

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/01 18:30:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR21672007.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_SRR21672007 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR21672007_1.fastq.gz SRR21672007_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 01 18:30:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR21672007.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	217,146,730
Mapped reads	215,149,128 / 99.08%
Unmapped reads	1,997,602 / 0.92%
Mapped paired reads	215,149,128 / 99.08%
Mapped reads, first in pair	107,684,757 / 49.59%
Mapped reads, second in pair	107,464,371 / 49.49%
Mapped reads, both in pair	214,438,848 / 98.75%
Mapped reads, singletons	710,280 / 0.33%
Secondary alignments	0
Supplementary alignments	1,954,902 / 0.9%
Read min/max/mean length	15 / 150 / 148.83
Duplicated reads (estimated)	51,173,495 / 23.57%
Duplication rate	19.56%
Clipped reads	14,686,512 / 6.76%

2.2. ACGT Content

Number/percentage of A's	9,282,368,690 / 29.38%
Number/percentage of C's	6,529,415,528 / 20.67%
Number/percentage of T's	9,208,737,948 / 29.15%
Number/percentage of G's	6,575,591,761 / 20.81%
Number/percentage of N's	45,856 / 0%

GC Percentage	41.48%
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2.3. Coverage

Mean	10.2109
Standard Deviation	125.157

2.4. Mapping Quality

Mean Mapping Quality	54.39
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2.5. Insert size

Mean	134,471.98
Standard Deviation	3,530,247.26
P25/Median/P75	305 / 389 / 482

2.6. Mismatches and indels

General error rate	0.84%
Mismatches	251,516,602
Insertions	4,546,912
Mapped reads with at least one insertion	1.99%
Deletions	4,853,222
Mapped reads with at least one deletion	2.16%
Homopolymer indels	44.5%

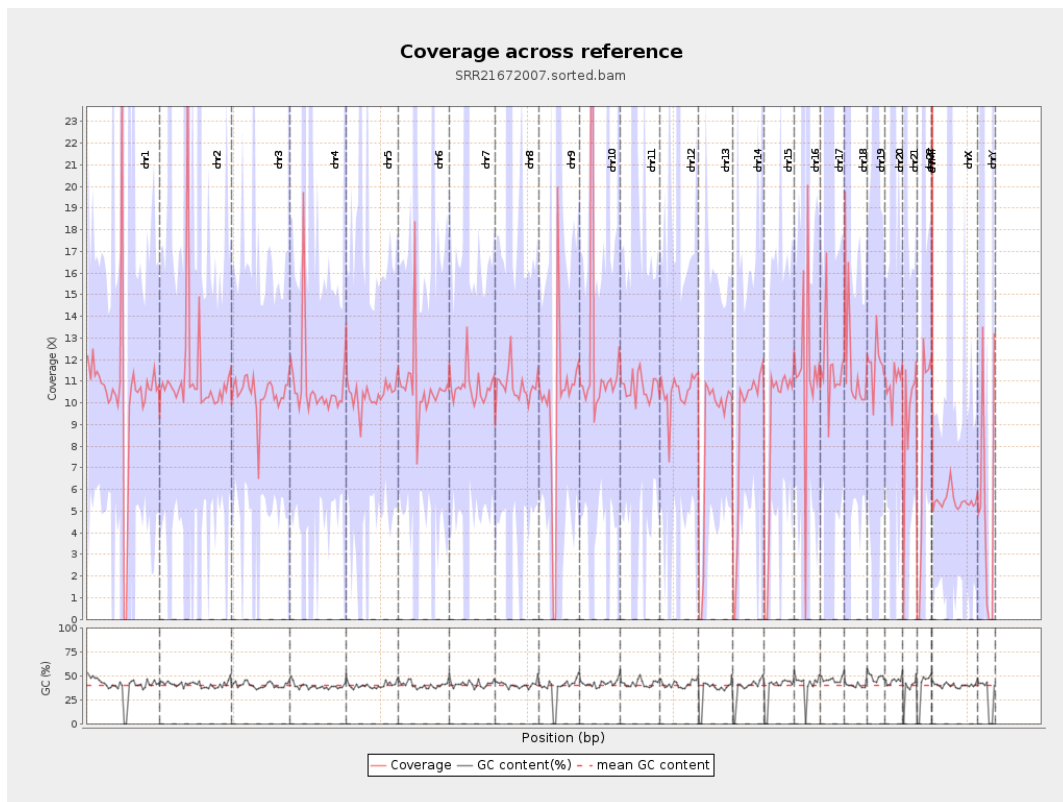
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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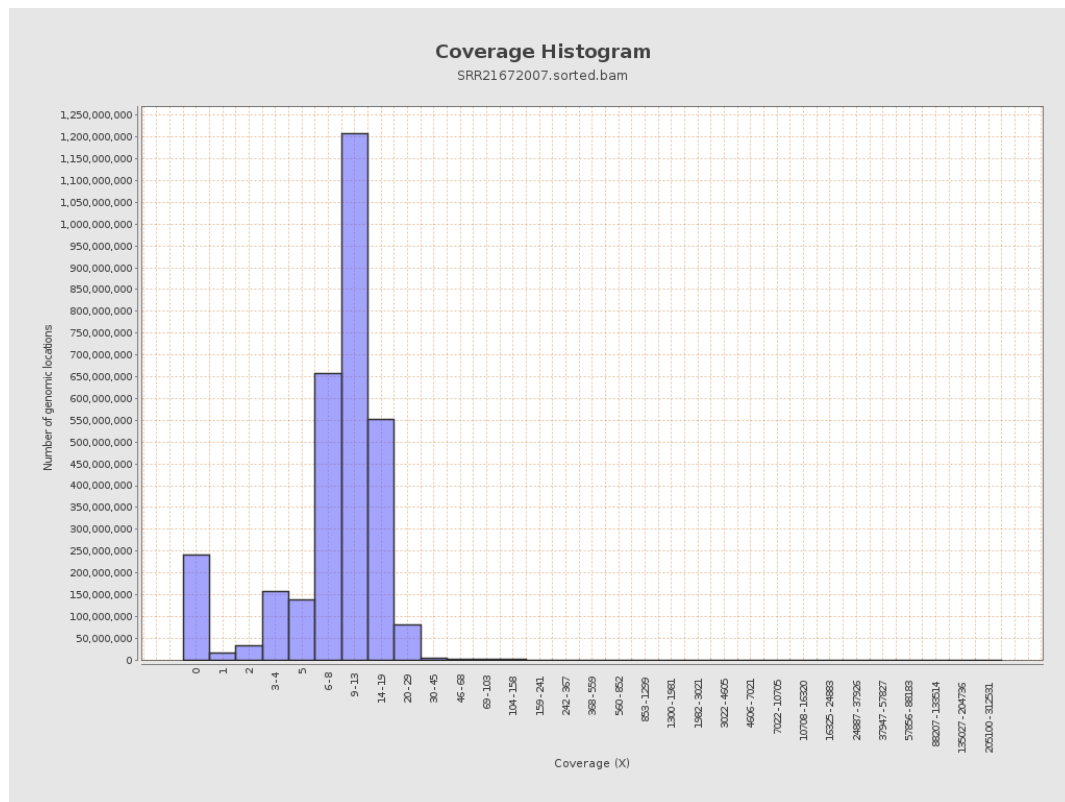
		bases	coverage	deviation
chr1	249250621	2631757494	10.5587	310.5047
chr2	243199373	2729204007	11.2221	81.3476
chr3	198022430	2061462305	10.4102	9.0401
chr4	191154276	2055626367	10.7538	81.2935
chr5	180915260	1881777130	10.4014	8.5457
chr6	171115067	1837006940	10.7355	88.9587
chr7	159138663	1713599281	10.768	67.6709
chr8	146364022	1585353161	10.8316	97.2851
chr9	141213431	1390860860	9.8494	212.4806
chr10	135534747	1662490818	12.2662	215.2344
chr11	135006516	1453677956	10.7675	40.938
chr12	133851895	1403689466	10.4869	22.628
chr13	115169878	989699098	8.5934	6.4374
chr14	107349540	953765199	8.8847	9.6442
chr15	102531392	907063062	8.8467	7.3758
chr16	90354753	1041075013	11.5221	73.4135
chr17	81195210	941850542	11.5998	63.4195
chr18	78077248	900524947	11.5338	170.5632
chr19	59128983	702044431	11.8731	139.8091
chr20	63025520	687843301	10.9137	28.5803
chr21	48129895	453136614	9.4149	44.2806
chr22	51304566	422166810	8.2286	23.5834
chrMT	16571	35926311	2,168.0231	247.8289
chrX	155270560	850230690	5.4758	17.4788

chrY	59373566	317985589	5.3557	98.2364
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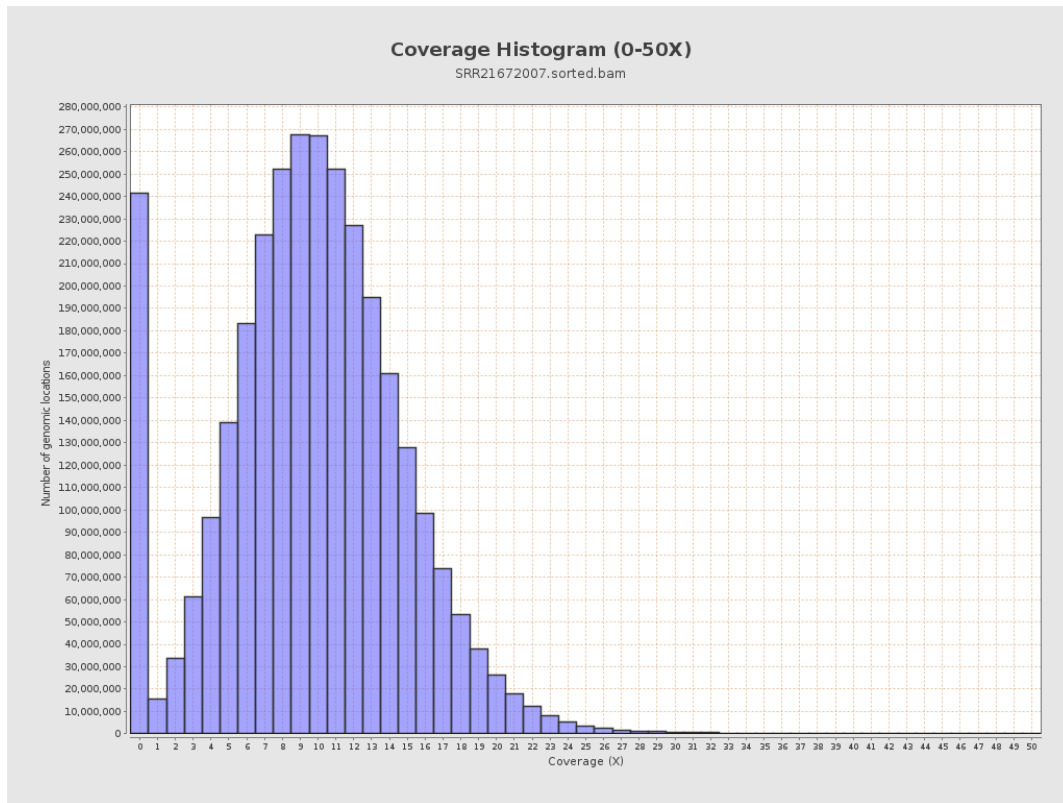
3. Results : Coverage across reference



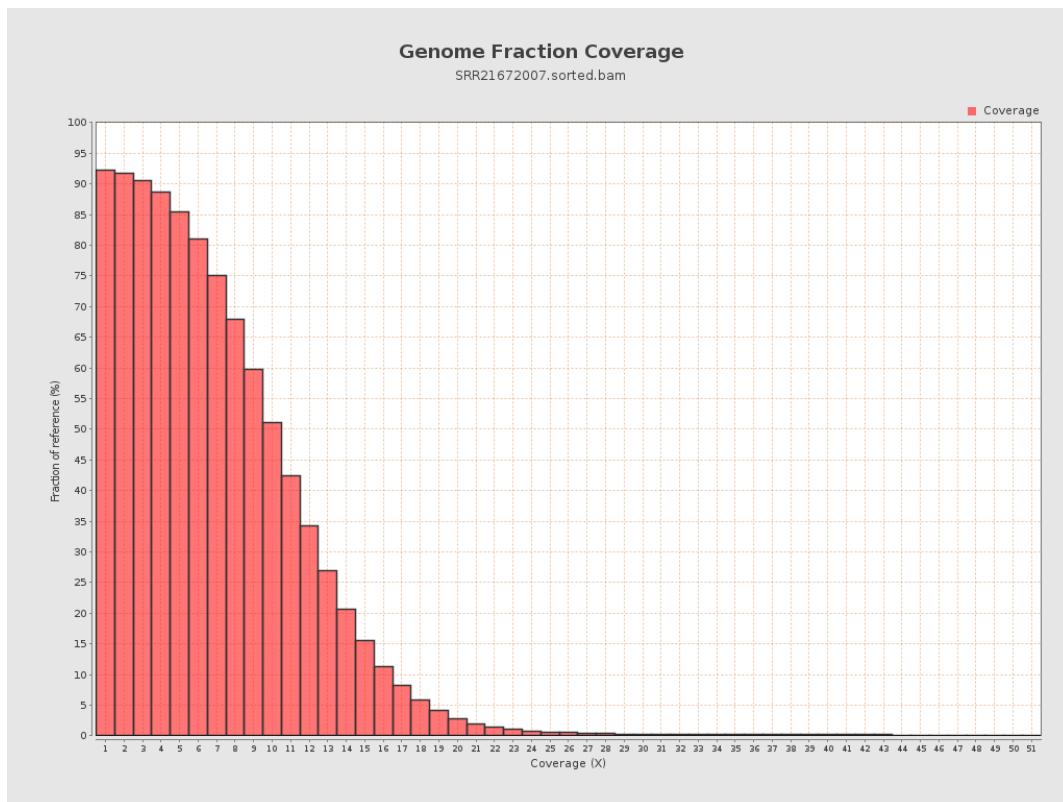
4. Results : Coverage Histogram



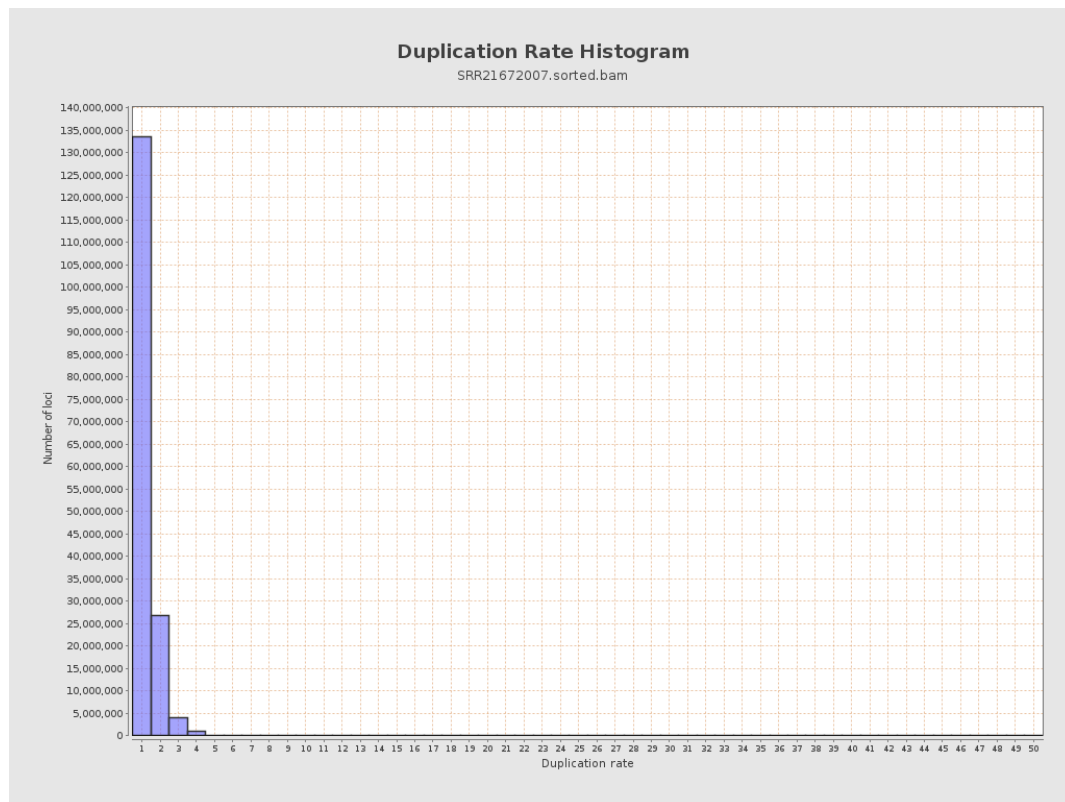
5. Results : Coverage Histogram (0-50X)



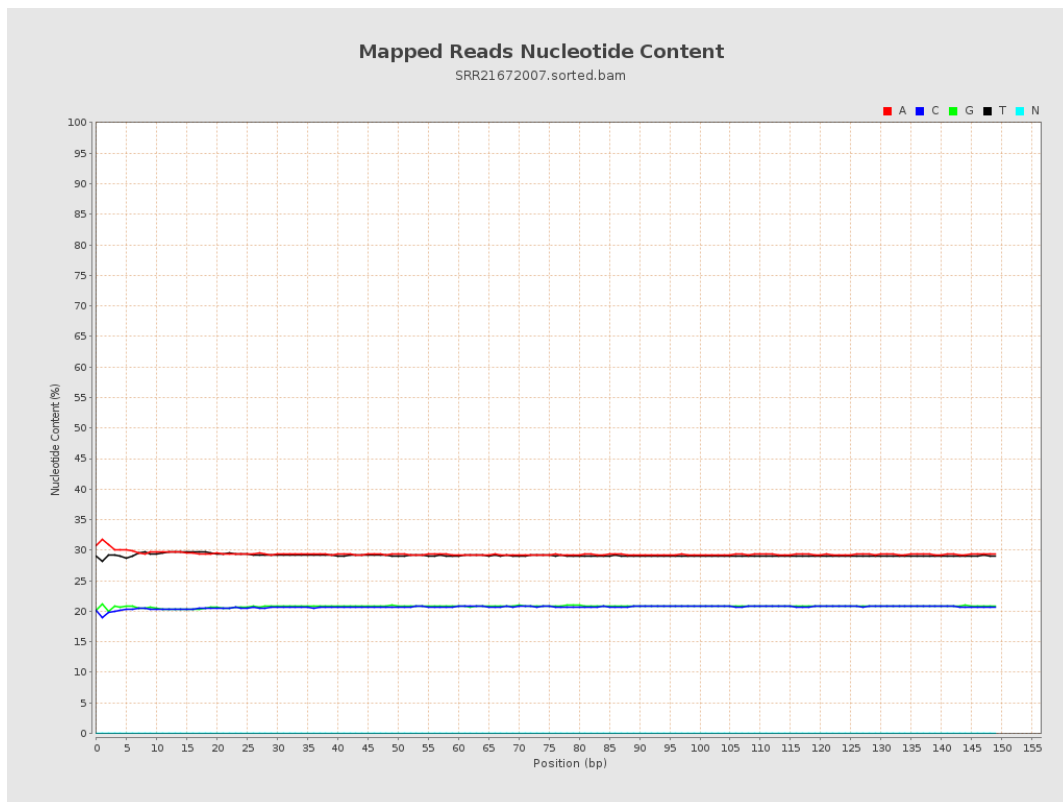
6. Results : Genome Fraction Coverage



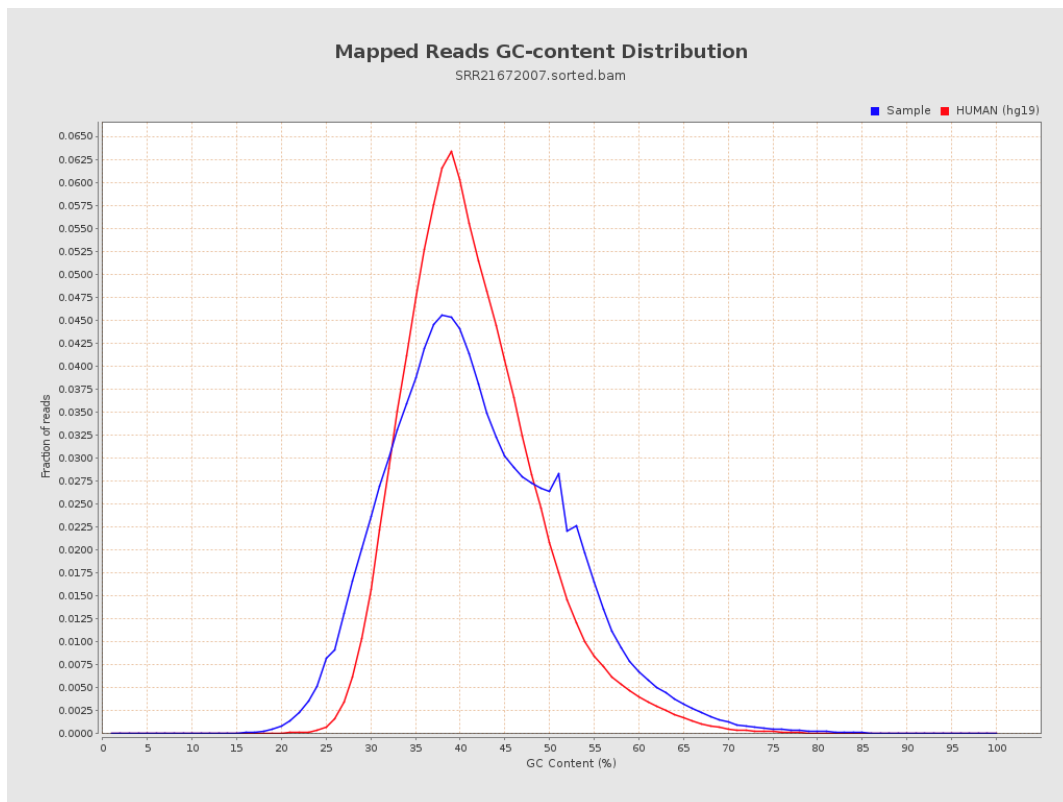
7. Results : Duplication Rate Histogram



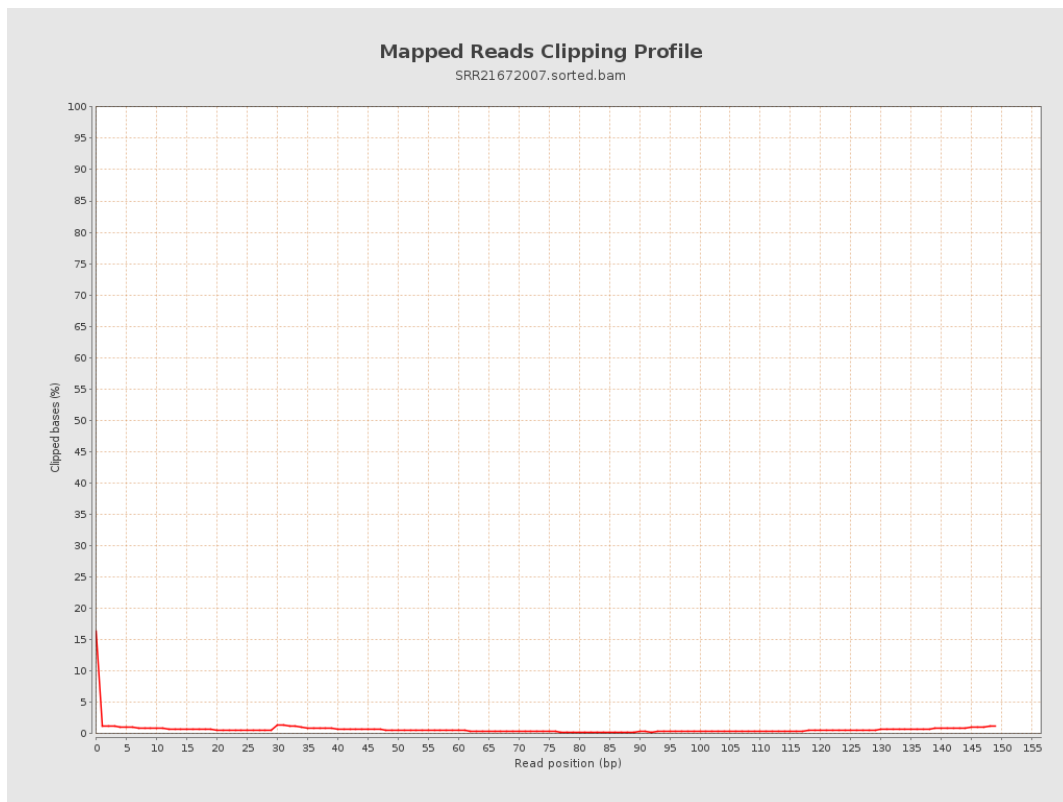
8. Results : Mapped Reads Nucleotide Content



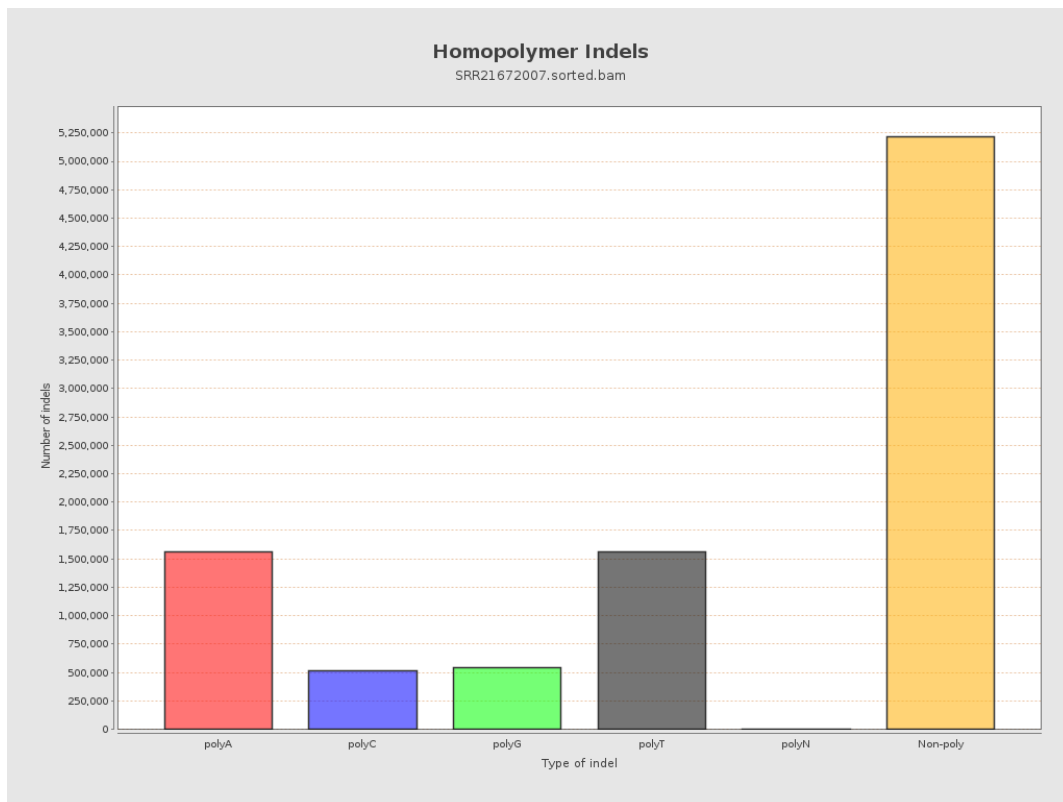
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



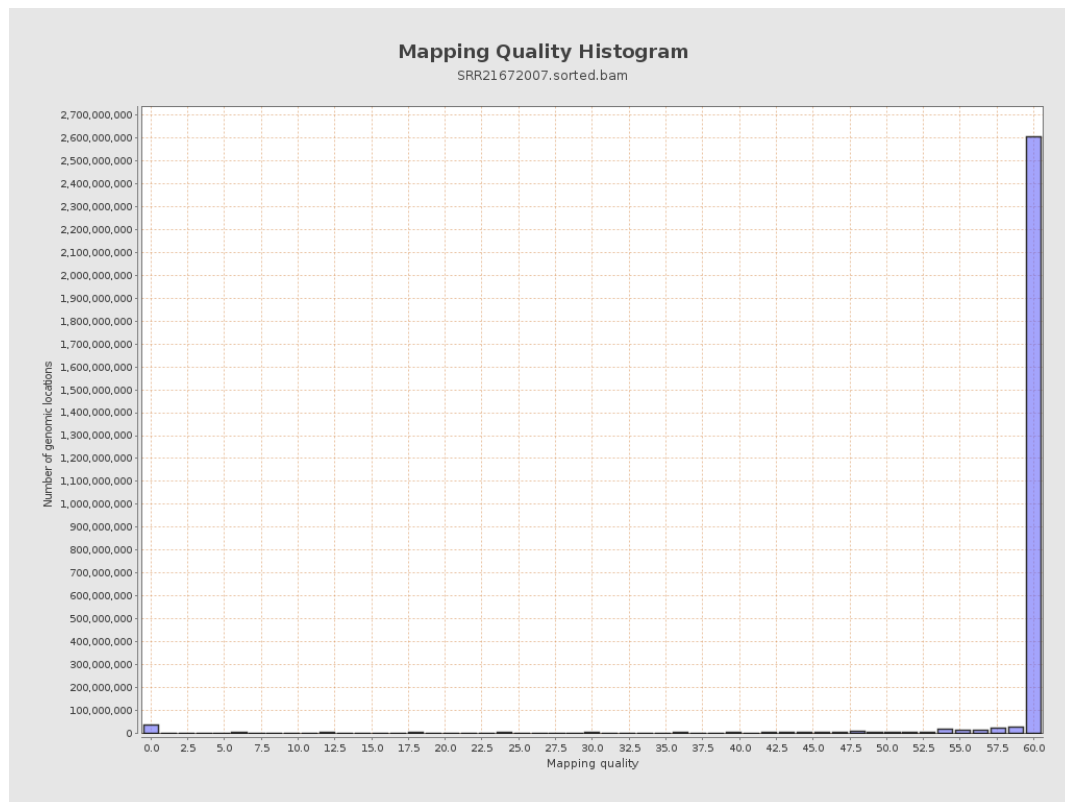
11. Results : Homopolymer Indels



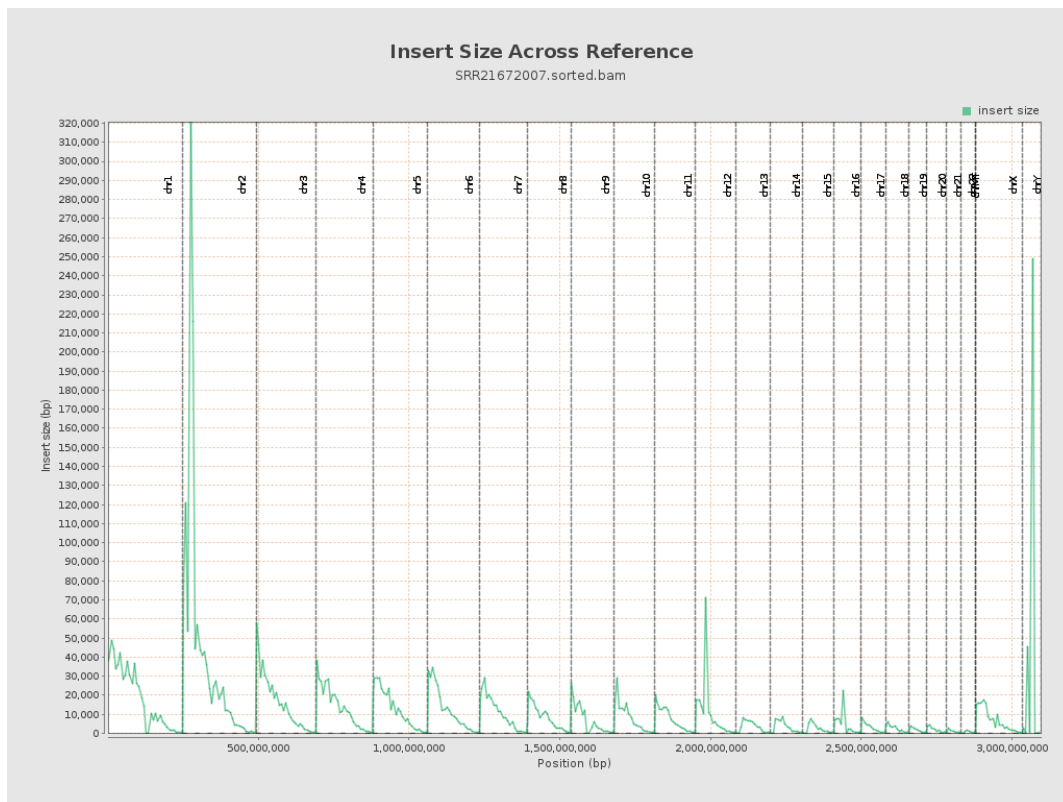
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

