

Supplemental Table S1. Analysis of spacers acquired in wild type *Sth* expressing increased Cas1/Cas2/Csn2 (Figures 1B, 2D, and 3).

spacer #	spacer	PAM ¹	source ²	strand ³
1	TTTATTGGCTTCACGAATAACCTTACGCCC	TG AGAAT TCT	G	plus
2	ATAACTAAACGAAATAAACGCTAAAACGTC	TC AGAAAC G	P	minus
3	GATATTAGCTTTTCGTCATCAACTACAGTT	ACA AATAAC	G	minus
4	TTTCGAGGAATATGATCCGCTTACAGGTGAG	AGAAT AAAA	G	minus
5	AAGCGCTTGAAAGAACAGCTGGATTGGTCT	CAGAA CAAA	G/P	plus
6	AGCTGTATTTGAGTTTATCACCCCTTGTCAC	TA AGAAA ATA	P	minus
7	AAGATATTGTTTCAACAAACTCTAGCGCCT	TT AGATT ATG	P	plus
8	TACCAACAATGATAGCTGGACGGTTAATCC	AG AGAAT GAA	G	plus
9	GAAACTAGTACAGTTATTACAGCACCAAGTA	CAGAAG TAGT	G	plus
10	AACCCATCTTTTCTAACTTAGCCATGTCAT	TAC GAAT GGT	G	minus
11	AGAGTTTTATGATTTATACCTTTCTGATGT	AG AGAAAT TAT	P	plus
12	AAGGACTTAAAAGAGCGTATTGAAAGATAC	AG AGAAAT TGG	P	plus
13	TAAGAGAAGTGTAATAATCATGAAAAACAA	AA AGAAAT TAT	P	minus
14	TATAAACCTTTAAGAACTTTCTTTT	GTTTTGGTCG TTTT TTCT TG ³	P	minus
15	AATTGCTTGCAATTTTGCCGAGCGGTAGCG	CT GGAAA ATT	P	plus
16	TCAAATCTGCGGTTGCGGCGTTAGCTATA	GA AGAAT ATG	P	plus
17	TCACTGGCCGTCGTTTTACAACGTCGTGAC	TG GGAAA ACC	P	minus
18	TAAAACATTCTCTGGTATTTGGACTCCTGT	AA AGAAT GAC	P	plus

19	GGCACTCGGCACTTAATGGGGGGTCGTAGT	ACGGAAGCAA	P	minus
20	GCTGTATTTGAGTTTATCACCCCTTGTCACT	AAGAAAATAA	P	minus
21	TTGAGAGGCTTTATGATGTTCAAAAAGAT	AGAGAAAAT	G	plus
22	ATAAATCTGTTAAGTCTCATCTCTTACAAG	GAATCTTAGA	G	minus
23	TTTAGGAGGCTTACTTGTCTGCTTTCTTCA	TTAGAATCAA	P	minus
24	AAATGCGTGGTGAACACTCTAAGGAATTAC	AAGAATTGCG	G	minus
25	AACGAGCTATTGAATTAGCTGAAGAATACC	CAGAAATTTA	G	minus
26	TTAAACCCAGTAAATGAAGTCCATGGAATA	ATAGAAAGAG	P	minus
27	GAGGCTCAACGTCAATAAAGCAATTGGAAT	AAAGAAGCGA	P	minus
28	AGTAAATGAAGTCCATGGAATAATAGAAAAG	AGAAAAAGCA	P	minus
29	AGTTATGCAAAGGTTCTTGATGCTGAAACG	GGGGAATAA	P	plus
30	TTATATCATGGCTATTA AAAATACTAAAG	CTAGAAATTT	P	plus
31	AATCGCCTTGCAGCACATCCCCCTTTCGCC	AGGGATAGA	P	minus
32	AGGTCTTGTGGCTAATTTAGCATAATTG	TTTGAAGTAG	G	minus
33	TTGGCAGATTATGCTGACTTCATGGCTATC	AAAGAATACT	G	minus
34	TCCGACTCTGAGAACTTCTGGAATCGCTA	GAGAATTTCT	P	plus
35	TTATATCCTGACTCAATTCCTAATGATTGG	AAAGAAAAT	P	plus
36	TTACAGGTACATCATTCTGTTTGTGATGGT	TATCATGCAG	P	plus
37	GAATAAAGAAGCGAAAAGGAGAAGTCGGT	TCAGAAAAG	P	minus

¹PAMs matching the previously identified motif (NNAGAAW, W = A or T) are highlighted in red. PAMs with 1 SNP, or position shift of 1 bp from NNAGAAW are highlighted in. PAMs with 2 SNPs, or 1 SNP and 1 position shift from NNAGAAW are highlighted in.

²G, protospacers originating from *Sth* genome; P, protospacers originating from the plasmid.

³Plus and minus, protospacer matching the plus or minus strand (arbitrarily assigned) of the source.

⁴Reverse complement of the upstream sequence of spacer #14 matches NNAGAAW