Supplementary Information

Viunalikeviruses are environmentally common agents of horizontal gene transfer in pathogens and biocontrol bacteria

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Supplementary Table S1: Frequency of transduction of different markers using the *Salmonella* phage ViI

Donor strain	Relevant marker/plasmid	Recipient strain	m.o.i.	Transduction efficiency[a,b,c]	Standard deviation[b]
BDR948	pECA1039-Km3	BDR948	10	$<1.0 \times 10^{-10}$	-
	pECA1039-Km3	BDR948	1	3.7×10^{-7}	7.7×10^{-8}
	pECA1039-Km3	BDR948	0.1	1.3×10^{-5}	1.1×10^{-6}
	pECA1039-Km3	BDR948	0.01	2.3×10^{-5}	2.5×10^{-6}
SW114	*STY1890-1891*::*cat*	BDR948	10	$<1.0 \times 10^{-10}$	-
	STY1890-1891::*cat*	BDR948	1	1.1×10^{-7}	8.8×10^{-9}
	STY1890-1891::*cat*	BDR948	0.1	5.6×10^{-6}	7.1×10^{-7}
	STY1890-1891::*cat*	BDR948	0.01	1.2×10^{-5}	3.5×10^{-6}
BA231	*STY3632*::*cat*	BDR948	10	$<1.0 \times 10^{-10}$	-
	STY3632::*cat*	BDR948	1	4.5×10^{-8}	5.7×10^{-8}
	STY3632::*cat*	BDR948	0.1	5.2×10^{-6}	2.8×10^{-7}
	STY3632::*cat*	BDR948	0.01	4.6×10^{-5}	8.1×10^{-6}

[a]Transduction efficiency is expressed as the number of transductants per plaque forming unit (p.f.u.)

[b]Mean and stardard deviation of three independent experiments are shown.

[c]Transduction experiments were performed using 10^9 bacterial cells.

Supplementary Table S2. Phages, bacteria, oomycete, and plasmids used in this study

Phage/Bacteria/ oomycete/plasmids	Genotype or relevant characteristic[a]	Reference or source
Phages		
ViI	*Salmonella* Typhi infecting phage	Pickard *et al.,* (2010)
LIMEstone1	*Dickeya solani* infecting phage	Adriaenssens *et al*., (2012)
LIMEstone2	*Dickeya solani* infecting phage	Adriaenssens *et al*., (2012)
CBA120	*Escherichia coli* O157:H7 infecting phage	Kutter *et al*., (2011)
φXF1	*Dickeya solani* infecting phage	This study
φXF3	*Dickeya solani* infecting phage	This study
φXF4	*Dickeya solani* infecting phage	This study
φXF28	*Dickeya solani* infecting phage	This study
Bacteria strains		
Salmonella Typhi BRD948	ViI host strain; Ty2 Δ*aroC aroD htrA*; Wild type "vaccine strain"	Bishop *et al*., (2008)
Salmonella Typhi SW114	BDR948 mutant *STY1890-1891*::*cat*; Cm^r	D. Pickard
Salmonella Typhi SW231	BDR948 mutant *STY3632*::*cat*; Cm^r	D. Pickard
Escherichia coli β2163	F^- RP4-2-Tc::Mu Δ*dapA*::(*erm-pir*), Km^rEm^r	Demarre *et al*., (2005)
E. coli O157:H7 NCTC 12900	CBA120 host strain; The strain lacks the shiga-toxin (Stx) genes; Km^r	ATCC 700728
Dickeya solani MK10	Wild type strain isolated from potato in Israel; LIMEstone phage host strain	Pritchard *et al*., (2013)
MK10P1	MK10 transposon mutant defective in secreted protease C precursor *spp*::Tn-KRCPN1; Protease-negative, Km^r	This study
MK10P7	MK10 transposon mutant defective in alkaline protease inhibitor precursor *api*::Tn-KRCPN1; Protease-negative, Km^r	This study
MK1610P1	MK10 transposon mutant defective in secreted protease C precursor *spp*::mini-Tn*5*Sm/Sp; Transduced from MK16P1 using LIMEstone phages; Protease-negative, Sm^r	This study
MK10MM1	MK10 transposon mutant defective in 3-isopropylmalate dehydratase (large subunit) *ipd*::Tn-KRCPN1; auxotrophic, Km^r	This study
MK10MM2	MK10 transposon mutant defective in glutamate synthase (large subunit) *gts*::mini-Tn*5*Sm/Sp; auxotrophic, Sm^r	This study
MK10oocF	MK10 transposon mutant *oocF*::Tn-KRCPN1; oocydin A negative, Km^r	This study
MK10oocN	MK10 transposon mutant *oocN*::Tn-KRCPN1; oocydin A negative, Km^r	This study
Dickeya solani MK16	Wild type strain isolated from river water in the United Kingdom; LIMEstone phage host strain	Pritchard *et al*., (2013)
MK16P1	MK16 transposon mutant defective in secreted protease C precursor *spp*::mini-Tn*5*Sm/Sp; Protease-negative, Sm^r	This study
MK16P2	MK16 transposon insertion in promoter region of gene for secreted protease C precursor *spp*::mini-Tn*5*Sm/Sp; Protease-negative, Sm^r	This study
MK16MM1	MK16 transposon mutant defective in dihydroorotate dehydrogenase *dhd*::mini-Tn*5*Sm/Sp; auxotrophic, Sm^r	This study
MK16MM3	MK16 transposon mutant defective in anthranilate phosphoribosyltransferase *apr*::mini-Tn*5*Sm/Sp; auxotrophic, Sm^r	This study
MK16MM4	MK16 transposon mutant defective in nitrite/sulfite reductase (beta-component) *nsr*::mini-Tn*5*Sm/Sp; auxotrophic, Sm^r	This study
MK16MM5	MK16 transposon mutant defective in phosphoribosylaminoimidazole carboxylase *ppc*::mini-Tn*5*Sm/Sp; auxotrophic, Sm^r	This study
MK1016P1	MK16 transposon mutant defective in secreted protease C precursor *spp*::Tn-KRCPN1; Transduced from MK10P1 using LIMEstone phages; Protease-negative, Km^r	This study
1016MM2	MK16 transposon mutant defective in glutamate synthase (large subunit) *gts*::mini-Tn*5*Sm/Sp; Transduced from MK10MM2 using LIMEstone phages; auxotrophic, Sm^r	This study
MK16oocF	MK16 transposon mutant *oocF*::Tn-KRCPN1; Transduced from MK10oocF using LIMEstone phages; oocydin A negative, Km^r	This study
MK16oocN	MK16 transposon mutant *oocN*::Tn-KRCPN1; Transduced from MK10oocN using LIMEstone phages; oocydin A negative, Km^r	This study
Dickeya solani IPO 2222	Wild type strain isolated from potato in the Netherlands; LIMEstone host strain	Pritchard *et al*., (2013)
10IPOP1	IPO 2222 transposon mutant defective in secreted protease C precursor *spp*::Tn-KRCPN1; Transduced from MK10P1 using LIMEstone phages; Protease-negative, Km^r	This study

IPOoocF	IPO 2222 transposon mutant *oocF*::Tn-KRCPN1; Transduced from MK10oocF using LIMEstone phages; oocydin A negative, Km^r	This study
IPOoocN	IPO 2222 transposon mutant *oocN*::Tn-KRCPN1; Transduced from MK10oocN using LIMEstone phages; oocydin A negative, Km^r	This study
Oomycete strains		
Pythium ultimum	Wild type, plant pathogen	R. Cooper
Plasmids		
pKRCPN1	Km^r, Tc^r; Derivative of pDS1028*uidA* with the *uidA* and *cat* genes replaced with *lacZ* and *km* genes. Plasmid used in transposon mutagenesis	K.J. Roberts (2010)
pUTmini-Tn*5*Sm/Sp	Ap^r, Sm^r, Sp^r; Delivery plasmid for mini-Tn*5*Sm/Sp; Plasmid used in transposon mutagenesis	De Lorenzo *et al*., (1990)
pACYC184	Cm^r, Tc^r; Plasmid cloning vector	Chang and Cohen (1978)
pECA1039-Km3	Km^r; Transposon-marked derivative of the original ToxIN plasmid, pECA1039, from *Pectobacterium atrosepticum*	Fineran *et al*., (2009)
pFR2	Ap^r; pBR322 containing the full *tenpin* locus from *Photorhabdus luminescens* TT01	Blower *et al*., (2012)
p34S-Km3	Km^r, Ap^r *km3* antibiotic resistance cassette	Dennis and Zylstra (1998)
pMAMV116	Km^r; 0.99-kb PstI fragment containing *km3* cassette of p34S-Km3 was inserted into PstI site of *amp* resistance gene in pFR2	Matilla and Salmond (submitted for publication)
pTA46	Ap^r; pBR322 containing the full toxin locus from *Pectobacterium atrosepticum*	Fineran *et al*., (2009)
pMAMV114	Km^r; 0.99-kb PstI fragment containing *km3* antibiotic resistance cassette of p34S-Km3 inserted into PstI site of amp resistance gene in pTA46	Matilla and Salmond (submitted for publication)

[a]Ap, ampicillin; Km, kanamycin; Cm, chloramphenicol; Sm, streptomycin; Sp, spectinomycin; Tc, tetracycline; Em, erythromycin; ATCC, American Type Culture Collection.

Supplementary Table S3: Oligonucleotide PCR primers used in this study

Name	Sequence (5´-3´)	Note
PF106	GACCACACGTCGACTAGTGCNNNNNNNNNNAGAG	Random primed PCR primer 1
PF107	GACCACACGTCGACTAGTGCNNNNNNNNNNACGCC	Random primed PCR primer 2
PF108	GACCACACGTCGACTAGTGCNNNNNNNNNNGATAC	Random primed PCR primer 3
PF109	GACCACACGTCGACTAGTGC	Random primed PCR adapter primer
MAMV1-KRCPN1	GGAATTGATCCGGTGGATG	TnKRCPN1 specific primer
MAMV2-KRCPN1	GCATAAAGCTTGCTCAATCAATCAC	TnKRCPN1 specific primer
MAMV3-Sm/Sp	CTAAGCTGATCCGGTGGATG	mini-Tn*5*Sm/Sp specific primer
MAMV4-Sm/Sp	AACGGTTTACAAGCATAAAGC	mini-Tn*5*Sm/Sp specific primer
MJ7	TTTTGAATTCGTTTTATCGACATTGTGAACC	pECA1039-Km3 specific primer
KD02	TTTTAAGCTTTTACGATCTTCAGTATGGG	pECA1039-Km3 specific primer
pTRB58	TGATGTCGGCGATATAGG	pACYC184 specific primer
pTRB59	AGAGATTACGCGCAGACC	pACYC184 specific primer

Supplementary Table S4: Transduction efficiencies of LIMEstone phages within and between *Dickeya solani* strains.

Donor strain	Relevant marker/plasmid	Recipient strain	Phenotype	Transduction efficiency LS1[a,b,c]	Standard deviation[b]	Transduction efficiency LS2[a,b,c]	Standard deviation[b]
Transduction within *Dickeya solani* MK10							
MK10P1	*spp*::Km	MK10	Protease$^-$	5.1×10^{-5}	1.4×10^{-7}	5.5×10^{-5}	4.2×10^{-6}
MK10P7	*api*::Km	MK10	Protease$^-$	6.1×10^{-5}	9.2×10^{-6}	7.6×10^{-5}	1.8×10^{-5}
MK10MM1	*ipd*::Km	MK10	Auxotrophy	6.3×10^{-5}	3.4×10^{-6}	6.2×10^{-5}	9.9×10^{-7}
MK10MM2	*gts*::Sm	MK10	Auxotrophy	1.2×10^{-5}	1.0×10^{-6}	1.7×10^{-5}	3.2×10^{-6}
MK10oocF	*oocF*::Km	MK10	Oocydin A$^-$	2.5×10^{-5}	2.5×10^{-6}	3.5×10^{-5}	1.7×10^{-6}
MK10oocN	*oocN*::Km	MK10	Oocydin A$^-$	3.5×10^{-5}	7.5×10^{-7}	3.3×10^{-5}	1.3×10^{-6}
MK10	pECA1039-km3	MK10	ToxIN$^+$	5.1×10^{-5}	9.8×10^{-6}	4.7×10^{-5}	4.0×10^{-6}
Transduction within *Dickeya solani* MK16							
MK16P1	*spp*::Sm	MK16	Protease$^-$	2.2×10^{-5}	1.2×10^{-6}	2.8×10^{-5}	3.5×10^{-7}
MK16P2	P_{spp}::Sm	MK16	Protease$^-$	2.5×10^{-5}	2.1×10^{-6}	3.2×10^{-5}	4.2×10^{-6}
MK16MM1	*dhd*::Sm	MK16	Auxotrophy	1.9×10^{-5}	3.1×10^{-6}	2.9×10^{-5}	3.3×10^{-6}
MK16MM3	*apr*::Sm	MK16	Auxotrophy	1.0×10^{-5}	6.6×10^{-7}	9.1×10^{-6}	1.3×10^{-6}
MK16MM4	*nsr*::Sm	MK16	Auxotrophy	1.7×10^{-5}	7.1×10^{-7}	1.7×10^{-5}	1.8×10^{-6}
MK16MM5	*ppc*::Sm	MK16	Auxotrophy	1.8×10^{-5}	2.4×10^{-6}	2.3×10^{-5}	1.9×10^{-6}
MK16	pECA1039-km3	MK16	ToxIN$^+$	4.1×10^{-5}	3.5×10^{-7}	4.4×10^{-5}	3.4×10^{-6}
Interstrain transduction							
MK10P1	*spp*::Km	MK16	Protease$^-$	1.7×10^{-5}	4.2×10^{-7}	3.3×10^{-5}	4.3×10^{-6}
MK10P1	*spp*::Km	IPO 2222	Protease$^-$	1.5×10^{-5}	5.7×10^{-7}	1.2×10^{-5}	6.4×10^{-6}
MK10MM2	*gts*::*Sm*	MK16	Auxotrophy	9.6×10^{-6}	1.1×10^{-6}	1.2×10^{-5}	1.3×10^{-6}
MK10oocF	*oocF*::Km	MK16	Oocydin A$^-$	9.3×10^{-6}	1.8×10^{-6}	1.1×10^{-5}	1.4×10^{-6}
MK10oocF	*oocF*::Km	IPO 2222	Oocydin A$^-$	1.1×10^{-5}	1.6×10^{-6}	1.4×10^{-5}	2.3×10^{-6}
MK10oocN	*oocN*::Km	MK16	Oocydin A$^-$	1.5×10^{-5}	1.9×10^{-7}	1.2×10^{-5}	1.5×10^{-6}
MK10oocN	*oocN*::Km	IPO 2222	Oocydin A$^-$	1.6×10^{-5}	4.7×10^{-6}	1.4×10^{-5}	8.5×10^{-7}
MK10	pECA1039-km3	MK16	ToxIN$^+$	2.4×10^{-5}	1.1×10^{-6}	2.3×10^{-5}	2.8×10^{-6}
MK10	pECA1039-km3	IPO 2222	ToxIN$^+$	1.5×10^{-5}	8.5×10^{-7}	1.3×10^{-5}	1.3×10^{-6}
MK16P1	*spp*::Sm	MK10	Protease$^-$	3.9×10^{-5}	9.9×10^{-7}	3.7×10^{-5}	1.3×10^{-6}
MK16	pECA1039-km3	MK10	ToxIN$^+$	7.0×10^{-5}	9.5×10^{-6}	6.6×10^{-5}	3.0×10^{-6}
MK16	pECA1039-km3	IPO 2222	ToxIN$^+$	4.3×10^{-5}	2.2×10^{-6}	4.1×10^{-5}	4.5×10^{-6}

[a]Transduction efficiency is expressed as the number of transductants per plaque forming unit (p.f.u.)

[b]Mean and standard deviation of three independent experiments are shown.

[c]Transduction experiments were performed using 10^9 cells with LIMEstone1 (LS1) and LIMEstone2 (LS2) at an m.o.i. of 0.1.

Supplementary Table S5: Transduction efficiency of LIMEstone phages

Number of cells	m.o.i.	Transduction efficiency LS1[a,b]	Standard deviation LS1[b]	Transduction efficiency LS2[a,b]	Standard deviation LS2[b]
1×10^{10}	10	$< 1.0 \times 10^{-11}$	-	$< 1.0 \times 10^{-11}$	-
	1	9.9×10^{-6}	2.3×10^{-6}	9.3×10^{-6}	1.1×10^{-6}
	0.1	4.1×10^{-5}	1.1×10^{-6}	7.6×10^{-5}	4.5×10^{-6}
	0.01	7.4×10^{-5}	9.9×10^{-6}	7.5×10^{-5}	5.7×10^{-6}
1×10^{9}	10	$< 1.0 \times 10^{-10}$	-	$< 1.0 \times 10^{-10}$	-
	1	1.1×10^{-6}	3.0×10^{-7}	1.2×10^{-6}	2.1×10^{-7}
	0.1	4.0×10^{-5}	2.1×10^{-6}	6.5×10^{-5}	1.4×10^{-6}
	0.01	7.5×10^{-5}	5.3×10^{-6}	1.3×10^{-4}	3.5×10^{-6}
1×10^{8}	10	$< 1.0 \times 10^{-9}$	-	$< 1.0 \times 10^{-9}$	-
	1	$< 1.0 \times 10^{-8}$	-	$< 1.0 \times 10^{-8}$	-
	0.1	1.1×10^{-6}	3.5×10^{-6}	1.0×10^{-6}	3.2×10^{-7}
	0.01	9.0×10^{-5}	7.1×10^{-6}	1.4×10^{-4}	1.1×10^{-5}

[a]Transduction efficiency of LIMEstone1 (LS1) and LIMEstone2 (LS2) phages, defined as the number of transductants obtained per p.f.u., of *api*::Tn-KRCPN1 into MK10.
[b]Mean and standard deviation of three independent experiments are shown.

Supplementary Table S6: Frequency of transduction of different markers using the *Escherichia coli* phage CBA120

Donor strain[a]	Relevant marker/plasmid	Recipient strain[a]	m.o.i.	Transduction efficiency[b,c,d]	Standard deviation[c]
O157:H7	pACYC184	O157:H7	10	$<1.0 \times 10^{-10}$	-
	pACYC184	O157:H7	1	5.8×10^{-5}	9.3×10^{-7}
	pACYC184	O157:H7	0.1	4.5×10^{-5}	1.2×10^{-5}
	pACYC184	O157:H7	0.01	1.4×10^{-4}	1.6×10^{-6}

[a] *Escherichia coli* O157:H7 NCTC 12900.
[b]Transduction efficiency is expressed as the number of transductants per plaque forming unit (p.f.u.)
[c]Mean and standard deviation of three independent experiments are shown.
[d]Transduction experiments were performed using 10^9 bacterial cells.

Supplementary Table S7: Frequency of transduction of different markers using the *Dickeya* phages φXF1, φXF3 and φXF4.

Donor strain	Relevant marker/plasmid	Recipient strain	m.o.i.	φXF1 Transduction efficiency[a,b,c]	φXF1 standard deviation[c]	φXF3 Transduction efficiency[a,b,c]	φXF3 standard deviation[c]	φXF4 Transduction efficiency[a,b,c]	φXF4 standard deviation[c]
MK10P1	*spp*::Km	MK10	10	$<1.0 \times 10^{-10}$	-	$<1.0 \times 10^{-10}$	-	$<1.0 \times 10^{-10}$	-
	spp::Km	MK10	1	2.6×10^{-8}	5.5×10^{-9}	1.3×10^{-8}	4.0×10^{-9}	1.8×10^{-8}	6.0×10^{-9}
	spp::Km	MK10	0.1	1.1×10^{-6}	7.0×10^{-8}	8.5×10^{-7}	1.3×10^{-8}	8.3×10^{-7}	7.3×10^{-8}
	spp::Km	MK10	0.01	3.5×10^{-6}	5.0×10^{-8}	2.4×10^{-6}	1.4×10^{-7}	2.1×10^{-6}	3.2×10^{-7}
MK10P1	*spp*::Km	MK16	10	$<1.0 \times 10^{-10}$	-	$<1.0 \times 10^{-10}$	-	$<1.0 \times 10^{-10}$	-
	spp::Km	MK16	1	6.6×10^{-8}	4.0×10^{-9}	2.6×10^{-8}	5.5×10^{-9}	2.9×10^{-8}	9.1×10^{-9}
	spp::Km	MK16	0.1	9.6×10^{-7}	1.0×10^{-8}	1.0×10^{-6}	5.0×10^{-8}	1.1×10^{-6}	9.1×10^{-8}
	spp::Km	MK16	0.01	2.6×10^{-6}	4.5×10^{-7}	2.0×10^{-6}	3.2×10^{-7}	2.0×10^{-6}	4.1×10^{-7}
MK10P1	*spp*::Km	IPO 2222	10	$<1.0 \times 10^{-10}$	-	$<1.0 \times 10^{-10}$	-	$<1.0 \times 10^{-10}$	-
	spp::Km	IPO 2222	1	2.6×10^{-8}	5.5×10^{-9}	8.2×10^{-9}	1.8×10^{-9}	4.6×10^{-9}	2.7×10^{-9}
	spp::Km	IPO 2222	0.1	1.3×10^{-6}	3.0×10^{-8}	1.1×10^{-6}	7.7×10^{-8}	7.4×10^{-7}	5.9×10^{-8}
	spp::Km	IPO 2222	0.01	2.4×10^{-6}	2.5×10^{-7}	2.1×10^{-6}	5.9×10^{-7}	1.4×10^{-6}	1.4×10^{-7}
MK10	pECA1039-km3	MK10	10	$<1.0 \times 10^{-10}$	-	$<1.0 \times 10^{-10}$	-	$<1.0 \times 10^{-10}$	-
	pECA1039-km3	MK10	1	2.0×10^{-8}	1.3×10^{-9}	1.4×10^{-8}	2.3×10^{-9}	4.1×10^{-9}	4.6×10^{-10}
	pECA1039-km3	MK10	0.1	9.1×10^{-7}	4.2×10^{-9}	9.2×10^{-7}	6.4×10^{-8}	1.4×10^{-6}	9.6×10^{-8}
	pECA1039-km3	MK10	0.01	2.6×10^{-6}	4.2×10^{-8}	2.2×10^{-6}	2.3×10^{-7}	1.4×10^{-6}	2.3×10^{-7}

[a]Transduction experiments were performed using 10^9 bacterial cells.
[b]Transduction efficiency defined as the number of transductants obtained per p.f.u.
[c]Mean and standard deviation of three independent experiments are shown.

Supplementary Figure S1: Nucleotide sequence alignments of structural and non-structural genes from LIMEstone 1, ϕXF1, ϕXF3, and ϕXF4. Alignments of DNA polymerase (non-structural) (**A**) and tail-spike protein (structural) (**B**) encoding genes are shown. Sequences of the genes encoding the tail-spike protein Orf158 (genome coordinates 119416-120966) and DNA polymerase Orf180 (genome coordinates 141743-142810) of LIMEstone1 (LS1) phage were used for the alignments. Multiple sequence alignments were carried out with ClustalW2 (European Bioinformatics Institute).

A

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XF1             TCTTCAGACGAAGAGTTAGAAATTGAGATTGAAAAACAAGATGAAAAAACAGCGACTCAA 60
XF3             TCTTCAGACGAAGAGTTAGAAATTGAGATTGAAAAACAAGATGAAAAAACAGCGACTCAA 60
XF4             TCTTCAGACGAAGAGTTAGAAATTGAGATTGAAAAACAAGATGAAAAAACAGCGACTCAA 60
LS1             CTGACGGACGAAGAGTTGGAAACAGAGATCCTTAACCAGGATGAGAGAACCGCCACCCAA 60
                    * *********** ****  *****    ** ** ***** * *** ** ** ***

XF1             GATACGATGCAGCAAGGGTTAAAAATCCTTATGAATGCTGGCTACGGGGCTTTGAGCAAC 120
XF3             GATACGATGCAGCAAGGGTTAAAAATCCTTATGAATGCTGGCTACGGGGCTTTGAGCAAC 120
XF4             GATACGATGCAGCAAGGGTTAAAAATCCTTATGAATGCTGGCTACGGGGCTTTGAGCAAC 120
LS1             GATACGATGCAGCAGGGGCTTAAAATCCTCATGAATGCTGGCTACGGCGCTCTGAGCAAC 120
                ************** *** * ******** ***************** *** ********

XF1             GTCTGGTTCAAAGAATACTTCAACCTCAACATCGCCGAGGCCATCACCACGTCCGGCCAG 180
XF3             GTCTGGTTCAAAGAATACTTCAACCTCAACATCGCCGAGGCCATCACCACGTCCGGCCAG 180
XF4             GTCTGGTTCAAAGAATACTTCAACCTCAACATCGCCGAGGCCATCACCACGTCCGGCCAG 180
LS1             GTCTGGTTCAAAGAGTACTTCAACCTCAACATCGCCGAAGCCATCACAACGTCCGGCCAG 180
                ************** ********************** ******** ************

XF1             CTGATCAACAAGTGGAACAAGCGTTACACCGATGATTATCTGAACAAGCTGTGTGGTACA 240
XF3             CTGATCAACAAGTGGAACAAGCGTTACACCGATGATTATCTGAACAAGCTGTGTGGTACA 240
XF4             CTGATCAACAAGTGGAACAAGCGTTACACCGATGATTATCTGAACAAGCTGTGTGGTACA 240
LS1             CTGATCAACAAGTGGAACAAGCGTTACACCGATGATTATCTGAACAAACTGTGTGGGACG 240
                ********************************************** ******** **

XF1             ACAGGACAGGACTTCGTCATCGCGGGTGATACTGACTCCAACTACATCTGCATTGAGCGT 300
XF3             ACAGGACAGGACTTCGTCATCGCGGGTGATACTGACTCCAACTACATCTGCATTGAGCGT 300
XF4             ACAGGACAGGACTTCGTCATCGCGGGTGATACTGACTCCAACTACATCTGCATTGAGCGT 300
LS1             ACAGGGCAGGACTTCGTCATTGCGGGTGACACTGACTCCAACTACATCTGCATTGAGCGC 300
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XF1             CTGGTCAAGCAGTTGTGGCCTGATGTTACGGACCACCACAAGATGGTTGATAACATCGAC 360
XF3             CTGGTCAAGCAGTTGTGGCCTGATGTTACGGACCACCACAAGATGGTTGATAACATCGAC 360
XF4             CTGGTCAAGCAGTTGTGGCCTGATGTTACGGACCACCACAAGATGGTTGATAACATCGAC 360
LS1             CTTGTCAAGCAACTGTGGCCGGATGAGACTGACCACCATAAGATGGTTGATAACATCGAT 360
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XF1             CAATGGATCAAAGACAACTACCAGCCCGAGACCAATGAGTGGGCGCAGCTTCTGTGCAAC 420
XF3             CAATGGATCAAAGACAACTACCAGCCCGAGACCAATGAGTGGGCGCAGCTTCTGTGCAAC 420
XF4             CAATGGATCAAAGACAACTACCAGCCCGAGACCAATGAGTGGGCGCAGCTTCTGTGCAAC 420
LS1             CAATGGATTAAGGACAACTATCAGCCTAAGACCAATGAGTGGGCACAGCTTCTGTGCAAC 420
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XF1             ACCATGAACGGGTTCGAGCAGCGCATGGTGTGGGAGCGTGAAGTAATTGCATCAGCCGCC 480
XF3             ACCATGAACGGGTTCGAGCAGCGCATGGTGTGGGAGCGTGAAGTAATTGCATCAGCCGCC 480
XF4             ACCATGAACGGGTTCGAGCAGCGCATGGTGTGGGAGCGTGAAGTAATTGCATCAGCCGCC 480
LS1             ACCATGAATGGGTTCGAGCAGCGCATGGTGTGGGAGCGTGAAGTAATTGCATCATCCGCC 480
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XF1             GTCTGGCGAGCCAAGAAGATGTACGCCATGGCCGTTTATGACAGTGAGGGCATCAAGTAC 540
XF3             GTCTGGCGAGCCAAGAAGATGTACGCCATGGCCGTTTATGACAGTGAGGGCATCAAGTAC 540
XF4             GTCTGGCGAGCCAAGAAGATGTACGCCATGGCCGTTTATGACAGTGAGGGCATCAAGTAC 540
LS1             GTCTGGCGAGCCAAGAAGATGTATGCGATGGCCGTGTATGACAGCGAGGGCATCAAGTAT 540
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XF1             GAGAAGTCGAAGATCAAGTTCAAAGGTCTTGAAGCCCGTAAGTCCACCACGCCCGAATGG 600
XF3             GAGAAGTCGAAGATCAAGTTCAAAGGTCTTGAAGCCCGTAAGTCCACCACGCCCGAATGG 600
XF4             GAGAAGTCGAAGATCAAGTTCAAAGGTCTTGAAGCCCGTAAGTCCACCACGCCCGAATGG 600
LS1             GAGAAGCCGAAGATTAAATTCAAAGGTCTGGAAGCCCGTAAGTCCACCACACCTGAATGG 600
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XF1             TGTCGTGACCGTCTTGTTAAGTGCTATGAGCGTATCCTGCTCGGCACCGAAGAGGAAGTG 660
XF3             TGTCGTGACCGTCTTGTTAAGTGCTATGAGCGTATCCTGCTCGGCACCGAAGAGGAAGTG 660
XF4             TGTCGTGACCGTCTTGTTAAGTGCTATGAGCGTATCCTGCTCGGCACCGAAGAGGAAGTG 660
LS1             TGCCGTGAGCGTCTTGTCAAGTGCTATGAGCGCATCCTGCTCGGCACCGAAGAGGAAGTA 660
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XF1             CAGACGCTCATCAGCGGCTACAAAGAGGAGTACATGAAGCTCTCTGTAGACGATATCGCC 720
XF3             CAGACGCTCATCAGCGGCTACAAAGAGGAGTACATGAAGCTCTCTGTAGACGATATCGCC 720
XF4             CAGACGCTCATCAGCGGCTACAAAGAGGAGTACATGAAGCTCTCTGTAGACGATATCGCC 720
LS1             CAGACGCTCATCAGCGGGTACAAAGAGGAGTACATGAAGCTGTCTGTGGATGATATCGCC 720
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XF1             AAGGCATCCGGCGTGTCCGACATAGAGAAGTGTGTGGCTGCCGACGGCTCGTTCATCTCT 780
XF3             AAGGCATCCGGCGTGTCCGACATAGAGAAGTGTGTGGCTGCCGACGGCTCGTTCATCTCT 780
XF4             AAGGCATCCGGCGTGTCCGACATAGAGAAGTGTGTGGCTGCCGACGGCTCGTTCATCTCT 780
LS1             AAGGCGTCCGGTGTGTCTGACATAGAGAAGTGTGTGGCCTCCGACGGTTCGTTCATCTCT 780
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XF1             GGTGCTCACTATGCTGCCAAGGCATGTGTGGGTTACAACCGCATGGTAGAGAAGAACGAA 840
XF3             GGTGCTCACTATGCTGCCAAGGCATGTGTGGGTTACAACCGCATGGTAGAGAAGAACGAA 840
XF4             GGTGCTCACTATGCTGCCAAGGCATGTGTGGGTTACAACCGCATGGTAGAGAAGAACGAA 840
LS1             GGCGCTCACTATGCTGCCAAGGCATGTGTGGGATACAACCGCCTTGTAGAGAAGAACGAA 840
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XF1             GACCTCGGCTTGCCAATGATTGAGTCGGGTGATAAGGTCAACATGGTACTGCTGAAGAAT 900
XF3             GACCTCGGCTTGCCAATGATTGAGTCGGGTGATAAGGTCAACATGGTACTGCTGAAGAAT 900
XF4             GACCTCGGCTTGCCAATGATTGAGTCGGGTGATAAGGTCAACATGGTACTGCTGAAGAAT 900
LS1             GATCTGGGTCTACCGATGATTGAGTCTGGCGATAAAGTGCAGATGGTATTGCTGAAACAG 900
                ** ** **  * ** *********** ** ***** **  * ****** *******  *

XF1             GGCAACCCGTTTGGCCAGAATTACTTCGCATATCCTGAGTTCTTCCCTGAGGAACTGGGT 960
XF3             GGCAACCCGTTTGGCCAGAATTACTTCGCATATCCTGAGTTCTTCCCTGAGGAACTGGGT 960
XF4             GGCAACCCGTTTGGCCAGAATTACTTCGCATATCCTGAGTTCTTCCCTGAGGAACTGGGT 960
LS1             GGCAACCCGTTTGGCCAGAACTACTTTGCATATCCTGAGTTCTTCCCTGAGGAACTGGGT 960
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XF1             ATGGGTAAATGGGTGGATTACCATACAGCCTTTGAGAAGTCCTTCATCGACCCGATTCAG 1020
XF3             ATGGGTAAATGGGTGGATTACCATACAGCCTTTGAGAAGTCCTTCATCGACCCGATTCAG 1020
XF4             ATGGGTAAATGGGTGGATTACCATACAGCCTTTGAGAAGTCCTTCATCGACCCGATTCAG 1020
LS1             ATGGGTAAATGGGTGGACTATCACACAGCCTTTGAGAAGTCCTTCATCGACCCGATTCAG 1020
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XF1             TCCATCCTTGACGTGGTCGGCTGGTCACACAAGCGCCGTGTGAACCTT 1068
XF3             TCCATCCTTGACGTGGTCGGCTGGTCACACAAGCGCCGTGTGAACCTT 1068
XF4             TCCATCCTTGACGTGGTCGGCTGGTCACACAAGCGCCGTGTGAACCTT 1068
LS1             TCTATCCTCGACGTGGTCGGCTGGTCACACAAGCGCCGTGTGAACCTT 1068
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XF1             CACGAGTGTTATGGTGTCCATTGGGAGTAATATTACGGTGCCGTTTGTTATACCGAGAGT 60
XF3             CACGAGTGTTATGGTGTCCATTGGGAGTAATATTACGGTGCCGTTTGTTATACCGAGAGT 60
XF4             CACGAGTGTTATGGTGTCCATTGGGAGTAATATTACGGTGCCGTTTGTTATACCGAGAGT 60
LS1             CACGAGTGTTATGGTGTCCATTGGGAGTAATATTACGGTGCCGTTTGTTATACCGAGAGT 60
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XF1             ACCCCCATTTCTGAGAATAGCACTAACAGTGCCACCCCCAATTGTAACGACAACAACACG 120
XF3             ACCCCCATTTCTGAGAATAGCACTAACAGTGCCACCCCCAATTGTAACGACAACAACACG 120
XF4             ACCCCCATTTCTGAGAATAGCACTAACAGTGCCACCCCCAATTGTAACGACAACAACACG 120
LS1             ACCCCCATTTCTGAGAATAGCACTAACAGTGCCACCCCCAATTGTAACGACAACAACACG 120
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XF1             CCCCGTCGTGTTTGTGACTGAAGACCCGGATGCAGGTAATCCTGGTGTGGTGATATCCAA 180
XF3             CCCCGTCGTGTTTGTGACTGAAGACCCGGATGCAGGTAATCCTGGTGTGGTGATATCCAA 180
XF4             CCCCGTCGTGTTTGTGACTGAAGACCCGGATGCAGGTAATCCTGGTGTGGTGATATCCAA 180
LS1             CCCCGTCGTGTTTGTGACTGAAGACCCGGATGCAGGTAATCCTGGTGTGGTGATATCCAA 180
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XF1             TTGATCATTCTGGAATTTTACACCCACTGCATTATTGGGATCTACCAACCCATCGACCTG 240
XF3             TTGATCATTCTGGAATTTTACACCCACTGCATTATTGGGATCTACCAACCCATCGACCTG 240
XF4             TTGATCATTCTGGAATTTTACACCCACTGCATTATTGGGATCTACCAACCCATCGACCTG 240
LS1             TTGATCATTCTGGAATTTTACACCCACTGCATTATTGGGATCTACCAACCCATCGACCTG 240
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XF1             AGAAACATTTGGATTGATTATCAAGAACCGGTTTGTTGAGCCAACTGGCGCTTGAGCCAA 300
XF3             AGAAACATTTGGATTGATTATCAAGAACCGGTTTGTTGAGCCAACTGGCGCTTGAGCCAA 300
XF4             AGAAACATTTGGATTGATTATCAAGAACCGGTTTGTTGAGCCAACTGGCGCTTGAGCCAA 300
LS1             AGAAACATTTGGATTGATTATCAAGAACCGGTTTGTTGAGCCAACTGGCGCTTGAGCCAA 300
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XF1             AAATTGTGTCCACAAACTGAACTGACAACCGATAAATGTATGTCCGCCAGAAGTCGGCAC 360
XF3             AAATTGTGTCCACAAACTGAACTGACAACCGATAAATGTATGTCCGCCAGAAGTCGGCAC 360
XF4             AAATTGTGTCCACAAACTGAACTGACAACCGATAAATGTATGTCCGCCAGAAGTCGGCAC 360
LS1             AAATTGTGTCCACAAACTGAACTGACAACCGATAAATGTATGTCCGCCAGAAGTCGGCAC 360
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XF1             TCCGTTATACAATGCGATGTTAATATTTTCAAAATCGCAACCGATAAAATTATTCGTGAA 420
XF3             TCCGTTATACAATGCGATGTTAATATTTTCAAAATCGCAACCGATAAAATTATTCGTGAA 420
XF4             TCCGTTATACAATGCGATGTTAATATTTTCAAAATCGCAACCGATAAAATTATTCGTGAA 420
LS1             TCCGTTATACAATGCGATGTTAATATTTTCAAAATCGCAACCGATAAAATTATTCGTGAA 420
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XF1             TGACACGCCATCAAGGAATGACACGCCATAGCTCGCATTTCCAAAACTACAAGACACATA 480
XF3             TGACACGCCATCAAGGAATGACACGCCATAGCTCGCATTTCCAAAACTACAAGACACATA 480
XF4             TGACACGCCATCAAGGAATGACACGCCATAGCTCGCATTTCCAAAACTACAAGACACATA 480
LS1             TGACACGCCATCAAGGAATGACACGCCATAGCTCGCATTTCCAAAACTACAAGACACATA 480
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XF1             GGTTGTAAACCCAACTTGTCGAACAACAAGCGCACGCCCCACATTAACACCAGTACCGGT 540
XF3             GGTTGTAAACCCAACTTGTCGAACAACAAGCGCACGCCCCACATTAACACCAGTACCGGT 540
XF4             GGTTGTAAACCCAACTTGTCGAACAACAAGCGCACGCCCCACATTAACACCAGTACCGGT 540
LS1             GGTTGTAAACCCAACTTGTCGAACAACAAGCGCACGCCCCACATTAACACCAGTACCGGT 540
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XF1             TGCATAACAATTGGCGCGCACATTAATTAACGAGCATTGGACACCGTATTCTAAACTCAG 600
XF3             TGCATAACAATTGGCGCGCACATTAATTAACGAGCATTGGACACCGTATTCTAAACTCAG 600
XF4             TGCATAACAATTGGCGCGCACATTAATTAACGAGCATTGGACACCGTATTCTAAACTCAG 600
LS1             TGCATAACAATTGGCGCGCACATTAATTAACGAGCATTGGACACCGTATTCTAAACTCAG 600
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XF1             GGCCACAACATTGTTATCACCAATGCTGCTGCTGTTTAGAAACGCCAAATCCTCAAGGCG 660
XF3             GGCCACAACATTGTTATCACCAATGCTGCTGCTGTTTAGAAACGCCAAATCCTCAAGGCG 660
XF4             GGCCACAACATTGTTATCACCAATGCTGCTGCTGTTTAGAAACGCCAAATCCTCAAGGCG 660
LS1             GGCCACAACATTGTTATCACCAATGCTGCTGCTGTTTAGAAACGCCAAATCCTCAAGGCG 660
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XF1             TGCCACATTCAAAGGATCCACAAAATTAGTGTTCCCGATTTGACACAAGATCCCAGCGTG 720
XF3             TGCCACATTCAAAGGATCCACAAAATTAGTGTTCCCGATTTGACACAAGATCCCAGCGTG 720
XF4             TGCCACATTCAAAGGATCCACAAAATTAGTGTTCCCGATTTGACACAAGATCCCAGCGTG 720
LS1             TGCCACATTCAAAGGATCCACAAAATTAGTGTTCCCGATTTGACACAAGATCCCAGCGTG 720
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XF1             TGATGAACGAACACTCATCCCTTCCCAAACAAAATCATACCAATCTGCGGTCGACTTGAT 780
XF3             TGATGAACGAACACTCATCCCTTCCCAAACAAAATCATACCAATCTGCGGTCGACTTGAT 780
XF4             TGATGAACGAACACTCATCCCTTCCCAAACAAAATCATACCAATCTGCGGTCGACTTGAT 780
LS1             TGATGAACGAACACTCATCCCTTCCCAAACAAAATCATACCAATCTGCGGTCGACTTGAT 780
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XF1             AATTAATTGAGTAACACCTGCAGCTGCGTTAGGAAACCTCAACTCTGTTCTGCTCACGCC 840
XF3             AATTAATTGAGTAACACCTGCAGCTGCGTTAGGAAACCTCAACTCTGTTCTGCTCACGCC 840
XF4             AATTAATTGAGTAACACCTGCAGCTGCGTTAGGAAACCTCAACTCTGTTCTGCTCACGCC 840
LS1             AATTAATTGAGTAACACCTGCAGCTGCGTTAGGAAACCTCAACTCTGTTCTGCTCACGCC 840
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XF1             CGCACCATATATTTTTATACCAGGCGCATCCATGTTTAATGTAACGGGGCTGGAGAAGTT 900
XF3             CGCACCATATATTTTTATACCAGGCGCATCCATGTTTAATGTAACGGGGCTGGAGAAGTT 900
XF4             CGCACCATATATTTTTATACCAGGCGCATCCATGTTTAATGTAACGGGGCTGGAGAAGTT 900
LS1             CGCACCATATATTTTTATACCAGGCGCATCCATGTTTAATGTAACGGGGCTGGAGAAGTT 900
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XF1             ATACACATGGGGAAGAAATTTTATTGGACGACCACTTGATAATGACTCGGTTAACACACG 960
XF3             ATACACATGGGGAAGAAATTTTATTGGACGACCACTTGATAATGACTCGGTTAACACACG 960
XF4             ATACACATGGGGAAGAAATTTTATTGGACGACCACTTGATAATGACTCGGTTAACACACG 960
LS1             ATACACATGGGGAAGAAATTTTATTGGACGACCACTTGATAATGACTCGGTTAACACACG 960
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XF1             TTGTATTGCATTGTCATAAGTTGTTTCTCCAGAAAATAAATAATCGTCTATAACGAGATC 1020
XF3             TTGTATTGCATTGTCATAAGTTGTTTCTCCAGAAAATAAATAATCGTCTATAACGAGATC 1020
XF4             TTGTATTGCATTGTCATAAGTTGTTTCTCCAGAAAATAAATAATCGTCTATAACGAGATC 1020
LS1             TTGTATTGCATTGTCATAAGTTGTTTCTCCAGAAAATAAATAATCGTCTATAACGAGATC 1020
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XF1             GGCGTGGTTATTAAGTTTTGTGGTGCTTATTTTAAGAGTAGATAAATCATTTTGCACGTT 1080
XF3             GGCGTGGTTATTAAGTTTTGTGGTGCTTATTTTAAGAGTAGATAAATCATTTTGCACGTT 1080
XF4             GGCGTGGTTATTAAGTTTTGTGGTGCTTATTTTAAGAGTAGATAAATCATTTTGCACGTT 1080
LS1             GGCGTGGTTATTAAGTTTTGTGGTGCTTATTTTAAGAGTAGATAAATCATTTTGCACGTT 1080
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XF1             TCCATCCGCTGAACCGATAACACCAGCGCCTGCCGAACTGAACAAATTTTCTCTCAAAGA 1140
XF3             TCCATCCGCTGAACCGATAACACCAGCGCCTGCCGAACTGAACAAATTTTCTCTCAAAGA 1140
XF4             TCCATCCGCTGAACCGATAACACCAGCGCCTGCCGAACTGAACAAATTTTCTCTCAAAGA 1140
LS1             TCCATCCGCTGAACCGATAACACCAGCGCCTGCCGAACTGAACAAATTTTCTCTCAAAGA 1140
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XF1             AGGATCATAAATTTTTATCCAAGTGGTAGGAGAAATACCACCACTTGCCTCTGGTGAAGA 1200
XF3             AGGATCATAAATTTTTATCCAAGTGGTAGGAGAAATACCACCACTTGCCTCTGGTGAAGA 1200
XF4             AGGATCATAAATTTTTATCCAAGTGGTAGGAGAAATACCACCACTTGCCTCTGGTGAAGA 1200
LS1             AGGATCATAAATTTTTATCCAAGTGGTAGGAGAAATACCACCACTTGCCTCTGGTGAAGA 1200
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XF1             ACCAAGAGGTACAATTTTAGGGAATGTGCCACCCCATCGATATTTACCATCATCGTGGGT 1260
XF3             ACCAAGAGGTACAATTTTAGGGAATGTGCCACCCCATCGATATTTACCATCATCGTGGGT 1260
XF4             ACCAAGAGGTACAATTTTAGGGAATGTGCCACCCCATCGATATTTACCATCATCGTGGGT 1260
LS1             ACCAAGAGGTACAATTTTAGGGAATGTGCCACCCCATCGATATTTACCATCATCGTGGGT 1260
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XF1             GAGTAATTCATTTTTTACGCCAAGTGTGCCACCAACTGTGAATGTGCCACCAACTGTGAC 1320
XF3             GAGTAATTCATTTTTTACGCCAAGTGTGCCACCAACTGTGAATGTGCCACCAACTGTGAC 1320
XF4             GAGTAATTCATTTTTTACGCCAAGTGTGCCACCAACTGTGAATGTGCCACCAACTGTGAC 1320
LS1             GAGTAATTCATTTTTTACGCCAAGTGTGCCACCAACTGTGAATGTGCCACCAACTGTGAC 1320
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XF1             AAATTCACCACGCAAAACAGCCAGTGCCCCCAAATCGACAGTCCCCCCATTATGAGTGAG 1380
XF3             AAATTCACCACGCAAAACAGCCAGTGCCCCCAAATCGACAGTCCCCCCATTATGAGTGAG 1380
XF4             AAATTCACCACGCAAAACAGCCAGTGCCCCCAAATCGACAGTCCCCCCATTATGAGTGAG 1380
LS1             AAATTCACCACGCAAAACAGCCAGTGCCCCCAAATCGACAGTCCCCCCATTATGAGTGAG 1380
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XF1             AATGGCATTTGTTAAGGAGATGAAGACGGAGTCGGAAGGTAAGTCGGAAGGTAAAGCATA 1440
XF3             AATGGCATTTGTTAAGGAGATGAAGACGGAGTCGGAAGGTAAGTCGGAAGGTAAAGCATA 1440
XF4             AATGGCATTTGTTAAGGAGATGAAGACGGAGTCGGAAGGTAAGTCGGAAGGTAAAGCATA 1440
LS1             AATGGCATTTGTTAAGGAGATGAAGACGGAGTCGGAAGGTAAGTCGGAAGGTAAAGCATA 1440
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XF1             AGAACGCTCTGTGTTCTTATCGTAGATTACTTTATACCCAGATAAAGATACGCCCGCTTT 1500
XF3             AGAACGCTCTGTGTTCTTATCGTAGATTACTTTATACCCAGATAAAGATACGCCCGCTTT 1500
XF4             AGAACGCTCTGTGTTCTTATCGTAGATTACTTTATACCCAGATAAAGATACGCCCGCTTT 1500
LS1             AGAACGCTCTGTGTTCTTATCGTAGATTACTTTATACCCAGATAAAGATACGCCCGCTTT 1500
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XF1             GGCATACAATACCTCAGACTTCTTACACCCGAATTTGCGGGCGATGGAATC 1551
XF3             GGCATACAATACCTCAGACTTCTTACACCCGAATTTGCGGGCGATGGAATC 1551
XF4             GGCATACAATACCTCAGACTTCTTACACCCGAATTTGCGGGCGATGGAATC 1551
LS1             GGCATACAATACCTCAGACTTCTTACACCCGAATTTGCGGGCGATGGAATC 1551
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Materials and methods

Bacterial strains, plasmids, phages, culture media and growth conditions. Bacterial strains and plasmids used in this study are listed in Supplementary Tables 2. *Salmonella, Dickeya* and their derivative strains were routinely grown at 30 ºC in Luria Broth (LB; 5 g yeast extract l^{-1},10 g Bacto tryptone l^{-1} and 5 g NaCl l^{-1}), Potato Dextrose (24 g potato dextrose broth l^{-1}) or minimal medium (0.1%, w/v, $(NH_4)_2SO_4$, 0.41 mM $MgSO_4$, 0.2% (w/v) glucose, 40 mM K_2HPO_4, 14.7 mM KH_2PO_4, pH 6.9–7.1). *S.* Typhi BRD948 LB broth was supplemented with a mixture of aromatic amino acids (0.01 g para-aminobenzoic acid l^{-1}, 0.04 g tryptophan l^{-1}, 0.04 g phenylalanine l^{-1} and 0.01 g dihydrobenzoic acid l^{-1}) and 0.04 g tyrosine l^{-1}, as described previously (Bishop *et al*., 2008). *Escherichia coli* strains were grown at 37 °C in LB. Media for propagation of *E. coli* β2163 were supplemented with 300 µM 2,6-diaminopimelic acid (DAPA). When appropriate, antibiotics were used at the following final concentrations (in µg ml^{-1}): kanamycin, 25 (*E. coli* strains) and 50 (*Dickeya* strains); streptomycin, 50; chloramphenicol, 25; tetracycline, 10. Phages were stored at 4 ºC in phage buffer (10 mM Tris-HCl pH 7.4, 10 mM $MgSO_4$, 0.01% w/v gelatine) over a few drops of $NaHCO_3$-saturated chloroform.

Isolation of novel bacteriophages and phage lysate preparation. Treated sewage effluent was collected from Milton (Cambridge, United Kingdom). To prepare phage enrichment, a 10 ml sample of the effluent was filter sterilized and added to 10 ml 2X LB broth. Then, 500 µL of an overnight culture of *Dickeya solani* MK10 was added to 250 ml flasks and incubated at 30 ºC with shaking at 225 rpm. After overnight incubation, 1 ml of the sample enrichment was mixed with 100 µL of chloroform and vortexed vigorously for 1 min to kill bacteria. The sample was centrifuge at 16,000 x g for 1 min and 100 µL dilution series of the sterilized supernatant was mixed with 200 µL of a *D. solani* MK10 overnight culture and 4 mL of top LB-agar (LBA, 0.35% w/v agar) and poured as an overlay onto LBA plates (1.5% w/v agar). Plates were incubated overnight at 30 ºC and single phage plaques were picked with a sterile toothpick into 0.2 ml phage buffer and shaken with 20 µL of chloroform to kill any bacteria. Phages obtained were plaque-purified three times. High-titre phage lysates were then obtained as described Petty *et al.* (2006). Phages were titrated by serial dilutions in phage buffer and the phage titre determined in plaque-forming units (p.f.u.) per millilitre. Phages ϕXF1, ϕXF3, ϕXF4 and ϕXF28 were isolated from four independent sewage effluent samples from Milton (Cambridge, UK).

Electron microscopy

High-titre lysates for transmission electron microscopy were obtained as described by Petty *et al.* (2006) using 0.35% (w/v) LB agarose instead of 0.35% (w/v) LB agar overlays. Phage samples were negatively stained by placing the grids in 25 µl drops of 2% phosphotungstic acid for 1 min. Phages were examined by transmission electron microscopy, in the Multi-Imaging Centre (Department of Physiology, Development and Neuroscience, University of Cambridge) using a FEI Tecnai G2 transmission electron microscope (FEI, Oregon, USA). The accelerating voltage was 120.0 kV and images were captured with an AMT XR60B digital camera running Deben software.

Transposon mutagenesis and isolation of auxotrophic, oocydin A negative and protease negative mutants.

Random transposon mutagenesis of *Dickeya solani* MK10 and MK16 using Tn-KRCPN1 and mini-Tn*5*Sm/Sp were performed as follows. In a biparental conjugal mating, 500 µl of overnight cultures *of E. coli* β2163 and *D. solani* were mixed, collected by centrifugation, resuspended in 30 µl of fresh LB, and spotted on an LB agar plate supplemented with 300 µM DAPA. After overnight incubation at 30 °C, cells were scraped off the plate and resuspended in 1 ml of LB. Serial dilutions were plated on LB agar medium containing the appropriate antibiotic, kanamycin and streptomycin for Tn-KRCPN1 and mini-Tn*5*Sm/Sp, respectively. 2,6-Diaminopimelic acid was not added to the LB agar medium, to allow counterselection of the *E. coli* donor. Auxotrophic, oocydin A negative and protease negative mutants were identified for their inability to grow on M9 glucose minimal medium agar, inhibit *Pythium ultimum* growth in potato dextrose agar and produce haloes when plated onto skimmed milk agar (nutrient broth agar, 10 g of Marvel skimmed milk powder per liter), respectively. Identification of the transposon insertion sites in mutants was determined using random primed PCR following the method described previously (Fineran *et al*., 2005) and using primers described in supplemental Table S3.

Transduction assays

Phage lysates were prepared on bacterial strains carrying the desired mutation or plasmid. For the transduction assays, an appropriate volume of a high-titre lysate was added to an overnight culture of the recipient strain to give the desired m.o.i. The mixture was incubated at 30 ºC (*Dickeya* and *Salmonella*) or 37 ºC (*E. coli*) for 1 h, pelleted by centrifugation (4.000 g for 10 min at 4 ºC), washed twice with LB to remove remaining phage and 100 µL aliquots of the phage-host mixture were spread on LBA plates containing the appropriate antibiotic. The drug-resistant transductants were re-streaked three times to reduce any bacteriophage carry-over. The number of

transductants was determined by co-inheritance of the antibiotic resistance and a secondary phenotype of either anti-*Pythium* activities, protease production or auxotrophy. The transposon insertion sites in the final transductants were confirmed by random primed PCR and sequencing, as described above. In the case of transduction of plasmids, the presence of the plasmids was confirmed by colony PCR in 10 of the final transductants per experiment, using primers listed in supplementary table S3. For the transduction assays, the protocol was optimized for incubation time, temperature, multiplicity of infection (m.o.i.) and number of bacterial cells. During the transduction assays, routine controls for spontaneous resistance to antibiotics were determined by spreading 100 µl of the overnight culture onto LBA plates containing the relevant antibiotic. A 100 µl volume of the high-titre lysate was also spread on non-LBA plates to confirm lysate sterility. Transduction efficiency was defined as the number of transductants obtained per p.f.u.

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