Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 01:02:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081181.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_SRR3081181 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081181.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 01:02:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081181.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,971,368
Mapped reads	1,783,662 / 90.48%
Unmapped reads	187,706 / 9.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,567 / 0.79%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	63,886 / 3.24%
Duplication rate	2.63%
Clipped reads	741,706 / 37.62%

2.2. ACGT Content

Number/percentage of A's	34,306,179 / 28.42%
Number/percentage of C's	22,482,691 / 18.62%
Number/percentage of T's	37,818,392 / 31.32%
Number/percentage of G's	26,087,150 / 21.61%
Number/percentage of N's	36,221 / 0.03%
GC Percentage	40.23%

2.3. Coverage

Mean	0.039

Standard Deviation	0.3759

2.4. Mapping Quality

Mean Mapping Quality	46.45

2.5. Mismatches and indels

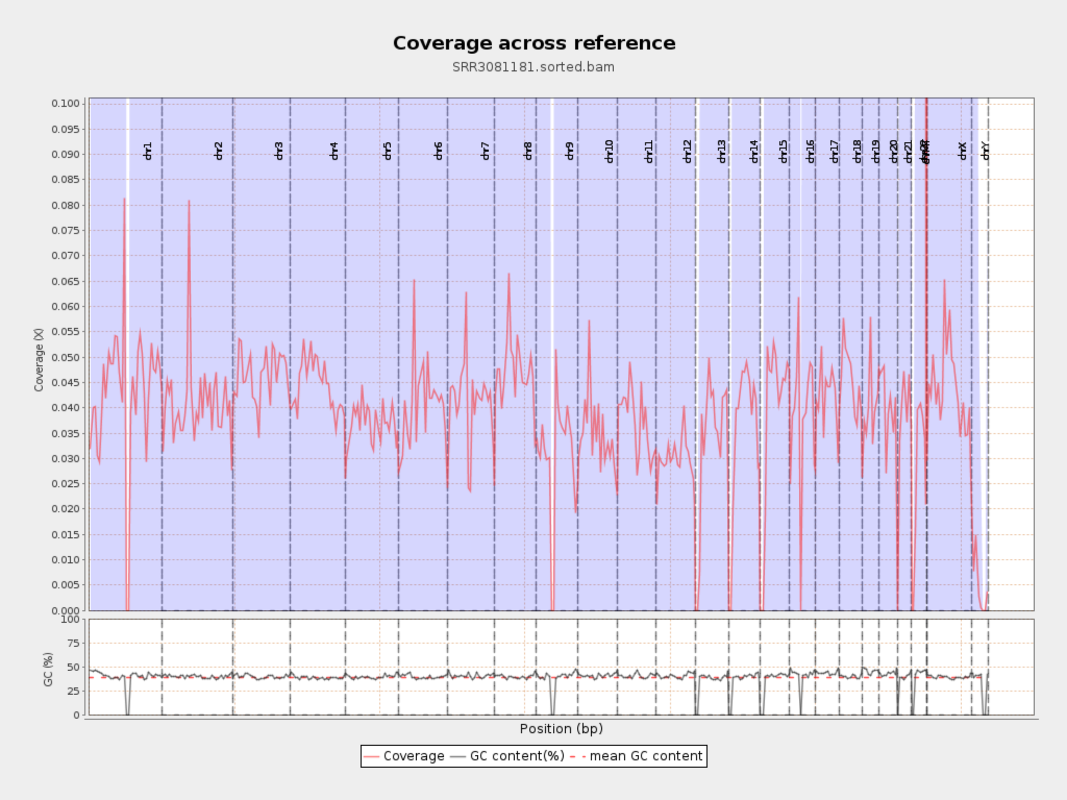
General error rate	0.87%
Mismatches	1,027,704
Insertions	9,771
Mapped reads with at least one insertion	0.54%
Deletions	29,657
Mapped reads with at least one deletion	1.64%
Homopolymer indels	46.37%

2.6. Chromosome stats

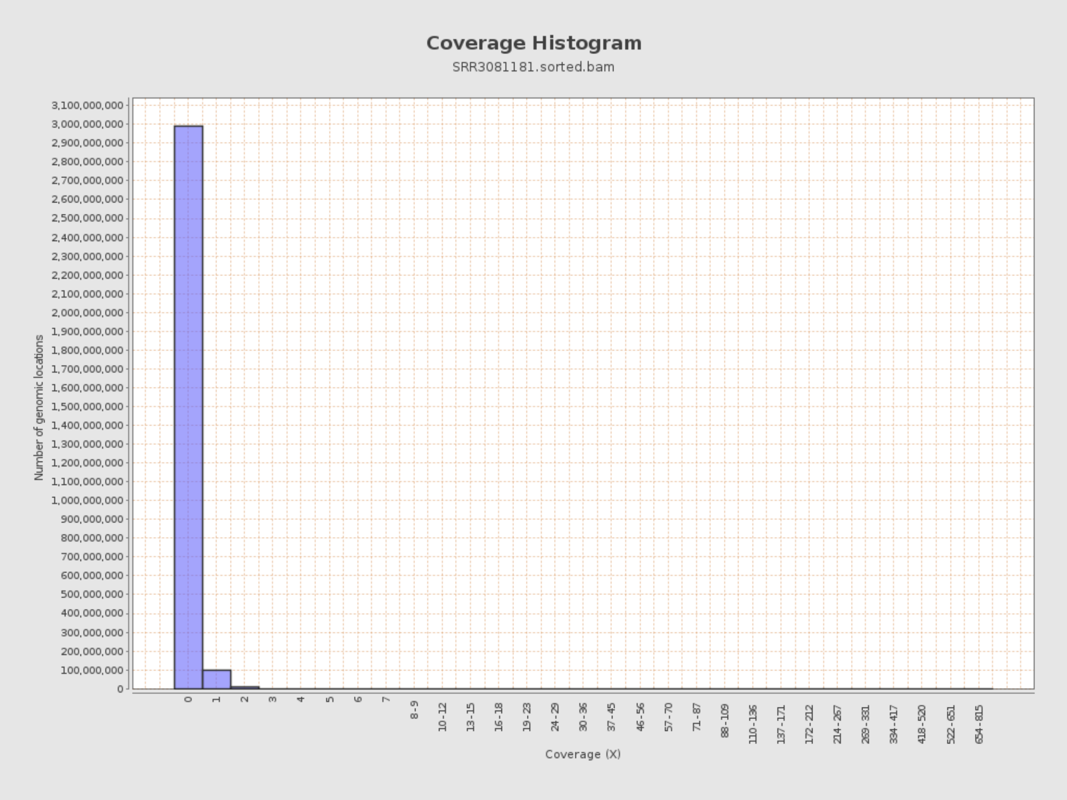
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10659660	0.0428	0.7419
chr2	243199373	10023122	0.0412	0.4197
chr3	198022430	9201339	0.0465	0.2339
chr4	191154276	8509402	0.0445	0.2359
chr5	180915260	6689428	0.037	0.2114
chr6	171115067	6906406	0.0404	0.312
chr7	159138663	6579330	0.0413	0.4742

chr8	146364022	6947915	0.0475	0.4726
chr9	141213431	4307589	0.0305	0.334
chr10	135534747	4751464	0.0351	0.289
chr11	135006516	5004329	0.0371	0.3407
chr12	133851895	4031804	0.0301	0.1956
chr13	115169878	3796228	0.033	0.1967
chr14	107349540	3782053	0.0352	0.2275
chr15	102531392	3948924	0.0385	0.2147
chr16	90354753	3486158	0.0386	0.2439
chr17	81195210	3413114	0.042	0.2705
chr18	78077248	3566923	0.0457	0.6593
chr19	59128983	2380815	0.0403	0.5092
chr20	63025520	2508794	0.0398	0.2221
chr21	48129895	1770524	0.0368	0.2243
chr22	51304566	1342673	0.0262	0.1747
chrMT	16571	78358	4.7286	3.0843
chrX	155270560	6788715	0.0437	0.266
chrY	59373566	304128	0.0051	0.1139

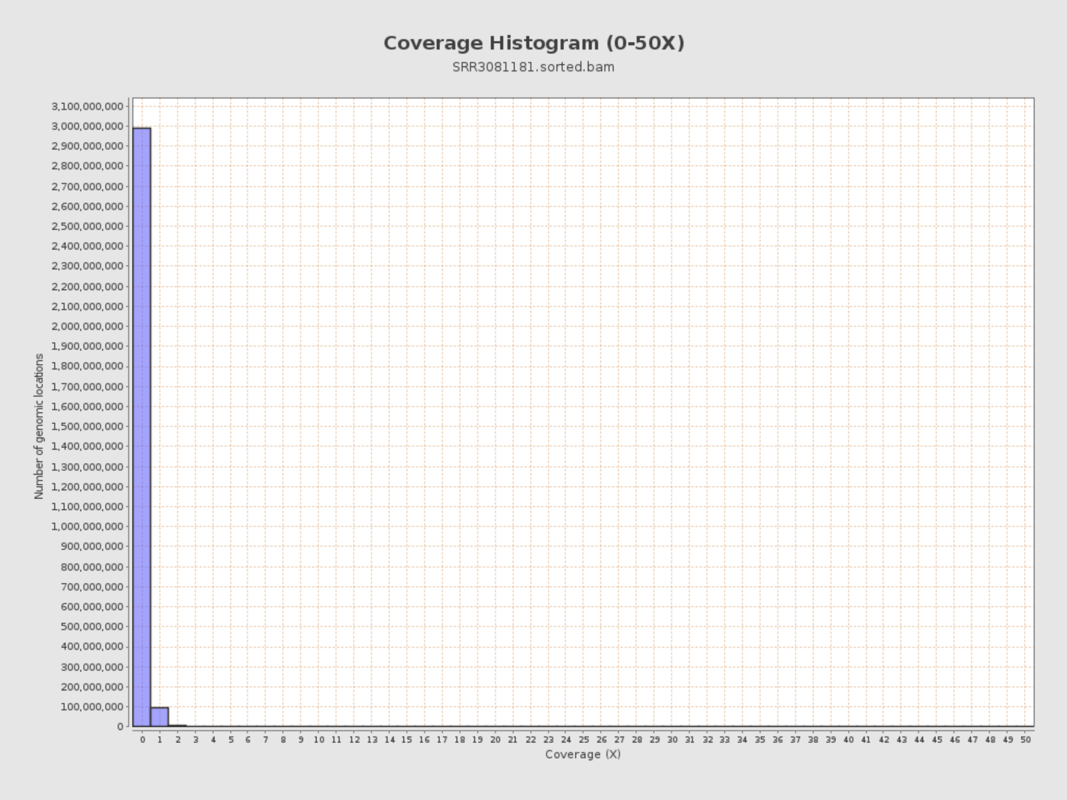
3. Results : Coverage across reference



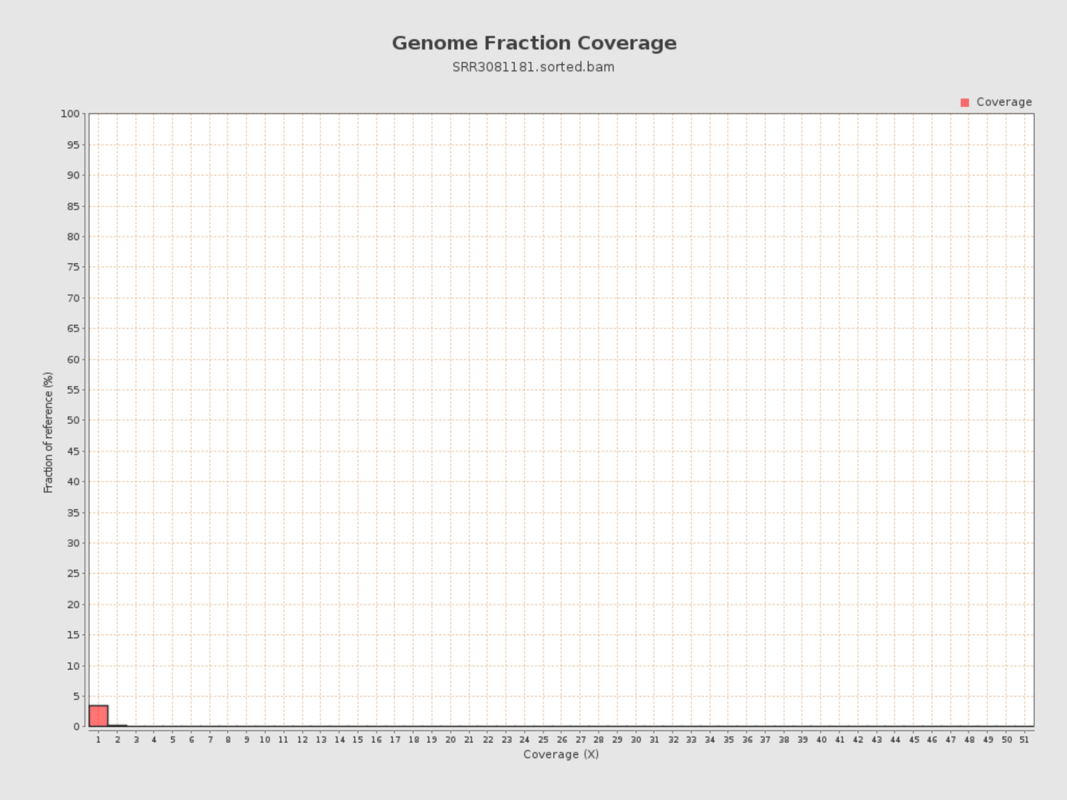
4. Results : Coverage Histogram



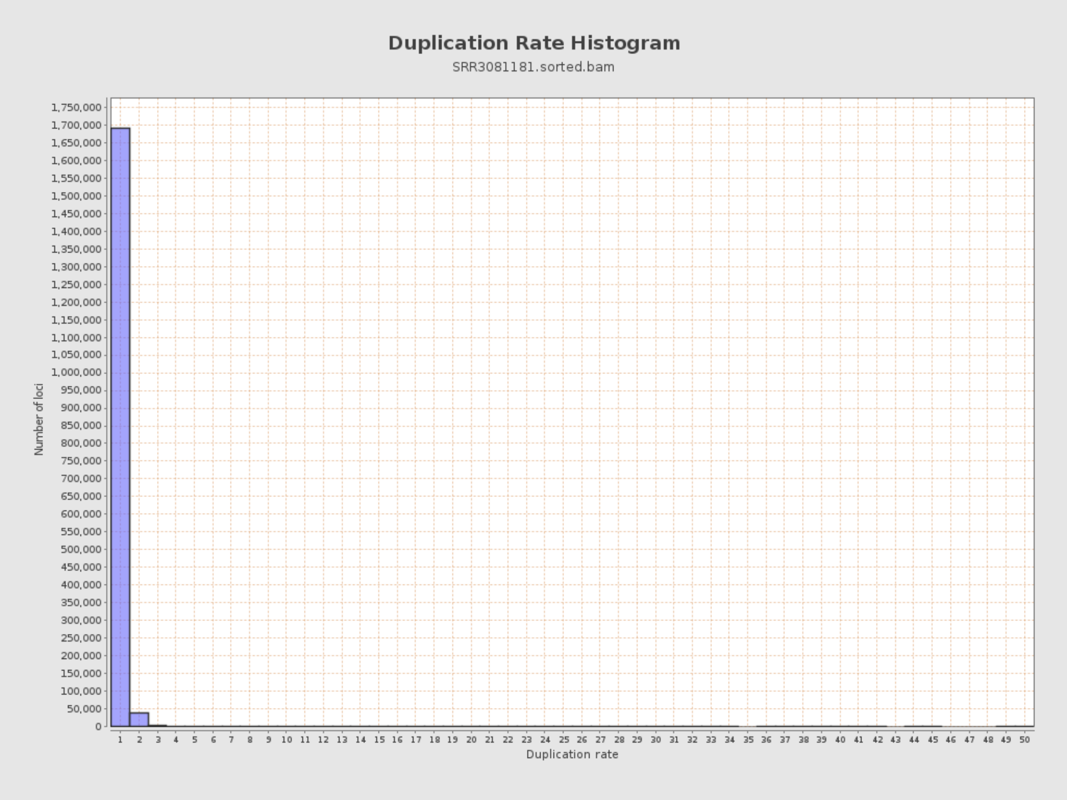
5. Results : Coverage Histogram (0-50X)



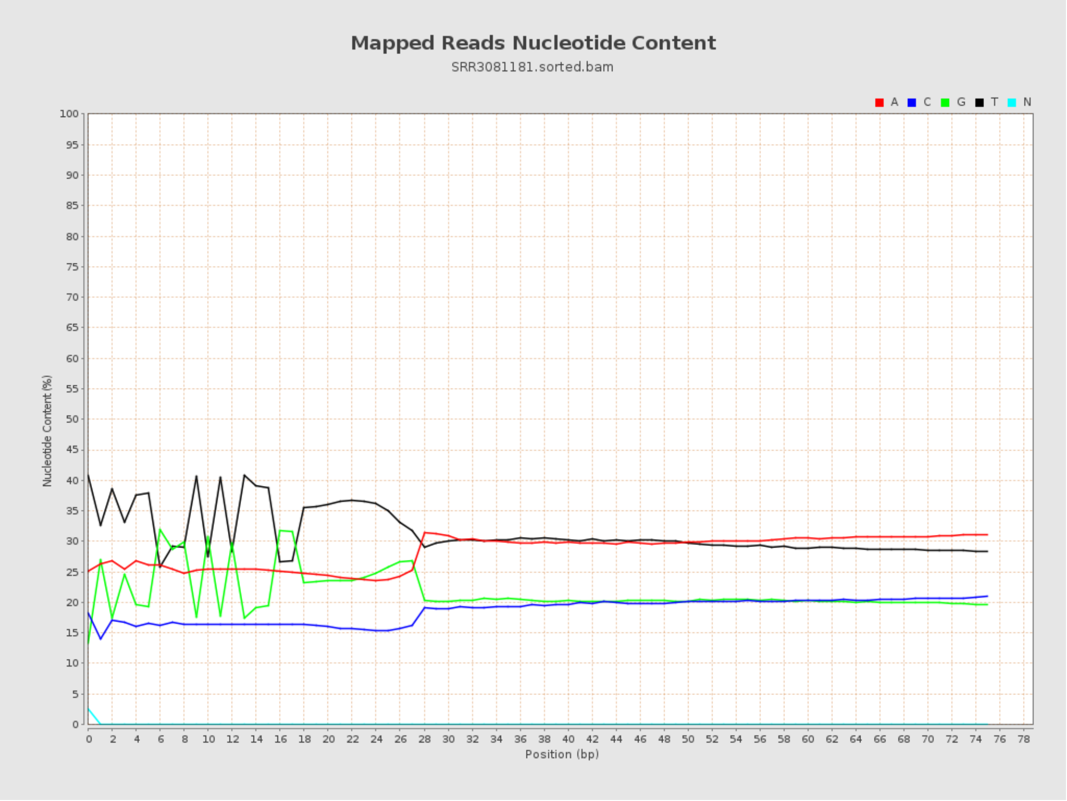
6. Results : Genome Fraction Coverage



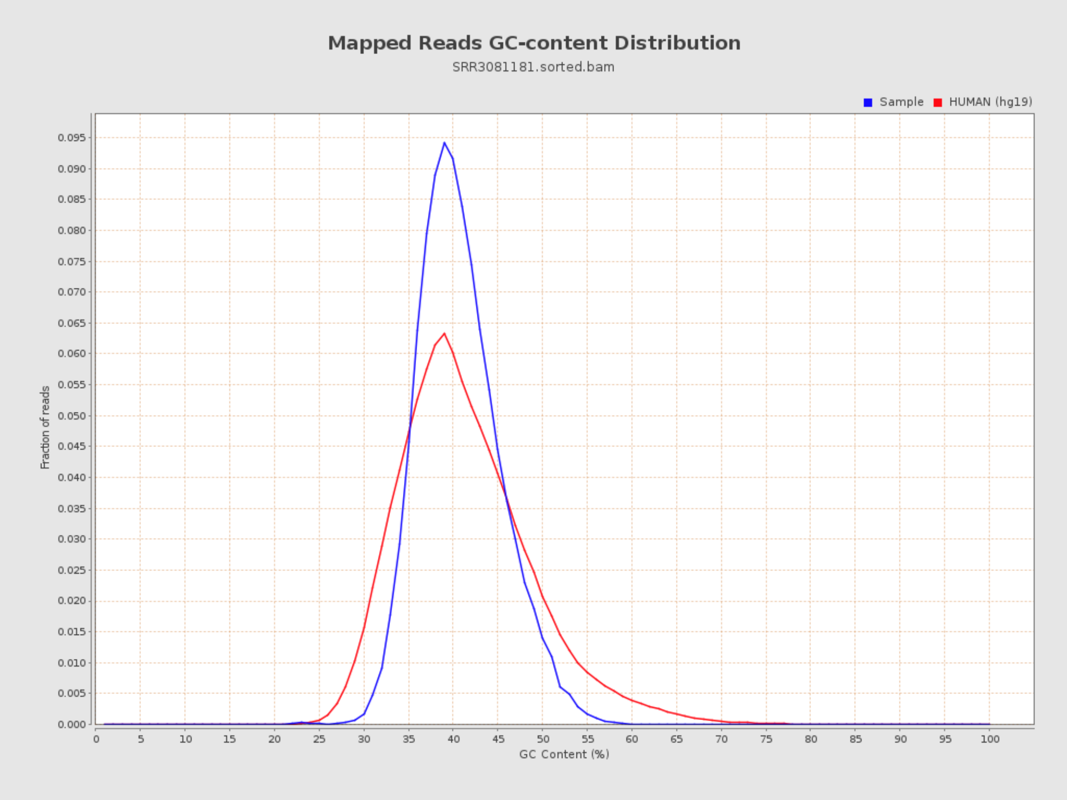
7. Results : Duplication Rate Histogram



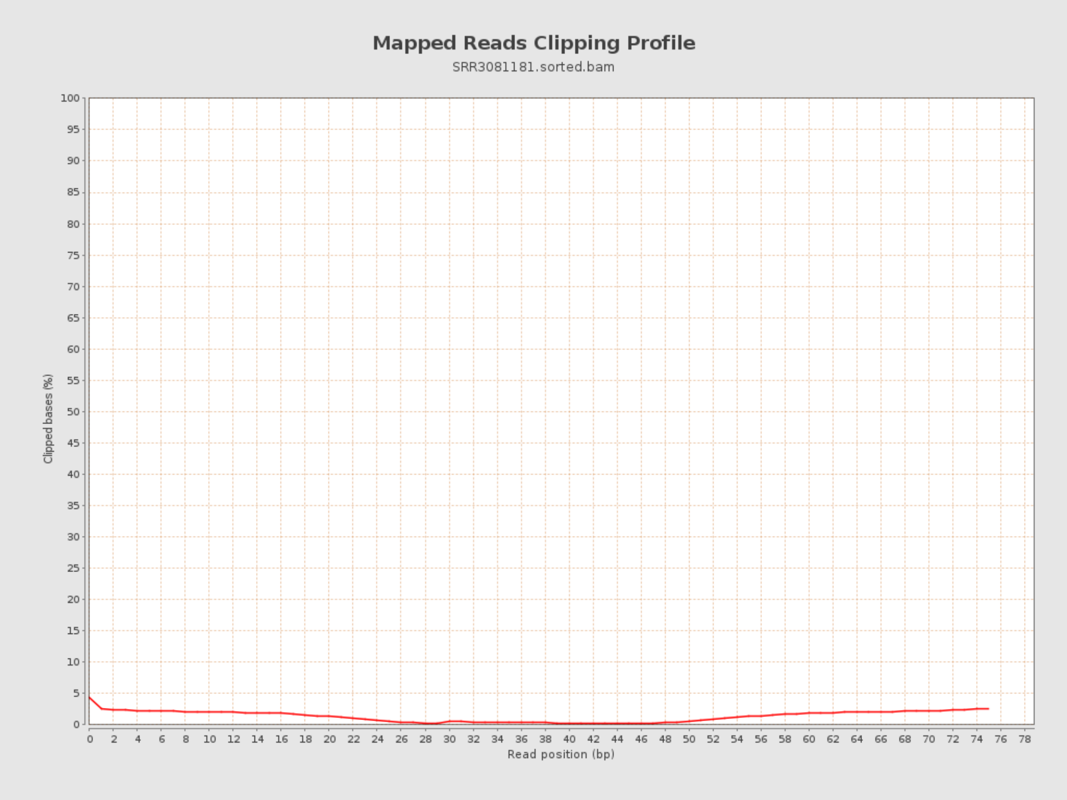
8. Results : Mapped Reads Nucleotide Content



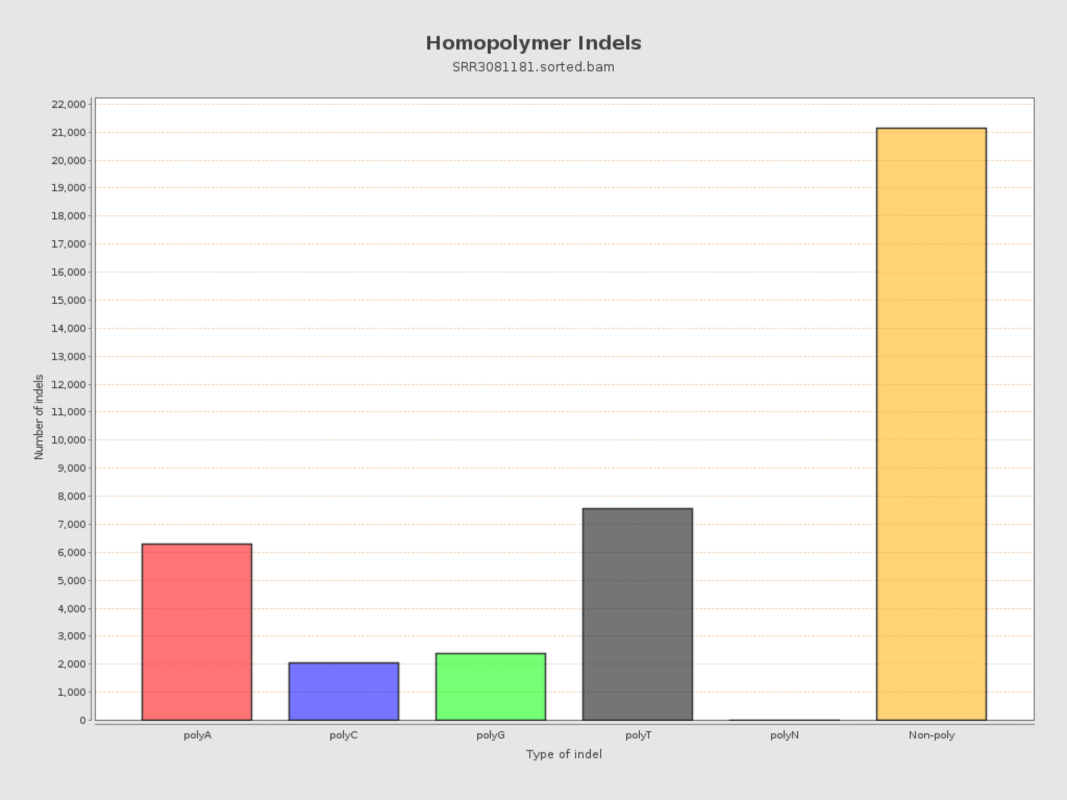
9. Results : Mapped Reads GC-content Distribution



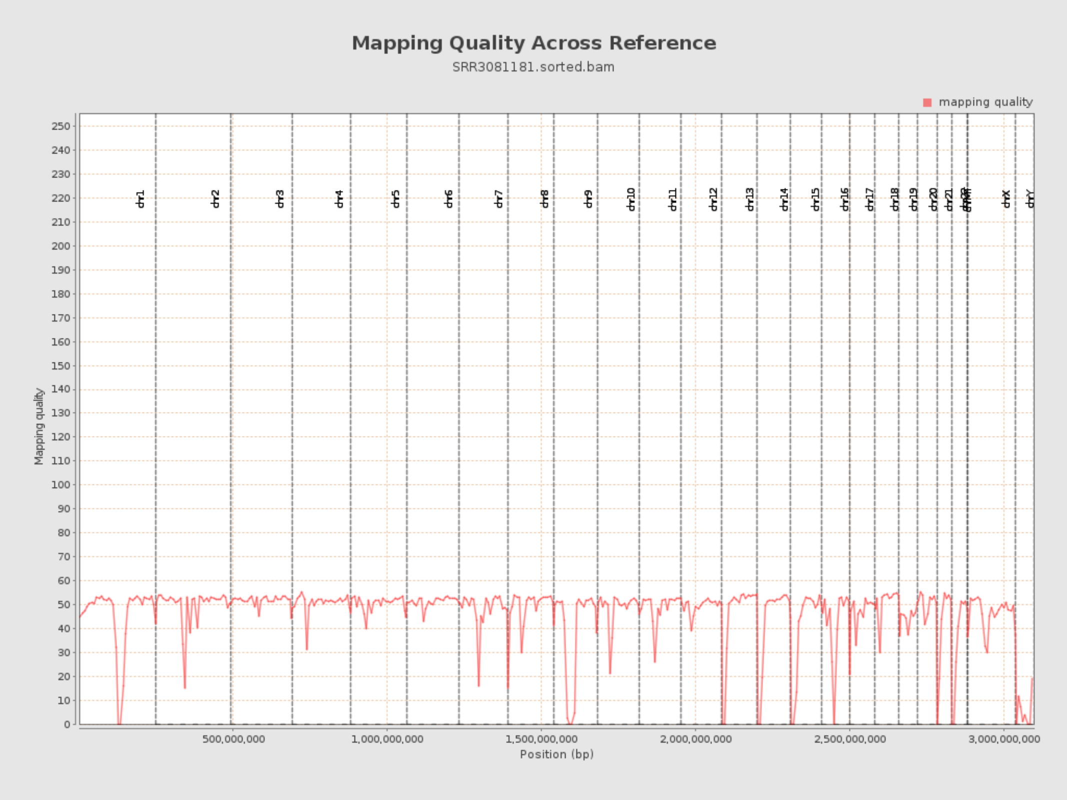
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram