

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 19:49:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174004.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_SRR10174004 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174004_1.fastq.gz SRR10174004_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 19:49:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174004.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,239,022
Mapped reads	13,891,110 / 97.56%
Unmapped reads	347,912 / 2.44%
Mapped paired reads	13,891,110 / 97.56%
Mapped reads, first in pair	6,941,667 / 48.75%
Mapped reads, second in pair	6,949,443 / 48.81%
Mapped reads, both in pair	13,658,146 / 95.92%
Mapped reads, singletons	232,964 / 1.64%
Secondary alignments	0
Supplementary alignments	1,388,291 / 9.75%
Read min/max/mean length	30 / 133 / 128.36
Duplicated reads (estimated)	11,381,774 / 79.93%
Duplication rate	67.02%
Clipped reads	5,409,494 / 37.99%

2.2. ACGT Content

Number/percentage of A's	492,387,464 / 29.84%
Number/percentage of C's	327,632,738 / 19.86%
Number/percentage of T's	491,364,983 / 29.78%
Number/percentage of G's	338,652,687 / 20.52%
Number/percentage of N's	20,306 / 0%

GC Percentage	40.38%
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2.3. Coverage

Mean	0.5333
Standard Deviation	7.0383

2.4. Mapping Quality

Mean Mapping Quality	52.83
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2.5. Insert size

Mean	834,500.29
Standard Deviation	8,423,662.01
P25/Median/P75	149 / 207 / 294

2.6. Mismatches and indels

General error rate	1.03%
Mismatches	16,531,426
Insertions	163,373
Mapped reads with at least one insertion	1.14%
Deletions	380,621
Mapped reads with at least one deletion	2.68%
Homopolymer indels	43.44%

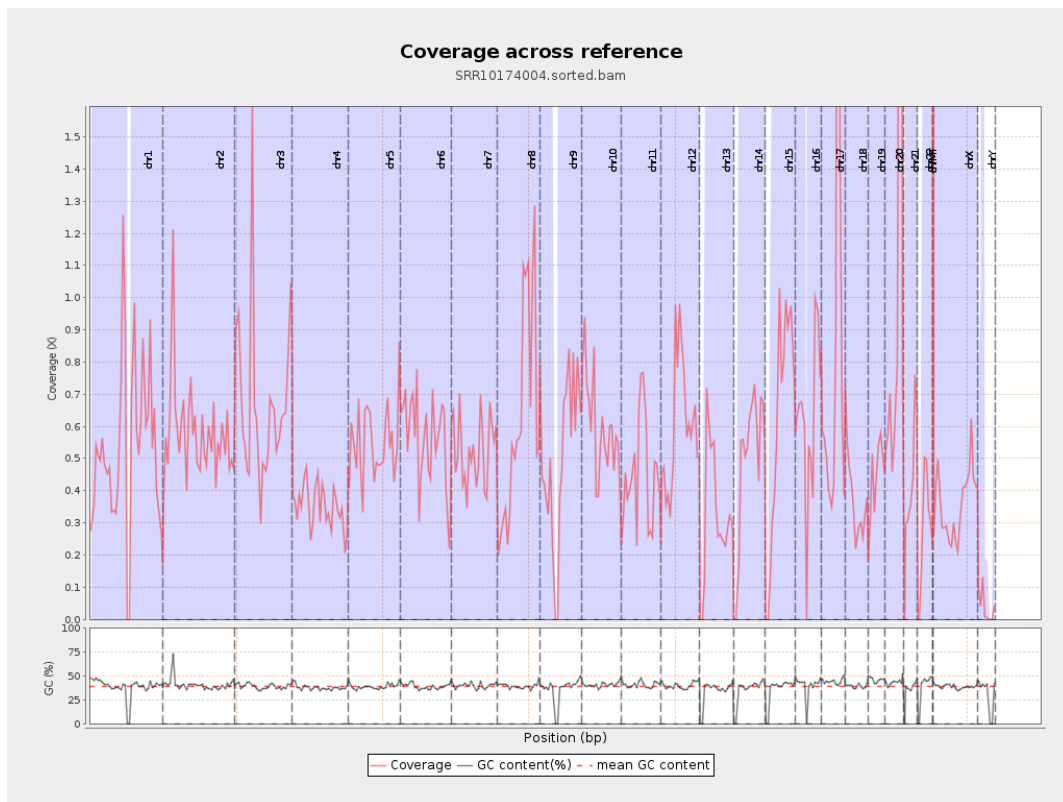
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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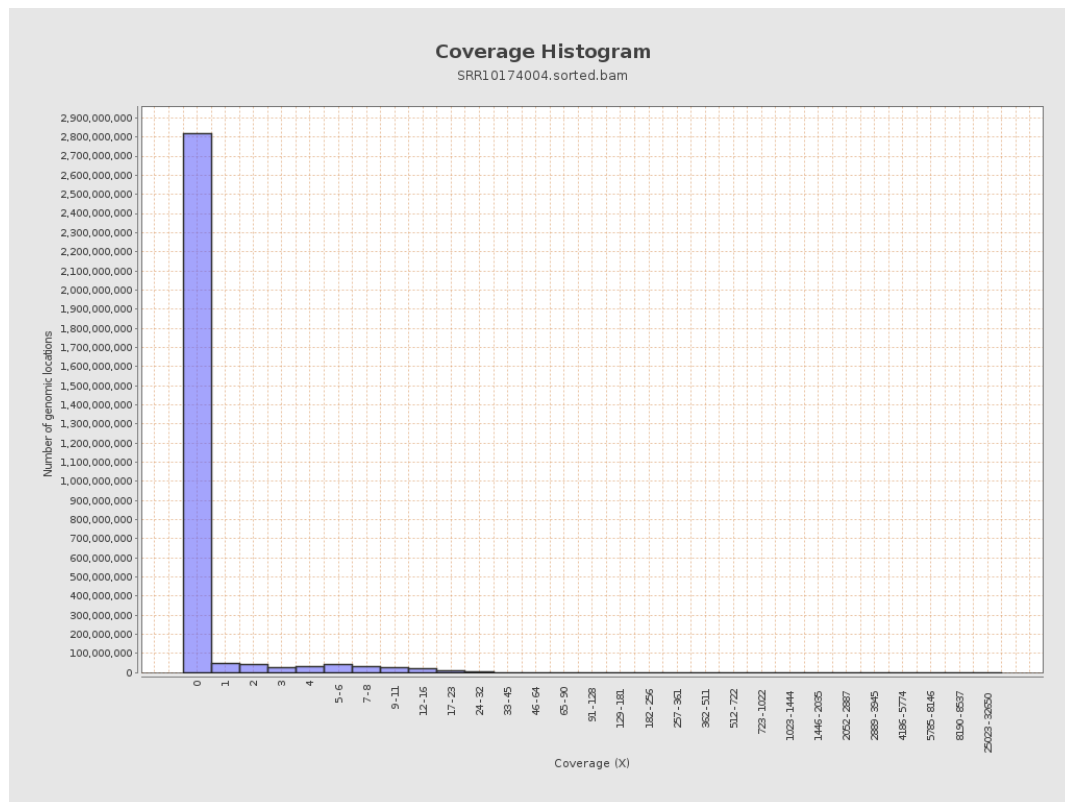
		bases	coverage	deviation
chr1	249250621	132344431	0.531	4.0644
chr2	243199373	140716200	0.5786	22.7285
chr3	198022430	131621179	0.6647	2.6374
chr4	191154276	67129029	0.3512	2.3188
chr5	180915260	99702910	0.5511	2.3212
chr6	171115067	96037641	0.5612	2.7483
chr7	159138663	83567182	0.5251	3.4001
chr8	146364022	90873175	0.6209	3.4379
chr9	141213431	69487647	0.4921	2.9235
chr10	135534747	80992463	0.5976	5.0878
chr11	135006516	60322768	0.4468	2.1541
chr12	133851895	81729154	0.6106	2.4965
chr13	115169878	37784382	0.3281	1.7929
chr14	107349540	52982727	0.4936	2.2245
chr15	102531392	61112477	0.596	2.4704
chr16	90354753	55038438	0.6091	3.0702
chr17	81195210	81119698	0.9991	3.9306
chr18	78077248	28969728	0.371	4.6756
chr19	59128983	26335782	0.4454	3.0082
chr20	63025520	77811741	1.2346	4.4851
chr21	48129895	19985502	0.4152	2.1454
chr22	51304566	14277590	0.2783	1.5882
chrMT	16571	3156080	190.458	145.8665
chrX	155270560	55640643	0.3583	1.877

chrY	59373566	2251754	0.0379	1.2903
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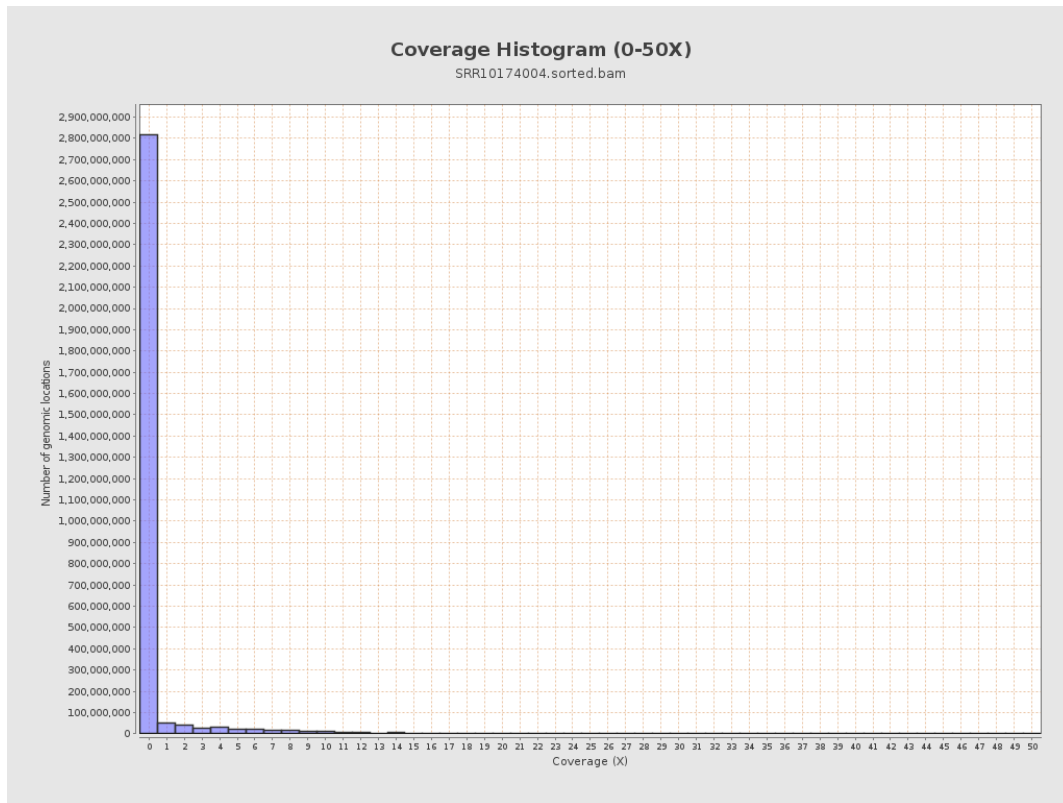
3. Results : Coverage across reference



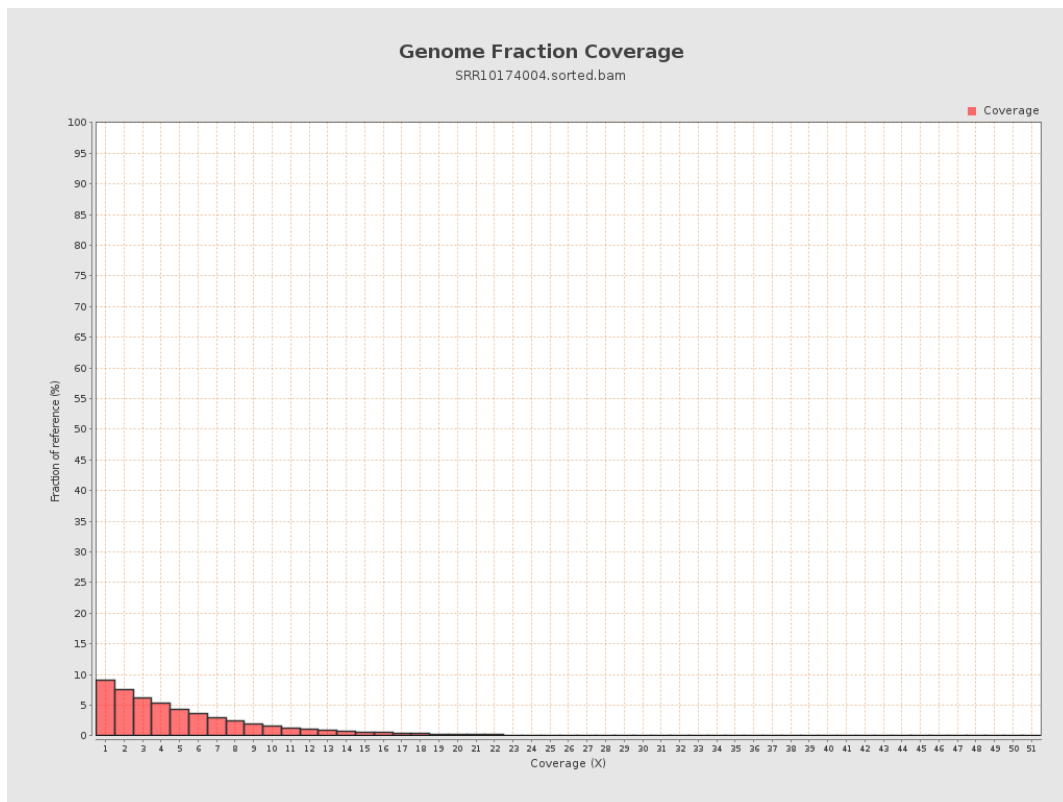
4. Results : Coverage Histogram



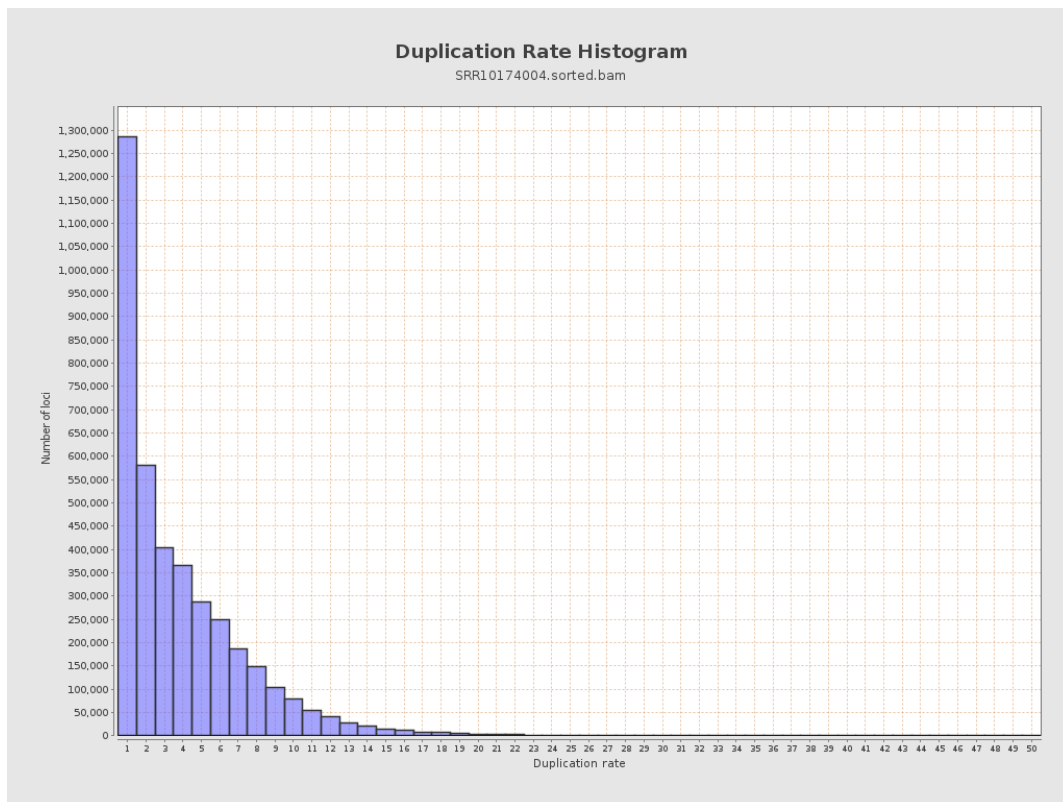
5. Results : Coverage Histogram (0-50X)



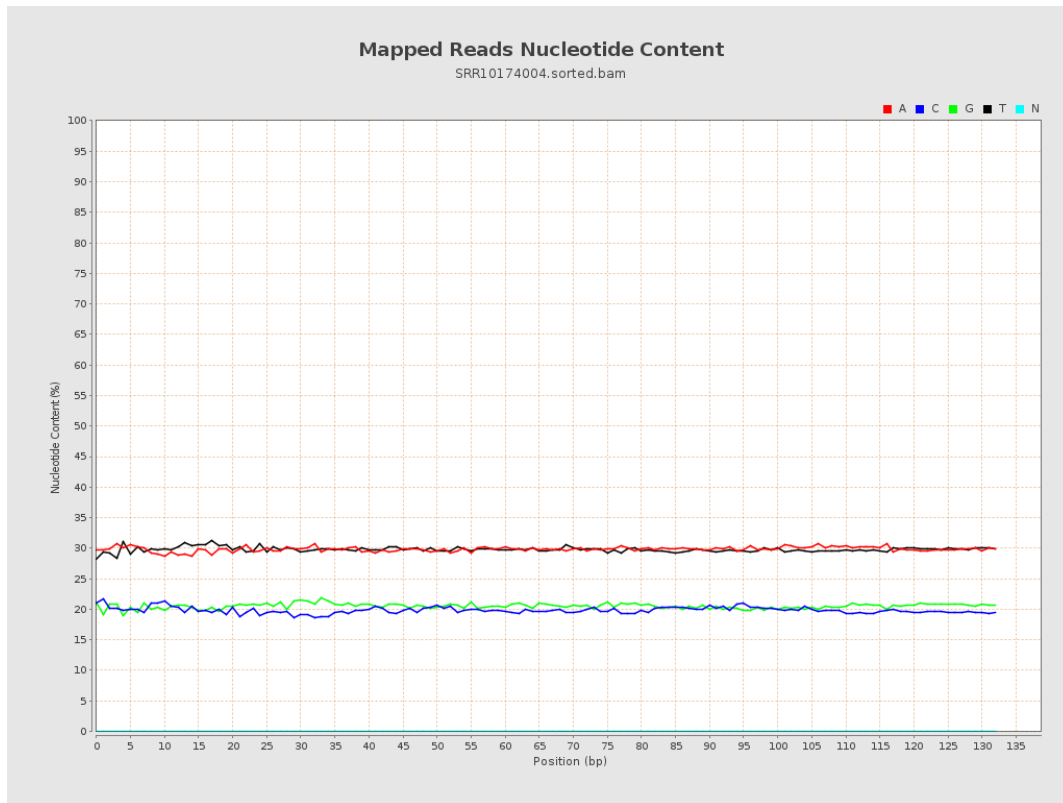
6. Results : Genome Fraction Coverage



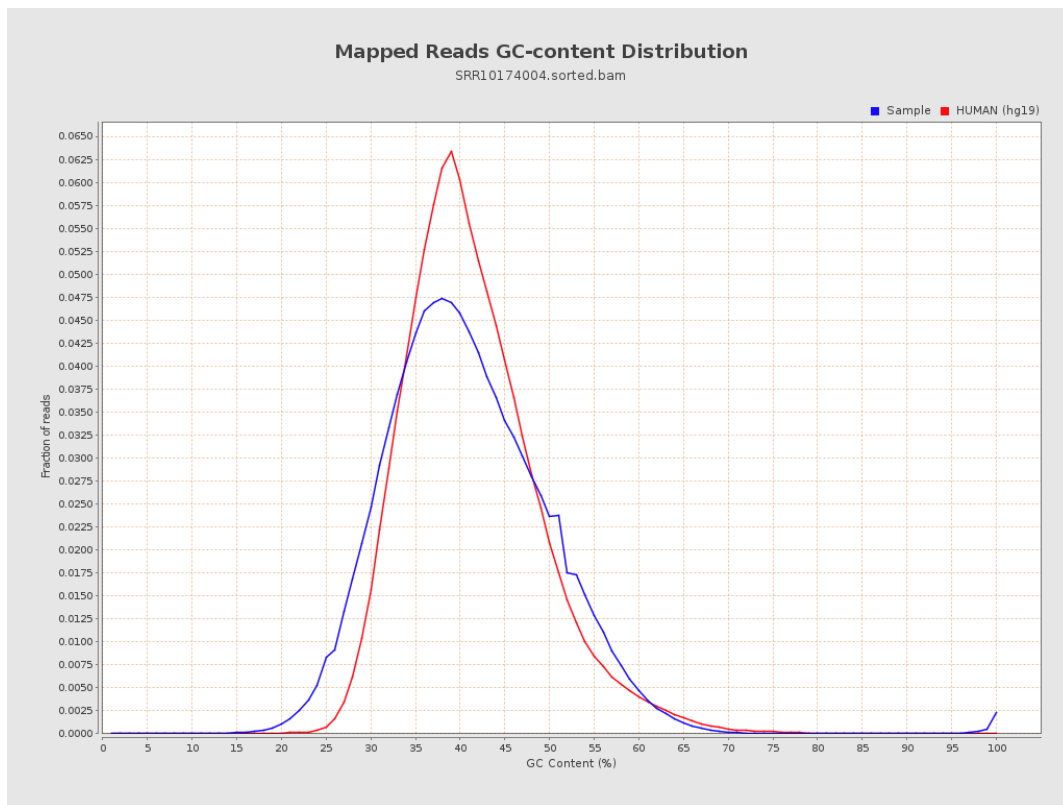
7. Results : Duplication Rate Histogram



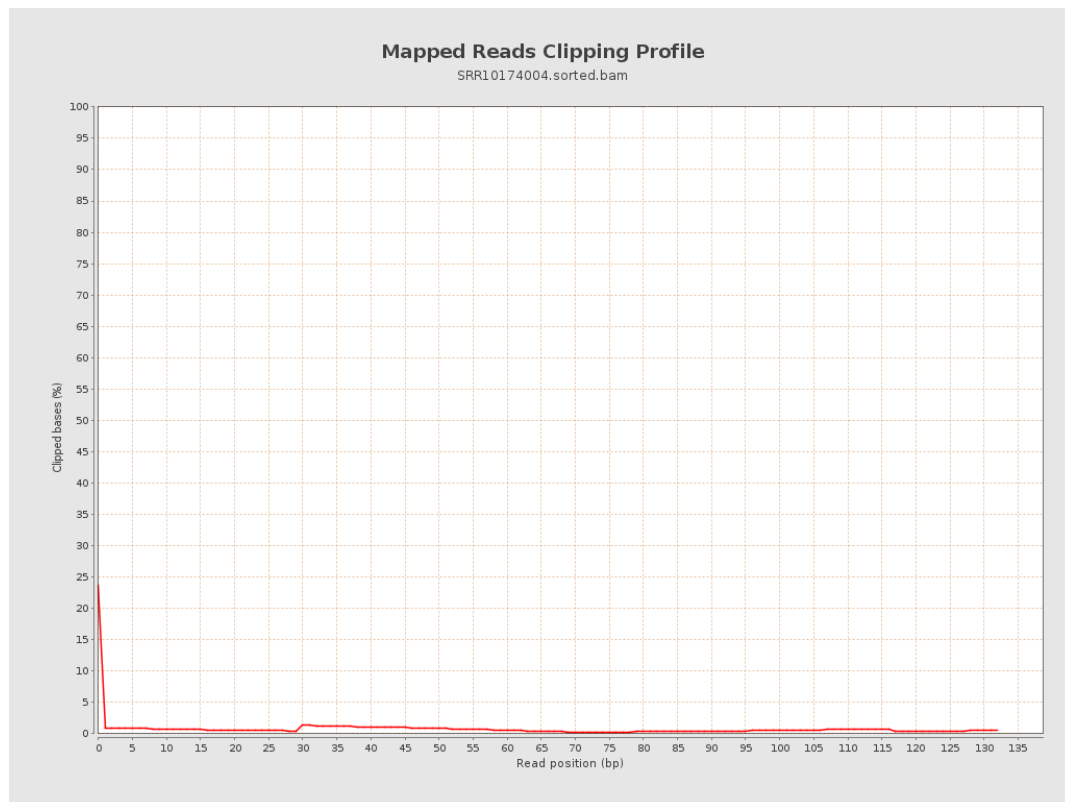
8. Results : Mapped Reads Nucleotide Content



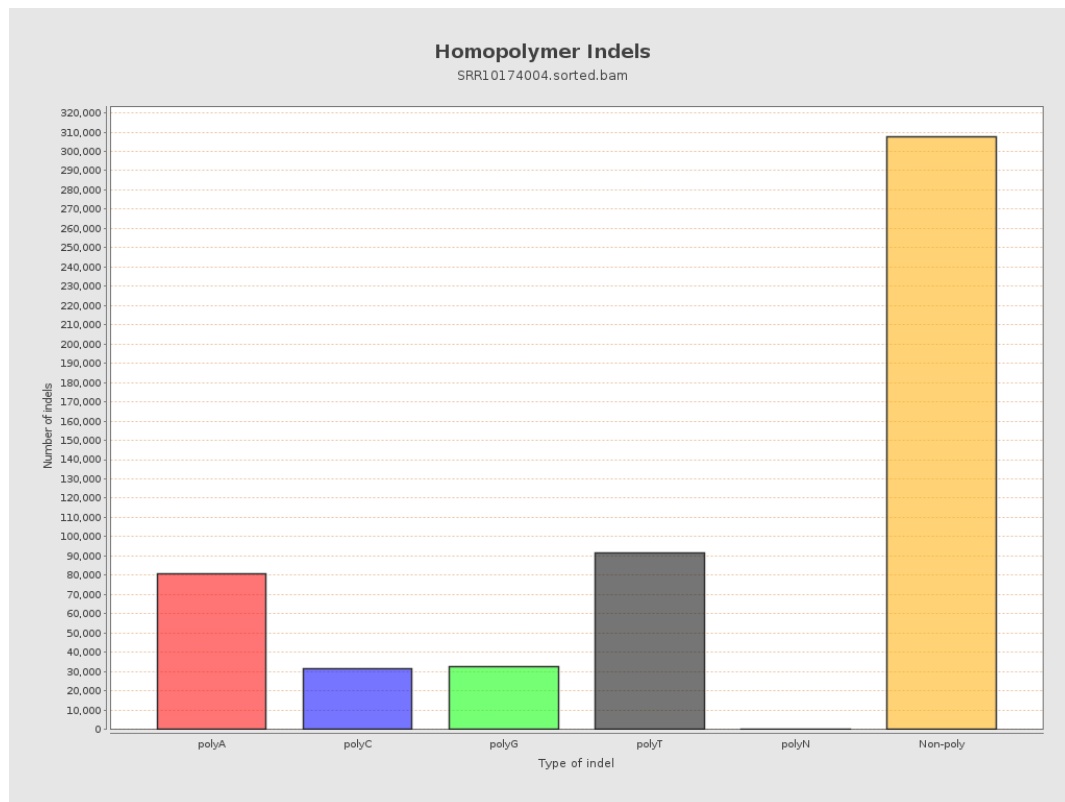
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



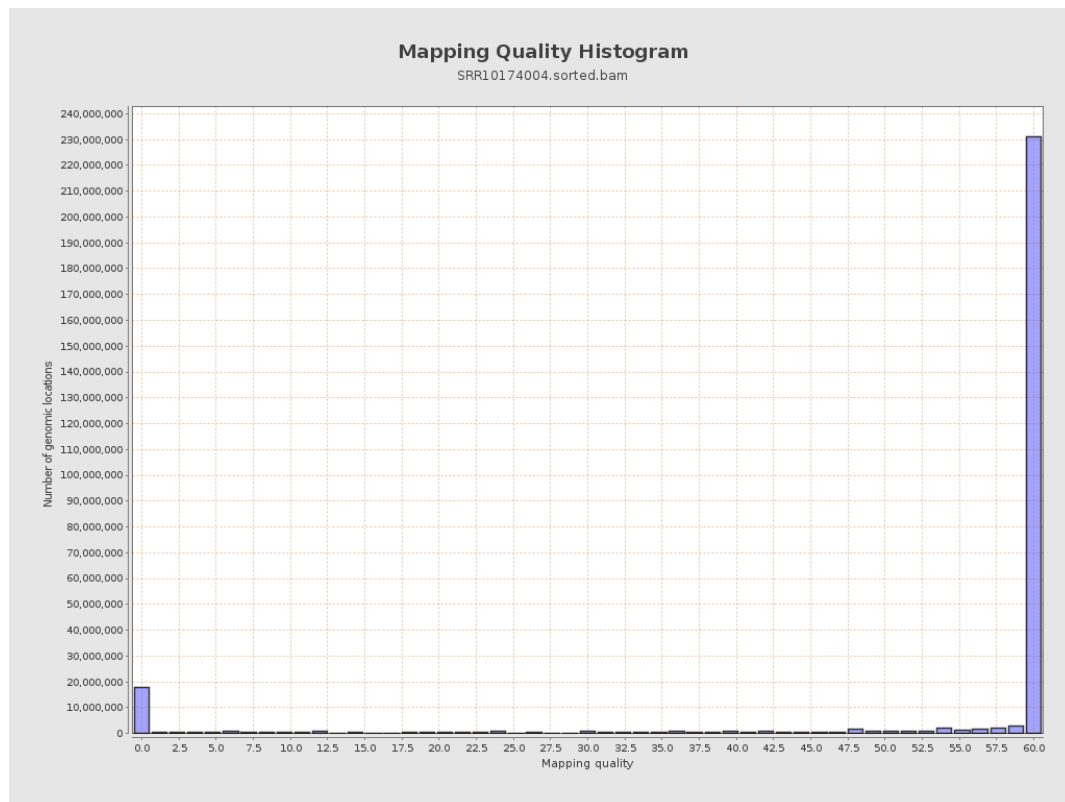
11. Results : Homopolymer Indels



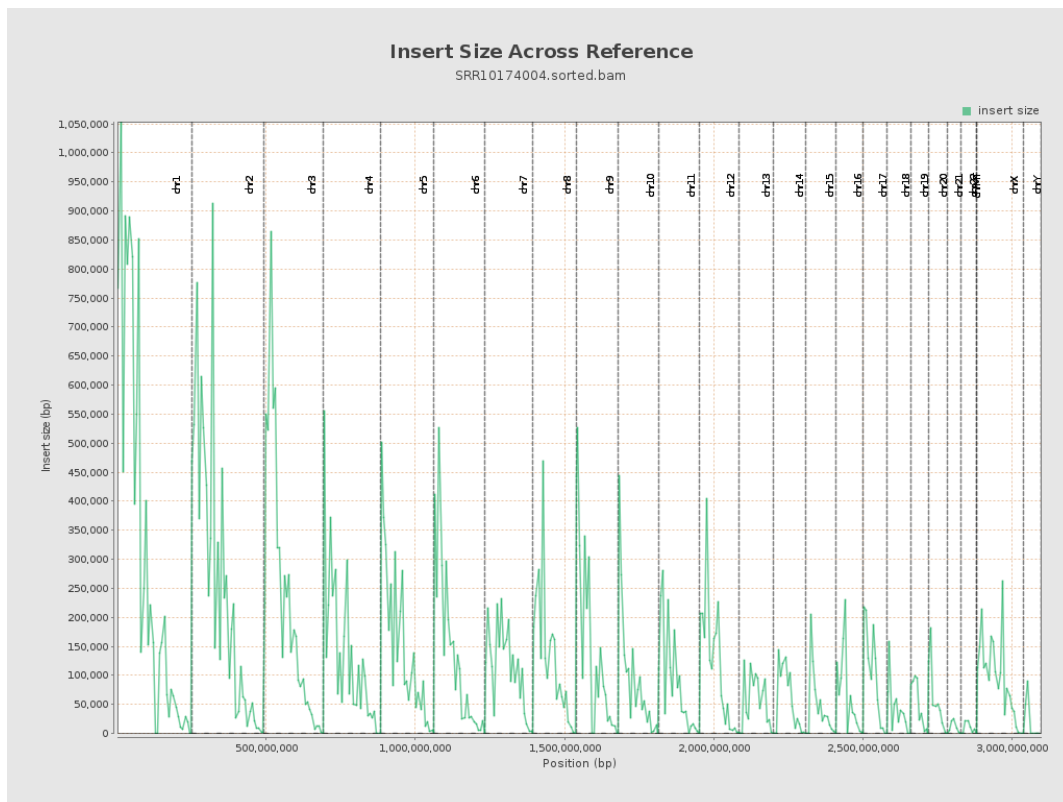
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

