

Supplementary information S8 (table) | Distribution of different types and subtypes of CRISPR-Cas in archaeal and bacterial phyla

	CAS-I-A	CAS-I-B	CAS-I-C	CAS-I-D	CAS-I-E	CAS-I-F	CAS-I-U	CAS-II-A	CAS-II-B	CAS-II-C	CAS-III-A	CAS-III-B	CAS-III-C	CAS-III-D	CAS-IV	CAS-V	part
A. Crenarchaeota	40.7	0	0	1	0	0	0	0	0	0	11	25.5	0	6.9	0	0	45.6
A. Euryarchaeota	9.2	72.1	5.4	18.5	12.4	0	2.7	0	0	0	22.2	4.6	7.7	3.2	0	4.3	21.8
A. Nanoarchaeota	0	6.8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
A. Thaumarchaeota	0	4.2	0	0	0	0	0	0	0	0	0	0	0	5.9	0	0	8.8
A. unclassified	0	0	0	2.3	0	0	0	0	0	0	0	0	0	0	0	0	0
B. Actinobacteria	0	1.4	7.8	0	44.8	0	3.5	8.6	0	2.7	1.2	0	0	9.2	7.2	0	22.2
B. Aquificae	0	9.1	0	0	0	0	0	0	0	0	4.2	0	2.8	0	0	0	3.3
B. Bacteroidetes/Chlorobi	0	22.4	12.9	0	5.8	0	0	0	0	25.1	12.9	11.7	2.3	4	0	0	26.4
B. Caldiseica	0	4.9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
B. Chlamydiae/Verrucomicrobia	0	0	0	0	0	0	0	0	0	4.8	0	0	0	5.3	0	0	5.3
B. Chloroflexi	4.4	12.5	6.6	6.7	8.8	0	0	0	0	0	15.1	12.8	5.5	11.3	0	0	9
B. Chrysiogenetes	0	0	0	0	0	3.7	0	0	0	0	3.7	0	0	0	0	0	0
B. Cyanobacteria	0.8	14.6	6.3	24	3.5	0	3.3	0	0	0	4	31.5	1	22.5	0	0	25.9
B. Deferribacteres	0	9.3	0	0	0	0	0	0	0	0	2.9	3.1	0	0	0	0	6
B. Deinococcus-Thermus	2	1	3.2	0	16	0	0.4	0	0	0	6.5	6.4	0	0	0	0	10.2
B. Dictyoglomi	0	3.5	0	0	0	0	0	0	0	0	1.7	0	0	0	0	0	0
B. Elusimicrobia	0	0	0	0	0	0	0	0	0	9.9	0	0	0	0	0	0	0
B. Fibrobacteres/Acidobacteria	0	4.4	3.8	0	0	0	13.3	0	0	5.7	3.4	8.9	0	0	0	0	5.7
B. Firmicutes	8.1	84.7	66.7	7.6	19.8	3.4	7.8	49.9	0	7.8	21.9	12.9	10.1	16.8	4.3	1.7	28.2
B. Fusobacteria	0	3.9	0	0	0	0	0	0.4	0	4.9	0	0	0	1.6	0	0	1.6
B. Nitrospirae	0	3.7	0	0	4.5	0	0	0	0	0	7.3	0	3.7	0	0	0	0
B. Planctomycetes	0	2.6	13	0	0	0	12.7	0	0	0	0	3.2	0	4.6	3.6	0	7
B. Proteobacteria	0	41.8	90.4	1	83.3	66.6	22.3	12.9	3.7	42.3	18.1	34	0	16.6	6.4	1.6	50.2
B. Spirochaetes	0	8.4	9.5	1.6	4.9	5.3	0	1.9	0	3.6	4.7	1.9	0	0	2.3	0	3
B. Synergistetes	0	6.7	0	0	0	0	0	0	0	0	0	2.2	0	0	0	0	10.1
B. Thermodesulfobacteria	0	0	0	0	0	0	0	0	0	0	2.7	2.4	0	0	0	0	2.7
B. Thermotogae	0	15.9	0	0	0	0	0	0	0	0	4.8	2.9	5.7	0	0	0	0
B. unclassified	0	7.9	0	0	3.1	0	4.2	0	0	0	4.8	3.1	0	0	0	0	4.8

Numbers and colors indicate the abundance of a system in a phylum (the sum of genome weights across single-unit loci; see Supplementary File 2 for details). “A” indicates archaeal phyla; “B” indicates bacterial phyla. The “part” column includes incomplete and ambiguously classified systems.