

: C.Dson_15_02_317Ma2_index13 : 5 : AGTCAA (5_120719_BD158KACXX_1_nophix-sort-dup)

| | | |
|-----------------------|-----------|--------------|
| Reference organism | hg19 | |
| Total | 135,414 | 101bp paired |
| Aligned | 123,958 | (91.5%) |
| Pairs aligned | 121,925 | (90.0%) |
| Pair duplicates | 55 | (0.0%) |
| Insert size | 198.0 | +/- 59.0 |
| On bait bases | 9,603,952 | (42.1%) |
| Near bait bases | 4,709,639 | (20.7%) |
| Off bait bases | 8,481,395 | (37.2%) |
| Mean bait coverage | 0.2 | |
| On target bases | 9,616,578 | (42.2%) |
| Mean target coverage | 0x | |
| 10x coverage targets | 0.0% | |
| Zero coverage targets | 86.7% | |
| Fold enrichment | 25x | |

Table 1: Summary of lane results

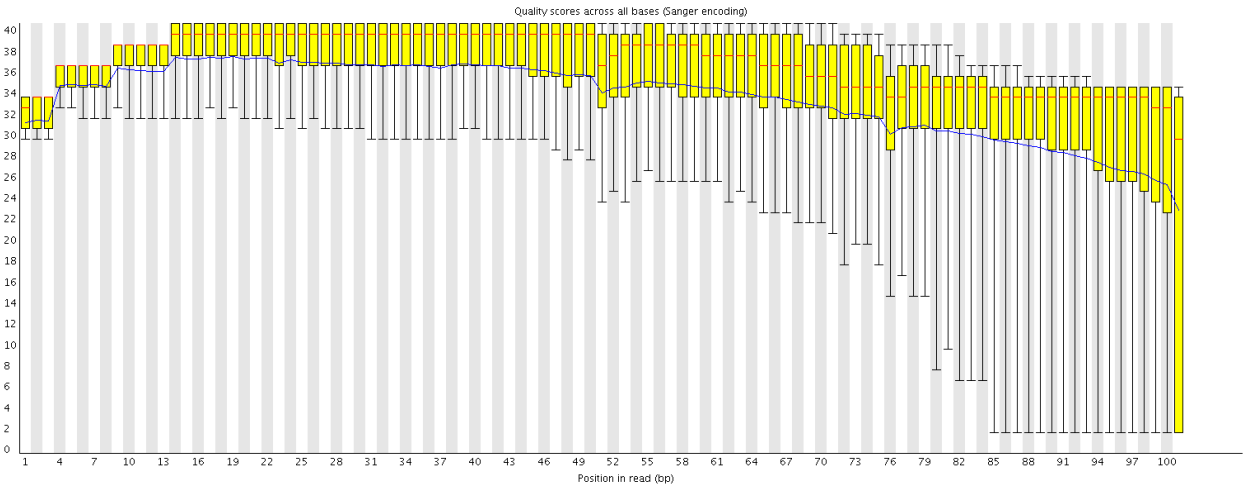


Figure 1:

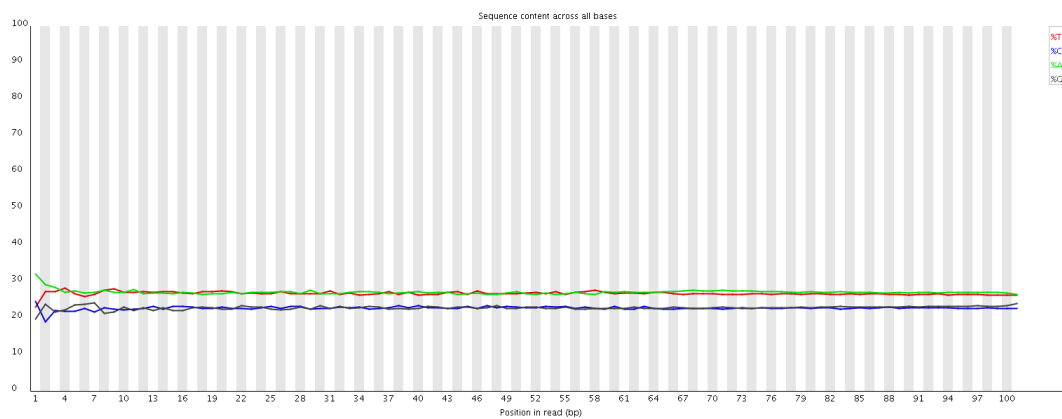


Figure 2:

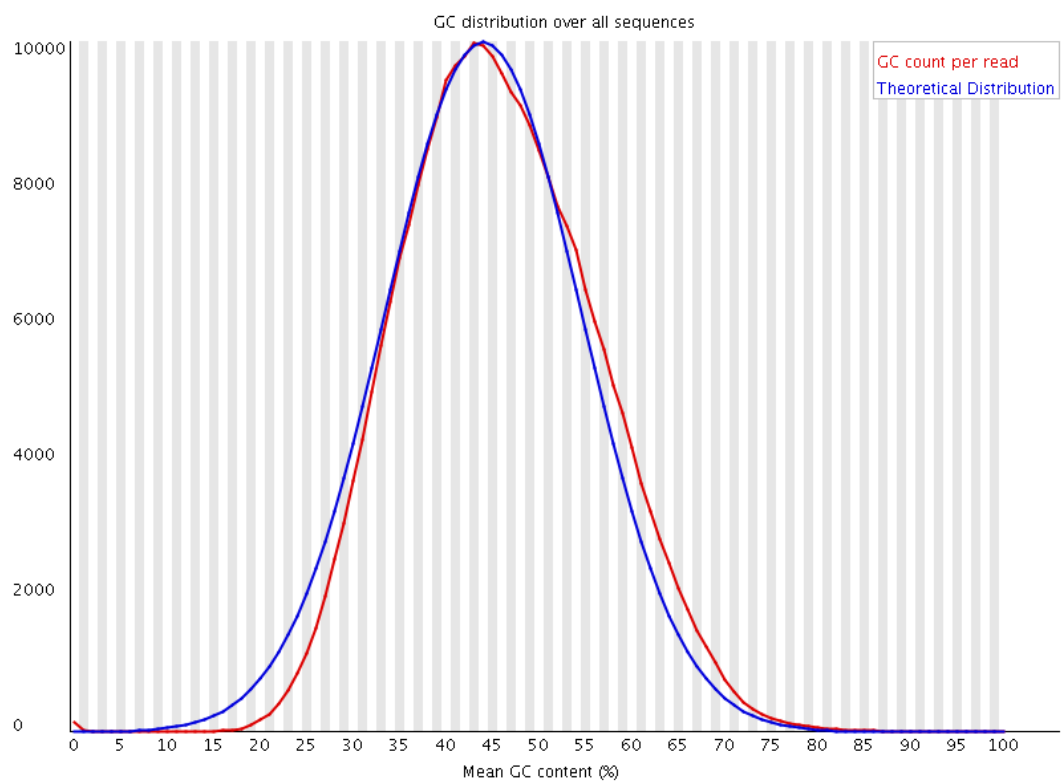


Figure 3:

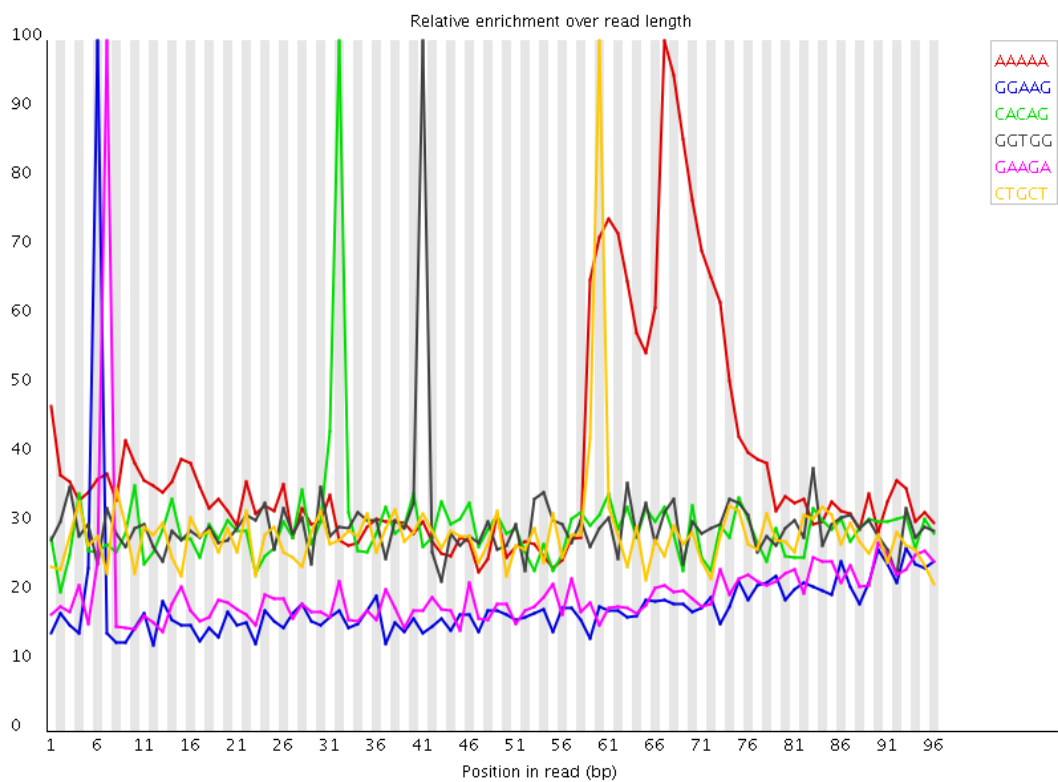


Figure 4:

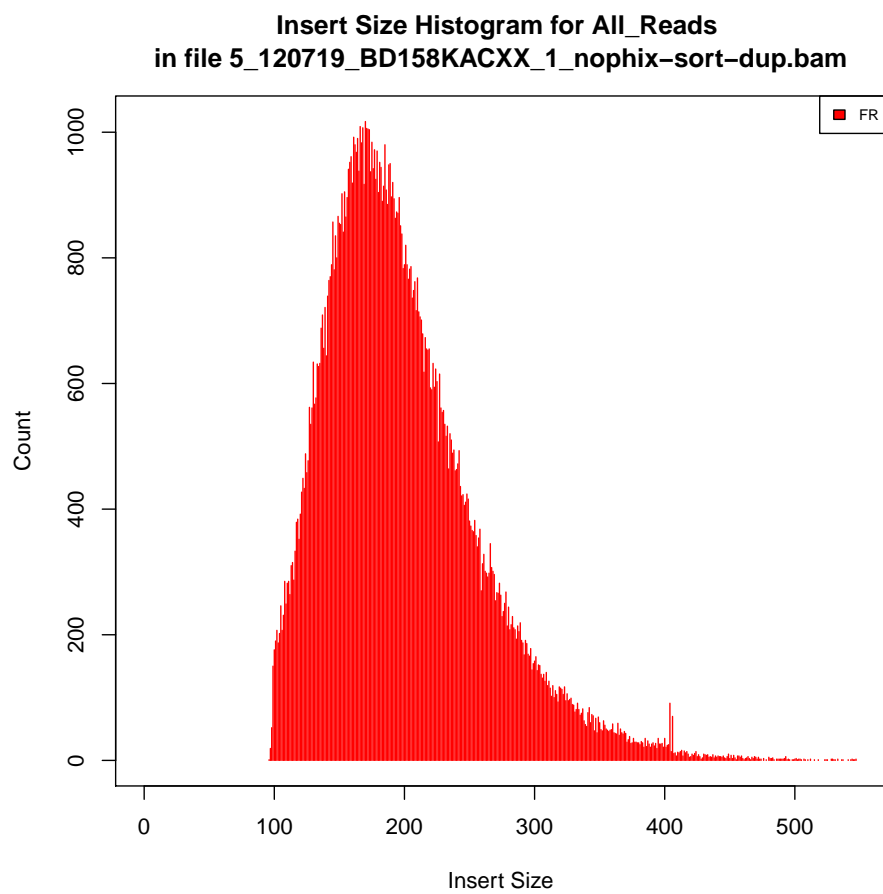


Figure 5: Distribution of paired end insert sizes