Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 22:11:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237246.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_SRR6237246 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237246.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 22:11:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237246.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,851,835
Mapped reads	2,603,185 / 91.28%
Unmapped reads	248,650 / 8.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,765 / 0.8%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	133,613 / 4.69%
Duplication rate	3.47%
Clipped reads	966,429 / 33.89%

2.2. ACGT Content

Number/percentage of A's	50,994,498 / 28.54%
Number/percentage of C's	33,065,425 / 18.51%
Number/percentage of T's	56,592,344 / 31.68%
Number/percentage of G's	37,995,146 / 21.27%
Number/percentage of N's	3,024 / 0%
GC Percentage	39.78%

2.3. Coverage

Mean	0.0577

Standard Deviation	0.673

2.4. Mapping Quality

Mean Mapping Quality	46.76

2.5. Mismatches and indels

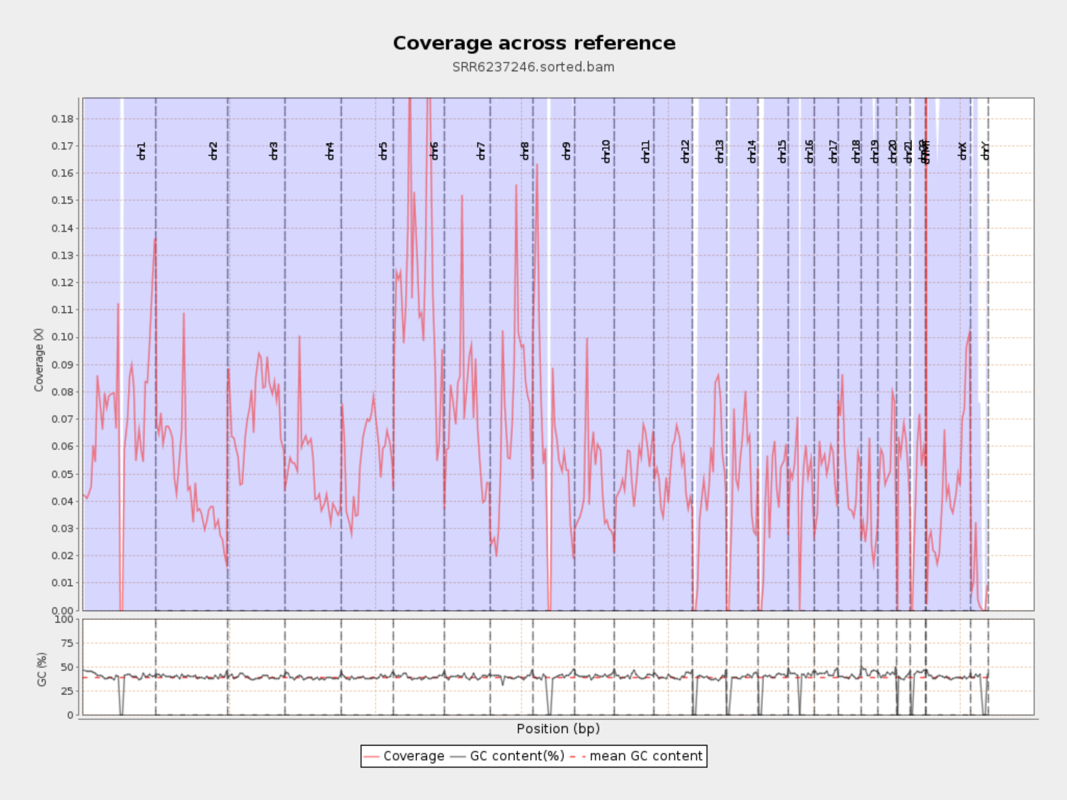
General error rate	0.79%
Mismatches	1,386,856
Insertions	15,534
Mapped reads with at least one insertion	0.59%
Deletions	41,971
Mapped reads with at least one deletion	1.59%
Homopolymer indels	47.71%

2.6. Chromosome stats

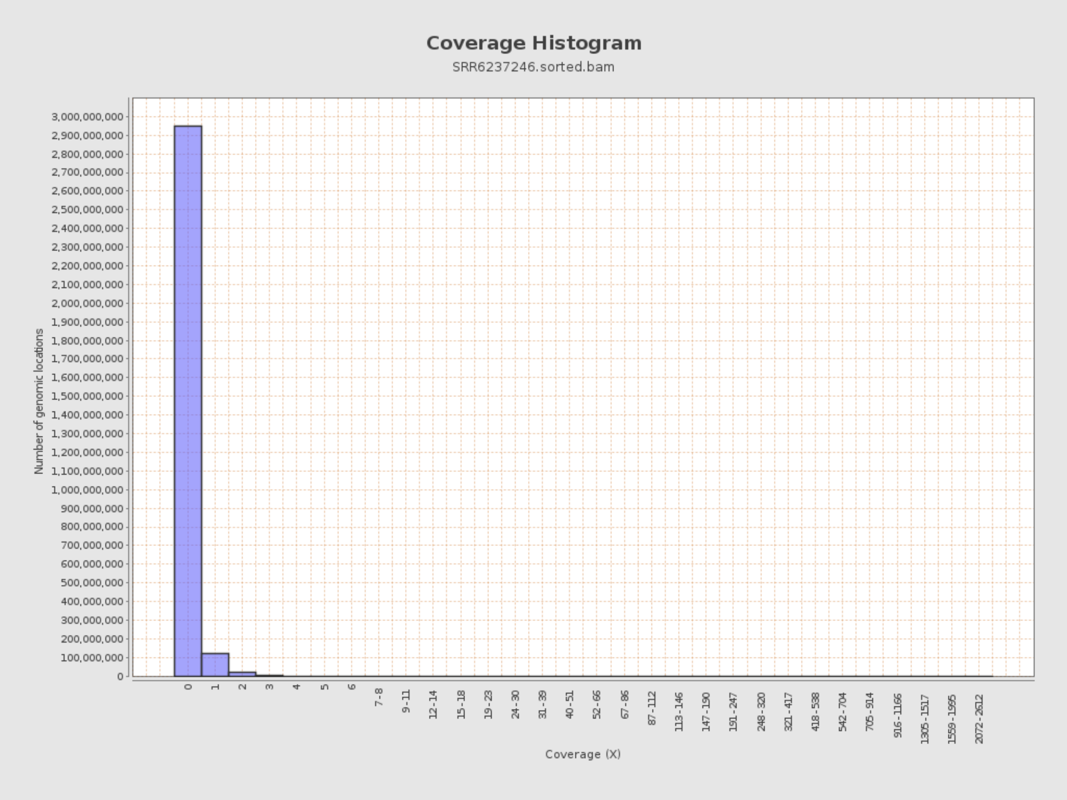
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17452445	0.07	1.0283
chr2	243199373	11610240	0.0477	0.557
chr3	198022430	14491508	0.0732	0.314
chr4	191154276	9494346	0.0497	0.3535
chr5	180915260	10170377	0.0562	0.278
chr6	171115067	20751662	0.1213	0.7693
chr7	159138663	11493160	0.0722	0.9945

chr8	146364022	10290899	0.0703	1.6908
chr9	141213431	8791493	0.0623	0.5667
chr10	135534747	6113903	0.0451	0.5499
chr11	135006516	7018926	0.052	0.4523
chr12	133851895	6615084	0.0494	0.2812
chr13	115169878	5324420	0.0462	0.2512
chr14	107349540	4840139	0.0451	0.3022
chr15	102531392	4037549	0.0394	0.228
chr16	90354753	4138984	0.0458	0.3273
chr17	81195210	4070392	0.0501	0.3446
chr18	78077248	4185099	0.0536	1.1391
chr19	59128983	1866158	0.0316	0.6634
chr20	63025520	3640141	0.0578	0.2973
chr21	48129895	2532002	0.0526	0.3481
chr22	51304566	2208051	0.043	0.2359
chrMT	16571	128878	7.7773	5.6544
chrX	155270560	6973928	0.0449	0.3007
chrY	59373566	480078	0.0081	0.2645

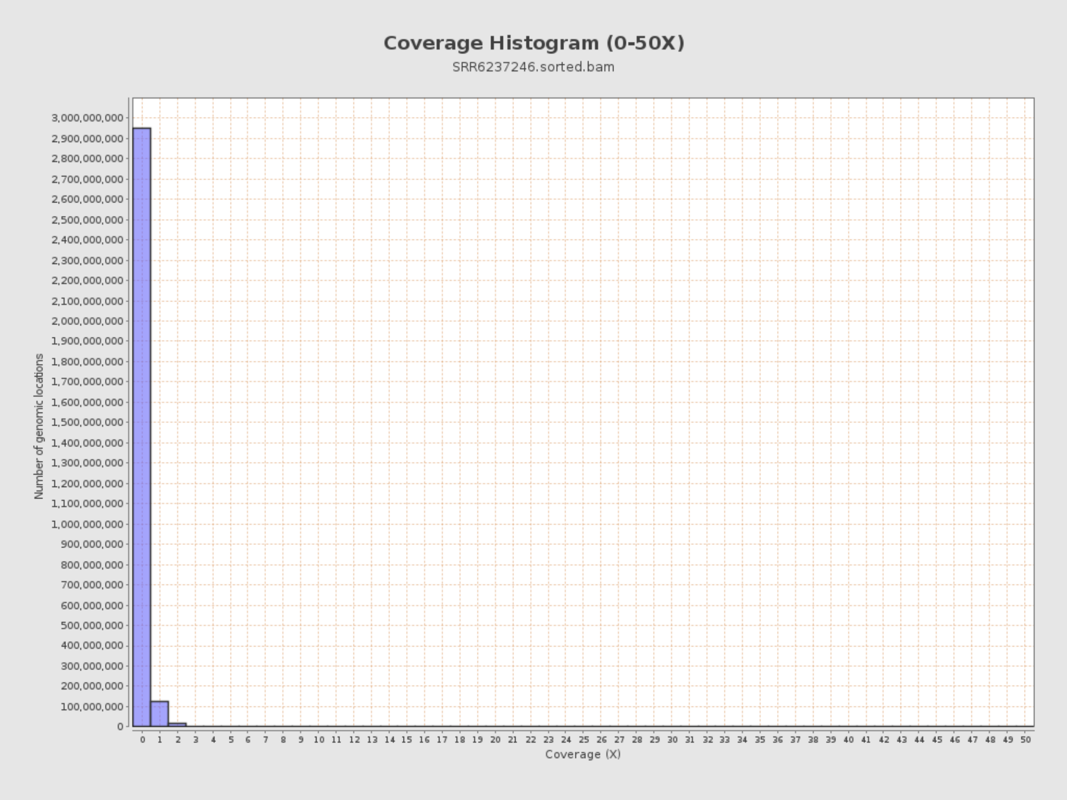
3. Results : Coverage across reference



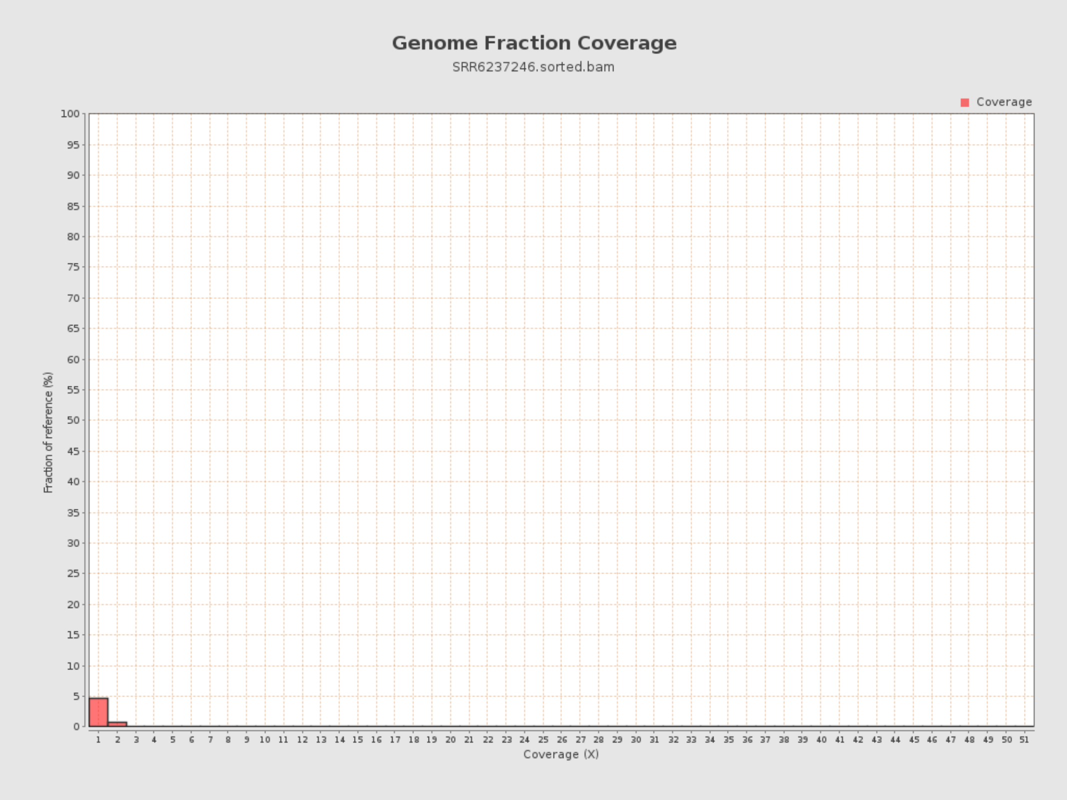
4. Results : Coverage Histogram



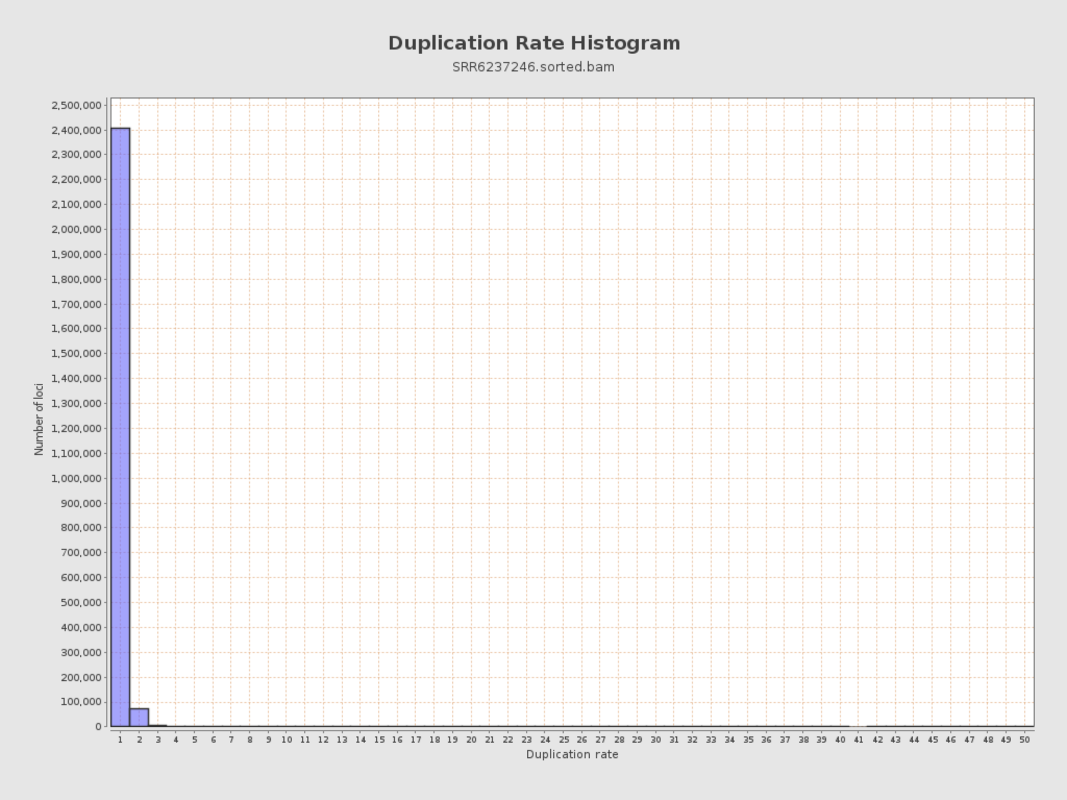
5. Results : Coverage Histogram (0-50X)



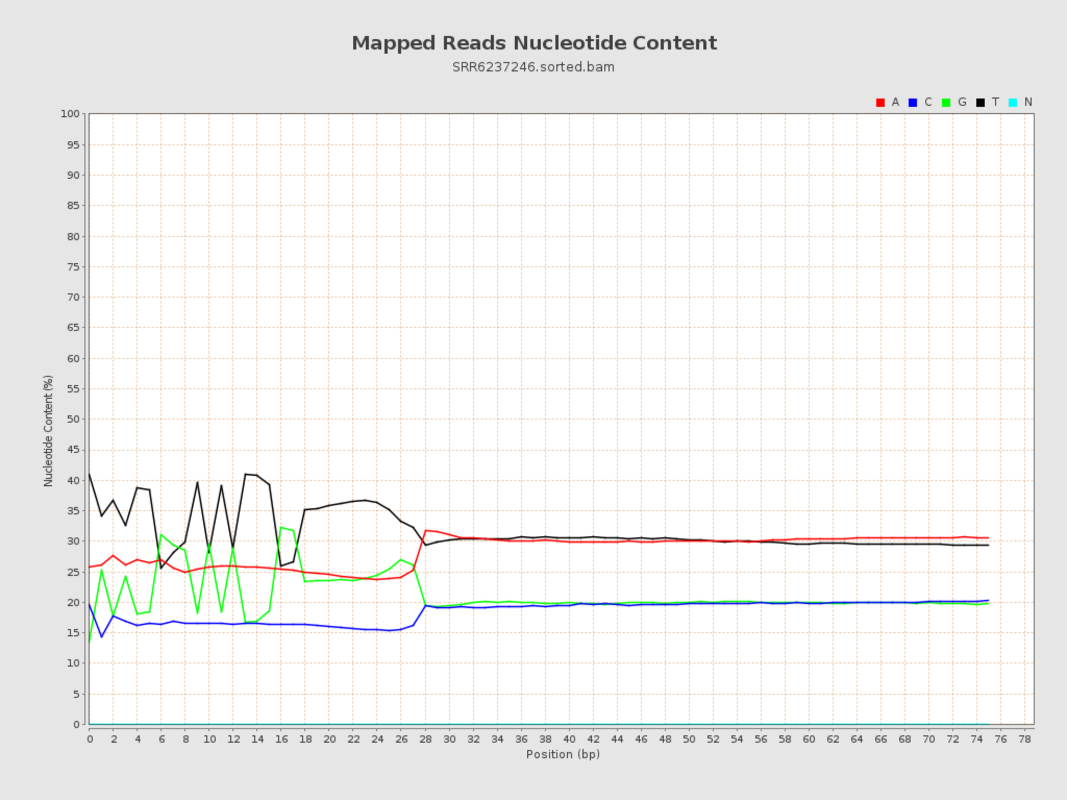
6. Results : Genome Fraction Coverage



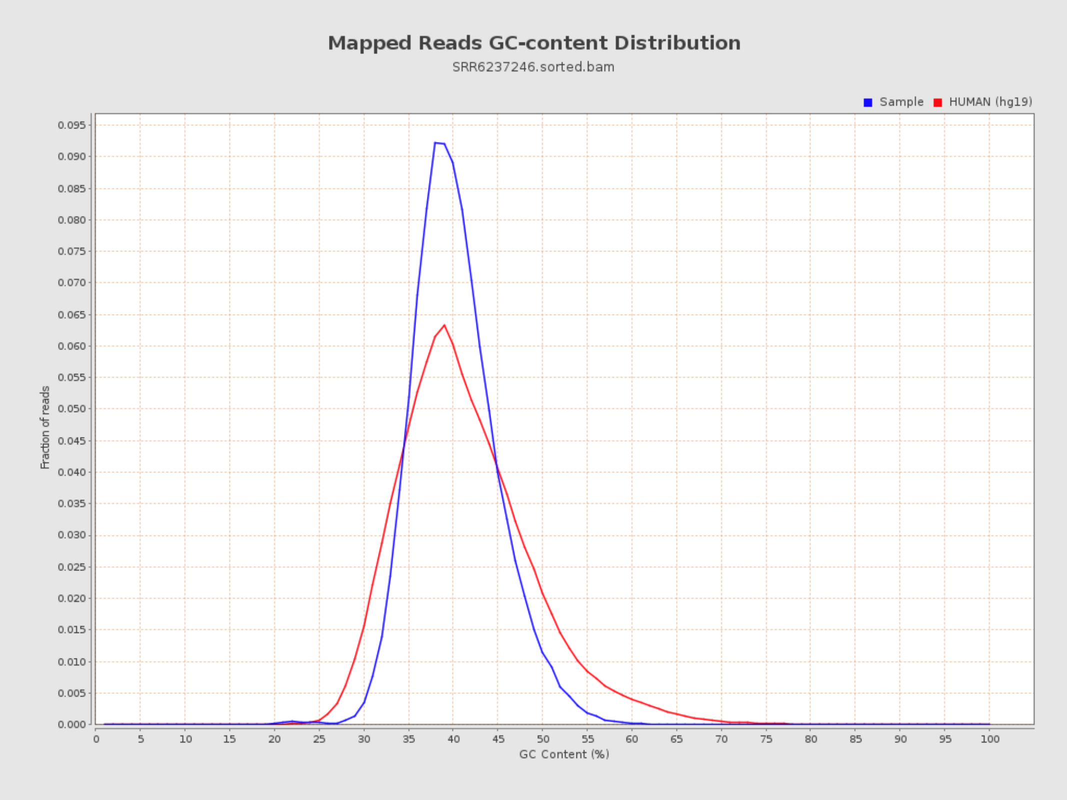
7. Results : Duplication Rate Histogram



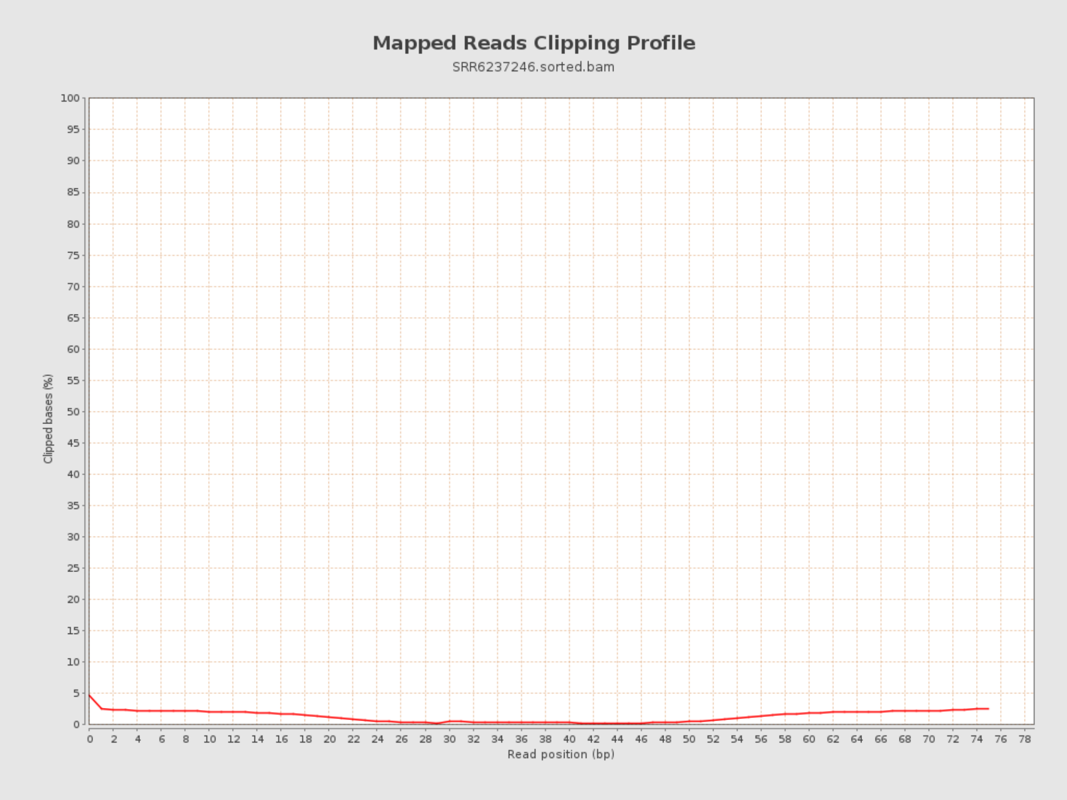
8. Results : Mapped Reads Nucleotide Content



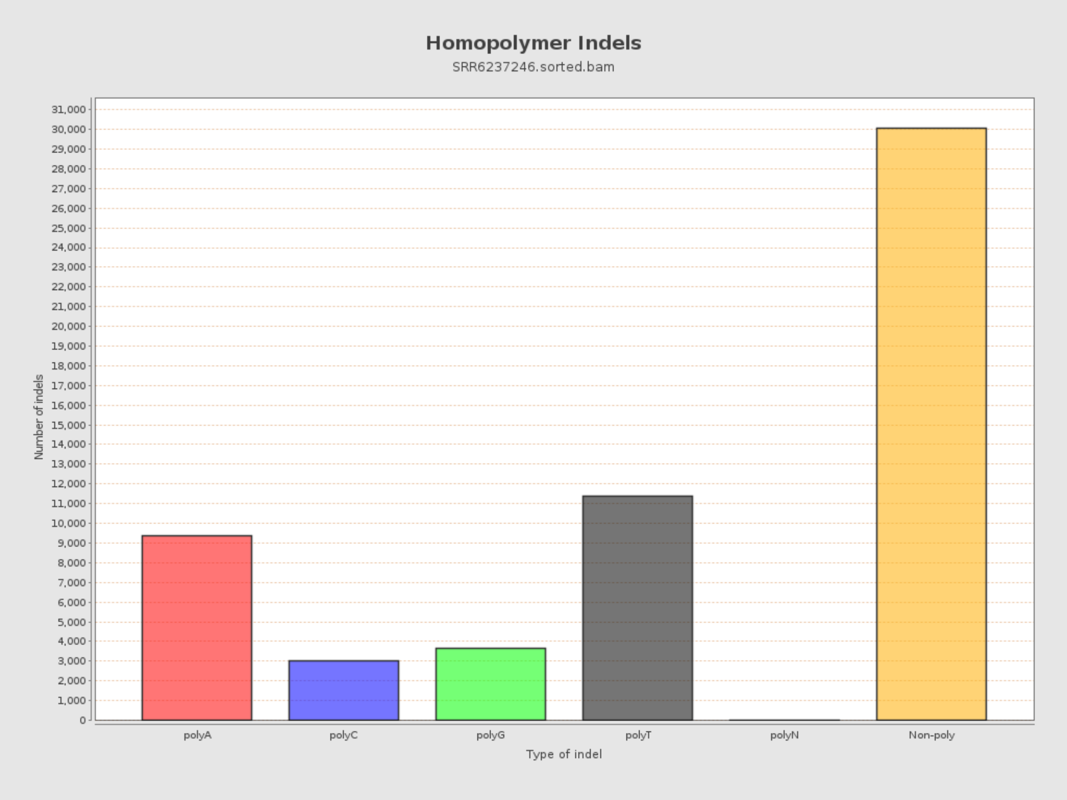
9. Results : Mapped Reads GC-content Distribution



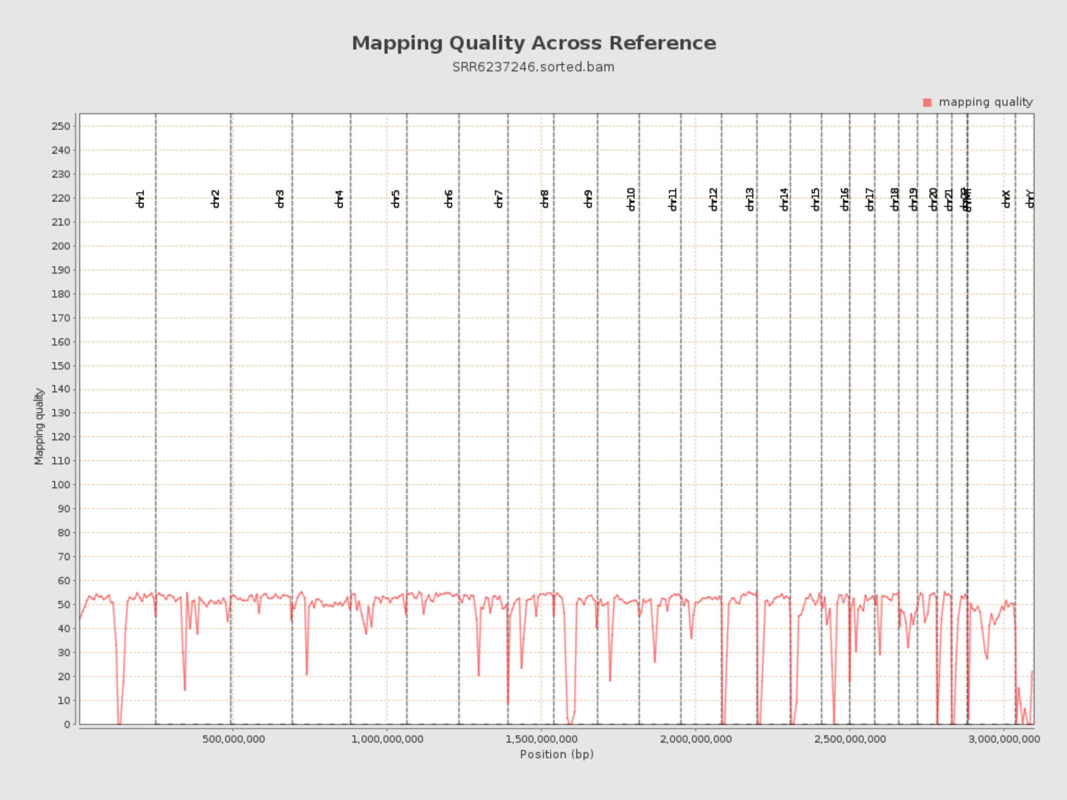
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram