

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/13 02:55:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695941.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 941 /seu_share/home/tujing/220232460/r eference/homo_bwa/hsa.fa SRR1695941_1.fastq.gz SRR1695941_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 02:55:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695941.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,672,416
Mapped reads	16,547,438 / 99.25%
Unmapped reads	124,978 / 0.75%
Mapped paired reads	16,547,438 / 99.25%
Mapped reads, first in pair	8,317,417 / 49.89%
Mapped reads, second in pair	8,230,021 / 49.36%
Mapped reads, both in pair	16,446,868 / 98.65%
Mapped reads, singletons	100,570 / 0.6%
Secondary alignments	0
Supplementary alignments	38,125 / 0.23%
Read min/max/mean length	30 / 100 / 100.09
Duplicated reads (estimated)	250,740 / 1.5%
Duplication rate	1.48%
Clipped reads	718,094 / 4.31%

2.2. ACGT Content

Number/percentage of A's	480,772,252 / 29.3%
Number/percentage of C's	338,153,534 / 20.6%
Number/percentage of T's	481,362,344 / 29.33%
Number/percentage of G's	340,128,178 / 20.73%
Number/percentage of N's	716,158 / 0.04%

GC Percentage	41.33%
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2.3. Coverage

Mean	0.5302
Standard Deviation	1.065

2.4. Mapping Quality

Mean Mapping Quality	54.77
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2.5. Insert size

Mean	28,541.72
Standard Deviation	1,684,969.25
P25/Median/P75	326 / 334 / 341

2.6. Mismatches and indels

General error rate	0.7%
Mismatches	11,213,351
Insertions	104,891
Mapped reads with at least one insertion	0.63%
Deletions	132,476
Mapped reads with at least one deletion	0.79%
Homopolymer indels	44.99%

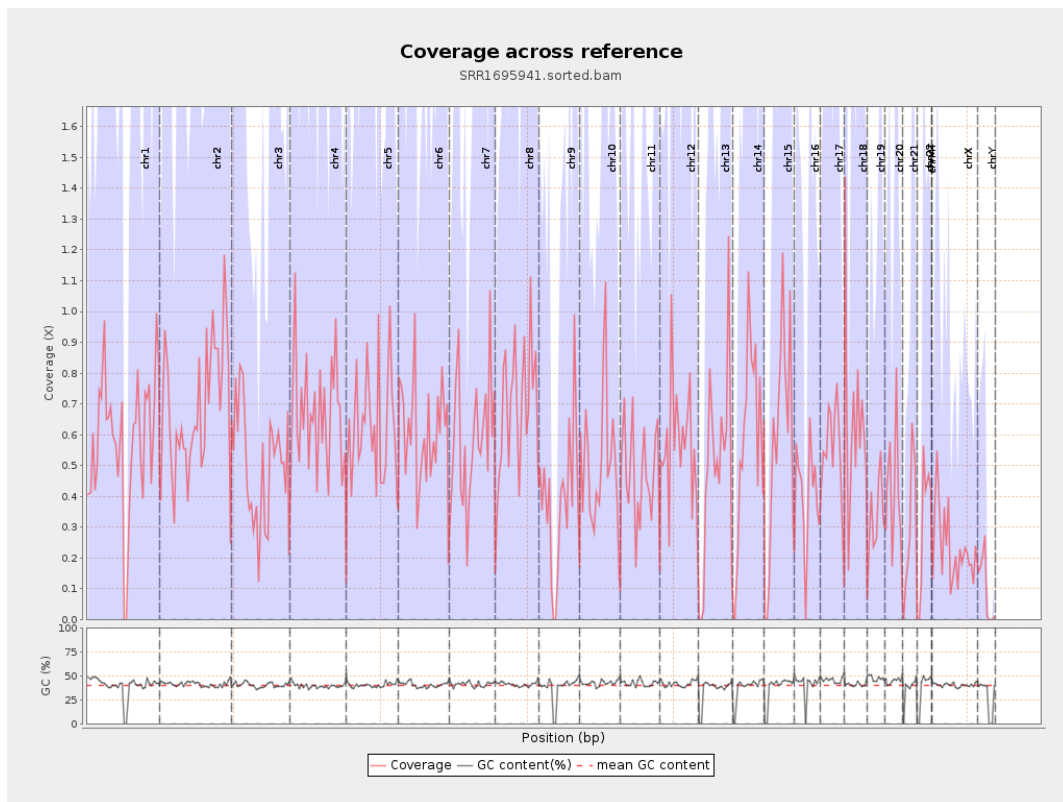
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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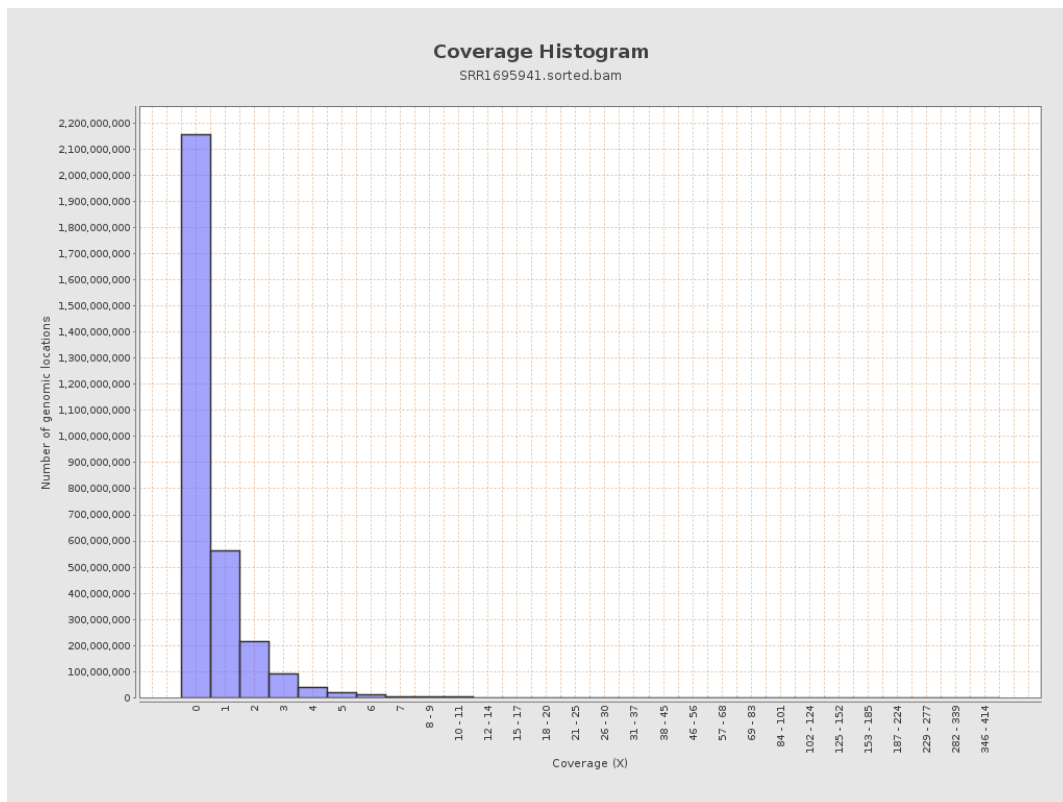
		bases	coverage	deviation
chr1	249250621	145806243	0.585	1.1454
chr2	243199373	167159837	0.6873	1.2276
chr3	198022430	99832743	0.5041	0.9847
chr4	191154276	128416874	0.6718	1.168
chr5	180915260	111946334	0.6188	1.0929
chr6	171115067	105191953	0.6147	1.1293
chr7	159138663	92823434	0.5833	1.1054
chr8	146364022	102537486	0.7006	1.2427
chr9	141213431	53342240	0.3777	0.9452
chr10	135534747	69946369	0.5161	1.005
chr11	135006516	63460789	0.4701	1.0027
chr12	133851895	75994860	0.5678	1.122
chr13	115169878	57476852	0.4991	1.009
chr14	107349540	61596309	0.5738	1.1118
chr15	102531392	58790761	0.5734	1.1509
chr16	90354753	35223911	0.3898	0.863
chr17	81195210	44109618	0.5433	1.0626
chr18	78077248	49473953	0.6337	1.1178
chr19	59128983	20444950	0.3458	0.8741
chr20	63025520	25590789	0.406	0.9439
chr21	48129895	14518770	0.3017	0.7691
chr22	51304566	15904799	0.31	0.814
chrMT	16571	4905	0.296	0.6044
chrX	155270560	35814437	0.2307	0.6657

chrY	59373566	6023672	0.1015	0.4155
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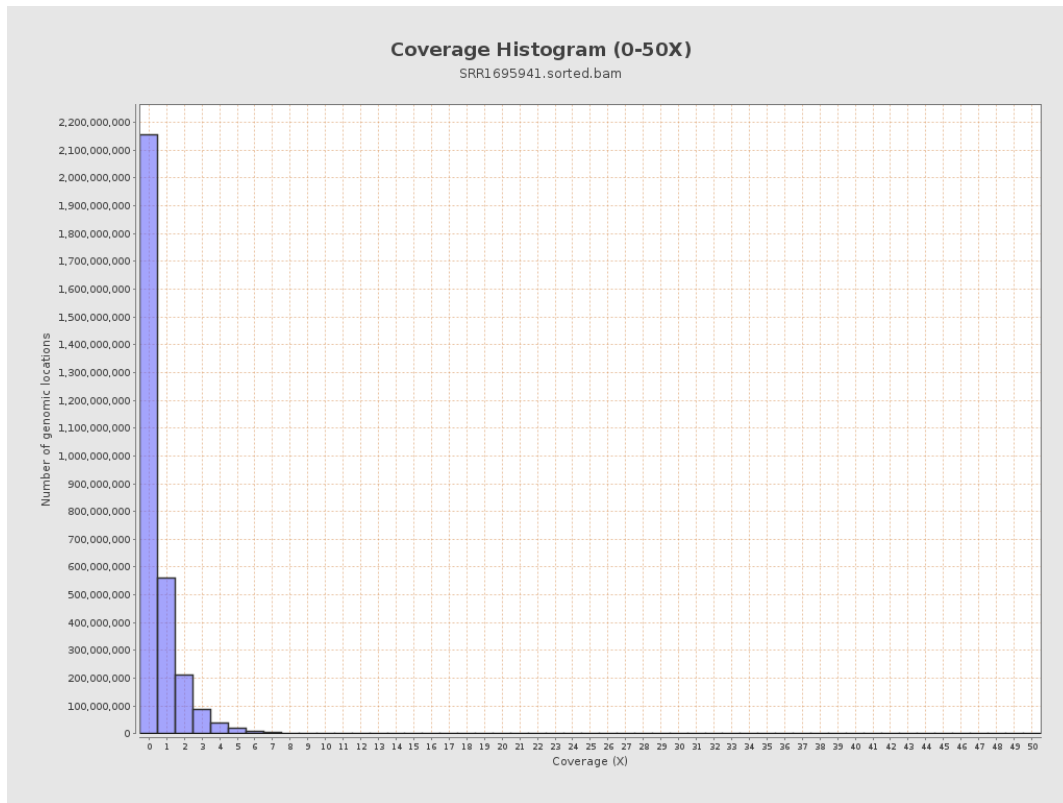
3. Results : Coverage across reference



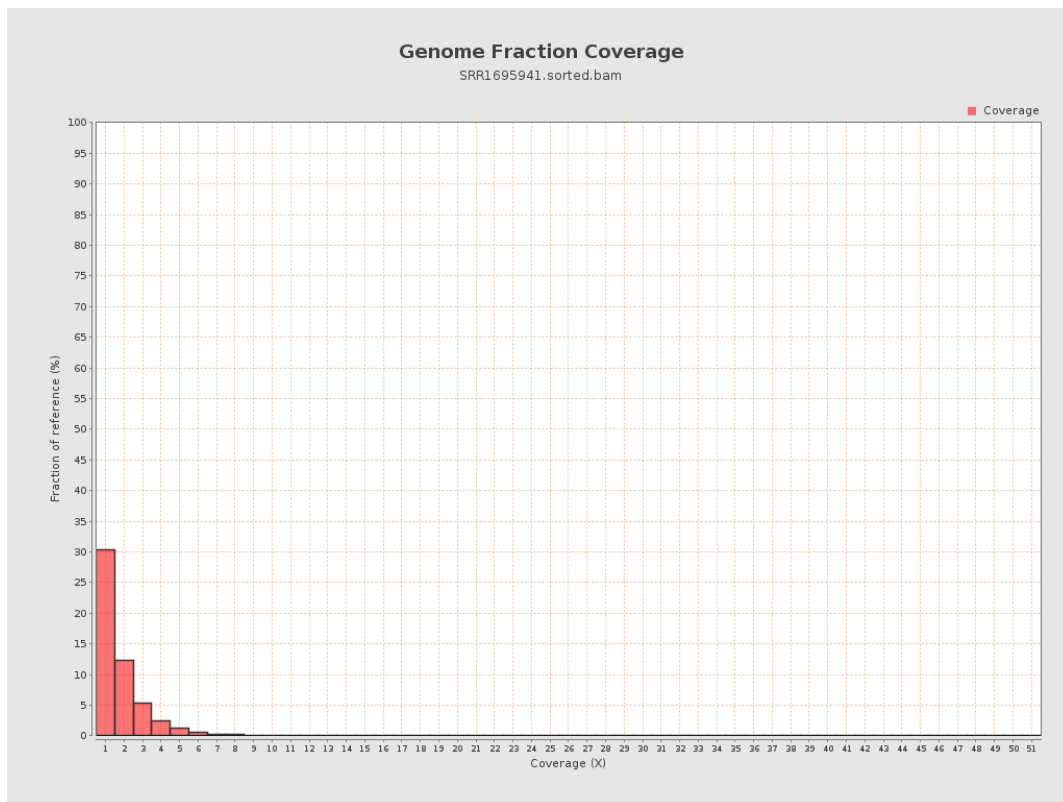
4. Results : Coverage Histogram



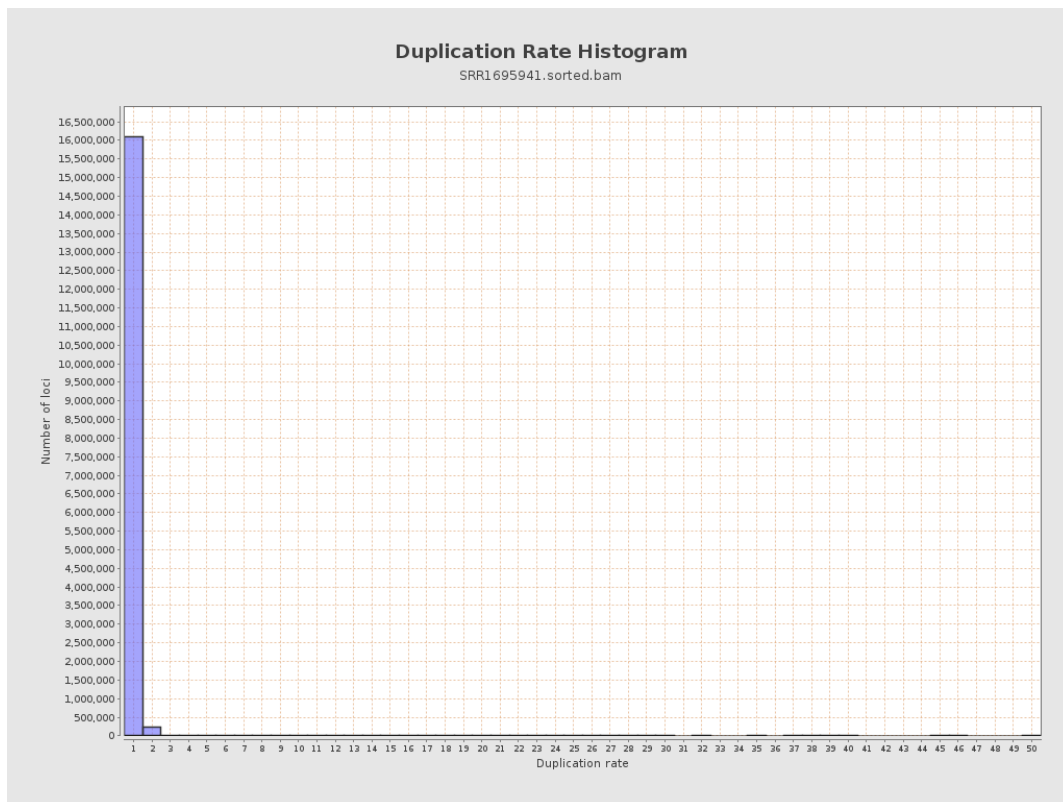
5. Results : Coverage Histogram (0-50X)



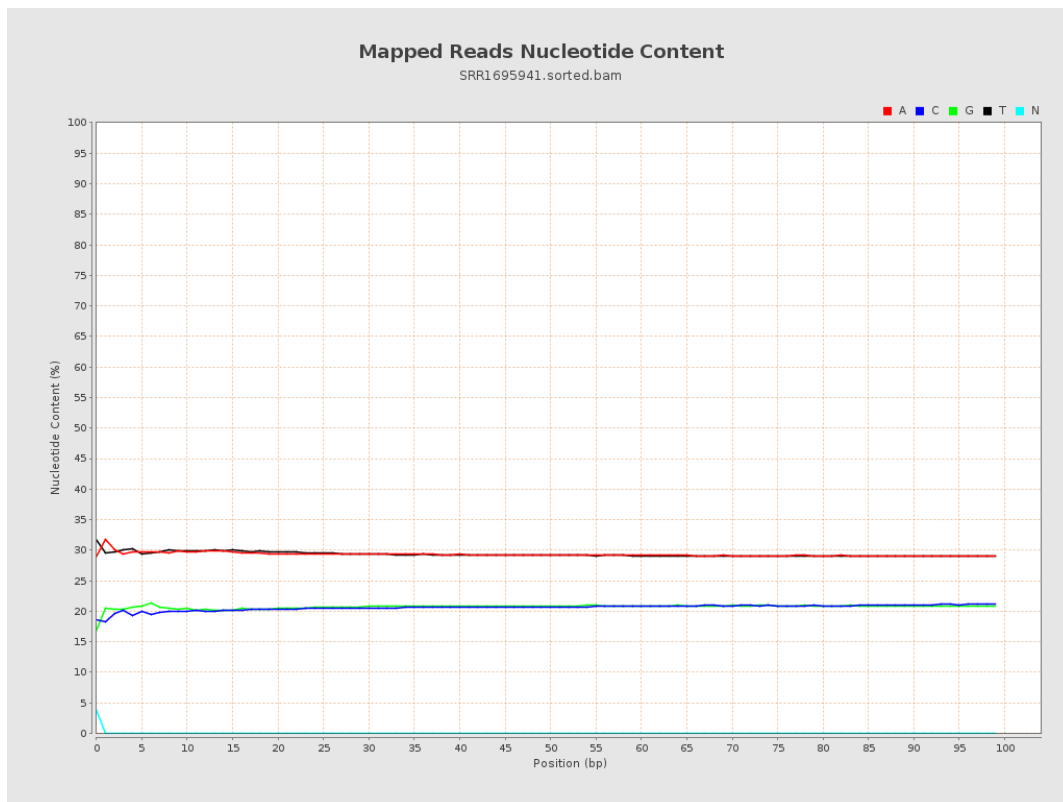
6. Results : Genome Fraction Coverage



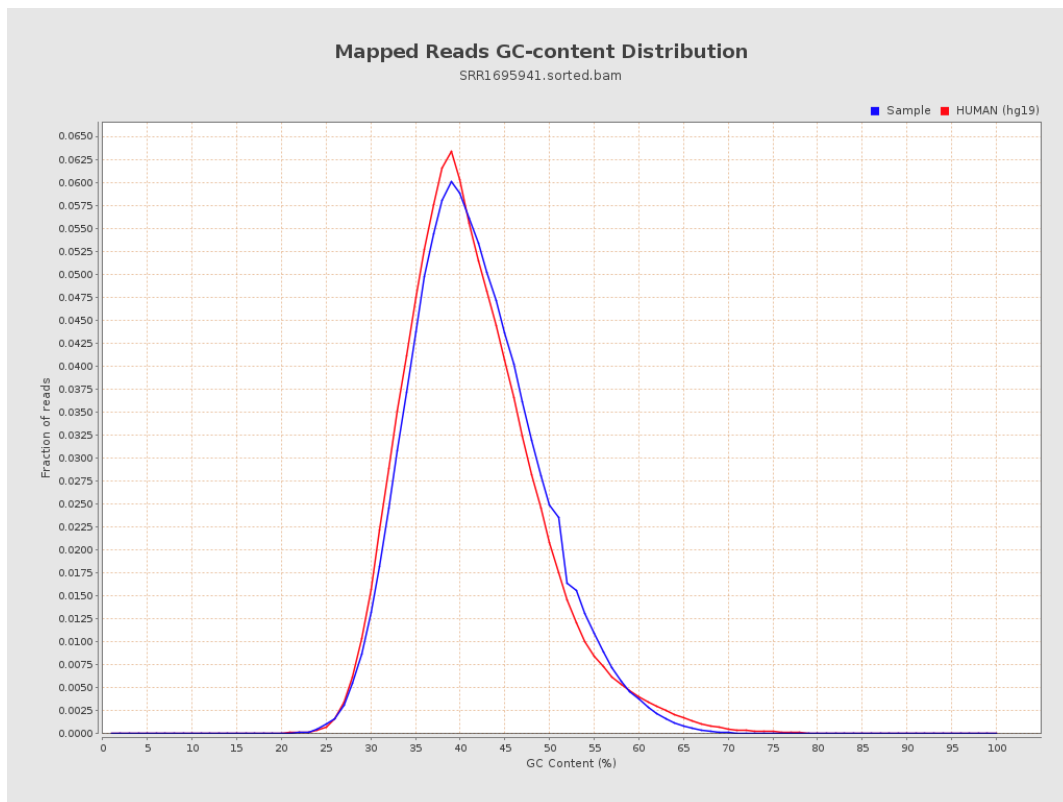
7. Results : Duplication Rate Histogram



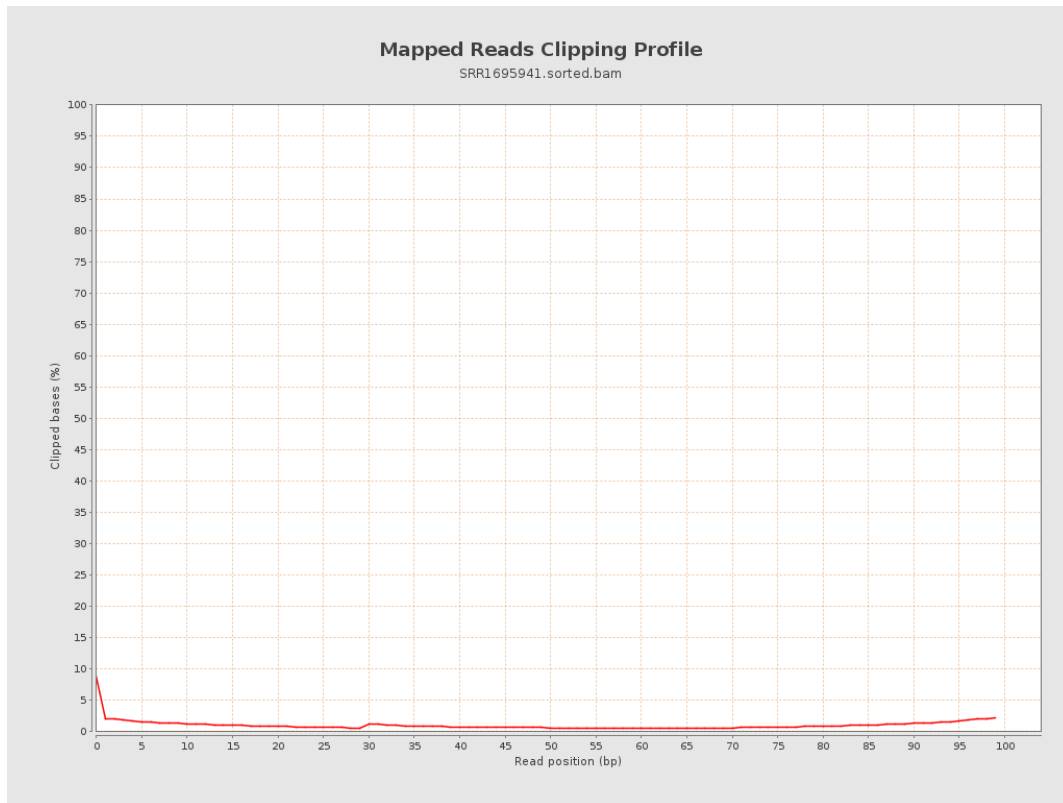
8. Results : Mapped Reads Nucleotide Content



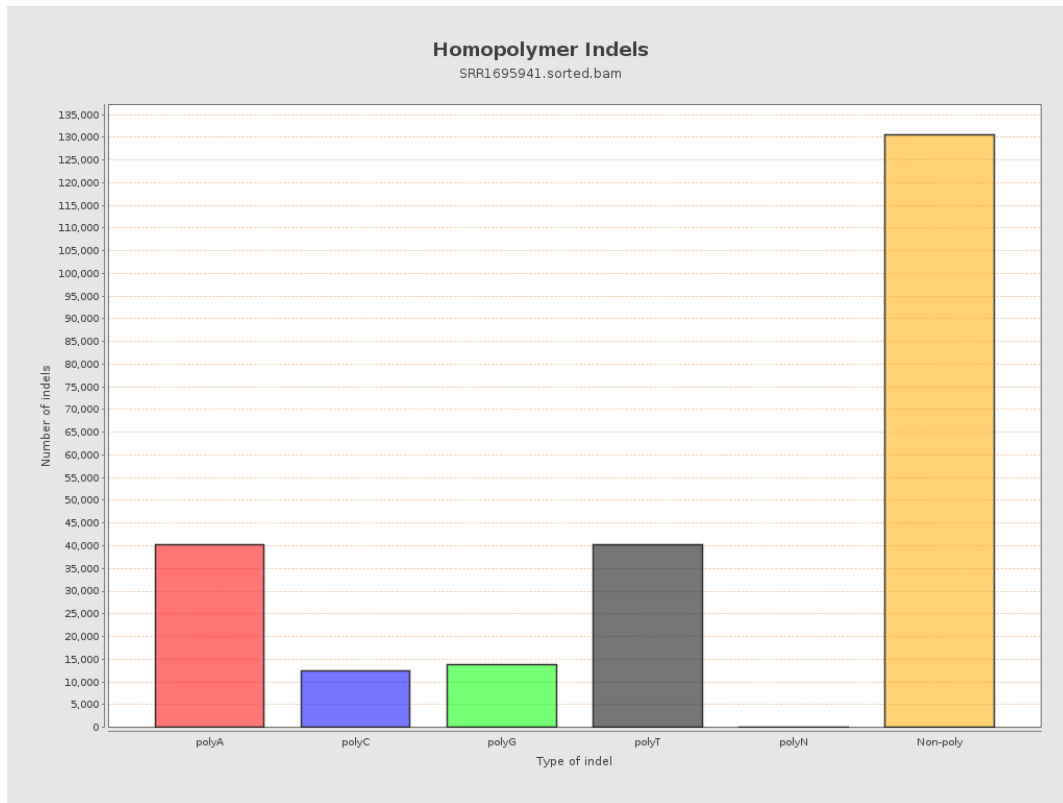
9. Results : Mapped Reads GC-content Distribution



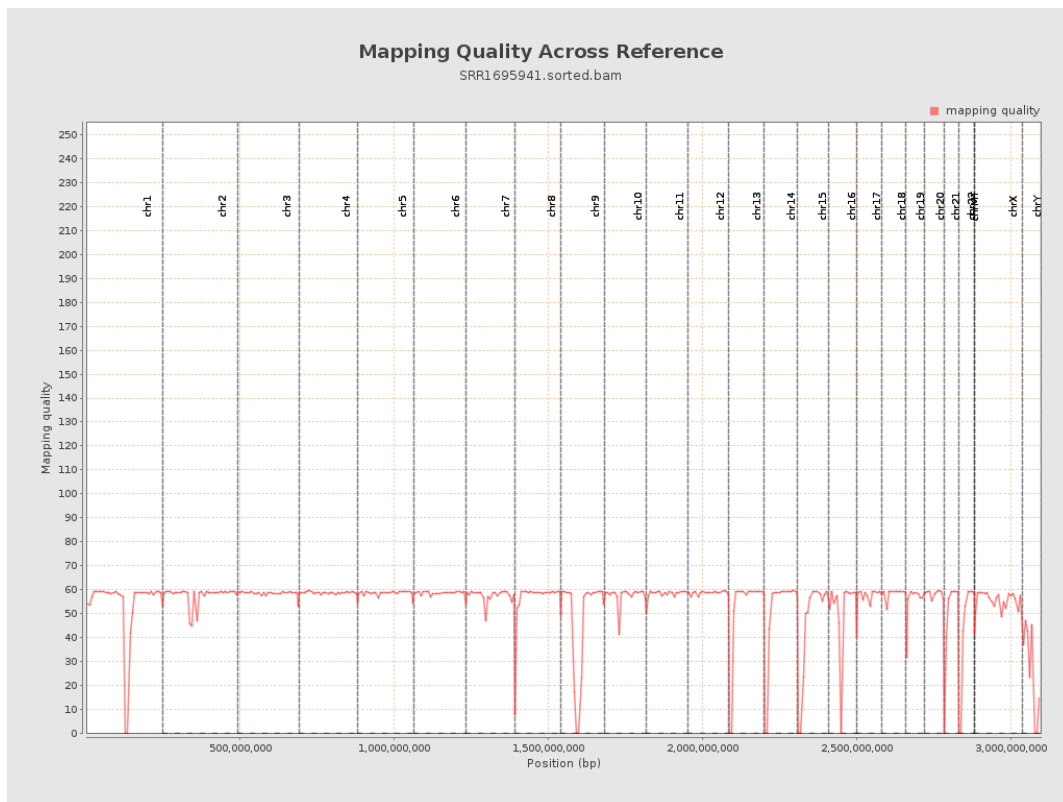
10. Results : Mapped Reads Clipping Profile



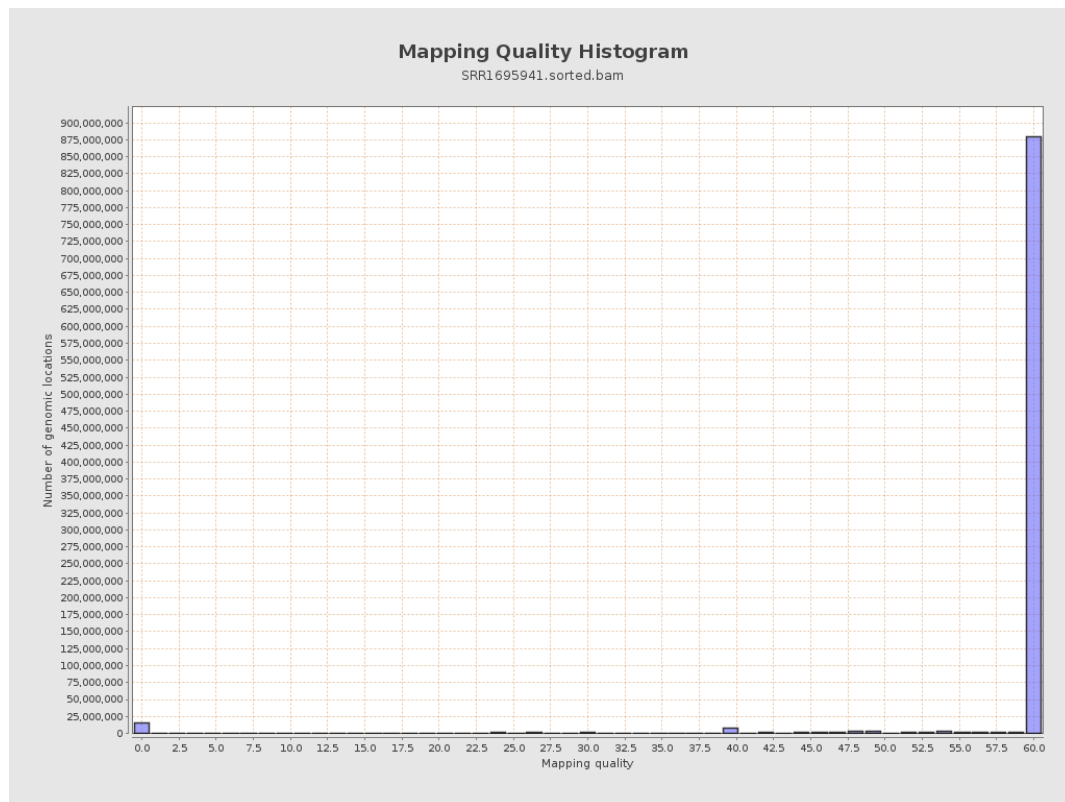
11. Results : Homopolymer Indels



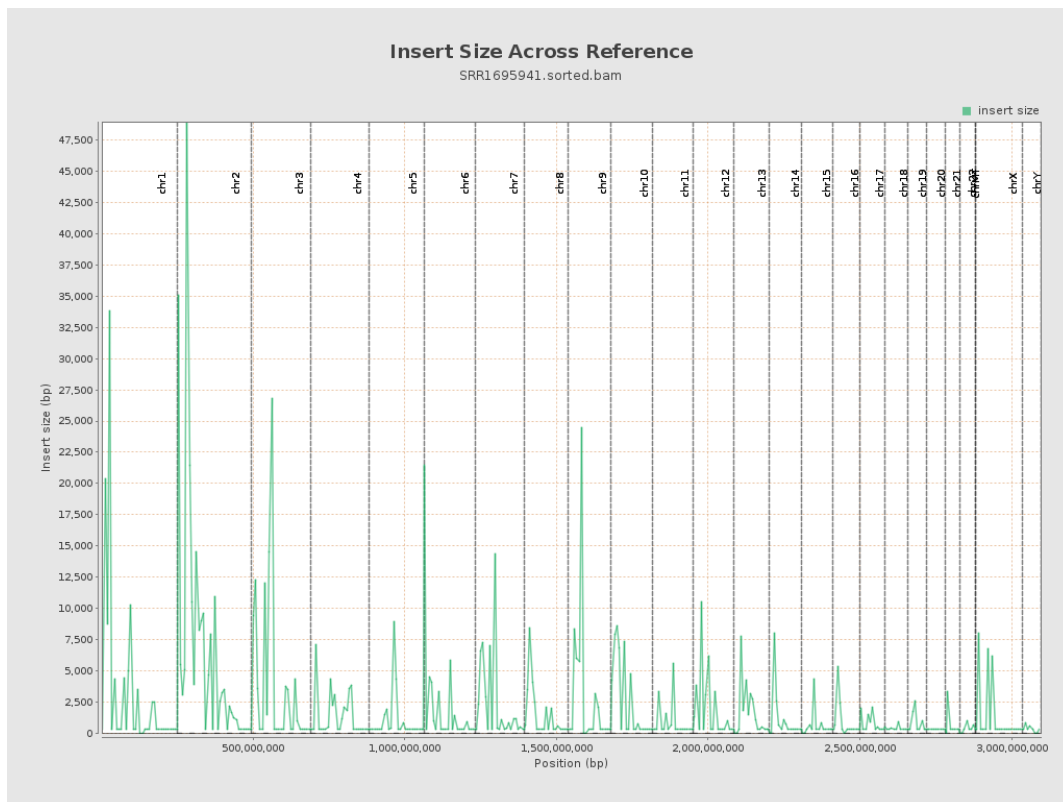
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

