

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/12 20:59:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695923.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_SRR1695923 /seu_share/home/tujing/220232460/reference/homo_bwa/hsa.fa SRR1695923_1.fastq.gz SRR1695923_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.18-r1243-dirty)
Analysis date:	Thu Sep 12 20:59:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695923.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,293,032
Mapped reads	2,284,865 / 99.64%
Unmapped reads	8,167 / 0.36%
Mapped paired reads	2,284,865 / 99.64%
Mapped reads, first in pair	1,144,687 / 49.92%
Mapped reads, second in pair	1,140,178 / 49.72%
Mapped reads, both in pair	2,279,378 / 99.4%
Mapped reads, singletons	5,487 / 0.24%
Secondary alignments	0
Supplementary alignments	38,846 / 1.69%
Read min/max/mean length	30 / 150 / 150.9
Duplicated reads (estimated)	6,219 / 0.27%
Duplication rate	0.24%
Clipped reads	142,321 / 6.21%

2.2. ACGT Content

Number/percentage of A's	102,556,392 / 30.09%
Number/percentage of C's	67,786,060 / 19.89%
Number/percentage of T's	102,370,298 / 30.04%
Number/percentage of G's	68,057,159 / 19.97%
Number/percentage of N's	45,007 / 0.01%

GC Percentage	39.86%
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2.3. Coverage

Mean	0.1101
Standard Deviation	0.3714

2.4. Mapping Quality

Mean Mapping Quality	55.19
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2.5. Insert size

Mean	34,661.81
Standard Deviation	1,768,741.8
P25/Median/P75	284 / 294 / 303

2.6. Mismatches and indels

General error rate	0.33%
Mismatches	1,078,432
Insertions	27,269
Mapped reads with at least one insertion	1.17%
Deletions	35,437
Mapped reads with at least one deletion	1.51%
Homopolymer indels	47.93%

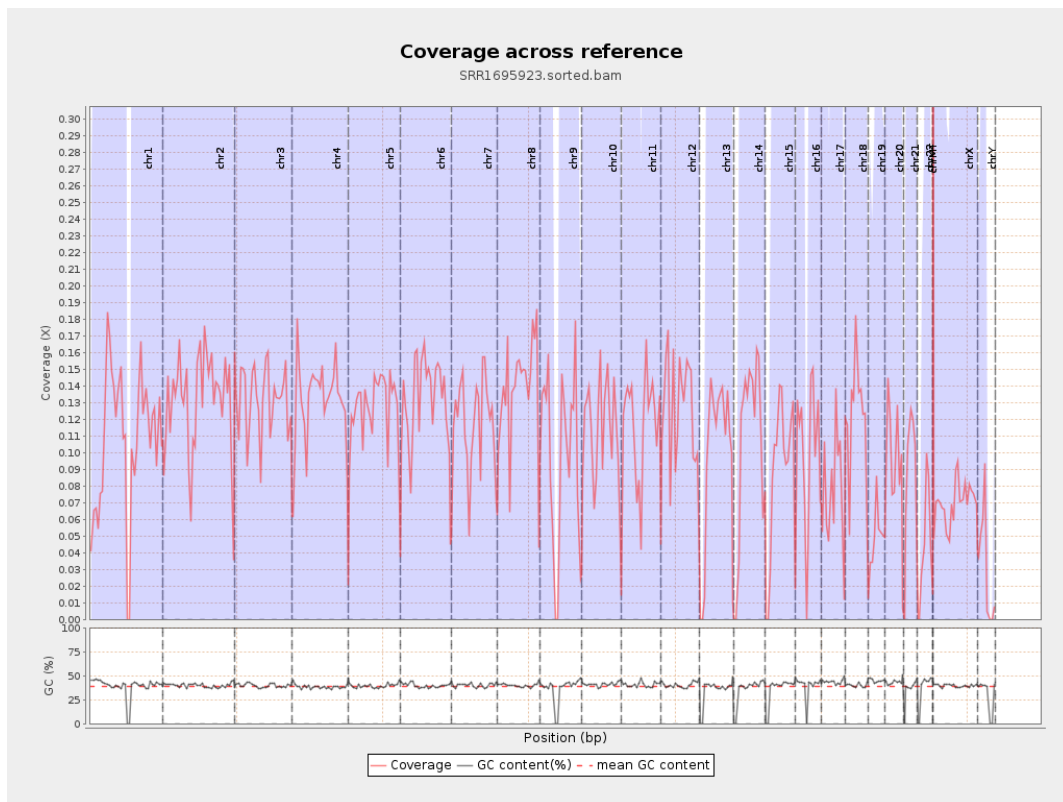
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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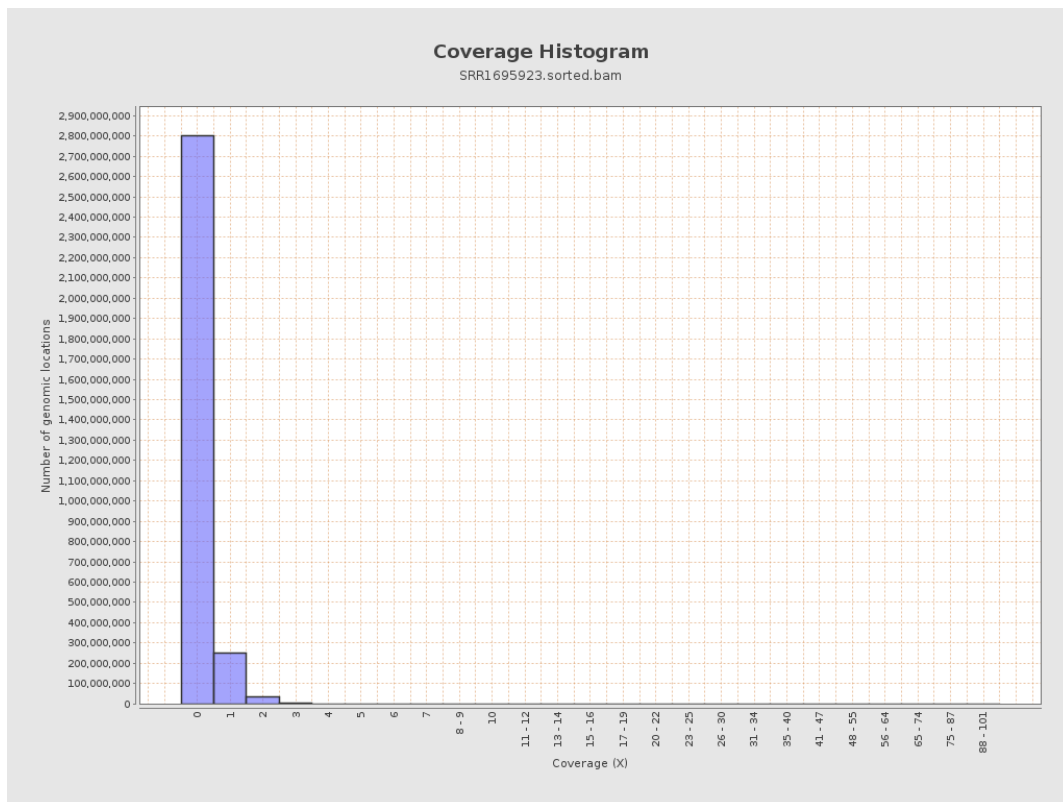
		bases	coverage	deviation
chr1	249250621	26738513	0.1073	0.378
chr2	243199373	31887997	0.1311	0.4049
chr3	198022430	26032148	0.1315	0.3978
chr4	191154276	25234560	0.132	0.3972
chr5	180915260	22686829	0.1254	0.3891
chr6	171115067	22710031	0.1327	0.407
chr7	159138663	18422861	0.1158	0.3753
chr8	146364022	20251014	0.1384	0.4178
chr9	141213431	13861233	0.0982	0.3541
chr10	135534747	15641284	0.1154	0.3837
chr11	135006516	15681833	0.1162	0.3753
chr12	133851895	16897787	0.1262	0.395
chr13	115169878	11455768	0.0995	0.3496
chr14	107349540	11505018	0.1072	0.3671
chr15	102531392	9043434	0.0882	0.3285
chr16	90354753	8733026	0.0967	0.3588
chr17	81195210	6349609	0.0782	0.3175
chr18	78077248	9491413	0.1216	0.3882
chr19	59128983	2926925	0.0495	0.2583
chr20	63025520	6130334	0.0973	0.3471
chr21	48129895	4143971	0.0861	0.3467
chr22	51304566	2349354	0.0458	0.2417
chrMT	16571	12796	0.7722	0.8587
chrX	155270560	10841003	0.0698	0.2899

chrY	59373566	1871991	0.0315	0.2013
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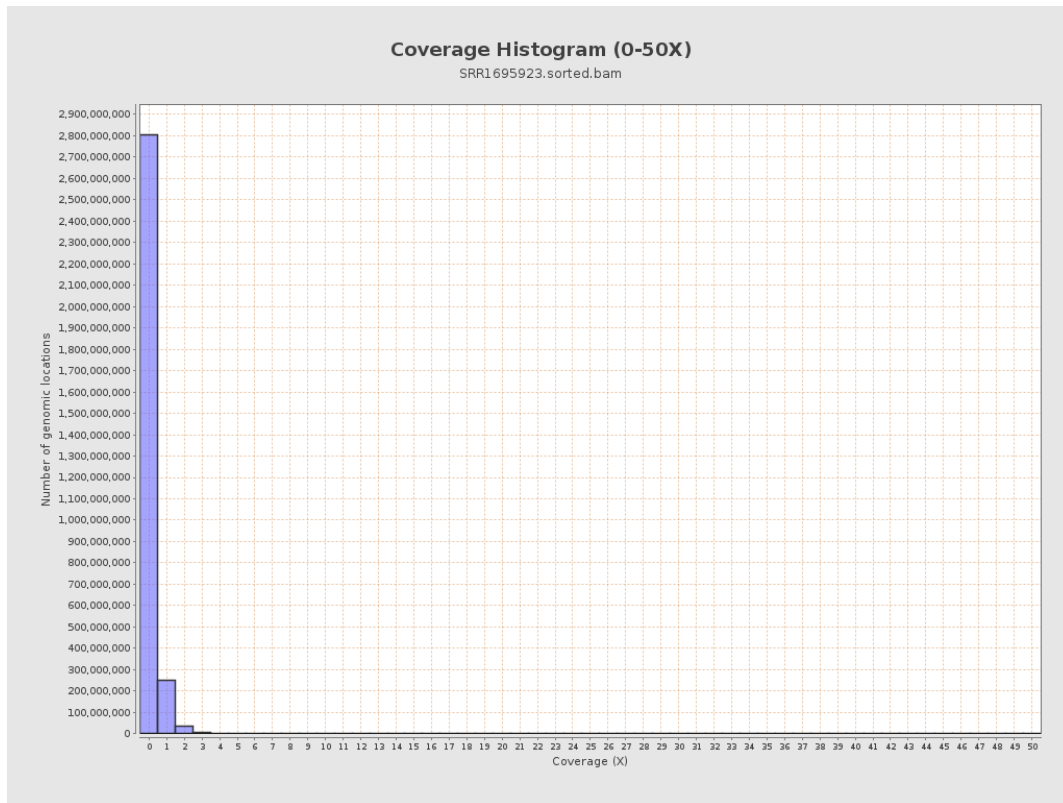
3. Results : Coverage across reference



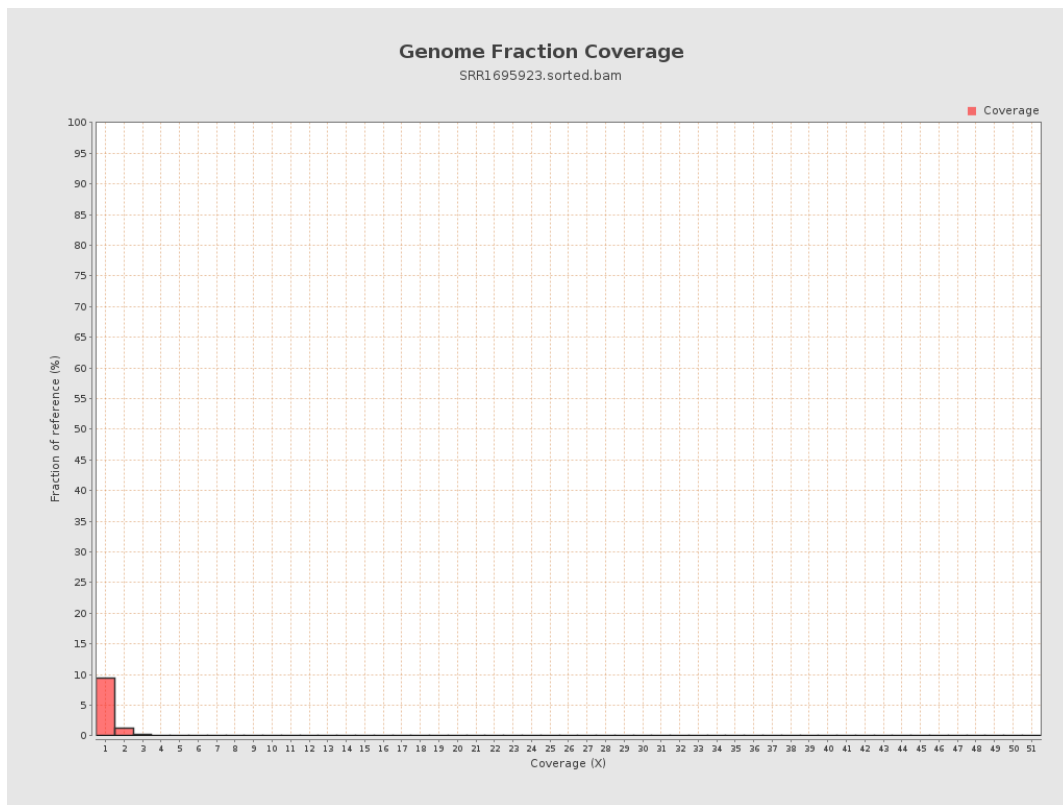
4. Results : Coverage Histogram



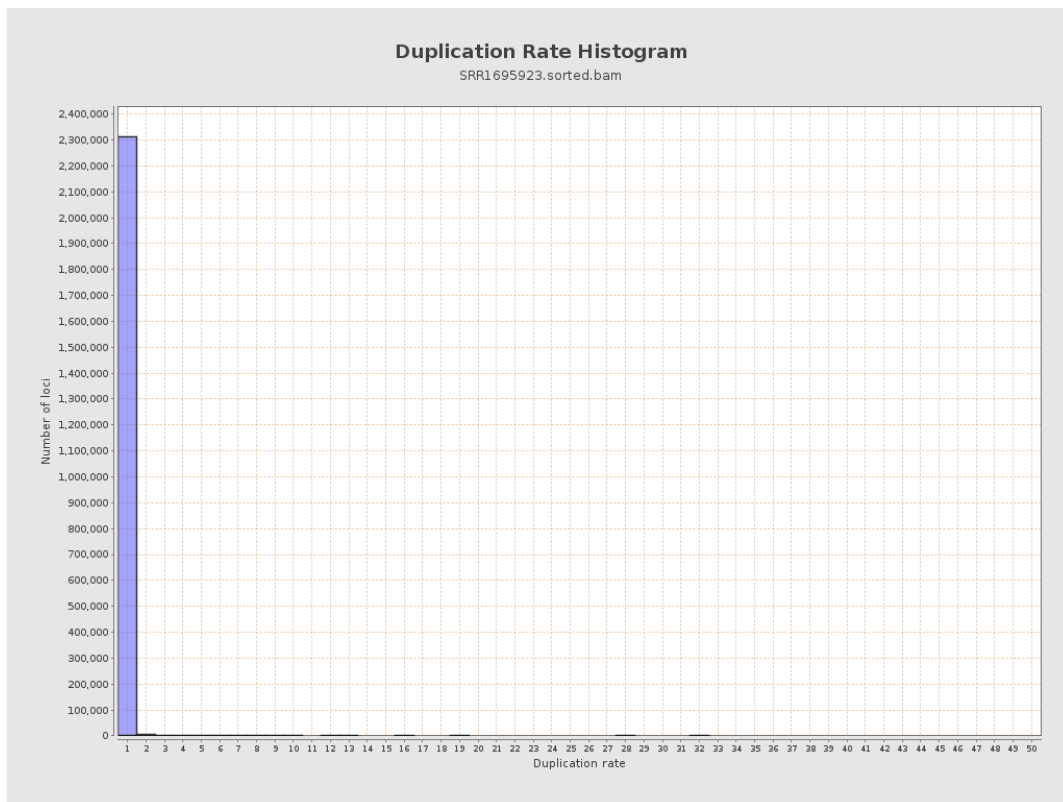
5. Results : Coverage Histogram (0-50X)



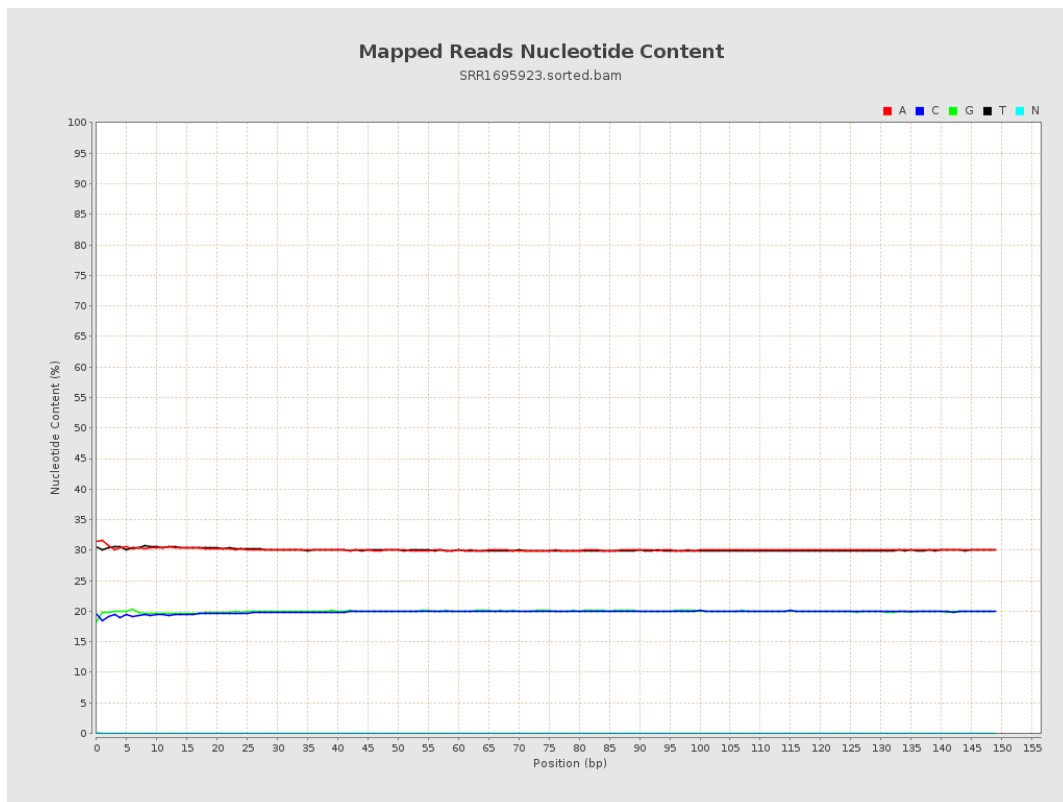
6. Results : Genome Fraction Coverage



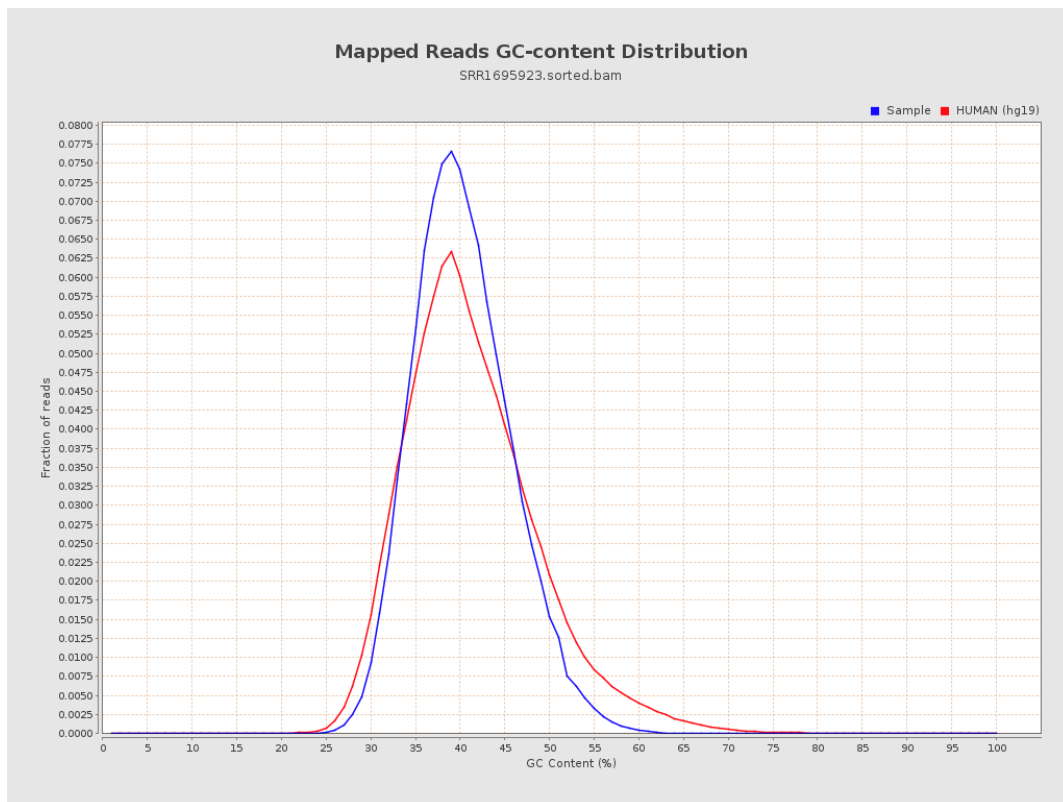
7. Results : Duplication Rate Histogram



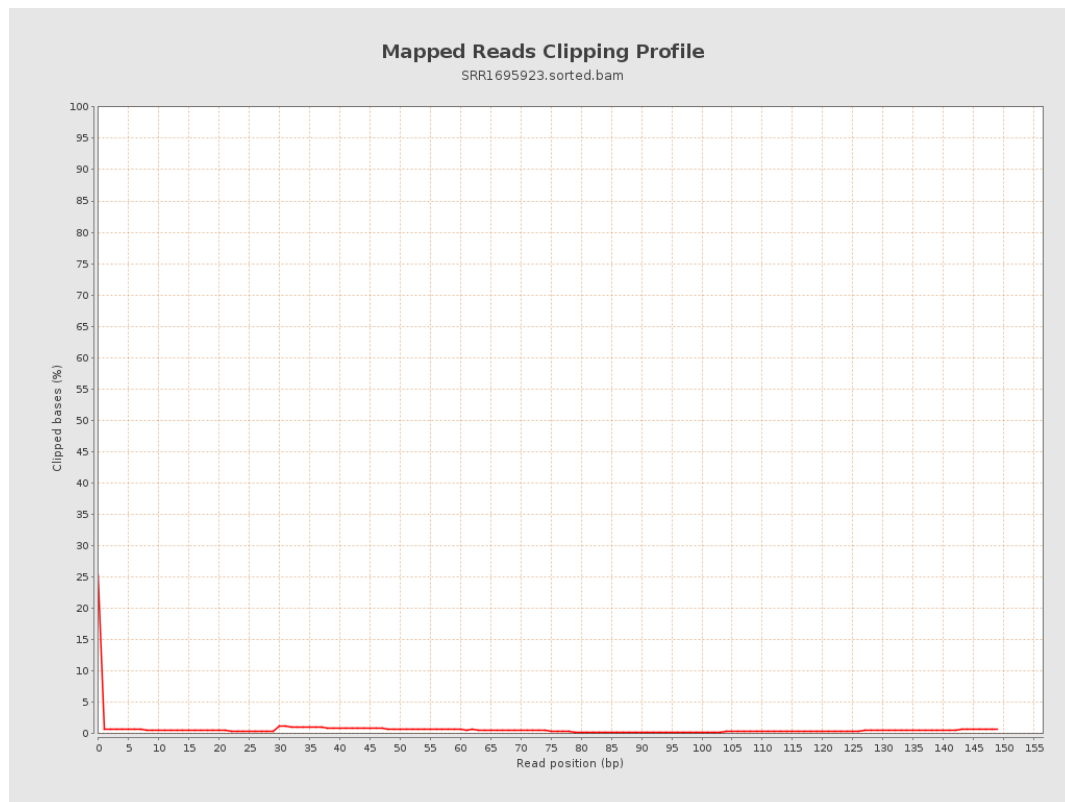
8. Results : Mapped Reads Nucleotide Content



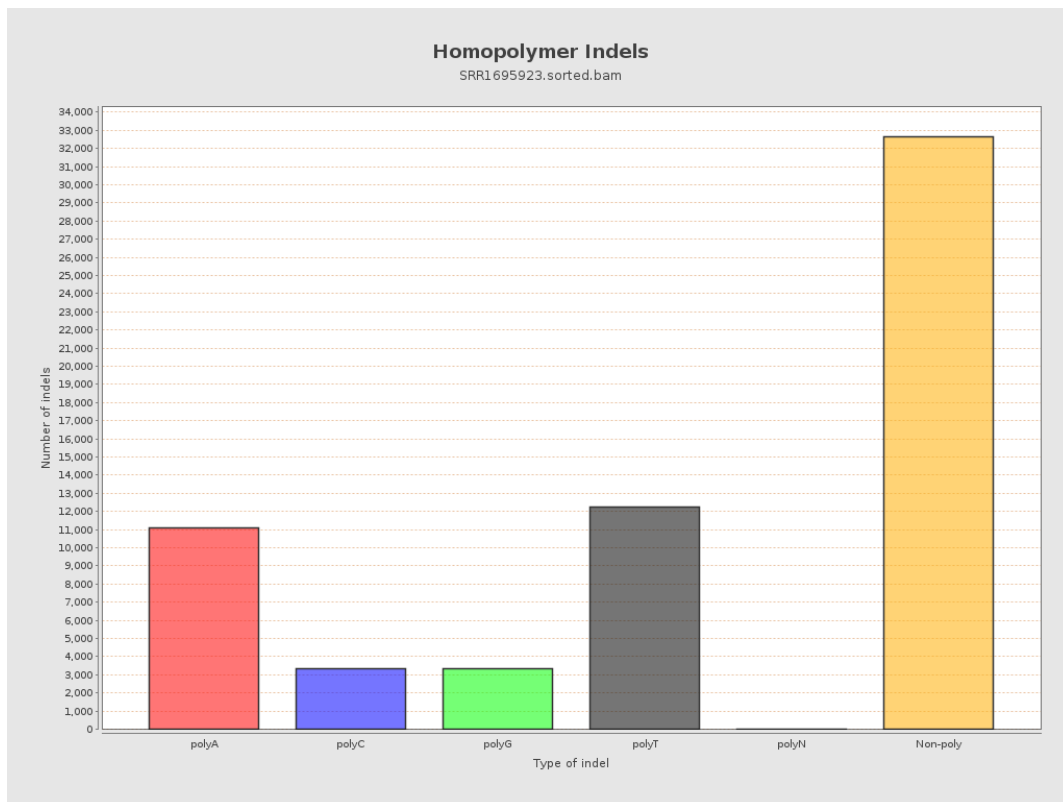
9. Results : Mapped Reads GC-content Distribution



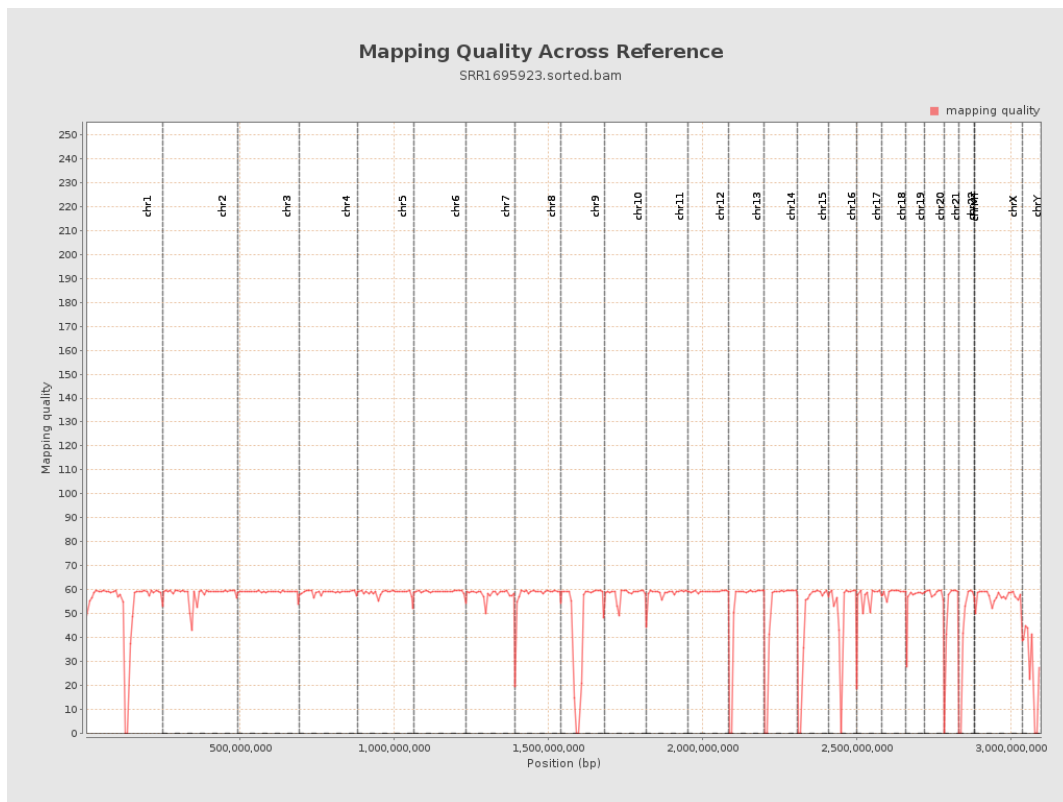
10. Results : Mapped Reads Clipping Profile



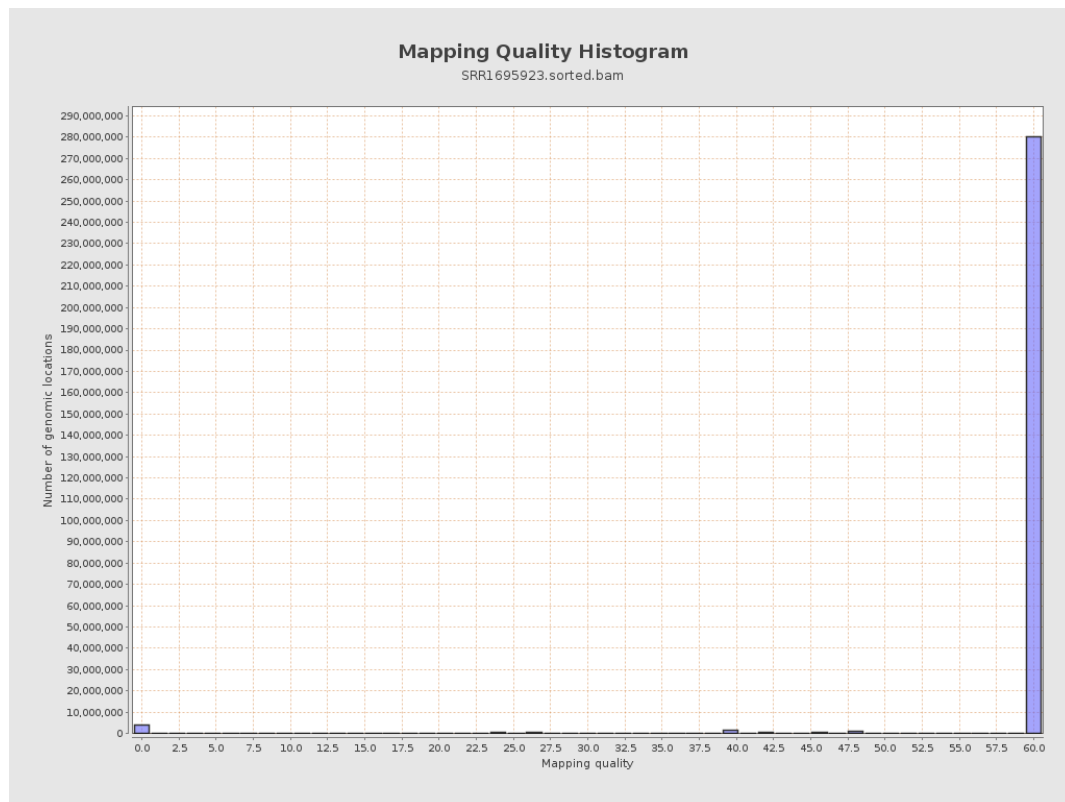
11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



15. Results : Insert Size Histogram

