Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 14:33:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234078.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_SRR6234078 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234078.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 14:33:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234078.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,811,888
Mapped reads	3,611,082 / 94.73%
Unmapped reads	200,806 / 5.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	35,446 / 0.93%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	461,506 / 12.11%
Duplication rate	10.75%
Clipped reads	1,895,187 / 49.72%

2.2. ACGT Content

Number/percentage of A's	59,655,831 / 25.55%
Number/percentage of C's	43,149,289 / 18.48%
Number/percentage of T's	74,866,717 / 32.06%
Number/percentage of G's	55,793,304 / 23.9%
Number/percentage of N's	23,043 / 0.01%
GC Percentage	42.38%

2.3. Coverage

Mean	0.0755

Standard Deviation	0.7157

2.4. Mapping Quality

Mean Mapping Quality	46.01

2.5. Mismatches and indels

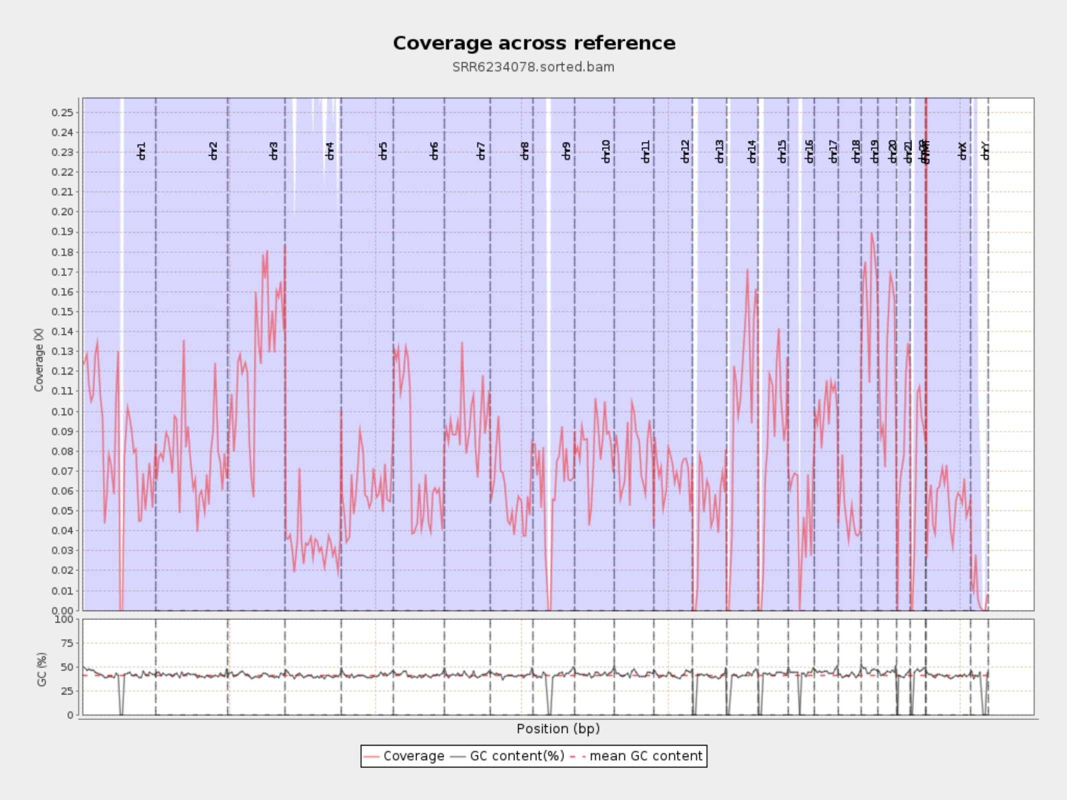
General error rate	0.54%
Mismatches	1,242,589
Insertions	14,663
Mapped reads with at least one insertion	0.4%
Deletions	50,096
Mapped reads with at least one deletion	1.37%
Homopolymer indels	44.39%

2.6. Chromosome stats

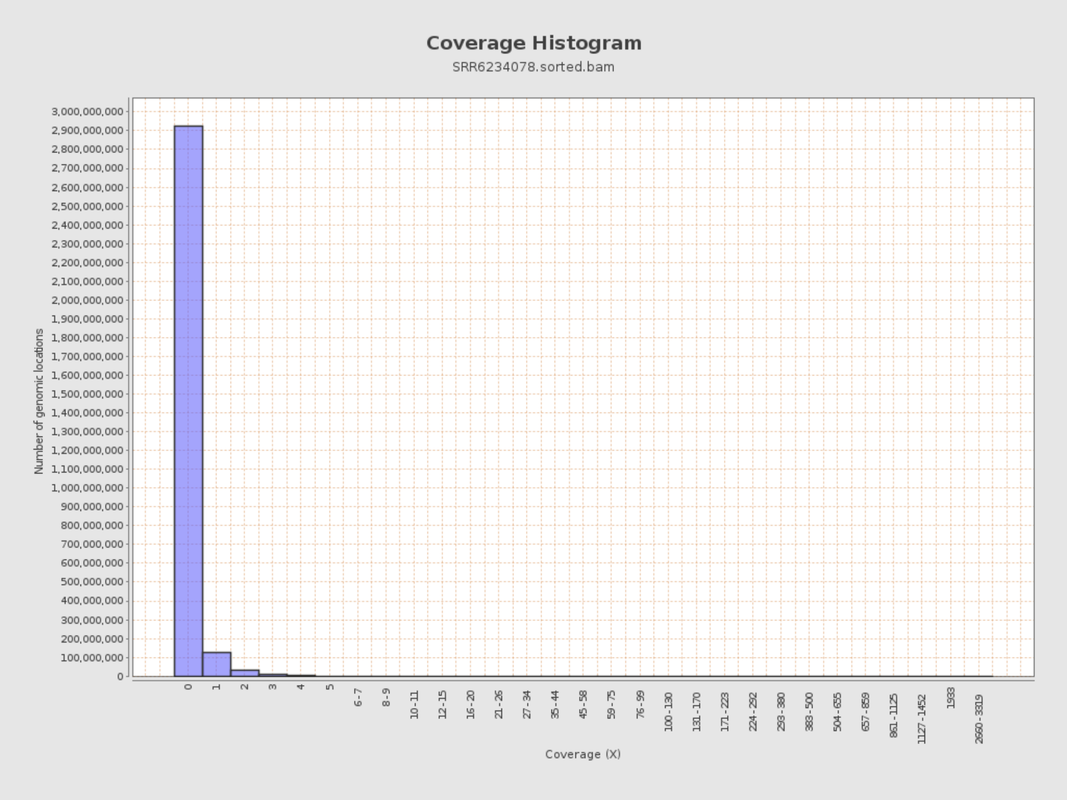
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20206852	0.0811	1.1746
chr2	243199373	18717807	0.077	1.5328
chr3	198022430	25029474	0.1264	0.4714
chr4	191154276	6307521	0.033	0.271
chr5	180915260	10972275	0.0606	0.3298
chr6	171115067	13008313	0.076	0.5333
chr7	159138663	15015433	0.0944	0.8155

chr8	146364022	8514669	0.0582	0.7639
chr9	141213431	8629724	0.0611	0.4486
chr10	135534747	11105633	0.0819	0.5105
chr11	135006516	10469573	0.0775	0.4774
chr12	133851895	9364651	0.07	0.3481
chr13	115169878	5695142	0.0494	0.3551
chr14	107349540	11401968	0.1062	0.438
chr15	102531392	8412311	0.082	0.389
chr16	90354753	4488995	0.0497	0.3332
chr17	81195210	8366030	0.103	0.4413
chr18	78077248	3781482	0.0484	1.0262
chr19	59128983	9554264	0.1616	0.7107
chr20	63025520	7810595	0.1239	0.4778
chr21	48129895	4096565	0.0851	0.3958
chr22	51304566	3562514	0.0694	0.3416
chrMT	16571	165778	10.0041	6.8838
chrX	155270560	8407579	0.0541	0.3439
chrY	59373566	489946	0.0083	0.2082

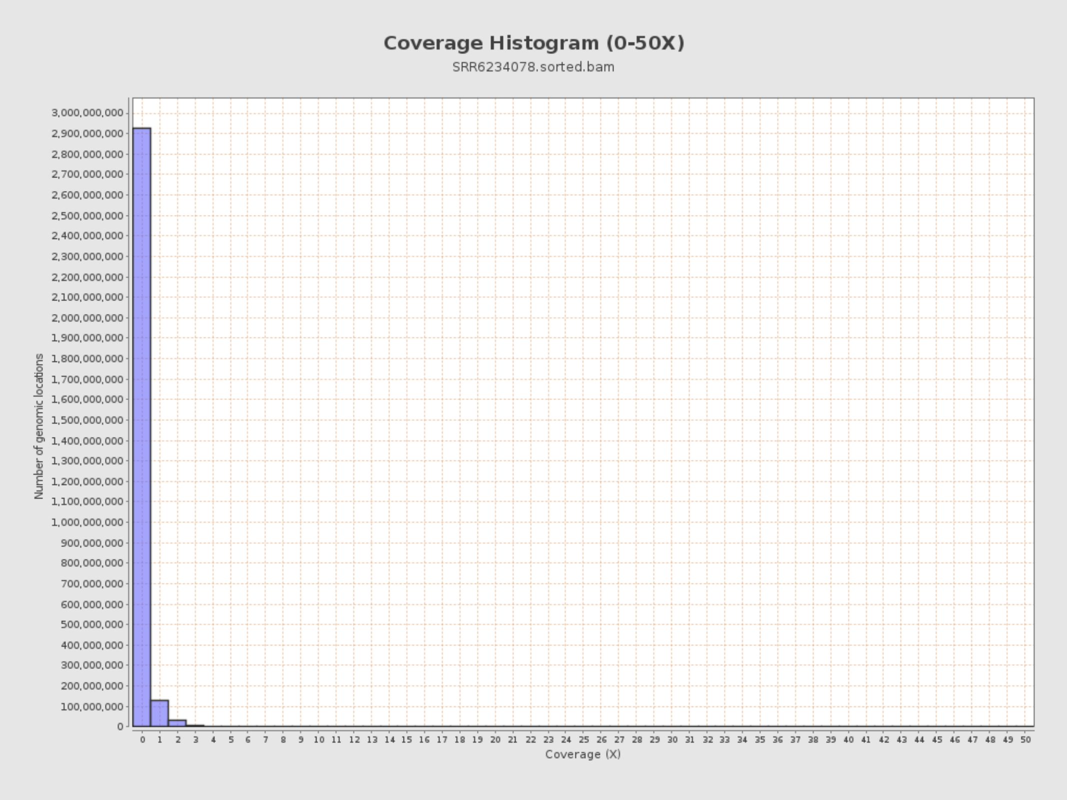
3. Results : Coverage across reference



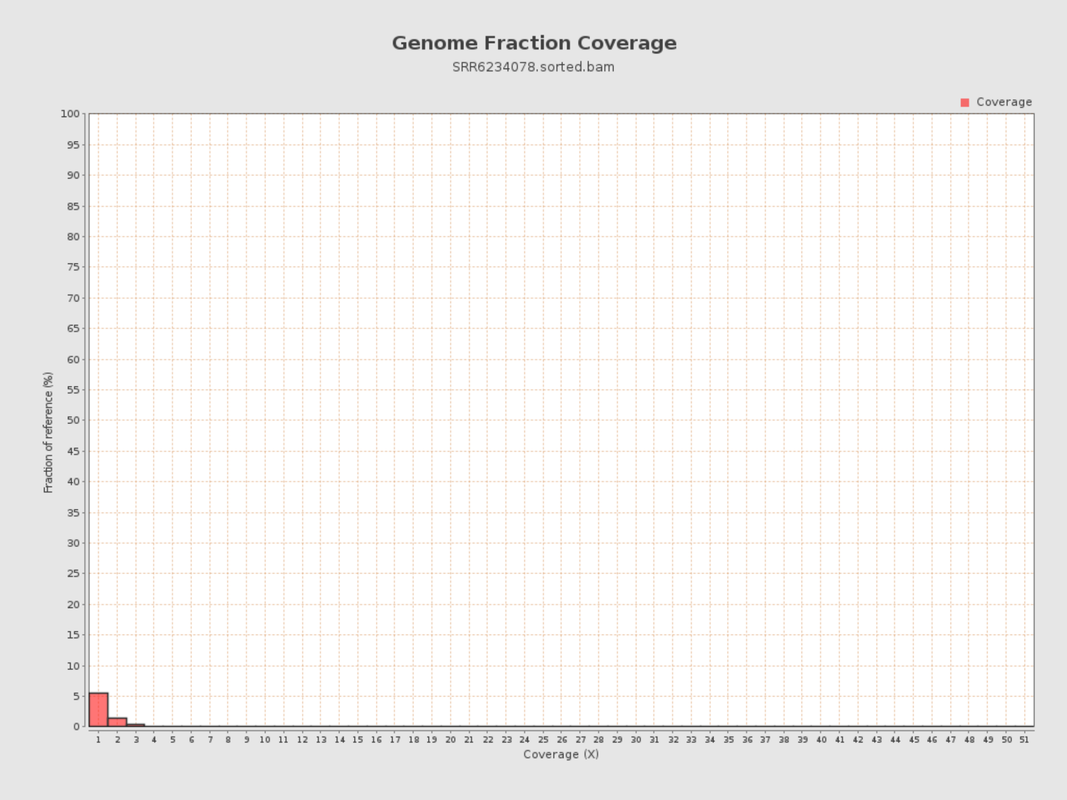
4. Results : Coverage Histogram



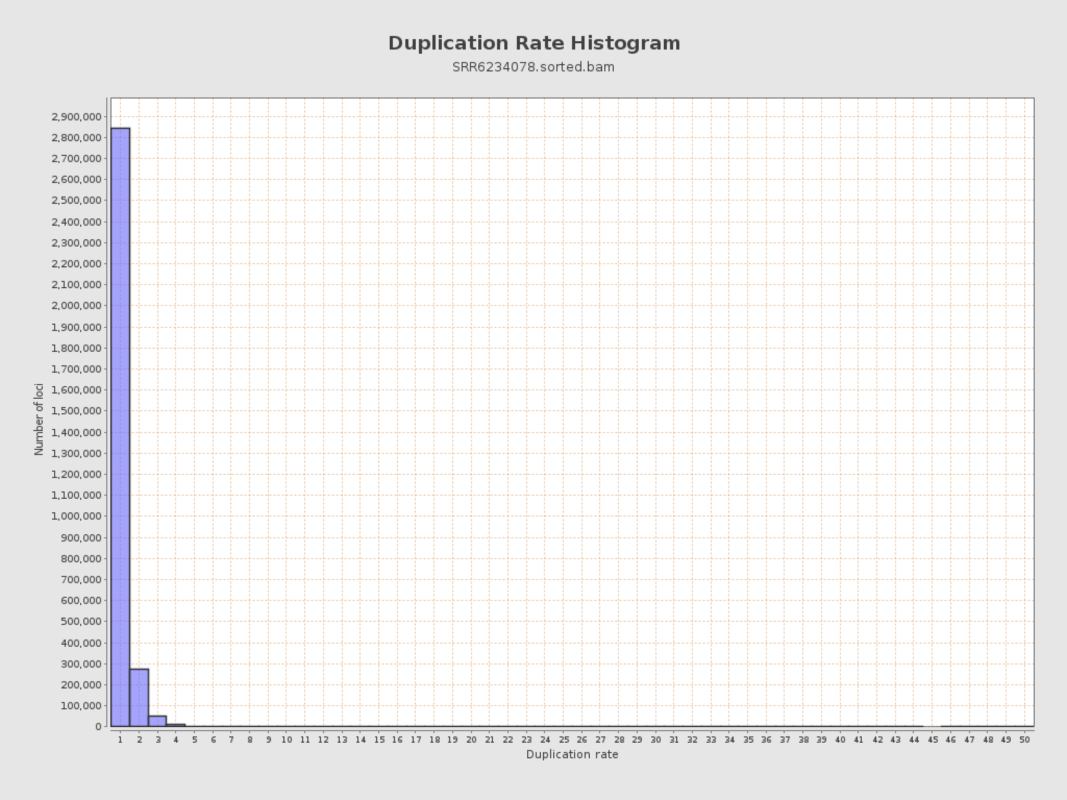
5. Results : Coverage Histogram (0-50X)



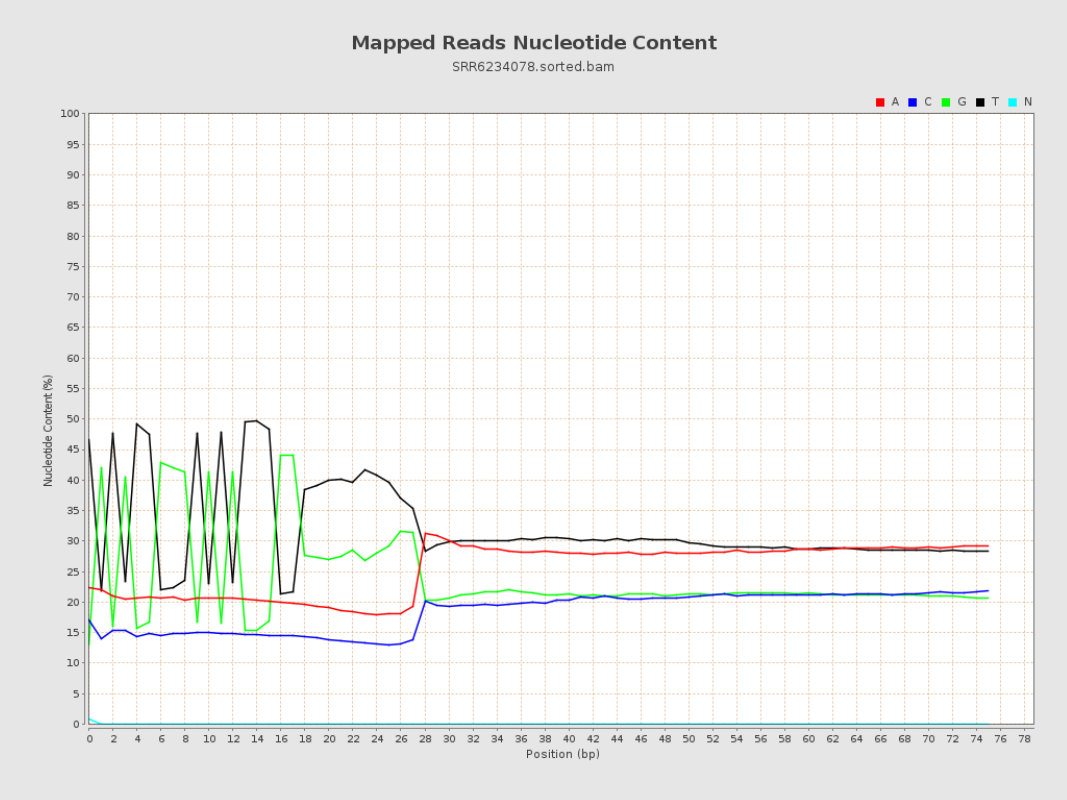
6. Results : Genome Fraction Coverage



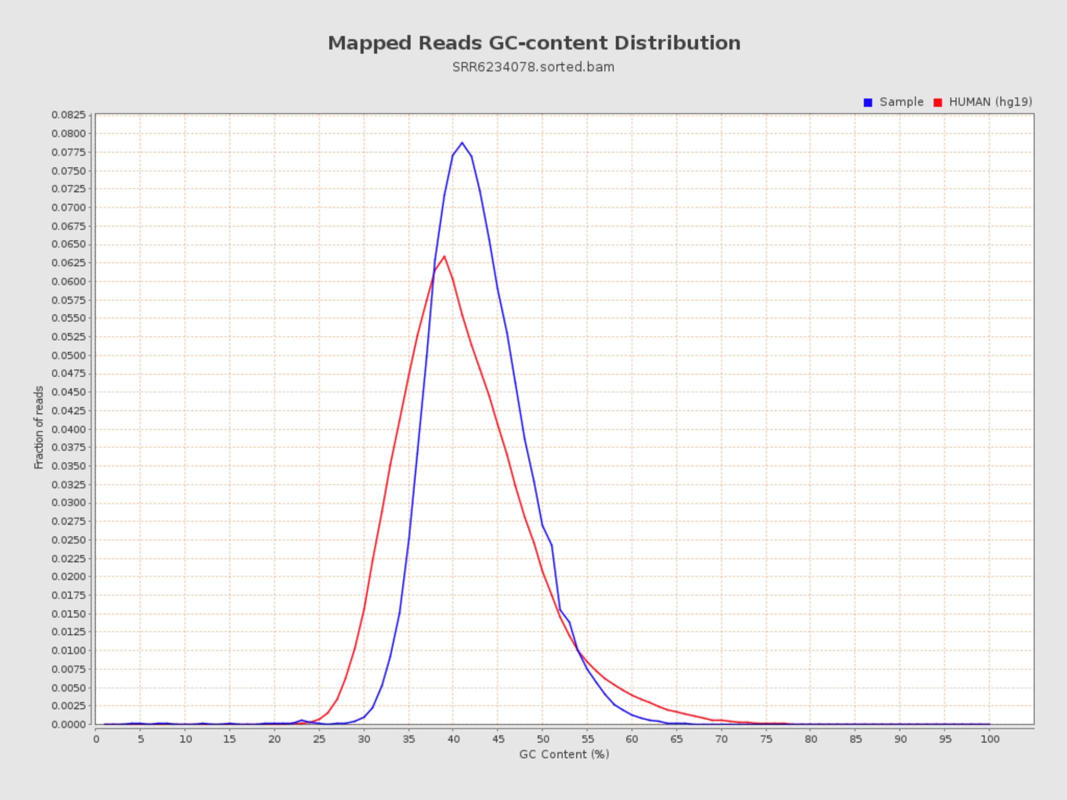
7. Results : Duplication Rate Histogram



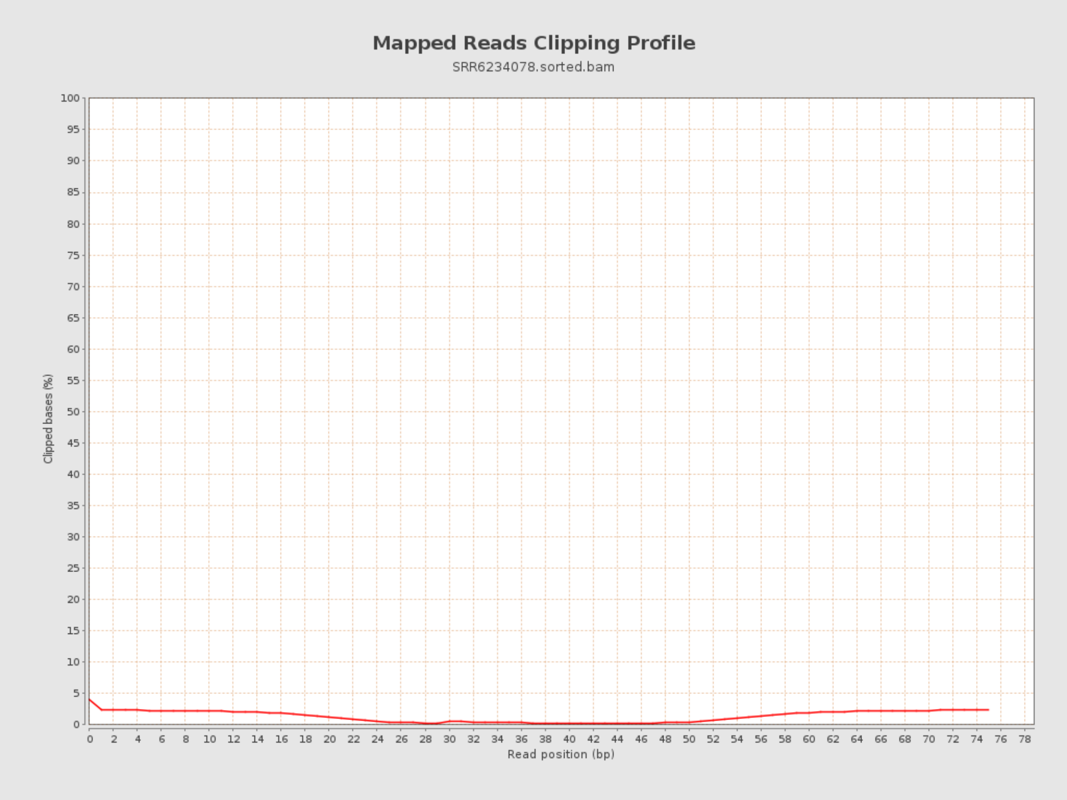
8. Results : Mapped Reads Nucleotide Content



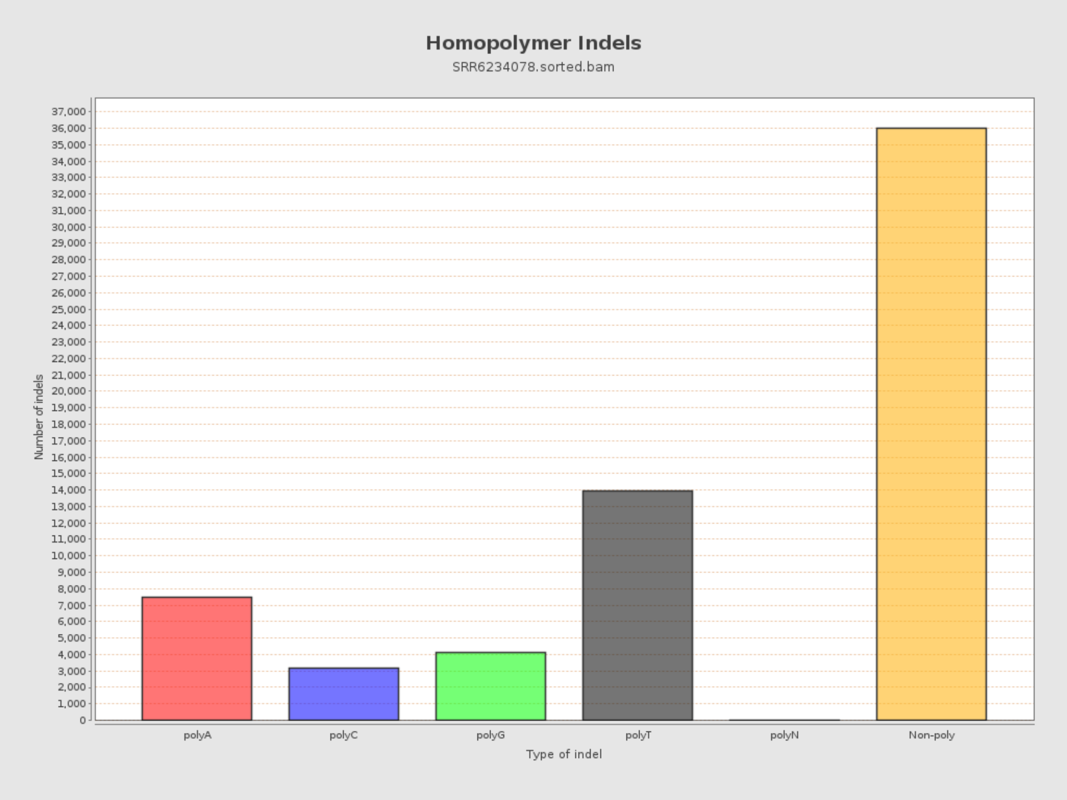
9. Results : Mapped Reads GC-content Distribution



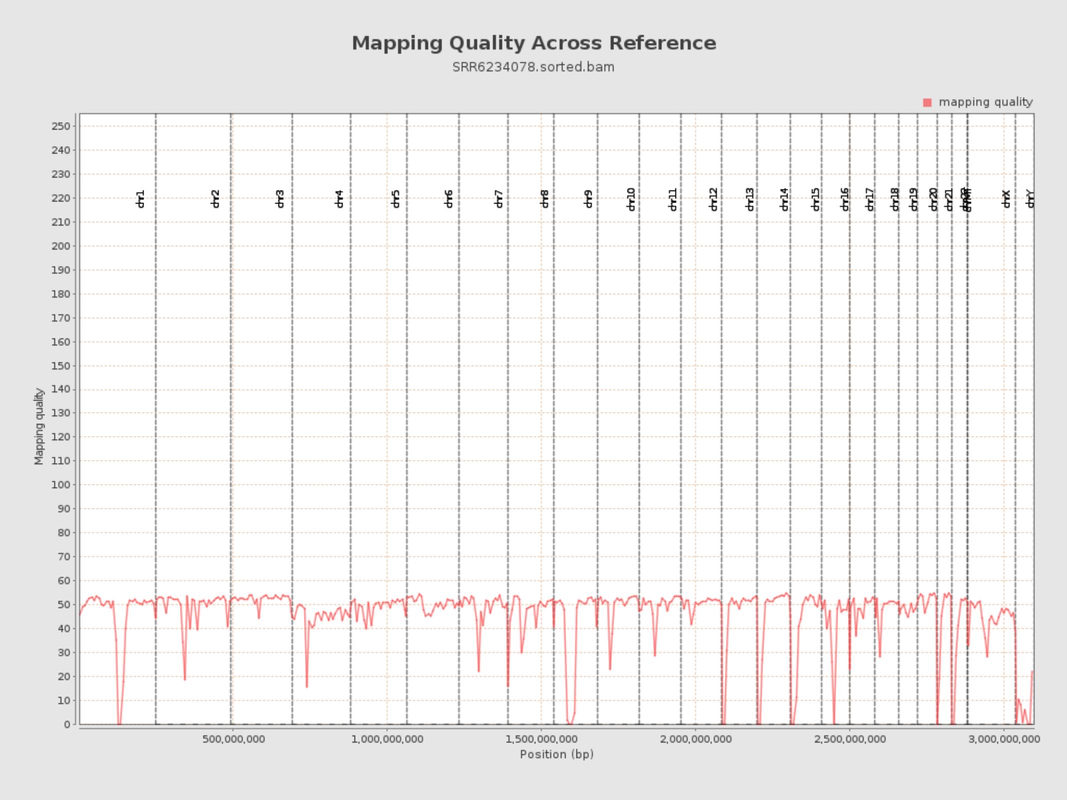
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram