Supplemental Table S3. Analysis of spacers acquired in *Sth cas1/cas2/cas2* deletions strain expressing increased Cas1/Cas2/Csn2 (Figures 1B and 3).

spacer #	spacer	PAM[1]	source[2]	strand
1	TATTTAAGTTAAACCCAGTAAATGAAGTCC	ATGGAATAAT	P	minus
2	TTCTAATGTCACTAACCTGCCCCGTTAGTT	GAAGAAGGTT	P	plus
3	TTTCCGACGAGAGAAGGTTTTAGGATGTCT	TTAGAAACTG	P	plus
4	AGACGCCAACTGAGGCAGTAGATCAGCCTT	CAGAAAAGAT	G	minus
5	TCAAAATCTGCGGTTGCGGCGTTAGCTATA	GAAGAATATG	P	plus
6	AATCAGCATATAAACTTAAACTGTGGACAG	GTAGAATACC	P	plus
7	AGAGTTTTATGATTTATACCTTTCTGATGT	AGAGAAATAT	P	plus
8	TTTTGGGCGCTAGAAGTGGCTAAGGAACTT	CAGAAAGACT	G	plus
9	TCTAATGTCACTAACCTGCCCCGTTAGTTG	AAGAAGGTTT	P	plus
10	GATGTCCAGATTATTGAGAGGTTCATCCAA	TAGAATAATA	G	plus
11	AGCTTCATCCAAAACAGTATCGGTCACTTG	TTCAGAAAAG	G	minus
12	CAAATTCTTGCAATGGCCTTTAGAATCATA	TAGAATAGGT	G	minus
13	ATAACTAAACGAAATAAACGCTAAAACGTC	TCAGAAACGA	P	minus
14	GCTTAAGAACGCTAGTATCGCCGGCATATC	GTGGTAATTC	G	minus
15	AAATATTGGTGCAATCACACAAATTGTTGG	TCAGAATAAT	P	plus
16	TTTGACTCATGAATCAAAGGACGCTATTGC	TAAGAATAAA	P	plus
17	TTATATCCTGACTCAATTCCTAATGATTGG	AAAGAAAAAT	P	plus
18	TTTCTAAAAAGAGGGATAGTTTATCAATA	TTAGAAACCC	P	minus
19	AGCTGTATTTGAGTTTATCACCCTTGTCAC	TAAGAAAATA	P	minus

20	AATATTGGTGCAATCACACAAATTGTTGGT	CAGAATAATG	P	plus
21	TTCACTGCCCAGTGGTATCAAGTTTAGAGT	GGAGAAAATA	P	plus
22	TGCCAATCAAGTTGATATAGTAACCCATTT	GGAGAAAATT	P	plus
23	TGTCTTGAAGTAAAAAATCAGCATGTGTT	TAGAAATTAT	G	minus
24	AAGGACTTAAAAGAGCGTATTGAAAGATAC	AGAGAAATGG	P	plus
25	TCTGTTAATTTTTTATCTTGCTCTTTTGTC	AGAGAAATCA	P	minus
26	TACGAGATCAGGAATTCCTTAAGTATGAGT	ATAGGTTGGG	P	plus
27	AAAAAGATGTTTTTTTGCCCATATCTCTA	TGAAAAAAAC	P	plus
28	TTTTAAGGATTTACTGGAGCAGATGGAATA	CAAGAAAGGA	P	plus
29	AGCCGAAATGAACTGCACCCCAAAAGTTAG	ACAGAAAAAA	G	plus
30	TTATATATATTGCACGAAATCCTGTAACA	ATAGAAAGCG	P	plus
31	TTAAACCCAGTAAATGAAGTCCATGGAATA	TAAGAAAATA	P	minus
32	AATTTTCGGTCTACTATCGCACTTGTCCTAA	TAGAAGCTTT	P	plus

[1]PAMs 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 and1 position shift from NNAGAAW are highlighted in.

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

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

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