Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 08:17:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231855.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_SRR6231855 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231855.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 08:17:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231855.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,232,519
Mapped reads	4,887,808 / 93.41%
Unmapped reads	344,711 / 6.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,621 / 0.59%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	481,166 / 9.2%
Duplication rate	7.92%
Clipped reads	2,659,352 / 50.82%

2.2. ACGT Content

Number/percentage of A's	80,707,840 / 25.73%
Number/percentage of C's	56,164,722 / 17.91%
Number/percentage of T's	102,817,742 / 32.78%
Number/percentage of G's	73,828,788 / 23.54%
Number/percentage of N's	121,541 / 0.04%
GC Percentage	41.45%

2.3. Coverage

Mean	0.1014

Standard Deviation	1.0361

2.4. Mapping Quality

Mean Mapping Quality	44.51

2.5. Mismatches and indels

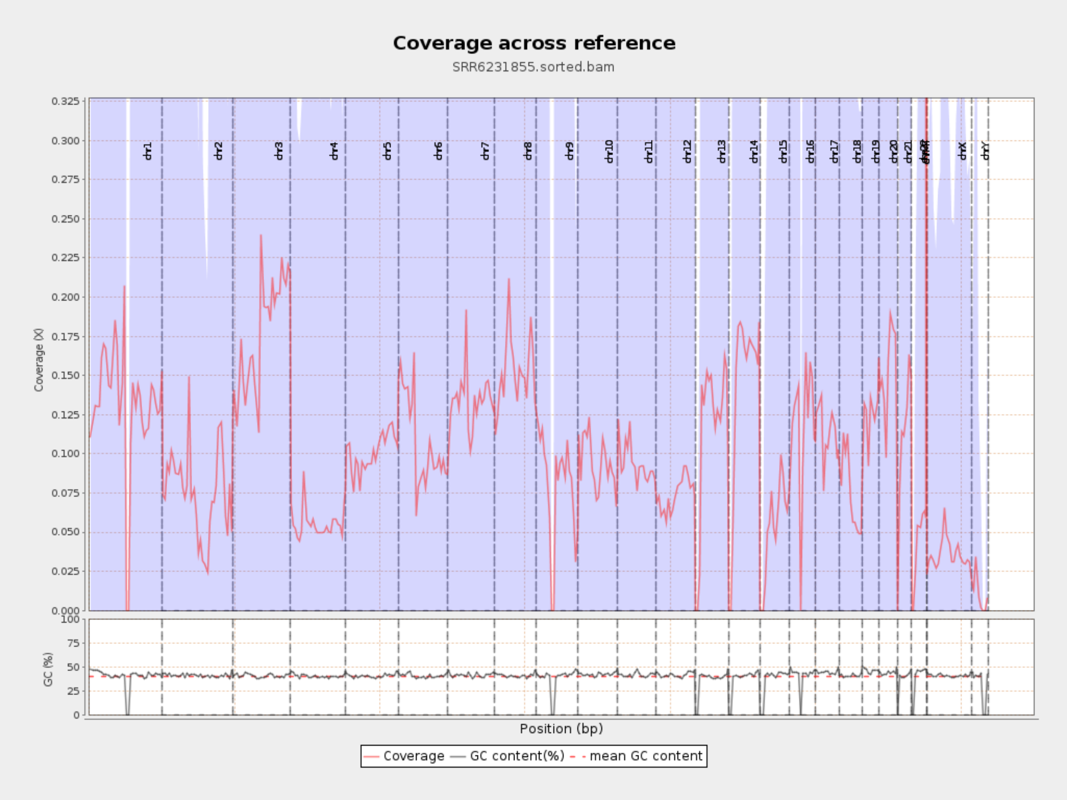
General error rate	0.65%
Mismatches	1,988,650
Insertions	20,169
Mapped reads with at least one insertion	0.41%
Deletions	68,735
Mapped reads with at least one deletion	1.39%
Homopolymer indels	43.45%

2.6. Chromosome stats

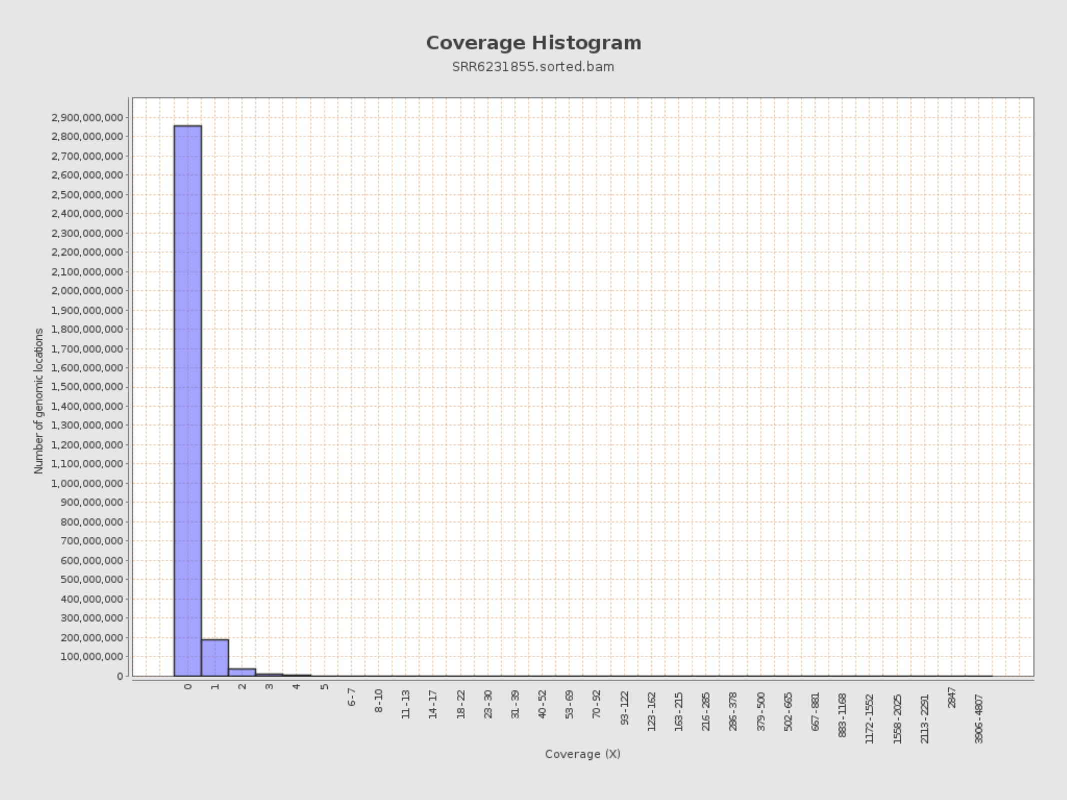
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	32699068	0.1312	1.8376
chr2	243199373	18263439	0.0751	2.1808
chr3	198022430	34715058	0.1753	0.5384
chr4	191154276	10518295	0.055	0.3991
chr5	180915260	18199023	0.1006	0.4089
chr6	171115067	18522554	0.1082	0.7524
chr7	159138663	21290110	0.1338	1.3329

chr8	146364022	22394156	0.153	1.164
chr9	141213431	11244943	0.0796	0.6317
chr10	135534747	12834120	0.0947	0.6451
chr11	135006516	12686010	0.094	0.6875
chr12	133851895	9936204	0.0742	0.3658
chr13	115169878	13341723	0.1158	0.5105
chr14	107349540	15024515	0.14	0.5252
chr15	102531392	5558102	0.0542	0.4235
chr16	90354753	10747608	0.1189	0.525
chr17	81195210	9172521	0.113	0.518
chr18	78077248	5902520	0.0756	1.4738
chr19	59128983	7331640	0.124	1.1414
chr20	63025520	9565818	0.1518	0.5508
chr21	48129895	5353461	0.1112	0.4459
chr22	51304566	2103915	0.041	0.2438
chrMT	16571	170751	10.3042	6.7133
chrX	155270560	5600711	0.0361	0.3733
chrY	59373566	582239	0.0098	0.2014

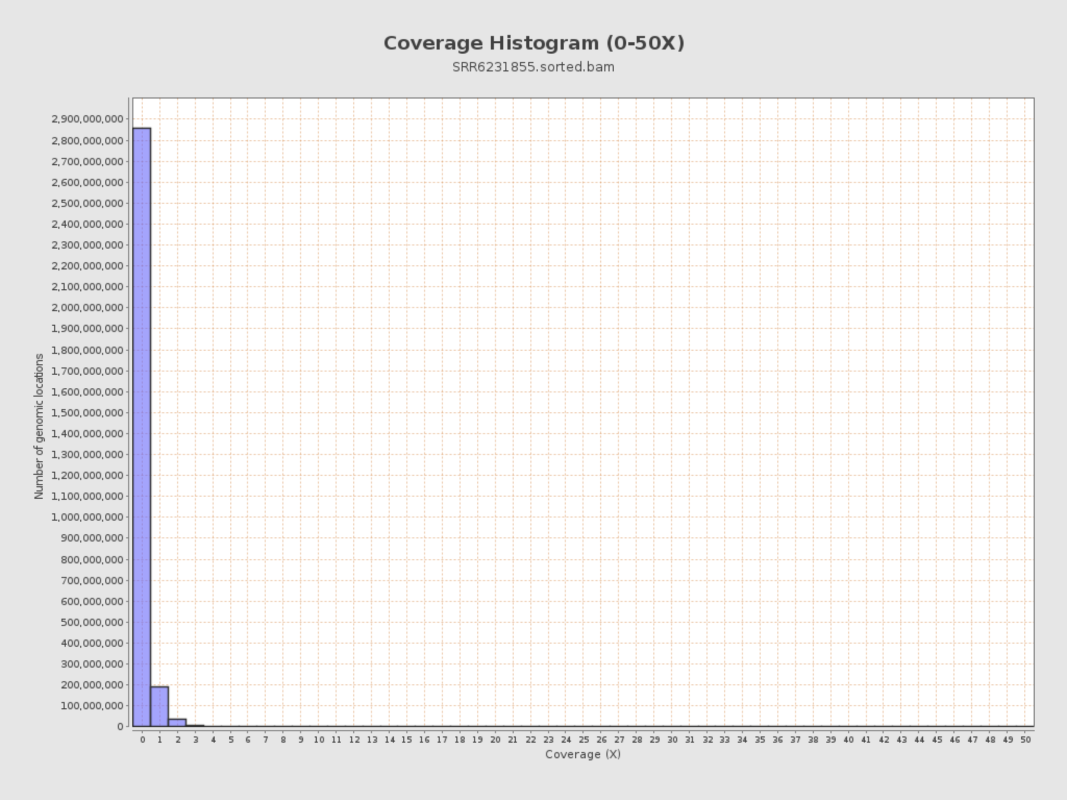
3. Results : Coverage across reference



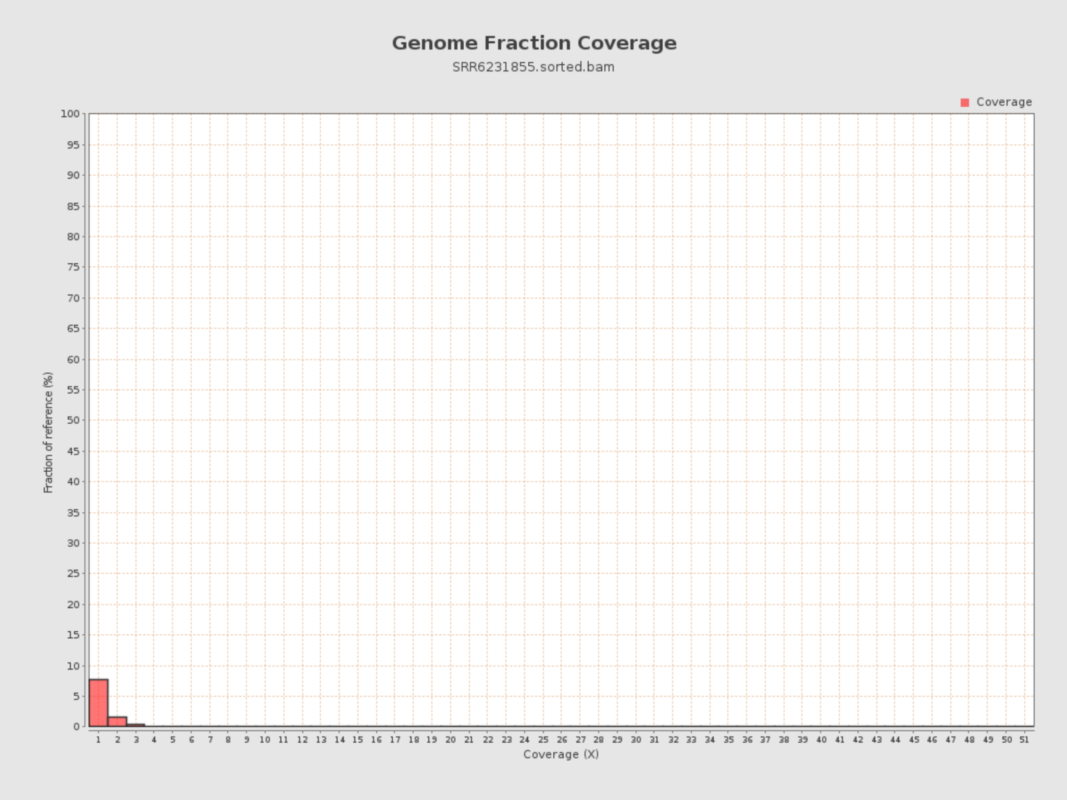
4. Results : Coverage Histogram



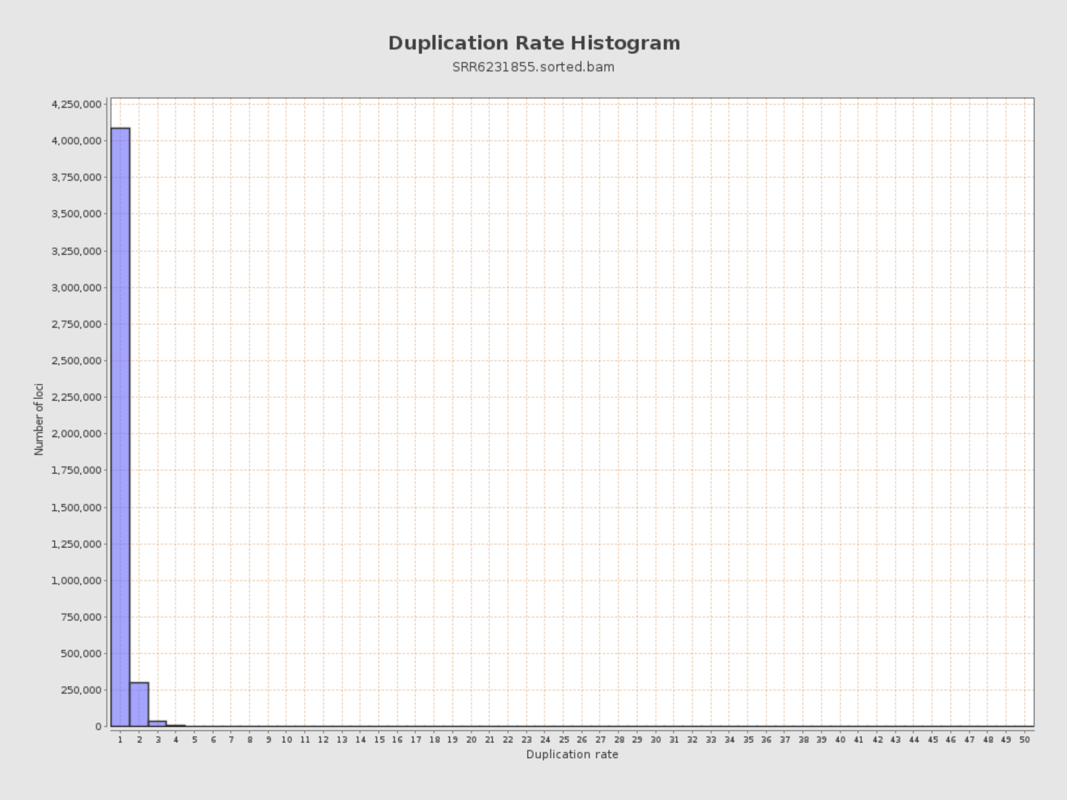
5. Results : Coverage Histogram (0-50X)



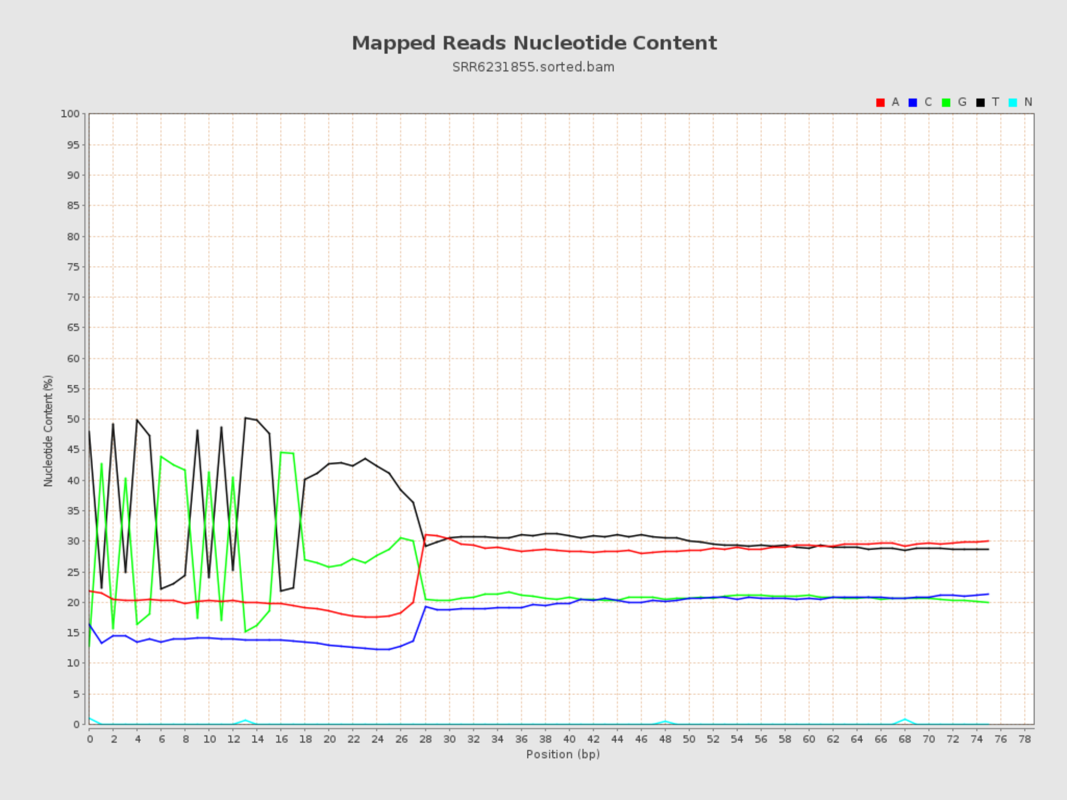
6. Results : Genome Fraction Coverage



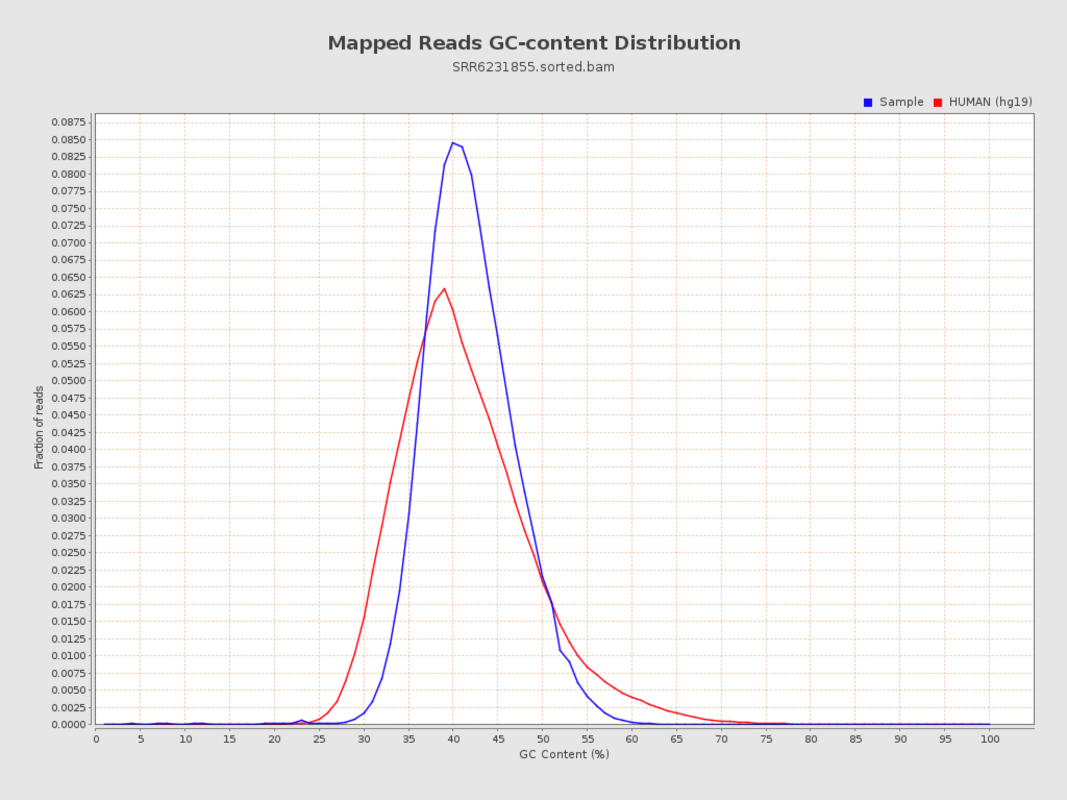
7. Results : Duplication Rate Histogram



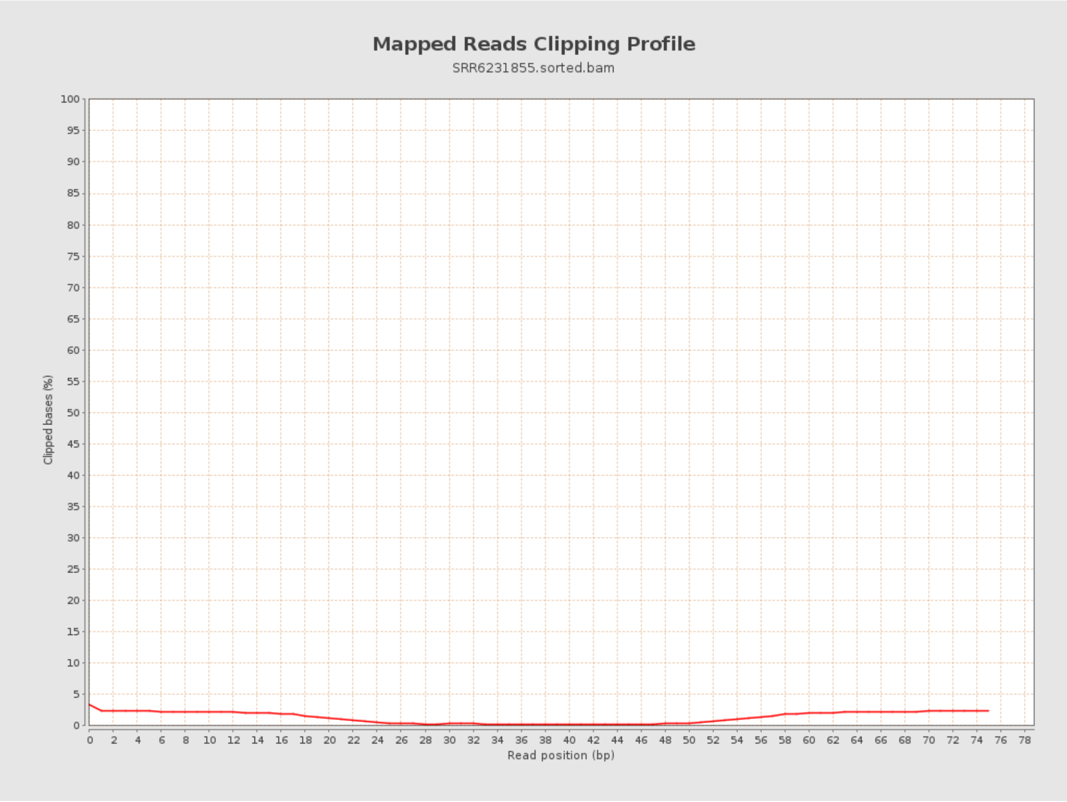
8. Results : Mapped Reads Nucleotide Content



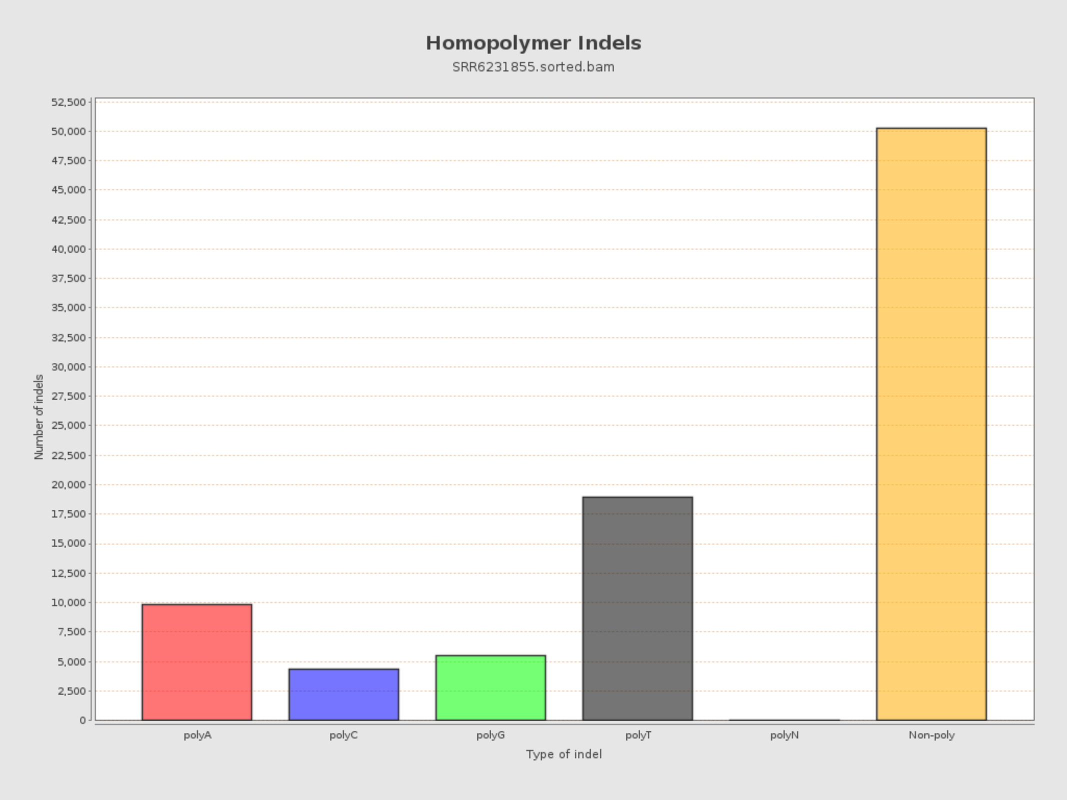
9. Results : Mapped Reads GC-content Distribution



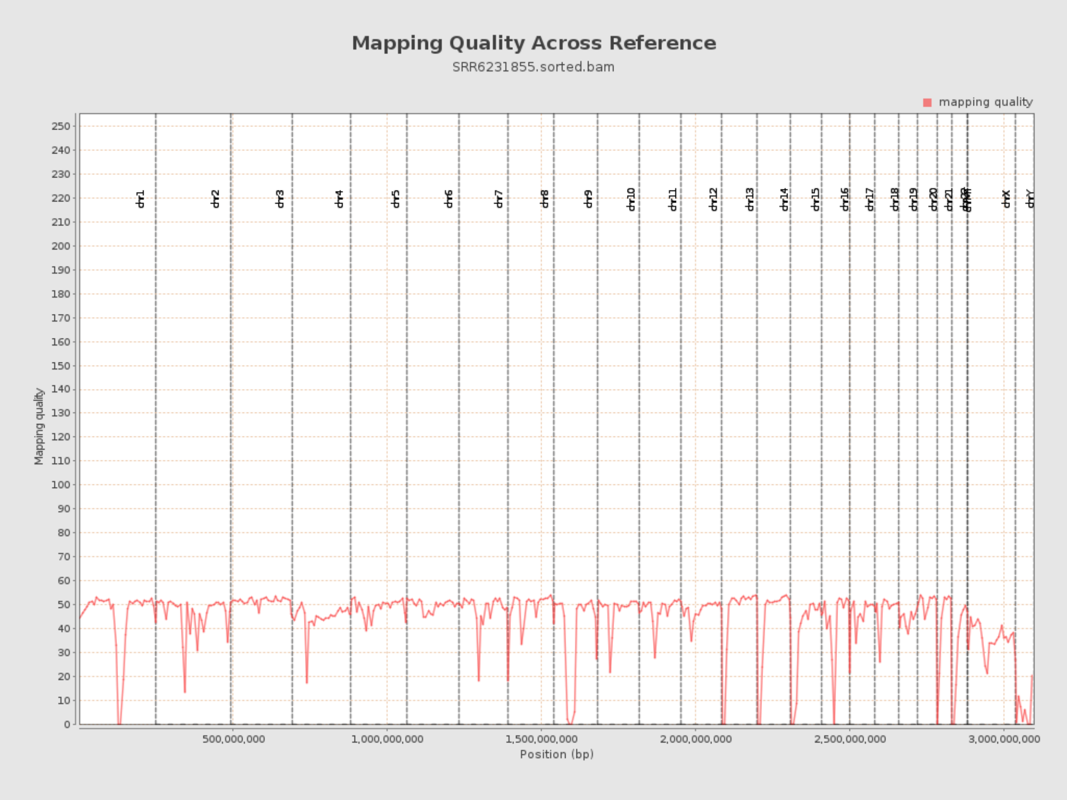
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram