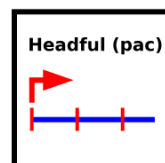
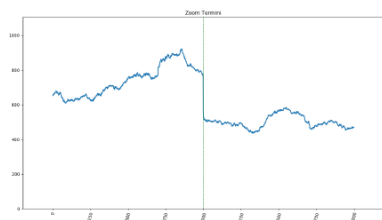


(a)

BF9_new PhageTerm Analysis



PhageTerm Method

Ends	Left (red)	Right (green)	Permuted	Orientation	Class	Type
Redundant	Distributed	28168	Yes	Reverse	Headful (pac)	P1

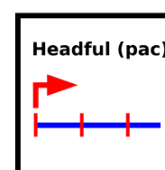
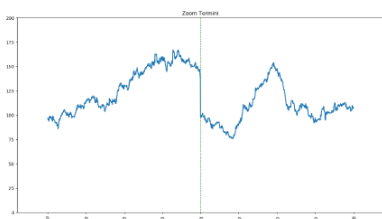
Strand	Location	T	pvalue	T (Start. Pos. Cov. / Whole Cov.)
+	4381	0.04	1.00e+00	strand (+)
	37563	0.03	1.00e+00	
	35182	0.03	1.00e+00	
	15890	0.03	1.00e+00	
	16012	0.03	1.00e+00	
-	28168	0.53	8.06e-65	strand (-)
	38030	0.04	3.27e-02	
	35314	0.03	1.00e+00	
	6351	0.03	1.00e+00	
	13386	0.03	1.00e+00	

Li's Method

Packaging	Termini	Forward	Reverse	Orientation
PAC	Fixed	Multiple-Pref. Term.	Obvious Termini	Reverse

(b)

BF15 PhageTerm Analysis



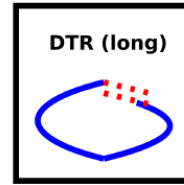
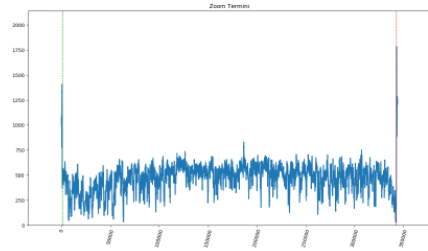
PhageTerm Method

Ends	Left (red)	Right (green)	Permuted	Orientation	Class	Type
Redundant	Distributed	31929	Yes	Reverse	Headful (pac)	P1

Strand	Location	T	pvalue	T (Start. Pos. Cov. / Whole Cov.)
+	89661	0.22	7.05e-03	strand (+)
	106113	0.21	8.35e-04	
	64992	0.18	9.41e-02	
	146351	0.16	1.00e+00	
	155006	0.15	2.13e-01	
-	31929	0.38	2.93e-08	strand (-)
	24329	0.19	1.00e+00	
	9398	0.17	1.00e+00	
	44358	0.17	3.97e-01	
	36015	0.16	1.00e+00	

(c)

BF17 PhageTerm Analysis



PhageTerm Method

Ends	Left (red)	Right (green)	Permuted	Orientation	Class	Type
Redundant	343150	838	No	NA	DTR (long)	T5

*Direct Terminal Repeats: 20590 bp

Strand	Location	T	pvalue	T (Start. Pos. Cov. / Whole Cov.)	
+	343150	0.76	0.00e+00		
	328452	0.04	1.00e+00		
	256072	0.04	1.00e+00		
	178079	0.04	1.00e+00		
	307012	0.04	1.00e+00		
-	838	0.61	3.89e-159		
	95609	0.04	1.00e+00		
	279233	0.04	1.00e+00		
	218577	0.04	5.38e-01		
	104749	0.03	1.00e+00		

Figure S1. PhageTerm analysis of the BF9 (a), BF15 (b), and BF17 (c) sequence read data demonstrating the genome packaging mechanism.