

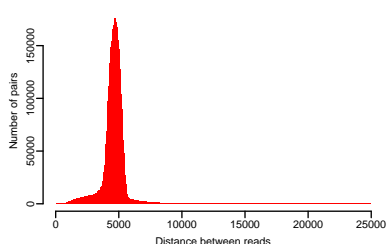
NextClip report for LIB4659 (*Arabidopsis thaliana*)

Overall

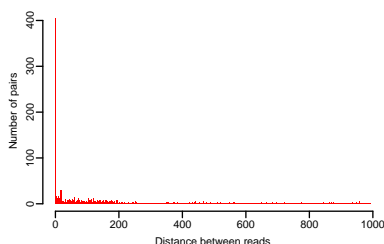
R1		R2	
19834858	Number of reads	19834858	
15226382 (76.77%)	With junction adaptor	14936152 (75.30%)	
12615077 (63.60%)	of which long enough (≥ 25)	12383578 (62.43%)	
2611305 (13.17%)	and too short (< 25)	2552574 (12.87%)	
4608476 (23.23%)	Without junction adaptor	4898706 (24.70%)	
Category	Number of pairs	Too short (< 25)	Long enough (≥ 25)
Adaptor in R1 and R2 (A)	11566407 (58.31%)	2856263 (14.40%)	8710144 (43.91%)
Adaptor in R2 only (B)	3369745 (16.99%)	1102366 (5.56%)	2267379 (11.43%)
Adaptor in R1 only (C)	3659975 (18.45%)	1175783 (5.93%)	2484192 (12.52%)
Adaptor in neither (D)	1238731 (6.25%)	416144 (2.10%)	822587 (4.15%)
All categories	19834858 (100%)	5550556 (27.98%)	14284302 (72.02%)
Total usable (A,B,C)			13461715 (67.87%)

Fragments with junction adaptor in R1 and R2 (A)

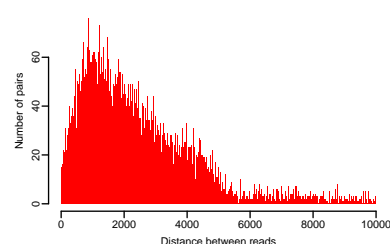
	Total	In range	Out of range	R1 mean	R2 mean
Pairs producing good mappings	4729115 (54.29%)	4716869 (54.15%)	12246 (0.14%)		
In Mate Pair orientation	4707977 (54.05%)	4706035 (54.03%)	1942 (0.02%)	120.71	121.23
In Pair End orientation	9226 (0.11%)	1496 (0.02%)	7730 (0.09%)	19.12	19.64
In Tandem orientation	11912 (0.14%)	9338 (0.11%)	2574 (0.03%)	90.07	90.65
Pairs producing bad mappings	3981029 (45.71%)				
Both reads unmapped	42340 (0.49%)				
One read unmapped	717944 (8.24%)				
Reads map to different ID	24297 (0.28%)				
Reads with MAPQ < 10	3196448 (36.70%)				



Mate pair



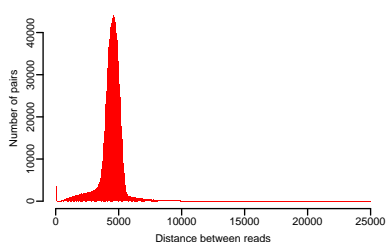
Pair end



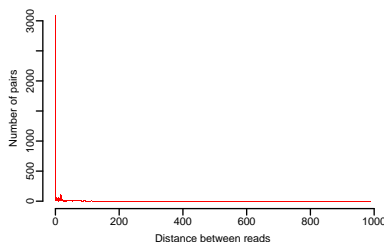
Tandem

Fragments with junction adaptor in R2 only (B)

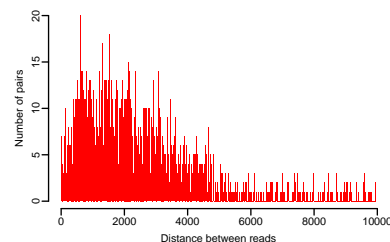
	Total	In range	Out of range	R1 mean	R2 mean
Pairs producing good mappings	1218190 (53.73%)	1214987 (53.59%)	3203 (0.14%)		
In Mate Pair orientation	1209188 (53.33%)	1208665 (53.31%)	523 (0.02%)	250.68	101.29
In Pair End orientation	6430 (0.28%)	4447 (0.20%)	1983 (0.09%)	141.58	105.48
In Tandem orientation	2572 (0.11%)	1875 (0.08%)	697 (0.03%)	182.75	65.99
Pairs producing bad mappings	1049189 (46.27%)				
Both reads unmapped	10518 (0.46%)				
One read unmapped	227859 (10.05%)				
Reads map to different ID	6534 (0.29%)				
Reads with MAPQ < 10	804278 (35.47%)				



Mate pair



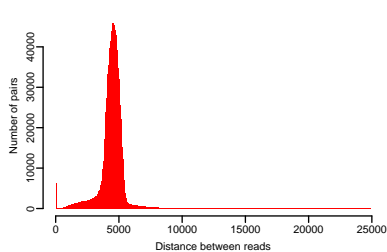
Pair end



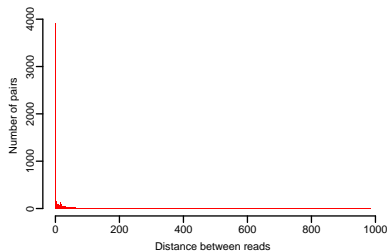
Tandem

Fragments with junction adaptor in R1 only (C)

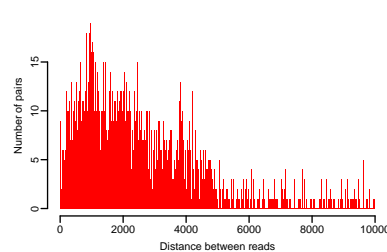
	Total	In range	Out of range	R1 mean	R2 mean
Pairs producing good mappings	1273837 (51.28%)	1270275 (51.13%)	3562 (0.14%)		
In Mate Pair orientation	1262520 (50.82%)	1261923 (50.80%)	597 (0.02%)	101.11	250.57
In Pair End orientation	8578 (0.35%)	6318 (0.25%)	2260 (0.09%)	111.35	153.48
In Tandem orientation	2739 (0.11%)	2034 (0.08%)	705 (0.03%)	65.08	186.31
Pairs producing bad mappings	1210355 (48.72%)				
Both reads unmapped	17631 (0.71%)				
One read unmapped	288490 (11.61%)				
Reads map to different ID	7412 (0.30%)				
Reads with MAPQ < 10	896822 (36.10%)				



Mate pair



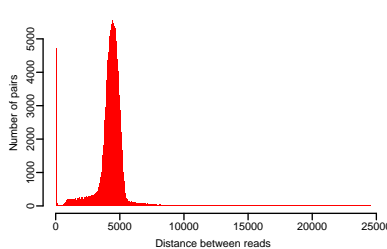
Pair end



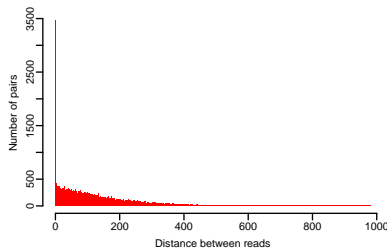
Tandem

Fragments where neither read contain the junction adaptor (D)

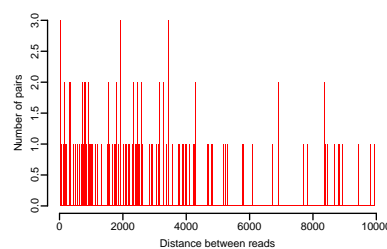
	Total	In range	Out of range	R1 mean	R2 mean
Pairs producing good mappings	190487 (23.16%)	189906 (23.09%)	581 (0.07%)		
In Mate Pair orientation	156411 (19.01%)	156307 (19.00%)	104 (0.01%)	249.85	249.82
In Pair End orientation	33796 (4.11%)	33472 (4.07%)	324 (0.04%)	245.51	245.45
In Tandem orientation	280 (0.03%)	127 (0.02%)	153 (0.02%)	113.85	113.67
Pairs producing bad mappings	632100 (76.84%)				
Both reads unmapped	412144 (50.10%)				
One read unmapped	60306 (7.33%)				
Reads map to different ID	1474 (0.18%)				
Reads with MAPQ < 10	158176 (19.23%)				



Mate pair



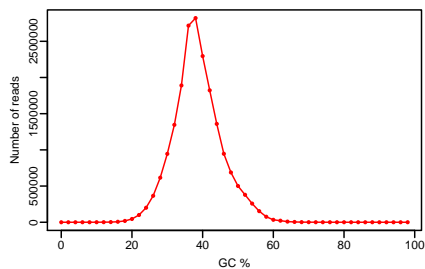
Pair end



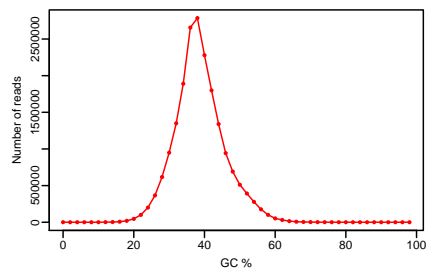
Tandem

GC content

Overall GC content 39.66%

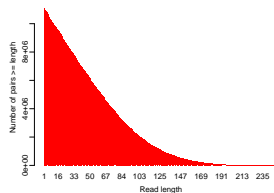


R1

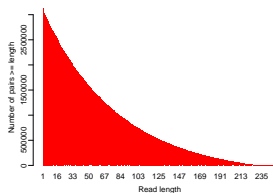


R2

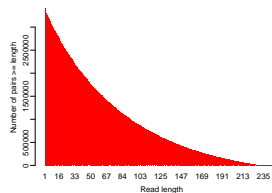
Shortest pair length



Category A pairs

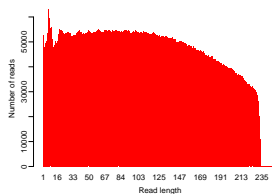


Category B pairs

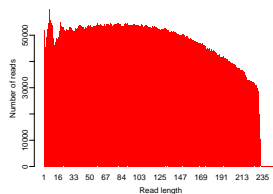


Category C pairs

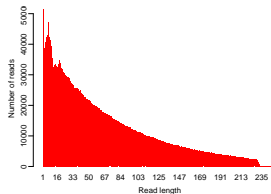
Clipped read lengths



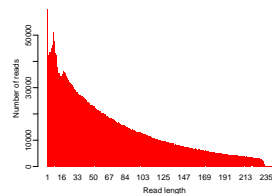
Category A R1 lengths



Category A R2 lengths



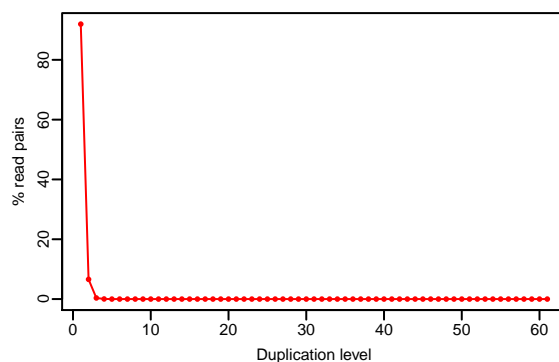
Category B R2 lengths



Category C R1 lengths

Duplication

Number of read pairs in library 19834858
PCR duplicates 206502 (3.56%)



Ambiguous bases

Number of pairs containing Ns 210354 (1.06%)

External adaptor

R1		R2
19834858	Number of reads	19834858
4476854 (22.57%)	With junction adaptor and external adaptor	4444180 (22.41%)
456531 (2.30%)	Without junction adaptor, but with external adaptor	302747 (1.53%)

Category A pairs also trimmed for external adaptor	12981 (0.07%)
Category B pairs also trimmed for external adaptor	32020 (0.16%)
Category C pairs also trimmed for external adaptor	45374 (0.23%)
Category D pairs also trimmed for external adaptor	437082 (2.20%)

Notes

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