

SHa47 : MitoGo Cohort 4 multiplexing_12 : HL1202 (/array0/projects/Sequencing/101216 HWI-EAS264 00028 FC62N4VAAXX/1 101216 FC62N4VAAXX 1-sort)

| | | |
|---------------------------------|-------------------------|-------------|
| Reference organism | Homo sapiens assembly19 | |
| Total | 8,921,383 | 72bp paired |
| Aligned | 8,865,660 | (99.4%) |
| Pairs aligned | 8,833,793 | (99.0%) |
| Pair duplicates | 999,001 | (11.3%) |
| Insert size | 187.8 | +/- 48.2 |
| On bait bases | 657,359,071 | (60.3%) |
| Near bait bases | 223,327,810 | (20.5%) |
| Off bait bases | 209,479,540 | (19.2%) |
| Mean bait coverage | 210.1 | |
| On target bases | 527,719,999 | (48.4%) |
| Mean target coverage | 234x | |
| 10x coverage targets | 95.0% | |
| Zero coverage targets | 2.5% | |
| Fold enrichment | 597x | |
| Total variations | 1334 | |
| In dbSNP | 95.7% | |
| Transition/Transversion (all) | 3.54 | |
| Transition/Transversion (dbSNP) | 3.61 | |
| Transition/Transversion (novel) | 2.35 | |

Table 1: Summary of lane results

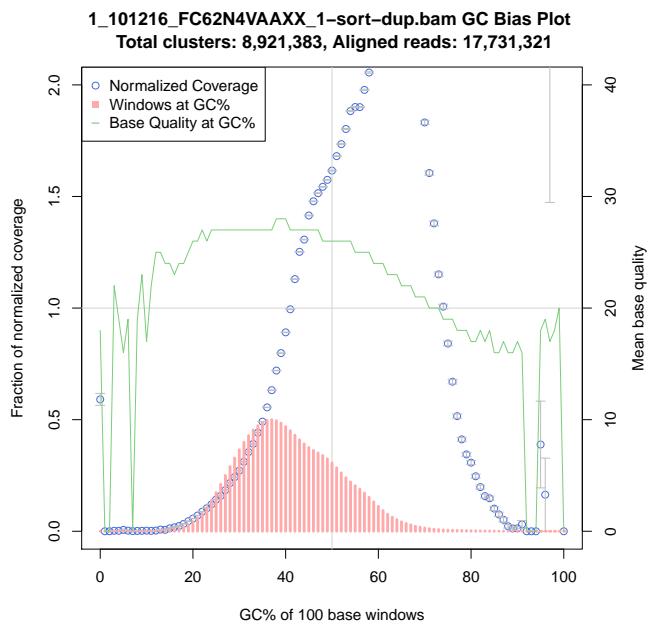


Figure 1: Distribution of GC content across reads

1_101216_FC62N4VAAXX_1-sort-dup.bam Insert Size Histogram

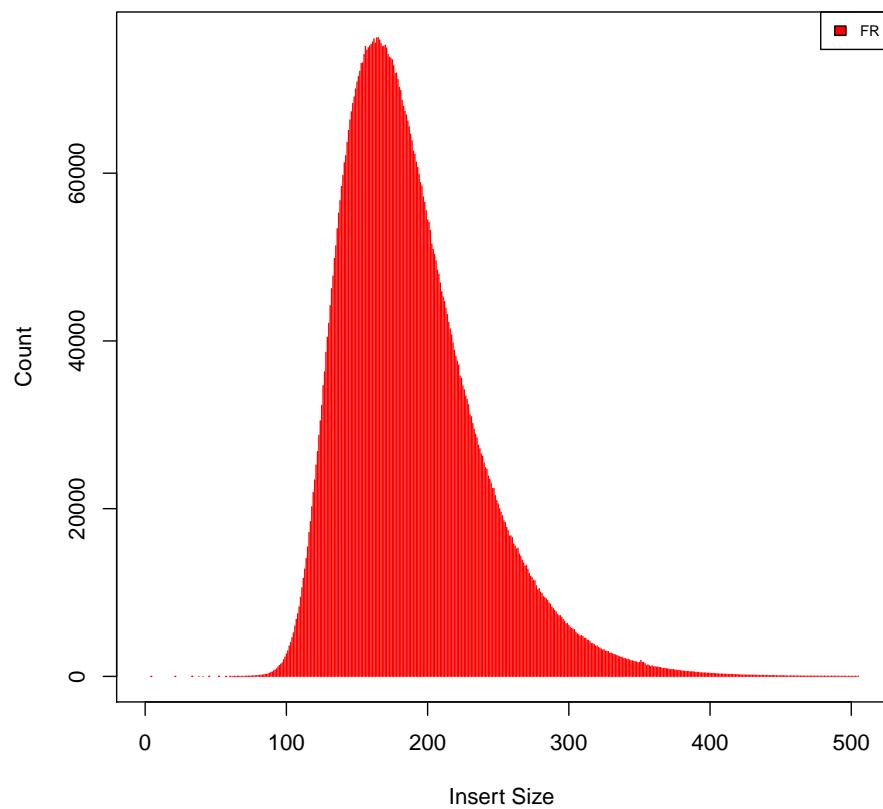


Figure 2: Distribution of paired end insert sizes

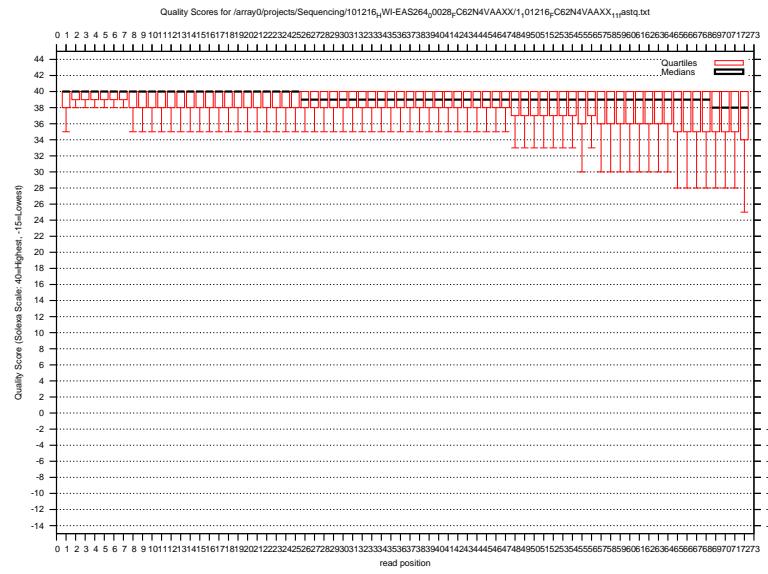


Figure 3: Quality score distribution per base for read 1

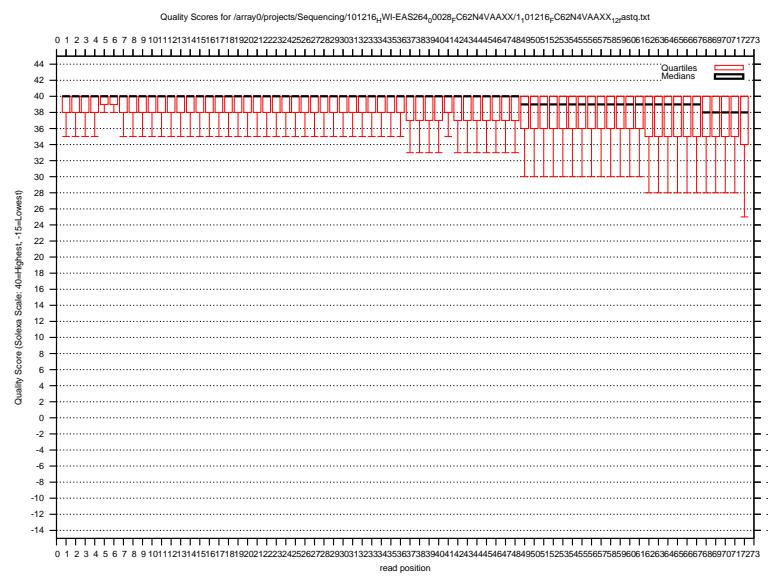


Figure 4: Quality score distribution per base for read 2

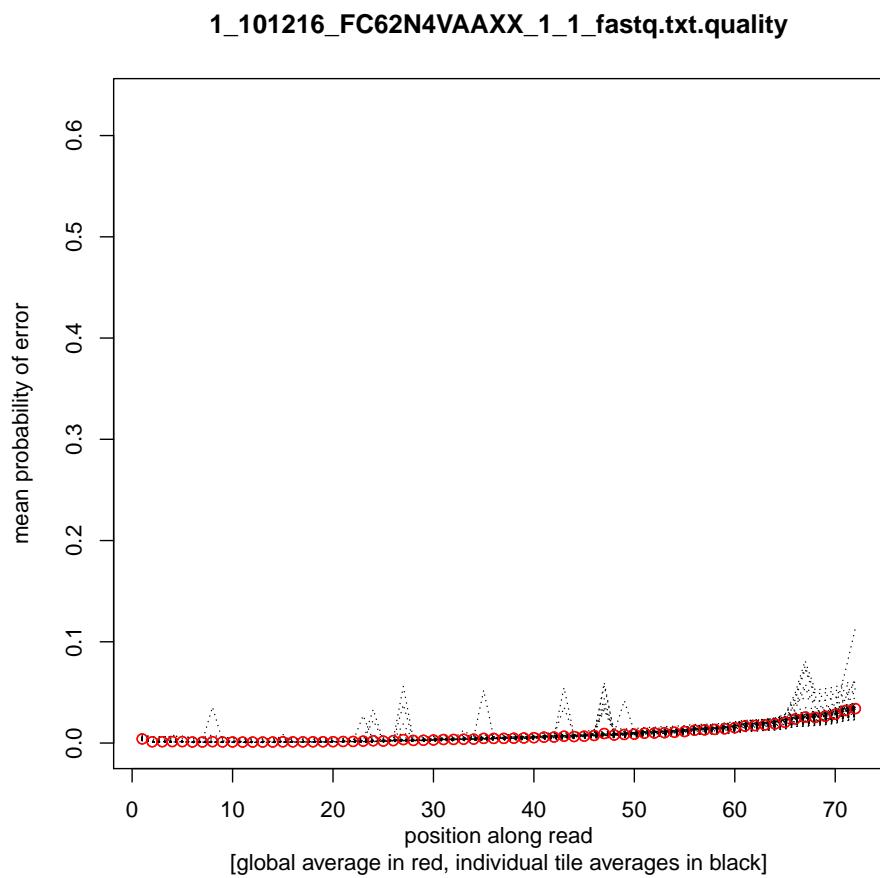


Figure 5: Mean error probability per read position and tile for read 1. Ideal flowcells will have a tight range of values for all tiles.

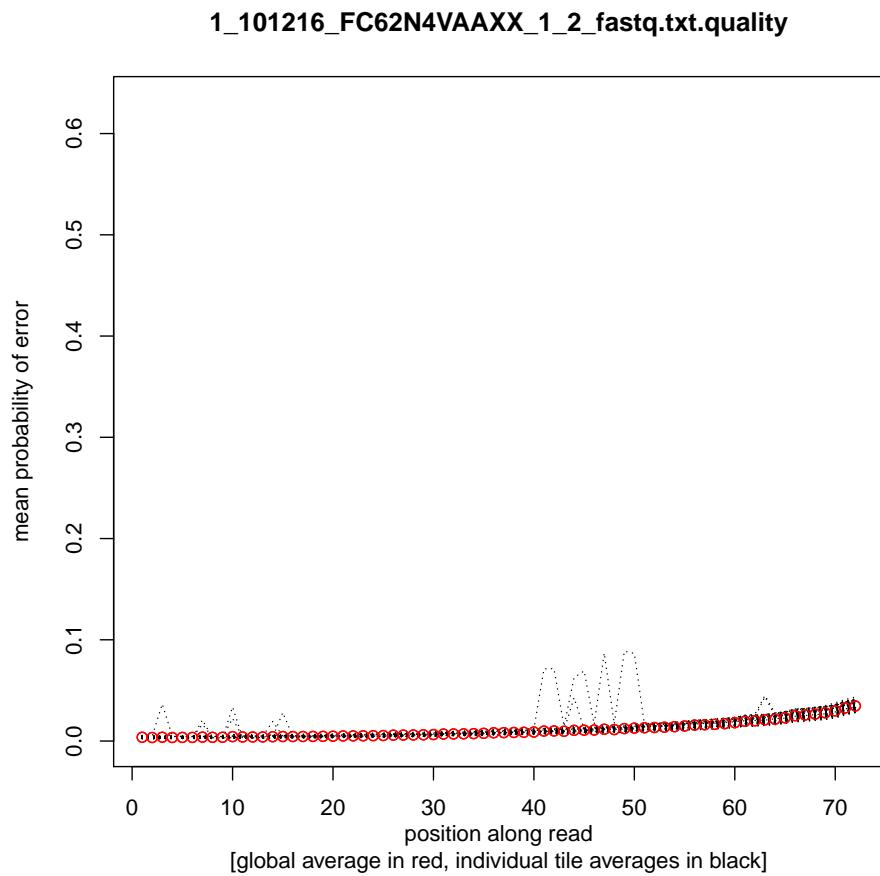


Figure 6: Mean error probability per read position and tile for read 2. Ideal flowcells will have a tight range of values for all tiles.

Quality score recalibration

