iScience, Volume *27*

Supplemental information

Diverse bacteriophages for biocontrol of ESBL- and AmpC-β-lactamase-producing *E. coli*

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Supplementary information

Table S2: The ability of each phage to infect diverse phylogroup and ST, related to Figure 4.
Table S3: List of primers for deletions of common bacteriophage receptor genes in *E. coli* strain ECOR4, related to Figure 5.
Table S4: List of primers for control of the deletion of genes expressing common bacteriophage receptor genes in *E. coli* strain ECOR4, related to Figure 5.
Figure S1: Protein sequence alignment of gp38 corresponding to the chaperone encoded by T4, related to Figure 5.
Figure S2: Protein sequence alignment of the tail fibers corresponding to the adhesins encoded by gp38 homologues of the phages T2 and T6, related to Figure 5.
Figure S3: Protein sequence alignment of gp37 of T4 and its homologues, related to Figure 5.

References

1. Vitt, A.R., Sørensen, M.C.H., Bortolaia, V., and Brøndsted, L. (2023). A Representative Collection of Commensal Extended-Spectrum- and AmpC-β-Lactamase-Producing Escherichia coli of Animal Origin for Phage Sensitivity Studies. PHAGE: Therapy, Applications, and Research *4*, 35–45. 10.1089/phage.2023.0002

Table S2: The ability of each phage to infect diverse phylogroup and STs, related to Figure 4.

Phage	Number of infected strains	Phylo-groups	STs based on MLST analysis
AV101	9	A, B1, C	ST-1800, ST-2040, ST-6206, ST-641, ST-88
AV102	4	B1, C	ST-162, ST-1431, ST-23
AV103	4	B1, C	ST-23, ST-641, ST-6254, ST-453
AV104	2	D	ST-69, ST-4243
AV105	2	D	ST-69, ST-4243
AV106	1	C	ST88
AV108	5	A, B1	ST-295, ST-10, ST-154, ST-6206
AV109	9	B1, C	ST-88, ST-7614, ST-4663, ST-295
AV110	48	A, B1, B2, C, G	ST-10, ST-101, ST-117, ST-1431, ST-154, ST-155, ST-156, ST-23, ST-295, ST-345, ST-3564, ST-429, ST-4580, ST-4663, ST-4980, ST-58, ST-665, ST-718, ST-75, ST-88
AV111	46	A, B1, C, D, E, F	ST-10, ST-1147, ST-1640, ST-23, ST-2607, ST-354, ST-4243, ST-453, ST-4663, ST-4980, ST-57, ST-58, ST-641
AV112	37	A, B1, C, D	ST-10, ST-101, ST-1011, ST-1431, ST-154, ST-155, ST-156, ST-1800, ST-2040, ST-295, ST-3564, ST-4580, ST-48, ST-4980, ST-58, ST-718, ST-75, ST-877, ST-88
AV113	25	A, B1, C, E	ST-295, ST-10, ST-101, ST-1431, ST-154, ST-155, ST-156, ST-1800, ST-295, ST-3564, ST-48, ST-57, ST-58, ST-718, ST-877, ST-88
AV114	29	A, B1, C, G	ST-117, ST-155, ST-165, ST-295, ST-3564, ST-453, ST-4663, ST-4980, ST-718, ST-7614, ST-88
AV115	33	A, B1, C, G	ST-101, ST-117, ST-1431, ST-165, ST-295, ST-3564, ST-453, ST-4663, ST-58, ST-88
AV116	17	A, B1, C	ST-101, ST-1431, ST-154, ST-155, ST-156, ST-1800, ST-2040, ST-295, ST-4580, ST-6206, ST-88
AV117	16	A, B1, C	ST-101, ST-1431, ST-154, ST-155, ST-156, ST-1800, ST-2040, ST-295, ST-4580, ST-6206, ST-88
AV118	9	A, B1, C	ST-155, ST-1850, ST-4580, ST-88
AV119	55	A, B1, B2, C, D, E, F	ST-10, ST-1147, ST-115, ST-131, ST-1640, ST-23, ST-355, ST-367, ST-4243, ST-453, ST-4663, ST-4980, ST-57, ST-6858, ST-69, ST-877, ST-88
AV120	50	A, B1, B2, C, D, E	ST-10, ST-131, ST-1640, ST-23, ST-2607, ST-367, ST-4243, ST-453, ST-4663, ST-4980, ST-57, ST-58, ST-602, ST-877, ST-88
AV121	26	Clade I, A, B1, B2, C, D	ST-115, ST-131, ST-2309, ST-355, ST-4243, ST-453, ST-4980, ST-770, ST-88
AV122	16	Clade I, B1, C, E	ST-101, ST-1431, ST-154, ST-155, ST-1640, ST-4580, ST-770, ST-877, ST-88
AV123	51	A, B1, B2, C, D, E	ST-101, ST-1056, ST-1147, ST-1286, ST-131, ST-1463, ST-154, ST-155, ST-162, ST-1800, ST-1850, ST-2040, ST-23, ST-2607, ST-38, ST-4243, ST-429, ST-4580, ST-4663, ST-4980, ST-57, ST-602, ST-6206, ST-718, ST-88
AV124	2	C	ST-23, ST-88
AV125	84	A, B1, B2, C, D, E	ST-10, ST-101, ST-1011, ST-1056, ST-1147, ST-115, ST-1431, ST-1463, ST-154, ST-155, ST-156, ST-162, ST-1640, ST-1800, ST-1850, ST-2040, ST-23, ST-2309, ST-2607, ST-295, ST-345, ST-3564, ST-367, ST-38, ST-4243, ST-429, ST-4580, ST-4663, ST-4980, ST-57, ST-602, ST-6206, ST-6254, ST-718, ST-88
AV126	65	Clade I, A, B1, B2, C, D, E	ST-770, ST-10, ST-101, ST-1011, ST-115, ST-1463, ST-154, ST-155, ST-1640, ST-1800, ST-1850, ST-2040, ST-23, ST-2607, ST-295, ST-345, ST-351, ST-38, ST-4243, ST-429, ST-4580, ST-4980, ST-57, ST-602, ST-6206, ST-718, ST-877, ST-88
AV127	13	A, B1, C	ST-1463, ST-155, ST-23, ST-4980, ST-4980, ST-57, ST-602, ST-88
AV128	8	A, B1, D, E	ST-101, ST-1640, ST-2197, ST-38, ST-57
AV129	12	A, B1, C, D, E	ST-1640, ST-23, ST-2952, ST-4243, ST-4980

Table S3: List of primers for deletions of common bacteriophage receptor genes in *E. coli* strain ECOR4, related to Figure 5.

Primers for deletion fragment amplification	
ompW-Up	ATGAAAAAGTTAACAGTGGCGGCTTTGGCAGTAACAACTCTTCTCTCTGG*AATTAACCCTCACTAAAGGGCG*
ompW-Dw	TTAAAAACGATATCCTGCTGAGAGCATAAACACCCACGGATCGAGGCGTA*TAATACGACTCACTATAGGGCTC*
tsx-Up	ATGAAAAAAACATTACTGGCAGCCGGTGCGGTACTGGCGCTCTCTTCGTC*AATTAACCCTCACTAAAGGGCG*
tsx-Dw	TCAGAAGTTGTAACCTACTACCAGGTAACCACCCCAGCCGGTAGAGCGAA*TAATACGACTCACTATAGGGCTC*
waaC-Up	ATGCGGGTTTTGATCGTTAAAACATCGTCGATGGGCGATGTTCTCCATAC*AATTAACCCTCACTAAAGGGCG*
waaC-Dw	TTAAATCAATGTGATTTTTTTATAAACAGCCGCTGCTTCTAAATTATTTA*TAATACGACTCACTATAGGGCTC*
tonB-Up	ATGACCCTTGATTTACCTCGCCGCTTCCCCTGGCCGACGTTACTTTCGGT*AATTAACCCTCACTAAAGGGCG*
tonB-Dw	TTACTGAATTTCGGTGGTGCCGTTAATTTTAAACAGGATATTCACCACAA*TAATACGACTCACTATAGGGCTC*
waaR-Up	ATGAATGAATTTATAAAAGAACGGTTTTCGTATTTAGCAGATAATAAAAA*AATTAACCCTCACTAAAGGGCG*
waaR-Dw	TTATTTCTTAAGCTTGTACTTAATTAATGAAGTTATGCCTTTTATATACT*TAATACGACTCACTATAGGGCTC*
ompF-Up	ATGATGAAGCGCAATATTCTGGCAGTGATCGTCCCTGCTCTGTTAGTAGC*AATTAACCCTCACTAAAGGGCG*
ompF-Dw	TTAGAACTGGTAAACGATACCCACAGCAACGGTGTCGTCTGAACCTACGC*TAATACGACTCACTATAGGGCTC*
fadL-Up	ATGAGCCAGAAAACCCTGTTTACAAAGTCTGCTCTCGCAGTCGCAGTGGC*AATTAACCCTCACTAAAGGGCG*
fadL-Dw	TCAGAACGCGTAGTTAAAGTTAGTACCGAACAGCCAGGCTTTACCTTCAG*TAATACGACTCACTATAGGGCTC*
ompA-Up	ATGAAAAAGACAGCTATCGCGATTGCAGTGGCACTGGCTGGTTTCGCTAC*AATTAACCCTCACTAAAGGGCG*
ompA-Dw	TTAAGCCTGCGGCTGAGTTACAACGTCTTTGATACCTTTAACTTCGATCT*TAATACGACTCACTATAGGGCTC*
ompC-Up	ATGAAAGTTAAAGTACTGTCCCTCCTGGTCCCAGCTCTGCTGGTAGCAGG*AATTAACCCTCACTAAAGGGCG*
ompC-Dw	TTAGAACTGGTAAACCAGACCCAGAGCTACGATGTTATCAGTGTTGATGC*TAATACGACTCACTATAGGGCTC*
fhuA-Up	ATGGCGCGTTCCAAAACTGCTCAGCCAAAACACTCACTGCGTAAAATCGC*AATTAACCCTCACTAAAGGGCG*
fhuA-Dw	TTAGAAACGGAAGGTTGCGGTTGCAACGACCTGACGTTCTGCGCCCCAGA*TAATACGACTCACTATAGGGCTC*
fepA-Up	ATGAACAAGAAGATTCATTCCCTGGCCTTGTTGGTCAATCTGGGGATTTA*AATTAACCCTCACTAAAGGGCG*
fepA-Dw	TCAGAAGTGGGTGTTTACGCTCATATACCACGTACGTCCCGGCTCGTTAT*TAATACGACTCACTATAGGGCTC*
btuB-Up	CCGCTTGGGCACAGGATACCAGCCCGGATACTCTCGTCGTTACTGCTAACC*AATTAACCCTCACTAAAGGGCG*
btuB-Dw	ATCGATCAAGTCACTGACATCGTTACGATATCCGGAAATACGCCAGTTCA*TAATACGACTCACTATAGGGCTC*
tolC-Up	ATGAAGAAATTGCTCCCCATTCTTATCGGCCTGAGCCTTTCTGGGTTCAG*AATTAACCCTCACTAAAGGGCG*
tolC-Dw	TCAGTTACGGAAAGGGTTATGACCGTTACTGGTGGTAGTGCGTGCGGATG*TAATACGACTCACTATAGGGCTC*

lamB-Up	ATGATGATTACTCTGCGCAAACTTCCTCTGGCGGTTGCCGTCGCAGCGGG*AATTAACCCTCACTAAAGGGCG*
lamB-Dw	TTACCACCAGATTTCCATCTGGGCACCGAAGGTCCACTCGTCGCTGTCGC*TAATACGACTCACTATAGGGCTC*

Table S4: List of primers for control of the deletion of genes expressing common bacteriophage receptor genes in *E. coli* strain ECOR4, related to Figure 5.

Primers for deletion control	
ompW-F	ATGAAAAAGTTAACAGTGGCG
ompW-R	TTAAAAACGATATCCTGCTGAGAG
tsx_F	ATGAAAAAAACATTACTGGCAGCC
tsx_R	TCAGAAGTTGTAACCTACTACCAGG
waaC_F	ATGCGGGTTTTGATCGTTAAAACATC
waaC_R	TTAAATCAATGTGATTTTTTTATAAACAGCCG
tonB-F	ATGACCCTTGATTTACCTCGC
tonB-R	TTACTGAATTTCGGTGGTGC
waaR_F	ATGAATGAATTTATAAAAGAACGGTTTTCG
waaR_R	TTATTTCTTAAGCTTGTACTTAATTAATGAAGTTA
ompF_F	ATGATGAAGCGCAATATTCTGGC
ompF_R	TTAGAACTGGTAAACGATACCCACAG
fadL_F	ATGAGCCAGAAAACCCTGTTTACAAAG
fadL_R	TCAGAACGCGTAGTTAAAGTTAGTAC
ompA_F	ATGAAAAAGACAGCTATCGCGATTG
ompA_R	TTAAGCCTGCGGCTGAGTTACAAC
ompC_F	ATGAAAGTTAAAGTACTGTCCCTCC
ompC_R	TTAGAACTGGTAAACCAGACCCAG
fhuA_F	ATGGCGCGTTCCAAAACTGC
fhuA_R	TTAGAAACGGAAGGTTGCGGTTG
fepA-F	ATGAACAAGAAGATTCATTCCCTG
fepA-R	TCAGAAGTGGGTGTTTACGC
btuB_F	ATGATTAAAAAAGCTTCGCTGCTGAC
btuB_R	TCAGAAGGTGTAGCTGCCAGACAAG
tolC_F	ATGAAGAAATTGCTCCCCATTCTTATC
tolC_R	TCAGTTACGGAAAGGGTTATGACC

lamB_F	ATGATGATTACTCTGCGCAAACTTC
lamB_R	TTACCACCAGATTTCCATCTGGG

Figure S1: Protein sequence alignment of gp38 corresponding to the chaperone encoded by T4, related to Figure 5.
Differing residues are highlighted in red colour.

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AV112_Gp38 MKLYHYYFDT KEFYKEENYK PLKGVGFPAH STPKKPLDPK EGYAIIFDER EQEWVYVEDH RGKTVWTYDK QKIVIDTPGA LQNVTTEEPG EFDIWTDDGW KEDEAYKRVV 110
AV113_Gp38 MKLYHYYFDT KEFYKEENYK PLKGVGFPAH STPKKPLDPK EGYAIIFDER EQEWVYVEDH RGKTVWTYDK QKIVIDTPGA LQNVTTEEPG EFDIWTDDGW KEDEAYKRVV 110
AV116_Gp38 MKLYHYYFDT KEFYKEENYK PLKGVGFPAH STPKKPLDPK EGYAVVFDER EQEWVYIEDH RGKTVWTYDK QKIVIDTPGA LQNVTTEEPG EFDIWTDDGW KEDEAYKRVV 110
AV118_Gp38 MKLYHYYFDT KEFYKEENYK PLKGVGFPAH STPKKPLDPK EGYAVVFDER EQEWVYIEDH RGKTVWTYDK QKIVIDTPGA LQNFTTEEPG EFDIWTDDGW KEDEAYKRVV 110
AV110_Gp38 MKLYHYYFDT KEFYKEENYK PLKGVGFPAH STPKKPLDPK EGYAVIFDER EQEWVYVEDH RGKTVWTYDK QKIVIDTPGA LQNVTTEEPG EFDLWTDDGW KEDEAYKRVV 110
AV117_Gp38 MKIYHYYFDT KEFYKEENYK LVKGLGLPAH STIKKPLDPK EGYAVVFDER EQEWVYVEDH RGKTVWTYDK QKIVIDTPGA LQNVTTEEPG EFDIWTGDGW KEDEAYKRVV 110
AV122_Gp38 MKIYHYYFDT KEFYKEENYK PVKGLGLPAH STIKKPLEPK EGYAVVFDER TQDWIYEEDH RGKRAWTFNK EEIFISEIGS PVGITFDEPG EFDIWTDDGW KEDETYKRVL 110
   T4_Gp38 MKIYHYYFDT KEFYKEENYK PVKGLGLPAH STIKKPLEPK EGYAVVFDER TQDWIYEEDH RGKRAWTFNK EEIFISDIGS PVGITFDEPG EFDIWTDDGW KEDETYKRVL 110
Conservation

AV112_Gp38 QRDKKIHELY KLFSVLSSLI DAEVANREEK RKFKELKKFF ALLEKHEHLG GEFPKFPDLE NKSIIKAIIN IFK 183
AV113_Gp38 QRDKKIHELY KLFSVLSSLI DAEVANREEK RKFKELKKFF ALLEKHEHLG GEFPKFPDLE NKSIIKAIIN IFK 183
AV116_Gp38 QRDKKIHELY KLFSVLSSLI DAEVANREEK RKFKELKKFF ALLEKHEHLG GEFPKFPDLE NKSIFKAIIN IFK 183
AV118_Gp38 QRDKKIHELY KLFSVLSSLI DAEVANREEK RKFKELKKFF ALLEKHEHLG GEFPKFPDLE NKSIFKAIIN IFK 183
AV110_Gp38 QRDKKIHELY KLFSVLSSLI DAEVANREEK RKFKELKKFF ALLEKHEHLG GEFPKFPDLE SKSLVKRIIN IFK 183
AV117_Gp38 QRDKKIHELY KLFSVLSSLI DAEVANREEK RKFKELKKFF ALLEKHEHLG GEFPKFPDLE NKSIIKAIIN IFK 183
AV122_Gp38 IRNRKIEELY KEFQVLNNMI EASVANKKEK FYYKNLKRFF ALLEKHEHLG GEFPAWPEKE QKPWYKRLFK HYV 183
   T4_Gp38 IRNRKIEELY KEFQVLNNMI EASVANKKEK FYYKNLKRFF ALLEKHEHLG GEFPSWPEKE QKPWYKRLFK HYV 183
Conservation
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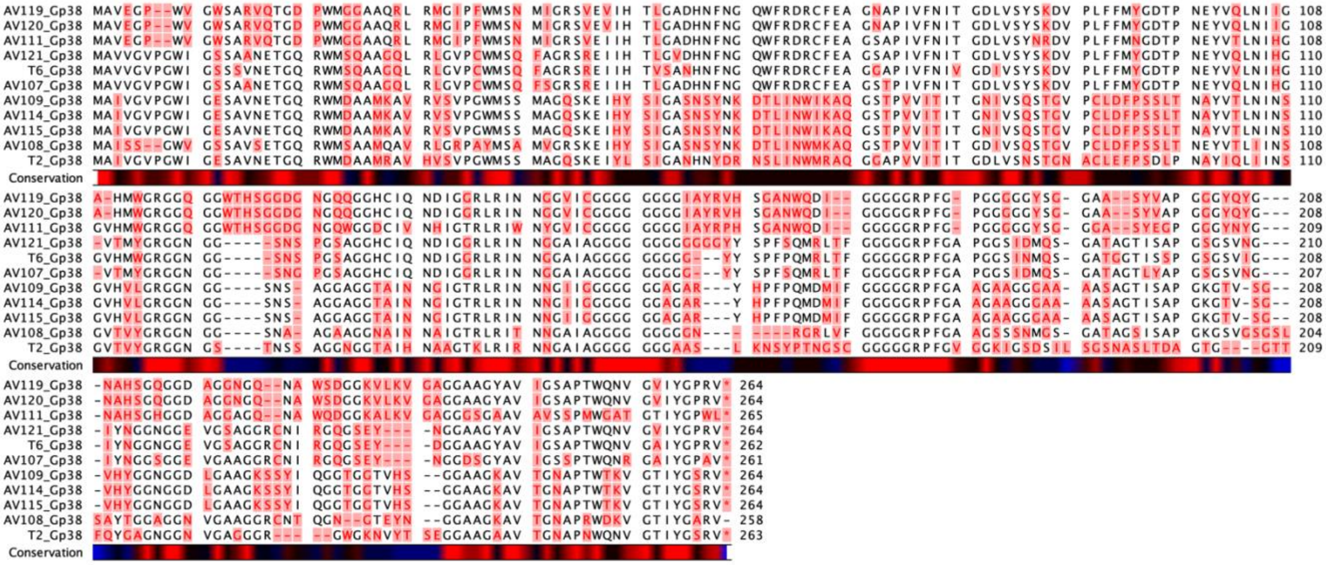
Figure S2 Protein sequence alignment of the tail fibers corresponding to the adhesins encoded by gp38 homologues of the phages T2 and T6, related to Figure 5. Differing residues are highlighted in red colour.



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AV119_Gp38 MAVEGP--WV GWSARVQTGD PWMGGAAQRL RMGIPFWMSN MIGRSVEVIH TLGADHNFNG QWFRDRCFEA GNAPIVFNIT GDLVSYSKDV PLFFMYGDTP NEYVQLNIIG 108
AV120_Gp38 MAVEGP--WV GWSARVQTGD PWMGGAAQRL RMGIPFWMSN MIGRSVEVIH TLGADHNFNG QWFRDRCFEA GNAPIVFNIT GDLVSYSKDV PLFFMYGDTP NEYVQLNIIG 108
AV111_Gp38 MAVEGP--WV GWSARVQTGD PWMGGAAQRL RMGIPFWMSN MIGRSVEIIH TLGADHNFNG QWFRDRCFEA GSAPIVFNIT GDLVSYNRDV PLFFMNGDTP NEYVTLNIHG 108
AV121_Gp38 MAVVGVPGWI GSSAANETGQ RWMSQAAGQL RLGVPCWMSQ FAGRSREIIH TLGVDHNFNG QWFRDRCFEA GSAPIVFNIT GDLVSYSKDV PLFFMYGDTP NEYVQLNIHG 110
   T6_Gp38 MAVVGVPGWI GSSSVNETGQ RWMSQAAGQL RLGVPCWMSQ FAGRSREIIH TVSANHNFNG QWFRDRCFEA GGAPIVFNIV GDIVSYSKDV PLFFMYGDTP NEYVVLNIHG 110
AV107_Gp38 MAVVGVPGWI GSSAANETGQ RWMSQAAGQL RLGVPCWMSQ FSGRSREIIH TLGADHNFNG QWFRDRCFEA GSTPIVFNIT GDLVSYSKDV PLFFMYGDTP NEYVQLNIHG 110
AV109_Gp38 MAIVGVPGWI GESAVNETGQ RWMDAAMKAV RVSVPGWMSS MAGQSKEIHY SIGASNSYNK DTLINWIKAQ GSTPVVITIT GNIVSQSTGV PCLDFPSSLT NAYVTLNINS 110
AV114_Gp38 MAIVGVPGWI GESAVNETGQ RWMDAAMKAV RVSVPGWMSS MAGQSKEIHY SIGASNSYNK DTLINWIKAQ GSTPVVITIT GNIVSQSTGV PCLDFPSSLT NAYVTLNINS 110
AV115_Gp38 MAIVGVPGWI GESAVNETGQ RWMDAAMKAV RVSVPGWMSS MAGQSKEIHY SIGASNSYNK DTLINWIKAQ GSTPVVITIT GNIVSQSTGV PCLDFPSSLT NAYVTLNINS 110
AV108_Gp38 MAISS--GWV GSSAVSETGQ RWMSAAMQAV RLGRPAYMSA MVGRSKEIHY SIGASNSYNK DTLINWMKAQ GSTPVVITIT GDIVSQSTGV PCLDFPSSLT NEYVTLIINS 108
   T2_Gp38 MAIVGVPGWI GESAVNETGQ RWMDAAMRAV HVSVPGWMSS MAGQSKEIYL SIGANHNYDR NSLINWMRAQ GGAPVVITIT GDLVSNSTGN ACLEFPSDLP NAYIQLIINS 110
Conservation

AV119_Gp38 A-HMWGRGGQ GGWTHSGGDG NGQQGGHCIQ NDIGGRLRIN NGGVICGGGG GGGGIAYRVH SGANWQDI-- GGGGGRPFG- PGGGGGYSG- GAA--SYVAP GGGYQYG--- 208
AV120_Gp38 A-HMWGRGGQ GGWTHSGGDG NGQQGGHCIQ NDIGGRLRIN NGGVICGGGG GGGGIAYRVH SGANWQDI-- GGGGGRPFG- PGGGGGYSG- GAA--SYVAP GGGYQYG--- 208
AV111_Gp38 GVHMWGRGGQ GGWTHSGGDG NGQWGGDCIV NHIGTRLRIW NYGVICGGGG GGGGIAYRPH SGANWQDI-- GGGGGRPFG- PGGGGGYSG- GGA--SYEGP GGGYNYG--- 209
AV121_Gp38 -VTMYGRGGN GG-----SNS PGSAGGHCIQ NDIGGRLRIN NGGAIAGGGG GGGGGGGGYY SPFSQMRLTF GGGGGRPFGA PGGSIDMQS- GATAGTISAP GSGSVNG--- 210
   T6_Gp38 GVHMWGRGGN GG-----SNS PGSAGGHCIQ NDIGGRLRIN NGGAIAGGGG GGGGG---YY SPFPQMRLTF GGGGGRPFGA PGGSINMQS- GATGGTISSP GSGSVIG--- 208
AV107_Gp38 -VTMYGRGGN GG-----SNG PGSAGGHCIQ NDIGGRLRIN NGGAIAGGGG GGGGG---YY SPFSQMRLTF GGGGGRPFGA PGGSIDMQS- GATAGTLYAP GSGSVNG--- 207
AV109_Gp38 GVHVLGRGGN GG----SNS- AGGAGGTAIN NGIGTRLRIN NNGIIGGGGG GGAGAR---Y HPFPQMDMIF GGGGGRPFGA AGAAGGGAA- AASAGTISAP GKGTV-SG-- 208
AV114_Gp38 GVHVLGRGGN GG----SNS- AGGAGGTAIN NGIGTRLRIN NNGIIGGGGG GGAGAR---Y HPFPQMDMIF GGGGGRPFGA AGAAGGGAA- AASAGTISAP GKGTV-SG-- 208
AV115_Gp38 GVHVLGRGGN GG----SNS- AGGAGGTAIN NGIGTRLRIN NNGIIGGGGG GGAGAR---Y HPFPQMDMIF GGGGGRPFGA AGAAGGGAA- AASAGTISAP GKGTV-SG-- 208
AV108_Gp38 GVTVYGRGGN GG----SNA- AGAAGGNAIN NAIGTRLRIT NNGAIAGGGG GGGGGN---- ----RGRLVF GGGGGRPFGA AGSSSNMGS- GATAGSISAP GKGSVGSGSL 204
   T2_Gp38 GVTVYGRGGN GS----TNSS AGGNGGTAIH NAAGTKLRIR NNGAIAGGGG GGGAAS---L KNSYPTNGSC GGGGGRPFGV GGKIGSDSIL SGSNASLTDA GTG----GTT 209
Conservation

AV119_Gp38 -NAHSGQGGD AGGNGQ--NA WSDGGKVLKV GAGGAAGYAV IGSAPTWQNV GVIYGPRV* 264
AV120_Gp38 -NAHSGQGGD AGGNGQ--NA WSDGGKVLKV GAGGAAGYAV IGSAPTWQNV GVIYGPRV* 264
AV111_Gp38 -NAHSGHGGD AGGAGQ--NA WQDGGKALKV GAGGGSGAAV AVSSPMWGAT GTIYGPWL* 265
AV121_Gp38 -IYNGGNGGE VGSAGGRCNI RGQGSEY--- -NGGAAGYAV IGSAPTWQNV GVIYGPRV* 264
   T6_Gp38 -IYNGGNGGE VGSAGGRCNI RGQGSEY--- -DGGAAGYAV IGSAPTWQNV GAIYGPRV* 262
AV107_Gp38 -IYNGGSGGE VGAAGGRCNI RGQGSEY--- -NGGDSGYAV IGSSPTWQNR GAIYGPAV* 261
AV109_Gp38 -VHYGGNGGD LGAAGKSSYI QGGTGGTVHS --GGAAGKAV TGNAPTWTKV GTIYGSRV* 264
AV114_Gp38 -VHYGGNGGD LGAAGKSSYI QGGTGGTVHS --GGAAGKAV TGNAPTWTKV GTIYGSRV* 264
AV115_Gp38 -VHYGGNGGD LGAAGKSSYI QGGTGGTVHS --GGAAGKAV TGNAPTWTKV GTIYGSRV* 264
AV108_Gp38 SAYTGGAGGN VGAAGGRCNT QGN--GTEYN --GGAAGKAV TGNAPRWDKV GTIYGARV- 258
   T2_Gp38 FQYGAGNGGN VGAGGGR--- --GWGKNVYT SEGGAAGAAV TGNAPNWQNV GTIYGSRV* 263
Conservation
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Figure S3. Protein sequence alignment of gp37 of T4 and full sequences of gp37 of phage T4 and AV110, AV112, AV113, AV116, AV117, AV118, AV122, related to Figure 5. Differing residues are highlighted in red.