

Suppl. Fig. 1: Protein sequence homology alignment of gp1 proteins from filamentous phages. M13 for Bacteriophage M13 gp1, uniprot number P03656. I2 for Bacteriophage I2-2 gp1, uniprot number P15418. IF1 for Bacteriophage If1 gp1, uniprot number O80299. fd for Bacteriophage fd gp1, uniprot number P03655. IKe for Bacteriophage IKe gp1, uniprot number P03658. f1 for Bacteriophage f1 gp1, uniprot number P03657. V\_VJF for *Vibrio cholerae* phage VJF-Phi ORF422. XantoPhiLf for *Xanthomonas* phage phiLf, uniprot number O55247. PropionibacB5 for Bacteriophage phiB5 of *Propionibacterium freudenreichii*.

Suppl. Fig. 2: Protein sequence homology alignment of the N-terminal region of gp1 proteins from filamentous phages. The putative Walker A and Walker B motifs are illustrated by red boxes. The consensus Walker motifs are depicted above the respective motifs. X represents any amino acid while h represents hydrophobic residues. M13 for Bacteriophage M13 gp1, uniprot number P03656. I2 for Bacteriophage I2-2 gp1, uniprot number P15418. IF1 for Bacteriophage If1 gp1, uniprot number O80299. fd for Bacteriophage fd gp1, uniprot number P03655. IKe for Bacteriophage IKe gp1, uniprot number P03658. f1 for Bacteriophage f1 gp1, uniprot number P03657. V\_VJF for *Vibrio cholerae* phage VJF-Phi ORF422. XantoPhiLf for *Xanthomonas* phage phiLf, uniprot number O55247. PropionibacB5 for Bacteriophage phiB5 of *Propionibacterium freudenreichii*.

Suppl. Fig. 3: Protein sequence homology alignment of gp1 proteins from filamentous phages. All cysteine residues of M13 are shown in yellow boxes and numbered above. The six tested glycine residues with putative hinge-like functions are boxed in green and numbered above. I2 for Bacteriophage I2-2 gp1, uniprot number P15418. IF1 for Bacteriophage If1 gp1, uniprot number O80299. fd for Bacteriophage fd gp1, uniprot

number P03655. IKe for Bacteriophage IKe gp1, uniprot number P03658. M13 for Bacteriophage M13 gp1, uniprot number P03656. f1 for Bacteriophage f1 gp1, uniprot number P03657.

Suppl. Fig. 4: Western blot analysis of His-tagged gp1 mutants and wild type (wt) expressed in the *E. coli* M15 strain used in complementation assays. Top panel depicts protein detected by  $\alpha$ -His antibody. Lower panel depicts protein detected by  $\alpha$ -OmpA antibody. The Outer membrane protein A, OmpA was used as an expression control. (A) Gp1 Walker A mutants K14A and K14R. (B) Gp1 Walker B mutants D88N and E89Q. (C) Gp1 glycine mutations G29P and G118P.

# Supplementary Figure 1

M13 1 MA-VY-----FVTGKLGSGKTLVSVG-KIQDKIVAGCKIATNLD-LRLQNLPO  
 I2 1 MA-VY-----VVTGKLGAGKTLVAVS-RIQRTLAKGGIVATNIN-LKLHHFPQ  
 IF1 1 MA-VY-----VVTGKLGAGKTLVAVG-KIQDKIVSCCR VATNLD-LRIHKLPR  
 fd 1 MA-VY-----FVTGKLGSGKTLVSVG-KIQDKIVAGCKIATNLD-LRLQNLPO  
 IKE 1 MA-VY-----VVTGKLGAGKTLVAVS-RIQRTLAKGGIVATNIN-LKLHHFPQ  
 f1 1 MA-VY-----FVTGKLGSGKTLVSVG-KIQDKIVAGCKIATNLD-LRLQNLPO  
 V\_VJF 1 MASVY-----FVTGKLGSGKSLI AVS-RIRDALMRGVPVATNIN-INLKEM--  
 XantoPhiLf 1 ML-VF-----NEGVPRAKGSYDAVKNHILPALKKGRVVFARLNGLRFDRIAK  
 PropionibacB5 1 MS-WQSKRDLRRRF GIVGYVGSNGSGKSLMAVL-DTMTPLEAGRQVLS TVR-LLDWENFR

M13 46 V-GRFAK-TPRVLRIPDKPSSIDLLAIGRGND---SYDENKNGLLVLDECGTWFNTRSW  
 I2 46 V-GRYAK-QCRMRIADKPTLEDLEAIGRGNL---SYDESKNGLIVLDECGTWFNSRNW  
 IF1 46 V-GIFAK-SPDVIRIPDKPSLDDLLAIGRGNN---SYDENKNGLLVLDECGTWFNSRSW  
 fd 46 V-GRFAK-TPRVLRIPDKPSSIDLLAIGRGND---SYDENKNGLLVLDECGTWFNTRSW  
 IKE 46 V-GRYAK-QCRMRIADKPTLEDLEAIGRGNL---TYDESKNGLLVLDECGTWFNSRNW  
 f1 46 V-GRFAK-TPRVLRIPDKPSSIDLLAIGRGND---SYDENKNGLLVLDECGTWFNTRSW  
 V\_VJF 45 I-GRDKR-NTRLRYRIPDKPTVEDIEILGYVVK---SYDTSKDGLIVLDECGTWFNSRTW  
 XantoPhiLf 47 HLGMAENDVQHLLVLDTKDVSKLFACTQDESGKWCIPDEFKDALVVIDEVHEFYVNER-  
 PropionibacB5 58 P-CDDP--GCDDLPGHPDHLAAHPLWVPLRELS---QMLDFEGGDIIILDEVTVGVASSRES

M13 100 NDKERQPII-DWFLHARKLGWDIIFLVQDLSIVDKQARSALAEHV VYCRRLDRITIP---  
 I2 100 SDKSRQPII-DWFLHARKLGWDVIFIIQDISLMDKQAREALAEHV VYCRRLDKINIP---  
 IF1 100 ADKERQSVI-NWFLHARKLGWDIIFLIQDLSIMDKQARVALAEHV VYCRRLDKITIP---  
 fd 100 NDKERQPII-DWFLHARKLGWDIIFLVQDLSIVDKQARSALAEHV VYCRRLDRITIP---  
 IKE 100 SDKSRQPII-DWFLHARKLGWDIIFIIQDISLMDKQARDALAEHV VYCRRLDKINIP---  
 f1 100 NDKERQPII-DWFLHARKLGWDIIFLVQDLSIVDKQARSALAEHV VYCRRLDRITIP---  
 V\_VJF 99 NDKNRQALL-DRFLHIRKLGWDVIFIVQNISMVDKQAREGLAEHV VYCRRLDRMQLP---  
 XantoPhiLf 106 --KPLAPAVENFWALLGQNGGDAVIMTQWINRLHSAVKAR-IEKKNTFQKLTATIGMK---  
 PropionibacB5 111 --MSLPPQIANMLVQLRRRDVVLRWTTPAWSRADLI IRET-TQAVVLCRGMASKTIPGRV

M13 156 -----F  
 I2 156 -----I  
 IF1 156 -----F  
 fd 156 -----F  
 IKE 156 -----I  
 f1 156 -----F  
 V\_VJF 155 -----F  
 XantoPhiLf 160 -----G  
 PropionibacB5 168 WPSHRLIMSRVVSAAATALSAGGQTAGRVSSSLARSVIRLEQCPAIQAYDTLDRVLSVPV

M13 157 VGTLYSLITGS--KMPLPKLHVGVVVKYG-----DSQLSPTVERWLYTGKNLYNAYD  
 I2 157 IGGLISVLSGG--RLPLPKVHFGIVVKYG-----DNPQSLTVDKWLYTGTDLYAAYD  
 IF1 157 IGSISVITGS--KLPLPKVHFGIVVKYG-----DSPQSM TVERWLYTGRDLYAAYD  
 fd 157 VGTLYSLVTGS--KMPLPKLHVGVVVKYG-----DSQLSPTVERWLYTGKNLYNAYD  
 IKE 157 IGGLISVLSGG--RLPLPKVHFGIVVKYG-----DNPQSLTVDKWVYTGTDLYAAYD  
 f1 157 VGTLYSLITGS--KMPLPKLHVGVVVKYG-----DSQLSPTVERWLYTGKNLYNAYD  
 V\_VJF 156 LSTIVWILTLGQLKIPMPKLIHIGIVVKYG-----DTINALTVDKWMLWGTDLYSSYD  
 XantoPhiLf 161 RYRVTYFHTTS--PGKFEKVGQOTLKYDPAIFPLYDGYAPGAENTEVEEYEGGKNVWAAMA  
 PropionibacB5 228 AEGGRCVVCGG--RRSVPGCSCGD--D-----GDSC-----

M13 206 TKQAFSSNYD-SGVYSYLTPLYSHGRYFKPLNLGQMKLTKIYLLKFSRVLCIAI----G  
 I2 206 TKQIFTS DRELSPPFCPVSPYYTHGIFAVKRD AKYYMRMTKIYFKKMN RVLMASFLALG  
 IF1 206 TKQAFSDAYE-HSSF SYLTPLYSHGRYAVKR DATFYMRLTRIYLLK KFSRVLCIFC----G  
 fd 206 TKQAFSSNYD-SGVYSYLTPLYSHGRYFKPLNLGQMKLTKIYLLKFSRVLCIAI----G  
 IKE 206 TKQIFTS DREISPPYCPYTHGIFSVKRD AKYYMRMTKIYFKKMN RVLMASFLALG  
 f1 206 TKQAFSSNYD-SGVYSYLTPLYSHGRYFKPLNLGQMKLTKIYLLKFSRVLCIAI----G  
 V\_VJF 207 TKQIFQNHYP-HGTYSVLP P WYIHGRYTVPYTARNIMRITKIYLLKFSRVAMFAV----G  
 XantoPhiLf 219 VRAAIFLTLGGVGIYF-FMHYFTKDRADPNKPMASA-----SQTTPKPTHVCA----G  
 PropionibacB5 255 -----GTERGAGPLGVARD-----

M13	261	FASAFTYSYITQPK--PEVK-----KVVS-----QTY-DFDKFTIDSSQRLNL
I2	266	ACVGFHYKSRQINEQLSNMPVASAQANTT-----KTDHTID-ELPRLSINSFAQMGY
IF1	261	FVSAFTYLSLSKPEATPOLKPVTT-QIIT-----SRY-KPSELRIITTSYRMGN
fd	261	FASAFTYSYITQPK--PEVK-----KVVS-----QTY-DFDKFTIDSSQRLNL
IKe	266	AACGIFYKSQAYSNQLQHIQDNSKTSVIS-----KTDQSAE-ILPRLSINSYSQMGY
f1	261	FASAFTYSYITQPK--PEVK-----KVVS-----QTY-DFDKFTIDSSQRLNL
V_VFJ	262	AAFCGAAFWHFTSPE--PELI-----QLVQAQNQMLTSESDHKLSELLGGFTISRYTALP-
XantoPhiLf	266	FANCAPSVPITQPPP--PDPL-----ADLTQEQ-----RYVAQLA-DKGRIRLSARARVGD
PropionibacB5	269	-----PSRAGREV--TALR-----AVES-----TSS-----

M13	301	SYR--YVEKDSK-GKLINSDD---LQKQGYSLTYIDLCTVSIKKGNSNEIVKC--N----
I2	317	DVN--VSEKDAK-GKIYSEF---LMKSGYALDIKDSCHITLRKRNYIQOVTG--EG---
IF1	307	AVG--FEEMDAK-KQKIASDD---LIKDGERMVTTPCSVELIKDGKHEKVT---C----
fd	301	SYR--YVEKDSK-GKLINSDD---LQKQGYSLTYIDLCTVSIKKGNSNEIVKC--N----
IKe	317	DVS--VTEKDAK-AKIYSEF---LIKDGYRVDIKDACHVTIVKKSIIQOITC--EG---
f1	301	SYR--YVEKDSK-GKLINSDD---LQKQGYSLTYIDLCTVSIKKGNSNEIVKC--N----
V_VFJ	314	DAP--VTEELSNQAKRLTSYE---LQSMGFEIEPLSRCEIILKSGAQNETIHC-----
XantoPhiLf	313	QDRAWIQWIDAS--NNVVEELDLSQIRALGYSVSVVTY--GVRLSAGK--HIMVATAWPWTA
PropionibacB5	288	-----DLAVRLGKKSEAEGMNPP-----

M13	-----
I2	-----
IF1	-----
fd	-----
IKe	-----
f1	-----
V_VFJ	-----
XantoPhiLf	369 PIREKDARLYNMAPDGSGGAAGVATAGSDGGGADRQVRGGVIEYGPRTQGTFFDNKGYS
PropionibacB5	306 -----

M13	-----
I2	-----
IF1	-----
fd	-----
IKe	-----
f1	-----
V_VFJ	-----
XantoPhiLf	429 SSTSTPATTLQM
PropionibacB5	306 -----ASA---

## Supplementary Figure 2

Putative  
Walker A

GXXXXGKS/T

M13	1	MA-VY-----FVTGKLGSGKTLVSVG-KIQDKIVAGCKIATNLD-LRLQNLPO
I2	1	MA-VY-----VVTGKLGAGKTLVAVS-RIQRTLAKGGIVATNLD-LKLHHFPQ
IF1	1	MA-VY-----VVTGKLGAGKTLVAVG-KIQDKIVSGCRVATNLD-LRLHKLPR
fd	1	MA-VY-----FVTGKLGSGKTLVSVG-KIQDKIVAGCKIATNLD-LRLQNLPO
IKe	1	MA-VY-----VVTGKLGAGKTLVAVS-RIQRTLAKGGIVATNLD-LKLHHFPQ
f1	1	MA-VY-----FVTGKLGSGKTLVSVG-KIQDKIVAGCKIATNLD-LRLQNLPO
V_VJF	1	MASVY-----FVTGKLGSGKSLI AVS-RIRDALMRGVPVATNLD-LNLKEM--
XantoPhiLf	1	ML-VF-----NEGVPRAKGSYDAVKNHILPALKKGRRVFARLNGLRFDRIAK
PropionibacB5	1	MS-WQSKRDLRRRFGIVGYVGSNGSGKSLMAVL-DTMPTLEAGROVLSTVR-LLDWENFR

Putative  
Walker B

hhhhDE

M13	46	V-GRFAK-TPRVLRIPDKPSISDLLAIGRGND----SYDENKNGLLVLDECGTWFNTRSW
I2	46	V-GRYAK-QCRMRIADKPTLEDLEAIGRGNL----SYDESKNGLLVLDECGTWFNSRNW
IF1	46	V-GIFAK-SPDVIRIPDKPSIDDLLAIGRGNN----SYDENKNGLLVLDECGTWFNSRSW
fd	46	V-GRFAK-TPRVLRIPDKPSISDLLAIGRGND----SYDENKNGLLVLDECGTWFNTRSW
IKe	46	V-GRYAK-QCRMRIADKPTLEDLESIGRGNL----TYDESKNGLLVLDECGTWFNSRNW
f1	46	V-GRFAK-TPRVLRIPDKPSISDLLAIGRGND----SYDENKNGLLVLDECGTWFNTRSW
V_VJF	45	I-GRDKR-NTRLRYRLPDKPTVEDIEILGYVVK----SYDTSKDGLIVLDECGTWFNSRTW
XantoPhiLf	47	HLCMAENDVQHLLVLVDTKDVSKLFACTQDESGKWCIPDEFKDALVVIDEVHEFYVNER-
PropionibacB5	58	P-CDDP--GCDLPGHPDHLAAHPLWVPLRELS----QMLDFEGCDIILDEVTVGVASSRES

# Supplementary Figure 3

Gly29 Cys30

M13	1	MA-VY-----FVTGKLGSGKTLVSVG-KIQDKIVACCKIATNLD-LRLQNLPO
I2	1	MA-VY-----VVTGKLGAGKTLVAVS-RIQRTLAKGGIVATNLN-LKLHHPFO
IF1	1	MA-VY-----VVTGKLGAGKTLVAVG-KIQDKIVSCRRVATNLD-LRTHKLPFR
fd	1	MA-VY-----FVTGKLGSGKTLVSVG-KIQDKIVACCKIATNLD-LRLQNLPO
IKe	1	MA-VY-----VVTGKLGAGKTLVAVS-RIQRTLAKGGIVATNLN-LKLHHPFO
f1	1	MA-VY-----FVTGKLGSGKTLVSVG-KIQDKIVACCKIATNLD-LRLQNLPO
V_VJF	1	MASVY-----FVTGKLGSGKSLIIVS-RIRDALMRCVVPVATNLN-INLKEM--
XantoPhiLf	1	ML-VF-----NEGVPRACKSYDAVKNEILPALKKCRVVFARLNGLRFDRIAK
PropionibacB5	1	MS-WQSKRDLRRRFGIVGVVGSNGSGKSLMAVL-DTMTPEAGROVLSIVR-LLDWENR

		Gly47		Cys90
M13	46	V-GRFAK-TPRVLRIPDKPSISDLLAIGRGND----SYDENKNGLLVLDECGTWFNTRSW		
I2	46	V-GRYAK-QCRVMRIADKPTLEDLEAIGRNL----SYDESKNGLLVLDECGTWFNSRNW		
IF1	46	V-GIFAK-SPDVLRIPDKPSISDLLAIGRNN----SYDENKNGLLVLDECGTWFNSRSW		
fd	46	V-GRFAK-TPRVLRIPDKPSISDLLAIGRGND----SYDENKNGLLVLDECGTWFNTRSW		
IKe	46	V-GRYAK-QCRVMRIADKPTLEDLEAIGRNL----TYDESKNGLLVLDECGTWFNSRNW		
f1	46	V-GRFAK-TPRVLRIPDKPSISDLLAIGRGND----SYDENKNGLLVLDECGTWFNTRSW		
V_VJF	45	I-GRDKR-NTRLVLRIPDKPTVEDTEILGYVMK----SYDTSKDGLLVLDECGTWFNSRTW		
XantoPhiLf	47	HLGMAENDVQHLLVLDTKDVSKLFACTQDES GKWCIPDEFKDALVVIDEVHEFVNER-		
PropionibacB5	58	P-CDDP--GCDLPGHPDHLAAHPLWVPLRELS----QMLDFEGGDIILDEVTGVASSRES		

		Gly118		Cys146
M13	100	NDKERQPII-DWFLHARKLGWDIIFLVQDISIVDKQARSALAEHVVYCRRLDRITLP---		
I2	100	SDKSRQPM-DWFLHARKLGWDVIFLIQDISLMDKQAREALAEHVVYCRRLDKINIP---		
IF1	100	ADKERQSVI-NWFLHARKLGWDIIFLIQDISIMDKQARVALAEHVVYCRRLDKITIP---		
fd	100	NDKERQPII-DWFLHARKLGWDIIFLVQDISIVDKQARSALAEHVVYCRRLDRITLP---		
IKe	100	SDKSRQPM-DWFLHARKLGWDIIFLIQDISLMDKQARDALAEHVVYCRRLDKINIP---		
f1	100	NDKERQPII-DWFLHARKLGWDIIFLVQDISIVDKQARSALAEHVVYCRRLDRITLP---		
V_VJF	99	NDKNRQALL-DRFLHTRKLGWDVIFIVQDISMVDKQAREGLAEHVVYCRRLDRMQLP---		
XantoPhiLf	106	--KPLAPAVENFWALLGQNGCDAVIMTQWINRLHSAVKAR-IEKKNTFOKLTALGK---		
PropionibacB5	111	--MSLPPQIANMLVQLRRRDVLRWTTPAWSRADLIIRET-TQAVVLCRGAMSKITLPGRV		

M13	156	-----F
I2	156	-----I
IF1	156	-----F
fd	156	-----F
IKe	156	-----I
f1	156	-----F
V_VJF	155	-----F
XantoPhiLf	160	-----G
PropionibacB5	168	WPSHRLIMSRVVSAAATALSAGGQTAGRVSSILARSVIRLEQCPAIQAYDTLDRVLSVPV

Gly197

M13	157	VGTLVSLITGS--KMPLPKLHVGVVKYG-----DSQLSPTVERWLYTGKNLVYAYD
I2	157	IGGLISVLSGG--RLPLPKVHFGIVKYG-----DNPQSLTVDKWLYTGTDLYAAYD
IF1	157	IGSIYSVITGS--KLPLPKVHVGVVKYG-----DSPQSMPTVERWLYTGTDLYAAYD
fd	157	VGTLVSLVITGS--KMPLPKLHVGVVKYG-----DSQLSPTVERWLYTGKNLVYAYD
IKe	157	IGGLISVLSGG--RLPLPKVHFGIVKYG-----DNPQSLTVDKWLYTGTDLYAAYD
f1	157	VGTLVSLITGS--KMPLPKLHVGVVKYG-----DSQLSPTVERWLYTGKNLVYAYD
V_VJF	156	LSTIVWLLTLGQLKIPMPKLIHIGIVKYG-----DITINALTVDKWMLWGTDLVSSYD
XantoPhiLf	161	RYRVTYFHHTS--PGKFEKVGQTLKYDPAIFPLYDGYAPGAENTEVVEEGKRVWAAMA
PropionibacB5	228	AEGGRCVVCVG--RRSVPGCSCGD--D-----GDS

		Gly229		Cys256		Gly260
M13	206	TKQAFSSNYD--SGVYSYLTPLYLSHGGRYFKPLNLCQMKLTKIYLKFSRVLCCLAI----				
I2	206	TKQIFTSDFRELSPPFCVPSPIYTHGIFAVKRDACYMRMTKIYFKKMNRVWLMASFLALG				
IF1	206	TKQAFSDAYE--HSSFYSYLTPLYLSHGGRYAVKRDATFYMRITRIYLLKFSRVLCCLFC----				
fd	206	TKQAFSSNYD--SGVYSYLTPLYLSHGGRYFKPLNLCQMKLTKIYLKFSRVLCCLAI----				
IKe	206	TKQIFTSDFREISPPYCPSPYIYTHGIFSVKRDACYMRMTKIYFKKMNRFVLMASFLALG				
f1	206	TKQAFSSNYD--SGVYSYLTPLYLSHGGRYFKPLNLCQMKLTKIYLKFSRVLCCLAI----				
V_VJF	207	TKQIFQNHYP--HCTYSVLPVYIHGRYTVPYTARNIMRITKILFRKYSRVVAMEFAV----				
XantoPhiLf	219	VRAAIFLTLGGVGIYF--FMHYFTKDRADPNKPMASA-----SQTTRPTEVCA----				
PropionibacB5	255	-----GTCRGAGLGVARD-----				

M13	261	FASAFTYSYITQPK--PEVK-----KVVS-----QTY-DFDKFTIDSSQRLNL
I2	266	ACVGFHYKSRQINEQLSNMPVASAQANTT-----KTDHTID-ELPRLSINSFAQMGY
IF1	261	FVSAFTYLSLSKPEATPOLKPVTT-QIIT-----SRY-KPSELRIITTSYRMGN
fd	261	FASAFTYSYITQPK--PEVK-----KVVS-----QTY-DFDKFTIDSSQRLNL
IKe	266	AACGIFYKSQAYSNQLQHIQDNSKTSVIS-----KTDQSAE-ILPRLSINSYSQMGY
f1	261	FASAFTYSYITQPK--PEVK-----KVVS-----QTY-DFDKFTIDSSQRLNL
V_VJF	262	AAFCGAAFWHFTSPE--PELI-----QLVQAQNQMLTSESDHKLSELLGGFTISRYTALP-
XantoPhiLf	266	FANCAPSVPITQPPP--PDPL-----ADLTQEQ-----RYVAQLA-DKGRIRLSARARVGD
PropionibacB5	269	-----PSRAGREV--TALR-----AVES-----TSS-----

Cys332                      Cys347

M13	301	SYR--YVEKDSK-GKLINSDD-----LQKQGYSITYIDLCTVSIKKGNSNEIVKC--N----
I2	317	DVN--VSEKDAK-GKIYSEF-----LMKSGYALDIKDSCHITLRKRNYIQOVTG--EG---
IF1	307	AVG--FEEMDAK-KQKIASDD-----LIKDGERMVTTPCSVELIKDGKHEKVT--C----
fd	301	SYR--YVEKDSK-GKLINSDD-----LQKQGYSITYIDLCTVSIKKGNSNEIVKC--N----
IKe	317	DVS--VTEKDAK-AKIYSEF-----LIKDGYRVDIKDACHVITIVKKSIIQOITC--EG---
f1	301	SYR--YVEKDSK-GKLINSDD-----LQKQGYSITYIDLCTVSIKKGNSNEIVKC--N----
V_VJF	314	DAP--VTEELSNAGKRLTSYE-----LQSMGFEIEPLSRCEIILKSGAQNETIHC-----
XantoPhiLf	313	QDRAWIQWIDAS--NNVVEELDLSQIRALGYSVSVVTY--GVRLSAGK--HIMVATAWPWTA
PropionibacB5	288	-----DLAVRLGKKSEAEGMNPP-----

M13	-----
I2	-----
IF1	-----
fd	-----
IKe	-----
f1	-----
V_VJF	-----
XantoPhiLf	369 PIREKDARLYNMAPDGSGGAAGVATAGSDGGGADRQVRGGVIEYGPRTQGTFFDNKGYS
PropionibacB5	306 -----

M13	-----
I2	-----
IF1	-----
fd	-----
IKe	-----
f1	-----
V_VJF	-----
XantoPhiLf	429 SSTSTPATTLQM
PropionibacB5	306 -----ASA---

# Supplementary Figure 4

