Supplementary Figures:

Figure S1:

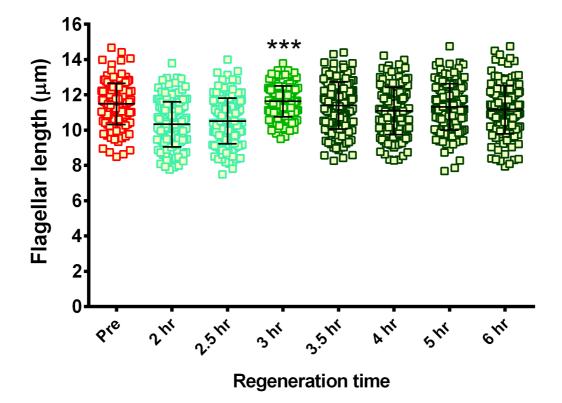


Figure S1: Wild type flagellar-length distribution at various time intervals during the regeneration after amputation. Pre-deflagellation non-synchronous cells (pre) are shown in red. Regeneration was carried out for indicated times after deflagellation by pH shock (green). Lighter and darker green indicates before and after the time of F-L synchronization respectively. Combined data from three independent experiments are represented (N=50/each, total 150). F test was performed for comparing variance (control= non-synchronous cells). Bonferroni corrected $\alpha_{altered} = 0.007$. Asterisk indicates significant difference below $\alpha_{altered}$ (***p=0.0006). Standard deviations are expressed as bar graphs in the lower panel. The filled SD bar represents F-L synchronization.

Figure S2:

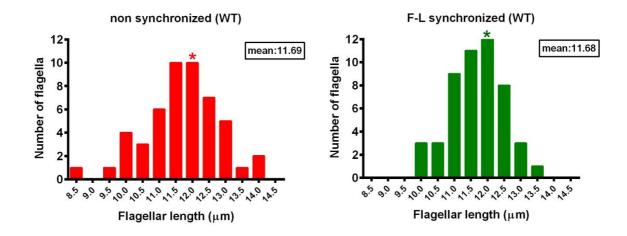


Figure S2: Distribution of flagellar length in wild type cells before and after F-L synchronization. Non-synchronized cells (red) and synchronized cells (green). N=50. Asterisk= mean flagellar length.

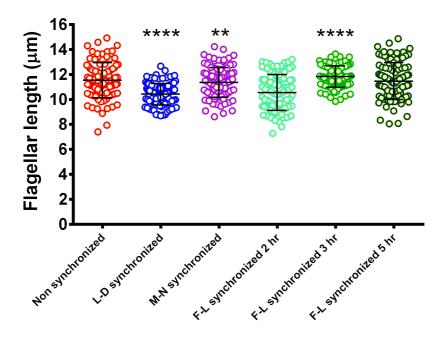


Figure S3:

Figure S3: Pre-deflagellation flagellar length distribution before precursor pool determination. These data confirm Fig 1 data showing the narrowest flagellar length distribution for L-D and F-L 3 hour synchronized cells. N=100 flagella. Bars are mean and standard deviation. F test was performed for comparing variance (control= non-synchronous cells). Asterisks indicate significant differences (**** p≤0.0001, ** p≤0.01).

Supplementary table:

	Non-	L-D	M-N	F-L synchronized	
	synchronized	synchronized	synchronized		
Mean	11.54	11.35	12.11	11.83	
SD	1.401	0.9614	1.059	0.8633	

Table S1: Flagellar length distribution after different synchronization methods.

Table S2: Distribution of flagellar length during regeneration following deflagellation.

	Pre	2 hour	2.5 hour	3 hour	3.5 hour	4 hour	5 hour	6 hour
Mean	11.70	11.00	11.40	11.68	12.12	11.64	11.54	11.26
SD	1.117	1.221	.9902	.7587	1.117	1.225	1.324	1.472

Table S3: Flagellar length distribution after length altering chemical treatment:

Chem		Non- synchronized		L-D synchronized		M-N synchronized		F-L synchronized		
-ical										
		Mean	SD	Mean	SD	Mean	SD	Mean	SD	
IBMX	Control	11.03	1.225	10.65	1.029	11.35	0.9315	10.70	1.029	
	Treated	7.063	1.103	5.965	1.122	6.657	1.015	5.863	1.015	
LatB	Control	12.11	1.052	10.65	1.029	11.31	1.200	11.63	0.8298	
	Treated	9.122	1.337	7.965	1.164	9.079	1.155	8.407	0.8109	
NaPPi	Control	11.07	1.195	10.42	0.8714	10.89	0.8654	11.94	0.8855	
	Treated	7.54	1.165	6.198	1.141	7.244	1.324	6.449	0.8925	
LiCl	Control	11.33	1.118	10.42	0.8714	12.10	1.051	12.13	0.8005	
	Treated	14.49	2.342	14.68	1.479	15.53	2.487	16.94	1.468	

	Time A	Time After Regeneration									
lf4-7		Pre	2 hr	3 hr	4hr	5 hr	6hr	7 hr	8 hr		
	Mean	20.8	12.07	17.36	19.42	21.51	20.96	22.07	20.16		
	SD	3.64	2.08	2.13	2.55	2.31	1.99	3.19	3.61		
shf1-		Pre	1 hr	1.5 hr	2hr	2.5 hr	3hr	3.5 hr	4 hr	5 hr	6 hr
253	Mean	6.4	5.07	6.24	6.73	6.7	7.13	6.78	6.54	6.77	6.56
	SD	0.92	0.96	0.92	0.81	0.56	0.80	0.98	1.05	0.98	1.21
cnk2-		Pre	2 hr	2.5 hr	3hr	3.5 hr	4 hr	5 hr	6 hr		
1	Mean	12.5	9.61	10.55	11.12	11.20	11.64	12.2	12.41		
	SD	1.05	1.12	1.27	1.05	1.15	0.87	0.71	1.01		

 Table S4: Flagellar length distribution of length mutants during regeneration.

Table S5: Flagellar length distribution prior to and after cycloheximide (cyclo)treatment:

		Non	L-D	M-N	F-L synchronized			
		synchronized	synchronized	synchronized	2 hr	3 hr	5 hr	
Before	Mean	11.54	10.42	11.36	10.56	11.83	11.46	
cyclo	SD	1.401	0.871	1.188	1.444	0.863	1.474	
After	Mean	5.600	4.191	4.513	5.409	6.162	6.156	
cyclo	SD	1.583	0.837	0.917	1.408	1.097	1.54	