## : C.Dson\_15\_02\_317Ma2\_index13 : 5 : GTGGCC (5\_120719\_BD158KACXX\_2\_nophix-sort-dup)

(	-	
Reference organism	hg19	
Total	191,205	101bp paired
Aligned	131,296	(68.7%)
Pairs aligned	124,077	(64.9%)
Pair duplicates	354	(0.3%)
Insert size	169.5	+/- 55.8
On bait bases	10,456,914	(45.3%)
Near bait bases	4,732,133	(20.5%)
Off bait bases	7,889,360	(34.2%)
Mean bait coverage	0.2	
On target bases	10,466,100	(45.4%)
Mean target coverage	0x	
10x coverage targets	0.0%	
Zero coverage targets	83.2%	
Fold enrichment	27x	

Table 1: Summary of lane results

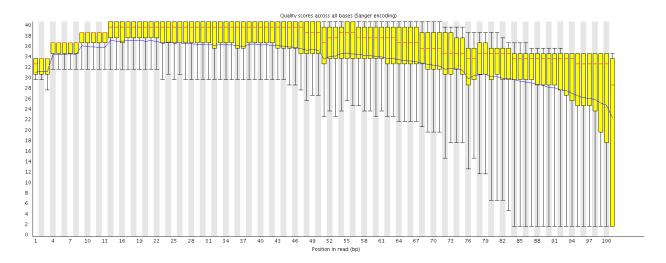


Figure 1:

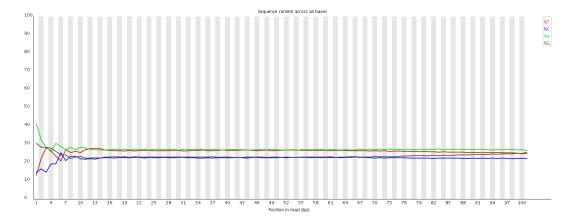


Figure 2:

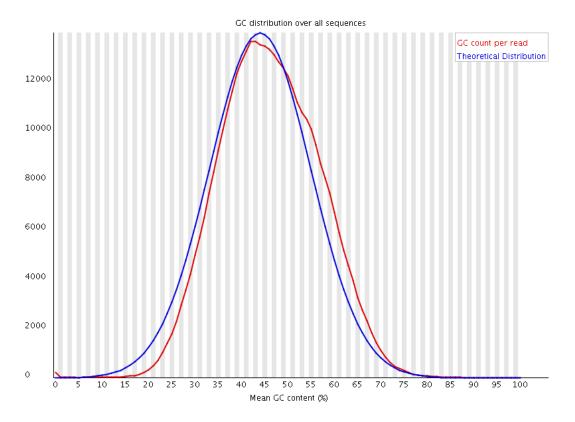


Figure 3:

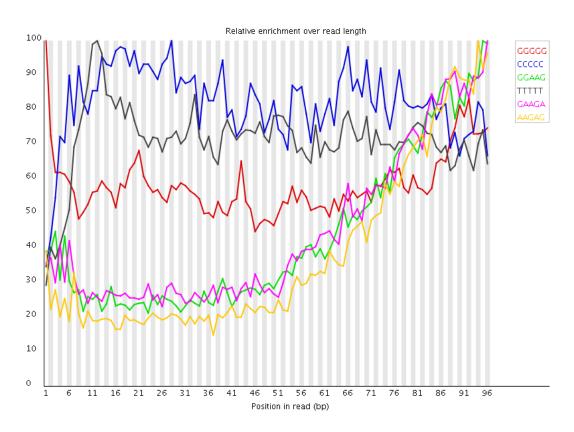


Figure 4:

## Insert Size Histogram for All\_Reads in file 5\_120719\_BD158KACXX\_2\_nophix-sort-dup.bam

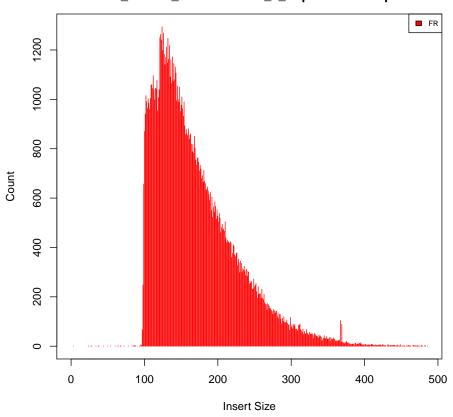


Figure 5: Distribution of paired end insert sizes