

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 05:26:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472594.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_SRR3472594 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472594_1.fastq.gz SRR3472594_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 05:26:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472594.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,787,444
Mapped reads	6,214,246 / 91.56%
Unmapped reads	573,198 / 8.44%
Mapped paired reads	6,214,246 / 91.56%
Mapped reads, first in pair	3,137,216 / 46.22%
Mapped reads, second in pair	3,077,030 / 45.33%
Mapped reads, both in pair	6,064,992 / 89.36%
Mapped reads, singletons	149,254 / 2.2%
Secondary alignments	0
Supplementary alignments	156,127 / 2.3%
Read min/max/mean length	30 / 100 / 100.89
Duplicated reads (estimated)	870,987 / 12.83%
Duplication rate	12.21%
Clipped reads	4,600,044 / 67.77%

2.2. ACGT Content

Number/percentage of A's	130,436,209 / 25.64%
Number/percentage of C's	101,557,080 / 19.97%
Number/percentage of T's	151,717,070 / 29.83%
Number/percentage of G's	124,632,742 / 24.5%
Number/percentage of N's	319,383 / 0.06%

GC Percentage	44.47%
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2.3. Coverage

Mean	0.1644
Standard Deviation	1.4653

2.4. Mapping Quality

Mean Mapping Quality	50.67
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2.5. Insert size

Mean	194,668.36
Standard Deviation	4,222,664.85
P25/Median/P75	96 / 136 / 189

2.6. Mismatches and indels

General error rate	1.19%
Mismatches	5,930,144
Insertions	48,087
Mapped reads with at least one insertion	0.76%
Deletions	120,719
Mapped reads with at least one deletion	1.91%
Homopolymer indels	43.18%

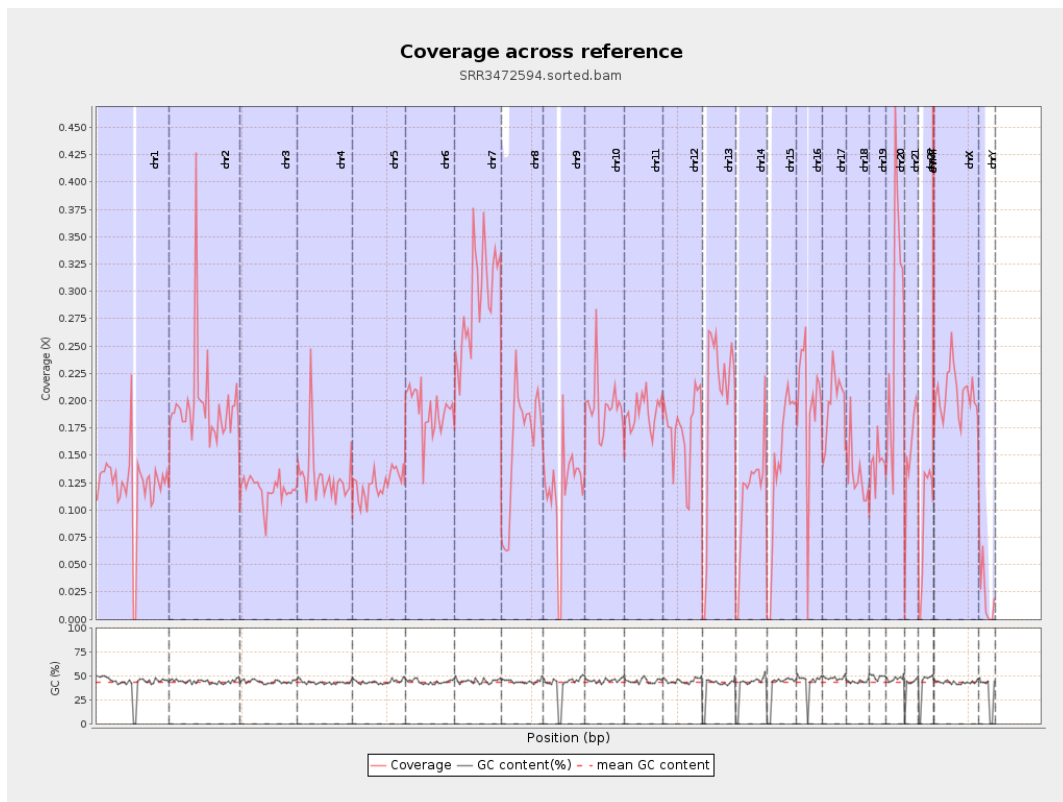
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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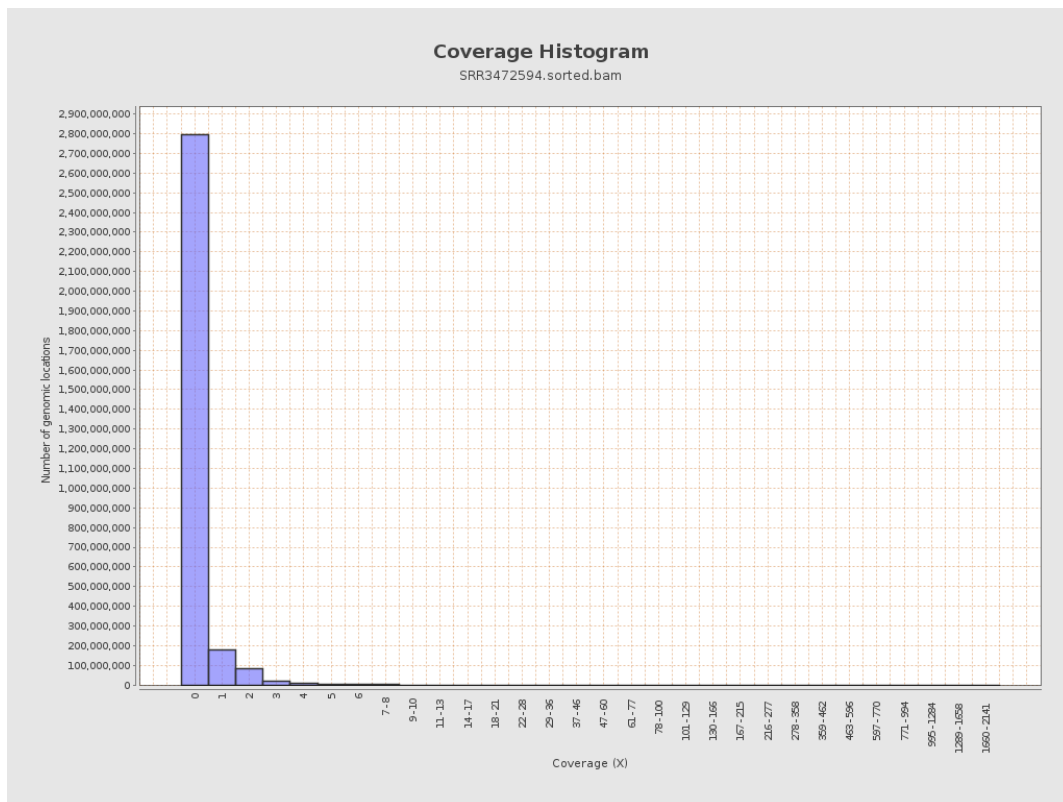
		bases	coverage	deviation
chr1	249250621	30424619	0.1221	1.8279
chr2	243199373	47666391	0.196	1.9098
chr3	198022430	23423401	0.1183	0.4923
chr4	191154276	24992085	0.1307	0.8296
chr5	180915260	22419868	0.1239	0.5211
chr6	171115067	32730965	0.1913	0.8821
chr7	159138663	46778719	0.2939	2.5705
chr8	146364022	23606833	0.1613	1.2059
chr9	141213431	16479247	0.1167	1.469
chr10	135534747	26390210	0.1947	1.4062
chr11	135006516	25456494	0.1886	1.4197
chr12	133851895	23260589	0.1738	0.6241
chr13	115169878	22653201	0.1967	0.6668
chr14	107349540	12272321	0.1143	3.5866
chr15	102531392	14596970	0.1424	0.5593
chr16	90354753	17920706	0.1983	0.907
chr17	81195210	16122221	0.1986	1.1402
chr18	78077248	10371961	0.1328	2.2459
chr19	59128983	8392815	0.1419	1.3557
chr20	63025520	17305095	0.2746	0.9931
chr21	48129895	7324223	0.1522	0.7212
chr22	51304566	4625003	0.0901	0.4444
chrMT	16571	323349	19.5129	12.0286
chrX	155270560	32056605	0.2065	0.8748

chrY	59373566	1295544	0.0218	0.6325
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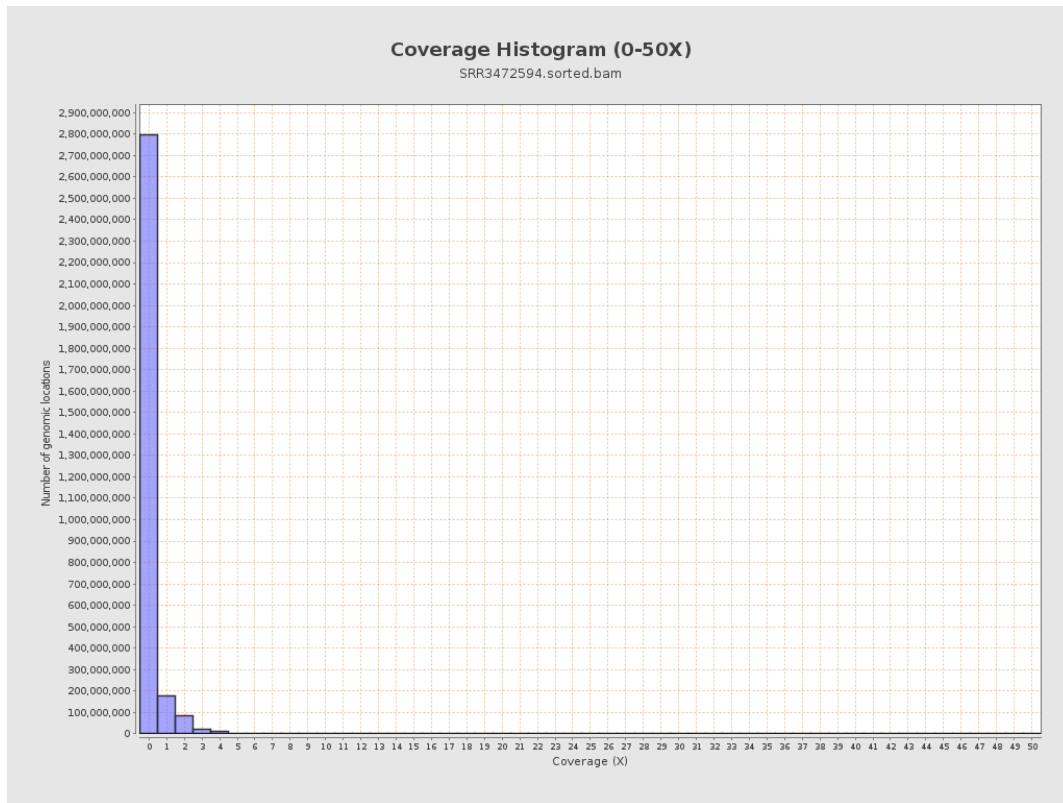
3. Results : Coverage across reference



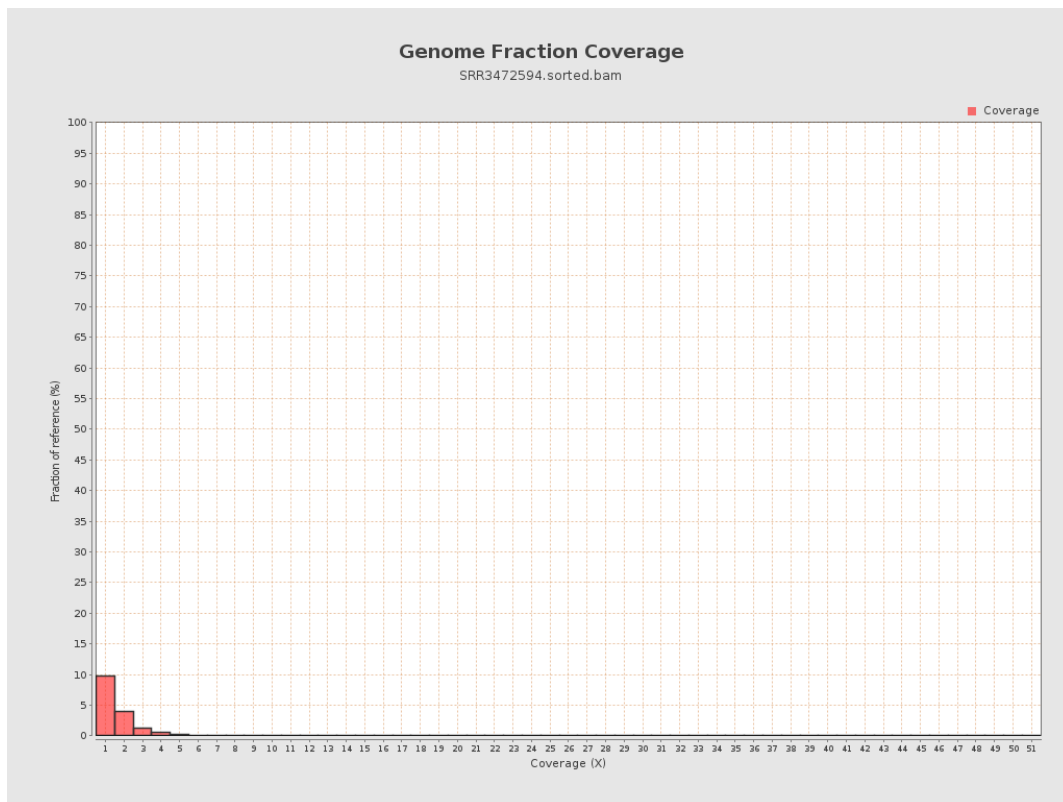
4. Results : Coverage Histogram



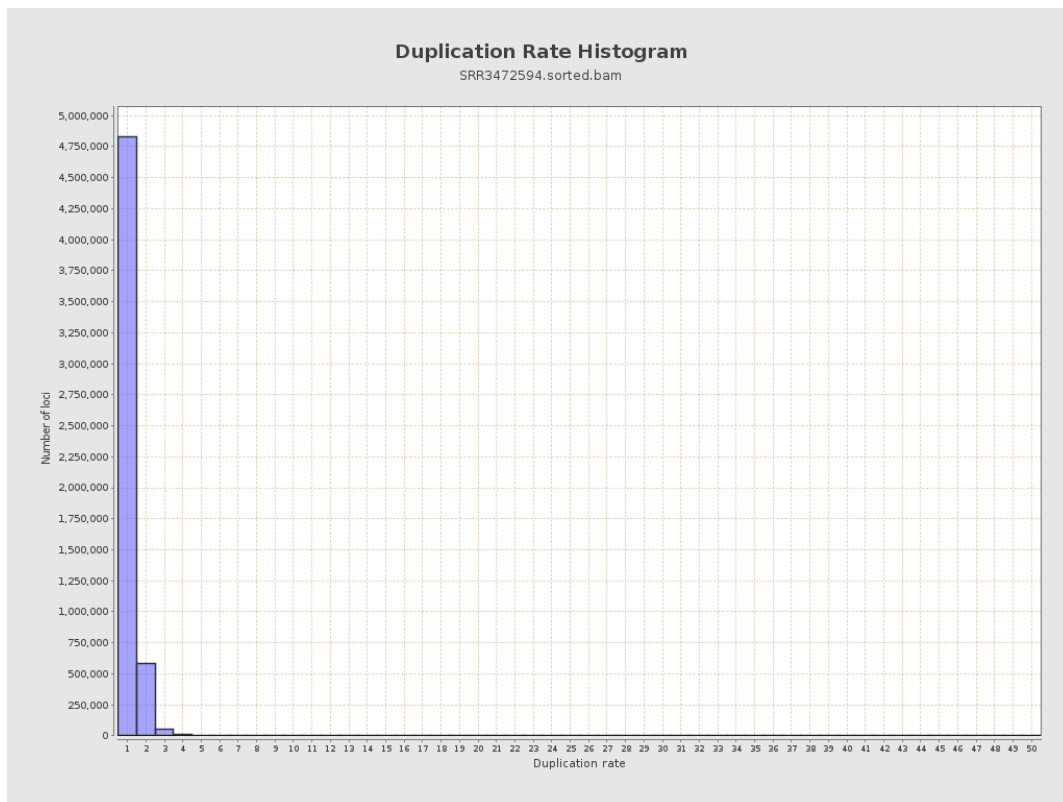
5. Results : Coverage Histogram (0-50X)



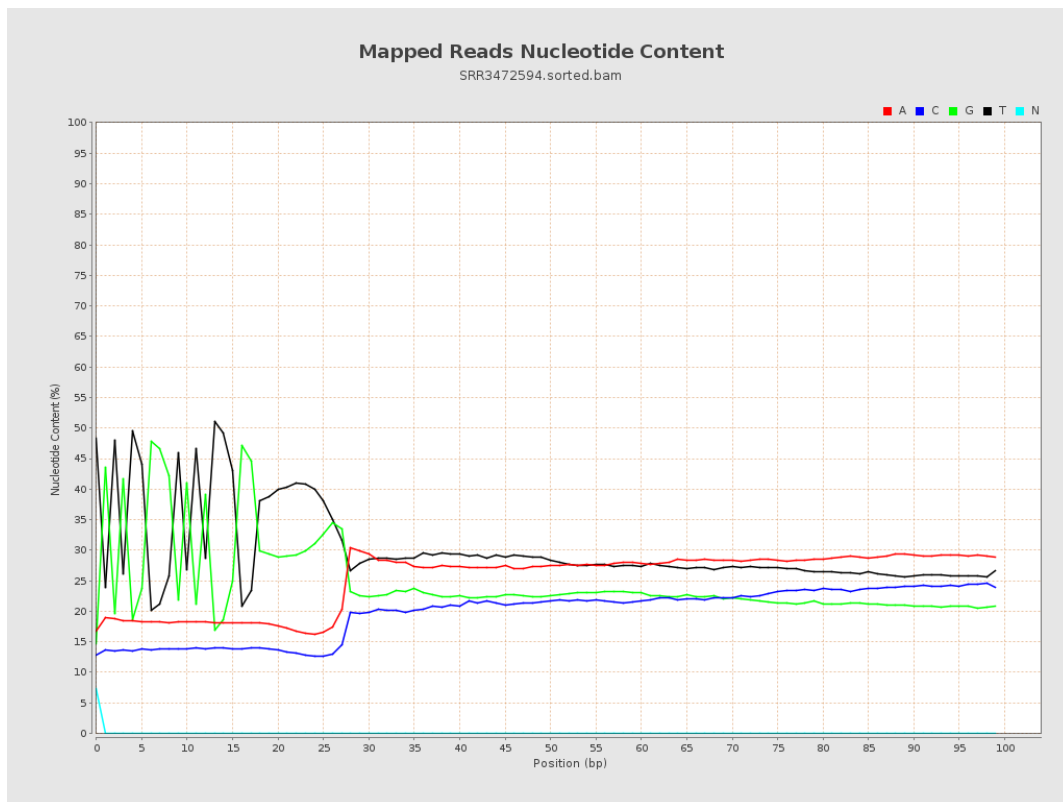
6. Results : Genome Fraction Coverage



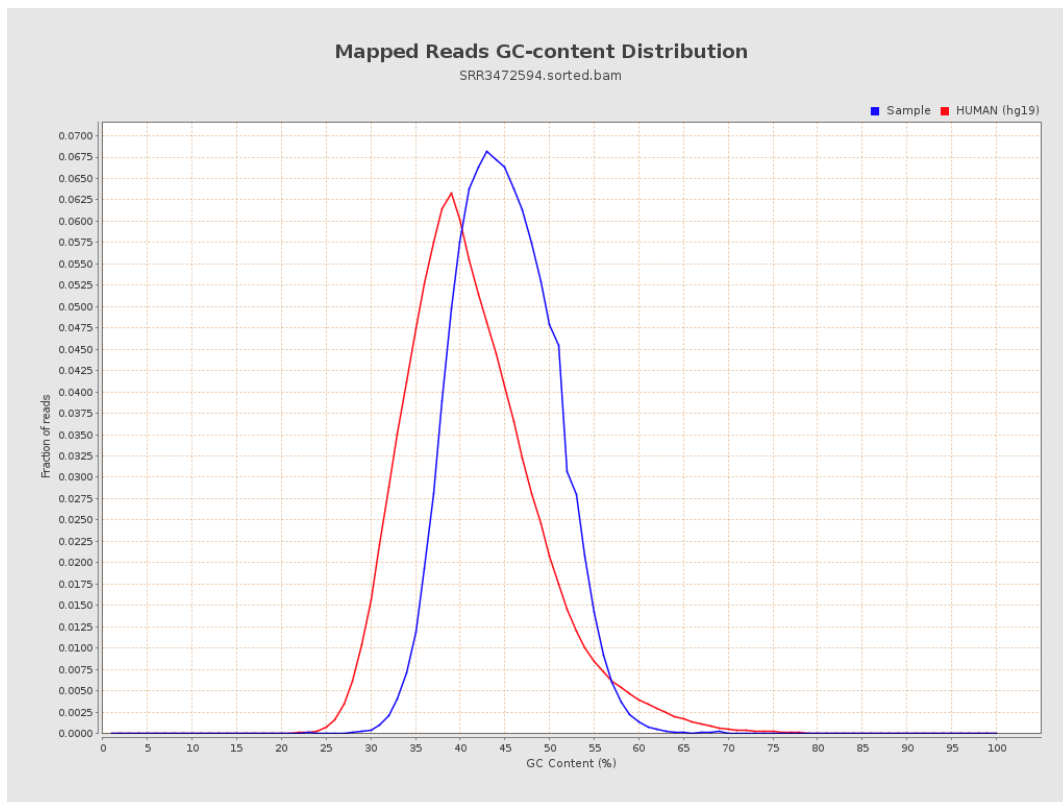
7. Results : Duplication Rate Histogram



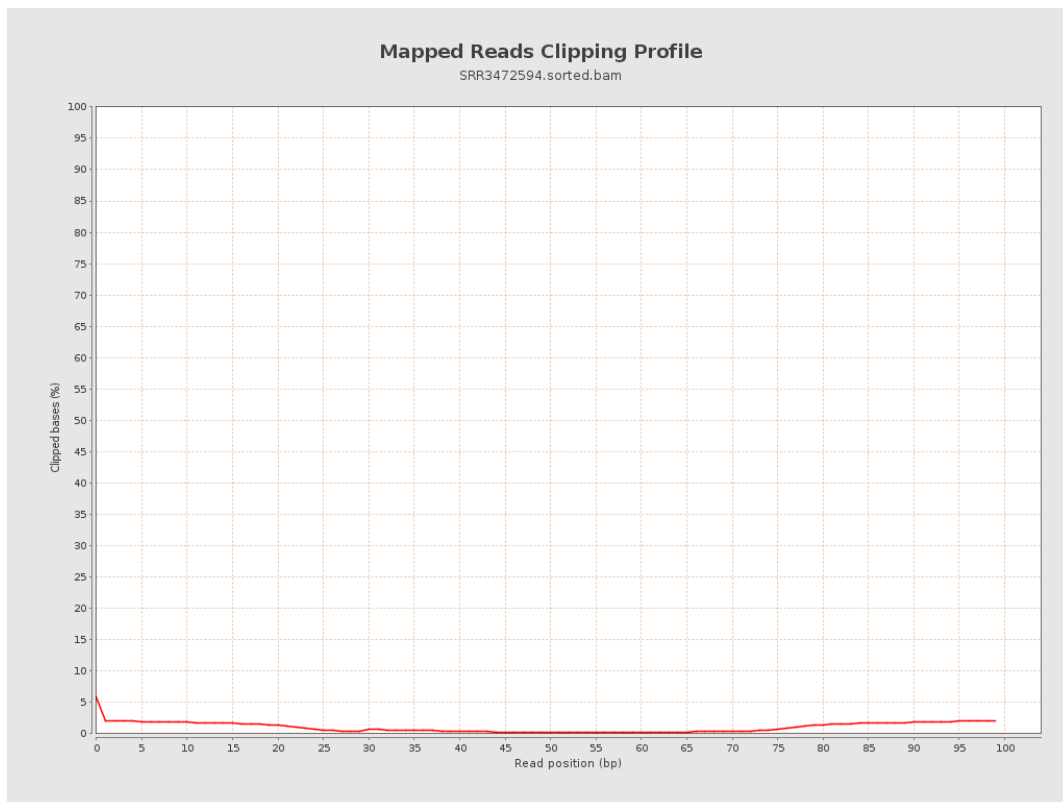
8. Results : Mapped Reads Nucleotide Content



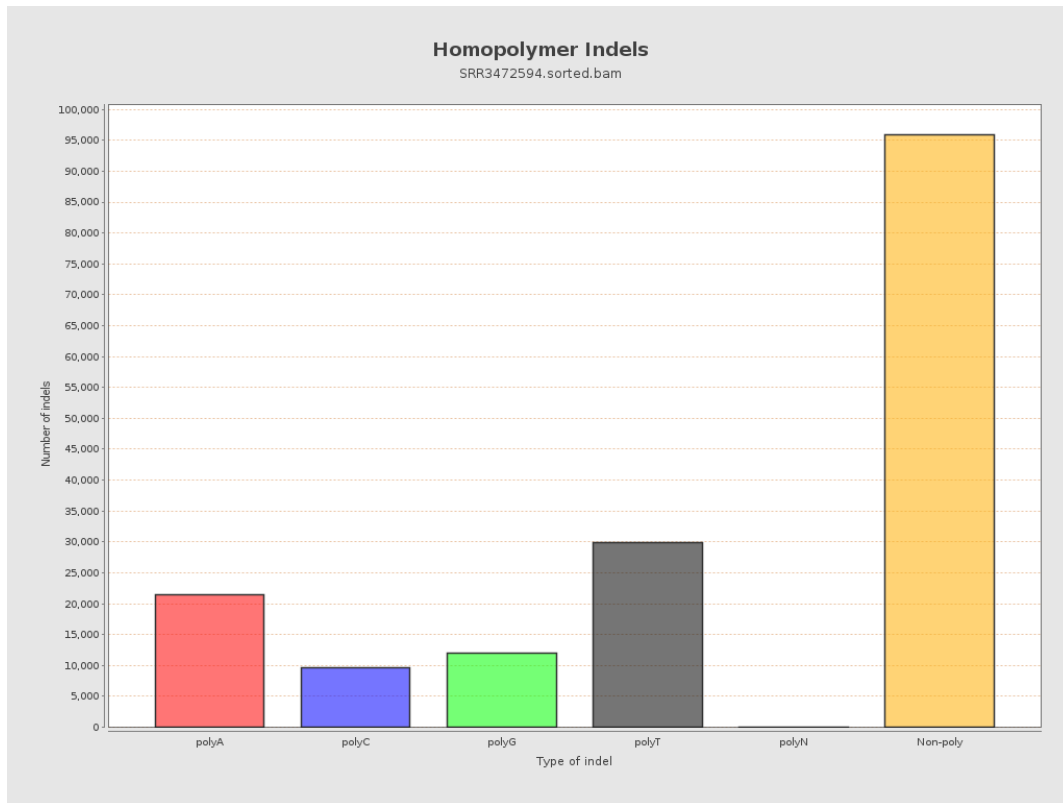
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



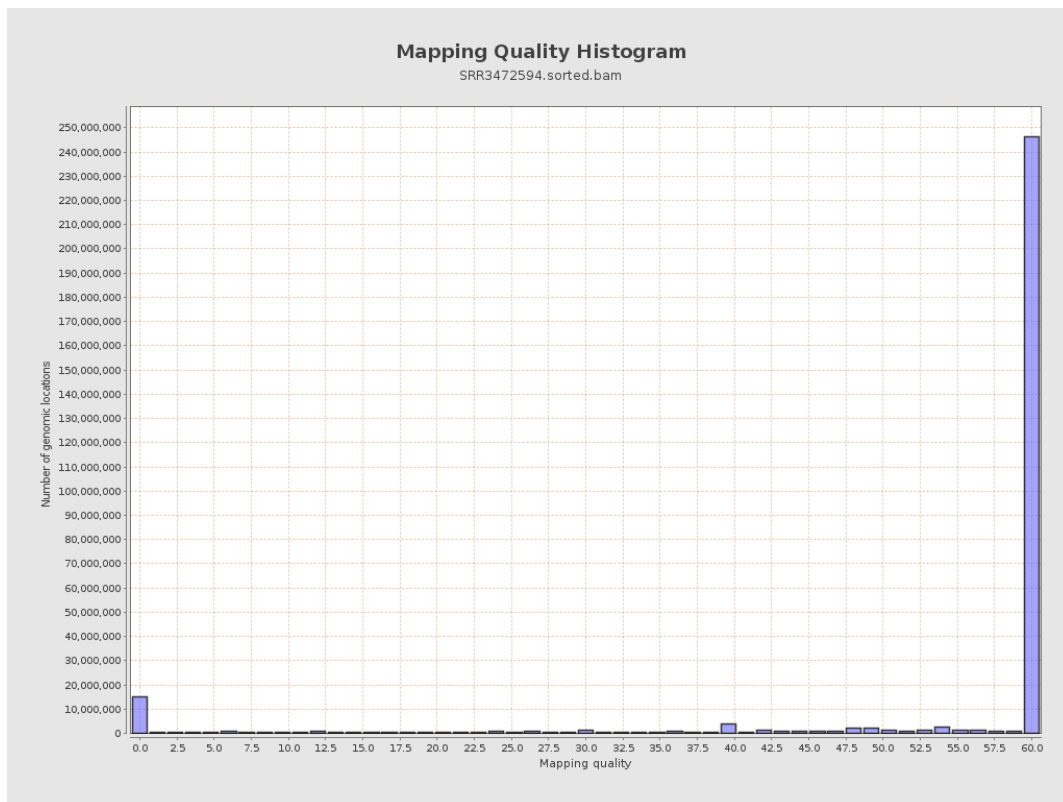
11. Results : Homopolymer Indels



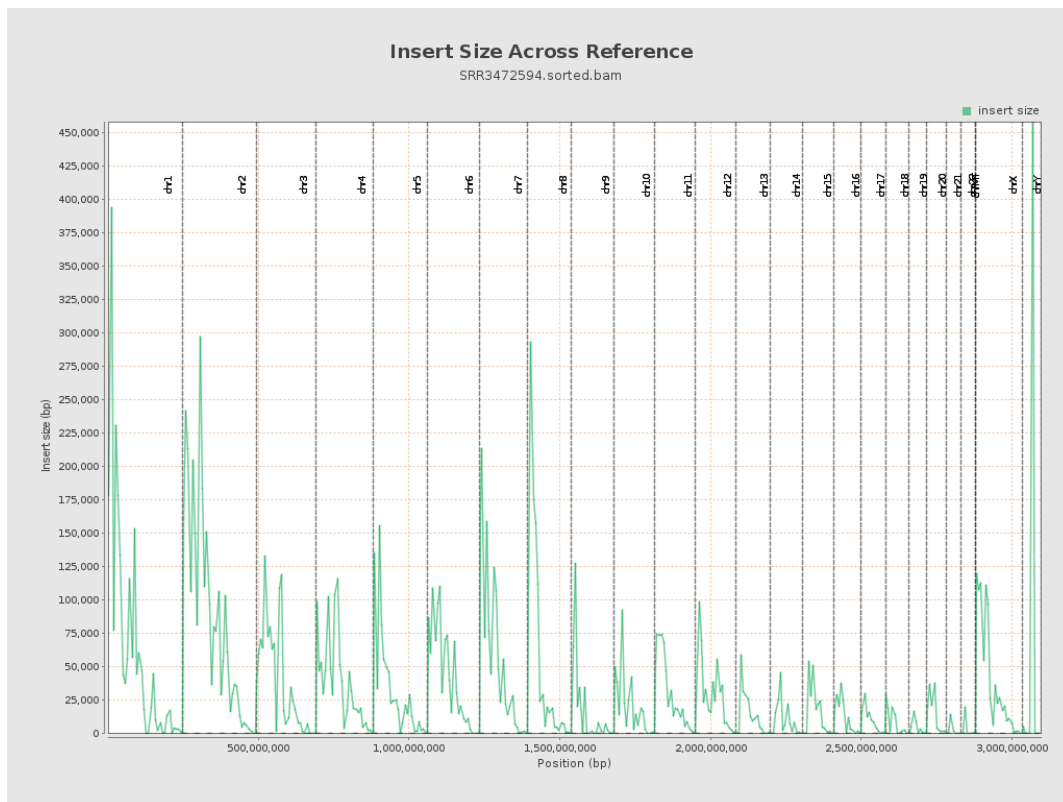
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

