Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 22:55:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231732.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_SRR6231732 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231732.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 22:55:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231732.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,059,657
Mapped reads	2,500,205 / 61.59%
Unmapped reads	1,559,452 / 38.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,521 / 0.73%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	702,783 / 17.31%
Duplication rate	12.35%
Clipped reads	884,684 / 21.79%

2.2. ACGT Content

Number/percentage of A's	41,867,331 / 24.3%
Number/percentage of C's	29,466,102 / 17.1%
Number/percentage of T's	45,333,026 / 26.31%
Number/percentage of G's	55,577,671 / 32.26%
Number/percentage of N's	35,933 / 0.02%
GC Percentage	49.36%

2.3. Coverage

Mean	0.0557

Standard Deviation	45.3344

2.4. Mapping Quality

Mean Mapping Quality	42.6

2.5. Mismatches and indels

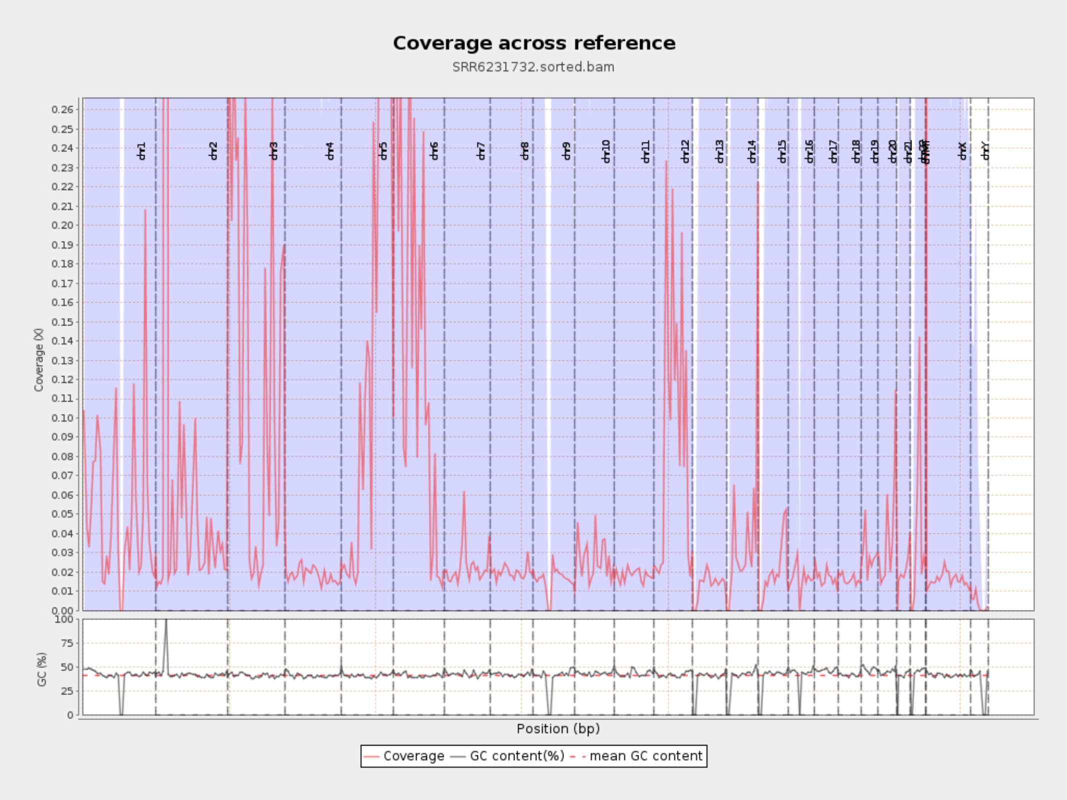
General error rate	0.59%
Mismatches	1,003,838
Insertions	10,254
Mapped reads with at least one insertion	0.41%
Deletions	33,109
Mapped reads with at least one deletion	1.31%
Homopolymer indels	47.18%

2.6. Chromosome stats

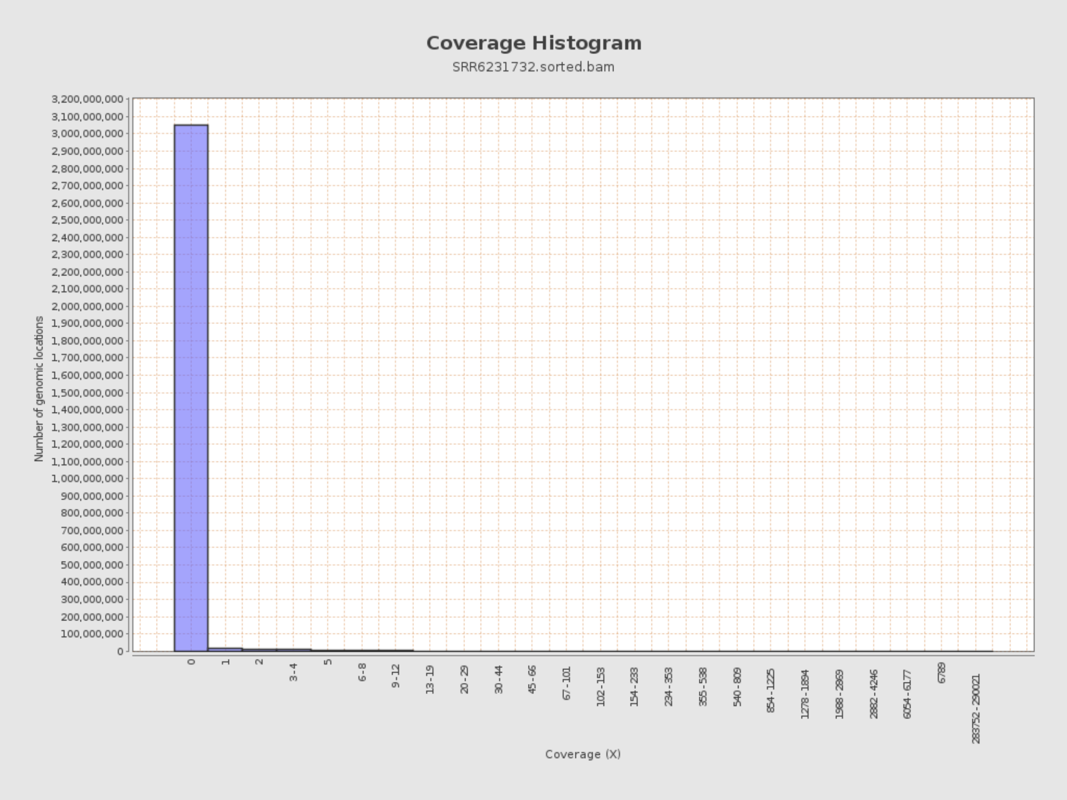
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13069413	0.0524	0.6239
chr2	243199373	31592326	0.1299	161.7291
chr3	198022430	25315420	0.1278	0.9372
chr4	191154276	3509755	0.0184	0.3296
chr5	180915260	26499323	0.1465	1.0078
chr6	171115067	24160917	0.1412	1.2781
chr7	159138663	3713715	0.0233	0.4241

chr8	146364022	2920404	0.02	0.3816
chr9	141213431	2243123	0.0159	0.3459
chr10	135534747	3600232	0.0266	0.453
chr11	135006516	2467149	0.0183	0.4022
chr12	133851895	12302955	0.0919	0.7832
chr13	115169878	1544453	0.0134	0.2839
chr14	107349540	3322128	0.0309	0.5463
chr15	102531392	2022970	0.0197	0.3612
chr16	90354753	1446399	0.016	0.3246
chr17	81195210	1414667	0.0174	0.3252
chr18	78077248	1271584	0.0163	0.3517
chr19	59128983	1735139	0.0293	0.463
chr20	63025520	2358042	0.0374	0.5127
chr21	48129895	984140	0.0204	0.3635
chr22	51304566	2061797	0.0402	0.5302
chrMT	16571	70139	4.2326	6.0775
chrX	155270560	2498157	0.0161	0.2948
chrY	59373566	209606	0.0035	0.1055

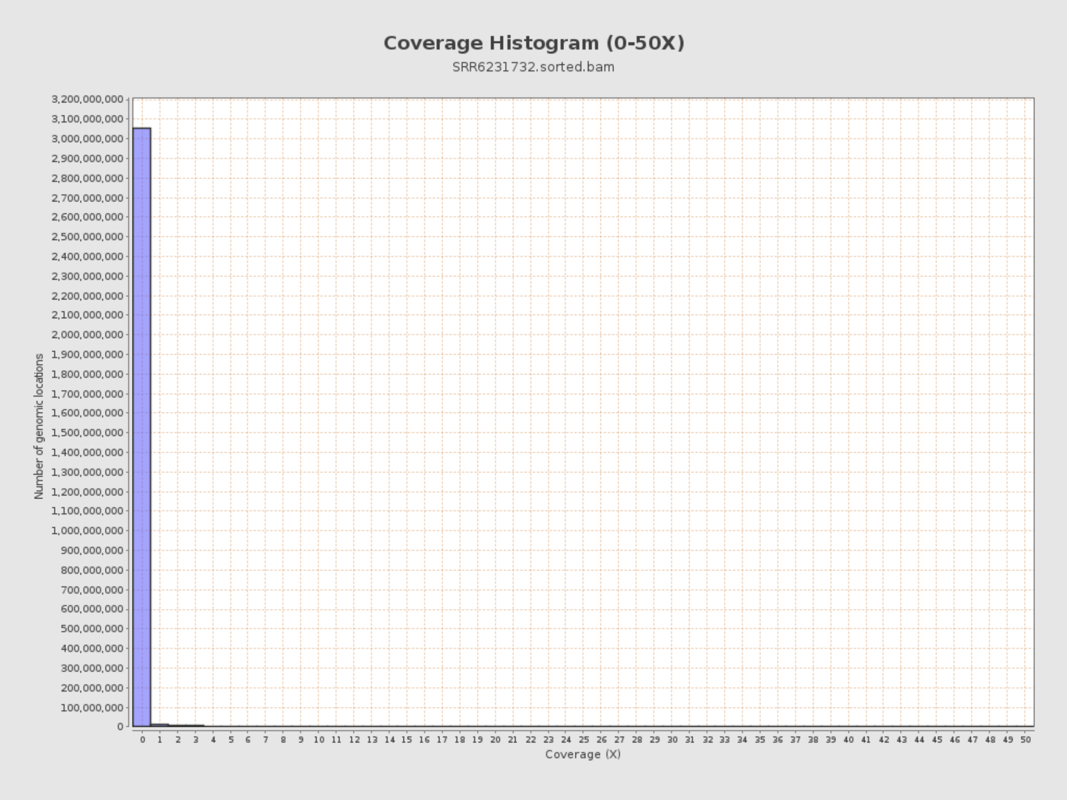
3. Results : Coverage across reference



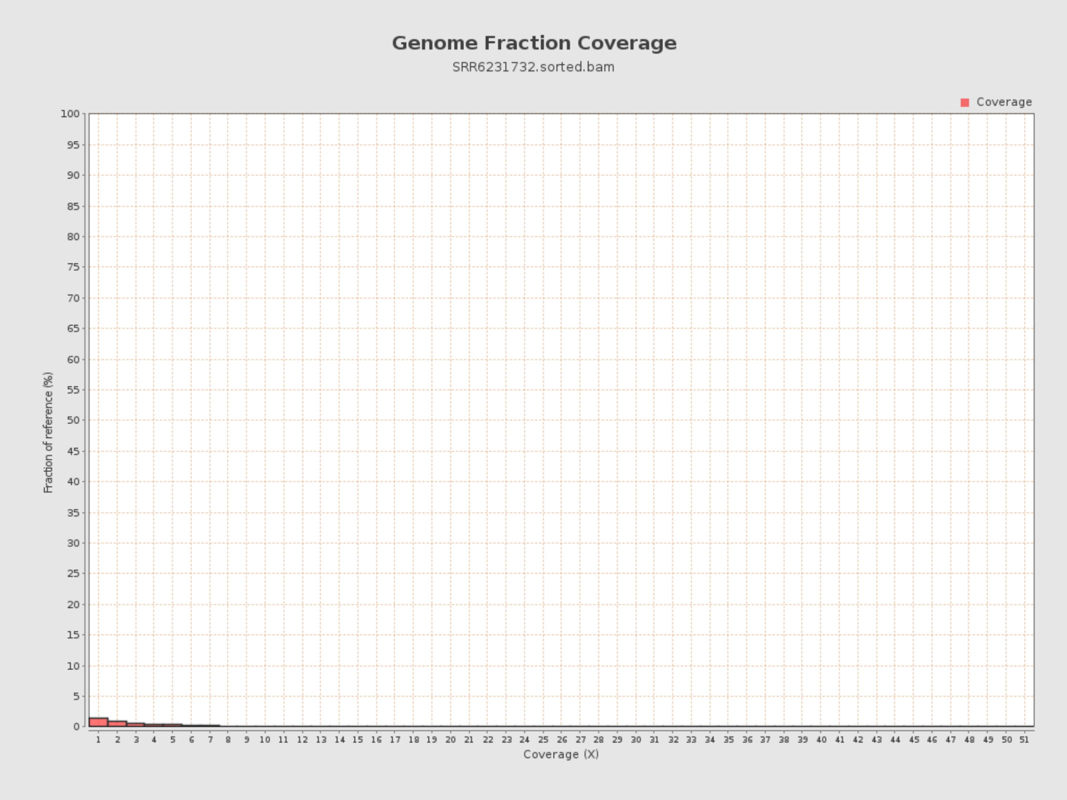
4. Results : Coverage Histogram



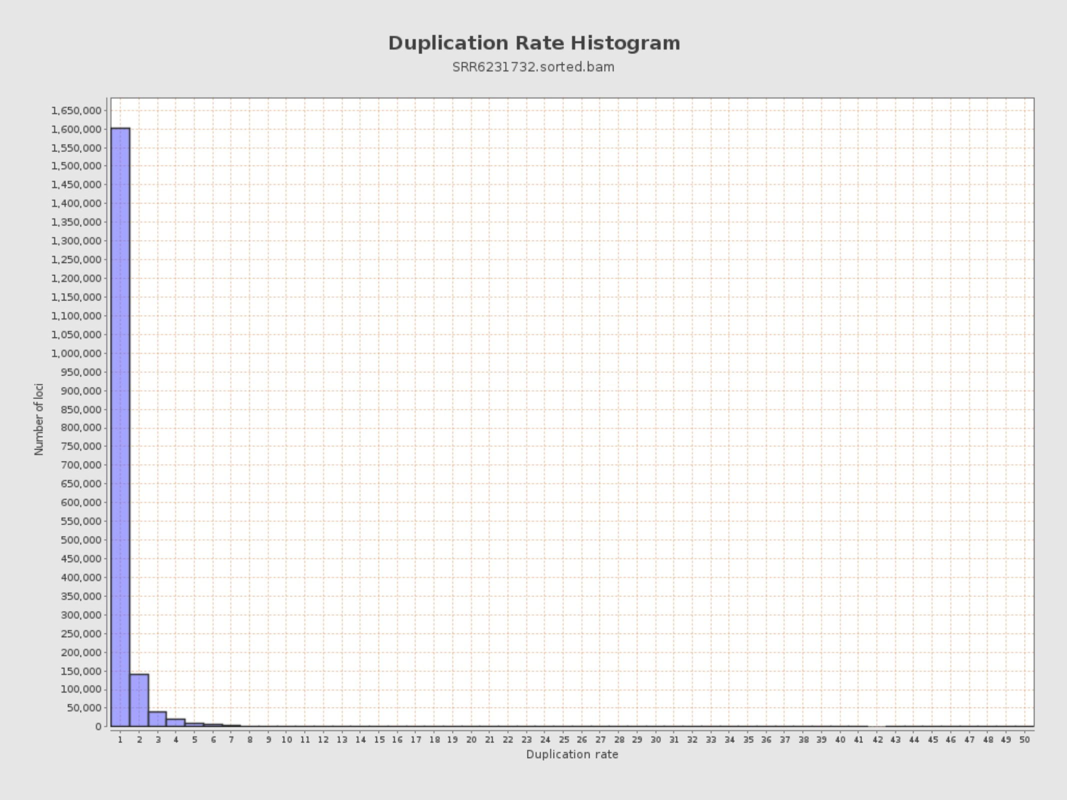
5. Results : Coverage Histogram (0-50X)



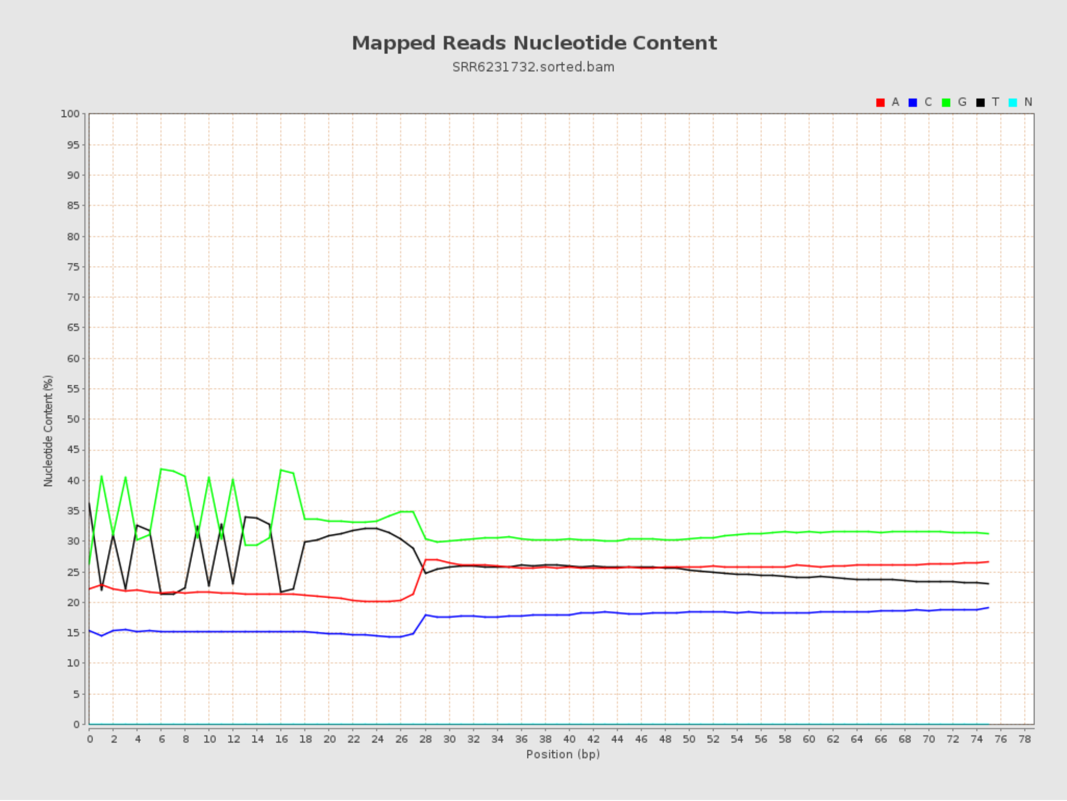
6. Results : Genome Fraction Coverage



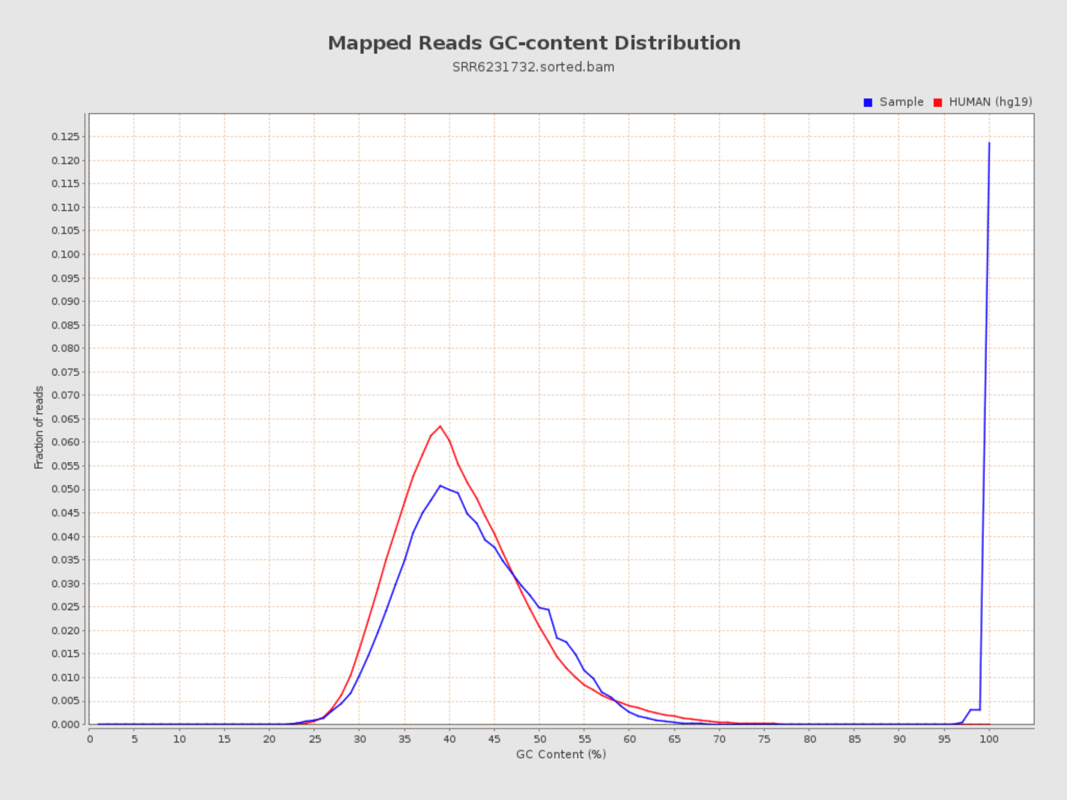
7. Results : Duplication Rate Histogram



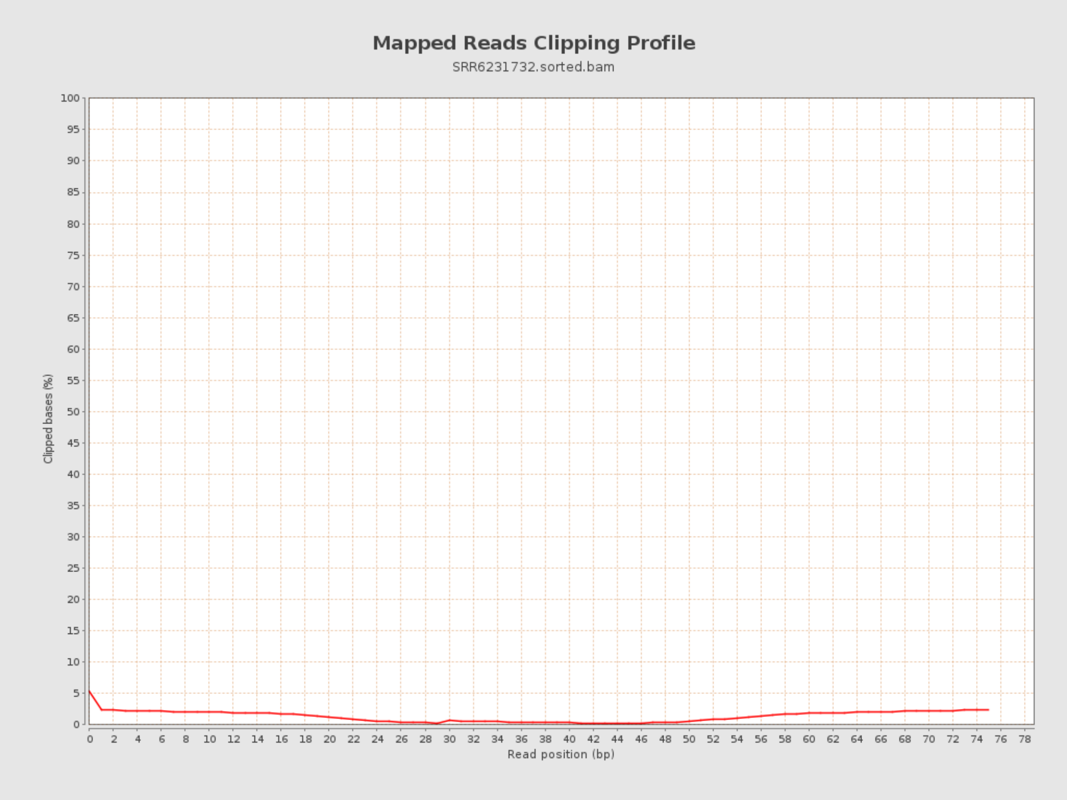
8. Results : Mapped Reads Nucleotide Content



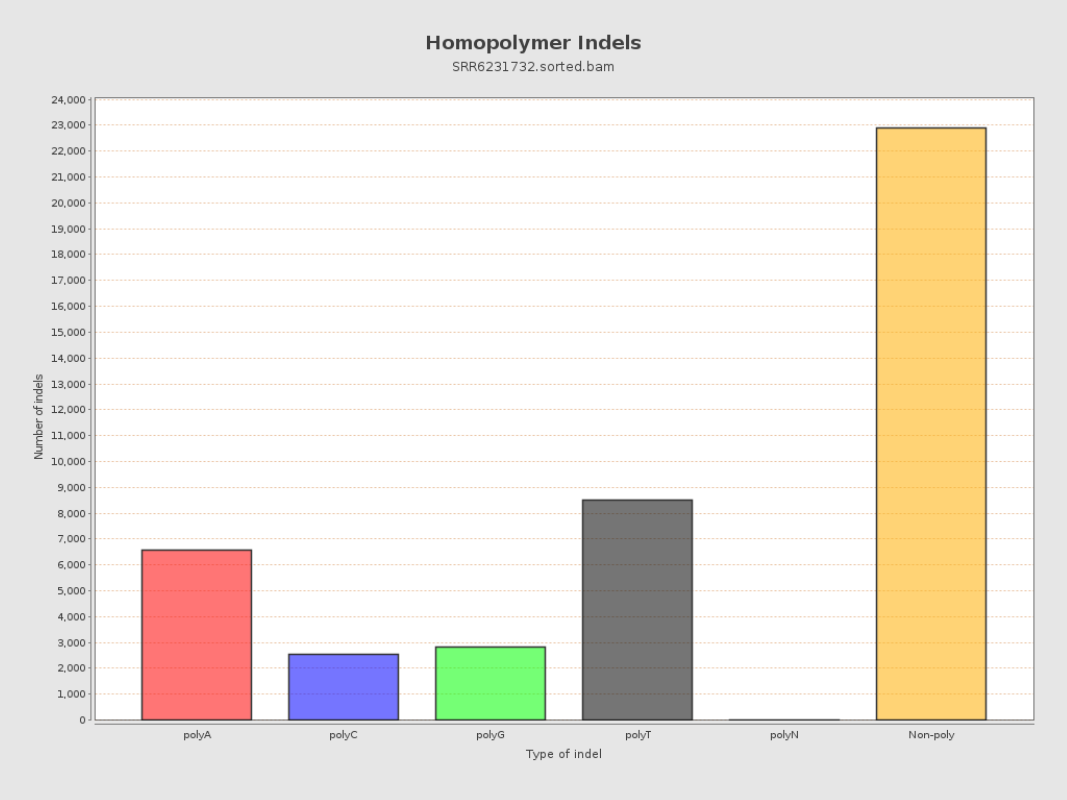
9. Results : Mapped Reads GC-content Distribution



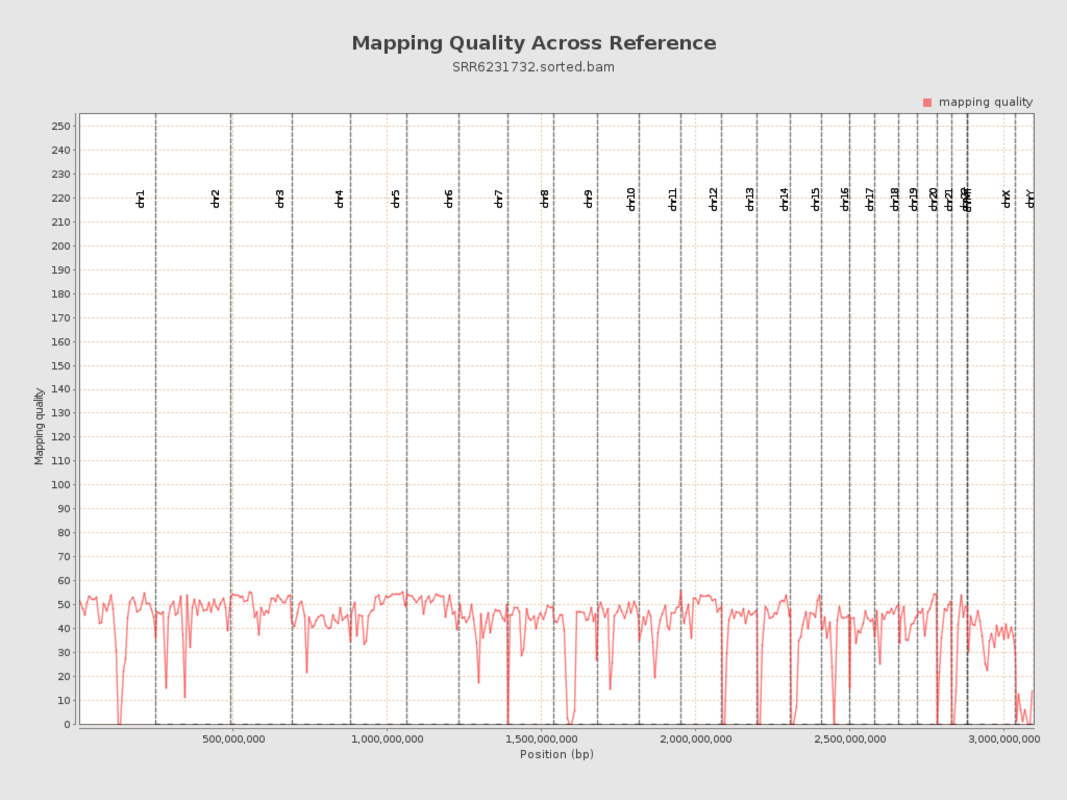
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram