SUPPLEMENTAL FIGURE LEGENDS

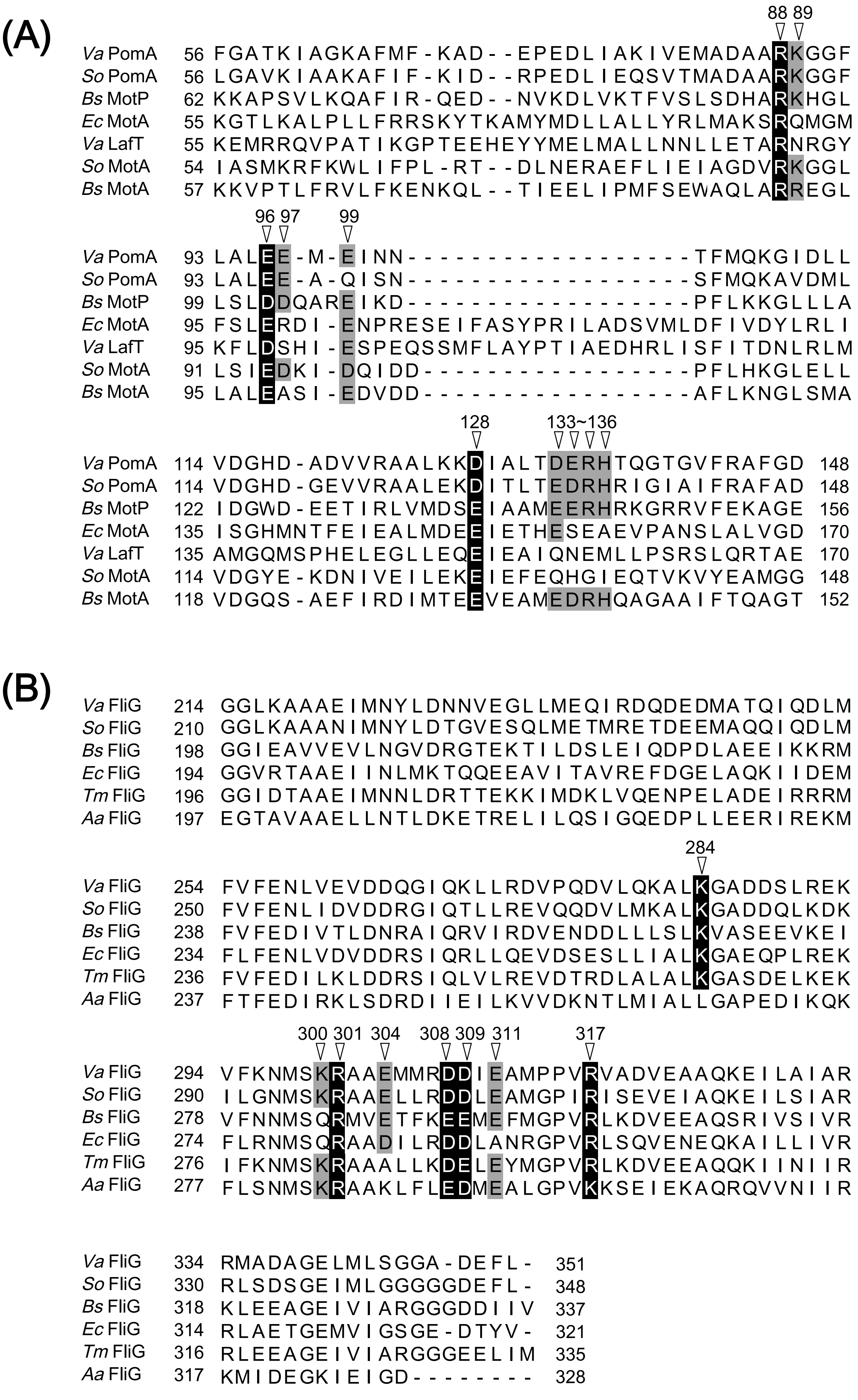
FIG. S1. Amino acid sequence alignment. Amino acid sequence alignment of the cytoplasmic loop regions of PomA (A) and the C-terminal regions of FliG (B) with residues mutated in this study. Residues shown in black boxes are residues that are conserved and are involved in torque generation of the H^+-driven flagellar motor in *E. coli* as described previously (14). Residues shown in gray boxes are additional residues mutated in this study. Numbers over the arrowheads indicate the residue numbers of PomA or FliG of *V. alginolyticus* mutated in this study. The multiple sequence alignment was carried out by the Clustal Omega application at the European Bioinformatics Institute website (http://www.ebi.ac.uk/Tools/msa/clustalo/). *Va*, *V. alginolyticus*; *So*, *S. oneidensis*; *Bs*, *B. subtilis*; *Ec*, *E. coli*; *Tm*, *T. maritima*; *Aa*, *A. aeolicus*. MotP, Na^+/K^+-driven stator protein in *B. subtilis*; LafT, H^+-driven stator protein in lateral flagella.

FIG. S2. Complementation of the *pomAB fliG* triple-mutant strain by wild-type *pomAB* and *fliG* genes on plasmids and detection of PomA and FliG proteins with mutations. (A) NMB301, Δ*pomAB*Δ*fliG* strain, was transformed with two plasmids, pSU41 (vector) or pYA303 (encoding the *pomAB* genes), and pMMB206 (vector) or pNT1 (encoding the *fliG* gene), and cells were inoculated in soft-agar plates and incubated at 30°C for 8 hr. (B) Expression of mutant PomA proteins. NMB301 cells harboring two plasmids, pSU41 or pYA303 encoding wild-type or mutant *pomA* with wild-type *pomB*, and pNT1 encoding the wild-type *fliG*, were grown at 30ºC for 4 hr, and whole-cell extracts were analyzed by immunoblotting with the anti-PomA antibody. (C) Expression of the mutant FliG proteins. NMB301 cells harboring two plasmids, pYA303 encoding wild-type *pomAB*, and pMMB206 or pNT1 encoding the wild-type or the mutant *fliG*, were grown at 30ºC for 4 hr, and whole-cell extracts were analyzed by immunoblotting with the anti-FliG antibody.

FIG. S3. Motilities of *pomA*/*fliG* combined mutants in soft-agar plates (i). Swimming abilities were observed in soft-agar plates of *pomA*/*fliG* combined mutants where highly conserved charged residues were substituted by single uncharged residues. Cells were incubated on VPG-soft-agar plates at 30ºC for 4.5 hr.

FIG. S4. Motilities of *pomA*/*fliG* combined mutants in soft-agar plates (ii). Swimming abilities were observed in soft-agar plates of *pomA*/*fliG* combined mutants where charged residues were substituted by charge-reversed residues. Cells were incubated on VPG-soft-agar plates at 30ºC for 5 hr.

FIG. S5. Motilities of *pomA*/*fliG* combined mutants in soft-agar plates (iii). Swimming abilities were observed in soft-agar plates of *pomA*/*fliG* combined mutants where charged residues were substituted by charge-reversed residues. Cells were incubated on VPG-soft-agar plates at 30ºC for 6 hr.



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(A)
Va PomA   56 FGATKIAGKAFMF-KAD--EPEDLIAKIVEMADAARKGGF
So PomA   56 LGAVKIAAKAFIF-KID--RPEDLIEQSVTMADAARKGGF
Bs MotP   62 KKAPSVLKQAFIR-QED--NVKDLVKTFVSLSDHARKHGL
Ec MotA   55 KGTLKALPLLFRRSKYTKAMYMDLLALLYRLMAKSRQMGM
Va LafT   55 KEMRRQVPATIKGPTEEHEYYMELMALLNNLLETARNRGY
So MotA   54 IASMKRFKWLIFPL-RT--DLNERAEFLIEIAGDVRKGGL
Bs MotA   57 KKVPTLFRVLFKENKQL--TIEELIPMFSEWAQLARREGL

Va PomA   93 LALEE-M-EINN------------------TFMQKGIDLL
So PomA   93 LALEE-A-QISN------------------SFMQKAVDML
Bs MotP   99 LSLDDQAREIKD------------------PFLKKGLLLA
Ec MotA   95 FSLERDI-ENPRESEIFASYPRILADSVMLDFIVDYLRLI
Va LafT   95 KFLDSHI-ESPEQSSMFLAYPTIAEDHRLISFITDNLRLM
So MotA   91 LSIEDKI-DQIDD-----------------PFLHKGLELL
Bs MotA   95 LALEASI-EDVDD-----------------AFLKNGLSMA

Va PomA  114 VDGHD-ADVVRAALKKDIALTDERHTQGTGVFRAFGD  148
So PomA  114 VDGHD-GEVVRAALEKDITLTEDRHRIGIAIFRAFAD  148
Bs MotP  122 IDGWD-EETIRLVMDSEIAAMEERHRKGRRVFEKAGE  156
Ec MotA  135 ISGHMNTFEIEALMDEEIETHESEAEVPANSLALVGD  170
Va LafT  135 AMGQMSPHELEGLLEQEIEAIQNEMLLPSRSLQRTAE  170
So MotA  114 VDGYE-KDNIVEILEKEIEFEQHGIEQTVKVYEAMGG  148
Bs MotA  118 VDGQS-AEFIRDIMTEEVEAMEDRHQAGAAIFTQAGT  152

(B)
Va FliG  214 GGLKAAAEIMNYLDNNVEGLLMEQIRDQDEDMATQIQDLM
So FliG  210 GGLKAAANIMNYLDTGVESQLMETMRETDEEMAQQIQDLM
Bs FliG  198 GGIEAVVEVLNGVDRGTEKTILDSLEIQDPDLAEEIKKRM
Ec FliG  194 GGVRTAAEIINLMKTQQEEAVITAVREFDGELAQKIIDEM
Tm FliG  196 GGIDTAAEIMNNLDRTTEKKIMDKLVQENPELADEIRRRM
Aa FliG  197 EGTAVAAELLNTLDKETRELILQSIGQEDPLLEERIREKM

Va FliG  254 FVFENLVEVDDQGIQKLLRDVPQDVLQKALKGADDSLREK
So FliG  250 FVFENLIDVDDRGIQTLLREVQQDVLMKALKGADDQLKDK
Bs FliG  238 FVFEDIVTLDNRAIQRVIRDVENDDLLLSLKVASEEVKEI
Ec FliG  234 FLFENLVDVDDRSIQRLLQEVDSESLLIALKGAEQPLREK
Tm FliG  236 FVFEDILKLDDRSIQLVLREVDTRDLALALKGASDELKEK
Aa FliG  237 FTFEDIRKLSDRDIIEILKVVDKNTLMIALLGAPEDIKQK

Va FliG  294 VFKNMSKRAAEMMRDDIEAMPPVRVADVEAAQKEILAIAR
So FliG  290 ILGNMSKRAAELLRDDLEAMGPIRISEVEIAQKEILSIAR
Bs FliG  278 VFNNMSQRMVETFKEEMEFMGPVRLKDVEEAQSRIVSIVR
Ec FliG  274 FLRNMSQRAADILRDDLANRGPVRLSQVENEQKAILLIVR
Tm FliG  276 IFKNMSKRAAALLKDELEYMGPVRLKDVEEAQQKIINIIR
Aa FliG  277 FLSNMSKRAAKLFLEDMEALGPVKKSEIEKAQRQVVNIIR

Va FliG  334 RMADAGELMLSGGA-DEFL-  351
So FliG  330 RLSDSGEIMLGGGGGDEFL-  348
Bs FliG  318 KLEEAGEIVIARGGGDDIIV  337
Ec FliG  314 RLAETGEMVIGSGE-DTYV-  321
Tm FliG  316 RLEEAGEIVIARGGGEELIM  335
Aa FliG  317 KMIDEGKIEIGD--------  328
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Fig. S1. Takekawa *et al.*

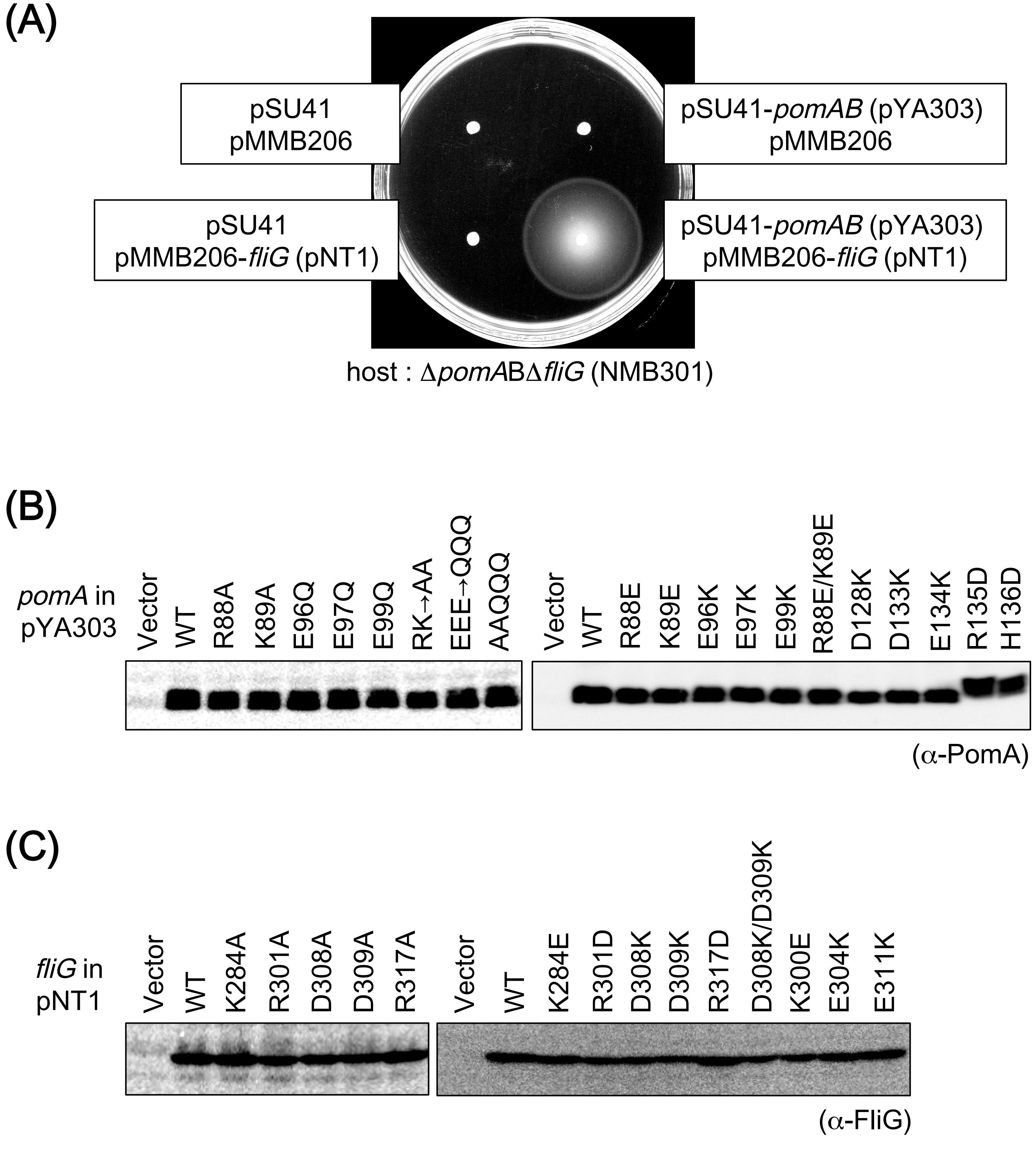

Fig. S2. Takekawa *et al*.

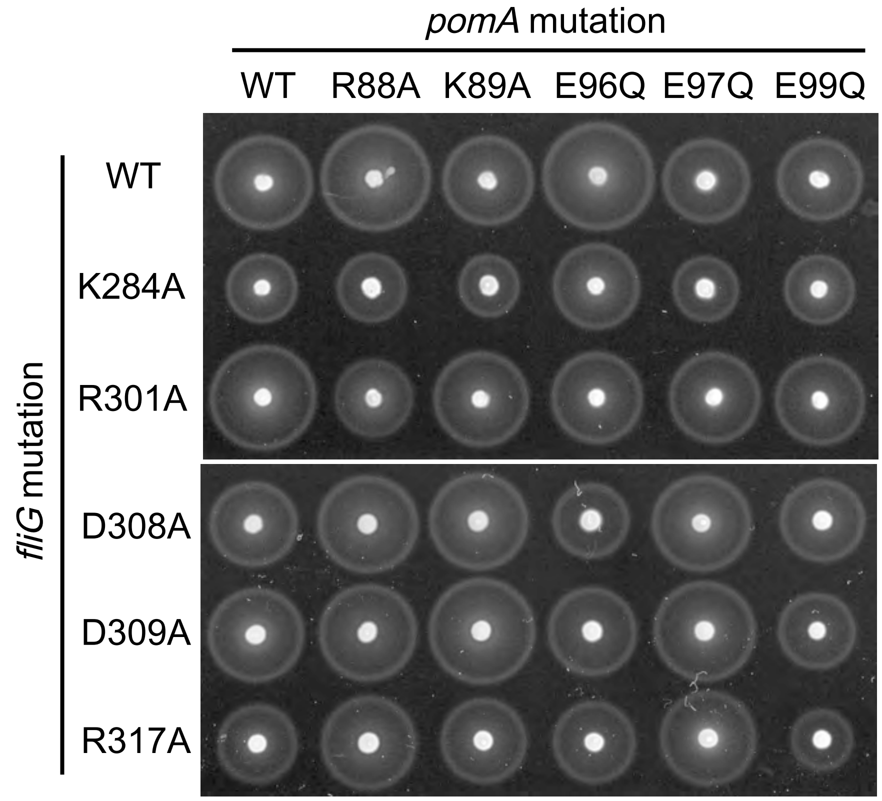

Fig. S3. Takekawa *et al*.

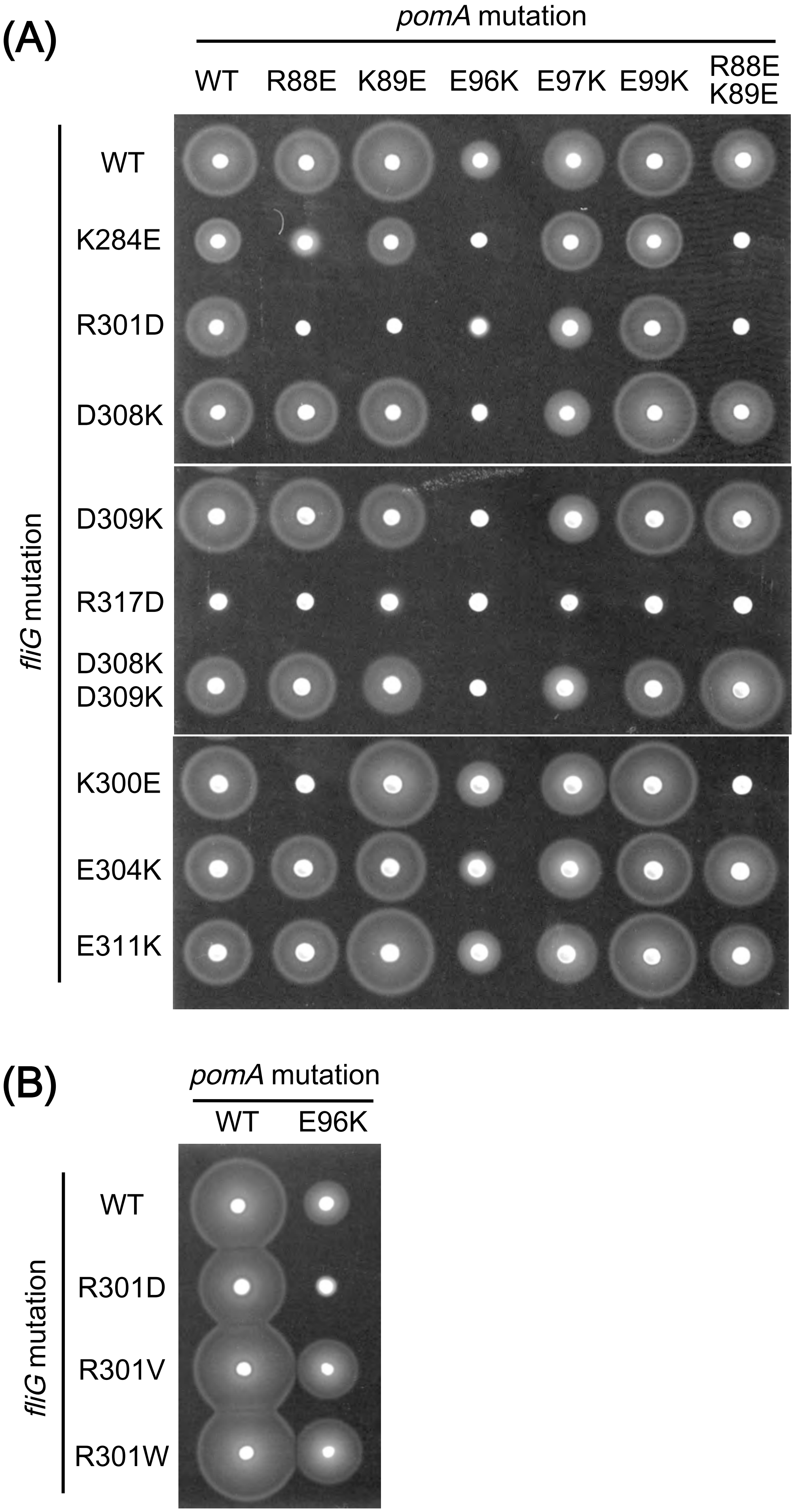

Fig. S4. Takekawa *et al.*

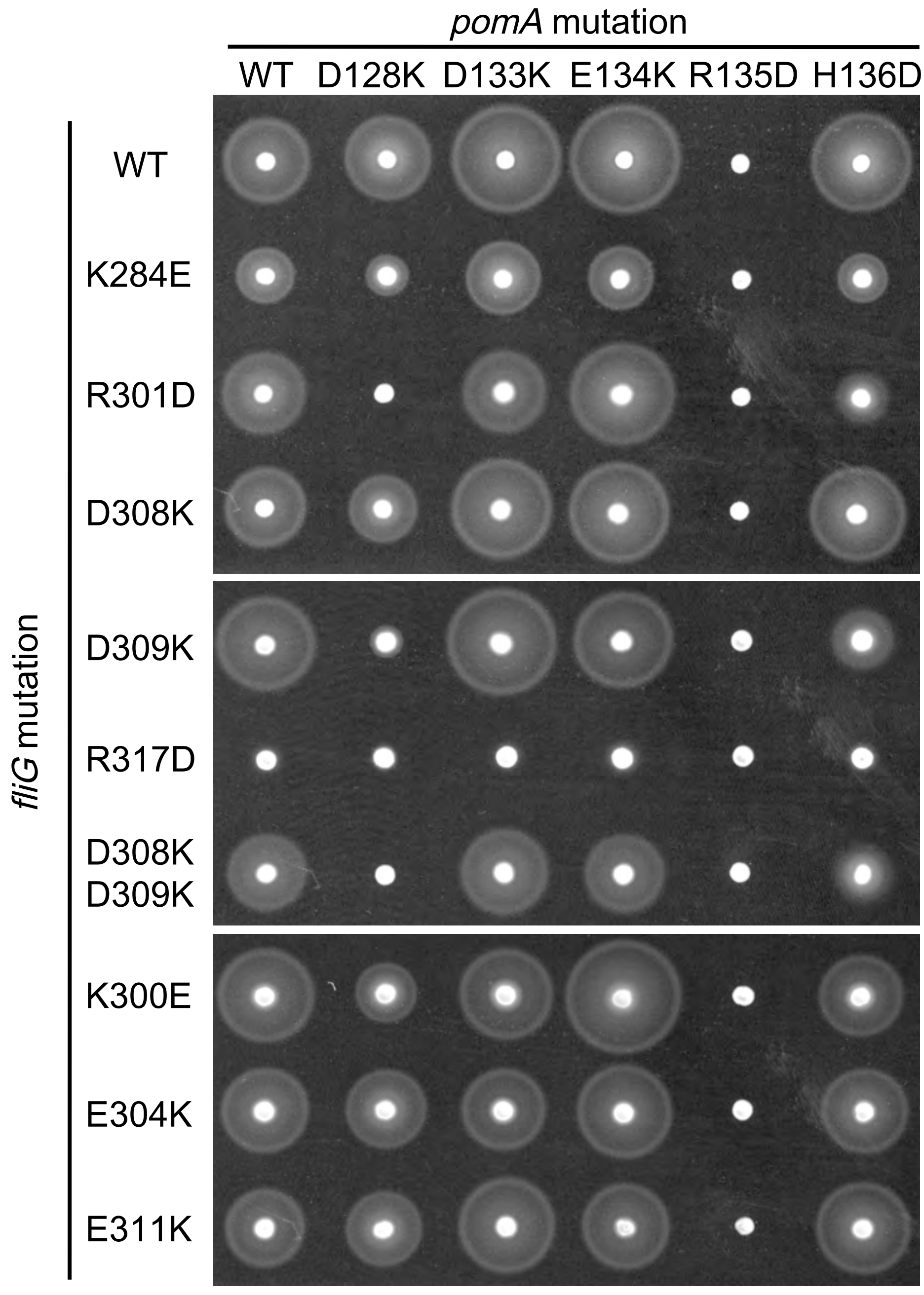

Fig. S5. Takekawa *et al*.