## : C.Dson\_15\_02\_317Ma1\_index12 : 5 : CTTGTA (5\_120719\_BD158KACXX\_1\_nophix-sort-dup)

Reference organism	hg19	
Total	80,006	101bp paired
Aligned	68,229	(85.3%)
Pairs aligned	66,936	(83.7%)
Pair duplicates	48	(0.1%)
Insert size	195.1	+/- 60.7
On bait bases	5,516,861	(44.2%)
Near bait bases	2,701,446	(21.6%)
Off bait bases	4,259,735	(34.1%)
Mean bait coverage	0.1	
On target bases	5,523,505	(44.3%)
Mean target coverage	0x	
10x coverage targets	0.0%	
Zero coverage targets	91.8%	
Fold enrichment	26x	

Table 1: Summary of lane results

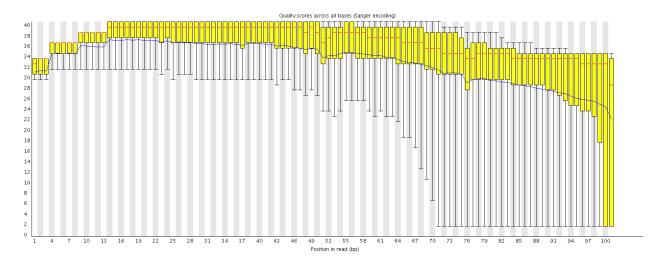


Figure 1:

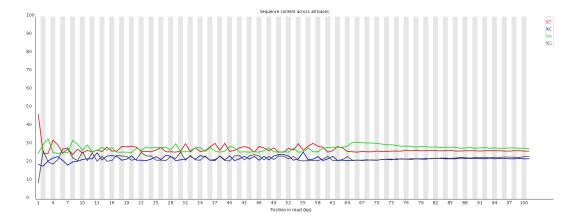


Figure 2:

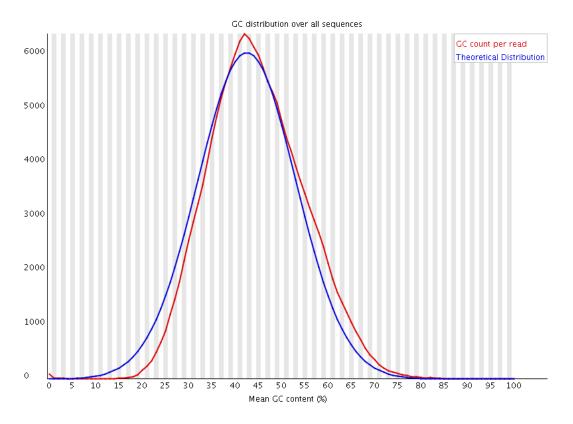


Figure 3:

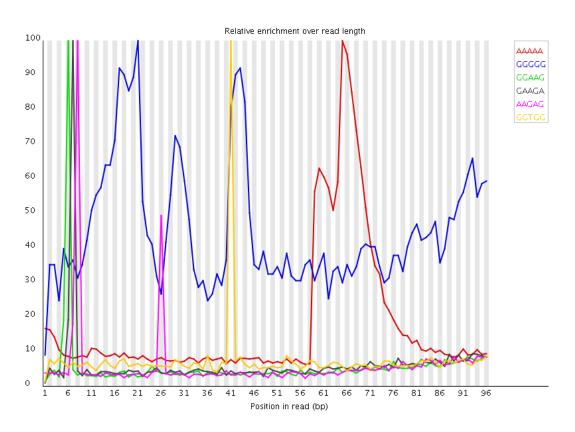


Figure 4:

## Insert Size Histogram for All\_Reads in file 5\_120719\_BD158KACXX\_1\_nophix-sort-dup.bam

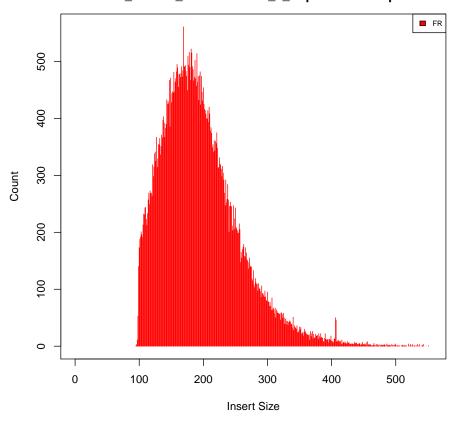


Figure 5: Distribution of paired end insert sizes