

NextClip report for LIB1468 (*Streptomyces coelicolor*)

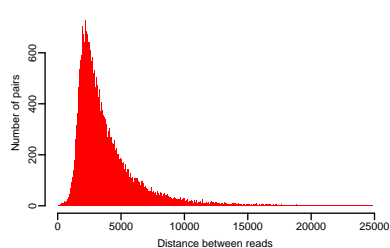
Overall

R1		R2
516923	Number of reads	516923
251263 (48.61%)	With adaptor	231003 (44.69%)
182481 (35.30%)	of which long enough (≥ 25)	164784 (31.88%)
68782 (13.31%)	and too short (< 25)	66219 (12.81%)
265660 (51.39%)	Without adaptor	285920 (55.31%)

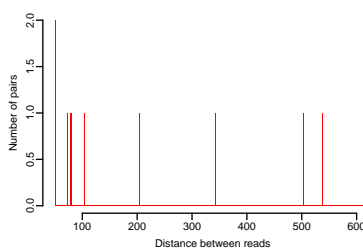
Category	Number of pairs	Too short (< 25)	Long enough (≥ 25)
Adaptor in R1 and R2 (A)	72146 (13.96%)	18997 (3.68%)	53149 (10.28%)
Adaptor in R2 only (B)	158857 (30.73%)	55653 (10.77%)	103204 (19.97%)
Adaptor in R1 only (C)	179117 (34.65%)	59471 (11.50%)	119646 (23.15%)
Adaptor in neither (D)	106803 (20.66%)	0 (0.00%)	106803 (20.66%)
All categories	516923 (100%)	134121 (25.95%)	382802 (74.05%)
Total usable (A,B,C)			275999 (53.39%)

Fragments with junction adaptor in R1 and R2 (A)

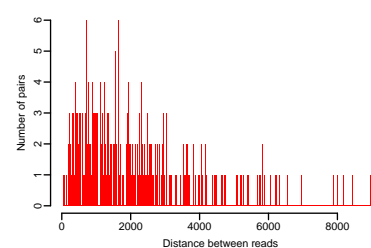
	Total	In range	Out of range	R1 mean	R2 mean
Pairs producing good mappings	41987 (79.00%)	40056 (75.37%)	1931 (3.63%)		
In Mate Pair orientation	40334 (75.89%)	39748 (74.79%)	586 (1.10%)	87.00	85.46
In Pair End orientation	472 (0.89%)	11 (0.02%)	461 (0.87%)	1.99	2.03
In Tandem orientation	1181 (2.22%)	297 (0.56%)	884 (1.66%)	21.24	22.17
Pairs producing bad mappings	11161 (21.00%)				
Both reads unmapped	214 (0.40%)				
One read unmapped	4884 (9.19%)				
Reads map to different ID	0 (0.00%)				
Reads with MAPQ < 10	6063 (11.41%)				



Mate pair



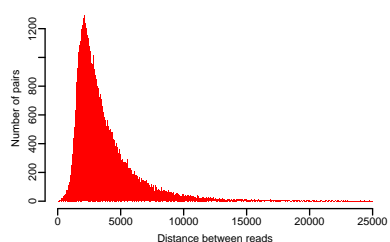
Pair end



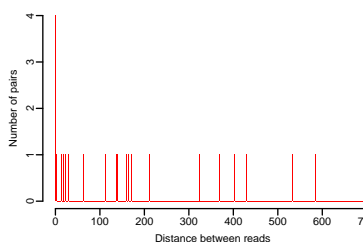
Tandem

Fragments with junction adaptor in R2 only (B)

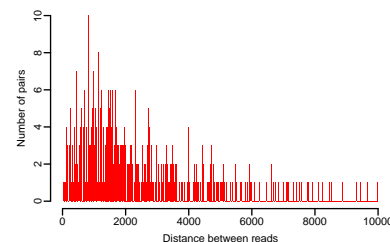
	Total	In range	Out of range	R1 mean	R2 mean
Pairs producing good mappings	78922 (76.47%)	75065 (72.74%)	3857 (3.74%)		
In Mate Pair orientation	75578 (73.23%)	74518 (72.21%)	1060 (1.03%)	148.88	75.56
In Pair End orientation	967 (0.94%)	24 (0.02%)	943 (0.91%)	3.75	2.22
In Tandem orientation	2377 (2.30%)	523 (0.51%)	1854 (1.80%)	33.22	16.60
Pairs producing bad mappings	24281 (23.53%)				
Both reads unmapped	348 (0.34%)				
One read unmapped	11689 (11.33%)				
Reads map to different ID	0 (0.00%)				
Reads with MAPQ < 10	12244 (11.86%)				



Mate pair



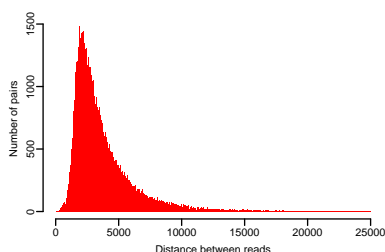
Pair end



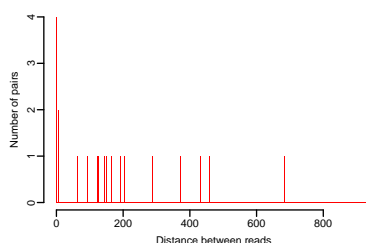
Tandem

Fragments with junction adaptor in R1 only (C)

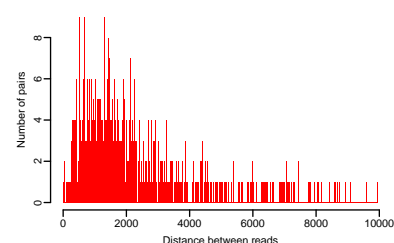
	Total	In range	Out of range	R1 mean	R2 mean
Pairs producing good mappings	91144 (76.18%)	85980 (71.86%)	5164 (4.32%)		
In Mate Pair orientation	86802 (72.55%)	85350 (71.34%)	1452 (1.21%)	77.35	148.47
In Pair End orientation	1304 (1.09%)	22 (0.02%)	1282 (1.07%)	1.20	2.55
In Tandem orientation	3038 (2.54%)	608 (0.51%)	2430 (2.03%)	15.71	30.22
Pairs producing bad mappings	28501 (23.82%)				
Both reads unmapped	834 (0.70%)				
One read unmapped	14499 (12.12%)				
Reads map to different ID	0 (0.00%)				
Reads with MAPQ < 10	13168 (11.01%)				



Mate pair



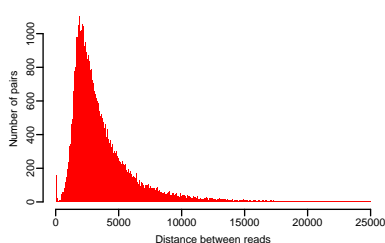
Pair end



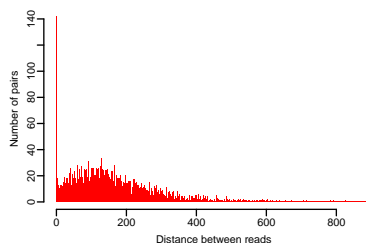
Tandem

Fragments where neither read contain the junction adaptor (D)

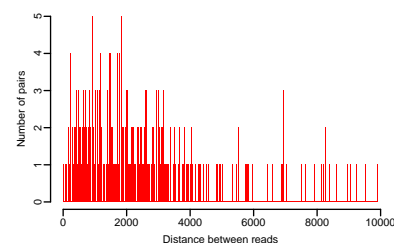
	Total	In range	Out of range	R1 mean	R2 mean
Pairs producing good mappings	71904 (67.32%)	65655 (61.47%)	6249 (5.85%)		
In Mate Pair orientation	64084 (60.00%)	62481 (58.50%)	1603 (1.50%)	147.22	147.22
In Pair End orientation	4422 (4.14%)	2875 (2.69%)	1547 (1.45%)	98.17	98.17
In Tandem orientation	3398 (3.18%)	299 (0.28%)	3099 (2.90%)	13.29	13.29
Pairs producing bad mappings	34898 (32.68%)				
Both reads unmapped	23695 (22.19%)				
One read unmapped	8322 (7.79%)				
Reads map to different ID	0 (0.00%)				
Reads with MAPQ < 10	2881 (2.70%)				



Mate pair



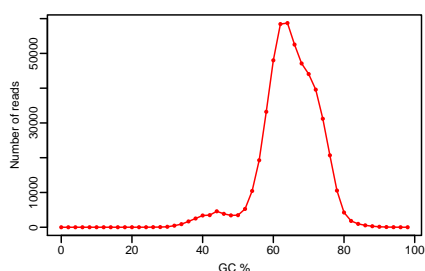
Pair end



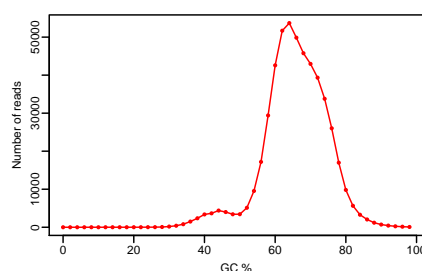
Tandem

GC content

Overall GC content 66.04%

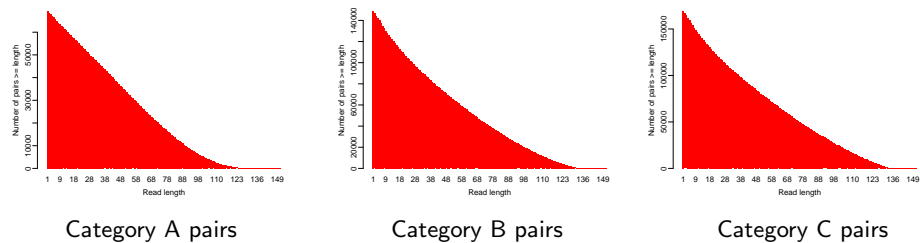


R1

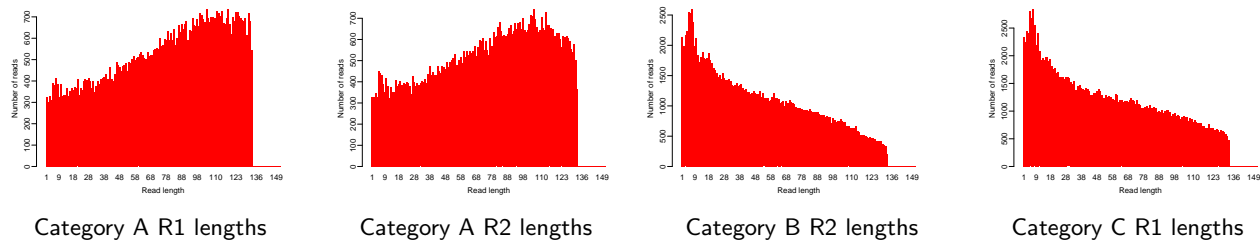


R2

Shortest pair length

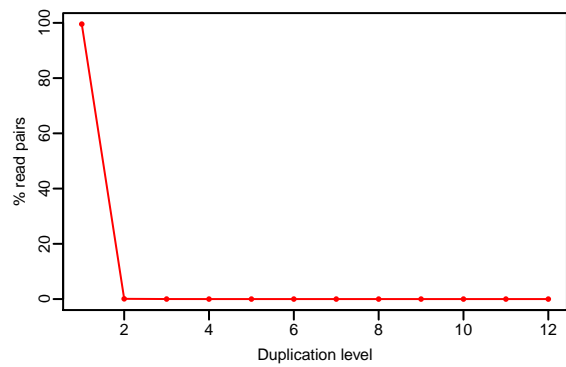


Clipped read lengths



Duplication

Number of read pairs in library 516923
PCR duplicates 293 (0.06%)



Ambiguous bases

Number of pairs containing Ns 1802 (0.35%)

Notes

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