Supplementary Table 4. Conserved genes in the pilus-dependent phages

Conserved Gene #		Protein Similarity	Pairwise % identity in Cluster	Number of Sequence Clusters*	Minimum %ID Between Clusters**
CG1	YP_001469130.1	cl-like repressor		4	54
CG2	YP_001469131.1	Ner-like repressor		2	67
CG3	YP_001469132.1		> 90		
CG4	YP_001469134.1	Transposase A	> 95		
CG5	YP_001469135.1	Transposase B	> 90		
CG6	YP_001469136.1		> 85		
CG7	YP_001469137.1		> 85		
CG8	YP_001469138.1		> 95		
CG9	YP_001469139.1		> 90		
CG10	YP_001469140.1	Similar to Mu Gam	> 90		
CG11	YP_001469142.1		> 90		
CG12	YP_001469143.1		> 90		
CG13	YP_001469145.1		> 95		
CG14	YP_001469146.1	Mor transcription activator	> 95		
CG15	YP_001469147.1		> 90		
CG16	YP_001469148.1	holin	> 95		
CG17	YP_001469149.1	peptidoglycan degrading	> 90		
CG18	YP_001469151.1	RZ-like lysis	> 85		
CG19	YP_001469152.1		> 95		
CG20	YP_001469153.1	Small Terminase Subunit	> 90		
CG21	YP_001469154.1	Large Terminase Subunit		2	36
CG22	YP_001469155.1	Portal	> 85		
CG23	YP_001469156.1	Similar to Mu gpF	> 90		
CG24	YP_001469157.1	Similar to Mu gpG	> 85		
CG25	YP_001469161.1	Head Protease	> 85		
CG26	YP_001469162.1	Major Head		2	32
CG27	YP_001469163.1	Packaging Chaperone		3	39
CG28	YP_001469164.1			2	63
CG29	YP_001469165.1	Head-Tail Connector		2	67
CG30	YP_001469166.1	Taill Terminator		2	71
CG31	YP_001469167.1			2	54
CG32	YP_001469168.1	Tail Tube		2	55
CG33	YP_001469169.1	Tail Chaperone		3	47
CG34	YP_001469170.1	Tail Chaperone		3	41
CG35	YP_001469171.1	Tape Measure		3	29
CG36	YP_001469172.1	Tail Protein-42	> 95		
CG37	YP_001469173.1	Tail Protein-43	> 90		
CG38	YP_001469174.1	Tail Protein-LM	> 95		
CG39	YP_001469175.1	Tail Protein-LL	> 90		
CG40	YP_001469176.1	Tail Protein-LI	> 85		
CG41	YP_001469177.1	Tail Protein-M5	> 90		
CG42	YP_001469178.1	Tail Protein-CF	> 95		
CG43	YP_001469179.1		> 90		
CG44	YP_001469180.1		> 85		

* These proteins can be clustered into groups with sequence identity >90%. The number of clusters above this cutoff are noted.

** Minimum percent identity between sequences within each cluster