

1 **SUPPLEMENTAL FIGURE LEGENDS**

2 Fig. S1. Amino acid sequence alignment and identity of RstAs. Identity indicated the results of
3 comparison to RstA1 of strain V06-18.

4 Fig. S2. Amino acid sequence alignment and identity of RstBs. Identity indicated the results of
5 comparison to RstB1 of strain V06-18.

6 Fig. S3. Amino acid sequence alignment and identity of RstRs. Identity indicated the results of
7 comparison to RstR1 of strain V06-18.

8 Fig. S4. Amino acid sequence alignment and identity of RstCs. Identity indicated the results of
9 comparison to RstC of strain V06-18.

10

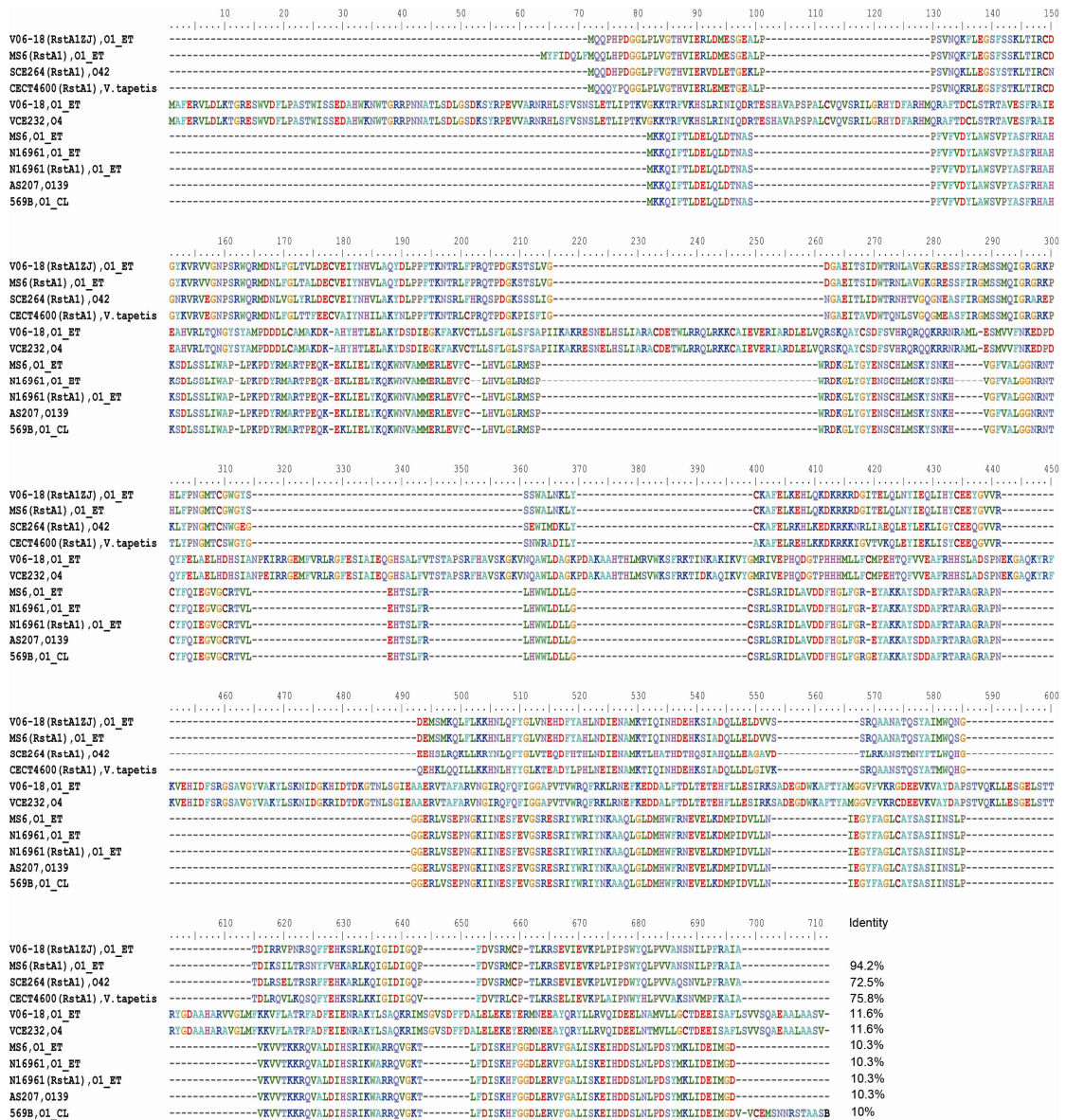
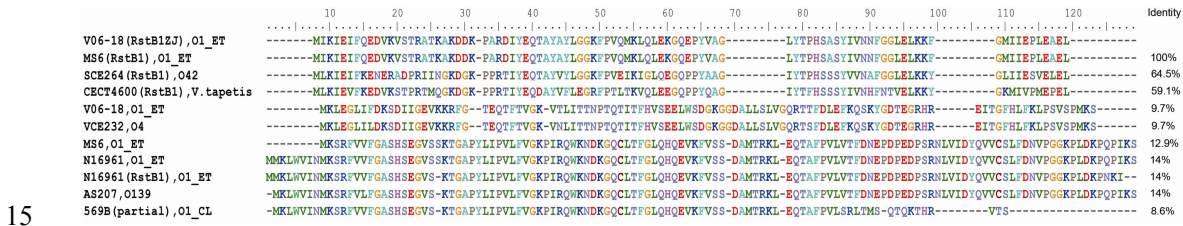
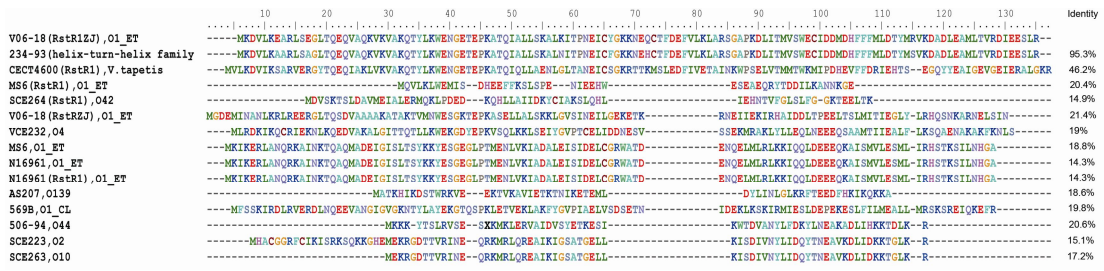


Fig. S1. Amino acid sequence alignment and identity of RstAs. Identity indicated the results of comparison to RstA1 of strain V06-18.



15
 16 Fig. S2. Amino acid sequence alignment and identity of RstBs. Identity indicated the results of
 17 comparison to RstB1 of strain V06-18.



18

19 Fig. S3. Amino acid sequence alignment and identity of RstRs. Identity indicated the results of
 20 comparison to RstR1 of strain V06-18.

	10	20	30	40	50	60	70	Identity
V06-18_01_ET	MSLKPYT	LM DVYDS	LEDLNNM	AVLRS	GAYTDE	IAHQVQ	NLICDK	II DLQGMV
MS6_01_ET	MSLKPYT	LM DVYDS	LEDLNNM	AVLRS	GAYTDE	IAHQVQ	NLICDK	II DLQGMV
SCE264_042	MSLKPYT	LM DVYDS	LEDLNNM	AVLRS	GAYTDE	IAHQVQ	NLICDK	II DLQGMV
N16961_01_ET	MSLKPYT	LM DVYDS	LEDLNNM	AVLRS	GAYTDE	IAHQVQ	NLICDK	II DLQGMV
E7946_01_ET	MSLKPYT	LM DVYDS	LEDLNNM	AVLRS	GAYTDE	IAHQVQ	NLICDK	II DLQGMV
V44_01_ET	MSLKPYT	LM DVYDS	LEDLNNM	AVLRS	GAYTDE	IAHQVQ	NLICDK	II DLQGMV
V52_037	MSLKPYT	LM DVYDS	LEDLNNM	AVLRS	GAYTDE	IAHQVQ	NLICDK	II DLQGMV
V51_0141	MSLKPYT	LM DVYDS	LEDLNNM	AVLRS	GAYTDE	IAHQVQ	NLICDK	II DLQGMV
CRIS101_01_ET	MSLKPYT	LM DVYDS	LEDLNNM	AVLRS	GAYTDE	IAHQVQ	NLICDK	II DLQGMV
INDRE91_1_01_ET	MSLKPYT	LM DVYDS	LEDLNNM	AVLRS	GAYTDE	IAHQVQ	NLICDK	II DLQGMV
IB1627_01_ET	MSLKPYT	LM DVYDS	LEDLNNM	AVLRS	GAYTDE	IAHQVQ	NLICDK	II DLQGMV
IB1346_01_ET	MSLKPYT	LM DVYDS	LEDLNNM	AVLRS	GAYTDE	IAHQVQ	NLICDK	II DLQGMV
E1781_01_ET	MSLKPYT	LM DVYDS	LEDLNNM	AVLRS	GAYTDE	IAHQVQ	NLICDK	II DLQGMV
IB4642_01_ET	MSLKPYT	LM DVYDS	LEDLNNM	AVLRS	GAYTDE	IAHQVQ	NLICDK	II DLQGMV
VC106_01_ET	MSLKPYT	LM DVYDS	LEDLNNM	AVLRS	GAYTDE	IAHQVQ	NLICDK	II DLQGMV
KMN002_01_ET	MSLKPYT	LM DVYDS	LEDLNNM	AVLRS	GAYTDE	IAHQVQ	NLICDK	II DLQGMV
MG116926_01_ET	MSLKPYT	LM DVYDS	LEDLNNM	AVLRS	GAYTDE	IAHQVQ	NLICDK	II DLQGMV
01_07vp_01_ET	MSLKPYT	LM DVYDS	LEDLNNM	AVLRS	GAYTDE	IAHQVQ	NLICDK	II DLQGMV
IB4322_01_ET	MSLKPYT	LM DVYDS	LEDLNNM	AVLRS	GAYTDE	IAHQVQ	NLICDK	II DLQGMV
CECT4600_V_tapetis	MTVKE	YTLSDA	EAKLDT	IASISL	FLSTG	NCPRE	IAENLQ	DHMQDE

22

23 Fig. S4. Amino acid sequence alignment and identity of RstCs. Identity indicated the results of
 24 comparison to RstC of strain V06-18.

25

26

27

28

29

30 **Table S1. Primers.**

Primers	Primer sequence (5'–3')	Target
zot1	AAACCTTGAACGCATGGC	<i>zot</i>
zot2	GCCCATAGACCACGATAA	
orfU1	TCTCCATCGGTAACGGCTTC	<i>gIII^{CTX}</i>
orfU2	GTTGTAACCAAACGCCTCGAC	
rstC1	GATGGCTCAGTCAATGCCTT	<i>rstC</i>
rstC2	TATATCTGCGTTCAGGCGCTTA	
inA	TCCTCCTTGCTTAATCTTG	VC1479
inB	ATGTGGACAGCTTTGTGGTG	<i>rtxA</i>
InI	GTCGCCATTGAATCTCTTCC	VCA0568
InJ	TGGATGTGGTGGAGCTGTAA	VCA0570
RstRZJF	GGTAAAACTTTGCACTAG	<i>rstR^{ZJ}</i>
RstAZJ-1	TGATAAATCATACCGCCCTGA	<i>rstA</i> of pre-CTX ^{ZJ} Φ
RstRN-1	GTAATAAGGAAGCTCGATTA	<i>rstR^{ZJ}</i> of pre-CTX ^{ZJ} Φ
RstRN-2	GCATTCCCAAGATACCATAG	
RstAN-1	CCACTGGTCGGGACGCATGTT	<i>rstA</i> in pre-CTX ^{ZJ} Φ of
RstAN-2	TCAAATGGCTGGCCGATA	VC06-18
rstRZJ1	CGGAATTCGGTAAAACTTTGCACTAG	<i>rstR^{ZJ}</i> in pre-CTX ^{ZJ} Φ
rstRZJ2	CGGAATTCGCGACGTAGCGTGCGGAG	
rstAZJP1	CGGAATTCATCCCCATGTTTGG	<i>rstA</i> promoter region of
rstAZJP2	CTTTCGAAGTCATGCACCAAAAACCTGTC	pre-CTX ^{ZJ} Φ
RlucZJ1	TTTTTGGTGCATGACTTCGAAAGTTTAT	<i>Rluc</i>
Rluc2	CGGAATTCACTGCATTCTAGTTGTGGTTTGTCC	
Rluc1	CGGAATTC ATGACTTCGAAAGTTTATG	<i>Rluc</i>
RS-F	ACGCGTTCGACCCGTTGCCGATTTCATCAC	<i>zot</i>
RS-R	CCGGAATTCGATTGCACAATGGGAGAGCC	<i>gIII^{CTX}</i>
zotF1	GATAAGAGAGGCGGCGGAG	<i>zot</i>
zotR1	CGTGGGTGGTCAGGGTAAAC	
ThyA1	GCCGATTTGACCTACGATG	<i>thyA</i>
ThyA2	ACGAATATAGCCGAGCAACTC	

32 **Table S2.** GenBank accession numbers

GenBank	Gene	Strain
KP768424	<i>rstR^{ZJ}, rstR1^{ZJ}, rstA, rstA1^{ZJ}, rstB, rstB1^{ZJ}, rstC</i>	V06-18
AF133307	<i>rstR-4**</i>	SCE223
AF133309	<i>rstR-4*</i>	SCE263
NC_010614	<i>rstR1, rstA1, rstB1, rstC</i>	<i>Vibrio tapetis</i> CECT4600
AF055890	<i>rstR^{class}, rstA, partial rstB</i>	569B
AF110029	<i>rstR^{Calc}, rstA, rstB</i>	AS207
AF452586	<i>rstR6</i>	506-94
DQ288668	<i>rstR-232, rstA, rstB</i>	VCE232
AE003852	<i>rstR^{ET}, rstR1^{ET}, rstA, rstA1, rstB, rstB1, rstC</i>	N16961
JMBO01000107	helix-turn-helix family protein	234-93
AP014524	<i>rstR1, rstA1, rstB1, rstC, rstR, rstA, rstB</i>	MS6
AF319656	<i>rstR1/rstR-5, rstA1, rstB1, rstC</i>	SCE264
U83795	<i>rstC</i>	E7946
EU860439	<i>rstC</i>	VC44
AAKJ02000045	<i>rstC</i>	V52
DS179738	<i>rstC</i>	V51
ACVW01000013	<i>rstC</i>	CIRS101
ADAK01000003	<i>rstC</i>	INDRE 91/1
GQ466610	<i>rstC</i>	IB1627
GQ466608	<i>rstC</i>	IB1346
GQ485653	<i>rstC</i>	E1781
GQ485651	<i>rstC</i>	IB4642
GU942563	<i>rstC</i>	VC106
HQ224500	<i>rstC</i>	KMN002
GQ485654	<i>rstC</i>	MG116926
GQ485652	<i>rstC</i>	01.07vp
GQ485650	<i>rstC</i>	IB4322

33

34