Supplementary Information to

Community-Wide Plasmid Gene Mobilization and Selection

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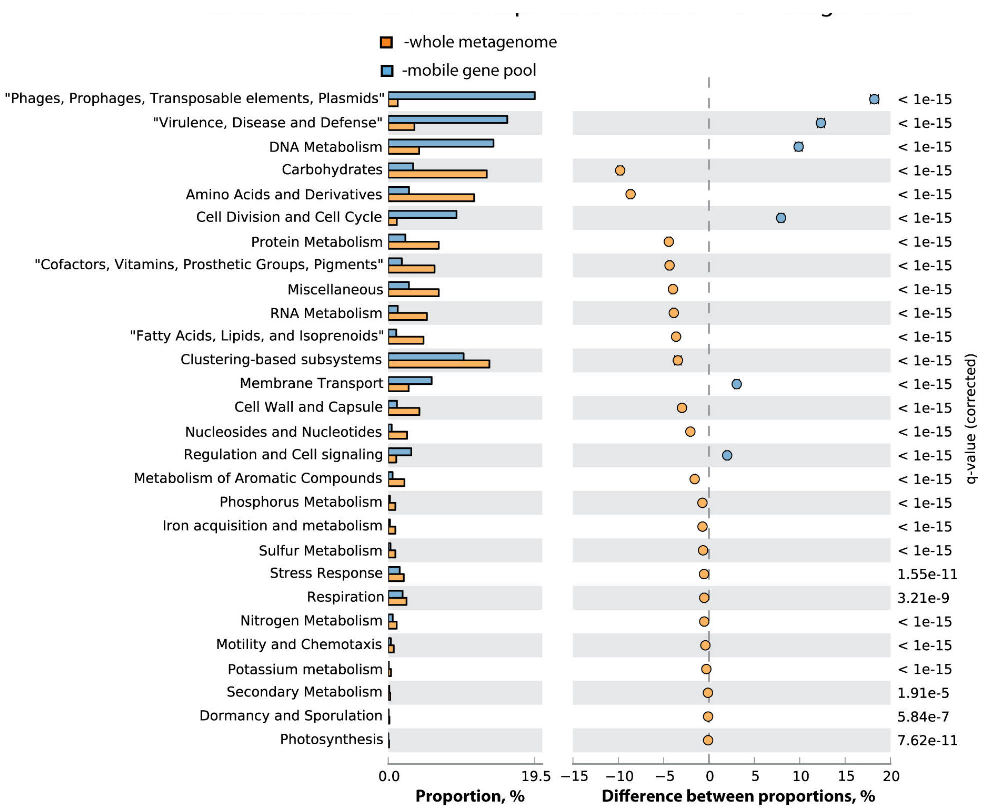
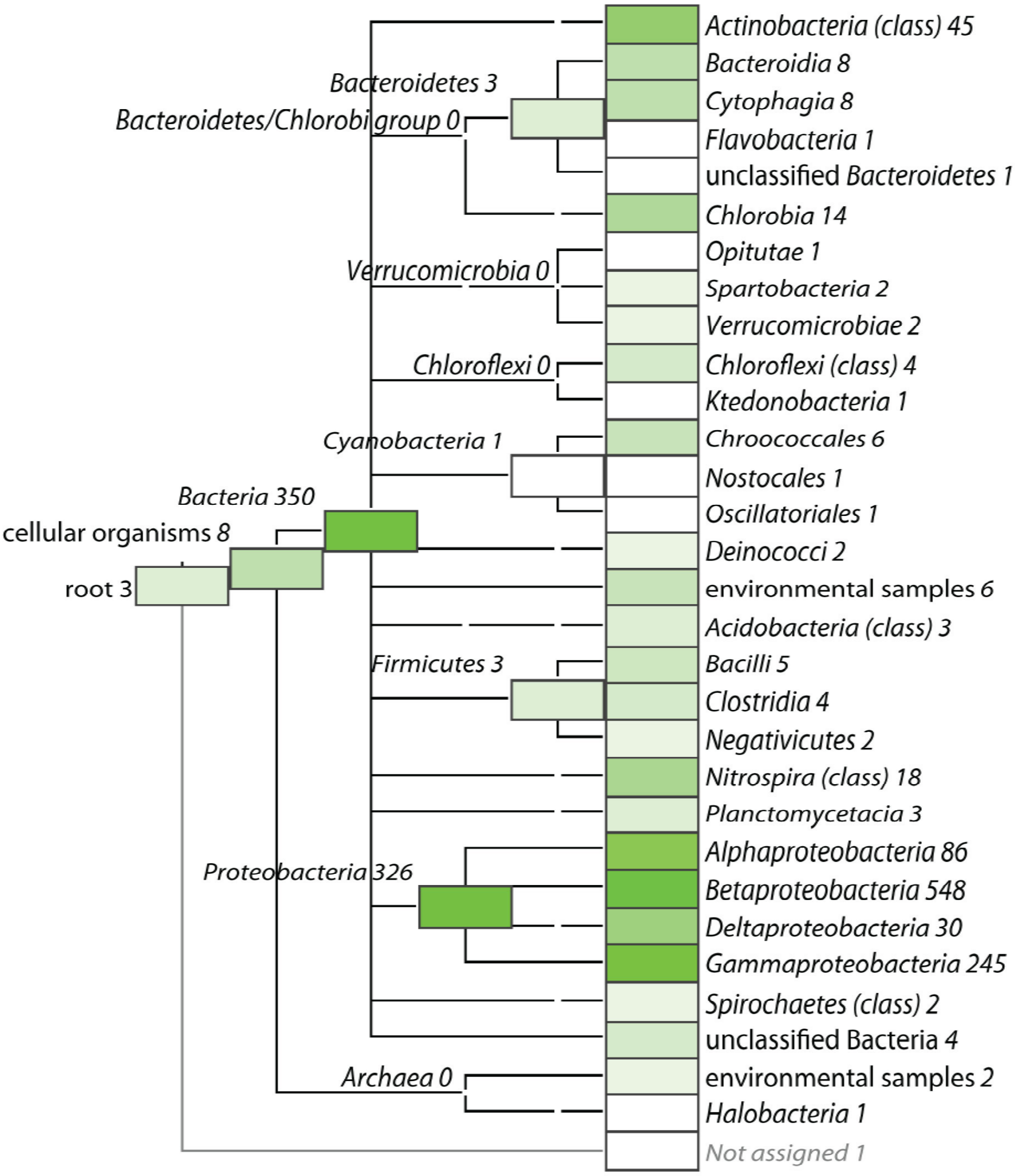


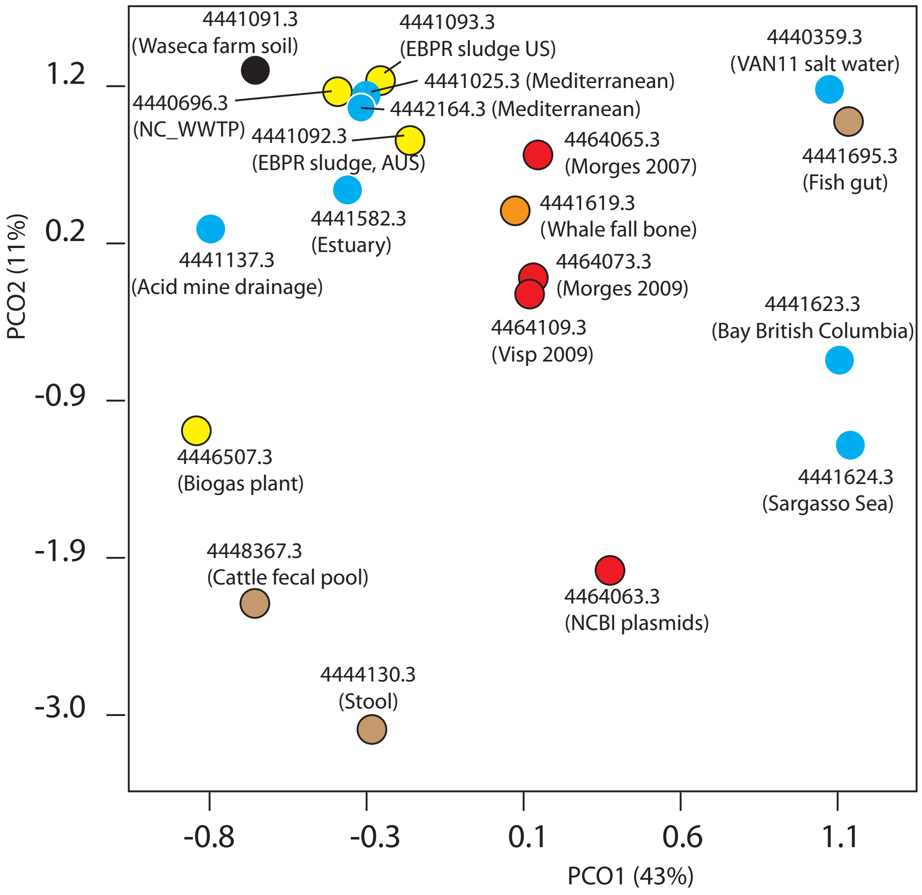
Supplementary Figure 1. Over- and underrepresentation of functionally categorizable protein coding genes from the Morges WWTP 2007 plasmid metagenome compared to the North Carolina complete WWTP metagenome. Diagram shows proportions within SEED level 1 subsystems and the difference between proportions in the two data sets. Whiskers denote calculated 95% confidence intervals.



Supplementary Figure 2. Phylogenetic inference of functionally predictable protein coding genes in the Morges WWTP plasmid metagenome. Diagram shows phylogeny and number of hits within taxonomic category for protein coding genes predicted from the MIRA CONTIGS non-redundant 5x covered dataset, as derived by BLASTP queries against 'All prokaryotic Proteins' within the CAMERA environment. Note that numbering at nodes is not cumulative but based on the direct count of hits in the closest phylogenetic group. As an example, 326 hits fall in the level of *Proteobacteria*, but cannot be more precisely assigned to lower phylogenetic levels. 548 Hits fall in *Betaproteobacteria*, but are not counted again at the level of *Proteobacteria*.

Supplementary Figure 3

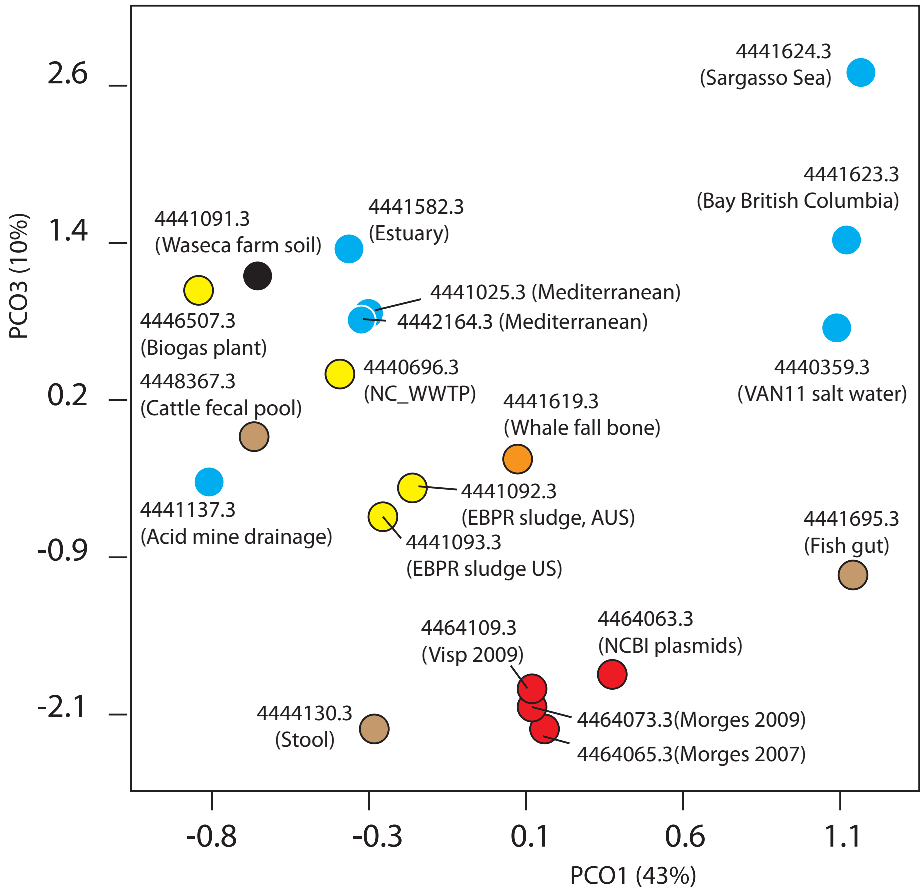
PCA analysis based on phylogenetic composition of mobile gene pools and selected whole microbial metagenomes representative for different environments. Phylogenetic classifications were obtained by BLAT searches {Kent, 2002} against the SEED protein database in the MG-RAST environment using a maximum *e*-value of 1e-5. **a.** Principal components 1 versus 2. **b.** Principal components 1 versus 3. Environmental color code: yellow, wastewater treatment processes; red, plasmid gene pools; blue, salt-water; black, soil; orange, whale fall; brown, gut/fecal communities.



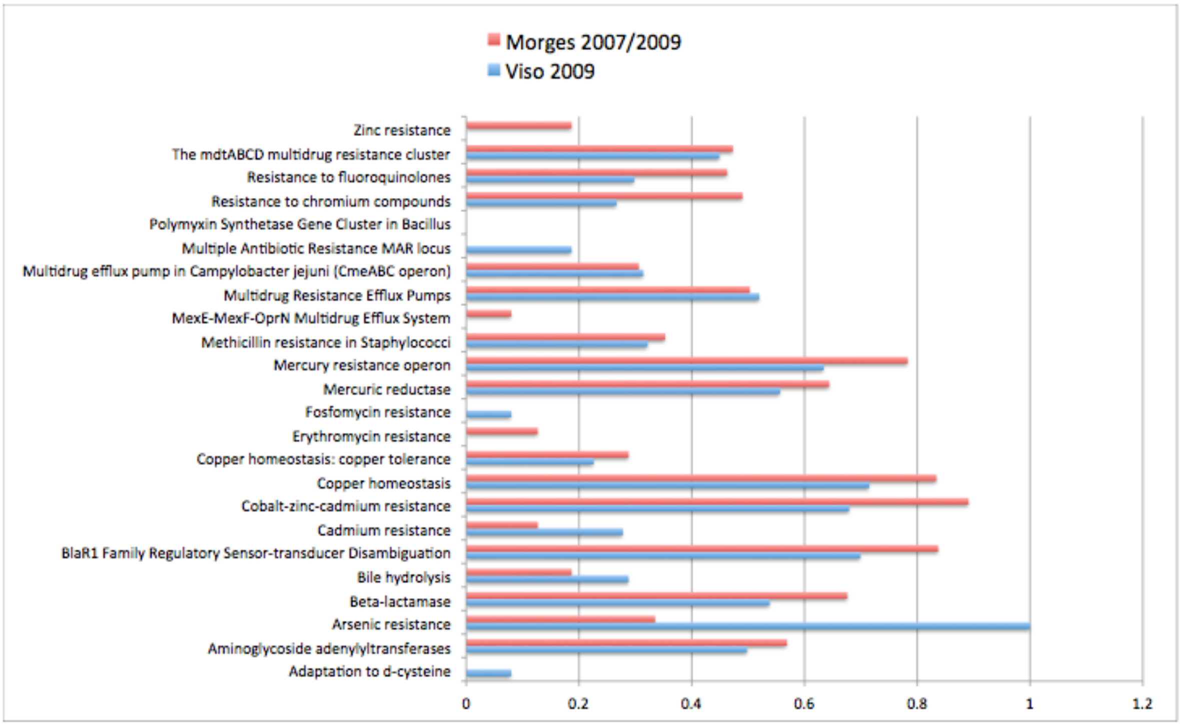
4464065.3	Morges2007
4464063.3	NCBI 1878 plasmids
4464109.3	Visp2009
4440696.3	NC_WWTP
4464073.3	Morges2009
4441025.3	Mediterranean bathypelagic habitat
4442464.3	Mediterranean bathypelagic habitat
4441091.3	Waseca Farm soil
4441092.3	Australian Phosphorus removing (EBPR) sludge
4441093.3	US Phosphorus removing (EBPR) sludge

4441137.3	5-Way (CG) acid mine drainage biofilm
4441619.3	Whale Fall Bone
4441623.3	Bay of British Columbia
4441582.3	GS006 Shotgun - Estuary - Bay of Fundy, Nova Scotia - Canada
4441624.3	Sargasso Sea
4444130.3	Stool Metagenome
4440359.3	VAN11 salt water metagenome
4441695.3	Fish—Healthy Gut bacteria
4446507.3	Biogas plant digestate
4448367.3	Cattle fecal pool

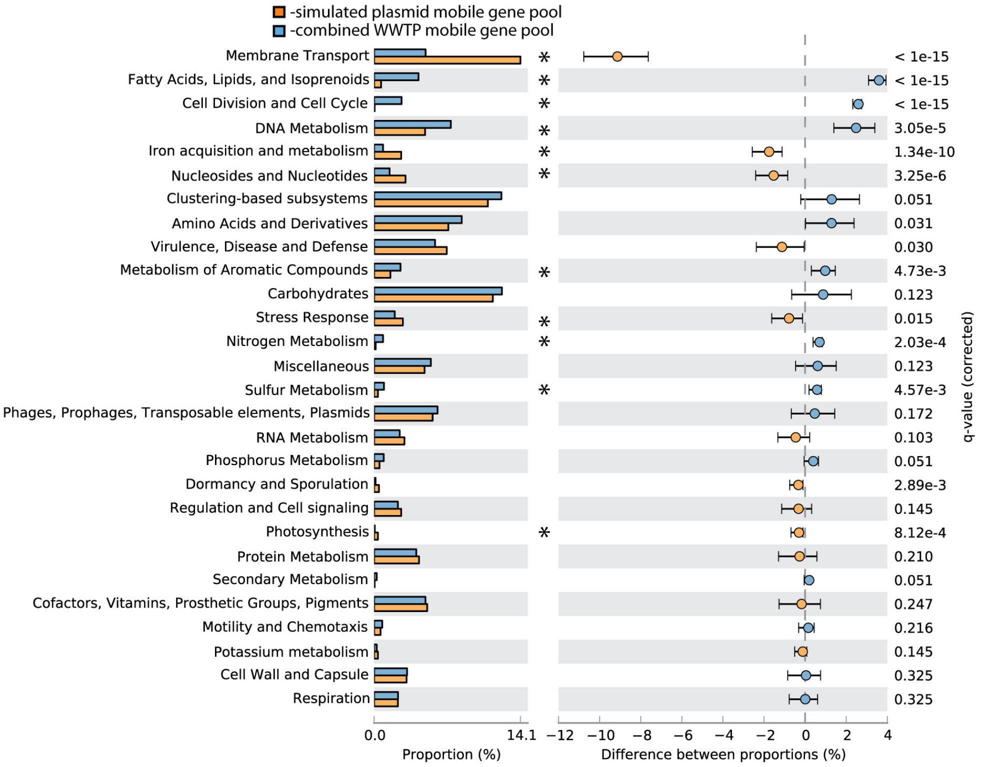
b. Principal components 1 versus 3. Environmental color code: yellow, wastewater treatment processes; red, plasmid gene pools; blue, salt-water; black, soil; orange, whale fall; brown, gut/fecal communities.



4464065.3	Morges2007	4441137.3	5-Way (CG) acid mine drainage biofilm
4464063.3	NCBI 1878 plasmids	4441619.3	Whale Fall Bone
4464109.3	Visp2009	4441623.3	Bay of British Columbia
4440696.3	NC_WWTP	4441582.3	GS006 Shotgun - Estuary - Bay of Fundy, Nova Scotia - Canada
4464073.3	Morges2009	4441624.3	Sargasso Sea
4441025.3	Mediterranean bathypelagic habitat	4444130.3	Stool Metagenome
4442464.3	Mediterranean bathypelagic habitat	4440359.3	VAN11 salt water metagenome
4441091.3	Waseca Farm soil	4441695.3	Fish—Healthy Gut bacteria
4441092.3	Australian Phosphorus removing (EBPR) sludge	4446507.3	Biogas plant digestate
4441093.3	US Phosphorus removing (EBPR) sludge	4448367.3	Cattle fecal pool



Supplementary Figure 4. Proportions (% of all functionally assignable reads) of subcategories within the SEED classification ‘Resistance to antibiotics and toxic compounds’ for the combined Morges 2007/2009 versus Visp 2009 plasmid metagenomes.



Supplementary Figure 5. Over- and underrepresentation of functionally categorizable protein coding genes from the combined Morges2007/2009, Visp2009 plasmid metagenomes compared to an artificially combined set of 1000 plasmids from NCBI. Diagram shows proportions within SEED level 1 subsystems and the difference between proportions in the two data sets. Whiskers denote calculated 95% confidence intervals. Asterisks mark categories with significant differences between the two data sets.

Supplementary Table 1

Abundance of CCSD sequence matches to 16S rRNA genes and to genes for ribosomal proteins indicated little contaminating prokaryotic chromosomal DNA

Metagenome	Number of reads	Genes for 16S rRNA	
CCS DNA Samples (unassembled reads)		**Number of matches**	**Matches per 100,000 reads**
Morges07	71224	5	7
Morges09	180048	103	57
Visp09	249017	11	4
Whole-WWTP metagenomes (unassembled reads)			
WWTP NC	353747	168	47
Sludge/Australian, Phrap Assembly	96563	40	41
Sludge/US, Phrap Assembly	127953	80	63

Presence of 16S rRNA genes in CCSD DNA samples in comparison to representative whole WWTP microbial community metagenomes according to MG-RAST annotation.

Supplementary Table 2

Proportions of significant hits to known cluster of orthologous groups (COGs) or protein families (Pfam and TIGRfam) in CCS DNAs compared to full WWTP metagenomes.

Genome Name	**IMG/M Taxon Object ID**	**Proportion of (%)**				
		Genes with functional prediction	**Enzymes**	**COG**	**Pfam**	**TIGR fam**
CCS DNA (assembled DNA)						
Morges07	2013843001	34	4	29	34	4
Morges09	2035918002	38	12	34	31	3
Visp09	2035918001	48	12	44	40	5
MIRA contigs	2209111023	37	3	29	32	4
Plasmids IMG	NA	57	6	38	56	12
Whole-community metagenomes (assembled DNA)						
Sludge/Australian Phrap Assembly	2000000001	60	19	66	64	21
Sludge/US, Phrap Assembly	2000000000	61	22	66	63	20
Sludge/US Virion (fgenesb)	2007300000	39	11	37	36	9

Supplementary Table S3. Ranking of 291 microbial metagenomes available in IMG/M according to the percentage of genes with functional prediction.

Genome Name	Taxon Obj ID	Phylum	Class	Order	Family	Genus	Genes	RANK	Genes with functional prediction, %	GC Perc	Bases
Aquatic microbial communities from Lake Kinneret (04)	2010483003	Environmental	Aquatic	Freshwater	Lentic	Limnetic zone	47	1	82.98	0.48	42224
Aquatic microbial communities from Lake Kinneret (05)	2010483004	Environmental	Aquatic	Freshwater	Lentic	Limnetic zone	41	2	82.93	0.53	41093
Aquatic microbial communities from Lake Kinneret (03)	2010483002	Environmental	Aquatic	Freshwater	Lentic	Limnetic zone	41	3	80.49	0.53	42973
Olavius algarvensis endosymbiont metagenome Gamma3	2004178004	Environmental	Aquatic	Marine	Neritic zone	Unclassified	4190	4	80.19	0.56	4647793
Marine Bacterioplankton communities from Antarctic, Sample 10335 (Summer fosmids)	2040502005	Environmental	Aquatic	Marine	Neritic zone	unclassified	1871	5	78.67	0.4	1866435
Sample 266	2018540003	Host-associated	Mammals	Digestive system	Large intestine	Fecal	42677	6	77.91	0	0
Aquatic microbial communities from Lake Kinneret (01)	2010483005	Environmental	Aquatic	Freshwater	Lentic	Limnetic zone	40	7	77.5	0.63	40450
Distal right leg ulcer DRU	2013505000	Host-associated	Human	Skin	Medial distal leg	Venous leg ulcers	4073	8	77.24	0	0
Venous leg ulcer VLU	2013505001	Host-associated	Human	Skin	Medial distal leg	Venous leg ulcers	5344	9	75.69	0	0
Sample 267	2018540002	Host-associated	Mammals	Digestive system	Large intestine	Fecal	124684	10	75.23	0	0
Water microbial communities from Great Boiling Spring, Nevada, sample from Cellulolytic enrichment S 77C (Cellulolytic enrichment S 77C water)	2149837005	Environmental	Aquatic	Thermal springs	Unclassified	Unclassified	264839	11	74.62	0.49	213546803
Marine Bacterioplankton communities from Antarctic, Sample 10334 (Winter fosmids)	2040502004	Environmental	Aquatic	Marine	Neritic zone	unclassified	2204	12	72.69	0.35	1933492
Sediment microbial communities from Great Boiling Spring, Nevada, sample from Cellulolytic enrichment S 77C (Cellulolytic enrichment S 77C sediment)	2149837004	Environmental	Aquatic	Thermal springs	Unclassified	Unclassified	243539	13	72.16	0.41	191954561
Mountain Pine Beetle microbial communities from Grand Prairie, Alberta, sample from Hybrid pine (MPB hybrid beetle)	2032320009	Host-associated	Arthropoda	Symbiotic fungal gardens and galleries	unclassified	Unclassified	42570	14	72	0.58	27077397
Marine microbial communities from the Eastern Subtropical North Pacific Ocean, Expanding Oxygen minimum zones, sample from Line P sample_J_08_P26_500 (J_08_P26_500)	2162886003	Environmental	Aquatic	Marine	Unclassified	Unclassified	130568	15	70.79	0.4	97610344
Marine microbial communities from the Eastern Subtropical North Pacific Ocean, Expanding Oxygen minimum zones, sample from Line P	2156126013	Environmental	Aquatic	Marine	Unclassified	Unclassified	95099	16	70.72	0.45	63838176

sample_A_09_P20_1000 (A_09_P20_1000)											
Marine Bacterioplankton communities from Antarctic, sample from Winter (Winter fosmids Sept 2010 assemblies)	2077657020	Environmental	Aquatic	Marine	Neritic zone	unclassified	4343	17	70.69	0.39	3492552
Olavius algarvensis endosymbiont metagenome Delta4	2004178002	Environmental	Aquatic	Marine	Neritic zone	Unclassified	3038	18	70.08	0.55	6382161
Uranium Contaminated Groundwater FW106	2006543007	Environmental	Aquatic	Freshwater	Groundwater	Contaminated	12420	19	69.96	0.63	9554544
Thermophilic enrichment culture SG0.5Z960 (454-Illumina assembly) (454-Illumina assembly)	2053563001	Engineered	Solid waste	Composting	Dissolved organics (aerobic)	Bioreactor	34856	20	69.69	0.65	29387211
Marine microbial communities from the Eastern Subtropical North Pacific Ocean, Expanding Oxygen minimum zones, sample from Line P sample_A_09_P20_1000 (sample_A_09_P20_1000 June 2011 assem)	2189573010	Environmental	Aquatic	Marine	Unclassified	Unclassified	60903	21	69.5	0.45	40909548
Marine microbial communities from the Eastern Subtropical North Pacific Ocean, Expanding Oxygen minimum zones, sample from Line P sample_J_09_P20_1000 (sample_J_09_P20_1000 June 2011 assem)	2189573014	Environmental	Aquatic	Marine	Unclassified	Unclassified	67353	22	68.95	0.47	46483313
MPB hybrid gallery (MPB hybrid gallery)	2029527007	Host-associated	Arthropoda	Symbiotic fungal gardens and galleries	Fungus gallery	Unclassified	53375	23	68.87	0.56	28121448
Marine microbial communities from the Eastern Subtropical North Pacific Ocean, Expanding Oxygen minimum zones, sample from Line P sample_A_09_P04_1300 (A_09_P04_1300)	2156126010	Environmental	Aquatic	Marine	Unclassified	Unclassified	149723	24	68.76	0.4	114098395
Marine microbial communities from the Eastern Subtropical North Pacific Ocean, Expanding Oxygen minimum zones, sample from Line P sample_A_09_P04_500 (sample_A_09_P04_500 June 2011 assem)	2189573006	Environmental	Aquatic	Marine	Unclassified	Unclassified	49811	25	68.58	0.44	32242365
Mouse Gut Community lean3	2004230000	Host-associated	Mammals	Digestive system	Large intestine	Fecal	2793	26	68.56	0.5	2143888
Mouse Gut Community lean1	2004230001	Host-associated	Mammals	Digestive system	Large intestine	Fecal	2935	27	68.48	0.51	2234664
Soil microbial community from bioreactor at Alameda Naval Air Station, CA, contaminated with Chloroethene, Sample 196 (Jan 2009 assem)	2199034002	Environmental	Terrestrial	Soil	Loam	Contaminated	43183	28	68.39	0.52	30615378
Marine microbial communities from the Eastern Subtropical North Pacific Ocean, Expanding Oxygen minimum zones, sample from Line P sample_A_09_P04_500 (A_09_P04_500)	2156126011	Environmental	Aquatic	Marine	Unclassified	Unclassified	63817	29	68.17	0.42	43645559
Marine microbial communities from the Eastern Subtropical North Pacific Ocean, Expanding Oxygen minimum zones, sample from Line P	2189573012	Environmental	Aquatic	Marine	Unclassified	Unclassified	60574	30	68.12	0.42	40827388

sample_J_08_P26_500 (sample_J_08_P26_500 June 2011 assem)											
Thermophilic enrichment culture SG0.5JP960 (454-Illumina assembly) - version 2 (454-Illumina assembly v2)	2061766001	Engineered	Solid waste	Composting	Dissolved organics (aerobic)	Bioreactor	64668	31	68.12	0.64	49664259
Marine microbial communities from the Eastern Subtropical North Pacific Ocean, Expanding Oxygen minimum zones, sample from Line P sample_J_09_P20_500 (sample_J_09_P20_500 June 2011 assem)	2189573013	Environmental	Aquatic	Marine	Unclassified	Unclassified	54923	32	68.04	0.46	36978437
Dendroctonus ponderosae beetle community (MPB hybrid beetle) (Lodgepole pine)	2032320008	Host-associated	Arthropoda	Symbiotic fungal gardens and galleries	Fungus gallery	Unclassified	66368	33	68.03	0.57	29279222
Fungus garden combined (combined)	2035918000	Host-associated	Arthropoda	Symbiotic fungal gardens and galleries	Fungus garden	unclassified	114620	34	68.03	0.53	61239920
Mouse Gut Community ob2	2004230002	Host-associated	Mammals	Digestive system	Large intestine	Fecal	2331	35	67.7	0.5	1841347
Hindgut microbiome of Nasutitermes sp. (Costa Rica), fosmids	2004175000	Host-associated	Arthropoda	Digestive system	Hindgut	unclassified	450	36	67.56	0.43	459633
Aquatic microbial communities from Lake Kinneret (02)	2010483006	Environmental	Aquatic	Freshwater	Lentic	Limnetic zone	46	37	67.39	0.42	38140
Marine microbial communities from the Eastern Subtropical North Pacific Ocean, Expanding Oxygen minimum zones, sample from Line P sample_A_09_P04_1300 (A_09_P04_1300 June 2011 assembly)	2166559025	Environmental	Aquatic	Marine	Unclassified	Unclassified	80550	38	66.98	0.41	56542842
Permafrost field sample	2067725009	Environmental	Terrestrial	Soil	Unclassified	unclassified	13277	39	66.9	0.54	9656814
Marine microbial communities from the Eastern Subtropical North Pacific Ocean, Expanding Oxygen minimum zones, sample from Line P sample_A_09_P04_1000 (A_09_P04_1000 June 2011 assem)	2189573007	Environmental	Aquatic	Marine	Unclassified	Unclassified	26183	40	66.78	0.35	17032716
Poplar biomass bioreactor microbial communities from Brookhaven National Lab, NY, sample from pooled GH fosmids	2020627002	Engineered	Solid waste	Composting	unclassified	Bioreactor	1485	41	66.6	0.52	1801402
Fungus garden microbial communities from Atta colombica in Panama, sample from fungus garden bottom (Fungus garden bottom)	2029527006	Host-associated	Arthropoda	Symbiotic fungal gardens and galleries	Fungus garden	unclassified	199573	42	66.5	0.55	83167033
Combined	2029527003	Host-associated	Arthropoda	Symbiotic fungal gardens and galleries	Fungus garden	unclassified	220873	43	66.11	0.57	97571324
Mountain Pine Beetle microbial communities from	2035918003	Host-associated	Arthropoda	Symbiotic	unclassified	Unclassified	87336	44	66.01	0.57	58839471

McBride, British Columbia, Canada, sample from Lodgepole pine (Lodgepole pine)				fungal gardens and galleries							
Mouse Gut Community lean2	2004230004	Host-associated	Mammals	Digestive system	Large intestine	Fecal	2782	45	65.82	0.52	2133081
Methylotrophic community from Lake Washington sediment Methylamine enrichment	2006207002	Environmental	Aquatic	Freshwater	Lentic	Sediment	54783	46	65.75	0.53	37225208
Cyphomyrmex longiscapus fungus garden	2030936005	Host-associated	Arthropoda	Symbiotic fungal gardens and galleries	Fungus garden	unclassified	190674	47	65.58	0.56	88331577
Mouse Gut Community ob1	2004230003	Host-associated	Mammals	Digestive system	Large intestine	Fecal	3051	48	65.49	0.46	2359017
Fungus garden microbial communities from Atta colombica in Panama, sample from fungus garden top	2029527005	Host-associated	Arthropoda	Symbiotic fungal gardens and galleries	Fungus garden	unclassified	241664	49	64.78	0.54	100904834
Atta cephalotes fungus garden (ACEF)	2029527004	Host-associated	Arthropoda	Symbiotic fungal gardens and galleries	Fungus garden	Unclassified	74196	50	64.17	0.51	40623338
Marine microbial communities from the Eastern Subtropical North Pacific Ocean, Expanding Oxygen minimum zones, sample from Line P sample_A_09_P20_500 (sample_A_09_P20_500 June 2011 assem)	2189573011	Environmental	Aquatic	Marine	Unclassified	Unclassified	62815	51	64.04	0.4	41083481
Human Gut Community Subject 7	2004002000	Host-associated	Human	Digestive system	Large intestine	Fecal	20956	52	63.68	0.49	15817685
Methylotrophic community from Lake Washington sediment Formate enrichment	2006207004	Environmental	Aquatic	Freshwater	Lentic	Sediment	28834	53	63.67	0.66	17570569
Fungus garden microbial community from termites in South Africa, sample from Oerleman's Farm	2065487014	Host-associated	Arthropoda	Symbiotic fungal gardens and galleries	Fungus garden	unclassified	23108	54	63.65	0.49	16028606
Trachymyrmex fungus garden	2084038018	Host-associated	Arthropoda	Symbiotic fungal gardens and galleries	Fungus garden	Unclassified	200369	55	63.63	0.54	79020976
TA reactor DNA contigs from 4 sample (Terephthalate degrading reactor metagenome contigs from 4 samples)	2081372008	Engineered	Wastewater	Industrial wastewater	Unclassified	Unclassified	50543	56	63.5	0.48	35830898
Marine microbial communities from the Eastern Subtropical North Pacific Ocean, Expanding Oxygen minimum zones, sample from Line P sample_F_10_SI03_135 (F_10_SI03_135)	2162886005	Environmental	Aquatic	Marine	Unclassified	Unclassified	677498	57	63.35	0.43	541536081
Soil microbial community from bioreactor at Alameda Naval Air Station, CA, contaminated with	2014730001	Environmental	Terrestrial	Soil	Loam	Contaminated	61557	58	63.1	0.52	41065977

Chloroethene, Sample 196											
Human Gut Community Subject 8	2004002001	Host-associated	Human	Digestive system	Large intestine	Fecal	26422	59	63.05	0.43	20486813
Marine microbial communities from the Eastern Subtropical North Pacific Ocean, Expanding Oxygen minimum zones, sample from Line P sample_F_10_SI03_150 (sample_F_10_SI03_150 June 2011 assem)	2189573019	Environmental	Aquatic	Marine	Unclassified	Unclassified	171988	60	62.75	0.44	126645598
Aquatic microbial communities from Lake Kinneret (07)	2010483007	Environmental	Aquatic	Freshwater	Lentic	Limnetic zone	32	61	62.5	0.61	35861
Sample 10205 (Test dataset. NOT FOR LOADING!)	2005137002	Engineered	Modeled	Simulated communities (sequence read mixture)	Sanger	Sanger	107218	62	62.25	0.57	81534405
Marine microbial communities from the Eastern Subtropical North Pacific Ocean, Expanding Oxygen minimum zones, sample from Line P sample_F_10_SI03_135 (sample_F_10_SI03_135 June 2011 assem)	2189573018	Environmental	Aquatic	Marine	Unclassified	Unclassified	178218	63	62.06	0.44	127666036
DNA Fragments from Six Antarctic Marine	2012990003	Environmental	Aquatic	Marine	Unclassified	Uncharacterized	39	64	61.54	0.5	43087
Marine microbial communities from the Eastern Subtropical North Pacific Ocean, Expanding Oxygen minimum zones, sample from Line P sample_F_10_SI03_200 (sample_F_10_SI03_200 June 2011 assem)	2189573008	Environmental	Aquatic	Marine	Unclassified	Unclassified	175334	65	61.32	0.41	131833497
Macropus eugenii forestomach microbiome from Canberra, Australia, sample 10206	2021593001	Host-associated	Mammals	Digestive system	Stomach	unclassified	2153	66	61.31	0.46	2471295
Switchgrass rhizosphere microbial community from Michigan, US, sample from East Lansing bulk soil (Bulk soil GOTP January 2011 combined assembly)	2124908023	Host-associated	Plants	Rhizoplane	Epiphytes	unclassified	44286	67	61.19	0.58	28451840
Hot spring microbial community from Yellowstone Hot Springs, sample from Calcite Springs, Tower Falls Region	2014031005	Environmental	Aquatic	Thermal springs	Hot (42-90C)	unclassified	23361	68	60.9	0.42	16071904
Mixed alcohol bioreactor microbial communities from Texas A&M University, sample 40C (40 degree reactor)	2049941001	Engineered	Biotransformation	Mixed alcohol bioreactor	Unclassified	Unclassified	296298	69	60.74	0.45	108660417
Switchgrass rhizosphere microbial community from Michigan, US, sample from Buena Vista Grasslands Wildlife Area, Rhizosphere BV2.1 (BV2.1 January 2011 combined assembly)	2124908019	Host-associated	Plants	Rhizoplane	Epiphytes	unclassified	5300	70	60.74	0.39	2825076
Sludge/US, Phrap Assembly	2000000000	Engineered	Wastewater	Nutrient removal	Biological phosphorus removal	Bioreactor	34656	71	60.7	0.6	56608360
Sample 10205 (Test dataset. NOT FOR LOADING!)	2005137001	Engineered	Modeled	Simulated communities (sequence read mixture)	Sanger	Sanger	94595	72	60.55	0.56	70870120

Bath Hot Springs, planktonic community	2007309001	Environmental	Aquatic	Non-marine Saline and Alkaline	Near-boiling (>90C)	Alkaline	29804	73	60.43	0.53	20451936
Marine microbial communities from the Eastern Subtropical North Pacific Ocean, Expanding Oxygen minimum zones, sample from Line P sample F_10_SI03_10 (F_10_S103_10)	2156126009	Environmental	Aquatic	Marine	Unclassified	Unclassified	339566	74	60.43	0.41	263651981
Hot spring microbial community from Yellowstone Hot Springs, sample from Bechler Spring	2013515002	Environmental	Aquatic	Thermal springs	Hot (42-90C)	unclassified	27144	75	60.16	0.47	18087467
Marine microbial communities from the Eastern Subtropical North Pacific Ocean, Expanding Oxygen minimum zones, sample from Line P sample F_10_SI03_10 (sample_F_10_SI03_10 June 2011 assem)	2189573015	Environmental	Aquatic	Marine	Unclassified	Unclassified	140093	76	60	0.42	97292779
Dump top (Dump top)	2030936006	Host-associated	Arthropoda	Symbiotic fungal gardens and galleries	Fungus garden	Garden dump	422825	77	59.97	0.59	160827138
Sample 10205 (Test dataset. NOT FOR LOADING!)	2005137000	Engineered	Modeled	Simulated communities (sequence read mixture)	Sanger	Sanger	150417	78	59.94	0.55	110456036
Xyleborus affinis microbiome from Bern, Switzerland, sample of gallery community (Gallery community)	2084038008	Host-associated	Arthropoda	Symbiotic fungal gardens and galleries	Fungus gallery	Unclassified	364117	79	59.86	0.58	146840147
1_050719N	2009439003	Environmental	Aquatic	Thermal springs	Hot (42-90C)	Acidic	40864	80	59.81	0.49	26884788
Sludge/Australian, Phrap Assembly	2000000001	Engineered	Wastewater	Nutrient removal	Biological phosphorus removal	Bioreactor	30672	81	59.63	0.55	53048954
Dendroctonus frontalis Fungal community	2044078007	Host-associated	Arthropoda	Symbiotic fungal gardens and galleries	Fungus gallery	Unclassified	130832	82	59.58	0.59	72612852
Hot spring microbial community from Yellowstone Hot Springs, sample from Obisdian Pool Prime	2016842005	Environmental	Aquatic	Thermal springs	Hot (42-90C)	unclassified	38984	83	59.2	0.45	24421805
Sludge/US, Jazz Assembly	2001000000	Engineered	Wastewater	Nutrient removal	Biological phosphorus removal	Bioreactor	16995	84	59.14	0.6	41128538
Freshwater-Acetate Anammox bacterial enrichment: gDNA_1	2030936003	Engineered	Wastewater	Nutrient removal	Nitrogen removal	Anammox	77567	85	58.65	0.58	41954873
Olavius algarvensis endosymbiont metagenome Gamma1	2004178003	Environmental	Aquatic	Marine	Neritic zone	Unclassified	1893	86	58.64	0.58	5317000
3_050719R	2010170001	Environmental	Aquatic	Thermal springs	Hot (42-90C)	Acidic	43764	87	58.6	0.59	28728092
5_050719P	2010170003	Environmental	Aquatic	Thermal	Hot (42-90C)	Acidic	74755	88	58.58	0.58	50211307

				springs							
Bath Hot Springs, filamentous community	2007309000	Environmental	Aquatic	Non-marine Saline and Alkaline	Near-boiling (>90C)	Alkaline	14864	89	58.56	0.5	10490501
Marine microbial communities from Deepwater Horizon Oil Spill, sample BP Oil Spill BM58: eDNA_1 (BM58 Illumina assembly)	2088090017	Environmental	Aquatic	Marine	Unclassified	Uncharacterized	41802	90	58.14	0.41	25346668
4_050719Q	2010170002	Environmental	Aquatic	Thermal springs	Hot (42-90C)	Acidic	84577	91	58.05	0.57	58029430
Sample 10166	2013843002	Engineered	Bioremedia-tion	Tetrachloroethylene and derivatives	Chloroethene	Bioreactor	41114	92	57.76	0.51	29947996
Guerrero Negro salt ponds hypersaline mat 01(G)	2004247000	Environmental	Aquatic	Non-marine Saline and Alkaline	Salt crystallizer ponds	Microbial mats	13353	93	57.73	0.55	8596350
Hot spring microbial community from Yellowstone Hot Springs, sample from Chocolate Pots	2014031006	Environmental	Aquatic	Thermal springs	Hot (42-90C)	unclassified	43924	94	57.49	0.5	31857986
Methylotrophic community from Lake Washington sediment combined (v2)	2006543005	Environmental	Aquatic	Freshwater	Lentic	Sediment	323777	95	57.41	0.58	211470570
Hot spring microbial community from Yellowstone Hot Springs, sample from Alice Springs, Crater Hills	2014031002	Environmental	Aquatic	Thermal springs	Hot (42-90C)	unclassified	13862	96	57.29	0.41	9888965
sept.09	2020627003	Engineered	Bioremedia-tion	Hydrocarbon	Benzene	Bioreactor	52548	97	57.15	0.5	33465768
Mixed alcohol bioreactor microbial communities from Texas A&M University, sample 55C (55 degree reactor, August 2010 assembly)	2077657005	Engineered	Biotransform-ation	Mixed alcohol bioreactor	Unclassified	Unclassified	154456	98	57.11	0.45	73615066
Freshwater microbial communities from Lake Mendota, WI, sample from Practice 29OCT2010 epilimnion (Lake Mendota Practice 29OCT2010 epilimnion June 2011 assem)	2199352005	Environmental	Aquatic	Freshwater	Lentic	Unclassified	157669	99	57.1	0.4	63922670
Methylotrophic community from Lake Washington sediment Methane enrichment	2006207000	Environmental	Aquatic	Freshwater	Lentic	Sediment	81582	100	56.98	0.59	52164993
Saline water microbial communities from Great Salt Lake, Utah, sample from South Arm Stromatolite (South Arm Stromatolite)	2058419002	Environmental	Aquatic	Non-marine Saline and Alkaline	Saline	unclassified	41679	101	56.89	0.47	14174075
Fossil microbial community from Whale Fall at Santa Cruz Basin of the Pacific Ocean Sample #1	2001200002	Environmental	Aquatic	Marine	Fossil	Whale fall	41932	102	56.73	0.44	31805936
Hot spring microbial community from Yellowstone Hot Springs, sample from Washburn Springs #1	2016842004	Environmental	Aquatic	Thermal springs	Hot (42-90C)	unclassified	62242	103	56.6	0.46	38709330
Poplar biomass bioreactor microbial communities from Brookhaven National Lab, NY sample from anaerobic community	2010388001	Engineered	Solid waste	Composting	unclassified	Bioreactor	20947	104	56.49	0.51	11096014
Hot spring microbial community from Yellowstone Hot Springs, sample from Mushroom Spring	2015219002	Environmental	Aquatic	Thermal springs	Hot (42-90C)	unclassified	76046	105	56.46	0.53	45311652
Bacterial community	2044078006	Host-associated	Arthropoda	Symbiotic fungal gardens and	unclassified	Unclassified	82571	106	56.42	0.6	41255331

				galleries							
Hindgut microbiome of Nasutitermes sp. (Costa Rica)	2004080001	Host-associated	Arthropoda	Digestive system	Hindgut	unclassified	83320	107	56.32	0.48	61533145
Sample 10594	2010170004	Environmental	Aquatic	Thermal springs	Hot (42-90C)	unclassified	6949	108	56.2	0.55	4270923
Dump bottom (Dump bottom)	2032320007	Host-associated	Arthropoda	Symbiotic fungal gardens and galleries	Fungus garden	Garden dump	525993	109	56.13	0.62	196100111
Hot spring microbial community from Yellowstone Hot Springs, sample from Dragon Spring, Norris Geyser Basin	2014031004	Environmental	Aquatic	Thermal springs	Hot (42-90C)	unclassified	27467	110	56.13	0.39	18602353
Hot spring microbial community from Yellowstone Hot Springs, sample from Nymph Lake 10 454-Titanium	2015219001	Environmental	Aquatic	Thermal springs	Hot (42-90C)	unclassified	10385	111	56.1	0.49	5509727
Air microbial communities Singapore indoor air filters 2	2003000007	Environmental	Air	Indoor Air	unclassified	Unclassified	45666	112	56	0.63	40148915
Marine microbial communities from the Eastern Subtropical North Pacific Ocean, Expanding Oxygen minimum zones, sample from Line P sample_A_09_P04_10 (sample_A_09_P04_10 June 2011 assem)	2189573009	Environmental	Aquatic	Marine	Unclassified	Unclassified	125307	113	55.95	0.4	82925362
Ultra Back A BS	2001200000	Environmental	Aquatic	Freshwater	Groundwater	Mine drainage	12820	114	55.94	0.46	10830886
Hot spring microbial community from Yellowstone Hot Springs, sample from Narrow Gauge - 454-Titanium	2015391001	Environmental	Aquatic	Thermal springs	Hot (42-90C)	unclassified	3891	115	55.92	0.32	2923224
Lake Itasca #1 (Itasca #1)	2077657006	Environmental	Aquatic	Freshwater	Lotic	Unclassified	628	116	55.89	0.52	222168
Hot spring microbial community from Yellowstone Hot Springs, sample from Bath Lake Vista Annex	2013954000	Environmental	Aquatic	Thermal springs	Hot (42-90C)	unclassified	51823	117	55.86	0.49	35743505
Methylotrophic community from Lake Washington sediment Methanol enrichment	2006207001	Environmental	Aquatic	Freshwater	Lentic	Sediment	77750	118	55.8	0.59	50245961
2_050719S	2009439000	Environmental	Aquatic	Thermal springs	Hot (42-90C)	Acidic	51132	119	55.56	0.51	31802272
Sample 10201	2017108002	Environmental	Aquatic	Marine	Oceanic	Sediment	22586	120	55.49	0.44	20878222
Minneapolis Minnesota #1 (Minneapolis #1)	2077657007	Environmental	Aquatic	Freshwater	Lotic	Unclassified	595	121	55.46	0.52	212691
Fungus-growing Termite worker microbial community from South Africa, sample from Oerleman's Farm	2065487013	Host-associated	Arthropoda	Digestive system	Hindgut	unclassified	359783	122	55.41	0.55	142578830
Hot spring microbial community from Yellowstone Hot Springs, sample from Bath Lake Vista Annex - Purple-Sulfur Mats	2016842008	Environmental	Aquatic	Thermal springs	Hot (42-90C)	unclassified	57652	123	54.98	0.48	41493403
Hot spring microbial community from Yellowstone Hot Springs, sample from Fairy Spring Red Layer	2016842003	Environmental	Aquatic	Thermal springs	Hot (42-90C)	unclassified	55048	124	54.83	0.6	36317514
Hot spring microbial community from Yellowstone Hot Springs, sample from OSP Spring YNP14	2013954001	Environmental	Aquatic	Thermal springs	Hot (42-90C)	unclassified	24201	125	54.8	0.39	16164785

Sediment microbial communities from Lake Washington, Seattle, for Methane and Nitrogen Cycles, original sample replicate 1	2149837030	Environmental	Aquatic	Freshwater	Lentic	Sediment	214899	126	54.8	0.48	111392199
Fungus garden microbial communities from Atta colombica in Panama, sample from dump top (Dump top)	2038011000	Host-associated	Arthropoda	Symbiotic fungal gardens and galleries	Fungus garden	unclassified	1292128	127	54.78	0.6	465469652
Hot spring microbial community from Yellowstone Hot Springs, sample from Octopus Springs	2014031007	Environmental	Aquatic	Thermal springs	Hot (42-90C)	unclassified	44662	128	54.73	0.47	28556353
TA reactor DNA contigs from 4 sample (Terephthalate degrading reactor metagenome contigs from 4 samples)	2007915000	Engineered	Wastewater	Industrial wastewater	Unclassified	Unclassified	94081	129	54.49	0.48	59647188
Air microbial communities Singapore indoor air filters 1	2003000006	Environmental	Air	Indoor Air	unclassified	Unclassified	46894	130	54.3	0.62	35449373
Aquatic microbial communities from Lake Kinneret (08)	2010483000	Environmental	Aquatic	Freshwater	Lentic	Limnetic zone	35	131	54.29	0.44	36738
Sediment microbial communities from Lake Washington, Seattle, for Methane and Nitrogen Cycles, original sample replicate 1	2149837029	Environmental	Aquatic	Freshwater	Lentic	Sediment	173648	132	54.2	0.47	92290447
Hot spring microbial community from Yellowstone Hot Springs, sample from OSP Spring YNP8	2013515001	Environmental	Aquatic	Thermal springs	Hot (42-90C)	unclassified	31801	133	54.17	0.44	21158971
Guerrero Negro salt ponds hypersaline mat 02(H)	2004247001	Environmental	Aquatic	Non-marine Saline and Alkaline	Salt crystallizer ponds	Microbial mats	12153	134	54.16	0.54	7469572
Marine microbial communities from the Eastern Subtropical North Pacific Ocean, Expanding Oxygen minimum zones, sample from Line P sample_F_10_SI03_120 (sample_F_10_SI03_120 June 2011 assem)	2189573017	Environmental	Aquatic	Marine	Unclassified	Unclassified	191444	135	54.04	0.4	133054468
Methylotrophic community from Lake Washington sediment Formaldehyde enrichment	2006207003	Environmental	Aquatic	Freshwater	Lentic	Sediment	90352	136	54.04	0.58	57622063
Fossil microbial community from Whale Fall at Santa Cruz Basin of the Pacific Ocean Sample #3	2001200004	Environmental	Aquatic	Marine	Fossil	Whale fall	38271	137	54.03	0.46	30784116
Poplar biomass bioreactor microbial communities from Brookhaven National Lab, NY, sample from total biomass decay community (13 April 2010 assembly with 454 paired-end)	2048955003	Engineered	Solid waste	Composting	unclassified	Bioreactor	893380	138	53.97	0.56	348781313
TCA/MEAL culture (TCA/MEAL culture Nov 2010 assembly with PE data)	2100351010	Engineered	Bioremediation	Tetrachloroethylene and derivatives	Chloroethene	Bioreactor	119855	139	53.9	0.5	64373035
Hot spring microbial community from Yellowstone Hot Springs, sample from Joseph's Coat Springs	2013843003	Environmental	Aquatic	Thermal springs	Hot (42-90C)	unclassified	26313	140	53.84	0.53	17963232
Sediment microbial communities from Great Boiling Spring, Nevada, sample from cellulolytic enrichment CS 77C (Cellulolytic enrichment CS 77C sediment)	2088090027	Environmental	Aquatic	Thermal springs	Unclassified	Unclassified	82728	141	53.54	0.45	42599697
Fungus garden microbial communities from Atta colombica in Panama, sample from dump bottom	2040502000	Host-associated	Arthropoda	Symbiotic fungal	Fungus garden	unclassified	1281334	142	53.49	0.65	482217958

(Dump bottom)				gardens and galleries							
September 2009 (Assembly with PE data)	2061766000	Engineered	Bioremedia-tion	Hydrocarbon	Benzene	Bioreactor	207753	143	53.4	0.51	80838838
Aquatic microbial communities from Lake Kinneret (06)	2010483001	Environmental	Aquatic	Freshwater	Lentic	Limnetic zone	30	144	53.33	0.69	38585
Marine microbial communities from the Eastern Subtropical North Pacific Ocean, Expanding Oxygen minimum zones, sample from Line P sample_A_09_P04_10 (A_09_P04_10)	2156126012	Environmental	Aquatic	Marine	Unclassified	Unclassified	242648	145	53.12	0.39	177724583
Compost Minireactor Metagenome (final assembly)	2029527000	Engineered	Solid waste	Composting	Grass	Bioreactor	258764	146	53.1	0.58	110687544
Hot spring microbial community from Yellowstone Hot Springs, sample from Cistern Spring	2015219000	Environmental	Aquatic	Thermal springs	Hot (42-90C)	unclassified	26749	147	52.84	0.5	17628346
Hot spring microbial community from Yellowstone Hot Springs, sample from White Creek Site 3	2013515000	Environmental	Aquatic	Thermal springs	Hot (42-90C)	unclassified	55998	148	52.77	0.51	38275783
Miscanthus rhizosphere microbial communities from Kellogg Biological Station, MSU, sample from Bulk Soil Replicate 2: eDNA_1 (Bulk soil 2 January 2011 combined assembly)	2124908025	Host-associated	Plants	Rhizoplane	Epiphytes	Unclassified	22426	149	52.48	0.57	10867947
Single-cell genome from subgingival tooth surface TM7c	2004000001	Host-associated	Human	Digestive system	Oral	unclassified	599	150	52.42	0.39	474179
Fossil microbial community from Whale Fall at Santa Cruz Basin of the Pacific Ocean Sample #2	2001200003	Environmental	Aquatic	Marine	Fossil	Whale fall	42521	151	52.23	0.53	32347432
Soil microbial communities from sample at FACE Site 4 Nevada Test Site Crust CO2-	2032320003	Environmental	Terrestrial	Soil	Unclassified	Unclassified	316494	152	51.98	0.68	123178563
Switchgrass rhizosphere microbial community from Michigan, US, sample from East Lansing bulk soil	2021593004	Host-associated	Plants	Rhizoplane	Epiphytes	unclassified	273689	153	51.92	0.62	113711136
Soil microbial communities from sample at FACE Site 3 Nevada Test Site Creosote CO2+	2032320002	Environmental	Terrestrial	Soil	Unclassified	Unclassified	534745	154	51.9	0.67	202685464
Sediment microbial communities from Great Boiling Spring, Nevada, sample from surface sediment (Surface sediment)	2053563014	Environmental	Aquatic	Thermal springs	Unclassified	Unclassified	93338	155	51.74	0.51	48184699
Olavius algarvensis endosymbiont metagenome Delta1	2004178001	Environmental	Aquatic	Marine	Neritic zone	Unclassified	12132	156	51.65	0.49	13536737
Miscanthus rhizosphere microbial communities from Kellogg Biological Station, MSU, sample Replicate 2: eDNA_1 (Rhizo 2 January 2011 combined assembly)	2124908027	Host-associated	Plants	Rhizoplane	Epiphytes	Unclassified	83119	157	51.52	0.54	44948785
Marine microbial communities from the Eastern Subtropical North Pacific Ocean, Expanding Oxygen minimum zones, sample from Line P sample_F_10_SI03_100 (F_10_SI03_100)	2162886004	Environmental	Aquatic	Marine	Unclassified	Unclassified	451236	158	51.22	0.4	345809224
Soil microbial communities from sample at FACE Site 3 Nevada Test Site Creosote CO2-	2029527002	Environmental	Terrestrial	Soil	Unclassified	Unclassified	318771	159	51.17	0.68	113475182
Oak Ridge Pristine Groundwater FRC FW301	2007427000	Environmental	Aquatic	Freshwater	Groundwater	Contaminated	170521	160	50.53	0.57	106573620
Guerrero Negro salt ponds hypersaline mat 04(N)	2004247003	Environmental	Aquatic	Non-marine Saline and	Salt crystallizer	Microbial mats	13330	161	50.32	0.56	8215056

				Alkaline	ponds						
Larvae (6 May 2010 assembly)	2084038013	Host-associated	Arthropoda	Digestive system	Unclassified	Unclassified	663502	162	50.12	0.56	280968062
Water microbial communities from Great Boiling Spring, Nevada, sample 1 (13 Aug 2010 assembly with PE data)	2077657003	Environmental	Aquatic	Thermal springs	Unclassified	Unclassified	11995	163	49.94	0.48	6283876
Switchgrass rhizosphere microbial community from Michigan, US, sample from Rose Lake bulk soil RL3 (Bulk soil RL3 January 2011 combined assembly)	2124908021	Host-associated	Plants	Rhizoplane	Epiphytes	unclassified	41246	164	49.82	0.53	20487337
Freshwater microbial communities from Antarctic Deep Lake, sample 24m 3.0um (24 m 3.0 um Illumina only)	2061766008	Environmental	Aquatic	Freshwater	Lentic	Limnetic zone	25462	165	49.75	0.59	18678739
Soil microbial communities from sample at FACE Site 1 Maryland Estuary CO2- (Maryland Estuary ambient)	2032320004	Environmental	Terrestrial	Soil	Unclassified	Unclassified	481014	166	49.73	0.6	189275844
Guerrero Negro salt ponds hypersaline mat 03(I)	2004247002	Environmental	Aquatic	Non-marine Saline and Alkaline	Salt crystallizer ponds	Microbial mats	13343	167	49.58	0.52	8286576
Soil microbial communities from sample at FACE Site 5 Oak Ridge CO2+ (Oak Ridge elevated CO2)	2032320006	Environmental	Terrestrial	Soil	Unclassified	Unclassified	341601	168	49.52	0.64	130858946
white/grey mat (white/grey mat, combined 454/Illumina assembly)	2084038012	Environmental	Aquatic	Marine	Hydrothermal vents	Sediment	173888	169	49.47	0.37	96236450
Freshwater microbial communities from Antarctic Deep Lake, sample 24m 0.8um (24 m 0.8 um 454/Illumina combined Jan 2011)	2140918017	Environmental	Aquatic	Freshwater	Lentic	Limnetic zone	106722	170	49.44	0.59	60876627
Freshwater microbial communities from Trout Bog Lake, WI, sample from Practice 18AUG2009 hypolimnion (Trout Bog Practice 18AUG2009 hypolimnion June 2011 assem)	2199352002	Environmental	Aquatic	Freshwater	Lentic	Unclassified	163413	171	48.96	0.45	72801538
Macropus eugenii forestomach microbiome from Canberra, Australia, sample Macropus_eugenii_combined	2013338003	Host-associated	Mammals	Digestive system	Stomach	unclassified	79862	172	48.95	0.44	53866884
Switchgrass rhizosphere microbial community from Michigan, US, sample from Rose Lake rhizosphere BV2.2 (BV2.2 January 2011 combined assembly)	2124908018	Host-associated	Plants	Rhizoplane	Epiphytes	unclassified	17507	173	48.91	0.58	8465840
4_Deep_abyss	2014642004	Environmental	Aquatic	Marine	Oceanic	unclassified	16740	174	48.54	0.54	11028821
Soil microbial communities from sample at FACE Site 2 North Carolina CO2-	2035918004	Environmental	Terrestrial	Soil	Unclassified	Unclassified	266562	175	48.46	0.61	124108791
Soil microbial communities from sample at FACE Site 5 Oak Ridge CO2- (Oak Ridge ambient)	2032320005	Environmental	Terrestrial	Soil	Unclassified	Unclassified	401954	176	48.44	0.63	157702128
Saline water microbial communities from Great Salt Lake, Utah, sample from South Arm Antelope Island 1 (South Arm Antelope Island)	2058419001	Environmental	Aquatic	Non-marine Saline and Alkaline	Saline	unclassified	173719	177	48.35	0.57	67538519
Soil microbial communities sample from Light Crust, Colorado Plateau, Green Butte (Light Crust, Colorado Plateau, Green Butte 2 June 2011 assem)	2199352006	Environmental	Terrestrial	Soil	Unclassified	Unclassified	18673	178	48.35	0.46	9280519
Soil microbial communities from sample at FACE Site	2040502001	Environmental	Terrestrial	Soil	Unclassified	Unclassified	364865	179	48.29	0.61	143751359

2 North Carolina CO2+ (North Carolina Elevated CO2)											
Saline water microbial communities from Great Salt Lake, Utah, sample from South Arm Stromatolite (South Arm Stromatolite)	2077657010	Environmental	Aquatic	Non-marine Saline and Alkaline	Saline	unclassified	408738	180	48.27	0.55	156436365
Sediment microbial communities from Lake Washington, Seattle, for Methane and Nitrogen Cycles, sample SIP 13C methane aerobic+nitrate (Aerobic with added nitrate, 13C SIP)	2046860006	Environmental	Aquatic	Freshwater	Lentic	Sediment	216380	181	48.24	0.55	80246742
7_Oxygen_minimum_layer	2014642003	Environmental	Aquatic	Marine	Oceanic	unclassified	16686	182	48.21	0.48	11811597
Sediment microbial communities from Great Boiling Spring, Nevada, sample from Cellulolytic enrichment CS 85C (GBS Cellulolytic enrichment CS 85C sediment)	2100351009	Environmental	Aquatic	Thermal springs	Unclassified	Unclassified	165257	183	48.17	0.47	74591189
Wastewater treatment plant plasmid pool from Canton de Vaud, Switzerland, sample from Visp2009	2035918001	Engineered	Wastewater	Nutrient removal	Dissolved organics (aerobic)	Activated sludge	23869	184	48.13	0.6	12200307
Guerrero Negro salt ponds hypersaline mat 06(P)	2004247005	Environmental	Aquatic	Non-marine Saline and Alkaline	Salt crystallizer ponds	Microbial mats	13462	185	48.03	0.57	8377132
Guerrero Negro salt ponds hypersaline mat 07(S)	2004247006	Environmental	Aquatic	Non-marine Saline and Alkaline	Salt crystallizer ponds	Microbial mats	16016	186	47.96	0.56	9864533
Guerrero Negro salt ponds hypersaline mat 05(O)	2004247004	Environmental	Aquatic	Non-marine Saline and Alkaline	Salt crystallizer ponds	Microbial mats	16053	187	47.88	0.57	9803980
Hot spring microbial community from Yellowstone Hot Springs, sample from Monarch Geyser, Norris Geyser Basin	2014031003	Environmental	Aquatic	Thermal springs	Hot (42-90C)	unclassified	20237	188	47.86	0.52	12778632
Freshwater microbial communities from Lake Mendota, WI, sample from Practice 20APR2010 epilimnion (Lake Mendota Practice 20APR2010 epilimnion June 2011 assem)	2199352003	Environmental	Aquatic	Freshwater	Lentic	Unclassified	60268	189	47.83	0.41	27640358
Marine sediment archaeal communities from Santa Barbara Basin, CA, that are methane-oxidizing, sample 15-18 cm (ANME Sed A12 15-18 cm)	2140918004	Environmental	Aquatic	Marine	Intertidal zone	Sediment	48112	190	47.69	0.44	21758522
Guerrero Negro salt ponds hypersaline mat 08(T)	2004247007	Environmental	Aquatic	Non-marine Saline and Alkaline	Salt crystallizer ponds	Microbial mats	13177	191	47.53	0.57	8017278
Freshwater microbial communities from Lake Mendota, WI, sample from Practice 15JUN2010 epilimnion (Lake Mendota Practice 15JUN2010 epilimnion June 2011 assem)	2199352004	Environmental	Aquatic	Freshwater	Lentic	Unclassified	160817	192	47.42	0.39	71094217
Saline water microbial communities from Great Salt Lake, Utah, sample from North Arm Stromatolite (North Arm Stromatolite)	2058419003	Environmental	Aquatic	Non-marine Saline and Alkaline	Saline	unclassified	130059	193	47.36	0.63	52414178
Freshwater microbial communities from Trout Bog	2199352000	Environmental	Aquatic	Freshwater	Lentic	Unclassified	183726	194	47.26	0.43	87219173

Lake, WI, sample from Practice 03JUN2009 hypolimnion (Trout Bog Practice 03JUN2009 hypolimnion June 2011 assem)											
Guerrero Negro salt ponds hypersaline mat 09(Y)	2004247008	Environmental	Aquatic	Non-marine Saline and Alkaline	Salt crystallizer ponds	Microbial mats	13798	195	47.14	0.59	8382678
5_Below_upper_mesopelagic	2014642002	Environmental	Aquatic	Marine	Oceanic	unclassified	13784	196	46.97	0.52	8764592
Water microbial communities from Great Boiling Spring, Nevada, sample 1 (Water borne 27 Oct 2010 assembly)	2084038020	Environmental	Aquatic	Thermal springs	Unclassified	Unclassified	14352	197	46.88	0.47	7181123
red mat (Red mat combined assembly)	2088090030	Environmental	Aquatic	Marine	Hydrothermal vents	Sediment	133323	198	46.86	0.48	69423586
sample 2	2019105002	Host-associated	Mammals	Digestive system	Large intestine	Fecal	480320	199	46.77	0.4	165356062
sample 1	2019105001	Host-associated	Mammals	Digestive system	Large intestine	Fecal	678420	200	46.7	0.41	241070849
Biofuel metagenome 1 (454/Illumina combined assembly)	2100351000	Engineered	Biotransformation	Unclassified	Unclassified	Unclassified	2706009	201	46.33	0.42	1275044948
Soil microbial communities from sample at FACE Site 4 Nevada Test Site Crust CO2+ (NTS Crust elevated CO2)	2035918005	Environmental	Terrestrial	Soil	Unclassified	Unclassified	629698	202	46.25	0.66	252083467
Sediment microbial communities from Lake Washington, Seattle, for Methane and Nitrogen Cycles, sample SIP 13C-methane anaerobic+nitrate (Anaerobic + nitrate SIP Nov 2010 with PE)	2088090009	Environmental	Aquatic	Freshwater	Lentic	Sediment	948029	203	46.01	0.61	354011745
Hot spring microbial communities from Yellowstone National Park, One Hundred Springs Plain, sample OSP_C (OSP_C)	2077657024	Environmental	Aquatic	Thermal springs	Unclassified	Unclassified	65660	204	45.9	0.41	27950878
Soil microbial communities sample from Dark Crust, Colorado Plateau, Green Butte (Dark Crust, Colorado Plateau, Green Butte June 2011 assem)	2209111000	Environmental	Terrestrial	Soil	Unclassified	Unclassified	1058313	205	45.87	0.61	396718301
Marine microbial communities from the Eastern Subtropical North Pacific Ocean, Expanding Oxygen minimum zones, sample from Line P sample_F_10_SI03_100 (sample_F_10_SI03_100 June 2011 assem)	2189573016	Environmental	Aquatic	Marine	Unclassified	Unclassified	204059	206	45.71	0.39	144622098
Soil microbial communities from sample at FACE Site 1 Maryland Estuary CO2+ (Maryland Estuary elevated)	2035918006	Environmental	Terrestrial	Soil	Unclassified	Unclassified	387519	207	45.6	0.59	156317799
Soil microbial communities from sample at FACE Site NTS_007 Nevada Test Site (NTS_007)	2119805009	Environmental	Terrestrial	Soil	Unclassified	Unclassified	1027241	208	45.56	0.66	384251082
Anaerobic methane oxidation (AOM) community from Eel River Basin sediment, California	2004175001	Environmental	Aquatic	Marine	Neritic zone	Sediment	2386	209	44.97	0.44	2116255
Marine sediment archaeal communities from Santa Barbara Basin, CA, that are methane-oxidizing, sample 6-9 cm (ANME Sed A12 6-9 cm)	2077657014	Environmental	Aquatic	Marine	Intertidal zone	Sediment	194553	210	44.87	0.45	92521799

Guerrero Negro salt ponds hypersaline mat 10(Z)	2004247009	Environmental	Aquatic	Non-marine Saline and Alkaline	Salt crystallizer ponds	Microbial mats	12094	211	44.86	0.56	7240715
Sediment microbial communities from Lake Washington, Seattle, for Methane and Nitrogen Cycles, sample SIP 13C-methane anaerobic+nitrate (Anaerobic with added nitrate, 13C SIP)	2046860004	Environmental	Aquatic	Freshwater	Lentic	Sediment	371171	212	44.43	0.65	139776104
Sediment microbial communities from Lake Washington, Seattle, for Methane and Nitrogen Cycles, sample SIP 13Cmethane anaerobic no nitrate (Anaerobic no nitrate SIP Nov 2010 with PE)	2088090013	Environmental	Aquatic	Freshwater	Lentic	Sediment	821124	213	44.35	0.52	308706277
Marine sediment archaeal communities from Santa Barbara Basin, CA, that are methane-oxidizing, sample 0-3 cm (ANME Sed A12 0-3 cm)	2077657018	Environmental	Aquatic	Marine	Intertidal zone	Sediment	556736	214	44.34	0.48	202177532
1_Upper_euphotic	2014613002	Environmental	Aquatic	Marine	Oceanic	unclassified	11252	215	44.25	0.49	7482595
Soil microbial communities from sample at Multiple FACE and OTC sites (NTS_010)	2119805011	Environmental	Terrestrial	Soil	Unclassified	Unclassified	913909	216	43.85	0.65	345080991
Soil microbial communities from sample at FACE Site Metagenome WIR_Oz2 (WIR_Oz2)	2124908006	Environmental	Terrestrial	Soil	Unclassified	Unclassified	930722	217	43.75	0.61	339617125
Marine sediment archaeal communities from Santa Barbara Basin, CA, that are methane-oxidizing, sample 12-15 cm (ANME Sed A12 12-15 cm)	2140918003	Environmental	Aquatic	Marine	Intertidal zone	Sediment	70150	218	43.58	0.44	30097641
Soil microbial communities from Minnesota Farm	2001200001	Environmental	Terrestrial	Soil	Unclassified	unclassified	185274	219	43.55	0.58	152406385
Soil microbial communities from sample at FACE Site North Carolina NCD_ElevF (NCD_ElevF)	2124908001	Environmental	Terrestrial	Soil	Unclassified	Unclassified	1200786	220	43.48	0.62	446081858
Soil microbial communities from sample at FACE Site NTS_067 Nevada Test Site (NTS_067)	2119805012	Environmental	Terrestrial	Soil	Unclassified	Unclassified	1036364	221	43.48	0.63	390792833
Single-cell genome from subgingival tooth surface TM7a	2004247010	Host-associated	Human	Digestive system	Oral	unclassified	3208	222	43.3	0.34	2864887
Soil microbial communities from sample at FACE Site North Carolina NCD_AmbF (NCD_AmbF)	2119805010	Environmental	Terrestrial	Soil	Unclassified	Unclassified	834028	223	43.29	0.61	324411358
Soil microbial communities from sample at FACE Site NTS_071 Nevada Test Site (NTS_071)	2081372006	Environmental	Terrestrial	Soil	Unclassified	Unclassified	835177	224	43.27	0.64	336899453
Hot spring microbial communities from Yellowstone National Park, One Hundred Springs Plain, sample OSP_B (OSP_B)	2077657023	Environmental	Aquatic	Thermal springs	Unclassified	Unclassified	81287	225	43.24	0.43	35803982
3_Below_base_of_euphotic	2014642001	Environmental	Aquatic	Marine	Oceanic	unclassified	11155	226	43.22	0.51	7829614
Sediment microbial communities from Lake Washington, Seattle, for Methane and Nitrogen Cycles, sample SIP 13C-methane aerobic no nitrate (Aerobic without added nitrate, 13C SIP)	2046860007	Environmental	Aquatic	Freshwater	Lentic	Sediment	210153	227	42.96	0.52	76631179
Soil microbial communities from sample at FACE Site Metagenome WIR_Amb2 (WIR_Amb2)	2124908009	Environmental	Terrestrial	Soil	Unclassified	Unclassified	1057446	228	42.92	0.61	380912680
Soil microbial communities from sample at FACE Site Metagenome WIR_ElevOz2 (WIR_ElevOz2)	2124908007	Environmental	Terrestrial	Soil	Unclassified	Unclassified	1040212	229	42.86	0.61	386839648

Endophytic microbiome from Rice	2010549000	Host-associated	Plants	Rhizoplane	Endophytes	Unclassified	64542	230	42.85	0.53	46747680
Hot spring microbial community from Beowulf Spring, Yellowstone National Park, sample YNP_Beowulf Spring_D (YNP_Beowulf Spring_D)	2119805007	Environmental	Aquatic	Thermal springs	Hot (42-90C)	Unclassified	128754	231	42.76	0.43	60745063
Freshwater microbial communities from Trout Bog Lake, WI sample from Practice 03JUN2009 epilimnion (Trout Bog Practice 03JUN2009 epilimnion June 2011 assem)	2199034001	Environmental	Aquatic	Freshwater	Lentic	Unclassified	250807	232	42.69	0.43	120283607
Sediment microbial communities from Lake Washington, Seattle, for Methane and Nitrogen Cycles, sample from flow sorted anaerobic no nitrate (Flow sorted anaerobic no nitrate Feb 2011 assembly)	2140918012	Environmental	Aquatic	Freshwater	Lentic	Sediment	96914	233	42.69	0.42	47869084
Soil microbial communities from sample at FACE Site Metagenome WIR_Elev2 (WIR_Elev2)	2124908008	Environmental	Terrestrial	Soil	Unclassified	Unclassified	1038025	234	42.46	0.61	380892539
Sediment microbial communities from Lake Washington, Seattle, for Methane and Nitrogen Cycles, sample from flow sorted anaerobic no nitrate (WGA anaerobic no nitrate)	2124908000	Environmental	Aquatic	Freshwater	Lentic	Sediment	69699	235	42.36	0.42	33111482
Marine sediment archaeal communities from Santa Barbara Basin, CA, that are methane-oxidizing, sample 9-12 cm (ANME Sed A12 9-12 cm)	2084038021	Environmental	Aquatic	Marine	Intertidal zone	Sediment	239177	236	42.31	0.43	90913355
Freshwater microbial communities from Antarctic Deep Lake, sample 24m 3.0um (24 m 3.0 um Sept 2010 combined)	2081372007	Environmental	Aquatic	Freshwater	Lentic	Limnetic zone	118816	237	42.09	0.58	56949331
Sakinaw Lake 454 metagenomics (120m): eDNA_2 (120 m)	2088090031	Environmental	Aquatic	Freshwater	Lentic	Unclassified	299533	238	41.97	0.45	120376854
Saline water microbial communities from Great Salt Lake, Utah, sample from North Arm Rozel Point	2051774008	Environmental	Aquatic	Non-marine Saline and Alkaline	Saline	unclassified	247708	239	41.94	0.6	99427575
Sediment microbial communities from Lake Washington, Seattle, for Methane and Nitrogen Cycles, original sample replicate 2 (Original sample replicate 2 12C fraction)	2088090006	Environmental	Aquatic	Freshwater	Lentic	Sediment	1147398	240	41.37	0.59	412615791
2_Base_of_chrolophyll_max	2014613003	Environmental	Aquatic	Marine	Oceanic	unclassified	7696	241	41.36	0.53	6091158
Single-cell genome from subgingival tooth surface TM7b	2005503000	Host-associated	Human	Digestive system	Oral	unclassified	194	242	41.24	0.37	112753
Crater Hills	2015391000	Host-associated	Microbial	Archaea	Viriome	Unclassified	2688	243	41.18	0.46	1715199
Sediment microbial communities from Lake Washington, Seattle, for Methane and Nitrogen Cycles, original sample replicate 1 (Original sample replicate 1)	2088090005	Environmental	Aquatic	Freshwater	Lentic	Sediment	1554721	244	40.81	0.57	559537102
Fresh water microbial communities from LaBonte Lake, Laramie, Wyoming, sample from peak-bloom 2 (Peak bloom metagenome 2)	2166559021	Environmental	Aquatic	Freshwater	Lentic	unclassified	475224	245	40.14	0.52	170450482
Hot spring microbial community from Beowulf	2100351008	Environmental	Aquatic	Thermal	Hot (42-90C)	Unclassified	140835	246	39.89	0.42	66680933

Spring, Yellowstone National Park, sample YNP_Beowulf Spring_E (YNP_Beowulf Spring_E)				springs						
Sediment microbial communities from Arctic Ocean, off the coast from Alaska, sample from low methane PC12-247-20cm (Low methane PC12-247-20cm)	2100351001	Environmental	Aquatic	Marine	Neritic zone	Unclassified	789043	247	39.7	0.53	312796620
Termite Protist Endosymbiont Community	2021593003	Host-associated	Microbial	Protists	Endosymbionts	Unclassified	39020	248	39.49	0.39	24858616
Sludge/US Virion (fgenesb)	2007300000	Engineered	Wastewater	Nutrient removal	Biological phosphorus removal	Bioreactor	8605	249	38.91	0.56	5822105
Hot spring microbial communities from Yellowstone National Park, One Hundred Springs Plain, sample OSP_D (OSP_D)	2140918001	Environmental	Aquatic	Thermal springs	Unclassified	Unclassified	116192	250	38.57	0.42	51518426
Sediment microbial communities from Lake Washington, Seattle, for Methane and Nitrogen Cycles, sample from flow sorted aerobic plus nitrate (Flow sorted aerobic plus nitrate)	2100351007	Environmental	Aquatic	Freshwater	Lentic	Sediment	1065361	251	38.48	0.46	386453037
Maize rhizosphere soil microbial communities from University of Illinois Energy Farm, Urbana, IL (Soil sample from rhizosphere of corn (Zea mays))	2044078001	Host-associated	Plants	Rhizoplane	Epiphytes	Unclassified	113040	252	38.38	0.63	39566506
Wastewater treatment plant plasmid pool from Canton de Vaud, Switzerland, sample from Bief Morges ,2009	2035918002	Engineered	Wastewater	Nutrient removal	Dissolved organics (aerobic)	Activated sludge	30169	253	38.25	0.51	13057318
Maize field bulk soil microbial communities from University of Illinois Energy Farm, Urbana, IL (Bulk soil sample from field growing corn (Zea mays))	2044078000	Host-associated	Plants	Rhizoplane	Epiphytes	Unclassified	124423	254	38.23	0.63	43495537
Sediment microbial communities from Lake Washington, Seattle, for Methane and Nitrogen Cycles, sample from flow sorted anaerobic plus nitrate (Flow sorted anaerobic plus nitrate)	2088090007	Environmental	Aquatic	Freshwater	Lentic	Sediment	1015830	255	38.15	0.46	372237563
Nymph Lake Bulk Water	2015219006	Host-associated	Microbial	Archaea	Viriome	Unclassified	1551	256	37.72	0.54	878429
Fresh water microbial communities from LaBonte Lake, Laramie, Wyoming, sample from Water peak-bloom 1 (Peak bloom metagenome 1)	2166559023	Environmental	Aquatic	Freshwater	Lentic	unclassified	377430	257	37.52	0.48	140026676
Miscanthus field bulk soil microbial communities from University of Illinois Energy Farm, Urbana, IL (Bulk soil sample from field growing Miscanthus x giganteus)	2044078003	Host-associated	Plants	Rhizoplane	Epiphytes	Unclassified	165002	258	37.45	0.62	58125848
Sediment microbial communities from Lake Washington, Seattle, for Methane and Nitrogen Cycles, sample from flow sorted aerobic no nitrate (Flow sorted aerobic no nitrate)	2084038009	Environmental	Aquatic	Freshwater	Lentic	Sediment	1059847	259	37.45	0.45	396601732
Fresh water microbial communities from LaBonte Lake, Laramie, Wyoming, sample from post-bloom (post-bloom)	2149837011	Environmental	Aquatic	Freshwater	Lentic	unclassified	144065	260	36.95	0.49	57916305
Miscanthus rhizosphere soil microbial communities from University of Illinois Energy Farm, Urbana, IL	2044078002	Host-associated	Plants	Rhizoplane	Epiphytes	Unclassified	81222	261	36.78	0.62	27992371

(Rhizosphere soil sample of Miscanthus x giganteus)											
6_Upper_euphotic	2014642000	Environmental	Aquatic	Marine	Oceanic	unclassified	16067	262	36.76	0.49	10828386
Switchgrass field bulk soil microbial communities from University of Illinois Energy Farm, Urbana, IL (Bulk soil sample from field growing switchgrass (Panicum virgatum))	2044078005	Host-associated	Plants	Rhizoplane	Epiphytes	Unclassified	52944	263	36.57	0.61	18598591
Wastewater treatment plant plasmid pool from Canton de Vaud, Switzerland, sample from Preverenges, Morges2007/09 (MIRA contigs, 5x coverage)	2209111023	Engineered	Wastewater	Nutrient removal	Dissolved organics (aerobic)	Activated sludge	3370	264	36.5	0.55	2205548
Switchgrass soil microbial communities from University of Illinois Energy Farm, Urbana, IL (Rhizosphere soil sample from switchgrass (Panicum virgatum))	2044078004	Host-associated	Plants	Rhizoplane	Epiphytes	Unclassified	79586	265	36.36	0.62	27453735
Marine sediment archaeal communities from Santa Barbara Basin, CA, that are methane-oxidizing, sample 3-6 cm (ANME Sed A12 3-6 cm)	2077657019	Environmental	Aquatic	Marine	Intertidal zone	Sediment	122604	266	36.3	0.43	58173635
Sediment microbial communities from Lake Washington, Seattle, for Methane and Nitrogen Cycles, sample SIP 13Cmethane anaerobic no nitrate (Anaerobic without added nitrate, 13C SIP)	2046860008	Environmental	Aquatic	Freshwater	Lentic	Sediment	160657	267	36.07	0.49	59711589
Sediment microbial communities from Arctic Ocean, off the coast from Alaska, sample from low methane PC12-244-90cm (Low methane PC12-244-90cm Sept2010 assembly)	2100351012	Environmental	Aquatic	Marine	Neritic zone	Unclassified	823046	268	35.77	0.48	339945372
Freshwater microbial communities from Trout Bog Lake, WI sample from Practice 18AUG2009 epilimnion (Trout Bog Practice 18AUG2009 epilimnion June 2011 assem)	2199352001	Environmental	Aquatic	Freshwater	Lentic	Unclassified	183791	269	35.2	0.43	82338961
Fresh water microbial communities from LaBonte Lake, Laramie, Wyoming, sample from algal/cyanobacterial bloom material peak-bloom 2 (algal/cyano bloom peak-bloom 2)	2189573023	Environmental	Aquatic	Freshwater	Lentic	unclassified	669817	270	35.02	0.51	268405022
Fresh water microbial communities from LaBonte Lake, Laramie, Wyoming, sample from algal/cyanobacterial bloom material peak-bloom 1 (algal/cyano bloom peak-bloom 1)	2166559022	Environmental	Aquatic	Freshwater	Lentic	unclassified	365628	271	34.75	0.52	147266570
Wastewater treatment plant plasmid pool from Canton de Vaud, Switzerland, sample from Preverenges, Morges	**2013843001**	**Engineered**	**Wastewater**	**Nutrient removal**	**Dissolved organics (aerobic)**	**Activated sludge**	**43340**	**272**	**34.05**	**0.53**	**28569177**
Sediment microbial communities from Arctic Ocean, off the coast from Alaska, sample from high methane PC12-236-260cm (High methane PC12-236-260cm)	2088090012	Environmental	Aquatic	Marine	Neritic zone	Unclassified	350243	273	33.98	0.46	191647483
Marine Trichodesmium cyanobacterial communities from the Bermuda Atlantic Time-Series	2156126005	Environmental	Aquatic	Marine	Neritic zone	Unclassified	242907	274	33.55	0.4	131475334
Fresh water microbial communities from LaBonte Lake, Laramie, Wyoming, sample from Water pre-	2149837010	Environmental	Aquatic	Freshwater	Lentic	unclassified	367751	275	32.62	0.49	139235803

bloom metagenome (pre-bloom)											
Sediment microbial communities from Arctic Ocean, off the coast from Alaska, sample from high methane PC12-225-485cm (High methane PC12-225-485cm Dec 2010 assembly)	2100351006	Environmental	Aquatic	Marine	Neritic zone	Unclassified	645119	276	31.76	0.45	310089302
Xyleborus affinis microbiome from Bern, Switzerland, sample of adult community (Ambrosia beetle adult)	2043231000	Host-associated	Arthropoda	Symbiotic fungal gardens and galleries	Fungus gallery	Unclassified	120235	277	31.28	0.41	88061459
Sediment microbial communities from Lake Washington, Seattle, for Methane and Nitrogen Cycles, sample from SIP 13C-methane aerobic no nitrate additional fraction (Aerobic without added nitrate, SIP additional fraction)	2046860005	Environmental	Aquatic	Freshwater	Lentic	Sediment	157525	278	31.23	0.44	58805457
Sediment microbial communities from Arctic Ocean, off the coast from Alaska, sample from high methane PC12-225-485cm (High methane PC12-225-485cm Jan 2011 assembly)	2140918005	Environmental	Aquatic	Marine	Neritic zone	Unclassified	674403	279	30.63	0.45	310086717
Xyleborus affinis microbiome from Bern, Switzerland, sample of larvae (Larvae community)	2044078011	Host-associated	Arthropoda	Symbiotic fungal gardens and galleries	Fungus gallery	Unclassified	83071	280	30.56	0.43	54155335
Freshwater microbial communities from Antarctic Deep Lake, sample 5mRS 0.1um (5 mRS 0.1um 454 only)	2084038019	Environmental	Aquatic	Freshwater	Lentic	Limnetic zone	125908	281	28.31	0.55	52160100
Freshwater microbial communities from Antarctic Deep Lake, sample 24m 0.1um (24 m 0.1 um 454 only)	2084038011	Environmental	Aquatic	Freshwater	Lentic	Limnetic zone	141524	282	27.58	0.56	59385153
Sediment microbial communities from Arctic Ocean, off the coast from Alaska, sample from medium methane PC12-240-170cm (Medium methane PC12-240-170cm Sept2010 assembly)	2100351011	Environmental	Aquatic	Marine	Neritic zone	Unclassified	1071024	283	26.87	0.45	386166283
Freshwater microbial communities from Antarctic Deep Lake, sample 36m 3.0um, 0.8um, 0.1um pool (HWGG+HTSY Jan 2011)	2140918027	Environmental	Aquatic	Freshwater	Lentic	Limnetic zone	475716	284	24.66	0.53	190563105
Freshwater microbial communities from Antarctic Deep Lake, sample 36m 3.0um, 0.8um, 0.1um pool (36m 3, 0.8 and 0.1 um pool)	2100351015	Environmental	Aquatic	Freshwater	Lentic	Limnetic zone	313035	285	24.41	0.52	124388753
Sirex noctilio microbiome from Pennsylvania, sample of adult community (Adult June 2010 assembly)	2100351016	Host-associated	Arthropoda	Symbiotic fungal gardens and galleries	Fungus garden	Unclassified	319145	286	21.12	0.44	177623549
Freshwater microbial communities from Antarctic Deep Lake, sample 13m 0.1um (13m 0.1um 454 only)	2100351014	Environmental	Aquatic	Freshwater	Lentic	Limnetic zone	201266	287	20.17	0.54	80245247
Bovine rumen viral communities from University of Illinois Dairy Farm in Urbana, IL, Cow rumen 7887 (Cow 7887)	2077657008	Host-associated	Mammals	Digestive system	Stomach	unclassified	211242	288	12.05	0.41	73827693

Bovine rumen viral communities from University of Illinois Dairy Farm in Urbana, IL, Cow rumen 7664 (Cow 7664)	2084038000	Host-associated	Mammals	Digestive system	Stomach	unclassified	445555	289	10.52	0.42	153674931
Water viral communities from Great Boiling Spring, Nevada (Water borne viral community)	2058419004	Environmental	Aquatic	Thermal springs	Unclassified	Unclassified	74224	290	10.29	0.43	27375388
Bovine rumen viral communities from University of Illinois Dairy Farm in Urbana, IL, Cow rumen 6993 (Cow 6993)	2077657009	Host-associated	Mammals	Digestive system	Stomach	unclassified	304432	291	9.8	0.37	100678798

Supplementary Table 4

List of IMG plasmids used to assemble a combined PLASMID-IMG metagenome.

taxon_oid	Genome Name	taxon_oid	Genome Name
648934901	'Rehmannia glutinosa' phytoplasma plasmid pPARG1	646556923	Lactococcus lactis SK11 plasmid pSK11B
640048201	Acetobacter aceti plasmid pAC5	640048385	Lactococcus lactis UC509.9 plasmid pCIS3
640048202	Acetobacter pasteurianus plasmid pAP12875	640048392	Lactococcus lactis W-1 plasmid pSRQ800
641507351	Acetobacter pasteurianus plasmid pGR7	640048393	Lactococcus lactis W-37 plasmid pSRQ900
641210201	Achromobacter denitrificans EST4002 plasmid pEST4011	641210327	Lactococcus lactis cremoris 712 plasmid pAG6
641210202	Achromobacter xylosoxidans A8 plasmid pA81	640048398	Lactococcus lactis cremoris Cremoris Wg2 plasmid pWVO2
641210203	Acidianus ambivalens Lei 10 plasmid pDL10	640048396	Lactococcus lactis cremoris HP plasmid pHP003
643660901	Acidianus hospitalis W1 plasmid pAH1	640048397	Lactococcus lactis cremoris NIZO B40 plasmid pNZ4000
641210204	Acidiphilium multivorum JCM8867 plasmid pAM5	640048395	Lactococcus lactis cremoris P8-2-47 plasmid pBM02
640048203	Acidithiobacillus caldus F plasmid pTC-F14	642914165	Lactococcus lactis diacetylactis DRC3 plasmid pNP40
642914101	Acidithiobacillus caldus MNG plasmid pTcM1	640048406	Lactococcus lactis lactis BGMN1-5 plasmid pMN5
640048205	Acidithiobacillus ferrooxidans ATCC33020 plasmid pTF5	640048404	Lactococcus lactis lactis IPLA 972 plasmid pBL1
640048204	Acidithiobacillus ferrooxidans MAL4-1 plasmid pTF4.1	641210329	Lactococcus lactis lactis K214 plasmid pK214
641210205	Acinetobacter baumannii 19606 plasmid pMAC	641210326	Lactococcus lactis lactis M127 plasmid pND324
646556902	Acinetobacter baumannii CU2 plasmid pMMCU2	640048463	Lactococcus lactis lactis MJC15 plasmid pCD4
645047301	Acinetobacter baumannii VA-566/00 plasmid pABVA01	640048405	Lactococcus lactis lactis UC317 plasmid pCI305
642481201	Acinetobacter baumannii plasmid pABIR	641210328	Lactococcus lactis lactis bv. diacetylactis DB0410 plasmid pDBORO
646556901	Acinetobacter baumannii plasmid pMMA2	640048403	Lactococcus lactis lactis bv. diacetylactis DPC220 plasmid pAH82
645047302	Acinetobacter calcoaceticus Acal H12O-07 plasmid pMMCU1	640048399	Lactococcus lactis lactis bv. diacetylactis DRC1 cryptic plasmid pDR1-1
640048206	Acinetobacter sp. EB104 plasmid pAC450	640048400	Lactococcus lactis lactis bv. diacetylactis DRC1 cryptic plasmid pDR1-1B
640048207	Acinetobacter sp. SUN plasmid pRAY	640048401	Lactococcus lactis lactis bv. diacetylactis plasmid pS7a
642481202	Acinetobacter venetianus plasmid pAV1	640048402	Lactococcus lactis lactis bv. diacetylactis plasmid pS7b
642481203	Acinetobacter venetianus plasmid pAV2	641210330	Lactococcus lactis lactis plasmid pL2
640048208	Actinobacillus actinomycetemcomitans plasmid pVT745	640048388	Lactococcus lactis plasmid pCRL291.1
642914102	Actinobacillus pleuropneumoniae 12494 plasmid p12494	640048481	Lactococcus lactis plasmid pWC1
646556903	Actinobacillus pleuropneumoniae APP11745 plasmid p11745	640048394	Lactococcus lactis plasmid pWV01
642914103	Actinobacillus pleuropneumoniae APPHB0503 plasmid pHB0503	648934922	Lactococcus lactis subsp. lactis M14 plasmid pAR141
641507352	Actinobacillus pleuropneumoniae plasmid p9555	641210331	Laribacter hongkongensis HLHK8 plasmid pHLHK8
641507353	Actinobacillus pleuropneumoniae plasmid p9956	642481238	Laribacter hongkongensis plasmid pHLHK22
641210206	Actinobacillus pleuropneumoniae plasmid pARD3079	642481239	Leptolyngbya boryana plasmid pPBS1
641210207	Actinobacillus pleuropneumoniae plasmid pKMA2425	640048407	Leptolyngbya foveolarum M-43 plasmid pPF1

641210208	Actinobacillus pleuropneumoniae plasmid pMS260	640048408	Leptolyngbya sp. PCC 6402 plasmid pRF1
641210209	Actinobacillus pleuropneumoniae plasmid pPSAS1522	641210332	Leptospirillum ferrooxidans ATCC 49879 plasmid p49879.1
640048209	Actinobacillus pleuropneumoniae plasmid pTYM1	641210333	Leptospirillum ferrooxidans ATCC 49879 plasmid p49879.2
641210210	Actinobacillus porcitonsillarum plasmid pIMD50	640048409	Leuconostoc citreum 22R plasmid pLC22R
641210211	Actinobacillus porcitonsillarum plasmid pKMA1467	645047360	Leuconostoc citreum C4 plasmid pCC3
641210212	Actinobacillus porcitonsillarum plasmid pKMA202	645047361	Leuconostoc citreum C4 plasmid pFMBL1
641210213	Actinobacillus porcitonsillarum plasmid pKMA5	642914166	Leuconostoc citreum plasmid pCB42
641210214	Actinobacillus porcitonsillarum plasmid pKMA505	642481240	Leuconostoc citreum plasmid pCB42
641210215	Actinobacillus porcitonsillarum plasmid pKMA757	641210334	Leuconostoc citreum plasmid pIH01
641210216	Aeromonas bestiarum 5S9 plasmid pAb5S9	640048465	Leuconostoc lactis 533 plasmid pCI411
648934902	Aeromonas hydrophila plasmid pAH3680	641210335	Leuconostoc mesenteroides SY2 plasmid pFMBL1
643660902	Aeromonas hydrophila AO1 plasmid pBRST7.6	641210336	Leuconostoc mesenteroides Y110 plasmid pTXL1
645047303	Aeromonas hydrophila plasmid pRA1	641210337	Leuconostoc mesenteroides mesenteroides FR52 plasmid pFR18
642914104	Aeromonas hydrophila plasmid pRA3	650625520	Listeria grayi DSM20601 plasmid pLGUG1
641210217	Aeromonas punctata HGB5 plasmid pFBAOT6	648934923	Listeria monocytogenes Lm1 plasmid pLM33
640048210	Aeromonas salmonicida plasmid pRAS3.2	650625521	Listeria monocytogenes SLCC2755 plasmid pLM1-2bUG1
641210218	Aeromonas salmonicida salmonicida RSP 74.1 plasmid pAsal5	641210338	Listonella anguillarum sv O1 775 plasmid pJM1
640048214	Aeromonas salmonicida salmonicida plasmid pAsal1	641210339	Listonella anguillarum sv O2 plasmid pLO2
640048215	Aeromonas salmonicida salmonicida plasmid pAsal2	641210340	Magnetospirillum gryphiswaldense MSR-1 plasmid
640048216	Aeromonas salmonicida salmonicida plasmid pAsal3	641210341	Magnetospirillum magneticum MGT-1 plasmid pMGT
640048217	Aeromonas salmonicida salmonicida plasmid pRAS3.1	641210342	Mannheimia haemolytica 3259 plasmid pCCK3259
642914105	Agrobacterium rhizogenes K599 plasmid pRi2659	640048410	Mannheimia haemolytica R122 plasmid pMHSCS1
640048218	Agrobacterium rhizogenes MAFF03-01724 plasmid pRi1724	640048411	Mannheimia varigena S131 plasmid pMVSCS1
642914106	Agrobacterium tumefaciens Bo542 plasmid Ti plasmid pTiBo542	640048412	Marinococcus halophilus DSM 20408 plasmid pPL1
640048221	Agrobacterium tumefaciens C58 plasmid pTiC58	641210345	Methanohalophilus mahii plasmid pML
641210219	Agrobacterium tumefaciens K84 plasmid pAgK84	640048414	Methanosarcina acetivorans C2A plasmid pC2A
640048220	Agrobacterium tumefaciens MAFF301001 plasmid pTi-SAKURA	640048417	Methanothermobacter thermautotrophicus Marburg plasmid pME2001
640048219	Agrobacterium tumefaciens plasmid Ti	640048415	Methanothermobacter thermautotrophicus THF plasmid pFV1
642914108	Amycolatopsis benzoatilytica DSM 43387 plasmid pA387	640048416	Methanothermobacter thermautotrophicus Z-245 plasmid pFZ1
642914109	Amycolatopsis mediterranei plasmid pMEA100	640048418	Methanothermobacter thermautotrophicus ZH3 plasmid pME2200
640048222	Arcanobacterium pyogenes BBR1 plasmid pAP1	640048419	Methylophaga thalassica S1 plasmid pMTS1
641210220	Arcanobacterium pyogenes plasmid pAP2	640048420	Micrococcus luteus NCIMB 13267 plasmid pMLU1
645047304	Archaeoglobus profundus AV18; DSM 5631 plasmid pGS5	640048421	Micrococcus sp. 28 plasmid pSD10
645047305	Arcobacter butzleri NCTC12481 plasmid unnamed	640048422	Microcystis aeruginosa Kutzing plasmid pMA1

641210221	Arthrobacter nitroguajacolicus Rue61a plasmid pAL1	640048423	Microcystis aeruginosa Kutzing plasmid pMA2
642481204	Arthrobacter sp. AK-1 plasmid pSI-1	640048424	Microcystis aeruginosa UV025 plasmid pMa025
642481205	Arthrobacter sp. Chr15 plasmid pChr15	641210346	Micromonospora rosaria plasmid pMR2
640048223	Aster yellows phytoplasma plasmid pJHW	640048425	Microscilla sp. PRE1 plasmid pSD15
642914110	Avibacterium paragallinarum A14 plasmid pYMH5	646556924	Moraxella bovis ATCC 10900 plasmid pMbo4.6
648018801	Bacillus amyloliquefaciens B3 plasmid pBSG3	642914167	Moraxella bovis Epp63 plasmid pMBO-1
640048226	Bacillus anthracis A2012 (Florida isolate)	642914168	Moraxella bovis Epp63 plasmid pMBO-2
640048227	Bacillus anthracis A2012 (Florida isolate)	642914169	Moraxella catarrhalis E22 plasmid pLQ510
640048225	Bacillus anthracis Pasteur plasmid pX02	641210347	Moraxella catarrhalis plasmid pEMCJH03
640048224	Bacillus anthracis Sterne plasmid pX01	642481241	Moraxella sp. TA144 plasmid pTA144 Dw
642914111	Bacillus cereus AH187; F4810/72 plasmid pCER270	640048426	Moraxella sp. TA144 plasmid pTA144 Up
642914112	Bacillus cereus AH818 plasmid pPER272	640048427	Mycobacterium avium MD1 plasmid pVT2
642914113	Bacillus cereus AH820 plasmid pPER272	640048428	Mycobacterium celatum 4 plasmid pCLP
643660903	Bacillus cereus G9241 plasmid pBC210	640048460	Mycobacterium fortuitum plasmid pAL5000
643660904	Bacillus cereus G9241 plasmid pBCXO1	643660931	Mycobacterium liflandii 128FXT 128FXT plasmid pMUM002
650625501	Bacillus cereus VPC1401 VPC1401 plasmid pLVP1401	640048429	Mycoplasma mycoides unnamed plasmid
640048461	Bacillus cereus plasmid pBC16	640048430	Mycoplasma sp. bovine group 7 plasmid pBG7AU
645047306	Bacillus cereus plasmid pPRS3a	642914170	Mycoplasma yeatsii GIH plasmid pMyBK1
642914114	Bacillus coagulans P4-102B plasmid pMSR0	642481242	Myxococcus fulvus plasmid pMF1
641210222	Bacillus licheniformis 63.1 plasmid pBL63.1	641210349	Natrinema sp. CX2021 plasmid pZMX201
641210223	Bacillus licheniformis FL5 plasmid pFL5	641210350	Natronobacterium sp. AS-7091 plasmid pNB101
641210224	Bacillus licheniformis FL7 plasmid pFL7	643660932	Neisseria gonorrhoeae plasmid pCmGFP
641507354	Bacillus megaterium QM B1551 plasmid pBM100	648018809	Neisseria gonorrhoeae 5289 plasmid pEP5289
641507355	Bacillus megaterium QM B1551 plasmid pBM200	640048432	Neisseria gonorrhoeae GC1-182 plasmid pJD4
641507356	Bacillus megaterium QM B1551 plasmid pBM300	640048431	Neisseria gonorrhoeae plasmid pJD1
640048228	Bacillus megaterium QM B1551 plasmid pBM400	642914171	Neisseria gonorrhoeae plasmid pSJ5.2
641210225	Bacillus methanolicus MGA3 plasmid pBM19	642914172	Neisseria lactamica 102739 plasmid pNL11
641210227	Bacillus mycoides DX plasmid pBMYdx	642914173	Neisseria lactamica 3207487 plasmid pNL3.1
641210228	Bacillus mycoides Dxv plasmid pDx14.2	642914174	Neisseria lactamica 3207487 plasmid pNL3.2
641210229	Bacillus mycoides Sinv plasmid pSin9.7	642914175	Neisseria lactamica 410838 plasmid pNL18.1
641210226	Bacillus mycoides sin96 plasmid pBMY1	642914176	Neisseria lactamica 410838 plasmid pNL18.2
640048229	Bacillus pumilus ATCC 12140 plasmid pPL10	642914177	Neisseria lactamica 5279613 plasmid pNL14
640048230	Bacillus pumilus ATCC 7065 plasmid pPL7065	642914178	Neisseria lactamica 750149 plasmid pNL750149
646556905	Bacillus pumilus ZZ84 plasmid pPZZ84	642914179	Neisseria lactamica 8101503 plasmid pNL9
640048231	Bacillus sp. B-3 plasmid pA01	642914180	Neisseria lactamica 811778 plasmid pNL15
648018802	Bacillus sp. BS-01 BS-01 plasmid pBS-01	642914181	Neisseria lactamica 871104 plasmid pNL871104
650625502	Bacillus sp. BS-02 BS-02 plasmid pBS-02	642914182	Neisseria lactamica 9225393 plasmid pNL7.1
650625503	Bacillus sp. JAMB750 JAMB750 plasmid pJAM1	642914183	Neisseria lactamica 932024 plasmid pNL932024

641210230	Bacillus sphaericus plasmid pLG	642481243	Neisseria lactamica plasmid pNL01
646556906	Bacillus subtilis ATCC 15841 plasmid pPL1	640048433	Neisseria meningitidis 537 plasmid pJS-B
640048233	Bacillus subtilis IAM1028 plasmid pTA1015	640048437	Nitrosomonas sp. ENI-11 plasmid pAYL
640048234	Bacillus subtilis IAM1232 plasmid pTA1040	640048438	Nitrosomonas sp. ENI-11 plasmid pAYS
640048235	Bacillus subtilis IF03022 plasmid pTA1060	646556925	Nocardia aobensis plasmid pYS1
640048232	Bacillus subtilis plasmid p1414	642914184	Nocardia sp. 107 plasmid pXT107
641210231	Bacillus subtilis plasmid pBS608	646556926	Nocardia sp. C-14-1 plasmid pC1
640048469	Bacillus subtilis plasmid pIM13	648018810	Nocardiopsis sp. 90127 plasmid pSQ10
641210232	Bacillus subtilis plasmid pLS30	641210351	Nostoc sp. PCC 7524 plasmid pDU1
640048237	Bacillus thuringiensis 4Q2 plasmid pTX14-2	640048439	Novosphingobium aromaticivorans F199 plasmid pNL1
641210234	Bacillus thuringiensis H1.1 plasmid pGI3	642914185	Ochrobactrum anthropi W24; CGMCC 1649 plasmid pW240
641210233	Bacillus thuringiensis HD-3a3b miniplasmid	641210352	Oenococcus oeni plasmid pOM1
641210235	Bacillus thuringiensis K1 plasmid pK1S1	640048440	Oenococcus oeni plasmid pRS2
641507357	Bacillus thuringiensis YBT-1520 plasmid pBMB67	640048441	Oenococcus oeni plasmid pRS3
643660905	Bacillus thuringiensis YBT-1520 plasmid pBMB7635	641210353	Oligotropha carboxidovorans OM5 - DSM 1227 plasmid pHCG3
640048236	Bacillus thuringiensis YBT-1520 plasmid pBMB9741	645047364	Onion yellows phytoplasma OY plasmid EcOYW1
642481206	Bacillus thuringiensis plasmid pDAN-involved	645047365	Onion yellows phytoplasma OY plasmid pOYM
642481207	Bacillus thuringiensis plasmid pFR12	645047366	Onion yellows phytoplasma OY plasmid pOYNIM
642481208	Bacillus thuringiensis plasmid pFR12.5	641210354	Onion yellows phytoplasma plasmid extrachromosomal DNA
642481209	Bacillus thuringiensis plasmid pFR55	643660933	Ornithobacterium rhinotracheale plasmid pOR1
642481210	Bacillus thuringiensis serovar kurstaki plasmid pAW63	642914186	Paenibacillus larvae 67E plasmid pMA67
641210236	Bacillus thuringiensis sv darmstadiensis INTA 14-4 plasmid pBMBt1	642914187	Paenibacillus popilliae NRRL B-2524 plasmid pBP68
640048239	Bacillus thuringiensis sv entomocidus LBIT-113 plasmid pUIBI-1	648934924	Pantoea agglomerans EGE6 plasmid pPAGA3
640048238	Bacillus thuringiensis sv israelensis HI4 plasmid pTX14-3	640048444	Pantoea citrea 1056R plasmid pUCD5000
641507358	Bacillus thuringiensis sv israelensis plasmid pBtoxis	640048443	Pantoea citrea ATCC31623 plasmid pPZG500
640048242	Bacillus thuringiensis sv israelensis plasmid pTX14-1	642914188	Paracoccus aminophilus JCM 7686 plasmid pAMI2
640048240	Bacillus thuringiensis sv kurstaki YBT-1520 plasmid pBMB2062	646556927	Paracoccus aminophilus JCM 7686 plasmid pAMI3
642914115	Bacillus thuringiensis sv tenebrionis YBT-1765 plasmid pBMB175	650625522	Paracoccus aminophilus JCM 7686 plasmid pAMI7
640048241	Bacillus thuringiensis sv thuringiensis H1.1 plasmid pGI1	641210355	Paracoccus methylutens DM12 plasmid pMTH1
642914116	Bacteroides fragilis P35 plasmid pBFP35	640048445	Paracoccus pantotrophus DSM 11072 plasmid pWKS1
640048243	Bacteroides fragilis plasmid pBI143	643660934	Pasteurella multocida plasmid pCCK1900
641210237	Bacteroides uniformis mobilizable transposon NBU1	641210356	Pasteurella multocida 381 plasmid pCCK381
640048244	Bartonella grahamii WM10 plasmid pBGR2	641210357	Pasteurella multocida 6647 plasmid pCCK647
641210238	Bartonella grahamii plasmid pBGR1	640048446	Pasteurella multocida Pm1096 plasmid pIG1
642914117	Bartonella tribocorum KM19-1 plasmid pKM19s	645047367	Pasteurella multocida plasmid pB1005
641210239	Beet leafhopper transmitted virescence phytoplasma plasmid pBLTVA-1	645047368	Pasteurella multocida plasmid pB1006

641210240	Beet leafhopper transmitted virescence phytoplasma plasmid pBLTVA-2	640048447	Pasteurella multocida plasmid pJR1
642914118	Bifidobacterium asteroides DSM 20089 plasmid pCIBAO89	640048448	Pasteurella multocida plasmid pJR2
643660906	Bifidobacterium bifidum B80 plasmid pB80	641210358	Pasteurella trehalosi 13698 plasmid pCCK13698
642914119	Bifidobacterium breve B21a plasmid pB21a	642481245	Paulownia witches-broom phytoplasma plasmid pPaWBNy-1
640048245	Bifidobacterium breve NCFB 2258 plasmid pCIBb1	642481246	Paulownia witches-broom phytoplasma plasmid pPaWBNy-2
641210241	Bifidobacterium catenulatum L48 plasmid pBC1	640048449	Peanut witches-broom phytoplasma plasmid pPNWB
642914120	Bifidobacterium longum DPC6043 plasmid p6043A	643660935	Pectobacterium atrosepticum SCRI1039 plasmid pECA1039
642914121	Bifidobacterium longum DPC6043 plasmid p6043B	640048450	Pediococcus acidilactici H plasmid pSMB74
642914122	Bifidobacterium longum FI10564 plasmid pFI2576	642914189	Pediococcus acidilactici NCIMB 6990 plasmid pEOC01
640048250	Bifidobacterium longum KJ plasmid pKJ36	641210359	Pediococcus damnosus 8801 plasmid pF8801
640048251	Bifidobacterium longum KJ plasmid pKJ50	648934925	Pediococcus pentosaceus ACA-DC 3431 plasmid pPS1
640048246	Bifidobacterium longum RW041 plasmid PNAC2	640048451	Pediococcus pentosaceus ATCC43200 plasmid pMD136
640048253	Bifidobacterium longum RW041 plasmid pNAC3	645047369	Pediococcus pentosaceus plasmid pRS5
640048252	Bifidobacterium longum RW048 plasmid pNAC1	645047370	Photobacterium damselae piscicida P9014 plasmid pP9014
640048247	Bifidobacterium longum VMKB44 plasmid pB44	641210361	Photobacterium damselae piscicida PT99-018 plasmid pP99-018
641210242	Bifidobacterium longum plasmid pMG1	641210360	Photobacterium damselae piscicida USA91278 plasmid pP91278
641210243	Bifidobacterium longum plasmid pTB6	650625523	Photobacterium damselae subsp. damselae plasmid pPHDD1
640048254	Bifidobacterium pseudocatenulatum VMKB4M plasmid p4M	648018811	Photobacterium damselae subsp. piscicida plasmid pPHDP10
642914123	Bifidobacterium pseudolongum globosum DPC479 plasmid pASV479	642481247	Phytoplasma sp. plasmid pPSE
643660907	Bifidobacterium sp. A24 A24 plasmid pBIFA24	646556928	Planococcus sp. ZOYM plasmid pPCZ1
642481211	Birmingham IncP-alpha plasmid	646556929	Planococcus sp. ZOYM plasmid pPCZ2
641210244	Bordetella pertussis BP136 plasmid pBP136	641210362	Plasmid QKH54
645047307	Borrelia burgdorferi 297 plasmid 297_lp54	641210363	Plasmid pB3
645047308	Borrelia burgdorferi JD1 plasmid JD1_lp54	648018812	Plasmid pGNB2 plasmid pGNB2
645047309	Borrelia burgdorferi N40 plasmid N40_lp54	640048471	Plasmid pIPO2T
640048256	Borrelia burgdorferi plasmid cp18-2	641210364	Plasmid pLB1
640048257	Borrelia burgdorferi strain ATCC 35210 plasmid lp16.9	642481248	Plasmid pNKH43
641210245	Borrelia burgdorferi strain Ip21 plasmid	640048482	Pleurotus ostreatus mitochondrial plasmid mlp1
641210246	Borrelia duttonii 44-kb linear plasmid	640048485	Prevotella ruminicola T31 plasmid pRAM4
640048259	Brevibacillus borstelensis HP926 plasmid pHT926	640048486	Propionibacterium acidipropionici E214 plasmid pRGO1
640048260	Brevibacterium linens plasmid LIM	640048487	Propionibacterium freudenreichii LMG16545 plasmid p545
640048263	Buchnera aphidicola Dn plasmid pLeu-Dn	641507374	Propionibacterium freudenreichii plasmid pLME108
640048262	Buchnera aphidicola Ps plasmid pBPS1	640048488	Propionibacterium granulosum PF283 cryptic plasmid pPG01

640048261	Buchnera aphidicola Sg plasmid pLeu-Sg	641210365	Propionibacterium jensenii DF1 plasmid pLME106
646556907	Buchnera aphidicola plasmid pleu-BTg	643660936	Proteus mirabilis plasmid pRPCMY
646556908	Burkholderia cepacia 2a plasmid pIJB1	640048490	Proteus vulgaris ATCC13315 plasmid pPvu1
641507359	Burkholderia cepacia plasmid PPC1	640048489	Proteus vulgaris UR-75 plasmid Rts1
643660908	Butyrivibrio fibrisolvens plasmid pRJF1	642914191	Providencia rettgeri plasmid R7K
643660909	Butyrivibrio fibrisolvens plasmid pRJF2	642914192	Pseudoalteromonas sp. 643A plasmid pKW1
640048264	Butyrivibrio fibrisolvens Bu49 plasmid pOM1	646556930	Pseudoalteromonas sp. BSi20327 plasmid pSM327
641210247	Caedibacter taeniospiralis plasmid pKAP298	640048491	Pseudoalteromonas sp. PS1M3 plasmid pPS1M3
641210248	Campylobacter coli 338 plasmid p3384	641210368	Pseudomonas aeruginosa 07-406 plasmid pMATVIM-7
641210249	Campylobacter coli 338 plasmid p3386	642914193	Pseudomonas aeruginosa E1 plasmid pMM1
641210253	Campylobacter coli CC31 plasmid pCC31	641210366	Pseudomonas aeruginosa Ps142 plasmid Rms149
641210250	Campylobacter coli RM2228 plasmid pCC2228-1	641210367	Pseudomonas aeruginosa plasmid pBS228
641210251	Campylobacter coli RM2228 plasmid pCC2228-2	641210369	Pseudomonas alcaligenes NCIB 9867 plasmid pRA2
641210252	Campylobacter coli RM2228 plasmid pCC2228-3	645047372	Pseudomonas fluorescens PC20 plasmid pNAH20
642914125	Campylobacter fetus venerealis 4111/108 plasmid pCFV108	640048492	Pseudomonas fulva IF-4 plasmid pNI10
640048370	Campylobacter fetus venerealis Azul-94	648934926	Pseudomonas putida HS1 plasmid pDK1
641210254	Campylobacter jejuni 21190 plasmid pCJ01	641210372	Pseudomonas putida MT53 plasmid pWW53
641210255	Campylobacter jejuni RM1170 plasmid pCJ1170	640048493	Pseudomonas putida NCIB 9816-4 plasmid pDTG1
640048265	Campylobacter jejuni plasmid pCJ419	640048494	Pseudomonas putida P8 plasmid pPP81
641507360	Campylobacter jejuni plasmid pTet (img:a)	645047373	Pseudomonas putida W2 plasmid pW2
641507361	Campylobacter jejuni plasmid pTet (img:b)	640048495	Pseudomonas putida mt-2 plasmid pWW0
641507362	Campylobacter jejuni plasmid pVir	641210371	Pseudomonas putida plasmid NAH7
641210259	Campylobacter lari 237 plasmid pUPTC237	640048496	Pseudomonas putida plasmid pYQ39
641210258	Campylobacter lari 300 plasmid pCL300	640048497	Pseudomonas resinovorans CA10 plasmid pCAR1
642914126	Candidatus Phytoplasma australiense plasmid pCPa	643660937	Pseudomonas resinovorans CA10 plasmid pCAR1.2
642914127	Candidatus Phytoplasma australiense plasmid pPAPh2	640048498	Pseudomonas sp. ADP plasmid pADP-1
642914128	Candidatus Phytoplasma australiense plasmid pPASb11	645047374	Pseudomonas sp. CG21 CG21 plasmid pMWHK01
648018803	Candidatus Rickettsia amblyommii AaR/SC plasmid pRAM18	642914194	Pseudomonas sp. CT14 plasmid pCT14
648018804	Candidatus Rickettsia amblyommii AaR/SC plasmid pRAM23	641210373	Pseudomonas sp. ND6 plasmid pND6-1
643660910	Capnocytophaga canimorsus 7 plasmid pCC7	641210374	Pseudomonas sp. S-47 plasmid p47L
645047310	Chlamydia trachomatis B/TZ1A828/OT plasmid pCTB	641210375	Pseudomonas sp. S-47 plasmid p47S
640048464	Chlamydia trachomatis D plasmid pCHL1	640048499	Pseudomonas sp. SLT2001 plasmid pQBR55
645047311	Chlamydia trachomatis Jali20 plasmid pJALI	640048500	Pseudomonas syringae maculicola M6 plasmid pFKN
645047312	Chlamydia trachomatis Sweden2 plasmid pSW2	641210376	Pseudomonas syringae pv. Maculicola ES4326 plasmid pPMA4326A
645047313	Chlamydia trachomatis Sweden3 plasmid pSW3	641210377	Pseudomonas syringae pv. maculicola ES4326 plasmid pPMA4326B
645047314	Chlamydia trachomatis Sweden4 plasmid pSW4	641210378	Pseudomonas syringae pv. maculicola ES4326 plasmid pPMA4326C

645047315	Chlamydia trachomatis Sweden5 plasmid pSW5	641210379	Pseudomonas syringae pv. maculicola ES4326 plasmid pPMA4326D
641507363	Chlamydia trachomatis plasmid pLGV440	641210380	Pseudomonas syringae pv. maculicola ES4326 plasmid pPMA4326E
640048267	Chlamydophila psittaci plasmid pCpA1	641210381	Pseudomonas syringae pv. syringae A2 plasmid pPSR1
640048268	Chlorobium limicola DSM 249 plasmid pCL1	650625525	Pseudonocardia autotrophica DSM 43082 plasmid pPA43082
640048270	Citrobacter rodentium DBS100 plasmid pCRP3	648018813	Pyrococcus sp. 12/1 12/1 plasmid pP12-1
640048269	Citrobacter rodentium DBS100 plasmid pCRP3	640048501	Pyrococcus sp. JT1 plasmid pRT1
645047316	Clostridium botulinum D 1873 plasmid pCLG1	641210382	Rahnella sp. WMR15 plasmid pHW15
645047317	Clostridium botulinum D 1873 plasmid pCLG2	642481250	Ralstonia pickettii plasmid pMBCP
645047318	Clostridium butyricum MIYAIRI 588 plasmid pCBM588	640048502	Ralstonia solanacearum M4S plasmid pJTPS1
650625504	Clostridium carboxidivorans P7 P7 plasmid p19	640048504	Rhodobacter blasticus TCRI-14 plasmid pMG160
641210260	Clostridium difficile CD6 plasmid pCD6	642914195	Rhodococcus aetherivorans I24 plasmid pRA1
641210262	Clostridium perfringens F4969 plasmid pCPF4969	640048505	Rhodococcus equi 103 plasmid p103
641210261	Clostridium perfringens F5603 plasmid pBCNF5603	642914196	Rhodococcus equi 103S plasmid pVAPA1037
641210263	Clostridium perfringens F5603 plasmid pCPF5603	640048506	Rhodococcus equi ATCC33701 plasmid pREAT701
643660911	Clostridium perfringens NCTC 8533B4D plasmid pCP8533etx	642914197	Rhodococcus equi PAM1593 plasmid pVAPB1593
642914129	Clostridium perfringens plasmid pCW3	640048507	Rhodococcus erythropolis BD2 plasmid pBD2
640048470	Clostridium perfringens plasmid pIP404	641210389	Rhodococcus erythropolis DSM 8424 plasmid pRE8424
640048271	Clostridium sp. MCF-1 indigenous plasmid pMCF-1	640048508	Rhodococcus erythropolis NI86/21 plasmid pFAJ2600
642481214	Collimonas fungivorans plasmid pTer331	641210392	Rhodococcus rhodochrous plasmid pNC500
642914130	Comamonas sp. CNB-1 plasmid pCNB	640048509	Rhodococcus sp. B264-1 plasmid pB264
642481215	Comamonas testosteroni plasmid pPT1	642914198	Rhodococcus sp. NS1 plasmid pNSL1
640048272	Corynebacterium callunae ATCC 15991 plasmid pCC1	646556931	Rhodopseudomonas palustris AS1.2352 plasmid pRPSZY
642914132	Corynebacterium casei JCM 12072 plasmid pCASE1	640048510	Rhodothermus marinus plasmid pRM21
640048273	Corynebacterium diphtheriae S601 plasmid pNG2	642914199	Rickettsia monacensis IrR/Munich plasmid pRM
640048274	Corynebacterium diphtheriae plasmid pNGA2	640048511	Riemerella anatipestifer 10 plasmid pCFC1
640048287	Corynebacterium glutamicum 1014 plasmid pXZ10142	640048512	Riemerella anatipestifer 20 plasmid pCFC2
640048285	Corynebacterium glutamicum 1014 plasmid pXZ10145.1	641210393	Ruegeria sp. PR1b plasmid pSD20
640048279	Corynebacterium glutamicum 22220 plasmid pAG3	641210394	Ruegeria sp. PR1b plasmid pSD25
640048286	Corynebacterium glutamicum 227 plasmid pXZ608	641210395	Ruminococcus flavefaciens R13e2 plasmid pBAW301
640048280	Corynebacterium glutamicum ATCC 13869 plasmid pAM330	640048513	Salmonella choleraesuis 79500 plasmid pSFD10
646556909	Corynebacterium glutamicum ATCC 14997 plasmid pCGR2	645047375	Salmonella enterica AM04528 plasmid pAM04528
640048283	Corynebacterium glutamicum ATCC 19223 plasmid pSR1	641210397	Salmonella enterica OU7025 plasmid pOU1113
640048281	Corynebacterium glutamicum ATCC 31832 plasmid pCG2	645047376	Salmonella enterica SGI-15 plasmid pSGI15
640048278	Corynebacterium glutamicum ATCC31830 R-plasmid pCG4	645047377	Salmonella enterica enterica sv 404ty plasmid pBSSB1
640048282	Corynebacterium glutamicum LP-6 plasmid pGA2	640048514	Salmonella enterica enterica sv Berta plasmid pBERT

640048284	Corynebacterium glutamicum LP-6 plasmid pTET3	640048515	Salmonella enterica enterica sv Choleraesuis RF-1 plasmid pKDSC50
640048277	Corynebacterium glutamicum YS-314 R-plasmid pAG1	641210398	Salmonella enterica enterica sv Choleraesuis cryptic
642481216	Corynebacterium glutamicum plasmid pBl1	642914200	Salmonella enterica enterica sv Dublin plasmid IncW pIE321
642481217	Corynebacterium glutamicum unnamed plasmid	642914201	Salmonella enterica enterica sv Enteritidis Sal550 plasmid pSE34
640048288	Corynebacterium jeikeium A501 plasmid pA501	645047378	Salmonella enterica enterica sv GSS-HN-2007057 plasmid p2007057
640048289	Corynebacterium jeikeium A505 plasmid pA505	642914202	Salmonella enterica enterica sv Kentucky CVM29188 plasmid pCVM29188_101
640048290	Corynebacterium jeikeium B85766 plasmid pB85766	642914203	Salmonella enterica enterica sv Kentucky CVM29188 plasmid pCVM29188_146
640048291	Corynebacterium jeikeium CJ84 plasmid pCJ84	642914204	Salmonella enterica enterica sv Kentucky CVM29188 plasmid pCVM29188_46
640048293	Corynebacterium jeikeium K64 plasmid pK64	642914205	Salmonella enterica enterica sv Paratyphi A plasmid pGY1
640048292	Corynebacterium jeikeium plasmid pK43	645047379	Salmonella enterica enterica sv SL491 plasmid pSL491_3
640048294	Corynebacterium renale plasmid pCR1	645047380	Salmonella enterica enterica sv SL491 plasmid pSL491_5
641210264	Corynebacterium sp. L2-79-05 plasmid pLEW279a	642914206	Salmonella enterica enterica sv Typhimurium ST728/06-2 plasmid pST728/06-2
641210265	Corynebacterium sp. L2-79-05 plasmid pLEW279b	640048516	Salmonella enterica enterica sv enteritidis plasmid pB
640048295	Corynebacterium striatum M82B plasmid pTP10	640048517	Salmonella enterica enterica sv enteritidis plasmid pC
650625505	Corynebacterium tuberculostearicum B146 plasmid p1B146	640048518	Salmonella enterica enterica sv enteritidis plasmid pK
642914133	Coxiella burnetii MSU Goat Q177 plasmid QpRS	640048519	Salmonella enterica enterica sv enteritidis plasmid pP
640048297	Coxiella burnetii Nine Mile phase I plasmid QpH1	648934927	Salmonella enterica subsp. enterica serovar plasmid pYT1
640048296	Coxiella burnetii R1140 plasmid QpDV	643660938	Salmonella enterica subsp. enterica serovar 05-686 plasmid pWES-1
642914134	Cupriavidus taiwanensis TJ86 plasmid pTJ86-1	642481251	Salmonella enterica subsp. enterica serovar Brandenburg plasmid
642914135	Cupriavidus taiwanensis TJ86 plasmid pTJ86-2	646556932	Salmonella enterica subsp. enterica serovar D23580 plasmid pSLT-BT
642914136	Cylindrospermum sp. A1345 plasmid pCYLM01	642481252	Salmonella enterica subsp. enterica serovar Dublin plasmid pOU1114
642914137	Cylindrospermum sp. A1345 plasmid pCYLM02	642481253	Salmonella enterica subsp. enterica serovar Dublin plasmid pOU1115
643660912	Deinococcus radiopugnans ATCC 19172 ATCC 19172 plasmid pUE30	642481254	Salmonella enterica subsp. enterica serovar Newport plasmid pA172
640048298	Delftia acidovorans B plasmid pUO1	648934928	Salmonella enterica subsp. enterica serovar PVCM07-2008 plasmid pVCM04
640048299	Dichelobacter nodosus plasmid DN1	648018814	Salmonella enterica subsp. enterica serovar SN11/00 plasmid pSN11/00Kan
640048303	Edwardsiella ictaluri plasmid pEI1	641507380	Salmonella enterica subsp. enterica sv Dublin L-789 plasmid pMAK2
640048304	Edwardsiella ictaluri plasmid pEI2	641507378	Salmonella enterica subsp. enterica sv Choleraesuis L-2454 plasmid pMAK1
650625506	Edwardsiella tarda CK41 plasmid pCK41	641507379	Salmonella enterica subsp. enterica sv Choleraesuis OU7519 plasmid pOU7519
641210266	Eikenella corrodens 1073 plasmid pMU1	641507381	Salmonella enterica subsp. enterica sv Dublin L-2156 plasmid pMAK3
640048531	Ensifer meliloti 1132 plasmid pRm1132f	641507382	Salmonella enterica subsp. enterica sv Typhimurium DT193 plasmid
640048476	Ensifer meliloti FP2 plasmid pSB102	640048520	Salmonella typhi plasmid R27

642914209	Ensifer meliloti SM11 plasmid pSmeSM11b	641210400	Salmonella typhimurium G8430 plasmid pU302L
640048305	Enterobacter aerogenes plasmid R751	641210401	Salmonella typhimurium G8430 plasmid pU302S
650625507	Enterobacter cloacae plasmid pS51A	640048357	Salmonella typhimurium IncN plasmid R46
645047321	Enterobacter cloacae CHE-2 plasmid pCHE-A	640048456	Salmonella typhimurium Plasmid NTP16
643660913	Enterobacter cloacae IFO 3320 plasmid pEC01	640048521	Salmonella typhimurium plasmid R64
645047319	Enterobacter cloacae plasmid pEC-IMP	642914207	Salmonella typhimurium plasmid pAnkS
645047320	Enterobacter cloacae plasmid pEC-IMPQ	640048522	Salmonella typhimurium plasmid pSC101
640048306	Enterobacter sp. RFL1396 plasmid pEsp1396	641210402	Selenomonas ruminantium 19 plasmid pSRD191
643660914	Enterococcus faecalis plasmid pMG2200	648018815	Selenomonas ruminantium 19 plasmid pSRD192
650625508	Enterococcus faecalis plasmid pTW9	640048526	Selenomonas ruminantium HD4 plasmid pSR1
648934903	Enterococcus faecalis plasmid pWZ1668	640048523	Selenomonas ruminantium JW13 plasmid pJW1
640048309	Enterococcus faecalis BFE 1071 plasmid pEF1071	640048524	Selenomonas ruminantium S20 plasmid pONE429
641210269	Enterococcus faecalis DS16 conjugative transposon Tn916	640048525	Selenomonas ruminantium S20 plasmid pONE430
640048308	Enterococcus faecalis DS5 plasmid pAMalpha1	640048527	Serratia entomophila A1MO2 plasmid pADAP
646556910	Enterococcus faecalis DS5 plasmid pAMbeta1	642914208	Serratia marcescens ACE4 plasmid pRK10
646556911	Enterococcus faecalis E99 plasmid pBEE99	640048528	Serratia marcescens plasmid R478
650625509	Enterococcus faecalis EF-01 plasmid pEF-01	641210403	Serratia marcescens plasmid R478
641210268	Enterococcus faecalis RE25 plasmid pRE25	645047381	Shewanella sp. 33B plasmid pSFKW33
640048307	Enterococcus faecalis plasmid pAM373	642481255	Shigella flexneri 2a plasmid p2457TS2
641210267	Enterococcus faecalis plasmid pCF10	640048457	Shigella flexneri 2b 222 plasmid R100
643660915	Enterococcus faecium plasmid pMG1	640048529	Shigella flexneri 5a virulence plasmid pWR501
641210274	Enterococcus faecium 399/F99/A9 plasmid pVEF2	646556933	Shigella sonnei EG0356 plasmid pEG356
641210273	Enterococcus faecium 399/F99/H8 plasmid pVEF1	640048454	Shigella sonnei P9 plasmid ColIb-P9
642914138	Enterococcus faecium 399/S99/A7 plasmid pVEF3	640048530	Shigella sonnei colicin type 7 plasmid ColJs
642914139	Enterococcus faecium 6T1a plasmid pEF1	641210404	Shigella sonnei plasmid pKKTET7
642914140	Enterococcus faecium BM4147 plasmid pIP816	640048472	Shigella sonnei plasmid pKYM
641210270	Enterococcus faecium L50 plasmid pCIZ2	646556934	Sinorhizobium meliloti plasmid pSmeSM11a
650625510	Enterococcus faecium S177 plasmid pS177	641210405	Sodalis glossinidius plasmid pSG1 (img:a)
640048310	Enterococcus faecium U37 plasmid pRUM	641210406	Sodalis glossinidius plasmid pSG1 (img:b)
641210271	Enterococcus faecium plasmid pHT beta	641210407	Sodalis glossinidius plasmid pSG2 (img:a)
641210272	Enterococcus faecium plasmid pJB01	641210408	Sodalis glossinidius plasmid pSG2 (img:b)
642481220	Enterococcus faecium plasmid pJS33	641210409	Sodalis glossinidius plasmid pSG3
642481221	Enterococcus faecium plasmid pJS42	641210410	Sodalis glossinidius plasmid pSG4 (img:a)
642481222	Enterococcus faecium plasmid pRI1	641210411	Sodalis glossinidius plasmid pSG4 (img:b)
641210275	Erwinia amylovora Ea88 plasmid pEA29	641210412	Sphingobium yanoikuyae JCM 7371 plasmid pYAN-1
641210276	Erwinia amylovora LebB66 plasmid pEL60	641210413	Sphingobium yanoikuyae JCM 7371 plasmid pYAN-2
641210277	Erwinia amylovora UTRJ2 plasmid pEU30	641210414	Sphingomonas sp. A1 plasmid pA1
640048311	Erwinia amylovora plasmid pEA1.7	641210415	Sphingomonas sp. KA1 plasmid pCAR3
640048312	Erwinia amylovora plasmid pEA2.8	648018816	Sphingomonas sp. MM-1 MM-1 plasmid pISP3

640048313	Erwinia pyrifoliae plasmid pEP36	641210416	Sphingomonas xenophaga QYY plasmid pSx-Qyy
640048314	Erwinia sp. Ejp 556 plasmid pEJ30	650625526	Sphingopyxis macrogoltabida 103 plasmid pSM103mini
640048315	Erysipelothrix rhusiopathiae plasmid pAP1	641210417	Spiroplasma citri plasmid pBJS-O
650625511	Escherichia coli plasmid p3521	641210418	Spiroplasma citri plasmid pSci1
642914141	Escherichia coli 1520 plasmid pIP1206	641210419	Spiroplasma citri plasmid pSci2
641210301	Escherichia coli 2001-10-678 plasmid pVI678	641210420	Spiroplasma citri plasmid pSci3
643660916	Escherichia coli 278B plasmid pEC278	641210421	Spiroplasma citri plasmid pSci4
640048321	Escherichia coli 29k plasmid pECO29	641210422	Spiroplasma citri plasmid pSci5
641210302	Escherichia coli 517-2H1 plasmid pLEW517	641210423	Spiroplasma citri plasmid pSci6
642914142	Escherichia coli 53638 plasmid p53638_226	641210424	Spiroplasma citri plasmid pSciA
642914143	Escherichia coli 53638 plasmid p53638_75	641210425	Spiroplasma kunkelii plasmid pSKU146
648934904	Escherichia coli 7 plasmid IncQ-type pQ7	648018817	Sporosarcina ureae DMV4 plasmid pSU1
642914144	Escherichia coli 86-24 plasmid pSP70	643660939	Staphylococcus aureus plasmid pC221
641210280	Escherichia coli 9705 plasmid p9705	643660940	Staphylococcus aureus plasmid pRJ6
645047323	Escherichia coli A plasmid pEK499	643660941	Staphylococcus aureus plasmid pVGA
641210281	Escherichia coli A2363 plasmid pAPEC-O2-ColV	640048542	Staphylococcus aureus 120-r plasmid pNVH01
641210282	Escherichia coli A2363 plasmid pAPEC-O2-R	641210432	Staphylococcus aureus CMRSA plasmid pWBG738
645047324	Escherichia coli APEC O103 plasmid pAPEC-O103-ColBM	648018818	Staphylococcus aureus E29 plasmid pDLK3
645047325	Escherichia coli AR060302 plasmid pAR060302	646556935	Staphylococcus aureus HUNSC491 plasmid pPR9
648934905	Escherichia coli B24 plasmid pEC_B24	641210429	Staphylococcus aureus IMCJ1308 plasmid pSA1308
648934906	Escherichia coli Bactec plasmid pEC_Bactec	641210430	Staphylococcus aureus IMCJ1379 plasmid pSA1379
645047326	Escherichia coli C plasmid pEK204	642914210	Staphylococcus aureus JY30 plasmid pKH20
648934907	Escherichia coli C14-9 plasmid pEC14-9	642914211	Staphylococcus aureus JY37 plasmid pKH19
648934908	Escherichia coli C159/11 plasmid pCT	642914212	Staphylococcus aureus JY43 plasmid pKH12
642914145	Escherichia coli CA46 plasmid pColG	642914213	Staphylococcus aureus JY50 plasmid pKH21
645047327	Escherichia coli D plasmid pEK516	640048537	Staphylococcus aureus SA5 plasmid pKH3
645047328	Escherichia coli D7-3 plasmid pRAx	648934929	Staphylococcus aureus SK18 plasmid pSK1
641210298	Escherichia coli DIJ1 plasmid pO86A1	640048547	Staphylococcus aureus TY4 plasmid pETB
641210278	Escherichia coli DU1040 plasmid NR1	640048546	Staphylococcus aureus WBG1576 plasmid pUB101
643660917	Escherichia coli E2348/69 plasmid p5217	642914214	Staphylococcus aureus WBG4364 plasmid pWBG1773
643660918	Escherichia coli E2348/69 plasmid p6148	646556936	Staphylococcus aureus a53 plasmid pBORa53
642914146	Escherichia coli E2348/69 plasmid pMAR7	645047383	Staphylococcus aureus aureus ST398 plasmid pKKS825
645047329	Escherichia coli EC14 plasmid pEC14_114	641507383	Staphylococcus aureus plasmid EDINA
650625512	Escherichia coli ED1a ED1a plasmid pECOED	640048532	Staphylococcus aureus plasmid J3356::POX7;1
641210297	Escherichia coli EH41 plasmid pO113	640048533	Staphylococcus aureus plasmid J3356::pOX7;3
648934909	Escherichia coli ETEC 1392/75 ETEC 1392/75 plasmid p1081	640048534	Staphylococcus aureus plasmid J3358
648934910	Escherichia coli ETEC 1392/75 ETEC 1392/75 plasmid p557	642481256	Staphylococcus aureus plasmid p21
648934911	Escherichia coli ETEC 1392/75 ETEC 1392/75 plasmid p746	640048535	Staphylococcus aureus plasmid pC194
648934912	Escherichia coli ETEC 1392/75 ETEC 1392/75 plasmid p75	640048536	Staphylococcus aureus plasmid pC221

646556912	Escherichia coli ETEC H10407 plasmid pEntH10407	641210426	Staphylococcus aureus plasmid pC223
646556913	Escherichia coli H22 plasmid pColE1-H22	641210427	Staphylococcus aureus plasmid pE194
645047330	Escherichia coli H30 plasmid pO26-S1	645047382	Staphylococcus aureus plasmid pGO1
645047331	Escherichia coli H30 plasmid pO26-S3	642481257	Staphylococcus aureus plasmid pKH13
645047332	Escherichia coli H30 plasmid pO26-S4	642481258	Staphylococcus aureus plasmid pKH14
645047333	Escherichia coli H30 plasmid pO26-Vir	642481259	Staphylococcus aureus plasmid pKH15
643660919	Escherichia coli H30 plasmid pO26I	642481260	Staphylococcus aureus plasmid pKH16
645047334	Escherichia coli H4H plasmid peH4H	642481261	Staphylococcus aureus plasmid pKH17
640048358	Escherichia coli IncQ-like plasmid pIE1107	642481262	Staphylococcus aureus plasmid pKH18
645047335	Escherichia coli J plasmid ColE9-J	640048538	Staphylococcus aureus plasmid pKH6
641210287	Escherichia coli JEF100 plasmid pCoo	640048539	Staphylococcus aureus plasmid pKH7
640048455	Escherichia coli K-12 CR63 plasmid F	640048540	Staphylococcus aureus plasmid pLW043
640048317	Escherichia coli K-12 plasmid R721	640048541	Staphylococcus aureus plasmid pMW2
640048316	Escherichia coli K12 P678-54 plasmid CloDF13	640048475	Staphylococcus aureus plasmid pNS1
640048322	Escherichia coli KL4 plasmid pKL1	641210428	Staphylococcus aureus plasmid pS194
648934913	Escherichia coli L46 plasmid pEC_L46	640048543	Staphylococcus aureus plasmid pSK3
648934914	Escherichia coli L8 plasmid pEC_L8	640048544	Staphylococcus aureus plasmid pSK41
645047336	Escherichia coli LF82 plasmid pILF82	640048545	Staphylococcus aureus plasmid pSK6
640048323	Escherichia coli LG74 plasmid pLG13	641210431	Staphylococcus aureus plasmid pSN2
641210291	Escherichia coli MG828 plasmid pMG828-1	640048477	Staphylococcus aureus plasmid pT181
641210292	Escherichia coli MG828 plasmid pMG828-2	640048478	Staphylococcus aureus plasmid pT48
641210293	Escherichia coli MG828 plasmid pMG828-3	642481263	Staphylococcus aureus plasmid pTZ2162
641210294	Escherichia coli MG828 plasmid pMG828-4	641507384	Staphylococcus aureus plasmid pTZ4
641210295	Escherichia coli MG828 plasmid pMG828-5	640048480	Staphylococcus aureus plasmid pUB110 (img:a)
646556914	Escherichia coli MS2027 plasmid pMAS2027	640048479	Staphylococcus aureus plasmid pUB110 (img:a)
650625513	Escherichia coli O102-ST405 plasmid pETN48	642481264	Staphylococcus aureus plasmid pV030-8
640048319	Escherichia coli O111:NM B171 (EPEC2)	650625527	Staphylococcus aureus subsp. aureus ST398 plasmid pKKS627
641210300	Escherichia coli O157:H- 3072/96 plasmid pSFO157	641507385	Staphylococcus aureus subsp. aureus USA300_TCH959 plasmid
646556915	Escherichia coli O26:H- O6877 plasmid pO26-CRL	641210434	Staphylococcus chromogenes KNS48 plasmid pLNU4
648934915	Escherichia coli ST131 plasmid pKC394	641210433	Staphylococcus chromogenes TS1 plasmid pLNU1
643660920	Escherichia coli TN38148 plasmid pTN38148	641210435	Staphylococcus chromogenes plasmid pLNU8 (naturally occurring)
645047337	Escherichia coli Vir68 plasmid pVir68	641210436	Staphylococcus chromogenes plasmid pLNU9 (naturally occurring)
641210299	Escherichia coli W ATCC 9637plasmid pRK2	640048548	Staphylococcus epidermidis CH plasmid pSepCH
646556916	Escherichia coli ZMF18 plasmid pPM18	641210438	Staphylococcus epidermidis SK398 plasmid pSK639
645047338	Escherichia coli chi7122 plasmid pAPEC-1	641210437	Staphylococcus epidermidis plasmid pLNU6 (naturally occurring)
640048452	Escherichia coli plasmid ColA	640048474	Staphylococcus epidermidis plasmid pNE131
640048453	Escherichia coli plasmid ColE1	641210442	Staphylococcus haemolyticus plasmid pLNU3

642481223	Escherichia coli plasmid MccC7-H22	641210443	Staphylococcus haemolyticus plasmid pLNU7 (naturally occurring)
640048458	Escherichia coli plasmid RSF1010	650625528	Staphylococcus hyicus plasmid pKKS966
640048318	Escherichia coli plasmid p1658/97	641210444	Staphylococcus lentus plasmid pSTE2
641210279	Escherichia coli plasmid p9123	640048549	Staphylococcus lugdunensis 995 plasmid pLUG10
641210283	Escherichia coli plasmid pBHRK18	641210445	Staphylococcus pasteuri plasmid pSP187
641210284	Escherichia coli plasmid pBHRK19	641210446	Staphylococcus saprophyticus plasmid pSES22
641210285	Escherichia coli plasmid pC15-1a	642914215	Staphylococcus sciuri 101 plasmid pC194-like
640048320	Escherichia coli plasmid pCol-let	640048550	Staphylococcus sciuri plasmid pSCFS1
645047322	Escherichia coli plasmid pColE8	641210447	Staphylococcus sciuri sciuri plasmid pACK6
641210286	Escherichia coli plasmid pColK-K235	641210448	Staphylococcus simulans 184/61 plasmid pLNU2
641210288	Escherichia coli plasmid pFL129	648018819	Staphylococcus simulans bv. staphylolyticus NRRL B-2628 plasmid pACK1
641210289	Escherichia coli plasmid pIGAL1	650625529	Staphylococcus simulans bv. staphylolyticus NRRL B-2628 plasmid pACK2
641210290	Escherichia coli plasmid pIGJC156	648018820	Staphylococcus simulans bv. staphylolyticus NRRL B-2628 plasmid pACK3
642914147	Escherichia coli plasmid pIGMS5	645047384	Staphylococcus simulans bv. staphylolyticus NRRL B-2628 plasmid pACK4
642914148	Escherichia coli plasmid pIGRW12	650625530	Staphylococcus simulans bv. staphylolyticus NRRL B-2628 plasmid pACK5
642914149	Escherichia coli plasmid pIGWZ12	641210449	Staphylococcus simulans plasmid pLNU5 (naturally occurring)
642481224	Escherichia coli plasmid pIS2	641210450	Staphylococcus sp. 693-2 plasmid pLEW6932
642481225	Escherichia coli plasmid pLEW517	648018821	Staphylococcus sp. JG-2009f plasmid SAP_104B
641507364	Escherichia coli plasmid pLMO226	648018822	Staphylococcus sp. SK85 SK85 plasmid SAP_108D
641210296	Escherichia coli plasmid pMUR050	648018823	Staphylococcus sp. SK939 SK939 plasmid SAP_106A
642481226	Escherichia coli plasmid pOLA52	641210451	Staphylococcus warneri ISK-1 plasmid pPI-1
642481227	Escherichia coli plasmid pVM01	641210452	Staphylococcus warneri ISK-1 plasmid pPI-2
641210303	Escherichia sp. Sflu5 plasmid pAK51	641210453	Staphylococcus warneri plasmid pSW174
642914150	Exiguobacterium sp. RFL1109 plasmid pEspA	641210454	Staphylococcus warneri plasmid pSW49
642914151	Exiguobacterium sp. RFL1109 plasmid pEspB	642481265	Stenotrophomonas maltophilia plasmid pSH1
640048324	Flavobacterium psychrophilum D12 plasmid pCP1	642481266	Stenotrophomonas maltophilia plasmid pSM76
642914152	Flavobacterium sp. KI723T1 plasmid Plasmid pOAD2	640048551	Streptococcus agalactiae plasmid pGB354
640048325	Flavobacterium sp. KP1 plasmid pFL1	640048552	Streptococcus agalactiae plasmid pGB3631
641507365	Fluoribacter dumoffii plasmid pLD-TEX-KL	640048473	Streptococcus agalactiae plasmid pLS1
645047339	Francisella philomiragia ATCC 25016 plasmid pF242	641507386	Streptococcus agalactiae plasmid pMV158
645047340	Francisella philomiragia philomiragia ATCC 25017 plasmid pF243	642914216	Streptococcus dysgalactiae equisimilis T132 plasmid pSdyT132
640048326	Francisella tularensis LVS plasmid pOM1	642481267	Streptococcus dysgalactiae subsp. equisimilis plasmid pW2580
640048327	Francisella tularensis novicida F6168 plasmid pFNL10	640048553	Streptococcus mutans LM7 plasmid pLM7
640048328	Frankia sp. CpI1 plasmid pFQ12	640048554	Streptococcus mutans UA140 plasmid pUA140
640048331	Fusobacterium nucleatum 12230 plasmid pFN1	645047385	Streptococcus parasanguinis plasmid pFW213
640048333	Fusobacterium nucleatum FDC 27-17 plasmid pPA52	640048556	Streptococcus pneumoniae A6011 plasmid pSMB1

640048332	Fusobacterium nucleatum KH9 plasmid pKH9	640048555	Streptococcus pneumoniae D39 plasmid pDP1
641210304	Fusobacterium nucleatum polymorphum ATCC 10953 plasmid pFN3	641210455	Streptococcus pneumoniae plasmid pSpnP1
640048334	Geobacillus stearothermophilus TKO15 plasmid pSTK1	641210456	Streptococcus pyogenes 71-724 plasmid pDN571
642481229	Geobacillus stearothermophilus plasmid pGS18	642481268	Streptococcus pyogenes plasmid pDN281
640048336	Gluconobacter oxydans DSM 3504 plasmid pGO128	642481269	Streptococcus pyogenes plasmid pRW35
640048335	Gluconobacter oxydans IFO 3171 plasmid pAG5	641210457	Streptococcus pyogenes plasmid pSM19035
641210305	Gordonia westfalica DSM44215 plasmid pKB1	640048557	Streptococcus suis DAT1 plasmid pSSU1
641210306	Haemophilus ducreyi ATCC 27722 plasmid pNAD1	640048564	Streptococcus thermophilus 2783 plasmid pt38
643660923	Haemophilus influenzae plasmid ICEhin1056	640048563	Streptococcus thermophilus SMQ-172 plasmid pSMQ172
650625514	Haemophilus influenzae BB1059 plasmid PB1000	641210458	Streptococcus thermophilus SMQ-173 plasmid pSMQ173b
640048343	Haemophilus influenzae aegyptius plasmid pF3031	640048559	Streptococcus thermophilus ST135 plasmid pER35
640048342	Haemophilus influenzae biotype aegyptius BPF plasmid pF3028	640048560	Streptococcus thermophilus ST136 plasmid pER36
641210307	Haemophilus influenzae biotype aegyptius plasmid pF1947	640048562	Streptococcus thermophilus ST2-1 plasmid pND103
641210308	Haemophilus paragallinarum HP250 plasmid p250	640048561	Streptococcus thermophilus ST371 plasmid pER371
645047341	Haemophilus parasuis HN7061 plasmid pHN61	640048558	Streptococcus thermophilus plasmid pER13
641210310	Haemophilus parasuis HS1543 plasmid pHS-Tet	642914217	Streptococcus thermophilus plasmid pSMQ-316
641210309	Haemophilus parasuis plasmid pHS-Rec	641210459	Streptococcus thermophilus plasmid pSMQ308
641210311	Hafnia alvei MISC230 plasmid pAlvA	641210460	Streptomyces albulus IFO 14147 plasmid pNO33
641210312	Hafnia alvei MISC261 plasmid pAlvB	640048565	Streptomyces clavuligerus NRRL 3585 plasmid pSCL
640048345	Haloarchaeal coccus LOC-1 plasmid pHGN1	640048566	Streptomyces coelicolor plasmid 2 SCP2*
641210313	Haloarcula sp. AS7094 plasmid pSCM201	642481270	Streptomyces cyaneus plasmid pSA1.1
640048346	Halobacterium salinarum SB3 plasmid pHSB	642481271	Streptomyces flavovirens plasmid pSN22
642481230	Halobacterium salinarum plasmid pHH205	641210461	Streptomyces ghanaensis DSM2932 plasmid pSG5
642481231	Halobacterium salinarum plasmid pPHIHL	641210462	Streptomyces laurentii ATCC 31255 plasmid pSLS
640048467	Haloferax volcanii DS2 plasmid pHV2	642481272	Streptomyces lavendulae plasmid pSLG33
640048347	Halorubrum saccharovorum plasmid pZMX101	640048567	Streptomyces lividans 1326 plasmid SLP2
646556917	Haloterrigena thermotolerans H13 plasmid pSN	640048468	Streptomyces lividans plasmid pIJ101
640048348	Helicobacter pylori 489 plasmid pHP489	640048568	Streptomyces natalensis plasmid pSNA1
642914153	Helicobacter pylori 69 plasmid pHP69	640048569	Streptomyces phaeochromogenes NRRL-B3559 plasmid pJV1
646556918	Helicobacter pylori AL226 plasmid pAL226	640048570	Streptomyces rochei 7434AN4 plasmid pSLA2-L
642914154	Helicobacter pylori CCUG 17874; NCTC 11638 plasmid pHP666	642914218	Streptomyces sp. 44030 plasmid pRL1
640048349	Helicobacter pylori HPM180 plasmid pHPM180	641210463	Streptomyces sp. 44414 plasmid pRL2
640048350	Helicobacter pylori HPM186 plasmid pHPM186	640048571	Streptomyces sp. EN27 plasmid pEN2701
640048351	Helicobacter pylori HPM8 plasmid pHPM8	641210464	Streptomyces sp. F11 plasmid pFP11
640048352	Helicobacter pylori OU145B plasmid pHPO100	641210465	Streptomyces sp. FQ1 plasmid pFP1
640048354	Helicobacter pylori P29 plasmid pHel5	642914219	Streptomyces sp. FR1 plasmid pFRL1

640048353	Helicobacter pylori P8 plasmid pHel4	642481273	Streptomyces sp. HK1 plasmid pSHK1
641210314	Helicobacter pylori plasmid pAL202	646556937	Streptomyces sp. W9 plasmid pCQ3
641210315	Helicobacter pylori plasmid pHP51	646556938	Streptomyces sp. Y27 plasmid pWTY27
640048344	Histophilus somni 57/98 plasmid p57/98	646556939	Streptomyces sp. ZL12 plasmid pZL12
640048355	Histophilus somni 9L plasmid p9L	646556940	Streptomyces sp. x3 plasmid pTSC2
641210316	IncP-1 plasmid pKJK5	641210466	Streptomyces venezuelae ETH14630 plasmid pSVH1
641210317	IncP-1beta multiresistance plasmid pB8	640048572	Streptomyces violaceoruber SANK95570 plasmid pSV2
648934916	Klebsiella oxytoca KOX105 KOX105 plasmid pKOX105	640048573	Sulfolobus islandicus HEN7H2 plasmid pHEN7
645047346	Klebsiella pneumoniae 0773 plasmid pCTXM360	640048574	Sulfolobus islandicus P1 plasmid pING1
645047347	Klebsiella pneumoniae 0773 plasmid pKpn114	640048575	Sulfolobus islandicus REN1H1 plasmid pRN1
645047348	Klebsiella pneumoniae 12 plasmid 12	640048576	Sulfolobus islandicus REN1H1 plasmid pRN2
645047349	Klebsiella pneumoniae 15 plasmid 15S	641507387	Sulfolobus islandicus Rey 15/4 plasmid pSSVx
640048361	Klebsiella pneumoniae 2kI plasmid pKPN2	641210467	Sulfolobus islandicus plasmid pARN3
645047350	Klebsiella pneumoniae 9 plasmid 9	641210468	Sulfolobus islandicus plasmid pARN4
650625515	Klebsiella pneumoniae 997 plasmid pc15-k	641210469	Sulfolobus islandicus plasmid pHVE14
640048359	Klebsiella pneumoniae BM4493 plasmid pIP843	641210470	Sulfolobus islandicus plasmid pKEF9
648934917	Klebsiella pneumoniae C132-98 plasmid unnamed	642914220	Sulfolobus islandicus plasmid pSOG1
641210318	Klebsiella pneumoniae CG43 plasmid pLVPK	642914221	Sulfolobus islandicus plasmid pSOG2
642914155	Klebsiella pneumoniae FC1 plasmid pMET-1	642481274	Sulfolobus islandicus plasmid pXZ1
640048360	Klebsiella pneumoniae JHCK1 plasmid pJHCMW1	641210471	Sulfolobus neozealandicus plasmid pORA1
648018805	Klebsiella pneumoniae KF3 plasmid pKF3-140	641210472	Sulfolobus solfataricus IT3 plasmid pIT3
646556919	Klebsiella pneumoniae KF3 plasmid pKF3-70	641210473	Sulfolobus sp. NOB8H2 plasmid pNOB8
648018806	Klebsiella pneumoniae KF3 plasmid pKF3-94	641210474	Sulfolobus tengchongensis plasmid pTC
648934918	Klebsiella pneumoniae KP048 plasmid pKP048	643660942	Synechococcus elongatus PCC 7942 PCC 7942 plasmid pANL
643660924	Klebsiella pneumoniae KP96 plasmid pKP96	640048578	Synechococcus elongatus PCC 7942 plasmid pUH24
648018807	Klebsiella pneumoniae Kpn557 plasmid pKpQIL	642481275	Synechococcus sp. plasmid pMA4
642914156	Klebsiella pneumoniae NK245 plasmid pK245	640048580	Synechocystis sp. PCC 6803 plasmid pCB2.4
642914157	Klebsiella pneumoniae NK29 plasmid pK29	642914222	Tetragenococcus halophilus H plasmid pHDC
648934919	Klebsiella pneumoniae NL194 plasmid pNL194	642914223	Tetragenococcus halophilus PB18 plasmid pSKPB18
642481232	Klebsiella pneumoniae NTUH-K2044 plasmid pK2044	640048581	Thermoanaerobacterium thermosaccharolyticum DSM 571 plasmid pNB2
645047342	Klebsiella pneumoniae plasmid p169	641210475	Thermococcus nautilus 30-1 plasmid pTN1
645047343	Klebsiella pneumoniae plasmid p9701	648018824	Thermococcus nautilus 30/1 plasmid pTN2
642481233	Klebsiella pneumoniae plasmid pH205	648018825	Thermococcus sp. 26/2 26/2 plasmid pT26-2
645047344	Klebsiella pneumoniae plasmid pIGMS31	645047386	Thermococcus sp. AMT11 plasmid pAMT11
645047345	Klebsiella pneumoniae plasmid pIGRK	641210476	Thermoplasma acidophilum H0-122 plasmid pTA1
640048362	Klebsiella pneumoniae plasmid pKlebB-k17/80	641210477	Thermotoga petrophila RKU1 plasmid pRKU1
640048363	Klebsiella sp. KCL-2 plasmid pMGD2	642914224	Thermus sp. 4C plasmid pL4C

648934920	Lactobacillus acidipiscis ACA-DC 1533 plasmid pLAC1	642914225	Thermus sp. 4C plasmid pS4C
640048364	Lactobacillus acidophilus TK8912 plasmid pLA103	643660943	Thermus thermophilus HB8 plasmid pTT8
640048365	Lactobacillus acidophilus TK8912 plasmid pLA106	642481276	Thermus thermophilus plasmid pTF62
645047351	Lactobacillus brevis 925A plasmid pLB925A01	650625531	Thiomonas sp. 3As 3As plasmid pTHI
645047352	Lactobacillus brevis 925A plasmid pLB925A02	642914226	Tomato big bud phytoplasma plasmid pTBBperi
645047353	Lactobacillus brevis 925A plasmid pLB925A03	640048582	Treponema denticola U9b plasmid pTS1
645047354	Lactobacillus brevis 925A plasmid pLB925A04	640048583	Uncultured bacterium plasmid pB10
641210320	Lactobacillus brevis ABBC45 plasmid pRH45II	640048584	Uncultured bacterium plasmid pB4
650625516	Lactobacillus brevis D11 plasmid pSD11	641210479	Uncultured bacterium plasmid pRSB101
640048366	Lactobacillus casei CRL705 plasmid pRC18	641210480	Uncultured bacterium plasmid pTB11
642481234	Lactobacillus casei plasmid pSMA23	641210481	Uncultured bacterium plasmid pTP6
641210321	Lactobacillus casei plasmid pYIT356	641210482	Uncultured bacterium plasmid pTRACA10
643660925	Lactobacillus casei str. Zhang Zhang plasmid plca36	641210483	Uncultured bacterium plasmid pTRACA17
640048367	Lactobacillus delbrueckii WS58 plasmid pWS58	640048585	Uncultured eubacterium pIE1115 plasmid pIE1115
642914158	Lactobacillus delbrueckii bulgaricus B36 plasmid pDOJ1	640048586	Uncultured eubacterium plasmid pIE1130
640048368	Lactobacillus delbrueckii bulgaricus plasmid pLBB1	645047387	Vibrio alginolyticus E259 plasmid pVAE259
640048369	Lactobacillus delbrueckii lactis JCL414 plasmid pJBL2	642914227	Vibrio cholerae G1.1 plasmid pVCG1.1
640048371	Lactobacillus delbrueckii lactis NCC88 plasmid pN42	642914228	Vibrio cholerae G1.1 plasmid pVCG1.2
643660926	Lactobacillus farciminis KCTC3681 plasmid pLF24	642914229	Vibrio cholerae G4.1 plasmid pVCG4.1
640048372	Lactobacillus fermentum KC5b plasmid pKC5b	640048587	Vibrio cholerae O395P plasmid pTLC
640048373	Lactobacillus fermentum ROT1 plasmid pLME300	641210484	Vibrio cholerae SIO plasmid pSIO1
643660927	Lactobacillus gasseri LA39 plasmid pLgLA39	643660944	Vibrio fischeri ES213 plasmid pES213
640048374	Lactobacillus helveticus ATCC15009 plasmid pLH1	643660945	Vibrio fluvialis BD146 plasmid pBD146
650625517	Lactobacillus helveticus R0052 R0052 plasmid pIR52-1	642914230	Vibrio nigripulchritudo SFn1 plasmid pSFn1
640048375	Lactobacillus helveticus jugurti SBT2161 plasmid pLJ1	645047388	Vibrio parahaemolyticus A5-5 plasmid pZY5
645047355	Lactobacillus johnsonii FI9785 plasmid p9785S	640048588	Vibrio parahaemolyticus KXV237 plasmid pO3K6
642914159	Lactobacillus paracasei MA3 plasmid pMA3	642481277	Vibrio parahaemolyticus plasmid pSA19
645047356	Lactobacillus paracasei paracasei BGSJ2-8 plasmid pSJ2-8	642914231	Vibrio shilonii AK1 plasmid pAK1
646556920	Lactobacillus paracasei subsp. paracasei NFBC338 plasmid pCD01	641507390	Vibrio sp. 09022 plasmid p09022A
646556921	Lactobacillus paracasei subsp. paracasei NFBC338 plasmid pCD02	641507391	Vibrio sp. 0908 plasmid p0908
645047357	Lactobacillus pentosus F121-1 plasmid p1-4	641507392	Vibrio sp. 23023 plasmid p23023
640048379	Lactobacillus plantarum 5057 plasmid pMD5057	642481278	Vibrio sp. 41 plasmid pPS41
641210324	Lactobacillus plantarum BIFI-38 plasmid pPB1	641210487	Vibrio sp. TC68 plasmid pTC68
643660928	Lactobacillus plantarum CICC 6002 plasmid pLP2111	642914232	Vibrio tapetis CECT4600; CIP104856; B1090 plasmid pVT1
645047359	Lactobacillus plantarum KLDS 1.0801	641210489	Vibrio vulnificus CECT4602 plasmid pC4602-1

	plasmid pLD1		
642914160	Lactobacillus plantarum L137 plasmid pLTK13	641210490	Vibrio vulnificus CECT4602 plasmid pC4602-2
640048378	Lactobacillus plantarum L137 plasmid pLTK2	641210488	Vibrio vulnificus CECT4999=R99 plasmid
642914161	Lactobacillus plantarum LR1 plasmid pLR1	645047389	Vibrio vulnificus MP-4 plasmid pMP1
641210323	Lactobacillus plantarum M4 plasmid pM4	641507393	Weissella cibaria plasmid pKLCA
641210322	Lactobacillus plantarum NC7 plasmid p256	641210491	Weissella cibaria plasmid pKLCB
650625518	Lactobacillus plantarum PC518 plasmid pLPI8	642914233	Weissella cibaria plasmid pKW2130
646556922	Lactobacillus plantarum S1 plasmid pLP2140	642914234	Xanthomonas axonopodis pv. glycines 8ra plasmid pXAG81
648018808	Lactobacillus plantarum TXW plasmid pTXW	642914235	Xanthomonas axonopodis pv. glycines 8ra plasmid pXAG82
648934921	Lactobacillus plantarum XY3 plasmid pXY3	642914236	Xanthomonas axonopodis pv. glycines AG1 plasmid pAG1
641507370	Lactobacillus plantarum plasmid pA1	640048589	Xanthomonas campestris pv. vesicatoria plasmid pXV64
640048462	Lactobacillus plantarum plasmid pC30il	641210492	Xanthomonas citri plasmid pXcB
645047358	Lactobacillus plantarum plasmid pLFE1	640048590	Xylella fastidiosa ATTC 35868 plasmid pXF868
640048376	Lactobacillus plantarum plasmid pLP2000	648934930	Xylella fastidiosa Riv11 plasmid pXF-RIV11
640048377	Lactobacillus plantarum plasmid pLP9000	648934931	Xylella fastidiosa Riv16 plasmid pXF-RIV16
640048380	Lactobacillus reuteri 100-23 plasmid pGT232	648934932	Xylella fastidiosa Riv19 plasmid pXF-RIV19
640048382	Lactobacillus reuteri AE78 plasmid pAE78	648934933	Xylella fastidiosa Riv25 plasmid pXF-RIV25
640048381	Lactobacillus reuteri AE78 plasmid pTE44	645047390	Yersinia enterocolitica 07-04449 plasmid pYe4449-1
650625519	Lactobacillus reuteri K50 plasmid pK50-2	645047391	Yersinia enterocolitica 07-04449 plasmid pYe4449-2
642914162	Lactobacillus reuteri L09 plasmid pILR091	640048591	Yersinia enterocolitica 127/90 plasmid pYVa127/90
642481235	Lactobacillus reuteri plasmid pLR581	641210493	Yersinia enterocolitica 29807 plasmid p29807
642481236	Lactobacillus reuteri plasmid pLR585	643660946	Yersinia enterocolitica 8081 plasmid pYVe8081
643660929	Lactobacillus sakei BM5 plasmid pYC2	640048592	Yersinia enterocolitica W22703 plasmid pYVe227
640048383	Lactobacillus sakei RV332 plasmid pRV500	642481279	Yersinia enterocolitica plasmid pYE854
642914163	Lactobacillus sakei YSI8 plasmid pYSI8	641210494	Yersinia pestis CA88-4125 plasmid pCD1
642481237	Lactobacillus sakei plasmid pLS55	641210495	Yersinia pestis CA88-4125 plasmid pMT1
640048459	Lactobacillus sp. PC121B plasmid p121BS	640048598	Yersinia pestis CH971662 plasmid pYC
642914164	Lactococcus garvieae plasmid pKL0018	641210496	Yersinia pestis bv Orientalis IP275 plasmid pIP1202
640048387	Lactococcus lactis CRL1127 plasmid pCRL1127	641210497	Yersinia pestis plasmid pG8786
640048391	Lactococcus lactis DCH-4 plasmid pSRQ700	643660947	Yersinia pseudotuberculosis IP32637 plasmid pGDT4
640048384	Lactococcus lactis DPC220 plasmid pAH33	641210498	Yersinia ruckeri YR71 plasmid pYR1
640048390	Lactococcus lactis DPC3147 plasmid pMRC01	641210500	Zymomonas mobilis ATCC 10988 plasmid pZMO2
640048389	Lactococcus lactis IL964 plasmid pIL105	640048602	Zymomonas mobilis ATCC10988 plasmid pZMO1
643660930	Lactococcus lactis KLDS4.0319-3 plasmid pKL001	640048601	Zymomonas mobilis ZM4 plasmid 1
640048386	Lactococcus lactis ML8 plasmid pCL2.1	645047392	Zymomonas mobilis mobilis ATCC 10988 plasmid pZMO1
641210325	Lactococcus lactis NCDO 1867 plasmid pGdh442	642914237	Zymomonas mobilis mobilis CP4 plasmid pCP4.2
		648934934	Zymomonas mobilis subsp. mobilis ZM4 ZM4 plasmid pZZM401
		648934935	Zymomonas mobilis subsp. mobilis ZM4 ZM4 plasmid pZZM402

648934936	Zymomonas mobilis subsp. mobilis ZM4 ZM4 plasmid pZZM403
648934937	Zymomonas mobilis subsp. mobilis ZM4 ZM4 plasmid pZZM404
648934938	Zymomonas mobilis subsp. mobilis ZM4 ZM4 plasmid pZZM405
641507400	Zymomonas mobilis unknown plasmid
642914107	alpha proteobacterium endosymbiont of Amoeba plasmid pAP3.9
645047393	endophytic bacterium LOB-07 plasmid pLK39
646556941	uncultured bacterium plasmid pTRACA18
646556942	uncultured bacterium plasmid pTRACA20
646556943	uncultured bacterium plasmid pTRACA22
646556944	uncultured bacterium plasmid pTRACA30

Supplementary Table 5

Phylogenetic classification of the functionally predictable protein coding genes in the non-redundant 5x covered Morges MIRA-CONTIGS data subset in comparison to the proportion of cells in Morges activated sludge hybridising to a fluorescently labeled rRNA-directed taxonomic probe

Taxons	**Nr. of BLASTP hits**	**Proportion of hits (%)**	**Proportion of cells by FISH (%)**
Betaproteobacteria	565	32	34.0
Gammaproteobacteria	265	15	3.0
Alphaproteobacteria	88	5	36.0
unclassified *Proteobacteria*	393	22	NA
Delta/Epsilon subdivisions	37	2	4.0
Actinobacteria	45	2.5	12.0
***Bacteroidetes/Chlorobi* group**	35	2.0	7.0
Cyanobacteria	9	0.5	NA
Firmicutes	14	1.8	<1
Other bacteria	239	14	4
Total	1739	100	100

Protein coding genes were predicted in the MIRA-CONTIGS data subset by using Metagene within CAMERA. The ‘All prokaryotic proteins’ database was queried by using BLASTP (e-value cutoff = 0.01). The output was analyzed within MEGAN with a BLAST score value cutoff set to 35 and the minimal number of hits per taxon limit set to 1. Hits were only scored within the top 10% of the maximum score value.

Supplementary Table 6. Assembled replicons from the Morges 2007 MIRA data set.

Contig Name	Length, bp	Fold Coverage	GenBank	Remark
M02_c2	4722	49	JX194161.1	
M02_c3	7462	40		
M02_c5	14573	48	JX194159.1	
M02_c6	36689	51	JX194160.1	
M02_c7	2314	50	JX202560.1	
M02_c11	1633	55	JX202561.1	
M02_c15	12062	39		
M02_c18	38015	50	awaiting nr	
M02_c22	26126	30		
M02_c24	7427	24		
M02_c37	4361	31		
M02_c41	3086	36		
M02_c42	2196	23		
M02_c47	2310	37		
M02_c50	13142	20		
M02_c54	2502	72	JX202562.1	
M02_c60	2517	32		
M02_c69	3636	20		
M02_c81	22374	18		
M02_c85	9199	23		
M02_c90	1934	60	JX202563.1	
M02_c104	1682	25		
M02_c128	1816	86		
M02_c139	1773	14		
M02_c169	2412	12		
M02_c189	2124	100		
M02_c191	10012	13		
M02_c192	12183	10		
M02_c222	1821	64		
M02_c243	2844	8		
M02_c1053	11295	9		
M02_c11577	17822	57	awaiting nr	
M02_c11584	12681	36	awaiting nr	
M02_c11700	48785	10	awaiting nr	phage
M02_c11704	22414	14		phage
M02_c11712	12313	8		phage
M02_c11728	9745	10		
M02_c11732	11718	19		
M02_c11740	4170	21	JX202564.1	
M02_c11742	21309	11		
Contig11697	59231	43	awating nr	
Min	*1633*	*8*		
Max	*59231*	*100*		
Average	*11864*	*34*		
Median	*7462*	*30*		

Supplementary Table S7

Abundance and number of hits in the sublevel 2 'Resistance to antibiotics and toxic compounds' in the Morges 2007 plasmid metagenome

level 3	function	abun-dance	avg eValue	avg % ident	avg align len	# hits
Multidrug Resistance Efflux Pumps	Acriflavin resistance protein	12	-23.54	62.51	89.31	12
Bile hydrolysis	Alpha-ketoglutarate-dependent taurine dioxygenase (EC 1.14.11.17)	5	-11	60.15	54	3
Arsenic resistance	Arsenate reductase (EC 1.20.4.1)	4	-25.2	71.84	72.4	4
Arsenic resistance	Arsenic resistance protein ArsH	1	-65	83.69	141	1
Arsenic resistance	Arsenical pump-driving ATPase (EC 3.6.3.16)	1	-17	64.52	62	1
Arsenic resistance	Arsenical-resistance protein ACR3	1	-23	77.14	70	1
Beta-lactamase	Beta-lactamase	133	-31	61.29	103.11	34
Beta-lactamase	Beta-lactamase (EC 3.5.2.6)	112	-31.98	60.99	106.2	21
BlaR1 Family Regulatory Sensor-transducer Disambiguation	Beta-lactamase (EC 3.5.2.6)	112	-31.98	60.99	106.2	21
Beta-lactamase	Beta-lactamase class C and other penicillin binding proteins	14	-27.91	62.02	95.36	8
Beta-lactamase	Beta-lactamase class D	5	-24	60.54	83.33	2
Cobalt-zinc-cadmium resistance	Cation efflux system protein CusA	563	-64.65	76.34	157.35	81
Cobalt-zinc-cadmium resistance	Cd(II)/Pb(II)-responsive transcriptional regulator	86	-21	64.18	76.23	9
Resistance to chromium compounds	Chromate resistance protein ChrB	4	-25.25	66.19	90.5	4
Resistance to chromium compounds	Chromate transport protein ChrA	8	-54	80.78	124.73	6
Cobalt-zinc-cadmium resistance	Cobalt-zinc-cadmium resistance protein	616	-59.01	75.82	145.64	97
Cobalt-zinc-cadmium resistance	Cobalt-zinc-cadmium resistance protein CzcA	563	-64.65	76.34	157.35	81
Cobalt-zinc-cadmium resistance	Cobalt-zinc-cadmium resistance protein CzcD	10	-31.7	68.76	93.8	10
Cobalt-zinc-cadmium resistance	Cobalt/zinc/cadmium efflux RND transporter, membrane fusion protein, CzcB family	134	-49.59	70.59	137.28	16
Copper homeostasis	CopG protein	6	-23.33	63.53	79.67	3
Copper	Copper chaperone	4	-18.67	73.18	63	2

homeostasis						
Copper homeostasis: copper tolerance	Copper homeostasis protein CutE	2	-13	61.58	61	2
Cobalt-zinc-cadmium resistance	Copper sensory histidine kinase CusS	74	-39.25	67.2	123	4
Copper homeostasis	Copper sensory histidine kinase CusS	74	-39.25	67.2	123	4
Copper homeostasis	Copper tolerance protein	4	-50.25	71.02	143.5	4
Cobalt-zinc-cadmium resistance	Copper-sensing two-component system response regulator CusR	58	-48.25	75.96	125.38	3
Copper homeostasis	Copper-sensing two-component system response regulator CusR	58	-48.25	75.96	125.38	3
BlaR1 Family Regulatory Sensor-transducer Disambiguation	Copper-translocating P-type ATPase (EC 3.6.3.4)	596	-59.4	77.4	146.85	57
Copper homeostasis	Copper-translocating P-type ATPase (EC 3.6.3.4)	596	-59.4	77.4	146.85	57
Copper homeostasis	Cytochrome c heme lyase subunit CcmF	1	-6	63.64	33	1
Copper homeostasis	Cytochrome c heme lyase subunit CcmH	2	-10.5	61.28	57	2
Resistance to fluoroquinolones	DNA gyrase subunit B (EC 5.99.1.3)	3	-81.33	77.14	186.67	3
Cobalt-zinc-cadmium resistance	DNA-binding heavy metal response regulator	62	-31	72.69	90	12
Cobalt-zinc-cadmium resistance	Heavy metal RND efflux outer membrane protein, CzcC family	151	-28.35	68.18	91.63	22
Cobalt-zinc-cadmium resistance	Heavy metal sensor histidine kinase	35	-26.71	66.14	95.24	5
Multidrug Resistance Efflux Pumps	Macrolide export ATP-binding/permease protein MacB (EC 3.6.3.-)	6	-28.83	71.92	88.17	6
Multidrug Resistance Efflux Pumps	Macrolide-specific efflux protein MacA	1	-63.5	64.39	199	1
Copper homeostasis: copper tolerance	Magnesium and cobalt efflux protein CorC	1	-17	72.58	62	1
Multidrug Resistance Efflux Pumps	Membrane fusion protein of RND family multidrug efflux pump	1	-6	64.29	42	1
Mercuric reductase	Mercuric ion reductase (EC 1.16.1.1)	136	-91.12	88.82	191.34	13
Mercury resistance operon	Mercuric ion reductase (EC 1.16.1.1)	136	-91.12	88.82	191.34	13
Mercury resistance operon	Mercuric resistance operon coregulator	44	-48.11	89.79	109.22	4
Mercury resistance operon	Mercuric resistance operon regulatory protein	146	-26.76	81.2	74.24	14
Mercury resistance	Mercuric transport protein, MerC	102	-45.12	87.13	98.81	5

operon						
Mercury resistance operon	Mercuric transport protein, MerE	1	-29	82.19	73	1
Mercury resistance operon	Mercuric transport protein, MerT	139	-25.54	85.7	63.82	14
Copper homeostasis	Multicopper oxidase	13	-55.17	72.87	130.08	10
Multidrug Resistance Efflux Pumps	Multidrug efflux RND transporter MexD	1	-40	55.63	151	1
MexE-MexF-OprN Multidrug Efflux System	Multidrug efflux transporter MexF	2	-67.5	62.85	198	2
Copper homeostasis	Multidrug resistance transporter, Bcr/CflA family	1	-37	58.82	136	1
Copper homeostasis: copper tolerance	Periplasmic divalent cation tolerance protein cutA	2	-9	51.79	56	1
Mercury resistance operon	Periplasmic mercury(+2) binding protein	65	-20.19	80.36	60.25	12
Mercuric reductase	PF00070 family, FAD-dependent NAD(P)-disulphide oxidoreductase	3	-16	64.95	67.33	3
Cobalt-zinc-cadmium resistance	Probable Co/Zn/Cd efflux system membrane fusion protein	8	-41	74.57	101	8
The mdtABCD multidrug resistance cluster	Probable RND efflux membrane fusion protein	14	-64.31	78.82	152.81	10
Zinc resistance	Response regulator of zinc sigma-54-dependent two-component system	3	-43.67	61.76	142.67	3
Multidrug Resistance Efflux Pumps	RND efflux system, outer membrane lipoprotein CmeC	4	-17	62.86	73.25	4
Multidrug efflux pump in Campylobacter jejuni (CmeABC operon)	RND efflux system, outer membrane lipoprotein CmeC	4	-17	62.86	73.25	4
Erythromycin resistance	rRNA adenine N-6-methyltransferase (EC 2.1.1.48)	1	-106	97.92	192	1
The mdtABCD multidrug resistance cluster	Sensory histidine kinase BaeS	1	-8	55.36	56	1
Aminoglycoside adenylyltransferases	Spectinomycin 9-O-adenylyltransferase	54	-69.4	93.49	138.73	5
Aminoglycoside adenylyltransferases	Streptomycin 3''-O-adenylyltransferase (EC 2.7.7.47)	54	-69.4	93.49	138.73	5
Resistance to chromium compounds	Superoxide dismutase ChrC	5	-9	70.07	41	1
Resistance to chromium compounds	Superoxide dismutase SodM-like protein ChrF	3	-16.2	72.37	52.8	3
Resistance to	Topoisomerase IV subunit A (EC	1	-52	67.65	136	1

fluoroquinolones	5.99.1.-)					
Resistance to fluoroquinolones	Topoisomerase IV subunit B (EC 5.99.1.-)	2	-20	72.33	68	2
Multidrug Resistance Efflux Pumps	Transcription regulator of multidrug efflux pump operon, TetR (AcrR) family	1	-10	67.35	49	1
Cobalt-zinc-cadmium resistance	Transcriptional regulator, MerR family	63	-22.12	68.9	76.46	16
Multidrug Resistance Efflux Pumps	Type I secretion outer membrane protein, TolC precursor	2	-9	60.77	52.5	2
Methicillin resistance in Staphylococci	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase (EC 6.3.2.13)	1	-19	79.66	59	1
Methicillin resistance in Staphylococci	UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate--D-alanyl-D-alanine ligase (EC 6.3.2.10)	1	-8	60	45	1
Methicillin resistance in Staphylococci	Undecaprenyl-phosphate N-acetylglucosaminyl 1-phosphate transferase (EC 2.7.8.-)	5	-11.4	67.26	48.6	5
Resistance to Vancomycin	Vancomycin B-type resistance protein VanW	1	-9	60.87	46	1

Seed subsystems categorization level 1: Virulence, Disease and Defense, plus level 2: Resistance to antibiotics and toxic compounds. Metagenome entry: 4464065.3

Supplementary Table S8:
Abundances and number of hits to functions within the SEED subcategory 'Resistance to antibiotics and toxic compounds'. Dataset Morges 2009.

function	abun-dance	avg eValue	avg % ident	avg align len	# hits
Cystine ABC transporter, permease protein	2	-8.5	61.87	49	2
D-cysteine desulfhydrase (EC 4.4.1.15)	1	-6	62.5	40	1
Spectinomycin 9-O-adenylyltransferase	78	-42.44	92.16	92.66	9
Streptomycin 3''-O-adenylyltransferase (EC 2.7.7.47)	78	-42.44	92.16	92.66	9
Arsenate reductase (EC 1.20.4.1)	2	-23	96.83	55	2
Arsenical pump-driving ATPase (EC 3.6.3.16)	4	-21	75.03	65.25	4
Arsenical resistance operon repressor	1	-13	70.59	51	1
Arsenical-resistance protein ACR3	2	-22.5	76.64	66.5	2
Beta-lactamase	157	-19.99	65.83	71.96	47
Beta-lactamase (EC 3.5.2.6)	148	-20.94	65.49	74.79	35
Beta-lactamase AmpS	1	-14	70.37	54	1
Beta-lactamase class A	1	-4	66.67	30	1
Beta-lactamase class C and other penicillin binding proteins	1	-27	71.25	80	1
Beta-lactamase class D	2	-8.5	64.48	46.5	2
Metal-dependent hydrolases of the beta-lactamase superfamily I	1	-46	69.49	118	1
Metal-dependent hydrolases of the beta-lactamase superfamily II	1	-46	69.49	118	1
Metal-dependent hydrolases of the beta-lactamase superfamily III	1	-46	69.49	118	1
Negative regulator of beta-lactamase expression	1	-11	56.14	57	1
Alpha-ketoglutarate-dependent taurine dioxygenase (EC 1.14.11.17)	1	-22	52.87	87	1
Choloylglycine hydrolase (EC 3.5.1.24)	1	-6	67.65	34	1
Beta-lactamase (EC 3.5.2.6)	148	-20.94	65.49	74.79	35
Beta-lactamase class A	1	-4	66.67	30	1
Copper-translocating P-type ATPase (EC 3.6.3.4)	408	-32.26	80.9	86.32	74
Peptidase M48, Ste24p precursor	1	-19	80	60	1
Transcriptional regulator, MecI family	1	-23	80.6	67	1
Cation efflux system protein CusA	352	-28.96	76.3	82.17	121
Cd(II)/Pb(II)-responsive transcriptional regulator	48	-17.8	65.86	68.2	12
Cobalt-zinc-cadmium resistance protein	376	-28	75.78	80.84	141
Cobalt-zinc-cadmium resistance protein CzcA	352	-28.96	76.3	82.17	121
Cobalt-zinc-cadmium resistance protein CzcD	14	-22.65	72.48	74.75	14
Cobalt/zinc/cadmium efflux RND transporter, membrane fusion protein, CzcB family	83	-27.42	78.95	79.31	16
Copper sensory histidine kinase CusS	37	-19.05	70.13	70.16	6
Copper-sensing two-component system response regulator CusR	24	-28.33	78.94	79.42	3
DNA-binding heavy metal response regulator	37	-17.94	73.72	59.87	11

Heavy metal RND efflux outer membrane protein, CzcC family	87	-13.47	71.05	56.09	25
Heavy metal sensor histidine kinase	29	-20.55	70.06	73.79	8
Probable Co/Zn/Cd efflux system membrane fusion protein	11	-21.77	68.09	75.08	9
Putative silver efflux pump	1	-15	67.24	58	1
Transcriptional regulator, MerR family	61	-18.71	76.07	61.29	20
Zinc transporter ZitB	1	-16	73.68	57	1
CopG protein	3	-20	64.41	70.67	3
Copper chaperone	3	-10.25	77.25	45	2
Copper resistance protein B	8	-18.12	68.02	63	8
Copper resistance protein D	5	-14.4	69.09	57	4
Copper sensory histidine kinase CusS	37	-19.05	70.13	70.16	6
Copper tolerance protein	7	-15.14	64.64	60.57	7
Copper-sensing two-component system response regulator CusR	24	-28.33	78.94	79.42	3
Copper-translocating P-type ATPase (EC 3.6.3.4)	408	-32.26	80.9	86.32	74
Cytochrome c heme lyase subunit CcmF	1	-25	78.57	70	1
Multicopper oxidase	33	-30.87	76.18	80.22	17
Sensor protein copS (EC 2.7.3.-)	3	-5.5	57.64	42	1
Cytoplasmic copper homeostasis protein cutC	1	-6	75.76	33	1
Magnesium and cobalt efflux protein CorC	2	-12.5	64.75	60.5	2
Periplasmic divalent cation tolerance protein cutA	2	-10.5	58.91	54.5	2
Dimethyladenosine transferase (EC 2.1.1.-)	1	-29	79.27	82	1
Mercuric ion reductase (EC 1.16.1.1)	84	-41.28	90.21	95	11
PF00070 family, FAD-dependent NAD(P)-disulphide oxidoreductase	1	-11	70.21	47	1
Mercuric ion reductase (EC 1.16.1.1)	84	-41.28	90.21	95	11
Mercuric resistance operon coregulator	13	-31.25	88.36	78.12	5
Mercuric resistance operon regulatory protein	32	-24.06	86.24	64.31	9
Mercuric transport protein, MerC	15	-36.57	84.87	84.71	4
Mercuric transport protein, MerE	5	-16.75	87.26	49.75	3
Mercuric transport protein, MerT	39	-17.27	83.88	51.8	11
Periplasmic mercury(+2) binding protein	27	-21.5	84.39	61.6	8
RNA polymerase sigma factor SigB	2	-13	90.43	40.5	2
UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase (EC 6.3.2.13)	6	-11.67	64.8	53.17	6
UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate--D-alanyl-D-alanine ligase (EC 6.3.2.10)	5	-9	82.3	39.5	4
Undecaprenyl-phosphate N-acetylglucosaminyl 1-phosphate transferase (EC 2.7.8.-)	1	-3	74.07	27	1
Acriflavin resistance protein	36	-13.5	70.58	53.13	27
Macrolide export ATP-binding/permease protein MacB (EC 3.6.3.-)	1	-9	57.69	52	1
Macrolide-specific efflux protein MacA	1	-6	81.82	33	1
Multi antimicrobial extrusion protein (Na(+)/drug antiporter), MATE family of MDR efflux pumps	1	-3	74.19	31	1

Multidrug efflux RND transporter MexD	1	-37	81.82	99	1
RND efflux system, inner membrane transporter CmeB	7	-26	72.6	81.56	7
RND efflux system, outer membrane lipoprotein CmeC	4	-15	62.58	67.75	4
RND efflux system, outer membrane lipoprotein, NodT family	1	-3	71.43	28	1
Transcription repressor of multidrug efflux pump acrAB operon, TetR (AcrR) family	1	-4	55.1	49	1
Type I secretion outer membrane protein, TolC precursor	3	-14.67	70.51	62.33	3
RND efflux system, inner membrane transporter CmeB	7	-26	72.6	81.56	7
RND efflux system, outer membrane lipoprotein CmeC	4	-15	62.58	67.75	4
Sensor histidine kinase VanS (EC 2.7.3.-)	1	-4	100	21	1
Chromate resistance protein ChrB	17	-15.62	71.98	58.38	9
Chromate transport protein ChrA	10	-27.87	75.37	80.67	8
Superoxide dismutase ChrC	5	-6.33	69.4	35.67	2
Superoxide dismutase SodM-like protein ChrF	13	-9.22	82.69	33.67	6
DNA gyrase subunit A (EC 5.99.1.3)	21	-25.83	73.93	75.28	18
DNA gyrase subunit B (EC 5.99.1.3)	11	-35.5	79.79	90.9	9
Topoisomerase IV subunit A (EC 5.99.1.-)	4	-37	74.14	98	4
Topoisomerase IV subunit B (EC 5.99.1.-)	6	-20.83	83.16	59.83	5
Multidrug transporter MdtC	1	-32	67	100	1
Probable RND efflux membrane fusion protein	18	-13.64	66.59	58.07	10
Sensory histidine kinase BaeS	1	-5	68.97	29	1
Response regulator of zinc sigma-54-dependent two-component system	3	-15.67	62.94	68.33	3

Seed subsystems categorization level 1: Virulence, Disease and Defense, plus level 2: Resistance to antibiotics and toxic compounds. Metagenome entry: 4464073.3

Supplementary Table S9. Abundance and number of hits in the sublevel 2 'Resistance to antibiotics and toxic compounds' in the Visp 2009 plasmid metagenome.

Level 3	function	abun-dance	avg eValue	avg % ident	avg align len	# hits
Adaptation to d-cysteine	Cystine ABC transporter, permease protein	1	-17	54.88	82	1
Aminoglycoside adenylyltransfe-rases	Spectinomycin 9-O-adenylyltransferase	44	-12.52	95.43	37.29	4
Aminoglycoside adenylyltransfe-rases	Spectinomycin 9-O-adenylyltransferase	1	-11	94.29	35	1
Aminoglycoside adenylyltransfe-rases	Streptomycin 3''-O-adenylyltransferase (EC 2.7.7.47)	44	-12.52	95.43	37.29	4
Aminoglycoside adenylyltransfe-rases	Streptomycin 3''-O-adenylyltransferase (EC 2.7.7.47)	1	-11	94.29	35	1
Arsenic resistance	Arsenate reductase (EC 1.20.4.1)	1369	-19.94	78.28	61.26	36
Arsenic resistance	Arsenate reductase (EC 1.20.4.1)	19	-37.5	73.68	102	8
Arsenic resistance	Arsenic resistance protein ArsH	1030	-32.97	85.56	80.41	27
Arsenic resistance	Arsenic resistance protein ArsH	5	-74.17	89.86	150	4
Arsenic resistance	Arsenical pump-driving ATPase (EC 3.6.3.16)	44	-18.38	70.75	65.54	17
Arsenic resistance	Arsenical pump-driving ATPase (EC 3.6.3.16)	4	-21	73.06	67.75	3
Arsenic resistance	Arsenical resistance operon repressor	3	-6	66.5	35.33	3
Arsenic resistance	Arsenical resistance operon repressor	1	-8	55.56	45	1
Arsenic resistance	Arsenical-resistance protein ACR3	3249	-29.88	81.63	79.9	35
Arsenic resistance	Arsenical-resistance protein ACR3	29	-64.3	74.23	157.35	15
Beta-lactamase	Beta-lactamase	116	-20.57	63.9	74.62	26
Beta-lactamase	Beta-lactamase	8	-26.67	60.89	99.17	6
Beta-lactamase	Beta-lactamase (EC 3.5.2.6)	108	-20.13	61.23	77.56	17
Beta-lactamase	Beta-lactamase (EC 3.5.2.6)	8	-26.67	60.89	99.17	6
Beta-lactamase	Beta-lactamase class C and other penicillin binding proteins	7	-23.4	71.15	71.4	7
Beta-lactamase	Metal-dependent hydrolases of the beta-lactamase superfamily I	27	-16.8	65.55	61.93	13
Beta-lactamase	Metal-dependent hydrolases of the beta-lactamase superfamily I	1	-13	70.21	47	1
Beta-lactamase	Metal-dependent hydrolases of the beta-lactamase superfamily II	1	-23	65.28	72	1
Beta-lactamase	Metal-dependent hydrolases of the beta-lactamase superfamily III	1	-23	65.28	72	1
Bile hydrolysis	Alpha-ketoglutarate-dependent taurine dioxygenase (EC 1.14.11.17)	19	-22.83	70.63	72.33	5

Bile hydrolysis	Alpha-ketoglutarate-dependent taurine dioxygenase (EC 1.14.11.17)	1	-22	75.36	69	1
Bile hydrolysis	Choloylglycine hydrolase (EC 3.5.1.24)	2	-27.5	68.53	84.5	2
BlaR1 Family Regulatory Sensor-transducer Disambiguation	Beta-lactamase (EC 3.5.2.6)	108	-20.13	61.23	77.56	17
BlaR1 Family Regulatory Sensor-transducer Disambiguation	Beta-lactamase (EC 3.5.2.6)	8	-26.67	60.89	99.17	6
BlaR1 Family Regulatory Sensor-transducer Disambiguation	Copper-translocating P-type ATPase (EC 3.6.3.4)	491	-30.54	74.97	89.21	131
BlaR1 Family Regulatory Sensor-transducer Disambiguation	Copper-translocating P-type ATPase (EC 3.6.3.4)	32	-50.64	74.99	131.21	25
BlaR1 Family Regulatory Sensor-transducer Disambiguation	Peptidase M48, Ste24p precursor	2	-43.5	85.33	102.5	2
BlaR1 Family Regulatory Sensor-transducer Disambiguation	Regulatory sensor-transducer, BlaR1/MecR1 family	1	-7	64.1	39	1
BlaR1 Family Regulatory Sensor-transducer Disambiguation	Transcriptional repressor, BlaI/MecI family	1	-50	86.44	118	1
Cadmium resistance	Cadmium efflux system accessory protein	1	-30	61.17	103	1
Cadmium resistance	Cadmium resistance protein	2	-14.5	89.17	44.5	1
Cadmium resistance	Cadmium-transporting ATPase (EC 3.6.3.3)	8	-20.43	71.16	71.43	3
Cadmium resistance	Cadmium-transporting ATPase (EC 3.6.3.3)	1	-18	69.12	68	1
Cobalt-zinc-cadmium resistance	Cadmium-transporting ATPase (EC 3.6.3.3)	8	-20.43	71.16	71.43	3
Cobalt-zinc-cadmium resistance	Cadmium-transporting ATPase (EC 3.6.3.3)	1	-18	69.12	68	1
Cobalt-zinc-cadmium resistance	Cation efflux system protein CusA	59	-28.92	74.56	85.55	41
Cobalt-zinc-cadmium resistance	Cd(II)/Pb(II)-responsive transcriptional regulator	1	-14	68.63	51	1
Cobalt-zinc-cadmium resistance	Cd(II)/Pb(II)-responsive transcriptional regulator	1	-46	66.67	126	1
Cobalt-zinc-cadmium resistance	Cobalt-zinc-cadmium resistance protein	293	-28.88	75.32	82.77	67

Cobalt-zinc-cadmium resistance	Cobalt-zinc-cadmium resistance protein	34	-45.91	72.51	121.09	16
Cobalt-zinc-cadmium resistance	Cobalt-zinc-cadmium resistance protein CzcA	61	-28.72	74.64	85.06	43
Cobalt-zinc-cadmium resistance	Cobalt-zinc-cadmium resistance protein CzcD	196	-26.84	74.53	77.37	17
Cobalt-zinc-cadmium resistance	Cobalt-zinc-cadmium resistance protein CzcD	28	-46.11	71.19	124	13
Cobalt-zinc-cadmium resistance	Cobalt/zinc/cadmium efflux RND transporter, membrane fusion protein, CzcB family	17	-18.62	71.27	65.25	12
Cobalt-zinc-cadmium resistance	Copper sensory histidine kinase CusS	1	-37	61.72	128	1
Cobalt-zinc-cadmium resistance	Copper-sensing two-component system response regulator CusR	3	-24.5	81.86	71.5	2
Cobalt-zinc-cadmium resistance	DNA-binding heavy metal response regulator	5	-28.4	73.39	83.2	5
Cobalt-zinc-cadmium resistance	Heavy metal RND efflux outer membrane protein, CzcC family	7	-14.86	70.02	60.57	7
Cobalt-zinc-cadmium resistance	Heavy metal resistance transcriptional regulator HmrR	28	-17.67	65.59	67.67	9
Cobalt-zinc-cadmium resistance	Heavy metal resistance transcriptional regulator HmrR	5	-24	68.29	79	3
Cobalt-zinc-cadmium resistance	Heavy metal sensor histidine kinase	3	-21	60.72	88	2
Cobalt-zinc-cadmium resistance	Heavy metal sensor histidine kinase	1	-49	71.74	138	1
Cobalt-zinc-cadmium resistance	Hypothetical protein involved in heavy metal export	3	-24.17	71.27	80.83	3
Cobalt-zinc-cadmium resistance	Probable Co/Zn/Cd efflux system membrane fusion protein	2	-14.5	72.36	53.5	2
Cobalt-zinc-cadmium resistance	Probable cadmium-transporting ATPase (EC 3.6.3.3)	2	-18	63.24	68	1
Cobalt-zinc-cadmium resistance	Putative silver efflux pump	2	-33	78.96	102	2
Cobalt-zinc-cadmium resistance	Transcriptional regulator, MerR family	35	-13.27	69.25	53.5	15
Cobalt-zinc-cadmium resistance	Transcriptional regulator, MerR family	5	-38	73.96	109.5	2
Copper	Blue copper oxidase CueO	2	-13.33	63.88	55.67	2

homeostasis	precursor				
Copper homeostasis	Blue copper oxidase CueO precursor	1	-14.33	66.26	57.33	1
Copper homeostasis	CopG protein	36	-25.7	75.43	72.3	6
Copper homeostasis	CopG protein	6	-43.75	76.45	105.25	4
Copper homeostasis	Copper chaperone	7	-6.17	69.66	36.17	4
Copper homeostasis	Copper resistance protein B	3	-20.5	71.57	77.5	3
Copper homeostasis	Copper sensory histidine kinase CusS	1	-37	61.72	128	1
Copper homeostasis	Copper tolerance protein	3	-20.33	79.54	61.33	3
Copper homeostasis	Copper-sensing two-component system response regulator CusR	3	-24.5	81.86	71.5	2
Copper homeostasis	Copper-translocating P-type ATPase (EC 3.6.3.4)	491	-30.54	74.97	89.21	131
Copper homeostasis	Copper-translocating P-type ATPase (EC 3.6.3.4)	32	-50.64	74.99	131.21	25
Copper homeostasis	Cu(I)-responsive transcriptional regulator	23	-17.5	63.89	67.75	12
Copper homeostasis	Cu(I)-responsive transcriptional regulator	3	-28	64.5	89.67	3
Copper homeostasis	Cytochrome c heme lyase subunit CcmF	4	-18.5	72.96	61.75	3
Copper homeostasis	Multicopper oxidase	49	-18.64	66.94	67.08	19
Copper homeostasis	Multicopper oxidase	6	-16.71	62.92	65.29	4
Copper homeostasis	Multidrug resistance transporter, Bcr/CflA family	1	-10	75	40	1
Copper homeostasis: copper tolerance	Copper homeostasis protein CutE	5	-11	60.66	51.5	4
Copper homeostasis: copper tolerance	Magnesium and cobalt efflux protein CorC	2	-7	74.26	40	2
Erythromycin resistance	Dimethyladenosine transferase (EC 2.1.1.-)	1	-22	58.62	87	1
Fosfomycin resistance	Fosfomycin resistance protein FosX	1	-32	80.72	83	1
Mercuric reductase	Mercuric ion reductase (EC 1.16.1.1)	187	-33.43	78.03	90.66	27
Mercuric reductase	Mercuric ion reductase (EC 1.16.1.1)	2	-22.5	75.47	76.5	2
Mercuric reductase	PF00070 family, FAD-dependent NAD(P)-disulphide oxidoreductase	1	-22	62.5	80	1
Mercury resistance operon	Mercuric ion reductase (EC 1.16.1.1)	187	-33.43	78.03	90.66	27
Mercury resistance operon	Mercuric ion reductase (EC 1.16.1.1)	2	-22.5	75.47	76.5	2
Mercury resistance operon	Mercuric resistance operon coregulator	1	-12	92.31	39	1
Mercury resistance	Mercuric resistance operon	59	-27.12	86.11	69.06	12

operon	regulatory protein					
Mercury resistance operon	Mercuric resistance operon regulatory protein	17	-42	93.98	92.12	6
Mercury resistance operon	Mercuric transport protein, MerE	1	-7	93.1	29	1
Mercury resistance operon	Mercuric transport protein, MerT	70	-21.82	82.01	59.43	15
Mercury resistance operon	Mercuric transport protein, MerT	16	-27	81.1	70.88	6
Mercury resistance operon	Periplasmic mercury(+2) binding protein	11	-16.67	72.99	59.22	6
Methicillin resistance in Staphylococci	UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate--D-alanyl-D-alanine ligase (EC 6.3.2.10)	3	-5	65.81	37.67	3
Methicillin resistance in Staphylococci	Undecaprenyl-phosphate N-acetylglucosaminyl 1-phosphate transferase (EC 2.7.8.-)	13	-12.8	66.53	52.9	9
Methicillin resistance in Staphylococci	Undecaprenyl-phosphate N-acetylglucosaminyl 1-phosphate transferase (EC 2.7.8.-)	5	-7.8	65.31	43.8	3
MexE-MexF-OprN Multidrug Efflux System	Multidrug efflux transporter MexF	2	-23.67	57.5	91.67	2
Multidrug Resistance Efflux Pumps	Acriflavin resistance protein	81	-17.33	64.49	69.1	28
Multidrug Resistance Efflux Pumps	Acriflavin resistance protein	6	-17.33	61.67	72.83	5
Multidrug Resistance Efflux Pumps	Macrolide export ATP-binding/permease protein MacB (EC 3.6.3.-)	8	-27.62	80.58	76.88	6
Multidrug Resistance Efflux Pumps	Macrolide-specific efflux protein MacA	4	-16	63.45	68.5	4
Multidrug Resistance Efflux Pumps	Multi antimicrobial extrusion protein (Na(+)/drug antiporter), MATE family of MDR efflux pumps	4	-5.67	64.43	37.33	1
Multidrug Resistance Efflux Pumps	Multidrug-efflux transporter, major facilitator superfamily (MFS) (TC 2.A.1)	2	-22	58.94	87.33	2
Multidrug Resistance Efflux Pumps	Probable transcription regulator protein of MDR efflux pump cluster	1	-23	69.74	76	1
Multidrug Resistance Efflux Pumps	RND efflux system, inner membrane transporter CmeB	20	-22.2	69.23	75.1	9
Multidrug Resistance Efflux Pumps	RND efflux system, inner membrane transporter CmeB	3	-43	73.96	121	3
Multidrug Resistance Efflux Pumps	RND efflux system, outer membrane lipoprotein CmeC	9	-21	68.74	70.71	7
Multidrug Resistance Efflux Pumps	RND efflux system, outer membrane lipoprotein, NodT family	3	-15	65.43	62	2

Multidrug Resistance Efflux Pumps	Transcription repressor of multidrug efflux pump acrAB operon, TetR (AcrR) family	3	-6.33	62.37	42.67	3
Multidrug Resistance Efflux Pumps	Type I secretion outer membrane protein, TolC precursor	3	-19.67	63.45	82.33	3
Multidrug efflux pump in Campylobacter jejuni (CmeABC operon)	RND efflux system, inner membrane transporter CmeB	20	-22.2	69.23	75.1	9
Multidrug efflux pump in Campylobacter jejuni (CmeABC operon)	RND efflux system, inner membrane transporter CmeB	3	-43	73.96	121	3
Multidrug efflux pump in Campylobacter jejuni (CmeABC operon)	RND efflux system, outer membrane lipoprotein CmeC	9	-21	68.74	70.71	7
Multiple Antibiotic Resistance MAR locus	Multiple antibiotic resistance protein MarC	6	-13.25	72.07	52.75	4
Multiple Antibiotic Resistance MAR locus	Multiple antibiotic resistance protein MarC	1	-30	67.68	99	1
Polymyxin Synthetase Gene Cluster in Bacillus	Polymyxin synthetase PmxA	1	-9	62.75	51	1
Resistance to chromium compounds	Chromate resistance protein ChrB	1	-16	93.48	46	1
Resistance to chromium compounds	Chromate transport protein ChrA	8	-21.62	71.33	71.12	8
Resistance to chromium compounds	Chromate transport protein ChrA	1	-30	71.28	94	1
Resistance to chromium compounds	Superoxide dismutase ChrC	1	-69	96.9	129	1
Resistance to chromium compounds	Superoxide dismutase SodM-like protein ChrF	2	-29.5	74.27	84	2
Resistance to fluoroquinolones	DNA gyrase subunit A (EC 5.99.1.3)	4	-42.75	76.91	113.75	4
Resistance to fluoroquinolones	DNA gyrase subunit B (EC 5.99.1.3)	6	-51.33	84.85	117.33	6
Resistance to fluoroquinolones	DNA gyrase subunit B (EC 5.99.1.3)	3	-22.33	77.14	68.33	3
Resistance to fluoroquinolones	Topoisomerase IV subunit A (EC 5.99.1.-)	4	-16	82	54	4
Resistance to fluoroquinolones	Topoisomerase IV subunit B (EC 5.99.1.-)	1	-83	91.52	165	1
The mdtABCD multidrug resistance cluster	Multidrug transporter MdtB	1	-22	63.22	87	1

The mdtABCD multidrug resistance cluster	Probable RND efflux membrane fusion protein	65	-8.88	64.15	50	5
The mdtABCD multidrug resistance cluster	Probable RND efflux membrane fusion protein	2	-7.5	60.52	47.5	2
Zinc resistance	Response regulator of zinc sigma-54-dependent two-component system	8	-9.14	63.91	47.29	5

Seed subsystems categorization level 1: Virulence, Disease and Defense, plus level 2: Resistance to antibiotics and toxic compounds. Metagenome entry: 4464109.3

Supplementary Table S10.

Accession numbers and sizes of plasmids that were combined to the metagenome dataset PLASMIDS-NCBI.

Accession number	size, bp	Accession number	size, bp
gi|259647811|ref|NC_013265.1|	4955	gi|85060490|ref|NC_007715.1|	10810
gi|259647806|ref|NC_013264.1|	3070	gi|85060466|ref|NC_007714.1|	27240
gi|259910328|ref|NC_013263.1|	35909	gi|85060411|ref|NC_007713.1|	83306
gi|189458505|ref|NC_010813.1|	29037	gi|84798614|ref|NC_007706.1|	3741
gi|219882535|ref|NC_011878.1|	6054	gi|116536719|ref|NC_007682.3|	56634
gi|71725141|ref|NC_007274.1|	131950	gi|83582730|ref|NC_007641.1|	53732
gi|45478502|ref|NC_005813.1|	70159	gi|81230333|ref|NC_007595.1|	46366
gi|206479926|ref|NC_011003.1|	92661	gi|78214253|ref|NC_007515.1|	13762
gi|16082691|ref|NC_003131.1|	70305	gi|78045242|ref|NC_007505.1|	19146
gi|21392893|ref|NC_003981.1|	94829	gi|78045239|ref|NC_007504.1|	1852
gi|224371993|ref|NC_012109.1|	68709	gi|77163517|ref|NC_007483.1|	40420
gi|31795262|ref|NC_004836.1|	70504	gi|76789623|ref|NC_007430.1|	7510
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gi|237640188|ref|NC_012690.1|	148105	gi|73663756|ref|NC_007351.1|	38454
gi|161867876|ref|NC_010119.1|	127212	gi|71061431|ref|NC_007203.1|	6909
gi|55275313|ref|NC_006385.1|	47829	gi|71024880|ref|NC_007191.1|	8663
gi|53793901|ref|NC_006352.1|	68869	gi|70887539|ref|NC_007190.1|	10402
gi|32469973|ref|NC_004998.1|	125491	gi|70724934|ref|NC_007188.1|	10816
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gi|84310666|ref|NC_007680.1|	54344	gi|70724865|ref|NC_007184.1|	27240
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gi|31795117|ref|NC_004840.1|	64508	gi|67078390|ref|NC_007107.1|	9150
gi|257070292|ref|NC_013176.1|	76494	gi|67078381|ref|NC_007106.1|	8191

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gi|133756440|ref|NC_009133.1|	94289	gi|56899872|ref|NC_006578.1|	77112
gi|133756175|ref|NC_009132.1|	63946	gi|56707090|ref|NC_006571.1|	36955
gi|133755324|ref|NC_009131.1|	65288	gi|56687495|ref|NC_006528.1|	846
gi|124111993|ref|NC_008821.1|	39714	gi|56410437|ref|NC_006509.1|	47890
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gi|93004786|ref|NC_007968.1|	41221	gi|10954579|ref|NC_002097.1|	5467
gi|92429516|ref|NC_007962.1|	3828	gi|10954553|ref|NC_001811.1|	8285
gi|89898813|ref|NC_007900.1|	7552	gi|10954545|ref|NC_001771.1|	5350
gi|85057971|ref|NC_007720.1|	4316	gi|10954476|ref|NC_001337.1|	11014
gi|85057963|ref|NC_007719.1|	5104	gi|10954462|ref|NC_001336.1|	13514
gi|85057958|ref|NC_007718.1|	4009	gi|76803367|ref|NC_007427.1|	130989
gi|85057952|ref|NC_007717.1|	3972	gi|76803317|ref|NC_007428.1|	23486
gi|16356922|ref|NC_003158.1|	16341	gi|207258116|ref|NC_011299.1|	28649

Supplementary Table S11. List of full REP_AC names used for phylogenetic assignment.

Contig or plasmid	Source	GenBank Accession	Species
M_c01	Morges		
M_c02	Morges		
M_c03	Morges		
M_c10	Morges		
M_c11	Morges		
M_c12	Morges		
M_c14	Morges		
M_c17	Morges		
M_c18	Morges		
M_c19	Morges		
M_c1904	Morges		
M_c22	Morges		
M_c226	Morges		
M_c278	Morges		
M_C3061	Morges		
M_c31	Morges		
M_c34	Morges		
M_c35	Morges		
M_c36	Morges		
M_c407	Morges		
M_c48	Morges		
M_c519	Morges		
M_c52	Morges		
M_c53	Morges		
M_c55	Morges		
M_c57	Morges		
M_c596	Morges		
M_c711	Morges		
M_c81	Morges		
V_c02227	Visp		
V_c02897	Visp		
V_c02909	Visp		
V_c03015	Visp		
CHR_		YP_002442095.1	[Pseudomonas aeruginosa LESB58]
CHR_GEI_SGI1-V		AED98694.1	[Proteus mirabilis]
CHR		EGQ98804.1	[Vibrio cholerae HE39]
CHR		YP_001641356.1	[Methylobacterium extorquens PA1]
CHR		YP_001754236.1	[Methylobacterium radiotolerans JCM 2831]
CHR		YP_004011810.1	[Rhodomicrobium vannielii ATCC 17100]
CHR		YP_004129265.1	[Taylorella equigenitalis MCE9]

CHR		YP_004302329.1	[Polymorphum gilvum SL003B-26A1]
CHR		YP_109866.1	[Burkholderia pseudomallei K96243]
CHR		YP_584967.1	[Cupriavidus metallidurans CH34]
CHR		YP_965444.1	[Shewanella sp. W3-18-1]
CHR		YP_968773.1	[Acidovorax citrulli AAC00-1]
CHR2		YP_001796446.1	[Cupriavidus taiwanensis LMG 19424]
cntg_1104196056139		ZP_01974633.1	[Vibrio cholerae B33]
cntg_11679kb		EGR08494.1	[Vibrio cholerae HE48]
cntg_247		ZP_00682678.1	[Xylella fastidiosa Ann-1]
cntg		ZP_02413388.1	[Burkholderia pseudomallei 14]
cntg00242		EGO80808.1	[Xylella fastidiosa EB92.1]
cntg00243		ZP_06895960.1	[Roseomonas cervicalis ATCC 49957]
cntg01383		ZP_08870552.1	[Azospirillum amazonense Y2]
cntg99		ZP_05880298.1	[Vibrio furnissii CIP 102972]
cntgNZ_ABBK01000836		ZP_02449509.1	[Burkholderia pseudomallei 91]
cntgPP100942		ZP_08124617.1	[Pseudonocardia sp. P1]
megaplasmid		YP_003749016.1	[Ralstonia solanacearum PSI07]
megaplasmid		YP_587945.1	[Cupriavidus metallidurans CH34]
OUT_RepA_C		EIJ25216.1	[Bifidobacterium longum subsp. longum 2-2B]
pAB510e		YP_003452890.1	[Azospirillum sp. B510]
pACMV1		YP_004277221.1	[Acidiphilium multivorum AIU301]
pAG1		YP_001965988.1	[Xanthomonas axonopodis pv. glycines]
pAPA01-020		YP_003189510.1	[Acetobacter pasteurianus IFO 3283-01]
pBFp1		AAQ94182.1	[uncultured bacterium]
pBGLA_1p		YP_004362442.1	[Burkholderia gladioli BSR3]
pBGLA_3p		YP_004351116.1	[Burkholderia gladioli BSR3]
pBGLU_4p			YP_002913205.1
pBI1063		AAP82047.1	[Stenotrophomonas maltophilia] aa
pCRY		AAO18205.1	RepA [Corynebacterium glutamicum]
pGLOV01		YP_001953900.1	[Geobacter lovleyi SZ]
pGOX2		YP_190413.1	[Gluconobacter oxydans 621H]
pGXY020		YP_004857926.1	[Gluconacetobacter xylinus NBRC 3288]
pHALHY02		YP_004451395.1	[Haliscomenobacter hydrossis DSM 1100]
pHLHK22		YP_001691017.1	[Laribacter hongkongensis]
pIPO2T		NP_444546.1	[uncultured bacterium
pKLC102		AAP22621.1	[Pseudomonas aeruginosa C]
plasmid_		YP_380325.1	[Geobacter metallireducens GS-15]
plasmid_4		YP_004210585.1	[Acidobacterium sp. MP5ACTX9]
plasmid2		YP_004219735.1	[Granulicella tundricola MP5ACTX9]
plasmid90kDa		CAB88201.1	[Azospirillum brasilense]
pLAtc2		YP_004750509.1	[Acidithiobacillus caldus SM-1]
pMG101		BAA89406.1	[Rhodopseudomonas palustris]
pMOL98		ACT97177.1	[Synthetic plasmid pMOL98]
pMRAD02		YP_001766469.1	[Methylobacterium radiotolerans JCM 2831]

pPAES01		YP_002019746.1	[Prosthecochloris aestuarii DSM 271]
pPRO2		YP_899682.1	[Pelobacter propionicus DSM 2379]
pR7K		YP_001874895.1	[Providencia rettgeri]
pRM21		NP_044344.1	[Rhodothermus marinus]
pRMAR01		YP_003292130.1	[Rhodothermus marinus DSM 4252]
pRSC35		CBJ36157.1	[Ralstonia solanacearum CMR15]
pSB102		NP_361015.1	[uncultured bacterium]
pSLIN03		YP_003391749.1	[Spirosoma linguale DSM 74]
pSM103mini		YP_003858293.1	[Sphingopyxis macrogoltabida]
pTer331_01		YP_001672027.1	[Collimonas fungivorans]
pUnnamed54kb		YP_425065.1	[Rhodospirillum rubrum ATCC 11170]
pXAC64		NP_644784.1	[Xanthomonas axonopodis pv. citri str. 306]
pXap41		YP_004888046.1	[Xanthomonas arboricola CFBP 5530]
pXCV183		YP_361657.1	[Xanthomonas campestris pv. vesicatoria str. 85-10]
pXV2		AF201825_1	[Xanthomonas euvesicatoria]