

Supplementary Table 1: Primers used in this study

Primer name	Sequence (5' – 3')	Function
<i>SmpilA</i> upF	GTAT <u>GTCGAC</u> GCCAATCGCCCCTATGCTGG	Anneals 1,047 to 1,028 bp upstream to the D1585 <i>pilA</i> start codon, <i>Sall</i> site underlined
<i>SmpilA</i> upR-OE	ATGGGATTAGCAGCCAGAGCACAGGATCGG TCTGG	The 20 nucleotides at the 3' end anneal to the seven codons following the D1585 <i>pilA</i> start codon and the first 15 nucleotides in bold overlap with the 5' end of the downstream fragment
<i>SmpilA</i> downF-OE	CCGATCCTGTGCTCTGGCTGCTAATCCCATC TGGA	The first 15 nucleotides in bold overlap with the 3' end of the upstream fragment, the last 20 nucleotides at the 3' end anneal to the last three codons in D1585 <i>pilA</i> and 11 bp following the stop codon
<i>SmpilA</i> downR	CCTC <u>AAGCTT</u> CCCCAACCACTTGTCTGC	Anneals 902 to 921 bp downstream to the D1585 <i>pilA</i> stop codon, <i>HindIII</i> site underlined
280 <i>pilA</i> upR	GCCCA <u>AAGCTT</u> CATGTTACGATCATCTGGG	Anneals 1,046 to 1,027 bp upstream to the 280 <i>pilA</i> start codon on the reverse strand. <i>HindIII</i> site underlined.
280 <i>pilA</i> upF-OE	GGCGTACTTCTTCAGCATTTTGGTACATCCC CAAG	The 20 nucleotides at the 3' end anneal to the 280 <i>pilA</i> start codon and 17 bp upstream, and the first 15 nucleotides in bold overlap with the 5' end of the downstream fragment.
280 <i>pilA</i> downR-OE	GGATGTACCAAAATGCTGAAGAAGTACGCC CCGAC	The first 15 nucleotides in bold overlap with the 3' end of the upstream fragment, and the last 20 nucleotides at the 3' end anneal to seven out of 12 codons upstream of the 280 <i>pilA</i> stop codon
280 <i>pilA</i> downF	GGCAG <u>TGACG</u> GAACTTGATCTCGTCCAGC	Anneals 1,082 to 1,063 bp downstream of the 280 <i>pilA</i> stop codon. <i>Sall</i> site underlined.
<i>PapilA</i> F	GCGT <u>GTCGAC</u> CCAGTTTCCTTGATCGTGCC	Anneals upstream of PA01 <i>pilA</i> gene. <i>Sall</i> site underlined.
<i>PapilA</i> R	GCCGA <u>AAGCTT</u> GAGGAACCAATCACAAACGG	Anneals downstream of PA01 <i>pilA</i> gene. <i>HindIII</i> site underlined.
<i>PapilE</i> F	CCGAGGATCCGATCGAGAAAGAACAGCCCC	Anneals upstream of the PA01 <i>pilE</i> gene. <i>BamHI</i> site underlined.
<i>PapilE</i> R	GCGGA <u>AAGCTT</u> GCGGGAGGAGAACATTACCT	Anneals downstream of the PA01 <i>pilE</i> gene. <i>HindIII</i> site underlined.
<i>SmpilA</i> F	CCA <u>AAGCTT</u> GACCCATCCGTGAAATAGCTGCC	Anneals upstream of D1585 <i>pilA</i> start codon. <i>Sall</i> site underlined.
<i>SmpilA</i> R	CGCC <u>AAGCTT</u> ACGAGCCGACAAAAGAAAGGC	Anneals downstream of D1585 <i>pilA</i> stop codon. <i>HindIII</i> site underlined.
<i>SmpilE</i> F	GTCTG <u>TGAC</u> CAGTAACCCAGTGCGAGGA	Anneals upstream of the D1585 <i>pilE</i> gene. <i>Sall</i> site underlined.
<i>SmpilE</i> R	GCCCA <u>AAGCTT</u> CTAACCGGTGAGCTATTCG	Anneals downstream of the D1585 <i>pilE</i> gene. <i>HindIII</i> site underlined.
280 <i>pilA</i> F	GCAAG <u>TGAC</u> CAGACCGATCCTGTGCTCTG	Anneals upstream of the 280 <i>pilA</i> gene. <i>Sall</i> site underlined.
280 <i>pilA</i> R	GACCA <u>AAGCTT</u> CCCCTAGTTCGCTTCATGGC	Anneals downstream of the 280 <i>pilA</i> gene. <i>HindIII</i> site underlined.

Supplementary Table 2: Characteristics of *P. aeruginosa* PA01 transposon mutants

Mutant ID/ Strain Name	Gene affected	Transposon	Genome Insertion Position	DLP1 lysis	Source
PW8621	<i>pilA</i>	<i>lacZ-hah</i>	5069310	-	[21]
PW8622	<i>pilA</i>	<i>phoA-hah</i>	5069368	-	[21]
PA01_lux_18_G2	<i>pilB</i>	<i>mini-Tn5-luxCDABE</i>	5069913	-	[20]
PA01_lux_50_H10	<i>pilB</i>	<i>mini-Tn5-luxCDABE</i>	5071244	-	[20]
PA01_lux_67_D1	<i>pilB</i>	<i>mini-Tn5-luxCDABE</i>	5070860	-	[20]
PA01_lux_97_B10	<i>pilB</i>	<i>mini-Tn5-luxCDABE</i>	5070077	-	[20]
PA01_lux_38_F5	<i>pilE</i>	<i>mini-Tn5-luxCDABE</i>	5104853	-	[20]
PA01_lux_41_C7	<i>pilE</i>	<i>mini-Tn5-luxCDABE</i>	5104839	-	[20]
PA01_lux_50_D5	<i>pilE</i>	<i>mini-Tn5-luxCDABE</i>	5104869	-	[20]
PW7438	<i>pilF</i>	<i>phoA-hah</i>	4264656	-	[21]
PA01_lux_44_E9	<i>pilJ</i>	<i>mini-Tn5-luxCDABE</i>	452821	-	[20]
PW9471	<i>pilN</i>	<i>phoA-hah</i>	5679378	-	[21]
PW9465	<i>pilQ</i>	<i>phoA-hah</i>	5676840	-	[21]
PW9466	<i>pilQ</i>	<i>phoA-hah</i>	5676900	-	[21]
PA01_lux_80_E5	<i>pilR</i>	<i>mini-Tn5-luxCDABE</i>	5096068	-	[20]
PA01_lux_18_G4	<i>pilS</i>	<i>mini-Tn5-luxCDABE</i>	5094527	-	[20]
PA01_lux_42_D11	<i>pilS</i>	<i>mini-Tn5-luxCDABE</i>	5094527	-	[20]
PA01_lux_53_B6	<i>pilS</i>	<i>mini-Tn5-luxCDABE</i>	5094527	-	[20]
PA01_lux_80_C7	<i>pilS</i>	<i>mini-Tn5-luxCDABE</i>	5094527	-	[20]
PA01_lux_32_G12	<i>pilT</i>	<i>mini-Tn5-luxCDABE</i>	436863	-	[20]
PA01_lux_46_D4	<i>pilT</i>	<i>mini-Tn5-luxCDABE</i>	436504	-	[20]
PW1730	<i>pilU</i>	<i>lacZ-hah</i>	438793	+	[21]
PA01_lux_19_D2	<i>pilV</i>	<i>mini-Tn5-luxCDABE</i>	5098940	-	[20]
PA01_lux_73_C10	<i>pilV</i>	<i>mini-Tn5-luxCDABE</i>	5099241	-	[20]
PA01_lux_20_D4	<i>pilYI</i>	<i>mini-Tn5-luxCDABE</i>	5101178	-	[20]
PA01_lux_51_H7	<i>pilYI</i>	<i>mini-Tn5-luxCDABE</i>	5102516	-	[20]
PA01_lux_82_C12	<i>pilYI</i>	<i>mini-Tn5-luxCDABE</i>	5102516	-	[20]
PA01_lux_97_G2	<i>pilYI</i>	<i>mini-Tn5-luxCDABE</i>	5100755	-	[20]
PA01_lux_67_E3	<i>fimV</i>	<i>mini-Tn5-luxCDABE</i>	3496099	+/-	[20]
PA01_lux_20_D1	<i>fimV</i>	<i>mini-Tn5-luxCDABE</i>	3497859	+/-	[20]
PA01_lux_21_F1	<i>fimV</i>	<i>mini-Tn5-luxCDABE</i>	3496114	+/-	[20]
PA01_lux_97_D2	<i>algR</i>	<i>mini-Tn5-luxCDABE</i>	5923165	+/-	[20]
PA01_lux_50_H9	<i>PA2806</i>	<i>mini-Tn5-luxCDABE</i>	3160973	-	[20]

More information on strains is available at <http://pseudomutant.pseudomonas.com> for *mini-Tn5-luxCDABE* mutants and <http://www.gs.washington.edu/labs/manoil/libraryindex.htm> for *lacZ-hah* and *phoA-hah* mutants.

Supplementary Table 3: Comparison of the presence of Phage-tail_3 domain and tail fiber domains of experimentally confirmed pili-receptor phages.

Bacteriophage	Accession	Morphology	Phage-tail_3 domain	Tail fiber domains
<i>Stenotrophomonas</i> phage DLP1	KR537872.1	<i>Siphoviridae</i>	Yes	-
<i>Stenotrophomonas</i> phage DLP2	KR537871.1	<i>Siphoviridae</i>	Yes	-
<i>Stenotrophomonas</i> phage DLP4	MG018224.1	<i>Siphoviridae</i>	Yes	Yes (1x)
<i>Pseudomonas</i> phage D3112	NC_005178	<i>Siphoviridae</i>	Yes	-
<i>Pseudomonas</i> phage MP22	NC_009818	<i>Siphoviridae</i>	Yes	-
<i>Pseudomonas</i> phage B3	NC_006548	<i>Siphoviridae</i>	Yes	-
<i>Pseudomonas</i> phage JBD26	JN811560	<i>Siphoviridae</i>	Yes	-
<i>Pseudomonas</i> phage JBD68	KY707339	<i>Siphoviridae</i>	-	-
<i>Pseudomonas</i> phage MP29	EU272036.1	<i>Siphoviridae</i>	Yes	-
<i>Pseudomonas</i> phage MP42	JQ762257.1	<i>Siphoviridae</i>	Yes	-
<i>Pseudomonas</i> phage JBD69	KU199708.1	<i>Siphoviridae</i>	Yes	-
<i>Pseudomonas</i> phage JBD93	NC_030918.1	<i>Siphoviridae</i>	Yes	-
<i>Pseudomonas</i> phage JBD88a	NC_020200.1	<i>Siphoviridae</i>	-	-
<i>Pseudomonas</i> phage JBD5	NC_020202.1	<i>Siphoviridae</i>	Yes	-
<i>Pseudomonas</i> phage JBD30	NC_020198.1	<i>Siphoviridae</i>	Yes	-
<i>Xylella</i> phage Paz	KF626666	<i>Siphoviridae</i>	-	Yes (1x) ^a
<i>Xylella</i> phage Prado	KF626667	<i>Siphoviridae</i>	-	Yes (1x) ^a
<i>Xylella</i> phage Salvo	KF626668	<i>Siphoviridae</i>	Yes	- ^b
<i>Xylella</i> phage Sano	KF626665	<i>Siphoviridae</i>	Yes	- ^b
<i>Caulobacter</i> phage phiCbK	JX100813	<i>Siphoviridae</i>	Yes	-
<i>Pseudomonas</i> phage phiKMV	AJ505558	<i>Podoviridae</i>	-	Yes (1x) ^c
<i>Pseudomonas</i> phage MPK7	JX501340	<i>Podoviridae</i>	-	Yes (2x)
<i>Pseudomonas</i> phage LUZ19	NC_010326	<i>Podoviridae</i>	-	Yes (3x)
<i>Pseudomonas</i> phage F116	NC_006552	<i>Podoviridae</i>	-	-
<i>Pseudomonas</i> phage Pf-10	NC_027292	<i>Podoviridae</i>	-	Yes (1x)
<i>Pseudomonas</i> phage JBD23	KM389462.1	N/A ^d	Yes	-

a. Three tail fiber genes annotated, but only one tail fiber hit on CD-search; therefore, only counted as 1x tail fiber domains.

b. One tail fiber gene annotated, but no tail fiber hits on CD-search, therefore not counting as tail fiber domains.

c. Two tail fiber proteins annotated, but only one hit on CD-search; therefore, only counting as 1x tail fiber domains.

d. Worked with phage experimentally in a lab (Bondy-Delomy *et al.*, 2016. Prophages mediate defense against phage infection through diverse mechanisms. ISME Journal (10); 2854–2866) and sequenced, but no annotations or TEM images.

Accession	Cov	pid	Seq
1 DLP1	100.0	100.0	M IATV VVA LIGALM P P VVA AA LQPF FSRG PMPV V VVQVPI I QI PPTFRM MGL
2 YP_001293432	100.0	99.54	M IATV VVA LIGALM P P VVA AA LQPF FSRG PMPV V VVQVPI I QI PPTFRM MGL
3 AVI4895	100.0	98.44	M IATV VVA LIGALM P P VVA AA LQPF FSRG PMPV V VVQVPI I QI PPTFRM MGL
4 YP_006299890	100.0	98.54	M IATV VVA LIGALM P P VVA AA LQPF FSRG PMPV V VVQVPI I QI PPTFRM MGL
5 ATR0189	100.0	98.44	M IATV VVA LIGALM P P VVA AA LQPF FSRG PMPV V VVQVPI I QI PPTFRM MGL
6 DLP2	100.0	98.38	M IATV VVA LIGALM P P VVA AA LQPF FSRG PMPV V VVQVPI I QI PPTFRM MGL
7 YP_00904360	100.0	97.98	M IATV VVA LIGALM P P VVA AA LQPF FSRG PMPV V VVQVPI I QI PPTFRM MGL
8 YP_009205621	99.4	69.38	M IATV VVA LIGALM P P VVA AA LQPF FSRG PMPV V VVQVPI I QI PPTFRM MGL
9 YP_006560777	98.3	46.84	M IATV VVA LIGALM P P VVA AA LQPF FSRG PMPV V VVQVPI I QI PPTFRM MGL
10 AHI12068	97.38	29.28	M IATV VVA LIGALM P P VVA AA LQPF FSRG PMPV V VVQVPI I QI PPTFRM MGL
11 AHI1243	96.68	28.78	M IATV VVA LIGALM P P VVA AA LQPF FSRG PMPV V VVQVPI I QI PPTFRM MGL
consensus/100			
consensus/80			
consensus/70			
1 DLP1	100.0	100.0	FSSRIVVGGHRLGICLCLGPPV-VL-----LQAGLV-LV-LGGLIIGIITPPLG
2 YP_001293432	100.0	99.54	FSSRIVVGGHRLGICLCLGPPV-VL-----LQAGLV-LV-LGGLIIGIITPPLG
3 AVI4895	100.0	98.68	FSSRIVVGGHRLGICLCLGPPV-VL-----LQAGLV-LV-LGGLIIGIITPPLG
4 YP_006299890	100.0	98.54	FSSRIVVGGHRLGICLCLGPPV-VL-----LQAGLV-LV-LGGLIIGIITPPLG
5 ATR0189	100.0	98.44	FSSRIVVGGHRLGICLCLGPPV-VL-----LQAGLV-LV-LGGLIIGIITPPLG
6 DLP2	100.0	98.38	FSSRIVVGGHRLGICLCLGPPV-VL-----LQAGLV-LV-LGGLIIGIITPPLG
7 YP_00904360	100.0	97.98	FSSRIVVGGHRLGICLCLGPPV-VL-----LQAGLV-LV-LGGLIIGIITPPLG
8 YP_009205621	99.4	69.38	FSSRIVVGGHRLGICLCLGPPV-VL-----LQAGLV-LV-LGGLIIGIITPPLG
9 YP_006560777	98.3	46.84	FSSRIVVGGHRLGICLCLGPPV-VL-----LQAGLV-LV-LGGLIIGIITPPLG
10 AHI12068	97.38	29.28	FSSRIVVGGHRLGICLCLGPPV-VL-----LQAGLV-LV-LGGLIIGIITPPLG
11 AHI1243	96.68	28.78	FSSRIVVGGHRLGICLCLGPPV-VL-----LQAGLV-LV-LGGLIIGIITPPLG
consensus/100			
consensus/80			
consensus/70			
1 DLP1	100.0	100.0	QRRGGGGLIIFTRGPPRGLVIRGIPVVAIGALALPATOQTPPPRPIIIGIIGLAIITP
2 YP_001293432	100.0	99.54	QRRGGGGLIIFTRGPPRGLVIRGIPVVAIGALALPATOQTPPPRPIIIGIIGLAIITP
3 AVI4895	100.0	98.44	QRRGGGGLIIFTRGPPRGLVIRGIPVVAIGALALPATOQTPPPRPIIIGIIGLAIITP
4 YP_006299890	100.0	98.54	QRRGGGGLIIFTRGPPRGLVIRGIPVVAIGALALPATOQTPPPRPIIIGIIGLAIITP
5 ATR0189	100.0	98.44	QRRGGGGLIIFTRGPPRGLVIRGIPVVAIGALALPATOQTPPPRPIIIGIIGLAIITP
6 DLP2	100.0	98.38	QRRGGGGLIIFTRGPPRGLVIRGIPVVAIGALALPATOQTPPPRPIIIGIIGLAIITP
7 YP_00904360	100.0	97.98	QRRGGGGLIIFTRGPPRGLVIRGIPVVAIGALALPATOQTPPPRPIIIGIIGLAIITP
8 YP_009205621	99.4	69.38	QRRGGGGLIIFTRGPPRGLVIRGIPVVAIGALALPATOQTPPPRPIIIGIIGLAIITP
9 YP_006560777	98.3	46.84	QRRGGGGLIIFTRGPPRGLVIRGIPVVAIGALALPATOQTPPPRPIIIGIIGLAIITP
10 AHI12068	97.38	29.28	QRRGGGGLIIFTRGPPRGLVIRGIPVVAIGALALPATOQTPPPRPIIIGIIGLAIITP
11 AHI1243	96.68	28.78	QRRGGGGLIIFTRGPPRGLVIRGIPVVAIGALALPATOQTPPPRPIIIGIIGLAIITP
consensus/100			
consensus/80			
consensus/70			
1 DLP1	100.0	100.0	HGLVPMIVIANHGGIGGIGIIMPVACALIRGGGLLVVATGIGLLVWVAQVLPAT
2 YP_001293432	100.0	99.54	HGLVPMIVIANHGGIGGIGIIMPVACALIRGGGLLVVATGIGLLVWVAQVLPAT
3 AVI4895	100.0	98.44	HGLVPMIVIANHGGIGGIGIIMPVACALIRGGGLLVVATGIGLLVWVAQVLPAT
4 YP_006299890	100.0	98.54	HGLVPMIVIANHGGIGGIGIIMPVACALIRGGGLLVVATGIGLLVWVAQVLPAT
5 ATR0189	100.0	98.44	HGLVPMIVIANHGGIGGIGIIMPVACALIRGGGLLVVATGIGLLVWVAQVLPAT
6 DLP2	100.0	98.38	HGLVPMIVIANHGGIGGIGIIMPVACALIRGGGLLVVATGIGLLVWVAQVLPAT
7 YP_00904360	100.0	97.98	HGLVPMIVIANHGGIGGIGIIMPVACALIRGGGLLVVATGIGLLVWVAQVLPAT
8 YP_009205621	99.4	69.38	HGLVPMIVIANHGGIGGIGIIMPVACALIRGGGLLVVATGIGLLVWVAQVLPAT
9 YP_006560777	98.3	46.84	HGLVPMIVIANHGGIGGIGIIMPVACALIRGGGLLVVATGIGLLVWVAQVLPAT
10 AHI12068	97.38	29.28	HGLVPMIVIANHGGIGGIGIIMPVACALIRGGGLLVVATGIGLLVWVAQVLPAT
11 AHI1243	96.68	28.78	HGLVPMIVIANHGGIGGIGIIMPVACALIRGGGLLVVATGIGLLVWVAQVLPAT
consensus/100			
consensus/80			
consensus/70			
1 DLP1	100.0	100.0	AIVA LVRG-DITVLLVLRVIV-LRQVQVETTRTRGCVVFRASSTVQVATQAIIPQ-IVIVST
2 YP_001293432	100.0	99.54	AIVA LVRG-DITVLLVLRVIV-LRQVQVETTRTRGCVVFRASSTVQVATQAIIPQ-IVIVST
3 AVI4895	100.0	98.44	AIVA LVRG-DITVLLVLRVIV-LRQVQVETTRTRGCVVFRASSTVQVATQAIIPQ-IVIVST
4 YP_006299890	100.0	98.54	AIVA LVRG-DITVLLVLRVIV-LRQVQVETTRTRGCVVFRASSTVQVATQAIIPQ-IVIVST
5 ATR0189	100.0	98.44	AIVA LVRG-DITVLLVLRVIV-LRQVQVETTRTRGCVVFRASSTVQVATQAIIPQ-IVIVST
6 DLP2	100.0	98.38	AIVA LVRG-DITVLLVLRVIV-LRQVQVETTRTRGCVVFRASSTVQVATQAIIPQ-IVIVST
7 YP_00904360	100.0	97.98	AIVA LVRG-DITVLLVLRVIV-LRQVQVETTRTRGCVVFRASSTVQVATQAIIPQ-IVIVST
8 YP_009205621	99.4	69.38	AIVA LVRG-DITVLLVLRVIV-LRQVQVETTRTRGCVVFRASSTVQVATQAIIPQ-IVIVST
9 YP_006560777	98.3	46.84	AIVA LVRG-DITVLLVLRVIV-LRQVQVETTRTRGCVVFRASSTVQVATQAIIPQ-IVIVST
10 AHI12068	97.38	29.28	AIVA LVRG-DITVLLVLRVIV-LRQVQVETTRTRGCVVFRASSTVQVATQAIIPQ-IVIVST
11 AHI1243	96.68	28.78	AIVA LVRG-DITVLLVLRVIV-LRQVQVETTRTRGCVVFRASSTVQVATQAIIPQ-IVIVST
consensus/100			
consensus/80			
consensus/70			
1 DLP1	100.0	100.0	IVVQVVAIVAVIAVILVPLVCLVVAALPGVIVLQVGIIMNHVIVVIGLISLIL
2 YP_001293432	100.0	99.54	IVVQVVAIVAVIAVILVPLVCLVVAALPGVIVLQVGIIMNHVIVVIGLISLIL
3 AVI4895	100.0	98.44	IVVQVVAIVAVIAVILVPLVCLVVAALPGVIVLQVGIIMNHVIVVIGLISLIL
4 YP_006299890	100.0	98.54	IVVQVVAIVAVIAVILVPLVCLVVAALPGVIVLQVGIIMNHVIVVIGLISLIL
5 ATR0189	100.0	98.44	IVVQVVAIVAVIAVILVPLVCLVVAALPGVIVLQVGIIMNHVIVVIGLISLIL
6 DLP2	100.0	98.38	IVVQVVAIVAVIAVILVPLVCLVVAALPGVIVLQVGIIMNHVIVVIGLISLIL
7 YP_00904360	100.0	97.98	IVVQVVAIVAVIAVILVPLVCLVVAALPGVIVLQVGIIMNHVIVVIGLISLIL
8 YP_009205621	99.4	69.38	IVVQVVAIVAVIAVILVPLVCLVVAALPGVIVLQVGIIMNHVIVVIGLISLIL
9 YP_006560777	98.3	46.84	IVVQVVAIVAVIAVILVPLVCLVVAALPGVIVLQVGIIMNHVIVVIGLISLIL
10 AHI12068	97.38	29.28	IVVQVVAIVAVIAVILVPLVCLVVAALPGVIVLQVGIIMNHVIVVIGLISLIL
11 AHI1243	96.68	28.78	IVVQVVAIVAVIAVILVPLVCLVVAALPGVIVLQVGIIMNHVIVVIGLISLIL
consensus/100			
consensus/80			
consensus/70			
1 DLP1	100.0	100.0	CVDFSSSLTAPPGQPIETPPTLIPPAAGGGDTPAIPGAGLAAVA-PGSLIYVAM
2 YP_001293432	100.0	99.54	CVDFSSSLTAPPGQPIETPPTLIPPAAGGGDTPAIPGAGLAAVA-PGSLIYVAM
3 AVI4895	100.0	98.68	CVDFSSSLTAPPGQPIETPPTLIPPAAGGGDTPAIPGAGLAAVA-PGSLIYVAM
4 YP_006299890	100.0	98.54	CVDFSSSLTAPPGQPIETPPTLIPPAAGGGDTPAIPGAGLAAVA-PGSLIYVAM
5 ATR0189	100.0	98.44	CVDFSSSLTAPPGQPIETPPTLIPPAAGGGDTPAIPGAGLAAVA-PGSLIYVAM
6 DLP2	100.0	98.38	CVDFSSSLTAPPGQPIETPPTLIPPAAGGGDTPAIPGAGLAAVA-PGSLIYVAM
7 YP_00904360	100.0	97.98	CVDFSSSLTAPPGQPIETPPTLIPPAAGGGDTPAIPGAGLAAVA-PGSLIYVAM
8 YP_009205621	99.4	69.38	CVDFSSSLTAPPGQPIETPPTLIPPAAGGGDTPAIPGAGLAAVA-PGSLIYVAM
9 YP_006560777	98.3	46.84	CVDFSSSLTAPPGQPIETPPTLIPPAAGGGDTPAIPGAGLAAVA-PGSLIYVAM
10 AHI12068	97.38	29.28	CVDFSSSLTAPPGQPIETPPTLIPPAAGGGDTPAIPGAGLAAVA-PGSLIYVAM
11 AHI1243	96.68	28.78	CVDFSSSLTAPPGQPIETPPTLIPPAAGGGDTPAIPGAGLAAVA-PGSLIYVAM
consensus/100			
consensus/80			
consensus/70			
1 DLP1	100.0	100.0	VAP--PFGPILLEAP--GGVLLAIAVAIVRERDGLVQVVAITGQTTLEAAG--GALL
2 YP_001293432	100.0	99.54	VAP--PFGPILLEAP--GGVLLAIAVAIVRERDGLVQVVAITGQTTLEAAG--GALL
3 AVI4895	100.0	98.68	VAP--PFGPILLEAP--GGVLLAIAVAIVRERDGLVQVVAITGQTTLEAAG--GALL
4 YP_006299890	100.0	98.54	VAP--PFGPILLEAP--GGVLLAIAVAIVRERDGLVQVVAITGQTTLEAAG--GALL
5 ATR0189	100.0	98.44	VAP--PFGPILLEAP--GGVLLAIAVAIVRERDGLVQVVAITGQTTLEAAG--GALL
6 DLP2	100.0	98.38	VAP--PFGPILLEAP--GGVLLAIAVAIVRERDGLVQVVAITGQTTLEAAG--GALL
7 YP_00904360	100.0	97.98	VAP--PFGPILLEAP--GGVLLAIAVAIVRERDGLVQVVAITGQTTLEAAG--GALL
8 YP_009205621	99.4	69.38	VAP--PFGPILLEAP--GGVLLAIAVAIVRERDGLVQVVAITGQTTLEAAG--GALL
9 YP_006560777	98.3	46.84	VAP--PFGPILLEAP--GGVLLAIAVAIVRERDGLVQVVAITGQTTLEAAG--GALL
10 AHI12068	97.38	29.28	VAP--PFGPILLEAP--GGVLLAIAVAIVRERDGLVQVVAITGQTTLEAAG--GALL
11 AHI1243	96.68	28.78	VAP--PFGPILLEAP--GGVLLAIAVAIVRERDGLVQVVAITGQTTLEAAG--GALL
consensus/100			
consensus/80			
consensus/70			
1 DLP1	100.0	100.0	HRLVWVWVGGGIPFVIVVQVLPAAHVVVIGRGLVVAIVVIGLIVVIGLIVVIGLIVV
2 YP_001293432	100.0	99.54	HRLVWVWVGGGIPFVIVVQVLPAAHVVVIGRGLVVAIVVIGLIVVIGLIVVIGLIVV
3 AVI4895	100.0	98.68	HRLVWVWVGGGIPFVIVVQVLPAAHVVVIGRGLVVAIVVIGLIVVIGLIVVIGLIVV
4 YP_006299890	100.0	98.54	HRLVWVWVGGGIPFVIVVQVLPAAHVVVIGRGLVVAIVVIGLIVVIGLIVVIGLIVV
5 ATR0189	100.0	98.44	HRLVWVWVGGGIPFVIVVQVLPAAHVVVIGRGLVVAIVVIGLIVVIGLIVVIGLIVV
6 DLP2	100.0	98.38	HRLVWVWVGGGIPFVIVVQVLPAAHVVVIGRGLVVAIVVIGLIVVIGLIVVIGLIVV
7 YP_00904360	100.0	97.98	HRLVWVWVGGGIPFVIVVQVLPAAHVVVIGRGLVVAIVVIGLIVVIGLIVVIGLIVV
8 YP_009205621	99.4	69.38	HRLVWVWVGGGIPFVIVVQVLPAAHVVVIGRGLVVAIVVIGLIVVIGLIVVIGLIVV
9 YP_006560777	98.3	46.84	HRLVWVWVGGGIPFVIVVQVLPAAHVVVIGRGLVVAIVVIGLIVVIGLIVVIGLIVV
10 AHI12068	97.38	29.28	HRLVWVWVGGGIPFVIVVQVLPAAHVVVIGRGLVVAIVVIGLIVVIGLIVVIGLIVV
11 AHI1243	96.68	28.78	HRLVWVWVGGGIPFVIVVQVLPAAHVVVIGRGLVVAIVVIGLIVVIGLIVVIGLIVV
consensus/100			
consensus/80			
consensus/70			
1 DLP1	100.0	100.0	PFPG LTRAGLPLPPL LAG RFP P VVA IAVARRRRAA L L VVDATRRRAGTRVWVGGGTT
2 YP_001293432	100.0	99.54	PFPG LTRAGLPLPPL LAG RFP P VVA IAVARRRRAA L L VVDATRRRAGTRVWVGGGTT
3 AVI4895	100.0	98.68	PFPG LTRAGLPLPPL LAG RFP P VVA IAVARRRRAA L L VVDATRRRAGTRVWVGGGTT
4 YP_006299890	100.0	98.54	PFPG LTRAGLPLPPL LAG RFP P VVA IAVARRRRAA L L VVDATRRRAGTRVWVGGGTT
5 ATR0189	100.0	98.44	PFPG LTRAGLPLPPL LAG RFP P VVA IAVARRRRAA L L VVDATRRRAGTRVWVGGGTT
6 DLP2	100.0	98.38	PFPG LTRAGLPLPPL LAG RFP P VVA IAVARRRRAA L L VVDATRRRAGTRVWVGGGTT
7 YP_00904360	100.0	97.98	PFPG LTRAGLPLPPL LAG RFP P VVA IAVARRRRAA L L VVDATRRRAGTRVWVGGGTT
8 YP_009205621	99.4	69.38	PFPG LTRAGLPLPPL LAG RFP P VVA IAVARRRRAA L L VVDATRRRAGTRVWVGGGTT
9 YP_006560777	98.3	46.84	PFPG LTRAGLPLPPL LAG RFP P VVA IAVARRRRAA L L VVDATRRRAGTRVWVGGGTT
10 AHI12068	97.38	29.28	PFPG LTRAGLPLPPL LAG RFP P VVA IAVARRRRAA L L VVDATRRRAGTRVWVGGGTT
11 AHI1243	96.68	28.78	PFPG LTRAGLPLPPL LAG RFP P VVA IAVARRRRAA L L VVDATRRRAGTRVWVGGGTT
consensus/100			
consensus/80			
consensus/70			
1 DLP1	100.0	100.0	VVAGSGLVIVG--GLVIVV--IISRR--TTRRGLMILAPPP--
2 YP_001293432	100.0	99.54	VVAGSGLVIVG--GLVIVV--IISRR--TTRRGLMILAPPP--
3 AVI4895	100.0	98.68	VVAGSGLVIVG--GLVIVV--IISRR--TTRRGLMILAPPP--
4 YP_006299890	100.0	98.54	VVAGSGLVIVG--GLVIVV--IISRR--TTRRGLMILAPPP--
5 ATR0189	100.0	98.44	VVAGSGLVIVG--GLVIVV--IISRR--TTRRGLMILAPPP--
6 DLP2	100.0	98.38	VVAGSGLVIVG--GLVIVV--IISRR--TTRRGLMILAPPP--
7 YP_00904360	100.0	97.98	VVAGSGLVIVG--GLVIVV--IISRR--TTRRGLMILAPPP--
8 YP_009205621	99.4	69.38	VVAGSGLVIVG--GLVIVV--IISRR--TTRRGLMILAPPP--
9 YP_006560777	98.3	46.84	VVAGSGLVIVG--GLVIVV--IISRR--TTRRGLMILAPPP--
10 AHI12068	97.38	29.28	VVAGSGLVIVG--GLVIVV--IISRR--TTRRGLMILAPPP--
11 AHI1243	96.68	28.78	VVAGSGLVIVG--GLVIVV--IISRR--TTRRGLMILAPPP--
consensus/100			
consensus/80			
consensus/70			

Supplementary Figure 1. An amino acid alignment of the DLP1 and DLP2 baseplate or central tail hub proteins with their ten nearest neighbours. Black lettered amino acids are identical; lighter shaded amino acids have less homology. Consensus cutoff levels and amino

acids are shown below the grouping. The alignment was performed using EMBL-EBI Multiple Sequence Alignment Tool and visually presented using M-view