Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 19:03:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236070.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_SRR6236070 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236070.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 19:03:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236070.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,204,285
Mapped reads	1,040,648 / 86.41%
Unmapped reads	163,637 / 13.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,913 / 0.49%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	38,788 / 3.22%
Duplication rate	3.04%
Clipped reads	528,173 / 43.86%

2.2. ACGT Content

Number/percentage of A's	18,276,892 / 27.02%
Number/percentage of C's	12,106,670 / 17.9%
Number/percentage of T's	21,678,103 / 32.05%
Number/percentage of G's	15,538,160 / 22.97%
Number/percentage of N's	37,726 / 0.06%
GC Percentage	40.87%

2.3. Coverage

Mean	0.0219

Standard Deviation	0.2274

2.4. Mapping Quality

Mean Mapping Quality	44.09

2.5. Mismatches and indels

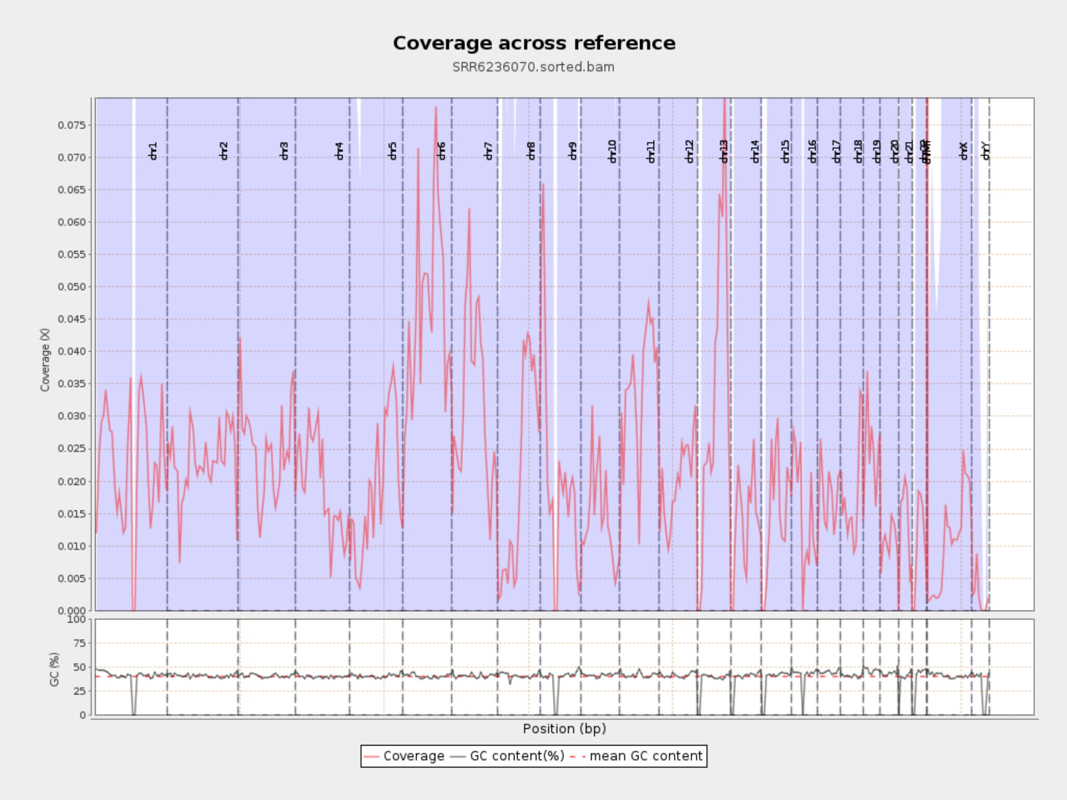
General error rate	0.83%
Mismatches	553,373
Insertions	4,751
Mapped reads with at least one insertion	0.45%
Deletions	19,935
Mapped reads with at least one deletion	1.89%
Homopolymer indels	45.92%

2.6. Chromosome stats

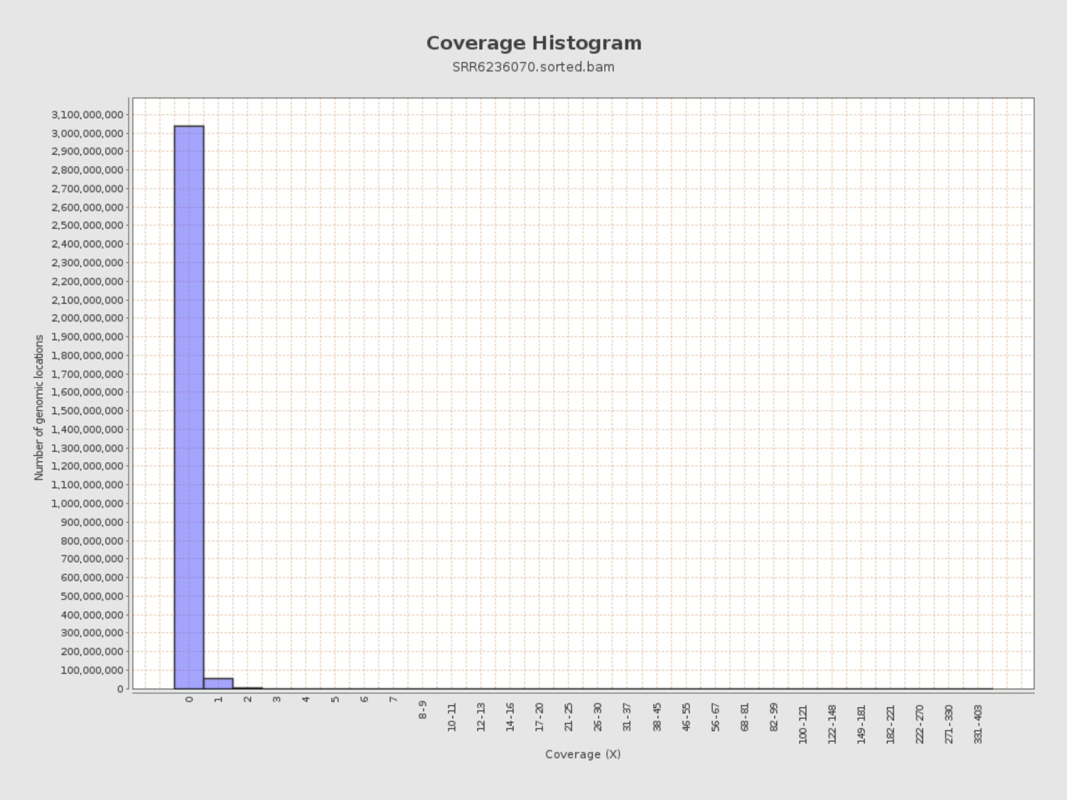
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5528456	0.0222	0.3587
chr2	243199373	5632105	0.0232	0.2203
chr3	198022430	4919762	0.0248	0.1708
chr4	191154276	3641023	0.019	0.1611
chr5	180915260	3456186	0.0191	0.1514
chr6	171115067	7896694	0.0461	0.2979
chr7	159138663	5193219	0.0326	0.4162

chr8	146364022	3013355	0.0206	0.247
chr9	141213431	2974003	0.0211	0.1957
chr10	135534747	1964436	0.0145	0.1784
chr11	135006516	4638460	0.0344	0.2469
chr12	133851895	2680152	0.02	0.1562
chr13	115169878	3848593	0.0334	0.2009
chr14	107349540	1422660	0.0133	0.1337
chr15	102531392	1559763	0.0152	0.1393
chr16	90354753	1349257	0.0149	0.1406
chr17	81195210	1434380	0.0177	0.1695
chr18	78077248	1359064	0.0174	0.2737
chr19	59128983	1490376	0.0252	0.2692
chr20	63025520	671624	0.0107	0.1163
chr21	48129895	637464	0.0132	0.1374
chr22	51304566	535119	0.0104	0.1094
chrMT	16571	41840	2.5249	2.3049
chrX	155270560	1648695	0.0106	0.1234
chrY	59373566	135808	0.0023	0.0793

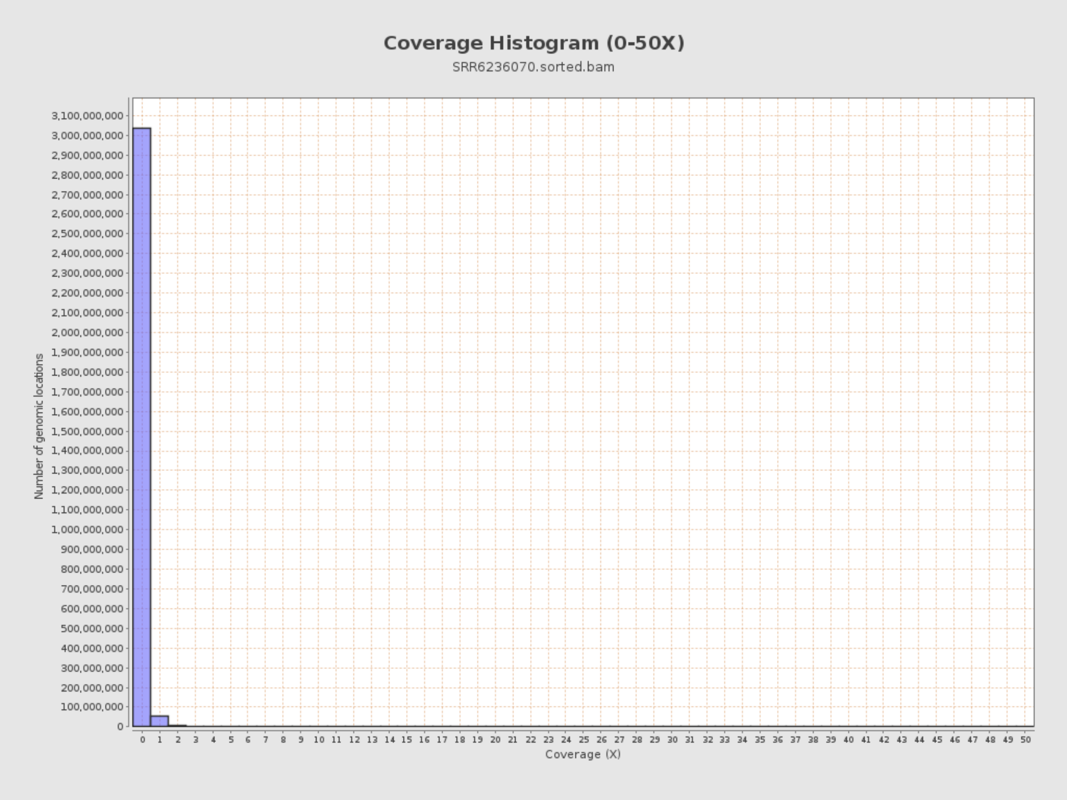
3. Results : Coverage across reference



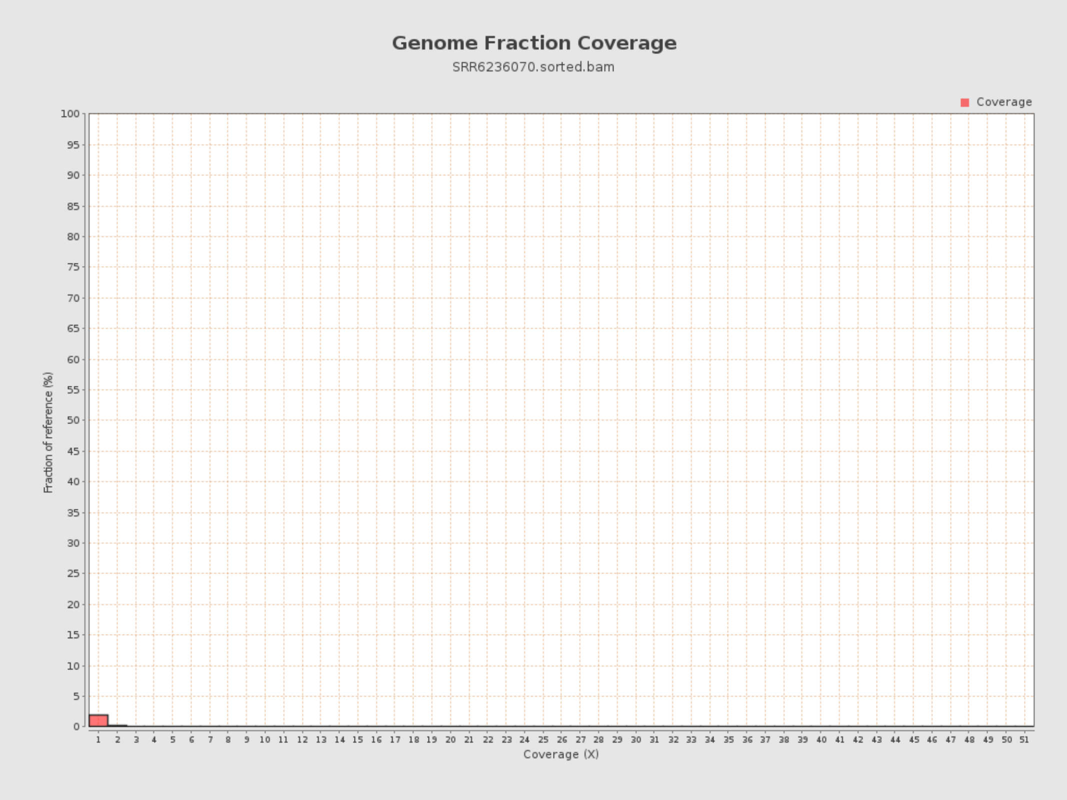
4. Results : Coverage Histogram



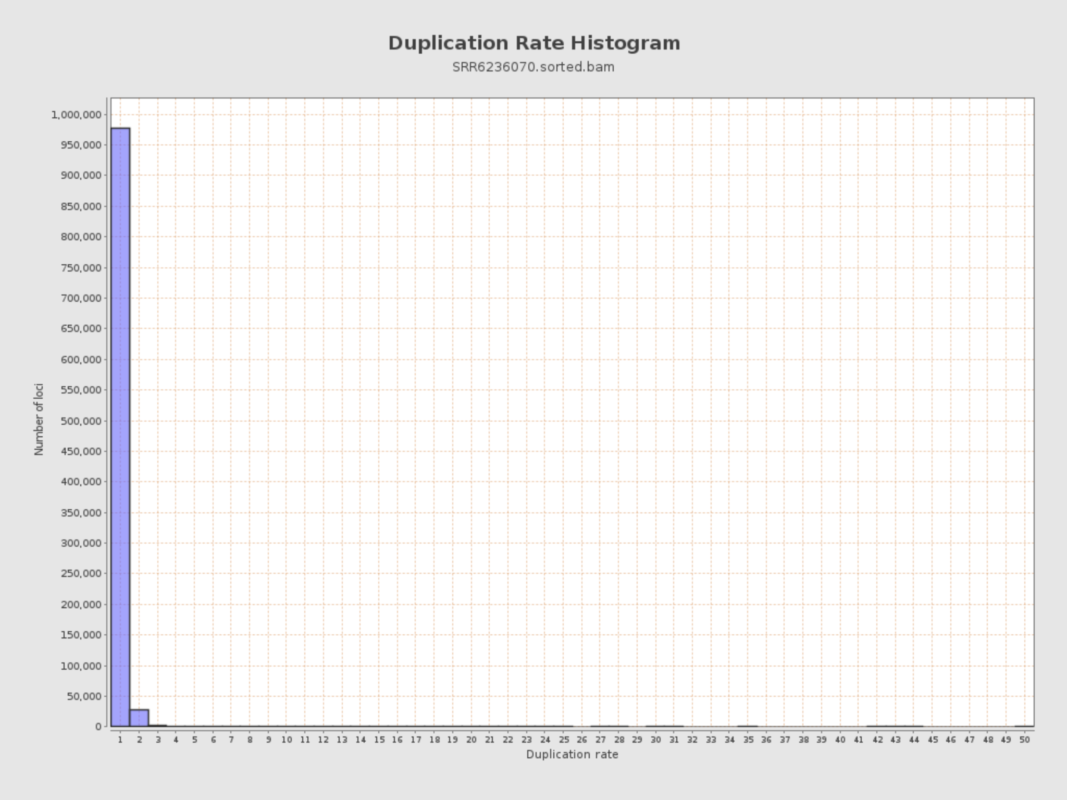
5. Results : Coverage Histogram (0-50X)



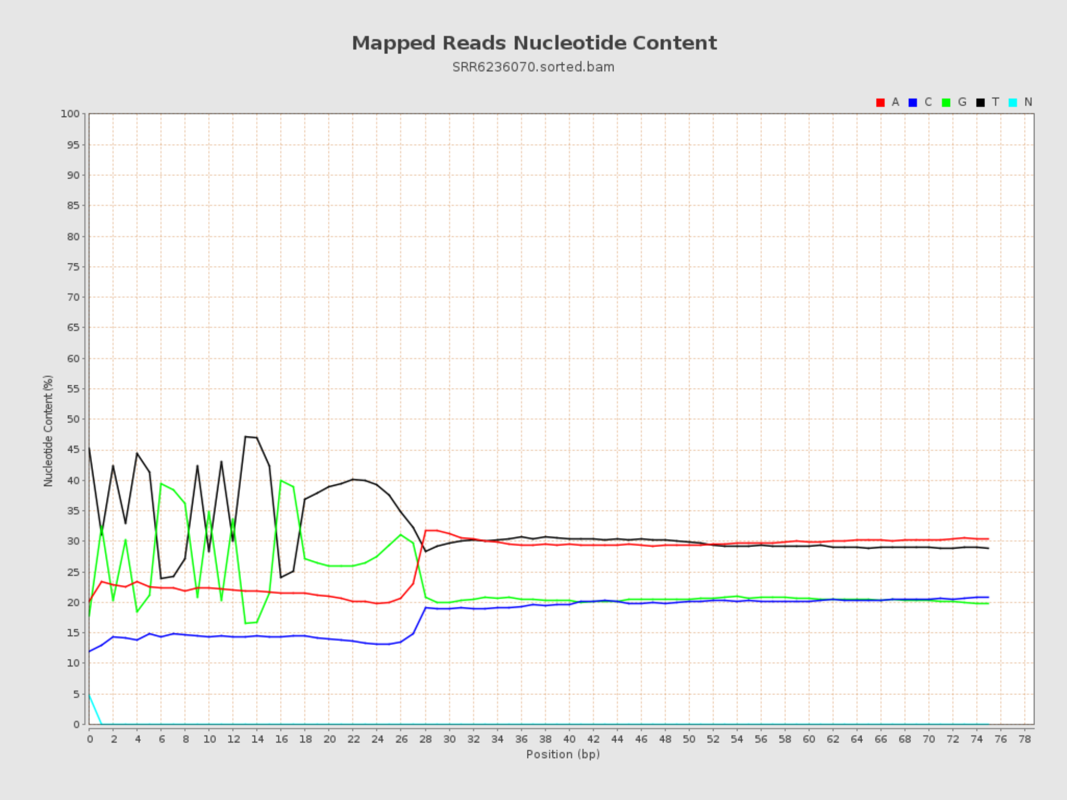
6. Results : Genome Fraction Coverage



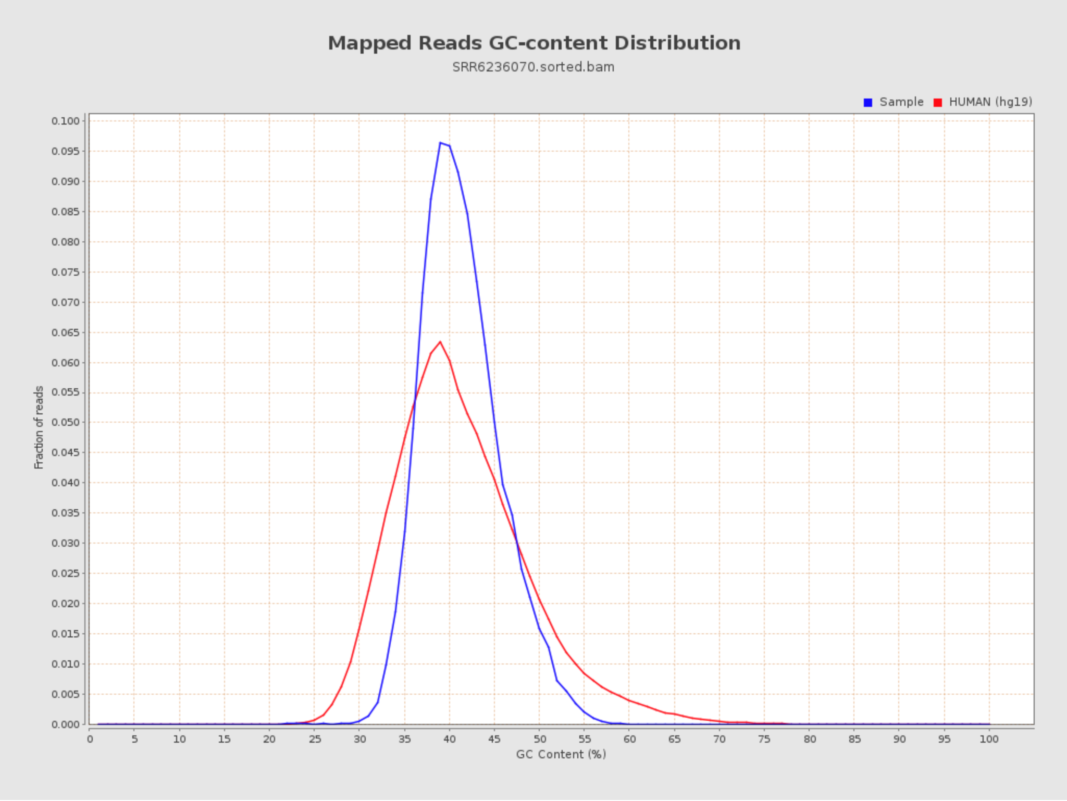
7. Results : Duplication Rate Histogram



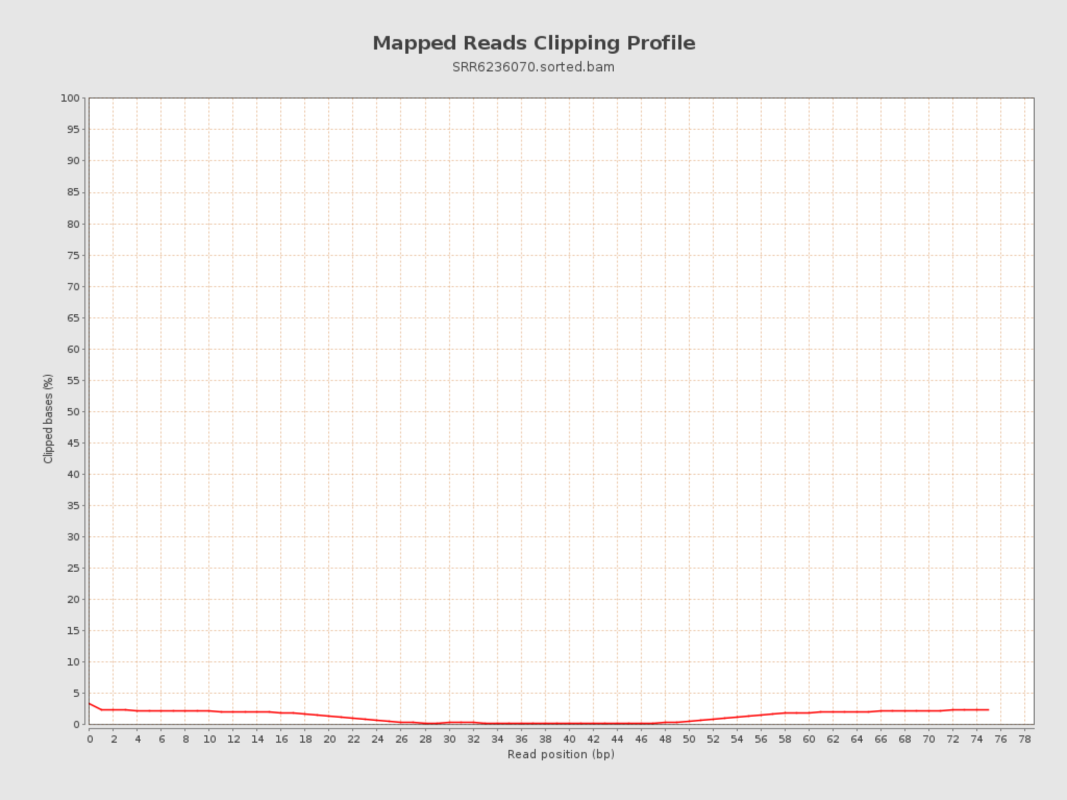
8. Results : Mapped Reads Nucleotide Content



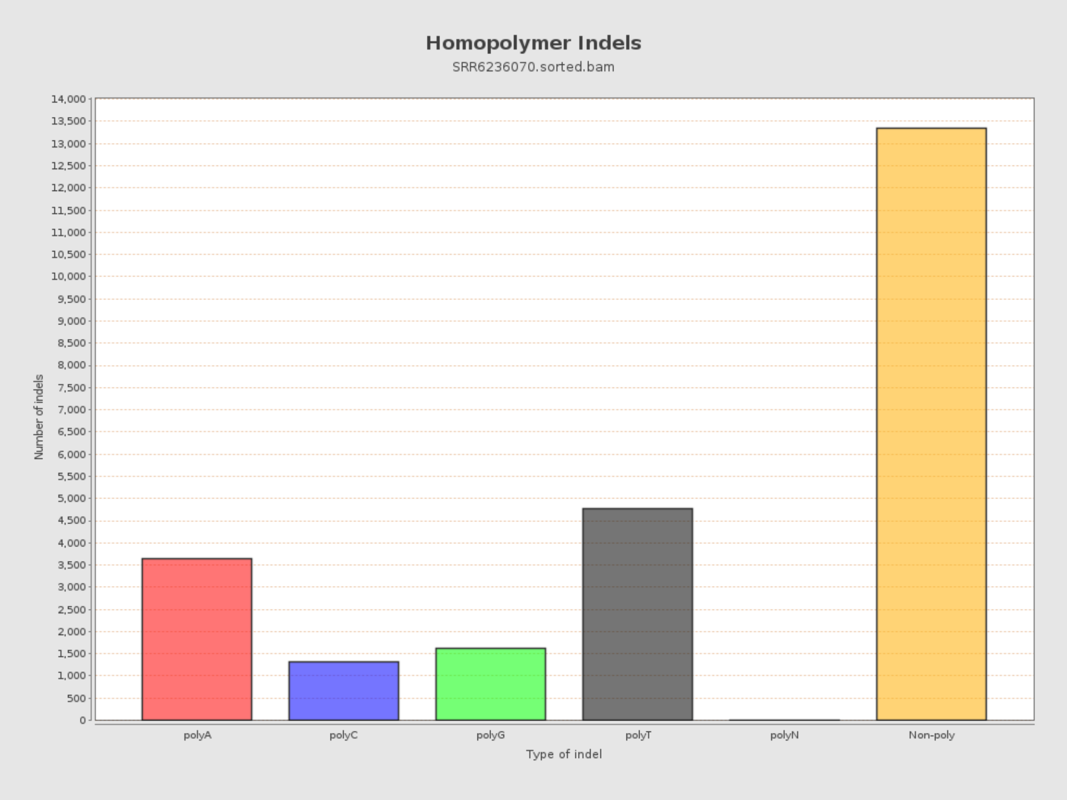
9. Results : Mapped Reads GC-content Distribution



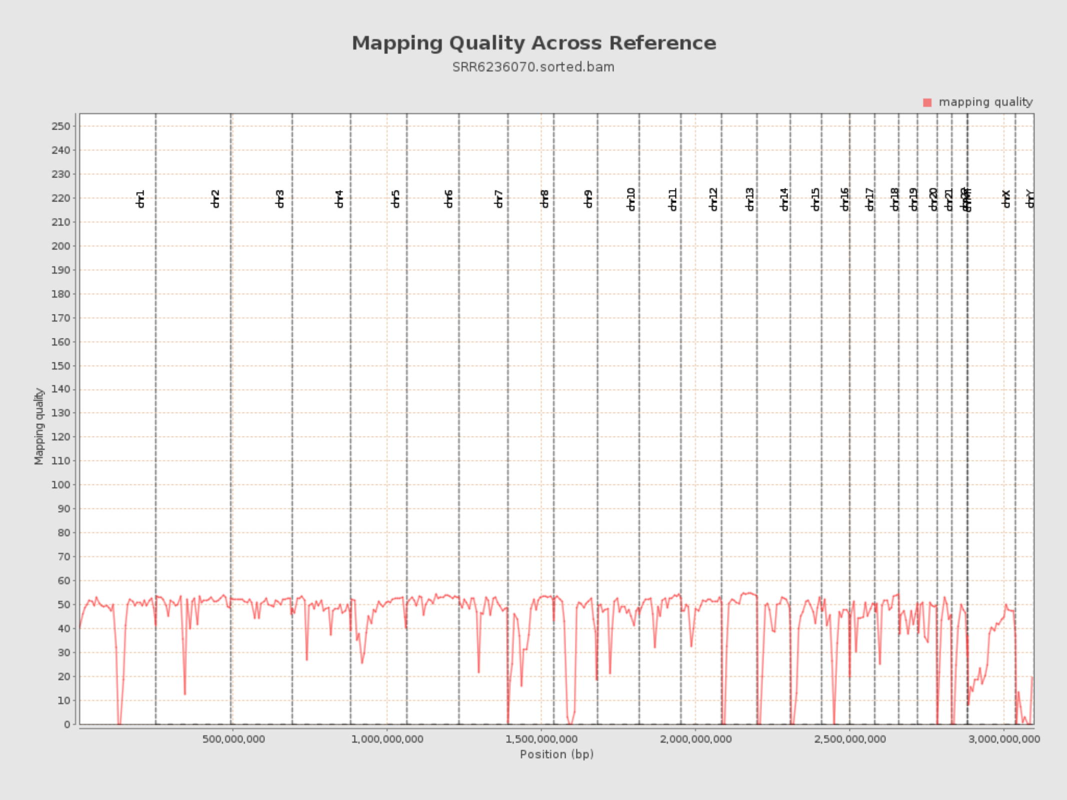
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram