

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/01 12:29:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR21672006.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_SRR21672006 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR21672006_1.fastq.gz SRR21672006_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 01 12:29:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR21672006.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	214,042,306
Mapped reads	213,039,048 / 99.53%
Unmapped reads	1,003,258 / 0.47%
Mapped paired reads	213,039,048 / 99.53%
Mapped reads, first in pair	106,529,212 / 49.77%
Mapped reads, second in pair	106,509,836 / 49.76%
Mapped reads, both in pair	212,672,012 / 99.36%
Mapped reads, singletons	367,036 / 0.17%
Secondary alignments	0
Supplementary alignments	915,311 / 0.43%
Read min/max/mean length	15 / 150 / 149.63
Duplicated reads (estimated)	56,971,157 / 26.62%
Duplication rate	24.1%
Clipped reads	9,707,192 / 4.54%

2.2. ACGT Content

Number/percentage of A's	9,207,219,293 / 29.15%
Number/percentage of C's	6,595,244,945 / 20.88%
Number/percentage of T's	9,158,870,078 / 29%
Number/percentage of G's	6,621,053,015 / 20.96%
Number/percentage of N's	136,582 / 0%

GC Percentage	41.85%
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2.3. Coverage

Mean	10.2062
Standard Deviation	106.5898

2.4. Mapping Quality

Mean Mapping Quality	54.55
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2.5. Insert size

Mean	64,150.99
Standard Deviation	2,438,779.82
P25/Median/P75	313 / 364 / 416

2.6. Mismatches and indels

General error rate	0.61%
Mismatches	181,493,130
Insertions	4,374,085
Mapped reads with at least one insertion	1.95%
Deletions	4,649,166
Mapped reads with at least one deletion	2.1%
Homopolymer indels	46.1%

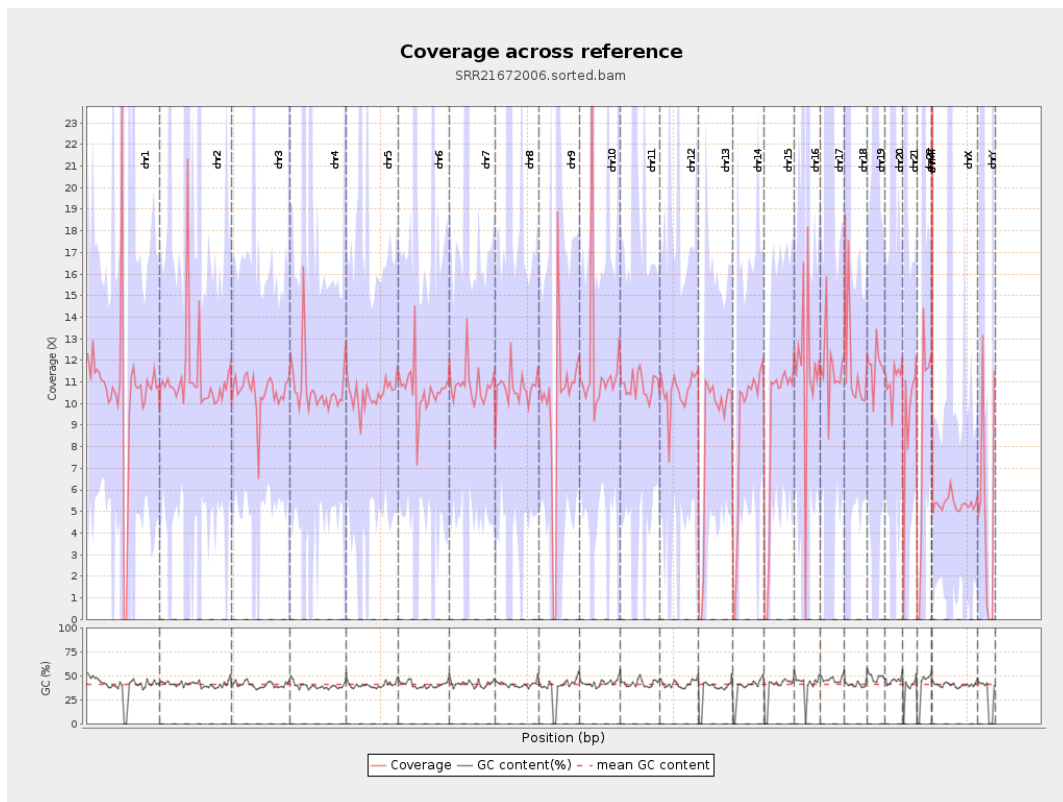
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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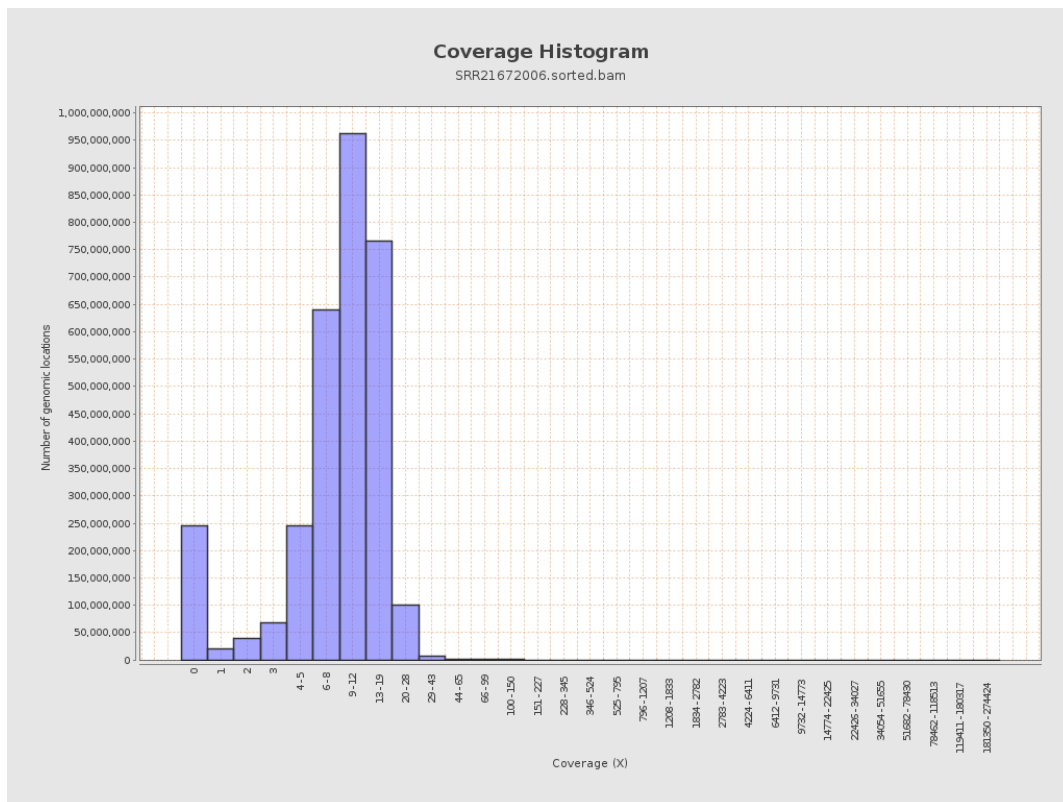
		bases	coverage	deviation
chr1	249250621	2648740442	10.6268	282.6345
chr2	243199373	2714234777	11.1605	63.6352
chr3	198022430	2082696900	10.5175	7.4486
chr4	191154276	2040385338	10.674	62.8876
chr5	180915260	1893034474	10.4637	9.1377
chr6	171115067	1819126727	10.631	49.1775
chr7	159138663	1732619780	10.8875	74.57
chr8	146364022	1580647759	10.7994	56.5169
chr9	141213431	1402289690	9.9303	179.6851
chr10	135534747	1592836604	11.7522	132.6882
chr11	135006516	1467928868	10.873	45.5202
chr12	133851895	1413128238	10.5574	8.5695
chr13	115169878	995268797	8.6417	6.481
chr14	107349540	963163394	8.9722	8.0397
chr15	102531392	910752428	8.8827	6.4543
chr16	90354753	1048182392	11.6007	63.5162
chr17	81195210	944868319	11.637	55.8383
chr18	78077248	910166027	11.6573	172.5645
chr19	59128983	696491012	11.7792	117.8165
chr20	63025520	696089826	11.0446	25.0323
chr21	48129895	452708299	9.406	40.4211
chr22	51304566	439125317	8.5592	39.8001
chrMT	16571	16539746	998.1139	115.8045
chrX	155270560	829175186	5.3402	15.5879

chrY	59373566	305215857	5.1406	87.2292
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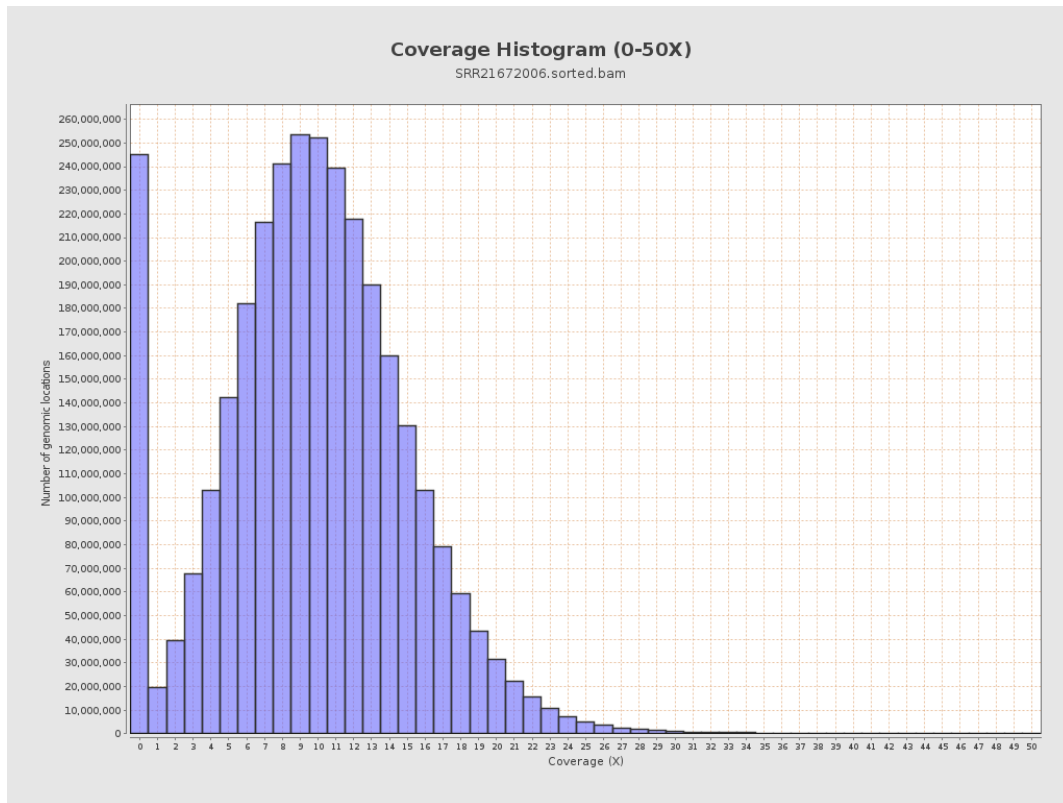
3. Results : Coverage across reference



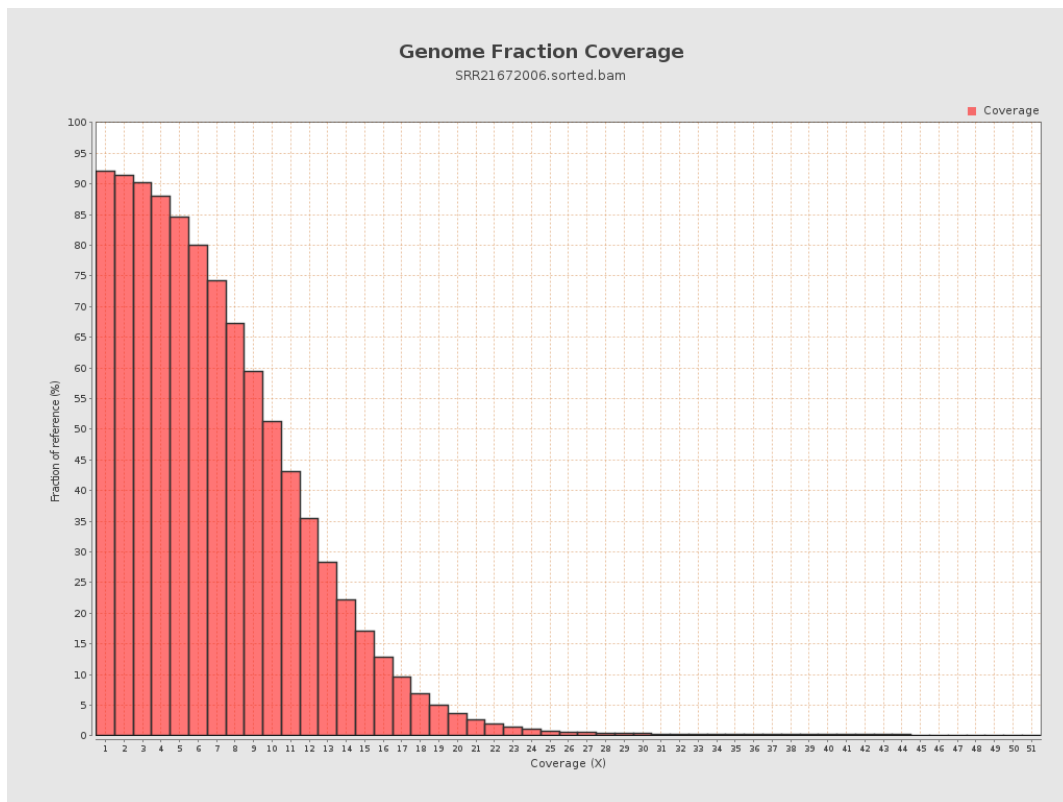
4. Results : Coverage Histogram



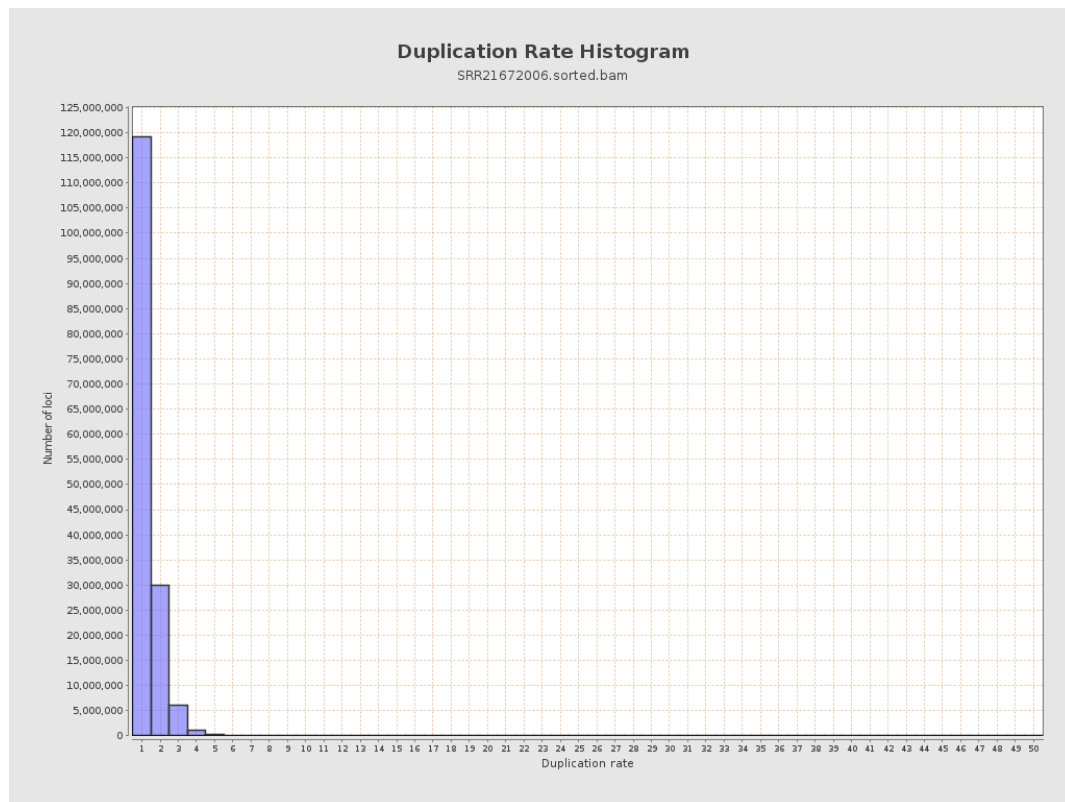
5. Results : Coverage Histogram (0-50X)



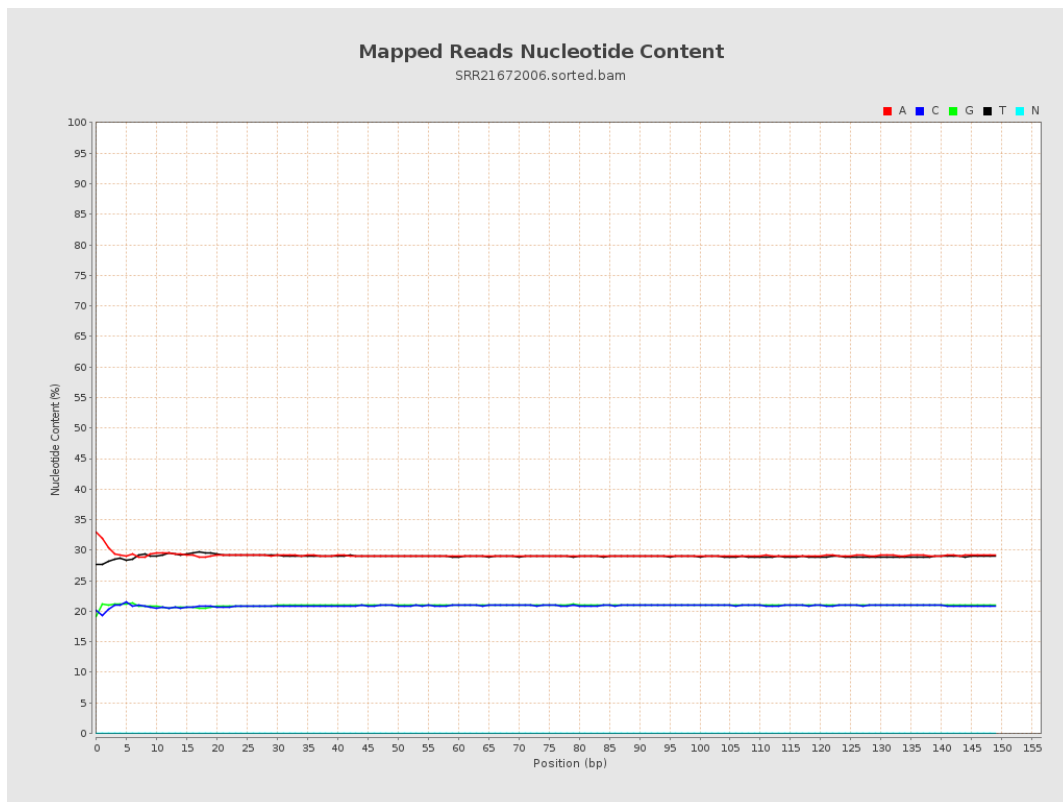
6. Results : Genome Fraction Coverage



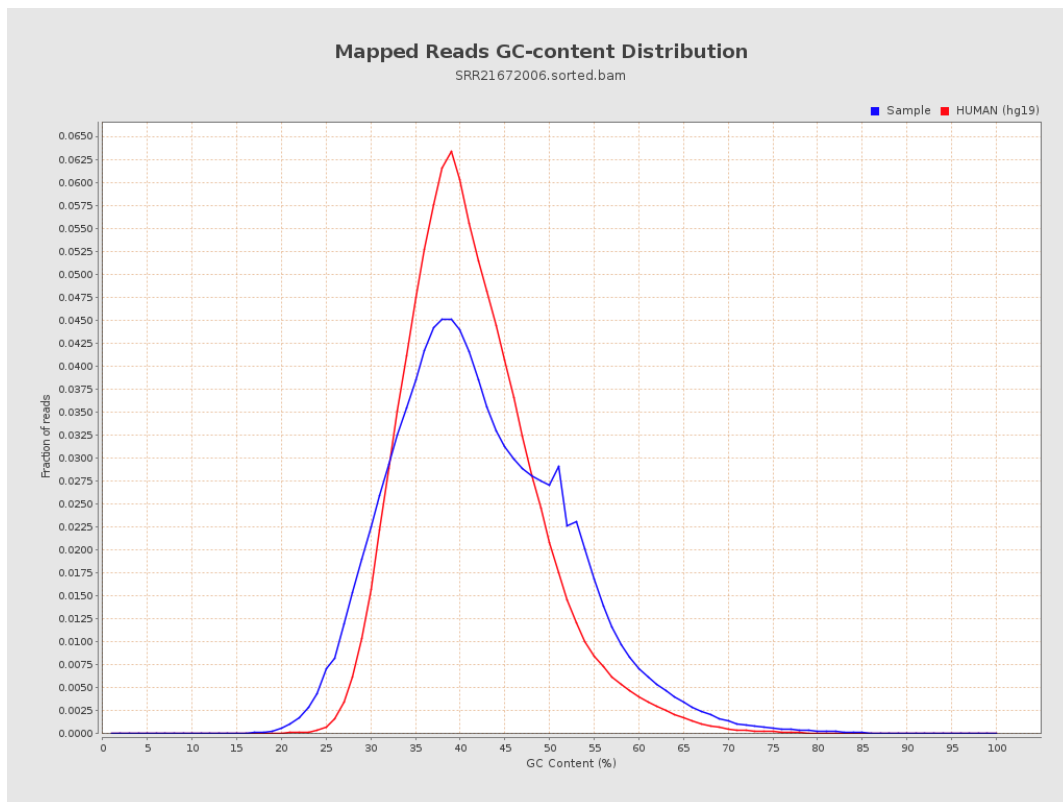
7. Results : Duplication Rate Histogram



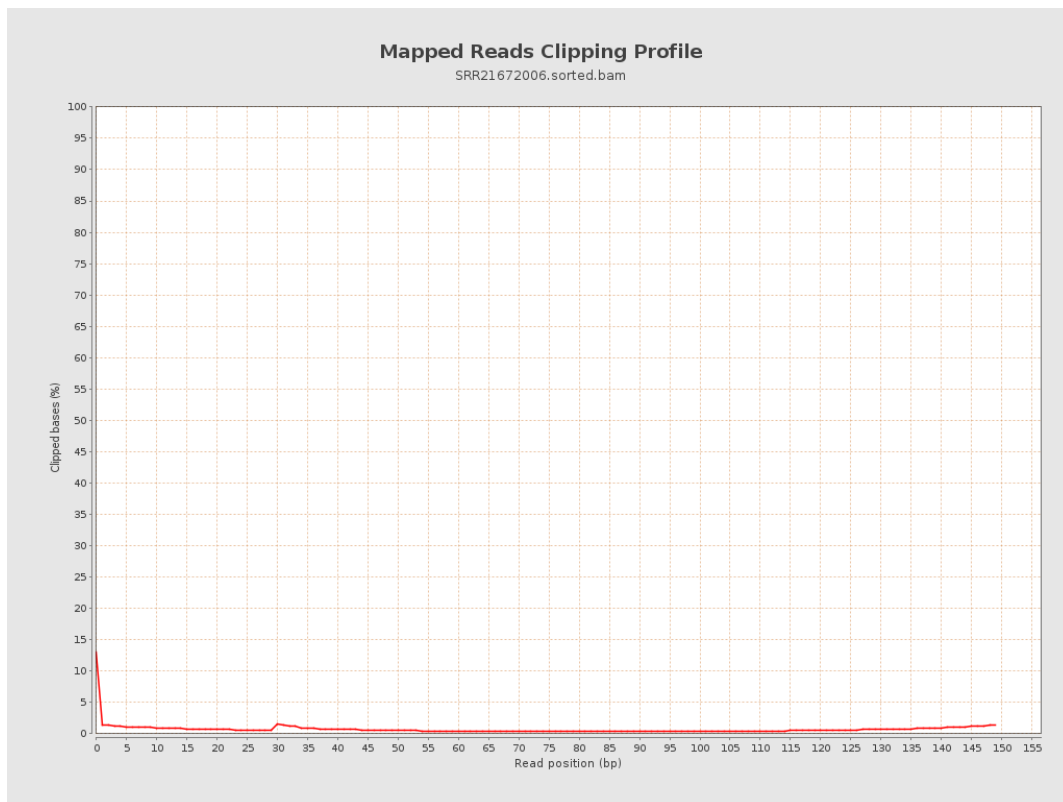
8. Results : Mapped Reads Nucleotide Content



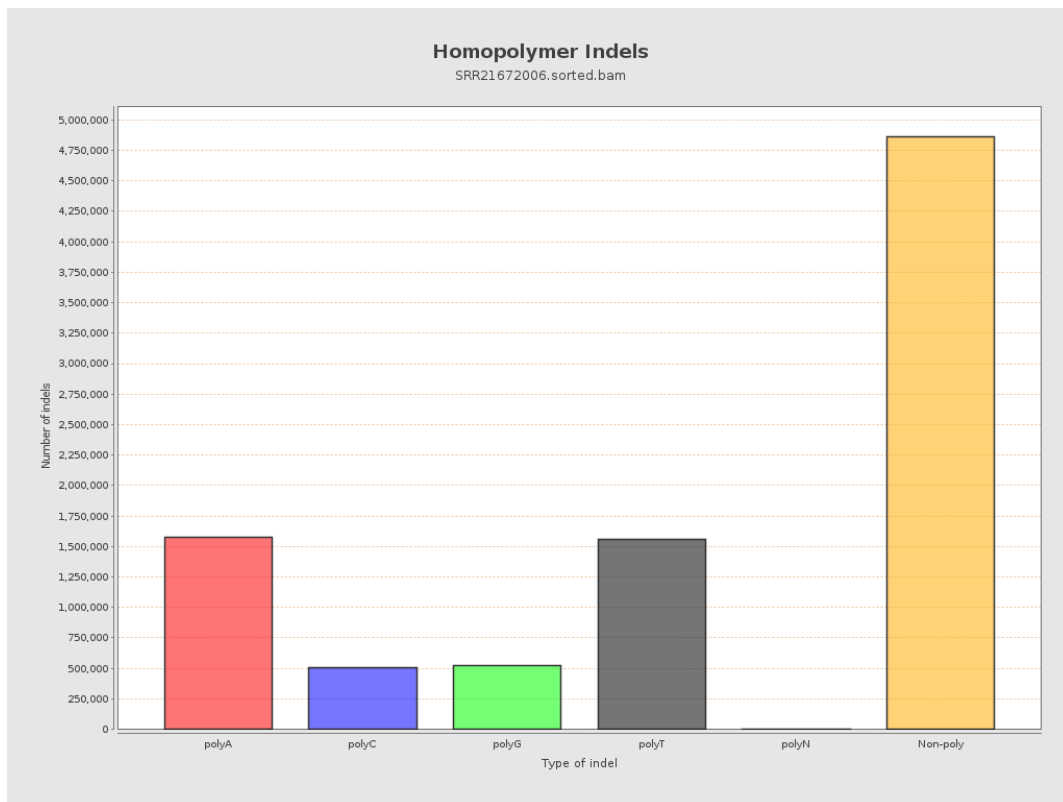
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



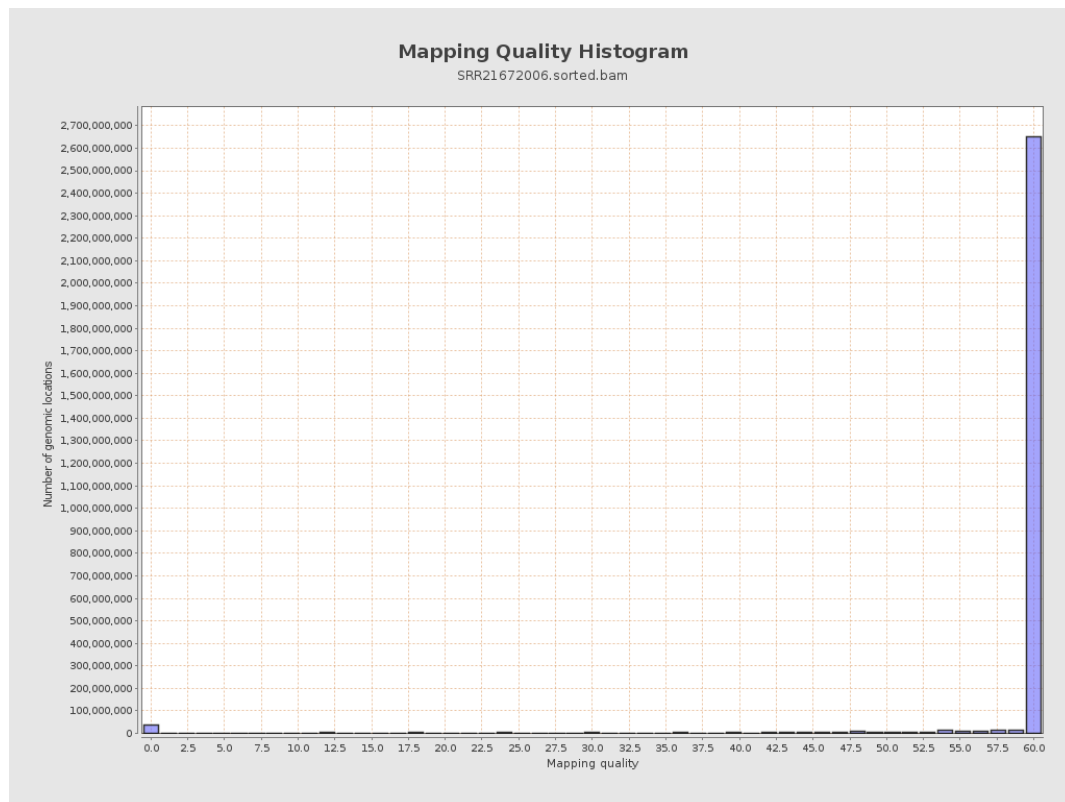
11. Results : Homopolymer Indels



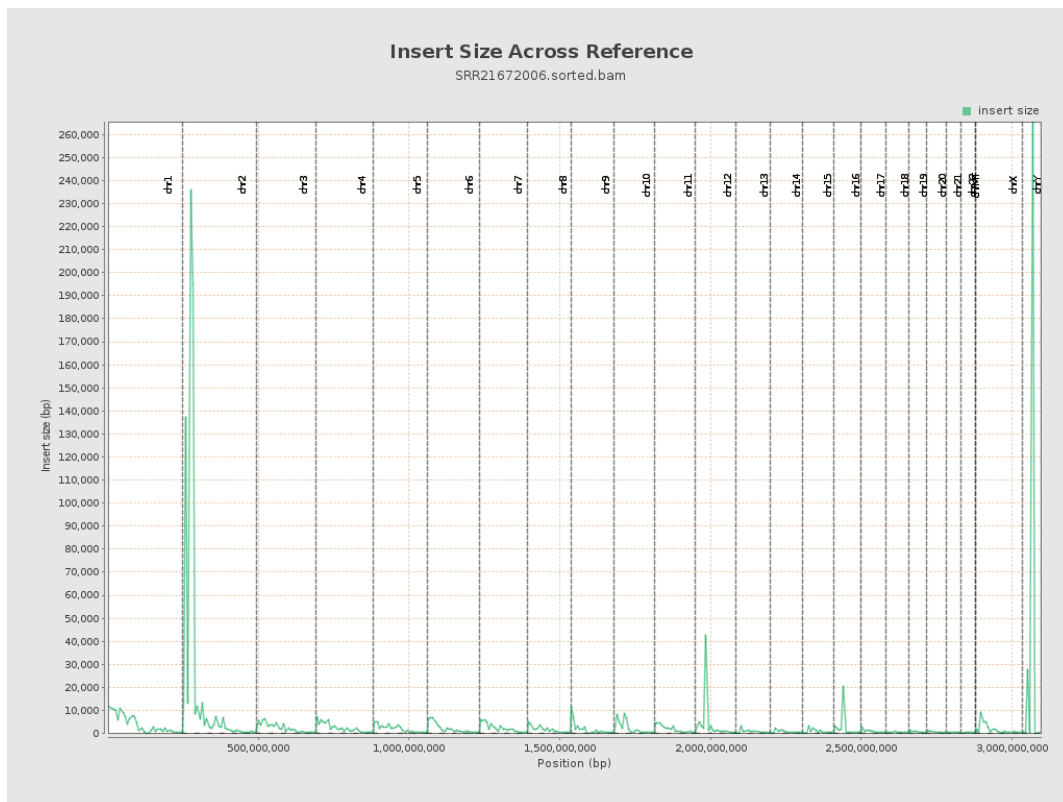
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

