

: C.Dson\_15\_02\_317Ma2\_index13 : 2 : AGTCAA (2\_120719\_BD158KACXX\_1\_nophix-sort-dup)

Reference organism	hg19	
Total	238,862	101bp paired
Aligned	215,891	(90.4%)
Pairs aligned	212,736	(89.1%)
Pair duplicates	325	(0.2%)
Insert size	182.5	+/- 58.5
On bait bases	17,862,556	(45.1%)
Near bait bases	8,032,040	(20.3%)
Off bait bases	13,754,850	(34.7%)
Mean bait coverage	0.3	
On target bases	17,883,810	(45.1%)
Mean target coverage	0x	
10x coverage targets	0.0%	
Zero coverage targets	74.7%	
Fold enrichment	27x	

Table 1: Summary of lane results

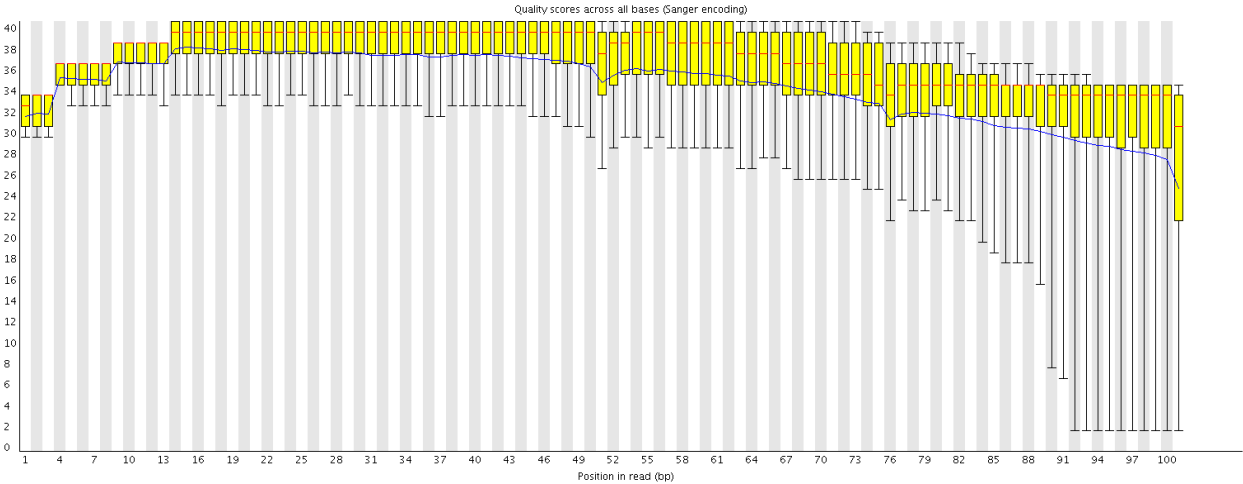


Figure 1:

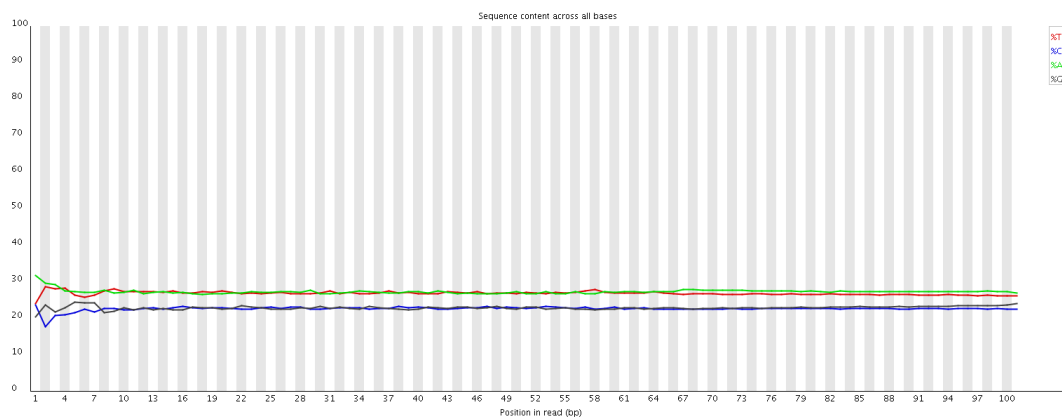


Figure 2:

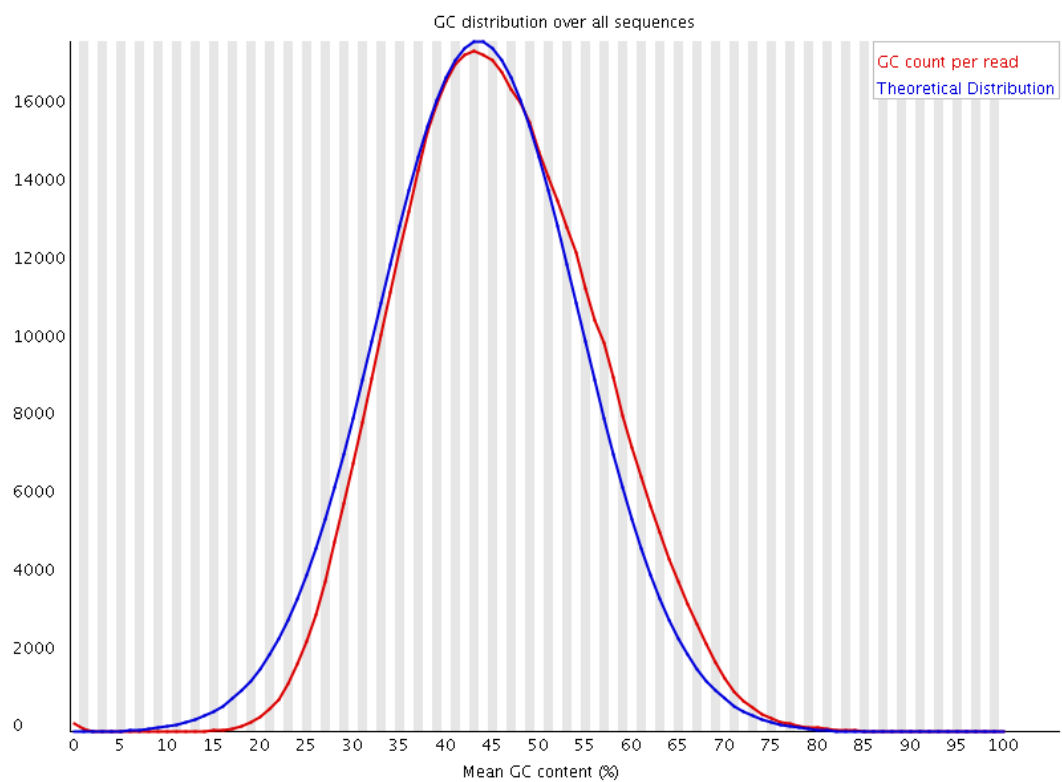


Figure 3:

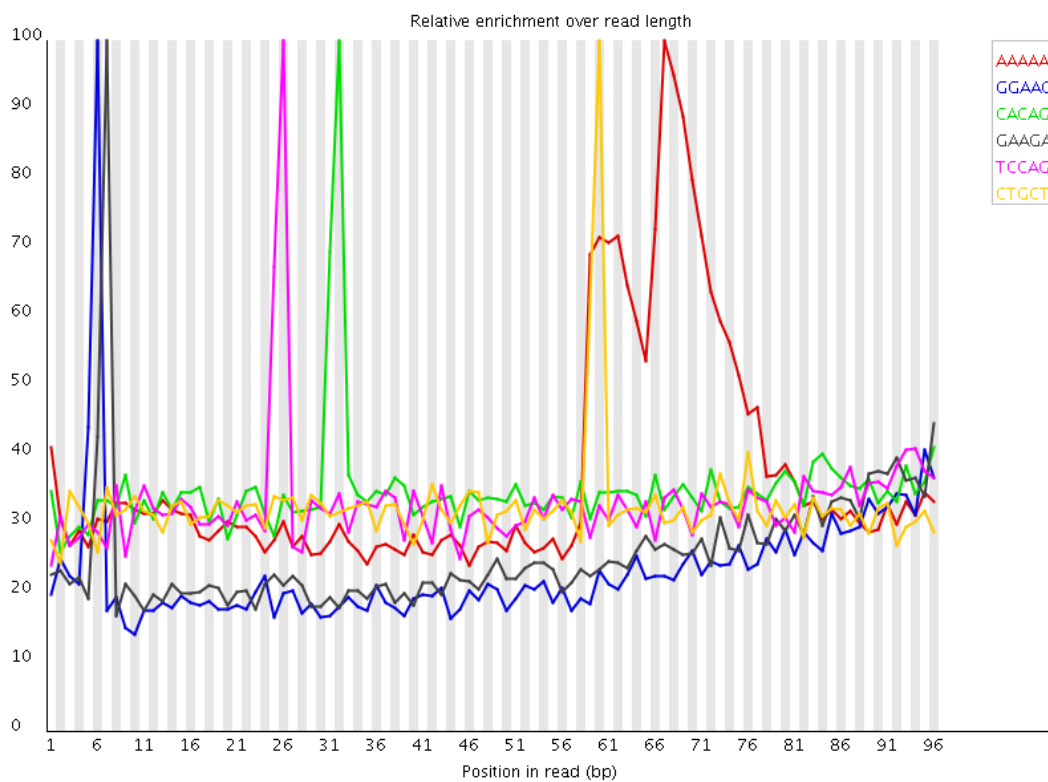


Figure 4:

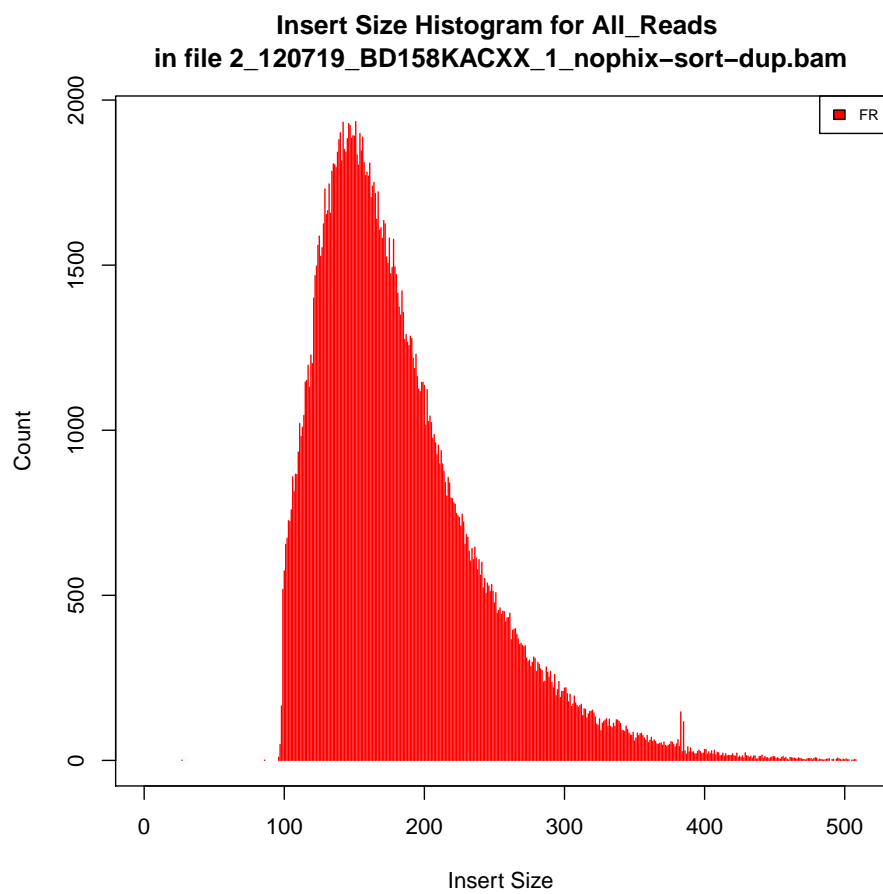


Figure 5: Distribution of paired end insert sizes