

Table 1: CRISPR locations per genome. First column indicates number of repeats of a CRISPR-locus. AAE – *Aquifex aeolicus*, HVI – *Hydrogenivirga sp.*, HTH – *Hydrogenobacter thermophilus*, HBA – *Hydrogenobaculum Y04AA1*, TAL – *Thermocrinis albus*, TRU – *Thermocrinis ruber*, PMA – *Persephonella marina*, SAZ – *Sulfurihydrogenibium azorense*, SSP – *Sulfurihydrogenibium YO3AOP1*. DTH – *Desulfurobacterium thermolithotrophum*, TAM – *Thermovibrio ammonificans*.

	AAE	HVI*	HTH	HBA	TAL	TRU	PMA	SAZ	SSP	DTH	TAM
3	0	0	0	0	0	1	0	0	0	0	0
4	2	1	0	0	0	0	0	1	1	0	1
5	3	0	0	0	0	0	0	0	1	0	1
6	0	2	0	0	0	0	1	0	0	1	0
7	0	2	0	0	0	0	1	1	0	0	1
8	0	0	0	0	0	0	0	2	0	0	0
9	0	2	0	0	0	1	0	2	0	0	0
10	0	1	0	0	0	0	0	1	0	0	2
11	0	0	0	0	0	1	0	1	0	0	1
12	0	1	0	0	0	0	1	0	0	0	0
13	0	1	0	0	0	0	0	0	0	0	0
14	0	0	0	0	0	1	0	0	0	0	1
15	0	1	0	0	0	0	1	0	0	0	0
16	0	1	0	0	0	0	0	0	0	0	0
17	0	0	0	0	0	0	0	1	0	0	0
18	0	0	0	0	0	1	0	0	1	0	0
19	0	0	0	0	0	1	0	0	0	0	0
20	0	0	0	0	0	0	0	2	0	0	0
21	0	0	0	0	0	0	0	0	1	0	0
22	0	0	0	0	0	0	0	1	0	0	0
24	0	0	0	0	0	0	0	0	0	0	1
25	0	0	0	0	0	0	1	0	0	0	0
30	0	0	0	1	0	0	0	0	0	0	0
34	0	0	(1)	0	0	0	0	0	0	0	0
36	0	0	(1)	0	1	0	0	0	0	0	0
41	0	0	0	0	1	0	0	0	0	0	0
57	0	0	0	0	1	0	0	0	0	0	0
63	0	0	0	0	1	0	0	0	0	0	0
88	0	0	0	0	0	0	0	0	0	0	0
total	5	12	1	1	4	6	4	12	4	1	8