NextClip report for LIB4659 (Arabidopsis thaliana)

Overall

R1		R2
R1		**R2**
19834858	Number of reads	19834858
15249255 (76.88%)	With adaptor	14961736 (75.43%)
12666156 (63.86%)	of which long enough ($\geq$ 25)	12417381 (62.60%)
2583099 (13.02%)	and too short ($<$ 25)	2544355 (12.83%)
4585603 (23.12%)	Without adaptor	4873122 (24.57%)

| Category	Number of pairs	Too short ($<$ 25)	Long enough ($\geq$ 25)
Adaptor in R1 and R2 (A)	11588027 (58.42%)	2856427 (14.40%)	8731600 (44.02%)
Adaptor in R2 only (B)	3373709 (17.01%)	1086389 (5.48%)	2287320 (11.53%)
Adaptor in R1 only (C)	3661228 (18.46%)	1152005 (5.81%)	2509223 (12.65%)
Adaptor in neither (D)	1211894 (6.11%)	0 (0.00%)	1211894 (6.11%)
All categories	19834858 (100%)	5094821 (25.69%)	14740037 (74.31%)
Total usable (A,B,C)			13528143 (68.20%)

Fragments with junction adaptor in R1 and R2 (A)

	Total	In range	Out of range	R1 mean	R2 mean
Pairs producing good mappings	4737301 (54.25%)	4725044 (54.11%)	12257 (0.14%)		
In Mate Pair orientation	4711475 (53.96%)	4709531 (53.94%)	1944 (0.02%)	120.74	121.25
In Pair End orientation	13910 (0.16%)	6174 (0.07%)	7736 (0.09%)	63.21	65.40
In Tandem orientation	11916 (0.14%)	9339 (0.11%)	2577 (0.03%)	90.07	90.64
Pairs producing bad mappings	3994299 (45.75%)				
Both reads unmapped	45732 (0.52%)				
One read unmapped	723789 (8.29%)				
Reads map to different ID	24326 (0.28%)				
Reads with MAPQ $<$ 10	3200452 (36.65%)				
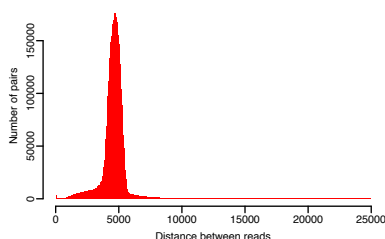
Mate pair
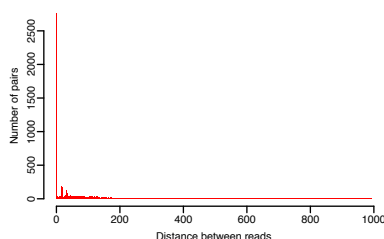
Pair end
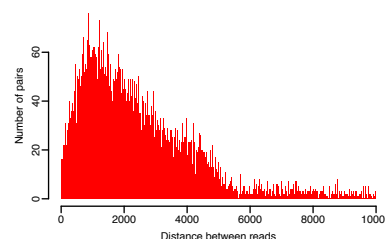
Tandem

Fragments with junction adaptor in R2 only (B)

	Total	In range	Out of range	R1 mean	R2 mean
Pairs producing good mappings	1221192 (53.39%)	1217984 (53.25%)	3208 (0.14%)		
In Mate Pair orientation	1209888 (52.90%)	1209364 (52.87%)	524 (0.02%)	250.89	101.33
In Pair End orientation	8730 (0.38%)	6743 (0.29%)	1987 (0.09%)	193.87	112.43
In Tandem orientation	2574 (0.11%)	1877 (0.08%)	697 (0.03%)	183.03	66.15
Pairs producing bad mappings	1066128 (46.61%)				
Both reads unmapped	18657 (0.82%)				
One read unmapped	235462 (10.29%)				
Reads map to different ID	6545 (0.29%)				
Reads with MAPQ $<$ 10	805464 (35.21%)				
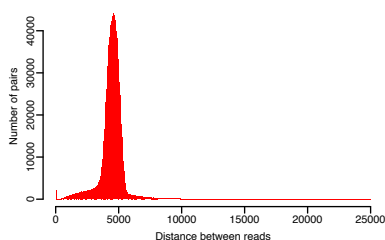
Mate pair
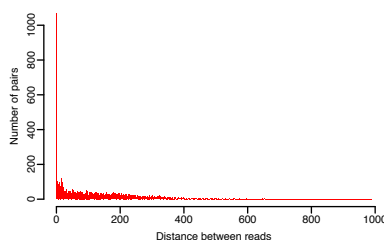
Pair end
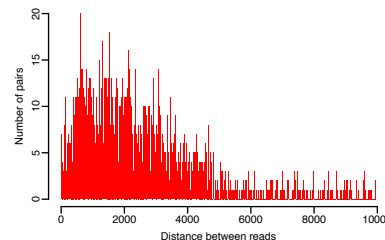
Tandem

Fragments with junction adaptor in R1 only (C)

	Total	In range	Out of range	R1 mean	R2 mean
Pairs producing good mappings	1275373 (50.83%)	1271805 (50.69%)	3568 (0.14%)		
In Mate Pair orientation	1262100 (50.30%)	1261503 (50.27%)	597 (0.02%)	101.14	250.88
In Pair End orientation	10517 (0.42%)	8257 (0.33%)	2260 (0.09%)	115.90	197.06
In Tandem orientation	2756 (0.11%)	2045 (0.08%)	711 (0.03%)	65.13	186.25
Pairs producing bad mappings	1233850 (49.17%)				
Both reads unmapped	31157 (1.24%)				
One read unmapped	297504 (11.86%)				
Reads map to different ID	7429 (0.30%)				
Reads with MAPQ < 10	897760 (35.78%)				
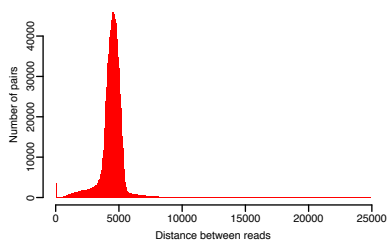
Mate pair
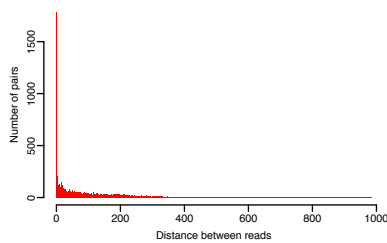
Pair end
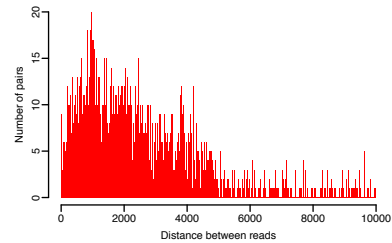
Tandem

Fragments where neither read contain the junction adaptor (D)

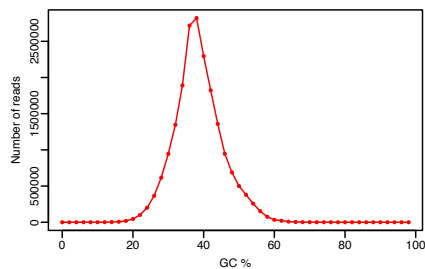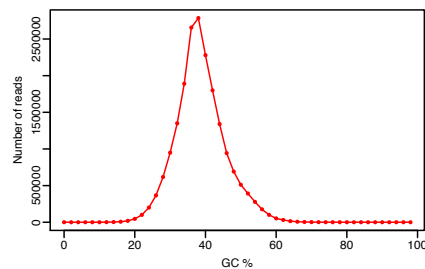|	Total	In range	Out of range	R1 mean	R2 mean
Pairs producing good mappings	177750 (14.67%)	177124 (14.62%)	626 (0.05%)		
In Mate Pair orientation	156436 (12.91%)	156330 (12.90%)	106 (0.01%)	250.83	250.83
In Pair End orientation	21038 (1.74%)	20672 (1.71%)	366 (0.03%)	246.63	246.63
In Tandem orientation	276 (0.02%)	122 (0.01%)	154 (0.01%)	110.95	110.95
Pairs producing bad mappings	1034144 (85.33%)				
Both reads unmapped	783634 (64.66%)				
One read unmapped	91916 (7.58%)				
Reads map to different ID	1503 (0.12%)				
Reads with MAPQ < 10	157091 (12.96%)				
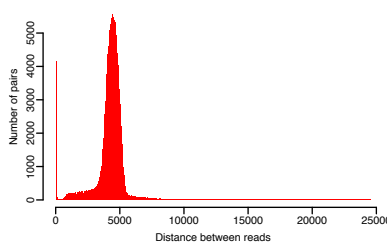
Mate pair
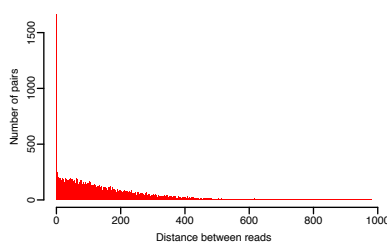
Pair end
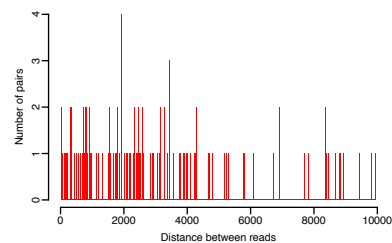
Tandem

GC content

Overall GC content   39.66%

R1

R2

Shortest pair length

Category A pairs

Category B pairs

Category C pairs

Clipped read lengths

Category A R1 lengths

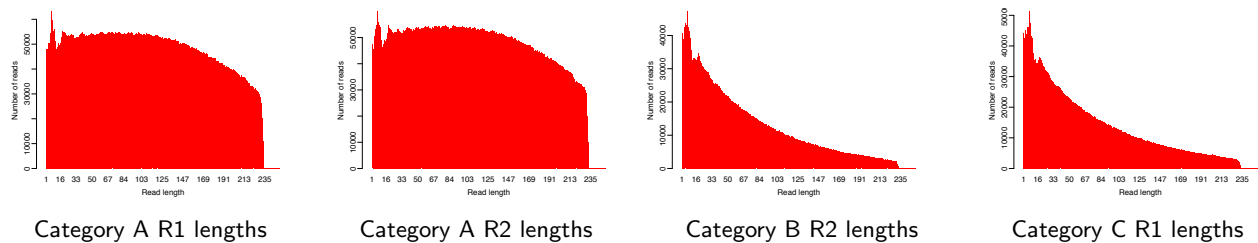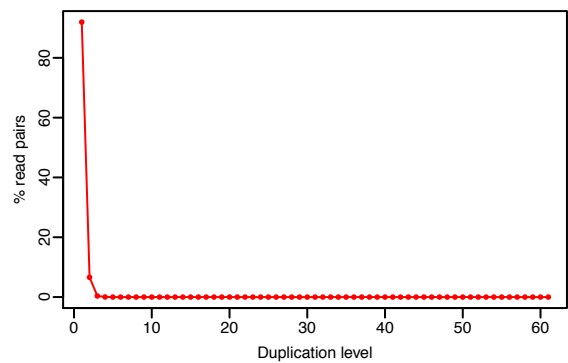Category A R2 lengths

Category B R2 lengths
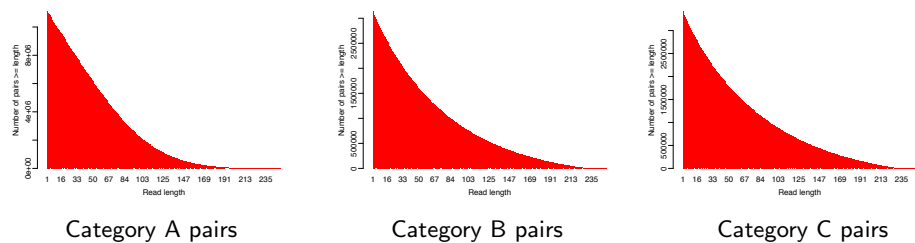
Category C R1 lengths

Duplication

Number of read pairs in library	19834858
PCR duplicates	706502 (3.56%)

Ambiguous bases

Number of pairs containing Ns	210354 (1.06%)

Notes

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