Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 20:36:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174008.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_SRR10174008 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174008_1.fastq.gz SRR10174008_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 20:36:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174008.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,381,396
Mapped reads	4,264,784 / 97.34%
Unmapped reads	116,612 / 2.66%
Mapped paired reads	4,264,784 / 97.34%
Mapped reads, first in pair	2,133,870 / 48.7%
Mapped reads, second in pair	2,130,914 / 48.64%
Mapped reads, both in pair	4,185,216 / 95.52%
Mapped reads, singletons	79,568 / 1.82%
Secondary alignments	0
Supplementary alignments	440,333 / 10.05%
Read min/max/mean length	30 / 133 / 128.41
Duplicated reads (estimated)	3,393,862 / 77.46%
Duplication rate	65.28%
Clipped reads	1,731,035 / 39.51%

2.2. ACGT Content

Number/percentage of A's	151,887,357 / 30.12%
Number/percentage of C's	98,633,099 / 19.56%
Number/percentage of T's	151,673,250 / 30.07%
Number/percentage of G's	102,129,300 / 20.25%
Number/percentage of N's	5,875 / 0%

GC Percentage	39.81%

2.3. Coverage

Mean	0.163
Standard Deviation	2.5567

2.4. Mapping Quality

Mean Mapping Quality	52.6

2.5. Insert size

Mean	1,068,356.84
Standard Deviation	9,892,493.73
P25/Median/P75	146 / 204 / 293

2.6. Mismatches and indels

General error rate	1.06%
Mismatches	5,226,273
Insertions	50,508
Mapped reads with at least one insertion	1.15%
Deletions	119,780
Mapped reads with at least one deletion	2.74%
Homopolymer indels	42.93%

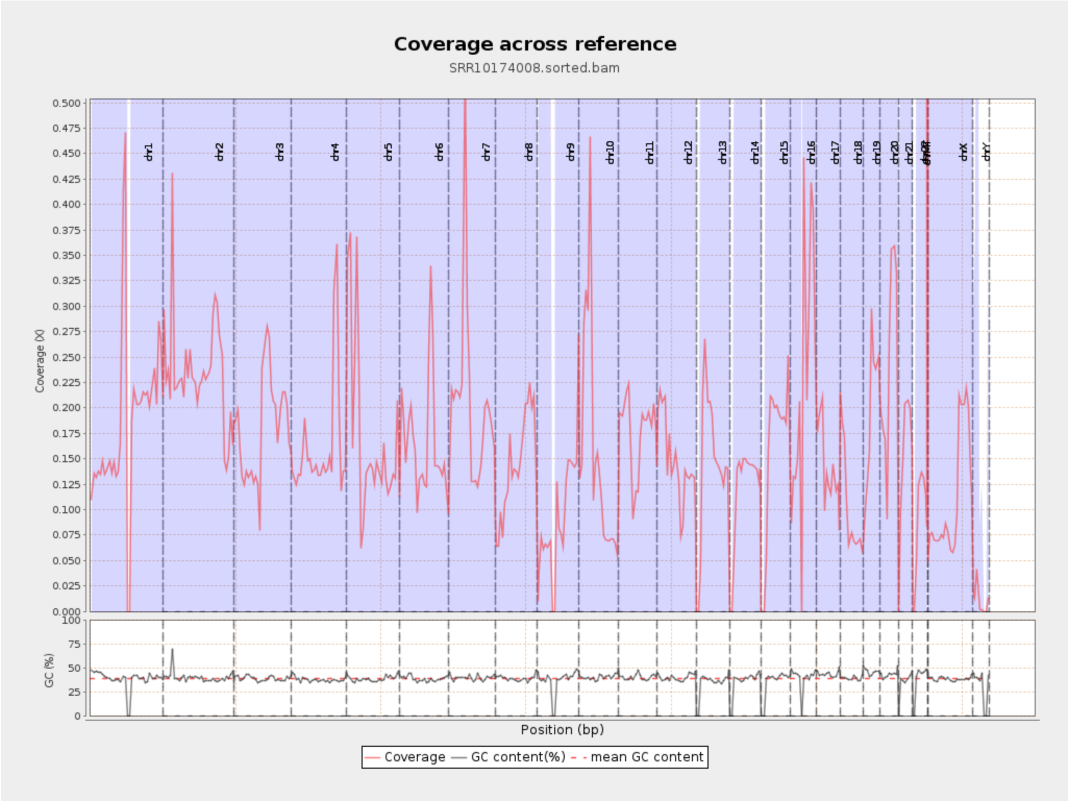
2.7. Chromosome stats

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

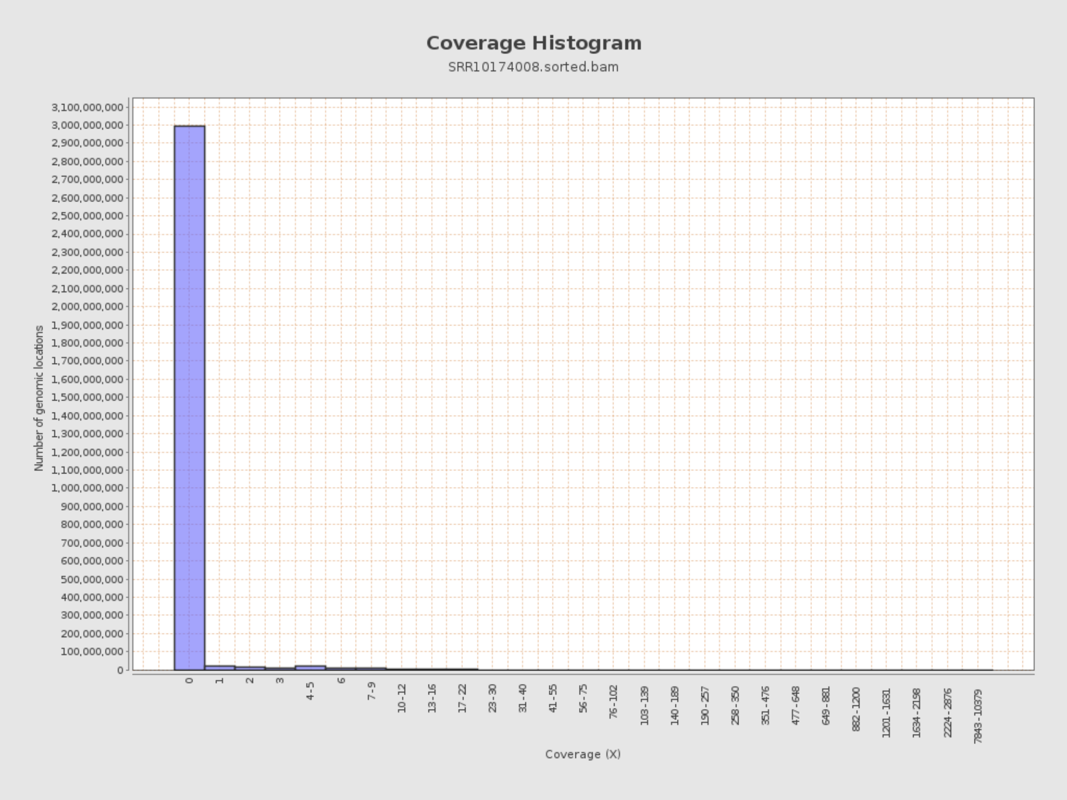
		bases	coverage	deviation
chr1	249250621	46075716	0.1849	1.9508
chr2	243199373	57314071	0.2357	7.3262
chr3	198022430	35810291	0.1808	1.2792
chr4	191154276	30413821	0.1591	1.333
chr5	180915260	31367946	0.1734	1.2496
chr6	171115067	28615816	0.1672	1.2638
chr7	159138663	32700571	0.2055	2.2893
chr8	146364022	21248623	0.1452	1.3637
chr9	141213431	12554452	0.0889	1.1262
chr10	135534747	21177105	0.1562	3.0149
chr11	135006516	23781568	0.1762	1.2672
chr12	133851895	19747312	0.1475	1.1503
chr13	115169878	16558865	0.1438	1.1487
chr14	107349540	12694137	0.1183	1.0272
chr15	102531392	16209887	0.1581	1.1757
chr16	90354753	20969946	0.2321	2.1618
chr17	81195210	11432598	0.1408	1.1971
chr18	78077248	7906994	0.1013	1.7874
chr19	59128983	11606794	0.1963	2.2324
chr20	63025520	15304234	0.2428	1.456
chr21	48129895	7443299	0.1547	1.201
chr22	51304566	4454577	0.0868	0.8347
chrMT	16571	1457206	87.9371	68.675
chrX	155270560	17125322	0.1103	0.9924

chrY	59373566	647733	0.0109	0.3987

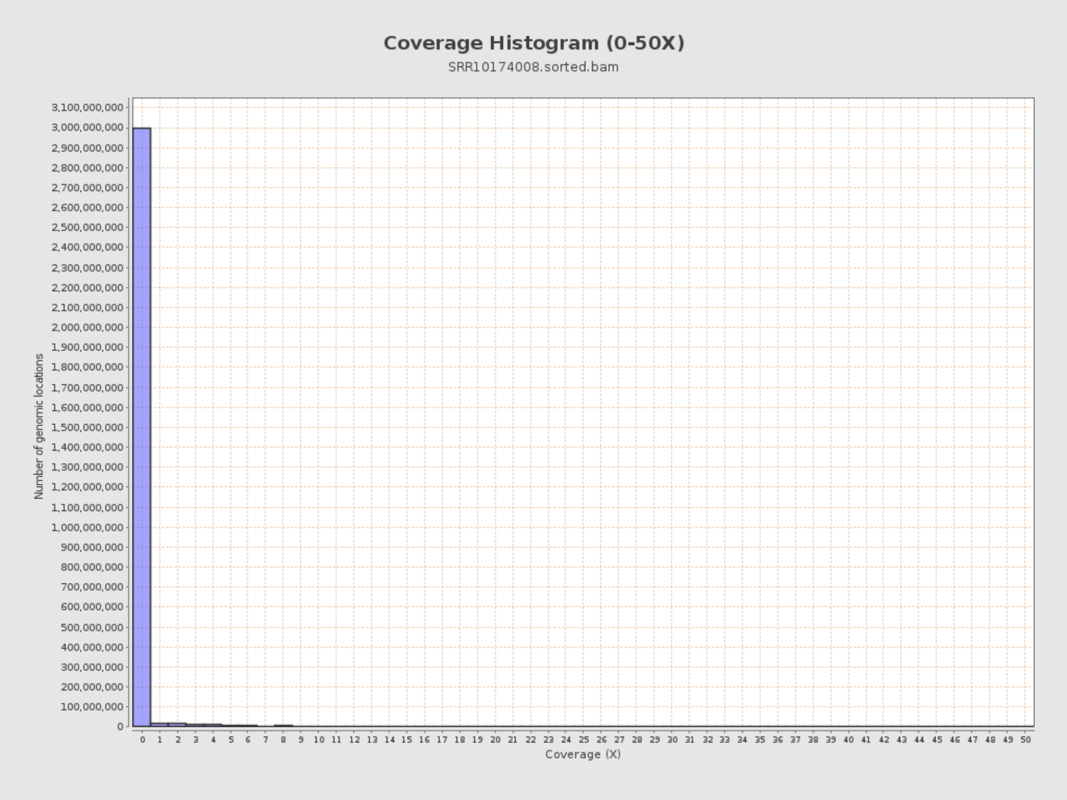
3. Results : Coverage across reference



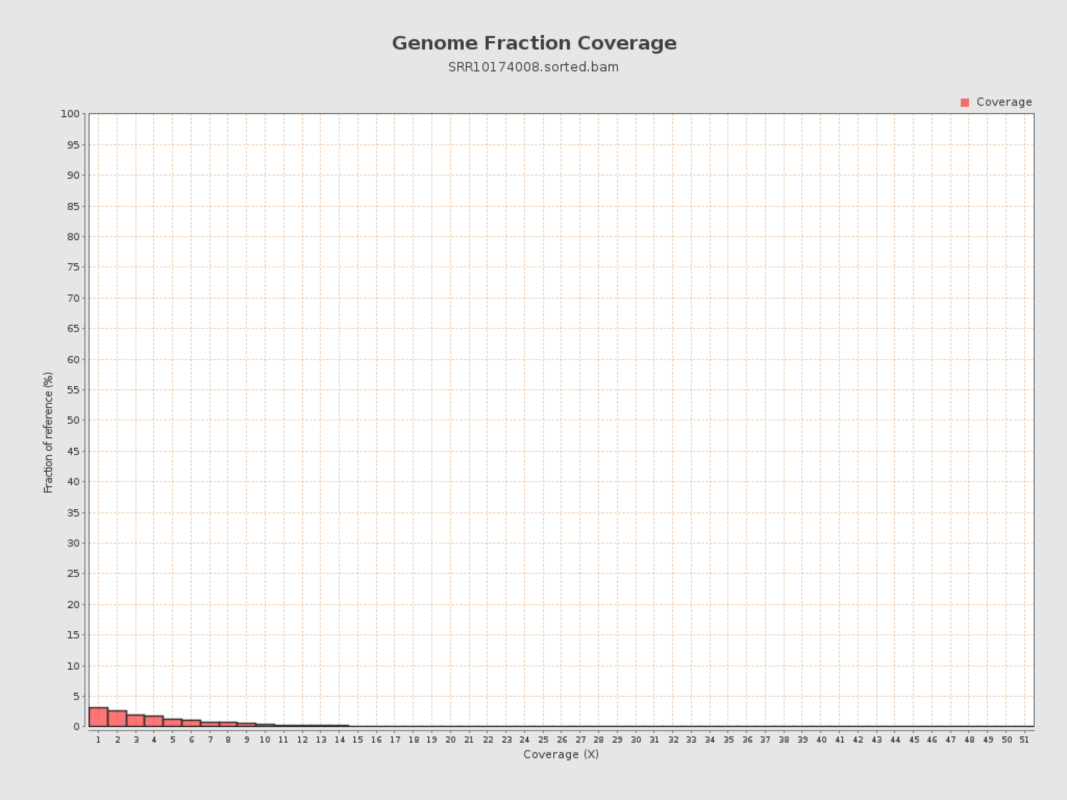
4. Results : Coverage Histogram



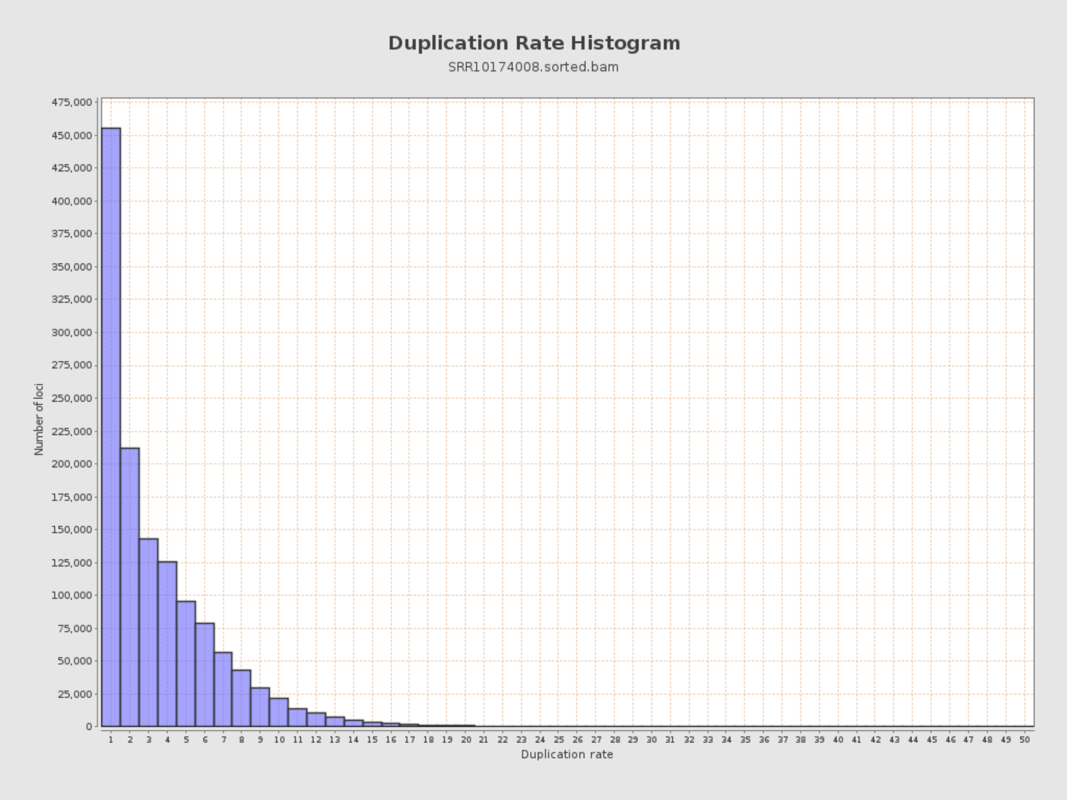
5. Results : Coverage Histogram (0-50X)



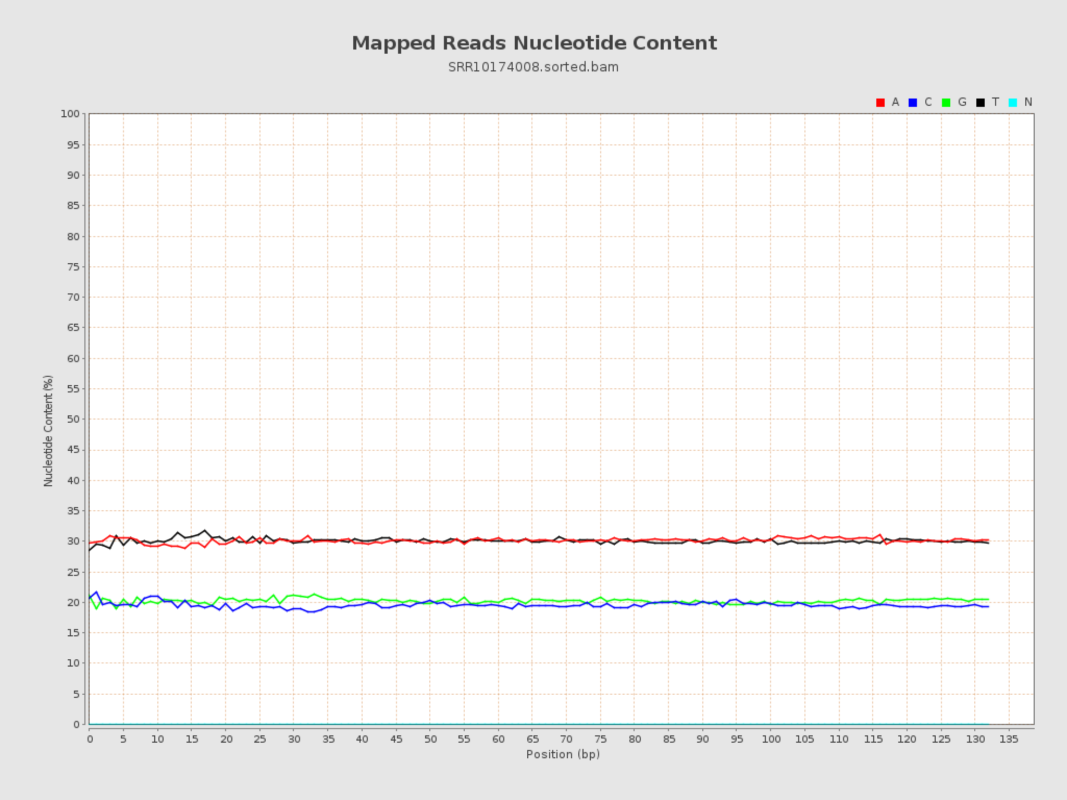
6. Results : Genome Fraction Coverage



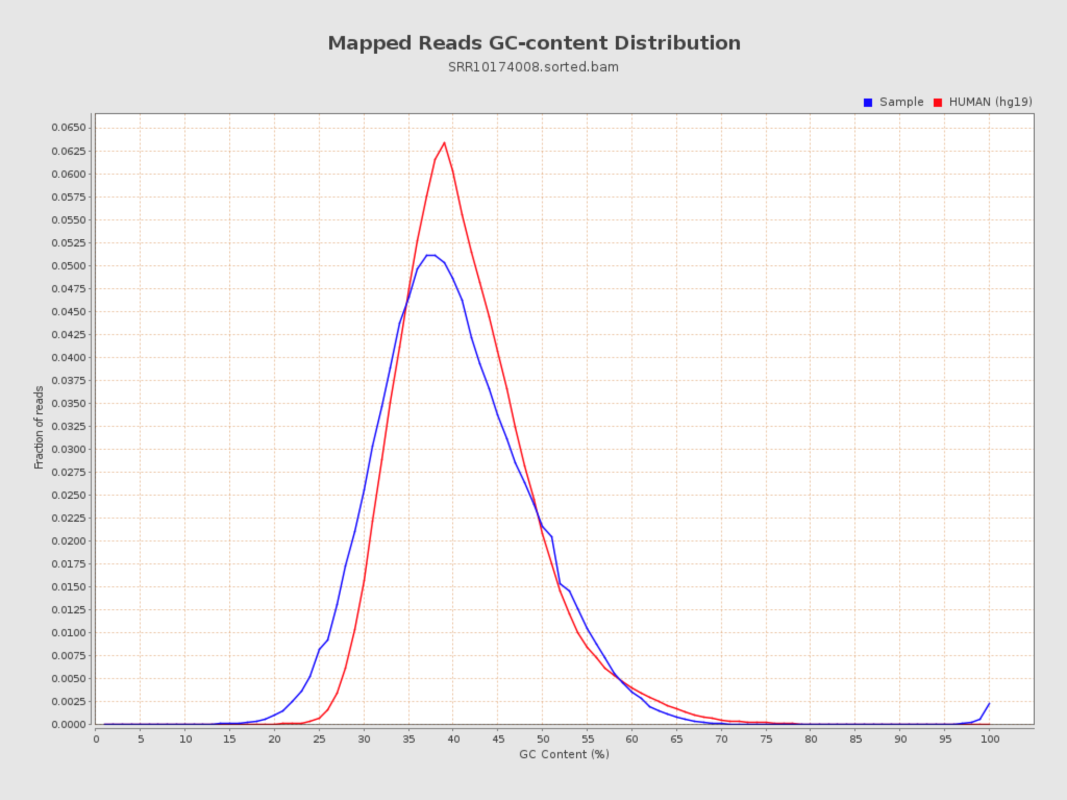
7. Results : Duplication Rate Histogram



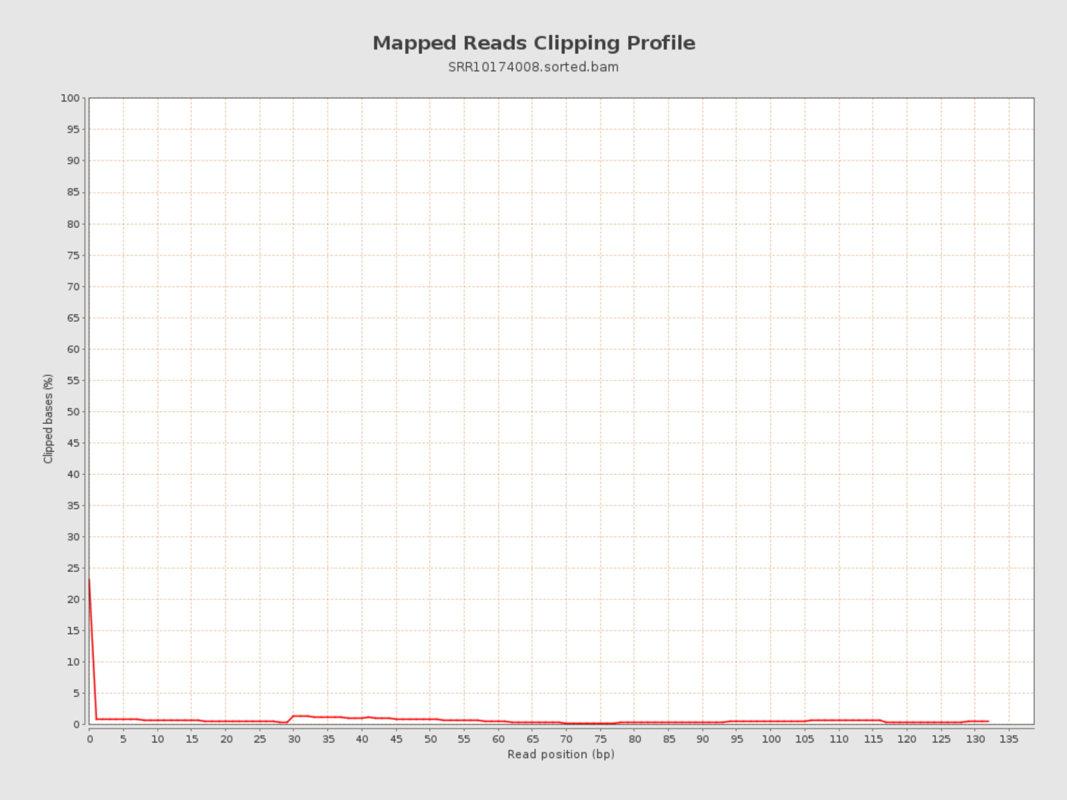
8. Results : Mapped Reads Nucleotide Content



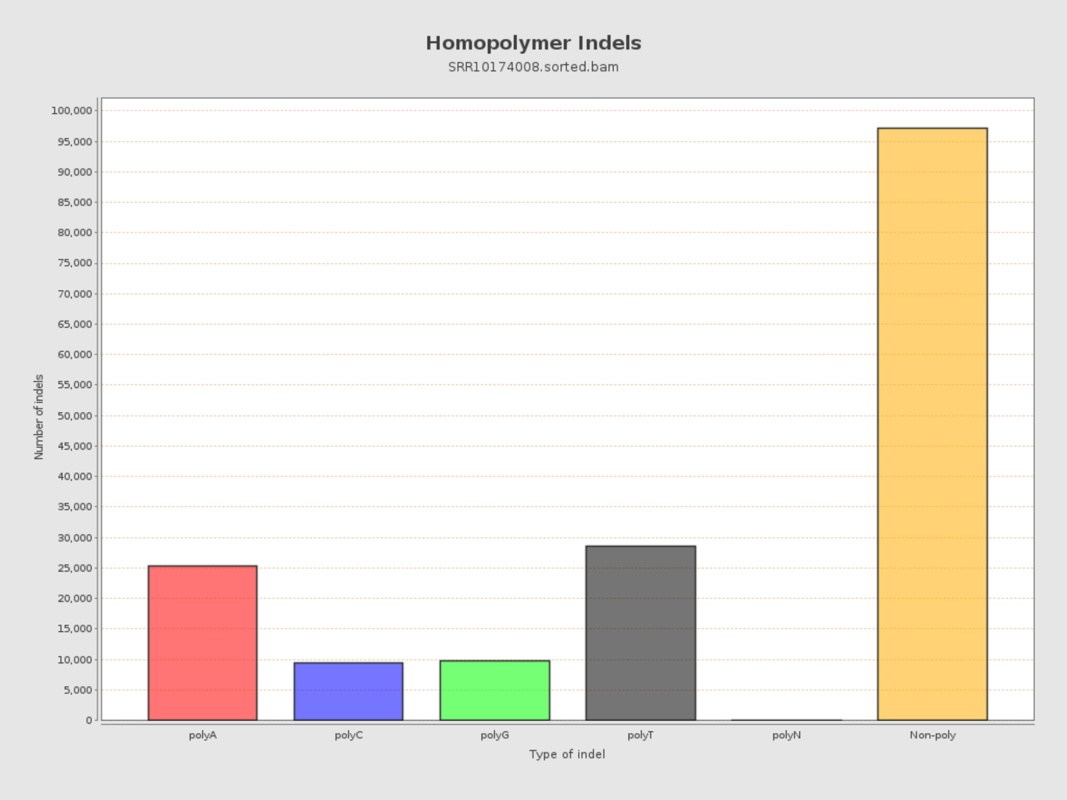
9. Results : Mapped Reads GC-content Distribution



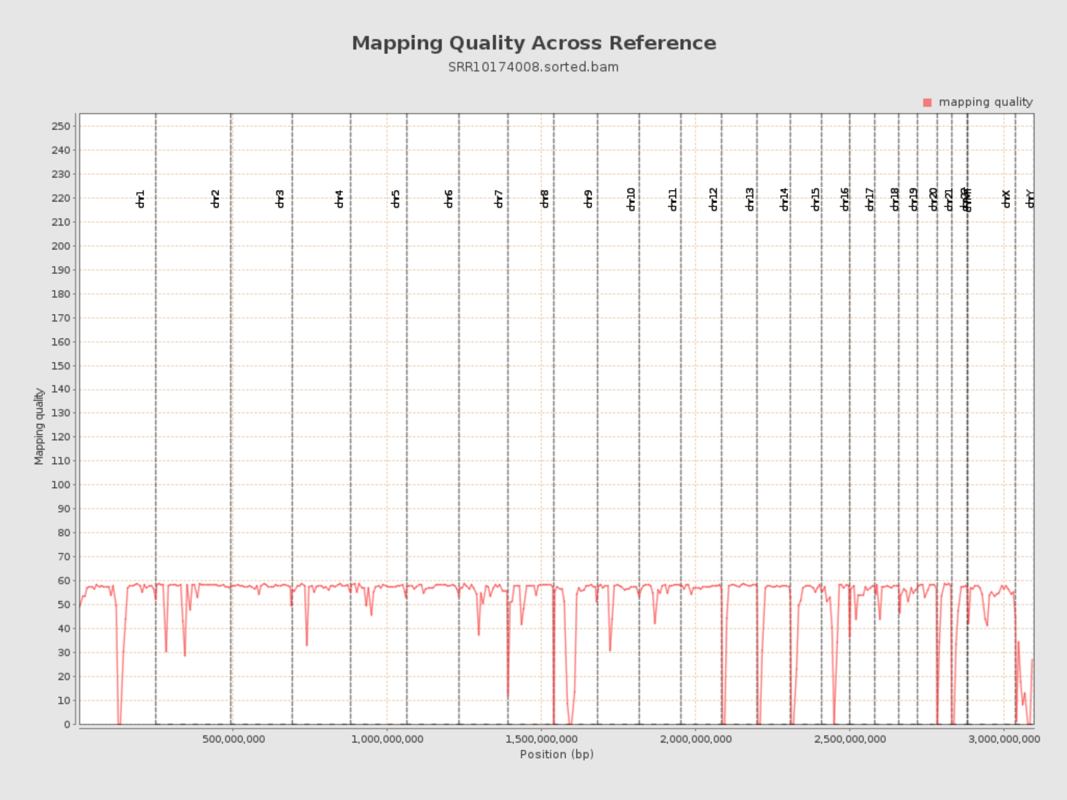
10. Results : Mapped Reads Clipping Profile



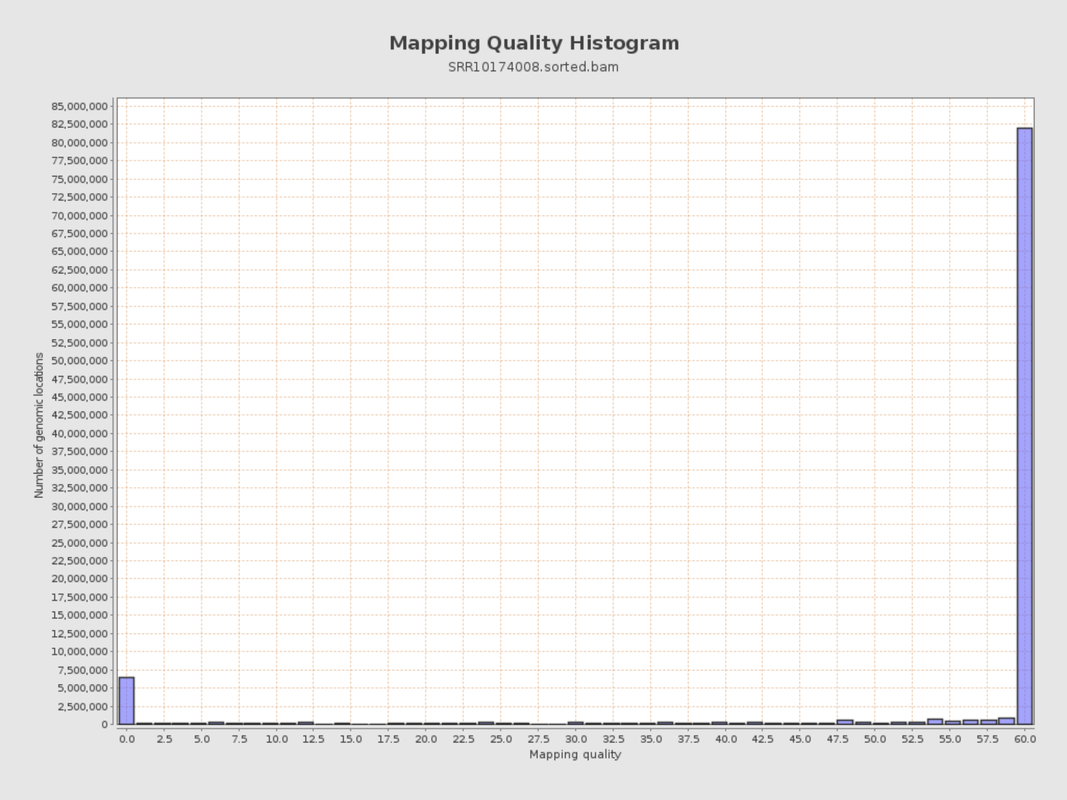
11. Results : Homopolymer Indels



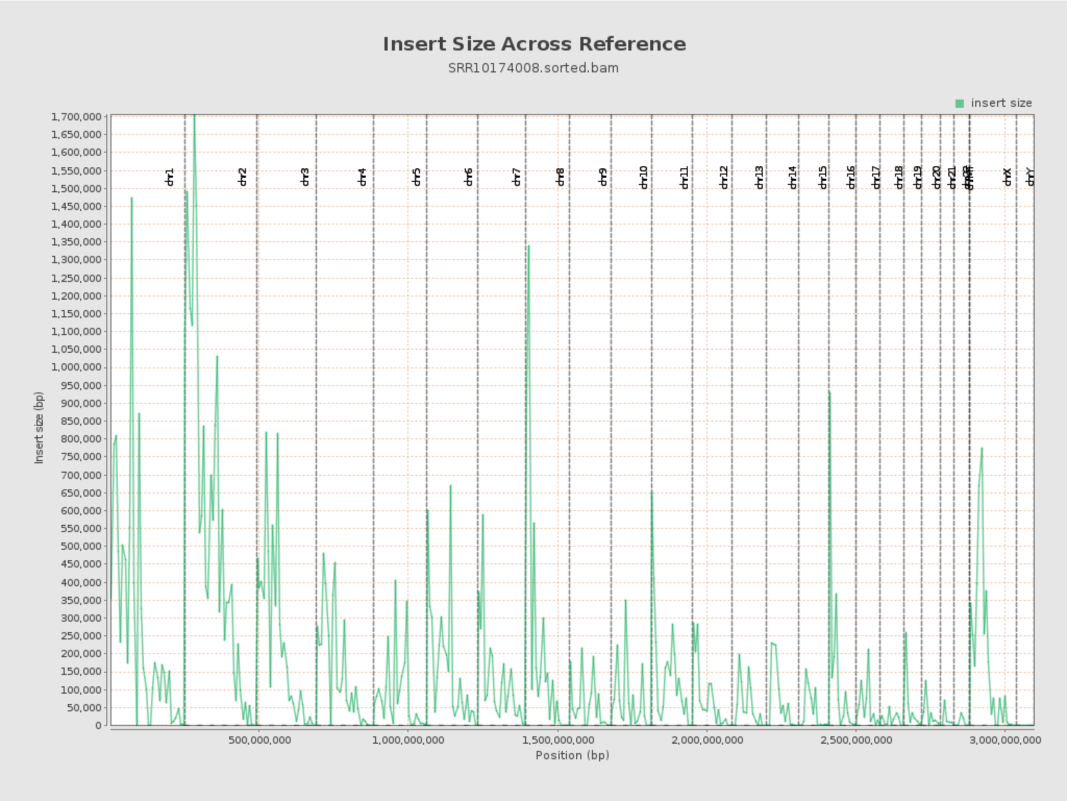
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram