Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 03:51:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081231.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_SRR3081231 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081231.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 03:51:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081231.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,052,811
Mapped reads	1,801,387 / 87.75%
Unmapped reads	251,424 / 12.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,552 / 1.15%
Read min/max/mean length	30 / 76 / 76.4
Duplicated reads (estimated)	73,810 / 3.6%
Duplication rate	3.43%
Clipped reads	926,167 / 45.12%

2.2. ACGT Content

Number/percentage of A's	33,501,357 / 28.4%
Number/percentage of C's	22,587,138 / 19.15%
Number/percentage of T's	36,342,531 / 30.81%
Number/percentage of G's	25,522,843 / 21.64%
Number/percentage of N's	15,831 / 0.01%
GC Percentage	40.78%

2.3. Coverage

Mean	0.0381

Standard Deviation	0.3036

2.4. Mapping Quality

Mean Mapping Quality	45.27

2.5. Mismatches and indels

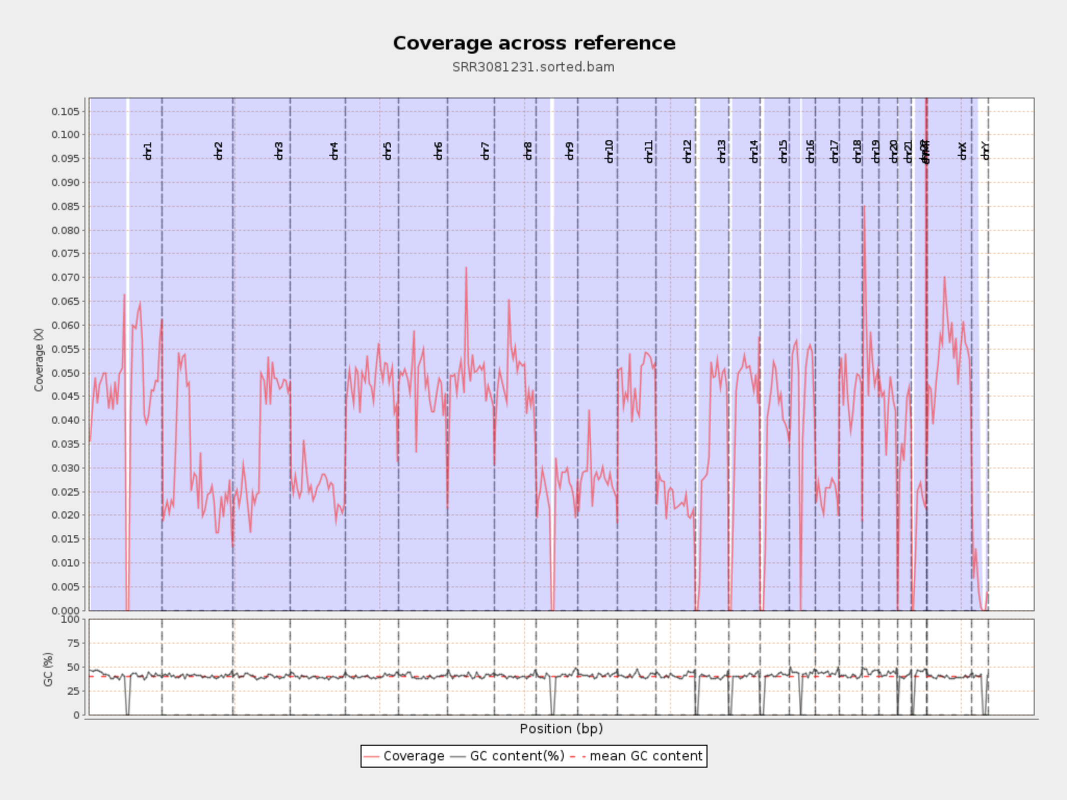
General error rate	0.89%
Mismatches	1,032,072
Insertions	8,702
Mapped reads with at least one insertion	0.48%
Deletions	26,748
Mapped reads with at least one deletion	1.47%
Homopolymer indels	48.38%

2.6. Chromosome stats

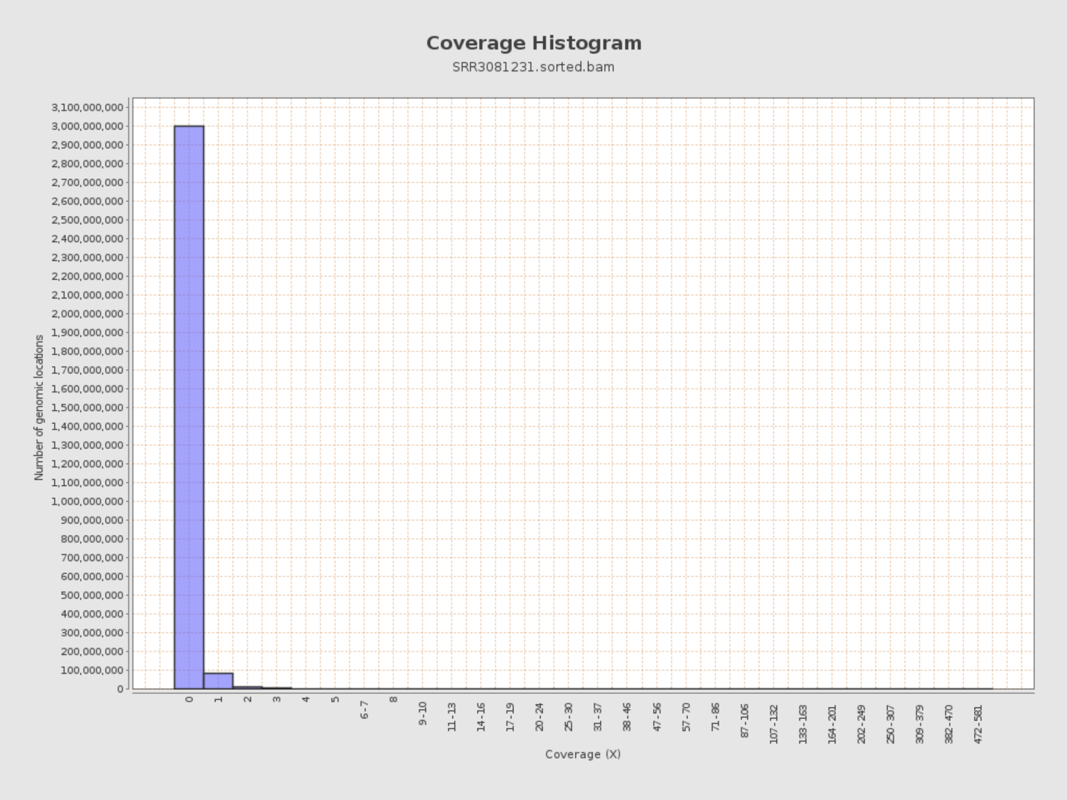
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11484699	0.0461	0.5334
chr2	243199373	6988464	0.0287	0.3063
chr3	198022430	7194979	0.0363	0.2213
chr4	191154276	4900933	0.0256	0.1918
chr5	180915260	8694488	0.0481	0.2557
chr6	171115067	8071807	0.0472	0.2777
chr7	159138663	7894720	0.0496	0.4432

chr8	146364022	7123151	0.0487	0.3701
chr9	141213431	3311897	0.0235	0.2161
chr10	135534747	3787602	0.0279	0.2477
chr11	135006516	6467285	0.0479	0.3137
chr12	133851895	3093122	0.0231	0.1782
chr13	115169878	4080209	0.0354	0.2201
chr14	107349540	4389544	0.0409	0.2406
chr15	102531392	3616488	0.0353	0.2222
chr16	90354753	4150258	0.0459	0.2524
chr17	81195210	1990158	0.0245	0.202
chr18	78077248	3658701	0.0469	0.34
chr19	59128983	3243020	0.0548	0.4208
chr20	63025520	2695617	0.0428	0.2423
chr21	48129895	1642173	0.0341	0.2215
chr22	51304566	886626	0.0173	0.1504
chrMT	16571	25220	1.5219	1.7024
chrX	155270560	8317662	0.0536	0.2818
chrY	59373566	304437	0.0051	0.0993

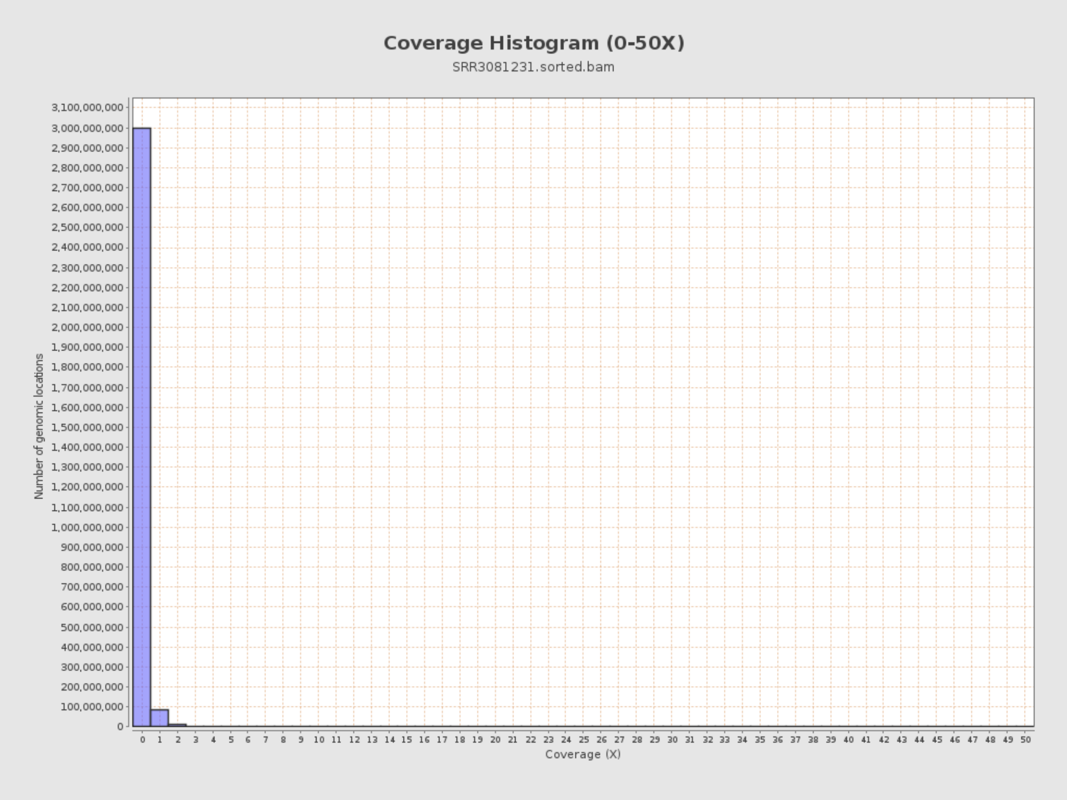
3. Results : Coverage across reference



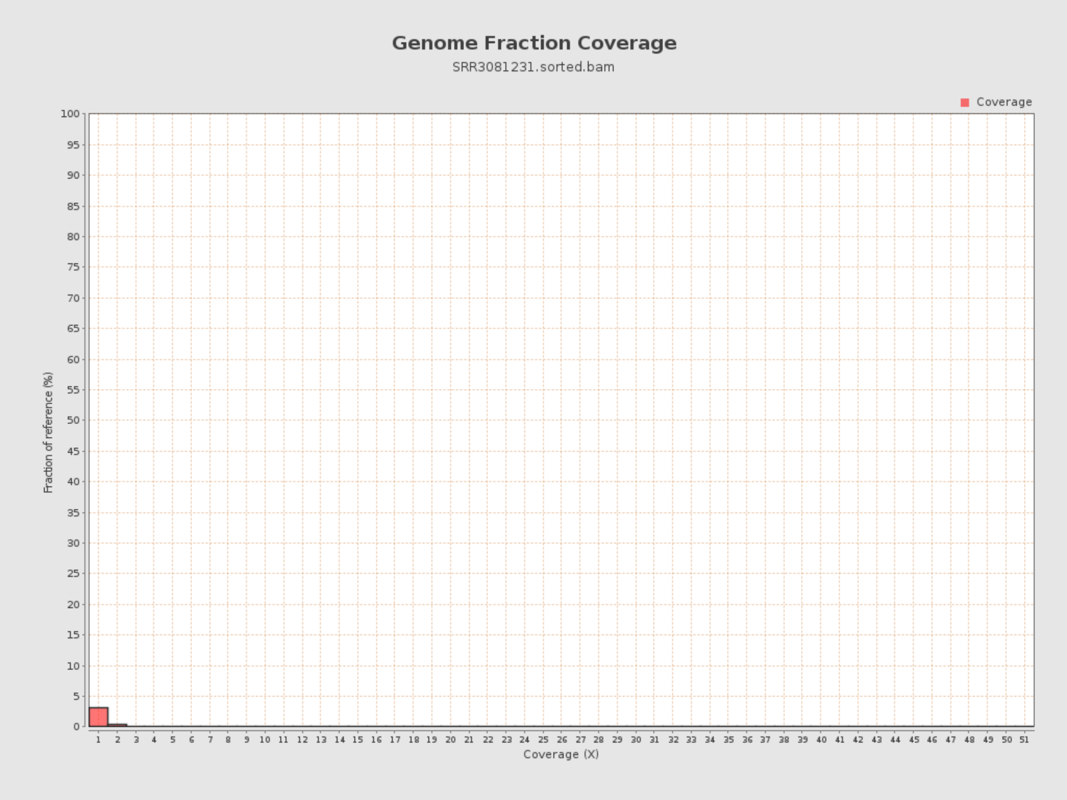
4. Results : Coverage Histogram



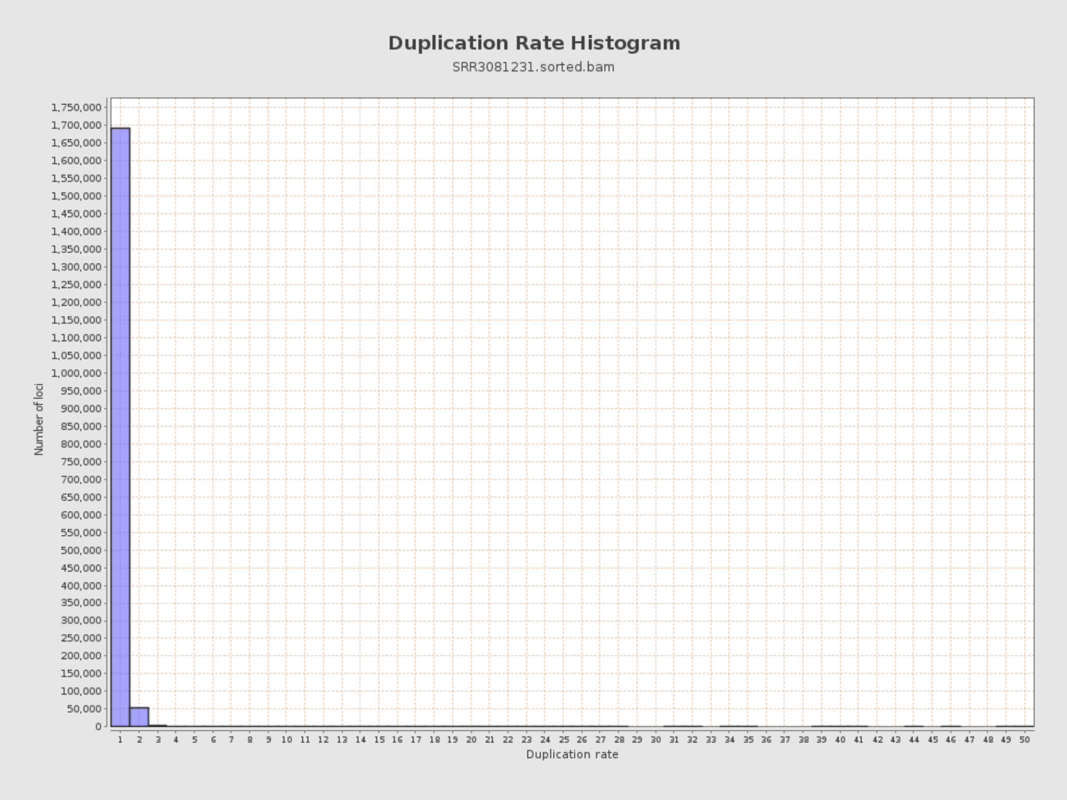
5. Results : Coverage Histogram (0-50X)



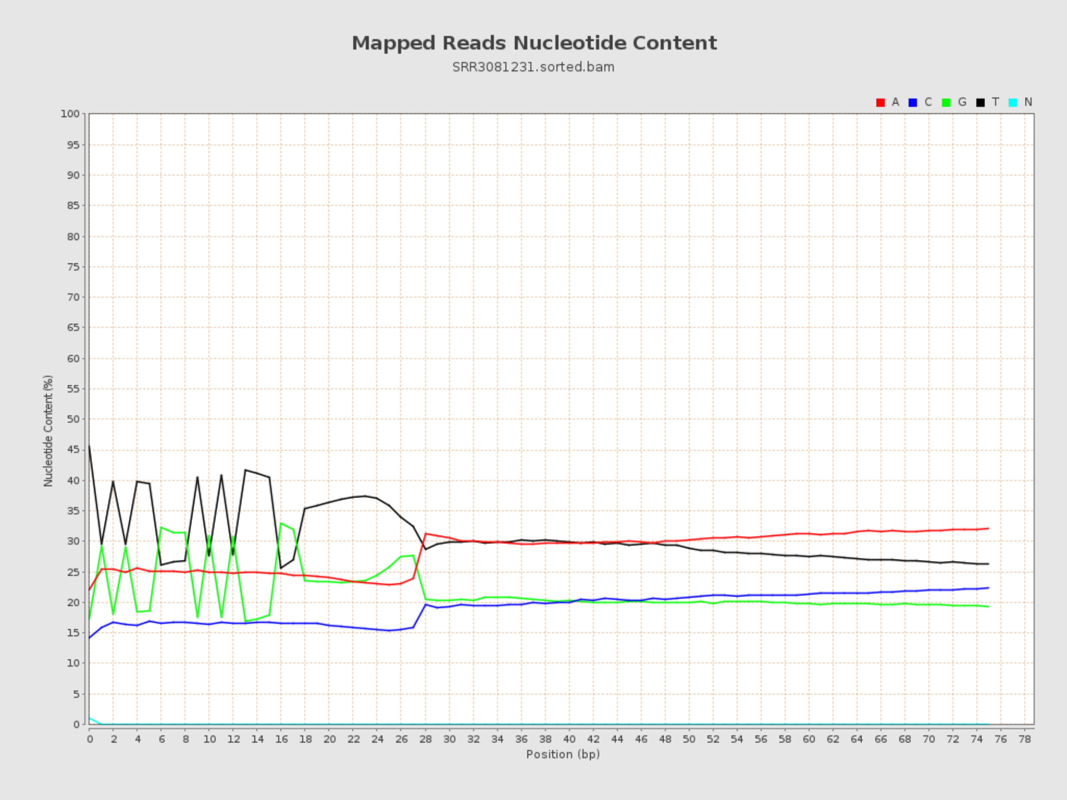
6. Results : Genome Fraction Coverage



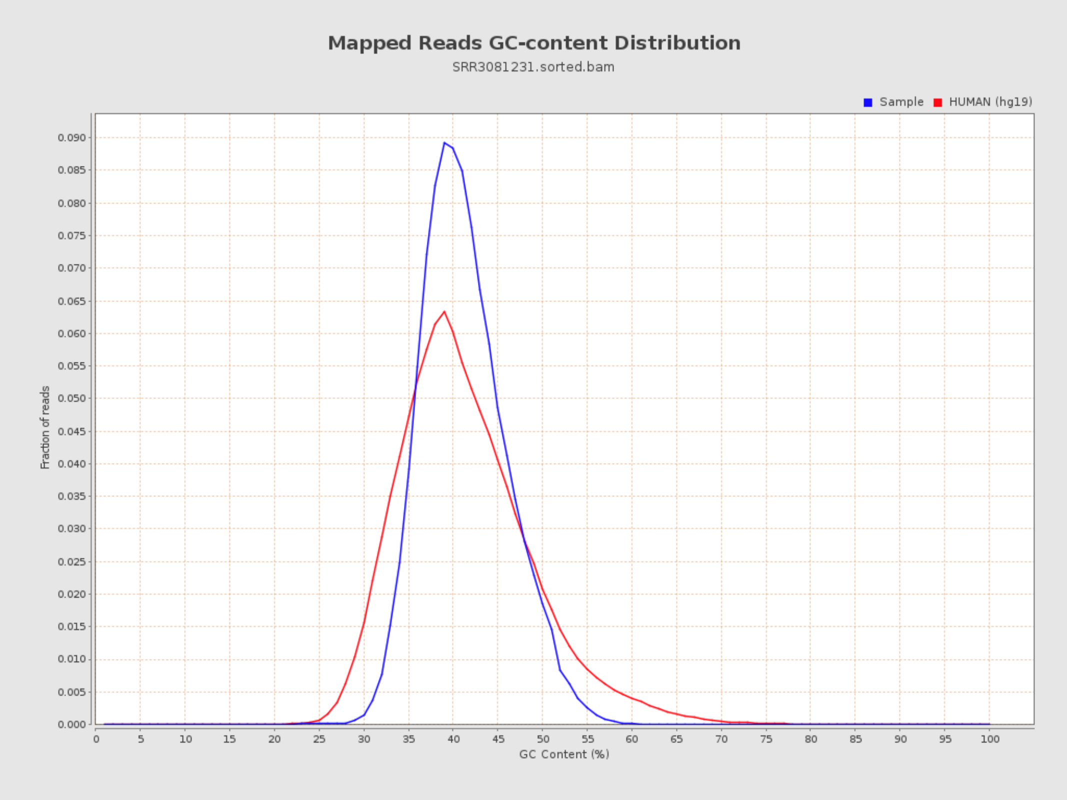
7. Results : Duplication Rate Histogram



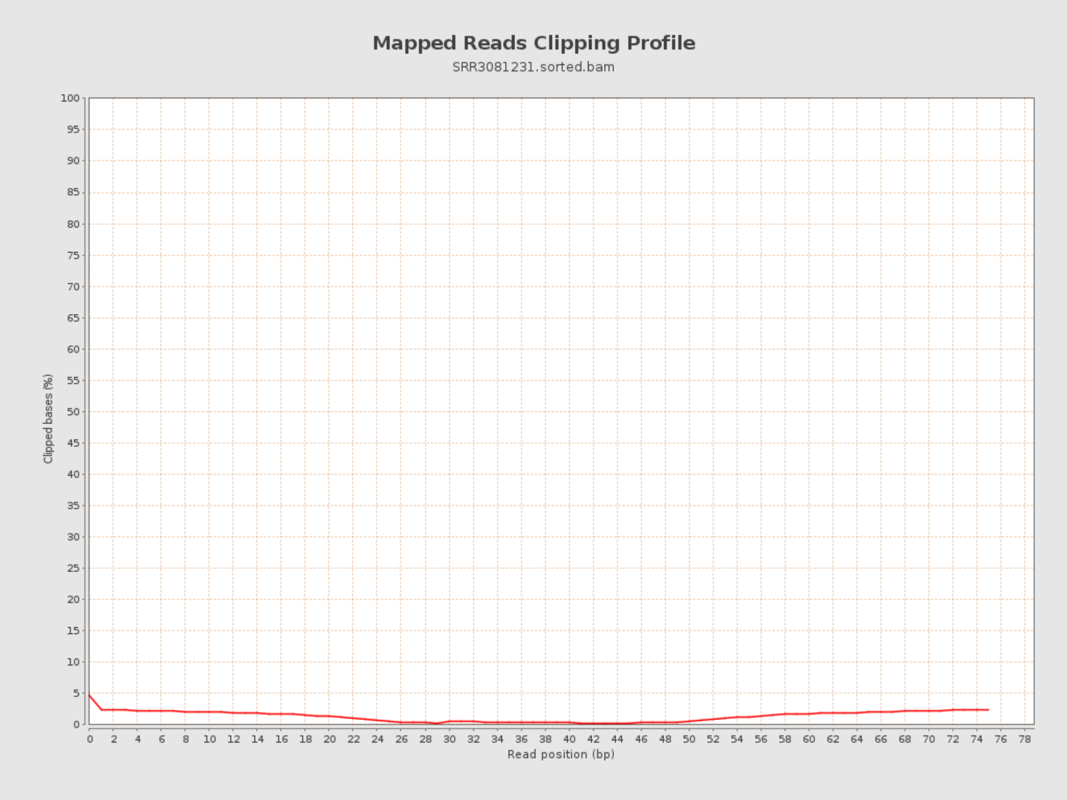
8. Results : Mapped Reads Nucleotide Content



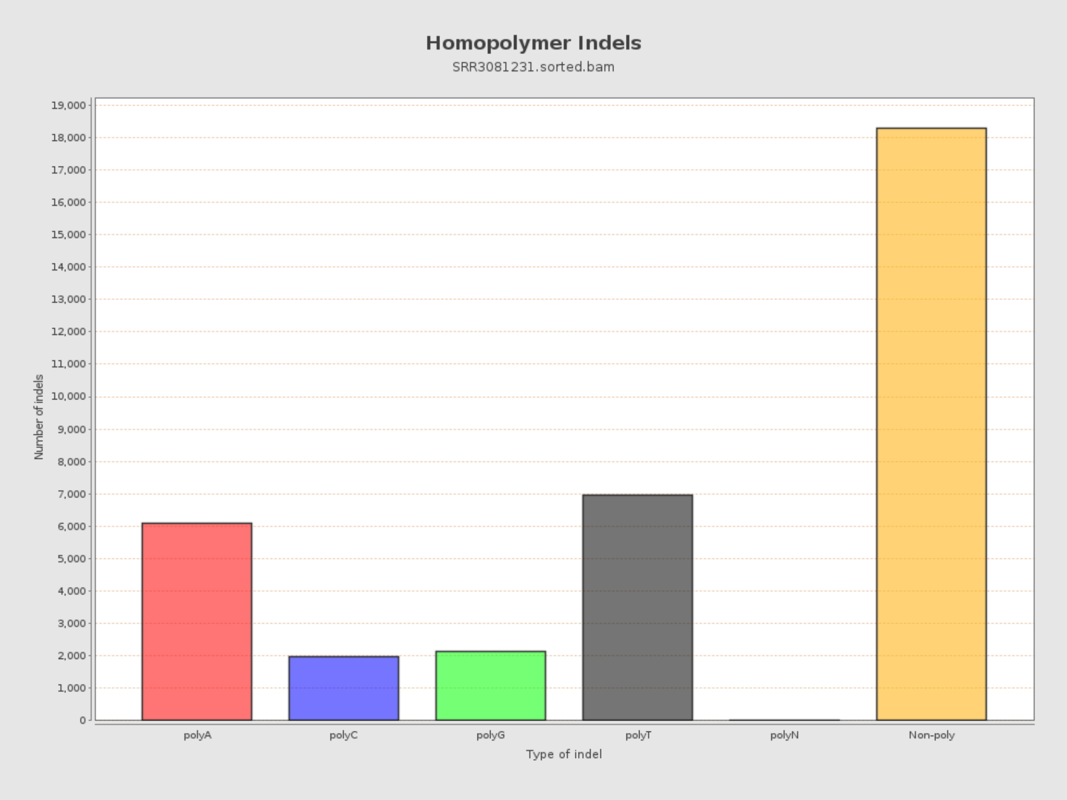
9. Results : Mapped Reads GC-content Distribution



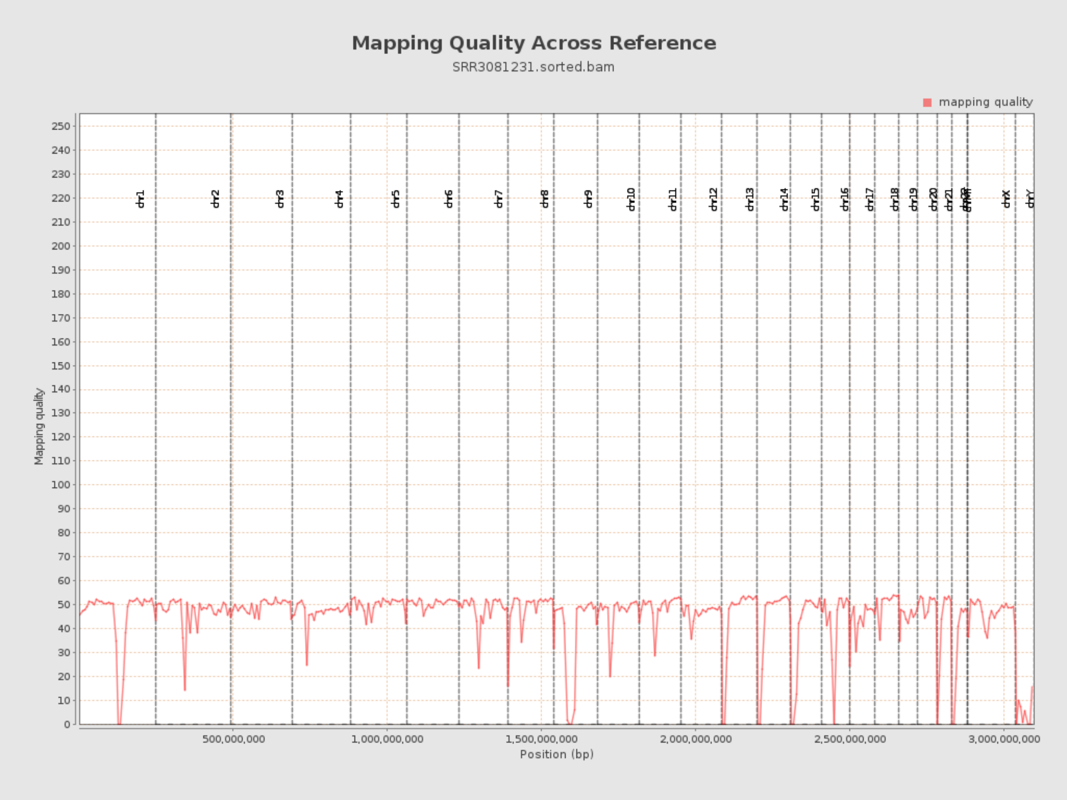
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram