Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 04:56:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472471.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_SRR3472471 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472471_1.fastq.gz SRR3472471_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 04:56:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472471.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,928,038
Mapped reads	17,731,679 / 98.9%
Unmapped reads	196,359 / 1.1%
Mapped paired reads	17,731,679 / 98.9%
Mapped reads, first in pair	8,889,688 / 49.59%
Mapped reads, second in pair	8,841,991 / 49.32%
Mapped reads, both in pair	17,633,136 / 98.36%
Mapped reads, singletons	98,543 / 0.55%
Secondary alignments	0
Supplementary alignments	64,372 / 0.36%
Read min/max/mean length	30 / 100 / 100.15
Duplicated reads (estimated)	11,102,214 / 61.93%
Duplication rate	46.2%
Clipped reads	1,667,698 / 9.3%

2.2. ACGT Content

Number/percentage of A's	479,760,259 / 27.57%
Number/percentage of C's	392,754,853 / 22.57%
Number/percentage of T's	476,641,117 / 27.39%
Number/percentage of G's	390,706,513 / 22.45%
Number/percentage of N's	270,780 / 0.02%

GC Percentage	45.02%

2.3. Coverage

Mean	0.5622
Standard Deviation	18.597

2.4. Mapping Quality

Mean Mapping Quality	55.07

2.5. Insert size

Mean	30,402.06
Standard Deviation	1,723,761.91
P25/Median/P75	162 / 228 / 310

2.6. Mismatches and indels

General error rate	0.6%
Mismatches	10,236,071
Insertions	94,604
Mapped reads with at least one insertion	0.53%
Deletions	87,469
Mapped reads with at least one deletion	0.49%
Homopolymer indels	44.2%

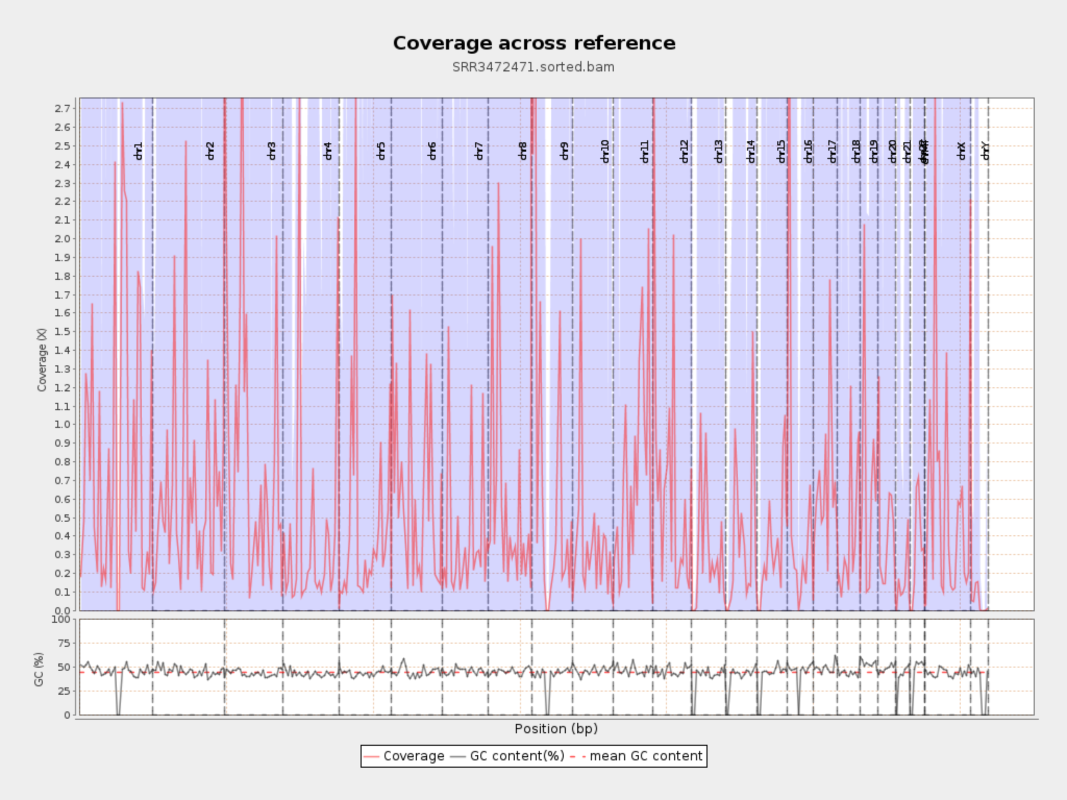
2.7. Chromosome stats

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

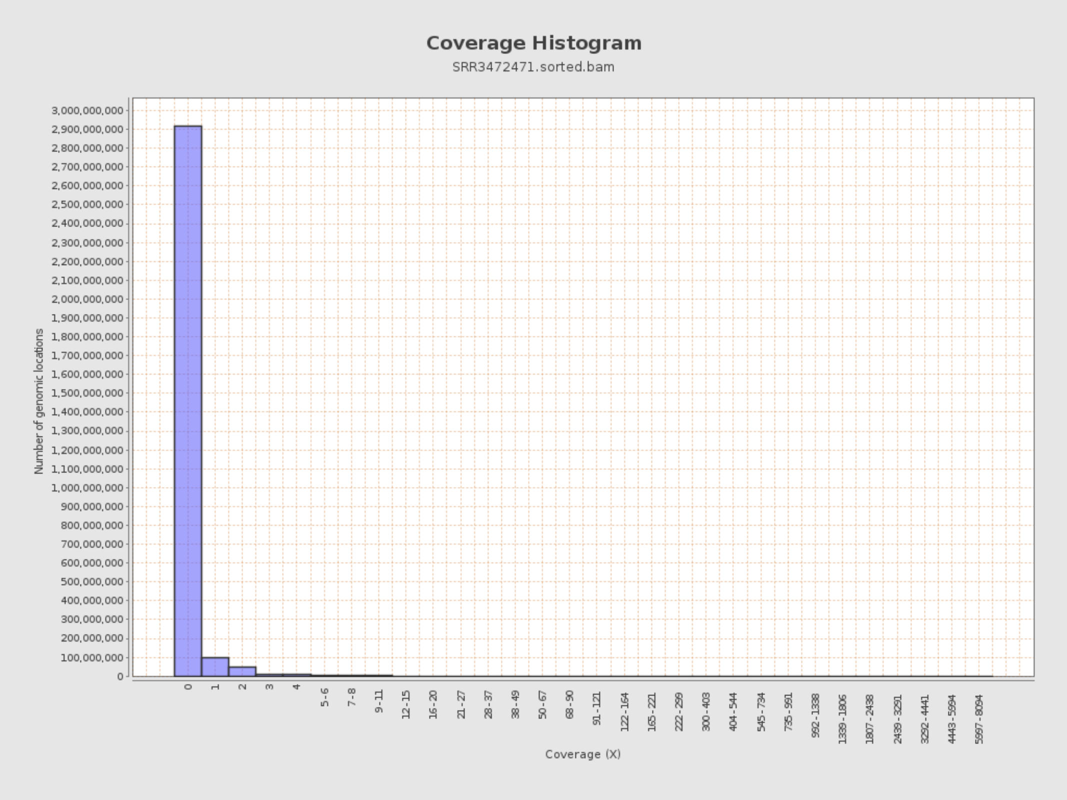
		bases	coverage	deviation
chr1	249250621	208022518	0.8346	24.9153
chr2	243199373	147320014	0.6058	19.3916
chr3	198022430	169903239	0.858	19.1389
chr4	191154276	76814616	0.4018	15.4291
chr5	180915260	86616863	0.4788	15.3446
chr6	171115067	104555088	0.611	18.8494
chr7	159138663	62173160	0.3907	15.9893
chr8	146364022	82404999	0.563	16.6862
chr9	141213431	119286553	0.8447	22.6011
chr10	135534747	52001766	0.3837	23.6302
chr11	135006516	97872961	0.7249	24.0747
chr12	133851895	93952854	0.7019	23.0846
chr13	115169878	36148610	0.3139	10.9492
chr14	107349540	39546405	0.3684	12.7169
chr15	102531392	35988386	0.351	9.9075
chr16	90354753	51740581	0.5726	19.1555
chr17	81195210	54947302	0.6767	17.5926
chr18	78077248	32715859	0.419	13.6017
chr19	59128983	41352637	0.6994	20.1176
chr20	63025520	27601366	0.4379	12.1129
chr21	48129895	7870478	0.1635	6.3403
chr22	51304566	16992779	0.3312	8.7787
chrMT	16571	1428	0.0862	0.3616
chrX	155270560	91389857	0.5886	21.3543

chrY	59373566	3133441	0.0528	2.0311

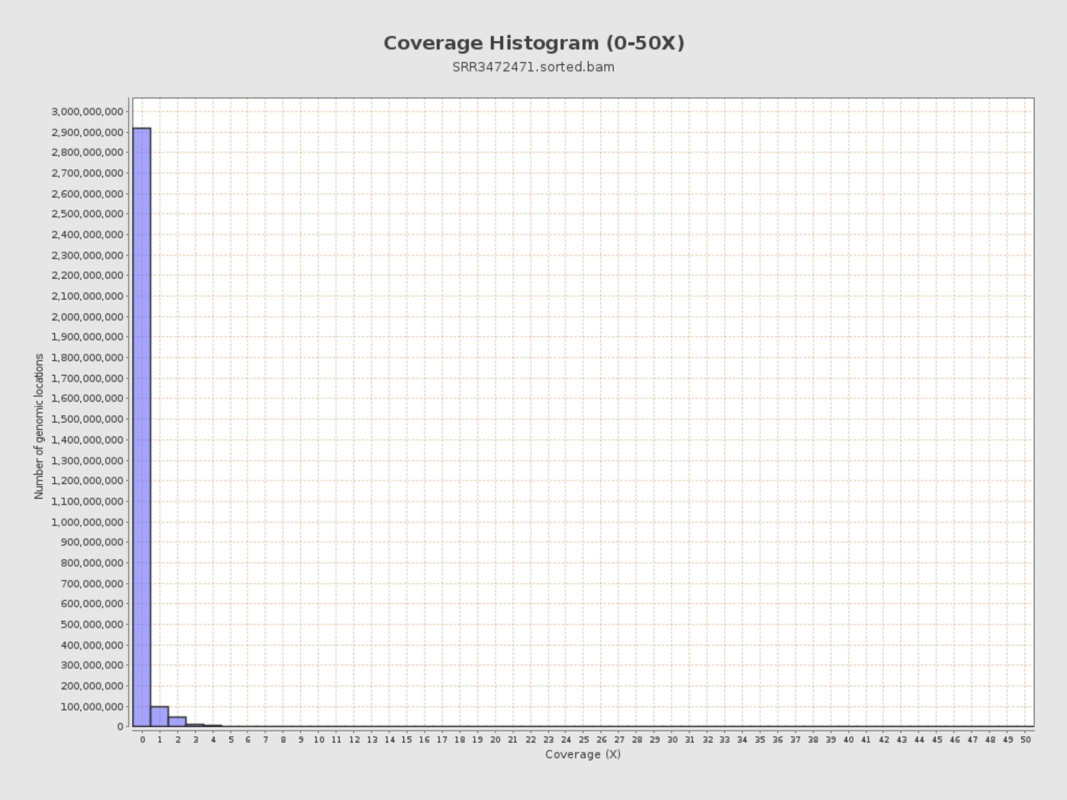
3. Results : Coverage across reference



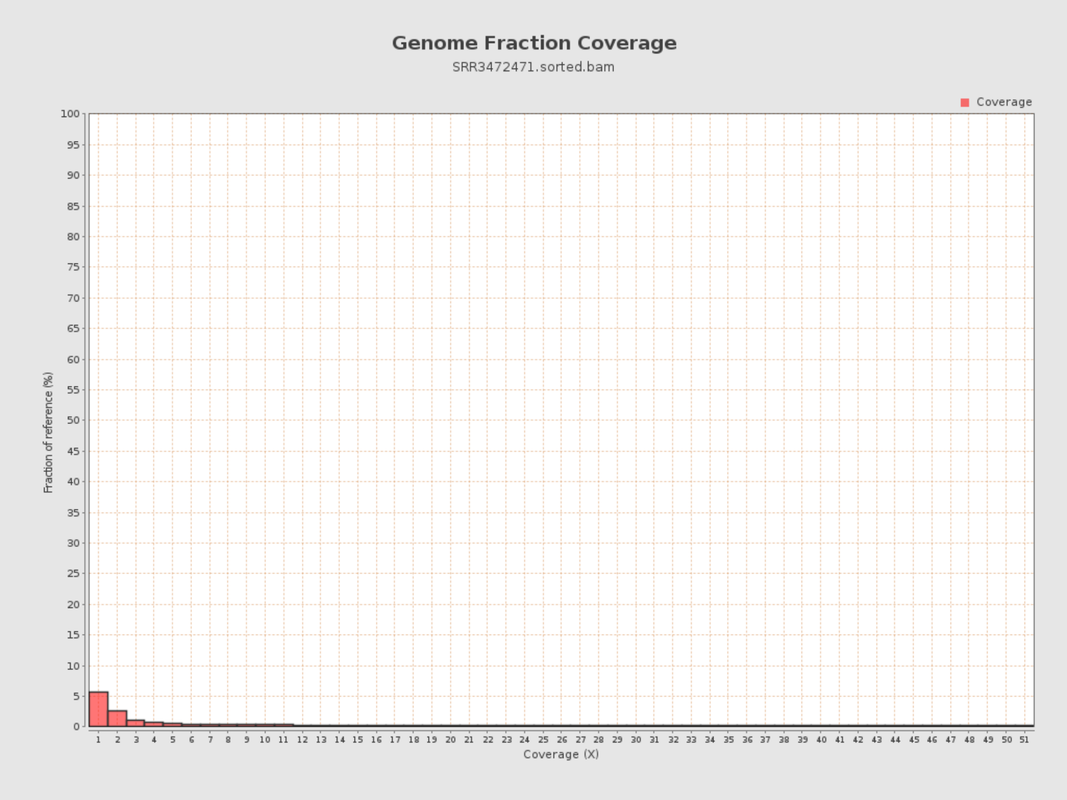
4. Results : Coverage Histogram



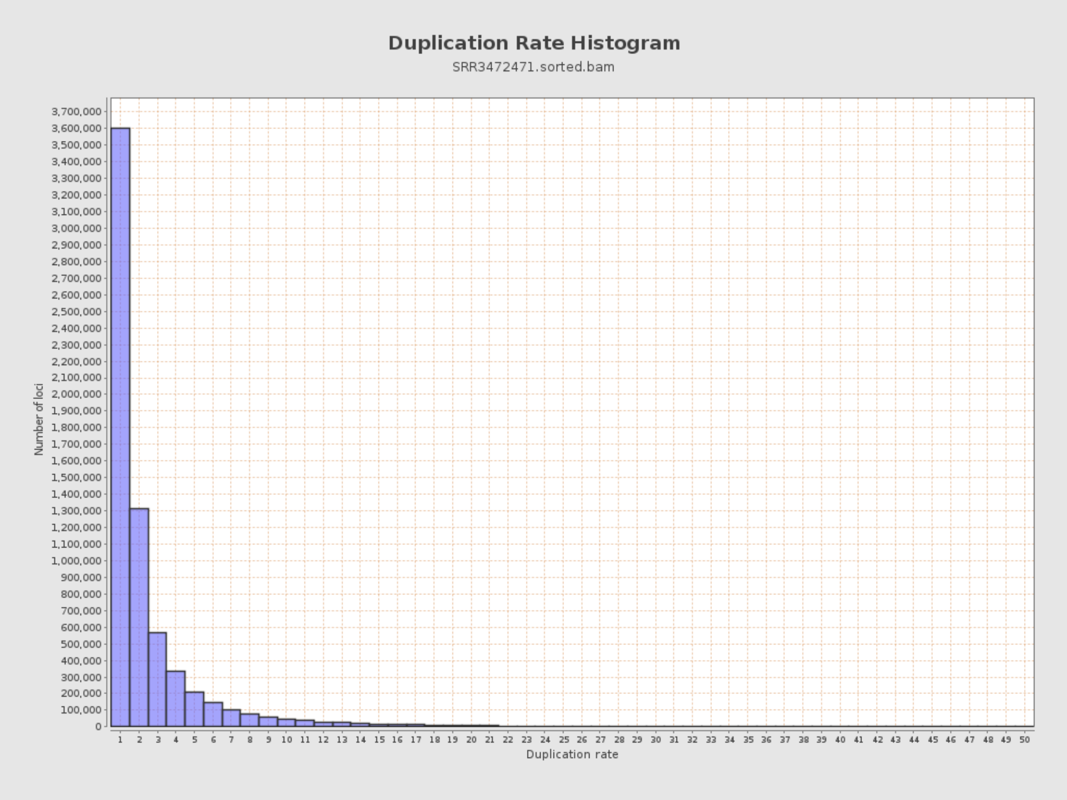
5. Results : Coverage Histogram (0-50X)



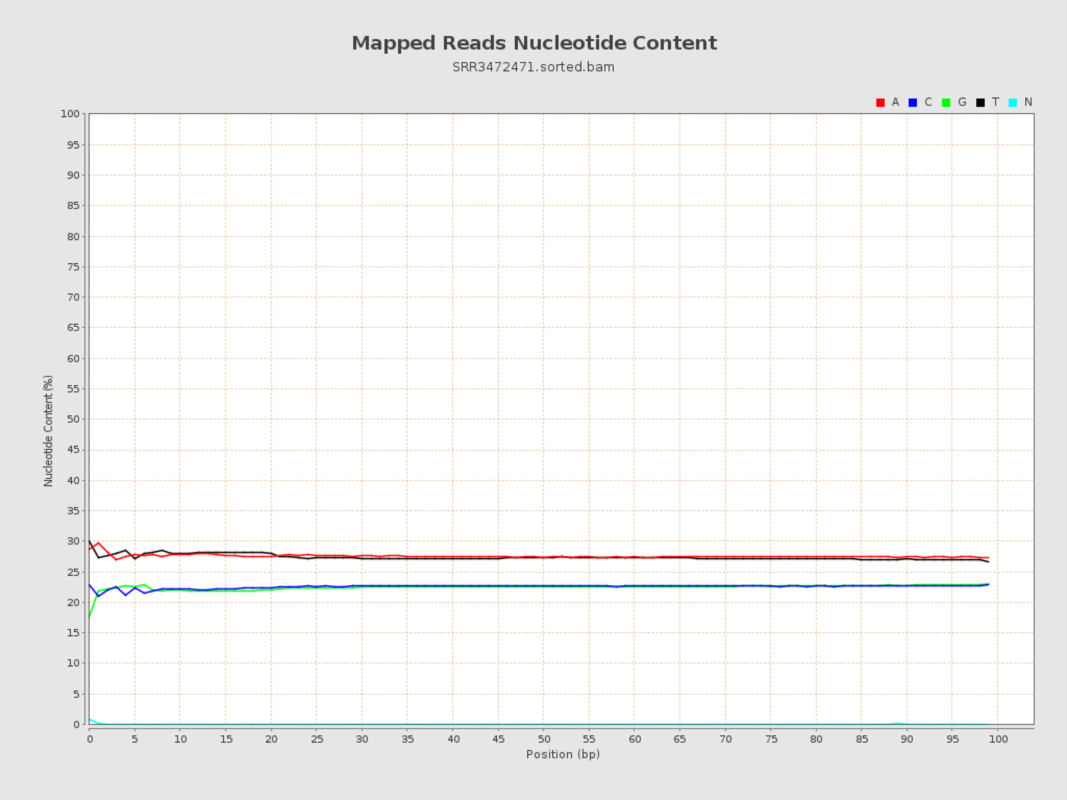
6. Results : Genome Fraction Coverage



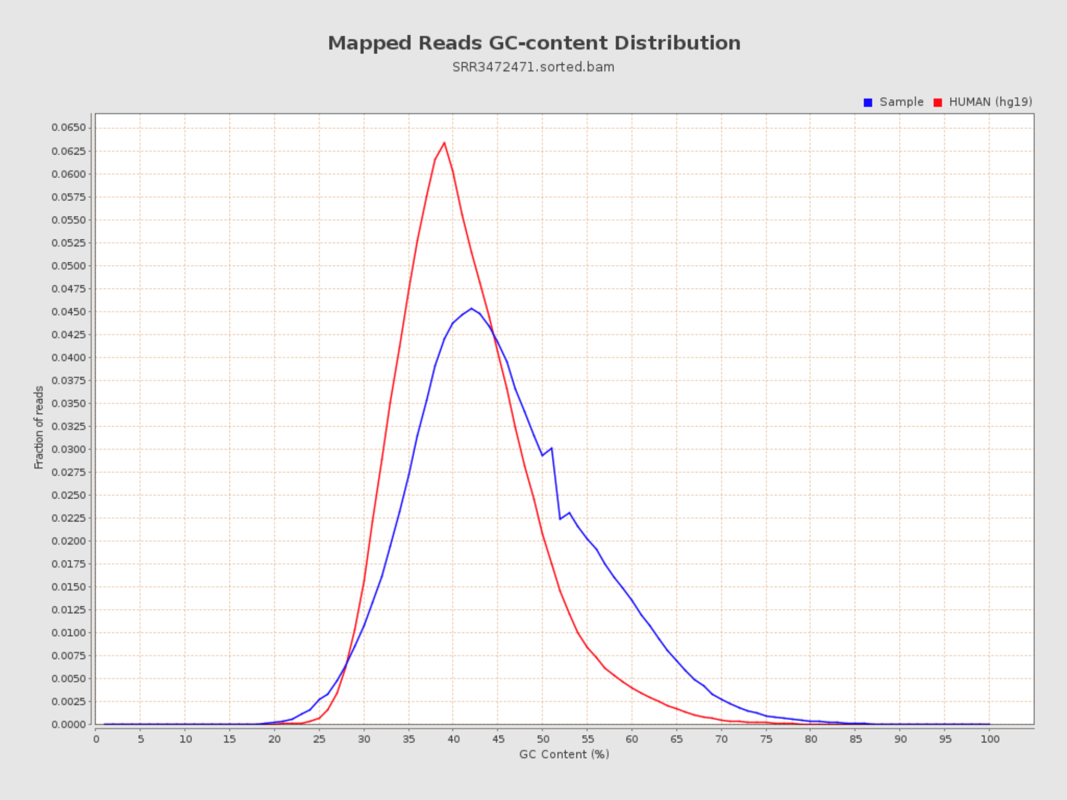
7. Results : Duplication Rate Histogram



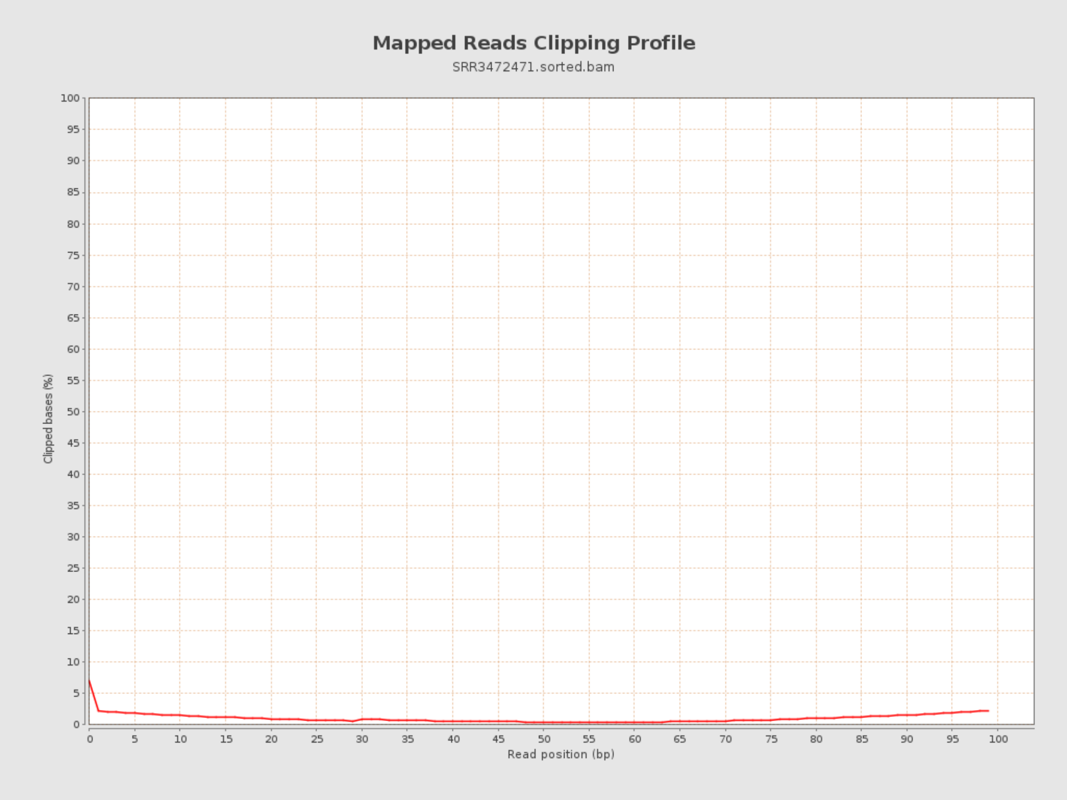
8. Results : Mapped Reads Nucleotide Content



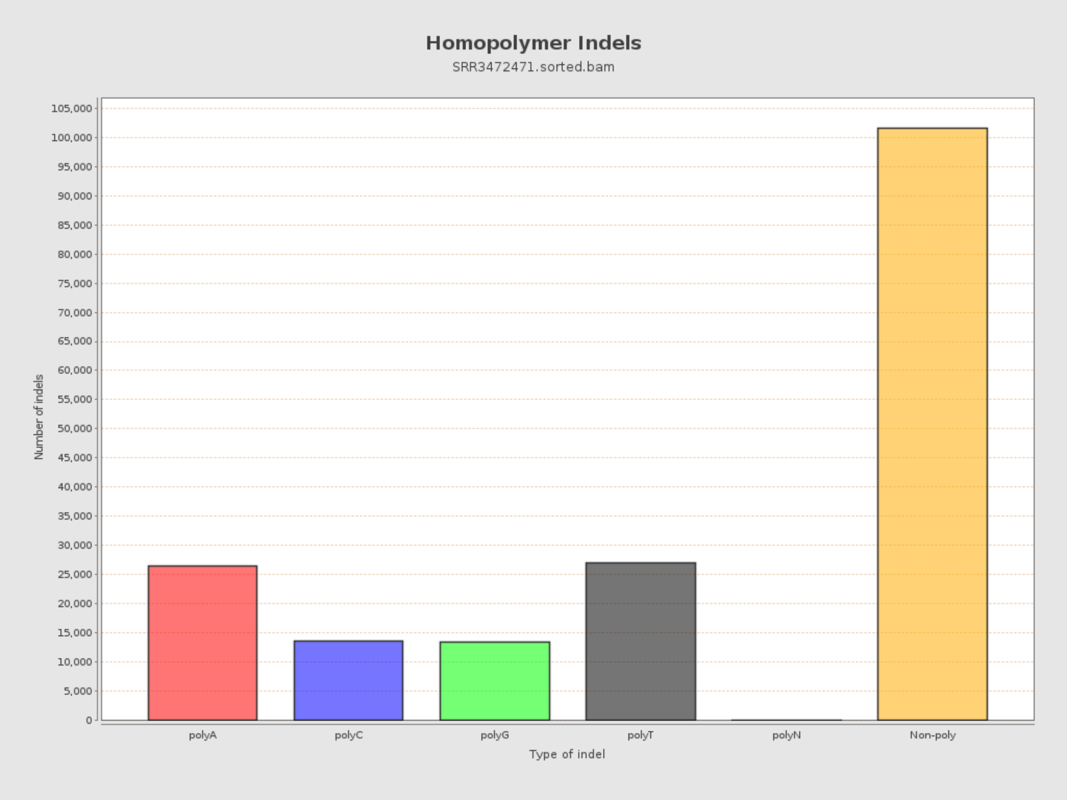
9. Results : Mapped Reads GC-content Distribution



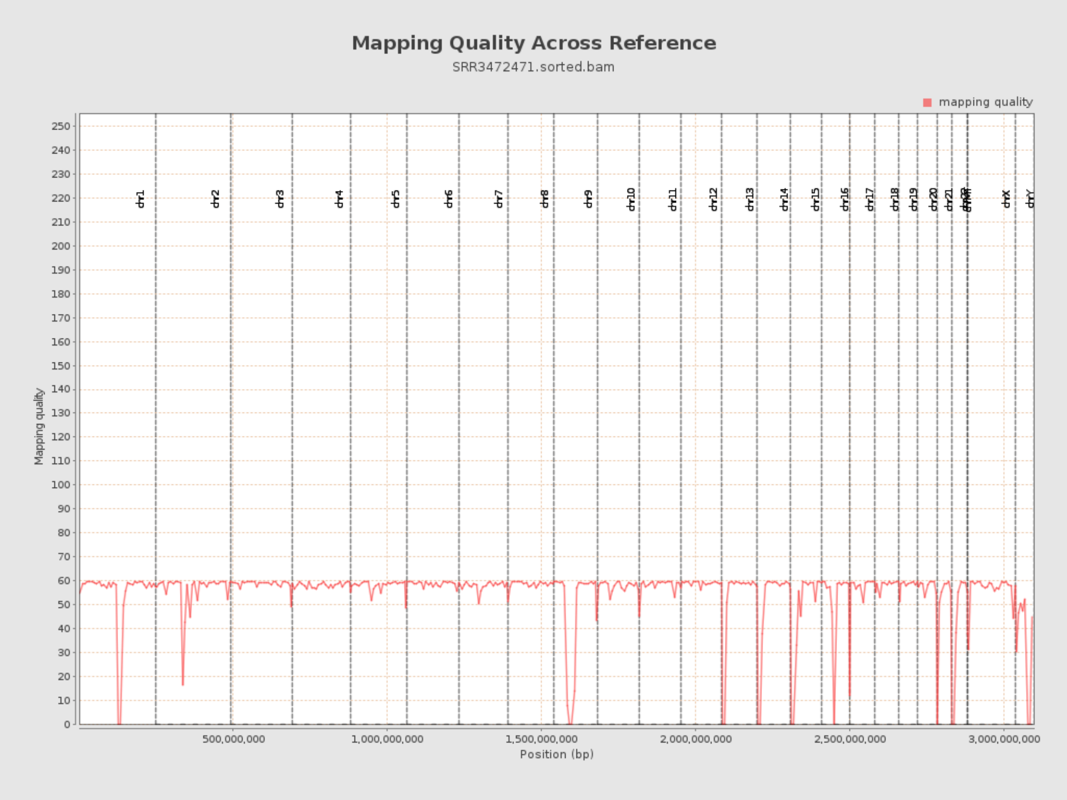
10. Results : Mapped Reads Clipping Profile



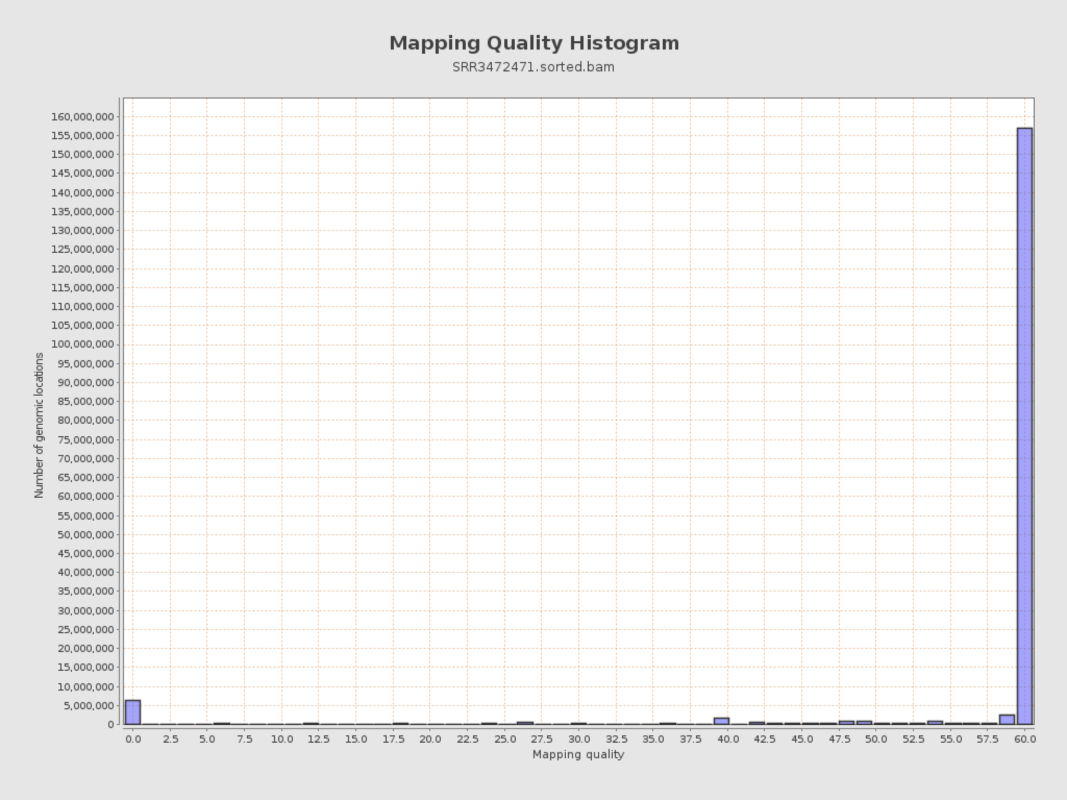
11. Results : Homopolymer Indels



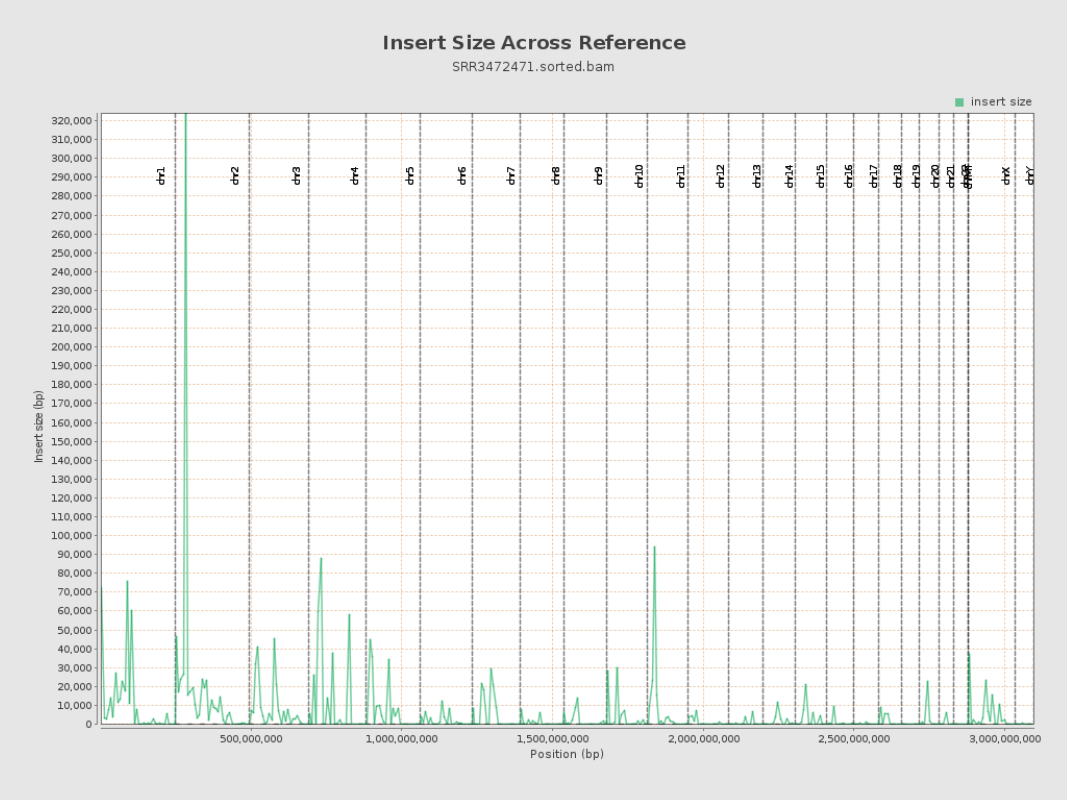
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram