Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 05:35:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472473.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_SRR3472473 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472473_1.fastq.gz SRR3472473_2.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 05:35:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472473.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,228,334
Mapped reads	18,898,369 / 98.28%
Unmapped reads	329,965 / 1.72%
Mapped paired reads	18,898,369 / 98.28%
Mapped reads, first in pair	9,474,826 / 49.28%
Mapped reads, second in pair	9,423,543 / 49.01%
Mapped reads, both in pair	18,787,392 / 97.71%
Mapped reads, singletons	110,977 / 0.58%
Secondary alignments	0
Supplementary alignments	86,470 / 0.45%
Read min/max/mean length	30 / 100 / 100.18
Duplicated reads (estimated)	12,359,910 / 64.28%
Duplication rate	45.33%
Clipped reads	1,900,340 / 9.88%

2.2. ACGT Content

Number/percentage of A's	513,124,735 / 27.7%
Number/percentage of C's	415,622,635 / 22.43%
Number/percentage of T's	508,992,443 / 27.47%
Number/percentage of G's	414,554,470 / 22.38%
Number/percentage of N's	289,876 / 0.02%

GC Percentage	44.81%

2.3. Coverage

Mean	0.5985
Standard Deviation	23.3997

2.4. Mapping Quality

Mean Mapping Quality	54.86

2.5. Insert size

Mean	29,978.89
Standard Deviation	1,641,089.13
P25/Median/P75	156 / 220 / 300

2.6. Mismatches and indels

General error rate	0.59%
Mismatches	10,654,389
Insertions	97,644
Mapped reads with at least one insertion	0.51%
Deletions	92,956
Mapped reads with at least one deletion	0.48%
Homopolymer indels	44.79%

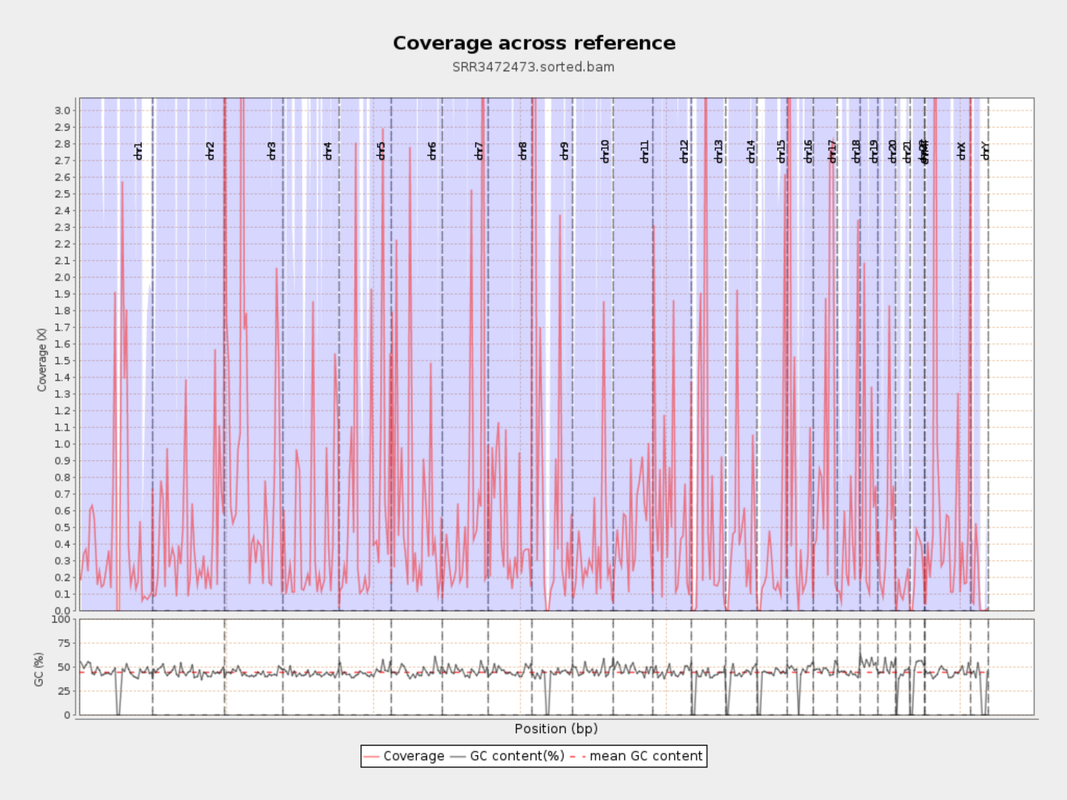
2.7. Chromosome stats

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

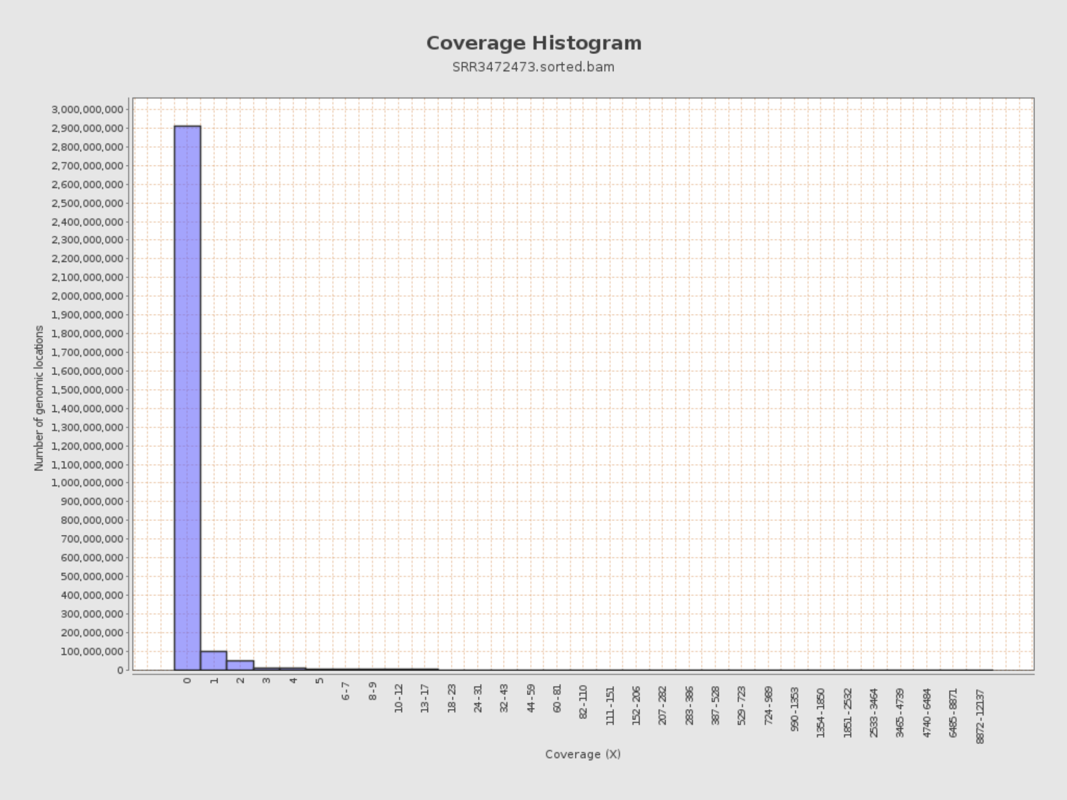
		bases	coverage	deviation
chr1	249250621	115728056	0.4643	15.9093
chr2	243199373	105818486	0.4351	16.7457
chr3	198022430	203805619	1.0292	27.5771
chr4	191154276	85510704	0.4473	16.4884
chr5	180915260	126944808	0.7017	26.008
chr6	171115067	111877586	0.6538	26.5019
chr7	159138663	109509497	0.6881	37.4311
chr8	146364022	71474278	0.4883	14.3578
chr9	141213431	124193953	0.8795	27.9726
chr10	135534747	50448367	0.3722	17.3427
chr11	135006516	69569025	0.5153	17.3826
chr12	133851895	88101608	0.6582	21.103
chr13	115169878	80499418	0.699	34.0086
chr14	107349540	50391567	0.4694	18.0255
chr15	102531392	44122761	0.4303	21.2504
chr16	90354753	78634991	0.8703	27.7209
chr17	81195210	83597450	1.0296	43.1423
chr18	78077248	41409339	0.5304	17.9327
chr19	59128983	42604109	0.7205	23.3562
chr20	63025520	35333862	0.5606	21.3289
chr21	48129895	6212100	0.1291	5.6786
chr22	51304566	13021642	0.2538	7.5928
chrMT	16571	5344	0.3225	0.9297
chrX	155270560	106676959	0.687	23.3828

chrY	59373566	7321438	0.1233	7.4646

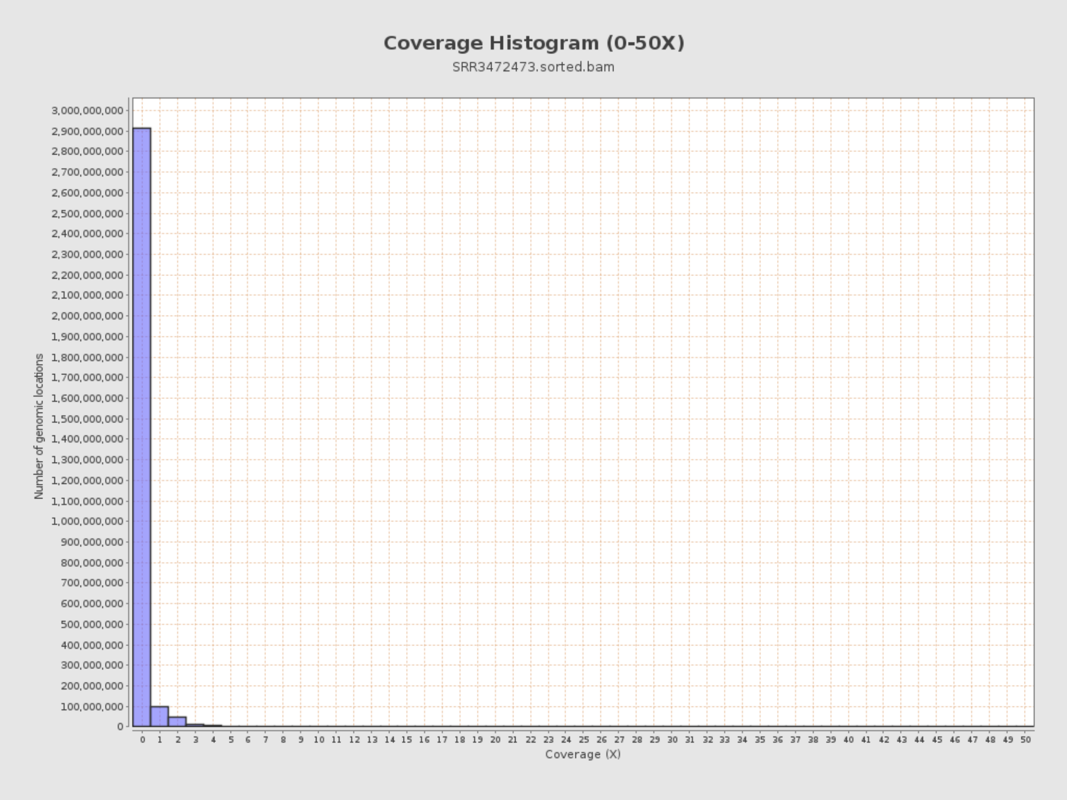
3. Results : Coverage across reference



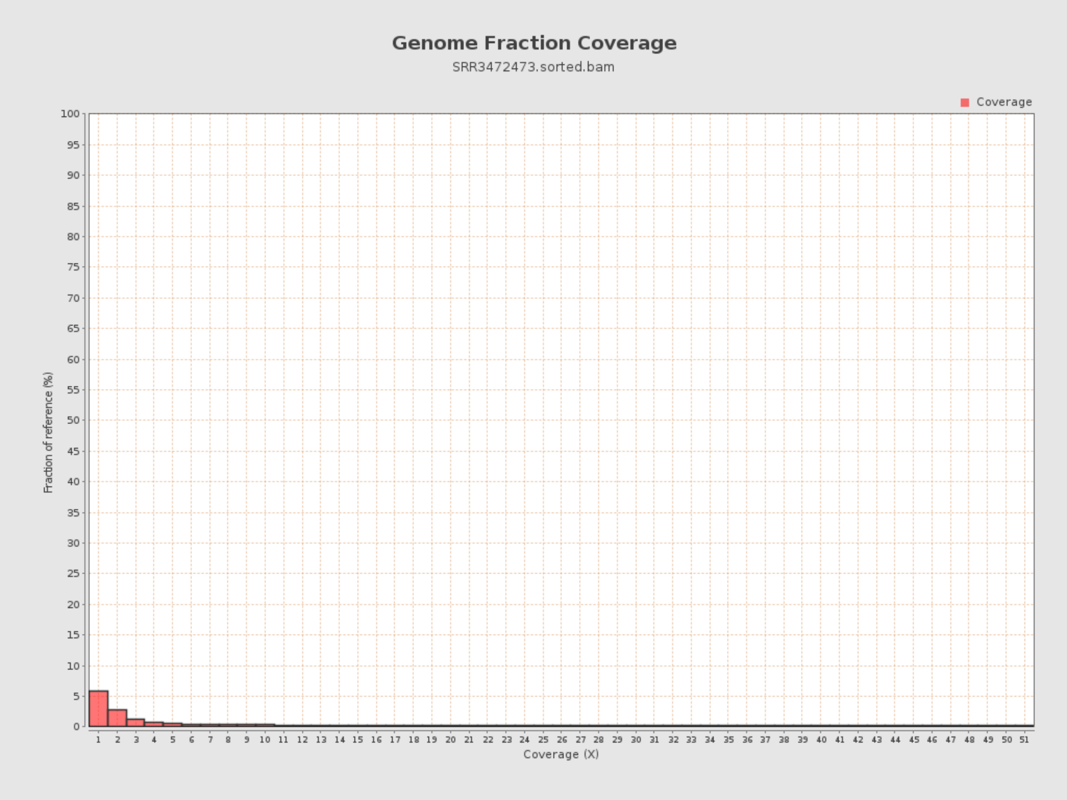
4. Results : Coverage Histogram



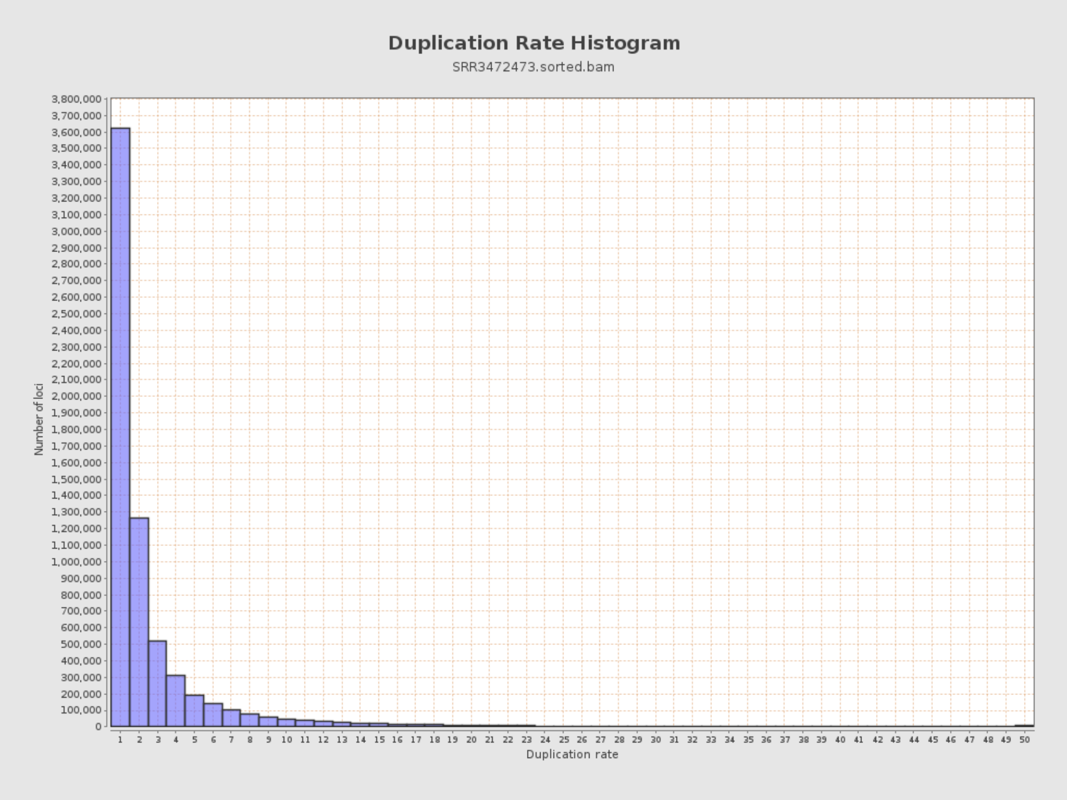
5. Results : Coverage Histogram (0-50X)



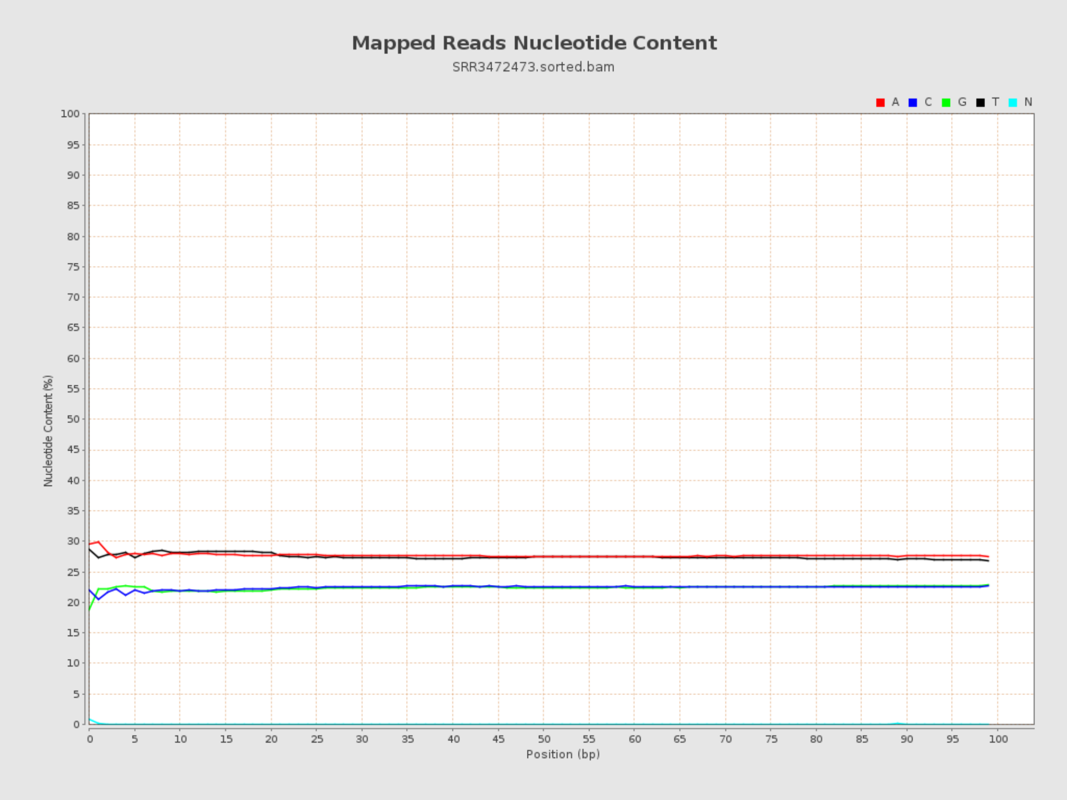
6. Results : Genome Fraction Coverage



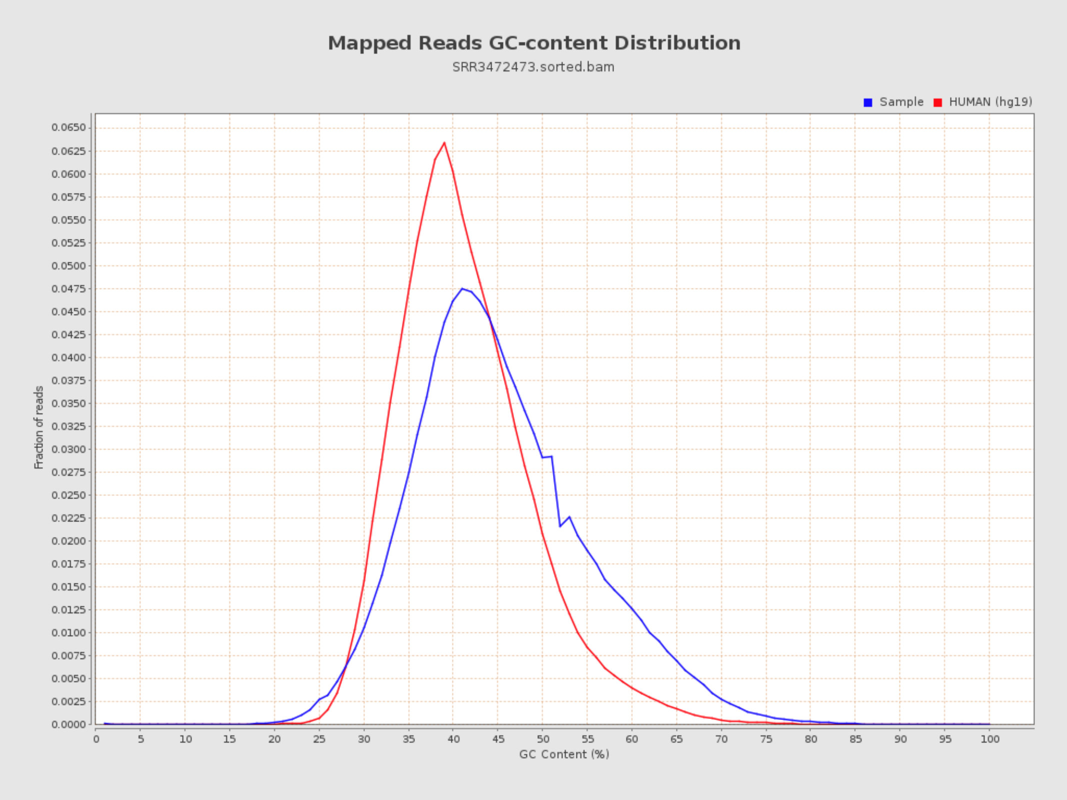
7. Results : Duplication Rate Histogram



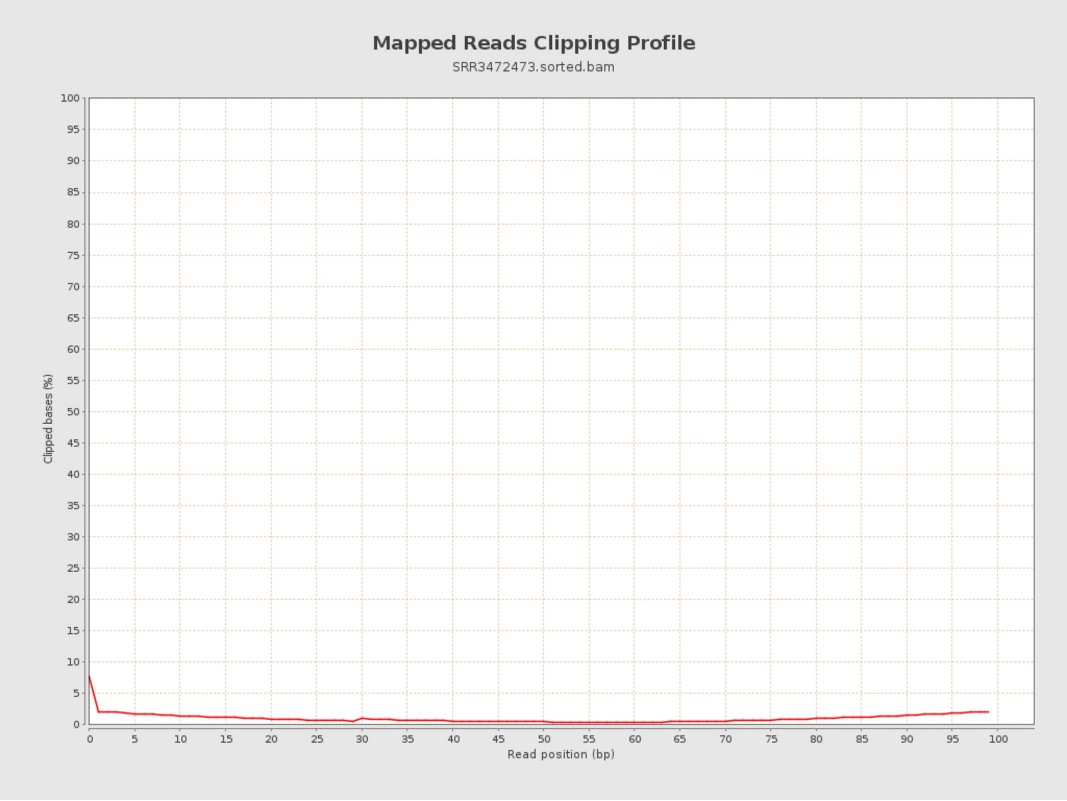
8. Results : Mapped Reads Nucleotide Content



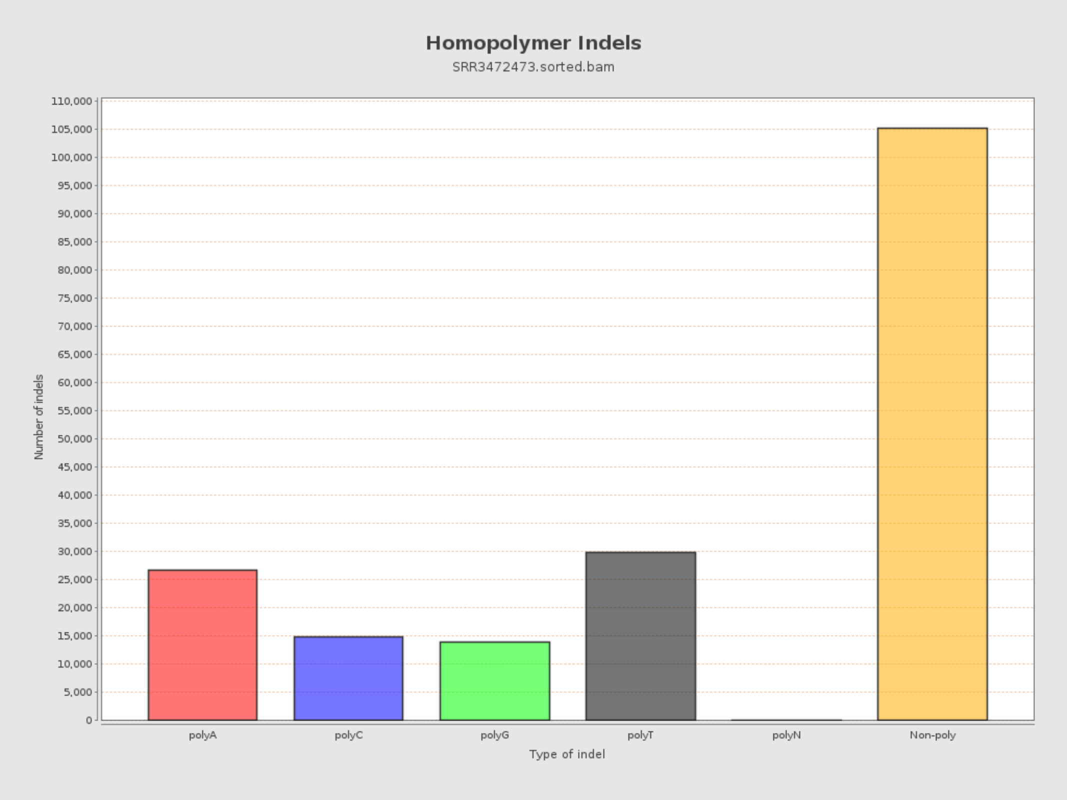
9. Results : Mapped Reads GC-content Distribution



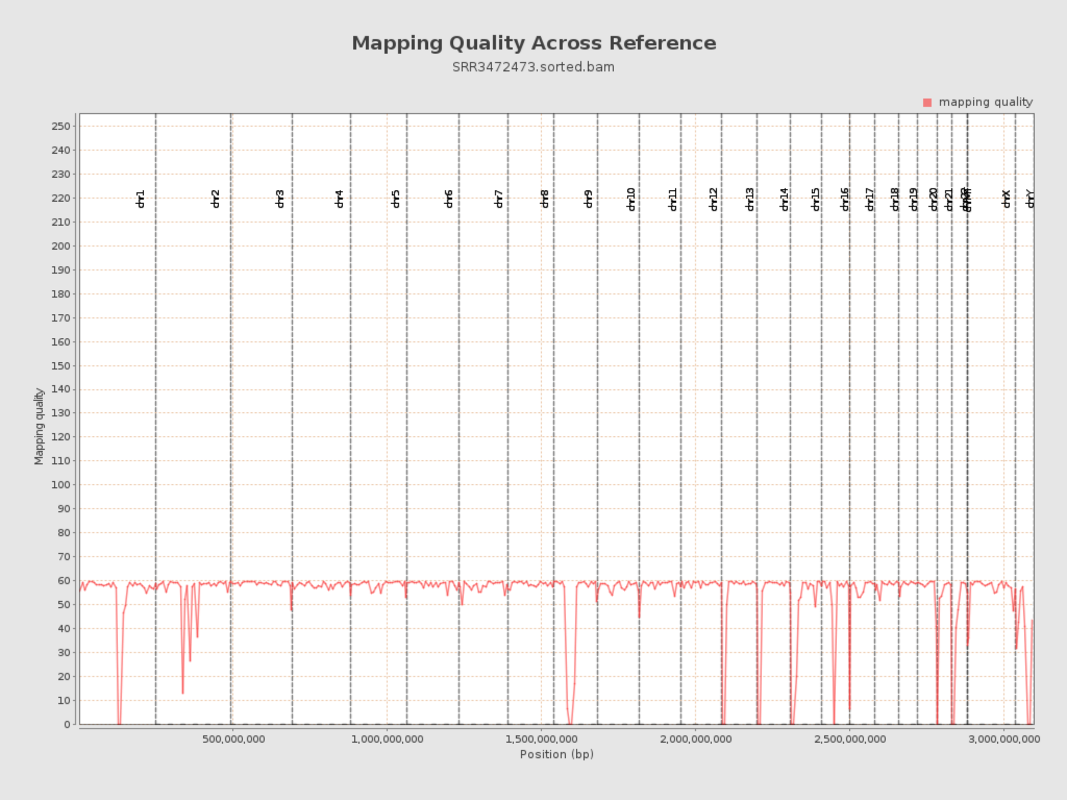
10. Results : Mapped Reads Clipping Profile



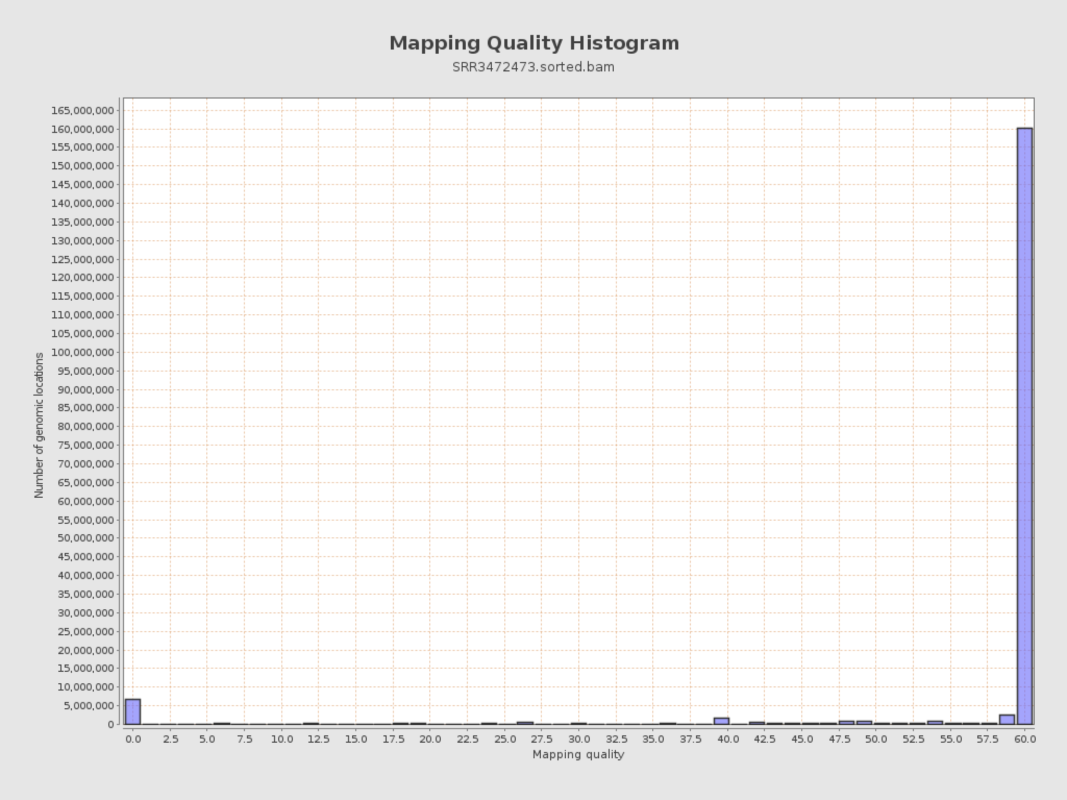
11. Results : Homopolymer Indels



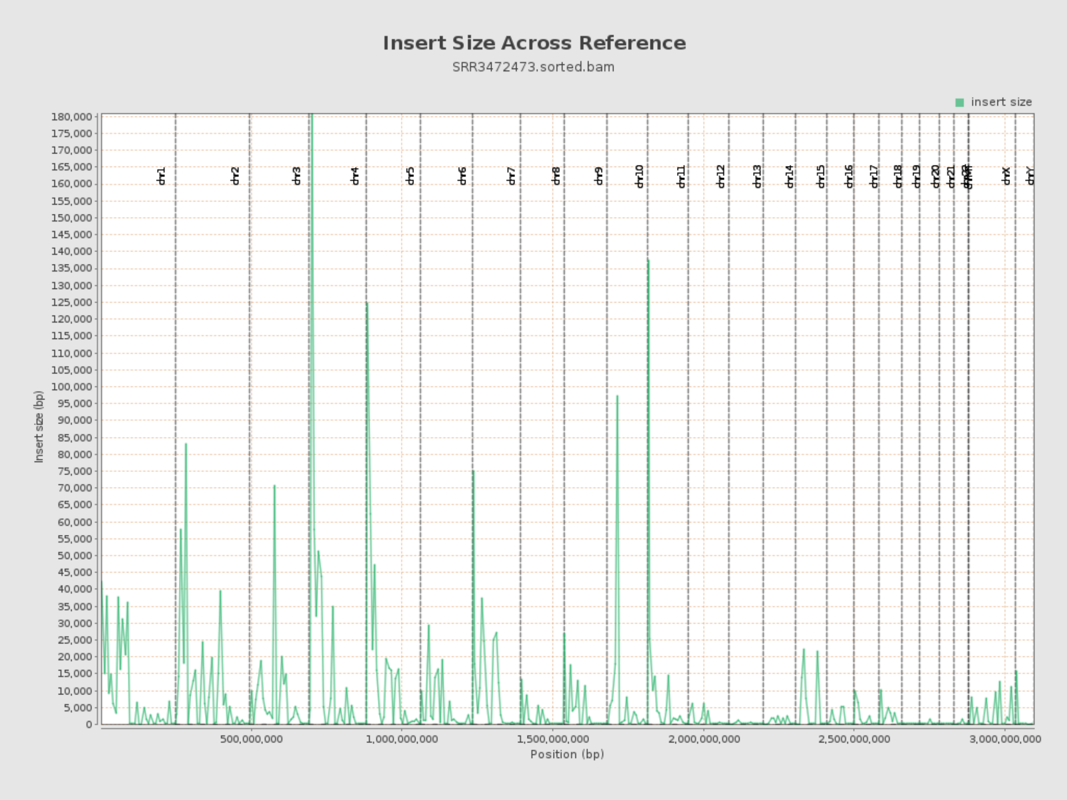
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram