Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 19:20:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472719.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_SRR3472719 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472719_1.fastq.gz SRR3472719_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 19:20:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472719.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,119,452
Mapped reads	13,006,171 / 99.14%
Unmapped reads	113,281 / 0.86%
Mapped paired reads	13,006,171 / 99.14%
Mapped reads, first in pair	6,525,790 / 49.74%
Mapped reads, second in pair	6,480,381 / 49.4%
Mapped reads, both in pair	12,934,374 / 98.59%
Mapped reads, singletons	71,797 / 0.55%
Secondary alignments	0
Supplementary alignments	46,415 / 0.35%
Read min/max/mean length	30 / 100 / 100.14
Duplicated reads (estimated)	7,715,916 / 58.81%
Duplication rate	46.62%
Clipped reads	991,433 / 7.56%

2.2. ACGT Content

Number/percentage of A's	358,472,902 / 27.96%
Number/percentage of C's	284,381,814 / 22.18%
Number/percentage of T's	356,183,017 / 27.78%
Number/percentage of G's	282,832,183 / 22.06%
Number/percentage of N's	248,073 / 0.02%

GC Percentage	44.24%

2.3. Coverage

Mean	0.4142
Standard Deviation	13.1834

2.4. Mapping Quality

Mean Mapping Quality	55.22

2.5. Insert size

Mean	21,965.28
Standard Deviation	1,489,748.99
P25/Median/P75	178 / 249 / 337

2.6. Mismatches and indels

General error rate	0.63%
Mismatches	7,928,585
Insertions	77,725
Mapped reads with at least one insertion	0.59%
Deletions	75,867
Mapped reads with at least one deletion	0.58%
Homopolymer indels	45.17%

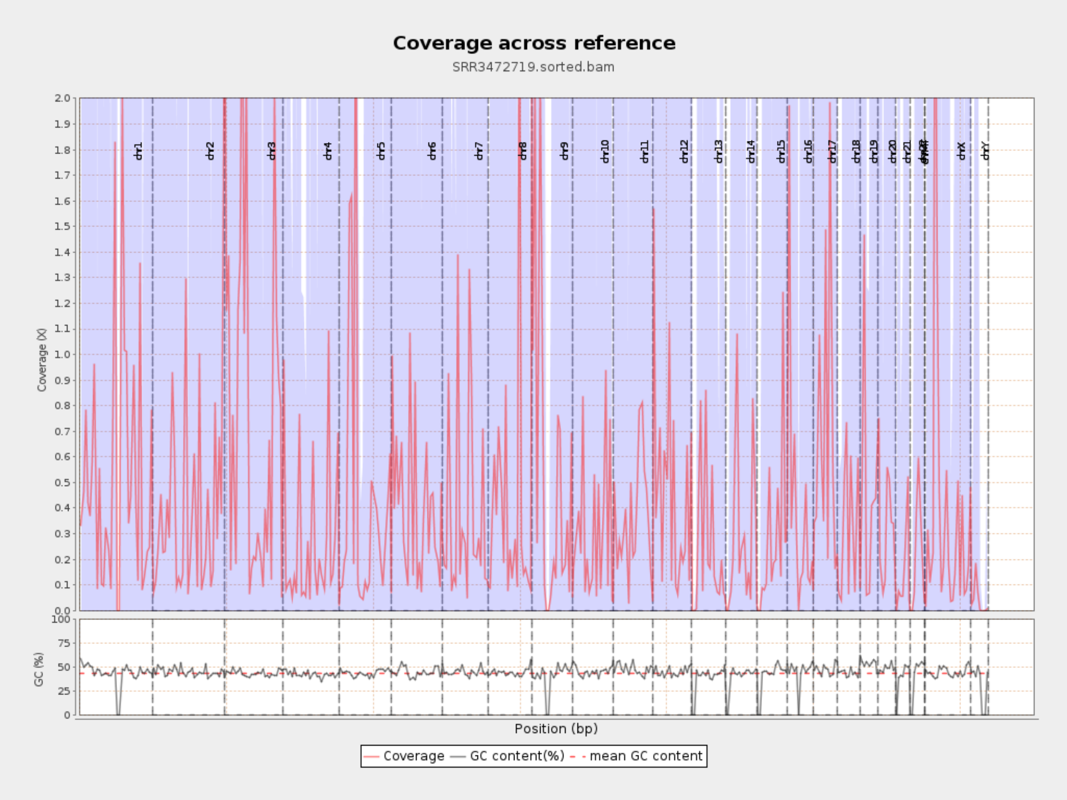
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard

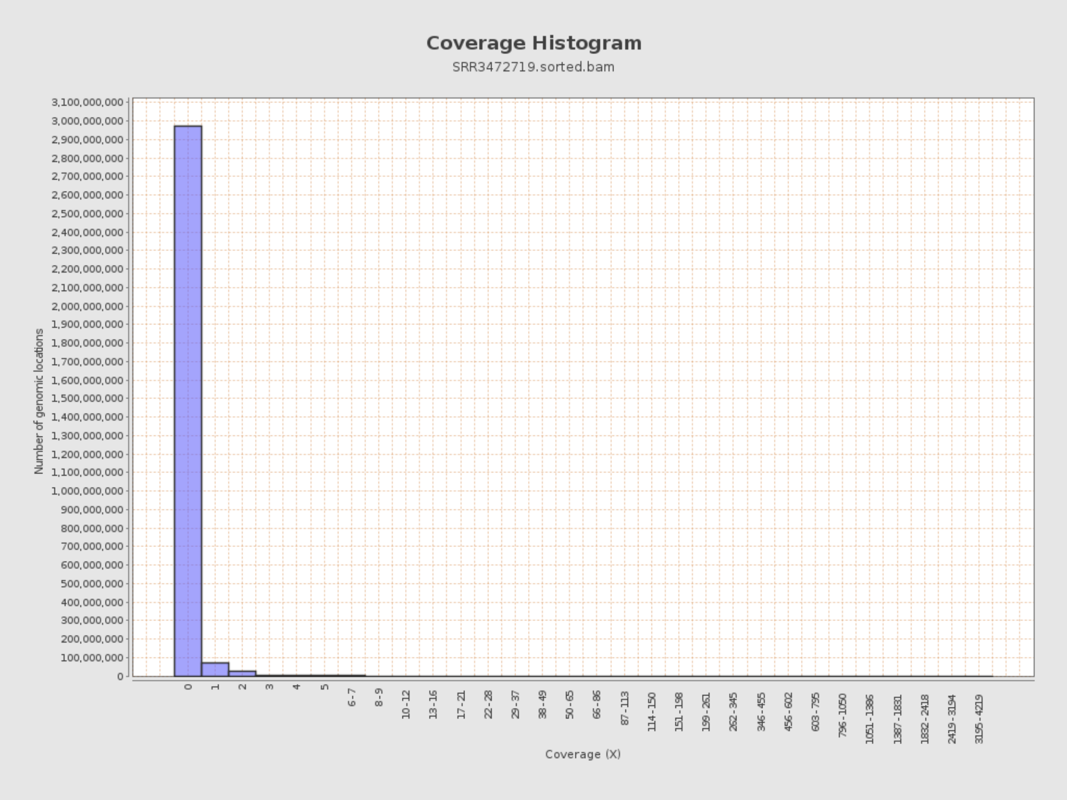
		bases	coverage	deviation
chr1	249250621	133328531	0.5349	15.6119
chr2	243199373	92860523	0.3818	12.0167
chr3	198022430	159464189	0.8053	19.6342
chr4	191154276	49822182	0.2606	10.1501
chr5	180915260	82885809	0.4581	16.5696
chr6	171115067	67614306	0.3951	11.7673
chr7	159138663	62020139	0.3897	13.4235
chr8	146364022	60945831	0.4164	15.5441
chr9	141213431	78568882	0.5564	14.3672
chr10	135534747	44270890	0.3266	11.7285
chr11	135006516	49537288	0.3669	12.1694
chr12	133851895	62880054	0.4698	13.1003
chr13	115169878	28520393	0.2476	9.2486
chr14	107349540	31953159	0.2977	9.1627
chr15	102531392	27577880	0.269	8.2101
chr16	90354753	36518892	0.4042	12.021
chr17	81195210	55751131	0.6866	15.7779
chr18	78077248	25966713	0.3326	12.3917
chr19	59128983	27784260	0.4699	11.6565
chr20	63025520	21123200	0.3352	9.5073
chr21	48129895	7368695	0.1531	6.1488
chr22	51304566	11000584	0.2144	6.9333
chrMT	16571	963	0.0581	0.2681
chrX	155270560	61987929	0.3992	13.5894

chrY	59373566	2561584	0.0431	1.7368

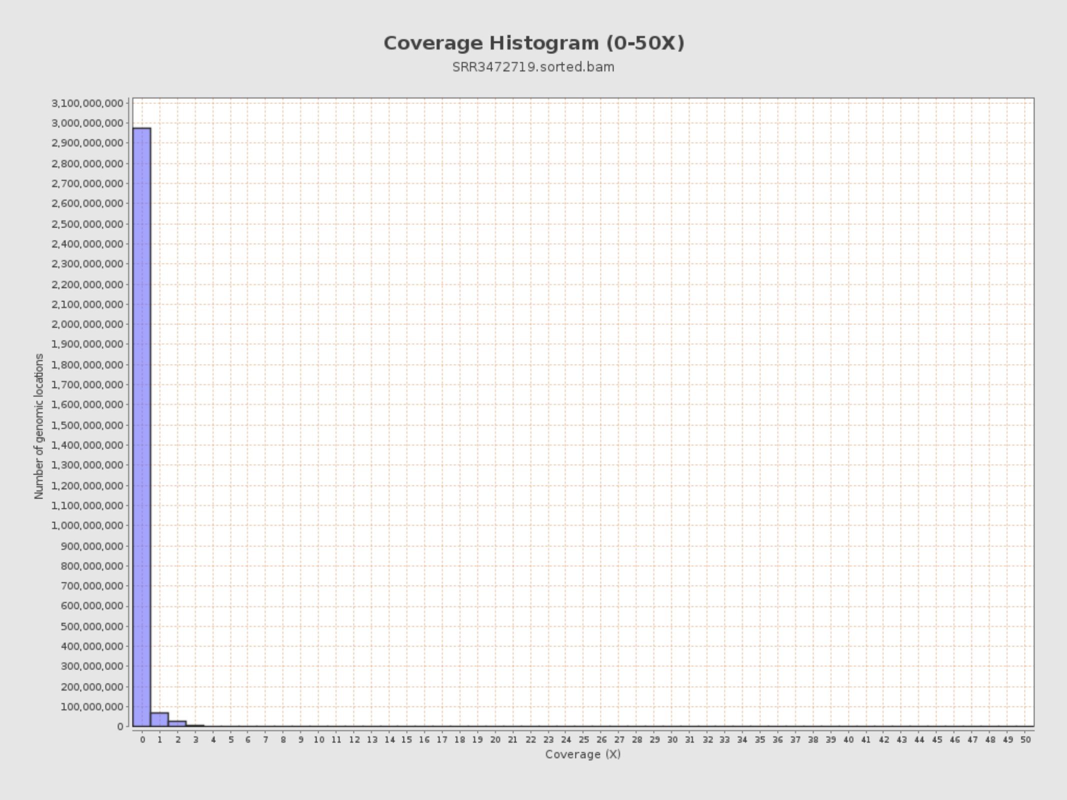
3. Results : Coverage across reference



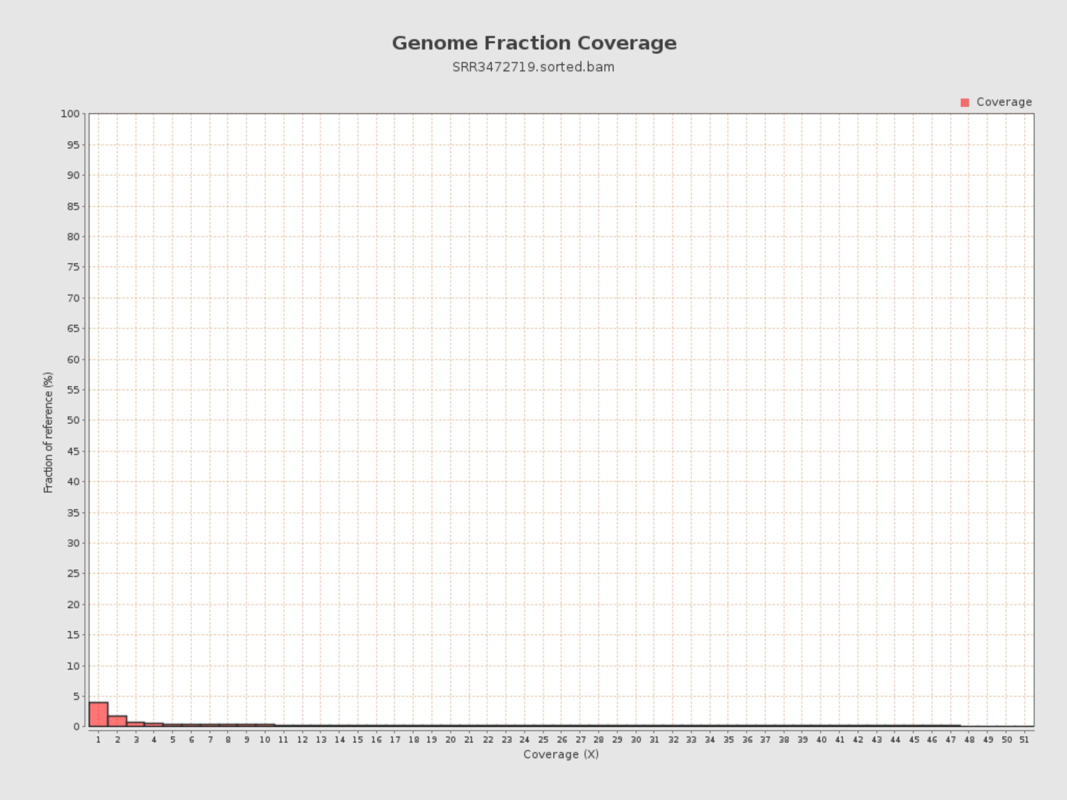
4. Results : Coverage Histogram



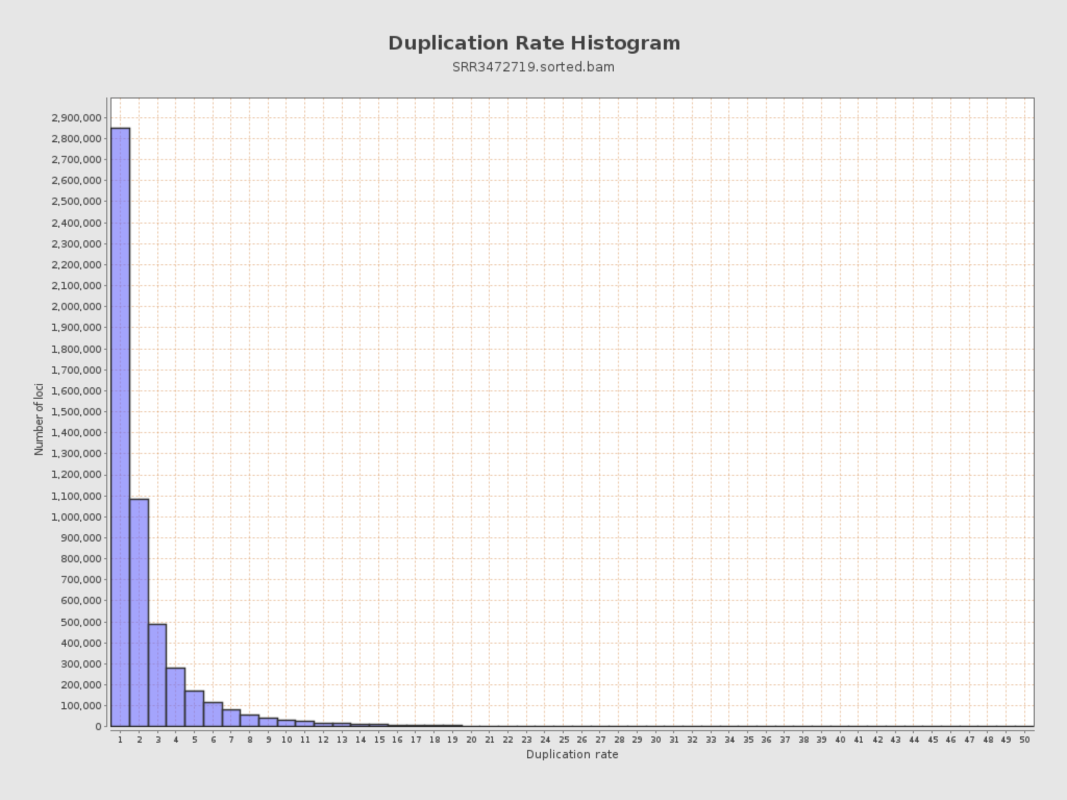
5. Results : Coverage Histogram (0-50X)



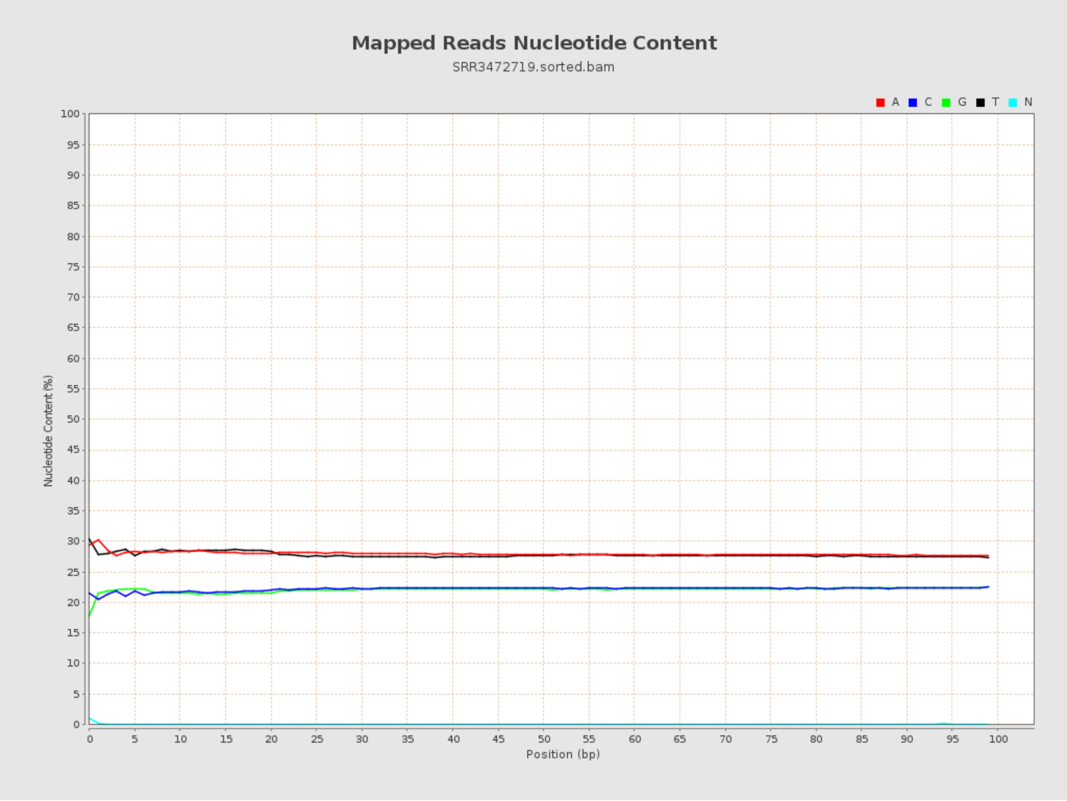
6. Results : Genome Fraction Coverage



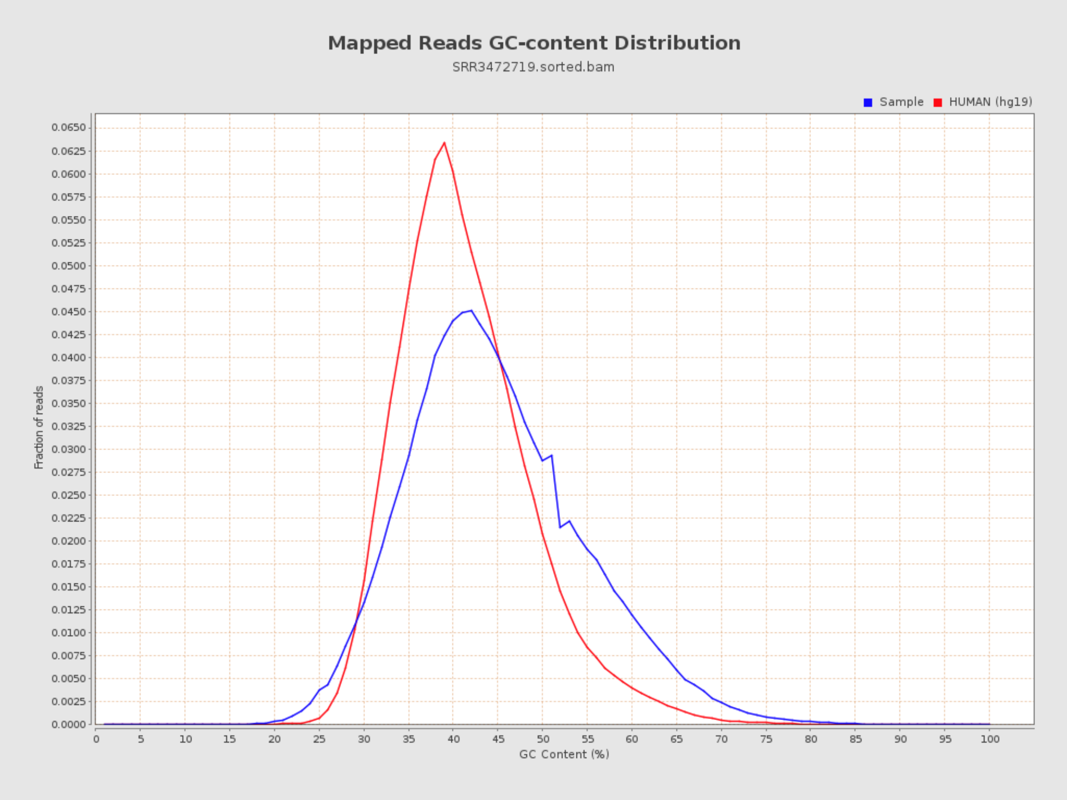
7. Results : Duplication Rate Histogram



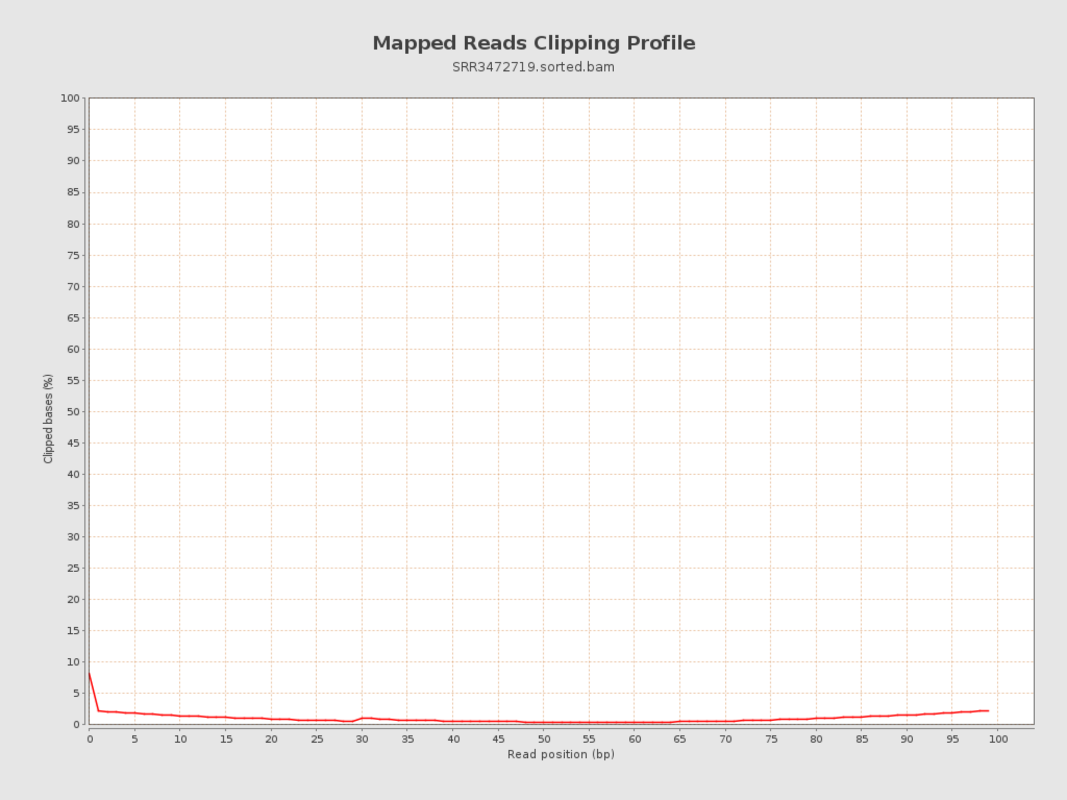
8. Results : Mapped Reads Nucleotide Content



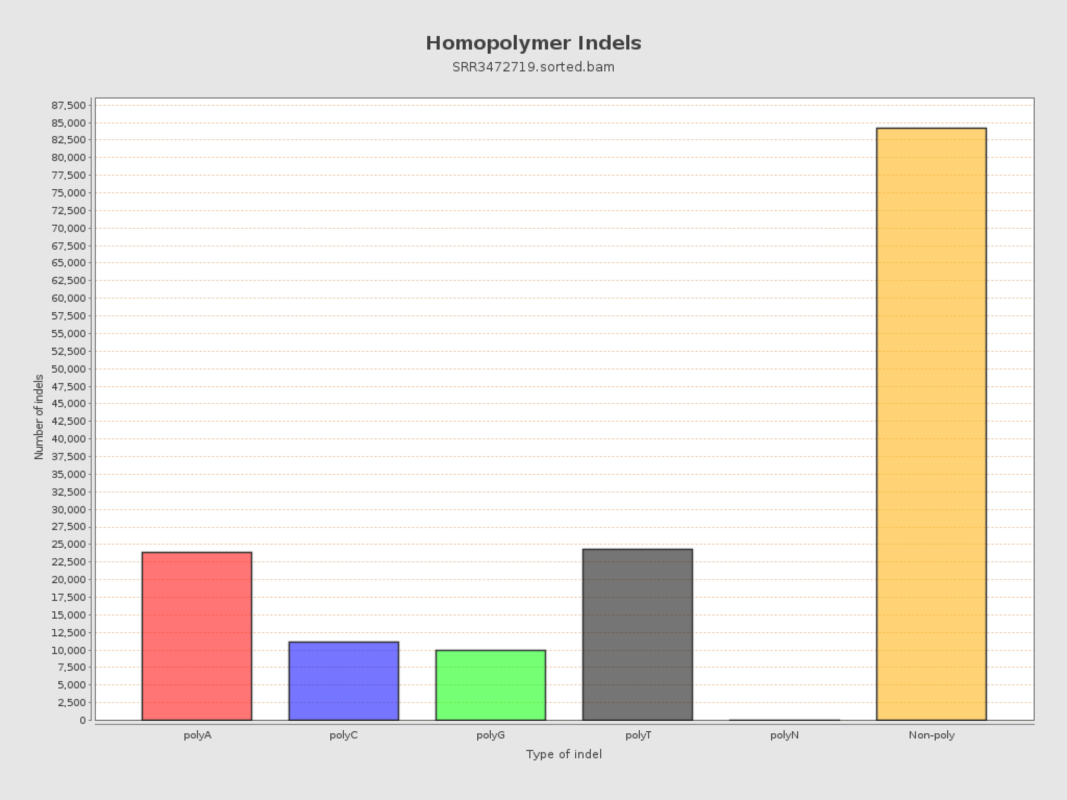
9. Results : Mapped Reads GC-content Distribution



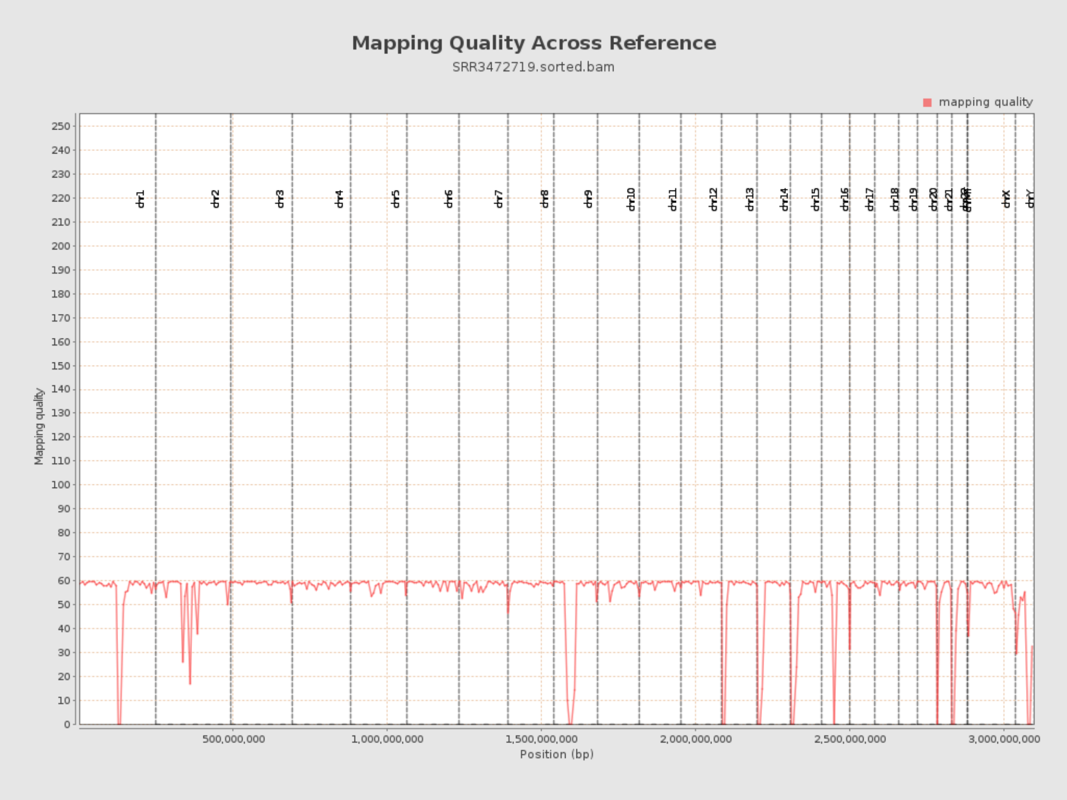
10. Results : Mapped Reads Clipping Profile



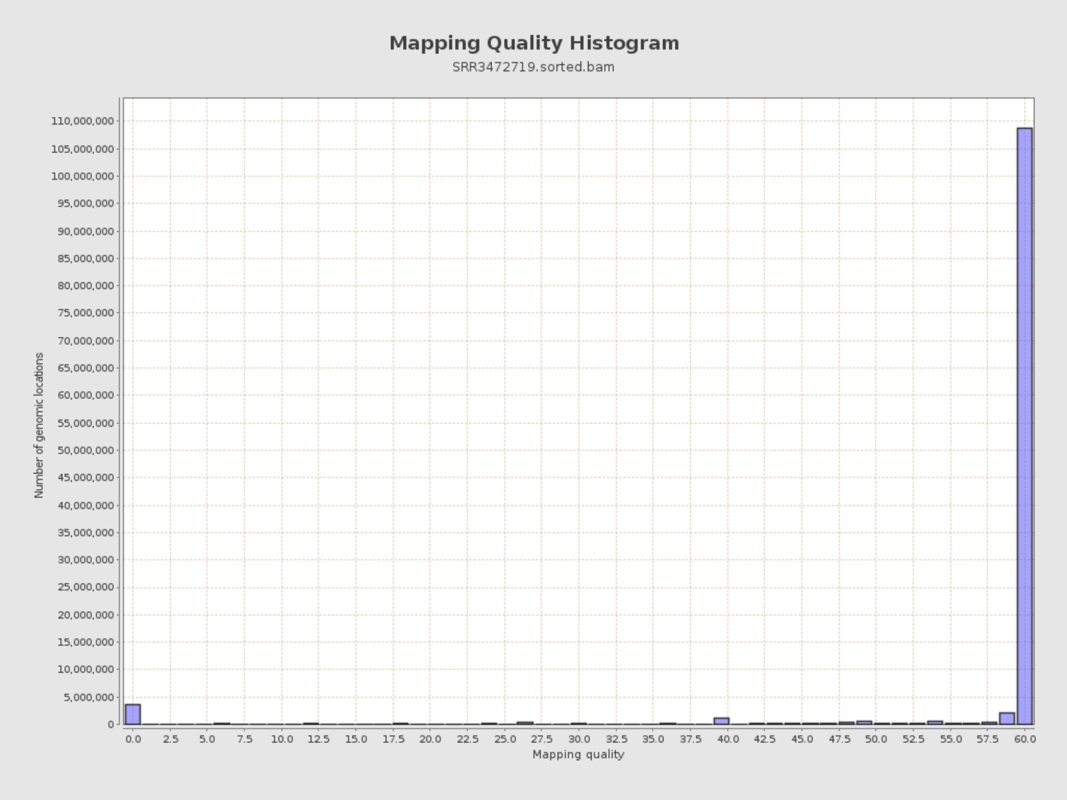
11. Results : Homopolymer Indels



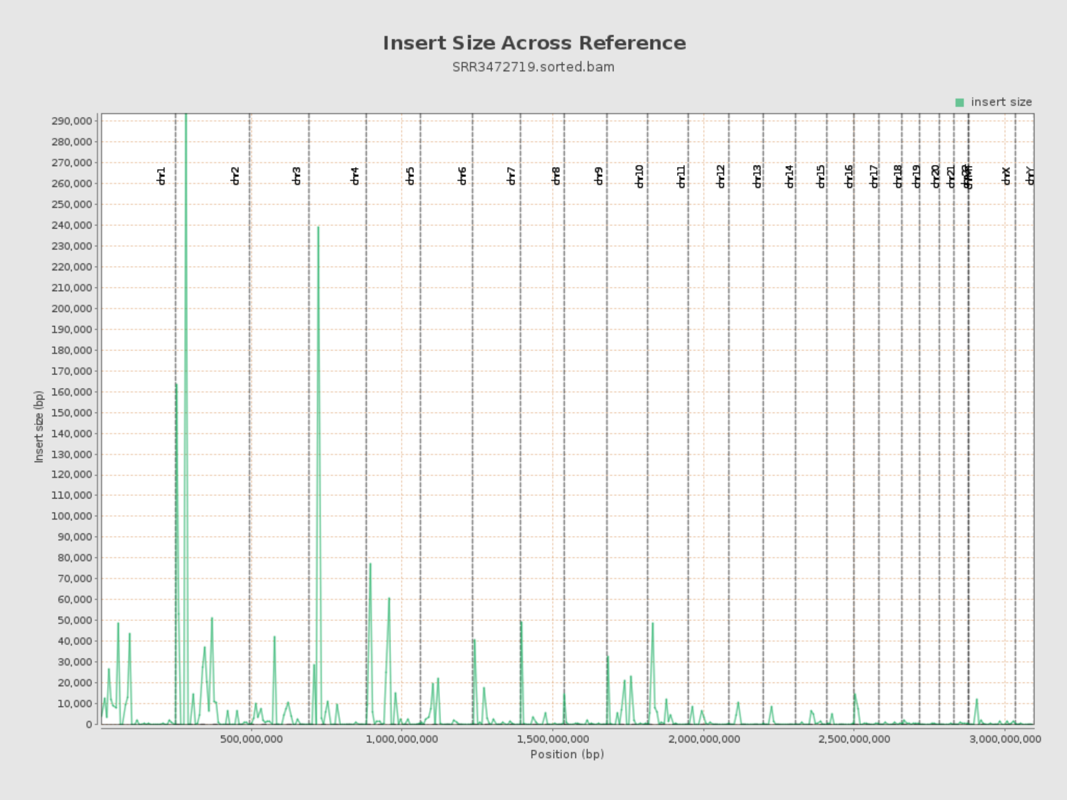
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram