Table S1. Genomic fragments and probes used for the data in Fig. 1.

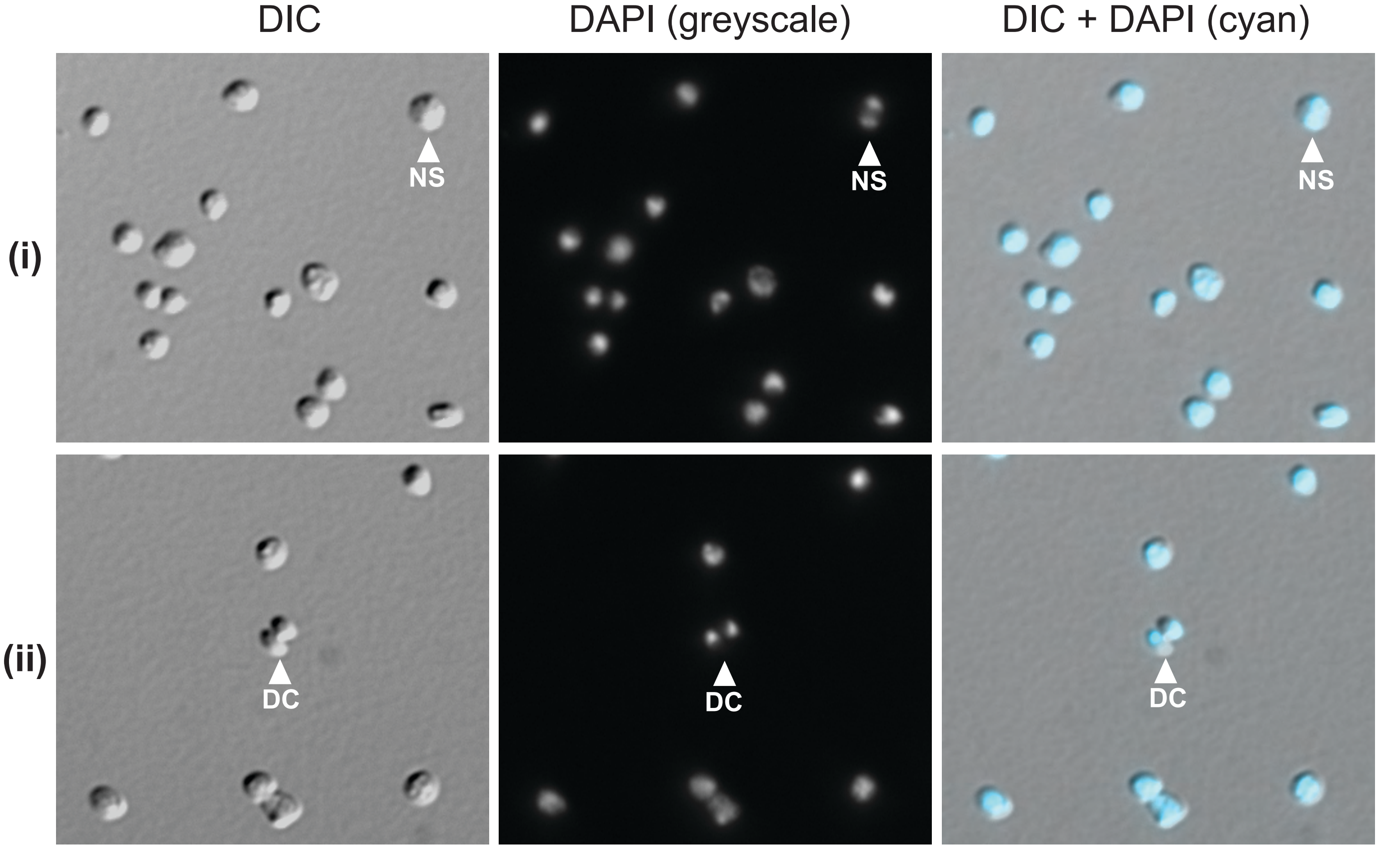
Panel	**Fragment coordinates[a] (and enzyme used)**	**Probe coordinates[a] (and name[b])**
B-a	453053-460881 (XmnI)	459927-460422 (460)
B-b	457492-461536 (PvuII)	459927-460422 (460)
B-c	459830-466464 (AflII)	462379-462887 (463)
B-d	465471-471399 (XmnI)	469111-469545 (469)
B-e	468606-472819 (NsiI)	469111-469545 (469)
B-f	471702-479483 (NheI)	478171-478700 (478)
B-g	478083-485927 (NsiI)	478171-478700 (478)
B-h	484422-491388 (HindIII)	490172-490836 (491)
B-i	489904-497758 (XcmI)	490172-490836 (491)
B-j	496443-503659 (XmnI)	501924-502331 (502)
B-k	500927-508444 (NdeI)	501924-502331 (502)
B-l	504093-510630 (HindIII)	510140-510594 (510)
B-m	510451-516935 (AflII)	515023-515440 (515)
B-n	515738-524102 (AvaII)	522970-523387 (523)
B-o	521377-529103 (NdeI)	522970-523387 (523)
B-p	528156-537640 (NsiI)	529876-530396 (530)
B-q	535642-542401 (AccI)	541998-542468 (542)
B-r	540496-547485 (AvaII)	541998-542468 (542)
B-s	545387-550078 (HindIII)	549021-549607 (549)
B-t	548788-560137 (AflII)	549021-549607 (549)
B-u	552983-561514 (BglII)	560209-560701 (560)
B-v	560137-115007 (AflII)	560209-560701 (560)
B-w	563283-567652 (AvaII)	566915-567458 (567)
B-x	566552-574236 (PvuII)	566915-567458 (567)
B-y	575726-580820 (AccI)	576206-576674 (576)
C-a	1345242-1352122 (HindIII)	1347147-1347671 (1347)
C-b	1348942-1356649 (XmnI)	1352885-1353521 (1353)
C-c	1354942-1360729 (PstI)	1355832-1356608 (1356)
C-d	1354906-1363717 (NcoI)	1355832-1356608 (1356)
C-e	1356288-1361481 (AccI)	1357634-1358044 (1358)
C-f	1361134-1366328 (NdeI)	1365171-1365713 (1365)
C-g	1363508-1368545 (HindIII)	1365171-1365713 (1365)
C-h	1367010-1373149 (NdeI)	1372096-1372606 (1372)
C-i	1371671-1375745 (AccI)	1372096-1372606 (1372)
C-j	1374710-1379882 (HindIII)	1375947-1376427 (1376)
C-k	1378005-1385788 (PvuII)	1385171-1385755 (1385)
C-l	1382653-1389706 (HindIII)	1385171-1385755 (1385)
C-m	1388173-1394122 (NdeI)	1393333-1393742 (1393)
C-n	1391606-1397850 (XmnI)	1393333-1393742 (1393)
C-o	1395277-1401341 (BglII)	1400793-1401343 (1401)
C-p	1399100-1405342 (PvuII)	1400793-1401343 (1401)
C-q	1403589-1408763 (XmnI)	1407835-1408240 (1408)
C-r	1407046-1416496 (NsiI)	1407835-1408240 (1408)
C-s	1413999-1419495 (XmnI)	1418177-1418628 (1418)

Table S1 continued

Panel	**Fragment coordinates**[a] **(and enzyme used)**	**Probe coordinates**[a] **(and name**[b]**)**
C-t	1418118-1424400 (XcmI)	1418177-1418628 (1418)
C-u	1424001-1429721 (XmnI)	1428924-1429391 (1429)
C-v	1427477-1432713 (AflII)	1428924-1429391 (1429)
C-w	1431025-1436248 (HindIII)	1435764-1436177 (1436)
C-x	1435723-1441754 (BglII)	1435764-1436177 (1436)
D-a	2560951-2565626 (NdeI)	2565210-2565614 (2565)
D-b	2563953-2567740 (AflII)	2565210-2565614 (2565)
D-c	2565189-2571376 (BamHI)	2565210-2565614 (2565)
D-d	2568956-2575384 (NheI)	2574388-2574806 (2575)
D-e	2573892-2578582 (EcoRV)	2574388-2574806 (2575)
D-f	2577110-2579961 (AccI)	2579201-2579623 (2579)
D-g	2574873-2583535 (XmnI)	2579201-2579623 (2579)
D-h	2581016-2587540 (PstI)	2586957-2587368 (2587)
D-i	2586827-2589742 (XmnI)	2586957-2587368 (2587)
D-j	2588677-2593947 (NdeI)	2593152-2593629 (2593)
D-k	2592168-2598198 (EcoRV)	2593152-2593629 (2593)
D-l	2596703-2601873 (XmnI)	2601124-2601582 (2601)
D-m	2600953-2606569 (NdeI)	2601124-2601582 (2601)
D-n	2605048-2609798 (XmnI)	2608795-2609229 (2609)
D-o	2608693-2615463 (AccI)	2608795-2609229 (2609)
D-p	2613935-2620904 (NheI)	2620349-2620846 (2621)
D-q	2619383-2625012 (HindIII)	2620349-2620846 (2621)
D-r	2623961-2629923 (AvaII)	2628313-2628783 (2629)
D-s	2628210-2635892 (NcoI)	2628313-2628783 (2629)
D-t	2634619-2640453 (BamHI)	2639369-2639867 (2640)
D-u	2639265-2643734 (AflII)	2639369-2639867 (2640)
D-v	2641968-2650017 (NcoI)	2648361-2648822 (2649)
D-w	2646742-2652078 (AvaII)	2648361-2648822 (2649)
D-x	2649818-2656723 (NheI)	2656043-2656494 (2656)
D-y	2655776-2659846 (AccI)	2656043-2656494 (2656)

[a] Coordinates relate to the genome sequence: She Q, Singh RK, Confalonieri F, Zivanovic Y, Allard G, Awayez MJ, Chan-Weiher CCY, Clausen IG, Curtis BA, De Moors A et al (2001) The complete genome of the crenarchaeon *Sulfolobus solfataricus* P2. *Proc Natl Acad Sci USA* **98**: 7835-7840.
http://www-archbac.u-psud.fr/projects/sulfolobus/

[b] Probes were generated using PCR and named relative to their nearest genomic location (kb).



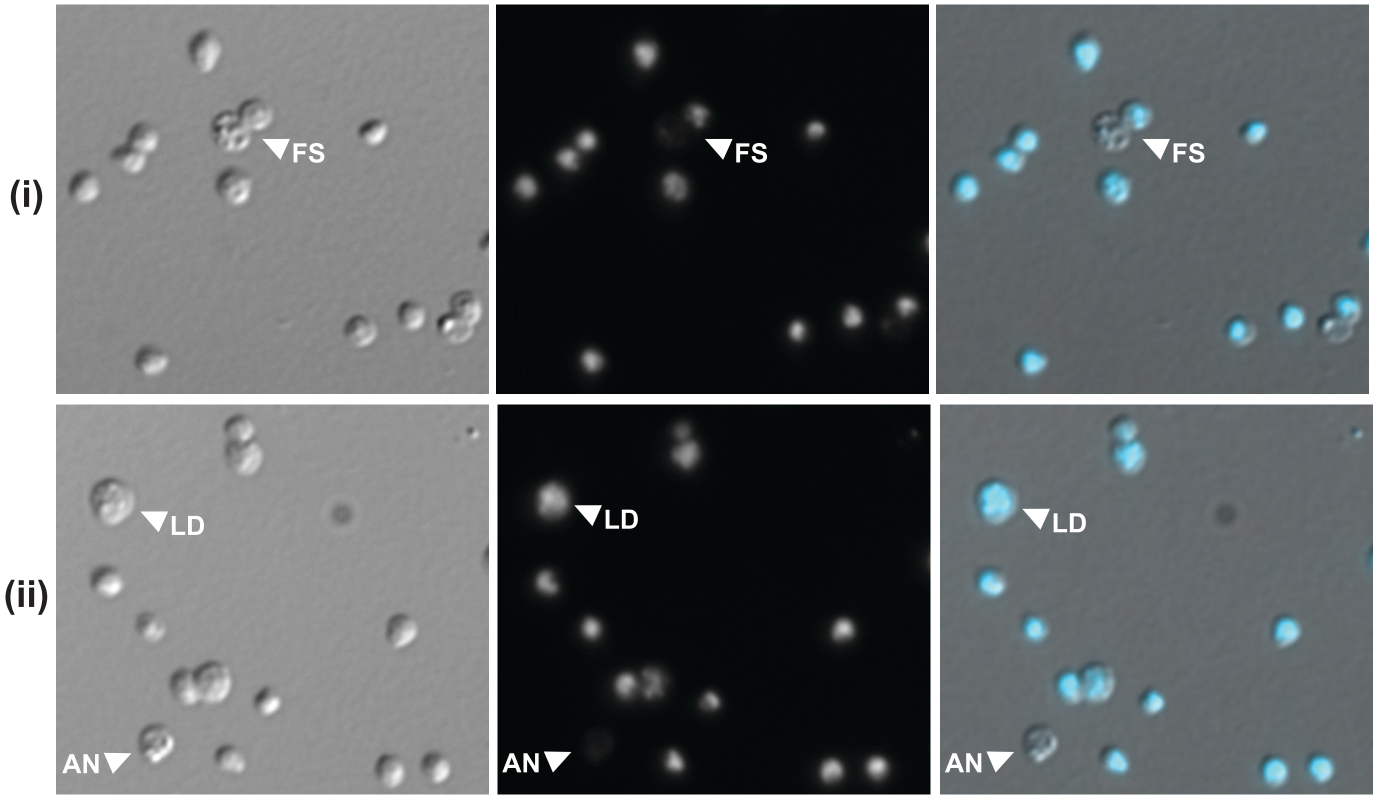


Fig. S2. Microscopy of *S. solfataricus* PBL2025 (**A**) and Δ*xer::lacS* (**B**). Cells were sampled at the same time as those for flow cytomtery in Fig. 2D and were prepared with the same method except the final resuspension contained 1 μg/ml DAPI instead of Sytox Green/RNase. Cells were applied to agarose pads for microscopy. Representative panels of both Differential Interference Contrast (DIC) and fluorescence (DAPI) micrographs acquired for each field are shown. The right-hand panels show an overlay of the two images, with DAPI coloured cyan. Examples of the types of cells observed are indicated by arrow-heads; abbreviations correspond to those specified in the abundance analysis in Fig. 2F (NS - Nucleoid segregation, DC - Doublet or dividing cell, FS - Failed segregation, LD - Large diffuse nucleoid, AN - Anucleate).