Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 07:17:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231842.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_SRR6231842 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231842.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 07:17:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231842.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,924,768
Mapped reads	2,318,317 / 59.07%
Unmapped reads	1,606,451 / 40.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,052 / 0.77%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	489,307 / 12.47%
Duplication rate	12.33%
Clipped reads	1,473,052 / 37.53%

2.2. ACGT Content

Number/percentage of A's	41,779,328 / 29.17%
Number/percentage of C's	28,061,047 / 19.59%
Number/percentage of T's	41,207,554 / 28.77%
Number/percentage of G's	32,187,110 / 22.47%
Number/percentage of N's	10,751 / 0.01%
GC Percentage	42.06%

2.3. Coverage

Mean	0.0463

Standard Deviation	5.6141

2.4. Mapping Quality

Mean Mapping Quality	44.38

2.5. Mismatches and indels

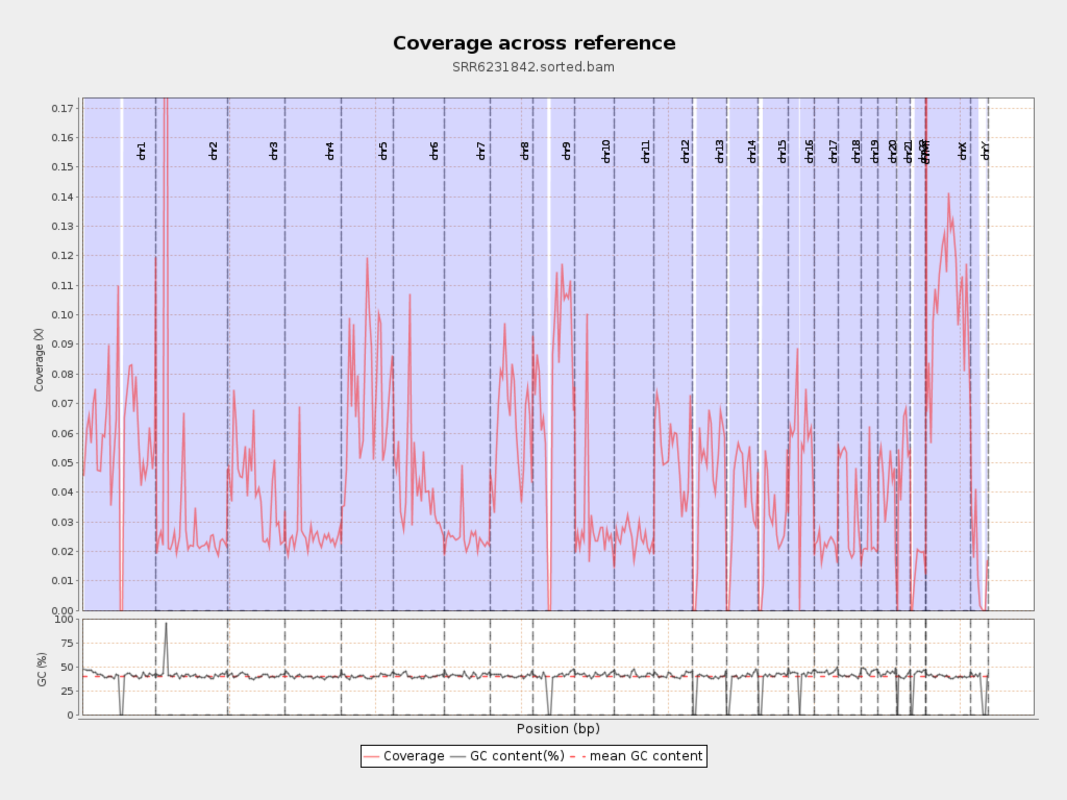
General error rate	0.62%
Mismatches	866,955
Insertions	9,578
Mapped reads with at least one insertion	0.41%
Deletions	28,878
Mapped reads with at least one deletion	1.23%
Homopolymer indels	44.4%

2.6. Chromosome stats

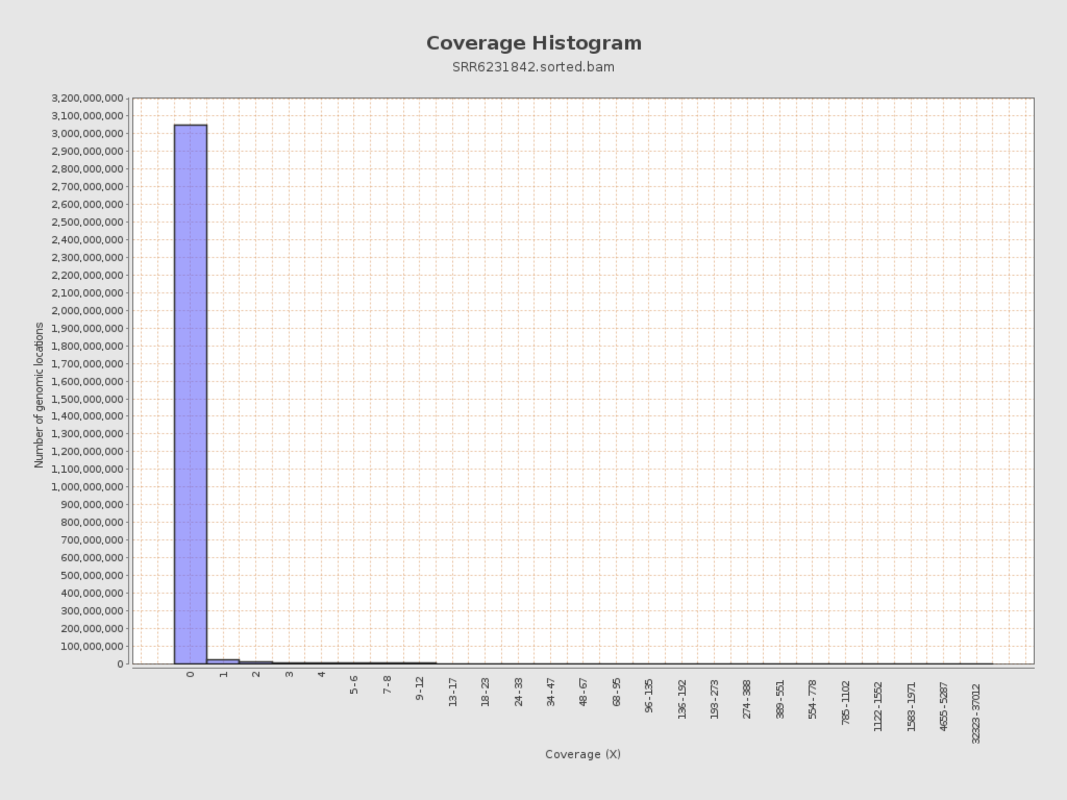
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14669127	0.0589	1.2346
chr2	243199373	9134442	0.0376	19.9008
chr3	198022430	8203582	0.0414	0.4771
chr4	191154276	4993496	0.0261	0.393
chr5	180915260	13295084	0.0735	0.6319
chr6	171115067	7372181	0.0431	0.6469
chr7	159138663	3974184	0.025	0.4474

chr8	146364022	9310433	0.0636	0.7425
chr9	141213431	11171135	0.0791	0.7239
chr10	135534747	3895488	0.0287	0.6548
chr11	135006516	3318206	0.0246	0.3771
chr12	133851895	7191260	0.0537	0.5433
chr13	115169878	5376891	0.0467	0.4986
chr14	107349540	4100460	0.0382	0.4894
chr15	102531392	2785540	0.0272	0.3701
chr16	90354753	4950636	0.0548	0.56
chr17	81195210	1821067	0.0224	0.3394
chr18	78077248	3019772	0.0387	0.836
chr19	59128983	1537068	0.026	0.9424
chr20	63025520	2776115	0.044	0.4821
chr21	48129895	2420287	0.0503	0.531
chr22	51304566	718223	0.014	0.2563
chrMT	16571	41502	2.5045	3.3275
chrX	155270560	16355221	0.1053	0.7951
chrY	59373566	863191	0.0145	0.319

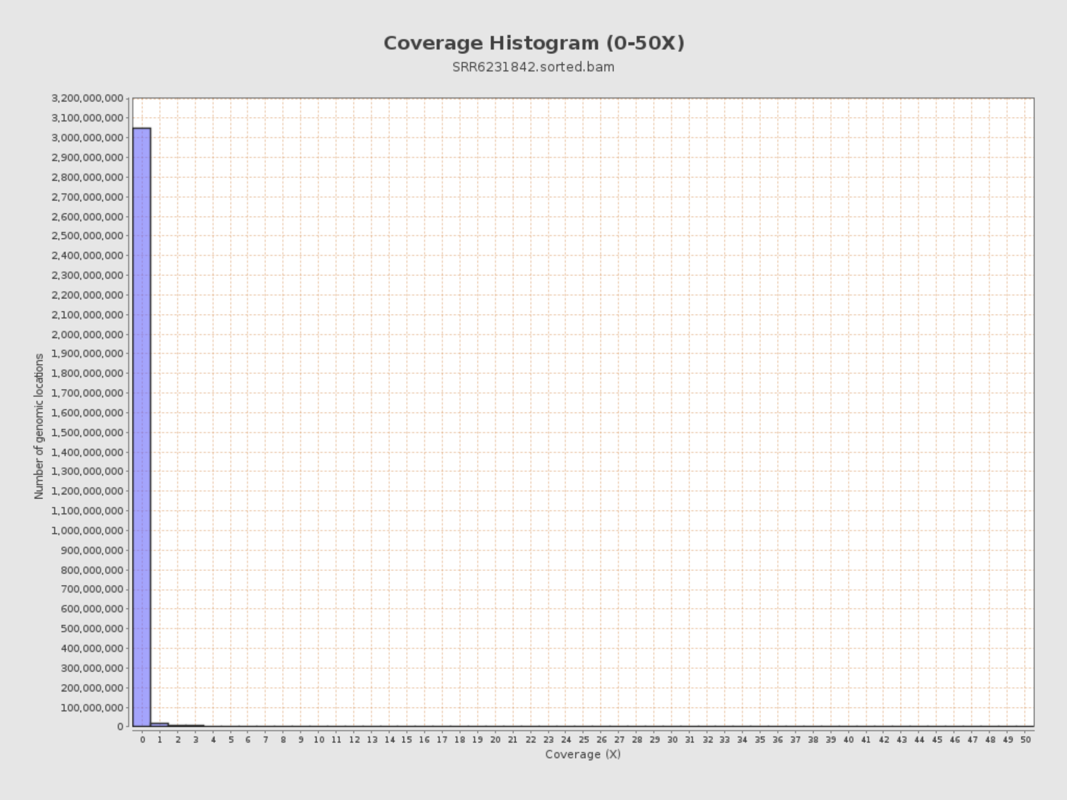
3. Results : Coverage across reference



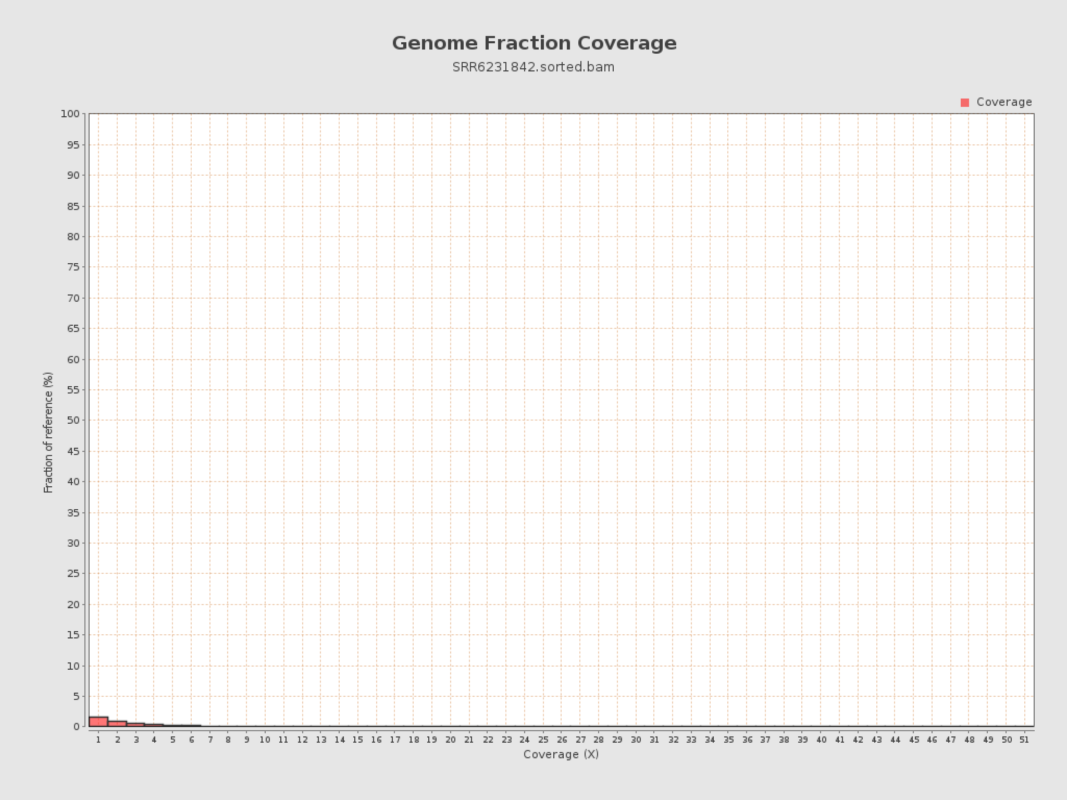
4. Results : Coverage Histogram



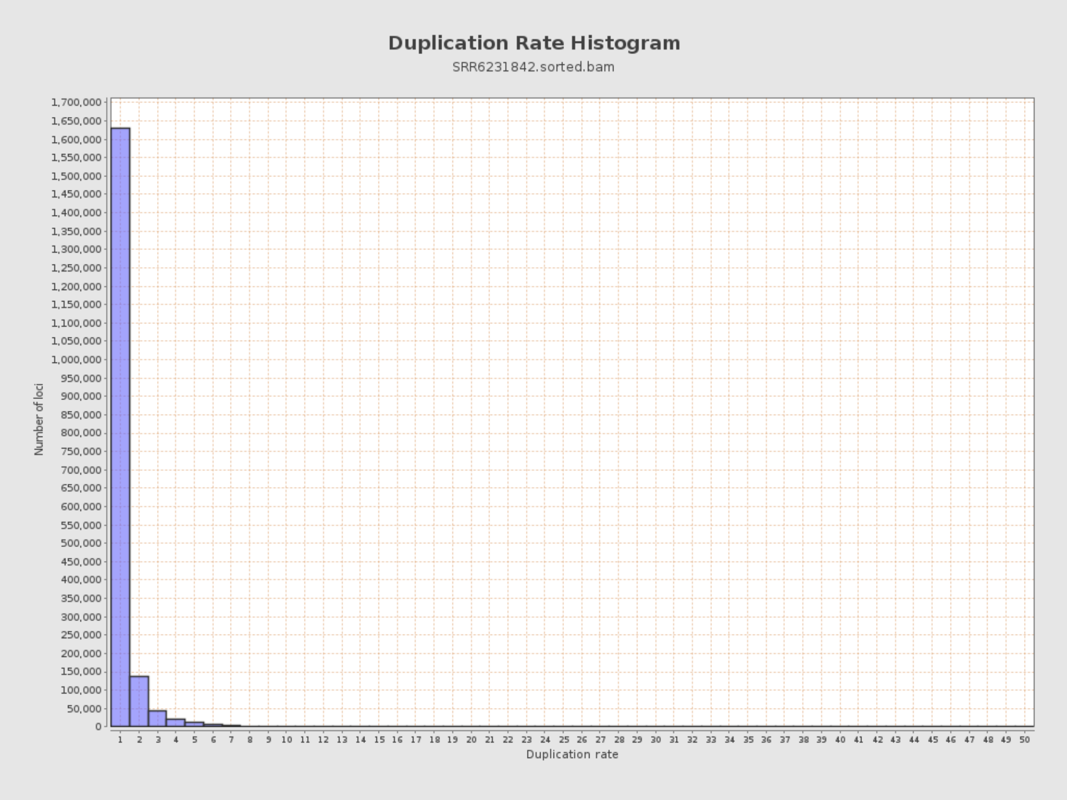
5. Results : Coverage Histogram (0-50X)



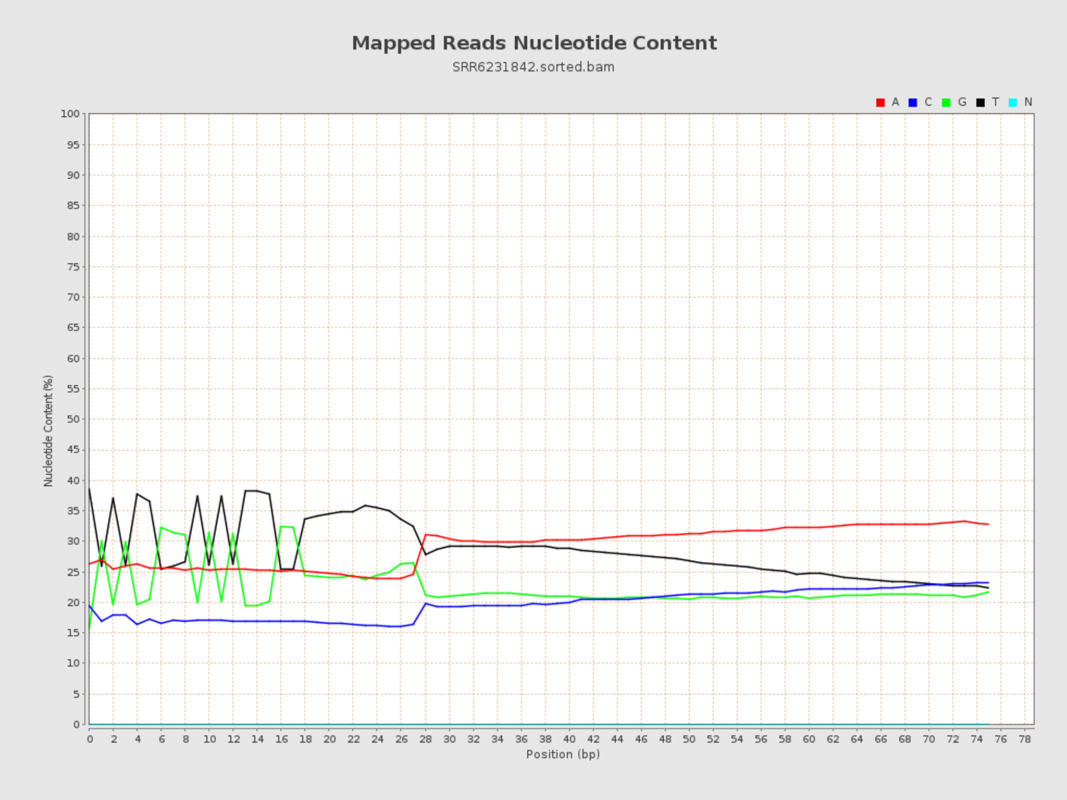
6. Results : Genome Fraction Coverage



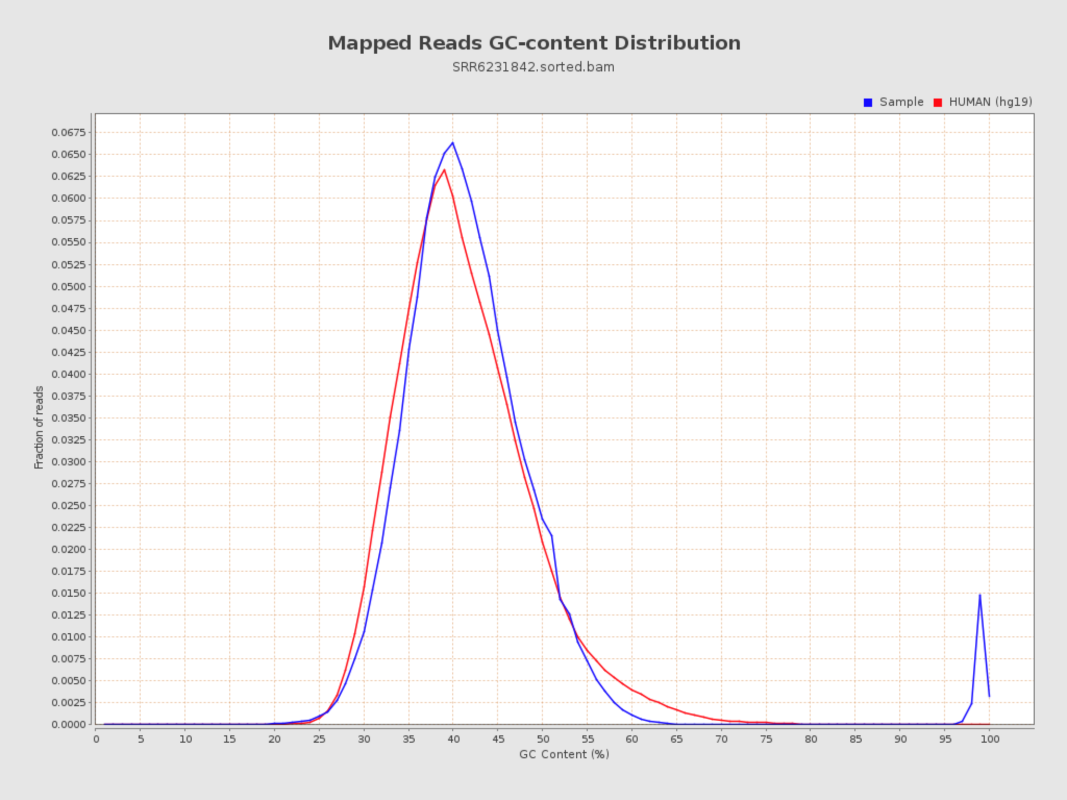
7. Results : Duplication Rate Histogram



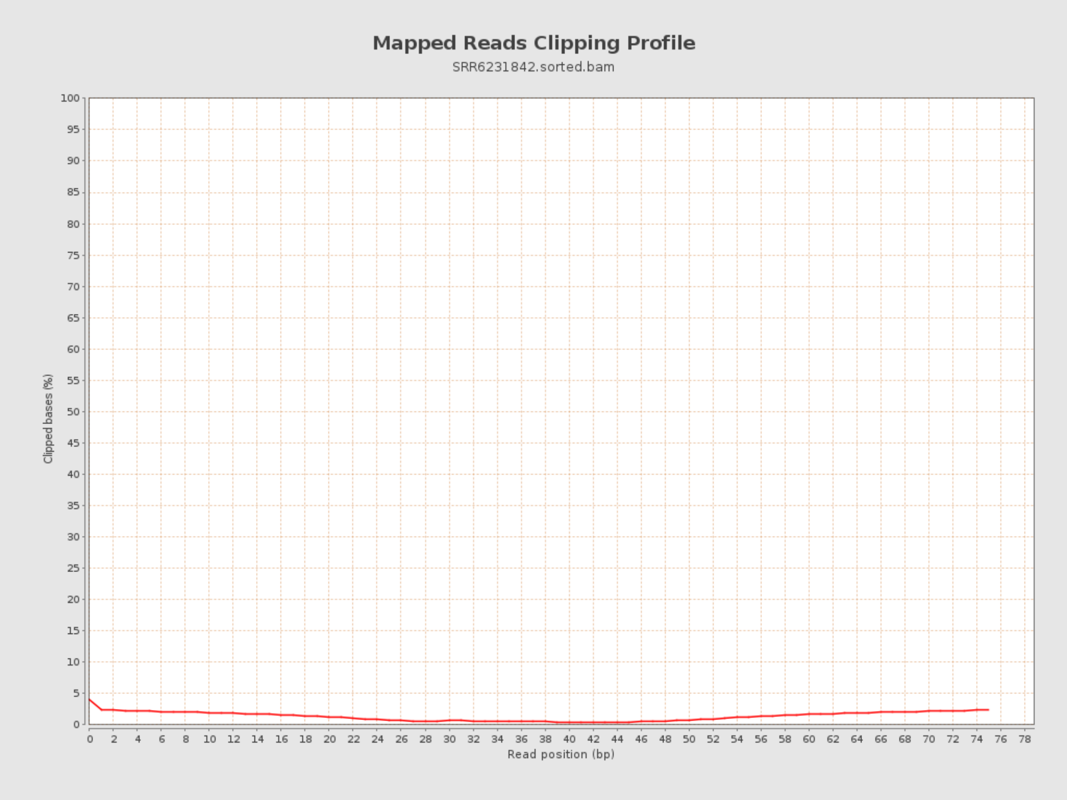
8. Results : Mapped Reads Nucleotide Content



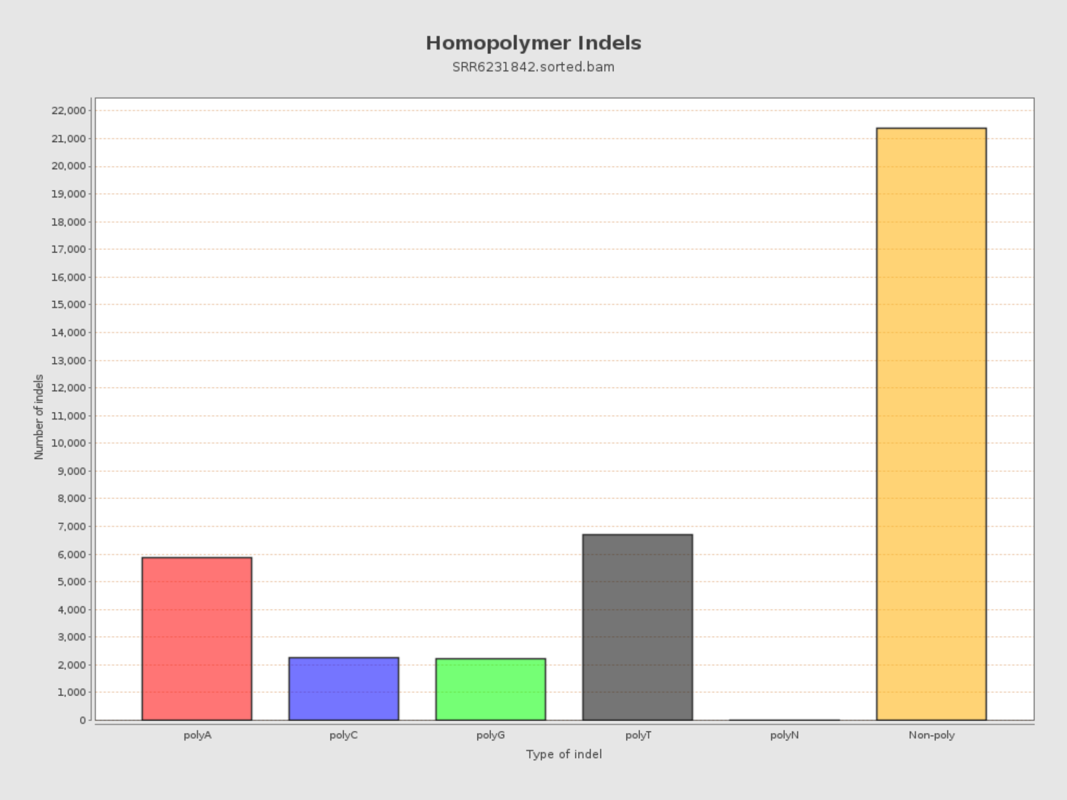
9. Results : Mapped Reads GC-content Distribution



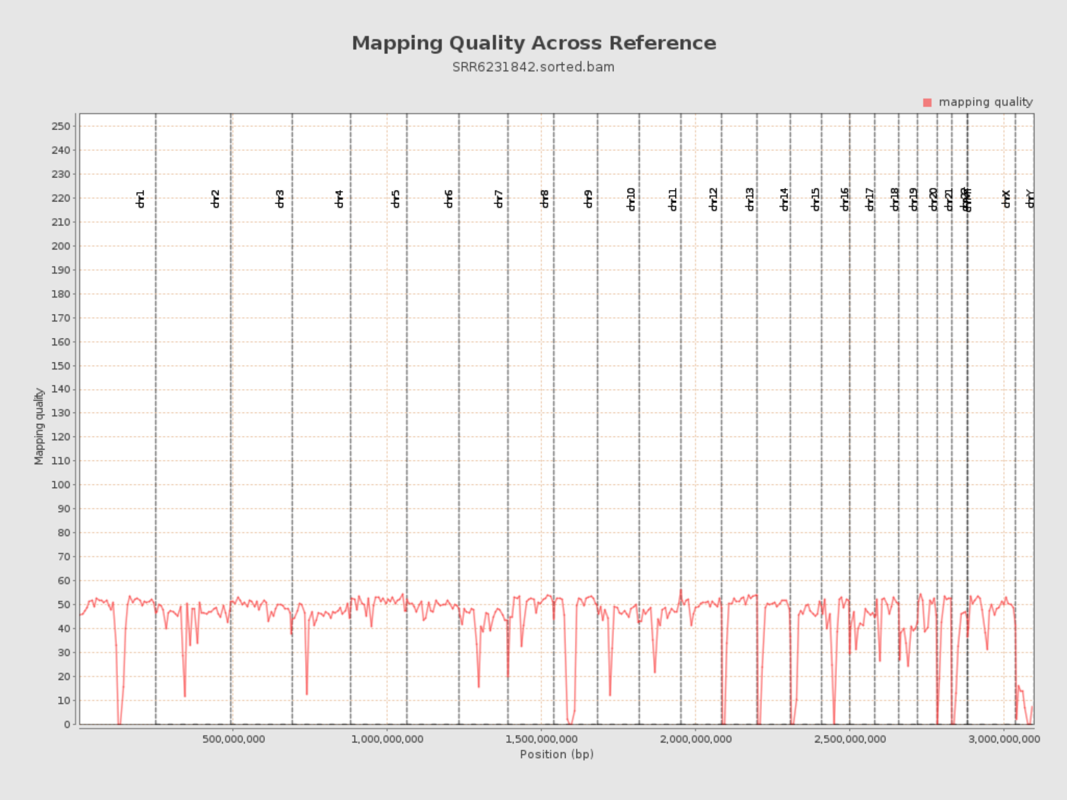
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram