Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 20:35:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236100.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_SRR6236100 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236100.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 20:35:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236100.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,609,768
Mapped reads	476,941 / 29.63%
Unmapped reads	1,132,827 / 70.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,143 / 0.2%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	27,499 / 1.71%
Duplication rate	4.9%
Clipped reads	228,874 / 14.22%

2.2. ACGT Content

Number/percentage of A's	8,559,059 / 27.41%
Number/percentage of C's	5,561,684 / 17.81%
Number/percentage of T's	10,148,049 / 32.5%
Number/percentage of G's	6,942,552 / 22.23%
Number/percentage of N's	12,673 / 0.04%
GC Percentage	40.05%

2.3. Coverage

Mean	0.0101

Standard Deviation	0.1605

2.4. Mapping Quality

Mean Mapping Quality	46.18

2.5. Mismatches and indels

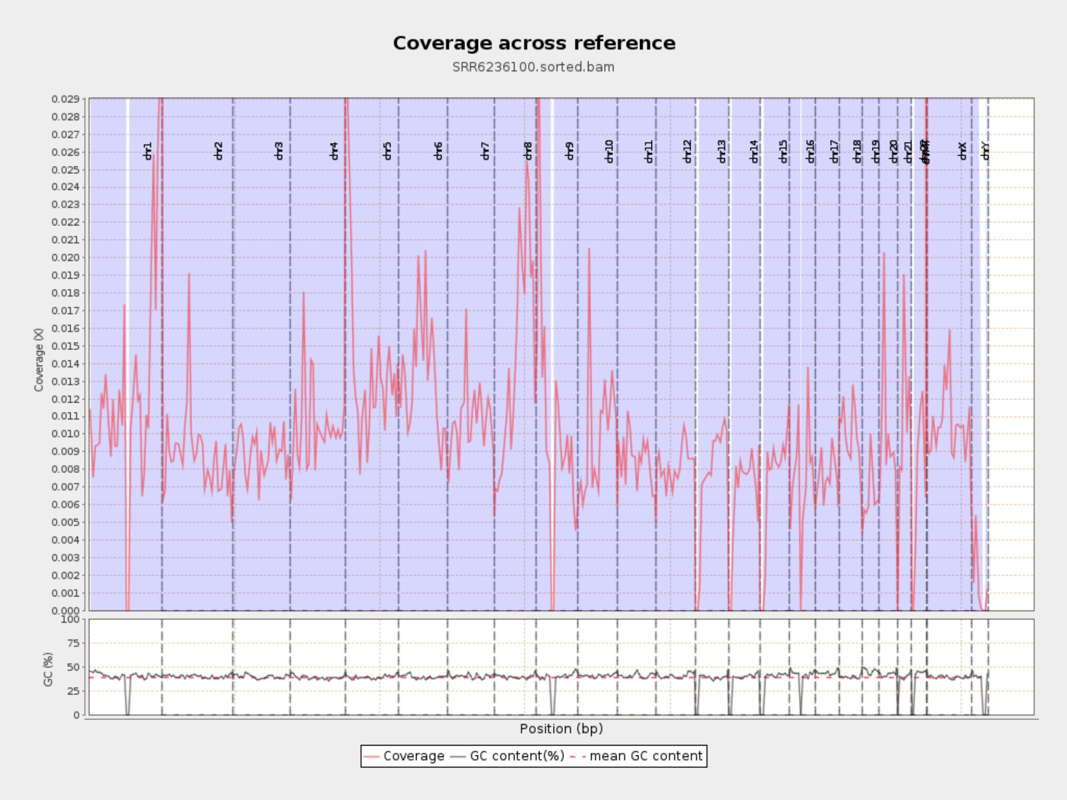
General error rate	0.84%
Mismatches	257,251
Insertions	2,388
Mapped reads with at least one insertion	0.5%
Deletions	7,523
Mapped reads with at least one deletion	1.56%
Homopolymer indels	48.32%

2.6. Chromosome stats

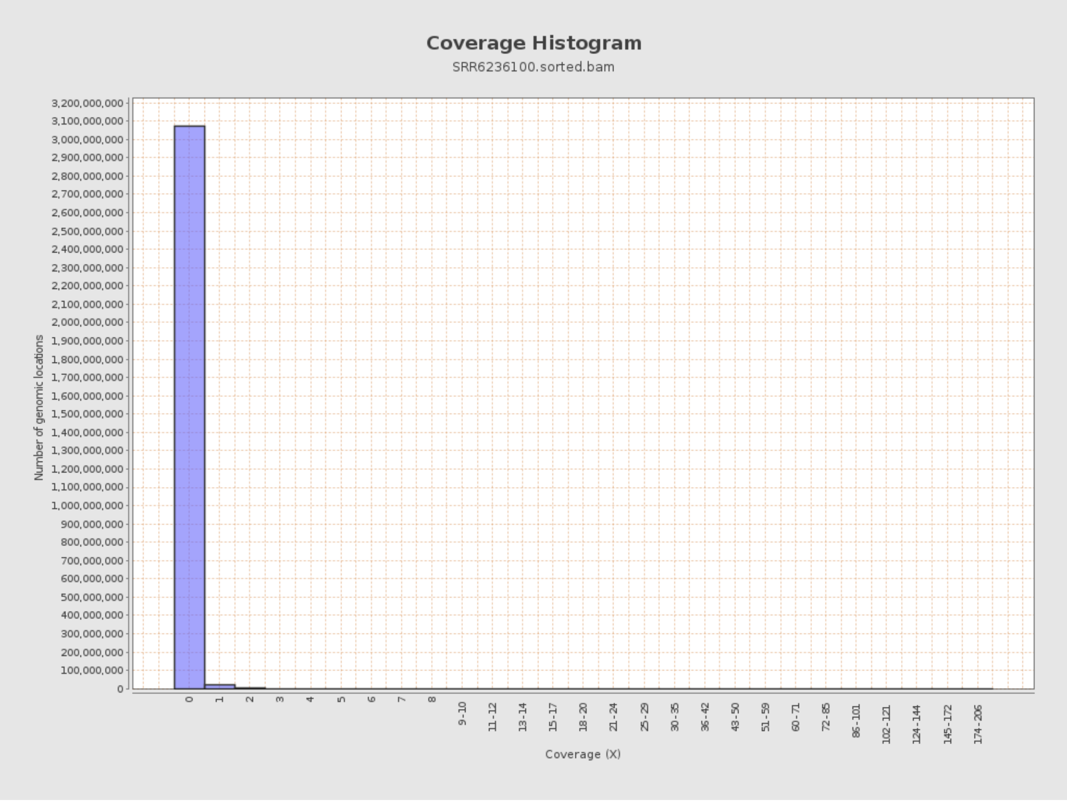
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3099224	0.0124	0.2252
chr2	243199373	2160979	0.0089	0.1446
chr3	198022430	1766922	0.0089	0.113
chr4	191154276	1991294	0.0104	0.1291
chr5	180915260	2517637	0.0139	0.1433
chr6	171115067	2268209	0.0133	0.1471
chr7	159138663	1731910	0.0109	0.1542

chr8	146364022	2110820	0.0144	0.1683
chr9	141213431	1536367	0.0109	0.1405
chr10	135534747	1337873	0.0099	0.1506
chr11	135006516	1153237	0.0085	0.1195
chr12	133851895	1108559	0.0083	0.1093
chr13	115169878	857433	0.0074	0.106
chr14	107349540	692983	0.0065	0.0971
chr15	102531392	726506	0.0071	0.1023
chr16	90354753	678536	0.0075	0.1056
chr17	81195210	614554	0.0076	0.1071
chr18	78077248	795822	0.0102	0.1734
chr19	59128983	392544	0.0066	0.1519
chr20	63025520	638589	0.0101	0.1213
chr21	48129895	498934	0.0104	0.1263
chr22	51304566	357786	0.007	0.0986
chrMT	16571	472827	28.5334	15.7761
chrX	155270560	1639388	0.0106	0.1262
chrY	59373566	88546	0.0015	0.0624

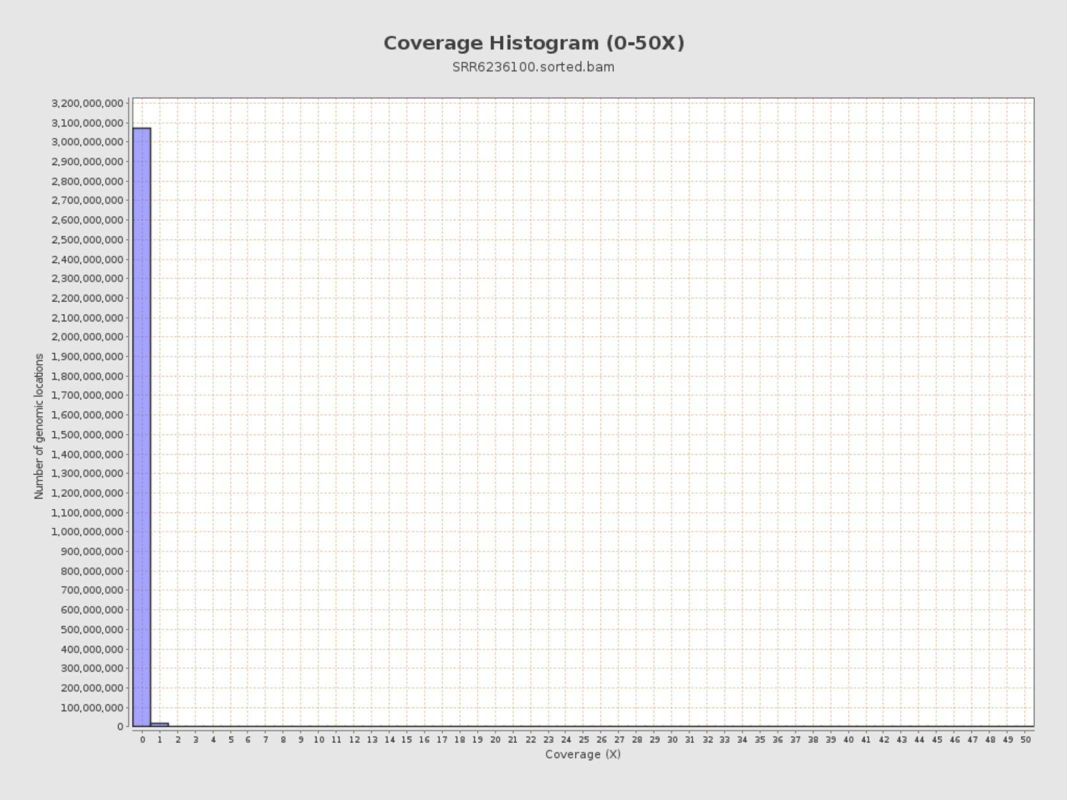
3. Results : Coverage across reference



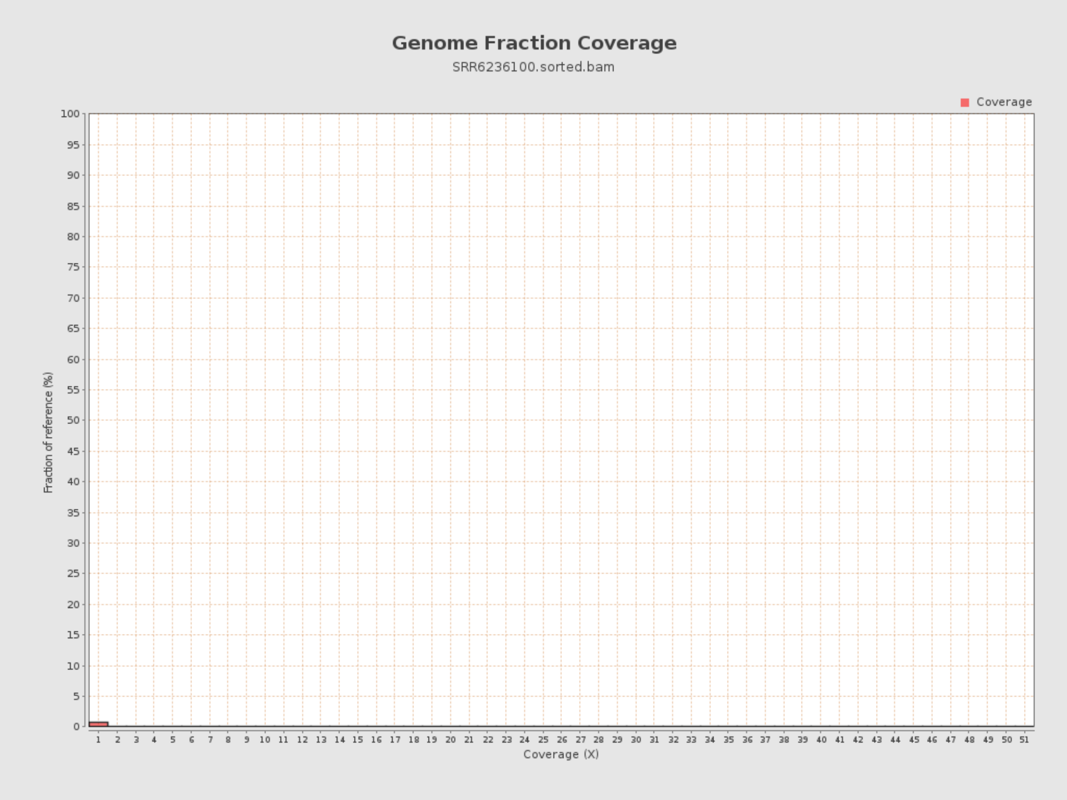
4. Results : Coverage Histogram



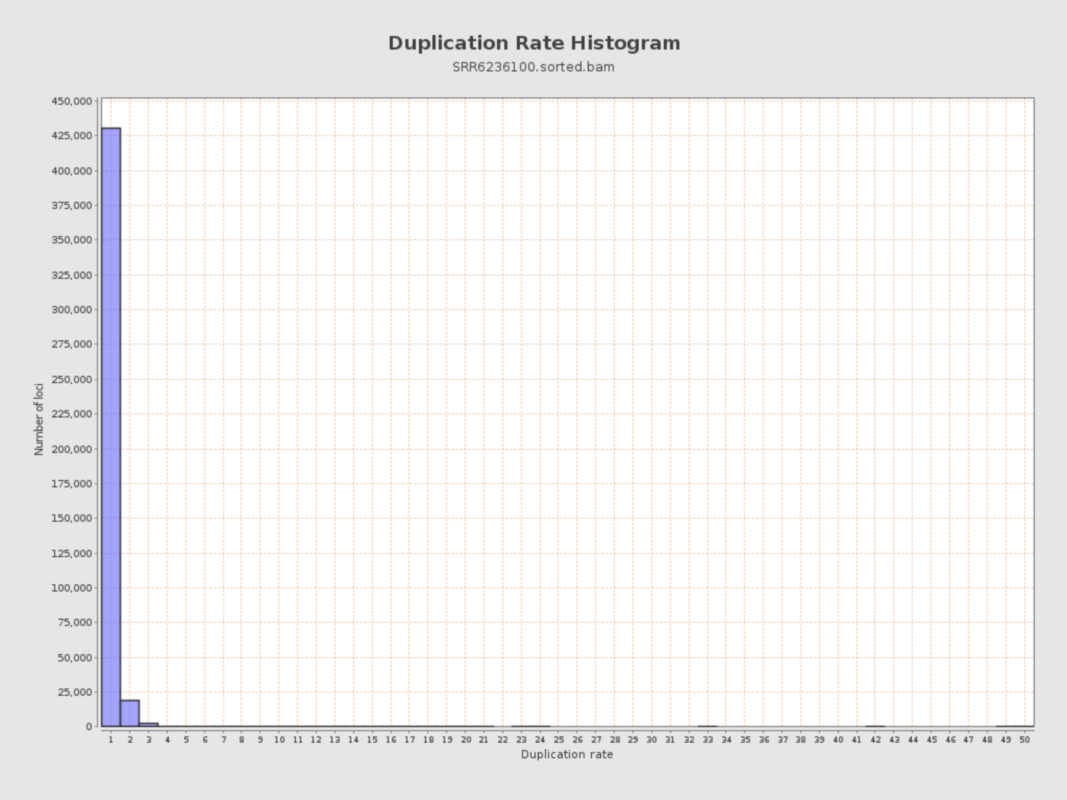
5. Results : Coverage Histogram (0-50X)



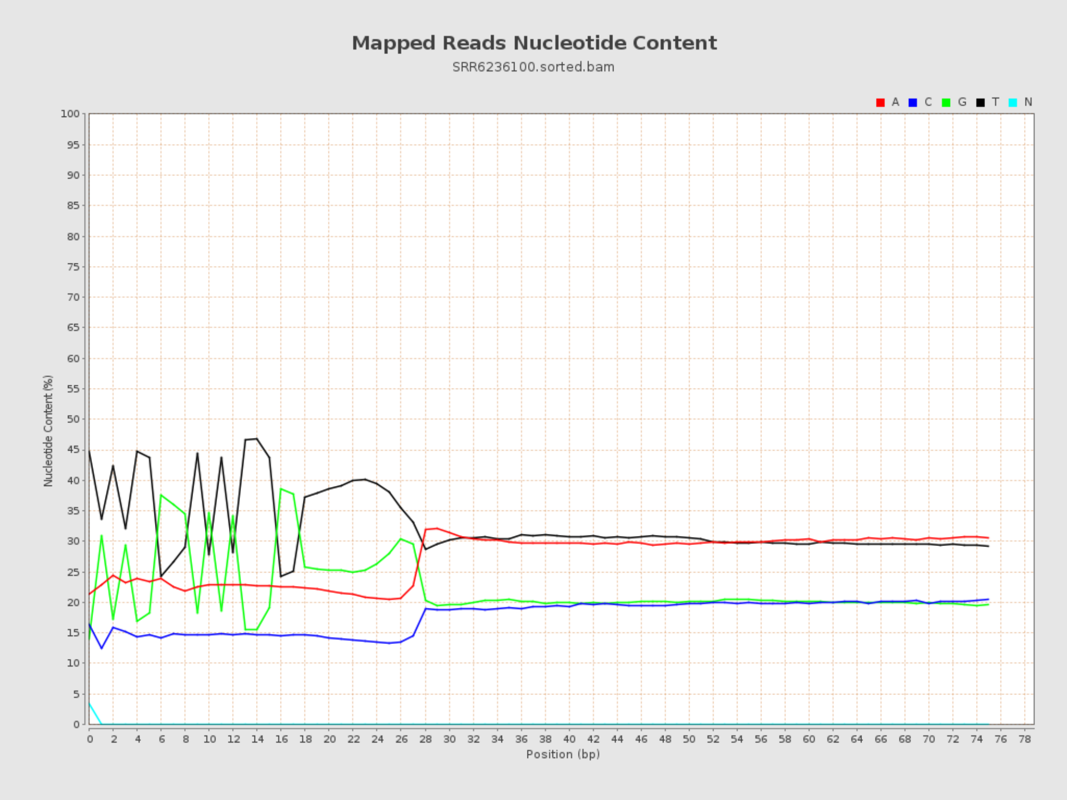
6. Results : Genome Fraction Coverage



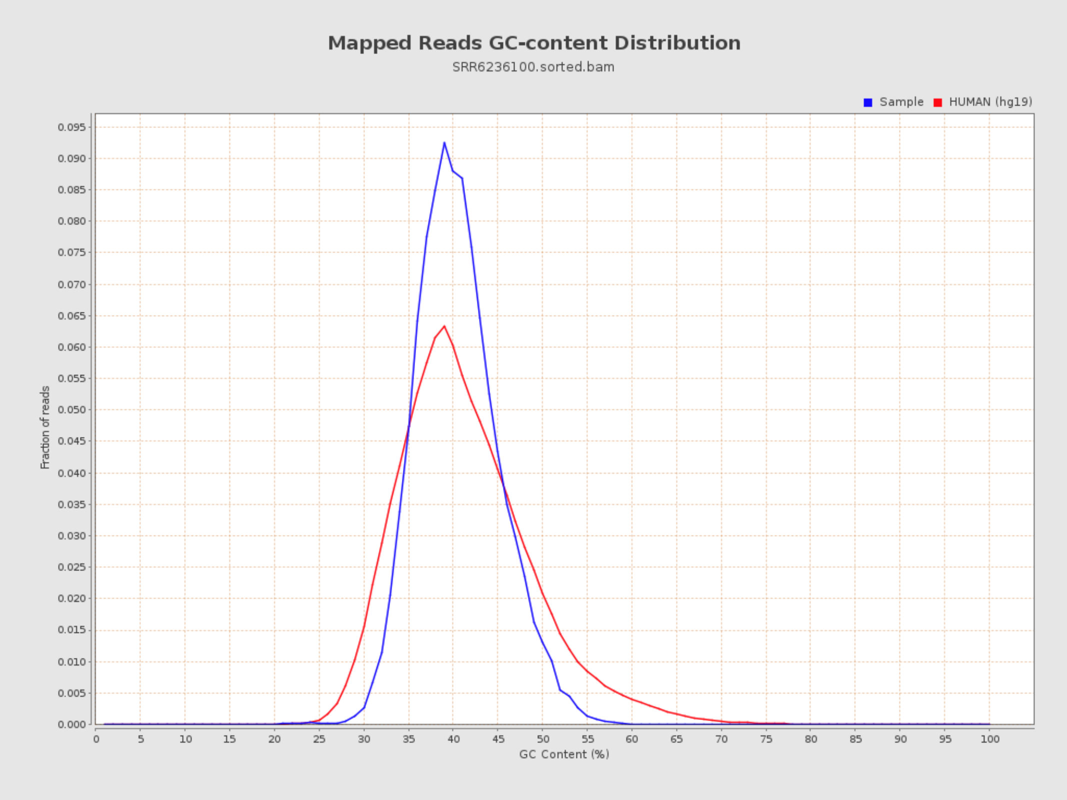
7. Results : Duplication Rate Histogram



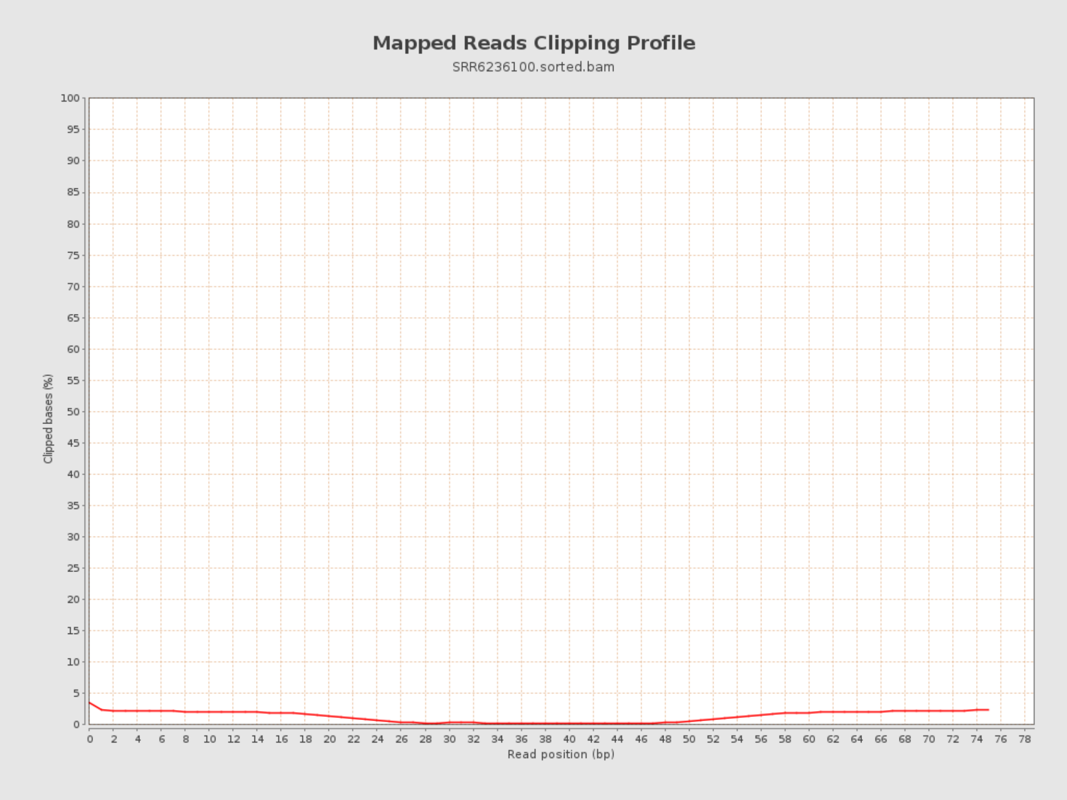
8. Results : Mapped Reads Nucleotide Content



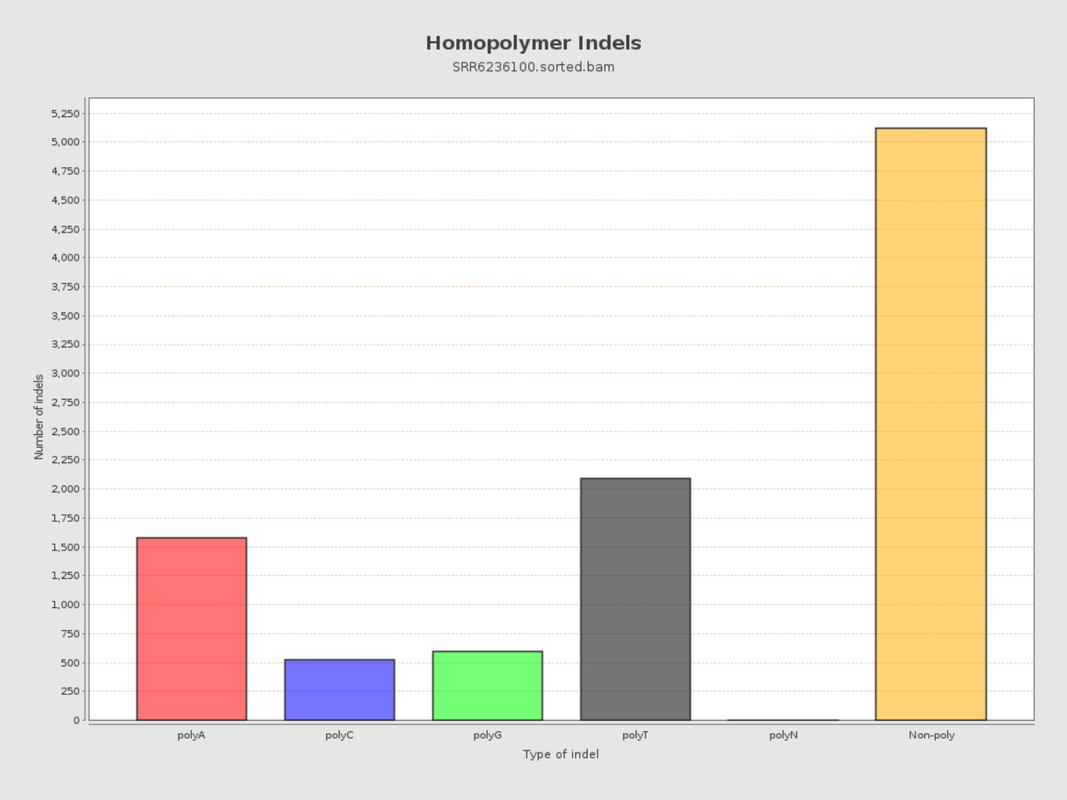
9. Results : Mapped Reads GC-content Distribution



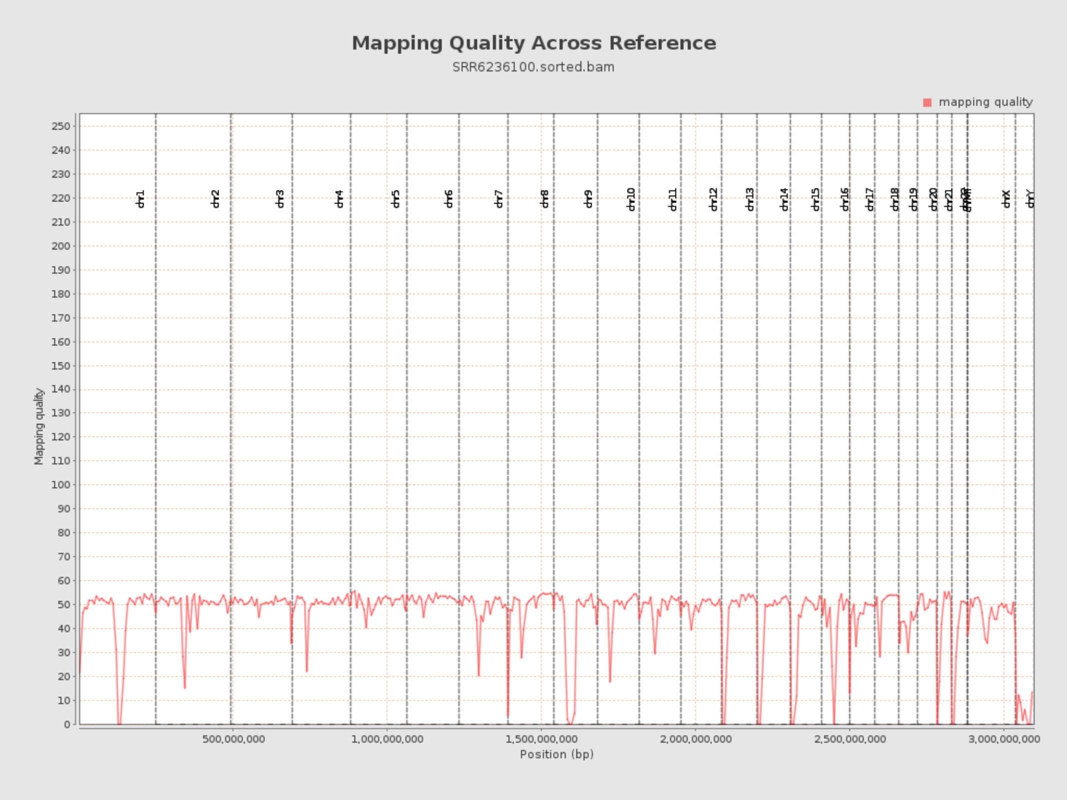
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram