Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 12:31:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472495.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_SRR3472495 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472495_1.fastq.gz SRR3472495_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 12:31:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472495.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,436,628
Mapped reads	15,279,379 / 98.98%
Unmapped reads	157,249 / 1.02%
Mapped paired reads	15,279,379 / 98.98%
Mapped reads, first in pair	7,664,915 / 49.65%
Mapped reads, second in pair	7,614,464 / 49.33%
Mapped reads, both in pair	15,192,878 / 98.42%
Mapped reads, singletons	86,501 / 0.56%
Secondary alignments	0
Supplementary alignments	51,557 / 0.33%
Read min/max/mean length	30 / 100 / 100.14
Duplicated reads (estimated)	9,416,685 / 61%
Duplication rate	44.72%
Clipped reads	1,225,853 / 7.94%

2.2. ACGT Content

Number/percentage of A's	409,707,628 / 27.23%
Number/percentage of C's	345,147,257 / 22.94%
Number/percentage of T's	406,967,624 / 27.05%
Number/percentage of G's	342,626,301 / 22.77%
Number/percentage of N's	232,342 / 0.02%

GC Percentage	45.71%

2.3. Coverage

Mean	0.4861
Standard Deviation	18.8035

2.4. Mapping Quality

Mean Mapping Quality	55.18

2.5. Insert size

Mean	26,235.6
Standard Deviation	1,655,760.19
P25/Median/P75	171 / 238 / 321

2.6. Mismatches and indels

General error rate	0.62%
Mismatches	9,191,630
Insertions	79,084
Mapped reads with at least one insertion	0.51%
Deletions	75,632
Mapped reads with at least one deletion	0.49%
Homopolymer indels	44.29%

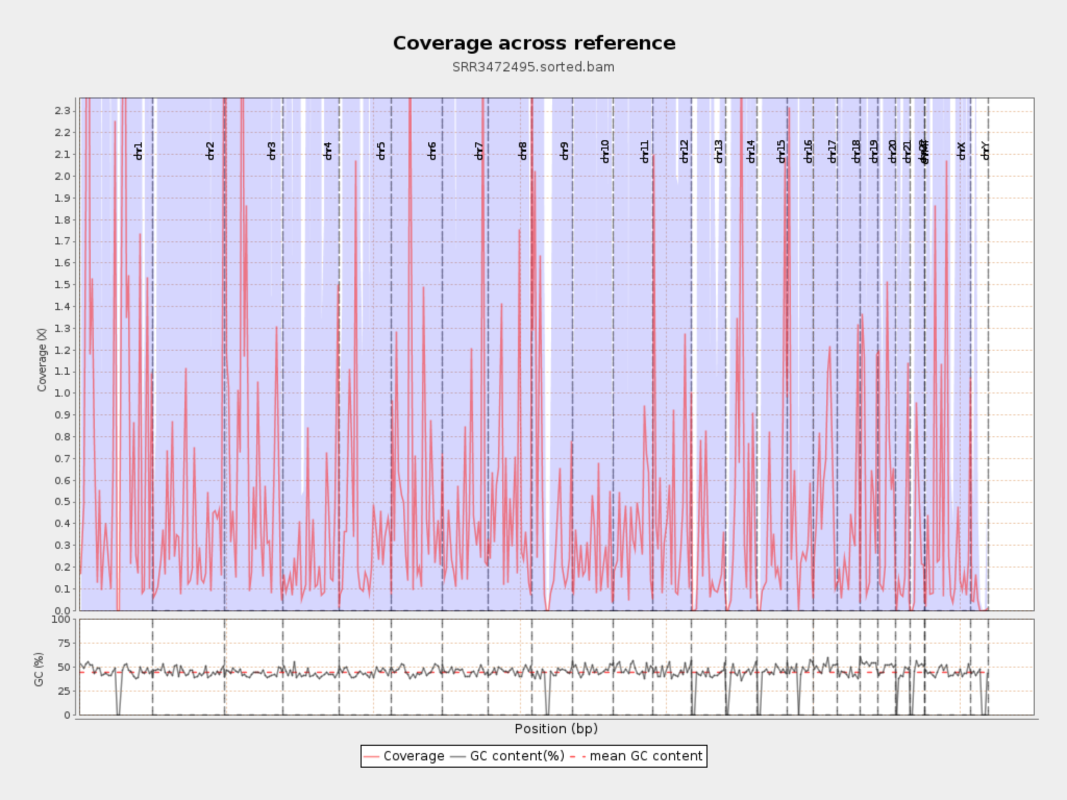
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard

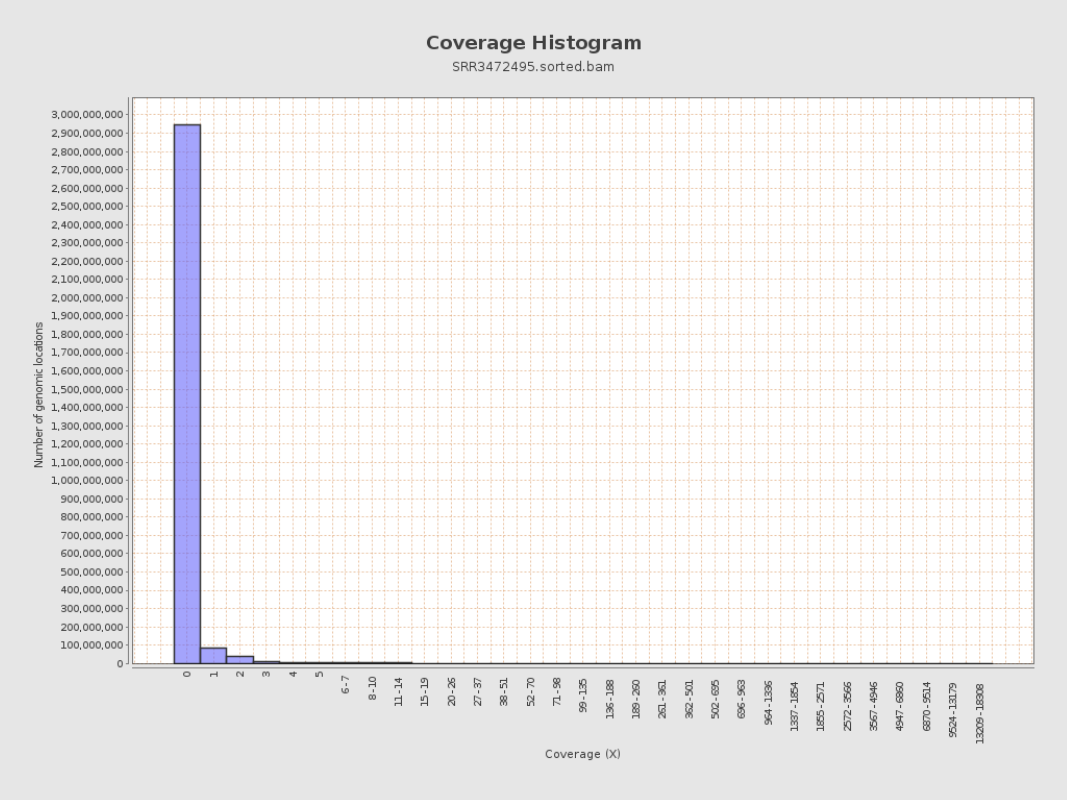
		bases	coverage	deviation
chr1	249250621	239069795	0.9592	43.5876
chr2	243199373	88639743	0.3645	13.1735
chr3	198022430	155105022	0.7833	17.9698
chr4	191154276	53144341	0.278	10.9944
chr5	180915260	70046476	0.3872	11.2952
chr6	171115067	102675881	0.6	17.2387
chr7	159138663	76995390	0.4838	21.1102
chr8	146364022	72062167	0.4923	15.6172
chr9	141213431	72488669	0.5133	12.9104
chr10	135534747	36093924	0.2663	9.4778
chr11	135006516	51958280	0.3849	13.8139
chr12	133851895	67525248	0.5045	17.2385
chr13	115169878	27395483	0.2379	8.3722
chr14	107349540	60875393	0.5671	22.6829
chr15	102531392	43350528	0.4228	14.9513
chr16	90354753	45097915	0.4991	14.4067
chr17	81195210	47939025	0.5904	15.1084
chr18	78077248	27907016	0.3574	11.8016
chr19	59128983	34835670	0.5891	19.0766
chr20	63025520	37567547	0.5961	15.2496
chr21	48129895	12443575	0.2585	13.4004
chr22	51304566	15848074	0.3089	10.5443
chrMT	16571	2070	0.1249	0.377
chrX	155270560	63551891	0.4093	12.6501

chrY	59373566	2266185	0.0382	1.0603

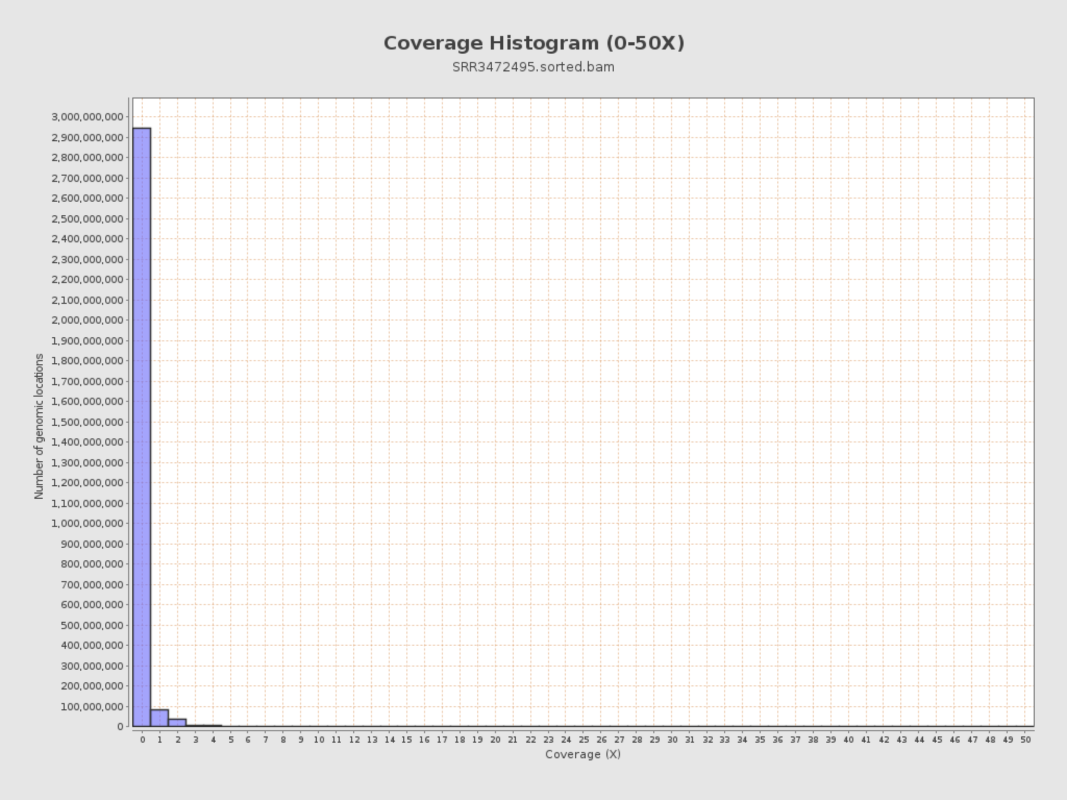
3. Results : Coverage across reference



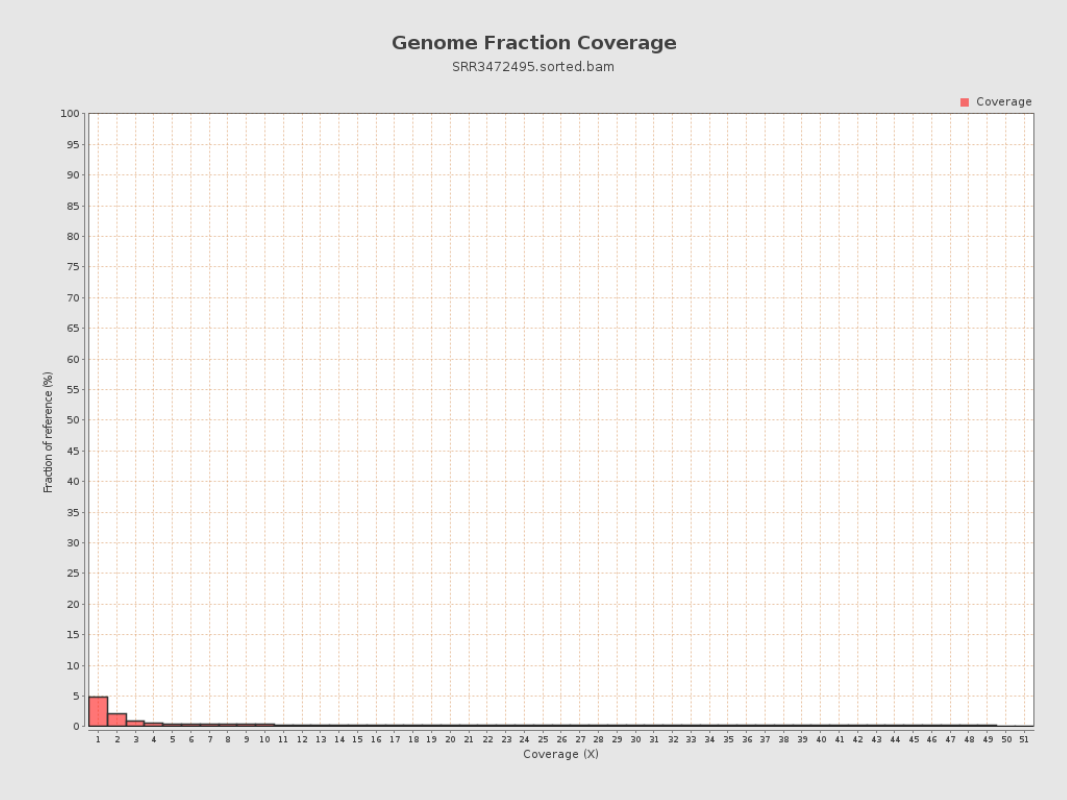
4. Results : Coverage Histogram



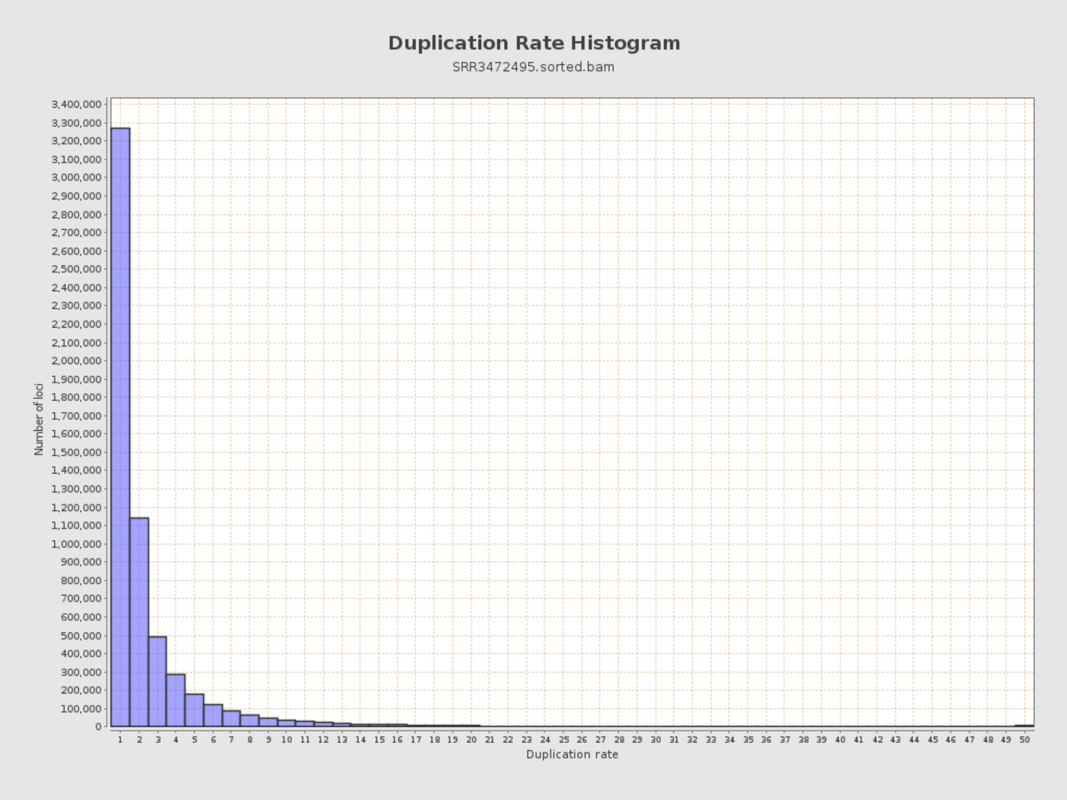
5. Results : Coverage Histogram (0-50X)



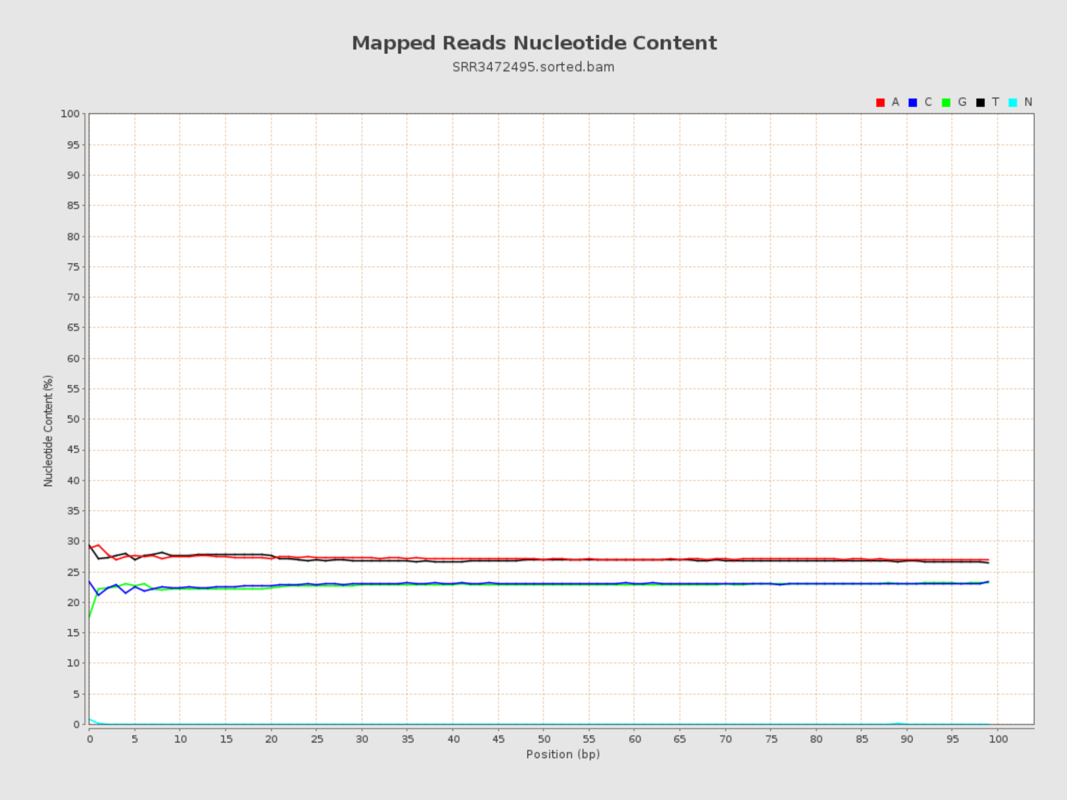
6. Results : Genome Fraction Coverage



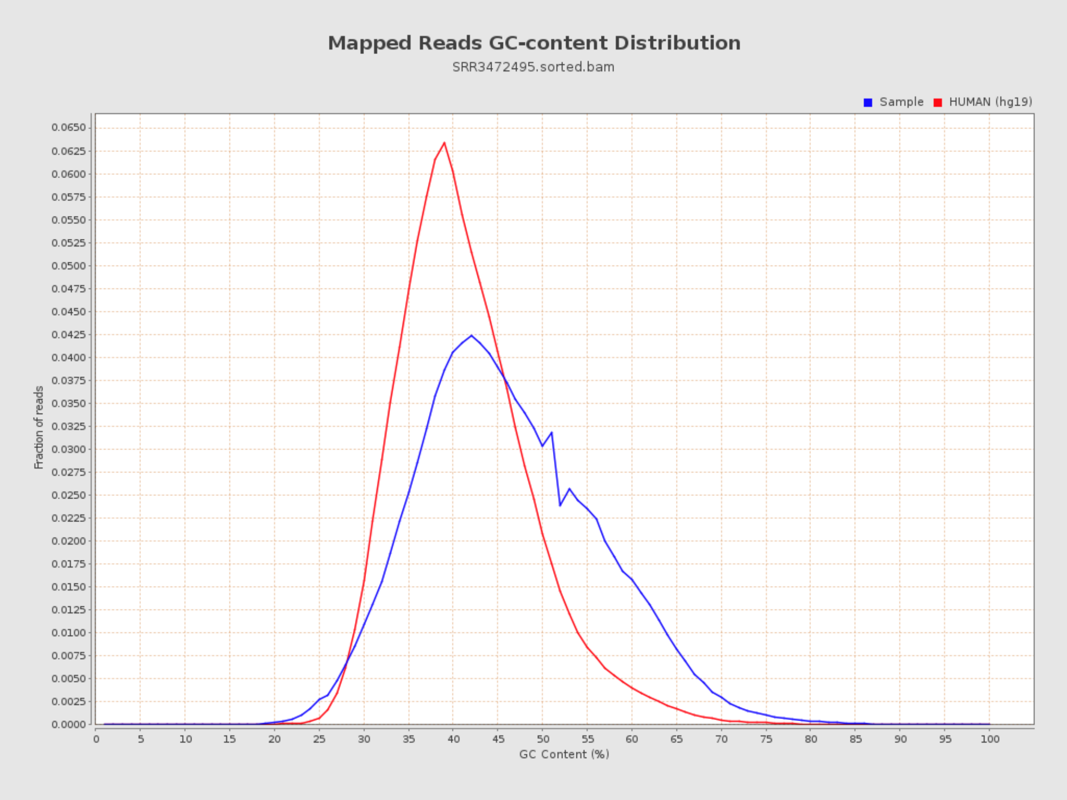
7. Results : Duplication Rate Histogram



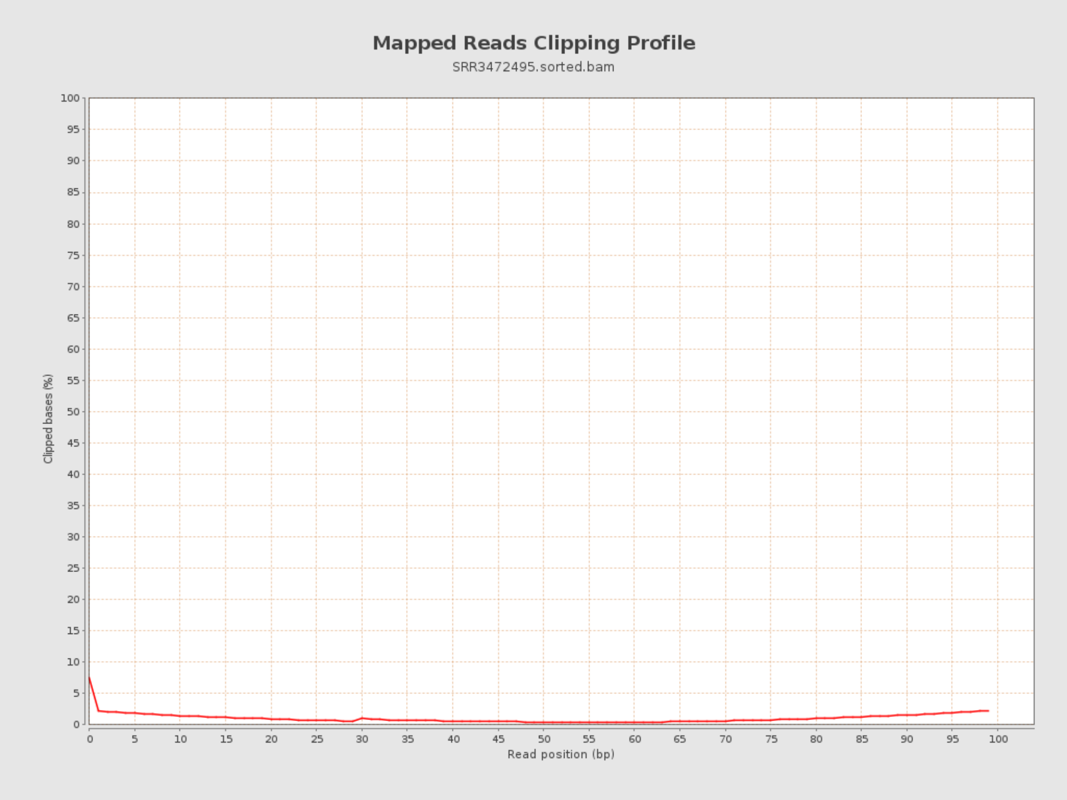
8. Results : Mapped Reads Nucleotide Content



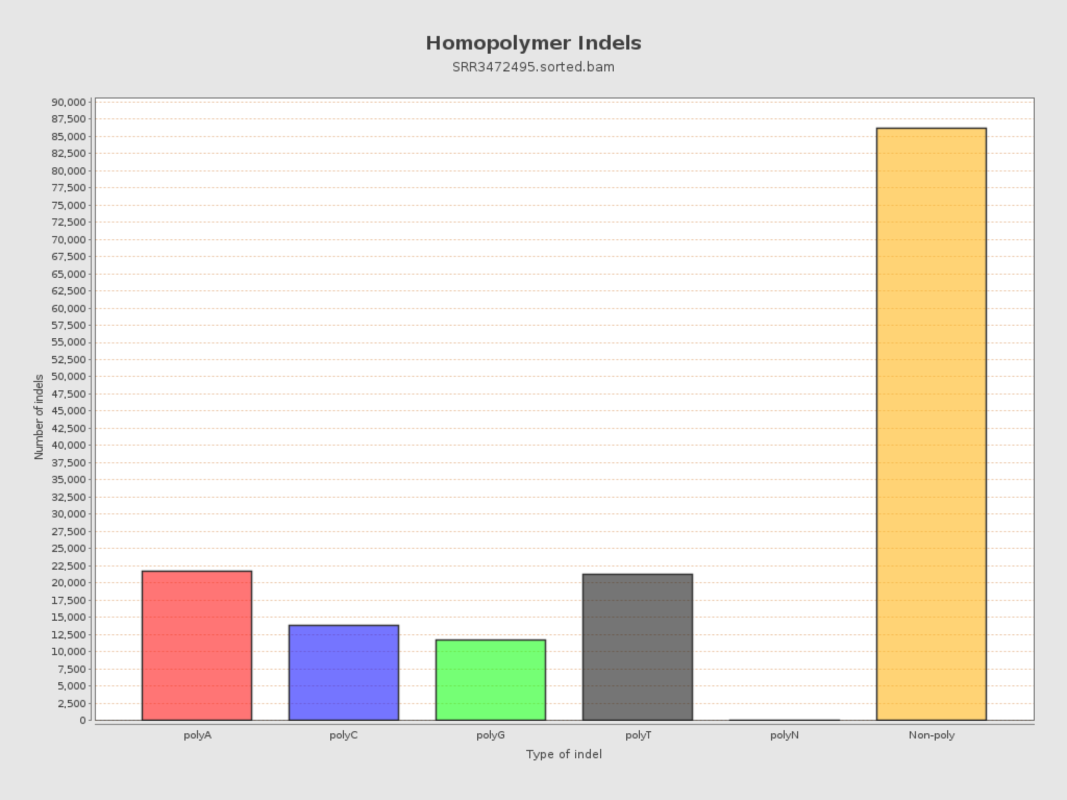
9. Results : Mapped Reads GC-content Distribution



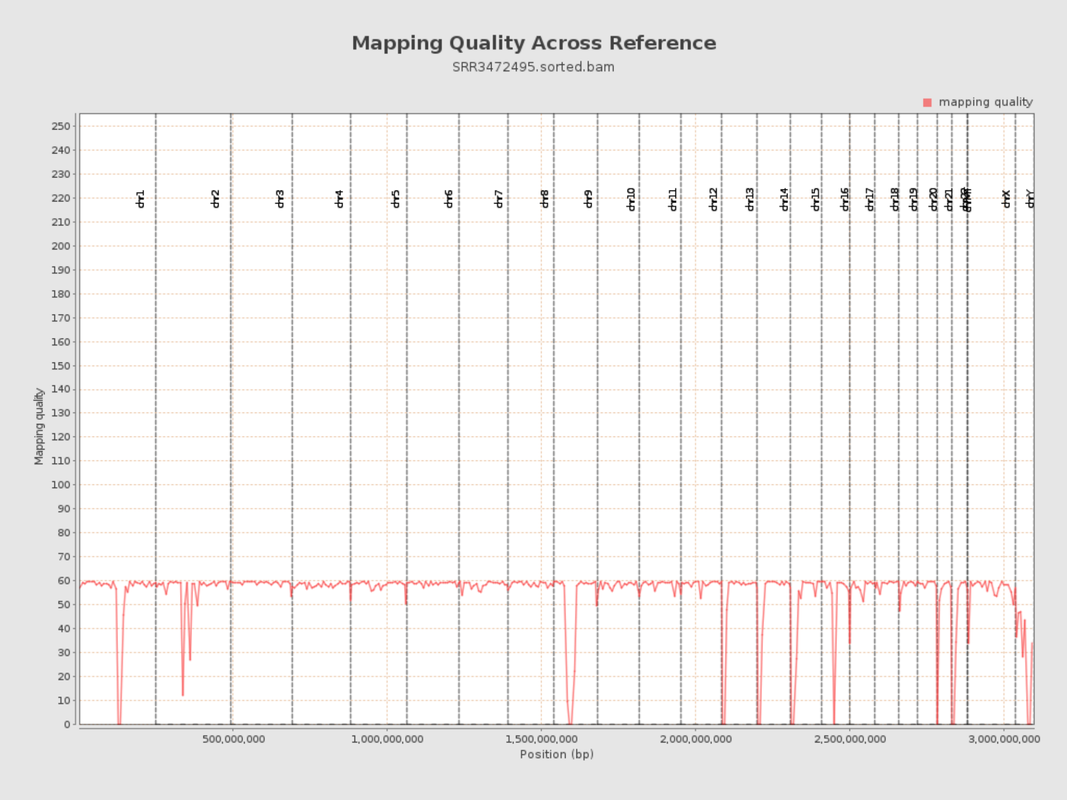
10. Results : Mapped Reads Clipping Profile



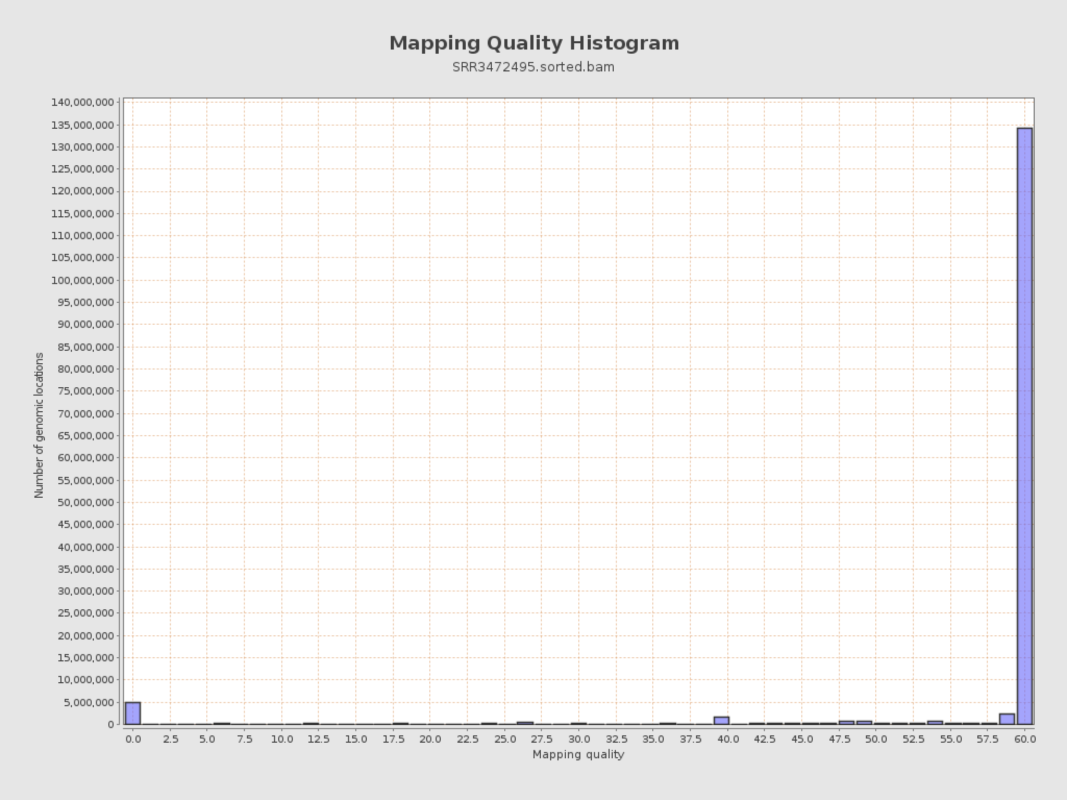
11. Results : Homopolymer Indels



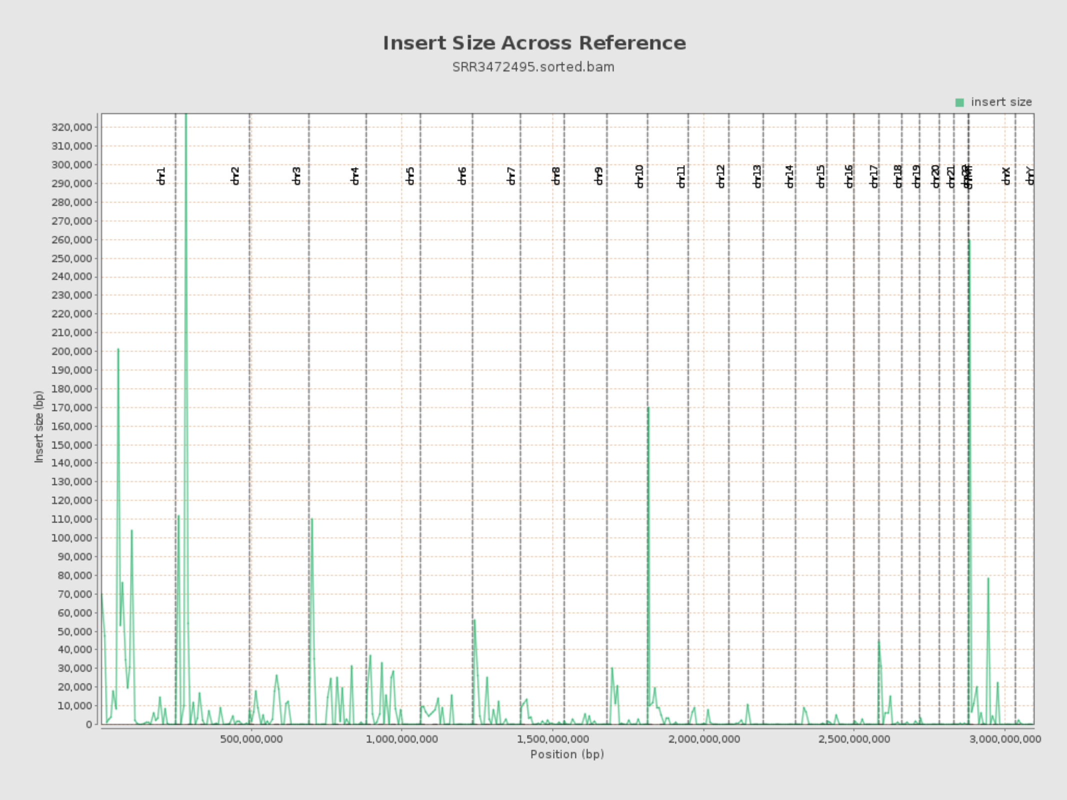
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram