

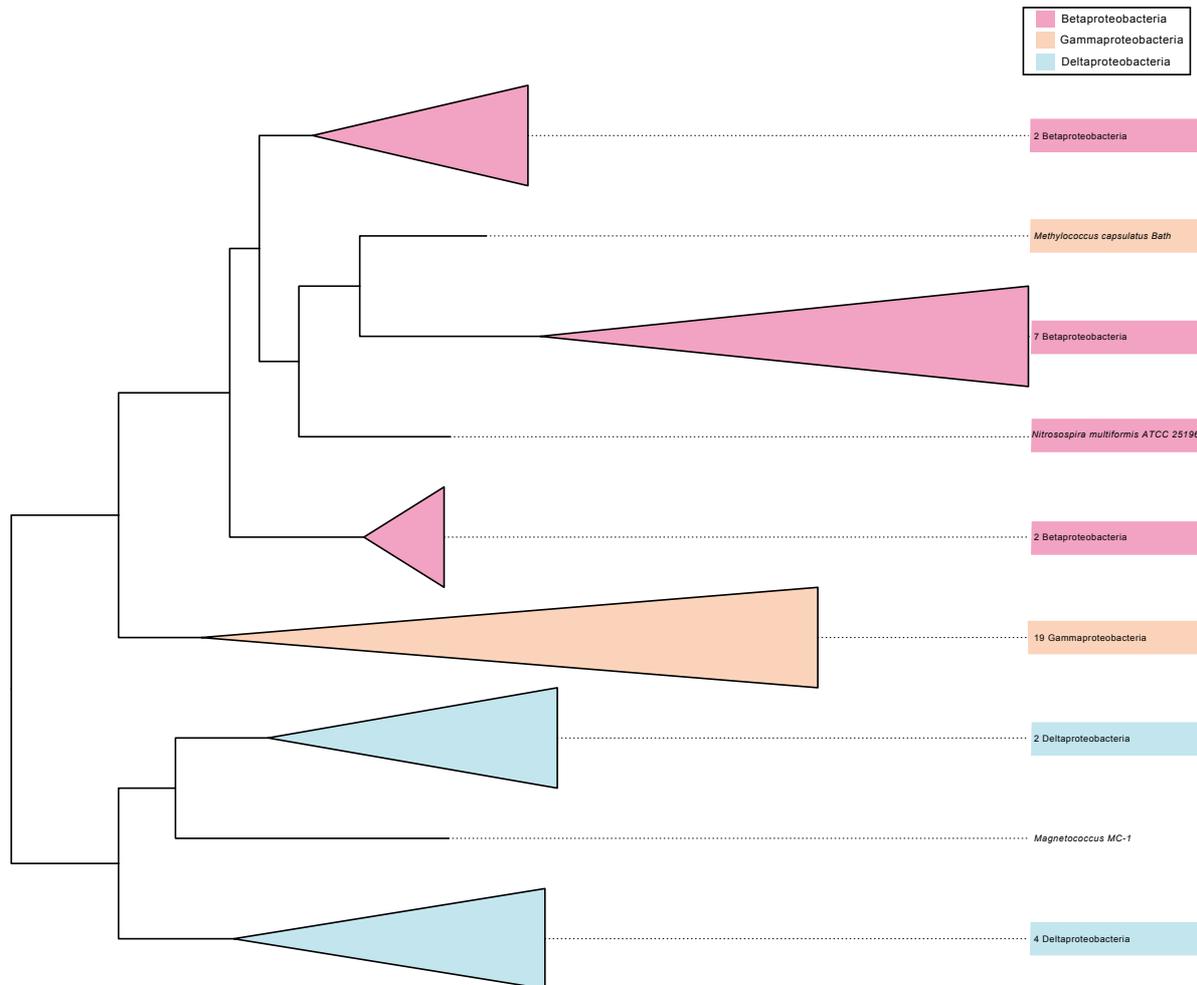
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**Figure S1: A maximum likelihood tree of the 39 ribosomal proteins L31 sharing one protein family at T<sub>60</sub>.**

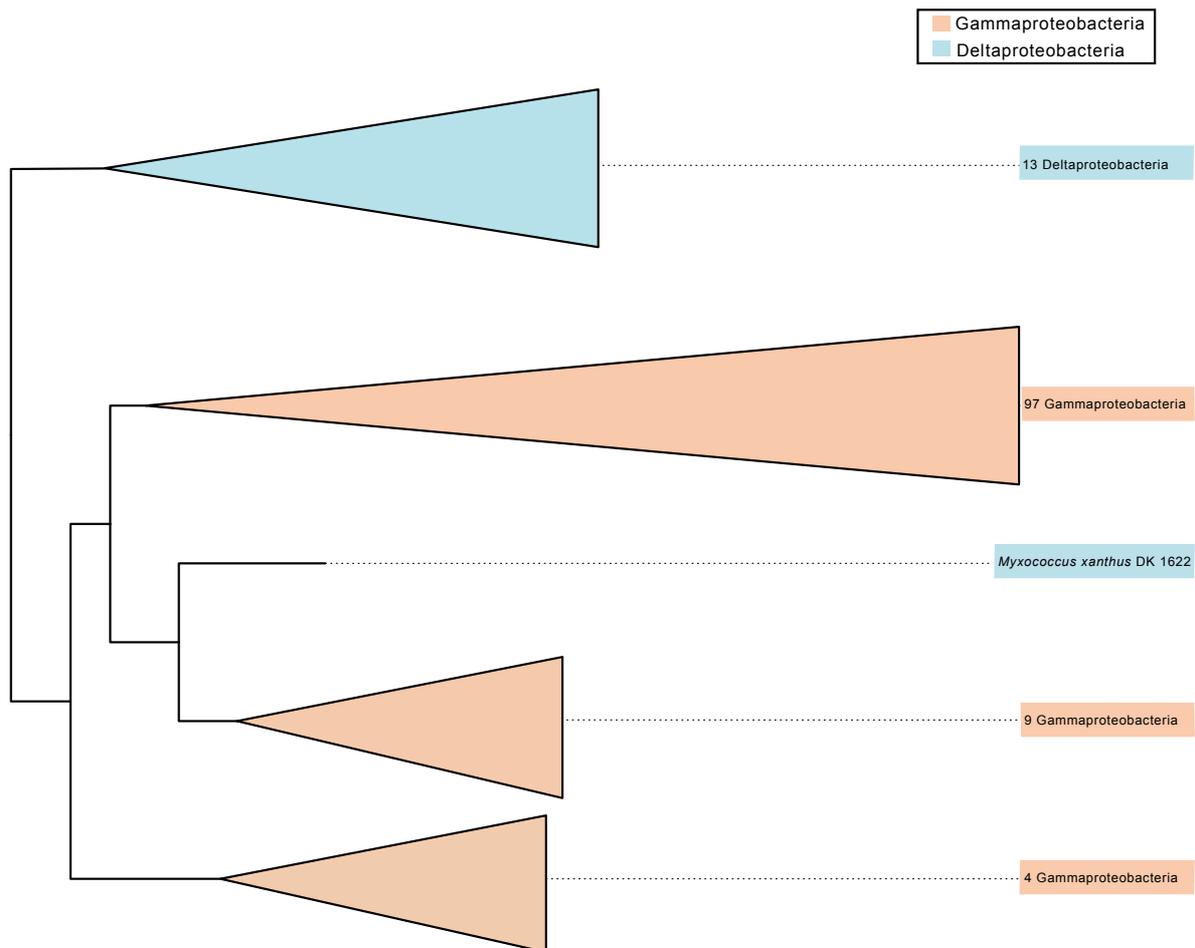
Including 12 Betaproteobacteria (magenta), 20 Gammaproteobacteria (yellow), 6 Deltaproteobacteria (cyan) and the unclassified proteobacteria *Magnetococcus MC-1*. Clades containing more than one specie of the same proteobacterial class are shown collapsed.



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**Figure S2: A maximum likelihood tree of the 124 asparaginyl-tRNA synthetase proteins sharing one proteine family at T<sub>55</sub>.**

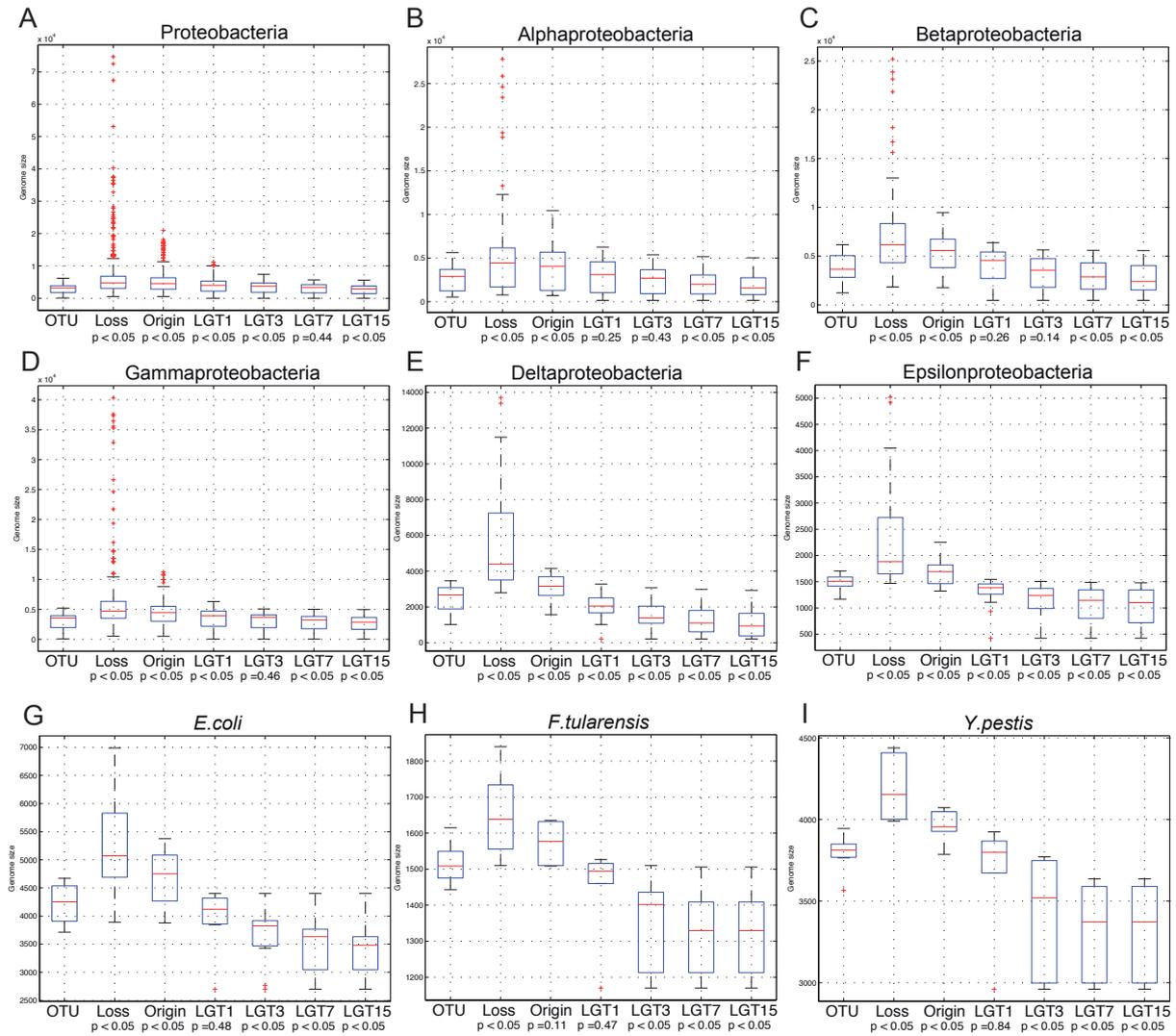
Including 110 Gammaproteobacteria (yellow) and 14 Deltaproteobacteria (cyan). Clades containing more than one species of the same proteobacterial class are shown collapsed.



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**Figure S3: Boxplots of the ancestral genome sizes calculated with the rRNA reference tree.**

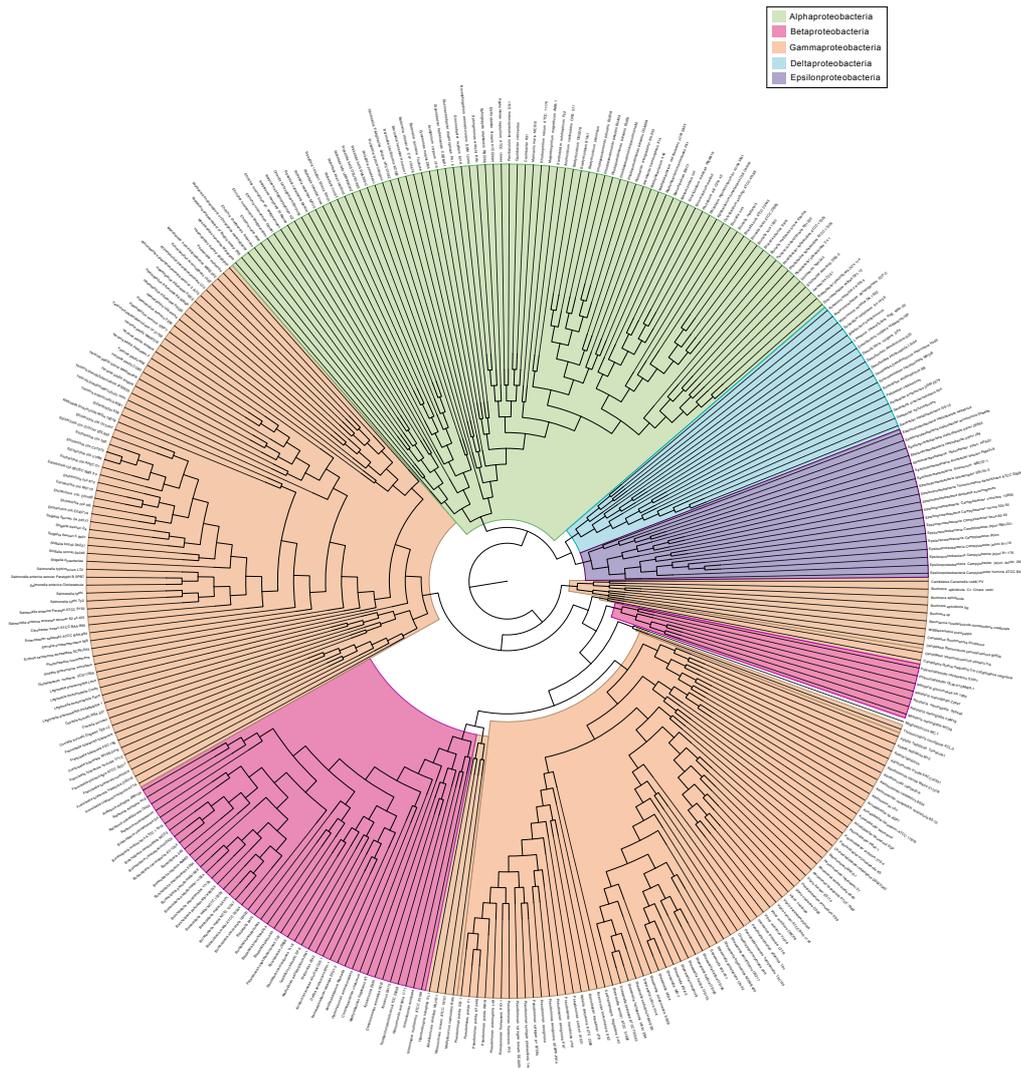
Calculated for the whole Dataset (A), the five proteobacterial classes (B-F) and the tree species *E. coli* (G), *F. tularensis* (H) and *Y. pestis* (I) allowing different amounts of LGT.



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**Figure S4: Gene content reference tree of 329 proteobacterial species.**

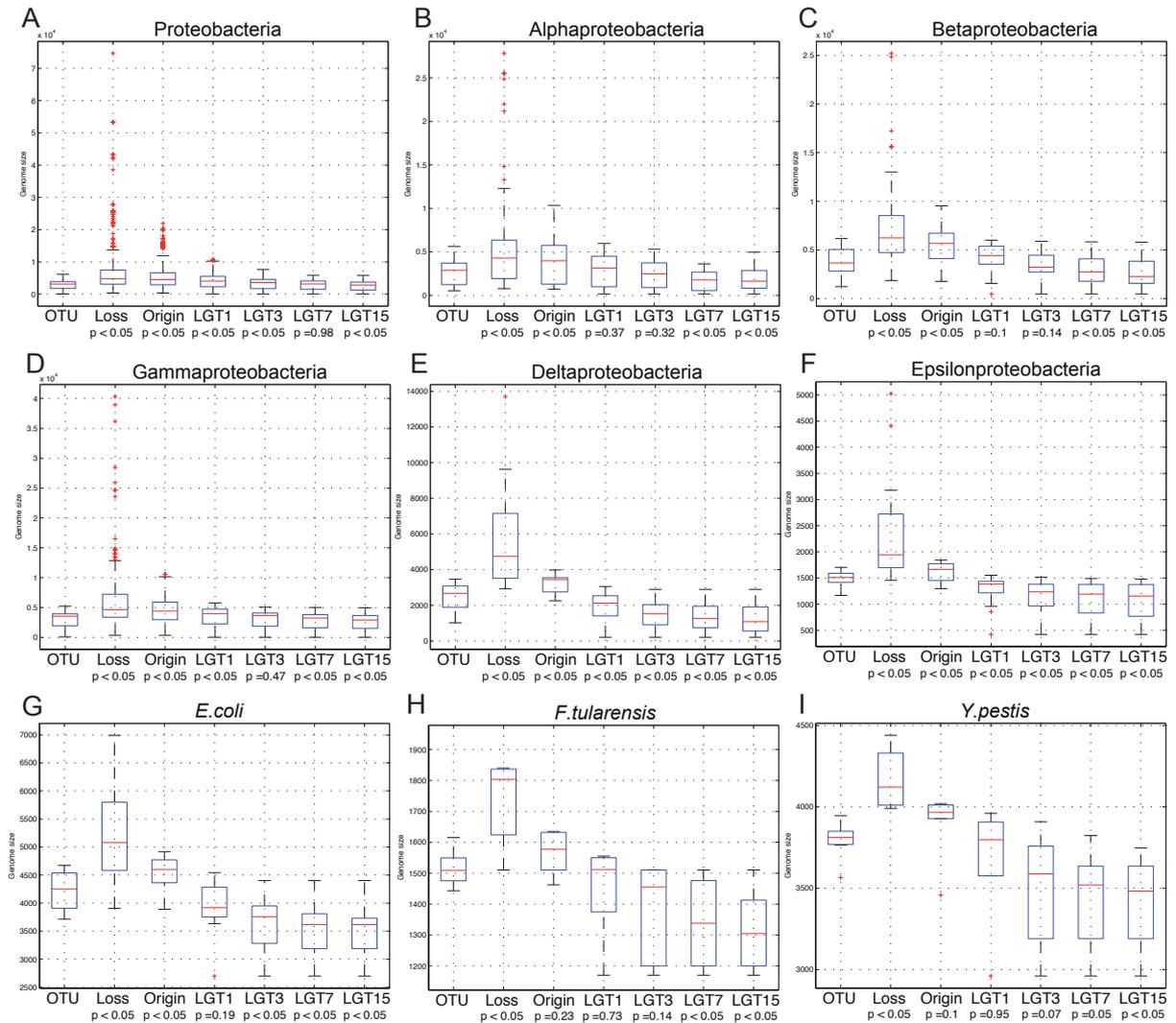
Containing 82 alphaproteobacteria (green), 52 betaproteobacteria (magenta), 157 gammaproteobacteria (yellow), 18 deltaproteobacteria (cyan), 19 epsilonproteobacteria (purple) and the unclassified proteobacteria *Magnetococcus* MC-1.



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**Figure S5: Boxplots of the ancestral genome sizes calculated with the gene content reference tree.**

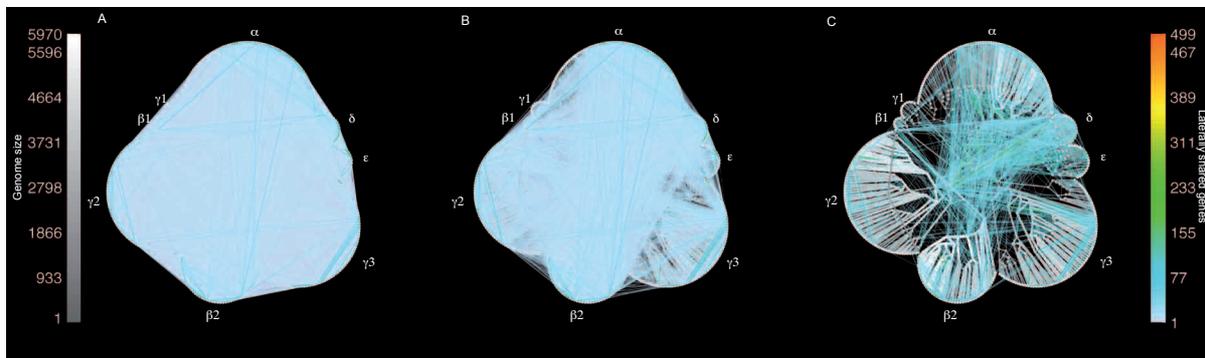
Calculated for the whole Dataset (A), the five proteobacterial classes (B-F) and the tree species *E. coli* (G), *F. tularensis* (H) and *Y. pestis* (I) allowing different amounts of LGT.



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**Figure S6: A minimal LGT network for 329 Proteobacteria using a gene content reference tree.**

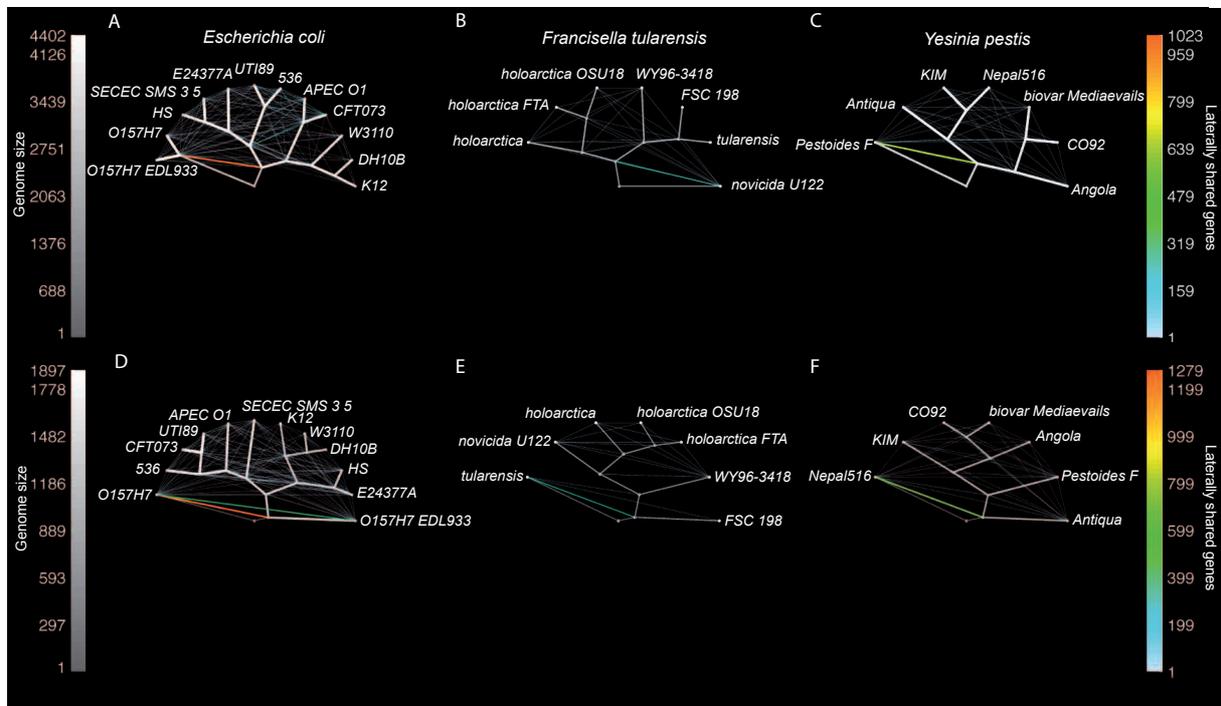
Vertical edges are indicated in gray, with both the width and the shading of the edge shown proportional to the number of inferred vertically inherited genes along the edge (see scale bar). The lateral network is indicated by edges that do not map onto the vertical component, with number of genes per edge indicated in color (see scale). The MLN showing all 61,964 edges of weight  $\geq 1$  gene in the MLN (A). The MLN showing only the 16,349 edges of weight  $\geq 5$  genes (B). The network showing only the 3,000 edges of weight  $\geq 20$  genes (C).



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**Figure S7: MLN for species datasets.**

A minimal LGT network for the proteobacterial species *Escherichia coli* (A), *Francisella tularensis* (B) and *Yersinia pestis* (C) using a ML-reference tree and a minimal LGT network for the same species using a gene content reference tree (D-F). Vertical edges are indicated in gray, with both the width and the shading of the edge shown proportional to the number of inferred vertically inherited genes along the edge (see scale bar). The lateral network is indicated by edges that do not map onto the vertical component, with number of genes per edge indicated in color (see scale bar).

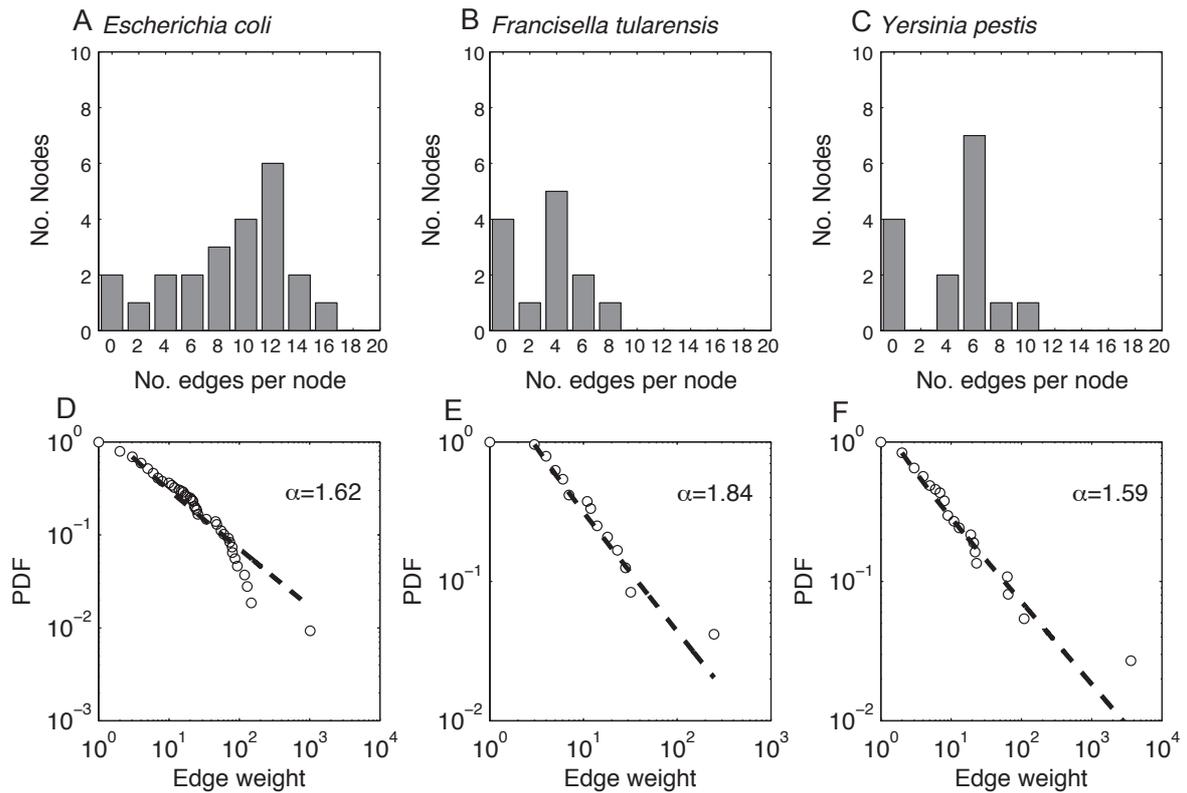




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**Figure S8. Properties of the minimal LGT networks in species scale.**

Properties are shown for a randomly selected replicate. (A-C) Distribution of connectivity, the number of one-edge-distanced neighbors for each vertex, in the MLN. (D-F) Frequency distribution of edge weight in the lateral component of the MLN.



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**Table S1: Universal proteome families at different proteome identity thresholds.**

<b>Proteins</b>	<b>Cutoff in %</b>	<b>25</b>	<b>30</b>	<b>35</b>	<b>40</b>	<b>45</b>	<b>50</b>	<b>55</b>	<b>60</b>	<b>65</b>	<b>70</b>
ATP-dependent Clp protease, proteolytic subunit ClpP		X	X	X	X	X	X	X			
Chaperonin GroEL		X	X	X	X	X	X				
ATP-dependent protease ATP-binding subunit		X	X	X	X	X					
50S ribosomal protein L2		X	X	X	X	X					
50S ribosomal protein L16		X	X	X	X						
30S ribosomal protein S5		X	X	X	X						
30S ribosomal protein S7		X	X	X							
50S ribosomal protein L5		X	X	X							
30S ribosomal protein S9		X	X	X							
50S ribosomal protein L15		X	X	X							
peptide deformylase		x	x								
30S ribosomal protein S4		X	X								
peptide chain release factor 1		X	X								
50S ribosomal protein L20		X	X								
DNA-directed RNA polymerase subunit alpha		X									
50S ribosomal protein L4		X									
30S ribosomal protein S2		X									
<b>Total</b>		<b>17</b>	<b>14</b>	<b>10</b>	<b>6</b>	<b>4</b>	<b>2</b>	<b>1</b>	<b>0</b>	<b>0</b>	<b>0</b>

Networks of gene sharing among 329 proteobacterial genomes reveal differences in lateral gene transfer frequency at different phylogenetic depths  
 Thorsten Kloesges, Ovidiu Popa, William Martin, Tal Dagan

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Table S2: Pairs of species disconnected in NSP<sub>70</sub>

Pairs of disconnected species at T <sub>70</sub>	
Anaplasma marginale St Maries	Zymomonas mobilis ZM4
Anaplasma marginale St Maries	Geobacter sulfurreducens
Anaplasma marginale St Maries	Syntrophus aciditrophicus SB
Anaplasma marginale St Maries	Campylobacter concisus 13826
Anaplasma marginale St Maries	Candidatus Carsonella ruddii PV
Anaplasma marginale St Maries	Citrobacter koseri ATCC BAA-895
Anaplasma marginale St Maries	Enterobacter sakazakii ATCC BAA-894
Anaplasma marginale St Maries	Escherichia coli DH10B
Anaplasma marginale St Maries	Salmonella enterica arizonae serovar 62 z4 z23
Anaplasma marginale St Maries	Salmonella enterica serovar Paratyphi B SPB7
Anaplasma phagocytophilum HZ	Zymomonas mobilis ZM4
Anaplasma phagocytophilum HZ	Geobacter sulfurreducens
Anaplasma phagocytophilum HZ	Syntrophus aciditrophicus SB
Anaplasma phagocytophilum HZ	Campylobacter concisus 13826
Anaplasma phagocytophilum HZ	Candidatus Carsonella ruddii PV
Anaplasma phagocytophilum HZ	Citrobacter koseri ATCC BAA-895
Anaplasma phagocytophilum HZ	Enterobacter sakazakii ATCC BAA-894
Anaplasma phagocytophilum HZ	Escherichia coli DH10B
Anaplasma phagocytophilum HZ	Salmonella enterica arizonae serovar 62 z4 z23
Anaplasma phagocytophilum HZ	Salmonella enterica serovar Paratyphi B SPB7
Ehrlichia canis Jake	Zymomonas mobilis ZM4
Ehrlichia canis Jake	Geobacter sulfurreducens
Ehrlichia canis Jake	Syntrophus aciditrophicus SB
Ehrlichia canis Jake	Campylobacter concisus 13826
Ehrlichia canis Jake	Candidatus Carsonella ruddii PV
Ehrlichia canis Jake	Citrobacter koseri ATCC BAA-895
Ehrlichia canis Jake	Enterobacter sakazakii ATCC BAA-894
Ehrlichia canis Jake	Escherichia coli DH10B
Ehrlichia canis Jake	Salmonella enterica arizonae serovar 62 z4 z23
Ehrlichia canis Jake	Salmonella enterica serovar Paratyphi B SPB7
Ehrlichia chaffeensis Arkansas	Zymomonas mobilis ZM4
Ehrlichia chaffeensis Arkansas	Geobacter sulfurreducens
Ehrlichia chaffeensis Arkansas	Syntrophus aciditrophicus SB
Ehrlichia chaffeensis Arkansas	Campylobacter concisus 13826
Ehrlichia chaffeensis Arkansas	Candidatus Carsonella ruddii PV
Ehrlichia chaffeensis Arkansas	Citrobacter koseri ATCC BAA-895
Ehrlichia chaffeensis Arkansas	Enterobacter sakazakii ATCC BAA-894
Ehrlichia chaffeensis Arkansas	Escherichia coli DH10B
Ehrlichia chaffeensis Arkansas	Salmonella enterica arizonae serovar 62 z4 z23
Ehrlichia chaffeensis Arkansas	Salmonella enterica serovar Paratyphi B SPB7
Ehrlichia ruminantium Gardel	Zymomonas mobilis ZM4
Ehrlichia ruminantium Gardel	Geobacter sulfurreducens
Ehrlichia ruminantium Gardel	Syntrophus aciditrophicus SB
Ehrlichia ruminantium Gardel	Campylobacter concisus 13826
Ehrlichia ruminantium Gardel	Candidatus Carsonella ruddii PV
Ehrlichia ruminantium Gardel	Citrobacter koseri ATCC BAA-895
Ehrlichia ruminantium Gardel	Enterobacter sakazakii ATCC BAA-894
Ehrlichia ruminantium Gardel	Escherichia coli DH10B
Ehrlichia ruminantium Gardel	Salmonella enterica arizonae serovar 62 z4 z23
Ehrlichia ruminantium Gardel	Salmonella enterica serovar Paratyphi B SPB7
Ehrlichia ruminantium Welgevonden	Zymomonas mobilis ZM4
Ehrlichia ruminantium Welgevonden	Geobacter sulfurreducens
Ehrlichia ruminantium Welgevonden	Syntrophus aciditrophicus SB
Ehrlichia ruminantium Welgevonden	Campylobacter concisus 13826
Ehrlichia ruminantium Welgevonden	Candidatus Carsonella ruddii PV
Ehrlichia ruminantium Welgevonden	Citrobacter koseri ATCC BAA-895
Ehrlichia ruminantium Welgevonden	Enterobacter sakazakii ATCC BAA-894
Ehrlichia ruminantium Welgevonden	Escherichia coli DH10B
Ehrlichia ruminantium Welgevonden	Salmonella enterica arizonae serovar 62 z4 z23
Ehrlichia ruminantium Welgevonden	Salmonella enterica serovar Paratyphi B SPB7
Ehrlichia ruminantium str. Welgevonden	Zymomonas mobilis ZM4
Ehrlichia ruminantium str. Welgevonden	Geobacter sulfurreducens
Ehrlichia ruminantium str. Welgevonden	Syntrophus aciditrophicus SB
Ehrlichia ruminantium str. Welgevonden	Campylobacter concisus 13826
Ehrlichia ruminantium str. Welgevonden	Candidatus Carsonella ruddii PV
Ehrlichia ruminantium str. Welgevonden	Citrobacter koseri ATCC BAA-895
Ehrlichia ruminantium str. Welgevonden	Enterobacter sakazakii ATCC BAA-894
Ehrlichia ruminantium str. Welgevonden	Escherichia coli DH10B
Ehrlichia ruminantium str. Welgevonden	Salmonella enterica arizonae serovar 62 z4 z23
Ehrlichia ruminantium str. Welgevonden	Salmonella enterica serovar Paratyphi B SPB7
Neorickettsia sennetsu Miyayama	Candidatus Carsonella ruddii PV
Neorickettsia sennetsu Miyayama	Citrobacter koseri ATCC BAA-895
Neorickettsia sennetsu Miyayama	Enterobacter sakazakii ATCC BAA-894
Rickettsia akari Hartford	Wolinella succinogenes
Rickettsia bellii OSU 85-389	Wolinella succinogenes
Rickettsia bellii RML369-C	Wolinella succinogenes
Rickettsia canadensis McKiel	Wolinella succinogenes
Rickettsia conorii	Wolinella succinogenes
Rickettsia felis URRWXC2	Wolinella succinogenes
Rickettsia massiliae MTU5	Wolinella succinogenes
Rickettsia prowazekii	Wolinella succinogenes
Rickettsia rickettsii Iowa	Wolinella succinogenes
Rickettsia rickettsii Sheila Smith	Wolinella succinogenes
Rickettsia typhi wilmington	Wolinella succinogenes
Zymomonas mobilis ZM4	Helicobacter pylori HPAG1
Helicobacter pylori HPAG1	Candidatus Carsonella ruddii PV
Wolinella succinogenes	Candidatus Carsonella ruddii PV

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Table S3: Class universal families at  $T_{70}$

class	proteine fam. no.	product
Betaproteobacteria	589	Glycine hydroxymethyltransferase
Betaproteobacteria	659	GTP-binding protein LepA
Betaproteobacteria	660	30S ribosomal protein S1
Betaproteobacteria	677	Holliday junction DNA helicase B
Betaproteobacteria	678	ribosomal protein S9
Betaproteobacteria	680	3-isopropylmalate dehydrogenase
Betaproteobacteria	681	ribosomal protein L19
Betaproteobacteria	682	DNA-directed RNA polymerase subunit beta'
Betaproteobacteria	684	ribosomal protein L32
Betaproteobacteria	685	bifunctional GMP synthase/glutamine amidotransferase protein
Betaproteobacteria	686	inosine-5'-monophosphate dehydrogenase
Betaproteobacteria	688	chorismate synthase
Betaproteobacteria	689	glutathione S-transferase, N-terminal domain
Betaproteobacteria	690	30S ribosomal protein S5
Betaproteobacteria	691	50S ribosomal protein L1
Betaproteobacteria	692	argininosuccinate lyase
Epsilonproteobacteria	4,506	50S ribosomal protein L14
Epsilonproteobacteria	4,513	ATP synthase F1 sector, beta subunit
Epsilonproteobacteria	4,531	nucleoside diphosphate kinase
Epsilonproteobacteria	4,532	50S ribosomal protein L20
Epsilonproteobacteria	4,533	DNA-dependent ATPase, RecA
Epsilonproteobacteria	4,534	30S ribosomal protein S7
Epsilonproteobacteria	4,535	ribose-phosphate pyrophosphokinase
Epsilonproteobacteria	4,536	GTP-binding protein LepA
Epsilonproteobacteria	4,537	heat shock protein HslVU, ATP-dependent protease subunit HslV
Epsilonproteobacteria	4,538	uridylyate kinase
Epsilonproteobacteria	4,539	ATP synthase F1 sector, alpha subunit
Epsilonproteobacteria	4,540	inosine-5-monophosphate dehydrogenase
Epsilonproteobacteria	4,541	DnaK-type molecular chaperone
Epsilonproteobacteria	4,542	riboflavin synthase, beta subunit
Epsilonproteobacteria	4,543	transcription termination factor Rho
Epsilonproteobacteria	4,544	60 kDa chaperonin
Epsilonproteobacteria	4,545	3-oxoacyl-(acyl carrier protein) reductase
Epsilonproteobacteria	4,546	50S ribosomal protein L2
Epsilonproteobacteria	4,547	30S ribosomal protein S3
Epsilonproteobacteria	4,548	50S ribosomal protein L16
Epsilonproteobacteria	4,549	30S ribosomal protein S5
Epsilonproteobacteria	4,550	translation initiation factor IF-1
Epsilonproteobacteria	4,551	30S ribosomal protein S13
Epsilonproteobacteria	4,552	30S ribosomal protein S11
Epsilonproteobacteria	4,553	30S ribosomal protein S4
Epsilonproteobacteria	4,554	GTP-binding elongation factor family protein
Epsilonproteobacteria	4,555	ribonucleoside-diphosphate reductase, alpha chain
Epsilonproteobacteria	4,556	50S ribosomal protein L7/L12
Epsilonproteobacteria	4,557	50S ribosomal protein L11

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Table S4: Classes, orders, species and effective genome size in the modules colored by modul at different proteine identity thresholds.

Class	Order	Species	EGS 30	EGS 35	EGS 40	EGS 45	EGS 50	EGS 55	EGS 60	EGS 65	EGS 70
Alphaproteobacteria	Caulobacterales	Caulobacter K31	3867	3800	3667	3452	3228	2923	2587	2205	1812
Alphaproteobacteria	Caulobacterales	Caulobacter crescentus	2987	2949	2888	2793	2659	2489	2269	2000	1695
Alphaproteobacteria	Rhizobiales	Agrobacterium tumefaciens CS8 Cereon	4057	4098	4076	3978	3784	3518	3150	2698	2181
Alphaproteobacteria	Rhizobiales	Azorhizobium caulinodans ORS 571	3680	3675	3596	3479	3243	2946	2572	2155	1648
Alphaproteobacteria	Rhizobiales	Bartonella bacilliformis KC583	1048	1042	1032	1022	1005	978	938	892	809
Alphaproteobacteria	Rhizobiales	Bartonella henselae Houston-1	1293	1301	1303	1299	1293	1281	1269	1248	1211
Alphaproteobacteria	Rhizobiales	Bartonella quintana Toulouse	1098	1106	1106	1101	1099	1091	1082	1073	1056
Alphaproteobacteria	Rhizobiales	Bartonella tribocorum CIP 105476	1388	1376	1364	1341	1325	1301	1274	1232	1175
Alphaproteobacteria	Rhizobiales	Bradyrhizobium BTA11	5630	5770	5854	5837	5813	5744	5627	5445	5243
Alphaproteobacteria	Rhizobiales	Bradyrhizobium ORS278	5252	5403	5475	5496	5486	5464	5391	5254	5068
Alphaproteobacteria	Rhizobiales	Bradyrhizobium japonicum	5495	5583	5553	5446	5269	4976	4595	4074	3406
Alphaproteobacteria	Rhizobiales	Brucella abortus 9-941	2928	2970	3009	3023	3035	3042	3041	3040	3040
Alphaproteobacteria	Rhizobiales	Brucella canis ATCC 23365	3047	3095	3134	3153	3170	3178	3180	3180	3182
Alphaproteobacteria	Rhizobiales	Brucella melitensis	2888	2932	2965	2969	2976	2961	2932	2915	2881
Alphaproteobacteria	Rhizobiales	Brucella melitensis biovar Abortus	2880	2920	2961	2978	2992	3001	3003	3000	2999
Alphaproteobacteria	Rhizobiales	Brucella ovis	2628	2674	2704	2717	2723	2724	2725	2717	2710
Alphaproteobacteria	Rhizobiales	Brucella suis 1330	3093	3138	3178	3197	3209	3219	3221	3219	3219
Alphaproteobacteria	Rhizobiales	Brucella suis ATCC 23445	3038	3085	3124	3142	3157	3164	3166	3165	3167
Alphaproteobacteria	Rhizobiales	Mesorhizobium BNC1	3427	3340	3228	2988	2749	2442	2107	1679	1273
Alphaproteobacteria	Rhizobiales	Mesorhizobium loti	4821	4716	4578	4312	3964	3489	2980	2371	1784
Alphaproteobacteria	Rhizobiales	Methylobacterium 4 46	4571	4575	4462	4292	4029	3668	3154	2570	1924
Alphaproteobacteria	Rhizobiales	Methylobacterium extorquens PA1	3763	3780	3730	3621	3454	3224	2872	2418	1917
Alphaproteobacteria	Rhizobiales	Methylobacterium radiotolerans JCM 2831	4521	4530	4475	4314	4110	3797	3337	2811	2219
Alphaproteobacteria	Rhizobiales	Nitrobacter hamburgensis X14	3184	3153	3127	3038	2962	2826	2689	2537	2352
Alphaproteobacteria	Rhizobiales	Nitrobacter winogradskyi Nb-255	2554	2536	2515	2452	2409	2330	2265	2198	2100
Alphaproteobacteria	Rhizobiales	Ochrobactrum anthropi ATCC 49188	3890	3923	3921	3853	3736	3553	3344	3150	2886
Alphaproteobacteria	Rhizobiales	Parvibaculum lavamentivorans DS-1	2760	2646	2462	2184	1861	1478	1109	778	499
Alphaproteobacteria	Rhizobiales	Rhizobium etli CFN 42	4755	4845	4897	4911	4881	4826	4769	4647	4489
Alphaproteobacteria	Rhizobiales	Rhizobium leguminosarum bv viciae 3841	5359	5456	5514	5520	5438	5309	5173	4947	4705
Alphaproteobacteria	Rhizobiales	Rhodopseudomonas palustris BisA53	4056	4093	4062	4011	3936	3851	3694	3505	3178
Alphaproteobacteria	Rhizobiales	Rhodopseudomonas palustris BisB18	4045	4074	4065	4028	3966	3867	3726	3507	3170
Alphaproteobacteria	Rhizobiales	Rhodopseudomonas palustris BisB5	3858	3893	3907	3901	3869	3852	3804	3729	3604
Alphaproteobacteria	Rhizobiales	Rhodopseudomonas palustris CGA009	4170	4230	4250	4235	4189	4110	3988	3785	3494
Alphaproteobacteria	Rhizobiales	Rhodopseudomonas palustris Haa2	4135	4171	4182	4192	4178	4122	4065	3932	3775
Alphaproteobacteria	Rhizobiales	Sinorhizobium medicae WSM419	4992	5068	5127	5118	5089	5043	4972	4876	4746
Alphaproteobacteria	Rhizobiales	Sinorhizobium meliloti	4966	5047	5133	5163	5122	5053	4966	4865	4716
Alphaproteobacteria	Rhizobiales	Xanthobacter autotrophicus Py2	3785	3747	3643	3472	3250	2930	2551	2140	1674
Alphaproteobacteria	Rhodobacterales	Dinoroseobacter shibae DFL 12	3235	3182	3082	2929	2704	2426	2092	1735	1319
Alphaproteobacteria	Rhodobacterales	Hyphomonas neptunium ATCC 15444	32515	2324	2090	1760	1383	1034	733	470	256
Alphaproteobacteria	Rhodobacterales	Jannaschia CCS1	2511	3147	2982	2759	2499	2193	1832	1459	1075
Alphaproteobacteria	Rhodobacterales	Maricaulis maris MCS10	2233	2062	1821	1517	1236	897	584	392	224
Alphaproteobacteria	Rhodobacterales	Paracoccus denitrificans PD1222	3646	3583	3478	3287	3020	2648	2203	1766	1289
Alphaproteobacteria	Rhodobacterales	Rhodobacter sphaeroides 2 4 1	3712	3745	3787	3769	3761	3752	3730	3722	3706
Alphaproteobacteria	Rhodobacterales	Rhodobacter sphaeroides ATCC 17025	3488	3476	3457	3388	3337	3272	3168	3070	2957
Alphaproteobacteria	Rhodobacterales	Rhodobacter sphaeroides ATCC 17029	3688	3735	3794	3789	3776	3766	3738	3721	3690
Alphaproteobacteria	Rhodobacterales	Roseobacter denitrificans OCH 114	3274	3241	3146	3013	2807	2549	2249	1905	1500
Alphaproteobacteria	Rhodobacterales	Silicibacter TM1040	3170	3120	3029	2906	2749	2510	2244	1897	1553
Alphaproteobacteria	Rhodobacterales	Silicibacter pomeroyi DSS-3	3474	3432	3344	3188	3015	2731	2408	2063	1668
Alphaproteobacteria	Rhodospirillales	Acidiphilium cryptum JF-5	2600	2489	2294	2049	1752	1399	1036	724	455
Alphaproteobacteria	Rhodospirillales	Gluconacetobacter diazotrophicus PAI 5	2595	2515	2400	2172	1902	1568	1195	864	545
Alphaproteobacteria	Rhodospirillales	Gluconobacter oxydans 621H	1925	1851	1745	1565	1368	1136	878	640	415
Alphaproteobacteria	Rhodospirillales	Granulobacter bethedensis CGDNH1	1988	1892	1766	1581	1347	1085	822	572	364
Alphaproteobacteria	Rhodospirillales	Magnetospirillum magnetium AMB-1	2697	2493	2229	1950	1645	1298	950	611	351
Alphaproteobacteria	Rhodospirillales	Rhodospirillum rubrum ATCC 11170	2914	2755	2536	2294	1947	1567	1180	783	489
Alphaproteobacteria	Rickettsiales	Anaplasma marginale St Maries	744	726	682	630	566	495	394	297	204
Alphaproteobacteria	Rickettsiales	Anaplasma phagocytophilum HZ	713	698	673	619	566	491	398	302	206
Alphaproteobacteria	Rickettsiales	Candidatus Pelagibacter ubique HTCC1062	985	867	721	531	389	269	169	94	47
Alphaproteobacteria	Rickettsiales	Ehrlichia canis Jake	796	789	783	771	764	752	738	725	698
Alphaproteobacteria	Rickettsiales	Ehrlichia chaffeensis Arkansas	798	788	783	771	762	748	736	722	696
Alphaproteobacteria	Rickettsiales	Ehrlichia ruminantium Gardel	919	920	920	917	914	913	912	909	905
Alphaproteobacteria	Rickettsiales	Ehrlichia ruminantium Weigelvonden	883	884	884	884	884	883	884	882	882
Alphaproteobacteria	Rickettsiales	Ehrlichia ruminantium str. Weigelvonden	921	923	923	924	924	922	917	916	915
Alphaproteobacteria	Rickettsiales	Neorickettsia sennetsu Miyayama	529	459	361	270	186	98	60	29	10
Alphaproteobacteria	Rickettsiales	Orientia tsutsugamushi Borjong	573	525	465	380	303	190	123	61	30
Alphaproteobacteria	Rickettsiales	Rickettsia akari Hartford	1002	983	969	952	921	894	877	854	841
Alphaproteobacteria	Rickettsiales	Rickettsia bellii OSU 85-389	1279	1282	1279	1274	1272	1260	1244	1230	1213
Alphaproteobacteria	Rickettsiales	Rickettsia bellii RML369-C	1310	1311	1309	1301	1294	1283	1267	1254	1228
Alphaproteobacteria	Rickettsiales	Rickettsia canadensis McKiel	840	829	822	816	807	803	787	775	769
Alphaproteobacteria	Rickettsiales	Rickettsia conorii	1231	1211	1185	1169	1139	1113	1089	1060	1033
Alphaproteobacteria	Rickettsiales	Rickettsia felis URWXCai2	1189	1158	1114	1084	1054	1018	980	961	937
Alphaproteobacteria	Rickettsiales	Rickettsia massiliae MTU5	948	942	935	930	924	917	903	889	881
Alphaproteobacteria	Rickettsiales	Rickettsia prowazekii	802	803	800	800	800	797	794	794	788
Alphaproteobacteria	Rickettsiales	Rickettsia rickettsii Iowa	1286	1281	1275	1272	1268	1264	1254	1246	1241
Alphaproteobacteria	Rickettsiales	Rickettsia rickettsii Sheila Smith	1271	1271	1271	1267	1263	1258	1256	1249	1246
Alphaproteobacteria	Rickettsiales	Rickettsia typhi wilmington	811	813	812	812	812	807	805	806	801
Alphaproteobacteria	Rickettsiales	Wolbachia endosymbiont of Brugia malayi TRS	669	664	657	651	645	633	629	619	597
Alphaproteobacteria	Rickettsiales	Wolbachia endosymbiont of Drosophila melanogaster	774	749	724	710	682	658	640	623	599
Alphaproteobacteria	Sphingomonadales	Erythrobacter litoralis HTCC2594	2271	2193	2070	1889	1670	1433	1142	876	617
Alphaproteobacteria	Sphingomonadales	Novosphingobium aromaticivorans DSM 12444	2919	2802	2627	2402	2118	1799	1444	1112	780
Alphaproteobacteria	Sphingomonadales	Sphingomonas wittichii RW1	3472	3280	3023	2652	2269	1879	1477	1083	721
Alphaproteobacteria	Sphingomonadales	Sphingopyxis alaskensis RB2256	2558	2492	2340	2118	1880	1578	1251	972	670
Alphaproteobacteria	Sphingomonadales	Zymomonas mobilis ZM4	1434	1357	1248	1104	962	782	593	406	262
Deltaproteobacteria	Bdellovibrionales	Bdellovibrio bacteriovorus	1412	1157	927	664	443	277	164	82	41
Deltaproteobacteria	Desulfobacterales	Candidatus Desulfococcus oleovorans Hxd3	1887	1672	1428	1129	851	581	344	183	90
Deltaproteobacteria	Desulfobacterales	Desulfotalea psychrophila L5v4	1885	1697	1448	1137	859	573	374	212	110
Deltaproteobacteria	Desulfovibrionales	Desulfovibrio desulfuricans G20	2465	2328	2166	1938	1705	1458	1196	913	688
Deltaproteobacteria	Desulfovibrionales	Desulfovibrio vulgaris DP4	2801	2816	2821	2807	2792	2774	2769	2761	2742
Deltaproteobacteria	Desulfovibrionales	Desulfovibrio vulgaris Hildenborough	2804	2827	2827	2825	2805	2786	2776	2763	2748
Deltaproteobacteria	Desulfuromonadales	Lawsonia intracellularis PHE MN1-00	1020	943	829	703	572	466	340	209	115
Deltaproteobacteria	Desulfuromonadales	Geobacter metallireducens GS-15	2813	2772	2720	2615	2497	2355	2194	1955	1692
Deltaproteobacteria	Desulfuromonadales	Geobacter sulfurireducens	2745	2704	2661	2558	2453	2288	2116	1897	1645
Deltaproteobacteria	Desulfuromonadales	Geobacter uraniumreducens Rf4	3081	2980	2816	2662	2475	2221	1915	1596	1243
Deltaproteobacteria	Desulfuromonadales	Pelobacter carbinolicus	2237	2061	1853	1593	1310	1003	730	492	290
Deltaproteobacteria	Desulfuromonadales	Pelobacter propionicus DSM 2379	2601	2501	2320	2133	1882	1613	1331	1022	742
Deltaproteobacteria	Mycococcales	Anaeromyxobacter Fw109-5	3462	3391	3300	3130	2919	2690	2460	2094	1678
Deltaproteobacteria	Mycococcales	Anaeromyxobacter dehalogenans 2CP-C	3424	3352	3255	3114	2920	2691	2458	2103	1682
Deltaproteobacteria	Mycococcales	Mycococcus xanthus DK 1622	3352	2986	2520	2019	1528	1079	722	416	224
Deltaproteobacteria	Mycococcales	Sorangium cellulosum So ce 56	3318	2805	2249	1723	1259	845	516	268	138
Deltaproteobacteria	Syntrophobacterales	Syntrophobacter fumarolicus MPOB	2335	2090	1839	1511	1134	788	509	302	187
Deltaproteobacteria	Syntrophobacterales	Syntrophus aciditrophicus SB	1766	1591	1357	1110	850	596	390	229	131

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SUPPLEMENTARY MATERIAL

Epsilonproteobacteria	Campylobacteriales	<i>Arcobacter butzleri</i> RM4018	1624	1506	1334	1140	931	719	542	356	214
Epsilonproteobacteria	Campylobacteriales	<i>Campylobacter concisus</i> 13826	1510	1482	1443	1395	1327	1243	1140	1027	866
Epsilonproteobacteria	Campylobacteriales	<i>Campylobacter curvus</i> 525 92	1568	1550	1516	1453	1376	1276	1158	1038	872
Epsilonproteobacteria	Campylobacteriales	<i>Campylobacter fetus</i> 82-40	1449	1399	1313	1218	1097	921	736	558	410
Epsilonproteobacteria	Campylobacteriales	<i>Campylobacter hominis</i> ATCC BAA-381	1168	1127	1055	959	871	725	579	423	303
Epsilonproteobacteria	Campylobacteriales	<i>Campylobacter jejuni</i>	1550	1553	1556	1552	1553	1547	1549	1546	1539
Epsilonproteobacteria	Campylobacteriales	<i>Campylobacter jejuni</i> 81-176	1585	1591	1581	1565	1563	1551	1541	1532	1521
Epsilonproteobacteria	Campylobacteriales	<i>Campylobacter jejuni</i> 81116	1537	1543	1542	1539	1537	1527	1523	1510	1502
Epsilonproteobacteria	Campylobacteriales	<i>Campylobacter jejuni</i> RM1221	1592	1585	1577	1569	1568	1559	1553	1542	1537
Epsilonproteobacteria	Campylobacteriales	<i>Campylobacter jejuni</i> doylei 269 97	1469	1463	1455	1447	1425	1411	1397	1384	1373
Epsilonproteobacteria	Campylobacteriales	<i>Helicobacter acinonychis</i> Sheeba	1295	1296	1282	1262	1252	1241	1237	1223	1209
Epsilonproteobacteria	Campylobacteriales	<i>Helicobacter hepaticus</i>	1279	1180	1048	901	745	584	439	297	209
Epsilonproteobacteria	Campylobacteriales	<i>Helicobacter pylori</i> 26695	1417	1420	1418	1408	1400	1389	1378	1363	1344
Epsilonproteobacteria	Campylobacteriales	<i>Helicobacter pylori</i> HPAG1	1415	1416	1412	1401	1395	1382	1374	1371	1356
Epsilonproteobacteria	Campylobacteriales	<i>Helicobacter pylori</i> J99	1417	1418	1412	1405	1393	1385	1378	1370	1362
Epsilonproteobacteria	Campylobacteriales	<i>Thiomicrospira denitrificans</i> ATCC 33889	1619	1515	1366	1202	1012	795	600	413	260
Epsilonproteobacteria	Campylobacteriales	<i>Wolinella succinogenes</i>	1615	1494	1337	1137	934	741	546	359	233
Epsilonproteobacteria	Nitratiruptor	<i>Nitratiruptor</i> SB155-2	1427	1315	1194	1060	903	722	545	386	228
Epsilonproteobacteria	Sulfurovum	<i>Sulfurovum</i> NBC37-1	1704	1558	1413	1234	1012	810	612	421	252
Betaproteobacteria	Burkholderiales	<i>Acidovorax</i> JS42	3336	3326	3315	3270	3191	3056	2860	2591	2240
Betaproteobacteria	Burkholderiales	<i>Acidovorax</i> avenae citrulli AACD0-1	3303	3549	3484	3381	3227	3034	2763	2454	2076
Betaproteobacteria	Burkholderiales	<i>Bordetella bronchiseptica</i>	4041	4168	4252	4346	4382	4389	4405	4400	4384
Betaproteobacteria	Burkholderiales	<i>Bordetella parapertussis</i>	3585	3717	3804	3912	3970	4017	4057	4071	4082
Betaproteobacteria	Burkholderiales	<i>Bordetella pertussis</i>	2900	2967	3023	3065	3093	3115	3132	3136	3138
Betaproteobacteria	Burkholderiales	<i>Bordetella petrii</i>	3720	3752	3764	3714	3594	3375	3114	2791	2440
Betaproteobacteria	Burkholderiales	<i>Burkholderia</i> 383	5820	5986	6137	6224	6236	6199	6085	5952	5819
Betaproteobacteria	Burkholderiales	<i>Burkholderia</i> cenocepacia AU 1054	5472	5668	5860	5998	6092	6182	6229	6268	6302
Betaproteobacteria	Burkholderiales	<i>Burkholderia</i> cenocepacia HI2424	5724	5934	6126	6275	6363	6452	6495	6535	6564
Betaproteobacteria	Burkholderiales	<i>Burkholderia</i> cenocepacia MCO 3	5696	5884	6073	6198	6253	6313	6312	6314	6303
Betaproteobacteria	Burkholderiales	<i>Burkholderia</i> cepacia AMMD	5282	5422	5567	5647	5683	5692	5668	5607	5537
Betaproteobacteria	Burkholderiales	<i>Burkholderia</i> mallei ATCC 23344	4153	4215	4273	4312	4329	4340	4329	4336	4318
Betaproteobacteria	Burkholderiales	<i>Burkholderia</i> mallei NCTC 10229	4896	4969	5035	5080	5102	5129	5134	5144	5139
Betaproteobacteria	Burkholderiales	<i>Burkholderia</i> mallei NCTC 10247	5198	5267	5340	5389	5411	5441	5443	5456	5456
Betaproteobacteria	Burkholderiales	<i>Burkholderia</i> mallei SAVP1	4628	4682	4744	4780	4794	4814	4822	4834	4824
Betaproteobacteria	Burkholderiales	<i>Burkholderia</i> multivorans ATCC 17616	5000	5128	5234	5280	5316	5304	5271	5196	5094
Betaproteobacteria	Burkholderiales	<i>Burkholderia</i> pseudomallei 1106a	6176	6273	6356	6411	6434	6460	6459	6451	6420
Betaproteobacteria	Burkholderiales	<i>Burkholderia</i> pseudomallei 1710b	5056	5138	5217	5261	5291	5316	5303	5294	5263
Betaproteobacteria	Burkholderiales	<i>Burkholderia</i> pseudomallei 668	6117	6207	6283	6340	6366	6381	6367	6338	6310
Betaproteobacteria	Burkholderiales	<i>Burkholderia</i> pseudomallei K96243	5049	5154	5248	5316	5349	5389	5404	5413	5410
Betaproteobacteria	Burkholderiales	<i>Burkholderia</i> thailandensis E264	4706	4780	4846	4873	4882	4876	4827	4775	4693
Betaproteobacteria	Burkholderiales	<i>Burkholderia</i> vietnamiensis G4	5340	5397	5453	5461	5426	5386	5293	5204	5083
Betaproteobacteria	Burkholderiales	<i>Burkholderia</i> xenovorans LB400	5448	5512	5495	5306	5068	4732	4343	3800	3225
Betaproteobacteria	Burkholderiales	<i>Deltaia acidovorans</i> SPH-1	4475	4490	4423	4264	4022	3694	3270	2750	2209
Betaproteobacteria	Burkholderiales	<i>Herrnlimonas arsenicoxydans</i>	2728	2726	2698	2643	2576	2499	2397	2271	2111
Betaproteobacteria	Burkholderiales	<i>Janthinobacterium</i> Marseille	3077	3077	3034	2954	2838	2712	2557	2368	2157
Betaproteobacteria	Burkholderiales	<i>Leptothrix cholodnii</i> SP 6	3416	3339	3218	3041	2819	2525	2133	1726	1301
Betaproteobacteria	Burkholderiales	<i>Methylubium petroleiphilum</i> PM1	3282	3197	3101	2914	2675	2416	2036	1647	1224
Betaproteobacteria	Burkholderiales	<i>Polaromonas</i> JS666	4006	4016	4008	3894	3712	3475	3237	2884	2507
Betaproteobacteria	Burkholderiales	<i>Polaromonas</i> naphthalenivorans CJ2	3730	3691	3632	3532	3410	3219	2976	2725	2421
Betaproteobacteria	Burkholderiales	<i>Polynucleobacter</i> QLW-P1DMWA-1	1799	1755	1707	1626	1533	1447	1341	1231	1115
Betaproteobacteria	Burkholderiales	<i>Polynucleobacter</i> necessarius ST1R1	1229	1208	1184	1168	1137	1116	1098	1061	1005
Betaproteobacteria	Burkholderiales	<i>Ralstonia eutropha</i> H16	5138	5207	5253	5254	5193	5037	4829	4549	4177
Betaproteobacteria	Burkholderiales	<i>Ralstonia eutropha</i> JMP134	5072	5136	5172	5196	5126	4985	4788	4530	4155
Betaproteobacteria	Burkholderiales	<i>Ralstonia</i> metallidurans CH34	4809	4846	4858	4831	4734	4547	4274	3953	3563
Betaproteobacteria	Burkholderiales	<i>Ralstonia</i> solanaceorum	3798	3733	3676	3533	3290	2997	2602	2187	1754
Betaproteobacteria	Burkholderiales	<i>Rhodoferrax</i> ferrireducens T118	3495	3447	3361	3247	3048	2800	2473	2095	1650
Betaproteobacteria	Burkholderiales	<i>Verminephrobacter</i> eiseniae EF01-2	3778	3578	3514	3405	3238	2953	2645	2260	1772
Betaproteobacteria	Hydrogenophiales	<i>Thiobacillus denitrificans</i> ATCC 25259	2523	2160	2031	1844	1615	1318	1017	723	459
Betaproteobacteria	Methylophilales	<i>Methylobacillus</i> flagellatus KT	2118	2016	1902	1731	1514	1240	974	704	485
Betaproteobacteria	Neisseriales	<i>Chromobacterium</i> violaceum	3153	2978	2780	2479	2104	1695	1303	898	579
Betaproteobacteria	Neisseriales	<i>Neisseria</i> gonorrhoeae FA 1090	1673	1663	1650	1635	1621	1600	1580	1556	1536
Betaproteobacteria	Neisseriales	<i>Neisseria</i> meningitidis 053442	1886	1887	1888	1883	1877	1860	1842	1821	1806
Betaproteobacteria	Neisseriales	<i>Neisseria</i> meningitidis FAM18	1791	1788	1787	1786	1788	1783	1778	1775	1768
Betaproteobacteria	Neisseriales	<i>Neisseria</i> meningitidis MCS8	1814	1810	1807	1804	1800	1789	1775	1758	1745
Betaproteobacteria	Neisseriales	<i>Neisseria</i> meningitidis Z2491	1859	1859	1865	1867	1862	1848	1838	1832	1822
Betaproteobacteria	Nitrosomonadales	<i>Nitrosomonas</i> europaea	2076	2072	2036	1999	1955	1892	1833	1741	1626
Betaproteobacteria	Nitrosomonadales	<i>Nitrosomonas</i> eutropha C71	2093	2065	2029	1990	1949	1879	1824	1746	1627
Betaproteobacteria	Nitrosomonadales	<i>Nitrosospira</i> multiformis ATCC 25196	2140	2049	1951	1804	1636	1381	1147	852	578
Betaproteobacteria	Rhodocyclales	<i>Azoarcus</i> BH72	3300	3273	3194	2994	2764	2505	2179	1788	1422
Betaproteobacteria	Rhodocyclales	<i>Azoarcus</i> sp EbN1	3064	3066	2923	2768	2598	2383	2114	1780	1451
Betaproteobacteria	Rhodocyclales	<i>Dechloromonas</i> aromatica RCB	3143	3062	2900	2698	2414	2058	1628	1188	819
Gammaproteobacteria	Aeromonadales	<i>Aeromonas</i> hydrophila ATCC 7966	3677	3711	3712	3710	3684	3618	3547	3462	3356
Gammaproteobacteria	Aeromonadales	<i>Aeromonas</i> salmonicida A449	3688	3693	3692	3667	3628	3562	3499	3418	3324
Gammaproteobacteria	Alteromonadales	<i>Colwellia</i> psychroerythraea 34H	3217	3035	2819	2522	2199	1819	1423	1075	713
Gammaproteobacteria	Alteromonadales	<i>Idiomarina</i> loihiensis L2TR	2168	2044	1904	1656	1393	1121	870	635	426
Gammaproteobacteria	Alteromonadales	<i>Marinobacter</i> aquaeolei VT8	3069	2886	2687	2396	2100	1733	1348	996	706
Gammaproteobacteria	Alteromonadales	<i>Pseudoalteromonas</i> atlantica T6c	3216	3011	2758	2404	2029	1651	1279	908	622
Gammaproteobacteria	Alteromonadales	<i>Pseudoalteromonas</i> haloplanktis TAC125	2741	2597	2441	2177	1887	1582	1266	942	659
Gammaproteobacteria	Alteromonadales	<i>Psychromonas</i> ingrahamii 37	2774	2665	2489	2283	2023	1720	1373	1060	737
Gammaproteobacteria	Alteromonadales	<i>Saccharophagus</i> degradans 2-40	2627	2373	2114	1793	1445	1119	836	578	377
Gammaproteobacteria	Alteromonadales	<i>Shewanella</i> ANA-3	3949	3966	3975	3972	3965	3950	3925	3901	3882
Gammaproteobacteria	Alteromonadales	<i>Shewanella</i> MR-4	3711	3744	3762	3779	3790	3786	3781	3783	3780
Gammaproteobacteria	Alteromonadales	<i>Shewanella</i> MR-7	3758	3789	3814	3814	3808	3800	3794	3789	3777
Gammaproteobacteria	Alteromonadales	<i>Shewanella</i> W3-18-1	3735	3750	3767	3776	3776	3755	3737	3723	3713
Gammaproteobacteria	Alteromonadales	<i>Shewanella</i> amazonensis SB2B	3333	3301	3234	3089	2900	2660	2391	2076	1746
Gammaproteobacteria	Alteromonadales	<i>Shewanella</i> baltica OS155	3874	3885	3894	3895	3887	3866	3839	3817	3798
Gammaproteobacteria	Alteromonadales	<i>Shewanella</i> baltica OS185	4041	4067	4095	4110	4113	4109	4100	4097	4090
Gammaproteobacteria	Alteromonadales	<i>Shewanella</i> baltica OS195	4184	4205	4222	4225	4216	4202	4191	4181	4172
Gammaproteobacteria	Alteromonadales	<i>Shewanella</i> denitrificans OS217	3150	3097	3021	2906	2761	2595	2359	2122	1799
Gammaproteobacteria	Alteromonadales	<i>Shewanella</i> frigidimarina NCIMB 400	3574	3552	3514	3415	3252	3066	2823	2544	2172
Gammaproteobacteria	Alteromonadales	<i>Shewanella</i> hallifaxensis HAW EB4	3815	3841	3868	3880	3861	3827	3787	3717	3593
Gammaproteobacteria	Alteromonadales	<i>Shewanella</i> loihica PV-4	3523	3524	3509	3426	3302	3109	2855	2555	2231
Gammaproteobacteria	Alteromonadales	<i>Shewanella</i> oneidensis	3751	3759	3746	3715	3688	3651	3618	3549	3480
Gammaproteobacteria	Alteromonadales	<i>Shewanella</i> pealeana ATCC 700345	3773	3809	3813	3813	3792	3763	3716	3647	3520
Gammaproteobacteria	Alteromonadales	<i>Shewanella</i> putrefaciens CN-32	3676	3697	3726	3744	3755	3739	3735	3719	3715
Gammaproteobacteria	Alteromonadales	<i>Shewanella</i> sediminis HAW-EB3	3856	3850	3840	3807	3725	3587	3447	3192	2885
Gammaproteobacteria	Alteromonadales	<i>Shewanella</i> woodyi ATCC 51908	4097	4077	4022	3902	3798	3612	3409	3139	2793
Gammaproteobacteria	Baumanni	<i>Baumanni</i> cicadellincola Homalodisa coagulata	586	586	584	572	548	519			

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Gammaproteobacteria	Chromatiales	Alkallimnicola ehrlichei MLHE-1	2348	2250	2081	1867	1607	1316	990	715	453
Gammaproteobacteria	Chromatiales	Halorhodospira halophila SL1	1953	1859	1720	1567	1377	1120	845	602	377
Gammaproteobacteria	Chromatiales	Nitrosococcus oceanii ATCC 19707	2227	2092	1922	1707	1409	1078	780	488	279
Gammaproteobacteria	Enterobacteriales	Buchnera aphidicola	493	486	465	417	368	274	201	150	95
Gammaproteobacteria	Enterobacteriales	Buchnera aphidicola Cc Clnara cedri	343	329	302	262	220	161	122	82	49
Gammaproteobacteria	Enterobacteriales	Buchnera aphidicola Sg	544	542	539	531	520	499	462	387	316
Gammaproteobacteria	Enterobacteriales	Buchnera sp.	564	563	561	553	539	512	469	394	320
Gammaproteobacteria	Enterobacteriales	Candidatus Blochmannia floridanus	578	576	571	566	541	476	389	282	195
Gammaproteobacteria	Enterobacteriales	Candidatus Blochmannia pennsylvanicus BPEN	601	599	595	589	559	496	403	299	205
Gammaproteobacteria	Enterobacteriales	Citrobacter koseri ATCC BAA-895	3834	3875	3896	3905	3881	3824	3787	3706	3621
Gammaproteobacteria	Enterobacteriales	Enterobacter 638	3719	3747	3761	3749	3735	3695	3603	3484	3305
Gammaproteobacteria	Enterobacteriales	Enterobacter sakazakii ATCC BAA-894	3547	3550	3520	3471	3391	3292	3135	2953	2713
Gammaproteobacteria	Enterobacteriales	Erwinia carotovora atroseptica SCRI1043	3624	3630	3566	3480	3330	3144	2882	2587	2214
Gammaproteobacteria	Enterobacteriales	Escherichia coli 536	4064	4107	4148	4196	4209	4220	4235	4236	4227
Gammaproteobacteria	Enterobacteriales	Escherichia coli APEC O1	4285	4322	4357	4391	4397	4400	4402	4384	4352
Gammaproteobacteria	Enterobacteriales	Escherichia coli CFT073	4536	4572	4618	4665	4678	4683	4695	4700	4691
Gammaproteobacteria	Enterobacteriales	Escherichia coli DH10B	3714	3758	3792	3836	3850	3873	3886	3900	3910
Gammaproteobacteria	Enterobacteriales	Escherichia coli E24377A	4241	4274	4296	4325	4321	4332	4345	4340	4337
Gammaproteobacteria	Enterobacteriales	Escherichia coli HS	3948	3988	4016	4051	4061	4073	4085	4081	4076
Gammaproteobacteria	Enterobacteriales	Escherichia coli K12	3804	3852	3889	3938	3954	3980	4001	4018	4031
Gammaproteobacteria	Enterobacteriales	Escherichia coli O157H7	4540	4602	4644	4694	4706	4726	4743	4760	4752
Gammaproteobacteria	Enterobacteriales	Escherichia coli O157H7 EDL933	4538	4603	4648	4702	4722	4745	4770	4778	4773
Gammaproteobacteria	Enterobacteriales	Escherichia coli SECEC SMS 3 5	4263	4306	4335	4374	4378	4392	4403	4400	4378
Gammaproteobacteria	Enterobacteriales	Escherichia coli UTI89	4671	4724	4775	4821	4843	4869	4893	4905	4906
Gammaproteobacteria	Enterobacteriales	Escherichia coli W3110	3867	3917	3957	4006	4024	4047	4065	4080	4090
Gammaproteobacteria	Enterobacteriales	Klebsiella pneumoniae MGH 78578	4182	4220	4242	4237	4199	4109	3971	3761	3502
Gammaproteobacteria	Enterobacteriales	Photorhabdus luminescens	3131	3035	2901	2775	2622	2420	2209	1941	1610
Gammaproteobacteria	Enterobacteriales	Salmonella enterica Choleraesuis	4145	4162	4187	4211	4211	4221	4226	4214	4211
Gammaproteobacteria	Enterobacteriales	Salmonella enterica Paratyphi ATCC 9150	3838	3882	3906	3942	3954	3960	3963	3962	3960
Gammaproteobacteria	Enterobacteriales	Salmonella enterica arizonae serovar 62 z4 z23	3714	3720	3719	3726	3707	3683	3636	3596	3558
Gammaproteobacteria	Enterobacteriales	Salmonella enterica serovar Paratyphi B SPB7	4262	4295	4319	4350	4350	4333	4302	4269	4236
Gammaproteobacteria	Enterobacteriales	Salmonella typhi	4292	4327	4356	4386	4395	4394	4400	4395	4392
Gammaproteobacteria	Enterobacteriales	Salmonella typhi Ty2	4035	4074	4107	4146	4169	4180	4192	4204	4218
Gammaproteobacteria	Enterobacteriales	Salmonella typhimurium LT2	4147	4190	4233	4277	4289	4294	4310	4306	4301
Gammaproteobacteria	Enterobacteriales	Serratia proteamaculans 568	4113	4122	4079	4004	3881	3690	3440	3138	2757
Gammaproteobacteria	Enterobacteriales	Shigella boydii Sb227	3479	3498	3513	3532	3542	3540	3533	3525	3508
Gammaproteobacteria	Enterobacteriales	Shigella dysenteriae	3285	3297	3297	3310	3308	3291	3265	3245	3225
Gammaproteobacteria	Enterobacteriales	Shigella flexneri 2a	3704	3731	3744	3769	3777	3793	3804	3799	3792
Gammaproteobacteria	Enterobacteriales	Shigella flexneri 2a 2457T	3482	3505	3522	3545	3554	3569	3573	3577	3577
Gammaproteobacteria	Enterobacteriales	Shigella flexneri 5 8401	3578	3593	3613	3636	3639	3652	3649	3639	3622
Gammaproteobacteria	Enterobacteriales	Shigella sonnei Ss046	3693	3719	3744	3762	3767	3773	3784	3785	3775
Gammaproteobacteria	Enterobacteriales	Sodalis glossinidius morsitans	2002	1941	1895	1807	1703	1589	1465	1322	1144
Gammaproteobacteria	Enterobacteriales	Wigglesworthia brevipalpis	587	567	528	451	341	254	173	115	71
Gammaproteobacteria	Enterobacteriales	Yersinia enterocolitica 8081	3576	3570	3555	3529	3499	3409	3303	3197	3053
Gammaproteobacteria	Enterobacteriales	Yersinia pestis Angola	3565	3573	3589	3597	3604	3593	3586	3573	3560
Gammaproteobacteria	Enterobacteriales	Yersinia pestis Antiqua	3945	3965	3988	4005	4016	4015	4012	4002	3999
Gammaproteobacteria	Enterobacteriales	Yersinia pestis CO92	3765	3783	3804	3816	3825	3833	3833	3832	3832
Gammaproteobacteria	Enterobacteriales	Yersinia pestis KIM	3779	3792	3813	3826	3831	3835	3836	3831	3829
Gammaproteobacteria	Enterobacteriales	Yersinia pestis Nepal516	3812	3832	3856	3872	3883	3889	3887	3884	3884
Gammaproteobacteria	Enterobacteriales	Yersinia pestis Pestoides F	3816	3834	3857	3869	3876	3880	3877	3868	3863
Gammaproteobacteria	Enterobacteriales	Yersinia pestis biovar Mediaevalis	3861	3880	3900	3914	3922	3927	3930	3928	3926
Gammaproteobacteria	Enterobacteriales	Yersinia pseudotuberculosis IP32953	3788	3801	3818	3828	3827	3817	3809	3794	3781
Gammaproteobacteria	Enterobacteriales	Yersinia pseudotuberculosis IP 31758	3874	3876	3877	3870	3861	3850	3829	3811	3786
Gammaproteobacteria	Enterobacteriales	Yersinia pseudotuberculosis YPIII	3783	3791	3797	3803	3795	3782	3764	3743	3720
Gammaproteobacteria	Legionellales	Coxiella burnetii	1798	1808	1810	1813	1810	1799	1790	1770	1756
Gammaproteobacteria	Legionellales	Coxiella burnetii Duqway 7E9-12	1889	1884	1864	1848	1827	1811	1781	1754	1727
Gammaproteobacteria	Legionellales	Coxiella burnetii RSA 331	1787	1794	1799	1802	1800	1798	1793	1786	1780
Gammaproteobacteria	Legionellales	Legionella pneumophila Corby	2838	2849	2846	2840	2830	2821	2816	2808	2779
Gammaproteobacteria	Legionellales	Legionella pneumophila Lens	2716	2716	2721	2717	2703	2691	2685	2680	2673
Gammaproteobacteria	Legionellales	Legionella pneumophila Paris	2852	2846	2842	2836	2832	2821	2812	2808	2795
Gammaproteobacteria	Legionellales	Legionella pneumophila Philadelphia 1	2686	2694	2689	2697	2697	2691	2684	2679	2667
Gammaproteobacteria	Methylocoales	Methylococcus capsulatus Bath	2164	2037	1868	1654	1411	1085	822	536	315
Gammaproteobacteria	Oceanospirillales	Alcanivorax borkumensis SK2	2221	2083	1927	1693	1417	1122	842	603	411
Gammaproteobacteria	Oceanospirillales	Chromohalobacter salexigens DSM 3043	2708	2584	2410	2160	1836	1464	1112	742	470
Gammaproteobacteria	Oceanospirillales	Hahella chejuensis KCTC 2396	3893	3621	3269	2809	2337	1824	1352	945	627
Gammaproteobacteria	Oceanospirillales	Marinomonas MWYL1	3400	3263	3014	2663	2269	1863	1411	1008	627
Gammaproteobacteria	Pasteurellales	Actinobacillus pleuropneumoniae L20	1901	1905	1903	1899	1899	1890	1880	1877	1865
Gammaproteobacteria	Pasteurellales	Actinobacillus pleuropneumoniae serovar 3 JL03	1876	1881	1884	1886	1883	1873	1869	1870	1860
Gammaproteobacteria	Pasteurellales	Actinobacillus succinogenes 130Z	1913	1898	1882	1839	1786	1718	1613	1501	1334
Gammaproteobacteria	Pasteurellales	Haemophilus ducreyi 35000HP	1368	1347	1328	1307	1284	1238	1186	1114	1018
Gammaproteobacteria	Pasteurellales	Haemophilus influenzae	1579	1573	1569	1561	1553	1541	1539	1530	1514
Gammaproteobacteria	Pasteurellales	Haemophilus influenzae 86 028NP	1704	1709	1705	1699	1688	1672	1663	1646	1627
Gammaproteobacteria	Pasteurellales	Haemophilus influenzae PITEE	1526	1523	1522	1520	1516	1503	1503	1494	1479
Gammaproteobacteria	Pasteurellales	Haemophilus influenzae PITGG	1544	1544	1540	1533	1526	1518	1512	1501	1480
Gammaproteobacteria	Pasteurellales	Haemophilus somnus 129PT	1620	1615	1606	1590	1575	1557	1544	1527	1508
Gammaproteobacteria	Pasteurellales	Haemophilus somnus 2336	1756	1746	1724	1691	1669	1637	1605	1575	1550
Gammaproteobacteria	Pasteurellales	Mannheimia succiniciproducens MBEL55E	1908	1892	1858	1811	1757	1684	1581	1467	1283
Gammaproteobacteria	Pasteurellales	Pasteurella multocida	1823	1814	1772	1742	1687	1614	1481	1354	1150
Gammaproteobacteria	Pseudomonadales	Acinetobacter baumannii	3053	3084	3100	3114	3096	3082	3064	3033	2983
Gammaproteobacteria	Pseudomonadales	Acinetobacter baumannii ATCC 17978	2880	2901	2911	2910	2872	2826	2796	2744	2552
Gammaproteobacteria	Pseudomonadales	Acinetobacter baumannii SDF	2325	2317	2312	2300	2280	2258	2247	2241	2232
Gammaproteobacteria	Pseudomonadales	Acinetobacter sp ADP1	2733	2720	2700	2639	2521	2390	2249	2036	1788
Gammaproteobacteria	Pseudomonadales	Pseudomonas aeruginosa	4975	5076	5186	5269	5334	5358	5372	5375	5381
Gammaproteobacteria	Pseudomonadales	Pseudomonas aeruginosa PA7	5161	5231	5296	5341	5360	5338	5305	5250	5185
Gammaproteobacteria	Pseudomonadales	Pseudomonas aeruginosa UCBBP-PA14	5213	5315	5411	5481	5540	5552	5573	5563	5568
Gammaproteobacteria	Pseudomonadales	Pseudomonas entomophila L48	4327	4404	4427	4423	4405	4360	4287	4163	4008
Gammaproteobacteria	Pseudomonadales	Pseudomonas fluorescens Pf-5	5066	5114	5166	5122	5021	4889	4681	4431	4066
Gammaproteobacteria	Pseudomonadales	Pseudomonas fluorescens PfO-1	4710	4769	4820	4801	4754	4640	4500	4307	3981
Gammaproteobacteria	Pseudomonadales	Pseudomonas mendocina ymp	3963	3990	3962	3901	3797	3615	3380	3038	2610
Gammaproteobacteria	Pseudomonadales	Pseudomonas putida F1	4537	4628	4717	4763	4790	4775	4766	4740	4718
Gammaproteobacteria	Pseudomonadales	Pseudomonas putida GB 1	4566	4664	4724	4737	4743	4724	4687	4642	4576
Gammaproteobacteria	Pseudomonadales	Pseudomonas putida KT2440	4473	4558	4622	4658	4681	4676	4652	4611	4569
Gammaproteobacteria	Pseudomonadales	Pseudomonas putida W619	4439	4506	4559	4561	4555	4522	4484	4412	4325
Gammaproteobacteria	Pseudomonadales	Pseudomonas stutzeri A1501	3514	3497	3462	3379	3238	3037	2788	2463	2058
Gammaproteobacteria	Pseudomonadales	Pseudomonas syringae phageolicola 1448A	4349	4401	4427	4441	4425	4400	4369	4315	4245
Gammaproteobacteria	Pseudomonadales	Pseudomonas syringae pv B728a	4456	4522	4547	4572	4576	4543	4509	4455	4386
Gammaproteobacteria	Pseudomonadales	Pseudomonas syringae tomato DC3000	4494	4528	4570	4566	4554	4513	4477	4406	4309
Gammaproteobacteria	Pseudomonadales	Psychrobacter PrWf-1	2011	1969	1889	1792	1671	1511	1315	1117	880
Gammaproteobacteria	Pseudomonadales	Psychrobacter arcticum 273-4	1905	1895	1879	1862	1839	1818	1801	1776	1756
Gammaproteobacteria	Pseudomonadales	Psychrobacter cryohalophilus K5	2207	2187	2157	2125	2075	2012	1962	1899	1842
Gammaproteobacteria	Ruthia	Candidatus Ruthia magnifica Cm Calyptogenia magnifica	925	919	910	891	873	862	853	839	809

Networks of gene sharing among 329 proteobacterial genomes reveal differences in lateral gene transfer frequency at different phylogenetic depths  
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Gammaproteobacteria	Thiotrichales	Francisella philomiragia ATCC 25017	1619	1596	1572	1546	1517	1472	1432	1366	1304
Gammaproteobacteria	Thiotrichales	Francisella tularensis FSC 198	1509	1516	1523	1525	1527	1529	1529	1530	1530
Gammaproteobacteria	Thiotrichales	Francisella tularensis WY96-3418	1527	1528	1537	1539	1541	1542	1542	1540	1539
Gammaproteobacteria	Thiotrichales	Francisella tularensis holarctica	1557	1557	1557	1552	1548	1534	1517	1504	1497
Gammaproteobacteria	Thiotrichales	Francisella tularensis holarctica FTA	1465	1466	1473	1476	1477	1477	1477	1475	1472
Gammaproteobacteria	Thiotrichales	Francisella tularensis holarctica OSU18	1443	1445	1452	1454	1456	1457	1454	1451	1449
Gammaproteobacteria	Thiotrichales	Francisella tularensis novidda U112	1615	1608	1614	1606	1595	1589	1583	1573	1561
Gammaproteobacteria	Thiotrichales	Francisella tularensis tularensis	1507	1515	1521	1523	1525	1527	1527	1528	1528
Gammaproteobacteria	Thiotrichales	Thiomicrospira crunogena XCL-2	1656	1524	1357	1127	905	685	466	309	180
Gammaproteobacteria	Vesicomysocius	Candidatus Vesicomysocius okutanii HA	901	895	888	878	866	859	847	834	807
Gammaproteobacteria	Vibrionales	Photobacterium profundum SS9	3846	3733	3556	3329	3064	2740	2400	1984	1575
Gammaproteobacteria	Vibrionales	Vibrio cholerae	3352	3376	3385	3401	3400	3404	3399	3393	3379
Gammaproteobacteria	Vibrionales	Vibrio cholerae O395	3431	3451	3453	3456	3446	3445	3438	3425	3401
Gammaproteobacteria	Vibrionales	Vibrio fischeri ES114	3132	3069	2977	2823	2642	2419	2153	1837	1518
Gammaproteobacteria	Vibrionales	Vibrio Harveyi ATCC BAA-1116	3994	3946	3891	3831	3755	3665	3571	3457	3304
Gammaproteobacteria	Vibrionales	Vibrio parahaemolyticus	3985	3999	4000	3978	3921	3846	3746	3612	3431
Gammaproteobacteria	Vibrionales	Vibrio vulnificus CMCP6	3952	3967	3959	3947	3928	3895	3861	3825	3789
Gammaproteobacteria	Vibrionales	Vibrio vulnificus YJ016	4052	4078	4064	4059	4046	4012	3966	3923	3879
Gammaproteobacteria	Xanthomonadales	Xanthomonas campestris	3945	3967	3997	4019	4027	4034	4037	4033	4027
Gammaproteobacteria	Xanthomonadales	Xanthomonas campestris 8004	3975	4005	4033	4059	4062	4062	4063	4048	4037
Gammaproteobacteria	Xanthomonadales	Xanthomonas campestris vesicatoria 85-10	3918	3920	3929	3935	3923	3890	3847	3799	3736
Gammaproteobacteria	Xanthomonadales	Xanthomonas citri	3841	3852	3850	3843	3811	3773	3734	3679	3627
Gammaproteobacteria	Xanthomonadales	Xanthomonas oryzae KACC10331	3438	3449	3455	3463	3459	3446	3431	3405	3371
Gammaproteobacteria	Xanthomonadales	Xanthomonas oryzae MAFF 311018	3629	3618	3618	3617	3603	3585	3561	3534	3510
Gammaproteobacteria	Xanthomonadales	Xylella fastidiosa	2156	2146	2125	2098	2075	2039	2020	1989	1950
Gammaproteobacteria	Xanthomonadales	Xylella fastidiosa M12	1939	1938	1936	1923	1911	1893	1878	1859	1835
Gammaproteobacteria	Xanthomonadales	Xylella fastidiosa Temecula1	1918	1913	1904	1901	1893	1884	1883	1866	1840
Unclassified Proteobacteria	Magnetococcus	Magnetococcus MC-1	1946	1714	1437	1142	860	596	380	209	98



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Table S5: Recent LGT estimated for the total Proteobacteria

Class	Order	Species	genome size	# recent	% recent
Alphaproteobacteria	Caulobacterales	Caulobacter crescentus	3,230	255	7.89%
Alphaproteobacteria	Caulobacterales	Caulobacter K31	4,543	742	16.33%
Alphaproteobacteria	Rhizobiales	Agrobacterium tumefaciens C58 Cereon	4,728	768	16.24%
Alphaproteobacteria	Rhizobiales	Azorhizobium caulinodans ORS 571	4,264	561	13.16%
Alphaproteobacteria	Rhizobiales	Bartonella bacilliformis KC583	1,105	35	3.17%
Alphaproteobacteria	Rhizobiales	Bartonella henselae Houston-1	1,384	21	1.52%
Alphaproteobacteria	Rhizobiales	Bartonella quintana Toulouse	1,124	23	2.05%
Alphaproteobacteria	Rhizobiales	Bartonella tribocorum CIP 105476	1,557	81	5.20%
Alphaproteobacteria	Rhizobiales	Bradyrhizobium BTAi1	6,929	470	6.78%
Alphaproteobacteria	Rhizobiales	Bradyrhizobium japonicum	6,893	942	13.67%
Alphaproteobacteria	Rhizobiales	Bradyrhizobium ORS278	6,069	318	5.24%
Alphaproteobacteria	Rhizobiales	Brucella abortus 9-941	3,078	72	2.34%
Alphaproteobacteria	Rhizobiales	Brucella canis ATCC 23365	3,205	461	14.38%
Alphaproteobacteria	Rhizobiales	Brucella melitensis	3,101	98	3.16%
Alphaproteobacteria	Rhizobiales	Brucella melitensis biovar Abortus	3,026	47	1.55%
Alphaproteobacteria	Rhizobiales	Brucella ovis	2,758	66	2.39%
Alphaproteobacteria	Rhizobiales	Brucella suis 1330	3,245	460	14.18%
Alphaproteobacteria	Rhizobiales	Brucella suis ATCC 23445	3,193	527	16.50%
Alphaproteobacteria	Rhizobiales	Mesorhizobium BNC1	3,975	653	16.43%
Alphaproteobacteria	Rhizobiales	Mesorhizobium loti	5,800	1,355	23.36%
Alphaproteobacteria	Rhizobiales	Methylobacterium 4 46	5,431	852	15.69%
Alphaproteobacteria	Rhizobiales	Methylobacterium extorquens PA1	4,256	322	7.57%
Alphaproteobacteria	Rhizobiales	Methylobacterium radiotolerans JCM 2831	5,265	648	12.31%
Alphaproteobacteria	Rhizobiales	Nitrobacter hamburgensis X14	3,657	537	14.68%
Alphaproteobacteria	Rhizobiales	Nitrobacter winogradskyi Nb-255	2,748	185	6.73%
Alphaproteobacteria	Rhizobiales	Ochrobactrum anthropi ATCC 49188	4,401	735	16.70%
Alphaproteobacteria	Rhizobiales	Parvibaculum lavamentivorans DS-1	3,082	853	27.68%
Alphaproteobacteria	Rhizobiales	Rhizobium etli CFN 42	5,477	309	5.64%
Alphaproteobacteria	Rhizobiales	Rhizobium leguminosarum bv viciae 3841	6,388	655	10.25%
Alphaproteobacteria	Rhizobiales	Rhodopseudomonas palustris BisA53	4,460	379	8.50%
Alphaproteobacteria	Rhizobiales	Rhodopseudomonas palustris BisB18	4,499	357	7.94%
Alphaproteobacteria	Rhizobiales	Rhodopseudomonas palustris BisB5	4,179	354	8.47%
Alphaproteobacteria	Rhizobiales	Rhodopseudomonas palustris CGA009	4,610	321	6.96%
Alphaproteobacteria	Rhizobiales	Rhodopseudomonas palustris HaA2	4,488	334	7.44%
Alphaproteobacteria	Rhizobiales	Sinorhizobium medicae WSM419	5,681	373	6.57%
Alphaproteobacteria	Rhizobiales	Sinorhizobium meliloti	5,628	288	5.12%
Alphaproteobacteria	Rhizobiales	Xanthobacter autotrophicus Py2	4,376	715	16.34%
Alphaproteobacteria	Rhodobacterales	Dinoroseobacter shibae DFL 12	3,662	774	21.14%
Alphaproteobacteria	Rhodobacterales	Hyphomonas neptunium ATCC 15444	2,730	535	19.60%
Alphaproteobacteria	Rhodobacterales	Jannaschia CCS1	3,536	696	19.68%
Alphaproteobacteria	Rhodobacterales	Maricaulis maris MCS10	2,350	512	21.79%
Alphaproteobacteria	Rhodobacterales	Paracoccus denitrificans PD1222	4,310	878	20.37%
Alphaproteobacteria	Rhodobacterales	Rhodobacter sphaeroides 2 4 1	4,032	177	4.39%
Alphaproteobacteria	Rhodobacterales	Rhodobacter sphaeroides ATCC 17025	3,816	388	10.17%
Alphaproteobacteria	Rhodobacterales	Rhodobacter sphaeroides ATCC 17029	3,966	160	4.03%
Alphaproteobacteria	Rhodobacterales	Roseobacter denitrificans OCH 114	3,511	529	15.07%
Alphaproteobacteria	Rhodobacterales	Silicibacter pomeroyi DSS-3	3,836	507	13.22%
Alphaproteobacteria	Rhodobacterales	Silicibacter TM1040	3,373	349	10.35%
Alphaproteobacteria	Rhodospirillales	Acidiphiliumcryptum JF-5	2,900	858	29.59%
Alphaproteobacteria	Rhodospirillales	Gluconacetobacter diazotrophicus PAI 5	3,018	631	20.91%
Alphaproteobacteria	Rhodospirillales	Gluconobacter oxydans 621H	2,088	269	12.88%
Alphaproteobacteria	Rhodospirillales	Granulobacter bethedensis CGDNIH1	2,053	463	22.55%
Alphaproteobacteria	Rhodospirillales	Magnetospirillum magneticum AMB-1	3,048	869	28.51%
Alphaproteobacteria	Rhodospirillales	Rhodospirillum rubrum ATCC 11170	3,175	992	31.24%
Alphaproteobacteria	Rickettsiales	Anaplasma marginale St Maries	765	16	2.09%
Alphaproteobacteria	Rickettsiales	Anaplasma phagocytophilum HZ	735	15	2.04%
Alphaproteobacteria	Rickettsiales	Candidatus Pelagibacter ubique HTCC1062	1,016	374	36.81%
Alphaproteobacteria	Rickettsiales	Ehrlichia canis Jake	813	4	0.49%
Alphaproteobacteria	Rickettsiales	Ehrlichia chaffeensis Arkansas	815	7	0.86%
Alphaproteobacteria	Rickettsiales	Ehrlichia ruminantium Gardel	924	39	4.22%
Alphaproteobacteria	Rickettsiales	Ehrlichia ruminantium str. Welgevonden	927	39	4.21%
Alphaproteobacteria	Rickettsiales	Ehrlichia ruminantium str. Welgevonden	886	1	0.11%
Alphaproteobacteria	Rickettsiales	Neorickettsia sennetsu Miyayama	530	38	7.17%
Alphaproteobacteria	Rickettsiales	Orientia tsutsugamushi Boryong	629	67	10.65%
Alphaproteobacteria	Rickettsiales	Rickettsia akari Hartford	1,010	85	8.42%
Alphaproteobacteria	Rickettsiales	Rickettsia bellii OSU 85-389	1,320	24	1.82%
Alphaproteobacteria	Rickettsiales	Rickettsia bellii RML369-C	1,346	44	3.27%
Alphaproteobacteria	Rickettsiales	Rickettsia canadensis McKiel	847	104	12.28%
Alphaproteobacteria	Rickettsiales	Rickettsia conorii	1,252	126	10.06%
Alphaproteobacteria	Rickettsiales	Rickettsia felis URRWXCal2	1,250	221	17.68%
Alphaproteobacteria	Rickettsiales	Rickettsia massiliae MTU5	955	58	6.07%
Alphaproteobacteria	Rickettsiales	Rickettsia prowazekii	810	7	0.86%
Alphaproteobacteria	Rickettsiales	Rickettsia rickettsii Iowa	1,293	48	3.71%
Alphaproteobacteria	Rickettsiales	Rickettsia rickettsii Sheila Smith	1,276	31	2.43%
Alphaproteobacteria	Rickettsiales	Rickettsia typhi wilmington	815	18	2.21%
Alphaproteobacteria	Rickettsiales	Wolbachia endosymbiont of Brugia malayi TRS	672	9	1.34%
Alphaproteobacteria	Rickettsiales	Wolbachia endosymbiont of Drosophila melanogaster	793	72	9.08%
Alphaproteobacteria	Sphingomonadales	Erythrobacter litoralis HTCC2594	2,483	359	14.46%
Alphaproteobacteria	Sphingomonadales	Novosphingobium aromaticivorans DSM 12444	3,258	775	23.79%
Alphaproteobacteria	Sphingomonadales	Sphingomonas wittichii RW1	4,123	1,378	33.42%
Alphaproteobacteria	Sphingomonadales	Sphingopyxis alaskensis RB2256	2,742	800	29.18%

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Alphaproteobacteria	Sphingomonadales	Zymomonas mobilis ZM4	1,466	194	13.23%
Betaproteobacteria	Burkholderiales	Acidovorax avenae citrulli AAC00-1	3,999	645	16.13%
Betaproteobacteria	Burkholderiales	Acidovorax JS42	3,823	418	10.93%
Betaproteobacteria	Burkholderiales	Bordetella bronchiseptica	4,830	256	5.30%
Betaproteobacteria	Burkholderiales	Bordetella parapertussis	4,146	22	0.53%
Betaproteobacteria	Burkholderiales	Bordetella pertussis	3,213	135	4.20%
Betaproteobacteria	Burkholderiales	Bordetella petrii	4,620	698	15.11%
Betaproteobacteria	Burkholderiales	Burkholderia 383	7,207	771	10.70%
Betaproteobacteria	Burkholderiales	Burkholderia cenocepacia AU 1054	6,428	13	0.20%
Betaproteobacteria	Burkholderiales	Burkholderia cenocepacia H12424	6,791	104	1.53%
Betaproteobacteria	Burkholderiales	Burkholderia cenocepacia MCO 3	6,836	652	9.54%
Betaproteobacteria	Burkholderiales	Burkholderia cepacia AMMD	6,265	414	6.61%
Betaproteobacteria	Burkholderiales	Burkholderia mallei ATCC 23344	4,475	175	3.91%
Betaproteobacteria	Burkholderiales	Burkholderia mallei NCTC 10229	5,248	481	9.17%
Betaproteobacteria	Burkholderiales	Burkholderia mallei NCTC 10247	5,577	933	16.73%
Betaproteobacteria	Burkholderiales	Burkholderia mallei SAVP1	4,940	492	9.96%
Betaproteobacteria	Burkholderiales	Burkholderia multivorans ATCC 17616	5,908	710	12.02%
Betaproteobacteria	Burkholderiales	Burkholderia pseudomallei 1106a	6,696	1,488	22.22%
Betaproteobacteria	Burkholderiales	Burkholderia pseudomallei 1710b	5,596	645	11.53%
Betaproteobacteria	Burkholderiales	Burkholderia pseudomallei 668	6,657	1,304	19.59%
Betaproteobacteria	Burkholderiales	Burkholderia pseudomallei K96243	5,609	183	3.26%
Betaproteobacteria	Burkholderiales	Burkholderia thailandensis E264	5,252	765	14.57%
Betaproteobacteria	Burkholderiales	Burkholderia vietnamiensis G4	6,337	722	11.39%
Betaproteobacteria	Burkholderiales	Burkholderia xenovorans LB400	7,262	1,358	18.70%
Betaproteobacteria	Burkholderiales	Delftia acidovorans SPH-1	5,267	968	18.38%
Betaproteobacteria	Burkholderiales	Hermiimonas arsenicoxidans	2,934	173	5.90%
Betaproteobacteria	Burkholderiales	Janthinobacterium Marseille	3,434	358	10.43%
Betaproteobacteria	Burkholderiales	Leptothrix cholodnii SP 6	3,808	554	14.55%
Betaproteobacteria	Burkholderiales	Methylobium petroleiphilum PM1	3,682	529	14.37%
Betaproteobacteria	Burkholderiales	Polaromonas JS666	4,714	706	14.98%
Betaproteobacteria	Burkholderiales	Polaromonas naphthalenivorans CJ2	4,202	597	14.21%
Betaproteobacteria	Burkholderiales	Polynucleobacter necessarius STIR1	1,242	21	1.69%
Betaproteobacteria	Burkholderiales	Polynucleobacter QLW-P1DMWA-1	1,877	127	6.77%
Betaproteobacteria	Burkholderiales	Ralstonia eutropha H16	6,173	545	8.83%
Betaproteobacteria	Burkholderiales	Ralstonia eutropha JMP134	6,055	531	8.77%
Betaproteobacteria	Burkholderiales	Ralstonia metallidurans CH34	5,644	724	12.83%
Betaproteobacteria	Burkholderiales	Ralstonia solanacearum	4,228	694	16.41%
Betaproteobacteria	Burkholderiales	Rhodoferrax ferrireducens T118	3,866	618	15.99%
Betaproteobacteria	Burkholderiales	Verminephrobacter eiseniae EF01-2	4,078	1,012	24.82%
Betaproteobacteria	Hydrogenophilales	Thiobacillus denitrificans ATCC 25259	2,378	492	20.69%
Betaproteobacteria	Methylophilales	Methylobacillus flagellatus KT	2,348	426	18.14%
Betaproteobacteria	Neisseriales	Chromobacterium violaceum	3,468	1,324	38.18%
Betaproteobacteria	Neisseriales	Neisseria gonorrhoeae FA 1090	1,740	241	13.85%
Betaproteobacteria	Neisseriales	Neisseria meningitidis 053442	1,963	193	9.83%
Betaproteobacteria	Neisseriales	Neisseria meningitidis FAM18	1,868	118	6.32%
Betaproteobacteria	Neisseriales	Neisseria meningitidis MC58	1,916	200	10.44%
Betaproteobacteria	Neisseriales	Neisseria meningitidis Z2491	1,917	254	13.25%
Betaproteobacteria	Nitrosomonadales	Nitrosomonas europaea	2,235	229	10.25%
Betaproteobacteria	Nitrosomonadales	Nitrosomonas eutropha C71	2,259	203	8.99%
Betaproteobacteria	Nitrosomonadales	Nitrospirilla multiformis ATCC 25196	2,296	394	17.16%
Betaproteobacteria	Rhodocyclales	Azoarcus BH72	3,644	696	19.10%
Betaproteobacteria	Rhodocyclales	Azoarcus sp EbN1	3,519	729	20.72%
Betaproteobacteria	Rhodocyclales	Dechloromonas aromatica RCB	3,563	860	24.14%
Deltaproteobacteria	Bdellovibrionales	Bdellovibrio bacteriovorus	1,534	864	56.32%
Deltaproteobacteria	Desulfobacterales	Candidatus Desulfococcus oleovorans Hxd3	2,050	778	37.95%
Deltaproteobacteria	Desulfobacterales	Desulfotalea psychrophila L5v54	2,073	1,677	80.90%
Deltaproteobacteria	Desulfovibrionales	Desulfovibrio desulfuricans G20	2,757	1,289	46.75%
Deltaproteobacteria	Desulfovibrionales	Desulfovibrio vulgaris DP4	2,958	106	3.58%
Deltaproteobacteria	Desulfovibrionales	Desulfovibrio vulgaris Hildenborough	2,951	119	4.03%
Deltaproteobacteria	Desulfovibrionales	Lawsonia intracellularis PHE MN1-00	1,043	129	12.37%
Deltaproteobacteria	Desulfuromonadales	Geobacter metallireducens GS-15	3,099	547	17.65%
Deltaproteobacteria	Desulfuromonadales	Geobacter sulfurreducens	2,972	455	15.31%
Deltaproteobacteria	Desulfuromonadales	Geobacter uraniumreducens Rf4	3,473	1,136	32.71%
Deltaproteobacteria	Desulfuromonadales	Pelobacter carbinolicus	2,476	916	37.00%
Deltaproteobacteria	Desulfuromonadales	Pelobacter propionicus DSM 2379	2,917	684	23.45%
Deltaproteobacteria	Myxococcales	Anaeromyxobacter dehalogenans 2CP-C	3,739	424	11.34%
Deltaproteobacteria	Myxococcales	Anaeromyxobacter Fw109-5	3,744	477	12.74%
Deltaproteobacteria	Myxococcales	Myxococcus xanthus DK 1622	3,768	1,577	41.85%
Deltaproteobacteria	Myxococcales	Sorangium cellulosum So ce 56	3,690	2,042	55.34%
Deltaproteobacteria	Syntrophobacterales	Syntrophobacter fumaroxidans MPOB	2,587	1,124	43.45%
Deltaproteobacteria	Syntrophobacterales	Syntrophus aciditrophicus SB	1,894	633	33.42%
Epsilonproteobacteria	Campylobacterales	Arcobacter butzleri RM4018	1,720	732	42.56%
Epsilonproteobacteria	Campylobacterales	Campylobacter concisus 13826	1,578	158	10.01%
Epsilonproteobacteria	Campylobacterales	Campylobacter curvus 525 92	1,627	161	9.90%
Epsilonproteobacteria	Campylobacterales	Campylobacter fetus 82-40	1,493	295	19.76%
Epsilonproteobacteria	Campylobacterales	Campylobacter hominis ATCC BAA-381	1,190	133	11.18%
Epsilonproteobacteria	Campylobacterales	Campylobacter jejuni	1,584	151	9.53%
Epsilonproteobacteria	Campylobacterales	Campylobacter jejuni 81-176	1,581	100	6.33%
Epsilonproteobacteria	Campylobacterales	Campylobacter jejuni 81116	1,631	51	3.13%
Epsilonproteobacteria	Campylobacterales	Campylobacter jejuni doylei 269 97	1,539	147	9.55%
Epsilonproteobacteria	Campylobacterales	Campylobacter jejuni RM1221	1,621	269	16.59%
Epsilonproteobacteria	Campylobacterales	Helicobacter acinonychis Sheeba	1,333	74	5.55%

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Epsilonproteobacteria	Campylobacteriales	<i>Helicobacter hepaticus</i>	1,301	347	26.67%
Epsilonproteobacteria	Campylobacteriales	<i>Helicobacter pylori</i> 26695	1,459	51	3.50%
Epsilonproteobacteria	Campylobacteriales	<i>Helicobacter pylori</i> HPAG1	1,456	47	3.23%
Epsilonproteobacteria	Campylobacteriales	<i>Helicobacter pylori</i> J99	1,430	71	4.97%
Epsilonproteobacteria	Campylobacteriales	<i>Thiomicrospira denitrificans</i> ATCC 33889	1,659	452	27.25%
Epsilonproteobacteria	Campylobacteriales	<i>Wolinella succinogenes</i>	1,659	801	48.28%
Epsilonproteobacteria	Nitratiruptor	<i>Nitratiruptor</i> SB155-2	1,464	1,006	68.72%
Epsilonproteobacteria	Sulfurovum	<i>Sulfurovum</i> NBC37-1	1,794	546	30.43%
Gammaproteobacteria	Aeromonadales	<i>Aeromonas hydrophila</i> ATCC 7966	3,939	180	4.57%
Gammaproteobacteria	Aeromonadales	<i>Aeromonas salmonicida</i> A449	3,978	251	6.31%
Gammaproteobacteria	Alteromonadales	<i>Colwellia psychrerythraea</i> 34H	3,586	662	18.46%
Gammaproteobacteria	Alteromonadales	<i>Idiomarina loihiensis</i> L2TR	2,263	231	10.21%
Gammaproteobacteria	Alteromonadales	<i>Marinobacter aquaeolei</i> VT8	3,454	468	13.55%
Gammaproteobacteria	Alteromonadales	<i>Pseudoalteromonas atlantica</i> T6c	3,492	659	18.87%
Gammaproteobacteria	Alteromonadales	<i>Pseudoalteromonas haloplanktis</i> TAC125	2,880	390	13.54%
Gammaproteobacteria	Alteromonadales	<i>Psychromonas ingrahamii</i> 37	2,995	617	20.60%
Gammaproteobacteria	Alteromonadales	<i>Saccharophagus degradans</i> 2-40	2,819	687	24.37%
Gammaproteobacteria	Alteromonadales	<i>Shewanella amazonensis</i> SB2B	3,471	573	16.51%
Gammaproteobacteria	Alteromonadales	<i>Shewanella</i> ANA-3	4,151	236	5.69%
Gammaproteobacteria	Alteromonadales	<i>Shewanella baltica</i> OS155	4,199	157	3.74%
Gammaproteobacteria	Alteromonadales	<i>Shewanella baltica</i> OS185	4,283	336	7.84%
Gammaproteobacteria	Alteromonadales	<i>Shewanella baltica</i> OS195	4,475	364	8.13%
Gammaproteobacteria	Alteromonadales	<i>Shewanella denitrificans</i> OS217	3,336	339	10.16%
Gammaproteobacteria	Alteromonadales	<i>Shewanella frigidimarina</i> NCIMB 400	3,811	422	11.07%
Gammaproteobacteria	Alteromonadales	<i>Shewanella halifaxensis</i> HAW EB4	4,112	230	5.59%
Gammaproteobacteria	Alteromonadales	<i>Shewanella loihica</i> PV-4	3,683	483	13.11%
Gammaproteobacteria	Alteromonadales	<i>Shewanella</i> MR-4	3,879	106	2.73%
Gammaproteobacteria	Alteromonadales	<i>Shewanella</i> MR-7	3,915	161	4.11%
Gammaproteobacteria	Alteromonadales	<i>Shewanella oneidensis</i>	3,967	334	8.42%
Gammaproteobacteria	Alteromonadales	<i>Shewanella pealeana</i> ATCC 700345	4,024	196	4.87%
Gammaproteobacteria	Alteromonadales	<i>Shewanella putrefaciens</i> CN-32	3,899	108	2.77%
Gammaproteobacteria	Alteromonadales	<i>Shewanella sediminis</i> HAW-EB3	4,183	441	10.54%
Gammaproteobacteria	Alteromonadales	<i>Shewanella</i> W3-18-1	3,913	151	3.86%
Gammaproteobacteria	Alteromonadales	<i>Shewanella woodyi</i> ATCC 51908	4,352	557	12.80%
Gammaproteobacteria	Baumannia	<i>Baumannia cicadellincola</i> Homalodisca coagulata	587	10	1.70%
Gammaproteobacteria	Cardiobacteriales	<i>Dichelobacter nodosus</i> VCS1703A	988	147	14.88%
Gammaproteobacteria	Carsonella	<i>Candidatus Carsonella ruddii</i> PV	80	1	1.25%
Gammaproteobacteria	Chromatiales	<i>Alkalilimnicola ehrlichei</i> MLHE-1	2,492	427	17.13%
Gammaproteobacteria	Chromatiales	<i>Halorhodospira halophila</i> SL1	2,042	255	12.49%
Gammaproteobacteria	Chromatiales	<i>Nitrosococcus oceani</i> ATCC 19707	2,364	692	29.27%
Gammaproteobacteria	Enterobacteriales	<i>Buchnera aphidicola</i>	494	11	2.23%
Gammaproteobacteria	Enterobacteriales	<i>Buchnera aphidicola</i> Cc Cinar cedri	343	2	0.58%
Gammaproteobacteria	Enterobacteriales	<i>Buchnera aphidicola</i> Sg	544	0	0.00%
Gammaproteobacteria	Enterobacteriales	<i>Buchnera</i> sp	566	2	0.35%
Gammaproteobacteria	Enterobacteriales	<i>Candidatus Blochmannia floridanus</i>	579	1	0.17%
Gammaproteobacteria	Enterobacteriales	<i>Candidatus Blochmannia pennsylvanicus</i> BPEN	602	1	0.17%
Gammaproteobacteria	Enterobacteriales	<i>Citrobacter koseri</i> ATCC BAA-895	4,194	521	12.42%
Gammaproteobacteria	Enterobacteriales	<i>Enterobacter</i> 638	4,059	613	15.10%
Gammaproteobacteria	Enterobacteriales	<i>Enterobacter sakazakii</i> ATCC BAA-894	3,812	480	12.59%
Gammaproteobacteria	Enterobacteriales	<i>Erwinia carotovora</i> atroseptica SCRI1043	4,018	681	16.95%
Gammaproteobacteria	Enterobacteriales	<i>Escherichia coli</i> 536	4,461	129	2.89%
Gammaproteobacteria	Enterobacteriales	<i>Escherichia coli</i> APEC O1	4,739	355	7.49%
Gammaproteobacteria	Enterobacteriales	<i>Escherichia coli</i> CFT073	5,045	548	10.86%
Gammaproteobacteria	Enterobacteriales	<i>Escherichia coli</i> DH10B	4,092	42	1.03%
Gammaproteobacteria	Enterobacteriales	<i>Escherichia coli</i> E24377A	4,656	385	8.27%
Gammaproteobacteria	Enterobacteriales	<i>Escherichia coli</i> HS	4,217	304	7.21%
Gammaproteobacteria	Enterobacteriales	<i>Escherichia coli</i> K12	4,100	21	0.51%
Gammaproteobacteria	Enterobacteriales	<i>Escherichia coli</i> O157H7	5,091	98	1.92%
Gammaproteobacteria	Enterobacteriales	<i>Escherichia coli</i> O157H7 EDL933	5,167	95	1.84%
Gammaproteobacteria	Enterobacteriales	<i>Escherichia coli</i> SECEC SMS 3 5	4,668	382	8.18%
Gammaproteobacteria	Enterobacteriales	<i>Escherichia coli</i> UTI89	5,072	549	10.82%
Gammaproteobacteria	Enterobacteriales	<i>Escherichia coli</i> W3110	4,180	45	1.08%
Gammaproteobacteria	Enterobacteriales	<i>Klebsiella pneumoniae</i> MGH 78578	4,808	651	13.54%
Gammaproteobacteria	Enterobacteriales	<i>Photobacterium luminescens</i>	3,495	724	20.72%
Gammaproteobacteria	Enterobacteriales	<i>Salmonella enterica</i> arizonae serovar 62 z4 z23	3,985	360	9.03%
Gammaproteobacteria	Enterobacteriales	<i>Salmonella enterica</i> Choleraesuis	4,434	377	8.50%
Gammaproteobacteria	Enterobacteriales	<i>Salmonella enterica</i> Paratyphi ATCC 9150	4,069	187	4.60%
Gammaproteobacteria	Enterobacteriales	<i>Salmonella enterica</i> serovar Paratyphi B SPB7	4,553	313	6.87%
Gammaproteobacteria	Enterobacteriales	<i>Salmonella typhi</i>	4,618	216	4.68%
Gammaproteobacteria	Enterobacteriales	<i>Salmonella typhi</i> Ty2	4,289	8	0.19%
Gammaproteobacteria	Enterobacteriales	<i>Salmonella typhimurium</i> LT2	4,472	166	3.71%
Gammaproteobacteria	Enterobacteriales	<i>Serratia proteamaculans</i> 568	4,590	658	14.34%
Gammaproteobacteria	Enterobacteriales	<i>Shigella boydii</i> Sb227	3,753	207	5.52%
Gammaproteobacteria	Enterobacteriales	<i>Shigella dysenteriae</i>	3,554	295	8.30%
Gammaproteobacteria	Enterobacteriales	<i>Shigella flexneri</i> 2a	4,055	227	5.60%
Gammaproteobacteria	Enterobacteriales	<i>Shigella flexneri</i> 2a 2457T	3,742	92	2.46%
Gammaproteobacteria	Enterobacteriales	<i>Shigella flexneri</i> 5 8401	3,820	124	3.25%
Gammaproteobacteria	Enterobacteriales	<i>Shigella sonnei</i> Ss046	3,959	235	5.94%
Gammaproteobacteria	Enterobacteriales	<i>Sodalis glossinidius</i> morsitans	2,121	242	11.41%
Gammaproteobacteria	Enterobacteriales	<i>Wigglesworthia brevialpilis</i>	588	23	3.91%
Gammaproteobacteria	Enterobacteriales	<i>Yersinia enterocolitica</i> 8081	3,801	402	10.58%
Gammaproteobacteria	Enterobacteriales	<i>Yersinia pestis</i> Angola	3,692	198	5.36%

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Gammaproteobacteria	Enterobacteriales	<i>Yersinia pestis</i> Antiqua	4,107	138	3.36%
Gammaproteobacteria	Enterobacteriales	<i>Yersinia pestis</i> biovar Mediaevalis	3,987	127	3.19%
Gammaproteobacteria	Enterobacteriales	<i>Yersinia pestis</i> CO92	3,879	45	1.16%
Gammaproteobacteria	Enterobacteriales	<i>Yersinia pestis</i> KIM	3,893	117	3.01%
Gammaproteobacteria	Enterobacteriales	<i>Yersinia pestis</i> Nepal516	3,942	91	2.31%
Gammaproteobacteria	Enterobacteriales	<i>Yersinia pestis</i> Pestoides F	3,942	445	11.29%
Gammaproteobacteria	Enterobacteriales	<i>Yersinia pseudotuberculosis</i> IP 31758	3,947	568	14.39%
Gammaproteobacteria	Enterobacteriales	<i>Yersinia pseudotuberculosis</i> IP32953	4,023	395	9.82%
Gammaproteobacteria	Enterobacteriales	<i>Yersinia pseudotuberculosis</i> YPIII	3,907	257	6.58%
Gammaproteobacteria	Legionellales	<i>Coxiella burnetii</i>	1,848	115	6.22%
Gammaproteobacteria	Legionellales	<i>Coxiella burnetii</i> Dugway 7E9-12	1,943	280	14.41%
Gammaproteobacteria	Legionellales	<i>Coxiella burnetii</i> RSA 331	1,820	125	6.87%
Gammaproteobacteria	Legionellales	<i>Legionella pneumophila</i> Corby	2,990	316	10.57%
Gammaproteobacteria	Legionellales	<i>Legionella pneumophila</i> Lens	2,813	173	6.15%
Gammaproteobacteria	Legionellales	<i>Legionella pneumophila</i> Paris	2,990	351	11.74%
Gammaproteobacteria	Legionellales	<i>Legionella pneumophila</i> Philadelphia 1	2,784	148	5.32%
Gammaproteobacteria	Methylococcales	<i>Methylococcus capsulatus</i> Bath	2,307	814	35.28%
Gammaproteobacteria	Oceanospirillales	<i>Alcanivorax borkumensis</i> SK2	2,339	346	14.79%
Gammaproteobacteria	Oceanospirillales	<i>Chromohalobacter salexigenis</i> DSM 3043	2,918	500	17.14%
Gammaproteobacteria	Oceanospirillales	<i>Hahella chejuensis</i> KCTC 2396	4,345	975	22.44%
Gammaproteobacteria	Oceanospirillales	<i>Marinomonas</i> MWV1	3,811	832	21.83%
Gammaproteobacteria	Pasteurellales	<i>Actinobacillus pleuropneumoniae</i> L20	1,973	41	2.08%
Gammaproteobacteria	Pasteurellales	<i>Actinobacillus pleuropneumoniae</i> serovar 3 J103	1,947	34	1.75%
Gammaproteobacteria	Pasteurellales	<i>Actinobacillus succinogenes</i> 130Z	2,004	140	6.99%
Gammaproteobacteria	Pasteurellales	<i>Haemophilus ducreyi</i> 35000HP	1,410	214	15.18%
Gammaproteobacteria	Pasteurellales	<i>Haemophilus influenzae</i>	1,621	81	5.00%
Gammaproteobacteria	Pasteurellales	<i>Haemophilus influenzae</i> 86 028NP	1,741	120	6.89%
Gammaproteobacteria	Pasteurellales	<i>Haemophilus influenzae</i> PittEE	1,550	52	3.35%
Gammaproteobacteria	Pasteurellales	<i>Haemophilus influenzae</i> PittGG	1,572	136	8.65%
Gammaproteobacteria	Pasteurellales	<i>Haemophilus somnus</i> 129PT	1,664	39	2.34%
Gammaproteobacteria	Pasteurellales	<i>Haemophilus somnus</i> 2336	1,815	104	5.73%
Gammaproteobacteria	Pasteurellales	<i>Mannheimia succiniciproducens</i> MBEL55E	2,001	122	6.10%
Gammaproteobacteria	Pasteurellales	<i>Pasteurella multocida</i>	1,879	152	8.09%
Gammaproteobacteria	Pseudomonadales	<i>Acinetobacter baumannii</i>	3,360	233	6.93%
Gammaproteobacteria	Pseudomonadales	<i>Acinetobacter baumannii</i> ATCC 17978	3,173	114	3.59%
Gammaproteobacteria	Pseudomonadales	<i>Acinetobacter baumannii</i> SDF	2,465	210	8.52%
Gammaproteobacteria	Pseudomonadales	<i>Acinetobacter</i> sp ADP1	2,948	365	12.38%
Gammaproteobacteria	Pseudomonadales	<i>Pseudomonas aeruginosa</i>	5,518	46	0.83%
Gammaproteobacteria	Pseudomonadales	<i>Pseudomonas aeruginosa</i> PA7	5,757	320	5.56%
Gammaproteobacteria	Pseudomonadales	<i>Pseudomonas aeruginosa</i> UCBPP-PA14	5,760	168	2.92%
Gammaproteobacteria	Pseudomonadales	<i>Pseudomonas entomophila</i> L48	4,778	452	9.46%
Gammaproteobacteria	Pseudomonadales	<i>Pseudomonas fluorescens</i> Pf-5	5,741	799	13.92%
Gammaproteobacteria	Pseudomonadales	<i>Pseudomonas fluorescens</i> PfO-1	5,339	705	13.20%
Gammaproteobacteria	Pseudomonadales	<i>Pseudomonas mendocina</i> ymp	4,329	472	10.90%
Gammaproteobacteria	Pseudomonadales	<i>Pseudomonas putida</i> F1	5,092	201	3.95%
Gammaproteobacteria	Pseudomonadales	<i>Pseudomonas putida</i> GB 1	5,162	349	6.76%
Gammaproteobacteria	Pseudomonadales	<i>Pseudomonas putida</i> KT2440	5,029	218	4.33%
Gammaproteobacteria	Pseudomonadales	<i>Pseudomonas putida</i> W619	4,956	395	7.97%
Gammaproteobacteria	Pseudomonadales	<i>Pseudomonas stutzeri</i> A1501	3,837	448	11.68%
Gammaproteobacteria	Pseudomonadales	<i>Pseudomonas syringae</i> phaseolicola 1448A	4,788	256	5.35%
Gammaproteobacteria	Pseudomonadales	<i>Pseudomonas syringae</i> pv B728a	4,866	361	7.42%
Gammaproteobacteria	Pseudomonadales	<i>Pseudomonas syringae</i> tomato DC3000	4,935	323	6.55%
Gammaproteobacteria	Pseudomonadales	<i>Psychrobacter arcticum</i> 273-4	1,971	70	3.55%
Gammaproteobacteria	Pseudomonadales	<i>Psychrobacter cryohalolentis</i> K5	2,331	168	7.21%
Gammaproteobacteria	Pseudomonadales	<i>Psychrobacter</i> PRwf-1	2,109	188	8.91%
Gammaproteobacteria	Ruthia	<i>Candidatus Ruthia magnifica</i> Cm Calyptogena magnifica	931	15	1.61%
Gammaproteobacteria	Thiotrichales	<i>Francisella philomiragia</i> ATCC 25017	1,693	267	15.77%
Gammaproteobacteria	Thiotrichales	<i>Francisella tularensis</i> FSC 198	1,553	0	0.00%
Gammaproteobacteria	Thiotrichales	<i>Francisella tularensis</i> holarctica	1,635	140	8.56%
Gammaproteobacteria	Thiotrichales	<i>Francisella tularensis</i> holarctica FTA	1,515	68	4.49%
Gammaproteobacteria	Thiotrichales	<i>Francisella tularensis</i> holarctica OSU18	1,486	51	3.43%
Gammaproteobacteria	Thiotrichales	<i>Francisella tularensis</i> novicida U112	1,661	265	15.95%
Gammaproteobacteria	Thiotrichales	<i>Francisella tularensis</i> tularensis	1,551	0	0.00%
Gammaproteobacteria	Thiotrichales	<i>Francisella tularensis</i> WY96-3418	1,552	70	4.51%
Gammaproteobacteria	Thiotrichales	<i>Thiomicrospira crunogena</i> XCL-2	1,719	401	23.33%
Gammaproteobacteria	Vesicomysocius	<i>Candidatus Vesicomysocius okutanii</i> HA	904	19	2.10%
Gammaproteobacteria	Vibrionales	<i>Photobacterium profundum</i> SS9	4,333	905	20.89%
Gammaproteobacteria	Vibrionales	<i>Vibrio cholerae</i>	3,520	44	1.25%
Gammaproteobacteria	Vibrionales	<i>Vibrio cholerae</i> O395	3,578	70	1.96%
Gammaproteobacteria	Vibrionales	<i>Vibrio fischeri</i> ES114	3,359	491	14.62%
Gammaproteobacteria	Vibrionales	<i>Vibrio harveyi</i> ATCC BAA-1116	4,308	359	8.33%
Gammaproteobacteria	Vibrionales	<i>Vibrio parahaemolyticus</i>	4,240	286	6.75%
Gammaproteobacteria	Vibrionales	<i>Vibrio vulnificus</i> CMCP6	4,178	129	3.09%
Gammaproteobacteria	Vibrionales	<i>Vibrio vulnificus</i> YJ016	4,266	205	4.81%
Gammaproteobacteria	Xanthomonadales	<i>Xanthomonas campestris</i>	4,117	483	11.73%
Gammaproteobacteria	Xanthomonadales	<i>Xanthomonas campestris</i> 8004	4,171	460	11.03%
Gammaproteobacteria	Xanthomonadales	<i>Xanthomonas campestris</i> vesicatoria 85-10	4,189	374	8.93%
Gammaproteobacteria	Xanthomonadales	<i>Xanthomonas citri</i>	4,022	323	8.03%
Gammaproteobacteria	Xanthomonadales	<i>Xanthomonas oryzae</i> KACC10331	3,625	29	0.80%
Gammaproteobacteria	Xanthomonadales	<i>Xanthomonas oryzae</i> MAFF 311018	3,759	123	3.27%
Gammaproteobacteria	Xanthomonadales	<i>Xylella fastidiosa</i>	2,317	372	16.06%
Gammaproteobacteria	Xanthomonadales	<i>Xylella fastidiosa</i> M12	2,018	175	8.67%
Gammaproteobacteria	Xanthomonadales	<i>Xylella fastidiosa</i> Temecula1	1,951	146	7.48%
unclassified Proteobacteria	Magnetococcus	<i>Magnetococcus</i> MC-1	2,232	1,280	57.35%