

ORGANISM	ACCESSION	SIZE	GC%	#	pgc%	end5	end3	loci	ori	#phgpb	Ty	class	att	target	In	Co	NC	Ly	Ta	Mu	dX	OC	
Corynebacterium jeikeium K411	NC_007164	2462499	61.40	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	
Coxiella burnetii RSA 493	NC_002971	1995275	42.66	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	
Cyanobacteria bacterium Yellowstone A-Prime	NC_007775	2932766	60.24	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	
Cyanobacteria bacterium Yellowstone B-Prime	NC_007776	3046682	58.45	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	
Dechloromonas aromatica RCB	NC_007298	4501104	59.25	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	
Dehalococcoides ethenogenes 195	NC_002936	1469720	48.85	1	51.01	969242	1021142	DET1067-DET1114	+	51901	PRO	LRG	Y	DET1066	2	7	1	2	2	0	119	48	
Dehalococcoides sp. CBDB1	NC_007356	1395502	47.03	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	
Deinococcus radiodurans R1	NC_001264	412348	66.69	1	65.50	90546	118664	DRA0094-DRA0121	+	28119	PRO	LRG	N	N.D.	0	3	0	0	0	0	0	29	
Deinococcus radiodurans R1	NC_001263	2648638	67.01	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	
Desulfotalea psychrophila Lsv54	NC_006138	3523383	46.81	1	41.89	455474	439461	DP0412-DP0425	-	16014	PRO	MED	SAT	Y	tRNA-Leu-3	2	0	0	1	0	0	218	14
Desulfotalea psychrophila Lsv54	NC_006138	3523383	46.81	2	46.71	1787949	1742488	DP1571-DP1604	-	45462	PRO	LRG	Y	tRNA-Leu-5	1	2	1	1	0	0	0	264	34
Desulfotalea psychrophila Lsv54	NC_006138	3523383	46.81	3	43.43	2262540	2322258	DP1991-DP2040	+	59719	PRO	LRG	Y	tRNA-Thr-3	2	1	0	0	0	0	0	285	50
Desulfovibrio desulfuricans G20	NC_007519	3730232	57.84	1	59.47	923315	994232	Dde_0896-Dde_0966	+	70918	PRO	LRG	Y	N.D.	3	3	0	0	5	0	52	71	
Desulfovibrio desulfuricans G20	NC_007519	3730232	57.84	2	60.53	1987435	1907643	Dde_1868-Dde_1936	-	79793	PRO	LRG	Y	N.D.	3	3	0	0	5	0	142	69	
Desulfovibrio desulfuricans G20	NC_007519	3730232	57.84	3	62.51	2560734	2573940	Dde_2544-Dde_2557	+	13207	PRO	MED	N	N.D.	0	1	0	1	0	0	0	14	
Desulfovibrio desulfuricans G20	NC_007519	3730232	57.84	4	56.45	3323331	3399211	Dde_3342-Dde_3434	+	75881	PRO	LRG	Mu	N	N.D.	1	3	1	1	2	1	0	92
Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough	NC_002937	3570858	63.14	1	63.62	270578	233143	tRNA-Pseudo-1-DVU0236	+	37436	PRO	LRG	Y	tRNA-Lys-1	1	3	1	2	6	0	153	48	
Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough	NC_002937	3570858	63.14	2	65.00	1204981	1240251	DVU1098-DVU1144	+	35271	PRO	LRG	Mu	N	N.D.	0	3	3	1	2	3	0	47
Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough	NC_002937	3570858	63.14	3	58.17	1596092	1556471	DVU1481-DVU1527	-	39622	PRO	LRG	Y	tRNA-Ser-4	1	10	1	1	0	0	0	190	47
Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough	NC_002937	3570858	63.14	4	60.77	2250660	2304061	NC_002937_tRNA-Gly-3-NC_0	+	53402	PRO	LRG	Y	tRNA-Gly-3	1	3	2	3	0	0	0	1036	58
Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough	NC_002937	3570858	63.14	5	65.06	2799591	2833587	DVU2686-DVU2732	+	33997	PRO	LRG	Mu	N	N.D.	0	4	2	1	7	2	0	48
Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough	NC_002937	3570858	63.14	6	62.54	2977702	2936186	DVU2828-DVU2881	-	41517	PRO	LRG	Y	tRNA-Arg-5	1	3	1	2	6	0	286	54	
Ehrlichia canis str. Jake	NC_007354	1315030	28.96	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	
Ehrlichia ruminantium str. Gardel	NC_006831	1499920	27.51	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	
Ehrlichia ruminantium str. Welgevonden	NC_006832	1512977	27.48	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	
Ehrlichia ruminantium str. Welgevonden	NC_005295	1516355	27.48	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	
Enterococcus faecalis V583	NC_004668	3218031	37.53	1	37.63	289300	326362	EF0303-NC_004668_tRNA-Met	+	37063	PRO	LRG	Y	pepC	1	3	2	0	3	0	54	53	
Enterococcus faecalis V583	NC_004668	3218031	37.53	2	36.20	1415824	1459644	EF1451-EF1503	+	43821	PRO	LRG	Y	tRNA-Lys-3	1	4	1	0	1	0	0	53	
Enterococcus faecalis V583	NC_004668	3218031	37.53	3	33.47	1962559	1922618	tRNA-Met-8-EF2043	-	39942	PRO	LRG	Y	N.D.	1	3	1	2	4	0	74	42	
Enterococcus faecalis V583	NC_004668	3218031	37.53	4	33.36	2004742	2048271	EF2084-EF2145	+	43530	PRO	LRG	SAT	Y	tRNA-Thr-2	1	0	0	1	0	0	125	62
Enterococcus faecalis V583	NC_004668	3218031	37.53	5	34.94	2736931	2700412	EF2802-EF2855	-	36520	PRO	LRG	Y	rpmG	1	8	1	0	3	0	123	51	
Erwinia carotovora subsp. atroseptica SCRI1043	NC_004547	5064019	50.97	1	50.77	2966914	2918980	pFlb-ECA2637	-	47935	PRO	LRG	Y	N.D.	1	8	1	1	18	0	243	42	
Erwinia carotovora subsp. atroseptica SCRI1043	NC_004547	5064019	50.97	2	52.22	4140147	4180770	ssb-ECA3742	+	40624	PRO	LRG	Mu	N	N.D.	0	5	0	1	14	2	0	54
Erwinia carotovora subsp. atroseptica SCRI1043	NC_004547	5064019	50.97	3	55.72	4809447	4784723	ECA4276-ECA4292	-	24725	PRO	LRG	SAT	Y	N.D.	4	0	0	1	0	0	337	17
Erythrobacter litoralis HTCC2594	NC_007722	3052398	63.07	1	59.46	157314	189261	ELI_00620-ELI_00770	+	31948	PRO	LRG	SAT	Y	ELI	3	0	0	1	0	0	241	31
Erythrobacter litoralis HTCC2594	NC_007722	3052398	63.07	2	67.44	2812472	2826784	ELI_13955-ELI_14035	+	14313	PRO	MED	N	N.D.	0	6	1	0	1	0	0	18	
Escherichia coli CFT073	NC_004431	5231428	50.47	1	50.22	908948	945479	intT-ybJc	+	36532	PRO	LRG	Y	N.D.	1	9	0	1	14	0	384	52	
Escherichia coli CFT073	NC_004431	5231428	50.47	2	50.09	1397105	1452282	c1516-c1602	+	55178	PRO	LRG	Y	icdA	1	11	0	2	9	0	265	84	
Escherichia coli CFT073	NC_004431	5231428	50.47	3	49.16	3018510	3067126	c3143-c3206	+	48617	PRO	LRG	Y	tmRNA-1	2	10	0	1	10	0	1811	64	
Escherichia coli K12	NC_000913	4639675	50.79	1	43.31	563978	585326	b0538-ompT	+	21349	PRO	LRG	Y	tRNA-Arg-1	2	1	0	2	1	0	60	29	
Escherichia coli K12	NC_000913	4639675	50.79	2	46.51	1433025	1409923	ydaQ-ynaE	-	23103	PRO	LRG	SAT	Y	ydaO	2	0	0	1	4	0	101	31
Escherichia coli K12	NC_000913	4639675	50.79	3	46.53	1631485	1662546	pinQ-ynfI	+	31062	PRO	LRG	Y	ynfI	2	1	0	1	3	0	161	45	
Escherichia coli K12	NC_000913	4639675	50.79	4	44.12	2464376	2474312	intS-yfdT	+	9937	PRO	MED	SAT	Y	tRNA-Arg-2	1	0	0	0	2	0	191	15
Escherichia coli O157:H7	NC_002695	5498450	50.54	1	45.15	300012	310644	ECs0271-ECs0288	+	10633	PRO	LRG	P2	Y	tRNA-Thr-1	3	0	0	0	3	0	60	14
Escherichia coli O157:H7	NC_002695	5498450	50.54	2	50.57	892240	925601	ECs0801-ECs0846	+	33362	PRO	LRG	N	N.D.	0	6	0	2	12	0	0	45	
Escherichia coli O157:H7	NC_002695	5498450	50.54	3	51.18	1210805	1161091	ECs1055-ECs1127	-	49715	PRO	LRG	Y	tRNA-Ser-2	1	7	0	2	10	0	206	66	
Escherichia coli O157:H7	NC_002695	5498450	50.54	4	50.37	1316408	1245903	ECs1160-ECs1259	-	70506	PRO	LRG	Y	ECs1260	1	2	0	2	3	0	137	99	
Escherichia coli O157:H7	NC_002695	5498450	50.54	5	50.00	1541478	1687839	ECs1501-ECs1692	+	146362	PRO	LRG	Y	N.D.	4	29	2	4	21	0	148	189	
Escherichia coli O157:H7	NC_002695	5498450	50.54	6	50.30	1757453	1815680	ECs1757-ECs1825	+	58228	PRO	LRG	Y	ECs1756	2	8	2	2	7	0	96	61	
Escherichia coli O157:H7	NC_002695	5498450	50.54	7	52.63	1940750	1987367	ECs1959-ECs2006	+	46618	PRO	LRG	Y	tRNA-Arg-6	1	8	2	2	8	0	0	48	
Escherichia coli O157:H7	NC_002695	5498450	50.54	8	52.74	2240563	2189516	tRNA-Arg-7-tRNA-Arg-8	-	51048	PRO	LRG	Y	tRNA-Arg-8	1	18	2	4	19	0	1384	73	
Escherichia coli O157:H7	NC_002695	5498450	50.54	9	50.10	2614141	2592901	ECs2617-ECs2646	-	21241	PRO	LRG	SAT	Y	tRNA-Leu-2	1	0	0	0	6	0	227	28
Escherichia coli O157:H7	NC_002695	5498450	50.54	10	52.02	2712096	2668007	ECs2716-ECs2773	-	44090	PRO	LRG	Y	tRNA-Ser-4	2	6	0	2	10	0	113	54	
Escherichia coli O157:H7	NC_002695	5498450	50.54	11	51.68	2943805	2895905	ECs2939-ECs3013	-	47901	PRO	LRG	SAT	Y	N.D.	1	6	0	2	12	0	58	72
Escherichia coli O157:H7	NC_002695	5498450	50.54	12	43.85	3475789	3494952	ECs3483-ECs3509	+	19164	PRO	LRG	SAT	Y	tmRNA-1	2	0	0	0	1	0	0	24
Escherichia coli O157:H7	NC_002695	5498450	50.54	13	53.74	5041814	5079469	ECs4944-ECs4998	+	37656	PRO	LRG	Mu	N	N.D.	1	4	0	1	8	2	0	56
Escherichia coli O157:H7 EDL933	NC_002655	5528445	50.38	1	45.15	300013	310645	intH-Z0322	+	10633	PRO	LRG	P2	Y	tRNA-Thr-1	3	0	0	0	3	0	60	15
Escherichia coli O157:H7 EDL933	NC_002655	5528445	50.38	2	49.93	935929	892627	Z0946-Z0985	-	43303	PRO	LRG	Y	ybhC	2	5	0	2	12	0	218	39	

ORGANISM	ACCESSION	SIZE	GC%	#	pgc%	end5	end3	loci	ori	#phgpb	Ty	class	att	target	In	Co	NC	Ly	Ta	Mu	dX	OC
Escherichia coli O157:H7 EDL933	NC_002655	5528445	50.38	3	51.95	1295622	1250314	Z1323-Z1383	-	45309	PRO	LRG	Y	tRNA-Ser-2	1	2	2	1	7	0	207	60
Escherichia coli O157:H7 EDL933	NC_002655	5528445	50.38	4	49.90	1330720	1400180	intW-ycdC	+	69461	PRO	LRG	Y	N.D.	1	1	0	2	3	0	137	77
Escherichia coli O157:H7 EDL933	NC_002655	5528445	50.38	5	48.24	1678525	1761710	Z1835-ycgN	+	83186	PRO	LRG	Y	ycgN	3	23	2	2	14	0	181	99
Escherichia coli O157:H7 EDL933	NC_002655	5528445	50.38	6	49.44	1866038	1893207	Z2063-tRNA-Met-6	+	27170	PRO	LRG	Y	tRNA-Arg-5	1	8	1	2	10	0	0	40
Escherichia coli O157:H7 EDL933	NC_002655	5528445	50.38	7	49.62	2115956	2165795	Z2337-ydaO	+	49840	PRO	LRG	Y	ydaO	1	7	1	2	9	0	101	67
Escherichia coli O157:H7 EDL933	NC_002655	5528445	50.38	8	51.93	2282874	2341960	Z6022-Z2583	+	59087	PRO	LRG	Y	N.D.	1	7	2	2	7	0	75	68
Escherichia coli O157:H7 EDL933	NC_002655	5528445	50.38	9	49.08	2668052	2712966	intT-flIE	+	44915	PRO	LRG	Y	fliF	2	1	0	0	7	0	287	55
Escherichia coli O157:H7 EDL933	NC_002655	5528445	50.38	10	52.25	2788461	2743224	Z3073-intU	-	45238	PRO	LRG	Y	tRNA-Ser-4	2	5	0	2	12	0	113	48
Escherichia coli O157:H7 EDL933	NC_002655	5528445	50.38	11	51.66	3015072	2966136	Z3305-intV	-	48937	PRO	LRG	Y	N.D.	1	8	1	2	7	0	58	64
Francisella tularensis subsp. tularensis SCHU 54	NC_006570	1892819	32.26	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Frankia sp. CcI3	NC_007777	5433628	70.08	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Fusobacterium nucleatum subsp. nucleatum ATCC 25586	NC_003454	2174500	27.15	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Geobacillus kaustophilus HTA426	NC_006510	3544776	52.09	1	43.59	535633	580399	GK0488-GK0555	+	44767	PRO	LRG	Y	GK0487	2	7	3	2	3	0	82	68
Geobacter metallireducens GS-15	NC_007517	3997420	59.51	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Geobacter sulfurreducens PCA	NC_002939	3814139	60.94	1	53.07	2335806	2345763	GSU2118-GSU2124	+	9958	PRO	LRG SAT	Y	N.D.	2	0	0	1	0	0	188	7
Gloeobacter violaceus PCC 7421	NC_005125	4659019	62.00	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Gluconobacter oxydans 621H	NC_006677	2702173	61.07	1	59.10	2537934	2581828	GOX2318-GOX2368	+	43895	PRO	LRG	Y	tRNA-Val-3	1	4	1	0	5	0	201	51
Gluconobacter oxydans 621H	NC_006677	2702173	61.07	2	58.66	2683373	2631060	GOX2431-GOX2485	-	52314	PRO	LRG	Y	tRNA-Cys-1	1	1	2	0	2	0	52	55
Haemophilus ducreyi 35000HP	NC_002940	1698955	38.22	1	48.23	73234	105391	HD0089-HD0154	+	32158	PRO	LRG Mu	N	N.D.	0	2	0	0	3	2	0	54
Haemophilus ducreyi 35000HP	NC_002940	1698955	38.22	2	42.81	382582	412066	HD0489-HD0539	+	29485	PRO	LRG Mu	N	N.D.	0	4	1	0	3	2	0	42
Haemophilus ducreyi 35000HP	NC_002940	1698955	38.22	3	41.15	1262080	1303775	HD1517-HD1581	+	41696	PRO	LRG Mu	N	N.D.	0	1	2	1	2	1	0	57
Haemophilus influenzae 86-028NP	NC_007146	1913428	38.15	1	40.96	1403911	1464344	dnab-prfA	+	60434	PRO	LRG Mu	N	N.D.	1	5	2	0	3	1	0	85
Haemophilus influenzae 86-028NP	NC_007146	1913428	38.15	2	37.88	1575155	1609932	NTHI1711-trpC	+	34778	PRO	LRG	Y	N.D.	1	6	1	2	0	0	133	47
Haemophilus influenzae 86-028NP	NC_007146	1913428	38.15	3	40.30	1707352	1727080	NTHI1856-NTHI1890	+	19729	PRO	LRG	N	N.D.	0	8	1	1	11	0	0	30
Haemophilus influenzae Rd KW20	NC_000907	1830138	38.15	1	39.54	1513224	1498816	HI1402-HI1424	-	14409	PRO	LRG	Y	tRNA-Leu-4	1	5	0	2	1	0	151	19
Haemophilus influenzae Rd KW20	NC_000907	1830138	38.15	2	43.75	1559962	1602497	HI1476-parC	+	42536	PRO	LRG Mu	N	N.D.	0	5	0	0	7	4	0	50
Haemophilus influenzae Rd KW20	NC_000907	1830138	38.15	3	38.30	1630955	1638288	prfA-ftnN	+	7334	PRO	LRG Mu	N	N.D.	0	1	0	0	2	1	0	7
Hahella chejuensis KCTC 2396	NC_007645	7215267	53.87	1	55.39	383094	416114	HCH_00366-HCH_00405	+	33021	PRO	LRG	Y	HCH	1	7	1	0	2	0	127	39
Hahella chejuensis KCTC 2396	NC_007645	7215267	53.87	2	53.18	2947108	2988255	HCH_02852-HCH_02910	+	41148	PRO	LRG	Y	N.D.	1	4	1	0	1	0	67	56
Hahella chejuensis KCTC 2396	NC_007645	7215267	53.87	3	53.65	4663633	4700154	HCH_04541-HCH_04582	+	36522	PRO	LRG	N	N.D.	0	12	0	0	2	0	0	43
Hahella chejuensis KCTC 2396	NC_007645	7215267	53.87	4	56.12	5815648	5765330	HCH_05648-HCH_05699	-	50319	PRO	LRG	Y	N.D.	1	3	1	0	0	0	383	50
Hahella chejuensis KCTC 2396	NC_007645	7215267	53.87	5	55.42	6867447	6901216	HCH_06750-HCH_06789	+	33770	PRO	LRG	Y	HCH	1	7	2	0	1	0	126	39
Helicobacter hepaticus ATCC 51449	NC_004917	1799146	35.93	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Helicobacter pylori 26695	NC_000915	1667867	38.87	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Helicobacter pylori J99	NC_000921	1643831	39.19	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Idiomarina loihiensis LZTR	NC_006512	2839318	47.04	1	43.38	1743546	1727886	IL1612-IL1631	-	15661	PRO	LRG SAT	Y	N.D.	1	0	0	0	2	0	247	17
Lactobacillus acidophilus NCFM	NC_006814	1993564	34.71	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Lactobacillus johnsonii NCC 533	NC_005362	1992676	34.61	1	35.17	327838	367873	LJ0288-LJ0330	+	40036	PRO	LRG	Y	N.D.	1	8	0	2	1	0	56	46
Lactobacillus johnsonii NCC 533	NC_005362	1992676	34.61	2	34.71	1330481	1292072	LJ1418-LJ1465	+	38410	PRO	LRG	Y	tRNA-Ser-3	1	8	0	1	2	0	104	50
Lactobacillus plantarum WCFS1	NC_004567	3308274	44.47	1	41.47	606331	6440559	lp_0658-dnaX	+	37729	PRO	LRG	Y	tRNA-Asn-2	1	7	1	1	5	0	0	37
Lactobacillus plantarum WCFS1	NC_004567	3308274	44.47	2	40.05	2204060	2162771	lp_2399-lp_2456	-	41290	PRO	LRG	Y	tRNA-Glu-3	2	18	0	0	5	0	0	56
Lactobacillus sakei subsp. sakei 23K	NC_007576	1884661	41.26	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Lactococcus lactis subsp. lactis IL1403	NC_002662	2365589	35.33	1	35.06	28825	56382	mtlR-tRNA-Lys-1	+	27558	PRO	LRG	Y	tRNA-Asn-1	1	1	0	0	0	0	6655	39
Lactococcus lactis subsp. lactis IL1403	NC_002662	2365589	35.33	2	35.68	447143	484094	pi101-NC_002662_tRNA-Unde	+	36952	PRO	LRG	Y	tRNA-Arg-2	1	12	1	4	5	0	93	56
Lactococcus lactis subsp. lactis IL1403	NC_002662	2365589	35.33	3	34.77	1036339	1100902	pi201-ykJK	+	64564	PRO	LRG	Y	radC	1	9	1	3	3	0	303	95
Lactococcus lactis subsp. lactis IL1403	NC_002662	2365589	35.33	4	35.31	1457116	1415289	pi303-pi360	-	41828	PRO	LRG	Y	tmRNA-1	1	11	0	3	7	0	167	61
Legionella pneumophila str. Lens	NC_006369	3345687	38.41	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Legionella pneumophila str. Paris	NC_006368	3503610	38.37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Legionella pneumophila subsp. pneumophila str. Philadelphia	NC_002942	3397754	38.27	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Leifsonia xyli subsp. xyli str. CTCB07	NC_006087	2584158	67.68	1	62.70	2447497	2485065	Lxx23845-Lxx24254	+	37569	PRO	LRG	Y	tRNA-Gly-3	1	4	2	0	0	0	0	38
Leptospira interrogans serovar Copenhageni str. Fiocruz L1-139B	NC_005823	4277185	35.05	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Leptospira interrogans serovar Copenhageni str. Fiocruz L1-139B	NC_005824	350181	34.98	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Leptospira interrogans serovar Lai str. 56601	NC_004343	358943	35.14	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Leptospira interrogans serovar Lai str. 56601	NC_004342	4332241	35.01	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Listeria innocua Clip11262	NC_003212	3011208	37.44	1	37.28	76060	115599	lin0071-lin0129	+	39540	PRO	LRG	Y	tRNA-Lys								

ORGANISM	ACCESSION	SIZE	GC%	#	pgc%	end5	end3	loci	ori	#phgpb	Ty	class	att	target	In	Co	NC	Ly	Ta	Mu	dX	OC
Listeria innocua Clip11262	NC_003212	3011208	37.44	5	35.13	2625922	2587434	lin2561-lin2610	-	38489	PRO	LRG	Y	tRNA-Arg-5	2	9	1	0	5	0	115	50
Listeria monocytogenes EGD-e	NC_003210	2944528	37.98	1	35.94	2402603	2358515	lmo2271-int	-	44089	PRO	LRG	Y	N.D.	1	7	0	1	2	0	237	62
Listeria monocytogenes str. 4b F2365	NC_002973	2905310	38.04	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Magnetospirillum magneticum AMB-1	NC_007626	4967148	65.09	1	64.88	380453	421095	amb0342-amb0394	+	40643	PRO	LRG	Y	tRNA-Ser-1	1	3	1	0	0	0	1878	53
Magnetospirillum magneticum AMB-1	NC_007626	4967148	65.09	2	64.32	1275245	1227221	amb1153-amb1202	-	48025	PRO	LRG	Y	N.D.	1	3	1	0	0	0	268	50
Magnetospirillum magneticum AMB-1	NC_007626	4967148	65.09	3	67.21	1657763	1631085	amb1491-amb1526	-	26679	PRO	LRG SAT	Y	tRNA-Thr-1	1	0	1	1	0	0	177	36
Magnetospirillum magneticum AMB-1	NC_007626	4967148	65.09	4	64.58	1874273	1920451	amb1724-amb1781	+	46179	PRO	LRG Mu	N	N.D.	1	4	0	1	1	2	0	58
Magnetospirillum magneticum AMB-1	NC_007626	4967148	65.09	5	64.23	2153641	2173856	amb1993-amb2001	+	20216	PRO	LRG	N	N.D.	0	1	0	1	0	0	0	9
Mannheimia succiniciproducens MBEL55E	NC_006300	2314078	42.54	1	45.86	76498	112399	MS0078-MS0129	+	35902	PRO	LRG Mu	N	N.D.	0	3	1	0	15	2	0	53
Mesoplasma florum L1	NC_006055	793224	27.02	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Mesorhizobium loti MAFF303099	NC_002678	7036071	62.75	1	60.23	6575119	6605246	tRNA-Arg-4-msr8019	+	30128	PRO	LRG	Y	N.D.	1	1	0	0	0	0	176	39
Mesorhizobium loti MAFF303099	NC_002678	7036071	62.75	2	60.90	6984118	7016855	m1r8517-m1r8553	+	32738	PRO	LRG	N	N.D.	0	5	0	0	0	0	0	36
Methylococcus capsulatus str. Bath	NC_002977	3304554	63.58	1	66.88	2818529	2842021	MCA2630-MCA2660	+	23493	PRO	LRG	Y	tmRNA-1	1	3	0	1	0	0	1484	31
Methylococcus capsulatus str. Bath	NC_002977	3304554	63.58	2	64.31	3091839	3143138	MCA2900-MCA2967	+	51300	PRO	LRG Mu	N	N.D.	0	4	2	0	10	2	0	64
Moorella thermoacetica ATCC 39073	NC_007644	2628784	55.79	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Mycobacterium avium subsp. paratuberculosis str. k10	NC_002944	4829781	69.30	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Mycobacterium bovis AF2122/97	NC_002945	4345492	65.63	1	66.62	1773889	1757290	Mb1602c-Mb1612c	-	16600	PRO	MED	Y	N.D.	1	5	0	0	0	0	18	11
Mycobacterium leprae TN	NC_002677	3268203	57.80	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Mycobacterium tuberculosis CDC1551	NC_002755	4403837	65.61	1	66.64	2966133	2975784	MT2723-MT2735	+	9652	PRO	MED	Y	tRNA-Val-3	3	5	0	0	0	0	147	14
Mycobacterium tuberculosis CDC1551	NC_002755	4403837	65.61	2	65.17	3870574	3896507	MT3573-MT3586	+	25934	PRO	LRG	Y	N.D.	1	5	0	0	0	0	248	31
Mycobacterium tuberculosis H37Rv	NC_000962	4411532	65.61	1	66.65	1788523	1771924	Rv1576c-Rv1586c	-	16600	PRO	MED	Y	N.D.	1	5	0	0	0	0	18	11
Mycobacterium tuberculosis H37Rv	NC_000962	4411532	65.61	2	66.32	2969989	2980998	Rv2645-Rv2659c	+	11010	PRO	MED	Y	tRNA-Val-3	3	5	0	0	0	0	180	15
Mycoplasma capricolum subsp. capricolum ATCC 27343	NC_007633	1010023	23.77	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Mycoplasma gallisepticum R	NC_004829	996422	31.45	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Mycoplasma genitalium G-37	NC_000908	580074	31.69	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Mycoplasma hyopneumoniae 232	NC_006360	892758	28.56	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Mycoplasma hyopneumoniae 7448	NC_007332	920079	28.49	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Mycoplasma hyopneumoniae J	NC_007295	897405	28.52	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Mycoplasma mobile 163K	NC_006908	777079	24.95	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Mycoplasma mycoides subsp. mycoides SC str. PGI	NC_005364	1211703	23.97	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Mycoplasma penetrans HF-2	NC_004432	1358633	25.72	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Mycoplasma pneumoniae M129	NC_000912	816394	40.01	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Mycoplasma pulmonis UAB CTIP	NC_002771	963879	26.64	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Mycoplasma synoviae 53	NC_007294	799476	28.50	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Neisseria gonorrhoeae FA 1090	NC_002946	2153922	52.69	1	53.59	454876	519904	tRNA-Ser-3-NGO0544	+	65029	PRO	LRG	Y	N.D.	2	3	2	0	0	0	297	79
Neisseria gonorrhoeae FA 1090	NC_002946	2153922	52.69	2	54.24	1044447	1088060	NGO1085-NGO1145	+	43614	PRO	LRG	N	N.D.	0	3	0	0	0	0	0	62
Neisseria meningitidis MC58	NC_003112	2272351	51.53	1	53.20	1099901	1133476	NMB1078-NMB1119	+	33576	PRO	LRG Mu	N	N.D.	0	5	0	0	6	2	0	39
Neisseria meningitidis Z2491	NC_003116	2184406	51.81	1	52.66	1208979	1235779	NMA1284-NMA1328	+	26801	PRO	LRG Mu	N	N.D.	0	4	0	0	7	2	0	43
Neisseria meningitidis Z2491	NC_003116	2184406	51.81	2	53.29	1769385	1807515	NMA1821-NMA1884	+	38131	PRO	LRG Mu	N	N.D.	0	5	0	0	7	2	0	62
Nitrobacter winogradskyi Nb-255	NC_007406	3402093	62.05	1	63.99	870660	903670	Nwi_0781-Nwi_0818	+	33011	PRO	LRG	N	N.D.	0	3	2	0	0	0	0	39
Nitrobacter winogradskyi Nb-255	NC_007406	3402093	62.05	2	63.55	1266020	1290759	Nwi_1154-Nwi_1182	+	24740	PRO	LRG	N	N.D.	0	7	1	0	1	0	0	29
Nitrobacter winogradskyi Nb-255	NC_007406	3402093	62.05	3	59.71	1627396	1584907	Nwi_1464-Nwi_1496	-	42490	PRO	LRG	Y	N.D.	2	12	2	0	1	0	244	33
Nitrobacter winogradskyi Nb-255	NC_007406	3402093	62.05	4	62.15	1682405	1709452	Nwi_1536-tRNA-Arg-3	+	27048	PRO	LRG	Y	tRNA-Arg-2	1	5	1	0	0	0	56	30
Nitrobacter winogradskyi Nb-255	NC_007406	3402093	62.05	5	58.55	1759813	1778157	Nwi_1612-Nwi_1633	+	18345	PRO	LRG	Y	tRNA-Glu-1	1	11	3	0	1	0	333	22
Nitrosococcus oceani ATCC 19707	NC_007484	3481691	50.32	1	55.10	663279	699441	Noc_0615-Noc_0650	+	36163	PRO	LRG SAT	Y	Noc	1	0	1	0	0	0	345	36
Nitrosomonas europaea ATCC 19718	NC_004757	2812094	50.72	1	59.12	2765264	2781779	NE2528-NE2542	+	16516	PRO	MED SAT	Y	NE2527	1	0	0	1	0	0	252	15
Nitrospira multiformis ATCC 25196	NC_007614	3184243	53.94	1	51.88	1650562	1673830	Nmul_A1438-Nmul_A1463	+	23269	PRO	LRG	N	N.D.	0	2	1	1	0	0	0	27
Nocardia farcinica IFM 10152	NC_006361	6021225	70.83	1	69.23	13860	53126	nfa90-nfa90	+	39267	PRO	LRG	Y	tRNA-Ala-1	1	9	1	0	0	0	117	61
Nocardia farcinica IFM 10152	NC_006361	6021225	70.83	2	67.76	1653636	1708473	nfa14720-nfa15600	+	54838	PRO	LRG	Y	tRNA-Asn-1	1	1	0	0	0	0	607	89
Nocardia farcinica IFM 10152	NC_006361	6021225	70.83	3	65.25	4103904	4170836	nfa38910-nfa39960	+	66933	PRO	LRG	Y	N.D.	1	1	3	0	1	0	364	106
Nostoc sp. PCC 7120	NC_003272	6413771	41.35	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Novosphingobium aromaticivorans DSM 12444	NC_007794	3561584	65.15	1	62.82	708247	665414	Saro_0617-Saro_0666	-	42834	PRO	LRG	Y	tRNA-Gly-2	1	8	1	0	1	0	48	50
Novosphingobium aromaticivorans DSM 12444	NC_007794	3561584	65.15	2	63.04	2932903	2980807	Saro_2692-tRNA-Val-4	+	47905	PRO	LRG	Y	tRNA-Val-3	1	2	2	0	1	0	69	69
Novosphingobium aromaticivorans DSM 12444	NC_007794	3561584	65.15	3	60.98	3202038	3235526	Saro_2985-Saro_3025	+	33489	PRO	LRG	N	N.D.	0	1	0	0	0	0	0	41
Novosphingobium aromaticivorans DSM 12444	NC_007794	3561584	65.15	4	66.93	3331159	3356191	Saro_3118-Saro_3145	+	25033	PRO	LRG	N	N.D.	0	7	1	0	1	0	0	29
Oceanobacillus ihelyensis HTE831	NC_004193	3																				

ORGANISM	ACCESSION	SIZE	GC%	#	pgc%	end5	end3	loci	ori	#phgpb	Ty	class	att	target	In	Co	NC	Ly	Ta	Mu	dX	OC	
Rickettsia conorii str. Malish 7	NC_003103	1268755	32.44	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	
Rickettsia felis URRWXCa12	NC_007109	1485148	32.45	1	33.72	501268	520630	RF_0471-RF_0484	+	19363	PRO	LRG	N	N.D.	0	2	0	0	0	0	0	15	
Rickettsia felis URRWXCa2	NC_007109	1485148	32.45	2	33.25	809940	824822	RF_0749-sppA2	+	14883	PRO	MED	N	N.D.	0	3	0	0	0	0	0	19	
Rickettsia prowazekii str. Madrid E	NC_000963	1111523	29.00	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	
Rickettsia typhi str. Wilmington	NC_006142	1111496	28.92	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	
Salinibacter ruber DSM 13855	NC_007677	3551823	66.22	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	
Salmonella enterica subsp. enterica serovar Choleraesuis st	NC_006905	4755700	52.16	1	47.66	372787	413236	int-gtrA	+	40450	PRO	LRG	SAT	Y	tRNA-Thr-1	1	0	1	4	0	0	60	47
Salmonella enterica subsp. enterica serovar Choleraesuis st	NC_006905	4755700	52.16	2	51.56	1093444	1124402	SC0975-SC1008	+	30959	PRO	LRG	N	N.D.	0	4	0	4	12	0	0	35	
Salmonella enterica subsp. enterica serovar Choleraesuis st	NC_006905	4755700	52.16	3	50.57	1306752	1357353	intE-icdA	+	50602	PRO	LRG	Y	N.D.	1	10	0	1	12	0	275	58	
Salmonella enterica subsp. enterica serovar Choleraesuis st	NC_006905	4755700	52.16	4	51.21	2751745	2803512	tfa-yfiK	+	51768	PRO	LRG	N	N.D.	1	1	1	4	2	0	0	71	
Salmonella enterica subsp. enterica serovar Paratyphi A str	NC_006511	4585229	52.16	1	47.38	2527642	2486436	SPA2385-int	-	41207	PRO	LRG	SAT	Y	tRNA-Thr-1	1	0	0	4	0	0	60	47
Salmonella enterica subsp. enterica serovar Paratyphi A str	NC_006511	4585229	52.16	2	50.79	2662064	2727922	SPA2554-SPA2625	+	65859	PRO	LRG	Y	N.D.	2	14	2	3	17	0	3113	71	
Salmonella enterica subsp. enterica serovar Typhi Ty2	NC_004631	4791961	52.05	1	54.76	1408218	1442892	t1346-t1397	-	34675	PRO	LRG	Mu	N	N.D.	1	5	0	1	13	2	0	49
Salmonella enterica subsp. enterica serovar Typhi Ty2	NC_004631	4791961	52.05	2	50.27	1972379	1927739	t1864-int	-	44641	PRO	LRG	Y	N.D.	1	4	1	1	2	0	49	64	
Salmonella enterica subsp. enterica serovar Typhi Ty2	NC_004631	4791961	52.05	3	52.44	2734604	2759937	t2647-iroC	+	25334	PRO	LRG	RET	Y	tmRNA-1	2	1	0	0	6	0	598	23
Salmonella enterica subsp. enterica serovar Typhi Ty2	NC_004631	4791961	52.05	4	51.79	3527603	3490720	t3400-t3438	-	36884	PRO	LRG	Y	N.D.	2	9	0	1	17	0	257	38	
Salmonella enterica subsp. enterica serovar Typhi Ty2	NC_004631	4791961	52.05	5	47.86	4489676	4539215	t4338-yjeK	+	49540	PRO	LRG	Y	N.D.	5	9	0	1	15	0	155	45	
Salmonella enterica subsp. enterica serovar Typhi str. CT18	NC_003198	4809037	52.09	1	51.08	1045191	1008467	int-SFY1067	-	36725	PRO	LRG	Y	N.D.	1	4	1	1	2	0	280	56	
Salmonella enterica subsp. enterica serovar Typhi str. CT18	NC_003198	4809037	52.09	2	54.75	1538899	1572919	STY1591-SFY1643	+	34021	PRO	LRG	Mu	N	N.D.	1	5	0	0	17	2	0	52
Salmonella enterica subsp. enterica serovar Typhi str. CT18	NC_003198	4809037	52.09	3	47.82	1933643	1879753	STY2000-SFY2077	-	53891	PRO	LRG	Y	N.D.	2	4	1	3	2	0	85	75	
Salmonella enterica subsp. enterica serovar Typhi str. CT18	NC_003198	4809037	52.09	4	54.34	2759379	2774080	STY2879-iroB	+	14702	PRO	MED	Y	N.D.	1	1	0	0	6	0	5309	12	
Salmonella enterica subsp. enterica serovar Typhi str. CT18	NC_003198	4809037	52.09	5	51.76	3541799	3492650	ilvY-pin	-	49150	PRO	LRG	Y	N.D.	2	9	0	1	17	0	113	47	
Salmonella enterica subsp. enterica serovar Typhi str. CT18	NC_003198	4809037	52.09	6	47.93	4506090	4556313	STY4645-yjeK	+	50224	PRO	LRG	Y	N.D.	5	9	0	1	16	0	155	48	
Salmonella typhimurium LT2	NC_003197	4857432	52.22	1	51.85	962430	1004496	STM0893-STM0929	+	42067	PRO	LRG	Y	N.D.	1	5	0	3	13	0	182	42	
Salmonella typhimurium LT2	NC_003197	4857432	52.22	2	51.08	1098179	1144034	STM1005-STM1056	+	45856	PRO	LRG	Y	N.D.	1	5	0	4	14	0	49	54	
Salmonella typhimurium LT2	NC_003197	4857432	52.22	3	48.09	2326826	2344711	STM2225-STM2242	+	17886	PRO	MED	N	N.D.	0	2	0	1	3	0	0	18	
Salmonella typhimurium LT2	NC_003197	4857432	52.22	4	51.09	2777063	2728534	STM2586-STM2636	-	48530	PRO	LRG	Y	N.D.	1	10	0	4	14	0	247	50	
Salmonella typhimurium LT2	NC_003197	4857432	52.22	5	52.49	2844265	2878004	STM2694-STM2739	+	33740	PRO	LRG	Y	N.D.	3	9	0	1	16	0	45		
Salmonella typhimurium LT2	NC_003197	4857432	52.22	6	50.59	4417918	4438335	STM4196-STM4219.S	+	20418	PRO	LRG	N	N.D.	0	1	0	1	10	0	24		
Shewanella oneidensis MR-1	NC_004347	4969803	45.96	1	48.45	669361	709641	S00641-S00691	+	40281	PRO	LRG	Mu	N	N.D.	0	4	0	0	2	3	0	50
Shewanella oneidensis MR-1	NC_004347	4969803	45.96	2	47.25	2788307	2825616	SO2652-SO2704	+	37310	PRO	LRG	Mu	N	N.D.	0	4	0	0	6	4	0	54
Shewanella oneidensis MR-1	NC_004347	4969803	45.96	3	46.71	3126442	3074590	SO2940-SO3013	-	51853	PRO	LRG	Y	N.D.	2	10	0	0	5	0	193	73	
Shigella boydii Sb227	NC_007613	4519823	51.21	1	50.02	783760	752858	ybjH-SBO_0774	-	30903	PRO	LRG	Y	N.D.	1	7	1	1	10	0	323	36	
Shigella boydii Sb227	NC_007613	4519823	51.21	2	49.96	1003598	972388	SBO_0951-SBO_0979	-	31211	PRO	LRG	SAT	Y	N.D.	1	0	0	0	2	0	339	28
Shigella boydii Sb227	NC_007613	4519823	51.21	3	52.18	1370533	1397798	SBO_1391-SBO_1421	+	27266	PRO	LRG	Y	N.D.	1	7	2	0	17	0	318	31	
Shigella boydii Sb227	NC_007613	4519823	51.21	4	51.01	1581115	1639266	insB-SBO_1654	+	58152	PRO	LRG	N	N.D.	0	2	0	0	10	0	65		
Shigella boydii Sb227	NC_007613	4519823	51.21	5	49.42	2108798	2094435	insB-SBO_2134	-	14364	PRO	LRG	Y	N.D.	1	2	0	0	0	0	281	20	
Shigella dysenteriae Sd197	NC_007606	4369232	51.25	1	50.20	671726	686610	SDY_0714-ybjF	+	14885	PRO	MED	N	N.D.	0	1	1	0	0	0	0	24	
Shigella dysenteriae Sd197	NC_007606	4369232	51.25	2	50.65	1024069	914859	SDY_0975-fljY	-	109211	PRO	LRG	SAT	Y	N.D.	2	0	0	0	1	0	215	115
Shigella dysenteriae Sd197	NC_007606	4369232	51.25	3	49.14	1341409	1277062	int-SDY_1453	-	64348	PRO	LRG	SAT	Y	N.D.	1	0	0	1	0	0	201	70
Shigella dysenteriae Sd197	NC_007606	4369232	51.25	4	50.58	2180707	2209296	clpA-artI	+	28590	PRO	LRG	Y	N.D.	2	1	0	0	0	0	0	27	
Shigella flexneri 2a str. 2457T	NC_004741	4599354	50.91	1	41.25	313783	324319	S0316-gtrAI	+	10537	PRO	LRG	SAT	Y	tRNA-Ser-4	2	0	0	0	1	0	60	10
Shigella flexneri 2a str. 2457T	NC_004741	4599354	50.91	2	52.24	692891	748241	S0684-ybhB	+	55351	PRO	LRG	Mu	N	N.D.	0	13	1	3	10	3	0	70
Shigella flexneri 2a str. 2457T	NC_004741	4599354	50.91	3	49.12	1225125	1177513	ycfD-ycgB	+	47613	PRO	LRG	Y	N.D.	1	11	0	0	0	0	324	46	
Shigella flexneri 2a str. 2457T	NC_004741	4599354	50.91	4	50.46	1900980	1954093	S1963-S2034	+	53114	PRO	LRG	SAT	Y	N.D.	2	0	0	0	1	0	57	53
Shigella flexneri 2a str. 2457T	NC_004741	4599354	50.91	5	49.31	2044618	1992538	dcm-S2152	-	52081	PRO	LRG	Y	N.D.	3	1	0	0	2	0	276	39	
Shigella flexneri 2a str. 2457T	NC_004741	4599354	50.91	6	49.28	2678152	2690370	S2781-S2796	+	12219	PRO	MED	SAT	Y	N.D.	1	0	0	1	1	0	367	15
Shigella flexneri 2a str. 301	NC_004337	4607203	50.89	1	45.93	311264	340154	SF0294-SF0329	+	28891	PRO	LRG	SAT	Y	tRNA-Thr-1	2	0	0	0	1	0	27	35
Shigella flexneri 2a str. 301	NC_004337	4607203	50.89	2	52.21	696659	750736	SF0661-SFH_1	+	54078	PRO	LRG	Mu	N	N.D.	0	13	1	1	10	3	0	63
Shigella flexneri 2a str. 301	NC_004337	4607203	50.89	3	52.13	1919854	1964934	SF1881-SF1929	+	45081	PRO	LRG	N	N.D.	0	3	0	0	10	0	0	47	
Shigella flexneri 2a str. 301	NC_004337	4607203	50.89	4	48.27	2066786	2029271	dcm-SF2045	-	37516	PRO	LRG	Y	N.D.	2	1	0	0	1	0	389	38	
Shigella flexneri 2a str. 301	NC_004337	4607203	50.89	5	49.42	2684565	2696926	SF2609-SF2623	+	12362	PRO	MED	SAT	Y	N.D.	1	0	0	1	1	0	367	15
Shigella sonnei Ss046	NC_007384	4825265	51.01	1	50.40	791261	754753	SSO_0718-intE	-	36509	PRO	LRG	Y	N.D.	2	3	0	2	0	0	294	28	
Shigella sonnei Ss046	NC_007384	4825265	51.01	2	46.92	2023422	1987927	SSO_1889-SSO_1926	-	35496	PRO	LRG	SAT	Y	N.D.	2	0	0	0	2	0	64	35
Shigella sonnei Ss046	NC_007384	4825265	51.01	3	49.88	2288136	2266851	SSO_2165-SSO_2182	-	21286	PRO	LRG	SAT	Y	N.D.	1	0	0	0	1	0	370	16
Shigella sonnei Ss046	NC_007384	4825265	51.01	4	53.44	2540442	2571825	intC-SSO_2435	+	31384	PRO	LRG	Y	N.D.	1	0	0	0	2	0	64	35	
Shigella sonnei Ss046	NC_007384	4825265	51.01	5	50.82	2884693	2916444	SSO_2723-yfiB	+	31752	PRO	LRG	N	N.D.	1	10	0	2	13	0	180	29	
Shigella sonnei Ss046	NC_007384	4825265	51.01	6	50.10	2927119	2965577	SSO_2775-nrdF	+	38459	PRO	LRG	N	N.D.	0	5	0	2	0	0	0	40	

ORGANISM	ACCESSION	SIZE	GC%	#	pgc%	end5	end3	loci	ori	#phgpb	Ty	class	att	target	In	Co	NC	Ly	Ta	Mu	dX	OC		
Silicibacter pomeroyi DSS-3	NC_003911	4109442	64.22	1	64.16	1735362	1753877	xerD-SPO1647	+	18516	PRO	LRG	SAT	Y	N.D.	2	0	0	1	0	0	352	16	
Silicibacter pomeroyi DSS-3	NC_003911	4109442	64.22	2	66.59	2393491	2405707	SPO2250-SPO2263	+	12217	PRO	MED	N	N.D.	0	9	1	0	1	0	0	14		
Sinorhizobium meliloti 1021	NC_003047	3654135	62.73	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0	
Sodalis glossinidius str. 'morsitans'	NC_007712	4171146	54.70	1	55.73	440946	499358	SG0243-SG0275	+	58413	PRO	LRG	N	N.D.	0	2	0	0	1	0	0	33		
Sodalis glossinidius str. 'morsitans'	NC_007712	4171146	54.70	2	56.67	569107	591575	SG0317-SG0325	+	22469	PRO	LRG	Mu	N	N.D.	0	1	0	0	0	1	0	10	
Sodalis glossinidius str. 'morsitans'	NC_007712	4171146	54.70	3	45.38	1188876	1228395	SG0707-SG0737	+	39520	PRO	LRG	Y	tRNA-Arg-2	1	10	0	2	8	0	0	2847	31	
Sodalis glossinidius str. 'morsitans'	NC_007712	4171146	54.70	4	56.43	1377753	1409605	SG0816-SG0857	+	31853	PRO	LRG	Mu	N	N.D.	0	5	0	1	11	2	0	42	
Sodalis glossinidius str. 'morsitans'	NC_007712	4171146	54.70	5	51.57	1575615	1520578	SG0929-SG0953	-	55038	PRO	LRG	SAT	Y	SG0956	2	0	0	1	0	0	157	25	
Sodalis glossinidius str. 'morsitans'	NC_007712	4171146	54.70	6	51.74	1973854	2066252	SG1173-SG11225	+	92399	PRO	LRG	Y	tRNA-Leu-4	2	3	0	2	6	0	0	170	53	
Sodalis glossinidius str. 'morsitans'	NC_007712	4171146	54.70	7	54.51	2301717	2315177	SG1387-SG1395	+	13461	PRO	MED	N	N.D.	0	3	2	1	0	0	0	9		
Sodalis glossinidius str. 'morsitans'	NC_007712	4171146	54.70	8	48.03	2798801	2822774	SG1638-SG1650	+	23974	PRO	LRG	Y	tRNA-Arg-3	1	2	0	2	2	0	0	186	13	
Sodalis glossinidius str. 'morsitans'	NC_007712	4171146	54.70	9	53.78	2858974	2908373	NC_007712_tRNA-Lys-5-SG16	+	49400	PRO	LRG	SAT	Y	tRNA-Val-4	1	0	0	1	0	0	857	23	
Sodalis glossinidius str. 'morsitans'	NC_007712	4171146	54.70	10	51.22	3075399	3104832	SG1806-SG1829	+	29434	PRO	LRG	N	N.D.	0	5	0	0	1	0	0	25		
Sodalis glossinidius str. 'morsitans'	NC_007712	4171146	54.70	11	48.62	4031669	4063482	SG2350-SG2364	+	31814	PRO	LRG	N	N.D.	0	6	0	1	3	0	0	16		
Staphylococcus aureus RF122	NC_007622	2742531	32.78	1	32.00	311846	322949	SAB0258c-SAB0270	+	11104	PRO	MED	SAT	Y	geh	1	0	0	2	0	0	111	12	
Staphylococcus aureus RF122	NC_007622	2742531	32.78	2	31.41	388732	404695	SAB0342c-sel	+	15964	PRO	MED	Y	guaA	1	1	0	0	0	0	0	108	23	
Staphylococcus aureus RF122	NC_007622	2742531	32.78	3	32.29	847894	873883	SAB0779c-SAB0807	+	25990	PRO	LRG	SAT	Y	SAB0778	1	0	0	2	0	0	239	28	
Staphylococcus aureus RF122	NC_007622	2742531	32.78	4	34.95	1887347	1844048	SAB1702c-SAB1760	+	43300	PRO	LRG	Y	tRNA-Ser-3	1	9	0	2	5	0	0	171	59	
Staphylococcus aureus subsp. aureus COL	NC_002951	2809422	32.82	1	33.81	354674	398267	int-SACOL0389	+	43594	PRO	LRG	Y	SACOL0317	1	7	2	2	2	0	0	111	72	
Staphylococcus aureus subsp. aureus COL	NC_002951	2809422	32.82	2	31.40	903332	919283	SACOL0885-SACOL0911	+	15952	PRO	MED	Y	SACOL0884	1	1	0	0	0	0	0	159	27	
Staphylococcus aureus subsp. aureus MRSA252	NC_002952	2902619	32.81	1	32.02	409864	437654	SAR0365-SAR0401a	+	27791	PRO	LRG	Y	N.D.	1	1	0	0	0	0	0	312	37	
Staphylococcus aureus subsp. aureus MRSA252	NC_002952	2902619	32.81	2	32.25	2168560	2112234	SAR2033-int	-	56327	PRO	LRG	Y	N.D.	1	6	0	3	4	0	0	127	66	
Staphylococcus aureus subsp. aureus MSSA476	NC_002953	2799802	32.85	1	33.26	980997	1025777	SAS0891-SAS0954	+	44781	PRO	LRG	Y	N.D.	1	7	2	2	2	0	0	111	64	
Staphylococcus aureus subsp. aureus MSSA476	NC_002953	2799802	32.85	2	32.15	2068117	2015022	SAS1864-SAS1922	-	53096	PRO	LRG	Y	N.D.	1	14	0	3	5	0	0	126	56	
Staphylococcus aureus subsp. aureus MW2	NC_003923	2820462	32.83	1	32.14	2035775	2088875	MW1869-hlb	+	53101	PRO	LRG	Y	hlb	1	15	0	3	5	0	0	126	71	
Staphylococcus aureus subsp. aureus Mu50	NC_002758	2878529	32.88	1	31.27	868335	882871	SAV0783-SAV0804	+	14537	PRO	LRG	Y	tmRNA-1	1	1	0	0	0	0	0	127	22	
Staphylococcus aureus subsp. aureus Mu50	NC_002758	2878529	32.88	2	34.03	917414	961983	int-SAV0917	+	44570	PRO	LRG	Y	SAV0846	1	8	0	2	5	0	0	93	70	
Staphylococcus aureus subsp. aureus Mu50	NC_002758	2878529	32.88	3	33.21	2083115	2126181	SAV1940-truncated_hlb	+	43067	PRO	LRG	Y	SAV1939	1	6	0	3	4	0	0	71	63	
Staphylococcus aureus subsp. aureus N315	NC_002745	2814816	32.84	1	31.99	2072446	2005190	SA1753-int	-	67257	PRO	LRG	Y	groEL	2	7	0	3	5	0	0	174	89	
Staphylococcus aureus subsp. aureus NCTC 8325	NC_007795	2821361	32.87	1	27.61	1244641	1261792	SAOIHSC_01288-SAOIHSC_013	+	17152	PRO	MED	N	N.D.	0	1	0	0	0	0	0	0	30	
Staphylococcus aureus subsp. aureus NCTC 8325	NC_007795	2821361	32.87	2	34.09	1918903	1966997	SAOIHSC_02010-SAOIHSC_020	+	48095	PRO	LRG	Y	SAOIHSC	1	8	0	2	5	0	0	68	75	
Staphylococcus aureus subsp. aureus NCTC 8325	NC_007795	2821361	32.87	3	32.60	2021475	2074700	SAOIHSC_02149-SAOIHSC_022	+	53226	PRO	LRG	Y	SAOIHSC	1	15	0	3	5	0	0	126	85	
Staphylococcus aureus subsp. aureus USA300	NC_007793	2872769	32.75	1	27.70	1325509	1341775	SAUSA300_1202-SAUSA300_12	+	16255	PRO	MED	N	N.D.	0	1	0	0	0	0	0	23		
Staphylococcus aureus subsp. aureus USA300	NC_007793	2872769	32.75	2	32.14	2074218	2127775	SAUSA300_1908-SAUSA300_19	+	53558	PRO	LRG	Y	SAUSA300	1	7	0	3	4	0	0	126	64	
Staphylococcus epidermidis ATCC 12228	NC_004461	2499279	32.10	1	29.28	998429	1012563	SE0988-SE1007	+	14135	PRO	MED	N	N.D.	0	2	0	0	0	0	0	0	20	
Staphylococcus epidermidis RP62A	NC_002976	2616530	32.15	1	30.52	1567708	1698611	SERP1501-SERP1659	+	130904	PRO	LRG	Y	N.D.	5	1	0	2	2	0	0	60	159	
Staphylococcus haemolyticus JCSC1435	NC_007168	2685015	32.79	1	32.85	1806792	1855840	SH1746-int	+	49049	PRO	LRG	Y	tRNA-Arg-2	2	3	1	2	4	0	0	172	63	
Staphylococcus haemolyticus JCSC1435	NC_007168	2685015	32.79	2	28.94	2133991	2117673	SH2076-SH2103	-	16319	PRO	LRG	Y	tmRNA-1	1	1	0	0	0	0	0	840	28	
Staphylococcus haemolyticus JCSC1435	NC_007168	2685015	32.79	3	35.15	2350727	2396658	SH2331-int	+	45932	PRO	LRG	Y	SH2397	1	8	1	2	4	0	0	365	66	
Staphylococcus haemolyticus JCSC1435	NC_007168	2685015	32.79	4	31.35	2593525	2580925	SH2569-int	-	12601	PRO	MED	Y	guaA	1	1	0	0	0	0	0	177	13	
Staphylococcus saprophyticus subsp. saprophyticus ATCC 1530	NC_007350	2516575	33.24	1	30.43	1989267	2006322	SSP1924-SSP1947	+	17056	PRO	LRG	Y	tRNA-Arg-3	1	2	0	0	0	0	0	141	24	
Streptococcus agalactiae 2603V/R	NC_004116	2160267	35.65	1	36.80	558767	599345	SAG0545-SAG0608	+	40579	PRO	LRG	SAT	Y	tRNA-Arg-3	1	0	0	2	3	0	0	59	62
Streptococcus agalactiae 2603V/R	NC_004116	2160267	35.65	2	40.24	1833085	1867188	SAG1835-SAG1885	+	34104	PRO	LRG	Y	tRNA-Cys-1	2	5	2	2	4	0	0	71	50	
Streptococcus agalactiae A909	NC_007432	2127839	35.62	1	37.13	548923	585664	SAK_0607-SAK_0654	+	36742	PRO	LRG	SAT	Y	N.D.	1	0	0	2	2	0	0	41	48
Streptococcus agalactiae A909	NC_007432	2127839	35.62	2	42.95	701934	661644	SAK_0725-SAK_0765	-	40291	PRO	LRG	Y	N.D.	2	8	2	2	4	0	0	227	40	
Streptococcus agalactiae A909	NC_007432	2127839	35.62	3	35.45	2086288	2071032	SAK_2076-SAK_2094	-	15257	PRO	LRG	SAT	Y	rpsD	1	0	0	1	0	0	124	19	
Streptococcus agalactiae NEM316	NC_004368	2211485	35.63	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0	
Streptococcus mutans UA159	NC_004350	2030921	36.83	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0	
Streptococcus pneumoniae R6	NC_003098	2038615	39.72	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0	
Streptococcus pneumoniae TIGR4	NC_003028	2160837	39.70	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0	
Streptococcus pyogenes M1 GAS	NC_002737	1852441	38.51	1	39.25	529591	570509	int1-pepD	+	40919	PRO	LRG	Y	pepD	1	4	0	2	2	0	0	40	48	
Streptococcus pyogenes M1 GAS	NC_002737	1852441	38.51	2	37.97	778526	821010	int3-speH	+	42485	PRO	LRG	Y	N.D.	1	7	0	0	5	0	0	116	57	
Streptococcus pyogenes M1 GAS	NC_002737	1852441	38.51	3	38.04	1222654	1189125	SPy1438-int2	-	33530	PRO	LRG	SAT	Y	N.D.	1	0	0	2	1	0	0	105	46
Streptococcus pyogenes MGAS10394	NC_006086	1899877	38.69	1	39.97	35451	71318	M6_Spy0020-M6_Spy0063	+	35868	PRO	LRG	Y	M6	1	8	0	2	5	0	0	148	44	
Streptococcus pyogenes MGAS10394	NC_006086	1899877	38.69	2	38.00	987286	1020478	M6_Spy0982-M6_Spy1027	+	33193	PRO	LRG	Y	tmRNA-1	1	10	0	2	4	0	0	138	46	
Streptococcus pyogenes MGAS10394	NC_006086	1899877	38.69	3	38.41	1231991	1200072	M6_Spy1196-M6_Spy1242	+	31920	PRO	LRG	SAT	Y	N.D.	1	0	0	2	1	0	0	106	47
Streptococcus pyogenes MGAS10394	NC_006086	1899877	38.69	4	41.11	1333928	1355794	M6_Spy1342-M6_Spy1365	+	21867	PRO	LRG	N	N.D.	0	4	0	0	2	0	0	25		
Streptococcus pyogenes MGAS10394	NC_006086	1899877	38.69	5	40.39	1546648																		

ORGANISM	ACCESSION	SIZE	GC%	#	pgc%	end5	end3	loci	ori	#phgpb	Ty	class	att	target	In	Co	NC	Ly	Ta	Mu	dX	OC	
Streptococcus pyogenes MGAS315	NC_004070	1900521	38.59	1	37.88	749180	787900	SpyM3_0681-SpyM3_0735	+	38721	PRO	LRG	Y	N.D.	2	3	1	2	4	0	33	55	
Streptococcus pyogenes MGAS315	NC_004070	1900521	38.59	2	38.26	977267	1018334	SpyM3_0919-intP	+	41068	PRO	LRG	Y	tmRNA-1	1	9	1	2	4	0	141	60	
Streptococcus pyogenes MGAS315	NC_004070	1900521	38.59	3	38.02	1171973	1137554	SpyM3_1096-SpyM3_1145	-	34420	PRO	LRG	SAT	Y	N.D.	1	0	0	3	1	0	106	50
Streptococcus pyogenes MGAS315	NC_004070	1900521	38.59	4	38.86	1271989	1221158	s1a-int315.4	-	50832	PRO	LRG	Y	msrA.1	1	5	0	0	2	0	174	63	
Streptococcus pyogenes MGAS315	NC_004070	1900521	38.59	5	38.08	1313194	1351399	SpyM3_1300-int315.5	+	38206	PRO	LRG	Y	SpyM3	1	6	0	1	3	0	149	55	
Streptococcus pyogenes MGAS315	NC_004070	1900521	38.59	6	39.76	1450484	1410657	SpyM3_1411-int315.6	-	39828	PRO	LRG	Y	N.D.	1	8	0	2	5	0	26	48	
Streptococcus pyogenes MGAS5005	NC_007297	1838554	38.53	1	38.02	983754	1021805	M5005_Spy_0995-int.1	+	38052	PRO	LRG	Y	tmRNA-1	1	7	0	1	2	0	138	58	
Streptococcus pyogenes MGAS5005	NC_007297	1838554	38.53	2	37.67	1178893	1145475	M5005_Spy_1171-int.2	-	33419	PRO	LRG	Y	N.D.	1	1	0	2	1	0	107	52	
Streptococcus pyogenes MGAS5005	NC_007297	1838554	38.53	3	39.78	1426021	1385205	M5005_Spy_1416-int.3	+	40817	PRO	LRG	Y	tRNA-Ser-4	1	8	0	0	5	0	62	52	
Streptococcus pyogenes MGAS6180	NC_007296	1897573	38.35	1	37.19	986212	1032479	M28_Spy0967-M28_Spy1033	+	46268	PRO	LRG	Y	tmRNA-1	1	8	0	0	5	0	138	67	
Streptococcus pyogenes MGAS6180	NC_007296	1897573	38.35	2	38.60	1224383	1269128	M28_Spy1218-M28_Spy1285	+	44746	PRO	LRG	Mu	N	N.D.	1	5	1	0	2	1	0	68
Streptococcus pyogenes MGAS8232	NC_003485	1895017	38.55	1	38.33	293804	382800	int-spyM18_0467	+	88997	PRO	LRG	Y	N.D.	4	3	1	3	4	0	78	107	
Streptococcus pyogenes MGAS8232	NC_003485	1895017	38.55	2	38.16	578053	619120	int-MF2	+	41068	PRO	LRG	Y	spyM18	1	11	0	2	4	0	40	60	
Streptococcus pyogenes MGAS8232	NC_003485	1895017	38.55	3	37.64	1041142	1087880	spyM18_1237-int	+	46739	PRO	LRG	Y	tmRNA-1	1	8	0	2	5	0	141	69	
Streptococcus pyogenes MGAS8232	NC_003485	1895017	38.55	4	37.69	1241522	1206171	spyM18_1448-int	-	35352	PRO	LRG	SAT	Y	N.D.	1	0	0	2	1	0	106	53
Streptococcus pyogenes MGAS8232	NC_003485	1895017	38.55	5	38.12	1441660	1493558	spyM18_1733-int	+	51899	PRO	LRG	Y	spyM18	1	5	0	0	1	0	185	67	
Streptococcus pyogenes SSI-1	NC_004606	1894275	38.55	1	39.58	446165	495314	SPs0408-SPs0463	+	49150	PRO	LRG	Y	SPs0407	1	8	0	2	4	0	262	55	
Streptococcus pyogenes SSI-1	NC_004606	1894275	38.55	2	38.08	583691	545487	SPs0507-SPs0557	-	38205	PRO	LRG	Y	SPs0506	1	5	0	1	2	0	149	51	
Streptococcus pyogenes SSI-1	NC_004606	1894275	38.55	3	38.87	624896	675726	SPs0597-SPs0667	+	50831	PRO	LRG	Y	SPs0596	1	5	0	0	1	0	174	71	
Streptococcus pyogenes SSI-1	NC_004606	1894275	38.55	4	38.01	724702	764502	SPs0717-SPs0776	+	39801	PRO	LRG	SAT	Y	N.D.	1	0	0	3	1	0	315	60
Streptococcus pyogenes SSI-1	NC_004606	1894275	38.55	5	38.89	878343	924839	SPs0876-SPs0940	+	46497	PRO	LRG	Y	N.D.	1	9	0	2	3	0	347	65	
Streptococcus pyogenes SSI-1	NC_004606	1894275	38.55	6	37.28	1107624	1152457	SPs1118-SPs1175	+	44834	PRO	LRG	Y	tmRNA-1	2	3	1	2	3	0	4914	58	
Streptococcus thermophilus CNR21066	NC_006449	1796226	39.08	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Streptococcus thermophilus LMG 18311	NC_006448	1796846	39.09	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Streptomyces avermitilis MA-4680	NC_003155	9025608	70.72	1	67.61	6711968	6667915	SAV5498-int13	-	44054	PRO	LRG	Y	N.D.	1	1	2	0	0	0	120	51	
Streptomyces coelicolor A3(2)	NC_003888	8667507	72.12	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Symbiobacterium thermophilum IAM 14863	NC_006177	3566135	68.67	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Synechococcus elongatus PCC 6301	NC_006576	2696255	55.48	1	57.06	909616	860877	syc0770_c-syc0814_c	-	48740	PRO	LRG	Y	tRNA-Leu-2	1	4	0	0	8	0	249	45	
Synechococcus elongatus PCC 7942	NC_007604	2695903	55.47	1	57.04	711254	759991	Synpcc7942_0716-Synpcc794	+	48738	PRO	LRG	Y	tRNA-Leu-2	1	4	0	0	10	0	192	51	
Synechococcus sp. CC9605	NC_007516	2510659	59.22	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Synechococcus sp. CC9902	NC_007513	2234828	54.16	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Synechococcus sp. WH 8102	NC_005070	2434428	59.41	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Synechocystis sp. PCC 6803	NC_000911	3573470	47.72	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Syntrophus aciditrophicus SB	NC_007759	3179300	51.46	1	59.49	527763	562382	SYN_02328-SYN_02282	+	34620	PRO	LRG	Mu	N	N.D.	0	4	1	0	7	2	0	49
Thermoanaerobacter tengcongensis MB4	NC_003869	2689445	37.57	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Thermobifida fusca YX	NC_007333	3642249	67.50	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Thermosynechococcus elongatus BP-1	NC_004113	2593857	53.92	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Thermotoga maritima MSB8	NC_000853	1860725	46.25	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Thermus thermophilus HB27	NC_005835	1894877	69.44	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Thermus thermophilus HB8	NC_006461	1849742	69.52	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Thiobacillus denitrificans ATCC 25259	NC_007404	2909809	66.07	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Thiomicrospira crunogena XCL-2	NC_007520	2427734	43.13	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Thiomicrospira denitrificans ATCC 33889	NC_007575	2201561	34.46	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Treponema denticola ATCC 35405	NC_002967	2843201	37.87	1	37.03	1202635	1164700	TDE1136-TDE1173	-	37936	PRO	LRG	SAT	Y	tRNA-Met-1	1	0	0	0	1	0	224	38
Treponema pallidum subsp. pallidum str. Nichols	NC_000919	1138011	52.77	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Tropheryma whipplei TW08/27	NC_004551	925938	46.31	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Tropheryma whipplei str. Twist	NC_004572	927303	46.33	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Ureaplasma parvum serovar 3 str. ATCC 700970	NC_002162	751719	25.50	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Vibrio cholerae O1 biovar eltor str. N16961	NC_002506	1072315	46.91	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Vibrio cholerae O1 biovar eltor str. N16961	NC_002505	2961149	47.69	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Vibrio fischeri ES114	NC_006841	1332022	37.02	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Vibrio fischeri ES114	NC_006840	2906179	38.96	1	39.81	2243452	2276673	VF2003-VF2041	+	33222	PRO	LRG	Y	tmRNA-1	1	5	1	0	8	0	126	39	
Vibrio parahaemolyticus RIMD 2210633	NC_004603	3288558	45.39	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Vibrio parahaemolyticus RIMD 2210633	NC_004605	1877212	45.35	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Vibrio vulnificus CMCP6	NC_004460	1844853	47.12	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Vibrio vulnificus CMCP6	NC_004459	3281945	46.45	1	47.97	68394	110846	VV10063-VV10124	+	42453	PRO	LRG	SAT	Y	tRNA-Pro-1	4	0	1	0	10	0	156	59
Vibrio vulnificus YJ016	NC_005140	1857073	47.21	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0
Vibrio vulnificus YJ016	NC_005139	3354505	46.41	1	46.76	289159	270165	VV0262-VV0277	-	18995	PRO	LRG	SAT	Y	VV0278	1	0	0	0	1	0	286	16

ORGANISM	ACCESSION	SIZE	GC%	#	pgc%	end5	end3	loci	ori	#phgbp	Ty	class	att	target	In	Co	NC	Ly	Ta	Mu	dX	OC	
Wigglesworthia glossinidia endosymbiont of Glossina brevipa	NC_004344	697724	22.48	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0	
Wolbachia endosymbiont of Drosophila melanogaster	NC_002978	1267782	35.23	1	36.30	231382	269052	WD0248-WD0290	+	37671	PRO	LRG	Y	WD0290	1	1	0	0	2	0	241	35	
Wolbachia endosymbiont of Drosophila melanogaster	NC_002978	1267782	35.23	2	34.60	628222	543609	WD0558-WD0634	-	84614	PRO	LRG	Y	N.D.	1	2	0	0	9	0	103	69	
Wolbachia endosymbiont strain TRS of Brugia malayi	NC_006833	1080084	34.18	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0	
Wolinella succinogenes DSM 1740	NC_005090	2110355	48.46	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0	
Xanthomonas axonopodis pv. citri str. 306	NC_003919	5175554	64.77	1	59.16	1209301	1229085	XAC1051-pol	+	19785	PRO	LRG	SAT	Y	tRNA-His-1	1	0	0	2	0	0	22	
Xanthomonas axonopodis pv. citri str. 306	NC_003919	5175554	64.77	2	62.40	3091075	3121181	uvrB-XAC2662	+	30107	PRO	LRG	N	N.D.	0	8	0	1	6	0	0	38	
Xanthomonas campestris pv. campestris str. 8004	NC_007086	5148708	64.96	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0	
Xanthomonas campestris pv. vesicatoria str. ATCC 33913	NC_003902	5076188	65.07	1	61.76	3560388	3523026	umuD-int	-	37363	PRO	LRG	Y	tRNA-Lys-2	1	9	0	1	14	0	190	50	
Xanthomonas campestris pv. vesicatoria str. 85-10	NC_007508	5178466	64.75	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0	
Xanthomonas oryzae pv. oryzae KACC10331	NC_006834	4941439	63.69	1	62.48	1741336	1782160	int-XOO1720	+	40825	PRO	LRG	Y	tRNA-Lys-2	1	8	1	1	16	0	167	41	
Xanthomonas oryzae pv. oryzae MAFF 311018	NC_007705	4940217	63.70	1	62.54	1723638	1761358	XOO1570-XOO1618	+	37721	PRO	LRG	Y	tRNA-Lys-2	1	9	0	1	16	0	166	49	
Xylella fastidiosa 9a5c	NC_002488	2679306	52.67	1	57.89	488229	530138	XF0480-XF0536	+	41910	PRO	LRG	N	N.D.	0	3	1	1	0	0	0	57	
Xylella fastidiosa 9a5c	NC_002488	2679306	52.67	2	55.64	648982	702996	NC_002488_tRNA-Val-1-XF07	+	54015	PRO	LRG	Y	XF0677	1	6	1	1	11	0	133	71	
Xylella fastidiosa 9a5c	NC_002488	2679306	52.67	3	56.24	1514046	1549021	XF1555-XF1607	+	34976	PRO	LRG	Y	XF1554	1	3	0	1	0	0	301	53	
Xylella fastidiosa 9a5c	NC_002488	2679306	52.67	4	55.25	1585873	1630687	XF1642-XF1710	+	44815	PRO	LRG	Y	N.D.	2	3	0	1	2	0	107	69	
Xylella fastidiosa 9a5c	NC_002488	2679306	52.67	5	56.52	2404570	2369149	XF2487-XF2530	-	35422	PRO	LRG	Y	N.D.	2	6	1	1	11	0	302	44	
Xylella fastidiosa Temeculal	NC_004556	2519802	51.78	1	57.53	467642	453721	D-int	-	13922	PRO	MED	SAT	Y	N.D.	2	0	2	0	5	0	31	22
Xylella fastidiosa Temeculal	NC_004556	2519802	51.78	2	55.96	1227979	1181498	PD0985-PD1028	-	46482	PRO	LRG	Y	PD0985	3	3	1	1	2	0	82	41	
Xylella fastidiosa Temeculal	NC_004556	2519802	51.78	3	56.55	1331648	1287845	D-int	-	43804	PRO	LRG	Y	N.D.	2	5	1	1	10	0	107	52	
Xylella fastidiosa Temeculal	NC_004556	2519802	51.78	4	57.56	1393090	1379639	PD1177-int	-	13452	PRO	LRG	SAT	Y	yheS	2	0	0	0	2	0	327	18
Xylella fastidiosa Temeculal	NC_004556	2519802	51.78	5	61.13	1848608	1855582	PD1598-ssb	+	6975	PRO	LRG	N	N.D.	0	1	0	0	0	0	0	6	
Yersinia pestis CO92	NC_003143	4653728	47.64	1	46.12	1245690	1224076	mltD-tnp	-	21615	PRO	LRG	SAT	Y	tmRNA-1	3	0	0	1	0	0	1007	22
Yersinia pestis CO92	NC_003143	4653728	47.64	2	47.10	2364324	2410325	YPO2085-YPO2140	+	46002	PRO	LRG	N	N.D.	0	2	0	2	5	0	0	54	
Yersinia pestis KIM	NC_004088	4600755	47.64	1	47.17	2456523	2415479	y2184-y2227	+	41045	PRO	LRG	Y	y2228	1	2	0	1	5	0	56	43	
Yersinia pestis KIM	NC_004088	4600755	47.64	2	46.11	3389136	3410732	y3080-y3100	+	21597	PRO	LRG	SAT	Y	tmRNA-1	3	0	0	1	0	0	974	21
Yersinia pestis biovar Medievalis str. 91001	NC_005810	4595065	47.65	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0	
Yersinia pseudotuberculosis IP 32953	NC_006155	4744671	47.61	1	46.74	2125573	2234945	YPTB1774-tnpA	+	109373	PRO	LRG	Y	YPTB1773	3	17	2	3	31	0	297	116	
Zymomonas mobilis subsp. mobilis ZM4	NC_006526	2056416	46.33	1	48.32	383933	396251	ZMO0378-ZMO0397	+	12319	PRO	MED	N	N.D.	0	1	1	0	0	0	0	20	

Out of 302 genomes processed, there are 403 putative prophages > 18 kb, totalling 15421400 bp in size and 1.61% of the bacterial genomes analyzed or 1.3 phage per genome on average

Of those 154 genomes with prophages, the phage constitute 2.74% of the chromosomal DNA, averaging 2.62 phage per genome
 There are a total of 285 out of 403 phages with att sites with an average distance from integrase to att site of 529.85 bp
 There were 32 (7.94%) Mu-like Phages!

Target distribution:

Ala = 1
 Arg = 18
 Asn = 4
 Cys = 3
 Gln = 1
 Glu = 2
 Gly = 6
 His = 1
 Leu = 14
 Lys = 7
 Met = 3
 ND = 104
 Phe = 2
 Pro = 6
 Ser = 13
 Thr = 11
 Val = 7
 genes = 84
 intergenic = 93
 tmRNA = 23

 Total = 403