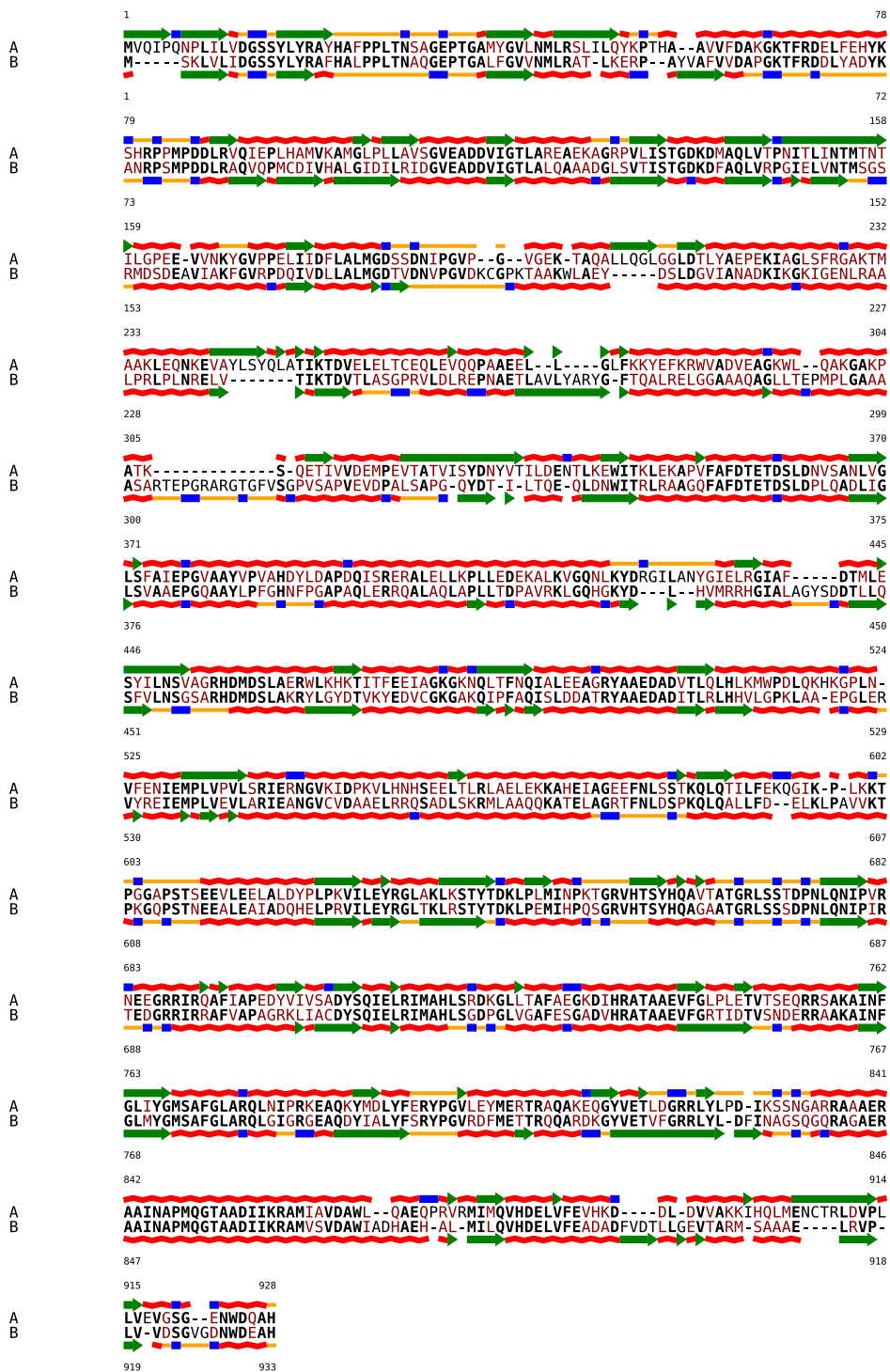# Additional file 1

Alignment and bi-alignment with at most one shift of the proteins DNA Polymerase I of *Escherichia* (`WP_016262675.1`) and *Xanthomonas hortorum* (`WP_095575020.1`); for comparison to Fig. 4 of the main text.

Alignment (Degenerated shift-free bi-alignment)

```
                1                                                                           78
A   MVQIPQNPLILVDGSSYLYRAYHAFPPLTNSAGEPTGAMYGVLNMLRSLILQYKPTHA--AVVFDAKGKTFRDELFEHYK
B   M-----SKLVLIDGSSYLYRAFHALPPLTNAQGEPTGALFGVVNMLRAT-LKERP--AYVAFVVDAPGKTFRDDLYADYK
                1                                                                           72

                79                                                                          158
A   SHRPPMPDDLRVQIEPLHAMVKAMGLPLLAVSGVEADDVIGTLAREAEKAGRPVLISTGDKDMAQLVTPNITLINTMTNT
B   ANRPSMPDDLRAQVQPMCDIVHALGIDILRIDGVEADDVIGTLALQAAADGLSVTISTGDKDFAQLVRPGIELVNTMSGS
                73                                                                          152

                159                                                                         232
A   ILGPEE-VVNKYGVPPELIIDFLALMGDSSDNIPGVP--G--VGEK-TAQALLQGLGGLDTLYAEPEKIAGLSFRGAKTM
B   RMDSDEAVIAKFGVRPDQIVDLLALMGDTVDNVPGVDKCGPKTAAKWLAEY-----DSLDGVIANADKIKGKIGENLRAA
                153                                                                         227

                233                                                                         304
A   AAKLEQNKEVAYLSYQLATIKTDVELELTCEQLEVQQPAAEEL--L-----GLFKKYEFKRWVADVEAGKWL--QAKGAKP
B   LPRLPLNRELV-------TIKTDVTLASGPRVLDLREPNAETLAVLYARYG-FTQALRELGGAAAQAGLLTEPMPLGAAA
                228                                                                         299

                305                                                                         370
A   ATK--------------S-QETIVVDEMPEVTATVISYDNYVTILDENTLKEWITKLEKAPVFAFDTETDSLDNVSANLVG
B   ASARTEPGRARGTGFVSGPVSAPVEVDPALSAPG-QYDT-I-LTQE-QLDNWITRLRAAGQFAFDTETDSLDPLQADLIG
                300                                                                         375

                371                                                                         445
A   LSFAIEPGVAAYVPVAHDYLDAPDQISRERALELLKPLLEDEKALKVGQNLKYDRGILANYGIELRGIAF-----DTMLE
B   LSVAAEPGQAAYLPFGHNFPGAPAQLERRQALAQLAPLLTDPAVRKLGQHGKYD---L--HVMRRHGIALAGYSDDTLLQ
                376                                                                         450

                446                                                                         524
A   SYILNSVAGRHDMDSLAERWLKHKTITFEEIAGKGKNQLTFNQIALEEAGRYAAEDADVTLQLHLKMWPDLQKHKGPLN-
B   SFVLNSGSARHDMDSLAKRYLGYDTVKYEDVCGKGAKQIPFAQISLDDATRYAAEDADITLRLHHVLGPKLAA-EPGLER
                451                                                                         529

                525                                                                         602
A   VFENIEMPLVPVLSRIERNGVKIDPKVLHNHSEELTLRLAELEKKAHEIAGEEFNLSSTKQLQTILFEKQGIK-P-LKKT
B   VYREIEMPLVEVLARIEANGVCVDAAELRRQSADLSKRMLAAQQKATELAGRTFNLDSPKQLQALLFD--ELKLPAVVKT
                530                                                                         607

                603                                                                         682
A   PGGAPSTSEEVLEELALDYPLPKVILEYRGLAKLKSTYTDKLPLMINPKTGRVHTSYHQAVTATGRLSSTDPNLQNIPVR
B   PKGQPSTNEEALEAIADQHELPRVILEYRGLTKLRSTYTDKLPEMIHPQSGRVHTSYHQAGAATGRLSSSDPNLQNIPIR
                608                                                                         687

                683                                                                         762
A   NEEGRRIRQAFIAPEDYVIVSADYSQIELRIMAHLSRDKGLLTAFAEGKDIHRATAAEVFGLPLETVTSEQRRSAKAINF
B   TEDGRRIRRAFVAPAGRKLIACDYSQIELRIMAHLSGDPGLVGAFESGADVHRATAAEVFGRTIDTVSNDERRAAKAINF
                688                                                                         767

                763                                                                         841
A   GLIYGMSAFGLARQLNIPRKEAQKYMDLYFERYPGVLEYMERTRAQAKEQGYVETLDGRRLYLPD-IKSSNGARRAAAER
B   GLMYGMSAFGLARQLGIGRGEAQDYIALYFSRYPGVRDFMETTRQQARDKGYVETVFGRRLYL-DFINAGSQGQRAGAER
                768                                                                         846

                842                                                                         914
A   AAINAPMQGTAADIIKRAMIAVDAWL--QAEQPRVRMIMQVHDELVFEVHKD----DL-DVVAKKIHQLMENCTRLDVPL
B   AAINAPMQGTAADIIKRAMVSVDAWIADHAEH-AL-MILQVHDELVFEADADFVDTLLGEVTARM-SAAAE----LRVP-
                847                                                                         918

                915           928
A   LVEVGSG--ENWDQAH
B   LV-VDSGVGDNWDEAH
                919           933
```

Bi-alignment with at most one shift of either sequence in either direction

```
     1                                                                        76
A  MVQIPQNPLILVDGSSYLYRAYHAFPPLT-NSAGEPTGAMYGVLNMLRSLI-LQYKPTHAA-VVFDAKGKTFRDELF-EH
B  M-----SKLVLIDGSSYLYRAFHALPPLT-NAQGEPTGALFGVVNMLRAT--LKERPAYVAFVV-DAPGKTFRDDLYAD-
     1                                                                        70

     77                                                                       150
A  YKSHRPPMPDDL-RVQIEPL-----HAMVKAMGLPLLA-VSGVEADDVIGTLAREAEKAGRPVLISTGDKDMAQLVTPNIT
B  YKANRPSMPDDL-RAQVQPMCDIVHA----LGIDILR-IDGVEADDVIGTLALQAAADGLSVTISTGDKDFAQLVRPGIE
     71                                                                      144

     151                                                                      226
A  LINTMTNTILGPEE-VVNKYGVPPELIIDFLALMGDS-SDNIPGVPGVGEKT-AQALLQGLGGLDTLYAEPEKIAG-LSF
B  LVNTMSGSRMDSDEAVIAKFGVRPDQIVDLLALMGDT-VDNVPGVDKCGPKTAAKWLAE-YDSLDGVIANADKIKGKI--
     145                                                                     220

     227                                                                      296
A  RGAKTMAA--KLEQNKEVAYLSYQLATIKTDVELELTCEQLEVQQPAAEEL--L----GLFKKYEFKRWV--ADVEAGKW
B  -GENLRAALPRLPLNRELV------TIKTDVTLASGPRVLDLREPNAETLAVLYARYG-FTQ-ALRE-LGGAAAQAGL-
     221                                                                     288

     297                                                                      354
A  L-QAK--GAKPATKSQE------T-IV---VDEMP-EVT-ATVIS----YDNYVTIL-DENTLKEWIT-KLEKAPV-FAF
B  LTEPMPLGAAAASARTEPGRARGTGFVSGPV-SAPVEVDPA--LSAPGQYD---TILTQEQ-LDNWIT-RLRAAGQ-FAF
     289                                                                     359

     355                                                                      431
A  DTETDSLDNVSANLVG-LSFAIEPGVAAYVPVAHDYLDAP-DQISRERALELLKPLLEDEKAL-KVGQNLKYDRGILANY
B  DTETDSLDPLQADLIG-LSVAAEPGQAAYLPFGHNFPGAP-AQLERRQALAQLAPLLTD-PAVRKLGQH---D-------
     360                                                                     425

     432                                                                      497
A  G-IELR-----GIAFD-----TMLESYILNSVAG--RHDMDSLAERWLKHKTITFEEIAGKGKNQLTFNQIALEEAG-RY
B  GKYDLHVMRRHGIALAGYSDDTLLQSFVLNS--GSARHDMDSLAKRYLGYDTVKYEDVCGKGAKQIPFAQISLDDAT-RY
     426                                                                     502

     498                                                                      573
A  AAEDAD-VTLQLHLKMWPDLQKHKGPLN-VFENIE-MPLVPVLSRIERNGVKIDPKVLHNHSEEL-TLRLAELEKKAHEI
B  AAEDAD-ITLRLHHVLGPKLAAEPG-LERVYREIE-MPLVEVLARIEANGVCVDAAELRRQSADL-SKRMLAAQQKATEL
     503                                                                     578

     574                                                                      648
A  A-GEEFNLSSTKQLQTILFEKQGIK-P-LKKTPGGAPSTSEEVLEELALD-YPLPKVI-LEYRGLAKLKSTYTDKLPLMI
B  A-GRTFNLDSPKQLQALLFDE--LKLPAVVKTPKGQPSTNEEALEAIA-DQHELPRVI-LEYRGLTKLRSTYTDKLPEMI
     579                                                                     653

     649                                                                      723
A  NPKT-GRVHT-SYHQAVTATGRLSSTDPNLQNIPVRN-EEGRRIRQAFIAP--EDYVIVSADYSQIELRIMAHLSRDKGL
B  HPQS-GRVHT-SYHQAGAATGRLSSSDPNLQNIPIRT-EDGRRIRRAFVAPAGRK--LIACDYSQIELRIMAHLSGDPGL
     654                                                                     728

     724                                                                      801
A  L-TAFAEGKDIHRATAAEVFGLPLETVTSEQRRSAKAINFGLIYGMSAFGLARQLNIPRKEAQKYMDLYFERYPG-VLEY
B  V-GAFESGADVHRATAAEVFGRTIDTVSNDERRAAKAINFGLMYGMSAFGLARQLGIGRGEAQDYIALYFSRYPG-VRDF
     729                                                                     806

     802                                                                      875
A  MERTRAQAKEQ-GYVETLDGRRLYLPD-IKS-SN-GARRAAAERAAINAPMQGTAADIIKRAMIAVDAWL--QAEQPRVR
B  METTRQQARDK-GYVETVFGRRLYL-DFINAGSQ-G-QRAGAERAAINAPMQGTAADIIKRAMVSVDAWIADHAEH-AL-
     807                                                                     880

     876                                                          928
A  MIMQVHDELVFEVHKD--D--L-D-VVAKKIHQLMENCTRLDVPLLVEV-GSG--ENWDQAH
B  MILQVHDELVFEADADFVDTLLGE-VTARM-SAAAE---LRVPLVVD---SGVGDNWDEAH
     881                                                          933
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