

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

Clone ¹	Spacer#	Spacer	PAM ²	Source ³	Location ⁴	Strand ⁵
1	1	TCCTTAGGAACCACGATGCTCATTCTACT	TCAGAAAATG	G	833792..833821	plus
	2	TGTTTAGTGAAAATTGCATCCGTTACTCGA	CTAGAAATAA	G	1492273..1492302	plus
2	1	TCAAGTCTTGCTTGCTAAACGTATGGGTAA	GAAGAAAATC	G	196047..196076	minus
	2	AGAGAAGATTACCAACGTGCTGAGAAGGCC	CTAGAAAGTG	G	1549996..1550025	plus
	3	AACACCTAGAAGTGCTACACCCGCGAGGGC	CAACCATTTG	G	68965..68994	plus
	4	AAGATGTCTTTGAGTTAGGTATTAATACTA	GTGGAATACC	G	792095..792124	plus
3	1	GAATTAATAATAAGGTAATAGATTTACATT	AGAAAATGAA	P		
	2	CTTCAAGGAAGTCATCATGTTTTTCAATCG	CAAGAATGAC	G	572859..572888	minus
4	1	AAAATCAAGCCAGAACATCAATACCTGATA	CCAGAAAAAA	G	788533..788562	plus
5	1	CATATGTAAGTAATTACATATAGATAGTAA	CAAGAAAATA	G	1792323..1792352	plus
	2	GGCTTCTTCAATTTACGACGCTCCAAGCC	AAGGCTGGTG TGGTTTCTTT ⁶	G	580391..580420	plus
	3	AACTTTCTATCATTCAAGCGATTTATCCC	AAAGAAATGG	G	549228..549257	minus
	4	AAGAGTCACGGTAGCTGAGACATCTATCGT	TGAGAAAAC	G	700732..700761	minus
6	1	same as 3-1				
	2	AGCTCTTTCATTGCTAAAGTTACCTGCTTT	GAAGAAAAGA	G	571256..571285	minus
7	1	same as 3-1				
	2	GAACTCGGCAAAATGGCCCCGTAAC TTCG	GAGAAGGGGC	G	1794107..1794136	plus

8	1	same as 3-1				
	2	TCCATTTCTTTGGGATAAAATCGCTTGAATG	ATAGAAAAGTT	G	549217..549246	plus
	3	CGAAAAGTTCTTCTCTATACCAGATTCTT	ACAGAAAAG	G	1427051..1427080	plus
9	1	TACTCTGGTAGACTCTATAACACTCAAACAG	GAGAAAGAAAT	G	488227..488257	minus
	2	ATGAGGTGCTTGATACCCCTTACAGACCGTG	AAGAAAATGT	G	99484..99513	minus
	3	AATTATCATTTACAGGAGAGCTTGTAGATT	TGATGGAAAT TTTATTCTTC ⁶	G	1682356..1682385	plus
	4	TACCAGTTTTACCAACAGACAAGACACCAT	AGAGAAGAGC	G	1728406..1728435	minus
	5	GCAGCAATGCTTAAGGCTGCTAACCAATAT	AATGGAAAGG	G	517776..517805	plus
	6	CAAAGACATCAAACGGTTGGGCTTTGGTTT	TAGAAACTTC	G	1736629..1736658	minus
	7	CAATACAAGAAAAATGGGTATACTCTTCTT	GAGAAAAGAA	G	1560601..1560630	plus
	8	TTAACCCATTCTTGCGTAGTGAGTTGCCT	AAAGAAATTT	G	1438643..1438672	plus
	9	TTAAGAGATTGTCTTAACCTCATCTCCCCT	TCAGAAAATT	G	18153..18182	plus
	10	CCTTCGCTATCTTAGGGACTGCCTTGCCA	GAAGAAATCT	G	514495..514523	plus
10	1	CTTCTTCTTGCAACGCCTGTTCTAGGTCTT	TAGAAATCT	G	1477793..1477822	minus
	2	AAAAAATTCGGCACAGAACCTCTGGTCACT	CTAGAAAAAA	G	539518..539547	minus
	3	GCAGTTCGTCGTCGTAGCAATCGAAATG	GCAGCAAGTC	G	1057015..1057044	plus
	4	ATTTGGCGTTGAAAATCAACTTAAAAAAGG	TAGAATGGTC	G	1168937..1168966	plus
11	1-3	same as 11-1,2,3				
	4	GCTGATATTGTGGAAGACTATAATATCCTA	GAAGAAGCAA	G	324199..324228	minus

12	1-3	same as 11-1,2,3				
	4	CTGCAAAATAAAATATAAGACCTATCATCC	TAAGAAAGAA	G	323990..324019	plus
13	1	CTACTCTATCTTTTCGTAAGATGCGTGACAA	GAAGAAACGC	G	918969..918998	plus
	2	AGCTGTATTTGAGTTTATCACCCCTTGTCAC	TAAGAAAATA	P		
14	1	ACCAATGGTATTGCAGACTATATCGGTTCT	GTAGAAGTTG	G	1031064..1031093	plus
	2	CATTCTGGTCAATCCGTCACCCAGCTGTCT	AAAGAATACG	G	510462..510491	plus
15	1	TTCATCTTGTGGACGTGACCAGTTTTTCAGT	TGAGAAAGCA	G	958812..958841	minus
	2	AGGACAAGATTGGACGCGACCGCCACGATC	GTAGAAAACG	G	972212..972241	minus
	3	GTAACCATGAATCCACCGATTGTTCCGACT	TTAGAAACTT	G	1086869..1086898	minus
	4	TCGTAACGCCCTTGGTGAGGATGGGACCAT	GCAGAATTAT	G	473222..473251	plus
	5	CTTATCGCCATAATAGTTGTTGATAACAATC	TTAGAATGTG	G	545894..545923	minus
16	1	TCATTTTTAACTTCTTAGCTTACATTCGTG	TAAGAAAAAA	G	376665..376694	minus
	2	AATCAGGCCGAAAAAGATTTCTTAGCTGGT	AAGAAAACCTC	G	1121023..1121052	plus
	3	GGATTACTTGGTTAACACTTTCAAAGCTA	AGAGAAAATA	G	773492..773521	plus
	4	TTCCAATTTCAACAGCACCTGATTGCACT	TGGGAAAGTC	G	752117..752146	minus
	5	TGTTTCATGATTATAGTGGTTATCAGCTGG	TAAGAAAATC	G	525465..525494	minus
	6	AAAGCAGTGAGACTGCCTCCACATGTGATG	CTAGAAAATA	G	508229..508258	minus

¹Each clone represents a series of adaptation events in a single CRISPR array. Sixteen CRISPR PCR clones with 1-10 new spacers were analyzed.

²PAMs 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 blue. PAMs with 2 SNPs, or 1 SNP and 1 position shift from NNAGAAW are highlighted in green.

³G, protospacer originating from *Sth* genome; P, protospacer originating from the plasmid.

⁴Protospacers are mapped to an assembly of 17 contigs (in order) of *Sth* DDCC7710 genome sequences.

⁵Plus and minus, protospacer matching the plus or minus strand (arbitrarily assigned) of the genome.

⁶Reverse complement of the upstream sequences of spacers match NNAGAAW motif