

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 08:38:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124945.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_SRR3124945 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124945_1.fastq.gz SRR3124945_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 08:38:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124945.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,985,280
Mapped reads	4,900,413 / 98.3%
Unmapped reads	84,867 / 1.7%
Mapped paired reads	4,900,413 / 98.3%
Mapped reads, first in pair	2,451,661 / 49.18%
Mapped reads, second in pair	2,448,752 / 49.12%
Mapped reads, both in pair	4,883,842 / 97.97%
Mapped reads, singletons	16,571 / 0.33%
Secondary alignments	0
Supplementary alignments	21,508 / 0.43%
Read min/max/mean length	30 / 101 / 101.17
Duplicated reads (estimated)	231,531 / 4.64%
Duplication rate	2.61%
Clipped reads	2,915,706 / 58.49%

2.2. ACGT Content

Number/percentage of A's	130,568,297 / 28.94%
Number/percentage of C's	88,456,954 / 19.61%
Number/percentage of T's	135,951,752 / 30.13%
Number/percentage of G's	95,886,141 / 21.25%
Number/percentage of N's	293,679 / 0.07%

GC Percentage	40.86%
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2.3. Coverage

Mean	0.1458
Standard Deviation	1.417

2.4. Mapping Quality

Mean Mapping Quality	52.9
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2.5. Insert size

Mean	73,176.53
Standard Deviation	2,592,645.44
P25/Median/P75	137 / 169 / 214

2.6. Mismatches and indels

General error rate	0.88%
Mismatches	3,827,870
Insertions	67,800
Mapped reads with at least one insertion	1.35%
Deletions	149,278
Mapped reads with at least one deletion	2.99%
Homopolymer indels	47.23%

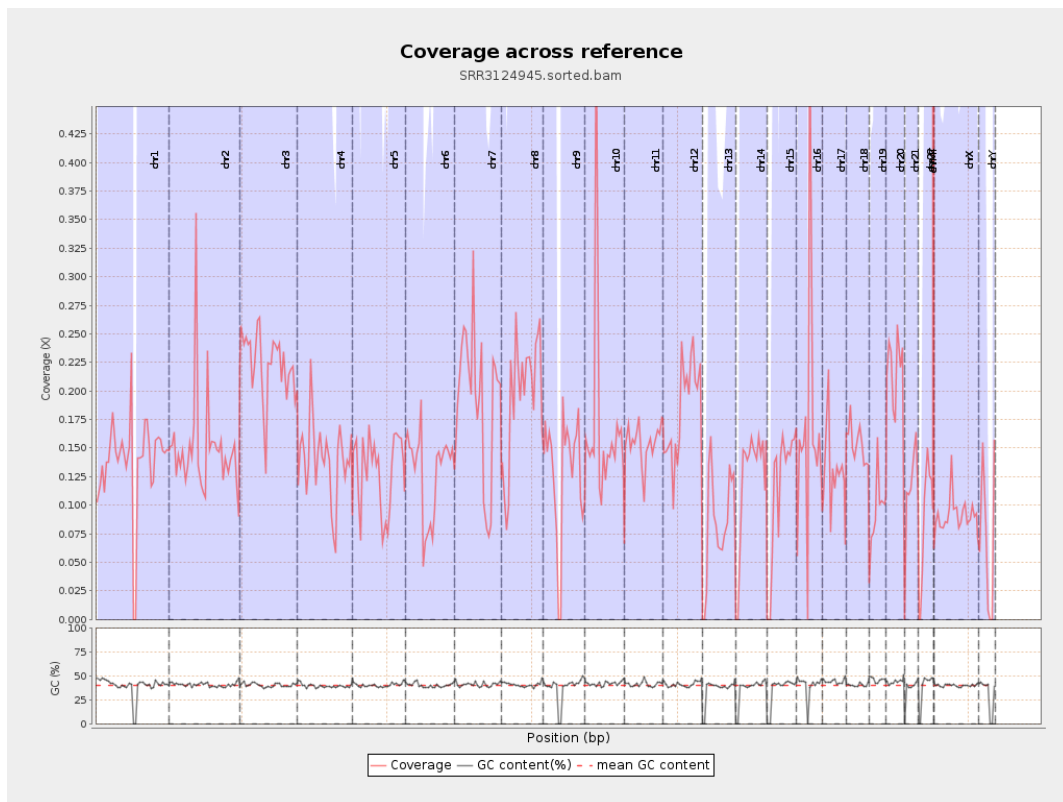
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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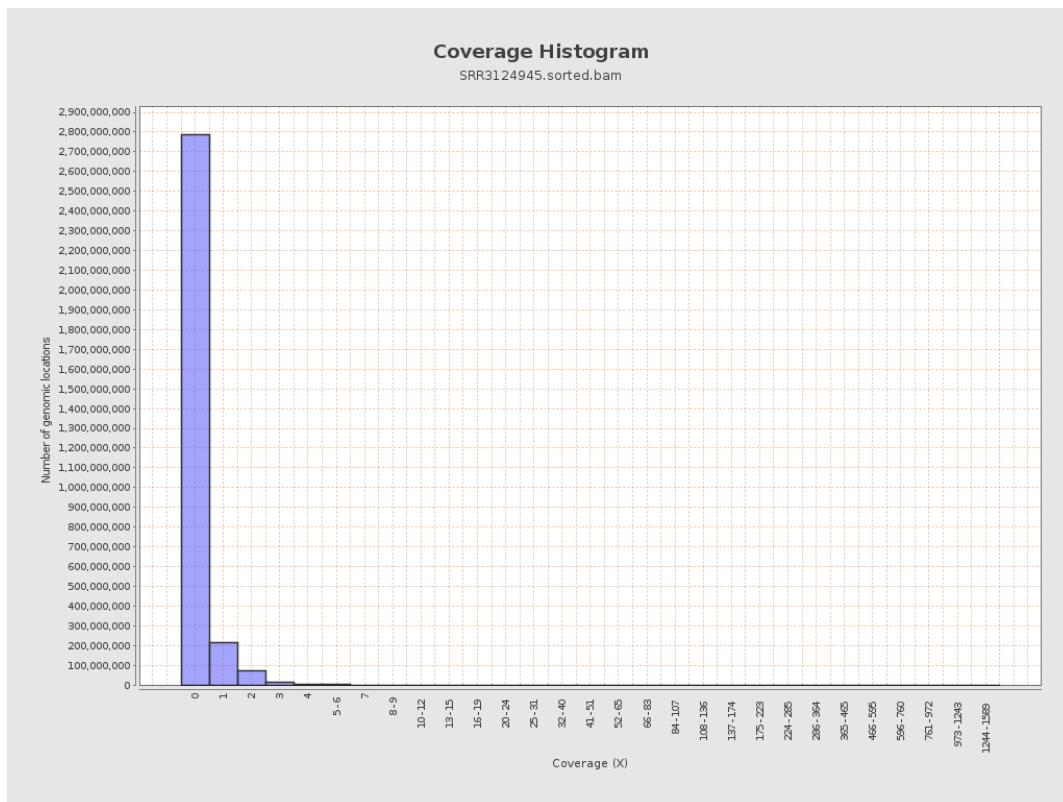
		bases	coverage	deviation
chr1	249250621	34414365	0.1381	1.446
chr2	243199373	36295860	0.1492	1.6117
chr3	198022430	44155020	0.223	0.6326
chr4	191154276	26445960	0.1383	0.7806
chr5	180915260	23411768	0.1294	0.4693
chr6	171115067	22119495	0.1293	0.9741
chr7	159138663	30918558	0.1943	2.7869
chr8	146364022	28554580	0.1951	0.7745
chr9	141213431	18261185	0.1293	1.7671
chr10	135534747	22500648	0.166	3.1942
chr11	135006516	20573413	0.1524	1.1424
chr12	133851895	24436405	0.1826	0.5564
chr13	115169878	9633319	0.0836	0.3646
chr14	107349540	13022297	0.1213	0.4882
chr15	102531392	11764514	0.1147	0.4365
chr16	90354753	14858038	0.1644	2.5519
chr17	81195210	10407575	0.1282	1.4089
chr18	78077248	12048527	0.1543	1.7961
chr19	59128983	5722991	0.0968	0.847
chr20	63025520	13568114	0.2153	0.6371
chr21	48129895	5492454	0.1141	0.562
chr22	51304566	4425694	0.0863	0.3923
chrMT	16571	86408	5.2144	3.6567
chrX	155270560	14190508	0.0914	0.6148

chrY	59373566	4095949	0.069	1.1823
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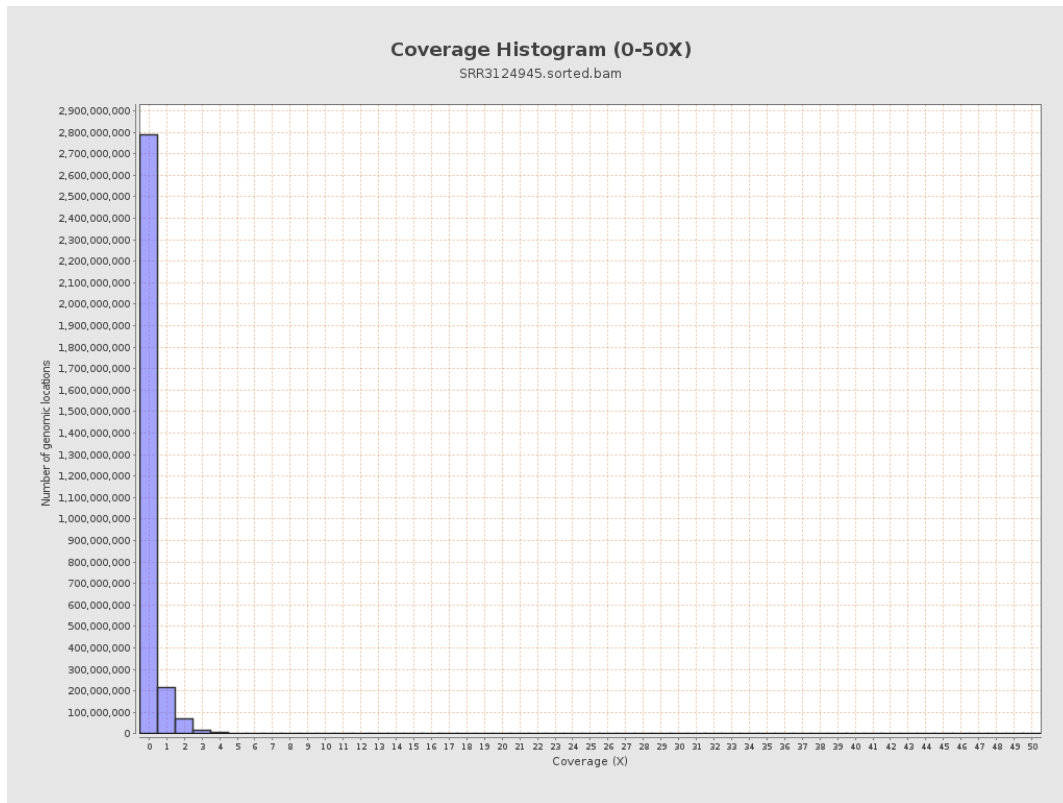
3. Results : Coverage across reference



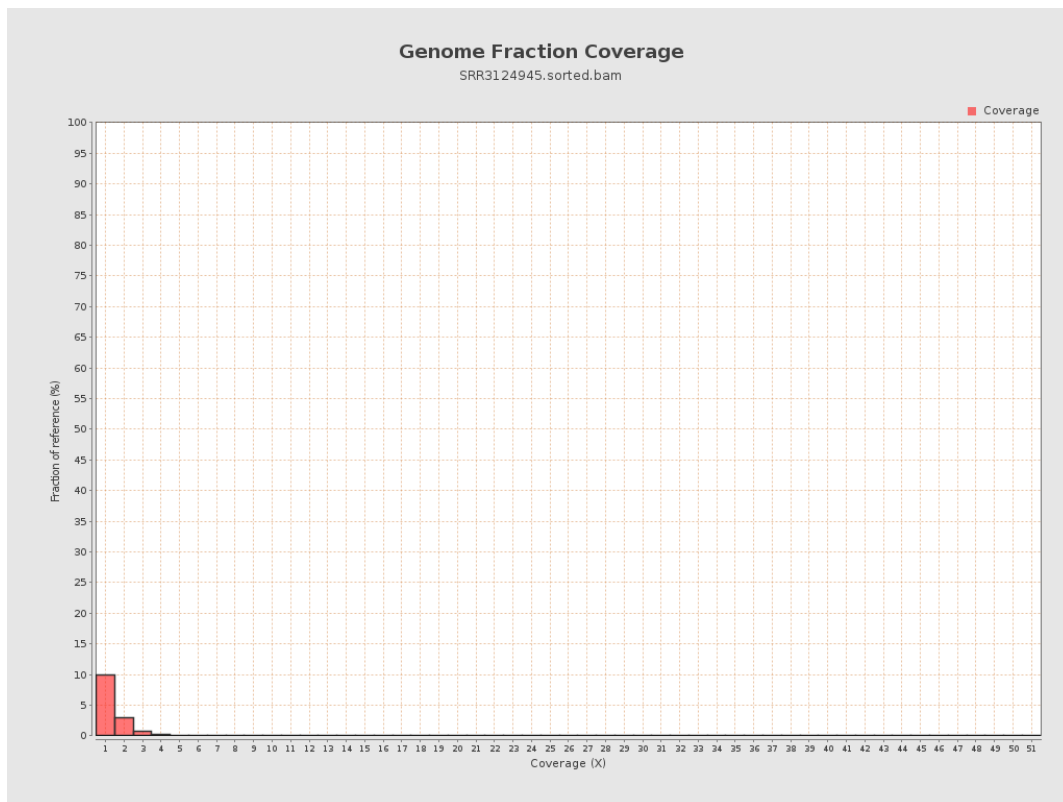
4. Results : Coverage Histogram



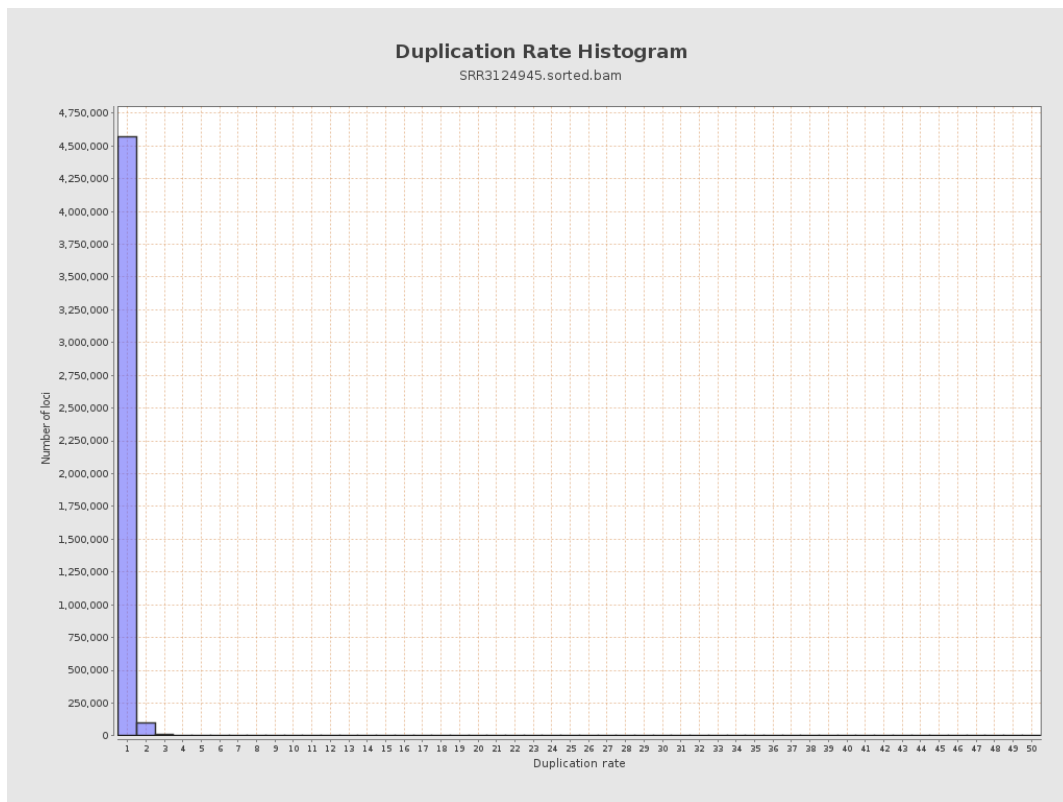
5. Results : Coverage Histogram (0-50X)



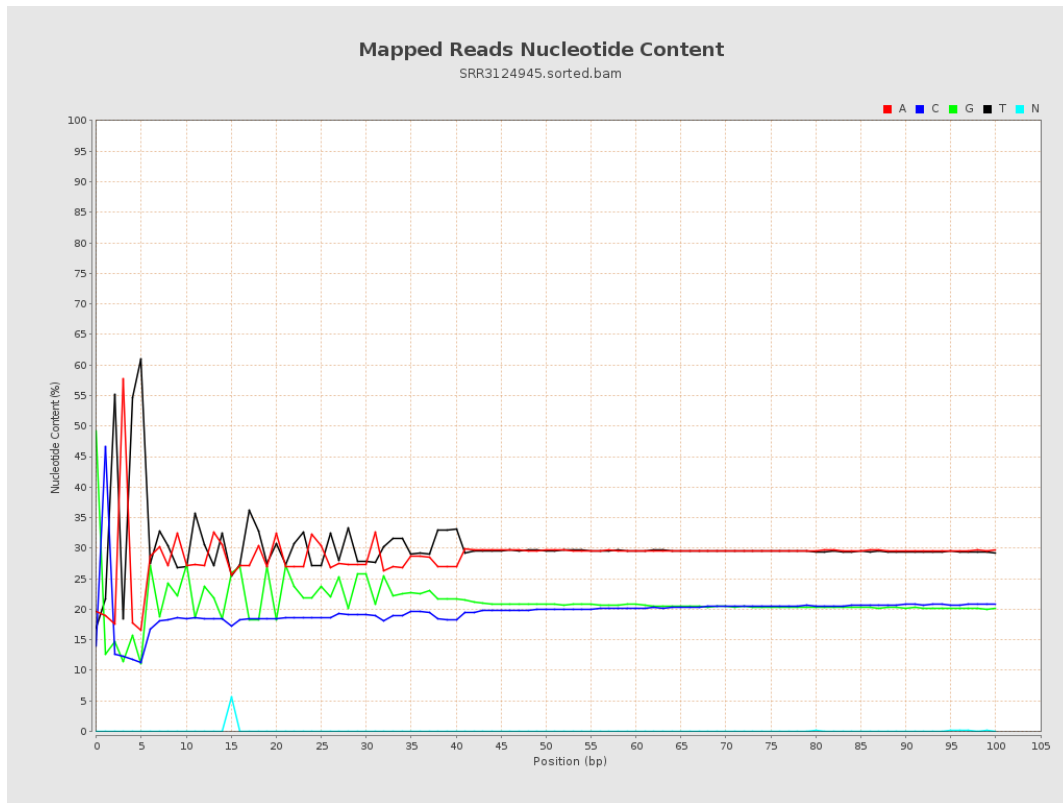
6. Results : Genome Fraction Coverage



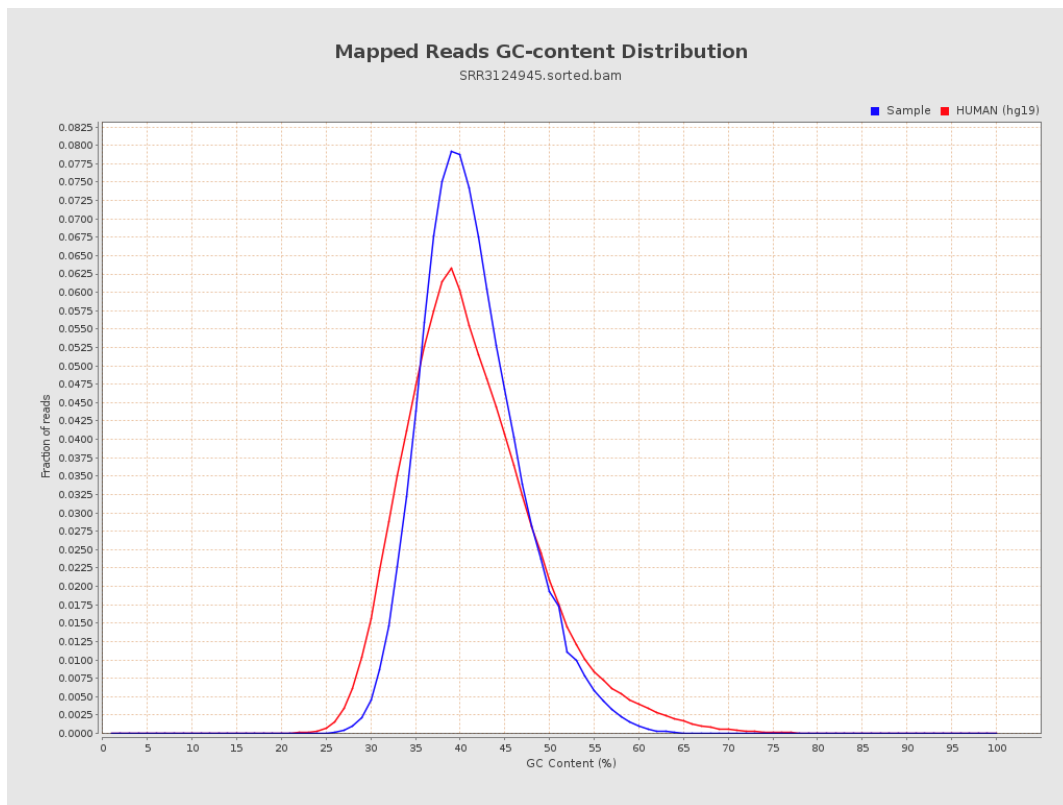
7. Results : Duplication Rate Histogram



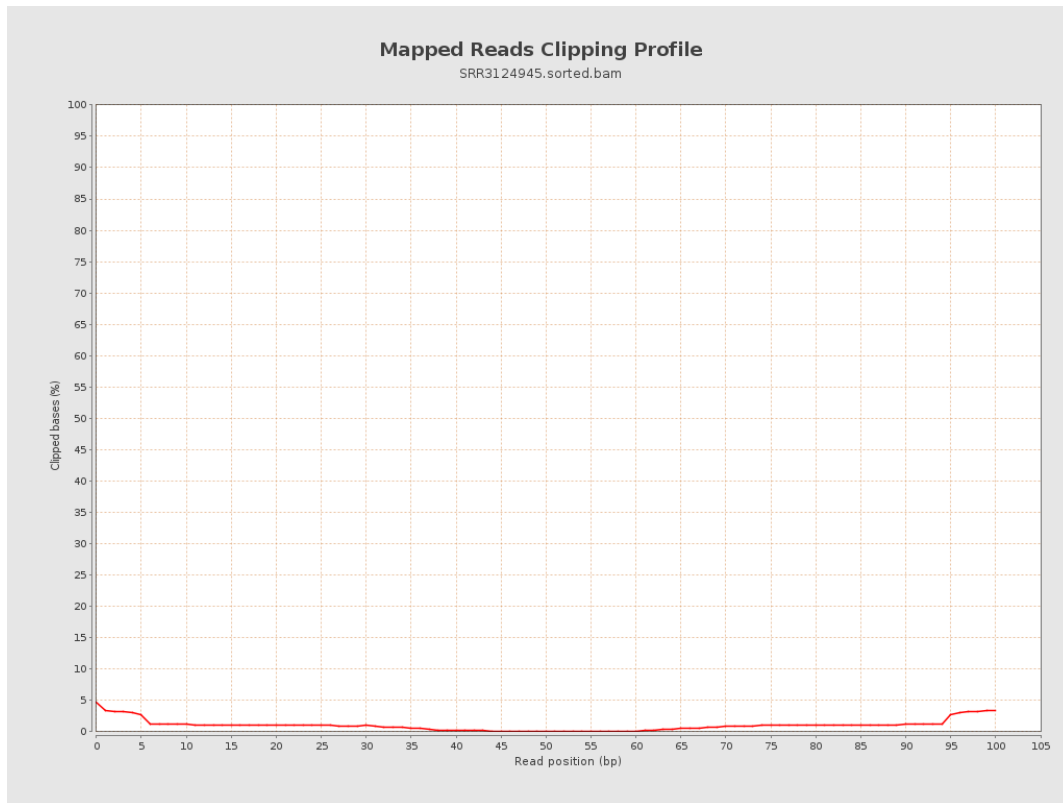
8. Results : Mapped Reads Nucleotide Content



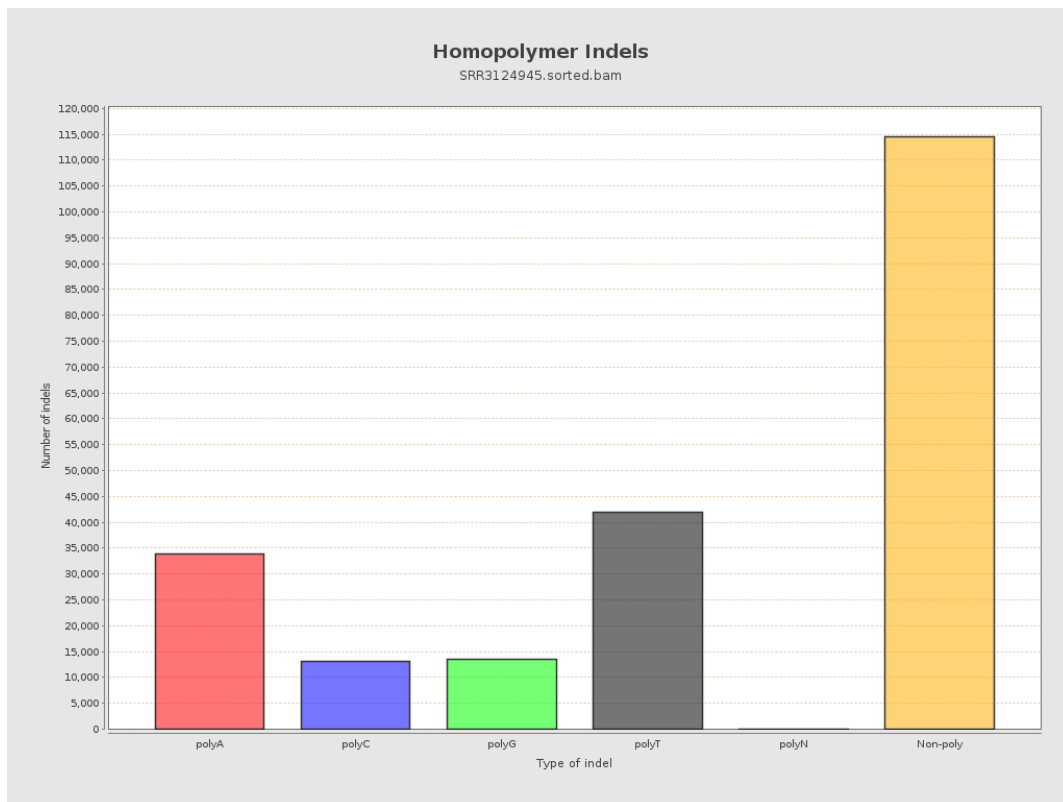
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



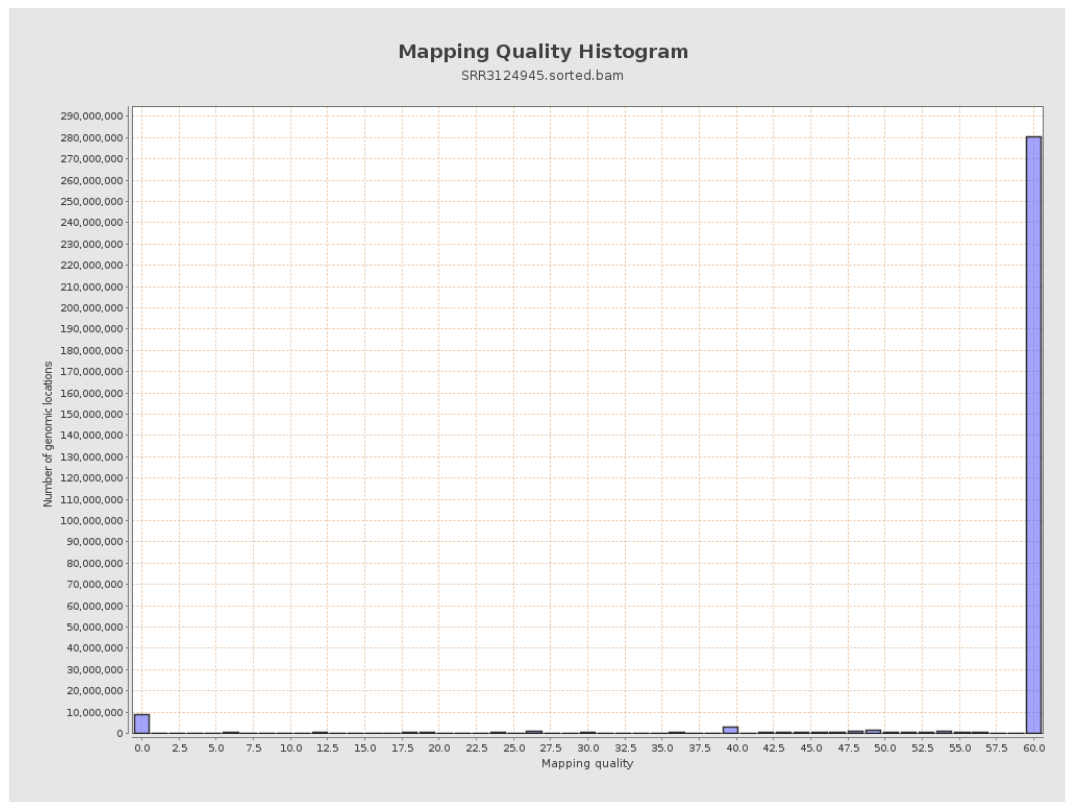
11. Results : Homopolymer Indels



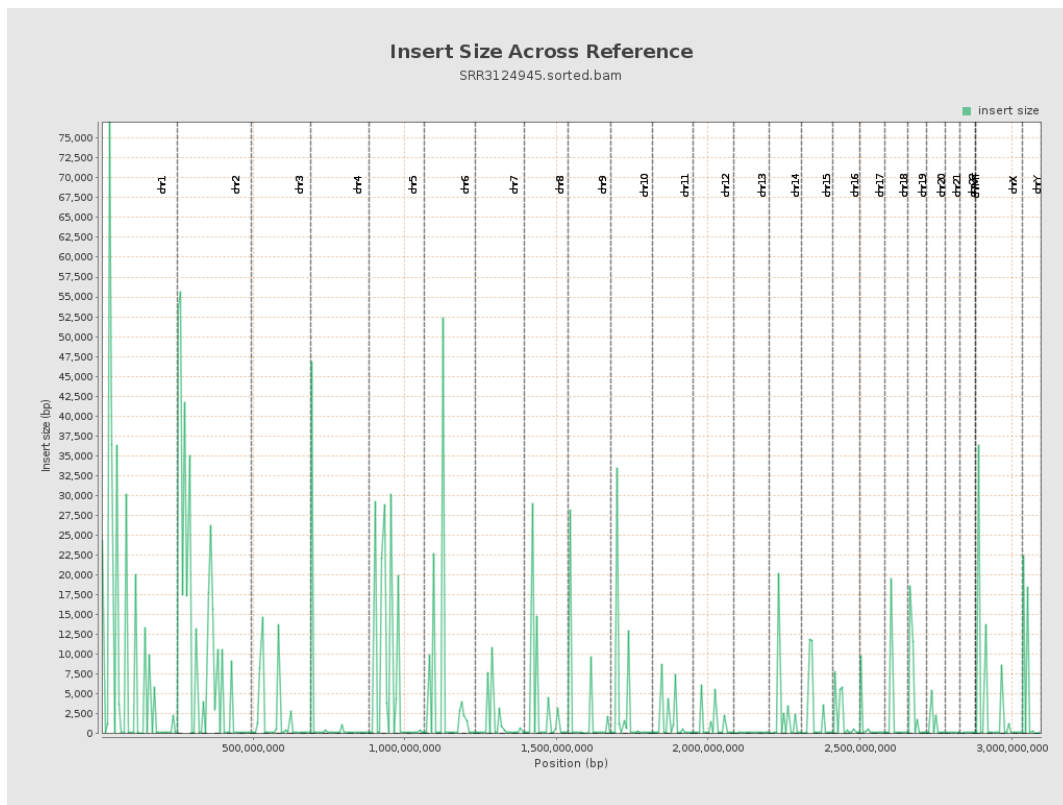
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

