Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 21:44:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236124.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_SRR6236124 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236124.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 21:44:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236124.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,147,735
Mapped reads	1,811,419 / 84.34%
Unmapped reads	336,316 / 15.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,553 / 0.58%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	113,330 / 5.28%
Duplication rate	5.13%
Clipped reads	846,142 / 39.4%

2.2. ACGT Content

Number/percentage of A's	32,583,552 / 27.35%
Number/percentage of C's	21,308,580 / 17.88%
Number/percentage of T's	38,634,644 / 32.43%
Number/percentage of G's	26,571,301 / 22.3%
Number/percentage of N's	48,251 / 0.04%
GC Percentage	40.19%

2.3. Coverage

Mean	0.0385

Standard Deviation	0.3904

2.4. Mapping Quality

Mean Mapping Quality	45.15

2.5. Mismatches and indels

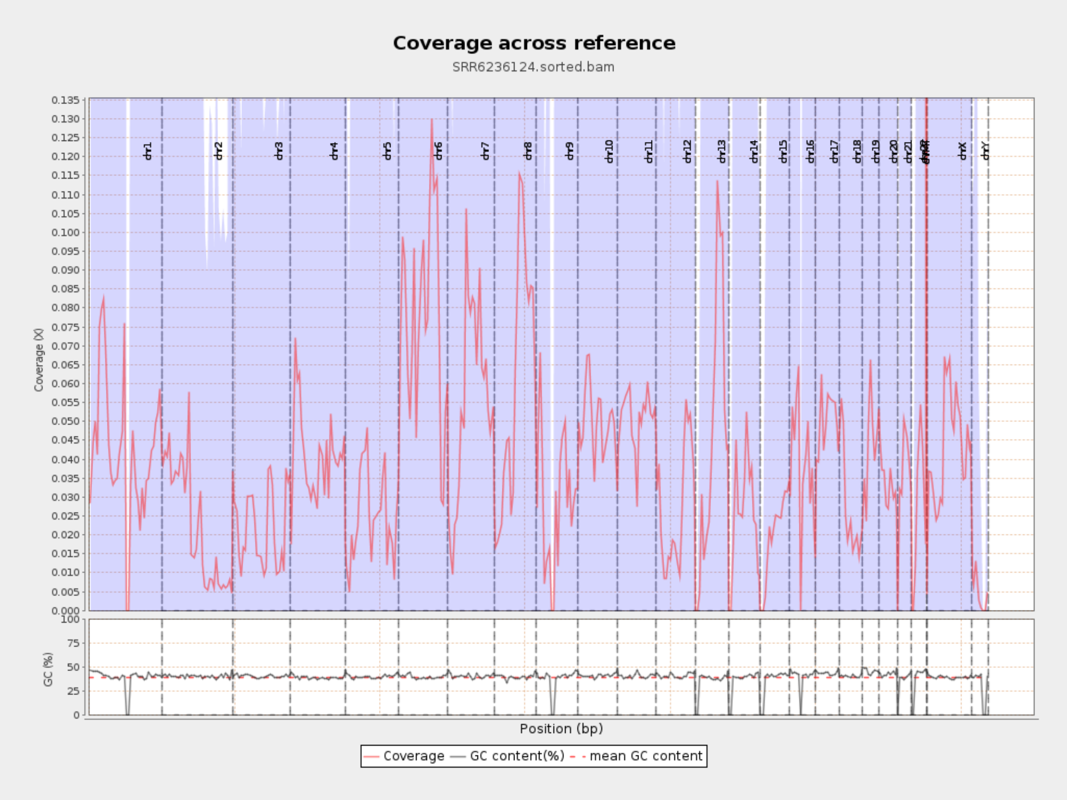
General error rate	0.81%
Mismatches	951,044
Insertions	8,316
Mapped reads with at least one insertion	0.45%
Deletions	34,232
Mapped reads with at least one deletion	1.87%
Homopolymer indels	46.6%

2.6. Chromosome stats

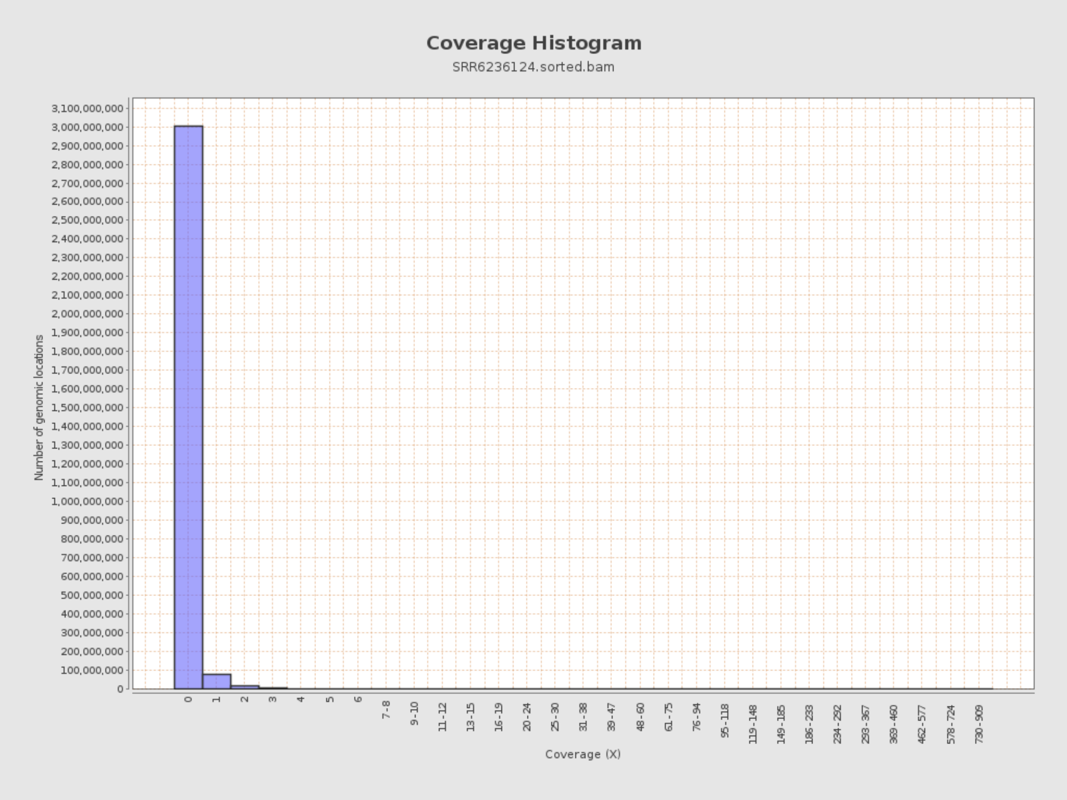
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10549014	0.0423	0.7491
chr2	243199373	5534518	0.0228	0.3387
chr3	198022430	4314419	0.0218	0.1785
chr4	191154276	7859083	0.0411	0.2532
chr5	180915260	4429156	0.0245	0.1919
chr6	171115067	13114436	0.0766	0.4218
chr7	159138663	8919931	0.0561	0.6325

chr8	146364022	8770889	0.0599	0.6535
chr9	141213431	4064059	0.0288	0.2569
chr10	135534747	6788393	0.0501	0.3263
chr11	135006516	6840057	0.0507	0.335
chr12	133851895	3621294	0.0271	0.2015
chr13	115169878	5222310	0.0453	0.2605
chr14	107349540	2731163	0.0254	0.1993
chr15	102531392	1994703	0.0195	0.1731
chr16	90354753	3488572	0.0386	0.2457
chr17	81195210	4064607	0.0501	0.3387
chr18	78077248	2118687	0.0271	0.3553
chr19	59128983	2589511	0.0438	0.5268
chr20	63025520	2102638	0.0334	0.2235
chr21	48129895	1697274	0.0353	0.232
chr22	51304566	1368845	0.0267	0.1944
chrMT	16571	154568	9.3276	5.9487
chrX	155270560	6609451	0.0426	0.264
chrY	59373566	258814	0.0044	0.0972

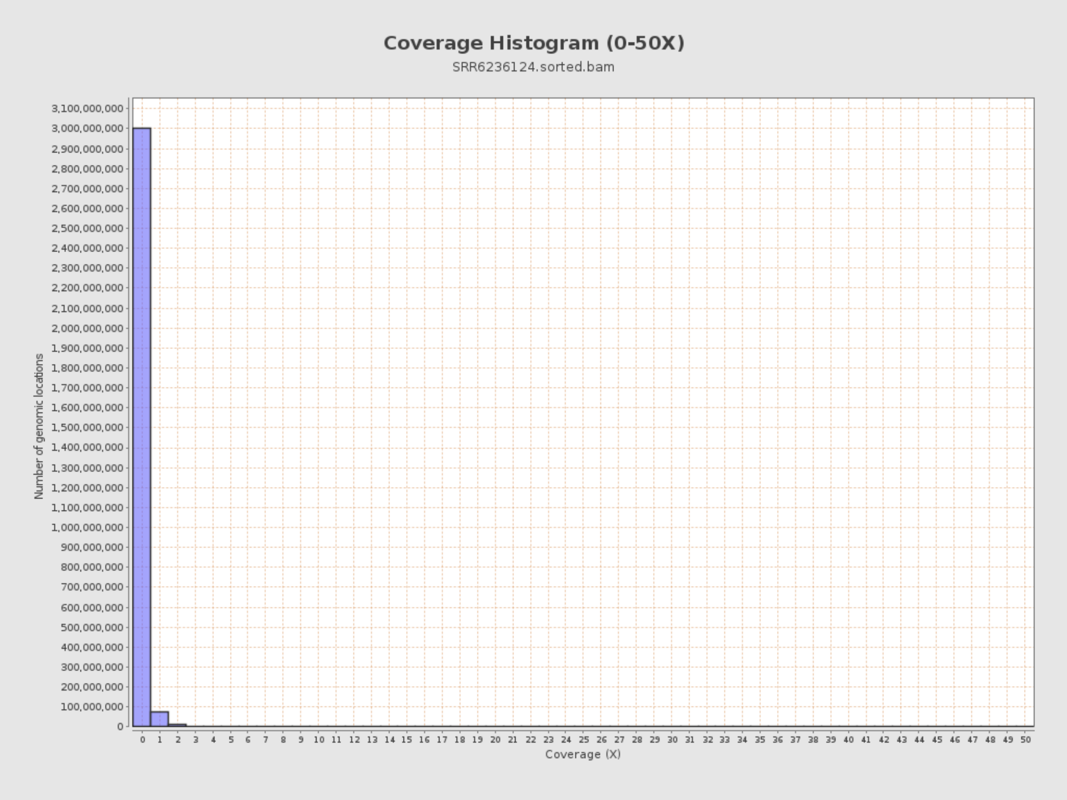
3. Results : Coverage across reference



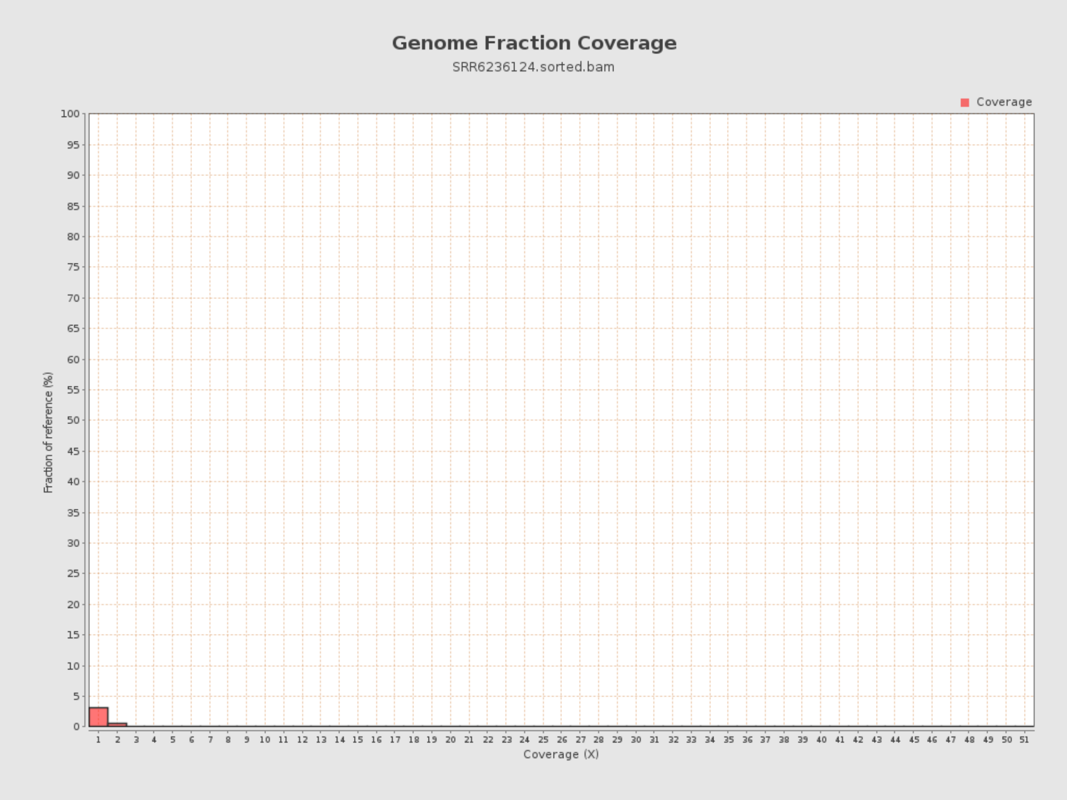
4. Results : Coverage Histogram



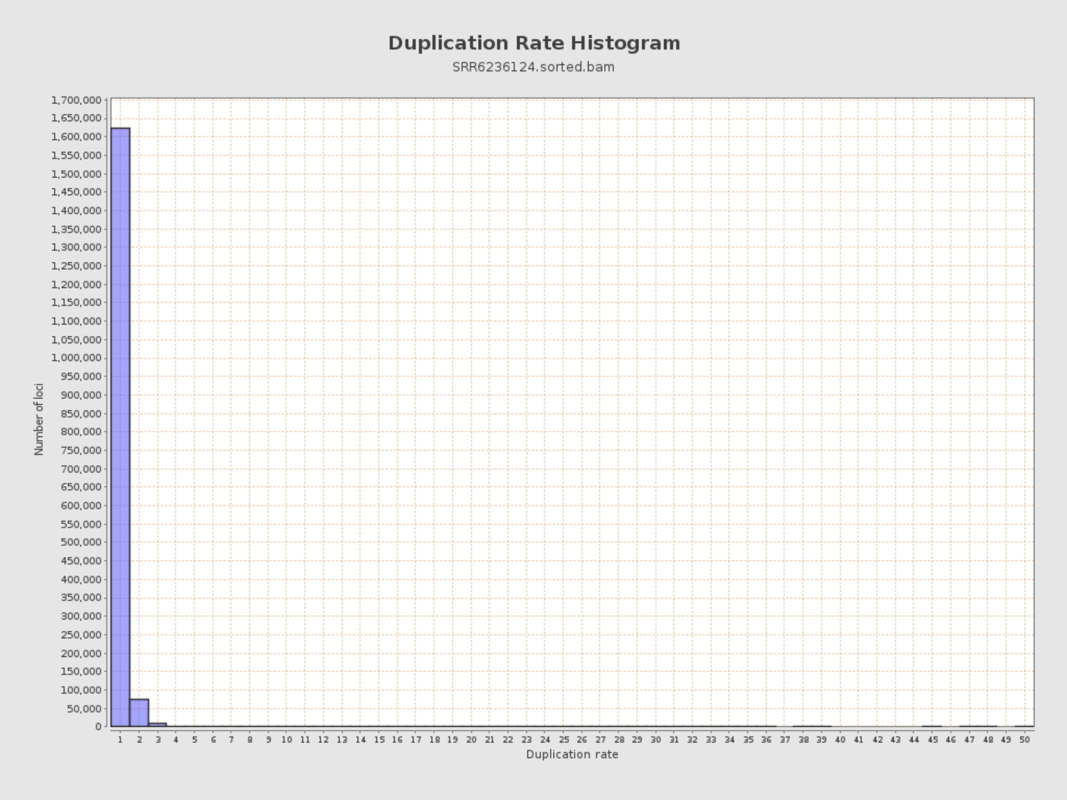
5. Results : Coverage Histogram (0-50X)



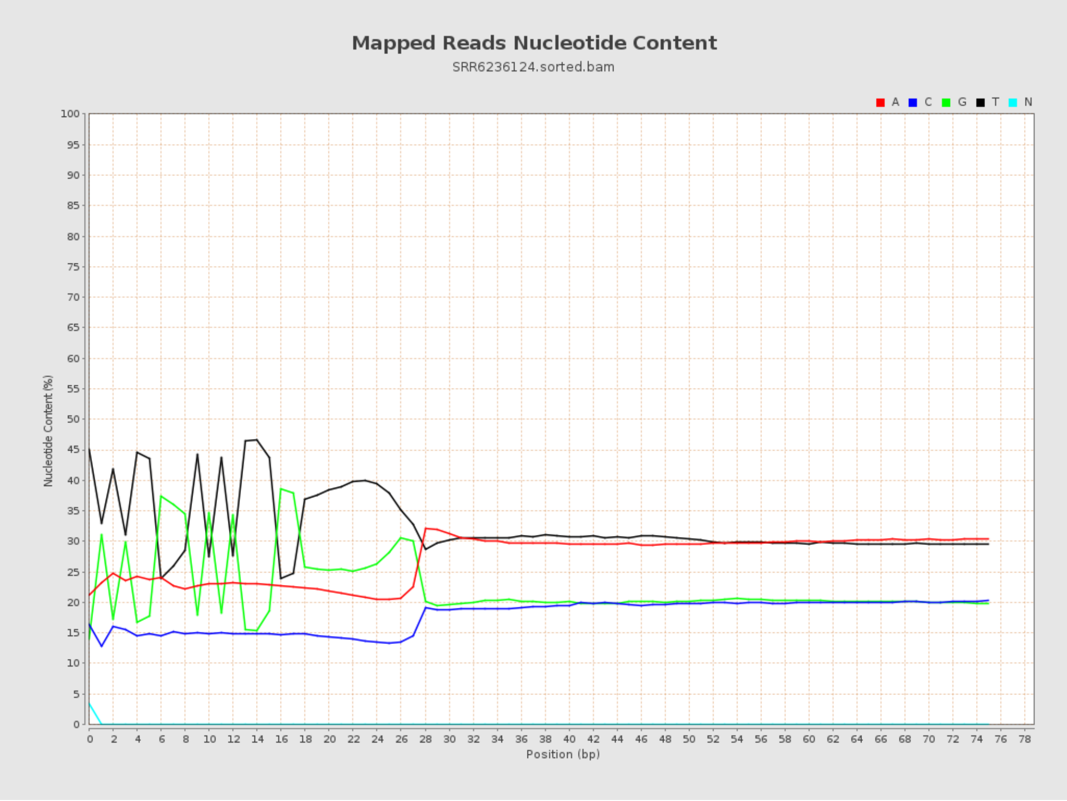
6. Results : Genome Fraction Coverage



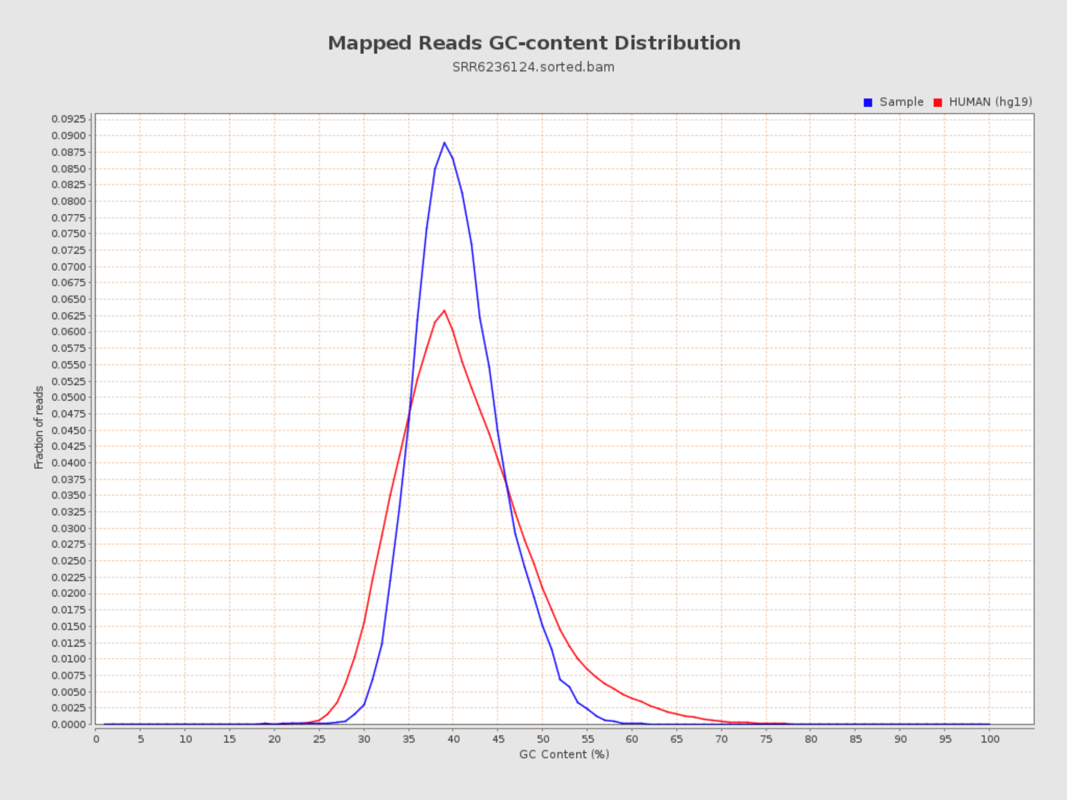
7. Results : Duplication Rate Histogram



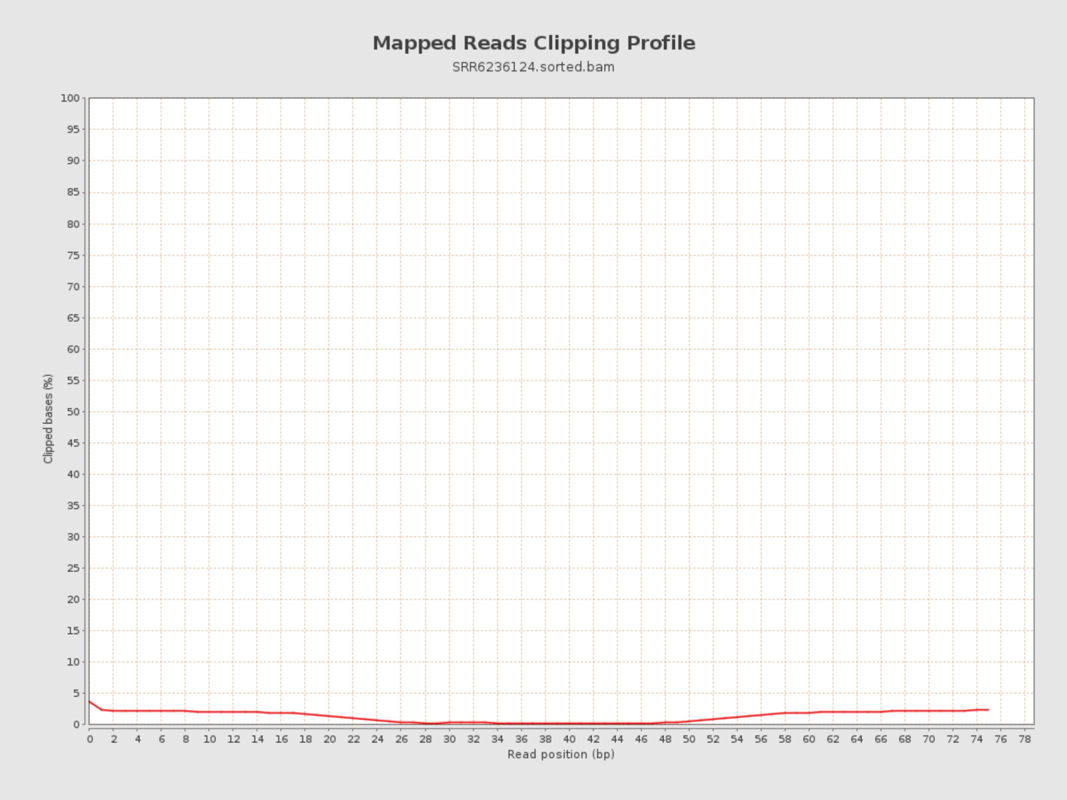
8. Results : Mapped Reads Nucleotide Content



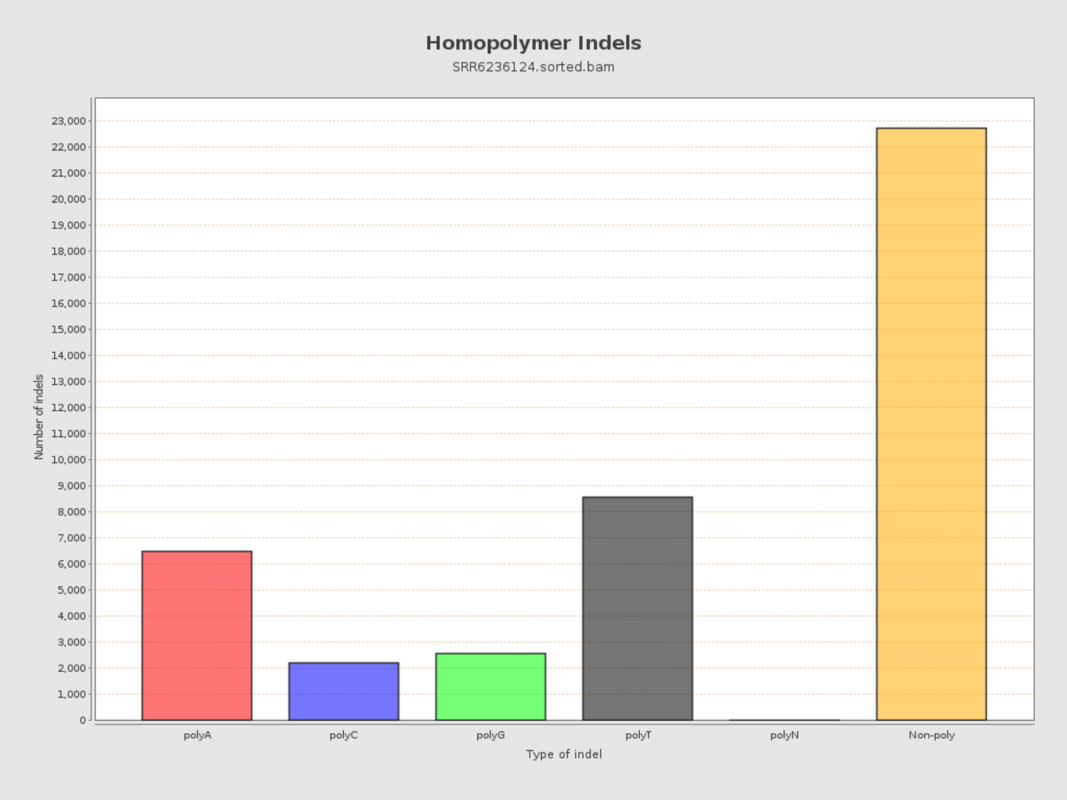
9. Results : Mapped Reads GC-content Distribution



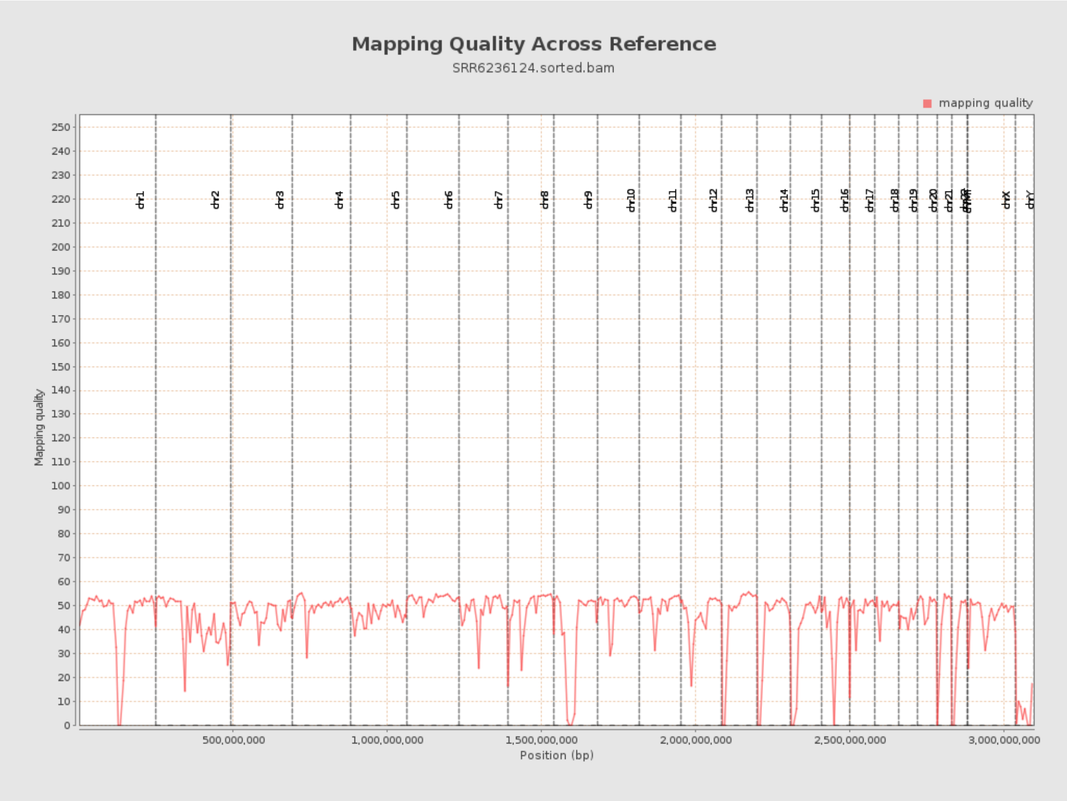
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram