SUPPLEMENTAL MATERIAL

Strain construction.

The serine to cysteine replacements were made by site-directed mutagenesis using PCR with the following primers. For S219C, forward primer AACCCAGCTTGCATTGAGGGTGTTTATAC, which changes TCA to TGC, and reverse primer GTATAAACACCCTCAATGCAAGCTGGGTT, which changes TGA to GCA. For S353C, forward primer TCCGGTGCCGCCTGCTCTCCAACCGCGGTCAAACTG, which changes AGT to TGC, and reverse primer CGCGGTTGGAGAGCAGGCGGCACCGGAAGAGTCAGT, which changes ACT to GCA. For S219C, the mutant PCR product was moved into the chromosome using the λ-Red system, as described previously [Yuan, 2008 #17]. The primers used for deletion of *fliC* were GCTAACCGTTTCACCTCTAACATTAAAGGCCTGACTCAGGTCAGAAGAACTCGTCAAGAA and GCCTGCTGGATGATCTGCGCTTTCGACATATTGGACACTTGGATATTATCGTGAGGATGC, where the *fliC* sequences are in blue and the pKD45 sequences are in green. For S353C, the mutant PCR product was cloned into pBAD33 using *Sac*I and *Xbc*I restriction sites, with the primers TGCGAGCTCGATTGAGCCGACGGG and TGCTCTAGATTAACCCTGCAGCAGAGACAG, respectively, where the restriction sites are shown in violet.

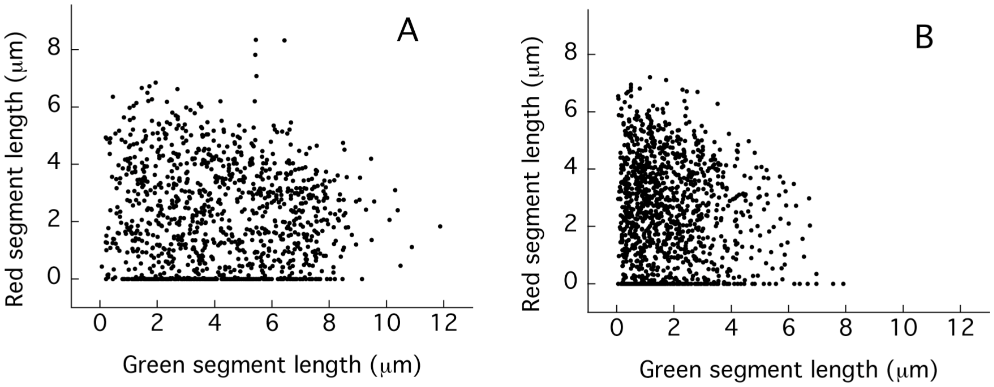

Figure S1. Plots of the lengths of red segments versus the lengths of the green segments from which they grew, for a single culture of strain HCB1668. **A**. Filaments of unsheared cells. **B**. Filaments of sheared cells.

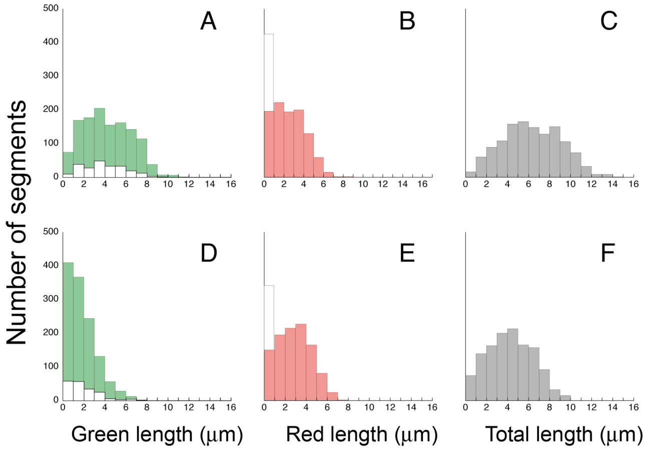

Figure S2. Distributions of segment lengths of filaments on cells of strain HCB1688, binned at 1-μm intervals. Green segments are shown in green, red segments are shown in red, and total lengths (green + red) are shown in grey. The distribution of the subset of green segments that failed to produce red extensions is shown by the white bars in panels A and D, while the total numbers of such green segments, which equals the numbers of red segments of zero length, are shown by the white bars in panels B and E. The top row (A-C) is for cells that were not sheared, and the bottom row (D-F) is for cells that were sheared.

Rejection of the hypothesis that broken filaments do not grow.

Consider the green segment-length distributions given in Figs. 4A and 4D of the main text. Assume that broken filaments do not grow (our data do not support this model). Let N_b be the number of filaments whose lengths fall in bin b of the sheared population, Fig. 4D. N_b can be written as a sum:

$$N_b = U_b + B_b, \tag{1}$$

where U_b is the number of unbroken filaments and B_b is the number of broken filaments in bin b. Prior to shearing, the distributions of filament lengths in the two populations (sheared and unsheared) must have been the same. Therefore

$$U_b \leq M_b, \tag{2}$$

where M_b is the number of filaments in bin b of the unsheared population, Fig. 4A.

The average growth of filaments in bin b from the unsheared population (F_b) that occurred during the second growth period is shown in Fig. 5; presumably the average growth of the unbroken filaments in bin b from the sheared population is the same. The average growth of *all* filaments in bin b from the sheared population (G_b) is shown in Fig. 7; according to the model it is predicted to be an average of F_b and 0, weighted according to the ratio of U_b to B_b:

$$< G_b > = (F_b U_b + 0 * B_b) / N_b, \qquad (3)$$

where $< G_b >$ is the predicted value of G_b. If we define H_b to be $F_b M_b / N_b$ then according to Eqs. (2) and (3),

$$< G_b > = (F_b U_b + 0 * B_b) / N_b \leq F_b M_b / N_b = H_b. \qquad (4)$$

Therefore, H_b should be an overestimate of G_b if the original assumption is correct. The actual values of F_b, G_b, and H_b are plotted as functions of b in Fig. S3. The figure shows only the first three bins; beyond that the analysis is inconclusive. Nevertheless, for the bins shown, the values of G_b are much higher than the values of H_b, indicating that the model's assumption (that broken filaments do not grow) is wrong.

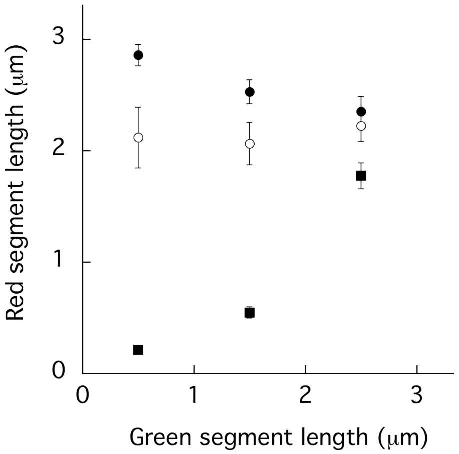

Figure S3. The mean value and standard errors of the lengths of red segments as a function of the lengths of the green segments from which they grew (plotted at bin mid-values): (●) actual data showing how the sheared filaments grew (G_b); (○) actual data showing how the unsheared filaments grew (F_b); (■) data expected if sheared filaments did not grow (H_b). All data are for cells of strain HCB1737.