

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 15:21:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR21671998.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_SRR21671998 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR21671998_1.fastq.gz SRR21671998_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 15:21:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR21671998.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	493,634,322
Mapped reads	327,436,445 / 66.33%
Unmapped reads	166,197,877 / 33.67%
Mapped paired reads	327,436,445 / 66.33%
Mapped reads, first in pair	163,744,447 / 33.17%
Mapped reads, second in pair	163,691,998 / 33.16%
Mapped reads, both in pair	326,082,662 / 66.06%
Mapped reads, singletons	1,353,783 / 0.27%
Secondary alignments	0
Supplementary alignments	5,794,044 / 1.17%
Read min/max/mean length	15 / 150 / 139.15
Duplicated reads (estimated)	134,462,966 / 27.24%
Duplication rate	40.77%
Clipped reads	28,556,108 / 5.78%

2.2. ACGT Content

Number/percentage of A's	13,423,869,560 / 29.97%
Number/percentage of C's	9,061,646,818 / 20.23%
Number/percentage of T's	13,249,236,368 / 29.58%
Number/percentage of G's	9,051,111,793 / 20.21%
Number/percentage of N's	439,939 / 0%

GC Percentage	40.44%
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2.3. Coverage

Mean	14.4734
Standard Deviation	200.4982

2.4. Mapping Quality

Mean Mapping Quality	54.04
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2.5. Insert size

Mean	66,351.83
Standard Deviation	2,471,911.72
P25/Median/P75	133 / 181 / 241

2.6. Mismatches and indels

General error rate	0.6%
Mismatches	249,742,422
Insertions	6,497,493
Mapped reads with at least one insertion	1.86%
Deletions	6,678,788
Mapped reads with at least one deletion	1.94%
Homopolymer indels	43.75%

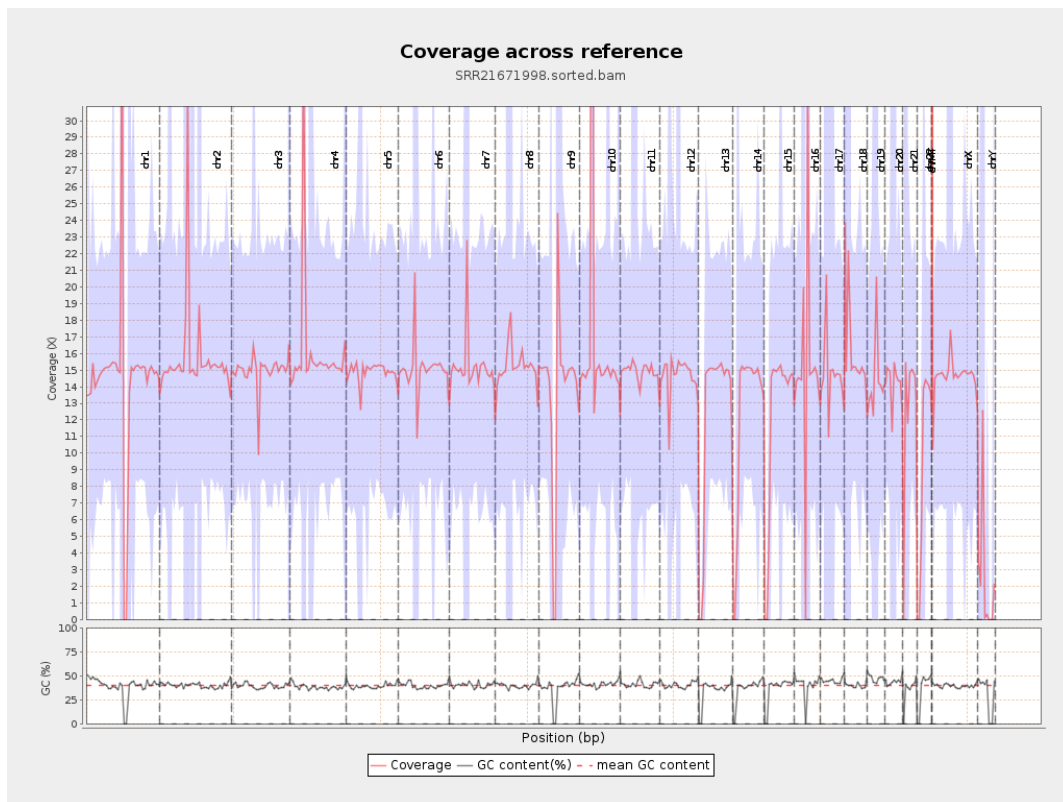
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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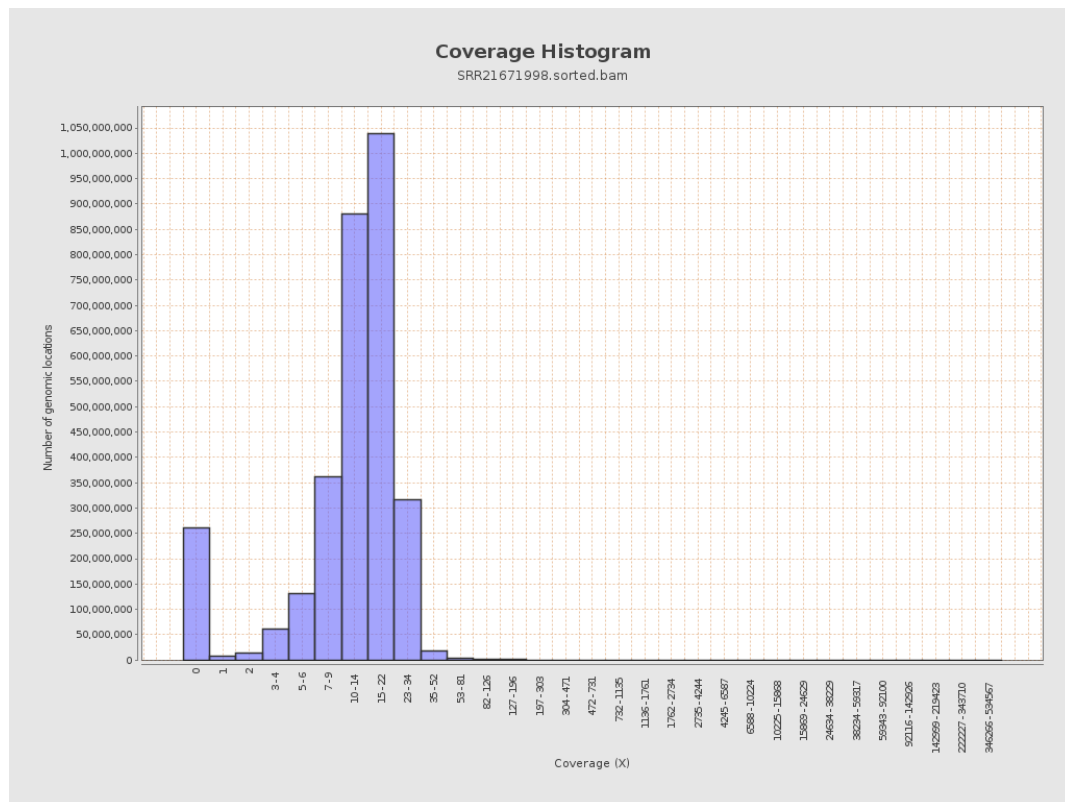
		bases	coverage	deviation
chr1	249250621	3650374795	14.6454	519.9811
chr2	243199373	3826906933	15.7357	109.808
chr3	198022430	2954099358	14.918	19.0888
chr4	191154276	3058570050	16.0005	154.3674
chr5	180915260	2686117817	14.8474	12.9498
chr6	171115067	2585314255	15.1086	67.5859
chr7	159138663	2419178706	15.2017	159.924
chr8	146364022	2234295057	15.2653	160.7324
chr9	141213431	1906945794	13.504	209.122
chr10	135534747	2365338242	17.4519	395.7768
chr11	135006516	2008163752	14.8746	71.7293
chr12	133851895	1961454585	14.6539	33.1585
chr13	115169878	1434334379	12.4541	8.6864
chr14	107349540	1324713946	12.3402	12.9684
chr15	102531392	1229130724	11.9878	11.4948
chr16	90354753	1372797931	15.1934	133.5931
chr17	81195210	1192242640	14.6837	94.5549
chr18	78077248	1251874716	16.0338	212.2222
chr19	59128983	852025395	14.4096	259.4789
chr20	63025520	894299440	14.1895	58.6563
chr21	48129895	620869400	12.8999	88.5714
chr22	51304566	495248096	9.6531	12.3611
chrMT	16571	57335308	3,459.9788	420.5768
chrX	155270560	2272988369	14.6389	38.9249

chrY	59373566	150612471	2.5367	166.9533
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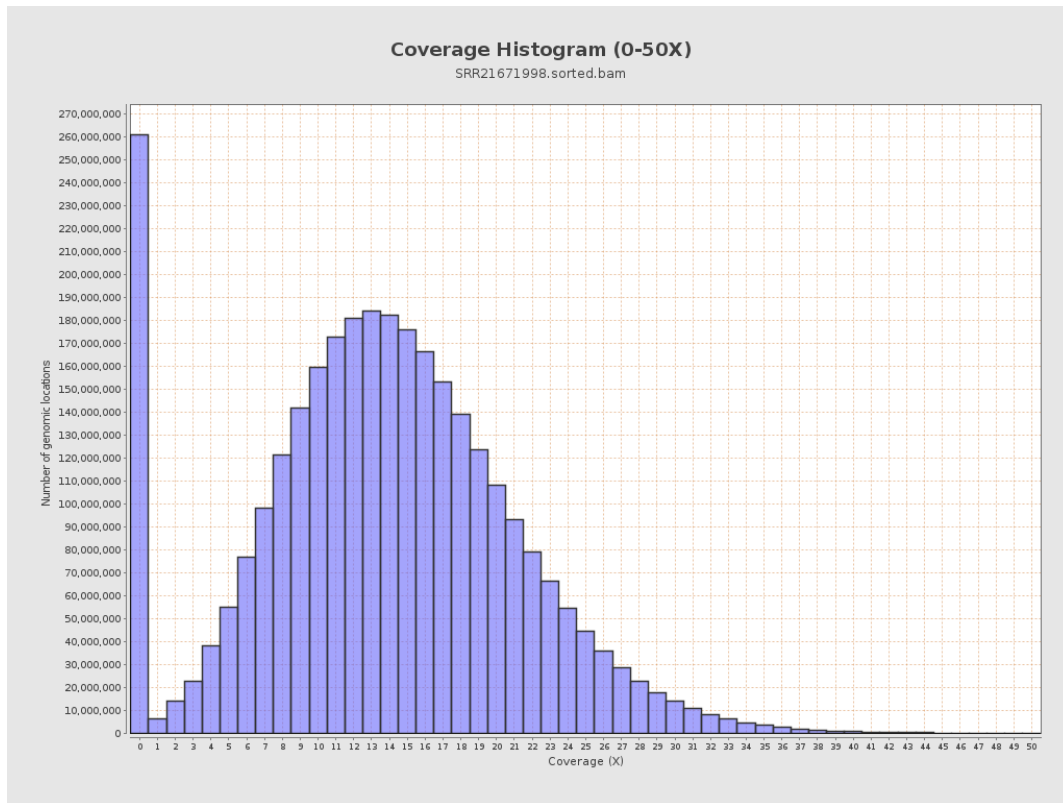
3. Results : Coverage across reference



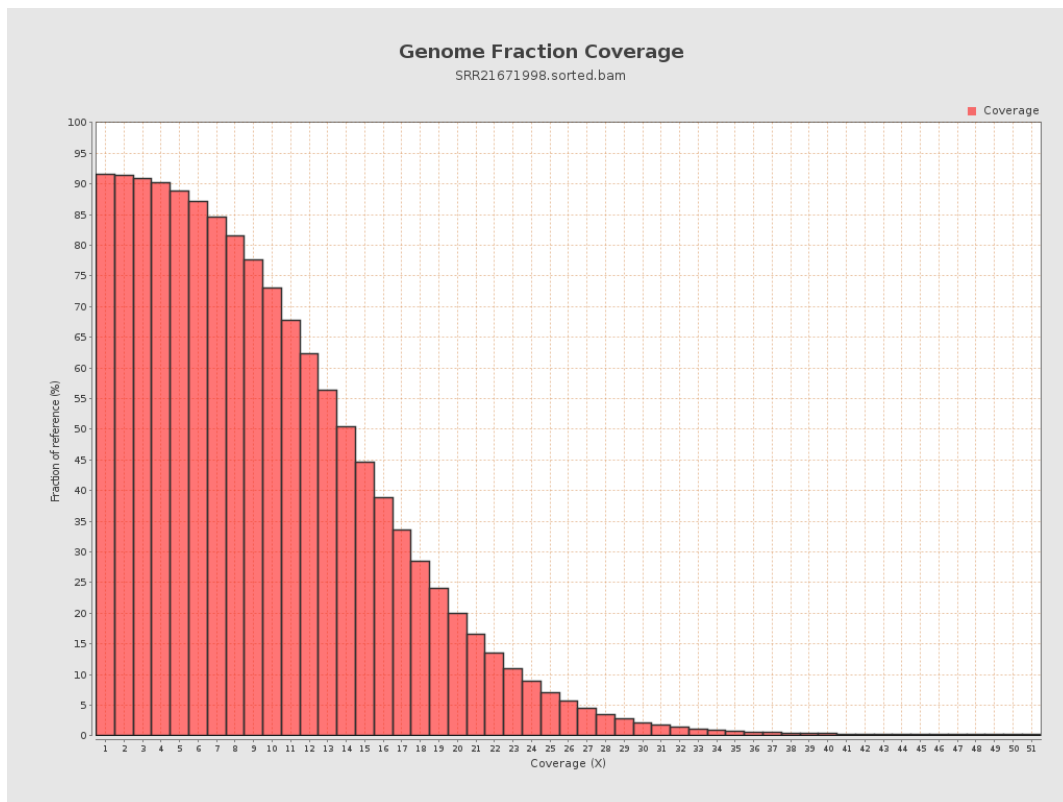
4. Results : Coverage Histogram



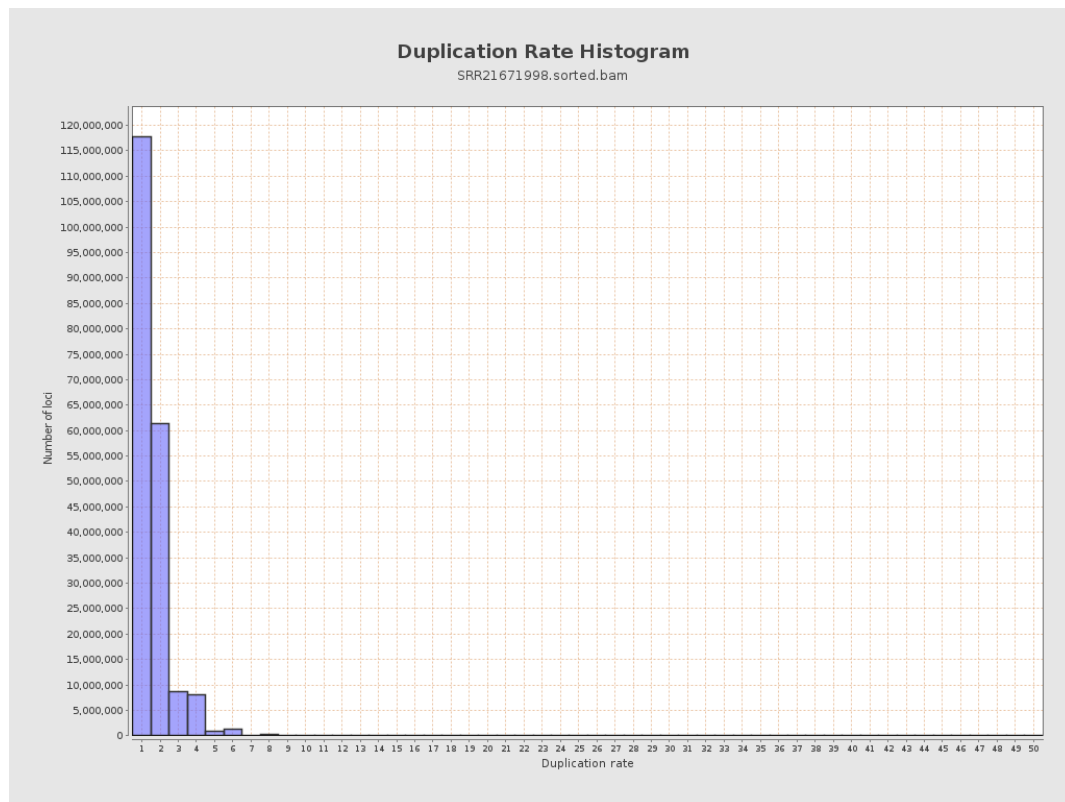
5. Results : Coverage Histogram (0-50X)



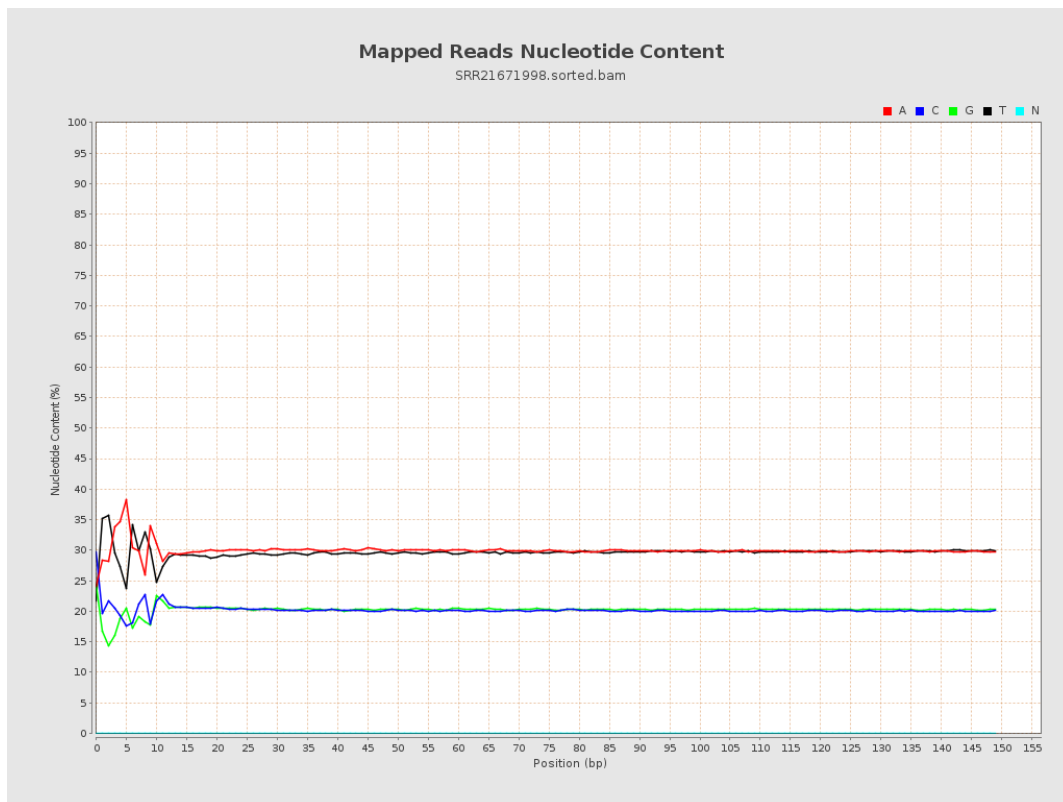
6. Results : Genome Fraction Coverage



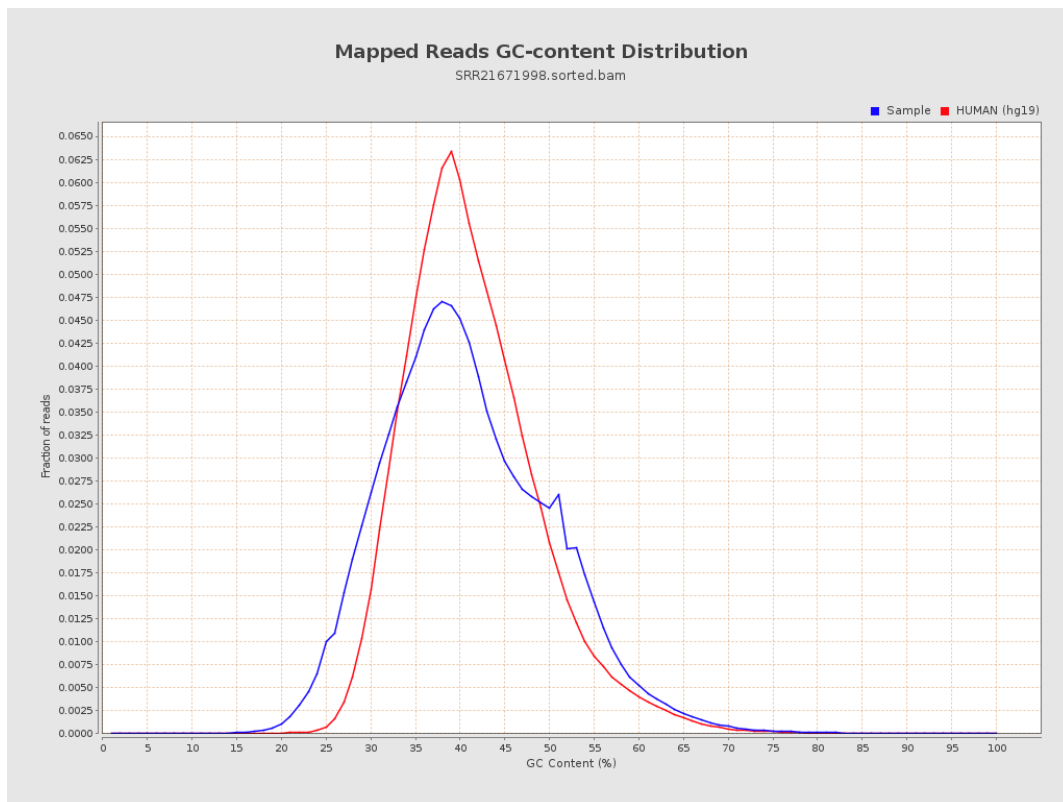
7. Results : Duplication Rate Histogram



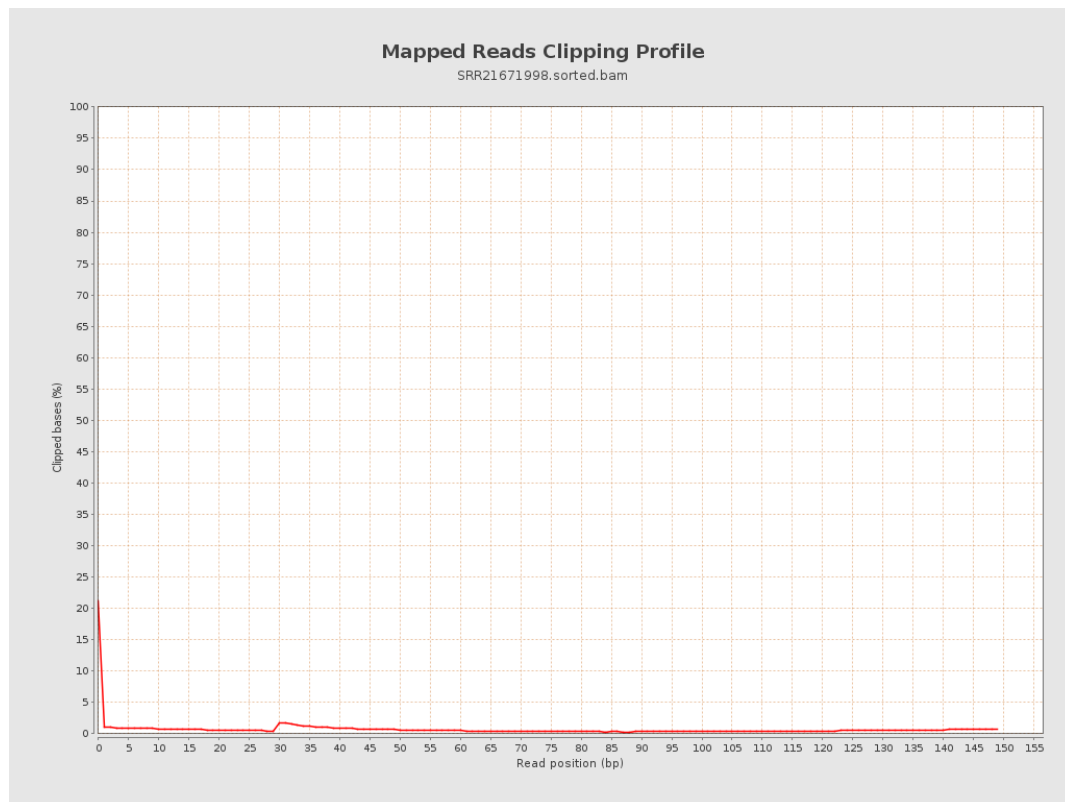
8. Results : Mapped Reads Nucleotide Content



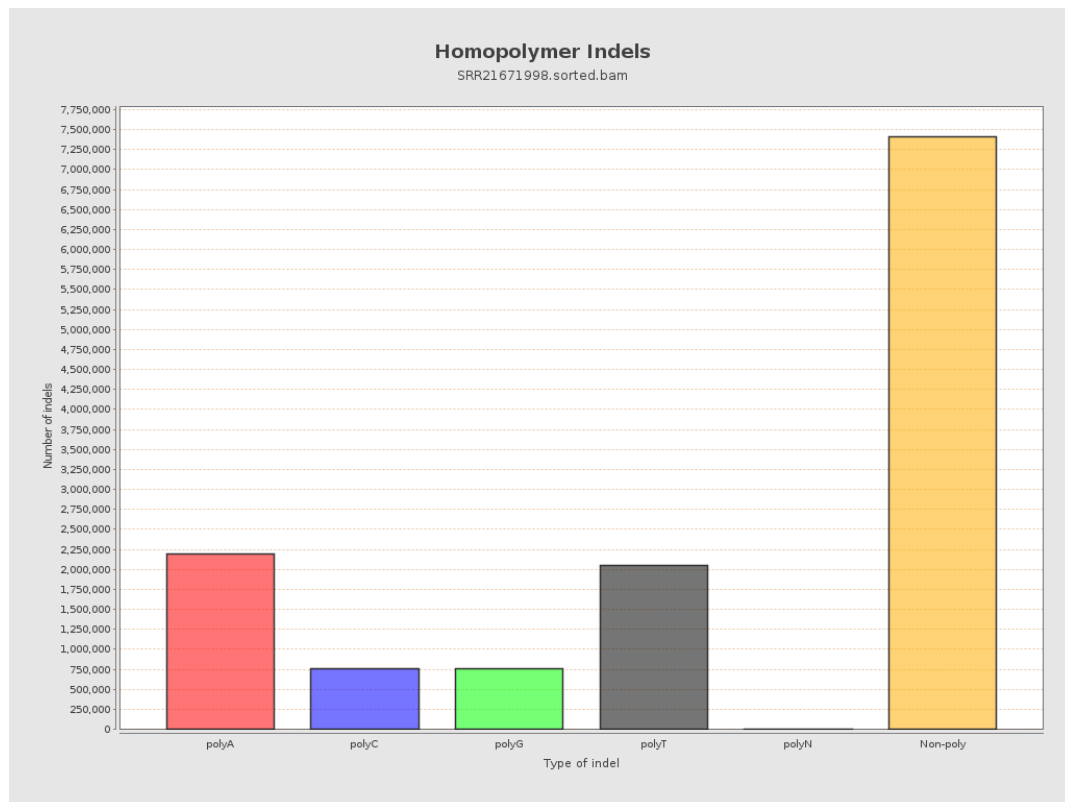
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



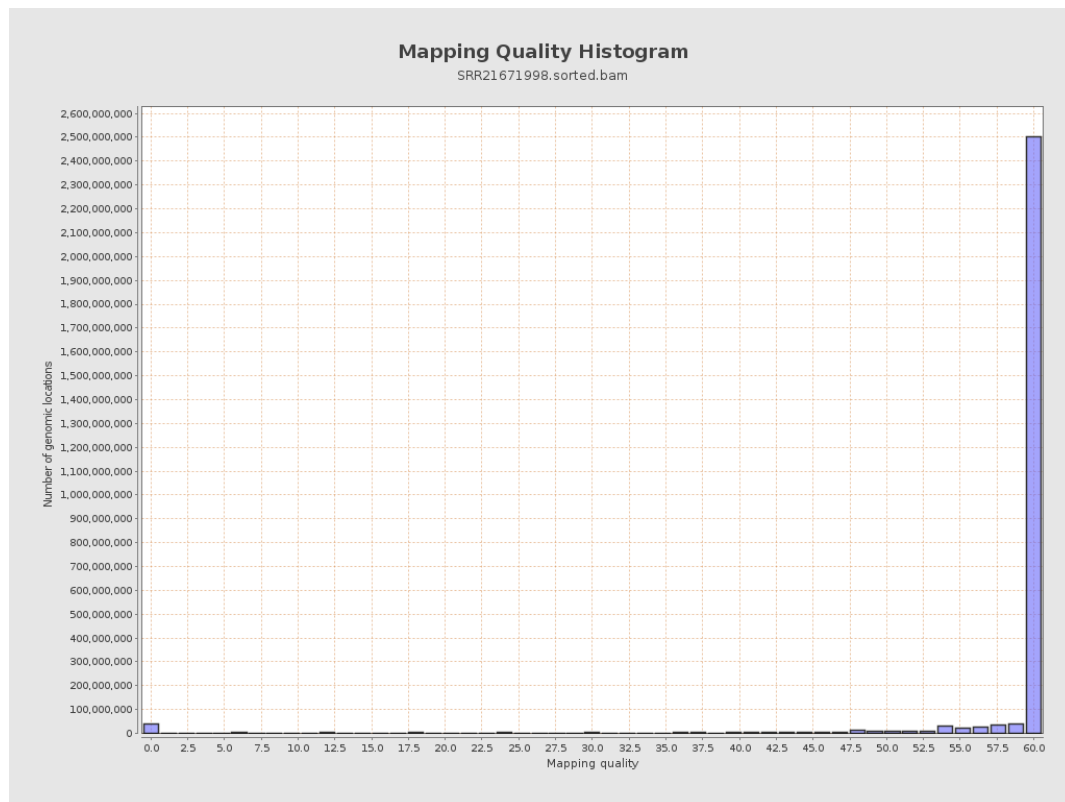
11. Results : Homopolymer Indels



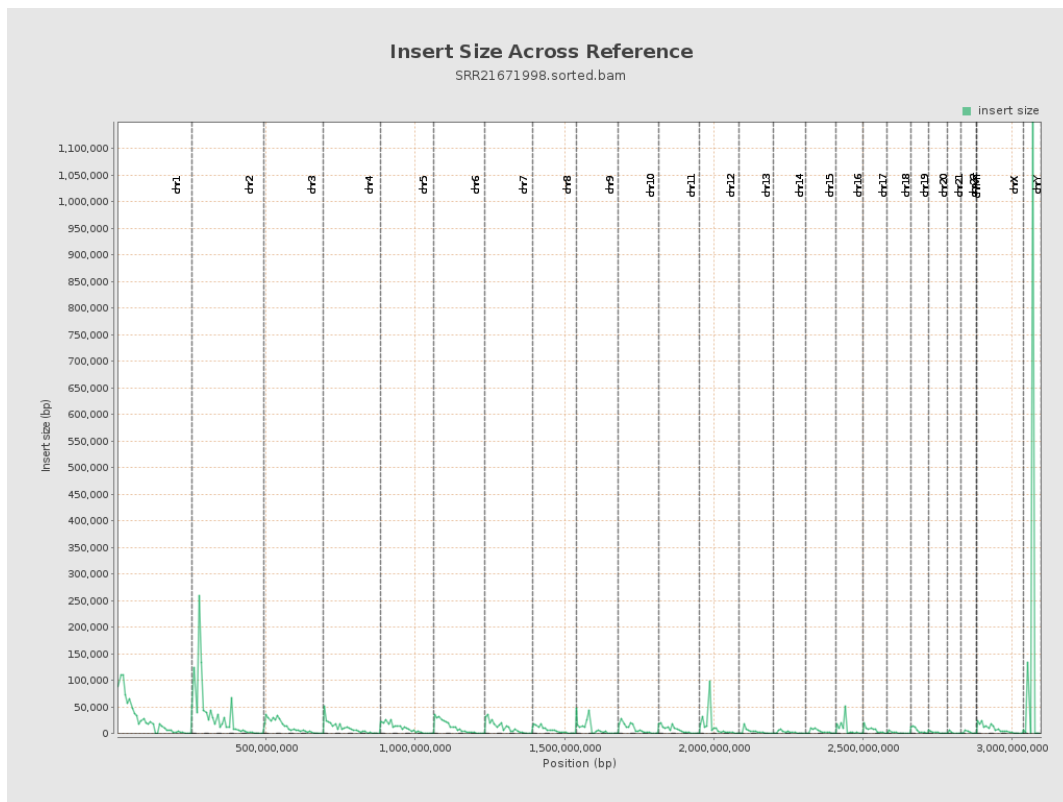
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

