

**Supplementary Table 1:** Features of genomes sequenced in the present study

<b>Population</b>	<b>Strain name</b>	<b>Number of contigs</b>	<b>Genome size (Mb)</b>	<b>Number of CDSs</b>	<b>Accession number</b>
F12	10N.286.45.A3	126	5.48	5124	PIGF00000000
	10N.286.46.E10	134	5.39	5009	PIGE00000000
	10N.286.48.B8	60	5.23	4822	PIGD00000000
	10N.286.51.C3	50	5.19	4758	PIGC00000000
	ZF 223	32	5.15	4727	PIGB00000000
F18	1F_55	117	5.74	5349	PIGA00000000
	1S_113	62	5.33	4842	PIFZ00000000
	1S_129	84	5.36	4875	PIFY00000000
	1S_14	41	5.33	4833	PIFX00000000
	1S_146	73	5.40	4934	PIFW00000000
	1S_296	48	5.40	4905	PIFV00000000
	5S_122	94	5.51	4998	PIFU00000000
	5S_210	41	5.28	4982	PIFT00000000
	5S_226	67	5.34	5070	PIFS00000000
	5S_238	68	5.41	4861	PIFR00000000
	5S_245	60	5.31	4781	PIFQ00000000
	5S_272	105	5.35	4853	PIFP00000000
	5S_279	69	5.40	4914	PIFO00000000
	5S_283	57	5.33	5050	PIFN00000000
	5S_57	53	5.41	5106	PIFM00000000
	FF_139	196	5.84	5641	PIFL00000000
	FF_144	195	5.90	5616	PIFK00000000
	ZS_107	56	5.46	4920	PIFJ00000000
	ZS_117	101	5.35	4847	PIFI00000000
	ZS_138	90	5.34	4865	PIFH00000000
	ZS_173	58	5.49	4906	PIFG00000000
	ZS_181	69	5.28	4968	PIFF00000000
	ZS_183	64	5.35	4841	PIFE00000000
	ZS_185	102	5.45	4960	PIFD00000000
	ZS_198	82	5.39	4873	PIFC00000000
	ZS_2	80	5.47	4966	PIFB00000000
	ZS_211	270	5.56	5282	PIFA00000000
	ZS_213	96	5.47	4953	PIEZ00000000
	ZS_58	78	5.37	4869	PIEY00000000
	ZS_82	53	5.38	5089	PIEX00000000
	ZS_90	46	5.38	5085	PIEW00000000
ZF_41	87	5.74	5310	PIEV00000000	

**Supplementary Table 2: Strains used in the present study**

<b>Name</b>	<b>Description</b>	<b>Reference</b>
PIR2	(F-) $\Delta$ lac169 rpoS(am) robA1 creC510 hsdR514 endA recA1 uidA( $\Delta$ Mlu I)::pir	Invitrogen, USA
$\beta$ 3914	$\beta$ 2163 <i>gyrA462</i> , <i>zei298::Tn10</i> [Km <sup>R</sup> Em <sup>R</sup> Tc <sup>R</sup> ]	Le Roux <i>et al.</i> , 2007
BL21 (DE3)	F <sup>-</sup> <i>ompT hsdS<sub>B</sub>(r<sub>B</sub><sup>-</sup> m<sub>B</sub><sup>-</sup>) gal dcm</i> (DE3)	Novagen, USA
GV1300	BL21 (DE3) + pFO4_GFP_R5-7 <sub>crass</sub>	This study
GV1549	BL21 (DE3) + pFO4_GFP_R5-7 <sub>F12</sub>	This study
TOP10	F- <i>mcrA</i> $\Delta$ ( <i>mrr-hsdRMS-mcrBC</i> ) $\phi$ 80 <i>lacZ</i> $\Delta$ M15 $\Delta$ lacX74 <i>recA1 araD139</i> $\Delta$ ( <i>ara-leu</i> )7697 <i>galU galK rpsL(Str<sup>R</sup>) endA1 nupG</i>	Invitrogen, USA
GV1460	J2-8 ( <i>Vibrio</i> sp. nov F13-like)	Lemire <i>et al.</i> , 2015
GV1422	J2-9 ( <i>V. crassostreae</i> )	Lemire <i>et al.</i> 2015
GV1495	J2-9 $\Delta$ R5.7	Lemire <i>et al.</i> , 2015
GV1040	10N.286.48.B8 (hereafter named B8)	Hunt <i>et al.</i> , 2008
GV1826	B8 $\Delta$ R-a	This study
GV1872	B8 $\Delta$ R-b	This study
GV1906	B8 $\Delta$ R-c	This study
GV1874	B8 $\Delta$ R-d	This study
GV1895	B8 $\Delta$ R-e	This study
GV1897	B8 $\Delta$ R-f	This study
GV1899	B8 $\Delta$ R-g	This study
GV1830	B8 $\Delta$ R-h	This study
GV1601	B8 $\Delta$ R-i	This study
GV1870	B8 $\Delta$ R-j	This study
GV1876	B8 $\Delta$ R-k	This study
GV1908	B8 $\Delta$ R-l	This study
GV1832	B8 $\Delta$ R-m	This study
GV1828	B8 $\Delta$ R-n	This study
GV1903	B8 $\Delta$ R-o	This study
GV1891	B8 $\Delta$ R-p	This study
GV1887	B8 $\Delta$ R-q	This study
GV1889	B8 $\Delta$ R-r	This study
GV1884	B8 $\Delta$ R-s	This study
GV1885	B8 $\Delta$ R-t	This study
GV1858	B8 $\Delta$ R-u	This study
GV1850	B8 $\Delta$ R-v	This study
GV1901	B8 $\Delta$ R-w	This study
GV1905	B8 $\Delta$ R-x	This study
GV1832	B8 $\Delta$ R-m	This study

GV1828	B8 $\Delta R-n$	This study
GV1903	B8 $\Delta R-o$	This study
GV1568	B8 $\Delta R5.7$	This study
GV2825	B8 $\Delta R5.8$	This study
GV2620	B8 $\Delta R-g$ + pMRB-PLACR-5.7 <sub>F12</sub>	This study
GV2621	B8 $\Delta R5-7$ + pMRB-PLACR-5.7 <sub>F12</sub>	This study
GV2288	8T2_11 ( <i>V. chagasii</i> , #3)	Bruto et al., 2016
GV2455	8T2_11 $\Delta R5.7$	This study
GV2423	7T7_2 ( <i>V. splendidus</i> , #24)	Bruto et al., 2016
GV2493	7T7_2 $\Delta R5.7$	This study
GV1054	ZS_173 ( <i>V. splendidus</i> , F18)	Hunt et al., 2008
GV2266	ZS_173 $\Delta MARTX$	This study
GV1065	ZS_185 ( <i>V. splendidus</i> , F18)	This study
GV1882	ZS_185 $\Delta MARTX$	This study
GV2466	ZS_185 $\Delta R5-7$	This study
GV1067	ZS_213 ( <i>V. splendidus</i> , F18)	Hunt et al., 2008
GV2267	ZS_213 $\Delta MARTX$	This study

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**Supplementary Table S3 : Plasmids used and constructed in this study**

<b>Name</b>	<b>Description</b>	<b>Reference</b>
pSW23T	<i>oriV<sub>R6K</sub></i> ; <i>oriT<sub>RP4</sub></i> ; $\square$ Cm <sup>R</sup> $\square$	Demarre <i>et al.</i> , 2005
pSW $\delta$ R5.7	pSW23T; $\Delta$ R5.7 <sub>8T2_11</sub> & ZS_185	This study
pSW7848T	<i>oriV<sub>R6K</sub></i> ; <i>oriT<sub>RP4</sub></i> ; <i>araC-P<sub>BAD</sub>ccdB</i> ; $\square$ Cm <sup>R</sup> $\square$	Le Roux <i>et al.</i> , 2007
pSW $\delta$ R-a	pSW7848T; $\Delta$ R-a	This study
pSW $\delta$ R-b	pSW7848T; $\Delta$ R-b	This study
pSW $\delta$ R-c	pSW7848T; $\Delta$ R-c	This study
pSW $\delta$ R-d	pSW7848T; $\Delta$ R-d	This study
pSW $\delta$ R-e	pSW7848T; $\Delta$ R-e	This study
pSW $\delta$ R-f	pSW7848T; $\Delta$ R-f	This study
pSW $\delta$ R-g	pSW7848T; $\Delta$ R-g	This study
pSW $\delta$ R-h	pSW7848T; $\Delta$ R-h	This study
pSW $\delta$ R-i	pSW7848T; $\Delta$ R-i	This study
pSW $\delta$ R-j	pSW7848T; $\Delta$ R-j	This study
pSW $\delta$ R-k	pSW7848T; $\Delta$ R-k	This study
pSW $\delta$ R-l	pSW7848T; $\Delta$ R-l	This study
pSW $\delta$ R-m	pSW7848T; $\Delta$ R-m	This study
pSW $\delta$ R-n	pSW7848T; $\Delta$ R-n	This study
pSW $\delta$ R-o	pSW7848T; $\Delta$ R-o	This study
pSW $\delta$ R-p	pSW7848T; $\Delta$ R-p	This study
pSW $\delta$ R-q	pSW7848T; $\Delta$ R-q	This study
pSW $\delta$ R-r	pSW7848T; $\Delta$ R-r	This study
pSW $\delta$ R-s	pSW7848T; $\Delta$ R-s	This study
pSW $\delta$ R-t	pSW7848T; $\Delta$ R-t	This study
pSW $\delta$ R-u	pSW7848T; $\Delta$ R-u	This study
pSW $\delta$ R-v	pSW7848T; $\Delta$ R-v	This study
pSW $\delta$ R-w	pSW7848T; $\Delta$ R-w	This study
pSW $\delta$ R-x	pSW7848T; $\Delta$ R-x	This study
pSW $\delta$ R5.7 <sub>F12</sub>	pSW7848T; $\Delta$ R5.7 <sub>F12</sub>	This study
pSW $\delta$ $\square$ 5.8 <sub>F12</sub>	pSW7848T; $\Delta$ R5.8 <sub>F12</sub>	This study
pSW $\delta$ MARTX	pSW7848T; $\Delta$ MARTX	This study
pMRB-PLACR-5.7 <sub>F12</sub>	<i>oriV<sub>R6K</sub></i> ; <i>oriT<sub>RP4</sub></i> ; <i>oriV<sub>pB1067</sub></i> ; P <sub>lac</sub> R-5.7 <sub>F12</sub> [Cm <sup>R</sup> ]	This study
pMRB-PLACGFP	<i>oriV<sub>R6K</sub></i> ; <i>oriT<sub>RP4</sub></i> ; <i>oriV<sub>pB1067</sub></i> ; P <sub>lac</sub> GFP [Cm <sup>R</sup> ]	Bruto <i>et al.</i> , 2016
pFO4	Amp <sup>R</sup> , T7lac promoter, His.Tag	Groisillier <i>et al.</i> , 2010
pFO4-R5.7 <sub>F12</sub>	pFO4-HisTag-GFP-R5.7 <sub>F12</sub>	This study
pFO4-R5.7 <sub>crass</sub>	pFO4-HisTag-GFP-R5.7 <sub>crass</sub>	This study

**Supplementary Table 4: Primers used in this study**

Use	Name	Sequence 5'-3' <sup>a</sup>
Deletion of R-a	R-a-1	GCCCCGAATTTCGACATATCCCGGTGGTTCAC
	R-a-2	CCAATAAAGAGAGGAGCCTGGGAAGTTAGTGG GCTTTGTG
	R-a-3	CACAAAGCCCCTAACTTCCCAGGCTCCTCTCT TTATTGG
	R-a-4	GCCCCGAATTCCAACACACCACCAACCTACG
Deletion of R-b	R-b-1	GCCCCGAATTCATCGCCCCAGATTTACTGG
	R-b-2	CACTCGTTATGCTGGTGAGTGGAGTCGTTTGTG TAAAGGG
	R-b-3	CCCTTTACACAAACGACTCCACTCACCAGCATA ACGAGTG
	R-b-4	GCCCCGAATTCGTGTGGTTACGCCTTCATCG
Deletion of R-c	R-c-1	GCCCCGAATTCCTTGCCGCTCTCGTAGATTG
	R-c-2	CGATACTTCTGGCTGCCATAGTGAGGCATTGAG CTTTGTG
	R-c-3	CACAAAGCTCAATGCCTCACTATGGCAGCCAG AAGTATCG
	R-c-4	GCCCCGAATTCGTCGCGATAAAAGTAAACGC
Deletion of R-d	R-d-1	GCCCCGAATTCGATTCATCAGAGTTCCAG
	R-d-2	CAGGGTACTGGAATTGTCCGCAAAGGTGAGG GTTTCAGG
	R-d-3	CCTGAAACCCTCACCTTTGCGGACAATTCCAGT AACCTG
	R-d-4	GCCCCGAATTCGGTAAACGTAAACGTGATGCG
Deletion of R-e	R-e-1	GCCCCGAATTCGGGTACTGTGTCCTGTCTC
	R-e-2	CAACTAGTGCAATGAGAGCCAAGCCAGTCAAT AGACTGGC
	R-e-3	GCCAGTCTATTGACTGGCTTGGCTCTCATTGCA CTAGTTG
	R-e-4	GCCCCGAATTCCTTGGCATCGCTTCAACACC
Deletion of R-f	R-f-1	GCCCCGAATTCCTGCATTGCTGAGTCGAAG
	R-f-2	GAGCCTGAAGCGTATCAGATCCATGCTATGTCG GCCTTTG
	R-f-3	CAAAGGCCGACATAGCATGGATCTGATACGCT TCAGGCTC
	R-f-4	GCCCCGAATTC AAGTTACTCTCCCACGGAG
Deletion of R-g	R-g-1	GCCCCGAATTCCTACGCAGCCAACATGCAAC
	R-g-2	GGCAAAGGCATTTTCACCGTGCCATAAAAAGG CCGACATC
	R-g-3	GATGTCGGCCTTTTTATGGCACGGTGAAAATGC CTTTGCC
	R-g-4	GCCCCGAATTCCTTCGATCTCGATTGGACTGC
Deletion of R-h	R-h-1	GCCCCGAATTCGTGATCCAGCCTTTGTTCAG

	R-h-2	GATATTCGCGAAGCAGCACCCCTGTTGAGTTGA CAGGAGG
	R-h-3	CCTCCTGTCAACTCAACAGGGGTGCTGCTTCGC GAATATC
	R-h-4	GCCCCGAATTCCTTTGGAGCTGCGTTCAAAC
Deletion of R-i	R-i-1	GCCCCGAATTCGGTAGTGGCTGATGAAGTTC
	R-i-2	GCTGCCGTGGTGATATGTATAAAATGTCCCGCA TTAGGCG
	R-i-3	CGCCTAATGCGGGACATTTTATACATATCACCA CGGCAGC
	R-i-4	GCCCCGAATTCCTGGCGCTGTATGACCAAAC
Deletion of R-j	R-j-1	GCCCCGAATTCGCAGAAGTATGGTAAGTCCC
	R-j-2	GAAGTACCCAGGGTCGTTTGAATGCCAATACC AAGCGCAG
	R-j-3	CTGCGCTTGGTATTGGCATTCAAACGACCCTGG GTACTION
	R-j-4	GCCCCGAATTCATGCTTTAGGTGCACACGC
Deletion of R-k	R-k-1	GCCCCGAATTCAGACACAGACATCGGCTATG
	R-k-2	GCATTGAAGTAGGGGACATCGTGAGCAAATAG CGTACCTG
	R-k-3	CAGGTACGCTATTTGCTCACGATGTCCCCTACT TCAATGC
	R-k-4	GCCCCGAATTCGGTATTGGTGATGTAGCCTC
Deletion of R-l	R-l-1	GCCCCGAATTCAGATAACGTAGCAGCAGG
	R-l-2	GTGCCTACAGTCCGAGTAATAAACAGCCAGCA TAAGGCTG
	R-l-3	CAGCCTTATGCTGGCTGTTTATTACTCGGACTG TAGGCAC
	R-l-4	GCCCCGAATTCCTGCGCTGTCGTTAGCAAAG
Deletion of R-m	R-m-1	GCCCCGAATTCACCAACCAACGAAAGTGGTG
	R-m-2	CAAGATGTTACCTCTGCGCTGTGTTGCAGCTTT CATTGGC
	R-m-3	GCCAATGAAAGCTGCAACACAGCGCAGAGGTA ACATCTTG
	R-m-4	GCCCCGAATTCCACTTCCATAACCTCTGTGC
Deletion of R-n	R-n-1	GCCCCGAATTCACCAAGACACAATCCATCACC
	R-n-2	CAGTGGTGAAGTTCAGAAGCTATTAGGTGACC TCCCAACG
	R-n-3	CGTTGGGAGGTCACCTAATAGCTTCTGAACTTC ACCACTG
	R-n-4	GCCCCGAATTCGACATCGAGAACTTGGTC
Deletion of R-o	R-o-1	GCCCCGAATTCGTTGCGTTTGCGGTATCAAG
	R-o-2	CCCGAAGGCTACACTTATTCGACTCTGTGAGCA TGTTTGG

	R-o-3	CCAAACATGCTCACAGAGTCGAATAAGTGTAG CCTTCGGG
	R-o-4	GCCCCGAATTCATAGTCTATCGTGCTGCAGG
Deletion of R-p	R-p-1	GCCCCGAATTCCTAATTCAGGATCGCCATC
	R-p-2	CATACGCTCAGCAGTATTCGCAAGCACGATGA CAGTTGAC
	R-p-3	GTCAACTGTCATCGTGCTTGCGAATACTGCTGA GCGTATG
	R-p-4	GCCCCGAATTCGGTCAGATCAAAGACCGATG
Deletion of R-q	R-q-1	GCCCCGAATTCGAGACTTCGTGTGTCTCTGC
	R-q-2	GTGGGCTTTTAAACGTCTGCCTGGTACATTAGC CAGCTTC
	R-q-3	GAAGCTGGCTAATGTACCAGGCAGACGTTAAA AAGCCAC
	R-q-4	GCCCCGAATTCGCAATGGAAGAGCAAGACAG
Deletion of R-r	R-r-1	GCCCCGAATTCCTCCTGAACAGTAAGCGGAC
	R-r-2	GAACATCGATTCTCAGCCTCAATTGGGGAGAG CATTAGGC
	R-r-3	GCCTAATGCTCTCCCAATTGAGGCTGAGAATC GATGTTC
	R-r-4	GCCCCGAATTCGGTAGGATGGATGAGGAAAC
Deletion of R-s	R-s-1	GCCCCGAATTCGCATCGAACAATGGGATTGG
	R-s-2	CGGTATTACCAACGGAAACGACATAGAGTAA GACCTCGC
	R-s-3	GCGAGGTCTTACTCTATGTCGTTTCCGTTGGGT AATACCG
	R-s-4	GCCCCGAATTCCTACTTCTCGGCCATCAAAC
Deletion of R-t	R-t-1	GCCCCGAATTCCTAAACAGTACTCAGCGCTC
	R-t-2	CTCGTATCTAGCTACCCTTCGTAAGCAAGCCAA GCATCAG
	R-t-3	CTGATGCTTGGCTTGCTTACGAAGGGTAGCTAG ATACGAG
	R-t-4	GCCCCGAATTCGTTCTACGTGAACTACCAG
Deletion of R-u	R-u-1	GCCCCGAATTC AAGGCTATCGTGCCGCATTC
	R-u-2	CCAATACTGCCACAAAGTGCATTTGTGCGGAC AACCTACG
	R-u-3	CGTAGGTTGTCCGCACAAATGCACTTTGTGGCA GTATTGG
	R-u-4	GCCCCGAATTCCTGAGGTTGACCACGTTTCG
Deletion of R-v	R-v-1	GCCCCGAATTCCTGAACAAGCGTGTGATCACC
	R-v-2	GGTAAGGGGTCGACTTTACCGCTCACGCTAAA GTAACCAC
	R-v-3	GTGGTACTTTAGCGTGAGCGGTAAAGTCGACC CCTTACC
	R-v-4	GCCCCGAATTCGCACACTATCGACATGACAG

Deletion of R-w	R-w-1	GCCCCGAATTCACAATGGACAAGTCCCATC
	R-w-2	GACACTTGTCAGCCAAACACCTTCCATGCCCAA ACTGGAG
	R-w-3	CTCCAGTTTGGGCATGGAAGGTGTTTGGCTGAC AAGTGTC
	R-w-4	GCCCCGAATTCGCACCGCTAAGTCATCAACC
Deletion of R-x	R-x-1	GCCCCGAATTC AAGTAATGCGGGACTGGAC
	R-x-2	CAACCCCAGTTCTCAACAGGGATGTTGCAACG TTACCGAC
	R-x-3	GTCGGTAACGTTGCAACATCCCTGTTGAGAACT GGGGTTG
	R-x-4	GCCCCGAATTCATGTTCAAGTGCCTCACCTC
Deletion of R5.7	R5.7-1	GTATCGATAAGCTTGATATCGAATTCCTCTTAC CATCGCTCTTCAG
	R5.7-2	CCAAAAAGGCCGACAAGATGGGGTAGCAGAA ACCAACACC
	R5.7-3	GGTGTGGTTTCTGCTACCCCATCTTGTCGGCC TTTTTGG
	R5.7-4	CCCCCGGGCTGCAGGAATTCCTACGCAGCCAA CATGCAAC
Deletion of R5.8	R5.8-1	GTATCGATAAGCTTGATATCGAATTCCTCTCCTG CAATCACAGTCAC
	R5.8-2	CTAATCACAAATCTAACAGGGATAAAACTCCA TACCCATCGACAAATAG
	R5.8-3	CTATTTGTCGATGGGTATGGAGTTTTATCCCTG TTAGATTTGTGATTAG
	R5.8-4	CCCCCGGGCTGCAGGAATTCACCTCTTAGTTAT TTGGCACAG
Inactivation of R5.7	0504-1	CGTATGCCTGAACATAGTTAG
	0504-2	GGGATCTGATGATCACCGAG
Deletion of <i>rtxA</i> CHBDE	MX1	GCCCCGAATTCAGATACATCGGACCATGCTG
	MX2	GGATACTCAGGTACAGCCTAAGGAAGTGACGT GATGGTAC
	MX3	GTACCATCACGTCACCTCCTTAGGCTGTACCTG AGTATCC
	MX4	GCCCCGAATTCGCTCGAATTGATAGGTTGCG
R5.7 <sub>F12</sub> in MRB	1102-1	GTGAGCGGATAACAAAGGAAGGGCCCATGAG AATTCTACCGATTATTATTTCTC
	1102-2	CGACGCGTCTGCAGCTCGAGTCAGTTAGAACA ACTGTTGCCATTC
	0207-1	CTCGAGCTGCAGACGCGTCG
	0207-2	GGGCCCTTCCTTTGTTATCCGCTCAC
R5.7 <sub>F12</sub> in pFO4	1102-3	GGTGGTGGTTCTGGTGGTGGTTCTAGTGACTGG CTAGAGCTTAATAAC



	1102-4	CATGCATGCTAGCCTCGAGTTAGTTAGAACAAC TGTTGCCATTC
	0904-1	CATCACCATCACCATGGATCCAGTAAAGGAGA AGAACTTTTC
	0904-2	AGAACCACCACCAGAACCACCACCTTTGTATA GTTTCATCCATGC
	2003-1	GGA TCC ATG GTG ATG GTG ATG
	2003-2	CTC GAG GCT AGC ATG CAT G
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R5.7 <sub>cras</sub> in pFO4	0904-5	GGTGGTGGTTCTGGTGGTGGTTCTAGCGACTGG CTTGAACTG
	0904-6	CATGCATGCTAGCCTCGAGTTAATTAGAGCAGC TATTGCC
		<hr/>

<sup>a</sup> restriction sites are indicated in bold

**Supplementary table 5:** Annotation of *Vibrio* sp. F12 specific regions.

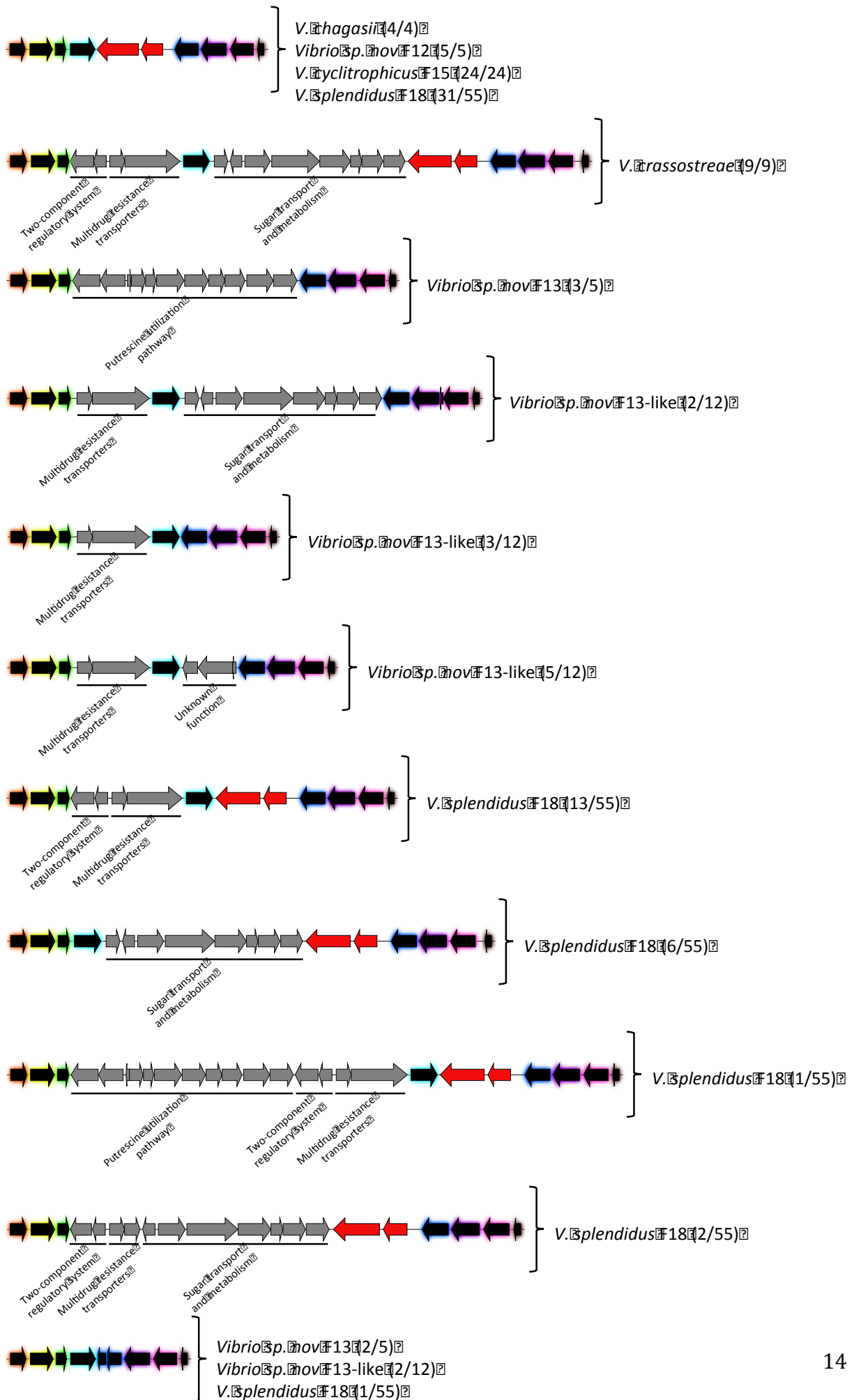
<b>Region</b>	<b>Locus tag<sup>a</sup></b>	<b>Product</b>
R-a	160071	AraC-type DNA-binding domain-containing protein
	160070	Putative MOSC domain protein
R-b	180051	Iron-hydroxamate transporter permease subunit
	180052	Ferrichrome-binding protein
	180053	Ferrichrome outer membrane transporter
	180055	Transcriptional activator
	180056	Conserved protein of unknown function with ferric iron reductase domains
	180057	Iron-hydroxamate transporter subunit ; ATP-binding component of ABC superfamily
R-c	10026	Putative Transcription regulator, AsnC-type protein
	10027	Conserved membrane protein of unknown function
R-d	10384	Putative Transcription regulator, TetR-like
	10385	Putative dihydrofolate reductase
	10386	Proton/sodium-glutamate symport protein
R-e	40063	NADH:flavorubredoxin oxidoreductase
	40065	Flavorubredoxin oxidoreductase
R-f	40179	Transcriptional regulator, LysR family protein
	40180	Conserved exported protein of unknown function
R-g	40197	Conserved exported protein of unknown function (R5.7)
	40198	Conserved exported protein of unknown function (R5.8)
R-h	40249	Conserved membrane protein of unknown function
	40250	Uncharacterized HTH-type transcriptional regulator
	40251	Putative glutathione S-transferase
	40252	Putative transcriptional regulator, LysR family protein
	40253	Putative methyl-accepting chemotaxis protein
	40254	Cryptochrome-like protein cry2
	40255	Sigma-54 dependent transcriptional regulator
	40256	Aldehyde dehydrogenase B
	40257	Putative NUDIX hydrolase
	40258	Conserved protein of unknown function
	40259	Putative multidrug efflux transporter
	40260	S-formylglutathione hydrolase
	40261	Alcohol dehydrogenase class 3 (Alcohol dehydrogenase class III)
	40262	Quaternary ammonium compound-resistance protein QacE
	200002	Murein peptide amidase A
	200003	Periplasmic oligopeptide-binding protein
	200004	Putative Ethylbenzene dehydrogenase
200006	Putative cytochrome c-type protein NrfB	
200007	Putative tetraheme cytochrome c3	
R-i	200027	Putative Organic hydroperoxide resistance protein
	200028	Putative Organic hydroperoxide resistance transcriptional regulator
R-j	200054	Putative two component histidine kinase

	200055	Two-component response regulator of C4-dicarboxylate transport
	200056	Putative glycerophosphoryl diester phosphodiesterase
	200057	Putative Phosphonate-binding periplasmic transporter
	200058	Putative Phosphonates import ATP-binding protein PhnC
	200059	Putative PhnE phosphonate ABC transporter, permease
	200060	Putative Phosphonate ABC transporter permease protein phnE1
R-k	310012	Conserved protein of unknown function
	310011	Conserved exported protein of unknown function
R-l	130064	Putative 5'-nucleotidase
	130062	Multiple antibiotic resistance protein marC
R-m	100119	Putative membrane bound peptidase; NefD homolog
	100118	Putative Stomatin like transmembrane protein
R-n	100095	Conserved exported protein of unknown function
	100094	Conserved protein of unknown function
R-o	30035	Putative Signal transduction protein containing an EAL and a GGDEF domains
	30034	Putative ABC-type sugar transport system, periplasmic component
	30033	Putative Ribose ABC transporter, periplasmic ribose-binding protein
R-p	170092	Conserved exported protein of unknown function
	170091	Conserved exported protein of unknown function
	170090	Conserved protein of unknown function
	170089	Conserved exported protein of unknown function
	170088	Conserved exported protein of unknown function
	170087	Putative Transcriptional regulator, LuxR family
	170081	Endonuclease/Exonuclease/phosphatase family protein
R-q	80118	GGDEF family protein
	80117	Putative Outer membrane protein and related peptidoglycan-associated (lipo)proteins
	80116	Conserved protein of unknown function
	80115	Conserved protein of unknown function
	80114	TadE-like protein
	80113	Conserved exported protein of unknown function
	80112	Conserved membrane protein of unknown function
	80111	Putative Flp pilus assembly protein TadB
	80109	Putative Flp pilus assembly ATPase TadZ/CpaE
	80108	Conserved exported protein of unknown function
	80106	Putative Flp pilus assembly protein RcpC/CpaB
	80105	Conserved membrane protein of unknown function
	80104	Putative pilin Flp
	80103	Bacterial regulatory helix-turn-helix , lysR family protein
R-r	80026	Conserved exported protein of unknown function
	80025	Conserved exported protein of unknown function
	80024	Conserved protein of unknown function
	80023	Conserved exported protein of unknown function
R-s	80012	Fe <sup>2+</sup> /Zn <sup>2+</sup> uptake regulation protein

	80011	Adenine deaminase family protein
	80010	Putative carbonate dehydratase
	80009	Putative Cobalamin (vitamin B12) biosynthesis CobW-like
R-t	250021	Transcriptional regulator
	250022	Conserved membrane protein of unknown function
R-u	60205	Conserved exported protein of unknown function
	60204	Conserved protein of unknown function
R-v	60093	Putative Cytochrome c556
	60092	Hydrogenase cytochrome B-type subunit-like protein
	60091	Transcriptional regulator, MarR family protein
R-w	60041	Transcriptional regulator
	60040	Conserved exported protein of unknown function
R-x	350020	Predicted Na <sup>+</sup> /dicarboxylate symporter
	440001	Coenzyme A disulfide reductase
	440002	Conserved exported protein of unknown function

<sup>a</sup>Locus tag in B8 (VB12B8\_v1\_XXXXXX)

**Supplementary Figure 1: Comparison of the genetic organization of the R5-7/8 locus in the Splendidus clade.** The first genetic organization (top of the figure) is mostly found in the populations of the Splendidus clade and was used as a reference for Figure 3. The R5.7 and R5.8 genes are represented with red arrows. The surrounding genes of R5-7/8 are represented by black arrows shrouded by colors to keep track in the different genetic organization shown in this figure. Genes in grey are intermittently present in the R5-7 locus and encode for different metabolic activities that are indicated when known. The distribution among different species the Splendidus clade of the different genetic organization of the R5-7/8 locus is shown on the right.



**Supplementary Figure 2: Virulence of R5.7 inactivated strains belonging to the Splendidus clade.** Comparison of mortalities induced by wild type strain (wt) and R5.7 inactivated mutant of a strain representative of *V. chagasii* (8T2\_11) and *V. splendidus* (7T7\_2) isolated in France (population #3 and 24 in Bruto et al., 2016) and *V. splendidus* isolated in Plum Island (population F18 in Hunt et al., 2008). All infections were performed in duplicate and at least twice by intramuscular injection of strains ( $10^7$  cfu/animal) in 20 oysters and counting the percentage of mortalities at 24H (y-axis).

