

Supplementary Materials to
Non-essential ribosomal proteins in bacteria and archaea identified using
COGs

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Supplementary Figures

Figure S1. Organization of the *spc* operon in bacteria with tiny genomes.

Supplementary Tables

Table S1. Core bacterial and archaeal ribosomal proteins. The table shows the RP gene names, corresponding entries in the COG and Pfam (1) databases, their universal nomenclature from Ban *et al.*, 2014 (2), phylogenetic distribution, and the UniProt (3) accession numbers in *Escherichia coli*, *Bacillus subtilis*, *Mycoplasma pneumoniae*, *Aeropyrum pernix*, *Haloarcula marismortui* and *Saccharomyces cerevisiae*.

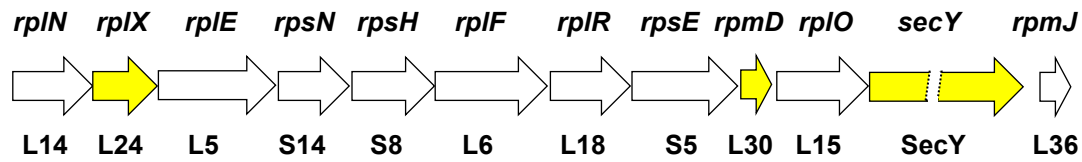
Table S2. Frameshifted ribosomal proteins in the genomes covered by the COG database

Table S3. Unannotated ORFs coding for ribosomal proteins in the genomes covered by the COG database

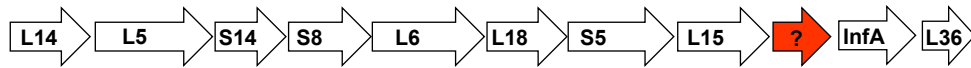
Table S4. Experimental data on large-scale inactivation of ribosomal proteins

Table S5. Loss of ribosomal proteins that differ in their rRNA interactions and the order of assembly

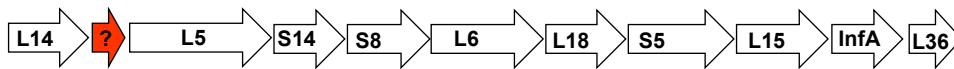
Escherichia coli



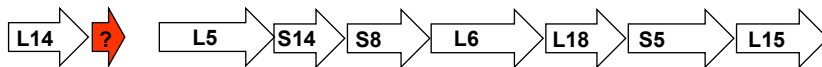
Ca. Nasuia deltocephalinicola



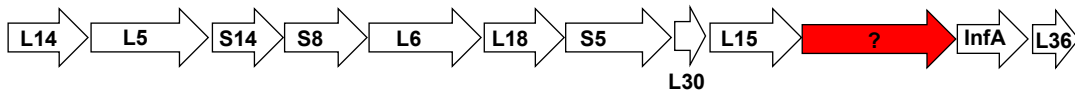
***Ca. Vidania fulgoroideae* OLIH**



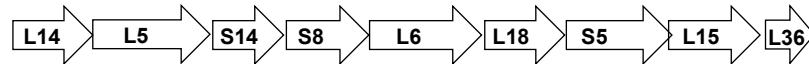
***Ca. Hodgkinia cicadicola* Dsem**



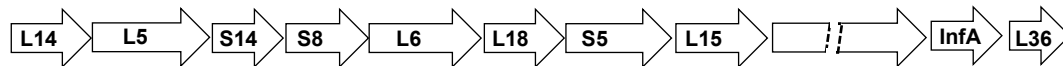
***Ca. Tremblaya phenacola* PAVE**



***Ca. Carsonella ruddii* DC**



***Ca. Sulcia muelleri* PUNC**



***Ca. Zinderia insecticola* CARI**

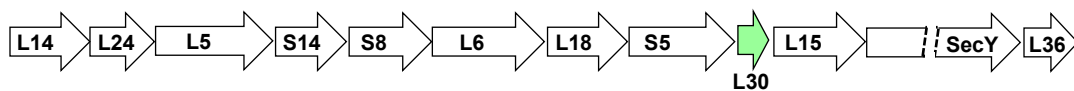


Figure S1. Organization of the *spc* operon in bacteria with tiny genomes.

The top row shows the *spc* operon organization in *E. coli* (4), which is widely conserved among various bacteria and archaea (5). The *rplX*, *rpmD* and *secY* genes, which are lost in some of the tiny genomes, are indicated by yellow shading. The *secY* gene, coding for a ~440-aa protein, is not drawn to scale. Red arrows indicate ORFs with no discernible similarity to any known proteins, the diverged but recognizable *rpmD* gene of “*Ca. Zinderia insecticola*” is shown in green.

Table S1. Core bacterial and archaeal ribosomal proteins, their gene names, corresponding entries in the COG and Pfam databases, their universal nomenclature, phylogenetic distribution, and the UniProt entries in *Escherichia coli*, *Bacillus subtilis*, *Mycoplasma pneumoniae*, *Aeropyrum pernix*, *Haloarcula marismortui* and *Saccharomyces cerevisiae*^a.

Protein name	Gene name	COG number ^b	Pfam entry ^b	Ban, 2014 ^c name	Distribution ^d		UniProt accession number ^e				
					Ban, 2014 ^d	COG	<i>E. coli</i>	<i>Bacillus subtilis</i>	<i>Haloarcula</i>	<i>Aeropyrum</i>	Yeast
50S subunit											
L1	<i>rplA</i>	COG0081	PF00687	uL1	BAE	A+B	P0A7L0	Q06797	P12738	Q9Y9W6	POCX44
L2	<i>rplB</i>	COG0090	PF00181+ PF03947	uL2	BAE	A+B	P60422	P42919	P20276	Q9YFN1	POCX45
L3	<i>rplC</i>	COG0087	PF00297	uL3	BAE	A+B	P60438	P42920	P20279	Q9YFM2	P14126
L4	<i>rplD</i>	COG0088	PF00573	uL4	BAE	A+B	P60723	P42921	P12735	Q9YFM1	P10664
L5	<i>rplE</i>	COG0094	PF00281	uL5	BAE	A+B	P62399	P12877	P14124	Q9YF87	POCOW9
L6	<i>rplF</i>	COG0097	PF00347	uL6	BAE	A+B	P0AG55	P46898	P14135	Q9YF91	P05738
L9	<i>rplI</i>	COG0359	PF03948	bL9	B	B	P0A7R1	P37437	–	–	–
L10	<i>rplJ</i>	COG0244	PF00466	uL10	BAE	A+B	P0A7J3	P42923	P15825	Q9Y9W8	P05317
L11	<i>rplK</i>	COG0080	PF03946+ PF00298	uL11	BAE	A+B	P0A7J7	Q06796	P14122	Q9Y9W5	POCX53
L7/L12	<i>rplL</i>	COG0222	PF16320+ PF00542	bL12	B	B	P0A7K2	P02394	–	–	–
L13	<i>rplM</i>	COG0102	PF00572	uL13	BAE	A+B	P0AA10	P70974	P29198	Q9YB50	P26784
L14	<i>rplN</i>	COG0093	PF00238	uL14	BAE	A+B	P0ADY3	P12875	P22450	Q9YF82	POCX41
L15	<i>rplO</i>	COG0200	PF00828	uL15	BAE	A+B	P02413	P19946	P12737	Q9YF98	P02406
L16/ L10AE	<i>rplP</i>	COG0197	PF00252	uL16	BAE	A+B	P0ADY7	P14577	P60617	Q9YF95	P41805
L17	<i>rplQ</i>	COG0203	PF01196	bL17	B	B	P0AG44	P20277	–	–	–
L18	<i>rplR</i>	COG0256	PF00861	uL18	BAE	A+B	P0C018	P46899	P14123	Q9YF94	P26321
L19	<i>rplS</i>	COG0335	PF01245	bL19	B	B	P0A7K6	O31742	–	–	–
L20	<i>rplT</i>	COG0292	PF00453	bL20	B	B	P0A7L3	P55873	–	–	–
L21	<i>rplU</i>	COG0261	PF00829	bL21	B	B	P0AG48	P26908	–	–	–
L22	<i>rplV</i>	COG0091	PF00237	uL22	BAE	A+B	P61175	P42060	P10970	Q9YF76	P05740
L23	<i>rplW</i>	COG0089	PF00276	uL23	BAE	A+B	P0ADZ0	P42924	P12732	Q9YFM0	P04456
L24	<i>rplX</i>	COG0198	PF00467	uL24	BAE	A+B	P60624	P0CI78	P10972	Q9YF83	P05743

L25	<i>rplY</i>	COG1825	PF01386	bL25	B	B	P68919	AOA6M3Z BP3	–	–	–
L27	<i>rpmA</i>	COG0211	PF01016	bL27	B	B	P0A7L8	P05657	–	–	–
L28	<i>rpmB</i>	COG0227	PF00830	bL28	B	B	P0A7M2	P37807	–	–	–
L29	<i>rpmC</i>	COG0255	PF00831	uL29	BAE	A+B	P0A7M6	P12873	P10971	P58085	P0CX84
L30/L7E	<i>rpmD</i>	COG1841	PF00327	uL30	BAE	A+B	P0AG51	P19947	P14121	Q9YF96	P05737
L31	<i>rpmE</i>	COG0254	PF01197	bL31	B	B	P0A7M9	Q03223	–	–	–
L32	<i>rpmF</i>	COG0333	PF01783	bL32	B	B	P0A7N4	O34687	–	–	–
L33	<i>rpmG</i>	COG0267	PF00471	bL33	B	B	P0A7N9	P56849	–	–	–
L34	<i>rpmH</i>	COG0230	PF00468	bL34	B	B	P0A7P5	P05647	–	–	–
L35	<i>rpmI</i>	COG0291	PF01632	bL35	B	B	P0A7Q1	P55874	–	–	–
L36	<i>rpmJ</i>	COG0257	PF00444	bL36	B	B	P0A7Q6	P20278	–	–	–
30S subunit											
S1	<i>rpsA</i>	COG0539	PF00575	bS1	B	B	P0AG67	P38494	–	–	–
S2	<i>rpsB</i>	COG0052	PF00318	uS2	BAE	A+B	P0A7V0	P21464	P29202	Q9YB45	P32905
S3	<i>rpsC</i>	COG0092	PF07650+ PF00189	uS3	BAE	A+B	P0A7V3	P21465	P20281	Q9YF78	P05750
S4	<i>rpsD</i>	COG0522	PF00163+ PF01479	uS4	BAE	A+B	P0A7V8	P21466	Q00862	Q9YB58	O13516
S5	<i>rpsE</i>	COG0098	PF00333+ PF03719	uS5	BAE	A+B	P0A7W1	P21467	P26815	Q9YF95	P25443
S6	<i>rpsF</i>	COG0360	PF01250	bS6	B	B	P02358	P21468	–	–	–
S7	<i>rpsG</i>	COG0049	PF00177	uS7	BAE	A+B	P02359	P21469	P32552	Q9YAU8	P26783
S8	<i>rpsH</i>	COG0096	PF00410	uS8	BAE	A+B	P0A7W7	P12879	P12742	Q9YF89	P0C0W1
S9	<i>rpsI</i>	COG0103	PF00380	uS9	BAE	A+B	P0A7X3	P21470	P05763	Q9YB48	P0CX51
S10	<i>rpsJ</i>	COG0051	PF00338	uS10	BAE	A+B	P0A7R5	P21471	P23357	Q9YAV2	P38701
S11	<i>rpsK</i>	COG0100	PF00411	uS11	BAE	A+B	P0A7R9	P04969	P10788	Q9YB55	P06367
S12	<i>rpsL</i>	COG0048	PF00164	uS12	BAE	A+B	P0A7S3	P21472	Q5UZR8	Q9YAU5	P0CX29
S13	<i>rpsM</i>	COG0099	PF00416	uS13	BAE	A+B	P0A7S9	P20282	Q00861	Q9YB60	P0CX55
S14	<i>rpsN</i>	COG0199	PF00253	uS14	BAE	A+B	P0AG59	P12878	P26816	P58731	P41057
S15	<i>rpsO</i>	COG0184	PF00312	uS15	BAE	A+B	P0ADZ4	P21473	P05762	Q9YCX3	P05756
S16	<i>rpsP</i>	COG0228	PF00886	bS16	B	B	P0A7T3	P21474	–	–	–
S17	<i>rpsQ</i>	COG0186	PF00366	uS17	BAE	A+B	P0AG63	P12874	P12741	Q9YF81	P0CX47
S18	<i>rpsR</i>	COG0238	PF01084	bS18	B	B	P0A7T7	P21475	–	–	–

S19	<i>rpsS</i>	COG0185	PF00203	uS19	BAE	A+B	P0A7U3	P21476	P20284	Q9YF74	Q01855
S20	<i>rpsT</i>	COG0268	PF01649	bS20	B	B	P0A7U7	P21477	–	–	–
S21	<i>rpsU</i>	COG0828	PF01165	bS21	B	B	P68681	P21478	–	–	–
Archaeal ribosomal proteins											
L7Ae	Rpl7Ae	COG1358	PF01248	eL8	AE	A+B	–	P46350	P12743	Q9YAX7	P48589
L12E/ L44/L45 /RPP1/ RPP2	RPP1A	COG2058	PF00428	P1/P2	AE	A	–	–	P15772	Q9Y9W9	P05318
L13E	RPL13	COG4352	PF01294	eL13	AE	A	–	–	P29198	Q9YEN9	P40212
L14E/L6 E/L27E	RPL14A	COG2163	PF01777	eL14	AE	A	–	–	–	Q9YDD7	POC2H6
L15E	RPL15A	COG1632	PF00827	eL15	AE	A	–	–	P60618	Q9YBZ8	P05748
L18E	RPL18A	COG1727	PF17135	eL18	AE	A	–	–	P12733	Q9YB51	POCX49
L19E	RPL19A	COG2147	PF01280	eL19	AE	A	–	–	P14119	Q9YF93	POCX82
L20A (L18A, LX)	RPL20A RPL18ae RplX	COG2157	PF01775	eL20	E	A	–	–	P14125	P58289	POCX23
L21E	RPL21A	COG2139	PF01157	eL21	AE	A	–	–	P12734	P58077	Q02753
L24E	RPL24A	COG2075	PF01246	eL24	AE	A	–	–	P14116	Q9Y9A7	P04449
L30E	RPL30E	COG1911	PF01248	eL30	AE	A	–	–	–	Q9YAX7	P14120
L31E	RPL31A	COG2097	PF01198	eL31	AE	A	–	–	P18138	Q9YD25	POC2H8
L32E	Rpl32e	COG1717	PF01655	eL32	AE	A	–	–	P12736	Q9YF92	P38061
L34E	RPL34A	COG2174	PF01199	eL34	AE	A	–	–	–	P58026	P87262
L35AE/ L33A	Rpl35A	COG2451	PF01247	eL33	AE	A	–	–	–	Q9Y9G4	P05744
L37E	RPL37A	COG2126	PF01907	eL37	AE	A	–	–	P32410	Q9YEQ4	P49166
L39E	RPL39	COG2167	PF00832	eL39	AE	A	–	–	P22452	P59472	P04650
L40E	RPL40A	COG1552	PF01020	eL40	AE	A	–	–	Q5UYU5	Q9YFY7	POCH08
L44E	RPL42A	COG1631	PF00935	eL42	AE	A	–	–	P32411	Q9YF00	POCX27
L37AE/ L43A	RPL43A	COG1997	PF01780	eL43	AE	A	–	–	P60619	Q9YC06	POCX25
S3AE	RPS3A	COG1890	PF01015	eS1	AE	A	–	–	Q5V296	Q9YCV8	P33442

S4E	RPS4A	COG1471	PF00900+ PF16121	eS4	AE	A	–	–	P22510	Q9YF85	POCX35
S6E (S10)	RPS6A	COG2125	PF01092	eS6	AE	A	–	–	P21509	Q9Y9B6	POCX37
S8E	RPS8A	COG2007	PF01201	eS8	AE	A	–	–	P49402	Q9YDY0	POCX39
S17E	RPS17A	COG1383	PF00833	eS17	AE	A	–	–	Q5V5R5	Q9YA67	P02407
S19E (S16A)	RPS19A	COG2238	PF01090	eS19	AE	A	–	–	P19952	Q9YD22	P07280
S24E	RPS24A	COG2004	PF01282	eS24	AE	A	–	–	P19953	Q9YCY0	POCX31
S25e	RPS25	COG4901	PF03297	eS25	AE	A	–	–	–	Q9Y914	Q3E792
S26e	RPS26B	COG4830	PF01283	eS26	E	A	–	–	–	Q05DX2	P39938
S27AE	RPS27ae	COG1998	PF01599	eS31	AE	A	–	–	Q06125	P61297	P05759
S27E	RPS27A	COG2051	PF01667	eS27	AE	A	–	–	Q5UX21	Q9YF01	P35997
S28E/ S33	RPS28A	COG2053	PF01200	eS28	AE	A	–	–	A0A4P8 K2X9	Q9Y9A6	Q3E7X9
S30	RPS30	COG4919	PF04758	eS30	AE	A	–	–	–	Q9Y9T9	POCX33

^a – A more detailed version of this table with UniProt names and the RP lists of the archaeon *Sulfolobus acidocaldarius*, chloroplast-encoded RPs in *Euglena gracilis*, and the chloroplast- and mitochondria-encoded RPs of the green alga *Chara vulgaris* is available in Excel format as Supplementary Table S6.

^b – These COG and Pfam numbers can be used to view the respective database entries, e.g., for L1 protein, as <https://www.ncbi.nlm.nih.gov/research/cog/cog/COG0081/> and <http://pfam.xfam.org/family/PF00687>.

^c – Ribosomal protein names in the universal nomenclature of Ban *et al.*, 2014 (2).

^d – Presence of the respective proteins in bacteria (B), archaea (A) and eukaryotes (E) according to Ban *et al.* (2014) and in COGs. Discrepancies between the two are highlighted in yellow.

^e – These accession numbers can be used to view the respective protein entries in the NCBI protein database and in UniProt, e.g. for L1 protein, as <https://www.ncbi.nlm.nih.gov/protein/P0A7L0> and <https://www.uniprot.org/uniprot/P0A7L0> (*E. coli*), <https://www.ncbi.nlm.nih.gov/protein/Q06797> and <https://www.uniprot.org/uniprot/Q06797> (*B. subtilis*), and so on.

Green shading indicates *E.coli* proteins with viable full-length deletion mutants in the Keio collection (6) and those *B. subtilis* proteins that are marked non-essential in SubtiWiki (7).

Table S2. Frameshifts and point mutations in ribosomal protein genes in the genomes covered by the COG database

Organism name, genome GenBank accession no.	Genome size, Mb	Taxonomy in COGs	Protein	COG	Frame 1 boundaries, protein ID (if available)	Frame 2 boundaries, protein ID (if available)
<i>Actinobaculum</i> sp. 313, CP029033.1	2.77	Actino-bacteria	L2	COG0090	Frame +1: 857650..858100	Frame +3: 858099..858464
			L14	COG0093	Frame +2: 861053..861328	Frame +1: 861334..861417
<i>Advenella kashmirensis</i> WT001, AFK64574.1	4.42	Beta	L1	COG0081	Frame -2: 4318292..4318771	Frame -1: 4318095..4318293
			L6	COG0097	Frame -2: 4158914..4159123	Frame -1: 4158609..4158920
			L21	COG0261	Frame -2: 1061612..1061875	Frame -1: 1061574..1061615
			S6	COG0360	Frame -1: 2704266..2704538	Frame -3: 2704189..2704242
<i>Anaerotignum propionicum</i> DSM 1682, CP014223.1	3.12	Clostridia	S4	COG0522	Frame +2: 585926..586072	Frame +1: 586075..586461
<i>Atlantibacter hermannii</i> NCTC12129, LR134136.1	4.55	Gamma	L23	COG0089	Frame +1: 428506..428781; VDZ71398.1	Frame +3: 428748..428789
			S9	COG0103	Frame +1: 504925..504996	Frame +2: 504992..505315
<i>Azorhizobium caulinodans</i> ORS 571, AP009384.1	5.37	Alpha	L9	COG0359	Frame -3: 4895567..4895716; BAF90303.1	Frame -2: 4895154..4895636; BAF90302.1
<i>Breoghania</i> sp. L-A4, CP031841.1	5.03	Alpha	S5	COG0098	Frame +1: 3228187..3228483	Frame -3: 3227942..3228184
<i>Brucella melitensis</i> str. 16M AE008917.1, AE008917.1	3.29	Alpha	L27	COG0211	Frame -2: 209218..209487, wrong translation start in AAL51384.1	
" <i>Ca. Atelocyanobacterium thalassa</i> " isolate ALOHA, CP001842.1	1.44	Cyano-bacteria	S17	COG0186	Frame +3: 1181154..1181309	Frame +1: 1181314..1181391
" <i>Ca. Methanomethylophilus alvus</i> " Mx-05, CP017686.1	1.67	Eury-archaeota	S14	COG0199	Frame -3: 1401381 to 1401527, no N-terminal fragment	
" <i>Ca. Nanopusillus acidilobi</i> ", CP010514.1	0.61	Other archaea	S14	COG0199	Frame -3: 604224..604298	Frame -1: 604160..604207
" <i>Ca. Tenderia electrophaga</i> " CP013099	3.76	Gamma	S19	COG0185	Frame +3: 877839..879123, 94 aa, no start codon	
" <i>Ca. Uzinura diaspidicola</i> " ASNER, CP003263.1	0.26	Bacteroidetes	L21	COG0261	Frame +1: 100210..100434	Frame +3: 100422..100508

<i>Desulfotalea psychrophila</i> LSv54, CR522870.1	3.66	Delta	L6	COG0097	Frame +2; 1279586..1279756, CAG35868.1	Frame +2: 1279755..1280131, CAG35869.1
			S8	COG0096	Frame +3: 1279164..1279361	Frame +2: 1279352..1279561
<i>Enterococcus faecalis</i> V583, AE016830.1	3.36	Bacilli	L13	COG0102	Frame -3: 3100862..3100966	Frame -1: 3100543..3100860
<i>Faecalibacterium prausnitzii</i> A2165, CP022479.1	3.11	Clostridia	L22	COG0091	Frame +1: 2112610..2112750	Frame +3: 2112726..2112941
<i>Fronohabitan</i> sp. PAMC 28766, CP014513.1	4.77	Actino- bacteria	L7/L12	COG0222	Frame -3: 3920472..3920576	Frame -2: 3920254..3920415
			S8	COG0096	Frame +3: 1279164..1279361	Frame +2: 1279352..1279561
<i>Gottschalkia acidurici</i> 9a, CP003326.1	3.11	Tissierellia	L9	COG0359	Frame -2: 3004298..3004453,	Frame -1: 3004155..3004271
<i>Ketogulonicigenium vulgare</i> Y25, CP002224.1	3.29	Alpha	S18	COG0238	Frame -3: 1093683..1093817	Frame -1: 1093583..1093654
<i>Lactobacillus acidophilus</i> NCFM, CP000033.3	1.99	Bacilli	S19	COG0185	Frame +3: 293403..293528	Frame +1: 293482..293685
<i>Laribacter hongkongensis</i> HLHK9, CP001154.1	3.17	Beta	S9	COG0103	Frame -2: 2660379..2660627	Frame -3: 2660237..2660416
<i>Massilia putida</i> 6NM-7T, CP019038.1	7.52	Beta	L11	COG0080	Frame +3: 4335990..4336055	Frame +2: 4336052..4336417
<i>Melioribacter roseus</i> P3M-2, CP003557.1	3.3	Other bacteria	S4	COG0522	Frame -1: 232066..232254	Frame -3: 231632..232075
<i>Methylomusa anaerophila</i> MMFC1, AP018449.1	4.78	Negati- vicutes	L35	COG0291	Frame +1: 3868123..3868230, BBB92833.1	Frame +2: 386226.. 3868318
Onion yellows phytoplasma OY-M, AP006628.2	0.85	Mollicutes	L3	COG0087	Frame +1: 243267..243902, BAD04285.1 Lost start codon results in 65 N-terminal aa missing	
			L24	COG0198	Frame +3: 248499..248693	Frame +1: 248680..248838
			S4	COG0522	Frame -3: 658421..658540; BAD04671.1	Frame +2: 657948..658430
<i>Paenalcaligenes hominis</i> 15S00501, CP019697.1	2.69	Beta	L2	COG0090	Frame -1: 1598924..1599670	Frame -3: 1598847..1598924
			L3	COG0087	Frame -3: 1601258..1600791	Frame -2: 1600585.. 1600788
<i>Parabacteroides distasonis</i> ATCC 8503, CP000140.1	4.81	Bactero- idetes	S4	COG0522	Frame -3: 2777237..2777734	Frame -2: 2777133..2777264
<i>Parachlamydia acanthamo- ebae</i> UV-7, FR872580.1	3.07	Chlamy- diae	S15	COG0184	Frame -1: 1022709..1022873	Frame -2: 1022606..1022704

<i>Paraglaciecola psychrophila</i> 170, CP003837.1	5.41	Gamma	L2	COG0090	Frame -3: 4969102..4969206	Frame -2: 4968386..4969063, AGH47270.1
			L31	COG0254	Frame +2: 218429..218527	Frame +1: 218527..218619, AGH42341.1
<i>Plesiomonas shigelloides</i> MS-17-188, CP027852.1	3.97	Gamma	S8	COG0096	Frame -2: 2081499..208159	Frame -1: 2081212..2081493
<i>Providencia stuartii</i> MRSN 2154	4.4	Gamma	L7/L12	COG0222	Frame -2: 1846220.. 1846558, AFH93584.1	Frame -3: 1846193.. 1846227
<i>Rodentibacter pneumotropicus</i> NCTC8284, LR134405.1	2.44	Gamma	L7/L12	COG0222	Frame +3: 225381..225467	Frame +2: 225530..225745
			S16	COG0228	Frame -3: 2228925..2228972	Frame -2: 2228728..2228937
			S20	COG0268	Frame +3: 2158104..2158226	Frame +1: 2158279..2158371
			L27	COG0211	Frame +1: 575761..576006, no start codon, point mutation	
<i>Salinicola tamaricis</i> F01, CP023559.1	4.28	Gamma	L6P	COG0097	Frame -2: 1172703..1172332	Frame -1: 1172314..1172180
			L7/L12	COG0222	Frame -3: 1193430..1193516	Frame -2: 1193182..1193373 Frame -1: 1193153..1193194
			L9	COG0359	Frame -1: 742979..743326	Frame -3: 742917..742979
			L25	COG1825	Frame -1: 3431492..3431671	Frame -3: 3431097..3431501
			S4	COG0522	Frame -3: 1167843..1168277	Frame -2: 1167665..1167730
<i>Simkania negevensis</i> Z, FR872582.1	2.63	Chlamydiae	L31	COG0254	Frame +1: 787441..787494	Frame +2: 787496..787678, CCB88630.1
<i>Sulfodiococcus acidiphilus</i> HS-1, AP018553.1	2.35	Crenarchaeota	L2	COG0090	Frame +1: 267295..267639, BBD71897.1	Frame: +3: 267636..268019, BBD71898.1
<i>Sulfuricella denitrificans</i> skB26, AP013066.1	3.22	Beta	L9	COG0359	Frame -2: 1812117..1812246, BAN35601.1	Frame -1: 1811804..1812166, BAN35600.1
<i>Syntrophus aciditrophicus</i> SB CP000252.1,	3.18	Delta	S12	COG0048	Frame +2: 311162..311347	Frame +3: 311373..311525
<i>Thioalkalivibrio nitratireducens</i> DSM 14787, CP003989.2	4.00	Gamma	L36	COG0257	Frame -2: 2648149..2648093	Frame -3: 2648085..2648038
<i>Thioclava nitratireducens</i> 25B10_4, CP019437.1	4.24	Alpha	S16	COG0228	Frame -3: 611211..611582, 123 aa, no start codon	
<i>Xanthobacter autotrophicus</i> Py2, CP000781.1	5.63	Alpha	L14	COG0093	Frame +1: 1902232..1902666, ABS66934.1	Frame +2: 5308729..5308830 (not adjacent)

Table S3. Examples of unannotated ORFs coding for ribosomal proteins in the genomes covered by the COG database

Organism name, GenBank accession no.	Genome size, Mb	Taxonomy in COGs	Ribosomal protein	COG no.	Newly translated ORF; locus tag, if available
BACTERIA					
<i>Sulfobacillus acidophilus</i> TPY, CP002901.1	3.55	Clostridia	L27	COG0211	ORF: 607200..607481 Frame: +3; 93 aa
			L28	COG0227	ORF: 1069175..1069366, Frame: -1; 63 aa
			L32	COG0333	ORF: 1133208..1133387, Frame: +3; 58 aa
			L33	COG0267	ORF: 306096..306302, Frame: +3; 68 aa
			L36	COG0257	ORF: 343563..343673, Frame: = +3; 37 aa
			S14	COG0199	ORF: 337812..337997, Frame: +3 ; 61 aa
<i>Pelotomaculum thermopropionicum</i> SI, AP009389.1	3.03	Clostridia	L28	COG0227	ORF: 1841595..1841786, Frame: +3; 63 aa
			L32	COG0333	ORF: 1830440..1830619, Frame: -1; 59 aa
			L34	COG0230	ORF: 3024909..3025082, Frame: -3; 57 aa
			S14	COG0199	ORF: 335426..335614, Frame: +2; 62 aa
			S21	COG0828	ORF: 901026..901331, Frame: +3; 101 aa
<i>Herpetosiphon aurantiacus</i> DSM 785, CP000875.1	6.79	Chloroflexi	L28	COG0227	ORF: 438793..438975, Frame: +1; 60 aa
			L29	COG0255	ORF: 6258620.. 6258832, Frame: +2; 70 aa
			L35	COG0291	ORF: 5927538..5927750, Frame: -2; 70 aa
			L36	COG0257	ORF: 6266198..6266311, Frame: +2; 38 aa
"Ca. Methylomirabilis oxyfera", FP565575.1	2.75	Other bacteria	L28	COG0227	ORF: 1181939..1182139, Frame: +2; 67 aa
			L33	COG0267	ORF:459805..459951, Frame: +1; 49 aa
			L34	COG0230	ORF: 2546125..2546259, Frame: +1; 44 aa
			L36	COG0257	ORF: 488708..488818, Frame: +2; 37 aa
			S13	COG0099	ORF: 488935..489300, Frame: +1, 124 aa
"Candidate division WWE3 bacterium RAAC2 WWE3 1", CP006914.1	0.88	Other bacteria	L34	COG0230	ORF: 795925..796083, Frame: -1; 52 aa
			L36	COG0257	ORF: 890953..890843, Frame: -2; 38 aa
			S14	COG0199	ORF: 73005..73229, Frame: +3; 74 aa
<i>Planktomarina temperata</i> RCA23, CP003984.1	3.29	Alphaproteo bacteria	L34	COG0230	ORF: 2522654..2522788, Frame: +2; 44 aa
			L36	COG0257	ORF: 3024835..3024960, Frame: = +1; 41 aa
"Ca. Paracaedimonas acanthamoebae", CP008936.1	2.18	Alphaproteo bacteria	L9	COG0359	ORF: 611520 to 611951, Frame: +3; 144 aa
			L32	COG0333	ORF: 164521..164676, Frame: -3; 59 aa
			L36	COG0257	ORF: 1218708..1218833, Frame: +3; 41 aa

<i>Rugosibacter aromatici-vorans</i> Ca6, CP010554.1	2.93	Betaproteobacteria	L36	COG0257	ORF: 2557159..2557269, Frame: -3; 37 aa
			S14	COG0199	ORF: 2561406..2561747, Frame: -1; 113 aa
"Candidatus Wolfebacteria bacterium GW2011 GWB1 47 1", CP011209.1	0.98	Other bacteria	L32	COG0333	ORF: 333695..333901, Frame: -3; 68 aa
			L34	COG0230	ORF: 178951..179097, Frame: -1; 48 aa
"Ca. Tenderia electrophaga" CP013099.1	3.76	Gammaproteobacteria	L36	COG0257	ORF: 885686..885796, Frame: +2; 37 aa
			L30/L7E	COG1841	ORF: 883593..883778, Frame: +3; 61 aa
<i>Hydrogenimonas</i> sp. MAG, AP019005.1	2.19	Epsilonproteobacteria	L36	COG0257	ORF: 2048969..2048859, Frame: -2; 37 aa
			S14	COG0199	ORF: 2053957..2054142, Frame: -1; 61 aa
<i>Paucimonas lemoignei</i> NCTC10937, LS483371.1	5.92	Betaproteobacteria	L36	COG0257	ORF: 5452130..5452246, Frame: -3; 38 aa
			S13	COG0099	ORF: 5451643..5451999, Frame: -1; 118 aa
			S12	COG0048	ORF: 5466930..5467298, Frame: -2; 123 aa
<i>Salinicola tamaricis</i> F01, CP023559.1	4.28	Gammaproteobacteria	L4	COG0088	ORF 1178149..1178727, Frame: -3; 192 aa
			S18	COG0238	ORF: 744224..744472, Frame: -1; 82 aa
"Ca. Tremblaya phenacola PAVE", CP003982.1	0.17	Betaproteobacteria	L28	COG0227	ORF: 59642..59827, Frame: -2; 62 aa (replaces AGO28266.1; locus tag=TPPAVE_073)
ARCHAEA					
<i>"Ca. Nanopusillus acidilobi"</i> , CP010514	0.61	Other archaea	L6P/L9E	COG0097	ORF: 501349..501882, Frame: -2; 177 aa; locus tag: Nps_02895
			L15e	COG1632	ORF: 250345..250866, Frame: +1; 173 aa; locus tag: Nps_01385
			L16/L10AE	COG0197	ORF 579086..579643, Frame: -1; 185 aa; locus tag: Nps_03305
			L22	COG0091	ORF: 586054..586629,(Frame: +1; 191 aa; locus_tag: Nps_03365
			L24	COG0198	ORF: 503210..50374, Frame: -1, 174 aa; locus_tag: Nps_02910
			S6e	COG2125	ORF: 329344..329733; Frame -2; 129 aa; locus tag: Nps_01880
			S15P/S13E	COG0184	ORF: 269039..269431, Frame: -1; 130 aa; locus tag: Nps_01520
			L35ae	COG2451	ORF: 558084..558428, Frame -3; 114 aa; locus tag: Nps_03205
			L37e	COG2126	ORF: 580869..581003, Frame -3; 54 aa

<i>Ca. Nitrosocosmicus oleophilus</i> , CP012850.1	3.43	Thaum-archaeota	L24e	COG2075	ORF: 865559..865771, Frame +2, 70 aa
<i>Nanoarchaeum equitans</i> Kin4-M, AE017199.1	0.49	Other archaea	L24e	COG2075	ORF: 297703..297867, Frame +1; 54 aa
			L37e	COG2126	ORF: 5537..5707, Frame: -1; 56 aa
"Nanohaloarchaea archaeon SG9", CP012986.1	1.12	Eury-archaeota	L18	COG0256	ORF: 47533..48027, Frame: -1; 169 aa; locus tag: AQV86_00305
			S2	COG0052	ORF: 413675..414298, Frame: -3; 207 aa; locus tag: AQV86_02305
			S28e	COG2053	ORF: 411826..411990, Frame: -1; 58 aa
			L24e	COG2075	ORF: 411666..411818, Frame +2, 50 aa
			L40e	COG1552	ORF: 708355..708516, Frame +1, 53 aa
<i>Thermofilum adornatus</i> , CP006646.1	1.75	Cren-archaeota	L34e	COG2174	ORF: 785414..785677, Frame -2, 87 aa

Table S4. Experimental data on large-scale inactivation of ribosomal protein-coding genes

Organism	Inactivated or deleted genes^a	Reference
<i>Acinetobacter baumannii</i>	L9, L19, L22, L27, L31, L32, L33, S1, S20	(8)
<i>Acinetobacter baylyi</i>	L9, L27, L31, L33, L36	(9)
<i>Agrobacterium fabrum</i>	L9, L11, L15, L31, L32, L33, S7, S12, S17, S19, S21	(10)
<i>Bacillus subtilis</i>	L11, L25, S1	(11)
	L1, L9, L11, L15, L22, L23, L25, L28, L29, L31, L32, L33, L34, L35, L36, S6, S20, S21	(12, 13)
	L1, L23, L34, L36, S6	(14)
<i>Bacteroides fragilis</i>	L9, L17, L19, L32, L34	(15)
<i>Bacteroides thetaiotaomicron</i>	L9, L19	(16)
<i>Brevundimonas subvibrioides</i>	L9, L30, L31, L35, S15, S16	(10)
<i>Burkholderia cenocepacia</i>	L9, L18, L19, L21, L25, L30, L36, S2, S13, S15, S17, S18, S21	(17, 18)
<i>Burkholderia thailandensis</i>	L1, L9, L21, L31, S2, S3, S15	(19)
<i>Campylobacter jejuni</i>	L9, L20, L25, L33, L35, S14	(20)
	L3, L9, L21, L33, S1, S2, S4, S5, S7, S17	(21)
	L9, L19, L20, L27, L31, S1, S4, S8, S15, S18	(22)
<i>Caulobacter crescentus</i>	L1, L10, L28, L29, L30, L31, L33, L35	(23)
<i>Escherichia coli</i>	L5, L9, L16, L22, S1, S3, S7	(24)
	L1, L9, L11, L25, L31, L32, L33, L35, L36, S6, S15, S20, S21	(6)
	S6, S9, S13, S15, S17, S20	(25)
	L15, L21, L24, L27, L29, L30, L34, S9, S17	(26)
	L1, L9, L31, L32, L33, S6, S9, S15, S18, S20 (L13, S1, S2, S4, S7, S12, S17, S18)	(27)
	L31, L36, S1, S15, S18	(28)
	L1, L9, L11, L25, L31, L32, L33, L35, L36, S6, S15, S20, S21	(29)
<i>Francisella novicida</i>	L9, L19, L33, S1, S21	(30)
<i>Francisella tularensis</i>	L1, S1	(31)
<i>Haemophilus influenzae</i>	L7, L9	(32)
<i>Helicobacter pylori</i>	L10, L18, L19, L33, S11, S13, S16	(33)
<i>Mycobacterium avium</i>	L7/L12, L9, L10, L19, L25, L28, L31, L32, L33, S6, S11, S14, S15, S17, S18	(34).
<i>Mycobacterium tuberculosis</i>	L1, L15, L28, L33, L36, S14, S16, S18	(35)
	L9, L15, L25, L28, L30, L33, S14, S16, S18	(36)
	L1, L5, L9, L22, L25, S1, S2	(37)
<i>Mycoplasma bovis</i>	L34	(38)
<i>Mycoplasma pulmonis</i>	L28, L33, S18	(39, 40)

<i>Neisseria gonorrhoeae</i>	L24, L27, L30, L31, L32, L33 , L36, S10, S21	(41)
<i>Porphyromonas gingivalis</i>	L9 , L17, L19, L31, L32 , L34, S1 , S16, S18, S21	(42)
<i>Providencia stuartii</i>	L19, L31, S1	(43)
<i>Pseudomonas aeruginosa</i>	L3, L4, L9, L19, L25, L32 , S3, S4, S5, S12	(44) as cited in (9)
	L2, L3, L4, L9, L19 , L21, L23, L25 , S4, S5, S6 , S8, S9, S12, S21	(45).
	L9 , L13, L17, L21, L25 , L27, L28, L31, L33 , L34, S1, S6 , S9, S10, S15, S18, S20	(46)
	L9, L25, L31, L32, L33 , S15	(47)
	L9, L25, L31, L32, L33 , S2, S21	(48)
<i>Pseudomonas protegens</i>	L9, L25, L31, L33 , L36	(49)
<i>Rhodopseudomonas palustris</i>	L9 , L21, L31, L33, S1 , S2, S16	(50)
<i>Rubrivivax gelatinosus</i>	L9, L25, L33	(51)
<i>Salmonella enterica</i>	L16	(52)
	L1, L9, L31, L32, L33 , L36, S20	(53)
	L1, L9, L10, L25, L31, L32, L33 , L36, S1 , S9, S15, S20, S21	(54)
<i>Shewanella oneidensis</i> MR-1	L19	(55)
<i>Staphylococcus aureus</i>	L6, S17	(56)
	L19, L25 , L27, L28, L33, S1 , S14	(57)
	L9, L33, S20	(58)
	L1, L9 , L11, L21, L23, L25, L28, L32, L33 , L34, S1, S20	(59)
<i>Streptococcus agalactiae</i>	L9, L28, S2, S6 , S14, S20	(60)
<i>Streptococcus mutans</i>	L9, L19, L28, L32, L33, L35, S1, S20, S21	(61)
<i>Streptococcus pyogenes</i>	L7/L12, L9 , L10, L15, L23, L28, L29, L32 , S14, S16, S20	(62)
<i>Streptococcus sanguinis</i>	L9 , L15, L21, L24, L28, L29 , L30, L31, L32, L33, L35 , L36, S9, S13, S15, S20, S21	(63)
<i>Streptococcus suis</i>	L9 , L10, L28, L32, L33, L35, S1 , S2, S12, S20	(64)
<i>Synechococcus elongatus</i>	L9 , L15, L28	(65)
<i>Vibrio cholerae</i>	L25, L31, L33	(66)
	L9, L31, L32	(67)
Candidate phyla radiation	L1, L9 , L30	(68)

^a – The proteins whose genes that could be inactivated in several distinct lineages are shown in bold. Those proteins for which the data varied between strains are shown in italics.

Table S5. Loss of ribosomal proteins that differ in their rRNA interactions and the order of assembly

50S subunit protein	Assembly order ^a	Missing in genomes ^b	30S subunit protein	Assembly order ^a	Missing in genomes ^b
L20	I	0	S4	I	0
L21	I	4	S6	I	2
L22	I	0	S8	I	0
L24	I	7	S15	I	2
L1	II	5	S16	I	1
L3	II	0	S17	I	0
L4	II	0	S18	I	0
L13	II	1	S20	I	5
L15	II	0	S5	II	0
L17	II	1	S7	II	1
L23	II	6	S11	II	0
L5	III	0	S12	II	1
L18	III	1	S9	III	1
L29	III	19	S10	III	0
L34	III	21	S13	III	0
L2	IV	0	S14	III	0
L14	IV	0	S19	III	0
L19	IV	4	S2	IV	1
L32	IV	13	S3	IV	0
L6	V	0	S21	IV	196
L9	V	14			
L11	V	1			
L28	V	1			
L33	V	6			
L7/L12	VI	1			
L10	VI	5			
L16	VI	0			
L25	VI	109			
L27	VI	2			
L30	VI	77			
L31	VI	5			
L35	VI	6			
L36	VI	2			

^a – Ribosome assembly order and cell coloring is according to Chen and Williamson, 2013 (69)

^b – Total number of genomes in COGs that are lacking the genes for respective proteins. L29 is mostly lost in tiny genomes (Table 1), absence of L25, L34, and S21 is mostly due to lineage-specific gene loss (Table 2).

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