Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 07:37:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240231.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_SRR6240231 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240231.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 07:37:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240231.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,233,003
Mapped reads	2,542,580 / 78.64%
Unmapped reads	690,423 / 21.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,585 / 0.61%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	485,427 / 15.01%
Duplication rate	13.15%
Clipped reads	1,416,325 / 43.81%

2.2. ACGT Content

Number/percentage of A's	45,190,937 / 27.71%
Number/percentage of C's	29,278,052 / 17.95%
Number/percentage of T's	52,443,810 / 32.16%
Number/percentage of G's	36,094,452 / 22.13%
Number/percentage of N's	59,538 / 0.04%
GC Percentage	40.09%

2.3. Coverage

Mean	0.0527

Standard Deviation	0.5659

2.4. Mapping Quality

Mean Mapping Quality	46.43

2.5. Mismatches and indels

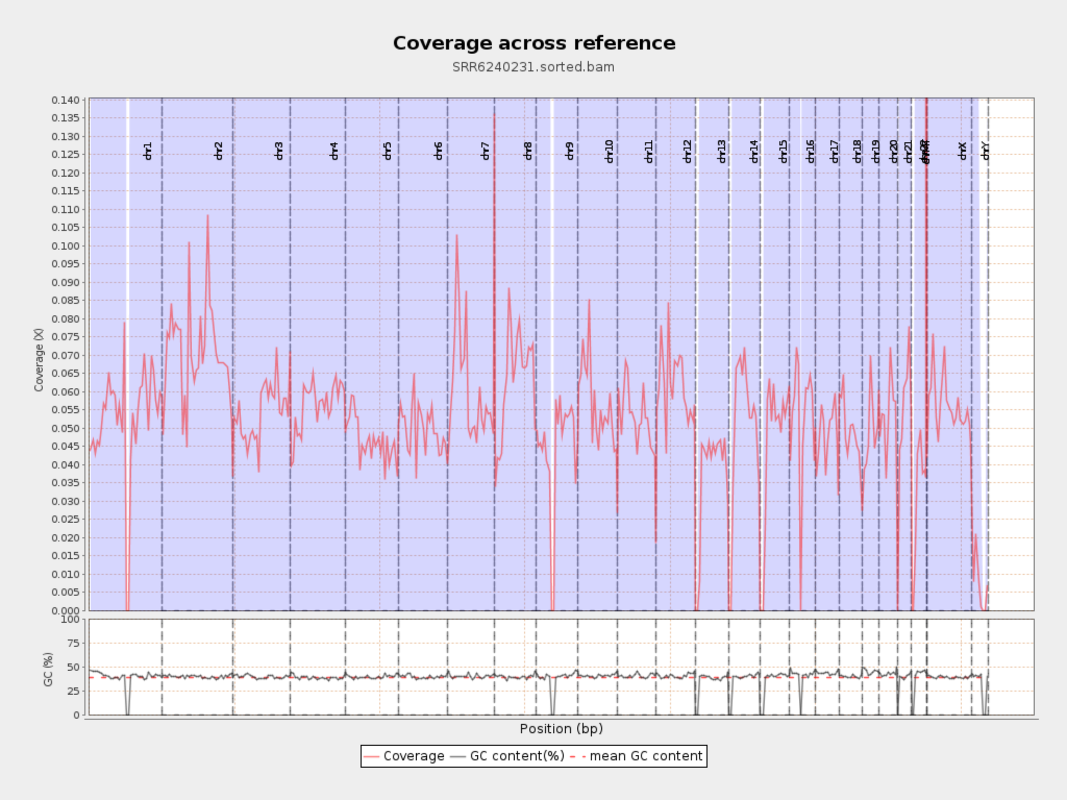
General error rate	0.9%
Mismatches	1,445,090
Insertions	11,557
Mapped reads with at least one insertion	0.45%
Deletions	45,312
Mapped reads with at least one deletion	1.76%
Homopolymer indels	47.85%

2.6. Chromosome stats

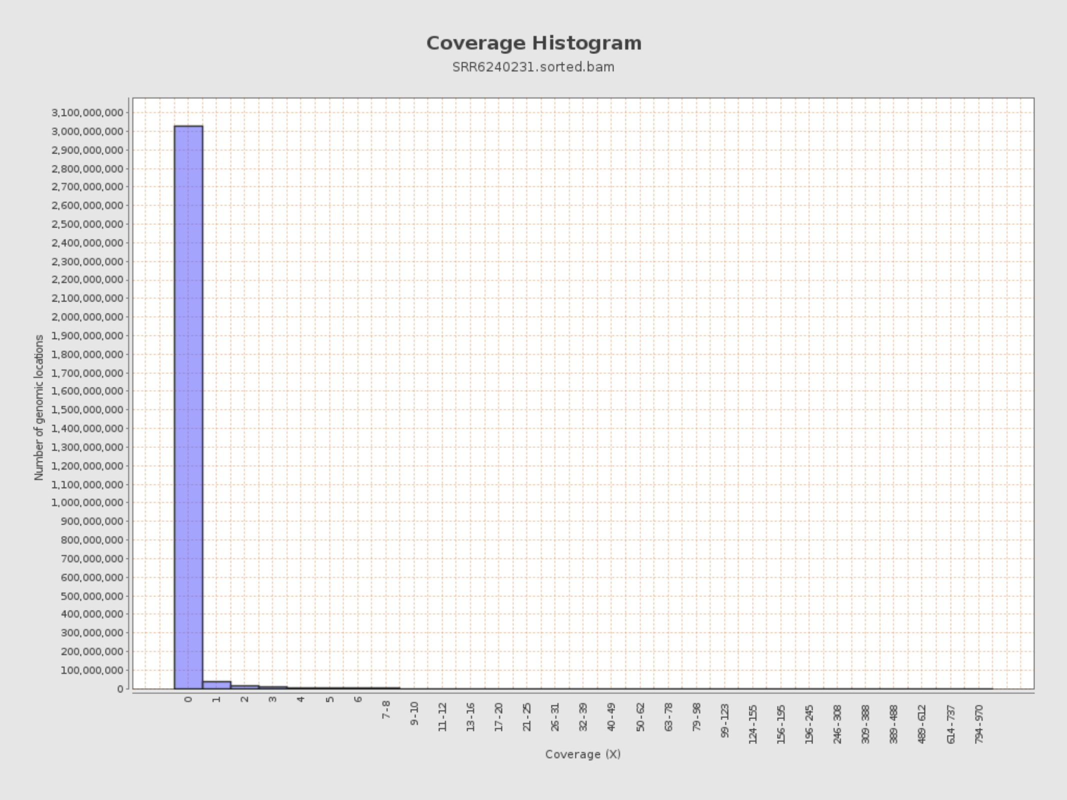
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13055682	0.0524	0.7693
chr2	243199373	17285203	0.0711	0.7139
chr3	198022430	10675447	0.0539	0.4642
chr4	191154276	10735993	0.0562	0.4894
chr5	180915260	8444670	0.0467	0.4305
chr6	171115067	8509918	0.0497	0.4878
chr7	159138663	9681866	0.0608	0.7583

chr8	146364022	9277660	0.0634	0.7593
chr9	141213431	6158779	0.0436	0.4941
chr10	135534747	7745063	0.0571	0.5612
chr11	135006516	7108784	0.0527	0.542
chr12	133851895	8262080	0.0617	0.5016
chr13	115169878	4199314	0.0365	0.3885
chr14	107349540	5398657	0.0503	0.471
chr15	102531392	4679848	0.0456	0.4658
chr16	90354753	4752744	0.0526	0.4605
chr17	81195210	3854297	0.0475	0.4421
chr18	78077248	3867197	0.0495	0.7525
chr19	59128983	2885134	0.0488	0.5701
chr20	63025520	3346344	0.0531	0.4549
chr21	48129895	2540552	0.0528	0.4604
chr22	51304566	1507685	0.0294	0.3267
chrMT	16571	30902	1.8648	2.9455
chrX	155270560	8703863	0.0561	0.4944
chrY	59373566	436356	0.0073	0.1689

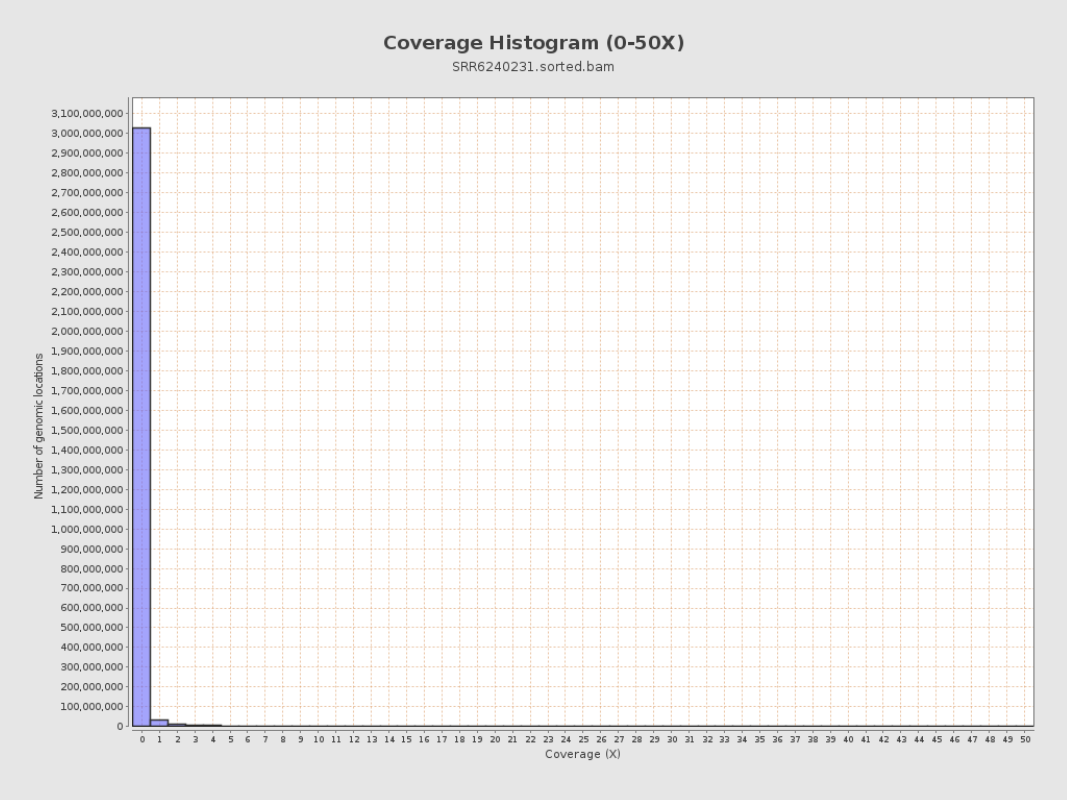
3. Results : Coverage across reference



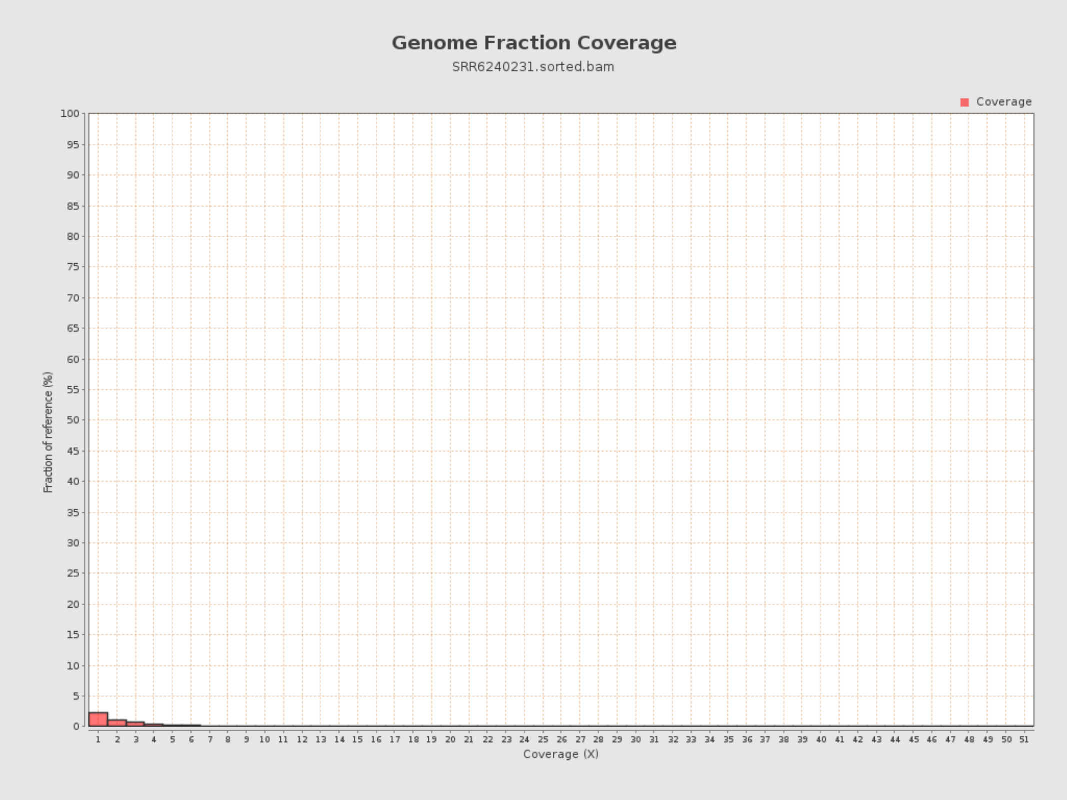
4. Results : Coverage Histogram



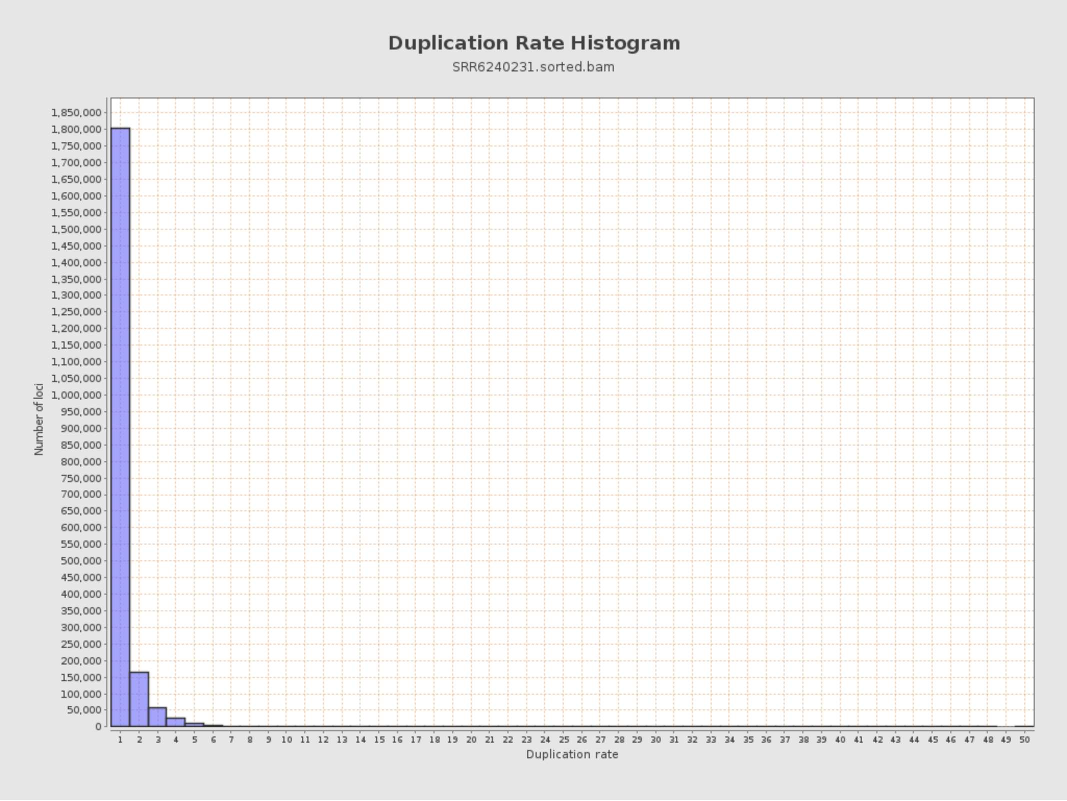
5. Results : Coverage Histogram (0-50X)



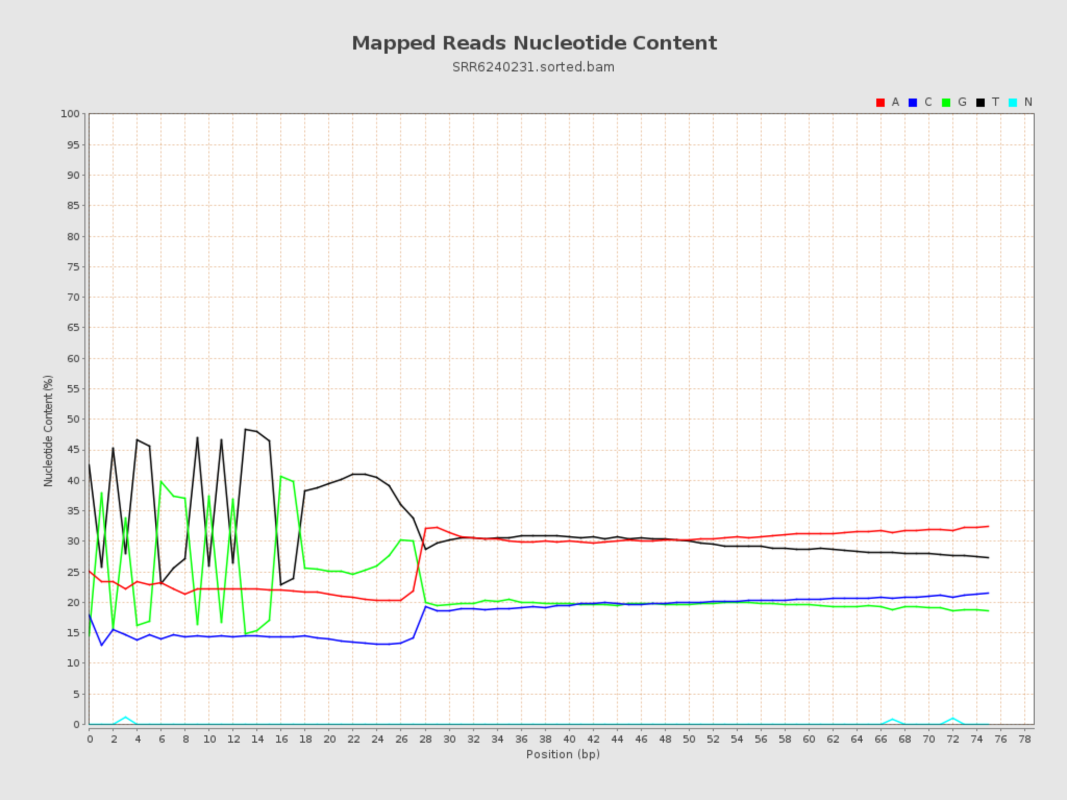
6. Results : Genome Fraction Coverage



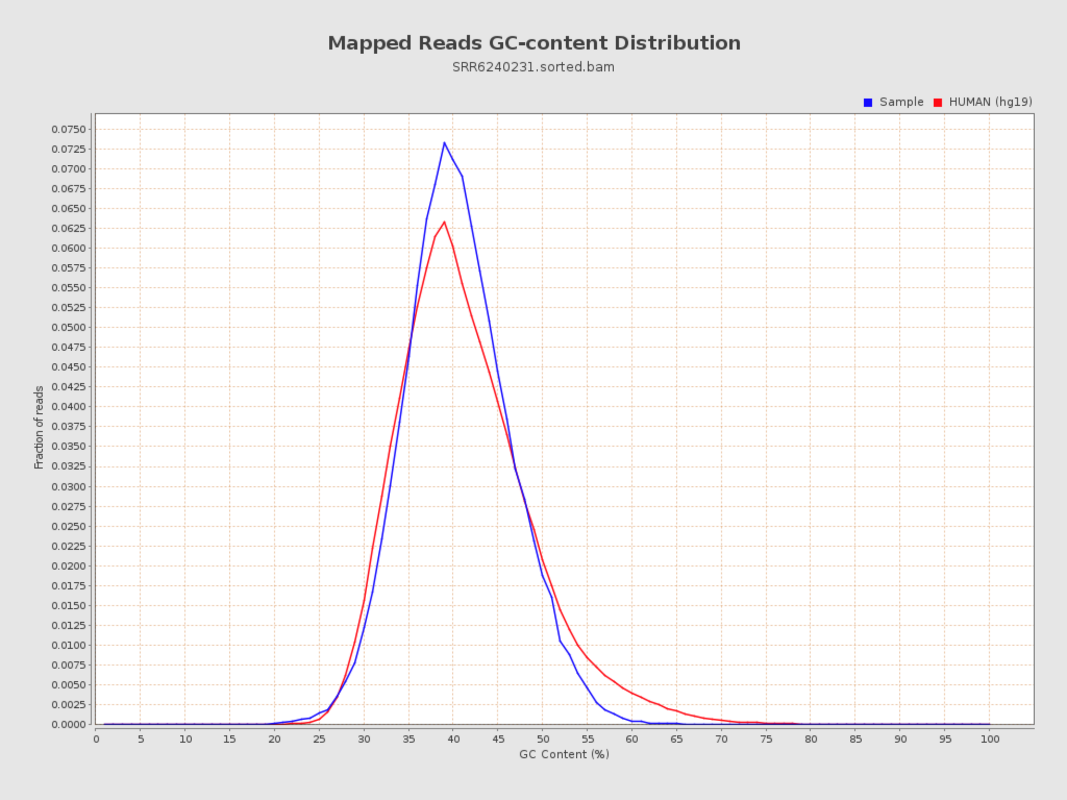
7. Results : Duplication Rate Histogram



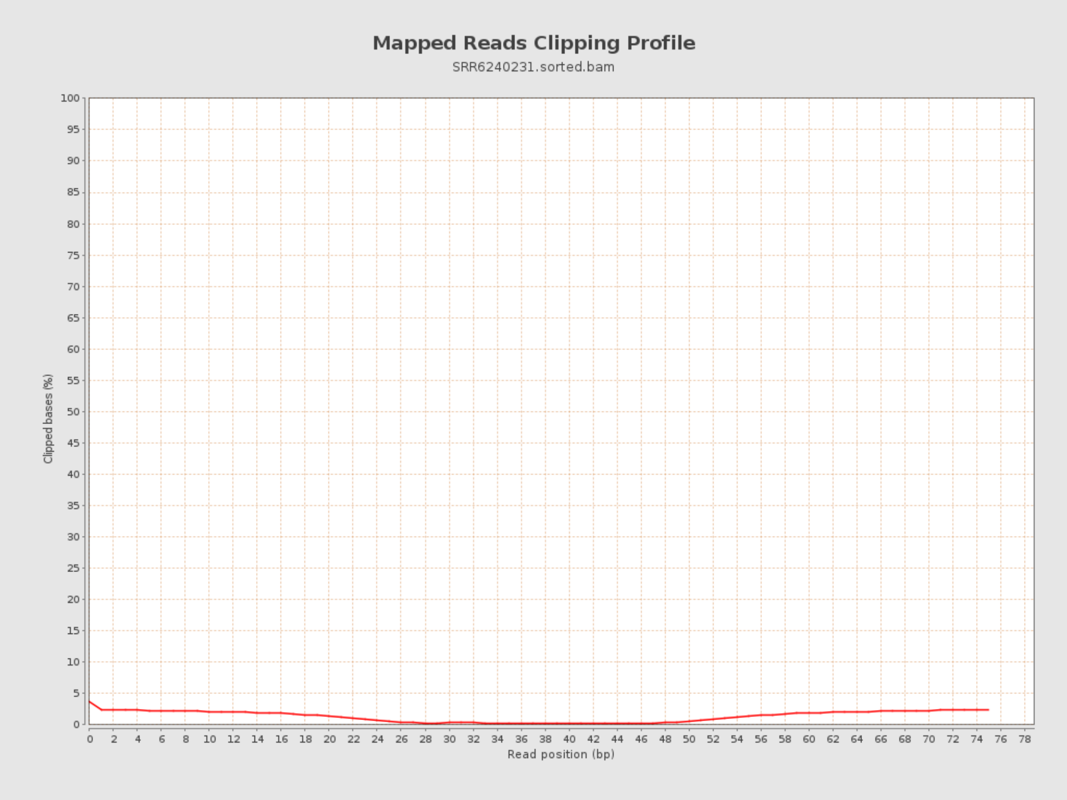
8. Results : Mapped Reads Nucleotide Content



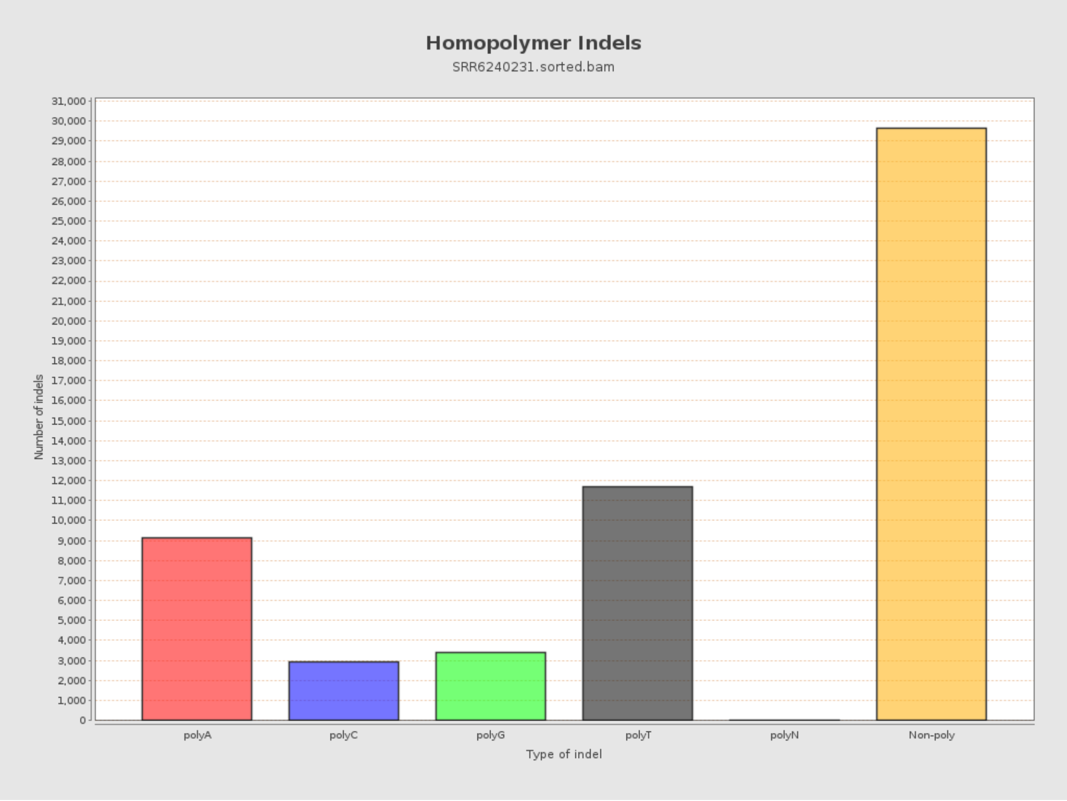
9. Results : Mapped Reads GC-content Distribution



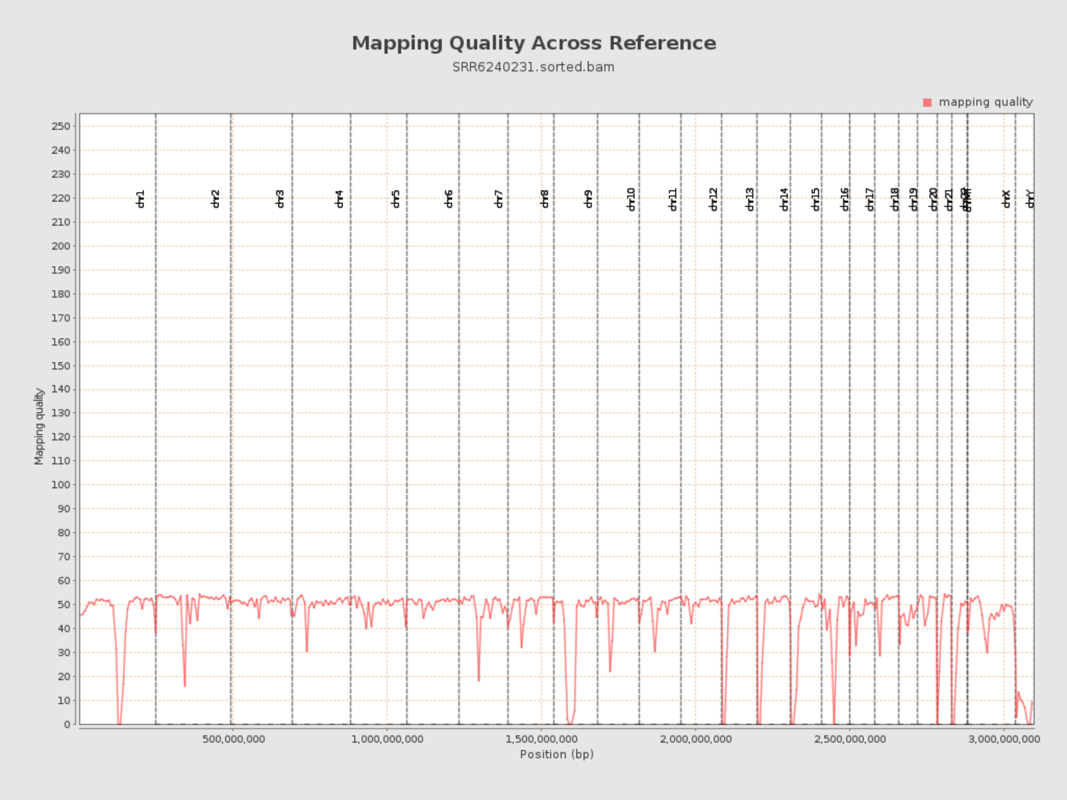
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram