

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 13:36:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472700.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_SRR3472700 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472700_1.fastq.gz SRR3472700_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 13:36:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472700.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,580,182
Mapped reads	12,436,574 / 98.86%
Unmapped reads	143,608 / 1.14%
Mapped paired reads	12,436,574 / 98.86%
Mapped reads, first in pair	6,239,072 / 49.59%
Mapped reads, second in pair	6,197,502 / 49.26%
Mapped reads, both in pair	12,367,674 / 98.31%
Mapped reads, singletons	68,900 / 0.55%
Secondary alignments	0
Supplementary alignments	39,400 / 0.31%
Read min/max/mean length	30 / 100 / 100.13
Duplicated reads (estimated)	7,486,352 / 59.51%
Duplication rate	46.75%
Clipped reads	1,024,138 / 8.14%

2.2. ACGT Content

Number/percentage of A's	328,888,298 / 26.87%
Number/percentage of C's	285,129,063 / 23.3%
Number/percentage of T's	326,470,814 / 26.67%
Number/percentage of G's	283,178,573 / 23.14%
Number/percentage of N's	239,802 / 0.02%

GC Percentage	46.43%
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2.3. Coverage

Mean	0.3954
Standard Deviation	13.3935

2.4. Mapping Quality

Mean Mapping Quality	55.06
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2.5. Insert size

Mean	21,543.48
Standard Deviation	1,424,830.36
P25/Median/P75	169 / 236 / 319

2.6. Mismatches and indels

General error rate	0.62%
Mismatches	7,421,141
Insertions	73,481
Mapped reads with at least one insertion	0.58%
Deletions	64,726
Mapped reads with at least one deletion	0.51%
Homopolymer indels	46.72%

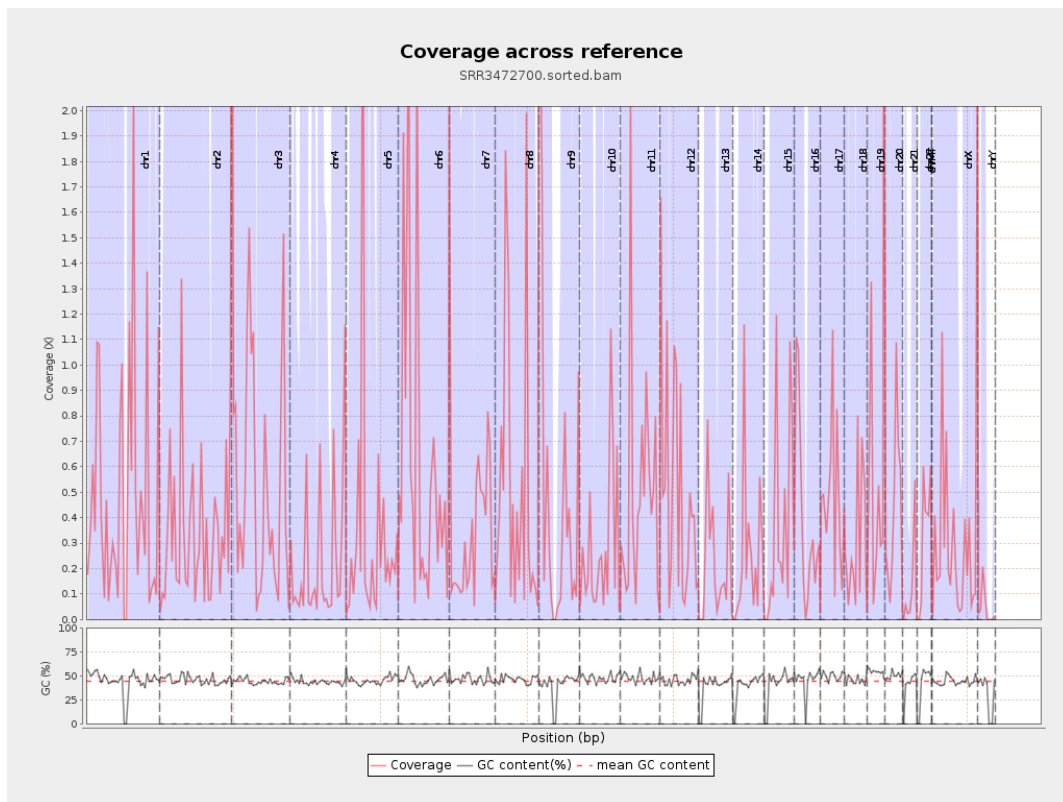
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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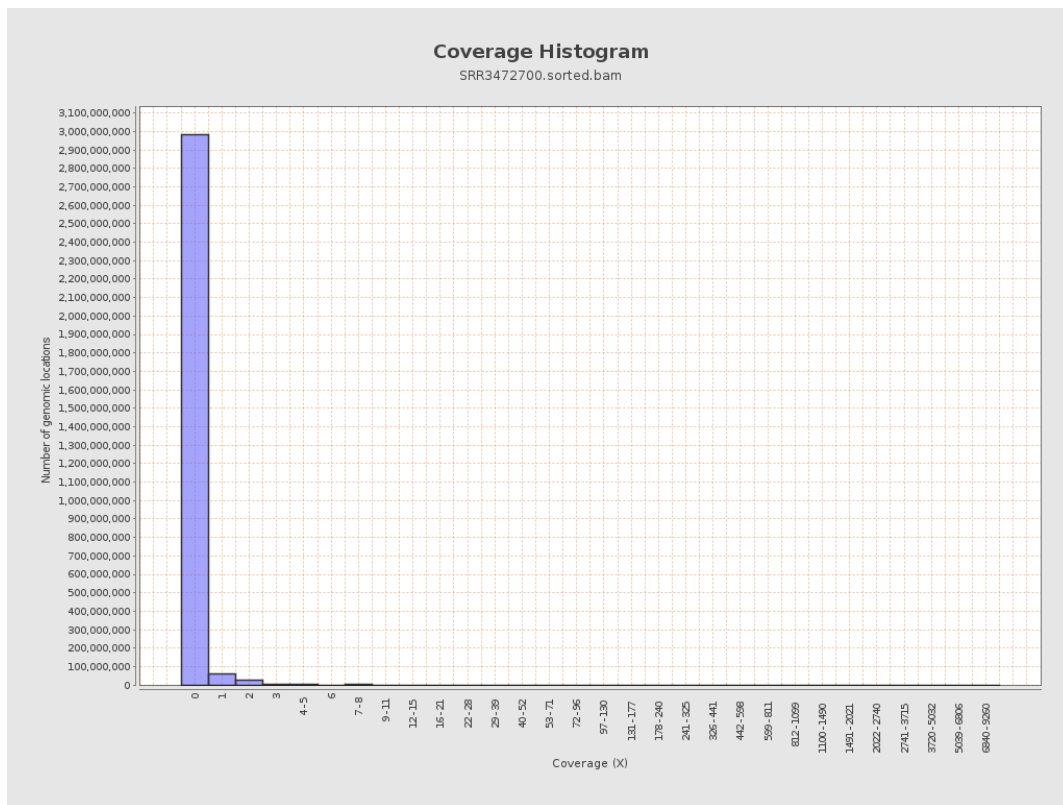
		bases	coverage	deviation
chr1	249250621	123327327	0.4948	13.8016
chr2	243199373	82300846	0.3384	11.0387
chr3	198022430	113760192	0.5745	14.166
chr4	191154276	42344056	0.2215	8.7593
chr5	180915260	61521188	0.3401	13.014
chr6	171115067	105775081	0.6182	18.2106
chr7	159138663	57253536	0.3598	12.2666
chr8	146364022	74872518	0.5116	17.4419
chr9	141213431	71782221	0.5083	16.0529
chr10	135534747	38466227	0.2838	14.8015
chr11	135006516	67790814	0.5021	19.125
chr12	133851895	69226146	0.5172	14.9511
chr13	115169878	25720804	0.2233	8.2263
chr14	107349540	26237414	0.2444	9.8191
chr15	102531392	36738921	0.3583	11.9382
chr16	90354753	32992154	0.3651	9.8109
chr17	81195210	39121274	0.4818	13.2229
chr18	78077248	23677379	0.3033	12.8922
chr19	59128983	32183323	0.5443	17.1312
chr20	63025520	27232143	0.4321	13.7931
chr21	48129895	6166262	0.1281	5.9926
chr22	51304566	16402374	0.3197	10.9128
chrMT	16571	4082	0.2463	0.8019
chrX	155270560	46210015	0.2976	10.302

chrY	59373566	2973228	0.0501	1.9106
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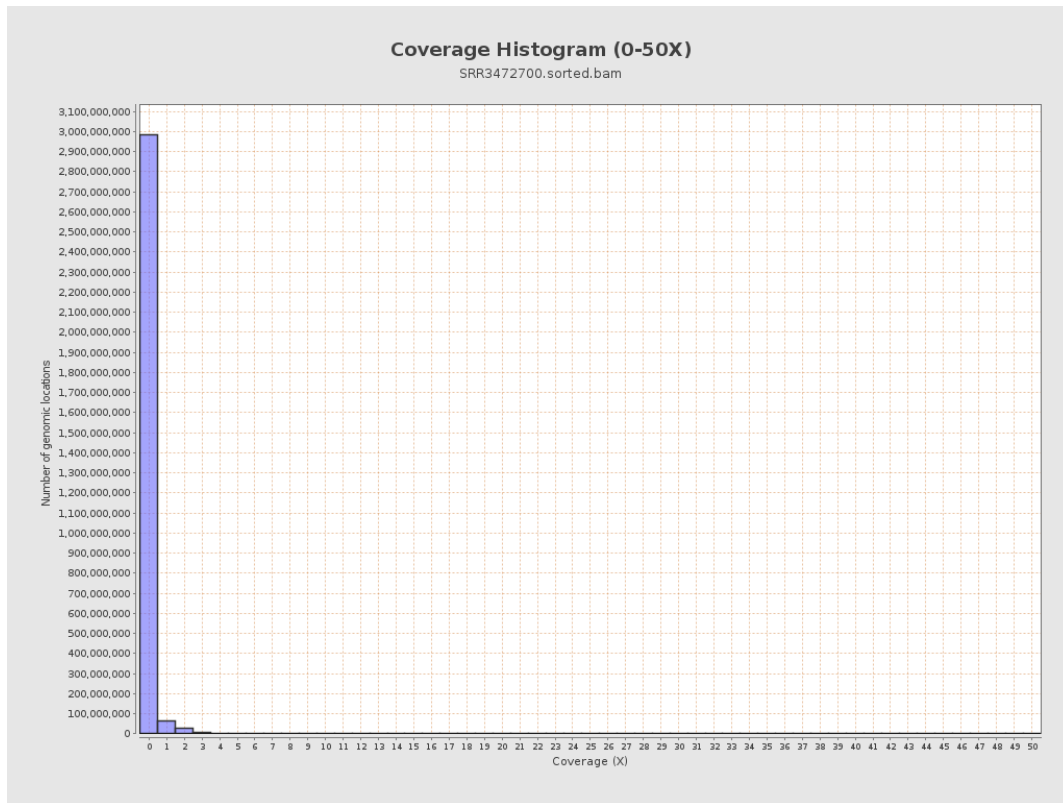
3. Results : Coverage across reference



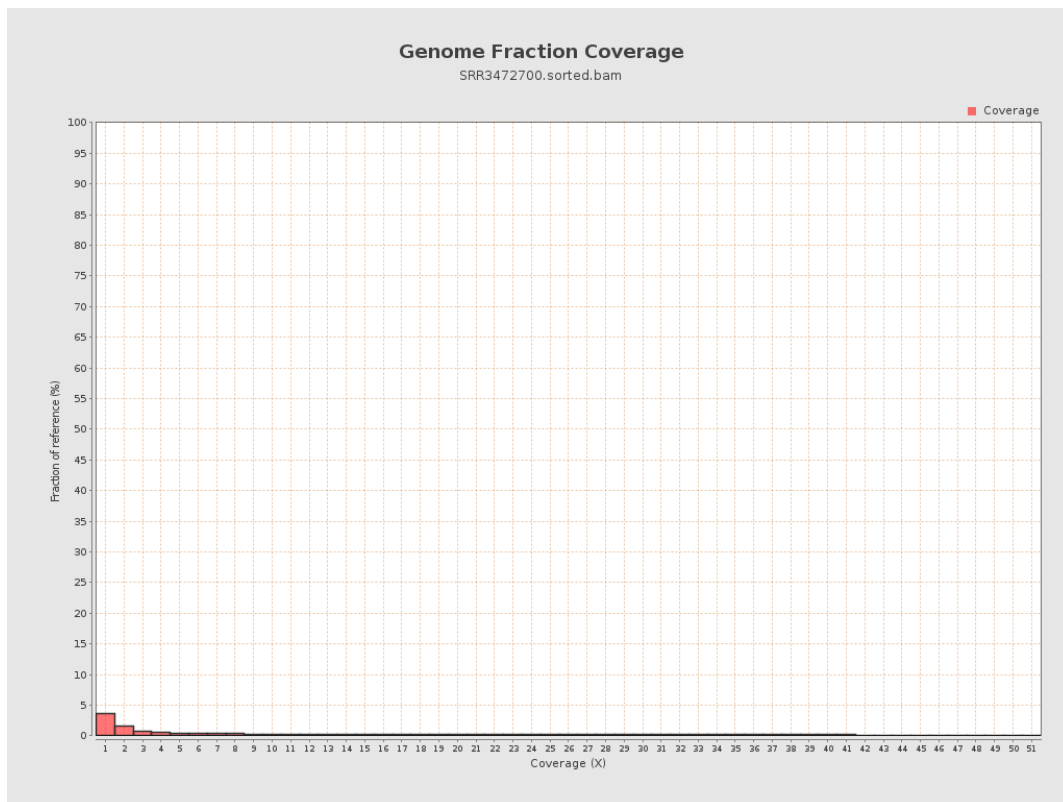
4. Results : Coverage Histogram



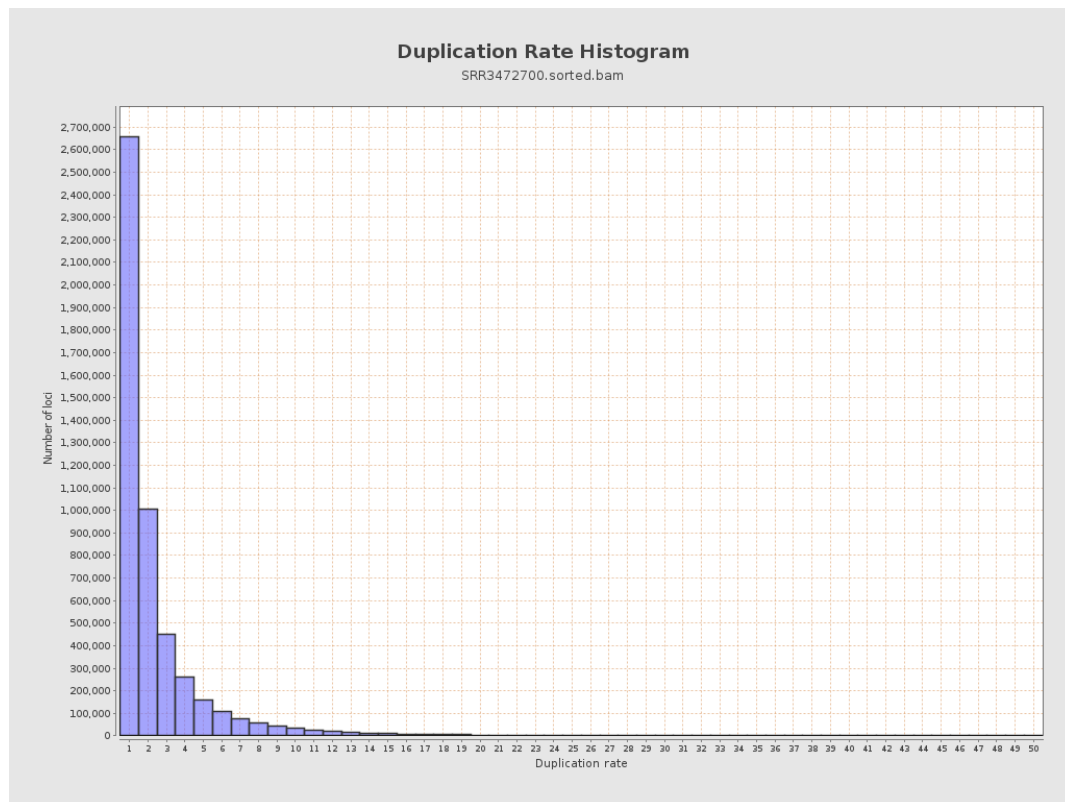
5. Results : Coverage Histogram (0-50X)



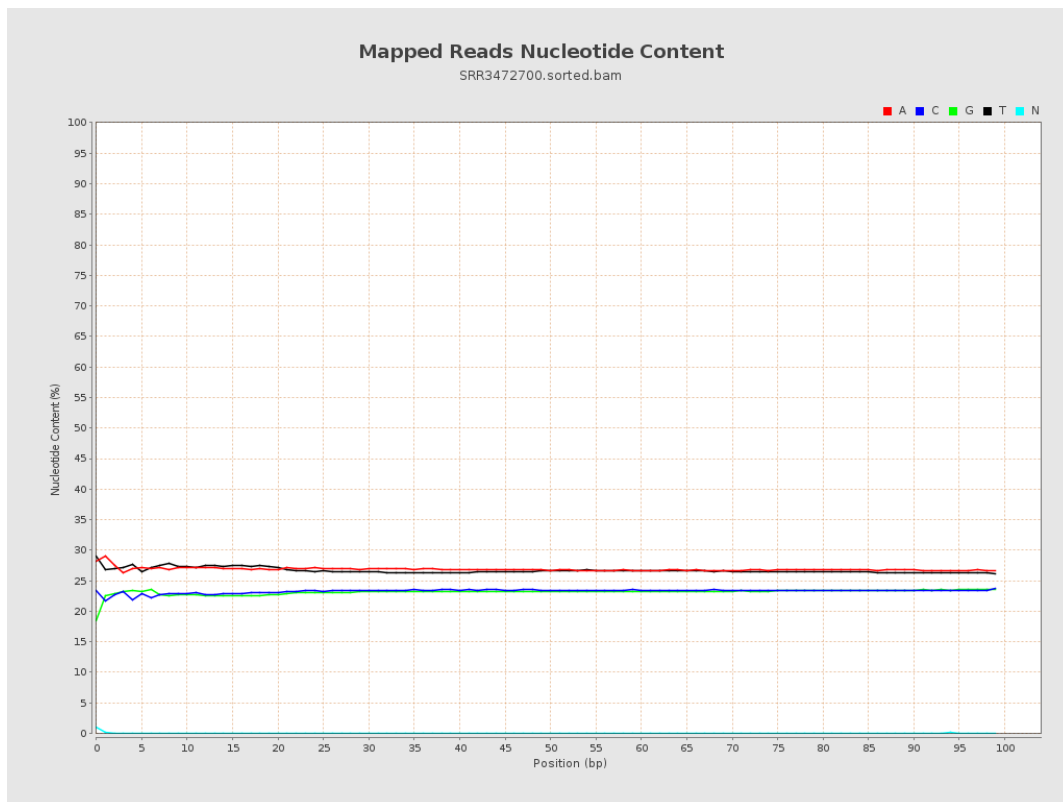
6. Results : Genome Fraction Coverage



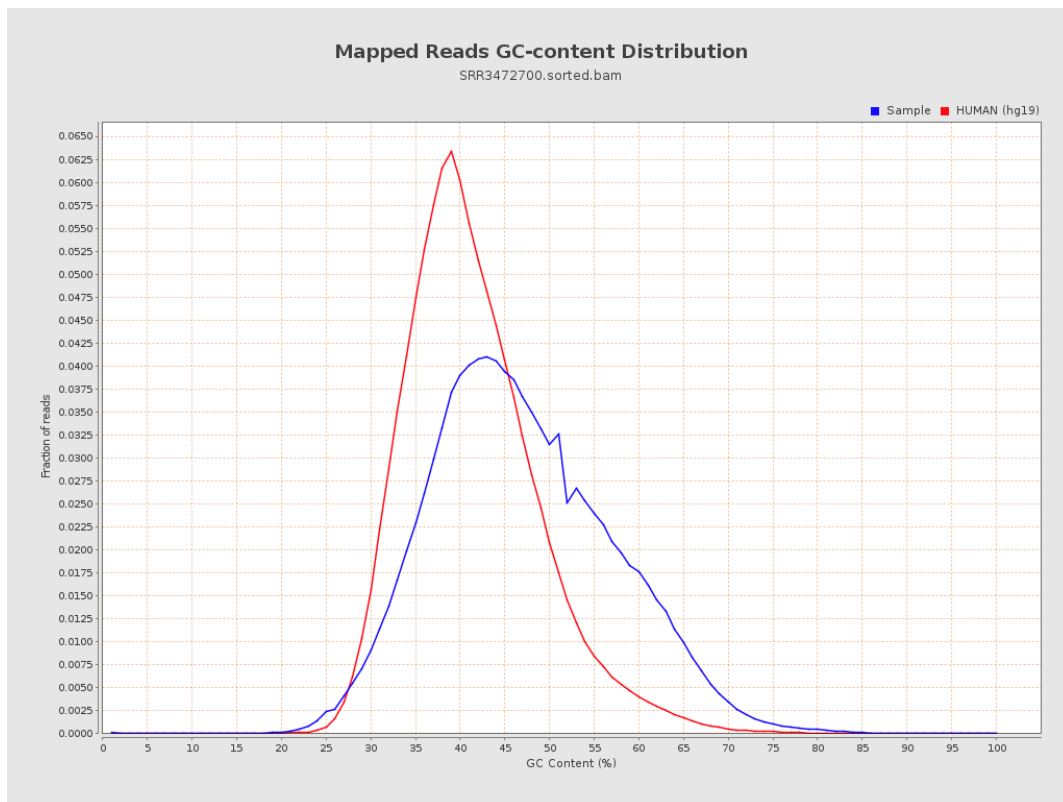
7. Results : Duplication Rate Histogram



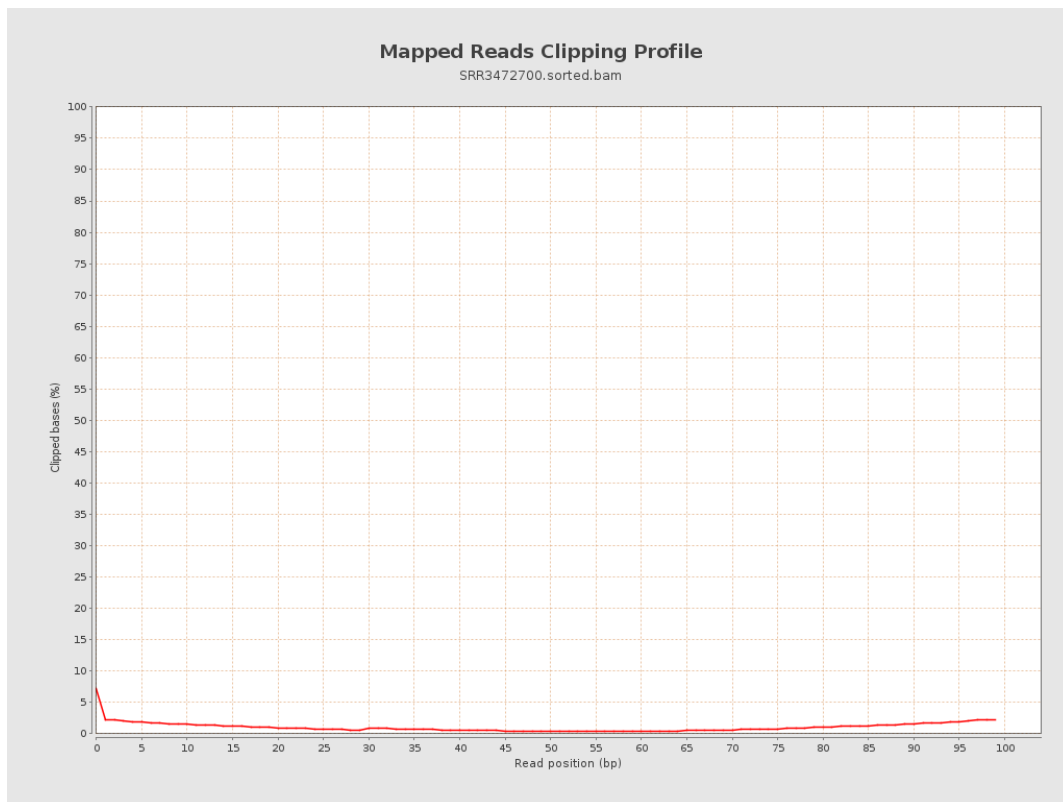
8. Results : Mapped Reads Nucleotide Content



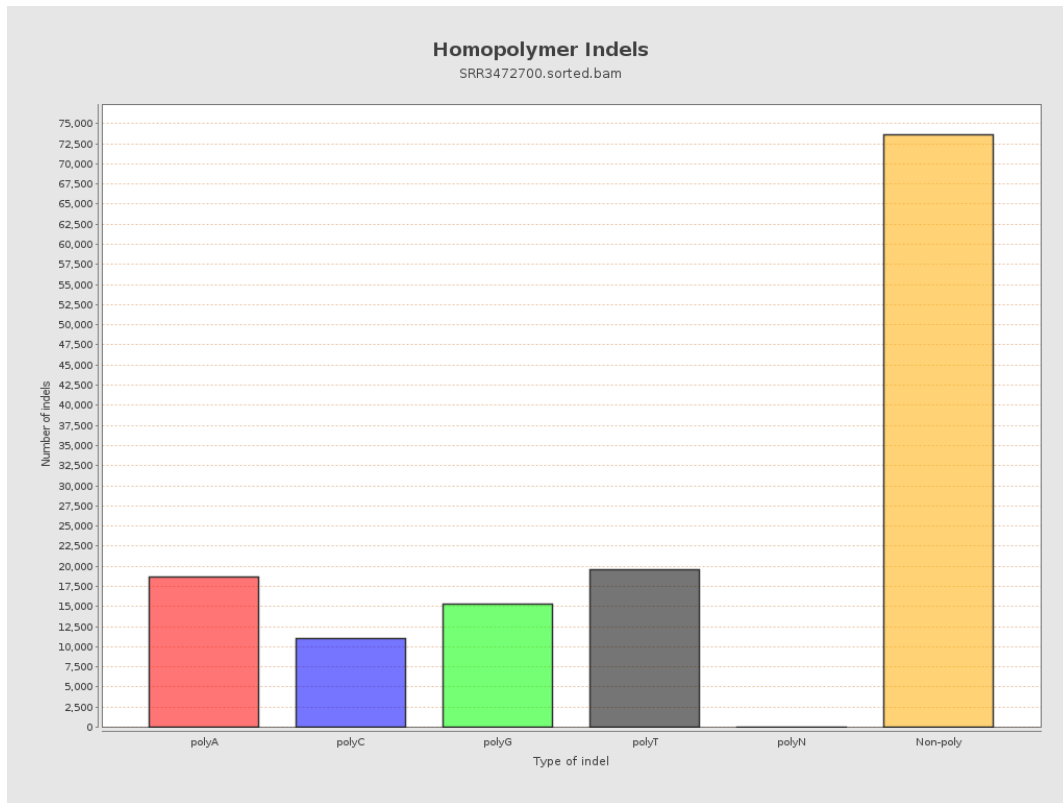
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



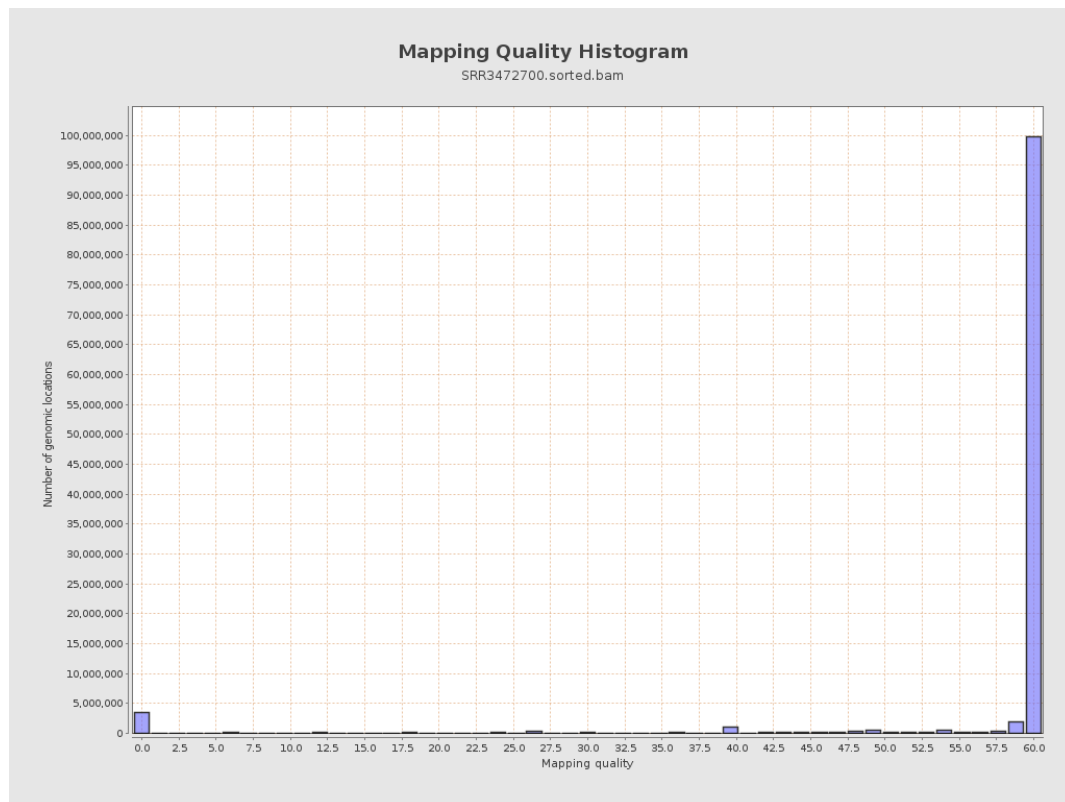
11. Results : Homopolymer Indels



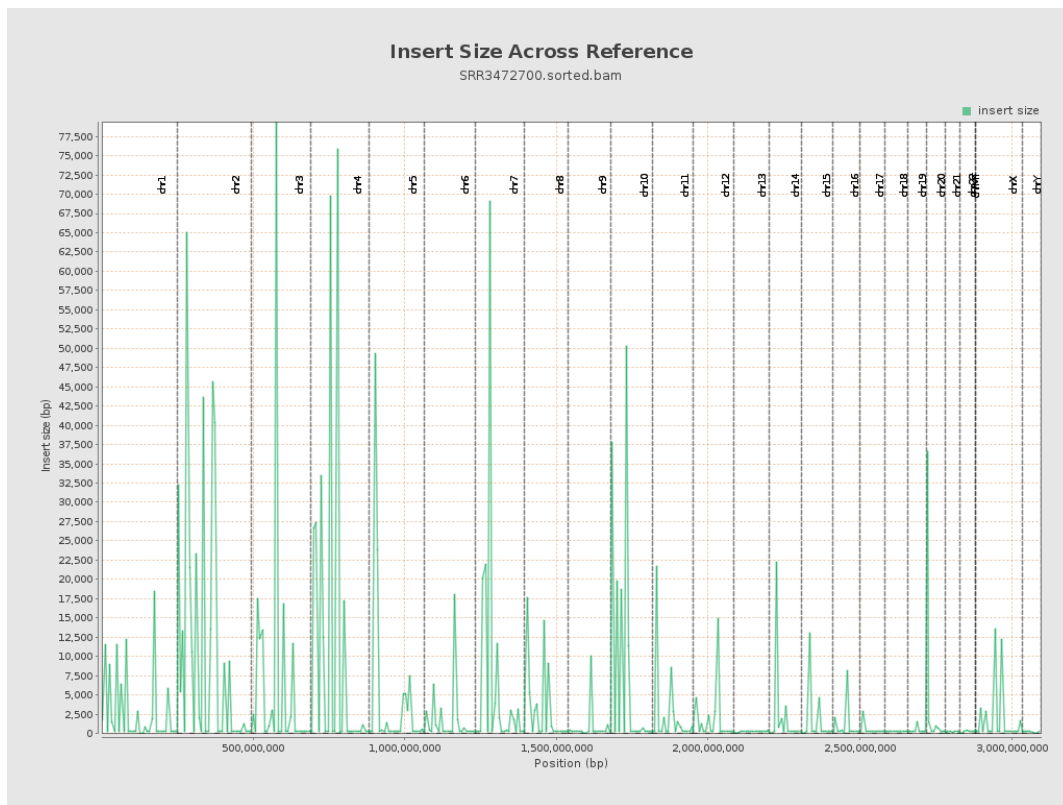
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

