

Supplementary Table S1. Oligonucleotides used in this study.

Target and oligonucleotides	Sequence	bp amplified
<i>dly</i>		
Dly-5'	CTCCTATGGGACATGAATGG	549
Dly-3'	TGCTCTAGGCTAAATGAATC	
<i>phlyP (hlyA_{pl})</i>		
PhlyP-5'	GCTATAAATGAATAAGAAAA	767
PhlyP-3'	TTGAAGCTAACTCAAAAA	
<i>phlyC (hlyA_{ch})</i>		
phlyC-5'	AATGTTTCTTTCCGTTGGGC	353
phlyC -3'	CCGGAGTTCCACCAGTAAAT	
<i>hlyAch-det(hlyA_{ch})</i>		
hlyAch-det-5'	GAAGAGTTAGCGATGGTCTA	288
hyAch-det-3'	TTGATATAGCGTCTGCGCCC	
<i>hyAch (upstream sequences)</i>		
hlyAch-3new	ACATATACAATACGATCTGG	variable
KefA-3'	TGTAGGTAGATATCGAGCTC	
<i>PlpV int (phospholipase)</i>		
plp int -F	TTCATAATAGCAGTAATCT	1618
plp int -R	TTACTAAGCAGAATCCAGCC	
<i>pPHDD1 replication origin</i>		
Ori_pPHDD1-F	TGGAATAACTATGAGTAACA	3052
Ori_pPHDD1-R	CATTACCAAAACATCTACAT	
<i>toxR</i>		
toxR-5'	GGGATTTTATGGTACACAAA	985
toxR-3'	ATCATAACCAGAGAGATGCT	
<i>Collagenase (internal fragment)</i>		
col - F	CCTGCTACAGTTCGAGCTCA	1617
col - R	TCAACCACTCGAGATATTCC	
<i>Collagenase (gene context)</i>		
ups_colP_F	GAGGACCATTTATTGCCAGT	variable
downs_colP_R	CGGCTAAGCAAACAGAAAAC	
<i>Urease</i>		
Ure-5'	TCCGGAATAGGTAAAGCGGG	448
Ure-3'	CTTGAATATCCATCTCATCTGC	
<i>rstAB system</i>		
Kinasa int - F	TCAGCTTCATAATCTTCTAG	236
Kinasa int - R	AATAAGATTGTGAGTCTACG	
<i>Tat-pathway protein</i>		
vda-002799-intF	TCCATTTTCGTTCTTGTTCTGA	1500
vda-002799-intR	GATTTTTCACGGACGATAT	
<i>Type III secretion system</i>		
vda-000187-intF	GCCGATCTCTTCACCATTAT	140
vda-000187-intR	TAGAACCGCAAACTGCAAC	
<i>Type III secretion system</i>		
vda-000193-intF	CCAACAATCGCGGCAAGAAT	240
vda-000193-intR	GAGGCTCTTGAATTGTTCTC	
<i>Type III secretion system</i>		
vda-000224-intF	AGTTATAACCGACTTTACTG	511
vda-000224-intR	ACATGCTGGGCGATCAAGC	

<i>Vibrio</i> ferrin synthesis PvsB		
DK2_PvsB-1000_F	AGCCTGTGCTCACGAAAGTT	980
DK2_PvsB-1000_R	CGTCATTTTGCCTTCTTTAT	
<i>Vibrio</i> ferrin synthesis PvsD		
DK2_PvsD_1200_F	AAATGGTGTTTTGTTGTTGC	1210
DK2_PvsD_1200_R	AATTCTGGAAGCAATTTGGT	
<i>Outer membrane usher</i>		
DK3_outer membrane_800_F	ATTGTGGGATCCTGGTGTTA	800
DK3_outer membrane_800_R	TTTCCATCCATGTTGAGTTT	
<i>Fimbrial protein</i>		
DK3_fimbria_600_F	CGCCTATGTCTATTTTTGGG	600
DK3_fimbria_600_R	GCTACTGCTAACTTTTCCAC	
<i>CRISPR-Cas3(System 1)</i>		
DK29-crispr-Cas3-400-F	AATGCGCTAAATCATAAATC	400
DK29-crispr-Cas3-400-R	AAATCCTTTATGTTGCGTAA	
<i>CRISPR-Csy1 (System 1)</i>		
DK29-crispr-Csy1-200-F	CAGAGCGTTATCAAACATAAG	200
DK29-crispr-Csy1-200-R	ATACTGATTTGATTGGCTCG	
<i>CRISPR-Cas3 (System 2)</i>		
cas3_sist2_F	AAGCTTTGCTACTGACAAGG	1000
cas3_sist2_R	TTAGATCCTTTAAATTCTGT	
<i>CRISPR-Cas2 (System 2)</i>		
cas2_sist2_F	ATCAGCAGGTAAAAATTTC	150
cas2_sist2_R	TCAGGGAAATGATTTGGGAA	
<i>CRISPR-csy4/cas6 (System 3)</i>		
csy4_sist3_F	TGCGCTGATGAACCGCTAGA	290
csy4_sist3_R	TTGCCTTTGTTGCTGAAGAT	
<i>DK3-hyAch (upstream sequences)</i>		
DK3_contorno_CDS6_F	AACGCTATCATGGGAACTGA	2000
DK3_contorno_CDS7_R	AAATATGTCTAACGGCCTGA	
<i>DK20-hyAch (upstream sequences)</i>		
DK20_contorno_CDS5_R	TCCAAAAGGAGTATTTATCA	2000
DK20_contorno_CDS6_F	GCACCAAGGAGCGGAGCAAA	
<i>DK29-hyAch (upstream sequences)</i>		
DK29_contorno_CDS7_R	CAATGTCTGTCCCTGTTAAG	900
HlyAchr_contorno_F	ATAAACAAAAATTAAATTCA	
