Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 11:38:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472384.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_SRR3472384 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472384_1.fastq.gz SRR3472384_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 11:38:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472384.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	21,759,060
Mapped reads	21,579,527 / 99.17%
Unmapped reads	179,533 / 0.83%
Mapped paired reads	21,579,527 / 99.17%
Mapped reads, first in pair	10,830,604 / 49.78%
Mapped reads, second in pair	10,748,923 / 49.4%
Mapped reads, both in pair	21,457,634 / 98.61%
Mapped reads, singletons	121,893 / 0.56%
Secondary alignments	0
Supplementary alignments	82,407 / 0.38%
Read min/max/mean length	30 / 100 / 99.44
Duplicated reads (estimated)	13,783,826 / 63.35%
Duplication rate	49.02%
Clipped reads	1,434,418 / 6.59%

2.2. ACGT Content

Number/percentage of A's	576,997,775 / 27.24%
Number/percentage of C's	483,973,013 / 22.85%
Number/percentage of T's	577,186,275 / 27.25%
Number/percentage of G's	479,796,038 / 22.65%
Number/percentage of N's	263,563 / 0.01%

GC Percentage	45.5%

2.3. Coverage

Mean	0.6843
Standard Deviation	19.3865

2.4. Mapping Quality

Mean Mapping Quality	54.89

2.5. Insert size

Mean	20,369.95
Standard Deviation	1,394,624.38
P25/Median/P75	161 / 225 / 304

2.6. Mismatches and indels

General error rate	0.56%
Mismatches	11,572,756
Insertions	126,447
Mapped reads with at least one insertion	0.58%
Deletions	108,882
Mapped reads with at least one deletion	0.49%
Homopolymer indels	46.37%

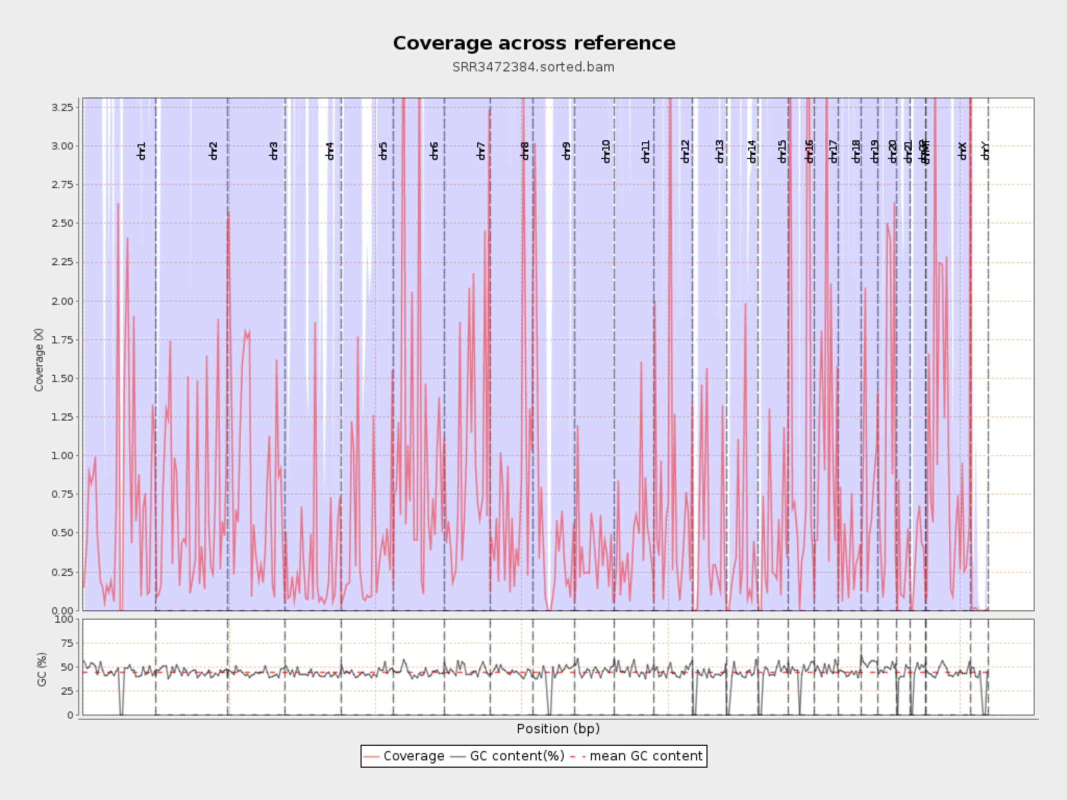
2.7. Chromosome stats

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

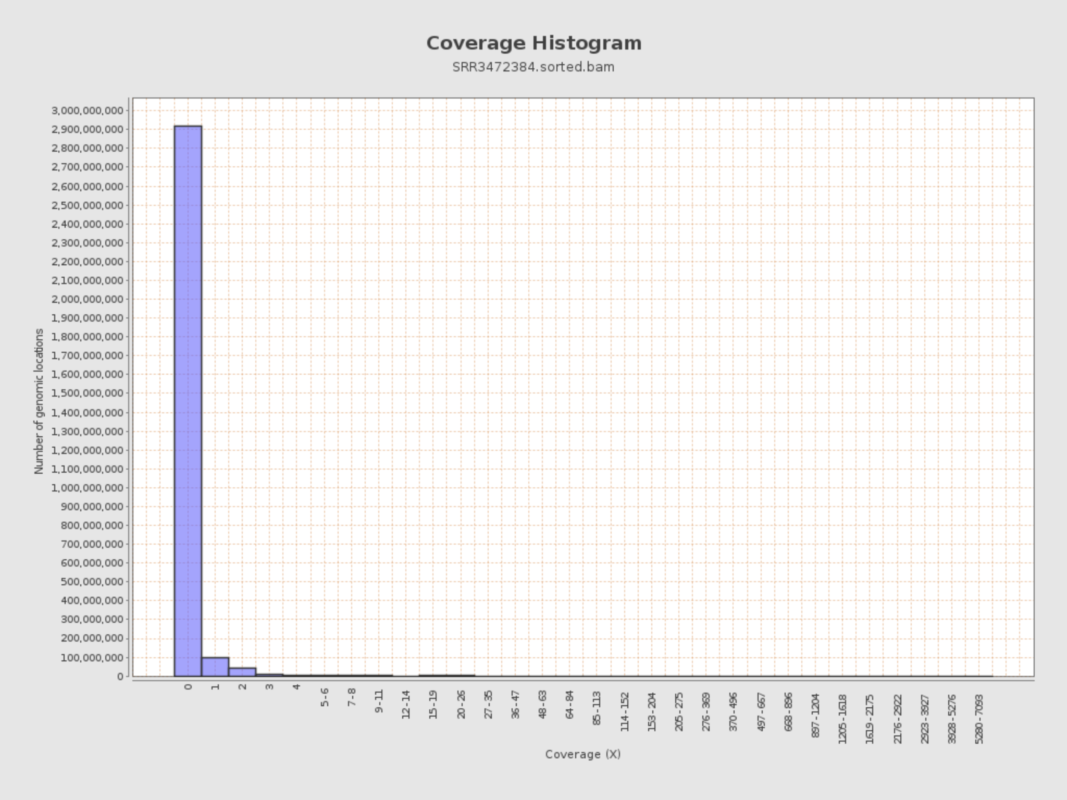
		bases	coverage	deviation
chr1	249250621	170330211	0.6834	19.2461
chr2	243199373	160712596	0.6608	17.1733
chr3	198022430	172202108	0.8696	20.1792
chr4	191154276	58523761	0.3062	11.9414
chr5	180915260	83441474	0.4612	15.2299
chr6	171115067	184440625	1.0779	26.9411
chr7	159138663	165874579	1.0423	25.1407
chr8	146364022	110541340	0.7552	20.4738
chr9	141213431	76635385	0.5427	19.311
chr10	135534747	51959128	0.3834	15.0659
chr11	135006516	62623947	0.4639	14.0778
chr12	133851895	104801479	0.783	17.2546
chr13	115169878	55778513	0.4843	15.3961
chr14	107349540	40536513	0.3776	11.2225
chr15	102531392	42466405	0.4142	11.4249
chr16	90354753	107399721	1.1886	32.1417
chr17	81195210	103378061	1.2732	29.4452
chr18	78077248	28253628	0.3619	11.1137
chr19	59128983	51082871	0.8639	17.0711
chr20	63025520	76083753	1.2072	28.0612
chr21	48129895	15373652	0.3194	13.3398
chr22	51304566	17777488	0.3465	9.9446
chrMT	16571	4469	0.2697	0.7619
chrX	155270560	177773432	1.1449	26.0059

chrY	59373566	481161	0.0081	0.5684

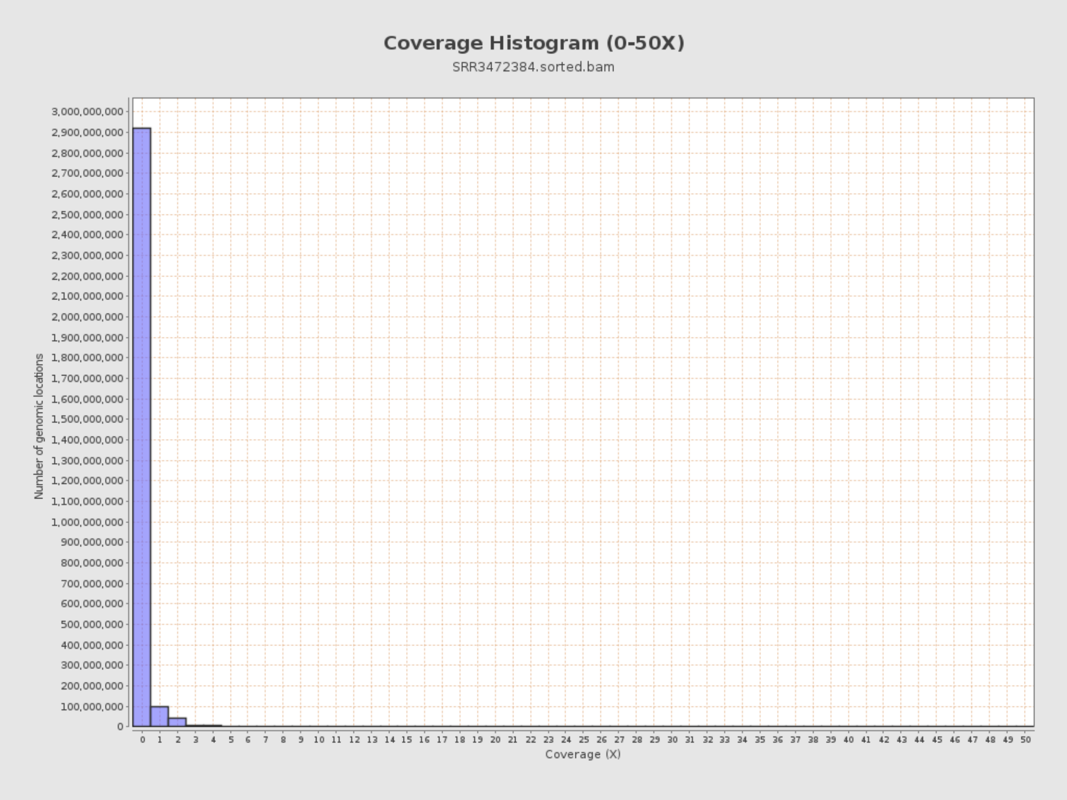
3. Results : Coverage across reference



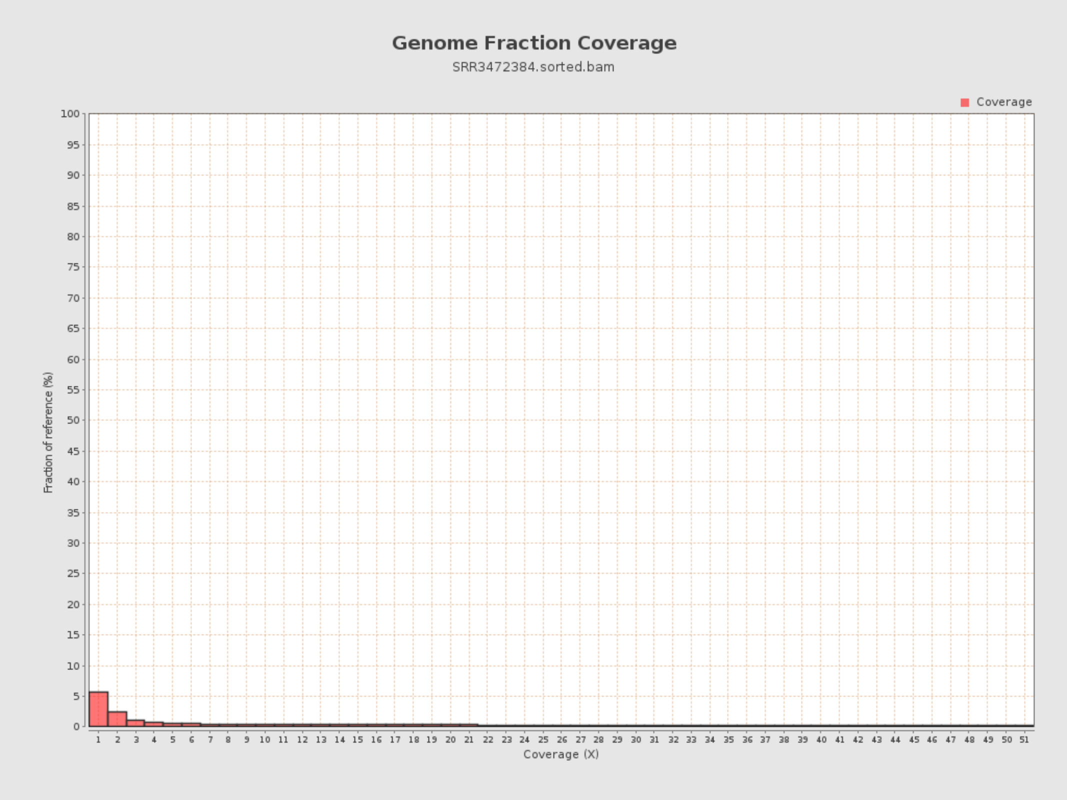
4. Results : Coverage Histogram



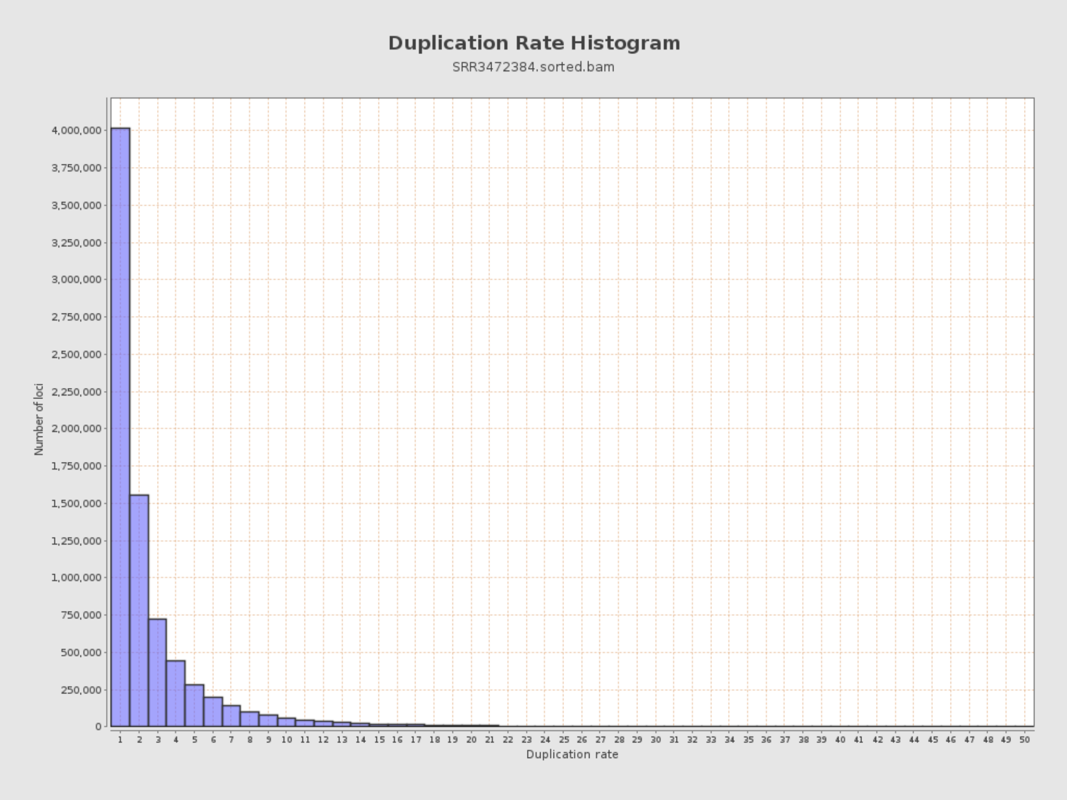
5. Results : Coverage Histogram (0-50X)



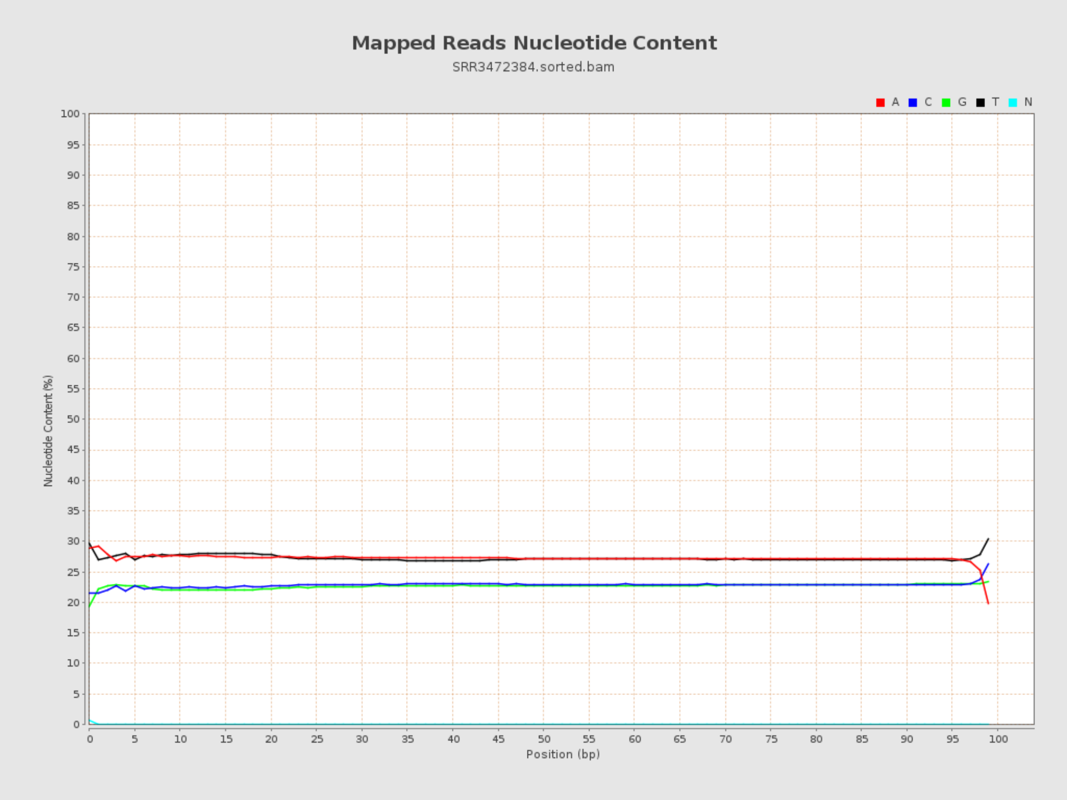
6. Results : Genome Fraction Coverage



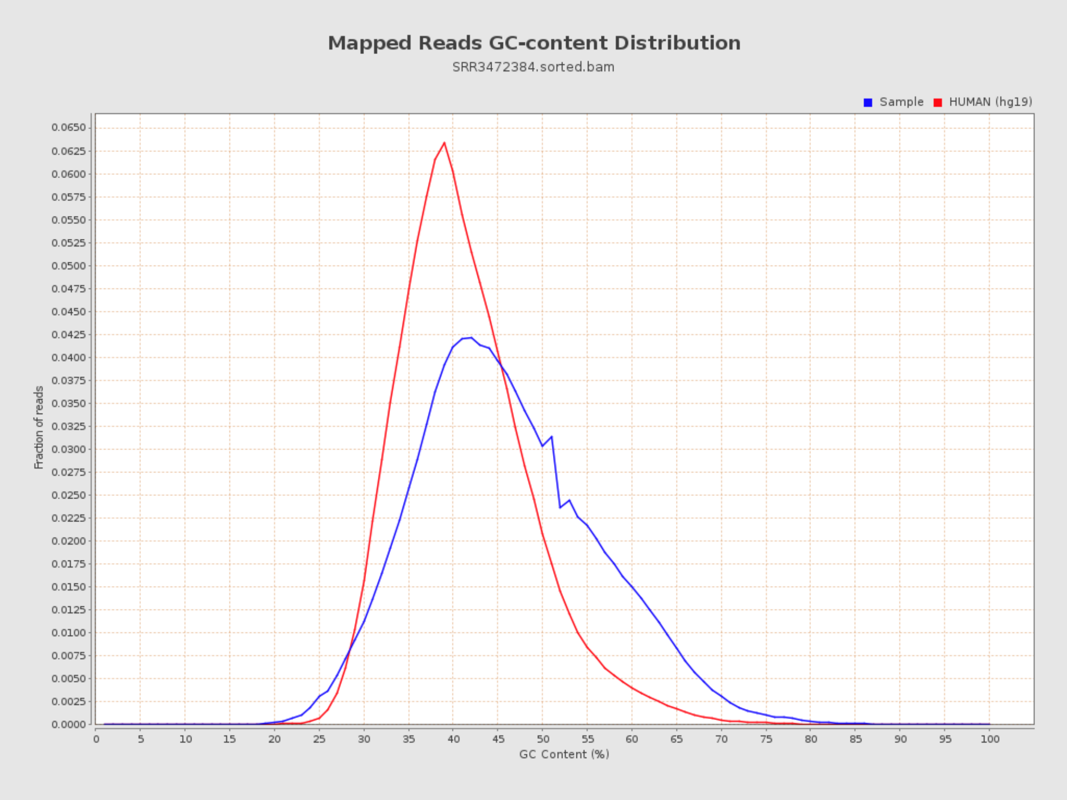
7. Results : Duplication Rate Histogram



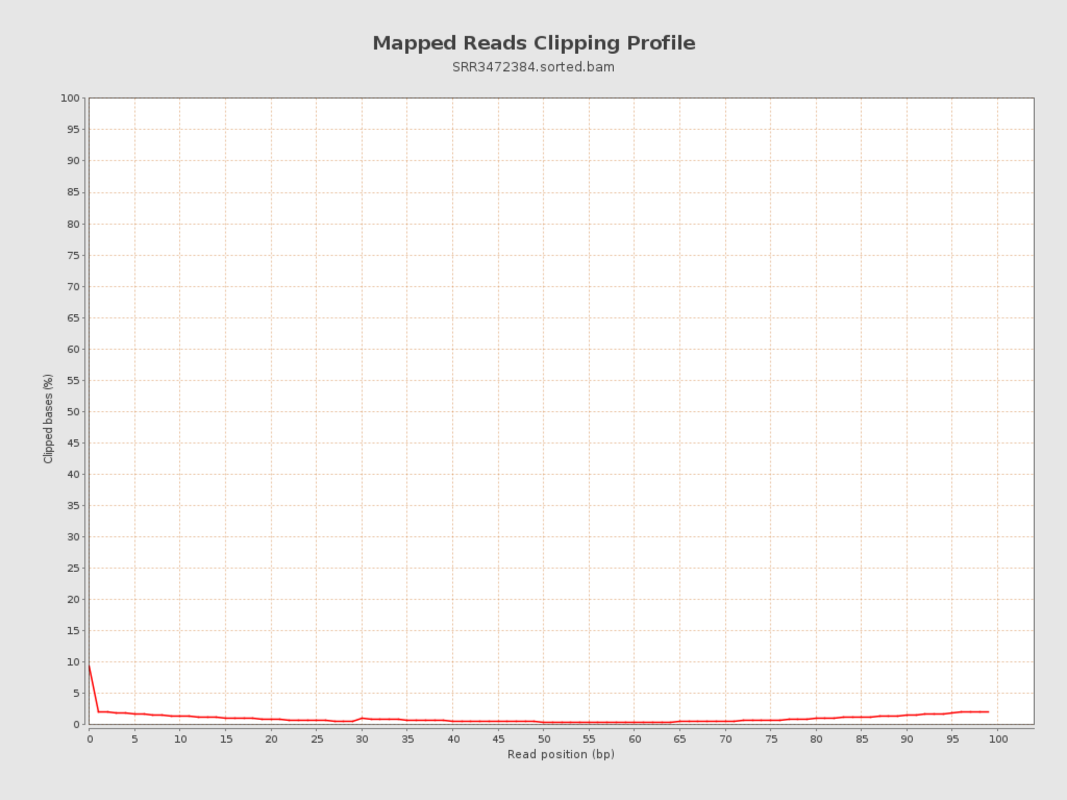
8. Results : Mapped Reads Nucleotide Content



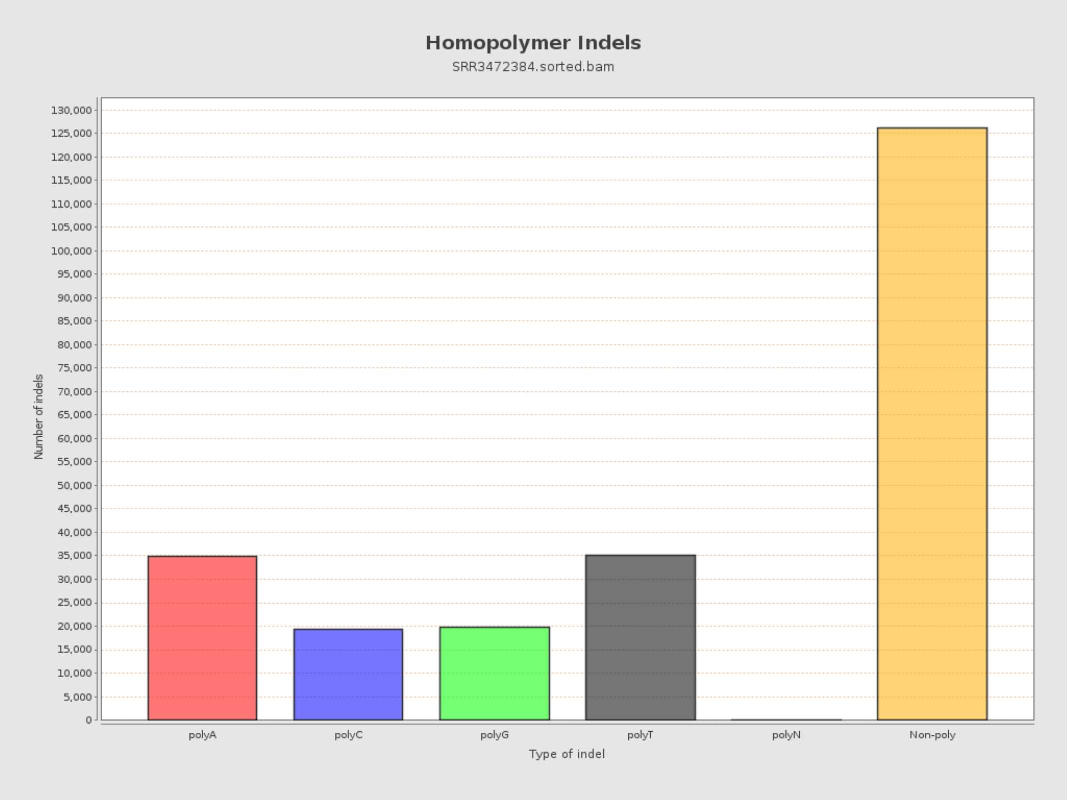
9. Results : Mapped Reads GC-content Distribution



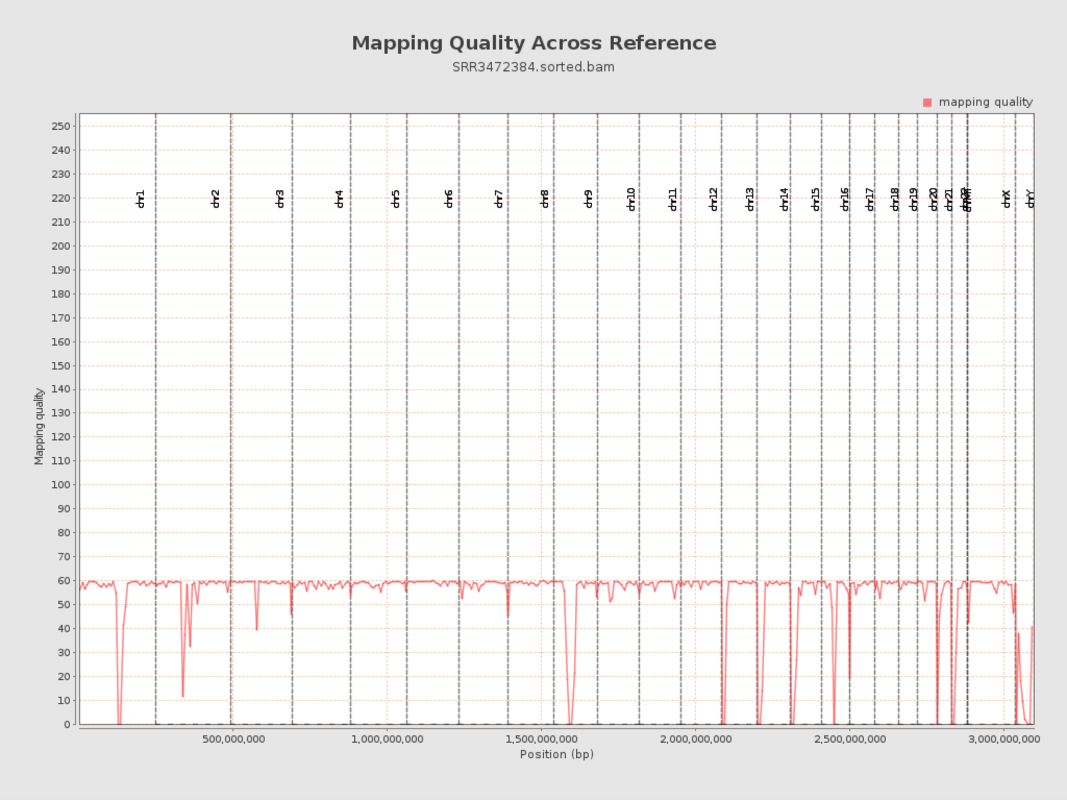
10. Results : Mapped Reads Clipping Profile



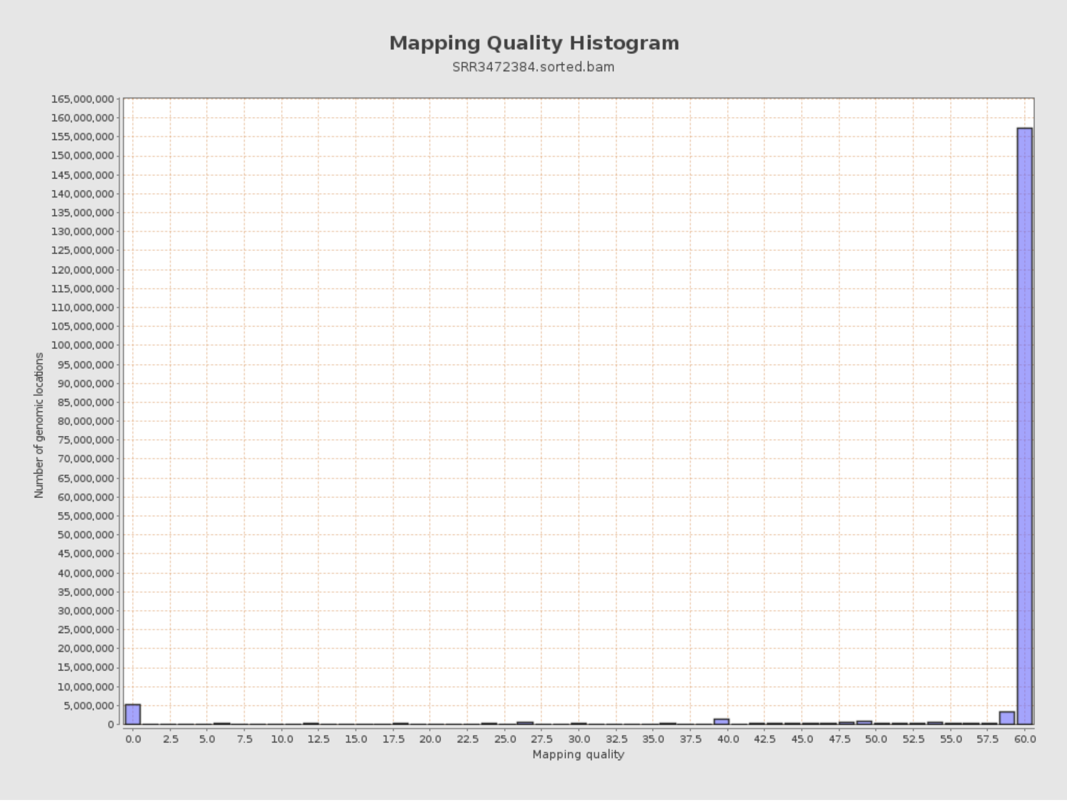
11. Results : Homopolymer Indels



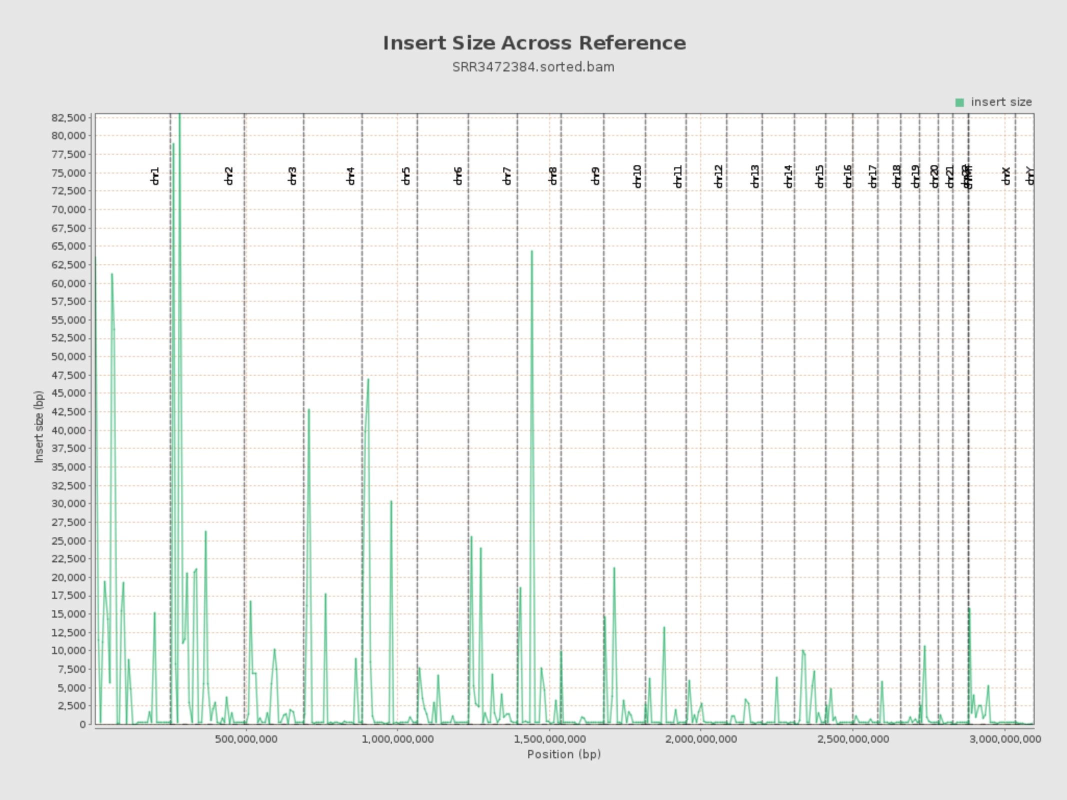
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram