Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 19:31:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472720.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_SRR3472720 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472720_1.fastq.gz SRR3472720_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 19:31:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472720.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	46,630
Mapped reads	45,898 / 98.43%
Unmapped reads	732 / 1.57%
Mapped paired reads	45,898 / 98.43%
Mapped reads, first in pair	23,163 / 49.67%
Mapped reads, second in pair	22,735 / 48.76%
Mapped reads, both in pair	45,368 / 97.29%
Mapped reads, singletons	530 / 1.14%
Secondary alignments	0
Supplementary alignments	166 / 0.36%
Read min/max/mean length	30 / 100 / 100.15
Duplicated reads (estimated)	8,776 / 18.82%
Duplication rate	19.24%
Clipped reads	3,854 / 8.27%

2.2. ACGT Content

Number/percentage of A's	1,236,551 / 27.37%
Number/percentage of C's	1,029,714 / 22.79%
Number/percentage of T's	1,230,262 / 27.23%
Number/percentage of G's	1,021,074 / 22.6%
Number/percentage of N's	923 / 0.02%

GC Percentage	45.39%

2.3. Coverage

Mean	0.0015
Standard Deviation	0.0618

2.4. Mapping Quality

Mean Mapping Quality	54.33

2.5. Insert size

Mean	29,088.57
Standard Deviation	1,383,780.8
P25/Median/P75	169 / 235 / 316

2.6. Mismatches and indels

General error rate	0.63%
Mismatches	27,916
Insertions	243
Mapped reads with at least one insertion	0.51%
Deletions	239
Mapped reads with at least one deletion	0.52%
Homopolymer indels	46.89%

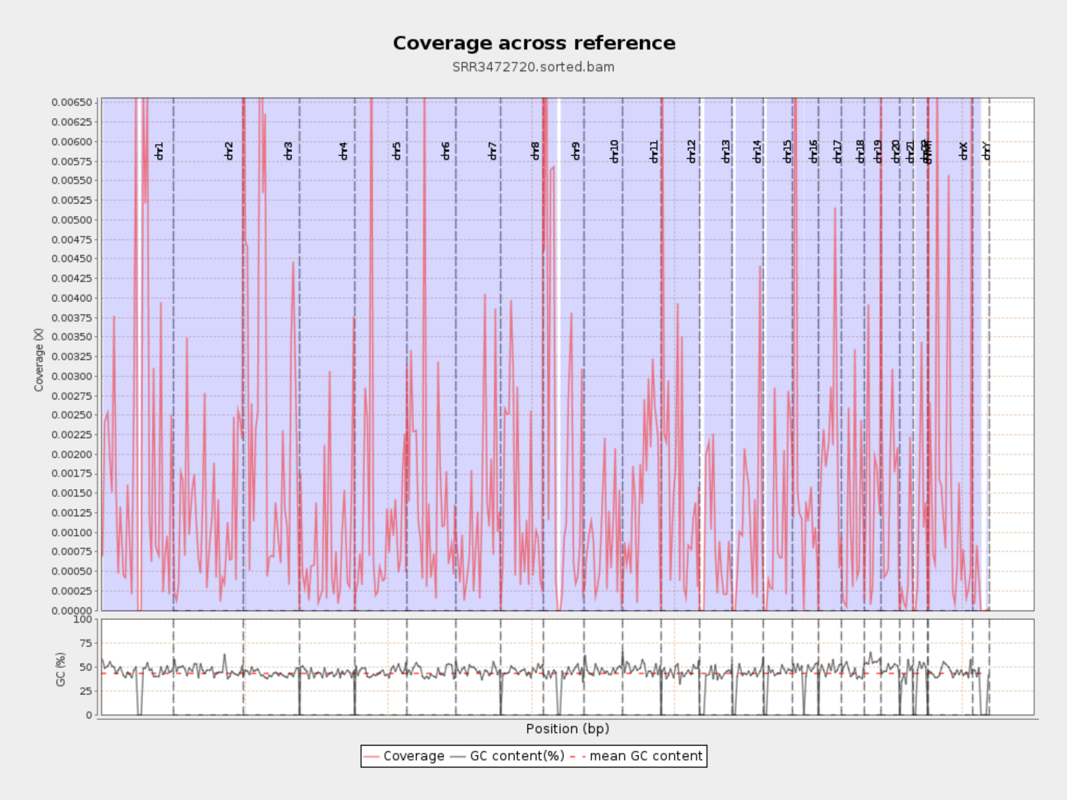
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

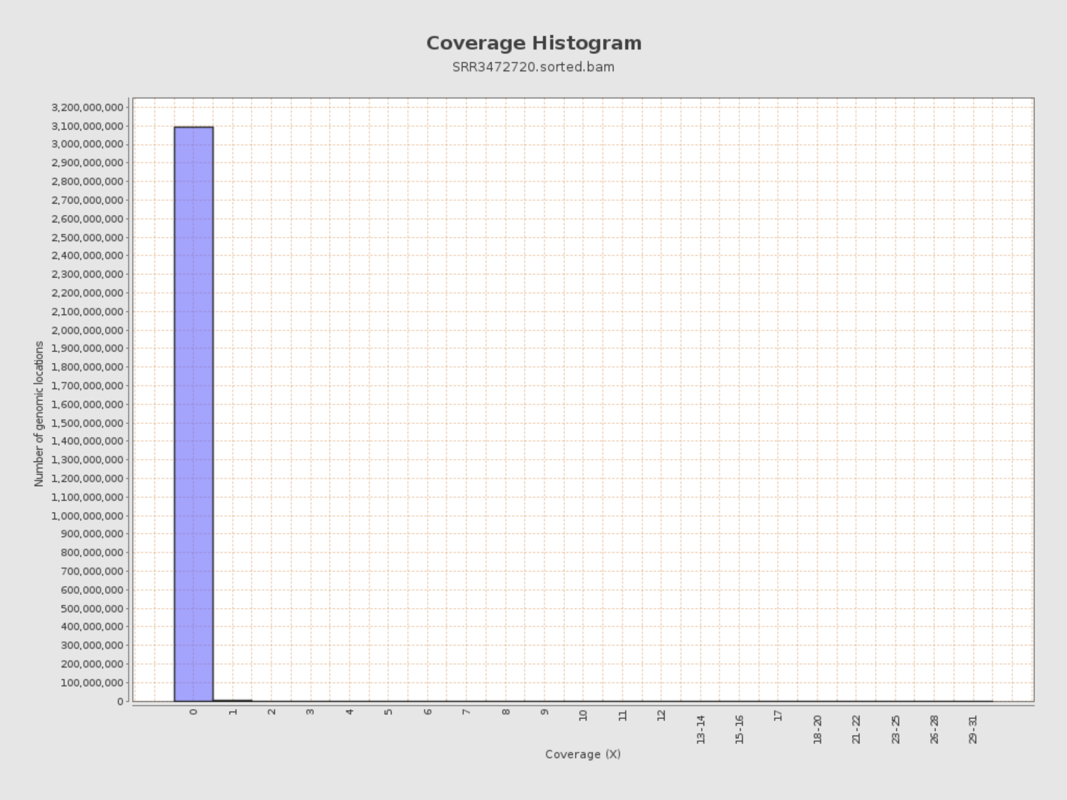
		bases	coverage	deviation
chr1	249250621	485514	0.0019	0.0799
chr2	243199373	290698	0.0012	0.0554
chr3	198022430	503847	0.0025	0.0793
chr4	191154276	163609	0.0009	0.0457
chr5	180915260	225423	0.0012	0.0529
chr6	171115067	275378	0.0016	0.0631
chr7	159138663	190372	0.0012	0.0544
chr8	146364022	212750	0.0015	0.0619
chr9	141213431	314106	0.0022	0.0796
chr10	135534747	119462	0.0009	0.0453
chr11	135006516	213143	0.0016	0.0639
chr12	133851895	246918	0.0018	0.068
chr13	115169878	89739	0.0008	0.0447
chr14	107349540	122790	0.0011	0.0629
chr15	102531392	109904	0.0011	0.0518
chr16	90354753	157499	0.0017	0.0661
chr17	81195210	177615	0.0022	0.0717
chr18	78077248	89801	0.0012	0.0607
chr19	59128983	99679	0.0017	0.062
chr20	63025520	95312	0.0015	0.0614
chr21	48129895	25309	0.0005	0.0351
chr22	51304566	60827	0.0012	0.0519
chrMT	16571	577	0.0348	0.1988
chrX	155270560	237803	0.0015	0.0601

chrY	59373566	11014	0.0002	0.0193

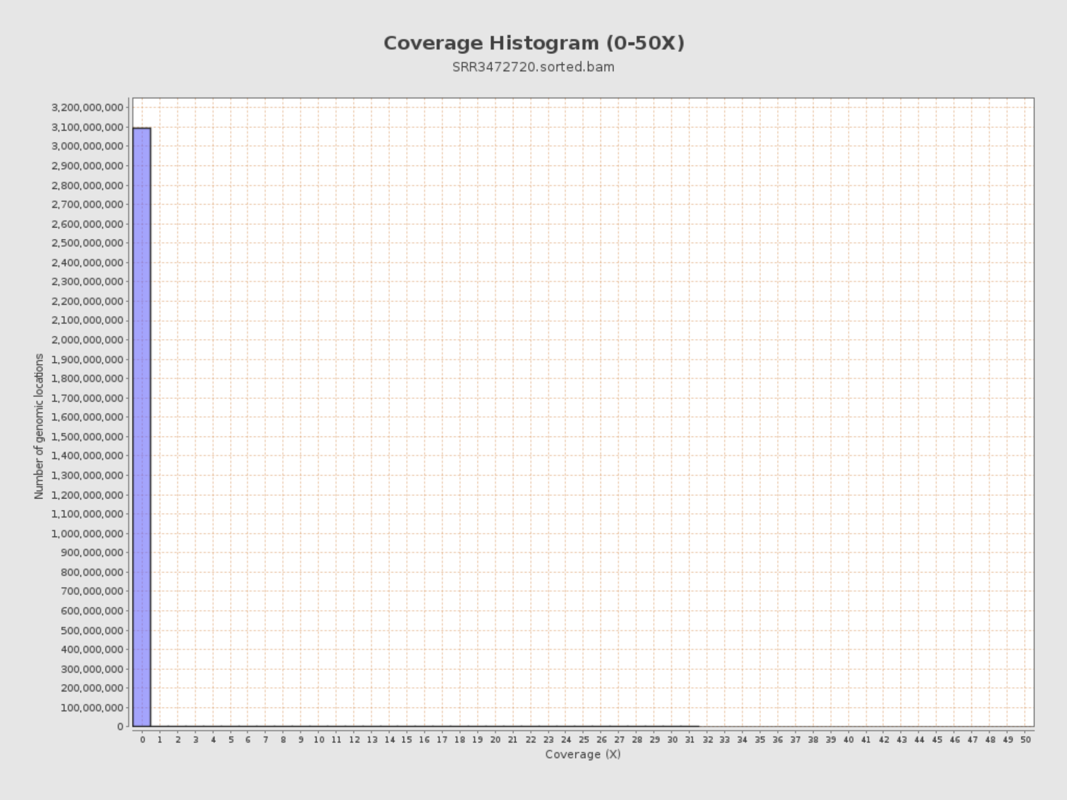
3. Results : Coverage across reference



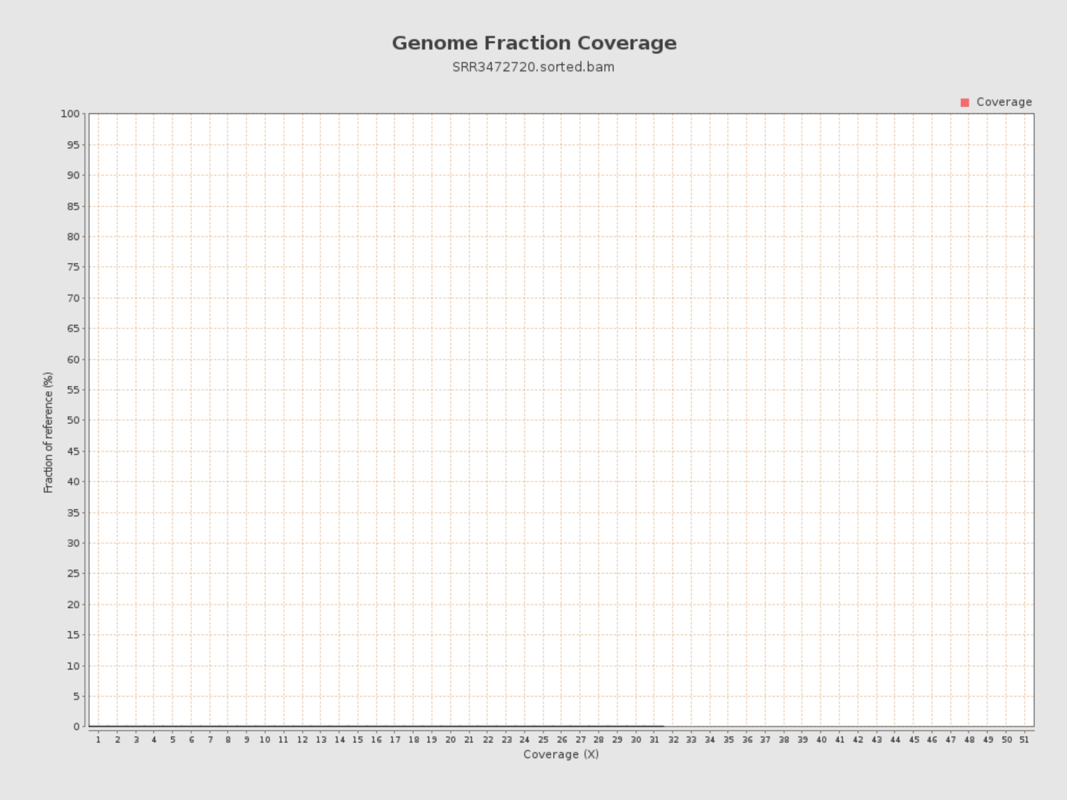
4. Results : Coverage Histogram



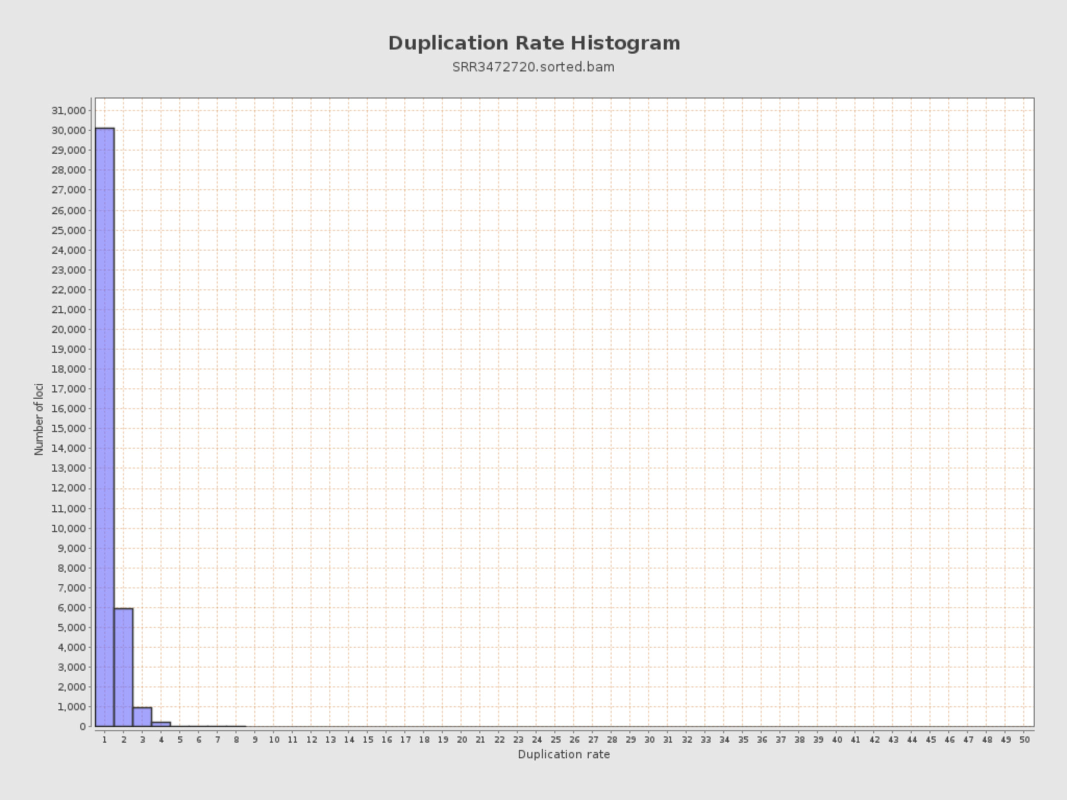
5. Results : Coverage Histogram (0-50X)



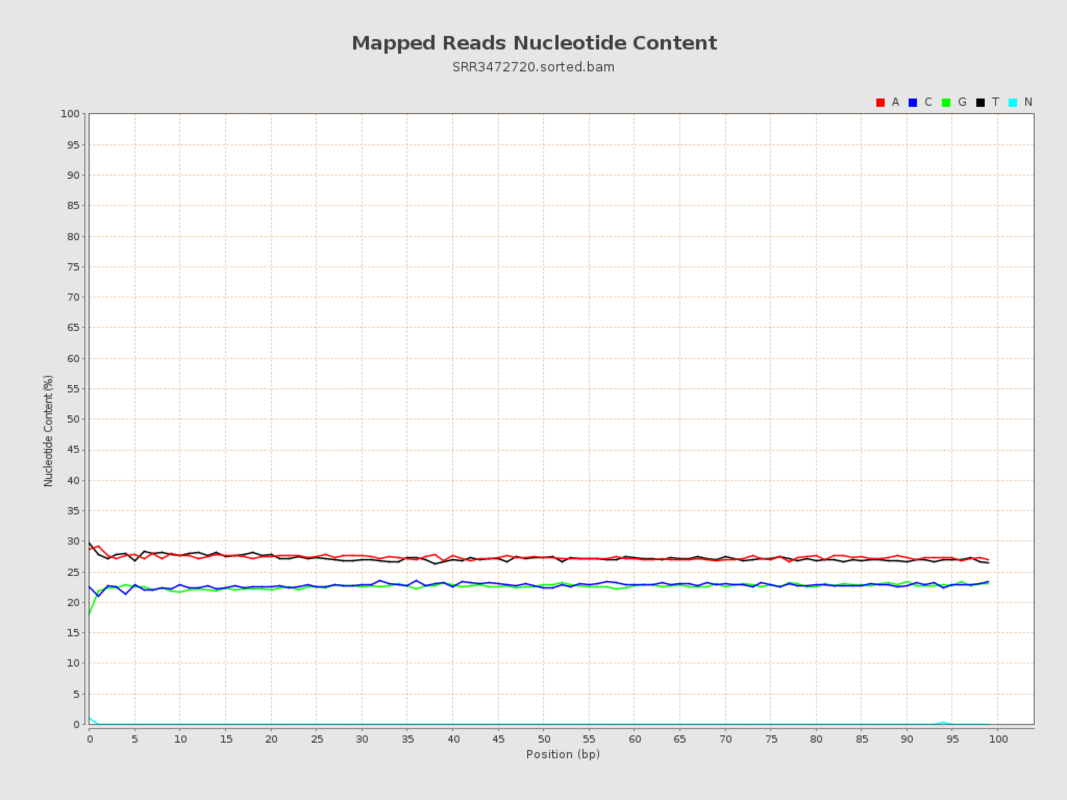
6. Results : Genome Fraction Coverage



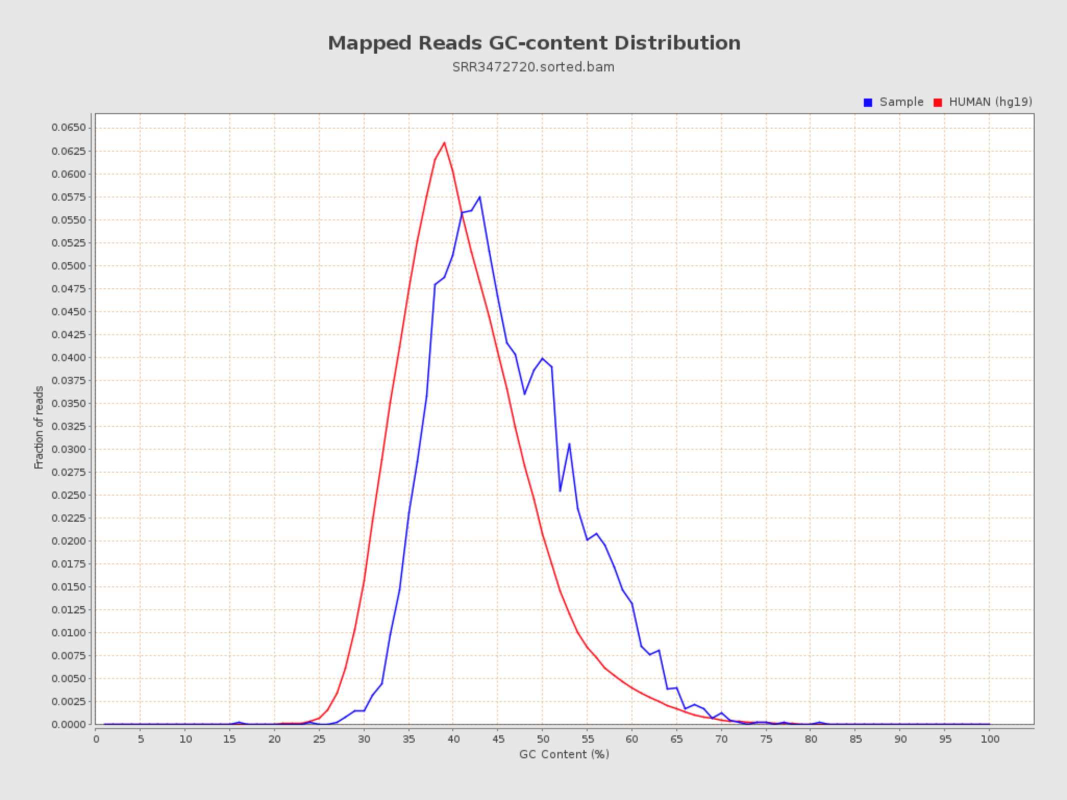
7. Results : Duplication Rate Histogram



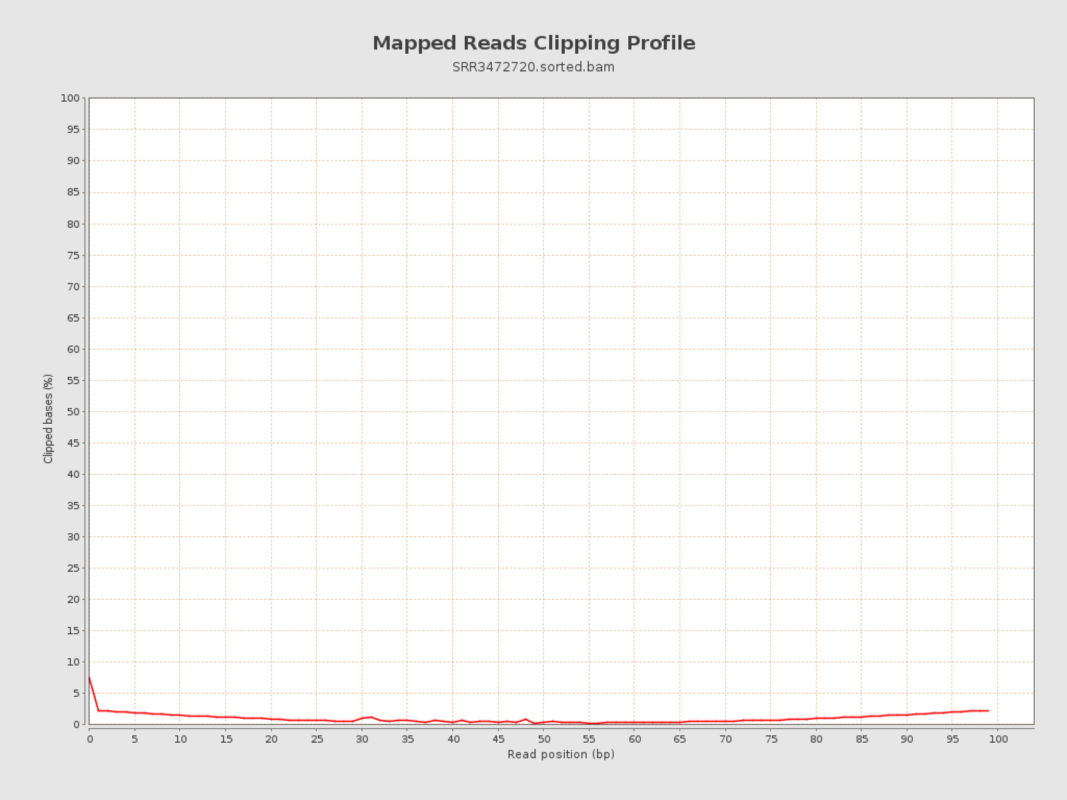
8. Results : Mapped Reads Nucleotide Content



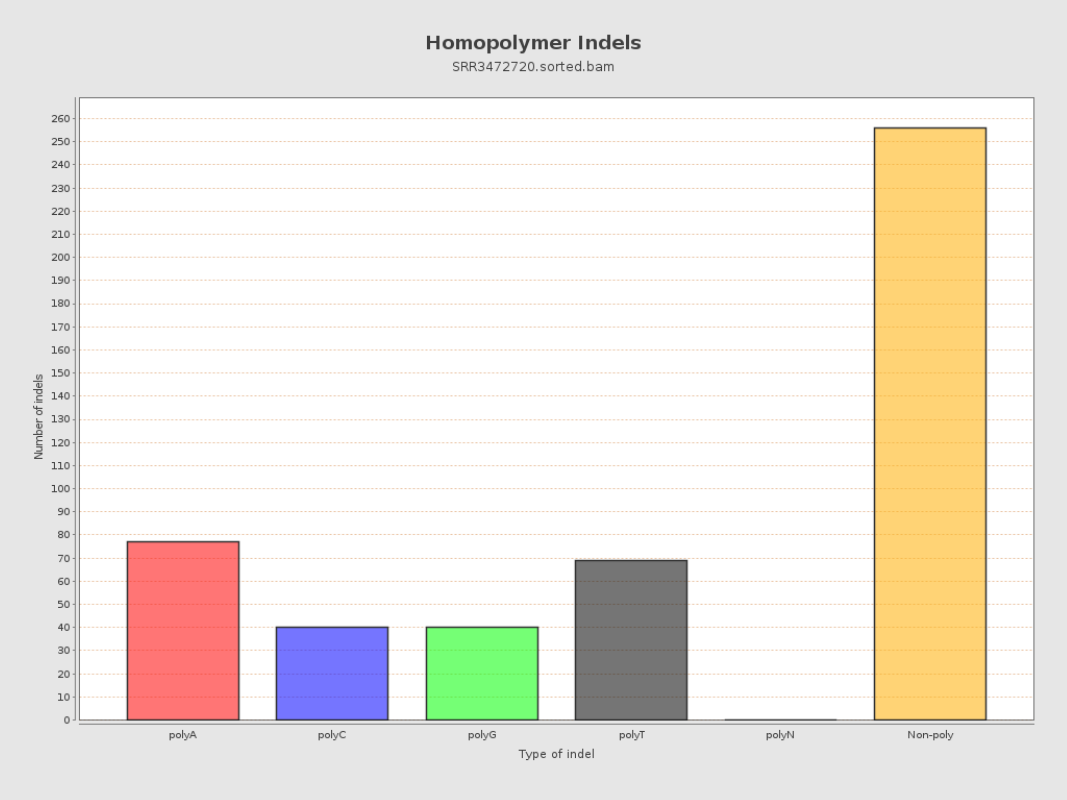
9. Results : Mapped Reads GC-content Distribution



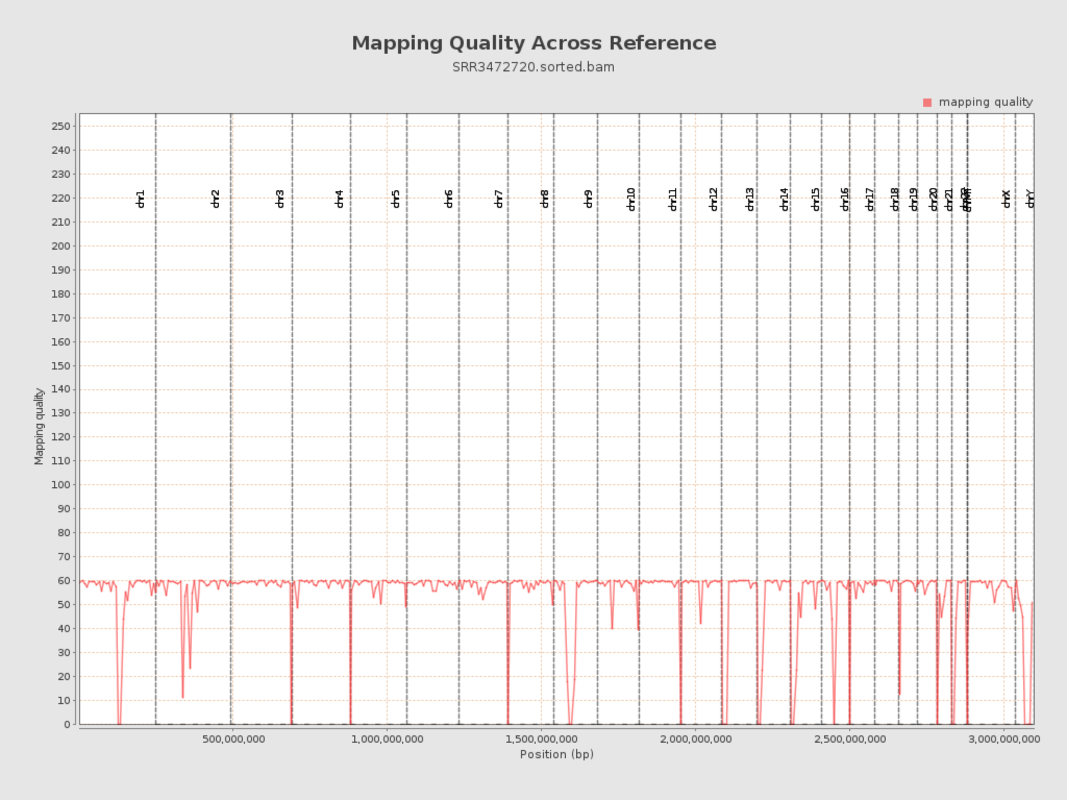
10. Results : Mapped Reads Clipping Profile



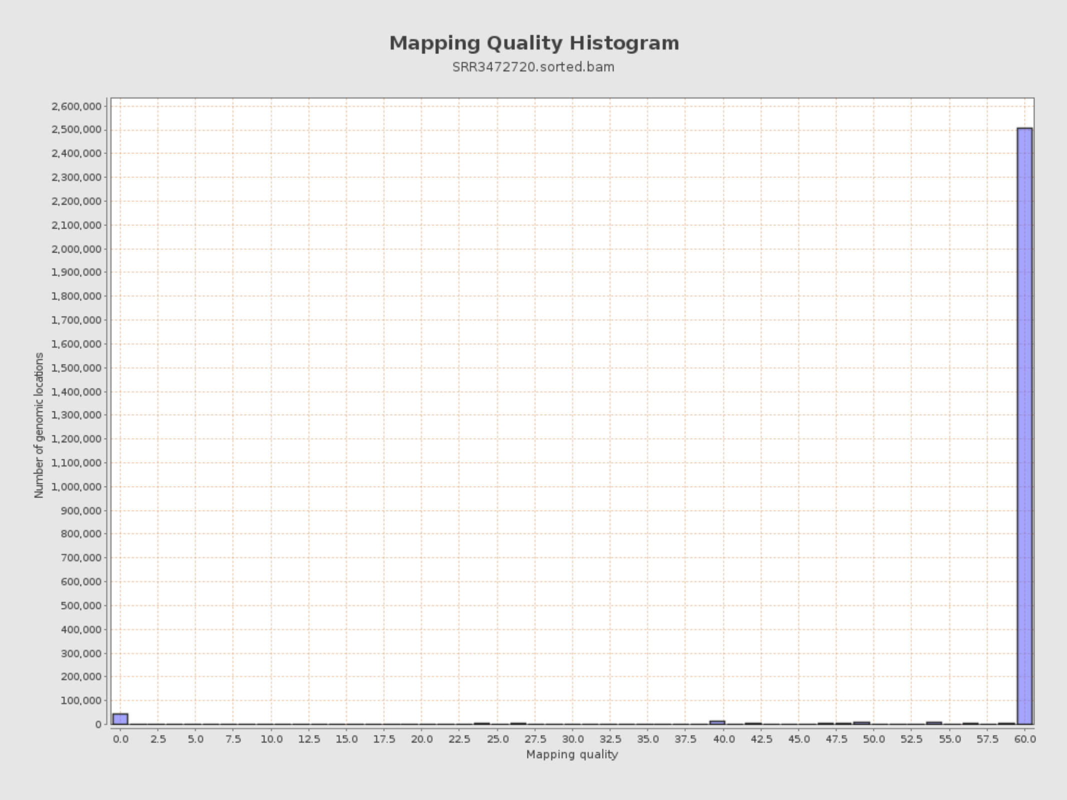
11. Results : Homopolymer Indels



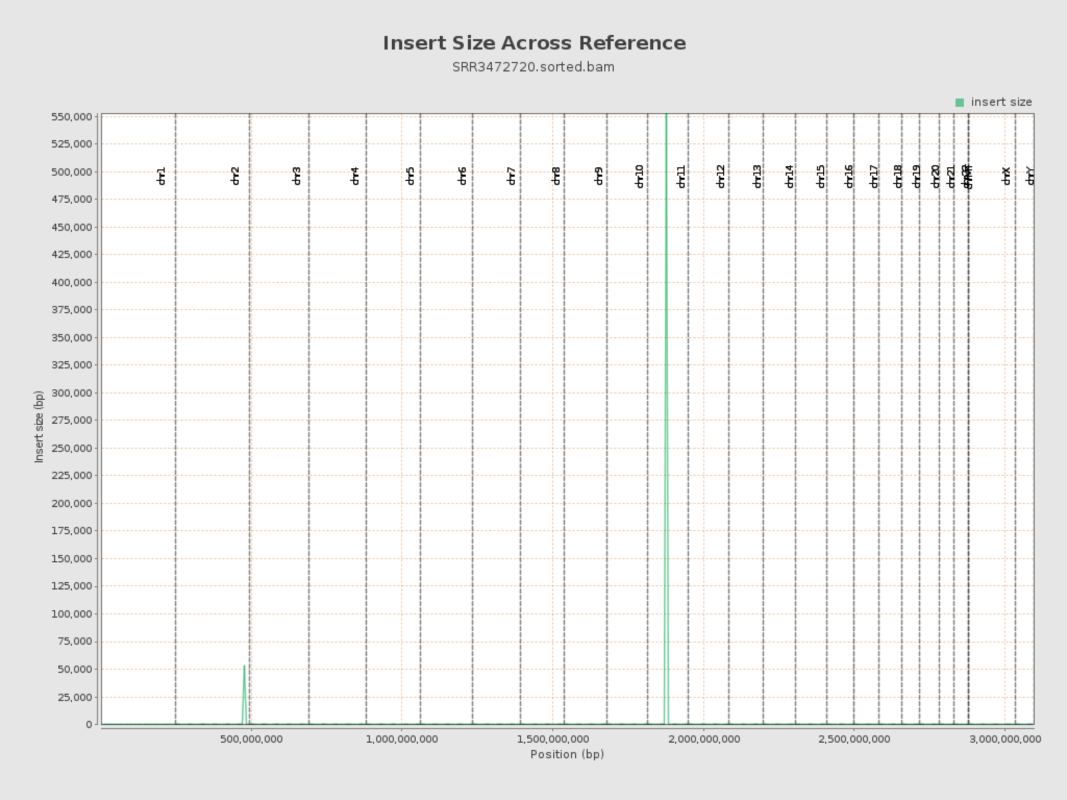
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram