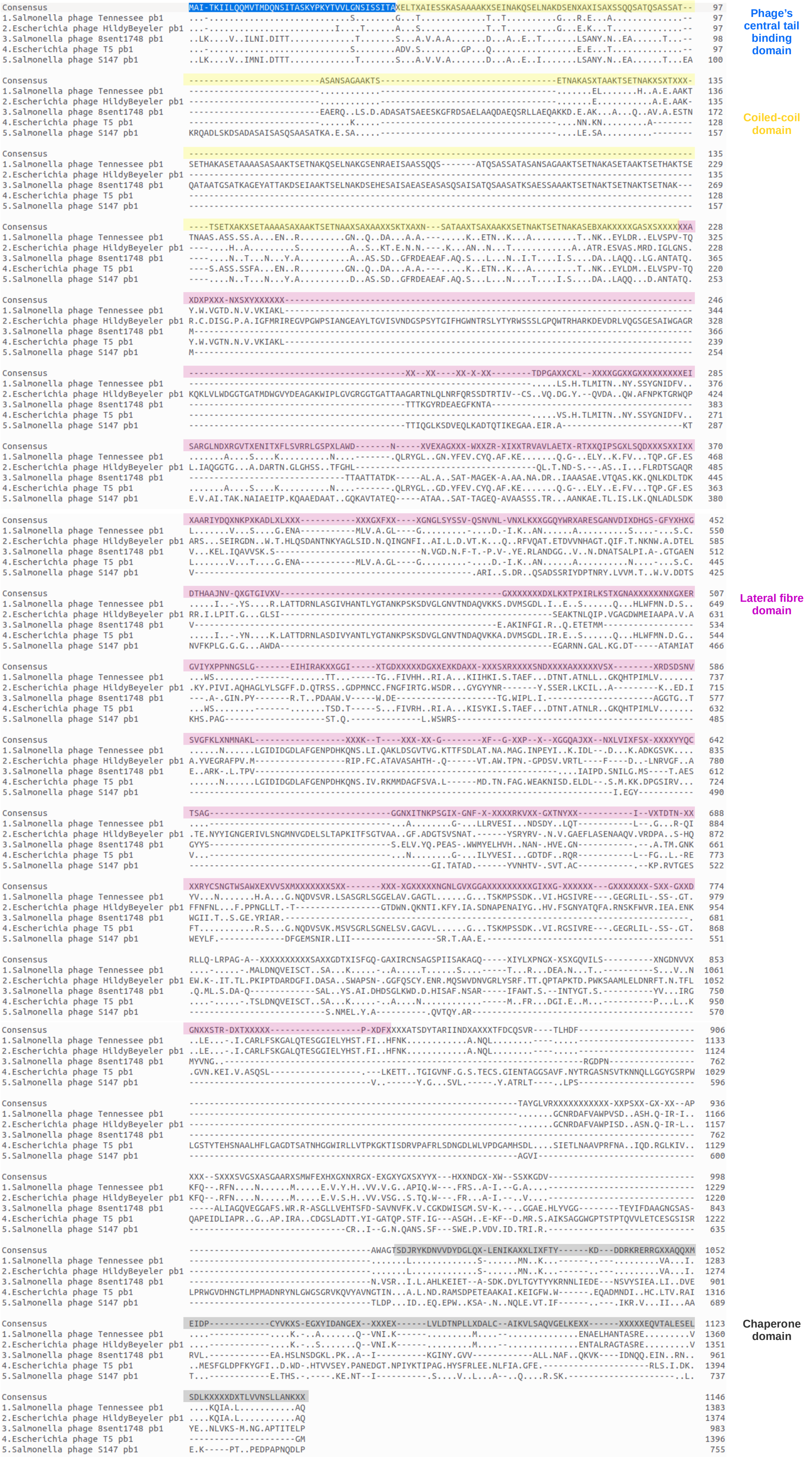

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Consensus                            MAI-TKIILQQMVTMDQNSITASKYPKYTVVLGNSISSITAXELTXAIESSKASAAAAKXSEINAKQSELNAKDSENXAXISAXSSQQSATQSASSAT--    97
1.Salmonella phage Tennessee pb1     ...-............................S........G...T.............T..T..........G...R.E...A..............--    97
2.Escherichia phage HildyBeyeler pb1 ...-.........................I....T......A...S.............T..T..........G...E.K...T..............--    97
3.Salmonella phage 8sent1748 pb1     ..LK....V..ILNI.DITT.............T.......S...A.V.A.A.......D...A..E..T.......LSANY.N..EA......T...--    98
4.Escherichia phage T5 pb1           ...-............................S........ADV.S........GP...Q.................E.E...T..............--    97
5.Salmonella phage S147 pb1          ..LK....V..IMNI.DTTT.............T.......S...A.V.V.A.......D...A..E..I.......LSANY.N..EA......T...EA   100

Consensus                            --------------------------ASANSAGAAKTS-----------------------------------ETNAKASXTAAKTSETNAKXSXTXXX-   135
1.Salmonella phage Tennessee pb1     --------------------------............-----------------------------------.......EL.......H..A.E.AAKT   136
2.Escherichia phage HildyBeyeler pb1 --------------------------............-----------------------------------.......E...........A.E.AAK-   135
3.Salmonella phage 8sent1748 pb1     --------------------------EAERQ..LS.D.ADASATSAEESKGFRDSAELAAQDAEQSRLLAEQAKKD.E.AK...A...Q..AV.A.ESTN   172
4.Escherichia phage T5 pb1           --------------------------......K.....-----------------------------------....NN.KN.........A--------   128
5.Salmonella phage S147 pb1          KRQADLSKDSADASAISASQSAASATKA.E.SA.....-----------------------------------....LE.SA..........--------   157

Consensus                            ----------------------------------------------------------------------------------------------------   135
1.Salmonella phage Tennessee pb1     SETHAKASETAAAASASAAKTSETNAKQSELNAKGSENRAEISAASSQQS-------ATQSASSATASANSAGAAKTSETNAKASETAAKTSETHAKTSE   229
2.Escherichia phage HildyBeyeler pb1 ----------------------------------------------------------------------------------------------------   135
3.Salmonella phage 8sent1748 pb1     QATAATGSATKAGEYATTAKDSEIAAKTSELNAKDSEHESAISAEASEASASQSAISATQSAASATKSAESSAAAKTSETNAKTSETNAKTSETNAK---   269
4.Escherichia phage T5 pb1           ----------------------------------------------------------------------------------------------------   128
5.Salmonella phage S147 pb1          ----------------------------------------------------------------------------------------------------   157

Consensus                            ----TSETXAKXSETAAAASAXAAKTSETNAAXSAXAAXXSKTXAXN---SATAAXTSAXAAKXSETNAKTSETNAKASEBXAKXXXXGASXSXXXXXXA   228
1.Salmonella phage Tennessee pb1     TNAAS.ASS.SS.A...EN..R.........GN..Q..DA...A.A.---.....K..ETN..K...A.........T..NK..EYLDR..ELVSPV-TQ   325
2.Escherichia phage HildyBeyeler pb1 ----....H..A.........S..........A..S..KT.E.N.N.---.K...AN..N...T............A..ATR.ESVAS.MRD.IGLGNS.   228
3.Salmonella phage 8sent1748 pb1     ----....N..T...N...Y.A..........A..AS.SD..GFRDEAEAF.AQ.S...L...N..I.T....I.S....DA..LAQQ..LG.ANTATQ.   365
4.Escherichia phage T5 pb1           ----S.ASS.SSFA...EN..R.........GN..Q..DA...A.A.---.....K..ETN..K...A.........T..NK..EYLDM..ELVSPV-TQ   220
5.Salmonella phage S147 pb1          ----....N..T...N...Y.A..........D..AS.SD..GFRDEAEAF.AQ.S...L...N....T....I.S....DA..LAQQ...D.ANTATQ.   253

Consensus                            XDXPXXX-NXSXYXXXXXX---------------------------------------------------------------------------------   246
1.Salmonella phage Tennessee pb1     Y.W.VGTD.N.V.VKIAKL---------------------------------------------------------------------------------   344
2.Escherichia phage HildyBeyeler pb1 R.C.DISG.P.A.IGFMRIREGVPGWPSIANGEAYLTGVISVNDGSPSYTGIFHGWNTRSLYTYRWSSSLGPQWTRHARKDEVDRLVQGSGESAIWGAGR   328
3.Salmonella phage 8sent1748 pb1     M---------------------------------------------------------------------------------------------------   366
4.Escherichia phage T5 pb1           Y.W.VGTN.N.V.VKIAKL---------------------------------------------------------------------------------   239
5.Salmonella phage S147 pb1          M---------------------------------------------------------------------------------------------------   254

Consensus                            ------------------------------------------XX--XX----XX-X-XX--------TDPGAXXCXL--XXXXGGXXGXXXXXXXXXXEI   285
1.Salmonella phage Tennessee pb1     --------------------------------------------------------------------.....LS.H.TLMITN..NY.SSYGNIDFV..   376
2.Escherichia phage HildyBeyeler pb1 KQKLVLWDGGTGATMDWGVYDEAGAKWIPLGVGRGGTGATTAAGARTNLQLNRFQRSSDTRTIV--CS..VQ.DG.Y.--QVDA..QW.AFNPKTGRWQP   424
3.Salmonella phage 8sent1748 pb1     ------------------------------------------TTTKGYRDEAEGFKNTA-----------------------------------------   383
4.Escherichia phage T5 pb1           --------------------------------------------------------------------.....VS.H.TLMITN..NY.SSYGNIDFV..   271
5.Salmonella phage S147 pb1          ------------------------------------------TTIQGLKSDVEQLKADTQTIKEGAA.EIR.A-------------------------KT   287

Consensus                            SARGLNDXRGVTXENITXFLSVRRLGSPXLAWD-------N-----XVEXAGXXX-WXXZR-XIXXTRVAVLAETX-RTXXQIPSGXLSQDXXXSXXIXX   370
1.Salmonella phage Tennessee pb1     .......A....S....K..........N....-------.QLRYGL..GN.YFEV.CYQ.AF.KE.......Q.G-..ELY..K.FV...TQP.GF.ES   468
2.Escherichia phage HildyBeyeler pb1 L.IAQGGTG...A.DARTN.GLGHSS..TFGHL------------------------------------QL.T.ND-S.--.AS..I...FLRDTSGAQR   485
3.Salmonella phage 8sent1748 pb1     -------------------------------TTAATTATDK-----AL.A..SAT-MAGEK-A.AA.NA.DR..IAAASAE.VTQAS.KK.QNLKDLTDK   445
4.Escherichia phage T5 pb1           .......A....S....K..........N....-------.QLRYGL..GD.YFEV.CYQ.AF.KE.......Q.G-..ELY..E.FV...TQP.GF.ES   363
5.Salmonella phage S147 pb1          E.V.AI.TAK.NAIAEITP.KQAAEDAAT..GQKAVTATEQ-----ATAA..SAT-TAGEQ-AVAASSS.TR...AANKAE.TL.IS.LK.QNLADLSDK   380

Consensus                            XAARIYDQXNKPXKADLXLXXX-----------XXXGXFXX----XGNGLSYSSV-QSNVNL-VNXLKXXGGQYWRXARESGANVDIXDHGS-GFYXHXG   452
1.Salmonella phage Tennessee pb1     L.......V...S....G.ENA-----------MLV.A.GL----G.........-....D.-I.K..AN.....A...........S....-...S.C.   550
2.Escherichia phage HildyBeyeler pb1 ARS...SEIRGDN..W.T.HLQSDANTNKYAGLSID.N.QINGNFI..AI.L.D.VT.K...Q..RFVQAT.ETDVVNHAGT.QIF.T.NKNW.A.DTEL   585
3.Salmonella phage 8sent1748 pb1     V...KEL.IQAVVSK.S-----------------------------N.VGD.N.F-T.-P.V-.YE.RLANDGG..V..N.DNATSALPI.A-.GTGAEN   512
4.Escherichia phage T5 pb1           L.......V...T....G.ENA-----------MLV.A.GL----G.........-....D.-I.K..AN.....A...........N....-...S.C.   445
5.Salmonella phage S147 pb1          V-------------------------------------------------------.ARI..S.DR..QSADSSRIYDPTNRY.LVVM.T..W.V.DDTS   425

Consensus                            DTHAAJNV-QXGTGIVXV-------------------------------------------GXXXXXXXDXLKXTPXIRLKSTXGNAXXXXXXXNXGXER   507
1.Salmonella phage Tennessee pb1     .....I..-.YS....R.LATTDRNLASGIVHANTLYGTANKPSKSDVGLGNVTNDAQVKKS.DVMSGDL.I..E..S......Q...HLWFMN.D.S..   649
2.Escherichia phage HildyBeyeler pb1 RR.I.LPIT.G...GLSI------------------------------------------------------SEAKTNLQIP.VGAGDWMEIAAPA.V.A   631
3.Salmonella phage 8sent1748 pb1     V------------------------------------------------------------E.AKINFGI.R..Q.ETETMM------------------   534
4.Escherichia phage T5 pb1           .....I..-.YN....K.LATTDRNLASDIVYANTLYGTANKPSKSDVGLGNVTNDAQVKKA.DVMSGDL.IR.E..S......Q...HLWFMN.D.G..   544
5.Salmonella phage S147 pb1          NVFKPLG.G.G...AWDA------------------------------------------------------EGARNN.GAL.KG.DT-----ATAMIAT   466

Consensus                            GVIYXPPNNGSLG-------EIHIRAKXXGGI-----XTGDXXXXXDGXXEXKDAXX-XXXSXRXXXXSNDXXXXAXXXXXVSX--------XRDSDSNV   586
1.Salmonella phage Tennessee pb1     ...WS........-------.......TT...-----TG..FIVHH..RI.A...KIIHKI.S.TAEF...DTNT.ATNLL..GKQHTPIMLV.......   737
2.Escherichia phage HildyBeyeler pb1 .KY.PIVI.AQHAGLYLSGFF.D.QTRSS..GDPMNCC.FNGFIRTG.WSDR...GYGYYNR-------Y.SSER.LKCIL..A---------K..ED.I   715
3.Salmonella phage 8sent1748 pb1     ---.A-.GIN.PY-------R.T..PDAAW.V-----W.DE--------------------TG.WIPL.I.---------------------AGGTG..T   577
4.Escherichia phage T5 pb1           ...WS........-------.......TSD.T-----S...FIVRH..RI.A...KISYKI.S.TAEF...DTNT.ATNLR..GKQHTPIMLV.......   632
5.Salmonella phage S147 pb1          KHS.PAG--------------------ST.Q.--------------L.WSWRS-----------------------------------------------   485

Consensus                            SVGFKLXNMNAKL------------------XXXK--T----XXX-XX-G--------XF--G-XXP--X--XGGQAJXX--NXLVIXFSX-XXXXYYQC   642
1.Salmonella phage Tennessee pb1     ......N......LGIDIDGDLAFGENPDHKQNS.LI.QAKLDSGVTVG.KTTFSDLAT.NA.MAG.INPEYI..K.IDL--.D...K.ADKGSVK....   835
2.Escherichia phage HildyBeyeler pb1 A.YVEGRAFPV.M------------------RIP.FC.ATAVASAHTH-.Q------VT.AW.TPN.-GPDSV.VRTL----F----D..-LNRVGF..A   780
3.Salmonella phage 8sent1748 pb1     E..ARK-.L.TPV------------------------------------------------------------....IAIPD.SNILG.MS----T.AES   612
4.Escherichia phage T5 pb1           ......N......LGIDIDGDLAFGENPDHKQNS.IV.RKMMDAGFSVA.L------MD.TN.FAG.WEAKNISD.ELDL--.S.M.KK.DPGSIRV...   724
5.Salmonella phage S147 pb1          ------------------------------------------------------------------------------------I.EGY-----------   490

Consensus                            TSAG------------------------------------GGNXITNKPSGIX-GNF-X-XXXXRKVXX-GXTNYXX-----------I--VXTDTN-XX   688
1.Salmonella phage Tennessee pb1     ....------------------------------------...A........G-...LLRVESI...NDSDY..LQT-----------L--.G...R-QI   884
2.Escherichia phage HildyBeyeler pb1 .TE.NYYIGNGERIVLSNGMNVGDELSLTAPKITFSGTVAA..GF.ADGTSVSNAT.------YSRYRV-.N.V.GAEFLASENAAQV.VRDPA..S-HQ   872
3.Salmonella phage 8sent1748 pb1     GYYS------------------------------------S.ELV.YQ.PEAS-.WWMYELHVH..NAN-.HVE.GN-----------.--.A.TM.GNK   661
4.Escherichia phage T5 pb1           V...------------------------------------...N........G-...ILYVESI...GDTDF..RQR-----------L--FG..L.-RE   773
5.Salmonella phage S147 pb1          ------------------------------------------------GI.TATAD.------YVNHTV-.SVT.AC-----------.--KP.RVTGES   522

Consensus                            XXRYCSNGTWSAWXEXVVSXMXXXXXXXXSXX------XXX-XGXXXXXNGNLGVXGGAXXXXXXXXXGIXXG-XXXXXX---GXXXXXXX-SXX-GXXD   774
1.Salmonella phage Tennessee pb1     YV...N.......H.A...G.NQDVSVR.LSASGRLSGGELAV.GAGTL......G...TSKMPSSDK..VI.HGSIVRE---.GEGRLIL-.SS-.GT.   979
2.Escherichia phage HildyBeyeler pb1 FFNFNL...F.PPNGLLT.-T-----------------GTDWN.QKNTI.KFY.IA.SDNAPENAIYG..HV.FSGNYATQFA.RNSKFWVR.IEA.ENK   954
3.Salmonella phage 8sent1748 pb1     WGII.T..S.GE.YRIAR.--------------------------------------------------------------------------------.   681
4.Escherichia phage T5 pb1           FT..........R.S...G.NQDVSVK.MSVSGRLSGNELSV.GAGVL......G...TSKMPSSDK..VI.RGSIVRE---.GEGRLIL-.SS-.GT.   868
5.Salmonella phage S147 pb1          WEYLF.-------------DFGEMSNIR.LII-----------------SR.T.AA.E.-----------------------------------------   551

Consensus                            RLLQ-LRPAG-A--XXXXXXXXXXXSAXXGDTXISFGQ-GAXIRCNSAGSPIISAKAGQ----XIYLXPNGX-XSXGQVILS----------XNGDNVVX   853
1.Salmonella phage Tennessee pb1     ....-.....-.MALDNQVEISCT..SA...K......-..A.....T......S....----T...R...DEA.N...T..----------S...V..N  1061
2.Escherichia phage HildyBeyeler pb1 EW.K-.IT.TL.PKIPTDARDGFI.DASA..SWAPSN-.GGFQSCY.ENR.MQSWVDNVGRLYSRF.TT.QPTAPKTD.PWKSAAMLELDNRFT.N.TFL  1052
3.Salmonella phage 8sent1748 pb1     .Q.ML.S.DA-Q-------------SAL..YS.AI.DHDSGLKWD.D.HISAF.NSAR-----IFAWT.S.--INTYGT.S.----------YV...IRG   750
4.Escherichia phage T5 pb1           ....-.....-.TSLDNQVEISCT..SA...K......-..A....N............----M..FR...DGI.E..M...----------P...L..K   950
5.Salmonella phage S147 pb1          ---------------------------S.NMEL.Y.A-----------.QVTQY.AR-------------------------------------------   570

Consensus                            GNXXSTR-DXTXXXXX------------------P-XDFXXXXATSDYTARIINDXAXXXTFDCQSVR----TLHDF-----------------------   906
1.Salmonella phage Tennessee pb1     ..LE...-.I.CARLFSKGALQTESGGIELYHST.FI..HFNK............A.NQL........----.....-----------------------  1133
2.Escherichia phage HildyBeyeler pb1 ..LE...-.I.CARLFSKGALQTESGGIELYHST.FI..HFNK............A.NQL........----.....-----------------------  1124
3.Salmonella phage 8sent1748 pb1     MYVNG..-----------------------------------------------------------------------RGDPN-----------------   762
4.Escherichia phage T5 pb1           .GVN.KEI.V.ASQSL------------------.---LKETT..TGIGVNF.G.S.TECS.GIENTAGGSAVF.NYTRGASNSVTKNNQLLGGYGSRPW  1029
5.Salmonella phage S147 pb1          ------------------------------------V..------Y.G...SVL.-----.Y.ATRLT----..LPS-----------------------   596

Consensus                            -----------------------------------------------------------------TAYGLVRXXXXXXXXXXX-XXPSXX-GX-XX--AP   936
1.Salmonella phage Tennessee pb1     -----------------------------------------------------------------.......GCNRDAFVAWPVSD..ASH.Q-IR-I..  1166
2.Escherichia phage HildyBeyeler pb1 -----------------------------------------------------------------.......GCNRDAFVAWPISD..ASN.Q-IR-L..  1157
3.Salmonella phage 8sent1748 pb1     ----------------------------------------------------------------------------------------------------   762
4.Escherichia phage T5 pb1           LGSTYTEHSNAALHFLGAGDTSATNHGGWIRLLVTPKGKTISDRVPAFRLSDNGDLWLVPDGAMHSDL....SIETLNAAVPRFNA..IQD.RGLKIV..  1129
5.Salmonella phage S147 pb1          -----------------------------------------------------------------AGVI-------------------------------   600

Consensus                            XXX--SXXXSVGSXASGAARXSMWFEXHXGXNXRGX-EXGXYGXSXYYX---HXXNDGX-XW--SSXKGDV-----------------------------   998
1.Salmonella phage Tennessee pb1     KFQ--.RFN....N......M.....E.V.Y.H..VV.V.G..APIQ.W---.FRS..A-I.--G.A....-----------------------------  1229
2.Escherichia phage HildyBeyeler pb1 KFQ--.RFN....N......M.....E.V.S.H..VV.VSG..S.TQ.W---.FR...A-I.--..V....-----------------------------  1220
3.Salmonella phage 8sent1748 pb1     -----ALIAGQVEGGAFS.WR.R-ASGLLVEHTSFD-SAVNVFK.V.CGKDWISGM.SV-K.--..GGAE.HLYVGG--------TEYIFDAAGNGSAS-   843
4.Escherichia phage T5 pb1           QAPEIDLIAPR..G..AP.IRA..CDGSLADTT.YI-GATQP.STF.IG---ASGH..E-KF--D.MR.S.AIKSAGGWGPTSTPTQVVLETCESGSISR  1222
5.Salmonella phage S147 pb1          -------------------------------CR..I--G.N.QANS.SF---SWE.P.VDV.ID.TRI.R.-----------------------------   635

Consensus                            ------------------------------------AWAGTSDJRYKDNVVDYDGLQX-LENIKAXXLIXFTY------KD---DDRKRERRGXXAQQXM  1052
1.Salmonella phage Tennessee pb1     ------------------------------------.......L.............S-......MN..K...------..---.........VA...I.  1283
2.Escherichia phage HildyBeyeler pb1 ------------------------------------.......L.............S-......MN..K...------..---.........VA...I.  1274
3.Salmonella phage 8sent1748 pb1     ------------------------------------N.VSR..I.L.AHLKEIET--A-SDK.DYLTGYTYYKRNNLIEDE---NSVYSIEA.LI..DVE   901
4.Escherichia phage T5 pb1           LPRWGVDHNGTLMPMADNRYNLGWGSGRVKQVYAVNGTIN...A.L.ND.RAMSDPETEAAKAI.KEIGFW.W------.EQADMNDI..HC.LTV.RAI  1316
5.Salmonella phage S147 pb1          ------------------------------------TLDP...ID..EQ.EPW..KSA-.N..NQLE.VT.IF------..---.IKR.V...II...AA   689

Consensus                            EIDP------------CYVKXS-EGXYIDANGEX--XXXEX------LVLDTNPLLXDALC--AIKVLSAQVGELKEXX------XXXXXEQVTALESEL  1123
1.Salmonella phage Tennessee pb1     ....------------....K.-..A.......Q--VNI.K------.........M....--..............ENAELHANTASRE.........V  1360
2.Escherichia phage HildyBeyeler pb1 ....------------....K.-..S.......Q--VNI.K------.........M....--..............ENTALRAGTASRE.........V  1351
3.Salmonella phage 8sent1748 pb1     RVL.------------EA.HSLNSDGKL.PK..A--I--------KGINY.GVV--------------ALL.NAF..QKVK----IDNQQ.EIN..RN..   961
4.Escherichia phage T5 pb1           ..MESFGLDPFKYGFI..D.WD-.HTVVSEY.PANEDGT.NPIYKTIPAG.HYSFRLEE.NLFIA.GFE.---------------------RLS.I.DK.  1394
5.Salmonella phage S147 pb1          T...------------E.THS.-.-----.KE.NT--I---------.S....V..L...A--..Q....R.SK.----------------------.L.   737

Consensus                            SDLKXXXXDXTLVVNSLLANKXX                                                                              1146
1.Salmonella phage Tennessee pb1     ....KQIA.L...........AQ                                                                              1383
2.Escherichia phage HildyBeyeler pb1 ....KQIA.L...........AQ                                                                              1374
3.Salmonella phage 8sent1748 pb1     YE..NLVKS-M.NG.APTITELP                                                                               983
4.Escherichia phage T5 pb1           ---------------------GM                                                                              1396
5.Salmonella phage S147 pb1          E.K-----PT..PEDPAPNQDLP                                                                               755
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Figure S2. MUSCLE (v.5.1) alignment of the five LTFpb1 protein sequences from the four representative Tequintaviruses and Salten. Dots represent an identical aminoacid compared to the consensus sequence, dashes represent gaps. Written aminoacid letters indicate a variation compared to the consensus sequence. Domains known thanks to T5 modeling (Garcia-Doval et al., 2015) are highlighted.