Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 21:20:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472450.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_SRR3472450 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472450_1.fastq.gz SRR3472450_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 21:20:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472450.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,733,818
Mapped reads	18,595,335 / 99.26%
Unmapped reads	138,483 / 0.74%
Mapped paired reads	18,595,335 / 99.26%
Mapped reads, first in pair	9,317,846 / 49.74%
Mapped reads, second in pair	9,277,489 / 49.52%
Mapped reads, both in pair	18,512,036 / 98.82%
Mapped reads, singletons	83,299 / 0.44%
Secondary alignments	0
Supplementary alignments	71,217 / 0.38%
Read min/max/mean length	30 / 100 / 99.32
Duplicated reads (estimated)	12,055,270 / 64.35%
Duplication rate	47.81%
Clipped reads	1,346,849 / 7.19%

2.2. ACGT Content

Number/percentage of A's	493,082,419 / 27.08%
Number/percentage of C's	418,731,921 / 22.99%
Number/percentage of T's	494,376,915 / 27.15%
Number/percentage of G's	414,655,357 / 22.77%
Number/percentage of N's	230,035 / 0.01%

GC Percentage	45.76%

2.3. Coverage

Mean	0.5883
Standard Deviation	19.5095

2.4. Mapping Quality

Mean Mapping Quality	54.66

2.5. Insert size

Mean	16,403.15
Standard Deviation	1,276,893.47
P25/Median/P75	149 / 206 / 276

2.6. Mismatches and indels

General error rate	0.54%
Mismatches	9,702,962
Insertions	104,566
Mapped reads with at least one insertion	0.56%
Deletions	86,717
Mapped reads with at least one deletion	0.46%
Homopolymer indels	46.88%

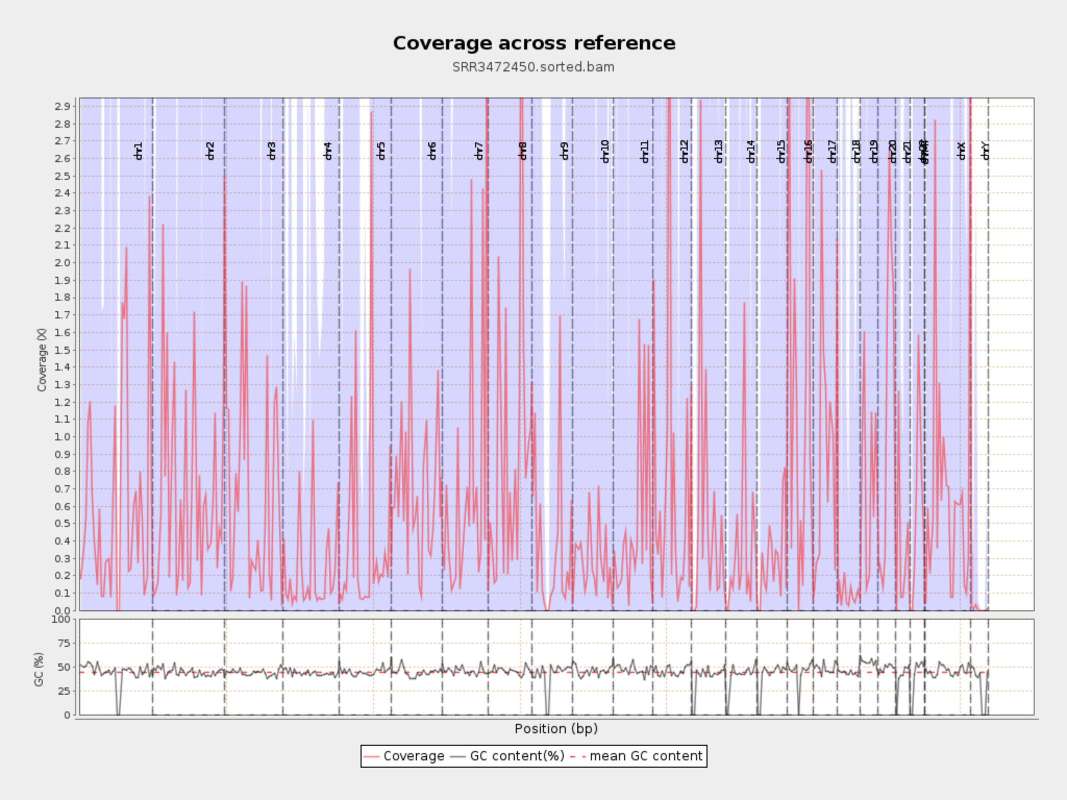
2.7. Chromosome stats

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

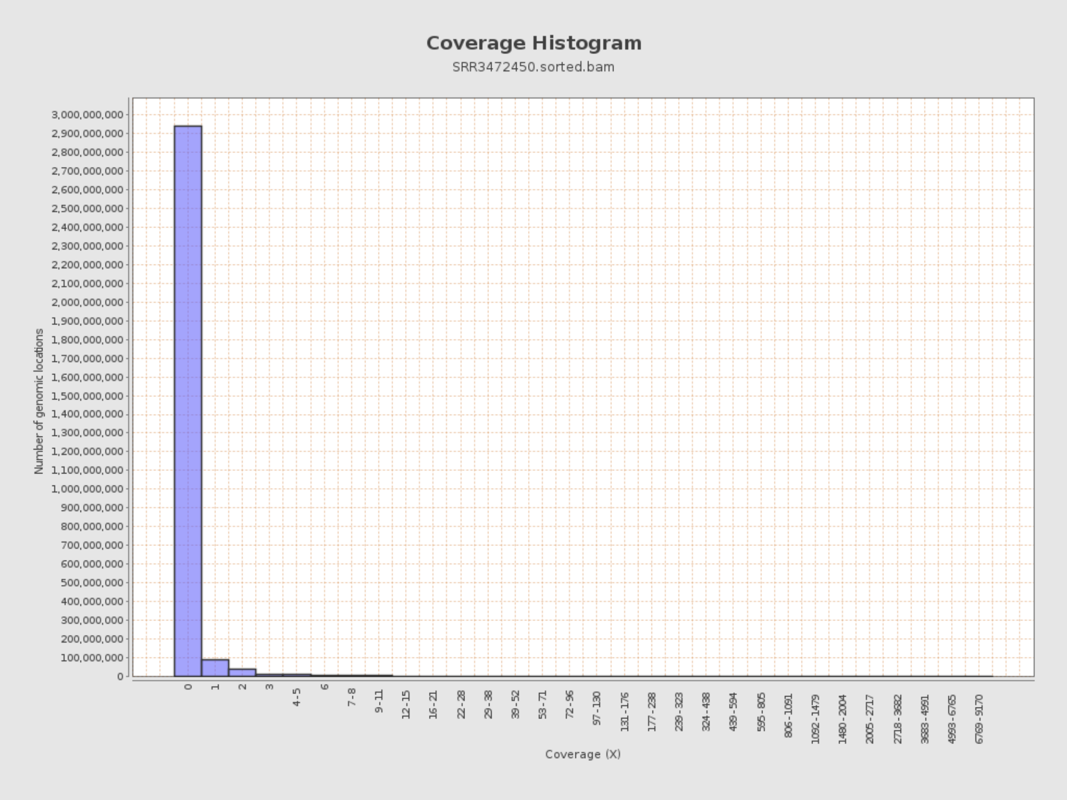
		bases	**coverage**	**deviation**
chr1	249250621	155225353	0.6228	17.9204
chr2	243199373	156091138	0.6418	22.078
chr3	198022430	137572165	0.6947	17.4248
chr4	191154276	43603413	0.2281	8.7794
chr5	180915260	77954945	0.4309	19.5095
chr6	171115067	117998250	0.6896	15.6148
chr7	159138663	125810095	0.7906	25.5402
chr8	146364022	141513108	0.9669	24.5211
chr9	141213431	51764130	0.3666	13.6683
chr10	135534747	38747961	0.2859	11.9687
chr11	135006516	66633236	0.4936	17.7318
chr12	133851895	102492942	0.7657	26.0641
chr13	115169878	61100571	0.5305	18.3786
chr14	107349540	35925300	0.3347	11.7811
chr15	102531392	31356968	0.3058	8.3465
chr16	90354753	122789804	1.359	36.0734
chr17	81195210	79187370	0.9753	26.4889
chr18	78077248	7379920	0.0945	3.2935
chr19	59128983	46326931	0.7835	18.5709
chr20	63025520	72626049	1.1523	32.1213
chr21	48129895	17091447	0.3551	22.5914
chr22	51304566	28875654	0.5628	20.7442
chrMT	16571	658	0.0397	0.2371
chrX	155270560	102691231	0.6614	18.7481

chrY	59373566	519983	0.0088	0.9494

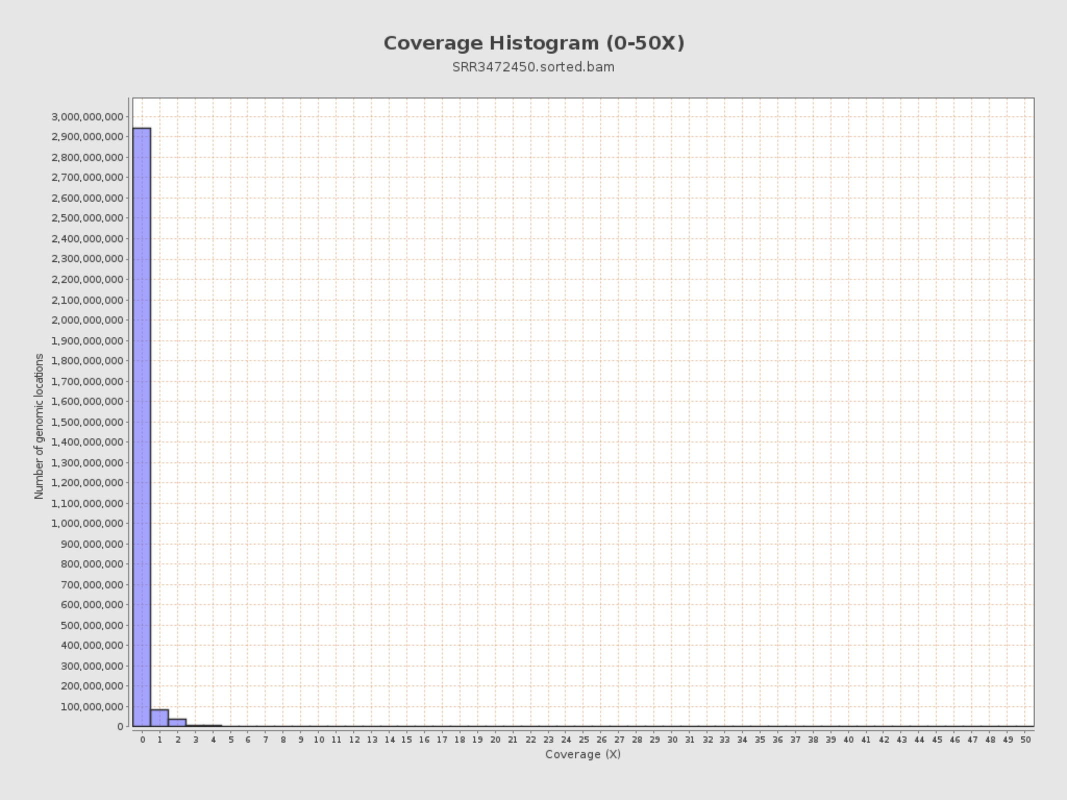
3. Results : Coverage across reference



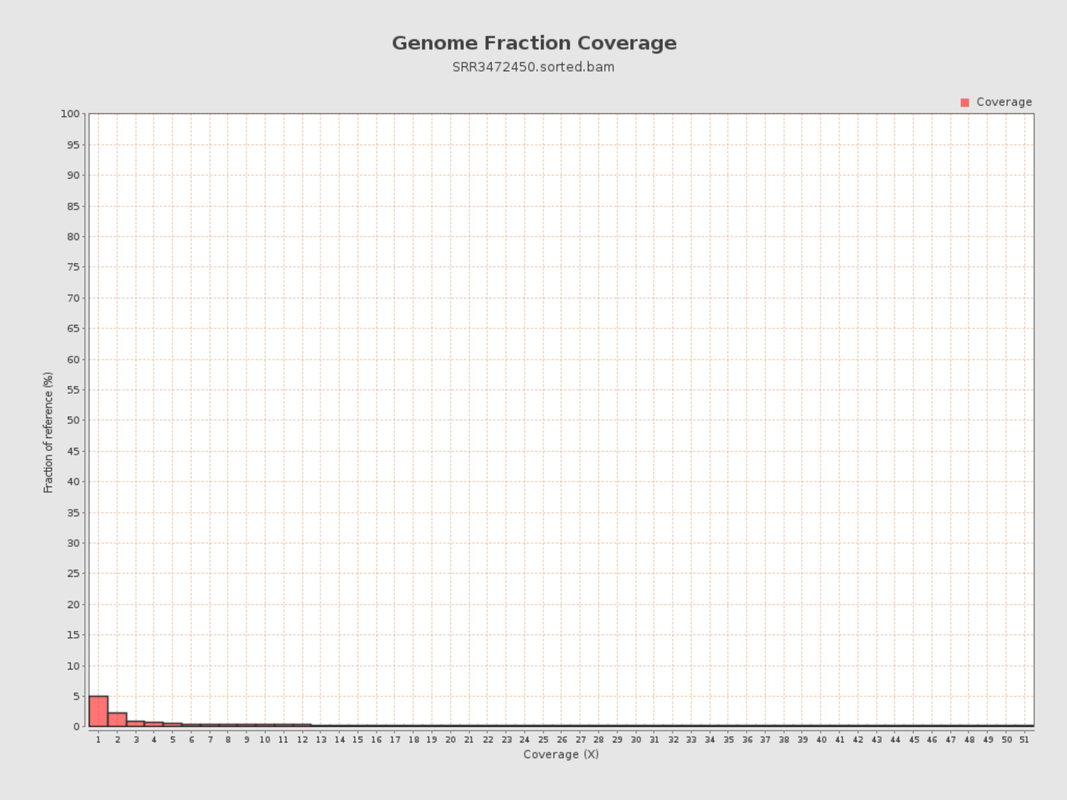
4. Results : Coverage Histogram



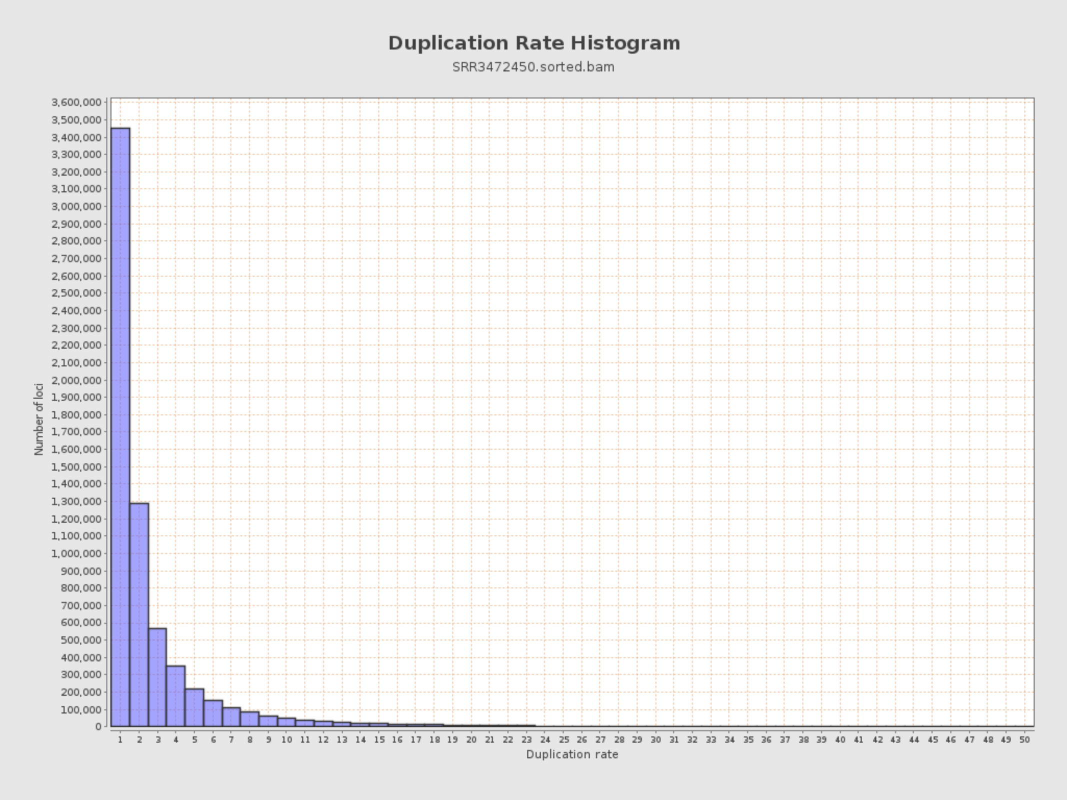
5. Results : Coverage Histogram (0-50X)



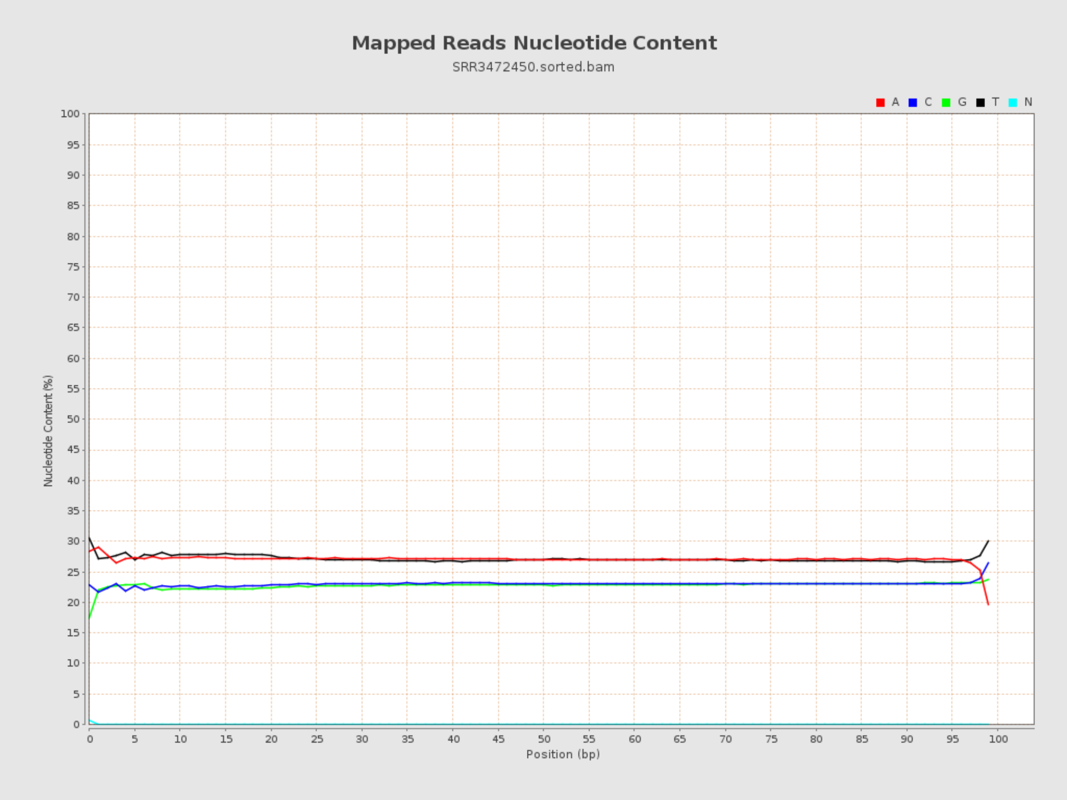
6. Results : Genome Fraction Coverage



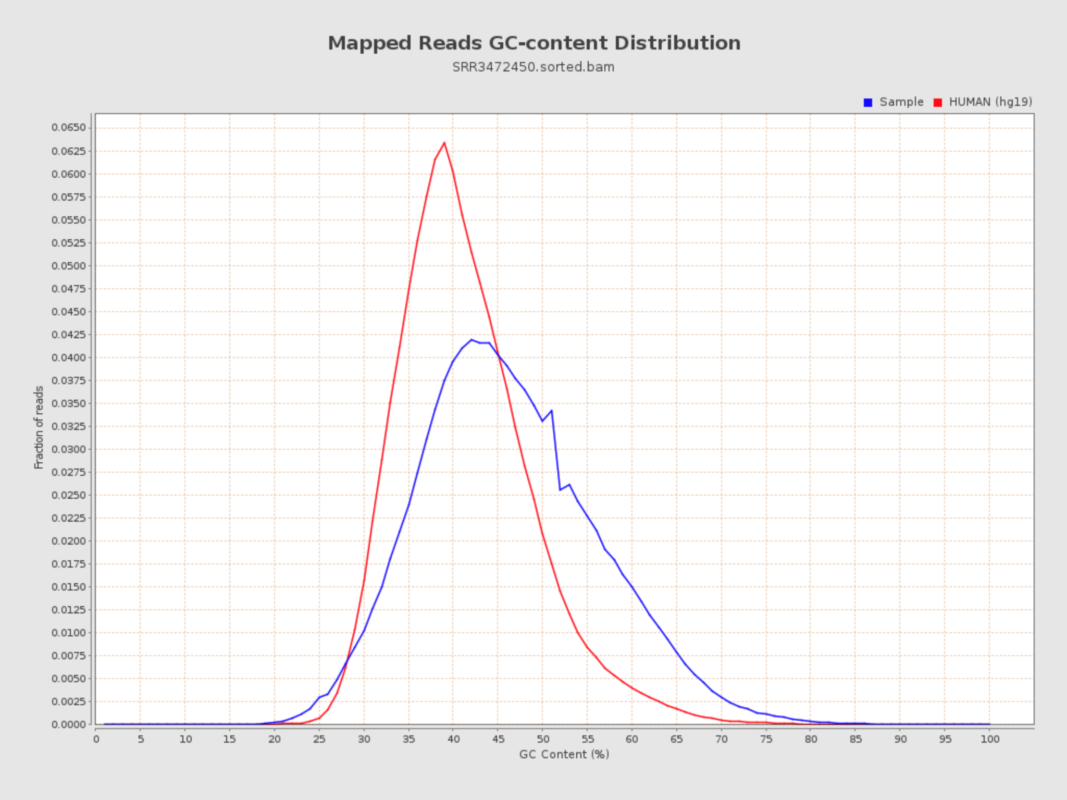
7. Results : Duplication Rate Histogram



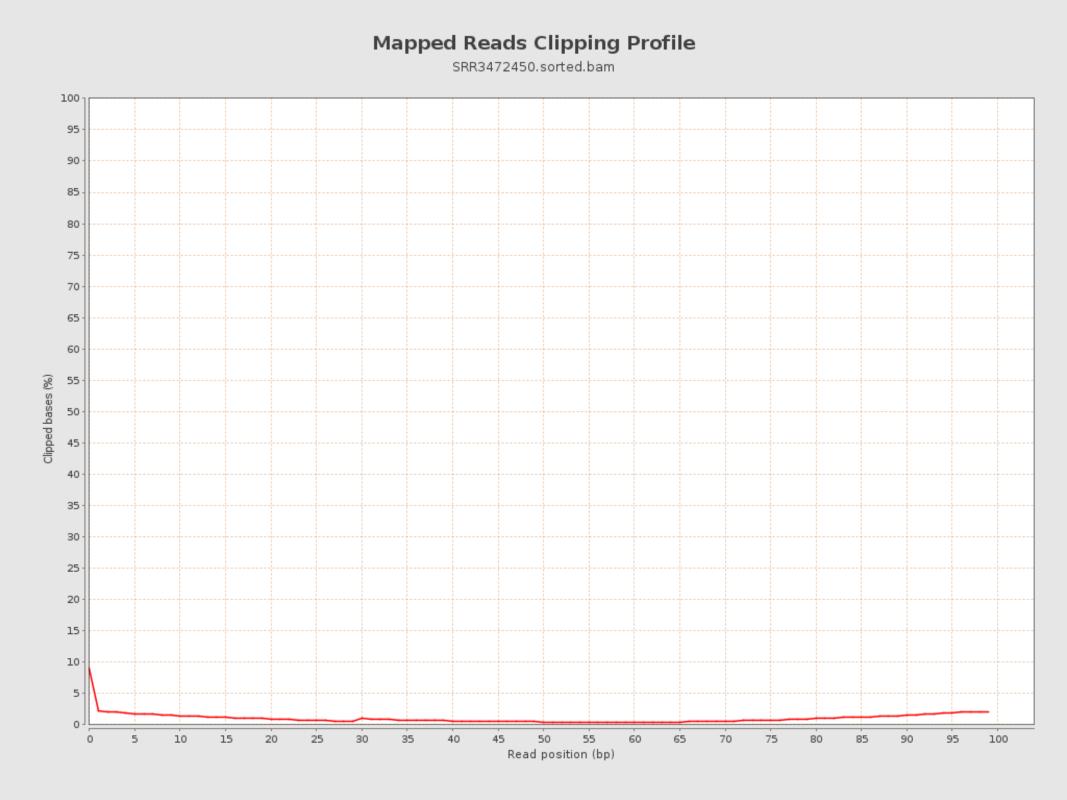
8. Results : Mapped Reads Nucleotide Content



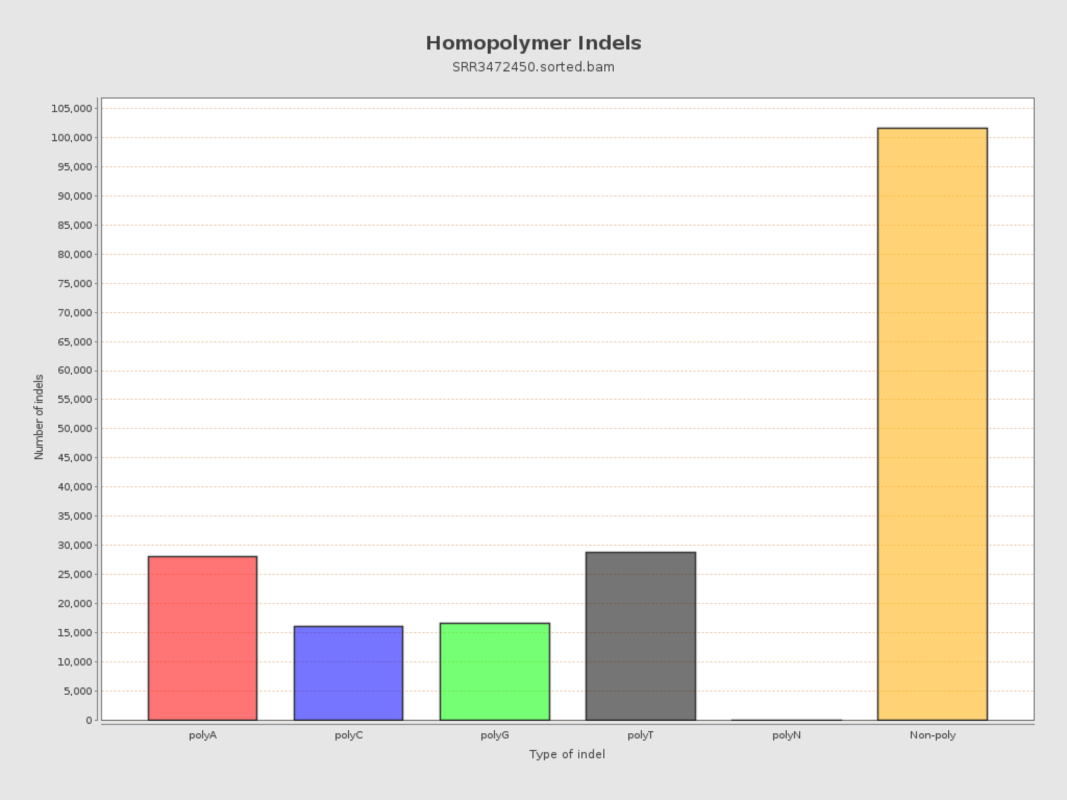
9. Results : Mapped Reads GC-content Distribution



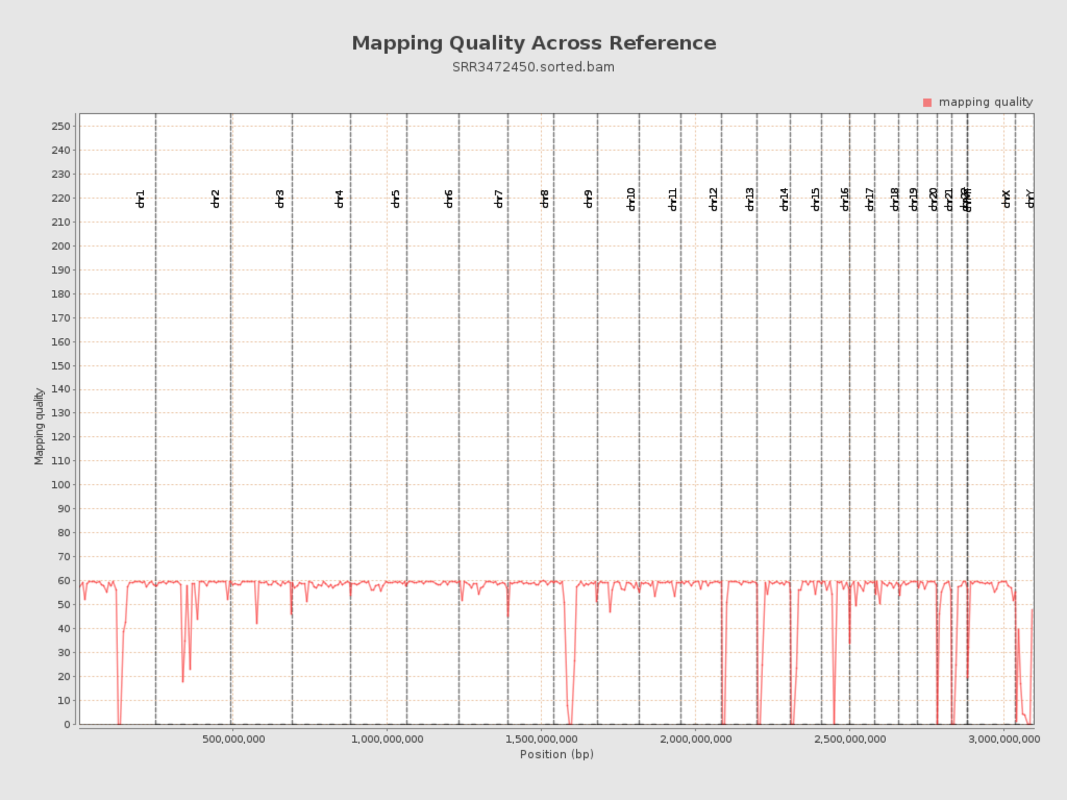
10. Results : Mapped Reads Clipping Profile



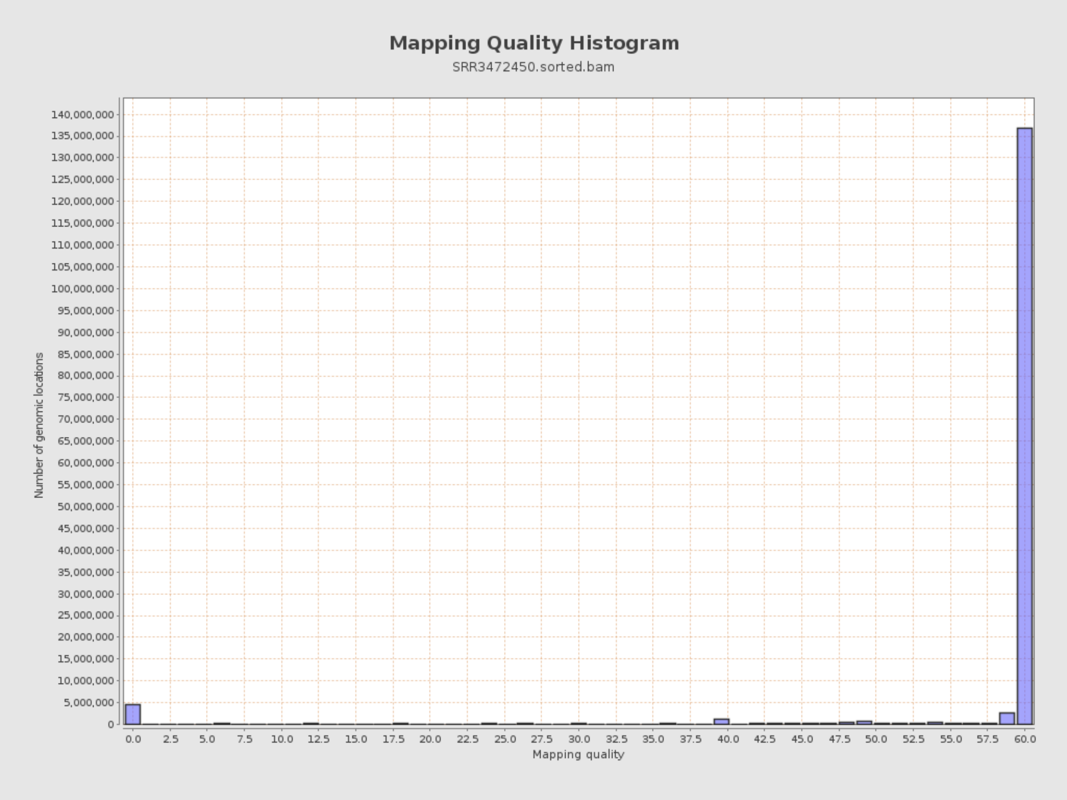
11. Results : Homopolymer Indels



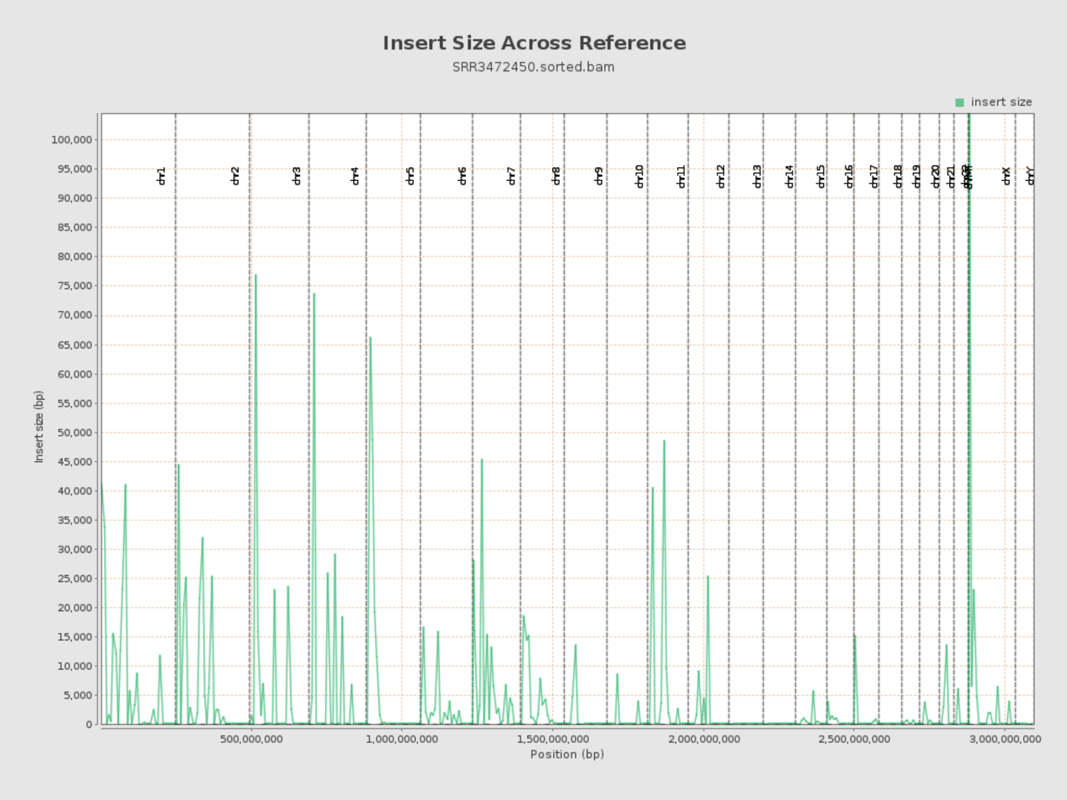
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram