

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 11:06:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR21671994.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_SRR21671994 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR21671994_1.fastq.gz SRR21671994_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 11:06:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR21671994.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	600,251,144
Mapped reads	592,406,711 / 98.69%
Unmapped reads	7,844,433 / 1.31%
Mapped paired reads	592,406,711 / 98.69%
Mapped reads, first in pair	296,704,971 / 49.43%
Mapped reads, second in pair	295,701,740 / 49.26%
Mapped reads, both in pair	588,652,946 / 98.07%
Mapped reads, singletons	3,753,765 / 0.63%
Secondary alignments	0
Supplementary alignments	10,441,937 / 1.74%
Read min/max/mean length	15 / 150 / 150.36
Duplicated reads (estimated)	327,404,697 / 54.54%
Duplication rate	38.61%
Clipped reads	339,169,359 / 56.5%

2.2. ACGT Content

Number/percentage of A's	20,439,765,576 / 25.52%
Number/percentage of C's	16,949,121,147 / 21.16%
Number/percentage of T's	22,046,736,137 / 27.52%
Number/percentage of G's	20,666,541,054 / 25.8%
Number/percentage of N's	221,825 / 0%

GC Percentage	46.96%
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2.3. Coverage

Mean	25.8905
Standard Deviation	186.6837

2.4. Mapping Quality

Mean Mapping Quality	53.74
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2.5. Insert size

Mean	201,788.39
Standard Deviation	4,566,053.69
P25/Median/P75	270 / 319 / 368

2.6. Mismatches and indels

General error rate	1.15%
Mismatches	895,456,892
Insertions	12,576,993
Mapped reads with at least one insertion	2.02%
Deletions	23,910,539
Mapped reads with at least one deletion	3.91%
Homopolymer indels	46.23%

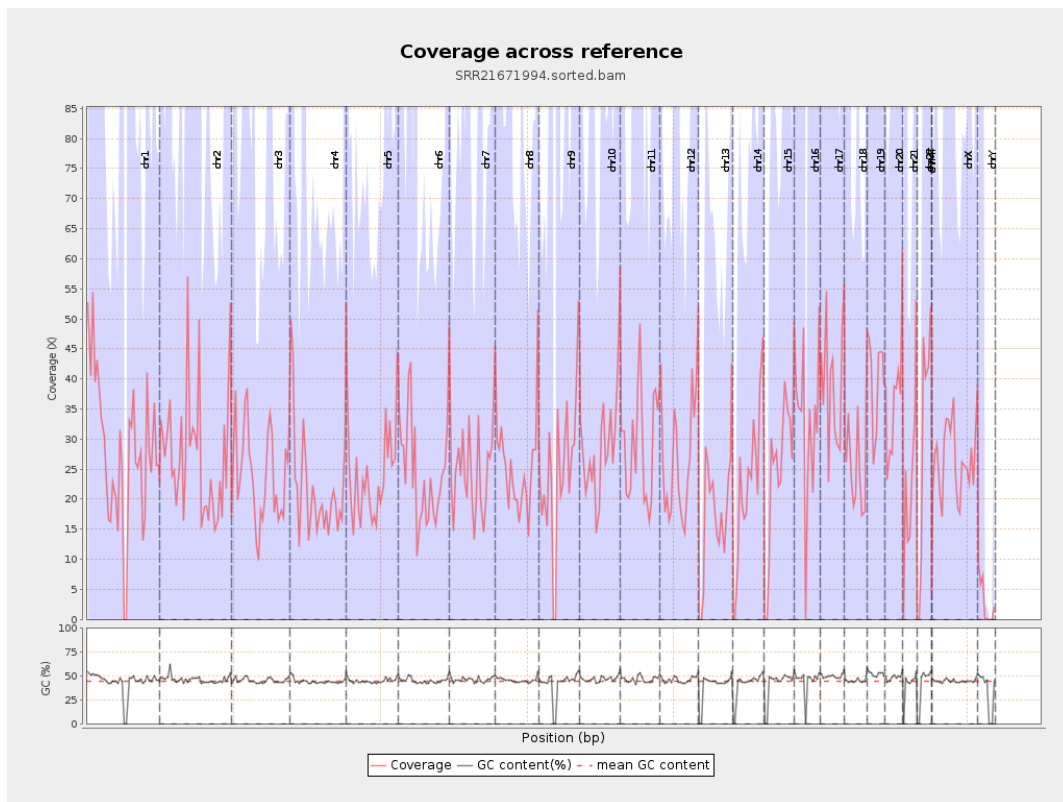
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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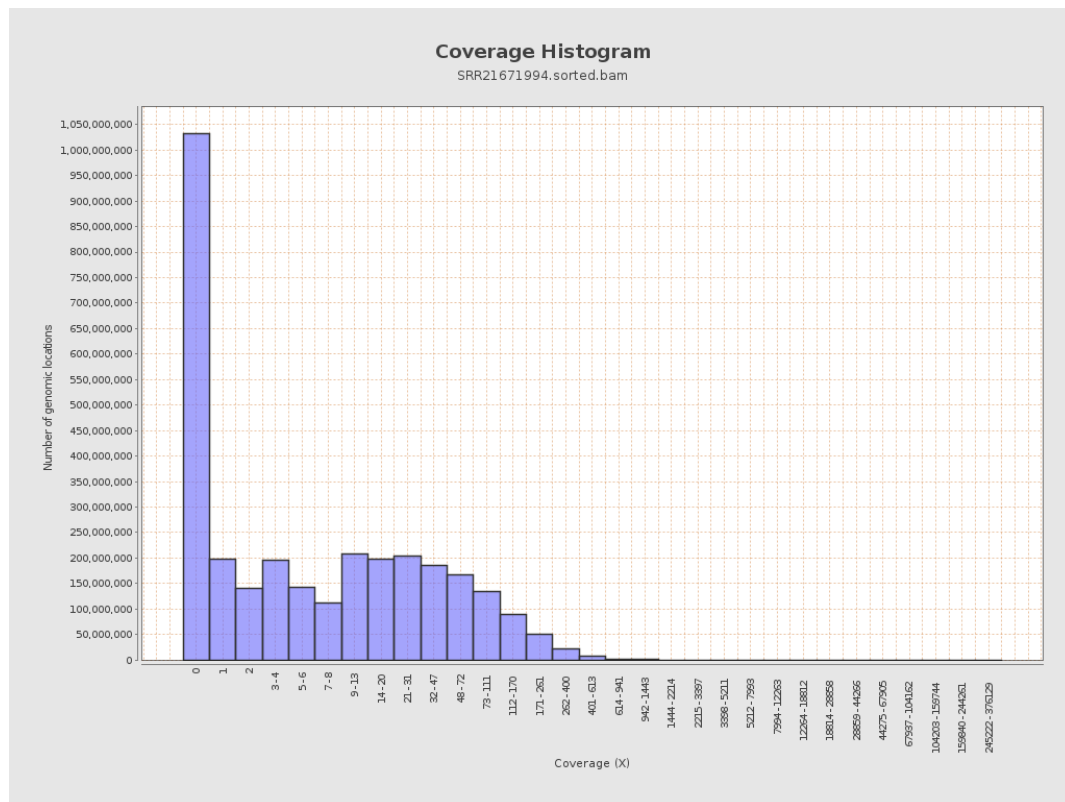
		bases	coverage	deviation
chr1	249250621	6975479261	27.9858	170.5517
chr2	243199373	6651489848	27.3499	433.7138
chr3	198022430	4790969295	24.1941	54.2907
chr4	191154276	4104752361	21.4735	103.9794
chr5	180915260	4403269697	24.3389	55.7683
chr6	171115067	4153402378	24.2726	184.7051
chr7	159138663	3980848931	25.015	97.1603
chr8	146364022	3652079788	24.952	67.2029
chr9	141213431	3534979462	25.0329	254.8421
chr10	135534747	3821984295	28.1993	65.3666
chr11	135006516	3996060507	29.599	221.1436
chr12	133851895	3559284919	26.5912	62.0159
chr13	115169878	1978970865	17.1831	44.8566
chr14	107349540	2399172310	22.3492	106.3108
chr15	102531392	2461318978	24.0055	56.5609
chr16	90354753	2998397504	33.1847	194.7074
chr17	81195210	3154190429	38.847	269.6544
chr18	78077248	1965432856	25.1729	357.8431
chr19	59128983	2386426164	40.3597	89.6036
chr20	63025520	2230893535	35.3967	79.826
chr21	48129895	1110815513	23.0795	214.8556
chr22	51304566	1580158677	30.7996	67.9383
chrMT	16571	66093	3.9885	12.1293
chrX	155270560	4092291213	26.3559	104.0311

chrY	59373566	166189177	2.799	100.7237
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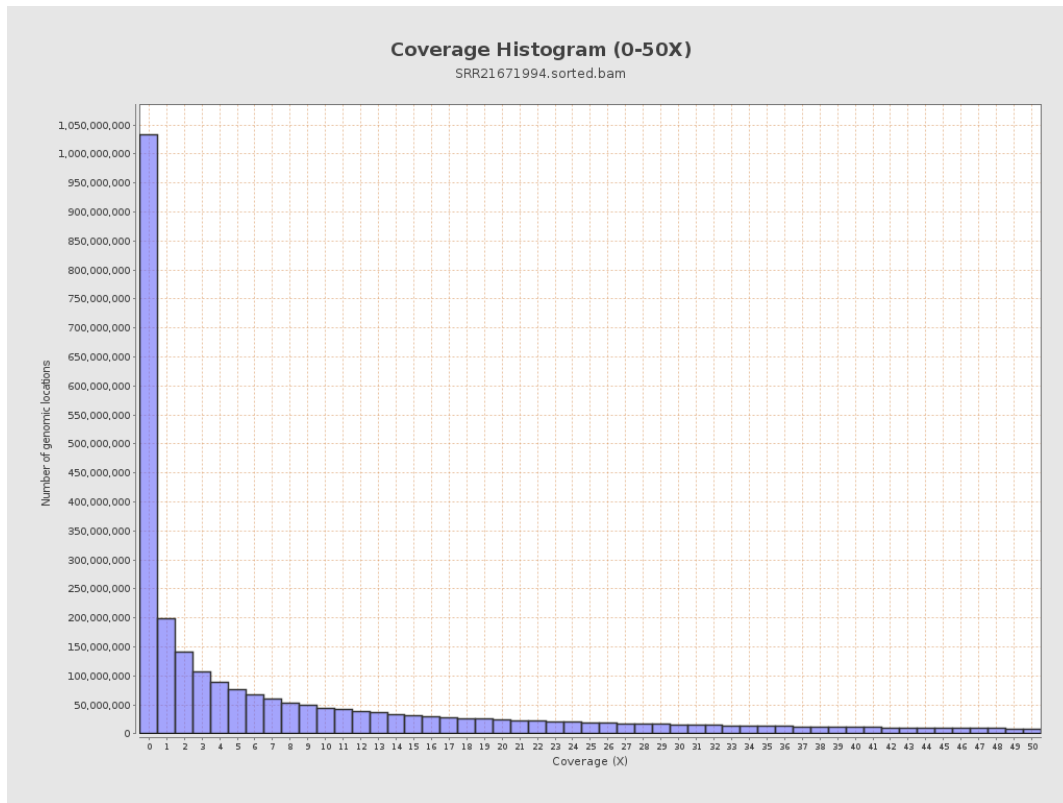
3. Results : Coverage across reference



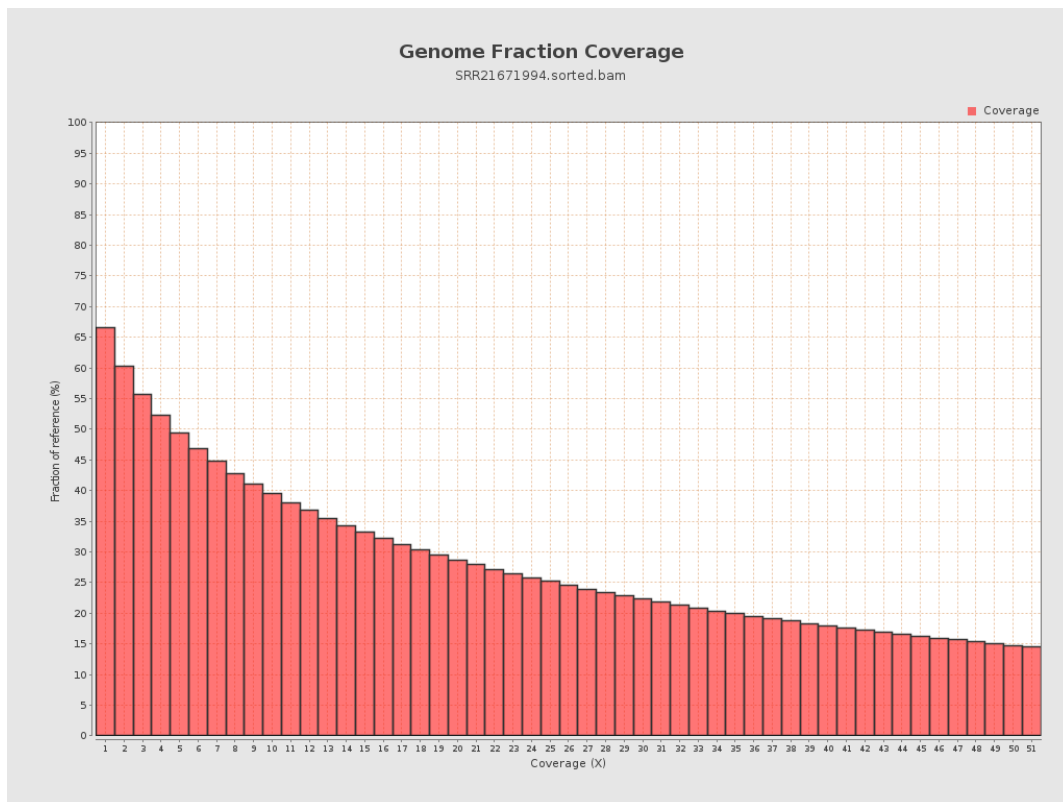
4. Results : Coverage Histogram



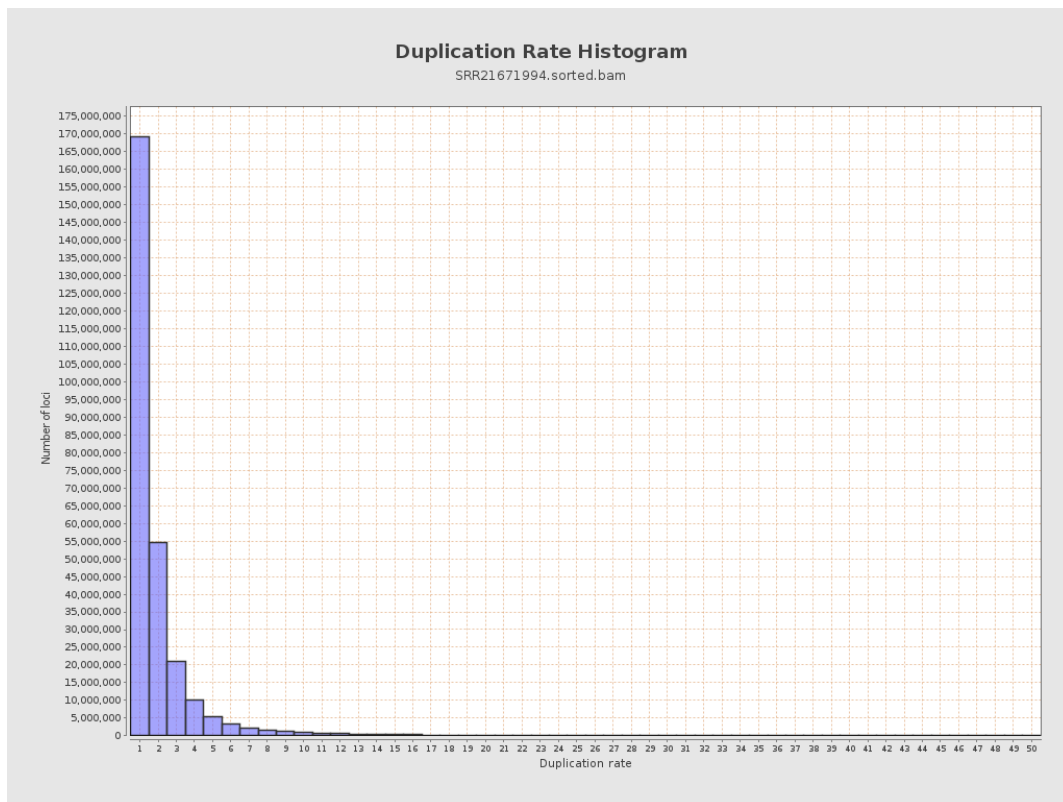
5. Results : Coverage Histogram (0-50X)



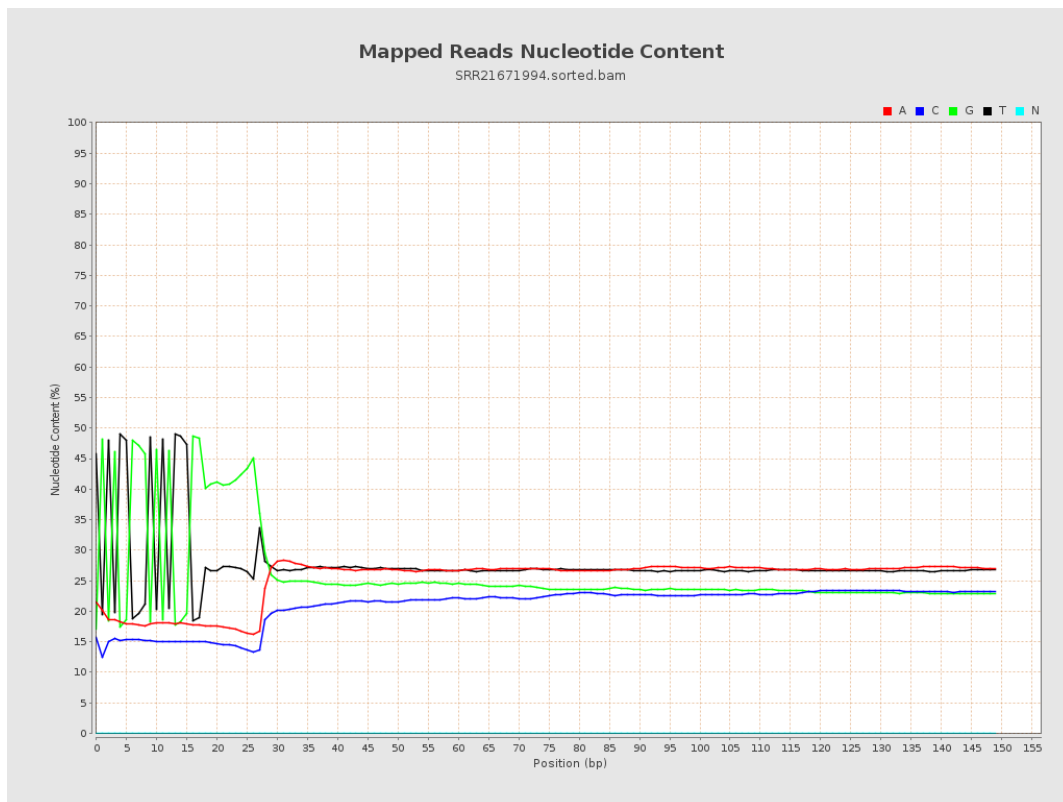
6. Results : Genome Fraction Coverage



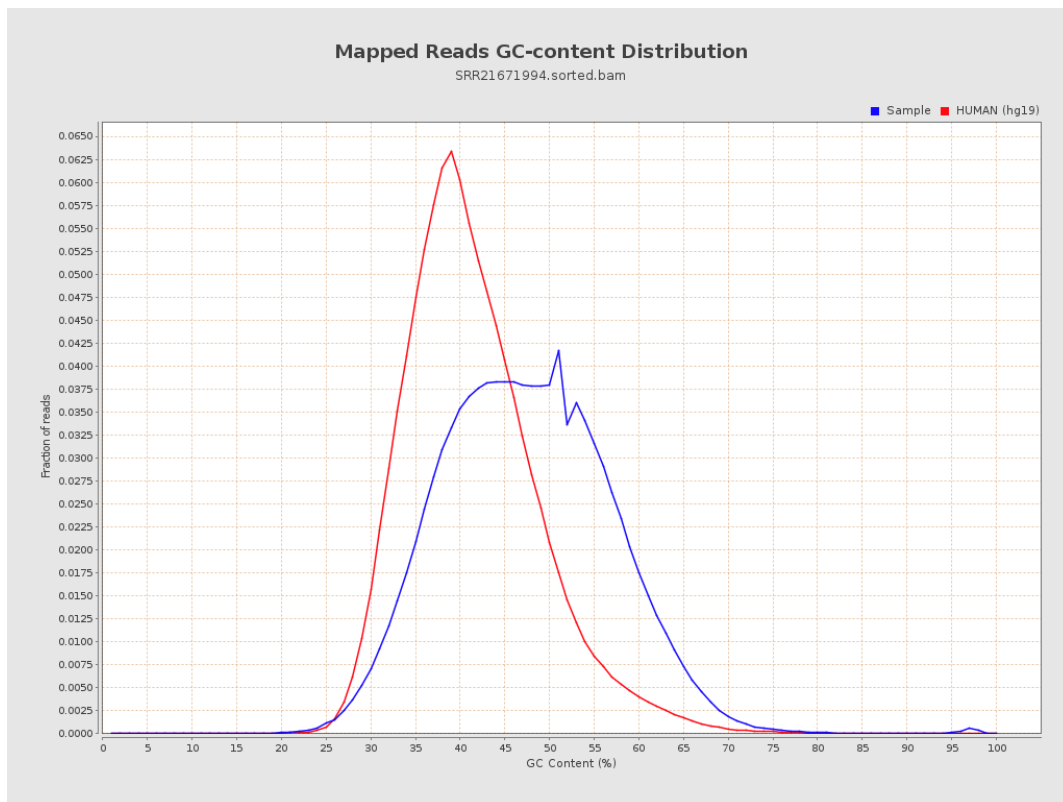
7. Results : Duplication Rate Histogram



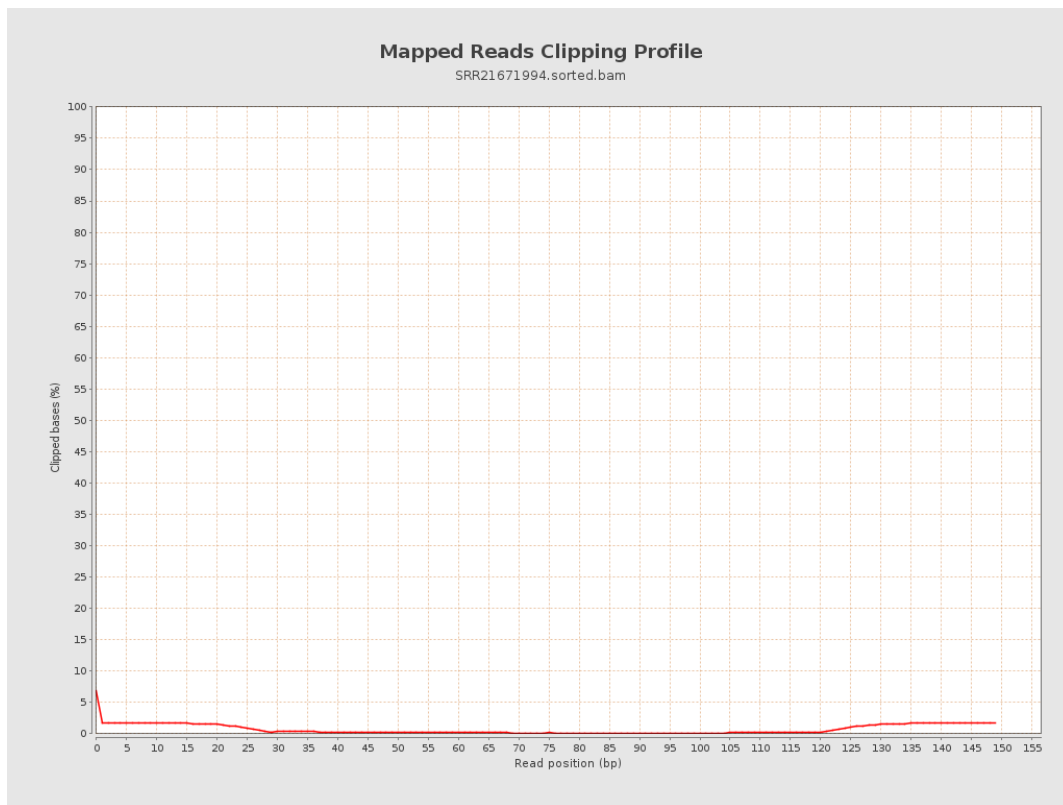
8. Results : Mapped Reads Nucleotide Content



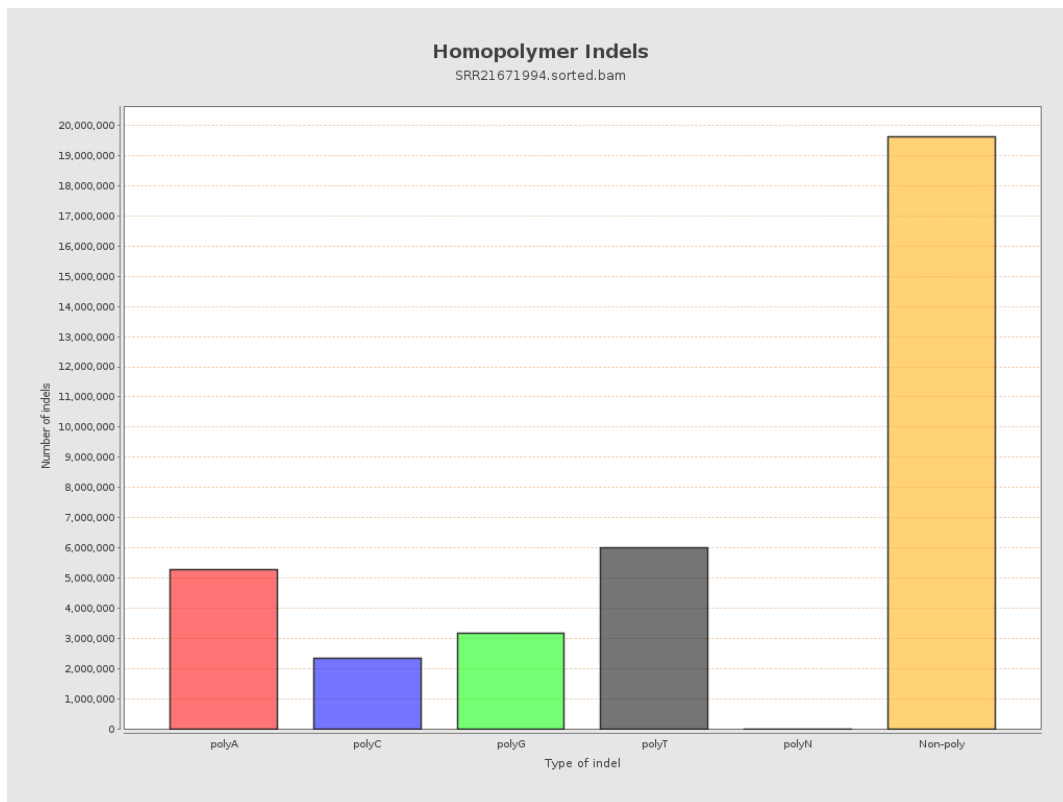
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



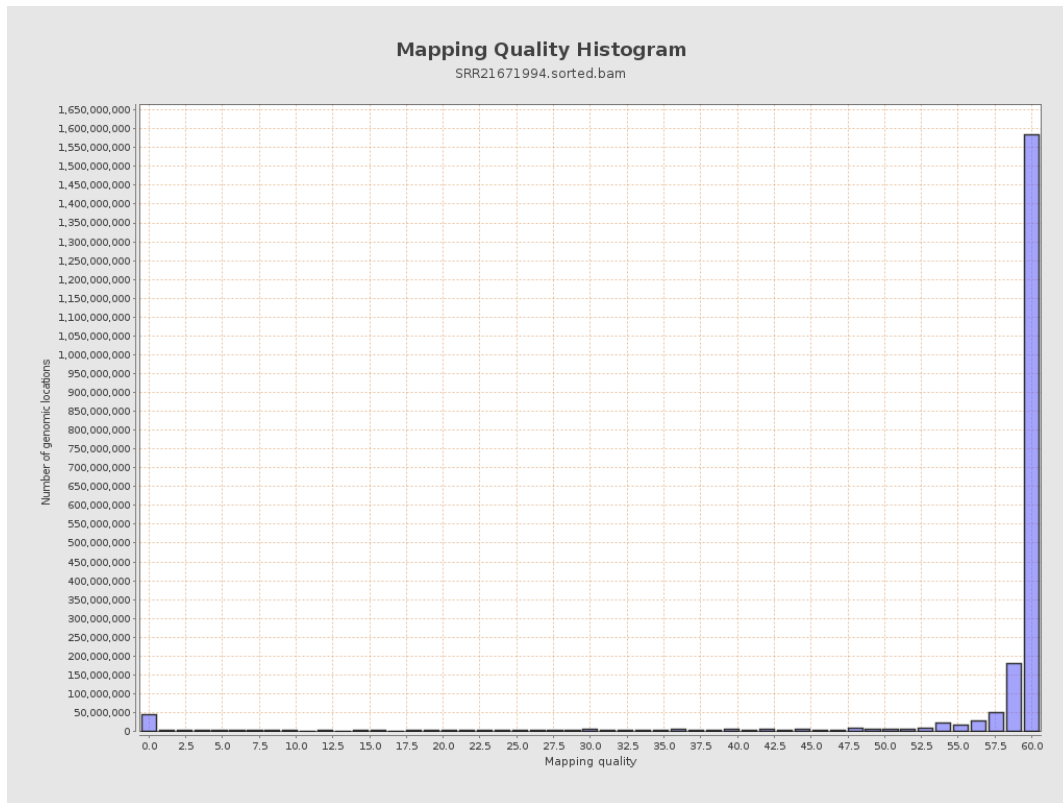
11. Results : Homopolymer Indels



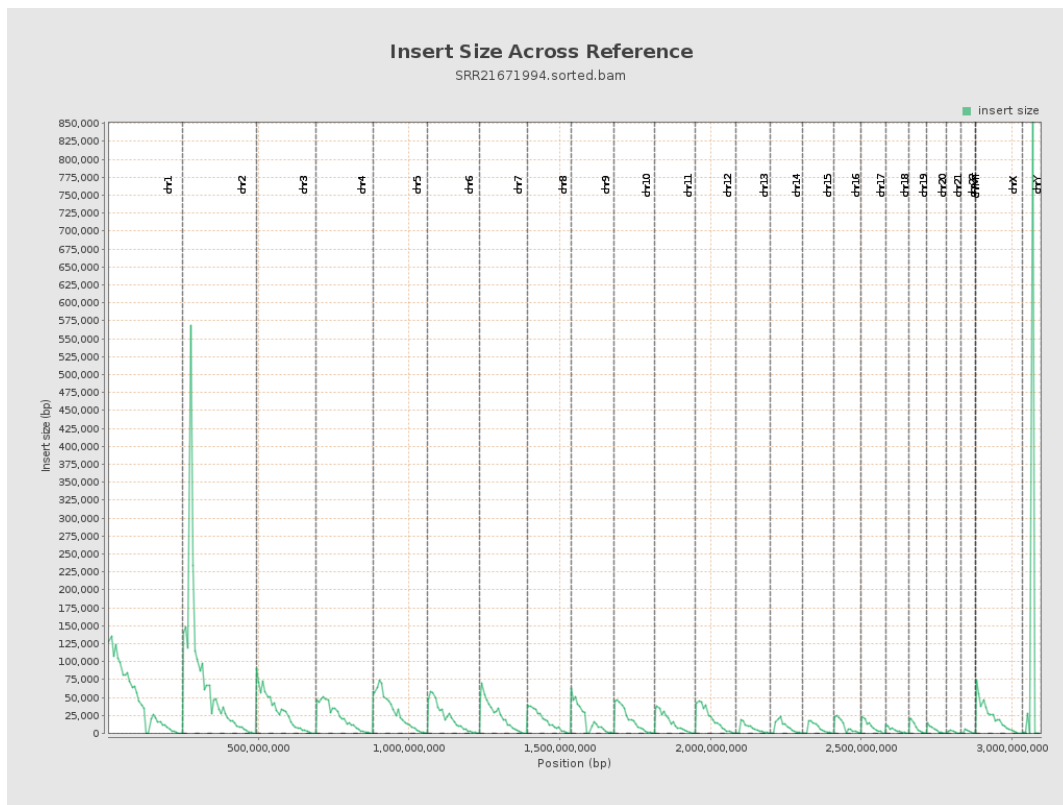
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

