## : C.Dson\_15\_02\_317Ma2\_index13 : 4 : AGTCAA (4\_120719\_BD158KACXX\_1\_nophix-sort-dup)

Reference organism	hg19	
Total	229,974	101bp paired
Aligned	207,396	(90.2%)
Pairs aligned	204,321	(88.8%)
Pair duplicates	294	(0.1%)
Insert size	182.7	+/- 58.7
On bait bases	17,152,148	(45.0%)
Near bait bases	7,681,712	(20.2%)
Off bait bases	13,253,386	(34.8%)
Mean bait coverage	0.3	
On target bases	17,169,975	(45.1%)
Mean target coverage	0x	
10x coverage targets	0.0%	
Zero coverage targets	75.6%	
Fold enrichment	27x	

Table 1: Summary of lane results

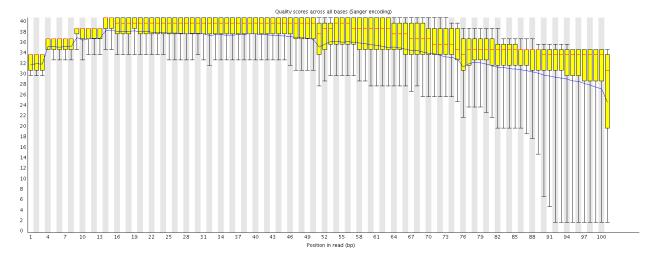


Figure 1:

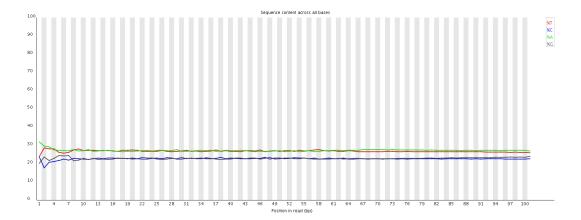


Figure 2:

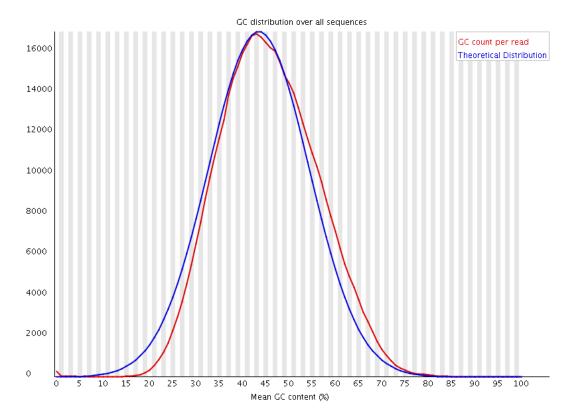


Figure 3:

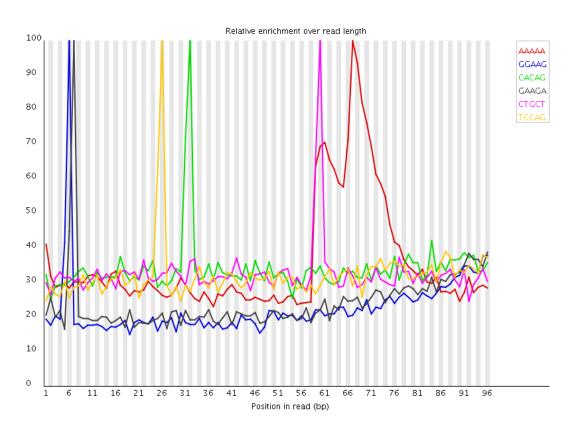


Figure 4:

## Insert Size Histogram for All\_Reads in file 4\_120719\_BD158KACXX\_1\_nophix-sort-dup.bam

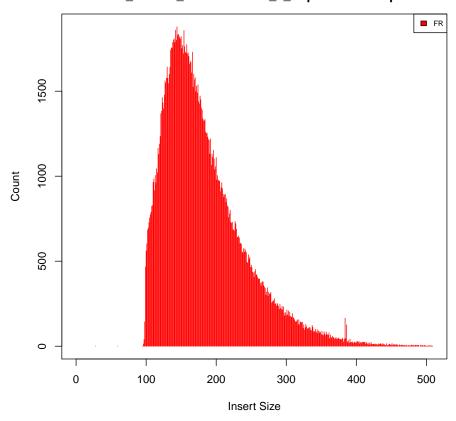


Figure 5: Distribution of paired end insert sizes