SUPPLEMENTARY MATERIAL

Dual control of lysogeny and phage defense by a phosphorylation-based toxin/antitoxin system

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Tables S1, S2, S4, S5, S8 and S9

References

Legends for the Tables S3, S6 and S7 which are uploaded as separate excel files:

Table S3. Published articles with sequencing raw data deposited in the NCBI SRA database. Sequencing reads were mapped to the reference genome of MPAO1 (CP079712). Average depths were calculated of Pf4 and Pf6 genome regions as well as the upstream and downstream 1000 bp regions flanking the prophage genomes. Y indicates yes and N indicates no.

Table S6. Distribution of KKP modules in bacteria. Data were retrieved from the IMG/G database. Gene IDs were indicated.

Table S7. List of phosphorylation sites in PAO1 genome that are modified by KK_{MP} or KKP_{MP} identified by phosphoproteome.

Table S1. **List of the Pf4 and Pf6 prophage genes in MPAO1 and their locations in PAO1 genome**. The core prophage genes are highlighted in bold letters.

Pf4 in MPAO1 (12416 bp)						Pf6 in MPAO1 (12148 bp)					Nucleotide		Protein	
Locus tag (MPAO1)	**Locus tag (PAO1)**	**Gene name**	**Start**	**Stop**	**Strand**	**Locus tag (MPAO1)**	**Gene name**	**Start**	**Stop**	**Strand**	**Coverage**	**Identity**	**Coverage**	**Identity**
		attR	4717479	4717505	-									
MP_4487	PA0729	*pfiT*	4717628	4717975	-									
MP_4488	PA0728.1	*pfiA*	4717985	4718236	-		*attR*	5241438	5241519					
MP_4489	PA0728	*intF4*	4718450	4719433	-	MP_4975	*intF6*	5241680	5242681	-	0	0	98%	40.66%
MP_4490	**PA0727**	***repF4***	**4719433**	**4720725**	**-**	**MP_4976**	***repF6***	**5242678**	**5243889**	**-**	**96%**	**92.30%**	**93%**	**95.29%**
MP_4491	**PA0726.1**		**4720857**	**4720958**	**-**	**MP_4977**		**5244102**	**5244203**	**-**	**100%**	**97.06%**	**100%**	**93.94%**
MP_4492	**PA0726**		**4720955**	**4722229**	**-**	**MP_4978**		**5244200**	**5245474**	**-**	**100%**	**98.27%**	**100%**	**97.88%**
MP_4493	**PA0725**	***gVI***	**4722233**	**4722589**	**-**	**MP_4979**	***gVI***	**5245478**	**5245834**	**-**	**100%**	**99.16%**	**100%**	**100%**
MP_4494	**PA0724**	***gIII***	**4722594**	**4723856**	**-**	**MP_4980**	***gIII***	**5245839**	**5247098**	**-**	**100%**	**98.10%**	**100%**	**98.81%**
MP_4495	**PA0723**	***gVIII***	**4723992**	**4724240**	**-**	**MP_4981**	***gVIII***	**5247234**	**5247482**	**-**	**100%**	**99.20%**	**100%**	**100%**
MP_4496	**PA0722**	***gIX***	**4724253**	**4724504**	**-**	**MP_4982**	***gIX***	**5247495**	**5247746**	**-**	**100%**	**100%**	**100%**	**100%**
MP_4497	**PA0721**	***gVII***	**4724517**	**4724609**	**-**	**MP_4983**	***gVII***	**5247759**	**5247851**	**-**	**100%**	**97.85%**	**100%**	**96.67%**
MP_4498	**PA0720**		**4724626**	**4725060**	**-**	**MP_4984**		**5247868**	**5248302**	**-**	**100%**	**96.09%**	**100%**	**97.92%**
MP_4499	**PA0719**		**4725195**	**4725572**	**-**	**MP_4985**		**5248469**	**5248813**	**-**	**99%**	**97.38%**	**79%**	**98.99%**
MP_4500	**PA0718**		**4725576**	**4725866**	**-**	**MP_4986**		**5248817**	**5249107**	**-**	**100%**	**96.91%**	**100%**	**96.88%**
MP_4501	**PA0717**		**4725870**	**4726082**	**-**	**MP_4987**		**5249111**	**5249239**	**-**	**60%**	**97.67%**	**60%**	**97.62%**
MP_4502	PA0716.2	*xisF4*	4726084	4726299	-	MP_4988	*xisF6*	5249319	5249549	-	0	0	49%	34.29%
MP_4503	PA0716.1	*pf4r*	4726418	4726684	+	MP_4989	*pf6r*	5249717	5249986	+	0	0	100%	50.56%
MP_4504	PA0716		4726973	4728298	-	MP_4990	*pfpC*	5250121	5251218	+				
MP_4505	PA0715		4728301	4729257	-	MP_4991	*pfkB*	5251221	5252270	+				
MP_4506	PA0714.1	*phrD*	4729635	4729707	-	MP_4992	*pfkA*	5252267	5253340	+				
		attL	4729868	4729894	-		*attL*	5253510	5253589					

Table S2. The presence of Pf4 and Pf6 loci in the selected *P. aeruginosa* strains were analyzed by BLASTN. The four genomes used in Fig. 2a are shown in blue fonts and two ATCC strains were shown in bold fonts. In addition, the strains with determined sources summarized by C. E., Chandler et al.[1] were also analyzed, and the assembly of these strains were downloaded from NCBI under BioProject accession number PRJNA490649. Y indicates yes and N indicates no.

GenBank/Assembly ID	Strain name	Pf4	Pf6	Source	Date acquired	PubMed ID	Date of publish
MPAO1 sublines							
CP079712	**MPAO1**	**Y**	**Y**	**McDermott, University of Washington**	**07/2020**	**this study**	
CP027857	**MPAO1 (C. Manoil)**	**Y**	**Y**	**C. Manoil, University of Washington**	**2017**	**33127897**	2020 Oct 30
GCA_003957075	MPAO-1 (C. Manoil)	Y	Y	C. Manoil, University of Washington	01/2003	30530517	2019 Feb 11
GCA_003957195	MPAO-1 (C. Manoil)	Y	Y	C. Manoil, University of Washington	08/2008	30530517	2019 Feb 11
GCA_003957175	PAO-1 (B. Iglewski)	Y	Y	E.P. Greenberg, University of Washington	10/2000	30530517	2019 Feb 11
CP050052	PAO1 (B. Iglewski)	Y	Y	E. P. Greenberg, University of Washington	04/2019	unpublished	
GCF_003957105	H103 PAO-1 AK957	Y	Y	R. Hancock, University of British Columbia	02/2000	30530517	2019 Feb 11
GCA_003957205	PAO-1 (B. Holloway)	Y	Y	D. Ohman, Virginia Commonwealth University	05/2001	30530517	2019 Feb 11
GCA_003957095	PAO-1 V	Y	Y	J. Goldberg, University of Virginia	07/2003	30530517	2019 Feb 11
GCA_003957085	PAO-1	Y	Y	H. Nikaido, University of California, Berkeley	08/2003	30530517	2019 Feb 11
GCA_003957115	PAO-1	Y	Y	A. Prince, Columbia University	11/2003	30530517	2019 Feb 11
CP050054/CP050053	PAO1	Y	Y	Y. Liu, South China Agricultural University	04/2018	unpublished	
CP053028	PAO1	Y	Y	S.P. Diggle, Georgia Institute of Technology	01/2014	32341475	2020 Mar 23
not available	PAO1	Y	Y	Scott A. Rice, Nanyang Technological University	not available	34452479	2021 Aug 15
LN871187	PAO1_Orsay1	Y	Y	Pourcel, Institut de Genetique et Microbiologie	not available	unpublished	
CP032126	PAO1161	Y	Y	A. Kawalek, Institute for Biochemistry and Biophysics PAS	11/2017	31906858	2020 Jan 6
NZ_CP017149	**PAO-1C (ATCC 15692)**	**Y**	**Y**	**ATCC (deposited by BW Holloway)**	**not available**	unpublished	
CP041008	**PAO1 (ATCC BAA-47)**	**Y**	**Y**	**ATCC (deposited by HW Ackermann)**	**not available**	unpublished	
PAO1 sublines							
CP085082	**PAO1**	**Y**	**N**	**J.J. Mekalanos, Harvard Medical School**	**10/2020**	**this study**	
AE004091	**PAO1**	**Y**	**N**	**P. Phibbs, University of Georgia**	**not available**	**10984043**	**2000 Aug 31**
GCA_003957185	PAO-1	Y	N	J. Burns, University of Washington	02/2000	30530517	2019 Feb 11
CP006832/CP006831	PAO1	Y	N	H.W.D., Yu, Marshall University	not available	24336371	2013 Dec 12
CP006705	PAO1 (PA0581)	Y	N	H.W.D., Yu, Marshall University	not available	24115549	2013 Oct 10
CP053110 to CP053119	PAO1	Y	N	S. Fong, University of Adelaide	12/2017	unpublished	
CP047061 to CP047068	PAO1	Y	N	Balint Csorgo, UCSF	not available	unpublished	
CP032540/CP032541	PAO1	Y	N	Progenesis Technologies, LLC	09/2014	unpublished	
CP034908	PA0750	Y	N	H.P. Schweizer, Colorado State University	2005	17005832	2006 Oct

Table S4. **RNA-seq reads of each Pf4 and Pf6 genes in the biofilm cells and in the planktonic cells of MPAO1 strain.** Three replicates were used and shown. NA indicates not available. FC, CPM and FDR indicate fold change, counts per million and false discovery rate, respectively.

Locus tag (MPAO1)	Gene product	Planktonic cells			Biofilm cells			LogFC	LogCPM	FDR
		# 1	# 2	# 3	# 1	# 2	# 3			
Pf4 prophage										
MP_4487	PfiT	59.0	69.9	45.6	583.1	272.6	468.9	3.0	6.4	5.29E-36
MP_4488	PfiA	60.2	47.0	63.6	539.2	302.2	369.8	2.9	5.9	1.55E-24
MP_4489	IntF4	1.7	4.0	2.3	459.7	103.6	155.5	6.5	6.8	2.72E-44
MP_4490	RepF4	2.9	3.8	3.6	892.8	196.0	316.5	7.1	8.2	6.83E-54
MP_4491	Hypothetical	0.0	0.0	0.0	41.5	1.8	9.3	6.3	0.1	0.00088
MP_4492	Hypothetical	1.0	0.6	1.0	576.3	122.4	177.4	8.3	7.5	8.38E-53
MP_4493	pVI	0.0	0.9	0.0	23.7	3.0	0.5	4.7	0.8	0.001108
MP_4494	pIII	0.3	1.2	1.3	1196.3	249.6	426.0	9.4	8.5	4.14E-62
MP_4495	pVIII	1.3	4.3	6.4	11773.3	1518.9	1889.6	10.2	9.2	2.20E-35
MP_4496	pIX	0.0	0.0	0.0	0.0	0.0	0.0	NA	NA	NA
MP_4497	pVII	0.0	0.0	0.0	123.4	15.5	34.5	7.9	1.4	1.12E-08
MP_4498	Hypothetical	8.3	23.8	9.2	20618.8	4612.1	8445.6	9.7	11.2	5.79E-77
MP_4499	Hypothetical	8.6	9.7	0.9	9635.9	2351.2	4761.3	9.8	10.0	1.07E-71
MP_4500	Hypothetical	3.4	4.7	8.8	5423.0	2356.9	3570.8	9.5	9.1	8.37-126
MP_4501	Hypothetical	0.8	0.7	3.0	1681.4	588.2	744.9	9.4	6.7	7.87E-83
MP_4502	XisF4	2.3	1.4	2.2	5079.5	950.1	1656.8	10.3	8.0	1.58E-62
MP_4503	Pf4r	24.4	23.9	18.6	48.3	58.0	110.9	1.9	3.7	1.36E-06
MP_4504	Hypothetical	48.2	38.2	32.7	39.9	68.0	94.3	0.99	6.2	0.01418
MP_4505	Hypothetical	48.4	22.9	23.4	33.9	60.2	91.3	1.2	5.6	0.01255
MP_4506	PhrD	464.6	878.3	875.3	391.6	254.0	434.2	-0.92	5.3	0.00379
Pf6 prophage										
MP_4975	IntF6	4.9	2.3	3.8	61.9	93.2	142.0	4.9	5.8	9.62E-27
MP_4976	RepF6	3.2	2.5	2.1	164.9	237.5	393.0	6.9	7.5	4.69E-49
MP_4977	Hypothetical	0.0	0.0	0.0	63.2	88.2	160.9	9.1	2.5	1.01E-18
MP_4978	Hypothetical	0.1	0.6	0.5	70.1	135.1	200.5	8.6	6.6	1.07E-44
MP_4979	pVI	0.0	0.0	0.0	10.7	9.1	9.5	7.5	1.0	2.15E-09

MP_4980	pIII	1.0	0.5	1.0	189.8	335.9	525.1	8.9	7.9	1.92E-52
MP_4981	pVIII	0.0	1.2	2.6	3837.9	2455.9	2303.2	11.2	8.5	8.44E-126
MP_4982	pIX	0.0	0.0	0.0	0.0	0.0	0.0	NA	NA	NA
MP_4983	pVII	0.0	0.0	0.0	10.8	7.7	24.3	6.0	-0.1	0.000402
MP_4984	Hypothetical	4.1	6.3	4.4	4002.7	4457.3	6895.2	10.2	10.2	1.91E-110
MP_4985	Hypothetical	3.8	4.4	0.9	4505.9	4766.5	8160.2	11.1	10.1	4.38E-108
MP_4986	Hypothetical	0.6	1.0	2.2	2020.1	2039.6	3080.0	11.0	8.5	8.22E-108
MP_4987	Hypothetical	2.5	0.0	2.5	1373.3	1618.7	1675.9	10.0	6.8	4.59E-81
MP_4988	XisF6	3.5	4.6	1.4	4576.2	6590.4	10843.9	11.4	9.9	1.21E-85
MP_4989	Pf6r	186.0	146.3	99.1	1427.1	462.0	666.6	2.6	7.0	8.03E-17
MP_4990	PfpC	93.1	67.4	46.4	468.6	209.2	306.5	2.3	7.8	1.02E-16
MP_4991	PfkB	162.3	109.5	76.3	2198.4	953.6	1415.6	3.8	9.7	3.64E-34
MP_4992	PfkA	731.0	674.1	431.5	933.8	319.8	466.5	-0.02	9.3	0.97

Table S5. List of proteins that are modified by PfkA kinase identified by phosphoproteome. The fold changes indicated the phosphorylation levels of proteins controlled by PfkA via pHERD20T-*pfkA* overproduction versus those in cells harboring pHERD20T vector. Two replicates were used, and those proteins with fold changes > 2.5 and coefficient of variation (CV) < 0.1) were selected.

Locus tag (MPAO1)	Locus tag (PAO1)	Protein	Position	Fold change	CV value	Description
MP_2627	PA2480		391T	4.554	0.006	Signal transduction histidine kinase
MP_4036	PA1155	NrdB	408T	3.968	0.008	Ribonucleotide-diphosphate reductase subunit beta
MP_618	PA0577	DnaG	527T	3.816	0.088	DNA primase
MP_1549	PA3481	ApbC	353S	3.777	0.022	ATPases involved in chromosome partitioning
MP_3583	PA1585	SucA	62T	3.616	0.072	Dehydrogenase (E1) component related enzymes
MP_82	PA0074	PpkA	270T	3.261	0.087	Ser/Thr kinase
MP_723	PA4274	RplK	71T	3.101	0.046	Ribosomal protein L11
MP_5588	PA5239	Rho	84S	3.010	0.060	Transcription termination factor
MP_2467	PA2629	PurB	296S	2.975	0.088	Adenylosuccinate lyase
MP_2427	**PA2667**	**MvaU**	**65T/67S**	**2.892**	**0.019**	**H-NS family protein**
MP_5084	PA4759	DapB	207T	2.640	0.069	Dihydrodipicolinate reductase
MP_4426	PA0787		79S	2.624	0.089	Predicted ATPase
MP_5631	PA5279		49S	2.609	0.085	Uncharacterized protein conserved in bacteria
MP_5697	PA5343		246S	2.604	0.026	Nucleoside-diphosphate-sugar epimerases
MP_5797	PA5435	PycB	462T	2.517	0.022	Pyruvate/oxaloacetate carboxyltransferase
MP_1500	PA3529		198S	0.229	0.049	Peroxidase
MP_1153	PA3861	RhlB	38S	0.129	0.044	ATP-dependent RNA helicase RhlB
MP_180	PA0170		68T	0.017	0.083	DUF1987 domain-containing protein

Table S8. Bacterial strains and plasmids used in this study. R indicates resistance, Gm indicates gentamycin, Amp indicates ampicillin, MP indicates MPAO1 strain. KKP indicates the *pfkA-pfkB-pfpC* cascade.

	Description	**Source**
Strains		
PAO1	wild-type	[2]
MPAO1	wild-type	[3]
MP-ΔPf4	whole Pf4 prophage removed from MPAO1 host chromosome	[3]
MP-ΔPf6core	the core genes from MP-4976 to MP_4987 removed from MPAO1 host chromosome	this study
MP-ΔPf4ΔPf6core	whole Pf4 prophage removed from MP-ΔPf6core host chromosome	this study
pVIII::GFP	*gVIII* gene encoding Pf4 major coat protein pVIII in-frame fused with *gfp* gene in PAO1 host chromosome	this study
MP-pVIII::GFP	*gVIII* gene encoding Pf4 major coat protein pVIII in-frame fused with *gfp* gene in MPAO1 host chromosome	this study
MP-Δ*mvaU*Δ*mvaT*	*mvaT* and *mvaU* double deletion mutant derived from MPAO1	[3]
PAO1::$pilC_{MP}$	*pilC* gene from MPAO1 was integrated into Δ*pilC* host chromosome	this study
PAO1::$pilC_{MP}$::KKP_{MP}	the KKP_{MP} cascades were integrated into PAO1::$pilC_{MP}$ host chromosome	this study
PAO1::KKP_{MP}	the KKP_{MP} cascades were integrated into PAO1 host chromosome	this study
PAO1::$pilC_{MP}$::$K^{GFI}KP_{MP}$	the mutant KKP_{MP} cascade (the 307th -309th aa codon GGATTCATT in *pfkA* was mutated to GACTATGCA) were integrated into PAO1::$pilC_{MP}$ host chromosome	this study
WM3064	*thrB*1004 *pro thi rpsL hsdS lacZ*ΔM15 RP4-1360) Δ(*araBAD*)567 Δ*dapA*1341::[*erm pir(*wt)]	W. Metcalf, UIUC
MG655	K-12 F^- *lambda*$^-$ *ilvG- rfb-50 rph-1*	lab stored
Plasmids		
pEX18Ap	Ap^R, $oriT^+$, $sacB^+$, gene replacement vector	[4]
pEX18Gm	Gm^R, $oriT^+$, $sacB^+$, gene replacement vector	[4]
pFLP2	Ap^R, Flp recombinase-expressing plasmid	[4]
pPS856	Ap^R, Gm^R; for amplifying gentamycin resistance cassette	[4]
pEX18Gm-ΔPf6core-up-down	Gm^R, Ap^R, for deleting Pf6core region	this study
pEX18Gm-up-pVIII::GFP-down	Gm^R, Ap^R, for Pf4 *gVIII* in-frame fused with *gfp* gene in MPAO1 host chromosome	this study
pEX18Gm-*pilC*-up-down	Gm^R, Ap^R, for deleting *pilC* in PAO1 host chromosome	this study
pEX18Gm-up-$pilC_{MP}$-down	Gm^R, Ap^R, for integration of $pilC_{MP}$ gene from MPAO1 into Δ*pilC* host chromosome	this study
pEX18Gm-up-Gm-KKP-down	Gm^R, Ap^R, for integration of KKP_{MP} cascade from MPAO1 into PAO1::$pilC_{MP}$ host chromosome	this study
pEX18Gm-up-Gm-K^{GFI}KP-down	Gm^R, Ap^R, for integration of $K^{GFI}KP_{MP}$ cascade mutant into PAO1:: $pilC_{MP}$ host chromosome	this study
pHERD20T	Ap^R, expression vector with araC-P_{BAD} promoter	[5]
pHERD20T-*mvaU*	Ap^R, *mvaU* in pHERD20T NcoI/HindIII	this study
pHERD20T-$mvaU^{S2A}$	Ap^R, the second aa codon TCC in *mvaU* was mutated to GCC in pHERD20T-*mvaU*	this study

pHERD20T-*mvaU*^{S2D}	Ap^R, the second aa codon TCC in *mvaU* was mutated to GAC in pHERD20T-*mvaU*	this study
pHERD20T-*mvaU*^{S26A}	Ap^R, the 26th aa codon AGC in *mvaU* was mutated to GCC in pHERD20T-*mvaU*	this study
pHERD20T-*mvaU*^{S26D}	Ap^R, the 26th aa codon AGC in *mvaU* was mutated to GAC in pHERD20T-*mvaU*	this study
pHERD20T-*mvaU*^{T50A}	Ap^R, the 50th aa codon ACC in *mvaU* was mutated to GCC in pHERD20T-*mvaU*	this study
pHERD20T-*mvaU*^{T50D}	Ap^R, the 50th aa codon ACC in *mvaU* was mutated to GAC in pHERD20T-*mvaU*	this study
pHERD20T-*mvaU*^{T65A}	Ap^R, the 65th aa codon ACC in *mvaU* was mutated to GCC in pHERD20T-*mvaU*	this study
pHERD20T-*mvaU*^{T65D}	Ap^R, the 65th aa codon ACC in *mvaU* was mutated to GAC in pHERD20T-*mvaU*	this study
pHERD20T-*mvaU*^{S67A}	Ap^R, the 67th aa codon AGC in *mvaU* was mutated to GCC in pHERD20T-*mvaU*	this study
pHERD20T-*mvaU*^{S67D}	Ap^R, the 67th aa codon AGC in *mvaU* was mutated to GAC in pHERD20T-*mvaU*	this study
pHERD20T-*mvaU*^{S108A}	Ap^R, the 108th aa codon TCC in *mvaU* was mutated to GCC in pHERD20T-*mvaU*	this study
pHERD20T-*mvaU*^{S108D}	Ap^R, the 108th aa codon TCC in *mvaU* was mutated to GAC in pHERD20T-*mvaU*	this study
pHERD20T-*mvaU*^{S113A}	Ap^R, the 113th aa codon TCC in *mvaU* was mutated to GCC in pHERD20T-*mvaU*	this study
pHERD20T-*mvaU*^{S113D}	Ap^R, the 113th aa codon TCC in *mvaU* was mutated to GAC in pHERD20T-*mvaU*	this study
pHERD20T-*mvaU*-His-*pfkA*	Ap^R, N terminal His tagged *mvaU* was coexpressed with *pfkA* in pHERD20T NcoI/HindIII	this study
pHERD20T-*mvaU*-His-*pfkB*	Ap^R, N terminal His tagged *mvaU* was coexpressed with *pfkB* in pHERD20T NcoI/HindIII	this study
pHERD20T-*mvaU*-His-*pfkA-pfkB*	Ap^R, N terminal His tagged *mvaU* was coexpressed with *pfkA-pfkB* in pHERD20T NcoI/HindIII	this study
pHERD20T-*mvaU*-His-KKP_{MP}	Ap^R, N terminal His tagged *mvaU* was coexpressed with KKP_{MP} in pHERD20T NcoI/HindIII	this study
pHERD20T-*pfkA*	Ap^R, *pfkA* in pHERD20T NcoI/HindIII	this study
pHERD20T-*pfkA*^{CSD}	Ap^R, mutant *pfkA* lacking CSD domain in pHERD20T NcoI/HindIII	this study
pHERD20T-*CSD*	Ap^R, CSD domain of *pfkA* in pHERD20T NcoI/HindIII	this study
pHERD20T-*pfkB*	Ap^R, *pfkB* in pHERD20T NcoI/HindIII	this study
pHERD20T-*pfkB*^{FHA}	Ap^R, mutant *pfkB* lacking FHA domain in pHERD20T NcoI/HindIII	this study
pHERD20T-*FHA*	Ap^R, FHA domain of *pfkB* in pHERD20T NcoI/HindIII	this study
pHERD20T-*pfpC*	Ap^R, *pfpc* in pHERD20T NcoI/HindIII	this study
pHERD20T-*pfkA-pfkB*	Ap^R, *pfkA-pfkB* in pHERD20T NcoI/HindIII	this study
pHERD20T-*pfkA*^{CSD}-*pfkB*	Ap^R, mutant *pfkA-pfkB* without CSD domain in pHERD20T NcoI/HindIII	this study
pHERD20T-*pfkA-pfkB*^{FHA}	Ap^R, mutant *pfkA-pfkB* without FHA domain in pHERD20T NcoI/HindIII	this study
pHERD20T-*pfkA*^{CSD}-*pfkB*^{FHA}	Ap^R, mutant *pfkA-pfkB* without both CSD and FHA domains in pHERD20T NcoI/HindIII	this study
pHERD20T-*pfkA*^{GGM}-*pfkB*	Ap^R, mutant GGM motif in PfkA in *pfkA-pfkB* in pHERD20T NcoI/HindIII	this study
pHERD20T-*pfkA*^{HRD}-*pfkB*	Ap^R, mutant HRD motif in PfkA in *pfkA-pfkB* in pHERD20T NcoI/HindIII	this study
pHERD20T-*pfkA*^{DFG}-*pfkB*	Ap^R, mutant DFG motif in PfkA in *pfkA-pfkB* in pHERD20T NcoI/HindIII	this study
pHERD20T-*pfkA*^{GFI}-*pfkB*	Ap^R, mutant GFI motif in PfkA in *pfkA-pfkB* in pHERD20T NcoI/HindIII	this study
pHERD20T-*pfkA-pfkB*^{GGM}	Ap^R, mutant GGM motif in PfkB in *pfkA-pfkB* in pHERD20T NcoI/HindIII	this study

pHERD20T-*pfkA-pfkB*^{HRD}	Ap^{R}, mutant HRD motif in PfkB in *pfkA-pfkB* in pHERD20T NcoI/HindIII	this study
pHERD20T-*pfkA-pfkB*^{DFG}	Ap^{R}, mutant DFG motif in PfkB in *pfkA-pfkB* in pHERD20T NcoI/HindIII	this study
pHERD20T-*pfkA*^{GGM}-*pfkB*^{GGM}	Ap^{R}, mutant GGM motifs in both PfkA and PfkB in *pfkA-pfkB* in pHERD20T NcoI/HindIII	this study
pHERD20T-*pfkA*^{HRD}-*pfkB*^{HRD}	Ap^{R}, mutant HRD motifs in both PfkA and PfkB in *pfkA-pfkB* in pHERD20T NcoI/HindIII	this study
pHERD20T-*pfkA*^{DFG}-*pfkB*^{DFG}	Ap^{R}, mutant DFG motifs in both PfkA and PfkB in *pfkA-pfkB* in pHERD20T NcoI/HindIII	this study
pHERD20T-*pfkA*$^{GGM+HRD+DFG}$-*pfkB*	Ap^{R}, the GGM, HRD and DFG motif in PfkA were mutated as PAO1::MP-*pilC*::K$^{GGM+HRD+DFG}$K$^{GGM+HRD+DFG}$P in *pfkA-pfkB,* and the generated *pfkA*$^{GGM+HRD+DFG}$-*pfkB* was ligated to pHERD20T NcoI/HindIII	this study
pHERD20T-*pfkA-pfkB*$^{GGM+HRD+DFG}$	Ap^{R}, the GGM, HRD and DFG motif in PfkB were mutated as PAO1::MP-*pilC*::K$^{GGM+HRD+DFG}$K$^{GGM+HRD+DFG}$P in *pfkA-pfkB,* and the generated *pfkA*$^{GGM+HRD+DFG}$-*pfkB* was ligated to pHERD20T NcoI/HindIII	this study
pHERD20T-*pfkA*$^{GGM+HRD+DFG}$ -*pfkB*$^{GGM+HRD+DFG}$	Ap^{R}, the GGM, HRD and DFG motif in both PfkA and PfkB were mutated as PAO1::MP-*pilC*::K$^{GGM+HRD+DFG}$K$^{GGM+HRD+DFG}$P in *pfkA-pfkB,* and the generated *pfkA*$^{GGM+HRD+DFG}$-*pfkB*$^{GGM+HRD+DFG}$ was ligated to pHERD20T NcoI/HindIII	this study
pHERD20T-*pfkA-pfpC*	Ap^{R}, *pfkA-pfpC* in pHERD20T NcoI/HindIII	this study
pHERD20T-*pfkB-pfpC*	Ap^{R}, *pfkB-pfpC* in pHERD20T NcoI/HindIII	this study
pHERD20T-*pfkA-pfkB-pfpC*	Ap^{R}, KKP$_{MP}$ (*pfkA-pfkB-pfpC*) in pHERD20T NcoI/HindIII	this study
pHERD20T-*pfkA*^{GGM}-*pfkB*	Ap^{R}, the 23th-25th aa codon GGAGGCATG in *pfkA* was mutated to GCAGCGTGT in pHERD20T-*pfkA-pfkB*	this study
pHERD20T-*pfkA*^{HRD}-*pfkB*	Ap^{R}, the 131th-133th aa codon CATCGCGAC in *pfkA* was mutated to TTCGAAAAT in pHERD20T-*pfkA-pfkB*	this study
pHERD20T-*pfkA*^{DFG}-*pfkB*	Ap^{R}, the 154th-157th aa codon GACTTCGGT in *pfkA* was mutated to AATTATGCA in pHERD20T-*pfkA-pfkB*	this study
pHERD20T-*pfkA-pfkB*^{GGM}	Ap^{R}, the 16th-18th aa codon GGCGGCATG in *pfkB* was mutated to GCAGCGTGT in pHERD20T-*pfkA-pfkB*	this study
pHERD20T-*pfkA-pfkB*^{HRD}	Ap^{R}, the 121th-123th aa codon CATAGAGAT in *pfkB* was mutated to TTCGAAAAT in pHERD20T-*pfkA-pfkB*	this study
pHERD20T-*pfkA-pfkB*^{DFG}	Ap^{R}, the 141th-143th aa codon GACTTTGGC in *pfkB* was mutated to AATTATGCA in pHERD20T-*pfkA-pfkB*	this study
pHERD20T-*2208*	Ap^{R}, *2208* in pHERD20T NcoI/HindIII	this study
pHERD20T-*2209*	Ap^{R}, *2209* in pHERD20T NcoI/HindIII	this study
pHERD20T-*2210*	Ap^{R}, *2210* in pHERD20T NcoI/HindIII	this study
pHERD20T-*2208-2209*	Ap^{R}, *2208-2209* in pHERD20T NcoI/HindIII	this study
pHERD20T-*2208-2210*	Ap^{R}, *2208-2210* in pHERD20T NcoI/HindIII	this study
pHERD20T-*2209-2210*	Ap^{R}, *2209-2210* in pHERD20T NcoI/HindIII	this study
pHERD20T-*2208-2209-2210*	Ap^{R}, *2208-2209-2210* (KKP$_{SW}$ in marine *Shewanella* W3-18-1) in pHERD20T NcoI/HindIII	this study
pHERD20T-K^{GFA}-KP$_{SW}$	Ap^{R}, *2208*^{GFA}*-2209-2210* (K^{GFA}KP$_{SW}$ with GFA mutation in marine *Shewanella* W3-18-1) in pHERD20T NcoI/HindIII	this study
pHERD20T-K$^{HRD+DFG}$-K$^{HRD+DFG}$P$_{SW}$	ApR, 2208-2209$^{HRD+DFG}$-2210$^{HRD+DFG}$ (K$^{HRD+DFG}$K$^{HRD+DFG}$P$_{SW}$ with GFA mutation in marine *Shewanella* W3-18-1) in pHERD20T NcoI/HindIII	this study
pHERD20T-K^{GFI}-KP$_{EC039}$	ApR, GFI mutation in *E. coli* 15EC039 KKP$_{EC039}$ (K^{GFI}KP$_{EC039}$) in pHERD20T NcoI/HindIII	this study

Table. S9 Oligonucleotides used for gene knockout and DNA sequencing. F indicates forward primer and R indicates reverse primer. The red letters indicate the mutation of nucleotides.

Primer name	Sequence (5'-3')	Purpose
Primers used for construction of MP-ΔPf6core and MP-ΔPf4ΔPf6core		
Pf6core-up-F	acgacggccagtgccaagcttTCTAAGTTCACATTCATGCACTCTTTC	Construction of pEX18Gm-ΔPf6core-up-down
Pf6core-up-R	tgagcgggtctcaTTAGTCACCGTCGTAATCCCCC	
Pf6core-down-F	tgactaaTGAGACCCGCTCAATGGACA	
Pf6core-down-R	ggtacccggggatcctctagaGAGTGGTGATAGCGAAACTCGAT	
Pf6core-conf-SF	TGAATCATCGCTACGCTCCTC	Verification of Pf6core knockout in MP-ΔPf6core and MP-ΔPf4ΔPf6core
Pf6core-conf-SR	ACGGCTGCTTGGTTGGTCT	
Pf6core-conf-LF	CATGGCAGACTCTATCAGCCA	
Pf6core-conf-LR	ATCGCATATCCCTTGCGCAGATA	
Primers used for construction of pVIII::GFP and MP-pVIII::GFP		
pVIII-gfp-up-F	gccagtgccaagcttgcatgcAGGACAAACAAGACAAGACCCCG	Construction of pEX18Gm-pVIII::GFP-up-down
pVIII-gfp-up-R	TTCTCCTTTACTCGCCTTGCGCAACATGCT	
pVIII-gfp-F2	GCAAGGCGAGTAAAGGAGAAGAACTTTTCACTGGA	
pVIII-gfp-R2	CCAGAGCACCCGTTATTTGTATAGTTCATCCATGCCATG	
pVIII-gfp-down-F	ACAAATAACGGGTGCTCTGGTCGGTG	
pVIII-gfp-down-R	tatgaccatgattacgaattcCGGTGCCCTTGAGGATGTAA	
pVIII-gfp-conf-SF	GCGAATACAACATCGAGCCG	Verification of strains pVIII::GFP and MP-pVIII::GFP
pVIII-gfp-conf-SR	GGTCTGGGAGAAGGTGTAGGAAT	
pVIII-gfp-conf-LF	ATGAACATGTTTGCAACCCAA	
pVIII-gfp-conf-LR	TCAGTCCTTCAGCAGAATGAG	
Primers used for construction of Δ*pilC* and PAO1::*pilC*$_{MP}$		
pilC-up-F	acgacggccagtgccaagcttTCTGCTCGTCTCAAGGTAAT	Construction of pEX18Gm-up-*pilC*-down, and pEX18Gm-up-*pilC*$_{MP}$-down
pilC-up-R	ATGGCTGGCCAGGTAGTCGAGGAGGGGCATGGATTAATCCTTGGTCACGCGGTTGACTT	
pilC-down-F	AAGTCAACCGCGTGACCAAGGATTAATCCATGCCCCTCCTCGACTACCTGGCCAGCCAT	
pilC-down-R	tatgaccatgattacgaattcAGTTGGTGATCGGCATCGAT	
pilC-conf-SF	GAGCAAGCCCGCAAAGAAG	Verification of strains Δ*pilC,* and PAO1::*pilC*$_{MP}$
pilC-conf-SR	CCAGTTGCGCTCCATCATCT	
pilC-conf-LF	AAGATGCTGCTGGATGCCAT	
pilC-conf-LR	GATCAGCGGGTGCAGCAATT	

Primers used for construction of PAO1::*pilC*$_{MP}$::KKP$_{MP}$ and PAO1::*pilC*$_{MP}$::K^{GFI}KP$_{MP}$

KKP$_{MP}$-F1	acgacggccagtgccaagcttTAGTTGATTACCACTGAGGAGGTGG	Amplification of the 697 bp downstream of *pfkA*
KKP$_{MP}$-R1	CGACCCAAGTACCGCCACCTAAATGGCACTCTAATAAATAAAATTAAATTTATCGCTTC	
KKP$_{MP}$-F2	GAAGCGATAAATTTAATTTTATTTATTAGAGTGCCATTTAGGTGGCGGTACTTGGGTCG	Amplification of Gm resistance gene with its 303 bp promoter
KKP$_{MP}$-R2	AGCACATCCTGTTATGATCCTTGATGAGTAGAGTTCCTATACTTTCTAGAGAATAGGAA	
KKP$_{MP}$-F3	TTCCTATTCTCTAGAAAGTATAGGAACTCTACTCATCAAGGATCATAACAGGATGTGCT	Amplification of KKP cascades and upstream 404 bp promoter the start codon of *pf6r* was mutated to TGA)
KKP$_{MP}$-R3	TGTCCCAGGTTCAAGTCCCGGTGTAGCCACCATGAGAATCAATACAGAGCAGAGCTAGG	
KKP$_{MP}$-F4	CCTAGCTCTGCTCTGTATTGATTCTCATGGTGGCTACACCGGGACTTGAACCTGGGACA	Amplification of the 836 bp from Pf6 *attR* to upstream
KKP$_{MP}$-R4	tatgaccatgattacgaattcGGGCAAGCCGGCGCGTTC	
KK^{GFI}P$_{MP}$-R3	GAAAATTTCTTTCCCCATCAAGGATGACTAGGAATGAGCACAATACCAGACCGATATGA	Amplification of *pfkA*^{GFI}-*pfkB* from pHERD20T-*pfkA*^{GFI}-*pfkB*
KK^{GFI}P$_{MP}$-F4	TCATATCGGTCTGGTATTGTGCTCATTCCTAGTCATCCTTGATGGGGAAAGAAATTTTC	Amplification of *pfpC* and the 836 bp from Pf6 *attR* to upstream with KKP$_{MP}$-R4, the template is PAO1::*pilC*$_{MP}$::KKP$_{MP}$ genomic DNA

Primers used for construction of pHERD20T-*mvaU* and related mutants

pHERD20T-*mvaU*-F	aagaaggagatatacataccATGTCCAAACTTGCCGAGTTC
pHERD20T-*mvaU*-R	cgacggccagtgccaagcttTTAGCGTTGCAGCCAGGATTC
pHERD20T-*mvaU*^{S2A}-F	aagaaggagatatacataccATGGCCAAACTTGCCGAGTTC
pHERD20T-*mvaU*^{S2D}-F	aagaaggagatatacataccATGGACAAACTTGCCGAGTTC
pHERD20T-*mvaU*^{S26A}-F	GCTGAAAGCCGACAGCAGCCTGAAGCAGGAACTGGAAT
pHERD20T-*mvaU*^{S26A}-R	GCTGCTGTCGGCTTTCAGCTTTTCCAGCAGGGCCAGTT
pHERD20T-*mvaU*^{S26D}-F	AAGCTGAAAGACGACAGCAGCCTGAAGCAGGAACTGGAAT
pHERD20T-*mvaU*^{S26D}-R	CAGGCTGCTGTCGTCTTTCAGCTTTTCCAGCAGGGCCAGT
pHERD20T-*mvaU*^{T50A}-F	TACGGCATGGCCCTGCACAACATCATCGCCATCCTCGACC
pHERD20T-*mvaU*^{T50A}-R	GTTGTGCAGGGCCATGCCGTACTTGTCCATCAACGCCTGC
pHERD20T-*mvaU*^{T50D}-F	TACGGCATGGACCTGCACAACATCATCGCCATCCTCGACC
pHERD20T-*mvaU*^{T50D}-R	GTTGTGCAGGTCCATGCCGTACTTGTCCATCAACGCCTGC
pHERD20T-*mvaU*^{T65A}-F	AAGGCTCCGGTCGCCGTCAGCGCCGCTCCGCAGCGCCGTGCCCGC
pHERD20T-*mvaU*^{T65A}-R	GGCGCTGACGGCGACCGGAGCCTTGGGGTCGAGGATGGCGATGAT
pHERD20T-*mvaU*^{T65D}-F	GCTCCGGTCGACGTCAGCGCCGCTCCGCAGCGCCGTGCC

Construction of pHERD20T-*mvaU* and related single site mutations in MvaU

pHERD20T-*mvaU*^{T65D}-R	GCTGACGTCGACCGGAGCCTTGGGGTCGAGGATGGCGAT	
pHERD20T-*mvaU*^{S67A}-F	AAGGCTCCGGTCACCGTCGCCGCCGCTCCGCAGCGCCGTGCCCGC	
pHERD20T-*mvaU*^{S67A}-R	GGCGGCGACGGTGACCGGAGCCTTGGGGTCGAGGATGGCGATGAT	
pHERD20T-*mvaU*^{S67D}-F	GCTCCGGTCACCGTCGACGCCGCTCCGCAGCGCCGTGCC	
pHERD20T-*mvaU*^{S67D}-R	GGAGCGGCGTCGACGGTGACCGGAGCCTTGGGGTCGAGGATGGCGAT	
pHERD20T-*mvaU*^{S108A}-R	cgacggccagtgccaagcttTTAGCGTTGCAGCCAGGATTCGACGGTTTCGGAACCGGCCTGTTCTTTC	
pHERD20T-*mvaU*^{S108D}-R	cgacggccagtgccaagcttTTAGCGTTGCAGCCAGGATTCGACGGTTTCGGAACCGTCCTGTTCTTTC	
pHERD20T-*mvaU*^{S113A}-R	cgacggccagtgccaagcttTTAGCGTTGCAGCCAGGCTTCGACGGTTTC	
pHERD20T-*mvaU*^{S113D}-R	cgacggccagtgccaagcttTTAGCGTTGCAGCCAGTCTTCGACGGTTTC	

Primers used for cloning KKP$_{MP}$ components and domains of PfkA and PfkB

pHERD20T-*pfkA*-F	aggagatatacatacccatgACGACTTCGAGAATCGGAAAGAC	
pHERD20T-*pfkA*-R	acgacggccagtgccaagcttCTACTCATCAAGGATCATAACAGGATG	
pHERD20T-*pfkB*-F	aggagatatacatacccatgAGCACAATACCAGACCGATATGAATT	Construction of pHERD20T-based constructions for expression of MPAO1 KKP components
pHERD20T-*pfkB*-R	acgacggccagtgccaagcttTCATAAGTTTATCTCCGGATGAGATAG	
pHERD20T-*pfpC*-F	aggagatatacatacccatgAATGTGAACTTAGAGAACGATATTACATTTC	
pHERD20T-*pfpC*-R	acgacggccagtgccaagcttCTAGTCATCCTTGATGGGGAAAGA	
pfkA^{CSD}-R	acgacggccagtgccaagcttTCAACATAAAAGTTCACATTTTTTTACC	Construction of pHERD20T-*pfkA*^{CSD}-*pfkB*, pHERD20T-*pfkA*-*pfkB*^{FHA} and pHERD20T-*pfkA*^{CSD}-*pfkB*^{FHA} together with primers pHERD20T-*pfkB*-F and pHERD20T-*pfkA*-R
pfkB^{FHA}-R1	TTAGCGCTTGATGTCTGTTTTCTAACTATATGTGCTTCTCAAGTGTCTCTTTGATTGAC	
pfkB^{FHA}-F2	GTCAATCAAAGAGACACTTGAGAAGCACATATAGTTAGAAAACAGACATCAAGCGCTAA	
pHERD20T-*pfkA*^{CSD}-R	acgacggccagtgccaagcttTCATATGTGCTTCTCAAGTGTCTCTTT	Construction of pHERD20T-*pfkA*^{CSD}, pHERD20T-*pfkA*^{CSD}, pHERD20T-*pfkB*^{FHA} and pHERD20T-*FHA* together with primers pHERD20T-*pfkB*-F/R and pHERD20T-*pfkA*-F/R
pHERD20T-*CSD*-R	aggagatatacatacccATGTTAGAAAACAGACATCAAGCGC	
pHERD20T-*pfkB*^{FHA}-R	acgacggccagtgccaagcttCTAACATAAAAGTTCACATTTTTTTACCA	
pHERD20T-*FHA*-R	aggagatatacatacccATGTATGCAAAAAACCCAAGATATATTG	

Primers used for construction of conserved domains in pHERD20T-*pfkA-pfkB*

pHERD20T-*pfkA*^{GGM}-*pfkB*-F	ATCTCGATATTTAATCGAGGACTTAATCGGCGAAGCAGCGTGTCAATATGTTTACCG	F primers/HERD20T-*pfkA*-R and pHERD20T-*pfkB*-F/R primers were used to amplify the second and first fragments separately, the two fragments were fused using pHERD20T-*pfkB*-F and pHERD20T-*pfkA*-R and ligated into pHERD20T plasmid.
pHERD20T-*pfkA*^{GGM}-*pfkB*-R	CGGTAAACATATTGACACGCTGCTTCGCCGATTAAGTCCTCGATTAAATATCGAGAT	
pHERD20T-*pfkA*^{HRD}-*pfkB*-F	TGCCGGAGTAGTTTTCGAAAATCTGAAACCAAC	
pHERD20T-*pfkA*^{HRD}-*pfkB*-R	GTTGGTTTCAGATTTTCGAAAACTACTCCGGCA	
pHERD20T-*pfkA*^{DFG}-*pfkB*-F	GTTAAAAATTACTAATTATGCAATTGCAAAAATG	
pHERD20T-*pfkA*^{DFG}-*pfkB*-R	CATTTTTGCAATTGCATAATTAGTAATTTTTAAC	

pHERD20T-*pfkA-pfkB*^{GGM}-F	TTGATGCAGCGTTAGGTACAATCTTCGTCTGC	
pHERD20T-*pfkA-pfkB*^{GGM}-R	GCAGACGAAGATTGTACCTAACGCTGCATCAA	
pHERD20T-*pfkA-pfkB*^{HRD}-F	GTAAACATAATTTTCGAAAATATCAAACCAAACAAC	
pHERD20T-*pfkA-pfkB*^{HRD}-R	GTTGTTTGGTTTGATATTTTCGAAAATTATGTTTAC	
pHERD20T-*pfkA-pfkB*^{DFG}-F	ATCATTAAAATATTTAATTATGCATTAGCAAGACACAC	
pHERD20T-*pfkA-pfkB*^{DFG}-R	GTGTGTCTTGCTAATGCATAATTAAATATTTTAATGAT	
pfkA-pfkB-linker-F	TTACGTTCGACCTATCTCATCCGGAGATAAACTTATGACGACTTCGAGAATCGGAAAGACTATA	Construction the double GGM, HDR, DFG mutations, the *pfkB* and *pfkA* single mutants were amplified using the above PCR products as templates, and fused with the primers and ligated into pHERD20T plasmid.
pfkA-pfkB -linker-R	TATAGTCTTTCCGATTCTCGAAGTCGTCATAAGTTTATCTCCGGATGAGATAGGTCGAACGTAA	
pfkB-in-R1	TAAGTCATTGCCGTAGATATATTCTTGTACGATGCCAAGCCCGCGTTCG	Construction of pHERD20T-*pfkA*$^{GGM+HRD+DFG}$-*pfkB*, pHERD20T-*pfkA-pfkB*$^{GGM+HRD+DFG}$ and pHERD20T-*pfkA*$^{GGM+HRD+DFG}$-*pfkB*$^{GGM+HRD+DFG}$, mutant *pfkB* and *pfkA* with were amplified using above mutants as templates, and fused with these primers, and *pfkA-pfkB*-linker-F/R, then ligated into pHERD20T plasmid.
pfkB-in-F1	CGAACGCGGGCTTGGCATCGTACAAGAATATATCTACGGCAATGACTTA	
pfkB-in-R2	AATATTTTAATGATGCTTTCATGGTCTAGCATCATGTTGTTTGGTTTGA	
pfkB-in-F2	TCAAACCAAACAACATGATGCTAGACCATGAAAGCATCATTAAAATATT	
pfkA-in-R1	GGCTACGTTATGATGATTGACTTTGGCTGCTACAATGGCACTACGCCG	
pfkA-in-F1	CGGCGTAGTGCCATTGTAGCAGCCAAAGTCAATCATCATAACGTAGCC	
pfkA-in-R2	AACTCATTTAGTGAATATCCGCCAGAGATCATAACGTTTGTTGGTTTCA	
pfkA-in-F2	TGAAACCAACAAACGTTATGATCTCTGGCGGATATTCACTAAATGAGTT	

Primers used for cloning *Shewanella* W3-18-1 KKP$_{SW}$ components and mutants

pHERD20T-*2208*-F	aggagatatacatacccatgTTTCAAAGGCTATTGCAAAAA	
pHERD20T-*2208*-R	acgacggccagtgccaagcttCTACTTGGAATCATCATCTTCAACCT	
pHERD20T-*2209*-F	aggagatatacatacccatgATGATTCCAAGTAGATATGAACTCTG	
pHERD20T-*2209*-R	acgacggccagtgccaagcttTCATGAAACCACCTCTGGGTTAG	
pHERD20T-*2210*-F	aggagatatacatacccatgATCACATCGAATACTCTGATCG	Construction of pHERD20T-based constructions for expression of KKP$_{SW}$ components and mutants
pHERD20T-*2210*^{GFA}-F	GCTATGTTGAGGGTTTGAAGCATAGTCACTATATCCGTTTTGAAT	
pHERD20T-*2210*^{GFA}-R	ATTCAAAACGGATATAGTGACTATGCTTCAAACCCTCAACATAGC	
pHERD20T-*2210*^{HRD}-F	CACACATTCAAGGAGTAATATTCGAAAATTTGAAGCCAAGTAATA	
pHERD20T-*2210*^{HRD}-R	TATTACTTGGCTTCAAATTTTCGAATATTACTCCTTGAATGTGTG	
pHERD20T-*2210*^{DFG}-F	TCGTCGGTAAAAGTTGCAATTGCATAATTGGTAATCTTTAGCTCT	
pHERD20T-*2210*^{DFG}-R	AGAGCTAAAGATTACCAATTATGCAATTGCAACTTTTACCGACGA	

pHERD20T-*2209*^{HRD}-F	TACATAAGGCAGGAATTATTTTCGAAAATATCAAACCAAACAATA	
pHERD20T-*2209*^{HRD}-R	TATTGTTTGGTTTGATATTTTCGAAAATAATTCCTGCCTTATGTA	
pHERD20T-*2209*^{DFG}-F	CGGAGTTATCAAGGTCTTTAATTATGCACTTTCGAGAAAACTTGA	
pHERD20T-*2209*^{DFG}-R	TCAAGTTTTCTCGAAAGTGCATAATTAAAGACCTTGATAACTCCG	
Primers used for cloning KKP components from other bacteria		
pHERD20T-*RS13785*-F	aggagatatacatacccatgCAAGATATATTAACAAAAAGGCTAA	
pHERD20T-*RS13795*-R	acgacggccagtgccaagcttTTATTTACAGCGAATAATTGGAAATGC	
pHERD20T-*STY4824*-F	aggagatatacatacccatgTTTACAGAACGACTTGCTCGC	
pHERD20T-*STY4822*-R	acgacggccagtgccaagcttTCAATCTTTCCAAAGAATTACAGGG	Construction of GFI mutants in PfkA homogues in the synthesized pHERD20T-KKP plasmids with different resources.
pHERD20T-*RS23220*-F	aggagatatacatacccatgAGCCGTGATTCTTACGAAAT	
pHERD20T-*RS23210*-R	acgacggccagtgccaagcttCTACTTAGCCTTGATAACTGGATGAGC	
pHERD20T-*3792*-F	aggagatatacatacccatgAGCCGTGATTCTTACGAAAT	
pHERD20T-*3794*-R	acgacggccagtgccaagcttCTACTTAGCCTTGATAACTGGATGAGC	
$K^{GFI}KP_{EC039}$-F	GATACTAGACTAGCTTATGACTATGCTCGTATACCAAACCAACCACAAG	
$K^{GFI}KP_{EC039}$-R	CTTGTGGTTGGTTTGGTATACGAGCATAGTCATAAGCTAGTCTAGTATC	
Plasmid verification primers		
pEX18Ap-F/pEX18Gm-F	AATCTTCTCTCATCCGCCAAAACA	
pEX18Ap-R/pEX18Gm-R	CGCCCAATACGCAAACCGCCTCTC	Verification of constructions used for gene knockout and expression
pHDRD20T-F	ATCGCAACTCTCTACTGTTTCT	
pHDRD20T-R	TGCAAGGCGATTAAGTTGGGT	
QPCR primers		
pfiA-qF	ATGCGGCTGACCTGGATT	
pfiA-qR	TGAGCGAACCTCCTGGAAA	
pfkA-qF	CGACCTGAAACCAACAAACGT	
pfkA-qR	TTAAACCATTGCTGAAAGGGAA	Quantification of Pf4 and Pf6 phages in effluents and expression levels of KKP_{MP} components in MPAO1 biofilm at different days
pfkB-qF	GAAATGAGGTGCGTCGGTAT	
pfkB-qR	ACAAGAATATATCTACGGCAATGAC	
pfpC-qF	GCCATGACAACTGCTCCACT	
pfpC-qR	TTTTCTATGCTCGCTTGCTTT	
gyrB-qF	CAAGTACGAAGGCGGTCTGAAG	

gyrB-qR	GCAGAGCAGGTTCTCGTTGAA
16SrRNA-qF	TGGTTCAGCAAGTTGGATGTG
16SrRNA-qR	GTTTGCTCCCCACGCTTTC

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