Table S1. Genomic information of *Vibrio* strains included in this study

Genome assembly	Strain	Species	Host / environmental origin	Geographic location
ASM1264146v1	SM6	*V. agarilyticus*	Seawater	China
ASM139945v2	605	*V. bivalvicida*	Grooved carpet shell	Spain
ASM155843v2	FDAARGOS_107	*V. harveyi*	Environment	Bahamas
ASM190843v2	QT520	*V. harveyi*	Golden pompano	China
ASM19609v1	RIMD 2210633	*V. parahaemolyticus*	Human	Japan
ASM2139773v1	XH2145	*V. harveyi*	Seawater	China
ASM216375v1	ATCC 25920	*V. campbellii*	Seawater	USA
ASM222426v1	ATCC 27562	*V. vulnificus*	Estuarine	USA
ASM2365091v1	E110	*V. alginolyticus*	Pacific white shrimp	-
ASM2497193v1	1	*V. harveyi*	Penaeus vannamei	China
ASM274198v1	CAIM 577	*V. rotiferianus*	Rotifer from water	Belgium
ASM284985v1	LC2-005	*V. azureus*	Seawater	Japan
ASM285029v1	345	*V. harveyi*	Grouper	China
ASM2855131v1	VH21FL	*V. harveyi*	Japanese flounder	South Korea
ASM2888554v1	A2	*V. harveyi*	European seabass	Croatia

ASM2888556v1	120-19	*V. harveyi*	Golden seabream	Croatia
ASM2888558v1	160-19	*V. harveyi*	European seabass	Croatia
ASM2888560v1	94/17	*V. harveyi*	European seabass	Croatia
ASM2889862v1	A27	*V. harveyi*	European seabass	Croatia
ASM2889864v1	FR9	*V. harveyi*	European seabass	France
ASM2889866v1	ESP	*V. harveyi*	Golden seabream	Spain
ASM2889868v1	FR5	*V. harveyi*	European seabass	Tunisia
ASM2889868v1	IT5	*V. harveyi*	European seabass	Turkey
ASM2889870v1	IT7	*V. harveyi*	European seabass	Italy
ASM2889872v1	IT2	*V. harveyi*	European seabass	Italy
ASM2889874v1	TUR2	*V. harveyi*	Golden seabream	Turkey
ASM2889878v1	IT8	*V. harveyi*	European seabass	Italy
ASM2889880v1	IT4	*V. harveyi*	European seabass	Italy
ASM2889882v1	FR10	*V. harveyi*	Golden seabream	France
ASM2899353v1	IT6	*V. harveyi*	Golden seabream	Italy
ASM290647v1	BoB-53	*V. campbellii*	Marine environments	India
ASM290665v1	090810a	*V. hyugaens*	Seawater	Japan
ASM2942895v1	PH1009	*V. harveyi*	Grass shrimp	Philippines

ASM3006043v1	SB1	*V. harveyi*	Asian seabass	India
ASM3038840v1	K2014767	*V. harveyi*	Caribbean spiny lobster	USA
ASM3635193v1	WHSS0915	*V. harveyi*	Korean rockfish	China
ASM3799714v1	NH-LM1	*V. harveyi*	Yellowsnout sea bass	China
ASM4269163v1	LcV6	*V. harveyi*	Large yellow croaker	China
ASM4284805v1	TUMSAT-2019	*V. harveyi*	Kuruma shrimp	Japan
ASM455152v1	BEI176	*V. ouci*	Seawater	China
ASM46443v1	BAA-1116	*V. campbellii*	Seawater	-
ASM46718v1	NBRC 102218	*V. ezurae*	Abalone	Japan
ASM653852v1	NBRC 102082	*V. inusitatus*	Red abalone	USA
ASM77011v2	ATCC 33843	*V. harveyi*	Marine environments	USA
ASM799093v1	NBRC 104589	*V. sagamiensis*	Seawater	Japan
ASM918474v1	WXL538	*V. harveyi*	Estuarine water	China
ASM936341v1	THAF100	*V.aquimaris*	Water	Germany
ASM966531v1	2011V-1164	*V. harveyi*	Brown shark	USA
S2394	S2394	*V. nigripulchritudo*	Jellyfish	Australia
S2757	S2757	*V. galatheae*	Mussel	Australia
Vsuperstes	JCM 21480	*V. superstes*	Red Abalone	Australia

Table S2. Bacterial strains and plasmids used for genetic manipulation in this study

Primer	Sequence (5'-3')	Description
45T2-F-*ompF*	AATGGGGCTACAACTCTGGC	To amplify a 337-bp gene fragment of *ompF*
45T2-R-*ompF*	TTCAGTGAGGCTGTCGCATT	
N8T11-F-*moxR*	AGGAGCTCAGCGCGTTATAC	To amplify a 668-bp gene fragment of *moxR*
N8T11-R-*moxR*	TTCCATCCAAGGGGGATTGC	
Plasmid conjugation efficiency and stability		
pN8T11a-*yejB*-F	TGTGCTCCGCAGGCTCTTAT	To amplify a 372- gene fragment of *yejB*
pN8T11a-*yejB*-R	AATGTCCACCCACCCAATGA	
pN8T11b-*OmpA*-F	TTTCTCGTTGGGTCTTATCGT	To amplify a 499-bp gene fragment of *OmpA*
pN8T11b-*OmpA*-R	GCTCACTTCGTCTGTTCCTTG	
pN8T11c-AAIA71_29215-F	ATCCCTCTCACATTACACCA	To amplify a 264-bp gene fragment at gene locus AAIA71_29215
pN8T11c-AAIA71_29215-R	CATAACTAACCAAGCCAACA	
pN8T11d-*tbpA*-F	GTGAAGGAGAACGAACGAGA	To amplify a 764- bp gene fragment of *tbpA*
pN8T11d-*tbpA*-R	AAATGGACTAACCGACCAAG	
pN8T11e-*abiQ*-F	AGAGGGGACAAGCGGAAAAGGA	To amplify a 238-bp gene fragment of *abiQ*
pN8T11e-*abiQ*-R	GCCGAGCGGAAGAGGTAAATGA	

Table S3. Predicted secretory system genes in *V. harveyi* strains N8T11 and 45T2

Gene name	Secretion system type	Gene Count	N8T11 Gene Locus	45T2 Gene Locus
tolC	Type I	2	AAIA71_06635/ AAIA71_08980	AAIA70_01825/ AAIA70_07235
gspM	Type II	1	AAIA71_17160	AAIA70_14505
gspL	Type II	1	AAIA71_17165	AAIA70_00595
gspK	Type II	1	AAIA71_17170	AAIA70_00590
gspJ	Type II	1	AAIA71_17175	AAIA70_00585
gspI	Type II	1	AAIA71_17180	AAIA70_00580
gspH	Type II	1	AAIA71_17185	AAIA70_00575
gspG	Type II	1	AAIA71_17190	AAIA70_00570
gspF	Type II	1	AAIA71_17195	AAIA70_00565
gspE	Type II	1	AAIA71_17200	AAIA70_00560
gspD	Type II	1	AAIA71_17205	AAIA70_00555
gspC	Type II	1	AAIA71_17210	AAIA70_00550
yscV	Type III	1	AAIA71_12100	AAIA70_05390
yscX	Type III	1	AAIA71_12110	AAIA70_05380
yscW	Type III	1	AAIA71_12125	AAIA70_05365
yscN	Type III	1	AAIA71_12130	AAIA70_05360
yscO	Type III	1	AAIA71_12135	AAIA70_05355
yscP	Type III	1	AAIA71_12140	AAIA70_05350
yscQ	Type III	1	AAIA71_12145	AAIA70_05345
yscR	Type III	1	AAIA71_12150	AAIA70_05340
yscS	Type III	1	AAIA71_12155	AAIA70_05335
yscT	Type III	1	AAIA71_12160	AAIA70_05330
yscU	Type III	1	AAIA71_12165	AAIA70_05325
yscL	Type III	1	AAIA71_12200	AAIA70_05290
yscJ	Type III	1	AAIA71_12210	AAIA70_05280
yscF	Type III	1	AAIA71_12230	AAIA70_05260
yscC	Type III	1	AAIA71_12245	AAIA70_05245
virD4	Type IV	1	AAIA71_05975	AAIA70_11270
virB11	Type IV	1	AAIA71_05980	AAIA70_11265
virB10	Type IV	1	AAIA71_05990	AAIA70_11255
virB9	Type IV	1	AAIA71_05995	AAIA70_11250
virB8	Type IV	1	AAIA71_06000	AAIA70_11245
virB6	Type IV	1	AAIA71_06005	AAIA70_11235
virB5	Type IV	1	AAIA71_06015	AAIA70_11225
virB4	Type IV	1	AAIA71_06020	AAIA70_11220
virB1	Type IV	1	AAIA71_06035	AAIA70_11205
vgrG	Type VI	3	AAIA71_10000/ AAIA71_19525/ AAIA71_21160	AAIA70_07145/ AAIA70_24455/ AAIA70_26120
hcp	Type VI	3	AAIA71_10020/ AAIA71_19520/ AAIA71_21165	AAIA70_06150/ AAIA70_24450/ AAIA70_26125
vasG	Type VI	3	AAIA71_10055/ AAIA71_19515/ AAIA71_21170	AAIA70_07090/ AAIA70_24445/ AAIA70_26130
vasD	Type VI	3	AAIA71_10070/ AAIA71_19610/ AAIA71_21245	AAIA70_07075/ AAIA70_24375/ AAIA70_26035

impK	Type VI	3	AAIA71_10080/ AAIA71_19620/ AAIA71_21235	AAIA70_07065/ AAIA70_24365/ AAIA70_26025
impL	Type VI	3	AAIA71_10085/ AAIA71_19590/ AAIA71_21230	AAIA70_07060/ AAIA70_24360/ AAIA70_26020
secA	Sec-SRP	1	AAIA71_15700	AAIA70_02015
secB	Sec-SRP	1	AAIA71_01135	AAIA70_15165
secD	Sec-SRP	2	AAIA71_14935/ AAIA71_18815	AAIA70_02660/ AAIA70_16885
secE	Sec-SRP	1	AAIA71_00715	AAIA70_15585
secF	Sec-SRP	2	AAIA71_14930/ AAIA71_18820	AAIA70_16880/ AAIA70_02665
secG	Sec-SRP	1	AAIA71_03945	AAIA70_13175
secY	Sec-SRP	1	AAIA71_14245	AAIA70_01265
yidC	Sec-SRP	1	AAIA71_18020	AAIA70_16460
yajC	Sec-SRP	1	AAIA71_14940	AAIA70_02655
ffh	Sec-SRP	1	AAIA71_03590	AAIA70_13530
ftsY	Sec-SRP	1	AAIA71_00500	AAIA70_15800
tatA	Tat	1	AAIA71_17355	AAIA70_00405
tatB	Tat	1	AAIA71_17350	AAIA70_00410
tatC	Tat	1	AAIA71_17345	AAIA70_00415

Table S4. Predicted secretory protein-Encoding genes in *Vibrio harveyi* strains N8T11 and 45T2

Gene locus	Stain	Source (Plasmid/Chromosome)	Start position	End position	Orientation	Protein description
AAIA70_00370	45T2	Chromosome 1	83616	83176	-	Hypothetical protein
AAIA70_00985	45T2	Chromosome 1	221577	221353	-	Hypothetical protein
AAIA70_05685	45T2	Chromosome 1	1240716	1243154	+	Collagenase
AAIA70_06800	45T2	Chromosome 1	1501296	1501865	+	Hypothetical protein
AAIA70_06805	45T2	Chromosome 1	1502450	1505194	+	TcfC E-set like domain-containing protein
AAIA70_06810	45T2	Chromosome 1	1505198	1505947	+	Hypothetical protein
AAIA70_06815	45T2	Chromosome 1	1505944	1507038	+	Hypothetical protein
AAIA70_06820	45T2	Chromosome 1	1508380	1508153	-	Hypothetical protein
AAIA70_08250	45T2	Chromosome 1	1840511	1839510	-	Haloacid dehalogenase-like hydrolase
AAIA70_08255	45T2	Chromosome 1	1841842	1840736	-	BatD family protein
AAIA70_08285	45T2	Chromosome 1	1847035	1848681	+	Sulfatase-like hydrolase/transferase
AAIA70_08290	45T2	Chromosome 1	1848745	1849101	+	Hypothetical protein
AAIA70_08300	45T2	Chromosome 1	1850550	1851545	+	Hypothetical protein
AAIA70_08305	45T2	Chromosome 1	1851553	1851951	+	Hypothetical protein
AAIA70_08335	45T2	Chromosome 1	1856654	1855842	-	Hypothetical protein
AAIA70_09370	45T2	Chromosome 1	2075894	2075403	-	Hypothetical protein
AAIA70_09865	45T2	Chromosome 1	2145549	2145022	-	Hypothetical protein
AAIA70_11855	45T2	Chromosome 1	2567674	2567928	+	CG2 omega domain protein
AAIA70_19270	45T2	Chromosome 2	593152	594237	+	Porin
AAIA70_23935	45T2	Chromosome 2	1633406	1631643	-	DUF3859 domain-containing protein
AAIA70_24605	45T2	Chromosome 2	1789658	1792414	+	NEW3 domain-containing protein
AAIA71_01500	N8T11	Chromosome 1	315503	316345	+	BspA family leucine-rich repeat surface protein
AAIA71_01640	N8T11	Chromosome 1	344035	346113	+	Hypothetical protein
AAIA71_01645	N8T11	Chromosome 1	346216	346746	+	Hypothetical protein

AAIA71_01665	N8T11	Chromosome 1	349932	350246	+	Hypothetical protein
AAIA71_01670	N8T11	Chromosome 1	350248	350601	+	Hypothetical protein
AAIA71_02565	N8T11	Chromosome 1	538472	539089	+	Hypothetical protein
AAIA71_02600	N8T11	Chromosome 1	549581	547257	-	Ig-like domain-containing protein
AAIA71_03435	N8T11	Chromosome 1	691274	691912	+	OmpA family protein
AAIA71_05940	N8T11	Chromosome 1	1242891	1242160	-	Peptidase
AAIA71_07565	N8T11	Chromosome 1	1581521	1581892	+	Hypothetical protein
AAIA71_07585	N8T11	Chromosome 1	1583764	1584237	+	DUF4476 domain-containing protein
AAIA71_09460	N8T11	Chromosome 1	1984583	1983093	-	Hypothetical protein
AAIA71_09465	N8T11	Chromosome 1	1984994	1984752	-	Hypothetical protein
AAIA71_09465	N8T11	Chromosome 1	2102555	2101011	-	Trypsin-like serine protease
AAIA71_10425	N8T11	Chromosome 1	2212106	2212540	+	Hypothetical protein
AAIA71_10490	N8T11	Chromosome 1	2228147	2228644	+	Hypothetical protein
AAIA71_11035	N8T11	Chromosome 1	2360605	2361429	+	Hypothetical protein
AAIA71_11490	N8T11	Chromosome 1	2455271	2455813	+	Hypothetical protein
AAIA71_11565	N8T11	Chromosome 1	2468065	2468469	-	Hypothetical protein
AAIA71_11570	N8T11	Chromosome 1	2469245	2468931	-	Hypothetical protein
AAIA71_11575	N8T11	Chromosome 1	2470317	2469367	-	Hypothetical protein
AAIA71_11595	N8T11	Chromosome 1	2473935	2473405	-	Hypothetical protein
AAIA71_11600	N8T11	Chromosome 1	2476116	2474038	-	Hypothetical protein
AAIA71_11605	N8T11	Chromosome 1	2479347	2476267	-	Hypothetical protein
AAIA71_11735	N8T11	Chromosome 1	2504637	2503795	-	BspA family leucine-rich repeat surface protein
AAIA71_11930	N8T11	Chromosome 1	2556683	2555769	-	Alpha/beta hydrolase fold domain-containing protein
AAIA71_12010	N8T11	Chromosome 1	2570080	2570760	+	DUF1007 family protein
AAIA71_13675	N8T11	Chromosome 1	2933387	2933569	+	Hypothetical protein
AAIA71_14570	N8T11	Chromosome 1	3113280	3112993	-	Hypothetical protein
AAIA71_14675	N8T11	Chromosome 1	3128436	3128945	+	Hypothetical protein

AAIA71_16605	N8T11	Chromosome 1	3534513	3535670	+	Hypothetical protein
AAIA71_16790	N8T11	Chromosome 1	3568514	3568723	+	Hypothetical protein
AAIA71_17410	N8T11	Chromosome 1	3705798	3705313	-	Hypothetical protein
AAIA71_20510	N8T11	Chromosome 2	591190	589589	-	Hypothetical protein
AAIA71_20515	N8T11	Chromosome 2	591550	591320	-	Membrane protein
AAIA71_20560	N8T11	Chromosome 2	597959	596367	-	Methyl-accepting chemotaxis protein
AAIA71_20565	N8T11	Chromosome 2	598323	598093	-	Membrane protein
AAIA71_20780	N8T11	Chromosome 2	640673	640209	-	Hypothetical protein
AAIA71_20785	N8T11	Chromosome 2	641218	640712	-	Hypothetical protein
AAIA71_20790	N8T11	Chromosome 2	641679	641221	-	Hypothetical protein
AAIA71_20930	N8T11	Chromosome 2	642024	641683	-	Nitrite reductase small subunit NirD
AAIA71_20975	N8T11	Chromosome 2	681048	682094	+	Hypothetical protein
AAIA71_21710	N8T11	Chromosome 2	846848	847672	+	DUF2861 family protein
AAIA71_21715	N8T11	Chromosome 2	847746	850016	+	Glycoside hydrolase
AAIA71_23075	N8T11	Chromosome 2	1145970	1145494	-	Hypothetical protein
AAIA71_23080	N8T11	Chromosome 2	1148864	1146048	-	Insulinase family protein
AAIA71_23090	N8T11	Chromosome 2	1152982	1150637	-	TonB-dependent receptor plug domain-containing protein
AAIA71_23095	N8T11	Chromosome 2	1153502	1154245	+	DUF3450 domain-containing protein
AAIA71_23120	N8T11	Chromosome 2	1157129	1158304	+	Tetratricopeptide repeat protein
AAIA71_28040	N8T11	Chromosome 2	2203612	2202659	-	DUF2860 family protein
AAIA71_28125	N8T11	Chromosome 2	2216275	2215937	-	Cardiolipin synthetase domain protein
AAIA71_28410	N8T11	pN8T11a	7479	9290	+	extracellular solute-binding protein
AAIA71_28445	N8T11	pN8T11a	17295	14998	-	TonB-dependent siderophore receptor
AAIA71_28525	N8T11	pN8T11a	56846	56157	-	Hypothetical protein
AAIA71_28740	N8T11	pN8T11b	2301	2921	+	OmpA family protein
AAIA71_28910	N8T11	pN8T11b	31002	31538	+	Hypothetical protein
AAIA71_29110	N8T11	pN8T11c	13369	13920	+	outer membrane beta-barrel protein

AAIA71_29345	N8T11	pN8T11c	47795	48151	+	Hypothetical protein
AAIA71_29520	N8T11	pN8T11d	24277	23744	-	Hypothetical protein
AAIA71_29705	N8T11	pN8T11d	58616	58230	-	Hydroxyisourate hydrolase

Table S5. Comparative analysis of predicted virulence genes in V. harveyi strains N8T11 and 45T2 based on VFDB

Gene ontology category	Function	Virulence Genes in N8T11	Gene Count in N8T11	Virulence Genes in 45T2	Gene Count in 45T2	Presence
Mannose-sensitive Hemagglutinin	Adhesion and Biofilm Formation	*mshA, mshD, mshE, mshF, mshG, mshH, mshI, mshJ,mshK, mshL, mshM, mshN*	12	*mshA, mshB, mshD, mshE, mshF, mshG, mshH, mshI, mshJ, mshK, mshL, mshM, mshN*	13	Both
Type IV Pilus	Assembly and Motility	*pilB, pilC, pilD*	3	*pilB, pilC, pilD*	3	Both
LPS O-antigen	Surface Antigen Variation	-	0	*wbpM*	1	45T2
The tad Locus	Biofilm Formation	-	0	*tadA*	1	45T2
Capsular Polysaccharide	Protective Capsule Formation	*cpsA, cpsB, cpsC, cpsD, cpsE, cpsF, cpsG, cpsH, cpsI, cpsJ, wbfV/wcvB, wecA, wza, wzb, wzc*	15	*cpsA, cpsB, cpsC, cpsD, cpsE, cpsF, cpsG, cpsH, cpsI, cpsJ, wbfV/wcvB, wbfY, wza, wzb, wzc*	15	Both
Flagellar Assembly	Motility and Sensory Functions	*cheA, cheB, cheR, cheV, cheW, cheY, cheZ, filM,*	53	*cheA, cheB, cheR, cheV, cheW, cheY,*	53	Both

		flaA, *flaB*, *flaC*, *flaD*, *flaE*, *flaG*, *flaI*, *flgA*, *flgB*, *flgC*, *flgD*, *flgE*, *flgF*, *flgG*, *flgH*, *flgI*, *flgJ*, *flgK*, *flgL*, *flgM*, *flgN*, *flhA*, *flhB*, *flhF*, *flhG*, *fliA*, *fliD*, *fliE*, *fliF*, *fliG*, *fliH*, *fliI*, *fliJ*, *fliK*, *fliL*, *fliN*, *fliO*, *fliP*, *fliQ*, *fliR*, *fliS*, *flrA*, *flrB*, *flrC*, *motA*, *motB*, *motX*, *motY*		*cheZ*, *filM*, *flaA*, *flaB*, *flaC*, *flaD*, *flaE*, *flaG*, *flaI*, *flgA*, *flgB*, *flgC*, *flgD*, *flgE*, *flgF*, *flgG*, *flgH*, *flgI*, *flgJ*, *flgK*, *flgL*, *flgM*, *flgN*, *flhA*, *flhB*, *flhF*, *flhG*, *fliA*, *fliD*, *fliE*, *fliF*, *fliG*, *fliH*, *fliI*, *fliJ*, *fliK*, *fliL*, *fliN*, *fliO*, *fliP*, *fliQ*, *fliR*, *fliS*, *flrA*, *flrB*, *flrC*, *motA*, *motB*, *motX*, *motY*		
Enterobactin Receptors	Iron Uptake	*vctA*	1	*vctA*	1	Both
Heme Receptors	Iron Acquisition	*hutA*, *hutR*	2	*hutA*, *hutR*	2	Both
Periplasmic Binding Protein-dependent ABC Transport Systems	Nutrient Transport	*vctC*, *vctD*, *vctG*, *vctP*, *vibE*	5	*vctC*, *vctD*, *vctG*, *vctP*, *vibE*	5	Both
Ferrous Iron Transport	Iron Transport	*sitC*	1	*sitC*	1	Both
Iron/Manganese Transport	Metal Ion Transport	*sitA*, *sitB*, *sitD*	3	*sitA*, *sitB*, *sitD*	3	Both
Autoinducer-2	Quorum Sensing	*luxS*	1	*luxS*	1	Both
Cholerae Autoinducer-1	Quorum Sensing	*cqsA*	1	*cqsA*	1	Both

EPS Type II Secretion System	Extracellular Protein Secretion	*epsC, epsE, epsF, epsG, epsH, epsI, epsJ, epsK, epsL, epsM, epsN, gspD*	12	*epsC, epsE, epsF, epsG, epsH, epsI, epsJ, epsK, epsL, epsM, epsN, gspD*	12	Both
T3SS1 Secreted Effectors	Host Interaction and Evasion	*vopQ, vopR, ati2*	3	*vopQ, vopR, ati2*	3	Both
Type III serection system	Host Interaction and Evasion	*sycN, tyeA, vcrD, vcrG, vcrH, vcrR, virF, vopB, vopD, vopN, vscA, vscB, vscC, vscD, vscF, vscG, vscH, vscI, vscJ, vscK, vscL, vscN, vscO, vscQ, vscR, vscS, vscT, vscU, vscX, vscY, vxsC*	30	*sycN, tyeA, vcrD, vcrG, vcrH, vcrR, virF, vopB, vopD, vopN, vscA, vscB, vscC, vscD, vscF, vscG, vscH, vscI, vscJ, vscK, vscL, vscN, vscO, vscQ, vscR, vscS, vscT, vscU, vscX, vscY, vxsC*	30	Both
Heat-stable Cytotonic Enterotoxin	Toxin Production	*ast*	1	*ast*	1	Both
Urease	Urea Hydrolysis	*ureB, ureG*	2	*ureB, ureG*	2	Both
Trehalose-recycling	Sugar Utilization	*sugC*	1	*sugC*	1	Both
LPS Glucosylation	Surface Antigen Modification	*gtrB*	1	-	0	N8T11
Capsule	Capsule Formation	-	0	*cap8E, cap8G*	2	45T2

LOS	Lipooligosaccharide Synthesis	-	0	*EIIC*	1	45T2

Table S6. Unique virulence genes identified in V. harveyi strain N8T11

Gene locus	Location	Virulence Factor	Start Position	End Position	Description	E-value
AAIA71_02600	Chromosome 1	VpadF	549581	547257	Ig-like domain-containing protein	3.60E-45
AAIA71_03345	Chromosome 1	Hemolysin	673697	675712	Peptidase domain-containing ABC transporter	1.30E-70
AAIA71_03405	Chromosome 1	Flp pili	686146	687048	Type II secretion system F family protein	2.10E-49
AAIA71_03410	Chromosome 1	Flp pili	687045	687887	Type II secretion system F family protein	1.40E-42
AAIA71_03435	Chromosome 1	Polar flagella	691274	691912	OmpA family protein	1.20E-06
AAIA71_05815	Chromosome 1	LetA/S	1218295	1216499	ATP-binding protein	1.10E-44
AAIA71_09450	Chromosome 1	Zot	1982742	1981357	Zonular occludens toxin domain-containing protein	2.70E-11
AAIA71_11935	Chromosome 1	Ent	2558602	2556683	TonB-dependent receptor	2.90E-24
AAIA71_11975	Chromosome 1	Hemolysin/ Cytolysin	2567516	2566668	Dipeptide/oligopeptide/nickel ABC transporter ATP-binding protein	7.80E-22
AAIA71_11980	Chromosome 1	Acinetobactin	2568298	2567537	ATP-binding cassette domain-containing protein	8.80E-17
AAIA71_14610	Chromosome 1	F1 antigen	3118592	3117741	AraC family transcriptional regulator	8.40E-08
AAIA71_14635	Chromosome 1	Capsule	3121637	3122350	TIGR04283 family arsenosugar biosynthesis glycosyltransferase	2.00E-07
AAIA71_14685	Chromosome 1	ACF	3131358	3133004	Methyl-accepting chemotaxis protein	1.90E-32
AAIA71_16685	Chromosome 1	Hyaluronic acid capsule	3548212	3547295	UTP--glucose-1-phosphate uridylyl transferase GalU	4.90E-62

AAIA71_16695	Chromosome 1	LOS	3549595	3550677	Nucleotide sugar dehydrogenase	5.00E-82
AAIA71_16750	Chromosome 1	Capsule	3560491	3559526	Glycosyl transferase family 2 protein	3.50E-26
AAIA71_16835	Chromosome 1	LPS	3578543	3577671	Glycosyltransferase family A protein	2.00E-17
AAIA71_16975	Chromosome 1	LPS	3605009	3604101	Glycosyltransferase	8.20E-86
AAIA71_18460	Chromosome 2	PhoP	846201	846851	LysR family transcriptional regulator	1.20E-22
AAIA71_23045	Chromosome 2	PDIM	1139861	1140910	Alcohol dehydrogenase family protein	6.90E-20
AAIA71_23050	Chromosome 2	TTSS secreted effectors	1141298	1142281	YopT-type cysteine protease domain-containing protein	2.60E-37
AAIA71_23085	Chromosome 2	LOS	1150564	1148861	ABC transporter ATP-binding protein/permease	1.00E-12
AAIA71_26175	Chromosome 2	Pyoverdine	1831214	1830324	LysR family transcriptional regulator	2.40E-37
AAIA71_28125	Chromosome 2	Phospholipase D	2216275	2215937	Phospholipase D family protein	3.10E-06
AAIA71_28405	pN8T11a	Pyoverdine	5830	7479	Cyclic peptide export ABC transporter	7.40E-77
AAIA71_28430	pN8T11a	HitABC	11396	12631	ABC transporter permease subunit	4.30E-29
AAIA71_28450	pN8T11a	Pyoverdine	17530	17330	MbtH family NRPS accessory protein	2.50E-16
AAIA71_28460	pN8T11a	Pyoverdine	18631	25419	Non-ribosomal peptide synthetase	9.30E-142
AAIA71_28465	pN8T11a	Pyoverdine	25423	31698	Amino acid adenylation domain-containing protein	3.30E-226
AAIA71_28475	pN8T11a	Pyoverdine	32142	44468	Amino acid adenylation domain-containing protein	0
AAIA71_28480	pN8T11a	Bacillibactin	44556	46109	Thioesterase domain-containing protein	2.30E-51

AAIA71_28965	pN8T11B	Ysa TTSS	45654	45409	Lytic trans glycosylase domain-containing protein	4.10E-08
AAIA71_29090	pN8T11C	TTSS	10940	10512	Lytic trans glycosylase domain-containing protein	7.60E-18
AAIA71_29420	pN8T11d	HmbR	230	2455	TonB-dependent hemoglobin/transferrin/lactoferrin family receptor	1.10E-83
AAIA71_29470	pN8T11d	Ysa TTSS	10155	10586	Lytic trans glycosylase domain-containing protein	1.10E-16

Table S7. Genomic islands predicted in *V. harveyi* strains N8T11 and 45T2

Location	Start position	End position	GI name
N8T11 Chromosome 1	312237	351141	N8T11 GI 1
	351932	367700	N8T11 GI 2
	411820	423427	N8T11 GI 3
	530789	556400	N8T11 GI 4
	583541	595635	N8T11 GI 5
	671331	682745	N8T11 GI 6
	963073	971710	N8T11 GI 7
	1181987	1252983	N8T11 GI 8
	1548668	1642056	N8T11 GI 9
	2456308	2472317	N8T11 GI 10
	2473026	2508099	N8T11 GI 11
	3108541	3135004	N8T11 GI 12
	3221653	3235910	N8T11 GI 13
	3551595	3566345	N8T11 GI 14
	3704921	3714607	N8T11 GI 15
	3718309	3728884	N8T11 GI 16
N8T11 Chromosome 2	474677	488757	N8T11 GI 17
	717646	726961	N8T11 GI 18
	727699	737103	N8T11 GI 19
	740314	749618	N8T11 GI 20
	1217352	1225974	N8T11 GI 21
	2207652	2217359	N8T11 GI 22
pN8T11a	3943	12409	N8T11 GI 23
	47703	55202	N8T11 GI 24
	81575	97019	N8T11 GI 25
pN8T11b	45200	58755	N8T11 GI 26
pN8T11c	22090	61668	N8T11 GI 27
pN8T11d	35490	60275	N8T11 GI 28
45T2 Chromosome 1	225746	242784	45T2 GI 1
	1127944	1138711	45T2 GI 2
	1501983	1512297	45T2 GI 3
	2069013	2153741	45T2 GI 4
	2450476	2490353	45T2 GI 5
	2692292	2700959	45T2 GI 6
45T2 Chromosome 2	315689	326652	45T2 GI 7
	1585249	1601259	45T2 GI 8
	1734700	1744005	45T2 GI 9
	1747216	1755355	45T2 GI 10
	1756093	1765408	45T2 GI 11
	1986151	2017027	45T2 GI 12

Table S8. IS predicted in *V. harveyi* strains N8T11 and 45T2

Stain	Start position	End position	Subject	Identity (%)	E-value
	1772657	1772727	ISPsy43	87.32	3.00E-08
	1724608	1724747	Vnal	82.27	4.00E-07
	1988387	1988841	ISShes8	79.43	9.00E-29
	1988241	1988841	ISShes8	90.2	4.00E-06
	1988645	1988291	ISShwo2	84.08	2.00E-26
	1988241	1988287	ISShwo2	91.49	4.00E-06
45T2	2015212	2015299	ISVch8	88.64	3.00E-16
	2015142	2015183	ISVch8	95.24	7.00E-08
	2015142	2015208	ISV-N52	91.04	3.00E-13
	2015212	2015299	ISV-N52	84.09	1.00E-06
	1879896	1879951	ISVbsp5	92.86	2.00E-11
	1879906	1879948	ISVnal	93.02	4.00E-06
	1988391	1988431	ISSham1	92.68	7.00E-05
	2449063	2450305	ISVal2	93.4	0
	1564077	1565319	ISVal2	93.4	0
	1593553	1594795	ISVal2	93.4	0
	1620799	1622041	ISVal2	93.4	0
	1570825	1572067	ISVal2	93.4	0
	1562503	1563745	ISVal2	93.4	0
	2480679	2481921	ISVal2	93.4	0
	1204502	1205744	ISVal2	93.4	0
	1201467	1202709	ISVal2	93.4	0
	320476	321718	ISVal2	93.4	0
	3699299	3700283	ISVa2	91.68	0
	3561154	3562138	ISVa2	91.68	0
	3554199	3555183	ISVa2	91.68	0
	3341688	3342672	ISVa2	91.68	0
	504763	505747	ISVa2	91.68	0
	549839	550823	ISVa2	91.68	0
	672689	673673	ISVa2	91.68	0
	679750	680734	ISVa2	91.68	0
	854172	855156	ISVa2	91.68	0
	865510	866494	ISVa2	91.68	0
	1234252	1235236	ISVa2	91.68	0
	2559102	2560086	ISVa2	91.68	0
	2464325	2465309	ISVa2	91.68	0
	1568882	1569866	ISVa2	91.68	0
	1605599	1606583	ISVa2	91.68	0
	1616556	1617540	ISVa2	91.68	0
	1990617	1991601	ISVa2	91.68	0
	2285003	2285987	ISVa2	91.68	0
	1522257	1523241	ISVa2	91.68	0
	2506075	2507059	ISVa2	91.68	0
	1243071	1244055	ISVa2	91.68	0
	1213094	1214078	ISVa2	91.68	0
	1202902	1203886	ISVa2	91.68	0
	2698900	2699884	ISVa2	91.68	0
	2933655	2934639	ISVa2	91.68	0
	3090663	3091647	ISVa2	91.68	0

662306	663290	ISVa2	91.68	0
567760	568744	ISVa2	91.68	0
457991	458975	ISVa2	91.68	0
1196662	1197343	ISVa2	92.52	0
3562836	3563273	ISVa2	88.81	9.00E-132
3555761	3556059	ISVa2	90.97	3.00E-101
1195094	1195400	ISVa2	89.9	1.00E-96
3555188	3555325	ISVa2	89.86	7.00E-34
3554035	3554129	ISVa2	90.53	1.00E-22
3127540	3127677	ISVa2	81.88	5.00E-10
3555477	3555608	ISVa2	81.82	8.00E-09
2449063	2450305	ISVpa2	88.17	0
1564077	1565319	ISVpa2	88.17	0
1593553	1594795	ISVpa2	88.17	0
1620799	1622041	ISVpa2	88.17	0
1570825	1572067	ISVpa2	88.17	0
1562503	1563745	ISVpa2	88.17	0
2480679	2481921	ISVpa2	88.17	0
1204502	1205744	ISVpa2	88.17	0
1201467	1202709	ISVpa2	88.17	0
320476	321718	ISVpa2	88.17	0
3699282	3700283	ISVal1	90.92	0
3561137	3562138	ISVal1	90.92	0
3554182	3555183	ISVal1	90.92	0
3341671	3342672	ISVal1	90.92	0
504763	505764	ISVal1	90.92	0
549839	550840	ISVal1	90.92	0
672689	673690	ISVal1	90.92	0
679750	680751	ISVal1	90.92	0
854172	855173	ISVal1	90.92	0
865510	866511	ISVal1	90.92	0
1234252	1235253	ISVal1	90.92	0
2559085	2560086	ISVal1	90.92	0
2464308	2465309	ISVal1	90.92	0
1568882	1569883	ISVal1	90.92	0
1605599	1606600	ISVal1	90.92	0
1616556	1617557	ISVal1	90.92	0
1990617	1991618	ISVal1	90.92	0
2285003	2286004	ISVal1	90.92	0
1522240	1523241	ISVal1	90.92	0
2506075	2507076	ISVal1	90.92	0
1243054	1244055	ISVal1	90.92	0
1213077	1214078	ISVal1	90.92	0
1202885	1203886	ISVal1	90.92	0
2698900	2699901	ISVal1	90.92	0
2933655	2934656	ISVal1	90.92	0
3090663	3091664	ISVal1	90.92	0
662289	663290	ISVal1	90.92	0
567743	568744	ISVal1	90.92	0
457974	458975	ISVal1	90.92	0
1196662	1197343	ISVal1	93.55	0
3562836	3563273	ISVal1	88.36	5.00E-127

3555760	3556056	ISVal1	87.54	3.00E-76
1195077	1195401	ISVal1	85.54	4.00E-69
3555188	3555457	ISVal1	83.76	3.00E-39
3560706	3560779	ISVal1	86.49	1.00E-07
3555567	3555608	ISVal1	92.86	3.00E-05
1564077	1565320	ISVisp3	86.66	0
1204501	1205744	ISVisp3	86.66	0
1201466	1202709	ISVisp3	86.66	0
2449063	2450305	ISVisp3	86.65	0
1593553	1594795	ISVisp3	86.65	0
1620799	1622041	ISVisp3	86.65	0
1570825	1572067	ISVisp3	86.65	0
1562503	1563745	ISVisp3	86.65	0
2480679	2481921	ISVisp3	86.65	0
320476	321718	ISVisp3	86.65	0
2449071	2450305	ISVpe1	86.15	0
1564077	1565311	ISVpe1	86.15	0
1593553	1594787	ISVpe1	86.15	0
1620807	1622041	ISVpe1	86.15	0
1570833	1572067	ISVpe1	86.15	0
1562511	1563745	ISVpe1	86.15	0
2480679	2481913	ISVpe1	86.15	0
1204510	1205744	ISVpe1	86.15	0
1201475	1202709	ISVpe1	86.15	0
320484	321718	ISVpe1	86.15	0
2449071	2450305	ISVisp5	86.15	0
1564077	1565311	ISVisp5	86.15	0
1593553	1594787	ISVisp5	86.15	0
1620807	1622041	ISVisp5	86.15	0
1570833	1572067	ISVisp5	86.15	0
1562511	1563745	ISVisp5	86.15	0
2480679	2481913	ISVisp5	86.15	0
1204510	1205744	ISVisp5	86.15	0
1201475	1202709	ISVisp5	86.15	0
320484	321718	ISVisp5	86.15	0
2213215	2214124	ISVch6	88.13	0
2214243	2214308	ISVch6	89.39	5.00E-10
3699295	3700215	ISVpa3	83.82	0
3561150	3562070	ISVpa3	83.82	0
3554195	3555115	ISVpa3	83.82	0
3341684	3342604	ISVpa3	83.82	0
504831	505751	ISVpa3	83.82	0
549907	550827	ISVpa3	83.82	0
672757	673677	ISVpa3	83.82	0
679818	680738	ISVpa3	83.82	0
854240	855160	ISVpa3	83.82	0
865578	866498	ISVpa3	83.82	0
1234320	1235240	ISVpa3	83.82	0
2559098	2560018	ISVpa3	83.82	0
2464321	2465241	ISVpa3	83.82	0
1568950	1569870	ISVpa3	83.82	0
1605667	1606587	ISVpa3	83.82	0

1616624	1617544	ISVpa3	83.82	0
1990685	1991605	ISVpa3	83.82	0
2285071	2285991	ISVpa3	83.82	0
1522253	1523173	ISVpa3	83.82	0
2506143	2507063	ISVpa3	83.82	0
1243067	1243987	ISVpa3	83.82	0
1213090	1214010	ISVpa3	83.82	0
1202898	1203818	ISVpa3	83.82	0
2698968	2699888	ISVpa3	83.82	0
2933723	2934643	ISVpa3	83.82	0
3090731	3091651	ISVpa3	83.82	0
662302	663222	ISVpa3	83.82	0
567756	568676	ISVpa3	83.82	0
457987	458907	ISVpa3	83.82	0
3562836	3563271	ISVpa3	85.78	2.00E-99
1196672	1197275	ISVpa3	82.12	5.00E-90
1195090	1195397	ISVpa3	87.66	2.00E-80
3555216	3555608	ISVpa3	82.11	4.00E-57
3555767	3555996	ISVpa3	82.68	6.00E-25
3560618	3560773	ISVpa3	82.69	5.00E-16
3554027	3554132	ISVpa3	85.85	8.00E-15
3699297	3700215	ISVvu5	83.46	6.00E-173
3561152	3562070	ISVvu5	83.46	6.00E-173
3554197	3555115	ISVvu5	83.46	6.00E-173
3341686	3342604	ISVvu5	83.46	6.00E-173
504831	505749	ISVvu5	83.46	6.00E-173
549907	550825	ISVvu5	83.46	6.00E-173
672757	673675	ISVvu5	83.46	6.00E-173
679818	680736	ISVvu5	83.46	6.00E-173
854240	855158	ISVvu5	83.46	6.00E-173
865578	866496	ISVvu5	83.46	6.00E-173
1234320	1235238	ISVvu5	83.46	6.00E-173
2559100	2560018	ISVvu5	83.46	6.00E-173
2464323	2465241	ISVvu5	83.46	6.00E-173
1568950	1569868	ISVvu5	83.46	6.00E-173
1605667	1606585	ISVvu5	83.46	6.00E-173
1616624	1617542	ISVvu5	83.46	6.00E-173
1990685	1991603	ISVvu5	83.46	6.00E-173
2285071	2285989	ISVvu5	83.46	6.00E-173
1522255	1523173	ISVvu5	83.46	6.00E-173
2506143	2507061	ISVvu5	83.46	6.00E-173
1243069	1243987	ISVvu5	83.46	6.00E-173
1213092	1214010	ISVvu5	83.46	6.00E-173
1202900	1203818	ISVvu5	83.46	6.00E-173
2698968	2699886	ISVvu5	83.46	6.00E-173
2933723	2934641	ISVvu5	83.46	6.00E-173
3090731	3091649	ISVvu5	83.46	6.00E-173
662304	663222	ISVvu5	83.46	6.00E-173
567758	568676	ISVvu5	83.46	6.00E-173
457989	458907	ISVvu5	83.46	6.00E-173
1196664	1197275	ISVvu5	82.35	9.00E-95
3562836	3563271	ISVvu5	83.94	2.00E-80

1195092	1195397	ISVvu5	85.95	3.00E-67
3555216	3555608	ISVvu5	81.37	5.00E-50
3555767	3555996	ISVvu5	82.25	1.00E-22
3560618	3560791	ISVvu5	83.33	6.00E-22
3554023	3554129	ISVvu5	85.05	5.00E-13
3119603	3120135	ISVa19	86.87	6.00E-136
3699304	3699860	ISVbsp3	83.12	2.00E-95
3561159	3561715	ISVbsp3	83.12	2.00E-95
3554204	3554760	ISVbsp3	83.12	2.00E-95
3341693	3342249	ISVbsp3	83.12	2.00E-95
505186	505742	ISVbsp3	83.12	2.00E-95
550262	550818	ISVbsp3	83.12	2.00E-95
673112	673668	ISVbsp3	83.12	2.00E-95
680173	680729	ISVbsp3	83.12	2.00E-95
854595	855151	ISVbsp3	83.12	2.00E-95
865933	866489	ISVbsp3	83.12	2.00E-95
1234675	1235231	ISVbsp3	83.12	2.00E-95
2559107	2559663	ISVbsp3	83.12	2.00E-95
2464330	2464886	ISVbsp3	83.12	2.00E-95
1569305	1569861	ISVbsp3	83.12	2.00E-95
1606022	1606578	ISVbsp3	83.12	2.00E-95
1616979	1617535	ISVbsp3	83.12	2.00E-95
1991040	1991596	ISVbsp3	83.12	2.00E-95
2285426	2285982	ISVbsp3	83.12	2.00E-95
1522262	1522818	ISVbsp3	83.12	2.00E-95
2506498	2507054	ISVbsp3	83.12	2.00E-95
1243076	1243632	ISVbsp3	83.12	2.00E-95
1213099	1213655	ISVbsp3	83.12	2.00E-95
1202907	1203463	ISVbsp3	83.12	2.00E-95
2699323	2699879	ISVbsp3	83.12	2.00E-95
2934078	2934634	ISVbsp3	83.12	2.00E-95
3091086	3091642	ISVbsp3	83.12	2.00E-95
662311	662867	ISVbsp3	83.12	2.00E-95
567765	568321	ISVbsp3	83.12	2.00E-95
457996	458552	ISVbsp3	83.12	2.00E-95
3562836	3563266	ISVbsp3	81.67	6.00E-56
1195099	1195394	ISVbsp3	83.11	1.00E-44
1196672	1196920	ISVbsp3	84.34	8.00E-43
3555216	3555608	ISVbsp3	79.9	1.00E-35
679113	679248	ISVbsp3	84.67	1.00E-16
3127471	3127677	ISVbsp3	80.68	2.00E-15
3699998	3700199	ISVbsp3	80.88	2.00E-12
3561853	3562054	ISVbsp3	80.88	2.00E-12
3554898	3555099	ISVbsp3	80.88	2.00E-12
3342387	3342588	ISVbsp3	80.88	2.00E-12
504847	505048	ISVbsp3	80.88	2.00E-12
549923	550124	ISVbsp3	80.88	2.00E-12
672773	672974	ISVbsp3	80.88	2.00E-12
679834	680035	ISVbsp3	80.88	2.00E-12
854256	854457	ISVbsp3	80.88	2.00E-12
865594	865795	ISVbsp3	80.88	2.00E-12
1234336	1234537	ISVbsp3	80.88	2.00E-12

2559801	2560002	ISVbsp3	80.88	2.00E-12
2465024	2465225	ISVbsp3	80.88	2.00E-12
1568966	1569167	ISVbsp3	80.88	2.00E-12
1605683	1605884	ISVbsp3	80.88	2.00E-12
1616640	1616841	ISVbsp3	80.88	2.00E-12
1990701	1990902	ISVbsp3	80.88	2.00E-12
2285087	2285288	ISVbsp3	80.88	2.00E-12
1522956	1523157	ISVbsp3	80.88	2.00E-12
2506159	2506360	ISVbsp3	80.88	2.00E-12
1243770	1243971	ISVbsp3	80.88	2.00E-12
1213793	1213994	ISVbsp3	80.88	2.00E-12
1203601	1203802	ISVbsp3	80.88	2.00E-12
1197058	1197259	ISVbsp3	80.88	2.00E-12
2698984	2699185	ISVbsp3	80.88	2.00E-12
2933739	2933940	ISVbsp3	80.88	2.00E-12
3090747	3090948	ISVbsp3	80.88	2.00E-12
663005	663206	ISVbsp3	80.88	2.00E-12
568459	568660	ISVbsp3	80.88	2.00E-12
458690	458891	ISVbsp3	80.88	2.00E-12
3560655	3560773	ISVbsp3	81.51	8.00E-06
3554047	3554132	ISVbsp3	83.72	3.00E-05
3560550	3560964	ISV-M52	85.58	5.00E-90
3700110	3700216	ISV-M52	89.72	6.00E-25
3561965	3562071	ISV-M52	89.72	6.00E-25
3555010	3555116	ISV-M52	89.72	6.00E-25
3342499	3342605	ISV-M52	89.72	6.00E-25
504830	504936	ISV-M52	89.72	6.00E-25
549906	550012	ISV-M52	89.72	6.00E-25
672756	672862	ISV-M52	89.72	6.00E-25
679817	679923	ISV-M52	89.72	6.00E-25
854239	854345	ISV-M52	89.72	6.00E-25
865577	865683	ISV-M52	89.72	6.00E-25
1234319	1234425	ISV-M52	89.72	6.00E-25
2559913	2560019	ISV-M52	89.72	6.00E-25
2465136	2465242	ISV-M52	89.72	6.00E-25
1568949	1569055	ISV-M52	89.72	6.00E-25
1605666	1605772	ISV-M52	89.72	6.00E-25
1616623	1616729	ISV-M52	89.72	6.00E-25
1990684	1990790	ISV-M52	89.72	6.00E-25
2285070	2285176	ISV-M52	89.72	6.00E-25
1523068	1523174	ISV-M52	89.72	6.00E-25
2506142	2506248	ISV-M52	89.72	6.00E-25
1243882	1243988	ISV-M52	89.72	6.00E-25
1213905	1214011	ISV-M52	89.72	6.00E-25
1203713	1203819	ISV-M52	89.72	6.00E-25
1197170	1197276	ISV-M52	89.72	6.00E-25
2698967	2699073	ISV-M52	89.72	6.00E-25
2933722	2933828	ISV-M52	89.72	6.00E-25
3090730	3090836	ISV-M52	89.72	6.00E-25
663117	663223	ISV-M52	89.72	6.00E-25
568571	568677	ISV-M52	89.72	6.00E-25
458802	458908	ISV-M52	89.72	6.00E-25

3699304	3699509	ISV-M52	82.04	1.00E-19
3561159	3561364	ISV-M52	82.04	1.00E-19
3554204	3554409	ISV-M52	82.04	1.00E-19
3341693	3341898	ISV-M52	82.04	1.00E-19
505537	505742	ISV-M52	82.04	1.00E-19
550613	550818	ISV-M52	82.04	1.00E-19
673463	673668	ISV-M52	82.04	1.00E-19
680524	680729	ISV-M52	82.04	1.00E-19
854946	855151	ISV-M52	82.04	1.00E-19
866284	866489	ISV-M52	82.04	1.00E-19
1235026	1235231	ISV-M52	82.04	1.00E-19
2559107	2559312	ISV-M52	82.04	1.00E-19
2464330	2464535	ISV-M52	82.04	1.00E-19
1569656	1569861	ISV-M52	82.04	1.00E-19
1606373	1606578	ISV-M52	82.04	1.00E-19
1617330	1617535	ISV-M52	82.04	1.00E-19
1991391	1991596	ISV-M52	82.04	1.00E-19
2285777	2285982	ISV-M52	82.04	1.00E-19
1522262	1522467	ISV-M52	82.04	1.00E-19
2506849	2507054	ISV-M52	82.04	1.00E-19
1243076	1243281	ISV-M52	82.04	1.00E-19
1213099	1213304	ISV-M52	82.04	1.00E-19
1202907	1203112	ISV-M52	82.04	1.00E-19
1195099	1195304	ISV-M52	82.04	1.00E-19
2699674	2699879	ISV-M52	82.04	1.00E-19
2934429	2934634	ISV-M52	82.04	1.00E-19
3091437	3091642	ISV-M52	82.04	1.00E-19
662311	662516	ISV-M52	82.04	1.00E-19
567765	567970	ISV-M52	82.04	1.00E-19
457996	458201	ISV-M52	82.04	1.00E-19
3555871	3556001	ISV-M52	83.97	2.00E-15
1196676	1196953	ISV-M52	78.78	2.00E-12
3562881	3562966	ISV-M52	86.05	5.00E-10
3563061	3563266	ISV-M52	80.1	5.00E-10
3560550	3560964	ISVch8	84.86	8.00E-83
3699304	3700283	ISVch8	78.08	2.00E-55
3561159	3562138	ISVch8	78.08	2.00E-55
3554204	3555183	ISVch8	78.08	2.00E-55
3341693	3342672	ISVch8	78.08	2.00E-55
504763	505742	ISVch8	78.08	2.00E-55
549839	550818	ISVch8	78.08	2.00E-55
672689	673668	ISVch8	78.08	2.00E-55
679750	680729	ISVch8	78.08	2.00E-55
854172	855151	ISVch8	78.08	2.00E-55
865510	866489	ISVch8	78.08	2.00E-55
1234252	1235231	ISVch8	78.08	2.00E-55
2559107	2560086	ISVch8	78.08	2.00E-55
2464330	2465309	ISVch8	78.08	2.00E-55
1568882	1569861	ISVch8	78.08	2.00E-55
1605599	1606578	ISVch8	78.08	2.00E-55
1616556	1617535	ISVch8	78.08	2.00E-55
1990617	1991596	ISVch8	78.08	2.00E-55

2285003	2285982	ISVch8	78.08	2.00E-55
1522262	1523241	ISVch8	78.08	2.00E-55
2506075	2507054	ISVch8	78.08	2.00E-55
1243076	1244055	ISVch8	78.08	2.00E-55
1213099	1214078	ISVch8	78.08	2.00E-55
1202907	1203886	ISVch8	78.08	2.00E-55
2698900	2699879	ISVch8	78.08	2.00E-55
2933655	2934634	ISVch8	78.08	2.00E-55
3090663	3091642	ISVch8	78.08	2.00E-55
662311	663290	ISVch8	78.08	2.00E-55
567765	568744	ISVch8	78.08	2.00E-55
457996	458975	ISVch8	78.08	2.00E-55
1196664	1197343	ISVch8	78.12	7.00E-34
3562848	3563266	ISVch8	79	2.00E-27
1195099	1195369	ISVch8	80.07	4.00E-20
3555896	3556059	ISVch8	84.34	2.00E-15
3562466	3562794	ISVvu1	84.8	2.00E-64
3553897	3553958	ISVvu1	91.94	2.00E-12
2213946	2214308	ISVa15	83.47	1.00E-60
3538196	3538363	ISVa15	81.66	8.00E-12
2213375	2213425	ISVa15	90.2	8.00E-06
670726	671418	ISVfl1	78.98	2.00E-55
670437	670608	ISVfl1	83.24	6.00E-19
1626236	1626471	ISShwo3	85.59	5.00E-47
3550905	3551112	ISVa1	87.5	5.00E-47
3551296	3551492	ISVa1	86.8	8.00E-43
3551668	3551818	ISVa1	84.87	9.00E-21
1626238	1626471	ISPtu2	86.02	1.00E-44
1626236	1626471	ISSpi5	85.23	8.00E-43
1625353	1625442	ISSpi5	84.44	1.00E-07
3699805	3700208	ISVba2	79.95	4.00E-35
3561660	3562063	ISVba2	79.95	4.00E-35
3554705	3555108	ISVba2	79.95	4.00E-35
3342194	3342597	ISVba2	79.95	4.00E-35
504838	505241	ISVba2	79.95	4.00E-35
549914	550317	ISVba2	79.95	4.00E-35
672764	673167	ISVba2	79.95	4.00E-35
679825	680228	ISVba2	79.95	4.00E-35
854247	854650	ISVba2	79.95	4.00E-35
865585	865988	ISVba2	79.95	4.00E-35
1234327	1234730	ISVba2	79.95	4.00E-35
2559608	2560011	ISVba2	79.95	4.00E-35
2464831	2465234	ISVba2	79.95	4.00E-35
1568957	1569360	ISVba2	79.95	4.00E-35
1605674	1606077	ISVba2	79.95	4.00E-35
1616631	1617034	ISVba2	79.95	4.00E-35
1990692	1991095	ISVba2	79.95	4.00E-35
2285078	2285481	ISVba2	79.95	4.00E-35
1522763	1523166	ISVba2	79.95	4.00E-35
2506150	2506553	ISVba2	79.95	4.00E-35
1243577	1243980	ISVba2	79.95	4.00E-35
1213600	1214003	ISVba2	79.95	4.00E-35

1203408	1203811	ISVba2	79.95	4.00E-35
1196865	1197268	ISVba2	79.95	4.00E-35
2698975	2699378	ISVba2	79.95	4.00E-35
2933730	2934133	ISVba2	79.95	4.00E-35
3090738	3091141	ISVba2	79.95	4.00E-35
662812	663215	ISVba2	79.95	4.00E-35
568266	568669	ISVba2	79.95	4.00E-35
458497	458900	ISVba2	79.95	4.00E-35
3560608	3560859	ISVba2	81.35	2.00E-25
3555896	3556052	ISVba2	86.08	2.00E-24
1626189	1626468	IS492	83.39	4.00E-35
1625353	1625532	IS492	81.67	5.00E-16
678825	679026	ISShes15	84.24	2.00E-27
693859	693964	ISShfr4	89.72	1.00E-22
678089	678233	ISSod13	84.83	2.00E-21
678801	678934	ISSod13	84.33	3.00E-17
677831	677868	ISSod13	94.74	3.00E-05
693860	694041	ISSpe3	84.24	9.00E-21
3700099	3700202	ISSpu11	87.5	2.00E-18
3561954	3562057	ISSpu11	87.5	2.00E-18
3554999	3555102	ISSpu11	87.5	2.00E-18
3342488	3342591	ISSpu11	87.5	2.00E-18
504844	504947	ISSpu11	87.5	2.00E-18
549920	550023	ISSpu11	87.5	2.00E-18
672770	672873	ISSpu11	87.5	2.00E-18
679831	679934	ISSpu11	87.5	2.00E-18
854253	854356	ISSpu11	87.5	2.00E-18
865591	865694	ISSpu11	87.5	2.00E-18
1234333	1234436	ISSpu11	87.5	2.00E-18
2559902	2560005	ISSpu11	87.5	2.00E-18
2465125	2465228	ISSpu11	87.5	2.00E-18
1568963	1569066	ISSpu11	87.5	2.00E-18
1605680	1605783	ISSpu11	87.5	2.00E-18
1616637	1616740	ISSpu11	87.5	2.00E-18
1990698	1990801	ISSpu11	87.5	2.00E-18
2285084	2285187	ISSpu11	87.5	2.00E-18
1523057	1523160	ISSpu11	87.5	2.00E-18
2506156	2506259	ISSpu11	87.5	2.00E-18
1243871	1243974	ISSpu11	87.5	2.00E-18
1213894	1213997	ISSpu11	87.5	2.00E-18
1203702	1203805	ISSpu11	87.5	2.00E-18
1197159	1197262	ISSpu11	87.5	2.00E-18
2698981	2699084	ISSpu11	87.5	2.00E-18
2933736	2933839	ISSpu11	87.5	2.00E-18
3090744	3090847	ISSpu11	87.5	2.00E-18
663106	663209	ISSpu11	87.5	2.00E-18
568560	568663	ISSpu11	87.5	2.00E-18
458791	458894	ISSpu11	87.5	2.00E-18
3699996	3700062	ISSpu11	89.55	1.00E-10
3561851	3561917	ISSpu11	89.55	1.00E-10
3554896	3554962	ISSpu11	89.55	1.00E-10
3342385	3342451	ISSpu11	89.55	1.00E-10

504984	505050	ISSpu11	89.55	1.00E-10
550060	550126	ISSpu11	89.55	1.00E-10
672910	672976	ISSpu11	89.55	1.00E-10
679971	680037	ISSpu11	89.55	1.00E-10
854393	854459	ISSpu11	89.55	1.00E-10
865731	865797	ISSpu11	89.55	1.00E-10
1234473	1234539	ISSpu11	89.55	1.00E-10
2559799	2559865	ISSpu11	89.55	1.00E-10
2465022	2465088	ISSpu11	89.55	1.00E-10
1569103	1569169	ISSpu11	89.55	1.00E-10
1605820	1605886	ISSpu11	89.55	1.00E-10
1616777	1616843	ISSpu11	89.55	1.00E-10
1990838	1990904	ISSpu11	89.55	1.00E-10
2285224	2285290	ISSpu11	89.55	1.00E-10
1522954	1523020	ISSpu11	89.55	1.00E-10
2506296	2506362	ISSpu11	89.55	1.00E-10
1243768	1243834	ISSpu11	89.55	1.00E-10
1213791	1213857	ISSpu11	89.55	1.00E-10
1203599	1203665	ISSpu11	89.55	1.00E-10
1197056	1197122	ISSpu11	89.55	1.00E-10
2699121	2699187	ISSpu11	89.55	1.00E-10
2933876	2933942	ISSpu11	89.55	1.00E-10
3090884	3090950	ISSpu11	89.55	1.00E-10
663003	663069	ISSpu11	89.55	1.00E-10
568457	568523	ISSpu11	89.55	1.00E-10
458688	458754	ISSpu11	89.55	1.00E-10
3555883	3555987	ISSpu11	83.81	2.00E-09
3699304	3699572	ISSpu11	78.44	2.00E-09
3561159	3561427	ISSpu11	78.44	2.00E-09
3554204	3554472	ISSpu11	78.44	2.00E-09
3341693	3341961	ISSpu11	78.44	2.00E-09
505474	505742	ISSpu11	78.44	2.00E-09
550550	550818	ISSpu11	78.44	2.00E-09
673400	673668	ISSpu11	78.44	2.00E-09
680461	680729	ISSpu11	78.44	2.00E-09
854883	855151	ISSpu11	78.44	2.00E-09
866221	866489	ISSpu11	78.44	2.00E-09
1234963	1235231	ISSpu11	78.44	2.00E-09
2559107	2559375	ISSpu11	78.44	2.00E-09
2464330	2464598	ISSpu11	78.44	2.00E-09
1569593	1569861	ISSpu11	78.44	2.00E-09
1606310	1606578	ISSpu11	78.44	2.00E-09
1617267	1617535	ISSpu11	78.44	2.00E-09
1991328	1991596	ISSpu11	78.44	2.00E-09
2285714	2285982	ISSpu11	78.44	2.00E-09
1522262	1522530	ISSpu11	78.44	2.00E-09
2506786	2507054	ISSpu11	78.44	2.00E-09
1243076	1243344	ISSpu11	78.44	2.00E-09
1213099	1213367	ISSpu11	78.44	2.00E-09
1202907	1203175	ISSpu11	78.44	2.00E-09
1195099	1195367	ISSpu11	78.44	2.00E-09
2699611	2699879	ISSpu11	78.44	2.00E-09

2934366	2934634	ISSpu11	78.44	2.00E-09
3091374	3091642	ISSpu11	78.44	2.00E-09
662311	662579	ISSpu11	78.44	2.00E-09
567765	568033	ISSpu11	78.44	2.00E-09
457996	458264	ISSpu11	78.44	2.00E-09
3699745	3699836	ISSpu11	84.78	8.00E-09
3561600	3561691	ISSpu11	84.78	8.00E-09
3554645	3554736	ISSpu11	84.78	8.00E-09
3342134	3342225	ISSpu11	84.78	8.00E-09
505210	505301	ISSpu11	84.78	8.00E-09
550286	550377	ISSpu11	84.78	8.00E-09
673136	673227	ISSpu11	84.78	8.00E-09
680197	680288	ISSpu11	84.78	8.00E-09
854619	854710	ISSpu11	84.78	8.00E-09
865957	866048	ISSpu11	84.78	8.00E-09
1234699	1234790	ISSpu11	84.78	8.00E-09
2559548	2559639	ISSpu11	84.78	8.00E-09
2464771	2464862	ISSpu11	84.78	8.00E-09
1569329	1569420	ISSpu11	84.78	8.00E-09
1606046	1606137	ISSpu11	84.78	8.00E-09
1617003	1617094	ISSpu11	84.78	8.00E-09
1991064	1991155	ISSpu11	84.78	8.00E-09
2285450	2285541	ISSpu11	84.78	8.00E-09
1522703	1522794	ISSpu11	84.78	8.00E-09
2506522	2506613	ISSpu11	84.78	8.00E-09
1243517	1243608	ISSpu11	84.78	8.00E-09
1213540	1213631	ISSpu11	84.78	8.00E-09
1203348	1203439	ISSpu11	84.78	8.00E-09
1196805	1196896	ISSpu11	84.78	8.00E-09
2699347	2699438	ISSpu11	84.78	8.00E-09
2934102	2934193	ISSpu11	84.78	8.00E-09
3091110	3091201	ISSpu11	84.78	8.00E-09
662752	662843	ISSpu11	84.78	8.00E-09
568206	568297	ISSpu11	84.78	8.00E-09
458437	458528	ISSpu11	84.78	8.00E-09
3555767	3555836	ISSpu11	87.14	1.00E-07
529035	529112	ISEc52	91.03	3.00E-17
1601998	1602075	ISEc52	91.03	3.00E-17
1553751	1553828	ISEc52	91.03	3.00E-17
1196264	1196341	ISEc52	91.03	3.00E-17
529050	529119	ISSlo2	92.86	3.00E-17
1601991	1602060	ISSlo2	92.86	3.00E-17
1553744	1553813	ISSlo2	92.86	3.00E-17
1196257	1196326	ISSlo2	92.86	3.00E-17
1625352	1625696	ISSde13	79.19	3.00E-17
1625845	1626054	ISSde13	79.05	1.00E-07
677831	678027	ISSde2	81.73	3.00E-17
678860	678938	ISSde2	89.87	2.00E-15
3133129	3133186	ISVvu4	96.55	3.00E-17
678075	678165	ISVvu4	86.81	5.00E-13
678885	678937	ISVvu4	92.45	2.00E-09
529048	529112	IS911	93.85	1.00E-16

	1601998	1602062	IS911	93.85	1.00E-16
	1553751	1553815	IS911	93.85	1.00E-16
	1196264	1196328	IS911	93.85	1.00E-16
	678077	678204	ISErsp1	84.38	5.00E-16
	678872	678934	ISErsp1	87.3	8.00E-06
	678801	678934	ISSma11	83.58	8.00E-15
	678044	678216	ISSma11	80.35	2.00E-09
	529014	529119	ISCfr25	85.85	8.00E-15
	1601991	1602096	ISCfr25	85.85	8.00E-15
	1553744	1553849	ISCfr25	85.85	8.00E-15
	1196257	1196362	ISCfr25	85.85	8.00E-15
	529436	529494	ISCfr25	89.83	3.00E-08
	1601616	1601674	ISCfr25	89.83	3.00E-08
	1553369	1553427	ISCfr25	89.83	3.00E-08
	1195882	1195940	ISCfr25	89.83	3.00E-08
	528713	528746	ISCfr25	97.06	3.00E-05
	1602364	1602397	ISCfr25	97.06	3.00E-05
	1554117	1554150	ISCfr25	97.06	3.00E-05
	1196630	1196663	ISCfr25	97.06	3.00E-05
	529047	529112	ISLad1	92.42	8.00E-15
	1601998	1602063	ISLad1	92.42	8.00E-15
	1553751	1553816	ISLad1	92.42	8.00E-15
	1196264	1196329	ISLad1	92.42	8.00E-15
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	679846	679922	ISSpu20	89.61	3.00E-14
	854268	854344	ISSpu20	89.61	3.00E-14
	865606	865682	ISSpu20	89.61	3.00E-14
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	2559914	2559990	ISSpu20	89.61	3.00E-14
	2465137	2465213	ISSpu20	89.61	3.00E-14
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	1605695	1605771	ISSpu20	89.61	3.00E-14
	1616652	1616728	ISSpu20	89.61	3.00E-14
	1990713	1990789	ISSpu20	89.61	3.00E-14
	2285099	2285175	ISSpu20	89.61	3.00E-14
	1523069	1523145	ISSpu20	89.61	3.00E-14
	2506171	2506247	ISSpu20	89.61	3.00E-14
	1243883	1243959	ISSpu20	89.61	3.00E-14
	1213906	1213982	ISSpu20	89.61	3.00E-14
	1203714	1203790	ISSpu20	89.61	3.00E-14
	1197171	1197247	ISSpu20	89.61	3.00E-14
	2698996	2699072	ISSpu20	89.61	3.00E-14
	2933751	2933827	ISSpu20	89.61	3.00E-14
	3090759	3090835	ISSpu20	89.61	3.00E-14
	663118	663194	ISSpu20	89.61	3.00E-14
	568572	568648	ISSpu20	89.61	3.00E-14

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394447	395365	ISVvu5	83.46	4.00E-173
1705430	1706348	ISVvu5	83.46	4.00E-173
1689547	1690465	ISVvu5	83.46	4.00E-173
1007497	1008415	ISVvu5	83.46	4.00E-173
1436627	1437545	ISVvu5	83.46	4.00E-173
787321	788239	ISVvu5	83.46	4.00E-173
774158	775076	ISVvu5	83.46	4.00E-173
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1646374	1647292	ISVvu5	83.46	4.00E-173
1665163	1666081	ISVvu5	83.46	4.00E-173
1798712	1799630	ISVvu5	83.46	4.00E-173
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774165	774721	ISVbsp3	83.12	1.00E-95
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1436559	1437538	ISVch8	78.08	1.00E-55

787328	788307	ISVch8	78.08	1.00E-55
774165	775144	ISVch8	78.08	1.00E-55
1591966	1592945	ISVch8	78.08	1.00E-55
1646306	1647285	ISVch8	78.08	1.00E-55
1665095	1666074	ISVch8	78.08	1.00E-55
1798644	1799623	ISVch8	78.08	1.00E-55
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1690055	1690458	ISVba2	79.95	3.00E-35
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787829	788232	ISVba2	79.95	3.00E-35
774666	775069	ISVba2	79.95	3.00E-35
1592041	1592444	ISVba2	79.95	3.00E-35
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1665170	1665573	ISVba2	79.95	3.00E-35
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1706243	1706349	ISV-M52	89.72	4.00E-25
1690360	1690466	ISV-M52	89.72	4.00E-25
1008310	1008416	ISV-M52	89.72	4.00E-25
1436626	1436732	ISV-M52	89.72	4.00E-25
788134	788240	ISV-M52	89.72	4.00E-25
774971	775077	ISV-M52	89.72	4.00E-25
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1646373	1646479	ISV-M52	89.72	4.00E-25
1665162	1665268	ISV-M52	89.72	4.00E-25
1798711	1798817	ISV-M52	89.72	4.00E-25
2125150	2125256	ISV-M52	89.72	4.00E-25
2215002	2215207	ISV-M52	82.04	8.00E-20
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1705437	1705642	ISV-M52	82.04	8.00E-20
1689554	1689759	ISV-M52	82.04	8.00E-20
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787328	787533	ISV-M52	82.04	8.00E-20
774165	774370	ISV-M52	82.04	8.00E-20
1592740	1592945	ISV-M52	82.04	8.00E-20
1647080	1647285	ISV-M52	82.04	8.00E-20
1665869	1666074	ISV-M52	82.04	8.00E-20
1799418	1799623	ISV-M52	82.04	8.00E-20
2125857	2126062	ISV-M52	82.04	8.00E-20
476487	476553	ISV-M52	89.55	8.00E-11
476416	476484	ISV-M52	87.14	2.00E-05

2215797	2215900	ISSpu11	87.5	1.00E-18
181994	182097	ISSpu11	87.5	1.00E-18
394460	394563	ISSpu11	87.5	1.00E-18
1706232	1706335	ISSpu11	87.5	1.00E-18
1690349	1690452	ISSpu11	87.5	1.00E-18
1008299	1008402	ISSpu11	87.5	1.00E-18
1436640	1436743	ISSpu11	87.5	1.00E-18
788123	788226	ISSpu11	87.5	1.00E-18
774960	775063	ISSpu11	87.5	1.00E-18
1592047	1592150	ISSpu11	87.5	1.00E-18
1646387	1646490	ISSpu11	87.5	1.00E-18
1665176	1665279	ISSpu11	87.5	1.00E-18
1798725	1798828	ISSpu11	87.5	1.00E-18
2125164	2125267	ISSpu11	87.5	1.00E-18
2215694	2215760	ISSpu11	89.55	8.00E-11
182134	182200	ISSpu11	89.55	8.00E-11
394600	394666	ISSpu11	89.55	8.00E-11
1706129	1706195	ISSpu11	89.55	8.00E-11
1690246	1690312	ISSpu11	89.55	8.00E-11
1008196	1008262	ISSpu11	89.55	8.00E-11
1436780	1436846	ISSpu11	89.55	8.00E-11
788020	788086	ISSpu11	89.55	8.00E-11
774857	774923	ISSpu11	89.55	8.00E-11
1592187	1592253	ISSpu11	89.55	8.00E-11
1646527	1646593	ISSpu11	89.55	8.00E-11
1665316	1665382	ISSpu11	89.55	8.00E-11
1798865	1798931	ISSpu11	89.55	8.00E-11
2125304	2125370	ISSpu11	89.55	8.00E-11
2215002	2215270	ISSpu11	78.44	1.00E-09
182624	182892	ISSpu11	78.44	1.00E-09
395090	395358	ISSpu11	78.44	1.00E-09
1705437	1705705	ISSpu11	78.44	1.00E-09
1689554	1689822	ISSpu11	78.44	1.00E-09
1007504	1007772	ISSpu11	78.44	1.00E-09
1437270	1437538	ISSpu11	78.44	1.00E-09
787328	787596	ISSpu11	78.44	1.00E-09
774165	774433	ISSpu11	78.44	1.00E-09
1592677	1592945	ISSpu11	78.44	1.00E-09
1647017	1647285	ISSpu11	78.44	1.00E-09
1665806	1666074	ISSpu11	78.44	1.00E-09
1799355	1799623	ISSpu11	78.44	1.00E-09
2125794	2126062	ISSpu11	78.44	1.00E-09
2215443	2215534	ISSpu11	84.78	5.00E-09
182360	182451	ISSpu11	84.78	5.00E-09
394826	394917	ISSpu11	84.78	5.00E-09
1705878	1705969	ISSpu11	84.78	5.00E-09
1689995	1690086	ISSpu11	84.78	5.00E-09
1007945	1008036	ISSpu11	84.78	5.00E-09
1437006	1437097	ISSpu11	84.78	5.00E-09
787769	787860	ISSpu11	84.78	5.00E-09
774606	774697	ISSpu11	84.78	5.00E-09
1592413	1592504	ISSpu11	84.78	5.00E-09

1646753	1646844	ISSpu11	84.78	5.00E-09
1665542	1665633	ISSpu11	84.78	5.00E-09
1799091	1799182	ISSpu11	84.78	5.00E-09
2125530	2125621	ISSpu11	84.78	5.00E-09
724794	724871	ISEc52	91.03	2.00E-17
724809	724878	ISSlo2	92.86	2.00E-17
724807	724871	IS911	93.85	8.00E-17
724773	724878	ISCfr25	85.85	5.00E-15
725195	725253	ISCfr25	89.83	2.00E-08
724472	724505	ISCfr25	97.06	2.00E-05
724806	724871	ISLad1	92.42	5.00E-15
2215809	2215885	ISSpu20	89.61	2.00E-14
182009	182085	ISSpu20	89.61	2.00E-14
394475	394551	ISSpu20	89.61	2.00E-14
1706244	1706320	ISSpu20	89.61	2.00E-14
1690361	1690437	ISSpu20	89.61	2.00E-14
1008311	1008387	ISSpu20	89.61	2.00E-14
1436655	1436731	ISSpu20	89.61	2.00E-14
788135	788211	ISSpu20	89.61	2.00E-14
774972	775048	ISSpu20	89.61	2.00E-14
1592062	1592138	ISSpu20	89.61	2.00E-14
1646402	1646478	ISSpu20	89.61	2.00E-14
1665191	1665267	ISSpu20	89.61	2.00E-14
1798740	1798816	ISSpu20	89.61	2.00E-14
2125179	2125255	ISSpu20	89.61	2.00E-14
724800	724872	ISSpu4	90.41	2.00E-14
724794	724871	ISBrsa1	88.46	1.00E-12
724800	724878	ISVch4	87.34	8.00E-11
2215815	2215897	ISSod12	86.75	8.00E-11
181997	182079	ISSod12	86.75	8.00E-11
394463	394545	ISSod12	86.75	8.00E-11
1706250	1706332	ISSod12	86.75	8.00E-11
1690367	1690449	ISSod12	86.75	8.00E-11
1008317	1008399	ISSod12	86.75	8.00E-11
1436643	1436725	ISSod12	86.75	8.00E-11
788141	788223	ISSod12	86.75	8.00E-11
774978	775060	ISSod12	86.75	8.00E-11
1592050	1592132	ISSod12	86.75	8.00E-11
1646390	1646472	ISSod12	86.75	8.00E-11
1665179	1665261	ISSod12	86.75	8.00E-11
1798728	1798810	ISSod12	86.75	8.00E-11
2125167	2125249	ISSod12	86.75	8.00E-11
2215458	2215534	ISSod12	85.71	3.00E-07
182360	182436	ISSod12	85.71	3.00E-07
394826	394902	ISSod12	85.71	3.00E-07
1705893	1705969	ISSod12	85.71	3.00E-07
1690010	1690086	ISSod12	85.71	3.00E-07
1007960	1008036	ISSod12	85.71	3.00E-07
1437006	1437082	ISSod12	85.71	3.00E-07
787784	787860	ISSod12	85.71	3.00E-07
774621	774697	ISSod12	85.71	3.00E-07
1592413	1592489	ISSod12	85.71	3.00E-07

1646753	1646829	ISSod12	85.71	3.00E-07
1665542	1665618	ISSod12	85.71	3.00E-07
1799091	1799167	ISSod12	85.71	3.00E-07
2125530	2125606	ISSod12	85.71	3.00E-07
2215002	2215240	ISSod12	78.24	4.00E-06
182654	182892	ISSod12	78.24	4.00E-06
395120	395358	ISSod12	78.24	4.00E-06
1705437	1705675	ISSod12	78.24	4.00E-06
1689554	1689792	ISSod12	78.24	4.00E-06
1007504	1007742	ISSod12	78.24	4.00E-06
1437300	1437538	ISSod12	78.24	4.00E-06
787328	787566	ISSod12	78.24	4.00E-06
774165	774403	ISSod12	78.24	4.00E-06
1592707	1592945	ISSod12	78.24	4.00E-06
1647047	1647285	ISSod12	78.24	4.00E-06
1665836	1666074	ISSod12	78.24	4.00E-06
1799385	1799623	ISSod12	78.24	4.00E-06
2125824	2126062	ISSod12	78.24	4.00E-06
724794	724871	ISPrre1	87.18	3.00E-10
724806	724878	ISVsa11	87.67	1.00E-09
724803	724840	ISSba5	97.37	7.00E-08
725642	725682	ISSba5	92.68	7.00E-05
725701	725733	ISSba5	96.97	7.00E-05
479862	479905	ISVa15	93.18	1.00E-06
724807	724858	ISEc31	90.38	1.00E-06
725701	725733	ISEc31	96.97	7.00E-05
724807	724878	ISAlg	86.11	1.00E-06
724800	724834	ISPa107	97.14	4.00E-06
724800	724834	ISPa98	97.14	4.00E-06
724806	724840	ISShfr6	97.14	4.00E-06
725642	725682	ISShfr6	92.68	7.00E-05
2215509	2215553	ISEc28	91.11	7.00E-05
182341	182385	ISEc28	91.11	7.00E-05
394807	394851	ISEc28	91.11	7.00E-05
1705944	1705988	ISEc28	91.11	7.00E-05
1690061	1690105	ISEc28	91.11	7.00E-05
1008011	1008055	ISEc28	91.11	7.00E-05
1436987	1437031	ISEc28	91.11	7.00E-05
787835	787879	ISEc28	91.11	7.00E-05
774672	774716	ISEc28	91.11	7.00E-05
1592394	1592438	ISEc28	91.11	7.00E-05
1646734	1646778	ISEc28	91.11	7.00E-05
1665523	1665567	ISEc28	91.11	7.00E-05
1799072	1799116	ISEc28	91.11	7.00E-05
2125511	2125555	ISEc28	91.11	7.00E-05
89544	90783	ISVal2	92.92	0
74387	75620	ISVal2	92.44	0
73395	74389	ISVal2	91.71	0
89544	90783	ISVpa2	87.77	0
74387	75620	ISVpa2	87.21	0
73395	74389	ISVpa2	85.51	0
89544	90783	ISVisp3	86.16	0

74387	75620	ISVisp3	85.84	0
73394	74389	ISVisp3	84.43	0
89544	90775	ISVpe1	85.67	0
74387	75612	ISVpe1	85.43	0
73395	74389	ISVpe1	83.42	0
89544	90775	ISVisp5	85.67	0
74387	75612	ISVisp5	85.43	0
73395	74389	ISVisp5	83.42	0
5434	5659	ISVa19	92.04	8.00E-81
75369	75408	ISAbe16	95	5.00E-08
90532	90571	ISAbe16	95	5.00E-08
75501	75561	ISSpu1	86.89	3.00E-06
90664	90724	ISSpu1	86.89	3.00E-06
74154	74192	ISShes1	92.31	5.00E-05
75143	75181	ISShes1	92.31	5.00E-05
90306	90344	ISShes1	92.31	5.00E-05
75369	75407	ISPto4	92.31	5.00E-05
90532	90570	ISPto4	92.31	5.00E-05
3604	4153	ISVal1	92.73	0
3228	3607	ISVal1	87.11	7.00E-99
61766	61917	ISVal1	86.93	7.00E-28
3604	4153	ISVa2	92.73	0
3245	3605	ISVa2	89.75	4.00E-116
61765	61917	ISVa2	91.5	2.00E-49
3241	3590	ISVpa3	88	1.00E-97
3641	4085	ISVpa3	82.7	8.00E-71
61772	61842	ISVpa3	85.92	1.00E-07
3243	3590	ISVvu5	86.78	6.00E-87
3641	4085	ISVvu5	83.37	6.00E-78
61772	61842	ISVvu5	84.51	4.00E-05
3250	3587	ISVbsp3	83.14	1.00E-54
3641	3730	ISVbsp3	92.22	5.00E-26
3868	4069	ISVbsp3	80.88	4.00E-14
3675	4078	ISVba2	79.95	8.00E-37
61805	61835	ISVba2	96.77	4.00E-05
3250	3599	ISVch8	80	8.00E-31
3980	4153	ISVch8	83.43	4.00E-20
61766	61917	ISVch8	83.66	2.00E-16
3639	3760	ISVch8	81.15	6.00E-07
62180	62351	ISVsa9	84.3	3.00E-27
3980	4086	ISV-M52	89.72	1.00E-26
3250	3455	ISV-M52	82.04	3.00E-21
3562	3607	ISV-M52	93.48	2.00E-09
3969	4072	ISSpu11	87.5	4.00E-20
3866	3932	ISSpu11	89.55	2.00E-12
3250	3518	ISSpu11	78.44	4.00E-11
3615	3706	ISSpu11	84.78	1.00E-10
3981	4057	ISSpu20	89.61	6.00E-16
2973	3031	ISVha3	93.22	2.00E-12
3987	4069	ISSod12	86.75	2.00E-12
3630	3706	ISSod12	85.71	9.00E-09
3250	3488	ISSod12	78.24	1.00E-07

3681	3725	ISEc28	91.11	2.00E-06
3681	3723	ISPrre2	90.7	4.00E-05
24164	24316	ISVa2	91.5	2.00E-49
29181	29416	ISShwo3	85.59	8.00E-49
28298	28477	ISShwo3	80.56	5.00E-13
29183	29416	ISPtu2	86.02	2.00E-46
29181	29416	ISSpi5	85.23	1.00E-44
28298	28387	ISSpi5	84.44	2.00E-09
29134	29413	IS492	83.39	7.00E-37
28298	28477	IS492	81.67	9.00E-18
28555	28646	IS492	82.61	8.00E-06
24165	24316	ISVal1	86.93	6.00E-28
28297	28641	ISSde13	79.19	6.00E-19
28790	28999	ISSde13	79.05	2.00E-09
24165	24316	ISVch8	83.66	1.00E-16
29224	29348	ISCps7	83.2	3.00E-11
24171	24241	ISVpa3	85.92	1.00E-07
24204	24234	ISVba2	96.77	3.00E-05
24171	24241	ISVvu5	84.51	3.00E-05
56553	57634	ISVa3	80.99	4.00E-146
52106	52921	ISVa3	80.07	5.00E-90
56082	56153	ISVa3	87.5	1.00E-10
59311	59499	ISVa2	91.53	1.00E-63
59332	59499	ISVal1	88.76	7.00E-40
53748	53993	ISVvu1	81.45	1.00E-25
59312	59499	ISVch8	82.54	5.00E-19
59332	59428	ISV-M52	87.63	2.00E-18
59332	59425	ISVba2	87.23	1.00E-16
59334	59407	ISSpu11	90.54	1.00E-16
59334	59407	ISSod12	90.54	1.00E-16
59324	59404	ISSpu20	88.89	5.00E-16
59332	59428	ISVpa3	86.6	5.00E-16
59332	59428	ISVvu5	85.57	1.00E-13
55540	55586	ISVha3	91.49	3.00E-05

Table S9. Prophage regions and associated genes in *V. harveyi* strain N8T11

Region	Start Position	End Position	Orientation	Predicted Function
Chromosome 1 region 1	1981357	1982742	-	Phage-like protein
	1982747	1983091	-	Hypothetical protein
	1983093	1984583	-	Phage-like protein
	1984752	1984994	-	Phage-like protein
	1985000	1985227	-	Phage-like protein
	1985231	1985587	-	Hypothetical protein
	1985591	1986736	-	Phage-like protein
	1986720	1986935	-	Hypothetical protein
	1986938	1987210	-	Hypothetical protein
	1987466	1987834	+	Hypothetical protein
	1988003	1989733	-	Hypothetical protein
	1989723	1990574	-	Hypothetical protein
	1990692	1991612	+	Transposase
Chromosome 2 region 1	589273	589587	-	Hypothetical protein
	589589	591190	-	Hypothetical protein
	591320	591550	-	Hypothetical protein
	591561	591806	-	Hypothetical protein
	591817	592155	-	Phage-like protein
	592157	593236	-	Phage-like protein
	593880	594164	+	Hypothetical protein
	594362	594607	-	Hypothetical protein
	594915	596054	-	Hypothetical protein
	596051	596365	-	Hypothetical protein
	596367	597959	-	Hypothetical protein
	598093	598323	-	Hypothetical protein
	598334	598579	-	Hypothetical protein
	598590	598940	-	Hypothetical protein
	598951	600255	-	Phage-like protein
	600424	600714	+	Phage-like protein
	601256	601996	-	Hypothetical protein
Chromosome 2 region 2	1914443	1914459	+	Attachment site
	1914604	1915626	-	Hypothetical protein
	1915638	1916168	-	Hypothetical protein
	1916201	1916740	-	Hypothetical protein
	1916765	1917409	-	Hypothetical protein
	1917559	1917804	+	Hypothetical protein
	1917915	1918454	+	Hypothetical protein
	1918464	1918799	+	Hypothetical protein
	1918866	1919369	+	Hypothetical protein
	1919371	1919655	+	Hypothetical protein
	1919652	1920053	+	Hypothetical protein
	1920055	1920282	+	Hypothetical protein
	1920286	1920906	+	Hypothetical protein
	1920903	1921331	+	Hypothetical protein
	1921342	1924008	+	Hypothetical protein
	1924022	1924213	+	Hypothetical protein
	1924296	1924628	-	Hypothetical protein
	1924874	1925128	+	Hypothetical protein

1925147	1925398	-	Hypothetical protein
1925477	1926508	-	Hypothetical protein
1926505	1928256	-	Hypothetical protein
1928476	1929354	+	Hypothetical protein
1929394	1930407	+	Hypothetical protein
1930418	1931134	+	Hypothetical protein
1931267	1931686	+	Hypothetical protein
1931683	1932174	+	Hypothetical protein
1932158	1932814	+	Hypothetical protein
1932818	1933948	+	Phage-like protein
1933952	1934407	+	Phage-like protein
1934420	1934638	+	Phage-like protein
1934635	1935132	+	Hypothetical protein
1935129	1935359	+	Hypothetical protein
1935362	1935649	+	Hypothetical protein
1935646	1935909	+	Hypothetical protein
1935951	1936094	+	Hypothetical protein
1936120	1938003	+	Phage-like protein
1938003	1938344	+	Phage-like protein
1938344	1939531	+	Hypothetical protein
1939626	1940120	+	Hypothetical protein
1940132	1942561	+	Phage-like protein
1942561	1942830	+	Hypothetical protein
1942841	1943377	+	Phage-like protein
1943387	1944076	+	Phage-like protein
1944067	1944762	+	Phage-like protein
1944764	1944961	+	Phage-like protein
1945571	1945825	+	Phage-like protein
1945934	1945950	+	Attachment site

Table S10. Genetic features of plasmids in *V. harveyi* strain N8T11

Plasmid	Gene name/ gene locus	Description
pN8T11a	AAIA71_28370	Hypothetical protein
	AAIA71_28375	Hypothetical protein
	AAIA71_28380	Group II intron maturase-specific domain-containing protein
	AAIA71_28385	Hypothetical protein
	AAIA71_ 28390	AAA family ATPase
	AAIA71_28395	Regulator
	AAIA71_ 28400	IS256 family transposase
	AAIA71_ 28405	Cyclic peptide export ABC transporter
	AAIA71_ 28410	Extracellular solute-binding protein
	AAIA71_ 28415	ABC transporter permease subunit
	AAIA71_ 28420	Hypothetical protein
	AAIA71_ 28425	ABC transporter permease subunit
	AAIA71_28430	ABC transporter ATP-binding protein
	AAIA71_ 28435	Nitro reductase
	AAIA71_ 28440	4'-phosphopantetheinyl transferase superfamily protein
	AAIA71_28445	TonB-dependent siderophore receptor
	AAIA71_ 28450	MbtH family NRPS accessory protein
	AAIA71_ 28455	TauD/TfdA family dioxygenase
	AAIA71_ 28460	Non-ribosomal peptide synthetase
	AAIA71_ 28465	Amino acid adenylation domain-containing protein
	AAIA71_ 28470	Phosphopantetheine-binding protein
	AAIA71_ 28475	Amino acid adenylation domain-containing protein
	AAIA71_ 28480	Thioesterase domain-containing protein
	AAIA71_ 28485	Hypothetical protein
	AAIA71_ 28490	Hypothetical protein
	AAIA71_ 28495	Hypothetical protein
	AAIA71_ 28500	Hypothetical protein
	AAIA71_ 28505	Tyrosine-type recombinase integrase
	AAIA71_ 28510	Hypothetical protein
	AAIA71_ 28515	Hypothetical protein
	AAIA71_ 28520	Tyrosine-type recombinase/integrase
	AAIA71_ 28525	Hypothetical protein
	AAIA71_ 28530	Replication initiator protein RctB domain-containing protein
	AAIA71_ 28535	Hypothetical protein
	AAIA71_ 28540	DNA replication terminus site-binding protein
	AAIA71_ 28545	Hypothetical protein
	AAIA71_ 28550	Hypothetical protein
	AAIA71_ 28555	Hypothetical protein
	AAIA71_ 28560	UyrD-helicase domain-containing protein
	AAIA71_ 28565	Hypothetical protein

	AAIA71_ 28570	PD-(D/E)XK nuclease-like domain-containing protein
	AAIA71_ 28575	ParA, family protein
	AAIA71_ 28580	Hypothetical protein
	AAIA71_28585	Hypothetical protein
	AAIA71_28590	IS3 family transposase
	AAIA71_ 28595	IS3 family transposase
	AAIA71_ 28600	Hypothetical protein
	AAIA71_ 28605	Hypothetical protein
	AAIA71_ 28610	Site-specific integrase
	AAIA71_28615	DUF2913 family protein
	AAIA71_ 28620	Type Il toxin-antitoxin system Pemk/MazF family toxin
	AAIA71_28625	Hypothetical protein
	AAIA71_ 28630	Hypothetical protein
	AAIA71_ 28635	Hypothetical protein
	AAIA71_28640	Hypothetical protein
	AAIA71_28645	Hypothetical protein
	AAIA71_ 28650	Hypothetical protein
	AAIA71_ 28655	Hypothetical protein
	AAIA71_ 28660	Hypothetical protein
	AAIA71_ 28665	Hypothetical protein
	AAIA71_ 28670	Hypothetical protein
	AAIA71_ 28675	Hypothetical protein
	AAIA71_28680	Hypothetical protein
	AAIA71_ 28685	Hypothetical protein
	AAIA71_ 28690	P-loop NTPase fold protein
	AAIA71_ 28695	IS3 family transposase
	AAIA71_ 28700	Hypothetical protein
	AAIA71_ 28705	Hypothetical protein
	AAIA71_28710	DUF2913 family protein
	AAIA71_ 28715	Hypothetical protein
	AAIA71_ 28720	Hypothetical protein
	AAIA71_ 28725	DNA cytosine methyltransferase
	AAIA71_ 28735	Tolc family outer membrane protein
	AAIA71_ 28740	OmpA family protein
	AAIA71_28745	IS5 family transposase
	AAIA71_ 28750	Hypothetical protein
	AAIA71_ 28755	Hypothetical protein
	AAIA71_28760	ParA family protein
pN8T11b	AAIA71_28765	Rpn family recombination-promoting nuclease/putative transposase
	AAIA71_28770	Hypothetical protein
	AAIA71_ 28775	Hypothetical protein
	AAIA71_28780	TraY domain-containing protein
	AAIA71_ 28780	Type IV conjugative transfer system pilin TraA
	AAIA71_ 28785	Type IV conjugative transfer system protein Tral

AAIA71_ 28790	Type IV conjugative transfer system protein TraE
AAIA71_ 28795	Type-F conjugative transfer system secretin TraK
AAIA71_ 28805	Trbl/virB10 family protein
AAIA71_ 28805	Type IV conjugative transfer system lipoprotein TraV
AAIA71_28815	Hypothetical protein
AAIA71_ 28815	Type IV secretion system protein TraC
TAAIA71_ 28820	Type-F conjugative transfer system protein TraW
AAIA71_ 28830	Hypothetical protein
AAIA71_ 28830	Conjugal transfer pilus assembly protein TraU
AAIA71_ 28840	Hypothetical protein
AAIA71_ 28840	Type-F conjugative transfer system pilin assembly protein TrbC
AAIA71_ 28845	Type-F conjugative transfer system mating-pair stabilization protein TraN
AAIA71_ 28855	Hypothetical protein
AAIA71_ 28860	Hypothetical protein
AAIA71_ 28865	Hypothetical protein
AAIA71_ 28870	Hypothetical protein
AAIA71_ 28875	Hypothetical protein
AAIA71_ 28875	Type-F conjugative transfer system pilin assembly protein TraF
AAIA71_28885	ATP-binding protein
AAIA71_ 28885	Type-F conjugative transfer system pilin assembly thiol-disulfide isomerase
AAIA71_ 28895	Conjugal transfer protein TraH
AAIA71_ 28900	Conjugal transfer protein TraG N-terminal domain-containing protein
AAIA71_ 28905	Hypothetical protein
AAIA71_28910	Hypothetical protein
AAIA71_ 28910	Type IV conjugative transfer system coupling protein TraD
AAIA71_ 28920	Hypothetical protein
AAIA71_ 28925	Adenosine deaminase
AAIA71_ 28930	Hypothetical protein
AAIA71_ 28935	Hypothetical protein
AAIA71_ 28940	Hypothetical protein
AAIA71_ 28945	Hypothetical protein
AAIA71_ 28950	Hypothetical protein
AAIA71_ 28950	Conjugative transfer relaxase/helicase TraI
AAIA71_28960	Hypothetical protein
AAIA71_ 28965	Lytic trans glycosylases domain-containing protein
AAIA71_ 28970	Type I restriction endonuclease subunit M
AAIA71_ 28975	Hypothetical protein
AAIA71_28980	Hypothetical protein
AAIA71_28985	Hok /Gef family protein
AAIA71_ 28990	DUF2913 family protein

	AAIA71_28995	Hypothetical protein
	AAIA71_ 29000	Panacea domain-containing protein
	AAIA71_ 29005	Hypothetical protein
	AAIA71_ 29010	ATP-binding protein
	AAIA71_ 29015	Recombinase family protein
	AAIA71_ 29020	HEPN domain-containing protein
	AAIA71_ 29025	Type II toxin-antitoxin system Phd/efM family antitoxin
	AAIA71_29030	Type II toxin-antitoxin system RelE/ParE family toxin
	AAIA71_ 29035	Transposase
	AAIA71_29040	DUF5710 domain-containing protein
	AAIA71_ 29045	Hypothetical protein
	AAIA71_29050	IS91 family transposase
	AAIA71_ 29055	Domain-containing protein
	AAIA71_ 28730	Lg-like domain-containing protein
	AAIA71_ 29060	Type IV conjugative transfer system coupling protein TraD
	AAIA71_29065	Hypothetical protein
	AAIA71_29070	Adenosine deaminase
	AAIA71_ _29075	Hypothetical protein
	AAIA71_ 29080	Conjugative transfer relaxase/helicase Tral
	AAIA71_ 29085	Hypothetical protein
	AAIA71_ 29090	Lytic trans glycosylase domain-containing protein
	AAIA71_ 29095	Type I restriction endonuclease subunit M
	AAIA71_ 29100	Hypothetical protein
	AAIA71_ 29105	Hypothetical protein
	AAIA71_ 29110	Outer membrane beta-barrel protein
	AAIA71_ 29115	Hypothetical protein
	AAIA71_ 29120	DNA, repair protein RadC
	AAIA71_ 29125	Hypothetical protein
pN8T11c	AAIA71_ 29130	Hypothetical protein
	AAIA71_29135	Hypothetical protein
	AAIA71_ 29140	Hypothetical protein
	AAIA71_ 29145	Hypothetical protein
	AAIA71_29150	Hypothetical protein
	AAIA71_29155	FRG domain-containing protein
	AAIA71_ 29160	Hypothetical protein
	AAIA71_ 29165	Hypothetical protein
	AAIA71_29170	Hypothetical protein
	AAIA71_ 29175	DNA-binding protein
	AAIA71_ 29180	Type II toxin-antitoxin system HigB family toxin
	AAIA71_ 29185	CesT family type Ill secretion system chaperone
	AAIA71_ 29190	Hypothetical protein
	AAIA71_ 29195	Hypothetical protein
	AAIA71_ _29200	Hypothetical protein
	AAIA71_ 29205	Hypothetical protein

AAIA71_29210	Recombinase family protein
AAIA71_29215	Hypothetical protein
AAIA71_ 29220	Type II toxin-antitoxin system RelE/ParE family toxin
AAIA71_ 29225	Type II toxin-antitoxin system Phd/yefM family antitoxin
AAIA71_ 29230	Hypothetical protein
AAIA71_ 29235	IS110 family transposase
AAIA71_ 29240	Hypothetical protein
AAIA71_29245	DUF3265 domain-containing protein
AAIA71_ 29250	Restriction endonucleases
AAIA71_29255	Hypothetical protein
AAIA71_ 29260	Abi family protein
AAIA71_ 29265	Hypothetical protein
AAIA71_ 29270	Hypothetical Protel
AAIA71_ 29275	Hypothetical protein
AAIA71_29280	ParA family protein
AAIA71_ 29285	Rpn family recombination-promoting nuclease/putative transposase
AAIA71_ 29290	Hypothetical protein
AAIA71_29295	TraY domain-containing protein
AAIA71_ 29300	Type IV conjugative transfer system pilin TraA
AAIA71_ 29305	Type IV conjugative transfer system protein Tral
AAIA71_ 28790	Type IV conjugative transfer system protein TraE
AAIA71_ 28795	Type-F conjugative transfer system secretin TraK
AAIA71_ 29320	Trbl virB10 family protein
AAIA71_ 29325	Type IV conjugative transfer system lipoprotein TraV
AAIA71_ 29330	Type IV secretion system protein TraC
AAIA71_ 29335	Type-F conjugative transfer system protein TraW
AAIA71_ 29340	Hypothetical protein
AAIA71_ 29345	Hypothetical protein
TAAIA71_ 29350	Conjugal transfer pilus assembly protein TraU
AAIA71_ 29355	Type-F conjugative transfer system pilin assembly protein TrbC
AAIA71_ 29360	Type-F conjugative transfer system mating-pair stabilization protein TraN
AAIA71_ 29365	Hypothetical protein
AAIA71_29370	Hypothetical protein
AAIA71_ 29375	Hypothetical protein
AAIA71_29380	Hypothetical protein
AAIA71_ 29385	Type-F conjugative transfer system pilin assembly protein TraF
AAIA71_ 29390	Type-F conjugative transfer system pilin assembly thiol-disulfide isomerase TrbB
AAIA71_ 29395	Conjugal transfer protein TraH
AAIA71_ 29400	Conjugal transfer mating-pair stabilization protein TraG
AAIA71_ 29405	Hypothetical protein
AAIA71_ 29410	Hypothetical protein

pN8T11d	AAIA71_ 29415	Hok/Gef family protein
	AAIA71_ 29420	TonB-dependent hemoglobin receptor
	AAIA71_ 29425	Recombinase family protein
	AAIA71_ 29430	Helix-turn-helix domain-containing protein
	AAIA71_ 29435	PIN domain-containing protein
	AAIA71_ 29440	Hypothetical protein
	AAIA71_ 29445	YegP family protein
	AAIA71_29450	3'-5' exonuclease
	AAIA71_ 29455	Hypothetical protein
	AAIA71_ 29460	Hypothetical protein
	AAIA71_29465	Type I restriction endonuclease subunit M
	AAIA71_ 29470	Lytic trans glycosylase domain-containing protein
	AAIA71_ 29475	Hypothetical protein
	AAIA71_ 29495	Conjugative transfer relaxase/helicase TraI
	AAIA71_29485	Hypothetical protein
	AAIA71_ 29490	Hypothetical protein
	AAIA71_29495	Hypothetical protein
	AAIA71_ 29500	Adenosine deaminase
	AAIA71_ 29505	Hypothetical protein
	AAIA71_ 29510	Type Iv conjugative transfer system coupling protein TraD
	AAIA71_ 29515	Hypothetical protein
	AAIA71_ 29520	Hypothetical protein
	AAIA71_ 29525	Conjugal transfer mating-pair stabilization protein TraG
	AAIA71_ 29530	Conjugal transfer protein TraH
	AAIA71_ 29535	Type-F conjugative transfer system pilin assembly thiol-disulfide isomerase TrbB
	AAIA71_ 29540	ATP-binding protein
	AAIA71_ 29545	Type-F conjugative transfer system pilin assembly protein
	AAIA71_ 29550	Hypothetical protein
	AAIA71_ 29555	Hypothetical protein
	AAIA71_ 29560	Hypothetical protein
	AAIA71_ 29565	Hypothetical protein
	AAIA71_ 29570	Hypothetical protein
	AAIA71_ 29575	Type-F conjugative transfer system mating-pair stabilization protein
	AAIA71_ 29580	Type-F conjugative transfer system pilin assembly protein TrbC
	AAIA71_ 29585	Hypothetical protein
	AAIA71_ 29590	Conjugal transfer pilus assembly protein TraU
	AAIA71_ 29595	Hypothetical protein
	AAIA71_ 29600	Type-F conjugative transfer system protein Trav
	AAIA71_ 29605	Type IV secretion system protein TraC
	AAIA71_ 29610	Hypothetical protein
	AAIA71_ 29615	Type IV conjugative transfer system lipoprotein Traw

	AAIA71_ 29620	TrbI/virB 10 family protein
	AAIA71_ 29625	Type-F conjugative transfer system secretin TraK
	AAIA71_ 29630	Type IV conjugative transfer system protein TraE
	AAIA71_ 29635	Type IV conjugative transfer system protein Tral
	AAIA71_ 29640	Type IV conjugative transfer system pilin TraA
	AAIA71_ 29645	TraY domain-containing protein
	AAIA71_ 29650	Helix-turn-helix transcriptional regulator
	AAIA71_ 29655	Hypothetical protein
	AAIA71_ 29660	Ron family recombination-promoting nuclease/putative transposase
	AAIA71_ 29665	ParA family protein
	AAIA71_ 29670	Hypothetical protein
	AAIA71_ 29675	Hypothetical protein
	AAIA71_ 29680	IS91 family transposases
	AAIA71_ 29685	IS1 family transposase
	AAIA71_ 29690	Hypothetical protein
	AAIA71_ 29695	Hypothetical protein
	AAIA71_ 29700	IS91 family transposase
	AAIA71_ 29705	Hydroxyisourate hydrolase
	AAIA71_ 29710	IS5/1S1182 family transposase
pN8T11e	AAIA71_ 29715	A lactococcal endoribonuclease belonging to the type III toxin–antitoxin system

Table S11. Plasmids from other sources similar to those found in N8T11

Plasmid ref	Results plasmid accession num	Results plasmid name	Shared hashes	Mash Neighbor Distance	Host species	Results plasmid host stain ID	Biosample location
pN8T11b	NZ CP018682.2	QT520 p1	263	0	*V. harveyi*	QT520	China: Chenmai
	NZ CP150471.1	Pvh4	255	0.0434809	*V. harveyi*	NH-LM1	China: Bohai Bay
	NZ CP150472.1	Pvh5	255	0.0583726	*V. harveyi*	NH-LM1	China: Bohai Bay
	NZ CP150469.1	Pvh2	236	0.0563082	*V. harveyi*	NH-LM1	China: Bohai Bay
	NZ CP150470.1	Pvh3	156	0.0465005	*V. harveyi*	NH-LM1	China: Bohai Bay
	NZ CP025540.1	P345-67	83	0	*V. harveyi*	345	China: Shenzhen
	NZ CP018684.2	QT520 p3	82	0	*V. harveyi*	QT520	China: Chenmai
	NZ CP150908.1	pHLE-202006	81	0.0450347	*V. parahaemolyticus*	Vp-HL-202006	China: Fujian
	NZ CP150915.1	pHLE-202008	81	0.0450347	*V. parahaemolyticus*	Vp-HL-202008	China: Fujian
	NZ CP117056.1	unnamed1	68	0.0567566	*V. harveyi*	VH21FL	South Korea: Pohang
	NZ CP018683.2	QT520 p2	67	0	*V. harveyi*	QT520	China: Chenmai
pN8T11c	NZ CP018683.2	QT520 p2	250	0	*V. harveyi*	QT520	China: Chenmai
	NZ CP117056.1	unnamed1	241	0.0567566	*V. harveyi*	VH21FL	China: Bohai Bay
	NZ CP150470.1	Pvh3	225	0.0465005	*V. harveyi*	NH-LM1	China: Bohai Bay
	NZ CP150908.1	PHLE-202006	205	0.0450347	*V. parahaemolyticus*	Vp-HL-202006	China: Fujian
	NZ CP150915.1	PHLE-202008	205	0.0450347	*V. parahaemolyticus*	Vp-HL-202008	China: Fujian
	NZ CP018684.2	QT520 p3	193	0	*V. harveyi*	QT520	China: Chenmai
	NZ CP150473.1	Pvh6	185	0.0455159	*V. harveyi*	NH-LM1	China: Bohai Bay

	NZ CP025540.1	p345-67	162	0	*V. harveyi*	345	China: Shenzhen
	NZ CP150468.1	Pvh1	156	0.0615839	*V. harveyi*	NH-LM1	China: Bohai Bay
	NZ CP150469.1	Pvh2	142	0.0563082	*V. harveyi*	NH-LM1	China: Bohai Bay
	NZ CP150472.1	Pvh5	88	0.0583726	*V. harveyi*	NH-LM1	China: Bohai Bay
	NZ CP150469.1	Pvh2	284	0.0563082	*V. harveyi*	NH-LM1	China: Bohai Bay
	NZ CP150471.1	Pvh4	275	0.0434809	*V. harveyi*	NH-LM1	China: Bohai Bay
	NZ CP150472.1	Pvh5	213	0.0583726	*V. harveyi*	NH-LM1	China: Bohai Bay
	NZ CP018682.2	QT520 p1	191	0	*V. harveyi*	QT520	China: Chenmai
	NZ CP150470.1	Pvh3	136	0.0465005	*V. harveyi*	NH-LM1	China: Bohai Bay
	NZ CP018684.2	QT520 p3	100	0	*V. harveyi*	QT520	China: Chenmai
	NZ CP012741.1	unnamed	99	0	*V. vulnificus*	FORC_017	South Korea: Jeju island
pN8T11d	NC 009703.1	PC4602-2	97	0.0123533	*V. vulnificus*	CECT4602	Spain
	NZ CP014638.1	PR99	97	0	*V. vulnificus*	CECT 4999	Spain
	NZ CP044208.1	PVv180806	95	0.0123533	*V. vulnificus*	Vv180806	China: Guangzhou
	NZ CP134786.1	PVv GCU-01-2	89	0.0165552	*V. vulnificus*	GCU-01	South Korea: Kimpo
	NZ CP025540.1	P345-67	86	0	*V. harveyi*	345	China: Shenzhen
	NZ CP117056.1	Unnamed1	84	0.0567566	*V. harveyi*	VH21FL	South Korea: Pohang
	NZ CP018683.2	QT520 p2	79	0	*V. harveyi*	QT520	China: Chenmai
	NZ CP150473.1	Pvh6	71	0.0455159	*V. harveyi*	NH-LM1	China: Bohai Bay
	NZ CP150908.1	PHLE-202006	70	0.0450347	*V. parahaemolyticus*	Vp-HL-202006	China: Fujian
	NZ CP150915.1	PHLE-202008	70	0.0450347	*V. parahaemolyticus*	Vp-HL-202008	China: Fujian