Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 10:07:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231884.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_SRR6231884 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231884.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 10:07:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231884.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,522,705
Mapped reads	2,141,402 / 32.83%
Unmapped reads	4,381,303 / 67.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,912 / 0.23%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	122,356 / 1.88%
Duplication rate	2.29%
Clipped reads	1,198,912 / 18.38%

2.2. ACGT Content

Number/percentage of A's	38,947,538 / 28.45%
Number/percentage of C's	27,940,014 / 20.41%
Number/percentage of T's	36,522,308 / 26.67%
Number/percentage of G's	33,502,639 / 24.47%
Number/percentage of N's	9,366 / 0.01%
GC Percentage	44.87%

2.3. Coverage

Mean	0.0442

Standard Deviation	6.7822

2.4. Mapping Quality

Mean Mapping Quality	41.46

2.5. Mismatches and indels

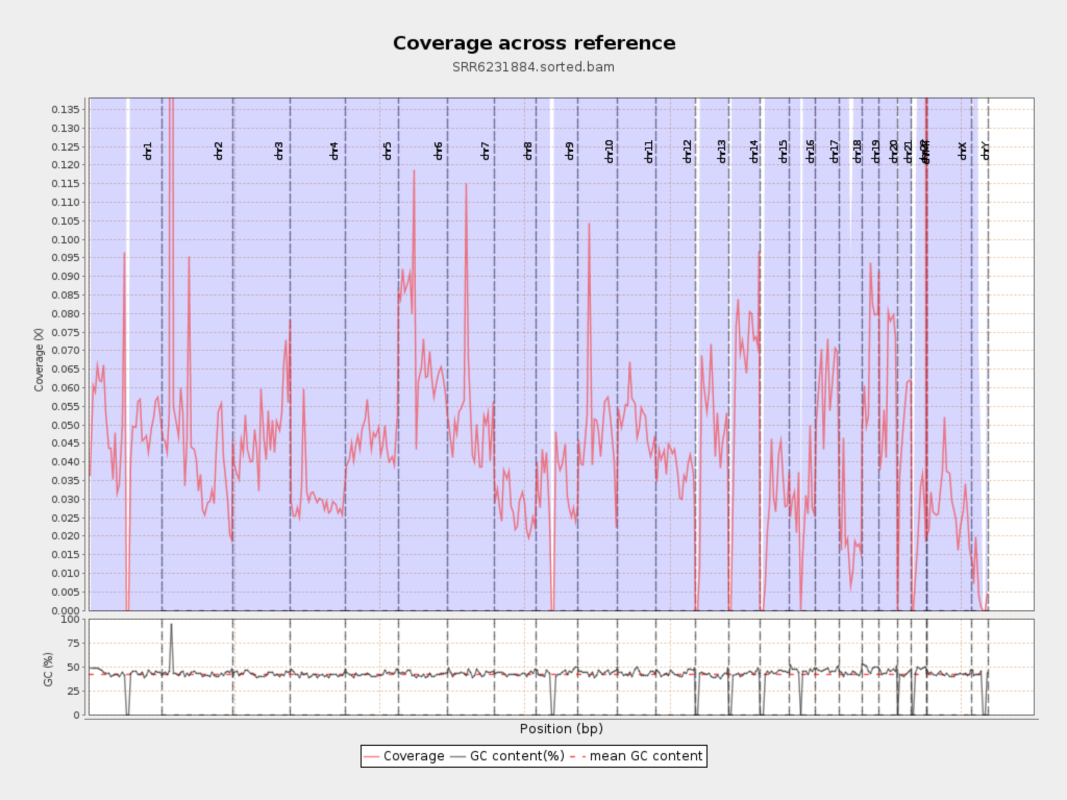
General error rate	0.72%
Mismatches	957,518
Insertions	11,745
Mapped reads with at least one insertion	0.54%
Deletions	28,265
Mapped reads with at least one deletion	1.31%
Homopolymer indels	42.52%

2.6. Chromosome stats

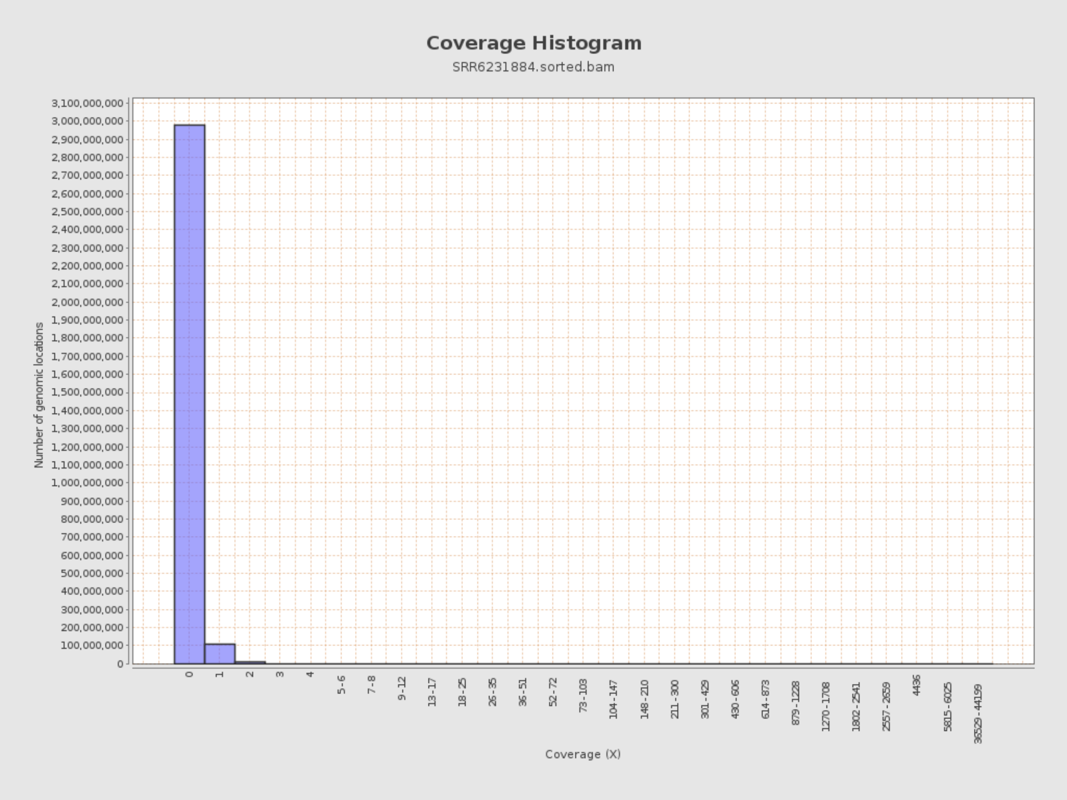
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12077543	0.0485	0.9613
chr2	243199373	13958780	0.0574	24.1443
chr3	198022430	9451146	0.0477	0.2395
chr4	191154276	5737153	0.03	0.2199
chr5	180915260	8221745	0.0454	0.2366
chr6	171115067	12340325	0.0721	0.4797
chr7	159138663	8346487	0.0524	0.7793

chr8	146364022	4059744	0.0277	0.2999
chr9	141213431	4350586	0.0308	0.3205
chr10	135534747	6742475	0.0497	0.5125
chr11	135006516	6943412	0.0514	0.4501
chr12	133851895	5180526	0.0387	0.2183
chr13	115169878	5207015	0.0452	0.2282
chr14	107349540	6617711	0.0616	0.3703
chr15	102531392	2746303	0.0268	0.1786
chr16	90354753	2429531	0.0269	0.2358
chr17	81195210	4953951	0.061	0.3582
chr18	78077248	1488937	0.0191	0.7948
chr19	59128983	4189933	0.0709	0.6013
chr20	63025520	3853465	0.0611	0.2891
chr21	48129895	2281353	0.0474	0.257
chr22	51304566	986481	0.0192	0.1486
chrMT	16571	23583	1.4231	1.6679
chrX	155270560	4432051	0.0285	0.2371
chrY	59373566	346809	0.0058	0.1371

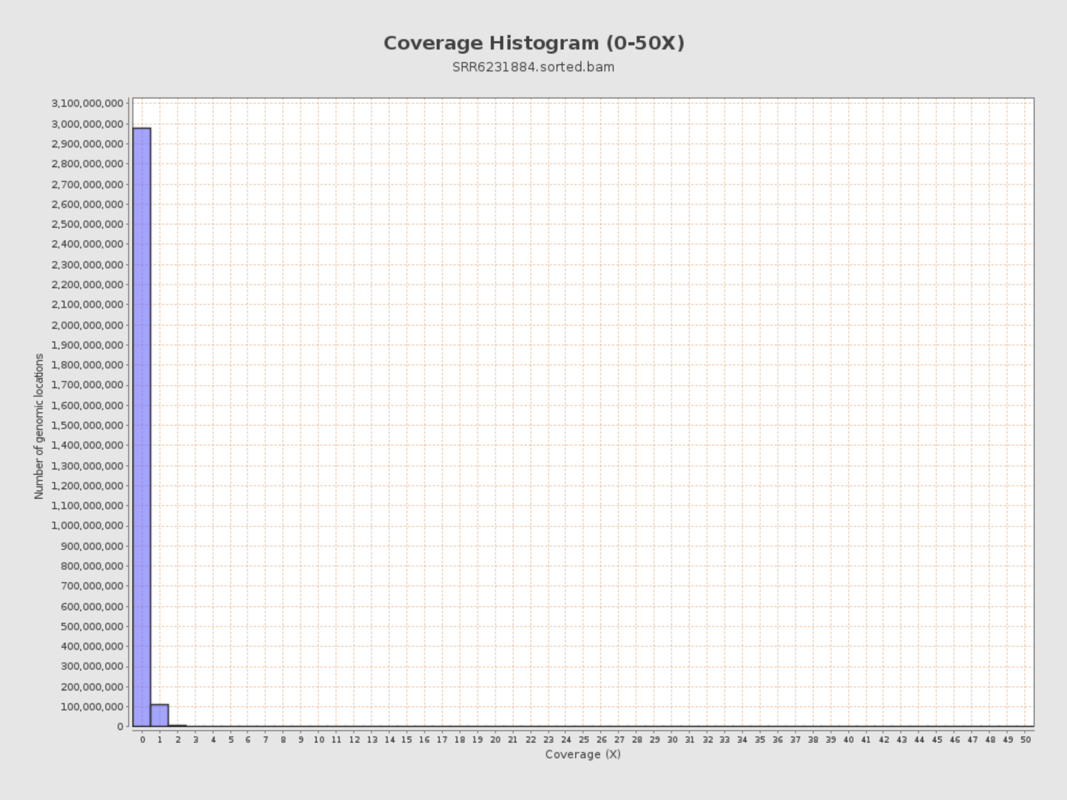
3. Results : Coverage across reference



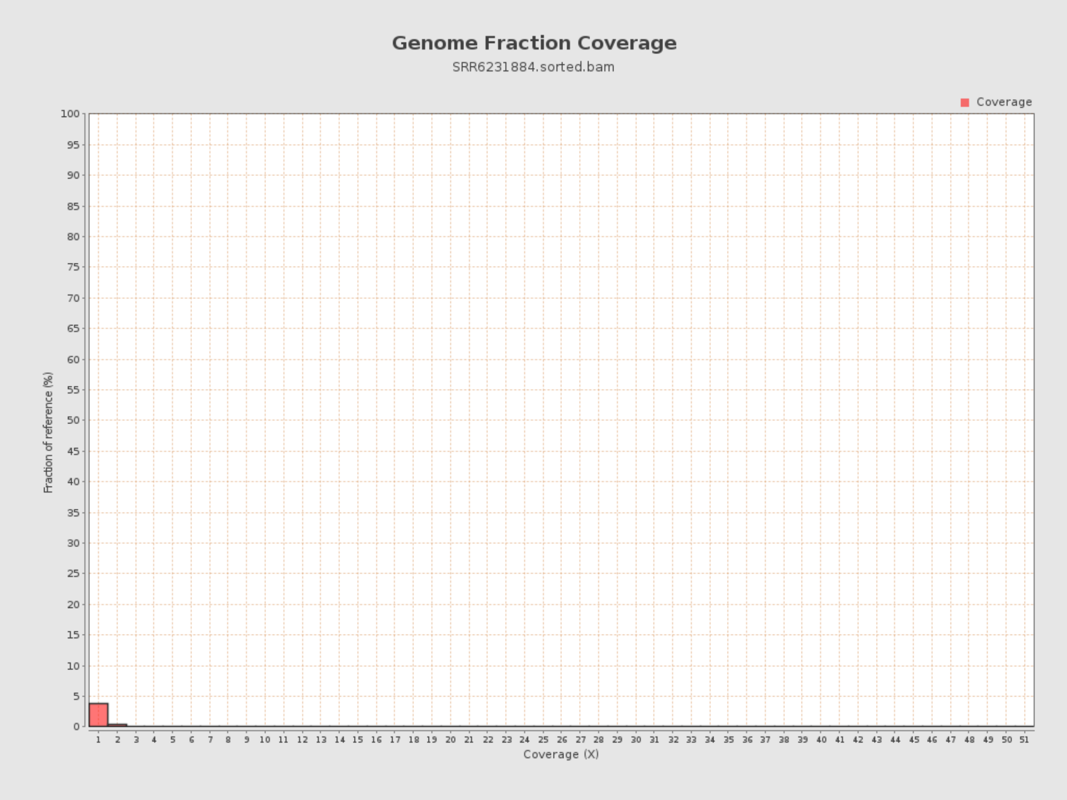
4. Results : Coverage Histogram



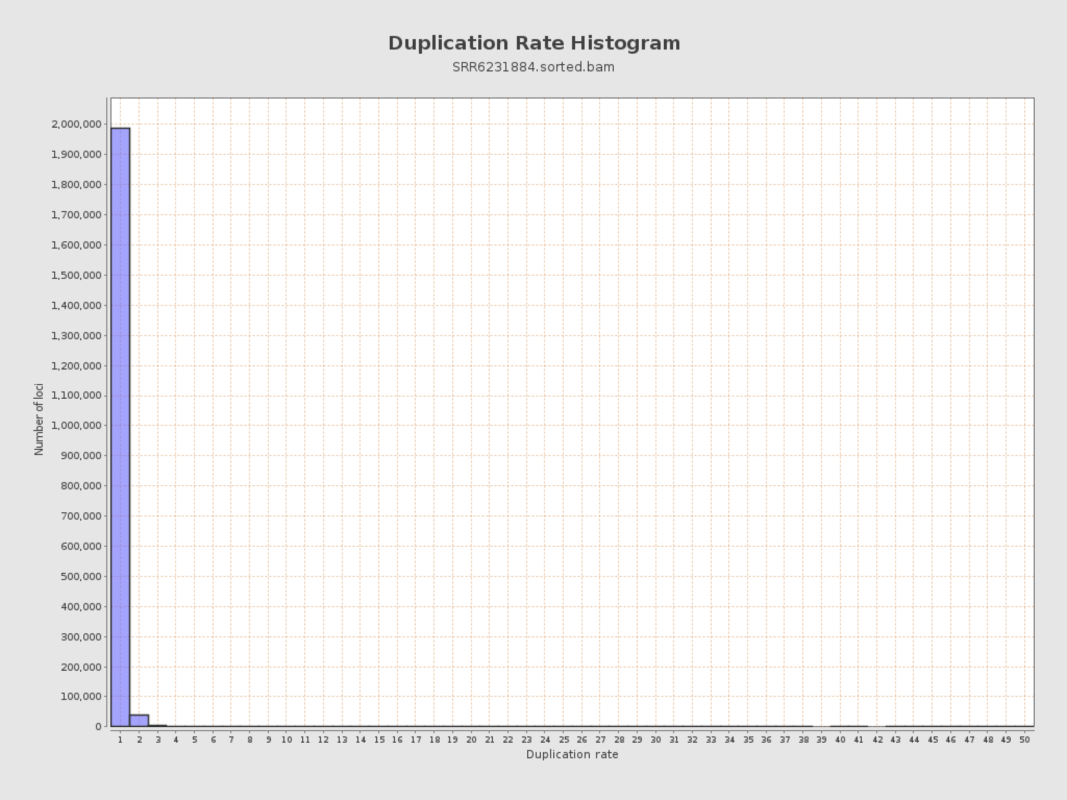
5. Results : Coverage Histogram (0-50X)



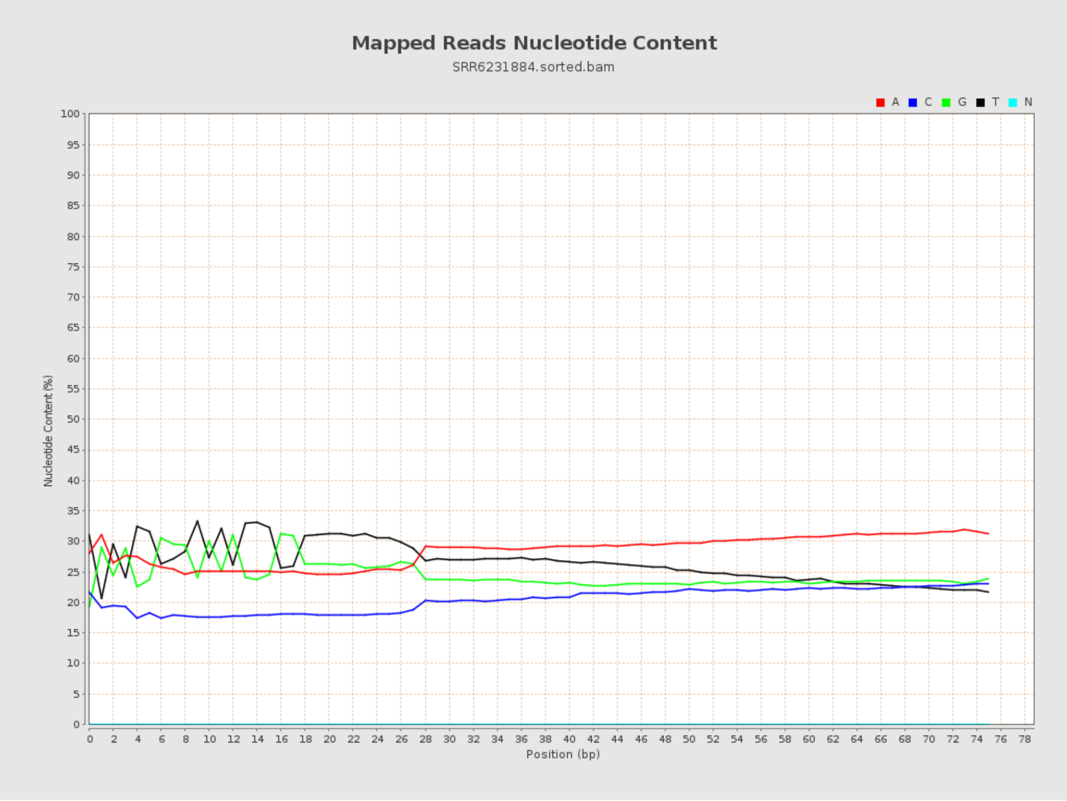
6. Results : Genome Fraction Coverage



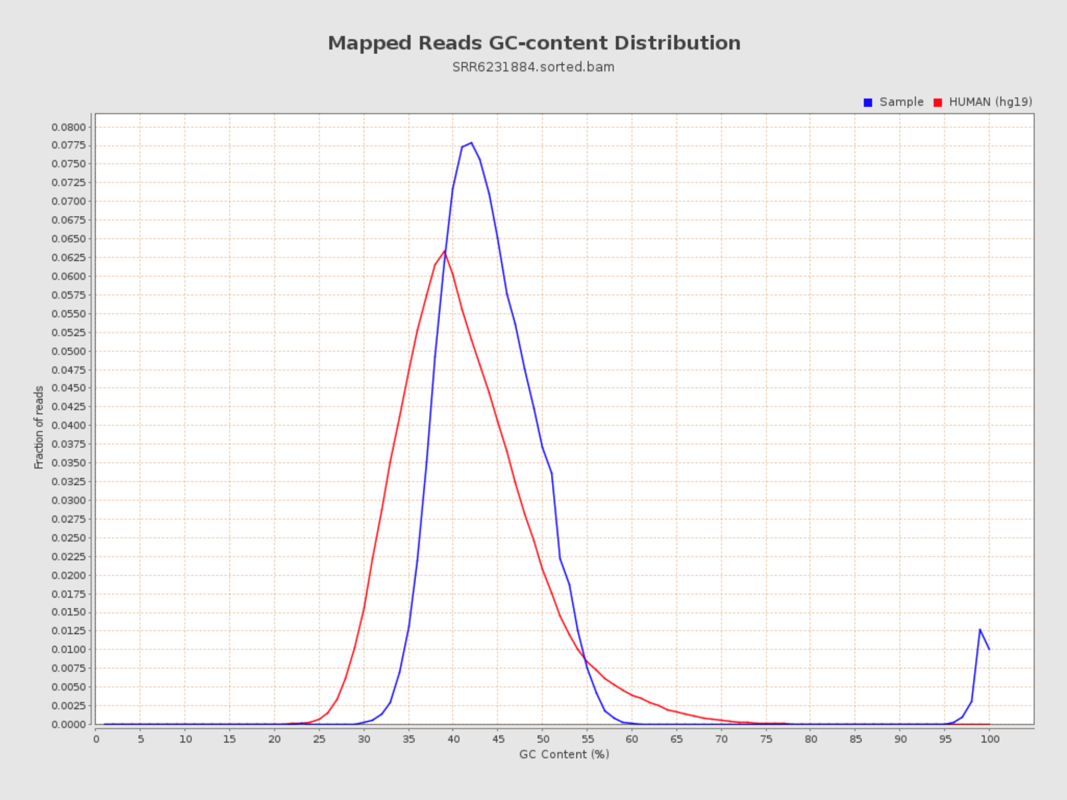
7. Results : Duplication Rate Histogram



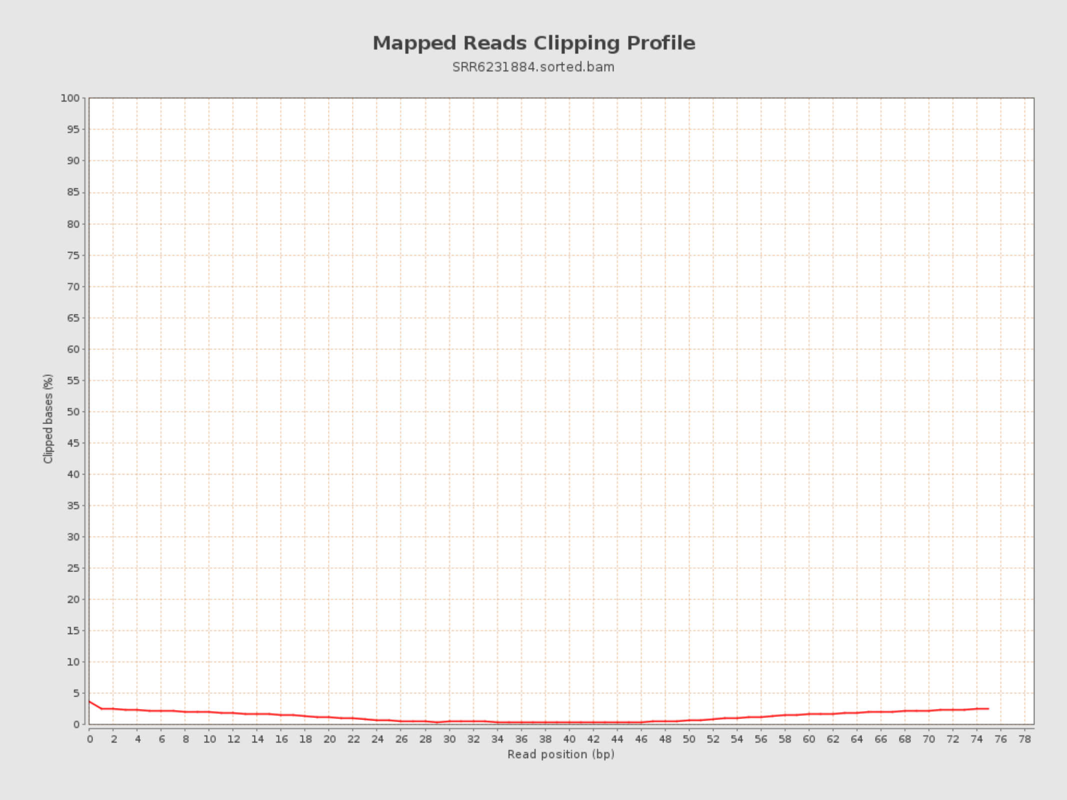
8. Results : Mapped Reads Nucleotide Content



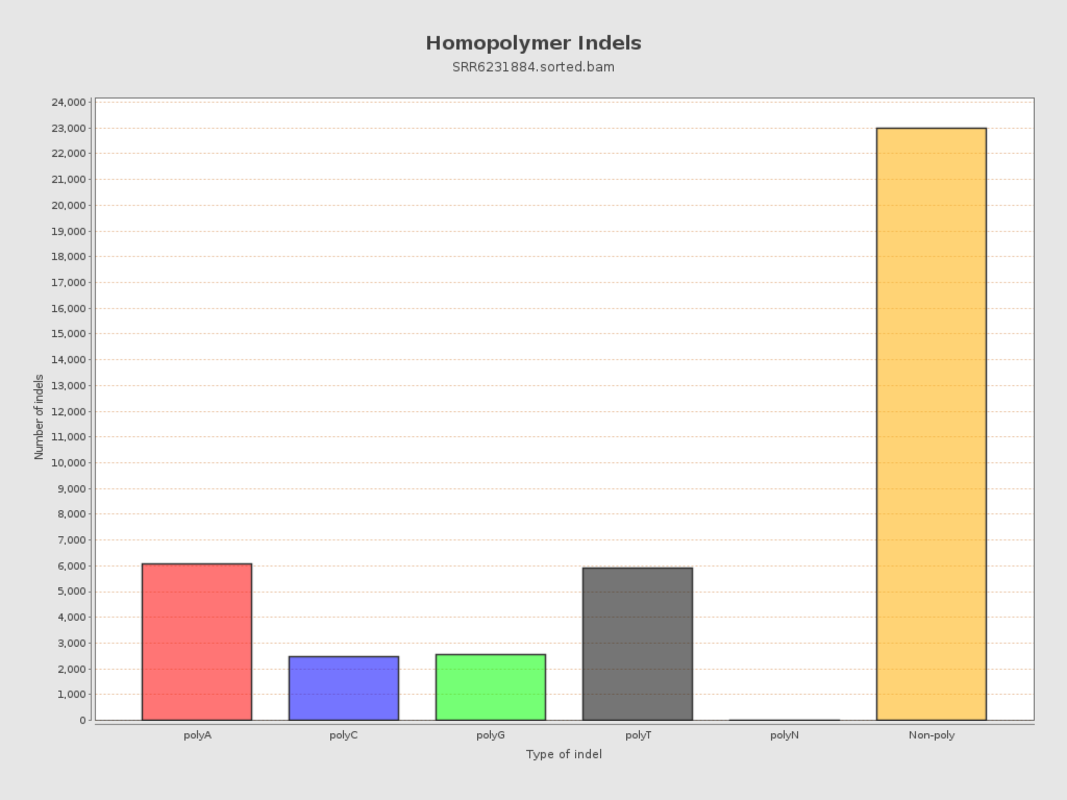
9. Results : Mapped Reads GC-content Distribution



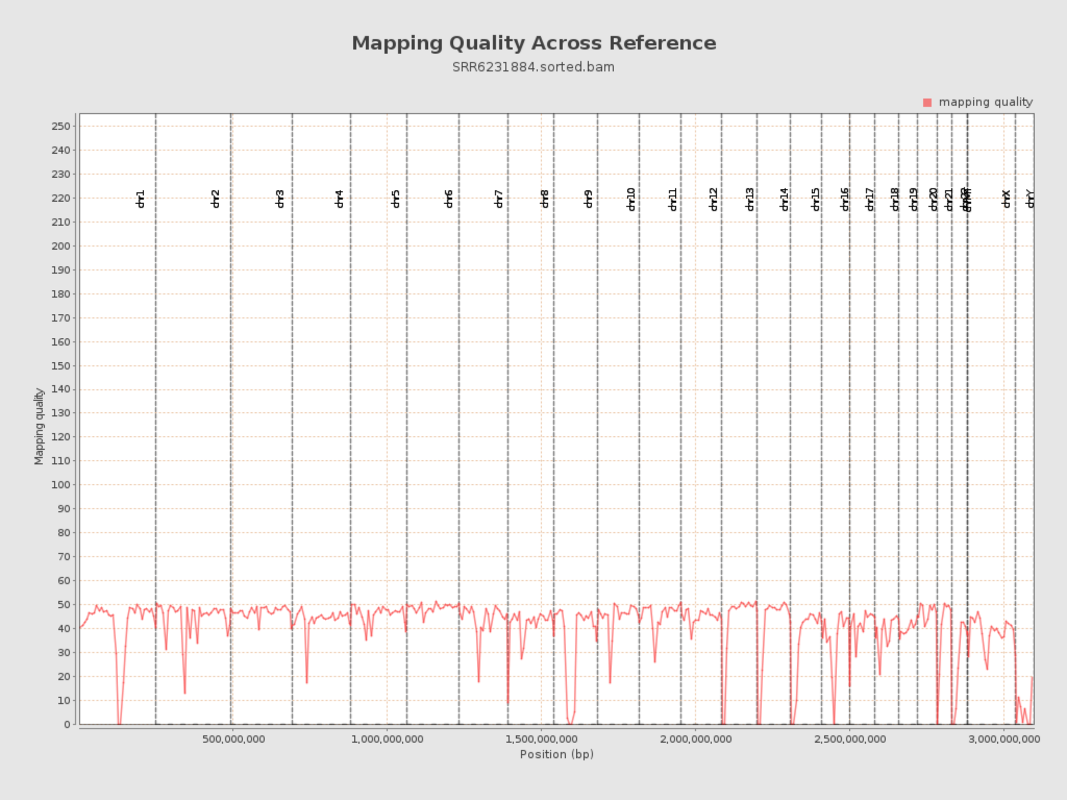
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram