Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/07 16:00:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617372.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_SRR617372 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617372_1.fastq.gz SRR617372_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Oct 07 16:00:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617372.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	29,580,656 / 92.44%
Unmapped reads	2,419,344 / 7.56%
Mapped paired reads	29,580,656 / 92.44%
Mapped reads, first in pair	14,920,260 / 46.63%
Mapped reads, second in pair	14,660,396 / 45.81%
Mapped reads, both in pair	28,884,774 / 90.26%
Mapped reads, singletons	695,882 / 2.17%
Secondary alignments	0
Supplementary alignments	85,471 / 0.27%
Read min/max/mean length	30 / 100 / 100.1
Duplicated reads (estimated)	1,546,519 / 4.83%
Duplication rate	1.5%
Clipped reads	2,745,818 / 8.58%

2.2. ACGT Content

Number/percentage of A's	878,187,872 / 30.37%
Number/percentage of C's	572,621,545 / 19.8%
Number/percentage of T's	864,823,609 / 29.91%
Number/percentage of G's	575,136,896 / 19.89%
Number/percentage of N's	644,054 / 0.02%

GC Percentage	39.7%

2.3. Coverage

Mean	0.9343
Standard Deviation	9.6064

2.4. Mapping Quality

Mean Mapping Quality	53.35

2.5. Insert size

Mean	57,680.36
Standard Deviation	2,294,683.6
P25/Median/P75	169 / 208 / 267

2.6. Mismatches and indels

General error rate	1.26%
Mismatches	35,686,507
Insertions	294,202
Mapped reads with at least one insertion	0.96%
Deletions	353,697
Mapped reads with at least one deletion	1.16%
Homopolymer indels	41.15%

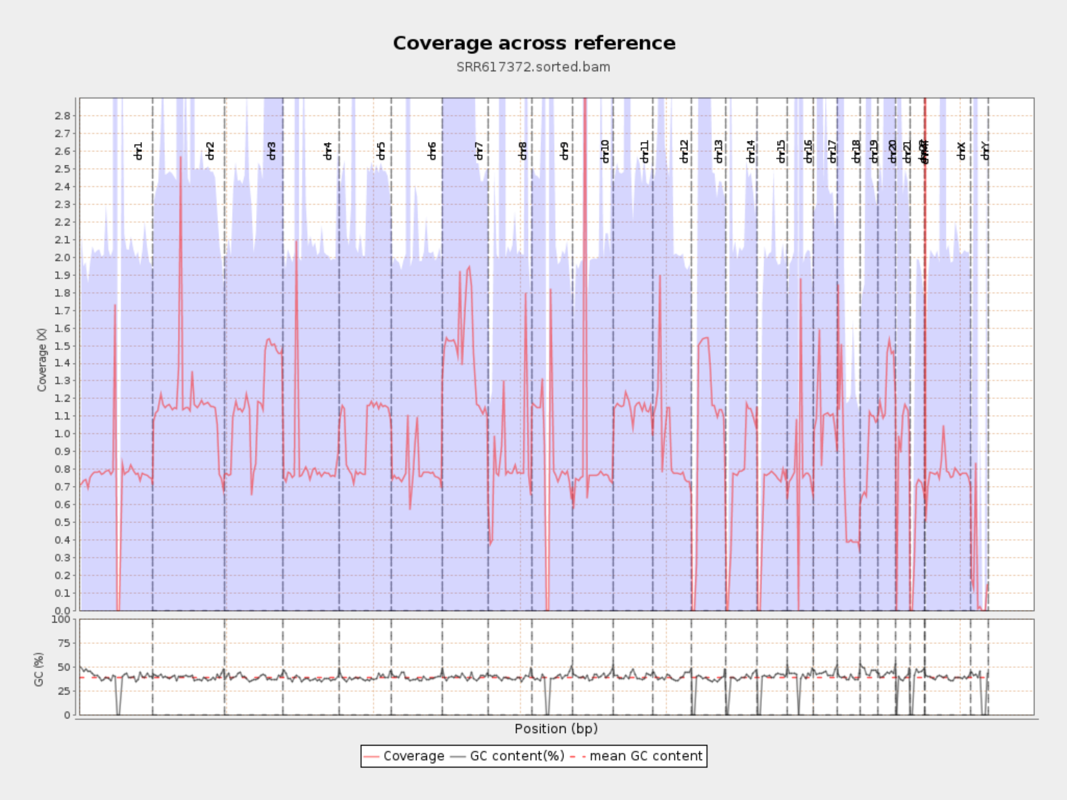
2.7. Chromosome stats

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

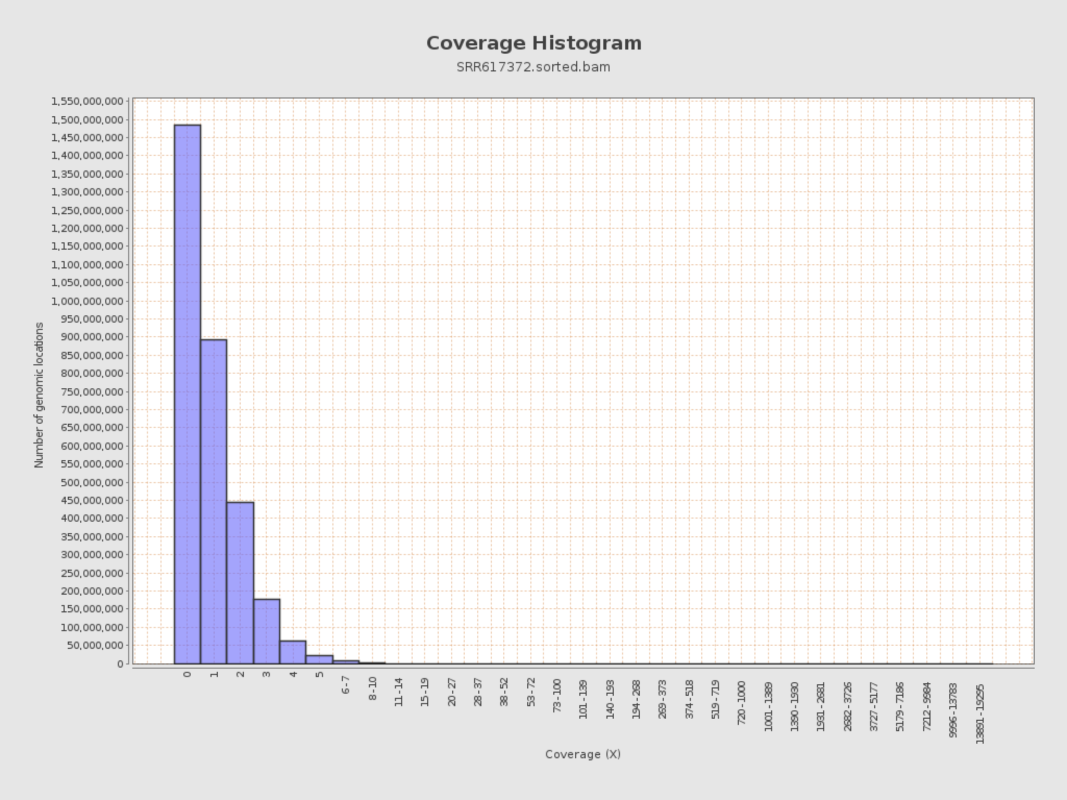
		bases	coverage	deviation
chr1	249250621	187542649	0.7524	19.705
chr2	243199373	285728085	1.1749	8.5868
chr3	198022430	230880196	1.1659	1.4672
chr4	191154276	158793687	0.8307	8.949
chr5	180915260	181970561	1.0058	1.4497
chr6	171115067	135686766	0.793	3.6368
chr7	159138663	234999124	1.4767	10.6255
chr8	146364022	121822222	0.8323	7.411
chr9	141213431	121497603	0.8604	14.4041
chr10	135534747	121950768	0.8998	19.9089
chr11	135006516	155160236	1.1493	5.4504
chr12	133851895	127713498	0.9541	1.3969
chr13	115169878	126404005	1.0975	1.2954
chr14	107349540	83503218	0.7779	1.3581
chr15	102531392	64913657	0.6331	1.0248
chr16	90354753	72729473	0.8049	7.812
chr17	81195210	89342552	1.1003	7.0124
chr18	78077248	52400657	0.6711	14.8648
chr19	59128983	53201515	0.8998	9.5745
chr20	63025520	82251616	1.3051	2.3582
chr21	48129895	45952890	0.9548	3.167
chr22	51304566	25419776	0.4955	0.9067
chrMT	16571	1941935	117.1888	22.1296
chrX	155270560	120689646	0.7773	2.9888

chrY	59373566	9765413	0.1645	8.1507

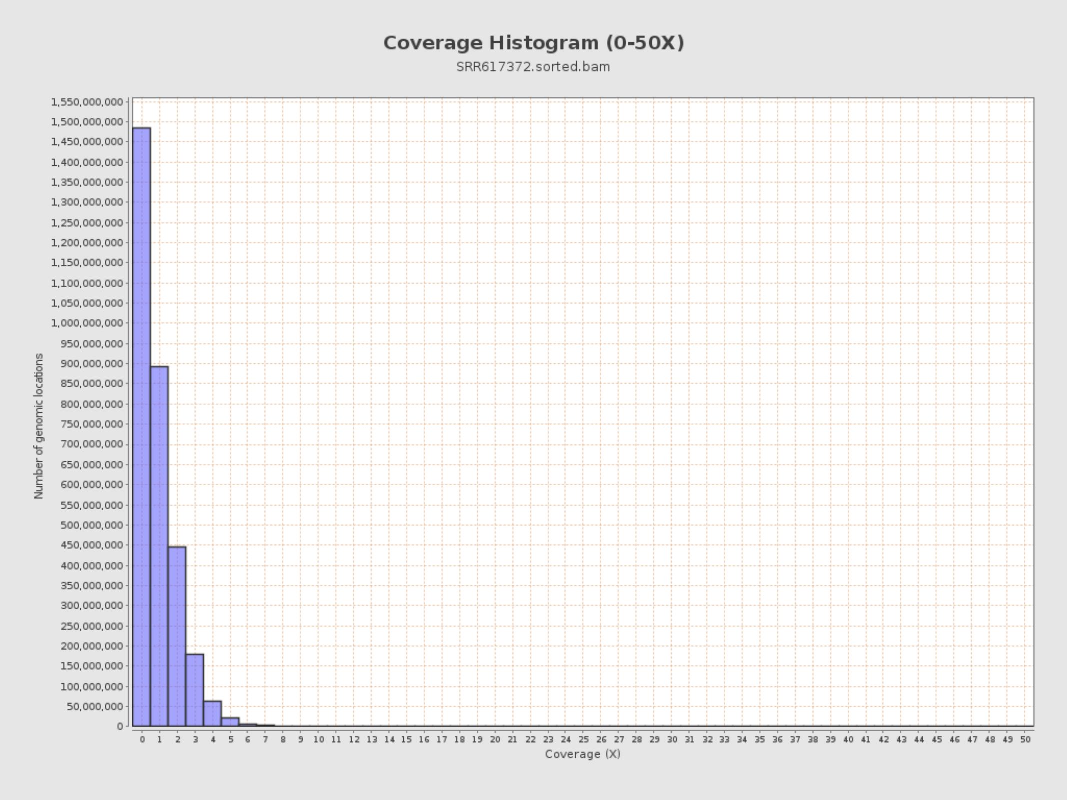
3. Results : Coverage across reference



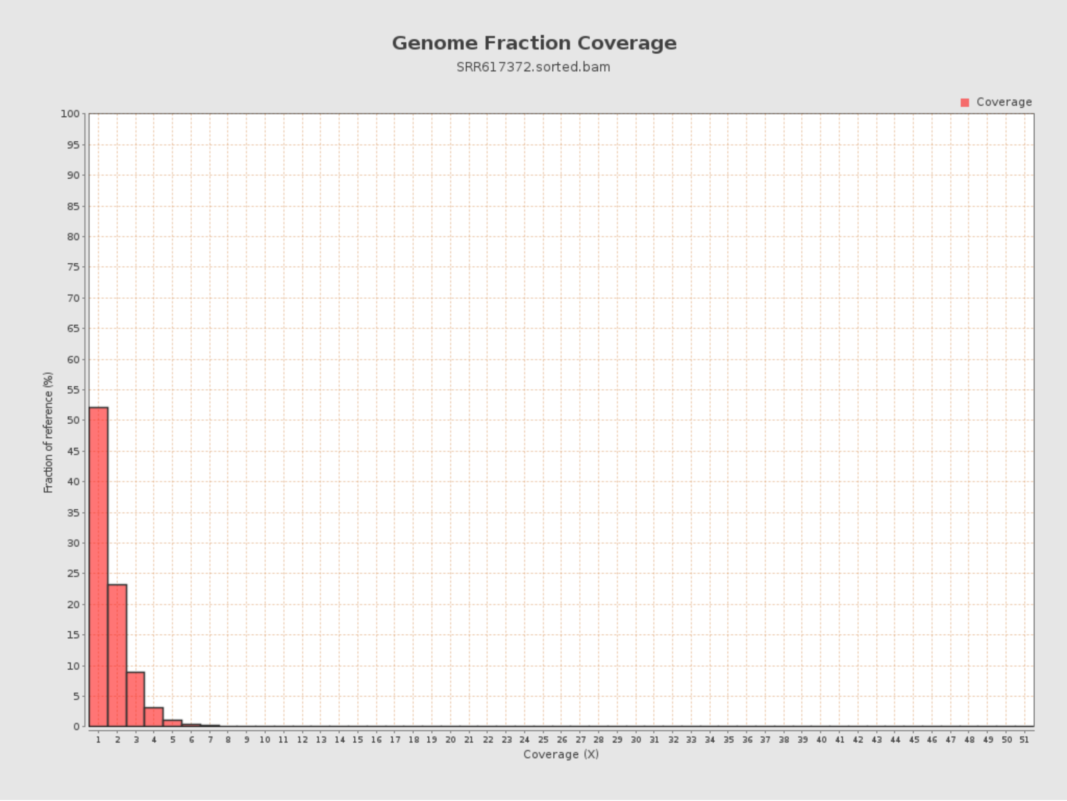
4. Results : Coverage Histogram



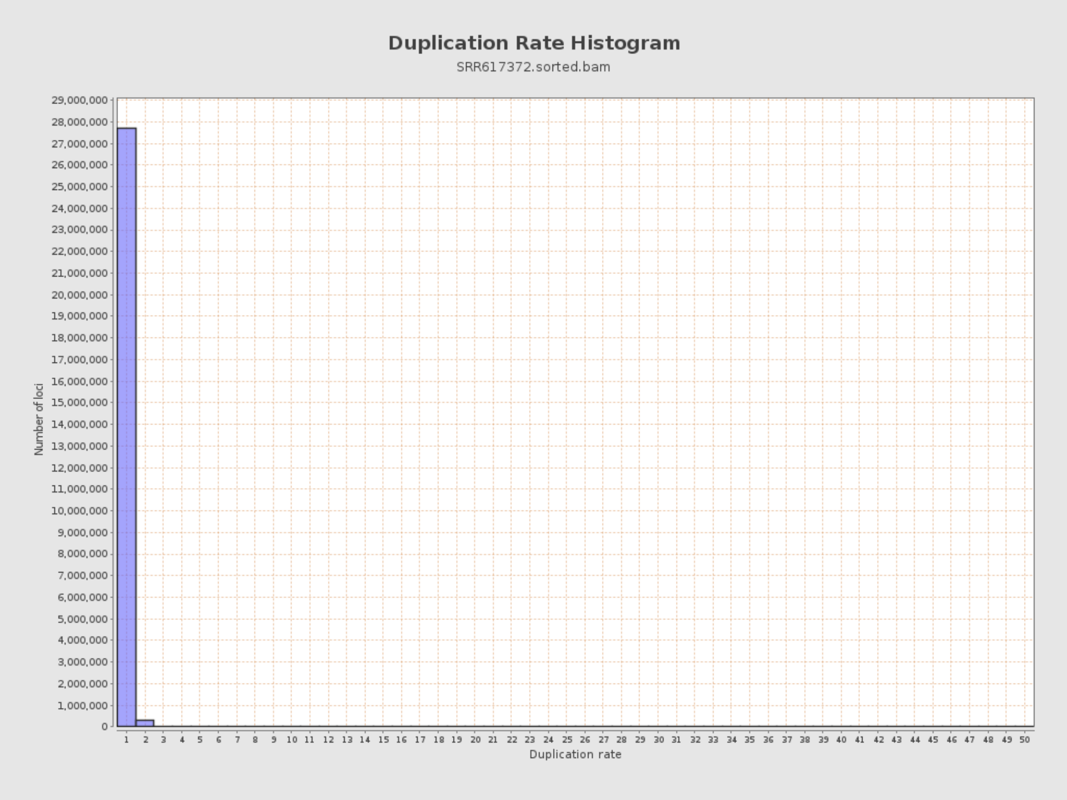
5. Results : Coverage Histogram (0-50X)



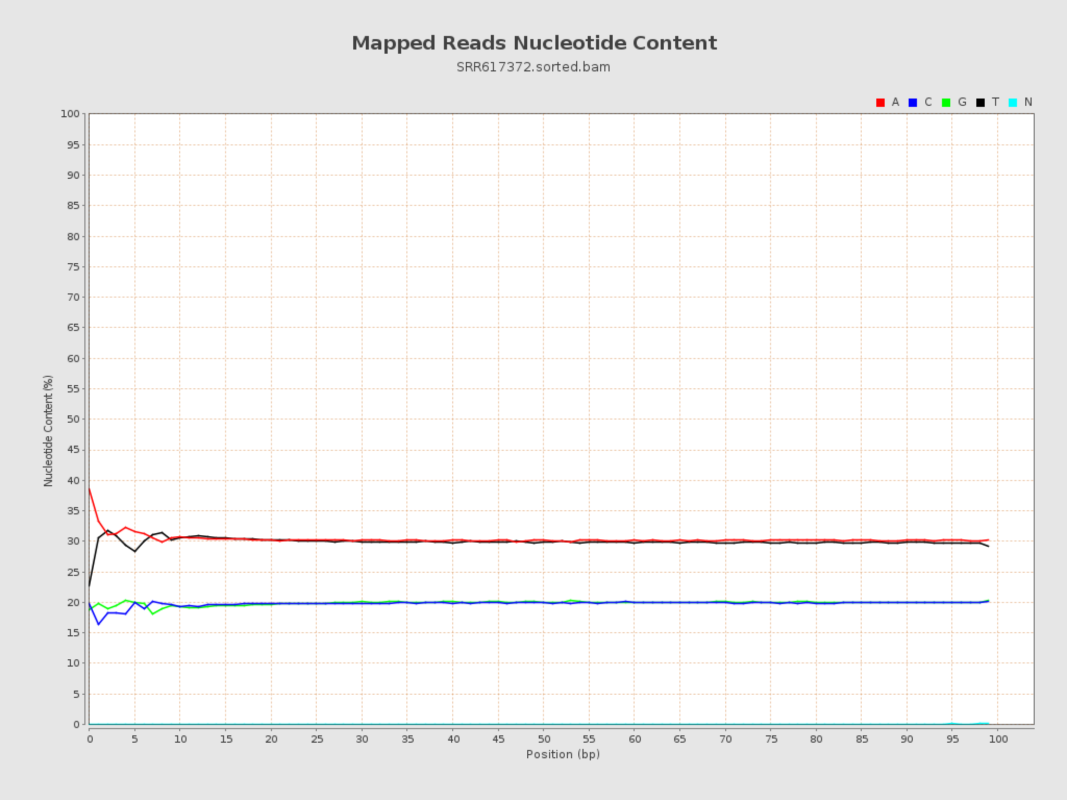
6. Results : Genome Fraction Coverage



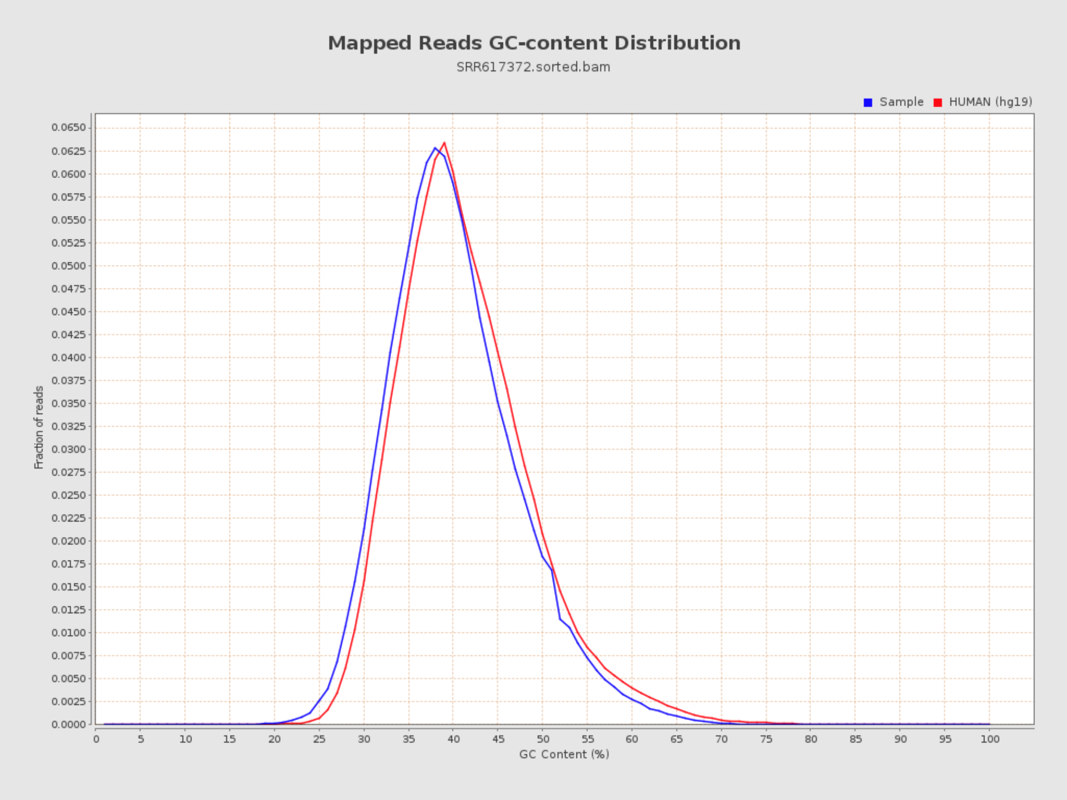
7. Results : Duplication Rate Histogram



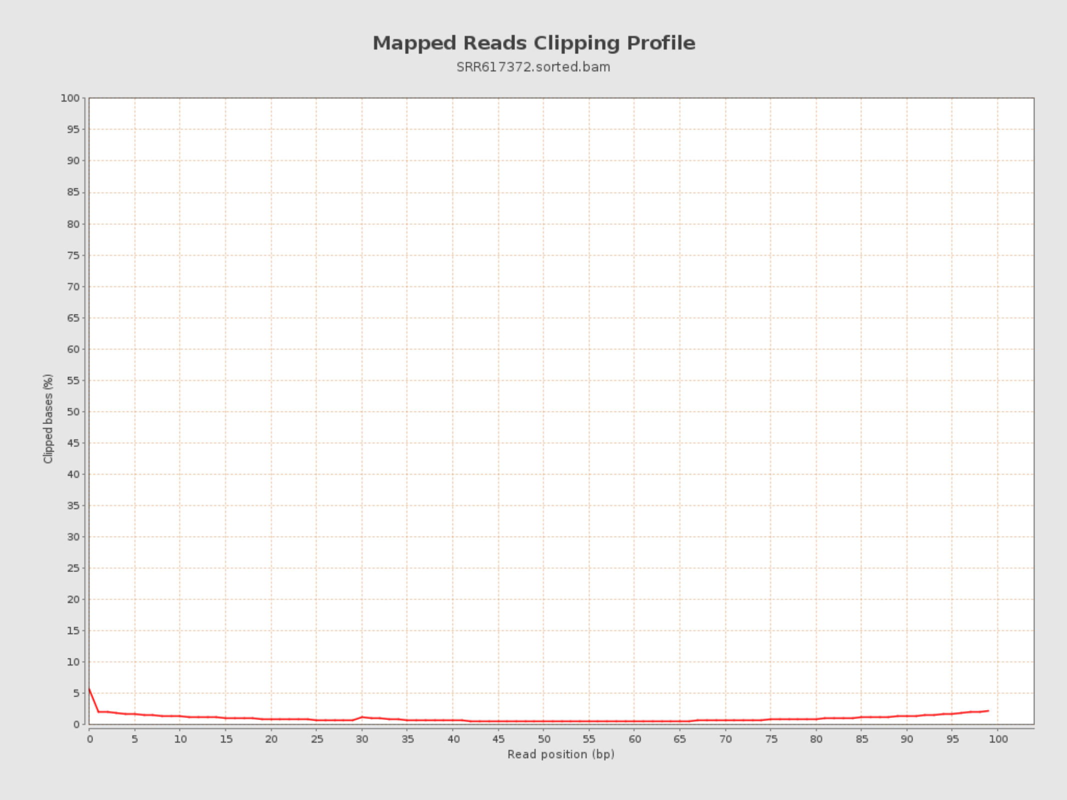
8. Results : Mapped Reads Nucleotide Content



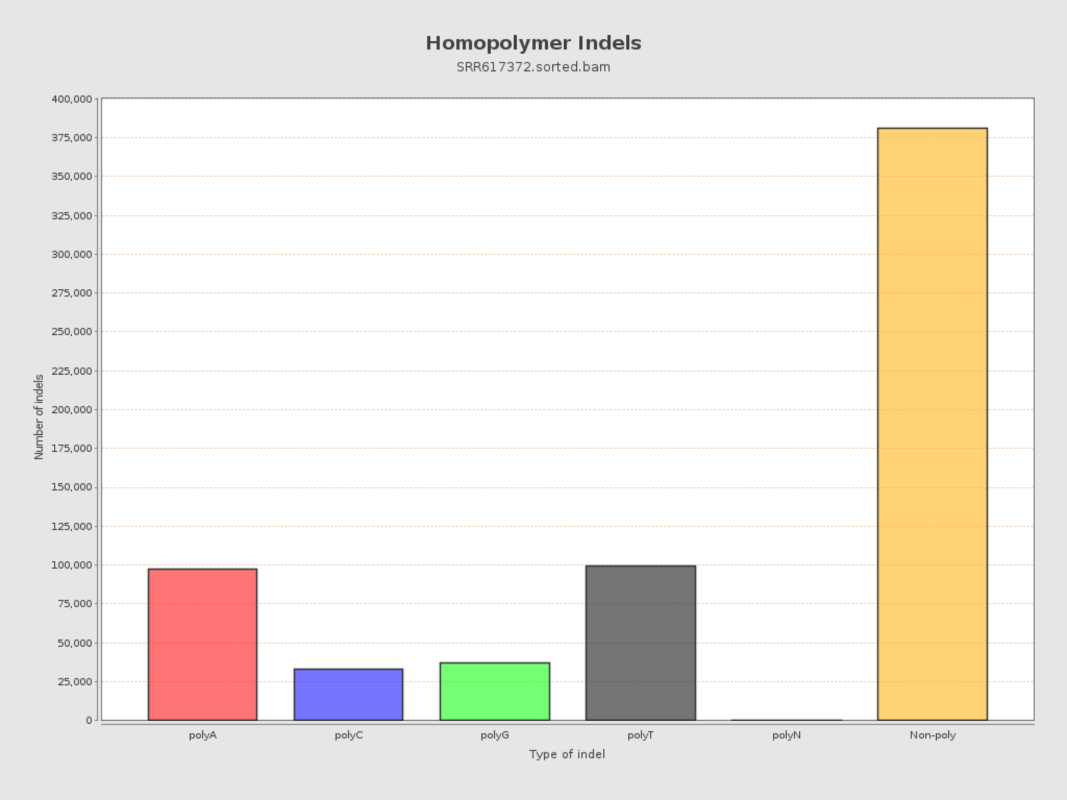
9. Results : Mapped Reads GC-content Distribution



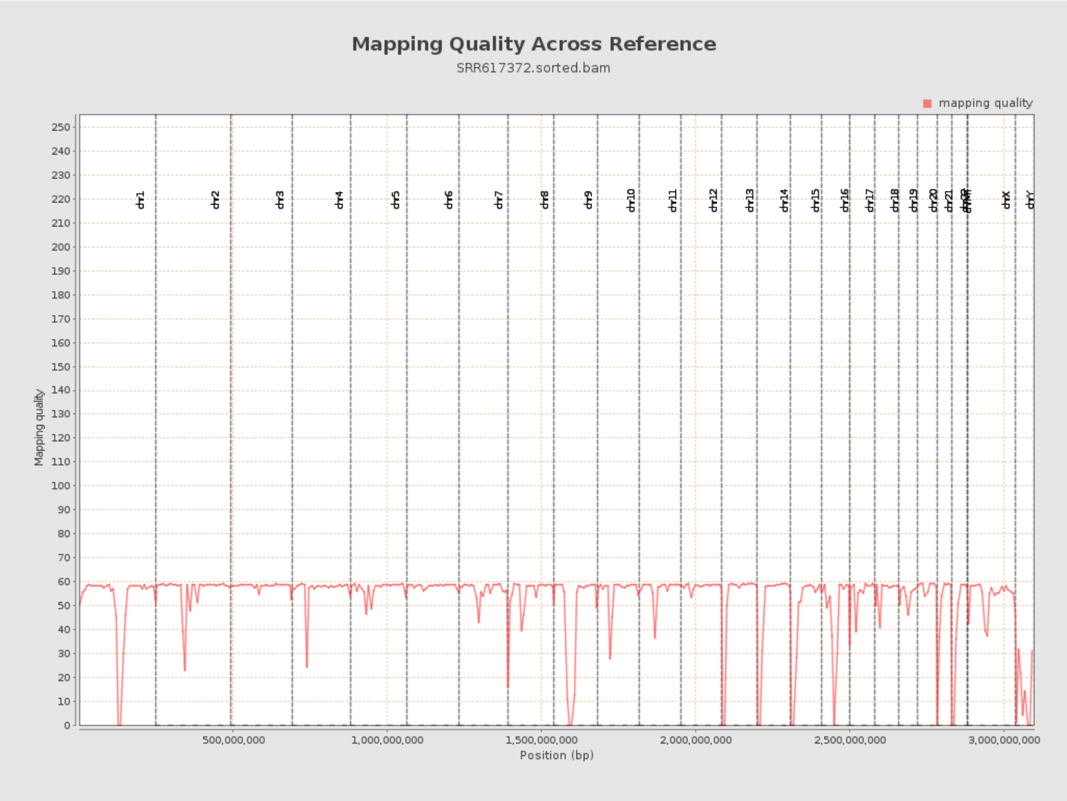
10. Results : Mapped Reads Clipping Profile



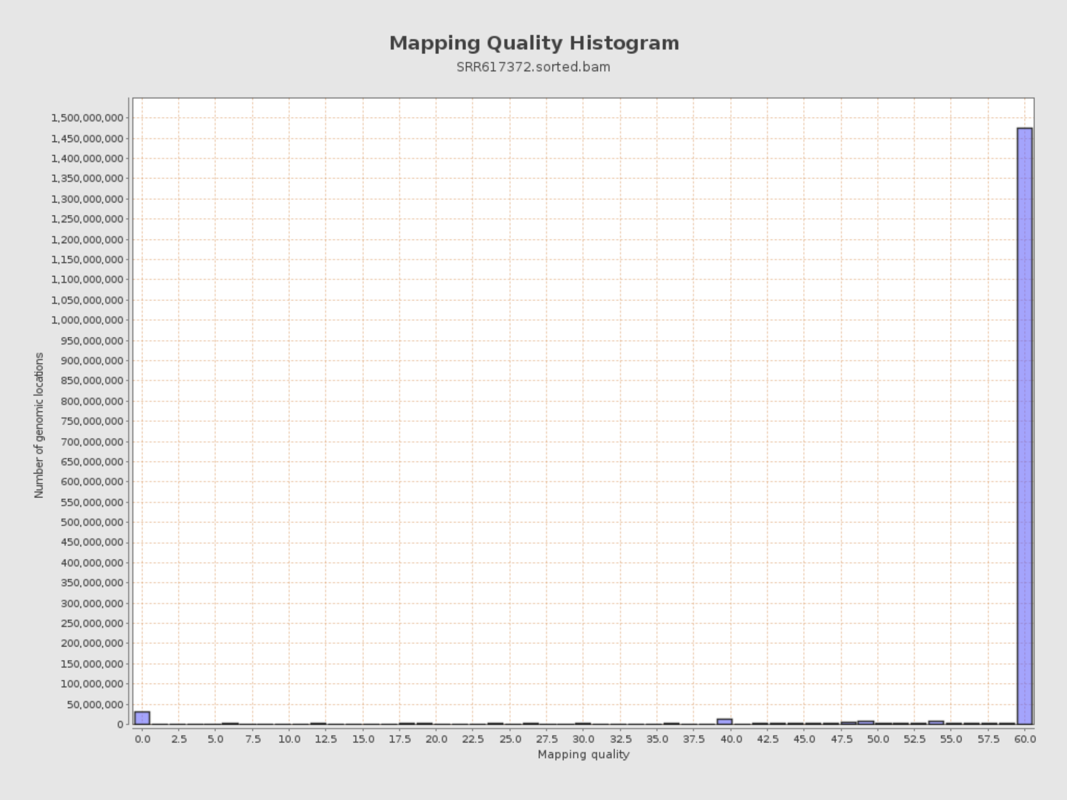
11. Results : Homopolymer Indels



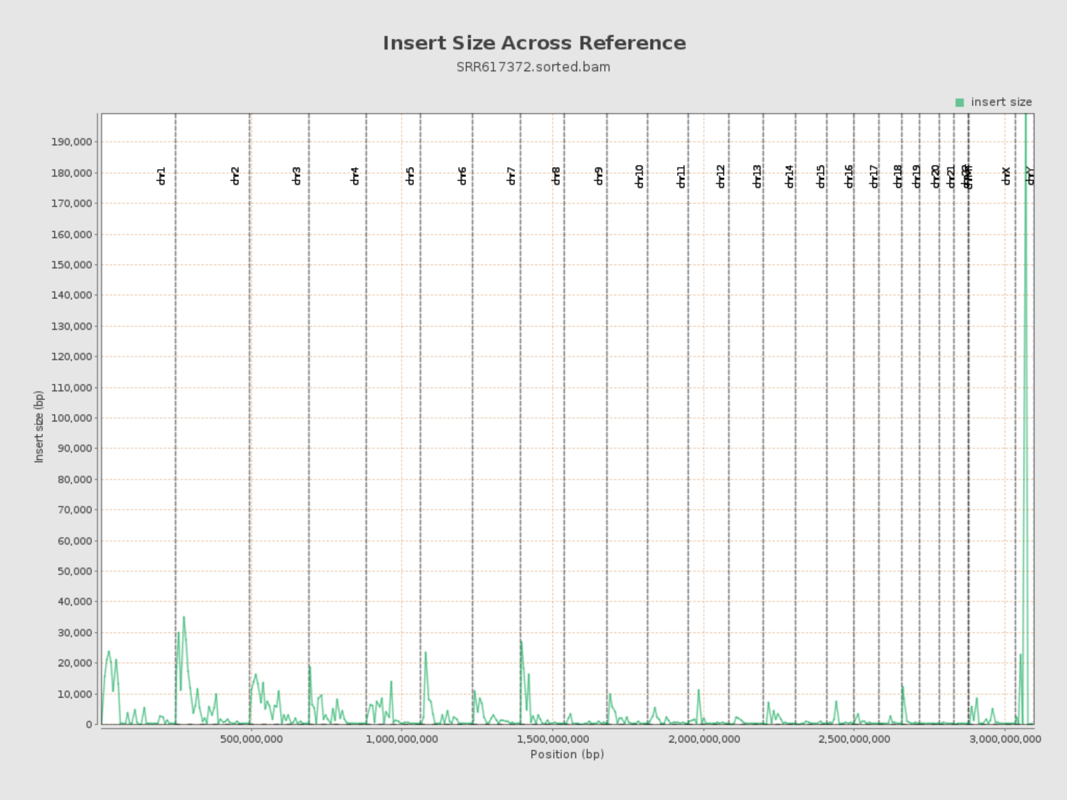
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram