Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 20:11:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472394.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_SRR3472394 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472394_1.fastq.gz SRR3472394_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 20:11:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472394.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,446,242
Mapped reads	18,272,647 / 99.06%
Unmapped reads	173,595 / 0.94%
Mapped paired reads	18,272,647 / 99.06%
Mapped reads, first in pair	9,164,361 / 49.68%
Mapped reads, second in pair	9,108,286 / 49.38%
Mapped reads, both in pair	18,161,200 / 98.45%
Mapped reads, singletons	111,447 / 0.6%
Secondary alignments	0
Supplementary alignments	68,819 / 0.37%
Read min/max/mean length	30 / 100 / 99.48
Duplicated reads (estimated)	11,180,018 / 60.61%
Duplication rate	47.47%
Clipped reads	1,269,099 / 6.88%

2.2. ACGT Content

Number/percentage of A's	483,471,503 / 26.96%
Number/percentage of C's	414,454,819 / 23.11%
Number/percentage of T's	483,208,701 / 26.95%
Number/percentage of G's	411,711,888 / 22.96%
Number/percentage of N's	223,047 / 0.01%

GC Percentage	46.08%

2.3. Coverage

Mean	0.5793
Standard Deviation	16.0124

2.4. Mapping Quality

Mean Mapping Quality	54.86

2.5. Insert size

Mean	18,295.31
Standard Deviation	1,324,397.79
P25/Median/P75	159 / 220 / 295

2.6. Mismatches and indels

General error rate	0.59%
Mismatches	10,472,943
Insertions	104,156
Mapped reads with at least one insertion	0.56%
Deletions	90,843
Mapped reads with at least one deletion	0.49%
Homopolymer indels	45.62%

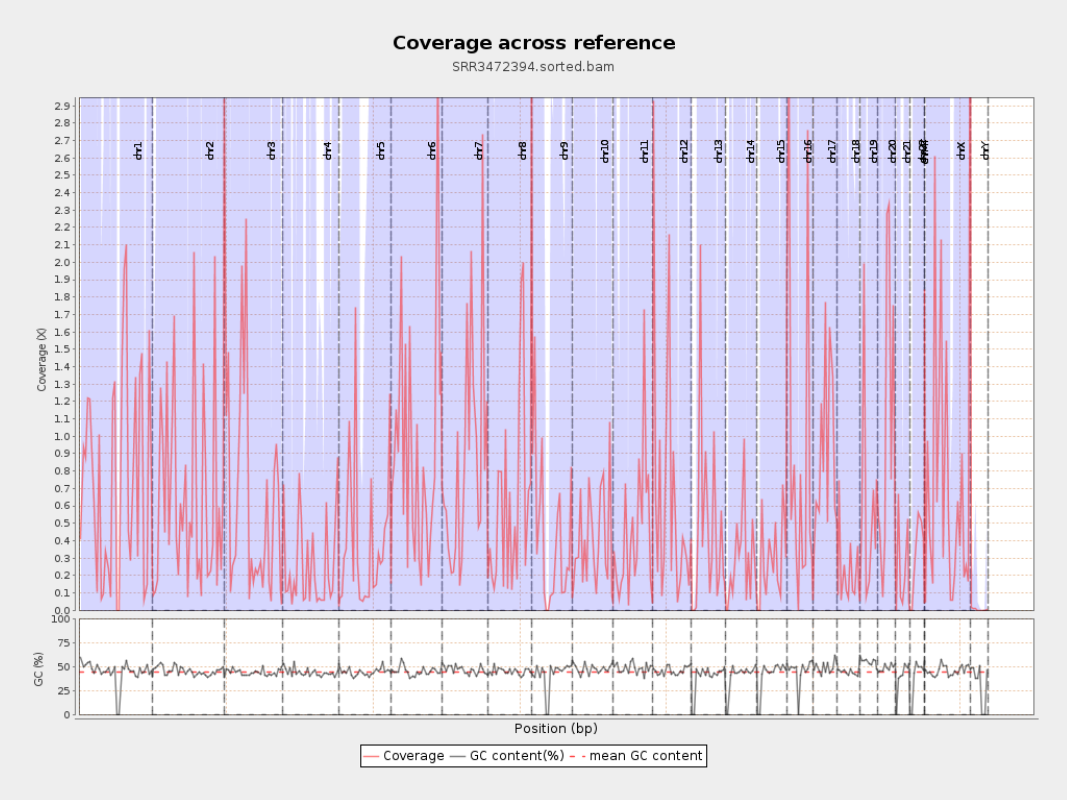
2.7. Chromosome stats

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

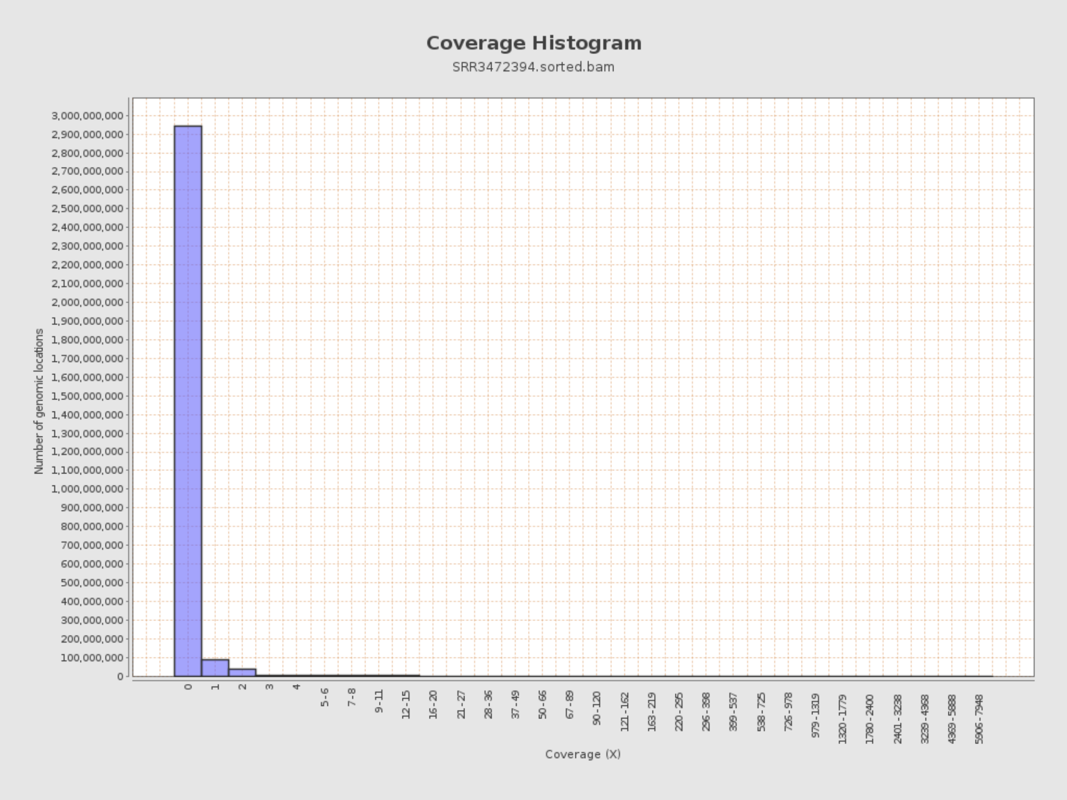
		bases	coverage	deviation
chr1	249250621	192915256	0.774	19.2209
chr2	243199373	157349256	0.647	18.4497
chr3	198022430	131540758	0.6643	14.7965
chr4	191154276	48210715	0.2522	8.5313
chr5	180915260	71738318	0.3965	13.7469
chr6	171115067	155268178	0.9074	22.3792
chr7	159138663	138329302	0.8692	21.0818
chr8	146364022	92819383	0.6342	16.1419
chr9	141213431	63364886	0.4487	10.5479
chr10	135534747	55417996	0.4089	11.7189
chr11	135006516	60630227	0.4491	15.479
chr12	133851895	90563905	0.6766	15.9476
chr13	115169878	54366456	0.4721	14.0177
chr14	107349540	30361009	0.2828	8.3577
chr15	102531392	30789444	0.3003	9.6984
chr16	90354753	83981979	0.9295	20.2993
chr17	81195210	74274719	0.9148	18.7292
chr18	78077248	18117712	0.232	6.494
chr19	59128983	34662857	0.5862	11.6905
chr20	63025520	66364520	1.053	25.5365
chr21	48129895	11637503	0.2418	10.9647
chr22	51304566	16264567	0.317	10.5833
chrMT	16571	30498	1.8404	1.665
chrX	155270560	114000172	0.7342	20.0549

chrY	59373566	287372	0.0048	0.3109

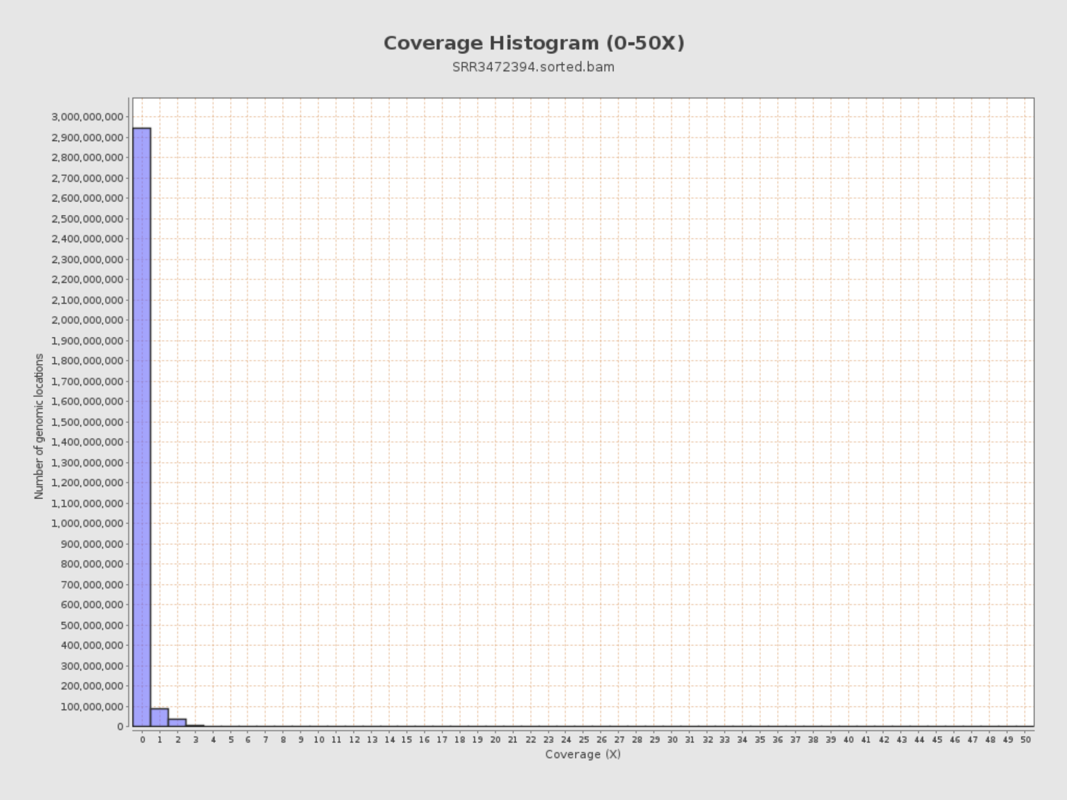
3. Results : Coverage across reference



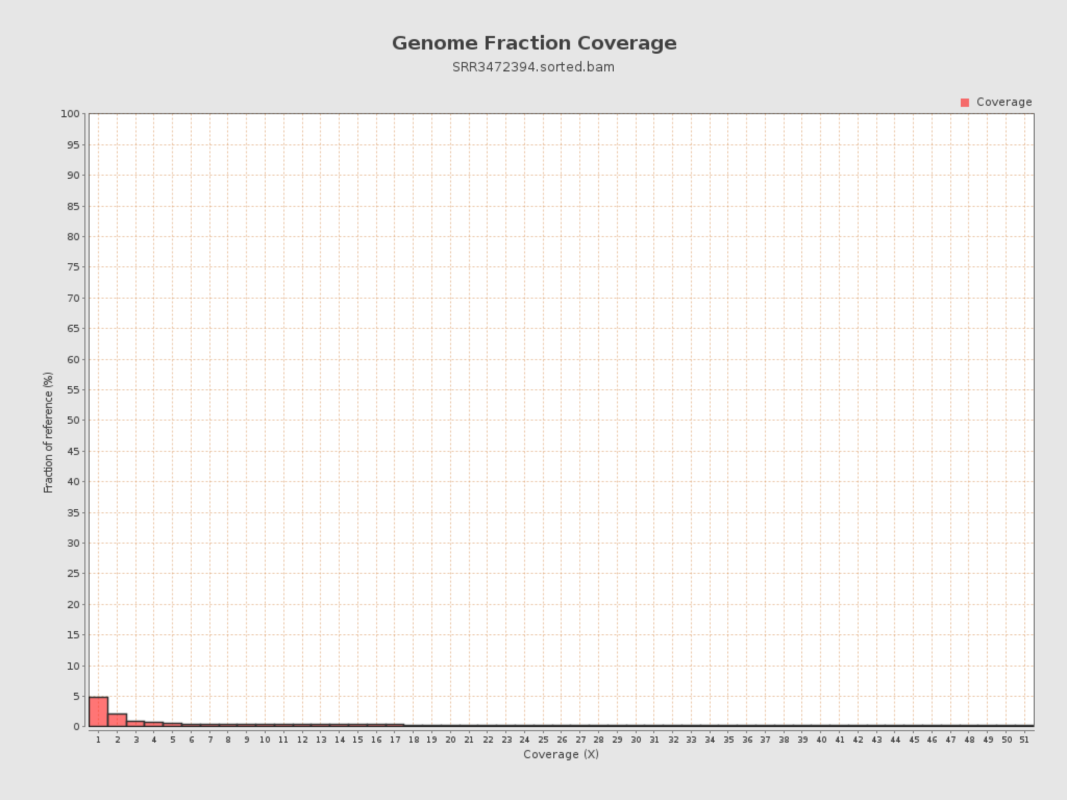
4. Results : Coverage Histogram



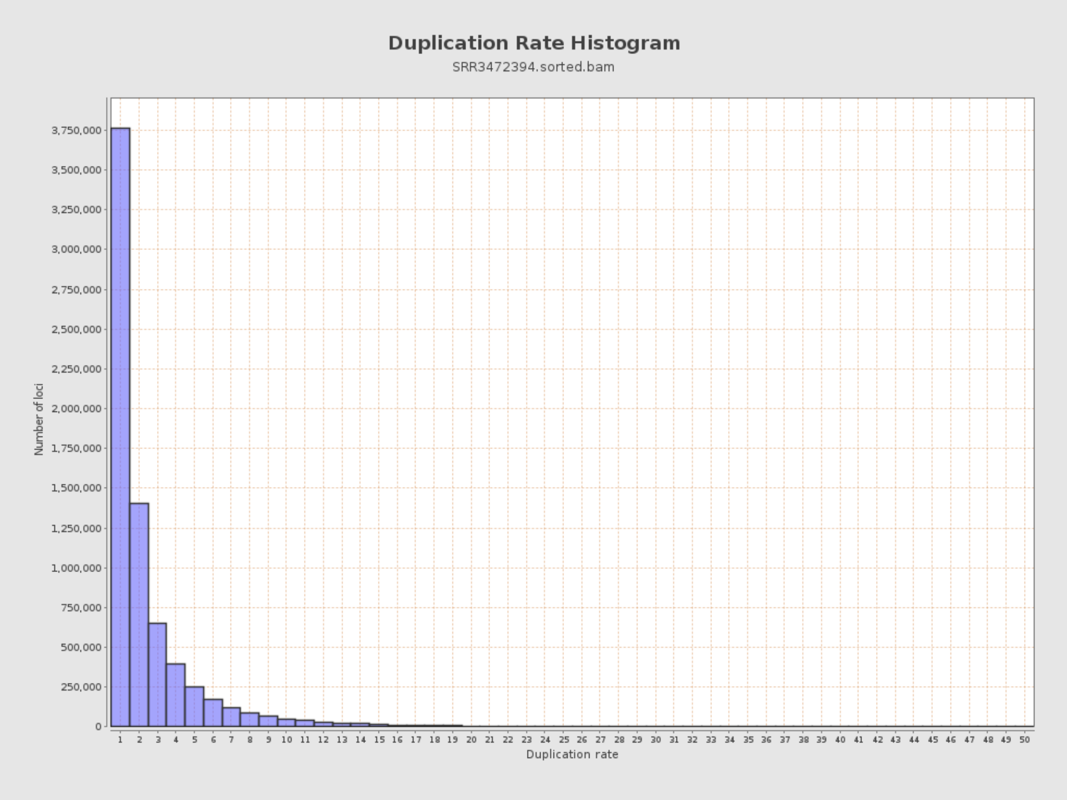
5. Results : Coverage Histogram (0-50X)



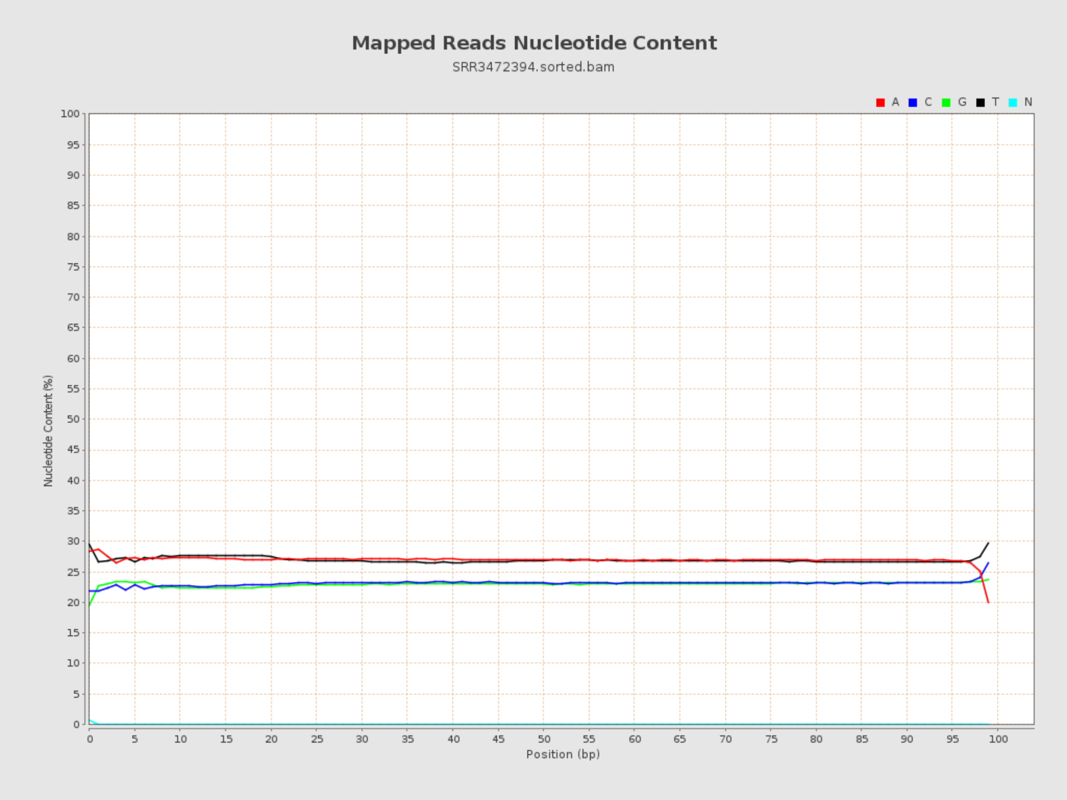
6. Results : Genome Fraction Coverage



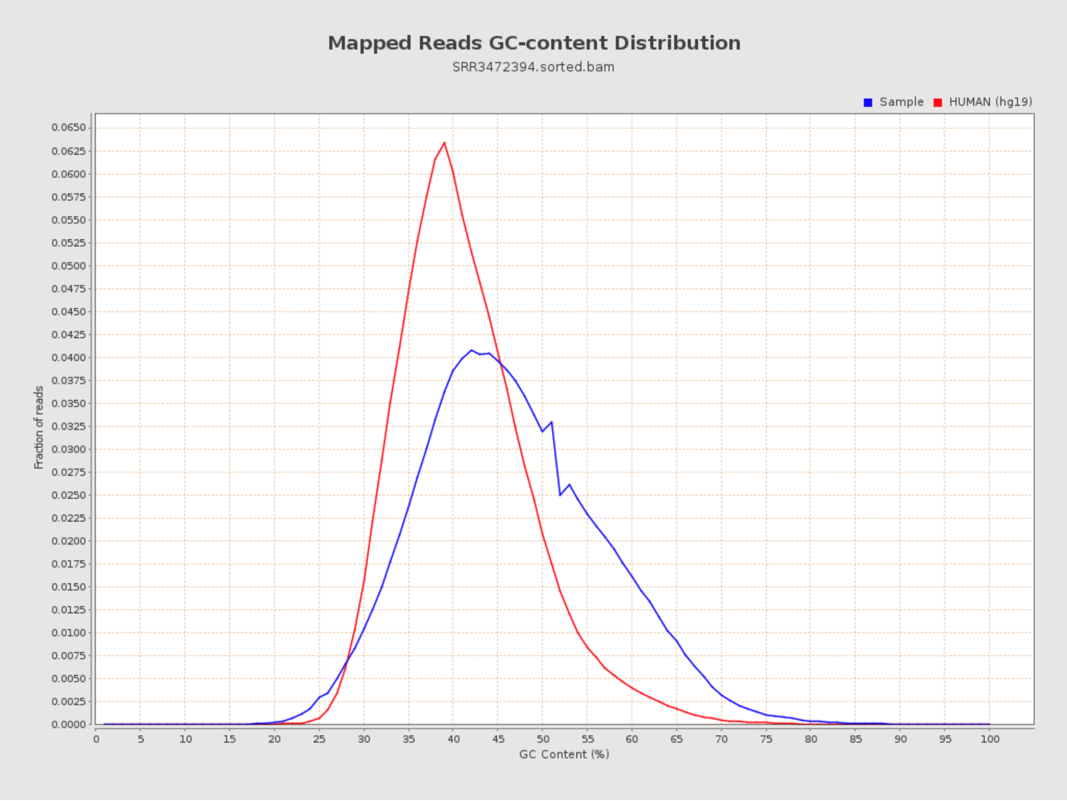
7. Results : Duplication Rate Histogram



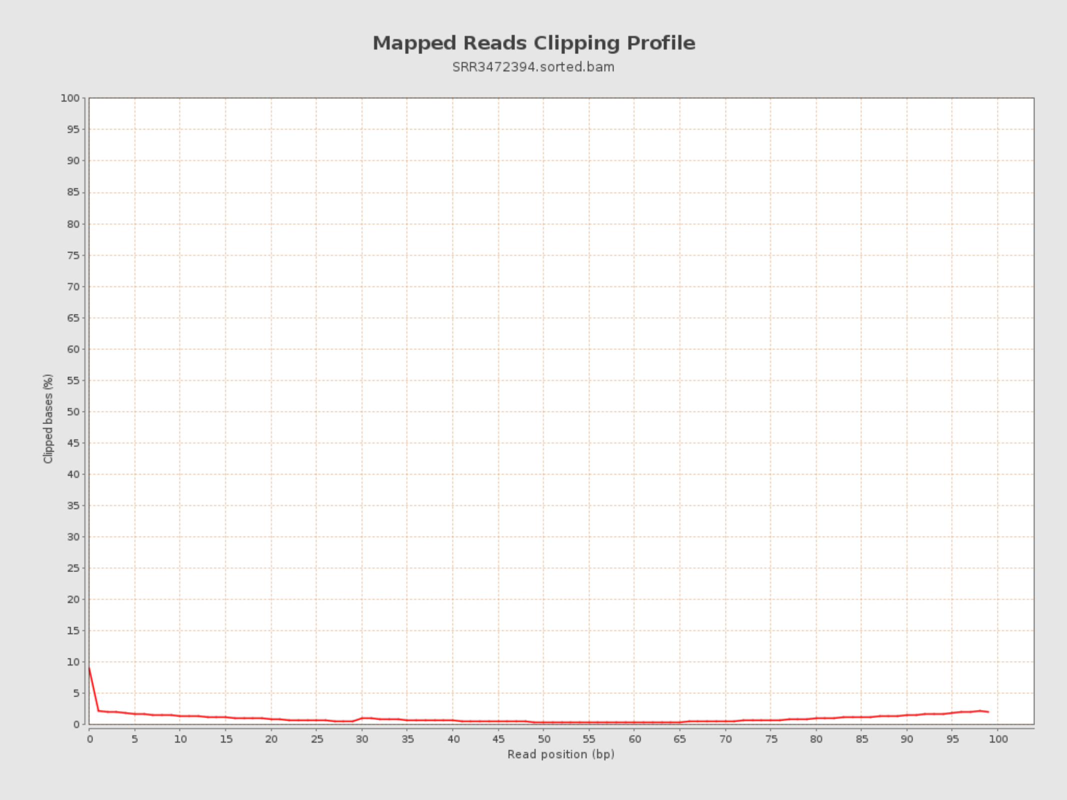
8. Results : Mapped Reads Nucleotide Content



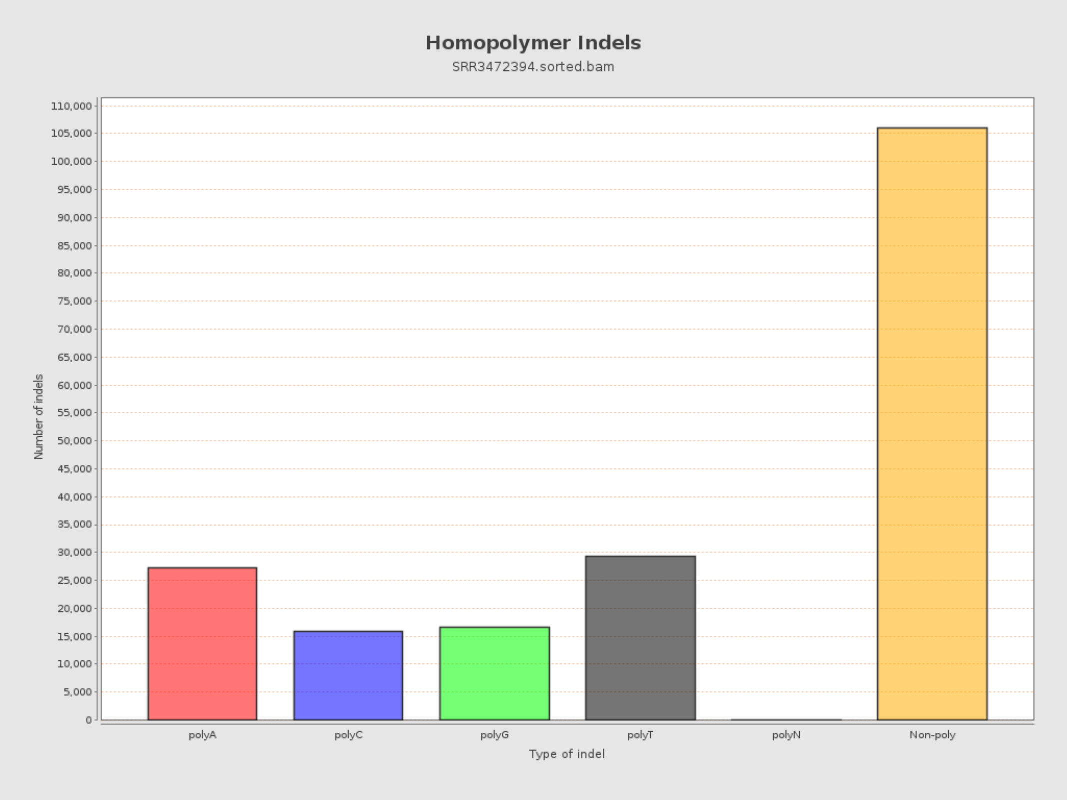
9. Results : Mapped Reads GC-content Distribution



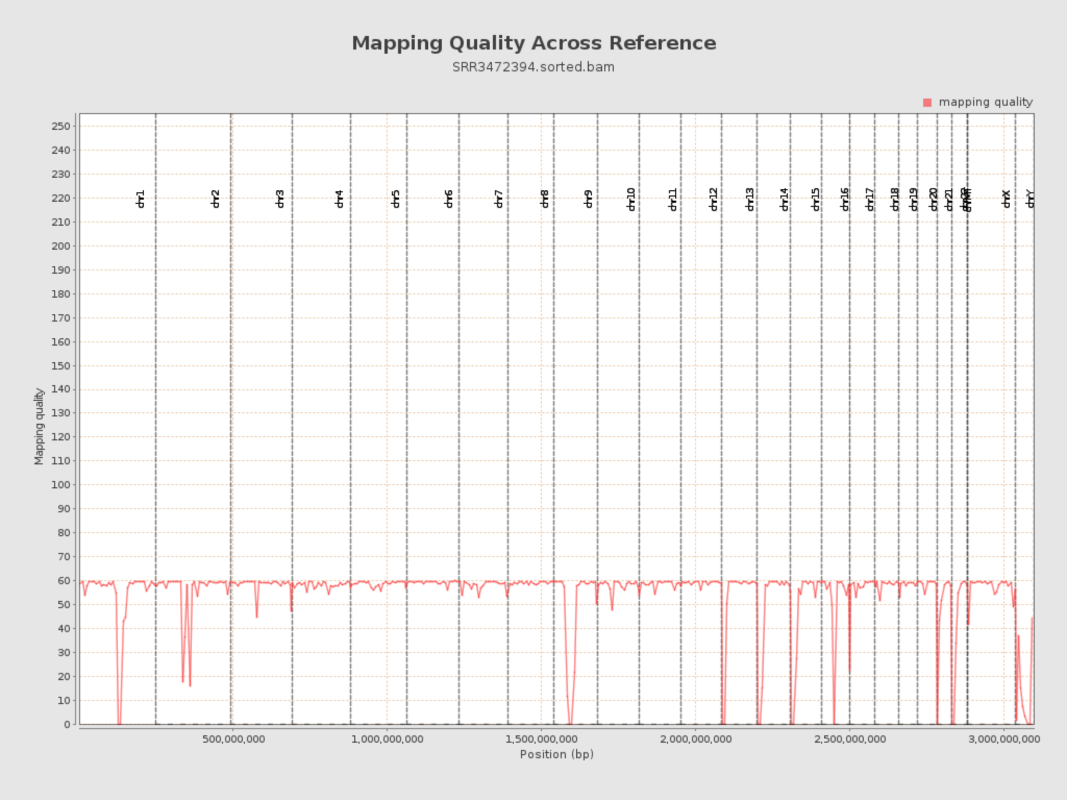
10. Results : Mapped Reads Clipping Profile



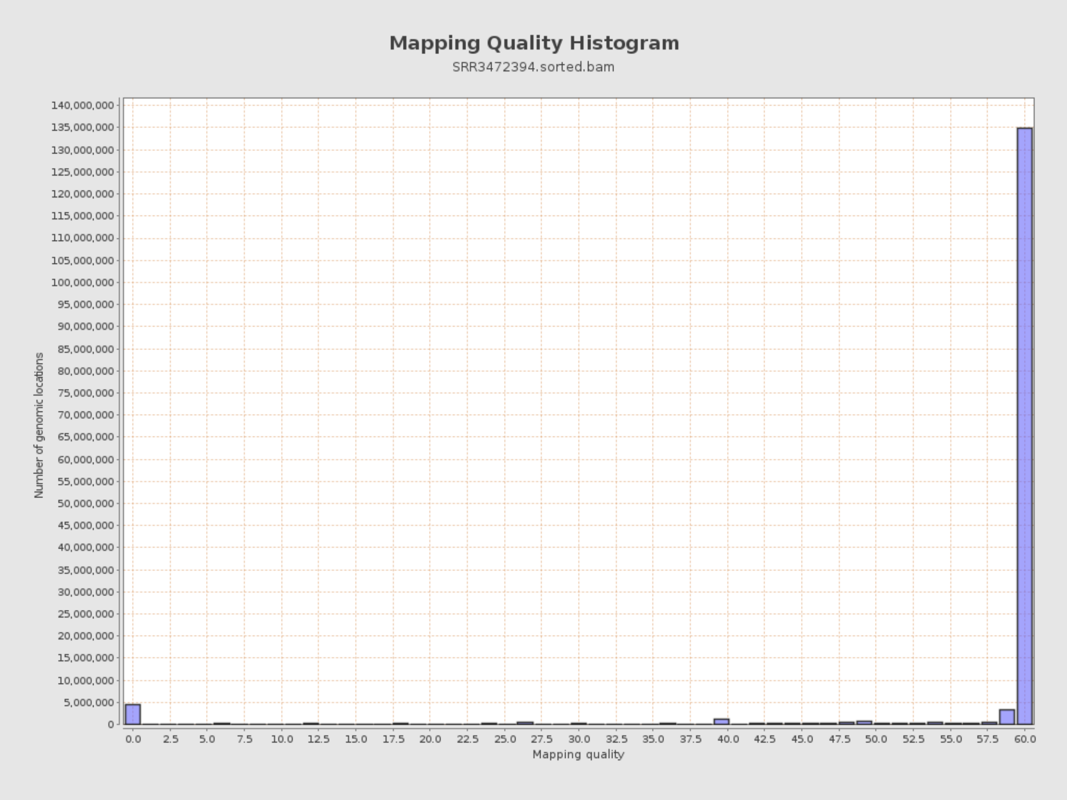
11. Results : Homopolymer Indels



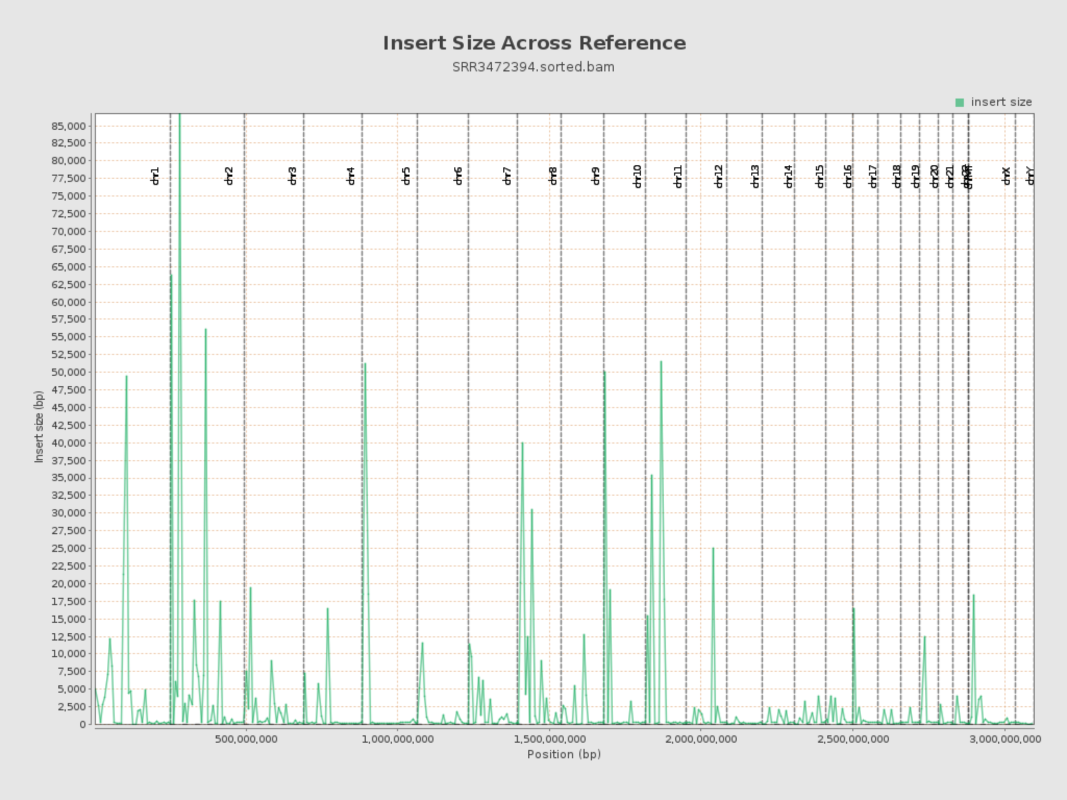
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram