Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 02:26:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472402.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_SRR3472402 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472402_1.fastq.gz SRR3472402_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 02:26:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472402.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,344,376
Mapped reads	20,191,266 / 99.25%
Unmapped reads	153,110 / 0.75%
Mapped paired reads	20,191,266 / 99.25%
Mapped reads, first in pair	10,122,247 / 49.75%
Mapped reads, second in pair	10,069,019 / 49.49%
Mapped reads, both in pair	20,098,592 / 98.79%
Mapped reads, singletons	92,674 / 0.46%
Secondary alignments	0
Supplementary alignments	77,654 / 0.38%
Read min/max/mean length	30 / 100 / 99.47
Duplicated reads (estimated)	13,034,895 / 64.07%
Duplication rate	48.18%
Clipped reads	1,424,092 / 7%

2.2. ACGT Content

Number/percentage of A's	536,293,373 / 27.07%
Number/percentage of C's	455,138,113 / 22.97%
Number/percentage of T's	536,670,722 / 27.09%
Number/percentage of G's	452,878,391 / 22.86%
Number/percentage of N's	255,611 / 0.01%

GC Percentage	45.83%

2.3. Coverage

Mean	0.6401
Standard Deviation	19.5748

2.4. Mapping Quality

Mean Mapping Quality	55.25

2.5. Insert size

Mean	16,249.38
Standard Deviation	1,259,290.15
P25/Median/P75	154 / 213 / 286

2.6. Mismatches and indels

General error rate	0.55%
Mismatches	10,732,692
Insertions	122,457
Mapped reads with at least one insertion	0.6%
Deletions	103,150
Mapped reads with at least one deletion	0.5%
Homopolymer indels	45.3%

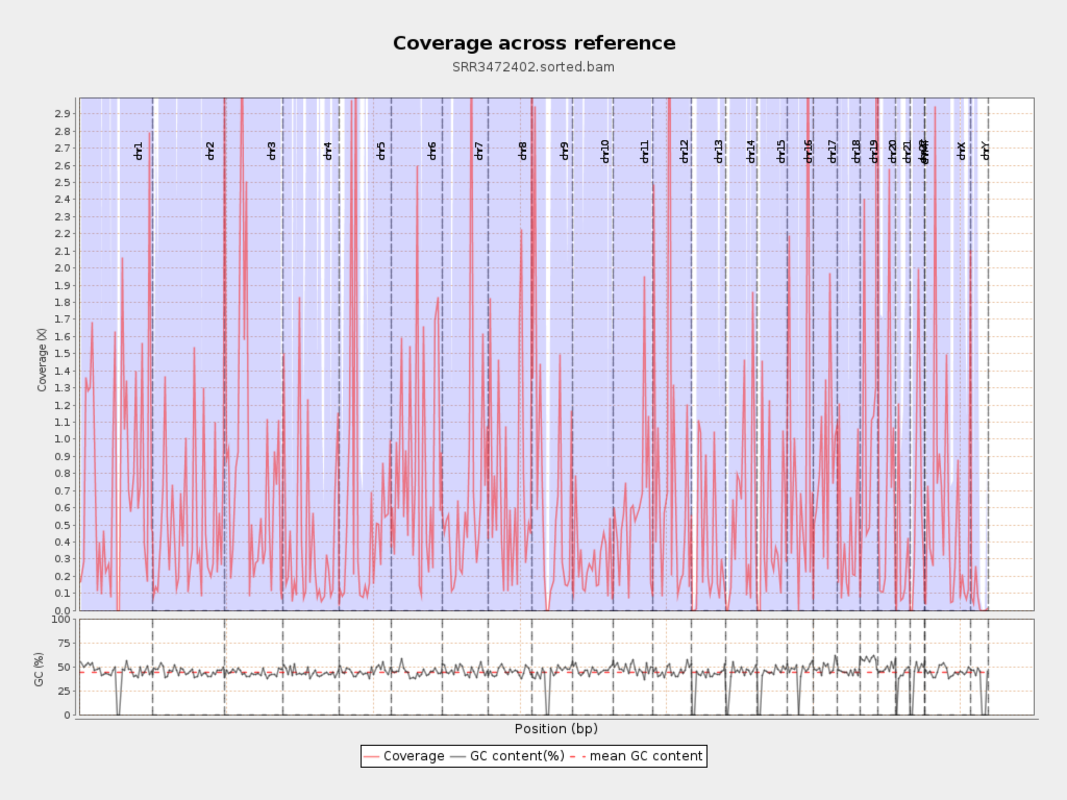
2.7. Chromosome stats

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

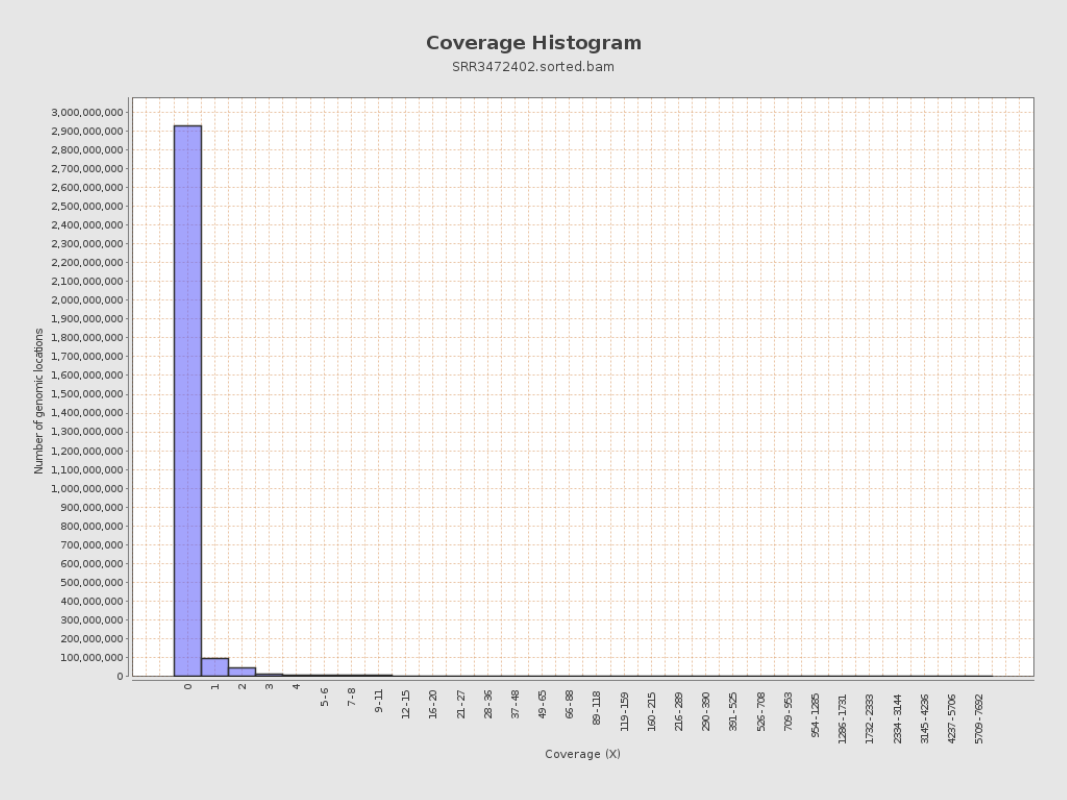
		bases	coverage	deviation
chr1	249250621	202679063	0.8132	22.6775
chr2	243199373	118695556	0.4881	14.6317
chr3	198022430	172024375	0.8687	18.7342
chr4	191154276	75400349	0.3944	14.4611
chr5	180915260	112695278	0.6229	20.9757
chr6	171115067	146248090	0.8547	23.2485
chr7	159138663	111491131	0.7006	19.3747
chr8	146364022	108852845	0.7437	19.8018
chr9	141213431	97773910	0.6924	17.3007
chr10	135534747	37891632	0.2796	9.0262
chr11	135006516	82075472	0.6079	16.8784
chr12	133851895	115354638	0.8618	26.4584
chr13	115169878	42497859	0.369	13.3119
chr14	107349540	57167648	0.5325	20.4721
chr15	102531392	48426945	0.4723	15.6638
chr16	90354753	86649603	0.959	28.9093
chr17	81195210	71332054	0.8785	22.3586
chr18	78077248	34449429	0.4412	12.8598
chr19	59128983	71790231	1.2141	35.4717
chr20	63025520	46446493	0.7369	24.8201
chr21	48129895	15739720	0.327	18.3948
chr22	51304566	32556380	0.6346	25.7692
chrMT	16571	1136	0.0686	0.2856
chrX	155270560	89728319	0.5779	15.5836

chrY	59373566	3504294	0.059	3.6181

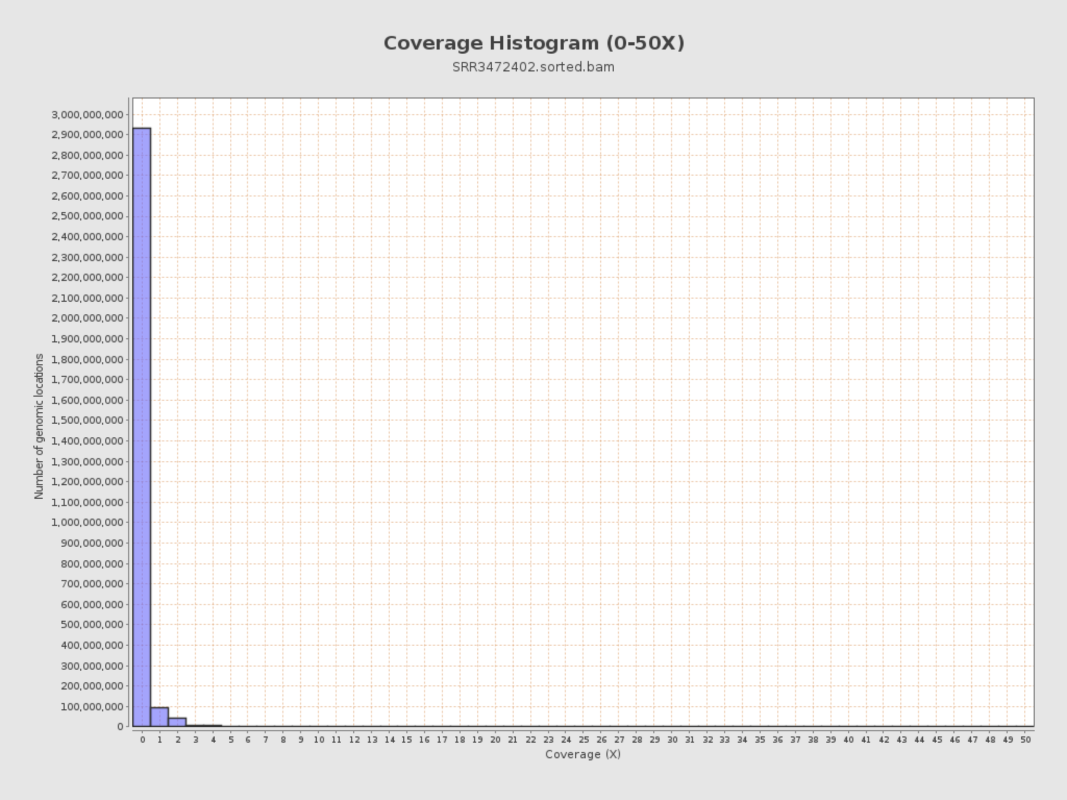
3. Results : Coverage across reference



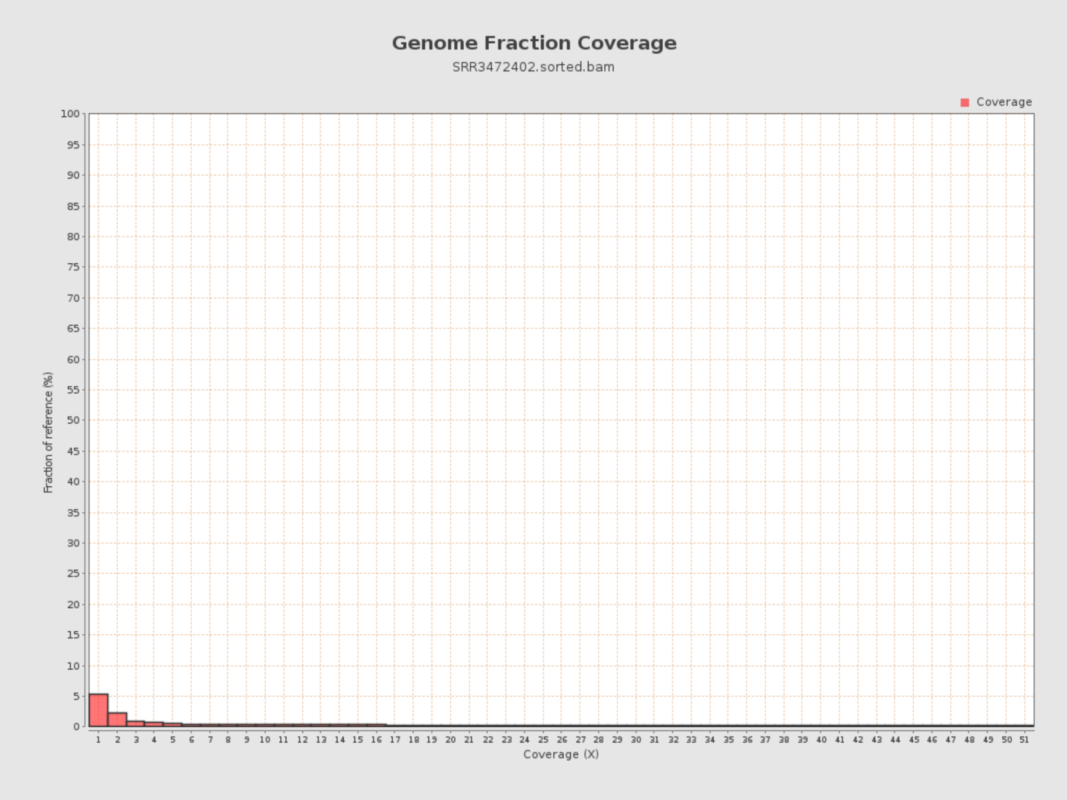
4. Results : Coverage Histogram



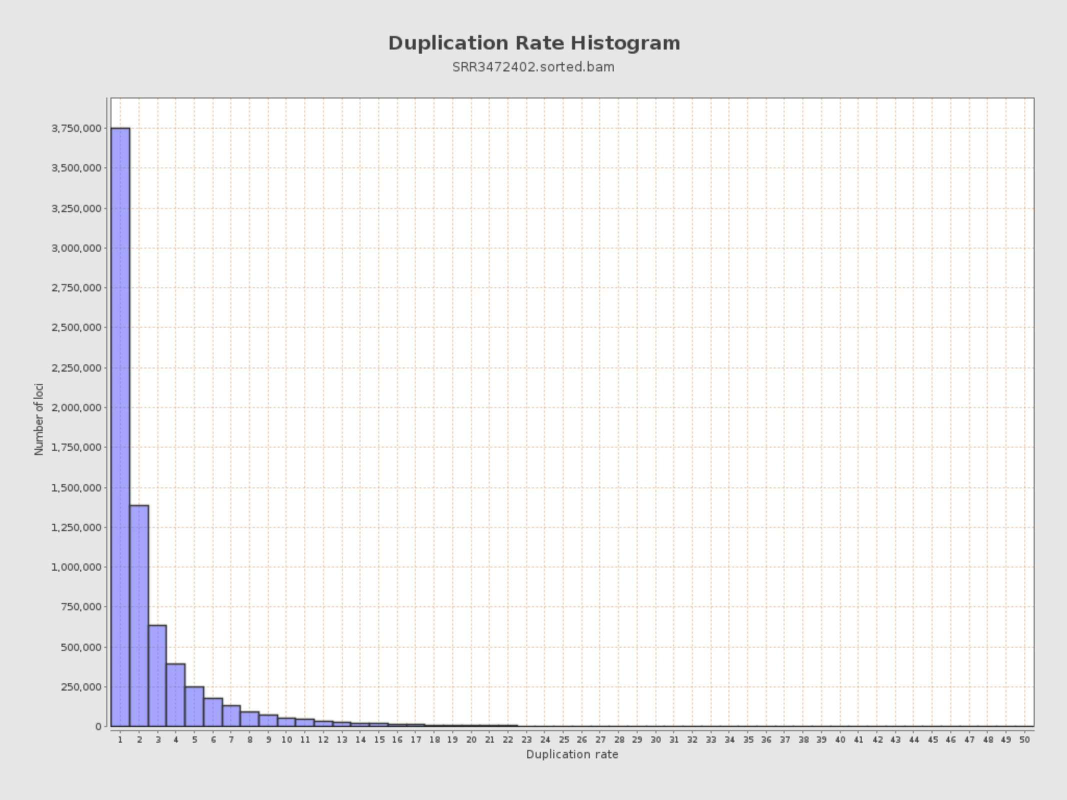
5. Results : Coverage Histogram (0-50X)



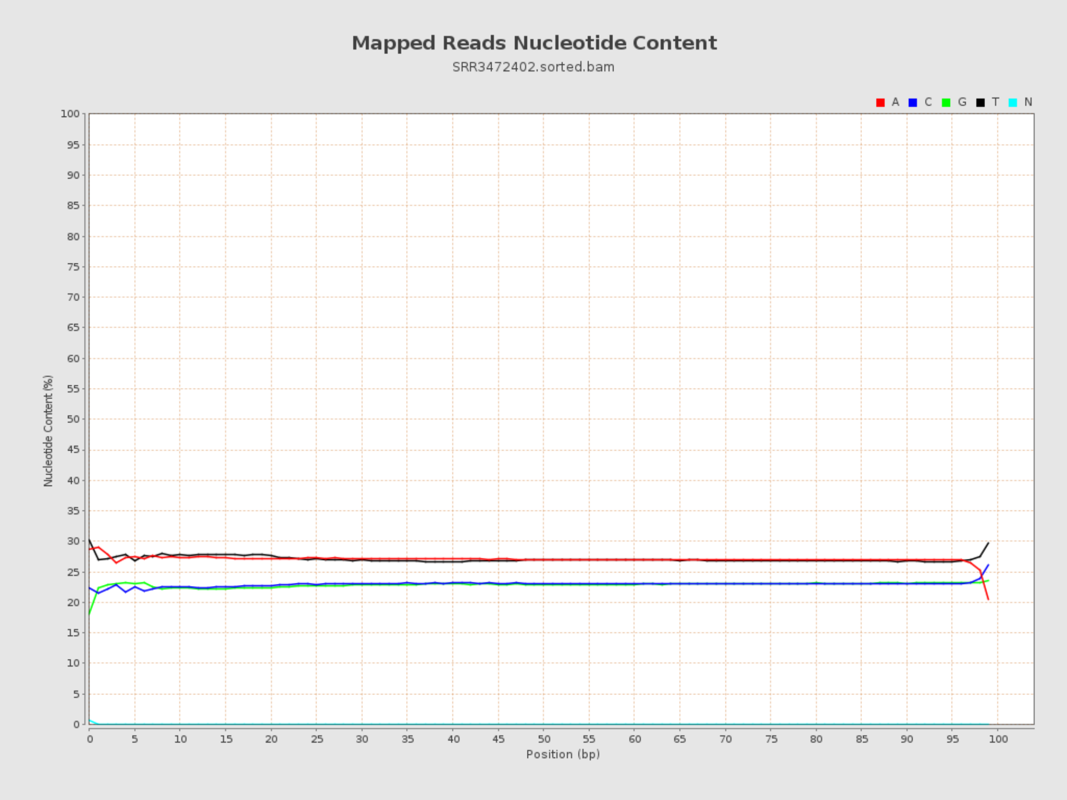
6. Results : Genome Fraction Coverage



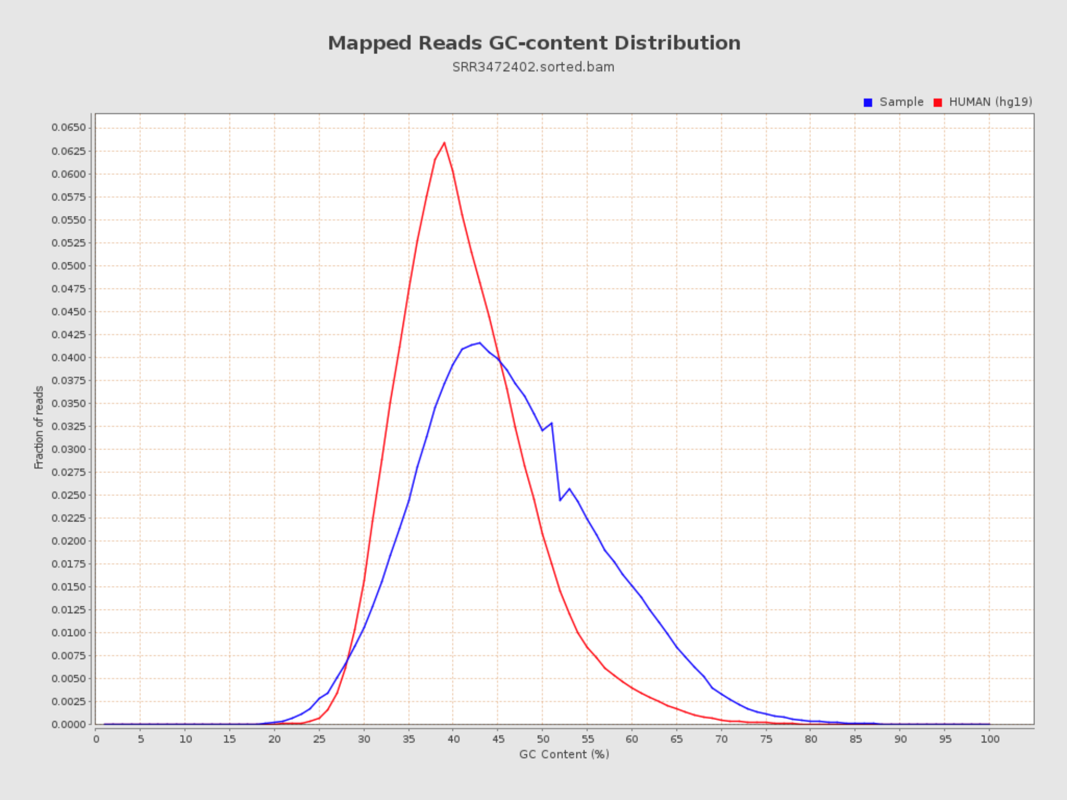
7. Results : Duplication Rate Histogram



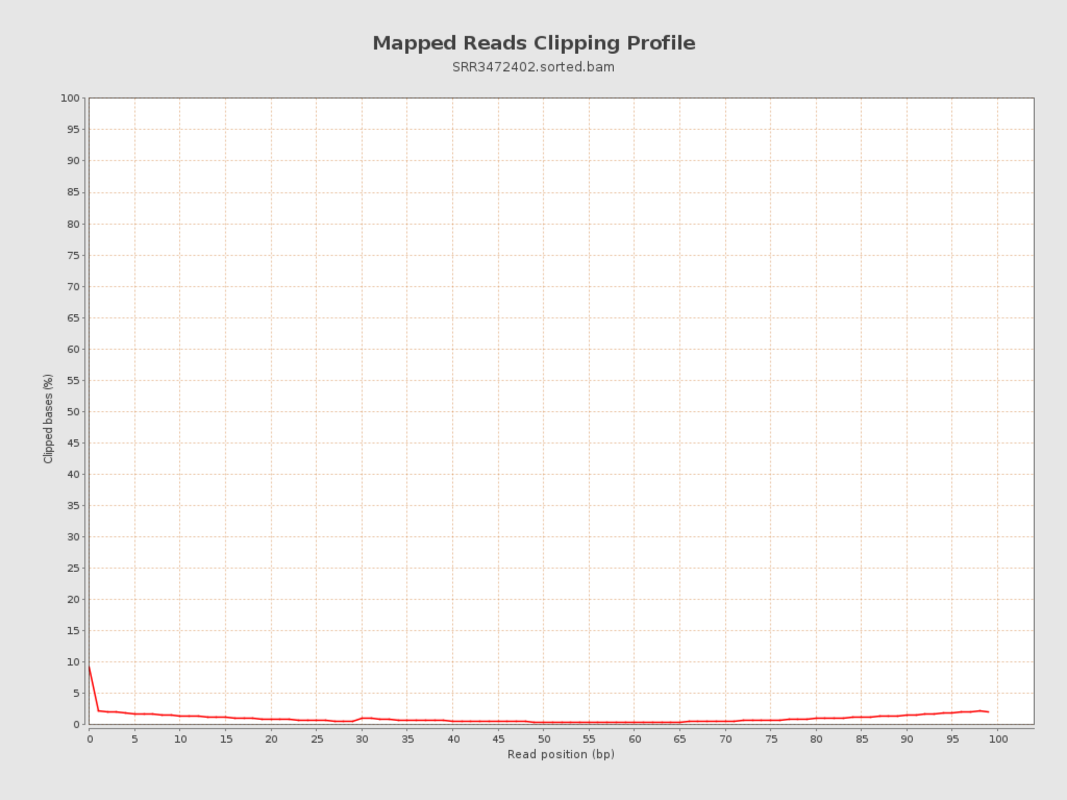
8. Results : Mapped Reads Nucleotide Content



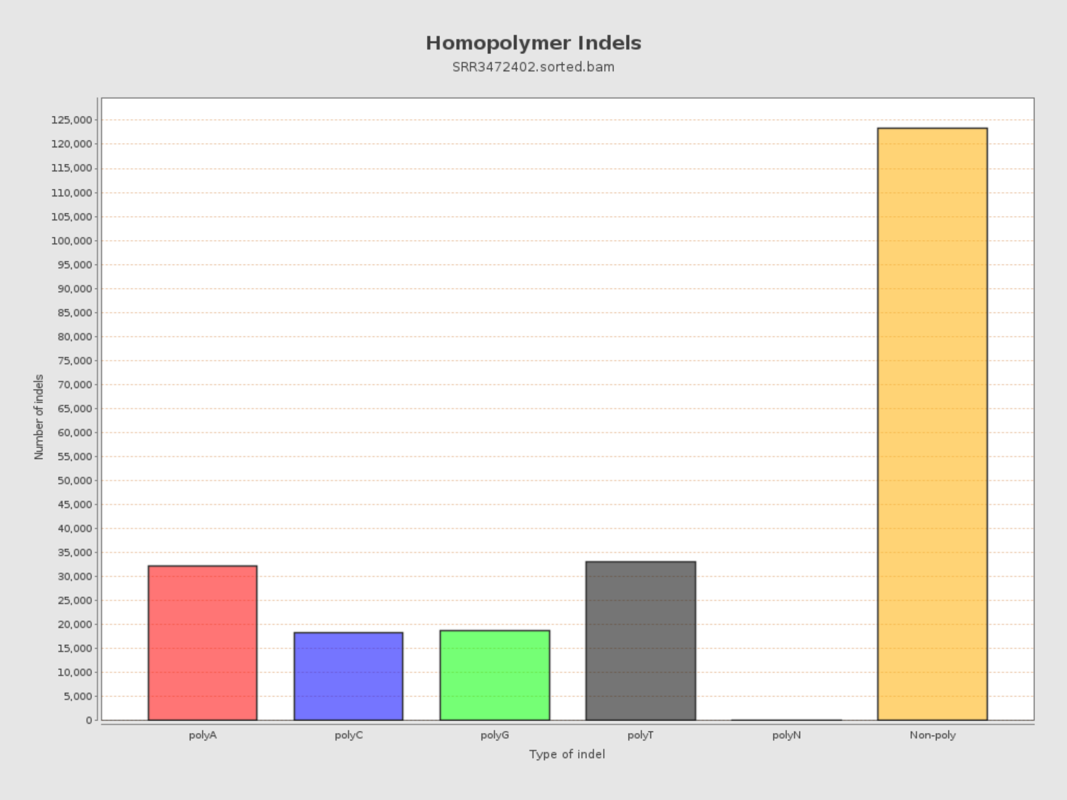
9. Results : Mapped Reads GC-content Distribution



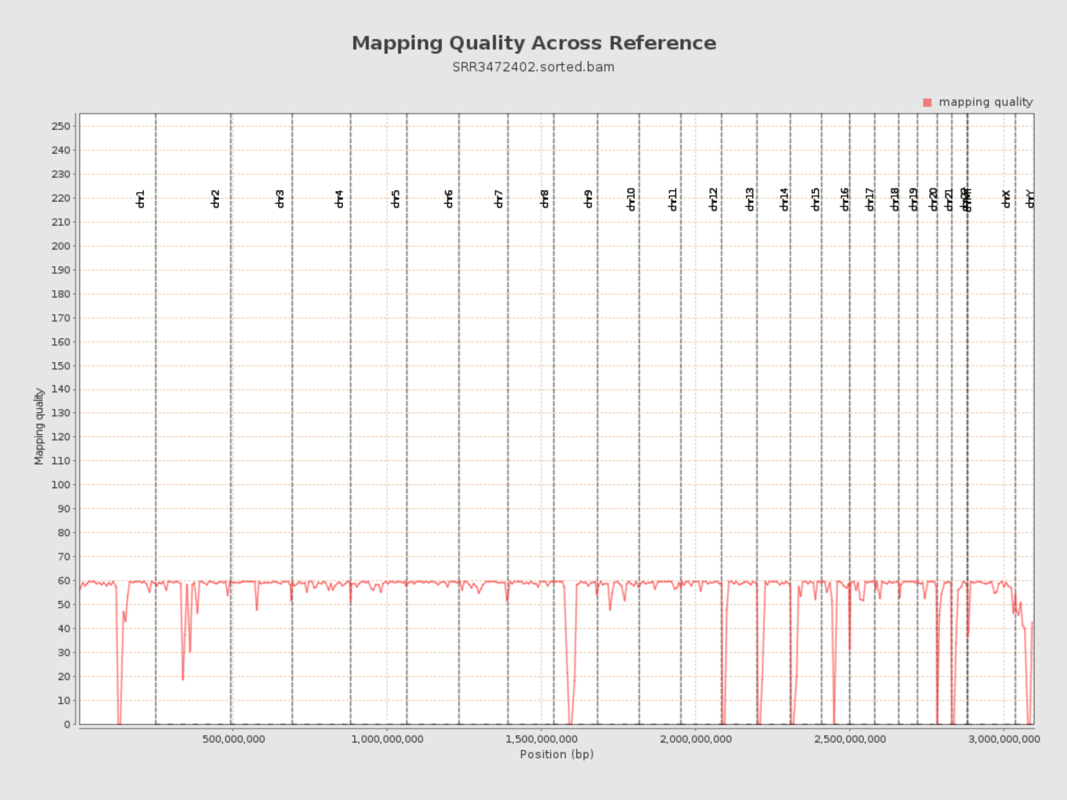
10. Results : Mapped Reads Clipping Profile



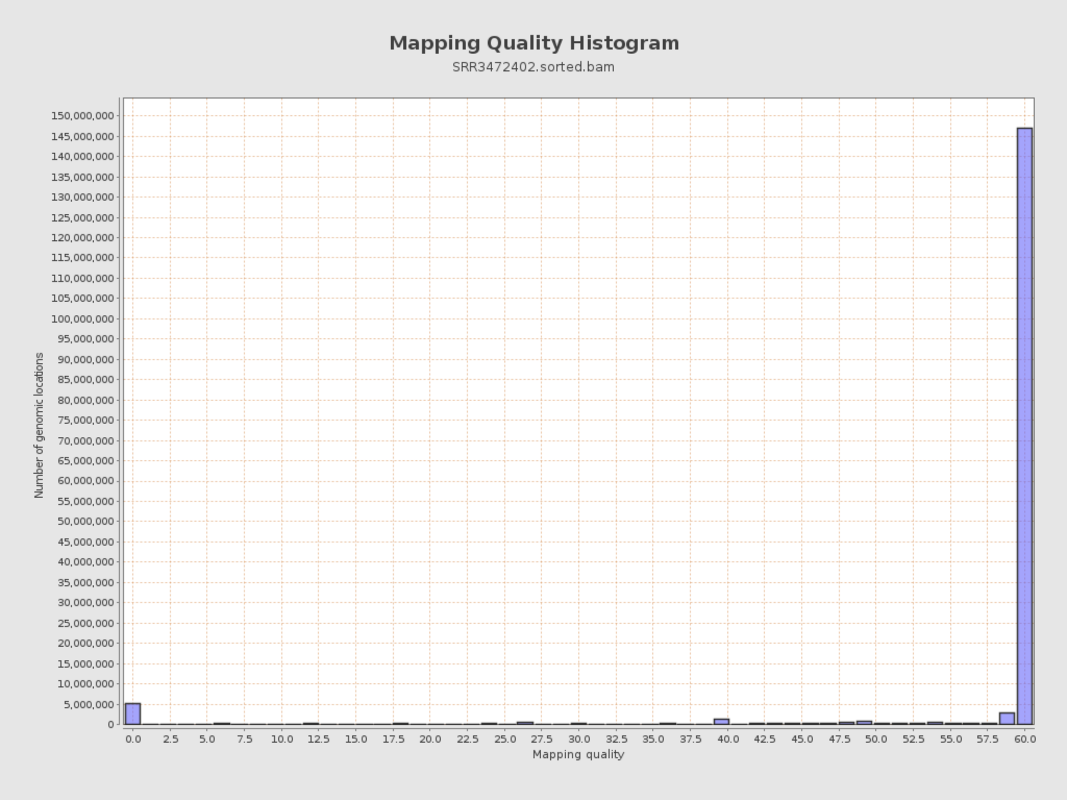
11. Results : Homopolymer Indels



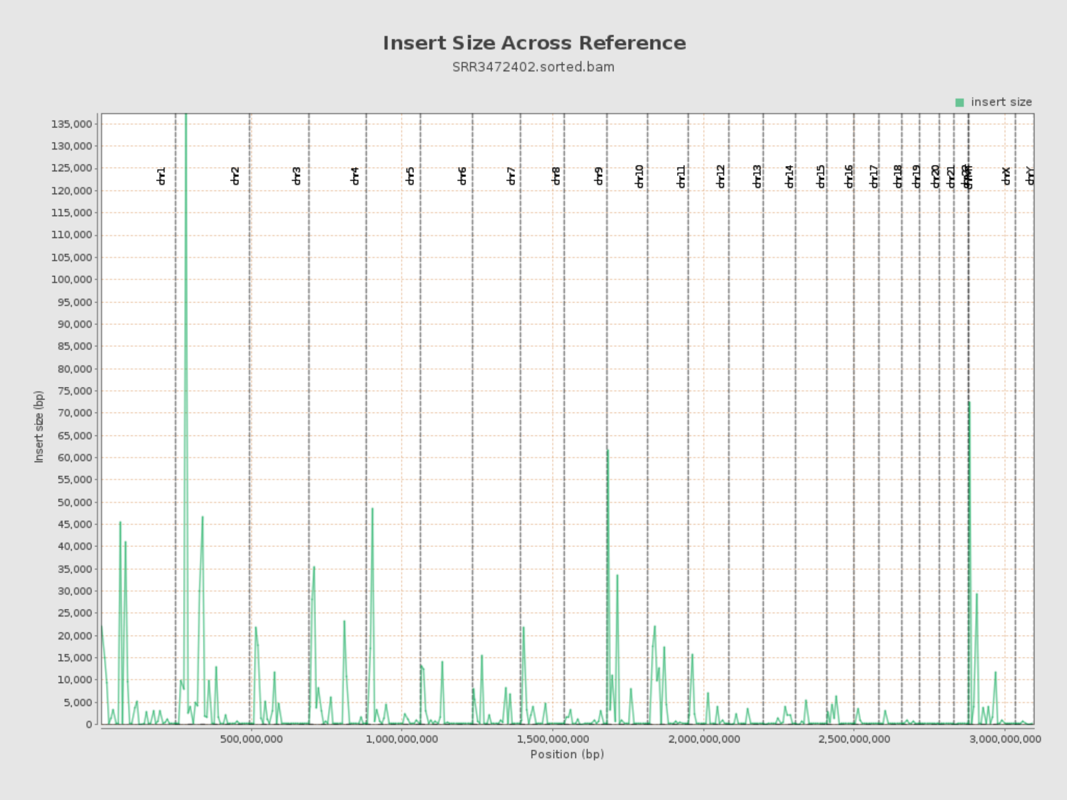
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram