

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 03:27:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472670.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_SRR3472670 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472670_1.fastq.gz SRR3472670_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 03:27:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472670.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,702,462
Mapped reads	19,569,395 / 99.32%
Unmapped reads	133,067 / 0.68%
Mapped paired reads	19,569,395 / 99.32%
Mapped reads, first in pair	9,808,609 / 49.78%
Mapped reads, second in pair	9,760,786 / 49.54%
Mapped reads, both in pair	19,488,194 / 98.91%
Mapped reads, singletons	81,201 / 0.41%
Secondary alignments	0
Supplementary alignments	103,962 / 0.53%
Read min/max/mean length	30 / 101 / 99.57
Duplicated reads (estimated)	14,145,339 / 71.79%
Duplication rate	50.24%
Clipped reads	1,389,254 / 7.05%

2.2. ACGT Content

Number/percentage of A's	508,590,848 / 26.46%
Number/percentage of C's	455,188,231 / 23.68%
Number/percentage of T's	509,961,673 / 26.53%
Number/percentage of G's	448,307,873 / 23.32%
Number/percentage of N's	364,811 / 0.02%

GC Percentage	47%
---------------	-----

2.3. Coverage

Mean	0.6211
Standard Deviation	28.9603

2.4. Mapping Quality

Mean Mapping Quality	54.79
----------------------	-------

2.5. Insert size

Mean	19,234.66
Standard Deviation	1,358,092.81
P25/Median/P75	149 / 203 / 270

2.6. Mismatches and indels

General error rate	0.57%
Mismatches	10,705,472
Insertions	110,599
Mapped reads with at least one insertion	0.56%
Deletions	108,982
Mapped reads with at least one deletion	0.54%
Homopolymer indels	46.48%

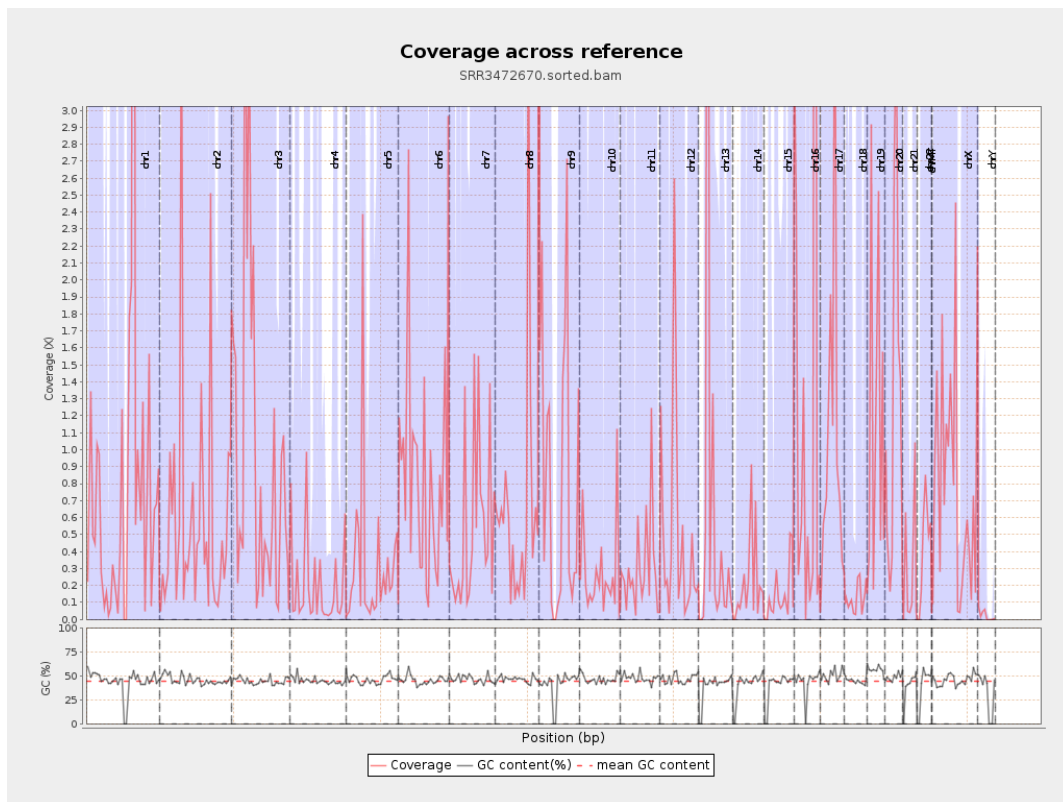
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
------	--------	--------	------	----------

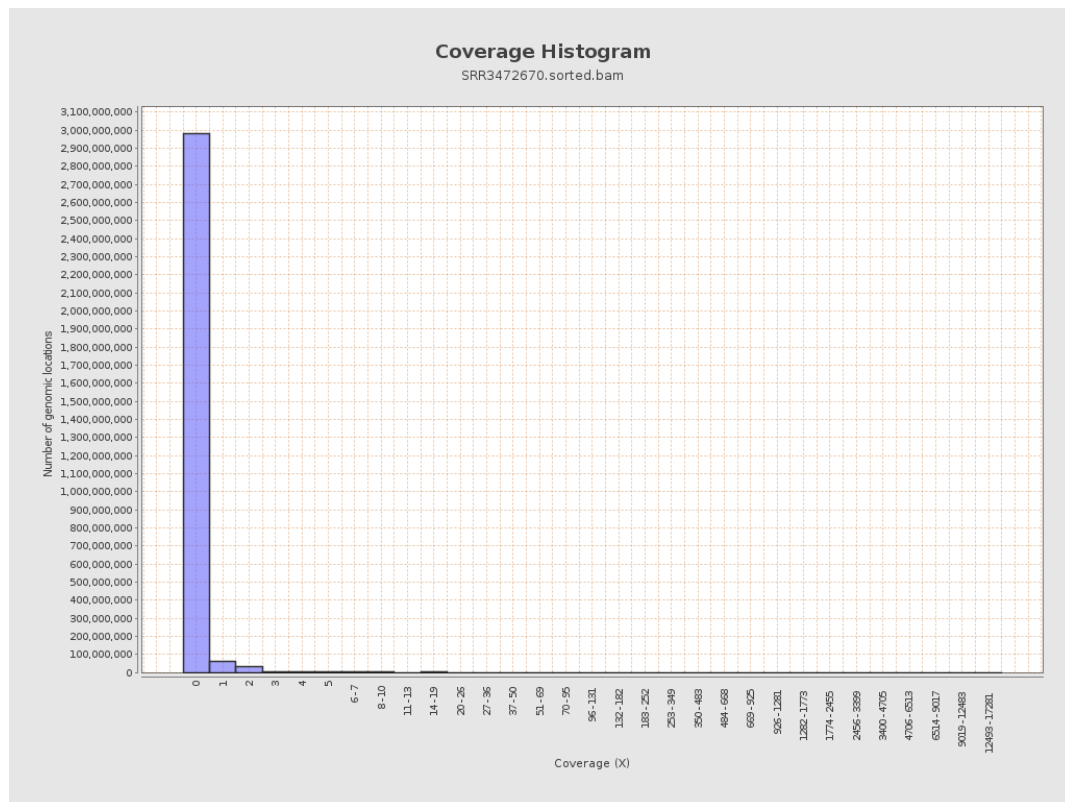
		bases	coverage	deviation
chr1	249250621	210919765	0.8462	35.7545
chr2	243199373	146955534	0.6043	27.6684
chr3	198022430	201631685	1.0182	37.2867
chr4	191154276	35961632	0.1881	9.2263
chr5	180915260	57417253	0.3174	14.5549
chr6	171115067	144652625	0.8454	26.5687
chr7	159138663	87477844	0.5497	23.6352
chr8	146364022	94616173	0.6464	27.3553
chr9	141213431	124147403	0.8791	28.5815
chr10	135534747	36076012	0.2662	12.8932
chr11	135006516	41260028	0.3056	14.8061
chr12	133851895	67035913	0.5008	17.275
chr13	115169878	82374302	0.7152	50.6071
chr14	107349540	22581729	0.2104	12.0707
chr15	102531392	15136212	0.1476	6.964
chr16	90354753	132527457	1.4667	63.2272
chr17	81195210	93305348	1.1491	43.2986
chr18	78077248	9898340	0.1268	6.6006
chr19	59128983	75088879	1.2699	42.1594
chr20	63025520	86635325	1.3746	38.597
chr21	48129895	14607081	0.3035	18.5145
chr22	51304566	20877161	0.4069	15.6744
chrMT	16571	6443	0.3888	0.8922
chrX	155270560	120127263	0.7737	33.4783

chrY	59373566	1366063	0.023	1.0769
------	----------	---------	-------	--------

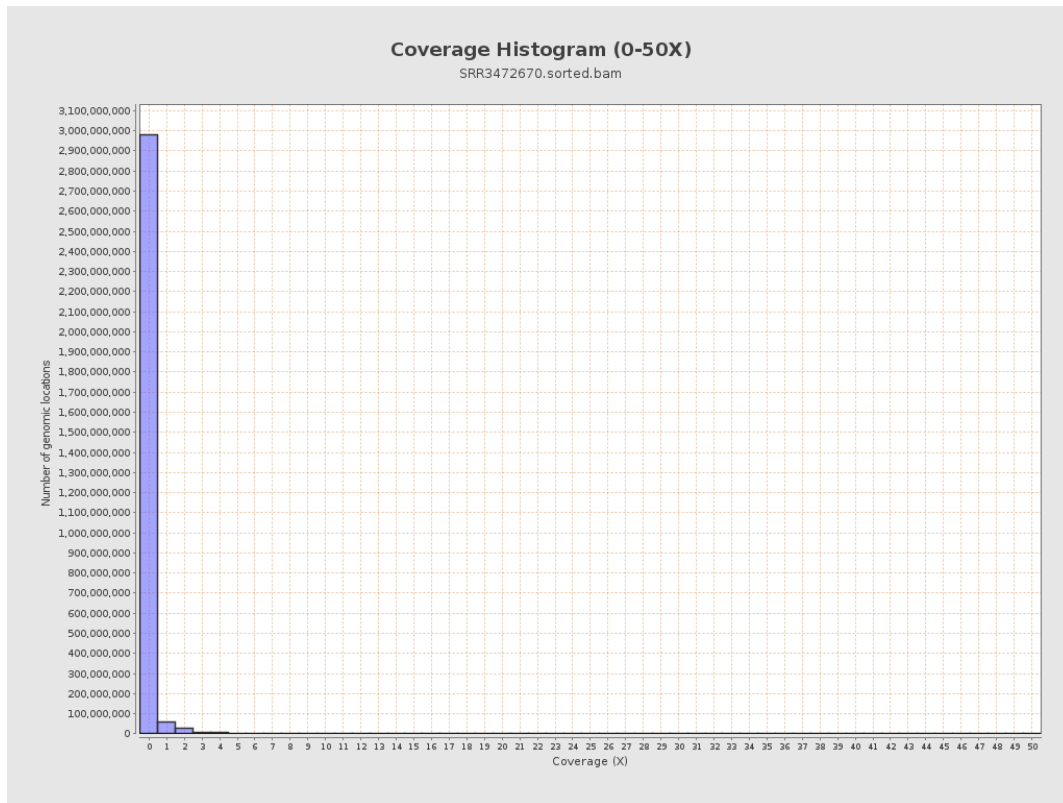
3. Results : Coverage across reference



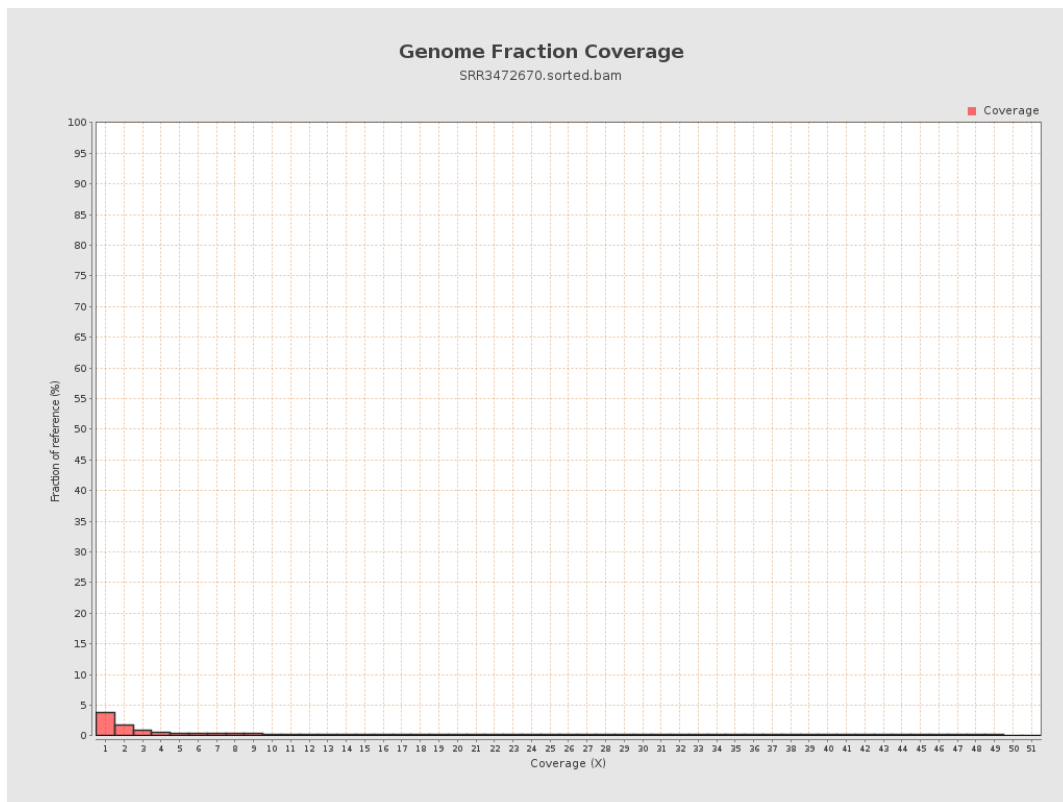
4. Results : Coverage Histogram



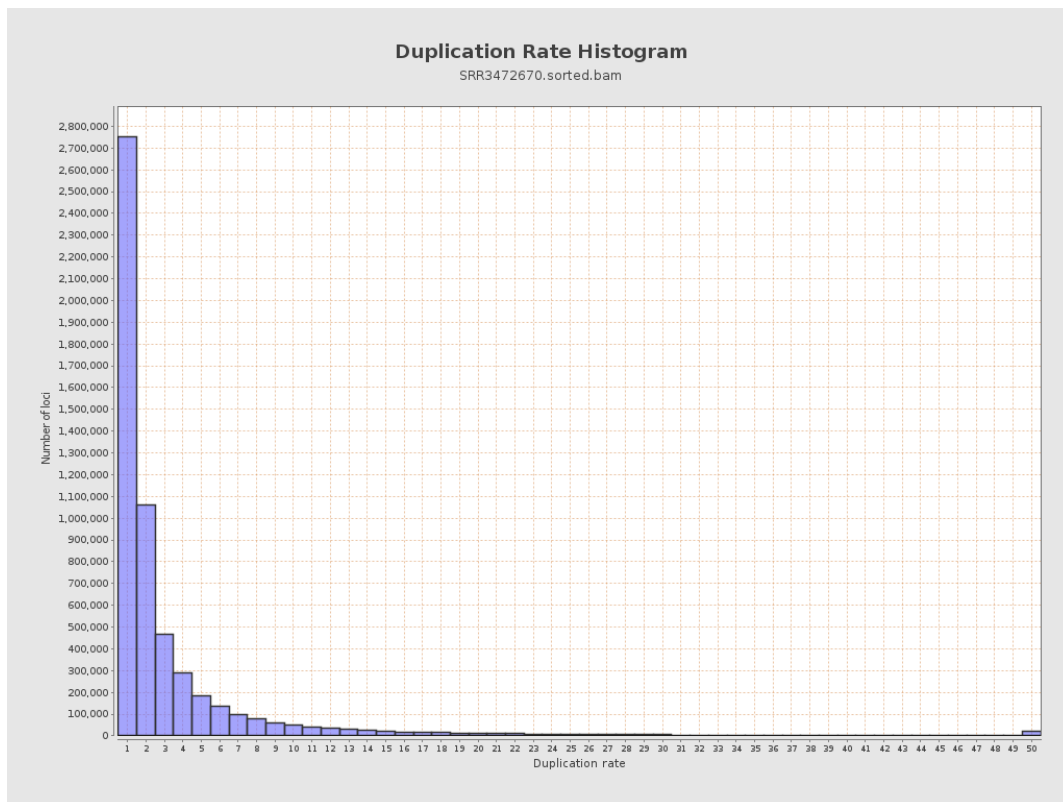
5. Results : Coverage Histogram (0-50X)



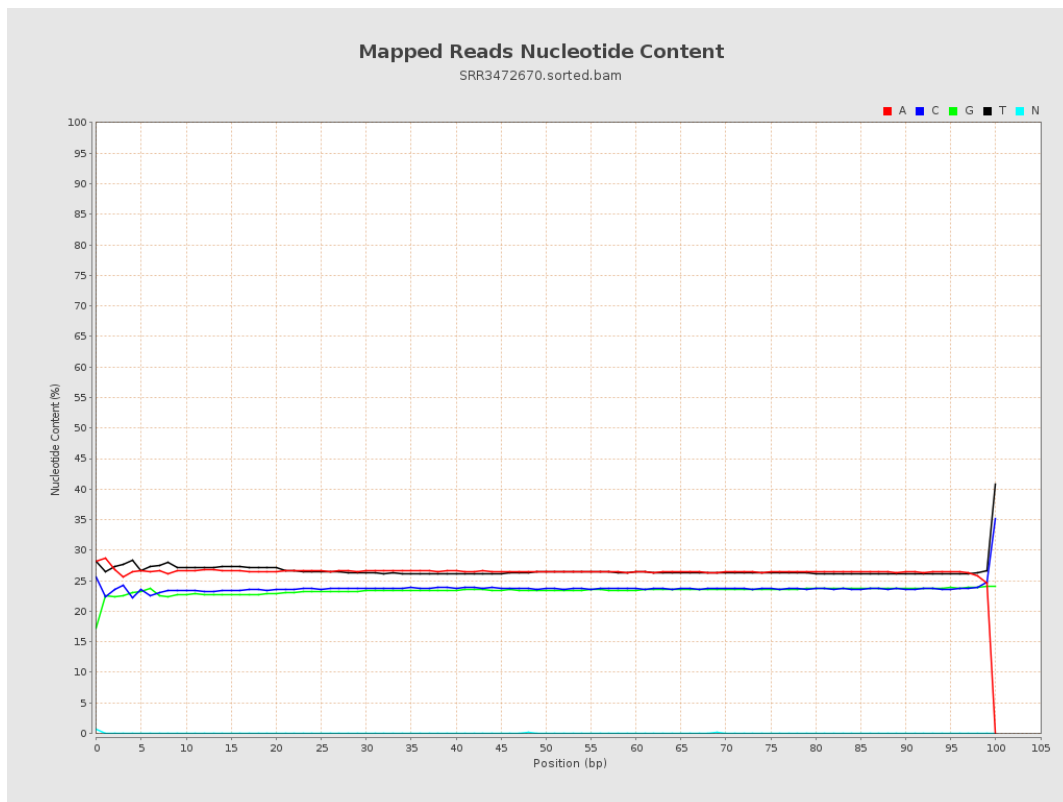
6. Results : Genome Fraction Coverage



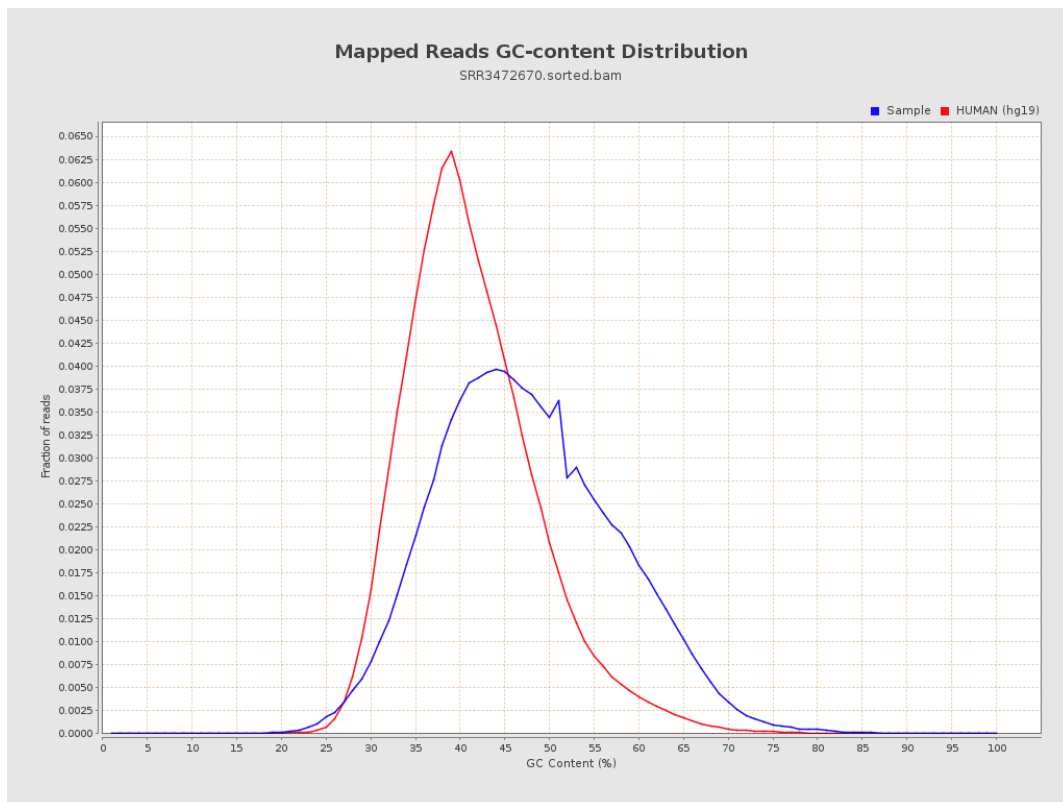
7. Results : Duplication Rate Histogram



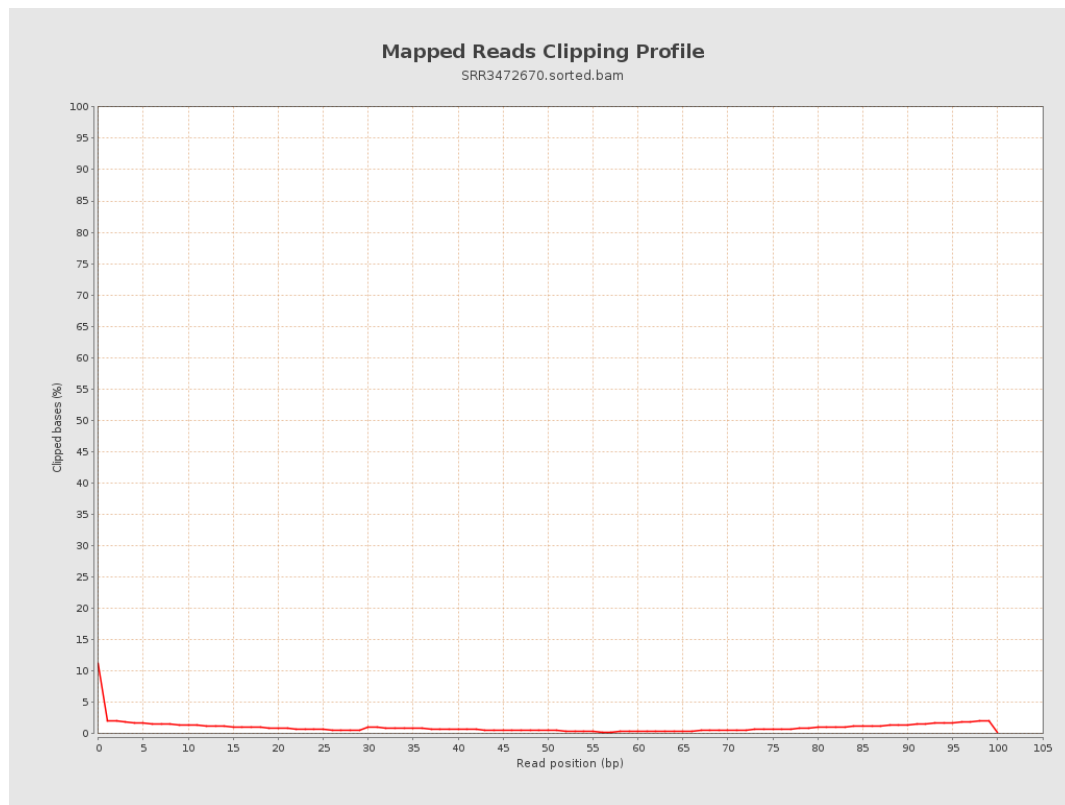
8. Results : Mapped Reads Nucleotide Content



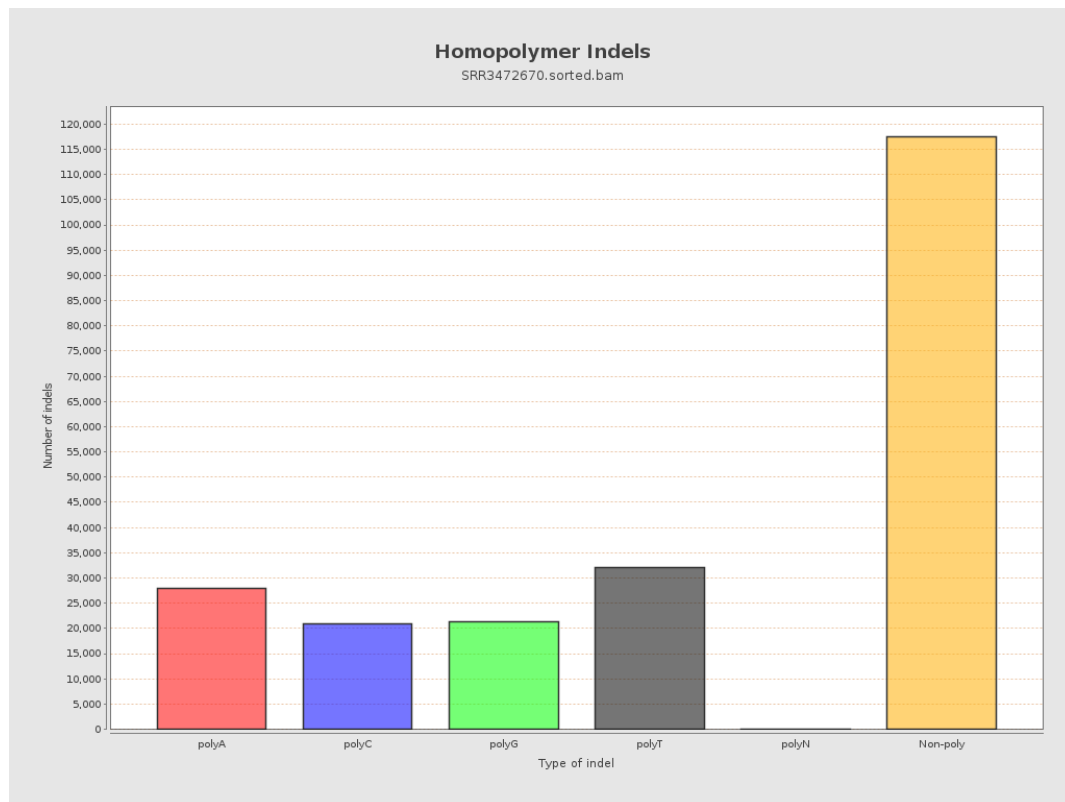
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



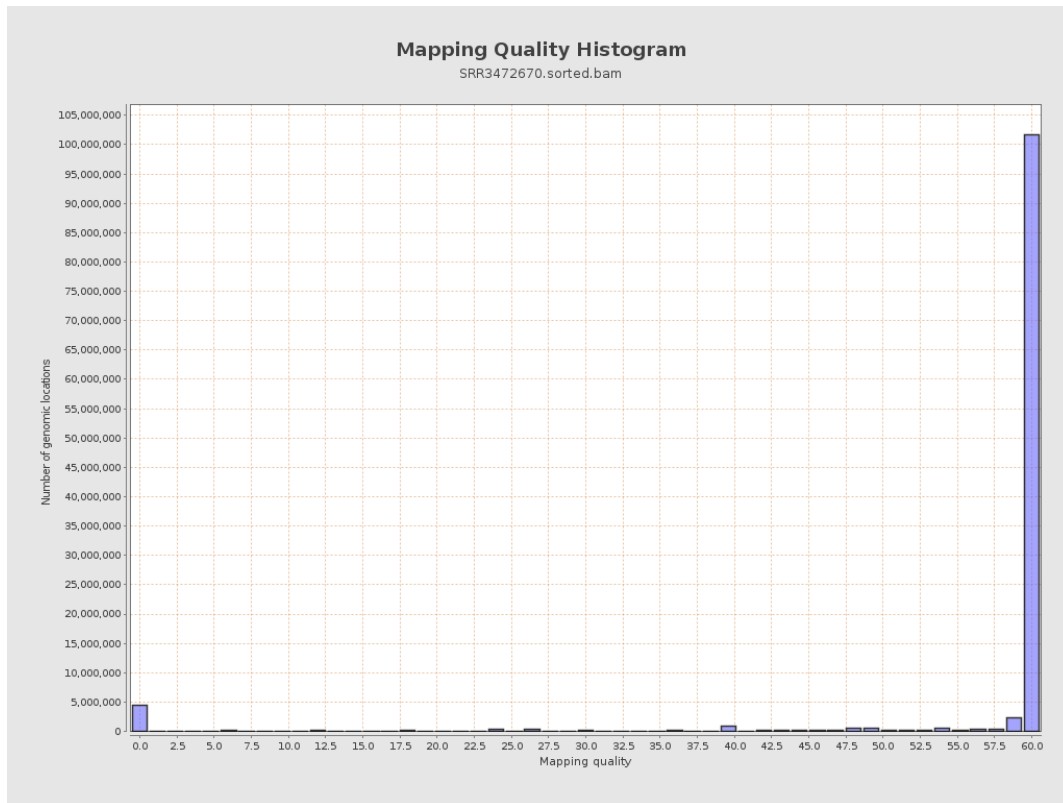
11. Results : Homopolymer Indels



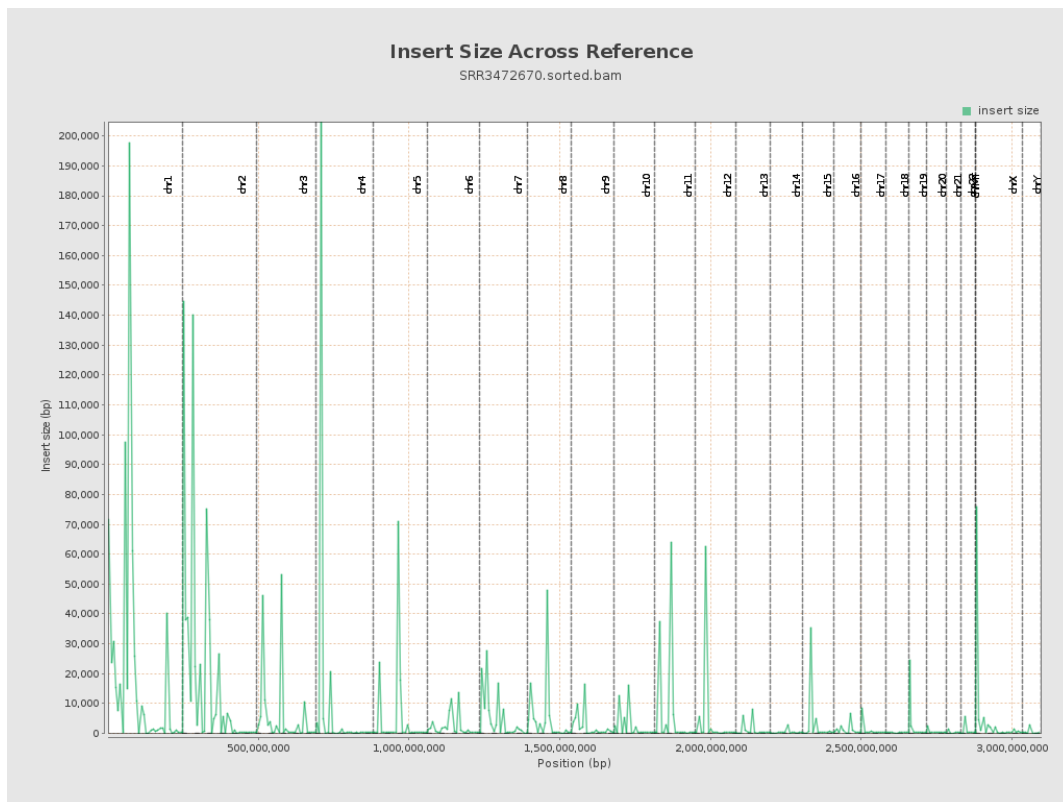
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

