

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 03:45:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472671.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR3472671 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472671_1.fastq.gz SRR3472671_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 03:45:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472671.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,160,876
Mapped reads	18,997,142 / 99.15%
Unmapped reads	163,734 / 0.85%
Mapped paired reads	18,997,142 / 99.15%
Mapped reads, first in pair	9,523,793 / 49.7%
Mapped reads, second in pair	9,473,349 / 49.44%
Mapped reads, both in pair	18,895,702 / 98.62%
Mapped reads, singletons	101,440 / 0.53%
Secondary alignments	0
Supplementary alignments	114,181 / 0.6%
Read min/max/mean length	30 / 101 / 99.74
Duplicated reads (estimated)	13,572,582 / 70.83%
Duplication rate	49.56%
Clipped reads	1,399,716 / 7.31%

2.2. ACGT Content

Number/percentage of A's	496,460,555 / 26.58%
Number/percentage of C's	439,600,966 / 23.54%
Number/percentage of T's	497,717,471 / 26.65%
Number/percentage of G's	433,518,155 / 23.21%
Number/percentage of N's	356,941 / 0.02%

GC Percentage	46.75%
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2.3. Coverage

Mean	0.6034
Standard Deviation	28.4965

2.4. Mapping Quality

Mean Mapping Quality	54.8
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2.5. Insert size

Mean	22,283.39
Standard Deviation	1,520,645.15
P25/Median/P75	155 / 213 / 283

2.6. Mismatches and indels

General error rate	0.62%
Mismatches	11,429,418
Insertions	125,292
Mapped reads with at least one insertion	0.65%
Deletions	113,275
Mapped reads with at least one deletion	0.59%
Homopolymer indels	48.52%

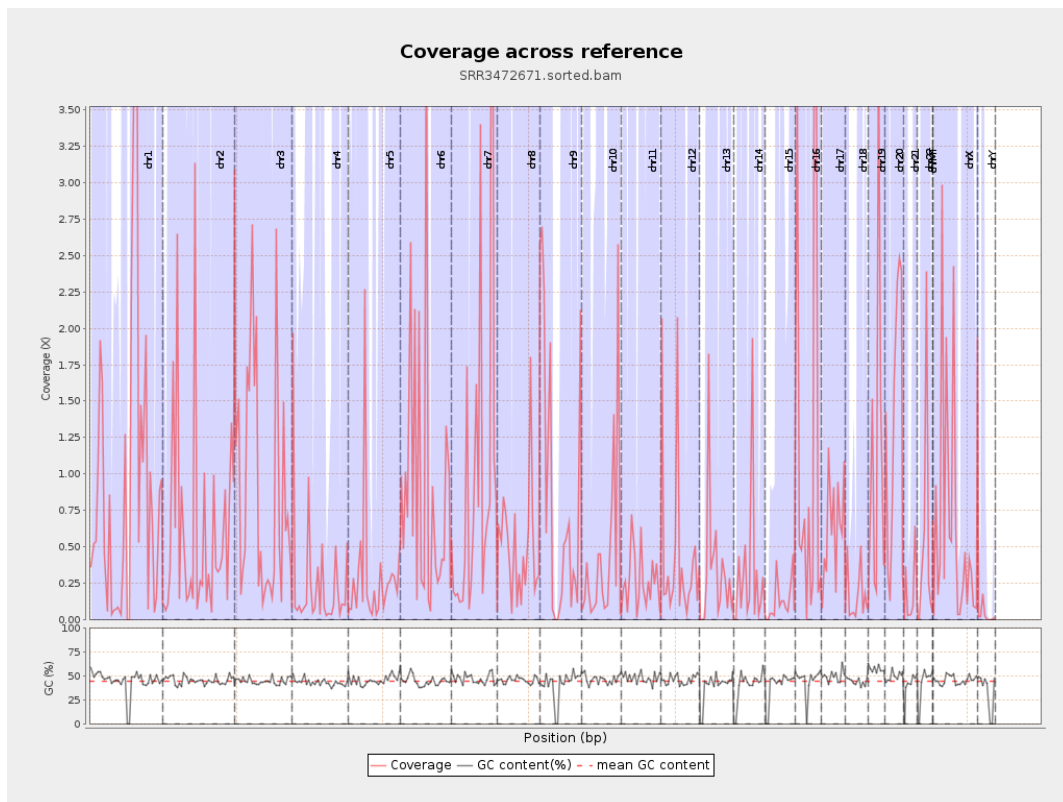
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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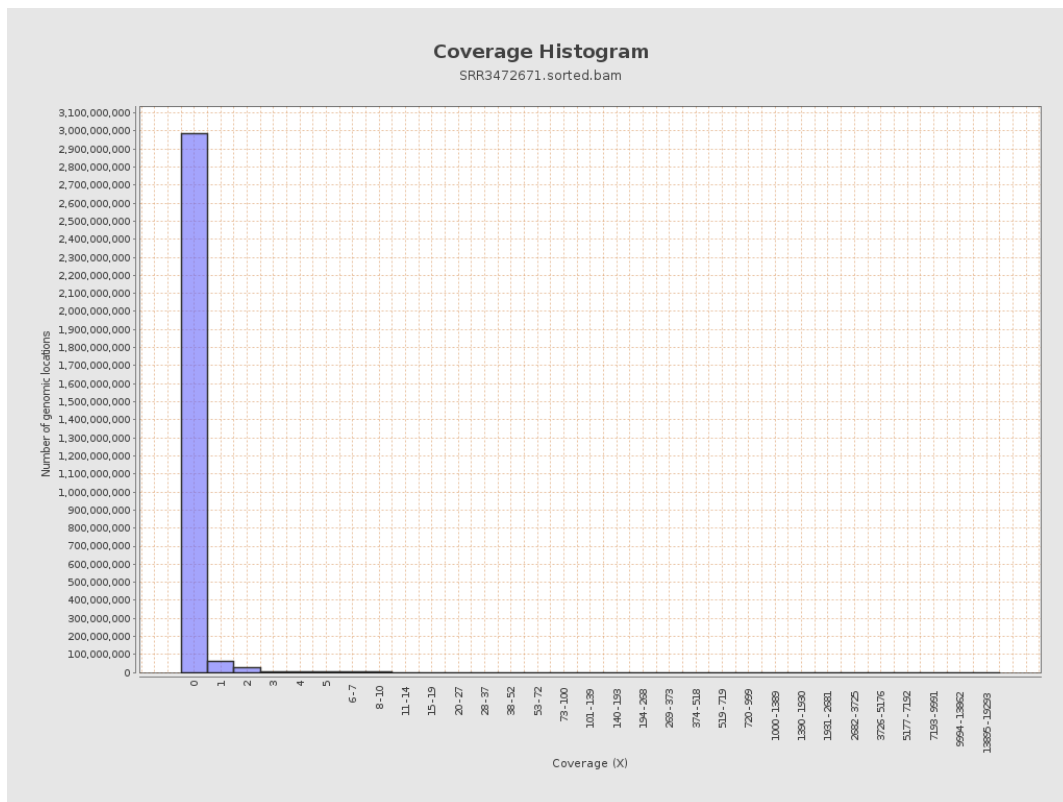
		bases	coverage	deviation
chr1	249250621	229902568	0.9224	35.7627
chr2	243199373	150400462	0.6184	34.5102
chr3	198022430	178435547	0.9011	28.0795
chr4	191154276	46601261	0.2438	13.0947
chr5	180915260	53488852	0.2957	11.6959
chr6	171115067	158055258	0.9237	39.5146
chr7	159138663	159934764	1.005	46.2438
chr8	146364022	73792656	0.5042	16.8581
chr9	141213431	108637174	0.7693	23.6812
chr10	135534747	60081506	0.4433	34.8411
chr11	135006516	35734784	0.2647	10.1047
chr12	133851895	59801642	0.4468	16.8295
chr13	115169878	37943337	0.3295	15.8289
chr14	107349540	32967710	0.3071	18.5074
chr15	102531392	13356077	0.1303	5.2976
chr16	90354753	109466520	1.2115	44.3937
chr17	81195210	49874009	0.6142	18.8128
chr18	78077248	12990572	0.1664	8.9422
chr19	59128983	67214737	1.1367	59.6736
chr20	63025520	86592005	1.3739	41.4982
chr21	48129895	9595790	0.1994	12.0948
chr22	51304566	28217991	0.55	23.3592
chrMT	16571	11195	0.6756	1.1059
chrX	155270560	102853149	0.6624	26.7128

chrY	59373566	1961522	0.033	2.777
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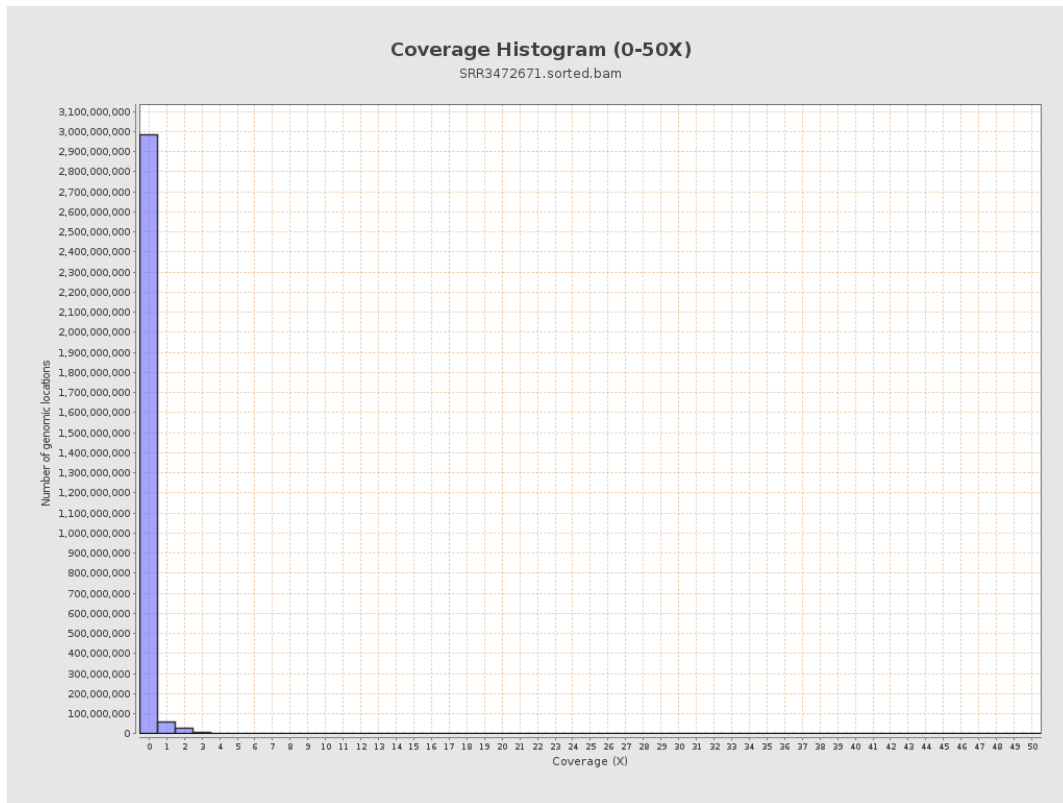
3. Results : Coverage across reference



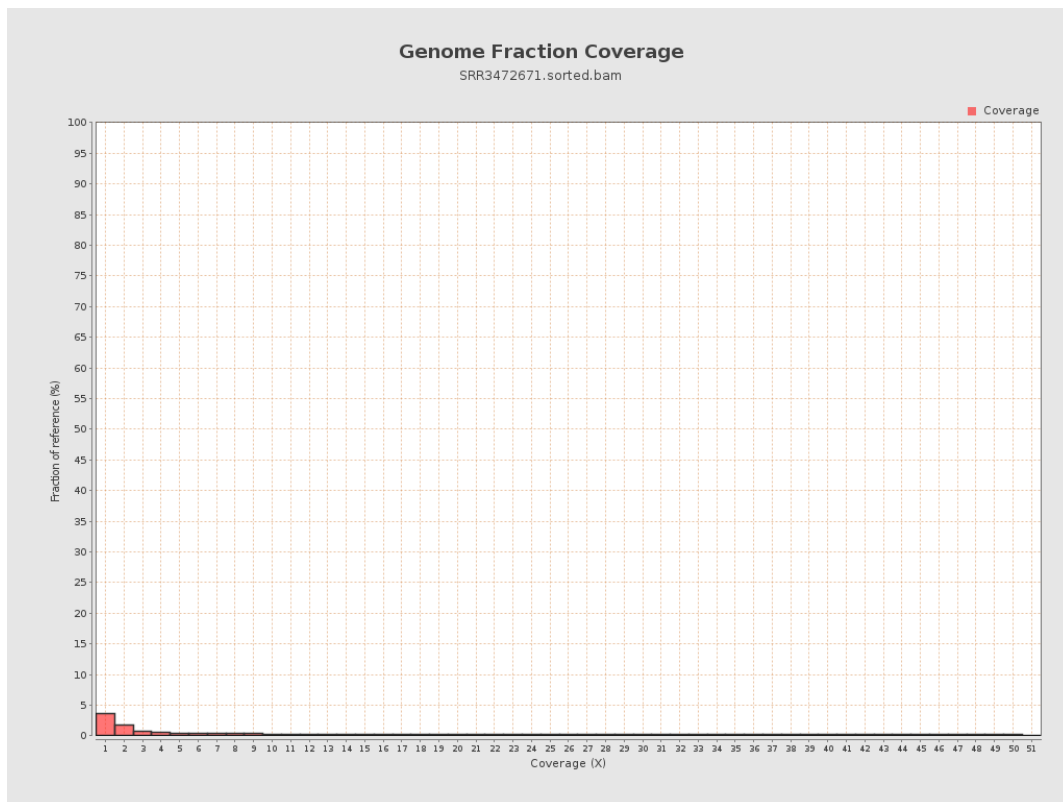
4. Results : Coverage Histogram



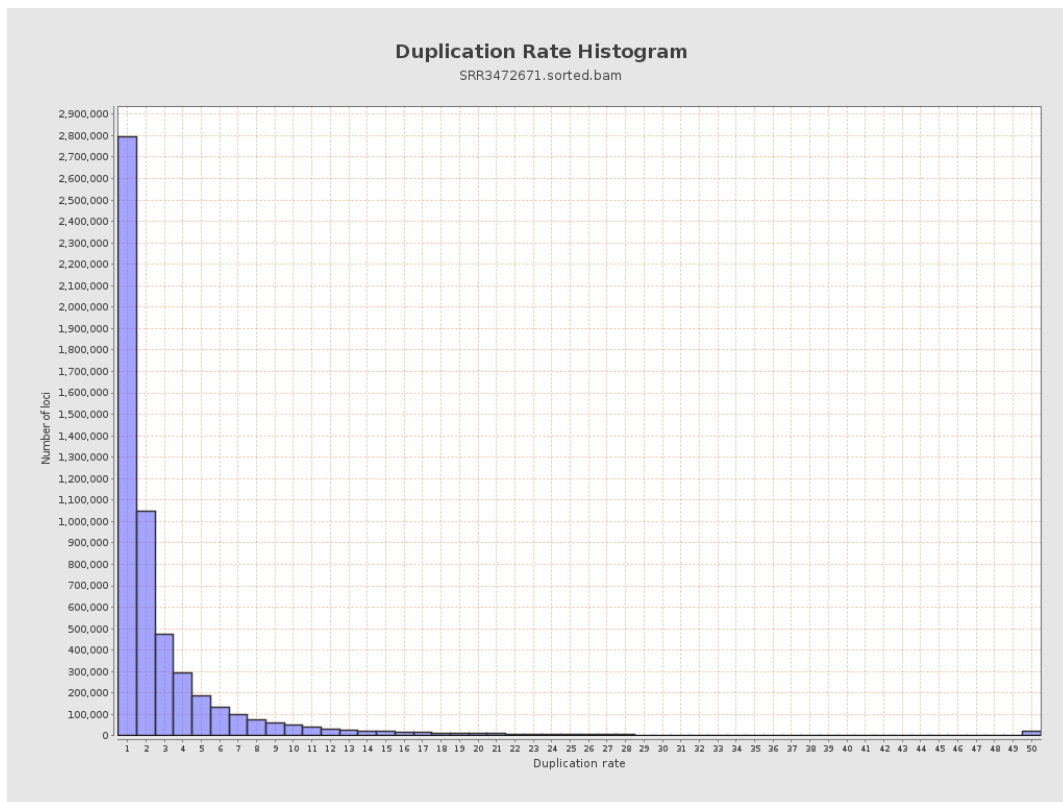
5. Results : Coverage Histogram (0-50X)



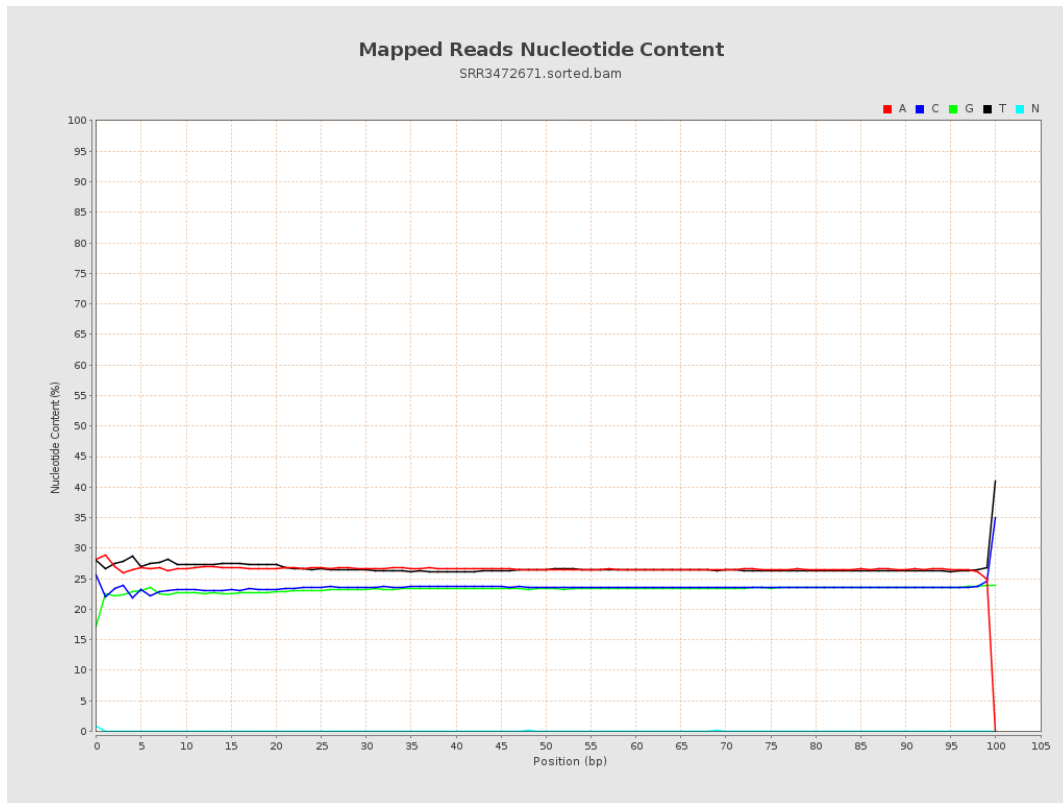
6. Results : Genome Fraction Coverage



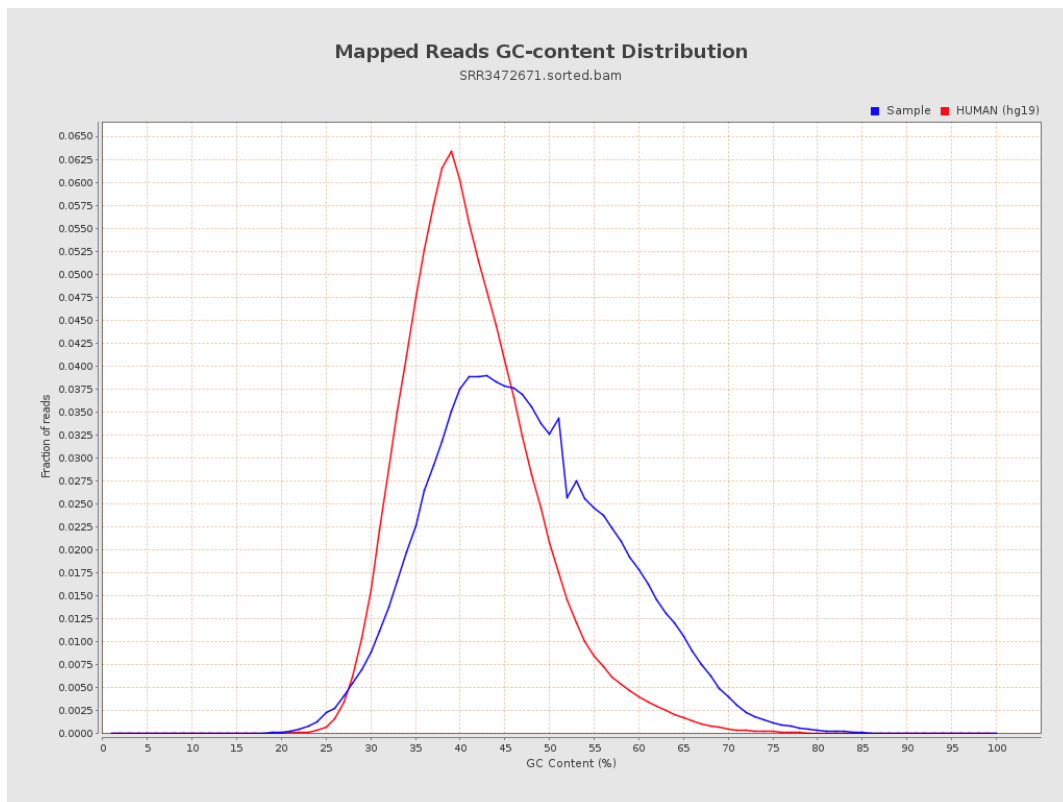
7. Results : Duplication Rate Histogram



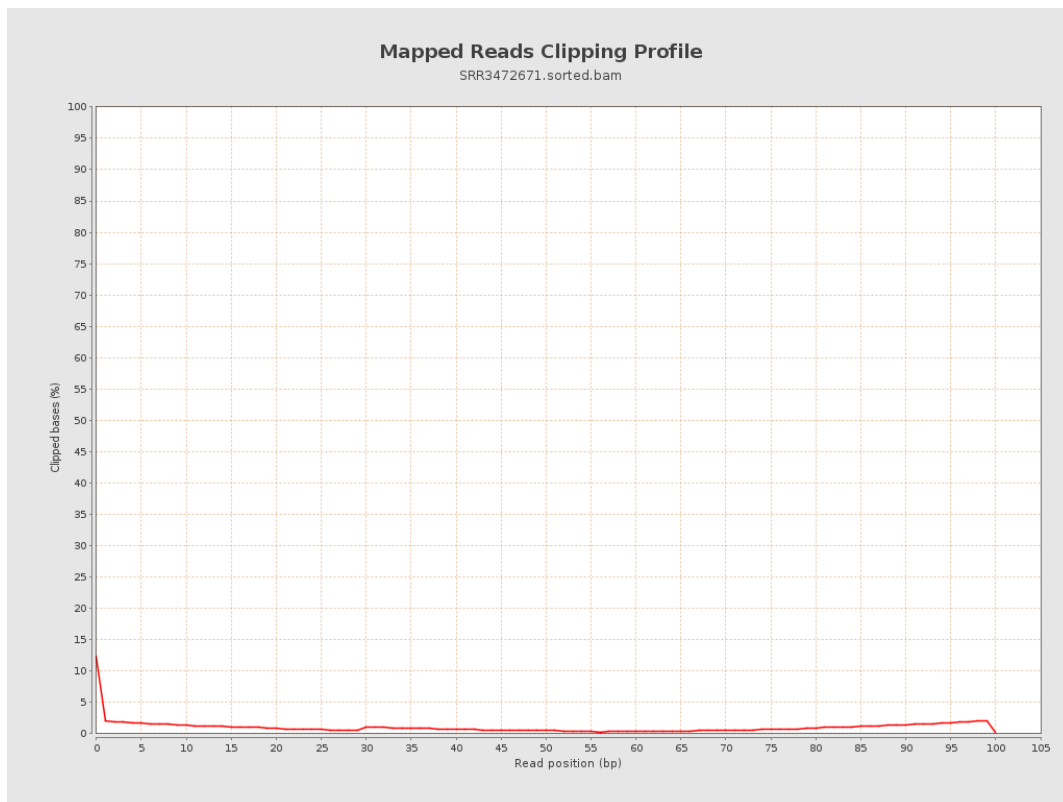
8. Results : Mapped Reads Nucleotide Content



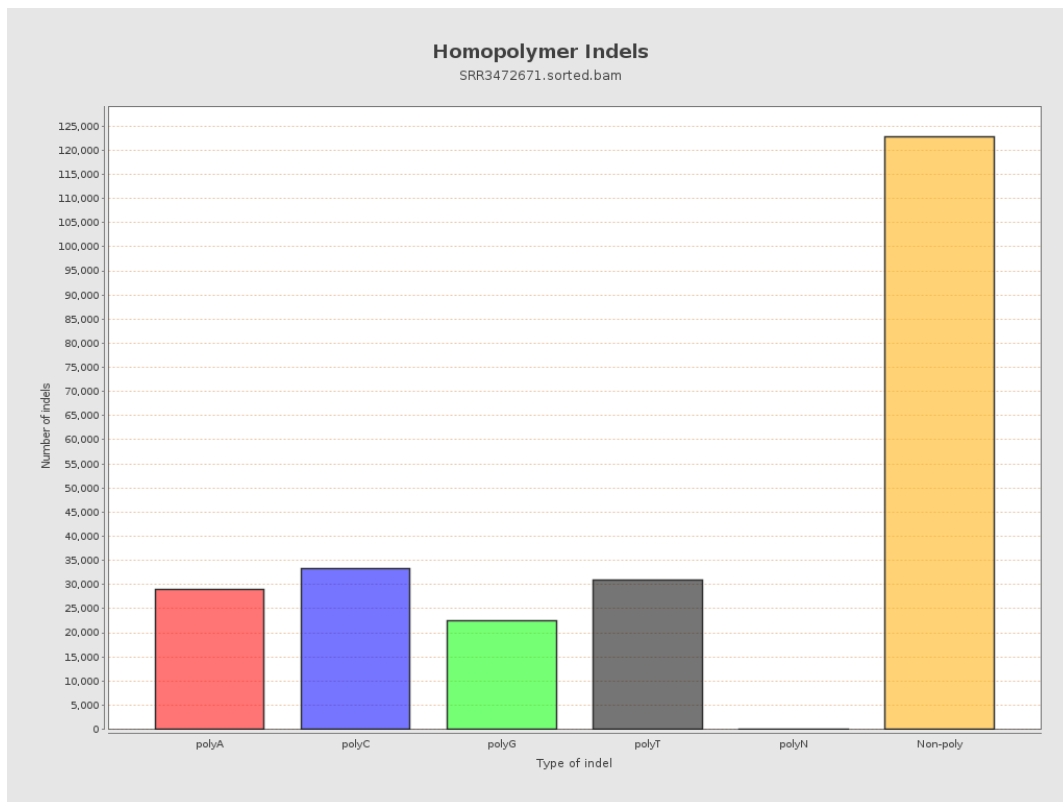
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



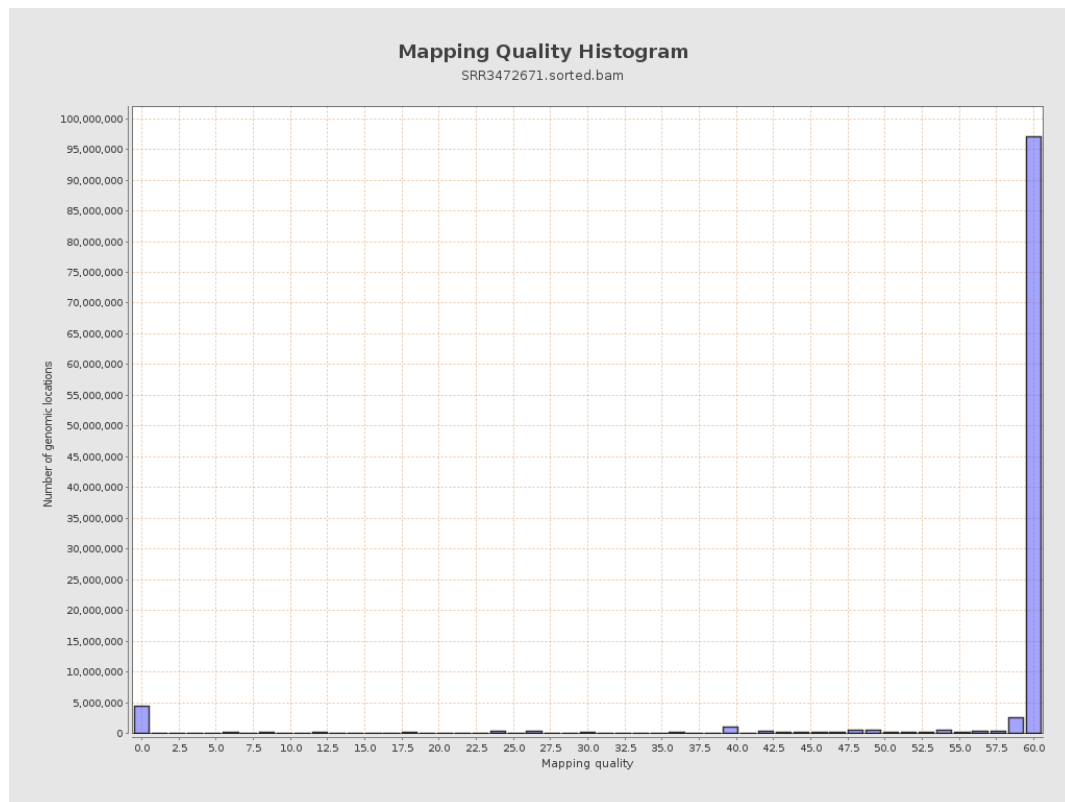
11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



15. Results : Insert Size Histogram

