Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 14:41:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472434.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_SRR3472434 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472434_1.fastq.gz SRR3472434_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 14:41:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472434.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,486,528
Mapped reads	20,268,262 / 98.93%
Unmapped reads	218,266 / 1.07%
Mapped paired reads	20,268,262 / 98.93%
Mapped reads, first in pair	10,165,838 / 49.62%
Mapped reads, second in pair	10,102,424 / 49.31%
Mapped reads, both in pair	20,168,360 / 98.45%
Mapped reads, singletons	99,902 / 0.49%
Secondary alignments	0
Supplementary alignments	72,086 / 0.35%
Read min/max/mean length	30 / 100 / 99.11
Duplicated reads (estimated)	13,159,374 / 64.23%
Duplication rate	48.86%
Clipped reads	1,533,030 / 7.48%

2.2. ACGT Content

Number/percentage of A's	534,099,832 / 26.96%
Number/percentage of C's	458,584,360 / 23.14%
Number/percentage of T's	535,102,021 / 27.01%
Number/percentage of G's	453,384,818 / 22.88%
Number/percentage of N's	246,777 / 0.01%

GC Percentage	46.03%

2.3. Coverage

Mean	0.6401
Standard Deviation	19.7937

2.4. Mapping Quality

Mean Mapping Quality	54.75

2.5. Insert size

Mean	15,569.33
Standard Deviation	1,247,345.18
P25/Median/P75	148 / 207 / 280

2.6. Mismatches and indels

General error rate	0.53%
Mismatches	10,206,866
Insertions	115,992
Mapped reads with at least one insertion	0.57%
Deletions	85,233
Mapped reads with at least one deletion	0.41%
Homopolymer indels	46.57%

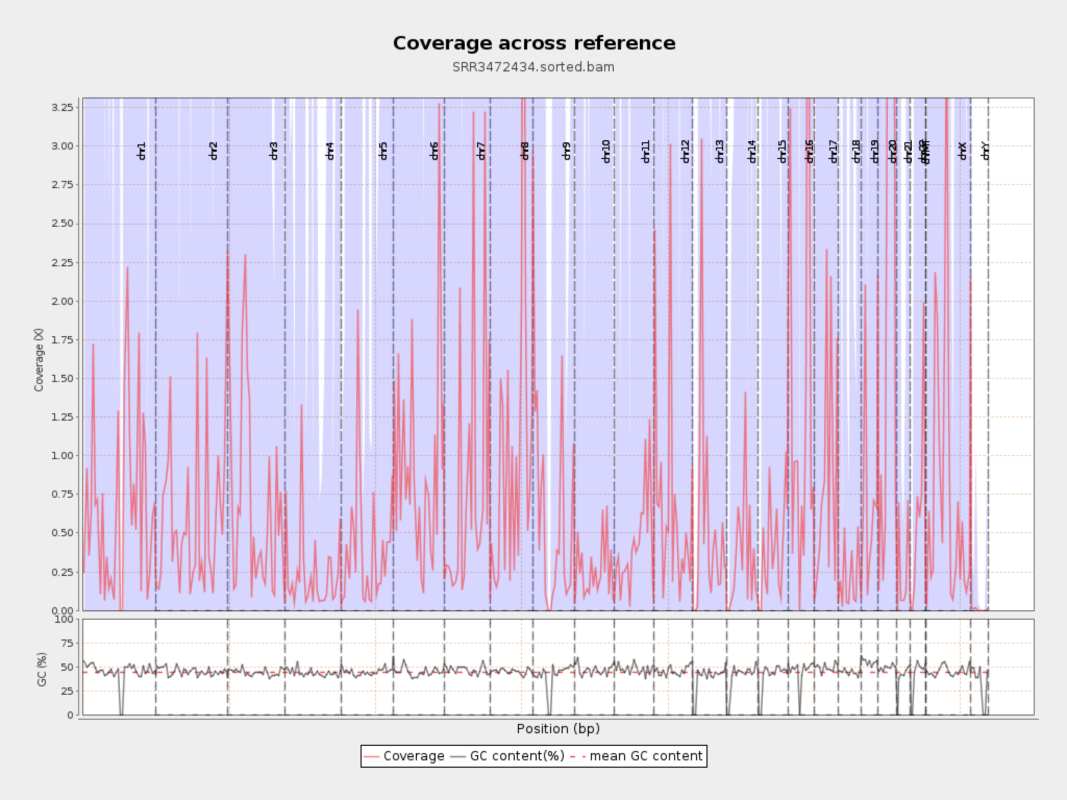
2.7. Chromosome stats

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

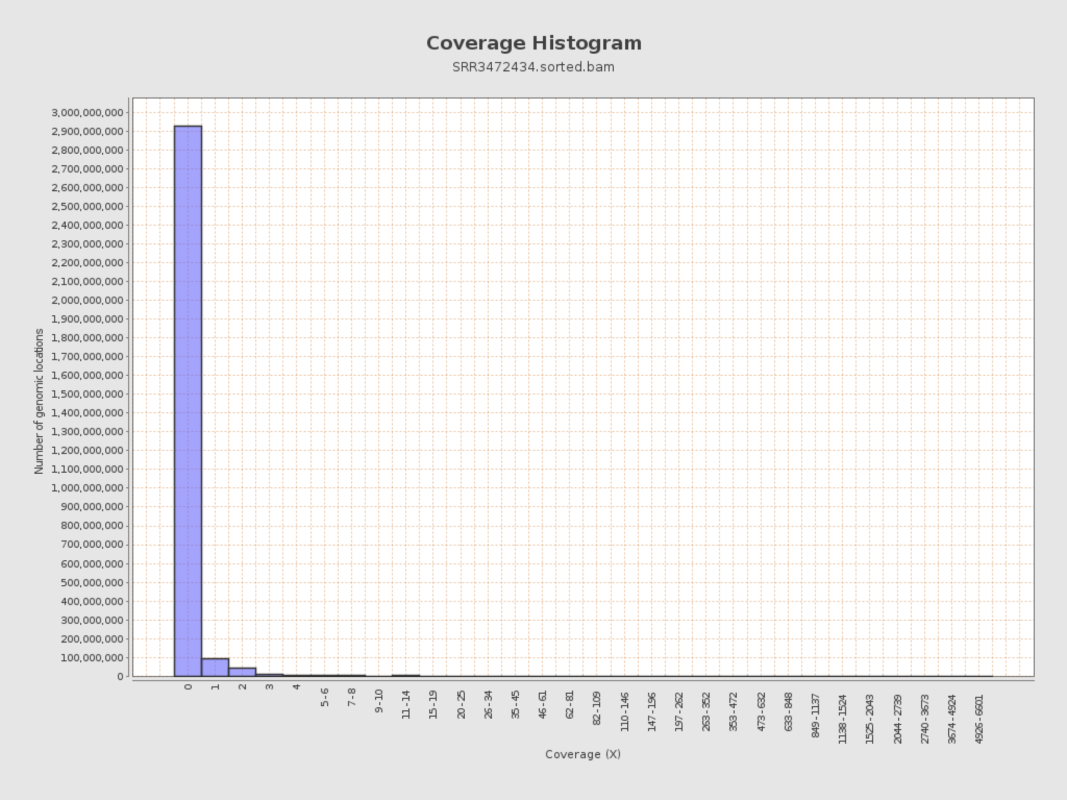
		bases	coverage	deviation
chr1	249250621	166559964	0.6682	19.7214
chr2	243199373	144102334	0.5925	18.1226
chr3	198022430	141838200	0.7163	16.4704
chr4	191154276	47411656	0.248	8.3915
chr5	180915260	73438730	0.4059	13.9022
chr6	171115067	155698437	0.9099	21.5415
chr7	159138663	132797522	0.8345	27.0722
chr8	146364022	157884276	1.0787	28.1016
chr9	141213431	75841946	0.5371	16.1766
chr10	135534747	37217275	0.2746	12.2304
chr11	135006516	58029937	0.4298	11.6067
chr12	133851895	95056954	0.7102	16.7553
chr13	115169878	63719449	0.5533	16.3669
chr14	107349540	37396076	0.3484	11.7995
chr15	102531392	40856462	0.3985	13.1728
chr16	90354753	123622081	1.3682	36.2311
chr17	81195210	70136555	0.8638	17.888
chr18	78077248	15957921	0.2044	8.7983
chr19	59128983	43494020	0.7356	16.0353
chr20	63025520	122175493	1.9385	47.7835
chr21	48129895	13273778	0.2758	12.8443
chr22	51304566	32796036	0.6392	23.6919
chrMT	16571	1026	0.0619	0.245
chrX	155270560	131932661	0.8497	25.2335

chrY	59373566	389135	0.0066	0.5304

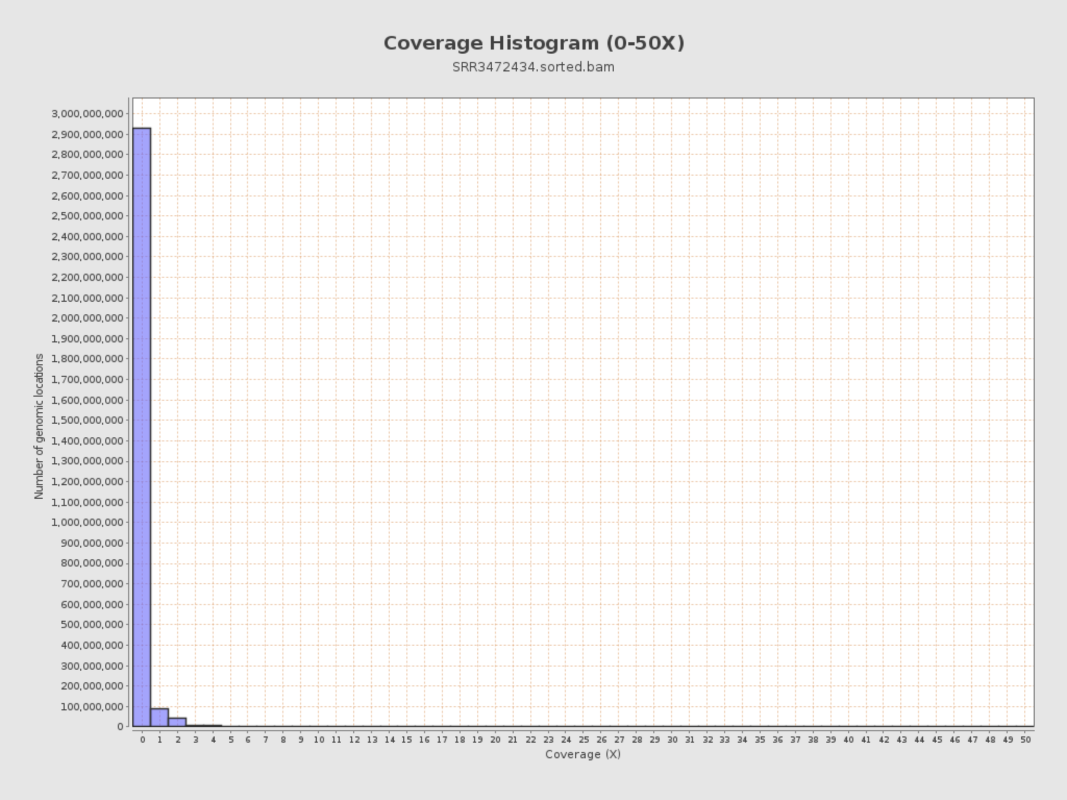
3. Results : Coverage across reference



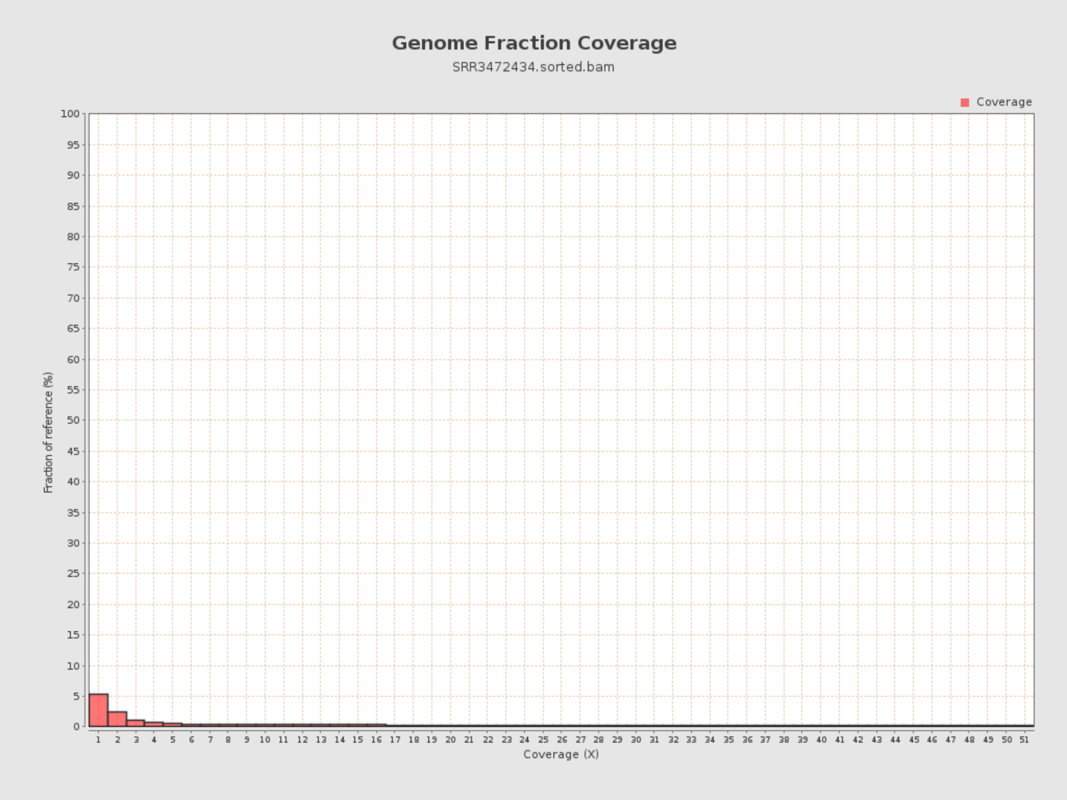
4. Results : Coverage Histogram



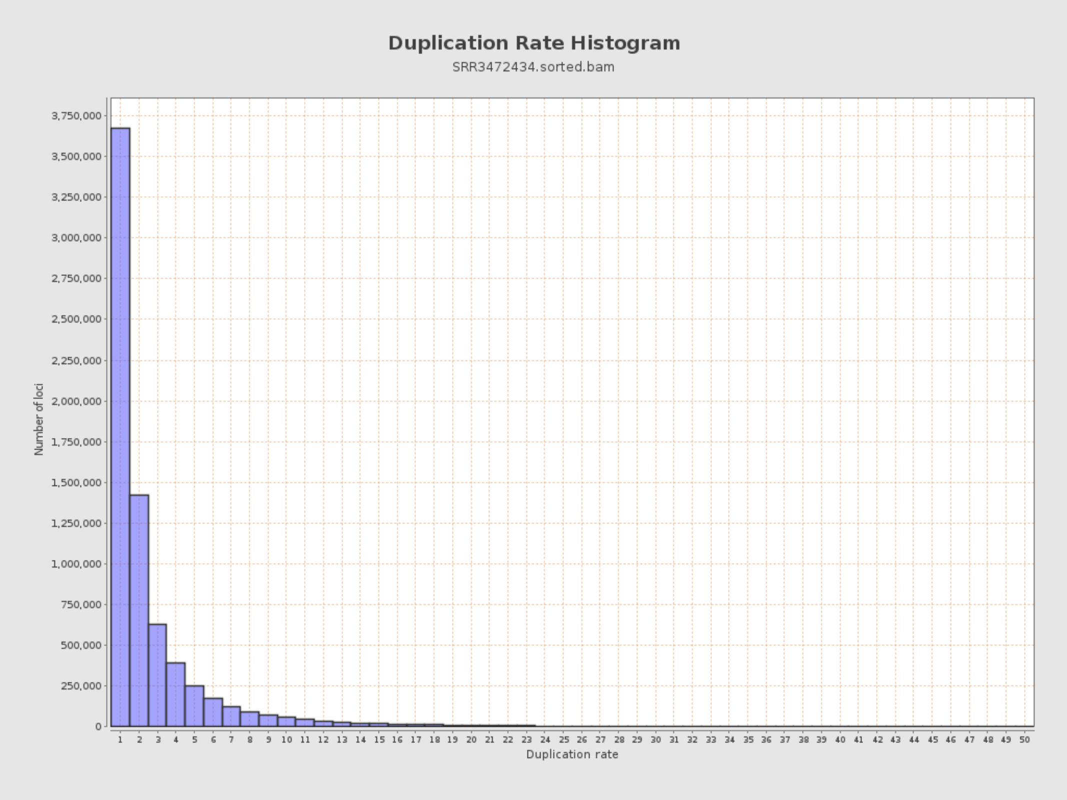
5. Results : Coverage Histogram (0-50X)



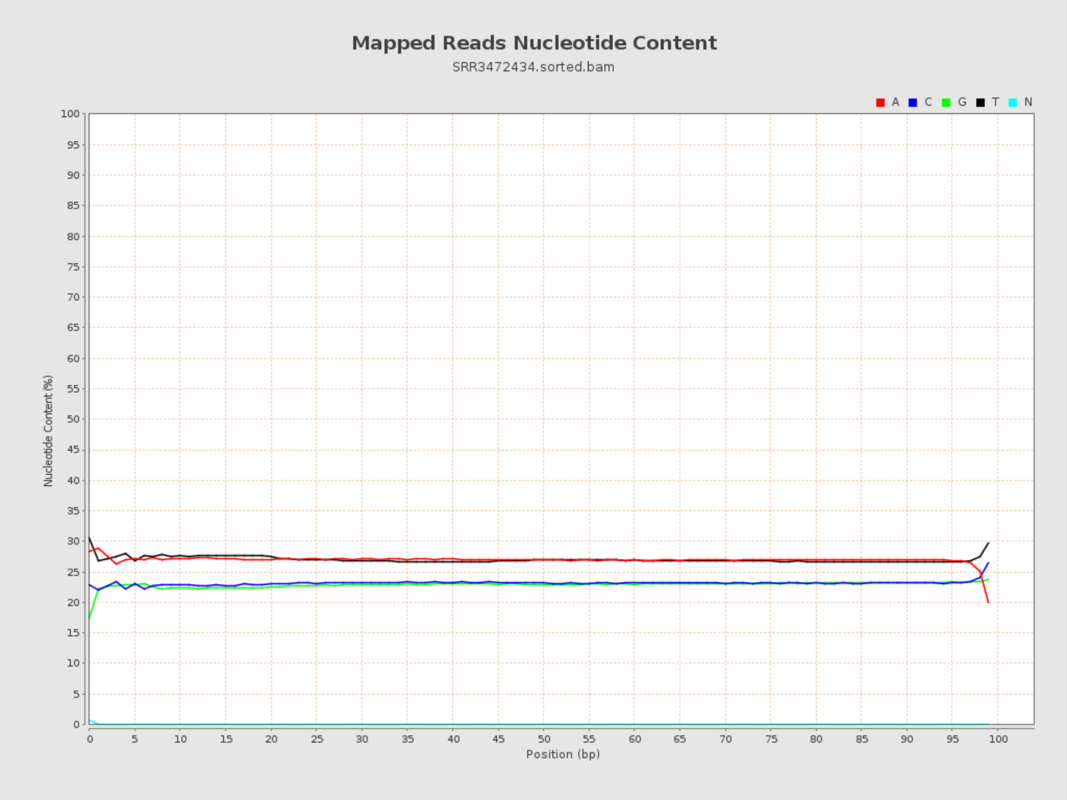
6. Results : Genome Fraction Coverage



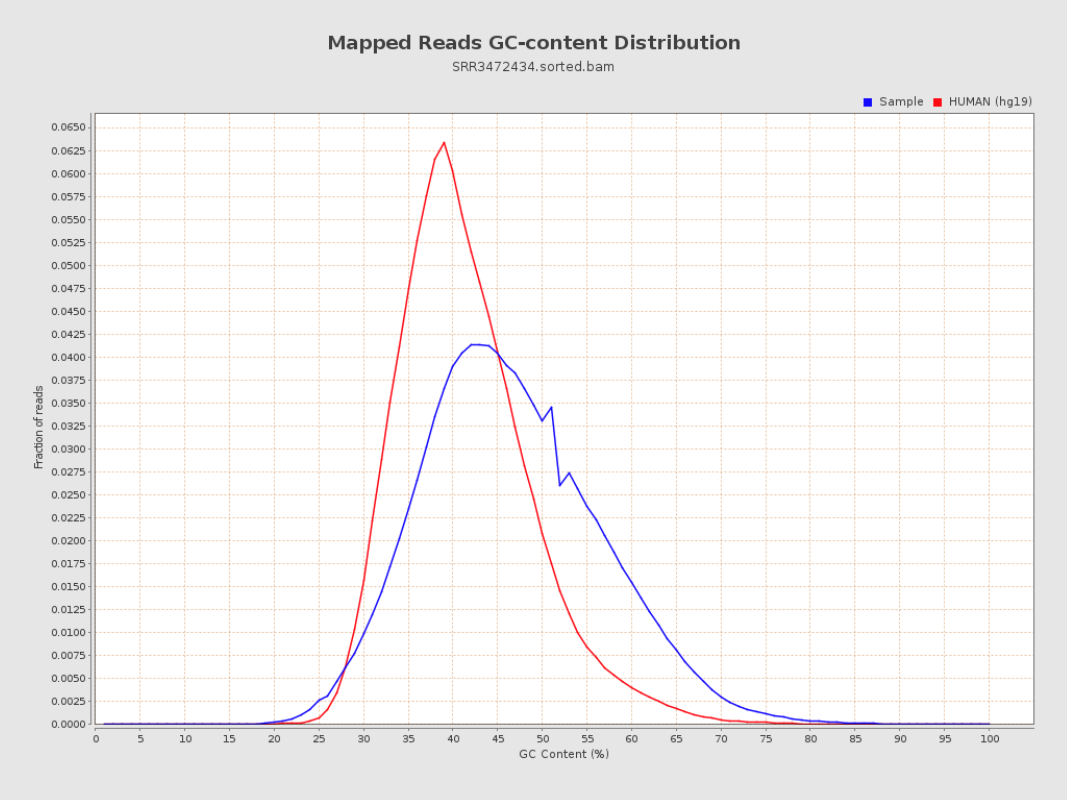
7. Results : Duplication Rate Histogram



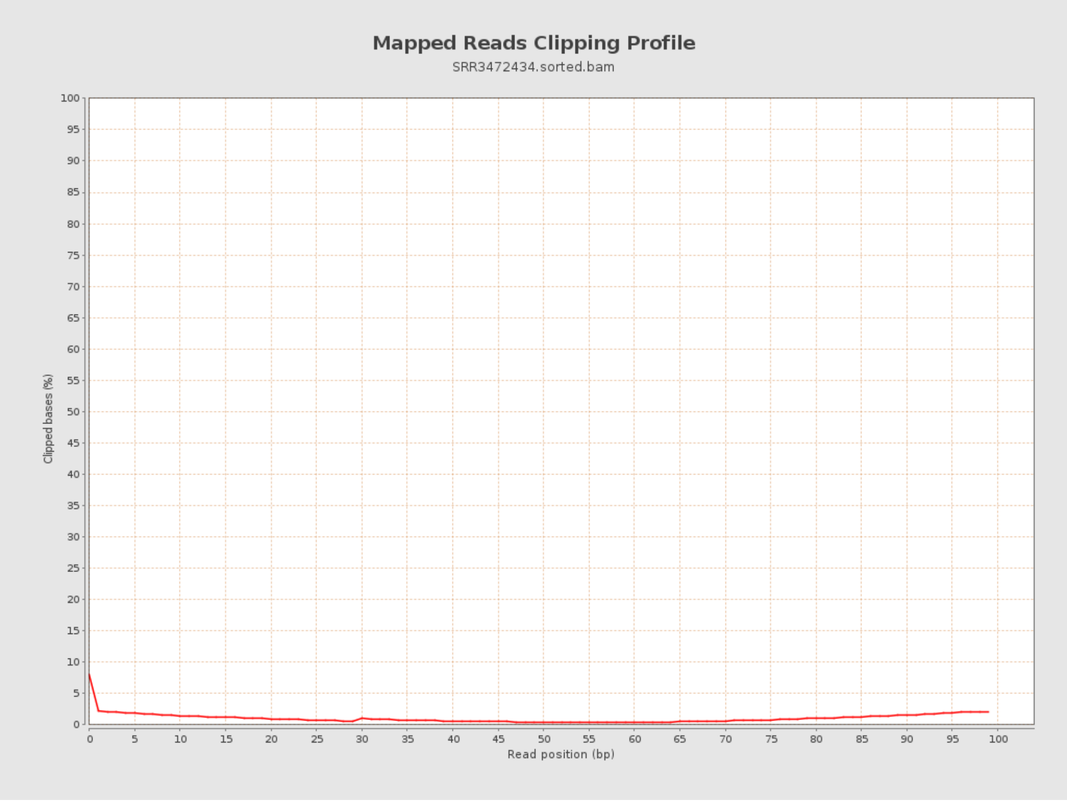
8. Results : Mapped Reads Nucleotide Content



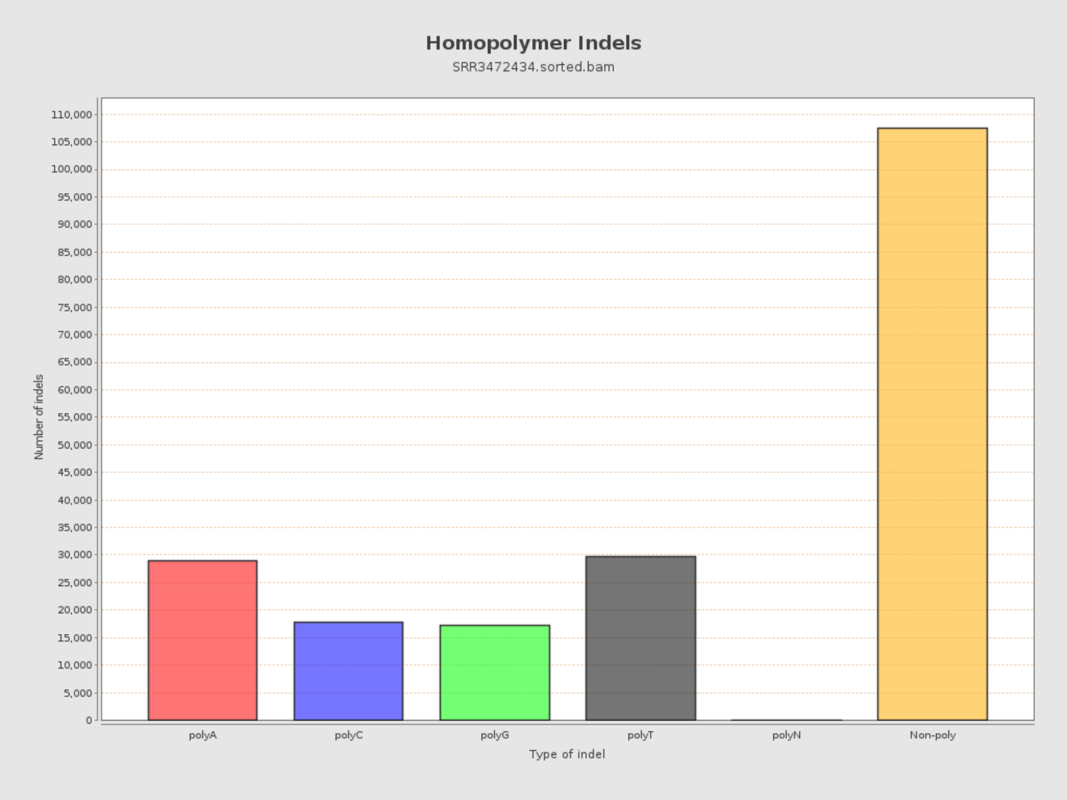
9. Results : Mapped Reads GC-content Distribution



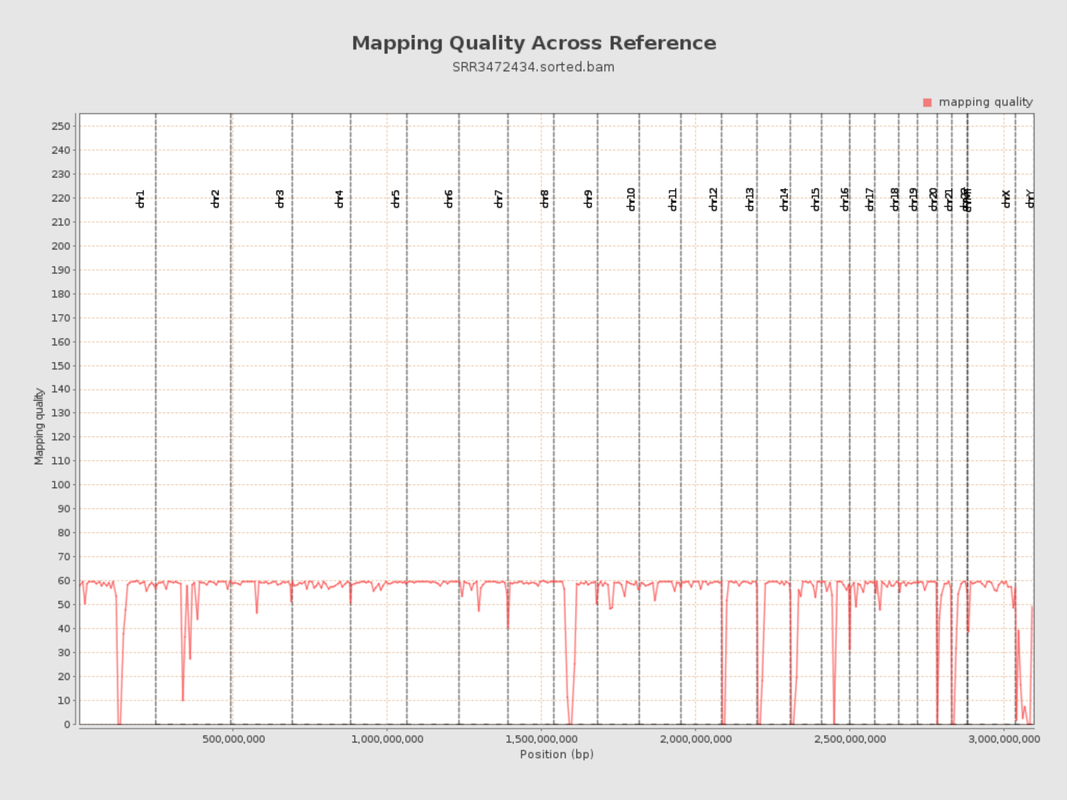
10. Results : Mapped Reads Clipping Profile



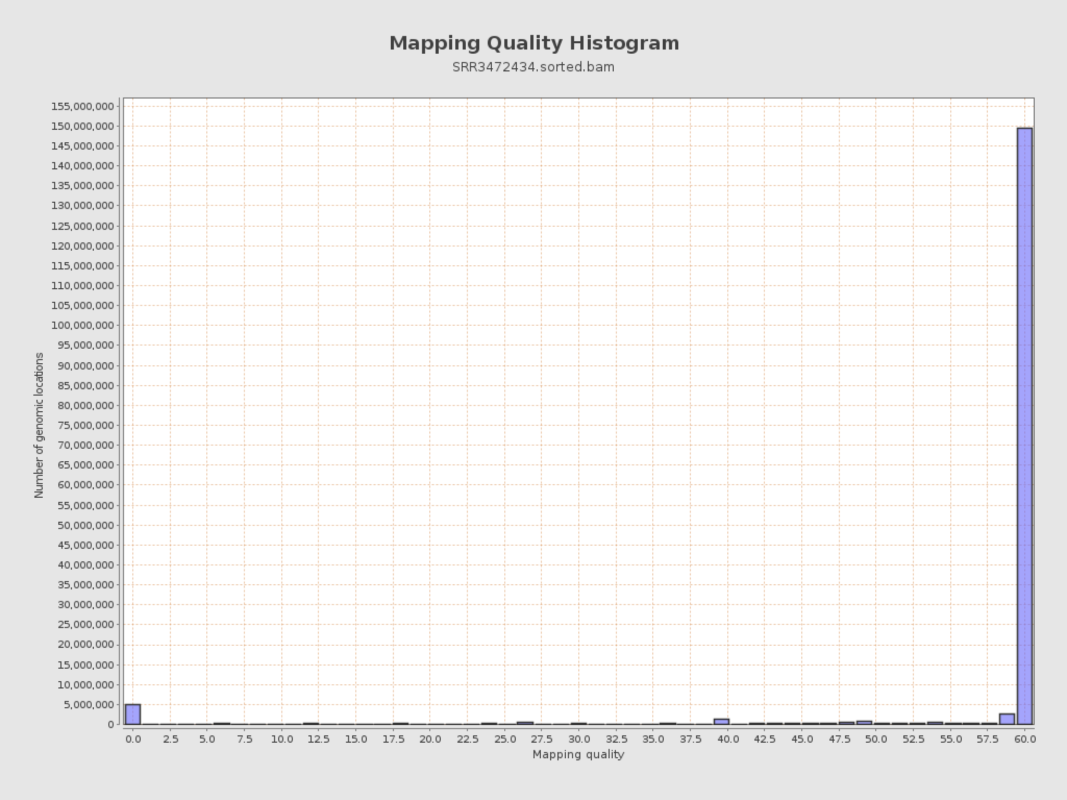
11. Results : Homopolymer Indels



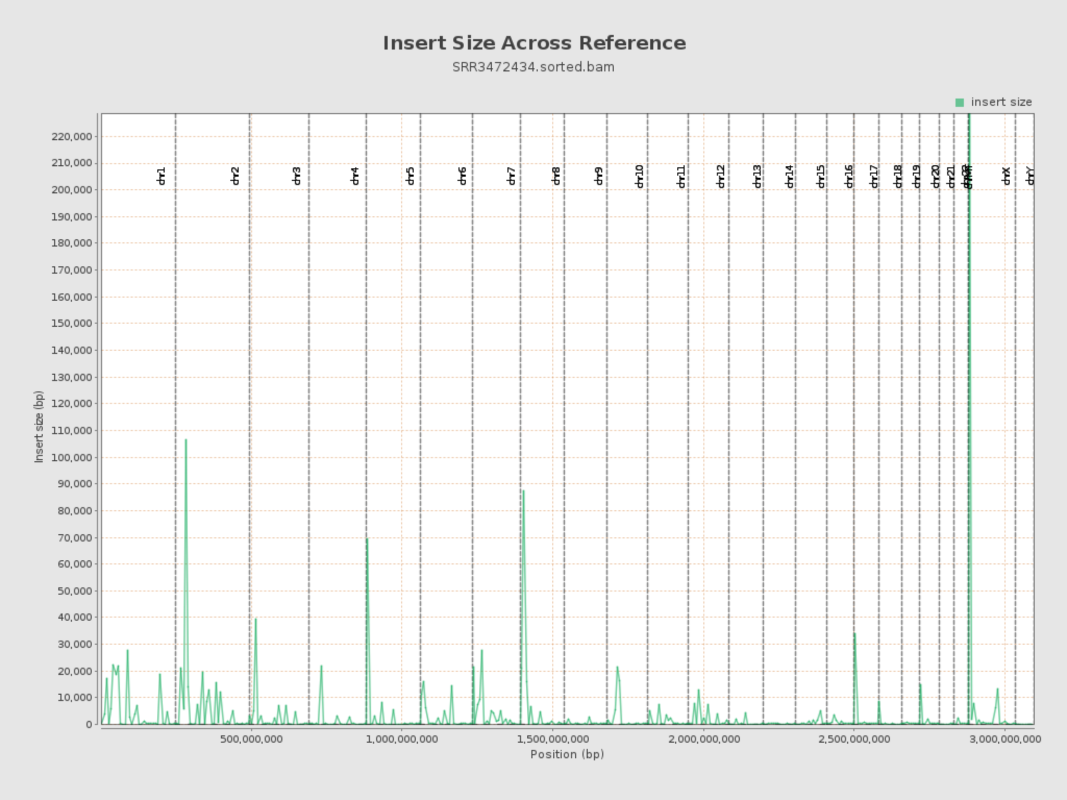
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram