: C.Dson_15_02_317Ma1_index12 : 3 : CTTGTA (3_120719_BD158KACXX_1_nophix-sort-dup)

D-f:	110	
Reference organism	hg19	
Total	222,178	101bp paired
Aligned	202,291	(91.0%)
Pairs aligned	199,514	(89.8%)
Pair duplicates	330	(0.2%)
Insert size	182.7	+/- 60.2
On bait bases	17,035,522	(45.9%)
Near bait bases	7,649,870	(20.6%)
Off bait bases	12,423,239	(33.5%)
Mean bait coverage	0.3	
On target bases	17,054,142	(46.0%)
Mean target coverage	0x	
10x coverage targets	0.0%	
Zero coverage targets	75.9%	
Fold enrichment	27x	

Table 1: Summary of lane results

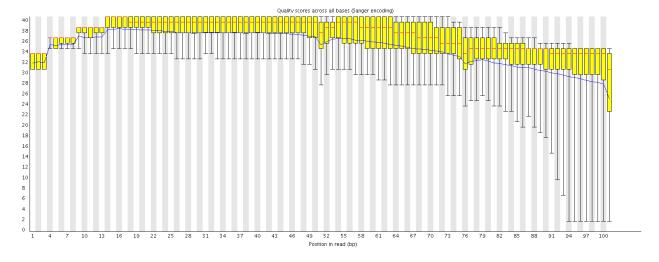


Figure 1:

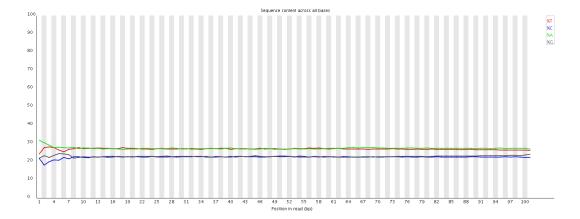


Figure 2:

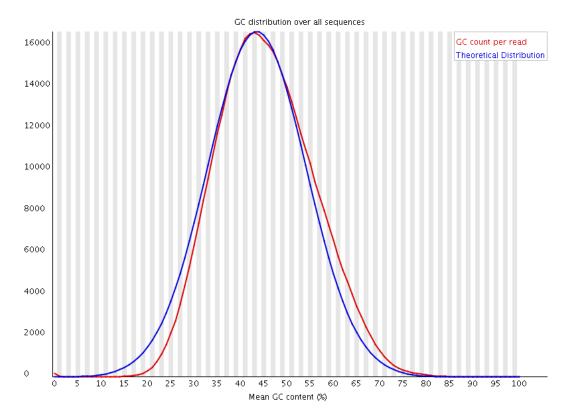


Figure 3:

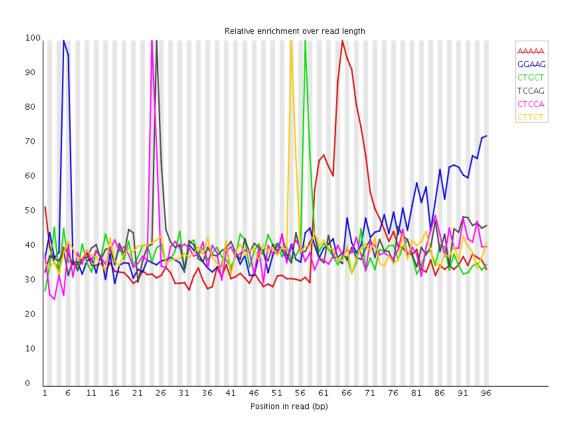


Figure 4:

Insert Size Histogram for All_Reads in file 3_120719_BD158KACXX_1_nophix-sort-dup.bam

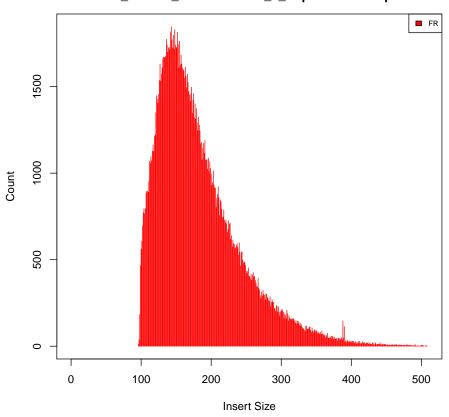


Figure 5: Distribution of paired end insert sizes