

group	organism	UUCGA	GGGGU	UUCGAA	CUUAUG	GCUAUG	CUUAGU	GUUAGC	ACUAUG	CUUAGC	UUCGCG	GGGCUU	GGGCAU	GGAACA	GACAGC	CUUUCU	UUUUUA	GUUUCU	AAAAUA	AGAAAA	CUUUCA	biased codon pairs in full genome (%)	biased codon pairs in st. genome (%)	genome size (Mb)
mollicutes	Mycoplasma pneumoniae																					26.2	16.8	0.82
	Mycoplasma penetrans																					13.0	5.3	1.36
	Mycoplasma capricolum																					9.7	4.8	1.01
	Mycoplasma hyopneumoniae																					17.4	9.7	0.92
fusobacteria	Fusobacterium nucleatum																					18.5	6.0	2.17
cyanobacteria	Synechococcus CC9605																					39.9	13.2	2.51
	Synechococcus CC9311																					37.2	10.2	2.61
	Trichodesmium erythraeum																					46.2	8.9	7.80
	Anabaena variabilis																					54.5	12.2	7.07
	Thermosynechococcus elongatus																					50.0	19.0	2.59
bacteroides/ chloroflexi	Bacteroides fragilis																					52.9	9.2	5.31
	Bacteroides thetaiotaomicron																					57.0	9.5	6.33
	Dehalococcoides ethenogens																					43.4	23.7	1.47
chlamydiae	Chlamydia trachomatis																					15.2	6.9	1.04
actinobacteria	Bifidobacterium longum																					32.5	10.8	2.26
	Leifsonia xyli subsp.xyli																					22.7	7.0	2.58
	Rhodococcus sp. RHA1																					53.1	11.8	9.67
	Corynebacterium jeikeium																					24.6	5.8	2.48
	Corynebacterium glutamicum																					38.4	8.7	3.30
	Frankia alni																					43.7	8.7	7.50
planctomycetes	Rhodopirellula baltica																					60.2	14.5	7.10
thermus- deinococcus	Thermus thermophilus HB8																					31.8	15.9	2.07
	Thermus thermophilus H27																					31.9	15.5	2.13
aquificae	Aquifex aeolicus																					37.5	17.3	1.59
thermotogae	Thermotoga maritima																					38.0	15.2	1.86
acidobacteria	Acidobacteria bacterium																					46.1	8.7	5.65
spirochaetes	Leptospira interrogans																					51.0	13.2	4.69
δ-proteobacteria	Syntrophus aciditrophicus SB																					46.5	9.9	3.20
ε-proteobacteria	Campylobacter jejuni Jejuni																					33.2	14.1	1.64
	Campylobacter jejuni RM1221																					33.5	14.4	1.80
	Helicobacter hepaticus																					43.7	19.0	1.80
	Helicobacter pylori																					51.2	27.7	1.67
γ-proteobacteria	Francisella tularensis																					21.0	6.6	1.90
	Xanthomonas campestris																					50.7	14.5	5.42
	Xantomonas oryzae																					52.3	15.2	4.94
	Dechloromonas aromatica																					50.2	12.6	4.50
β-proteobacteria	Rhodoferax ferrireducens																					50.5	13.1	4.97
γ-proteobacteria	Chromobacterium violaceum																					50.6	12.4	4.80
	Burkholderia xenovorans																					60.0	13.3	9.77
	Burkholderia pseudomallei 1710b																					63.9	18.0	7.31
	Burkholderia pseudomallei K96243																					53.6	16.0	7.30
	Burkholderia thailandensis																					54.6	15.9	6.72
	Burkholderia sp. 383																					58.5	15.3	8.68
	Legionella pneumophila str. Lens																					33.7	5.4	3.41
	Legionella pneumophila str. Paris																					34.3	4.7	3.64
	Methylococcus capsulatus																					40.4	10.2	3.30
	Hahella chejuensis																					56.2	11.4	7.22
	Pseudomonas putida																					51.3	12.7	6.18
	Pseudomonas syringae pv.Tomato																					55.4	13.2	6.54
	Pseudomonas syringae pv.Syringae																					54.8	13.3	6.09
	Psychrobacter arcticus																					42.9	16.0	2.65
	Chromohalobacter salexigens																					46.2	13.6	3.70
	Haemophilus ducrey																					24.0	8.2	1.70
	Haemophilus influenzae																					29.6	8.7	1.91
	Buchnera aphidicola																					2.0	1.7	0.64
	Candidatus blochmannia																					2.3	1.5	0.79
	Sodalis glossinidius																					37.1	12.3	4.29
	Yersinia pestis Nepal516																					49.6	10.9	4.61
	Yersinia pestis CO92																					49.9	9.9	4.88
	Salmonella enterica																					52.7	14.5	4.59
	Escherichia coli																					53.6	13.3	4.64
	Shigella sonnei																					54.7	15.2	5.06
	Shigella flexneri 2a str. 301																					53.5	13.9	4.83
	Shigella flexneri 2a str. 2457T																					52.7	13.0	4.60
	Idiomarina loihiensis																					41.4	10.3	2.84
	Pseudoalteromonas haloplanktis																					47.7	13.9	3.85
	Vibrio fisheri																					40.7	8.2	4.28
	Vibrio vulnificus																					50.4	11.0	5.26