

Table S4. Phylogenetic distribution of bacterial and archaea genomes in groups A, B, C, D, and E.

Group A

- a: Total number of genomes in the taxon
- b: Number of group A genomes in the taxon
- c: Percentage of group A genomes in the taxon
- d: Average percentage of first-genes-in-operon in the genomes of the taxon in prediction
- e: Average percentage of predicted leaderless genes among FGIO
- f: Average percentage of predicted leaderless genes among all genes

Colors Legend - Column f

- Values between 10 and 25 percent
- Values between 25 and 40 percent
- Values between 40 and 55 percent
- Values between 55 and 70 percent
- "Higher level" groups that contain several of the above ranges have been left blank

	a	b	c	d	e	f
cellular organisms	5007	199	4.0	72.4	56.6	44.9
__ Archaea	238	199	83.6	72.4	56.6	44.9
__ Euryarchaeota	190	163	85.8	72.7	53.9	42.8
__ Halobacteria	74	74	100.0	79.2	70.8	58.8
__ Halobacteriales	26	26	100.0	78.1	70.5	57.9
__ Haloarculaceae	9	9	100.0	78.4	73.4	60.0
__ Halococcaceae	7	7	100.0	78.0	66.8	55.2
__ Halococcus	7	7	100.0	78.0	66.8	55.2
__ Halobacteriaceae	7	7	100.0	77.9	68.4	56.4
__ Halobacterium	3	3	100.0	77.2	70.7	57.6
__ unclassified Halobacteriales	3	3	100.0	78.3	75.0	61.4
__ Natrionalbales	25	25	100.0	81.5	71.1	60.5
__ Natrionalbaceae	25	25	100.0	81.5	71.1	60.5
__ Halopiger	4	4	100.0	81.9	73.0	62.2
__ Natronorubrum	3	3	100.0	81.2	71.9	61.2
__ Natrinema	3	3	100.0	81.2	70.0	59.4
__ Natronococcus	3	3	100.0	81.9	65.7	56.0
__ Natrionalba	3	3	100.0	81.8	70.8	60.7
__ Haloferacales	23	23	100.0	77.8	71.0	57.9

		Halorubraceae	12	12	100.0	77.2	72.0	58.0
		__ Halorubrum	9	9	100.0	77.5	70.7	57.2
		__ Haloferacaceae	11	11	100.0	78.5	69.8	57.8
		__ Haloferax	5	5	100.0	77.7	71.7	58.8
	__	Methanomicrobia	42	40	95.2	72.5	36.4	28.8
		__ Methanosarcinales	26	24	92.3	76.6	29.6	24.9
		__ Methanosarcinaceae	22	20	90.9	78.6	28.2	24.4
		__ Methanosarcina	13	12	92.3	83.0	27.4	24.5
		__ Methanococcoides	3	3	100.0	71.9	29.2	24.1
		__ Methanomicrobiales	14	14	100.0	65.8	47.0	35.1
		__ Methanomicrobiaceae	7	7	100.0	67.0	47.3	35.6
		__ Methanoculleus	3	3	100.0	66.5	49.2	36.2
		__ Methanoregulaceae	4	4	100.0	67.0	42.9	32.1
	__	Thermococci	21	21	100.0	63.0	30.3	21.4
		__ Thermococcales	21	21	100.0	63.0	30.3	21.4
		__ Thermococcaceae	21	21	100.0	63.0	30.3	21.4
		__ Thermococcus	14	14	100.0	64.2	31.7	22.8
		__ Pyrococcus	5	5	100.0	59.1	28.3	19.0
	__	Thermoplasmata	11	11	100.0	65.7	63.2	45.8
		__ Thermoplasmatales	6	6	100.0	67.5	72.3	52.7
		__ Methanomassiliicoccales	5	5	100.0	63.5	52.3	37.6
		__ Methanomassiliicoccaceae	5	5	100.0	63.5	52.3	37.6
	__	Archaeoglobi	7	7	100.0	57.7	64.1	42.2
		__ Archaeoglobales	7	7	100.0	57.7	64.1	42.2
		__ Archaeoglobaceae	7	7	100.0	57.7	64.1	42.2
		__ Archaeoglobus	4	4	100.0	59.2	63.8	43.3
	__	Methanobacteria	18	5	27.8	66.3	26.2	21.3
		__ Methanobacteriales	18	5	27.8	66.3	26.2	21.3
		__ Methanobacteriaceae	17	5	29.4	66.3	26.2	21.3
	__	Methanococci	15	3	20.0	63.6	12.5	11.9
		__ Methanococcales	15	3	20.0	63.6	12.5	11.9
		__ Methanocaldococcaceae	8	3	37.5	63.6	12.5	11.9
	__	TACK group	47	35	74.5	70.8	68.8	54.1
	__	Crenarchaeota	35	23	65.7	69.4	67.3	52.3
		__ Thermoprotei	35	23	65.7	69.4	67.3	52.3
		__ Sulfolobales	11	11	100.0	66.6	69.0	52.0
		__ Sulfolobaceae	11	11	100.0	66.6	69.0	52.0
		__ Sulfolobus	6	6	100.0	66.4	67.2	51.2
		__ Metallosphaera	3	3	100.0	66.7	68.3	50.5
		__ Thermoproteales	9	9	100.0	71.6	76.0	59.9
		__ Thermoproteaceae	6	6	100.0	72.7	81.2	65.6
		__ Thermofilaceae	3	3	100.0	69.3	65.6	48.4
		__ Thermofilum	3	3	100.0	69.3	65.6	48.4

Group B

- a: Total number of genomes in the taxon
- b: Number of group B genomes in the taxon
- c: Percentage of group B genomes in the taxon
- d: Average percentage of first-genes-in-operon in the genomes of the taxon in prediction
- e: Average percentage of predicted leaderless genes among FGIO
- f: Average percentage of predicted leaderless genes among all genes

Colors Legend - Column c

- Individual colors have no specific meaning - colors are used to highlight members of the same "cluster", in particular, those clusters with a significant number of genomes that have been classified as class B.

Colors Legend - Column f

- Values between 10 and 20 percent
- Values between 20 and 30 percent
- Values between 30 and 40 percent
- Values between 40 and 60 percent
- "Higher level" groups that contain several of the above ranges have been left blank

	a	b	c	d	e	f
cellular organisms	5007	1028	20.5	70.4	36.7	31.4
__ Bacteria	4769	1028	21.6	70.4	36.7	31.4
__ Terrabacteria group	2228	877	39.4	71.2	37.3	31.7
__ Actinobacteria	859	773	90.0	72.1	37.7	32.2
__ Actinobacteria	807	764	94.7	72.1	37.6	32.1
__ Micrococcales	211	198	93.8	69.6	39.5	33.2
__ Microbacteriaceae	82	78	95.1	68.3	41.0	34.0
__ Microbacterium	34	34	100.0	67.0	41.7	33.9
__ Leifsonia	9	8	88.9	68.4	39.8	33.6
__ Leucobacter	8	7	87.5	68.8	38.4	31.7
__ Micrococcaceae	51	43	84.3	72.3	35.4	31.0
__ Arthrobacter	19	16	84.2	71.8	36.3	31.7
__ Kocuria	9	9	100.0	73.7	32.0	28.5
__ Intrasporangiaceae	25	25	100.0	67.4	42.9	35.5
__ Cellulomonadaceae	17	17	100.0	69.6	40.5	33.6
__ Cellulomonas	14	14	100.0	69.6	40.3	33.4
__ Brevibacteriaceae	7	7	100.0	69.8	35.2	29.5
__ Brevibacterium	7	7	100.0	69.8	35.2	29.5
__ Dermacoccaceae	6	6	100.0	70.5	42.4	35.2
__ Corynebacteriales	202	197	97.5	70.4	41.0	35.0
__ Corynebacteriaceae	72	70	97.2	70.7	40.8	35.3
__ Corynebacterium	70	68	97.1	70.7	40.9	35.4
__ Mycobacteriaceae	57	56	98.2	67.2	43.6	36.7
__ Mycobacterium	56	55	98.2	67.2	43.7	36.8

			__ Nocardiaceae	43	41	95.3	74.2	36.9	32.0
			__ __ Nocardia	30	28	93.3	75.8	36.3	31.6
			__ __ Rhodococcus	12	12	100.0	71.0	37.8	32.6
			__ Gordoniaceae	19	19	100.0	70.8	42.5	35.8
			__ __ Gordonia	19	19	100.0	70.8	42.5	35.8
		__	Streptomycetales	129	129	100.0	78.2	31.9	28.2
		__	__ Streptomycetaceae	129	129	100.0	78.2	31.9	28.2
		__	__ __ Streptomyces	117	117	100.0	78.0	32.0	28.2
		__	__ __ Kitasatospora	6	6	100.0	79.5	30.2	27.4
		__	Propionibacteriales	50	50	100.0	67.3	41.3	33.7
		__	__ Nocardioideaceae	32	32	100.0	66.7	42.7	35.0
		__	__ __ Nocardioides	18	18	100.0	66.2	43.0	35.2
		__	__ __ Aeromicrobium	6	6	100.0	66.0	44.0	35.9
		__	__ Propionibacteriaceae	18	18	100.0	68.5	38.7	31.3
		__	Pseudonocardiales	46	45	97.8	71.8	37.0	31.2
		__	__ Pseudonocardiaceae	46	45	97.8	71.8	37.0	31.2
		__	__ __ Saccharomonospora	9	9	100.0	72.7	37.4	31.3
		__	__ __ Amycolatopsis	7	7	100.0	70.7	36.2	30.1
		__	__ __ Pseudonocardia	7	7	100.0	70.6	38.0	32.3
		__	Actinomycetales	36	35	97.2	70.8	35.1	29.2
		__	__ Actinomycetaceae	36	35	97.2	70.8	35.1	29.2
		__	__ __ Actinomyces	23	22	95.7	71.0	36.3	30.1
		__	Streptosporangiales	34	32	94.1	76.6	32.3	28.2
		__	__ Nocardioisporaceae	18	16	88.9	78.6	30.4	26.9
		__	__ __ Nocardioopsis	15	15	100.0	78.4	30.5	26.9
		__	__ Streptosporangiaceae	9	9	100.0	74.4	35.4	30.7
		__	__ Thermomonosporaceae	7	7	100.0	74.7	32.6	28.2
		__	Bifidobacteriales	36	20	55.6	79.1	26.4	23.5
		__	__ Bifidobacteriaceae	36	20	55.6	79.1	26.4	23.5
		__	__ __ Bifidobacterium	30	14	46.7	80.1	26.7	23.8
		__	Micromonosporales	18	18	100.0	73.2	39.6	34.2
		__	__ Micromonosporaceae	18	18	100.0	73.2	39.6	34.2
		__	__ __ Actinoplanes	7	7	100.0	71.8	41.4	36.0
		__	Geodermatophilales	10	10	100.0	71.1	40.2	35.1
		__	__ Geodermatophilaceae	10	10	100.0	71.1	40.2	35.1
		__	Frankiales	11	8	72.7	75.6	34.8	31.6
		__	__ Frankiaceae	9	6	66.7	78.3	33.7	31.2
		__	__ __ Frankia	9	6	66.7	78.3	33.7	31.2
		__	Deinococcus-Thermus	38	37	97.4	68.1	48.3	39.0
		__	__ Deinococci	38	37	97.4	68.1	48.3	39.0
		__	__ Deinococcales	20	20	100.0	75.4	48.8	40.3
		__	__ __ Deinococcaceae	19	19	100.0	75.5	49.3	40.7
		__	__ __ Deinococcus	19	19	100.0	75.5	49.3	40.7
		__	Thermales	18	17	94.4	59.5	47.7	37.4
		__	__ Thermaceae	18	17	94.4	59.5	47.7	37.4
		__	__ __ Thermus	10	10	100.0	53.3	48.3	37.1
		__	__ __ Meiothermus	6	6	100.0	70.4	47.9	38.8

__ Firmicutes	1064	36	3.4	64.1	19.4	17.1
__ Bacilli	597	24	4.0	66.8	19.8	17.6
__ Lactobacillales	255	24	9.4	66.8	19.8	17.6
__ Streptococcaceae	41	19	46.3	66.8	18.8	16.9
__ Streptococcus	39	18	46.2	66.5	18.5	16.6
__ Tenericutes	116	30	25.9	61.5	32.7	26.5
__ Mollicutes	115	30	26.1	61.5	32.7	26.5
__ Mycoplasmatales	73	26	35.6	59.5	33.8	26.8
__ Mycoplasmataceae	73	26	35.6	59.5	33.8	26.8
__ Mycoplasma	70	26	37.1	59.5	33.8	26.8
__ Proteobacteria	1854	104	5.6	66.5	32.2	29.9
__ Gammaproteobacteria	711	34	4.8	70.2	32.0	29.5
__ Xanthomonadales	62	18	29.0	69.8	35.7	32.4
__ Xanthomonadaceae	48	18	37.5	69.8	35.7	32.4
__ Lysobacter	12	7	58.3	72.7	35.2	32.2
__ Alphaproteobacteria	667	34	5.1	67.9	33.2	31.4
__ Sphingomonadales	105	13	12.4	68.1	32.6	30.3
__ Sphingomonadaceae	83	10	12.0	68.3	32.5	30.4
__ Sphingomonas	34	9	26.5	68.7	32.2	30.1
__ delta/epsilon subdivisions	196	20	10.2	57.6	25.6	24.5
__ Deltaproteobacteria	123	10	8.1	60.7	30.8	27.0
__ Bdellovibrionales	8	7	87.5	65.6	30.0	26.9
__ Epsilonproteobacteria	73	10	13.7	54.6	20.5	21.9
__ Campylobacteriales	67	9	13.4	54.5	20.5	22.2
__ Betaproteobacteria	273	15	5.5	66.8	39.1	35.4
__ Burkholderiales	166	15	9.0	66.8	39.1	35.4
__ Comamonadaceae	50	8	16.0	67.0	40.0	35.7
__ Spirochaetes	60	24	40.0	63.5	28.6	22.7
__ Spirochaetia	60	24	40.0	63.5	28.6	22.7
__ Spirochaetales	40	24	60.0	63.5	28.6	22.7
__ Spirochaetaceae	28	21	75.0	63.7	29.2	22.8
__ Treponema	17	12	70.6	64.3	29.7	23.6
__ FCB group	455	8	1.8	70.2	56.9	52.5
__ Bacteroidetes/Chlorobi group	450	7	1.6	70.3	59.9	55.7
__ Bacteroidetes	436	7	1.6	70.3	59.9	55.7
__ Deferribacteres	6	3	50.0	51.6	21.2	18.2
__ Aquificae	14	3	21.4	45.4	39.4	29.9
__ PVC group	52	2	3.8	74.8	50.8	46.1
__ Acidobacteria	24	2	8.3	67.5	31.1	25.5
__ Elusimicrobia	2	2	100.0	58.4	30.3	29.5
__ unclassified Bacteria	5	1	20.0	70.9	41.4	35.3
__ Fusobacteria	19	1	5.3	49.7	16.9	11.3
__ Thermodesulfobacteria	6	1	16.7	53.0	33.0	30.0

Group C

a: Total number of genomes in the taxon

b: Number of group C genomes in the taxon

c: Percentage of group C genomes in the taxon

	a	b	c
cellular organisms	5007	495	9.9
__ Bacteria	4769	495	10.4
__ FCB group	455	409	89.9
__ Bacteroidetes/Chlorobi group	450	408	90.7
__ Bacteroidetes	436	400	91.7
__ Flavobacteria	190	187	98.4
__ Flavobacteriales	188	185	98.4
__ Flavobacteriaceae	174	172	98.9
__ Flavobacterium	30	30	100.0
__ Chryseobacterium	24	24	100.0
__ Capnocytophaga	8	8	100.0
__ Lacinutrix	5	5	100.0
__ Aquimarina	5	5	100.0
__ Psychroserpens	5	5	100.0
__ Maribacter	4	4	100.0
__ Polaribacter	4	4	100.0
__ Nonlabens	5	4	80.0
__ Cellulophaga	4	4	100.0
__ Tenacibaculum	4	4	100.0
__ Arenibacter	3	3	100.0
__ Mangrovimonas	3	3	100.0
__ Leeuwenhoekella	3	3	100.0
__ Muricauda	3	3	100.0
__ Kordia	3	3	100.0
__ Gillisia	3	3	100.0
__ Psychroflexus	3	3	100.0
__ Blattabacteriaceae	8	7	87.5
__ Blattabacterium	8	7	87.5
__ Bacteroidia	137	130	94.9
__ Bacteroidales	127	120	94.5
__ Prevotellaceae	52	51	98.1
__ Prevotella	49	49	100.0
__ Porphyromonadaceae	33	31	93.9
__ Porphyromonas	15	13	86.7
__ Dysgonomonas	5	5	100.0

			__ Parabacteroides	3	3	100.0
			__ Bacteroidaceae	23	21	91.3
			__ Bacteroides	23	21	91.3
			__ Rikenellaceae	12	11	91.7
			__ Alistipes	10	10	100.0
			__ Odoribacteraceae	4	4	100.0
			__ Marinilabiliales	10	10	100.0
			__ Marinilabiliaceae	5	5	100.0
			__ Prolixibacteraceae	3	3	100.0
			__ Cytophagia	70	46	65.7
			__ Cytophagales	70	46	65.7
			__ Cyclobacteriaceae	16	16	100.0
			__ Algoriphagus	6	6	100.0
			__ Cytophagaceae	22	11	50.0
			__ Dyadobacter	4	3	75.0
			__ Hymenobacteraceae	14	7	50.0
			__ Pontibacter	4	3	75.0
			__ Hymenobacter	8	3	37.5
			__ Flammeovirgaceae	8	4	50.0
			__ Amoebophilaceae	3	3	100.0
			__ Sphingobacteriia	21	20	95.2
			__ Sphingobacteriales	21	20	95.2
			__ Sphingobacteriaceae	21	20	95.2
			__ Sphingobacterium	8	8	100.0
			__ Pedobacter	7	7	100.0
			__ Chitinophagia	12	12	100.0
			__ Chitinophagales	12	12	100.0
			__ Chitinophagaceae	12	12	100.0
			__ Flaviumibacter	3	3	100.0
			__ Chlorobi	11	7	63.6
			__ Chlorobia	11	7	63.6
			__ Chlorobiales	11	7	63.6
			__ Chlorobiaceae	11	7	63.6
			__ Chlorobium/Pelodictyon group	8	6	75.0
			__ Chlorobium	6	4	66.7
			__ Proteobacteria	1854	38	2.0
			__ Alphaproteobacteria	667	24	3.6
			__ Rickettsiales	42	16	38.1
			__ Rickettsiaceae	18	12	66.7
			__ Rickettsieae	18	12	66.7
			__ Rickettsia	15	10	66.7
			__ spotted fever group	12	8	66.7
			__ Anaplasmataceae	21	4	19.0

__ Pelagibacterales	8	6	75.0
__ Pelagibacteraceae	8	6	75.0
__ Candidatus Pelagibacter	5	3	60.0
__ Candidatus Pelagibacter ubique	3	3	100.0
__ unclassified Pelagibacteraceae	3	3	100.0
__ Gammaproteobacteria	711	9	1.3
__ Enterobacterales	112	5	4.5
__ Enterobacteriaceae	41	3	7.3
__ Betaproteobacteria	273	5	1.8
__ unclassified Betaproteobacteria	12	5	41.7
__ Kinetoplastibacterium	5	4	80.0
__ Terrabacteria group	2228	38	1.7
__ Cyanobacteria/Melainabacteria group	127	32	25.2
__ Cyanobacteria	127	32	25.2
__ Nostocales	31	13	41.9
__ Nostocaceae	10	9	90.0
__ Nostoc	4	4	100.0
__ Anabaena	3	3	100.0
__ Oscillatoriothyracaceae	31	9	29.0
__ Oscillatoriales	22	7	31.8
__ Synechococcales	55	8	14.5
__ Synechococcaceae	27	4	14.8
__ Synechococcus	24	4	16.7
__ Tenericutes	116	4	3.4
__ Mollicutes	115	4	3.5
__ Mycoplasmatales	73	4	5.5
__ Mycoplasmataceae	73	4	5.5
__ Mycoplasma	70	4	5.7
__ PVC group	52	7	13.5
__ Verrucomicrobia	17	5	29.4
__ Spirochaetes	60	2	3.3
__ Acidobacteria	24	1	4.2

Group D

a: Total number of genomes in the taxon
 b: Number of group D genomes in the taxon
 c: Percentage of group D genomes in the taxon

	a	b	c
cellular organisms	5007	2974	59.4
__ Bacteria	4769	2935	61.5
__ Proteobacteria	1854	1570	84.7
__ Gammaproteobacteria	711	631	88.7
__ Enterobacterales	112	97	86.6
__ Enterobacteriaceae	41	32	78.0
__ unclassified Enterobacteriaceae	13	7	53.8
__ Erwiniaceae	30	28	93.3
__ Erwinia	10	10	100.0
__ Buchnera	8	8	100.0
__ Buchnera aphidicola	8	8	100.0
__ Pantoea	8	8	100.0
__ Yersiniaceae	14	14	100.0
__ Serratia	8	8	100.0
__ Morganellaceae	13	10	76.9
__ Pectobacteriaceae	8	8	100.0
__ Alteromonadales	94	94	100.0
__ Alteromonadaceae	34	34	100.0
__ Marinobacter	12	12	100.0
__ Shewanellaceae	17	17	100.0
__ Shewanella	17	17	100.0
__ Pseudoalteromonadaceae	16	16	100.0
__ Pseudoalteromonas	15	15	100.0
__ Idiomarinaceae	9	9	100.0
__ Idiomarina	9	9	100.0
__ Colwelliaceae	6	6	100.0
__ Pseudomonadales	81	81	100.0
__ Moraxellaceae	41	41	100.0
__ Acinetobacter	25	25	100.0
__ Psychrobacter	8	8	100.0
__ Moraxella	6	6	100.0
__ Pseudomonadaceae	40	40	100.0
__ Pseudomonas	38	38	100.0
__ Oceanospirillales	73	72	98.6
__ Oceanospirillaceae	28	28	100.0

	__ Marinomonas	7	7	100.0
	__ Halomonadaceae	28	27	96.4
	__ __ Halomonas	19	19	100.0
	__ Alcanivoracaceae	6	6	100.0
	__ __ Alcanivorax	6	6	100.0
	__ Hahellaceae	6	6	100.0
__	Vibrionales	49	48	98.0
	__ Vibrionaceae	49	48	98.0
	__ __ Vibrio	27	26	96.3
	__ __ Photobacterium	13	13	100.0
__	Chromatiales	42	40	95.2
	__ Ectothiorhodospiraceae	21	20	95.2
	__ __ Thioalkalivibrio	11	11	100.0
	__ Chromatiaceae	18	17	94.4
__	Xanthomonadales	62	35	56.5
	__ Xanthomonadaceae	48	22	45.8
	__ __ Stenotrophomonas	10	8	80.0
	__ Rhodanobacteraceae	14	13	92.9
__	Thiotrichales	34	31	91.2
	__ Piscirickettsiaceae	21	20	95.2
	__ __ Thiomicrospira	10	10	100.0
	__ Thiotrichaceae	7	6	85.7
__	Cellvibrionales	31	31	100.0
	__ Cellvibrionaceae	13	13	100.0
	__ Halieaceae	8	8	100.0
	__ Spongiibacteraceae	6	6	100.0
__	Legionellales	38	31	81.6
	__ Legionellaceae	32	28	87.5
	__ __ Legionella	30	26	86.7
__	unclassified Gammaproteobacteria	26	18	69.2
	__ unclassified Gammaproteobacteria (miscellaneous)	7	6	85.7
__	Pasteurellales	19	16	84.2
	__ Pasteurellaceae	19	16	84.2
__	Aeromonadales	15	14	93.3
	__ Aeromonadaceae	9	9	100.0
	__ __ Aeromonas	7	7	100.0
__	Methylococcales	20	11	55.0
	__ Methylococcaceae	19	10	52.6
__	Nevskiales	7	6	85.7
__	Alphaproteobacteria	667	583	87.4
	__ Rhizobiales	225	221	98.2
	__ __ Bradyrhizobiaceae	44	43	97.7
	__ __ Bradyrhizobium	18	18	100.0

__ unclassified Alphaproteobacteria	13	12	92.3
__ __ unclassified Alphaproteobacteria (miscellaneous)	7	6	85.7
__ Betaproteobacteria	273	177	64.8
__ __ Burkholderiales	166	88	53.0
__ __ __ Oxalobacteraceae	30	26	86.7
__ __ __ __ Massilia	8	8	100.0
__ __ __ __ Herbaspirillum	7	7	100.0
__ __ __ Burkholderiaceae	34	25	73.5
__ __ __ __ Paraburkholderia	8	7	87.5
__ __ __ Alcaligenaceae	23	20	87.0
__ __ __ Comamonadaceae	50	10	20.0
__ __ Neisseriales	42	42	100.0
__ __ __ Neisseriaceae	23	23	100.0
__ __ __ __ Neisseria	10	10	100.0
__ __ __ Chromobacteriaceae	19	19	100.0
__ __ Rhodocyclales	19	19	100.0
__ __ __ Rhodocyclaceae	19	19	100.0
__ __ Methylophilales	14	10	71.4
__ __ __ Methylophilaceae	12	10	83.3
__ delta/epsilon subdivisions	196	173	88.3
__ __ Deltaproteobacteria	123	110	89.4
__ __ __ Desulfovibrionales	44	44	100.0
__ __ __ __ Desulfovibrionaceae	35	35	100.0
__ __ __ __ __ Desulfovibrio	31	31	100.0
__ __ __ Desulfobacterales	22	22	100.0
__ __ __ __ Desulfobacteraceae	15	15	100.0
__ __ __ __ Desulfobulbaceae	7	7	100.0
__ __ __ Desulfuromonadales	16	16	100.0
__ __ __ __ Geobacteraceae	10	10	100.0
__ __ __ __ __ Geobacter	7	7	100.0
__ __ __ __ Desulfuromonadaceae	6	6	100.0
__ __ __ Myxococcales	15	11	73.3
__ __ __ __ Cystobacterineae	11	10	90.9
__ __ Epsilonproteobacteria	73	63	86.3
__ __ __ Campylobacterales	67	58	86.6
__ __ __ __ Helicobacteraceae	34	30	88.2
__ __ __ __ __ Helicobacter	28	27	96.4
__ __ __ __ Campylobacteraceae	32	28	87.5
__ __ __ __ __ Campylobacter	19	17	89.5
__ __ __ __ __ Arcobacter	7	6	85.7
__ Terrabacteria group	2228	1206	54.1
__ __ Firmicutes	1064	1028	96.6
__ __ __ Bacilli	597	573	96.0

—	Bacillales	342	342	100.0
—	Bacillaceae	165	165	100.0
—	Bacillus	97	97	100.0
—	Lysinibacillus	8	8	100.0
—	Oceanobacillus	6	6	100.0
—	Paenibacillaceae	71	71	100.0
—	Paenibacillus	50	50	100.0
—	Brevibacillus	8	8	100.0
—	Staphylococcaceae	38	38	100.0
—	Staphylococcus	28	28	100.0
—	Planococcaceae	24	24	100.0
—	Listeriaceae	11	11	100.0
—	Listeria	9	9	100.0
—	Alicyclobacillaceae	11	11	100.0
—	Alicyclobacillus	8	8	100.0
—	Bacillales incertae sedis	9	9	100.0
—	Thermoactinomycetaceae	6	6	100.0
—	Lactobacillales	255	231	90.6
—	Lactobacillaceae	141	140	99.3
—	Lactobacillus	131	130	99.2
—	Pediococcus	9	9	100.0
—	Enterococcaceae	23	23	100.0
—	Enterococcus	17	17	100.0
—	Streptococcaceae	41	22	53.7
—	Streptococcus	39	21	53.8
—	Leuconostocaceae	23	19	82.6
—	Weissella	10	10	100.0
—	Leuconostoc	8	6	75.0
—	Carnobacteriaceae	19	19	100.0
—	Carnobacterium	10	10	100.0
—	Aerococcaceae	8	8	100.0
—	Clostridia	370	366	98.9
—	Clostridiales	335	334	99.7
—	Lachnospiraceae	101	101	100.0
—	unclassified Lachnospiraceae	33	33	100.0
—	Lachnoclostridium	14	14	100.0
—	Butyrivibrio	10	10	100.0
—	Blautia	9	9	100.0
—	Clostridiaceae	82	82	100.0
—	Clostridium	57	57	100.0
—	Ruminococcaceae	45	45	100.0
—	Ruminococcus	14	14	100.0
—	Ruminiclostridium	13	13	100.0

	__ Peptococcaceae	28	27	96.4
	__ Desulfotomaculum	9	9	100.0
	__ Desulfosporosinus	7	7	100.0
	__ Peptostreptococcaceae	19	19	100.0
	__ unclassified Clostridiales	18	18	100.0
	__ unclassified Clostridiales (miscellaneous)	6	6	100.0
	__ Eubacteriaceae	17	17	100.0
	__ Eubacterium	12	12	100.0
	__ Clostridiales incertae sedis	10	10	100.0
	__ Clostridiales Family XIII. Incertae Sedis	7	7	100.0
	__ Thermoanaerobacterales	24	21	87.5
	__ Thermoanaerobacteraceae	13	13	100.0
	__ Thermoanaerobacterales Family III. Incertae Sedis	7	7	100.0
	__ Halanaerobiales	8	8	100.0
	__ Negativicutes	41	41	100.0
	__ Selenomonadales	21	21	100.0
	__ Selenomonadaceae	15	15	100.0
	__ Selenomonas	8	8	100.0
	__ Sporomusaceae	6	6	100.0
	__ Veillonellales	16	16	100.0
	__ Veillonellaceae	16	16	100.0
	__ Megasphaera	7	7	100.0
	__ Tissierellia	32	29	90.6
	__ Tissierellales	26	23	88.5
	__ Peptoniphilaceae	26	23	88.5
	__ Peptoniphilus	13	10	76.9
	__ Anaerococcus	8	8	100.0
	__ unclassified Tissierellia	6	6	100.0
	__ Erysipelotrichia	21	17	81.0
	__ Erysipelotrichales	21	17	81.0
	__ Erysipelotrichaceae	21	17	81.0
	__ Actinobacteria	859	78	9.1
	__ Actinobacteria	807	38	4.7
	__ Bifidobacteriales	36	16	44.4
	__ Bifidobacteriaceae	36	16	44.4
	__ Bifidobacterium	30	16	53.3
	__ Micrococcales	211	10	4.7
	__ Micrococcaceae	51	8	15.7
	__ Coriobacteriia	34	34	100.0
	__ Coriobacteriales	23	23	100.0
	__ Atopobiaceae	12	12	100.0
	__ Atopobium	7	7	100.0
	__ Coriobacteriaceae	11	11	100.0

		__ Eggerthellales	11	11	100.0
		__ __ Eggerthellaceae	11	11	100.0
	__ Tenericutes		116	72	62.1
	__ __ Mollicutes		115	71	61.7
		__ __ Mycoplasmatales	73	33	45.2
		__ __ __ Mycoplasmataceae	73	33	45.2
		__ __ __ Mycoplasma	70	30	42.9
		__ __ Entomoplasmatales	22	19	86.4
		__ __ __ Spiroplasmataceae	15	12	80.0
		__ __ __ __ Spiroplasma	15	12	80.0
		__ __ __ Entomoplasmataceae	7	7	100.0
		__ __ Acholeplasmatales	20	19	95.0
		__ __ __ Acholeplasmataceae	20	19	95.0
		__ __ __ Acholeplasma	10	10	100.0
		__ __ __ Candidatus Phytoplasma	10	9	90.0
	__ Chloroflexi		21	21	100.0
	__ __ Chloroflexia		6	6	100.0
__ PVC group			52	28	53.8
	__ Chlamydiae		17	15	88.2
	__ __ Chlamydiia		17	15	88.2
		__ __ Parachlamydiales	8	8	100.0
		__ __ Chlamydiales	9	7	77.8
		__ __ __ Chlamydiaceae	9	7	77.8
		__ __ __ Chlamydia/Chlamydoxila group	9	7	77.8
		__ __ __ Chlamydia	9	7	77.8
	__ Planctomycetes		16	11	68.8
	__ __ Planctomycetia		15	11	73.3
	__ __ __ Planctomycetales		13	9	69.2
__ Spirochaetes			60	26	43.3
	__ Spirochaetia		60	26	43.3
	__ __ Spirochaetales		40	16	40.0
		__ __ Borreliaceae	12	9	75.0
		__ __ Spirochaetaceae	28	7	25.0
	__ Leptospirales		16	6	37.5
	__ __ Leptospiraceae		16	6	37.5
	__ __ __ Leptospira		14	6	42.9
__ Thermotogae			19	19	100.0
	__ Thermotogae		19	19	100.0
	__ __ Thermotogales		12	12	100.0
	__ __ __ Thermotogaceae		7	7	100.0
__ Fusobacteria			19	18	94.7
	__ Fusobacteriia		19	18	94.7
	__ __ Fusobacteriales		19	18	94.7

				Fusobacteriaceae	11	11	100.0
				__ Fusobacterium	8	8	100.0
				__ Leptotrichiaceae	8	7	87.5
				__ Acidobacteria	24	17	70.8
				__ Acidobacteriia	17	15	88.2
				__ Acidobacteriales	17	15	88.2
				__ Acidobacteriaceae	17	15	88.2
				__ Synergistetes	13	13	100.0
				__ Synergistia	13	13	100.0
				__ Synergistales	13	13	100.0
				__ Synergistaceae	13	13	100.0
				__ Aquificae	14	11	78.6
				__ Aquificae	14	11	78.6
				__ Aquificales	11	8	72.7
				__ Nitrospirae	6	6	100.0
				__ Nitrospira	6	6	100.0
				__ Nitrospirales	6	6	100.0
				__ Nitrospiraceae	6	6	100.0
				__ Thermodesulfobacteria	6	5	83.3
				__ unclassified Bacteria	5	4	80.0
				__ FCB group	455	3	0.7
				__ Deferribacteres	6	3	50.0
				__ Chrysiogenetes	2	2	100.0
				__ Dictyoglomi	1	1	100.0
				__ Calditrichaeota	1	1	100.0
				__ Caldiserica	1	1	100.0
				__ Nitrospinae/Tectomicrobia group	1	1	100.0
				__ Archaea	238	39	16.4
				__ Euryarchaeota	190	27	14.2
				__ Methanobacteria	18	13	72.2
				__ Methanobacteriales	18	13	72.2
				__ Methanobacteriaceae	17	12	70.6
				__ Methanobacterium	7	6	85.7
				__ Methanococci	15	12	80.0
				__ Methanococcales	15	12	80.0
				__ Methanococcaceae	7	7	100.0
				__ TACK group	47	12	25.5
				__ Crenarchaeota	35	12	34.3
				__ Thermoprotei	35	12	34.3
				__ Desulfurococcales	13	12	92.3
				__ Desulfurococcaceae	9	9	100.0

Group E

a: Total number of genomes in the taxon
 b: Number of group E genomes in the taxon
 c: Percentage of group E genomes in the taxon

	a	b	c
cellular organisms	5007	311	6.2
__ Bacteria	4769	311	6.5
__ Proteobacteria	1854	142	7.7
__ Betaproteobacteria	273	76	27.8
__ Burkholderiales	166	63	38.0
__ Comamonadaceae	50	32	64.0
__ Acidovorax	7	6	85.7
__ Comamonas	7	5	71.4
__ unclassified Burkholderiales	24	16	66.7
__ Burkholderiales Genera incertae sedis	21	14	66.7
__ Thiomonas	4	3	75.0
__ Burkholderiaceae	34	8	23.5
__ Oxalobacteraceae	30	3	10.0
__ Alcaligenaceae	23	3	13.0
__ unclassified Betaproteobacteria	12	5	41.7
__ unclassified Betaproteobacteria (miscellaneous)	5	4	80.0
__ Methylophilales	14	4	28.6
__ Nitrosomonadales	9	4	44.4
__ Nitrosomonadaceae	9	4	44.4
__ Gammaproteobacteria	711	37	5.2
__ Xanthomonadales	62	9	14.5
__ Xanthomonadaceae	48	8	16.7
__ Xanthomonas	6	3	50.0
__ Methylococcales	20	8	40.0
__ Methylococcaceae	19	8	42.1
__ Methyломicrobium	3	3	100.0
__ unclassified Gammaproteobacteria	26	6	23.1
__ Enterobacteriales	112	5	4.5
__ Enterobacteriaceae	41	5	12.2
__ unclassified Enterobacteriaceae	13	5	38.5
__ ant, tsetse, mealybug, aphid, etc. endosymbionts	10	5	50.0
__ ant endosymbionts	5	4	80.0
__ Candidatus Blochmannia	5	4	80.0
__ Legionellales	38	3	7.9
__ Alphaproteobacteria	667	26	3.9

__ Rickettsiales	42	17	40.5
__ Anaplasmataceae	21	12	57.1
__ Ehrlichia	6	6	100.0
__ canis group	5	5	100.0
__ Wolbachieae	8	4	50.0
__ Wolbachia	8	4	50.0
__ Rickettsiaceae	18	5	27.8
__ Rickettsieae	18	5	27.8
__ Rickettsia	15	4	26.7
__ spotted fever group	12	3	25.0
__ Rhizobiales	225	3	1.3
__ delta/epsilon subdivisions	196	3	1.5
__ Deltaproteobacteria	123	3	2.4
__ Myxococcales	15	3	20.0
__ Sorangiineae	4	3	75.0
__ Terrabacteria group	2228	107	4.8
__ Cyanobacteria/Melainabacteria group	127	90	70.9
__ Cyanobacteria	127	90	70.9
__ Synechococcales	55	43	78.2
__ Synechococcaceae	27	20	74.1
__ Synechococcus	24	17	70.8
__ Prochloraceae	11	9	81.8
__ Prochlorococcus	11	9	81.8
__ Prochlorococcus marinus	9	8	88.9
__ Leptolyngbyaceae	10	9	90.0
__ Leptolyngbya	8	7	87.5
__ Pseudanabaenaceae	4	3	75.0
__ Oscillatoriophyycideae	31	22	71.0
__ Oscillatoriales	22	15	68.2
__ Microcoleaceae	6	5	83.3
__ Oscillatoriaceae	6	4	66.7
__ Cyanothecaceae	5	3	60.0
__ Cyanothece	5	3	60.0
__ Chroococcales	9	7	77.8
__ Aphanothecaceae	4	3	75.0
__ Nostocales	31	18	58.1
__ Rivulariaceae	5	4	80.0
__ Calothrix	4	4	100.0
__ Hapalosiphonaceae	4	4	100.0
__ Aphanizomenonaceae	4	4	100.0
__ Tolypothrichaceae	4	3	75.0
__ Tolypothrix	4	3	75.0
__ Pleurocapsales	5	5	100.0

		__ Hyellaceae	3	3	100.0
	__ Tenericutes		116	10	8.6
	__ Mollicutes		115	10	8.7
		__ Mycoplasmatales	73	10	13.7
		__ Mycoplasmataceae	73	10	13.7
		__ Mycoplasma	70	10	14.3
	__ Actinobacteria		859	7	0.8
	__ Actinobacteria		807	4	0.5
	__ Thermoleophilia		8	3	37.5
	__ Solirubrobacterales		8	3	37.5
__ FCB group			455	35	7.7
	__ Bacteroidetes/Chlorobi group		450	34	7.6
	__ Bacteroidetes		436	29	6.7
	__ Cytophagia		70	24	34.3
	__ Cytophagales		70	24	34.3
		__ Cytophagaceae	22	11	50.0
		__ Spirosoma	3	3	100.0
		__ Hymenobacteraceae	14	7	50.0
		__ Hymenobacter	8	5	62.5
		__ Flammeovirgaceae	8	4	50.0
	__ Bacteroidia		137	3	2.2
	__ Bacteroidales		127	3	2.4
	__ Chlorobi		11	4	36.4
	__ Chlorobia		11	4	36.4
	__ Chlorobiales		11	4	36.4
	__ Chlorobiaceae		11	4	36.4
__ PVC group			52	15	28.8
	__ Verrucomicrobia		17	12	70.6
	__ Verrucomicrobiae		7	5	71.4
	__ Verrucomicrobiales		7	5	71.4
	__ Opitutae		4	3	75.0
	__ Planctomycetes		16	3	18.8
	__ Planctomycetia		15	3	20.0
	__ Planctomycetales		13	3	23.1
	__ Planctomycetaceae		9	3	33.3
__ Spirochaetes			60	8	13.3
	__ Spirochaetia		60	8	13.3
	__ Leptospirales		16	8	50.0
	__ Leptospiraceae		16	8	50.0
	__ Leptospira		14	6	42.9
__ Acidobacteria			24	4	16.7