Table S1: Plasmids

Plasmid	Genotype
pDG364	*amyE::cat amp*
pDP357	*amyE::$P_{fla/che}$-swrD cat amp*
pANR21	*amyE::P_{fliD}-lacZ cat*
pANR22	*amyE::P_{fliD}^{sod4}-lacZ cat*
pDG268	*amyE::lacZ cat amp*

Table S2: Primers

Primer	Sequence
609	TGAGCGAATTCACAAAGAACAACAT
1510	CTCCTAAGCTTATGCCCCAATCTATCGTTTATATCG
1802	CTCCTCTCGAGAATATCCTTGTCGAGAATTGTAAAACT
2460	AGGAGGAATTCAGGTACTTATATCAAGGTACTAA
2462	AGGAGCTCGAGCTTCAAGAACTGGTTAACCTTA
2463	CTCCTGGATCCGAGAGCACCAATTACGATAAG

Table S3: β-galactosidase activities used to construct Figure 5.

Genotype	$P_{fla/che}$-*lacZ*	P_{hag}-*lacZ*	P_{motA}-*lacZ*	P_{flgM}-*lacZ*	P_{fliD}-*lacZ*	P_{fliD}^{sod4}-*lacZ*
WT	424 ± 43 (DS791)	295 ± 21 (DS793)	248 ± 16 (DS1849)	12 ± 1 (DS811)	312 ± 26 (DK4698)	28 ± 1 (DK4805)
swrD	486 ± 15 (DK67)	312 ± 7 (DK68)	294 ± 27 (DK3046)	22 ± 1 (DK2925)	154 ± 4 (DK4699)	32 ± 1 (DK4812)
swrD sod2	444 ± 15 (DK4758)	833 ± 10 (DK4757)	833 ± 43 (DK4759)	144 ± 7 (DK2926)	N.D.	N.D.
swrD sod4	506 ± 10 (DK3187)	764 ± 28 (DK2968)	688 ± 25 (DK2919)	76 ± 8 (DK2927)	N.D.	N.D.
swrD sod48	448 ± 22 (DK3188)	882 ± 26 (DK2970)	844 ± 45 (DK2907)	126 ± 2 (DK2929)	N.D.	N.D.

The genotype column indicates the genetic background into which the reporter construct was introduced.

The reporter columns indicate the promoter fused to *lacZ* integrated at the ectopic *amyE* site in the chromosome. Each value is the average ± the standard deviation of three replicates. The strain used to generate each data point is indicated in parentheses below the values.

N.D. is not determined.

Supplemental Figure Legends

Figure S1: Mutation of *swrD* does not reduce the frequency of σ^D ON cells. Left) Bar graph indicating the percentage of cells that express P_{hag}-*GFP* in a wild type (DS908) and *swrD* mutant (DS7696) background. Each bar is the average of three replicates in which over 600 cells were counted in each experiment. Right, sample fluorescence microscopy images used to generate counts presented in the bar graph. Membranes were stained with FM4-64 and false colored red. GFP false colored green.

Figure S2: Overexpression of *motAB* does not improve swarming to cells mutated for *fliL*. Quantitative swarm expansion assay of wild type (3610), Δ*fliL* (DS6540) and Δ*fliL* *(motAB*$^{+++}$*)* (DK5113) in which *motAB* was overexpressed from a $P_{hyspank}$ promoter in the presence of 1 mM IPTG. Each point is the average of three replicates.

Figure S3. The *swrD* gene is linked to *motA*, *motB*, and *fliL* in multiple phylogenetic lineages. The phylogenetic trees were presented using the Interactive Tree of Life visualization software (67). The genomes of 191 organisms identified by Ciccarelli, *et al.* were annotated with the Pfam 29 library using the software hmmer v 3.1b2 and an E value threshold of 1e-10 (68-70). If a genome encoded a SwrD homolog (established by the presence of a FlbD domain) any open reading frames co-oriented with the *swrD* open reading frame and within 4000 bp downstream of the *swrD* open reading frame were also annotated with the Pfam 29 library using hmmer software using an E value threshold of 1e-5. The presence of MotA was established by a MotA_ExbB domain, the presence of MotB was established by a MotB_plug domain, and the presence of FliL was established by a FliL domain. Genes are drawn as boxes radiating outward from the encoding species. The 5' of each gene is oriented towards the center of the circle. Homologs of *swrD* are colored green, homologs of *motA* and *motB* are colored orange, and homologs of *fliL* are colored blue. A full list of all bacterial species that encode *swrD* homologs including the genes encoded downstream of *swrD* is presented in table S4.

Supplemental references

67. **Letunic I, Bork P. 2016.** Interactive tree of life (iTOL) v3: an online tool for the display and annotation of phylogenetic and other trees. *Nucleic Acids Res* **44**:W242-W245.

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Figure S1

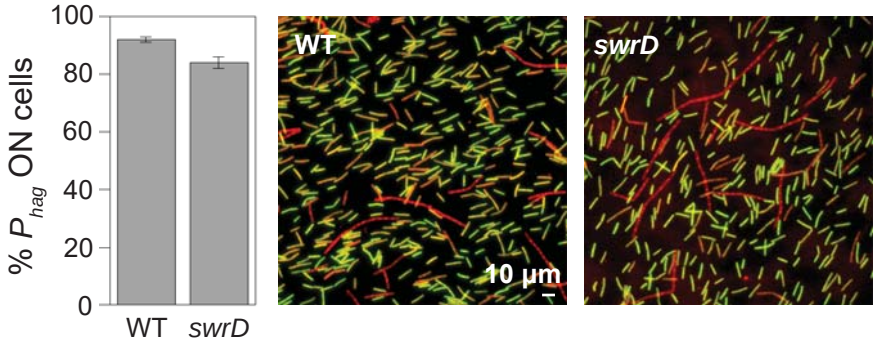

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Figure S2

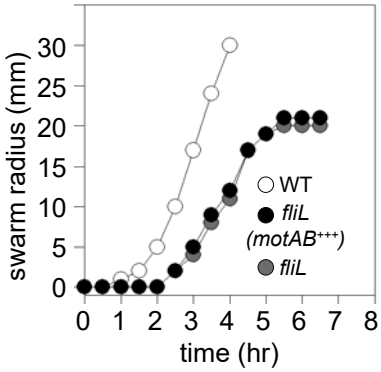

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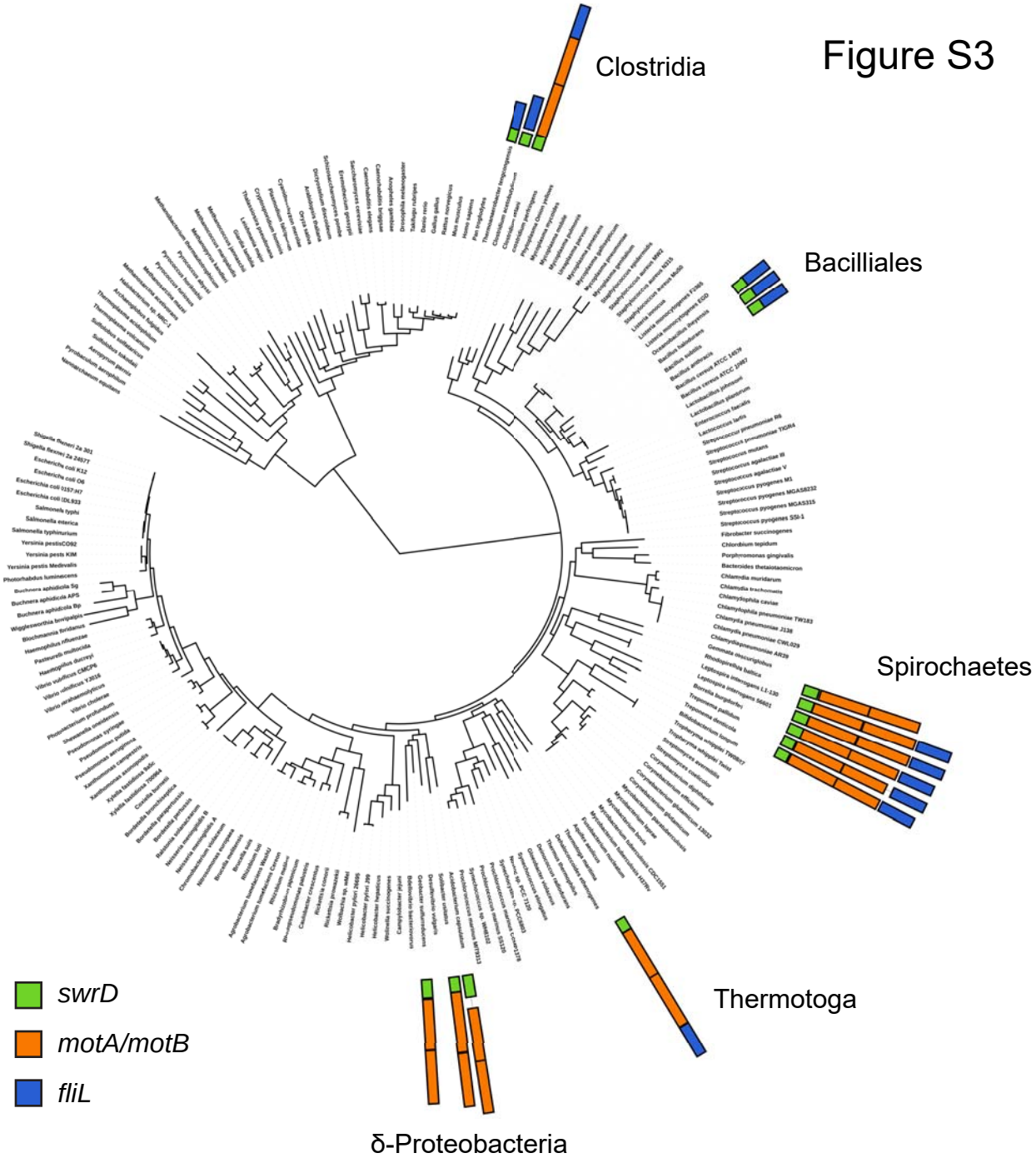
Figure S3



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