

1 **Supplementary Material**

2
3
4 Supplementary movie S1: Exponentially growing *B. subtilis* cells expressing SftA-
5 YFP from the original gene locus, 30 ms stream acquisition of YFP fluorescence,
6 shown are 33 frames/s

7
8 Supplementary movie S2: Exponentially growing *B. subtilis* cells expressing SftA-
9 YFP from the original gene locus, mobile single signals are shown within the cell
10 borders (determined through an overlay of fluorescence with bright field
11 acquisition), 30 ms stream acquisition of YFP fluorescence, shown are 10
12 frames/s

13
14 Supplementary movie S3: Exponentially growing *B. subtilis* cells expressing SftA-
15 YFP from the original gene locus, static single signal is shown within the cell
16 borders, 30 ms stream acquisition of YFP fluorescence, shown are 10 frames/s

17
18 Supplementary movie S4: Exponentially growing *B. subtilis* cells expressing
19 SpoIIIE-YFP from the original gene locus, 30 ms stream acquisition of YFP
20 fluorescence, shown are 33 frames/s

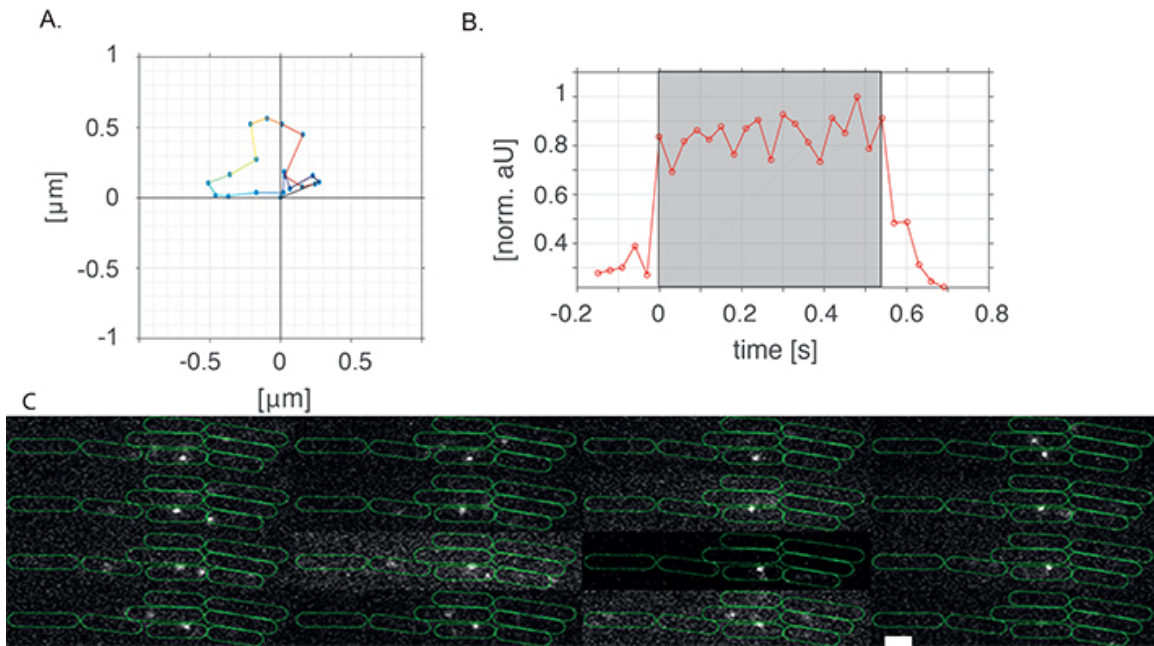
21
22 Supplementary movie S5: Exponentially growing *B. subtilis* cells expressing
23 SpoIIIE-YFP from the original gene locus, mobile single signals are shown at the
24 cell borders, 30 ms stream acquisition of YFP fluorescence, shown are 10
25 frames/s

26
27 Supplementary movie S6: Exponentially growing *B. subtilis* cells expressing
28 PfkA-YFP from an ectopic gene locus, 30 ms stream acquisition of YFP
29 fluorescence, shown are 33 frames/s

30
31 Supplementary movie S7: Exponentially growing *B. subtilis* cells expressing
32 PfkA-YFP from the original gene locus, mobile single signals are shown within
33 the cell borders, 30 ms stream acquisition of YFP fluorescence, shown are 10
34 frames/s

35

36



37

38

39 **Fig. S1** Movement of a single SftA-YFP molecule within a *B. subtilis* cell. A) Trajectory

40 of a single molecule, shown in panel C. The timing of movement is from blue to red. B)

41 Fluorescence intensity of the single molecules. C) 15 ms stream showing the movement

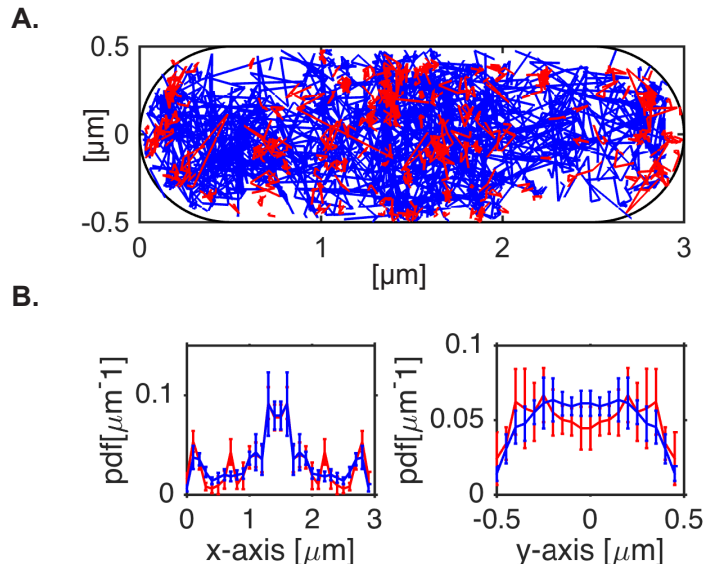
42 of a dynamic SftA-YFP molecule, left to right, top to bottom. White bar 2 μm .

43

44

45

46



47

48

49 **Fig. S2** A) Determination of the subcellular localization of slow and of fast moving
50 molecules of FtsA-YFP, tracked at 30 ms. Tracks were projected into a standardized cell
51 of 3 x 1 μm size, and were sorted into slow moving (not leaving an area of 3 x 3 pixels)
52 molecules indicated by red line, and fast molecules, indicated by blue lines. B)
53 Superimposition of slow (red line) and fast moving (blue line) molecules sorted in x- and
54 y-orientation (long and short axis of the cell). Shown are the mean and the standard
55 deviation of a bootstrap analysis sampling 50 times tracks with replacement.

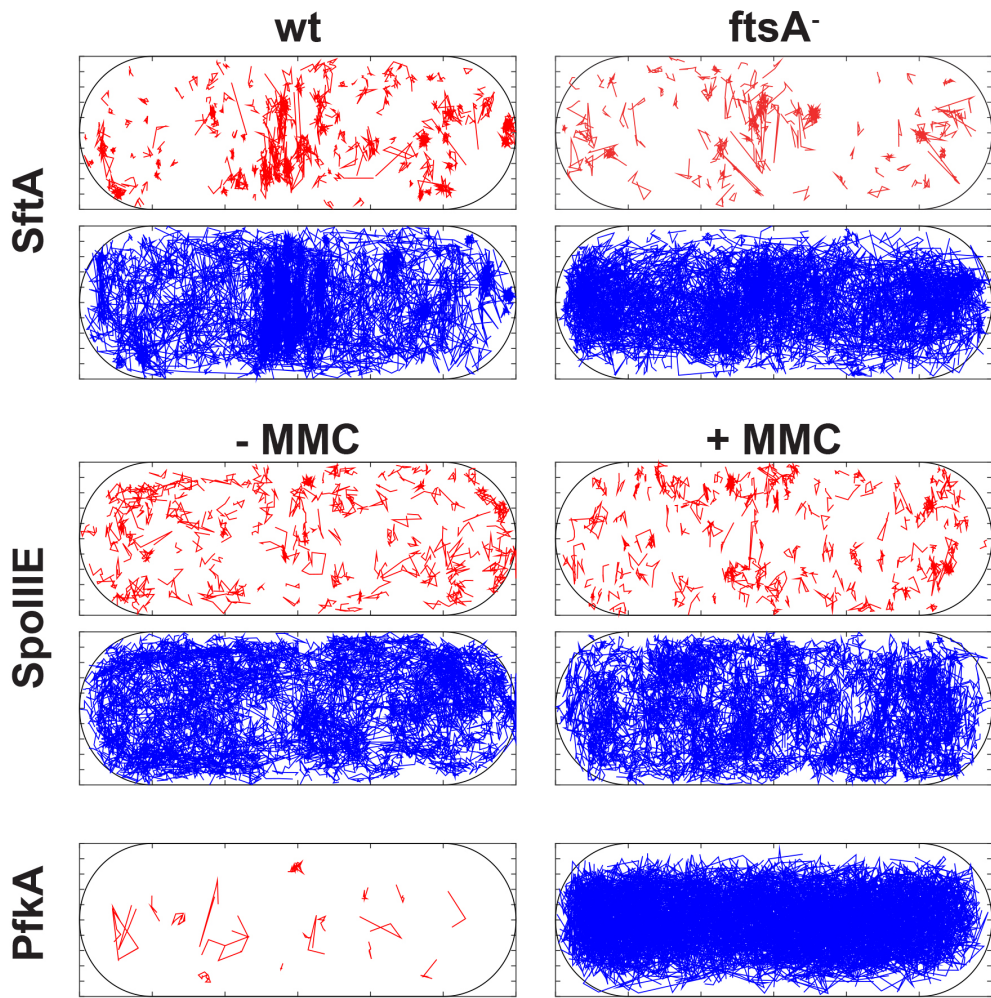
56 Figure S2: Superimposition of slow moving (red bars) and fast moving (blue bars)
57 molecules sorted in x-orientation (along the length of cells), data are the same as in Fig.
58 6.

59

60

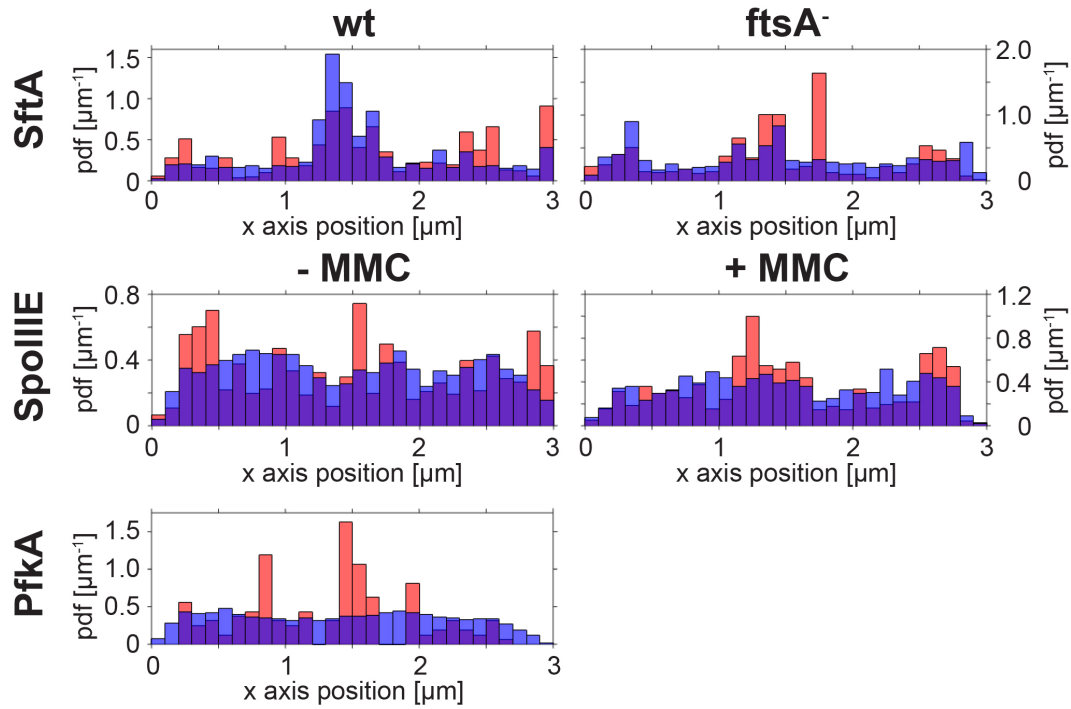
61

62



63
64
65
66
67
68
69
70
71
72
73
74

Figure S3 Determination of the subcellular localization of slow and of fast moving molecules. 1000 tracks of SftA-YFP, SpoIIIE-YFP or PfkA-YFP were projected into a standardized cells of 3 x 1 μm size, and were sorted into slow moving (not leaving an area of 3 x 3 pixels) molecules, indicated by the red tracks, and fast molecules, indicated by blue tracks. FtsA⁻ indicates depletion of FtsA for 1 hour, + MMC the addition of MMC for 1 hour.



75

76

77 **Figure S4** Superimposition of slow moving (red bars) and fast moving (blue bars)

78 molecules sorted in x-orientation (along the length of cells), data are the same as in Fig.

79 S2.

80

81

82

83

84

Table S1

Oligonucleotide	Sequence	Construct
2622	5'-CATGGGCCCAATCATCATGAAA-3'	1164-sftAN-tap
2624	5'-CATATCGATCGGAAATACATAGCTGCC-3'	
4406	5'-CATGAATTCATGAACAACAATGAACT TTAC-3'	pPR-IBA 101-FtsA ₁₋₄₂₅
4407	5'-CATGGATCCATGTTCGGCTTGTGTTTTTT-3'	
5509	5'-CATGGTACCATGTTGGAGTTCGAAAC AAAC-3'	pFD1-ftsZ
5510	5'-CATACTAGTGCCGCGTTTATTACGGTT-3'	
5517	5'-CATCTCGAGGCCGCGTTTATTACGGTT-3'	pFD1-ftsZ-yfp
5456	5'-CATGGTACCATGAACAACAATGAACT TTAC-3'	pFD1-ftsA
5457	5'-CATACTAGTTTCCCAAACATGCTTAA TAG-3'	
4281	5'-CATGGGCCCATGAACAACAATGAACT TTAC-3'	pFD1-ftsA-yfp
4295	5'-CATCTCGAGTTCCCAAACATGCTTA ATAG-3'	
2342	5'-CATGGGCCCCGACGAACCGAAATCCGCG-3'	pFD1-sftA-yfp
4088	5'-CATGATATCTTCGTTTATTAAATCACT TGC-3'	
2523	5'-CATGGGCCCCGGAATAACATAGCTGCC-3'	pFD1-sftAN-yfp
2624	5'-CATATCGATCGGAAATACATAGCTGCC-3'	