

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 04:54:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472407.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_SRR3472407 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472407_1.fastq.gz SRR3472407_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 04:54:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472407.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,647,306
Mapped reads	18,512,999 / 99.28%
Unmapped reads	134,307 / 0.72%
Mapped paired reads	18,512,999 / 99.28%
Mapped reads, first in pair	9,283,215 / 49.78%
Mapped reads, second in pair	9,229,784 / 49.5%
Mapped reads, both in pair	18,428,810 / 98.83%
Mapped reads, singletons	84,189 / 0.45%
Secondary alignments	0
Supplementary alignments	74,213 / 0.4%
Read min/max/mean length	30 / 100 / 99.46
Duplicated reads (estimated)	11,943,797 / 64.05%
Duplication rate	47.7%
Clipped reads	1,244,919 / 6.68%

2.2. ACGT Content

Number/percentage of A's	488,691,107 / 26.88%
Number/percentage of C's	421,877,079 / 23.2%
Number/percentage of T's	489,616,784 / 26.93%
Number/percentage of G's	417,763,619 / 22.98%
Number/percentage of N's	224,731 / 0.01%

GC Percentage	46.18%
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2.3. Coverage

Mean	0.5874
Standard Deviation	19.1604

2.4. Mapping Quality

Mean Mapping Quality	55.24
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2.5. Insert size

Mean	17,194.08
Standard Deviation	1,317,561.81
P25/Median/P75	157 / 216 / 288

2.6. Mismatches and indels

General error rate	0.53%
Mismatches	9,522,030
Insertions	105,886
Mapped reads with at least one insertion	0.57%
Deletions	84,766
Mapped reads with at least one deletion	0.45%
Homopolymer indels	46.47%

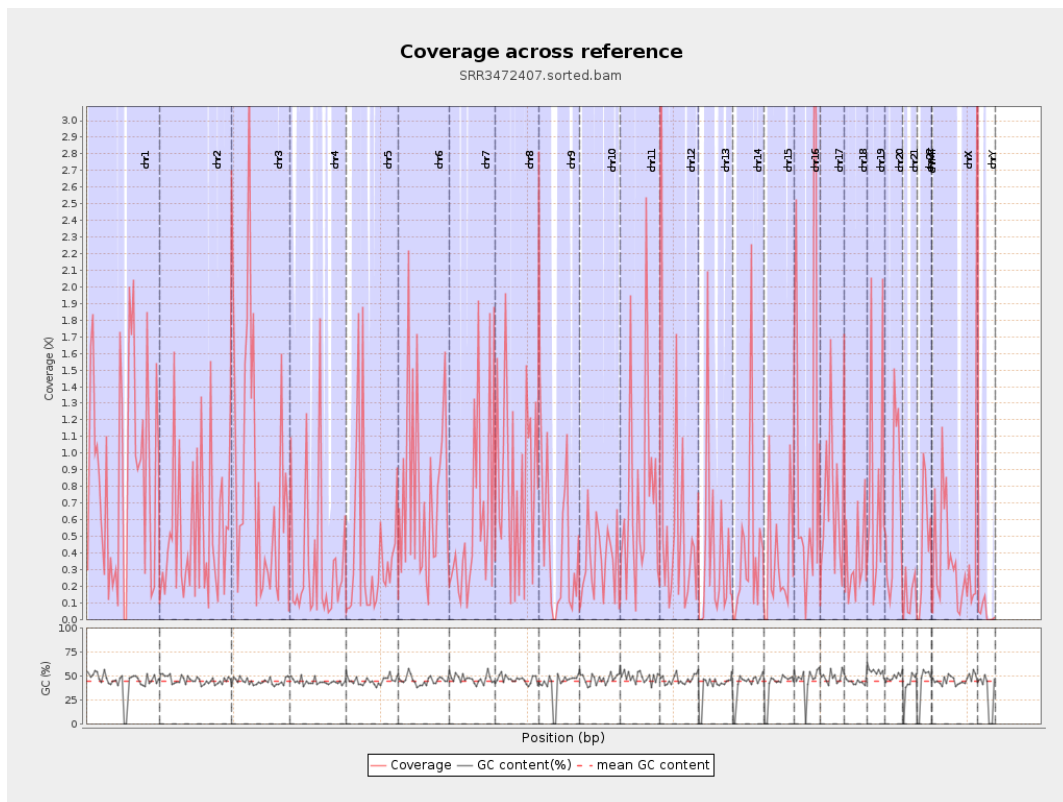
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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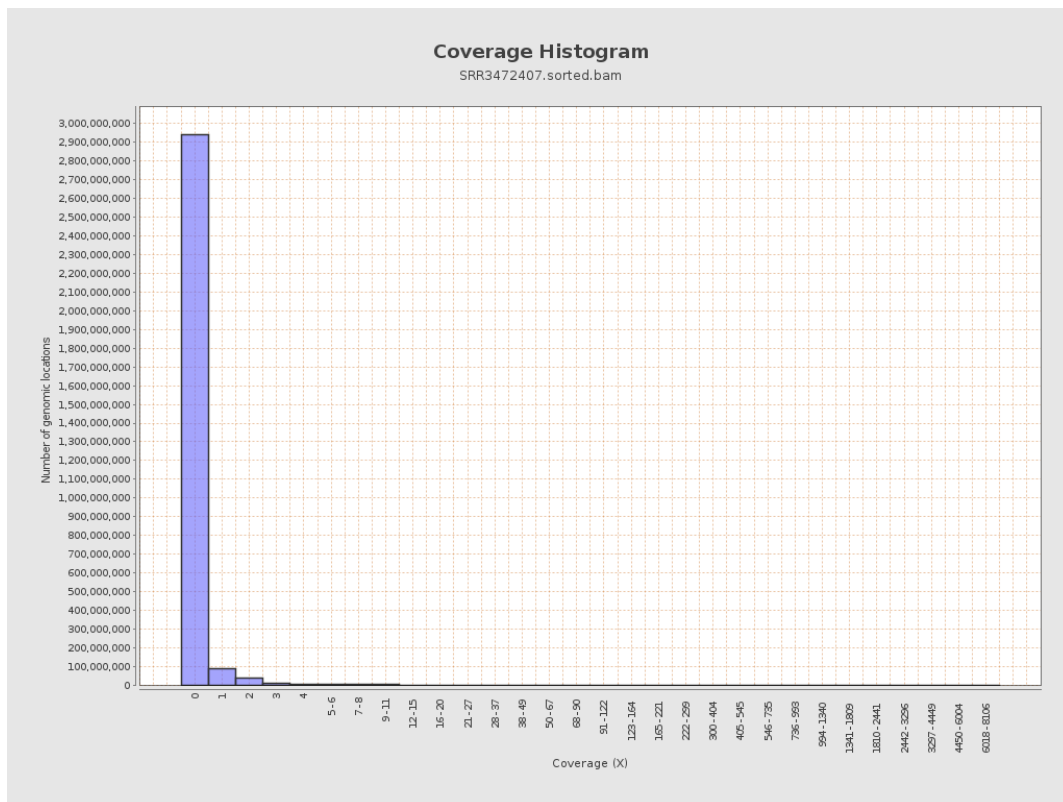
		bases	coverage	deviation
chr1	249250621	221326359	0.888	22.5855
chr2	243199373	127307880	0.5235	16.8897
chr3	198022430	171854151	0.8679	21.543
chr4	191154276	61395746	0.3212	15.7425
chr5	180915260	75881707	0.4194	14.7331
chr6	171115067	129485654	0.7567	19.0522
chr7	159138663	98293211	0.6177	18.7782
chr8	146364022	123566001	0.8442	25.1002
chr9	141213431	66686986	0.4722	14.8071
chr10	135534747	48080125	0.3547	12.6609
chr11	135006516	98168269	0.7271	27.3772
chr12	133851895	91344179	0.6824	23.9186
chr13	115169878	43564163	0.3783	13.9478
chr14	107349540	43602257	0.4062	12.0042
chr15	102531392	36562128	0.3566	11.1198
chr16	90354753	102665562	1.1362	37.0486
chr17	81195210	59921031	0.738	18.2137
chr18	78077248	28142149	0.3604	11.5804
chr19	59128983	51111705	0.8644	28.6055
chr20	63025520	43672777	0.6929	19.2654
chr21	48129895	7207289	0.1497	7.1079
chr22	51304566	23962126	0.4671	12.3096
chrMT	16571	3421	0.2064	0.5647
chrX	155270560	62001479	0.3993	12.9913

chrY	59373566	2573131	0.0433	1.8284
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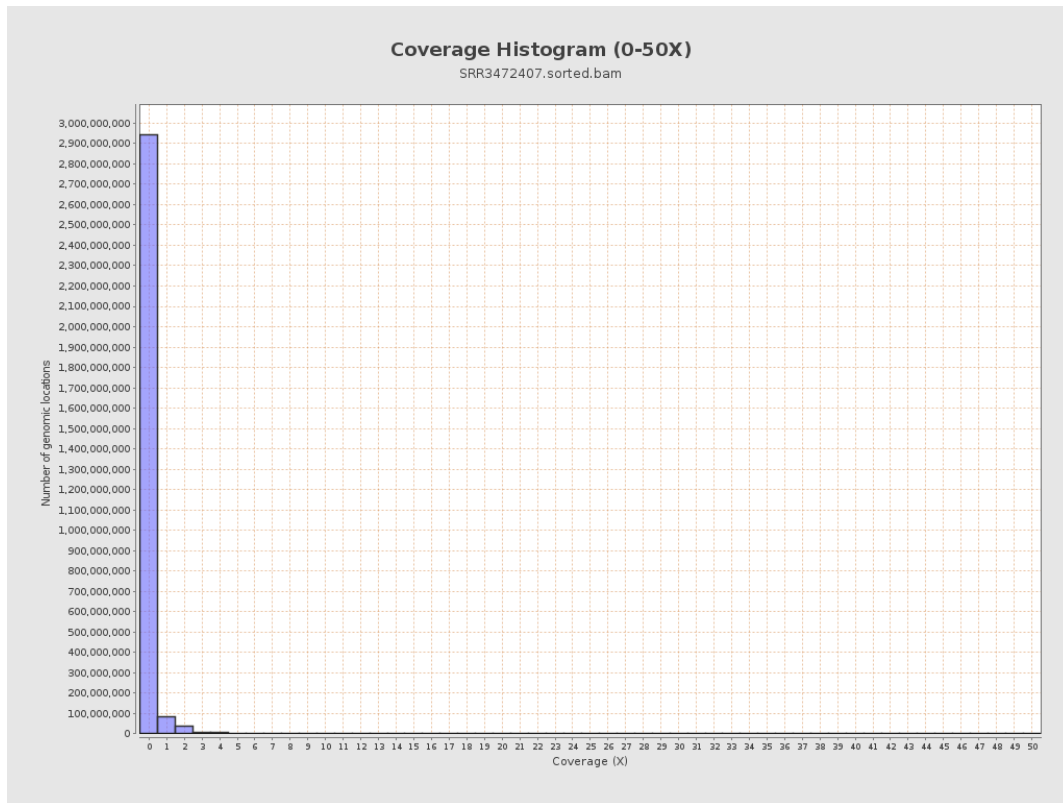
3. Results : Coverage across reference



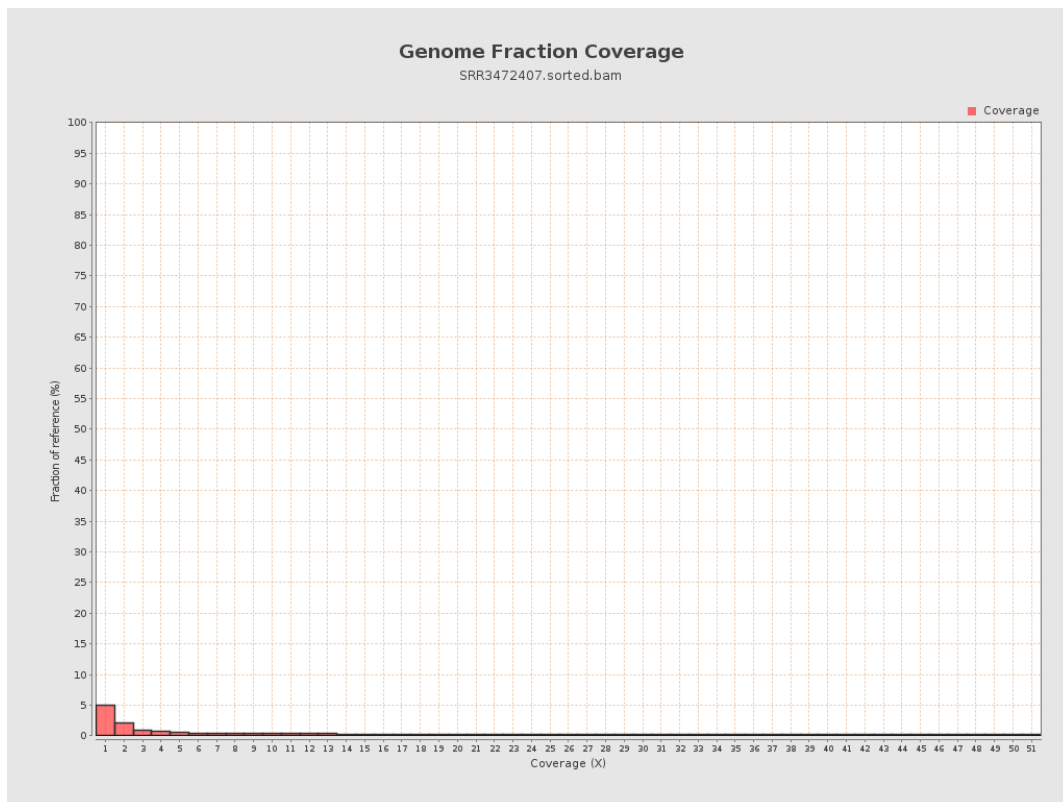
4. Results : Coverage Histogram



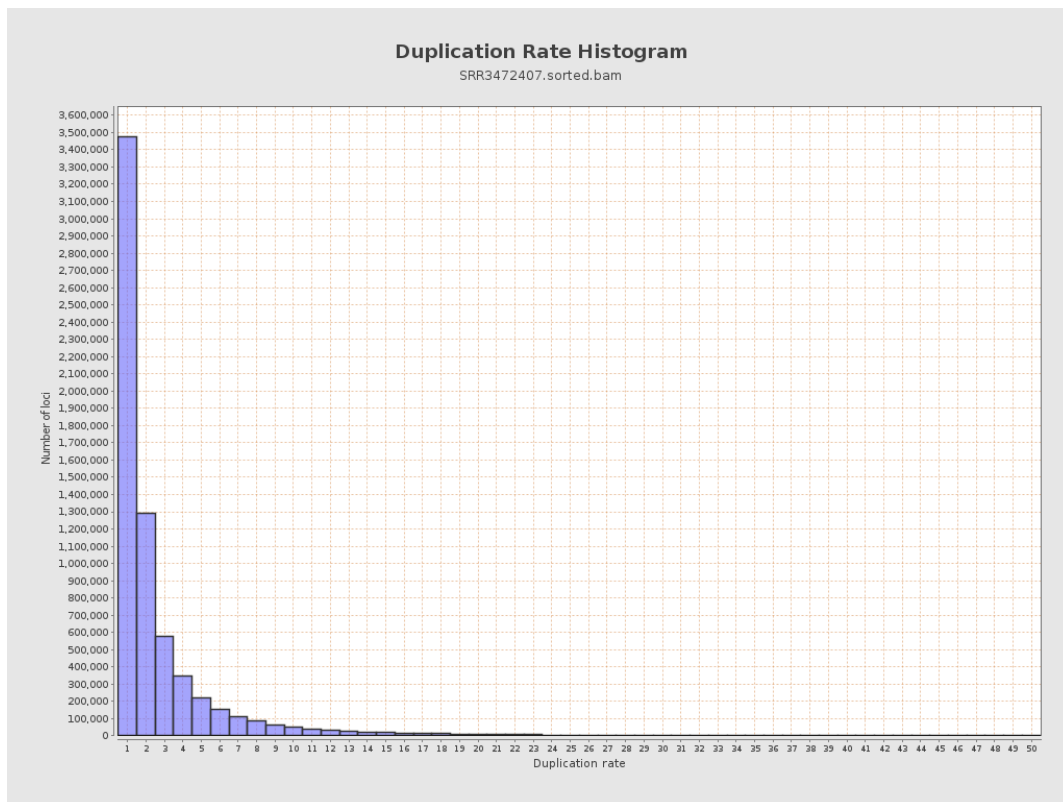
5. Results : Coverage Histogram (0-50X)



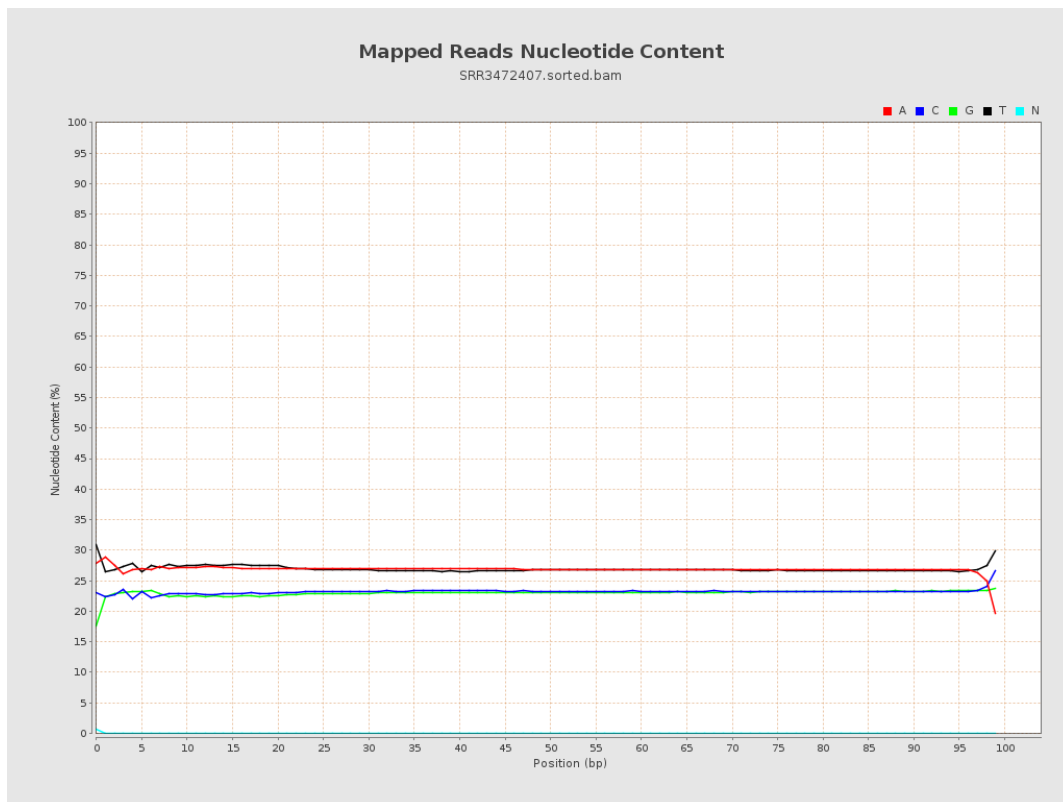
6. Results : Genome Fraction Coverage



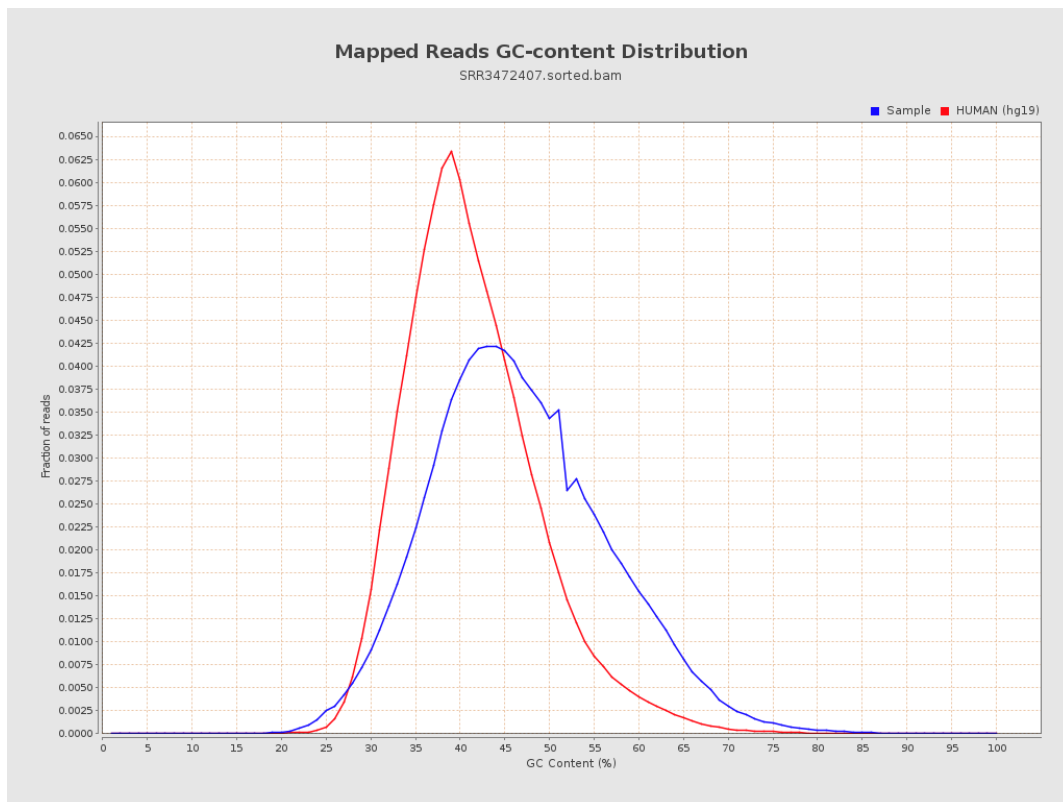
7. Results : Duplication Rate Histogram



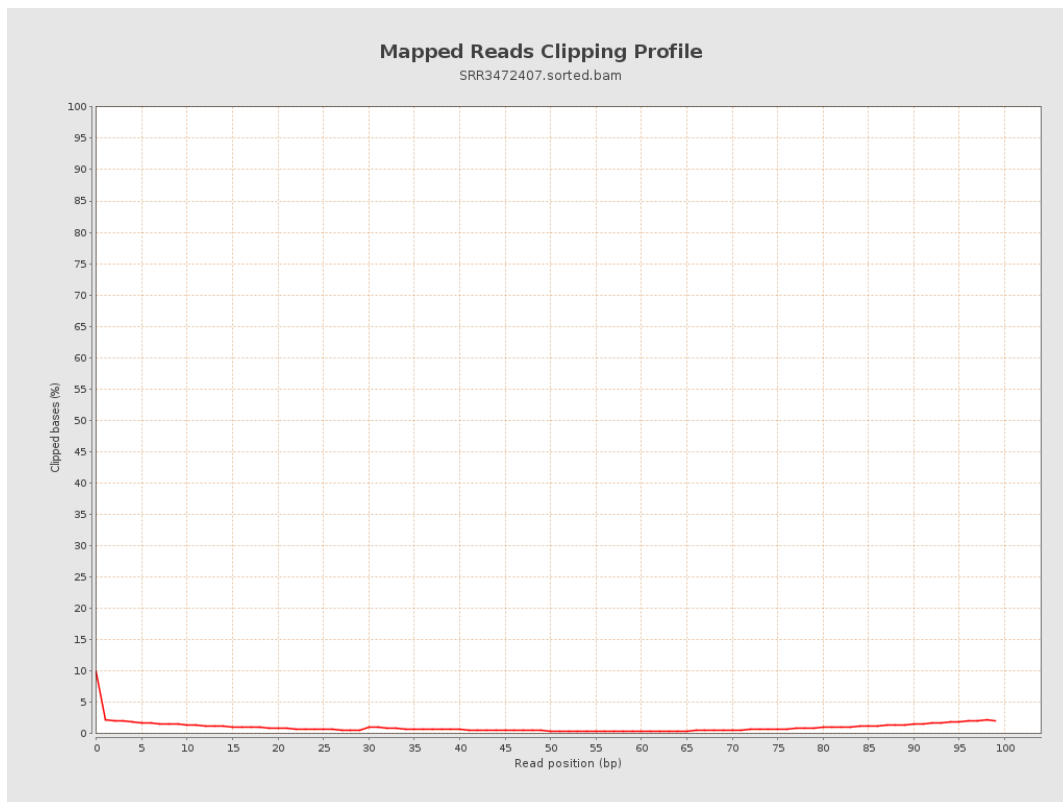
8. Results : Mapped Reads Nucleotide Content



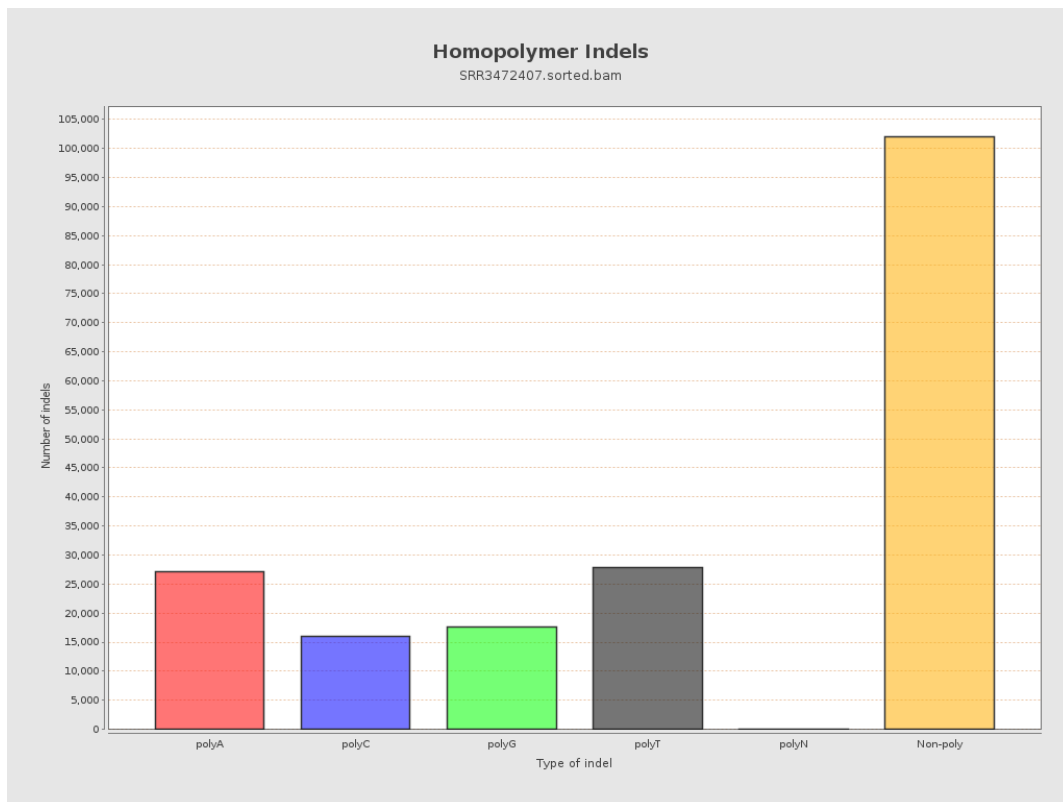
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



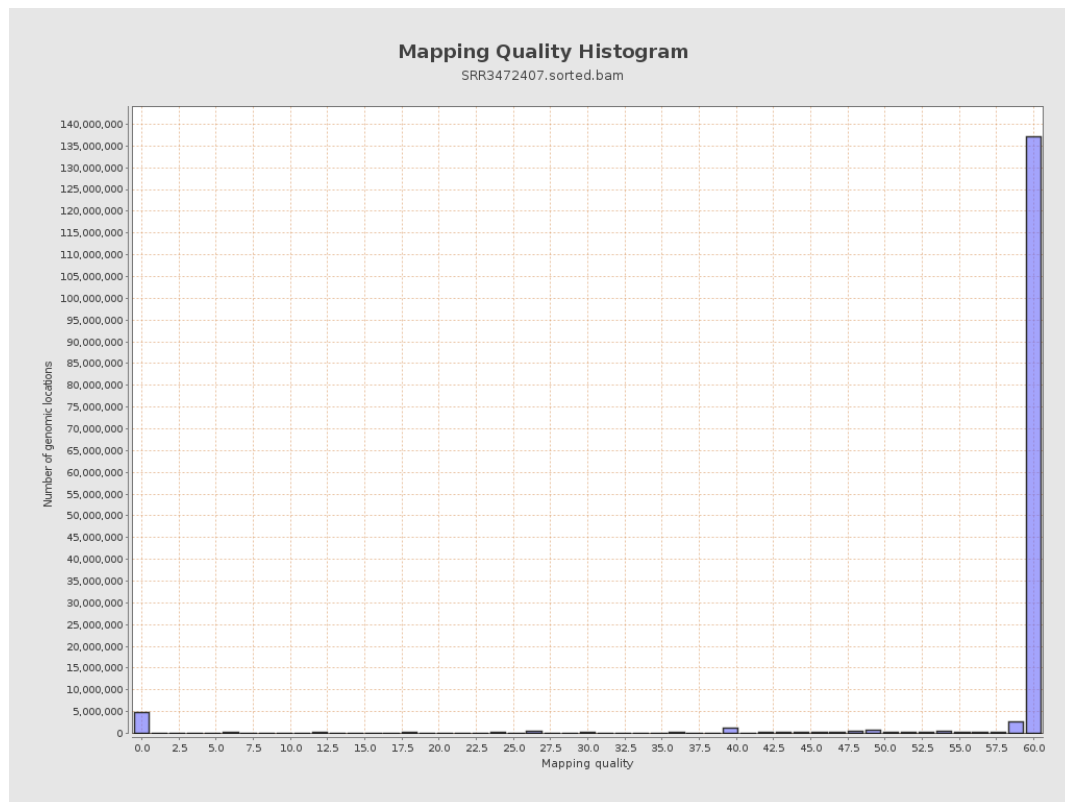
11. Results : Homopolymer Indels



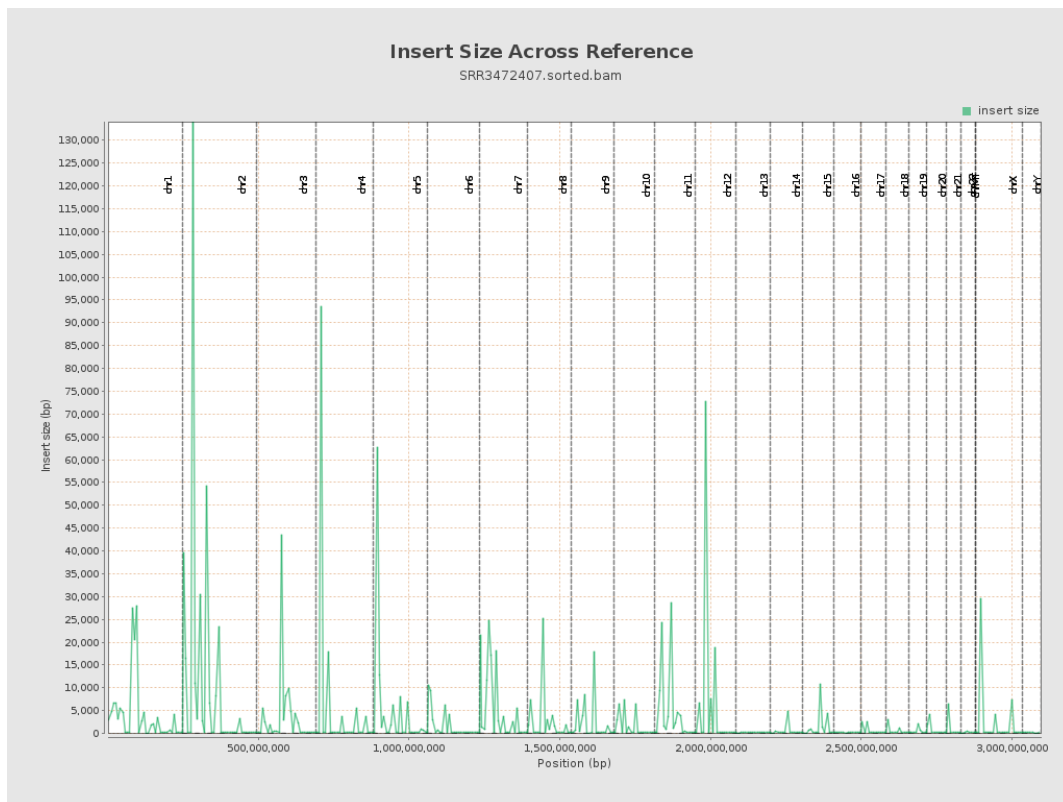
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

