Supplemental Table S2. PAM analysis of spacers acquired in wild-type *Sth* expressing increased Cas1/Cas2/Csn2 (Figure 1B and Supplemental Table S1)

PAM[2] Source[1]	NNAGAAW	1 SNP	2 SNPs	Reverse	No similarity	Total
Genome	4 (33%)[3]	4 (33%)	3 (25%)	0	1 (8%)	12
Plasmid	12 (48%)	9 (36%)	2 (8%)	1 (4%)	1 (4%)	25
Total	16 (43%)	13 (35%)	5 (14%)	1 (3%)	2 (5%)	37

[1] Genome, protospacers originating from *Sth* genome; Plasmid, protospacers originating from the plasmid.

[2] PAMs are classified as matching the previously identified motif (NNAGAAW, W = A or T), with 1 SNP, or position shift of 1 bp from NNAGAAW (1 SNP), with 2 SNPs, or 1 SNP and 1 position shift (2 SNPs) from NNAGAAW, reverse (reverse complement of the upstream sequence matches NNAGAAW), and no similarity to NNAGAAW.

[3] Percentage of spacers with the designated PAM among all spacers from the same protospacer source is shown in parentheses.