Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 10:49:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234021.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_SRR6234021 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234021.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 10:49:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234021.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,754,021
Mapped reads	1,117,268 / 63.7%
Unmapped reads	636,753 / 36.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,573 / 0.89%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	155,722 / 8.88%
Duplication rate	10.49%
Clipped reads	559,148 / 31.88%

2.2. ACGT Content

Number/percentage of A's	19,998,863 / 27.35%
Number/percentage of C's	13,778,395 / 18.84%
Number/percentage of T's	22,963,655 / 31.4%
Number/percentage of G's	16,374,995 / 22.39%
Number/percentage of N's	18,284 / 0.03%
GC Percentage	41.23%

2.3. Coverage

Mean	0.0236

Standard Deviation	0.3039

2.4. Mapping Quality

Mean Mapping Quality	35.95

2.5. Mismatches and indels

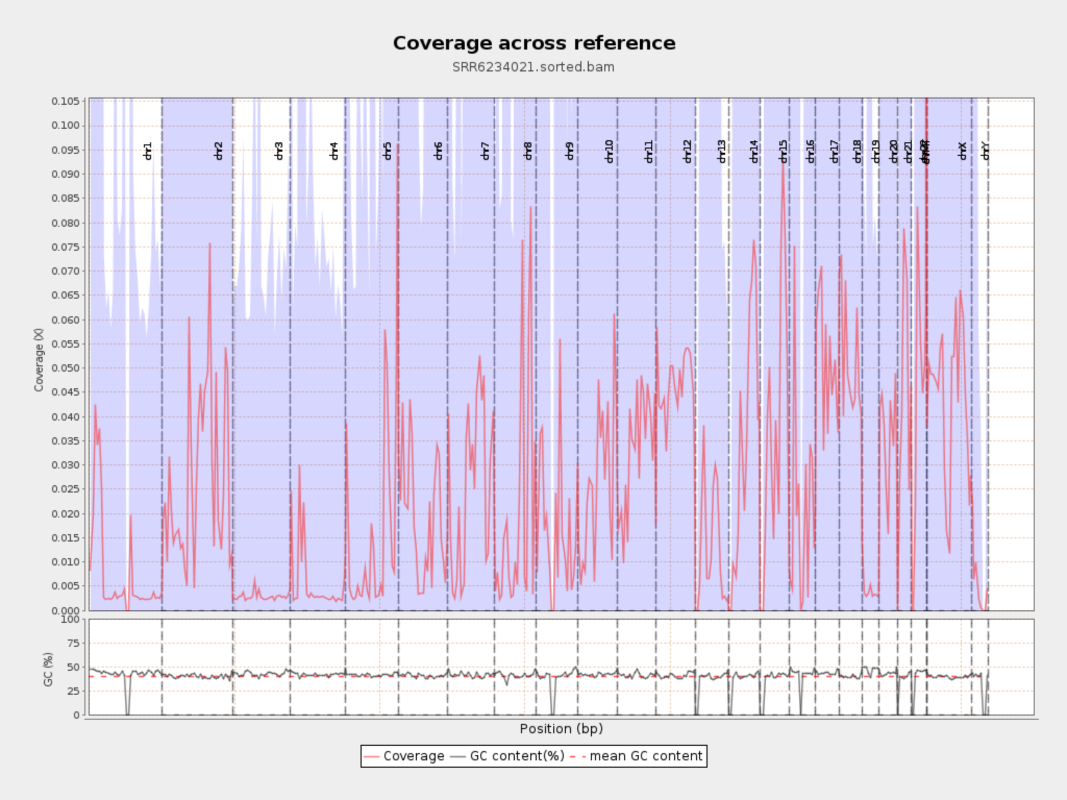
General error rate	0.8%
Mismatches	573,754
Insertions	5,735
Mapped reads with at least one insertion	0.51%
Deletions	21,567
Mapped reads with at least one deletion	1.91%
Homopolymer indels	44.52%

2.6. Chromosome stats

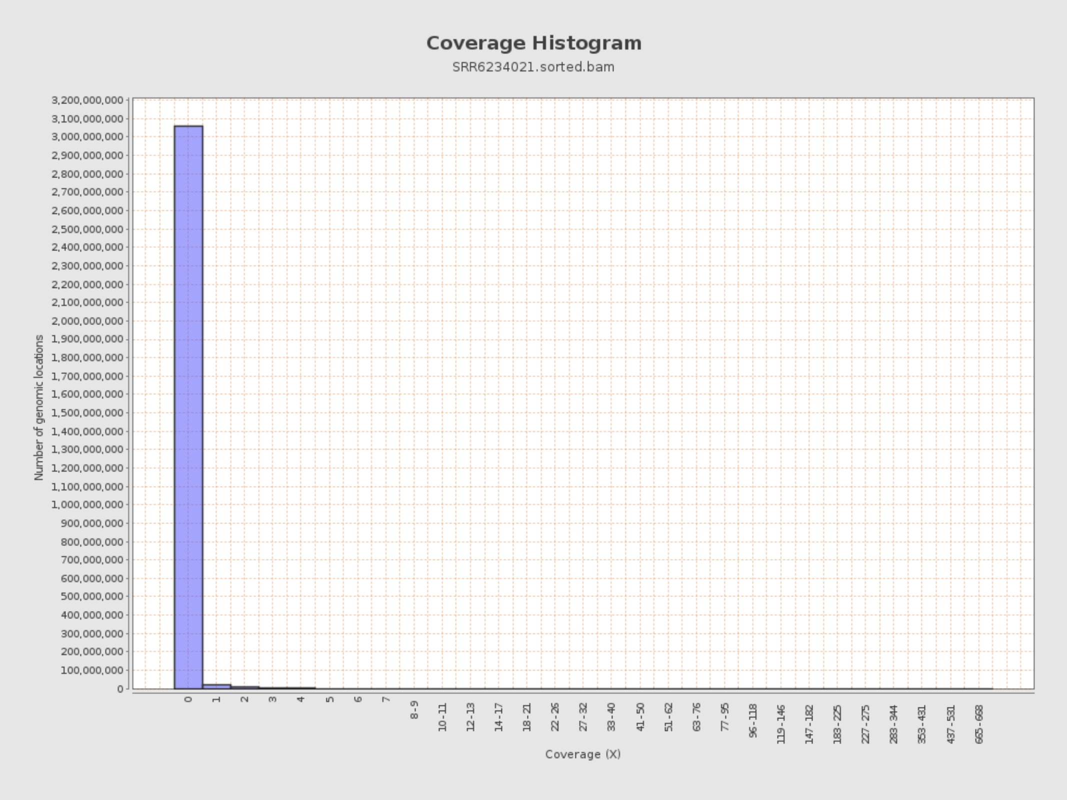
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1954326	0.0078	0.1424
chr2	243199373	6756644	0.0278	0.4369
chr3	198022430	583556	0.0029	0.0768
chr4	191154276	1087948	0.0057	0.1286
chr5	180915260	2772218	0.0153	0.2039
chr6	171115067	3286459	0.0192	0.2402
chr7	159138663	4106721	0.0258	0.2973

chr8	146364022	2845635	0.0194	0.3678
chr9	141213431	2384456	0.0169	0.2929
chr10	135534747	3510334	0.0259	0.2853
chr11	135006516	4450980	0.033	0.3681
chr12	133851895	6284557	0.047	0.3665
chr13	115169878	1461272	0.0127	0.1971
chr14	107349540	3777881	0.0352	0.3247
chr15	102531392	3938231	0.0384	0.3326
chr16	90354753	1882023	0.0208	0.2516
chr17	81195210	4142111	0.051	0.3919
chr18	78077248	4059620	0.052	0.643
chr19	59128983	238349	0.004	0.1204
chr20	63025520	2282466	0.0362	0.3292
chr21	48129895	2083020	0.0433	0.3549
chr22	51304566	2104572	0.041	0.3364
chrMT	16571	11488	0.6933	1.2438
chrX	155270560	6868358	0.0442	0.3662
chrY	59373566	299024	0.005	0.1091

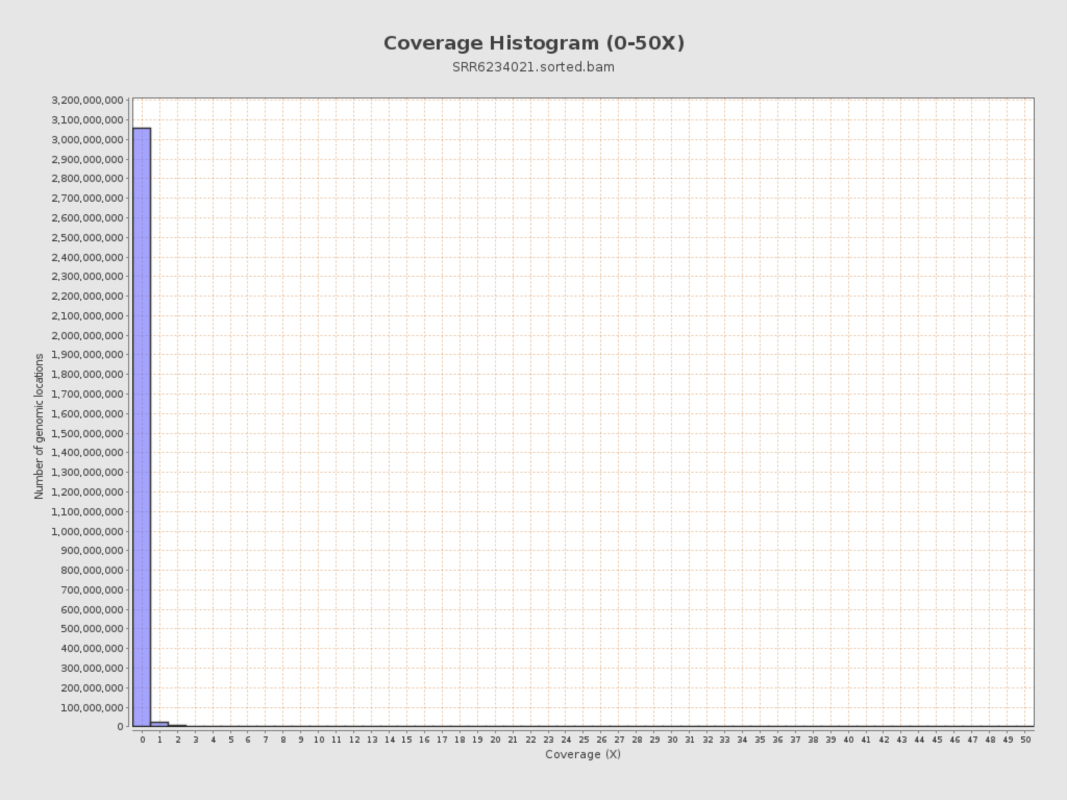
3. Results : Coverage across reference



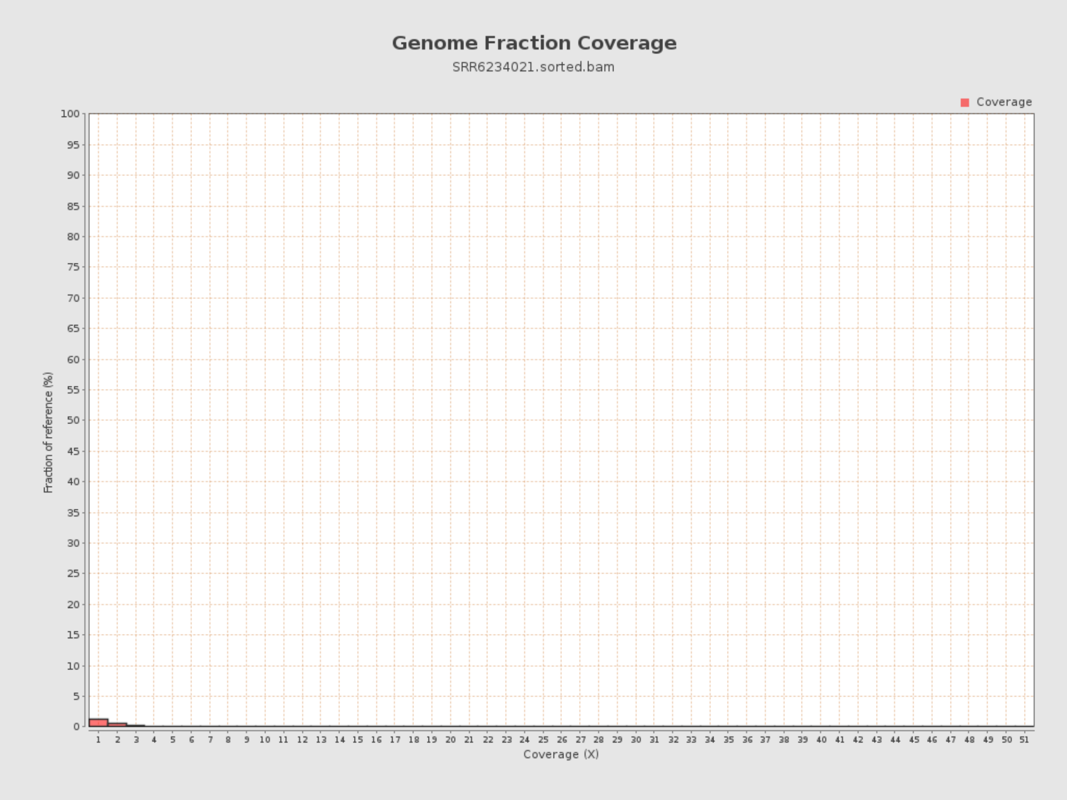
4. Results : Coverage Histogram



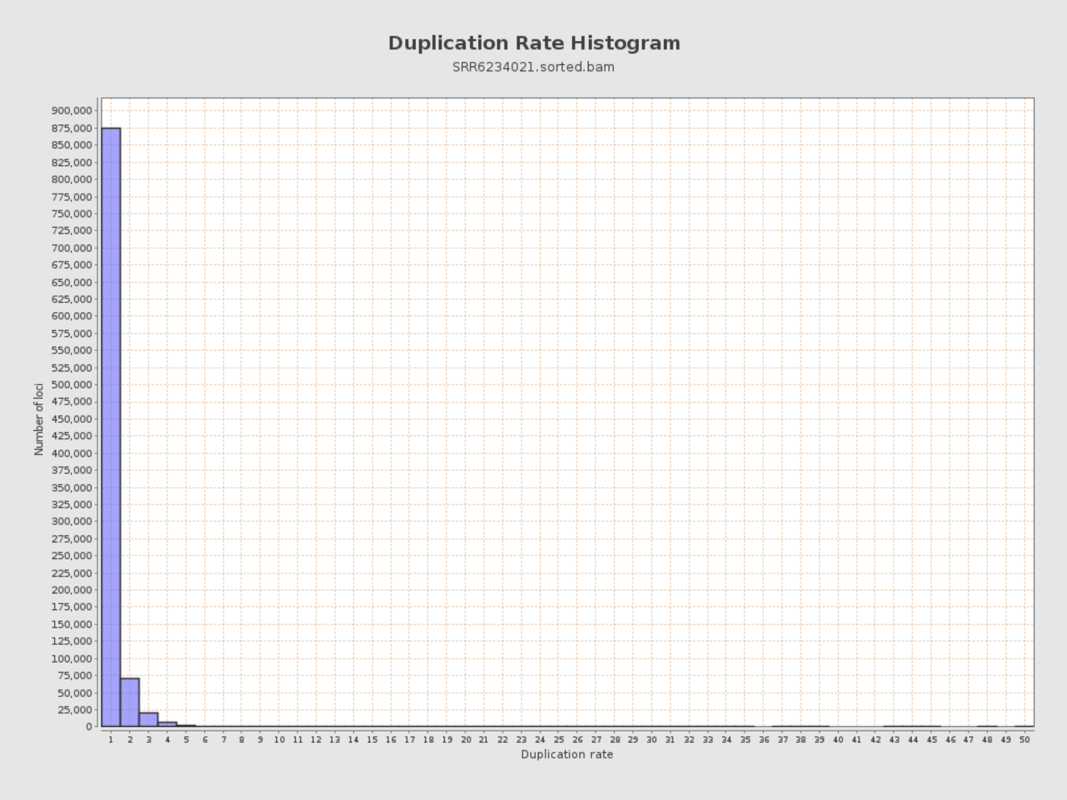
5. Results : Coverage Histogram (0-50X)



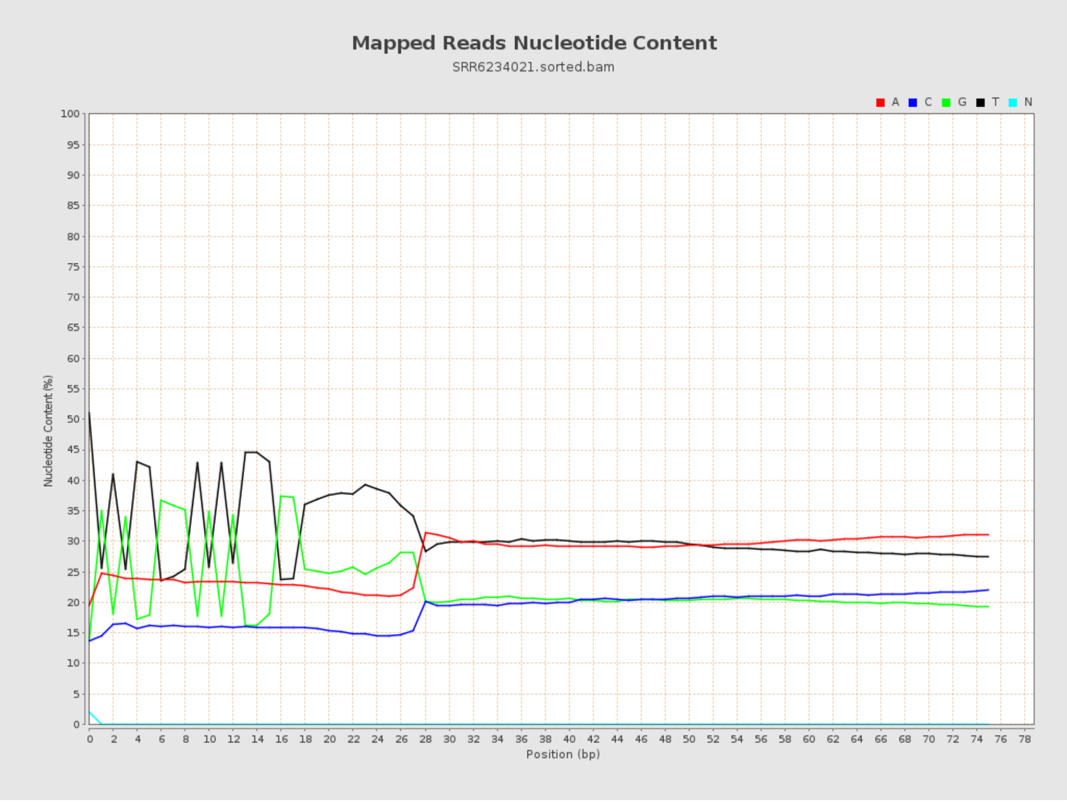
6. Results : Genome Fraction Coverage



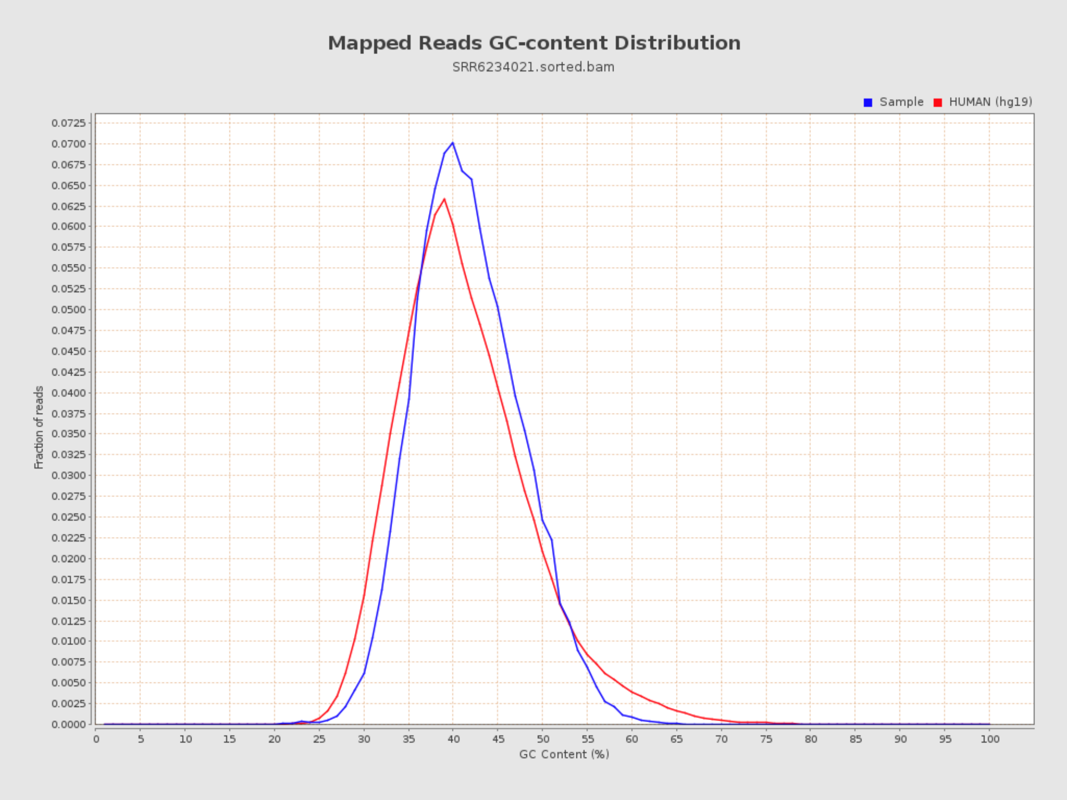
7. Results : Duplication Rate Histogram



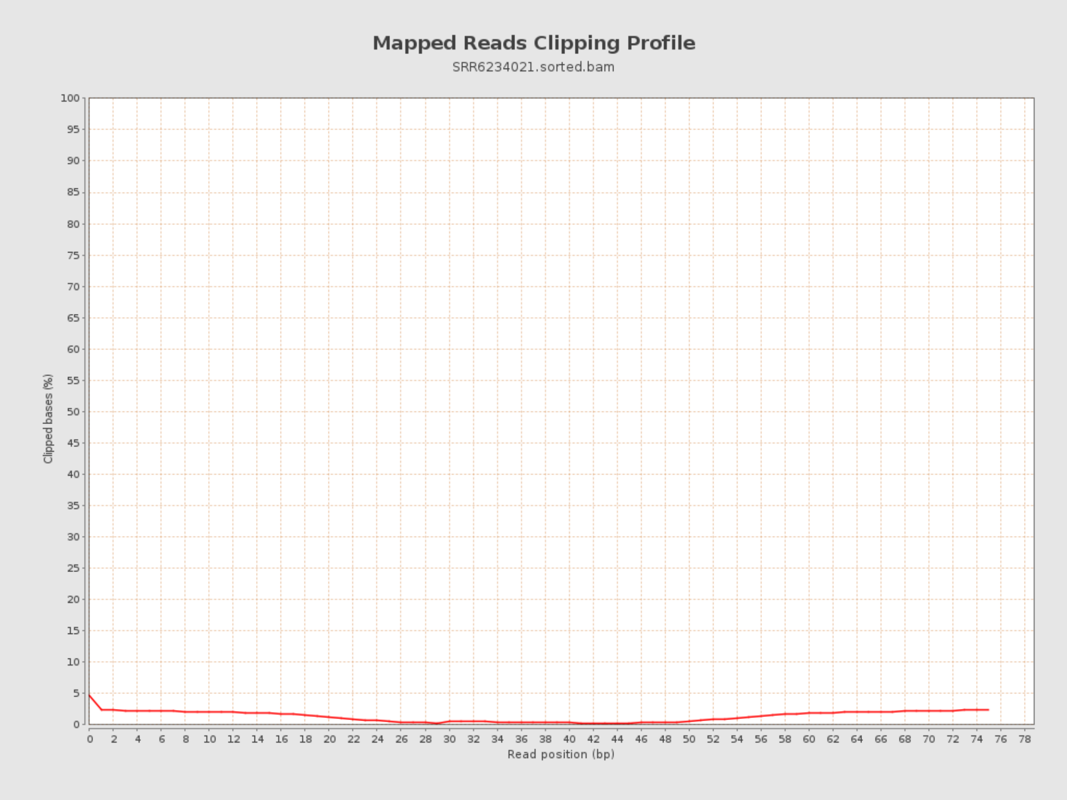
8. Results : Mapped Reads Nucleotide Content



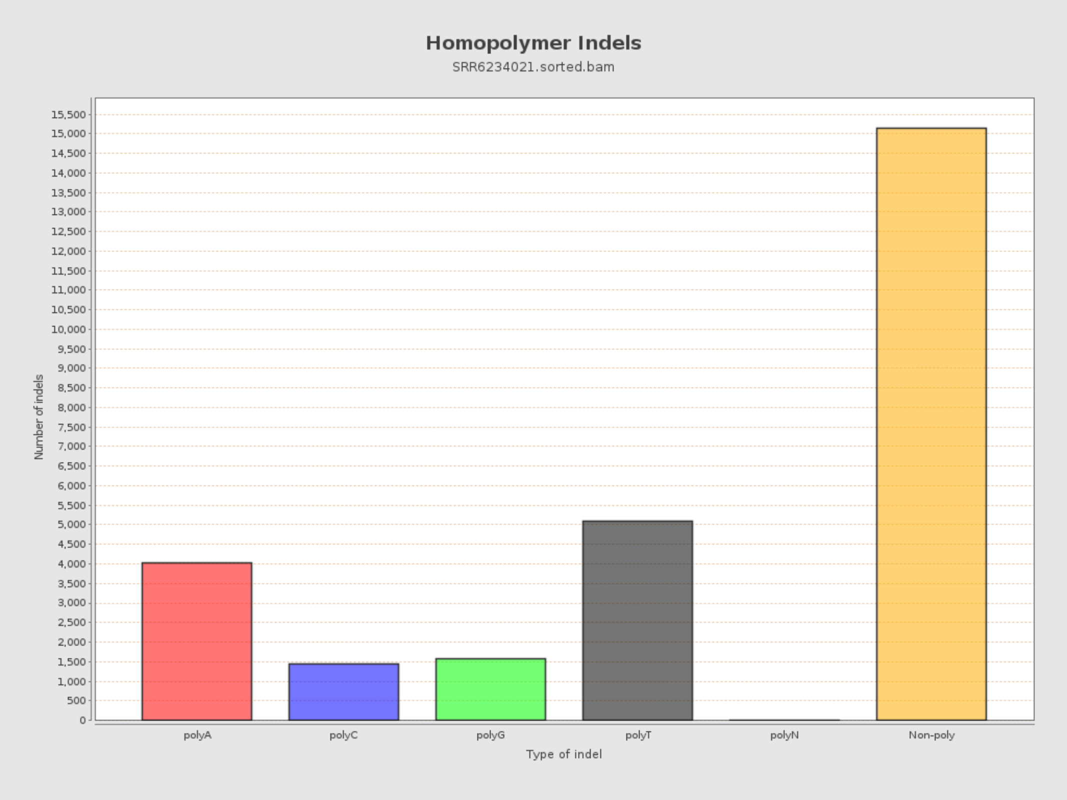
9. Results : Mapped Reads GC-content Distribution



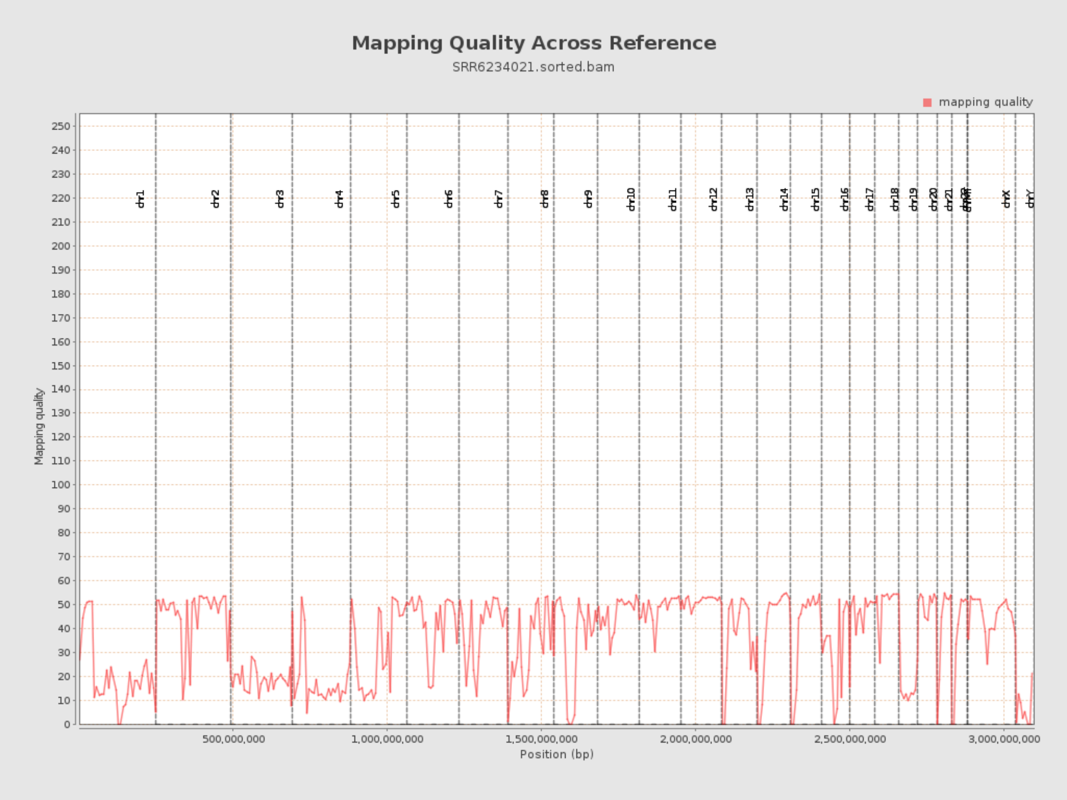
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram