

## Supplementary data to

### A type III-B CRISPR–Cas effector complex mediating massive target DNA destruction

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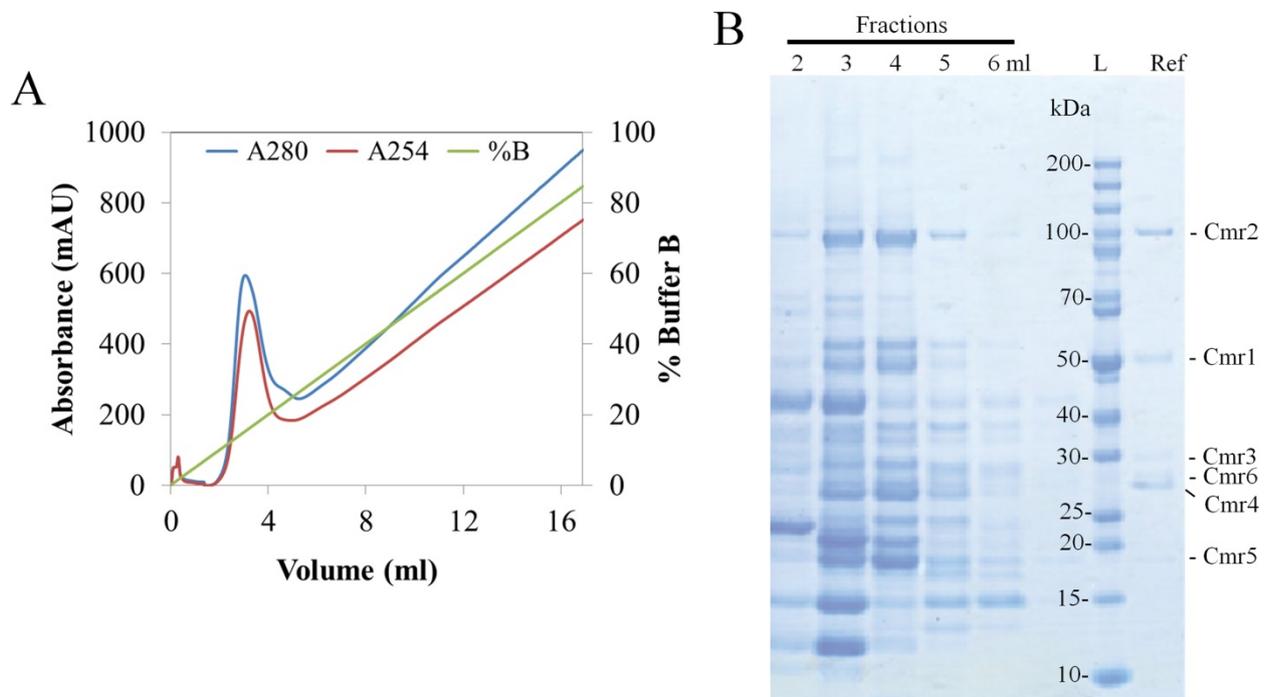
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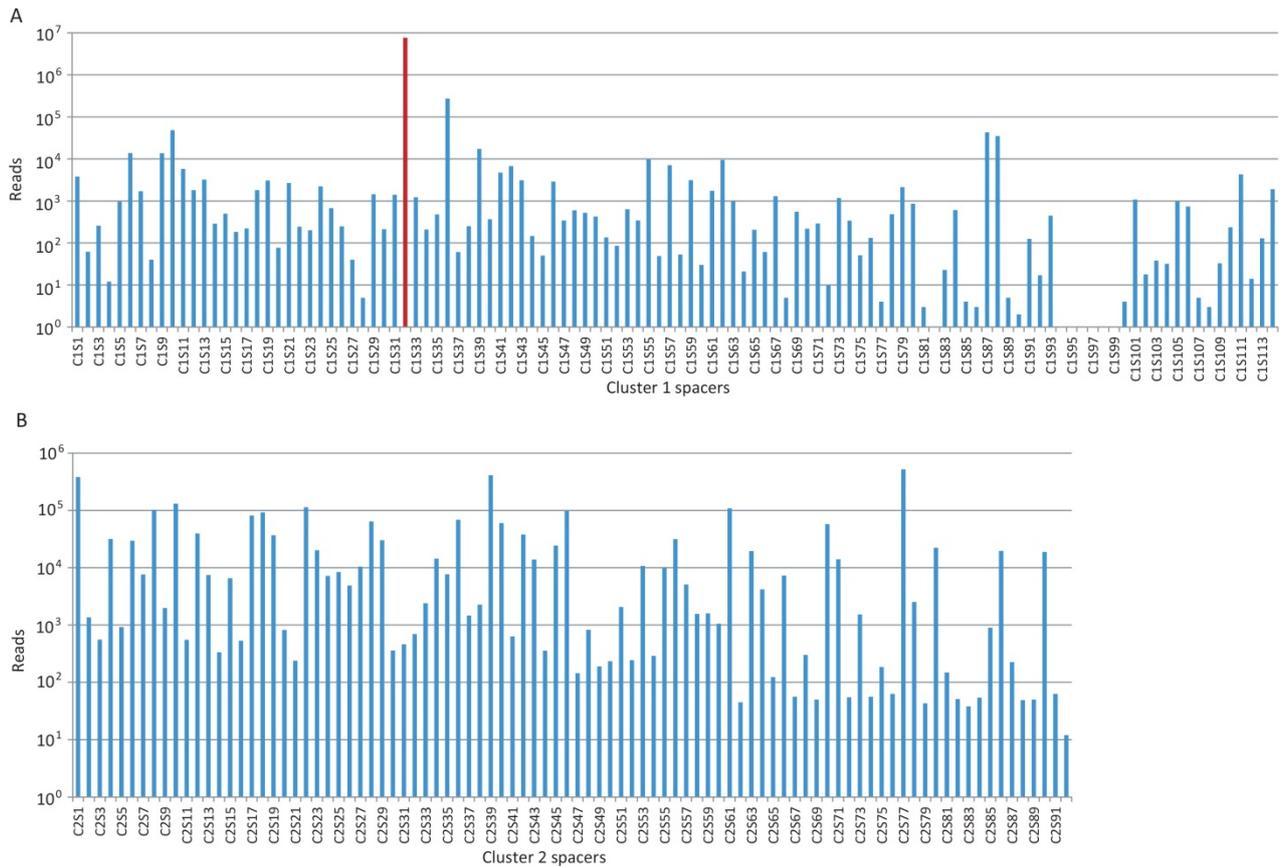
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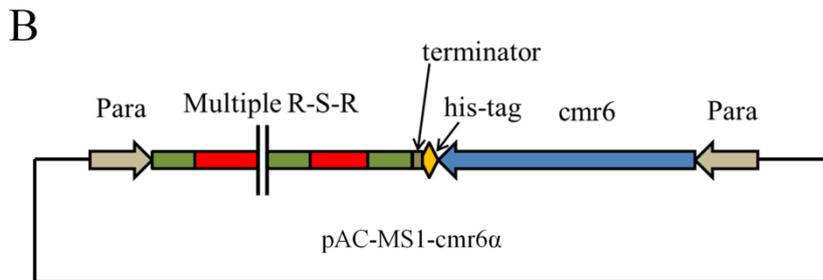
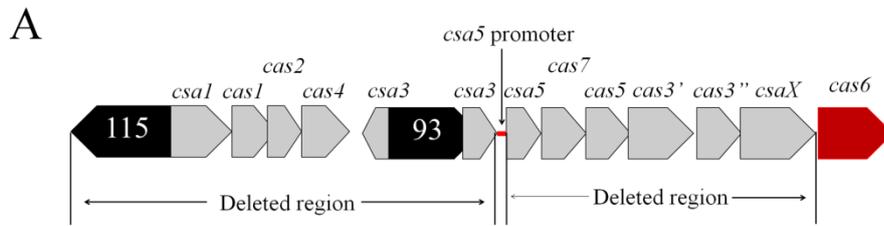
## Supplementary figures and tables



**Supplementary figure S1.** (A) UV-Vis spectrograms of the Ni-sepharose affinity chromatography of the His-tagged Cmr- $\alpha$  complex. Depicted is the absorbance at 280 nm (blue), 254 nm (red) as well as the elution buffer gradient (green). (B) SDS-PAGE of the selected peak fractions after the HisTrap purification. Ref represents purified Cmr- $\alpha$  complex.



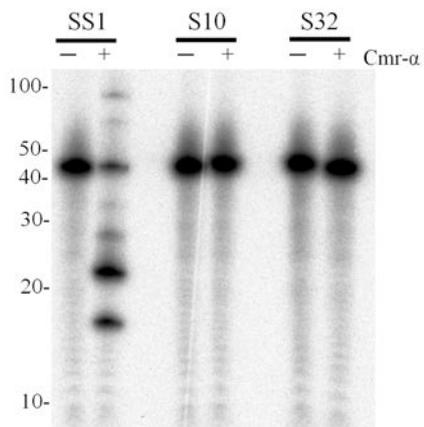
**Supplementary figure S2.** Distribution of Cmr- $\alpha$  mature crRNAs on the chromosomal CRISPR loci revealed from RNA sequencing of crRNAs extracted from the Cmr- $\alpha$  complex. Reads number matching each spacer is plotted to the position corresponding spacer in the CRISPR locus 1 (A) and 2 (B) of the *S. islandicus* REY15A chromosome



**Supplementary figure S3.**

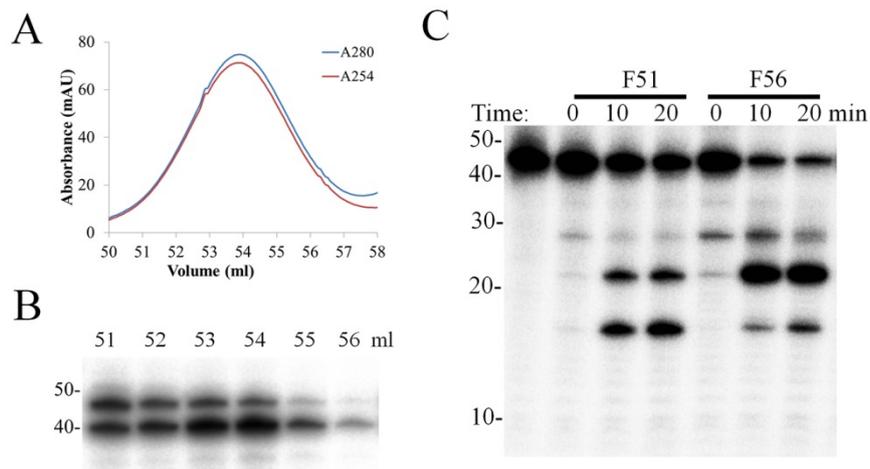
(A) Schematic of deleted regions in the *S. islandicus* MF1 strain. The first deleted region contains two CRISPR loci (indicated in black) and all type I-A adaptation *cas* genes plus a regulatory gene *csa3b* (indicated in gray). The second region includes all type I-A interference genes except *cas6*. An active *cas6* gene is generated by the fusion of the promoter of *csa5* and the coding sequence of *cas6* (shown in red) by SOE-PCR.

(B) Schematic of the pAC-MS1-*cmr6* $\alpha$  plasmid employed for purifying a native Cmr- $\alpha$  complex harboring a single type of crRNA. The expression of the artificial CRISPR array consisting of 10 repeat-spacer units (Multiple R-S-R) and the gene coding for the 6xHis-Cmr6- $\alpha$  is under the control of the promoter of the arabinose-inducible *araS* gene coding for a arabinose-binding protein. terminator: transcriptional terminator signal.



**Supplementary figure S4.** Cmr- $\alpha$ -SS1 does not cleave S10 or S32 RNA substrate.

Twenty five nM of labelled S10 and S32 RNA substrate was incubated with 25 nM Cmr- $\alpha$ -SS1 for 20 min and resolved on a denaturing polyacrylamide gel.



**Supplementary figure S5.** RNA cleavage sites correlate with the length of crRNAs present in the Cmr- $\alpha$  complex.

(A) UV spectrum of gel filtration chromatography of the His-tagged Cmr- $\alpha$ -SS1. Only the Cmr- $\alpha$  region (fraction no. 50-58 ml) is shown. Blue: UV absorbance at 280 nm; red: UV absorbance at 254 nm. (B) Denaturing gel electrophoresis analysis of crRNA extracted from different fractions in (A). The RNA samples were labelled with T4 polynucleotide kinase using  $^{32}\text{P}$ - $\gamma$ -ATP. (C) RNA cleavage by the 51-ml fraction (F51) and 56-ml fraction (F56), respectively. 5'-labelled SS1 RNA substrate was incubated with 1.5  $\mu\text{l}$  of F51 or 7.5  $\mu\text{l}$  of F56 for indicated times, and then analyzed by denaturing gel electrophoresis.



substrate from 4B. The percentage was normalized by the amount of SS1 RNA without Cmr- $\alpha$ -SS1.

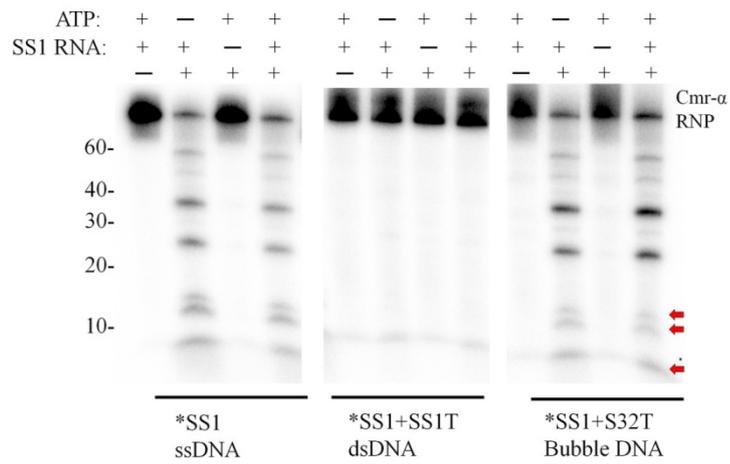
Bubble DNA:

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SS1: 5-TAATACGACTCACTATAGGGAGA      TGTTAAGTCTGGTTTCCCTCCAGGGTATCTAAGCTTTGAACCCCCCCCCCCCCC      ACGCGTCTCCGGATGTACAAA-3
S32T: 3-ATTATGCTGAGTGATATCCCTCT      TAGCGTTACGACCCTTAACCCACCACCGATCCAAGAAGTATTTTTTTTTTTTTTTT      TCGCGAGAGGCCTACATGTTT-5
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R-loop DNA:

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SS1: 5-TAATACGACTCACTATAGGGAGA      TGTTAAGTCTGGTTTCCCTCCAGGGTATCTAAGCTTTGAACCCCCCCCCCCCCC      ACGCGTCTCCGGATGTACAAA-3
S32T: 3-ATTATGCTGAGTGATATCCCTCT      TAGCGTTACGACCCTTAACCCACCACCGATCCAAGAAGTATTTTTTTTTTTTTTTT      TCGCGAGAGGCCTACATGTTT-5
S32*RNA: 5-AUCGCAAUGCUGGAAUUGGGUGGUGGCUAGGUUCUUCAUAAAAAAAAAAAAAAAAA-3
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**Supplementary figure S7.** Schematic map of bubble DNA and R-loop DNA used in Fig. 6A. Bubble DNA was produced by annealing of SS1 and S32T ssDNA, while R-loop DNA was yielded by annealing of S32\* RNA and S32T ssDNA followed by SS1 ssDNA.



**Supplementary figure S8.** Twenty five nM of ssDNA (labelled SS1), dsDNA (labelled SS1 + unlabeled SS1T) and bubble DNA (labelled SS1 + unlabeled S32T) were incubated with (+) without (-) 50 nM Cmr- $\alpha$ -SS1, 200 nM SS1 RNA and 1 mM ATP for 1 h, and then the samples were analyzed by denaturing PAGE. The three red arrows indicate that the cleavage sites are located in the double strand region of the bubble DNA.

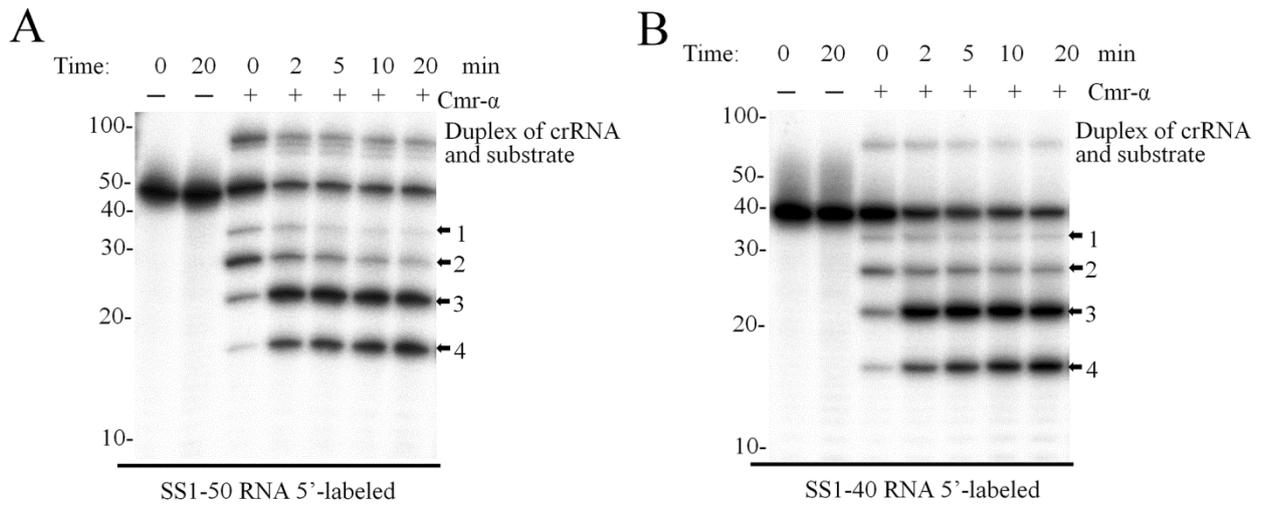
SS1;  
TAATACGACTCACTATAGGGAGATGTTAAGTCTGGTTCCCTCCAGGTATCTAAGCTTTGAACCCCCCCCCCCCCACGCGTCTCCGGATGTACAAA  
↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑

SS1 anti-tag;  
TAATACGACTCACTATAGGGAGATGTTAAGTCTGGTTCCCTCCAGGTATCTAAGCTTTGAACCTTCAATCCCCCCCCACGCGTCTCCGGATGTACAAA  
↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑

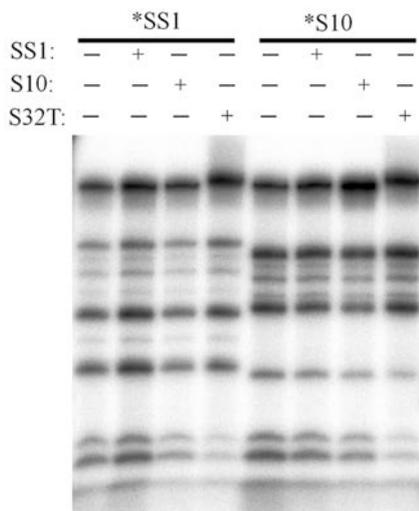
S10;  
TAATACGACTCACTATAGGGAGAAATAGAATGCCCCATTATACAATATCTACGTTTTAGATGACCCCCCCCCCCCCACGCGTCTCCGGATGTACAAA  
↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑

S32T;  
TTTGTACATCCGGAGACGCGTTTTTTTTTTTTTTTTATGAAGAACCTAGCCACCACCAATTCCCAGCATTGCGATTCTCCCTATAGTGAGTCGTATTA  
↑ ↑

**Supplementary figure S9.** Schematic depicting the cleavage sites on the ssDNA substrates.



**Supplementary figure S10.** Cleavage of SS1-50 (A) and SS1-40 (B) by Cmr- $\alpha$ -SS1. Twenty five nM of the labelled substrates were incubated with (+) or without (-) 25 nM of Cmr- $\alpha$ -SS1 for indicated time and then analyzed by denaturing PAGE.



**Supplementary figure S11.** Additional 10 times of unlabeled ssDNA substrate does not affect the cleavage of labeled substrate by Cmr- $\alpha$ . Twenty five nM labeled SS1 and S10 ssDNA substrate were incubated with 50 nM Cmr- $\alpha$ -SS1 and 200 nM SS1 RNA in the presence of 250 nM of unlabeled SS1, S10 or S32T ssDNA as indicated. After 1 h's incubation, the samples were analyzed by denaturing PAGE.

Supplementary Table 1. *Sulfolobus* strains used in this work

Strains	Genotype and features	Reference
<i>S. islandicus</i> E233S1	$\Delta pyrEF\Delta lacS$	(1)
<i>S. islandicus</i> MF1	Derived from E233S1. The genes for CRISPR cascade and the two CRISPR modules are deleted.	This work
<i>S. islandicus</i> $\Delta cmr-\beta$	Derived from E233, carrying deletion of IIIB <i>Cmr</i> - $\beta$ locus including 7 <i>cmr</i> - $\beta$ genes	(2)
<i>S. islandicus</i> <i>Cmr</i> -2 $\alpha$ HD-M1	Derived from <i>S. islandicus</i> $\Delta cmr-\beta$ , carrying a double mutation in the HD motif (H14N, D15N) of <i>Cmr</i> -2 $\alpha$	(2)
<i>S. islandicus</i> <i>Cmr</i> -2 $\alpha$ HD-M2	Derived from <i>S. islandicus</i> $\Delta cmr-\beta$ , carrying a quadruple mutation in the HD domain (H14N, D15N, K19A and I23A) of <i>Cmr</i> -2 $\alpha$	(2)
<i>S. islandicus</i> <i>Cmr</i> -2 $\alpha$ Palm-M1	Derived from <i>S. islandicus</i> $\Delta cmr-\beta$ , carrying a double mutation in the GGDD motif (G666K, D667K) of <i>Cmr</i> -2 $\alpha$	This work
<i>S. islandicus</i> <i>Cmr</i> -2 $\alpha$ Palm-M2	Derived from <i>S. islandicus</i> $\Delta cmr-\beta$ , carrying an octal mutation in the Palm domain (from IYIGGDDiLA to AAIAAAiAS) of <i>Cmr</i> -2 $\alpha$	This work

Supplementary Table 2. Plasmids used in this work

Plasmids	Genotype and features	Reference
pSeSD1	A <i>Sulfolobus-E. coli</i> shuttle vector with an expression cassette controlled under ParaS-SD promoter	(3)
pSe-Rp	A cloning vector for constructing mini-CRISPR arrays for <i>Sulfolobus</i>	(4)
pAC-MS1	Derived from pSeSD1, carrying an artificial CRISPR locus with 10 copies of 43 nt SS1 spacer.	This work
pcmr6 $\alpha$	Derived from pSeSD1, expressing His-tagged Cmr6	This work
pAC-MS1-cmr6 $\alpha$	Derived from pAC-MS1, both carrying an artificial CRISPR locus with 10 copies of SS1 spacer and expressing His-tagged Cmr6	This work

Supplementary Table S3. Primers used in this work

<b>Name</b>	<b>Sequence (5'~3')</b>
SS1- fwd	GCTAATCTACTATAGAATTGAAAGTTCAAAGCTTAGATACCCTGGAGGGAAACCAGACTT
SS1- rev	CGCAGTCGACTTTCAATTCTATAGTAGATTAGCTGGTGTTAAGTCTGGTTTCCCTCCAGG
Cmr6α fwd	TTTTTTTCATATGCAAGGTAATCGGATTCTTAATG
Cmr6α fwd	TTTTAGGCCTAGAACTCGGACATTTTAATTCCACC
MCS-fwd	ATGCCCCGGGATGTAAACAAGTTAGG
MCS-rev	GGCACTCGAGAAAAAAGATTTTGCTTAATGGTG
IA-L-F_Sall	TTACGC GTCGAC ATTGCAGAGAGGCCTAAGAGGACCA
IA-SOE-R	AATATATAAACTTTCTATTTCTTGTGAACGAAAAGATTTTCATACGTTTCCCCGACT
IA-SOE-F	AATAGAAAGTTTTATATATTGGGGTAGTAAAGAGAATAATGTGCCATTAATTTTCAAG
IA-R-R_NotI	AAGGAAAAAA GCGGCCGC CAATGTAGGGGAAACAAACCTCACT
IAspacer1F	aaagAAGGATATACATTTTGATGGAAGAGATACGGACTCGGCTG
IAspacer1R	tagcCAGCCGAGTCCGTATCTCTTCCATCAAATGTATATCCTT
2α-GD-SpF	aagCCACCCAAATATATAGCTACAGCATTATTATCGCGTAATA
2α-GD-SpR	agcTATTACGCGATAATAATGCTGTAGCTATATATTTGGGTGG
2α-GD-SOEF	CTGTAGCTATATATTTGGGTAAGAAAGACATATTGG
2α-GD-SOER	ACCCAAATATATAGCTACAG
2α-I-A-SpF	aaagATATGTCGTCACCACCCAAATATATAGCTACAGCATTATT
2α-I-A-SpR	tagcAATAATGCTGTAGCTATATATTTGGGTGGTGACGACATAT
2α-I-A-SOEF	GCAGCTTTGGCTGCTAACAAACATAGCTTCGTTATCGCCTATAAAGTTTAACG
2α-I-A-SOER	AAGCTATGTTGTTAGCAGCCAAAGCTGCAGCTACAGCATTATTATCGCGTAAT
2α-Palm-SallF	ACGCGTCGACTACTGTGCAATCAAACGCG
2α-Palm-NotIR	ATAAGAATGCGGCCGCCCTTAAGTAAGATACTG

Supplementary Table S4. Nucleic acid substrates used in this work

Name	Sequence (5'~3')	Size (mer)
RNA		
SS1	UGUUAAGUCUGGUUUCUCCUCCAGGGUAUCUAAGCUUUGAAAAAAAA	46
SS1-50	UGUUAAGUCUGGUUUCUCCUCCAGGGUAUCUAAGCUUUGAACTTTCAATAA	50
SS1-40	UGUUAAGUCUGGUUUCUCCUCCAGGGUAUCUAAGCUUUGAA	40
S10	AUAGAAUGCCCCAUUAUACAAUAUCUACGUUUUAGAUGAAAAAAAA	46
S32	AUCGCAAUGCUGGGAAUUGGGUGGUGGCUAGGUUCUUCAUUAAAAAAAA	46
S32*	AUCGCAAUGCUGGGAAUUGGGUGGUGGCUAGGUUCUUCAUUAAAAAAAAAAAAAAAAA A	55
DNA		
SS1	TAATACGACTCACTATAGGGAGaTGTTAAGTCTGGTTTCCCTCCAGGGTATCTAAGC TTTGAAccccccccccccccACGCGTCTCCGGATGTACAAA	99
SS1T	TTTGTACATCCGGAGACGCGTggggggggggggggTTCAAAGCTTAGATACCCTGGAG GGAAACCAGACTTAACA <sub>t</sub> CTCCCTATAGTGAGTCGTATTA	99
SS1 anti-tag	TAATACGACTCACTATAGGGAGaTGTTAAGTCTGGTTTCCCTCCAGGGTATCTAAGC TTTGA <sub>ACTTTCAAT</sub> ccccccACGCGTCTCCGGATGTACAAA	99
S10	TAATACGACTCACTATAGGGAGaATAGAATGCCCCATTATACAATATCTACGTTTTTA GATGAccccccccccccccccACGCGTCTCCGGATGTACAAA	99
S32T	TTTGTACATCCGGAGACGCGTTTTTTTTTTTTTTTTTATGAAGAACCTAGCCACCACCC AATCCCAGCATTGCGAT <sub>i</sub> CTCCCTATAGTGAGTCGTATTA	99

## References

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- Peng, N., Deng, L., Mei, Y., Jiang, D., Hu, Y., Awayez, M., Liang, Y. and **She, Q.** (2012) A synthetic arabinose-inducible promoter confers high levels of recombinant protein expression in hyperthermophilic archaeon *Sulfolobus islandicus*. *Appl Environ Microbiol*, **78**, 5630-5637.

4. Peng, W., Feng, M., Feng, X., Liang, Y.X. and **She, Q.** (2015) An archaeal CRISPR type III-B system exhibiting distinctive RNA targeting features and mediating dual RNA and DNA interference. *Nucleic Acids Res*, **43**, 406-417.