Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 03:31:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081223.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_SRR3081223 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081223.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 03:31:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081223.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,411,709
Mapped reads	2,124,615 / 88.1%
Unmapped reads	287,094 / 11.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,510 / 1.06%
Read min/max/mean length	30 / 76 / 76.37
Duplicated reads (estimated)	92,803 / 3.85%
Duplication rate	3.59%
Clipped reads	1,107,453 / 45.92%

2.2. ACGT Content

Number/percentage of A's	39,524,544 / 28.5%
Number/percentage of C's	26,758,770 / 19.29%
Number/percentage of T's	42,465,252 / 30.62%
Number/percentage of G's	29,940,199 / 21.59%
Number/percentage of N's	9,251 / 0.01%
GC Percentage	40.88%

2.3. Coverage

Mean	0.0448

Standard Deviation	0.3529

2.4. Mapping Quality

Mean Mapping Quality	45.31

2.5. Mismatches and indels

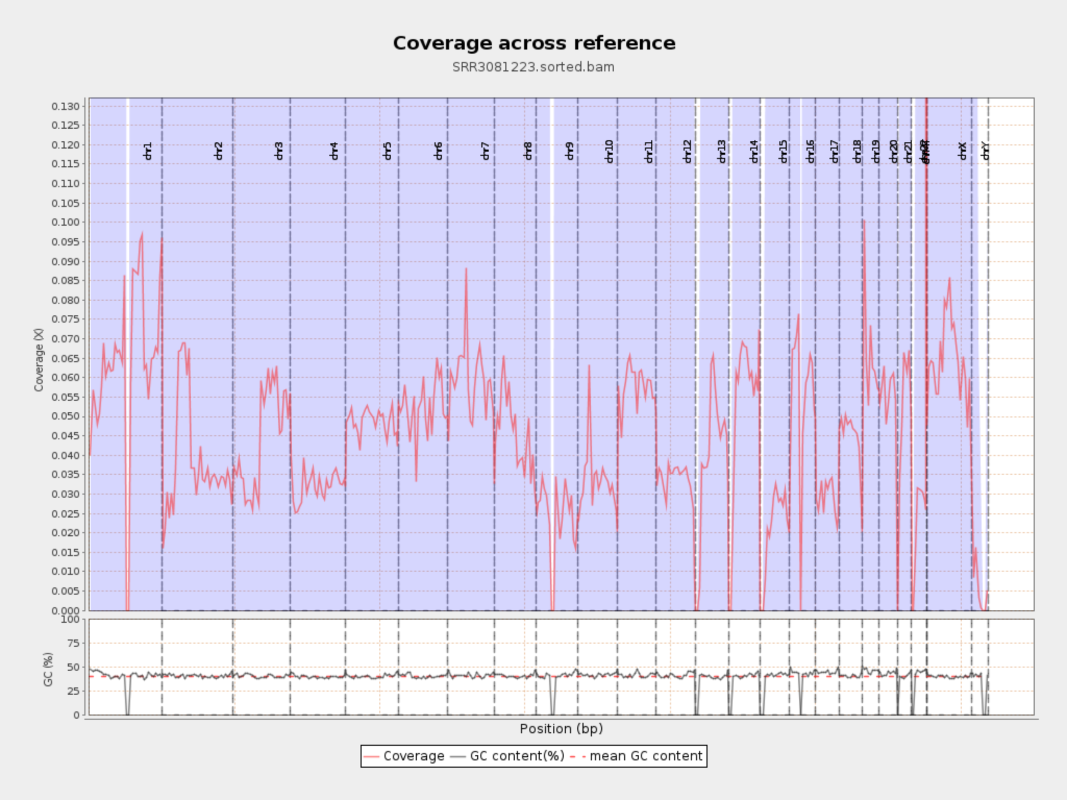
General error rate	0.89%
Mismatches	1,214,569
Insertions	10,023
Mapped reads with at least one insertion	0.47%
Deletions	31,517
Mapped reads with at least one deletion	1.47%
Homopolymer indels	48.41%

2.6. Chromosome stats

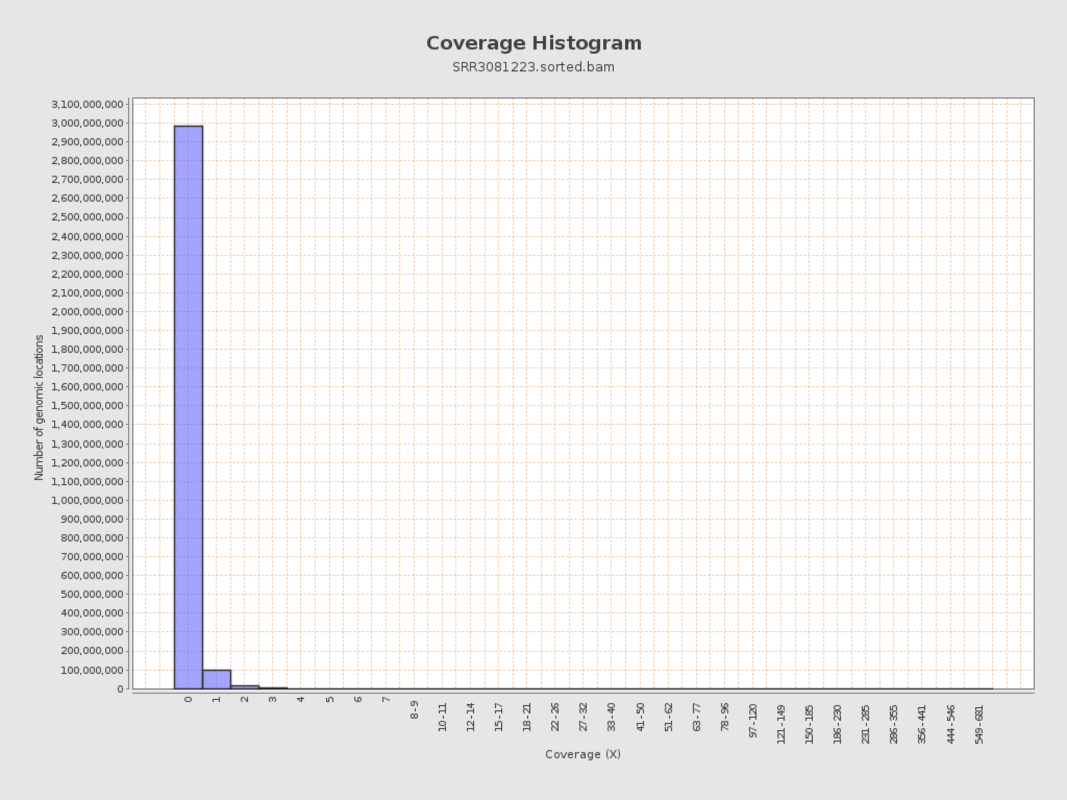
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15779525	0.0633	0.6426
chr2	243199373	9426866	0.0388	0.3787
chr3	198022430	8747416	0.0442	0.2493
chr4	191154276	6116688	0.032	0.2157
chr5	180915260	8791251	0.0486	0.2587
chr6	171115067	8930702	0.0522	0.2909
chr7	159138663	9529567	0.0599	0.4947

chr8	146364022	6709292	0.0458	0.3843
chr9	141213431	3374894	0.0239	0.2405
chr10	135534747	4592174	0.0339	0.3403
chr11	135006516	7715045	0.0571	0.431
chr12	133851895	4506844	0.0337	0.2177
chr13	115169878	4558144	0.0396	0.2343
chr14	107349540	5562875	0.0518	0.2732
chr15	102531392	2159926	0.0211	0.1731
chr16	90354753	5081504	0.0562	0.2878
chr17	81195210	2351358	0.029	0.233
chr18	78077248	3586009	0.0459	0.4064
chr19	59128983	3833632	0.0648	0.4993
chr20	63025520	3466595	0.055	0.2776
chr21	48129895	2384240	0.0495	0.2711
chr22	51304566	1103908	0.0215	0.1701
chrMT	16571	49887	3.0105	2.5937
chrX	155270560	10010045	0.0645	0.319
chrY	59373566	381223	0.0064	0.1117

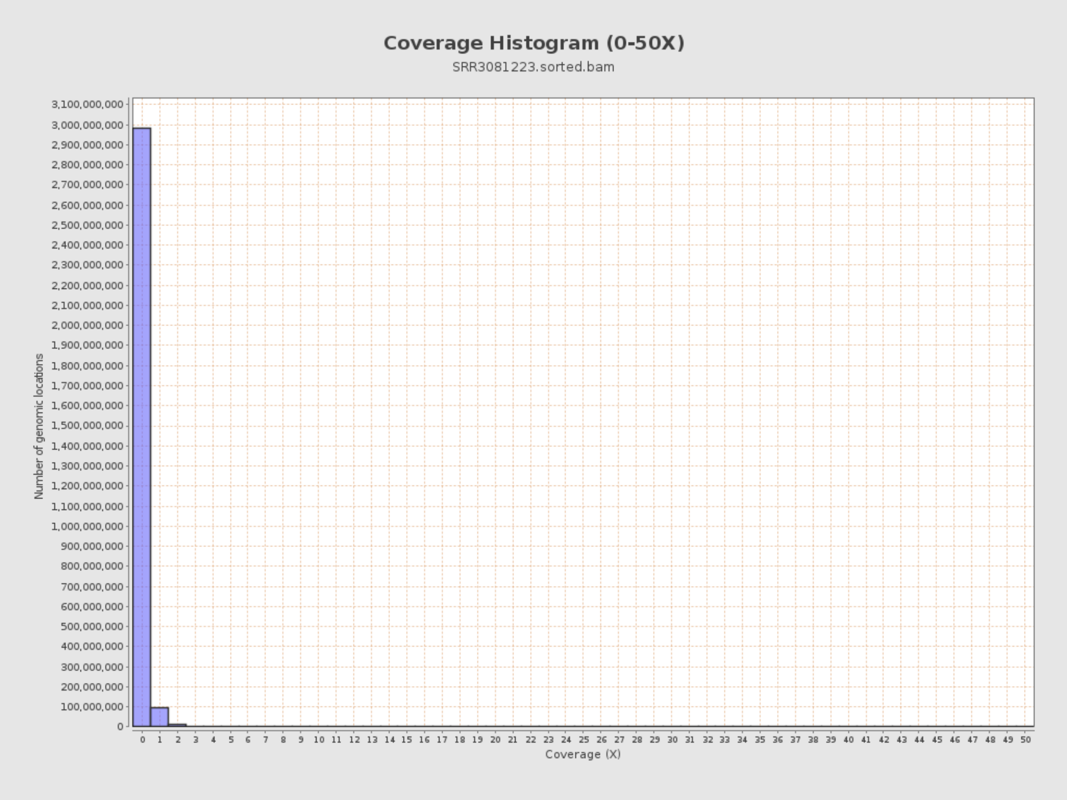
3. Results : Coverage across reference



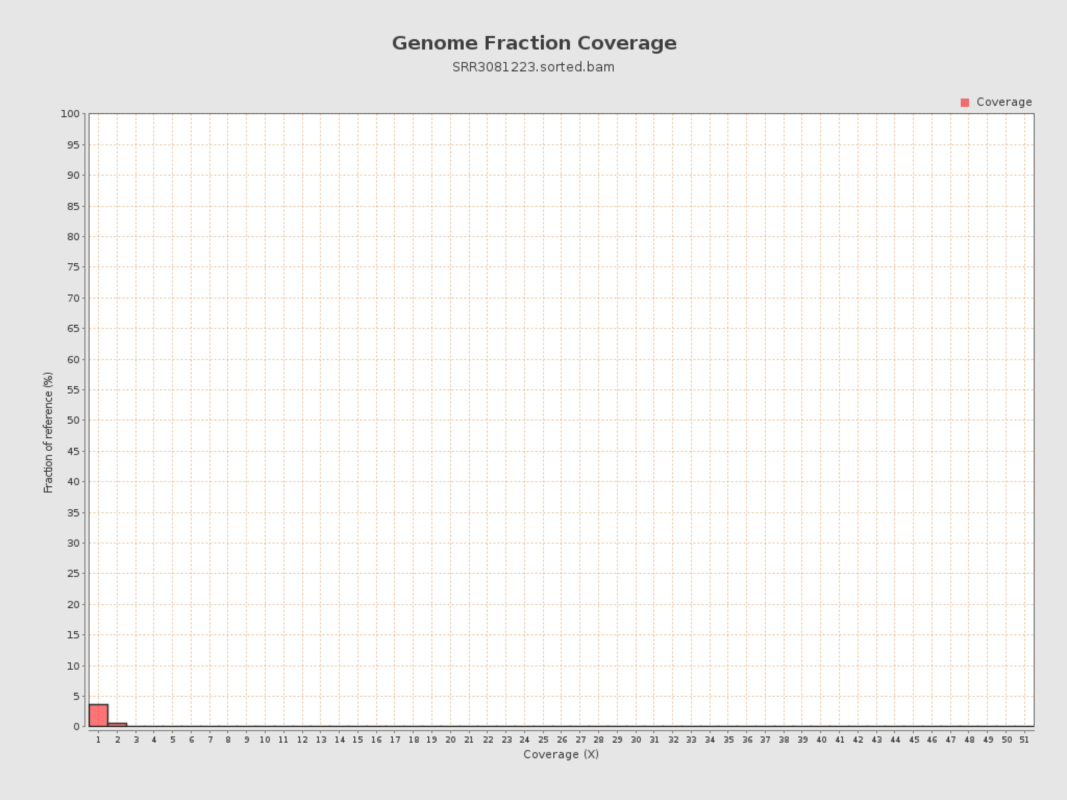
4. Results : Coverage Histogram



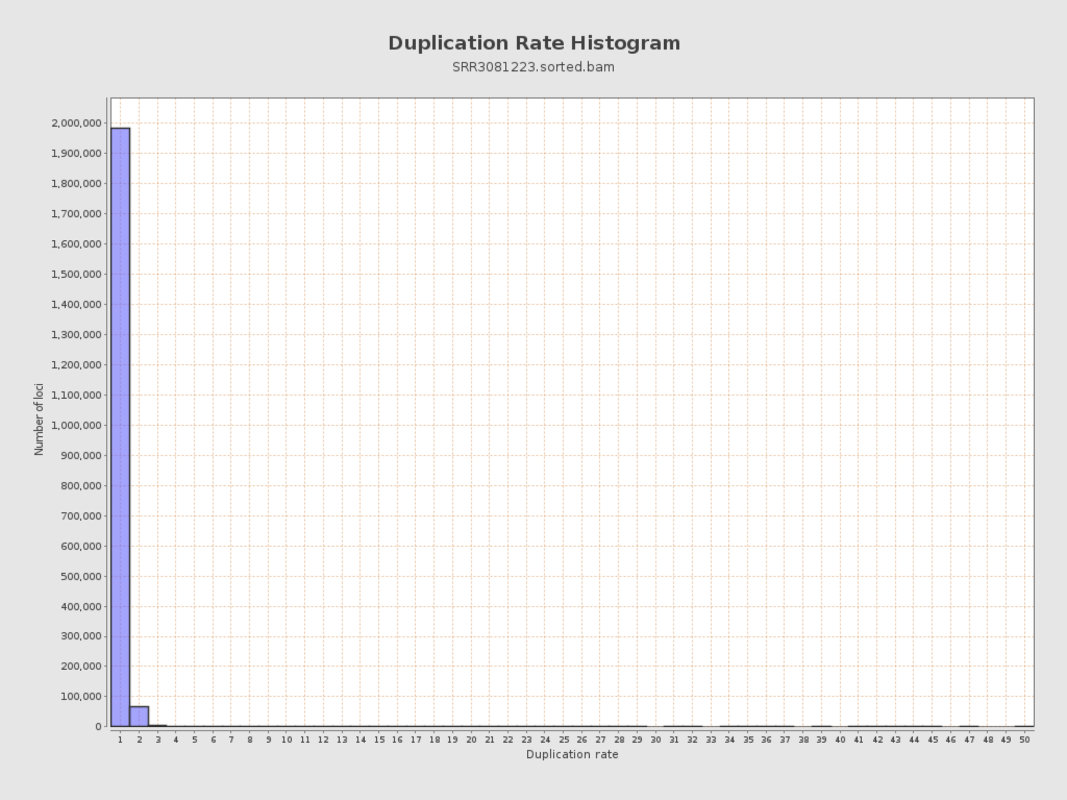
5. Results : Coverage Histogram (0-50X)



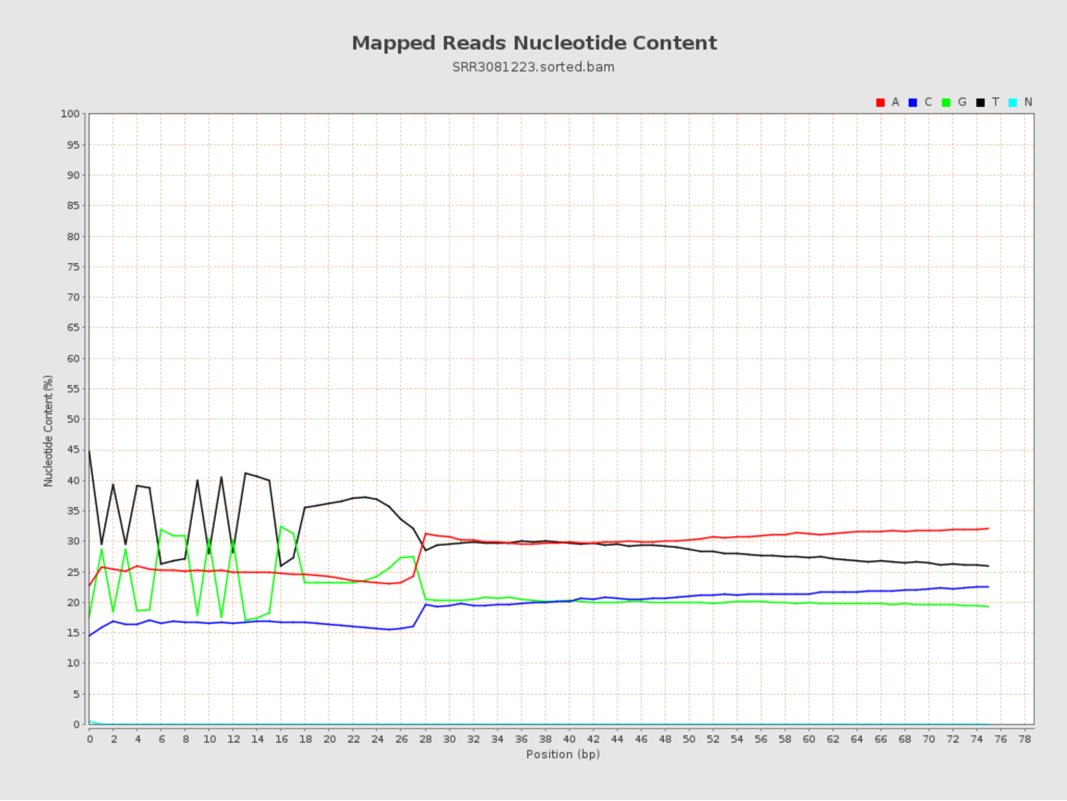
6. Results : Genome Fraction Coverage



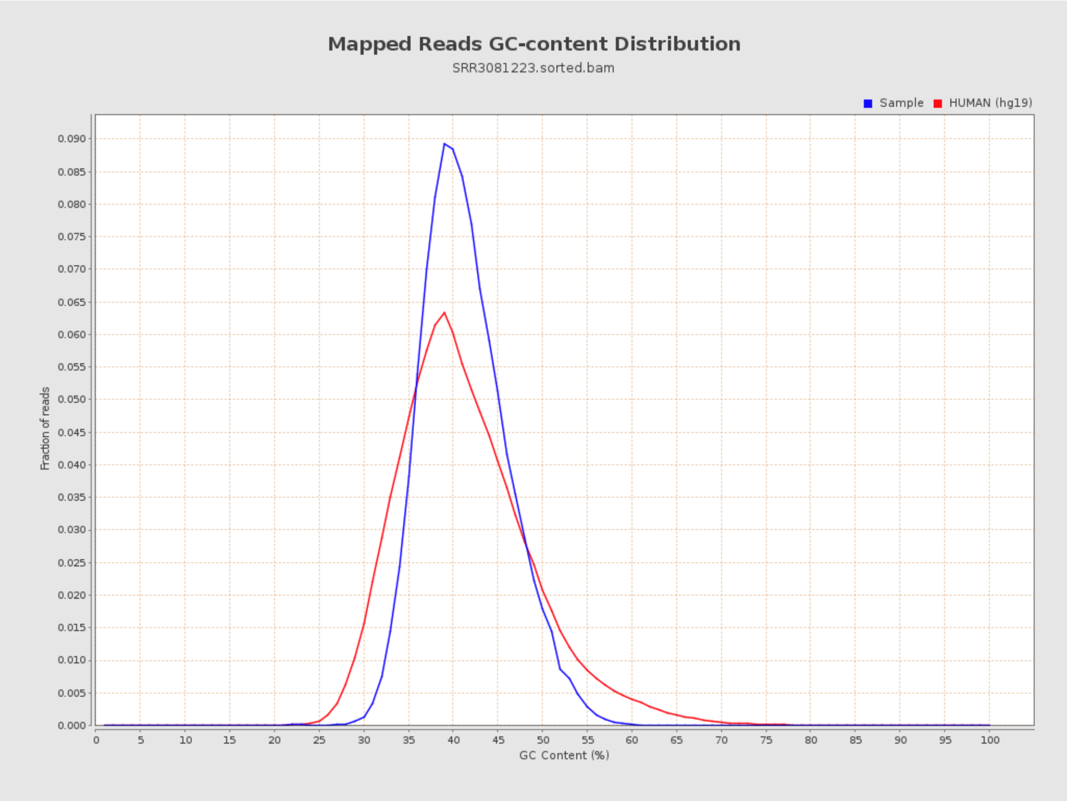
7. Results : Duplication Rate Histogram



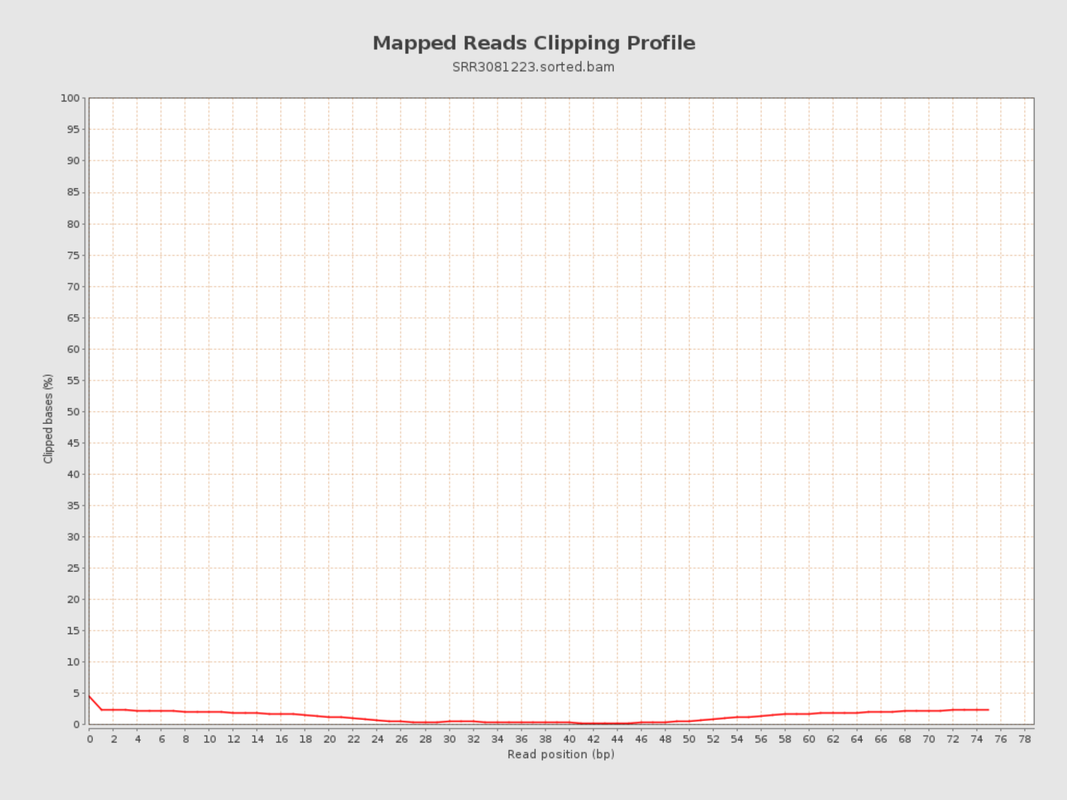
8. Results : Mapped Reads Nucleotide Content



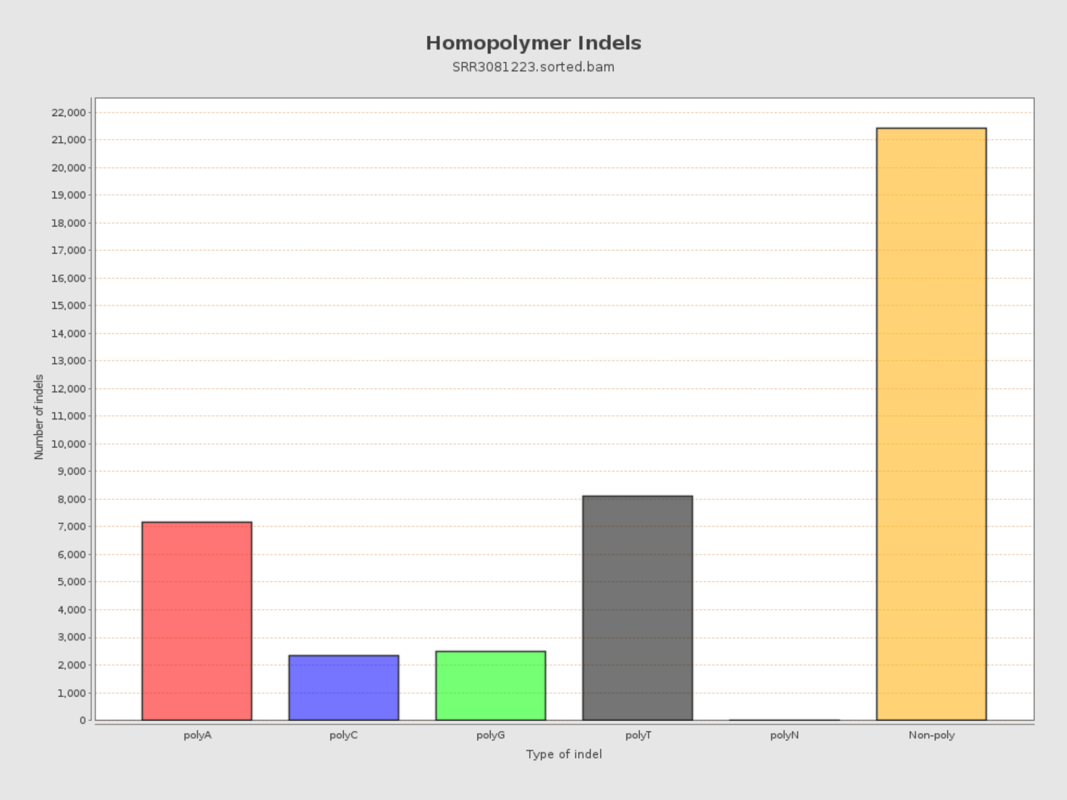
9. Results : Mapped Reads GC-content Distribution



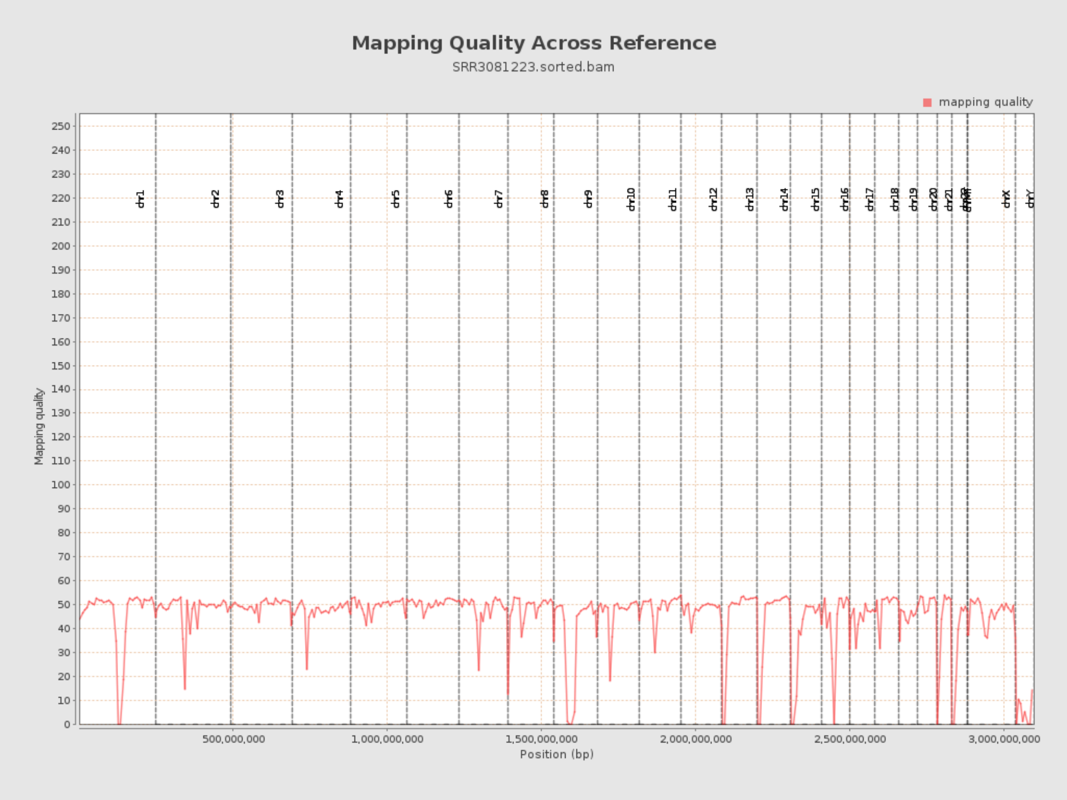
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram