

: C.Dson_15_02_317Ma1_index12 : 4 : CTTGTA (4_120719_BD158KACXX_1_nophix-sort-dup)

Reference organism	hg19	
Total	223,898	101bp paired
Aligned	203,628	(90.9%)
Pairs aligned	200,651	(89.6%)
Pair duplicates	273	(0.1%)
Insert size	182.8	+/- 60.2
On bait bases	17,115,136	(45.8%)
Near bait bases	7,662,254	(20.5%)
Off bait bases	12,591,167	(33.7%)
Mean bait coverage	0.3	
On target bases	17,131,658	(45.8%)
Mean target coverage	0x	
10x coverage targets	0.0%	
Zero coverage targets	75.9%	
Fold enrichment	27x	

Table 1: Summary of lane results

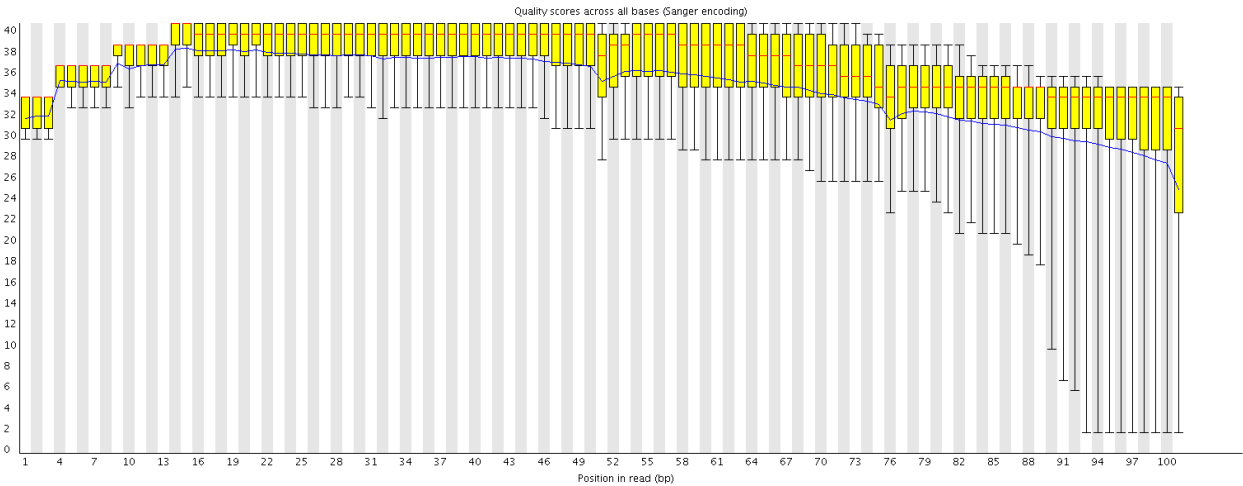


Figure 1:

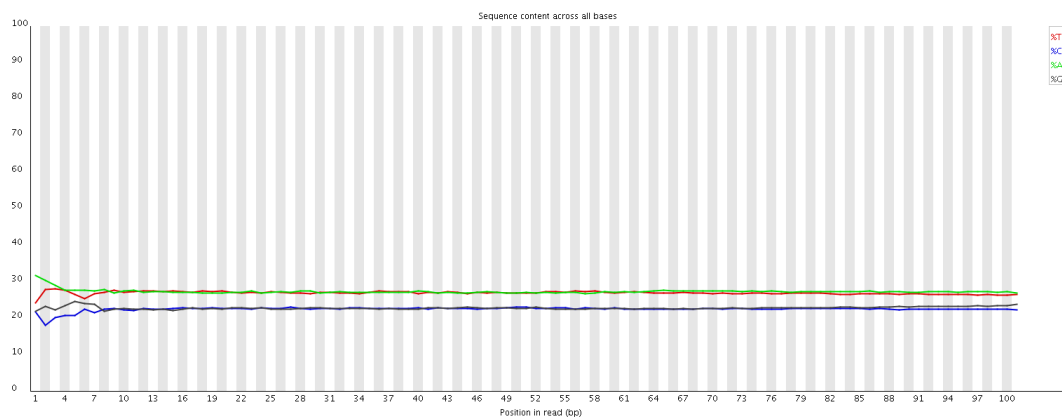


Figure 2:

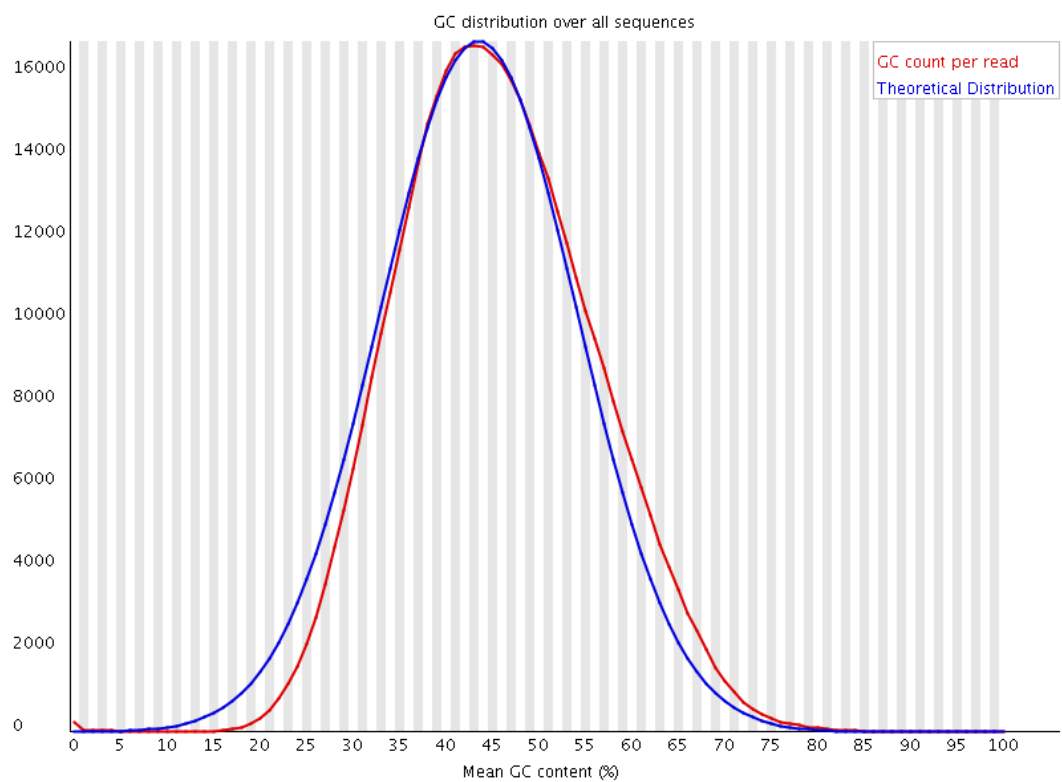


Figure 3:

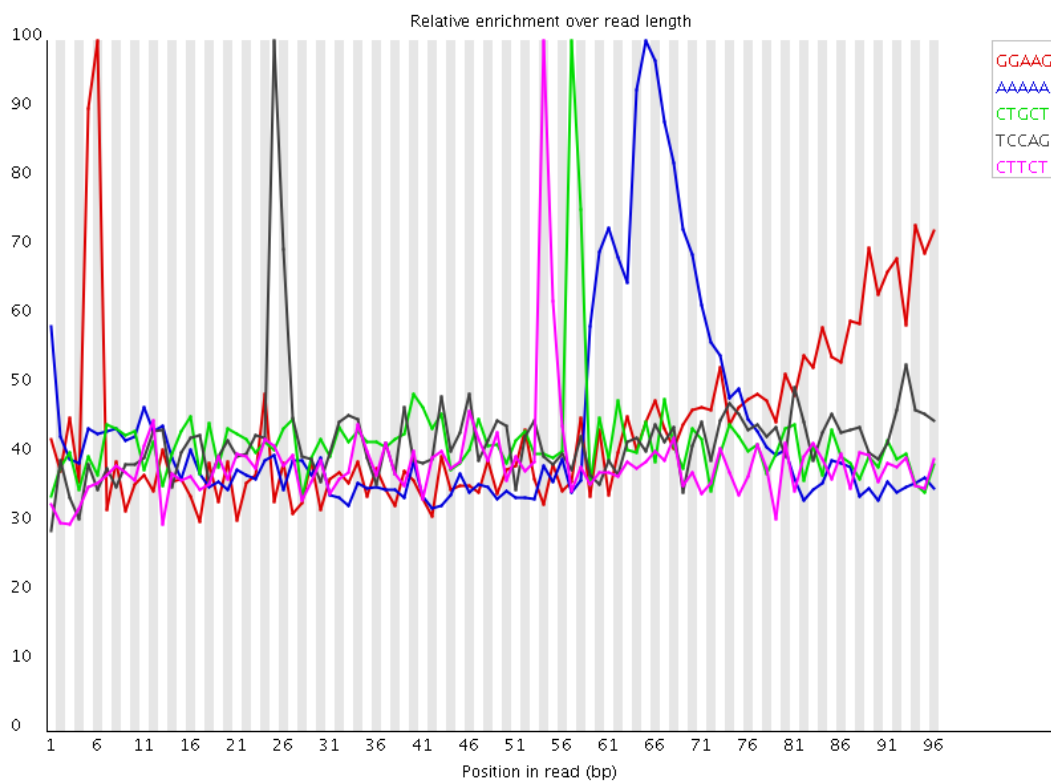


Figure 4:

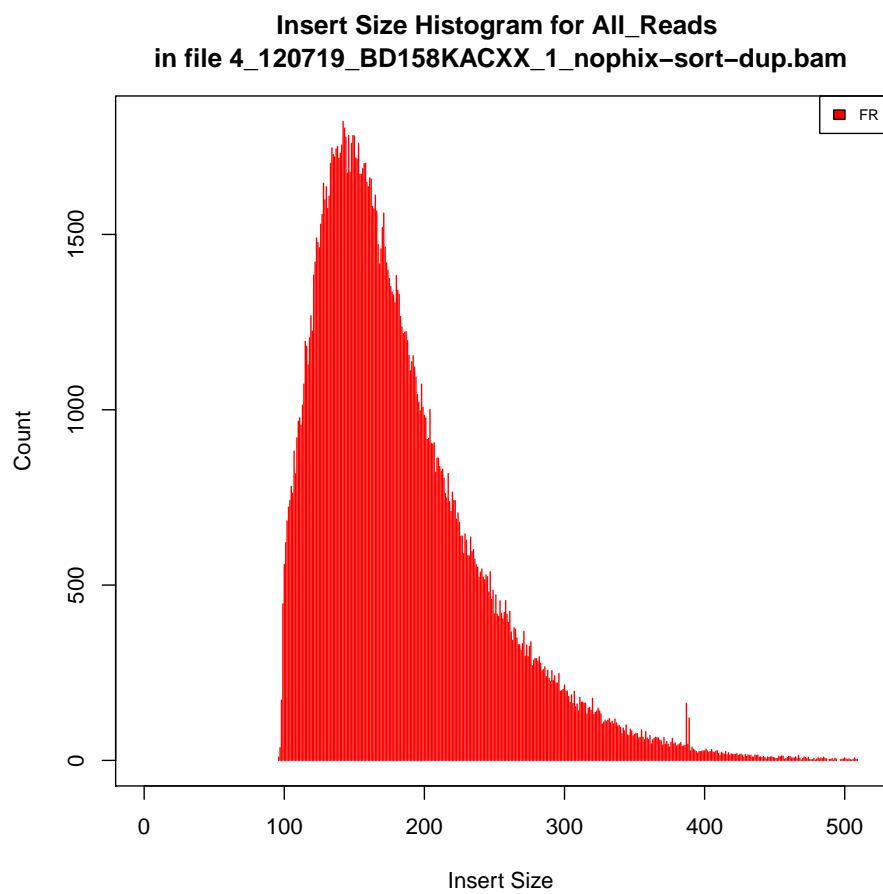


Figure 5: Distribution of paired end insert sizes