Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 02:35:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081210.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_SRR3081210 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081210.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 02:35:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081210.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,412,412
Mapped reads	8,977,983 / 86.22%
Unmapped reads	1,434,429 / 13.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	88,205 / 0.85%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	1,065,156 / 10.23%
Duplication rate	7.59%
Clipped reads	4,666,528 / 44.82%

2.2. ACGT Content

Number/percentage of A's	166,151,126 / 28.35%
Number/percentage of C's	116,898,150 / 19.95%
Number/percentage of T's	176,146,396 / 30.06%
Number/percentage of G's	126,683,325 / 21.62%
Number/percentage of N's	148,683 / 0.03%
GC Percentage	41.56%

2.3. Coverage

Mean	0.1894

Standard Deviation	2.6521

2.4. Mapping Quality

Mean Mapping Quality	41.87

2.5. Mismatches and indels

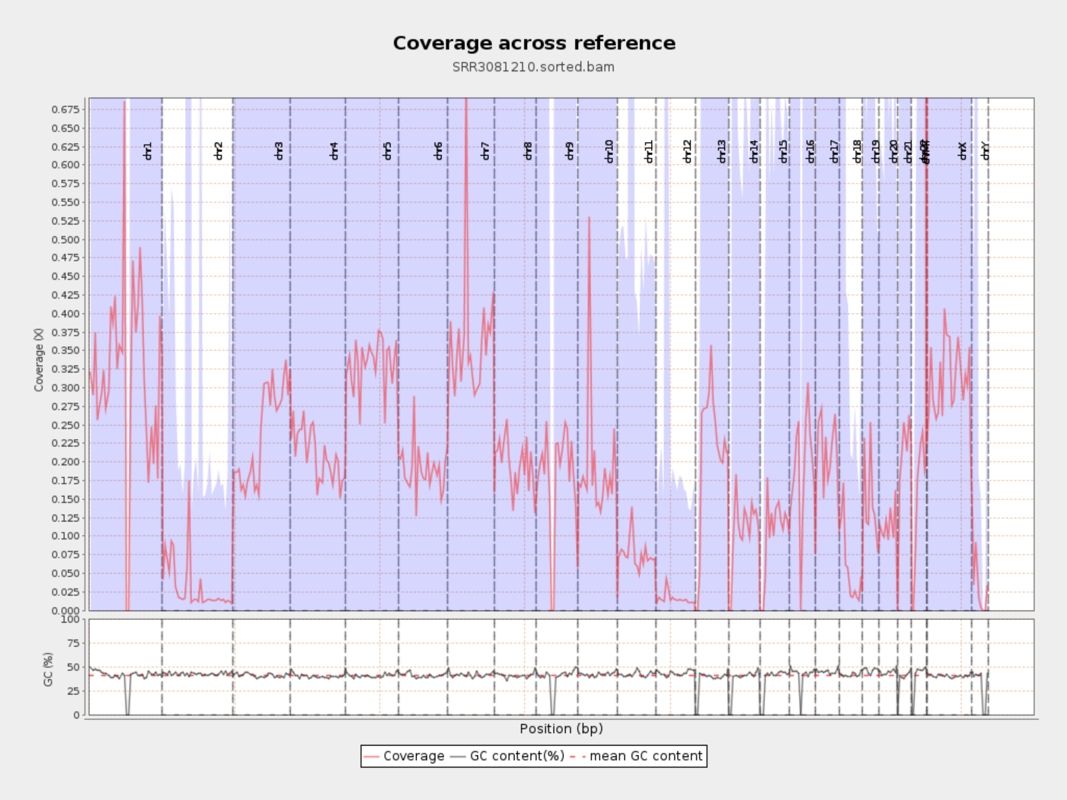
General error rate	1.12%
Mismatches	6,476,957
Insertions	40,464
Mapped reads with at least one insertion	0.45%
Deletions	118,162
Mapped reads with at least one deletion	1.3%
Homopolymer indels	45.16%

2.6. Chromosome stats

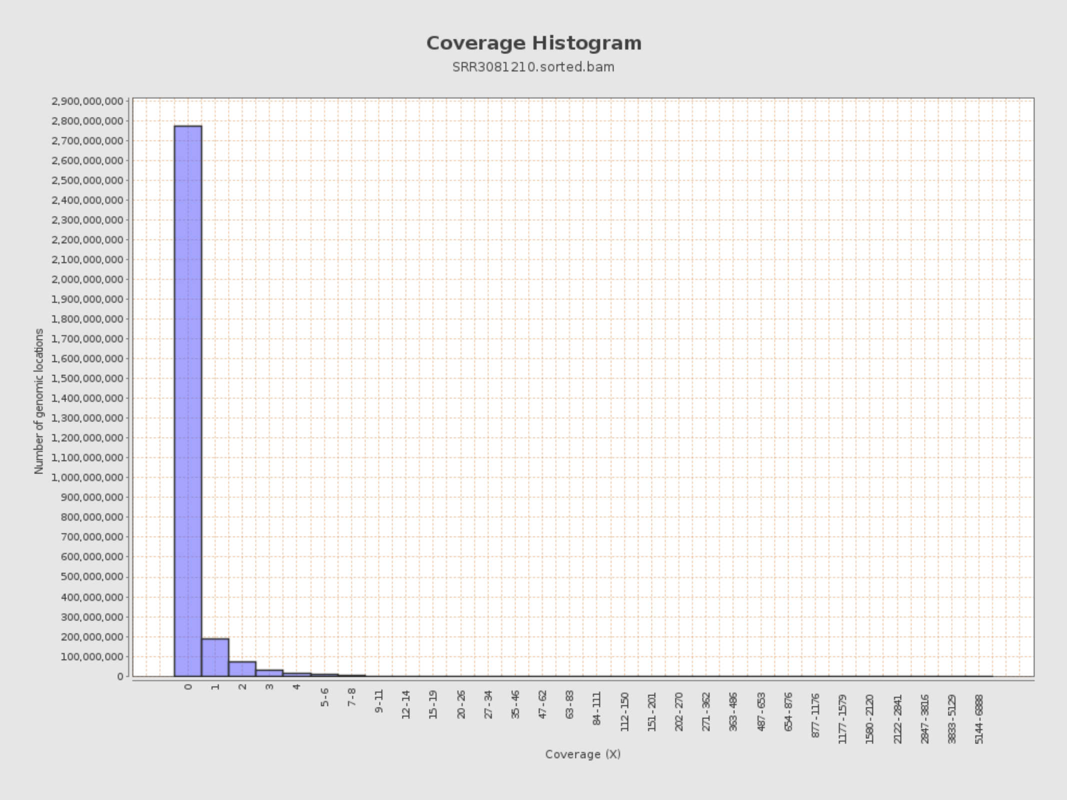
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	78866249	0.3164	5.9764
chr2	243199373	7965924	0.0328	0.8918
chr3	198022430	46793257	0.2363	0.9576
chr4	191154276	40191772	0.2103	0.7986
chr5	180915260	60262094	0.3331	0.9211
chr6	171115067	32530103	0.1901	1.0525
chr7	159138663	58029268	0.3646	6.2531

chr8	146364022	28672084	0.1959	3.2517
chr9	141213431	25524719	0.1808	1.3624
chr10	135534747	25923160	0.1913	3.3548
chr11	135006516	10091442	0.0747	1.0758
chr12	133851895	2188934	0.0164	0.4819
chr13	115169878	24530313	0.213	0.7173
chr14	107349540	11513823	0.1073	1.0345
chr15	102531392	10541237	0.1028	0.4874
chr16	90354753	17273839	0.1912	0.9737
chr17	81195210	17124257	0.2109	1.0958
chr18	78077248	4570070	0.0585	2.747
chr19	59128983	8528984	0.1442	4.0236
chr20	63025520	7219154	0.1145	0.6601
chr21	48129895	9764023	0.2029	0.8489
chr22	51304566	7395063	0.1441	0.596
chrMT	16571	207215	12.5047	8.0575
chrX	155270560	48490574	0.3123	1.1987
chrY	59373566	2017668	0.034	0.5525

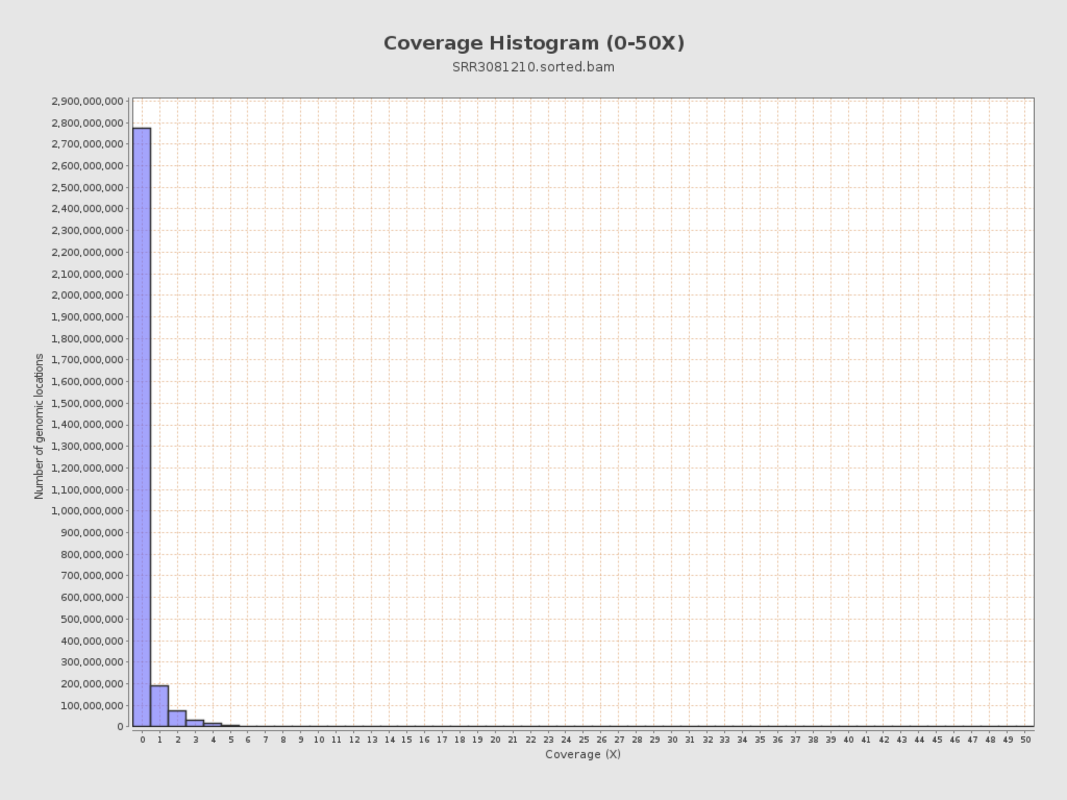
3. Results : Coverage across reference



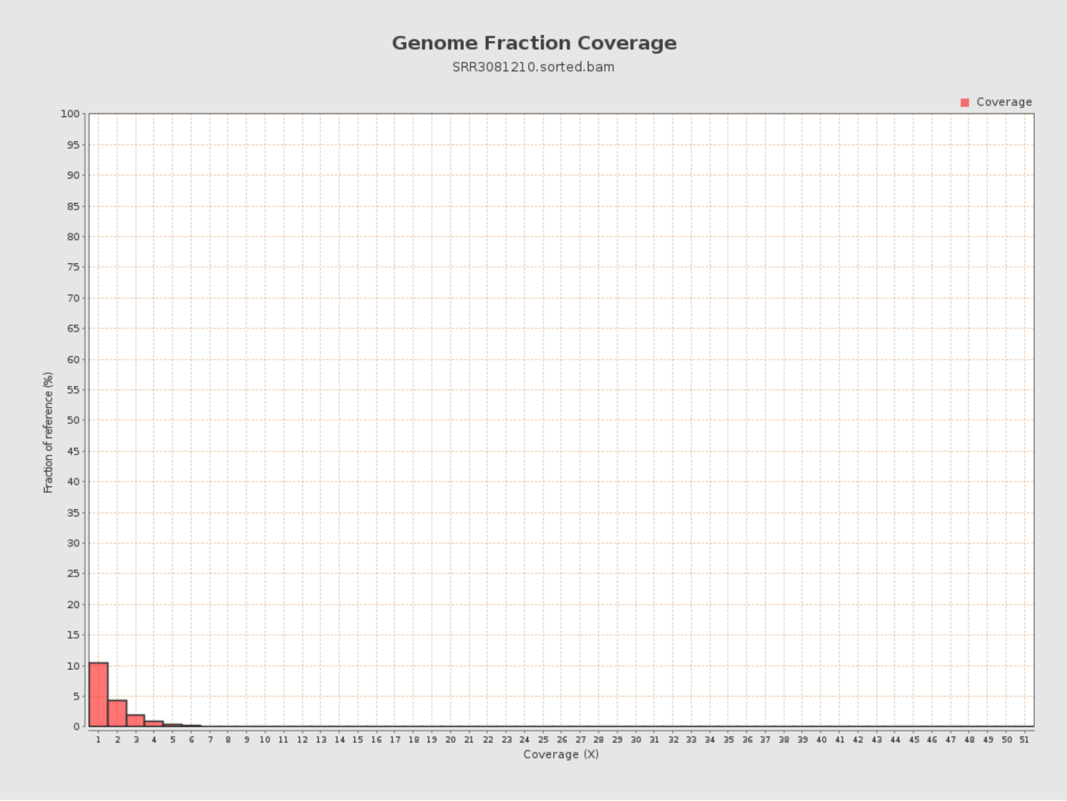
4. Results : Coverage Histogram



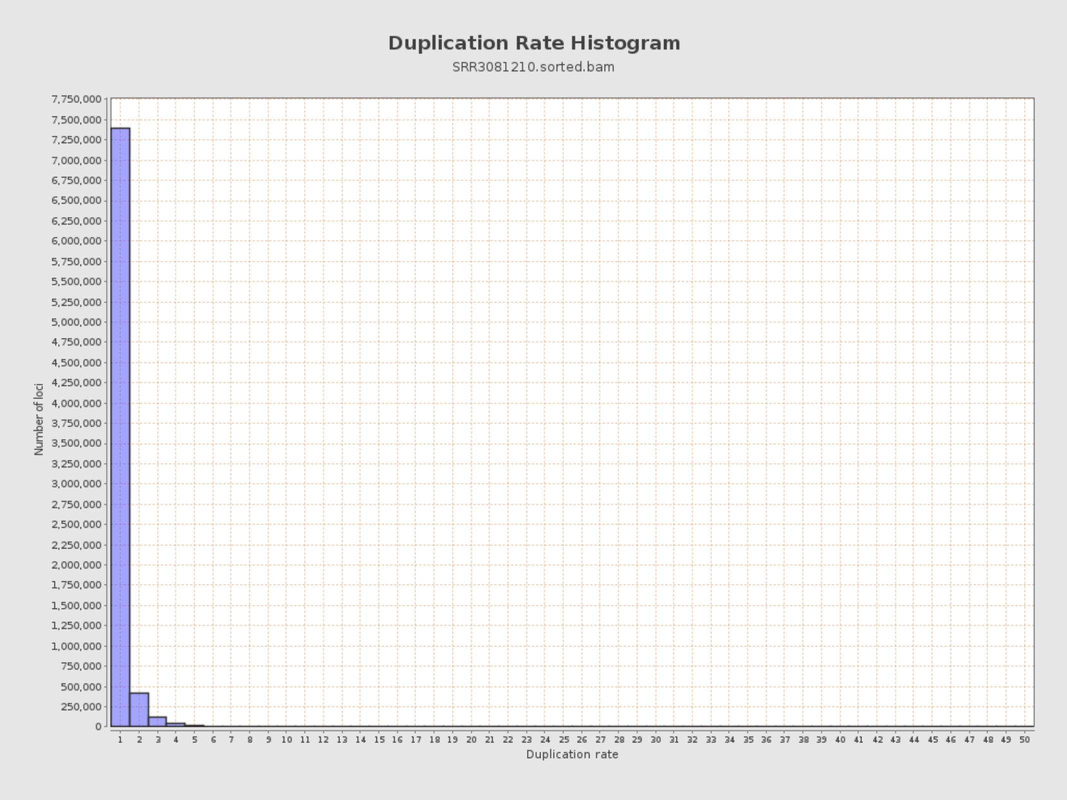
5. Results : Coverage Histogram (0-50X)



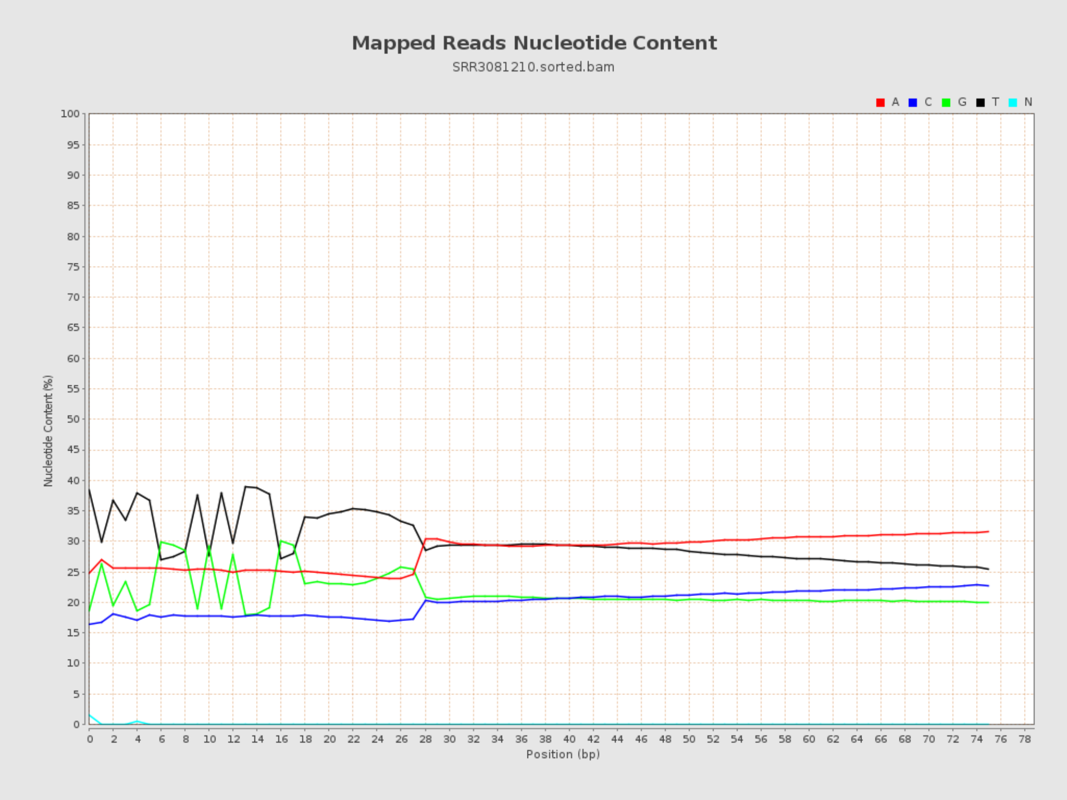
6. Results : Genome Fraction Coverage



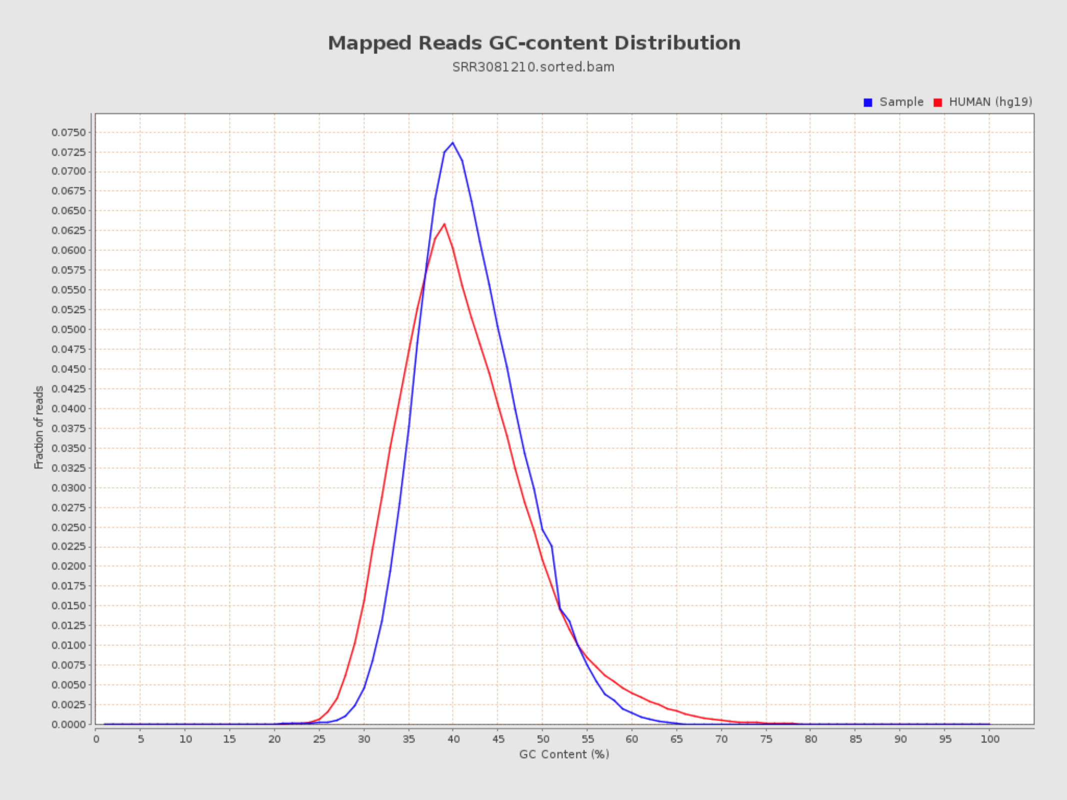
7. Results : Duplication Rate Histogram



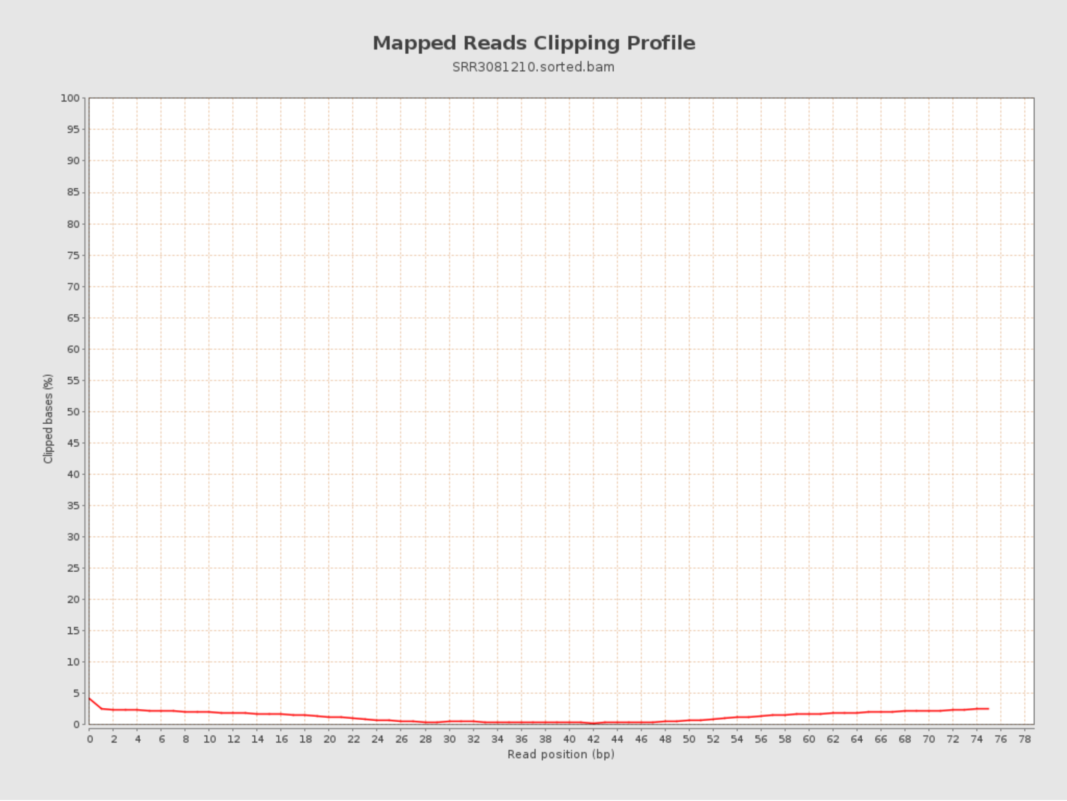
8. Results : Mapped Reads Nucleotide Content



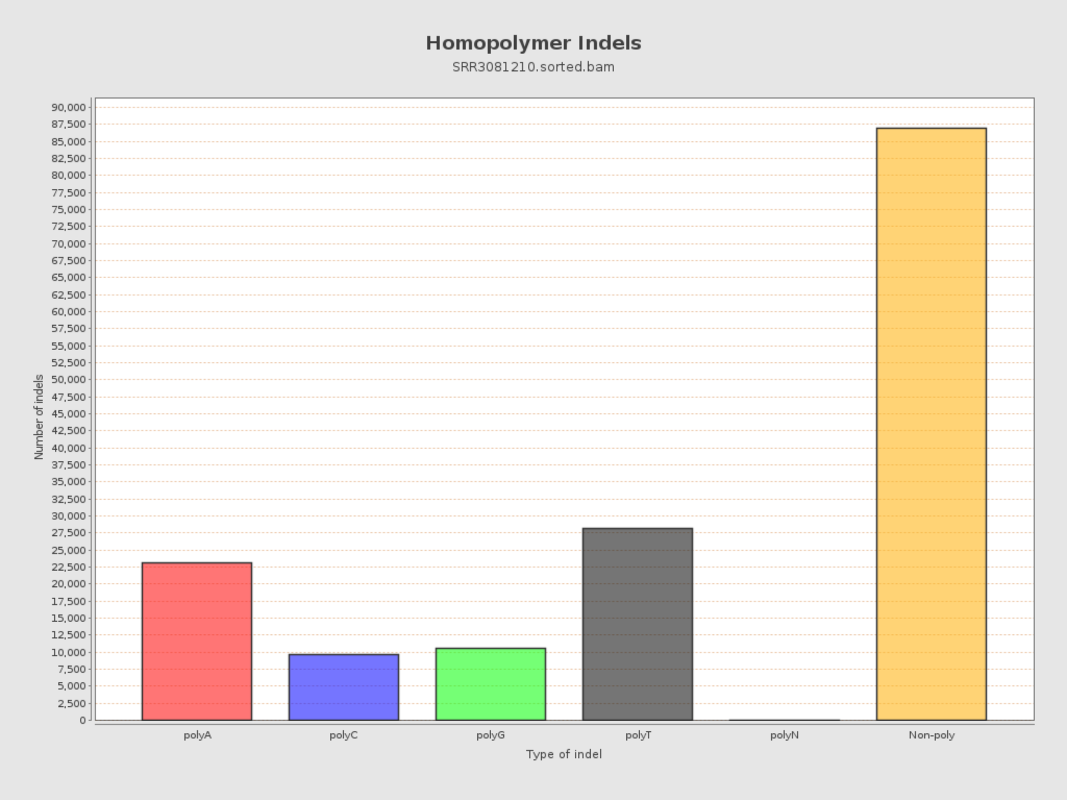
9. Results : Mapped Reads GC-content Distribution



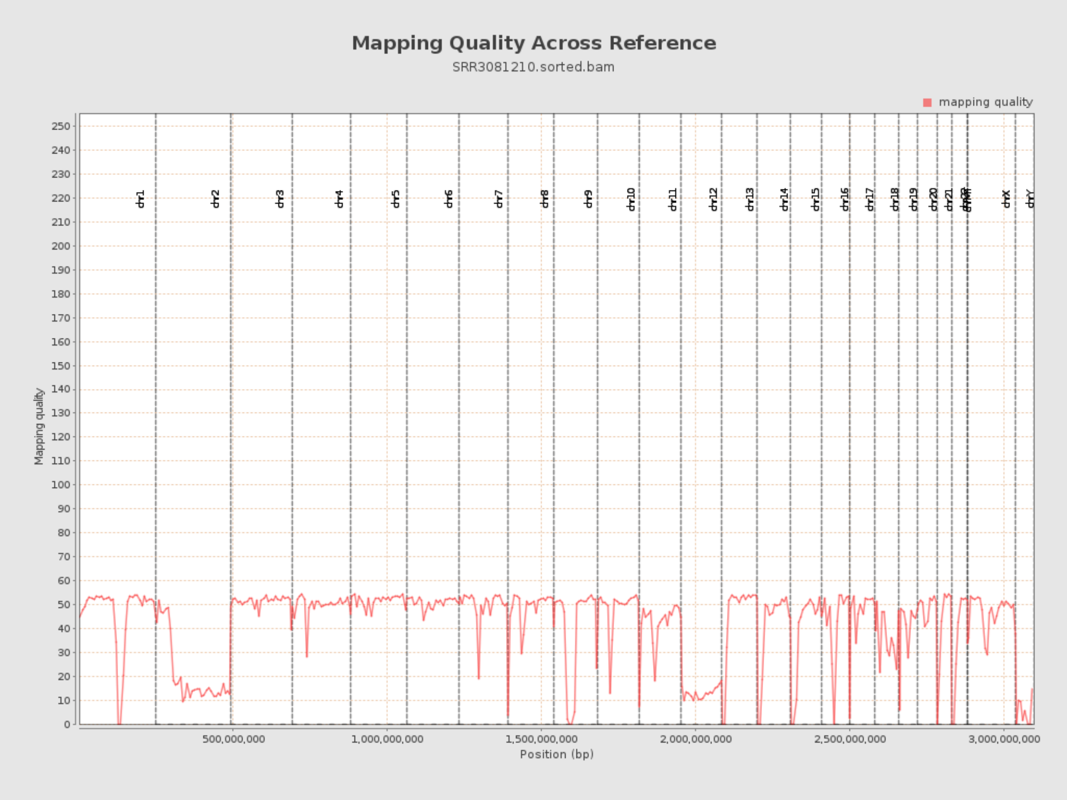
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram