Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 00:05:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231751.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_SRR6231751 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231751.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 00:05:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231751.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,923,684
Mapped reads	4,540,087 / 92.21%
Unmapped reads	383,597 / 7.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,567 / 0.58%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	635,344 / 12.9%
Duplication rate	6.74%
Clipped reads	1,635,243 / 33.21%

2.2. ACGT Content

Number/percentage of A's	81,641,375 / 26.28%
Number/percentage of C's	56,725,856 / 18.26%
Number/percentage of T's	88,855,072 / 28.6%
Number/percentage of G's	83,401,031 / 26.84%
Number/percentage of N's	65,545 / 0.02%
GC Percentage	45.1%

2.3. Coverage

Mean	0.1004

Standard Deviation	37.6254

2.4. Mapping Quality

Mean Mapping Quality	37.69

2.5. Mismatches and indels

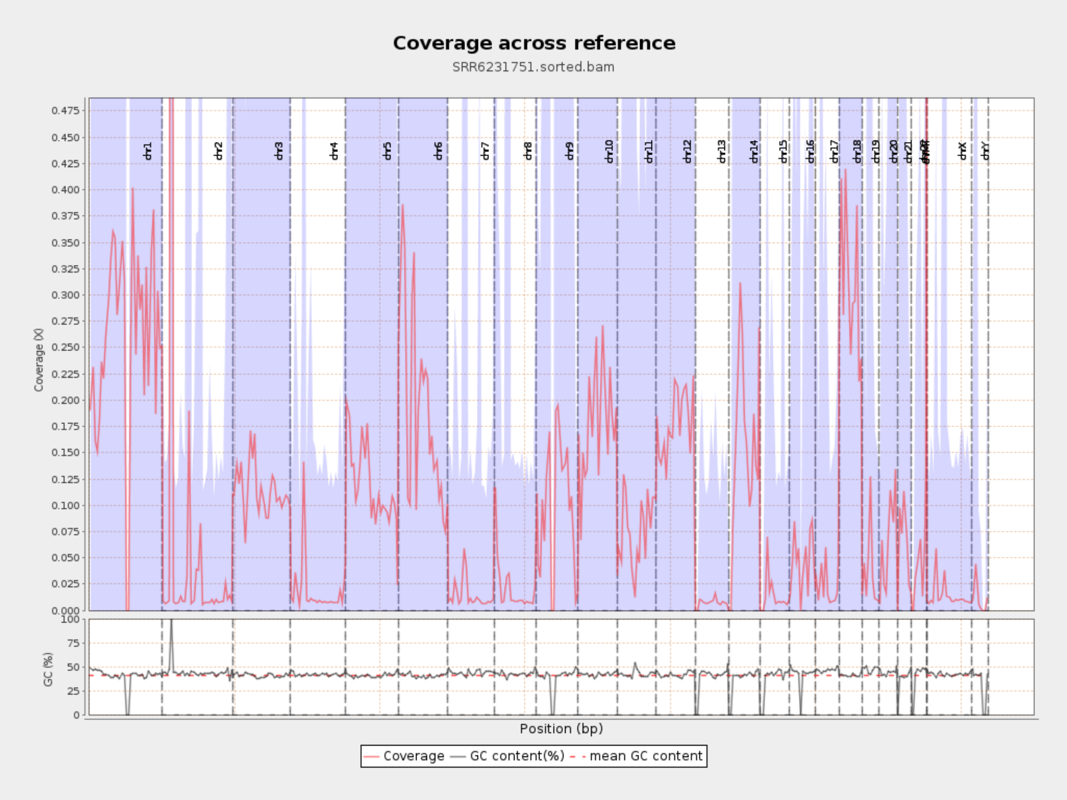
General error rate	0.67%
Mismatches	2,040,663
Insertions	21,918
Mapped reads with at least one insertion	0.48%
Deletions	63,806
Mapped reads with at least one deletion	1.39%
Homopolymer indels	47.23%

2.6. Chromosome stats

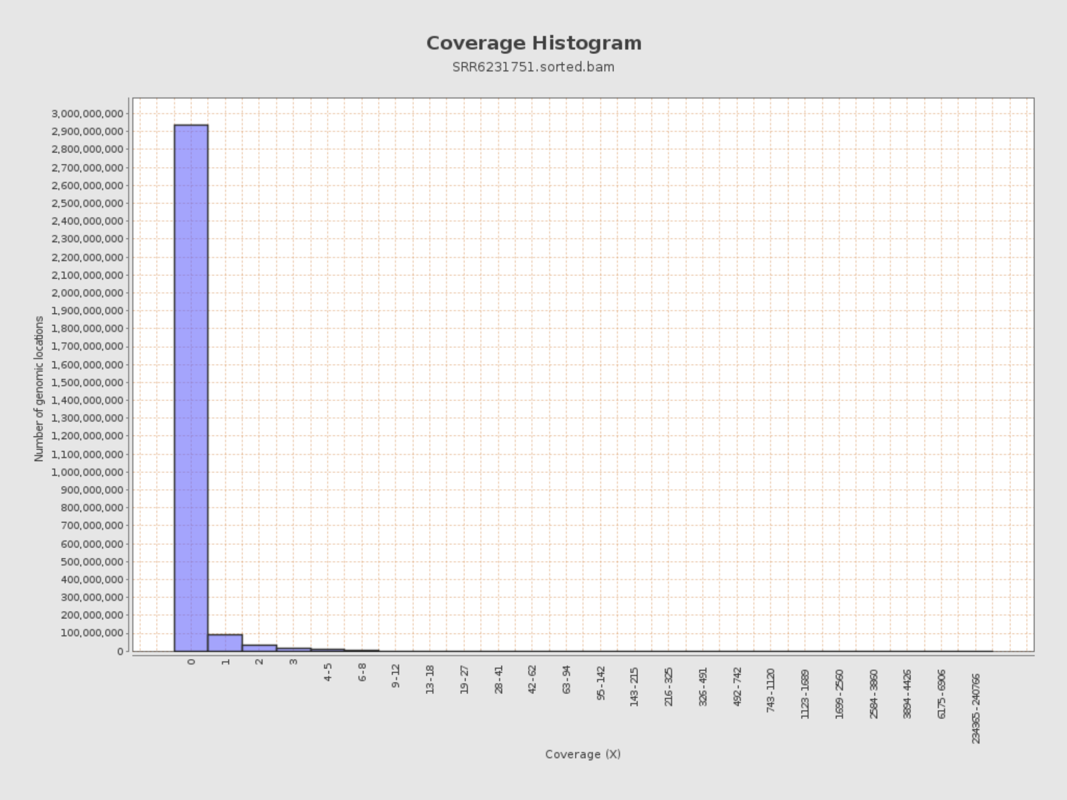
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	64495354	0.2588	1.6677
chr2	243199373	23713648	0.0975	134.2055
chr3	198022430	22656640	0.1144	0.5606
chr4	191154276	3338682	0.0175	0.3233
chr5	180915260	21744521	0.1202	0.569
chr6	171115067	33228373	0.1942	1.0723
chr7	159138663	2285979	0.0144	0.464

chr8	146364022	3115518	0.0213	0.9291
chr9	141213431	14056796	0.0995	0.9537
chr10	135534747	24454232	0.1804	1.0816
chr11	135006516	10323846	0.0765	0.7901
chr12	133851895	23721289	0.1772	0.7145
chr13	115169878	878357	0.0076	0.1352
chr14	107349540	16256293	0.1514	0.7608
chr15	102531392	1474943	0.0144	0.2397
chr16	90354753	4311233	0.0477	0.5134
chr17	81195210	1839600	0.0227	0.3581
chr18	78077248	24567922	0.3147	1.7051
chr19	59128983	2313075	0.0391	1.4327
chr20	63025520	4224100	0.067	0.4498
chr21	48129895	2990682	0.0621	0.4804
chr22	51304566	1972255	0.0384	0.3146
chrMT	16571	12247	0.7391	1.2379
chrX	155270560	2150015	0.0138	0.6207
chrY	59373566	670806	0.0113	0.3596

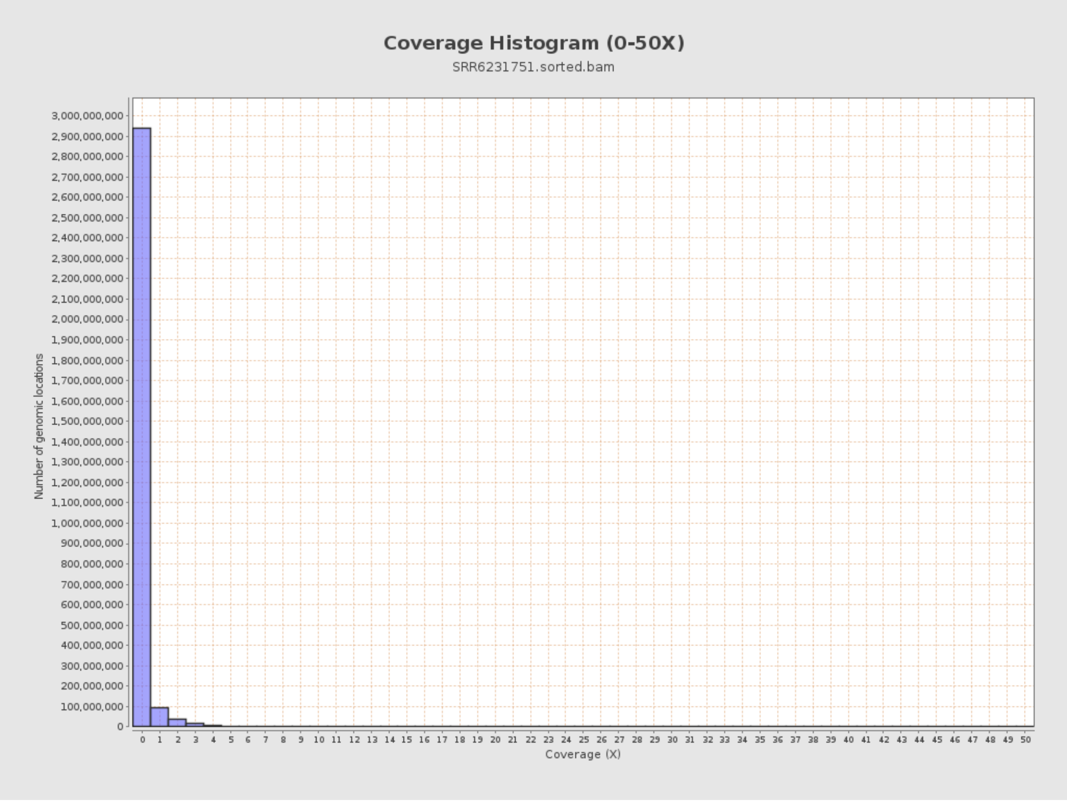
3. Results : Coverage across reference



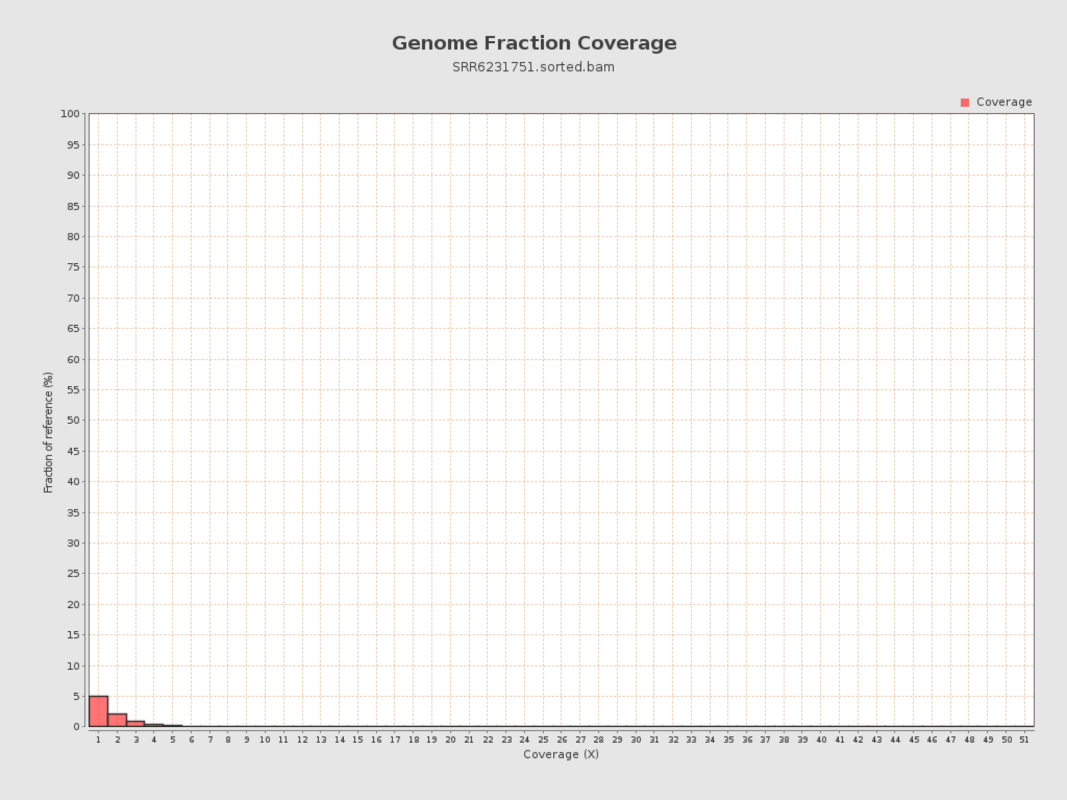
4. Results : Coverage Histogram



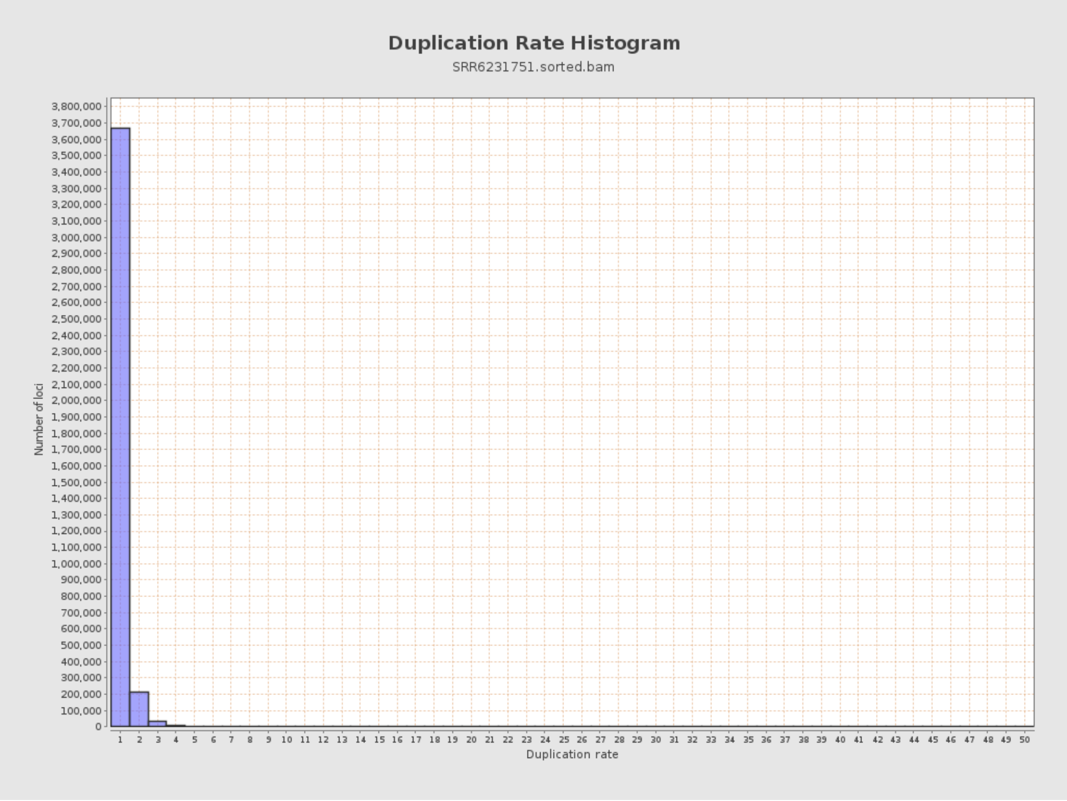
5. Results : Coverage Histogram (0-50X)



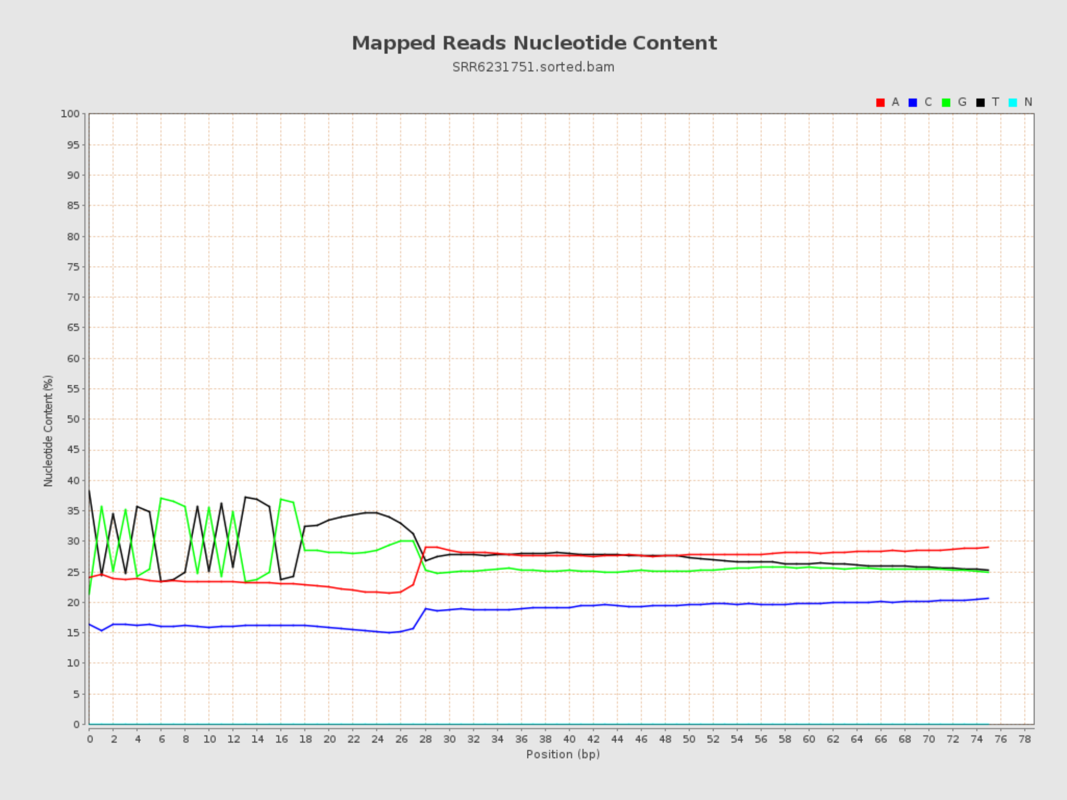
6. Results : Genome Fraction Coverage



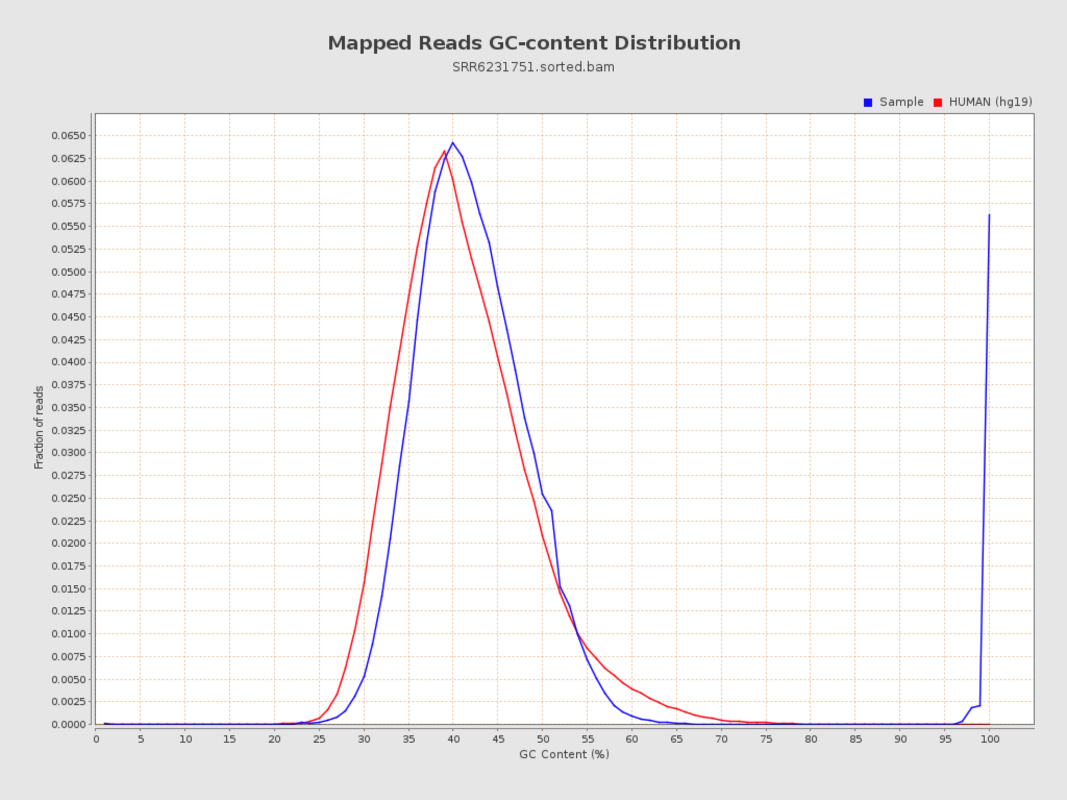
7. Results : Duplication Rate Histogram



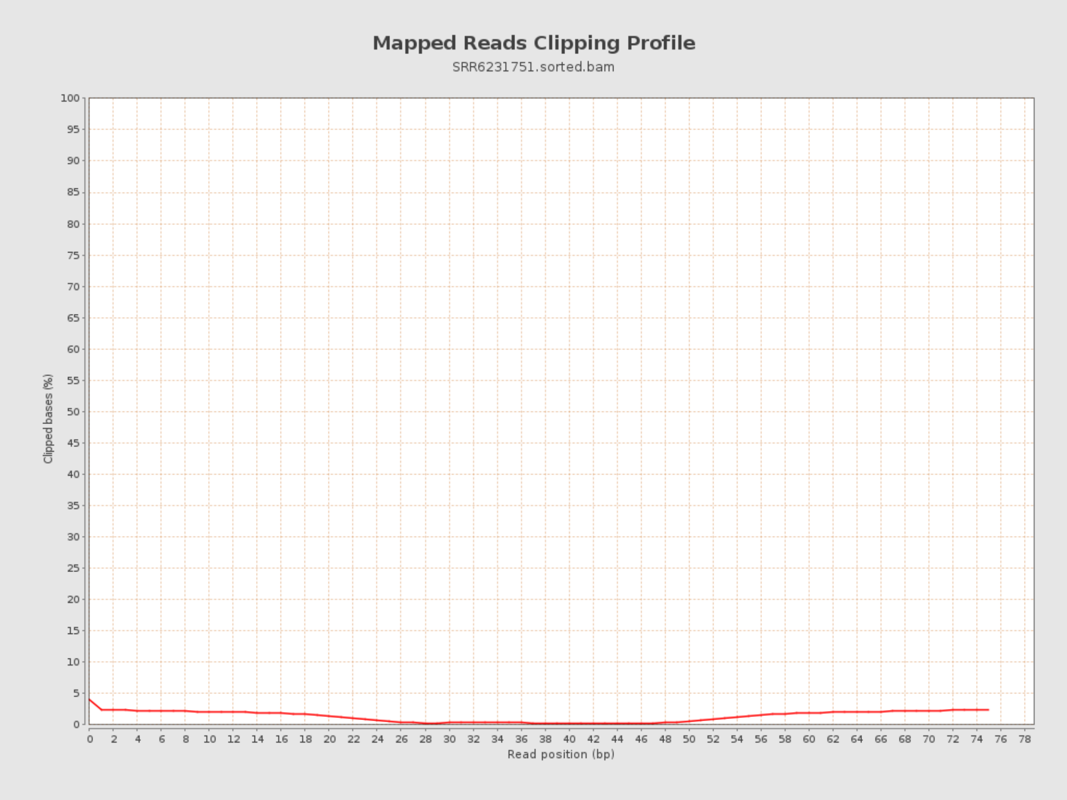
8. Results : Mapped Reads Nucleotide Content



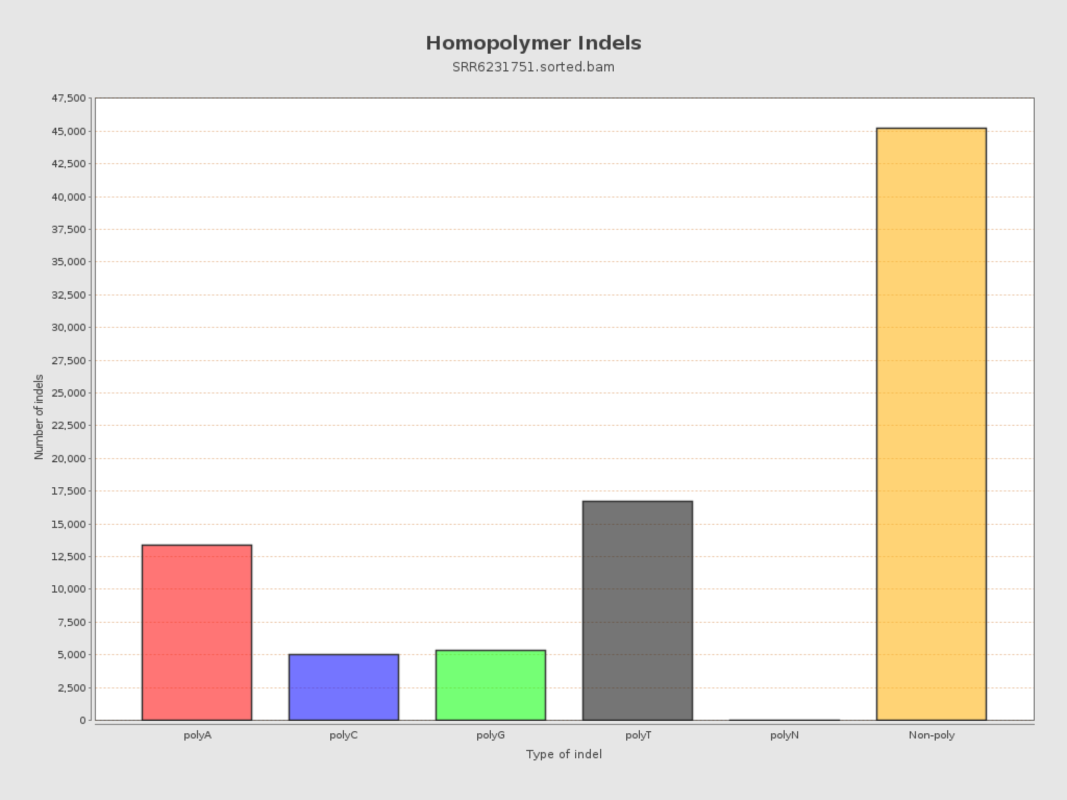
9. Results : Mapped Reads GC-content Distribution



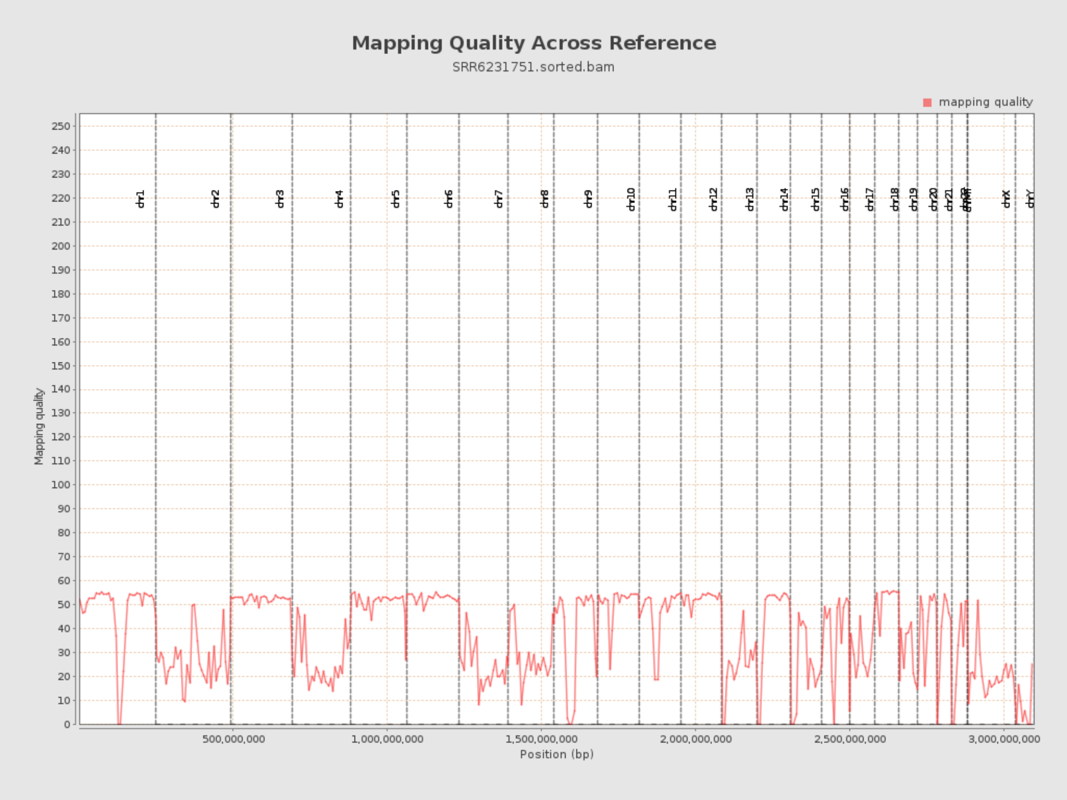
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram