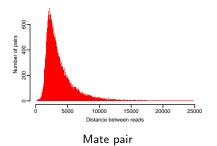
## NextClip report for LIB1468 (Streptomyces coelicolor)

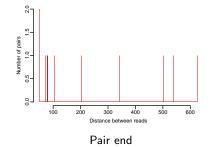
## Overall

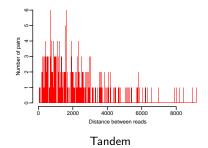
R1			R2	
516923	Num	ber of reads	516923	
251244 (48.60%)	With ju	inction adaptor	230971 (44.68%)	
182299 (35.27%)	of which lo	ong enough ( $\geq$ 25)	164662 (31.85%)	
68945 (13.34%)	and to	o short (< 25)	66309 (12.83%)	
265679 (51.40%)	Without	junction adaptor	285952 (55.32%)	
Category	N	umber of pairs	Too short $(< 25)$	Long enough ( $\geq$ 25)
Caregory		umber of pairs	100 siloit (< 23)	Long chough ( $\leq 23$ )
Adaptor in R1 and		2133 (13.95%)	18997 (3.68%)	53136 (10.28%)
0,	R2 (A) 7	•	, ,	,
Adaptor in R1 and	R2 (A) 7 (B) 1!	2133 (13.95%)	18997 (3.68%)	53136 (10.28%)
Adaptor in R1 and Adaptor in R2 only	R2 (A) 7 (B) 1! (C) 1	2133 (13.95%) 58838 (30.73%)	18997 (3.68%) 55751 (10.79%)	53136 (10.28%) 103087 (19.94%)
Adaptor in R1 and Adaptor in R2 only Adaptor in R1 only	R2 (A) 7 (B) 1! (C) 1 (D) 10	2133 (13.95%) 58838 (30.73%) 79111 (34.65%)	18997 (3.68%) 55751 (10.79%) 59631 (11.54%)	53136 (10.28%) 103087 (19.94%) 119480 (23.11%)
Adaptor in R1 and Adaptor in R2 only Adaptor in R1 only Adaptor in neither	R2 (A) 7 (B) 1! (C) 1: (D) 10	2133 (13.95%) 58838 (30.73%) 79111 (34.65%) 06841 (20.67%)	18997 (3.68%) 55751 (10.79%) 59631 (11.54%) 9505 (1.84%)	53136 (10.28%) 103087 (19.94%) 119480 (23.11%) 97336 (18.83%)

## Fragments with junction adaptor in R1 and R2 (A)

	Total	In range	Out of range	R1 mean	R2 mean
Pairs producing good mappings	41984 (79.01%)	40053 (75.38%)	1931 (3.63%)		
In Mate Pair orientation	40331 (75.90%)	39745 (74.80%)	586 (1.10%)	87.00	85.46
In Pair End orientation	472 (0.89%)	11 (0.02%)	461 (0.87%)	1.99	2.03
In Tandem orientation	1181 (2.22%)	297 (0.56%)	884 (1.66%)	21.24	22.17
Pairs producing bad mappings	11151 (20.99%)				
Both reads unmapped	204 (0.38%)				
One read unmapped	4884 (9.19%)				
Reads map to different ID	0 (0.00%)				
Reads with MAPQ $< 10$	6063 (11.41%)				

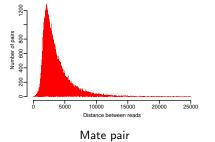


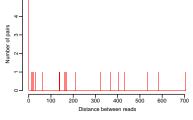


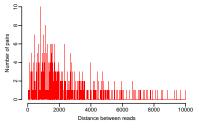


## Fragments with junction adaptor in R2 only (B)

	Total	In range	Out of range	R1 mean	R2 mean
Pairs producing good mappings	78916 (76.55%)	75058 (72.81%)	3858 (3.74%)		
In Mate Pair orientation	75573 (73.31%)	74512 (72.28%)	1061 (1.03%)	148.88	75.56
In Pair End orientation	966 (0.94%)	23 (0.02%)	943 (0.91%)	3.57	2.16
In Tandem orientation	2377 (2.31%)	523 (0.51%)	1854 (1.80%)	33.22	16.60
Pairs producing bad mappings	24170 (23.45%)	, ,	,		
Both reads unmapped	245 (0.24%)				
One read unmapped	11684 (11.33%)				
Reads map to different ID	0 (0.00%)				
Reads with MAPQ $< 10$	12241 (11.87%)				

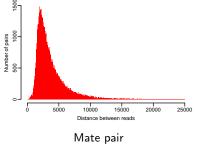


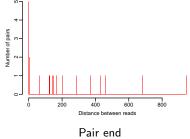


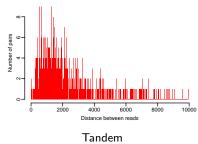


# Fragments with junction adaptor in R1 only (C)

	Total	In range	Out of range	R1 mean	R2 mean	
Pairs producing good mappings	91153 (76.29%)	85991 (71.97%)	5162 (4.32%)			
In Mate Pair orientation	86813 (72.66%)	85362 (71.45%)	1451 (1.21%)	77.35	148.48	
In Pair End orientation	1302 (1.09%)	21 (0.02%)	1281 (1.07%)	1.15	2.39	
In Tandem orientation	3038 (2.54%)	608 (0.51%)	2430 (2.03%)	15.71	30.22	
Pairs producing bad mappings	28326 (23.71%)	, ,	, ,			
Both reads unmapped	671 (0.56%)					
One read unmapped	14490 (12.13%)					
Reads map to different ID	0 (0.00%)					
Reads with MAPQ $< 10$	13165 (11.02%)					
	,					
997 <b>.</b>	72					
#				∞¬		
, 8	4-					
pairs 1000	pairs			pairs 6		

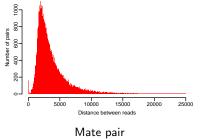


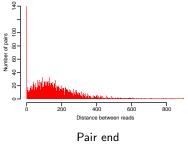


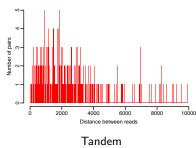


## Fragments where neither read contain the junction adaptor (D)

	Total	In range	Out of range	R1 mean	R2 mean
Pairs producing good mappings	71933 (73.90%)	65685 (67.48%)	6248 (6.42%)		
In Mate Pair orientation	64090 (65.84%)	62488 (64.20%)	1602 (1.65%)	147.16	147.17
In Pair End orientation	4445 (4.57%)	2899 (2.98%)	1546 (1.59%)	97.82	97.87
In Tandem orientation	3398 (3.49%)	298 (0.31%)	3100 (3.18%)	13.24	13.24
Pairs producing bad mappings	25402 (26.10%)				
Both reads unmapped	14203 (14.59%)				
One read unmapped	8324 (8.55%)				
Reads map to different ID	0 (0.00%)				
Reads with MAPQ $< 10$	2875 (2.95%)				
8 <b>-</b>	6 <sup>4</sup>	1		ا [ء	1

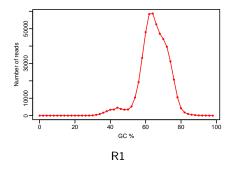


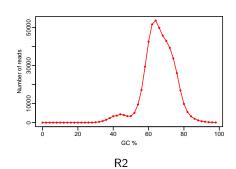




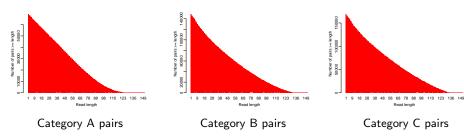
#### **GC** content

Overall GC content 66.04%

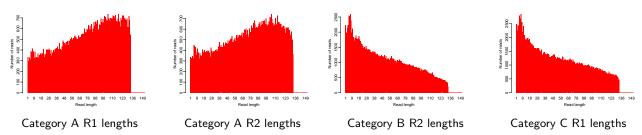




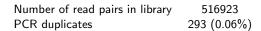
### Shortest pair length

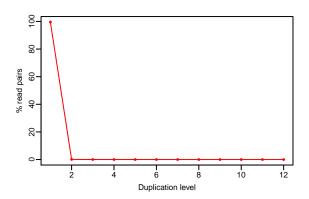


### Clipped read lengths



#### **Duplication**





### **Ambiguous bases**

Number of pairs containing Ns 1802 (0.35%)

#### **External adaptor**

R1			R2
516923	Number of reads		516923
9704 (1.88%)	With junction adaptor and exte	rnal adaptor	8973 (1.74%)
9702 (1.88%)	Without junction adaptor, but with	external adaptor	9760 (1.89%)
Category A pair	s also trimmed for external adaptor	11 (0.00%)	
Category B pair	s also trimmed for external adaptor	132 (0.03%)	
Category C pair	s also trimmed for external adaptor	198 (0.04%)	
Category D pair	s also trimmed for external adaptor	10187 (1.97%)	

#### **Notes**

Minimum contig size for alignment to reference	0
Maximum allowed MP insert	25000
Maximum allowed PE insert	1000
Maximum allowed tandem insert	10000