Supplemental Figure 1: Lindner *et al.* 2011

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PfPrex          SATSTFVSKYYKININDVYNYLHRKK--YEFIETDIKITLKYCPFCPPHK
Dm              MA--------------------------------SIVKAHLPCNTCGSH-
Vi06            MDNM--------------------------LDSDSIFLYHEPCPSCGSS-
T3              MER----------------------------EDDSIFLFHAPCENCGSS-
T7              MDNS--------------------------HDSDSVFLYHIPCDNCGSS-
K1F             MSYDD-------------------------QDDESVFLYHTQCPDCGSS-
phiIBB-PF7A     MSE---------------------------HEEESVLMHKGPCEFCGSS-
Pp              MPMKN-----------------RK------HETVSEFVRHLPCENCGSS-
285P            MDME--------------------------EQQESIFLYHLPCENCGPS-
TJI-51          ME------------------------------------------------
Bo              MAD------------------------------A----------------
phi15           MSHE--------------------------DREEAVLLHKGPCDHCGSS-
Vv              MAQ------------------------------ESNFLQKEPCPKCGSK-
VP4             MSYEY-----------------E-------DREESIFLYHLPCENCGSS-
Bw              MNNRK-----------------NDKSSERHPYEDSTFSHHEPCPQCQRNG
CPm             MQIT--------------------------NDEQTEFIRHESCPKCGSS-


PfPrex          YKYDNMYKHEIFKNTG------NSYCHR--CGYKGSFYDFKLKMGDLITS
Dm              ------DALC-TYSDG------STYCFS--CNTCIQK-------G-----
Vi06            ------DAGA-RYSDN------HFHCFV--CGHYIK--------G-----
T3              ------DGNS-VYSDG------HEWCFV--CEHRVP--------A-----
T7              ------DGNS-LFSDG------HTFCYV--CEKWTA--------G-----
K1F             ------DANG-VYSDG------HQFCFA--CDPSVA--------W-----
phiIBB-PF7A     ------DARA-VYSDG------HSFCYA--CPEGDA--------W-----
Pp              ------DANS-IYTDN------HQYCFA--CEHYVH--------G-----
285P            ------NGNG-MYSDG------HQYCFV--CQNHVR--------G-----
TJI-51          --------------------------------------------------
Bo              --------------------------------------------------
phi15           ------DARA-VYSDG------HSFCFA--CPEETA--------W-----
Vv              ------DNLA-RYDDG------HAHCFTNGCDYFEP--------A-----
VP4             ------DANS-MFSDG------HTFCYV--CEKYVP--------P-----
Bw              GDWNG-DNLA-RYSDG------HGYCHV--CGYYET--------A-----
CPm             ------DALA-VYGDSATQEVHHGWCFS--CQTFQK--------G-----


PfPrex          NFESTVVHNNNFYEEEEEKI----TLNDVKVYNMNLLYSKE-AENARNYL
Dm              --------NNDTVTI-------------------------PQ-DSLVISS
Vi06            --------DGYGPERSYK------RTGG-TPMTKG-VWSFGE-ANGRFSA
T3              --------NEEREAKLSTRR----RTGGSKPMSYD-VWNFGD-SNGRYSD
T7              --------NEDTKERASKRK----PSGG-KPMTYN-VWNFGE-SNGRYSA
K1F             --------KKGDMELTEGYT----PSGG-RKQVSN-LLTFGE-NAGRYVP
phiIBB-PF7A     --------KPGDGEYVPNA-----ARST-KPAAEG-TISFNE-KQGRYTA
Pp              --------DGETPTTGGRT-----------K------RMEGL-ISGEFKP
285P            --------TEETRETVAKTRRSSYNTGG-DKM-SN-LLNFGD-SDGRYTN
TJI-51          ----------------------------------------GL-ISGEFKP
Bo              ----------------------------------D-TASTGL-LRGEYRP
phi15           --------QAGEDYQGSQK-----EGVG-KTRSEG-TISFSE-KQGRYAA
Vv              --------TDNQ--RPPKQ-----KQQA-KPKK-E-RKEFTP-IEGEVRP
VP4             --------SGVEQTDSY-SN----TTGG-KKKMSN-VYSMQE-LNGGYQA
Bw              --------QGGSGRMDRQK-----------D-----PVPFDPVPVDAFMA
CPm             --------DNVDGSYTNTPKR-------------N-SSSANL-LDGEYNE
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PfPrex          MNVRKLSIDTLKKFLIGFSVME-FQSFESSGKFEKHECIIFPFIKKVDEI
Dm              LKKRGITKATCHKYGYYISKNA-KTPMQVACY------------------
Vi06            LTARGISKETCQKAGYWLAKVD-GVVYQVADY------------------
T3              LTARGISKETCQKAGYWLAKVD-NRMYQVADY------------------
T7              LTARGISKETCQKAGYWIAKVD-GVMYQVADY------------------
K1F             LPARSLSMEICKKYSYWVGNMG-GKMVQVADY------------------
phiIBB-PF7A     LKARGLMEDVCKQYGYWVGTFS-GESKQVANY------------------
Pp              LMKRKLTLETCRKFGYFVSEVR-GRLVQVAPY------------------
285P            LKARGLMEAICRKYGYWVAKVN-GEMLQVANY------------------
TJI-51          LMKRKLTLETCRKFGYFVSEVR-GRLVQVAPY------------------
Bo              LGKRGIAEETCRKYGYLVGEDRDGVPVQIATY------------------
phi15           LPKRGLMEAVCRQYGYWLGTFN-GETKQVANY------------------
Vv              LTKRGIREDTCKKYGYKVGKLSGGEWVQYIDV------------------
VP4             LNARGITEDTCRKYGYWVGKDQ-KVTYQIANY------------------
Bw              LKARGITQETCEHFGYGIGKAG-GKYCHIAPL------------------
CPm             IKSRGLTEETCRKFNYTTAIHN-GEPVQVATY------------------
                :  * :     .:     .        .

PfPrex          NMIETNGINSNMNKMNNNNNNNNNNNNNNNNNNNINDN-YEVVRIKIRSL
Dm              ----------------------------------YDD-NGECIGKKIRY-
Vi06            ----------------------------------RDQ-NGTIVSQKIRD-
T3              ----------------------------------RDQ-NGSIVSQKVRD-
T7              ----------------------------------RDQ-NGNIVSQKVRD-
K1F             ----------------------------------YDR-SGTKVGQKVRD-
phiIBB-PF7A     ----------------------------------YDM-DRNLVAQKVRD-
Pp              ----------------------------------FDN-SGVMVAQKLRD-
285P            ----------------------------------YDV-EGNLVGQKVRD-
TJI-51          ----------------------------------FDN-SGVMVAQKLRD-
Bo              ----------------------------------CDS-AGSPVAQKLRN-
phi15           ----------------------------------YGD-DGSIVAQKVRD-
Vv              ----------------------------------RDPLTRQLVAQKIRT-
VP4             ----------------------------------YDE-TGTLVFQKLRD-
Bw              ----------------------------------YDH-EGILVAQHLRF-
CPm             ----------------------------------LDE-NGRPVAQKVRT-
                                                   .      :  ::*

PfPrex          KDKGYMRLYPKNVRNEMKLFFFGDHLIK-NS--EEIVLTEGEIDAMTISQ
Dm              PDKHFAVE-----GTIS-HRFFGQHLWA-NGHMKKLVITEGEIDCLTVSQ
Vi06            KDKNFKTT-----GSHKSDALFGKHLWS-GG--KKIVVTEGEVDMLTVME
T3              KDKNFKTT-----GSHKSDALFLKHLWS-GG--KKIVVTEGEIDALTVME
T7              KDKNFKTT-----GSHKSDALFGKHLWN-GG--KKIVVTEGEIDMLTVME
K1F             AEKNFTAI-----GSVKSDMLFGSQLWN-GG--KKIVITEGEIDALSVAQ
phiIBB-PF7A     RHKEFFIA-----GKMPKDGLFGKHLWT-GG--KKIVVTEGEIDCLTVAQ
Pp              QDKGFAIL-----GDGAKLTLFGQNLWASGG--KKIVVTEGELDAMSVSQ
285P            KNKEFSAK-----GKLKADLLFGKQLWN-GG--KKIVVTEGEIDCLTVAQ
TJI-51          QDKGFAIL-----GDGAKLTLFGQNLWASGG--KKIVVTEGELDAMSVSQ
Bo              ADKEFVVV-----GKLKHAGLFGQHLWRTTG--KKVIVTEGEIDCLSVAQ
phi15           RNKEFFIA-----GSMPKDALFGKHLWS-GG--KKVVVTEGEIDCLTVAQ
Vv              ENKQFLVK-----GTLTG-ELIGAHLFS-GG--KKLIITEGEIDMLTVSQ
VP4             KDKNFKTR-----GKSSDSLMFGKNLWN-GG--RKLIITEGEIDCLTVAQ
Bw              EGKEFRWR-----GSASEAVLFGQTLWRRGG--RKVIVTEGEIDCLSISQ
CPm             KSKKFTML-----GDAKAATLYGSHLYK-TG--KKLVICEGEIDAMTVSQ
                  * :               :    *    .  .:::: ***:* ::: :
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PfPrex          --ETKYPAISLPNGSKSLPI---YLLPYLERFKKIHLWLDFDKAGKSSVF
Dm              LQENKYPCVSIPNGAASAKKVFKENMEWLNTFEEVIVMFDMDEAGRKAVE
Vi06            LQDCKYPVVSLGHGASAAKKTCAANYEYFDQFEQIILMFDMDEAGRKAVE
T3              LQDCKYPVVSLGHGASAAKKTCAANYEYFDQFEQIILMFDMDDAGRKAVE
T7              LQDCKYPVVSLGHGASAAKKTCAANYEYFDQFEQIILMFDMDEAGRKAVE
K1F             VQDGKYPVVSLPLGAKSAKKAMAANLEYLDQFEEIILMFDMDEPGRQAIE
phiIBB-PF7A     IQGGKYPVVSIPRGAEDAKKVCAANFEYFNQFEQIILMFDMDAPGRAASL
Pp              VQNNKWPVVSLPNGAPAARKAIQRNIEYLESFEEVILMFDMDEPGREAAQ
285P            LQEGKYPVVSLPMGAQAAKKTCAANFEYFDQFDEIILMFDMDEPGRKAIE
TJI-51          VQNNKWPVVSLPNGAPAARKAIQRNIEYLESFEEVILMFDMDEPGREAAQ
Bo              ALSLKWPVVSVPNGAQGAAKSLAAQIEWLRGYEEIVLWFDNDDPGREAVA
phi15           LQGGKYPVVSIPRGAKDAKKTIAANKDWFSGFQEIILMFDMDEDGRKAAL
Vv              VQSNKYPVVSLPNGISSAKKAIMNNLDYLSNFEEIILCFDMDEVGREGAV
VP4             IQGCKYPVVSIPLGAKAAKKCIAANLDYFEQFEEIILMFDQDDAGRAAAQ
Bw              LQGNKWPVVSLPNGSSSGAKYIRASLEWLESFDEVVFAFDMDEPGQKAAK
CPm             VQGHKWATVSLTQGCSSAVKTMKNNWEFITKFEEVILMFDMDSVGQKAAQ
                    *:. :*:  *             ::  :.:: . :* *  *: .

PfPrex          NFVNKIGLGRTNVI------TDANVHYLN-------PD
Dm              DVQGLLKPRKLKIANLP--LKDPNECLIAGRGQ----E
Vi06            EAAQVLPAGKVRVAVLP--CKDANECHLNGH------D
T3              EAAQVLPAGKVRVAVLP--CKDANECHIMGE------D
T7              EAAQVLPAGKVRVAVLP--CKDANECHLNGH------D
K1F             DAAPVLPAGRVKVAFIN-GYKDANAALQA-K------D
phiIBB-PF7A     EAADVLPAGKVHIAVLP--LKDPNECLLAGNSKAVIDQ
Pp              ECAELFSPGKCKIATLS--MKDANELLVAGREQ----E
285P            ECAPVLPSGKVRVAVLP--LKDANECLLNGQAKAV-TD
TJI-51          ECAELFSPGKCKIATLS--MKDANELLVAGREQ----E
Bo              ACAAILPPGRVKFITTPHELKDANDLLREHGPKAV-VD
phi15           EAAEVLPAGRVFIAKLP--LKDANECILNGHAKAV-MD
Vv              EAAELLIDHNVKIMSLP--LKDPNEMLLAGRT----EE
VP4             ECAEIMPMGKTKIAVLP--LKDANECLLAGKTKEV-ID
Bw              ECALLLSPGKAKIARLP--MKDANECLVAGKGKEL-ID
CPm             EAAATLPVGKAKIAYLP--CKDANECLLQGKSAEI-IQ
                     :   .  .       .*.*             :
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Abbreviations: **PfPrex**: PfPrex (AA115-465); **Dm**: Dialister microaerophilus DNA primase/helicase; **Vi06**: Salmonella phage Vi06 predicted DNA primase-helicase; **T3**: Enterobacteria phage T3 4A; **T7**: Enterobacteria phage T7 unnamed protein product; **K1F**: Enterobacteria phage K1F gp4A protein; **phiIBB-PF7A**: Pseudomonas phage phiIBB-PF7A putative primase/helicase; **Pp**: Pseudomonas putida KT2440 DNA primase/helicase; **285P**: Enterobacteria phage 285P gp4a; **TJI-51**: Pseudomonas sp. TJI-51 DNA primase/helicase; **Bo**: Burkholderia oklahomensis EO147 DNA primase; **phi15**: Pseudomonas phage phi15 putative DNA primase/helicase; **Vv**: Vibrio vulnificus MO6-24/O DNA primase/helicase; **VP4**: Vibriophage VP4 Primase/Helicase; **Bw**: Bilophila wadsworthia 3_1_6 toprim domain-containing protein; **CPm**: Candidatus Puniceispirillum marinum IMCC1322 DNA primase

Consensus Key:
* / asterisk: Identity
: / double-dot: Conserved Physiochemical Group
. / single-dot: Semi-Conserved Physiochemical Group