

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 03:59:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472745.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_SRR3472745 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472745_1.fastq.gz SRR3472745_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 03:59:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472745.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,270,426
Mapped reads	18,062,968 / 98.86%
Unmapped reads	207,458 / 1.14%
Mapped paired reads	18,062,968 / 98.86%
Mapped reads, first in pair	9,080,725 / 49.7%
Mapped reads, second in pair	8,982,243 / 49.16%
Mapped reads, both in pair	17,926,934 / 98.12%
Mapped reads, singletons	136,034 / 0.74%
Secondary alignments	0
Supplementary alignments	90,607 / 0.5%
Read min/max/mean length	30 / 100 / 100.2
Duplicated reads (estimated)	12,199,446 / 66.77%
Duplication rate	46.85%
Clipped reads	1,342,418 / 7.35%

2.2. ACGT Content

Number/percentage of A's	494,250,390 / 27.72%
Number/percentage of C's	400,834,447 / 22.48%
Number/percentage of T's	491,326,534 / 27.55%
Number/percentage of G's	396,454,648 / 22.23%
Number/percentage of N's	340,691 / 0.02%

GC Percentage	44.71%
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2.3. Coverage

Mean	0.5761
Standard Deviation	26.565

2.4. Mapping Quality

Mean Mapping Quality	54.92
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2.5. Insert size

Mean	31,450.63
Standard Deviation	1,717,706.97
P25/Median/P75	186 / 261 / 352

2.6. Mismatches and indels

General error rate	0.68%
Mismatches	11,983,529
Insertions	98,690
Mapped reads with at least one insertion	0.54%
Deletions	98,441
Mapped reads with at least one deletion	0.54%
Homopolymer indels	46.83%

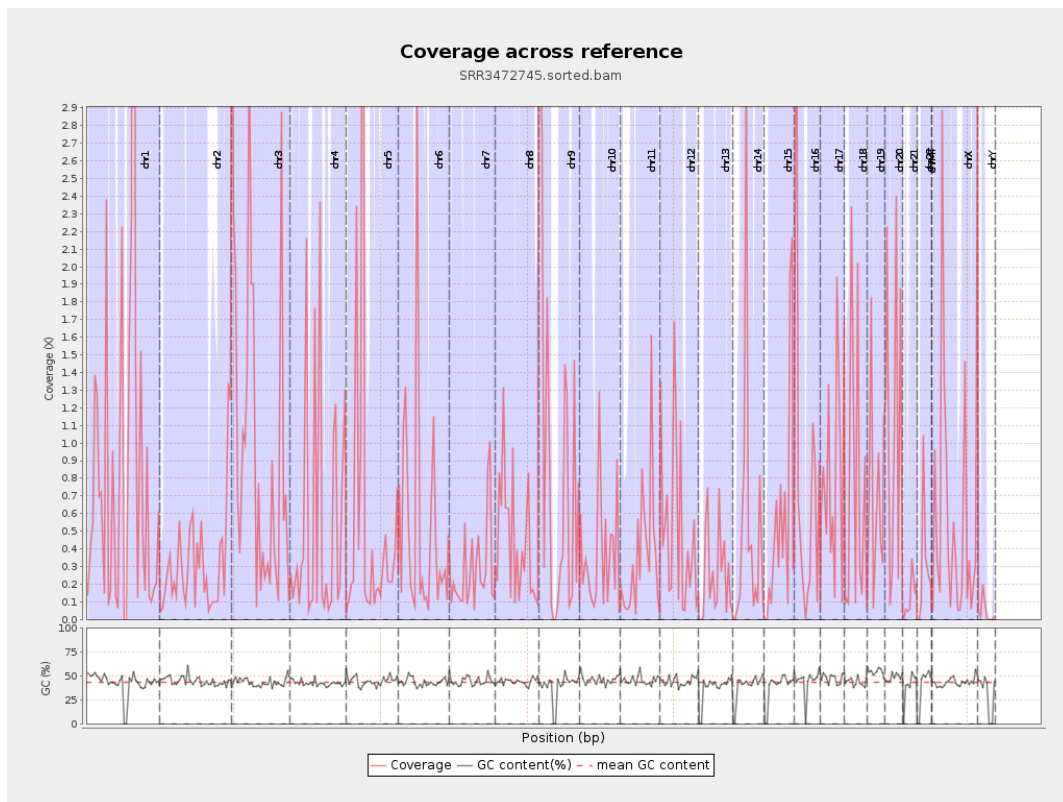
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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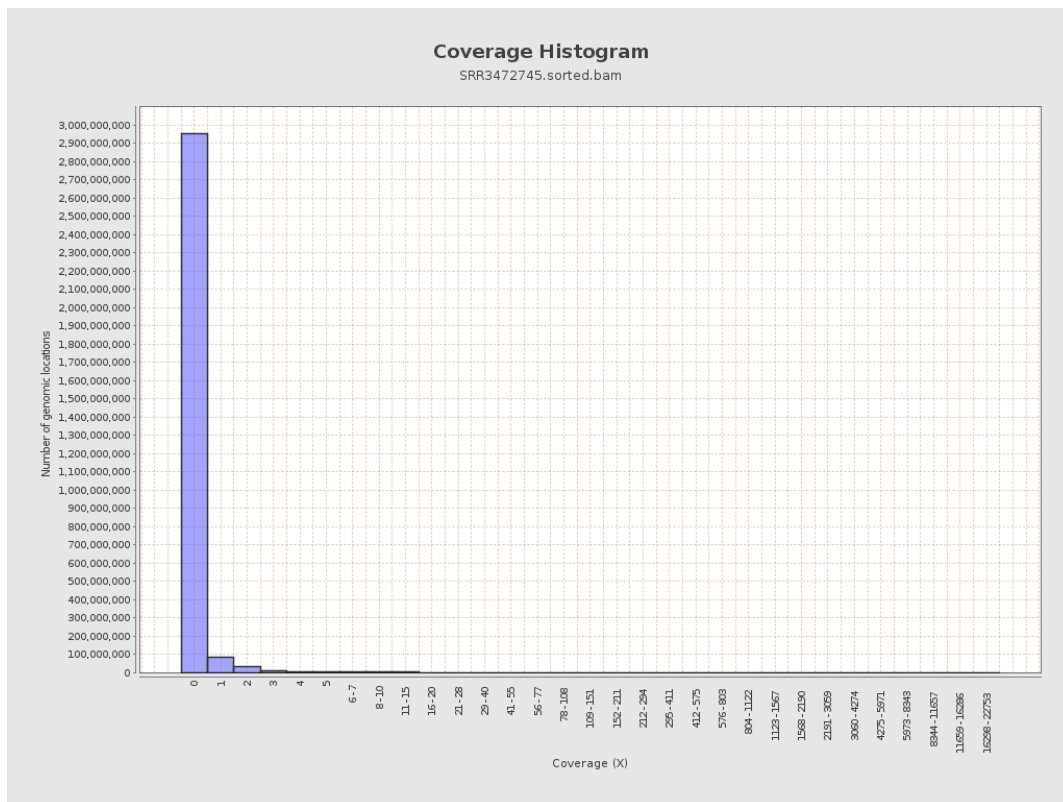
		bases	coverage	deviation
chr1	249250621	241197368	0.9677	56.581
chr2	243199373	76030507	0.3126	11.4105
chr3	198022430	199383480	1.0069	24.6897
chr4	191154276	102811450	0.5378	28.4185
chr5	180915260	106759258	0.5901	23.3829
chr6	171115067	85131513	0.4975	16.2462
chr7	159138663	45931058	0.2886	10.2152
chr8	146364022	65920675	0.4504	18.7746
chr9	141213431	130165349	0.9218	34.1156
chr10	135534747	50365120	0.3716	15.0442
chr11	135006516	50103844	0.3711	15.1361
chr12	133851895	69017817	0.5156	18.4422
chr13	115169878	29423104	0.2555	10.0499
chr14	107349540	53521427	0.4986	23.5765
chr15	102531392	59935213	0.5846	29.445
chr16	90354753	70824040	0.7838	28.8924
chr17	81195210	64621274	0.7959	19.3021
chr18	78077248	57386969	0.735	42.2702
chr19	59128983	40392283	0.6831	21.0053
chr20	63025520	69788658	1.1073	39.1834
chr21	48129895	6109108	0.1269	7.4102
chr22	51304566	15326241	0.2987	9.9111
chrMT	16571	3444	0.2078	0.6325
chrX	155270560	90549623	0.5832	19.6194

chrY	59373566	2751394	0.0463	2.1442
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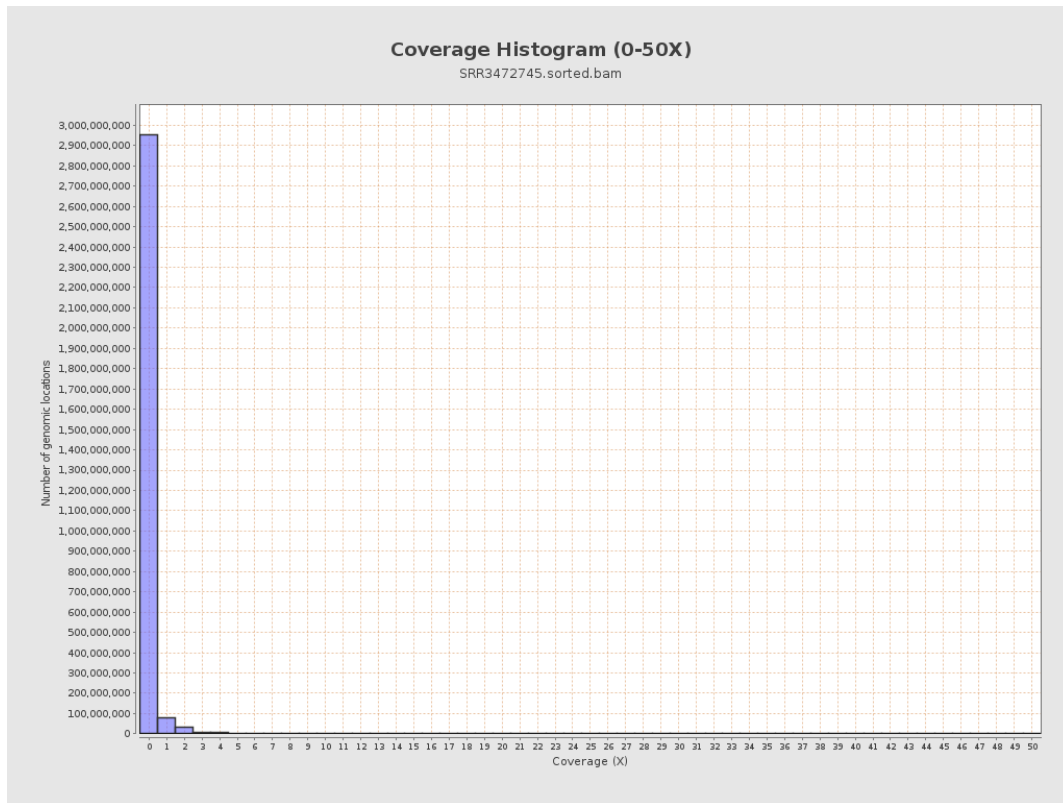
3. Results : Coverage across reference



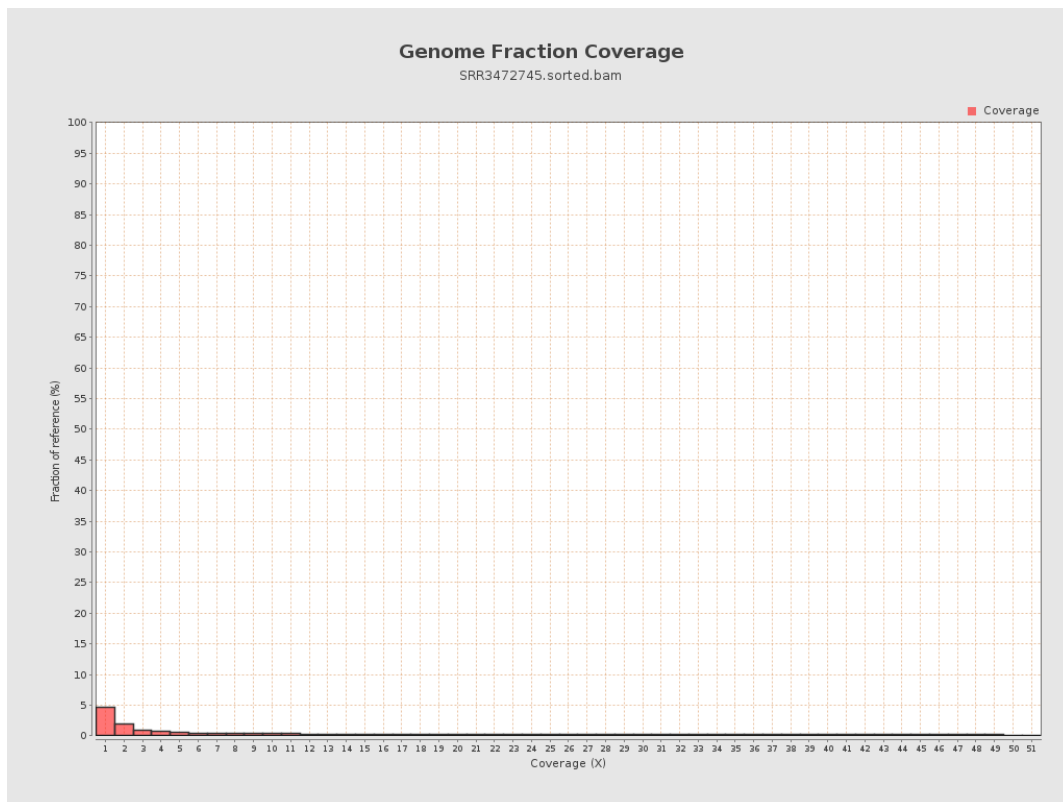
4. Results : Coverage Histogram



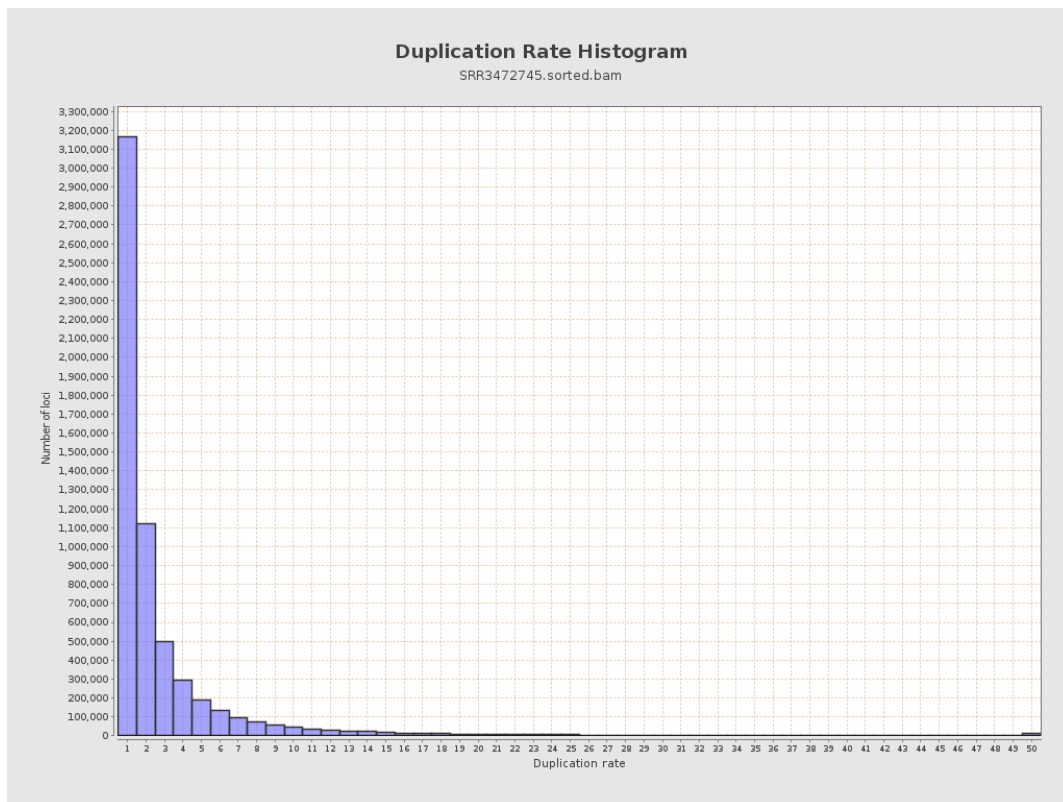
5. Results : Coverage Histogram (0-50X)



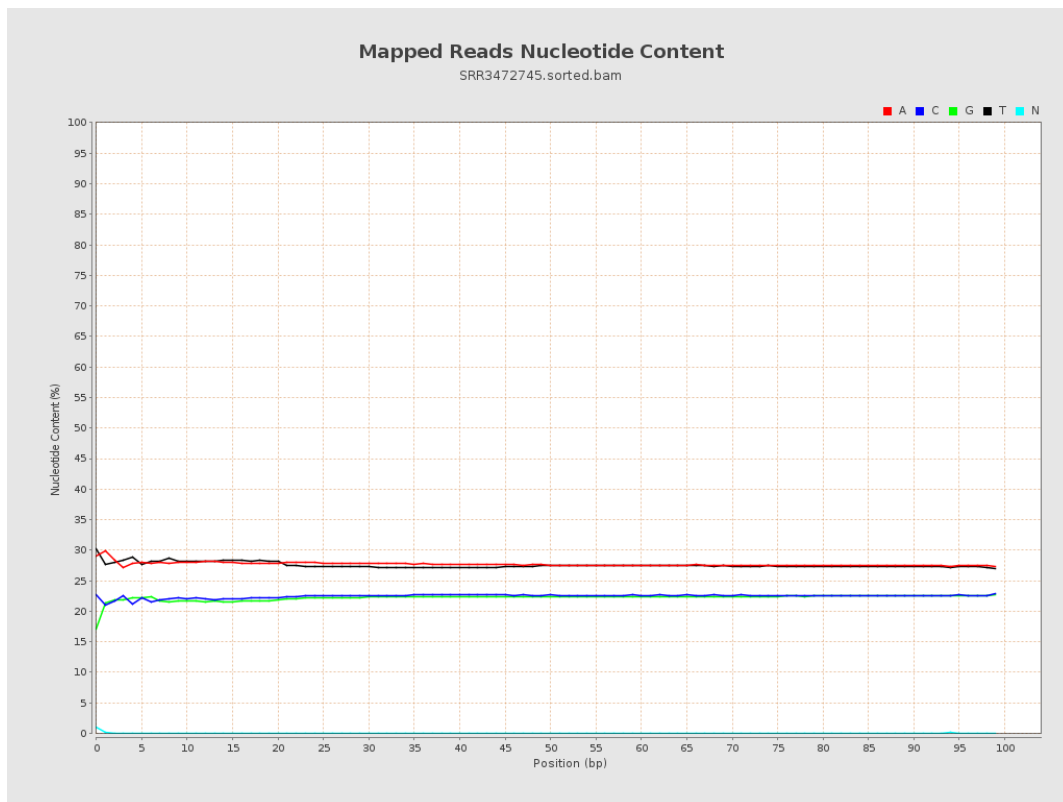
6. Results : Genome Fraction Coverage



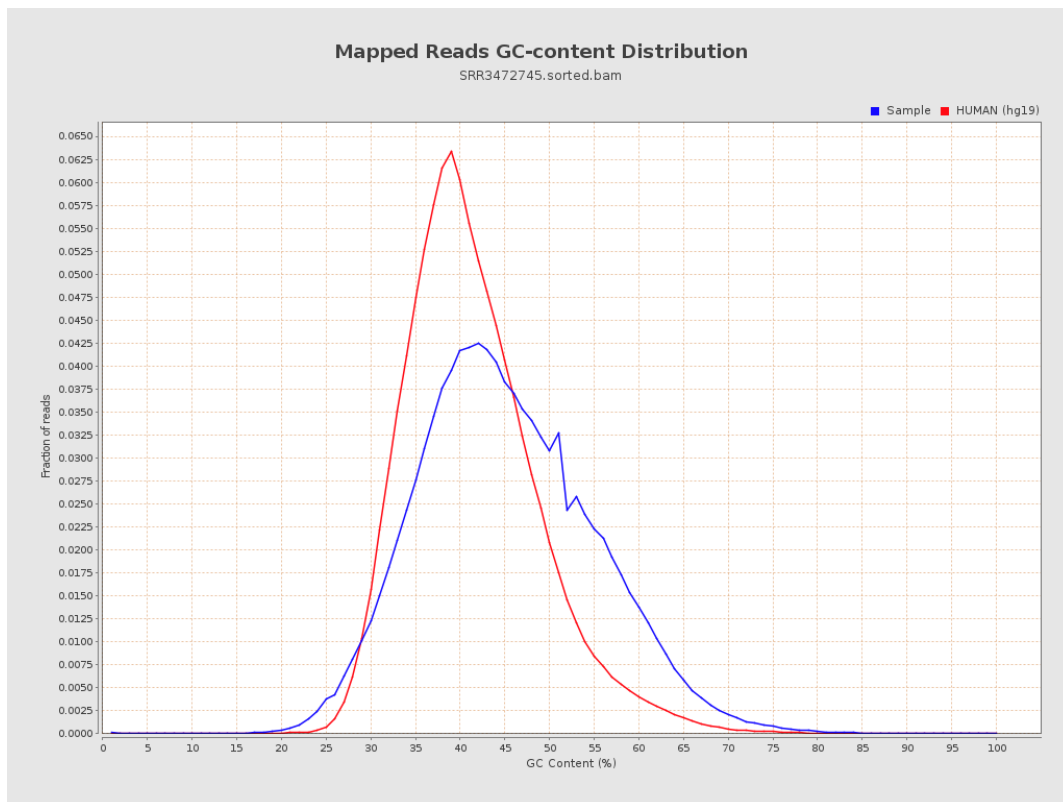
7. Results : Duplication Rate Histogram



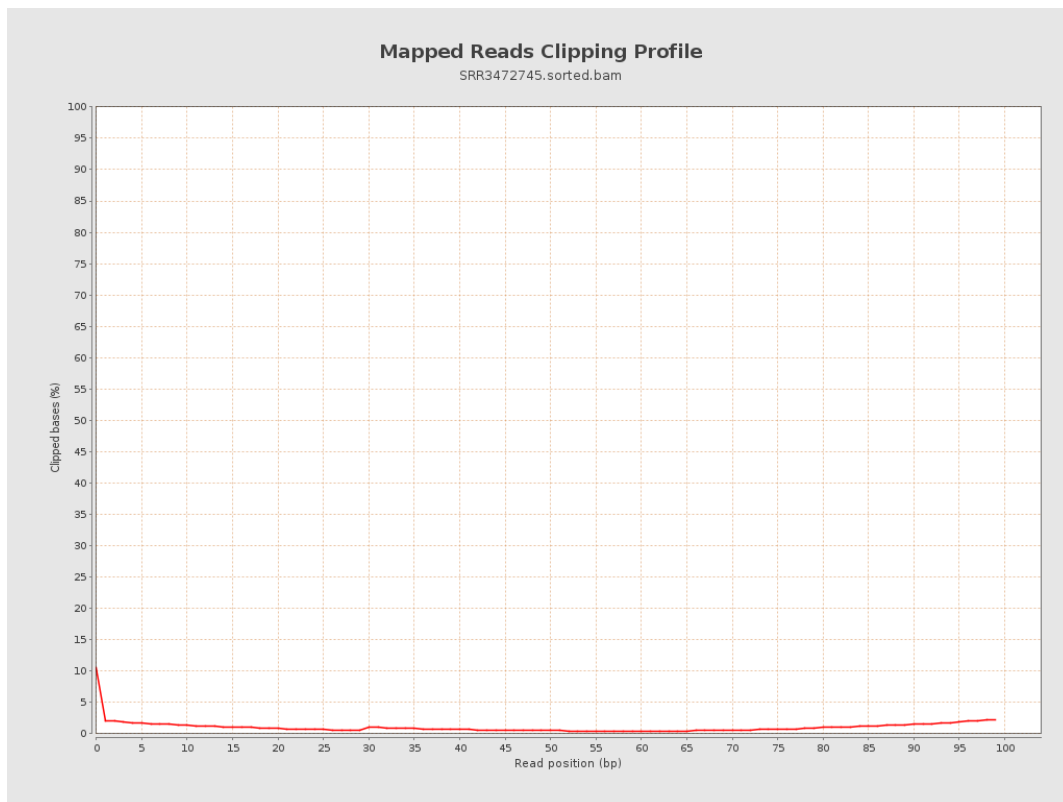
8. Results : Mapped Reads Nucleotide Content



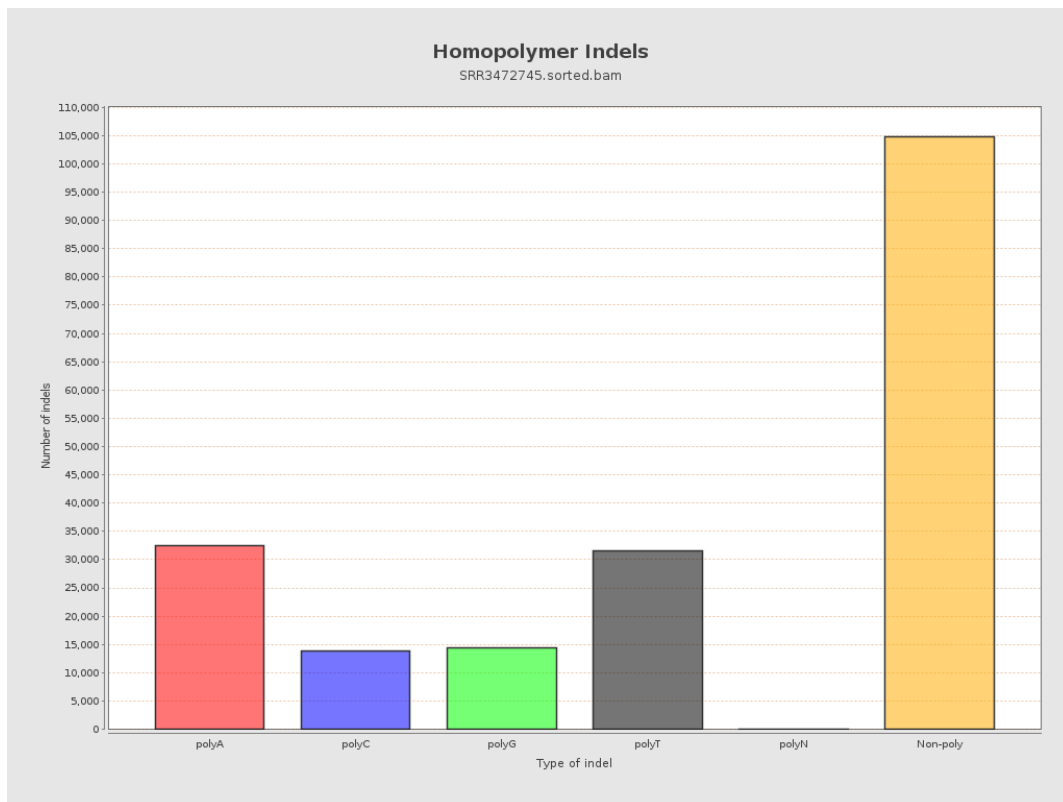
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



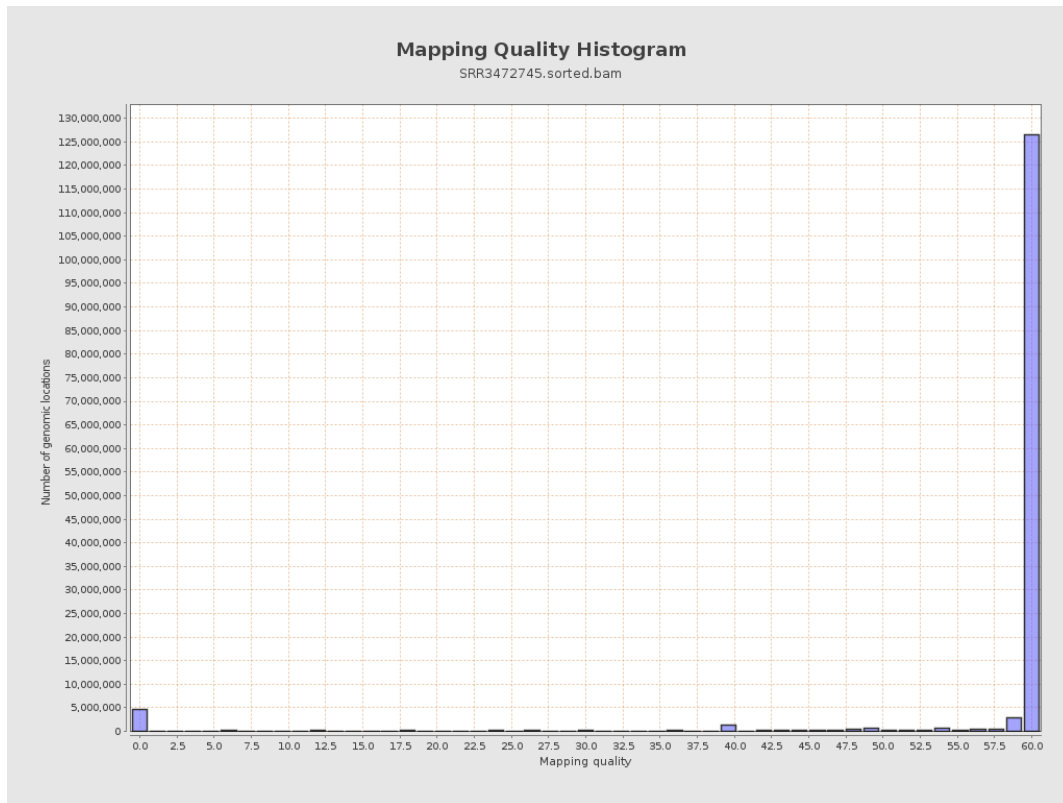
11. Results : Homopolymer Indels



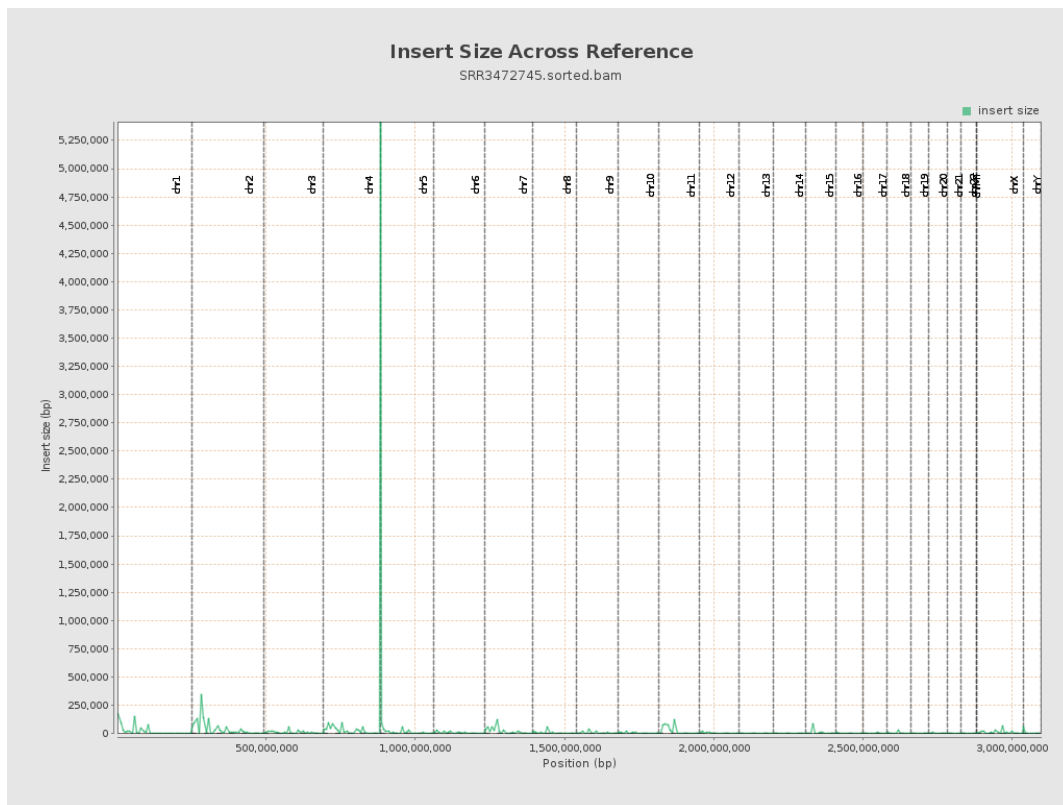
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

