

1 **Supplemental Information for:**  
2 **Alterations in gp37 expand the host range of a T4-like phage**

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11 Running title: gp37 replacement expands phage host range

12

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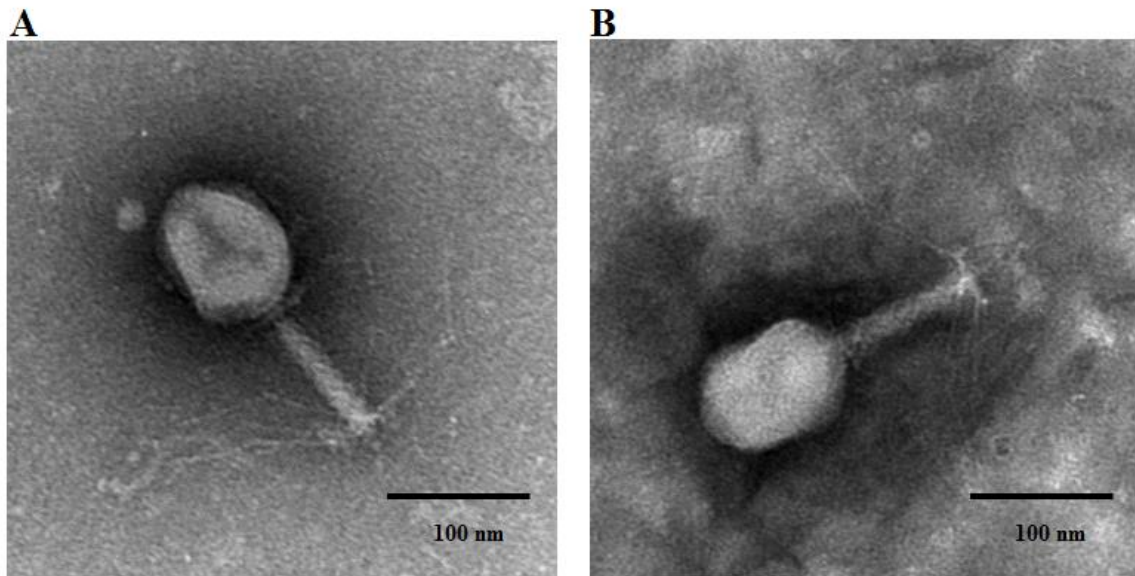
20 **Tables**

21 **Table S1** strains used in phage isolation and host range analysis of recombinant  
22 phages

23 **Table S2** T4-like phages that show a high homology with the WG01 genome sequence

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25 **Table S4** The DNA sequences of chimeric phages and mutants from the WQT  
26 chimeric phage



27

28 **Fig. S1 Electron microscopy images of QL01 and WG01**

29 **(A) Electron microscopy image of WG01.**

30 **(B) Electron microscopy image of QL01.**

31 The phage filtrate was applied to a copper grid coated with a carbon support film

32 before negative staining with phosphotungstic acid (PTA, 2% w/v). Electron

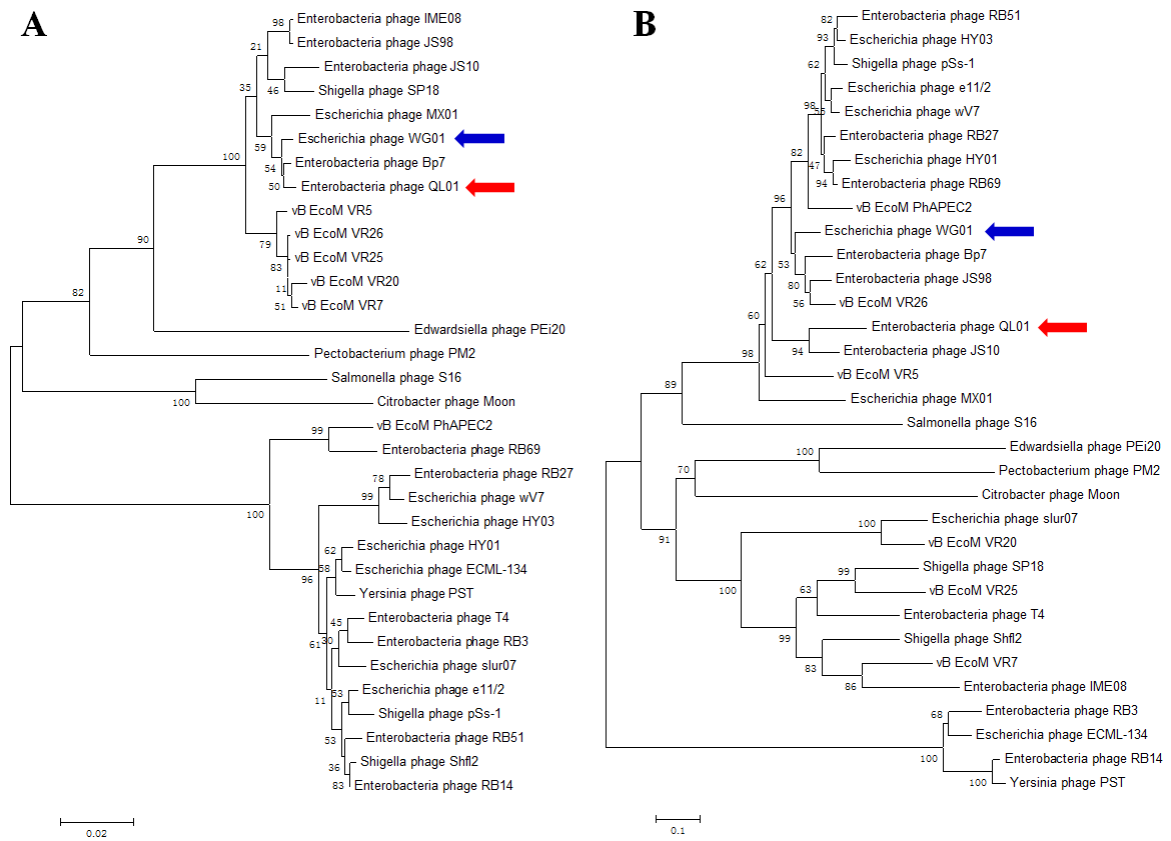
33 micrographs were generated with an H\_7650 (Hitachi, Japan) transmission electron

34 microscope (TEM).

35 WG01 possessed an icosahedral head and a contractile tail, which exhibited the same

36 morphology as QL01.

37



38

39 **Fig. S2 Phylogenetic trees for the amino acid sequences of gp23 and gp37**

40 A neighbor-joining tree analysis and bootstrap analysis (1000 bootstrap replicates)

41 based on the alignment of the amino acid sequence of gp23 (A) and gp37 (B) of 33

42 T4-like phages. The numbers at the nodes indicate the bootstrap probabilities of that

43 particular branch. The phylogenetic tree based on gp23 revealed that WG01 shared a

44 close phylogenetic relationship with Bp7 and QL01; however, in the distance tree of

45 gp37, WG01 shared a close phylogenetic relationship with Bp7, JS98, and

46 vB\_EcoM-VR26, but a distant phylogenetic relationship with QL01. Moreover, QL01

47 and JS10 shared a close evolutionary relationship.

48

# A

```
wV7 1 MATLKQIQFKRSKTAGARPAASVLAEGELAINLKDRVLFTRKDDGQNIIDLGFAKGGSIDGNVITHGNYNQTGDYTLNGFTQIGNFNIGIARVTRDITAG
WG01 1 MATLKQIQFKRSKTAGARPAASVLAEGELAINLKDRVLFTRKDDGQNIIDLGFAKGGSIDGNVITHGNYNQTGDYTLNGFTQIGNFNIGIARVTRDITAG
JS10 1 MATLKQIQFKRSKTAGARPAASVLAEGELAINLKDRVLFTRKDDGQNIIDLGFAKGGSIDGNVITHGNYNQTGDYTLNGFTQIGNFNIGIARVTRDITAG
QL01 1 MATLKQIQFKRSKTAGARPAASVLAEGELAINLKDRVLFTRKDDGQNIIDLGFAKGGSIDGNVITHGNYNQTGDYTLNGFTQIGNFNIGIARVTRDITAG

wV7 101 AGQIMTEGGELTIKSSGTAAHVRFFD-CNSRREGIITAPANDGLTQVNIIRVQDYAAGSESTYAFSGSGLFTSPEVSAWKSISSEPCITLIDKVIITNGKRIK
WG01 101 AGQIMTEGGELTIKSSGTAAHVRFFD-CNSRREGIITAPANDGLTQVNIIRVQDYAAGSESTYAFSGSGLFTSPEVSAWKSISSEPCITLIDKVIITNGKRIK
JS10 101 AGQIMTEGGELTIKSSGTAAHVRFFD-CNSRREGIITAPANDGLTQVNIIRVQDYAAGSESTYAFSGSGLFTSPEVSAWKSISSEPCITLIDKVIITNGKRIK
QL01 101 KSRIMTTEGIVVGNSTAAHVRFFD-CNSRREGIITAPANDGLTQVNIIRVQDYAAGSESTYAFSGSGLFTSPEVSAWKSISSEPCITLIDKVIITNGKRIK

wV7 200 DYDIYSLANNTPISESTFAINHLRVMRNVAGSGIFHEVKDNDGITWYAGDGLAYLWSFTWSGGLKAGHSISIGTPGGPKGYSELGTASIALGDNDTGLK
WG01 200 DYDIYSLANNTPISESTFAINHLRVMRNVAGSGIFHEVKDNDGITWYAGDGLAYLWSFTWSGGLKAGHSISIGTPGGPKGYSELGTASIALGDNDTGLK
JS10 200 DYDIYSLANNTPISESTFAINHLRVMRNVAGSGIFHEVKDNDGITWYAGDGLAYLWSFTWSGGLKAGHSISIGTPGGPKGYSELGTASIALGDNDTGLK
QL01 201 DYDIYSLANNTPISESTFAINHLRVMRNVAGSGIFHEVKDNDGITWYAGDGLAYLWSFTWSGGLKAGHSISIGTPGGPKGYSELGTASIALGDNDTGLK

wV7 300 WIIHDGYFVSNNGKIKLIFSESEITSLRKFVAGYSTNGDLDLPEPTONYALATVITYHDNAFGDQGLLGYQCGNYHHYFRGKGTINVTAGGLLVTF
WG01 300 WIIHDGYFVSNNGKIKLIFSESEITSLRKFVAGYSTNGDLDLPEPTONYALATVITYHDNAFGDQGLLGYQCGNYHHYFRGKGTINVTAGGLLVTF
JS10 300 WIIHDGYFVSNNGKIKLIFSESEITSLRKFVAGYSTNGDLDLPEPTONYALATVITYHDNAFGDQGLLGYQCGNYHHYFRGKGTINVTAGGLLVTF
QL01 297 WIIHDGYFVSNNGKIKLIFSESEITSLRKFVAGYSTNGDLDLPEPTONYALATVITYHDNAFGDQGLLGYQCGNYHHYFRGKGTINVTAGGLLVTF

wV7 400 GNIIDVYGGSVNIDGRNNSSTLMEFGNTTGSSSVDNMTIISWGNFTFNIPSEGRKKNVME
WG01 400 GNIIDVYGGSVNIDGRNNSSTLMEFGNTTGSSSVDNMTIISWGNFTFNIPSEGRKKNVME
JS10 400 GNIIDVYGGSVNIDGRNNSSTLMEFGNTTGSSSVDNMTIISWGNFTFNIPSEGRKKNVME
QL01 397 GNIIDVYGGSVNIDGRNNSSTLMEFGNTTGSSSVDNMTIISWGNFTFNIPSEGRKKNVME
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# B

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wV7 458 IISDATSWMSYIQRTTAGKVESYLNQITMNIENLTVKNAIFLGHISAAECISGAVNALRIWNDYGAIFRNSEGLLHIPTAFGGCKNGITIGPLRPFST
WG01 457 IISDATSWMSYIQRTTAGKVESYLNQITMNIENLTVKNAIFLGHISAAECISGAVNALRIWNDYGAIFRNSEGLLHIPTAFGGCKNGITIGPLRPFST
QL01 454 IISDATSWMSYIQRTTAGKVESYLNQITMNIENLTVKNAIFLGHISAAECISGAVNALRIWNDYGAIFRNSEGLLHIPTAFGGCKNGITIGPLRPFST
JS10 457 IISDATSWMSYIQRTTAGKVESYLNQITMNIENLTVKNAIFLGHISAAECISGAVNALRIWNDYGAIFRNSEGLLHIPTAFGGCKNGITIGPLRPFST

wV7 558 ALDTGKVVIFDILSSMNTFAANGITKRVGHGAGAGGYDICYSAAPITFQIDDAAVSKYPIVQKQFTNGKAVWSLSTETNSGTFVLHLLKEDGSCGHTS
WG01 551 ALDTGKVVIFDILSSMNTFAANGITKRVGHGAGAGGYDICYSAAPITFQIDDAAVSKYPIVQKQFTNGKAVWSLSTETNSGTFVLHLLKEDGSCGHTS
QL01 554 ALDTGKVVIFDILSSMNTFAANGITKRVGHGAGAGGYDICYSAAPITFQIDDAAVSKYPIVQKQFTNGKAVWSLSTETNSGTFVLHLLKEDGSCGHTS
JS10 557 ALDTGKVVIFDILSSMNTFAANGITKRVGHGAGAGGYDICYSAAPITFQIDDAAVSKYPIVQKQFTNGKAVWSLSTETNSGTFVLHLLKEDGSCGHTS

wV7 658 ----RFNADGTVNFPDNDVQVGGGEATIARNGNIFSDIWKTEISAGDITNIRDALATRVAKEGDVTMTG
WG01 651 ----RFNADGTVNFPDNDVQVGGGEATIARNGNIFSDIWKTEISAGDITNIRDALATRVAKEGDVTMTG
QL01 651 GIKYWRFTKRG--NEVITRNLRYAGTAFMNTDGNLAGSIWKNYSGA---FNLDAAVNTRVKSGSDVTMTG
JS10 654 GIKYWRFTKRG--NEVITRNLRYAGTAFMNTDGNLAGSIWKNYSGA---FNLDAAVNTRVKSGSDVTMTG
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# C

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JS10 714 RLITKINSDAVVIDYPADEAGYVKKKGVDNWNVGNGGADNGLAIFWSPQSGGINTHNGEVVLSPOGASVFNINRDRITMNGSNWIAHKSAGWDQW
WG01 714 RLITKINSDAVVIDYPADEAGYVKKKGVDNWNVGNGGADNGLAIFWSPQSGGINTHNGEVVLSPOGASVFNINRDRITMNGSNWIAHKSAGWDQW
QL01 714 KLIVKRGSDAINIAADENDSAYLLGTSGGANSWYIGKGGADDTASFYNEKTTAGLITNSVGDIDFVNRQATAASLNRYLYLNGRQWATQGHGYNNQW
wV7 721 KLIVKRGSDAINIAADENDSAYLLGTSGGANSWYIGKGGADDTASFYNEKTTAGLITNSVGDIDFVNRQATAASLNRYLYLNGRQWATQGHGYNNQW

JS10 816 GLPAPYFLEFG-SVGEDSYPIIKGRSVISGQYITTSVELGMRNPE--QAWCOAIRVGNABRGDC--EVGIFEFHSSGLYAPITLVQITLAIIGVGTINQ
WG01 813 GLPAPYFLEFG-SVGEDSYPIIKGRSVISGQYITTSVELGMRNPE--QAWCOAIRVGNABRGDC--EVGIFEFHSSGLYAPITLVQITLAIIGVGTINQ
QL01 814 QTEAPFVDFEGSVPKDSYPIIKGRSVISGQYITTSVELGMRNPE--QAWCOAIRVGNABRGDC--EVGIFEFHSSGLYAPITLVQITLAIIGVGTINQ
wV7 821 QTEAPFVDFEGSVPKDSYPIIKGRSVISGQYITTSVELGMRNPE--QAWCOAIRVGNABRGDC--EVGIFEFHSSGLYAPITLVQITLAIIGVGTINQ

JS10 909 LQSP
WG01 906 LQAS
QL01 913 WGGG
wV7 920 WGGG
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# D

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QL01 918 STAIGDDDTGLVHGGDGRINMYANSMHIASWAGYHIHGLWDTTGALWTEGTRAITISFGHLVQANDSYSTVVRDYYVRSRDIKVKKDLVKFENASQILSKL
WG01 911 STAIGDDDTGLVHGGDGRINMYANSMHIASWAGYHIHGLWDTTGALWTEGTRAITISFGHLVQANDSYSTVVRDYYVRSRDIKVKKDLVKFENASQILSKL
JS10 914 STAIGDDDTGLVHGGDGRINMYANSMHIASWAGYHIHGLWDTTGALWTEGTRAITISFGHLVQANDSYSTVVRDYYVRSRDIKVKKDLVKFENASQILSKL
wV7 925 STAIGDDDTGLVHGGDGRINMYANSMHIASWAGYHIHGLWDTTGALWTEGTRAITISFGHLVQANDSYSTVVRDYYVRSRDIKVKKDLVKFENASQILSKL

QL01 1018 INGYTYMOKRGLDEEGNQKWPENAGLIAQEVQAILPELVEGDDPGEALLRLNNGVIGLNTAAINEHTAEIABLKSEIEELKALIKSLK
WG01 1011 INGYTYMOKRGLDEEGNQKWPENAGLIAQEVQAILPELVEGDDPGEALLRLNNGVIGLNTAAINEHTAEIABLKSEIEELKALIKSLK
JS10 1014 INGYTYMOKRGLDEEGNQKWPENAGLIAQEVQAILPELVEGDDPGEALLRLNNGVIGLNTAAINEHTAEIABLKSEIEELKALIKSLK
wV7 1025 INGYTYMOKRGLDEEGNQKWPENAGLIAQEVQAILPELVEGDDPGEALLRLNNGVIGLNTAAINEHTAEIABLKSEIEELKALIKSLK
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49

50 **Fig. S3 Alignment results of gp37 of WG01 with other homologous T4-like**

51 **phages**

52 The different amino acids domains (1–456, 457–713, 714–910, and 911–1100) of

53 WG01 gp37 was compared with the corresponding protein sequences of QL01, JS10,

54 and wV7.

55 (A) The N-terminal domain (amino acids 1–456) of WG01 gp37 was compared with  
56 the corresponding protein sequences of QL01, JS10, and wV7.

57 (B) The N-terminal domain (amino acids 457–713) of WG01 gp37 was compared  
58 with the corresponding protein sequences of QL01, JS10, and wV7.

59 (C) The WG01 gp37 C-terminal domain (amino acids 714–910) was compared with  
60 the corresponding protein sequences of QL01, JS10, and wV7.

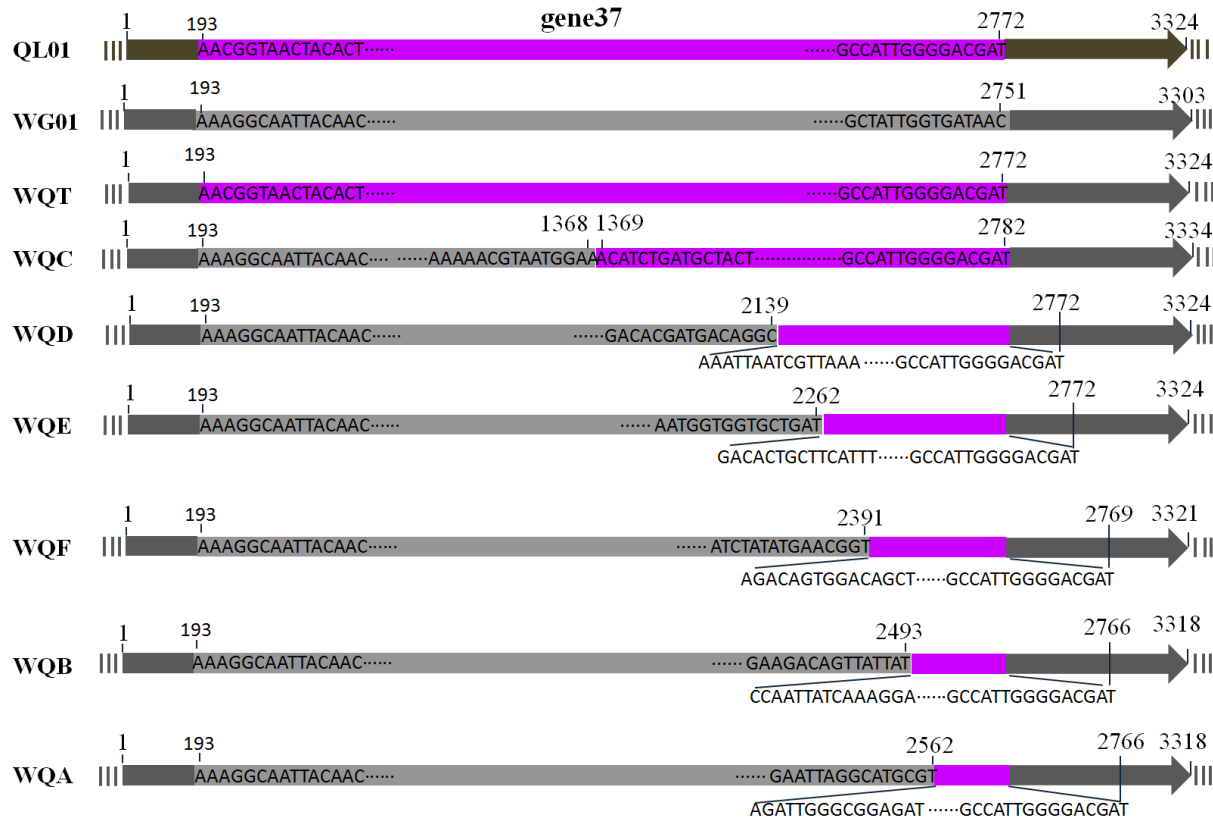
61 (D) The WG01 gp37 C-terminal receptor attachment domain (amino acids 911–1100)  
62 was compared with the corresponding protein sequences of QL01, JS10, and  
63 wV7.

64 The black boxes represent the same amino acids. Grey boxes represent the amino  
65 acids in the same classification. In (B) and (C), the amino acid sequences exhibited a  
66 higher homology with the corresponding parts of WG01 marked with red boxes. The  
67 amino acid sequences exhibiting a lower homology with the corresponding parts of  
68 WG01 are marked with blue boxes.

A

WG01 1 MATLKQIQFKRSKVAGVRPAPAQLAEGELAINLKRLLFTKDDTGAIIDLGFAGKGNIDGNVHFGNYNQTGLYPLNEVFE  
 QL01 1 MATLKQIQFKRSKVAGVRPAPAQLAEGELAINLKRLLFTKDDTGAIIDLGFAGKGNIDGNVHFGNYNQTGLYPLNEVFE  
 WG01 81 TQICEDNINLSTARVTRDTHAQQNTTCCGELISFSASFSRFFFLSPDRERGLTISFNNAFCHNOVAVNRVQDYAAGEE  
 QL01 81 TQCSSTTTSSTITANGDITAKSRNMTMGEVTVRGGNGAHVRFDDLADARERAILISGRRTSPTRKILINRVRQDYTNSSGS  
 WG01 160 STYAFSGNGVFSSEWVFWKRSVSTPVIYTNRVINRKRVRSDYDIYSLADNTPFEEGEGATNHLRVMNAVCACTPHEMNV  
 QL01 161 NIPAFNCGEFTFYAFSSSAGTSVRSEVYITNVAWDSRNIQDVIDLSSLANNN----SAPDRNMLRVVMTDPSAHLHEHCE  
 WG01 240 NNGIHWYSGGDLDTYVWSPNNAAGLKAHSTISVGLPGGSKGYSLELCTASTALGDNDFGRKWHODGYFFSVNNGTRRFRISG  
 QL01 237 NNGIHWYSGGSTPTDYVWSPNNAAGLKAHSTISVGLPGGSKGYSLELCTASTALGDNDFGRKWHODGYFFSVNNGTRRFRISG  
 WG01 320 PADHTSLKIKVMEYSVNGDITTEPSENYALATVWYHNNAGDGGTLLGYDQGNVHHYFRGKGTINVTAGGLLVTB  
 QL01 317 PDEWTSLQQLVAGSYNNGSDILLETQNYFPIVWNTNDRNSEGQDGLLGYDQGNVHHYFRGKGTINVTAGGLLVTB  
 WG01 400 GNIIVVGGSVNIDGRNASTMEKGNITTCSSVDNMTDAVGNFTNTDGRKNVMEISDATSNMNYIQRTDKVBAH  
 QL01 397 GNIIVVGGSVNIDGRNASTMEKGNITTCSSVDNMTDAVGNFTNTDGRKNVMEISDATSNMNYIQRTDKVBAH  
 WG01 480 NG-----FRVNGSSIDVGEVNVVSTLAGVNVNLRINWDTYCAIFRSESSLHLIPTAFGEKRTEDGPIRPSALD  
 QL01 477 NGPTMNVIEGLVWQDTSIKRNIYVSENLKVRASGLRINWDRYGVIFRSEDLHLIPTANANAGESSGGLRPLSLTLD  
 WG01 554 TGRVLPDLDLSHTLBAENGTIKGCHGAGGCDIYQAAPITQEDDIDAVSKYPIVVKORFLQGKAVWSTLCTEINS  
 QL01 557 TGRVLPDLDLSHTLBAENGTIKGCHGAGGCDIYQAAPITQEDDIDAVSKYPIVVKORFLQGKAVWSTLCTEINS  
 WG01 634 TGVVHHYKDGTCGHTS----RENALGTVNEPDNVQVGGGPAITARNNGNIFSDIWNQNGAGNITNIRDALATRVSRG  
 QL01 634 EPRIVAQGLLGDSDAGLQVWRFKKCF--NFIITRNRYGCFAPNNTIGNIAGSLWNKISGA---TNLDAAVNRVQRG  
 WG01 709 DVTMGILVTRTNSDAMVIDYPADLASYVTRKKGVDNMYVNGGADNGLAFVSEVQSGCININPNSEVILSPQ-GNSIFG  
 QL01 709 DVTMGILVTRTNSDAMVIDYPADLASYVTRKKGVDNMYVNGGADNGLAFVSEVQSGCININPNSEVILSPQ-GNSIFG  
 WG01 788 INRIRIYINGAHVVRKSGAGDQVGLQAPVLEFG-SVGGSDSYPIIKGSEVSGQYITVSLGCRTP--CQWGAJ  
 QL01 789 INRIRIYINGAHVVRKSGAGDQVGLQAPVLEFG-SVGGSDSYPIIKGSEVSGQYITVSLGCRTP--CQWGAJ  
 WG01 865 IIRVGNARSGS--EVEIFEEHSSSEFYSFSSVQT-PSISVNDMLGSSIAIGDNTGLVHGGDGRINMYANSMHIAW  
 QL01 869 IIRVGSABSSSHEVMAIVEQANSEKRAAGLRAGVNGVSEIPIVWGEASIAIGDNTGLVHGGDGRINMYANSMHIAW  
 WG01 942 GAGYVHIEGLWDTTGALWTFETGRAIISFGHLVQQNDSYSTFVRDYYVRSDIRVKKDLVKFENASQTLKINGYTYMQRG  
 QL01 949 GAGYVHIEGLWDTTGALWTFETGRAIISFGHLVQQNDSYSTFVRDYYVRSDIRVKKDLVKFENASQTLKINGYTYMQRG  
 WG01 1022 LDEEGNQKWEPNAGLIAEQVQAILPELVGDPDGEALLRINVNGVIGLNTAAINEHTAEIAELKSEIEELKALIKSLK  
 QL01 1029 LDEEGNQKWEPNAGLIAEQVQAILPELVGDPDGEALLRINVNGVIGLNTAAINEHTAEIAELKSEIEELKALIKSLK

B



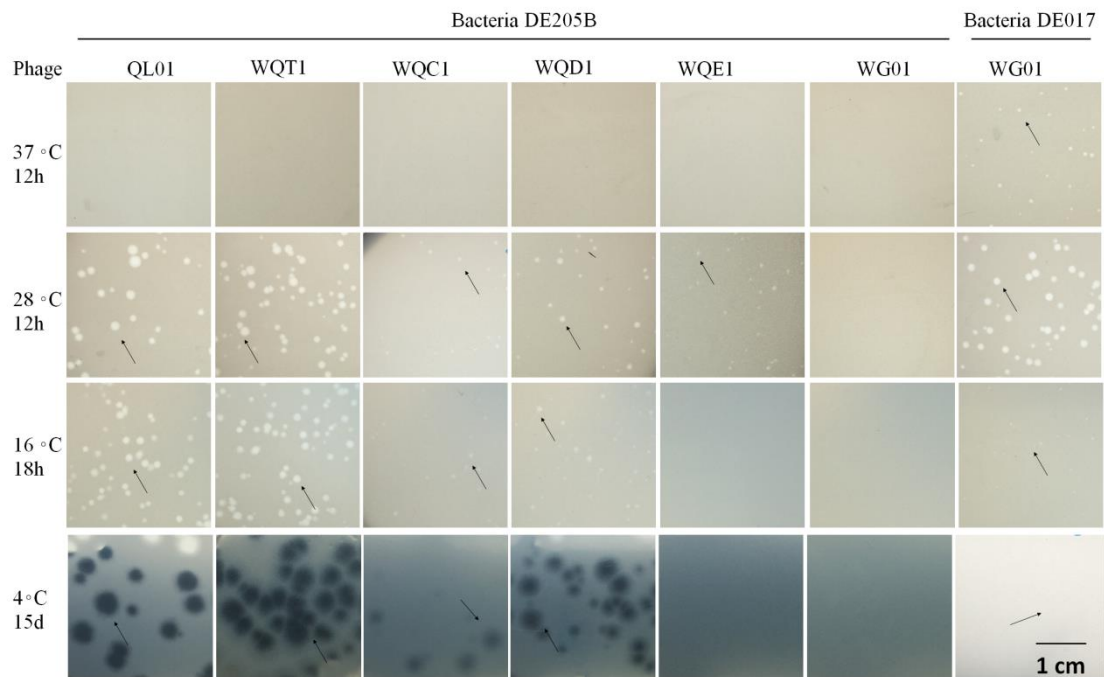
72 **Fig. S4 Comparison and recombination positions between QL01 and WG01 on gene37**

73 **(A) Alignment results of gp37 from WG01 and QL01**

74 The gp37 of WG01 exhibited a relatively low degree of sequence conservation with 59% identity associated with QL01. A high identity (100%)  
75 of the amino acid alignment in the first 64 aa of the gp37 N-terminal domain and the first 183 aa of gp37 C-terminal domain between WG01 and  
76 QL01 was observed. In contrast, minimal homology was observed in the other regions of gp37. The positions of the initiation sites for the  
77 different recombinant fragments and the name of the DNA fragments are indicated above the sequence.

78 **(B) The recombination positions between QL01 and WG01 on gene37**

79 Gene37 diagrams of the QL01, WG01, and WG01 derivatives (WQT, WQC, WQD, WQE, WQF, WQB, and WQA) are displayed. The nucleic  
80 acid sequences of the changes are indicated on or in the diagram. The recombination positions between QL01 and WG01 on the gene37 locus are  
81 indicated above the diagrams. The color gray represents WG01, which was modified in this study. The color mauve represents the exchanged  
82 regions which are derived from QL01. For example, in WQT, the region from 193 to 2772 was the exchanged region from QL01.



84

85 **Fig. S5 Growth characteristics of WG01, QL01, and WG01 derivatives**

86 The results of the growth characteristics for WG01, QL01, WQT1, WQC1, WQD1,  
87 and WQE1 were displayed. On the lawn of DE205B, QL01, WQT1, WQC1, and  
88 WQD1 all formed plaques at 28 °C, 16 °C, and 4 °C, rather than at 37 °C; WQE1 only  
89 formed plaques at 28 °C. WG01 could not infect DE205B, but could form plaques at  
90 37 °C, 28 °C, 16 °C and 4 °C with DE017.



91

92 **Table S1** strains used in phage isolation and host range analysis of recombinant phages

Strains	WQT2	WQT3	WQT4	WQT5	WQT6	WQT7	WQT8	WQT9	WQT10	WQT11	WQT12	QL01	WQC	WQD	WQE	WG01	WQT1
DE001	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-
DE002	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE003	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	+
DE005	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE007	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE008	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	+
DE010	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE011	-	-	-	-	-	-	-	-	-	-	-	-	+	+	+	-	-
DE013	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE015	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
DE017	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
DE018	+	+	+	+	+	+	+	+	+	+	+	-	+	+	-	-	+
DE019	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE020	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE021	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
DE022	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE023	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	+
DE028	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	+
DE032	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	+
DE034	-	-	-	-	-	-	-	-	-	-	-	-	+	+	+	+	-
DE037	+	+	+	+	+	+	+	+	+	+	+	-	+	+	-	-	+

DE041	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE044	-	-	-	-	-	-	-	-	-	-	-	-	+	+	+	+	-
DE046	-	-	-	-	-	+	-	-	-	-	-	-	-	+	-	-	-
DE049	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE050	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE054	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE056	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE060	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE061	-	-	-	-	-	-	-	-	-	-	-	-	+	+	+	-	-
DE064	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE065	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE069	-	-	-	-	-	-	-	-	-	-	-	-	+	+	+	+	-
DE070	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE071	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE072	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
DE074	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE075	-	-	-	-	-	-	-	-	-	-	-	-	+	+	+	-	-
DE077	-	-	-	-	-	-	-	-	-	-	-	-	+	+	+	-	-
DE083	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE085	-	-	-	-	-	+	-	-	-	-	-	-	-	+	-	-	-
DE094	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE098	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE101	+	+	+	+	+	+	+	+	+	+	+	+	-	+	+	+	-
DE102	+	+	+	+	+	+	+	+	+	+	+	+	-	+	-	+	-
DE104	+	+	+	+	+	+	+	+	+	+	+	+	-	+	+	-	+
DE119	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-





DE426	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE432	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DE452	+	+	+	+	+	+	+	+	+	+	+	+	-	+	-	+	+	
DE458	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
DE464	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
XM	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	
HX01	-	-	-	-	-	+	-	-	-	-	-	+	-	+	-	-	-	
HX04	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
NT-1	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	
MC1061	+	+	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	
MG1655	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
O157:H7	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
RS218	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	
5155	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	
Host range	49	49	49	49	49	52	49	49	49	49	49	50	47	63	28	22	46	

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94 +, clear lysis; -, no reaction

95 **Table S2** T4-like phages that showed homology with the genome sequence of QL01

Phage	Host strain	RefSeq	Size (bp)	Query %	Ident %
Enterobacteria phage WG01	<i>Escherichia coli</i>	NC_031928.1	169936	100	100
Enterobacteria phage Bp7	<i>Escherichia coli</i>	NC_019500.1	168066	92	98
Enterobacteria phage JS98	<i>Escherichia coli</i>	NC_010105.1	170523	94	92
Enterobacteria phage QL01	<i>Escherichia coli</i>	NC_028847.1	170527	95	98
Enterobacteria phage JS10	<i>Escherichia coli</i>	NC_012741.1	171451	93	93
Enterobacteria phage MX01	<i>Escherichia coli</i>	NC_031934.1	168929	93	94
Enterobacteria phage vB_EcoM_VR5	<i>Escherichia coli</i>	NC_028881.1	170473	90	90
Enterobacteria phage IME08	<i>Escherichia coli</i>	NC_014260.1	172253	91	92
Enterobacteria phage vB_EcoM_VR20	<i>Escherichia coli</i>	NC_028894.1	170336	76	79
Enterobacteria phage vB_EcoM_VR25	<i>Escherichia coli</i>	NC_028925.1	170822	74	79
Shigella phage SP18	<i>Shigella sonnei</i>	NC_014595.1	170605	76	77
Enterobacteria phage vB_EcoM_VR26	<i>Escherichia coli</i>	NC_028957.1	171541	74	81
Enterobacteria phage vB_EcoM_VR7	<i>Escherichia coli</i>	NC_014792.1	169285	72	80
Edwardsiella phage PEi20	<i>Edwardsiella ictaluri</i>	NC_028683.1	177643	52	80
Pectobacterium bacteriophage PM2	<i>Pectobacterium carotovorum</i> subsp. <i>Carotovorum</i>	NC_028940.1	170286	51	78
Escherichia phage slur07	<i>Escherichia coli</i>	NC_028780.1	167124	48	76
Escherichia phage ECML-134	<i>Escherichia coli</i>	NC_025449.1	166783	48	75
Escherichia phage HY01	<i>Escherichia coli</i>	NC_027349.1	166977	50	76
Shigella phage pSs-1	<i>Shigella sonnei</i>	NC_025829.1	164999	49	75
Enterobacteria phage T4	<i>Escherichia coli</i>	NC_000866.4	168903	46	76
Enterobacteria phage RB27	<i>Escherichia coli</i>	NC_025448.1	165179	48	76
Yersinia phage PST	<i>Yersinia pseudotuberculosis</i>	NC_027404.1	167785	49	76
Enterobacteria phage RB3	<i>Escherichia coli</i>	NC_025419.1	168402	44	76
Enterobacteria phage RB14	<i>Escherichia coli</i>	NC_012638.1	165429	48	76
Escherichia phage wV7	<i>Escherichia coli</i>	NC_019505.1	166452	49	75
Shigella phage Shfl2	<i>Shigella flexneri</i>	NC_015457.1	165919	48	75
Escherichia phage HY03	<i>Escherichia coli</i>	NC_031047.1	170770	47	75
Escherichia phage e11/2	<i>Escherichia coli</i>	NC_024125.2	168470	48	75
Escherichia phage vB_EcoM_PhAPEC2	<i>Escherichia coli</i>	NC_024794.1	167318	57	75
Enterobacteria phage RB69	<i>Escherichia coli</i>	NC_004928.1	167560	58	75

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Enterobacteria phage RB51	<i>Escherichia coli</i>	NC_012635.1	168394	50	75
Citrobacter phage Moon	<i>Citrobacter freundii</i>	NC_027331.1	170341	41	75
Salmonella phage S16	<i>Salmonella enterica</i>	NC_020416.1	160221	33	72

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100 **Table S3.** Comparison results for WG01 and QL01

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QL01 ORF	WG01 ORF	WG01 protein identity with the proteins of QL01		Protein (from NCBI) identity with either WG01 or QL01 proteins			Product
		query	iden	phage	query	iden	
1	1	100	99				rIIA protects from prophage-induced early lysis
2	2	100	99				hypothetical protein
3	3	100	99				hypothetical protein
4	4	100	96				hypothetical protein
5	5	100	100				topoisomerase II large subunit
6	6	100	100				hypothetical protein
7	7	100	100				hypothetical protein
8	8	100	99				putative RNA metabolism modulator
9	9	100	100				modifier of suppressor tRNAs
10	10	100	87				modifier of transcription
11	11	100	97				hypothetical protein
12	12	100	97				hypothetical protein
13	13	100	99				hypothetical protein
14	14	100	97				hypothetical protein
15	15	100	99				DNA helicase
16	16	100	100				hypothetical protein
17	17	100	99				putative Srd anti-sigma factor
18	18	100	99				hypothetical protein
19	19	100	99				hypothetical protein
-	20	-	-	Shigella phage SP18_gp021	100	59	hypothetical protein



20	21	100	97	hypothetical protein
21	22	100	88	hypothetical protein
22	23	100	93	hypothetical protein
23	24	100	98	Srh transcription modulator
24	25	81	92	hypothetical protein
25	26	100	100	hypothetical protein
26	27	100	92	hypothetical protein
27	28	100	100	dCTPase
28	29	100	100	hypothetical protein
29	30	100	100	hypothetical protein
30	31	100	100	hypothetical protein
31	32	100	100	hypothetical protein
32	33	100	99	hypothetical protein
33	34	100	96	spackle periplasmic protein
34	35	100	99	hypothetical protein
35	36	100	98	hypothetical protein
36	37	100	97	discriminator of mRNA degradation
37	38	100	100	hypothetical protein
38	39	100	100	DNA primase-helicase subunit
39	40	100	100	hypothetical protein
40	41	100	100	UvsX RecA-like recombination protein
41	42	100	99	hypothetical protein
42	43	100	100	hypothetical protein
43	44	100	100	hypothetical protein
44	45	100	100	hypothetical protein
45	46	100	100	hypothetical protein

46	47	100	100				hypothetical protein
47	48	100	100				immunity to superinfection membrane protein
48	49	100	99				DNA polymerase
49	50	100	99				hypothetical protein
50	51	100	100				translational repressor protein
51	52	100	99				clamp loader subunit DNA polymerase
52	53	100	99				hypothetical protein
53	54	100	100				sliding clamp DNA polymerase accessory protein
54	55	100	100				hypothetical protein
55	56	100	100				hypothetical protein
56	57	100	99				hypothetical protein
57	58	100	100				hypothetical protein
58	59	100	100				hypothetical protein
59	60	100	97				recombination endonuclease subunit
60	-	-	-	BP7_0131	55	61	N-terminal catalytic GIY-YIG domain of bacteriophage T4 segABCDEFGF gene encoding proteins
-	61	-	-	JS98_058	100	98	gp47.1 hypothetical predicted membrane protein
61	62	100	100				hypothetical protein
62	63	100	100				hypothetical protein
63	64	100	100				hypothetical protein
64	65	100	100				hypothetical protein
65	66	100	99				hypothetical protein
66	67	100	97				hypothetical protein
67	68	100	100				hypothetical protein
68	69	100	99				hypothetical protein

69	70	100	100				hypothetical protein
70	71	100	88				hypothetical protein
71	72	100	100				hypothetical protein
72	73	100	100				hypothetical protein
73	74	100	68				hypothetical protein
74	75	100	100				hypothetical protein
75	76	100	100				hypothetical protein
76	77	100	100				putative membrane protein
77	78	100	100				hypothetical protein
78	79	100	100				hypothetical protein
79	80	100	100				hypothetical protein
80	81	100	100				hypothetical protein
81	82	100	100				hypothetical protein
82	83	100	100				thioredoxin
83	84	100	100				hypothetical protein
84	85	100	99				hypothetical protein
85	86	100	99				hypothetical protein
86	87	100	97				hypothetical protein
87	88	100	100				hypothetical protein
88	89	100	100				hypothetical protein
89	90	100	100				hypothetical protein
90	91	100	81				hypothetical protein
91	92	100	98				hypothetical protein
-	93	-	-	Edwardsiella phage PEi20_098, Edwardsiella phage PEi26_098	96	51	hypothetical protein
92	94	100	91				hypothetical protein

93	95	98	99				hypothetical protein
94	96	100	100				hypothetical protein
95	97	100	100				hypothetical protein
96	98	100	95				hypothetical protein
97	99	100	100				hypothetical protein
98	100	100	100				hypothetical protein
99	101	100	100				hypothetical protein
100	102	100	100				hypothetical protein
101	103	100	100				thymidine kinase
102	104	100	59				hypothetical protein
103	105	100	100				hypothetical protein
104	106	100	99				hypothetical protein
105	107	100	100				valyl-tRNA synthetase modifier
106	108	100	98				hypothetical protein
107	109	100	98				site-specific RNA endonuclease
108	-	-	-	Edwardsiella phage PEi26_122	100	88	conserved hypothetical protein
109	110	100	98				hypothetical protein
110	111	100	100				hypothetical protein
111	112	100	100				hypothetical protein
112	113	100	99				hypothetical protein
113	144	97	51				IP7
-	114	-	-	-	-	-	hypothetical protein
-	115	-	-	Escherichia phage Av-05_183	94	37	hypothetical protein
114	116	100	99				endonuclease V N-glycosylase UV repair enzyme
115	117	100	99				internal head protein
116	118	100	100				hypothetical protein

117	119	100	99	hypothetical protein
118	120	100	100	nudix hydrolase
119	121	100	100	hypothetical protein
120	122	100	53	putative membrane protein
121	123	100	93	hypothetical protein
122	124	100	100	hypothetical protein
123	125	100	99	hypothetical protein
124	126	100	100	hypothetical protein
125	127	100	100	hypothetical protein
126	128	100	100	hypothetical protein
127	129	100	100	hypothetical protein
128	130	100	100	hypothetical protein
129	131	100	100	hypothetical protein
130	132	100	100	hypothetical protein
131	133	100	99	hypothetical protein
132	134	100	77	hypothetical protein
133	135	100	98	hypothetical protein
134	136	100	97	hypothetical protein
135	137	100	99	hypothetical protein
136	138	100	99	hypothetical protein
137	139	100	100	hypothetical protein
138	140	100	99	hypothetical protein
139	141	100	100	hypothetical protein
140	142	100	92	hypothetical protein
141	143	100	69	hypothetical protein
142	145	100	98	hypothetical protein

143	146	100	91				hypothetical protein
-	147	-	-	Citrobacter phage Merlin_166	95	53	hypothetical protein
144	148	100	99				hypothetical protein
145	149	100	100				chaperone for tail fiber formation
146	150	100	100				hypothetical protein
147	151	100	99				tail completion and sheath stabilizer protein
148	-	-	-	vB_EcoM_VR25_162	100	62	hypothetical protein
149	152	100	98				DNA end protector protein
150	153	100	100				head completion protein
151	154	100	100				hypothetical protein
152	155	95	95				baseplate hub subunit and tail lysozyme
153	-	-	-	IME08_142	100	95	5.1 gene product
154	-	-	-	IME08_143	100	100	5.4 gene product
-	156	-	-	Bp7_254	100	100	hypothetical protein
155	157	100	100				baseplate wedge subunit
156	158	100	99				baseplate wedge initiator
157	159	100	100				baseplate wedge subunit
158	160	100	100				baseplate wedge tail fiber
159	161	100	99				baseplate wedge subunit and tail pin
160	162	100	100				baseplate wedge subunit and tail pin
161	163	100	100				short tail fibers protein
162	164	100	99				fibritin neck whiskers
163	165	100	100				neck protein
164	166	100	100				neck protein
165	167	100	100				tail sheath stabilizer and completion protein
166	168	100	97				terminase DNA packaging enzyme small subunit

167	169	100	100				terminase DNA packaging enzyme large subunit
168	170	100	98				tail sheath protein
169	-	-	-	Klebsiella phage PKO111_028	99	65	hypothetical protein
170	171	100	100				hypothetical protein
171	-	-	-	Bp7_237	100	100	hypothetical protein
172	172	100	100				hypothetical protein
173	173	100	100				prohead core protein precursor
174	174	100	100				prohead core protein
175	175	100	100				prohead core scaffold protein and protease
176	176	100	99				prohead core scaffold protein
177	177	100	99				major head protein
178	178	100	100				hypothetical protein
179	179	100	99				head vertex protein
180	180	100	100				head vertex protein
181	181	100	84				RNA ligase 2
182	182	100	100				hypothetical protein
183	183	100	98				head outer capsid protein
184	184	100	99				inhibitor of prohead protease
185	185	100	100				hypothetical protein
186	186	100	100				hypothetical protein
187	187	100	100				hypothetical protein
188	188	100	100				hypothetical protein
189	189	100	100				UvsY recombination repair and ssDNA binding protein
190	190	100	100				baseplate hub subunit
191	191	100	99				baseplate hub subunit

192	192	100	100				baseplate hub assembly catalyst
193	193	100	100				aseplate hub subunit
194	194	100	100				hypothetical protein
195	195	100	99				baseplate hub subunit
196	196	100	99				baseplate tail tube cap
197	197	100	96				baseplate tail tube initiator
198	198	100	98				hypothetical protein
199	199	100	98				RNA polymerase ADP-ribosylase
200	200	100	46				RNA polymerase ADP-ribosylase
201	200	99	99				RNA polymerase ADP-ribosylase
201	201	94	41				RNA polymerase ADP-ribosylase
202	202	100	98				hypothetical protein
203	203	100	99				DNA ligase
204	204	100	100				hypothetical protein
205	205	100	99				hypothetical protein
206	206	100	99				hypothetical protein
207	207	100	57				hypothetical protein
207	208	100	97				hypothetical protein
208	209	100	98				hypothetical protein
209	-	-	-	vB_EcoM_VR5_207	97	92	hypothetical protein
210	210	100	99				hypothetical protein
211	211	100	98				hypothetical protein
212	212	100	100				hypothetical protein
213	213	100	100				hypothetical protein
214	214	100	99				hypothetical protein
215	215	100	100				head assembly cochaperone with GroEL



216	216	100	100				hypothetical protein
217	217	100	100				hypothetical protein
218	218	100	99				hypothetical protein
219	219	100	99				hypothetical protein
220	220	100	88				hypothetical protein
221	221	100	97				hypothetical protein
222	222	100	100				hypothetical protein
223	223	100	100				hypothetical protein
224	-	-	-	RB14_217	100	78	hypothetical protein
225	224	100	97				PseT polynucleotide 5'-kinase and 3'-phosphatase
226	225	100	100				hypothetical protein
227	226	100	100				hypothetical protein
228	227	100	100				hypothetical protein
229	228	100	99				putative membrane protein
230	229	100	100				hypothetical protein
231	230	100	100				hypothetical protein
232	231	100	100				hypothetical protein
233	232	100	99				hypothetical protein
234	233	100	99				aerobic NDP reductase small subunit
235	234	100	99				aerobic NDP reductase large subunit
236	235	74	99				hypothetical protein
237	236	100	100				dTMP thymidylate synthase
238	237	100	95				dihydrofolate reductase
239	238	100	100				hypothetical protein
240	239	100	100				hypothetical protein
241	240	100	100				hypothetical protein

242	241	100	96				hypothetical protein
243	242	100	100				hypothetical protein
244	243	100	98				hypothetical protein
245	244	100	100				late promoter transcription accessory protein
246	245	100	100				hypothetical protein
247	246	100	99				RNaseH ribonuclease
248	247	100	98				long tail fiber proximal subunit
249	248	100	99				long tail fiber proximal connector
250	249	100	99				long tail fiber distal connector
251	250	100	58				long tail fiber distal subunit
252	251	100	99				tail fiber adhesin
253	252	100	100				hypothetical protein
254	253	100	100				anti-sigma 70 protein
255	254	100	93				hypothetical protein
256	255	100	97				hypothetical protein
257	256	100	98				hypothetical protein
258	257	100	85				hypothetical protein
259	-	-	-	RB32_252	100	90	hypothetical protein
-	258	-	-	Bp7_151	100	100	hypothetical protein
260	259	100	75				hypothetical protein
261	260	100	100				hypothetical protein
262	261	100	100				hypothetical protein
263	262	99	98				topoisomerase II medium subunit
264	263	100	100				hypothetical protein
265	264	100	98				putative membrane protein
266	265	100	100				nucleoid disruption protein

267	266	100	100					hypothetical protein
268	267	100	100					hypothetical protein
269	268	100	100					putative inner membrane
270	269	100	98					hypothetical protein
271	-	-	-	-	-	-	-	hypothetical protein
272	270	100	100					hypothetical protein
273	271	100	99					hypothetical protein
274	272	100	100					hypothetical protein
275	273	100	93					hypothetical protein

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104 **Table S4.** The DNA sequences of chimeric phages and mutants from the WQT chimeric phage

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106 **WQT2**

107 ATGGCTACTTTAAAGCAAATCCAATTTAAAGAAGTAAAGTAGCCGGTGTACGTCCGGCACCGGCCA  
108 GTTGGCTGAAGGCGAACTGGCTATTAACCTAAAGGACCGTTTACTTTTTACTAAAGACGATACTGGAG  
109 CGATTATCGACCTTGGCTTTGCTAAGGGTGGAAATATCGATGGTAATGTTATTCATAAAGGCAATTACAA  
110 CAAAACCGGTAATTATAATCTGTCTGGTACTTTTACCCAAACAGGTAGTTATACGACATCCGGAAGTATA  
111 ACAGCAAATGGTGATATTACTGCAAAATCTCGCCTAATGACGGATATGGGCGAAGTTTTGGTACGTGGC  
112 AATGGTACCGCACATGTTTCGATTCCAGGATTTAGCTGATGCGCGGAAAGAGCTATAATTTATTCTCAA  
113 AACCGTACTGGGGATACCAAGCAAATCTGAACGTTCTGTTCAGGATTACACTAATTCGACATCTAAT  
114 ATTTTGCATTCAACGGCGACGGTTTATTTTATGCTCCGTCTATTTCCGCCGGAACATCAGTAAAATCTC  
115 CGGTAATTTATACTAATACTGTTAATACAGACAGTAAGAATATTGGCGATTATGATATATCTTCATTAGCA  
116 AATAATAATTCTGCCACGGATAAAAACCTATTTGCGCGTTGTACGTACCGACCCAGCGTCTGCAATACTT  
117 CATGAAATTTGTGAAAATAACGGTATCAGTTGGTATTCTGGTTCAACCCCTACTGATTATATGTTGTCTT  
118 TTGCTTATCCGGTGGTTTTCAAGCAGGTCATTCGATTGCAGTAAAGTATGGAATCAGGGCCTTTGACATA  
119 TTCAACCTTAGGTAAAGTTCTATTGTTCTTGGTGATAATGATACCGGGTTAAATGGAAACAAGACGG  
120 CCTGTTCTATACAATTAATAATGGAGCTTATACTTTACTTACAACCTCAACTGAAGTTACAAGCCTTAAA  
121 CAGTTAGTTGCGGGTTATTCAACCAACGGTTCTGATTTAATTCTTCTACAACCTCAAACTATCCATTAG  
122 TTATTGTTAATACTACTAATGATAAAAACAGCTTCGGCGACGGTCAAACCTTTTTAGGTTATCACCAGA  
123 GCGGCAAATATCACCATTATTTTCGTGGCAAAGGTGTAACAAACGTTAACACCGCCGGCGGGTTGTTG  
124 GTTACTCCTGGTAACGTTGAAGTCCGGGGCGGTTTCGGTTAATATTGATGGTCTCAGTAATGCTTCTACA  
125 GTGCTTTTTAAAGGAAATACTACAGGATATAGTTTCAGTCGATAATATAGAGCTCAAAGTTTGGGGTGAC  
126 ACTTTTAATACGGTAGGTGGTTCTCGTAAAAACGTAATGGAAACATCTGATGCTACTGGCTGGATGCAT  
127 TATATTCAACGAACTACAGAAGGTAAAGTCAATCCTATTTAAATGGTACCATGAATGTAATTGAAGGA  
128 TTGACTGTCAATCAAGATACATCCTTAAAACGTAATCTGTATGTTTCCAATGAAATTAAGTTTCGCGCTG  
129 CTAGTGGTCTTCGTATTTGGAACGATAAGTATGGTGTATTTTTTCGAAATTCGGAAGACCAACTGCATAT  
130 TATCCGACCAATGCCAATGCCGGCGAAAGTGGTGGATTGGGCCATTACGACCGTTAAGTATTACATT  
131 AGACACCGGCATAGTTAAAATTCCTAACTTAGCAGCCAACCAGGTTTCTTTTAGTAGCACAGGTGTATT  
132 GGAATTCATCGCCGTAACGGTTCATCTTATGCTAACCAGAACACAACCTAAAGCTCCATTGTATCAAAC  
133 GCTTGGTTCTGCGACTCAAGCATTCTATCCTATTACTAAGCAGAAAAATACAGTTTCTAACGTAACTGTT  
134 ACTCAAGGTATGGACCGAGCTACGAGCGAATACCGAATTGTTGCTCAAGGTGATTTGCTTGGTGATGG  
135 TGATGCTACAGGATTGCAATACTGGCGATTTACCAAAGAAGGTAACCTTATAACTCGGAACCGCTTATA  
136 TGCCGGTACAGCTTTCATGAATACCGATGGTAATATTGCAGGTTCTATTTGGAACAAGTATAGCGGTGCT  
137 ACTAACCTTGATGCTGCAGTGAATACTCGTGTTGGTAAAGGCGGCGATAAATGACTGGCAAATTAATC  
138 GTTAAAAGAGGCTCTGACGCTATTAACATTGCTGCCGATGAAAATGATTCTGCTTATTTACTTGGAAACA  
139 TCGGGTGGAGCGAATTCGTGGTACATCGTAAAGGCGGAGCAGATGACACTGCTTCATTTTATAATTC  
140 AAAACTACCGCAGGAATTACTCTTAATAGTGAGGCGATATTGATTTAATGTTAAAAACAATCTACTG  
141 CAGCTTCATTAATTTTTATCGTTTATATTTAAACGGAAGACAGTGGACAGCTACTCAAGGCCACGGAT  
142 ATAATAATCAATGGCAAACAGAAGCCCATCTTCGTTGACTTTGGTGAATCTGTTCCGAAAGATAGTT  
143 ATATGCCAATTATCAAAGGAAAAAGCCAAATCATTAACGAAGGATATGCCACAAAGGCAGATTTTGGTA  
144 TTATTAGATTGGGCGGAGATGCTACTTGGGGAAATGCAGTAATTCGTGTTGGTTCTGCGGAAAGTGGA  
145 GATAGCAGTCATCCTAATGCAATATTTGTGTTTCAGGCTAATGGCGATTTTAAAGCTCCGGCTGGTCTTC  
146 GCGCTGGTGTTAACTTGGGTGTCGGTACAATCCAGCATGGGGCGGAGCATCTATCGCCATTGGGGAC

147 GATGACACCGGCTTGGTCCATGGCGGTGACGGCCGAATTAATATGTATGCCAATAGTATGCATATTGCA  
148 AGCTGGGGAGCTGGTTACCATATCCATGAAGGTCTTTGGGATACCACTGGTGCCTTGTGGACTGAAAC  
149 AGGAAGAGCTATTATTTCTTTTGGTCATTTAGTCCAACAAAACGATAGCTATTCAACATTTGTTTCGTGAC  
150 GTTTATGTTTCGTTCTGATATTCGTGTTAAAAAAGACCTTGTTAAATTTGAAAATGCTTCACAGACACTTT  
151 CAAAAATTAACGGTTACACTTATATGCAGAAACGTGGCCTGGATGAAGAAGGTAATCAGAAATGGGAA  
152 CCTAATGCCGGTTTAATTGCTCAAGAAGTTCAAGCTATTTTACCTGAATTGGTTGAAGGGGACCCCTGAC  
153 GGTGAAGCTTTACTTCGTTTAAACTATAACGGTGTAAATTGGTTTAAATACAGCTGCAATCAATGAGCAC  
154 ACTGCAGAAATAGCAGAATTGAAATCAGAGATTGAAGAACTTAAAGCACTAATTAATCATTGTTAAA  
155 ATAA

156

157 **WQT3**

158 ATGGCTACTTTAAAGCAAATCCAATTTAAAGAAGTAAAGTAGCCGGTGTACGTCCGGCACCGGCCCA  
159 GTTGGCTGAAGGCGAACTGGCTATTAACTTAAAGGACCGTTTACTTTTACTAAAGACGATACTGGAG  
160 CGATTATCGACCTTGGCTTTGCTAAGGGTGGAAATATCGATGGTAATGTTATTCAAAAAGGCAATTACAA  
161 CCAAACCGTAATTATAATCTGTCTGGTACTTTTACCCAAACAGGTAGTTATACGACATCCGGAAGTATA  
162 ACAGCAAATGGTGATATTACTGCAAAATCTCGCCTAATGACGGATATGGGCGAAGTTTTGGTACGTGGC  
163 AATGGTACCGCACATGTTTCGATTCCAGGATTTAGCTGATGCGCGCGAAAGAGCTATAATTTATTCTCAA  
164 AACCGTACTGGGGATACCAAGCAAATCTTGAACGTTTCGTGTTTCAGGATTACACTAATTCGACATCTAAT  
165 ATTTTTGCATTCAACGGCGACGGTTTATTTTATGCTCCGTCTATTTCCGCCGGAACATCAGTAAAATCTC  
166 CGGTAATTTATACTAATACTGTTAATACAGACAGTAAGAATATTGGCGATTATGATATATCTTCATTAGCA  
167 AATAATAATTCTGCCACGGATAAAAACCTATTTGCGCGTTGTACGTACCGACCCAGCGTCTGCAATACTT  
168 CATGAAATTTGTGAAAATAACGGTATCAGTTGGTATTCTGGTTCAACCCCTACTGATTATATGTTGTCTT  
169 TTGCTTATCCGGTGGTTTTCAAGCAGGTCATTCGATTGCAGTAGGTATGGAATCAGGGCCTTTGACATA  
170 TTCAACCTTAGGTAAAGGTTCTATTGTTCTTGGTGATAATGATACCGGGTTTAAATGGAAACAAGACGG  
171 CCTGTTCTATACAATTAATAATGGAGCTTATACTTTACTTACAACCTCCAACTGAAGTTACAAGCCTTAAA  
172 CAGTTAGTTGCGGGTTATTCAACCAACGGTTCTGATTTAATTCTTCTACAACCTCAAACCTATCCATTAG  
173 TTATTGTTAATACTACTAATGATAAAAACAGCTTCGCGCAGCGTCAAACCTCTTTTAGGTTATCACCAGA  
174 GCGGCAAATATCACCATTATTTTCGTGGCAAAGGTGTAACAAACGTTAACACCGCCGGCGGGTTGTTG  
175 GTTACTCCTGGTAACGTTGAAGTCCGGGGCGGTTTCGGTTAATATTGATGGTCTCAGTAATGCTTCTACA  
176 GTGCTTTTTAAAGGAAATACTACAGGATATAGTTTCAGTCGATAATATAGAGCTCAAAGTTTGGGGTGAC  
177 ACTTTTAATACGGTAGGTGGTTCTCGTAAAAACGTAATGGAAACATCTGATGCTACTGGCTGGATGCAT  
178 TATATTCAACGAACTACAGAAGGTAAAGTCAATCCTATTTAAATGGTACCATGAATGTAATTGAAGGA  
179 TTGACTGTCAATCAAGATACATCCTTAAAACGTAATCTGTATGTTTCCAATGAAATTAAGTTTCGCGCTG  
180 CTAGTGGTCTTCGTATTTGGAACGATAAGTATGGTGTATTTTTCGAAATTCGGAAGACCAACTGCATAT  
181 TATCCGACCAATGCCAATGCCGGCGAAAGTGGTGGATTGGGCCATTACGACCGTTAAGTATTACATT  
182 AGACACCGGCATAGTTAAAATTCCTAACTTAGCAGCCAACCAGGTTTCTTTTAGTAGCACAGGTGTATT  
183 GGAATTCATCGCCGTAACGGTTCATCTTATGCTAACCAGAACACAACCTAAAGCTCCATTGTATCAAAC  
184 GCTTGGTTCTGCGACTCAAGCATTCTATCCTATTAAGCAGAAAAATACAGTTTCTAACGTAACCTGTT  
185 ACTCAAGGTATGGACCGAGCTACGAGCGAATACCGAATTGTTGCTCAAGGTGATTTGCTTGGTGATGG  
186 TGATGCTACAGGATTGCAATACTGGCGATTTACCAAAGAAGGTAACCTTATAACTCGGAACCGCTTATA  
187 TGCCGGTACAGCTTTCATGAATACCGATGGTAATATTGCAGGTTCTATTTGGAACAAGTATAGCGGTGCT  
188 ACTAACCTTGATGCTGCAGTGAATACTCGTGTTGGTAAAGGCGGCGATACAATGACTGGCAAATTAATC  
189 GTTAAAAGAGGGCTCTGACGCTATTAACATTGCTGCCGATGAAAATGATTCTGCTTATTTACTTGGAAACA  
190 TCGGGTGGAGCGAATTCGTGGTACATCGGTAAAGGCGGAGCAGATGACACTGCTTCATTTTATAATTC

191 AAAACTACCGCAGGAATTACTCTTAATAGTGTAGGGGATATTGATTTTAATGTTAAAAACAATCTACTG  
192 CAGCTTCATTAATTTTTATCGTTTATATTTAAACGGAAGACAGTGGACAGCTACTCAAGGCCACGGAT  
193 ATAATAATCAATGGCAAACAGAAAGCCCATCTTCGTTGACTTTGGTGAATCTGTTCCGAAAGATAGTT  
194 ATATGCCAATTATCAAAGGAAAAAGCCAAATCATTAACGAAGGATATGCCACAAAGGCAGATTTTGGTA  
195 TTATTAGATTGGGCGGAGATGCTACTTGGGGAAATGCAGTAATTCGTGTTGGTTCTGCGGAAAGTGGA  
196 GATAGCAGTCATCCTAATGCAATATTTGTGTTTCAGGCTAATGGCGATTTTAAAGCTCCGGCTGGTCTTC  
197 GCGCTGGTGTTAACTTGGGTGTCGGTACAATCCAGCATGGGGCGGAGCATCTATCGCTATTGGTGATA  
198 ACGACACAGGTTTAGTCCATGGTGGTGACGGCCGAATTAATATGTATGCCAATAGTATGCATATTGCAA  
199 GCTGGGGAAGCCGGTTACCATATCCATGAAGGTCTTTGGGATACCACTGGTGCCTTGTGGACTGAAACA  
200 GGAAGAGCTATTATTTCTTTGGTCATTTAGTCCAACAAAACGATAGCTATTCAACATTTGTTCGTGACG  
201 TTTATGTTCTGTTCTGATATTCGTGTTAAAAAGACCTTGTTAAATTTGAAAATGCTTCACAGACACTTTC  
202 AAAAATTAACGGTTACACTTATATGCAGAAACGTGGCCTGGATGAAGAAGGTAATCAGAAATGGGAAC  
203 CTAATGCCGGTTTAAATTGCTCAAGAAGTTCAAGCTATTTTACCTGAATTGGTTGAAGGCGACCCCTGACG  
204 GTGAAGCTTTACTTTCGTTTAAACTATAACGGTGTAATTGGTTTAAATACAGCTGCAATCAATGAGCACA  
205 CTGCAGAAATAGCAGAATTGAAATCAGAGATTGAAGAACTTAAAGCACTAATTAATCATTGTTAAAT  
206 AA

207

208 **WQT4**

209 ATGGCTACTTTAAAGCAAATCCAATTTAAAAGAAGTAAAGTAGCCGGTGTACGTCCGGCACCGGCCCA  
210 GTTGGCTGAAGGCGAACTGGCTATTAACTTAAAGGACCGTTTACTTTTACTAAAGACGATACTGGAG  
211 CGATTATCGACCTTGGCTTTGCTAAAGGCGGTAATATCGACGGAACGTTATTCATAACGGTAACTACA  
212 CTCAAACCGGTAATTATAATCTGTCTGGTACTTTTACCCAAACAGGTAGTTATACGACATCCGGAAGTAT  
213 AACAGCAAATGGTGATTAATCTGCAAAATCTCGCCTAATGACGGATATGGGCGAAGTTTGGTACGTGG  
214 CAATGGTACCGCATGTTTCGATTCCAGGATTTAGCTGATGCGCGGAAAGAGCTATAATTTATTCTCA  
215 AAACCGTACTGGGGATACCAAGCAAATCTTGAACGTTTCGTGTTTCAGGATTACACTAATTCGACATCTAA  
216 TATTTTTGCATTCAACGGCGACGGTTTATTTATGCTCCGCTATTTCCGCCGGAACATCAGTAAAATCT  
217 CCGGTAATTTATACTAATACTGTTAATACAGACAGTAAGAATATTGGCGATTATGATATATCTTCATTAGC  
218 AAATAATAATTCTGCCACGGATAAAAATTTGCGCGTTGTACGTACCGACCCAGCGTCTGCAATACT  
219 TCATGAAATTTGTGAAAATAACGGTATCAGTTGGTATTCTGGTTCAACCCCTACTGATTATATGTTGTCT  
220 TTTGCTTATCCGGTGGTTTTCAAGCAGGTCATTGATTGCAGTAGGTATGGAATCAGGGCCTTTGACAT  
221 ATTC AACCTTAGGTAAAGGTTCTATTGTTCTTGGTGATAATGATACCGGGTTTAAATGGAAACAAGACG  
222 GCCTGTTCTATAACAATTAATAATGGAGCTTATACTTTACTTACAACCTCCAACCTGAAGTTACAAGCCTTAA  
223 ACAGTTAGTTGCGGGTATTCAACCAACGGTTCTGATTAAATCTTCTTACAACCTCAAACTATCCATTA  
224 GTTATTGTTAATACTACTAATGATAAAAACAGCTTCGCGACGGTCAAACCTTTTTAGGTTATCACCAG  
225 AGCGGCAAATATCACCATTATTTTCGTGGCAAAGGTGTAACAAACGTTAACACCGCCGGCGGGTTGTT  
226 GGTTACTCCTGGTAACGTTGAAGTCCGGGGCGGTTCCGGTTAATATTGATGGTCTCAGTAATGCTTCTAC  
227 AGTGCTTTTTAAAGGAAATACTACAGGATATAGTTCAGTCGATAATATAGAGCTCAAAGTTTGGGGTGA  
228 CACTTTTAATACGGTAGGTGGTTCTCGTAAAAACGTAATGGAAACATCTGATGCTACTGGCTGGATGCA  
229 TTATATCAACGAACACAGAAGGTAAAGTCGAATCCTATTTAAATGGTACCATGAATGTAATTGAAGG  
230 ATTGACTGTCAATCAAGATACATCCTTAAAACGTAATCTGTATGTTTCCAATGAAATTAAGTTCGCGCT  
231 GCTAGTGGTCTTCGTATTTGGAACGATAAGTATGGTGTATTTTTCGAAATTCGGAAGACCAACTGCATA  
232 TTATCCGACCAATGCCAATGCCGGCGAAAGTGGTGGATTGGGCCATTACGACCGTTAAGTATTACAT  
233 TAGACACCGGCATAGTTAAAATTCCTAACTTAGCAGCCAACCAGGTTTCTTTTAGTAGCACAGGTGTAT  
234 TGGAATTCATCGCCGGTAACGGTTCATCTTATGCTAACGAAACACAACCTAAAGCTCCATTGTATCAA

235 CGCTTGGTTCTGCGACTCAAGCATTCTATCCTATTAAGCAGAAAAATACAGTTTCTAACGTAACGTG  
236 TTAAGGTATGGACCGAGCTACGAGCGAATACCGAATTGTTGCTCAAGGTGATTTGCTTGGTGATG  
237 GTGATGCTACAGGATTGCAATACTGGCGATTTACCAAAGAGGTAACCTTATAACTCGGAACCGCTTAT  
238 ATGCCGGTACAGCTTTCATGAATACCGATGGTAATATTGCAGGTTCTATTTGGAACAAGTATAGCGGTGC  
239 TACTAACCTTGATGCTGCAGTGAATACTCGTGTGGTAAAGGCGGCGATACAATGACTGGCAAATTAAT  
240 CGTAAAAAGAGGCTCTGACGCTATTAACATTGCTGCCGATGAAAATGATTCTGCTTATTTACTTGGAAC  
241 ATCGGGTGGAGCGAATTCGTGGTACATCGGTAAAGGCGGAGCAGATGACTGCTTCATTTTATAATTT  
242 CAAAACCTACCGCAGGAATTACTCTTAATAGTGTAGGCGATATTGATTTTAATGTAAAAACAATCTACT  
243 GCAGCTTCATTAATTTTTATCGTTTATATTTAAACGGAAGACAGTGGACAGCTACTCAAGGCCACGGA  
244 TATAATAATCAATGGCAAACAGAAGCCCCATTCTTCGTTGACTTTGGTGAATCTGTTCCGAAAGATAGT  
245 TATATGCCAATTATCAAAGGAAAAAGCCAAATCATTAACGAAGGATATGCCACAAAGGCAGATTTTGGT  
246 ATTATTAGATTGGGCGGAGATGCTACTTGGGGAAATGCAGTAATTCGTGTTGGTTCTGCGGAAAGTGGA  
247 GATAGCAGTCATCCTAATGCAATATTTGTGTTTCAGGCTAATGGCGATTTAAAGCTCCGGCTGGTCTTC  
248 GCGCTGGTGTTAACTTGGGTGTCGGTACAATTCAGCATGGGGCGGAGCATCTATCGCCATTGGGGAC  
249 GATGACACCGGCTTGGTCCATGGTGGTGACGGCCGAATTAATATGTATGCCAATAGTATGCATATTGCAA  
250 GCTGGGGA<sup>GCC</sup>GGTTACCATATCCATGAAGGCTTTGGGATAACCACTGGTGCCTTGTGGACTGAAACA  
251 GGAAGAGCTATTATTTCTTTTGGTCATTTAGTCCAACAAAACGATAGCTATTCAACATTTGTTCGTGACG  
252 TTTATGTTTCGTTCTGATATTCGTGTTAAAAAGACCTTGTAAATTTGAAAATGCTTCACAGACACTTTC  
253 AAAAAATTAACGGTTACACTTATATGCAGAAACGTGGCCTGGATGAAGAAGGTAATCAGAAATGGGAAC  
254 CTAATGCCGGTTTAATTGCTCAAGAAGTTCAAGCTATTTTACCTGAATTGGTTGAAGGCGACCCCTGACG  
255 GTGAAGCTTTACTTTCGTTTAAACTATAACGGTGTAAATGGTTTAAATACAGCTGCAATCAATGAGCACA  
256 CTGCAGAAATAGCAGAATTGAAATCAGAGATTGAAGAACTTAAAGCACTAATTAATCATTGTTAAAT  
257 AA

258

259 **WQT5**

260 ATGGCTACTTTAAAGCAAATCCAATTTAAAGAAAGTAAAGTAGCCGGTGTACGTCCGGCACCGGCCCA  
261 GTTGGCTGAAGGCGAACTGGCTATTAACCTTAAAGGACCGTTTACTTTTTACTAAAGACGATACTGGAG  
262 CGATTATCGACCTTGGCTTTGCTAAAGGCGGTAATATCGACGGAAACGTTATTCATAACGGTAACTACA  
263 CTCAAACCGGTAATTATAATCTGTCTGGTACTTTTACCAAACAGGTAGTTATACGACATCCGGAAGTAT  
264 AACAGCAAATGGTGATTAATGCAAAAATCTCGCCTAATGACGGATATGGGCGAAGTTTGGTACGTGG  
265 CAATGGTACCGCACATGTTTCGATTCCAGGATTTAGCTGATGCGCGGAAAGAGCTATAATTTATTCTCA  
266 AAACCGTACTGGGGATACCAAGCAAATCTTGAACGTTTCGTGTTTCAGGATTACACTAATTCGACATCTAA  
267 TATTTTGCATTCAACGGCGACGGTTTATTTATGCTCCGCTATTTCCGCCGGAACATCAGTAAAAATCT  
268 CCGGTAATTTATACTAATACTGTAAATACAGACAGTAAGAATATTGGCGATTATGATATATCTTCATTAGC  
269 AAATAATAATTCTGCCACGGATAAAAACTATTTGCGCGTTGTACGTACCGACCCAGCGTCTGCAATACT  
270 TCATGAAATTTGTGAAAATAACGGTATCAGTTGGTATTCTGGTTCAACCCCTACTGATTATATGTTGTCT  
271 TTTGCTTATCCGGTGGTTTTCAAGCAGGTCATTGATTGCAGTAGGTATGGAATCAGGGCCTTTGACAT  
272 ATTCAACCTTAGGTAAAGGTTCTATTGTTCTTGGTGATAATGATACCGGGTTTAAATGGAAACAAGACG  
273 GCCTGTTCTATACAATTAATAATGGAGCTTATACTTTACTTACAACCTCAACTGAAGTTACAAGCCTTAA  
274 ACAGTTAGTTGCGGGTATTCAACCAACGGTTCGATTTAATTCTTCCTACAACCTCAAACTATCCATTA  
275 GTTATTGTTAATACTACTAATGATAAAAACAGCTTCGGCGACGGTCAAACCTCTTTTAGGTTATCACCAG  
276 AGCGGCAAATATCACCAATTATTTTCGTGGCAAAGGTGTAACAAACGTTAACACCGCCGGCGGGTTGTT  
277 GGTTACTCCTGGTAAACGTTGAAGTCCGGGGCGGTTTCGGTTAATATTGATGGTCTCAGTAATGCTTCTAC  
278 AGTGCTTTTTAAAGGAAATACTACAGGATATAGTTCAGTCGATAATATAGAGCTCAAAGTTGGGGTGA

279 CACTTTTAATACGGTAGGTGGTTCTCGTAAAAACGTAATGGAAACATCTGATGCTACTGGCTGGATGCA  
280 TTATATCAACGAACACAGAAGGTAAAGTCGAATCCTATTTAAATGGTACCATGAATGTAATTGAAGG  
281 ATTGACTGTCAATCAAGATACATCCTTAAAACGTAATCTGTATGTTTCCAATGAAATTAAGTTCGCGCT  
282 GCTAGTGGTCTTCGTATTTGGAACGATAAGTATGGTGTATTTTTTCGAAATTCGGAAGACCAACTGCATA  
283 TTATCCGACCAATGCCAATGCCGGCGAAAGTGGTGGATTGGGCCATTACGACCGTTAAGTATTACAT  
284 TAGACACCGGCATAGTTAAAATTCCTAACTTAGCAGCCAACCAGGTTTCTTTTAGTAGCACAGGTGTAT  
285 TGGAATTCATCGCCGGTAACGGTTCATCTTATGCTAACCCAGAACAACAACTAAAGCTCCATTGTATCAAA  
286 CGCTTGGTTCTGCGACTCAAGCATTCTATCTATTAAGCAGAAAAATACAGTTTCTAACGTAACCTG  
287 TTAACAAGGTATGGACCGAGCTACGAGCGAATACCGAATTGTTGCTCAAGGTGATTGCTTGGTGATG  
288 GTGATGCTACAGGATTGCAATACTGGCGATTTACCAAAGAAGGTAACTTATAACTCGGAACCGCTTAT  
289 ATGCCGGTACAGCTTTCATGAATACCGATGGTAATATTGCAGGTTCTATTTGGAACAAGTATAGCGGTGC  
290 TACTAACCTTGATGCTGCAGTGAATACTCGTGTGGTAAAGGCGCGATACAATGACTGGCAAATTAAT  
291 CGTTAAAAGAGGCTCTGACGCTATTAACATTGCTGCCGATGAAAATGATTCTGCTTATTTACTTGGAAC  
292 ATCGGGTGGAGCGAATTCGTGGTACATCGGTAAAGGCGGAGCAGATGACTGCTTCATTTTATAATTT  
293 CAAAACCTACCGCAGGAATTACTCTTAATAGTGTAGGCGATATTGATTTAATGTAAAAACAATCTACT  
294 GCAGCTTCATTAATTTTTATCGTTTATTTAAACGGAAGACAGTGGACAGCTACTCAAGGCCACGGA  
295 TATAATAATCAATGGCAAACAGAAGCCCCATTCTTCGTTGACTTTGGTGAATCTGTTCCGAAAGATAGT  
296 TATATGCCAATTATCAAAGGAAAAAGCCAAATCATTAACGAAGGATATGCCACAAAGGCAGATTTTGGT  
297 ATTATTAGATTGGGCGGAGATGCTACTTGGGGAAATGCAGTAATTCGTGTTGGTTCTGCGGAAAGTGGA  
298 GATAGCAGTCATCCTAATGCAATATTTGTGTTTCAGGCTAATGGCGATTTTAAAGCTCCGGCTGGTCTTC  
299 GCGCTGGTGTTAACTTGGGTGTCGGTACAATTCAGCATGGGGCGGAGCATCTATCGCCATTGGGGAC  
300 GATGACACCGGCTTGGTCCATGGCGGTGACGGCCGAATTAATATGTATGCCAATAGTATGCATATTGCA  
301 AGCTGGGGA **GCC**GGTTACCATATCCATGAAGGTCTTTGGGATACCACTGGTGCCTTGTGGACTGAAAC  
302 AGGAAGAGCTATTATTTCTTTTGGTCATTTAGTCCAACAAAACGATAGCTATTCAACATTTGTTCTGTGAC  
303 GTTTATGTTCTGTTCTGATATTCTGTGTTAAAAAAGACCTTGTTAAATTTGAAAATGCTTCACAGACACTTT  
304 CAAAAATTAACGGTTACTTATATGCAGAAACGTGGCTGGATGAAGAAGGTAATCAGAAATGGGAA  
305 CCTAATGCCGGTTAATTGCTCAAGAAGTTCAAGCTATTTTACCTGAATTGGTTGAAGGCGACCTGAC  
306 GGTGAAGCTTTACTTCGTTTAAACTATAACGGTGTAAATTGGTTTAAATACAGCTGCAATCAATGAGCAC  
307 ACTGCAGAAATAGCAGAATTGAAATCAGAGATTGAAGAACTTAAAGCACTAATTAATCATTGTAAAA  
308 ATAA

309

310 **WQT6**

311 ATGGCTACTTTAAAGCAAATCCAATTTAAAGAAGTAAAGTAGCCGGTGTACGTCCGGCACCGGCCCA  
312 GTTGGCTGAAGGCGAACTGGCTATTAACCTAAAGGACCGTTTACTTTTTACTAAAGACGATACTGGAG  
313 CGATTATCGACCTTGGCTTTGCT **AAGGGTGGAA**AATATC **GATGGTAAT**GTTATTCA **AAAGGCAAT**TACAA  
314 **C**CAAACCGTAATTATAATCTGTCTGGTACTTTTACCCAAACAGGTAGTTATACGACATCCGGAAGTATA  
315 ACAGCAAATGGTGATATTACTGCAAAATCTCGCCTAATGACGGATATGGGCGAAGTTTGGTACGTGGC  
316 AATGGTACCGCACATGTTTCGATTCCAGGATTTAGCTGATGCGCGGAAAGAGCTATAATTTATTCTCAA  
317 AACCGTACTGGGATACCAAGCAAATCTTGAACGTTCTGTTCAGGATTACACTAATTCGACATCTAAT  
318 ATTTTGCATCAACGGCGACGGTTTATTTATGCTCCGCTATTTCCGCCGGAACATCAGTAAAAATCTC  
319 CGGTAATTTATACTAATACTGTTAATACAGACAGTAAGAATATTGGCGATTATGATATATCTTCATTAGCA  
320 AATAATAATTCTGCCACGGATAAAAACCTATTTGCGCGTTGTACGTACCGACCCAGCGTCTGCAATACTT  
321 CATGAAATTTGTGAAAATAACGGTATCAGTTGGTATTCTGGTTCAACCCCTACTGATTATATGTTGTCTT  
322 TTGCTTATCCGGTGGTTTTCAAGCAGGTCATTCGATTGCAGTAGGTATGGAATCAGGGCCTTTGACATA



323 TTCAACCTTAGGTAAAGGTTCTATTGTTCTTGGTGATAATGATACCGGGTTTAAATGGAAACAAGACGG  
324 CCTGTTCTATAACAATTAATAATGGAGCTTATACTTTACTTACAACCTCCAAGTTACAAGCCTTAAA  
325 CAGTTAGTTGCGGGTTATTCAACCAACGGTCTGATTTAATTCTTCCTACAACCTCAAAACTATCCATTAG  
326 TTATTGTTAATACTACTAATGATAAAAACAGCTTCGGCGACGGTCAAACCTCTTTTAGGTTATCACCAGA  
327 GCGGCAAATATCACCATTATTTTCGTGGCAAAGGTGTAACAAACGTTAACACCGCCGGCGGGTTGTTG  
328 GTTACTCCTGGTAACGTTGAAGTCCGGGGCGGTTCCGGTTAATATTGATGGTCTCAGTAATGCTTCTACA  
329 GTGCTTTTTAAAGGAAATACTACAGGATATAGTTCAGTCGATAATATAGAGCTCAAAGTTTGGGGTGAC  
330 ACTTTTAATACGGTAGGTGGTTCTCGTAAAAACGTAATGGAAACATCTGATGCTACTGGCTGGATGCAT  
331 TATATTCAACGAACTACAGAAGGTAAAGTCGAATCCTATTTAAATGGTACCATGAATGTAATTGAAGGA  
332 TTGACTGTCAATCAAGATACATCCTTAAAACGTAATCTGTATGTTCCAATGAAATTAAGTTCGCGCTG  
333 CTAGTGGTCTTCGTATTTGGAACGATAAGTATGGTGTATTTTTCGAAATTCGGAAGACCAACTGCATAT  
334 TATTCCGACCAATGCCAATGCCGGCGAAAGTGGTGGATTGGGCCATTACGACCGTTAAGTATTACATT  
335 AGACACCGGCATAGTTAAAATTCCTAACTTAGCAGCCAACCAGGTTTCTTTTAGTAGCACAGGTGTATT  
336 GGAATTCATCGCCGGTAACGGTTCATCTTATGCTAACCAGAACACAACCTAAAGCTCCATTGTATCAAAC  
337 GCTTGGTTCTGCGACTCAAGCATTCTATCCTATTACTAAGCAGAAAAATACAGTTTCTAACGTAACCTGTT  
338 ACTCAAGGTATGGACCGAGCTACGAGCGAATACCGAATTGTTGCTCAAGGTGATTTGCTTGGTGATGG  
339 TGATGCTACAGGATTGCAATACTGGCGATTTACCAAAGAAGGTAACCTTATAACTCGGAACCGCTTATA  
340 TGCCGGTACAGCTTTCATGAATACCGATGGTAATATTGCAGGTTCTATTTGGAACAAGTATAGCGGTGCT  
341 ACTAACCTTGATGCTGCAGTGAATACTCGTGTGGTAAAGGCGGCGATAACAATGACTGGCAAATTAATC  
342 GTTAAAAGAGGCTCTGACGCTATTAACATTGCTGCCGATGAAAATGATTCTGCTTATTTACTTGAACA  
343 TCGGGTGGAGCGAATTCGTGGTACATCGGTAAAGGCGGAGCAGATGACACTGCTTCATTTTATAATTC  
344 AAAACTACCGCAGGAATTACTCTTAATAGTGTAGGCGATATTGATTTAATGTTAAAAACAATCTACTG  
345 CAGCTTCATTAATTTTTATCGTTTATATTTAAACGGAAGACAGTGGACAGCTACTCAAGGCCACGGAT  
346 ATAATAATCAATGGCAAACAGAAGCCCCATTCTTCGTTGACTTTGGTGAATCTGTTCCGAAAGATAGTT  
347 ATATGCCAATTATCAAAGGAAAAAGCCAAATCATTAAACGAAGGATATGCCACAAAGGCAGATTTTGGTA  
348 TTATTAGATTGGGCGGAGATGCTACTTGGGGAAATGCAGTAATTCGTGTTGGTTCTGCGGAAAGTGGA  
349 GATAGCAGTCATCCTAATGCAATATTTGTGTTTCAGGCTAATGGCGATTTTAAAGCTCCGGCTGGTCTTC  
350 GCGCTGGTGTTAACTTGGGTGTCGGTACAATTCAGCATGGGGCGGAGCATCTATCGCCATTGGGGAC  
351 GATGACACCGGCTTGGTCCATGGCGGTGACGGCCGAATTAATATGTATGCCAATAGTATGCATATTGCA  
352 AGCTGGGGAGCTGGTTACCATATCCATGAAGGTCTTGGGATACCACTGGTGCCTTGTGGACTGAAAC  
353 AGGAAGAGCTATTATTTCTTTTGGTCATTTAGTCCAACAAAACGATAGCTATTCAACATTTGTTCTGTGAC  
354 GTTTATGTTCTGTTCTGATATTCTGTGTTAAAAAAGACCTTGTTAAATTTGAAAATGCTTCACAGACACTTT  
355 CAAAAATTAACGGTTACACTTATATGCAGAAACGTGGCCTGGATGAAGAAGGTAATCAGAAATGGGAA  
356 CCTAATGCCGGTTAATTGCTCAAGAAGTTCAAGCTATTTTACCTGAATTGGTTGAAGGCGACCTGAC  
357 GGTGAAGCTTACTTCGTTTAAACTATAACGGTGTAAATTGGTTTAAATACAGCTGCAATCAATGAGCAC  
358 ACTGCAGAAATAGCAGAATTGAAATCAGAGATTGAAGAACTTAAAGCACTAATTAATCATTGTTAAA  
359 ATAA

360

361 **WQT7**

362 ATGGCTACTTTAAAGCAAATCCAATTTAAAGAAGTAAAGTAGCCGGTGTACGTCCGGCACCGGCCCA  
363 GTTGGCTGAAGGCGAACTGGCTATTAACCTAAAGGACCGTTTACTTTTTACTAAAGACGATACTGGAG  
364 CGATTATCGACCTTGGCTTTGCTAAAGGCGGTAATATCGACGGAAACGTTATTCATAACGGTAACTACA  
365 CTCAAACCGGT(AATTATAATCTGTCTGGTACTTTTACCCAAACAGGT)AGTTATACGACATCCGGAAGT  
366 ATAACAGCAAATGGTGATTAATGCAAAAATCTCGCCTAATGACGGATATGGGCGAAGTTTTGGTACGT

367 GGCAATGGTACCGCACATGTTTCGATTCCAGGATTTAGCTGATGCGCGGAAAGAGCTATAATTTATTCT  
368 CAAAACCGTACTGGGGATACCAAGCAAATCTTGAACGTTTCGTGTTTCAGGATTACACTAATTCGACATCT  
369 AATATTTTGCATTCAACGGCGACGGTTTATTTTATGCTCCGCTATTTCCGCCGGAACATCAGTAAAAT  
370 CTCCGGTAATTTATACTAATACTGTTAATACAGACAGTAAGAATATTGGCGATTATGATATATCTTCATTA  
371 GCAAATAATAATTCTGCCACGGATAAAAACTATTTGCGCGTTGTACGTACCGACCCAGCGTCTGCAATA  
372 CTTTCATGAAATTTGTGAAAATAACGGTATCAGTTGGTATTCTGGTTCAACCCCTACTGATTATATGTTGT  
373 CTTTTGCTTATCCGGTGGTTTTCAAGCAGGTCATTTCGATTGCAGTAGGTATGGAATCAGGGCCTTTGA  
374 CATATTCAACCTTAGGTAAAGGTTCTATTGTTCTTGGTGATAATGATACCGGGTTTAAATGGAAACAAG  
375 ACGGCCTGTTCTATAACAATTAATAATGGAGCTTATACTTTACTTACAACCTCCAACCTGAAGTTACAAGCCT  
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377 TTAGTTATTGTTAATACTACTAATGATAAAAACAGCTTCGGCGACGGTCAAACCTCTTTTAGGTTATCACC  
378 AGAGCGGCAAATATCACCATTATTTTCGTGGCAAAGGTGTAACAAACGTTAACACCGCCGGCGGGTTG  
379 TTGGTTACTCCTGGTAACGTTGAAGTCCGGGGCGGTTCCGGTTAATATTGATGGTCTCAGTAATGCTTCT  
380 ACAGTGCTTTTTAAAGGAAATACTACAGGATATAGTTCAGTCGATAATATAGAGCTCAAAGTTTGGGGT  
381 GACACTTTTAATACGGTAGGTGGTTCTCGTAAAAACGTAATGGAAACATCTGATGCTACTGGCTGGATG  
382 CATTATATTCAACGAACTACAGAAGGTAAGTCAATCCTATTTAAATGGTACCATGAATGTAATTGAAG  
383 GATTGACTGTCAATCAAGATACATCCTTAAAACGTAATCTGTATGTTCCAATGAAATTAAGTTCGCGC  
384 TGCTAGTGGTCTTCGTATTTGGAACGATAAGTATGGTGTATTTTTCGAAATTCGGAAGACCAACTGCAT  
385 ATTATCCGACCAATGCCAATGCCGGCGAAAAGTGGTGGATTGGGCCATTACGACCGTTAAGTATTACA  
386 TTAGACACCGGCATAGTTAAAATTCCTAACTTAGCAGCCAACCAGGTTTCTTTTAGTAGCACAGGTGTA  
387 TTGGAATTCATCGCCGTAACGGTTCATCTTATGCTAACCAGAACACAACCTAAAGCTCCATTGTATCAA  
388 ACGCTTGGTTCTGCGACTCAAGCATTCTATCCTATTACTAAGCAGAAAAATACAGTTTCTAACGTAAC  
389 GTTACTCAAGGTATGGACCGAGCTACGAGCGAATACCGAATTGTTGCTCAAGGTGATTTGCTTGGTGAT  
390 GGTGATGCTACAGGATTGCAATACTGGCGATTTACCAAAGAAGGTAACCTTTATACTCGGAACCGCTTA  
391 TATGCCGGTACAGCTTTCATGAATACCGATGGTAATATTGCAGGTTCTATTTGGAACAAGTATAGCGGTG  
392 CTACTAACCTTGATGCTGCAGTGAATACTCGTGTGGTAAAGGCGGCGATACAATGACTGGCAAATTA  
393 TCGTTAAAAGAGGCTCTGACGCTATTAACATTGCTGCCGATGAAAATGATTCTGCTTATTTACTTGGA  
394 CATCGGGTGGAGCGAATTCGTGGTACATCGGTAAAGGCGGAGCAGATGACTGCTTCATTTTATAATT  
395 TCAAAACTACCGCAGGAATTACTCTTAATAGTGTAGGCGATATTGATTTAATGTTAAAAACAATCTAC  
396 TGCAGCTTCATTAAATTTTATCGTTTATATTTAAACGGAAGACAGTGGACAGCTACTCAAGGCCACGG  
397 ATATAATAATCAATGGCAAACAGAAGCCCCATTCTTCGTTGACTTTGGTGAATCTGTTCCGAAAGATAG  
398 TTATATGCCAATTATCAAAGGAAAAAGCCAAATCATTAAACGAAGGATATGCCACAAAGGCAGATTTTGG  
399 TATTATTAGATTGGGCGGAGATGCTACTTGGGGAATGCAGTAATTCGTGTTGGTTCTGCGGAAAAGTGG  
400 AGATAGCAGTCATCCTAATGCAATATTTGTGTTTCAGGCTAATGGCGATTTTAAAGCTCCGGCTGGTCTT  
401 CGCGCTGGTGTAACTTGGGTGTCGGTACAATTCCAGCATGGGGCGGAGCATCTATCGCCATTGGGGA  
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403 AGCTGGGGA**GCC**GGTTACCATATCCATGAAGGTCTTTGGGATACCACTGGTGCCTTGTGGACTGAAAC  
404 AGGAAGAGCTATTATTTCTTTTGGTCAATTTAGTCCAACAAAACGATAGCTATTCAACATTTGTTCTGTGAC  
405 GTTTATGTTCTGATATTTCGTGTTAAAAAAGACCTTGTTAAATTTGAAAATGCTTCACAGACACTTT  
406 CAAAATTAACGGTTACACTTATATGCAGAAACGTGGCCTGGATGAAGAAGGTAATCAGAAATGGGAA  
407 CCTAATGCCGGTTAATTGCTCAAGAAGTTCAAGCTATTTTACCTGAATTGGTTGAAGGCGACCTGAC  
408 GGTGAAGCTTTACTTCGTTTAAACTATAACGGTGTAAATGGTTTAAATACAGCTGCAATCAATGAGCAC  
409 ACTGCAGAAATAGCAGAATTGAAATCAGAGATTGAAGAACTTAAAGCACTAATTAATCATTGTTAAA  
410 ATAA

411

412 **WQT8**

413 ATGGCTACTTTAAAGCAAATCCAATTTAAAGAAGTAAAGTAGCCGGTGTACGTCCGGCACCCGCCCA  
414 GTTGGCTGAAGGCCAACTGGCTATTAACCTAAAGGACCGTTTACTTTTTACTAAAGACGATACTGGAG  
415 CGATTATCGACCTTGGCTTTGCTAAGGGTGGAAATATCGATGGTAATGTTATTCATAAAGGCAATTACAC  
416 TCAAACCGGTAAATTATAATCTGTCTGGTACTTTTACCCAAACAGGTAGTTATAACGACATCCGGAAGTATA  
417 ACAGCAAATGGTGATATTACTGCAAAATCTCGCCTAATGACGGATATGGGCGAAGTTTTGGTACGTGGC  
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457 AAAAATTAACGGTTACACTTATATGCAGAAACGTGGCCTGGATGAAGAAGGTAATCAGAAATGGGAAC  
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459 GTGAAGCTTTACTTTCGTTTAAACTATAACGGTGTAAATTGGTTTAAATACAGCTGCAATCAATGAGCACA  
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461 AA

462 **WQT9**

463 ATGGCTACTTTAAAGCAAATCCAATTTAAAGAAGTAAAGTAGCCGGTGTACGTCCGGCACCGGCCA  
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467 AACAGCAAATGGTGATTAATGCAAAAATCTCGCCTAATGACGGATATGGGCGAAGTTTGGTACGTGG  
468 CAATGGTACCGCACATGTTTCGATTCCAGGATTTAGCTGATGCGCGGAAAGAGCTATAATTTATTCTCA  
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509 GGTGAAGCTTTACTTCGTTTAAACTATAACGGTGTAATTGGTTTAAATACAGCTGCAATCAATGAGCAC  
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511 ATAA  
512 **WQT10**  
513 ATGGCTACTTTAAAGCAAATCCAATTTAAAGAAGTAAAGTAGCCGGTGTACGTCCGGCACCGGCCCA  
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558 CCTAATGCCGGTTAATTGCTCAAGAAGTTCAAGCTATTTTACCTGAATTGGTTGAAGGCGACCCTGAC  
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560 ACTGCAGAAATAGCAGAATTGAAATCAGAGATTGAAGAACTTAAAGCACTAATTAATCATTGTAAA  
561 ATAA

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563 **WQT11**

564 ATGGCTACTTTAAAGCAAATCCAATTTAAAGAAGTAAAGTAGCCGGTGTACGTCCGGCACCGGCCCA  
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611 CTGCAGAAATAGCAGAATTGAAATCAGAGATTGAAGA ACTTAAAGCACTAATTAATCATTGTTAAAT  
612 AA

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614 **WQT12**

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625 TCATGAAATTTGTGAAAATAACGGTATCAGTTGGTATTCTGGTTCAACCCCTACTGATTATATGTTGTCT  
626 TTTGCTTATCCGGTGGTTTTCAAGCAGGTCATTGATTGCAGTAGGTATGGAATCAGGGCCTTTGACAT  
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628 GCCTGTTCTATACAATTAATAATGGAGCTTATACTTTACTTACA ACTCCA ACTGAAGTTACAAGCCTTAA  
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631 AGCGGCAAATATCACCATTATTTTCGTGGCAAAGGTGTAACAAACGTTAACACCGCCGGCGGGTTGTT  
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633 AGTGCTTTTTAAAGGAAATACTACAGGATATAGTTCAGTCGATAATATAGAGCTCAAAGTTGGGGTGA  
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637 GCTAGTGGTCTTCGTATTTGGAACGATAAGTATGGTGTATTTTTCGAAATTCGGAAGACCAACTGCATA  
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663 ATAA

664

665 **WQC1**

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714 ATCATTGTAAAATAA

715

716 **WQD1**

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765 TGTTAAAATAA  
766  
767 **WQE1**  
768  
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817 TGTTAAAATAA

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819 **WQT1**

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858 GATAGCAGTCATCCTAATGCAATATTTGTGTTTCAGGCTAATGGCGATTTTAAAGCTCCGGCTGGTCTTC  
859 GCGCTGGTGTTAACTTGGGTGTCGGTACAATTCCAGCATGGGGCGGAGCATCTATCGCCATTGGTGATA  
860 ACGACACAGGTTTAGTCCATGGTGGTGACGGCCGAATTAATATGTATGCCAATAGTATGCATATTGCAA  
861 GCTGGGGAGCTGGTTACCATATCCATGAAGGTCCTTTGGGATACCACTGGTGCCTTGTGGACTGAAACA  
862 GGAAGAGCTATTATTTCTTTTGGTCATTTAGTCCAACAAAACGATAGCTATTCAACATTTGTTTCGTGACG  
863 TTTATGTTTCGTTCTGATATTCGTGTTAAAAAAGACCTTGTTAAATTTGAAAATGCTTCACAGACACTTC  
864 AAAAATTAACGGTTACACTTATATGCAGAAACGTGGCCTGGATGAAGAAGGTAATCAGAAATGGGAAC  
865 CTAATGCCGGTTTAATTGCTCAAGAAGTTCAAGCTATTTTACCTGAATTGGTTGAAGGCGACCCTGACG  
866 GTGAAGCTTTACTTCGTTTAAACTATAACGGTGTAAATTGGTTTAAATACAGCTGCAATCAATGAGCACA  
867 CTGCAGAAATAGCAGAATTGAAATCAGAGATTGAAGAACTTAAAGCACTAATTAATCATTGTTAAAAT  
868 AA

869

870

871 Yellow and green color: nucleic acid mutation which occurred didn't cause amino acid  
872 substitution

873 Red color: nucleic acid mutation which occurred caused amino acid substitution.

874

875

876