

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/13 02:08:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695933.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 933 /seu_share/home/tujing/220232460/r eference/homo_bwa/hsa.fa SRR1695933_1.fastq.gz SRR1695933_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 02:08:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695933.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,401,036
Mapped reads	14,676,339 / 95.29%
Unmapped reads	724,697 / 4.71%
Mapped paired reads	14,676,339 / 95.29%
Mapped reads, first in pair	7,391,093 / 47.99%
Mapped reads, second in pair	7,285,246 / 47.3%
Mapped reads, both in pair	14,320,458 / 92.98%
Mapped reads, singletons	355,881 / 2.31%
Secondary alignments	0
Supplementary alignments	340,359 / 2.21%
Read min/max/mean length	30 / 100 / 100.9
Duplicated reads (estimated)	4,361,663 / 28.32%
Duplication rate	14.52%
Clipped reads	8,467,102 / 54.98%

2.2. ACGT Content

Number/percentage of A's	348,372,383 / 26.91%
Number/percentage of C's	289,441,831 / 22.36%
Number/percentage of T's	356,958,854 / 27.57%
Number/percentage of G's	299,288,206 / 23.12%
Number/percentage of N's	463,503 / 0.04%

GC Percentage	45.48%
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2.3. Coverage

Mean	0.4183
Standard Deviation	10.0976

2.4. Mapping Quality

Mean Mapping Quality	49.68
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2.5. Insert size

Mean	873,824.5
Standard Deviation	9,125,767.15
P25/Median/P75	275 / 288 / 299

2.6. Mismatches and indels

General error rate	1.29%
Mismatches	16,053,348
Insertions	192,324
Mapped reads with at least one insertion	1.26%
Deletions	222,565
Mapped reads with at least one deletion	1.47%
Homopolymer indels	39.07%

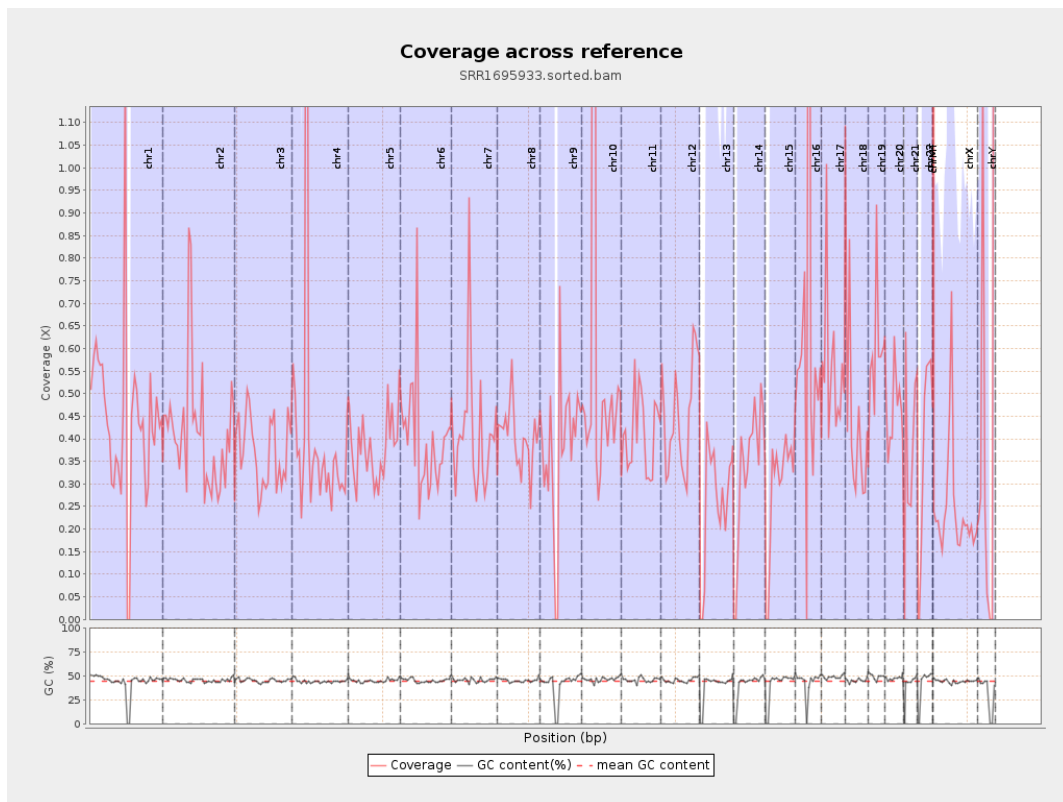
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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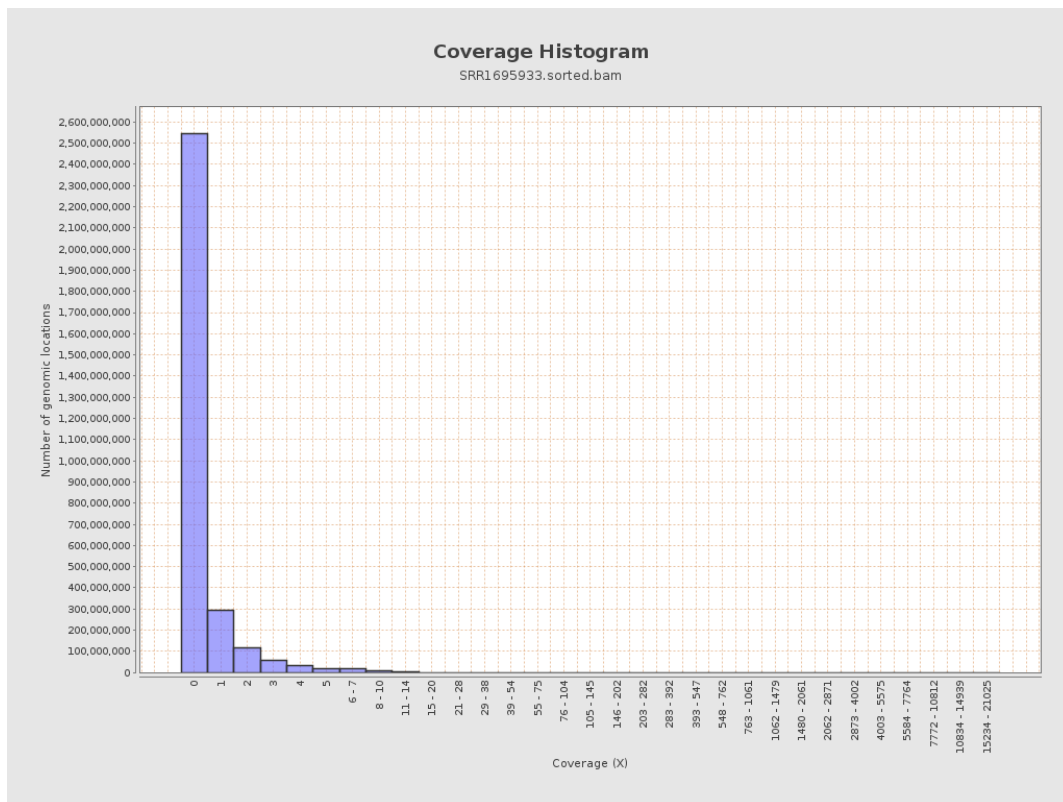
		bases	coverage	deviation
chr1	249250621	109652509	0.4399	16.4701
chr2	243199373	100816949	0.4145	5.38
chr3	198022430	73450421	0.3709	1.2636
chr4	191154276	81574768	0.4267	12.4113
chr5	180915260	69537880	0.3844	1.6654
chr6	171115067	67819044	0.3963	7.6367
chr7	159138663	66284626	0.4165	6.7171
chr8	146364022	58771707	0.4015	2.5907
chr9	141213431	53023855	0.3755	6.1413
chr10	135534747	78050910	0.5759	21.6167
chr11	135006516	55258654	0.4093	1.8509
chr12	133851895	60767834	0.454	1.8856
chr13	115169878	30156106	0.2618	0.9019
chr14	107349540	36520962	0.3402	1.2575
chr15	102531392	29708437	0.2897	0.9466
chr16	90354753	60852277	0.6735	17.3051
chr17	81195210	45397395	0.5591	6.1714
chr18	78077248	33965511	0.435	11.9965
chr19	59128983	35345605	0.5978	19.6283
chr20	63025520	29115653	0.462	5.037
chr21	48129895	18701566	0.3886	5.2229
chr22	51304566	19256189	0.3753	1.2139
chrMT	16571	10748477	648.6318	1,417.8596
chrX	155270560	37833874	0.2437	3.5293

chrY	59373566	32439904	0.5464	14.9336
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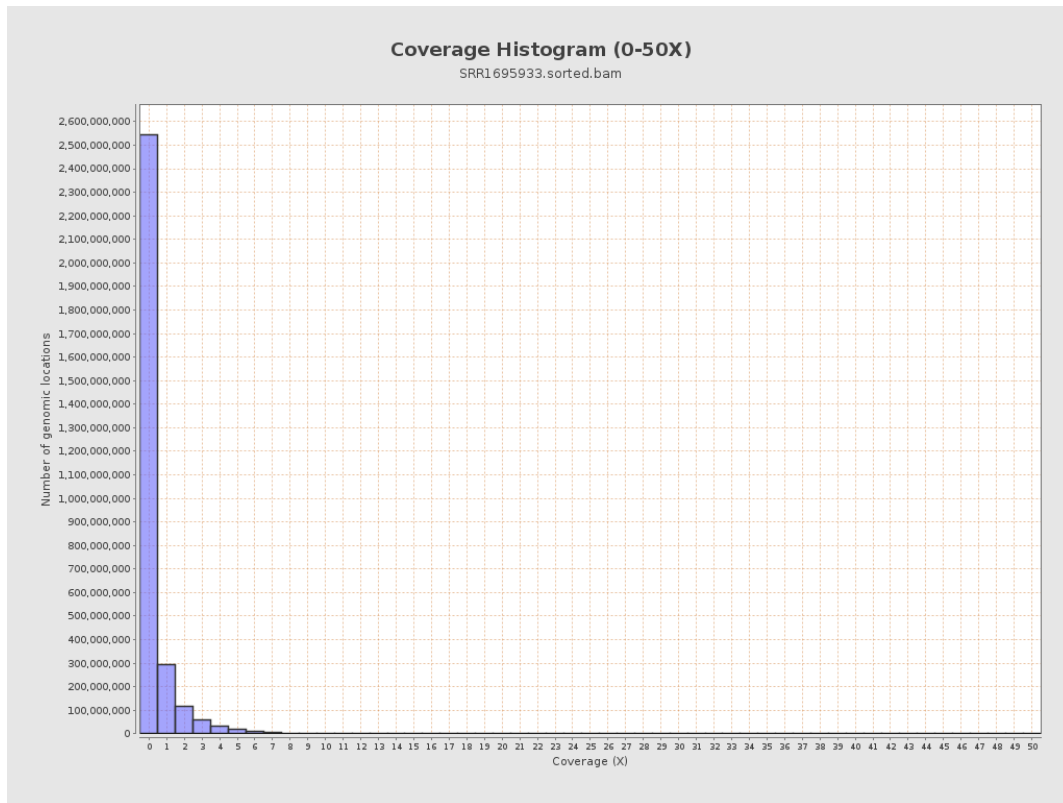
3. Results : Coverage across reference



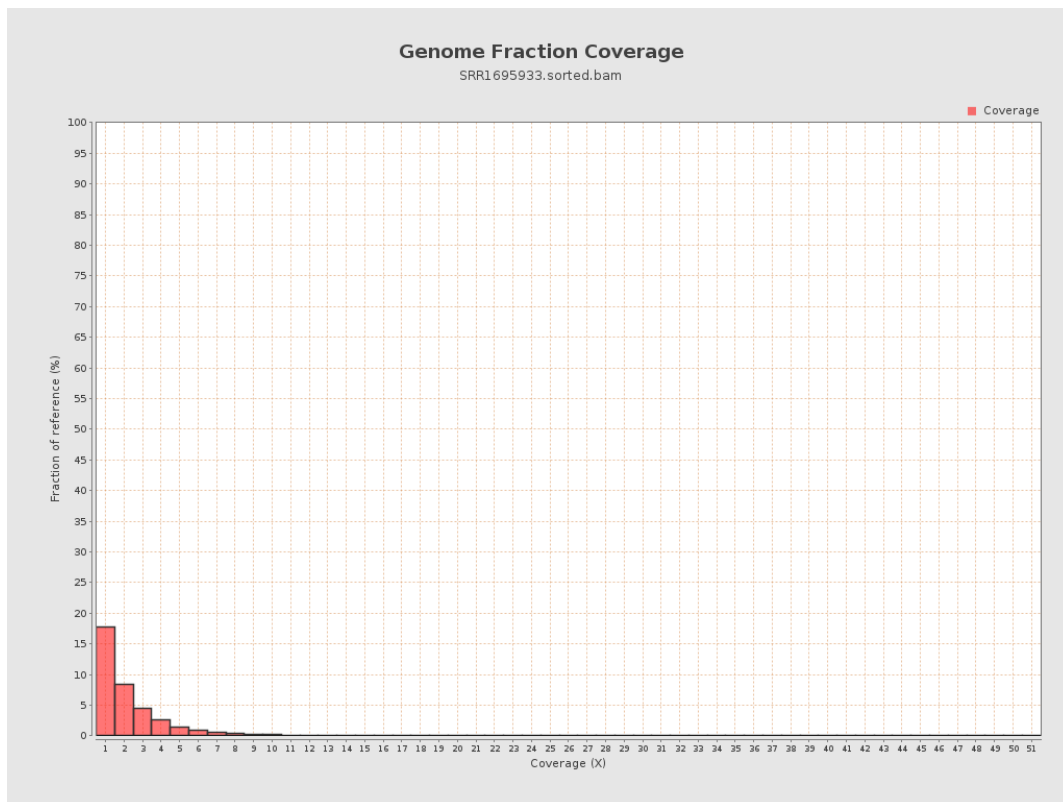
4. Results : Coverage Histogram



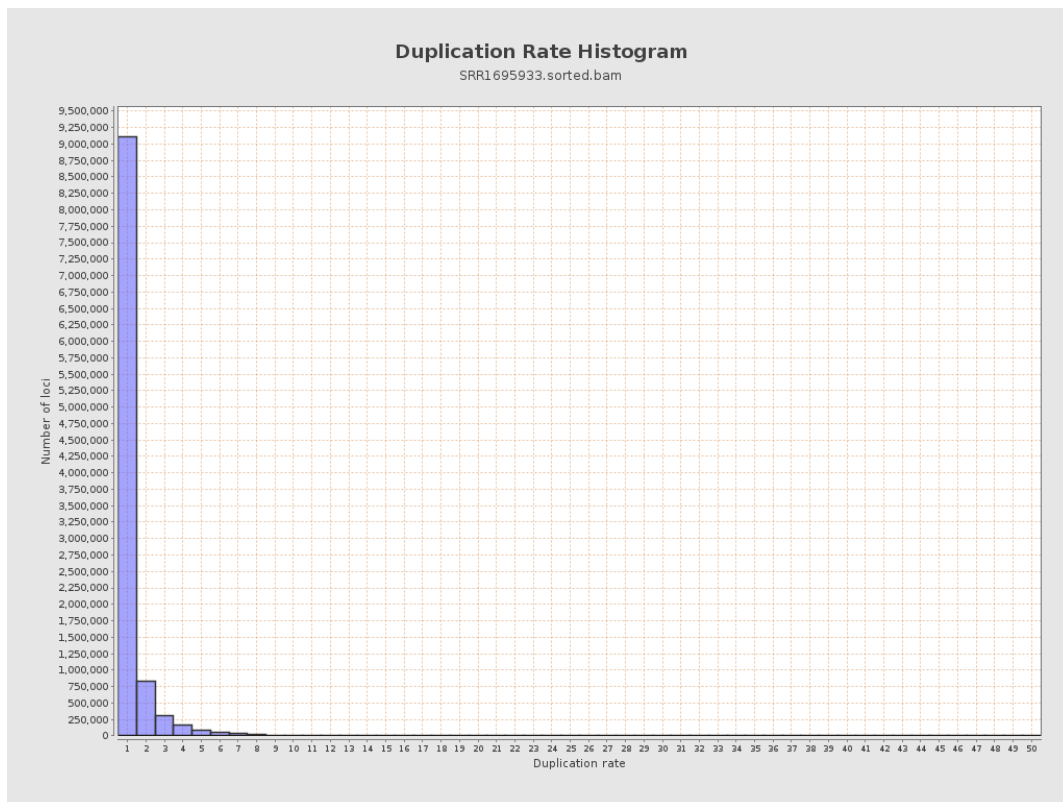
5. Results : Coverage Histogram (0-50X)



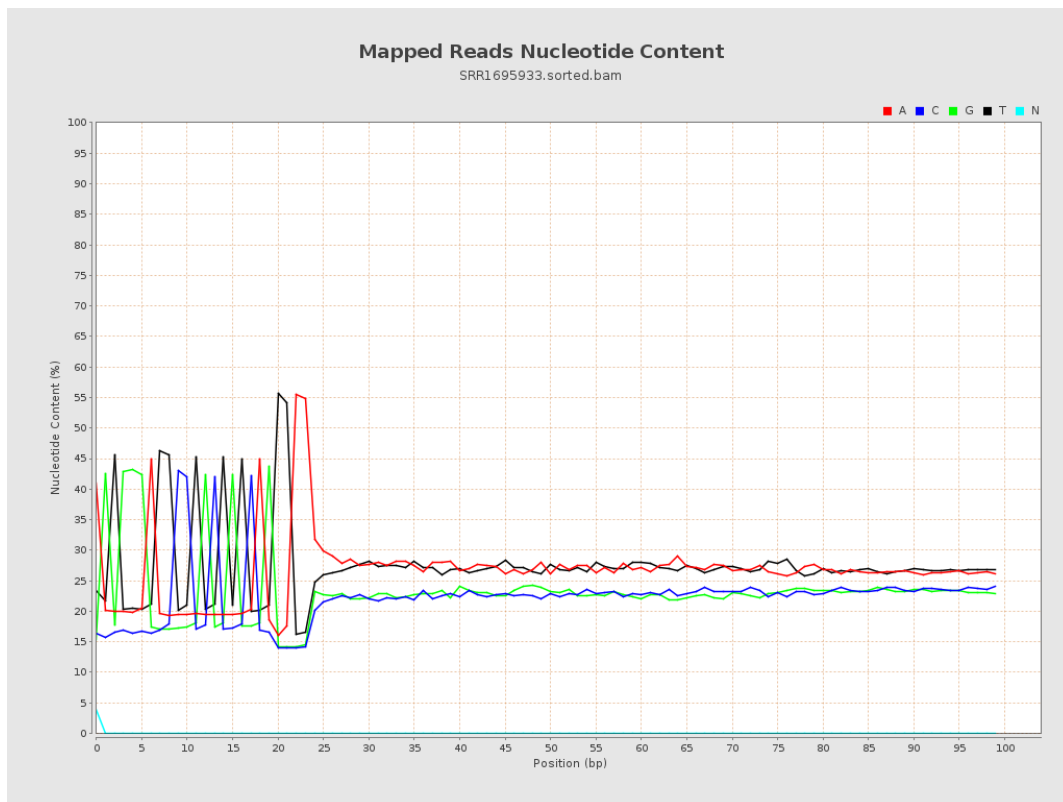
6. Results : Genome Fraction Coverage



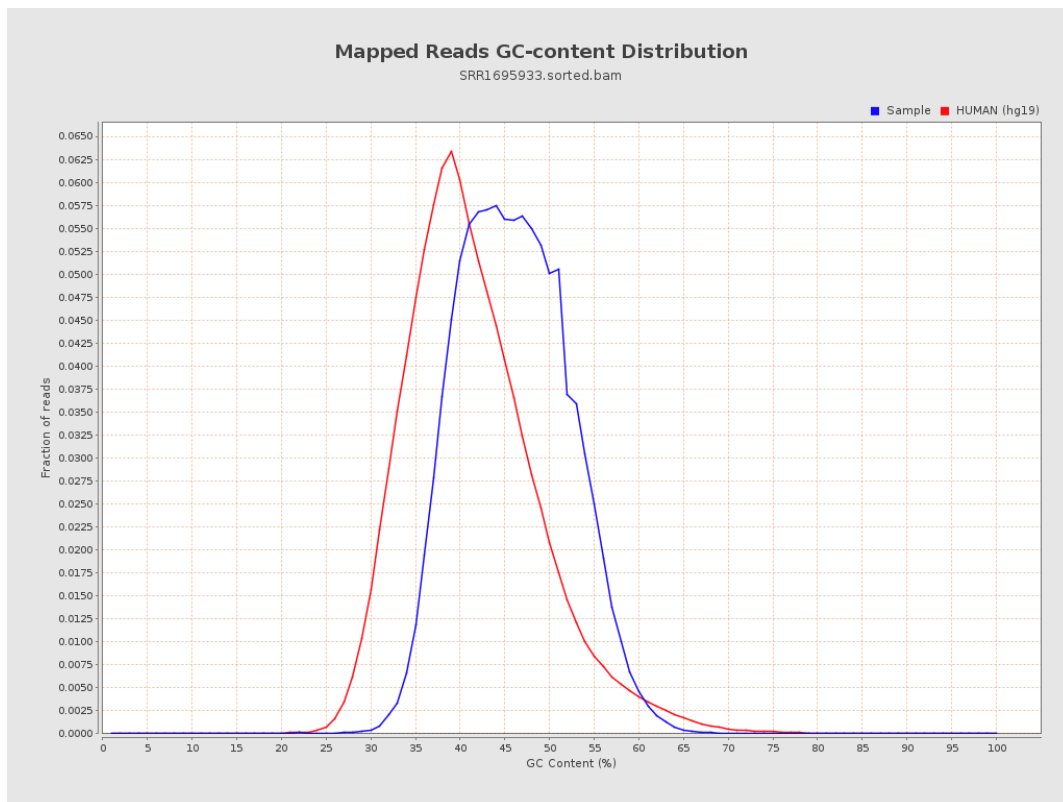
7. Results : Duplication Rate Histogram



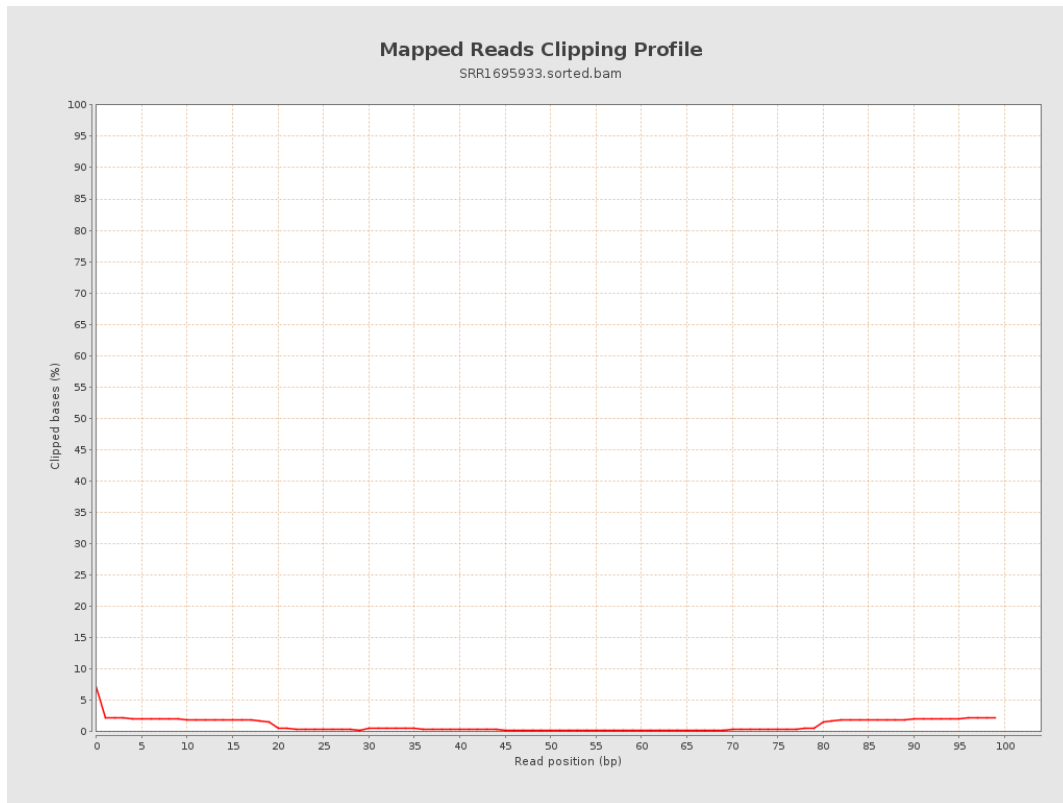
8. Results : Mapped Reads Nucleotide Content



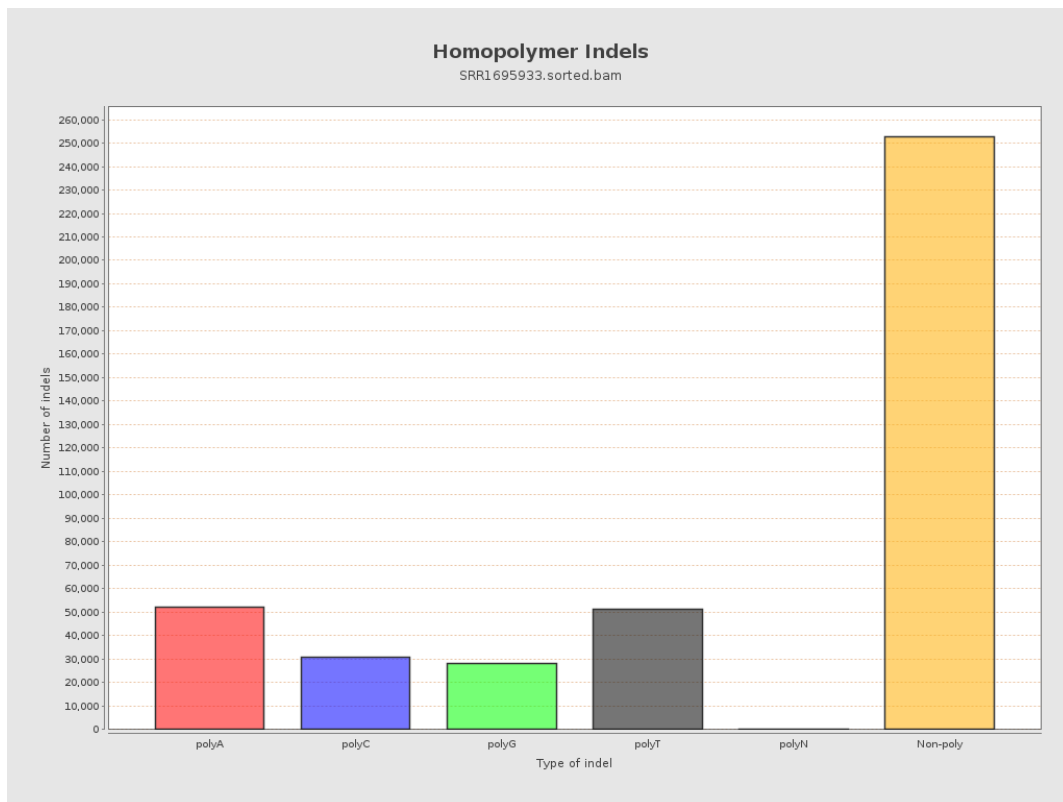
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



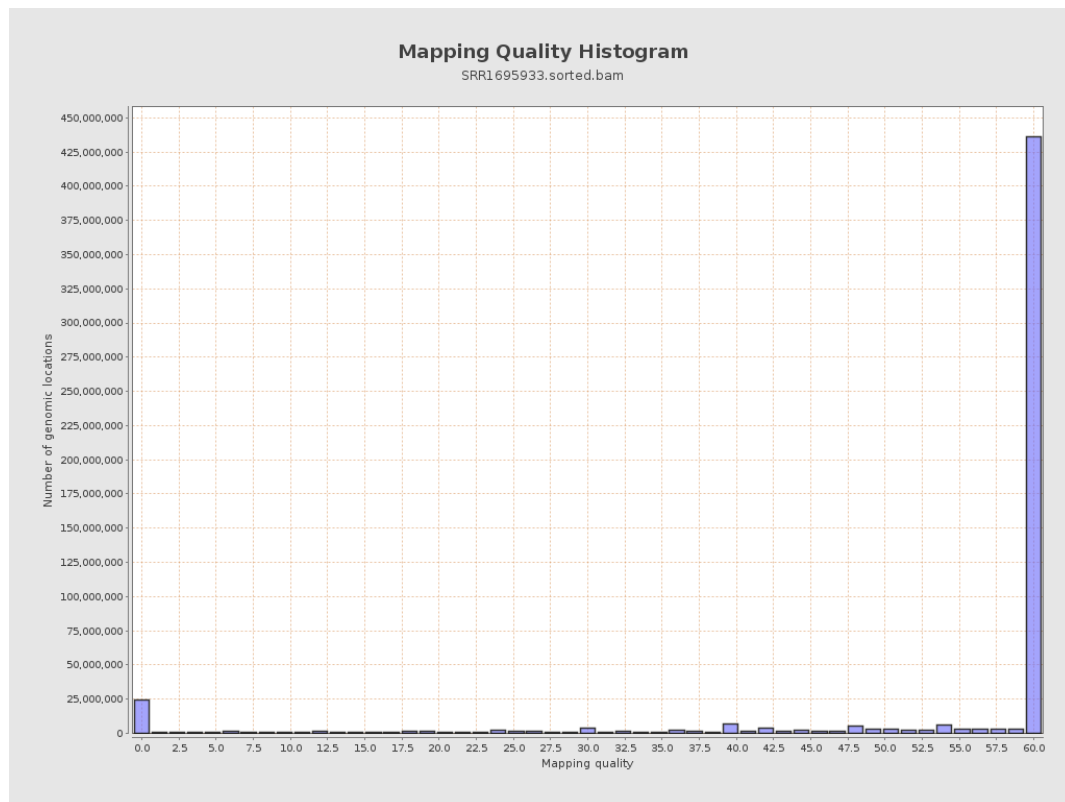
11. Results : Homopolymer Indels



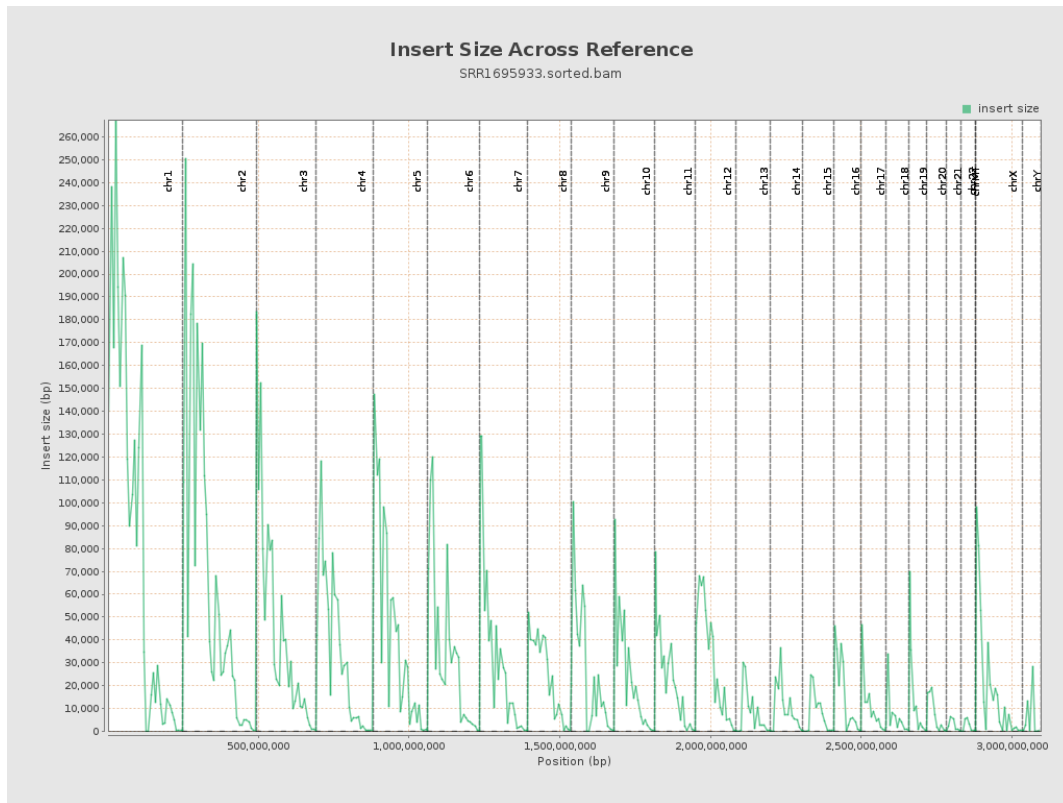
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

