

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/13 18:09:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695956.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/seu_share/home/tujing/220232460/software/bwa-0.7.18/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR1695956 /seu_share/home/tujing/220232460/reference/homo_bwa/hsa.fa SRR1695956_1.fastq.gz SRR1695956_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 18:09:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695956.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	349,287,082
Mapped reads	344,385,903 / 98.6%
Unmapped reads	4,901,179 / 1.4%
Mapped paired reads	344,385,903 / 98.6%
Mapped reads, first in pair	173,291,127 / 49.61%
Mapped reads, second in pair	171,094,776 / 48.98%
Mapped reads, both in pair	341,058,108 / 97.64%
Mapped reads, singletons	3,327,795 / 0.95%
Secondary alignments	0
Supplementary alignments	5,358,008 / 1.53%
Read min/max/mean length	30 / 100 / 100.63
Duplicated reads (estimated)	59,281,043 / 16.97%
Duplication rate	13.82%
Clipped reads	29,336,209 / 8.4%

2.2. ACGT Content

Number/percentage of A's	9,481,607,459 / 27.85%
Number/percentage of C's	7,445,347,752 / 21.87%
Number/percentage of T's	9,434,484,579 / 27.71%
Number/percentage of G's	7,676,012,417 / 22.54%
Number/percentage of N's	10,516,769 / 0.03%

GC Percentage	44.41%
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2.3. Coverage

Mean	11.0022
Standard Deviation	41.0453

2.4. Mapping Quality

Mean Mapping Quality	53.9
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2.5. Insert size

Mean	80,894.89
Standard Deviation	2,720,263.28
P25/Median/P75	313 / 321 / 329

2.6. Mismatches and indels

General error rate	0.52%
Mismatches	166,803,691
Insertions	5,338,750
Mapped reads with at least one insertion	1.49%
Deletions	4,396,865
Mapped reads with at least one deletion	1.23%
Homopolymer indels	40.69%

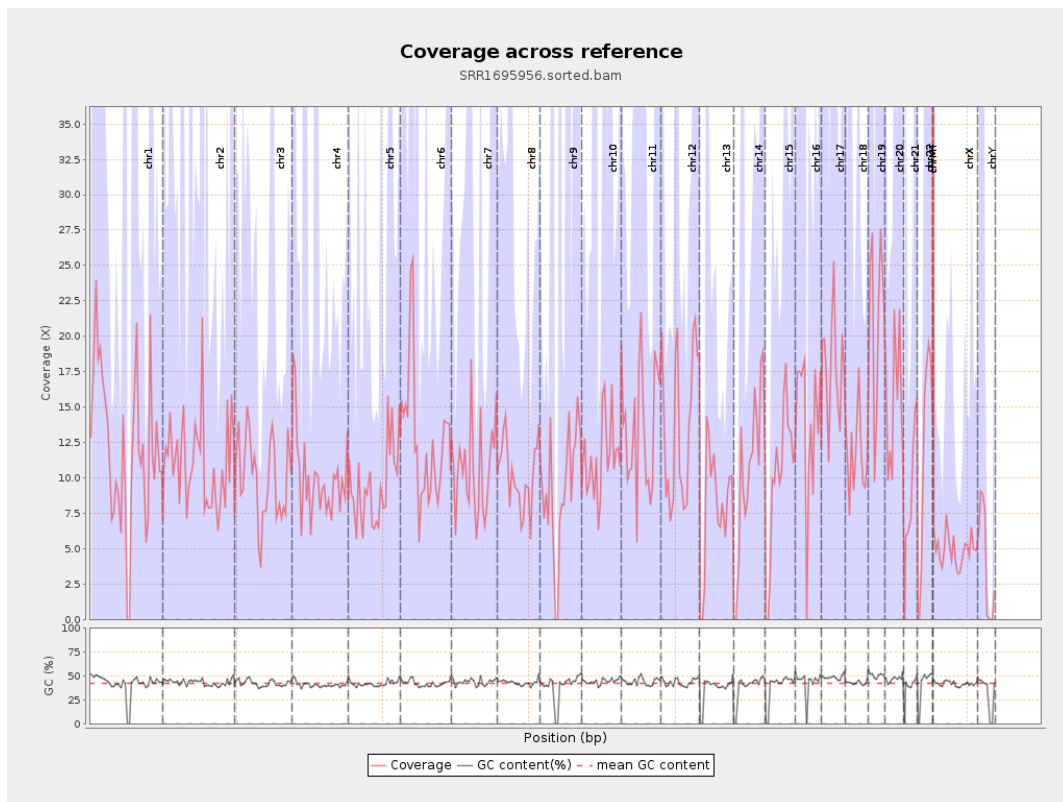
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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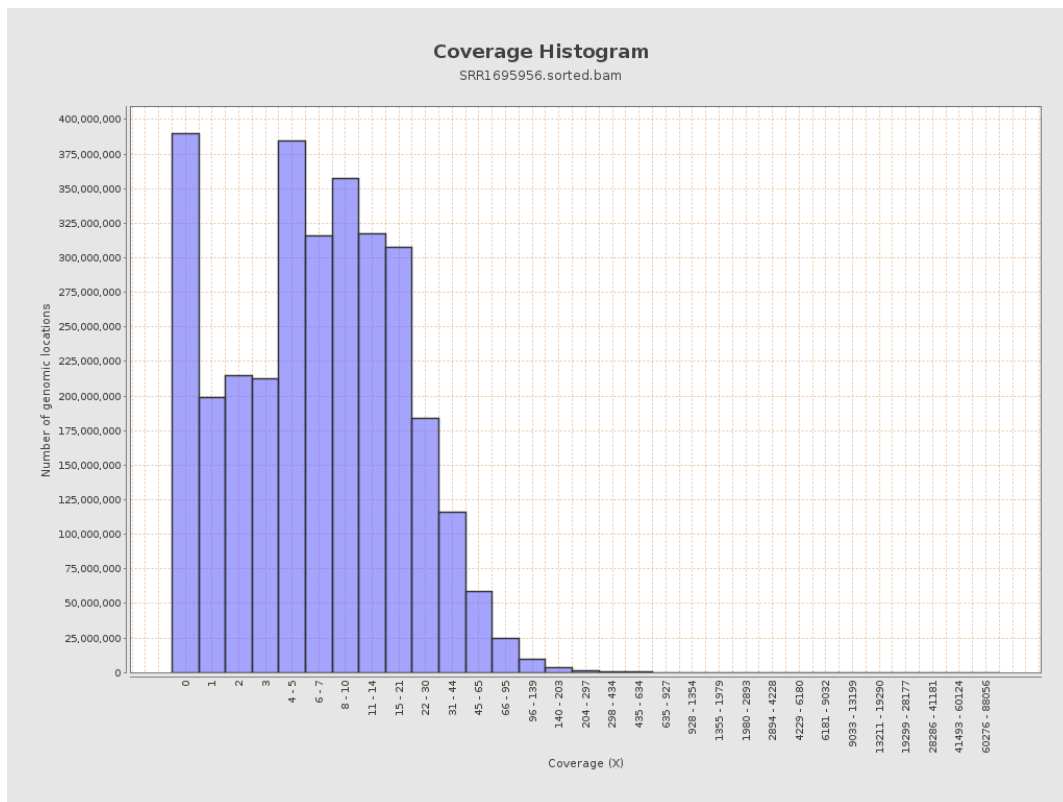
		bases	coverage	deviation
chr1	249250621	3010636856	12.0788	33.886
chr2	243199373	2688576604	11.055	84.165
chr3	198022430	1976455587	9.981	18.1232
chr4	191154276	1906011611	9.9711	24.3677
chr5	180915260	1719360439	9.5037	19.2787
chr6	171115067	2158472111	12.6142	30.8121
chr7	159138663	1692910224	10.638	23.2724
chr8	146364022	1486953634	10.1593	28.7878
chr9	141213431	1280452151	9.0675	59.4536
chr10	135534747	1547428500	11.4172	59.6012
chr11	135006516	1815010353	13.4439	27.7737
chr12	133851895	1848793060	13.8122	20.5335
chr13	115169878	924456064	8.0269	18.239
chr14	107349540	1128225645	10.5098	41.5703
chr15	102531392	1016204374	9.9112	22.2951
chr16	90354753	1241232186	13.7373	62.0202
chr17	81195210	1457921673	17.9558	35.191
chr18	78077248	894803238	11.4605	43.3401
chr19	59128983	1236567435	20.9131	37.5522
chr20	63025520	952540831	15.1136	22.972
chr21	48129895	432194237	8.9797	25.1929
chr22	51304566	609954654	11.8889	24.4006
chrMT	16571	22393065	1,351.3406	477.2331
chrX	155270560	764465211	4.9234	12.5018

chrY	59373566	247444017	4.1676	73.2901
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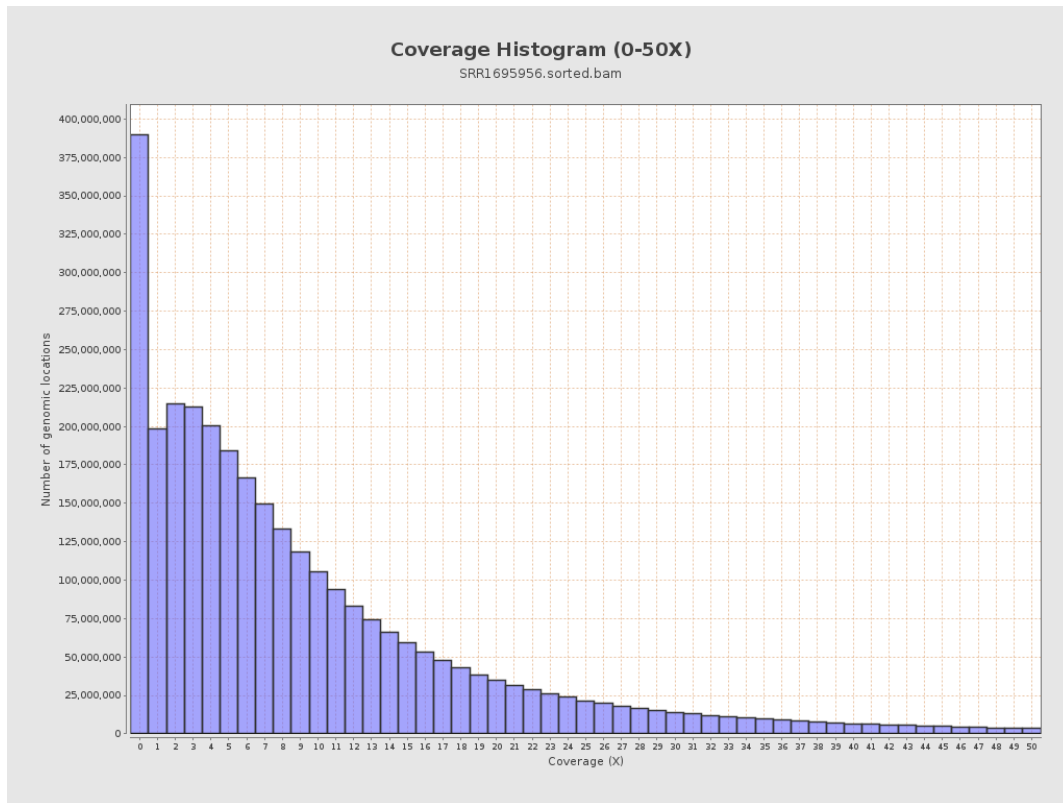
3. Results : Coverage across reference



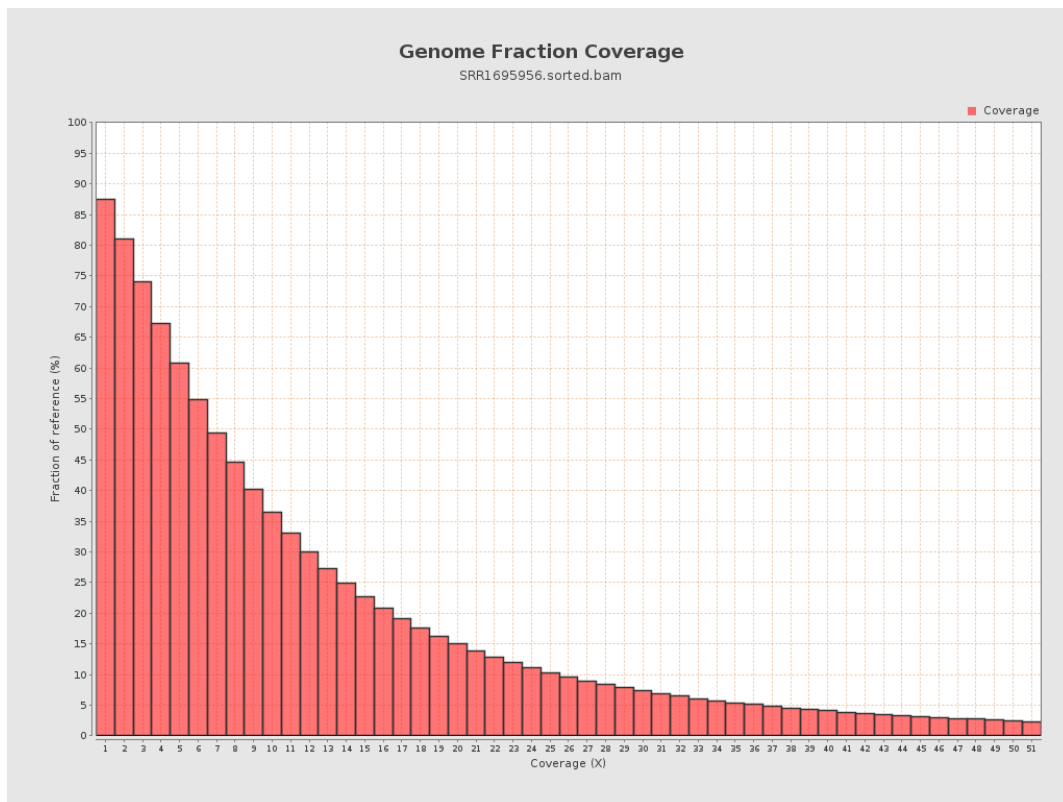
4. Results : Coverage Histogram



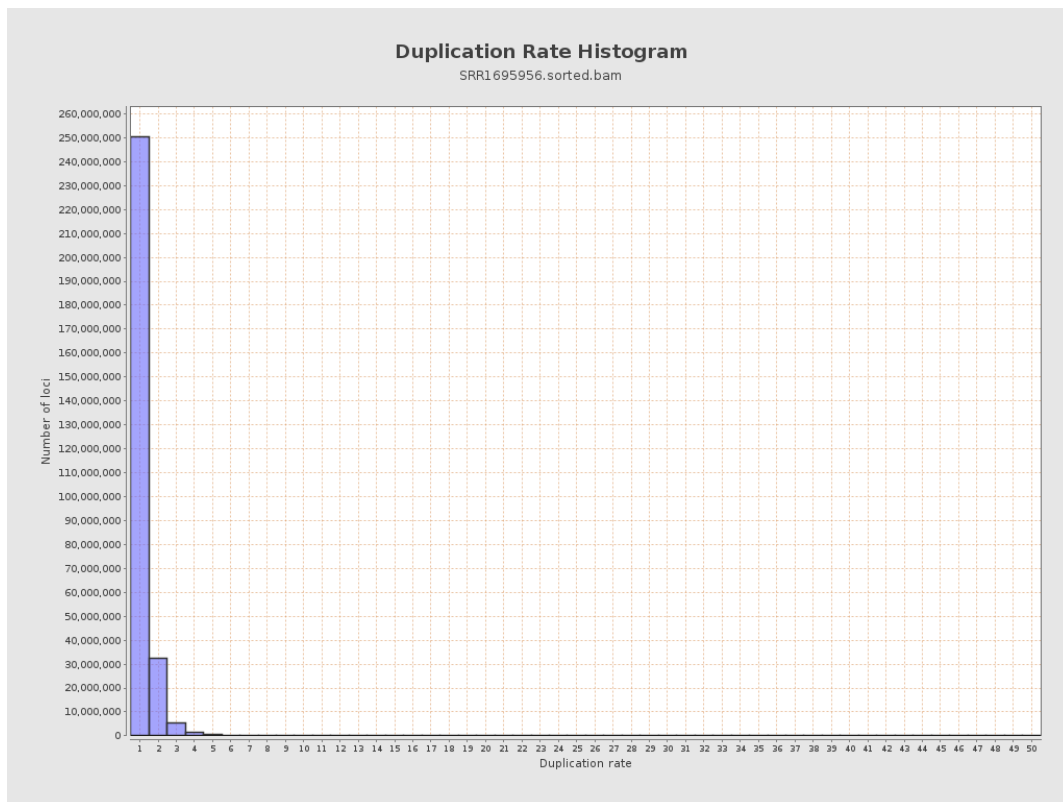
5. Results : Coverage Histogram (0-50X)



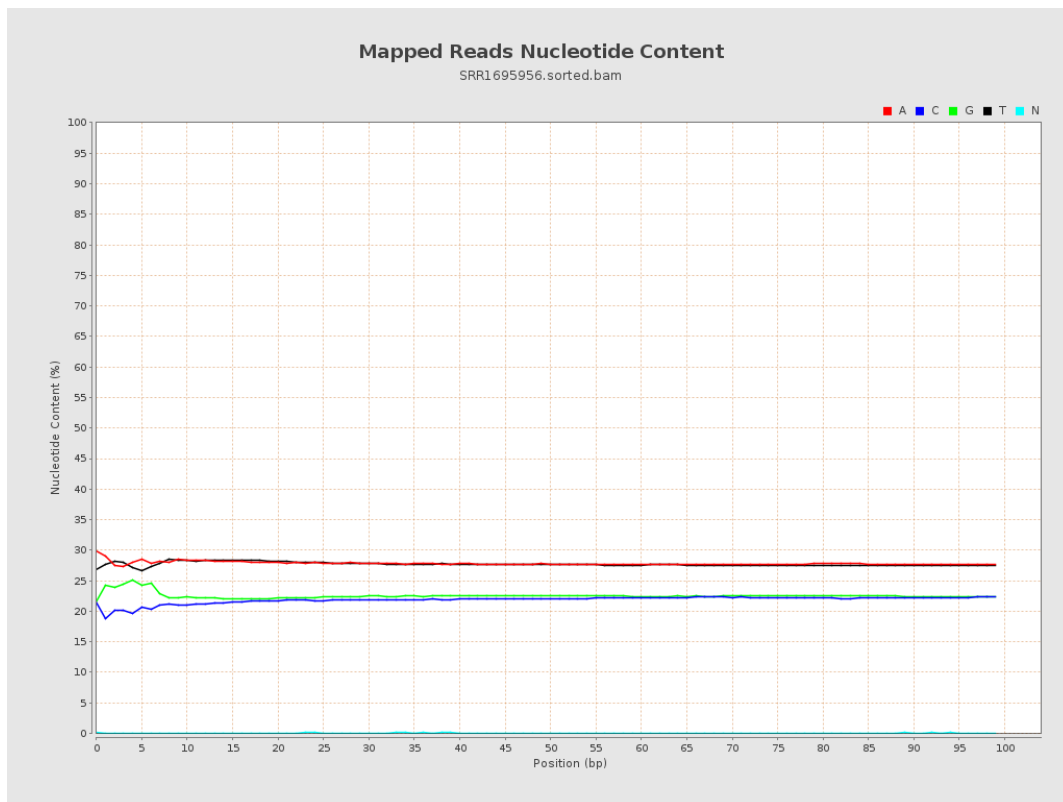
6. Results : Genome Fraction Coverage



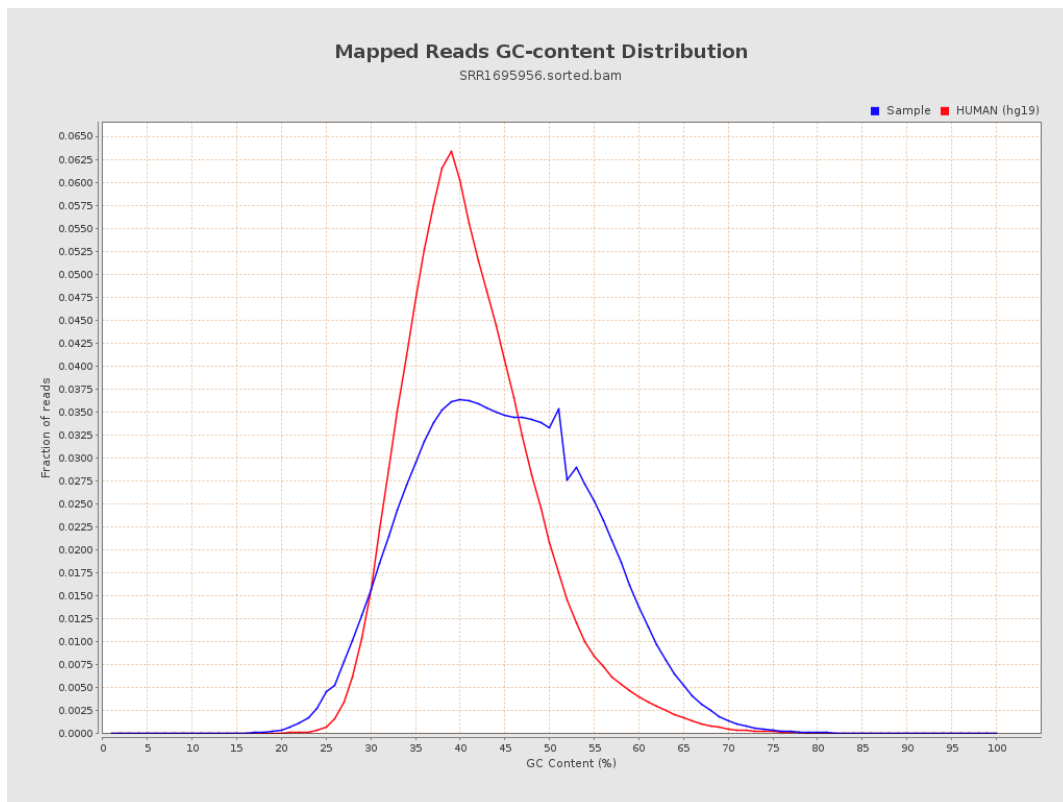
7. Results : Duplication Rate Histogram



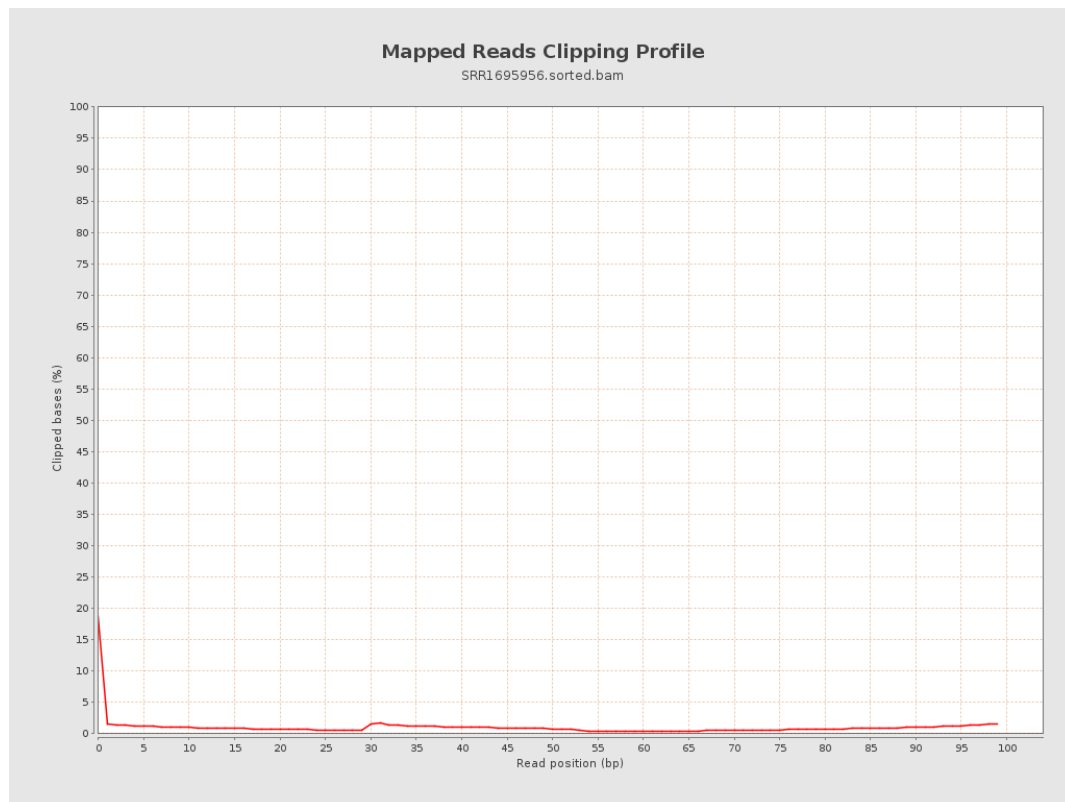
8. Results : Mapped Reads Nucleotide Content



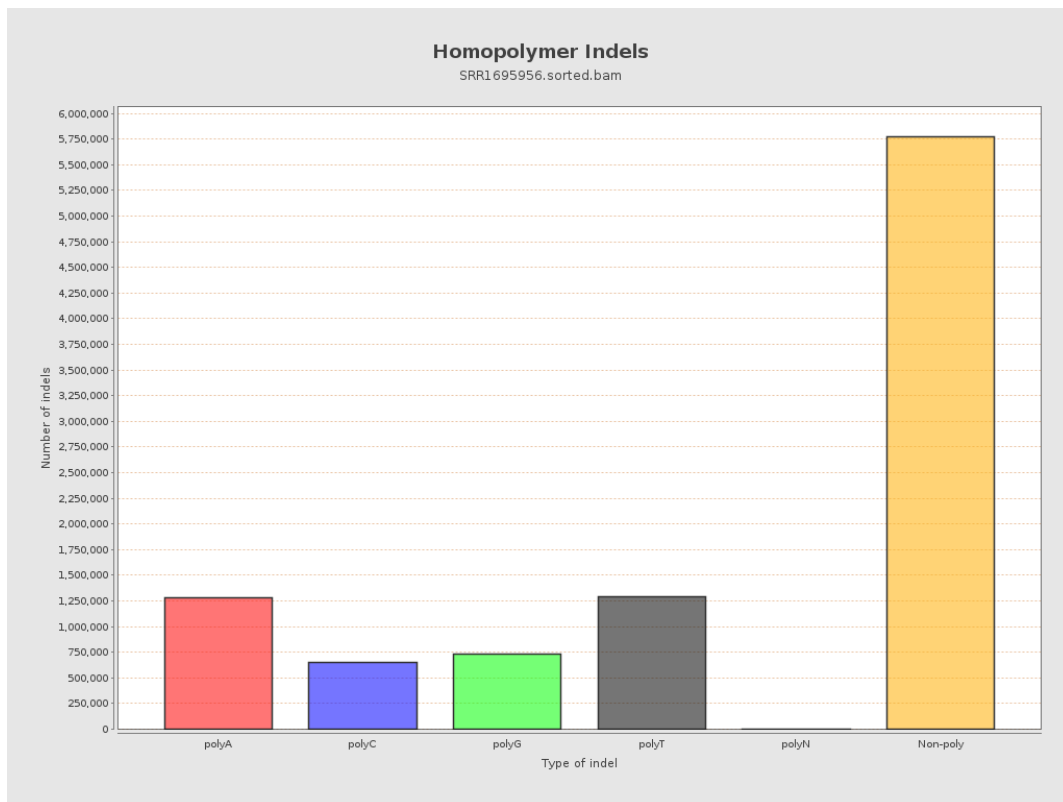
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



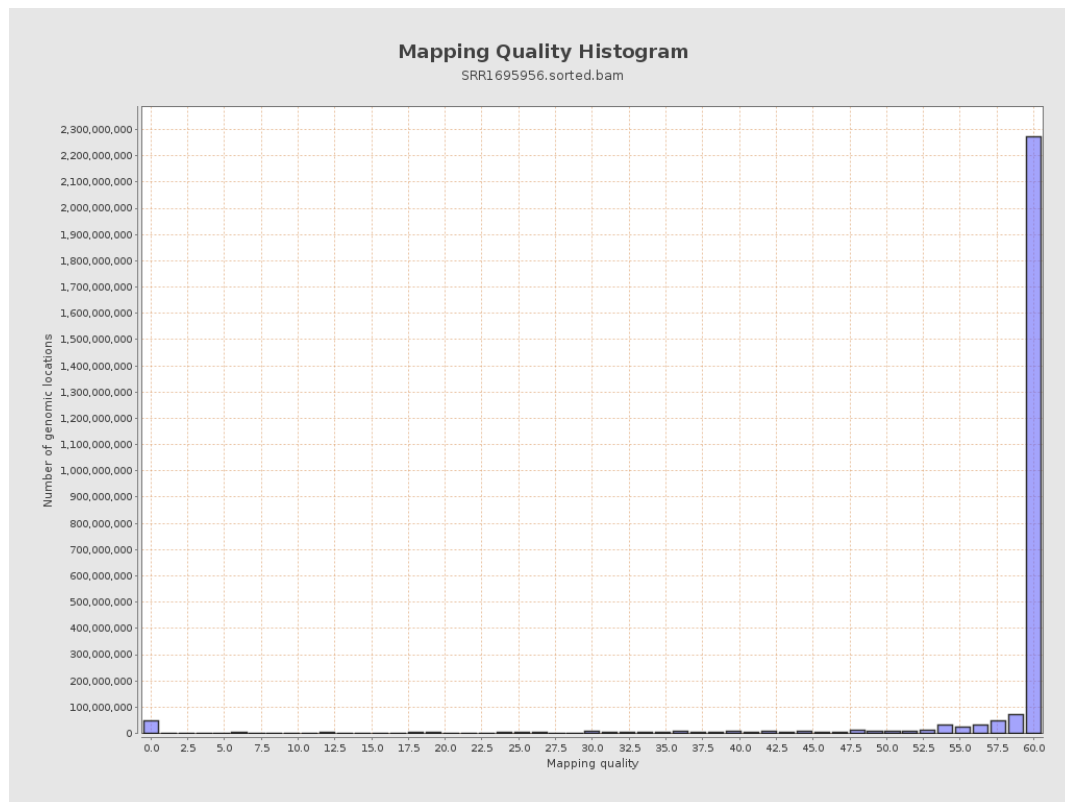
11. Results : Homopolymer Indels



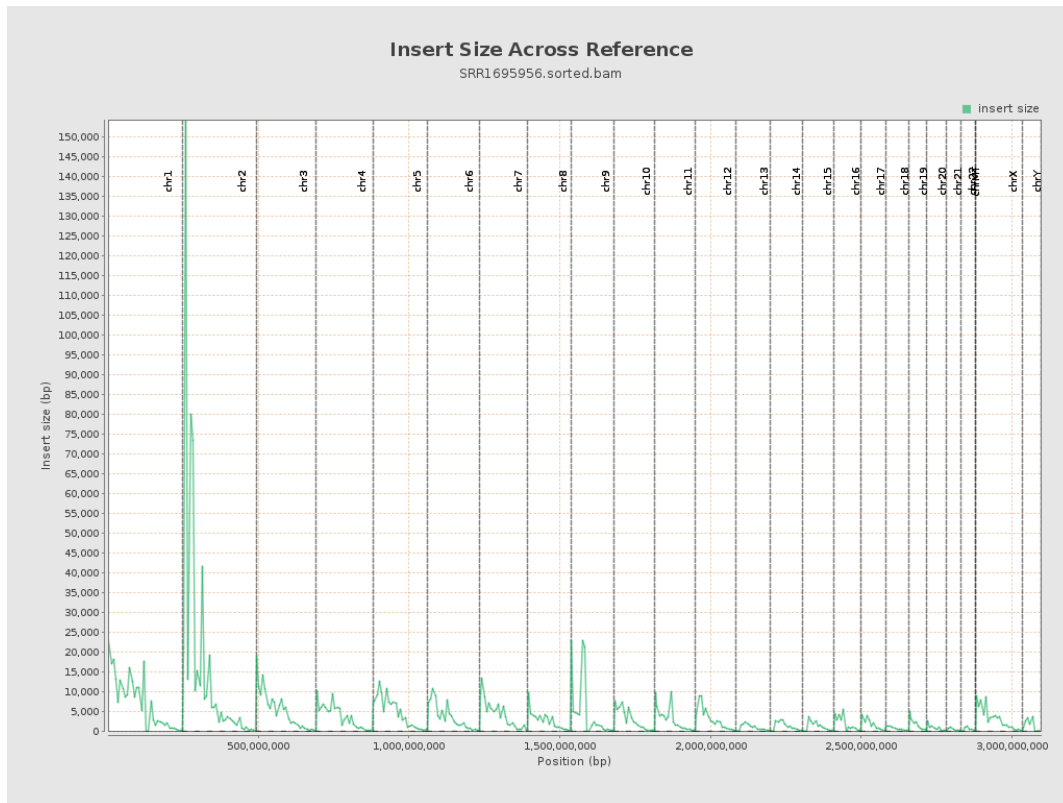
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

