

: C.Dson\_15\_02\_317Ma1\_index12 : 2 : CTTGTA (2\_120719\_BD158KACXX\_1\_nophix-sort-dup)

Reference organism	hg19	
Total	233,287	101bp paired
Aligned	212,507	(91.1%)
Pairs aligned	209,408	(89.8%)
Pair duplicates	306	(0.1%)
Insert size	182.9	+/- 60.5
On bait bases	17,823,907	(45.7%)
Near bait bases	8,010,333	(20.5%)
Off bait bases	13,181,542	(33.8%)
Mean bait coverage	0.3	
On target bases	17,843,534	(45.7%)
Mean target coverage	0x	
10x coverage targets	0.0%	
Zero coverage targets	75.1%	
Fold enrichment	27x	

Table 1: Summary of lane results

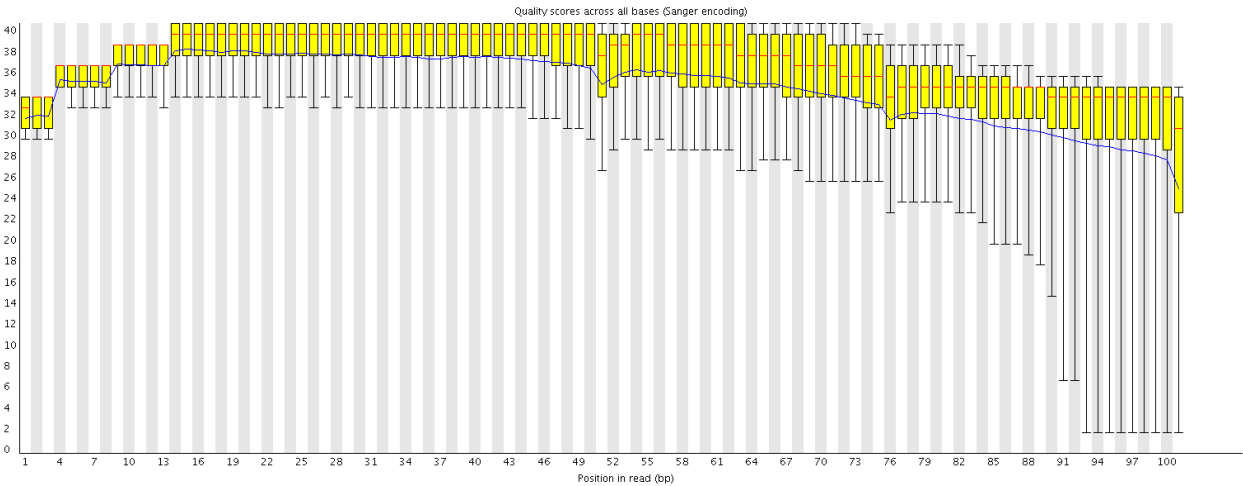


Figure 1:

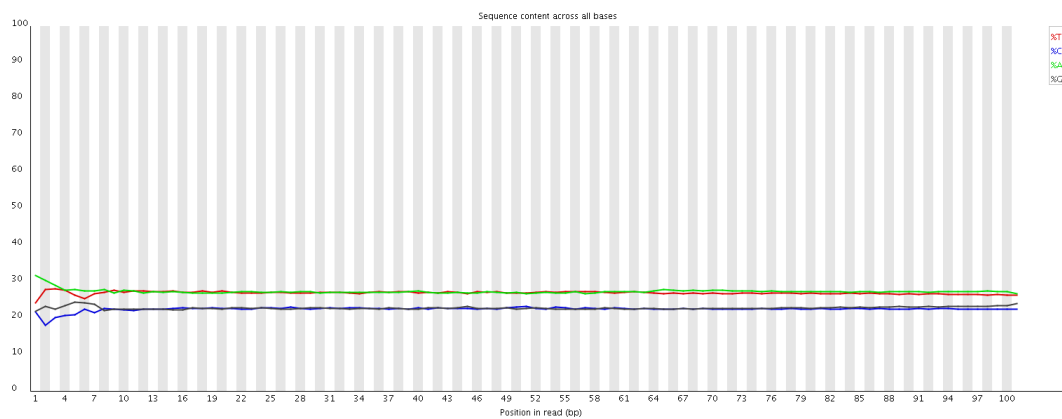


Figure 2:

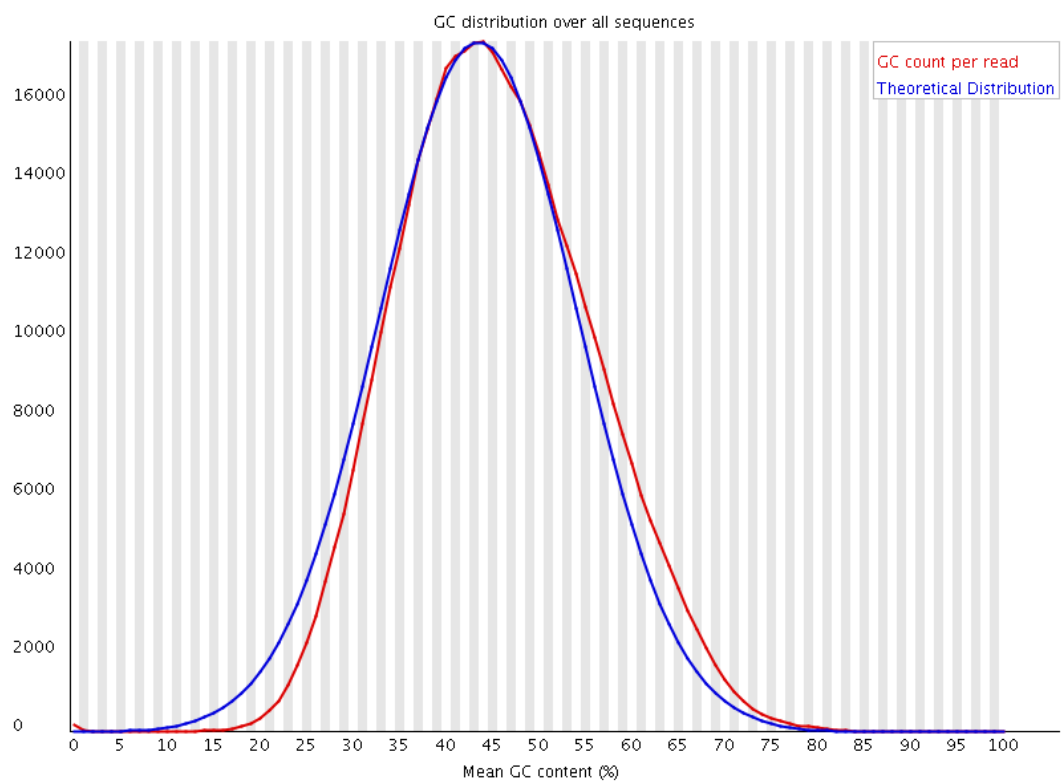


Figure 3:

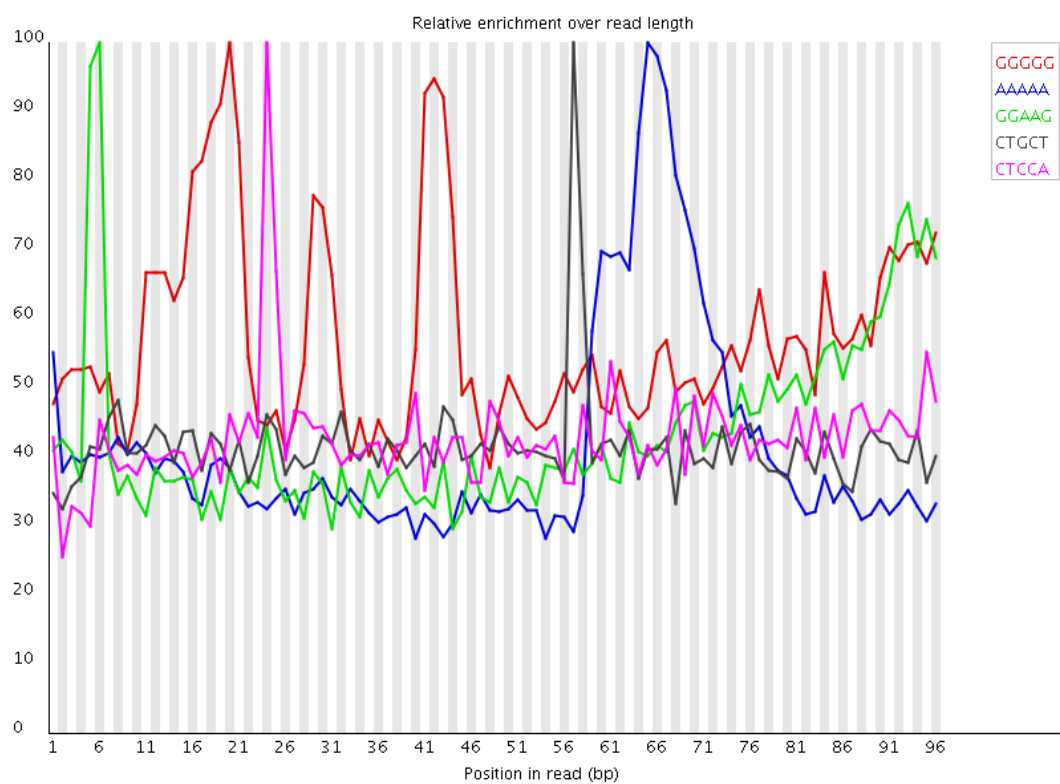


Figure 4:

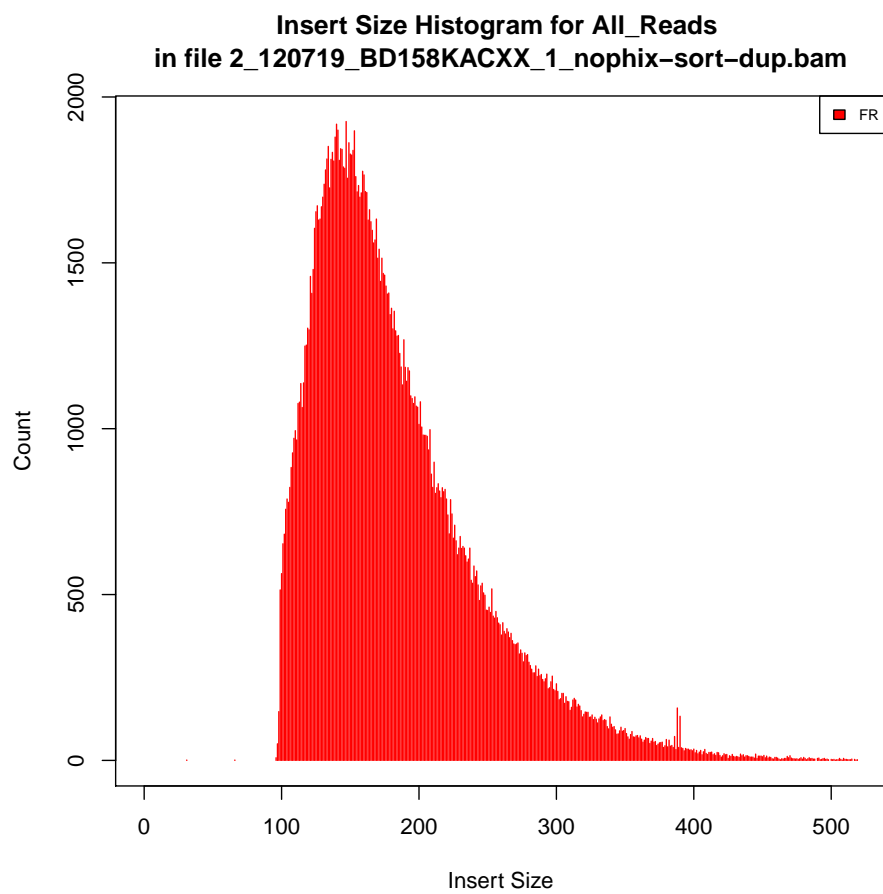


Figure 5: Distribution of paired end insert sizes