Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 06:05:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231831.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_SRR6231831 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231831.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 06:05:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231831.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,942,502
Mapped reads	4,115,522 / 46.02%
Unmapped reads	4,826,980 / 53.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	34,620 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	693,297 / 7.75%
Duplication rate	10.6%
Clipped reads	2,661,665 / 29.76%

2.2. ACGT Content

Number/percentage of A's	74,977,781 / 29.63%
Number/percentage of C's	50,343,866 / 19.9%
Number/percentage of T's	72,410,591 / 28.62%
Number/percentage of G's	55,256,296 / 21.84%
Number/percentage of N's	18,950 / 0.01%
GC Percentage	41.74%

2.3. Coverage

Mean	0.0818

Standard Deviation	7.1833

2.4. Mapping Quality

Mean Mapping Quality	45.3

2.5. Mismatches and indels

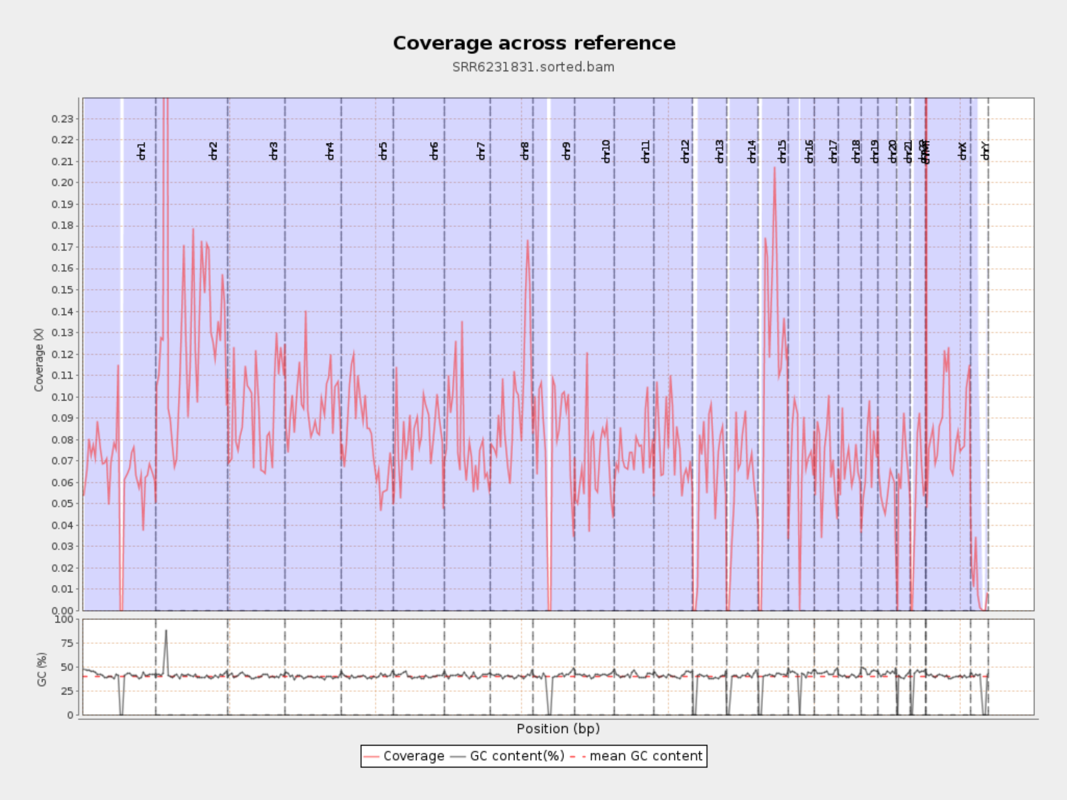
General error rate	0.58%
Mismatches	1,422,809
Insertions	17,172
Mapped reads with at least one insertion	0.41%
Deletions	50,488
Mapped reads with at least one deletion	1.21%
Homopolymer indels	45.26%

2.6. Chromosome stats

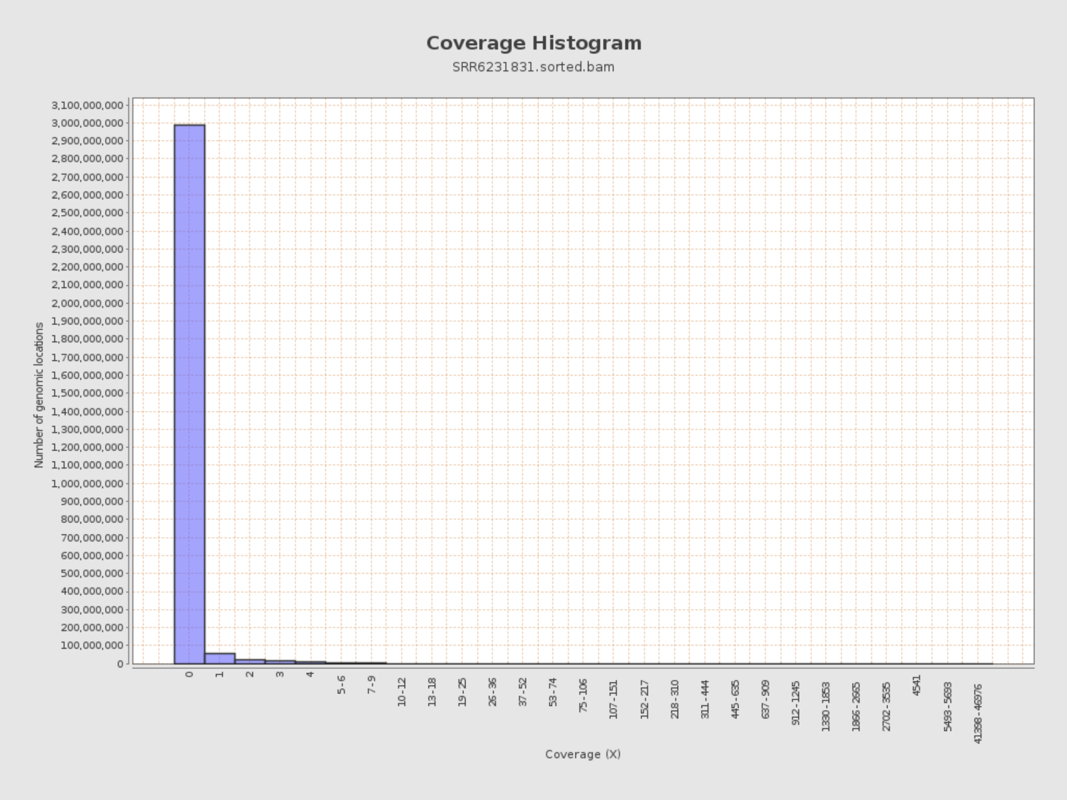
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16047837	0.0644	1.2785
chr2	243199373	34132552	0.1403	25.4999
chr3	198022430	18340002	0.0926	0.5964
chr4	191154276	18428785	0.0964	0.6295
chr5	180915260	14530493	0.0803	0.5524
chr6	171115067	14068117	0.0822	0.6196
chr7	159138663	12542868	0.0788	0.8557

chr8	146364022	14346618	0.098	0.8499
chr9	141213431	11060636	0.0783	0.7335
chr10	135534747	9221492	0.068	0.708
chr11	135006516	10124901	0.075	0.642
chr12	133851895	10317787	0.0771	0.5551
chr13	115169878	7249966	0.063	0.489
chr14	107349540	6237827	0.0581	0.5537
chr15	102531392	12184137	0.1188	0.6718
chr16	90354753	6103314	0.0675	0.5481
chr17	81195210	5640577	0.0695	0.5721
chr18	78077248	5330886	0.0683	1.3394
chr19	59128983	4242072	0.0717	0.9884
chr20	63025520	3460164	0.0549	0.459
chr21	48129895	2990832	0.0621	0.5166
chr22	51304566	2668172	0.052	0.4341
chrMT	16571	27254	1.6447	2.5532
chrX	155270560	13201403	0.085	0.636
chrY	59373566	594120	0.01	0.2591

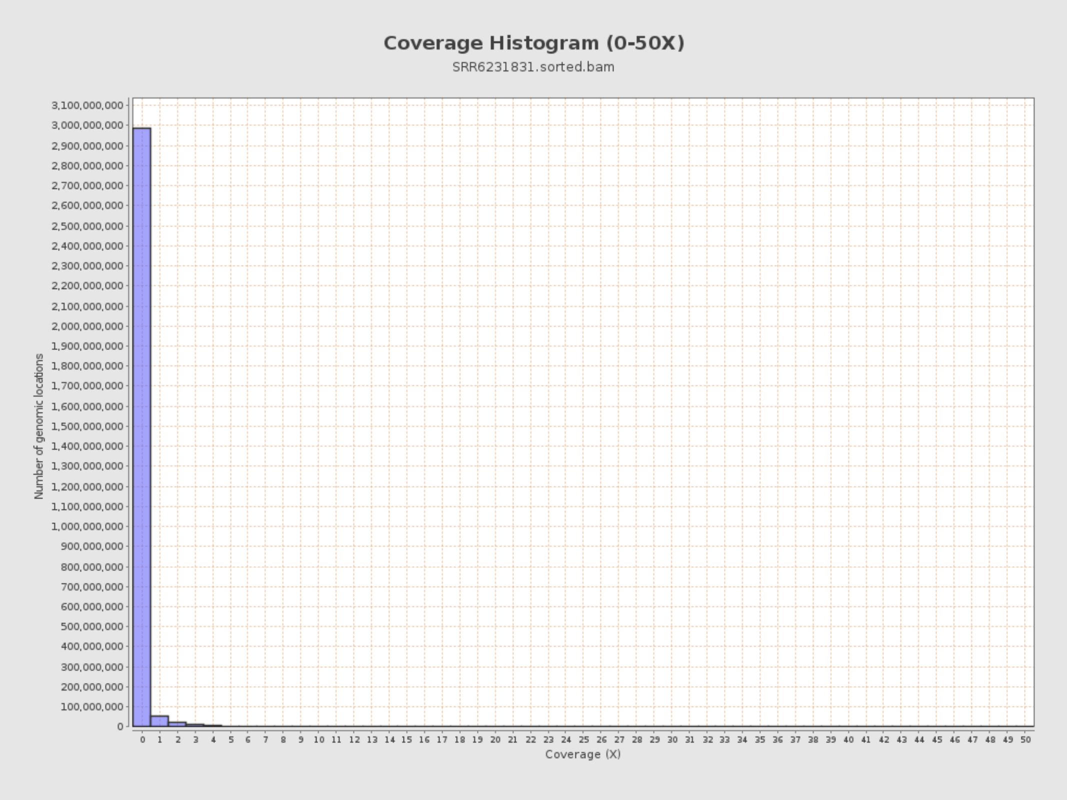
3. Results : Coverage across reference



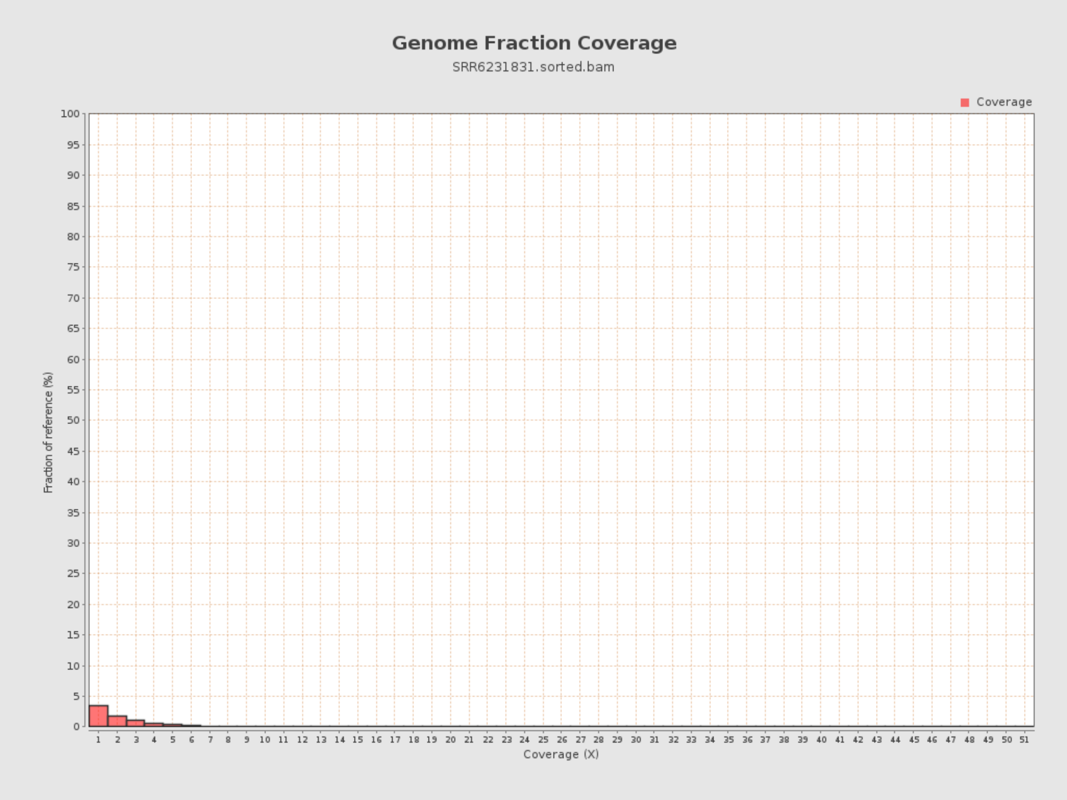
4. Results : Coverage Histogram



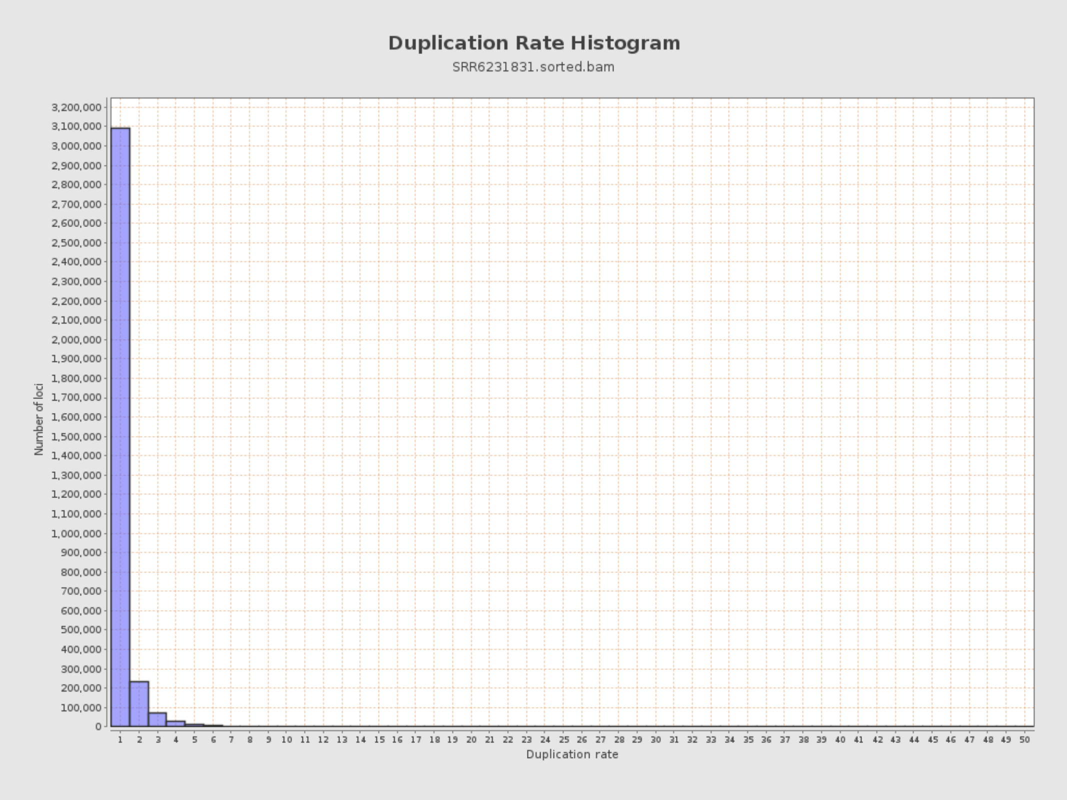
5. Results : Coverage Histogram (0-50X)



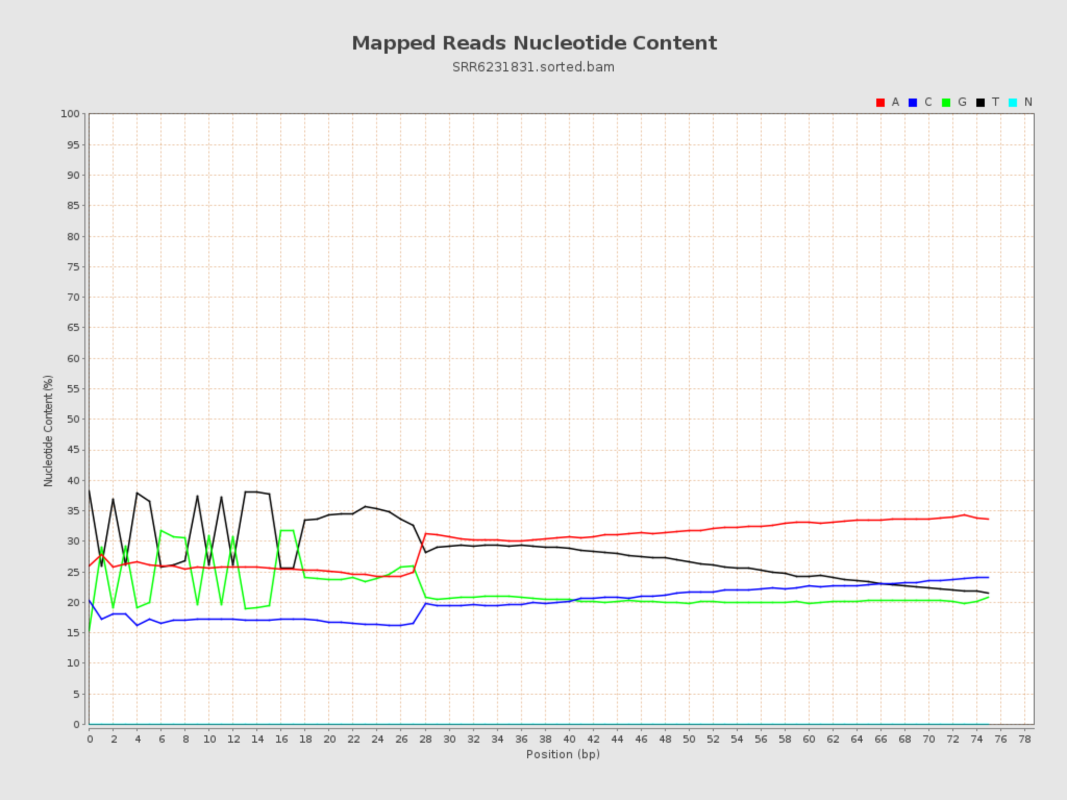
6. Results : Genome Fraction Coverage



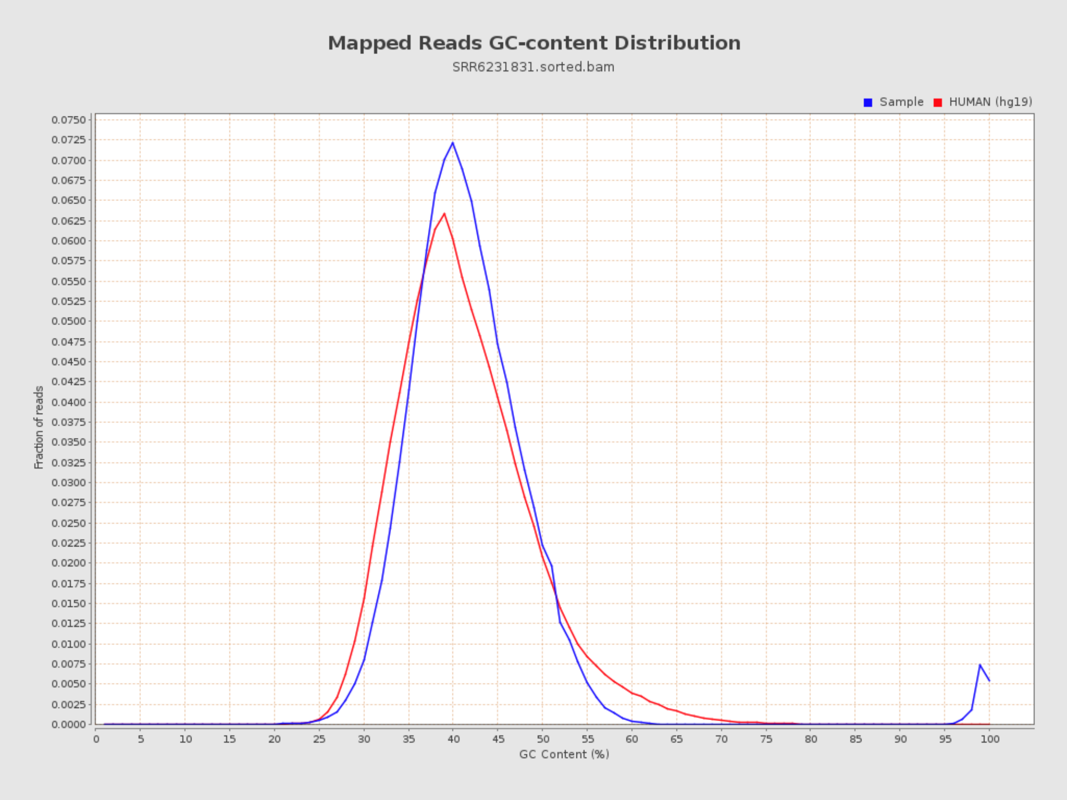
7. Results : Duplication Rate Histogram



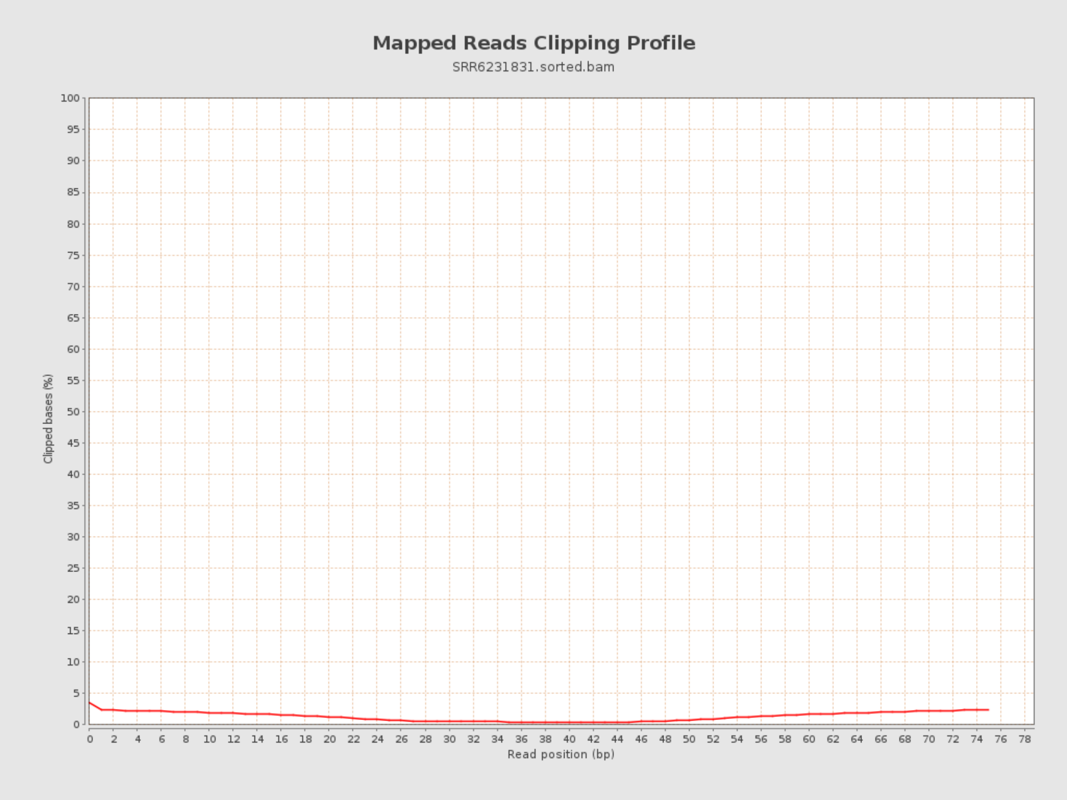
8. Results : Mapped Reads Nucleotide Content



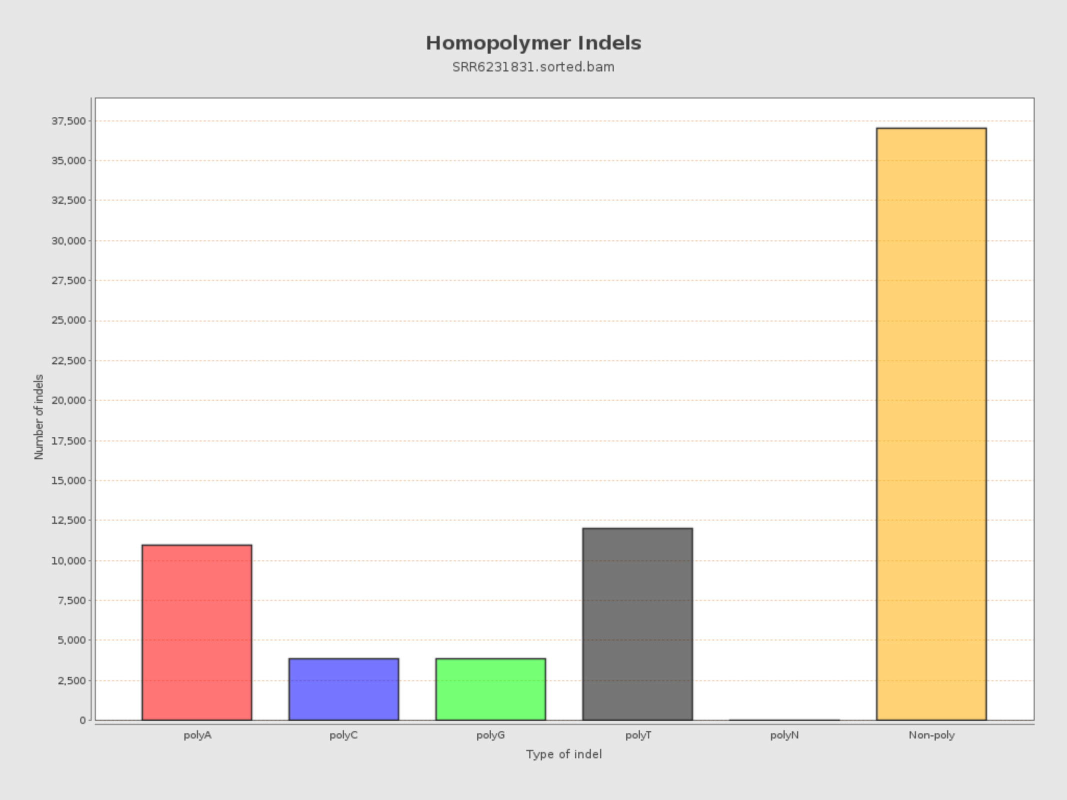
9. Results : Mapped Reads GC-content Distribution



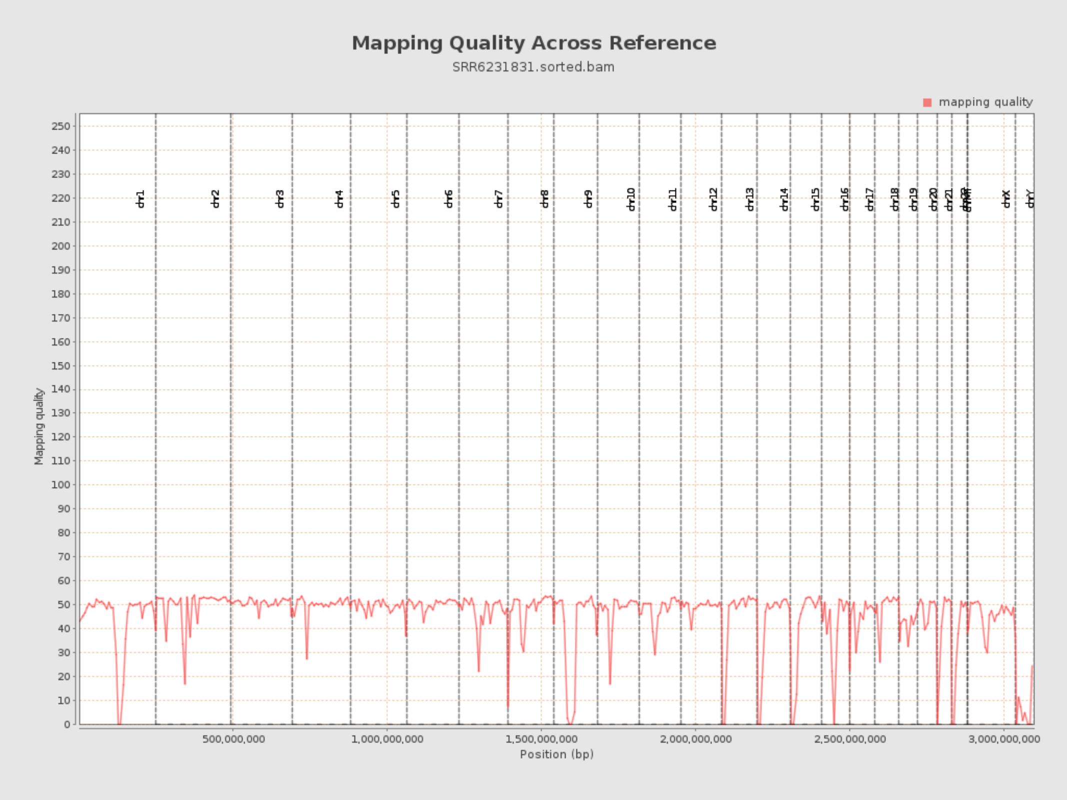
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram