

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 23:08:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472732.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_SRR3472732 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472732_1.fastq.gz SRR3472732_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 23:08:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472732.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,284,288
Mapped reads	17,126,139 / 99.09%
Unmapped reads	158,149 / 0.91%
Mapped paired reads	17,126,139 / 99.09%
Mapped reads, first in pair	8,596,564 / 49.74%
Mapped reads, second in pair	8,529,575 / 49.35%
Mapped reads, both in pair	17,024,402 / 98.5%
Mapped reads, singletons	101,737 / 0.59%
Secondary alignments	0
Supplementary alignments	61,070 / 0.35%
Read min/max/mean length	30 / 100 / 100.14
Duplicated reads (estimated)	10,704,114 / 61.93%
Duplication rate	47.49%
Clipped reads	1,222,698 / 7.07%

2.2. ACGT Content

Number/percentage of A's	469,471,254 / 27.77%
Number/percentage of C's	377,693,860 / 22.34%
Number/percentage of T's	467,803,084 / 27.67%
Number/percentage of G's	375,264,510 / 22.2%
Number/percentage of N's	325,526 / 0.02%

GC Percentage	44.54%
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2.3. Coverage

Mean	0.5462
Standard Deviation	17.9435

2.4. Mapping Quality

Mean Mapping Quality	55.23
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2.5. Insert size

Mean	25,997.56
Standard Deviation	1,588,991.82
P25/Median/P75	183 / 254 / 339

2.6. Mismatches and indels

General error rate	0.65%
Mismatches	10,792,980
Insertions	101,669
Mapped reads with at least one insertion	0.59%
Deletions	99,747
Mapped reads with at least one deletion	0.58%
Homopolymer indels	45.18%

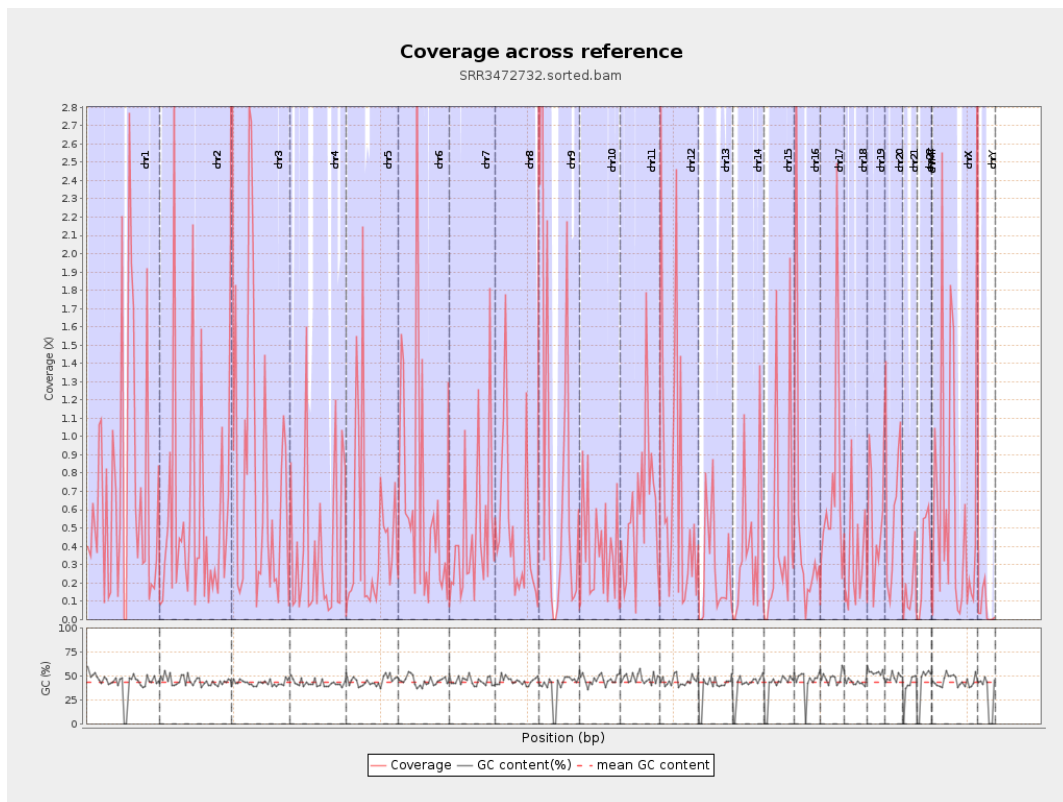
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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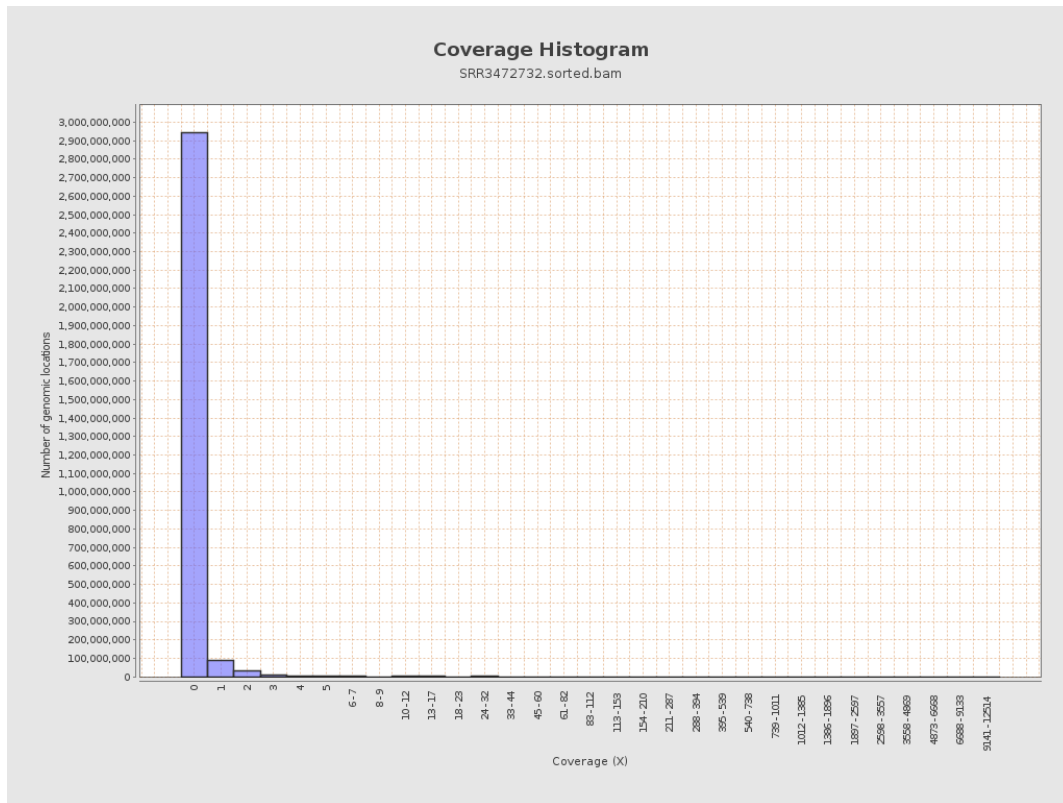
		bases	coverage	deviation
chr1	249250621	173708169	0.6969	19.6709
chr2	243199373	138298153	0.5687	19.2535
chr3	198022430	168479727	0.8508	20.3495
chr4	191154276	72920279	0.3815	13.5847
chr5	180915260	81963415	0.453	13.7433
chr6	171115067	112866708	0.6596	18.2097
chr7	159138663	74686632	0.4693	14.4002
chr8	146364022	71496786	0.4885	16.7874
chr9	141213431	126244356	0.894	33.864
chr10	135534747	51639253	0.381	15.9902
chr11	135006516	80224339	0.5942	18.8252
chr12	133851895	99791343	0.7455	22.5055
chr13	115169878	31427725	0.2729	9.0901
chr14	107349540	39610559	0.369	15.2741
chr15	102531392	45726428	0.446	17.4485
chr16	90354753	46965806	0.5198	11.6029
chr17	81195210	56984431	0.7018	16.4686
chr18	78077248	25342596	0.3246	12.0569
chr19	59128983	30812990	0.5211	13.0951
chr20	63025520	38274379	0.6073	17.7864
chr21	48129895	7557653	0.157	8.021
chr22	51304566	17171258	0.3347	8.9231
chrMT	16571	1631	0.0984	0.3731
chrX	155270560	94982467	0.6117	20.6784

chrY	59373566	3617997	0.0609	2.5191
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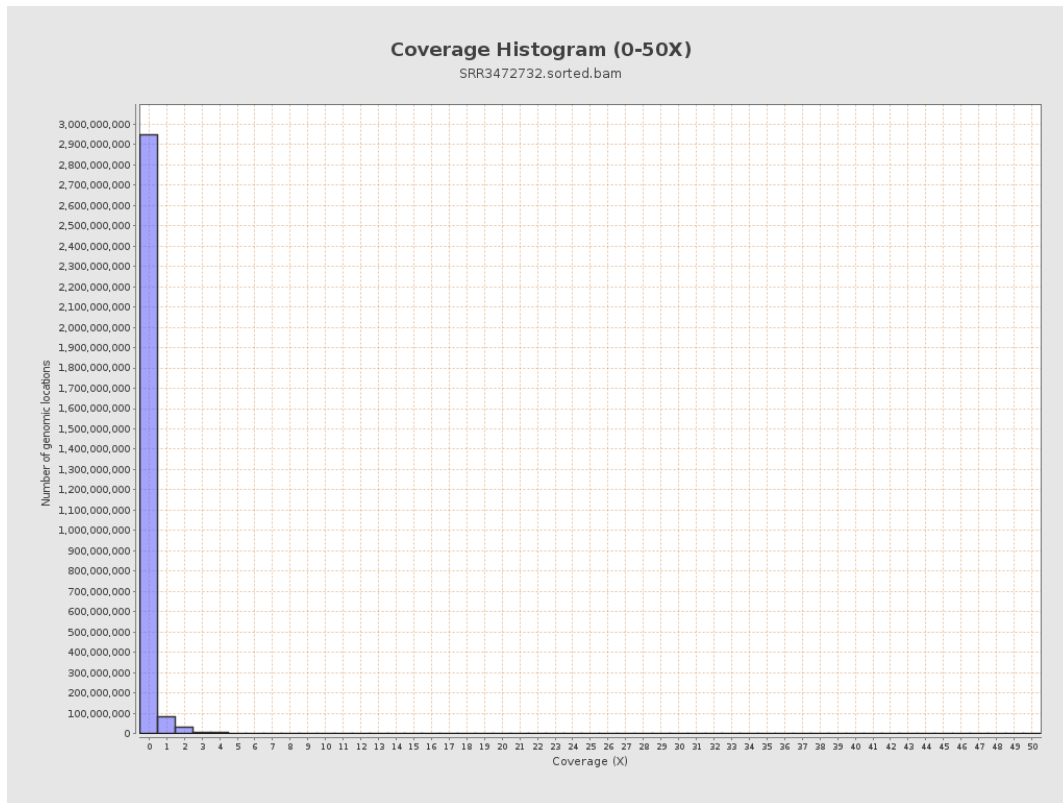
3. Results : Coverage across reference



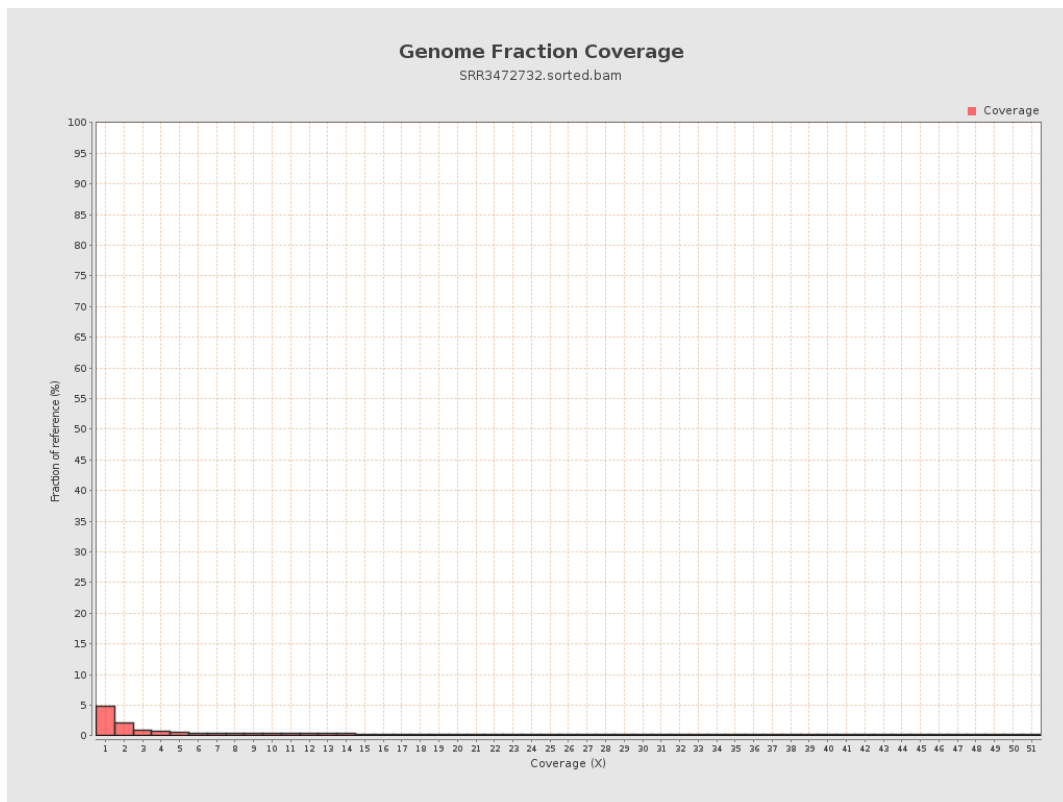
4. Results : Coverage Histogram



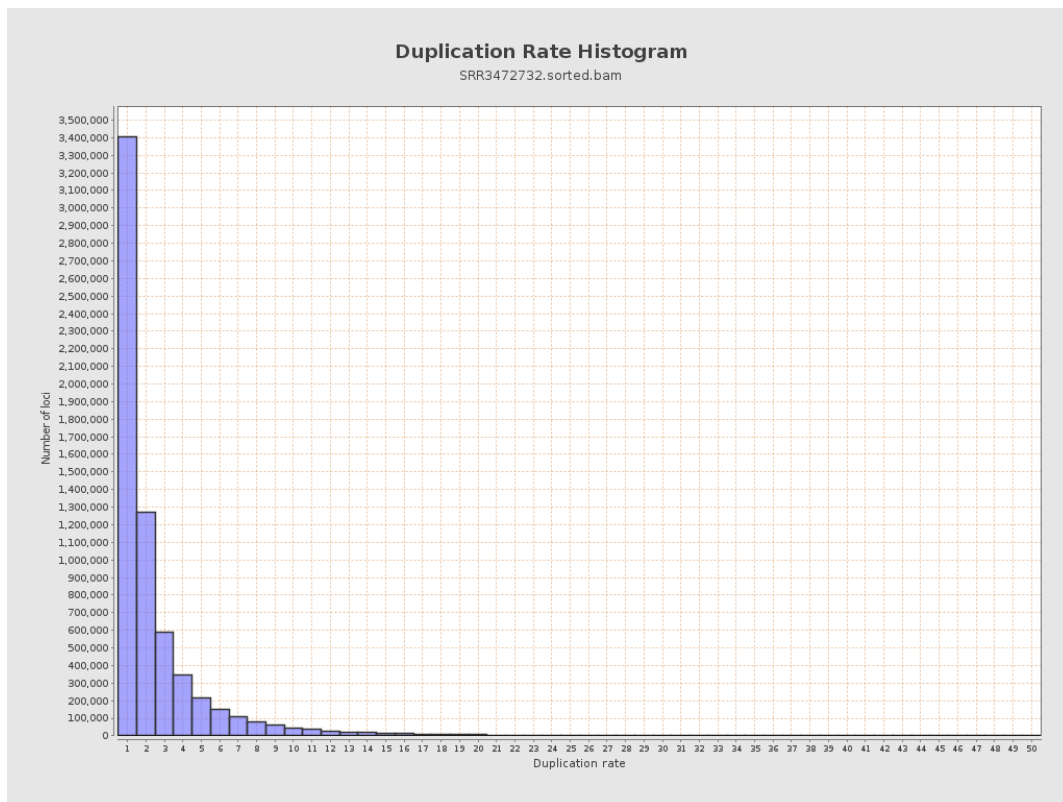
5. Results : Coverage Histogram (0-50X)



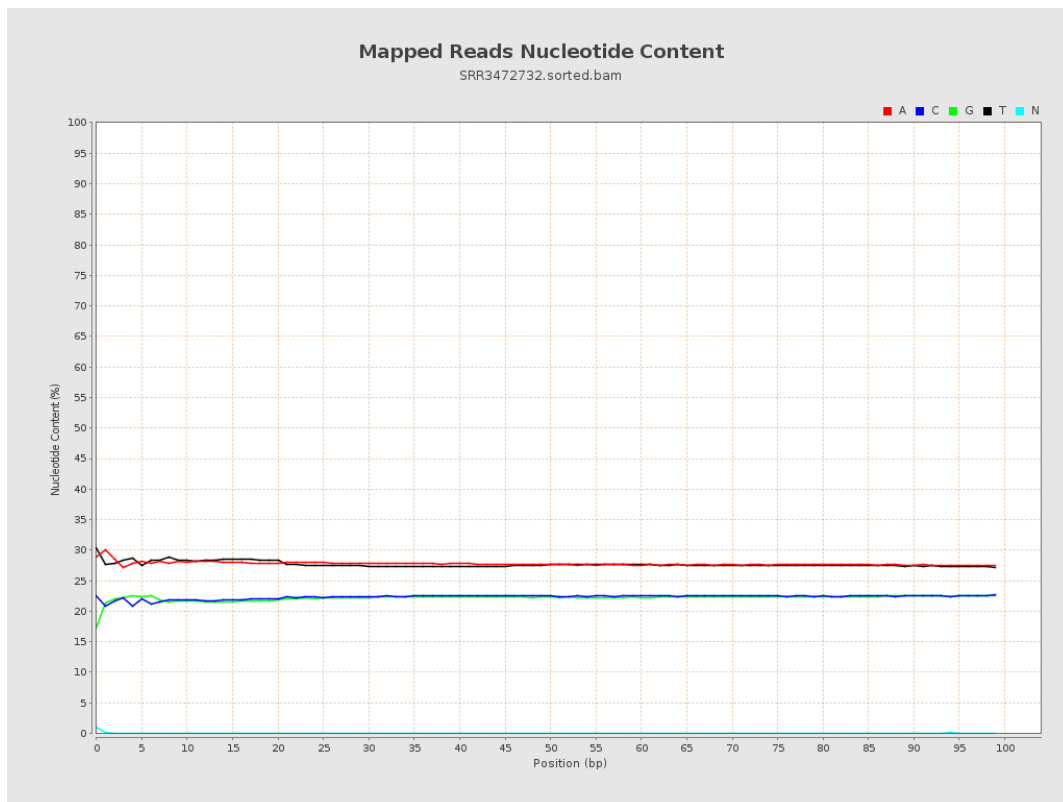
6. Results : Genome Fraction Coverage



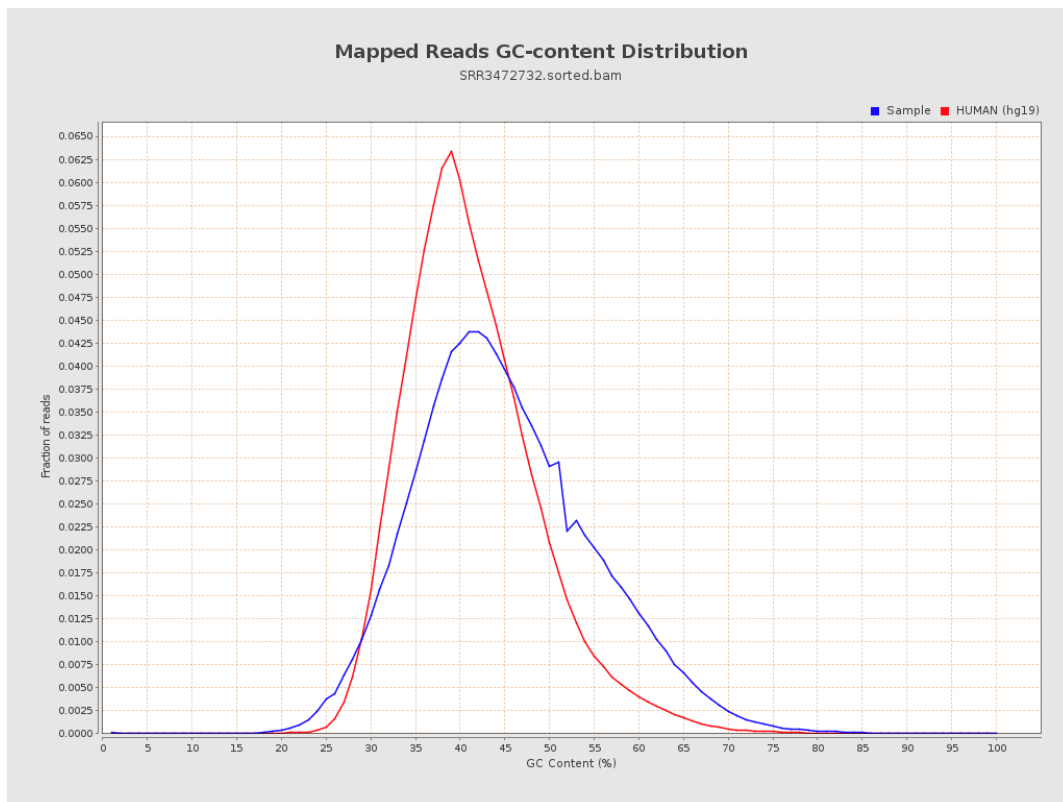
7. Results : Duplication Rate Histogram



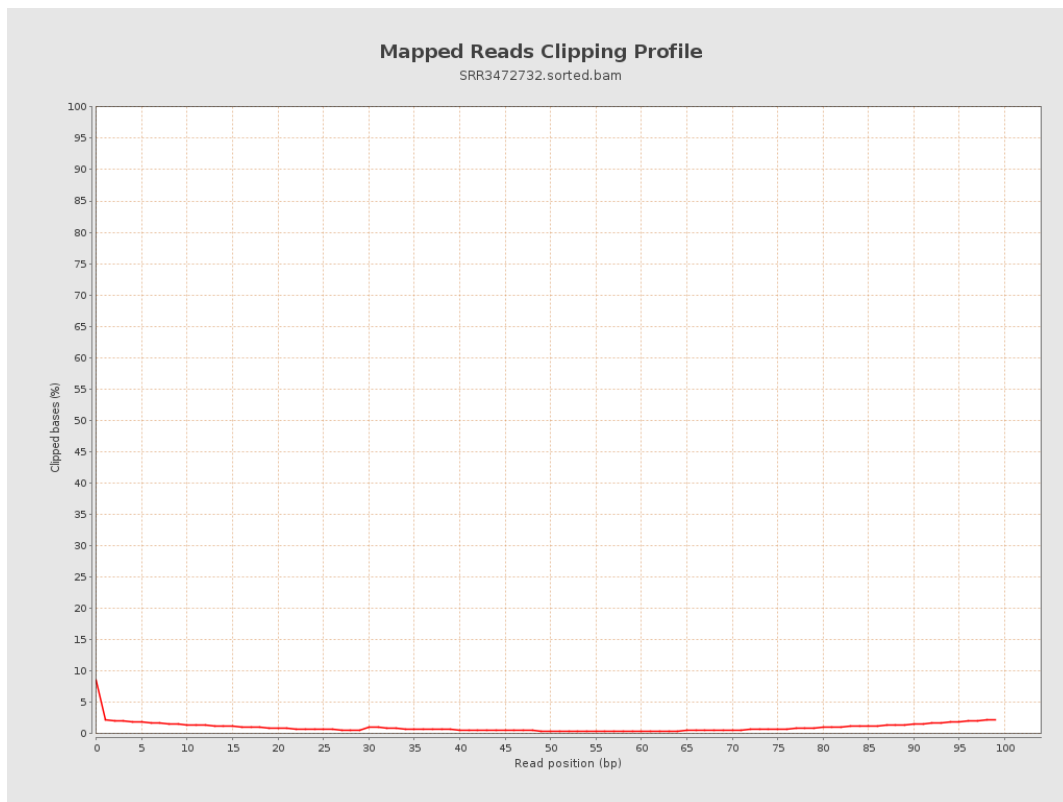
8. Results : Mapped Reads Nucleotide Content



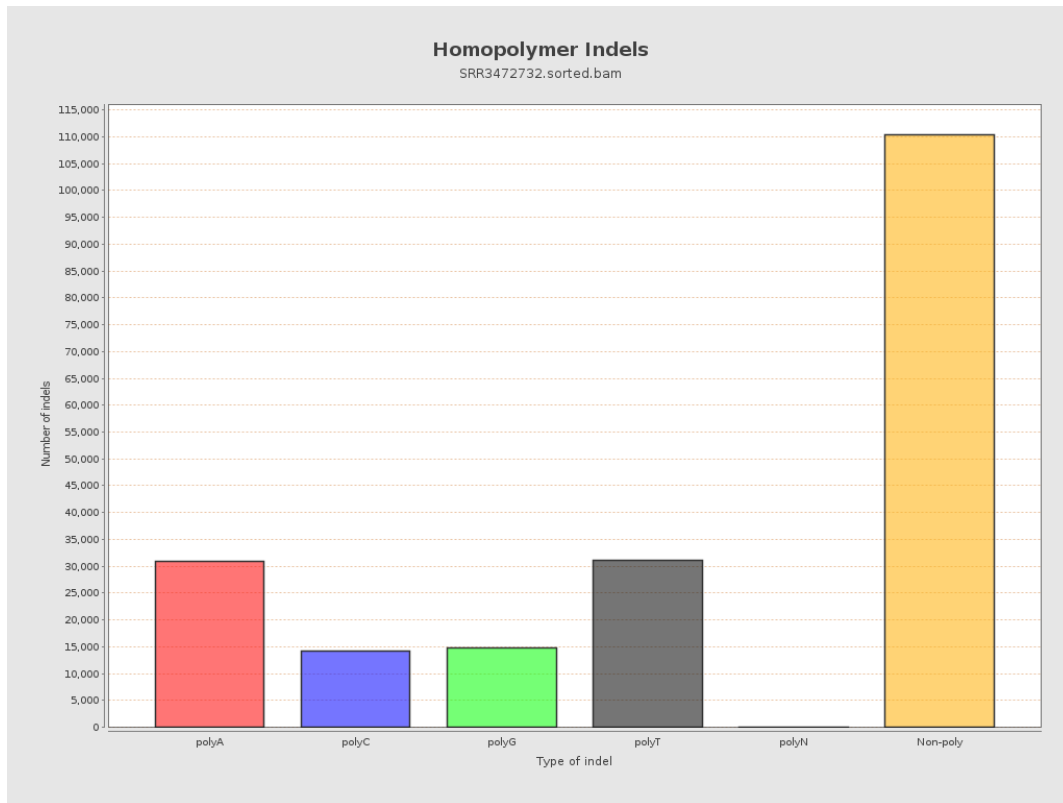
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



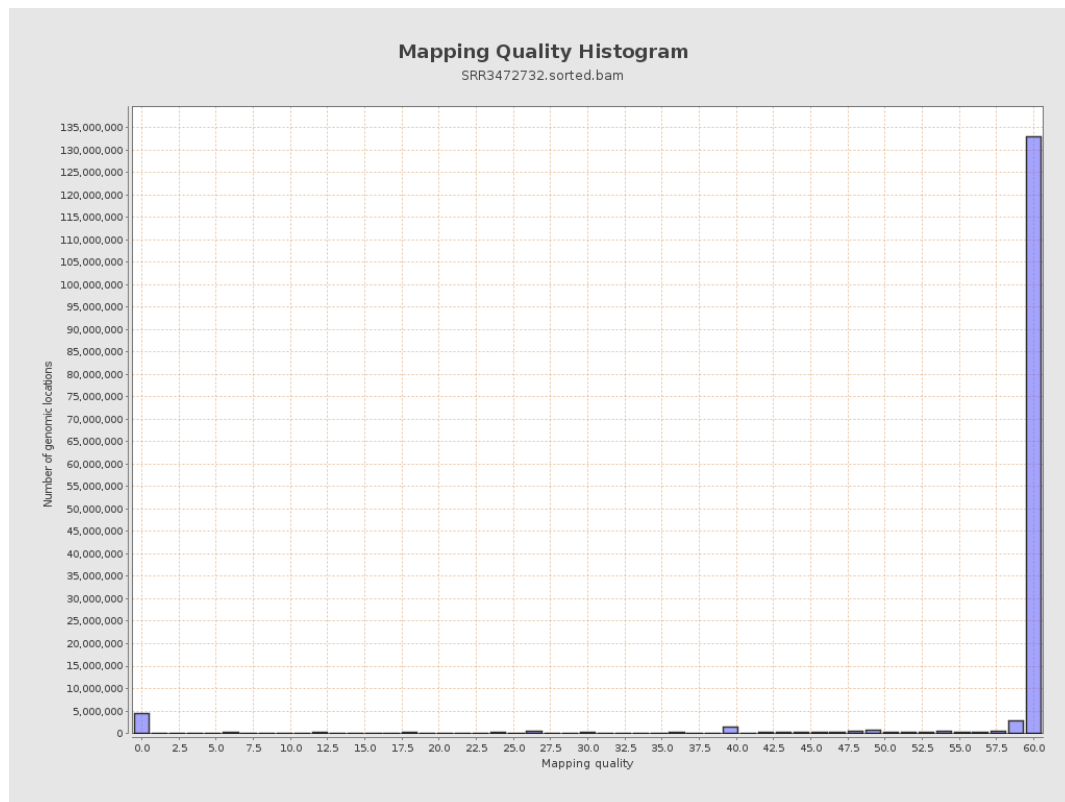
11. Results : Homopolymer Indels



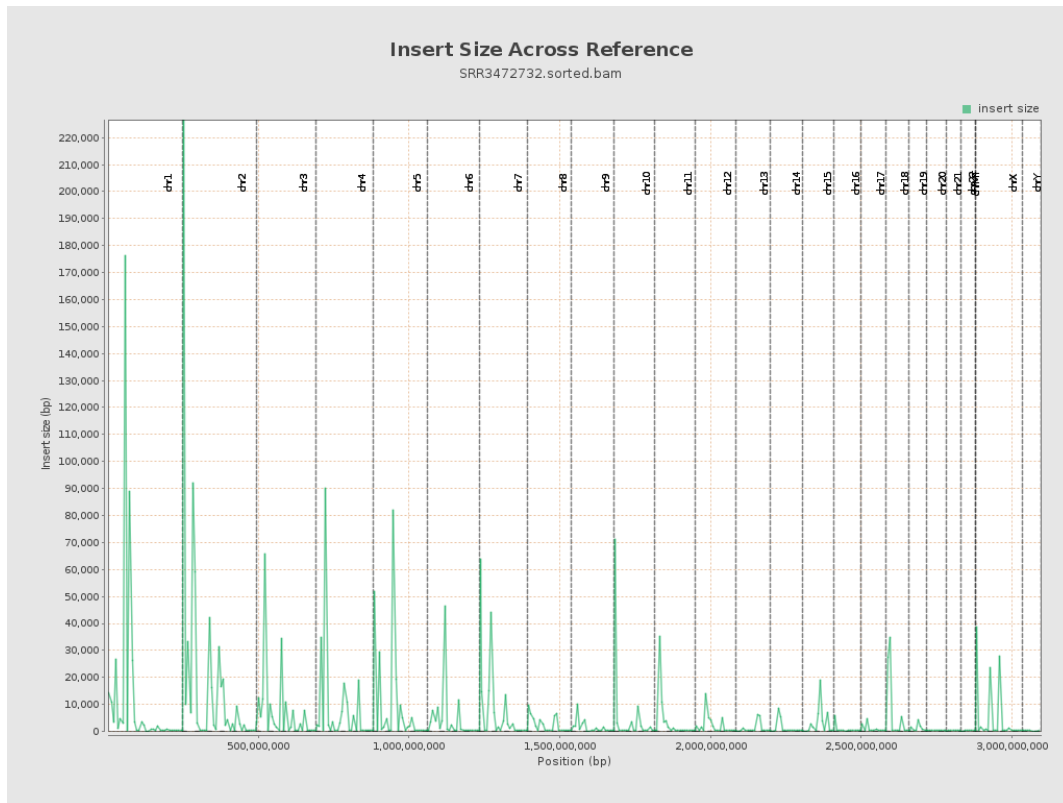
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

