Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 18:52:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081101.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_SRR3081101 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081101.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 18:52:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081101.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,698,863
Mapped reads	2,462,251 / 91.23%
Unmapped reads	236,612 / 8.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,858 / 0.88%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	116,567 / 4.32%
Duplication rate	3.51%
Clipped reads	1,045,412 / 38.74%

2.2. ACGT Content

Number/percentage of A's	46,070,399 / 27.74%
Number/percentage of C's	31,511,818 / 18.97%
Number/percentage of T's	51,637,803 / 31.09%
Number/percentage of G's	36,859,473 / 22.19%
Number/percentage of N's	1,799 / 0%
GC Percentage	41.17%

2.3. Coverage

Mean	0.0537

Standard Deviation	0.4652

2.4. Mapping Quality

Mean Mapping Quality	45.26

2.5. Mismatches and indels

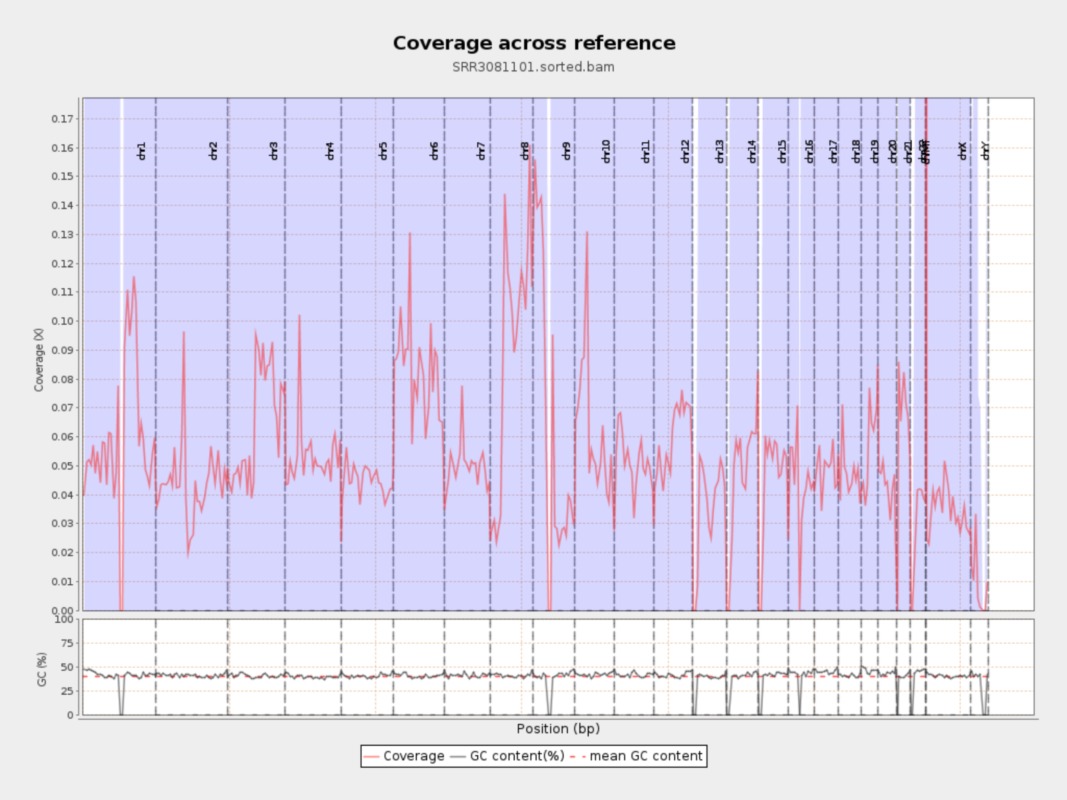
General error rate	0.96%
Mismatches	1,559,477
Insertions	14,121
Mapped reads with at least one insertion	0.57%
Deletions	38,495
Mapped reads with at least one deletion	1.55%
Homopolymer indels	45.74%

2.6. Chromosome stats

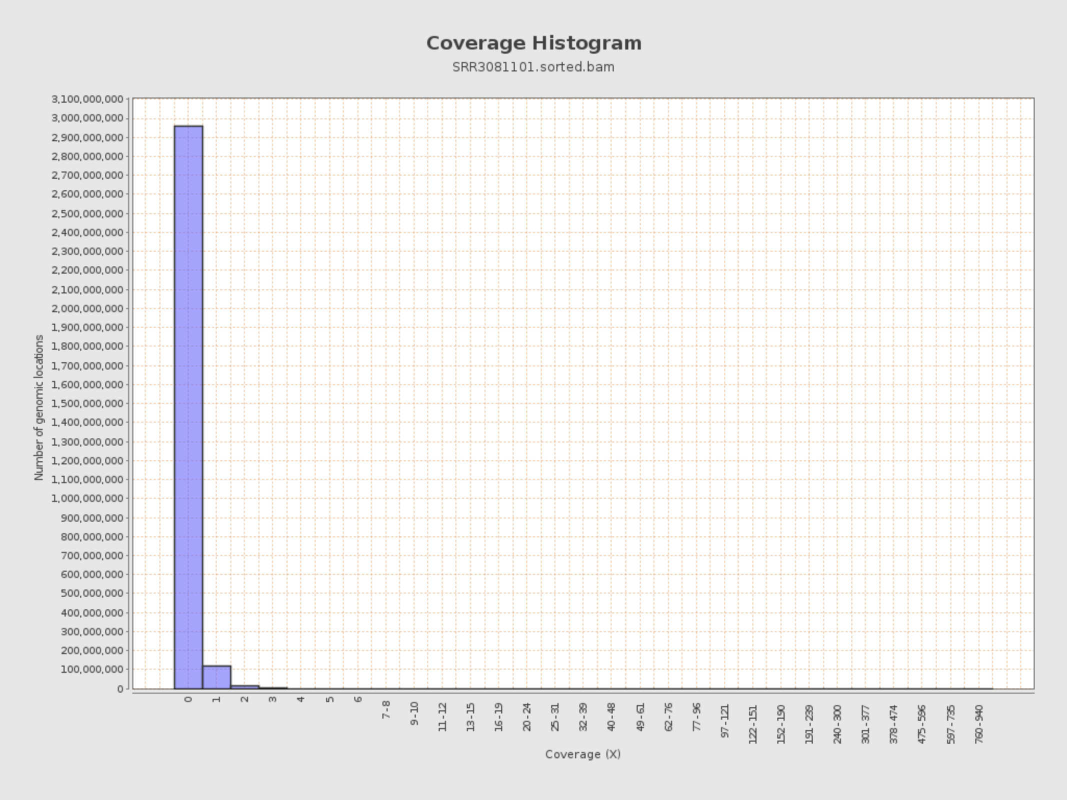
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14772947	0.0593	0.6964
chr2	243199373	10764902	0.0443	0.52
chr3	198022430	12650389	0.0639	0.2955
chr4	191154276	10228311	0.0535	0.3256
chr5	180915260	8132360	0.045	0.25
chr6	171115067	14263839	0.0834	0.5338
chr7	159138663	7943512	0.0499	0.453

chr8	146364022	13196962	0.0902	0.558
chr9	141213431	9021220	0.0639	0.5889
chr10	135534747	8355129	0.0616	0.5836
chr11	135006516	6944778	0.0514	0.3592
chr12	133851895	8010466	0.0598	0.3105
chr13	115169878	4081074	0.0354	0.216
chr14	107349540	4986078	0.0464	0.3499
chr15	102531392	4539342	0.0443	0.2415
chr16	90354753	3805187	0.0421	0.3562
chr17	81195210	3975403	0.049	0.2691
chr18	78077248	3738328	0.0479	1.1023
chr19	59128983	3374220	0.0571	0.5237
chr20	63025520	2731902	0.0433	0.2696
chr21	48129895	3142127	0.0653	0.3953
chr22	51304566	1470634	0.0287	0.1924
chrMT	16571	62433	3.7676	2.7921
chrX	155270560	5419226	0.0349	0.2589
chrY	59373566	534934	0.009	0.2395

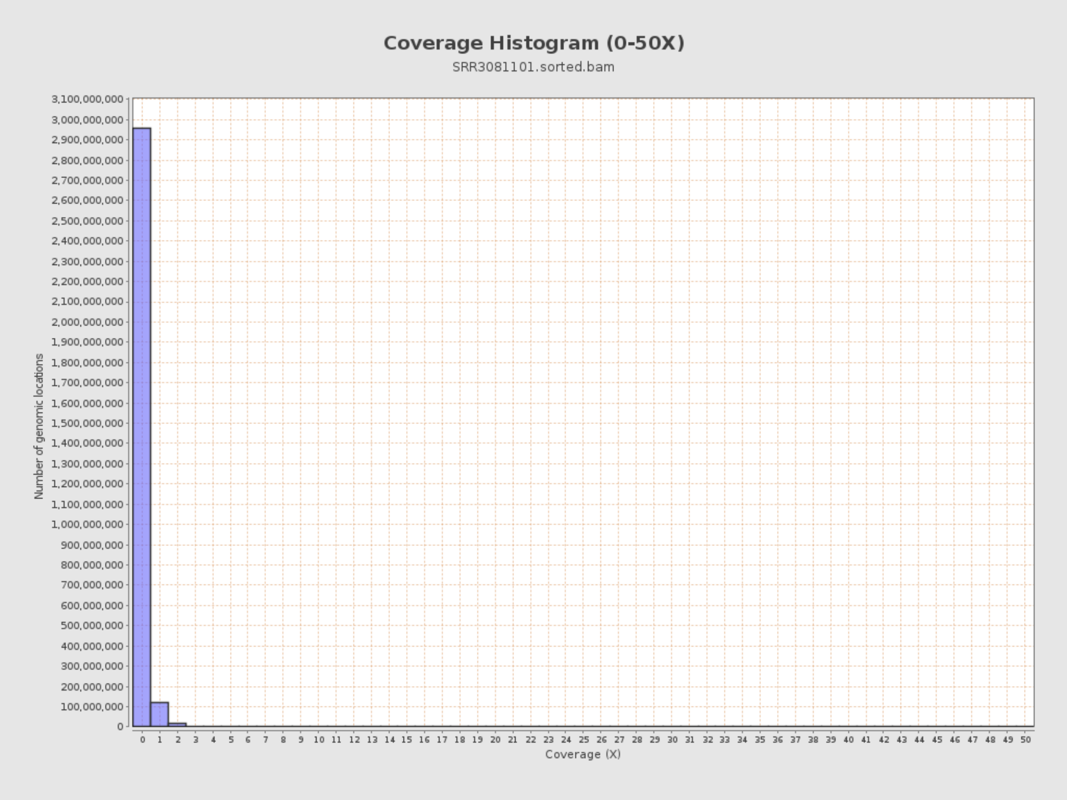
3. Results : Coverage across reference



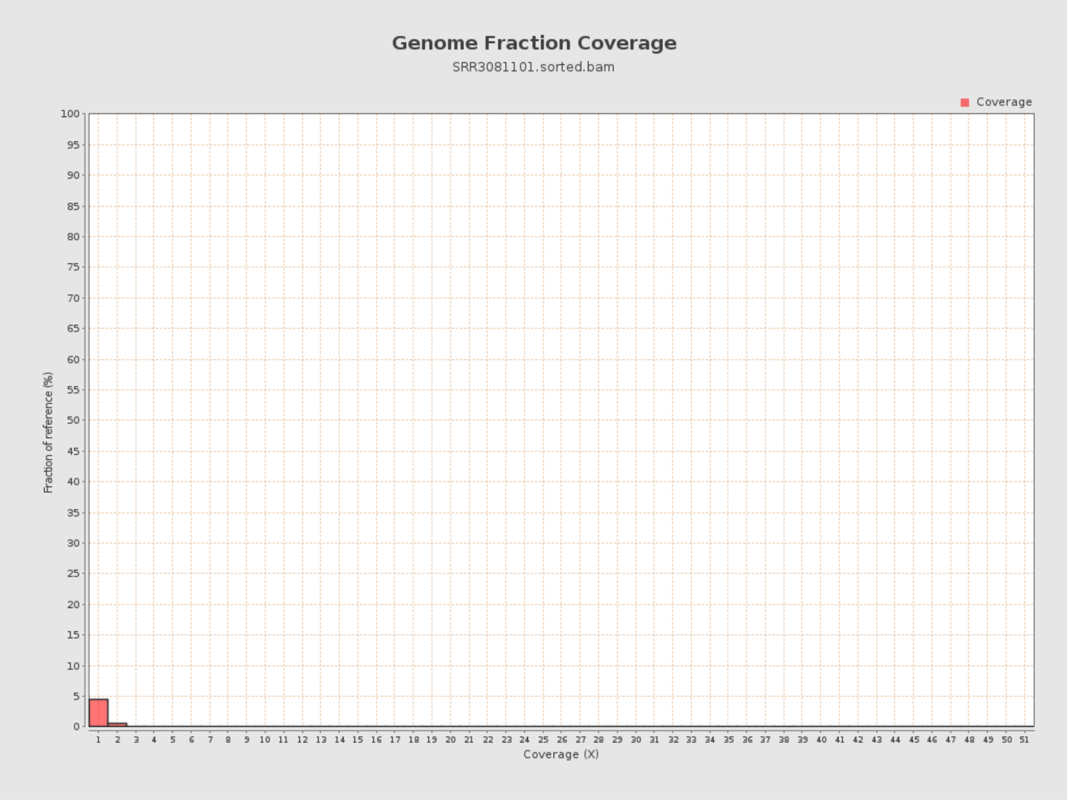
4. Results : Coverage Histogram



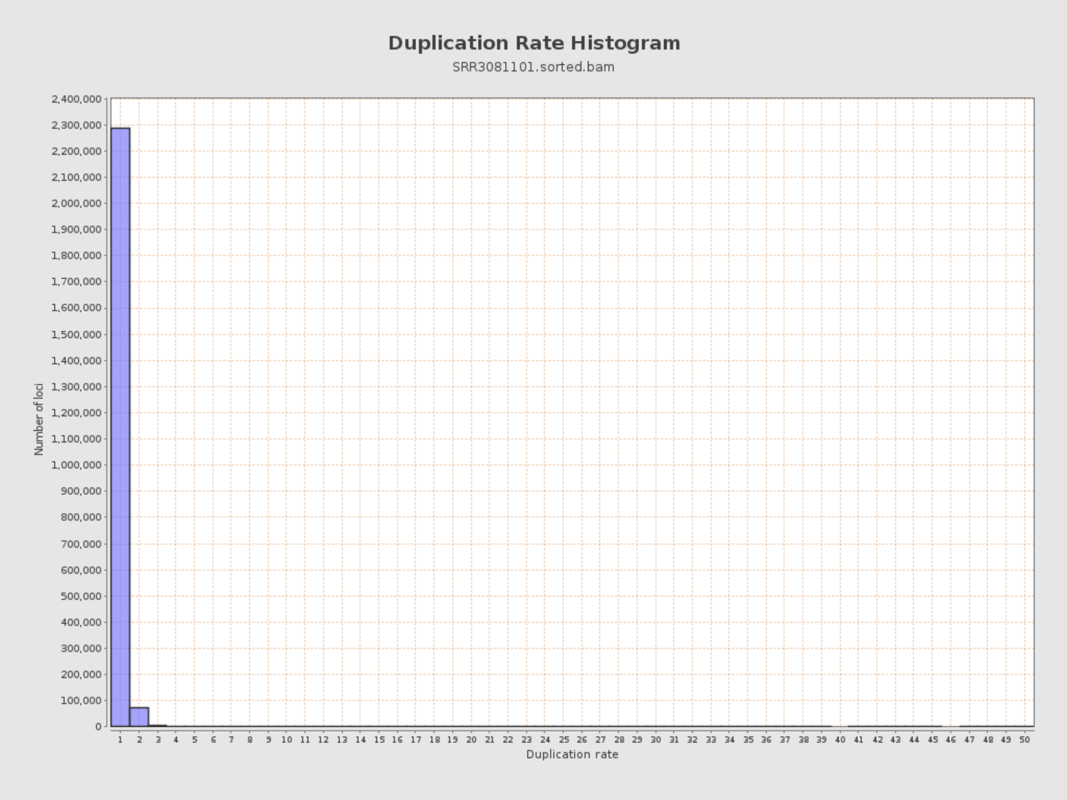
5. Results : Coverage Histogram (0-50X)



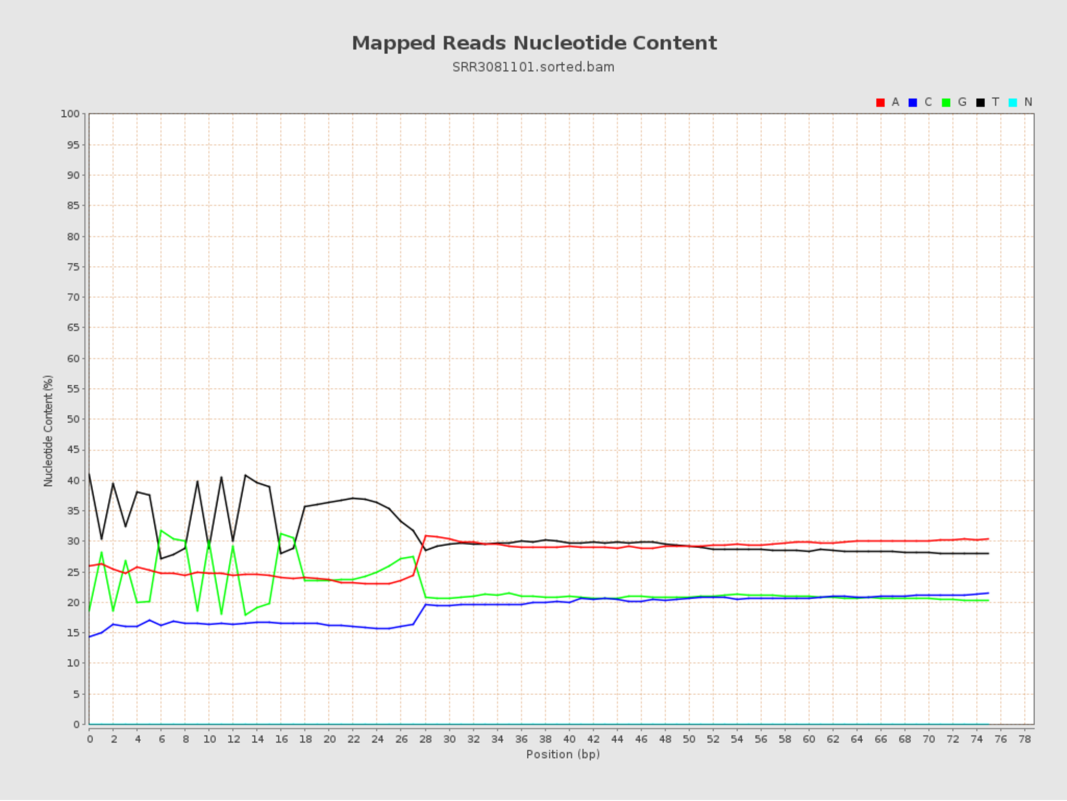
6. Results : Genome Fraction Coverage



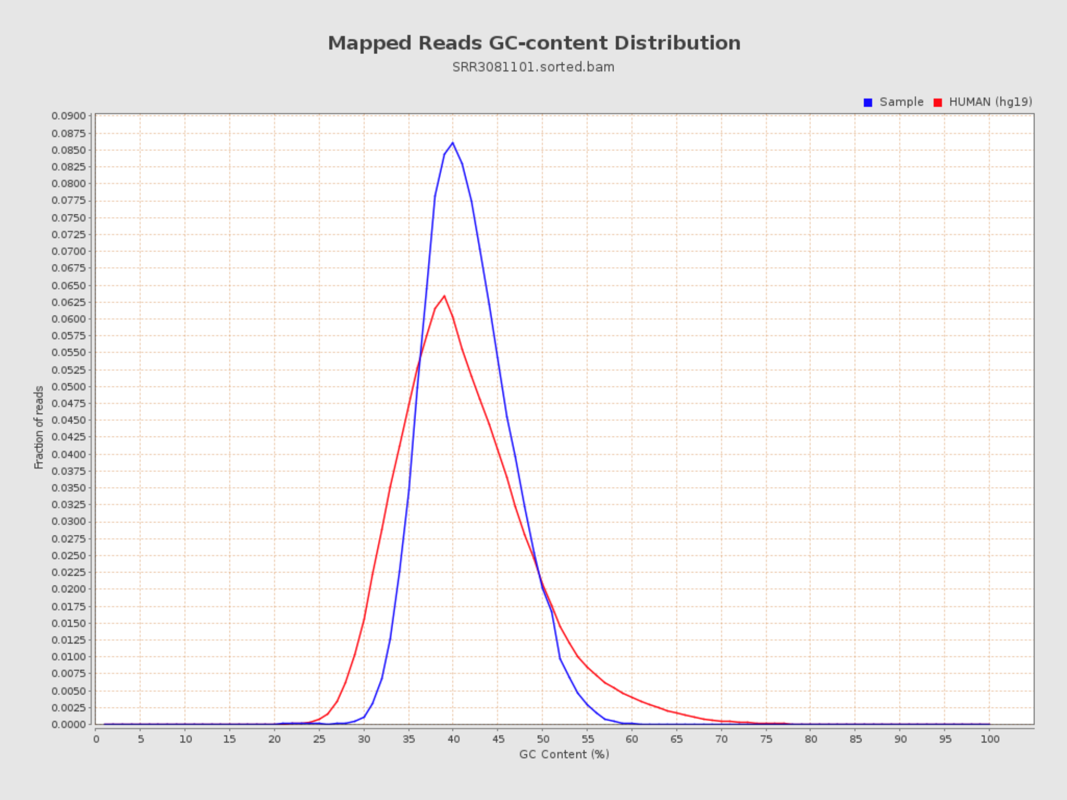
7. Results : Duplication Rate Histogram



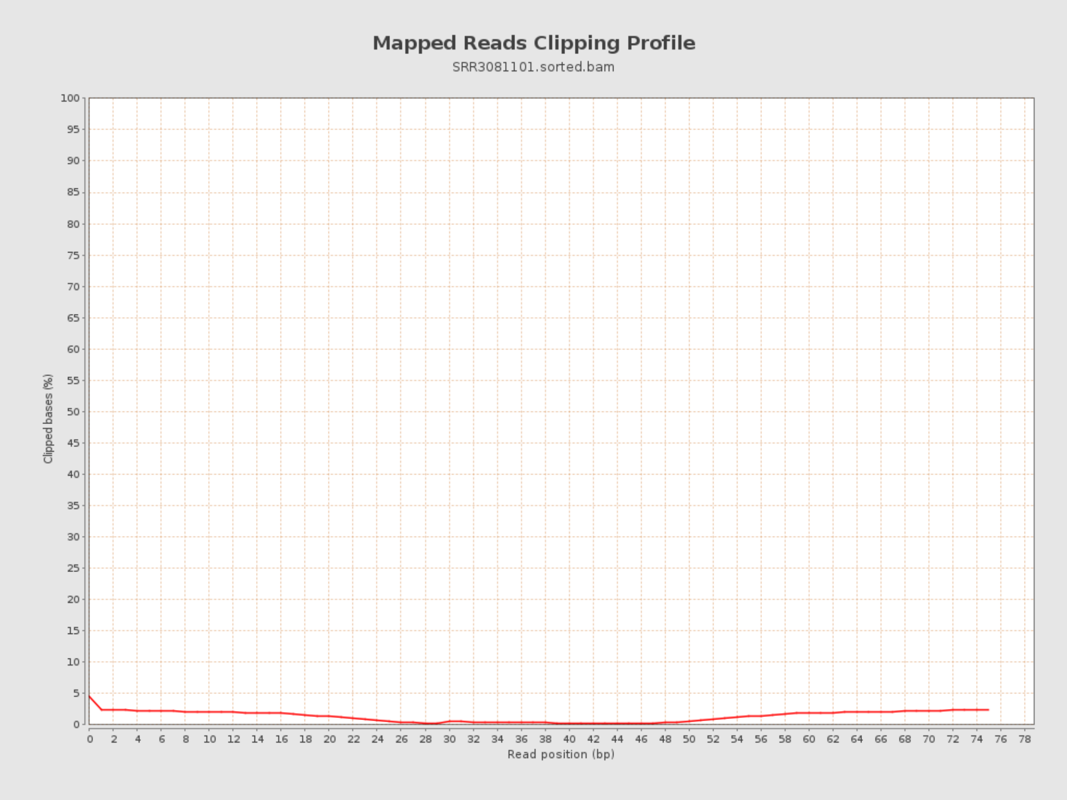
8. Results : Mapped Reads Nucleotide Content



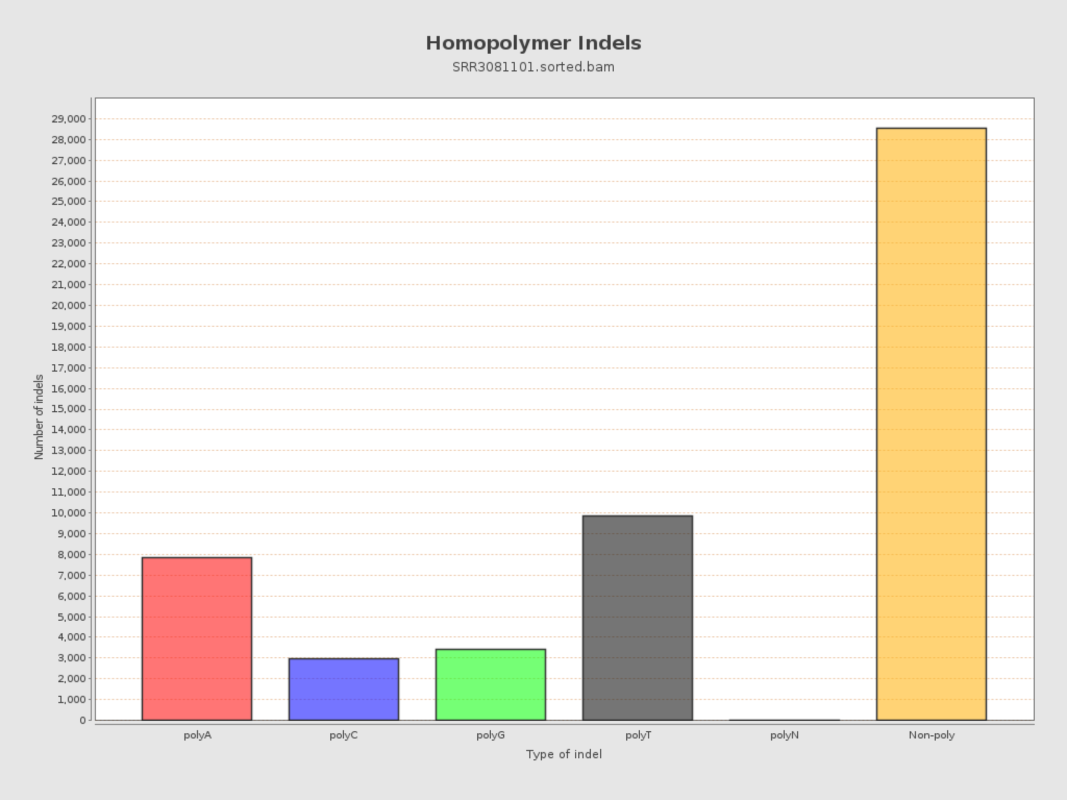
9. Results : Mapped Reads GC-content Distribution



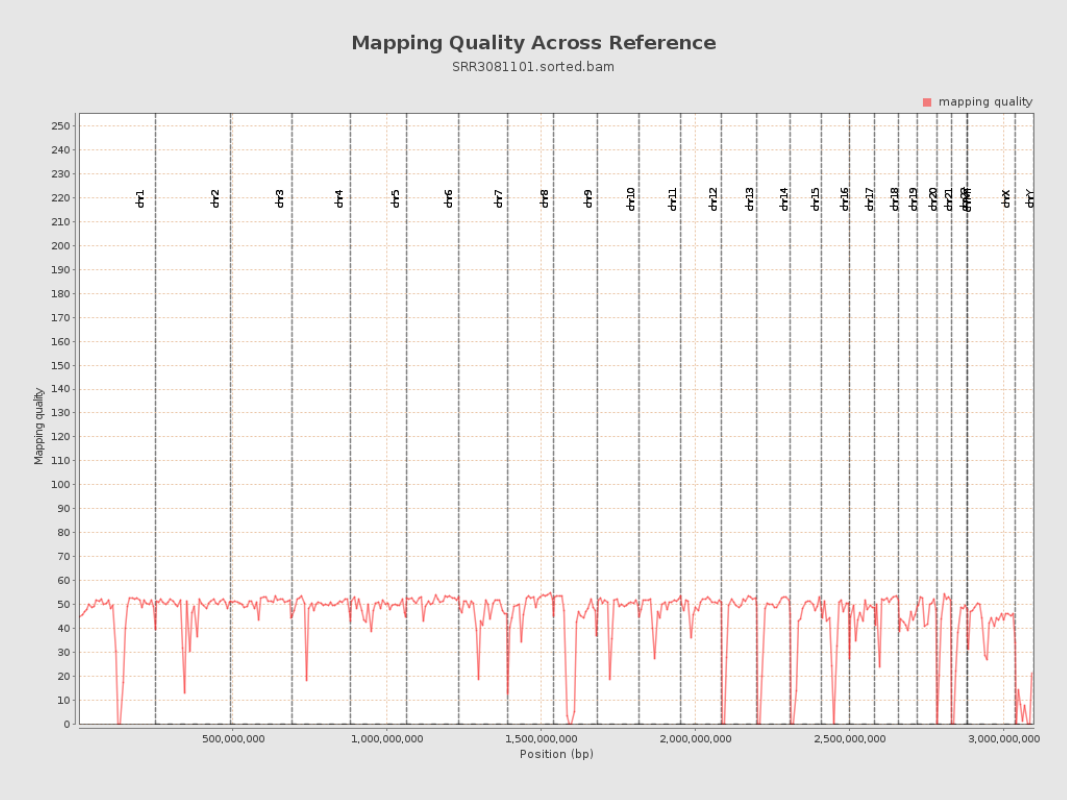
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram