

SUPPLEMENTAL FIGURE LEGENDS

Figure S1. Excess FliW doesnot disrupt FliS-Hag interaction. Protein pull-down assay using the indicated amounts of His-Hag (gray caret) loaded onto a nickel column with the indicated amounts of FliS (black caret) and/or FliW proteins (open caret) added. Gel was stained with Coomassie Brilliant blue. “Supernatant” indicates the proteins that failed to bind to the beads, and “pellet” indicates the proteins that remained bound to the beads following a series of washes.

Figure S2. FliS is required for swimming motility. Qualitative swim expansion assays were done for WT (DK374), *hag* (DK378), *fliS* (DK397), *fliW* (DK377), *fliS csrA* (DK396), *fliWcsrA* (DK376), *csrA* (DK375). Each plate is representative of three replicates.

Supplemental Table S1: Plasmids

Plasmid	Genotype	Reference
pDP362	$\Omega\Delta fliD$ <i>mls amp</i>	
pDP363	$\Omega\Delta fliS$ <i>mls amp</i>	
pDR111	<i>amyE::P_{hyspank} spec amp</i>	(31)
pJP4	<i>P_{T7}-His₆-Hag amp</i>	
pMiniMAD	<i>ori^{BsTs} mls</i>	(30)
pSM6	<i>P_{T7}-GST-CsrA amp</i>	(23)
pSM12	<i>P_{T7}-His₆-SUMO-FliW amp</i>	(23)
pSM25	<i>P_{T7}-His₆-SUMO-FliS amp</i>	
pSM36	$\Omega\Delta fliDfliS$ <i>mls amp</i>	
pSM56	<i>P_{T7}-His₆-SUMO-Hag amp</i>	
pTB146	<i>PT₇-His₆-SUMO amp</i>	(33)

Supplemental Table S2: Primers

Primer	Sequence
575	aggagggatccctagttttatcgcgaaaataaacga
576	ctcctgctgacaccctcagctgttggataagaga
577	aggaggtcgacaatcgctagagcacacaattaacaa
578	ctcctccatggagatgaactgccaaggttccaaaa
2537	aggaggaattcacaacctgttgggatcgta
2538	ctcctctcgagagacatattaatcttgaattcttt
2539	aggagctcgagaaccgctattattcaaaattcag
2540	ctcctggatcctccgctcactttgaatggct
2541	aggaggaattcgataaagaggtagagctctgg
2542	ctcctctcgagctgataggctgtatatggatt
2543	aggagctcgaggcttggaaacaagccattcaa
2544	ctcctggatccataatgaagagaagtgttgaatg
2769	aggaggctcttcaggatggcgatccaaaatccatatacag
2770	ctcctctcgagcatcgcttccggcgattttgta
2906	aggagaagcttgcgtcctatttatcacagcttct
2907	ctcctgctagccatcgcttccggcgattttg
3317	aggaggtcgaccaatgagaattaaccacaatattgc
3331	ctcctggatccggcaacgccaaggtctttttaaaa

Supplemental Table S3: β -galactosidase activities for Fig 3A and Fig 3B.

Genotype	<i>amyE::P_{hag}^{translational}-lacZ</i>	<i>amyE::P_{hag}^{transcriptional}-lacZ</i>
Wild type	6133 \pm 468 (DS278)	462 \pm 93 (DS793)
<i>csrA</i>	5275 \pm 822 (DS7596)	466 \pm 80 (DS8323)
<i>hag</i>	7109 \pm 362 (DS8622)	493 \pm 28 (DS9904)
<i>fliW</i>	738 \pm 11 (DS7598)	800 \pm 281 (DS8325)
<i>fliW csrA</i>	6003 \pm 982 (DS7597)	808 \pm 68 (DS8324)
<i>fliW hag</i>	427 \pm 33 (DK72)	698 \pm 51 (DK85)
<i>fliS</i>	669 \pm 35 (DS7814)	969 \pm 58 (DS8525)
<i>fliS csrA</i>	5439 \pm 77 (DS8526)	429 \pm 48 (DS8527)
<i>fliS hag</i>	3848 \pm 98 (DS9902)	243 \pm 59 (DS9905)

Figure S1

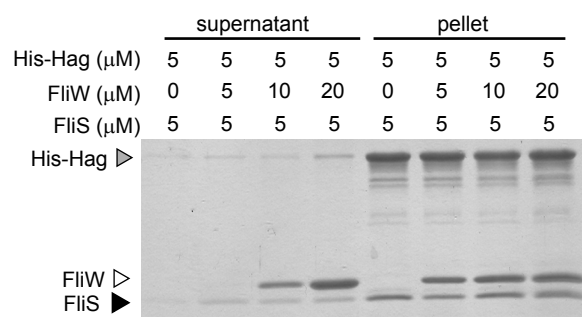


Figure S2

