

1                   ***Vibrio parahaemolyticus* RhsP Represents a Widespread Group of**  
2                   **Pro-effectors for Type VI Secretion System**

3  
4  
5           Nan Jiang<sup>1, #</sup>, Le Tang<sup>2,3,4, #</sup>, Ruiqiang Xie<sup>1</sup>, Zhi Li<sup>1</sup>, Brianne Burkinshaw<sup>2,3,4</sup>, Xiaoye Liang<sup>5</sup>,  
6           Dylan Sosa<sup>6</sup>, L. Aravind<sup>7</sup>, Tao Dong<sup>2,3,4,5,\*</sup>, Dapeng Zhang<sup>6,8,\*</sup> and Jun Zheng<sup>1,\*</sup>

7  
8  
9   **Affiliations:**

10  
11   <sup>1</sup> Faculty of Health Sciences, University of Macau, Macau SAR, China

12   <sup>2</sup> Department of Ecosystem and Public Health, University of Calgary, Calgary, AB, T2N 4Z6,  
13   Canada

14   <sup>3</sup> Department of Biochemistry and Molecular Biology, University of Calgary, Calgary, AB, T2N  
15   4Z6, Canada

16   <sup>4</sup> Snyder Institute for Chronic Diseases, University of Calgary, Calgary, AB, T2N 4Z6, Canada

17   <sup>5</sup> State Key Laboratory of Microbial Metabolism, Joint International Laboratory on Metabolic and  
18   Developmental Sciences, School of Life Sciences and Biotechnology, Shanghai Jiao Tong  
19   University, Shanghai, 200240, China

20   <sup>6</sup> Program of Bioinformatics and Computational Biology, College of Arts and Sciences, Saint  
21   Louis University, Saint Louis, MO, 63103, USA

22   <sup>7</sup> National Center for Biotechnology Information, National Library of Medicine, National  
23   Institutes of Health, Bethesda, MD, 20894, USA

24   <sup>8</sup> Department of Biology, College of Arts and Sciences, Saint Louis University, Saint Louis, MO,  
25   63103, USA

26  
27  
28   # These two authors contributed equally to this work

29  
30   \* Correspondence should be addressed to:

31  
32           Jun Zheng, [junzheng@umac.mo](mailto:junzheng@umac.mo)  
33           or Dapeng Zhang, [dapeng.zhang@slu.edu](mailto:dapeng.zhang@slu.edu)  
34           or Tao Dong, [tdong@ucalgary.ca](mailto:tdong@ucalgary.ca)

35  
36   **Running title: A widespread pro-effector for T6SS**

38 **Keywords:** T6SS, Rhs, Pro-effector, PAAR, social cheater

39

40 **Supporting Information**

41 **Supplementary Methods**

42 **Quantitative Real-time PCR.** The total bacterial RNA was extracted using RNeasy Mini Kit  
43 (Qiagen) after being treated with RNAprotect Bacteria Reagent (Qiagen). Synthesis of cDNA  
44 was performed using PrimeScript RT reagent Kit (Takara). Quantitative PCR was carried on  
45 cDNA using SYBR Premix Ex TagII (Takara) on a CFX96 Real-Time PCR machine (BioRad).  
46 16S rRNA gene was used as an internal control.

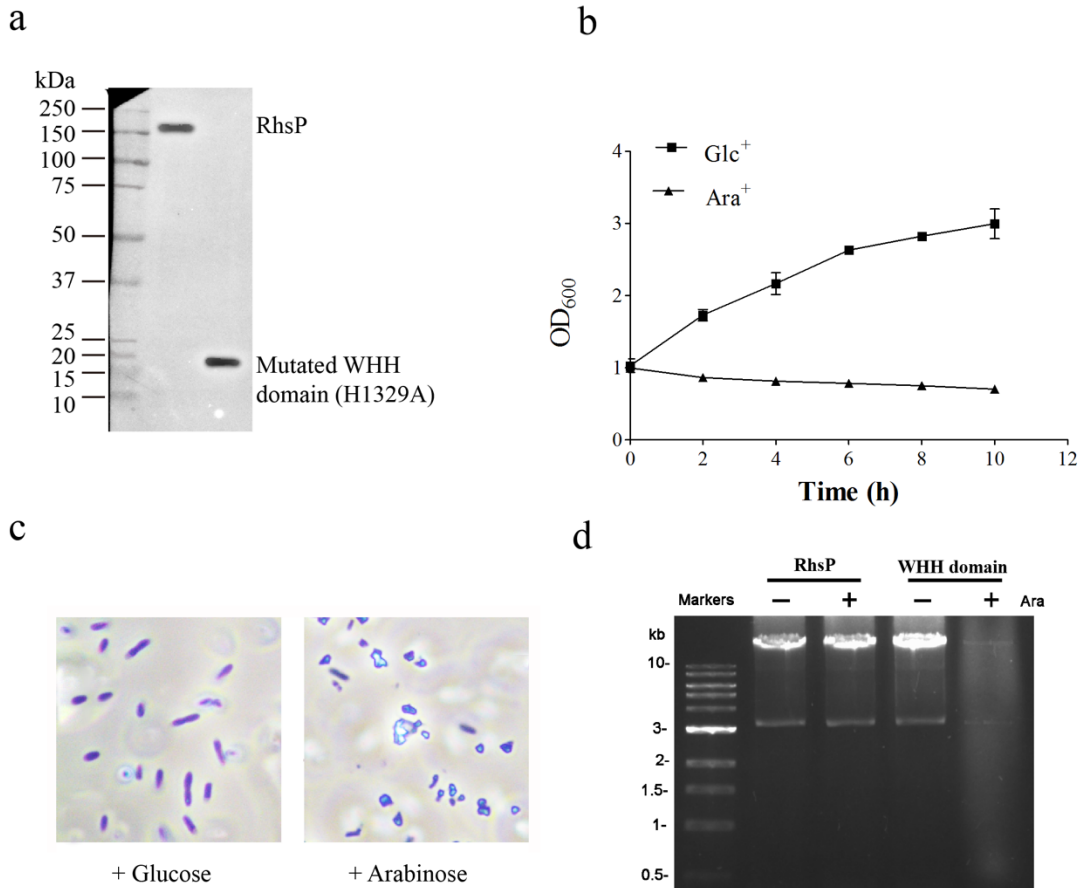
47 **Microscopy imaging of bacteria.** *E. coli* cells containing pBAD24-WHH domain were  
48 recovered in 5ml LB to  $OD_{600} = 0.6$ , and induced by 0.2% arabinose and glucose respectively for  
49 2 hours. Five microliters of bacteria were dropped on the object slide and imaged using a Nikon  
50 eclipse E200 microscope.

51

52

53

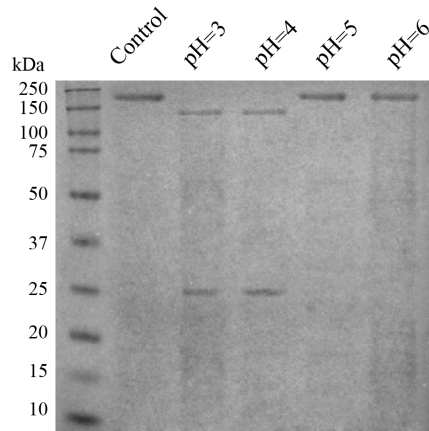
54 **Supplementary Figures**



55

56 **Supplementary Fig. 1. Toxicity of RhsP and its WHH domain on *E. coli*.** (a) Western blot  
 57 analysis of the expression of RhsP-FLAG in *E. coli* DH5 $\alpha$ . A WHH domain with site-directed  
 58 mutagenesis (H1329A) expressed in *E. coli* DH5 $\alpha$  was included as a control. (b) Growth curve  
 59 of *E. coli* expressing WHH domain (pBAD24-WHH domain-F). 0.2 % glucose (Glc<sup>+</sup>) or 0.2%  
 60 arabinose (Ara<sup>+</sup>) was added into cultures when the bacterial OD<sub>600</sub> reached 1.0 to repress or  
 61 induce the expression of WHH domain respectively. Bacterial number as measured by OD<sub>600</sub>  
 62 decreased gradually when the expression of WHH domain was induced by arabinose, contrary to  
 63 the increase when bacteria were supplemented with glucose. (c) Microscopy images of *E. coli*  
 64 expressing WHH domain (pBAD24-WHH domain-F). Cells died and broke upon WHH domain  
 65 induction, while remained intact when the expression of WHH domain was repressed. Images  
 66 were captured under 100  $\times$  visual field. (d) The electrophoresis of the DNA extracted from *E.*  
 67 *coli* containing pBAD24-*rhsP*-F or pBAD24-WHH domain-F. The expression of RhsP and  
 68 WHH domain in *E. coli* DH5 $\alpha$  was induced by arabinose for 4 hours and the total DNA from  
 69 bacterial cells was extracted and analysed by 1% agarose gel.

a



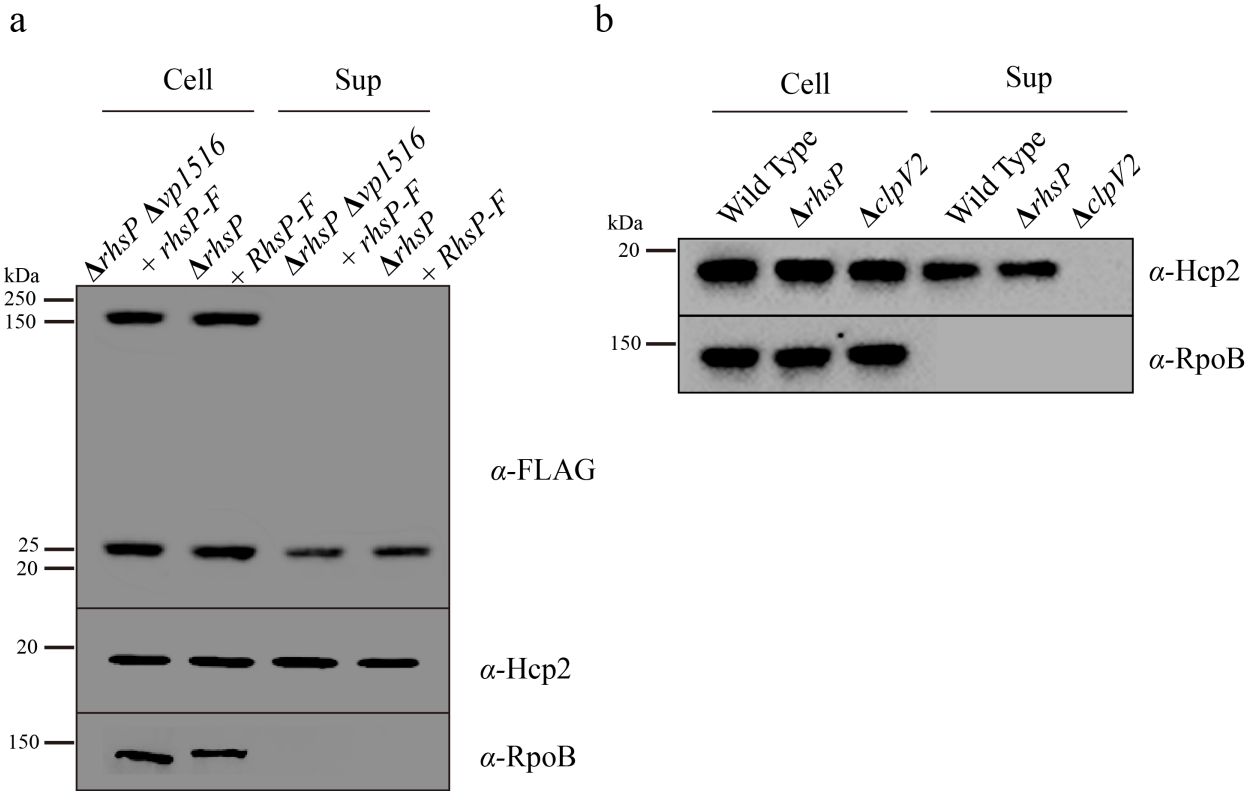
b

MIPQFVIPLTNCLGQSYHFSSQPIPKGEHKKFDSEQSAKAFLLDDFVPLRSSRVEELYHLLGQ  
FPPNVPDEELTPELYAPVFAKALVNGSLYVASFPKTKKNATISSEPTVPKQVKAKSKQNK  
AHTSSKTQAKNSASAKPLQTGSECHEKAGDPVSLVTGEEILTLNDVELPNGFVWSRTYRS  
SKASRNQGLGYGWRHAFQFELKEVTDEKHNVTSEFISDSADEIEFEPVEHGSTSYQVYV  
GASCHFLNPINIRIVTLSSGDQYRFELVEDIWLKQVRNGIFSTFQLRYSRNHRLIEVAHNK  
RPVLECQYDKQGRLEVLLNAKTEQVLTTYIYDEQDDLVGATNDLGLTEREYEQDQHLLIA  
KRVRPTGFTHYFEWSGEGSSAKCIRNFGDSGIYDYRFHYEGAKSSYSDSLDNEWTFIHDE  
QGHLLKSSPTGRTWQWHYDHLGRKEKAVFPDNSTTQYQYNQQGQLISKLHSSGAQIQY  
GYDSLGLKLVKTVSPDGDLEKAYNSLQQRVWDIDALGCVTEYEYDKHKGQVVKRESEDG  
KKSRRWWWDKQQRLLVAHEVDGTLRLYSYGATDLVNGIAYPDGCVAQISYDDYGRRTSIR  
YFNDEDKVGYSSEYAYDEFSRVAQIQTPGVTSYQWGALAQQAQVIFPDGSHISYEYDQ  
QRNLTKLVRSDGLAFEFWYDSEGLLSGTVGFDDLHLSQFKYDSMGRIIRKDVADRTVLYS  
YDDAGFLQHIKAGNGKNIVENHFNYTLGGRLTLASNRHQTLQYQYSSFGHLTKRIQGQFE  
IGEEFNVRVQQRVSQTLPKTTSFNFSYDTNGRLSEIRFSDDSLPKIEFQYDVMGRSLVTETES  
FRESKLYDGVGRLVEQQWSGREKKYIYNAQNRISILDNTAGATHYQYDTLGYVTKVSE  
AGSTSTFESDSFGNPALADSKVMSDRIEAYAGVRYKYDQQGNQVKREGDGTQKRVPFD  
ALSQLEVEVHGDSISHYEYDALGRRTKKITQNGITEFLWEGERLLGERTADGFRWYLYQP  
ETYIPLAVLENGSIYLYECDQVGKPERLKDSAGNIVWSASYDVHGFASIDVEEVRNPLRFQ  
GQYFDQETNLHYNLARYYDPKLGRFIQQDPISIAAGGINHYQYAVNPIQWIDPTGFLCEEGL  
KRLQQMLAEYQAQSDVPQEVCDQILEAAKESSVGEDGVRSQVKIRKPNGKNNIRYEYD  
LDHIDCKKNEITFYRHINYS DGSKRKIQYTVGIEGFVDIYDFVNVQKCD AQVYDTKTSKT  
VGGRKIINSEFAGKTVTTKGGDVRFDSDGFPDFTPYSKKTVRVIGLTGDMANDVPLAMA  
RAKITKYDKSKYVWHHHQDGKTMMLIPKSVHSVRNGGVAHTGGRSVIQHNLLNPNNKL  
NYSSPEELV

70

71

72 **Supplementary Fig. 2. Auto-proteolysis of RhsP.** (a) RhsP was self-cleaved and its C-terminal  
73 toxin domain was released upon incubation in acidic condition. The pH value of the incubation  
74 condition was shown. (b) Sequence annotation of RhsP. Different domains are shown in colours.  
75 Green: RHS repeats; Red: intrinsic aspartic protease; Orange: PAAR-interacting domain PID;  
76 Blue: WHH domain. The larger font highlighted methionine (M) is the cleavage site.



78

79

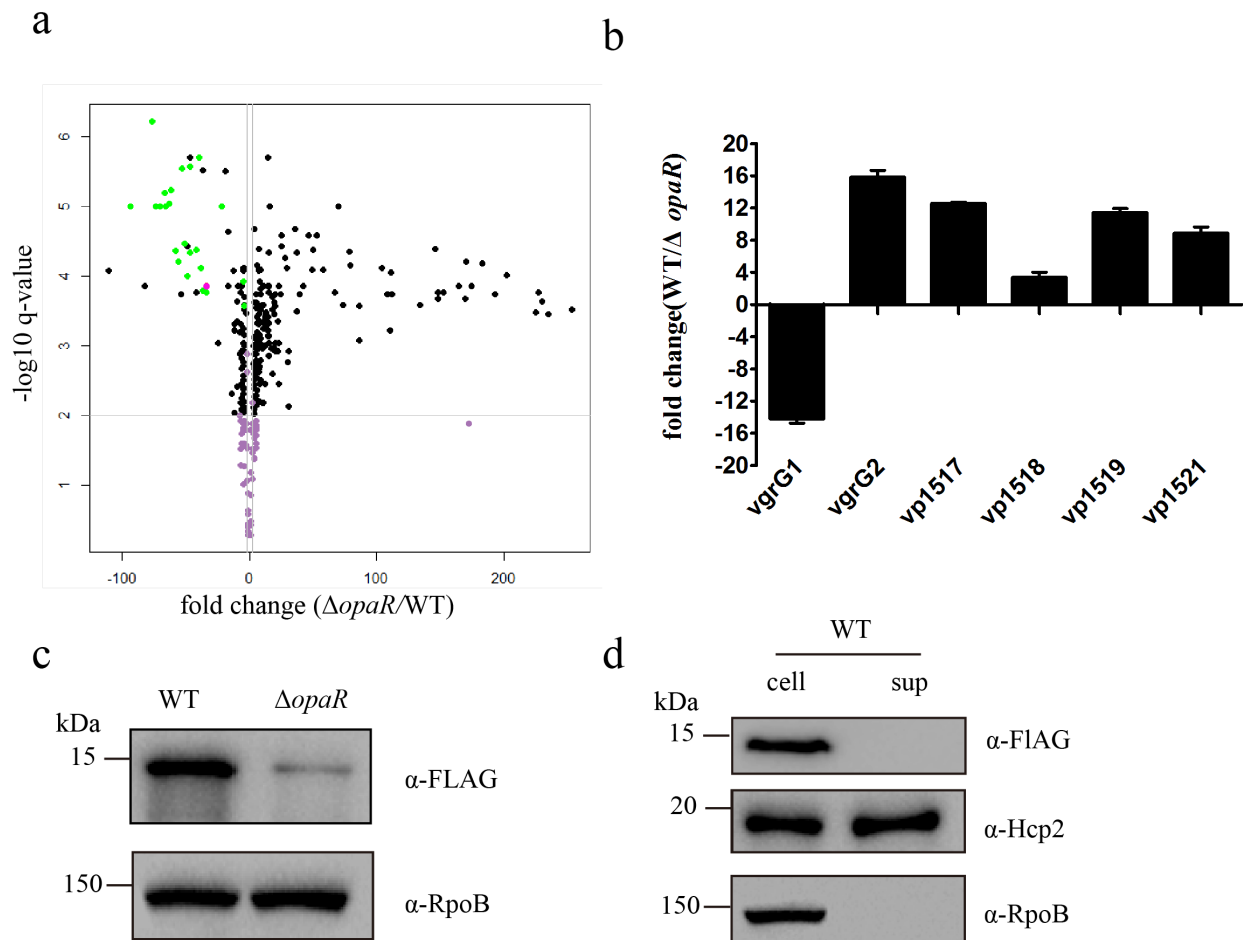
80

81

82 **Supplementary Fig. 3.** (a) Deletion of *vp1516* in *V. parahaemolyticus* RIMD 2210633 has no  
 83 effect on the secretion of RhsP. FLAG tagged RhsP (RhsP-F) was expressed in  $\Delta rhsP$  or  
 84  $\Delta rhsP \Delta vp1516$  and the secretion of RhsP and its derivatives were examined by Western blot  
 85 analysis of the total (Cell) and secreted proteins (Sup) by  $\alpha$ -FLAG antibody. (b) Deletion of *rhsP*  
 86 in *V. parahaemolyticus* RIMD 2210633 did not affect Hcp2 secretion.

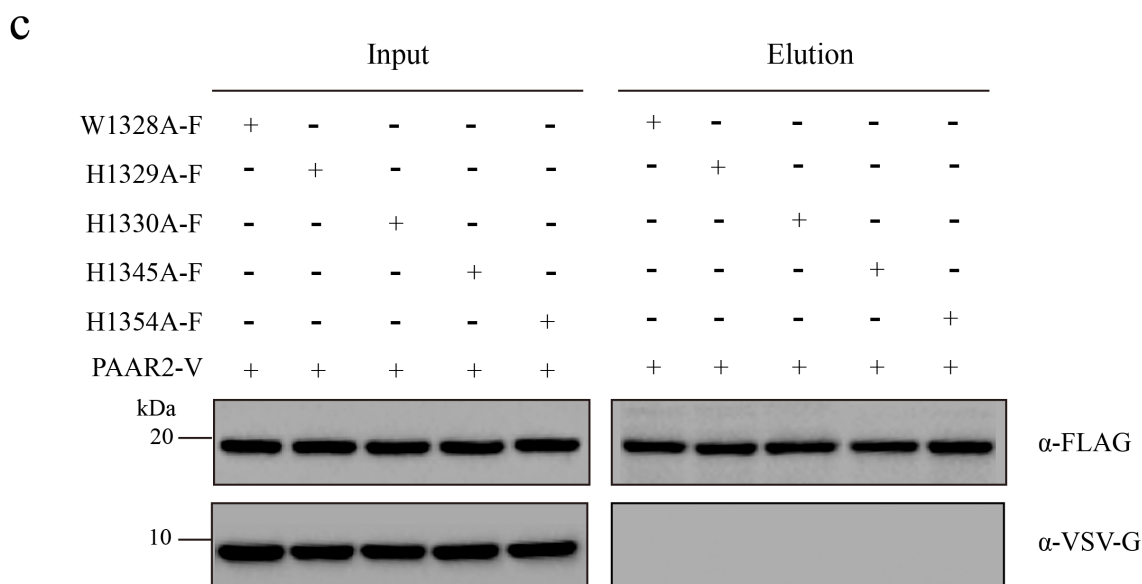
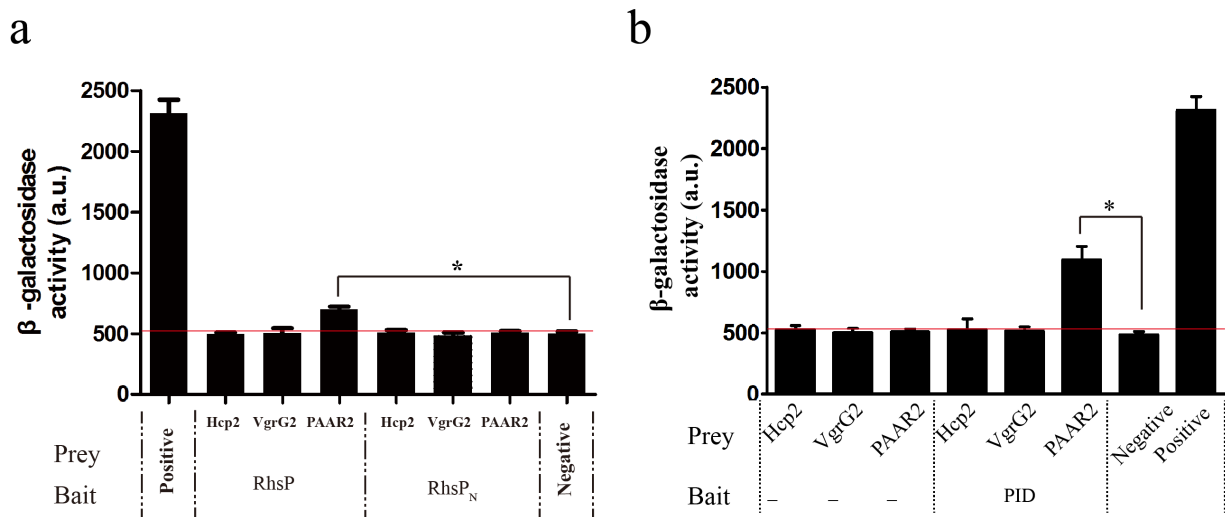
87

88



89  
 90  
 91  
 92  
 93  
 94  
 95  
 96  
 97  
 98  
 99  
 100

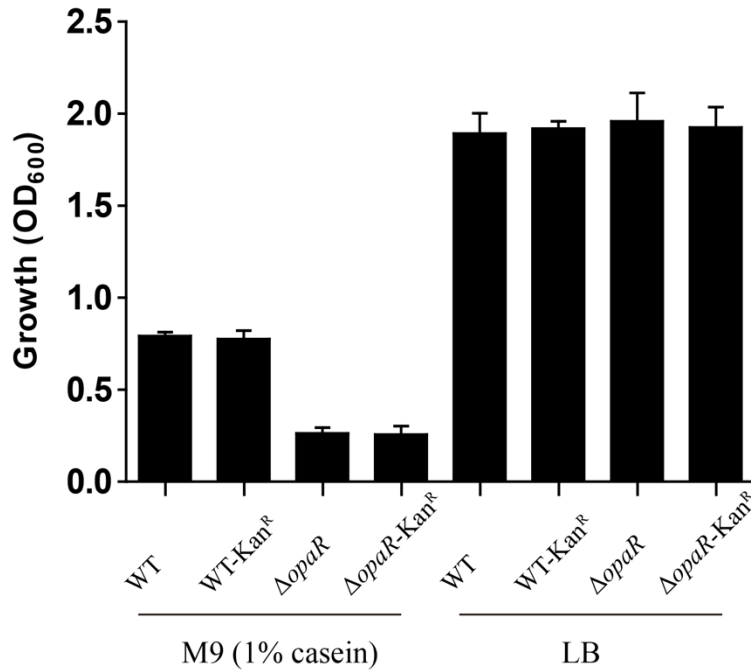
**Supplementary Fig. 4. The expression of *rhsP* and *rhsPi* is positively regulated by OpaR.** (a) Volcano map visualization of the genes regulated by OpaR based on the microarray data published previously<sup>1</sup>. *rhsP* (magenta dot) and the T6SS2 genes (green dot) are marked. (b) Real-time PCR validation of OpaR regulation on genes in *rhsP* loci. *vgrG1* from T6SS1 and *vgrG2* from T6SS2 were included as controls. (c) Western blot analysis of the expression level of FLAG tagged RhsPi in wild-type *V. parahaemolyticus* and the corresponding  $\Delta opaR$ , both of which contain a chromosomal *rhsPi::flag* (*vp1518::flag*). (d) RhsPi is not secreted. Western blot analysis of the secretion of the RhsPi in wild-type *V. parahaemolyticus*, which contains a chromosomal *rhsPi::flag*.



101  
 102 **Supplementary Fig. 5. RhsP interacts with PAAR2.** (a) Bacterial two-hybrid assay to detect  
 103 the interaction of full-length RhsP or N-terminal of RhsP (RhsP<sub>N</sub>) with selected T6SS2  
 104 components. (b) Bacterial two-hybrid assay to detect the interaction between PAAR-interacting  
 105 domain PID (the first 102 amino acids after the auto-proteolysis site) and the components of  
 106 T6SS puncture device. For (a) and (b), the values represent the means ± s.d. from one  
 107 representative experiment performed with triplicate samples. Equivalent results were obtained at  
 108 least three times. Significance was determined by the two-tailed Student *t* test. \**p*<0.05. (c)  
 109 Co-immunoprecipitation between WHH domain derivatives (different site-directed mutants) and  
 110 PAAR2. Results showed that various WHH domain derivatives do not interact with PAAR2.  
 111 WHH domain derivatives and PAAR2 were expressed in *E. coli* DH5α.  
 112







119

120

121 **Supplementary Fig. 7. Growth of *V. parahaemolyticus* wild-type (WT) and  $\Delta opaR$  in LB**  
 122 **broth and M9 broth minimum media with 1% casein as carbon source.** Each strain was  
 123 inoculated independently and grown overnight in either M9 broth medium containing 1% casein  
 124 or in LB broth at 37°C for 16 h, the OD<sub>600</sub> was then measured. The means of each data set in one  
 125 representative experiment performed with triplicates was shown. Equivalent results were  
 126 obtained twice.

127

128

129

130

131

a

PID domain:

```

Sec_Structure  -HHHHHHH-----HHHHHHHHH-----EEEEEE-----EEEEEE-----EEEEEE-----EEEEEEEEEEEEEEEE-----
>NP_797896.1   LQQHAEYQAQSDPQEVCDQEAARKEVGEDG--VRQVKKKNGKKNHIREDDHIDCKRNEFRHNYSDGSKRKIQYTGREGVDIYDFVNVQKCD
>EVU18727.1   ---HAEYQAQSDPQEVCDQEAARKEVGEDG--VRQVKKKNGKKNHIREDDHIDCKRNEFRHNYSDGSKRKIQYTGREGVDIYDFVNVQKCD
>WP_079854477.1 ---HAEYQAQNNPQEVCDQEAARKEVGEDG--VRQVKKKNGKKNHIREDDHIDCKRNEFRHNYSDGSKRKIQYTGREGVDIYDFVNVQKCD
>OXX42947.1   ---HAEYQAQNNPQEVCDQEAARKEVGEDG--VRQVKKKNGKKNHIREDDHIDCKRNEFRHNYSDGSKRKIQYTGREGVDIYDFVNVQKCD
>ODY69660.1   LQQHAEYQAQNNPQEVCDQEAARKEVGEDG--ARQVKKKNGKKNHIREDDHIDCKRNEFRHNYSDGSKRKIQYTGREGVDIYDFVNVQKCD
>WP_006742583.1 LQQHAEYQAQNNPQEVCDQEAARKEVGEDG--VRQVKKKNGKKNHIREDDHIDCKRNEFRHNYSDGSKRKIQYTGREGVDIYDFVNVQKCD
>WP_021449074.1 LQQHAEYQAQSDPQEVCDQEAARKEVGEDG--VRQVKKKNGKKNHIREDDHIDCKRNEFRHNYSDGSKRKIQYTGREGVDIYDFVNVQKCD
>WP_079851964.1 LQQHAEYQAQNNPQEVCDQEAARKEVGEDG--VRQVKKKNGKKNHIREDDHIDCKRNEFRHNYSDGSKRKIQYTGREGVDIYDFVNVQKCD
>EQM46614.1   LQQHAEYQAQNNPQEVCDQEAARKEVGEDG--VRQVKKKNGKKNHIREDDHIDCKRNEFRHNYSDGSKRKIQYTGREGVDIYDFVNVQKCD
>EQM11800.1   LQKHAEYQAQNNPQEVCDQEAARKEVGEDG--VRQVKKKNGKKNHIREDDHIDCKRNEFRHNYSDGSKRKIQYTGREGVDIYDFVNVQKCD
>AOW89994.1   LQKHAEYQAQNNPQEVCDQEAARKEVGEDG--VRQVKKKNGKKNHIREDDHIDCKRNEFRHNYSDGSKRKIQYTGREGVDIYDFVNVQKCD
>KJR14643.1   LQQHAEYQAQNNPQEVCDQEAARKEVGEDG--VRQVKKKNGKKNHIREDDHIDCKRNEFRHNYSDGSKRKIQYTGREGVDIYDFVNVQKCD
>AGV16404.1   LQQHAEYQAQSDPQEVCDQEAARKEVGEDG--VRQVKKKNGKKNHIREDDHIDCKRNEFRHNYSDGSKRKIQYTGREGVDIYDFVNVQKCD
>OO110452.1   LQQHAEYQAQNNPQEVCDQEAARKEVGEDG--VRQVKKKNGKKNHIREDDHIDCKRNEFRHNYSDGSKRKIQYTGREGVDIYDFVNVQKCD
>KFF89385.1   LQQHAEYQAQSDPQEVCDQEAARKEVGEDG--VRQVKKKNGKKNHIREDDHIDCKRNEFRHNYSDGSKRKIQYTGREGVDIYDFVNVQKCD
>GAJ75183.1   LQQHAEYQAQNNPQEVCDQEAARKEVGEDG--VRQVKKKNGKKNHIREDDHIDCKRNEFRHNYSDGSKRKIQYTGREGVDIYDFVNVQKCD
>WP_005396166.1 LQQHAEYQAQNNPQEVCDQEAARKEVGEDG--VRQVKKKNGKKNHIREDDHIDCKRNEFRHNYSDGSKRKIQYTGREGVDIYDFVNVQKCD
>OQJ06944.1   LQKHAEYQAQNNPQEVCDQEAARKEVGEDG--VRQVKKKNGKKNHIREDDHIDCKRNEFRHNYSDGSKRKIQYTGREGVDIYDFVNVQKCD
>ARC17275.1   ---HAEYQAQNNPQEVCDQEAARKEVGEDG--VRQVKKKNGKKNHIREDDHIDCKRNEFRHNYSDGSKRKIQYTGREGVDIYDFVNVQKCD
>ODZ79473.1   ---HAEYQAQNNPQEVCDQEAARKEVGEDG--VRQVKKKNGKKNHIREDDHIDCKRNEFRHNYSDGSKRKIQYTGREGVDIYDFVNVQKCD
>EXJ24942.1   LQQHAEYQAQSDPQEVCDQEAARKEVGEDG--VRQVKKKNGKKNHIREDDHIDCKRNEFRHNYSDGSKRKIQYTGREGVDIYDFVNVQKCD
>ODX22356.1   MQQHAEYQAQNNPQEVCDQEAARKEVGEDG--VRQVKKKNGKKNHIREDDHIDCKRNEFRHNYSDGSKRKIQYTGREGVDIYDFVNVQKCD
>KZC47345.1   ---HAEYQAQNNPQEVCDQEAARKEVGEDG--VRQVKKKNGKKNHIREDDHIDCKRNEFRHNYSDGSKRKIQYTGREGVDIYDFVNVQKCD
>OQK14945.1   LQQHAEYQAQNNPQEVCDQEAARKEVGEDG--VRQVKKKNGKKNHIREDDHIDCKRNEFRHNYSDGSKRKIQYTGREGVDIYDFVNVQKCD
>GAK16033.1   LQQHAEYQAQSDPQEVCDQEAARKEVGEDG--VRQVKKKNGKKNHIREDDHIDCKRNEFRHNYSDGSKRKIQYTGREGVDIYDFVNVQKCD
>OEX33162.1   LQQHAEYQAQSDPQEVCDQEAARKEVGEDG--VRQVKKKNGKKNHIREDDHIDCKRNEFRHNYSDGSKRKIQYTGREGVDIYDFVNVQKCD
>EVT83419.1   LQQHAEYQAQSDPQEVCDQEAARKEVGEDG--VRQVKKKNGKKNHIREDDHIDCKRNEFRHNYSDGSKRKIQYTGREGVDIYDFVNVQKCD
>ETZ10275.1   LQQHAEYQAQSDPQEVCDQEAARKEVGEDG--VRQVKKKNGKKNHIREDDHIDCKRNEFRHNYSDGSKRKIQYTGREGVDIYDFVNVQKCD
>WP_024612975.1 LKNHGTLVG-NGFDETVKAYRIIACTPINK--DIITNYVIEGKVNRRTHESEFKLPERNKIITRELPS---GTRISQTSIEDAQOHIDNNEKVAN
>WP_055023366.1 LSAHDTLVG-NGIDKQTKKQKSIDLAITD---PEAKLKKOKDGVNKNIAATSEMDVNNITVQRND----GQIKEMDLTKEAGHGFDFGKVDVE
>WP_018693037.1 LQGHDTALEK-DGLTPMRKVEARQAGNVNNSDEQPKLIKRRKGGTFLVHEDKLGLDPENGTVMRKVG----DDVSPKVLTKKAGGHLVDGSLVNE
>KPZ55502.1   ---SKMIG-DIIPATKAKIKIREDPADA---RTGNIKIVTRNGENRLEHSESMDVDNGKILTEVGV---DKVITETMTIQVGGHVIDGKVVNE
Consensus/90%  ...MLtpbpt.ssVspElp-pILEtAc-SSst-st...s+SpkIR+PpGnpIcYEsL-+LDspNcITbYrCIs.....p+chphsV.IppFl.hlas.sp.....

```

b

```

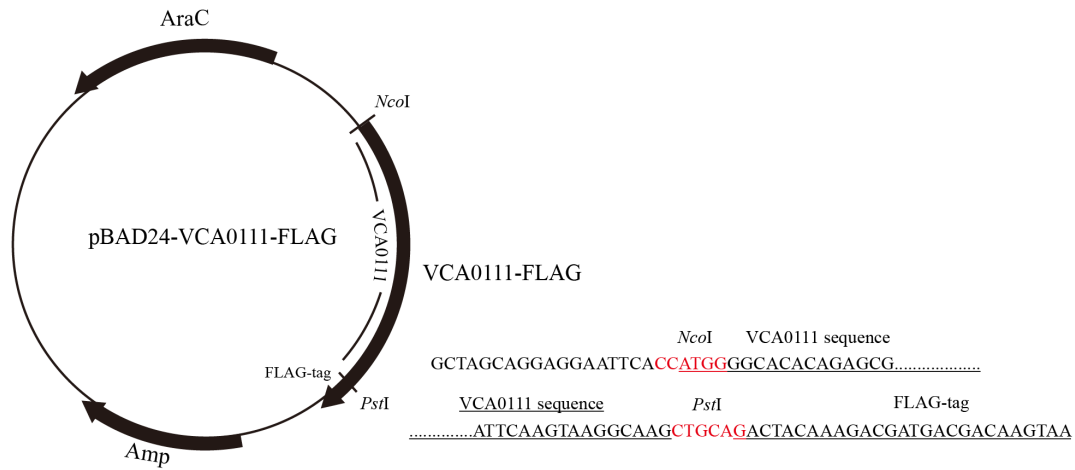
          *          *          *
FAVQ-D E SGL YN- RYY P G-F- DP- GGG -N Y Y x N P wvDP G
RhsP F Q G Q Y F D K E T N L H Y N - A N Y Y D P K L G R I I Q Q D P I S I A G G - - - I N H Y Q Y A V N - P I Q W I D P T G
idrD F Q G Q Y F D K E T G L H Y N T F N Y Y A D L G R E T Q Q D P I G L A G G - - - I N L Y A Y A P N - P L T W V D P W G
RhsP1 F Q G Q Y H D E E S G L Y Y N R Y Y Y L E A G R M A S Q D P L G L G G G - - - P N P Y A Y A L N A P T L A Y D P T G
RhsP2 F Q G Q Y F D A E T G L H Y N R I I N Y Y N R S T G R M L T P D P I R L A G G - - - L N S Y R Y V P N - P T G W V D P L G
RhsCT1 Y A G Q W Q D A E S G L C Y N R F Y Y Y E H E T G M Y L V S D P L G L L G G - - - E Q T Y R Y V P N - P C G W V D P L G
RhsT F T G H E H L E E S G L V H M N G R Y Y D P V I G R E L S A D I V Y Q D T A N A Q A Y N R Y S Y G W N P I A S V D P T G
WapA Y A G Y Q Y D E E T G L Y Y L M A Y Y E F R N G V F L S L D P D P G S D G S L D Q N G Y A Y G N N P V M N V D P D G
RhsC Y Q G Q V Y D A E T G L Y Y N R H I Y Y D F E L G Q V I S A D P I G L A G G - - - L R P Q G Y V H N - P M E W V D P F G
RhsB F A G Q L R D S E S G L C Y N R F Y Y D P A G G C Y V S P D P I G I A G G - - - E S N Y G Y V Q N - P N T R V D P L G
RhsA F A G Q L R D S E S G L C Y N R F Y Y D P A G G C Y V S P D P I G I A G G - - - E S N Y G Y V S N - P M C W V D P F G
Rhs2 Y A G Q Y Q D D E S G L H Y N L F Y Y Y E V G R E T T Q D P I G I E G G - - - L N L Y A Y G P N - P L T W I D P F G
Rhs1 L Q G Q Y L D R E T G L H Y N L F Y Y D P I G R E T Q H D P I G L A G G - - - I N L Y Q Y A P N - P L G W V D P W G

```

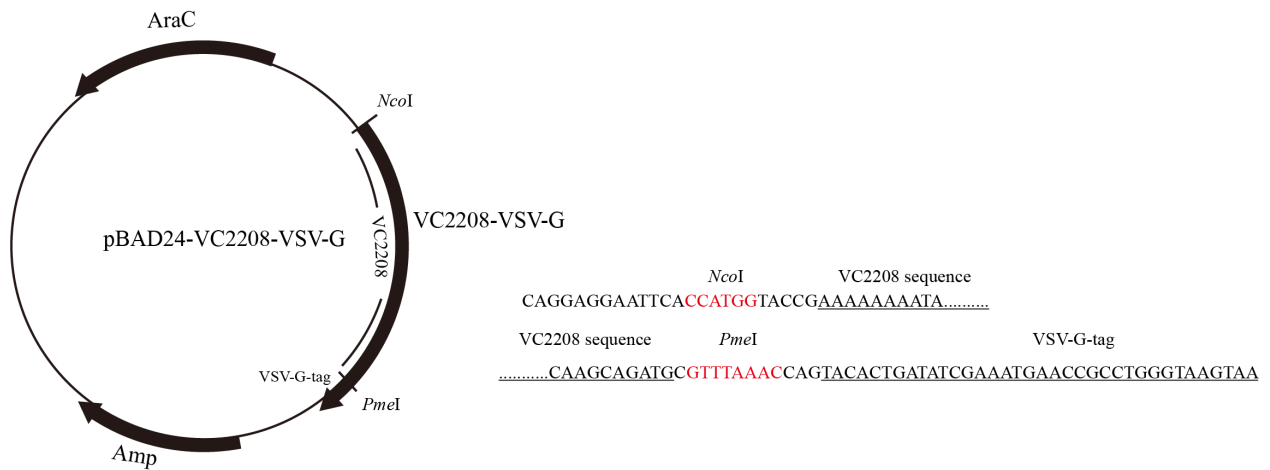
132  
133  
134  
135  
136  
137  
138

**Supplementary Fig. 8.** (a) Alignment of amino acid sequences of PID from different pro-effectors identified in Fig. 5a. (b) Alignment of the conserved aspartic protease domain in PAAR-Rhs effectors that have been reported previously<sup>2-9</sup>. Characteristic residues (RDD) are indicated by asterisks.

a



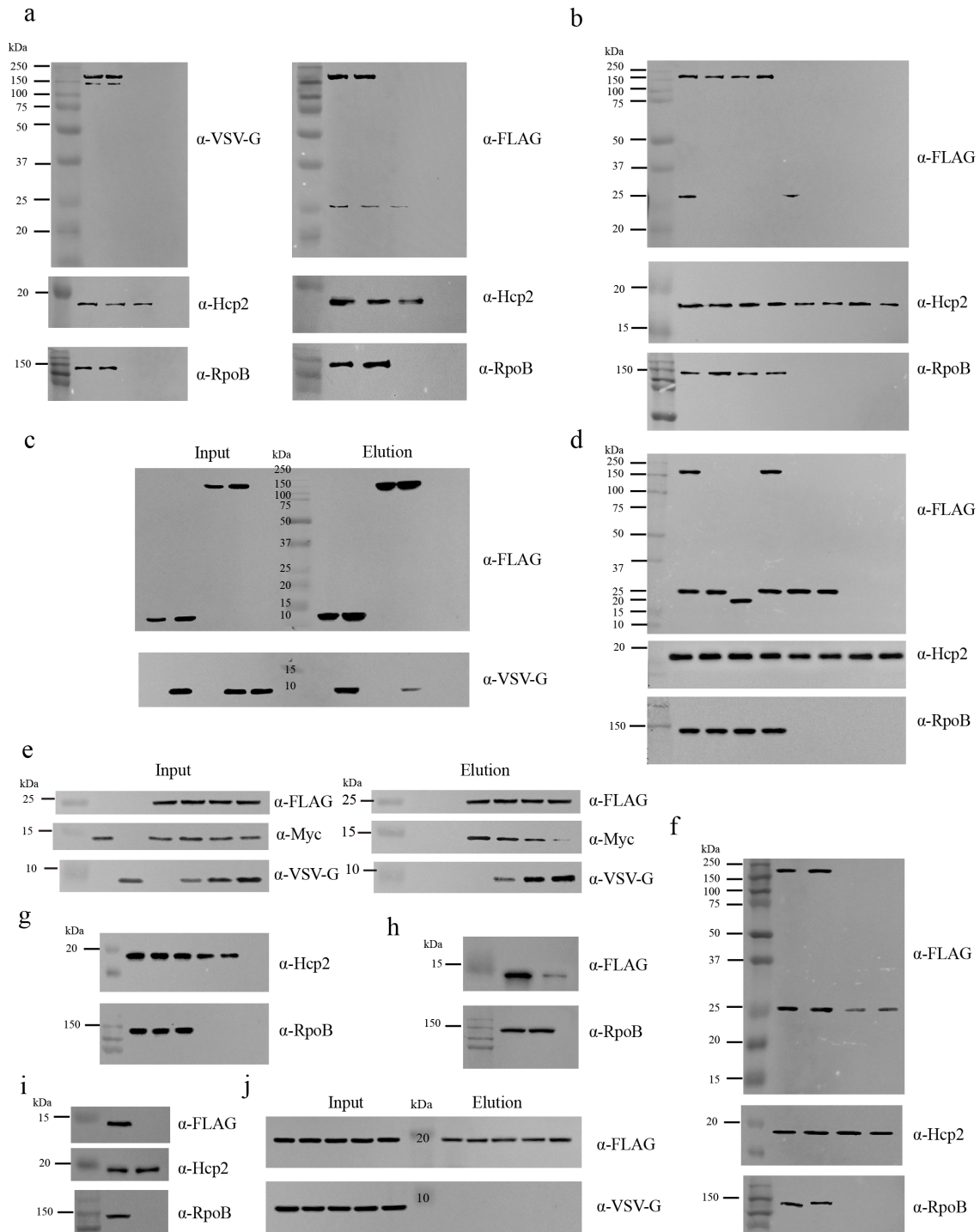
b



139  
140

141 **Supplementary Fig. 9.** The map and nucleic acids sequences of cloning sites for vector  
142 expressing (a) FLAG tag and (b) VSV-G tag. Tested gene was amplified by primers listed in  
143 Supplementary Table 5 and the PCR product was ligated into *NcoI/PstI* digested  
144 pBAD24-VCA0111-FLAG to construct FLAG tagged protein or ligated into *NcoI/PmeI* digested  
145 pBAD24-VC2208-VSV-G to construct VSV-G tagged protein.

146



147  
 148 **Supplementary Fig. 10.** Original figure of western blot analysis for results used in the article. (a)  
 149 Full picture for Fig. 2e. (b) Full picture for Fig. 3a. (c) Full picture for Fig. 3b. (d) Full picture  
 150 for Fig. 3c. (e) Full picture for Fig. 4c. (f) Full picture for Supplementary Fig. 3a. (g) Full picture  
 151 for Supplementary Fig. 3b. (h) Full picture for Supplementary Fig. 4c. (i) Full picture for  
 152 Supplementary Fig. 4d. (j) Full picture for Supplementary Fig. 5c. All images in this study were  
 153 acquired with a ChemiDoc imaging system.  
 154



**Supplementary Table 2. Bacterial strains and plasmids used in this study**

Bacterial strains/plasmids	Description	Source
<i>Vibrio parahaemolyticus</i>		
RIMD 2210633	Wild-type <i>V. parahaemolyticus</i> , Amp <sup>R</sup>	10
$\Delta rhsP$	RIMD 2210633, in-frame deletion of <i>rhsP</i>	This study
$\Delta rhsP\Delta paar2$	RIMD 2210633, in-frame deletion of <i>rhsP</i> and <i>paar2</i>	This study
$\Delta rhsP\Delta clpV2$	RIMD 2210633, in-frame deletion of <i>rhsP</i> and <i>clpV2</i>	This study
$\Delta rhsP + V-rhsP-F$	$\Delta rhsP$ complemented with pBAD33- <i>V-RhsP-F</i>	This study
$\Delta rhsP\Delta clpV2 + V-rhsP-F$	$\Delta rhsP\Delta clpV2$ complemented with pBAD33- <i>V-RhsP-F</i>	This study
$\Delta rhsP + rhsP-F$	$\Delta rhsP$ complemented with pBAD33- <i>RhsP-F</i>	This study
$\Delta rhsP + rhsP_C-F$	$\Delta rhsP$ complemented with pBAD33- <i>rhsP_C-F</i>	This study
$\Delta rhsP +$ WHH domain-F	$\Delta rhsP$ complemented with pBAD33-WHH domain-F	This study
$\Delta rhsP\Delta paar2 + rhsP-F$	$\Delta rhsP\Delta paar2$ complemented with pBAD33- <i>RhsP-F</i>	This study
$\Delta rhsP\Delta rhsPi$	RIMD 2210633, in-frame deletion of <i>rhsP</i> and <i>rhsPi</i>	This study
$\Delta clpV2$	RIMD 2210633, in-frame deletion of <i>clpV2</i>	This study
$\Delta clpV2 + clpV2$	$\Delta clpV2$ complemented with pBAD33- <i>clpV2</i>	This study
$\Delta opaR$	RIMD 2210633, in-frame deletion of <i>opaR</i> ( <i>vp2516</i> )	This study
$\Delta opaR$ -Kan <sup>R</sup>	$\Delta opaR$ complemented with pBBR1MCS2, Kan <sup>R</sup>	This study
$\Delta opaR$ -Chl <sup>R</sup>	$\Delta opaR$ containing pBAD33, Chl <sup>R</sup>	This study
$\Delta opaR + rhsPi$	$\Delta rhsP$ complemented with pBAD33- <i>rhsPi</i>	This study
$\Delta rhsP\Delta vp1516$	RIMD 2210633, in-frame deletion of <i>rhsP</i> and <i>vp1516</i>	This study
$\Delta rhsP\Delta vp1516 + rhsP-F$	$\Delta rhsP\Delta vp1516$ complemented with pBAD33- <i>RhsP-F</i>	This study
<i>E. coli</i>		
DH5 $\alpha$ <i>pir</i>	F- $\phi 80$ <i>lacZ</i> $\Delta$ M15 $\Delta$ ( <i>lacZYA-argF</i> ) <i>LAMpir</i> U169 <i>endA1 recA1 hsdR17</i> (rk-,mk+) <i>supE44</i> $\lambda$ - <i>thi</i> -1 <i>gyrA96 relA1 phoA</i>	Invitrogen
BL21(DE3)	F- <i>dcm ompT hsdS gal</i> $\lambda$ (DE3)	Novagen
MFD <i>pir</i>	MG1655 RP4-2-Tc:: Mu1:: <i>aac(3)IV-aphA-nic35-Mu2::zeo dapA::(erm-pir) recA</i>	11
Plasmid		

pET28a	cloning vector, PT7, Kan <sup>R</sup>	Invitrogen
pET28a- <i>rhsP</i>	pET28a expressing RhsP tagged with 6×His at C-terminal	This study
pET28a- R1092A	pET28a expressing RhsP mutant of R1092A tagged with 6×His at C-terminal	This study
pET28a- D1105A	pET28a expressing RhsP mutant of R1105A tagged with 6×His at C-terminal	This study
pET28a- D1127A	pET28a expressing RhsP mutant of R1127A tagged with 6×His at C-terminal	This study
pBAD24	cloning vector, arabinose induced, Amp <sup>R</sup>	Invitrogen
pBAD24-VCA0111-FLAG	pBAD24 expressing VCA0111-FLAG	This study
pBAD24-VC2208-VSV-G	pBAD24 expressing VC2208-VSV-G	This study
pBAD24- <i>rhsP-F</i>	pBAD24 expressing RhsP tagged with FLAG epitope at C-terminal	This study
pBAD24-WHH domain-F	pBAD24 expressing WHH domain tagged with FLAG epitope at C-terminal	This study
pBAD24-W1328A	pBAD24 expressing WHH domain with point mutation of W1328A tagged with FLAG epitope at C-terminal	This study
pBAD24-H1329A	pBAD24 expressing WHH domain with point mutation of W1329A tagged with FLAG epitope at C-terminal	This study
pBAD24-H1330A	pBAD24 expressing WHH domain with point mutation of W1330A tagged with FLAG epitope at C-terminal	This study
pBAD24-H1345A	pBAD24 expressing WHH domain with point mutation of W1345A tagged with FLAG epitope at C-terminal	This study
pBAD24-H1354A	pBAD24 expressing WHH domain with point mutation of W1354A tagged with FLAG epitope at C-terminal	This study
pBAD24-PID-F	pBAD24 expressing PID (from M1143 to D1244 of RhsP) tagged with FLAG epitope at C-terminal	This study
pBAD24- <i>paar2-V</i>	pBAD24 expressing PAAR2 tagged with VSV-G epitope at C-terminal	This study
pBAD33	cloning vector, arabinose induced, Chl <sup>R</sup>	Invitrogen
pBAD33- <i>V-rhsP-F</i>	pBAD33 expressing RhsP tagged with FLAG epitope at C-terminal and VSV-G at its N-terminal	This study
pBAD33- <i>rhsP-F</i>	pBAD33 expressing RhsP tagged with FLAG epitope at C-terminal	This study



pBAD33- <i>rhsP-F</i> (R1092A)	pBAD33 expressing point mutated RhsP (R1092A) tagged with FLAG epitope at C-terminal	This study
pBAD33- <i>rhsP-F</i> (D1105A)	pBAD33 expressing point mutated RhsP (D1105A) tagged with FLAG epitope at C-terminal	This study
pBAD33- <i>rhsP-F</i> (D1127A)	pBAD33 expressing point mutated RhsP (D1127A) tagged with FLAG epitope at C-terminal	This study
pBAD33- <i>rhsPc-F</i>	pBAD33 expressing RhsPc tagged with FLAG epitope at C-terminal	This study
pBAD33-WHH domain-F	pBAD33 expressing WHH domain tagged with FLAG epitope at C-terminal	This study
pBAD33- <i>clpV2</i>	pBAD33 expressing ClpV2	This study
pBAD33- <i>rhsPi</i> ( <i>vp1518</i> )	<i>Vp1518</i> cloned into pBAD33	This study
pCX340	pBBR322 derivative, IPTG induced, Tet <sup>R</sup>	<sup>12</sup>
pCX340- <i>rhsPi</i> ( <i>vp1518</i> )	pCX340 with <i>vp1518</i> including stop codon	This study
pCX340- <i>vp1519</i>	pCX340 with <i>vp1519</i> including stop codon	This study
pCX340- <i>vp1520</i>	pCX340 with <i>vp1520</i> including stop codon	This study
pCX340- <i>rhsPi-M</i>	pCX340 expressing RhsPi (VP1518) tagged with Myc epitope at C-terminal	This study
pAC $\lambda$ CI	Plasmid for bacterial two-hybrid; Encodes $\lambda$ CI (residues 1-236) under the control of lacUV5 promoter; Chl <sup>R</sup>	<sup>13</sup>
pBR $\alpha$	Plasmid for bacterial two-hybrid; Encodes the full-length $\alpha$ subunit of RNAP under the control of tandem <i>placUV5</i> and <i>plpp</i> promoters; Carb <sup>R</sup>	<sup>13</sup>
pAC $\lambda$ CI- $\beta$ -flap (831–1057)	Positive control for bacterial two-hybrid; Encodes residues 1-248 of $\alpha$ fused by a three-alanine linker residues 831–1057 of the $\beta$ subunit of <i>E. coli</i> RNAP under the control of tandem <i>placUV5</i> and <i>plpp</i> promoters; confers resistance to Carb; used to generate <i>NotI/Bam</i> HI-digested backbone to construct various $\alpha$ fusions; Chl <sup>R</sup>	<sup>13</sup>
pBR $\alpha$ - $\beta$ -flap (831–1057)	Positive control for bacterial two-hybrid; Encodes residues 1-248 of $\alpha$ fused by a three-alanine-linker residues 831–1057 of the $\beta$ subunit of <i>E. coli</i> RNAP under the control of tandem <i>placUV5</i> and <i>plpp</i> promoters; used to generate <i>NotI/Bam</i> HI-digested backbone to construct various $\alpha$ fusions; Carb <sup>R</sup>	<sup>13</sup>
pAC- <i>hcp2</i>	pAC $\lambda$ CI with <i>hcp2</i>	This study

pAC- <i>paar2</i>	pAC $\lambda$ cI with <i>paar2</i>	This study
pAC- <i>vgrG2</i>	pAC $\lambda$ cI with <i>vgrG2</i>	This study
pBR- <i>rhsP</i>	pBR $\alpha$ with <i>rhsP</i>	This study
pBR-PID	pBR $\alpha$ with fragment encoding PID	This study
pBR- <i>rhsP<sub>N</sub></i>	pBR $\alpha$ with <i>rhsP<sub>N</sub></i>	This study

163

164

165 **Supplementary Table 3. Buffers formula for auto-proteolysis testing of RhsP and its derivatives**  
166

<b>pH</b>	<b>0.1M acetic acid (ml)</b>	<b>0.1 sodium acetate (tri-hydrate) (ml)</b>
3	982.3	17.7
4	847	153
5	357	643
6	52.2	947.8

167  
168

169 **Supplementary Table 4. Primers used in this study**

170

Name	Sequence	Destination
Primers for mutant construction		
VP1517up-F	<u>AAAAAGGATCGATCCTCTAGATTTGGATTGCGTAT</u> ATCC	For construction of deletion mutant of <i>ΔrhsP</i>
VP1517up-R	ATCAACTCCAGTTGTAACGAGTGTGTCC	
VP1517down-F	GTTACAACCTGGAGTTGATATATGATTAGCC	
VP1517down-R	<u>ATCGCATGCGGTACCTCTAGAATT</u> CAGCACAAGAT CTTT	
VP1517-18 cluster up -F	<u>AAAAAGGATCGATCCTCTAGATTTGGATTGCGTAT</u> ATCC	For construction of deletion mutant of <i>ΔrhsPΔrhsPi</i>
VP1517-1518 cluster up-R	TTGTCAAAGAGTTGTAACGAGTGTG	
VP1517-18 cluster down -F	GTTACAACCTCTTTGACAAAACAGGG	
VP1517-1518 cluster down-R	<u>ATCGCATGCGGTACCTCTAGATACAAATTTGTTTCG</u> TCTTCA	
VP1518FLAG-up-F	<u>AAAAAGGATCGATCCTCTAGACTATT</u> CAGATGGTA GTAAAC	To insert Flag tag following RhsPi (VP1518)
VP1518FLAG-up-R	TTACTTGTCTCGTCATCGTCTTTGTAGTCAGATTCTAG AAGCTTTTCCA	
VP1518FLAG-down-F	GACGATGACGACAAGTAACTTTGACAAAACAGGG AAGA	
VP1518FLAG-down-R	<u>ATCGCATGCGGTACCTCTAGACAAATTTGTTTCGTC</u> TTCATG	
VPA1025up-F	<u>AAAAAGGATCGATCCTCTAGACACGAAGATAAAT</u> CGCGA	For construction of deletion mutant of <i>Δpaar2</i> (VPA1025)
VPA1025up-R	ACCGACGAGTCTAAGTTCCTCTTAATTCA	
VPA1025down-F	GAACTTAGACTCGTCGGTGTACCGACCGTC	
VPA1025down-R	<u>ATCGCATGCGGTACCTCTAGAATGTGGTTTGTGTT</u> GATT	
VPA1028up-F	<u>AAAAAGGATCGATCCTCTAGAGTTACTTCTTTACC</u> C	For construction of deletion mutant of <i>clpV2</i> (VPA1028)
VPA1028up-R	TTTAAAGGAAACATACAAGTTTAACTCTGT	
VPA1028down-F	ACAGAGTTAACTTGTATGTTTCCTTTAAA	
VPA1028down-R	<u>ATCGCATGCGGTACCTCTAGAACCGGAGCTAAA</u> GC	
VP2516up-F	<u>AAAAAGGATCGATCCTCTAGAAACGCCCATTTATA</u> TGGG	For construction of deletion mutant of <i>ΔopaR</i> (VP2516)

VP2516up-R	AAATCTGAGCTATCCATTTTCCTTGCCATT	
VP2516down-F	AAAATGGATAGCTCAGATTTGAACACGAAC	
VP2516down-R	<u>ATCGCATGCGGTACCTCTAGACGTTAAGGTTTACA</u> CCAA	
Primers for constructs for complementation		
VP1517-WHH-FLA Gcom-F	<u>GGGCTAGCGAATTCGAGCTC</u> <b>AGGAGGAATTCACC</b> ATGGCTCAAGTATATGATAC	For cloning variable length of <i>RhsP</i> into pBAD33
VP1517C-FLA Gcom -F	<u>GGGCTAGCGAATTCGAGCTC</u> <b>AGGAGGAATTCACC</b> ATGTTCCCTTTGTGAAGAAGG	
VP1517-FLA Gcom- F	<u>GGGCTAGCGAATTCGAGCTC</u> <b>AGGAGGAATTCACC</b> ATGATTCCCTCAATTTGTTAT	
VSVG-VP1517-FL A Gcom-F	<u>GGGCTAGCGAATTCGAGCTC</u> <b>AGGAGGAATTCACC</b> ATGTATACAGACATAGAGATGAACCGACTTGAA AGATTCCCTCAATTTGTTAT	
VP1517FLA Gcom- R	<u>GATCCCCGGGTACCGAGCTCTTACTTGTGCGTCATC</u> GTCTT	
VP1517-FLA Gcom- F	<u>GGGCTAGCGAATTCGAGCTC</u> <b>AGGAGGAATTCACC</b> ATGATTCCCTCAATTTGTTAT	For construction of <i>RhsP</i> mutant R1092A in pBAD33
VP1517-R1092A-R	GTCGTAATACGCAGCGAGGTT	
VP1517-R1092A-F	AACCTCGCTGCGTATTACGAC	
VP1517FLA Gcom- R	<u>GATCCCCGGGTACCGAGCTCTTACTTGTGCGTCATC</u> GTCTT	
VP1517-FLA Gcom- F	<u>GGGCTAGCGAATTCGAGCTC</u> <b>AGGAGGAATTCACC</b> ATGATTCCCTCAATTTGTTAT	For construction of <i>RhsP</i> mutant D1105A in pBAD33
VP1517-D1105A-R	AGATATCGGGGCTTGTGGAT	
VP1517-D1105A-F	ATCCAACAAGCCCCGATATCT	
VP1517FLA Gcom- R	<u>GATCCCCGGGTACCGAGCTCTTACTTGTGCGTCATC</u> GTCTT	
VP1517-FLA Gcom- F	<u>GGGCTAGCGAATTCGAGCTC</u> <b>AGGAGGAATTCACC</b> ATGATTCCCTCAATTTGTTAT	For construction of <i>RhsP</i> mutant D1127A in pBAD33
VP1517-D1127A-R	ACCTGTTGGGGCAATCCACTG	
VP1517-D1127A-F	CAGTGGATTGCCCAACAGGT	
VP1517FLA Gcom- R	<u>GATCCCCGGGTACCGAGCTCTTACTTGTGCGTCATC</u> GTCTT	
VP1518com-F	<u>GGGCTAGCGAATTCGAGCTC</u> <b>AGGAGGAATTCACC</b> ATGATTAGCCTTTCAGATATTG	For construction of <i>RhsPi</i> in pBAD33
VP1518com-R	<u>GATCCCCGGGTACCGAGCTCTTAAGATTCTAGAAG</u> CTTTTCC	
VPA1028com-F	<u>GGGCTAGCGAATTCGAGCTC</u> <b>AGGAGGAATTCACC</b> ATGGCTTCATTATCA	For construction of ClpV2 in pBAD33

VPA1028com-R	<u>GATCCCCGGGTACCGAGCTCTTAAATAAGTGAGA</u> CTTCT	
VP2516com-F	<u>GGGCTAGCGAATTCGAGCTC</u> <b><i>AGGAGGAATTCACC</i></b> ATGGACTCAATTGCA	For cloning <i>opaR</i> into plasmid pBAD33
VP2516com-R	<u>GATCCCCGGGTACCGAGCTCTTAGTGTTTCGCGATT</u> GTAG	
*Bold: Alanine substituted site; Bold and Italic: ribosome-binding site		
Primers for constructs used in Co-IP		
pBAD24-vpa1025V SVG-F	<u>GAGGAATTCACCATGGGTAAACCAGCAGCAGTGA</u> T	For cloning <i>paar2</i> into plasmid pBAD24-VC2208-VSV-G plasmid
pBAD24-VPA1025 VSVG-R	<u>GATATCAGTGTACTGGTTTAAACGTCCCCCGATGA</u> GGACGGTCG	
pBAD24-PID-FLA G-F	<u>GAGGAATTCACCATGTTCTTTGTGAAGAAGG</u>	For cloning PID into plasmid pBAD24- VCA0111-FLAG plasmid
pBAD24-PID-FLA G-R	<u>ATCGTCTTTGTAGTCGTCACATTTTGAACATT</u>	
Primers for expressing toxin and antitoxin		
pBAD24-1517FLA G-F	<u>GAGGAATTCACCATGATTCTCTCAATTTGTTAT</u>	For cloning <i>rhsP</i> and WHH domain into plasmid pBAD24-VCA0111-FLAG
pBAD24-1517CT-F LAG-F	<u>GAGGAATTCACCATGGCTCAAGTATATGATACTAA</u>	
pPAD24-1517CT-F LAG-R	<u>ATCGTCTTTGTAGTCTACGAGCTCTTCTGGAGACG</u> AGTA	
pBAD24-1517CT-F LAG-F	<u>GAGGAATTCACCATGGCTCAAGTATATGATACTAA</u>	Overlapping primers to amplify mutated WHH(W1328A)
WHH-W1328A-R	CTTGATGATGATGCGCAACAT	
WHH-W1328A-F	ATGTTGCGCATCATCAAG	
pPAD24-1517CT-F LAG-R	<u>ATCGTCTTTGTAGTCTACGAGCTCTTCTGGAGACG</u> AGTA	
pBAD24-1517CT-F LAG-F	<u>GAGGAATTCACCATGGCTCAAGTATATGATACTAA</u>	Overlapping primers to amplify mutated WHH (H1329A)
WHH-H1329A-R	CATCTTGATGATGTGCCCAA	
WHH-H1329A-F	TTTGGGCACATCAAGATG	
pPAD24-1517CT-F LAG-R	<u>ATCGTCTTTGTAGTCTACGAGCTCTTCTGGAGACG</u> AGTA	
pBAD24-1517CT-F LAG-F	<u>GAGGAATTCACCATGGCTCAAGTATATGATACTAA</u>	Overlapping primers to amplify mutated WHH (H1330A)
WHH-H1330A-R	ACCATCTTGATGGGCATGCCA	
WHH-H1330A-F	TGGCATGCCATCAAGATGGT	
pPAD24-1517CT-F	<u>ATCGTCTTTGTAGTCTACGAGCTCTTCTGGAGACG</u>	

LAG-R	AGTA	
pBAD24-1517CT-F LAG-F	<u>GAGGAATTCACCATGGCTCAAGTATATGATACTAA</u>	Overlapping primers to amplify mutated WHH (H1345A)
WHH-H1345A-R	TTCTAACTGAGGCCACACTTT	
WHH-H1345A-F	AAAGTGTGGCCTCAGTTAGAA	
pPAD24-1517CT-F LAG-R	<u>ATCGTCTTTGTAGTCTACGAGCTCTTCTGGAGACG</u> AGTA	
pBAD24-1517CT-F LAG-F	<u>GAGGAATTCACCATGGCTCAAGTATATGATACTAA</u>	Overlapping primers to amplify mutated WHH (H1354A)
WHH-H1354A-R	CTACCACCTGTGGCAGCTACA	
WHH-H1354A-F	TGTAGCTGCCACAGGTGGTAG	
pPAD24-1517CT-F LAG-R	<u>ATCGTCTTTGTAGTCTACGAGCTCTTCTGGAGACG</u> AGTA	
	*Bold: Alanine substituted site	
pCX340-1518-F	<u>CATATGGGAAGCTTGGGTACCATGATTAGCCTTTC</u> AGATATTG	For cloning <i>rhsPi</i> into plasmid pCX340 to express RhsPi-Myc
pCX340-1518-R	<u>AGCGTTTCTGGGTGCGAATTC</u> TTAAGATTCTAGAA GCTTTTCC	
pCX340-1518myc-R	<u>AGCGTTTCTGGGTGCGAATTC</u> TTACAGGTCTTCTT CAGAGATCAGTTTCTGTTTCAGATTCTAGAAGCTTT TCC	
pCX340-1519-F	<u>CATATGGGAAGCTTGGGTACCATGCTGGCAGAGTA</u> TCAGGCGC	For cloning <i>vp1519</i> into plasmid pCX340
pCX340-1519-R	<u>AGCGTTTCTGGGTGCGAATTC</u> TTAGCACAAAGATCT TTAGTGAAG	
pCX340-1520-F	<u>CATATGGGAAGCTTGGGTACCATGCTGAATAAAGC</u> AGAATATAA	For cloning <i>vp1520</i> into plasmid pCX340
pCX340-1520-R	<u>AGCGTTTCTGGGTGCGAATTC</u> TTAATCAATTTTAA ACTCAGCTA	
pBAD24-WP021FL AG-F	<u>GAGGAATTCACCATGTTGAATAAAAAGTCAA</u>	For cloning the fragment of the AHH domain in strain WP-021449074 into pBAD24 plasmid
pBAD24-WP021FL AG-R	<u>ATCGTCTTTGTAGTCTCTACTTCTACTTTT</u>	
pBAD24-WP005FL AG-F	<u>GAGGAATTCACCATGGTTGGTGGGGAGAAA</u>	For cloning the fragment of the REase-6 domain in strain WP-005396166 into pBAD24 plasmid
pBAD24-WP005FL AG-R	<u>ATCGTCTTTGTAGTCTTTAGTCTTCTC</u>	
pBAD24-WP006-F	<u>GAGGAATTCACCATGAATGAAGGATCTGGT</u>	For cloning the fragment of the AHH domain in strain WP-006742583 into
pBAD24-WP006-R	<u>ATCGTCTTTGTAGTCTCTCTCACAGC</u>	

		pBAD24 plasmid
pCX340-antiWP012-F	<u>CATATGGGAAGCTTGGGTACC</u> ATGACACTTAAAATTTGG	For cloning the fragment of the immunity protein of the AHH domain in strain WP-021449074 into pCX340 plasmid
pCX340-antiWP012-R	AGCGTTTCTGGGTGCGAATTC <u>TAAAAAGGACGC</u> CATTC	
pCX340-WP005FL-AG-F	<u>CATATGGGAAGCTTGGGTACC</u> ATGCAAAGCAAAGAATCG	For cloning the fragment of the immunity protein of the REase-6 domain in strain WP-005396166 into pCX340 plasmid
pCX340-WP005FL-AG-R	AGCGTTTCTGGGTGCGAATTC <u>TATCGAGTGATCT</u> TCCC	
pCX340-WP006-F	<u>CATATGGGAAGCTTGGGTACC</u> ATGGCAGGTGAGCATAGC	For cloning the fragment of the immunity protein of the AHH domain in strain WP-006742583 into pCX340 plasmid
pCX340-WP006-R	AGCGTTTCTGGGTGCGAATTC <u>TAAAGCGTCCTAT</u> TGTG	
Primer for pET28a cloning		
28a-vp1517-F	<u>TAAGAAGGAGATATACCATG</u> ATTCCTCAATTTGTTAT	For cloning <i>rhsP</i> into pET28a plasmid
28a-vp1517-R	<u>GTGGTGGTGGTGGTGT</u> ACGAGCTCTTCTGGAGACGA	
28a-vp1517-F	<u>TAAGAAGGAGATATACCATG</u> ATTCCTCAATTTGTTAT	For construction of RhsP mutant R1092A in pET28a
VP1517-R1092A-R	GTCGTAATACGCAGCGAGGTT	
VP1517-R1092A-F	AACCTCGCTGCGTATTACGAC	
28a-vp1517-R	<u>GTGGTGGTGGTGGTGT</u> ACGAGCTCTTCTGGAGACGA	
28a-vp1517-F	<u>TAAGAAGGAGATATACCATG</u> ATTCCTCAATTTGTTAT	
VP1517-D1105A-R	AGATATCGGGGCTTGTGGAT	For construction of RhsP mutant D1105A in pET28a
VP1517-D1105A-F	ATCCAACAAGCCCCGATATCT	
28a-vp1517-R	<u>GTGGTGGTGGTGGTGT</u> ACGAGCTCTTCTGGAGACGA	
28a-vp1517-F	<u>TAAGAAGGAGATATACCATG</u> ATTCCTCAATTTGTTAT	
VP1517-D1127A-R	ACCTGTTGGGGCAATCCACTG	
VP1517-D1127A-F	CAGTGGATTGCCCAACAGGT	For construction of RhsP mutant D1127A in pET28a
28a-vp1517-R	<u>GTGGTGGTGGTGGTGT</u> ACGAGCTCTTCTGGAGACGA	
28a-vp1517-F	<u>TAAGAAGGAGATATACCATG</u> ATTCCTCAATTTGTTAT	
Primers for bacterial two hybrid		
pAC-Hcp2-F	<u>ACGTTTGGCGCGGCCGCT</u> ATGCAGTCTAATACGTATCT	For cloning Hcp2 into pAC $\lambda$ CI plasmid
pAC-Hcp2-R	<u>CTGCGATGCGGATCC</u> TACATTTGTTGACCTTTA	



	A	
pAC-VgrG2-F	<u>ACGTTTGGCGCGGCCGCT</u> ATGAAAAAGCAAGTC AAGA	For cloning VgrG2 into pAC $\lambda$ CI plasmid
pAC-VgrG2-R	<u>CCTGCGATGCGGATCC</u> TAAATCAAGAGATTTGT C	
pAC-PAAR2-F	<u>ACGTTTGGCGCGGCCGCT</u> ATGGGTAAACCAGCAG CAGT	For cloning PAAR2 into pAC $\lambda$ CI plasmid
pAC-PAAR2-R	<u>CCTGCGATGCGGATCC</u> TATCCCCGATGAGGACG G	
pBR-RhsP-F	<u>AAACCAGAGGCGGCCGCT</u> ATGATTCCTCAATTTGT TAT	For cloning RhsP into pBR $\alpha$ plasmid
pBR-RhsP-R	<u>CCGGCGTAGAGGATCC</u> TACATACGAGCTCTTCTGGA G	
		For cloning RhsP <sub>N</sub> into pBR $\alpha$ plasmid
pBR-RhsP <sub>N</sub> -R	<u>CCGGCGTAGAGGATCC</u> ACCRGTTGGGTCAATCCA CTGG	
pBR-PID-F	<u>AAACCAGAGGCGGCCGCT</u> ATGTTCTTTGTGAAG AAGG	For cloning PID into pBR $\alpha$ plasmid
pBR-PID-R	<u>CCGGCGTAGAGGATCC</u> TACGTCACATTTTGAACA TT	
Primers for Real time PCR		
RT-vp-vgrG1-F	TGCCGATGATAACCAAACAG	For RT-PCR to targeting <i>vgrG1</i>
RT-vp-vgrG1-R	CCACCTTTCACGACGACTTT	
RT-vp-vgrG2-F	TAAAGTCTTCAAACAGCCA	For RT-PCR to targeting <i>vgrG2</i>
RT-vp-vgrG2-R	TTGCCCTACCCGAGGATGAA	
RT-vp1517-F	ATTAACCATTACCAATATGC	For RT-PCR to targeting <i>rhsP</i>
RT-vp1517-R	GCGAGCGAACGCCATCTTCT	
RT-vp1518-F	GCCTTTCAGATATTGAAAAT	For RT-PCR to targeting <i>rhsPi</i>
RT-vp1518-R	ATCCAAATACTCCTCATAGT	
RT-vp1519-F	TCCGTCGGAGAAGATGGTGT	For RT-PCR to targeting <i>vp1519</i>
RT-vp1519-R	GCGCATTACAAATTCCTCA	
RT-vp1521-F	AATTGTGCGTGATAGACCAA	For RT-PCR to targeting <i>vp1521</i>
RT-vp1521-R	CCAGTTATCCCCTTGATCTA	
RT-16s-F	ACTCCTACGGGAGGCAGCAG	For RT-PCR to targeting 16srDNA
RT-16s-R	ATTACCGCGGCTGCTGG	

171

172

173  
174  
175  
176  
177  
178  
179  
180  
181  
182  
183  
184  
185  
186  
187  
188  
189  
190  
191  
192  
193  
194  
195  
196  
197  
198  
199  
200  
201  
202  
203  
204  
205  
206

## References

- 1 Gode-Potratz, C. J. & McCarter, L. L. Quorum sensing and silencing in *Vibrio parahaemolyticus*. *J Bacteriol* **193**, 4224-4237, doi:10.1128/JB.00432-11 (2011).
- 2 Alcoforado Diniz, J. & Coulthurst, S. J. Intraspecies Competition in *Serratia marcescens* Is Mediated by Type VI-Secreted Rhs Effectors and a Conserved Effector-Associated Accessory Protein. *J Bacteriol* **197**, 2350-2360, doi:10.1128/JB.00199-15 (2015).
- 3 Koskiniemi, S. *et al.* Rhs proteins from diverse bacteria mediate intercellular competition. *Proc Natl Acad Sci U S A* **110**, 7032-7037, doi:10.1073/pnas.1300627110 (2013).
- 4 Cianfanelli, F. R. *et al.* VgrG and PAAR Proteins Define Distinct Versions of a Functional Type VI Secretion System. *PLoS Pathog* **12**, e1005735, doi:10.1371/journal.ppat.1005735 (2016).
- 5 Kung, V. L. *et al.* An rhs gene of *Pseudomonas aeruginosa* encodes a virulence protein that activates the inflammasome. *Proc Natl Acad Sci U S A* **109**, 1275-1280, doi:10.1073/pnas.1109285109 (2012).
- 6 Ma, J. *et al.* PAAR-Rhs proteins harbor various C-terminal toxins to diversify the antibacterial pathways of type VI secretion systems. *Environ Microbiol* **19**, 345-360, doi:10.1111/1462-2920.13621 (2017).
- 7 Wenren, L. M., Sullivan, N. L., Cardarelli, L., Septer, A. N. & Gibbs, K. A. Two independent pathways for self-recognition in *Proteus mirabilis* are linked by type VI-dependent export. *MBio* **4**, doi:10.1128/mBio.00374-13 (2013).
- 8 Whitney, J. C. *et al.* Genetically distinct pathways guide effector export through the type VI secretion system. *Mol Microbiol* **92**, 529-542, doi:10.1111/mmi.12571 (2014).
- 9 Hachani, A., Allsopp, L. P., Oduko, Y. & Filloux, A. The VgrG proteins are "a la carte" delivery systems for bacterial type VI effectors. *J Biol Chem* **289**, 17872-17884, doi:10.1074/jbc.M114.563429 (2014).
- 10 Park, K. S. *et al.* Functional characterization of two type III secretion systems of *Vibrio parahaemolyticus*. *Infect Immun* **72**, 6659-6665, doi:10.1128/IAI.72.11.6659-6665.2004 (2004).
- 11 Ferrieres, L. *et al.* Silent mischief: bacteriophage Mu insertions contaminate products of *Escherichia coli* random mutagenesis performed using suicidal transposon delivery plasmids mobilized by broad-host-range RP4 conjugative machinery. *Journal of bacteriology* **192**, 6418-6427 (2010).
- 12 Charpentier, X. & Oswald, E. Identification of the secretion and translocation domain of the enteropathogenic and enterohemorrhagic *Escherichia coli* effector Cif, using TEM-1  $\beta$ -lactamase as a new fluorescence-based reporter. *Journal of bacteriology* **186**, 5486-5495 (2004).
- 13 Dove, S. L., Joung, J. K. & Hochschild, A. Activation of prokaryotic transcription through arbitrary protein-protein contacts. *Nature* **386**, 627-630, doi:DOI 10.1038/386627a0 (1997).