

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 09:24:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472689.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_SRR3472689 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472689_1.fastq.gz SRR3472689_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 09:24:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472689.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,315,992
Mapped reads	14,191,937 / 99.13%
Unmapped reads	124,055 / 0.87%
Mapped paired reads	14,191,937 / 99.13%
Mapped reads, first in pair	7,130,054 / 49.8%
Mapped reads, second in pair	7,061,883 / 49.33%
Mapped reads, both in pair	14,118,908 / 98.62%
Mapped reads, singletons	73,029 / 0.51%
Secondary alignments	0
Supplementary alignments	92,860 / 0.65%
Read min/max/mean length	30 / 101 / 99.54
Duplicated reads (estimated)	10,490,547 / 73.28%
Duplication rate	46.77%
Clipped reads	942,340 / 6.58%

2.2. ACGT Content

Number/percentage of A's	371,062,810 / 26.6%
Number/percentage of C's	326,470,931 / 23.4%
Number/percentage of T's	375,639,085 / 26.93%
Number/percentage of G's	321,543,749 / 23.05%
Number/percentage of N's	297,322 / 0.02%

GC Percentage	46.45%
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2.3. Coverage

Mean	0.4509
Standard Deviation	53.3535

2.4. Mapping Quality

Mean Mapping Quality	54.8
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2.5. Insert size

Mean	17,869.17
Standard Deviation	1,289,170.04
P25/Median/P75	151 / 208 / 275

2.6. Mismatches and indels

General error rate	0.5%
Mismatches	6,834,903
Insertions	100,914
Mapped reads with at least one insertion	0.7%
Deletions	119,274
Mapped reads with at least one deletion	0.83%
Homopolymer indels	40.82%

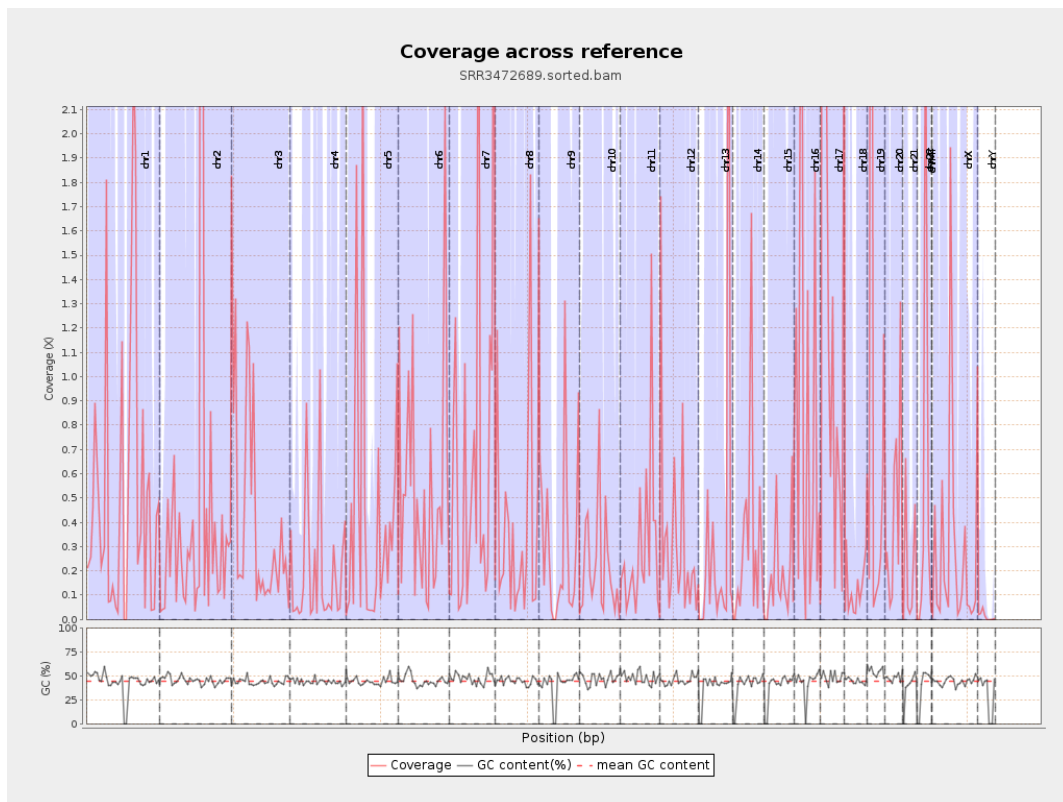
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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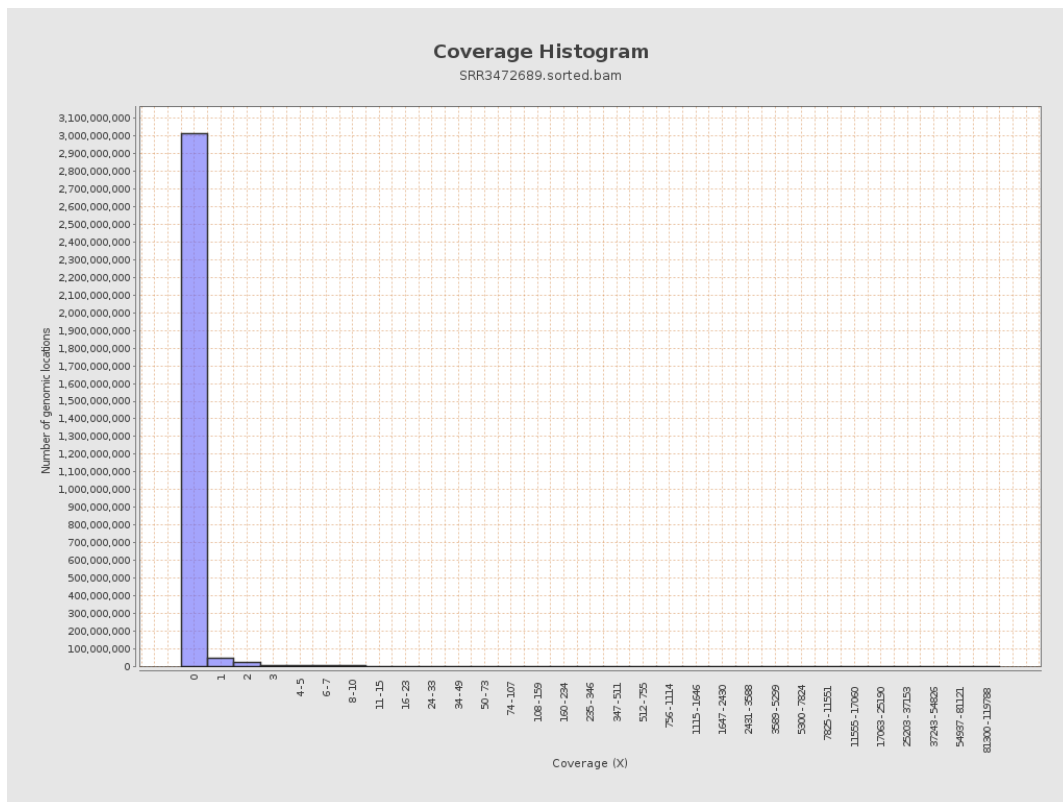
		bases	coverage	deviation
chr1	249250621	135661727	0.5443	25.0269
chr2	243199373	110313040	0.4536	78.6412
chr3	198022430	81463058	0.4114	17.2436
chr4	191154276	37007107	0.1936	13.378
chr5	180915260	79581426	0.4399	23.422
chr6	171115067	90815382	0.5307	21.4046
chr7	159138663	119710755	0.7522	37.316
chr8	146364022	56003036	0.3826	22.0382
chr9	141213431	46329651	0.3281	19.3247
chr10	135534747	29624003	0.2186	15.3865
chr11	135006516	40110970	0.2971	14.5854
chr12	133851895	43754911	0.3269	15.763
chr13	115169878	41961346	0.3643	40.5791
chr14	107349540	33131291	0.3086	16.5222
chr15	102531392	18942443	0.1847	10.1124
chr16	90354753	79236875	0.877	46.6521
chr17	81195210	175170449	2.1574	262.848
chr18	78077248	10533904	0.1349	4.9425
chr19	59128983	61295188	1.0366	65.2135
chr20	63025520	27093950	0.4299	28.2072
chr21	48129895	10838512	0.2252	18.6168
chr22	51304566	26044046	0.5076	23.5574
chrMT	16571	600	0.0362	0.1868
chrX	155270560	40379289	0.2601	19.1529

chrY	59373566	864044	0.0146	0.5666
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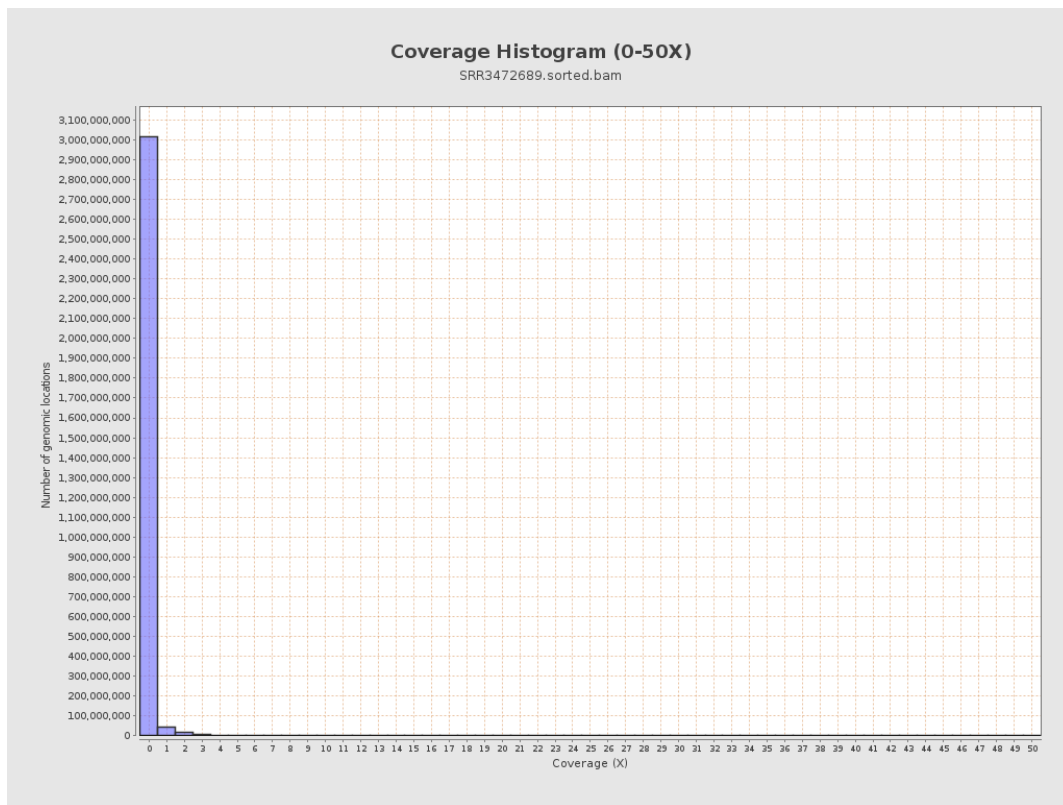
3. Results : Coverage across reference



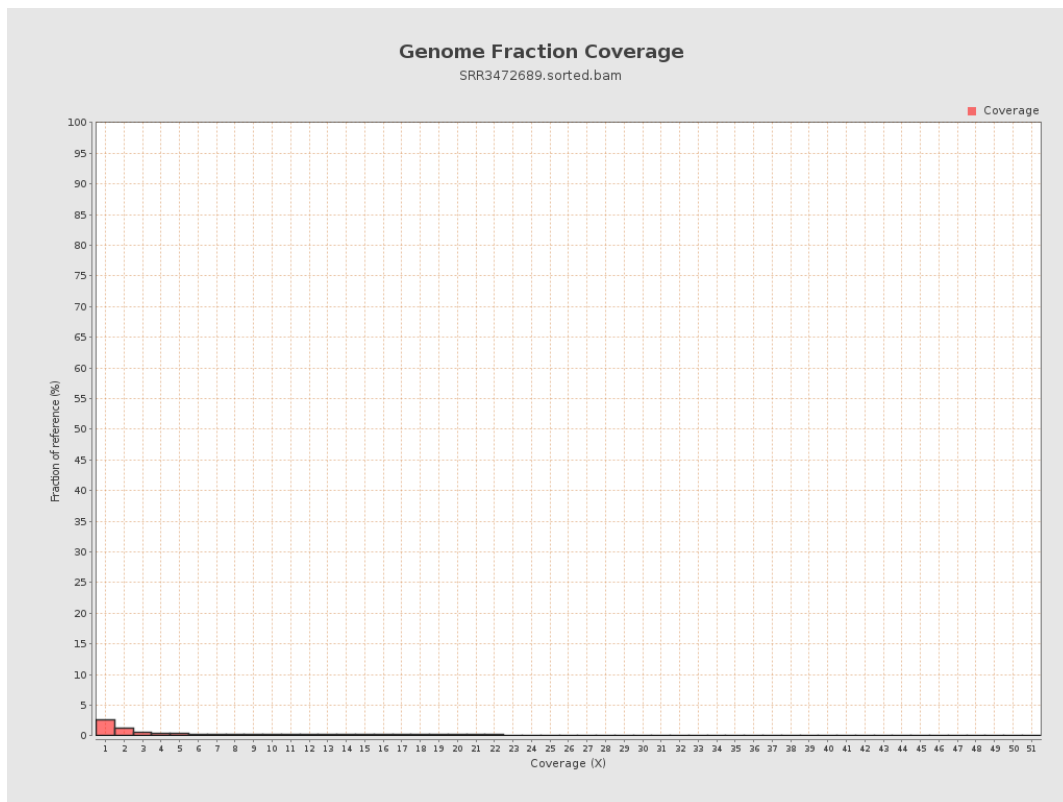
4. Results : Coverage Histogram



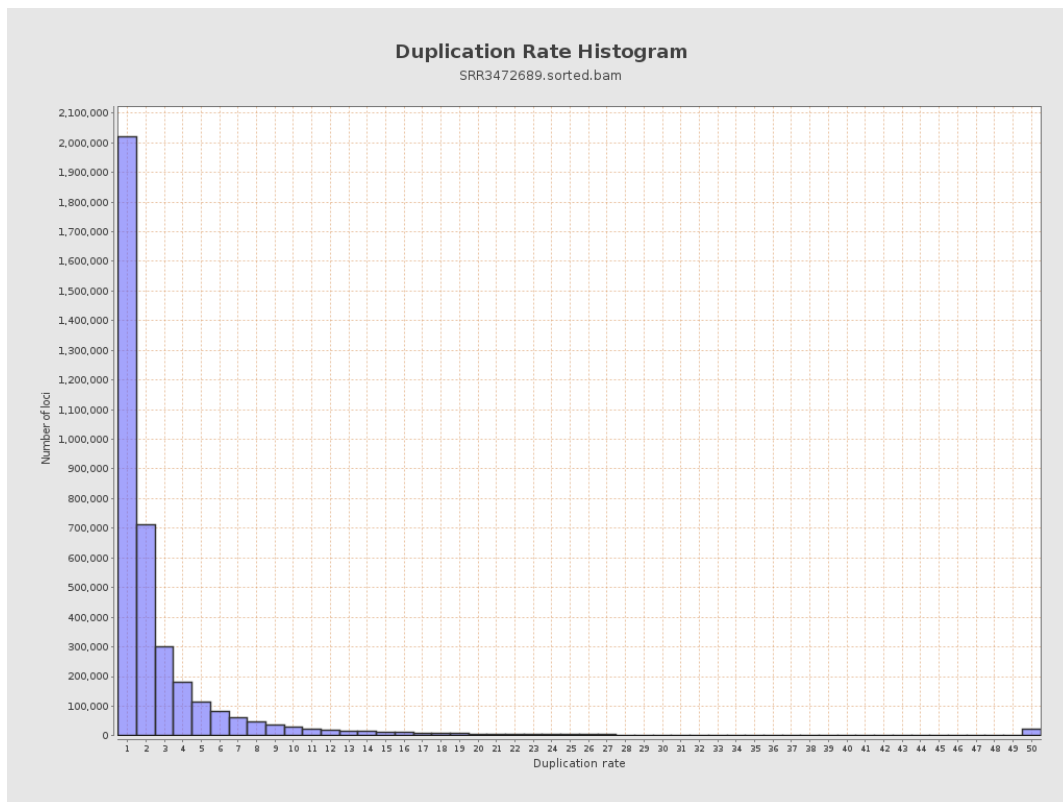
5. Results : Coverage Histogram (0-50X)



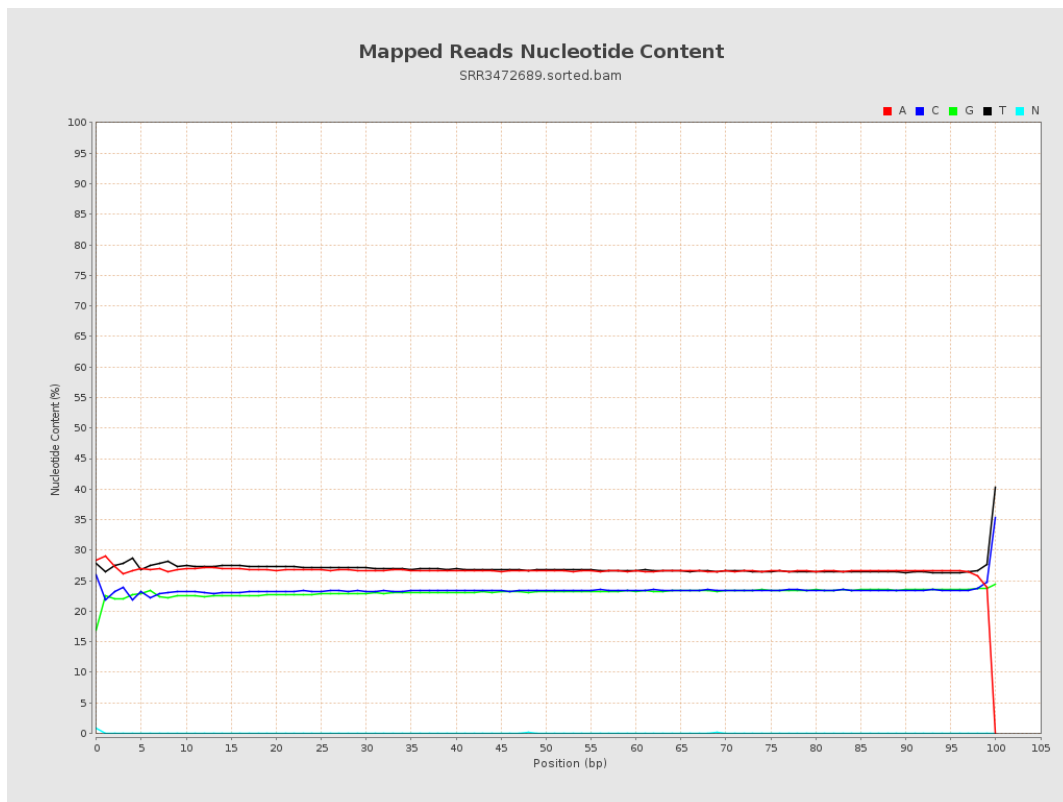
6. Results : Genome Fraction Coverage



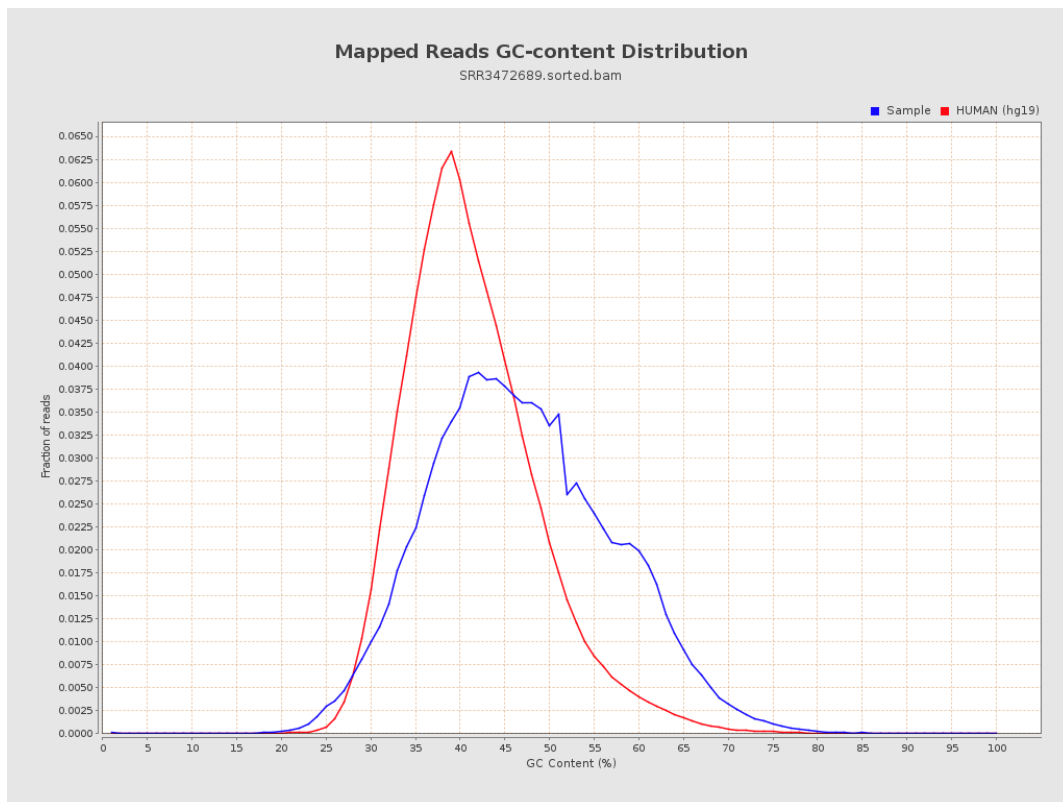
7. Results : Duplication Rate Histogram



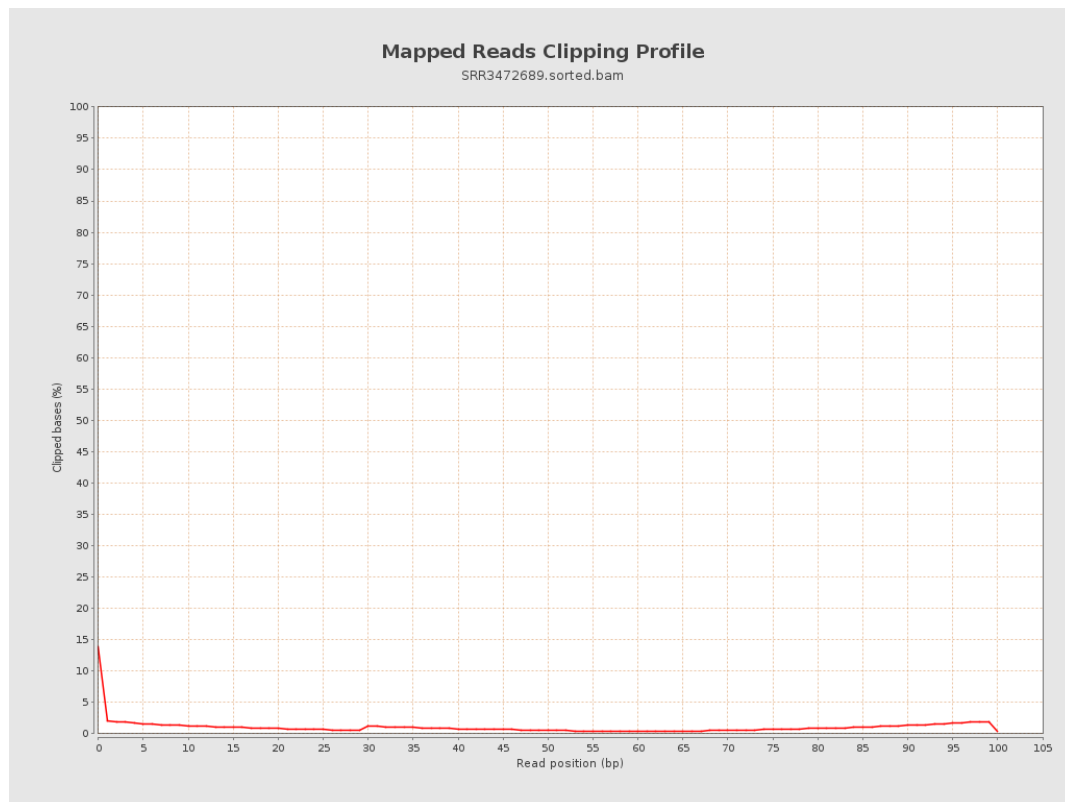
8. Results : Mapped Reads Nucleotide Content



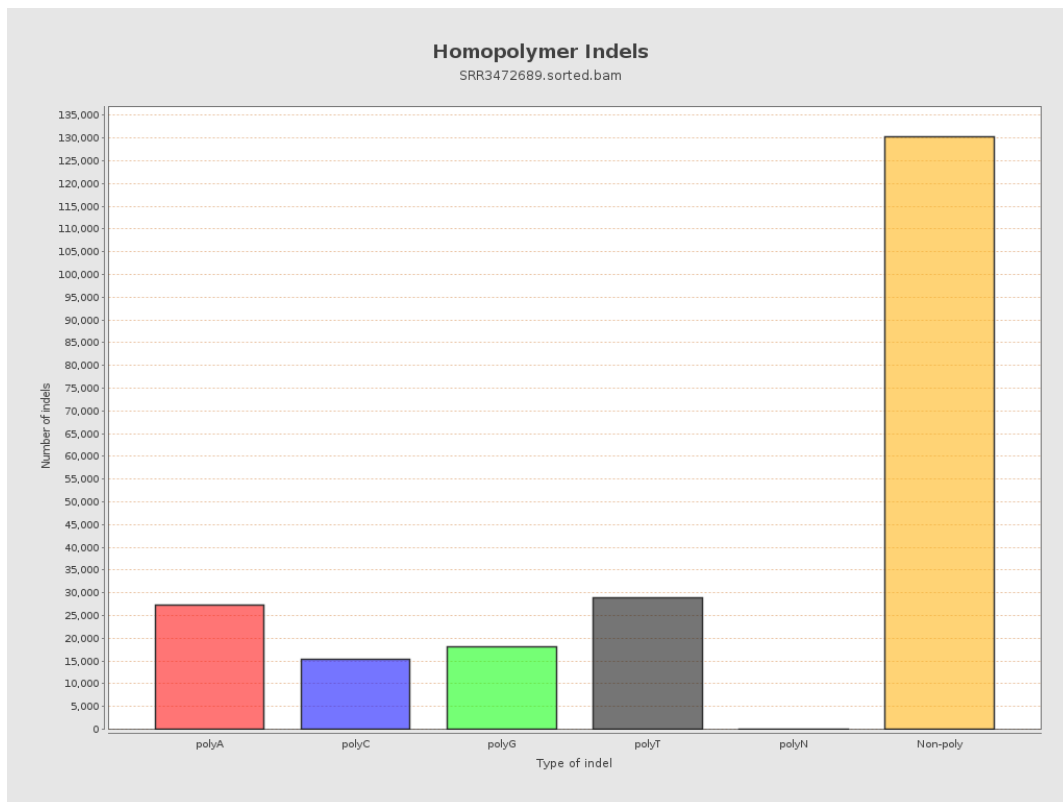
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



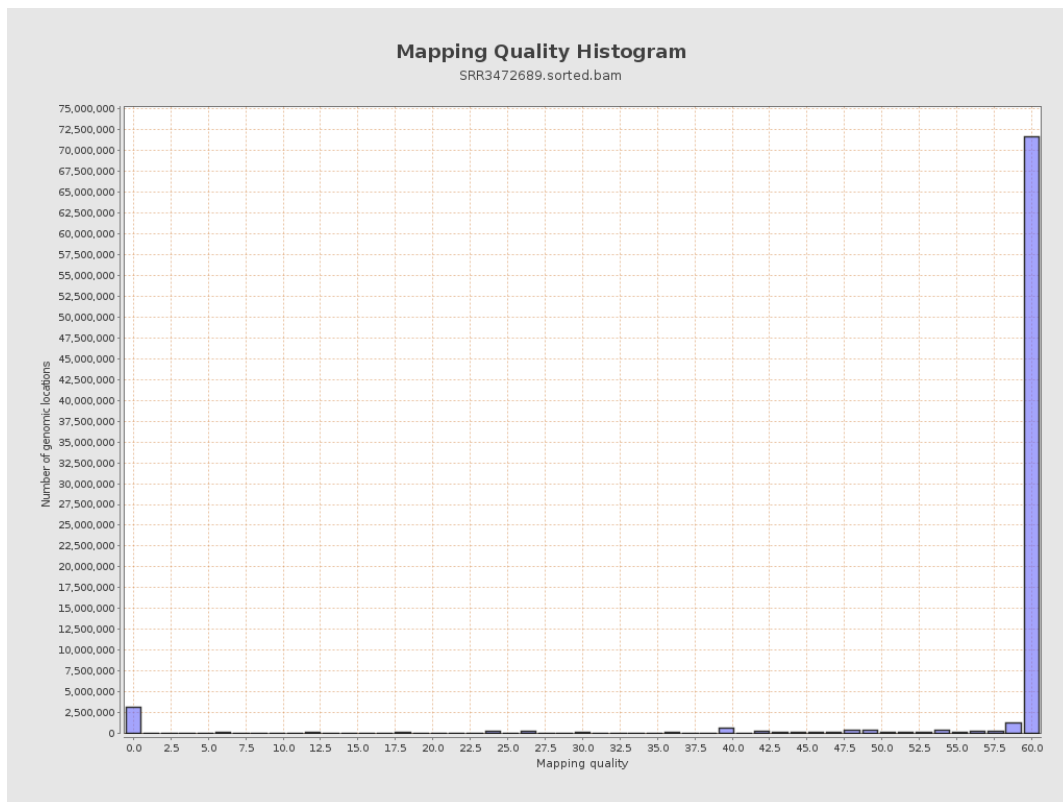
11. Results : Homopolymer Indels



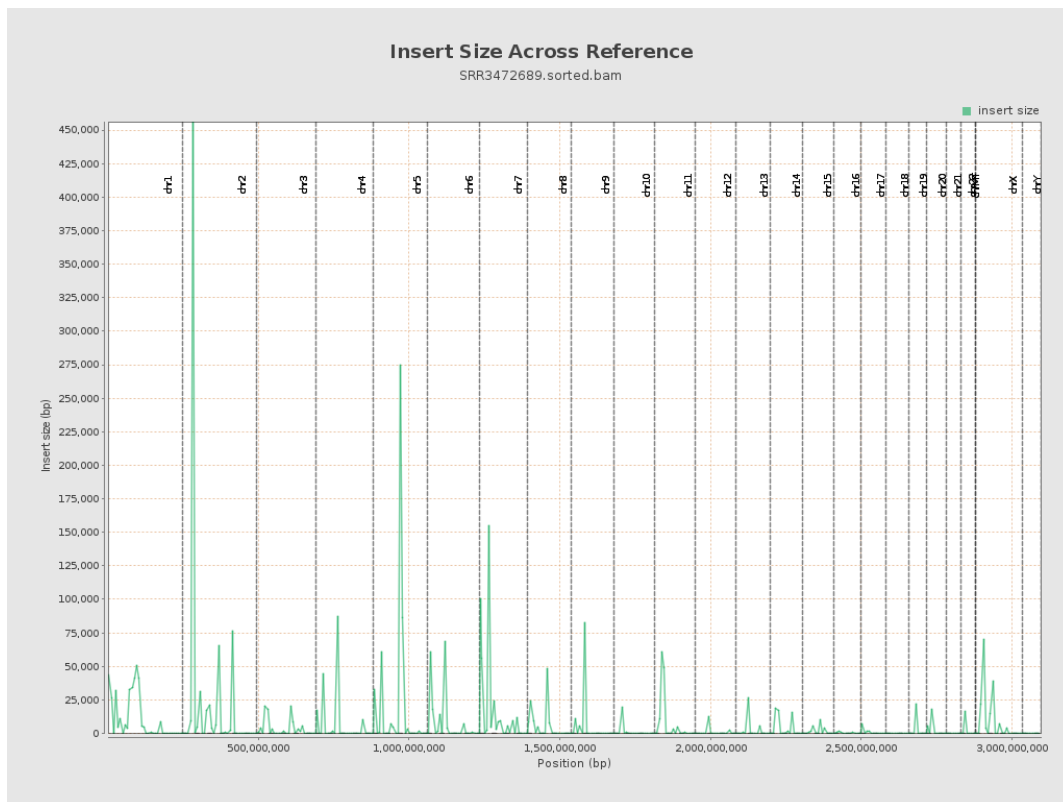
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

