Supplementary Data

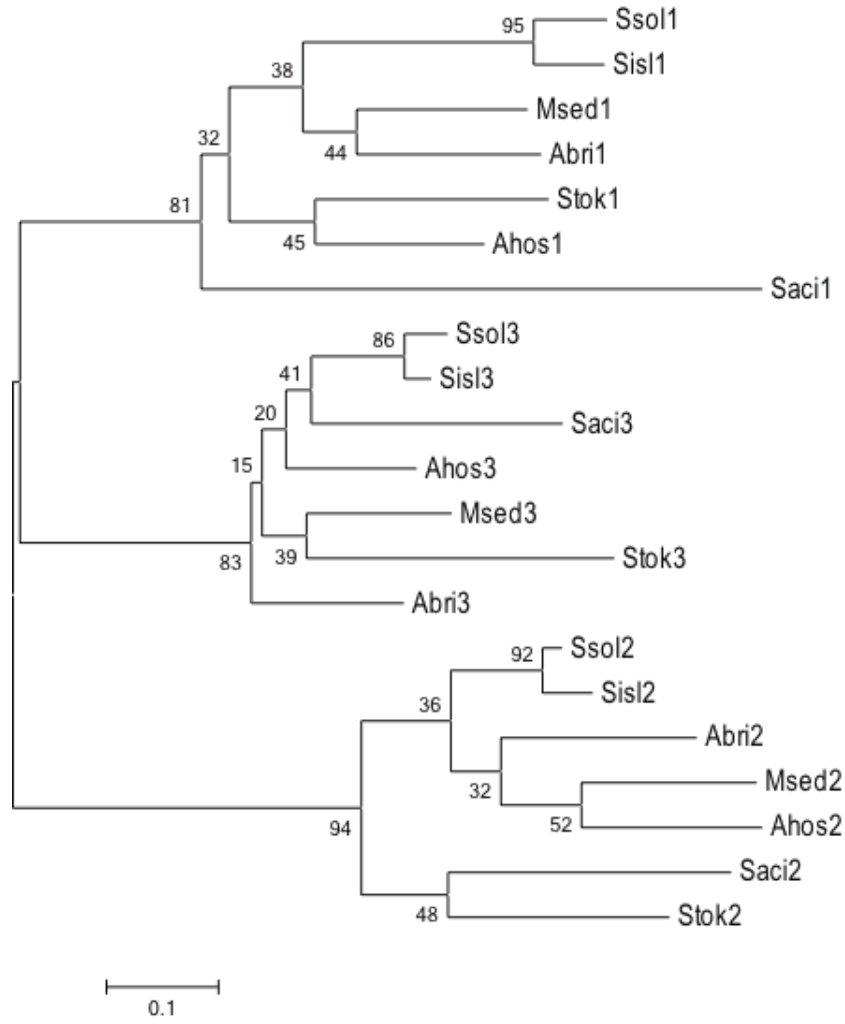

Figure S1. Distance tree showing clustering of the individual Cbp1 repeats. Results are presented for members of the Sulfolobales: *S. solfataricus* P2 (Ssol-0454), *S. islandicus* REY15A (Sisl-1547), *S. acidocaldarius* DSM 639 (Saci-0449), *S. tokodaii* str. 7 (Stok-0170), *M. sedula* DSM 5348 (Msed-2177), *A. brierleyi* (Abri-2346) and *A. hospitalis* W1 (Ahos-0975) which are labeled by four-letter prefixes. Protein repeats are numbered from the N-terminus. The tree was constructed using MEGA4 with neighbour joining and bootstrap values (53).

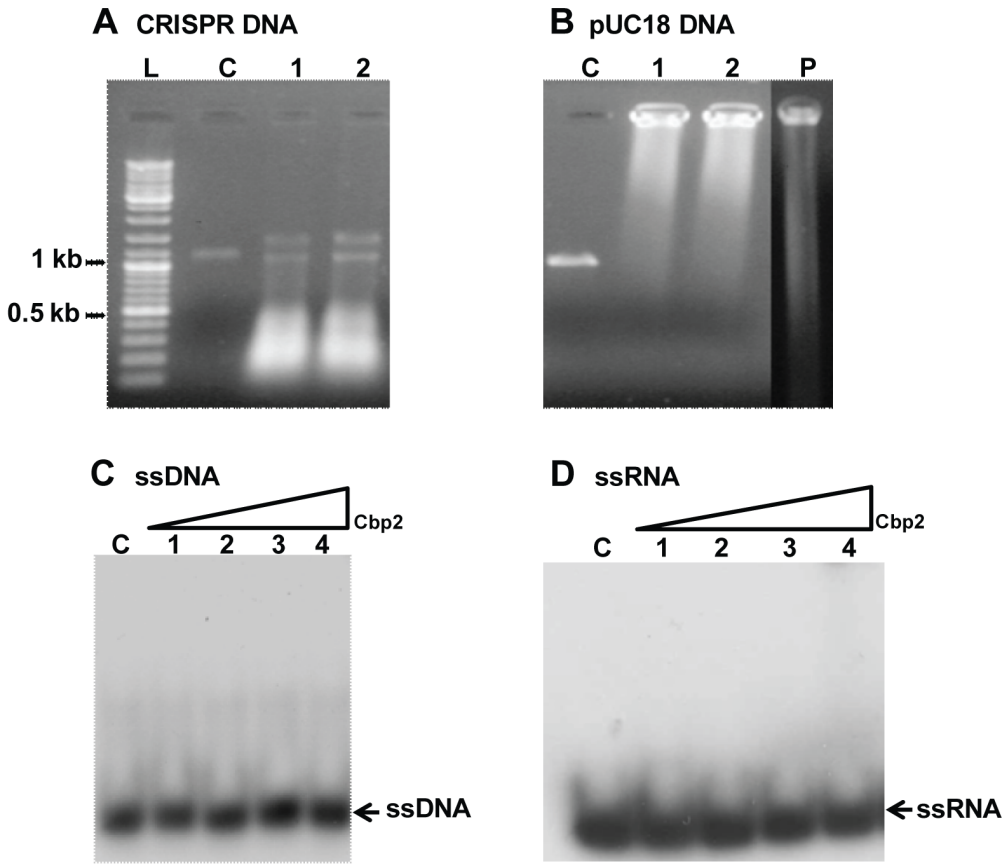

Figure S2. (A) 1158 bp CRISPR$_{Hb}$ DNA carrying 17 repeats and 16 spacers was PCR amplified using the respective forward and reverse primers 5´-CCTGCTCGGCGGCCTGCTCT-3´ and 5´-TGGAGGCTGCACCGGACCGC-3´. 5 nM DNA was incubated at 50°C for 20 min with Cbp2 copurified with *E. coli* DNA in binding buffer 15 µl of 10 mM Tris-HCl, pH 7.6, 150 mM KCl, 2 mM DTT, 10% glycerol. Lane 1 - 5 nM DNA and 25 nM Cbp2; lane 2 - 10 nM DNA and 50 nM Cbp2; lane L - 0.1 kb to 10 kb DNA size ladder; lane C - DNA with no protein. (B) A 1062 bp DNA fragment amplified from pUC18 with respective forward and reverse primers 5´-GCTTTCCAGTCGGGAAACCTGTC-3´ and 5´-CGCTGAGATAGGTGCCTCACTG-3´ was incubated with Cbp2 under the same solution conditions as in (A). Lane 1 - 5 nM DNA and 25 nM Cbp2; lane 2 - 10 nM dsDNA with 50 nM Cbp2; lane C - DNA with no protein, and lane P, Cbp2 copurified with *E. coli* DNA. Complexes were run in 0.8 % agarose gels. (C) and (D) 40 nM 55 nt ssDNA (from CRISPR-1r$_{Hb}$) and 8 nM of single stranded RNA (single 25 nt repeat) were [^{32}P] 5´-end labelled and incubated with 2, 5, 10 and 20 molar excess of Cbp2 in lanes 1 to 4, respectively, in binding buffer for 20 min at 50°C. Lane C - no protein was added. Reactions were run on native 8% polyacrylamide gels (as in Figure 2).

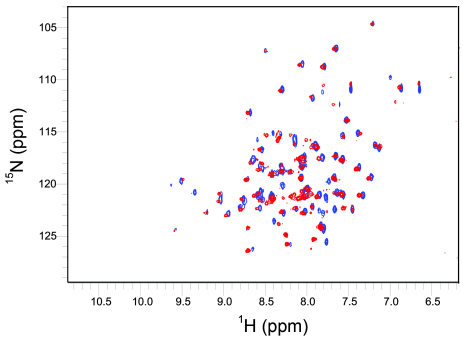

Figure S3. ^{1}H, ^{15}N-HSQCs of Cbp2-DNA binding. The spectrum of Cbp2 in complex with CRISPR-1r$_{Hb}$ (red) overlaid with the spectrum of Cbp2 in complex with the 12 bp downstream conserved region of CRISPR-1r$_{Hb}$ (blue). The spectra were recorded using 32 and 64 scans for CRISPR-1r$_{Hb}$ 12 bp region and CRISRPR-1r$_{Hb}$, respectively, and are drawn with different contour levels for clarity.

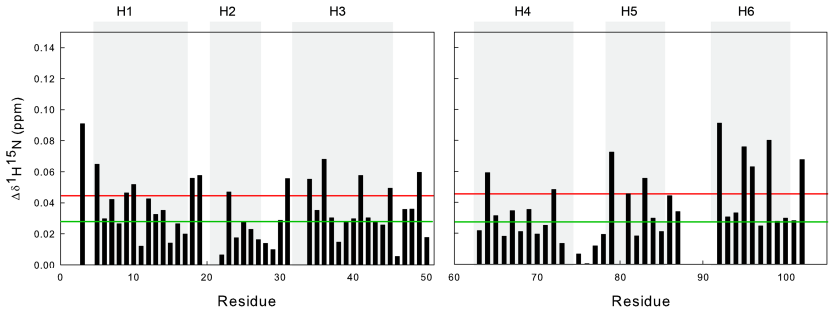

Figure S4. Combined ^{1}H,^{15}N chemical shift differences between the free form and CRISPR-1r$_{Hb}$ 12 bp conserved DNA-bound Cbp2 domains. N-domain (left) and C-domain (right) chemical shift differences, plotted as a function of amino acid residue number. Helices H1 to H6 are indicated, green lines denote trimmed average values and red lines denote trimmed average values plus one standard deviation.

53. Kumar,S., Dudley,J., Nei,M. and Tamura,K. (2008) MEGA4: A biologist-centric software for evolutionary analysis of DNA and protein sequences. *Briefs. Bioinform.,* **9,** 299-306