

Supplementary Table S1. General genomic features of genomes used in this study.

Name	Assembly NCBI		Scaffolds	Size (Mb)	GC (%)	Genes	Proteins
	ID / IMG Genome ID	RefSeq Ascc. No.					
<i>Afipia birgiae</i> 34632 ^T	GCA_000308295.2	CAJQ02	65	5.33	60.8	5166	4871
<i>Afipia broomeae</i> ATCC 49717 ^T	GCA_000314675.2	AGWX01	4	5.26	61.3	5086	4953
<i>Afipia clevelandensis</i> ATCC 49720 ^T	GCA_000336555.1	AGWY01	19	4.4	61.7	4248	4151
<i>Agrobacterium fabrum</i> C58 ^T	GCA_000092025.1	NC_003062.2 NC_003063.2	-	5.67	59.1	5459	5355
<i>Agrobacterium</i> sp. H13-3	GCA_000192635.1	NC_015183.1 NC_015508.1	-	5.57	58.5	5365	5154
<i>Agrobacterium tumefaciens</i> Ach5	GCA_000971565.1	NZ_CP011246.1 NZ_CP011247.1	-	5.67	58.5	5404	5184
<i>Agrobacterium tumefaciens</i> ATCC 31700	GCA_001975795.1	MTKI01	117	5.94	58.4	5709	5462
<i>Aminobacter aminovorans</i> KCTC 2477	GCA_001605015.1	NZ_CP015005.1	-	5.62	63.4	5542	5362
<i>Aquamicrobium aerolatum</i> DSM 21857 ^T	GCA_900113935.1	FORF01	50	3.64	60.1	3573	3513
<i>Aquamicrobium defluvii</i> W13Z1	GCA_000585625.1	JENY01	65	4.77	63.1	4703	4455
<i>Aurantimonas coralicida</i> DSM 14790 ^T	GCA_000421645.1	ATXK01	38	4.62	66.7	4359	4198
<i>Aurantimonas manganoxydans</i> DSM 21871 ^T	GCA_001463865.1	BBWP01	94	4.25	66.8	3944	3821
<i>Aureimonas altamirensis</i> DSM 21988 ^T	GCA_900141975.1	FQZC01	11	4.19	64.8	3983	3894
<i>Aureimonas frigidaquae</i> JCM 14755 ^T	GCA_001463905.1	BBWR01	30	4.10	66.1	3864	3774
<i>Aureimonas jatrophae</i> DSM 25025 ^T	GCA_900104035.1	FNIT01	27	4.59	67.8	4360	4304
<i>Aureimonas phyllosphaerae</i> DSM 25026 ^T	GCA_900113065.1	FOOA01	62	4.72	67.5	4538	4479
<i>Aureimonas ureilytica</i> DSM 18598 ^T	GCA_000382705.1	ARQE01	44	5.09	67.3	4792	4637
<i>Bartonella ancashensis</i> 20.00 ^T	GCA_001281405.1	NZ_CP010401.1	-	1.47	38.4	1317	1203
<i>Bartonella bacilliformis</i> ATCC 35685 ^T	GCA_001559035.1	NZ_CP014012.1	-	1.44	38.2	1284	1183
<i>Bartonella bovis</i> 91-4 ^T	GCA_000384965.1	NZ_CM001844.1	1	1.63	37.4	2809	2627
<i>Bartonella clarridgeiae</i> ATCC 51734 ^T	GCA_000518185.1	JADC01	17	1.49	35.7	1275	1170
<i>Bartonella schoenbuchensis</i> R1 ^T	GCA_002022685.1	NZ_CP019789.1	2	1.73	37.8	1587	1330
<i>Beijerinckia indica</i> ATCC 9039 ^T	GCA_000019845.1	NC_010581.1	-	4.17	57.1	3767	3619
<i>Beijerinckia mobilis</i> UQM 1969 ^T	GCA_000745425.1	JQJH01	58	4.32	57.2	-	3680
<i>Blastochloris viridis</i> ATCC 19567	GCA_001402875.1	NZ_CP012946.1	-	3.72	67.9	3265	3157
<i>Blastochloris viridis</i> DSM 133 ^T	GCA_001548155.2	NZ_AP014854.2	-	3.73	67.9	3260	3149
<i>Bosea robiniae</i> DSM 26672 ^T	GCA_900102525.1	FNBZ01	21	5.28	66.3	5067	5006
<i>Bosea vaviloviae</i> Vaf-18 ^T	GCA_001741865.1	NZ_CP017147.1	-	6.71	65.4	6271	6105
<i>Bradyrhizobium arachidis</i> LMG 26795	GCA_900116675.1	FPBQ01	98	9.79	63.6	9374	9312

<i>Bradyrhizobium canariense</i> GAS369	GCA_900105125.1	LT629750.1	-	7.84	60.9	7549	7291
<i>Bradyrhizobium daqingense</i> CGMCC 1.10947 ^a	2596583556	-	107	7.89	63.7	7559	7480
<i>Bradyrhizobium diazoefficiens</i> NK6	GCA_001549695.1	AP014685.1	-	10.5	63.6	10249	8598
<i>Bradyrhizobium diazoefficiens</i> SEMIA 5080	GCA_000648595.2	ADOU02	13	9.09	64.0	8726	8252
<i>Bradyrhizobium diazoefficiens</i> USDA 110	GCA_000011365.1	BA000040.2	-	9.11	64.1	8373	8317
<i>Bradyrhizobium diazoefficiens</i> USDA 122	GCA_000473025.1	AXAX01	101	8.98	64.0	8673	8184
<i>Bradyrhizobium elkanii</i> 587	GCA_000257685.2	AJJK01	2430	8.67	63.6	-	-
<i>Bradyrhizobium elkanii</i> BLY3-8	GCA_001718205.1	LWUI01	90	9.20	63.8	8553	8143
<i>Bradyrhizobium elkanii</i> BLY6-1	GCA_001718185.1	LXEM01	79	9.20	63.8	8549	8148
<i>Bradyrhizobium elkanii</i> CCBAU 05737	GCA_000261505.1	AJPV01	751	9.77	63.5	9578	8527
<i>Bradyrhizobium elkanii</i> CCBAU 43297	GCA_000261525.1	AJPW01	654	9.35	63.7	9092	8193
<i>Bradyrhizobium elkanii</i> UASWS1015	GCA_000878305.1	JXOF01	187	7.82	64.6	7306	7077
<i>Bradyrhizobium elkanii</i> USDA 3254	GCA_000472765.1	AXAH01	85	8.98	63.8	8497	7977
<i>Bradyrhizobium elkanii</i> USDA 3259	GCA_000473005.1	AXAW01	101	8.72	63.9	8264	7782
<i>Bradyrhizobium elkanii</i> USDA 76	GCA_000379145.1	ARAG01	2	9.49	63.7	8969	8534
<i>Bradyrhizobium elkanii</i> USDA 94	GCA_000519225.1	JAF01	164	9.56	63.7	9038	8504
<i>Bradyrhizobium elkanii</i> WSM1741	GCA_000472965.1	AXAU01	69	7.95	62.1	7520	7116
<i>Bradyrhizobium elkanii</i> WSM2783	GCA_000472865.1	AXAP01	217	9.90	62.4	9510	8824
<i>Bradyrhizobium embrapense</i> SEMIA 6208	GCA_001189235.2	LFIP02	36	8.27	64.0	7729	7404
<i>Bradyrhizobium erythrophlei</i> GAS138	GCA_900129425.1	LT670817.1	-	9.09	61.4	8638	8280
<i>Bradyrhizobium erythrophlei</i> GAS242	GCA_900129505.1	LT670818.1	-	9.19	61.9	8690	8320
<i>Bradyrhizobium erythrophlei</i> GAS401	GCA_900142985.1	LT670849.1	-	7.53	61.2	7214	7027
<i>Bradyrhizobium erythrophlei</i> MT12	GCA_900105845.1	FNTH01	2	8.97	63.8	8417	8054
<i>Bradyrhizobium huanghuaihaiense</i> CGMCC 1.10948 ^a	2596583587	-	101	9.23	63.9	8760	8654
<i>Bradyrhizobium icense</i> LMTR 13	GCA_001693385.1	CP016428.1	-	8.32	62.0	7868	7456
<i>Bradyrhizobium japonicum</i> 22	GCA_000482425.1	AXVG01	4	7.51	64.5	7121	6860
<i>Bradyrhizobium japonicum</i> CCBAU 15354	GCA_000261545.1	AJPX01	951	10.1	63.3	10250	8898
<i>Bradyrhizobium japonicum</i> CCBAU 15517	GCA_000261565.1	AJPY01	1129	9.92	63.4	10050	8694
<i>Bradyrhizobium japonicum</i> CCBAU 15618	GCA_000261585.1	AJPZ01	691	9.82	63.4	9846	8828
<i>Bradyrhizobium japonicum</i> CCBAU 25435	GCA_000261605.1	AJQA01	520	9.46	63.5	9292	8475
<i>Bradyrhizobium japonicum</i> CCBAU 83623	GCA_000261625.1	AJQB01	1212	10.1	63.3	10277	8854
<i>Bradyrhizobium japonicum</i> E109	GCA_000807315.1	CP010313.1	-	9.22	63.7	8741	8404
<i>Bradyrhizobium japonicum</i> FN1	GCA_001038185.1	JGCL01	87	9.14	63.7	8664	8320
<i>Bradyrhizobium japonicum</i> in8p8	GCA_000426845.1	AUGD01	52	7.59	63.8	7270	6947
<i>Bradyrhizobium japonicum</i> ls-1	GCA_001280585.1	LGUJ01	104	8.98	64.0	8656	8201
<i>Bradyrhizobium japonicum</i> ls-34	GCA_000773865.1	JRPN01	248	10.3	63.0	9921	9376
<i>Bradyrhizobium japonicum</i> is5	GCA_000421305.1	ATWP01	60	7.59	63.8	7257	6929
<i>Bradyrhizobium japonicum</i> SEMIA 5079	GCA_000661935.1	CP007569.1	-	9.58	63.5	9143	8675

<i>Bradyrhizobium japonicum</i> USDA 123	GCA_000482525.1	AXVP01	517	10.6	63.3	10272	9181
<i>Bradyrhizobium japonicum</i> USDA 124	GCA_000374205.1	ARFJ01	123	9.00	64.0	8593	8182
<i>Bradyrhizobium japonicum</i> USDA 135	GCA_000472945.1	AXAT01	547	7.70	64.0	7662	6704
<i>Bradyrhizobium japonicum</i> USDA 38	GCA_000472745.1	AXAG01	107	9.61	63.5	9225	8760
<i>Bradyrhizobium japonicum</i> USDA 4	GCA_000472725.1	AXAF01	97	8.74	63.7	8235	7778
<i>Bradyrhizobium japonicum</i> USDA 6	GCA_000472985.1	AXAV01	87	9.13	63.7	8715	8321
<i>Bradyrhizobium jicamae</i> PAC68	GCA_001440395.1	LLXZ01	235	8.74	62.2	8277	7745
<i>Bradyrhizobium lablabi</i> GAS522	GCA_900104755.1	FNTI01	2	8.27	62.3	7822	7504
<i>Bradyrhizobium liaoningense</i> CCBAU 05525	GCA_000261645.1	AJQC01	1040	8.16	63.8	8111	6957
<i>Bradyrhizobium liaoningense</i> CCBAU 83689	GCA_000261665.1	AJQD01	1133	8.01	63.8	7966	6843
<i>Bradyrhizobium liaoningense</i> CCNWSX0360	GCA_001595995.1	LUKO01	242	8.59	63.7	8155	7651
<i>Bradyrhizobium manausense</i> BR3351	GCA_001440035.1	LJYG01	127	9.15	62.8	8404	7794
<i>Bradyrhizobium neotropiale</i> BR 10247	GCA_001641695.1	LSEF01	125	8.68	63.6	7989	7682
<i>Bradyrhizobium oligotrophicum</i> S58	GCA_000344805.1	AP012603.1	-	8.26	65.1	7291	7061
<i>Bradyrhizobium ottawaense</i> GAS524	GCA_900099825.1	LT629693.1	-	8.34	62.3	7956	7624
<i>Bradyrhizobium pachyrhizi</i> BR3262	GCA_001440015.1	LJYE01	116	8.97	63.7	8290	7621
<i>Bradyrhizobium pachyrhizi</i> PAC 48	GCA_001189245.1	LFIQ019.09	124	8.71	63.8	8096	7479
<i>Bradyrhizobium paxllaeri</i> LMTR 21	GCA_001693515.1	MAXB01	146	8.29	62.5	7713	7430
<i>Bradyrhizobium retamae</i> Ro19	GCA_001440415.1	LLYA01	235	8.47	61.9	7995	7481
<i>Bradyrhizobium</i> sp. 17-4	GCA_001312945.1	BBEX01	2463	7.11	64.5	-	-
<i>Bradyrhizobium</i> sp. Ai1a-2	GCA_000426245.1	AUEZ01	246	9.03	62.6	8411	7810
<i>Bradyrhizobium</i> sp. ARR65	GCA_000472385.1	AWZU01	139	8.61	62.0	8126	7603
<i>Bradyrhizobium</i> sp. AT1	GCA_001590795.1	JXDL01	8	7.54	64.2	7029	6673
<i>Bradyrhizobium</i> sp. BF49 ^a	2751185896	-	1	7.55	63.8	7398	7328
<i>Bradyrhizobium</i> sp. BR 10245	GCA_001641635.1	LUUB01	133	10.1	63.2	9486	8827
<i>Bradyrhizobium</i> sp. BR 10303	GCA_001542415.1	LNCU01	137	8.72	63.2	8162	7593
<i>Bradyrhizobium</i> sp. BTAi1	GCA_000015165.1	CP000494.1	-	8.49	64.8	7716	7496
<i>Bradyrhizobium</i> sp. CCBAU 15544	GCA_000261705.1	AJQF01	612	8.48	63.7	8340	7529
<i>Bradyrhizobium</i> sp. CCBAU 15615	GCA_000261725.1	AJQG01	453	8.85	63.7	8600	7815
<i>Bradyrhizobium</i> sp. CCBAU 15635	GCA_000261745.1	AJQH01	456	8.29	63.8	8091	7410
<i>Bradyrhizobium</i> sp. CCBAU 41267	GCA_000261765.1	AJQI01	563	9.12	64.0	9076	8388
<i>Bradyrhizobium</i> sp. CCBAU 43298	GCA_000261685.1	AJQE01	508	7.92	63.9	7836	7123
<i>Bradyrhizobium</i> sp. CCGE-LA001	GCA_000296215.2	CP013949.1	-	7.83	63.6	7234	6988
<i>Bradyrhizobium</i> sp. CCH10-C7	GCA_001556255.1	LSIN01	366	5.59	60.7	5487	5116
<i>Bradyrhizobium</i> sp. CCH4-A6	GCA_001556245.1	LSIM01	249	5.30	60.9	5151	4852
<i>Bradyrhizobium</i> sp. CCH5-F6	GCA_001556045.1	LSIC01	222	8.16	64.1	7720	7383
<i>Bradyrhizobium</i> sp. CF659	GCA_900113725.1	FOQJ01	25	8.47	64.5	7968	7608
<i>Bradyrhizobium</i> sp. Cp5.3	GCA_000426265.1	AUFA01	148	8.92	63.4	8486	8000

<i>Bradyrhizobium</i> sp. DFCI-1	GCA_000465325.1	AMFB01	89	7.65	64.4	7164	7112
<i>Bradyrhizobium</i> sp. DOA1	GCA_001593325.1	JXJM01	4	7.54	63.6	7085	6648
<i>Bradyrhizobium</i> sp. DOA9	GCA_000617845.2	BAWE01	2	7.85	64.5	7364	7109
<i>Bradyrhizobium</i> sp. Ec3.3	GCA_000472925.1	AXAS01	154	10.0	62.6	9477	8845
<i>Bradyrhizobium</i> sp. ERR11	GCA_900094605.1	FMAI01	102	9.16	63.2	8688	8037
<i>Bradyrhizobium</i> sp. G22	GCA_900011265.1	CZWJ01	20	9.09	63.7	8606	8188
<i>Bradyrhizobium</i> sp. Gha	GCA_900113735.1	FOQM01	95	8.25	62.9	7934	7318
<i>Bradyrhizobium</i> sp. Ghvi	GCA_900115265.1	FOVU01	41	7.93	63.0	7536	7137
<i>Bradyrhizobium</i> sp. Leaf396	GCA_001424605.1	LMQJ01	66	7.71	63.8	7324	7020
<i>Bradyrhizobium</i> sp. LMTR 3	GCA_001693485.1	MAXC01	55	7.84	62.3	7328	7024
<i>Bradyrhizobium</i> sp. LTSP849	GCA_000938255.1	JYMR01	57	8.57	63.2	8063	7841
<i>Bradyrhizobium</i> sp. LTSP857	GCA_000938285.1	JYMS01	50	8.43	63.3	7947	7719
<i>Bradyrhizobium</i> sp. LTSP885	GCA_000938305.1	JYMT01	43	7.85	63.4	7295	7143
<i>Bradyrhizobium</i> sp. LTSPM299	GCA_000938235.1	JYMU01	100	9.09	62.8	8488	8171
<i>Bradyrhizobium</i> sp. OHSU III	GCA_000497675.1	APJD01	82	7.94	64.7	7417	7217
<i>Bradyrhizobium</i> sp. OK095	GCA_900109945.1	FOBX01	51	7.85	63.9	7417	7204
<i>Bradyrhizobium</i> sp. ORS 278	GCA_000026145.1	CU234118.1	-	7.46	65.5	6788	6589
<i>Bradyrhizobium</i> sp. ORS 285	GCA_900176205.1	LT859959.1	-	7.80	65.2	7015	6749
<i>Bradyrhizobium</i> sp. ORS 375	GCA_000239775.2	CAFI01	497	7.86	65.5	7230	6821
<i>Bradyrhizobium</i> sp. R5	GCA_900101405.1	FMZW01	124	9.45	63.6	8887	8309
<i>Bradyrhizobium</i> sp. Rc2d	GCA_900099855.1	FNCU01	117	9.58	62.8	9149	8477
<i>Bradyrhizobium</i> sp. Rc3b	GCA_900114915.1	FOUS01	49	8.38	63.7	7874	7487
<i>Bradyrhizobium</i> sp. S23321	GCA_000284275.1	AP012279.1	-	7.23	64.3	6849	6733
<i>Bradyrhizobium</i> sp. STM 3809	GCA_000239795.2	CAFJ01	803	7.31	66.2	6897	6413
<i>Bradyrhizobium</i> sp. STM 3843	GCA_000239815.2	CAFK01	350	8.44	63.6	7822	7470
<i>Bradyrhizobium</i> sp. th.b2	GCA_000426785.1	AUGA01	266	10.1	63.3	9677	8877
<i>Bradyrhizobium</i> sp. Tv2a-2	GCA_000472425.1	AXAI01	87	8.50	62.2	7955	7609
<i>Bradyrhizobium</i> sp. URHA0002	GCA_000426105.1	AUES01	144	6.97	62.2	6757	6390
<i>Bradyrhizobium</i> sp. URHA0013	GCA_000518345.1	JADK01	23	7.19	63.8	6856	6620
<i>Bradyrhizobium</i> sp. URHD0069	GCA_000701345.1	JNIJ01	129	6.79	60.7	6595	6156
<i>Bradyrhizobium</i> sp. USDA 3384	GCA_000472685.1	AXAD01	51	9.80	63.6	9242	8791
<i>Bradyrhizobium</i> sp. WSM1253	GCA_000244935.1	AHMB01	2	8.72	63.1	8346	7851
<i>Bradyrhizobium</i> sp. WSM1417	GCA_000515415.1	AZXU01	1	8.05	63.2	7628	7292
<i>Bradyrhizobium</i> sp. WSM1743	GCA_000473065.1	AXAZ01	163	8.34	63.4	7858	7222
<i>Bradyrhizobium</i> sp. WSM2254	GCA_000472645.1	AXAB01	100	9.09	63.9	8586	8130
<i>Bradyrhizobium</i> sp. WSM2793	GCA_000379585.1	ARBF01	84	8.87	63.5	8409	7865
<i>Bradyrhizobium</i> sp. WSM3983	GCA_000473045.1	AXAY01	70	8.79	63.0	8416	7942
<i>Bradyrhizobium</i> sp. WSM4349	GCA_000373125.1	ARDH01	104	8.29	63.1	8029	7404

<i>Bradyrhizobium</i> sp. WSM471	GCA_000244915.1	CM001442.1	-	7.78	63.4	7336	6996
<i>Bradyrhizobium</i> sp. YR681	GCA_000282615.1	AKIY01	351	7.83	64.7	7575	7139
<i>Bradyrhizobium stylosanthis</i> BR 446	GCA_001641335.1	LVEM01	22	8.80	64.6	8195	7957
<i>Bradyrhizobium tropiciagri</i> SEMIA 6148	GCA_001189845.1	LFLZ01	189	9.77	63.5	-	-
<i>Bradyrhizobium valentinum</i> LmjM3	GCA_001440405.1	LLXX01	242	8.85	61.9	8566	7796
<i>Bradyrhizobium valentinum</i> LmjM6	GCA_001440385.1	LLXY01	242	9.15	61.9	8718	8034
<i>Bradyrhizobium viridifuturi</i> SEMIA 690	GCA_001238275.1	LGTB01	152	8.81	64.0	8372	7130
<i>Bradyrhizobium yuanmingense</i> BR3267	GCA_001439885.1	LJYF01	55	7.90	63.9	7318	6847
<i>Bradyrhizobium yuanmingense</i> CCBAU 05623	GCA_000261785.1	AJQJ01	570	8.25	63.8	8077	7249
<i>Bradyrhizobium yuanmingense</i> CCBAU 10071	GCA_900094575.1	FMAE01	108	8.20	63.8	7826	7334
<i>Bradyrhizobium yuanmingense</i> CCBAU 25021	GCA_000261805.1	AJQK01	490	7.99	63.8	7810	7021
<i>Bradyrhizobium yuanmingense</i> CCBAU 35157	GCA_000261825.1	AJQL01	457	7.85	63.9	7612	6906
<i>Bradyrhizobium yuanmingense</i> CGMCC 1.3531 ^a	2596583575	-	111	8.20	63.8	7860	7777
<i>Brucella abortus</i> 544 ^T	GCA_000369945.1	AQIS01	3	3.30	57.2	3386	3155
<i>Brucella abortus</i> NCTC 10505	GCA_000740175.1	NZ_CP007700.1 NZ_CP007701.1	-	3.29	57.2	3371	3140
<i>Brucella canis</i> RM6/66 ^T	GCA_000740335.1	NZ_CP007758.1 NZ_CP007759.1	-	3.31	57.2	3361	3152
<i>Brucella melitensis</i> 16M ^T	GCA_000007125.1	NC_003317.1 NC_003318.1	-	3.31	57.2	3369	3099
<i>Brucella melitensis</i> 20236	GCA_001431745.1	NZ_CP008750.1 NZ_CP008751.1	-	3.31	57.2	3381	3140
<i>Brucella microti</i> CCM 4915 ^T	GCA_000022745.1	NC_013119.1 NC_013118.1	-	3.34	57.2	3366	3198
<i>Brucella ovis</i> ATCC 25840 ^T	GCA_000016845.1	NC_009505.1 NC_009504.1	-	3.28	57.2	3395	3043
<i>Chelatococcus daeguensis</i> TAD1	GCA_001887265.1	NZ_CP018095.1	-	4.10	67.9	3848	3724
<i>Chelatococcus sambhunathii</i> DSM 18167 ^T	GCA_001418005.1	LIOL01	35	4.37	67.8	4173	4018
<i>Cohaesibacter marisflavi</i> CGMCC 1.9157 ^T	GCA_900115225.1	FOVR01	44	5.34	53.8	4868	4804
<i>Cucumibacter marinus</i> DSM 18995 ^T	GCA_000429865.1	AUCR01	27	3.71	62.2	3586	3499
<i>Devosia chinhatensis</i> IPL18 ^T	GCA_000969445.1	JZEY01	98	3.50	62.4	3398	3257
<i>Devosia enhydra</i> ATCC 23634 ^T	GCA_900119845.1	FPKU01	11	4.22	65.6	4080	3975
<i>Devosia lucknowensis</i> L15 ^T	GCA_900177655.1	FXWK01	3	3.72	62.8	3665	3584
<i>Devosia soli</i> GH2-10 ^T	GCA_000970455.1	LAJG01	48	4.14	61.0	4062	3709
<i>Ensifer sojae</i> CCBAU 05684 ^T	GCA_002288525.1	NZ_CP023067.1	-	6.09	62.0	5887	5474
<i>Filomicrobium insigne</i> CGMCC 1.6497 ^T	GCA_900104305.1	FNJC01	11	3.85	57.4	3676	3562
<i>Fulvimarina manganoxydans</i> CGMCC 1.10972 ^T	GCA_900176465.1	FWXR01	55	4.83	62.9	4528	4469
<i>Fulvimarina pelagi</i> DSM 15513 ^T	GCA_001463845.1	BBWO01	61	3.77	61.3	3523	3419

<i>Hoeflea olei</i> JC234 ^T	GCA_001703635.1	LQZT01	74	4.72	65.5	4357	4181
<i>Hoeflea phototrophica</i> DFL-43 ^T	GCA_000154705.2	NZ_CM002917.1	-	4.47	59.8	4227	4118
<i>Hyphomicrobium denitrificans</i> ATCC 51888 ^T	GCA_000143145.1	NC_014313.1	-	3.64	60.8	3542	3473
<i>Hyphomicrobium nitrativorans</i> NL23 ^T	GCA_000503895.1	NC_022997.1	-	3.65	63.9	3400	3279
<i>Hyphomicrobium zavarzinii</i> ATCC 27496 ^T	GCA_000383415.1	ARTG01	20	4.65	63.7	4276	4175
<i>Kaistia adipata</i> DSM 17808 ^T	GCA_000423225.1	AUHO01	14	4.84	67.1	4545	4423
<i>Kaistia soli</i> DSM 19436 ^T	GCA_900129325.1	FQUP01	18	5.24	64.5	4892	4851
<i>Liberibacter crescens</i> BT-0	GCA_001543305.1	NZ_CP010522.1	-	1.52	35.4	1372	1299
<i>Liberibacter crescens</i> BT-1 ^T	GCA_000325745.1	NC_019907.1	-	1.51	35.4	1363	1245
<i>Maritalea myrionectae</i> DSM 19524 ^T	GCA_000423365.1	AUHV01	12	3.54	52.6	3472	3416
<i>Martelella endophytica</i> YC6887 ^T	GCA_000960975.1	NZ_CP010803.1	-	4.82	62.1	4526	4393
<i>Martelella mediterranea</i> DSM 17316 ^T	GCA_000376125.1	AQWH01	75	5.64	62.4	5301	5068
<i>Mesorhizobium australicum</i> WSM2073 ^T	GCA_000230995.3	NC_019973.1	-	6.20	62.8	6068	5795
<i>Mesorhizobium ciceri</i> CC1192	GCA_001618825.1	NZ_CP015062.1	-	6.94	62.5	6826	6551
<i>Mesorhizobium ciceri</i> WSM1271	GCA_000185905.1	NC_014923.1	-	6.69	62.6	6532	6264
<i>Mesorhizobium huakuii</i> 7653R	GCA_000709395.1	NZ_CP006581.1	-	6.36	63.3	6288	5885
<i>Mesorhizobium japonicum</i> MAFF303099	GCA_000009625.1	NC_002678.2	-	7.04	62.5	7487	7114
<i>Mesorhizobium opportunistum</i> WSM2075 ^T	GCA_000176035.2	NC_015675.1	-	6.88	62.9	6779	6514
<i>Mesorhizobium sophorae</i> ICMP 19535 ^T	GCA_002270415.1	NNRI01	24	8.05	62.2	7780	7205
<i>Mesorhizobium</i> sp. WSM1497	GCA_001672455.2	NZ_CP021070.1	-	7.20	62.4	7008	6654
<i>Methylobacterium extorquens</i> DM4 ^T	GCA_000083545.1	NC_012988.1	-	6.12	68.0	5763	5503
<i>Methylobacterium nodulans</i> ORS 2060 ^T	GCA_000022085.1	NC_011894.1	-	8.84	68.5	7471	7020
<i>Methylobacterium oryzae</i> CBMB20 ^T	GCA_000757795.1	NZ_CP003811.1	-	6.29	69.8	5771	5530
<i>Methylobacterium phyllosphaerae</i> CBMB27 ^T	GCA_001936175.1	NZ_CP015367.1	-	6.32	69.6	5722	5506
<i>Methylobacterium populi</i> BJ001 ^T	GCA_000019945.1	NC_010725.1	-	5.85	69.4	5480	5289
<i>Methylocapsa aurea</i> KYG ^T	GCA_000746085.1	JQKO01	37	3.97	61.3	3703	3551
<i>Methylocapsa palsarum</i> NE2 ^T	GCA_900114285.1	FOSN01	78	4.11	61.7	3885	3820
<i>Methylocella silvestris</i> BL2 ^T	GCA_000021745.1	NC_011666.1	-	4.31	63.1	4011	3873
<i>Methylocystis bryophila</i> S285	GCA_002117405.1	NZ_CP019948.1	-	4.53	63.2	4286	4150
<i>Methylocystis rosea</i> SV97 ^T	GCA_000372845.1	ARCT01	2	3.91	62.5	3895	3709
<i>Methyloferula stellata</i> AR4 ^T	GCA_000385335.1	ARWA01	1	4.24	59.6	3961	3877
<i>Methylosinus trichosporium</i> OB3b ^T	GCA_0002752655.1	CP023737.1	-	5.18	65.8	4806	4565
<i>Microvirga lotononidis</i> WSM3557 ^T	GCA_000262405.1	AJUA01	104	7.08	63.1	6915	6524
<i>Microvirga massiliensis</i> JC119 ^T	GCA_001006805.1	CDSD01	50	9.17	62.8	8575	8045
<i>Neomegalonema perideroedes</i> DSM 15528 ^T	GCA_000374145.1	ARFG01	22	3.41	67.2	3121	3023
<i>Neorhizobium galegae</i> HAMBI 540 ^T	GCA_000731315.1	NZ_HG938353.1	-	6.46	61.3	6271	6033
<i>Nitratireductor basaltis</i> RR3-28	GCA_001953055.1	NZ_CP019044.1	-	3.36	58.6	3237	3082
<i>Nitratireductor soli</i> ZZ-1 ^T	GCA_001050155.1	LFVY01	60	5.13	64.1	5000	4839

<i>Nitrobacter hamburgensis</i> X14 ^T	GCA_000013885.1	NC_007964.1	-	4.41	61.7	4240	396
<i>Nitrobacter vulgaris</i> Ab1	GCA_002028545.1	MWPQ01	96	3.90	59.8	3739	3501
<i>Nitrobacter winogradskyi</i> Nb-255 ^T	GCA_000012725.1	NC_007406.1	-	3.40	62.0	3224	2984
<i>Ochrobactrum anthropi</i> ATCC 49188 ^T	GCA_000017405.1	NC_009667.1 NC_009668.1	-	5.21	56.2	5087	4870
<i>Ochrobactrum intermedium</i> LMG 3301 ^T	GCA_000182645.1	ACQA01	4	4.73	57.7	4571	4269
<i>Oligotropha carboxidovorans</i> ATCC 49405 ^T	GCA_000021365.1	NC_011386.1	-	3.75	62.4	3616	3518
<i>Paramesorhizobium deserti</i> A-3-E ^T	GCA_001558695.1	LNTU011	41	5.48	60.9	5149	4946
<i>Pararhizobium polonicum</i> F5.1 ^T	GCA_001687365.1	LGLV01	31	5.90	61.2	5591	5430
<i>Pelagibacterium halotolerans</i> B2 ^T	GCA_000230555.1	NC_016078.1	-	3.94	61.4	3858	3755
<i>Pelagibacterium luteolum</i> CGMCC 1.10267 ^T	GCA_900100665.1	FNCS01	51	4.30	60.4	4327	4266
<i>Pleomorphomonas koreensis</i> DSM 23070 ^T	GCA_000425185.1	AULH01	76	4.62	67.2	4318	4230
<i>Pleomorphomonas oryzae</i> DSM 16300 ^T	GCA_000422965.1	AUHB01	39	5.23	63.0	4857	4733
<i>Prosthecomicrobium hirschii</i> 16	GCA_001305515.1	LJYW01	52	6.48	68.8	5710	5502
<i>Pseudaminobacter manganicus</i> JH-7 ^T	GCA_002075885.1	MEDT01	60	4.84	61.2	4685	4504
<i>Pseudaminobacter salicylatoxidans</i> KCT001	GCA_000304395.1	CAIU01	53	4.61	62.8	4456	3981
<i>Pseudorhizobium pelagicum</i> R1-200B4	GCA_000722615.1	JAKI01	62	5.14	62.8	4998	4791
<i>Rhizobium etli</i> CFN 42 ^T	GCA_000092045.1	NC_007761.1	-	6.53	61.1	6435	5992
<i>Rhizobium favelukesii</i> LPU83 ^T	GCA_000577275.1	NZ_HG916852.1	-	7.04	59.6	8202	7513
<i>Rhizobium gallicum</i> R602 ^T	GCA_000816845.1	NZ_CP006877.1	-	7.31	59.6	7138	6674
<i>Rhizobium grahamii</i> CCGE 502 ^T	GCA_000298315.2	AEYE02	80	7.15	59.4	6898	6844
<i>Rhizobium leguminosarum</i> WSM1689	GCA_000517605.1	NZ_CP007045.1	-	6.90	60.9	6760	6429
<i>Rhizobium tropici</i> CIAT 899 ^T	GCA_000330885.1	NC_020059.1	-	6.69	59.5	6419	6208
<i>Rhodoblastus acidophilus</i> DSM 137 ^T	GCA_900187365.1	FYDG01	74	4.71	65.3	4490	4422
<i>Rhodomicrobium vannielii</i> ATCC 17100 ^T	GCA_000166055.1	NC_014664.1	-	4.02	62.2	3724	3600
<i>Rhodopseudomonas palustris</i> BisA53	GCA_000014825.1	NC_008435.1	-	5.51	64.4	4959	4834
<i>Rhodopseudomonas palustris</i> BisB18	GCA_000013745.1	NC_007925.1	-	5.51	65.0	5000	4858
<i>Rhodopseudomonas palustris</i> CGA009	GCA_000195775.1	NC_005296.1	-	5.47	65.0	4996	4874
<i>Rhodopseudomonas palustris</i> HaA2	GCA_000013365.1	NC_007778.1	-	5.33	66.0	4785	4673
<i>Rhodopseudomonas pseudopalustris</i> DSM 123 ^T	GCA_900110435.1	FODT01	29	5.27	64.6	4883	4821
<i>Salinarimonas rosea</i> DSM 21201 ^T	GCA_000429045.1	AUBC01	62	5.25	71.8	4903	4735
<i>Sinorhizobium fredii</i> NGR234	GCA_000018545.1	NC_012587.1	-	6.89	62.4	6472	6362
<i>Sinorhizobium fredii</i> USDA 205T	GCA_001461695.1	AUTC01	209	6.58	62.3	6377	5774
<i>Sinorhizobium meliloti</i> 1021	GCA_000006965.1	NC_003047.1	-	6.69	62.2	6292	6218
<i>Tardiphaga robiniae</i> Vaf-07	GCA_001618955.1	LVYV01	56	6.36	61.5	5883	5722
<i>Tardiphaga</i> sp. OK246	GCA_900188215.1	FZOX01	19	6.75	61.4	6346	6165
<i>Terasakiella pusilla</i> DSM 6293 ^T	GCA_000688235.1	JHYO01	85	4.05	50.0	3967	3783

^aGenomes downloaded from the JGI IMG server instead of the NCBI ftp server.