

Table S1. Details of mutation datasets.

Groups	Species	Approach	Average generations during MA
Bacteria	<i>Agrobacterium tumefaciens</i> C58	MA	5819
Bacteria	<i>Arthrobacter</i> sp. KBS0703	MA	5194
Bacteria	<i>Bacillus subtilis</i> NCIB 3610	MA	5077
Bacteria	<i>Burkholderia cenocepacia</i> HI2424	MA	5554
Bacteria	<i>Caulobacter crescentus</i> NA1000	MA	4284
Bacteria	<i>Colwellia psychrerythraea</i> 34H	MA	1078
Bacteria	<i>Deinococcus radiodurans</i> BAA-816	MA	5961
Bacteria	<i>Escherichia coli</i> K-12 MG1655	MA	1682
Bacteria	<i>Flavobacterium</i> sp. KBS0721	MA	5940
Bacteria	<i>Gemmata obscuriglobus</i> DSM5831	MA	2336
Bacteria	<i>Janthinobacterium lividum</i> KBS0711	MA	5023
Bacteria	<i>Kineococcus radiotolerans</i> SRS30216	MA	4724
Bacteria	<i>Lactococcus lactis</i> DSMZ20481	MA	3973
Bacteria	<i>Mesoplasma florum</i> L1	MA	2351
Bacteria	<i>Micrococcus</i> sp. KBS0714	MA	3834
Bacteria	<i>Mycobacterium smegmatis</i> MC2 155	MA	4900
Bacteria	<i>Rhodobacter sphaeroides</i> ATCC17025	MA	4544
Bacteria	<i>Ruegeria pomeroyi</i> DSS-3	MA	5386
Bacteria	<i>Staphylococcus aureus</i> ATCC 25923	MA	2716
Bacteria	<i>Staphylococcus epidermidis</i> ATCC 12228	MA	7101
Bacteria	<i>Teredinibacter turnerae</i> T7901	MA	3025
Bacteria	<i>Vibrio cholerae</i> 2740-80	MA	6453
Bacteria	<i>Vibrio fischeri</i> ES114	MA	5187
MultiEuk	<i>Arabidopsis thaliana</i> Col-0	MA	30
MultiEuk	<i>Caenorhabditis elegans</i> N2	MA	255
MultiEuk	<i>Daphnia pulex</i> ASEX without ASEX-12	MA	196
MultiEuk	<i>Drosophila melanogaster</i> IVE	MA	147
MultiEuk	<i>Ficedula albicollis</i>	Trio	N/A

MultiEuk	Homo sapiens CEU, YRI, Iceland	Trio	N/A
MultiEuk	Mus musculus C57BL/6	MA	12
MultiEuk	Oryza sativa	Trio	N/A
MultiEuk	Pan troglodytes verus	Trio	N/A
UniEuk	Chlamydomonas reinhardtii (CC1373, CC1952, CC2342, CC2937)	MA	940
UniEuk	Plasmodium falciparum (3D7,Dd2,HB3,KH1-01,KH2-01,W2)	MA	117
UniEuk	Rhodotorula toruloides ATCC10788	MA	3486
UniEuk	Saccharomyces cerevisiae S288C	MA	2062
UniEuk	Schizosaccharomyces pombe ED668	MA	1716
UniEuk	Sphaeroforma arctica JP610	MA	1789
<p>abbreviations: 0-fold, nonsynonymous sites; 2-fold, two fold degenerate sites; 4-fold, four fold degenerate sites; BPS, base-pair substitution; delta, difference in G/C content between different genomic sites; Equilibrium, genome G/C composition at mutation equilibrium; inter, intergenic region; m, mutation bias to the G/C direction: $A/T > G/C \div G/C > A/T$ mutation rate; MA, mutation accumulation; MultiEuk, multicellular eukaryotes; neutral, G/C content based on the neutral expectation, i.e. G/C content solely determined by mutation rate; S, popula</p>			

- ¹ Based on list of base substitutions in the supplemental materials;
² CC2344 and CC2931 are excluded due to presence of mutator lines;
³ Mean mutation rate of three human populations;
⁴ Mutation rate per erythrocytic life cycle per site;
⁵ All standard errors of these G/C compositions are < 0.001

Abbreviations:

BPS, base-pair substitution;

Equilibrium, genome G/C composition at mutation equilibrium;

m, mutation bias to the G/C direction: $A/T > G/C \div G/C > A/T$ mutation rate;

MA, mutation accumulation;

MultiEuk, multicellular eukaryotes;

S, population-scaled selection strength;

Trio, parents-offspring trio genome sequencing;

UniEuk, unicellular eukaryotes

No. of lines/trios	No. sites analyzed per line ($\times 10^6$)	Total BPS ¹	BPS rate ($\times 10^{-10}$ / nucleotide site / generation)	G:C>A:T ($\times 10^{-10}$ / site / generation)	G:C>T:A ($\times 10^{-10}$ / site / generation)
47	5.37	425	2.92	1.91	0.75
58	4.70	451	3.18	1.95	0.68
50	4.25	350	3.28	2.80	0.51
47	7.70	245	1.33	0.70	0.23
44	3.97	259	3.46	2.11	0.14
84	5.27	400	8.38	9.69	0.94
43	3.03	388	4.99	3.01	0.63
46	4.57	79	2.23	1.50	0.39
43	5.81	580	3.91	4.53	2.75
41	8.64	197	2.38	1.87	0.36
49	3.52	106	1.22	1.33	0.19
44	3.45	280	3.90	3.42	0.28
63	1.95	813	16.62	20.42	18.51
28	0.79	548	97.80	172.19	96.77
60	2.32	170	3.18	1.18	0.84
49	6.77	856	5.27	2.76	1.58
46	4.38	107	1.17	1.31	0.13
47	4.01	161	1.39	0.67	0.07
83	2.77	274	4.38	5.08	3.18
22	2.55	294	7.40	7.45	6.20
42	4.81	640	11.40	11.10	2.22
46	3.83	127	1.07	1.02	0.44
48	4.25	219	2.07	1.80	1.92
5	99.85	99	59.00	98.70	15.32
10	58.38	391	27.00	12.74	17.52
3	120.64	235	40.00	31.78	11.88
8	114.96	732	54.90	58.83	14.58
7	848.30	55	46.00	51.42	5.71

G:C>C:G ($\times 10^{-10}$ / site / generation)	A:T>G:C ($\times 10^{-10}$ / site / generation)	A:T>C:G (\times 10^{-10} / site / generation)	A:T>T:A (\times 10^{-10} / site / generation)	m (mutation bias to the A:T direction)	Equilibrium
0.80	1.32	0.60	0.39	1.3836	0.4195
0.46	1.86	1.05	0.46	0.9050	0.5249
0.17	2.16	0.44	0.46	1.2739	0.4398
0.22	0.60	0.49	0.25	0.8514	0.5401
0.38	3.87	0.61	0.69	0.5011	0.6662
0.83	5.15	0.77	0.57	1.7926	0.3581
0.17	3.43	3.19	0.74	0.5511	0.6447
0.22	0.86	0.86	0.63	1.1003	0.4761
1.64	0.68	0.20	0.43	8.1879	0.1088
0.18	1.55	0.55	0.22	1.0554	0.4865
0.15	0.36	0.15	0.00	2.9555	0.2528
0.60	1.59	0.93	0.22	1.4703	0.4048
2.08	2.21	1.25	0.40	11.2652	0.0815
49.09	13.65	3.15	4.20	16.0060	0.0588
0.36	3.15	1.96	0.28	0.3945	0.7171
0.43	3.95	2.10	0.26	0.7170	0.5824
0.10	0.24	0.07	0.07	4.6487	0.1770
0.13	1.18	0.52	0.35	0.4379	0.6955
0.34	1.33	0.48	0.52	4.5699	0.1795
0.86	1.26	0.81	1.96	6.5888	0.1318
0.98	5.17	1.17	2.12	2.1009	0.3225
0.11	0.31	0.33	0.12	2.2989	0.3031
0.25	0.43	0.40	0.06	4.4600	0.1832
13.61	13.19	7.69	5.49	5.4614	0.1548
4.78	4.44	4.76	9.30	3.2908	0.2331
3.21	9.27	5.76	7.27	2.9036	0.2562
8.69	13.08	6.20	11.86	3.8077	0.2080
9.52	19.62	6.04	4.53	2.2263	0.3100

GC composition at different genomic sites		
95% confidence interval of equilibrium G/C	Genome-wide ⁵	Nonsynonymous (0-fold) ⁵
(0.3258, 0.5132)	0.5904	0.4456
(0.4158, 0.634)	0.6623	0.4842
(0.3425, 0.5371)	0.4335	0.3597
(0.3842, 0.6961)	0.6679	0.4774
(0.4913, 0.8411)	0.6717	0.4789
(0.2848, 0.4313)	0.3801	0.3694
(0.5112, 0.7782)	0.6659	0.4776
(0.2423, 0.7099)	0.5079	0.4070
(0.0834, 0.1343)	0.3413	0.3375
(0.3341, 0.6389)	0.6718	0.4845
(0.122, 0.3836)	0.6060	0.4505
(0.2755, 0.5341)	0.7425	0.5185
(0.065, 0.098)	0.3545	0.3414
(0.0432, 0.0744)	0.2695	0.2900
(0.4892, 0.945)	0.7304	0.5013
(0.4999, 0.6649)	0.6740	0.4864
(0.0558, 0.2982)	0.6823	0.4844
(0.4339, 0.957)	0.6407	0.4631
(0.1309, 0.2282)	0.3286	0.3243
(0.0921, 0.1714)	0.3205	0.3179
(0.2645, 0.3804)	0.5089	0.4122
(0.1856, 0.4206)	0.4751	0.3872
(0.1264, 0.2399)	0.3835	0.3686
(0.0759, 0.2336)	0.3606	0.4004
(0.1722, 0.2939)	0.3544	0.3944
(0.1788, 0.3335)	0.4054	0.4145
(0.1688, 0.2472)	0.4201	0.4207
(0.1255, 0.4944)	0.4422	0.4156

(0.264, 0.3029)	0.4102	0.4210
(0.1292, 0.2672)	0.4172	0.4287
(0.0953, 0.4216)	0.4356	0.4493
(0.1709, 0.3205)	0.4079	0.4146
(0.2575, 0.3135)	0.6408	0.5749
(0.0744, 0.254)	0.1936	0.2212
(0.4365, 0.6061)	0.6205	0.4902
(0.2571, 0.3975)	0.3815	0.3647
(0.2137, 0.3315)	0.3604	0.3823
(0.1734, 0.2904)	0.4179	0.4331

Two-fold ⁵	Four-fold ⁵	Intergenic ⁵	<i>S_{4-fold}</i>	<i>S_{0-fold}</i>	<i>S_{2-fold}</i>	<i>S_{inter}</i>
0.5508	0.7731	0.5292	1.5507	0.1061	0.5285	0.4418
0.7838	0.8511	0.6211	1.6431	-0.1631	1.1879	0.3943
0.3607	0.4811	0.3624	0.1665	-0.3346	-0.3302	-0.3228
0.7272	0.9195	0.6213	2.2753	-0.2515	0.8195	0.3344
0.7761	0.9014	0.6195	1.5214	-0.7754	0.5524	-0.2036
0.2680	0.3143	0.3233	-0.1964	0.0489	-0.4212	-0.1550
0.7740	0.8947	0.5951	1.5443	-0.6855	0.6351	-0.2108
0.4216	0.6330	0.4212	0.6408	-0.2808	-0.2206	-0.2221
0.2391	0.2713	0.2746	1.1147	1.4283	0.9449	1.1313
0.8296	0.8959	0.6337	2.2062	-0.0082	1.6367	0.6019
0.5869	0.8431	0.5278	2.7649	0.8850	1.4349	1.1951
0.9582	0.9572	0.7281	3.4919	0.4596	3.5164	1.3706
0.2090	0.2489	0.3014	1.3170	1.7648	1.0908	1.5811
0.1455	0.0620	0.2139	0.0560	1.8776	1.0027	1.4716
0.9465	0.9500	0.7312	2.0143	-0.9249	1.9438	0.0705
0.8047	0.8678	0.6147	1.5489	-0.3871	1.0831	0.1344
0.7657	0.9102	0.6531	3.8530	1.4741	2.7209	2.1691
0.6280	0.8771	0.5833	1.1396	-0.9738	-0.3020	-0.4896
0.1911	0.2063	0.2949	0.1720	0.7855	0.0765	0.6476
0.1862	0.1907	0.2640	0.4401	1.1219	0.4107	0.8603
0.4710	0.6097	0.4591	1.1884	0.3876	0.6264	0.5784
0.3720	0.5503	0.4166	1.0344	0.3732	0.3086	0.4957
0.2716	0.2527	0.3403	0.4110	0.9568	0.5087	0.8333
0.4327	0.3367	0.3063	1.0196	1.2937	1.4269	0.8802
0.3805	0.3514	0.3342	0.5782	0.7624	0.7039	0.5018
0.4433	0.4857	0.3977	1.0088	0.7204	0.8383	0.6511
0.5823	0.6095	0.4029	1.7820	1.0171	1.6693	0.9438
0.5819	0.5456	0.4385	0.9832	0.4595	1.1309	0.5532

Insertion/deletion rates ($\times 10^{-10}$ / site / generation) if first reported in this study	Reference genome
	NCBI RefSeq: GCF_000092025.1_ASM9202v1
Insertion rate: 0.25, deletion rate: 0.37	NCBI BioProject: PRJNA373913
	GCF_000186085.1_ASM18608v1
	GCF_000203955.1_ASM20395v1
Insertion rate: 0.33, deletion rate: 0.21	GCF_000022005.1_ASM2200v1
Insertion rate: 0.29, deletion rate: 0.63	GCF_000012325.1_ASM1232v1
	GCA_001638825.1_ASM163882v1
	GCF_000005845.2_ASM584v2
Insertion rate: 0.36, deletion rate: 0.21	PRJNA370526
Insertion rate: 0.13, deletion rate: 0.22	GCF_000171775.1_ASM17177v1
Insertion rate: 0.02, deletion rate: 0.08	GCF_000242815.1_ASM24281v2
Insertion rate: 0.71, deletion rate: 0.88	GCF_000017305.1_ASM1730v1
Insertion rate: 0.35, deletion rate: 0.79	GCF_900088425.1_A12
	GCF_000479355.1_ASM47935v1
Insertion rate: 0.81, deletion rate: 0.75	PRJNA373912
	GCF_000283295.1_ASM28329v1
Insertion rate: 0.07, deletion rate: 0.10	GCF_000016405.1_ASM1640v1
	GCF_000011965.2_ASM1196v2
Insertion rate: 0.14, deletion rate: 0.30	GCF_000756205.1_ASM75620v1
	GCF_000007645.1_ASM764v1
	GCF_000023025.1_ASM2302v1
	GCF_000168915.2_ASM16891v3
	GCF_000011805.1_ASM1180v1
	GCF_000001735.3_TAIR10
	GCF_000002985.6_WBcel235
	PRJEB14656; PA42, version 3.
	GCF_000001215.4_Release_6_plus_ISO1_MT
	GCF_000247815.1_FicAlb1.5

	GCF_000001405.35_GRCh38.p9
	GCF_000001635.25_GRCm38.p5
	GCF_000005425.2_Build_4.0
	GCF_000001515.7_Pan_tro_3.0
	Phytozome, Joint Genome Institute: creinhardtii_281_v5.0
	GCF_000002765.3_ASM276v1
	GCF_000320785.1_RHOziaDV1.0
	GCF_000146045.2_R64
	GCF_000002945.1_ASM294v2
Insertion rate: 0.04, deletion rate: 0.09	GCA_001186125.1 Spha_arctica_JP610_V1

Data and strain sources

Sung et al. (2016) G3 6:2583-2591

This study; strain was from Jay Lennon lab, Indiana University, Bloomington

Sung et al. (2015) Mol. Biol. Evol. 32:1672-1683

Dillon et al. (2015) Genetics 200: 935-946;

This study; strain was from Yves Brun lab, Indiana University, Bloomington

This study; strain was ordered from ATCC (catalogue number: BAA-681)

Long et al. (2015) Mol. Biol. Evol. 32: 2383-2392.

Mutations are based on those of the wild-type negative control,
Long et al. (2016) Proc Natl Acad Sci U S A 113: E2498-E2505

This study; strain was from Jay Lennon lab, Indiana University, Bloomington

This study; strain was ordered from DSMZ (catalogue number: DSM5831)

This study; strain was from Jay Lennon lab, Indiana University, Bloomington

This study; strain was ordered from ATCC (catalogue number: BAA-149)

This study; strain was ordered from DSMZ (catalogue number: DSM20481)

Sung et al. (2012) Proc Natl Acad Sci U S A 109: 18488-18492

This study; strain was from Jay Lennon lab, Indiana University, Bloomington

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This study; strain was ordered from ATCC (catalogue number: ATCC17025)

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This study; strain was ordered from ATCC (catalogue number: ATCC25923)

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Senra et al. in press; strain was ordered from ATCC (catalogue number: ATCC39867)

Dillon et al. (2017) Mol Biol Evol 34: 93-109; Sung et al. (2016) G3 6:2583-2591

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Ossowski et al. (2010) Science 327:92-94.

Denver et al. (2009) Proc Natl Acad Sci U S A. 106: 16310-16314.

Keith et al. (2016) Genome Res. 26:60-69;

Schrider et al. (2013) Genetics 194: 937-954

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Conrad et al. (2011) Nature Genetics 43: 712-714; Kong et al. (2012) Nature 488: 471-475;
Lynch et al. (2016) Nat. Rev. Genet. 17: 704-714.

Uchimura et al. (2015) Genome Res. 25: 1125-1134

Yang et al. (2015) Nature 523:463-467

Venn et al. (2014) Science 344: 1272-1275

Ness et al. (2015) Genome Res. 25: 1739-1749--
mutations of strains CC-2391, CC-2344 are excluded due to presence of mutator MA lines in these two

Hamilton et al. (2017) Nucleic Acids Res 45: 1889-1901.

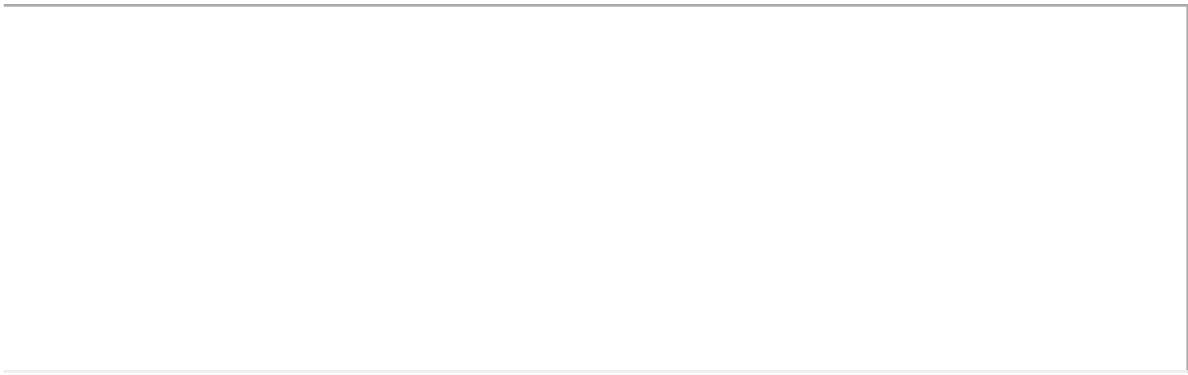
Long et al. (2016) Genome Biol Evol 8: 3815-3821

Zhu et al. (2014) Proc Natl Acad Sci U S A. 111: E2310-E2318.

Farlow et al. (2015) Genetics 201: 737-744

This study; the strain was provided by the Iñaki Ruiz-Trillo lab, Institut de Biologia Evolutiva (CSIC-UPF)

Other notes
peptone yeast extract agar plus (PYE+); culturing temperature: 25 °C
peptone yeast extract agar (PYE); culturing temperature: 25 °C
marine agar; culturing temperature: 10 °C
nutrient agar; culturing temperature: 25 °C
Staley's Maintenance Agar; culturing temperature: 30 °C
nutrient agar; culturing temperature: 25 °C
peptone tryptone yeast extract glucose agar (PTYG); culturing temperature: 25 °C
LB agar; culturing temperature: 25 °C
peptone yeast extract agar (PYE); culturing temperature: 25 °C
nutrient agar; culturing temperature: 30 °C
LB agar; culturing temperature: 37 °C
MMB medium; culturing temperature: 30 °C



⌵ Orange = Fasta/GBK Issue Blue = Baseball Data Missing Red = Multiple file issues
GBK file is fragmented among scaffolds/contigs, currently investigating way to insert whole
only have WT basecalls, no MMR baseball data
de novo assembly. bioproject only contains contigs; no unified fasta/gbk files
WGS shotgun sequence, no completed genome for fast/gbk files
fasta/gbk was assembly only
(Fasta/GBK issue) scaffold level assembly only - does not contain unified sequence data W
no basecall data published
Indel data only published, however no base call supplemental dataset
Sung, et al, 2016 referenced, no baseball data published for this article for S.epidermitis
assembly only?
assembly only

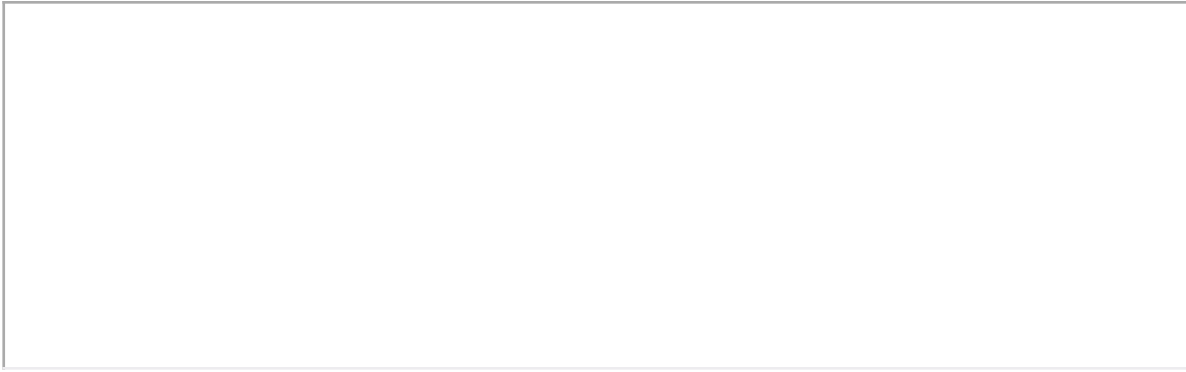


Table S2. List of base-pair substitutions detected in MA lines of the 12 species reported on for

Group	Species	Line name	Chromosome/Scaffold
Bacteria	Arthrobacter sp. KBS0703	AR1	G_contig000013
Bacteria	Arthrobacter sp. KBS0703	AR1	G_contig000013
Bacteria	Arthrobacter sp. KBS0703	AR1	G_contig000040
Bacteria	Arthrobacter sp. KBS0703	AR1	G_contig000040
Bacteria	Arthrobacter sp. KBS0703	AR1	G_contig000040
Bacteria	Arthrobacter sp. KBS0703	AR1	G_contig000043
Bacteria	Arthrobacter sp. KBS0703	AR1	G_contig000057
Bacteria	Arthrobacter sp. KBS0703	AR1	G_contig000058
Bacteria	Arthrobacter sp. KBS0703	AR1	G_contig000058
Bacteria	Arthrobacter sp. KBS0703	AR2	G_contig000012
Bacteria	Arthrobacter sp. KBS0703	AR2	G_contig000026
Bacteria	Arthrobacter sp. KBS0703	AR2	G_contig000026
Bacteria	Arthrobacter sp. KBS0703	AR2	G_contig000028
Bacteria	Arthrobacter sp. KBS0703	AR2	G_contig000040
Bacteria	Arthrobacter sp. KBS0703	AR2	G_contig000043
Bacteria	Arthrobacter sp. KBS0703	AR2	G_contig000045
Bacteria	Arthrobacter sp. KBS0703	AR2	G_contig000048
Bacteria	Arthrobacter sp. KBS0703	AR2	G_contig000057
Bacteria	Arthrobacter sp. KBS0703	AR2	G_contig000067
Bacteria	Arthrobacter sp. KBS0703	AR2	G_contig000071
Bacteria	Arthrobacter sp. KBS0703	AR2	G_contig000089
Bacteria	Arthrobacter sp. KBS0703	AR3	G_contig000015
Bacteria	Arthrobacter sp. KBS0703	AR3	G_contig000026
Bacteria	Arthrobacter sp. KBS0703	AR3	G_contig000028
Bacteria	Arthrobacter sp. KBS0703	AR3	G_contig000038
Bacteria	Arthrobacter sp. KBS0703	AR3	G_contig000040
Bacteria	Arthrobacter sp. KBS0703	AR3	G_contig000040
Bacteria	Arthrobacter sp. KBS0703	AR3	G_contig000045
Bacteria	Arthrobacter sp. KBS0703	AR3	G_contig000057
Bacteria	Arthrobacter sp. KBS0703	AR3	G_contig000064
Bacteria	Arthrobacter sp. KBS0703	AR3	G_contig000067
Bacteria	Arthrobacter sp. KBS0703	AR3	G_contig000067
Bacteria	Arthrobacter sp. KBS0703	AR3	G_contig000072
Bacteria	Arthrobacter sp. KBS0703	AR3	G_contig000074
Bacteria	Arthrobacter sp. KBS0703	AR4	G_contig000013
Bacteria	Arthrobacter sp. KBS0703	AR4	G_contig000021
Bacteria	Arthrobacter sp. KBS0703	AR4	G_contig000032
Bacteria	Arthrobacter sp. KBS0703	AR4	G_contig000040
Bacteria	Arthrobacter sp. KBS0703	AR4	G_contig000048
Bacteria	Arthrobacter sp. KBS0703	AR4	G_contig000073
Bacteria	Arthrobacter sp. KBS0703	AR4	G_contig000073
Bacteria	Arthrobacter sp. KBS0703	AR4	G_contig000074
Bacteria	Arthrobacter sp. KBS0703	AR5	G_contig000013

Bacteria	Arthrobacter sp. KBS0703	AR29	G_contig000038
Bacteria	Arthrobacter sp. KBS0703	AR29	G_contig000044
Bacteria	Arthrobacter sp. KBS0703	AR29	G_contig000050
Bacteria	Arthrobacter sp. KBS0703	AR29	G_contig000057
Bacteria	Arthrobacter sp. KBS0703	AR29	G_contig000068
Bacteria	Arthrobacter sp. KBS0703	AR31	G_contig000026
Bacteria	Arthrobacter sp. KBS0703	AR31	G_contig000026
Bacteria	Arthrobacter sp. KBS0703	AR31	G_contig000028
Bacteria	Arthrobacter sp. KBS0703	AR31	G_contig000040
Bacteria	Arthrobacter sp. KBS0703	AR31	G_contig000065
Bacteria	Arthrobacter sp. KBS0703	AR31	G_contig000067
Bacteria	Arthrobacter sp. KBS0703	AR31	G_contig000089
Bacteria	Arthrobacter sp. KBS0703	AR31	G_contig000093
Bacteria	Arthrobacter sp. KBS0703	AR32	G_contig000002
Bacteria	Arthrobacter sp. KBS0703	AR32	G_contig000012
Bacteria	Arthrobacter sp. KBS0703	AR32	G_contig000038
Bacteria	Arthrobacter sp. KBS0703	AR32	G_contig000038
Bacteria	Arthrobacter sp. KBS0703	AR32	G_contig000043
Bacteria	Arthrobacter sp. KBS0703	AR32	G_contig000055
Bacteria	Arthrobacter sp. KBS0703	AR32	G_contig000063
Bacteria	Arthrobacter sp. KBS0703	AR32	G_contig000067
Bacteria	Arthrobacter sp. KBS0703	AR33	G_contig000028
Bacteria	Arthrobacter sp. KBS0703	AR33	G_contig000040
Bacteria	Arthrobacter sp. KBS0703	AR33	G_contig000057
Bacteria	Arthrobacter sp. KBS0703	AR33	G_contig000058
Bacteria	Arthrobacter sp. KBS0703	AR33	G_contig000064
Bacteria	Arthrobacter sp. KBS0703	AR33	G_contig000089
Bacteria	Arthrobacter sp. KBS0703	AR34	G_contig000028
Bacteria	Arthrobacter sp. KBS0703	AR34	G_contig000040
Bacteria	Arthrobacter sp. KBS0703	AR34	G_contig000050
Bacteria	Arthrobacter sp. KBS0703	AR34	G_contig000055
Bacteria	Arthrobacter sp. KBS0703	AR34	G_contig000064
Bacteria	Arthrobacter sp. KBS0703	AR34	G_contig000064
Bacteria	Arthrobacter sp. KBS0703	AR35	G_contig000013
Bacteria	Arthrobacter sp. KBS0703	AR35	G_contig000032
Bacteria	Arthrobacter sp. KBS0703	AR35	G_contig000038
Bacteria	Arthrobacter sp. KBS0703	AR35	G_contig000040
Bacteria	Arthrobacter sp. KBS0703	AR35	G_contig000043
Bacteria	Arthrobacter sp. KBS0703	AR36	G_contig000001
Bacteria	Arthrobacter sp. KBS0703	AR36	G_contig000040
Bacteria	Arthrobacter sp. KBS0703	AR36	G_contig000043
Bacteria	Arthrobacter sp. KBS0703	AR36	G_contig000043
Bacteria	Arthrobacter sp. KBS0703	AR36	G_contig000045
Bacteria	Arthrobacter sp. KBS0703	AR36	G_contig000050
Bacteria	Arthrobacter sp. KBS0703	AR36	G_contig000067

Bacteria	Flavobacterium sp. KBS0721	FL53	G_contig000007
Bacteria	Flavobacterium sp. KBS0721	FL53	G_contig000007
Bacteria	Flavobacterium sp. KBS0721	FL53	G_contig000007
Bacteria	Flavobacterium sp. KBS0721	FL55	G_contig000001
Bacteria	Flavobacterium sp. KBS0721	FL55	G_contig000001
Bacteria	Flavobacterium sp. KBS0721	FL55	G_contig000001
Bacteria	Flavobacterium sp. KBS0721	FL55	G_contig000001
Bacteria	Flavobacterium sp. KBS0721	FL55	G_contig000002
Bacteria	Flavobacterium sp. KBS0721	FL55	G_contig000002
Bacteria	Flavobacterium sp. KBS0721	FL55	G_contig000003
Bacteria	Flavobacterium sp. KBS0721	FL55	G_contig000003
Bacteria	Flavobacterium sp. KBS0721	FL55	G_contig000004
Bacteria	Flavobacterium sp. KBS0721	FL55	G_contig000004
Bacteria	Flavobacterium sp. KBS0721	FL55	G_contig000004
Bacteria	Flavobacterium sp. KBS0721	FL55	G_contig000006
Bacteria	Flavobacterium sp. KBS0721	FL55	G_contig000006
Bacteria	Flavobacterium sp. KBS0721	FL56	G_contig000001
Bacteria	Flavobacterium sp. KBS0721	FL56	G_contig000003
Bacteria	Flavobacterium sp. KBS0721	FL56	G_contig000003
Bacteria	Flavobacterium sp. KBS0721	FL56	G_contig000003
Bacteria	Flavobacterium sp. KBS0721	FL56	G_contig000004
Bacteria	Flavobacterium sp. KBS0721	FL56	G_contig000004
Bacteria	Flavobacterium sp. KBS0721	FL56	G_contig000004
Bacteria	Flavobacterium sp. KBS0721	FL56	G_contig000004
Bacteria	Flavobacterium sp. KBS0721	FL56	G_contig000007
Bacteria	Gemmata obscuriglobus DSM5831	GE1	NZ_ABGO01000477.1
Bacteria	Gemmata obscuriglobus DSM5831	GE1	NZ_ABGO01000155.1
Bacteria	Gemmata obscuriglobus DSM5831	GE1	NZ_ABGO01000145.1
Bacteria	Gemmata obscuriglobus DSM5831	GE1	NZ_ABGO01000058.1
Bacteria	Gemmata obscuriglobus DSM5831	GE4	NZ_ABGO01000308.1
Bacteria	Gemmata obscuriglobus DSM5831	GE4	NZ_ABGO01000137.1
Bacteria	Gemmata obscuriglobus DSM5831	GE4	NZ_ABGO01000130.1
Bacteria	Gemmata obscuriglobus DSM5831	GE4	NZ_ABGO01000060.1
Bacteria	Gemmata obscuriglobus DSM5831	GE5	NZ_ABGO01000447.1
Bacteria	Gemmata obscuriglobus DSM5831	GE5	NZ_ABGO01000055.1
Bacteria	Gemmata obscuriglobus DSM5831	GE5	NZ_ABGO01000004.1
Bacteria	Gemmata obscuriglobus DSM5831	GE8	NZ_ABGO01000509.1
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Bacteria	Gemmata obscuriglobus DSM5831	GE8	NZ_ABGO01000196.1
Bacteria	Gemmata obscuriglobus DSM5831	GE8	NZ_ABGO01000115.1
Bacteria	Gemmata obscuriglobus DSM5831	GE8	NZ_ABGO01000050.1
Bacteria	Gemmata obscuriglobus DSM5831	GE8	NZ_ABGO01000021.1
Bacteria	Gemmata obscuriglobus DSM5831	GE8	NZ_ABGO01000057.1

Bacteria	Gemmata obscuriglobus DSM5831	GE9	NZ_ABGO01000114.1
Bacteria	Gemmata obscuriglobus DSM5831	GE9	NZ_ABGO01000106.1
Bacteria	Gemmata obscuriglobus DSM5831	GE9	NZ_ABGO01000002.1
Bacteria	Gemmata obscuriglobus DSM5831	GE10	NZ_ABGO01000311.1
Bacteria	Gemmata obscuriglobus DSM5831	GE10	NZ_ABGO01000291.1
Bacteria	Gemmata obscuriglobus DSM5831	GE10	NZ_ABGO01000198.1
Bacteria	Gemmata obscuriglobus DSM5831	GE10	NZ_ABGO01000057.1
Bacteria	Gemmata obscuriglobus DSM5831	GE10	NZ_ABGO01000019.1
Bacteria	Gemmata obscuriglobus DSM5831	GE11	NZ_ABGO01000413.1
Bacteria	Gemmata obscuriglobus DSM5831	GE11	NZ_ABGO01000108.1
Bacteria	Gemmata obscuriglobus DSM5831	GE11	NZ_ABGO01000009.1
Bacteria	Gemmata obscuriglobus DSM5831	GE12	NZ_ABGO01000301.1
Bacteria	Gemmata obscuriglobus DSM5831	GE12	NZ_ABGO01000028.1
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Bacteria	Gemmata obscuriglobus DSM5831	GE13	NZ_ABGO01000026.1
Bacteria	Gemmata obscuriglobus DSM5831	GE13	NZ_ABGO01000005.1
Bacteria	Gemmata obscuriglobus DSM5831	GE14	NZ_ABGO01000393.1
Bacteria	Gemmata obscuriglobus DSM5831	GE14	NZ_ABGO01000308.1
Bacteria	Gemmata obscuriglobus DSM5831	GE14	NZ_ABGO01000269.1
Bacteria	Gemmata obscuriglobus DSM5831	GE14	NZ_ABGO01000224.1
Bacteria	Gemmata obscuriglobus DSM5831	GE14	NZ_ABGO01000150.1
Bacteria	Gemmata obscuriglobus DSM5831	GE14	NZ_ABGO01000101.1
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Bacteria	Gemmata obscuriglobus DSM5831	GE14	NZ_ABGO01000071.1
Bacteria	Gemmata obscuriglobus DSM5831	GE14	NZ_ABGO01000035.1
Bacteria	Gemmata obscuriglobus DSM5831	GE14	NZ_ABGO01000028.1
Bacteria	Gemmata obscuriglobus DSM5831	GE15	NZ_ABGO01000415.1
Bacteria	Gemmata obscuriglobus DSM5831	GE15	NZ_ABGO01000146.1
Bacteria	Gemmata obscuriglobus DSM5831	GE15	NZ_ABGO01000134.1
Bacteria	Gemmata obscuriglobus DSM5831	GE15	NZ_ABGO01000029.1
Bacteria	Gemmata obscuriglobus DSM5831	GE15	NZ_ABGO01000017.1
Bacteria	Gemmata obscuriglobus DSM5831	GE15	NZ_ABGO01000010.1
Bacteria	Gemmata obscuriglobus DSM5831	GE15	NZ_ABGO01000002.1
Bacteria	Gemmata obscuriglobus DSM5831	GE19	NZ_ABGO01000180.1
Bacteria	Gemmata obscuriglobus DSM5831	GE19	NZ_ABGO01000050.1
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Bacteria	Gemmata obscuriglobus DSM5831	GE23	NZ_ABGO01000187.1
Bacteria	Gemmata obscuriglobus DSM5831	GE23	NZ_ABGO01000116.1
Bacteria	Gemmata obscuriglobus DSM5831	GE23	NZ_ABGO01000040.1

Bacteria	Gemmata obscuriglobus DSM5831	GE23	NZ_ABGO01000004.1
Bacteria	Gemmata obscuriglobus DSM5831	GE23	NZ_ABGO01000004.1
Bacteria	Gemmata obscuriglobus DSM5831	GE25	NZ_ABGO01000249.1
Bacteria	Gemmata obscuriglobus DSM5831	GE25	NZ_ABGO01000234.1
Bacteria	Gemmata obscuriglobus DSM5831	GE26	NZ_ABGO01000520.1
Bacteria	Gemmata obscuriglobus DSM5831	GE26	NZ_ABGO01000493.1
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Bacteria	Gemmata obscuriglobus DSM5831	GE26	NZ_ABGO01000287.1
Bacteria	Gemmata obscuriglobus DSM5831	GE26	NZ_ABGO01000253.1
Bacteria	Gemmata obscuriglobus DSM5831	GE26	NZ_ABGO01000240.1
Bacteria	Gemmata obscuriglobus DSM5831	GE26	NZ_ABGO01000079.1
Bacteria	Gemmata obscuriglobus DSM5831	GE26	NZ_ABGO01000032.1
Bacteria	Gemmata obscuriglobus DSM5831	GE26	NZ_ABGO01000020.1
Bacteria	Gemmata obscuriglobus DSM5831	GE26	NZ_ABGO01000005.1
Bacteria	Gemmata obscuriglobus DSM5831	GE26	NZ_ABGO01000004.1
Bacteria	Gemmata obscuriglobus DSM5831	GE27	NZ_ABGO01000366.1
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Bacteria	Gemmata obscuriglobus DSM5831	GE27	NZ_ABGO01000036.1
Bacteria	Gemmata obscuriglobus DSM5831	GE27	NZ_ABGO01000009.1
Bacteria	Gemmata obscuriglobus DSM5831	GE27	NZ_ABGO01000007.1
Bacteria	Gemmata obscuriglobus DSM5831	GE34	NZ_ABGO01000432.1
Bacteria	Gemmata obscuriglobus DSM5831	GE34	NZ_ABGO01000274.1
Bacteria	Gemmata obscuriglobus DSM5831	GE34	NZ_ABGO01000144.1
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Bacteria	Gemmata obscuriglobus DSM5831	GE34	NZ_ABGO01000054.1
Bacteria	Gemmata obscuriglobus DSM5831	GE34	NZ_ABGO01000003.1
Bacteria	Gemmata obscuriglobus DSM5831	GE35	NZ_ABGO01000239.1
Bacteria	Gemmata obscuriglobus DSM5831	GE35	NZ_ABGO01000102.1
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Bacteria	Gemmata obscuriglobus DSM5831	GE44	NZ_ABGO01000107.1
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Bacteria	Gemmata obscuriglobus DSM5831	GE45	NZ_ABGO01000084.1

Bacteria	Gemmata obscuriglobus DSM5831	GE54	NZ_ABGO01000008.1
Bacteria	Gemmata obscuriglobus DSM5831	GE61	NZ_ABGO01000140.1
Bacteria	Gemmata obscuriglobus DSM5831	GE61	NZ_ABGO01000073.1
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Bacteria	Gemmata obscuriglobus DSM5831	GE70	NZ_ABGO01000306.1
Bacteria	Gemmata obscuriglobus DSM5831	GE70	NZ_ABGO01000133.1
Bacteria	Gemmata obscuriglobus DSM5831	GE70	NZ_ABGO01000133.1
Bacteria	Gemmata obscuriglobus DSM5831	GE70	NZ_ABGO01000119.1
Bacteria	Gemmata obscuriglobus DSM5831	GE70	NZ_ABGO01000071.1
Bacteria	Gemmata obscuriglobus DSM5831	GE74	NZ_ABGO01000519.1
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Bacteria	Gemmata obscuriglobus DSM5831	GE75	NZ_ABGO01000381.1
Bacteria	Gemmata obscuriglobus DSM5831	GE75	NZ_ABGO01000170.1
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Bacteria	Gemmata obscuriglobus DSM5831	GE76	NZ_ABGO01000017.1
Bacteria	Gemmata obscuriglobus DSM5831	GE77	NZ_ABGO01000529.1
Bacteria	Gemmata obscuriglobus DSM5831	GE77	NZ_ABGO01000311.1
Bacteria	Gemmata obscuriglobus DSM5831	GE77	NZ_ABGO01000144.1
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Bacteria	Gemmata obscuriglobus DSM5831	GE77	NZ_ABGO01000010.1
Bacteria	Gemmata obscuriglobus DSM5831	GE77	NZ_ABGO01000005.1
Bacteria	Janthinobacterium lividum KBS0711	JA1	NZ_AHHB01000032.1

Bacteria	Micrococcus sp. KBS0714	MI11	G_contig000025
Bacteria	Micrococcus sp. KBS0714	MI11	G_contig000032
Bacteria	Micrococcus sp. KBS0714	MI11	G_contig000036
Bacteria	Micrococcus sp. KBS0714	MI11	G_contig000039
Bacteria	Micrococcus sp. KBS0714	MI11	G_contig000050
Bacteria	Micrococcus sp. KBS0714	MI14	G_contig000014
Bacteria	Micrococcus sp. KBS0714	MI14	G_contig000025
Bacteria	Micrococcus sp. KBS0714	MI14	G_contig000038
Bacteria	Micrococcus sp. KBS0714	MI15	G_contig000022
Bacteria	Micrococcus sp. KBS0714	MI15	G_contig000026
Bacteria	Micrococcus sp. KBS0714	MI16	G_contig000008
Bacteria	Micrococcus sp. KBS0714	MI16	G_contig000036
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Bacteria	Micrococcus sp. KBS0714	MI16	G_contig000037
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Bacteria	Micrococcus sp. KBS0714	MI17	G_contig000027
Bacteria	Micrococcus sp. KBS0714	MI18	G_contig000008
Bacteria	Micrococcus sp. KBS0714	MI19	G_contig000037
Bacteria	Micrococcus sp. KBS0714	MI19	G_contig000039
Bacteria	Micrococcus sp. KBS0714	MI20	G_contig000025
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Bacteria	Micrococcus sp. KBS0714	MI20	G_contig000051
Bacteria	Micrococcus sp. KBS0714	MI21	G_contig000032
Bacteria	Micrococcus sp. KBS0714	MI21	G_contig000037
Bacteria	Micrococcus sp. KBS0714	MI21	G_contig000038
Bacteria	Micrococcus sp. KBS0714	MI22	G_contig000022
Bacteria	Micrococcus sp. KBS0714	MI22	G_contig000025
Bacteria	Micrococcus sp. KBS0714	MI22	G_contig000027
Bacteria	Micrococcus sp. KBS0714	MI22	G_contig000039
Bacteria	Micrococcus sp. KBS0714	MI23	G_contig000019
Bacteria	Micrococcus sp. KBS0714	MI23	G_contig000032
Bacteria	Micrococcus sp. KBS0714	MI24	G_contig000032
Bacteria	Micrococcus sp. KBS0714	MI24	G_contig000044
Bacteria	Micrococcus sp. KBS0714	MI25	G_contig000009
Bacteria	Micrococcus sp. KBS0714	MI25	G_contig000020
Bacteria	Micrococcus sp. KBS0714	MI25	G_contig000050
Bacteria	Micrococcus sp. KBS0714	MI26	G_contig000015
Bacteria	Micrococcus sp. KBS0714	MI26	G_contig000025
Bacteria	Micrococcus sp. KBS0714	MI26	G_contig000025
Bacteria	Micrococcus sp. KBS0714	MI26	G_contig000025
Bacteria	Micrococcus sp. KBS0714	MI27	G_contig000019
Bacteria	Micrococcus sp. KBS0714	MI27	G_contig000042
Bacteria	Micrococcus sp. KBS0714	MI27	G_contig000051
Bacteria	Micrococcus sp. KBS0714	MI27	G_contig000051
Bacteria	Micrococcus sp. KBS0714	MI30	G_contig000051

Bacteria	Micrococcus sp. KBS0714	MI31	G_contig000039
Bacteria	Micrococcus sp. KBS0714	MI34	G_contig000025
Bacteria	Micrococcus sp. KBS0714	MI34	G_contig000039
Bacteria	Micrococcus sp. KBS0714	MI35	G_contig000037
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Bacteria	Micrococcus sp. KBS0714	MI36	G_contig000020
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Bacteria	Micrococcus sp. KBS0714	MI36	G_contig000025
Bacteria	Micrococcus sp. KBS0714	MI36	G_contig000031
Bacteria	Micrococcus sp. KBS0714	MI37	G_contig000032
Bacteria	Micrococcus sp. KBS0714	MI37	G_contig000037
Bacteria	Micrococcus sp. KBS0714	MI38	G_contig000022
Bacteria	Micrococcus sp. KBS0714	MI38	G_contig000039
Bacteria	Micrococcus sp. KBS0714	MI39	G_contig000008
Bacteria	Micrococcus sp. KBS0714	MI39	G_contig000009
Bacteria	Micrococcus sp. KBS0714	MI39	G_contig000014
Bacteria	Micrococcus sp. KBS0714	MI39	G_contig000023
Bacteria	Micrococcus sp. KBS0714	MI39	G_contig000037
Bacteria	Micrococcus sp. KBS0714	MI41	G_contig000022
Bacteria	Micrococcus sp. KBS0714	MI41	G_contig000031
Bacteria	Micrococcus sp. KBS0714	MI41	G_contig000031
Bacteria	Micrococcus sp. KBS0714	MI42	G_contig000019
Bacteria	Micrococcus sp. KBS0714	MI42	G_contig000025
Bacteria	Micrococcus sp. KBS0714	MI44	G_contig000036
Bacteria	Micrococcus sp. KBS0714	MI44	G_contig000037
Bacteria	Micrococcus sp. KBS0714	MI44	G_contig000050
Bacteria	Micrococcus sp. KBS0714	MI45	G_contig000032
Bacteria	Micrococcus sp. KBS0714	MI45	G_contig000038
Bacteria	Micrococcus sp. KBS0714	MI45	G_contig000042
Bacteria	Micrococcus sp. KBS0714	MI45	G_contig000051
Bacteria	Micrococcus sp. KBS0714	MI46	G_contig000026
Bacteria	Micrococcus sp. KBS0714	MI46	G_contig000032
Bacteria	Micrococcus sp. KBS0714	MI46	G_contig000032
Bacteria	Micrococcus sp. KBS0714	MI46	G_contig000032
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Bacteria	Micrococcus sp. KBS0714	MI46	G_contig000037
Bacteria	Micrococcus sp. KBS0714	MI46	G_contig000051
Bacteria	Micrococcus sp. KBS0714	MI47	G_contig000020
Bacteria	Micrococcus sp. KBS0714	MI47	G_contig000022
Bacteria	Micrococcus sp. KBS0714	MI47	G_contig000035
Bacteria	Micrococcus sp. KBS0714	MI47	G_contig000037
Bacteria	Micrococcus sp. KBS0714	MI47	G_contig000038
Bacteria	Micrococcus sp. KBS0714	MI47	G_contig000038

Bacteria	Micrococcus sp. KBS0714	MI47	G_contig000039
Bacteria	Micrococcus sp. KBS0714	MI47	G_contig000050
Bacteria	Micrococcus sp. KBS0714	MI48	G_contig000025
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Bacteria	Micrococcus sp. KBS0714	MI50	G_contig000004
Bacteria	Micrococcus sp. KBS0714	MI50	G_contig000014
Bacteria	Micrococcus sp. KBS0714	MI50	G_contig000020
Bacteria	Micrococcus sp. KBS0714	MI50	G_contig000032
Bacteria	Micrococcus sp. KBS0714	MI50	G_contig000032
Bacteria	Micrococcus sp. KBS0714	MI50	G_contig000037
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Bacteria	Micrococcus sp. KBS0714	MI50	G_contig000039
Bacteria	Micrococcus sp. KBS0714	MI50	G_contig000039
Bacteria	Micrococcus sp. KBS0714	MI50	G_contig000042
Bacteria	Micrococcus sp. KBS0714	MI50	G_contig000044
Bacteria	Micrococcus sp. KBS0714	MI53	G_contig000020
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Bacteria	Micrococcus sp. KBS0714	MI54	G_contig000008
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Bacteria	Micrococcus sp. KBS0714	MI55	G_contig000031
Bacteria	Micrococcus sp. KBS0714	MI56	G_contig000028
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Bacteria	Micrococcus sp. KBS0714	MI56	G_contig000037
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Bacteria	Micrococcus sp. KBS0714	MI57	G_contig000032
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Bacteria	Rhodobacter sphaeroides ATCC17025	RH1	NC_009430.1
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Bacteria	Staphylococcus aureus ATCC 25923	ST1	CP009361.1
Bacteria	Staphylococcus aureus ATCC 25923	ST1	CP009361.1

Bacteria	Staphylococcus aureus ATCC 25923	ST100	CP009361.1
Bacteria	Staphylococcus aureus ATCC 25923	ST100	CP009361.1

the first time in this study.				
Position	Ancestral	Mutation		
226200	C	T		
239568	G	A		
79012	G	A		
93742	C	A		
128911	T	C		
212702	A	C		
34727	A	G		
1076	C	A		
15834	G	A		
32292	C	T		
75538	C	T		
143351	G	C		
142953	C	T		
100318	C	G		
298880	G	A		
227059	A	G		
13152	C	G		
83902	G	T		
168656	T	C		
17815	G	A		
35765	T	G		
26918	C	T		
196941	A	C		
67671	A	G		
90087	G	A		
154019	G	A		
161627	G	A		
250063	T	C		
170820	G	T		
238012	T	C		
265308	T	C		
265779	T	C		
2591	C	A		
204825	A	G		
2324	G	A		
21410	A	C		
212657	G	A		
136599	G	T		
6213	C	T		
400	A	T		
403	C	A		
254389	A	C		
83947	G	A		

13769	C	A		
65303	A	C		
322	A	T		
169000	T	A		
7149	A	G		
270786	G	A		
129280	A	G		
35135	C	A		
142568	G	A		
166089	G	C		
38131	C	T		
197251	G	T		
60990	G	A		
193699	C	T		
303358	G	T		
39997	G	T		
51957	T	G		
52524	A	G		
108121	A	C		
17701	C	A		
189274	T	C		
197374	C	T		
206313	G	A		
85872	T	C		
24589	G	A		
37393	C	T		
214404	A	G		
62566	A	C		
188007	T	G		
63675	C	T		
88778	G	A		
23177	G	A		
33112	C	T		
90814	A	C		
42466	A	T		
37848	T	G		
29400	A	G		
174314	G	A		
264618	T	G		
18169	A	G		
5512	C	G		
39880	T	C		
145241	C	T		
114850	A	G		
82997	G	A		

135579	G	A		
141669	C	T		
88974	G	T		
10411	A	G		
134209	A	C		
134582	A	T		
10113	C	T		
72076	C	A		
23743	C	T		
186530	G	A		
26791	T	C		
139837	C	T		
47790	C	A		
330466	T	G		
213645	C	A		
53917	G	A		
133185	G	A		
233098	C	T		
72961	G	A		
142358	G	C		
40801	C	T		
71038	G	A		
62805	C	T		
88700	C	T		
88758	C	T		
102842	A	G		
206943	A	C		
49751	C	A		
71338	C	A		
76523	G	C		
120556	G	A		
65842	T	C		
44285	G	A		
102777	G	A		
292630	C	A		
310357	C	T		
183171	C	G		
191526	C	T		
154916	G	A		
110206	G	A		
297355	A	C		
26382	A	G		
52995	T	G		
7098	A	G		
33363	A	G		

156508	G	A		
151606	C	A		
210955	A	G		
125140	G	A		
64782	A	T		
193348	C	T		
230505	A	G		
85360	C	T		
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50743	G	A		
222089	A	C		
5177	G	A		
32859	C	T		
2857	G	T		
38435	G	C		
40550	C	T		
251040	C	T		
8741	C	T		
96207	G	A		
19638	G	T		
19639	A	G		
136658	G	A		
16129	A	G		
25818	A	T		
160662	C	T		
150825	C	G		
233057	A	G		
2020	C	T		
66058	C	G		
203335	C	T		
40856	C	A		
101375	A	G		
258239	A	G		
183914	T	A		
23024	C	T		
132382	C	G		
127549	T	G		
215852	A	C		
148615	G	T		
17269	C	G		
118931	T	G		
38715	G	A		
119067	A	T		
46647	C	T		
40781	G	T		

196720	C	A		
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59251	C	T		
32015	T	G		
9910	G	C		
57098	C	T		
78458	C	T		
120141	G	A		
163350	G	T		
25994	G	A		
236290	T	C		
156191	G	C		
21458	G	A		
164	A	G		
22373	T	C		
118256	A	G		
119805	T	C		
211284	C	G		
21531	G	A		
1299	A	G		
164302	C	A		
141232	G	A		
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32387	A	G		
65723	C	T		
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12801	A	C		
1794	C	T		
4208	C	T		
33375	A	G		
198362	C	T		
275931	T	G		
194540	G	A		
124141	A	T		
190680	C	T		
41894	G	A		
27802	A	T		
41398	G	A		
197161	G	A		
316016	G	A		
2119	G	C		
30721	A	G		
172391	G	T		

333843	C	T		
44724	C	T		
26322	C	A		
10930	G	T		
66698	G	T		
72889	A	G		
235562	G	A		
140967	A	G		
141406	G	C		
166728	G	A		
57645	C	T		
67992	C	A		
170501	C	G		
8822	A	G		
27168	G	A		
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122057	G	A		
96967	G	T		
259226	A	G		
163503	C	T		
30603	C	T		
40564	G	T		
159798	C	T		
117475	C	T		
13944	A	C		
19887	A	G		
103830	G	A		
274294	G	A		
62152	A	T		
253881	G	A		
5826	G	A		
227500	G	C		
302744	C	T		
84094	G	T		
164279	G	A		
33165	G	A		
75324	C	G		
42940	C	A		
161440	C	T		
80052	C	A		
215770	C	T		
261230	C	T		
46608	G	A		
199654	C	T		
59375	T	C		

61344	G	A		
127928	T	C		
25889	A	C		
90135	C	T		
98897	G	A		
28005	C	T		
99841	C	A		
52921	G	A		
166238	C	G		
243078	T	A		
61892	T	C		
155801	C	T		
270749	G	A		
131543	C	T		
184654	T	G		
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27996	A	G		
26960	G	C		
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3206	C	T		
159671	T	A		
177100	A	G		
37474	G	A		

20586	C	A		
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794	C	A		
1476	G	A		
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1607	C	A		
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1613	T	G		
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36488	G	A		
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109994	G	A		
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264066	A	G		
91991	C	G		
77666	G	A		
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252113	C	A		
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146731	A	G		
151135	G	A		
72749	C	A		
104186	C	T		
165945	G	C		
16312	T	A		
4416	G	T		
10420	T	G		
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113271	G	A		
15103	C	A		
206681	C	T		
71048	G	A		
14629	G	T		
206308	C	G		
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10647	G	A		
61337	A	T		
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32920	C	T		
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34211	T	G		
109502	T	G		
1119	C	G		
31019	G	C		
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507729	G	A		
1020104	G	A		
1140995	C	T		
1620447	C	T		
464589	G	A		
568934	A	T		
787627	C	T		
894708	A	G		
1763421	G	A		
358592	T	C		
1661009	G	A		
1941963	C	G		
1997570	A	G		
669533	G	A		
803150	G	T		

1292048	G	A		
1498119	T	C		
2457536	C	A		
347098	G	A		
1475360	C	A		
2564032	G	A		
2594179	T	A		
252109	A	G		
362337	A	G		
1348954	C	A		
1348963	C	T		
1349490	C	T		
1794002	G	T		
1535868	T	C		
1347235	C	G		
1349711	T	A		
1611313	C	A		
1663040	G	A		
1881942	T	C		
1486904	C	A		
871208	G	T		
1009009	C	G		
1089857	C	T		
1272191	G	A		
2245575	G	A		
15813	A	G		
99190	G	T		
1270869	C	T		
1672266	C	T		
55866	A	T		
155481	C	T		
414327	C	T		
560172	T	C		
891086	T	C		
996631	C	A		
1227693	G	A		
1323744	C	T		
1568299	C	A		
2724031	G	T		
537116	C	A		
709880	A	G		
1543621	T	C		
2407570	G	T		
2616720	T	C		
613706	G	T		

2053750	C	T		
1519242	G	A		
2060538	C	T		
1383685	A	C		
1438565	G	A		
2607805	A	G		
1216477	T	C		
1370457	T	G		
2172987	G	A		
1453009	A	T		
2205297	G	T		
175683	G	T		
1191449	T	A		
1191450	C	A		
2182104	C	T		
2754896	C	T		
2754909	A	G		
2754924	T	C		
1646742	A	G		
2275230	A	T		
851595	G	A		
1750806	A	G		
2617875	G	A		
313322	A	C		
735502	T	C		
871323	G	T		
1501310	C	T		
166758	A	G		
670465	C	T		
807305	G	A		
876459	C	A		
1743846	G	A		
2578369	A	C		
645605	A	T		
1046125	G	C		
1288872	A	G		
225840	A	C		
303226	G	A		
314248	G	T		
363765	C	T		
1168757	T	G		
1349497	T	A		
1396816	A	G		
1809222	A	G		
2285366	C	A		

149473	G	T		
222843	T	A		
420295	G	T		
769565	T	G		
939538	C	T		
2164484	G	T		
985620	T	C		
1075714	A	G		
1078328	A	G		
1546745	G	A		
1711228	G	A		
1967101	G	T		
2299462	C	T		
723466	A	T		
2233676	C	T		
410220	T	G		
724372	G	A		
936457	T	C		
1053013	G	A		
7150	C	T		
160120	C	A		
756365	T	C		
2536875	G	A		
137187	C	A		
1419181	T	C		
1597017	C	A		
1960688	T	C		
519412	C	T		
2244156	A	G		
1077188	A	G		
1524212	G	T		
1608968	G	C		
1953064	G	T		
2503975	C	T		
2627348	G	A		
2610617	C	T		
1771010	G	A		
229457	G	T		
543610	G	A		
736934	T	G		
1644624	G	A		
1715921	C	A		
1771010	G	A		
2478095	G	A		
2659517	C	A		

358186	C	T		
576892	G	A		
1816089	C	A		
2438180	A	G		
2561663	G	T		
154858	C	T		
343435	T	C		
987501	C	T		
2058296	G	A		
2322389	C	A		
313839	C	T		
622022	T	C		
719874	G	T		
881148	G	A		
1942277	T	A		
334149	C	T		
1349806	G	A		
1459520	C	A		
1894488	G	A		
373849	C	T		
508328	A	G		
1021052	C	T		
1450245	C	A		
1612271	T	C		
1744608	G	A		
2407557	G	A		
508328	A	G		
886772	C	A		
1021052	C	T		
1390378	T	C		
1450245	C	A		
1612271	T	C		
1744608	G	A		
1648410	T	C		
1940544	G	A		
1966237	G	T		
354247	G	A		
798889	T	C		
1044582	G	A		
598355	G	C		
1699394	C	G		
2449471	C	T		
2727580	T	C		
369903	A	G		
2493624	G	A		

2678421	C	T		
2756717	C	A		

Table S3. List of indels detected in MA lines of the 12 species reported on for the first time in t

Group	Species	Line name	Chromosome/Scaffold	Position
Bacteria	Arthrobacter sp. KBS0703	AR1	G_contig000012	66128
Bacteria	Arthrobacter sp. KBS0703	AR1	G_contig000058	61558
Bacteria	Arthrobacter sp. KBS0703	AR1	G_contig000058	107117
Bacteria	Arthrobacter sp. KBS0703	AR1	G_contig000074	192971
Bacteria	Arthrobacter sp. KBS0703	AR2	G_contig000026	5196
Bacteria	Arthrobacter sp. KBS0703	AR2	G_contig000028	130248
Bacteria	Arthrobacter sp. KBS0703	AR2	G_contig000045	158065
Bacteria	Arthrobacter sp. KBS0703	AR3	G_contig000013	170955
Bacteria	Arthrobacter sp. KBS0703	AR4	G_contig000035	17939
Bacteria	Arthrobacter sp. KBS0703	AR4	G_contig000064	119222
Bacteria	Arthrobacter sp. KBS0703	AR4	G_contig000089	241724
Bacteria	Arthrobacter sp. KBS0703	AR7	G_contig000045	37991
Bacteria	Arthrobacter sp. KBS0703	AR8	G_contig000013	72940
Bacteria	Arthrobacter sp. KBS0703	AR8	G_contig000064	207006
Bacteria	Arthrobacter sp. KBS0703	AR11	G_contig000074	89190
Bacteria	Arthrobacter sp. KBS0703	AR12	G_contig000026	222830
Bacteria	Arthrobacter sp. KBS0703	AR12	G_contig000028	259353
Bacteria	Arthrobacter sp. KBS0703	AR13	G_contig000064	62537
Bacteria	Arthrobacter sp. KBS0703	AR15	G_contig000045	218761
Bacteria	Arthrobacter sp. KBS0703	AR16	G_contig000013	2875
Bacteria	Arthrobacter sp. KBS0703	AR16	G_contig000032	206939
Bacteria	Arthrobacter sp. KBS0703	AR16	G_contig000038	59493
Bacteria	Arthrobacter sp. KBS0703	AR16	G_contig000040	120413
Bacteria	Arthrobacter sp. KBS0703	AR16	G_contig000043	202652
Bacteria	Arthrobacter sp. KBS0703	AR19	G_contig000014	25760
Bacteria	Arthrobacter sp. KBS0703	AR19	G_contig000067	179416
Bacteria	Arthrobacter sp. KBS0703	AR21	G_contig000038	181692
Bacteria	Arthrobacter sp. KBS0703	AR21	G_contig000043	57580
Bacteria	Arthrobacter sp. KBS0703	AR21	G_contig000064	27567
Bacteria	Arthrobacter sp. KBS0703	AR21	G_contig000067	10098
Bacteria	Arthrobacter sp. KBS0703	AR22	G_contig000032	29083
Bacteria	Arthrobacter sp. KBS0703	AR22	G_contig000038	52579
Bacteria	Arthrobacter sp. KBS0703	AR22	G_contig000074	9177
Bacteria	Arthrobacter sp. KBS0703	AR24	G_contig000032	124353
Bacteria	Arthrobacter sp. KBS0703	AR25	G_contig000072	14498
Bacteria	Arthrobacter sp. KBS0703	AR27	G_contig000028	211184
Bacteria	Arthrobacter sp. KBS0703	AR28	G_contig000050	44971
Bacteria	Arthrobacter sp. KBS0703	AR28	G_contig000057	71480
Bacteria	Arthrobacter sp. KBS0703	AR28	G_contig000067	66701
Bacteria	Arthrobacter sp. KBS0703	AR29	G_contig000012	41259
Bacteria	Arthrobacter sp. KBS0703	AR32	G_contig000040	64785
Bacteria	Arthrobacter sp. KBS0703	AR32	G_contig000067	250970
Bacteria	Arthrobacter sp. KBS0703	AR33	G_contig000057	39835

Bacteria	Arthrobacter sp. KBS0703	AR34	G_contig000012	53886
Bacteria	Arthrobacter sp. KBS0703	AR35	G_contig000026	115809
Bacteria	Arthrobacter sp. KBS0703	AR35	G_contig000074	175257
Bacteria	Arthrobacter sp. KBS0703	AR36	G_contig000038	168472
Bacteria	Arthrobacter sp. KBS0703	AR38	G_contig000040	63702
Bacteria	Arthrobacter sp. KBS0703	AR42	G_contig000055	48760
Bacteria	Arthrobacter sp. KBS0703	AR42	G_contig000058	58773
Bacteria	Arthrobacter sp. KBS0703	AR43	G_contig000050	89064
Bacteria	Arthrobacter sp. KBS0703	AR43	G_contig000050	104548
Bacteria	Arthrobacter sp. KBS0703	AR43	G_contig000057	19224
Bacteria	Arthrobacter sp. KBS0703	AR44	G_contig000052	35845
Bacteria	Arthrobacter sp. KBS0703	AR45	G_contig000012	17564
Bacteria	Arthrobacter sp. KBS0703	AR45	G_contig000012	53595
Bacteria	Arthrobacter sp. KBS0703	AR45	G_contig000015	7737
Bacteria	Arthrobacter sp. KBS0703	AR45	G_contig000067	339545
Bacteria	Arthrobacter sp. KBS0703	AR47	G_contig000067	335626
Bacteria	Arthrobacter sp. KBS0703	AR48	G_contig000045	184029
Bacteria	Arthrobacter sp. KBS0703	AR49	G_contig000012	150291
Bacteria	Arthrobacter sp. KBS0703	AR49	G_contig000026	44699
Bacteria	Arthrobacter sp. KBS0703	AR49	G_contig000071	934
Bacteria	Arthrobacter sp. KBS0703	AR49	G_contig000071	944
Bacteria	Arthrobacter sp. KBS0703	AR49	G_contig000071	946
Bacteria	Arthrobacter sp. KBS0703	AR50	G_contig000043	80041
Bacteria	Arthrobacter sp. KBS0703	AR50	G_contig000044	28594
Bacteria	Arthrobacter sp. KBS0703	AR50	G_contig000064	193265
Bacteria	Arthrobacter sp. KBS0703	AR52	G_contig000057	177399
Bacteria	Arthrobacter sp. KBS0703	AR52	G_contig000064	45876
Bacteria	Arthrobacter sp. KBS0703	AR52	G_contig000089	128192
Bacteria	Arthrobacter sp. KBS0703	AR54	G_contig000032	14026
Bacteria	Arthrobacter sp. KBS0703	AR54	G_contig000032	66305
Bacteria	Arthrobacter sp. KBS0703	AR54	G_contig000074	157508
Bacteria	Arthrobacter sp. KBS0703	AR62	G_contig000045	166239
Bacteria	Arthrobacter sp. KBS0703	AR62	G_contig000064	96916
Bacteria	Arthrobacter sp. KBS0703	AR62	G_contig000067	177694
Bacteria	Arthrobacter sp. KBS0703	AR62	G_contig000089	93038
Bacteria	Arthrobacter sp. KBS0703	AR63	G_contig000058	101652
Bacteria	Arthrobacter sp. KBS0703	AR66	G_contig000045	124691
Bacteria	Arthrobacter sp. KBS0703	AR66	G_contig000045	218761
Bacteria	Arthrobacter sp. KBS0703	AR66	G_contig000057	51249
Bacteria	Arthrobacter sp. KBS0703	AR69	G_contig000026	123187
Bacteria	Arthrobacter sp. KBS0703	AR69	G_contig000045	7939
Bacteria	Arthrobacter sp. KBS0703	AR70	G_contig000068	88083
Bacteria	Arthrobacter sp. KBS0703	AR75	G_contig000040	146992
Bacteria	Arthrobacter sp. KBS0703	AR75	G_contig000043	242990
Bacteria	Arthrobacter sp. KBS0703	AR76	G_contig000089	244544

Bacteria	Caulobacter crescentus NA1000	CA1	NC_011916.1	1194945
Bacteria	Caulobacter crescentus NA1000	CA5	NC_011916.1	997057
Bacteria	Caulobacter crescentus NA1000	CA6	NC_011916.1	3116059
Bacteria	Caulobacter crescentus NA1000	CA10	NC_011916.1	2233133
Bacteria	Caulobacter crescentus NA1000	CA10	NC_011916.1	3423227
Bacteria	Caulobacter crescentus NA1000	CA12	NC_011916.1	2703739
Bacteria	Caulobacter crescentus NA1000	CA13	NC_011916.1	2065735
Bacteria	Caulobacter crescentus NA1000	CA14	NC_011916.1	3797966
Bacteria	Caulobacter crescentus NA1000	CA15	NC_011916.1	1698562
Bacteria	Caulobacter crescentus NA1000	CA15	NC_011916.1	3478629
Bacteria	Caulobacter crescentus NA1000	CA16	NC_011916.1	3288201
Bacteria	Caulobacter crescentus NA1000	CA18	NC_011916.1	1575805
Bacteria	Caulobacter crescentus NA1000	CA19	NC_011916.1	128226
Bacteria	Caulobacter crescentus NA1000	CA19	NC_011916.1	973923
Bacteria	Caulobacter crescentus NA1000	CA21	NC_011916.1	2871971
Bacteria	Caulobacter crescentus NA1000	CA23	NC_011916.1	1515939
Bacteria	Caulobacter crescentus NA1000	CA23	NC_011916.1	3038846
Bacteria	Caulobacter crescentus NA1000	CA23	NC_011916.1	3673789
Bacteria	Caulobacter crescentus NA1000	CA25	NC_011916.1	1186886
Bacteria	Caulobacter crescentus NA1000	CA25	NC_011916.1	3458056
Bacteria	Caulobacter crescentus NA1000	CA28	NC_011916.1	1645174
Bacteria	Caulobacter crescentus NA1000	CA28	NC_011916.1	3447983
Bacteria	Caulobacter crescentus NA1000	CA39	NC_011916.1	2195145
Bacteria	Caulobacter crescentus NA1000	CA39	NC_011916.1	3763068
Bacteria	Caulobacter crescentus NA1000	CA40	NC_011916.1	3141007
Bacteria	Caulobacter crescentus NA1000	CA42	NC_011916.1	3643860
Bacteria	Caulobacter crescentus NA1000	CA46	NC_011916.1	2848442
Bacteria	Caulobacter crescentus NA1000	CA46	NC_011916.1	3713958
Bacteria	Caulobacter crescentus NA1000	CA50	NC_011916.1	966217
Bacteria	Caulobacter crescentus NA1000	CA50	NC_011916.1	1847682
Bacteria	Caulobacter crescentus NA1000	CA52	NC_011916.1	3911516
Bacteria	Caulobacter crescentus NA1000	CA53	NC_011916.1	1286372
Bacteria	Caulobacter crescentus NA1000	CA53	NC_011916.1	2309009
Bacteria	Caulobacter crescentus NA1000	CA55	NC_011916.1	2353024
Bacteria	Caulobacter crescentus NA1000	CA58	NC_011916.1	98165
Bacteria	Caulobacter crescentus NA1000	CA60	NC_011916.1	3811800
Bacteria	Caulobacter crescentus NA1000	CA61	NC_011916.1	3665986
Bacteria	Caulobacter crescentus NA1000	CA69	NC_011916.1	485239
Bacteria	Caulobacter crescentus NA1000	CA69	NC_011916.1	1160529
Bacteria	Caulobacter crescentus NA1000	CA69	NC_011916.1	847479
Bacteria	Caulobacter crescentus NA1000	CA72	NC_011916.1	3456225
Bacteria	Colwellia psychrerythraea 34H	CO3	NC_003910	1598331
Bacteria	Colwellia psychrerythraea 34H	CO9	NC_003910	3482936
Bacteria	Colwellia psychrerythraea 34H	CO13	NC_003910	2604631
Bacteria	Colwellia psychrerythraea 34H	CO15	NC_003910	900548

Bacteria	Colwellia psychrerythraea 34H	CO15	NC_003910	2212846
Bacteria	Colwellia psychrerythraea 34H	CO39	NC_003910	3567808
Bacteria	Colwellia psychrerythraea 34H	CO40	NC_003910	5344308
Bacteria	Colwellia psychrerythraea 34H	CO43	NC_003910	3184617
Bacteria	Colwellia psychrerythraea 34H	CO43	NC_003910	4473192
Bacteria	Colwellia psychrerythraea 34H	CO47	NC_003910	3339461
Bacteria	Colwellia psychrerythraea 34H	CO50	NC_003910	3057296
Bacteria	Colwellia psychrerythraea 34H	CO52	NC_003910	1018090
Bacteria	Colwellia psychrerythraea 34H	CO57	NC_003910	4623008
Bacteria	Colwellia psychrerythraea 34H	CO60	NC_003910	3675814
Bacteria	Colwellia psychrerythraea 34H	CO60	NC_003910	4920030
Bacteria	Colwellia psychrerythraea 34H	CO67	NC_003910	3933539
Bacteria	Colwellia psychrerythraea 34H	CO67	NC_003910	4660385
Bacteria	Colwellia psychrerythraea 34H	CO70	NC_003910	1994376
Bacteria	Colwellia psychrerythraea 34H	CO80	NC_003910	1594218
Bacteria	Colwellia psychrerythraea 34H	CO84	NC_003910	1989610
Bacteria	Colwellia psychrerythraea 34H	CO87	NC_003910	1067199
Bacteria	Colwellia psychrerythraea 34H	CO87	NC_003910	2409749
Bacteria	Colwellia psychrerythraea 34H	CO95	NC_003910	3328895
Bacteria	Colwellia psychrerythraea 34H	CO96	NC_003910	4419992
Bacteria	Colwellia psychrerythraea 34H	CO101	NC_003910	973485
Bacteria	Colwellia psychrerythraea 34H	CO101	NC_003910	1518366
Bacteria	Colwellia psychrerythraea 34H	CO102	NC_003910	3501933
Bacteria	Colwellia psychrerythraea 34H	CO102	NC_003910	3699845
Bacteria	Colwellia psychrerythraea 34H	CO117	NC_003910	751258
Bacteria	Colwellia psychrerythraea 34H	CO118	NC_003910	2084781
Bacteria	Colwellia psychrerythraea 34H	CO122	NC_003910	4856503
Bacteria	Colwellia psychrerythraea 34H	CO133	NC_003910	1926890
Bacteria	Colwellia psychrerythraea 34H	CO133	NC_003910	4011920
Bacteria	Colwellia psychrerythraea 34H	CO142	NC_003910	2366111
Bacteria	Colwellia psychrerythraea 34H	CO142	NC_003910	4347210
Bacteria	Colwellia psychrerythraea 34H	CO147	NC_003910	3479365
Bacteria	Colwellia psychrerythraea 34H	CO147	NC_003910	3953502
Bacteria	Colwellia psychrerythraea 34H	CO148	NC_003910	2255009
Bacteria	Colwellia psychrerythraea 34H	CO150	NC_003910	596062
Bacteria	Colwellia psychrerythraea 34H	CO156	NC_003910	1168068
Bacteria	Colwellia psychrerythraea 34H	CO165	NC_003910	4022733
Bacteria	Colwellia psychrerythraea 34H	CO168	NC_003910	4754784
Bacteria	Colwellia psychrerythraea 34H	CO169	NC_003910	3809158
Bacteria	Colwellia psychrerythraea 34H	CO169	NC_003910	3898219
Bacteria	Flavobacterium sp. KBS0721	FL1	G_contig000002	451803
Bacteria	Flavobacterium sp. KBS0721	FL1	G_contig000002	1124413
Bacteria	Flavobacterium sp. KBS0721	FL1	G_contig000003	102953
Bacteria	Flavobacterium sp. KBS0721	FL1	G_contig000007	38869
Bacteria	Flavobacterium sp. KBS0721	FL1	G_contig000003	890924

Bacteria	Flavobacterium sp. KBS0721	FL2	G_contig000005	551749
Bacteria	Flavobacterium sp. KBS0721	FL2	G_contig000007	34139
Bacteria	Flavobacterium sp. KBS0721	FL4	G_contig000001	1397723
Bacteria	Flavobacterium sp. KBS0721	FL4	G_contig000003	26920
Bacteria	Flavobacterium sp. KBS0721	FL4	G_contig000004	173685
Bacteria	Flavobacterium sp. KBS0721	FL4	G_contig000004	402571
Bacteria	Flavobacterium sp. KBS0721	FL4	G_contig000007	106492
Bacteria	Flavobacterium sp. KBS0721	FL6	G_contig000002	60006
Bacteria	Flavobacterium sp. KBS0721	FL6	G_contig000002	856247
Bacteria	Flavobacterium sp. KBS0721	FL6	G_contig000002	1107486
Bacteria	Flavobacterium sp. KBS0721	FL6	G_contig000001	522520
Bacteria	Flavobacterium sp. KBS0721	FL6	G_contig000002	636771
Bacteria	Flavobacterium sp. KBS0721	FL6	G_contig000004	333737
Bacteria	Flavobacterium sp. KBS0721	FL9	G_contig000006	294326
Bacteria	Flavobacterium sp. KBS0721	FL9	G_contig000004	669220
Bacteria	Flavobacterium sp. KBS0721	FL10	G_contig000002	294474
Bacteria	Flavobacterium sp. KBS0721	FL10	G_contig000004	590231
Bacteria	Flavobacterium sp. KBS0721	FL10	G_contig000004	677813
Bacteria	Flavobacterium sp. KBS0721	FL10	G_contig000005	524682
Bacteria	Flavobacterium sp. KBS0721	FL11	G_contig000007	71123
Bacteria	Flavobacterium sp. KBS0721	FL12	G_contig000002	189845
Bacteria	Flavobacterium sp. KBS0721	FL12	G_contig000003	230693
Bacteria	Flavobacterium sp. KBS0721	FL12	G_contig000005	55739
Bacteria	Flavobacterium sp. KBS0721	FL13	G_contig000002	50348
Bacteria	Flavobacterium sp. KBS0721	FL13	G_contig000002	1221571
Bacteria	Flavobacterium sp. KBS0721	FL14	G_contig000003	219571
Bacteria	Flavobacterium sp. KBS0721	FL15	G_contig000001	537901
Bacteria	Flavobacterium sp. KBS0721	FL15	G_contig000002	766144
Bacteria	Flavobacterium sp. KBS0721	FL16	G_contig000002	785094
Bacteria	Flavobacterium sp. KBS0721	FL16	G_contig000002	1313560
Bacteria	Flavobacterium sp. KBS0721	FL17	G_contig000003	172595
Bacteria	Flavobacterium sp. KBS0721	FL20	G_contig000007	285146
Bacteria	Flavobacterium sp. KBS0721	FL20	G_contig000001	862598
Bacteria	Flavobacterium sp. KBS0721	FL21	G_contig000002	426935
Bacteria	Flavobacterium sp. KBS0721	FL21	G_contig000005	363088
Bacteria	Flavobacterium sp. KBS0721	FL22	G_contig000001	1419274
Bacteria	Flavobacterium sp. KBS0721	FL22	G_contig000003	592754
Bacteria	Flavobacterium sp. KBS0721	FL22	G_contig000004	288933
Bacteria	Flavobacterium sp. KBS0721	FL24	G_contig000004	291735
Bacteria	Flavobacterium sp. KBS0721	FL25	G_contig000001	99781
Bacteria	Flavobacterium sp. KBS0721	FL25	G_contig000002	1135382
Bacteria	Flavobacterium sp. KBS0721	FL25	G_contig000003	822812
Bacteria	Flavobacterium sp. KBS0721	FL28	G_contig000005	374184
Bacteria	Flavobacterium sp. KBS0721	FL29	G_contig000005	82613
Bacteria	Flavobacterium sp. KBS0721	FL29	G_contig000005	388793

Bacteria	Flavobacterium sp. KBS0721	FL29	G_contig000004	538076
Bacteria	Flavobacterium sp. KBS0721	FL30	G_contig000002	817206
Bacteria	Flavobacterium sp. KBS0721	FL32	G_contig000003	708098
Bacteria	Flavobacterium sp. KBS0721	FL33	G_contig000002	449191
Bacteria	Flavobacterium sp. KBS0721	FL33	G_contig000003	51366
Bacteria	Flavobacterium sp. KBS0721	FL33	G_contig000003	848417
Bacteria	Flavobacterium sp. KBS0721	FL33	G_contig000004	130126
Bacteria	Flavobacterium sp. KBS0721	FL33	G_contig000005	597344
Bacteria	Flavobacterium sp. KBS0721	FL33	G_contig000003	890924
Bacteria	Flavobacterium sp. KBS0721	FL34	G_contig000001	1047652
Bacteria	Flavobacterium sp. KBS0721	FL34	G_contig000005	133020
Bacteria	Flavobacterium sp. KBS0721	FL36	G_contig000002	643808
Bacteria	Flavobacterium sp. KBS0721	FL36	G_contig000003	693422
Bacteria	Flavobacterium sp. KBS0721	FL38	G_contig000001	93658
Bacteria	Flavobacterium sp. KBS0721	FL38	G_contig000002	388349
Bacteria	Flavobacterium sp. KBS0721	FL38	G_contig000002	1137962
Bacteria	Flavobacterium sp. KBS0721	FL39	G_contig000002	468718
Bacteria	Flavobacterium sp. KBS0721	FL39	G_contig000004	359545
Bacteria	Flavobacterium sp. KBS0721	FL39	G_contig000005	392339
Bacteria	Flavobacterium sp. KBS0721	FL41	G_contig000003	734306
Bacteria	Flavobacterium sp. KBS0721	FL46	G_contig000001	925940
Bacteria	Flavobacterium sp. KBS0721	FL47	G_contig000002	730140
Bacteria	Flavobacterium sp. KBS0721	FL47	G_contig000004	458876
Bacteria	Flavobacterium sp. KBS0721	FL47	G_contig000004	538076
Bacteria	Flavobacterium sp. KBS0721	FL48	G_contig000001	214139
Bacteria	Flavobacterium sp. KBS0721	FL48	G_contig000002	274691
Bacteria	Flavobacterium sp. KBS0721	FL48	G_contig000002	1251514
Bacteria	Flavobacterium sp. KBS0721	FL48	G_contig000005	43646
Bacteria	Flavobacterium sp. KBS0721	FL48	G_contig000005	125687
Bacteria	Flavobacterium sp. KBS0721	FL49	G_contig000003	157283
Bacteria	Flavobacterium sp. KBS0721	FL49	G_contig000006	196809
Bacteria	Flavobacterium sp. KBS0721	FL52	G_contig000002	728403
Bacteria	Flavobacterium sp. KBS0721	FL53	G_contig000002	557493
Bacteria	Flavobacterium sp. KBS0721	FL55	G_contig000001	793402
Bacteria	Flavobacterium sp. KBS0721	FL56	G_contig000001	1290797
Bacteria	Gemmata obscuriglobus DSM5831	GE1	NZ_ABGO01000081.1	27260
Bacteria	Gemmata obscuriglobus DSM5831	GE5	NZ_ABGO01000245.1	2028
Bacteria	Gemmata obscuriglobus DSM5831	GE13	NZ_ABGO01000074.1	26862
Bacteria	Gemmata obscuriglobus DSM5831	GE13	NZ_ABGO01000101.1	6217
Bacteria	Gemmata obscuriglobus DSM5831	GE13	NZ_ABGO01000101.1	6220
Bacteria	Gemmata obscuriglobus DSM5831	GE14	NZ_ABGO01000258.1	9357
Bacteria	Gemmata obscuriglobus DSM5831	GE15	NZ_ABGO01000059.1	7407
Bacteria	Gemmata obscuriglobus DSM5831	GE15	NZ_ABGO01000109.1	3223
Bacteria	Gemmata obscuriglobus DSM5831	GE15	NZ_ABGO01000222.1	9605
Bacteria	Gemmata obscuriglobus DSM5831	GE23	NZ_ABGO01000251.1	2292

Bacteria	Gemmata obscuriglobus DSM5831	GE25	NZ_ABGO01000492.1	3685
Bacteria	Gemmata obscuriglobus DSM5831	GE26	NZ_ABGO01000182.1	14806
Bacteria	Gemmata obscuriglobus DSM5831	GE35	NZ_ABGO01000090.1	4707
Bacteria	Gemmata obscuriglobus DSM5831	GE35	NZ_ABGO01000201.1	7171
Bacteria	Gemmata obscuriglobus DSM5831	GE44	NZ_ABGO01000444.1	2975
Bacteria	Gemmata obscuriglobus DSM5831	GE46	NZ_ABGO01000361.1	1362
Bacteria	Gemmata obscuriglobus DSM5831	GE52	NZ_ABGO01000211.1	4472
Bacteria	Gemmata obscuriglobus DSM5831	GE52	NZ_ABGO01000287.1	2964
Bacteria	Gemmata obscuriglobus DSM5831	GE66	NZ_ABGO01000078.1	3376
Bacteria	Gemmata obscuriglobus DSM5831	GE66	NZ_ABGO01000387.1	3481
Bacteria	Gemmata obscuriglobus DSM5831	GE70	NZ_ABGO01000030.1	42439
Bacteria	Gemmata obscuriglobus DSM5831	GE74	NZ_ABGO01000039.1	24208
Bacteria	Gemmata obscuriglobus DSM5831	GE75	NZ_ABGO01000022.1	31210
Bacteria	Gemmata obscuriglobus DSM5831	GE75	NZ_ABGO01000207.1	6094
Bacteria	Gemmata obscuriglobus DSM5831	GE75	NZ_ABGO01000313.1	220
Bacteria	Gemmata obscuriglobus DSM5831	GE75	NZ_ABGO01000493.1	716
Bacteria	Gemmata obscuriglobus DSM5831	GE76	NZ_ABGO01000024.1	39902
Bacteria	Gemmata obscuriglobus DSM5831	GE76	NZ_ABGO01000065.1	25635
Bacteria	Gemmata obscuriglobus DSM5831	GE77	NZ_ABGO01000003.1	52660
Bacteria	Janthinobacterium lividum KBS0711	JA6	NZ_AHHB01000037.1	520353
Bacteria	Janthinobacterium lividum KBS0711	JA7	NZ_AHHB01000043.1	26519
Bacteria	Janthinobacterium lividum KBS0711	JA12	NZ_AHHB01000037.1	40173
Bacteria	Janthinobacterium lividum KBS0711	JA17	NZ_AHHB01000028.1	409028
Bacteria	Janthinobacterium lividum KBS0711	JA43	NZ_AHHB01000028.1	87019
Bacteria	Janthinobacterium lividum KBS0711	JA44	NZ_AHHB01000042.1	302936
Bacteria	Janthinobacterium lividum KBS0711	JA52	NZ_AHHB01000019.1	208980
Bacteria	Janthinobacterium lividum KBS0711	JA53	NZ_AHHB01000036.1	254555
Bacteria	Janthinobacterium lividum KBS0711	JA60	NZ_AHHB01000021.1	165230
Bacteria	Kineococcus radiotolerans SRS30216	KI1	NC_009664.2	428152
Bacteria	Kineococcus radiotolerans SRS30216	KI1	NC_009664.2	443044
Bacteria	Kineococcus radiotolerans SRS30216	KI1	NC_009664.2	946383
Bacteria	Kineococcus radiotolerans SRS30216	KI1	NC_009664.2	1702183
Bacteria	Kineococcus radiotolerans SRS30216	KI1	NC_009664.2	1743246
Bacteria	Kineococcus radiotolerans SRS30216	KI3	NC_009664.2	2919736
Bacteria	Kineococcus radiotolerans SRS30216	KI3	NC_009664.2	4571148
Bacteria	Kineococcus radiotolerans SRS30216	KI4	NC_009664.2	4121369
Bacteria	Kineococcus radiotolerans SRS30216	KI5	NC_009664.2	2276106
Bacteria	Kineococcus radiotolerans SRS30216	KI5	NC_009664.2	2276457
Bacteria	Kineococcus radiotolerans SRS30216	KI5	NC_009664.2	3675552
Bacteria	Kineococcus radiotolerans SRS30216	KI6	NC_009664.2	1144
Bacteria	Kineococcus radiotolerans SRS30216	KI6	NC_009664.2	9942
Bacteria	Kineococcus radiotolerans SRS30216	KI6	NC_009664.2	65900
Bacteria	Kineococcus radiotolerans SRS30216	KI6	NC_009664.2	174029
Bacteria	Kineococcus radiotolerans SRS30216	KI6	NC_009664.2	2444476
Bacteria	Kineococcus radiotolerans SRS30216	KI6	NC_009664.2	3094635

Bacteria	Kineococcus radiotolerans SRS30216	KI9	NC_009664.2	206686
Bacteria	Kineococcus radiotolerans SRS30216	KI9	NC_009664.2	2758097
Bacteria	Kineococcus radiotolerans SRS30216	KI12	NC_009664.2	1245457
Bacteria	Kineococcus radiotolerans SRS30216	KI12	NC_009664.2	4544654
Bacteria	Kineococcus radiotolerans SRS30216	KI13	NC_009664.2	680968
Bacteria	Kineococcus radiotolerans SRS30216	KI13	NC_009664.2	786345
Bacteria	Kineococcus radiotolerans SRS30216	KI13	NC_009664.2	2070217
Bacteria	Kineococcus radiotolerans SRS30216	KI14	NC_009664.2	1127814
Bacteria	Kineococcus radiotolerans SRS30216	KI14	NC_009664.2	1580173
Bacteria	Kineococcus radiotolerans SRS30216	KI14	NC_009664.2	4636169
Bacteria	Kineococcus radiotolerans SRS30216	KI14	NC_009664.2	4683042
Bacteria	Kineococcus radiotolerans SRS30216	KI15	NC_009664.2	1022769
Bacteria	Kineococcus radiotolerans SRS30216	KI15	NC_009664.2	2855011
Bacteria	Kineococcus radiotolerans SRS30216	KI15	NC_009664.2	3541419
Bacteria	Kineococcus radiotolerans SRS30216	KI15	NC_009664.2	3559970
Bacteria	Kineococcus radiotolerans SRS30216	KI15	NC_009664.2	3737677
Bacteria	Kineococcus radiotolerans SRS30216	KI16	NC_009664.2	64631
Bacteria	Kineococcus radiotolerans SRS30216	KI16	NC_009664.2	1765898
Bacteria	Kineococcus radiotolerans SRS30216	KI16	NC_009664.2	4059546
Bacteria	Kineococcus radiotolerans SRS30216	KI17	NC_009664.2	301666
Bacteria	Kineococcus radiotolerans SRS30216	KI17	NC_009664.2	1353637
Bacteria	Kineococcus radiotolerans SRS30216	KI17	NC_009664.2	3127794
Bacteria	Kineococcus radiotolerans SRS30216	KI17	NC_009664.2	3127795
Bacteria	Kineococcus radiotolerans SRS30216	KI17	NC_009664.2	3267208
Bacteria	Kineococcus radiotolerans SRS30216	KI17	NC_009664.2	3627138
Bacteria	Kineococcus radiotolerans SRS30216	KI17	NC_009664.2	3687168
Bacteria	Kineococcus radiotolerans SRS30216	KI17	NC_009664.2	4619357
Bacteria	Kineococcus radiotolerans SRS30216	KI17	NC_009664.2	4746962
Bacteria	Kineococcus radiotolerans SRS30216	KI18	NC_009664.2	1247733
Bacteria	Kineococcus radiotolerans SRS30216	KI18	NC_009664.2	3225130
Bacteria	Kineococcus radiotolerans SRS30216	KI20	NC_009664.2	200020
Bacteria	Kineococcus radiotolerans SRS30216	KI20	NC_009664.2	2852902
Bacteria	Kineococcus radiotolerans SRS30216	KI20	NC_009664.2	3304592
Bacteria	Kineococcus radiotolerans SRS30216	KI20	NC_009664.2	3471685
Bacteria	Kineococcus radiotolerans SRS30216	KI20	NC_009664.2	3987915
Bacteria	Kineococcus radiotolerans SRS30216	KI21	NC_009664.2	30520
Bacteria	Kineococcus radiotolerans SRS30216	KI21	NC_009664.2	424765
Bacteria	Kineococcus radiotolerans SRS30216	KI21	NC_009664.2	615499
Bacteria	Kineococcus radiotolerans SRS30216	KI21	NC_009664.2	2934342
Bacteria	Kineococcus radiotolerans SRS30216	KI22	NC_009664.2	2928952
Bacteria	Kineococcus radiotolerans SRS30216	KI22	NC_009664.2	3247197
Bacteria	Kineococcus radiotolerans SRS30216	KI23	NC_009664.2	679518
Bacteria	Kineococcus radiotolerans SRS30216	KI23	NC_009664.2	2093872
Bacteria	Kineococcus radiotolerans SRS30216	KI23	NC_009664.2	3056701
Bacteria	Kineococcus radiotolerans SRS30216	KI24	NC_009664.2	779326

Bacteria	Kineococcus radiotolerans SRS30216	KI24	NC_009664.2	2602929
Bacteria	Kineococcus radiotolerans SRS30216	KI25	NC_009664.2	1902235
Bacteria	Kineococcus radiotolerans SRS30216	KI25	NC_009664.2	2968308
Bacteria	Kineococcus radiotolerans SRS30216	KI25	NC_009664.2	3414865
Bacteria	Kineococcus radiotolerans SRS30216	KI26	NC_009664.2	2597959
Bacteria	Kineococcus radiotolerans SRS30216	KI26	NC_009664.2	3043945
Bacteria	Kineococcus radiotolerans SRS30216	KI27	NC_009664.2	1990698
Bacteria	Kineococcus radiotolerans SRS30216	KI27	NC_009664.2	2031051
Bacteria	Kineococcus radiotolerans SRS30216	KI28	NC_009664.2	3627742
Bacteria	Kineococcus radiotolerans SRS30216	KI28	NC_009664.2	4119039
Bacteria	Kineococcus radiotolerans SRS30216	KI28	NC_009664.2	4119043
Bacteria	Kineococcus radiotolerans SRS30216	KI29	NC_009664.2	1265158
Bacteria	Kineococcus radiotolerans SRS30216	KI29	NC_009664.2	3023162
Bacteria	Kineococcus radiotolerans SRS30216	KI33	NC_009664.2	2747865
Bacteria	Kineococcus radiotolerans SRS30216	KI34	NC_009664.2	1551997
Bacteria	Kineococcus radiotolerans SRS30216	KI34	NC_009664.2	3404095
Bacteria	Kineococcus radiotolerans SRS30216	KI35	NC_009664.2	1992385
Bacteria	Kineococcus radiotolerans SRS30216	KI35	NC_009664.2	3162662
Bacteria	Kineococcus radiotolerans SRS30216	KI36	NC_009664.2	3162662
Bacteria	Kineococcus radiotolerans SRS30216	KI37	NC_009664.2	419621
Bacteria	Kineococcus radiotolerans SRS30216	KI37	NC_009664.2	826675
Bacteria	Kineococcus radiotolerans SRS30216	KI37	NC_009664.2	1260616
Bacteria	Kineococcus radiotolerans SRS30216	KI38	NC_009664.2	348375
Bacteria	Kineococcus radiotolerans SRS30216	KI41	NC_009664.2	462744
Bacteria	Kineococcus radiotolerans SRS30216	KI41	NC_009664.2	899132
Bacteria	Kineococcus radiotolerans SRS30216	KI42	NC_009664.2	366965
Bacteria	Kineococcus radiotolerans SRS30216	KI44	NC_009664.2	133274
Bacteria	Kineococcus radiotolerans SRS30216	KI44	NC_009664.2	206914
Bacteria	Kineococcus radiotolerans SRS30216	KI44	NC_009664.2	2897528
Bacteria	Kineococcus radiotolerans SRS30216	KI46	NC_009664.2	1245457
Bacteria	Kineococcus radiotolerans SRS30216	KI46	NC_009664.2	3304592
Bacteria	Kineococcus radiotolerans SRS30216	KI47	NC_009664.2	900615
Bacteria	Kineococcus radiotolerans SRS30216	KI47	NC_009664.2	1927160
Bacteria	Kineococcus radiotolerans SRS30216	KI47	NC_009664.2	4590235
Bacteria	Kineococcus radiotolerans SRS30216	KI48	NC_009664.2	381383
Bacteria	Kineococcus radiotolerans SRS30216	KI48	NC_009664.2	1475704
Bacteria	Kineococcus radiotolerans SRS30216	KI48	NC_009664.2	1555371
Bacteria	Kineococcus radiotolerans SRS30216	KI50	NC_009664.2	3095307
Bacteria	Kineococcus radiotolerans SRS30216	KI54	NC_009664.2	277901
Bacteria	Kineococcus radiotolerans SRS30216	KI54	NC_009664.2	1127799
Bacteria	Kineococcus radiotolerans SRS30216	KI54	NC_009664.2	2844907
Bacteria	Kineococcus radiotolerans SRS30216	KI57	NC_009664.2	2096984
Bacteria	Kineococcus radiotolerans SRS30216	KI57	NC_009664.2	3956326
Bacteria	Kineococcus radiotolerans SRS30216	KI58	NC_009664.2	668841
Bacteria	Kineococcus radiotolerans SRS30216	KI58	NC_009664.2	2076393

Bacteria	Kineococcus radiotolerans SRS30216	KI60	NC_009664.2	22914
Bacteria	Kineococcus radiotolerans SRS30216	KI60	NC_009664.2	887704
Bacteria	Kineococcus radiotolerans SRS30216	KI60	NC_009664.2	3234784
Bacteria	Kineococcus radiotolerans SRS30216	KI61	NC_009664.2	1795353
Bacteria	Kineococcus radiotolerans SRS30216	KI61	NC_009664.2	3085641
Bacteria	Kineococcus radiotolerans SRS30216	KI61	NC_009664.2	3709159
Bacteria	Kineococcus radiotolerans SRS30216	KI67	NC_009664.2	69487
Bacteria	Kineococcus radiotolerans SRS30216	KI67	NC_009664.2	1840540
Bacteria	Kineococcus radiotolerans SRS30216	KI67	NC_009664.2	1930779
Bacteria	Kineococcus radiotolerans SRS30216	KI67	NC_009664.2	2854089
Bacteria	Kineococcus radiotolerans SRS30216	KI67	NC_009664.2	2923145
Bacteria	Kineococcus radiotolerans SRS30216	KI67	NC_009664.2	4618265
Bacteria	Kineococcus radiotolerans SRS30216	KI68	NC_009664.2	3679514
Bacteria	Kineococcus radiotolerans SRS30216	KI70	NC_009664.2	522597
Bacteria	Kineococcus radiotolerans SRS30216	KI70	NC_009664.2	2656121
Bacteria	Lactococcus lactis DSMZ20481	LA1	NZ_LT599049.1	433507
Bacteria	Lactococcus lactis DSMZ20481	LA2	NZ_LT599049.1	711244
Bacteria	Lactococcus lactis DSMZ20481	LA4	NZ_LT599049.1	2220113
Bacteria	Lactococcus lactis DSMZ20481	LA5	NZ_LT599049.1	548090
Bacteria	Lactococcus lactis DSMZ20481	LA5	NZ_LT599052.1	32666
Bacteria	Lactococcus lactis DSMZ20481	LA7	NZ_LT599049.1	72817
Bacteria	Lactococcus lactis DSMZ20481	LA7	NZ_LT599051.1	4478
Bacteria	Lactococcus lactis DSMZ20481	LA8	NZ_LT599049.1	1593399
Bacteria	Lactococcus lactis DSMZ20481	LA8	NZ_LT599049.1	2057595
Bacteria	Lactococcus lactis DSMZ20481	LA15	NZ_LT599049.1	1399282
Bacteria	Lactococcus lactis DSMZ20481	LA16	NZ_LT599049.1	2285309
Bacteria	Lactococcus lactis DSMZ20481	LA17	NZ_LT599049.1	446406
Bacteria	Lactococcus lactis DSMZ20481	LA17	NZ_LT599049.1	1616196
Bacteria	Lactococcus lactis DSMZ20481	LA19	NZ_LT599049.1	2555689
Bacteria	Lactococcus lactis DSMZ20481	LA21	NZ_LT599049.1	1725866
Bacteria	Lactococcus lactis DSMZ20481	LA21	NZ_LT599049.1	2543398
Bacteria	Lactococcus lactis DSMZ20481	LA22	NZ_LT599049.1	1813970
Bacteria	Lactococcus lactis DSMZ20481	LA23	NZ_LT599049.1	1857875
Bacteria	Lactococcus lactis DSMZ20481	LA24	NZ_LT599049.1	934056
Bacteria	Lactococcus lactis DSMZ20481	LA27	NZ_LT599049.1	2457956
Bacteria	Lactococcus lactis DSMZ20481	LA29	NZ_LT599049.1	1496045
Bacteria	Lactococcus lactis DSMZ20481	LA30	NZ_LT599049.1	2004119
Bacteria	Lactococcus lactis DSMZ20481	LA31	NZ_LT599049.1	2161536
Bacteria	Lactococcus lactis DSMZ20481	LA32	NZ_LT599049.1	2401329
Bacteria	Lactococcus lactis DSMZ20481	LA33	NZ_LT599049.1	298895
Bacteria	Lactococcus lactis DSMZ20481	LA38	NZ_LT599049.1	526613
Bacteria	Lactococcus lactis DSMZ20481	LA38	NZ_LT599049.1	809472
Bacteria	Lactococcus lactis DSMZ20481	LA39	NZ_LT599049.1	531683
Bacteria	Lactococcus lactis DSMZ20481	LA42	NZ_LT599049.1	298672
Bacteria	Lactococcus lactis DSMZ20481	LA42	NZ_LT599049.1	2324781

Bacteria	Lactococcus lactis DSMZ20481	LA50	NZ_LT599049.1	2471417
Bacteria	Lactococcus lactis DSMZ20481	LA52	NZ_LT599049.1	25955
Bacteria	Lactococcus lactis DSMZ20481	LA52	NZ_LT599049.1	138658
Bacteria	Lactococcus lactis DSMZ20481	LA52	NZ_LT599049.1	1015921
Bacteria	Lactococcus lactis DSMZ20481	LA55	NZ_LT599049.1	1068973
Bacteria	Lactococcus lactis DSMZ20481	LA56	NZ_LT599049.1	87674
Bacteria	Lactococcus lactis DSMZ20481	LA56	NZ_LT599049.1	856338
Bacteria	Lactococcus lactis DSMZ20481	LA56	NZ_LT599049.1	900625
Bacteria	Lactococcus lactis DSMZ20481	LA56	NZ_LT599049.1	911059
Bacteria	Lactococcus lactis DSMZ20481	LA56	NZ_LT599049.1	911136
Bacteria	Lactococcus lactis DSMZ20481	LA56	NZ_LT599049.1	1076652
Bacteria	Lactococcus lactis DSMZ20481	LA56	NZ_LT599049.1	1136367
Bacteria	Lactococcus lactis DSMZ20481	LA56	NZ_LT599049.1	1228377
Bacteria	Lactococcus lactis DSMZ20481	LA56	NZ_LT599049.1	1298727
Bacteria	Lactococcus lactis DSMZ20481	LA56	NZ_LT599049.1	1561483
Bacteria	Lactococcus lactis DSMZ20481	LA56	NZ_LT599049.1	2328232
Bacteria	Lactococcus lactis DSMZ20481	LA58	NZ_LT599049.1	1215198
Bacteria	Lactococcus lactis DSMZ20481	LA61	NZ_LT599049.1	335692
Bacteria	Lactococcus lactis DSMZ20481	LA61	NZ_LT599049.1	2451955
Bacteria	Lactococcus lactis DSMZ20481	LA61	NZ_LT599049.1	2451957
Bacteria	Lactococcus lactis DSMZ20481	LA61	NZ_LT599049.1	1017833
Bacteria	Lactococcus lactis DSMZ20481	LA62	NZ_LT599049.1	11005
Bacteria	Lactococcus lactis DSMZ20481	LA63	NZ_LT599049.1	17544
Bacteria	Lactococcus lactis DSMZ20481	LA65	NZ_LT599049.1	1007040
Bacteria	Lactococcus lactis DSMZ20481	LA66	NZ_LT599049.1	585080
Bacteria	Lactococcus lactis DSMZ20481	LA73	NZ_LT599049.1	941362
Bacteria	Micrococcus sp. KBS0714	MI2	G_contig000022	56604
Bacteria	Micrococcus sp. KBS0714	MI2	G_contig000037	65922
Bacteria	Micrococcus sp. KBS0714	MI3	G_contig000026	53170
Bacteria	Micrococcus sp. KBS0714	MI6	G_contig000022	8306
Bacteria	Micrococcus sp. KBS0714	MI6	G_contig000032	192435
Bacteria	Micrococcus sp. KBS0714	MI7	G_contig000039	278186
Bacteria	Micrococcus sp. KBS0714	MI10	G_contig000039	21915
Bacteria	Micrococcus sp. KBS0714	MI11	G_contig000020	1773
Bacteria	Micrococcus sp. KBS0714	MI11	G_contig000037	143253
Bacteria	Micrococcus sp. KBS0714	MI13	G_contig000022	76208
Bacteria	Micrococcus sp. KBS0714	MI13	G_contig000039	84300
Bacteria	Micrococcus sp. KBS0714	MI17	G_contig000019	6689
Bacteria	Micrococcus sp. KBS0714	MI20	G_contig000014	13627
Bacteria	Micrococcus sp. KBS0714	MI20	G_contig000014	13778
Bacteria	Micrococcus sp. KBS0714	MI20	G_contig000036	73613
Bacteria	Micrococcus sp. KBS0714	MI21	G_contig000035	1929
Bacteria	Micrococcus sp. KBS0714	MI22	G_contig000026	57924
Bacteria	Micrococcus sp. KBS0714	MI22	G_contig000026	57928
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Bacteria	Micrococcus sp. KBS0714	MI26	G_contig000040	35637
Bacteria	Micrococcus sp. KBS0714	MI27	G_contig000014	86655
Bacteria	Micrococcus sp. KBS0714	MI30	G_contig000031	47343
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Bacteria	Micrococcus sp. KBS0714	MI30	G_contig000039	18406
Bacteria	Micrococcus sp. KBS0714	MI34	G_contig000040	8289
Bacteria	Micrococcus sp. KBS0714	MI35	G_contig000032	215930
Bacteria	Micrococcus sp. KBS0714	MI35	G_contig000042	60682
Bacteria	Micrococcus sp. KBS0714	MI35	G_contig000050	58900
Bacteria	Micrococcus sp. KBS0714	MI36	G_contig000025	70707
Bacteria	Micrococcus sp. KBS0714	MI36	G_contig000025	70708
Bacteria	Micrococcus sp. KBS0714	MI36	G_contig000044	27126
Bacteria	Micrococcus sp. KBS0714	MI37	G_contig000043	21954
Bacteria	Micrococcus sp. KBS0714	MI37	G_contig000050	69462
Bacteria	Micrococcus sp. KBS0714	MI38	G_contig000019	58309
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Bacteria	Micrococcus sp. KBS0714	MI39	G_contig000027	27446
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Bacteria	Micrococcus sp. KBS0714	MI42	G_contig000038	75028
Bacteria	Micrococcus sp. KBS0714	MI44	G_contig000022	74485
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Ancestral

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Table S4. Parameters from linear regression of G/C composition of genomic sites vs. mutation equilibrium is calculated with equation 1 in the text; slope is the amount α to a change of 1 unit of the G/C composition under mutation equilibrium; intercept is

Genomic sites	Slope (SE)	P value ($\times 10^{-4}$) for the slope = 0	r^2	Intercept (SE)
All	0.636 (0.087)	0.000134	0.585	0.276 (0.033)
0-fold	0.212 (0.055)	4.440000	0.274	0.347 (0.021)
2-fold	0.902 (0.159)	0.019500	0.457	0.223 (0.060)
4-fold	1.137 (0.161)	0.000272	0.569	0.193 (0.061)
Intergenic	0.624 (0.093)	0.000853	0.542	0.240 (0.035)

under mutation equilibrium. The G/C composition under
of change in G/C composition of the first column sites due
s G/C composition in the range of 0 to 1

P value (x10 ⁻⁴) for the Intercept = 0	Degree of freedom
0.00000535	36
<0.00000001	36
7.23	36
31.6	36
0.000613	36

Table S5. Expression level vs. GC content of four-fold degenerate sites in genes.
 FPKM (fragments per kilobase per million);
 RPK (reads per kilobase of transcripts);
 RPKM (reads per kilobase per million);
 TMM (Trimmed Mean of M-values normalization method) normalized reads;
 TPM (transcripts per million mapped reads);
 slope is the amount of change in expression level due to a change of 1 unit of the G/C compo

Group	Species name	r ²	Slope	P value for the slope = 0	Standard error of the slope
Bacteria	<i>Escherichia coli</i>	0.000339	-6254.00	0.120000	4021.00
Bacteria	<i>Kineococcus radiotolerans</i>	0.000636	-1582.00	0.118600	1013.40
Bacteria	<i>Mycobacterium smegmatis</i>	0.002848	-2332.20	0.000018	544.10
Bacteria	<i>Ruegeria pomeroyi</i>	0.014650	-1796.10	<0.00001	228.10
Bacteria	<i>Staphylococcus aureus</i>	0.010160	-61488.00	<0.00001	11562.00
Bacteria	<i>Vibrio cholerae</i>	0.109100	-65648.00	<0.00001	3258.00
Bacteria	<i>Vibrio fischeri</i>	0.007172	-25558.00	<0.00001	4783.00
UniEuk	<i>Chlamydomonas reinhardtii</i>	0.008738	405.25	<0.00001	36.01
UniEuk	<i>Plasmodium falciparum</i>	0.000078	-4848.90	0.232700	4062.80
UniEuk	<i>Rhodotorula toruloides</i>	0.016680	1079.16	<0.00001	99.57
UniEuk	<i>Saccharomyces cerevisiae</i>	0.004492	-4766.60	<0.00001	867.60
UniEuk	<i>Schizosaccharomyces pombe</i>	0.022860	9483.90	<0.00001	1185.10
MultiEuk	<i>Arabidopsis thaliana</i>	0.000044	13.26	0.140300	8.99
MultiEuk	<i>Caenorhabditis elegans</i>	0.002773	337.35	<0.00001	47.61
MultiEuk	<i>Drosophila melanogaster</i>	0.002049	173.13	0.000145	45.53
MultiEuk	<i>Homo sapiens</i>	0.002971	-76.62	<0.00001	11.22
MultiEuk	<i>Mus musculus</i>	0.000044	-11.85	0.193000	9.10

position at four-fold degenerate sites of genes; intercept is in the

Intercept	P value for the intercept = 0	Standard error of the slope	Degree of freedom
5344.00	0.032900	2504.00	4187
1913.90	0.047600	965.60	2257
2279.20	0.000001	464.90	6083
1791.10	<0.00001	200.20	4102
20443.00	<0.00001	2666.00	2656
40514.00	<0.00001	1784.00	3306
10218.00	<0.00001	1278.00	3813
-254.30	<0.00001	28.95	14256
7446.40	<0.00001	884.10	5467
-704.02	<0.00001	74.21	6867
3086.20	<0.00001	316.00	6467
-1861.00	<0.00001	354.30	2694
21.43	<0.00001	3.28	26079
-36.28	0.042500	17.88	17689
-54.57	0.076300	30.78	6555
105.87	<0.00001	6.62	15319
38.07	<0.00001	5.30	15742

unit of gene expression level.

RNA-seq Expression data source (NCBI GEO accession numbers or literature)
negative control wild-type strain cultured on LB plates; Long et al. (2016) Proc Natl Acad Sci U S A 113: E2498-E2505; unit of expression level: FPKM
negative control wild-type strain cultured in PTYG solution; GSM1238698; unit of expression level: RPKM
log-phase MC2 155 strain cultured in Middlebrook 7H9 broth are used; GSM1715076-GSM1715078; unit of expression level: normalized read counts by the python package Hts
rapid-growing DSS-3 strain aerated in darkness; GSM1622557-1622559; normalized read counts by the Rockhopper program
IPLA1 untreated control cells; GSM2339170-2339172; unit of expression level: RPKM
mid-log-phase O395 strain cultured in LB; GSM1906935; unit of expression level: read counts of transcripts of each gene after mapping reads to genome
ES114 strain in rich medium; GSM2131525-2131527; unit of expression level: normalized read counts by the python package Htseq
CPCC11 strain in artificial freshwater medium; GSM1716651-1716653; unit of expression level: normalized read counts by the python package Htseq
3D7 strain in RPMI 1640 medium with human serum; GSM2051314-GSM2051319; unit of expression level: normalized read counts by the R package Deseq
wild-type strain cultured in MM medium; GSM954176; unit of expression level: TPM
S288c wild-type strain in complete medium; GSM811071, GSM811072; unit of expression level: aligned-read counts
mid-log-phase 972 h ⁻ strain in Edinburgh minimal medium; Marguerate et al. (2012) Cell 151: 671-683; unit of expression level: RPK
rosettes of Col-0 strain grown for 10 days in full ES medium; GSM2339943-2339945; unit of expression level: TMM
L4 stage N2 strain maintained at standard lab conditions; GSM1507712; unit of expression level: FPKM
day 10 adult midgut tissue cells; GSM2029238-2029241; unit of expression level: RPKM
5-week gestation embryo; GSM2306011; unit of expression level: TPM
lung tissue of C57BL/6 strain at 12.5 dpc developmental stage; GSM2451667-2451669; unit of expression level: normalized read counts by the Maverix Biomixs Analytic