

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 04:20:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472673.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_SRR3472673 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472673_1.fastq.gz SRR3472673_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 04:20:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472673.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,555,610
Mapped reads	15,434,651 / 99.22%
Unmapped reads	120,959 / 0.78%
Mapped paired reads	15,434,651 / 99.22%
Mapped reads, first in pair	7,735,089 / 49.73%
Mapped reads, second in pair	7,699,562 / 49.5%
Mapped reads, both in pair	15,355,786 / 98.72%
Mapped reads, singletons	78,865 / 0.51%
Secondary alignments	0
Supplementary alignments	91,846 / 0.59%
Read min/max/mean length	30 / 101 / 99.72
Duplicated reads (estimated)	10,395,514 / 66.83%
Duplication rate	49.46%
Clipped reads	1,124,102 / 7.23%

2.2. ACGT Content

Number/percentage of A's	405,634,441 / 26.73%
Number/percentage of C's	354,971,442 / 23.39%
Number/percentage of T's	406,696,956 / 26.8%
Number/percentage of G's	350,118,503 / 23.07%
Number/percentage of N's	284,515 / 0.02%

GC Percentage	46.46%
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2.3. Coverage

Mean	0.4903
Standard Deviation	19.9238

2.4. Mapping Quality

Mean Mapping Quality	54.93
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2.5. Insert size

Mean	21,513.37
Standard Deviation	1,429,630.67
P25/Median/P75	155 / 210 / 279

2.6. Mismatches and indels

General error rate	0.62%
Mismatches	9,238,268
Insertions	97,399
Mapped reads with at least one insertion	0.62%
Deletions	85,091
Mapped reads with at least one deletion	0.54%
Homopolymer indels	45.78%

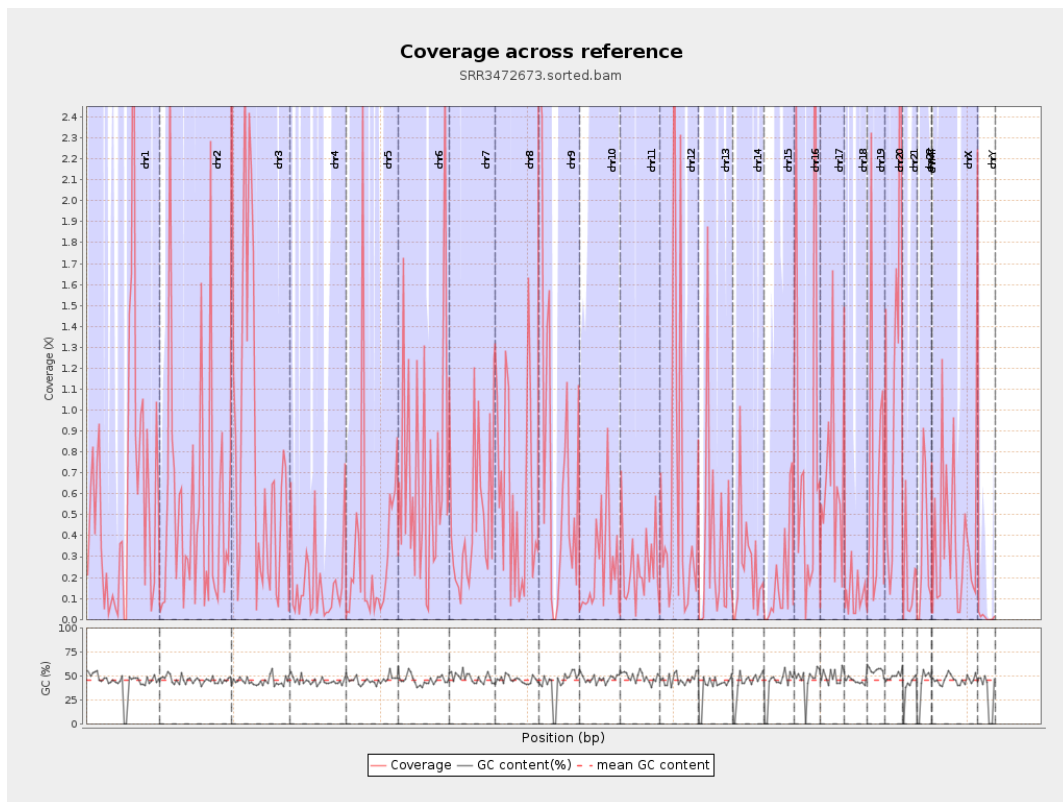
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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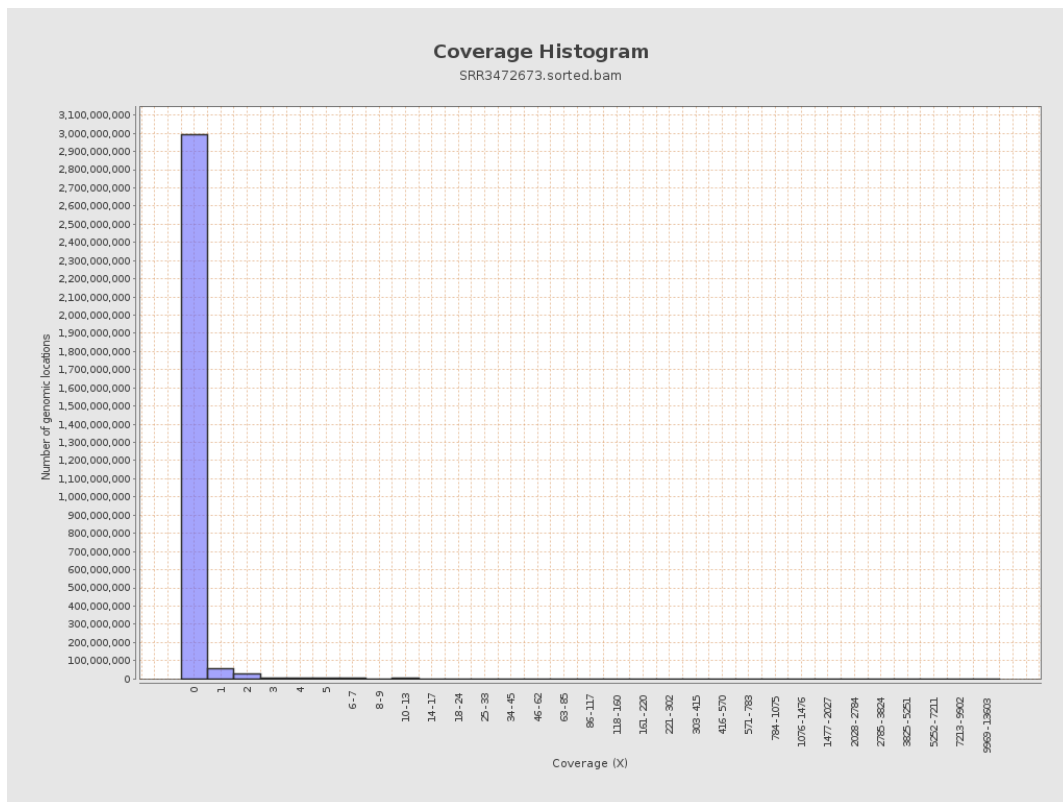
		bases	coverage	deviation
chr1	249250621	146086607	0.5861	20.7307
chr2	243199373	129373456	0.532	25.6038
chr3	198022430	165918838	0.8379	28.9608
chr4	191154276	32751331	0.1713	9.5491
chr5	180915260	62080472	0.3431	17.6695
chr6	171115067	118578678	0.693	20.6317
chr7	159138663	77456579	0.4867	18.1827
chr8	146364022	84930172	0.5803	21.9163
chr9	141213431	112675400	0.7979	26.8521
chr10	135534747	33840485	0.2497	13.3418
chr11	135006516	34379843	0.2547	9.9958
chr12	133851895	77920382	0.5821	24.8595
chr13	115169878	40441038	0.3511	14.9537
chr14	107349540	27354466	0.2548	15.6303
chr15	102531392	19928828	0.1944	10.0611
chr16	90354753	81737470	0.9046	27.0805
chr17	81195210	56179911	0.6919	21.2444
chr18	78077248	9178982	0.1176	5.425
chr19	59128983	44834468	0.7582	18.7984
chr20	63025520	75890748	1.2041	35.5418
chr21	48129895	9371948	0.1947	13.1168
chr22	51304566	16658556	0.3247	10.521
chrMT	16571	12473	0.7527	1.1294
chrX	155270560	59628142	0.384	11.9391

chrY	59373566	696004	0.0117	0.8751
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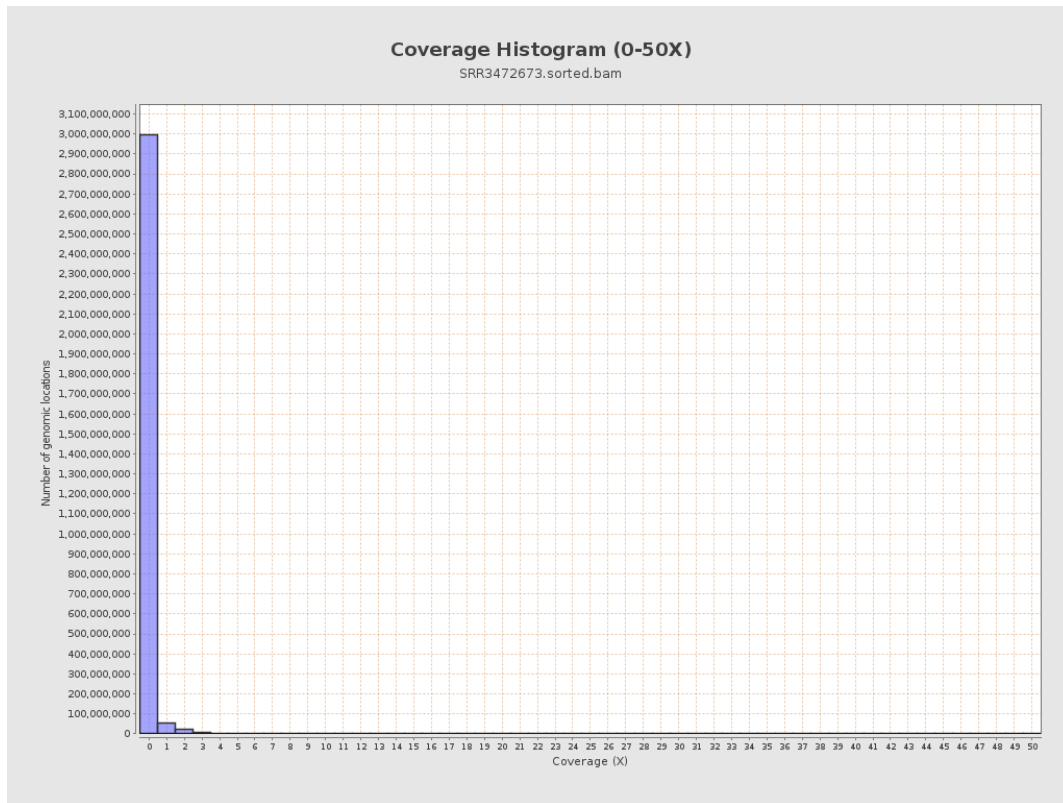
3. Results : Coverage across reference



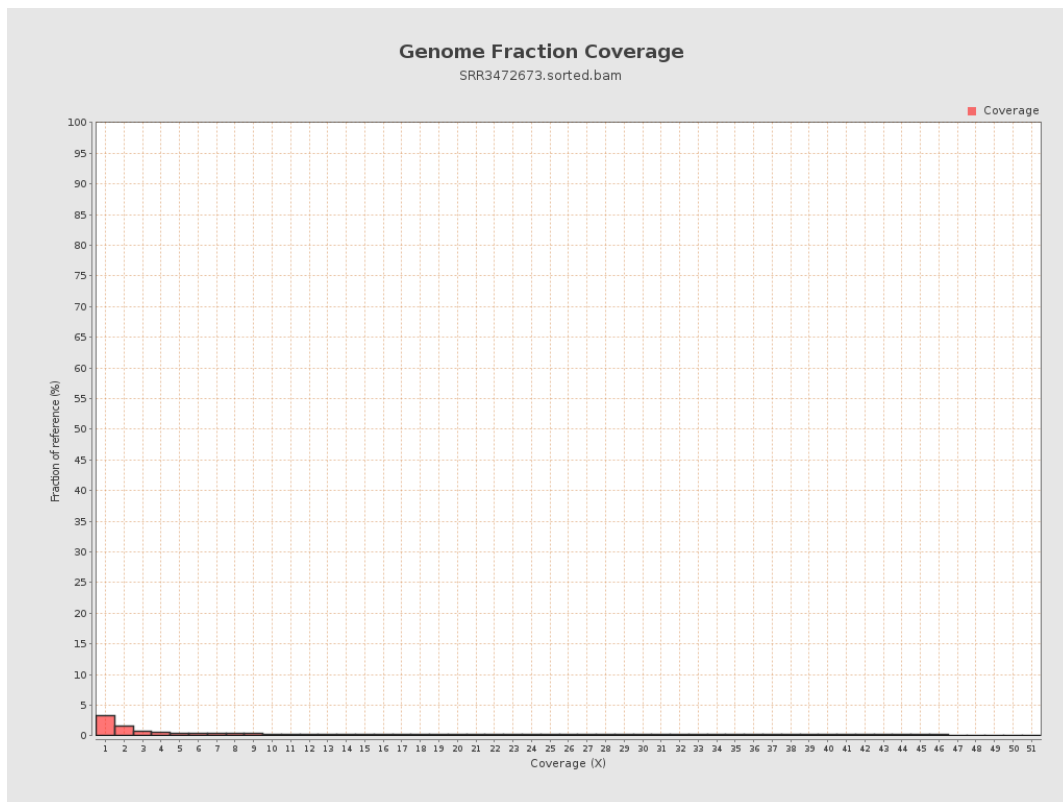
4. Results : Coverage Histogram



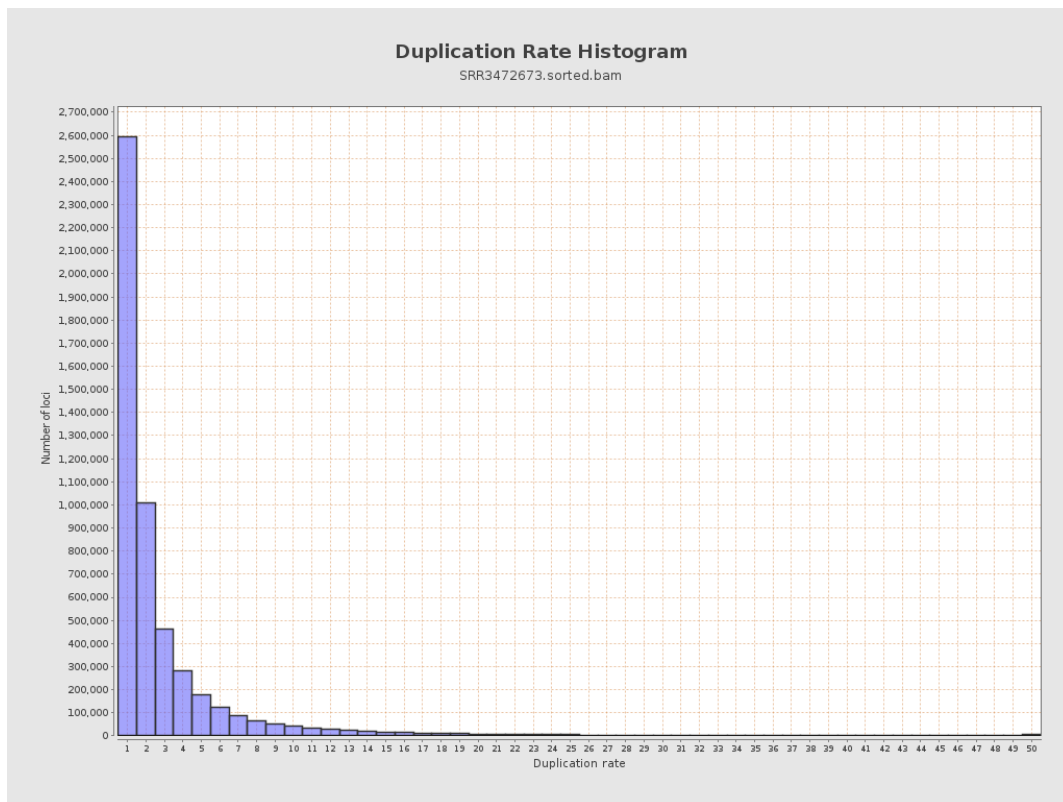
5. Results : Coverage Histogram (0-50X)



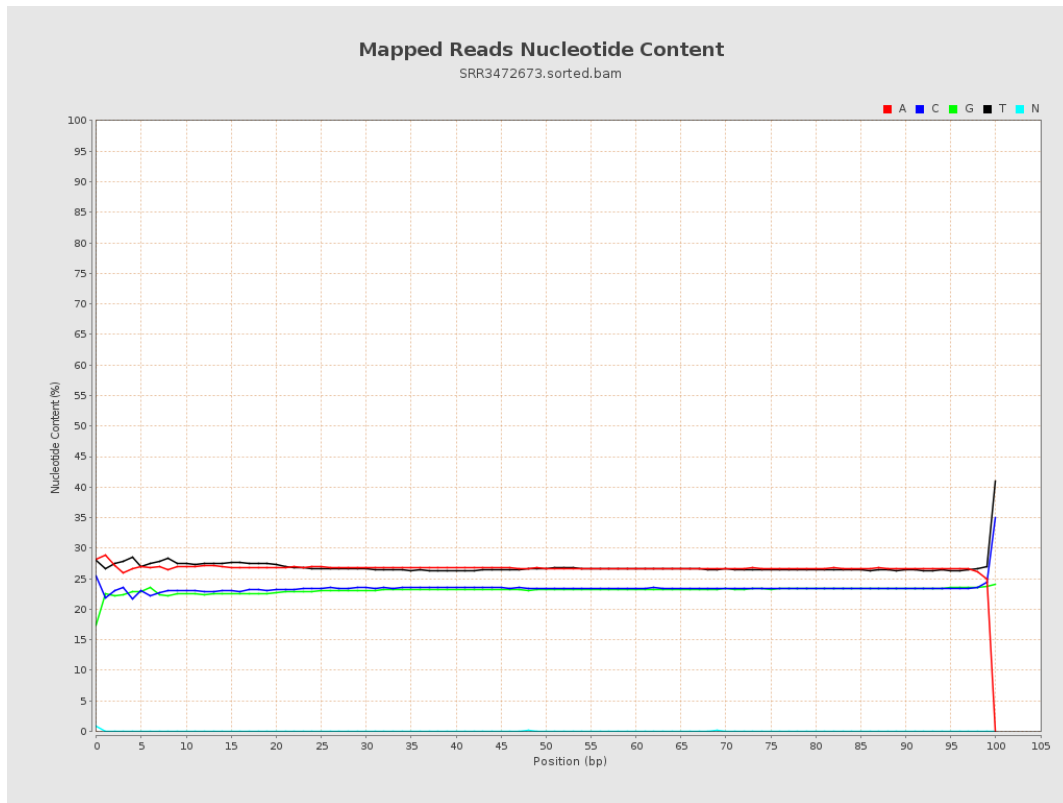
6. Results : Genome Fraction Coverage



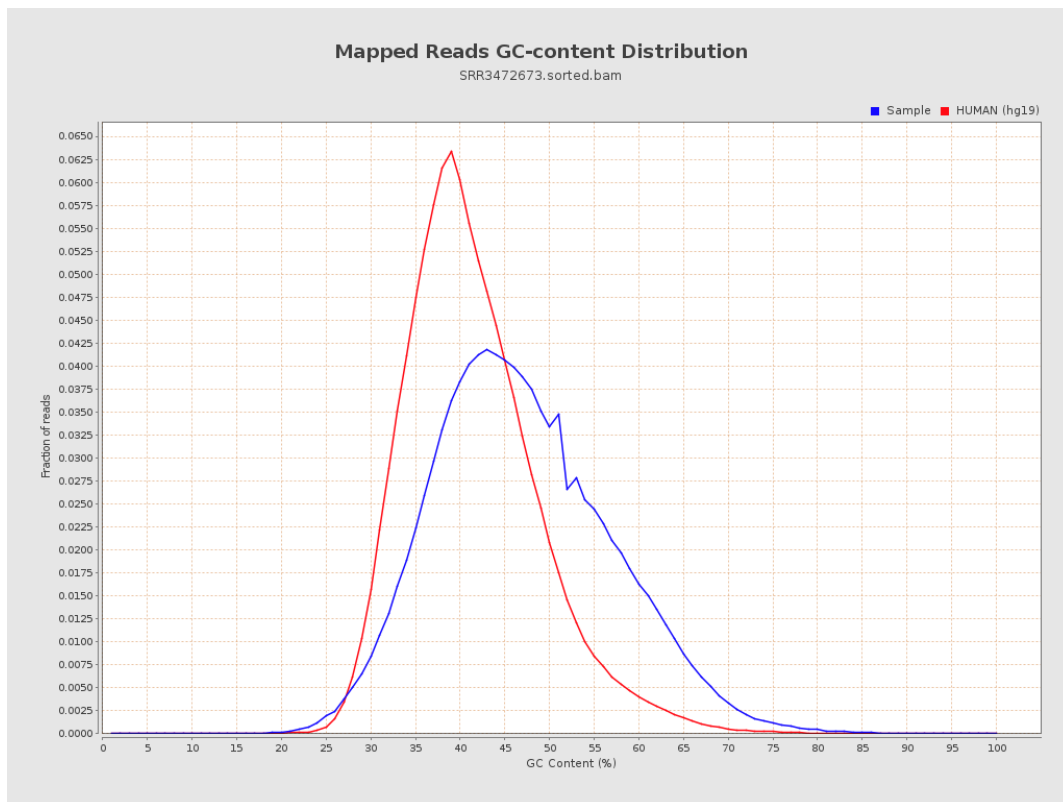
7. Results : Duplication Rate Histogram



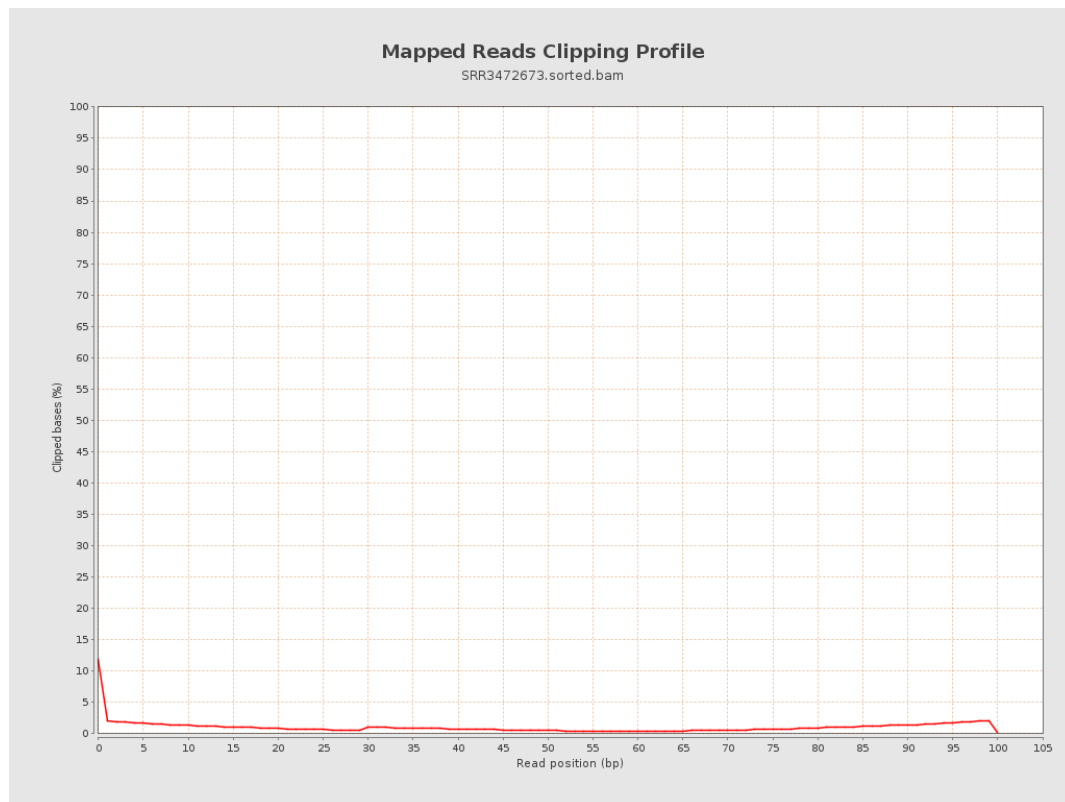
8. Results : Mapped Reads Nucleotide Content



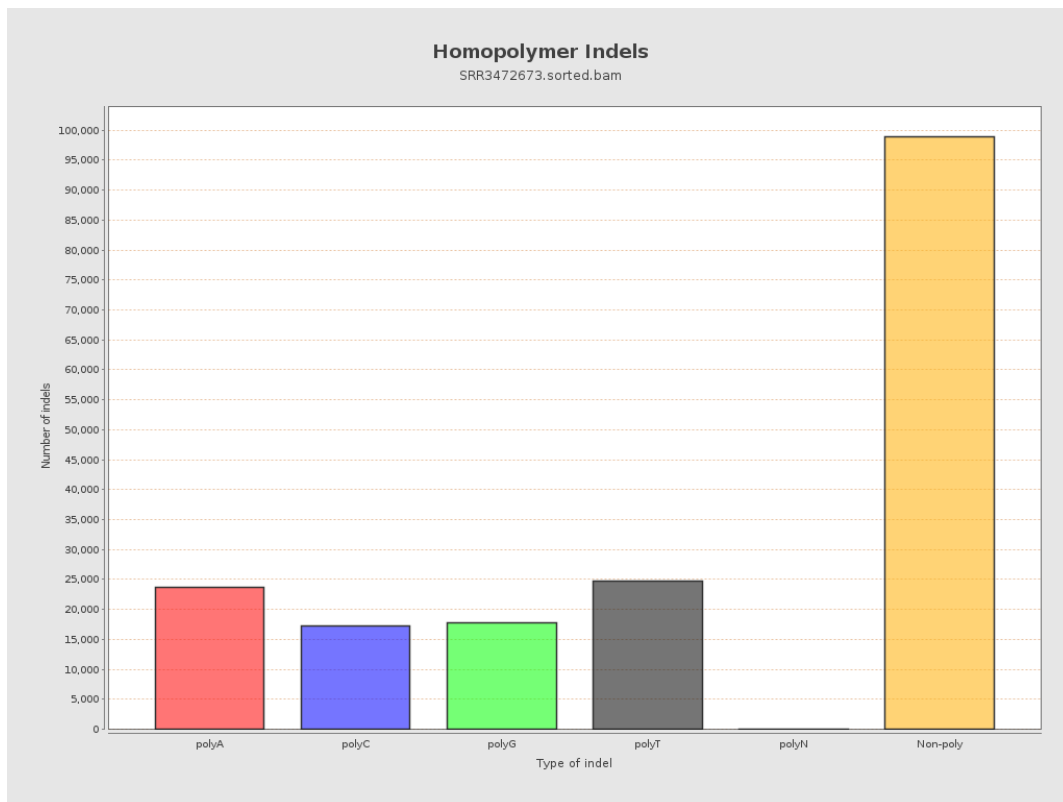
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



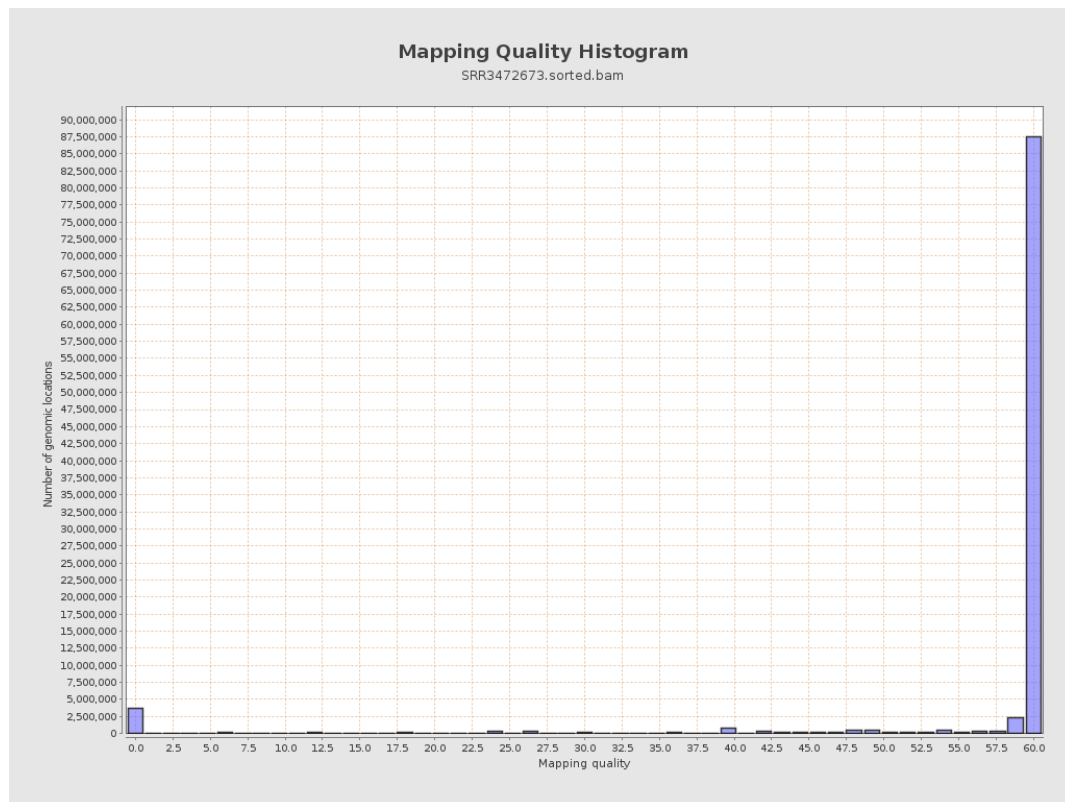
11. Results : Homopolymer Indels



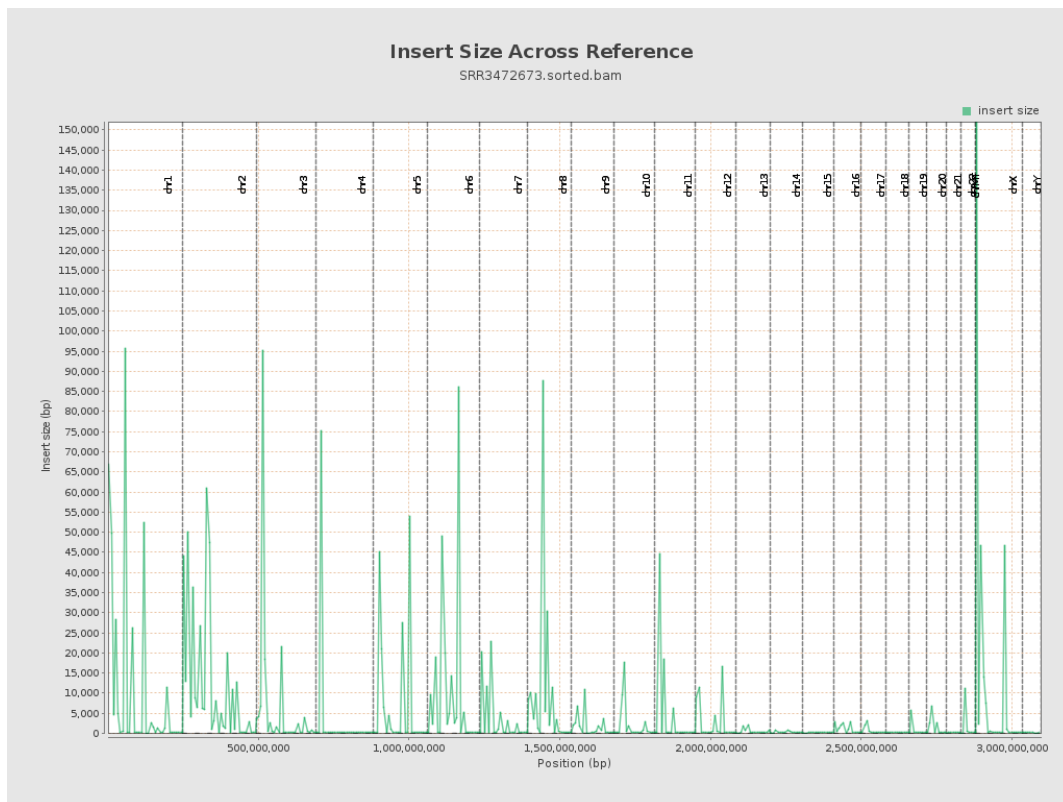
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

