

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/13 01:59:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695932.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/seu_share/home/tujing/220232460/s oftware/bwa-0.7.18/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\t PL:ILLUMINA\tSM:sample_SRR1695 932 /seu_share/home/tujing/220232460/r eference/homo_bwa/hsa.fa SRR1695932_1.fastq.gz SRR1695932_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.18-r1243-dirty)
Analysis date:	Fri Sep 13 01:59:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695932.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,634,480
Mapped reads	14,819,848 / 94.79%
Unmapped reads	814,632 / 5.21%
Mapped paired reads	14,819,848 / 94.79%
Mapped reads, first in pair	7,452,929 / 47.67%
Mapped reads, second in pair	7,366,919 / 47.12%
Mapped reads, both in pair	14,518,960 / 92.87%
Mapped reads, singletons	300,888 / 1.92%
Secondary alignments	0
Supplementary alignments	233,545 / 1.49%
Read min/max/mean length	30 / 100 / 100.6
Duplicated reads (estimated)	4,516,857 / 28.89%
Duplication rate	16.06%
Clipped reads	8,336,967 / 53.32%

2.2. ACGT Content

Number/percentage of A's	355,477,051 / 27.12%
Number/percentage of C's	290,457,823 / 22.16%
Number/percentage of T's	361,538,828 / 27.59%
Number/percentage of G's	302,573,370 / 23.09%
Number/percentage of N's	471,104 / 0.04%

GC Percentage	45.25%
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2.3. Coverage

Mean	0.4235
Standard Deviation	7.1233

2.4. Mapping Quality

Mean Mapping Quality	51.2
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2.5. Insert size

Mean	399,846.17
Standard Deviation	6,107,694.86
P25/Median/P75	276 / 287 / 297

2.6. Mismatches and indels

General error rate	1.07%
Mismatches	13,632,936
Insertions	142,083
Mapped reads with at least one insertion	0.93%
Deletions	193,705
Mapped reads with at least one deletion	1.27%
Homopolymer indels	41.34%

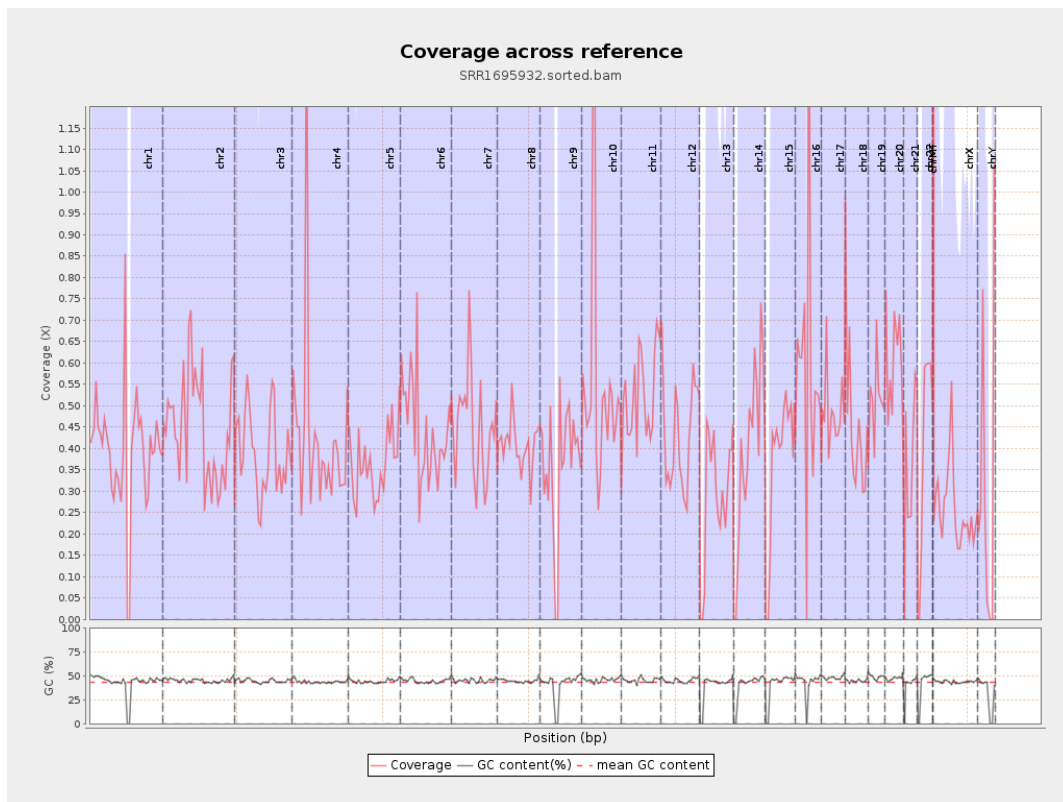
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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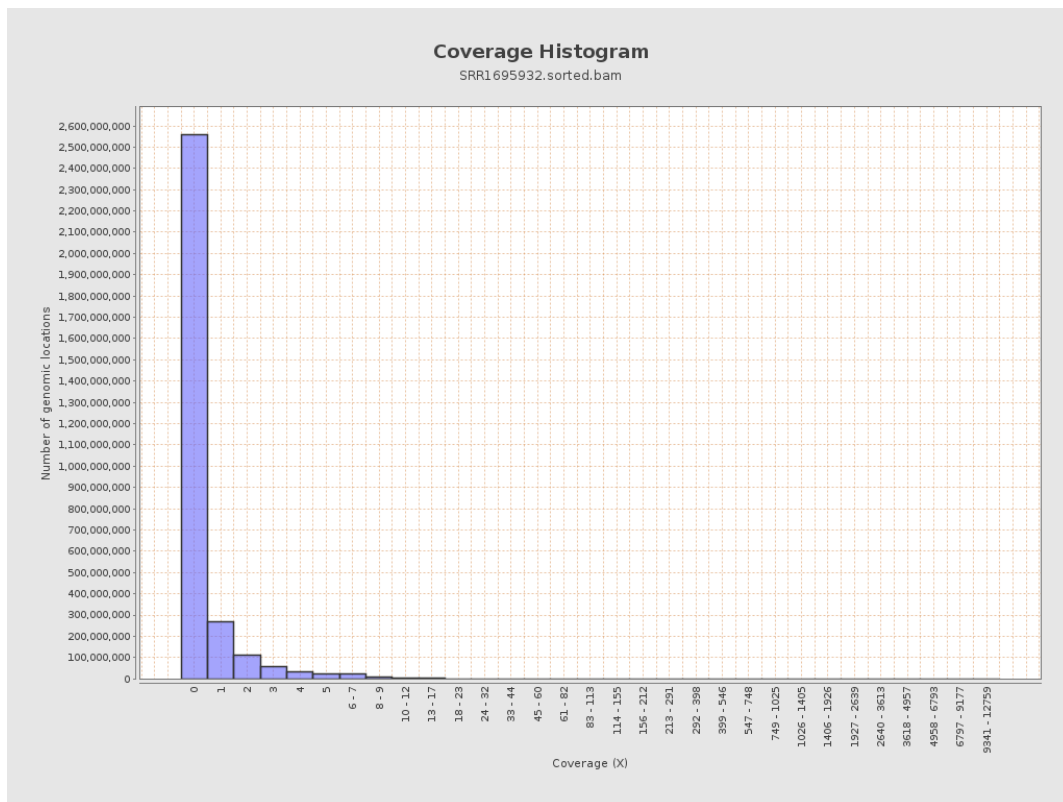
		bases	coverage	deviation
chr1	249250621	97793901	0.3924	10.0818
chr2	243199373	108941107	0.4479	3.6647
chr3	198022430	77069336	0.3892	1.212
chr4	191154276	82579903	0.432	7.0891
chr5	180915260	66736645	0.3689	1.3927
chr6	171115067	75122941	0.439	6.6122
chr7	159138663	71848744	0.4515	5.0033
chr8	146364022	59411516	0.4059	2.1748
chr9	141213431	50522457	0.3578	3.9248
chr10	135534747	73357075	0.5412	13.8095
chr11	135006516	70831823	0.5247	1.7162
chr12	133851895	58135989	0.4343	1.6616
chr13	115169878	33019736	0.2867	1.0126
chr14	107349540	42822655	0.3989	1.3275
chr15	102531392	37328746	0.3641	1.1513
chr16	90354753	53255092	0.5894	11.0967
chr17	81195210	39567810	0.4873	4.6031
chr18	78077248	34360410	0.4401	9.2458
chr19	59128983	30660269	0.5185	12.2849
chr20	63025520	37979752	0.6026	3.0513
chr21	48129895	18031896	0.3747	3.4232
chr22	51304566	20760250	0.4046	1.3192
chrMT	16571	10950717	660.8362	1,435.0329
chrX	155270560	40353680	0.2599	2.8715

chrY	59373566	19506788	0.3285	8.7111
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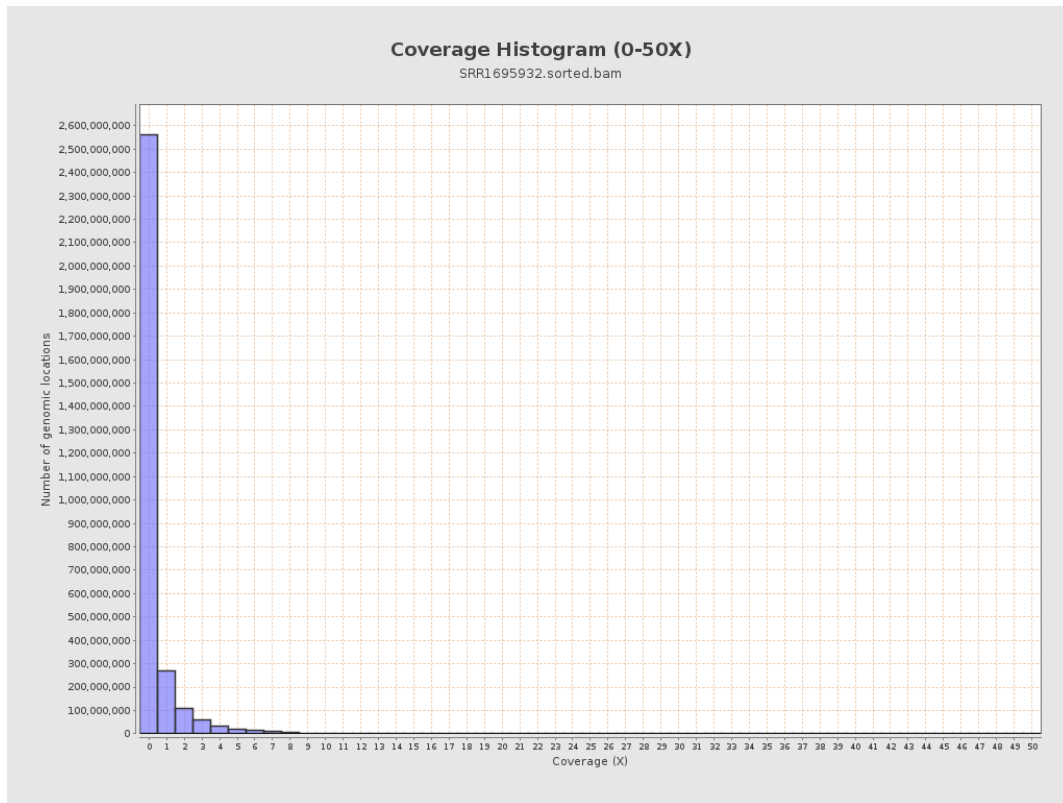
3. Results : Coverage across reference



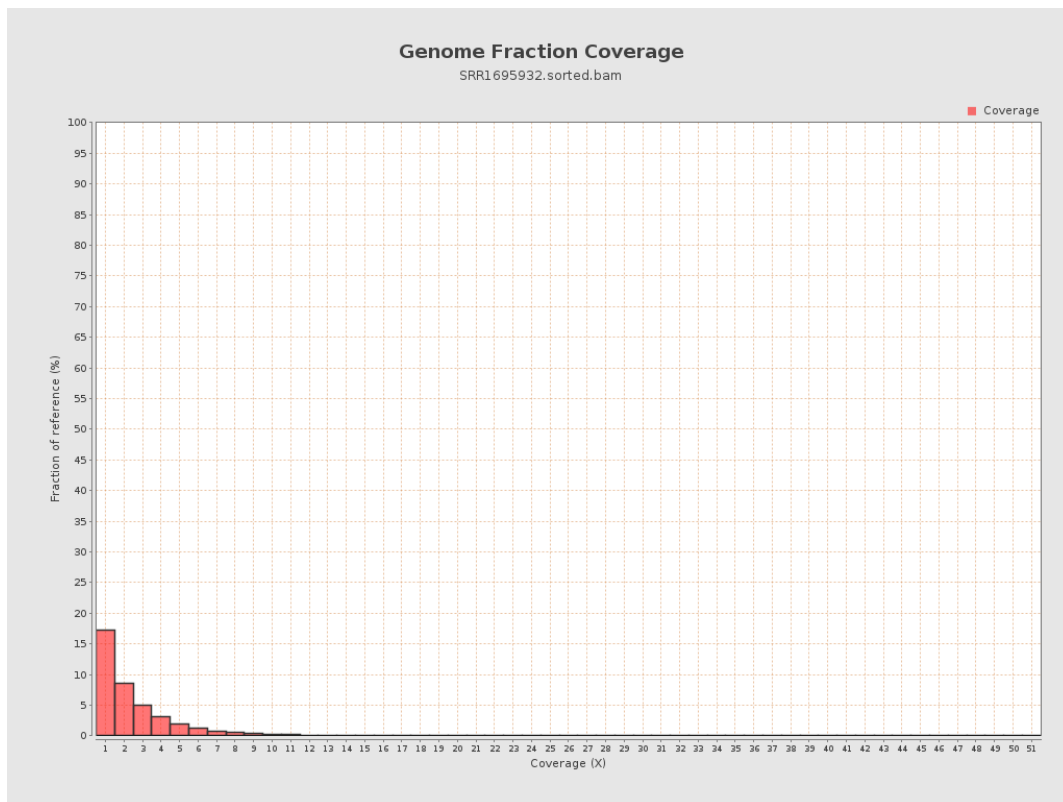
4. Results : Coverage Histogram



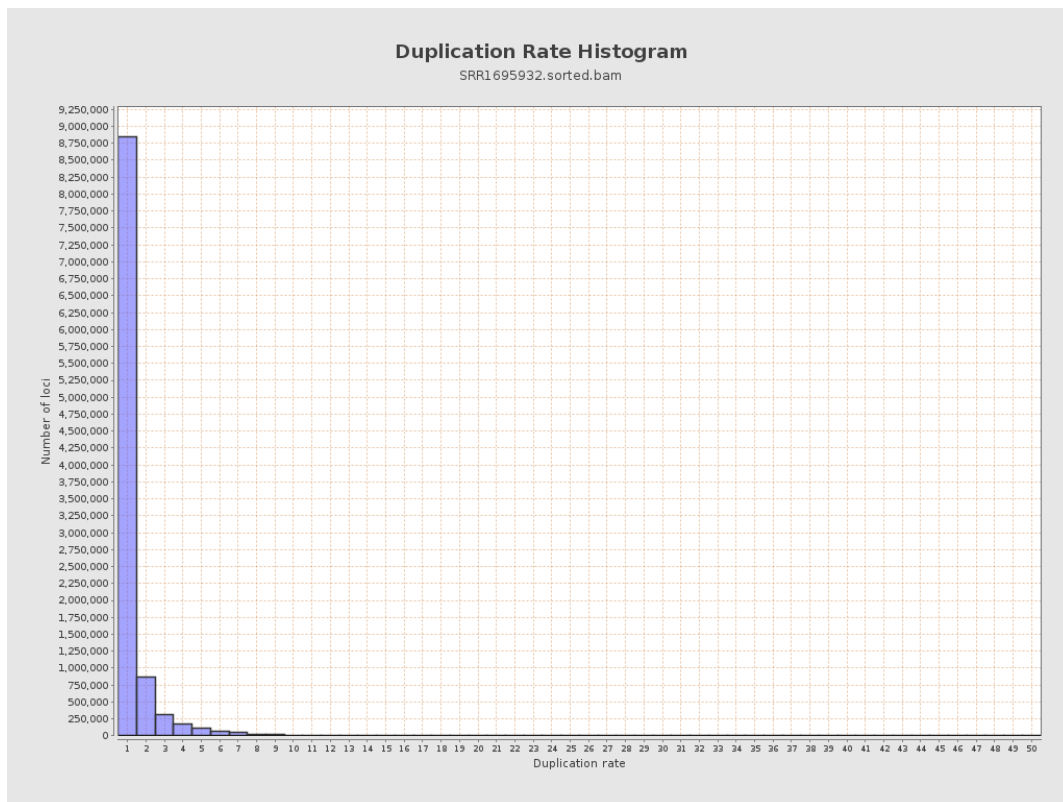
5. Results : Coverage Histogram (0-50X)



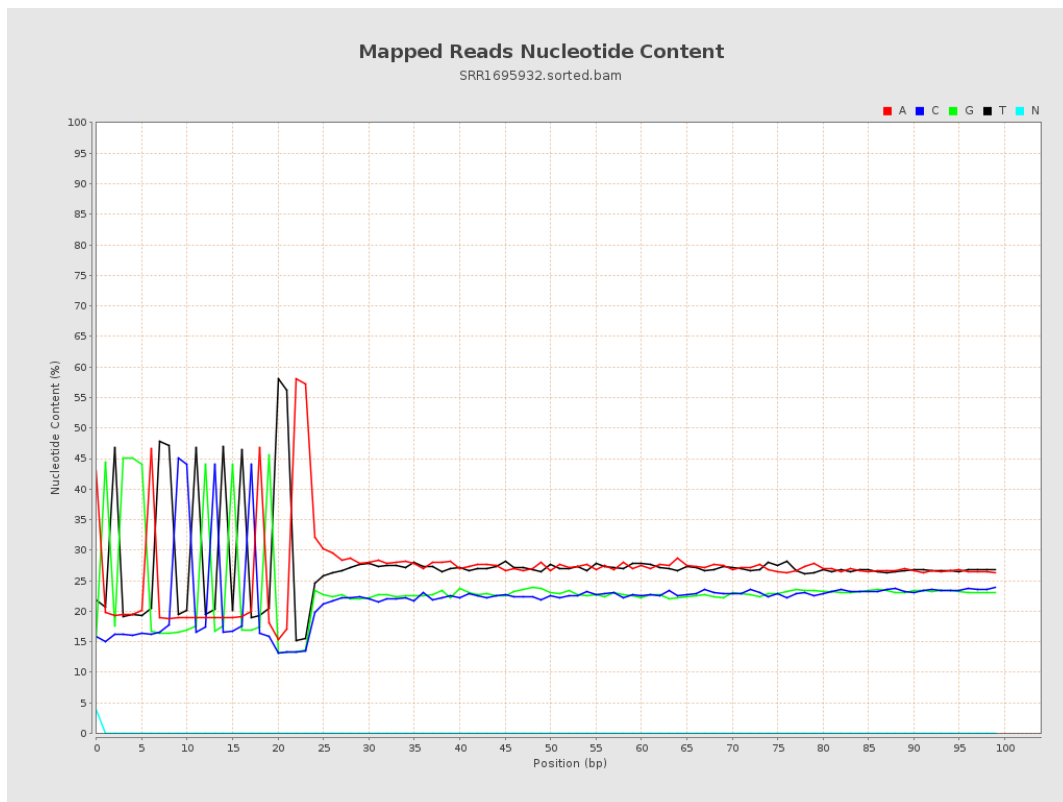
6. Results : Genome Fraction Coverage



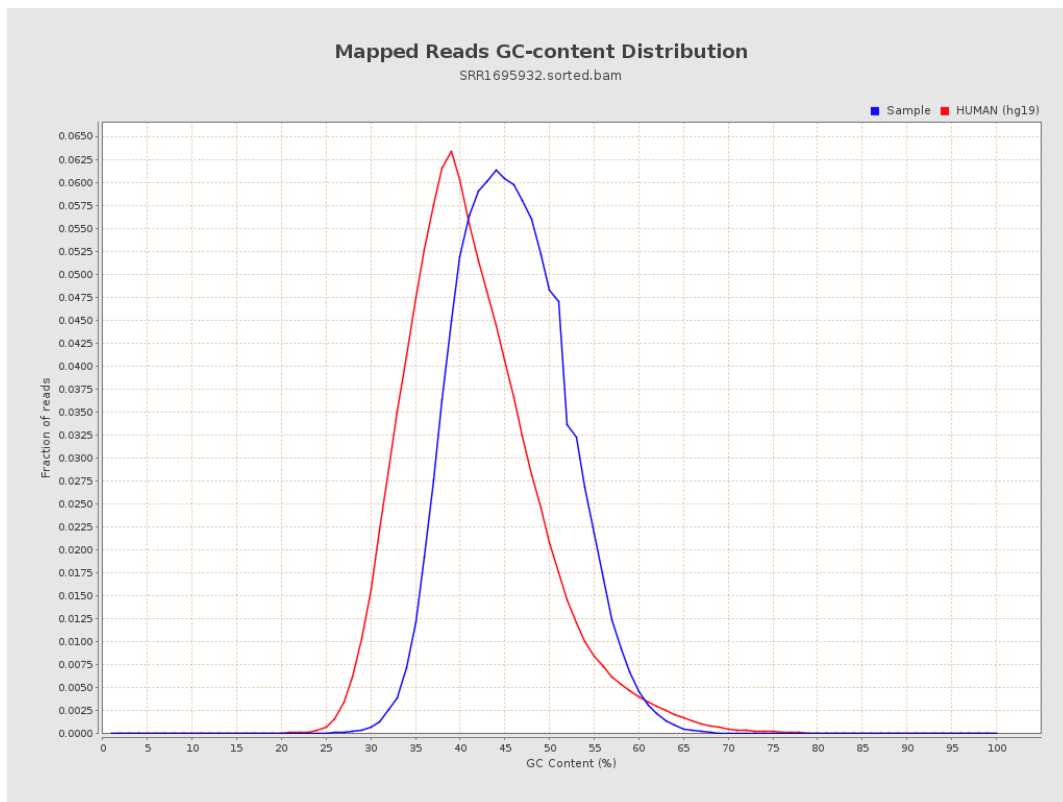
7. Results : Duplication Rate Histogram



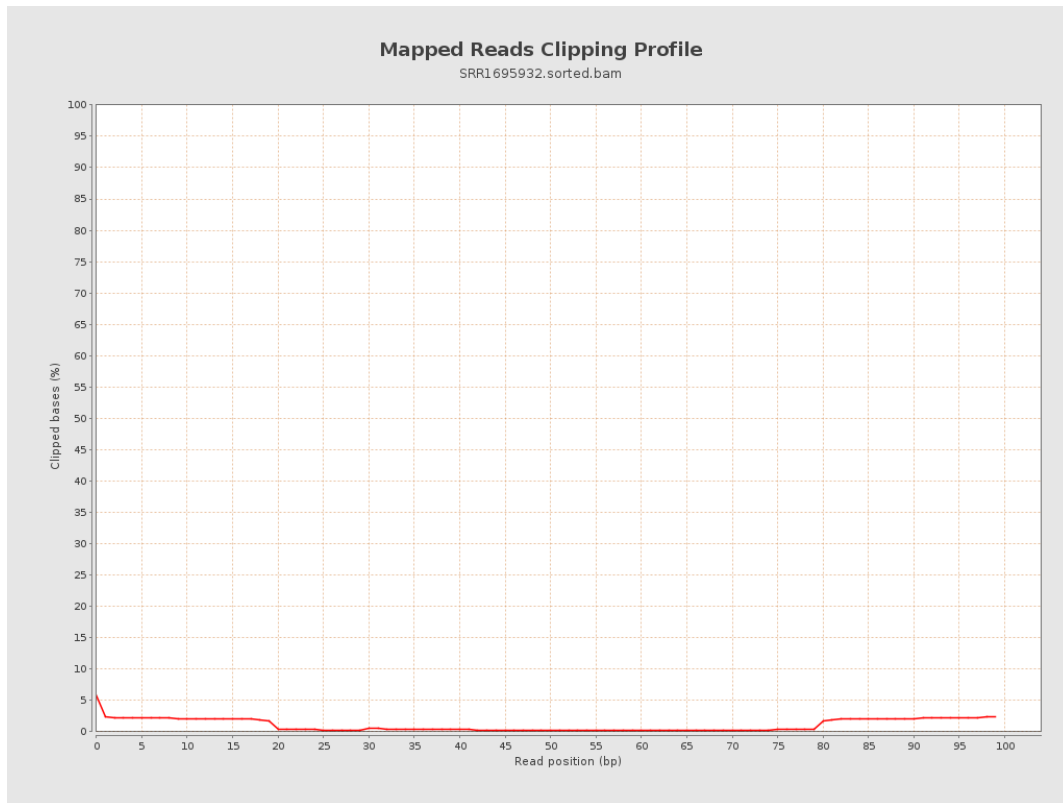
8. Results : Mapped Reads Nucleotide Content



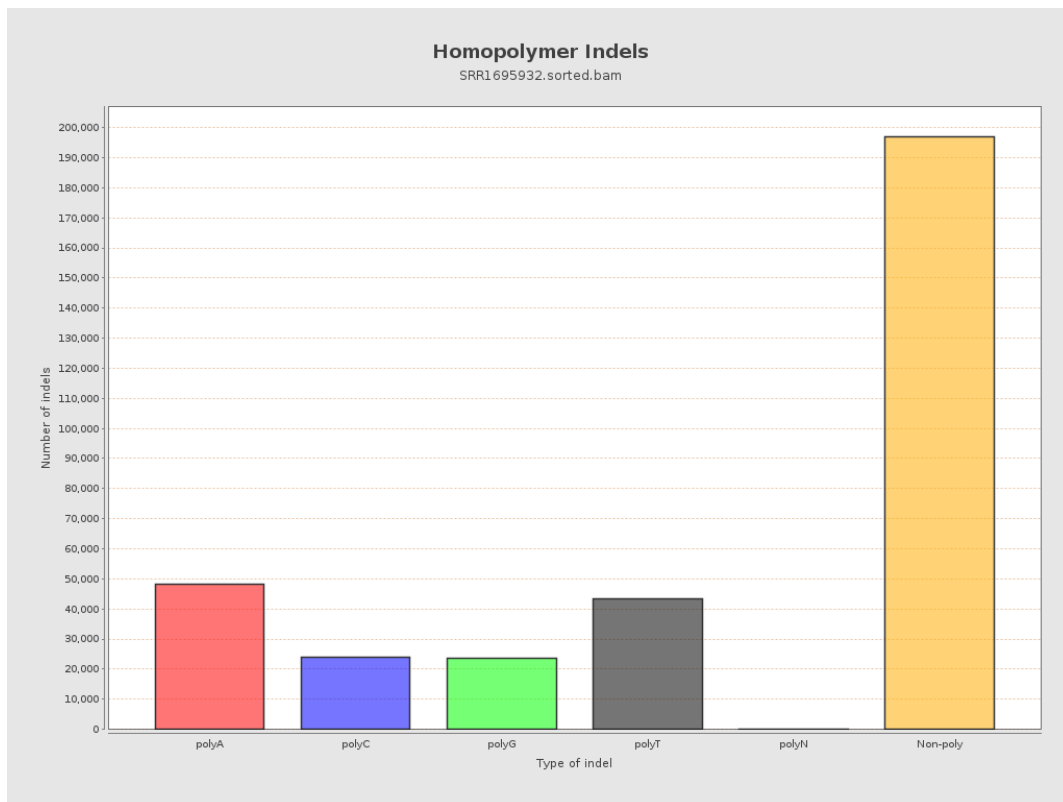
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



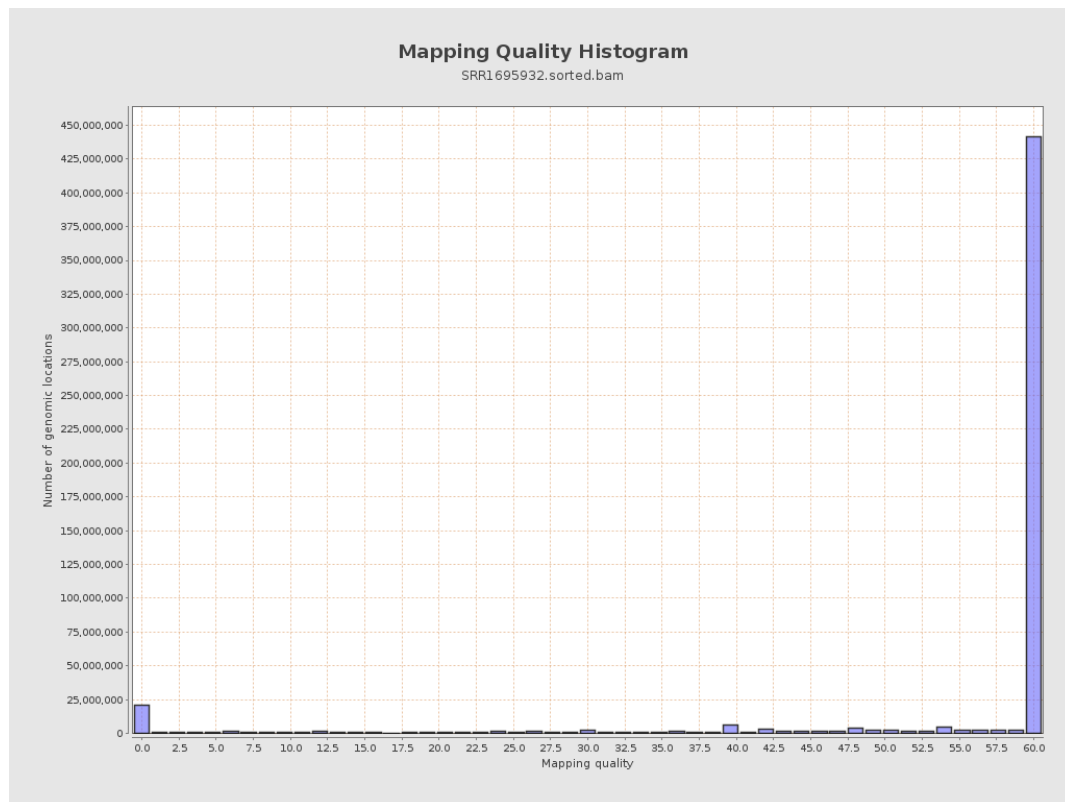
11. Results : Homopolymer Indels



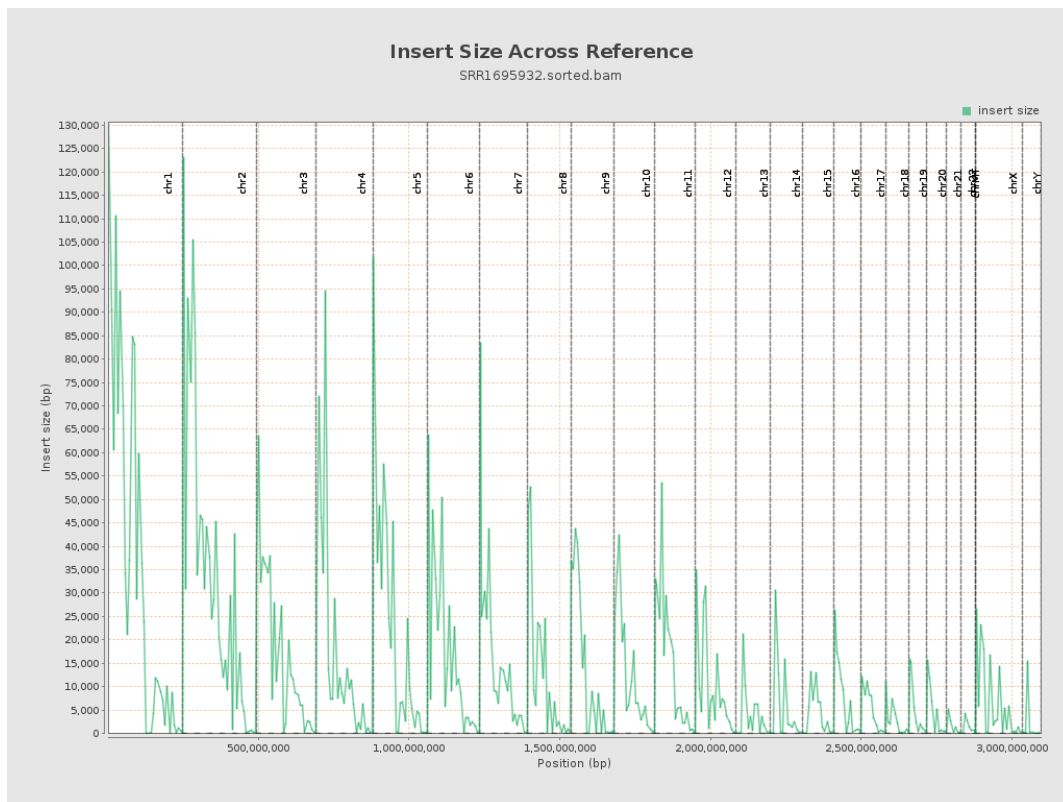
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

