Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 05:49:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240193.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_SRR6240193 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240193.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 05:49:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240193.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	826,821
Mapped reads	648,030 / 78.38%
Unmapped reads	178,791 / 21.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,770 / 0.34%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	19,258 / 2.33%
Duplication rate	2.37%
Clipped reads	345,268 / 41.76%

2.2. ACGT Content

Number/percentage of A's	12,142,535 / 29.02%
Number/percentage of C's	7,040,674 / 16.83%
Number/percentage of T's	13,178,899 / 31.49%
Number/percentage of G's	9,473,093 / 22.64%
Number/percentage of N's	10,312 / 0.02%
GC Percentage	39.46%

2.3. Coverage

Mean	0.0135

Standard Deviation	0.1668

2.4. Mapping Quality

Mean Mapping Quality	45.84

2.5. Mismatches and indels

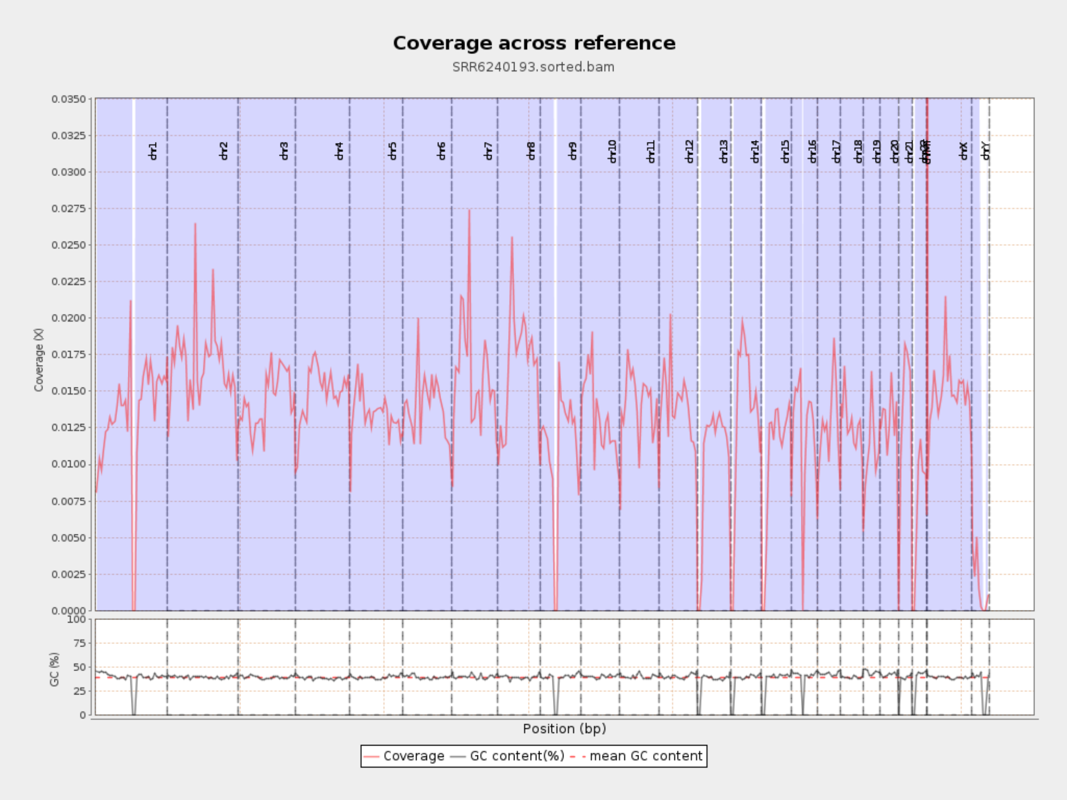
General error rate	1.13%
Mismatches	468,669
Insertions	3,493
Mapped reads with at least one insertion	0.53%
Deletions	14,390
Mapped reads with at least one deletion	2.19%
Homopolymer indels	49.19%

2.6. Chromosome stats

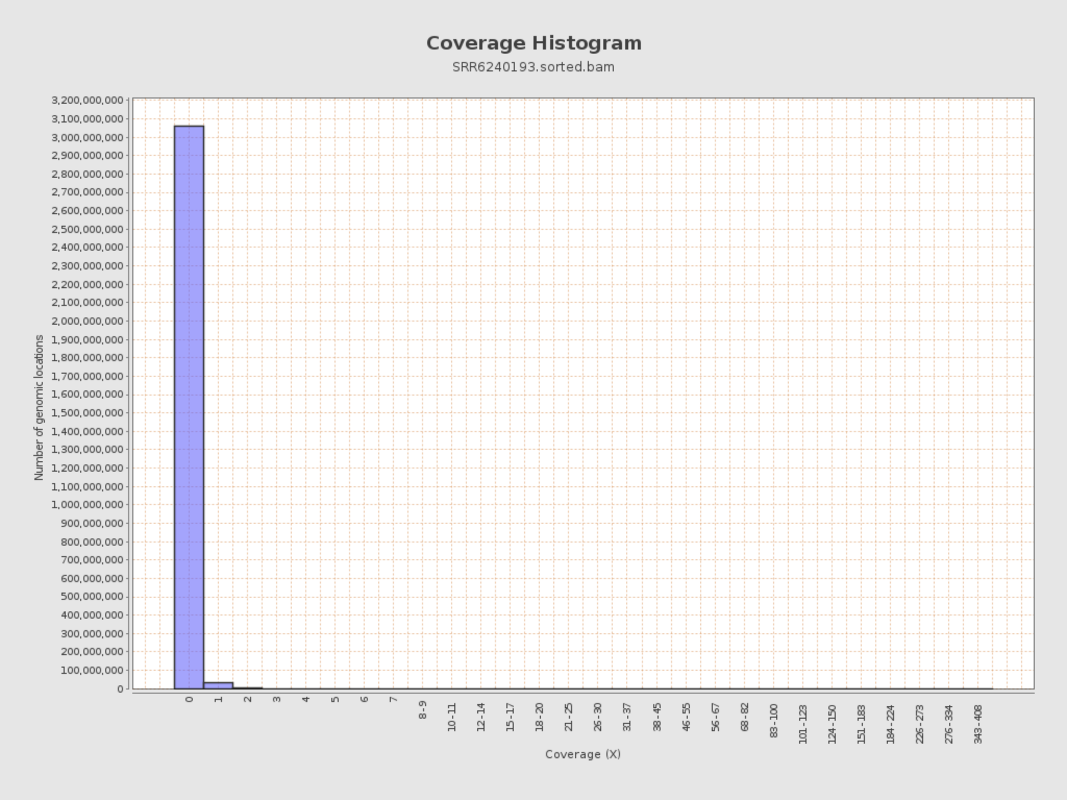
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3292061	0.0132	0.2341
chr2	243199373	4095649	0.0168	0.1867
chr3	198022430	2851924	0.0144	0.131
chr4	191154276	2838938	0.0149	0.1342
chr5	180915260	2458037	0.0136	0.1261
chr6	171115067	2393962	0.014	0.1385
chr7	159138663	2576674	0.0162	0.2468

chr8	146364022	2470580	0.0169	0.2867
chr9	141213431	1563418	0.0111	0.1528
chr10	135534747	1805448	0.0133	0.141
chr11	135006516	1907353	0.0141	0.1552
chr12	133851895	1888300	0.0141	0.1297
chr13	115169878	1181200	0.0103	0.1096
chr14	107349540	1427323	0.0133	0.1291
chr15	102531392	1062369	0.0104	0.1132
chr16	90354753	1074148	0.0119	0.1217
chr17	81195210	1034121	0.0127	0.1283
chr18	78077248	996236	0.0128	0.2164
chr19	59128983	656621	0.0111	0.1559
chr20	63025520	815422	0.0129	0.126
chr21	48129895	657819	0.0137	0.1305
chr22	51304566	368133	0.0072	0.0911
chrMT	16571	19185	1.1577	1.4797
chrX	155270560	2334522	0.015	0.1398
chrY	59373566	100767	0.0017	0.0503

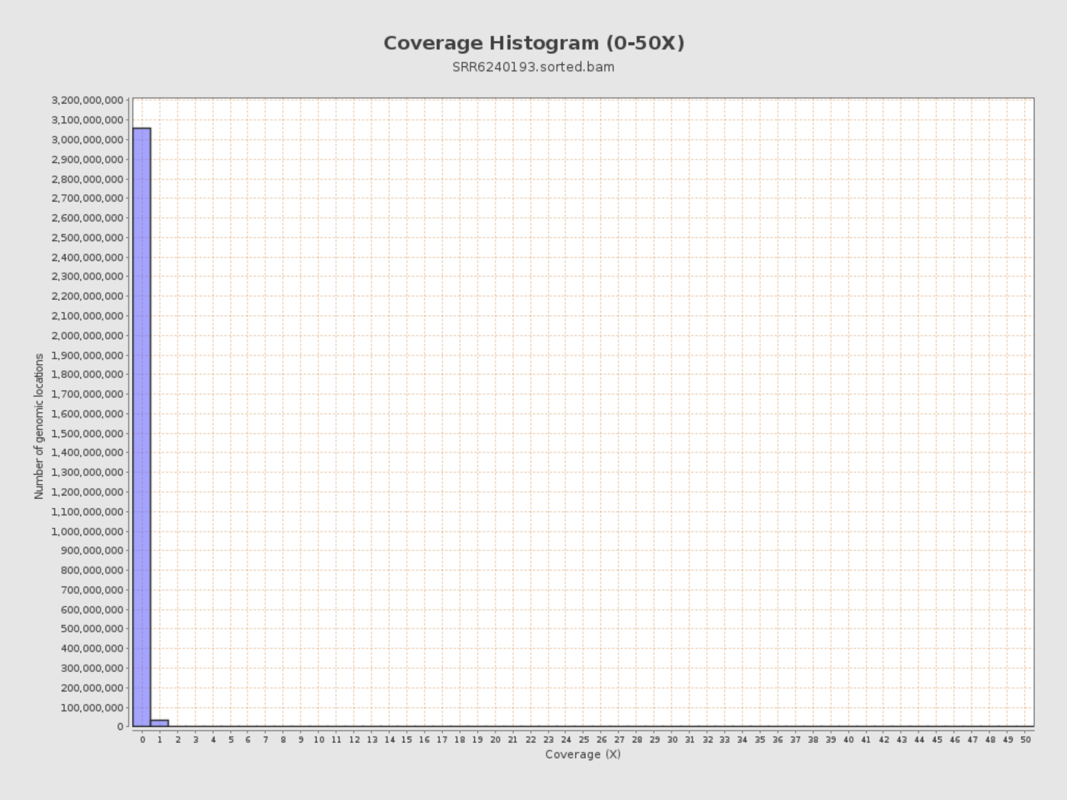
3. Results : Coverage across reference



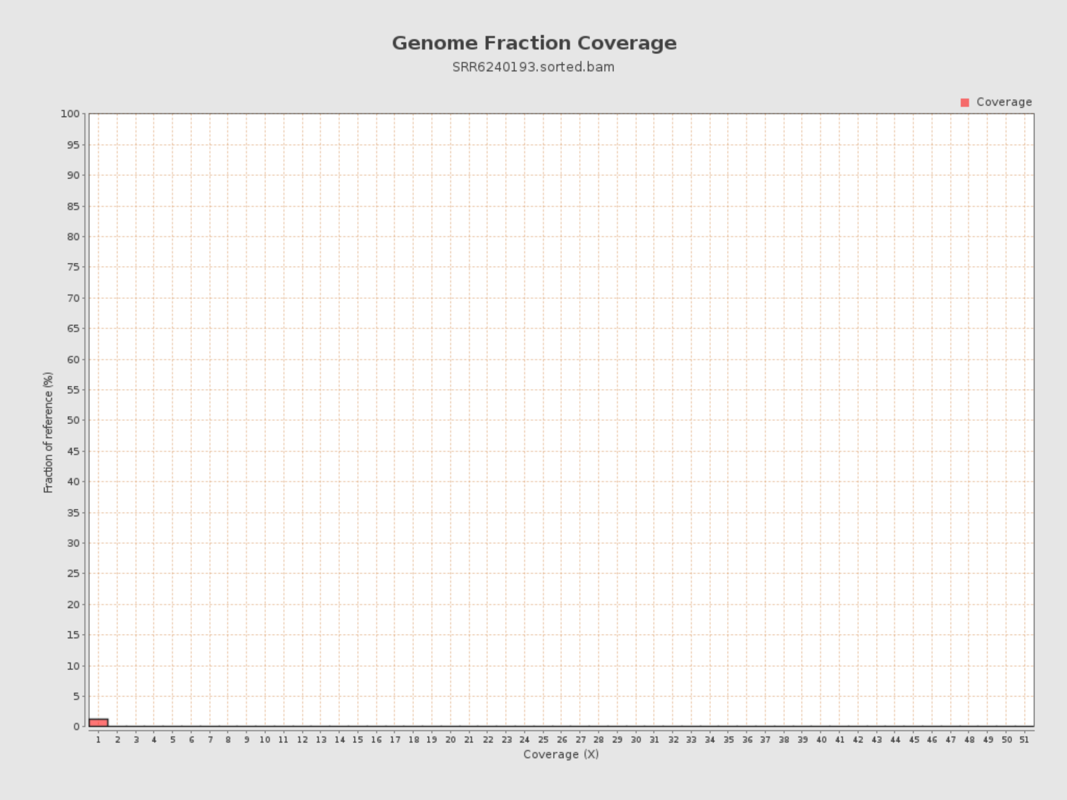
4. Results : Coverage Histogram



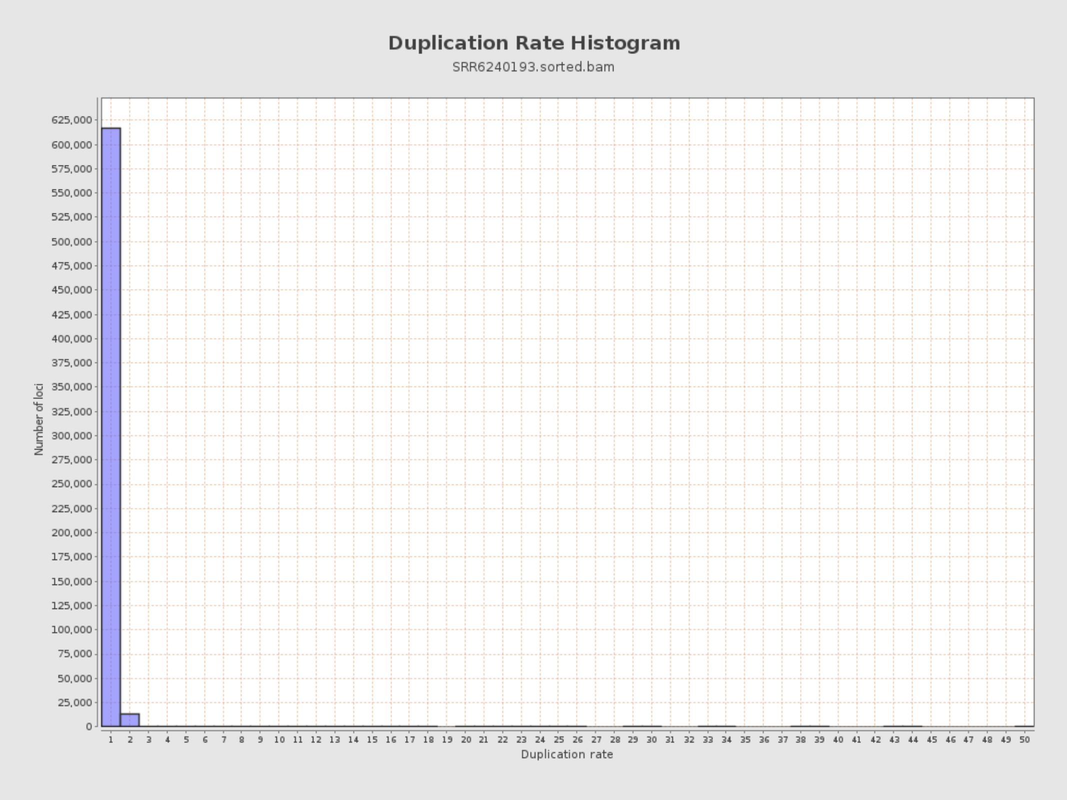
5. Results : Coverage Histogram (0-50X)



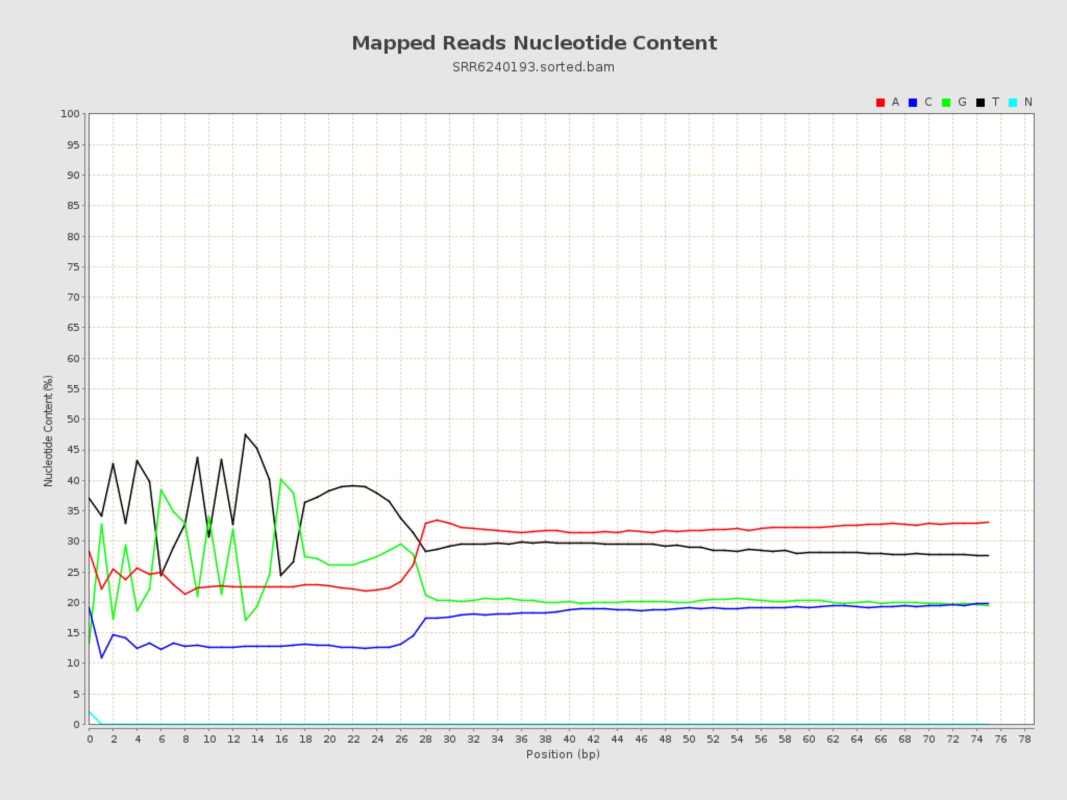
6. Results : Genome Fraction Coverage



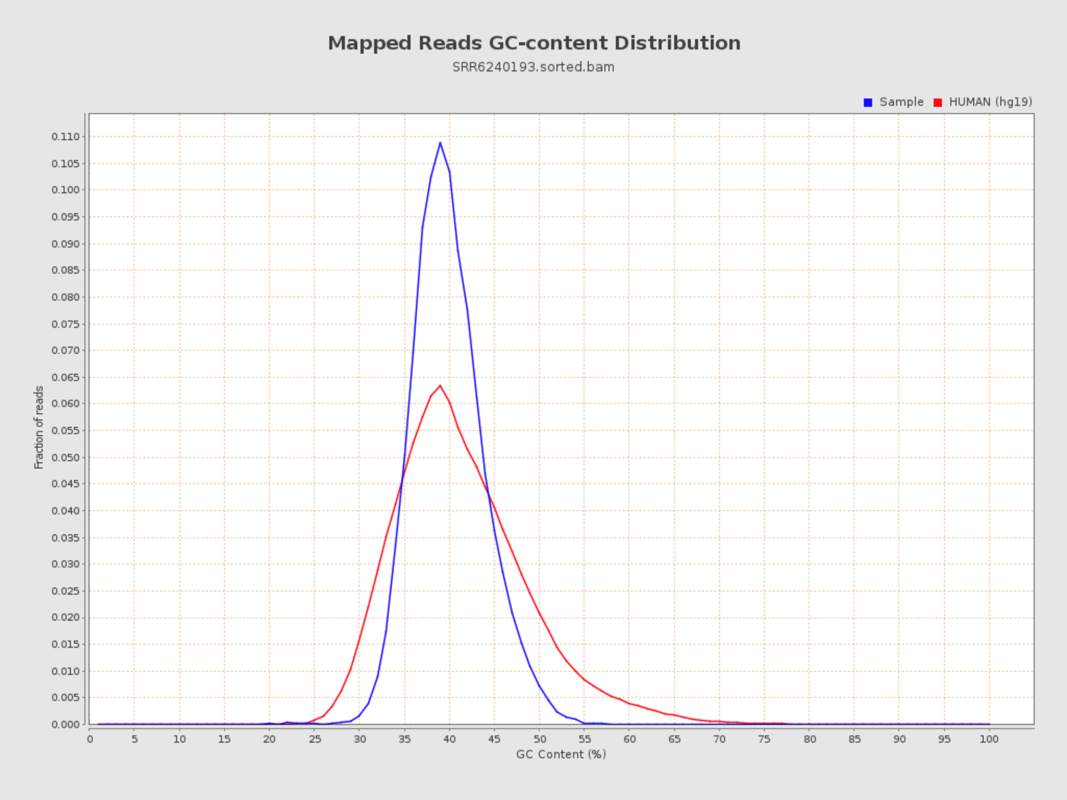
7. Results : Duplication Rate Histogram



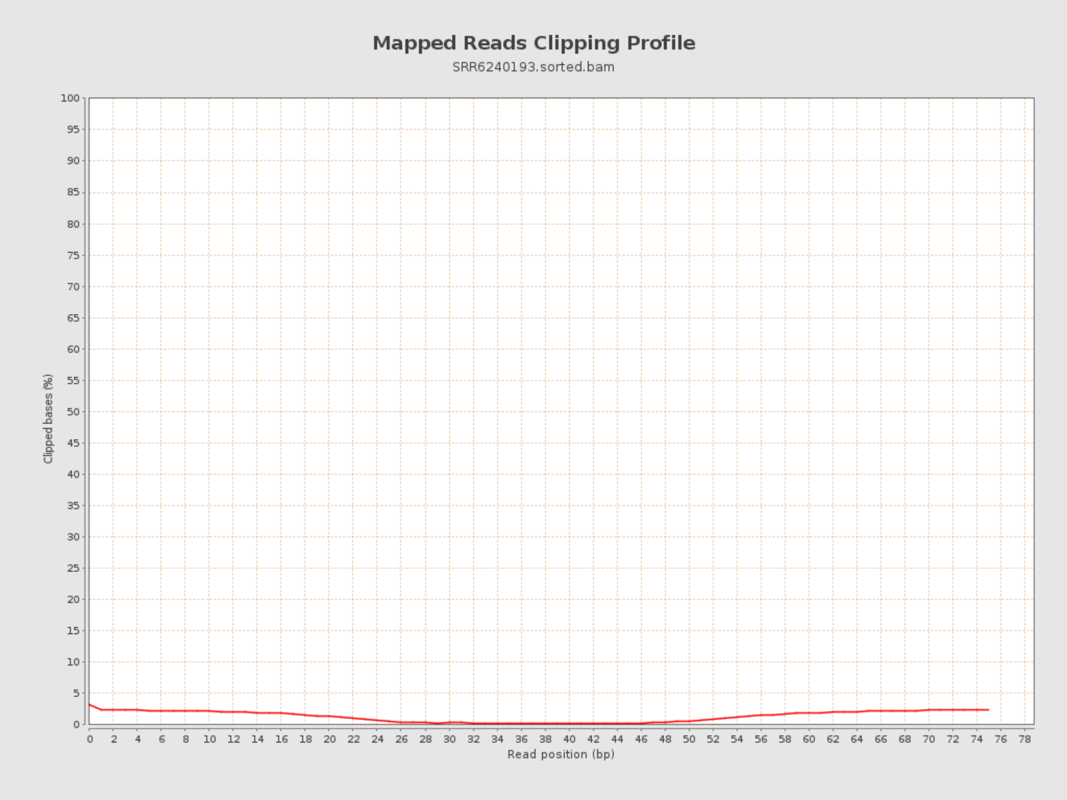
8. Results : Mapped Reads Nucleotide Content



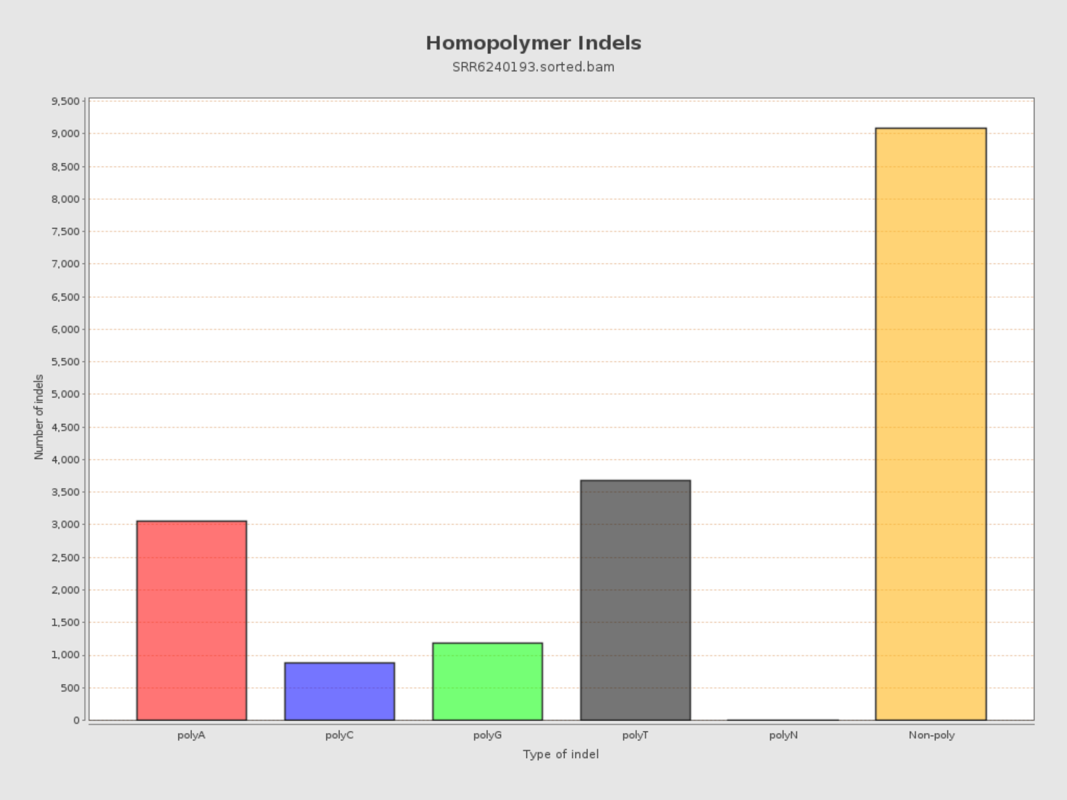
9. Results : Mapped Reads GC-content Distribution



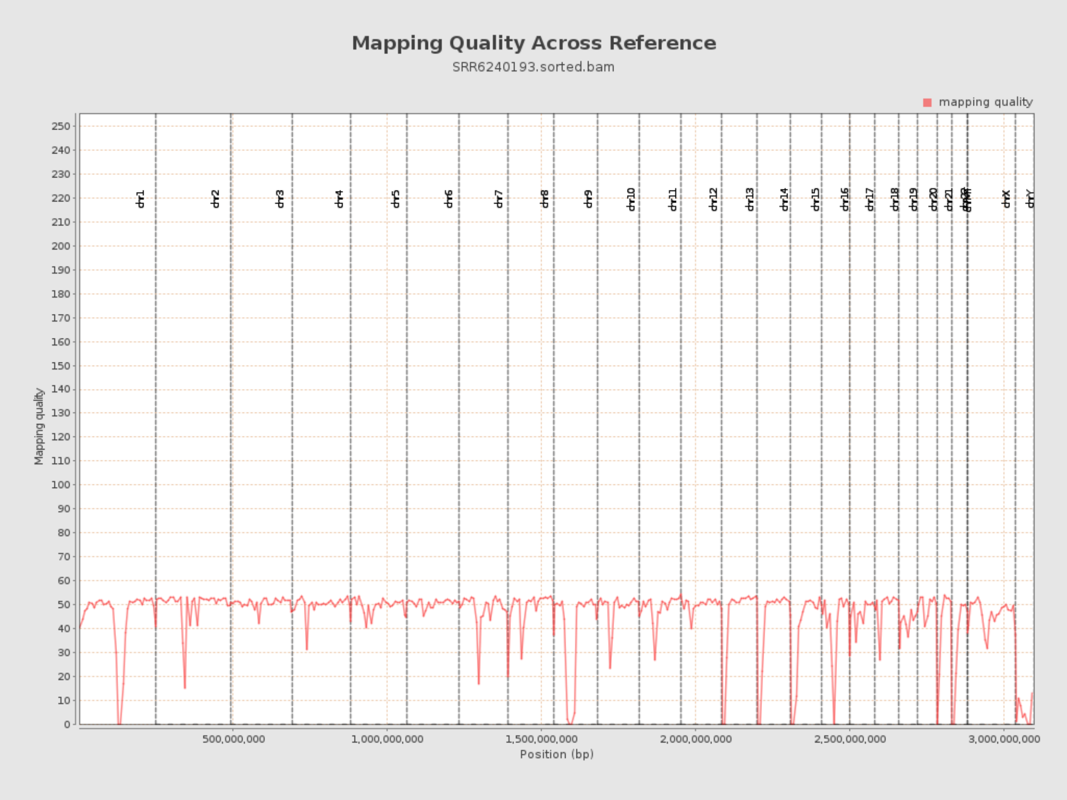
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram