Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 06:51:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3212674.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_SRR3212674 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3212674.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 06:51:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3212674.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,599,490
Mapped reads	2,281,331 / 87.76%
Unmapped reads	318,159 / 12.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,795 / 0.76%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	82,471 / 3.17%
Duplication rate	2.81%
Clipped reads	859,038 / 33.05%

2.2. ACGT Content

Number/percentage of A's	44,672,965 / 28.75%
Number/percentage of C's	27,186,393 / 17.5%
Number/percentage of T's	50,103,956 / 32.25%
Number/percentage of G's	32,673,706 / 21.03%
Number/percentage of N's	724,528 / 0.47%
GC Percentage	38.53%

2.3. Coverage

Mean	0.0502

Standard Deviation	0.398

2.4. Mapping Quality

Mean Mapping Quality	47.66

2.5. Mismatches and indels

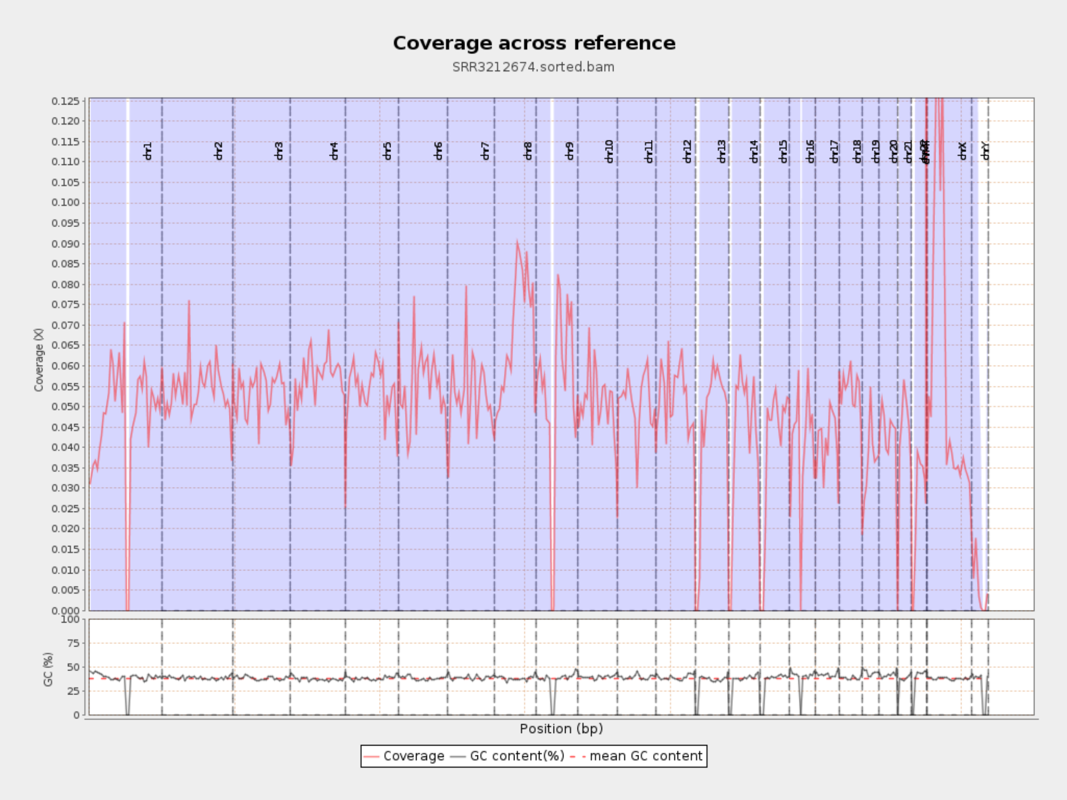
General error rate	1.16%
Mismatches	1,781,693
Insertions	11,877
Mapped reads with at least one insertion	0.52%
Deletions	33,987
Mapped reads with at least one deletion	1.47%
Homopolymer indels	49.57%

2.6. Chromosome stats

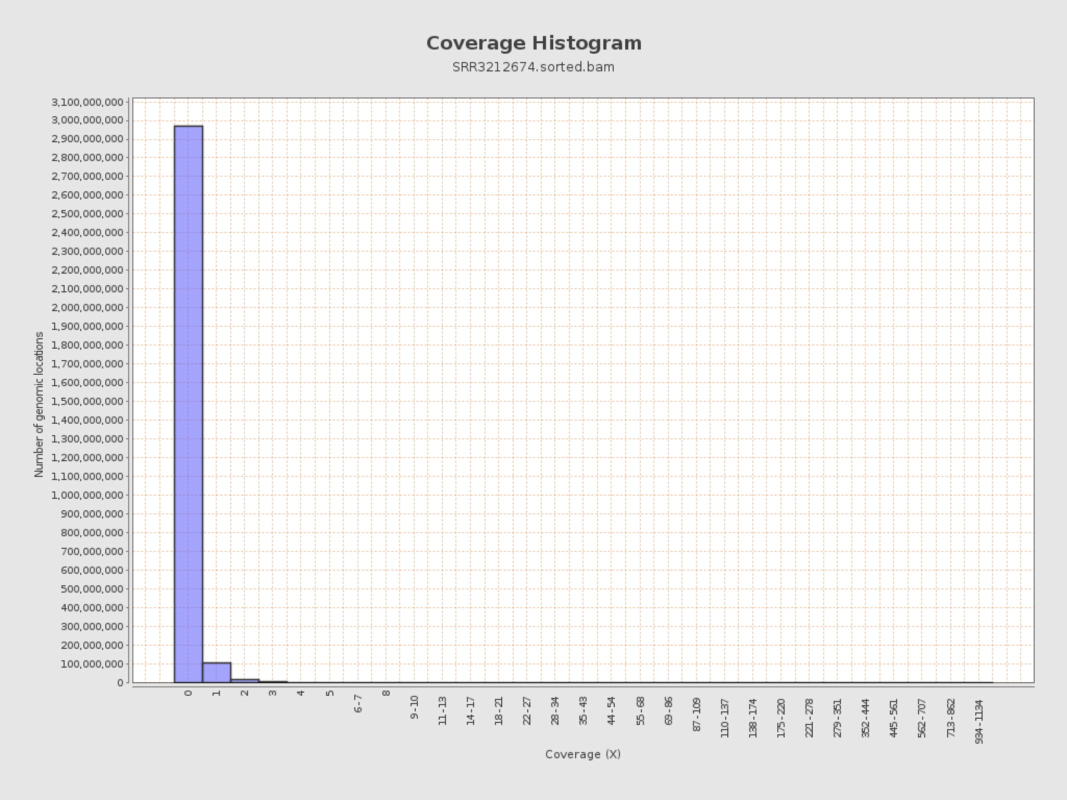
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11751027	0.0471	0.5985
chr2	243199373	13201233	0.0543	0.3773
chr3	198022430	10631635	0.0537	0.2724
chr4	191154276	10820940	0.0566	0.2901
chr5	180915260	9800085	0.0542	0.2757
chr6	171115067	9432264	0.0551	0.3569
chr7	159138663	8524150	0.0536	0.5631

chr8	146364022	9990824	0.0683	0.7526
chr9	141213431	7690628	0.0545	0.3956
chr10	135534747	6950523	0.0513	0.3468
chr11	135006516	6853675	0.0508	0.3254
chr12	133851895	7004659	0.0523	0.2727
chr13	115169878	5107765	0.0443	0.2474
chr14	107349540	4580033	0.0427	0.2567
chr15	102531392	4053569	0.0395	0.2338
chr16	90354753	3674256	0.0407	0.258
chr17	81195210	3326894	0.041	0.2582
chr18	78077248	4248327	0.0544	0.6439
chr19	59128983	2194415	0.0371	0.4331
chr20	63025520	2751044	0.0436	0.2527
chr21	48129895	2016028	0.0419	0.2557
chr22	51304566	1277738	0.0249	0.1825
chrMT	16571	12298	0.7421	0.9516
chrX	155270560	9194884	0.0592	0.3536
chrY	59373566	328566	0.0055	0.1263

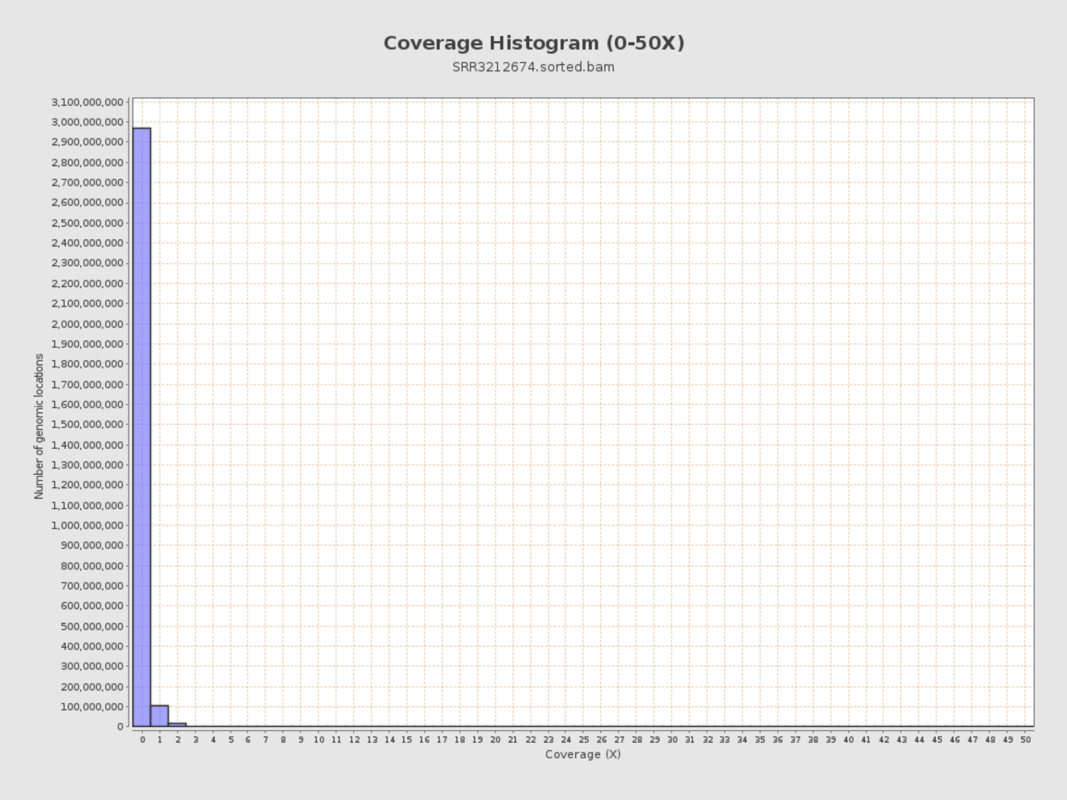
3. Results : Coverage across reference



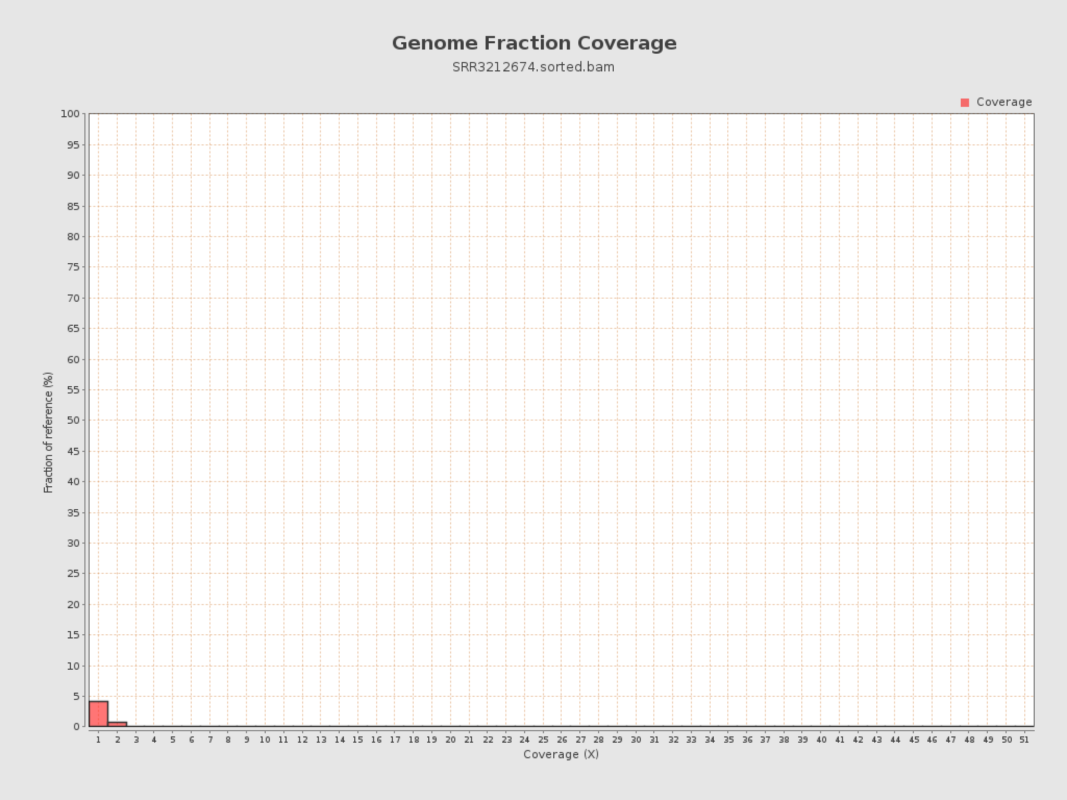
4. Results : Coverage Histogram



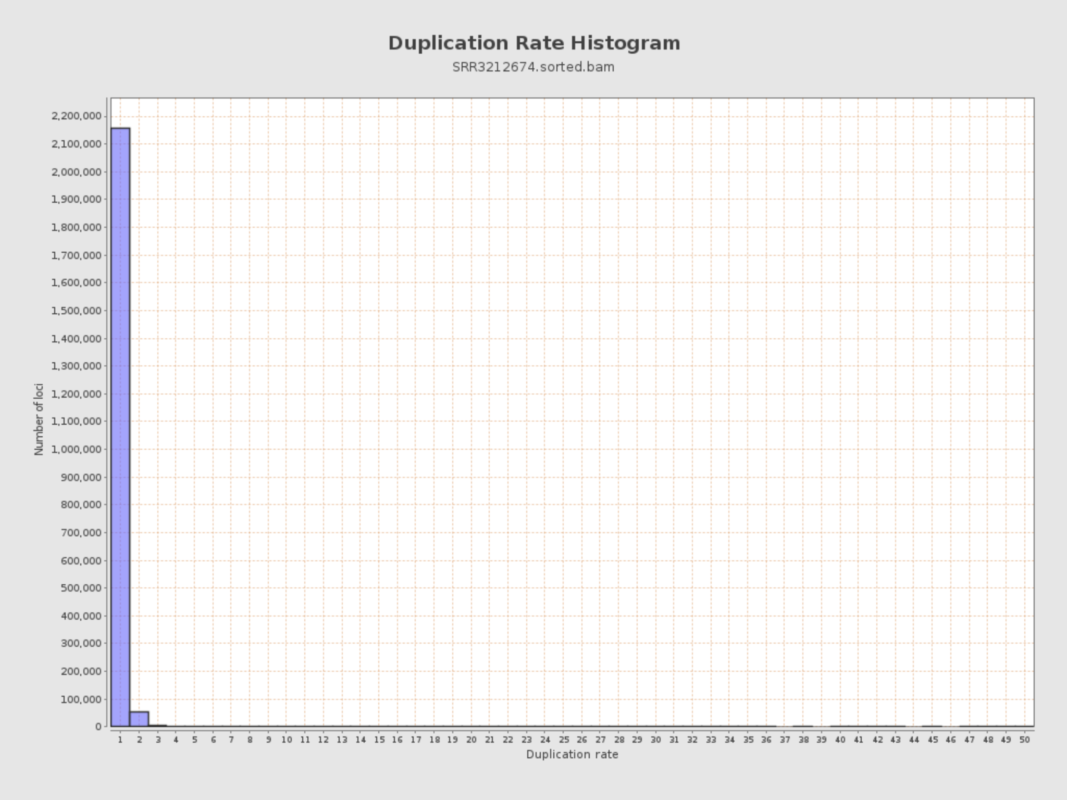
5. Results : Coverage Histogram (0-50X)



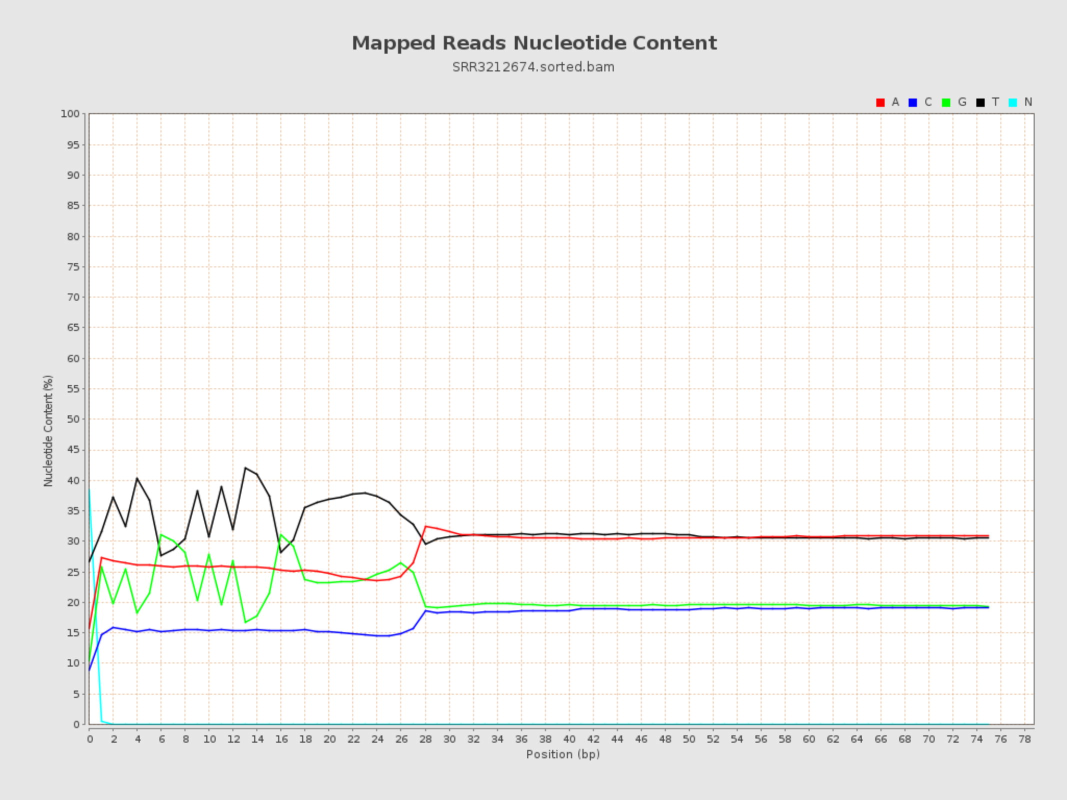
6. Results : Genome Fraction Coverage



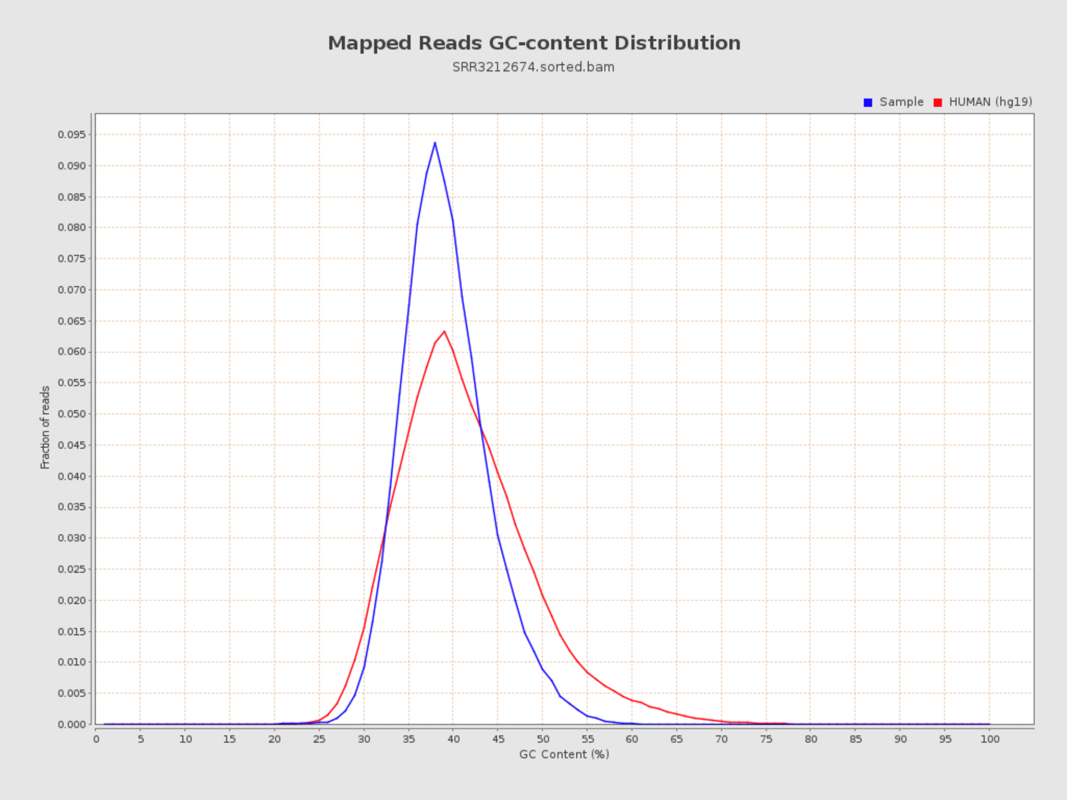
7. Results : Duplication Rate Histogram



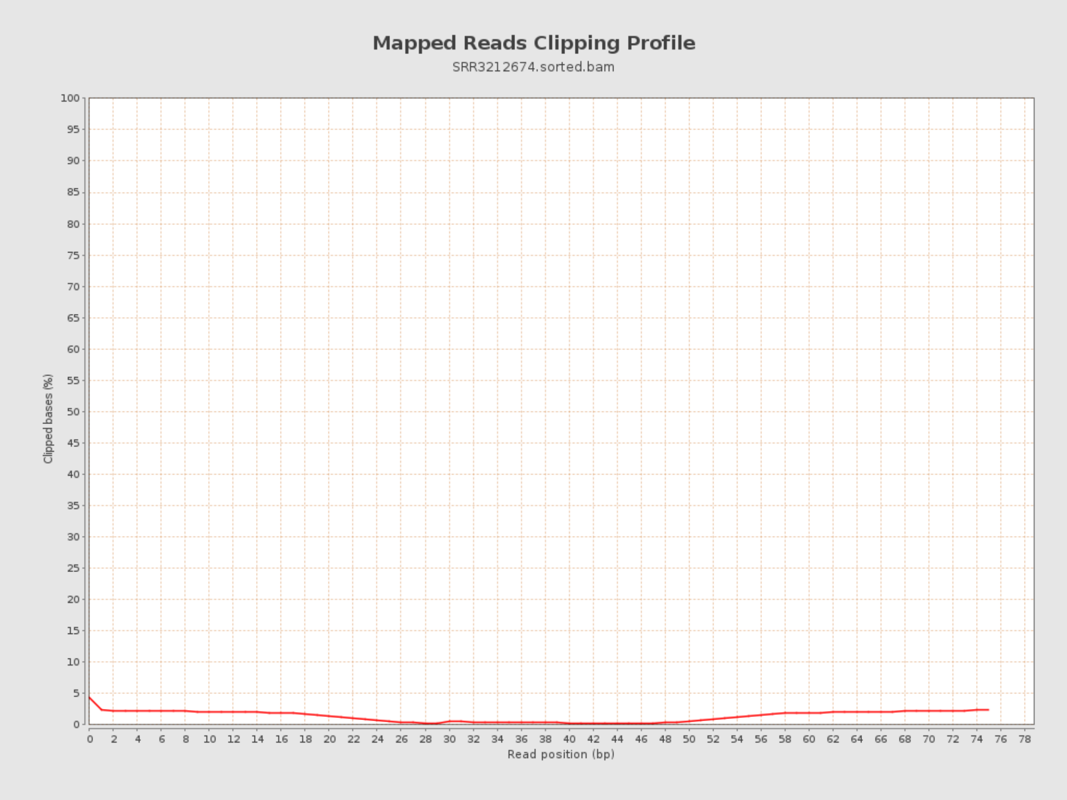
8. Results : Mapped Reads Nucleotide Content



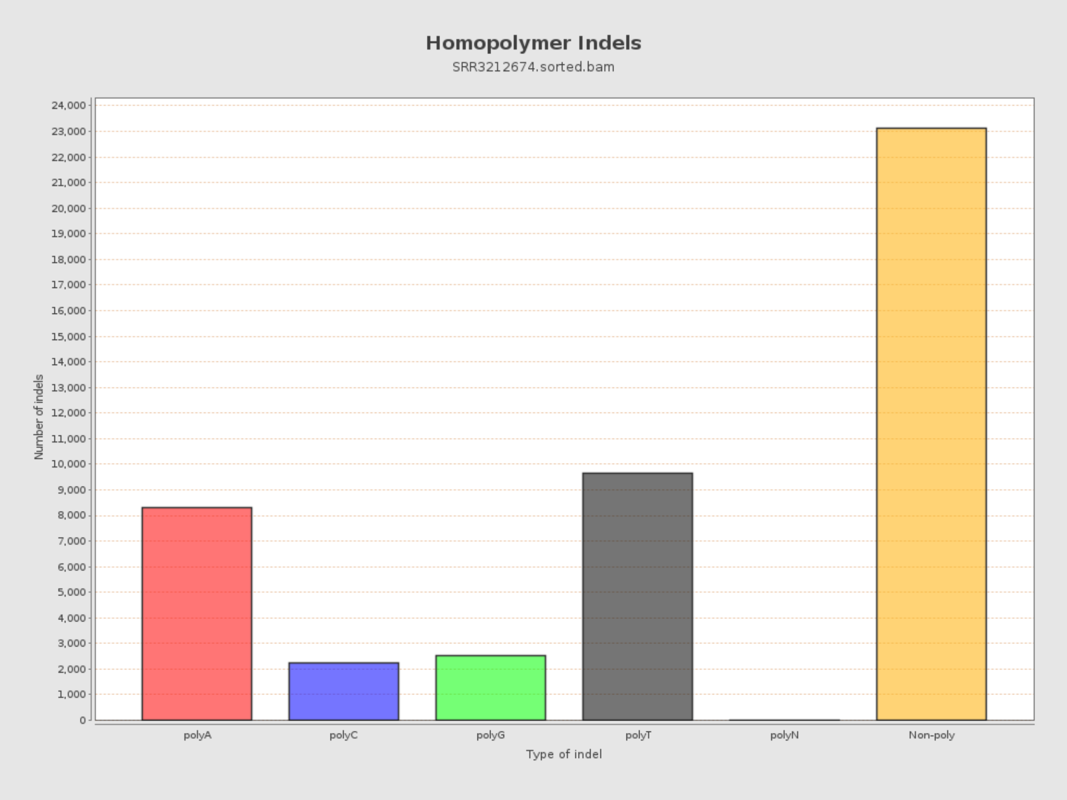
9. Results : Mapped Reads GC-content Distribution



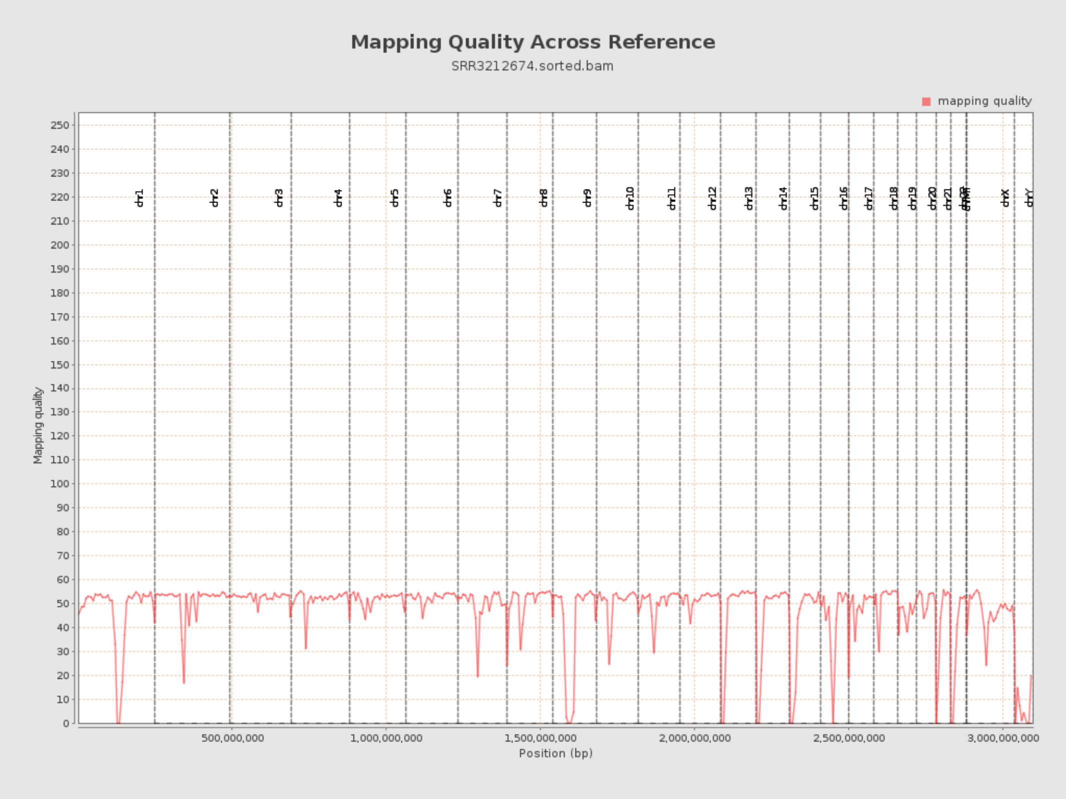
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram