

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 23:43:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716597.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_SRR9716597 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716597.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 23:43:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716597.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,271,269
Mapped reads	1,156,533 / 90.97%
Unmapped reads	114,736 / 9.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,754 / 0.61%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	36,466 / 2.87%
Duplication rate	2.47%
Clipped reads	1,160,883 / 91.32%

2.2. ACGT Content

Number/percentage of A's	16,962,815 / 24.94%
Number/percentage of C's	13,808,301 / 20.3%
Number/percentage of T's	20,636,813 / 30.34%
Number/percentage of G's	16,608,045 / 24.42%
Number/percentage of N's	859 / 0%
GC Percentage	44.72%

2.3. Coverage

Mean	0.022

Standard Deviation	0.2027
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	45.05
----------------------	-------

2.5. Mismatches and indels

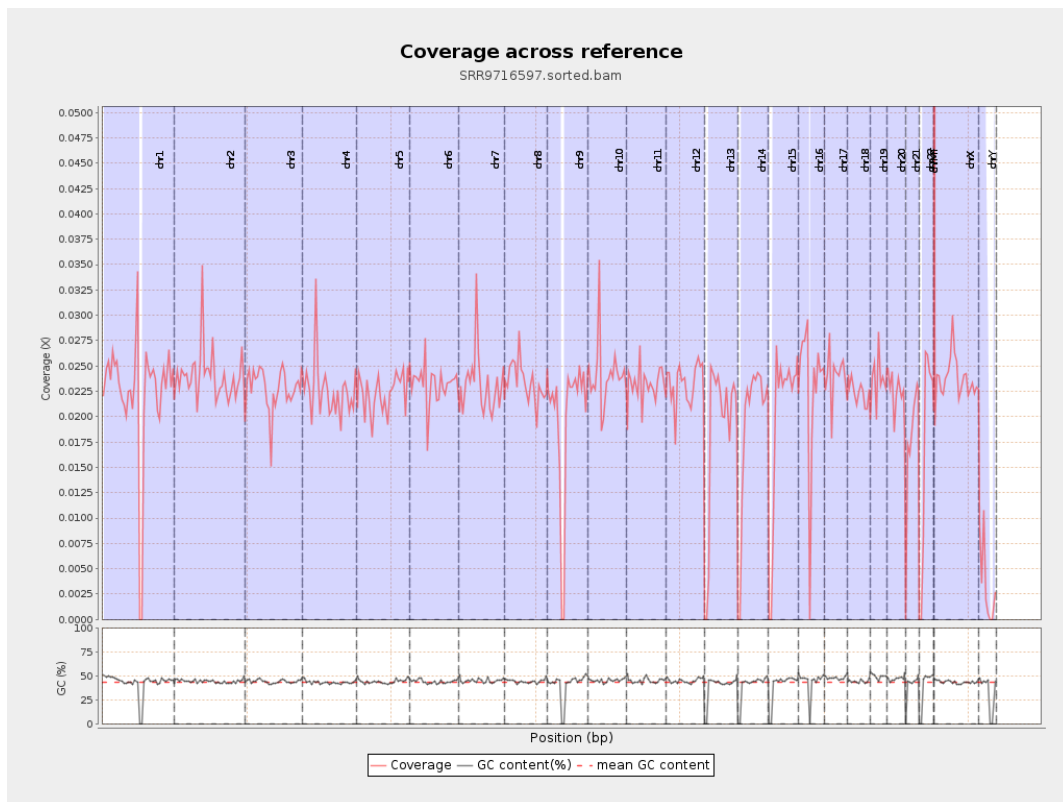
General error rate	0.51%
Mismatches	333,811
Insertions	5,356
Mapped reads with at least one insertion	0.46%
Deletions	12,033
Mapped reads with at least one deletion	1.03%
Homopolymer indels	39.54%

2.6. Chromosome stats

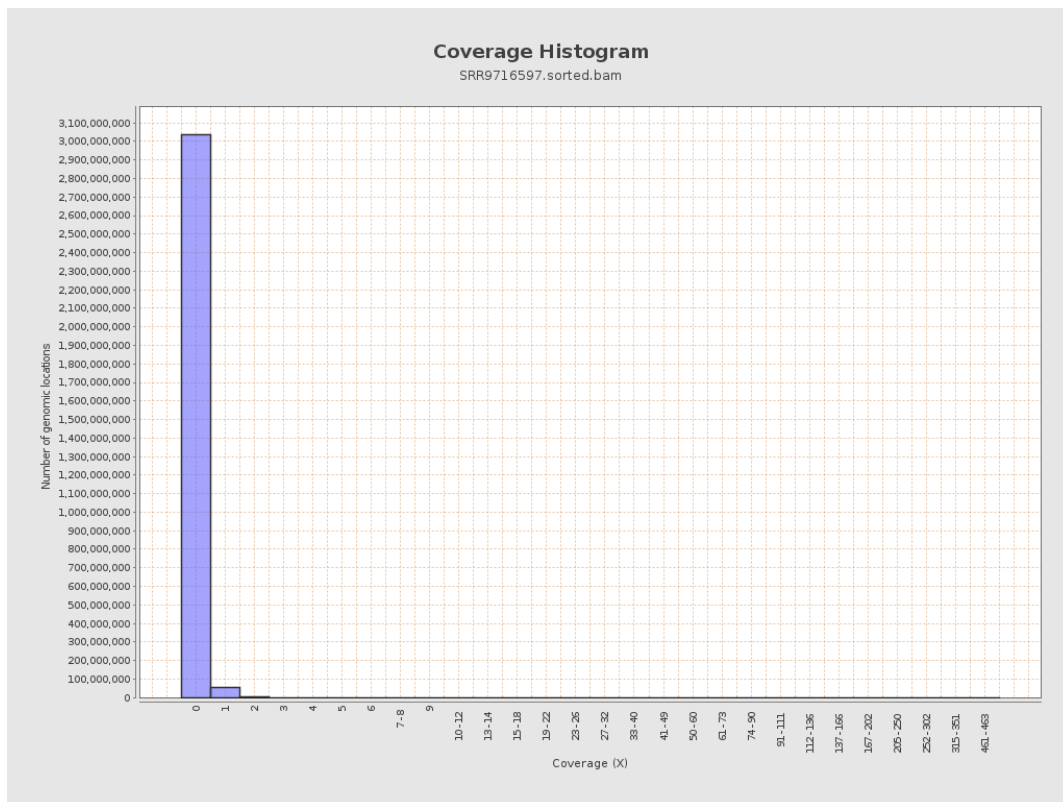
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5545251	0.0222	0.3118
chr2	243199373	5845983	0.024	0.2604
chr3	198022430	4511014	0.0228	0.1637
chr4	191154276	4317777	0.0226	0.1734
chr5	180915260	4050796	0.0224	0.1618
chr6	171115067	3968356	0.0232	0.1761
chr7	159138663	3687451	0.0232	0.2454

chr8	146364022	3426404	0.0234	0.2056
chr9	141213431	2785869	0.0197	0.1722
chr10	135534747	3268643	0.0241	0.2065
chr11	135006516	3141319	0.0233	0.195
chr12	133851895	3103097	0.0232	0.1662
chr13	115169878	2136899	0.0186	0.1474
chr14	107349540	2048813	0.0191	0.1526
chr15	102531392	2010007	0.0196	0.1523
chr16	90354753	2059925	0.0228	0.1692
chr17	81195210	1945463	0.024	0.1765
chr18	78077248	1746197	0.0224	0.2677
chr19	59128983	1402460	0.0237	0.2478
chr20	63025520	1406257	0.0223	0.1642
chr21	48129895	858211	0.0178	0.1537
chr22	51304566	880356	0.0172	0.1417
chrMT	16571	5141	0.3102	0.6153
chrX	155270560	3685110	0.0237	0.1751
chrY	59373566	199431	0.0034	0.0874

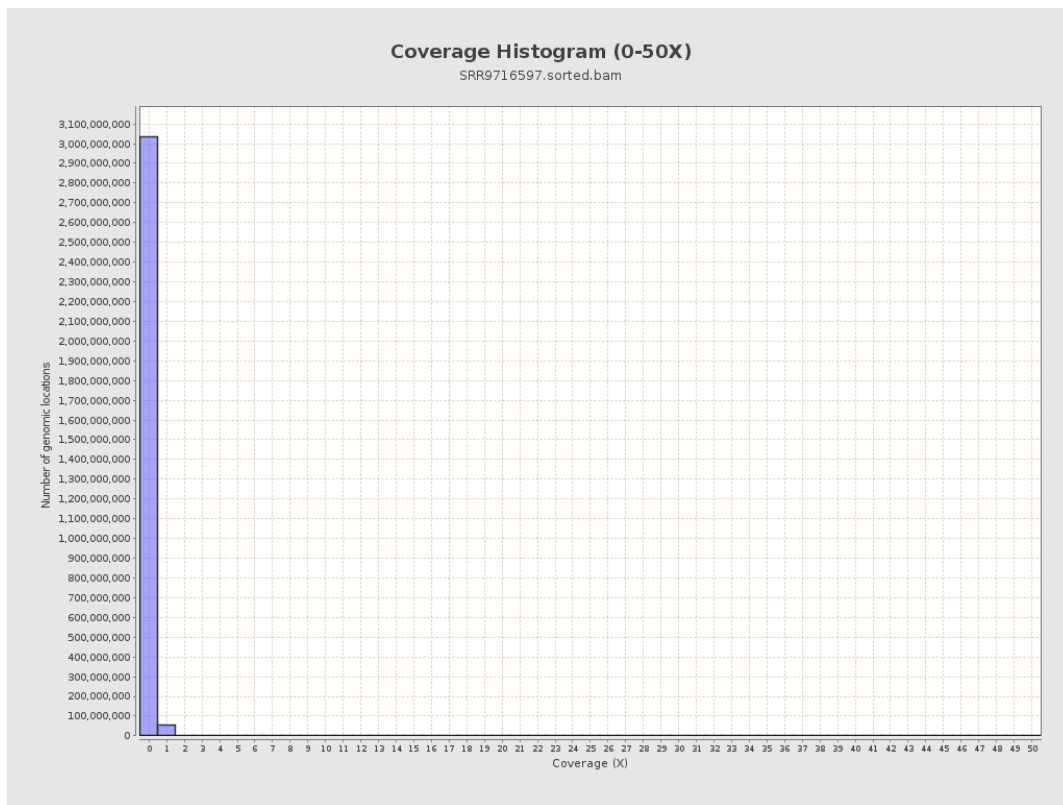
3. Results : Coverage across reference



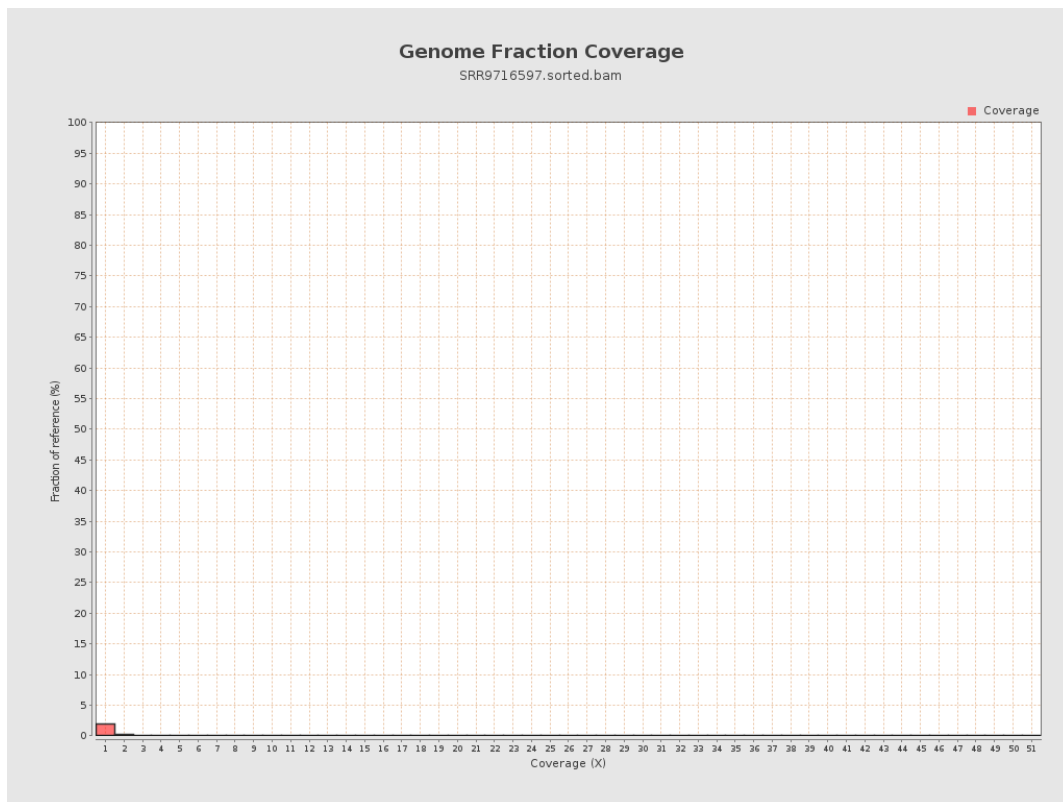
4. Results : Coverage Histogram



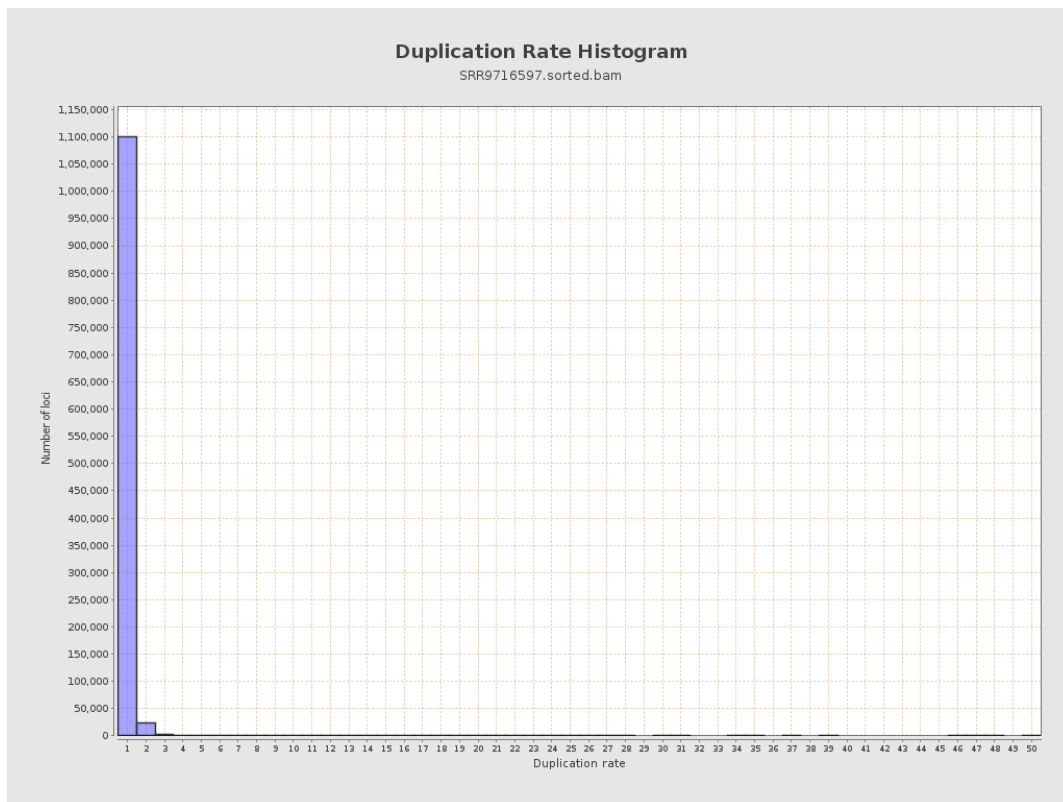
5. Results : Coverage Histogram (0-50X)



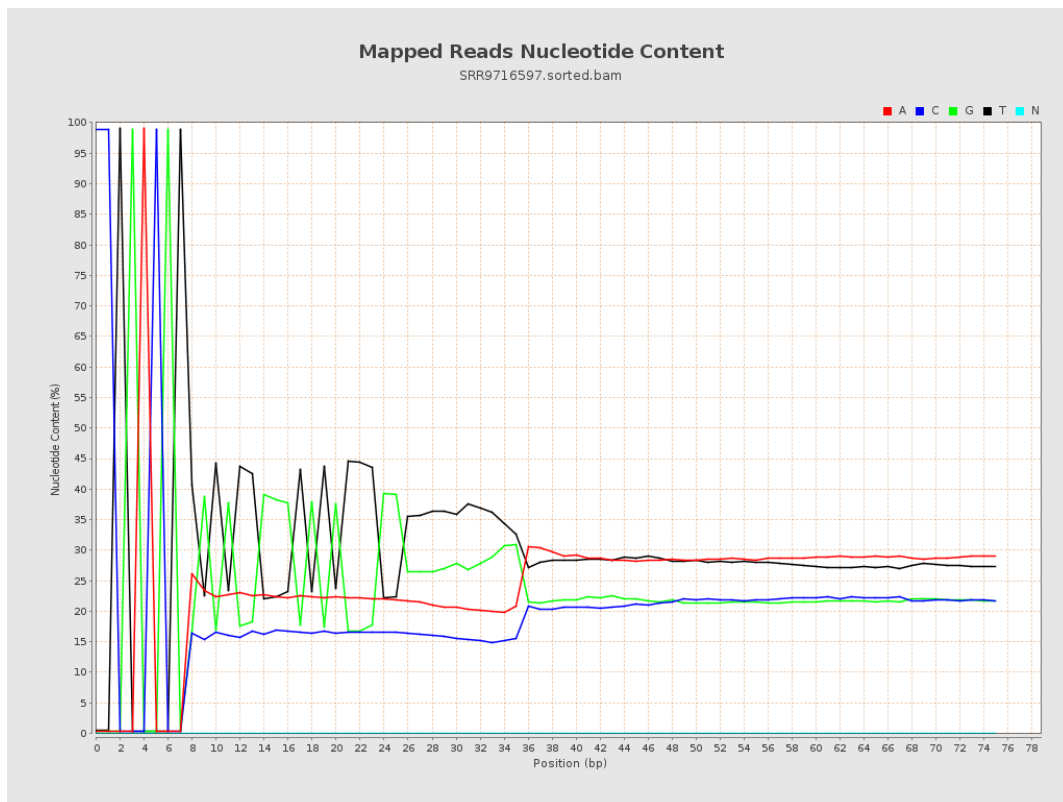
6. Results : Genome Fraction Coverage



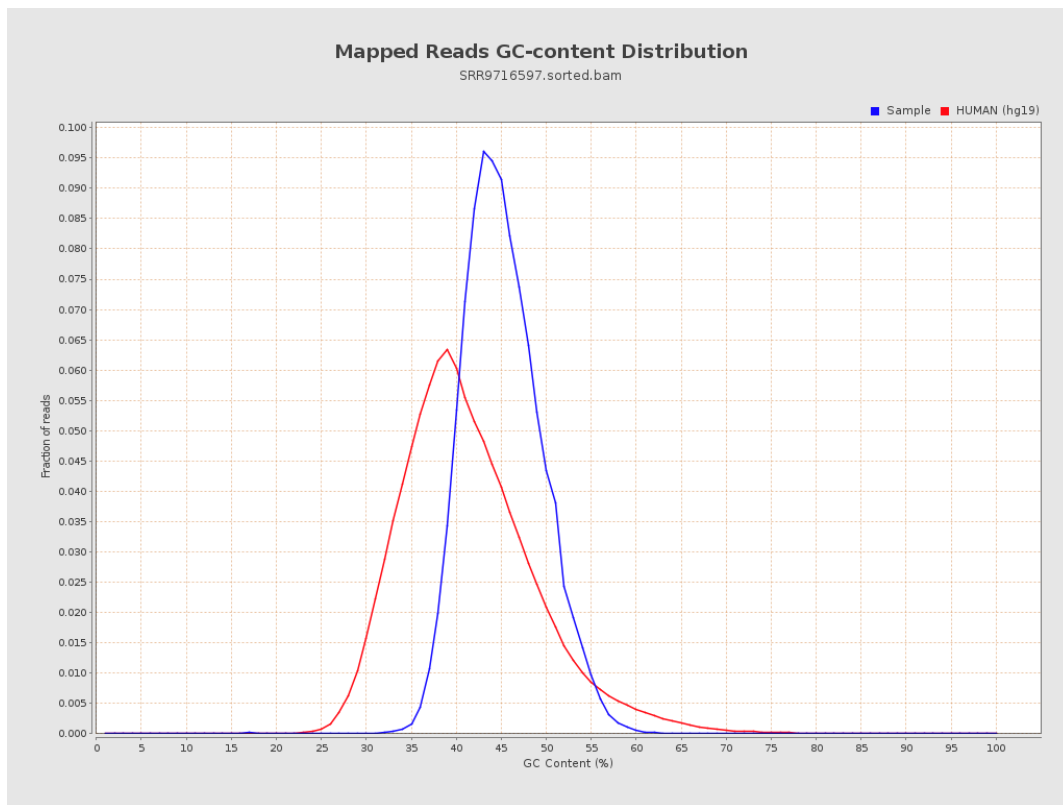
7. Results : Duplication Rate Histogram



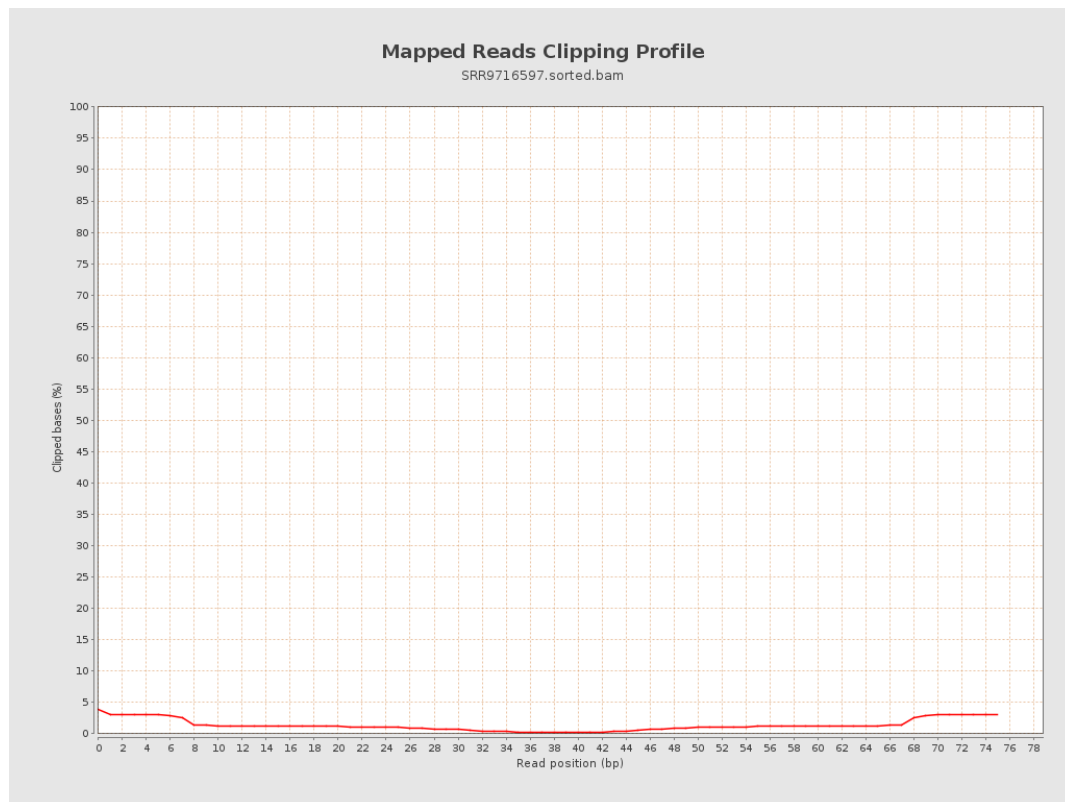
8. Results : Mapped Reads Nucleotide Content



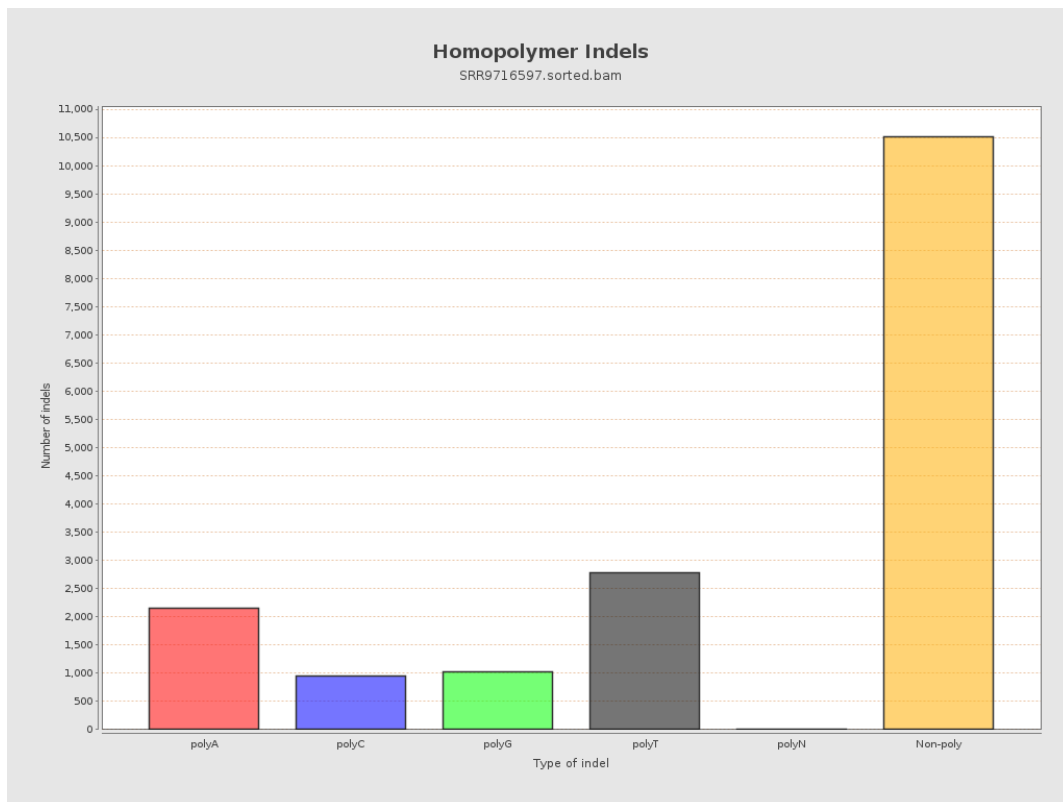
9. Results : Mapped Reads GC-content Distribution



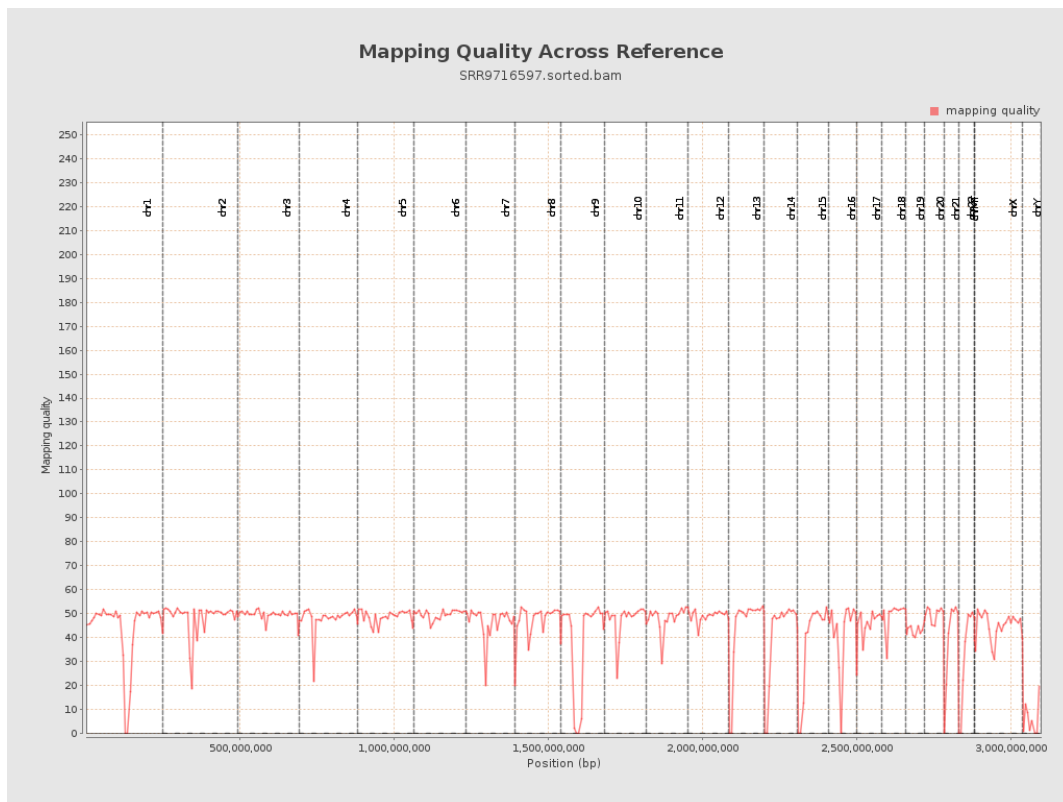
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

