

Supplemental material

TABLE S1 Oligonucleotides used in this work

RSP0035B	5' CGGAATTCGTGACCCCGAAAGGCAGCGAC 3'
ORF12	5' GCTCTAGACGTTTCAGCGCCTCCACATGG 3'
pRK6086 F	5' CGTCTAGAGTCACGCCGAAGGGCAGCGAC 3'
pRK6086 R	5' GCGAATTCCGTTTCAGCGCCTCCACATGG 3'
pBADmyc6086SPS-fw	5' TAGAATTCGACAGCCCGCCGTC 3'
pBADmyc6086SPS-rv	5' ATAAGCTTCCGGCCGGTCTCCA 3'
6086DHFw	5' CGGAATTCGCCGTCCGGGTCGAGGCCGA 3'
6086DHRV	5' CGCTGCAGGCCGGCCGGTCTCCACGAACTGC 3'
GAD6086Rv	5' ATCCCGGGGCCGGCCGGTCTCCACGA 3'
DH67CoilF	5' GAATTCGCTCGGTCGCCGATCTGCGCGA 3'
pG67FCOOH	5' GAATTCACCGAGCTCGGCGAGGCCATCG 3'
RSP0067-GSTRvsSTOP	5' CCCGGGTCACGGATAACGGATCGGATTG 3'
ADBDmotB1	5' GCGAATTCTCGTTTCAGCAAGATGGCGGGG 3'
ADmotB2	5' GCGAGCTCTCAGTCCTTGTAGGAAATCTC 3'

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R.spha/1-361      1 VRRLL LLL LAL - - - LAPLAASADSPAVRV EAEGFAMVAGPGDRDAARRRAVSDALLA 55
Va/1-377         1 MKKILNSLFSITLVMLVLPFKVMA S - - - - WY E V T G V A T I V S S - - E E T A R L H A L E D A L F K 52

R.spha/1-361     56 AALAAGADVSGHTAVNRGIVTSDVAIVRSVGRILRHRILSETLSGATWRVRIEALVGE 113
Va/1-377         53 AVNFSGADI- GSI SNLMP LLEESRNEYQFTNHEVR Y - I L V E S E R K R R G K V E V K I R V D I 108

R.spha/1-361     110 G P G P L - C P V R T L I V T A Y P A T L A V D P H A P A W S G E L A R T I A E R L V E R L A L H P A A S L S R V A 170
Va/1-377         109 Y P S A T G C H - - - - - T D Q Y K K T I L V - - - - - - - G N I E V A S P Q Q A V M G Q I Y Q V G D D F S R V V 153

R.spha/1-361     171 E R R P T R L G R - - - - - G G E A F D Y Q S L T Q G S V R L P A N G H G - - - - - - - - - F L P T I R L R R V 212
Va/1-377         150 N R Q L D Q T S R S F V S V G T T D Y S I S S N Y P A R T Q M I A Q D N G A Q Y I I G G V I T D L T A T V E S Q L L 211

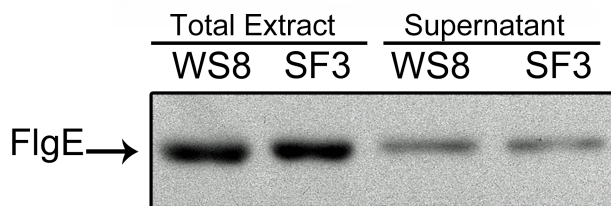
R.spha/1-361     213 A G P R L E L A L E L K L V A A D G T A S V Q Q F - - - - - V R R V P L P R P S L L G D L S V L V Q P Q R E A L A 260
Va/1-377         212 Q D D I I N R Q F A L E M K V F D G K T G H E V F N K A Y R E V A R W P F A K T S Q V D T R S A R F W A S - - T Y G 267

R.spha/1-361     265 S A L L E G S D R A L D A L F D R A G C E P A S A R L V A A - G G L L E V P V G Q A N G L T P G - - - - - S L A 310
Va/1-377         268 E M M L R V S R N I M L D L E S E L S C K I T L P E V V A V F G N T V T M D L G R M H G V K E G D K L Q L W H T A S 325

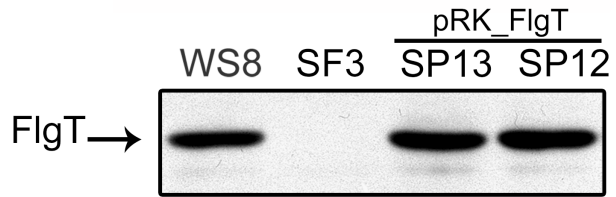
R.spha/1-361     315 F T A D G G - - - - - S T E I - L E I V A L R S G S A R L R P L D P T R P P A A F A G R R V Q F V E T G R      361
Va/1-377         326 F I D Q N G L P R N K V S Q S E I T L T V S R I Y E H E A E L T I D Q P N L A S S V Q I G D V M N K I L - - -      377

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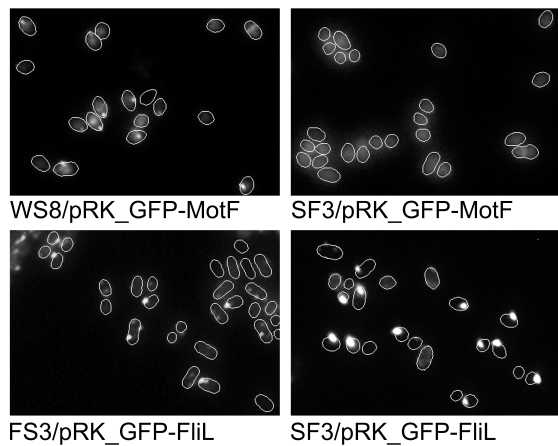
Suppl. Fig 1. Sequence alignment of FlgT from *Vibrio alginolyticus* with the gene product of RSP_6086 (FlgT_{RS})



Suppl. Fig 2. Exponentially growing cultures of WS8 and FS3 were fractionated, and the supernatant and cell pellet were analyzed by Western blot using anti-FlgE antibodies.



Suppl. Fig 3. Presence of FlgT in total cell extracts from SP13 ($\Delta fleQ1::Kan$) and SP12 ($\Delta fleT1::aadA$) strains expressing *flgT* from *lacp* present in pRK415. Total cell extracts from WS8 and SF3 were used as positive and negative controls, respectively.



Suppl. Fig 4. GFP-MotF and GFP-FliL localization in SF3 strain. Representative images of GFP-MotF and GFP-FliL in WS8 and SF3 cells. Bar=1 μm . Cell contours are shown.