

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 22:29:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174024.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_SRR10174024 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174024_1.fastq.gz SRR10174024_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 22:29:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174024.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,438,072
Mapped reads	5,297,882 / 97.42%
Unmapped reads	140,190 / 2.58%
Mapped paired reads	5,297,882 / 97.42%
Mapped reads, first in pair	2,651,805 / 48.76%
Mapped reads, second in pair	2,646,077 / 48.66%
Mapped reads, both in pair	5,204,848 / 95.71%
Mapped reads, singletons	93,034 / 1.71%
Secondary alignments	0
Supplementary alignments	529,639 / 9.74%
Read min/max/mean length	30 / 133 / 127.99
Duplicated reads (estimated)	4,118,041 / 75.73%
Duplication rate	65.7%
Clipped reads	2,306,154 / 42.41%

2.2. ACGT Content

Number/percentage of A's	187,686,448 / 30.03%
Number/percentage of C's	122,313,660 / 19.57%
Number/percentage of T's	187,319,361 / 29.97%
Number/percentage of G's	127,606,301 / 20.42%
Number/percentage of N's	7,745 / 0%

GC Percentage	39.99%
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2.3. Coverage

Mean	0.202
Standard Deviation	2.9576

2.4. Mapping Quality

Mean Mapping Quality	52.8
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2.5. Insert size

Mean	760,498.17
Standard Deviation	8,130,163.53
P25/Median/P75	142 / 198 / 283

2.6. Mismatches and indels

General error rate	1.05%
Mismatches	6,392,743
Insertions	64,285
Mapped reads with at least one insertion	1.17%
Deletions	163,917
Mapped reads with at least one deletion	3.02%
Homopolymer indels	42.03%

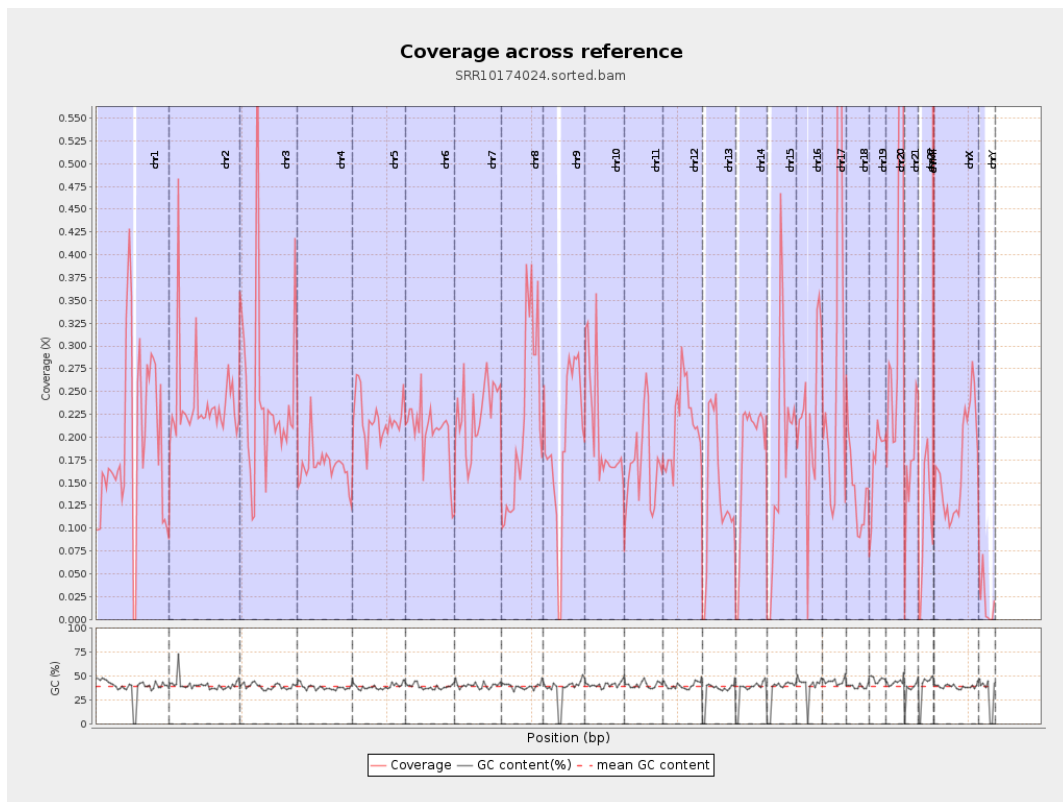
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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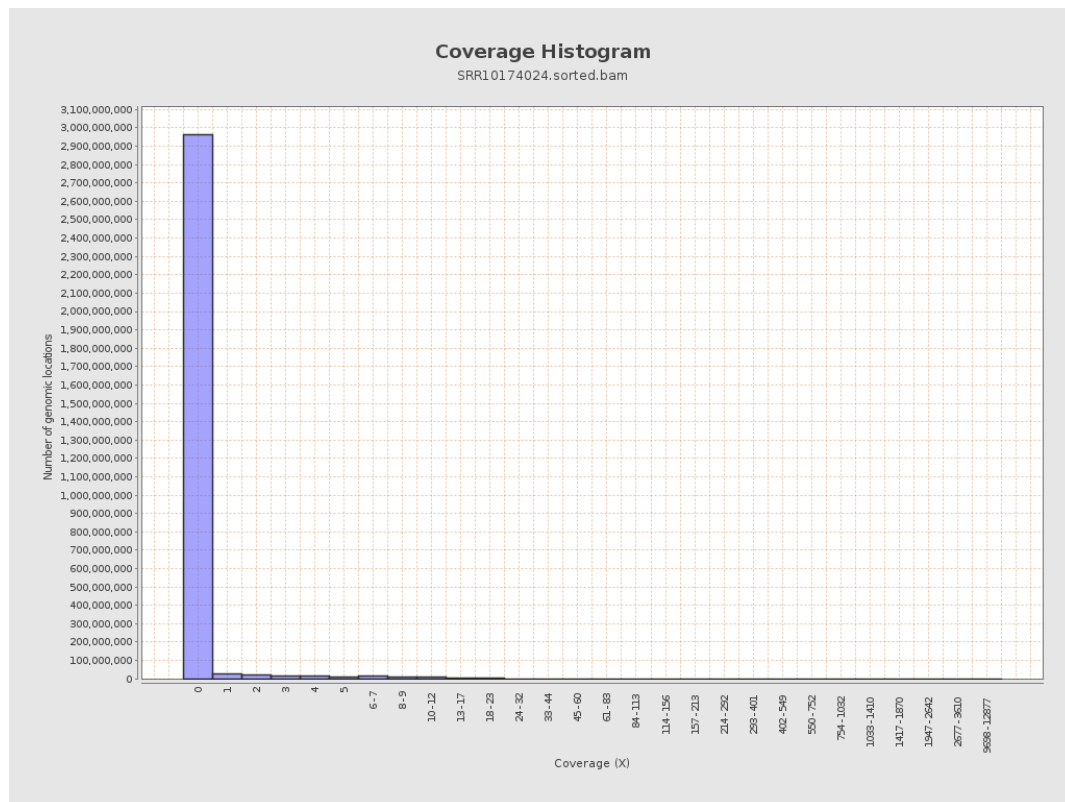
		bases	coverage	deviation
chr1	249250621	47408753	0.1902	1.9761
chr2	243199373	57537926	0.2366	9.0248
chr3	198022430	48002723	0.2424	1.4421
chr4	191154276	32042533	0.1676	1.3808
chr5	180915260	39797705	0.22	1.345
chr6	171115067	35009415	0.2046	1.471
chr7	159138663	36292018	0.2281	1.8927
chr8	146364022	31209422	0.2132	1.8053
chr9	141213431	27507424	0.1948	1.5371
chr10	135534747	27821152	0.2053	2.3586
chr11	135006516	23013191	0.1705	1.2208
chr12	133851895	28684437	0.2143	1.3423
chr13	115169878	15440744	0.1341	1.0567
chr14	107349540	19372410	0.1805	1.2214
chr15	102531392	18395436	0.1794	1.236
chr16	90354753	20315758	0.2248	1.641
chr17	81195210	26303902	0.324	1.8025
chr18	78077248	11083331	0.142	2.3839
chr19	59128983	10404340	0.176	1.5971
chr20	63025520	28402193	0.4506	2.1339
chr21	48129895	8224738	0.1709	1.232
chr22	51304566	5348304	0.1042	0.8878
chrMT	16571	631247	38.0935	32.8025
chrX	155270560	25979200	0.1673	1.1802

chrY	59373566	1090342	0.0184	0.7352
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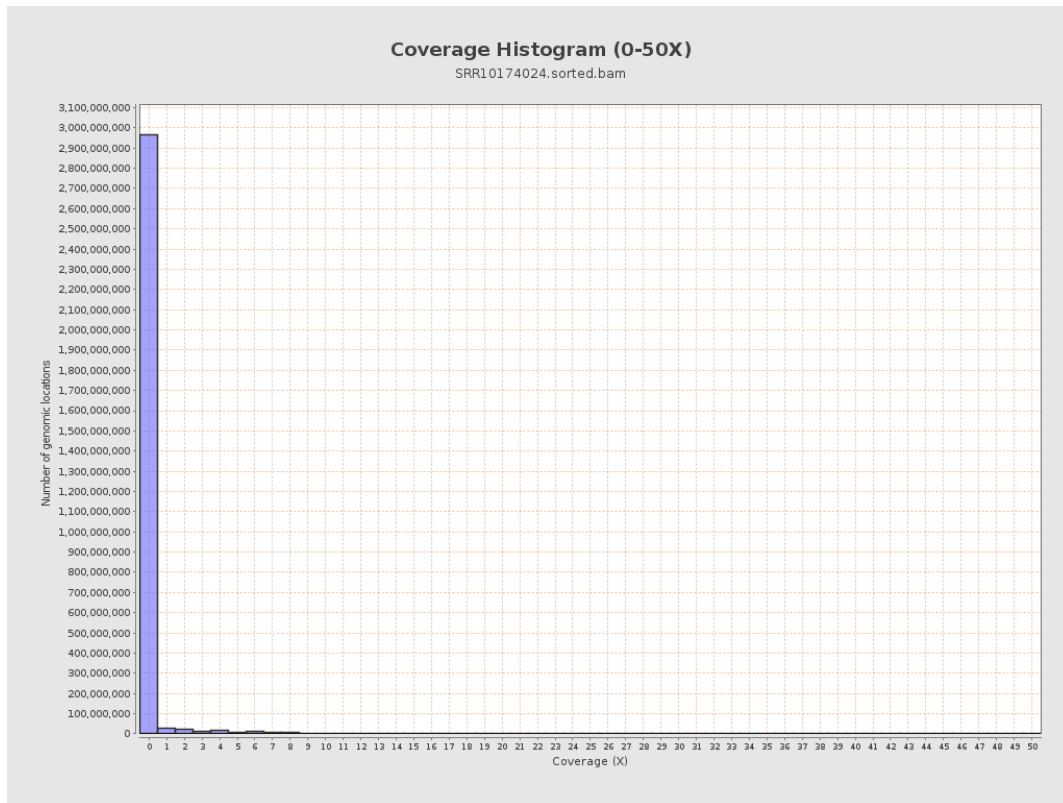
3. Results : Coverage across reference



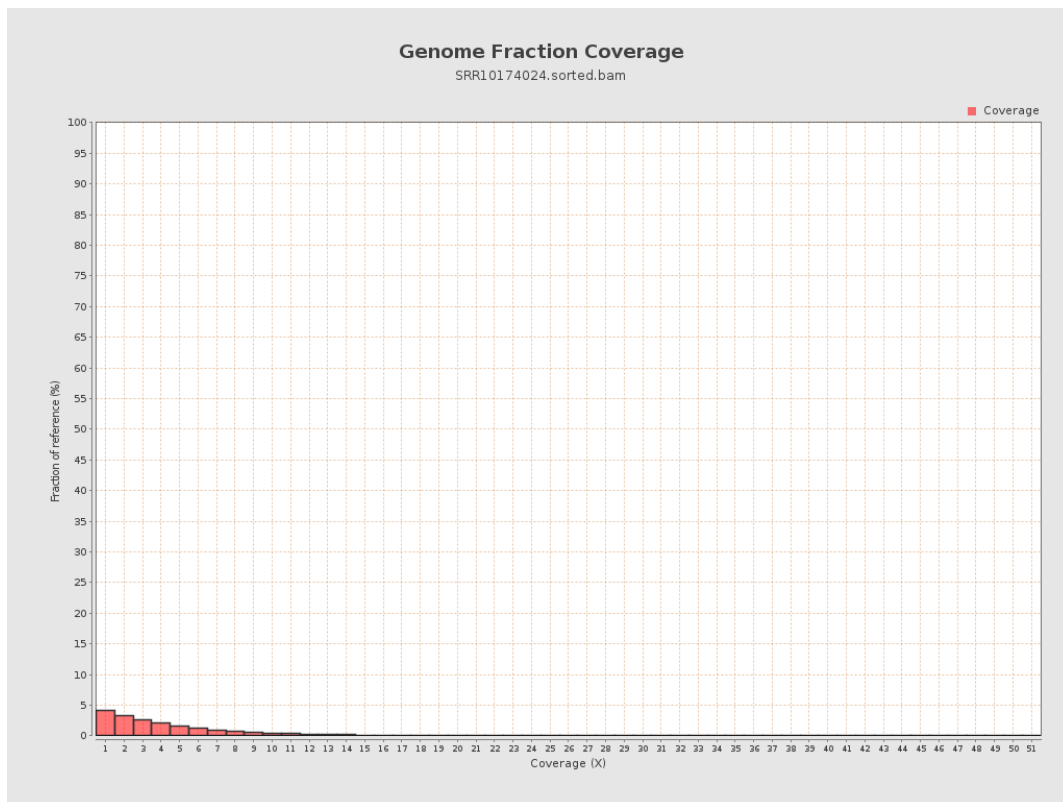
4. Results : Coverage Histogram



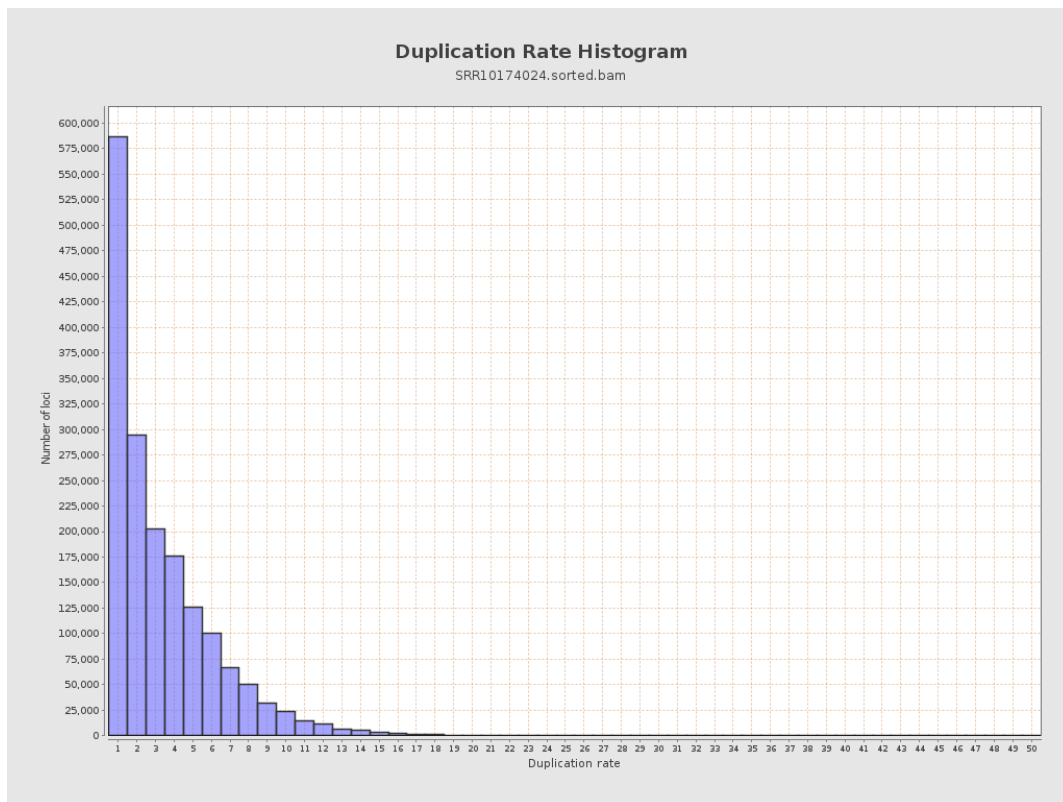
5. Results : Coverage Histogram (0-50X)



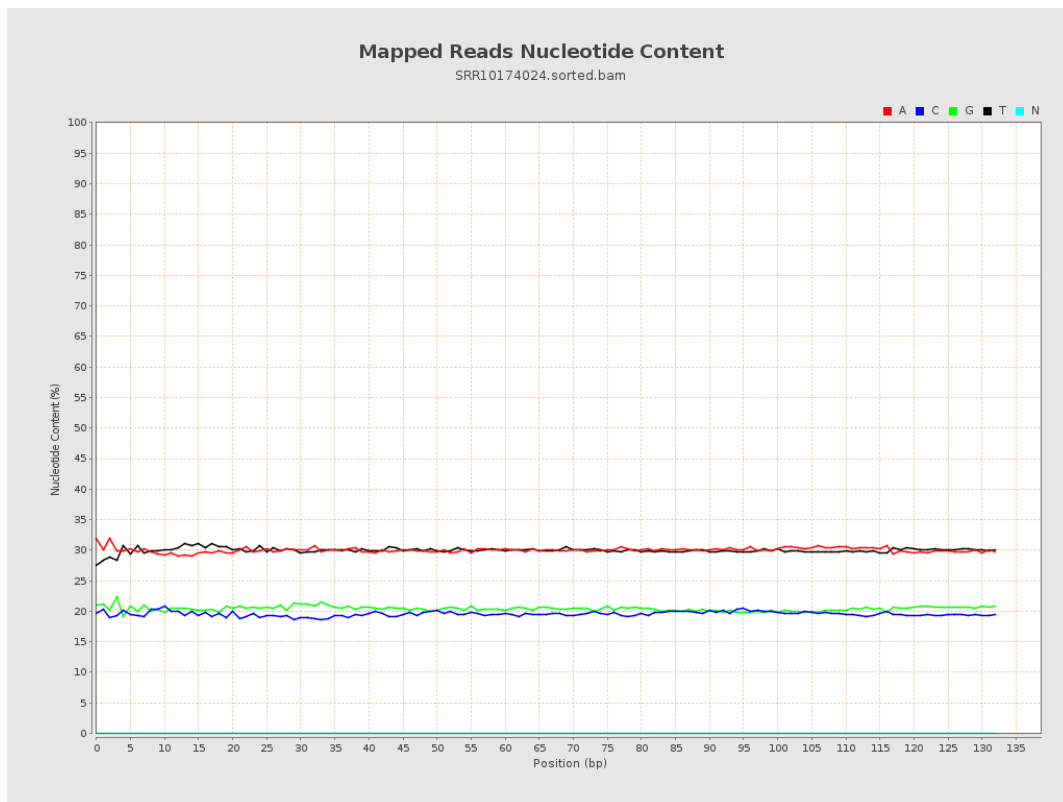
6. Results : Genome Fraction Coverage



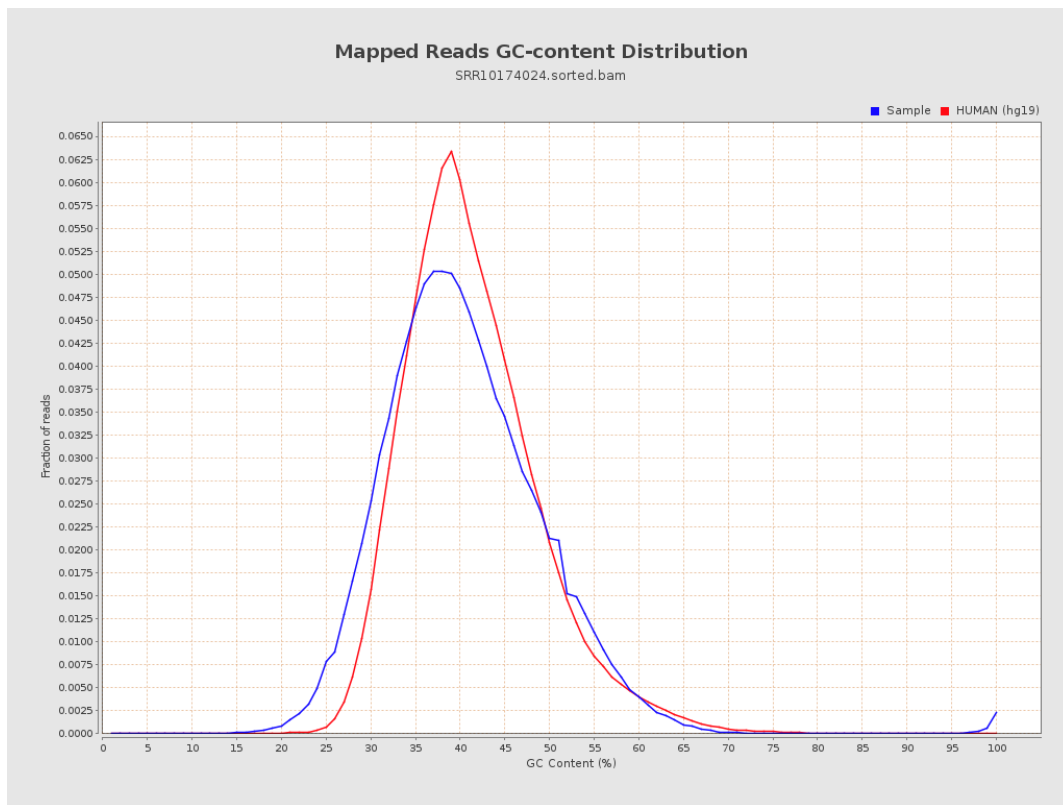
7. Results : Duplication Rate Histogram



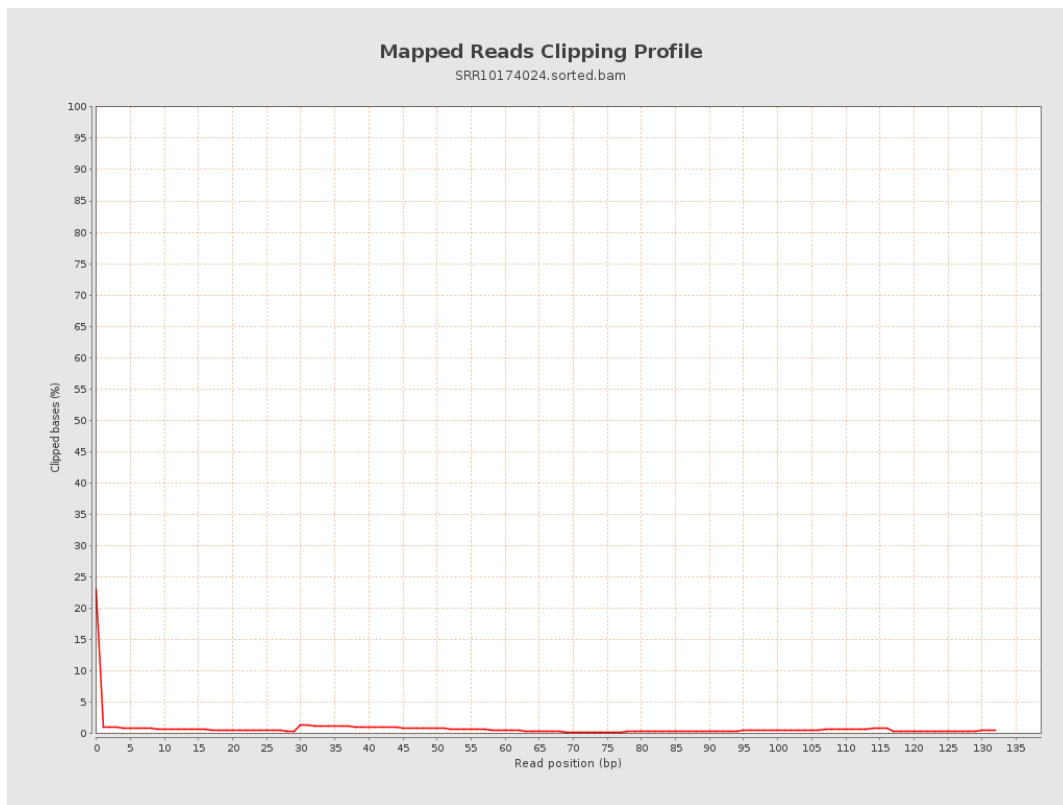
8. Results : Mapped Reads Nucleotide Content



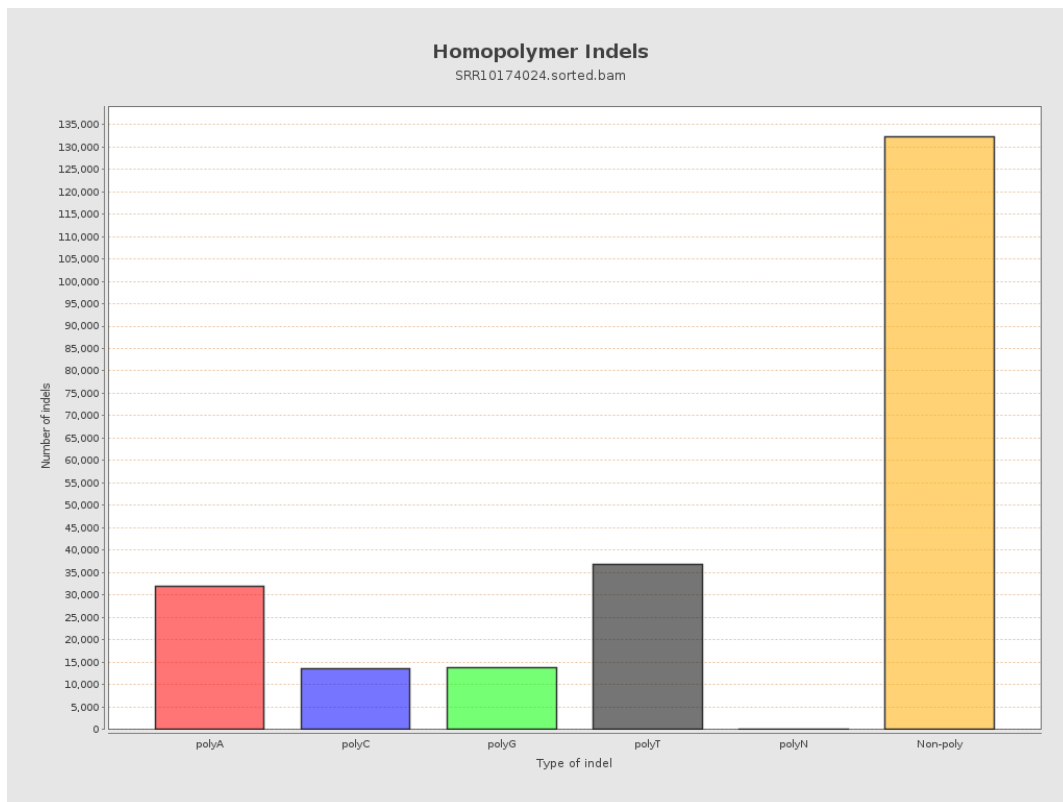
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



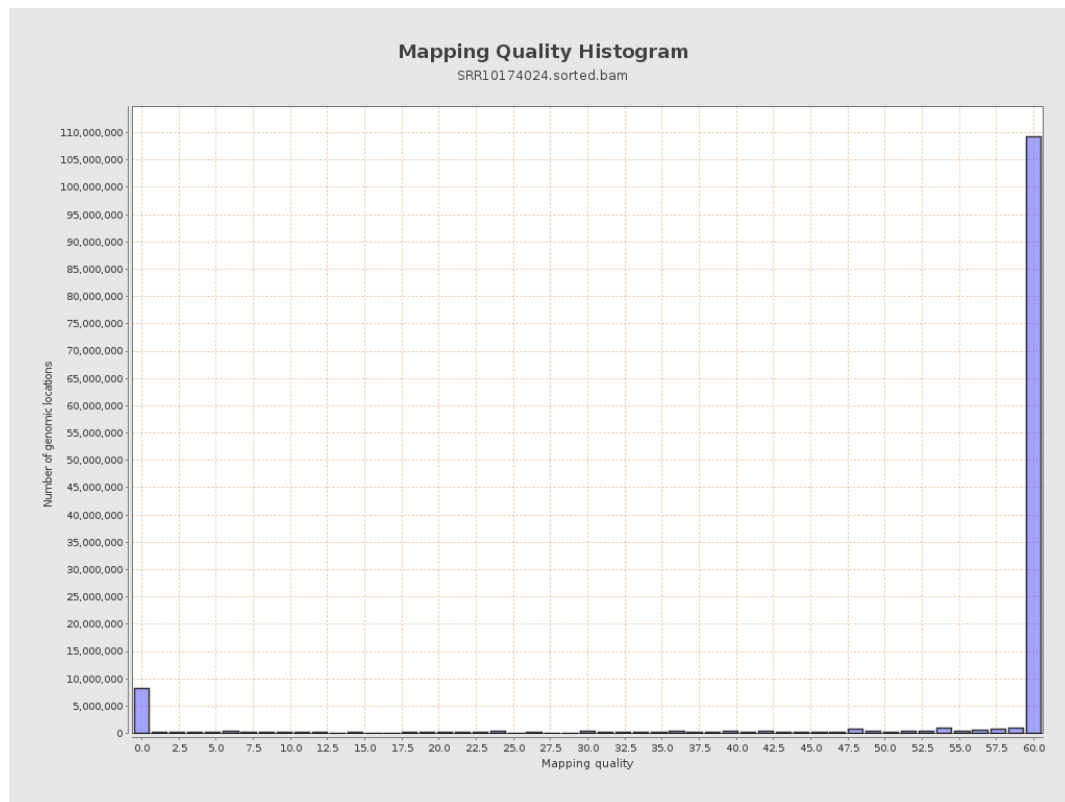
11. Results : Homopolymer Indels



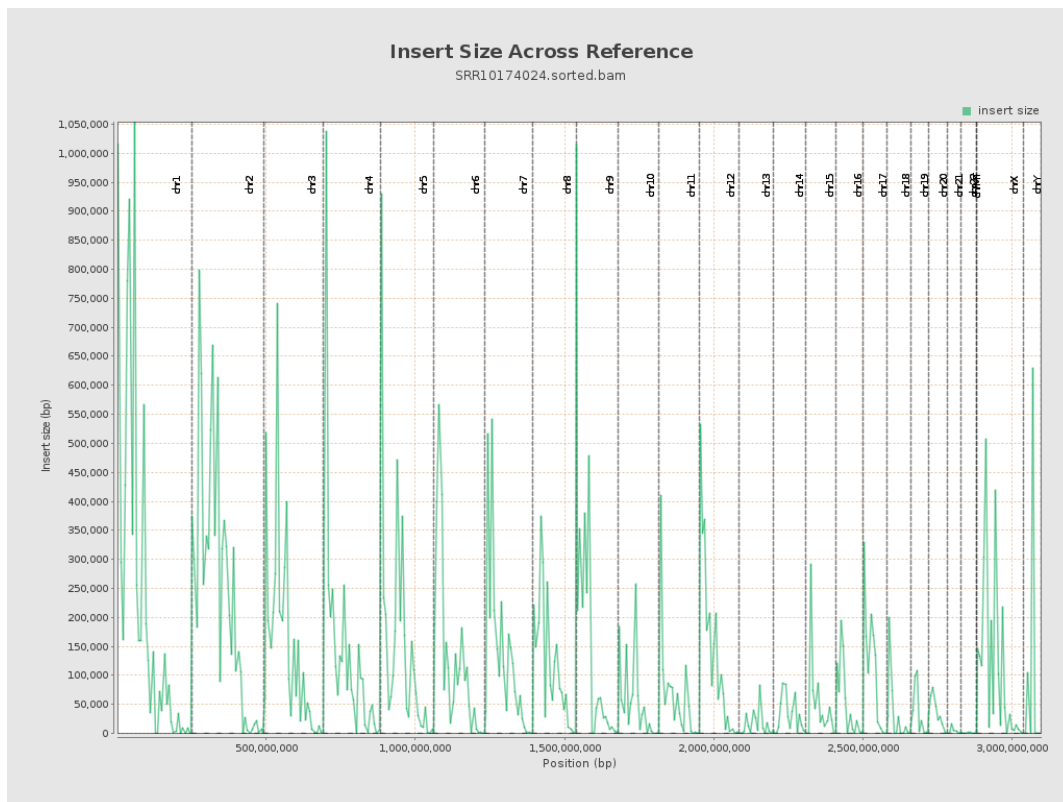
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

