Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 19:59:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174005.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_SRR10174005 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174005_1.fastq.gz SRR10174005_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 19:59:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174005.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,427,264
Mapped reads	3,356,538 / 97.94%
Unmapped reads	70,726 / 2.06%
Mapped paired reads	3,356,538 / 97.94%
Mapped reads, first in pair	1,678,579 / 48.98%
Mapped reads, second in pair	1,677,959 / 48.96%
Mapped reads, both in pair	3,310,870 / 96.6%
Mapped reads, singletons	45,668 / 1.33%
Secondary alignments	0
Supplementary alignments	273,399 / 7.98%
Read min/max/mean length	30 / 133 / 127.34
Duplicated reads (estimated)	2,528,817 / 73.79%
Duplication rate	64.82%
Clipped reads	1,168,049 / 34.08%

2.2. ACGT Content

Number/percentage of A's	121,640,907 / 30.47%
Number/percentage of C's	76,977,950 / 19.28%
Number/percentage of T's	121,303,387 / 30.38%
Number/percentage of G's	79,312,313 / 19.87%
Number/percentage of N's	5,070 / 0%

GC Percentage	39.15%

2.3. Coverage

Mean	0.129
Standard Deviation	2.0161

2.4. Mapping Quality

Mean Mapping Quality	52.98

2.5. Insert size

Mean	665,097.68
Standard Deviation	7,409,298.17
P25/Median/P75	146 / 200 / 285

2.6. Mismatches and indels

General error rate	1.04%
Mismatches	4,029,685
Insertions	41,965
Mapped reads with at least one insertion	1.21%
Deletions	90,384
Mapped reads with at least one deletion	2.62%
Homopolymer indels	43.39%

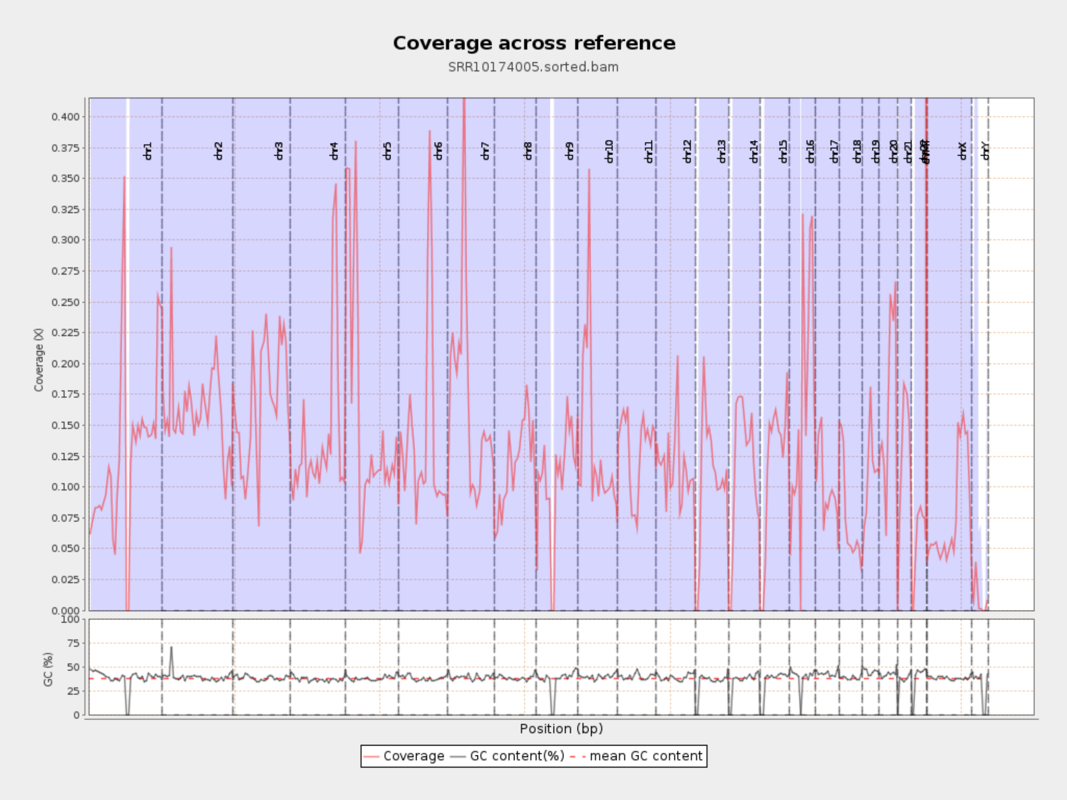
2.7. Chromosome stats

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

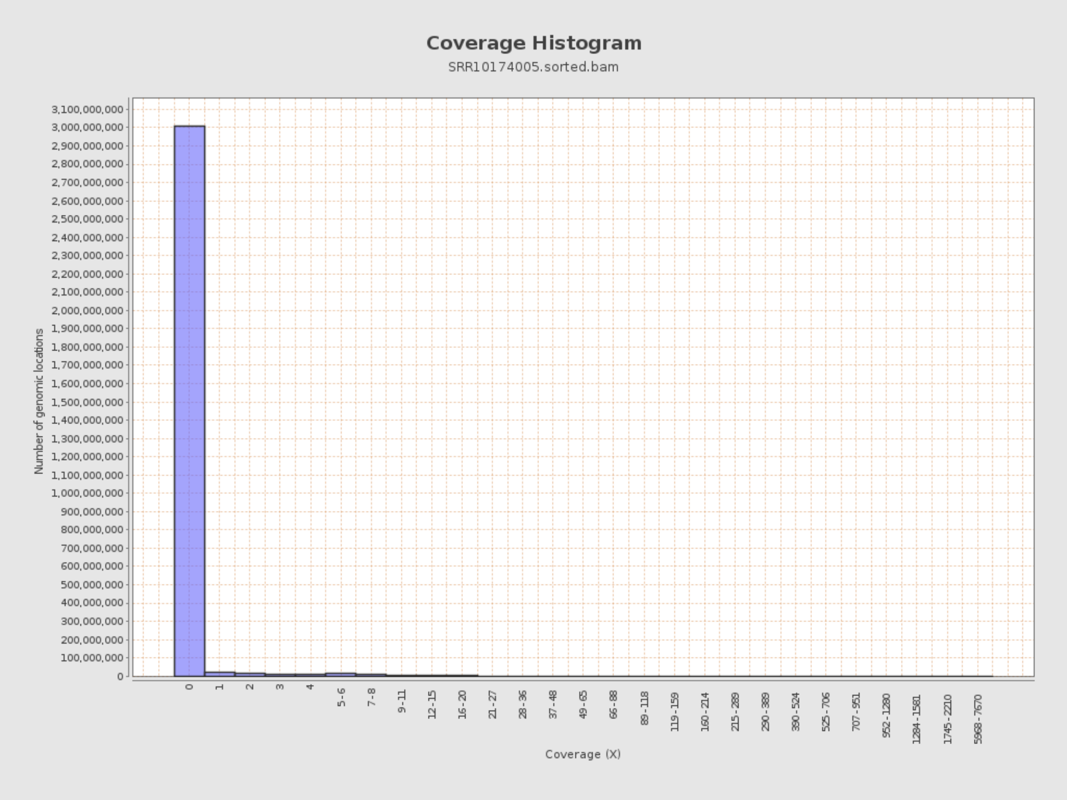
		bases	coverage	deviation
chr1	249250621	31756670	0.1274	1.7997
chr2	243199373	39354515	0.1618	5.4038
chr3	198022430	33441231	0.1689	1.1759
chr4	191154276	26018236	0.1361	1.2214
chr5	180915260	28480138	0.1574	1.1322
chr6	171115067	24012167	0.1403	1.0999
chr7	159138663	27152268	0.1706	2.2898
chr8	146364022	17311837	0.1183	1.1488
chr9	141213431	15293271	0.1083	1.1081
chr10	135534747	18429245	0.136	2.5832
chr11	135006516	17573327	0.1302	1.0402
chr12	133851895	15429355	0.1153	0.9723
chr13	115169878	12177814	0.1057	0.9186
chr14	107349540	12592775	0.1173	0.9768
chr15	102531392	12059323	0.1176	0.9662
chr16	90354753	15106515	0.1672	1.6557
chr17	81195210	7881535	0.0971	0.9933
chr18	78077248	5892434	0.0755	1.3811
chr19	59128983	6576375	0.1112	1.7636
chr20	63025520	10657852	0.1691	1.1525
chr21	48129895	6025256	0.1252	1.0323
chr22	51304566	2843145	0.0554	0.6262
chrMT	16571	845426	51.0184	44.9019
chrX	155270560	12046686	0.0776	0.7818

chrY	59373566	509425	0.0086	0.4482

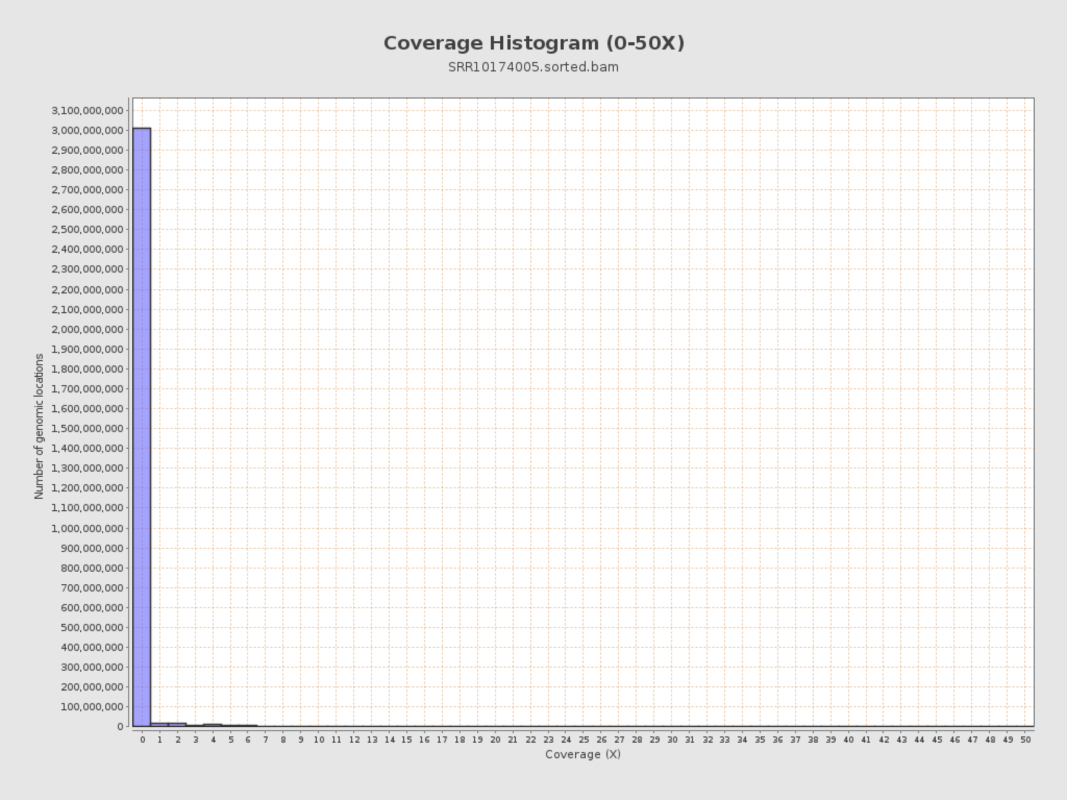
3. Results : Coverage across reference



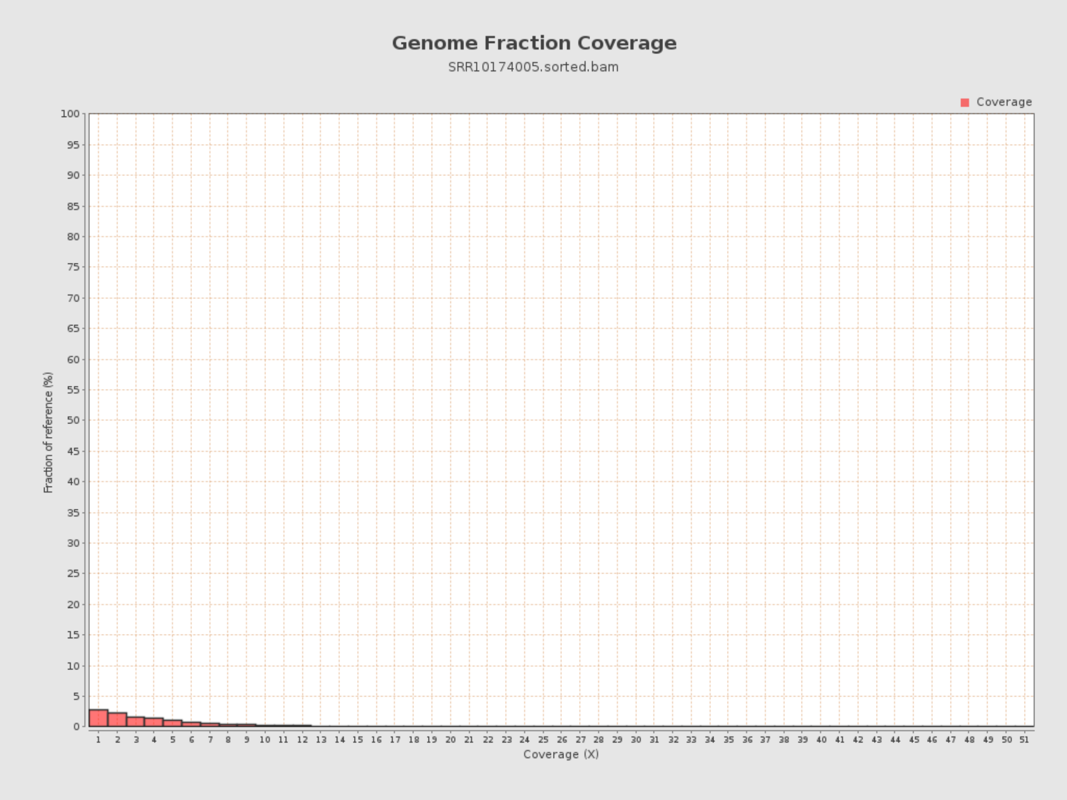
4. Results : Coverage Histogram



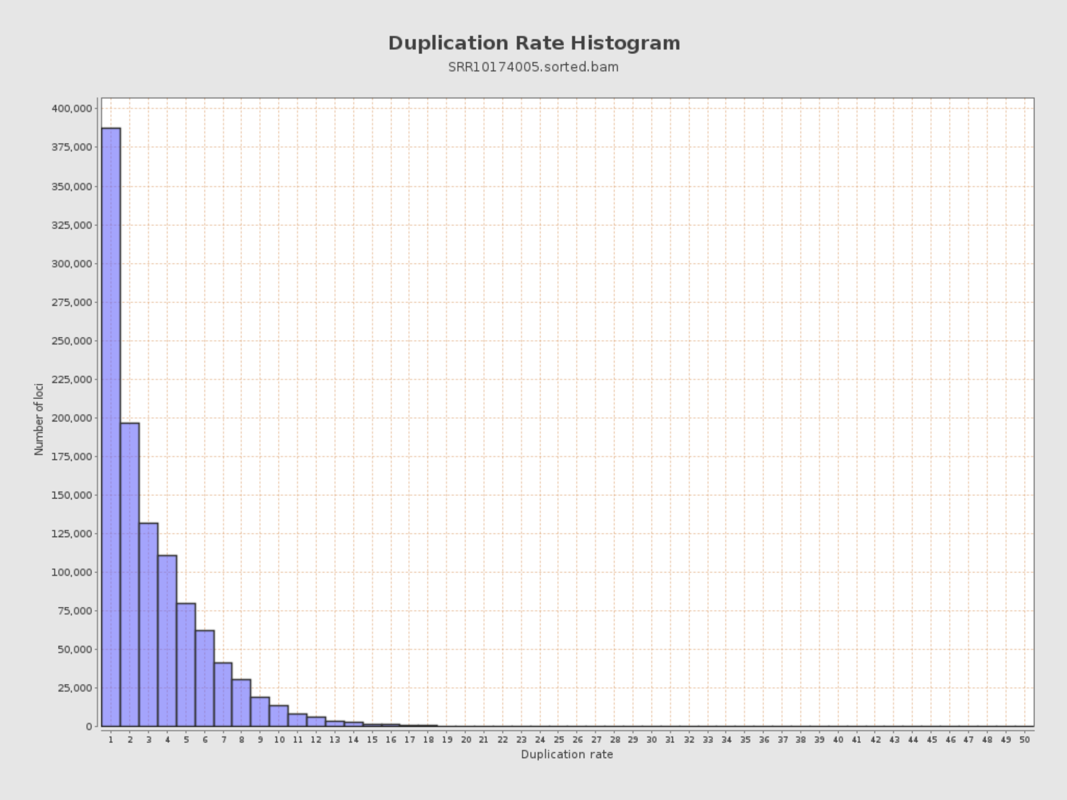
5. Results : Coverage Histogram (0-50X)



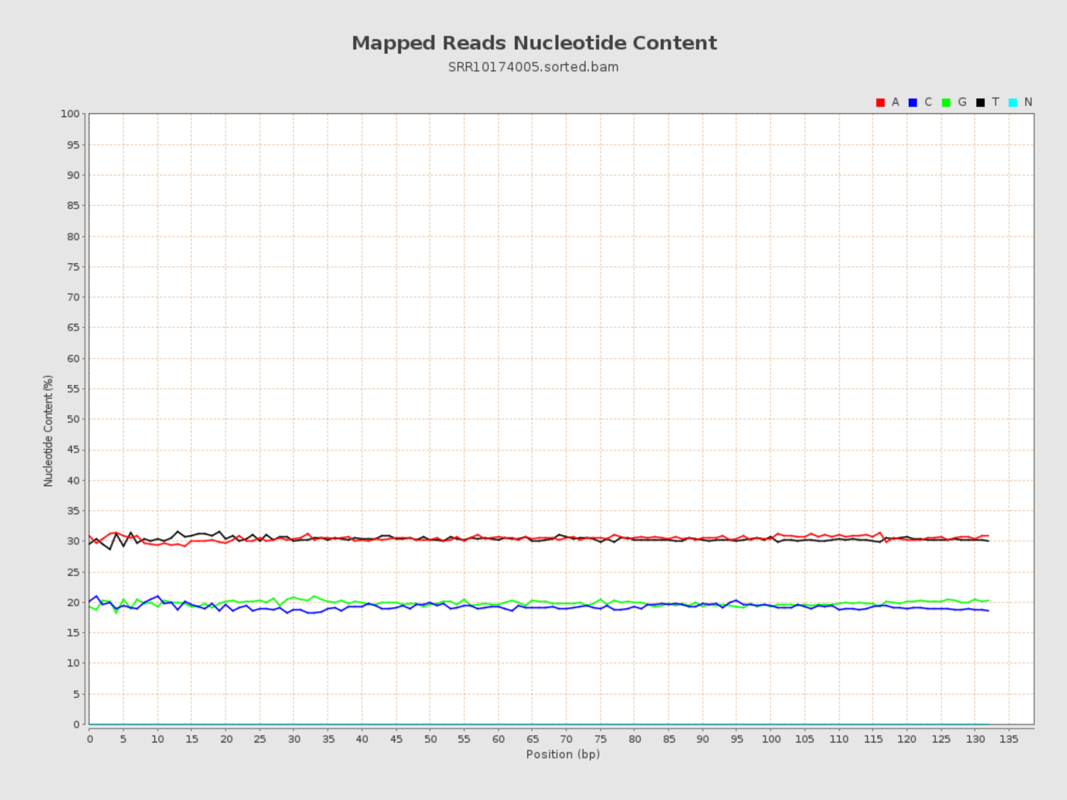
6. Results : Genome Fraction Coverage



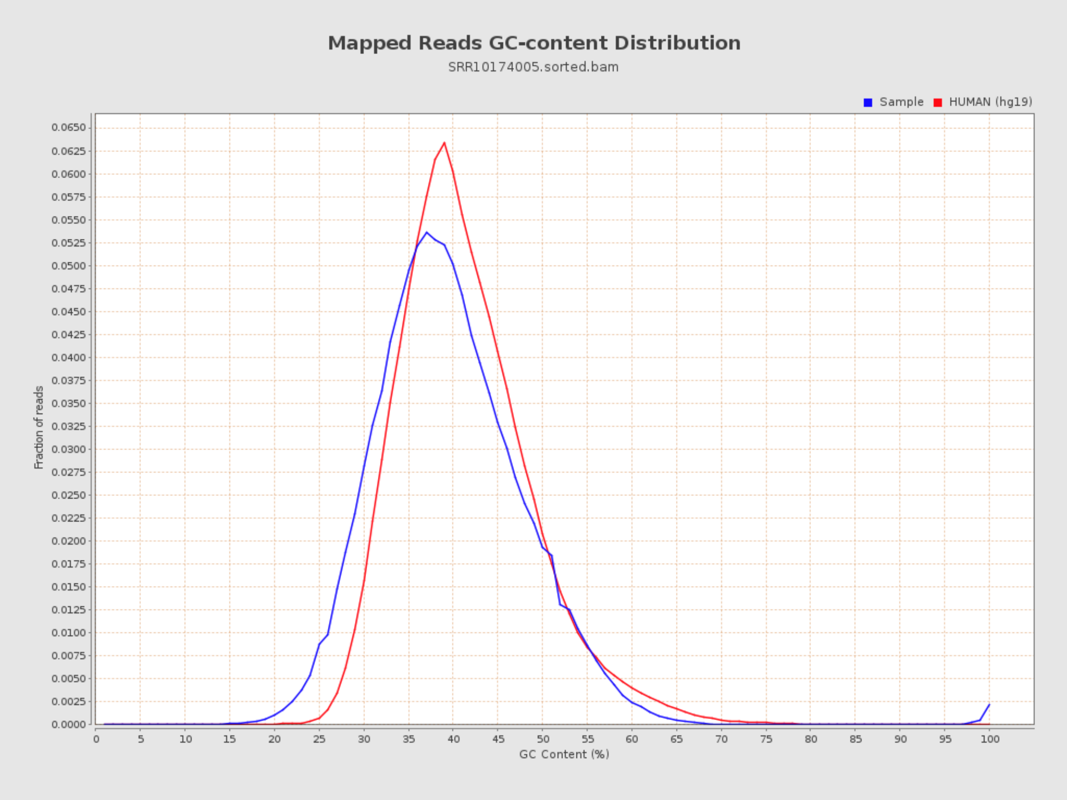
7. Results : Duplication Rate Histogram



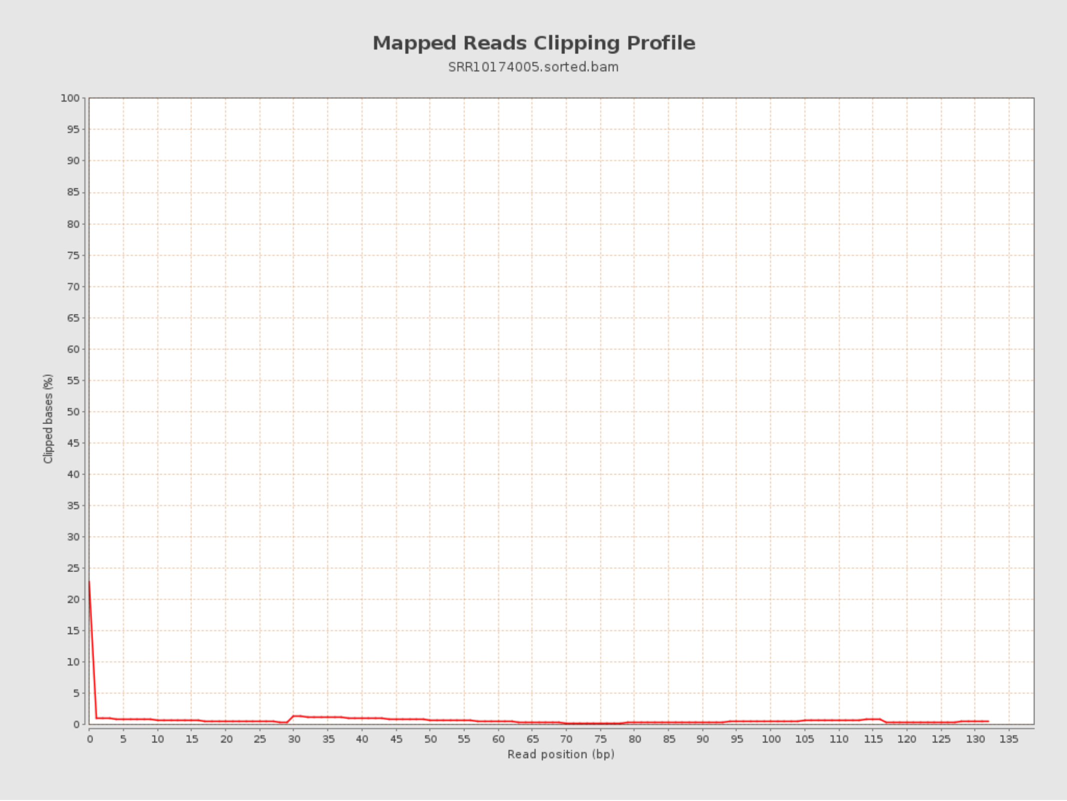
8. Results : Mapped Reads Nucleotide Content



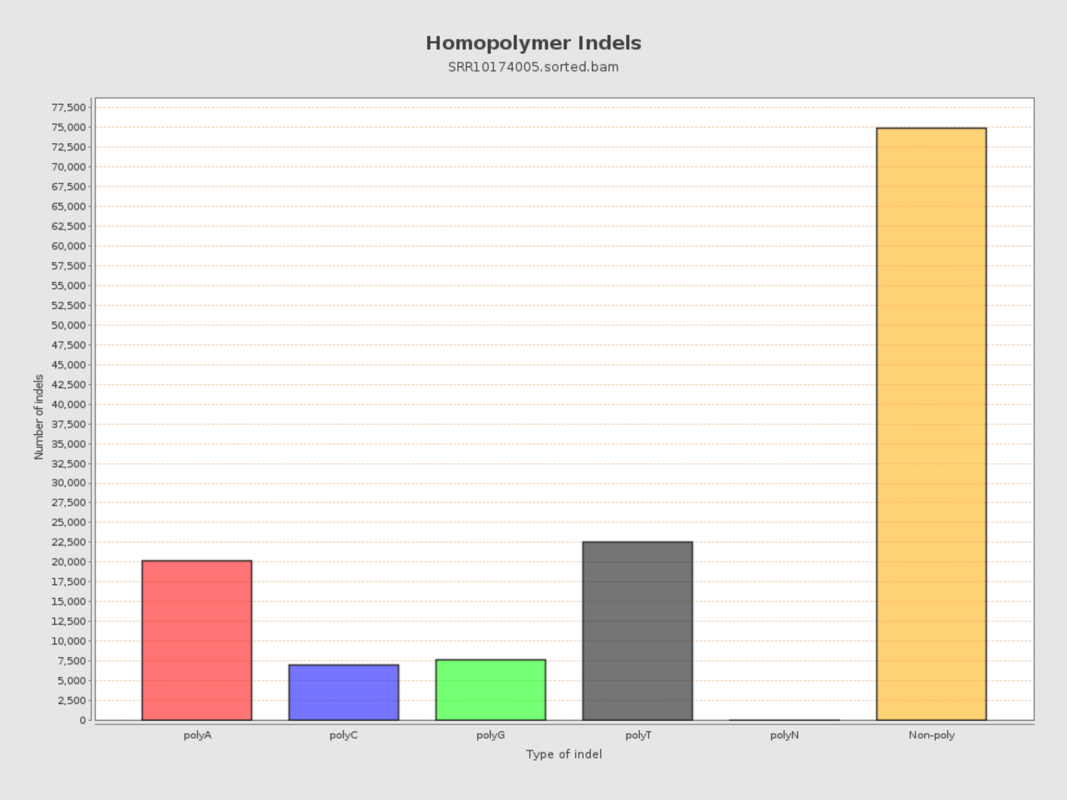
9. Results : Mapped Reads GC-content Distribution



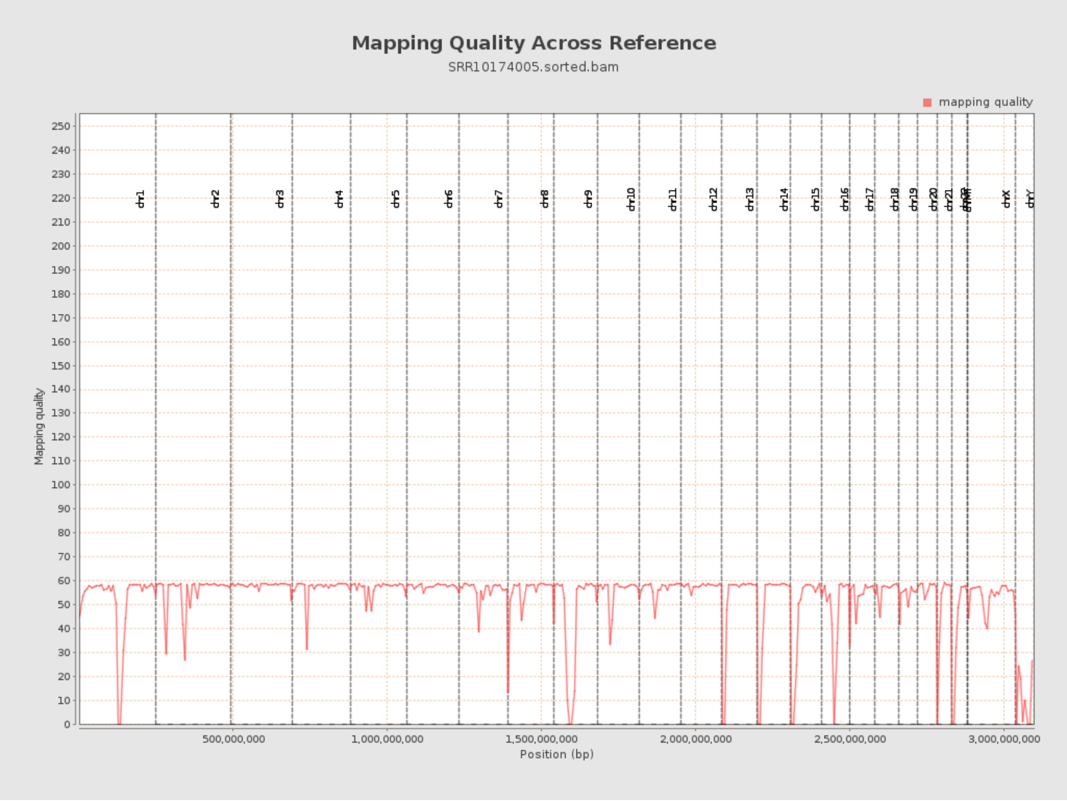
10. Results : Mapped Reads Clipping Profile



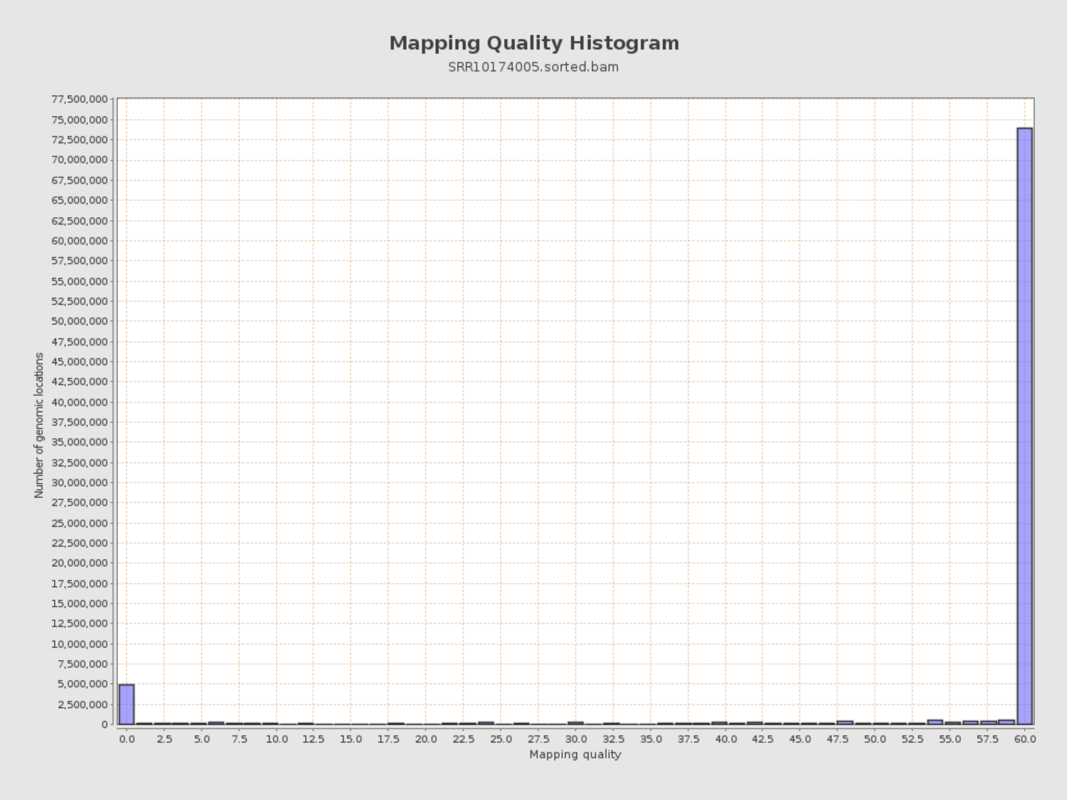
11. Results : Homopolymer Indels



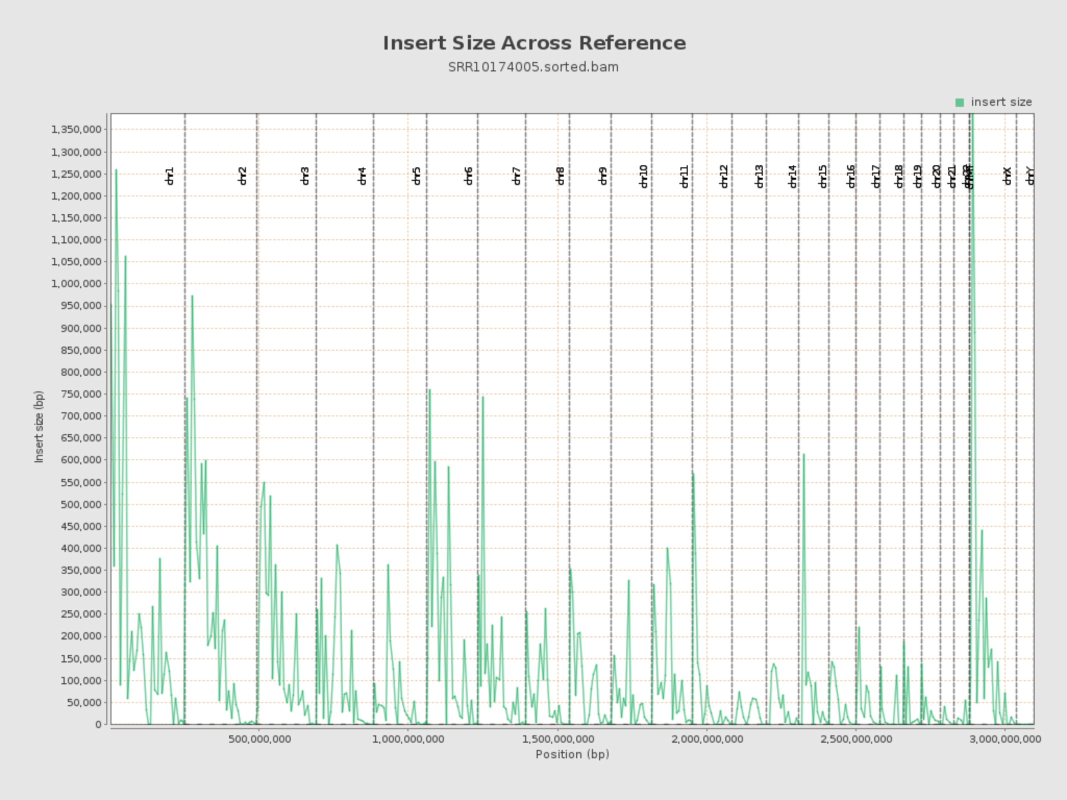
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram