: C.Dson_15_02_317Ma1_index12 : 5 : GGCTAC (5_120719_BD158KACXX_2_nophix-sort-dup)

Reference organism	hg19	
Total	113,969	101bp paired
Aligned	67,738	(59.4%)
Pairs aligned	60,100	(52.7%)
Pair duplicates	114	(0.2%)
Insert size	173.1	+/-56.6
On bait bases	5,149,315	(44.5%)
Near bait bases	2,299,339	(19.9%)
Off bait bases	4,110,952	(35.6%)
Mean bait coverage	0.1	
On target bases	5,153,300	(44.6%)
Mean target coverage	0x	
10x coverage targets	0.0%	
Zero coverage targets	92.7%	
Fold enrichment	27x	

Table 1: Summary of lane results

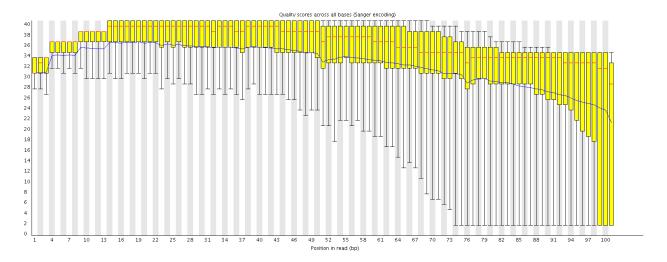


Figure 1:

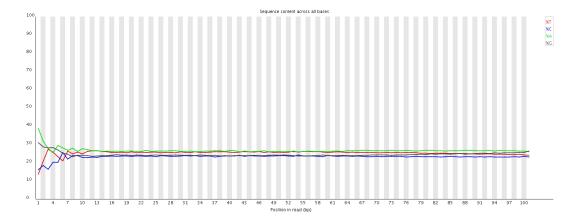


Figure 2:

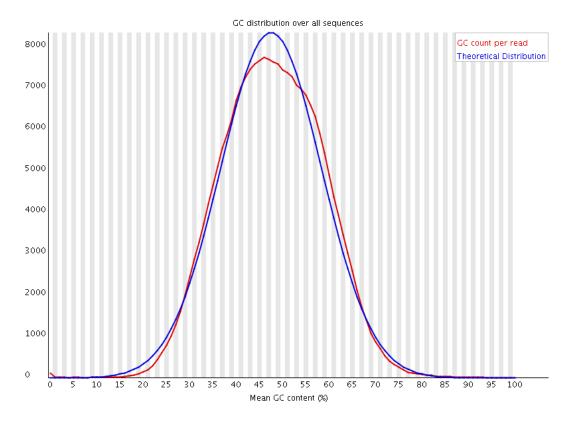


Figure 3:

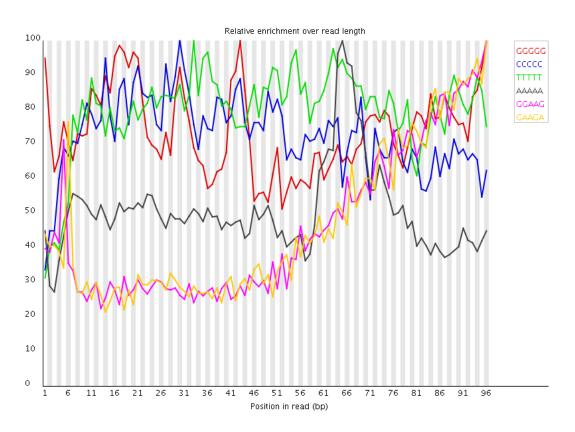


Figure 4:

Insert Size Histogram for All_Reads in file 5_120719_BD158KACXX_2_nophix-sort-dup.bam

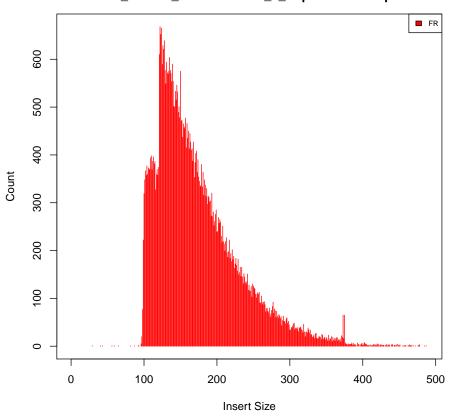


Figure 5: Distribution of paired end insert sizes