Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 07:07:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231841.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_SRR6231841 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231841.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 07:07:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231841.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,070,718
Mapped reads	16,520,590 / 86.63%
Unmapped reads	2,550,128 / 13.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	213,137 / 1.12%
Read min/max/mean length	30 / 76 / 76.39
Duplicated reads (estimated)	3,466,131 / 18.18%
Duplication rate	11.9%
Clipped reads	8,326,623 / 43.66%

2.2. ACGT Content

Number/percentage of A's	314,652,215 / 28.98%
Number/percentage of C's	213,653,574 / 19.68%
Number/percentage of T's	320,223,445 / 29.49%
Number/percentage of G's	237,253,498 / 21.85%
Number/percentage of N's	82,833 / 0.01%
GC Percentage	41.53%

2.3. Coverage

Mean	0.3509

Standard Deviation	17.0648

2.4. Mapping Quality

Mean Mapping Quality	40.17

2.5. Mismatches and indels

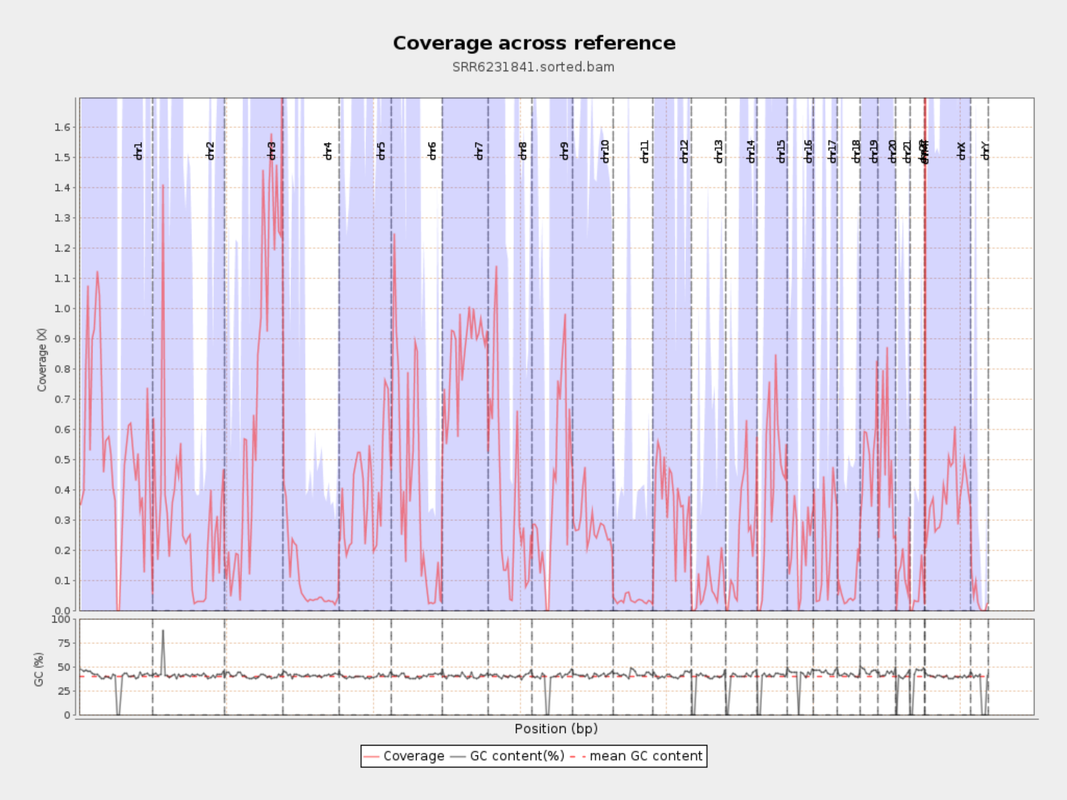
General error rate	0.56%
Mismatches	5,942,872
Insertions	70,472
Mapped reads with at least one insertion	0.42%
Deletions	233,001
Mapped reads with at least one deletion	1.4%
Homopolymer indels	47.26%

2.6. Chromosome stats

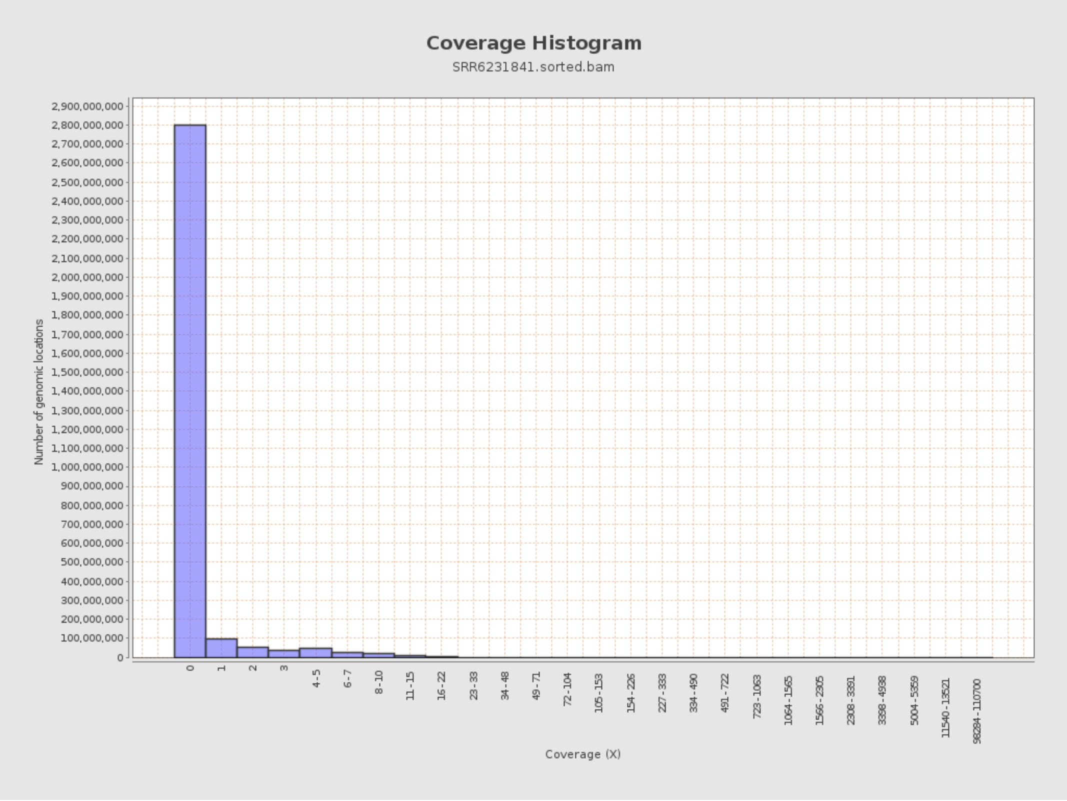
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	131689315	0.5283	4.3903
chr2	243199373	71462005	0.2938	60.2488
chr3	198022430	137890498	0.6963	2.2502
chr4	191154276	18958071	0.0992	1.08
chr5	180915260	72067810	0.3984	1.6015
chr6	171115067	68070804	0.3978	2.5194
chr7	159138663	135103490	0.849	6.4418

chr8	146364022	54638024	0.3733	1.8588
chr9	141213431	55121485	0.3903	1.8824
chr10	135534747	38173455	0.2817	2.9044
chr11	135006516	4594963	0.034	0.6399
chr12	133851895	48255121	0.3605	1.486
chr13	115169878	9160888	0.0795	0.7008
chr14	107349540	24860014	0.2316	1.254
chr15	102531392	41002206	0.3999	1.5915
chr16	90354753	19877622	0.22	1.1463
chr17	81195210	19203069	0.2365	1.1978
chr18	78077248	5279457	0.0676	0.912
chr19	59128983	30141537	0.5098	2.5114
chr20	63025520	29998938	0.476	1.7597
chr21	48129895	6435136	0.1337	0.9587
chr22	51304566	2751699	0.0536	0.52
chrMT	16571	365612	22.0634	16.2445
chrX	155270560	58962632	0.3797	1.6672
chrY	59373566	2191382	0.0369	0.6658

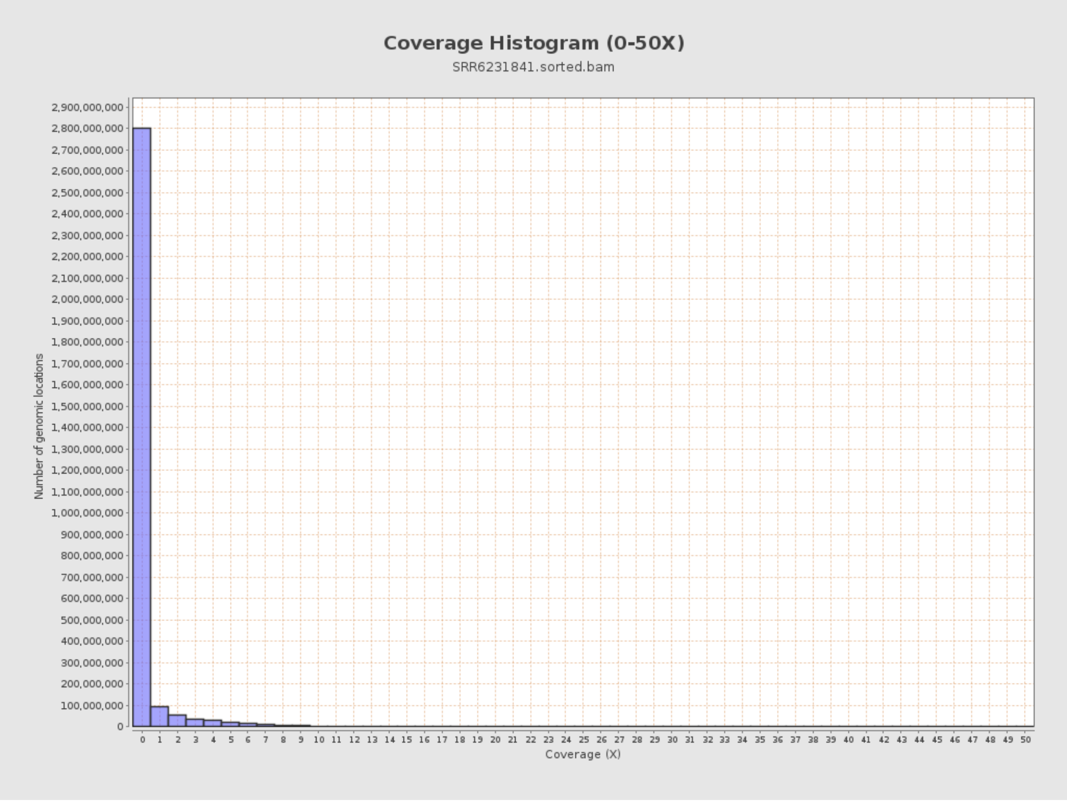
3. Results : Coverage across reference



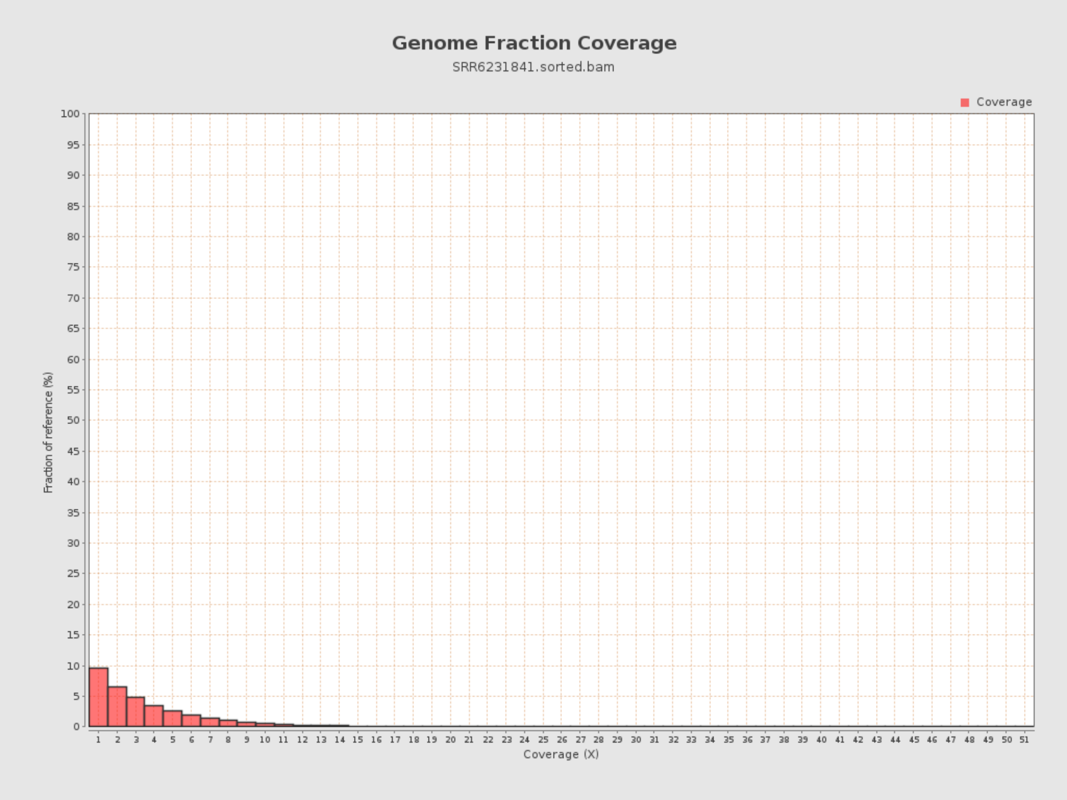
4. Results : Coverage Histogram



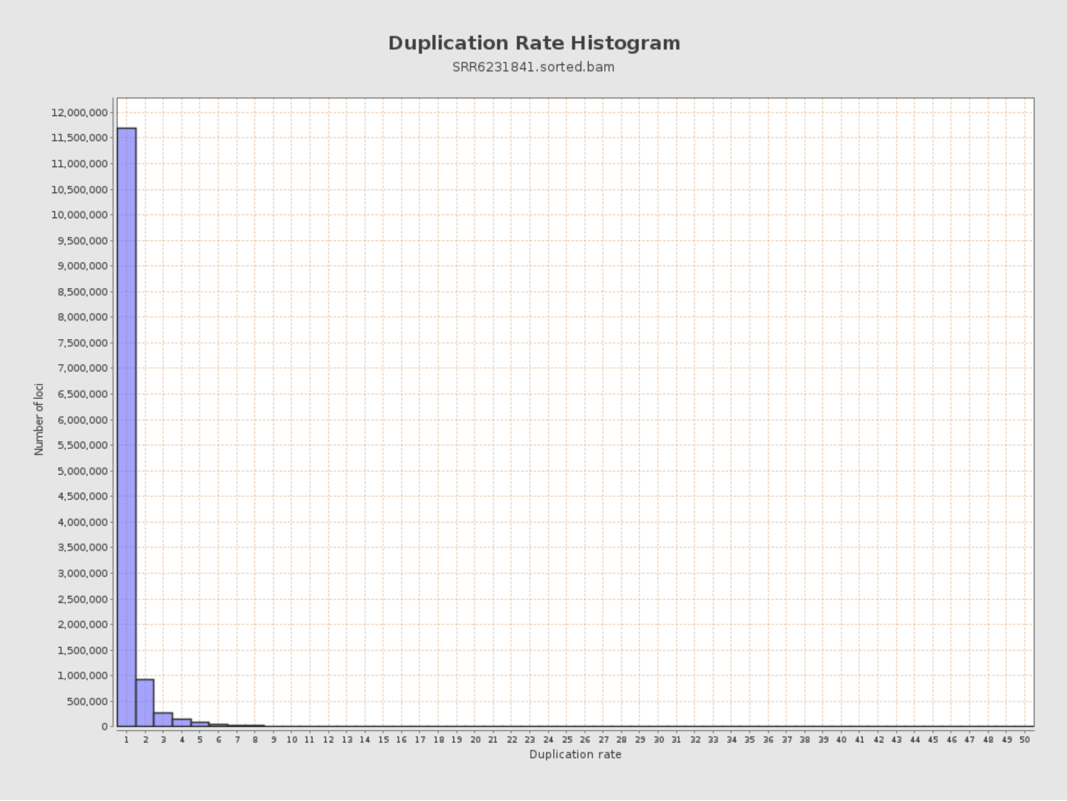
5. Results : Coverage Histogram (0-50X)



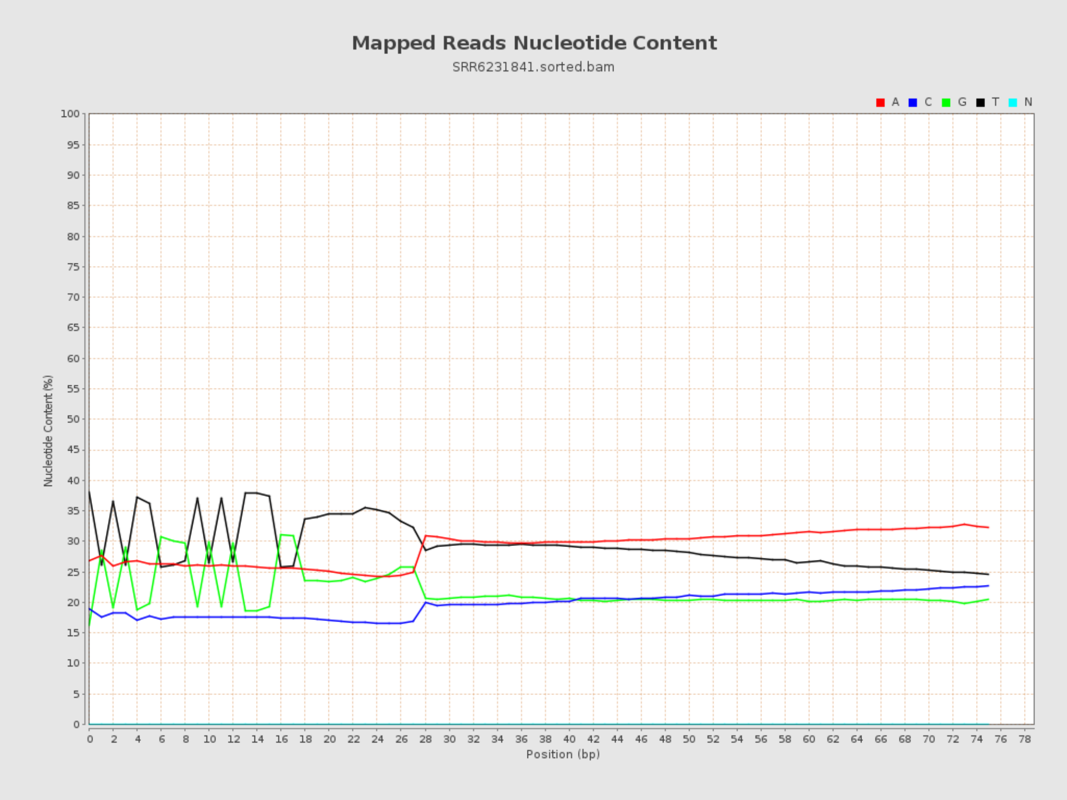
6. Results : Genome Fraction Coverage



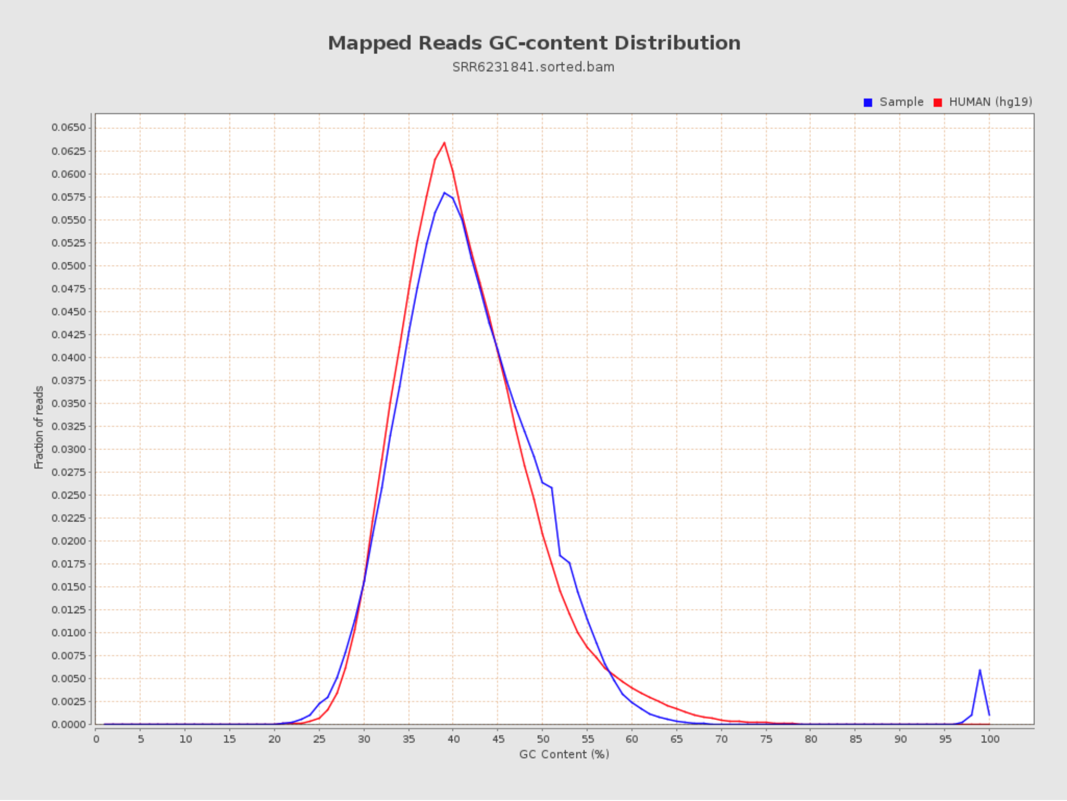
7. Results : Duplication Rate Histogram



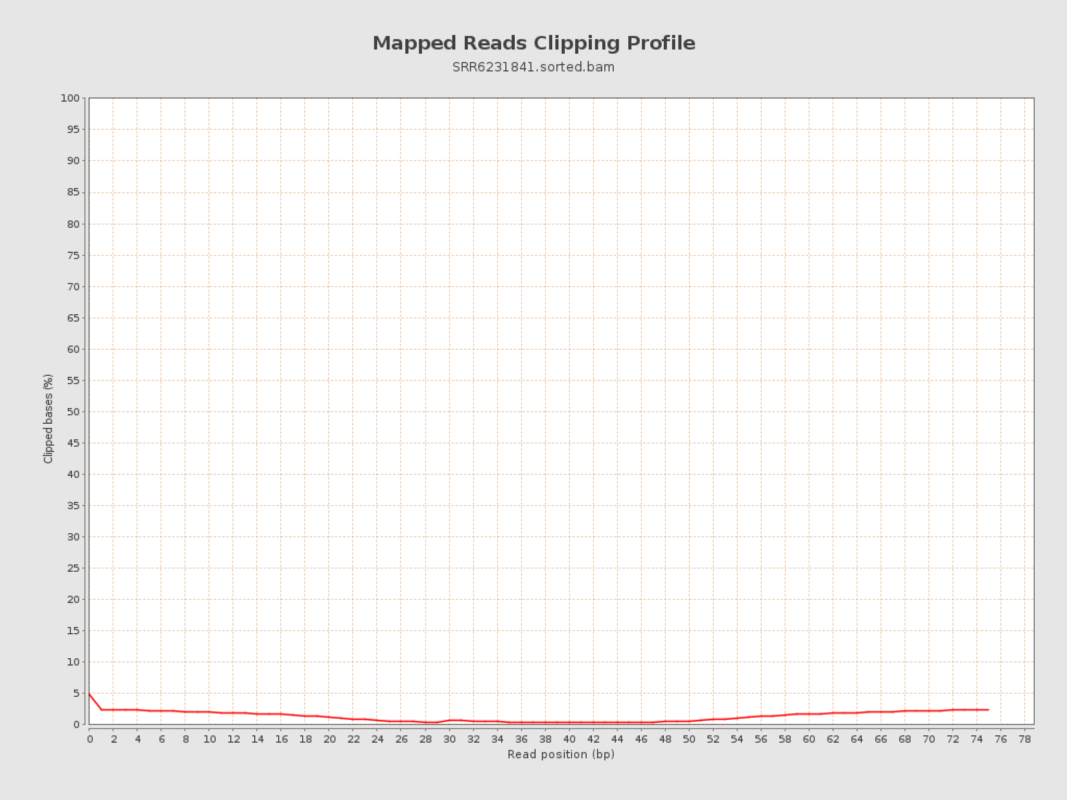
8. Results : Mapped Reads Nucleotide Content



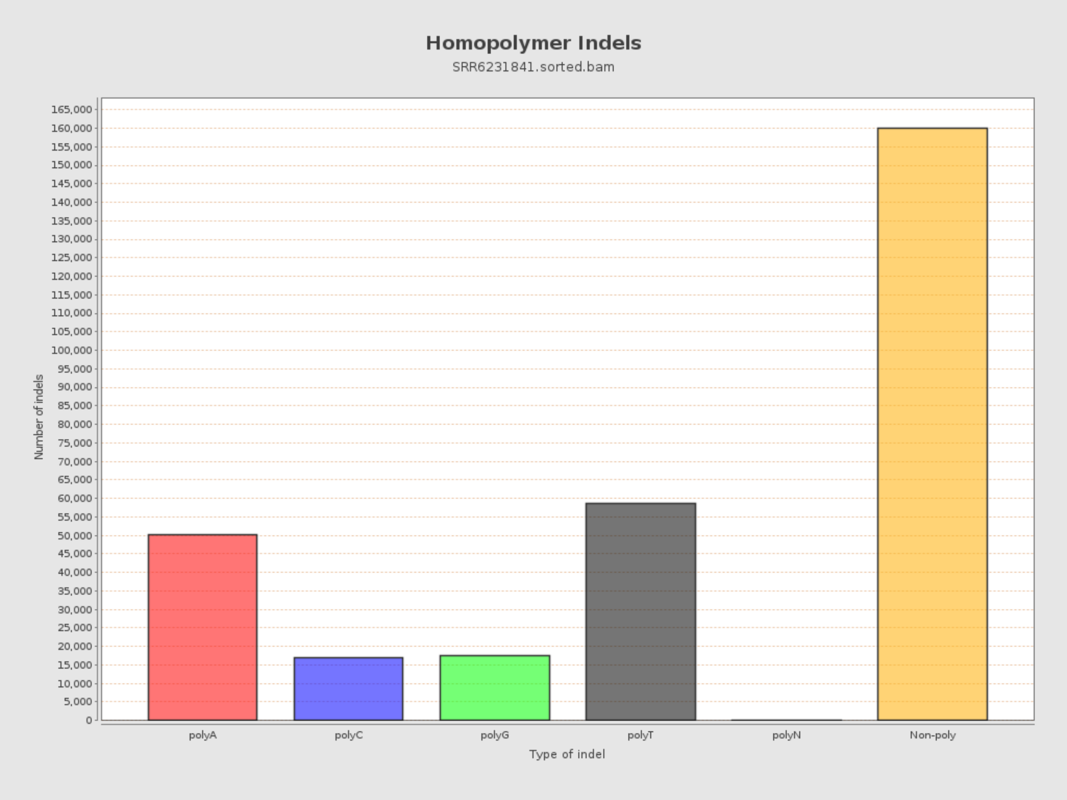
9. Results : Mapped Reads GC-content Distribution



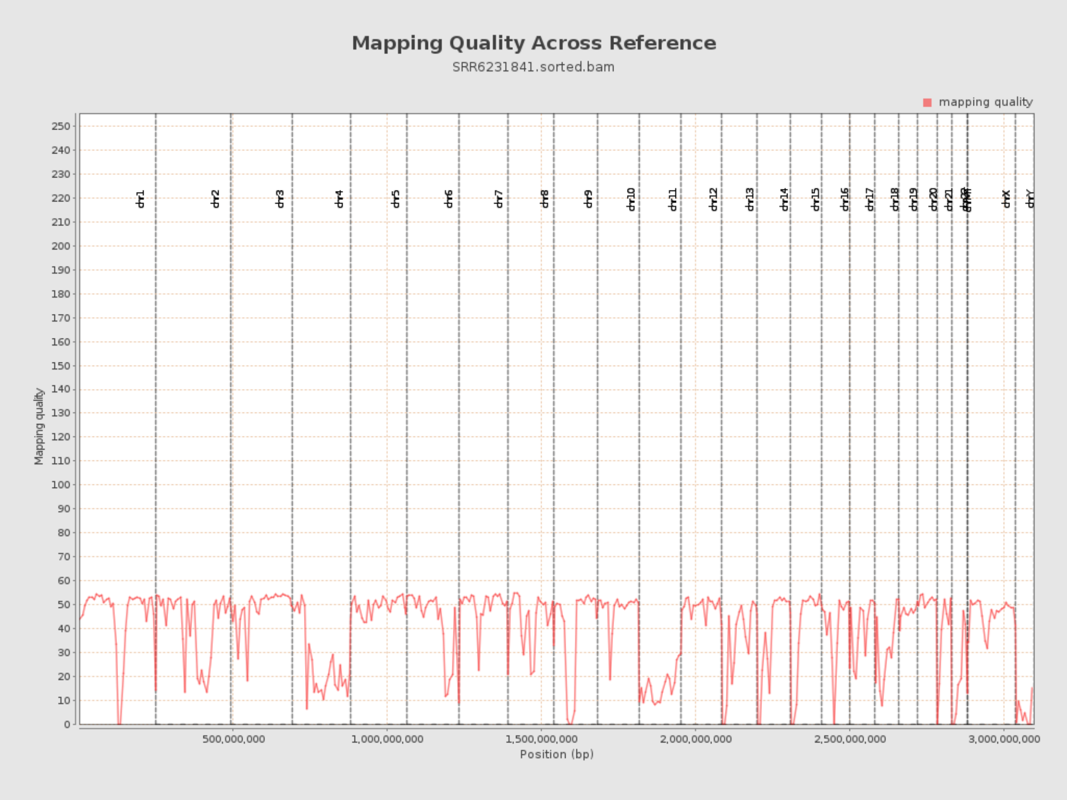
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram