

Supplemental Table S5. PAM analysis of spacers acquired in the *cas9* deletion strain expressing dCas9 and Cas1/Cas2/Csn2 (Figures 2C, and Supplemental Table S4)

Source ¹ \ PAM ²	NNAGAAW	1 SNP	2 SNPs	Reverse	No similarity	Total
Genome	28 (61%) ³	12 (26%)	4 (9%)	2 (4%)	0	46
Plasmid	1 (50%)	1 (50%)	0	0	0	2
Total	29 (60%)	13 (27%)	4 (8%)	2 (4%)	0	48

¹Genome, protospacer originated from *Sth* genome; Plasmid, protospacer originated from the plasmid.

²PAMs 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.

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