Suppl. Fig. 1: Protein sequence homology alignment of gp1 proteins from filamentous phages. M13 for Bacteriophage M13 g1p, uniprot number P03656. I2 for Bacteriophage I2-2 g1p, uniprot number P15418. IF1 for Bacteriophage If1 g1p, uniprot number O80299. fd for Bacteriophage fd g1p, uniprot number P03655. IKe for Bacteriophage IKe g1p, uniprot number P03658. f1 for Bacteriophage f1 g1p, 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*.

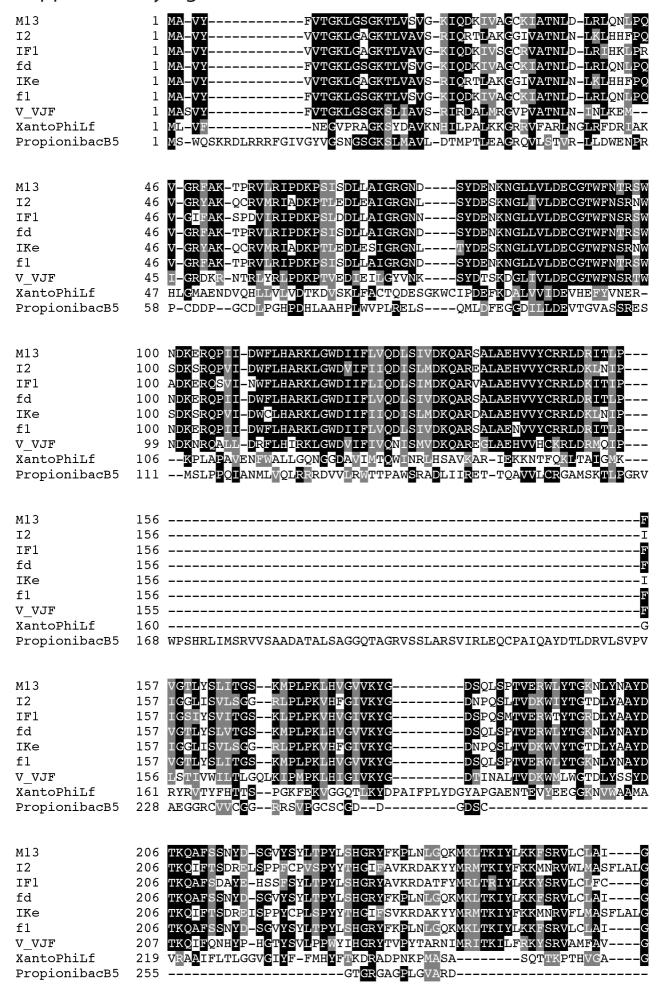
Suppl. Fig. 2: Protein sequence homology alignment of the N-terminal region of gp1 proteins from filamentous phages. The putative Walker A and Walker B motifs are illustrated by red boxes. The consensus Walker motifs are depicted above the respective motifs. X represents any amino acid while h represents hydrophobic residues. M13 for Bacteriophage M13 g1p, uniprot number P03656. I2 for Bacteriophage I2-2 g1p, uniprot number P15418. IF1 for Bacteriophage If1 g1p, uniprot number O80299. fd for Bacteriophage fd g1p, uniprot number P03655. IKe for Bacteriophage IKe g1p, uniprot number P03658. f1 for Bacteriophage f1 g1p, 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 g1p, uniprot number P15418. IF1 for Bacteriophage If1 g1p, uniprot number O80299. fd for Bacteriophage fd g1p, uniprot

number P03655. IKe for Bacteriophage IKe g1p, uniprot number P03658. M13 for Bacteriophage M13 g1p, uniprot number P03656. f1 for Bacteriophage f1 g1p, 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 α-His antibody. Lower panel depicts protein detected by α-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 I2 IF1 fd IKe f1 V_VFJ XantoPhiLf PropionibacB5	261 FASAFTYSYITQPKPEVKKVVSQTY-DFDKFTIDSSQRLNL 266 AGVGFFYKSRQINEQLSNMPVASAQANTTKTDHTID-ELPRLSINSFAQMGY 261 FVSAFTYLSLSKPEATPQIKPVTT-QIITSRY-KPSELRITTSYRMGN 261 FASAFTYSYITQPKPEVK
M13 I2 IF1 fd IKe f1 V_VFJ XantoPhiLf PropionibacB5	301 SYRYVFKDSK-GKLINSDDIQKQGYSLTYIDLCTVSIKKGNSNEIVKCN 317 DVNVSFKDAK-GKIYYSFDIMKSGYALDIKDSCHITLRKRNYIQQVTCEG 307 AVGFEEMDAK-KQKIASDDLIKDGFRMVYITPCSVELIKDGKHEKVTC 301 SYRYVFKDSK-GKLINSDDLQKQGYSITYIDLCTVSIKKGNSNEIVKCN 317 DVSVTFKDAK-AKIYNSFDLIKDGYRVDIKDACHVTIVKKSYIQQITCEG 301 SYRYVFKDSK-GKLINSDDLQKQGYSLTYIDLCTVSIKKGNSNEIVKCN 314 DAPVTFELSNGAKRITSYELQSMGFEIEPLSRCEIIIKSGAQNETIHC 313 QDRAWIQWIDAS-NNVVEELDLSQLRALGYSVSVVTY-GVRLSAGKHIMVATAWPWTA
M13 I2 IF1 fd IKe f1 V_VFJ XantoPhiLf PropionibacB5	369 PIREKDARLYNMAPDGSGGAAGVATAGSDGGGADRDQVRGGVIEYGPRTQGTFPDNKGYS 306
M13 I2 IF1 fd IKe f1 V_VFJ XantoPhiLf PropionibacB5	

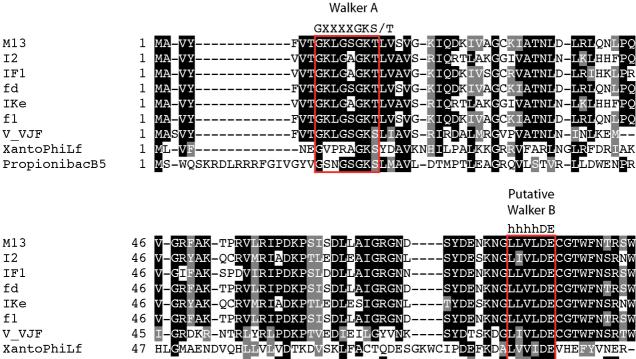
Supplementary Figure 2

 V_VJF XantoPhiLf

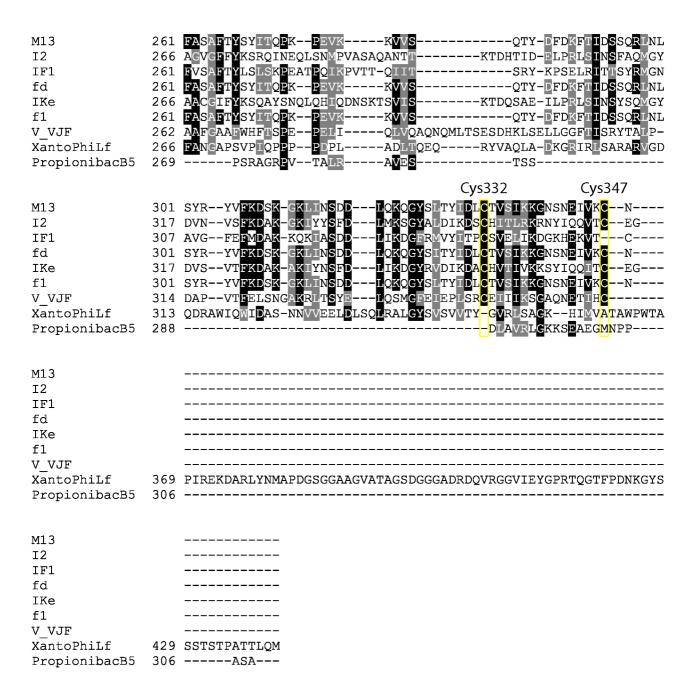
PropionibacB5

Putative

58 P-CDDP--GCDLPGHPDHLAAHPLWVPLRELS----QMLDFEGGDILLDEVTGVASSRES



Supplementary Figure 3 Gly29 Cys30 M13 FVTGKLGSGKTLVSVG KIQDKIVACCKIATNLD-LRLQNLPQ -RIQ<mark>RTL</mark>AKG<mark>G</mark>IVATNLN-LKLHHFPQ -KIQDKIVSGCRVATNLD-LRIHKLPR -KIQDKIVAGC<mark>KIATNL</mark>D-LRLQNLPQ VVTGKLG<mark>A</mark>GKTLVAVS 12 1 MA-VY VVTGKLGAGKTLVAVG-IF1 FVTGKLGSGKTLVSVG-1 MA-VY fd -VVTGKLGAGKTLVAVS-RIQRTLAKGGIVATNLN-LKLHHFPQ -FVTGKLGSGKTLVSVG-KIQDKIVAGCKIATNLD-LRLQNLPQ -FVTGKLGSGKSLIAVS-RIRDALMRGVPVATNLN-INLKEM---NEGVPRAGKSYDAVKNHILPALKKGRRVFARLNGLRFDRIAK 1 MA-VY IKe 1 MA-VY f1 V_VJF 1 MASVY 1 ML-XantoPhiLf 1 MS-WQSKRDLRRRFGIVGYVCSNGSGKSLMAVL-DTMPTLEAGRQVLSTVR-LLDWENPR PropionibacB5 Gly47 Cys90 46 V-GRFAK-TPRVLRIPDKPSISDLLAIGRGND----SYDENKNGLLVLDECGTWFNTRSW 46 V-GRYAK-QCRVMRIADKPTLEDLEAIGRGNL----SYDENKNGLIVLDECGTWFNSRNW 46 V-GIFAK-SPDVIRIPDKPSLDDLLAIGRGNN----SYDENKNGLLVLDECGTWFNSRSW 46 V-GRFAK-TPRVLRIPDKPSISDLLAIGRGND----SYDENKNGLLVLDECGTWFNTRSW 46 V-GRYAK-QCRVMRIADKPTLEDLESIGRGNL----TYDESKNGLLVLDECGTWFNSRNW 46 V-GRFAK-TPRVLRIPDKPSISDLLAIGRGND----SYDENKNGLLVLDECGTWFNTRSW 46 V-GRFAK-TPRVLRIPDKPSISDLLAIGRGND----SYDENKNGLLVLDECGTWFNTRSW 47 HLGMAENDVQHLLVLVDTKDVSKLFACTQDESGKWCIPDEFKDALVVIDEVHEFYVNER58 P-CDDP--GCDLPGHPDHLAAHPLWVPLRELS----QMLDFEGGDILLDEVTGVASSRES M13 12 IF1 fd IKe f1 V VJF XantoPhiLf PropionibacB5 Gly118 Cys146 100 NDKERQPII-DWFLHARKIGWDIIFLVQDLSIVDKQARSALAEHVVYCRRLDRITLP--100 SDKSRQPVI-DWFLHARKIGWDVIFIIQDISLMDKQAREALAEHVVYCRRLDKINIP--100 ADKERQSVI-NWFLHARKIGWDIIFLIQDLSIMDKQARVALAEHVVYCRRLDKITIP--100 NDKERQPII-DWFLHARKIGWDIIFLVQDLSIVDKQARSALAEHVVYCRRLDRITLP--100 SDKSRQPVI-DWCLHARKIGWDIIFIIQDISLMDKQARDALAEHVVYCRRLDKINIP--100 NDKERQPII-DWFLHARKIGWDIIFIVQDLSIVDKQARSALAENVVYCRRLDRITLP--99 NDKNRQALL-DRFLHIRKIGWDVIFIVQNISMVDKQAREGLAEHVVHCKRLDRMQIP--106 --KPLAPAVENFWALLGQNGGDAVIMTQWINRLHSAVKAR-IEKKNTFQKLTAIGMK---111 --MSLPPOTANMIVOIRRRDVYJRWTTPAWSRADLITRET-TOAVVICRGAMSKTIPGRV M13 IF1 fd IKe f1 V VJF XantoPhiLf PropionibacB5 111 --MSLPPQIANMLVQLRRRDVVLRWTTPAWSRADLIIRET-TQAVVLCRGAMSKTLEGRV M13 Ι2 IF1fd IKe 155 -----V VJF XantoPhiLf PropionibacB5 168 WPSHRLIMSRVVSAADATALSAGGQTAGRVSSLARSVIRLEQCPAIQAYDTLDRVLSVPV Gly197 M13 157 KLPLPKVHVGIVKYG-IGSTYSVITGS--KLPLPKVHVGTVKYG------DSF QSFTVERWLYTGKNLYNAYD /GTLYSLVTGS--KMPLPKLHVGVVKYG-----DSQLSPTVERWLYTGKNLYNAYD IGGLISVLSGG--RLPLPKVHFGIVKYG-----DNPQSLTVDKWVYTGTDLYAAYD /GTLYSLITGS--KMPLPKLHVGVVKYG-----DSQLSPTVERWLYTGKNLYNAYD 157 VGTLYSLITGS-KMPLPKLHVGVVKYG-----DSQLSPTVERWLYTGKNLYNAYD 156 LSTIVWILTLGQLKIPMPKLHIGIVKYG-----DTINALTVDKWMLWGTDLYSSYD V VJF 161 RYRVTYFHTTS--PGKFEKVGGQTLKYDPAIFPLYDGYAPGAENTEVYEEGGKNVWAAMA XantoPhiLf PropionibacB5 228 AEGGRCVVCGG--RRSVPGCSCGD--D------GDSC------Gly229 Cys256 Gly260 M13 Ι2 IF1 fd IKe V VJF XantoPhiLf PropionibacB5 255 -----



Supplementary Figure 4

