# Supplementary Tables and Figures

## Table S1 Oligonucleotides used in this study

| Primer | 5'–3' sequence[a] |
|---|---|
| P12-seq | AGTTGAGACCGTCGCGCCCG |
| P12-F | CTCGCTTTCGCTTCCGTC |
| Repeat-probe | CTTCAACCCAACGAGGGTCCGTCTGTAAC |
| C2S1-probe | GAAGGCGGCGATTACTCGCTGCGCATCGTCC |
| C18S1-probe | CAACTCATCCGCGTCGACGCGGACGACTCCTC |
| C22S1-probe | AACTGGCGCAGACACCGCGTTCGCCATCCTGTTC |
| C26S1-probe | AAGTCAACGCAACGCGCAAGGCACACG |
| P12S1-probe | AGTTGAGACCGTCGCGCCCGGATTCCCATGTGACT |
| P12S3-probe | ACCGACGTAACACTCTCGGTTGATGGGGGAGACCT |
| P23S1-probe | TCGGCGTCTACGCGCTCTACTGGGACCGGAT |
| C2-leaderprobe | CATGGCCAATCTGGCCGC |
| C18-leaderprobe | CATGCCCAATCTGAGGGC |
| C22-leaderprobe | CATGCCCGATTCGAGGGT |
| C26-leaderprobe | CATGGCCGATTTGAGTGC |
| P12-leaderprobe | CATGCCCAATTCAGGGGC |
| P23-leaderprobe | CATGGCCGATTTAAGCGC |
| 7S-probe-F | CCAACGTAGAAACCTCGTC |
| 7S-probe-R | GATGGTCCGCTGCTCGCTTC |
| PV1-testF | TGCCGCGTGTCTTTCATT |
| PV1-testR | CGCGCCTCACGAGTACAA |
| PV1-ctrlF | CGCTGTGTGGGAGGTTCAT |
| PV1-ctrlR | CGACGGCGAGCACATCTT |
| P12S3-RTF | TCAACCGAGAGTGTTACGTCGGT |
| P12S3-RTR | CGGTTGATGGGGGAGACCTGCT |
| phiH-PCR1 | TCTGCAAGCGAACGAAGTC |
| phiH-PCR2 | GGAAGGCGTCTACGAACTCAC |
| phiH-PCR3 | TGCCGGTCGTAGTCAATGTT |
| phiH-PCR4 | AGGCGACGGCATACATTCTG |
| C2-139 | TATAGGGTACCGCCGTGGATAGTGGATGCGA |
| C2-37 | TATAGGGTACCACGGAAACACTTGAGTGAGATGC |
| C2-31 | TATAGGGTACCACACTTGAGTGAGATGCGACAGTA |
| C2-R | GACGGATCCTCGAATCTCACATTTCCCAATTATC |
| VC2-UR | **GGGTCCGTCTGTAACCTGGCCGCTATAGAG**CTAGTA |
| VC2-DF | **CTCTATAGCGGCCAGGTTACAGACGGACCC**TCGTT |
| NCG-UR | **ACTTCAATCCAATGAGGAATCGCCTGTAAC**CATGGCCAA |
| NCG-DF | **TTACAGGCGATTCCTCATTGGATTGAAGT**GGACGATGCG |
| DCAS1-UF | CGCGGATCCCAGTTGAGGACCGATTCCTAT |
| DCAS1-UR | **GATAATGTACACCACGCTAGCAACTCCAGC**AGAAGT |

| | |
|---|---|
| DCAS1-DF | **GCTGGAGTTGCTAGCGTGGTGTACATTATC**GTCGTGTA |
| DCAS1-DR | ATAGGGTACCCCCAATCGTCTTCGACAA |
| DCAS2-UF | CGCGGATCCCTCGTCTCACCGAGACAACA |
| DCAS2-UR | **ACAGAAACCGTGACTTTACCACCACCGCTT**GAA |
| DCAS2-DF | **AAGCGGTGGTGGTAAAGTCACGGTTTCTGT**AGCAGT |
| DCAS2-DR | ATAGGGTACCGAGTTCGGGTCCGGTGTA |
| DCAS3-UF | CGCGGATCCCGCGGACGGTCAGCAAT |
| DCAS3-UR | **ATCGACGTCGGTCATCTCAAACGAACATCA**CCGTGTTT |
| DCAS3-DF | **TGATGTTCGTTTGAGATGACCGACGTCGAT**CCAGTT |
| DCAS3-DR | ATAGGGTACCGGCACCCATCGCTGAATAT |
| DCAS4-UF | CGCGGATCCTGCGGTCTACGATACTCAAGGA |
| DCAS4-UR | **GTAGTTTCGGTCCATGGTCATAGGAATCGG**TCCTCAA |
| DCAS4-DF | **CCGATTCCTATGACCATGGACCGAAACTAC**CACAT |
| DCAS4-DR | ATAGGGTACCCCGCCGTCCGTTGAAGA |
| DCAS5-UF | CGCGGATCCGGCGGGTTTGGATTGGAC |
| DCAS5-UR | **GTATTCAGCGGTCATAGTTAGTTGGGAAGC**GTCTCTA |
| DCAS5-DF | **GCTTCCCAACTAACTATGACCGCTGAATAC**GAACG |
| DCAS5-DR | ATAGGGTACCCCCGGTTGCTTCCTCGA |
| DCAS6-UF | AAACTGCAGTGTTTGGCTCCCGATCTACTGA |
| DCAS6-UR | **GCATCCTGAT**ACCTCACCCCG |
| DCAS6-DF | **ATCAGGATGC**TTTCGCCTGAGGAGTTC |
| DCAS6-DR | ATAGGGTACCCCGCGTCGAGCTTTACTTGG |
| DCAS7-UF | CGCGGATCCGGGAAGCAGCGACCGATTA |
| DCAS7-UR | **TGTCTGTTGGGTCACGGGTTTAATTTGCGG**TGGG |
| DCAS7-DF | **CCGCAAATTAAACCCGTGACCCAACAGACA**CTCACC |
| DCAS7-DR | ATAGGGTACCCCTCGAAGCGTCCGTGGTA |
| DCAS8-UF | CGCGGATCCGGGGCCTGCAACGAAACC |
| DCAS8-UR | **TGTATGTACAGTCATCTCAGGCGAAAGCAT**CTGCTC |
| DCAS8-DF | **ATGCTTTCGCCTGAGATGACTGTACATACA**GACCCCG |
| DCAS8-DR | ATAGGGTACCCGCCCTGTTCTTTCCCTGTT |
| DC2-UF | AAACTGCAGTGGCGATGCGACCGAAGA |
| DC2-UR | **CTGTGGGGCC**GCTGCCAACCACCA |
| DC2-DF | **GGCCCCACAG**ATAATTGGGAAATGTG |
| DC2-DR | ATAGGGTACCTGCCCCGTATGCTGTCGA |
| DC18-UF | ACGCGTCGACCTGCAGCGAATCCCACCACTGAACTCT |
| DC18-UR | **ACTGATGTCGCCCGTTCGGGTTTTCTCGGA**GTAGA |
| DC18-DF | **TCCGAGAAAACCCGAACGGGCGACATCAGT**GAAT |
| DC18-DR | GACGGATCCCTCCAGGCGAGCTACGATT |
| DC22-UF | CGCGGATCCGGCTGCGAGTATTCCGAG |
| DC22-UR | **AACGCTGCAGACTGGGCGCGATACACCAAT**TCCT |
| DC22-DF | **ATTGGTGTATCGCGCCCAGTCTGCAGCGTT**ACATT |
| DC22-DR | ATAGGGTACCGGTGCCTTGACGCCGTTA |
| DC26-UF | ACGCGTCGACGCATGCACCGCGATTCATAGTGTCA |
| DC26-UR | **TTGGTGGGTTCGAAGACTGGCTGTAGGAGA**CTCTGAT |

| | |
|---|---|
| DC26-DF | **TCTCCTACAGCCAGTCTTCGAACCCACCAA**CCA |
| DC26-DR | CGCGGATCCCGAAGCGAGGTCATCCAAAT |
| DP12-UF | CGCGGATCCGGTGCGGACACCGTAATGAT |
| DP12-UR | **TGAATGAACACCAGCGCGCCCCCACTAGGA**AATA |
| DP12-DF | **TCCTAGTGGGGGCGCGCTGGTGTTCATTCA**AGGATT |
| DP12-DR | ATAGGGTACCCGTGTCTGAAAATGGGATGAA |
| DP23-UF | CGCGGATCCTCAATCGACAGCAACTCACA |
| DP23-UR | **CACCCATCTGGACCGTGTTTCCGTCGACCT**CCAATA |
| DP23-DF | **AGGTCGACGGAAACACGGTCCAGATGGGTG**TTTA |
| DP23-DR | ATAGGGTACCGAAGGCTTGGTCGATCACAT |
| Cas6-F | TATAGGGTACCCACGAGAGCCCGGATCAAAGAG |
| Cas6-R | GACGGATCCAAAATCAGGCGAAAGCATCTGCTCTC |

[a] Restriction endonuclease sites are underlined. The complementary 5' end sequences in UR and DF primers are shown in bold.

## Figure S1

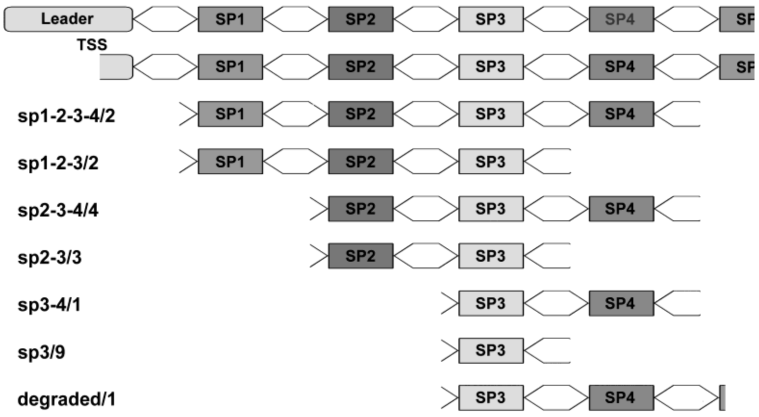

**Fig S1.** RT-PCR analysis of transcripts containing the spacer P12S3 with a pair of divergent primers P12S3-RTF and P12S3-RTR (indicated by black arrows), showing that most products could be cyclized with their two ends perfectly forming an intact repeat. Preceding RT-PCR procedures, the RNA sample was preliminarily 5’ to 3’-end-ligated (see Materials and Methods). The products are labeled with their spacer content and the number of sequenced colonies, separated by a slash.

## Figure S2

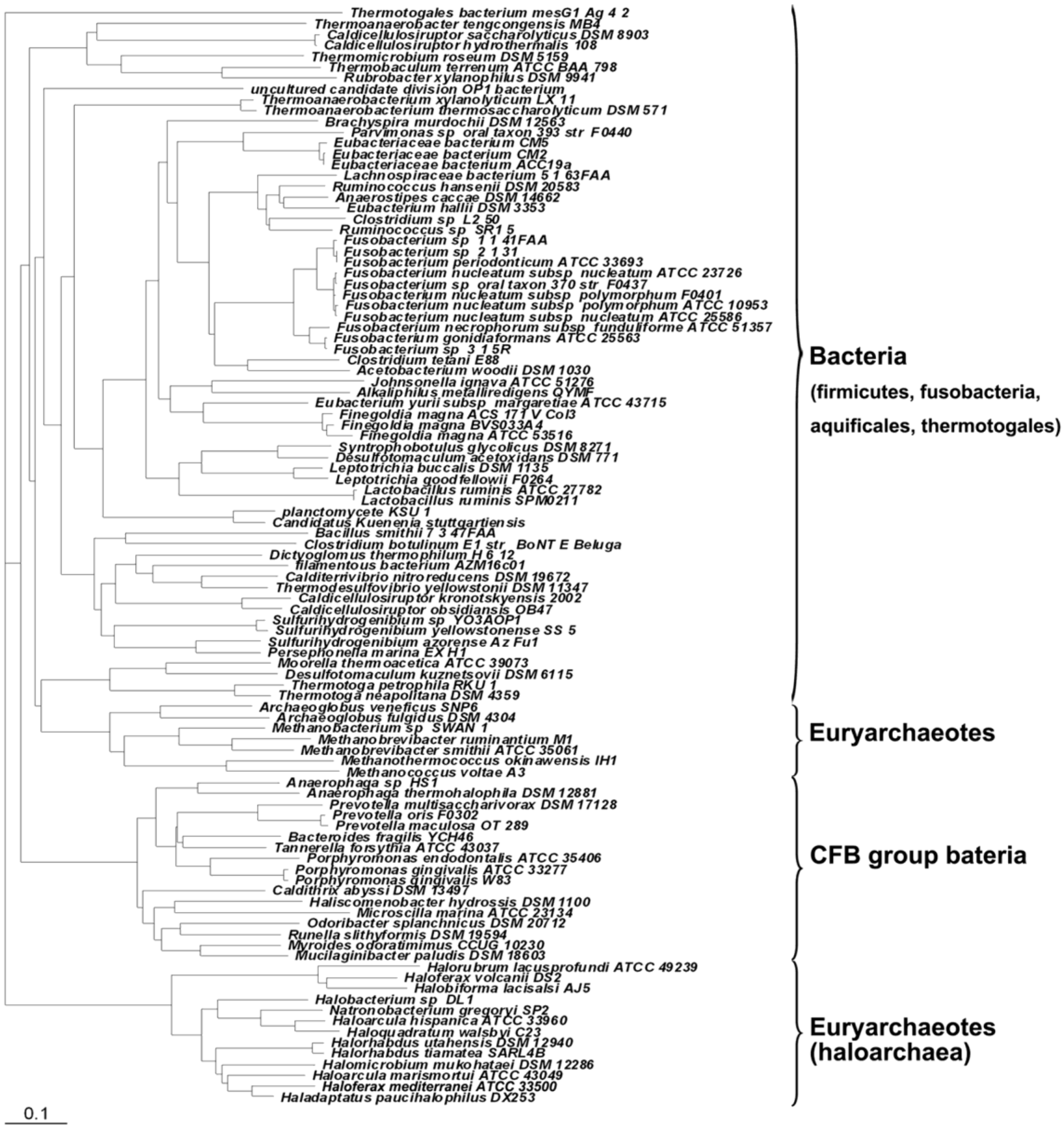

**Fig S2.** Phylogenetic tree of the haloarchaeal Cas1 proteins and their most related homologues.

## Figure S3

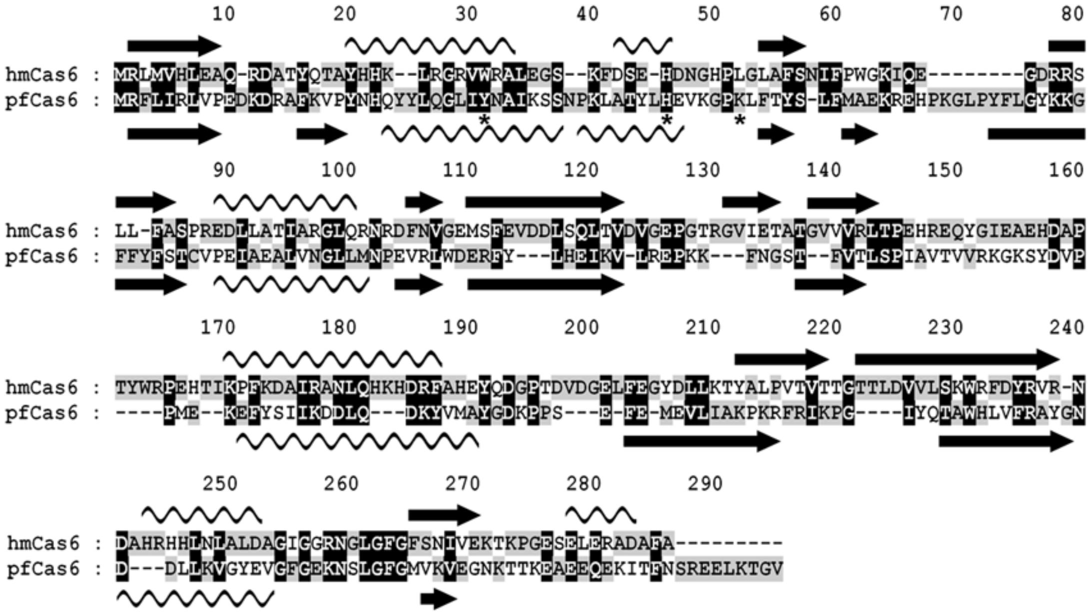

**Fig S3.** The alignment of *H. mediterranei* (hm) and *P. furious* (pf) Cas6 proteins showing their similar secondary structure arrangement. The helix and strand are respectively shown as wavy lines and black arrows. The nucleolytic triad of pfCas6 is labeled with asterisks. The secondary structure of hmCas6 was predicted with PSIPRED server (http://bioinf.cs.ucl.ac.uk/psipred/) and that of pfCas6 was according to the crystal structure data (PDB ID: 3I4H).