

Table S1. Observed (O) and expected (E) quantities of intergenic IS elements in fully sequenced bacterial chromosomes that have too few ISs for statistical analysis.

	Neighboring gene orientation (NGO)					
	→→, ←←		→←		←→	
	O	E	O	E	O	E
ACTINOBACTERIA						
<i>Actinomyces naeslundii</i> MG1	8	7.0	5	4.6	0	1.5
<i>Bifidobacterium longum</i> NCC2705	2	1.7	1	0.6	0	0.7
<i>Corynebacterium diphtheriae</i> NCTC13129	14	15.6	10	3.5	3	7.9
<i>Corynebacterium glutamicum</i> ATCC 13032	12	11.9	6	2.9	3	6.2
<i>Leifsonia xyli</i> CTCB07	13	11.7	4	3.2	2	4.2
<i>Mycobacterium leprae</i> TN	1	1.0	0	0.5	1	0.5
<i>Nocardia farcinica</i> IFM10152	16	15.3	7	4.0	6	9.7
<i>Propionibacterium acnes</i> KPA171202	4	3.5	2	0.9	0	1.6
<i>Symbiobacterium thermophilum</i> IAM14863	19	25.2	8	4.4	11	8.4
<i>Thermobifida fusca</i> YX	6	5.3	1	1.3	2	2.4
<i>Tropheryma whipplei</i> Twist	2	1.7	1	0.6	0	0.7
<i>T. whipplei</i> TW08/27	2	1.7	1	0.7	0	0.6
AQUIFICAE						
<i>Aquifex aeolicus</i> VF5	0	1.7	1	0.3	2	0.9
BACTERIODETES						
<i>Bacteroides fragilis</i> NCTC9343	8	9.9	1	2.3	7	3.8
<i>B. fragilis</i> YCH46	12	12.7	3	2.7	6	5.6
CHLAMYDIAE						
<i>Chlamydia muridarum</i> Nigg	2	1.1	0	0.2	0	0.7
<i>Chlamydia pneumoniae</i> AR39	3	1.8	0	0.3	0	0.9
<i>C. pneumoniae</i> CWL029	3	1.7	0	0.2	0	1.0
<i>C. pneumoniae</i> J138	3	1.8	0	0.2	0	1.0
<i>C. pneumoniae</i> TW-183	3	1.8	0	0.3	0	0.9
<i>Chlamydia trachomatis</i> A/HAR-13	3	1.8	0	0.2	0	1.0
<i>C. trachomatis</i> serovar D	2	1.7	0	0.2	1	1.1
<i>Chlamydophila abortus</i> S26 3	3	1.7	0	0.2	0	1.1
<i>Chlamydophila caviae</i> GPIC	2	1.1	0	0.2	0	0.7
<i>Chlamydophila felis</i> Fe/C-56	2	1.1	0	0.2	0	0.7
CHLOROBI						
<i>Chlorobium chlorochromatii</i> CaD3	11	11.3	6	2.4	1	4.4
<i>Chlorobium tepidum</i> TLS	11	11.4	6	4.2	4	5.5
<i>Pelodictyon luteolum</i> DSM 273	4	3.8	2	1.2	1	2.0
CHLOROFLEXI						
<i>Dehalococcoides ethenogenes</i> 195	5	7.6	5	2.1	4	4.3
<i>Dehalococcoides</i> sp. CBDB1	3	2.9	0	0.6	2	1.4
CYANOBACTERIA						
<i>Prochlorococcus marinus</i> CCMP1375	0	0.0	0	0.0	0	0.0
<i>P. marinus</i> CCMP1378 MED4	0	0.5	0	0.1	1	0.3

<i>P. marinus</i> MIT 9312	0	0.5	0	0.1	1	0.3
<i>P. marinus</i> MIT 9313	0	0.5	0	0.2	1	0.3
<i>P. marinus</i> NATL2A	0	0.0	0	0.0	0	0.0
<i>Synechococcus elongatus</i> PCC 6301	3	3.9	3	1.3	1	1.8
<i>S. elongatus</i> PCC 7942	2	3.3	4	1.0	0	1.7
<i>Synechococcus</i> sp. CC9311	0	0.0	0	0.0	0	0.0
<i>Synechococcus</i> sp. CC9605	1	0.6	0	0.2	0	0.3
<i>Synechococcus</i> sp. CC9902	0	0.5	0	0.2	1	0.3
<i>Synechococcus</i> sp. WH8102	2	1.1	0	0.4	0	0.5
DEINOCOCCUS						
<i>Thermus thermophilus</i> HB8	10	10.5	2	1.3	5	5.1
<i>T. thermophilus</i> HB27	11	9.6	4	1.7	2	5.7
FIRMICUTES						
<i>Bacillus anthracis</i> Kruger B	27	26.5	8	4.2	6	10.3
<i>B. anthracis</i> Sterne	27	24.1	5	4.6	7	10.2
<i>Bacillus clausii</i> KSM-k16	17	15.5	7	4.3	2	6.3
<i>Bacillus licheniformis</i> ATCC 14580	8	24.9	16	1.4	3	0.6
<i>B. licheniformis</i> ATCC 14580 (DSM 13)	7	14.6	14	2.3	2	6.1
<i>Bacillus subtilis</i> 168	8	8.6	5	1.9	2	4.5
<i>Carboxydotherrnus hydrogenoformans</i> Z-2901	15	14.1	0	1.7	4	3.3
<i>Clostridium acetobutylicum</i> ATCC 824	6	8.1	2	1.1	4	2.8
<i>Clostridium perfringens</i> 13	8	8.3	1	1.4	3	2.3
<i>C. perfringens</i> ATCC 13124	5	5.3	1	0.9	2	1.7
<i>Clostridium tetani</i> E88	12	14.9	7	2.7	3	4.4
<i>Enterococcus faecalis</i> V583	17	17.9	5	2.6	3	4.5
<i>Lactobacillus acidophilus</i> NCFM	10	11.4	4	1.8	3	3.8
<i>Lactobacillus johnsonii</i> NCC 533	13	12.3	4	3.7	3	4.0
<i>Lactobacillus plantarum</i> WCFS1	10	9.3	3	2.2	2	3.5
<i>Lactobacillus sakei</i> 23K	6	9.9	6	2.2	3	2.9
<i>Lactobacillus salivarius</i> UCC118	17	16.7	5	2.1	0	3.1
<i>Lactococcus lactis</i> subsp. <i>lactis</i> IL1403	27	28.4	7	3.7	5	6.9
<i>Listeria innocua</i> CLIP 11262	6	8.1	2	0.6	3	2.3
<i>Listeria monocytogenes</i> 1/2a F6854	5	7.3	3	0.8	3	2.9
<i>L. monocytogenes</i> 4b F2365	4	7.2	2	0.6	4	2.2
<i>L. monocytogenes</i> 4b H7858	4	5.0	1	0.4	2	1.7
<i>L. monocytogenes</i> EGD-e	8	10.8	3	0.9	4	3.3
<i>Mesoplasma florum</i> L1	0	0.0	0	0.0	0	0.0
<i>Moorella thermoacetica</i> ATCC 39073	18	21.7	6	2.9	5	4.5
<i>Mycoplasma capricolum</i> ATCC 27343	0	0.7	1	0.1	0	0.2
<i>Mycoplasma gallisepticum</i> strain R	1	0.6	0	0.1	0	0.4
<i>Mycoplasma genitalium</i> G-37	0	0.0	0	0.0	0	0.0
<i>Mycoplasma hyopneumoniae</i> 232	1	1.8	2	0.5	0	0.8
<i>M. hyopneumoniae</i> 7448	3	6.5	7	1.2	0	2.3
<i>M. hyopneumoniae</i> J	6	8.0	6	1.6	1	3.4
<i>Mycoplasma mobile</i> 163K	0	0.0	0	0.0	0	0.0
<i>Mycoplasma mycoides</i> SC PG1	20	31.2	16	4.2	6	6.6

<i>Mycoplasma penetrans</i> HF-2	10	10.5	3	1.3	1	2.3
<i>Mycoplasma pneumoniae</i> M129	0	0.0	0	0.0	0	0.0
<i>Mycoplasma pulmonis</i> UAB CTIP	3	3.6	3	1.0	0	1.3
<i>Mycoplasma synoviae</i> 53	8	9.9	8	3.5	1	3.5
<i>Oceanobacillus iheyensis</i> HTE831	20	20.6	9	4.2	2	6.1
<i>Phytoplasma asteris</i> AYWB	6	5.6	3	1.5	0	1.9
<i>P. asteris</i> Onion Yellow's strain	6	8.2	4	1.2	1	1.6
<i>Staphylococcus aureus</i> COL	12	17.1	12	4.6	3	5.2
<i>S. aureus</i> MRSA252	15	20.5	15	4.3	1	6.2
<i>S. aureus</i> MSSA476	8	8.7	5	2.6	1	2.6
<i>S. aureus</i> Mu50	17	17.9	9	4.8	2	5.3
<i>S. aureus</i> MW2	10	10.1	6	2.9	0	2.9
<i>S. aureus</i> N315	13	15.4	9	3.9	2	4.7
<i>S. aureus</i> NCTC 8325	9	12.5	9	3.2	2	4.3
<i>S. aureus</i> RF122	10	12.2	9	3.2	0	3.6
<i>S. aureus</i> USA300-FPR3757	11	13.5	9	3.4	1	4.0
<i>Staphylococcus saprophyticus</i> ATCC 15305	8	10.2	8	3.3	1	3.5
<i>Streptococcus agalactiae</i> 18RS21	13	14.4	3	2.5	5	4.1
<i>S. agalactiae</i> 515	10	9.2	2	1.8	2	3.0
<i>S. agalactiae</i> 2603V/R	23	18.5	3	3.4	1	5.2
<i>S. agalactiae</i> A909	14	14.8	6	1.9	1	4.2
<i>S. agalactiae</i> CJB111	6	6.9	2	1.2	2	1.9
<i>S. agalactiae</i> COH1	18	19.1	9	4.3	3	6.6
<i>S. agalactiae</i> H36B	14	15.1	4	2.5	4	4.4
<i>S. agalactiae</i> NEM316	3	3.5	1	0.6	1	0.9
<i>Streptococcus mitis</i> NCTC 12261	9	11.0	4	2.1	3	2.9
<i>Streptococcus mutans</i> UA159	11	11.9	5	2.4	1	2.7
<i>Streptococcus pyogenes</i> MGAS315	6	7.1	3	1.3	1	1.6
<i>S. pyogenes</i> MGAS2096	11	14.9	8	2.6	4	5.5
<i>S. pyogenes</i> MGAS5005	12	14.2	6	2.4	4	5.3
<i>S. pyogenes</i> MGAS6180	9	8.8	5	1.8	0	3.4
<i>S. pyogenes</i> MGAS8232	3	4.9	2	0.8	2	1.3
<i>S. pyogenes</i> MGAS9429	11	13.4	8	4.1	4	5.5
<i>S. pyogenes</i> MGAS10270	7	7.2	4	1.3	0	2.5
<i>S. pyogenes</i> MGAS10394	10	12.7	5	2.4	6	5.9
<i>S. pyogenes</i> MGAS10750	13	16.2	8	2.9	3	4.9
<i>S. pyogenes</i> SF370 serotype M1	1	1.4	1	0.2	0	0.4
<i>S. pyogenes</i> SSI-1	4	5.6	4	1.2	0	1.2
<i>Streptococcus thermophilus</i> CNRZ1066	16	27.9	17	4.6	5	5.5
<i>S. thermophilus</i> LMG 18311	15	26.7	19	4.1	2	5.2
FUSOBACTERIA						
<i>Fusobacterium nucleatum</i> ATCC 25586	17	18.3	8	1.9	1	5.8
PLANCTOMYCETES						
<i>Pirellula</i> sp. strain 1	12	16.4	8	7.8	9	4.8
SPIROCHAETES						

<i>Borrelia burgdorferi</i> B31	1	0.6	0	0.1	0	0.3
<i>Borrelia garinii</i> PBi	2	1.1	0	0.2	0	0.8
<i>Leptospira interrogans</i> Copenhageni	9	10.2	7	4.6	3	4.1
<i>Treponema denticola</i> ATCC 35405	8	8.1	1	1.8	5	4.2
<i>Treponema pallidum</i> Nichols	2	1.2	0	0.3	0	0.5
TENERICUTES						
<i>Ureaplasma urealyticum</i> parvum serovar 3	1	1.9	2	0.5	0	0.5
THERMOTOGAE						
<i>Thermotoga maritima</i> MSB8	6	5.7	2	0.7	2	3.6
ALPHAPROTEOBACTERIA						
<i>Agrobacterium tumefaciens</i> C58 Cereon	5	2.8	0	0.7	0	1.5
<i>A. tumefaciens</i> C58 UWash	14	12.3	2	2.8	5	5.8
<i>Anaplasma marginale</i> St Maries	2	1.1	0	0.4	0	0.5
<i>Anaplasma phagocytophilum</i> HZ	2	1.3	0	0.4	0	0.3
<i>Bartonella henselae</i> Houston-1	2	2.9	2	1.2	1	0.9
<i>Bartonella quintana</i> Toulouse	0	2.4	3	0.8	1	0.9
<i>Brucella abortus</i> 9-941	6	7.6	3	1.8	4	3.6
<i>Brucella melitensis</i> 16M	13	12.4	1	3.2	8	6.4
<i>B. melitensis</i> Abortus	11	12.2	5	3.2	6	6.5
<i>Brucella suis</i> 1330	14	12.3	2	3.2	5	5.6
<i>Ehrlichia canis</i> Jake	2	1.1	0	0.6	0	0.3
<i>Ehrlichia chaffeensis</i> Arkansas	2	1.7	1	0.7	0	0.6
<i>Ehrlichia ruminantium</i> Gardel	2	1.1	0	0.6	0	0.3
<i>E. ruminantium</i> Welgevonden France	2	1.6	1	0.9	0	0.5
<i>E. ruminantium</i> Welgevonden South Africa	2	1.6	1	0.9	0	0.5
<i>Erythrobacter litoralis</i> HTCC2594	11	10.8	4	2.3	4	5.9
<i>Hyphomonas neptunium</i> ATCC 15444	16	13.6	7	3.3	2	8.1
<i>Neorickettsia sennetsu</i> Miyayama	2	2.0	2	0.8	0	1.2
<i>Novosphingobium aromaticivorans</i> DSM12444	10	7.7	4	1.8	1	5.5
<i>Pelagibacter ubique</i> HTCC1062	2	1.2	0	0.2	0	0.7
<i>Rhizobium etli</i> CFN 42	9	11.4	5	2.8	6	5.8
<i>Rhodobacter sphaeroides</i> 2.4.1	5	5.0	2	1.6	2	2.4
<i>Rhodopseudomonas palustris</i> CGA009	6	8.4	5	2.5	5	5.1
<i>R. palustris</i> HaA2	9	8.2	3	2.5	3	4.3
<i>Rhodospirillum rubrum</i> ATCC 11170	15	16.6	12	4.4	3	9.0
<i>Rickettsia conorii</i> Malish 7	2	2.1	0	0.5	1	0.5
<i>Rickettsia felis</i> URRWXC12	16	22.1	12	4.6	5	6.2
<i>Rickettsia prowazekii</i> Madrid E	1	1.2	0	0.5	1	0.3
<i>Rickettsia typhi</i> Wilmington	1	1.3	0	0.4	1	0.3
<i>Ruegeria pomeroyi</i> DSS-3	9	7.8	2	2.2	3	4.0
<i>Wolbachia pipientis</i> Bm	4	5.8	4	1.8	2	2.4
<i>Zymomonas mobilis</i> ZM4	6	7.6	2	1.8	4	2.7
BETAPROTEOBACTERIA						
<i>Bordetella bronchiseptica</i> RB50	5	4.5	1	0.8	2	2.7
<i>Bordetella parapertussis</i> 12822	18	17.1	9	3.0	3	9.8
<i>Chromobacterium violaceum</i> ATCC 12472	15	14.4	5	3.1	3	5.5

<i>Dechloromonas aromatica</i> RCB	15	15.6	6	3.6	5	6.7
<i>Neisseria gonorrhoeae</i> FA1090	9	11.1	7	4.0	4	4.9
<i>Ralstonia eutropha</i> JMP134	13	14.9	8	2.7	5	8.4
<i>Rhodoferrax ferrireducens</i> DSM 15236	16	15.9	9	4.0	3	8.1
<i>Thiobacillus denitrificans</i> ATCC 25259	2	5.1	3	0.8	3	2.1
DELTAPROTEOBACTERIA						
<i>Anaeromyxobacter dehalogenans</i> 2CP-C	5	5.0	1	1.0	3	3.0
<i>Bdellovibrio bacteriovorus</i> HD100	4	3.4	2	0.6	0	1.9
<i>Desulfotalea psychrophila</i> LSv54	14	13.0	2	2.7	5	5.2
<i>Desulfovibrio vulgaris</i> Hildenborough	11	10.7	4	4.0	4	4.2
<i>Geobacter sulfurreducens</i> PCA	13	16.2	5	4.1	9	6.6
EPSILONPROTEOBACTERIA						
<i>Campylobacter jejuni</i> NCTC 11168	0	1.2	0	0.3	2	0.5
<i>C. jejuni</i> RM1221	0	1.8	1	0.4	2	0.8
<i>Helicobacter hepaticus</i> ATCC 51449	0	2.5	2	0.5	2	1.0
<i>Helicobacter pylori</i> 26695	3	4.9	4	1.8	2	2.3
<i>H. pylori</i> J99	1	1.5	1	0.8	1	0.7
<i>Thiomicrospira denitrificans</i> ATCC 33889	4	3.3	1	1.0	1	1.8
<i>Wolinella succinogenes</i> DSMZ 1740	3	5.4	2	0.8	5	3.8
GAMMAPROTEOBACTERIA						
<i>Acinetobacter</i> sp. ADP1	8	8.2	3	1.9	3	3.9
<i>Baumannia cicadellincola</i>	1	0.6	0	0.1	0	0.3
<i>Blochmannia floridanus</i>	0	0.0	0	0.0	0	0.0
<i>B. pennsylvanicus</i> BPEN	1	0.6	0	0.1	0	0.3
<i>Buchnera aphidicola</i> APS	1	0.6	0	0.1	0	0.3
<i>B. aphidicola</i> Baizongia pistaciae	1	0.5	0	0.2	0	0.3
<i>B. aphidicola</i> Sg	1	0.6	0	0.1	0	0.3
<i>Colwellia psychrerythraea</i> 34H	19	19.7	8	4.8	6	8.5
<i>Erwinia carotovora</i> atroseptica SCRI1043	14	12.9	6	2.8	2	6.4
<i>Haemophilus ducreyi</i> 35000HP	6	5.0	1	1.5	3	3.5
<i>Haemophilus influenzae</i> 86 028NP	5	6.8	6	2.0	0	2.2
<i>H. influenzae</i> Rd KW20	8	6.6	3	1.7	0	2.8
<i>Idiomarina loihiensis</i> L2TR	17	18.4	10	3.7	5	9.9
<i>Legionella pneumophila</i> Lens	19	17.4	11	4.7	3	10.9
<i>L. pneumophila</i> Philadelphia	12	11.9	9	3.5	1	6.6
<i>Mannheimia succiniciproducens</i> MBEL55E	7	8.8	7	3.4	2	3.8
<i>Pasteurella multocida</i> PM70	5	3.7	2	1.3	0	2.0
<i>Pseudoalteromonas haloplanktis</i> TAC125	13	9.6	3	2.9	2	5.5
<i>Pseudomonas aeruginosa</i> PAO1	12	17.1	11	3.9	7	9.0
<i>Pseudomonas fluorescens</i> Pf-5	6	10.6	7	2.4	5	5.0
<i>P. fluorescens</i> PfO-1	13	13.7	7	3.9	5	7.4
<i>Saccharophagus degradans</i> 2-40	15	12.6	4	2.4	2	6.0
<i>Salmonella enterica</i> Paratyphi ATCC 9150	10	15.0	11	2.6	4	7.4
<i>S. enterica</i> Typhi CT18	9	11.9	7	2.5	4	5.6
<i>S. enterica</i> Typhi Ty2	16	19.9	16	4.5	3	10.7
<i>Salmonella typhimurium</i> LT2 SGSC1412	18	18.0	8	3.3	5	9.7

<i>Thiomicrospira crunogena</i> XCL-2	5	5.7	3	1.1	1	2.2
<i>Vibrio fischeri</i> ES114	4	4.4	2	1.2	2	2.5
<i>Vibrio parahaemolyticus</i> RIMD 2210633	7	10.5	4	2.6	7	5.0
<i>Vibrio vulnificus</i> CMCP6	14	15.5	11	3.5	2	8.0
<i>Wigglesworthia glossinidia</i> brevipalpis	0	0.0	0	0.0	0	0.0
<i>Xylella fastidiosa</i> 9a5c	6	5.0	0	1.8	3	2.1
<i>X. fastidiosa</i> Temecula 1	4	2.9	1	0.9	0	1.1

Table S2. Quantities of IS element loci eliminated from the analysis for various reasons, all ultimately because the ISs do not neighbor genes annotated as functional, native bacterial genes (see Materials and Methods for details).

	Neighboring gene(s) annotated as:			
	disrupted	pseudogene	non-consecutive	phage
ACTINOBACTERIA				
<i>Corynebacterium efficiens</i> YS-314	0	0	0	0
<i>Corynebacterium glutamicum</i> ATCC 13032	0	0	0	0
<i>Corynebacterium jeikeium</i> K411	0	0	0	0
<i>Frankia</i> sp. CcI3	0	0	0	3
<i>Mycobacterium avium</i> paratuberculosis	0	0	0	0
<i>Mycobacterium bovis</i> AF2122/97	1	0	0	0
<i>Mycobacterium smegmatis</i> MC2	11	0	3	0
<i>Mycobacterium tuberculosis</i> CDC1551	0	2	1	0
<i>M. tuberculosis</i> H37Rv	2	0	0	0
<i>Streptomyces avermitilis</i> MA-4680	0	0	1	0
<i>Streptomyces coelicolor</i> A3(2)	0	0	14	0
BACTERIODETES				
<i>Bacteroides thetaiotaomicron</i> VPI-5482	0	0	0	0
<i>Porphyromonas gingivalis</i> W83	3	3	19	0
<i>Prevotella intermedia</i> 17	0	0	0	0
<i>Salinibacter ruber</i> DSM 13855	0	0	0	1 (1) ^a
CHLAMYDIAE				
<i>Protochlamydia amoebophila</i> UWE25	0	0	0	0
CYANOBACTERIA				
<i>Anabaena variabilis</i> ATCC 29413	0	0	0	1
<i>Gloeobacter violaceus</i> PCC7421	0	0	0	0
<i>Nostoc</i> sp. PCC 7120	0	0	1	0
<i>Synechococcus</i> sp. JA-2-3Ba(2-13)	4	1	4	0
<i>Synechococcus</i> sp. JA-3-3Ab	9	2	2	0
<i>Synechocystis</i> sp. PCC6803	0	0	8	0
<i>Thermosynechococcus elongatus</i> BP-1	0	0	0	0

DEINOCOCCUS

Deinococcus radiodurans R1 1 0 0 0

FIRMICUTES

Bacillus anthracis A0039 0 0 0 0

B. anthracis Ames 2 1 3 0

B. anthracis Ames Ancestor 2 1 3 0

B. anthracis CNEVA-9066 0 0 0 0

B. anthracis USA6153 0 0 0 0

B. anthracis Vollum 0 0 0 0

Bacillus cereus 10987 1 0 0 0

B. cereus ATCC 14579 0 0 2 2

B. cereus Zk 1 0 1 0

Bacillus halodurans C-125 0 0 0 0

Bacillus thuringiensis konkukian 1 0 1 0

Clostridium perfringens SM101 2 5 4 0

Desulfitobacterium hafniense Y51 0 0 0 0

Geobacillus kaustophilus HTA426 0 0 1 0

Staphylococcus epidermidis ATCC 12228 0 0 0 0

S. epidermidis RP62A 6 1 0 0

Staphylococcus haemolyticus JCSC1435 5 0 0 1

Streptococcus pneumoniae G54 0 0 0 0

S. pneumoniae R6 5 0 1 0

S. pneumoniae TIGR4 11 5 0 1

Thermoanaerobacter tengcongensis MB4(T) 0 0 12 0

SPIROCHAETES

Leptospira interrogans lai 56601 0 0 0 0

UNCLASSIFIED PROTEOBACTERIA

Magnetococcus sp. MC-1 0 0 22 0

ALPHAPROTEOBACTERIA

Bradyrhizobium japonicum USDA 110 0 0 0 0

Caulobacter crescentus CB15 2 0 0 0

Gluconobacter oxydans 621H 2 0 6 1

Magnetospirillum magneticum AMB-1 0 0 0 1

<i>Mesorhizobium loti</i> MAFF303099	0	0	23	0
<i>Nitrobacter winogradskyi</i> Nb-255	0	0	0	6
<i>Rhodopseudomonas palustris</i> BisB18	0	0	0	2
<i>Rickettsia bellii</i> RML369-C	0	0	0	0
<i>Sinorhizobium meliloti</i> 1021	0	0	0	1
<i>Wolbachia pipientis</i> wMel	7	1	1	3
BETAPROTEOBACTERIA				
<i>Azoarcus</i> sp. EbN1	0	0	0	4
<i>Bordetella pertussis</i> Tohama I	25	72	14	4
<i>Burkholderia cenocepacia</i> AU 1054	0	0	0	3
<i>Burkholderia mallei</i> ATCC 23344	22	10	24	4
<i>Burkholderia pseudomallei</i> 1710b	1	0	5	2
<i>B. pseudomallei</i> K96243	5	3	1	5
<i>Burkholderia thailandensis</i> E264	3	0	7	4
<i>Burkholderia</i> sp. 383	0	0	0	0
<i>Neisseria meningitidis</i> MC58	3	2	0	0
<i>N. meningitidis</i> Z2491	0	3	9	1
<i>Nitrosomonas europaea</i> ATCC 19718	2	1	0	1 (2) ^a
<i>Nitrospira multififormis</i> ATCC 25196	0	0	0	1
<i>Ralstonia solanacearum</i> GMI1000	1	0	1	6
DELTAPROTEOBACTERIA				
<i>Desulfovibrio desulfuricans</i> G20	0	0	0	2
<i>Geobacter metallireducens</i> GS-15	0	0	1	0 (2) ^a
<i>Myxococcus xanthus</i> DK 1622	0	1	9	0
<i>Pelobacter carbinolicus</i> DSM 2380	0	0	0	1
GAMMAPROTEOBACTERIA				
<i>Acidithiobacillus ferrooxidans</i> ATCC 23270	1	0	0	4
<i>Coxiella burnetii</i> RSA 493	1	1	0	0
<i>Escherichia coli</i> CFT073	0	0	1	5
<i>E. coli</i> K12 MG1655	2	0	0	2
<i>E. coli</i> O157:H7 EDL933	2	0	13	20
<i>E. coli</i> O157:H7 VT2-Sakai	1	0	0	3
<i>E. coli</i> UTI89	0	0	3	2

<i>Francisella tularensis</i> holarctica	5	0	0	0
<i>F. tularensis</i> tularensis	7	18	0	0
<i>Hahella chejuensis</i> KCTC 2396	0	0	8	0
<i>Legionella pneumophila</i> Paris	1	0	0	0
<i>Methylococcus capsulatus</i> Bath	6	3	9	1
<i>Nitrosococcus oceani</i> ATCC 19707	0	0	1	1
<i>Photobacterium profundum</i> SS9	0	0	16	0
<i>Photorhabdus luminescens</i> TTO1	39	6	0	1
<i>Pseudomonas putida</i> KT2440	5	1	0	2
<i>Pseudomonas syringae</i> DC3000	21	8	0	5
<i>P. syringae</i> pv B728a	0	0	0	0
<i>P. syringae</i> pv phaseolicola	12	5	4	1
<i>Psychrobacter arcticum</i> 273-4	0	0	0	1
<i>Salmonella enterica</i> Choleraesuis	0	0	0	3
<i>Shewanella oneidensis</i> MR-1	7	1	0	6
<i>Shigella boydii</i> Sb227	21	23	38	18
<i>Shigella dysenteriae</i> Sd197	20	28	67	17
<i>Shigella flexneri</i> 2a 301	49	3	1	10
<i>S. flexneri</i> 2a 2457T	0	0	106	33
<i>Shigella sonnei</i> Ss046	22	11	67	23
<i>Sodalis glossinidius</i> morsitans	0	0	0	10
<i>Vibrio cholerae</i> El Tor N16961	1	1	0	0
<i>Vibrio vulnificus</i> YJ016	0	0	1	2 (1) ^a
<i>Xanthomonas axonopodis</i> pv. citri 306	1	0	2	4
<i>Xanthomonas campestris</i> 8004	1	0	11	5
<i>X. campestris</i> ATCC 33913	0	0	1	6
<i>X. campestris</i> pv. armoraciae 756C	1	0	1	0
<i>X. campestris</i> pv. vesicatoria 85-10	4	0	0	6
<i>Xanthomonas oryzae</i> KACC10331	0	0	5	1
<i>X. oryzae</i> pv. oryzae MAFF 311018	8	3	0	0
<i>X. oryzae</i> pv. oryzicola BLS256	0	1	11	1
<i>Yersinia pestis</i> biovar Medievalis 91001	41	8	0	3
<i>Y. pestis</i> CO92	3	0	43	8

<i>Y. pestis</i> KIM	0	0	10	2
<i>Yersinia pseudotuberculosis</i> IP32593	5	0	0	4

^a parenthetical values represent the number of IS elements that were eliminated because they are annotated as being or bordering an integron or an integrative genetic element

Table S3. Calculation of expected intergenic IS elements in *Corynebacterium efficiens* YS-314.

Neighboring gene orientation (NGO)	Total count (A)	Mean intergenic space (in bp) (B)	A × B (C)	C proportion (D)	Total intergenic IS count ^a (E)	Expected IS quantity: D × E
→→ , ←←	1804	83.2	150,003	0.55	73	39.8
→←	487	112.5	54,799	0.20		14.5
←→	485	144.7	70,166	0.26		18.6
Sum			274,968	1.00		73

^a this is the total quantity of intergenic IS elements across the entire chromosome