Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 09:27:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008743.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR6008743 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008743.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 09:27:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008743.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,316,467
Mapped reads	995,948 / 42.99%
Unmapped reads	1,320,519 / 57.01%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,497 / 0.15%
Read min/max/mean length	30 / 76 / 76.05
Duplicated reads (estimated)	46,503 / 2.01%
Duplication rate	3.21%
Clipped reads	691,431 / 29.85%

2.2. ACGT Content

Number/percentage of A's	14,761,971 / 24.46%
Number/percentage of C's	11,392,774 / 18.88%
Number/percentage of T's	18,141,589 / 30.06%
Number/percentage of G's	16,053,133 / 26.6%
Number/percentage of N's	2,663 / 0%
GC Percentage	45.48%

2.3. Coverage

Mean	0.0195

Standard Deviation	0.2067

2.4. Mapping Quality

Mean Mapping Quality	40.53

2.5. Mismatches and indels

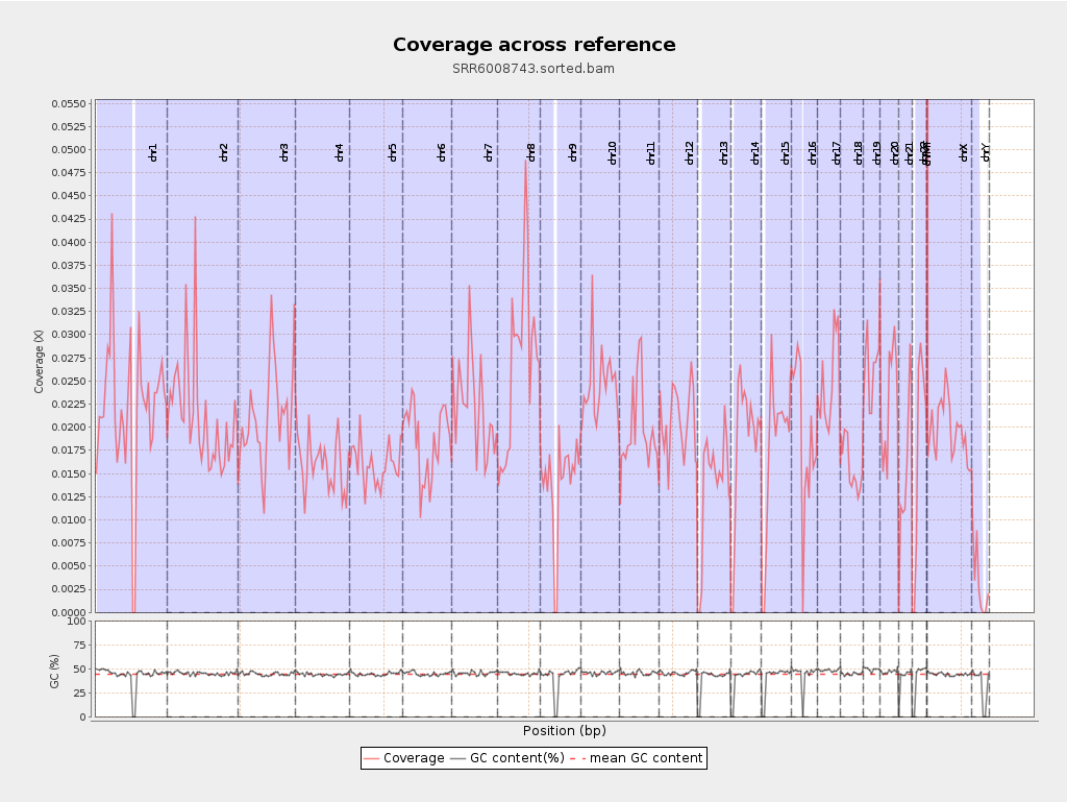
General error rate	0.92%
Mismatches	549,776
Insertions	4,837
Mapped reads with at least one insertion	0.48%
Deletions	21,664
Mapped reads with at least one deletion	2.15%
Homopolymer indels	45.42%

2.6. Chromosome stats

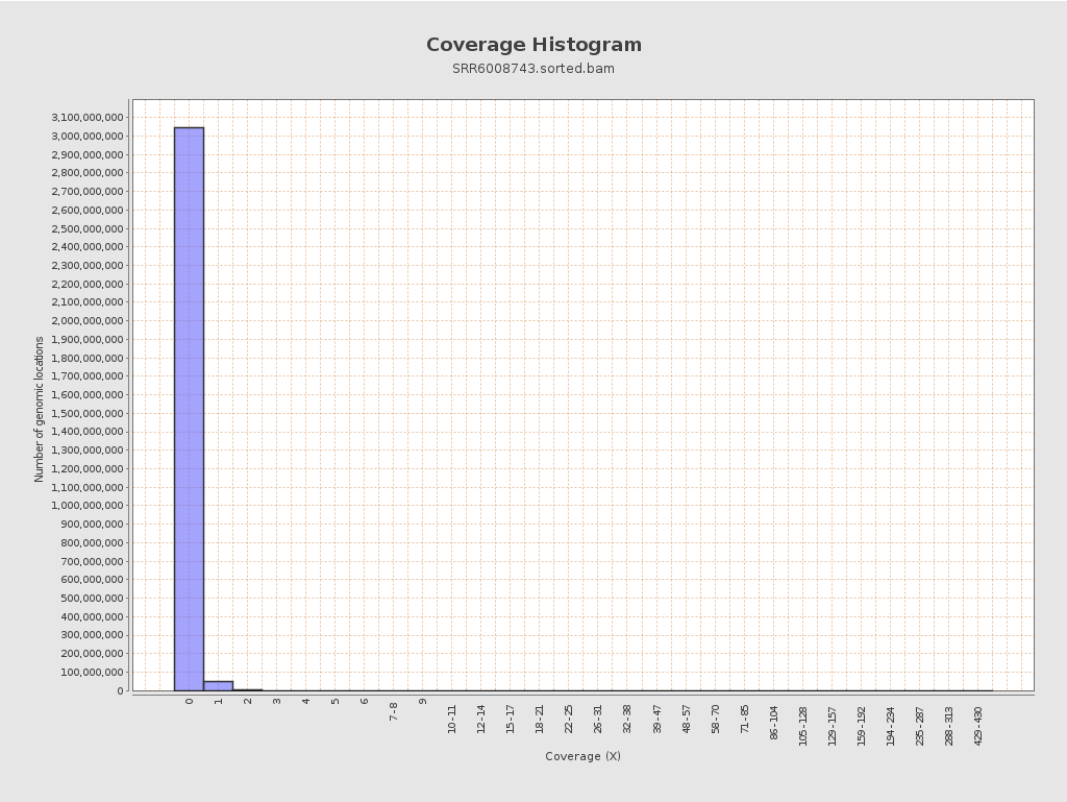
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5458532	0.0219	0.2586
chr2	243199373	5161604	0.0212	0.3077
chr3	198022430	4161414	0.021	0.1678
chr4	191154276	3084646	0.0161	0.1521
chr5	180915260	2913320	0.0161	0.1459
chr6	171115067	3167520	0.0185	0.1722
chr7	159138663	3565997	0.0224	0.3026

chr8	146364022	3963572	0.0271	0.2157
chr9	141213431	1960392	0.0139	0.1829
chr10	135534747	3330808	0.0246	0.2254
chr11	135006516	2693886	0.02	0.1984
chr12	133851895	2746295	0.0205	0.1713
chr13	115169878	1571600	0.0136	0.1423
chr14	107349540	1961687	0.0183	0.1567
chr15	102531392	1807842	0.0176	0.16
chr16	90354753	1712713	0.019	0.1732
chr17	81195210	2000413	0.0246	0.1978
chr18	78077248	1213501	0.0155	0.2534
chr19	59128983	1568858	0.0265	0.2287
chr20	63025520	1426423	0.0226	0.1766
chr21	48129895	732517	0.0152	0.1469
chr22	51304566	903376	0.0176	0.165
chrMT	16571	29998	1.8103	1.955
chrX	155270560	3064413	0.0197	0.1775
chrY	59373566	185357	0.0031	0.0764

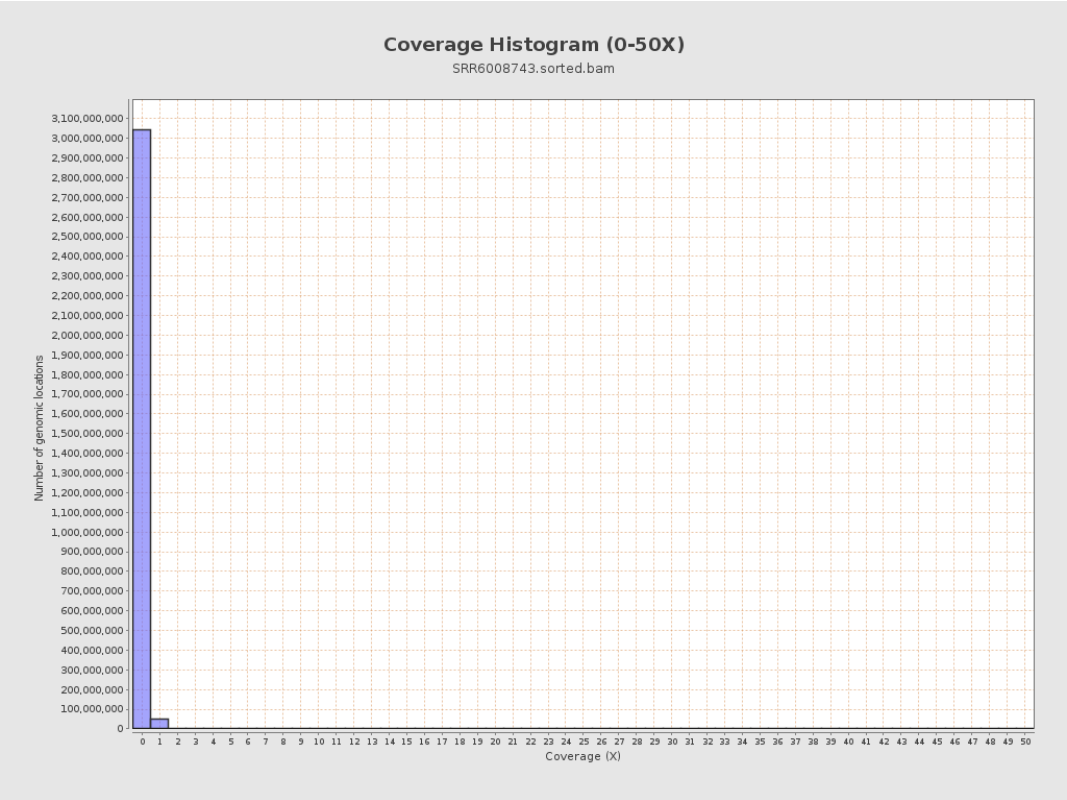
3. Results : Coverage across reference



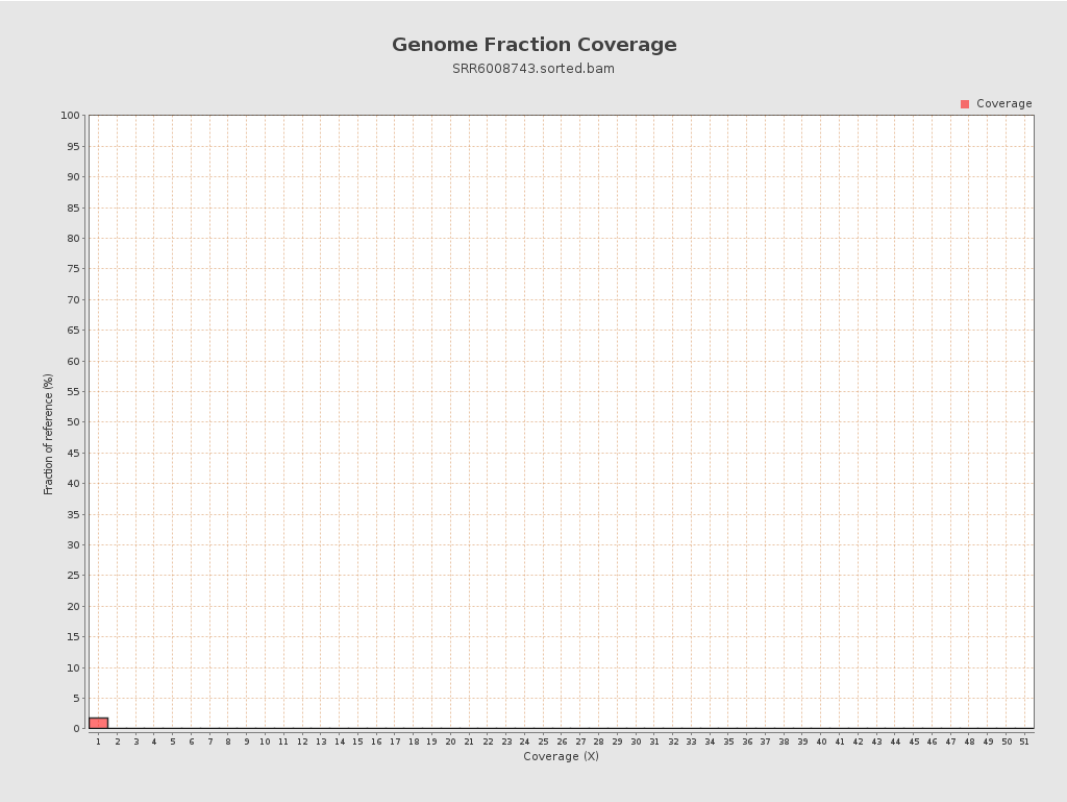
4. Results : Coverage Histogram



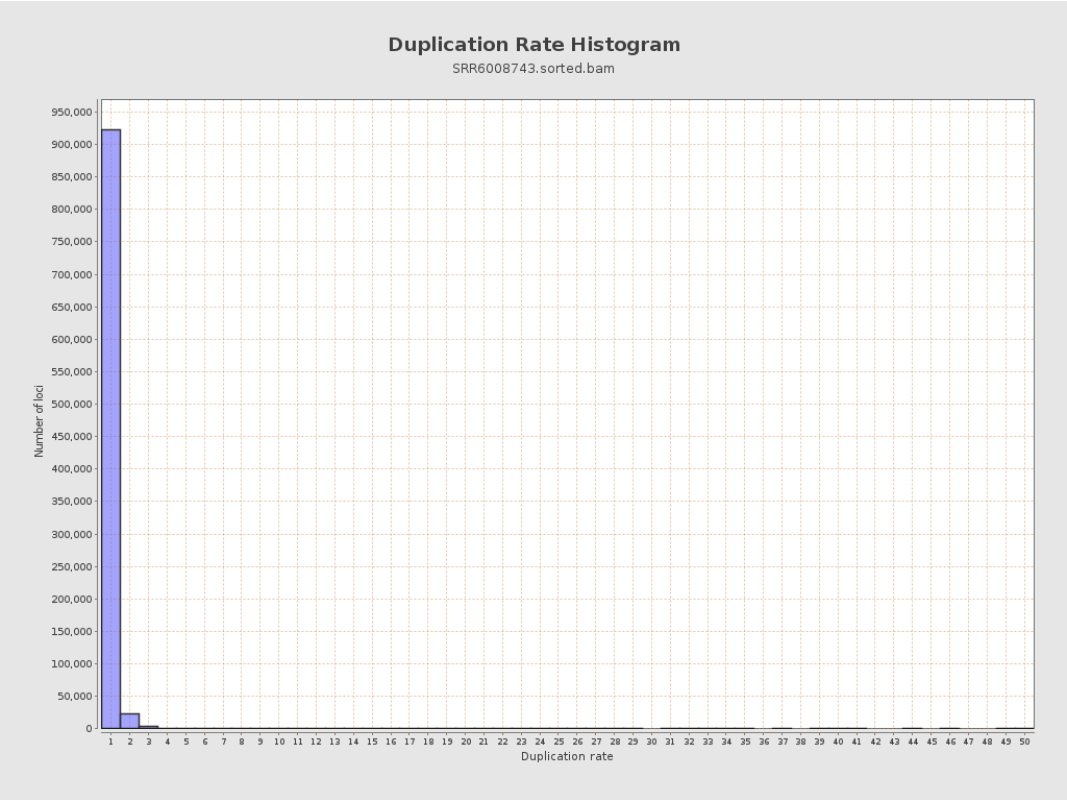
5. Results : Coverage Histogram (0-50X)



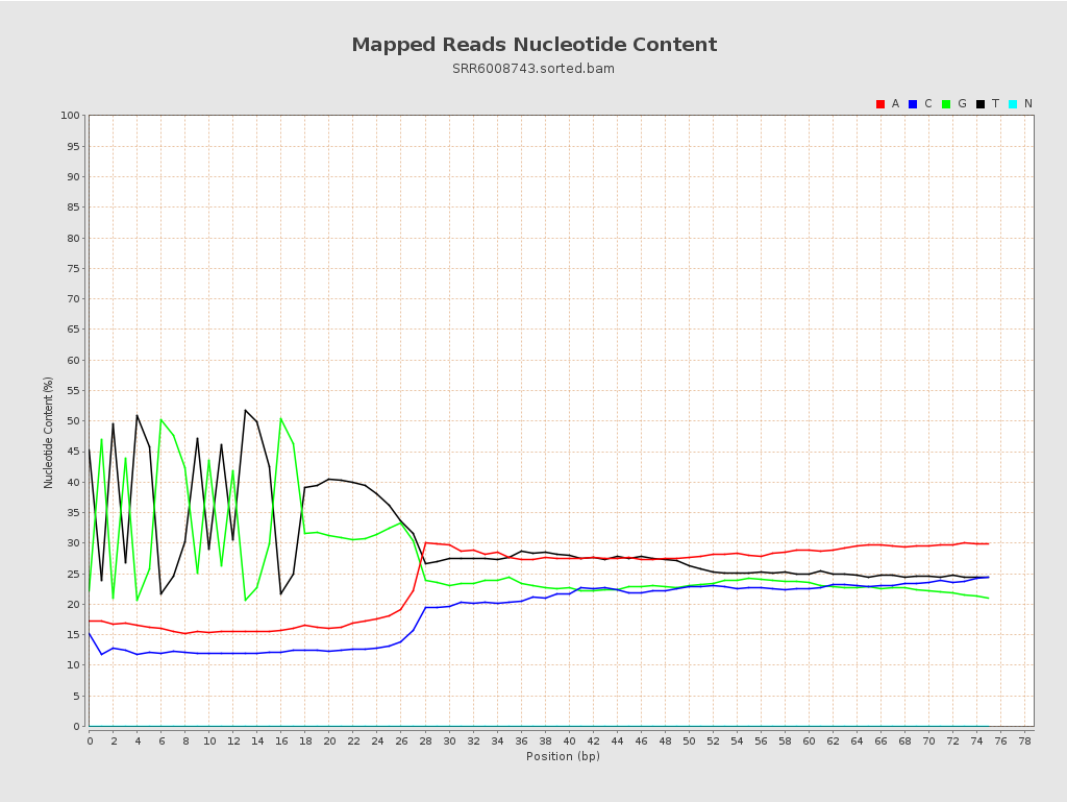
6. Results : Genome Fraction Coverage



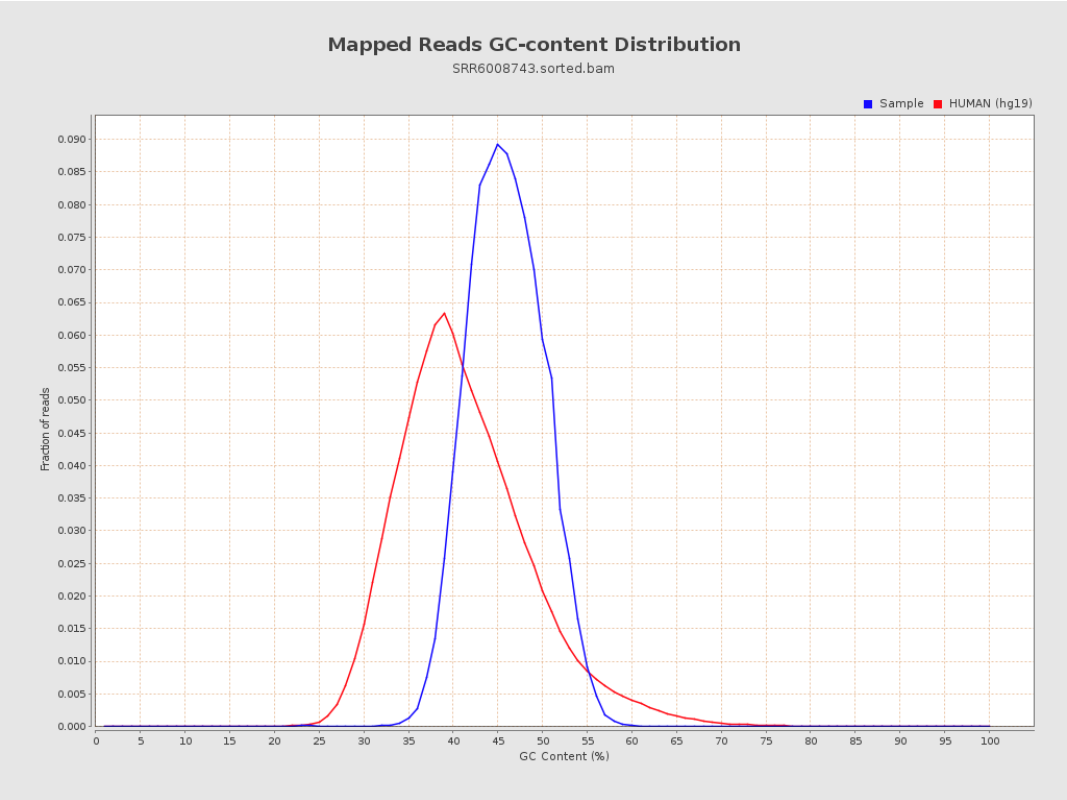
7. Results : Duplication Rate Histogram



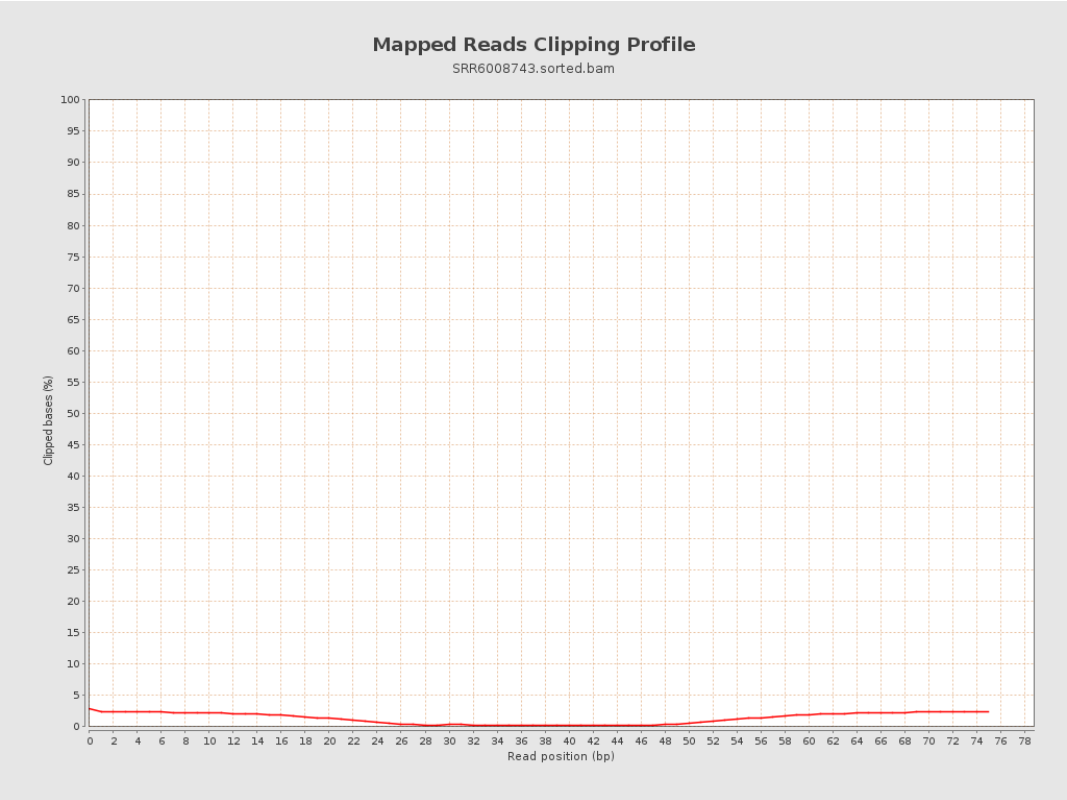
8. Results : Mapped Reads Nucleotide Content



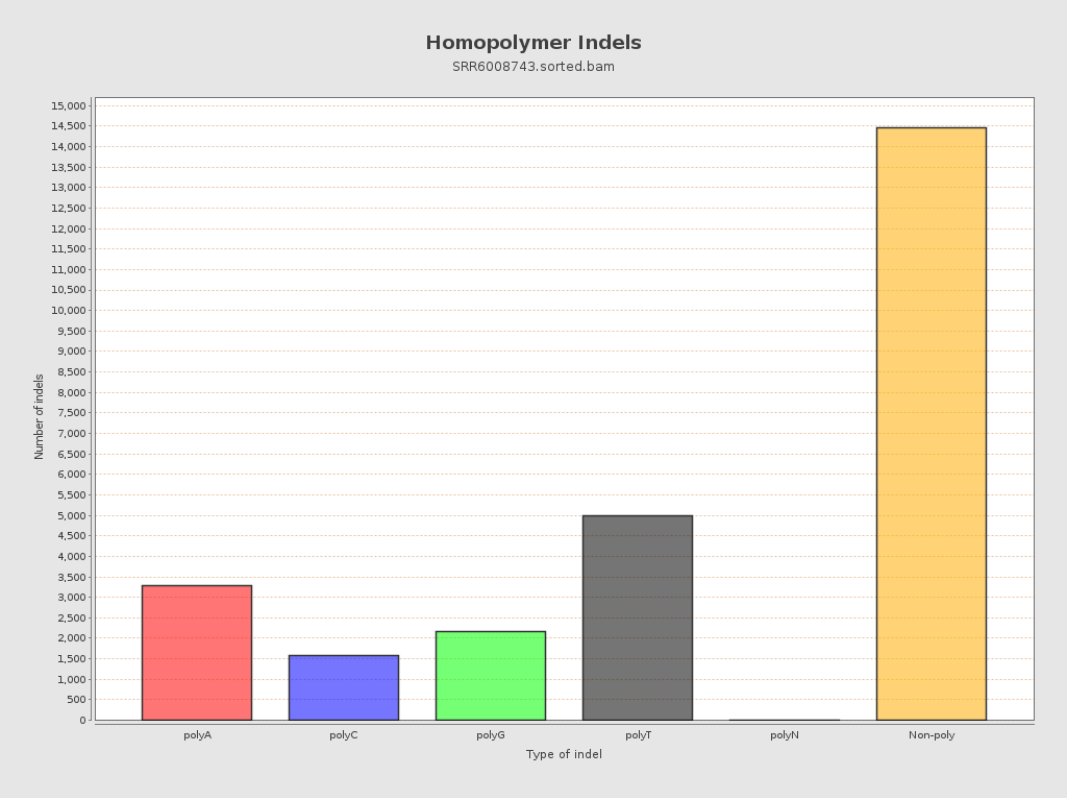
9. Results : Mapped Reads GC-content Distribution



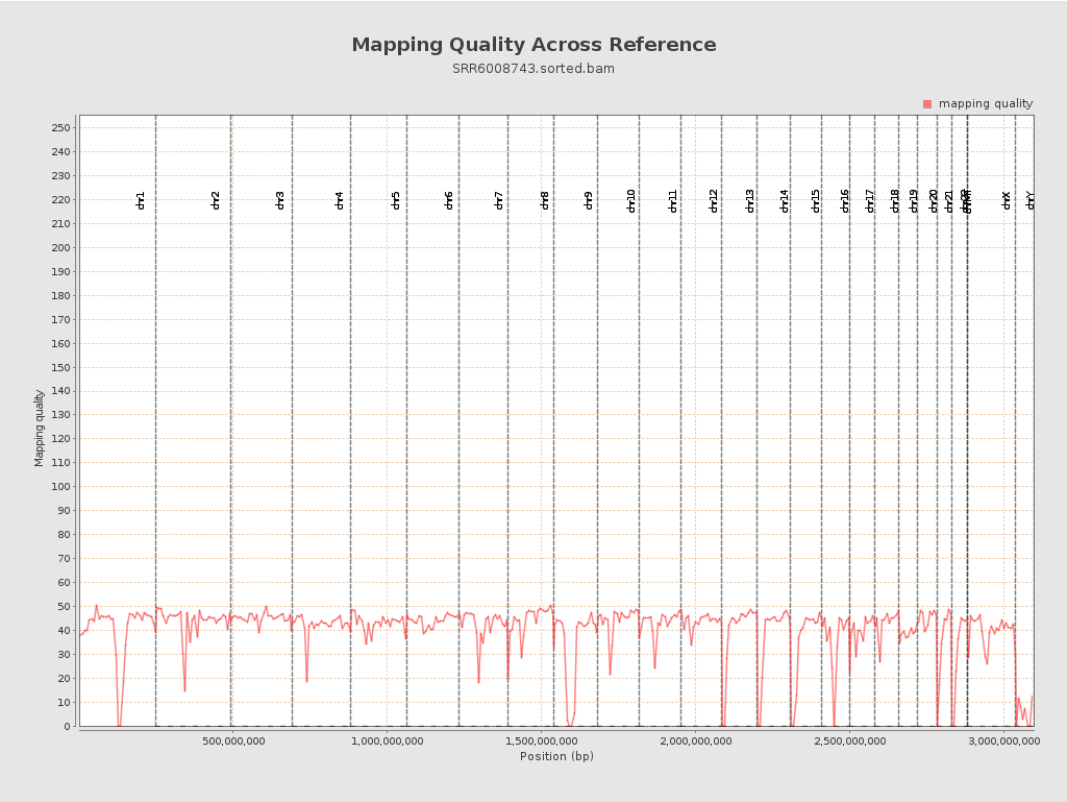
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram