Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 05:15:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472472.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_SRR3472472 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472472_1.fastq.gz SRR3472472_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 05:15:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472472.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,945,522
Mapped reads	16,774,887 / 98.99%
Unmapped reads	170,635 / 1.01%
Mapped paired reads	16,774,887 / 98.99%
Mapped reads, first in pair	8,409,899 / 49.63%
Mapped reads, second in pair	8,364,988 / 49.36%
Mapped reads, both in pair	16,685,666 / 98.47%
Mapped reads, singletons	89,221 / 0.53%
Secondary alignments	0
Supplementary alignments	58,131 / 0.34%
Read min/max/mean length	30 / 100 / 100.14
Duplicated reads (estimated)	10,758,796 / 63.49%
Duplication rate	44.62%
Clipped reads	1,744,946 / 10.3%

2.2. ACGT Content

Number/percentage of A's	447,119,829 / 27.23%
Number/percentage of C's	376,944,330 / 22.95%
Number/percentage of T's	444,210,013 / 27.05%
Number/percentage of G's	373,691,884 / 22.76%
Number/percentage of N's	257,313 / 0.02%

GC Percentage	45.71%

2.3. Coverage

Mean	0.5306
Standard Deviation	21.4533

2.4. Mapping Quality

Mean Mapping Quality	54.92

2.5. Insert size

Mean	29,325.43
Standard Deviation	1,620,902.55
P25/Median/P75	153 / 216 / 294

2.6. Mismatches and indels

General error rate	0.58%
Mismatches	9,394,113
Insertions	74,318
Mapped reads with at least one insertion	0.44%
Deletions	79,357
Mapped reads with at least one deletion	0.47%
Homopolymer indels	42.98%

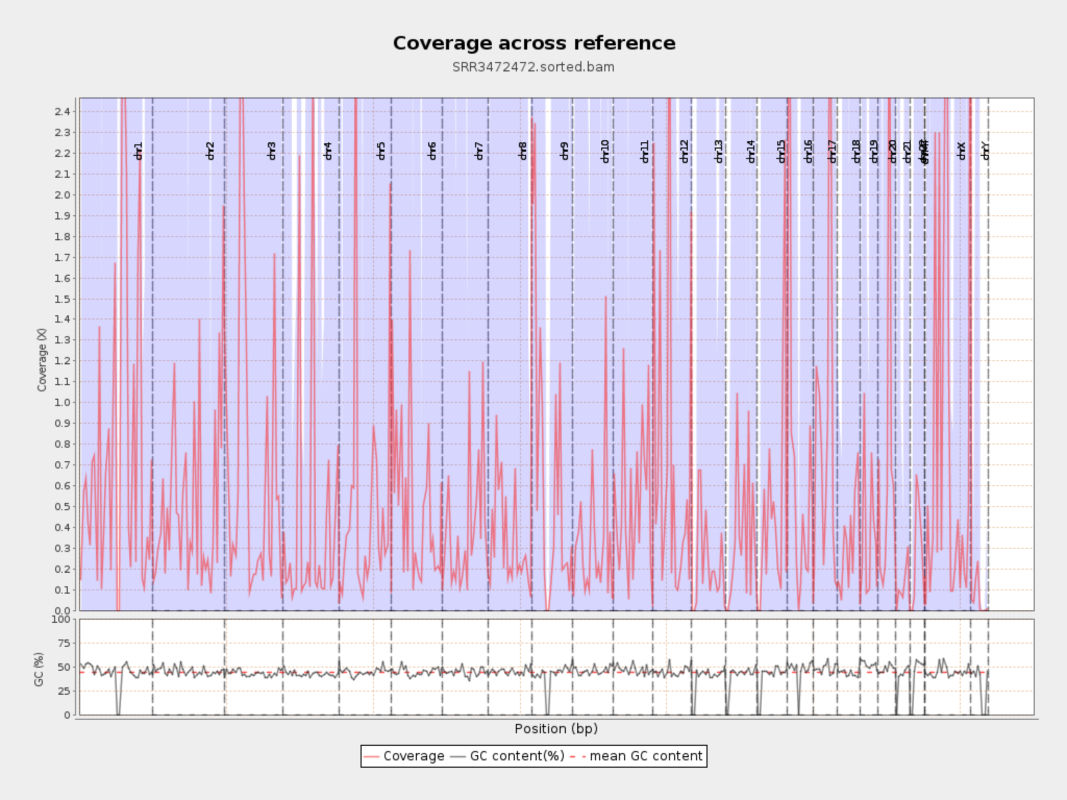
2.7. Chromosome stats

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

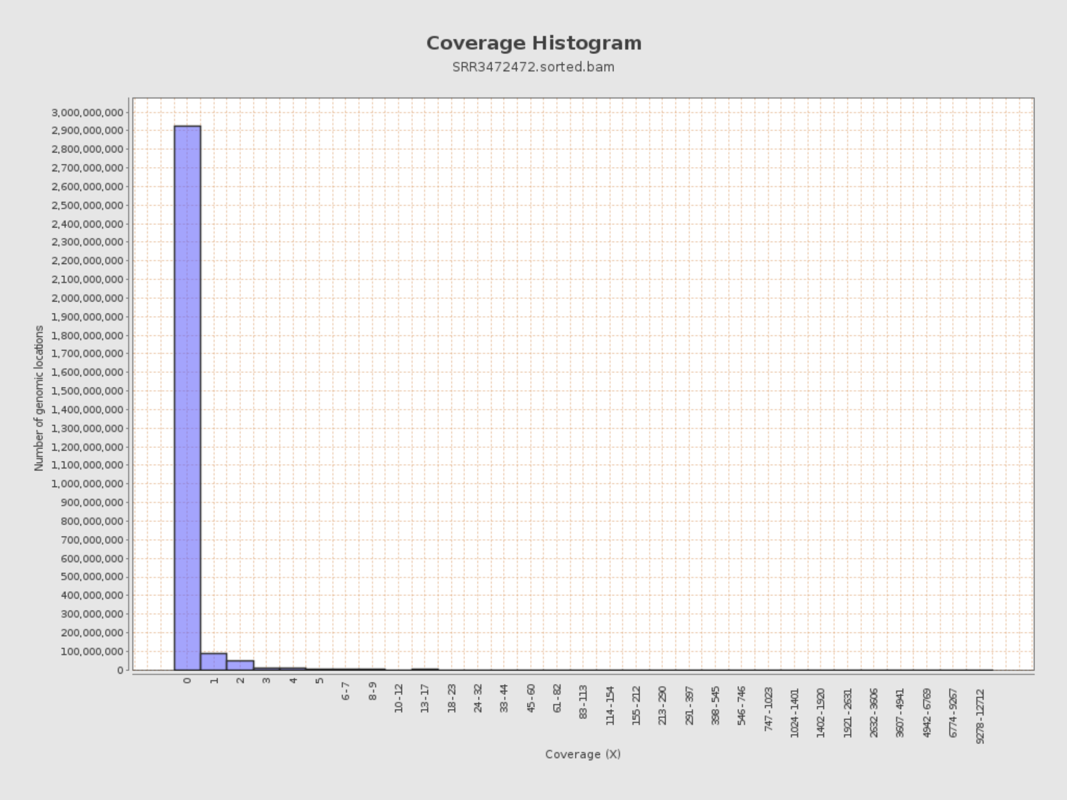
		bases	coverage	deviation
chr1	249250621	194326943	0.7796	29.3253
chr2	243199373	124828643	0.5133	18.4396
chr3	198022430	140946453	0.7118	17.4947
chr4	191154276	77634395	0.4061	19.5719
chr5	180915260	96707756	0.5345	24.9941
chr6	171115067	86015621	0.5027	14.7014
chr7	159138663	63028059	0.3961	14.6043
chr8	146364022	49062013	0.3352	11.5507
chr9	141213431	91023397	0.6446	17.1609
chr10	135534747	45558094	0.3361	15.8932
chr11	135006516	72474461	0.5368	18.9042
chr12	133851895	100713809	0.7524	30.7663
chr13	115169878	26903585	0.2336	8.1665
chr14	107349540	37833990	0.3524	18.81
chr15	102531392	55239732	0.5388	27.1071
chr16	90354753	64959517	0.7189	21.6801
chr17	81195210	69412011	0.8549	28.5261
chr18	78077248	25804485	0.3305	9.7544
chr19	59128983	23320324	0.3944	11.394
chr20	63025520	49908356	0.7919	34.3955
chr21	48129895	5860468	0.1218	4.492
chr22	51304566	13594016	0.265	12.9037
chrMT	16571	2696	0.1627	0.5257
chrX	155270560	123602313	0.796	36.7927

chrY	59373566	3666851	0.0618	3.265

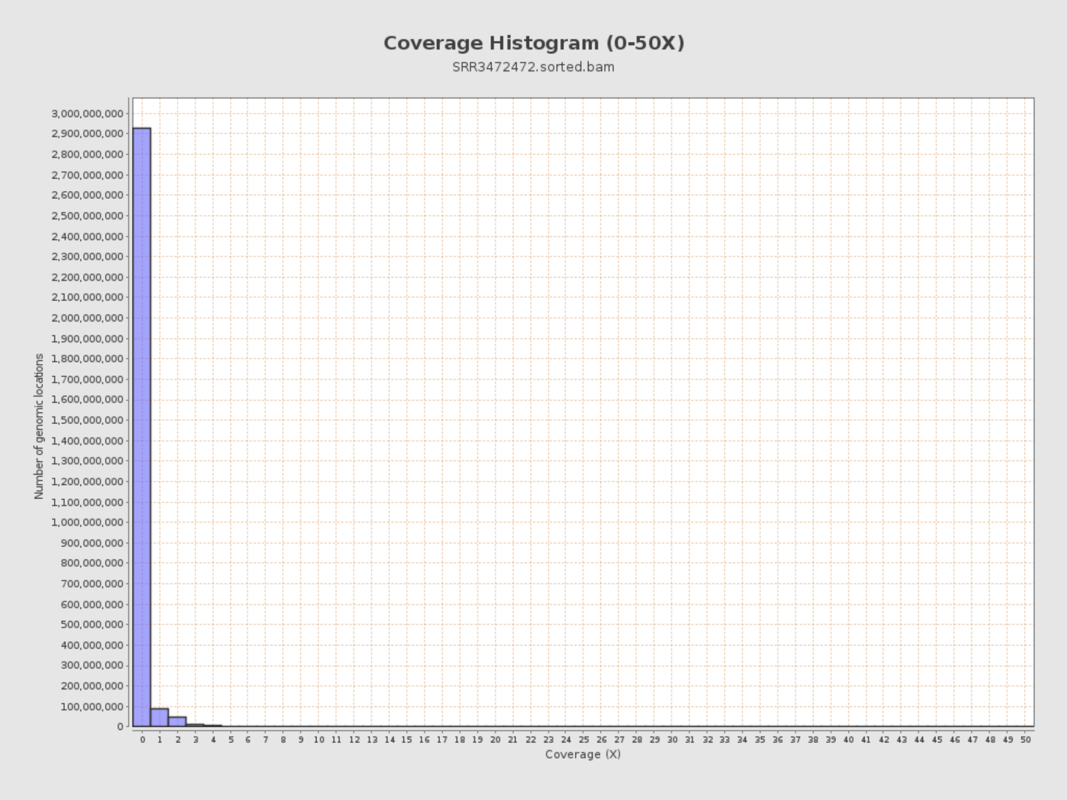
3. Results : Coverage across reference



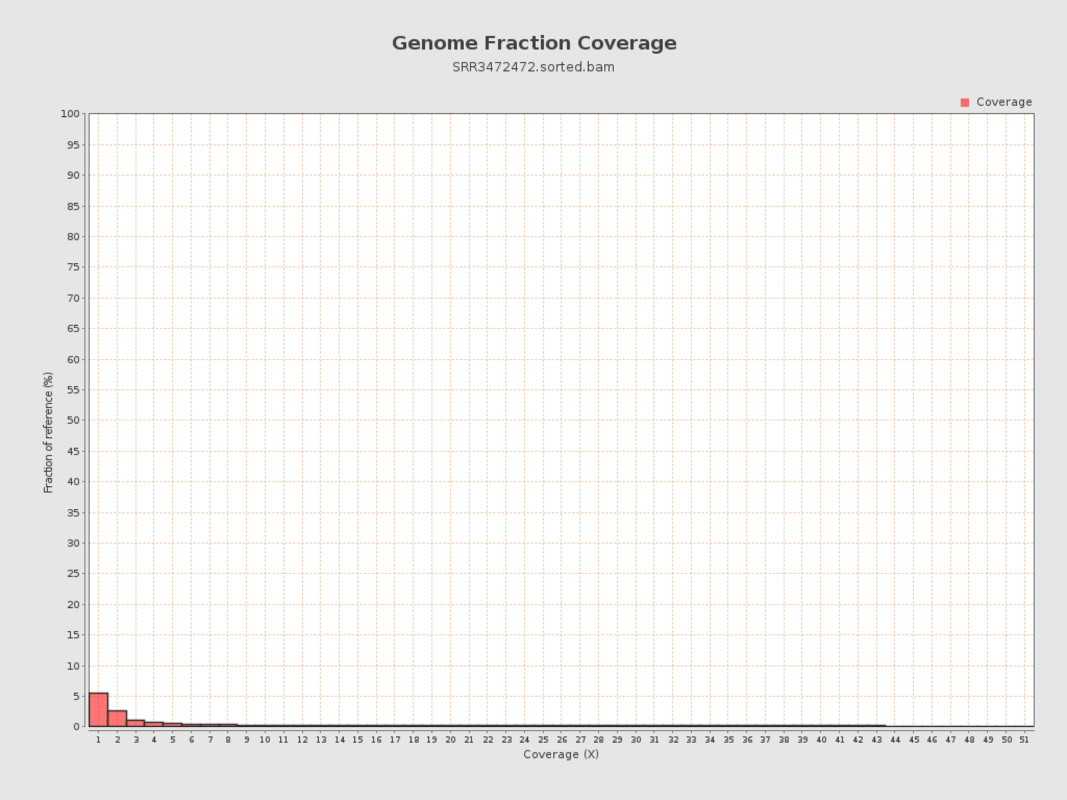
4. Results : Coverage Histogram



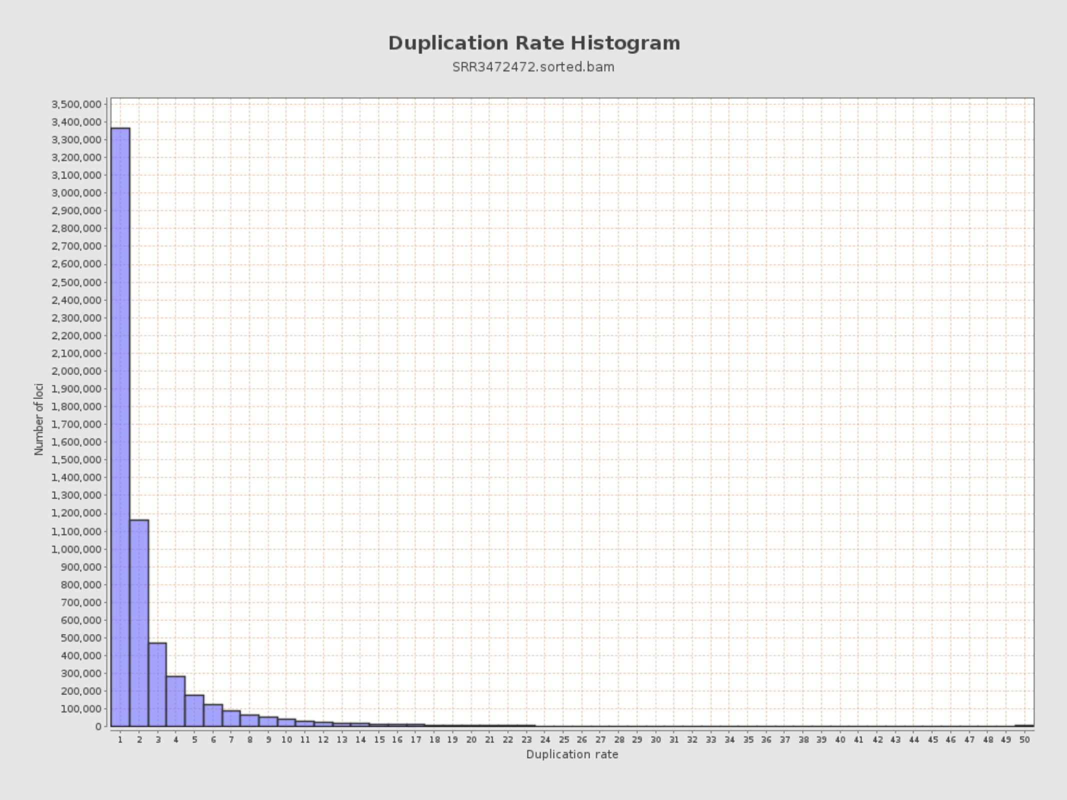
5. Results : Coverage Histogram (0-50X)



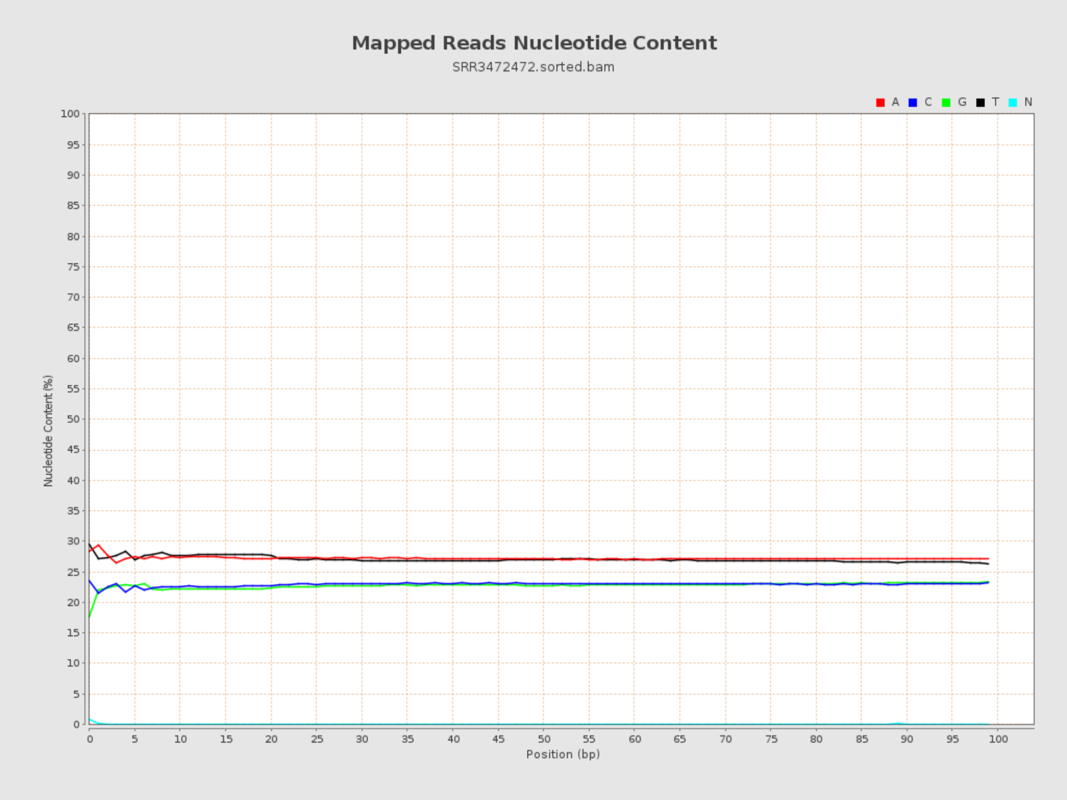
6. Results : Genome Fraction Coverage



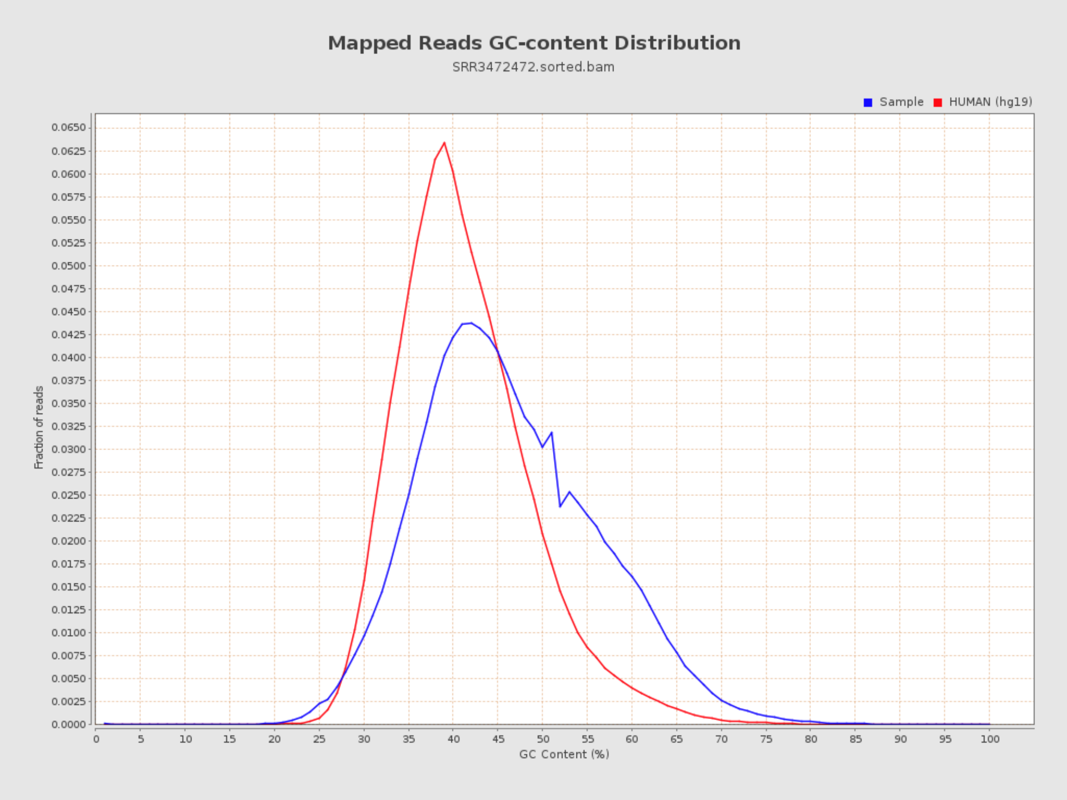
7. Results : Duplication Rate Histogram



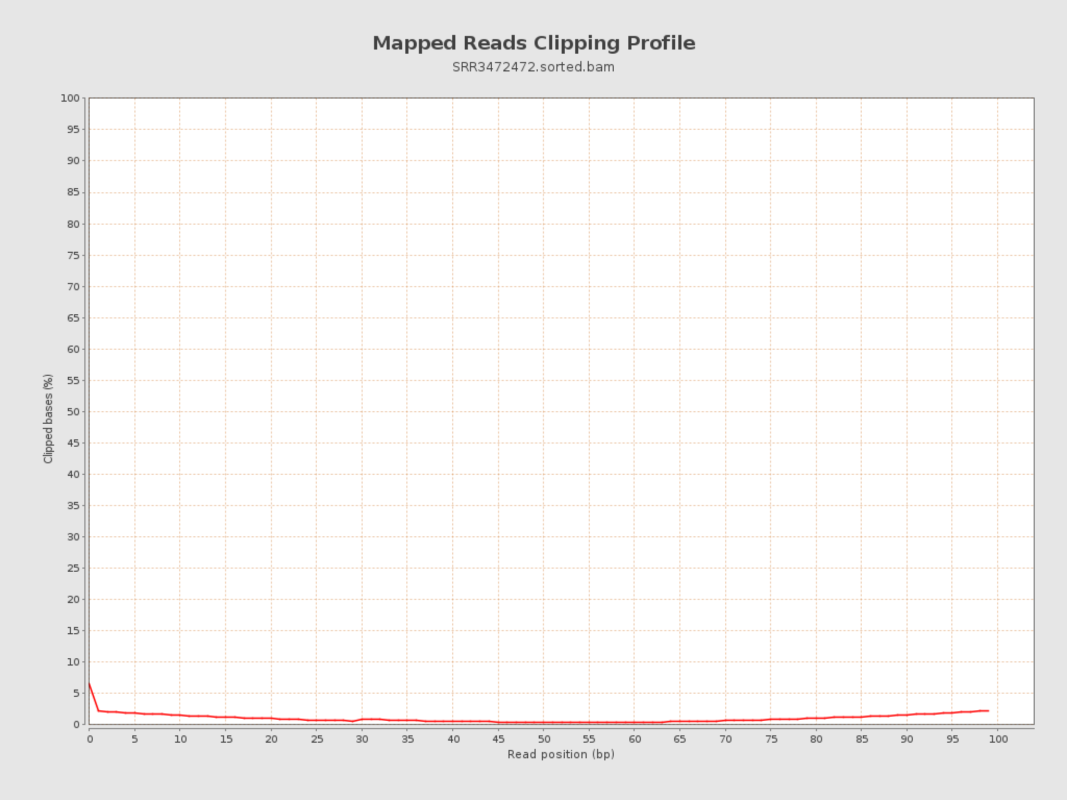
8. Results : Mapped Reads Nucleotide Content



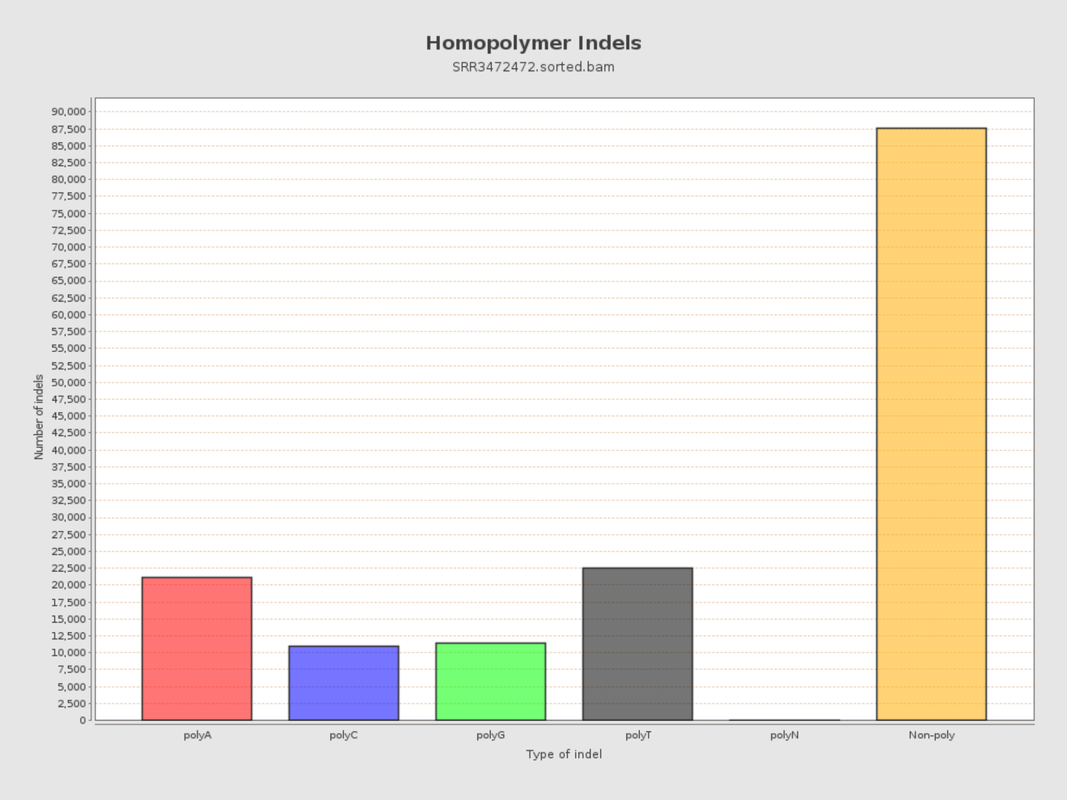
9. Results : Mapped Reads GC-content Distribution



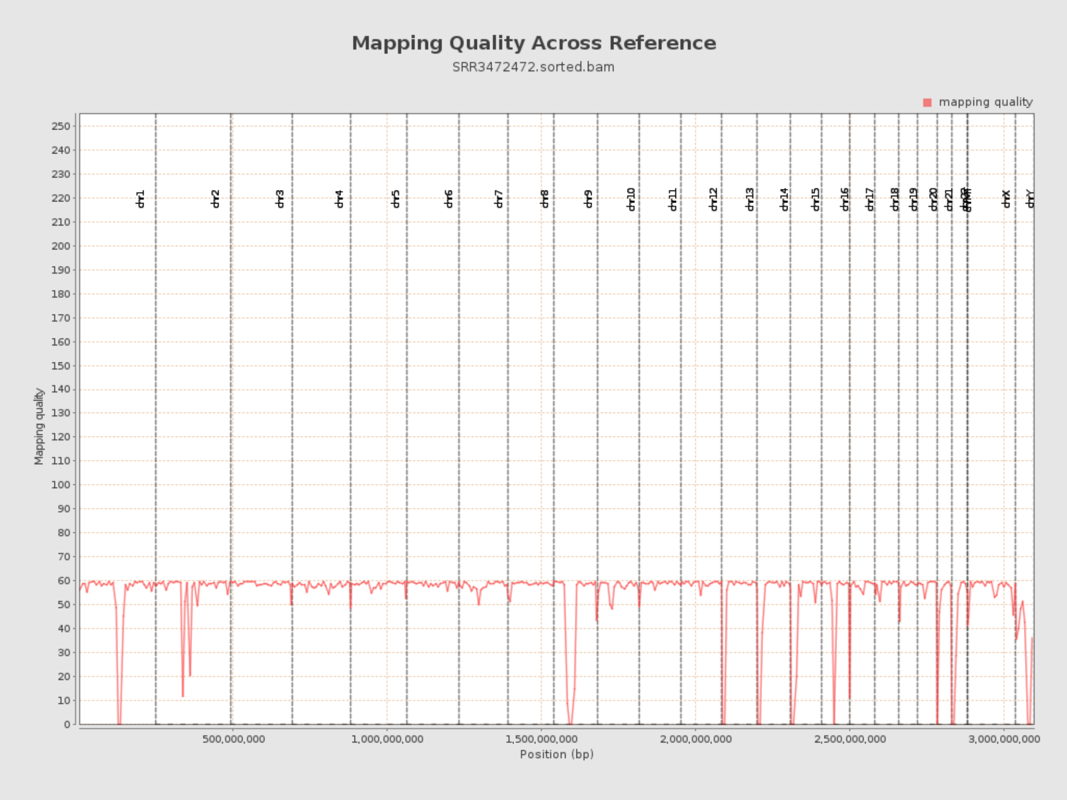
10. Results : Mapped Reads Clipping Profile



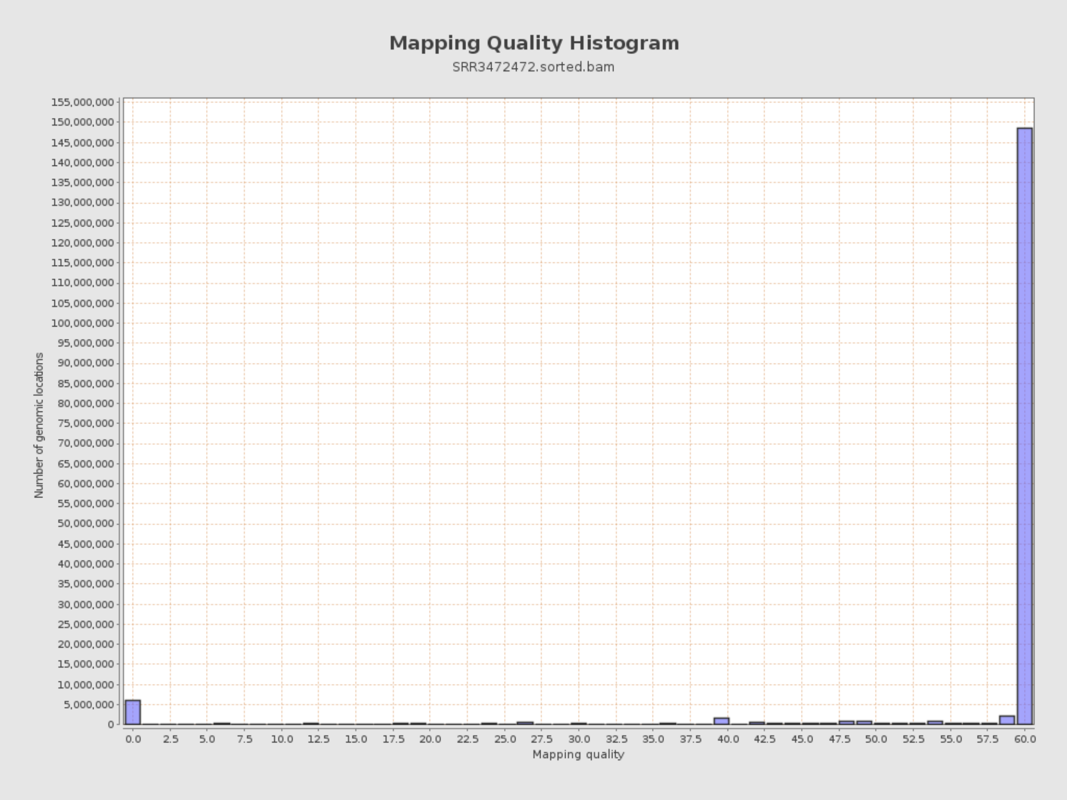
11. Results : Homopolymer Indels



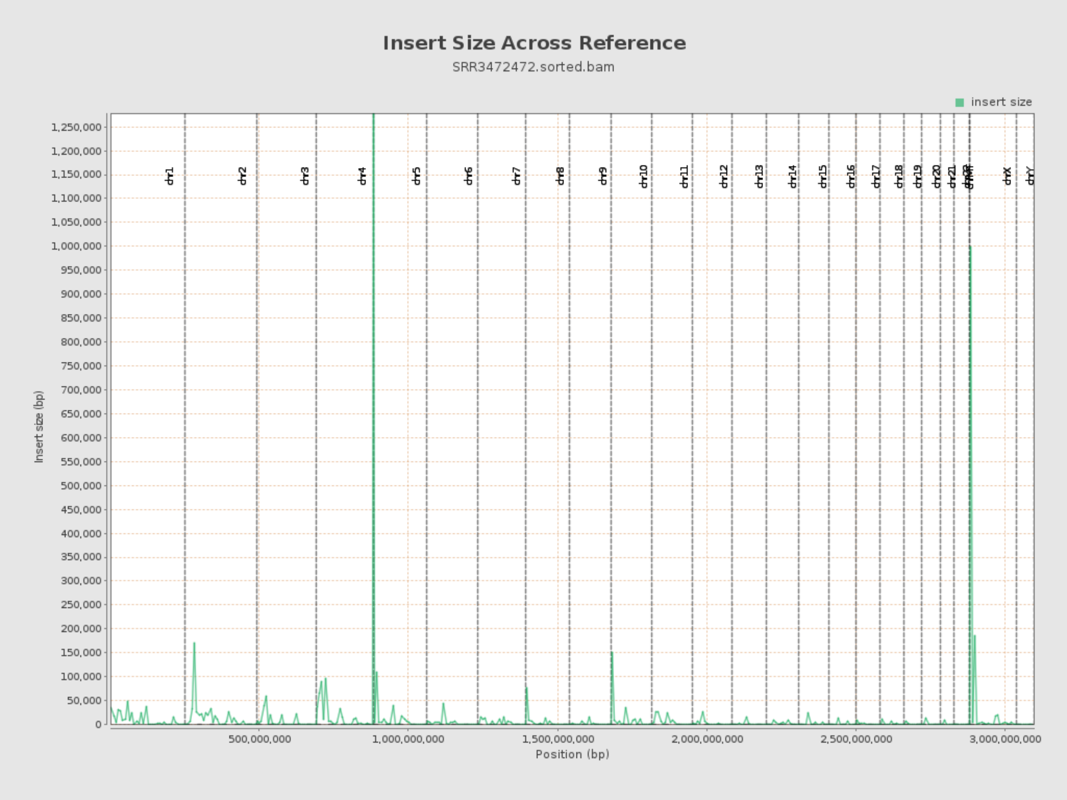
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram