

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 02:06:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472374.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_SRR3472374 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472374_1.fastq.gz SRR3472374_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 02:06:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472374.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,446,924
Mapped reads	19,281,553 / 99.15%
Unmapped reads	165,371 / 0.85%
Mapped paired reads	19,281,553 / 99.15%
Mapped reads, first in pair	9,673,870 / 49.74%
Mapped reads, second in pair	9,607,683 / 49.4%
Mapped reads, both in pair	19,174,734 / 98.6%
Mapped reads, singletons	106,819 / 0.55%
Secondary alignments	0
Supplementary alignments	73,404 / 0.38%
Read min/max/mean length	30 / 100 / 99.43
Duplicated reads (estimated)	11,982,397 / 61.62%
Duplication rate	48.01%
Clipped reads	1,274,126 / 6.55%

2.2. ACGT Content

Number/percentage of A's	521,713,508 / 27.56%
Number/percentage of C's	425,812,392 / 22.49%
Number/percentage of T's	522,561,000 / 27.6%
Number/percentage of G's	422,789,108 / 22.33%
Number/percentage of N's	236,144 / 0.01%

GC Percentage	44.83%
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2.3. Coverage

Mean	0.6116
Standard Deviation	17.1386

2.4. Mapping Quality

Mean Mapping Quality	54.86
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2.5. Insert size

Mean	20,282.03
Standard Deviation	1,402,785.59
P25/Median/P75	162 / 227 / 305

2.6. Mismatches and indels

General error rate	0.57%
Mismatches	10,646,120
Insertions	114,843
Mapped reads with at least one insertion	0.59%
Deletions	100,753
Mapped reads with at least one deletion	0.51%
Homopolymer indels	45.88%

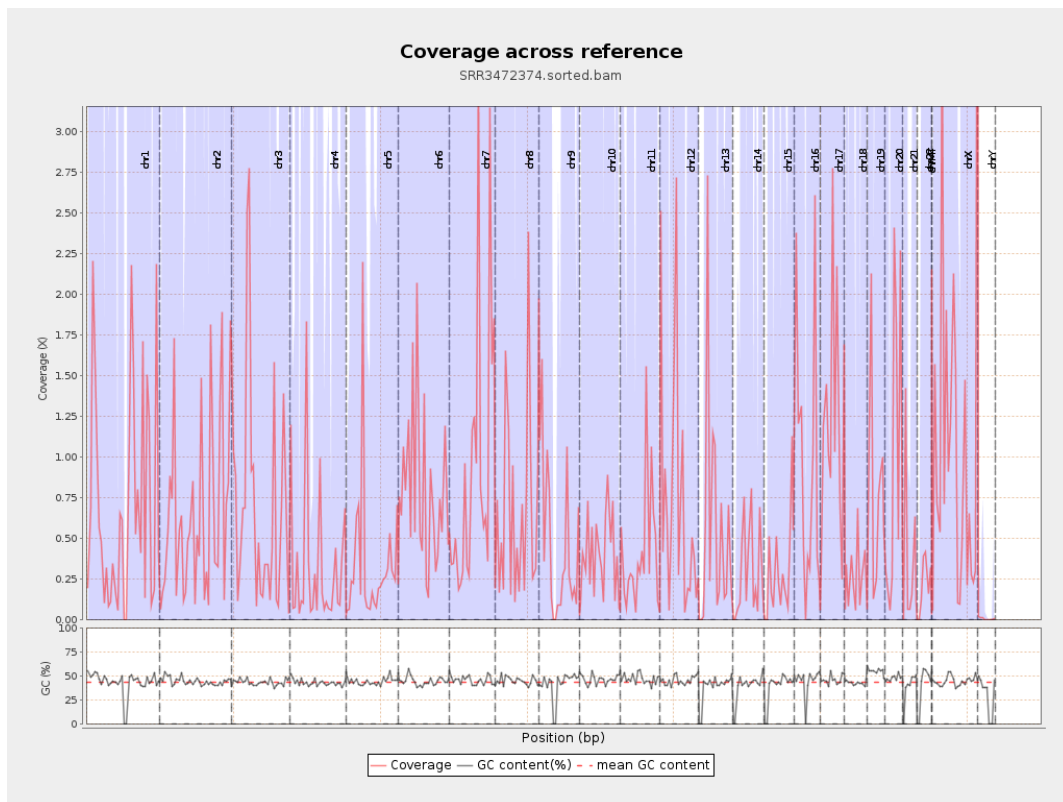
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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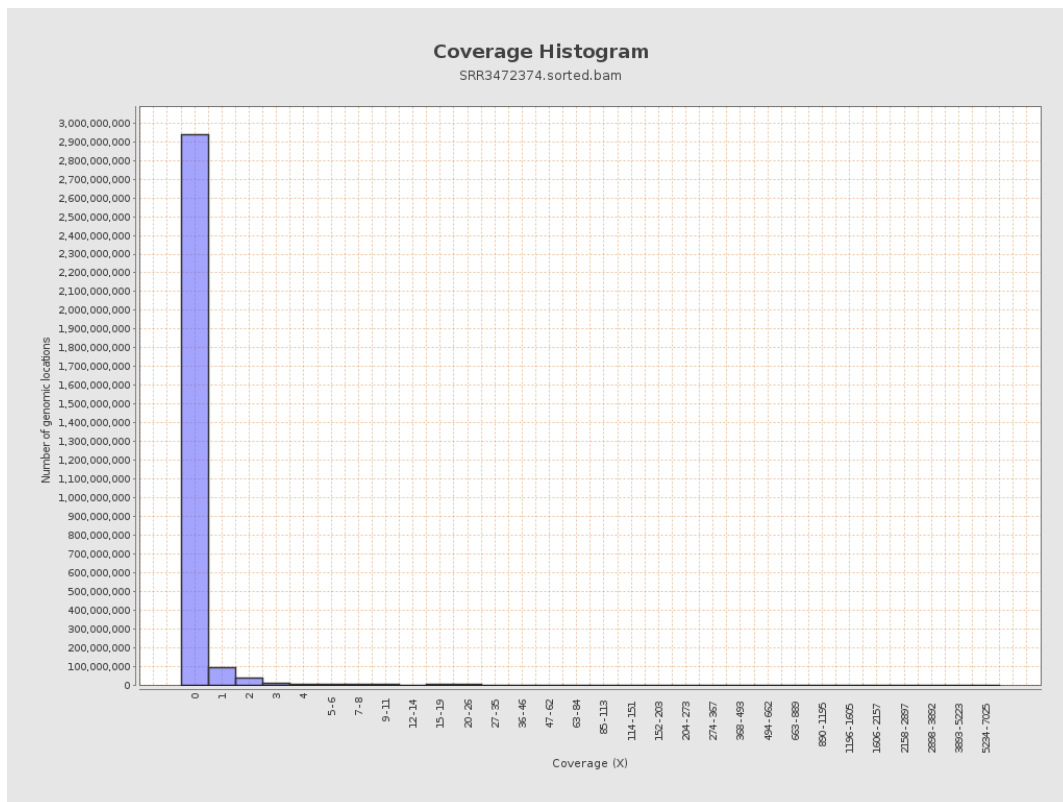
		bases	coverage	deviation
chr1	249250621	180211226	0.723	20.4534
chr2	243199373	158471370	0.6516	19.9044
chr3	198022430	143471162	0.7245	16.8107
chr4	191154276	59556496	0.3116	12.1373
chr5	180915260	61576368	0.3404	9.7717
chr6	171115067	133879198	0.7824	15.3514
chr7	159138663	150530713	0.9459	26.2585
chr8	146364022	98455290	0.6727	17.2217
chr9	141213431	65700091	0.4653	12.2845
chr10	135534747	55377532	0.4086	11.9525
chr11	135006516	55481144	0.411	12.5201
chr12	133851895	100499022	0.7508	17.5891
chr13	115169878	63161898	0.5484	17.0464
chr14	107349540	30373530	0.2829	7.5916
chr15	102531392	30680890	0.2992	8.7846
chr16	90354753	84997839	0.9407	22.7228
chr17	81195210	98190249	1.2093	26.9048
chr18	78077248	20948627	0.2683	8.391
chr19	59128983	50057739	0.8466	15.9639
chr20	63025520	61419808	0.9745	22.3741
chr21	48129895	18587098	0.3862	23.2336
chr22	51304566	10944064	0.2133	5.5766
chrMT	16571	35669	2.1525	2.1172
chrX	155270560	160421064	1.0332	22.3644

chrY	59373566	325994	0.0055	0.3487
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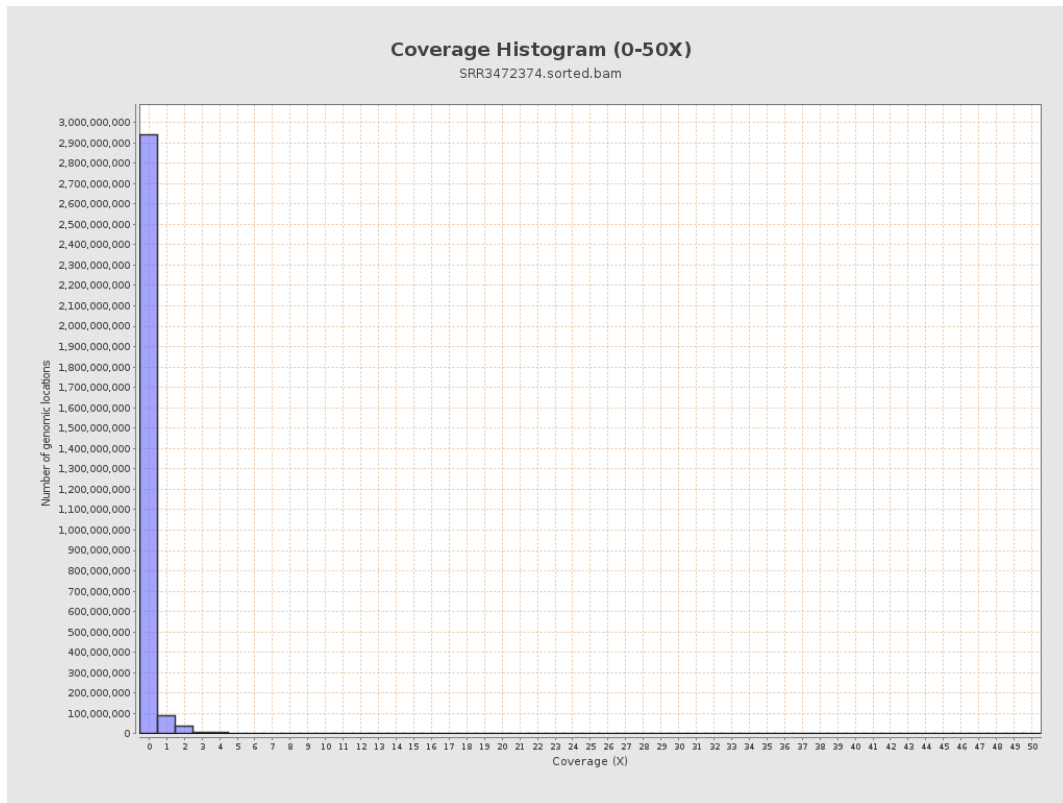
3. Results : Coverage across reference



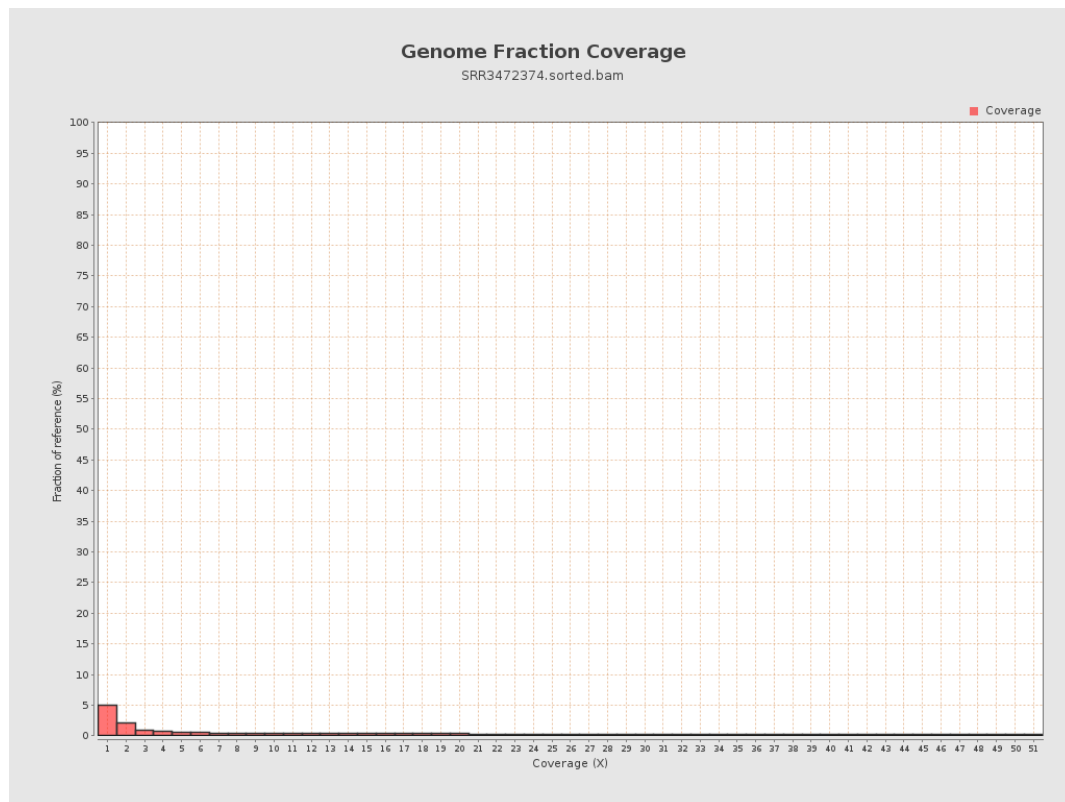
4. Results : Coverage Histogram



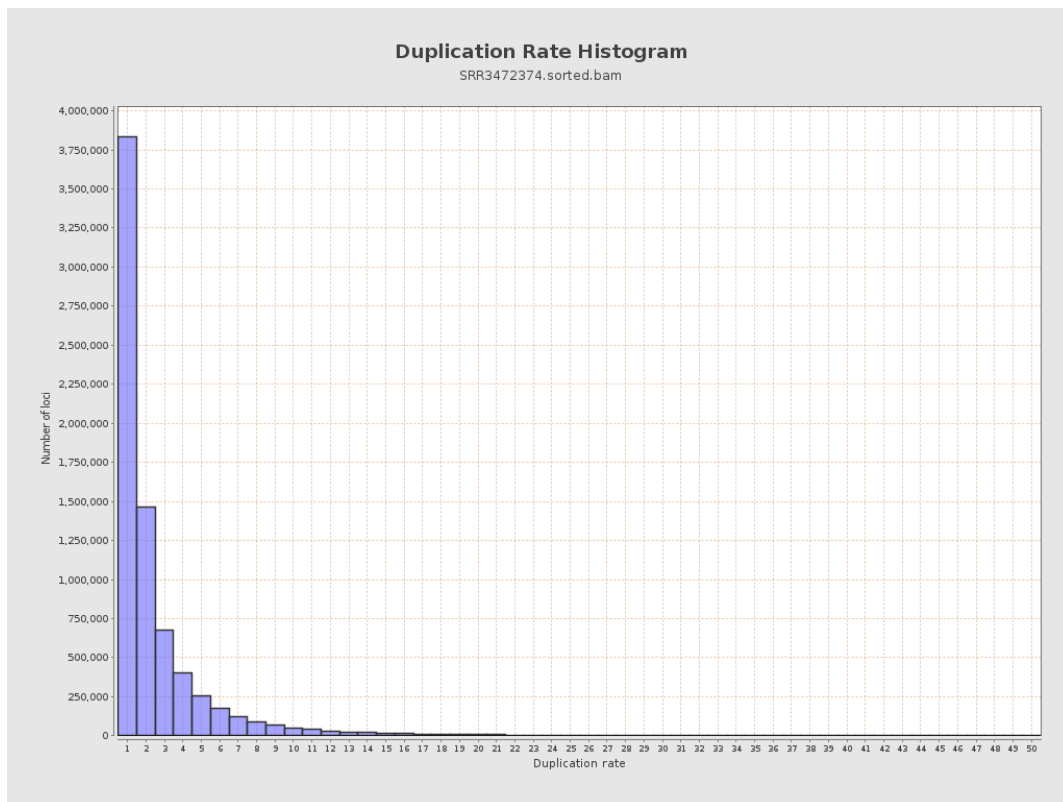
5. Results : Coverage Histogram (0-50X)



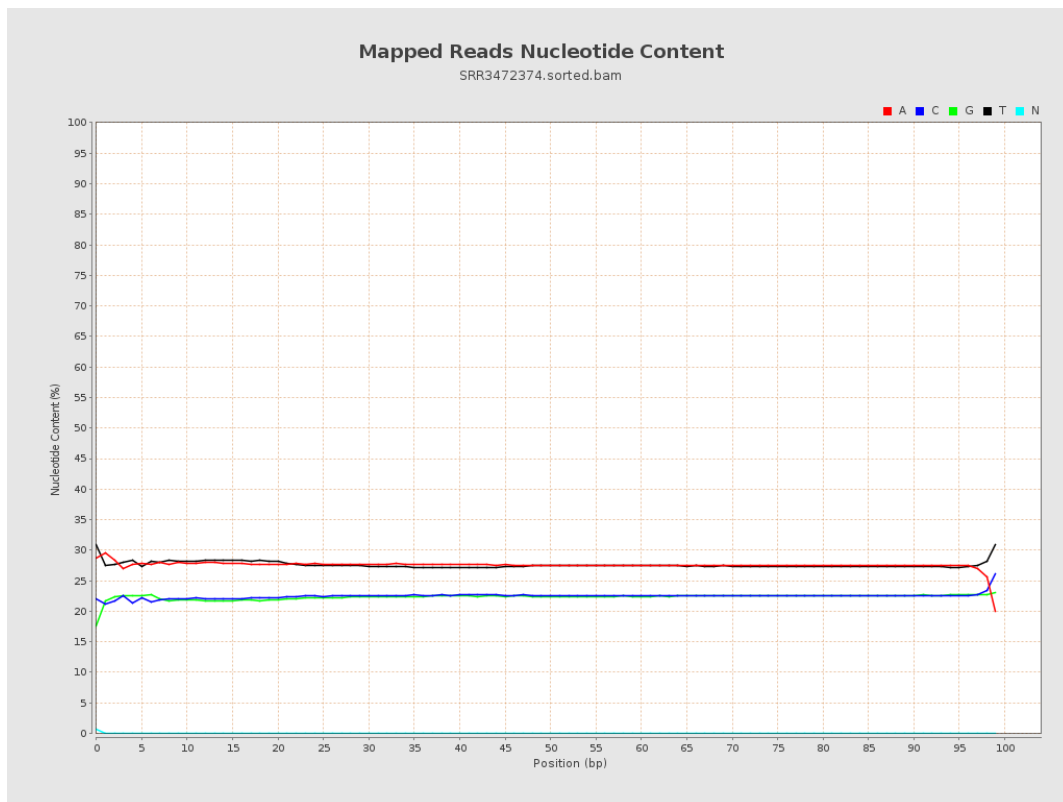
6. Results : Genome Fraction Coverage



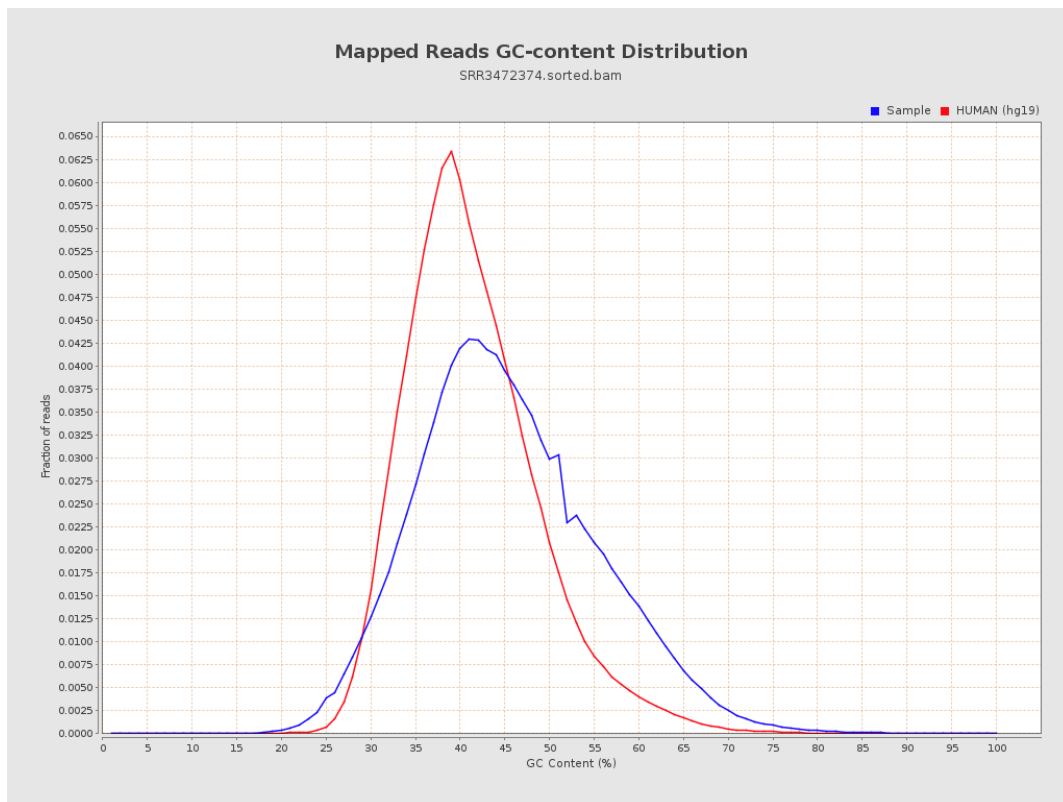
7. Results : Duplication Rate Histogram



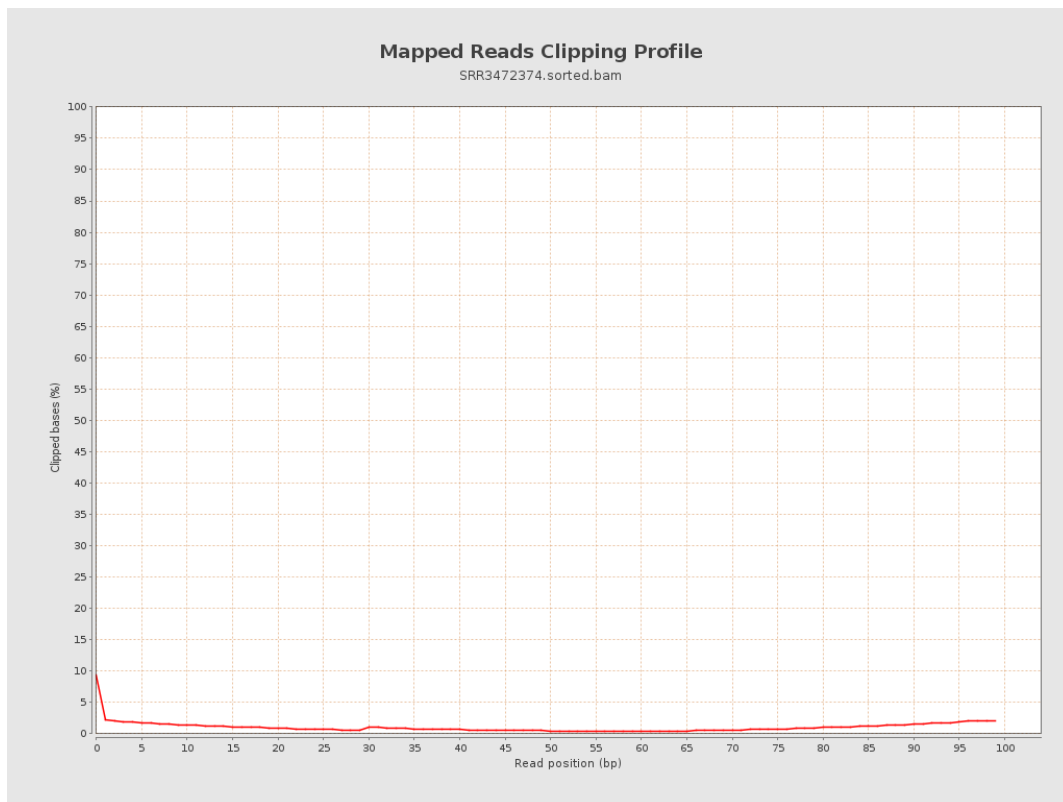
8. Results : Mapped Reads Nucleotide Content



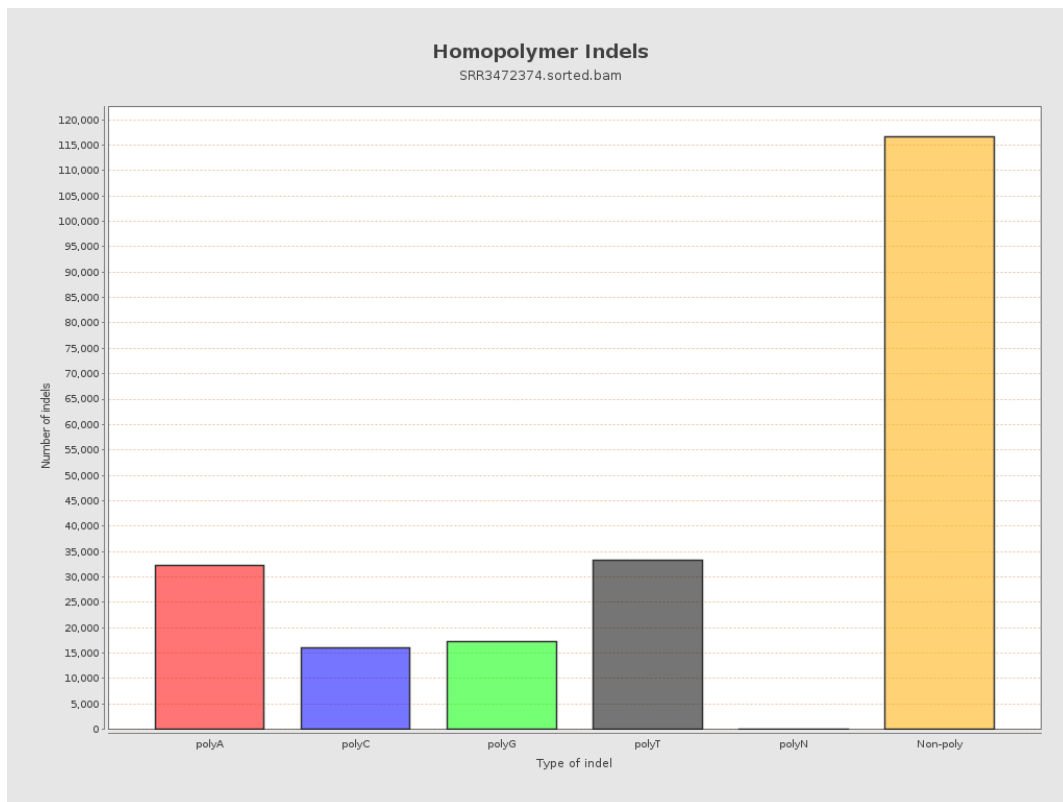
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



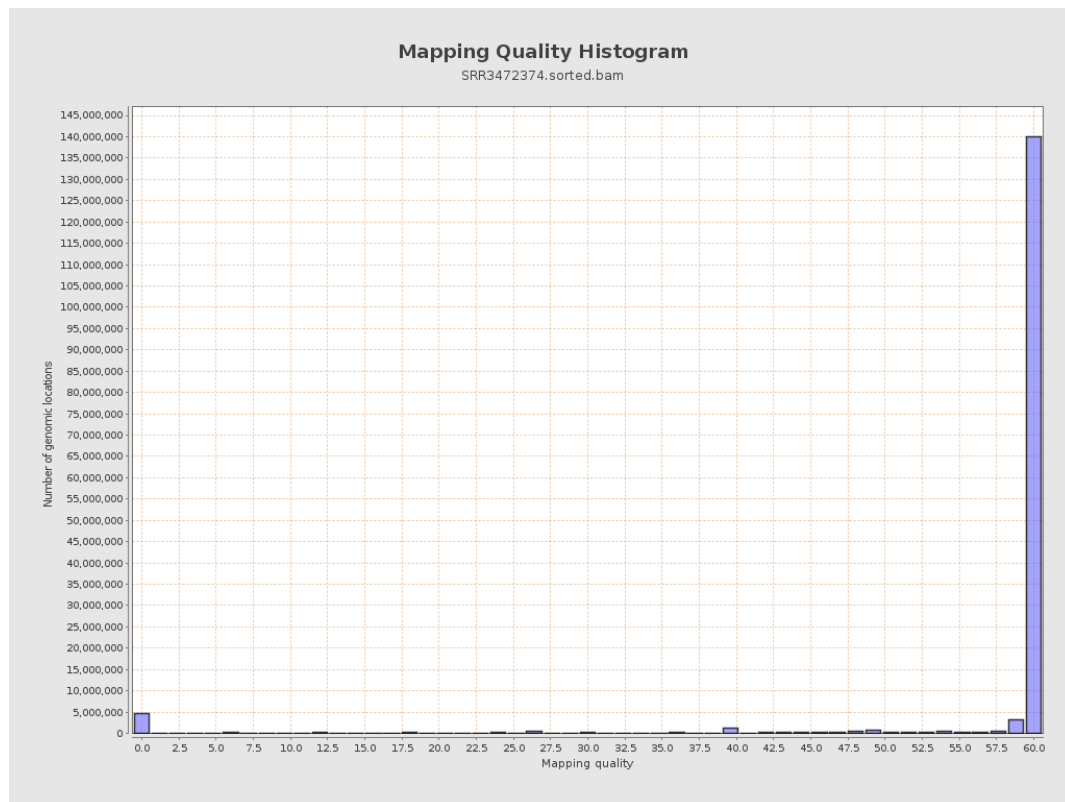
11. Results : Homopolymer Indels



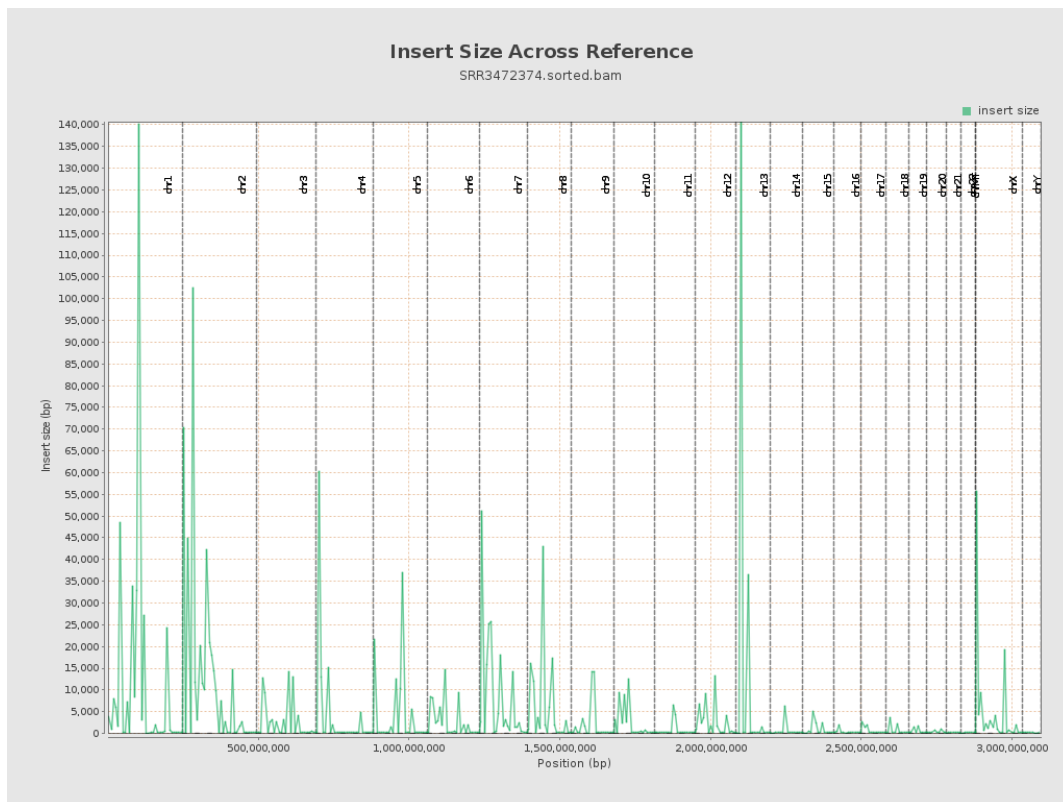
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

