Strain or plasmid Genotype or description Reference or source E. coli DH5a $F^- \Phi 80 dlac Z \Delta M15 \Delta (lac ZYA$ argF)U169 deoR recA1 endA1 $hsdR17(r_{K}, m_{K}) phoA supE44 \lambda$ thi-1 gyrA96 relA1 **BL21(DE3)** $F^- ompT hsdS_B (r_B^- m_B^-) gal dcm (DE3)$ Novagen V. alginolyticus VIK4 (Rif⁺ Pof⁺ Laf⁻) VIO5 (1) LPN1 VIO5 $\Delta flhF$ (Rif⁺ Pof⁺ Laf⁻) (2) **NMB196** $VIO5\Delta fliF$ (Rif⁺ Pof⁺ Laf⁻) (3)Plasmids pCold I Amp^r , P_{cspA} Takara Cm^r, P_{tac} P_{lac} UV5 pMMB206 (4)pBAD33 Cm^r , P_{BAD} (5)pTY60 Km^r, P_{BAD} (6)pTY57 Cm^r, P_{BAD} (7)pCold I-his-fliF pRO101 (8)This study pRO101-his-fliF(31-580) pRO101-*AN30* pRO101-AN50 pRO101-his-fliF(51-580) This study pRO101-*AC83* pRO101-his-fliF(1-497) This study pRO101-*AC110* pRO101-his-fliF(1-470) This study pTSK137 pCold I-his-fliFG (9) pTSK122 (9) pMMB206-flhF pTY57-fliF (8) pTY502 pTY502-*AN30* pTY57-fliF(31-580) This study pTY502-AN50 pTY57-fliF(51-580) This study рТҮ502-*ДС83* pTY57-fliF(1-497) This study pTY502-*AC110* pTY57-fliF(1-470) This study pHHT103 pBAD33-his-fliF (9) This study рННТ103-ДN30 pBAD33-his-fliF(31-580) pHHT103-⊿N50 pBAD33-his-fliF(51-580) This study pYI101 (9) pTY60-fliF-egfp pYI101-*N*⊿30 pTY60-*fliF*(Δ2-30)-*egfp* This study pYI101-NA50 pTY60-*fliF*(Δ2-50)-*egfp* This study Amp^r, ampicillin-resistant; Cm^r, chloramphenicol-resistant; Rif^r, Rifampicin-resistant; Pof⁺, possessing a polar flagellum; Laf⁻, lack of lateral flagella

Table S1. Bacterial strains and plasmids used in this study

References

- 1. Okunishi I, Kawagishi I, Homma M. 1996. Cloning and characterization of *motY*, a gene coding for a component of the sodium-driven flagellar motor in *Vibrio alginolyticus*. J Bacteriol 178:2409-2415.
- Kusumoto A, Shinohara A, Terashima H, Kojima S, Yakushi T, Homma M. 2008. Collaboration of FlhF and FlhG to regulate polar-flagella number and localization in *Vibrio alginolyticus*. Microbiology 154:1390-1399.
- 3. Yorimitsu T, Sato K, Asai Y, Kawagishi I, Homma M. 1999. Functional interaction between PomA and PomB, the Na⁺-driven flagellar motor components of *Vibrio alginolyticus*. J Bacteriol 181:5103-5106.
- 4. Morales BM, Backman A, Bagdasarian M. 1991. A series of wide-host-range lowcopy-number vectors that allow direct screening for recombinants. Gene 97:39-47.
- Guzman LM, Belin D, Carson MJ, Beckwith J. 1995. Tight regulation, modulation, and high-level expression by vectors containing the arabinose pBAD promoter. J Bacteriol 177:4121-4130.
- Kojima S, Nonoyama N, Takekawa N, Fukuoka H, Homma M. 2011. Mutations targeting the C-terminal domain of FliG can disrupt motor assembly in the Na⁺-driven flagella of *Vibrio alginolyticus*. J Mol Biol 414:62-74.
- Li N, Kojima S, Homma M. 2011. Characterization of the periplasmic region of PomB, a Na⁺-driven flagellar stator protein in *Vibrio alginolyticus*. J Bacteriol 193:3773-3784.
- Ogawa R, Abe-Yoshizumi R, Kishi T, Homma M, Kojima S. 2015. Interaction of the C-Terminal Tail of FliF with FliG from the Na⁺-Driven Flagellar Motor of *Vibrio alginolyticus*. J Bacteriol 197:63-72.
- Terashima H, Hirano K, Inoue Y, Tokano T, Kawamoto A, Kato T, Yamaguchi E, Namba K, Uchihashi T, Kojima S, Homma M. 2020. Assembly mechanism of a supramolecular MS-ring complex to initiate bacterial flagellar biogenesis in *Vibrio* species. J Bacteriol 202:e00236-20.

	30 50
1 1	MADKSTDLTVTEGGSDGALVASSDVDVESQNPDLEERSASKFDMAVGDLDLLRQVVLVLS
61	ISICVALIVMLFFW/KEPEMRPL-GAYETEELIPVLDYLDQQKINYKLDGNTISVESS
32	GSAAVAIVVAMVLW <mark>AKTPDYRTL</mark> FSNLSDQDGGAIVAQLTQMNIPYRFANGSGAIEVPAD
118	EYNSIKLGMVRSGVNQATEAGDDILLQDMGFGVSQRLEQERLKLSRERQLAQAIEEMKQV
92	KVHELRLRLAQQGLPKGGAVGFE-LLDQEKFGISQFSEQVNYQRALEGELARTIETLGPV
178	RK <mark>ARVLLALPKHSVFVR</mark> HNQEA <mark>SASV</mark> FLTLSTGTNLKQQEVDSIVDMVASAVPGMKTSRI
151	KS <mark>ARV</mark> HLAMPK <mark>PSLFVR</mark> EQKSP <mark>SASV</mark> TVTLEPGRALDEGQISAVVHLVSSAVAGLPPGNV
238	TVTDQHGRLLSSGSQDPASAARRKEQELERSQEQALREKIDSVLLPILGYGNYTAQVDIQ
211	TLVDQSGHLLTQ-SNTSGRDLNDAQLKFANDVESRIQRRIEAILSPIVGNGNVHAQVTAQ
298	MDFSAVEQTRKRFDPNTPATRSEYALEDYNNGNMVAGIPGALSNQPPADASI-
270	LDFANKEQTEEHYSPNGDASKATLRSRQLNISEQVGAGYPGGVPGALSNQPAPPNEAPIA
350	PQDVAQMKDGSVMGQGSVRKESTRNFELDTTISHERKQTGTVARQTVSV
330	TPPTNQQNAQNTPQTSTSTNSNSAGPRSTQRNETSNYEVDRTIRHTKMNVGDIERLSVAV
399	AIKDRRQVNPDTGEVTYTPMSESEINAIRQVLIGTVGFDQGRGDLLNVLSVKFAEPEAEQ
390	VVNYKTLADGKPLPLTADQMKQIEDLTREAMGFSDKRGDTLNVVNSPFSAVDNTG
459	LEEPPIWEHPNFSLWVRWFASALVIIVVVLVLVRPAMKKLLNPTSDDEDEMYGPDGLPIG
445	-GELPFWQQQSFILQLLAAGRWLLVLVVAWILWRKAVRPQLTRRVEEAKAAQEQAQVR
519	ADGETSLIGSDIESSELFEFGSSIDLPNLHKDEDVLKAVRALVANEPELAAQVVKNWMND
502	QETEEA-VEVRLSKDEQLQQRRANQRLG-AEVMSQRIREMSDNDPRVVALVIRQWMSN
579	NG-
558	DHE

Fig. S1. Comparison of amino acid sequences of *Salmonella* FliF and *Vibrio* FliF. Amino acid sequence homology is about 27%. The red frames indicate transmembrane regions. Arrows indicate mutation sites.



Fig. S2. Detection of N-terminal deletion FliF. The *fliF* deletion mutant (NMB196) producing wild-type FliF, Δ N30FliF, or Δ N50FliF from the pBAD plasmids was grown to mid-log phase in the presence of 0.02% arabinose and cells were disrupted by sonication. The membrane and the soluble fraction were separated by ultracentrifugation. After separating the proteins from the membrane and the soluble fraction by SDS-PAGE, the FliF protein was detected by immunoblotting with an anti-FliF antibody.



Fig. S3. (A) Motility of N-terminal deletion His-FliF in soft agar plate. Fresh single colonies of the *fliF* deletion mutant (NMB196) containing pTY502 (FliF), pHHT103 (His-FliF), pHHT103- $\Delta N30$ (His- $\Delta N30$ FliF), or pHHT103- $\Delta N50$ (His- $\Delta N50$ FliF) inoculated by toothpicks on the VPG-Cm 0.25% soft agar containing 0.02% arabinose, and incubated at 30 °C for 4.5 hours. (B) Detection of N-terminal deletion FliF. The *fliF* deletion mutant (NMB196) containing the same plasmids and pBAD33 was grown to mid-log phase and the whole cells were subjected to SDS-PAGE, and the separated FliF protein was detected by immunoblotting with an anti-FliF antibody.



Fig. S4. Purification process of MS ring made by N-terminal deleted FliF. *E. coli* BL21 (DE3) cells harboring pRO101 (A), pRO101 and pTSK22 (B), pRO101- Δ N30 (C), pRO101- Δ N30 and pTSK122 (D), pRO101- Δ N50 (E), or pRO101- Δ N50 and pTSK122 (F) were cultured and MS ring was isolated. The purification procedure is described in the bottom of the figure. The samples indicated by number in the procedure were subjected to SDS-PAGE, and the separated FliF protein was detected by immunoblotting with an anti-FliF antibody.



Fig. S5. Purification process of MS ring made by C-terminal deleted FliF. *E. coli* BL21 (DE3) cells harboring pRO101- $\Delta C83$ (A), pRO101- $\Delta C83$ and pTSK22 (B), pRO101- $\Delta C110$ (C) were cultured and MS ring was isolated as Fig. S4. The samples indicated by number in the procedure described in Fig. S4 were subjected to SDS-PAGE, and the separated FliF protein was detected by immunoblotting with an anti-FliF antibody.