooth, convex	99% Paenibacillus polymyxa	HQ538845.1	Firmicutes	-	-	-	-	-	-	-

Bac269	MM/K	5	Peach, flat, media, large colony, smooth	99% <i>Salinivibrio costicola</i>	JX913853.1	Proteobacteria	-	-	-	-	1.8	6.3	1
Bac270	MM/K	2	white, circular, smooth, convex, moist	99% <i>Aneurinibacillus migulanus</i>	AB680889.1	Firmicutes	-	-	-	4	2	3.25	3.5
Bac271	MM/K	2	Orange, microcolony, circular, smooth, moist	99% <i>Aneurinibacillus migulanus</i>	AB680889.1	Firmicutes	-	-	-	5.5	3	4.5	3.5
Bac272	MM/K	1	creamy, circular, rough, stick on media media	99% <i>Marinobacter mobilis</i>	NR_044456.1	Proteobacteria	+	-	-	-	-	-	-
Bac273	MM/K	1	Clear, large colony, smooth, moist	99% <i>Salinivibrio costicola</i>	JX913853.1	Proteobacteria	+	-	-	-	-	-	-
Bac274	BS/K	2	white, circular, flat, smooth, microcolony, moist	99% <i>Fulvivirga kasyanovii</i>	AB682457.1	Bacteroidetes	+	-	+	-	-	-	-
Bac275	BS/K	2	white, circular, flat, smooth, microcolony, moist	99% <i>Bacillus benzoovorans</i>	AY043085.1	Firmicutes	-	-	-	-	-	-	-
Bac277	BS/K	3	white, circular, flat, smooth, microcolony, moist	99% <i>Bacillus sonorensis</i>	JN700094.1	Firmicutes	-	-	-	-	-	-	-
							81% non-ribosomal peptide synthase [Bacillus licheniformis] AJO61325.1						
Bac278	BS/K	3	Pink, circular, smooth, convex, moist	99% <i>Bacillus subtilis</i>	JQ973708.1	Firmicutes	+	-	+	1	5	-	-
Bac279	BS/K	1	white, circular, smooth, convex, moist	99% <i>Virgibacillus pantothenicus</i>	JN791392.1	Firmicutes	-	-	-	-	-	-	-
Bac280	BS/K	1	Beige, circular, smooth, convex, moist	99% <i>Sporosarcina koreensis</i>	KC355330.1	Firmicutes	-	-	-	-	-	-	-
Bac282	BS/K	5	Clear, filamentous, smooth, conex, moist	99% <i>Bacillus sonorensis</i>	HQ696443.1	Firmicutes	+	+	-	-	-	-	-
Bac283	BS/K	5	Pink, rough, rhizoid, convex	99% <i>Bacillus sonorensis</i>	JN700094.1	Firmicutes	+	+	-	-	-	-	-
Bac284	BS/K	3	white, circular, flat, stick on media	99% <i>Bacillus sonorensis</i>	JN700094.1	Firmicutes	-	+	-	-	-	-	-
Bac287	BS/K	2	white, microcolony, smooth, flat, circular, moist	99% <i>Pseudoalteromonas hodoensis</i>	NR_126232.1	Proteobacteria	-	-	-	-	-	-	-
Bac288	BS/K	2	white, microcolony, smooth, flat, circular, moist	93% <i>Pseudoalteromonas atlantica</i>	KP645203.1	Proteobacteria	+	+	-	-	-	-	-
Bac289	BS/K	5	Pink, irregular, large colony, rough	99% <i>Bacillus halodenitrificans</i>	AY543168.1	Firmicutes	-	-	-	-	-	-	-
Bac291	BS/K	2	Pink, flat, large colony, wrinkled	99% <i>Pseudoalteromonas atlantica</i>	KP645203.1	Proteobacteria	-	-	-	-	-	-	-
							70% nonribosomal peptide synthase [Burkholderia pseudomallei] WP_044368416.1						
Bac292	BS/K	2	creamy, microcolony, circular, smooth, convex, moist	99% <i>Pseudoalteromonas espejiana</i>	KC178899.1	Proteobacteria	-	-	-	-	-	-	-
Bac295	BS/K	5	white, circular, smooth, flat, moist	99% <i>Bacillus niabensis</i>	JF496450.1	Firmicutes	-	+	-	-	-	-	-
Bac296	BS/K	5	pink, circular, smooth, convex, moist	99% <i>Bacillus halodenitrificans</i>	AY543168.1	Firmicutes	-	-	-	-	-	-	-
Bac298	MM/K	5	creamy, circular, smooth, convex, moist	99% <i>Bacillus pumilus</i>	JF496399.1	Firmicutes	-	-	-	-	-	-	-
Bac299	MM/K	5	Orange, circular, smooth, convex, moist	99% <i>Virgibacillus salarius</i>	NR_041270.1	Firmicutes	-	-	-	-	-	-	-
Bac301	MM/K	1	creamy, circular, smooth, flat, moist	99% <i>Pseudoalteromonas</i> sp.	JX075059.1	Proteobacteria	-	-	-	-	-	-	-
Bac302	MM/K	2	creamy, rhizoid, flat, rough, moist	99% <i>Pseudoalteromonas</i> sp.	JX045665.1	Proteobacteria	-	+	-	-	-	-	-
Bac306	MN/K	1	creamy, circular, smooth convex, moist	99% <i>Pseudoalteromonas piscicida</i>	AB681918.1	Proteobacteria	-	+	-	-	-	-	-
Bac318	MM/R	1	creamy, flat, smooth, moist, convex, circular	99% <i>Virgibacillus dokdonensis</i>	JN903905.1	Firmicutes	-	-	-	3	-	1.9	-
Bac319	MM/R	2	white, circular, smooth, convex, moist	98% <i>Pseudoalteromonas espejiana</i>	KC178899.1	Proteobacteria	+	+	+	1	-	-	-
Bac320	MM/R	5	Clear, irregular, flat, microcolony, smooth, moist	98% <i>Pseudoalteromonas atlantica</i>	KP645203.1	Proteobacteria	-	-	-	1	-	1	-
Bac323	MN/R	5	white, irregular, smooth, flat, moist	99% <i>Bacillus foraminis</i>	NR_042274.1	Firmicutes	-	-	+	-	-	-	-
Bac324	MN/R	5	Orange, smooth, circular, convex, moist	99% <i>Virgibacillus halodenitrificans</i>	NR_042967.1	Firmicutes	-	-	-	-	-	-	-
Bac325	MN/R	5	Orange, smooth, circular, convex, moist	99% <i>Pseudoalteromonas espejiana</i>	KC178899.1	Proteobacteria	-	+	-	0.5	-	-	-
Bac326	MN/R	2	white, irregular, smooth, flat, moist	99% <i>Pseudoalteromonas elyakovii</i>	DQ517879.1	Proteobacteria	+	+	-	-	-	-	-
Bac327	MN/R	5	white, circular, smooth, flat	99% <i>Virgibacillus pantothenicus</i>	JN791392.1	Firmicutes	+	-	-	1.8	-	6	-
Bac330	MN/R	1	Light Yellow, smooth, circular, convex, moist	99% <i>Virgibacillus dokdonensis</i>	JN903905.1	Firmicutes	-	-	-	3	-	2	-
Bac332	MN/R	1	white, circular and from the end rhizoid, smooth, flat	99% <i>Virgibacillus pantothenicus</i>	JN791392.2	Firmicutes	-	-	-	1.13	-	1	2.8
Bac333	MN/R	1	white, smooth, flat, moist, circular, convex	99% <i>Virgibacillus salarius</i>	NR_041270.1	Firmicutes	-	-	+	-	-	-	2

Bac334	BS/R	3	Yellow, circular, smooth, convex, moist	99% <i>Micrococcus luteus</i>	EU379288.1	Actinobacteria	-	-	-	-	-	-	-	
Bac335	BS/R	3	creamy, circular, smooth, convex, moist	99% <i>Gordonia aichiensis</i>	FJ536314.1	Actinobacteria	+	-	-	-	-	-	-	
Bac336	BS/R	1	white, circular, smooth, convex, moist	99% <i>Pseudoalteromonas atlantica</i>	KP645203.1	Proteobacteria	+	+	-	-	2	-	1	
Bac337	BS/R	1	white, circular, smooth, convex, moist	99% <i>Pseudoalteromonas espejiana</i>	JX867735.1	Proteobacteria	+	+	-	-	2.5	-	1.5	
Bac338	BS/R	2	white, circular, smooth, convex, moist	99% <i>Pseudoalteromonas hodoensis</i>	HM598083.1	Proteobacteria	-	+	-	-	-	-	-	
Bac342	BS/K	2	white, circular, smooth, convex, moist	99% <i>Pseudoalteromonas atlantica</i>	NR_126232.1	Proteobacteria	-	-	-	-	-	-	-	
Bac344	BS/R	5	creamy, circular, smooth, convex, moist	99% <i>Staphylococcus epidermidis</i>	KC443110.1	Firmicutes	-	-	-	-	1	-	-	
Bac345	BS/R	5	Clear,Irrgular, flat, smooth, moist	99% <i>Bacillus subtilis</i>	HM585050.1	Firmicutes	-	-	-	-	1	-	2	
Bac351	MN/K	5	Yellow, smooth, flat, moist, circular, moist	99% <i>Pseudoalteromonas piscicida</i>	AB681918.1	Proteobacteria	-	+	-	-	-	-	-	
Bac353	MN/K	3	creamy smooth, flat, circular, moist	99% <i>Ruegeria pelagia</i>	AB681677.1	Proteobacteria	-	-	-	-	-	-	-	
Bac355	BS/K	5	ight Pink, Irrgular, flat, smooth, moist	99% <i>Bacillus cereus</i>	JQ248587.1	Firmicutes	-	-	-	-	4	-	-	
Bac358	BS/K	2	white, microcolony, circular, smooth, convex	99% <i>Bacillus vietnamensis</i>	HQ699497.1	Firmicutes	+	-	-	-	-	-	-	
Bac361	BS/K	1	creamy, circular, smooth, convex	99% <i>Ruegeria pelagia</i>	AB681677.1	Proteobacteria	-	-	+	-	-	-	-	
Bac363	MM/K	5	Clear,microcolony, convex, smooth, circular	99% <i>Paenibacillus dendritiformi</i>	HM071942.1	Firmicutes	80% non-ribosomal peptide synthetase [Paenibacillus elgii] WP_050900668.1	+	+	-	0.5	3	1	5
Bac366	MM/K	3	creamy, smooth, flat, circular, moist	99% <i>Stenotrophomonas maltophilia</i>	JX262392.1	Proteobacteria	-	-	+	-	-	-	-	
Bac369	MM/K	2	white, circular, smooth, convex, moist	99% <i>Pseudoalteromonas nigrifaciens</i>	GU726859.1	Proteobacteria	65% nonribosomal peptide synthetase subunit [Paenibacillus alvei DSM 29] E JW20318.1	+	+	-	-	-	-	
Bac370	MM/K	1	creamy, smooth, flat, moist, circular	99% <i>Marinobacter mobilis</i>	NR_044456.1	Proteobacteria	-	-	-	-	-	-	-	
Bac371	MM/K	1	Creamy,circular, smooth, convex, moist	99% <i>Ruegeria pelagia</i>	AB681677.1	Proteobacteria	-	-	-	-	-	-	-	
Bac372	BS/R	5	Clear, circular, smooth, convex, moist	99% <i>Bacillus methylotrophicus</i>	KC405629.1	Firmicutes	-	-	-	-	1	-	1	
Bac373	BS/R	5	white, circular, smooth, flat, moist	99% <i>Bacillus cereus</i>	KC178715.1	Firmicute	-	-	-	-	-	-	-	
Bac374	BS/R	3	creamy, circular,smooth , convex, moist	99% <i>Pseudomonas syncyanea</i>	JX192650.1	Proteobacteria	-	-	-	-	-	-	-	
Bac375	BS/R	3	creamy, circular,smooth , flat	99% <i>Pseudomonas fluorescens</i>	HQ420253.1	Proteobacteria	-	-	-	-	3	-	-	
Bac376	BS/R	1	creamy, circular,smooth, convex	99% <i>Virgibacillus olivae</i>	HM179177.1	Firmicutes	+	-	-	-	-	-	7	
Bac378	BS/R	2	Clear, circular, smooth, convex	99% <i>Ruegeria pelagia</i>	AB681677.1	Proteobacteria	-	-	-	-	-	-	-	
Bac380	MN/R	3	white, circular, smooth, convex	99% <i>Stenotrophomonas maltophilia</i>	JX262392.1	Proteobacteria	-	-	-	-	5	-	-	
Bac381	MM/R	5	ight Pink, circular, convex, smooth, moist	99% <i>Bacillus cereus</i>	JN934390.1	Firmicutes	-	-	-	-	-	-	-	
Bac383	MM/R	1	creamy, smooth, flat , circular, moist	99% <i>Pseudoalteromonas ruthenica</i>	NR_025140.1	Proteobacteria	-	-	-	-	-	-	2	
Bac384	MM/R	1	creamy, circular, convex, smooth , moist	99% <i>Pseudoalteromonas ruthenica</i>	NR_025140.1	Proteobacteria	-	-	-	-	-	-	-	
Bac385	MM/R	3	white, circular, smooth, convex, moist	99% <i>Bacillus subtilis</i>	FJ959367.1	Firmicutes	+	-	-	-	-	-	-	
Bac386	MM/R	3	white, microcolony, circular, smooth, convex, moist	99% <i>Bacillus cereus</i>	KC248212.1	Firmicutes	-	-	-	-	-	-	-	
Bac387	MN/R	1	creamy, flat, smooth, moist, circular	96% <i>Exiguobacterium profundum</i>	JX112643.1	Firmicutes	83% non-ribosomal peptide synthase [Bacillus licheniformis] AJO61326.1	-	53% hypothetical protein [Psychrobacter sp. JCM 18902] WP_045445323.1	-	-	-	-	
Bac389	MN/R	5	ight Pink, circular, convex, smooth, moist	99% <i>Bacillus cereus</i>	JF895490.1	Firmicutes	+	-	+	-	-	-	0.5	
Bac390	MN/R	5	ight Pink, circular, convex, smooth, moist	99% <i>Paenibacillus dendritiformis</i>	JX499920.1	Firmicutes	80% non-ribosomal peptide synthetase [Paenibacillus polymyxa] WP_050900668.1	-	86% hypothetical protein [Bacillus thuringiensis] gi 803756437 KKB2720 0.1	+	2	2	5	3

Bac391	MN/R	2	creamy, microcolony ,circular, convex, smooth, moist	99% Exiguobacterium arabatum	JX913842.1	Firmicutes	-	-	-	-	-	-	-
Bac393	MN/R	3	white, irrular, convex, smooth	99% Bacillus cereus	HQ143564.1	Firmicutes	-	-	-	-	-	-	1
Bac394	MN/R	3	white, circular, smooth, convex, moist	99% Bacillus cereus	HQ143564.1	Firmicutes	-	-	-	-	-	2	-
Bac395	MN/R	3	white, circular, smooth, convex, moist	99% Stenotrophomonas maltophilia	JX262392.1	Proteobacteria	+	-	+	-	-	-	-
Bac396	MN/R	3	white, circular, smooth, convex, moist	99% Stenotrophomonas maltophilia	JX262392.1	Proteobacteria	-	-	-	-	-	-	-

Abbreviation	
MN	Mangrove Mud
MM	Microbial Mat
BS	Bareen Soil
K	Al-Kharrar
R	Rabigh

Media Name	NO.
Difco Marine Agar 2216 (MA)	1
10% Difco Marine Agar 2216 (10% MA)	2
Actinomyces Isolation Agar (AIA)	3
Difco Marine Agar 2216 with 1g/L streptomycin (Anti- MA)	4
Difco Marine Broth 2216 Gellan gum (MA-GM)	5

Table S5.2. NRPS and PKS results of strains that exhibited antimicrobial activity.

Sample ID	Type of samples	Location	Closest Relative by BLAST	PKS/NRPS			Zone of Inhibition (mm)							
				NRPS	PKSI	PKSII	<i>Staphylococcus</i>		<i>Salmonella</i>		<i>Pseudomonas</i>		<i>Escherichia coli</i>	
							Annular radius	Diameter	Annular radius	Diameter	Annular radius	Diameter	Annular radius	Diameter
Bac4	MN	RHL	99% <i>Bacillus licheniformis</i>	+	+	-	1	7	-	-	-	-	-	-
Bac5	MN	RHL	99% <i>Bacillus licheniformis</i>	+	-	-	0.5	6	-	-	2.5	10	1	6.7
Bac57	MN	RHL	99% <i>Bacillus amyloliquefaciens</i>	-	-	-	-	-	-	-	5	15	-	-
Bac75	MM	RHL	99% <i>Virgibacillus dokdonensis</i>	-	-	-	1	7	-	-	1	7	-	-
Bac84	MM	RHL	99% <i>Bacillus licheniformis</i>	95% non-ribosomal peptide synthetase [Bacillus sp. MSP5.4] WP_039073180.1	74% hypothetical protein [Bacillus subtilis] WP_015252614.1	+	4.5	14	3	11	3	11	3	10.8
Bac90	MM	RHL	99% <i>Bacillus sonorensis</i>	-	-	-	3.75	9.5	2.7	10	3	11	3	10.7
Bac98	MM	RHL	99% <i>Brevibacillus borstelensis</i>	-	-	-	5	15	0.5	6	4.2	13	4	12.8
Bac111	MM	RHL	99% <i>Bacillus vallismortis</i>	78% non-ribosomal peptide synthetase [Paenibacillus elgii] WP_050900668.1	89% hypothetical protein [Bacillus thuringiensis] KKB27200.1	99% hypothetical protein [Paenibacillus dendritiformis] WP_006677536	2	9	4	13	0.5	6	5	15
Bac119	BS	RHL	99% <i>Bacillus sonorensis</i> - R23	+	-	-	2.5	10	-	-	1	7	-	-
Bac129	BS	RHL	99% <i>Pontibacter korlensis</i>	+	-	-	1	7	-	-	-	-	-	-
Bac139	BS	RHL	99% <i>Bacillus sonorensis</i>	-	-	-	1	7	-	-	-	-	-	-
Bac144	BS	RHL	99% <i>Bacillus aquimaris</i>	-	-	-	3	11	-	-	4	13	3	10.8
Bac177	MN	AKL	99% <i>Microbulbifer salipaludis</i>	-	-	-	3.3	11	6.5	18	1	7	3.8	12.4
Bac189	MN	AKL	99% <i>Bacillus subtilis</i>	-	-	-	5.5	16	2	9	-	-	-	-
Bac207	MN	AKL	99% <i>Bacillus pumilus</i>	-	-	-	5	15	-	-	1	7	3.7	12.2
Bac218	MM	AKL	99% <i>Bacillus pumilus</i>	-	-	-	6	17	-	-	2	9	-	-
Bac247	BS	AKL	99% <i>Bacillus sonorensis</i>	-	+	-	2	9	-	-	1	7	-	-
Bac248	BS	AKL	99% <i>Bacillus sonorensis</i>	-	+	-	1	7	-	-	1	7	-	-
Bac250	BS	AKL	99% <i>Bacillus sonorensis</i>	-	-	-	4.2	13	-	-	-	-	1.5	7.8
Bac253	BS	AKL	99% <i>Bacillus sonorensis</i>	-	+	-	-	-	-	-	1	7	3.5	12
Bac254	MN	AKL	99% <i>Bacillus subtilis</i>	88% nonribosomal peptide synthase [Paenibacillus alvei] WP_021255906.1	89% hypothetical protein [Bacillus thuringiensis] KKB27200.1	78% hypothetical protein [Bacteria]gi WP_000919062.1	5	15	3	11	0.5	6	2.5	10
Bac256	MN	AKL	99% <i>Bacillus subtilis</i>	+	-	+	1	7	-	-	5	15	-	-
Bac267	MM	AKL	99% <i>Salinivibrio costicola</i>	+	-	-	4	13	-	-	-	-	1.5	7.7
Bac268	MM	AKL	99% <i>Bacillus circulansi</i>	+	-	-	-	-	4.8	14	2	9	1	5.6
Bac269	MM	AKL	99% <i>Salinivibrio costicola</i>	-	-	-	-	-	1.8	8	6.3	17	1	5.7
Bac270	MM	AKL	99% <i>Aneurinibacillus migulanus</i>	-	-	-	4	13	2	9	3.2	11	3.5	12

Bac271	MM	AKL	99% <i>Aneurinibacillus migulanus</i>	-	-	-	5.5	16	3	11	4.5	14	3.5	11.7
Bac278	BS	AKL	99% <i>Bacillus subtilis</i>	+	-	+	1	7	5	15	-	-	-	-
Bac291	BS	AKL	99% <i>Pseudoalteromonas atlantica</i>	70 % nonribosomal peptide synthase [Burkholderia pseudomallei] WP_044368416.1	+	-	1.5	7.5	-	-	-	-	-	-
Bac318	MM	RHL	99% <i>Virgibacillus dokdonensis</i>	-	-	-	3	11	-	-	1.9	8.5	-	-
Bac319	MM	RHL	98% <i>Pseudoalteromonas espejiana</i>	+	+	+	1	7	-	-	-	-	-	-
Bac320	MM	RHL	98% <i>Pseudoalteromonas atlantica</i>	-	-	-	1	7	-	-	1	7	-	-
Bac325	MN	RHL	99% <i>Pseudoalteromonas espejiana</i>	-	+	-	0.5	6	-	-	-	-	-	-
Bac327	MN	RHL	99% <i>Virgibacillus pantothenicus</i>	+	-	-	1.8	-	-	-	6	16	-	-
Bac330	MN	RHL	99% <i>Virgibacillus dokdonensis</i>	-	-	-	3	11	-	-	2	9	-	-
Bac332	MN	RHL	99% <i>Virgibacillus pantothenicus</i>	-	-	-	1.13	6	-	-	1	7	2.8	10.4
Bac333	MN	RHL	99% <i>Virgibacillus salarius</i>	-	-	+	-	-	-	-	-	-	2	9
Bac336	BS	RHL	99% <i>Pseudoalteromonas atlantica</i>	+	+	-	2	9	-	-	1	7	-	-
Bac337	BS	RHL	99% <i>Pseudoalteromonas espejiana</i>	+	+	-	2.5	10	-	-	1.5	8	-	-
Bac344	BS	RHL	99% <i>Staphylococcus epidermidis</i>	-	-	-	1	7	-	-	-	-	-	-
Bac345	BS	RHL	99% <i>Bacillus subtilis</i>	-	-	-	1	7	-	-	2	9	-	-
Bac355	BS	RHL	99% <i>Bacillus cereus</i>	-	-	-	4	13	-	-	-	-	-	-
Bac363	MM	AKL	99% <i>Paenibacillus dendritiformis</i>	80% non-ribosomal peptide synthetase [Paenibacillus elgii] WP_050900668.1	+	+	0.5	6	3	11	1	7	5	15
Bac372	BS	RHL	99% <i>Bacillus methylotrophicus</i>	-	-	-	1	7	-	-	1	7	-	-
Bac375	BS	RHL	99% <i>Pseudomonas fluorescens</i>	-	-	-	3	11	-	-	-	-	-	-
Bac376	BS	RHL	99% <i>Virgibacillus olivae</i>	+	-	-	-	-	-	-	7	18	-	-
Bac380	MN	RHL	99% <i>Stenotrophomonas maltophilia</i>	-	-	-	5	15	-	-	-	-	-	-
Bac383	MM	RHL	99% <i>Pseudoalteromonas rutherfordiana</i>	-	-	-	-	-	-	-	-	-	2	9
Bac389	MN	RHL	99% <i>Bacillus cereus</i>	+	-	+	-	-	-	-	-	-	0.5	6
Bac390	MN	RHL	99% <i>Paenibacillus dendritiformis</i>	80% non-ribosomal peptide synthetase [Paenibacillus polymyxa] WP_050900668.1	86% hypothetical protein [Bacillus thuringiensis] gi 803756437 KKB27200.1	+	2	9	2	9	5	15	3	11
Bac393	MN	RHL	99% <i>Bacillus cereus</i>	-	-	-	-	-	-	-	-	-	1	6.5
Bac394	MN	RHL	99% <i>Bacillus cereus</i>	-	-	-	-	-	-	-	2	9	-	0

Table S5.2: Genus abundance

Genus	BS/K	BS/R	MN/K	MN/R	MM/K	MM/R
Total number of different species	8	18	10	11	8	12
Arnithinibacillus	1	0	0	0	2	0
Bacillus	22	21	10	18	9	17
Blastopirellula	0	0	2	0	0	2
Brevibacillus	0	2	1	0	0	3
Enterococcus	0	0	1	0	0	0
Exiguobacterium	0	0	0	2	0	0
Flavobacteriaceae	0	1	0	0	0	0
Fulvivirga	1	0	0	0	0	0
Gordonia	0	1	0	2	0	0
Isopteriola	0	0	0	1	0	0
Labrenzia	0	1	0	0	0	0
Marinobacter	0	0	0	0	3	1
Microbulbifer	0	0	4	7	0	1
Micrococcus	0	1	0	0	0	0
Oceanicaulis	0	1	0	0	0	0
Oceanobacillus	0	1	0	0	0	0
Paenibacillus	0	2	0	1	1	0
Planctomycete	0	1	0	0	0	1
Pontibacter	0	3	0	0	0	0
Pseudoalteromonas	5	4	9	2	4	7

Psudomonas	0	2	0	0	0	0
Psychrobacter	0	0	0	0	0	4
Ruegeria	1	1	2	0	1	0
Saccharosirillum	0	0	0	0	0	1
Salinibacillus	1	0	0	0	0	0
Salinivibrio	0	0	0	0	4	3
Sporosarcina	1	0	0	0	0	0
Staphylococcus	0	1	0	0	0	0
Stappia	0	0	1	0	0	0
Stenotrophomonas	0	0	0	3	0	0
Terribacillus	0	1	0	0	0	0
vibrio	0	2	9	14	0	1
Virgibacillus	1	2	1	8	1	5