Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 11:20:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472423.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_SRR3472423 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472423_1.fastq.gz SRR3472423_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 11:20:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472423.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	30,909,406
Mapped reads	30,612,991 / 99.04%
Unmapped reads	296,415 / 0.96%
Mapped paired reads	30,612,991 / 99.04%
Mapped reads, first in pair	15,348,945 / 49.66%
Mapped reads, second in pair	15,264,046 / 49.38%
Mapped reads, both in pair	30,460,918 / 98.55%
Mapped reads, singletons	152,073 / 0.49%
Secondary alignments	0
Supplementary alignments	115,136 / 0.37%
Read min/max/mean length	30 / 100 / 99.28
Duplicated reads (estimated)	20,616,118 / 66.7%
Duplication rate	49.58%
Clipped reads	2,267,870 / 7.34%

2.2. ACGT Content

Number/percentage of A's	817,120,149 / 27.27%
Number/percentage of C's	683,492,079 / 22.81%
Number/percentage of T's	817,493,379 / 27.28%
Number/percentage of G's	678,415,604 / 22.64%
Number/percentage of N's	376,397 / 0.01%

GC Percentage	45.44%

2.3. Coverage

Mean	0.9682
Standard Deviation	26.9786

2.4. Mapping Quality

Mean Mapping Quality	55.19

2.5. Insert size

Mean	17,841.38
Standard Deviation	1,325,841.21
P25/Median/P75	152 / 213 / 287

2.6. Mismatches and indels

General error rate	0.55%
Mismatches	16,131,435
Insertions	176,058
Mapped reads with at least one insertion	0.57%
Deletions	149,815
Mapped reads with at least one deletion	0.48%
Homopolymer indels	46.56%

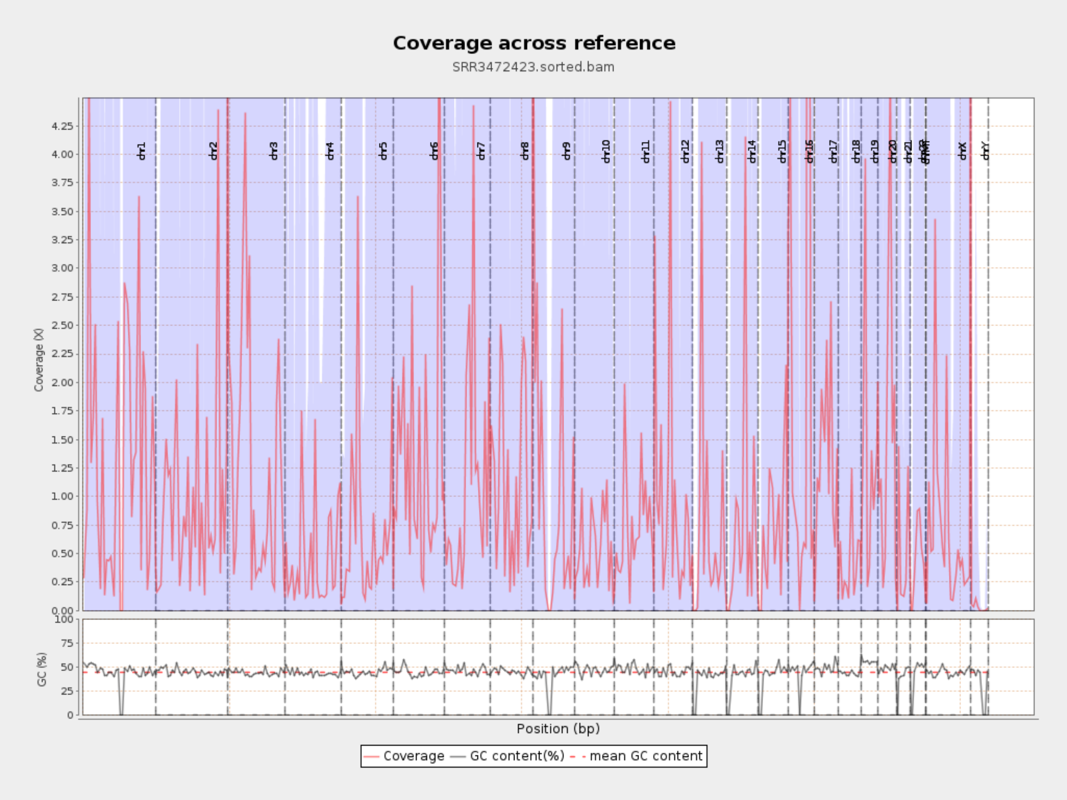
2.7. Chromosome stats

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

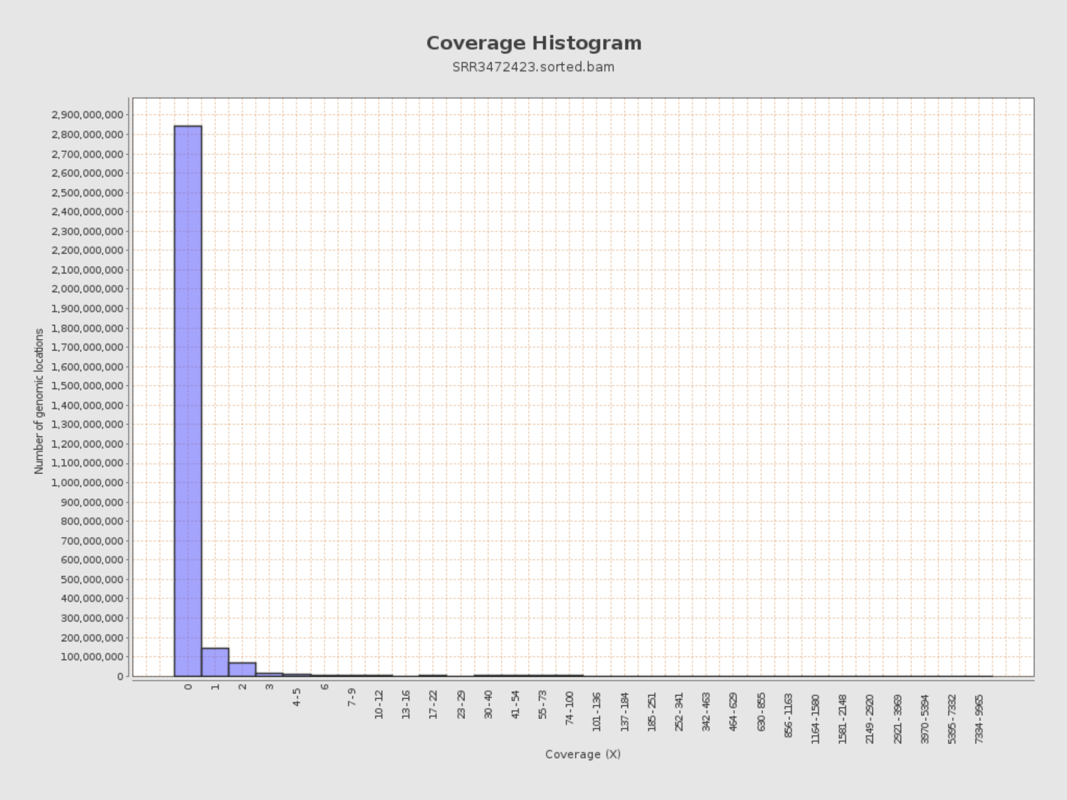
		bases	**coverage**	**deviation**
chr1	249250621	333679141	1.3387	38.003
chr2	243199373	227673887	0.9362	26.1394
chr3	198022430	263536232	1.3308	26.4003
chr4	191154276	92493451	0.4839	18.3672
chr5	180915260	128831779	0.7121	20.4813
chr6	171115067	229987398	1.3441	29.7505
chr7	159138663	179700615	1.1292	28.3358
chr8	146364022	166280832	1.1361	27.3791
chr9	141213431	130405879	0.9235	24.0816
chr10	135534747	77768654	0.5738	18.574
chr11	135006516	98150685	0.727	21.2587
chr12	133851895	139480699	1.0421	23.4718
chr13	115169878	83022131	0.7209	22.6337
chr14	107349540	82133674	0.7651	21.3759
chr15	102531392	75140434	0.7329	20.0968
chr16	90354753	188396840	2.0851	60.0567
chr17	81195210	109756302	1.3518	25.4637
chr18	78077248	31099447	0.3983	14.1524
chr19	59128983	80731638	1.3653	28.3302
chr20	63025520	100196406	1.5898	41.7391
chr21	48129895	26642175	0.5535	27.1787
chr22	51304566	23346208	0.4551	10.32
chrMT	16571	7008	0.4229	0.8361
chrX	155270560	127044405	0.8182	18.6102

chrY	59373566	1741689	0.0293	1.5444

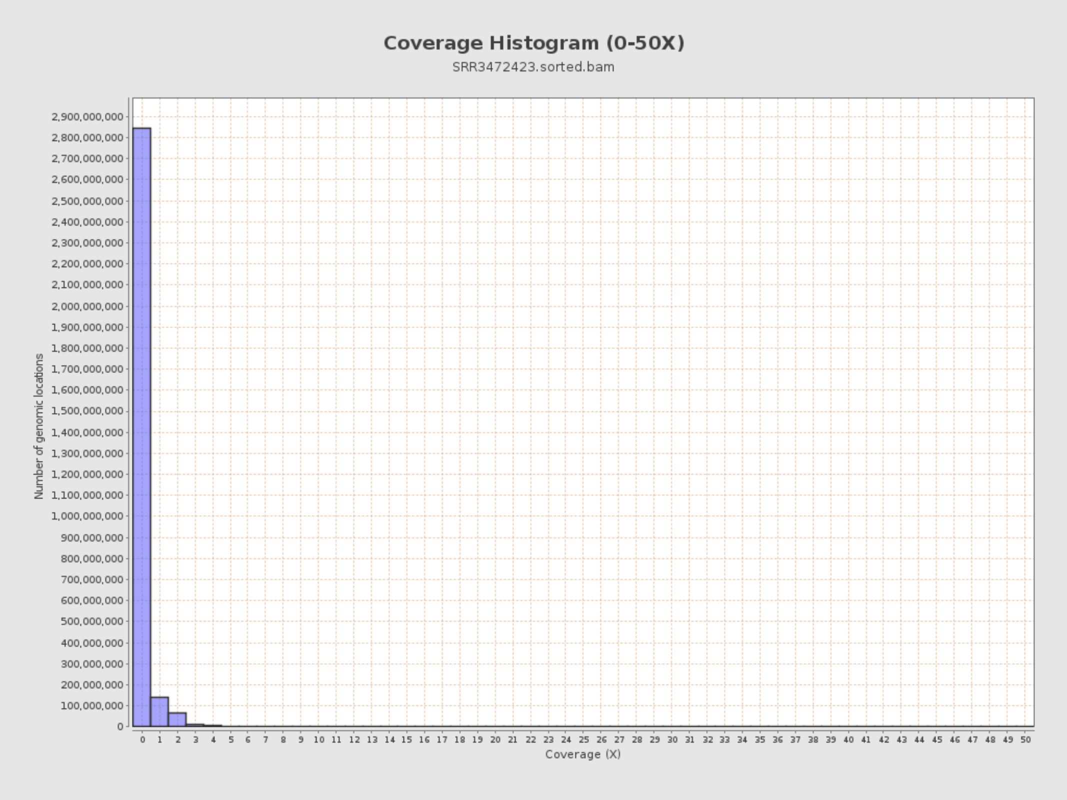
3. Results : Coverage across reference



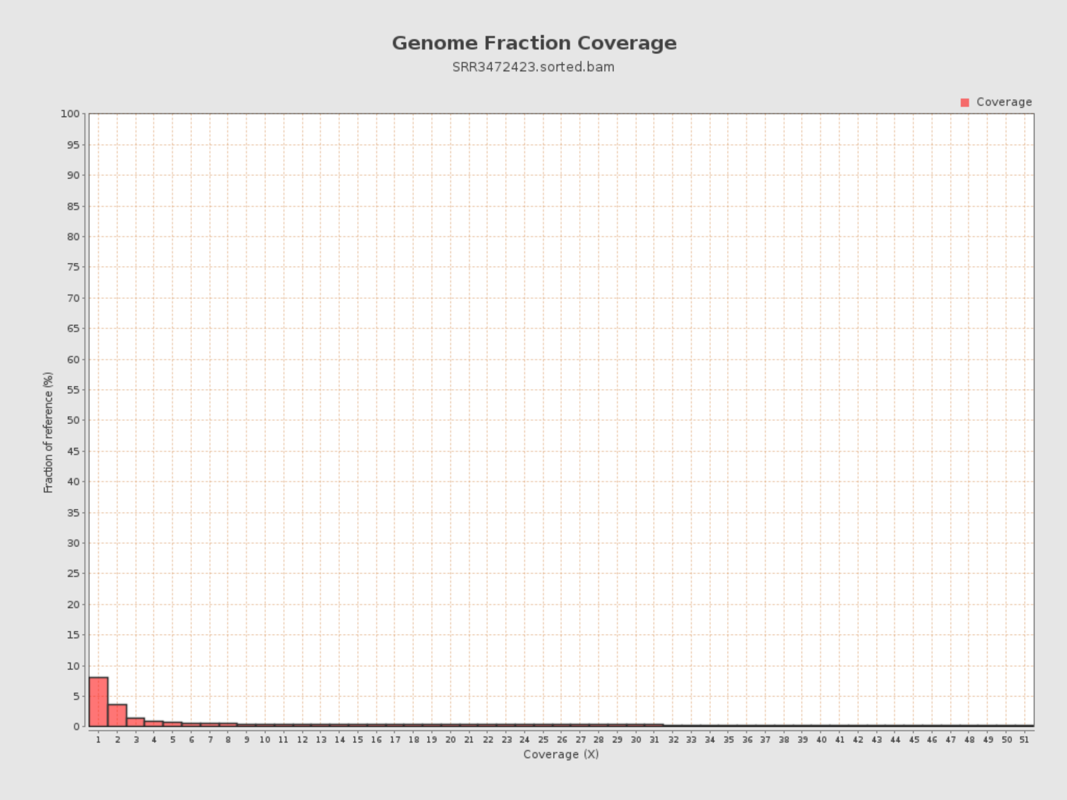
4. Results : Coverage Histogram



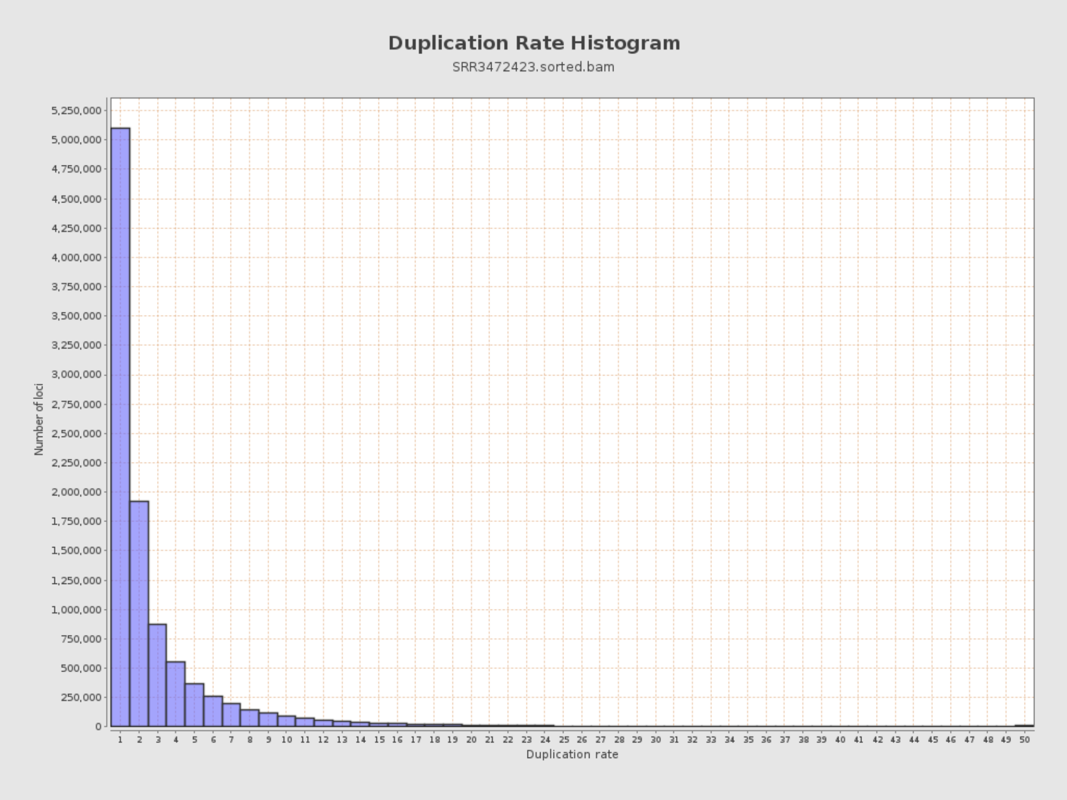
5. Results : Coverage Histogram (0-50X)



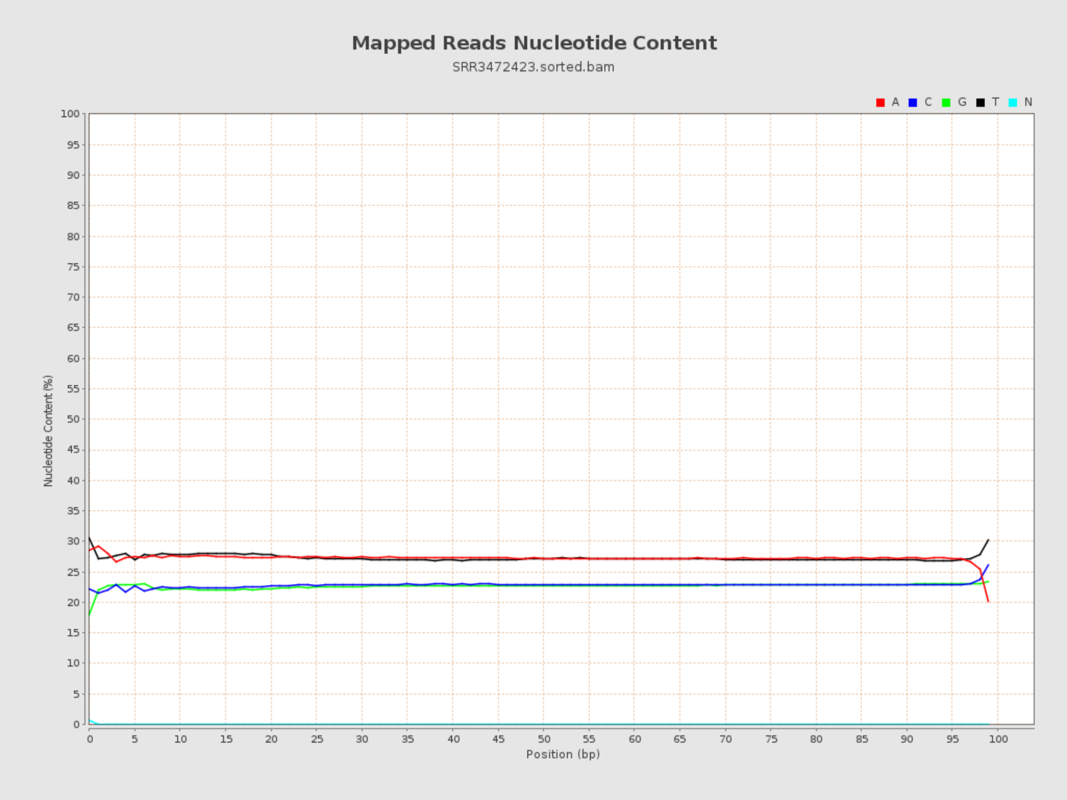
6. Results : Genome Fraction Coverage



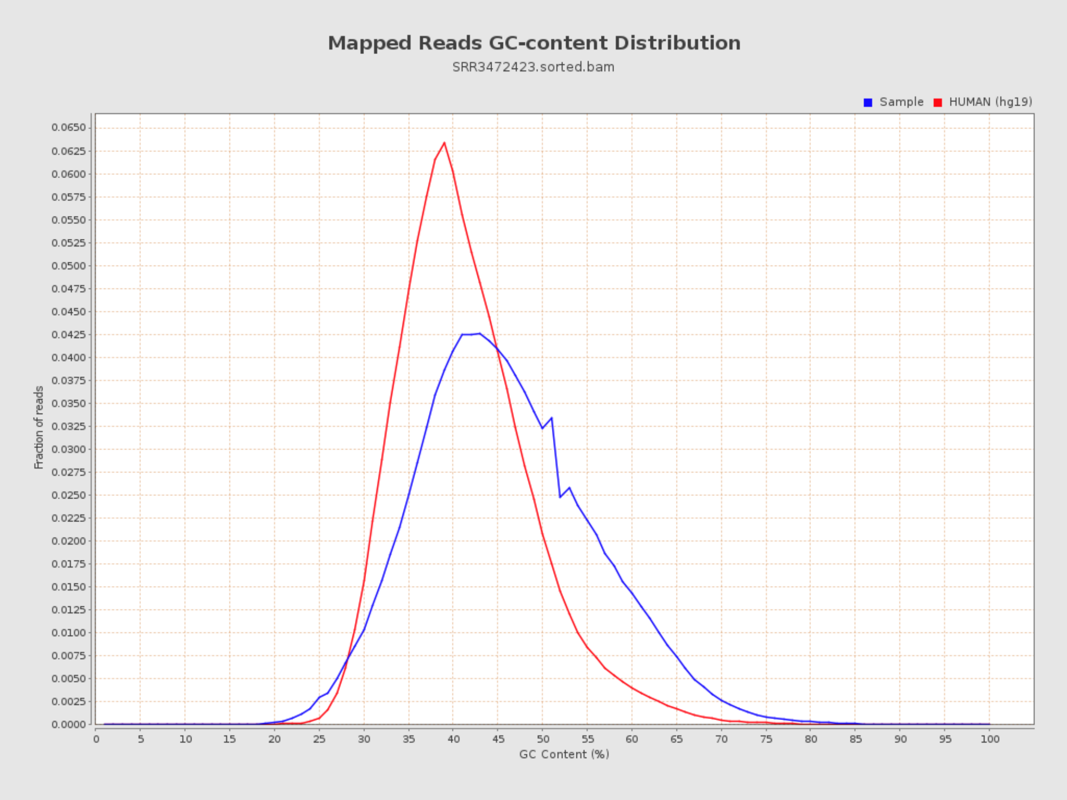
7. Results : Duplication Rate Histogram



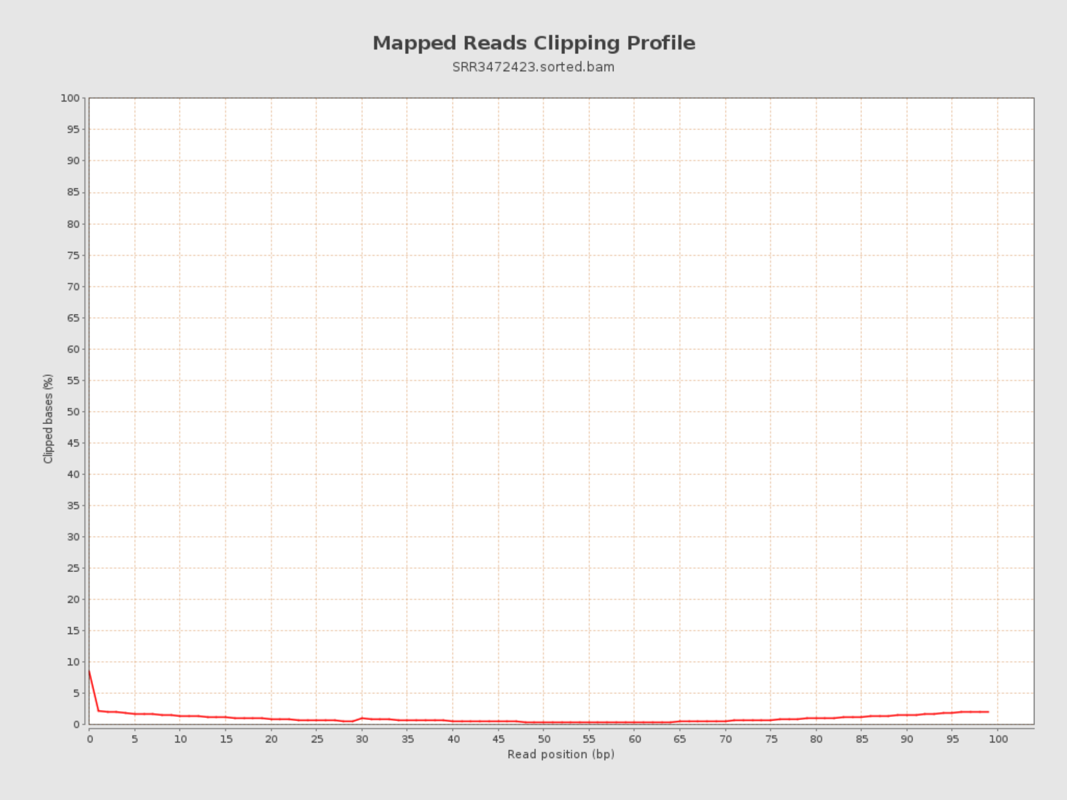
8. Results : Mapped Reads Nucleotide Content



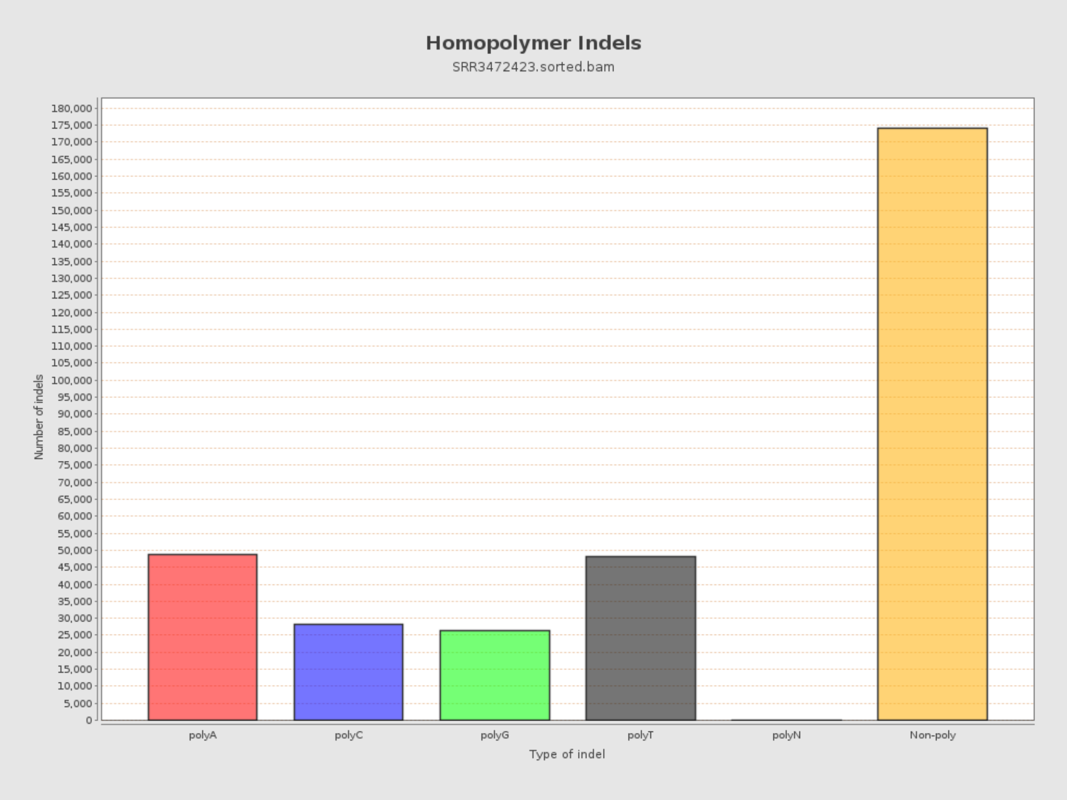
9. Results : Mapped Reads GC-content Distribution



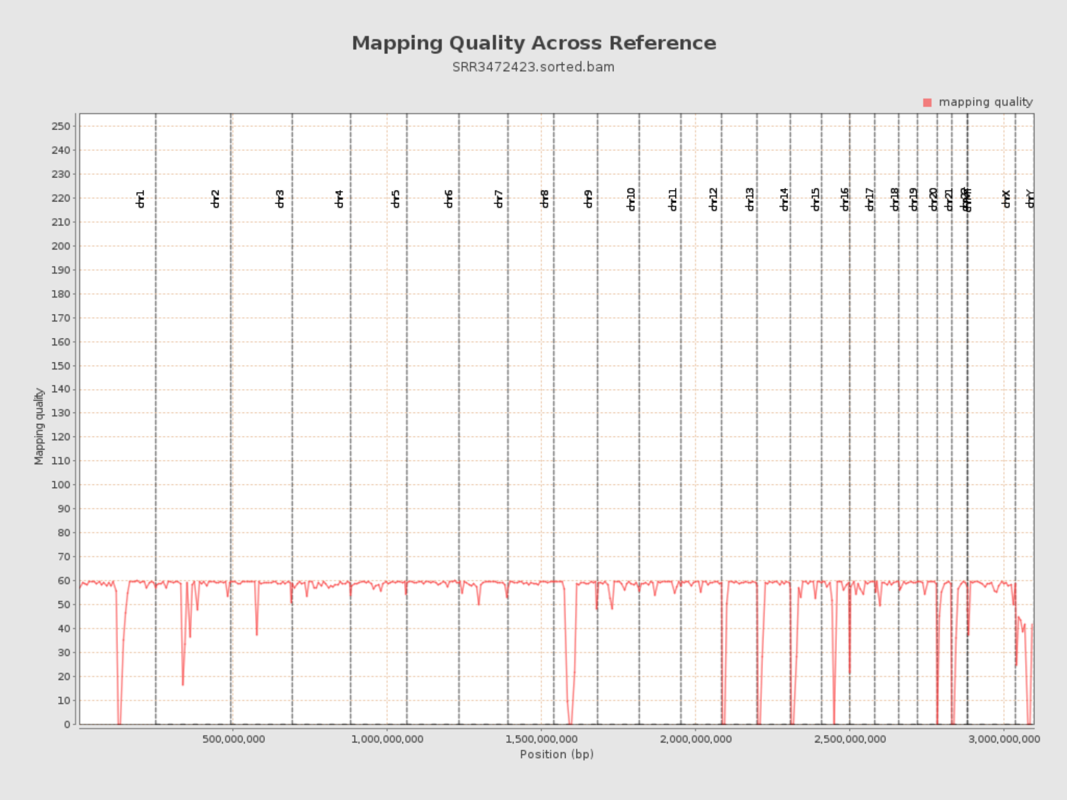
10. Results : Mapped Reads Clipping Profile



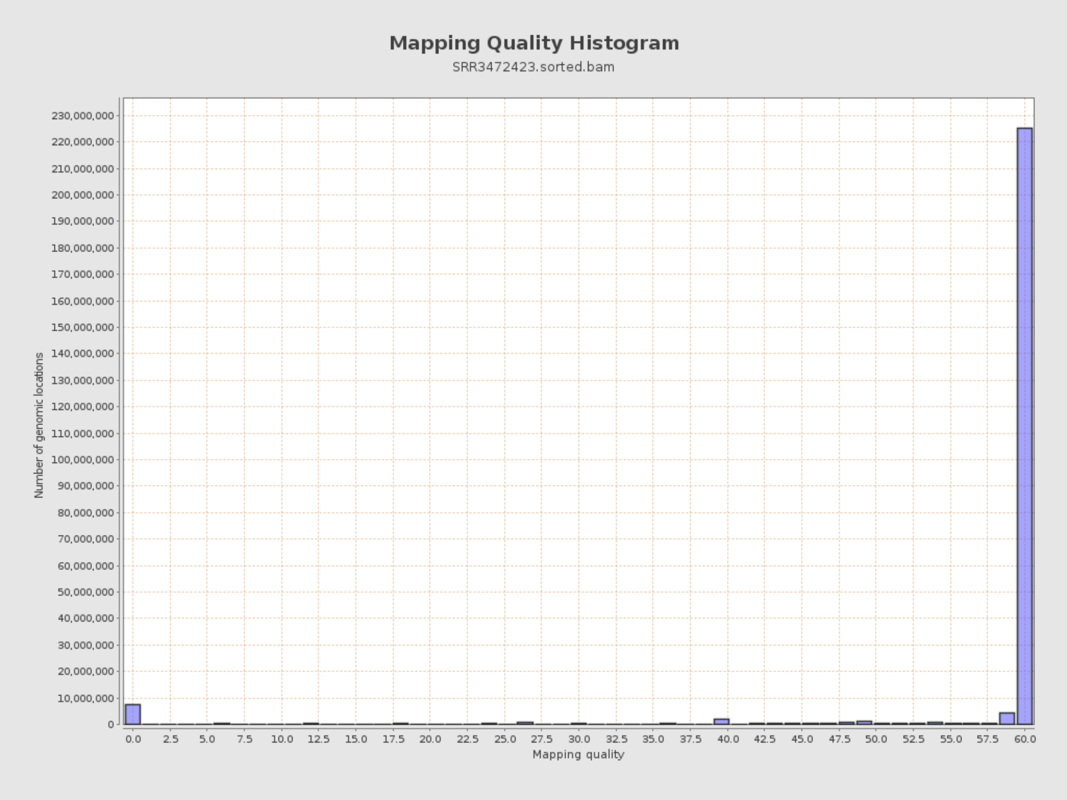
11. Results : Homopolymer Indels



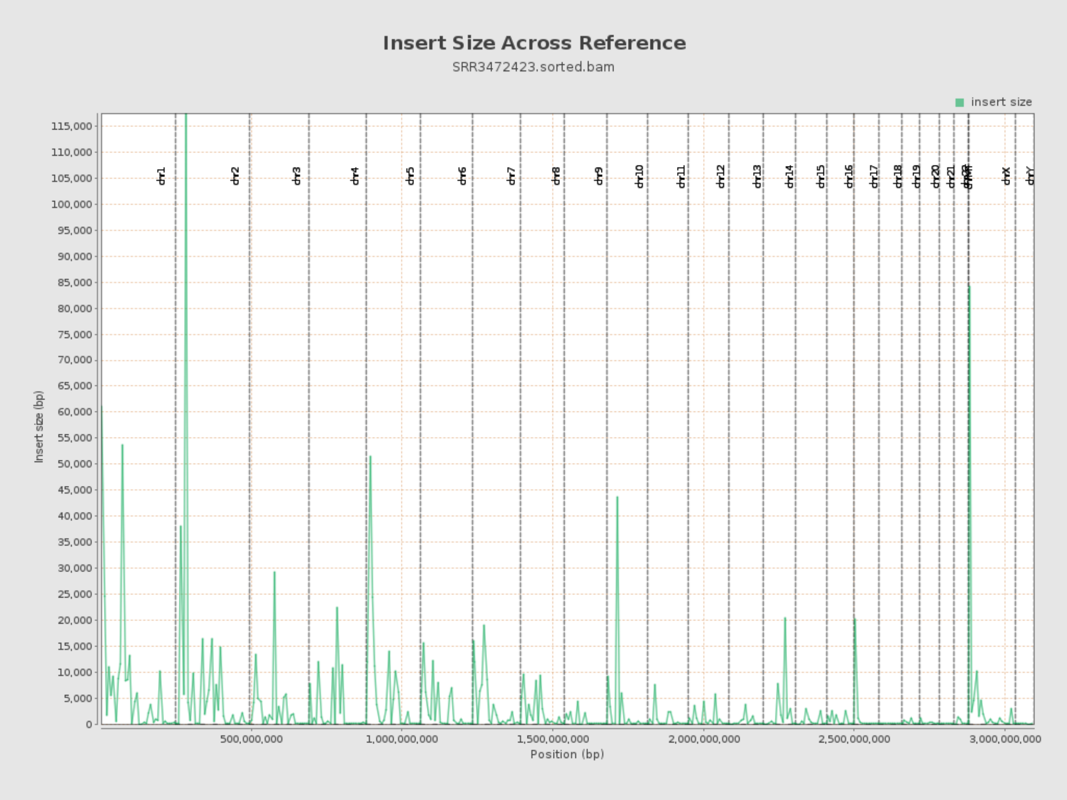
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram