Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 05:54:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472474.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_SRR3472474 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472474_1.fastq.gz SRR3472474_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 05:54:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472474.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,531,970
Mapped reads	17,341,860 / 98.92%
Unmapped reads	190,110 / 1.08%
Mapped paired reads	17,341,860 / 98.92%
Mapped reads, first in pair	8,701,371 / 49.63%
Mapped reads, second in pair	8,640,489 / 49.28%
Mapped reads, both in pair	17,236,528 / 98.31%
Mapped reads, singletons	105,332 / 0.6%
Secondary alignments	0
Supplementary alignments	76,541 / 0.44%
Read min/max/mean length	30 / 100 / 100.18
Duplicated reads (estimated)	10,968,991 / 62.57%
Duplication rate	45.31%
Clipped reads	1,541,601 / 8.79%

2.2. ACGT Content

Number/percentage of A's	477,051,281 / 27.98%
Number/percentage of C's	378,967,429 / 22.22%
Number/percentage of T's	472,901,114 / 27.73%
Number/percentage of G's	376,037,002 / 22.05%
Number/percentage of N's	262,576 / 0.02%

GC Percentage	44.28%

2.3. Coverage

Mean	0.5509
Standard Deviation	19.7579

2.4. Mapping Quality

Mean Mapping Quality	54.99

2.5. Insert size

Mean	34,515.4
Standard Deviation	1,831,215.01
P25/Median/P75	166 / 233 / 315

2.6. Mismatches and indels

General error rate	0.61%
Mismatches	10,279,879
Insertions	92,433
Mapped reads with at least one insertion	0.52%
Deletions	86,496
Mapped reads with at least one deletion	0.49%
Homopolymer indels	46.37%

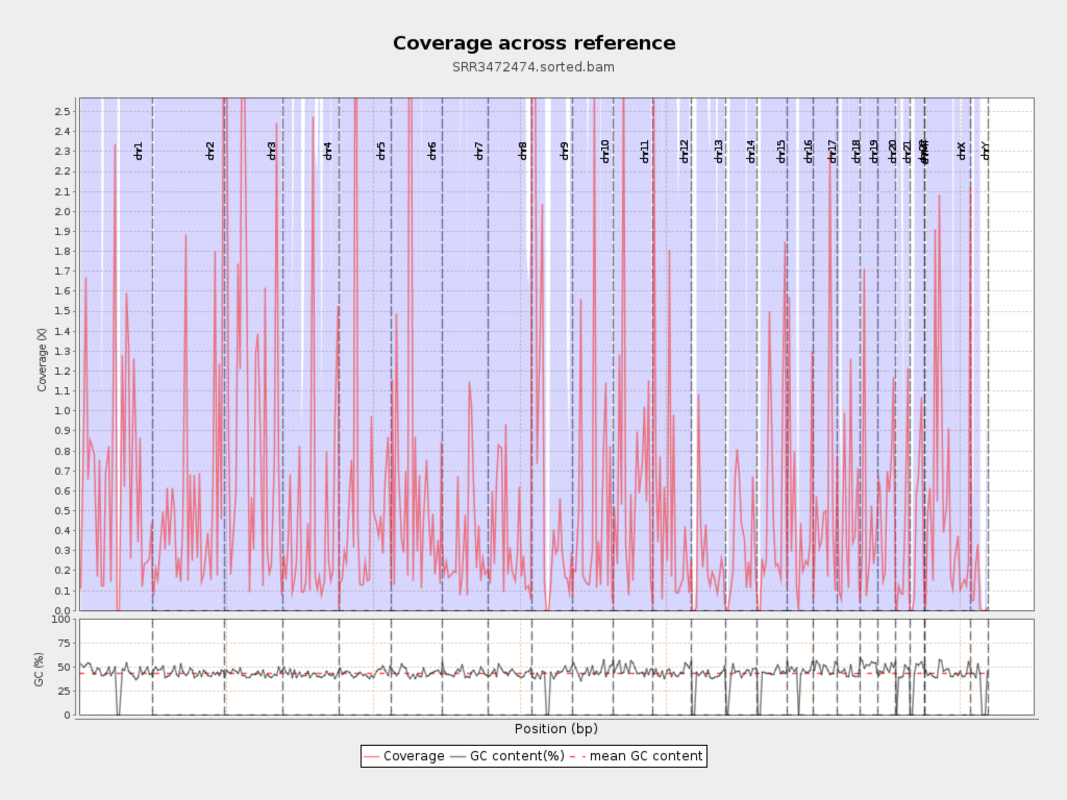
2.7. Chromosome stats

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

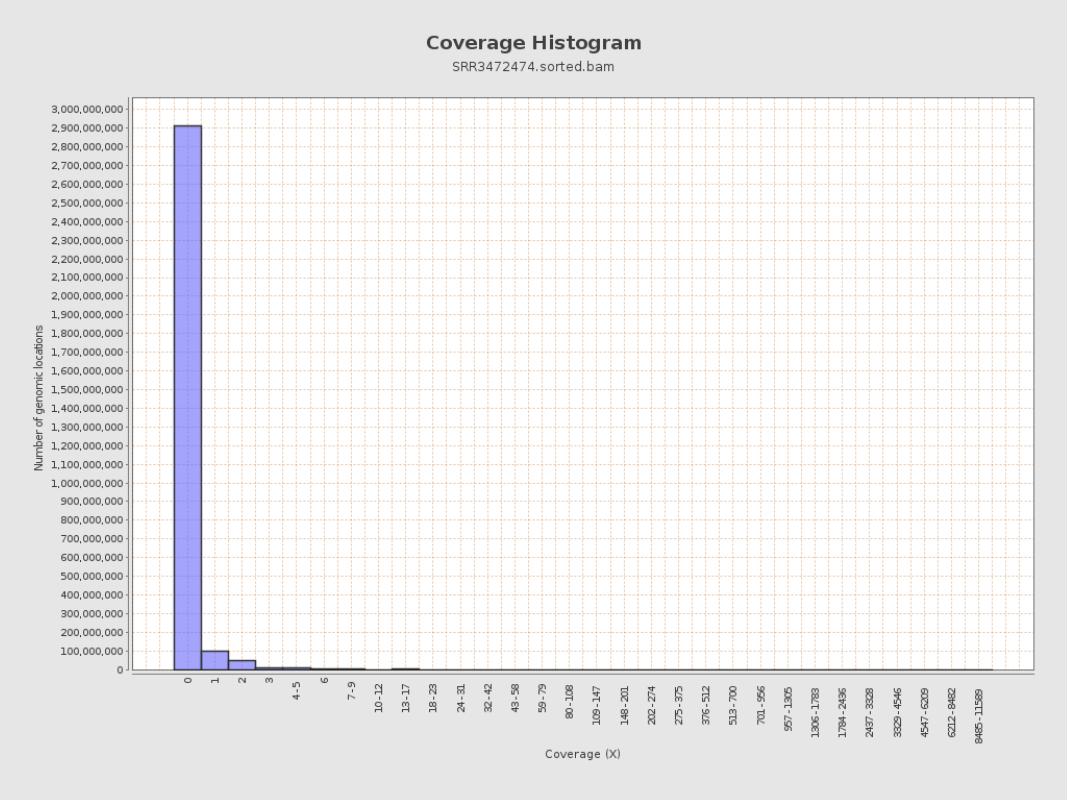
		bases	**coverage**	**deviation**
chr1	249250621	168304631	0.6752	21.977
chr2	243199373	127504672	0.5243	17.1728
chr3	198022430	219496666	1.1084	27.9016
chr4	191154276	80943461	0.4234	16.1508
chr5	180915260	101660460	0.5619	16.1018
chr6	171115067	118871207	0.6947	18.6344
chr7	159138663	54669378	0.3435	10.6284
chr8	146364022	52252662	0.357	12.676
chr9	141213431	107429526	0.7608	23.9447
chr10	135534747	73311660	0.5409	30.2961
chr11	135006516	94278184	0.6983	32.8132
chr12	133851895	72699412	0.5431	15.7658
chr13	115169878	27523045	0.239	8.8101
chr14	107349540	35311415	0.3289	10.2341
chr15	102531392	57736694	0.5631	17.1457
chr16	90354753	43463310	0.481	15.1728
chr17	81195210	44822751	0.552	14.255
chr18	78077248	34896454	0.4469	20.3996
chr19	59128983	27277778	0.4613	14.8334
chr20	63025520	36165227	0.5738	16.49
chr21	48129895	15317704	0.3183	13.8523
chr22	51304566	19821936	0.3864	13.8018
chrMT	16571	1891	0.1141	0.4192
chrX	155270560	86542825	0.5574	26.5445

chrY	59373566	5123326	0.0863	5.3985

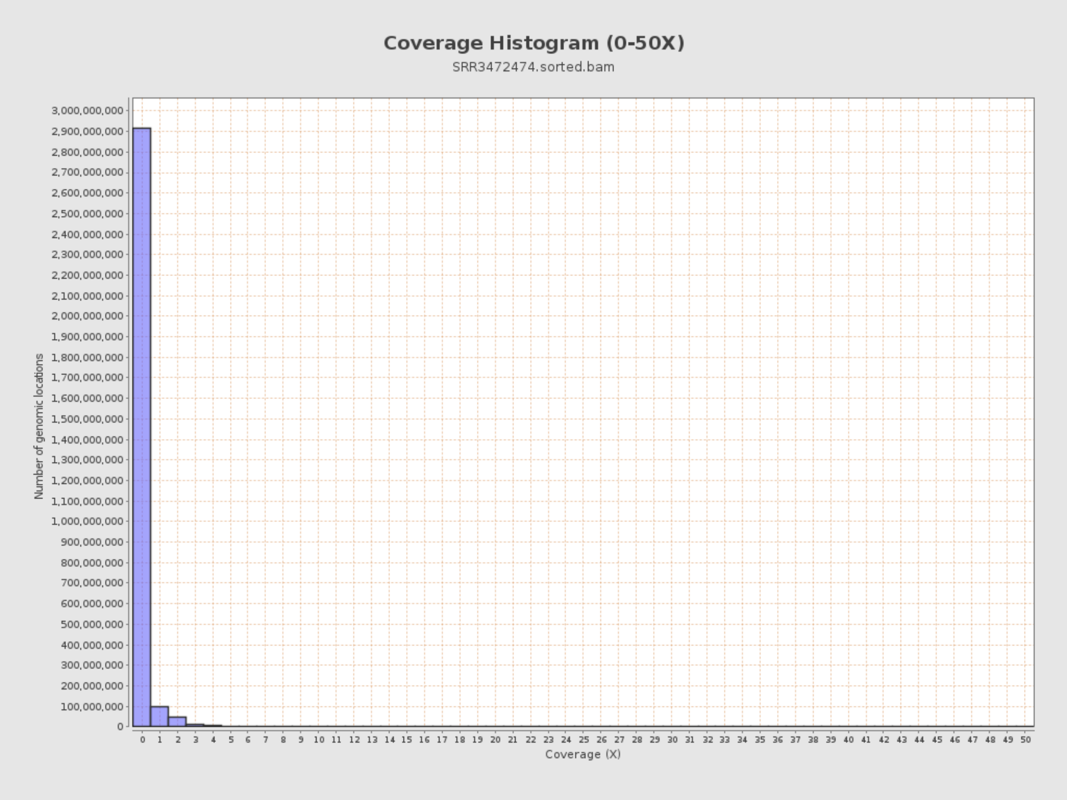
3. Results : Coverage across reference



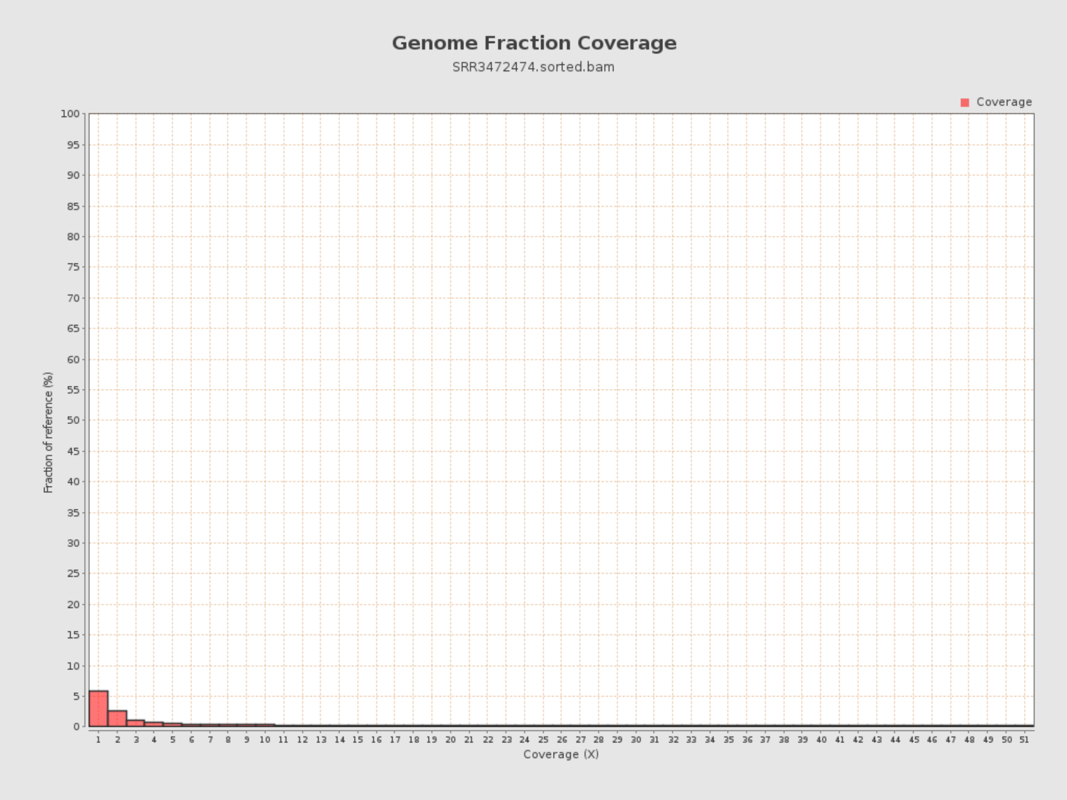
4. Results : Coverage Histogram



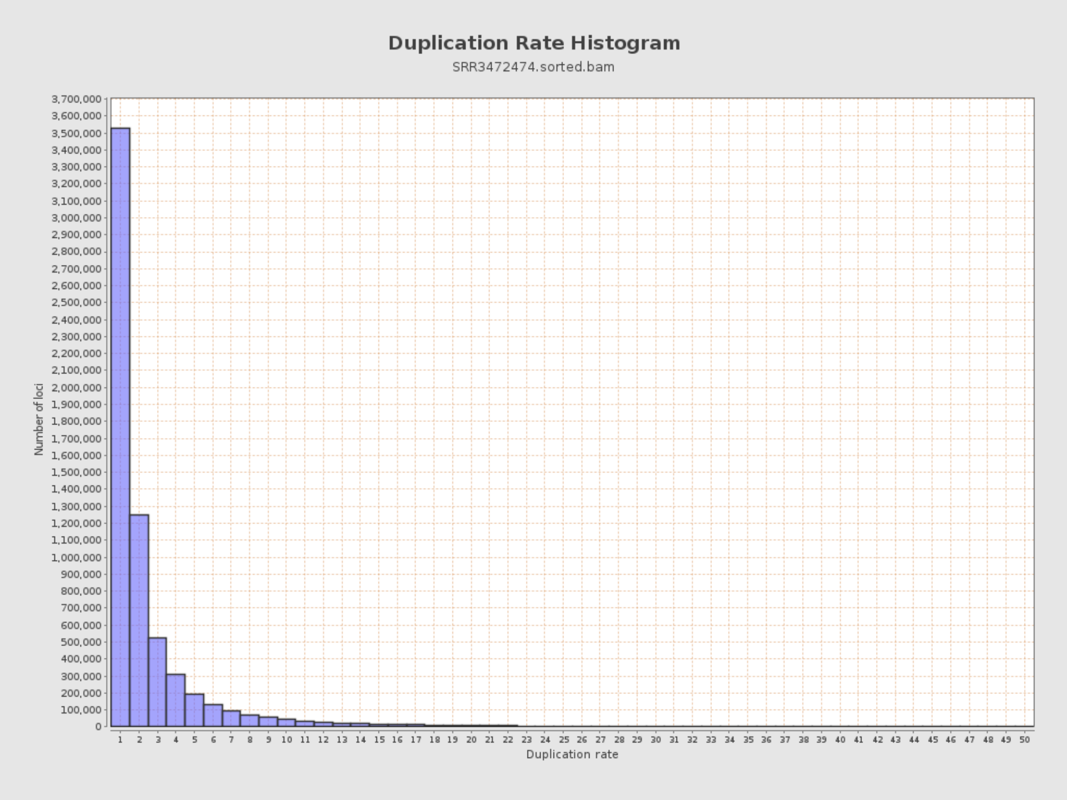
5. Results : Coverage Histogram (0-50X)



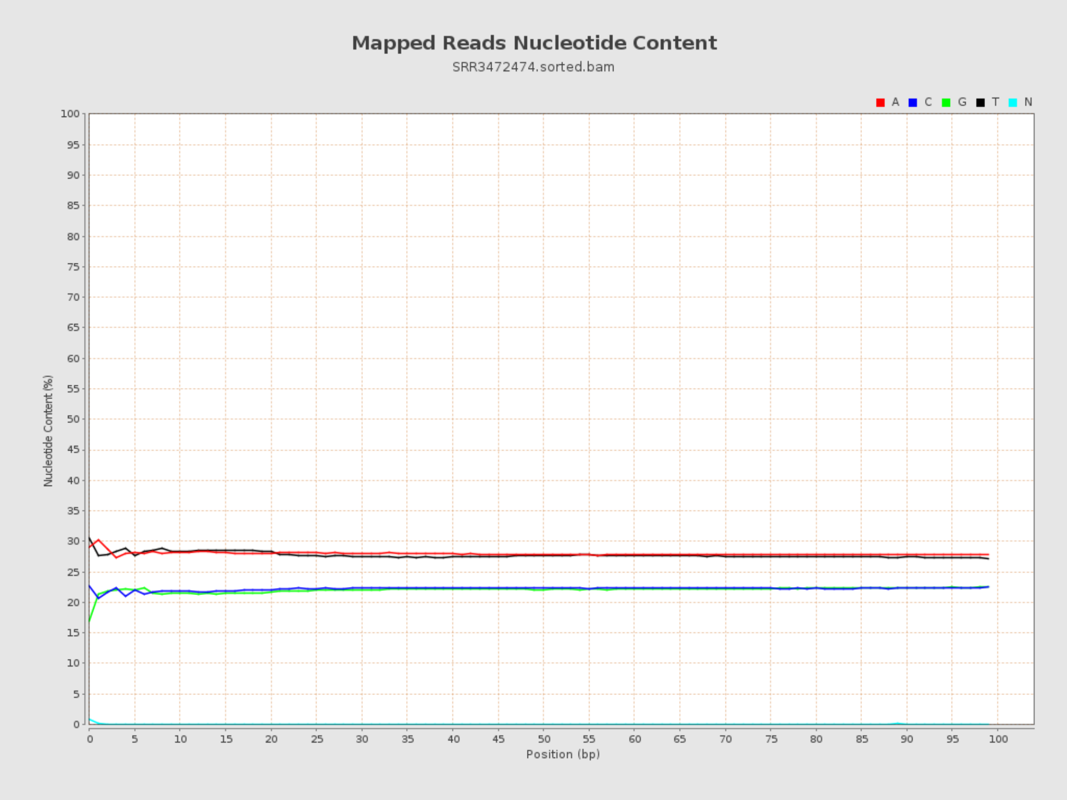
6. Results : Genome Fraction Coverage



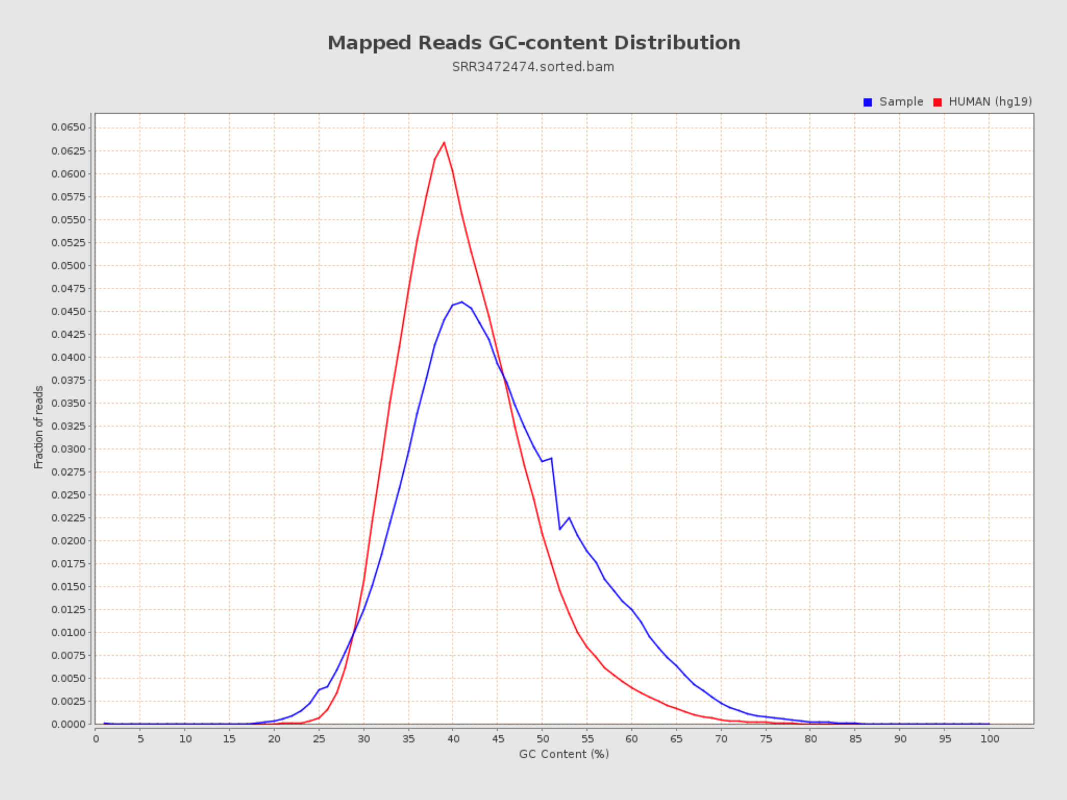
7. Results : Duplication Rate Histogram



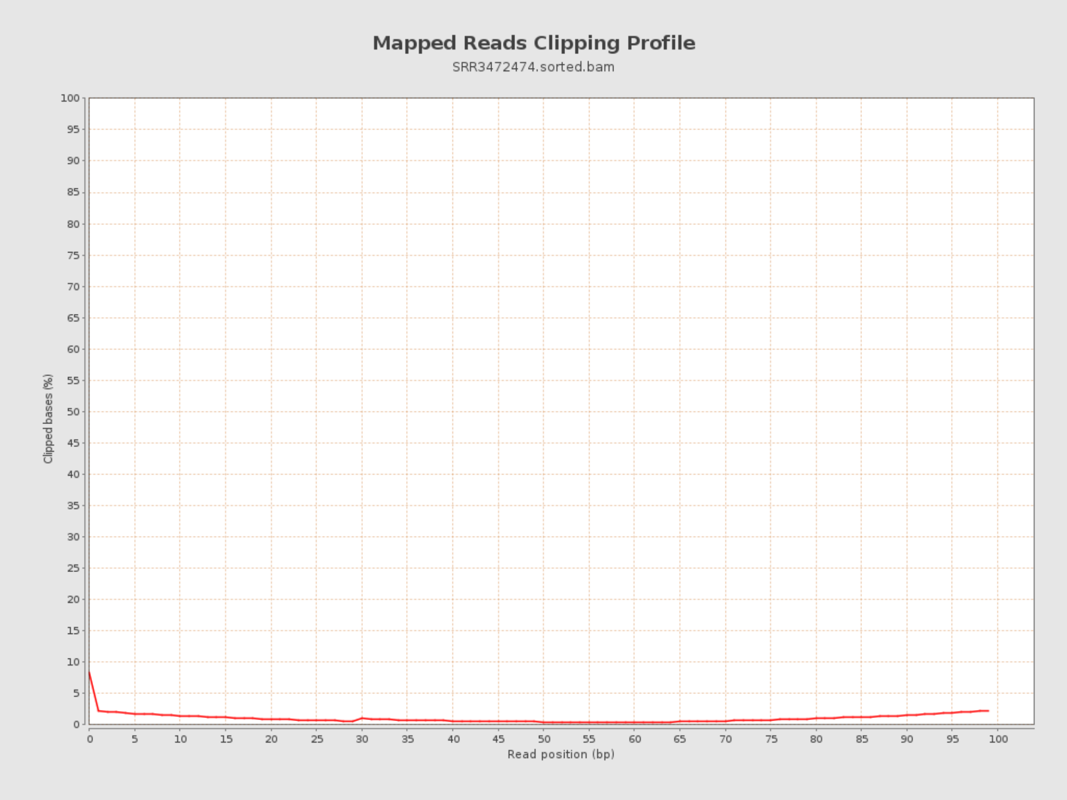
8. Results : Mapped Reads Nucleotide Content



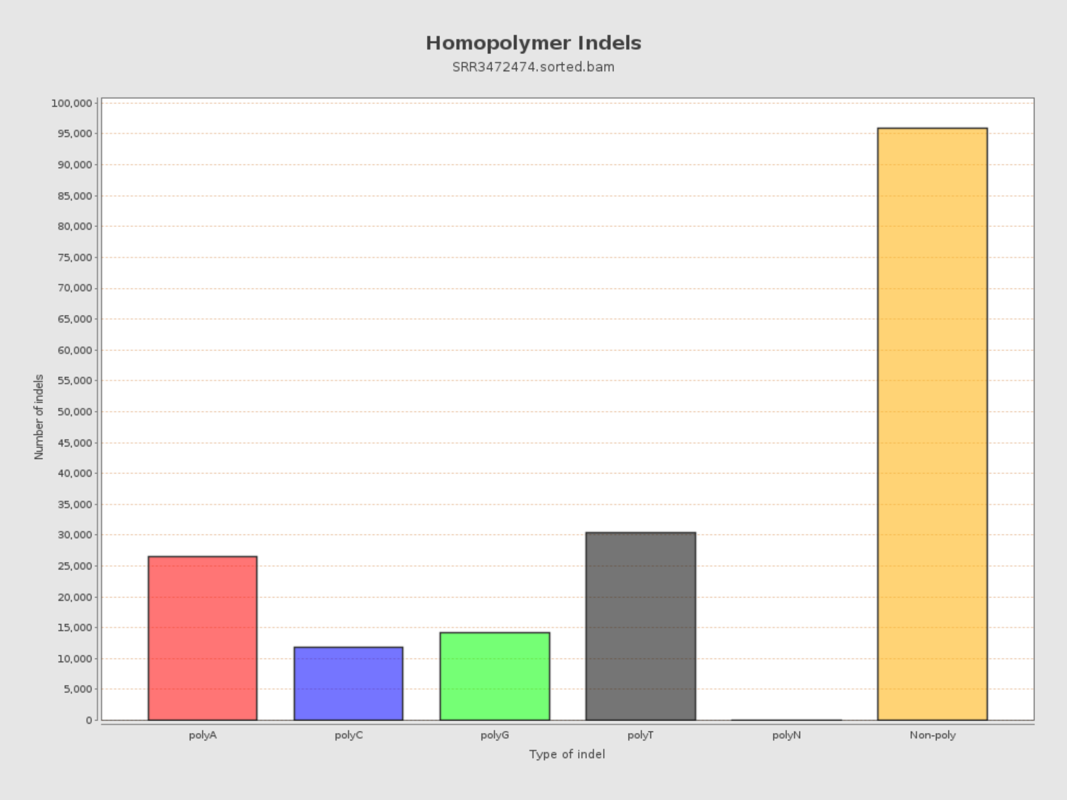
9. Results : Mapped Reads GC-content Distribution



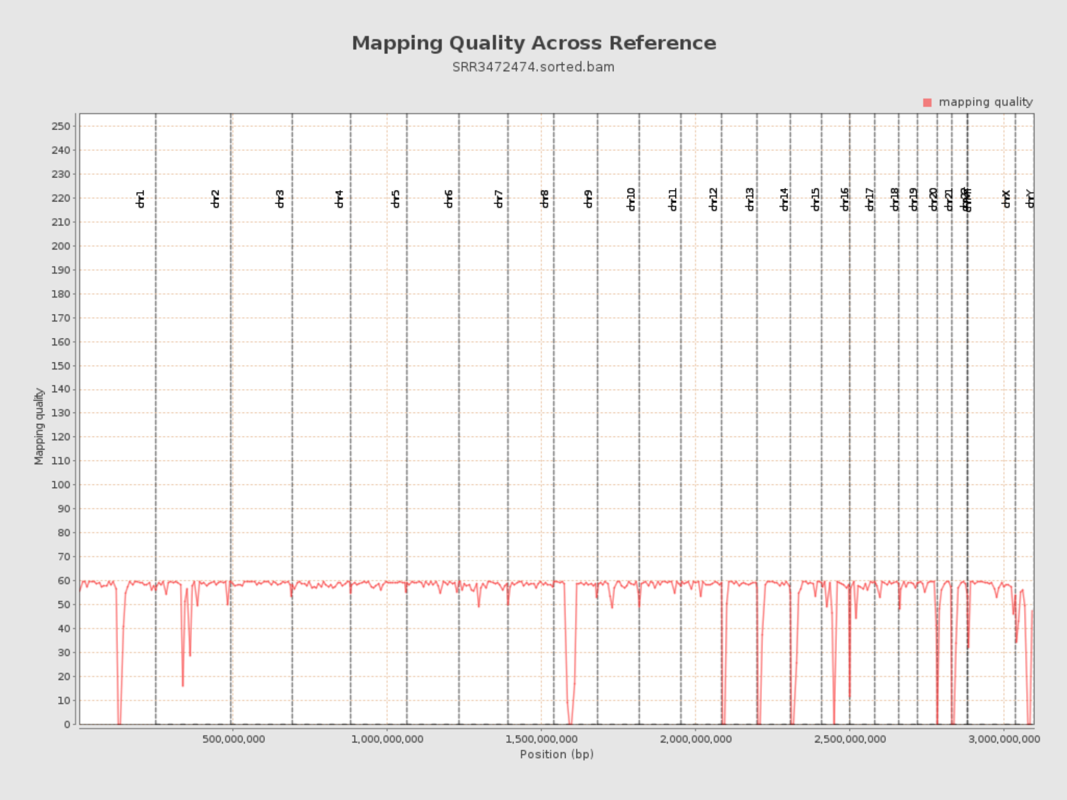
10. Results : Mapped Reads Clipping Profile



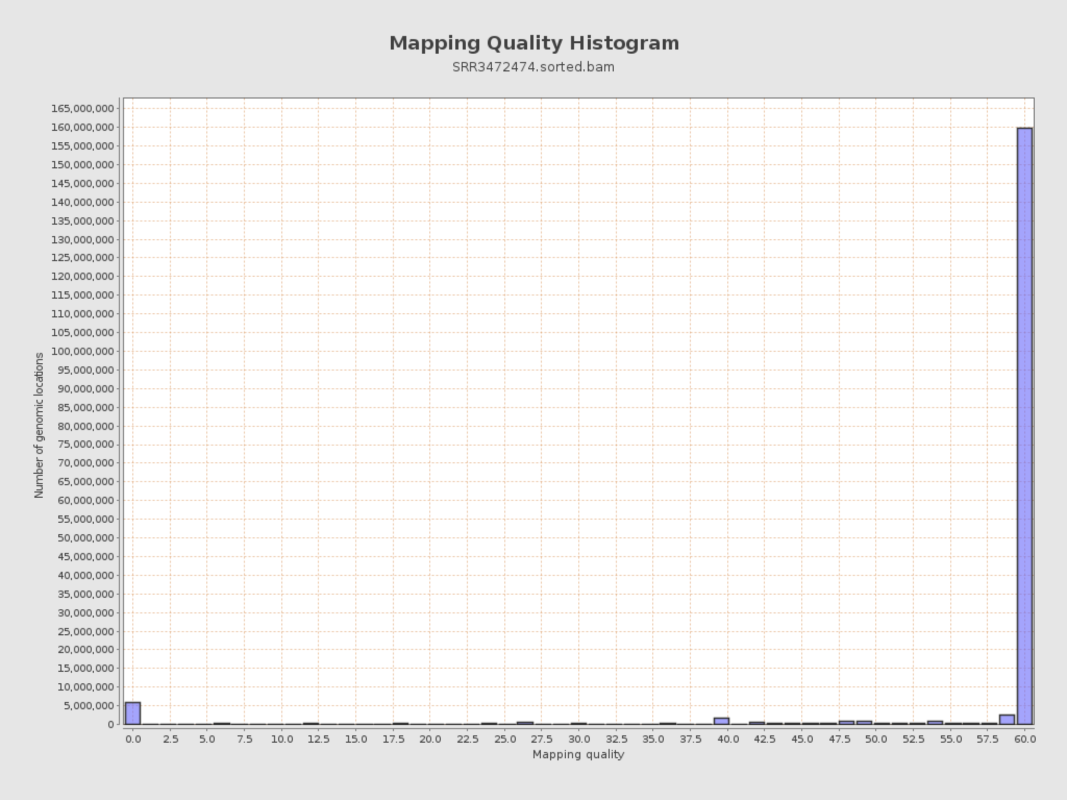
11. Results : Homopolymer Indels



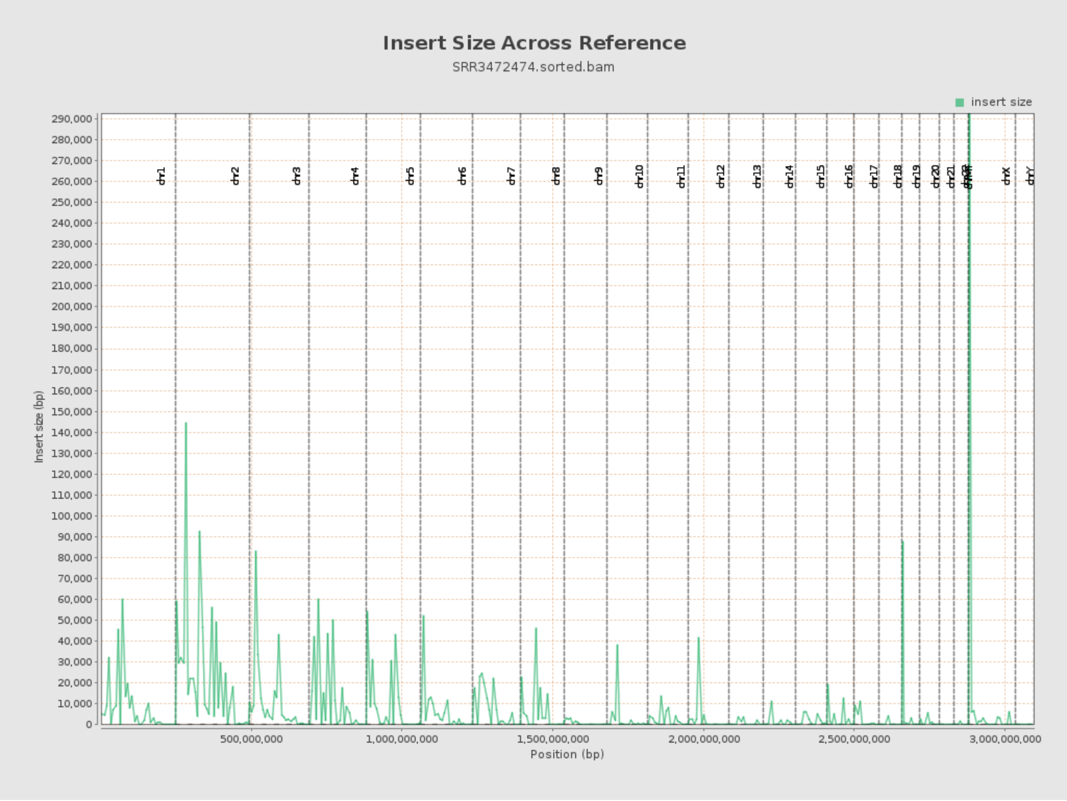
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram