

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/13 12:10:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695948.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 948 /seu_share/home/tujing/220232460/r eference/homo_bwa/hsa.fa SRR1695948_1.fastq.gz SRR1695948_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 12:10:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695948.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	344,762,632
Mapped reads	342,929,621 / 99.47%
Unmapped reads	1,833,011 / 0.53%
Mapped paired reads	342,929,621 / 99.47%
Mapped reads, first in pair	171,763,418 / 49.82%
Mapped reads, second in pair	171,166,203 / 49.65%
Mapped reads, both in pair	341,824,294 / 99.15%
Mapped reads, singletons	1,105,327 / 0.32%
Secondary alignments	0
Supplementary alignments	3,024,478 / 0.88%
Read min/max/mean length	30 / 100 / 100.36
Duplicated reads (estimated)	37,926,616 / 11%
Duplication rate	10.14%
Clipped reads	18,345,627 / 5.32%

2.2. ACGT Content

Number/percentage of A's	9,799,768,395 / 28.78%
Number/percentage of C's	7,141,836,548 / 20.98%
Number/percentage of T's	9,754,197,838 / 28.65%
Number/percentage of G's	7,343,725,075 / 21.57%
Number/percentage of N's	7,911,813 / 0.02%

GC Percentage	42.55%
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2.3. Coverage

Mean	11.0009
Standard Deviation	16.4549

2.4. Mapping Quality

Mean Mapping Quality	54.12
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2.5. Insert size

Mean	59,992.58
Standard Deviation	2,371,860.51
P25/Median/P75	312 / 320 / 327

2.6. Mismatches and indels

General error rate	0.39%
Mismatches	127,582,150
Insertions	3,400,469
Mapped reads with at least one insertion	0.97%
Deletions	3,385,112
Mapped reads with at least one deletion	0.96%
Homopolymer indels	45.22%

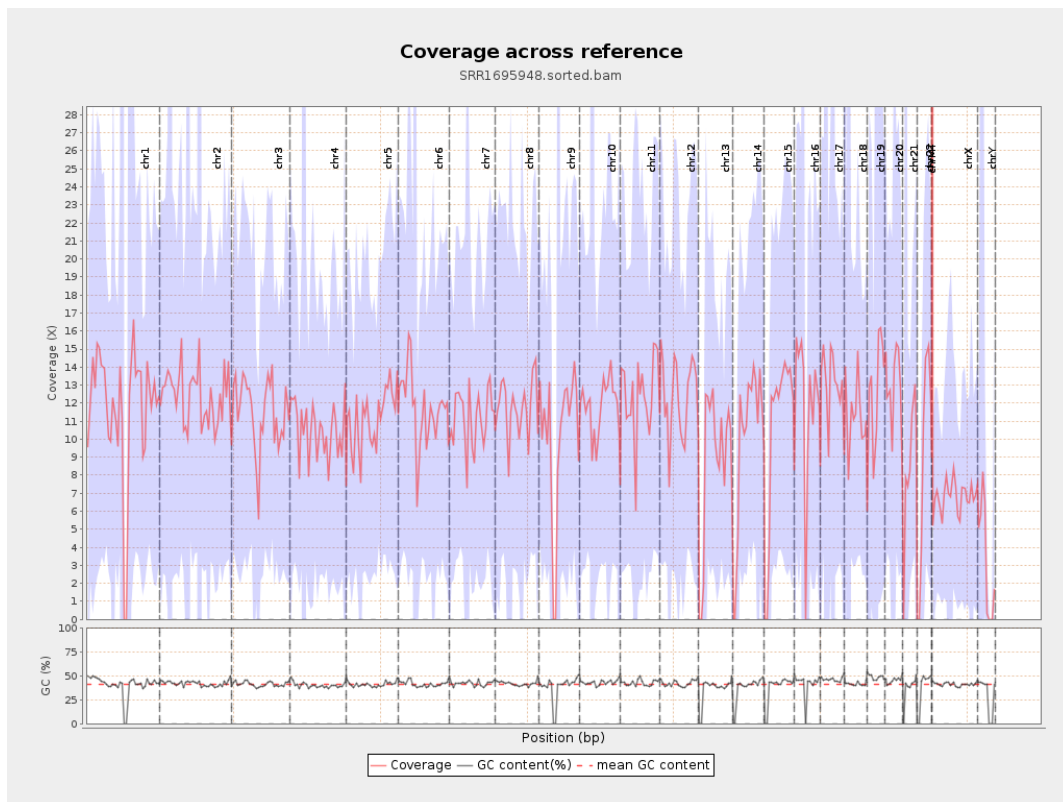
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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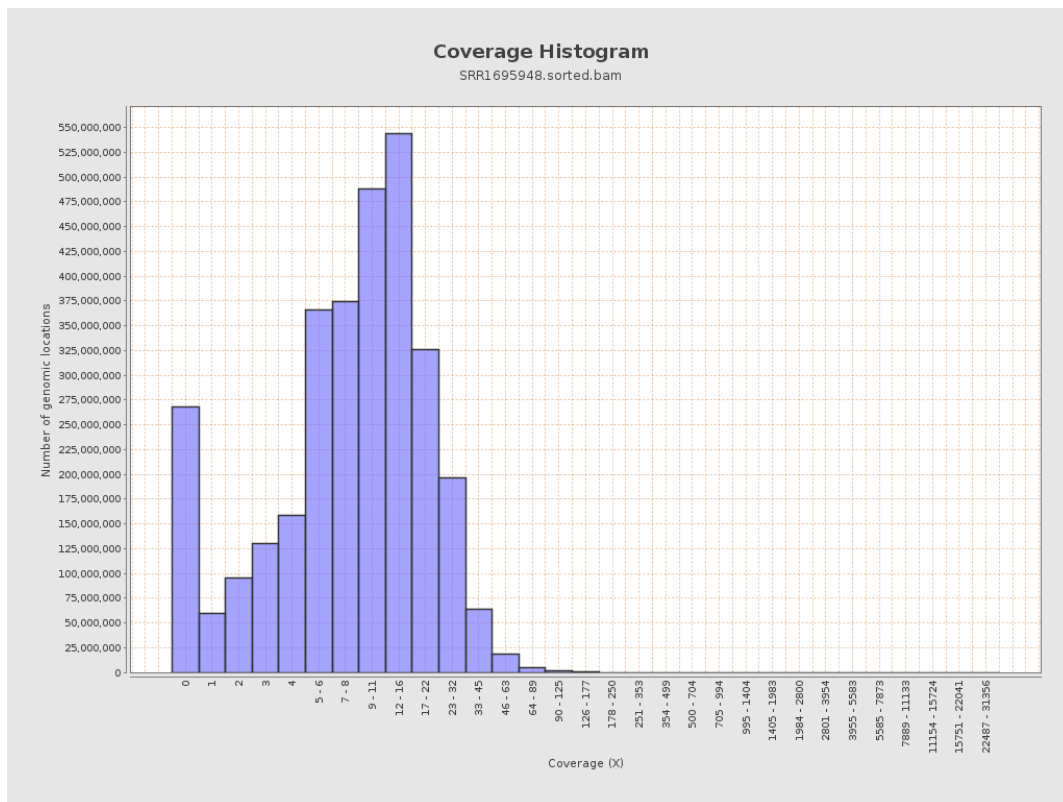
		bases	coverage	deviation
chr1	249250621	2943028516	11.8075	22.7185
chr2	243199373	3014306654	12.3944	27.8698
chr3	198022430	2277113107	11.4993	8.7026
chr4	191154276	2006511347	10.4968	14.3747
chr5	180915260	2023504708	11.1848	8.6093
chr6	171115067	2004350232	11.7135	11.8347
chr7	159138663	1773652793	11.1453	10.561
chr8	146364022	1721674347	11.763	10.3182
chr9	141213431	1421733109	10.068	14.2391
chr10	135534747	1607268935	11.8587	18.2266
chr11	135006516	1675023236	12.407	11.2647
chr12	133851895	1654770812	12.3627	10.2417
chr13	115169878	1018725548	8.8454	8.7381
chr14	107349540	1076671405	10.0296	9.9801
chr15	102531392	1080895644	10.5421	10.2286
chr16	90354753	1063200337	11.767	15.0668
chr17	81195210	1057740286	13.0271	17.8792
chr18	78077248	892543494	11.4315	24.974
chr19	59128983	759536314	12.8454	18.1938
chr20	63025520	815354171	12.9369	11.7698
chr21	48129895	423255275	8.794	21.4095
chr22	51304566	458714127	8.941	11.0396
chrMT	16571	33054026	1,994.6911	609.7502
chrX	155270560	1052459750	6.7782	6.605

chrY	59373566	200254006	3.3728	18.6626
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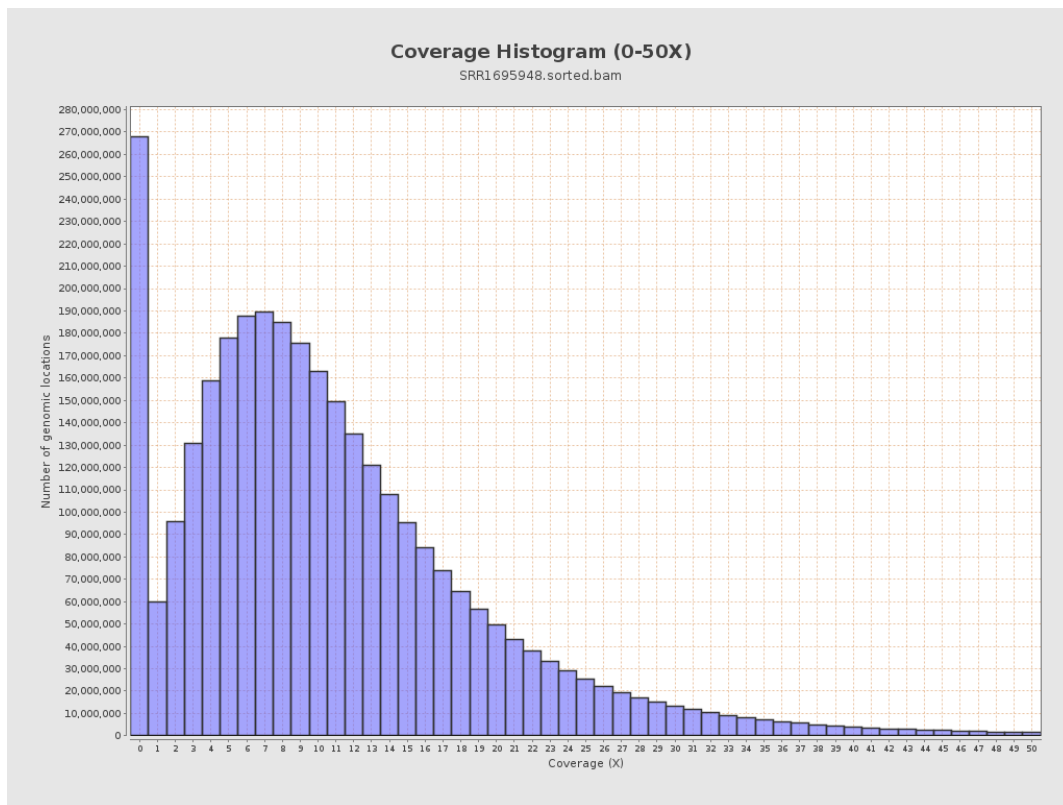
3. Results : Coverage across reference



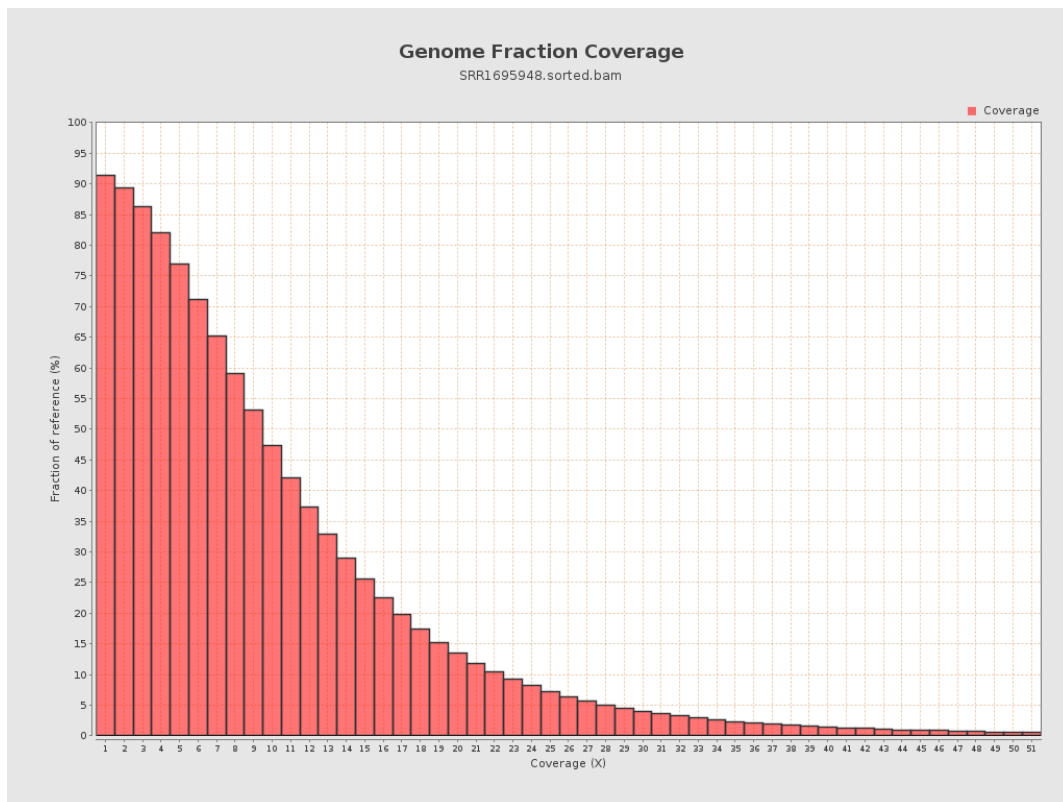
4. Results : Coverage Histogram



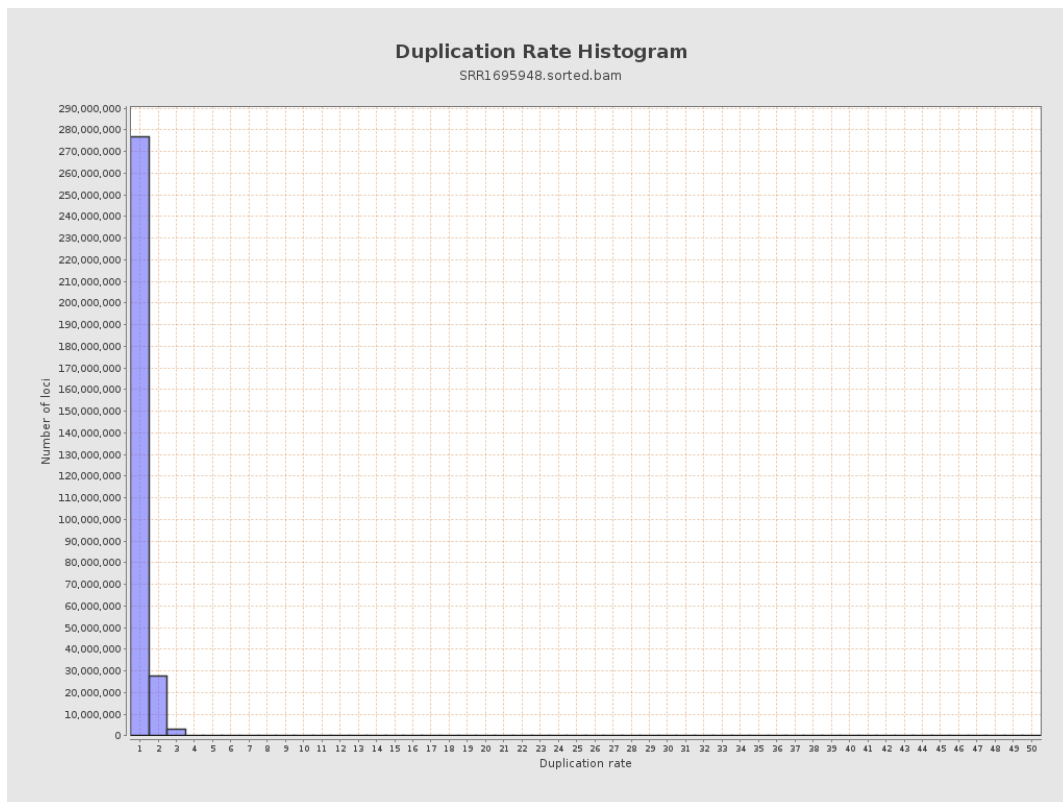
5. Results : Coverage Histogram (0-50X)



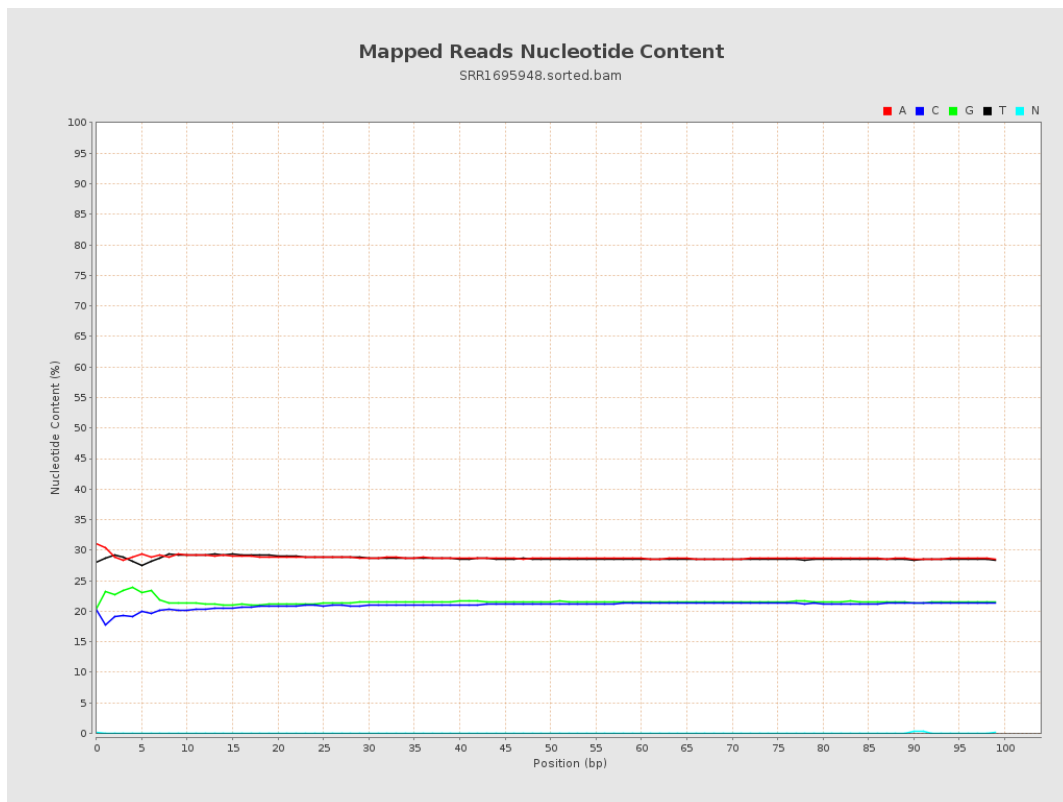
6. Results : Genome Fraction Coverage



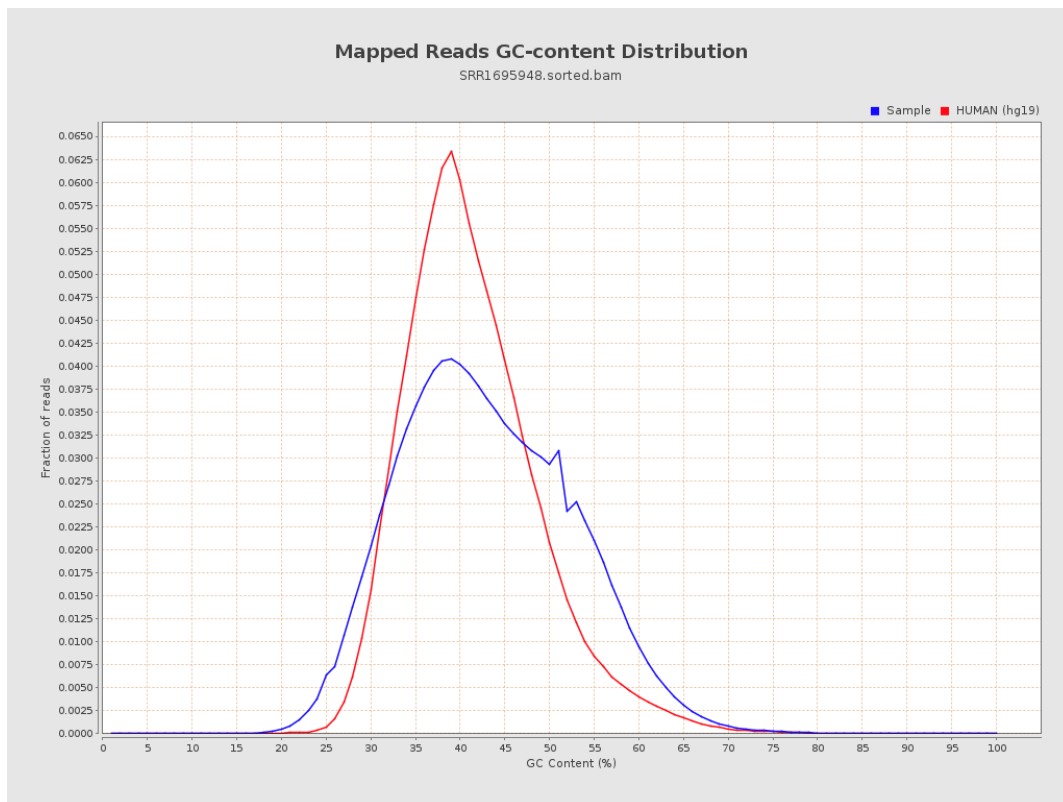
7. Results : Duplication Rate Histogram



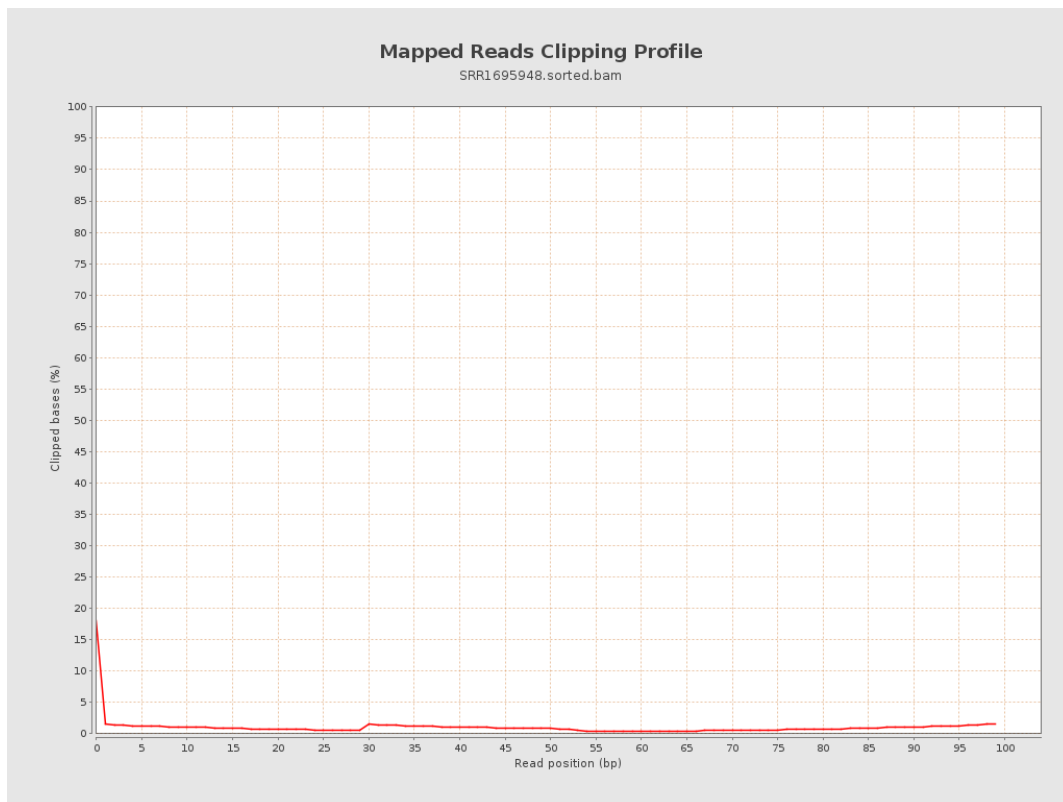
8. Results : Mapped Reads Nucleotide Content



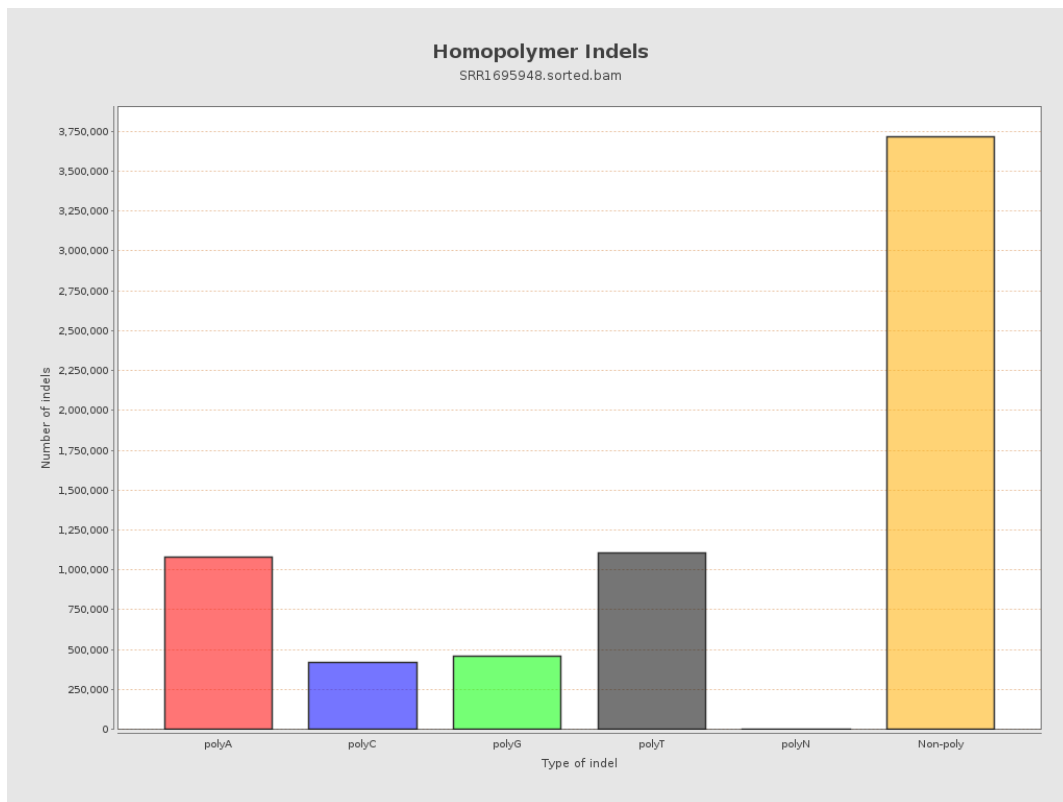
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



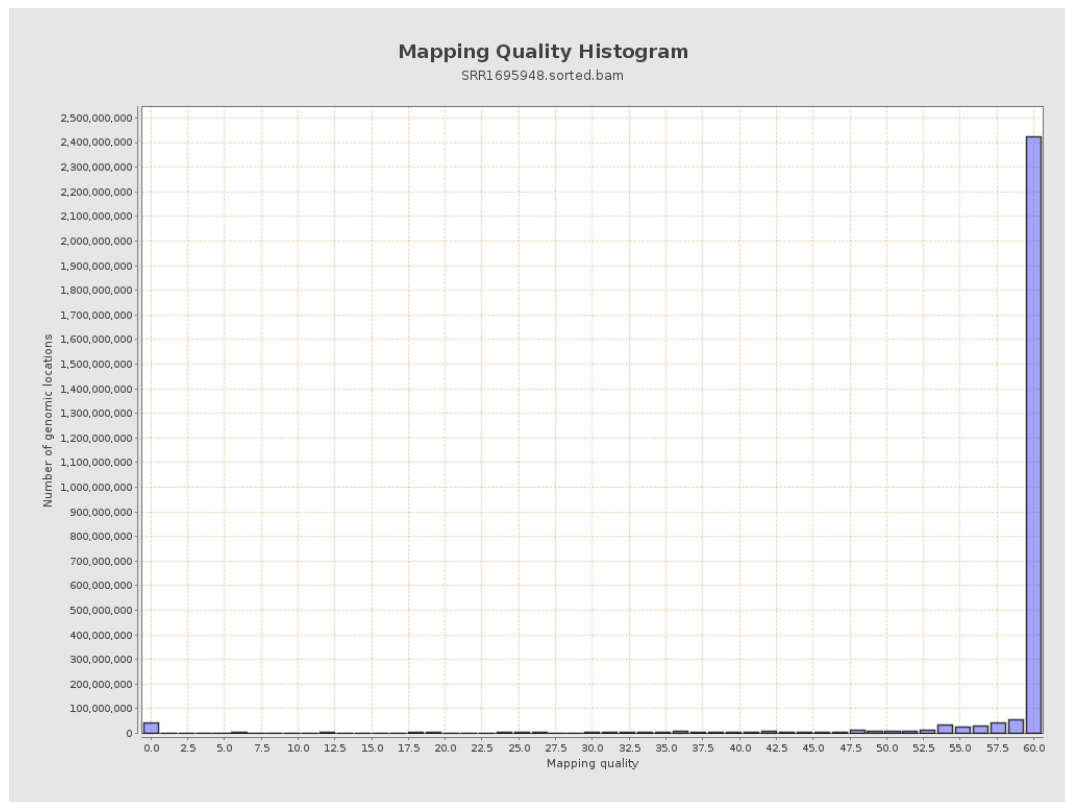
11. Results : Homopolymer Indels



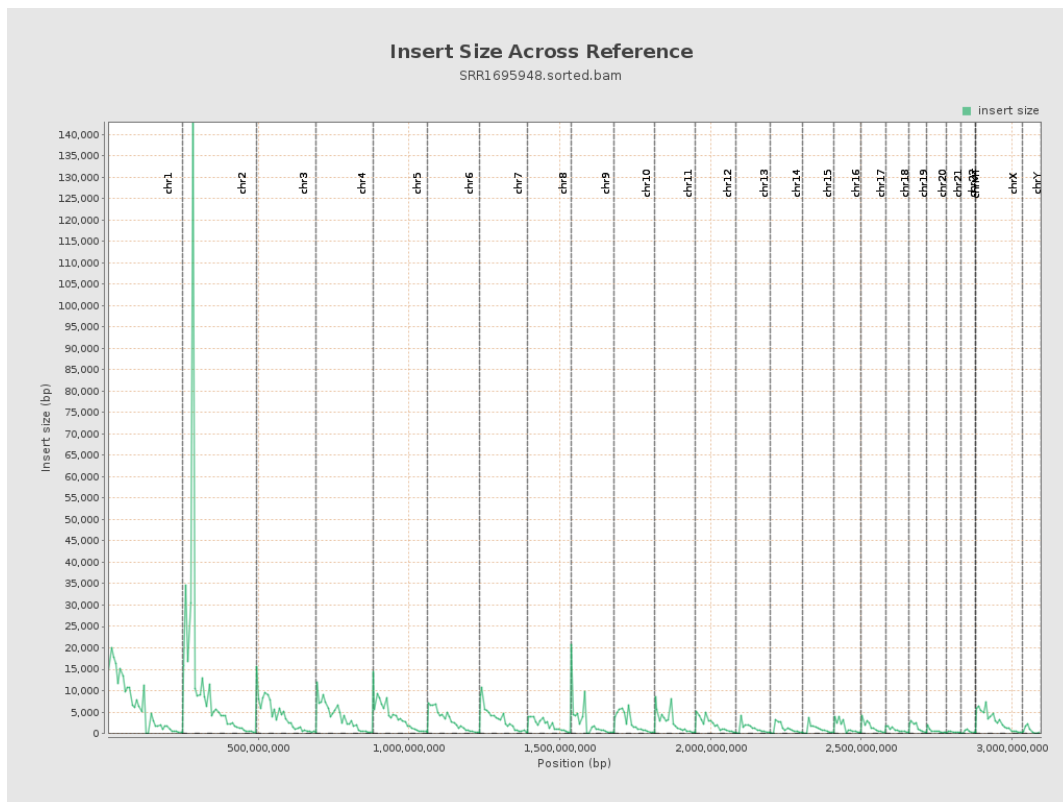
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

