

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 04:09:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472545.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_SRR3472545 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472545_1.fastq.gz SRR3472545_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 04:09:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472545.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,407,146
Mapped reads	18,183,899 / 98.79%
Unmapped reads	223,247 / 1.21%
Mapped paired reads	18,183,899 / 98.79%
Mapped reads, first in pair	9,133,411 / 49.62%
Mapped reads, second in pair	9,050,488 / 49.17%
Mapped reads, both in pair	18,055,052 / 98.09%
Mapped reads, singletons	128,847 / 0.7%
Secondary alignments	0
Supplementary alignments	63,200 / 0.34%
Read min/max/mean length	30 / 100 / 100.14
Duplicated reads (estimated)	11,185,509 / 60.77%
Duplication rate	47.26%
Clipped reads	1,392,529 / 7.57%

2.2. ACGT Content

Number/percentage of A's	494,731,685 / 27.61%
Number/percentage of C's	403,777,851 / 22.53%
Number/percentage of T's	492,228,339 / 27.47%
Number/percentage of G's	401,006,459 / 22.38%
Number/percentage of N's	277,030 / 0.02%

GC Percentage	44.91%
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2.3. Coverage

Mean	0.5789
Standard Deviation	16.7133

2.4. Mapping Quality

Mean Mapping Quality	55.01
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2.5. Insert size

Mean	28,865.2
Standard Deviation	1,687,170.3
P25/Median/P75	173 / 241 / 325

2.6. Mismatches and indels

General error rate	0.64%
Mismatches	11,184,554
Insertions	93,498
Mapped reads with at least one insertion	0.51%
Deletions	86,193
Mapped reads with at least one deletion	0.47%
Homopolymer indels	45.44%

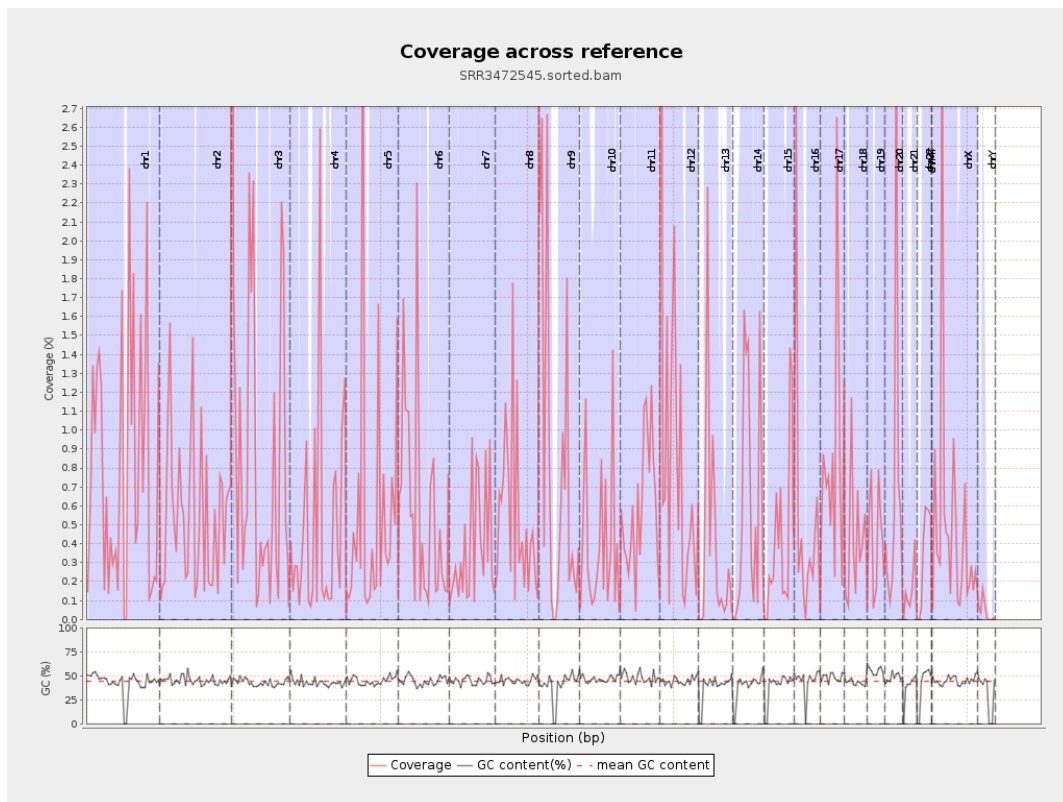
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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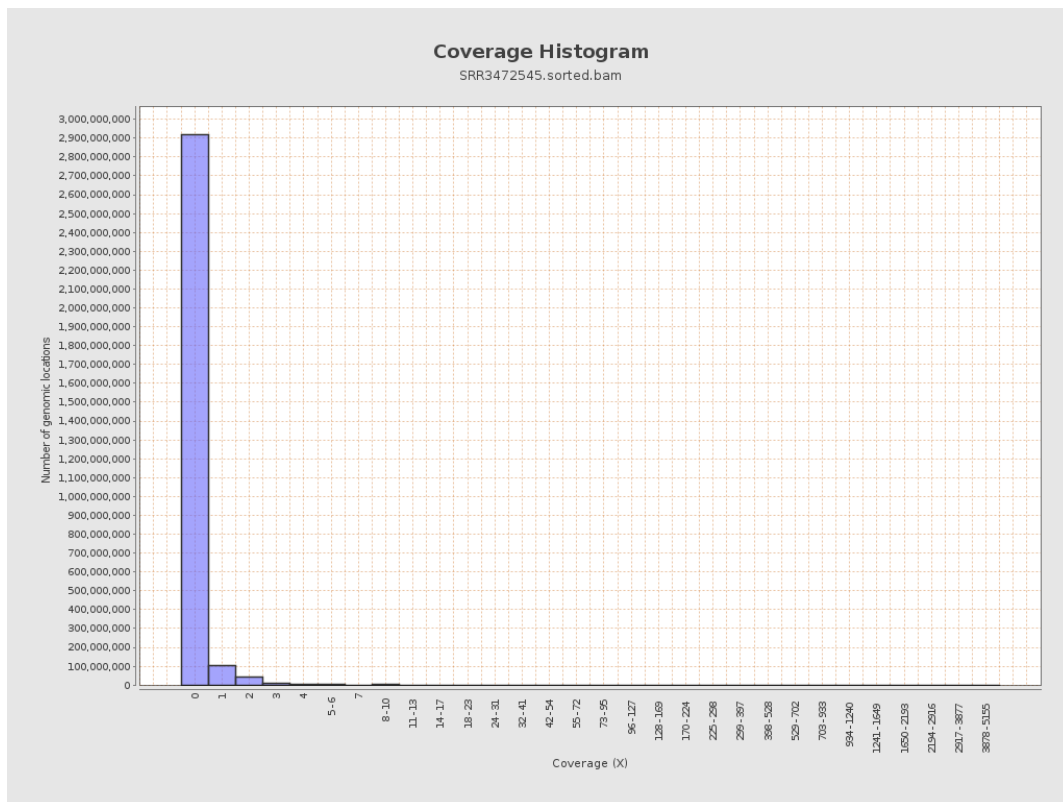
		bases	coverage	deviation
chr1	249250621	201778286	0.8095	21.1864
chr2	243199373	132714951	0.5457	16.2878
chr3	198022430	176936300	0.8935	20.4217
chr4	191154276	90146799	0.4716	17.7846
chr5	180915260	103668656	0.573	18.1261
chr6	171115067	98103788	0.5733	14.3791
chr7	159138663	60728478	0.3816	9.9719
chr8	146364022	79237970	0.5414	14.4967
chr9	141213431	112560474	0.7971	17.3193
chr10	135534747	53707098	0.3963	14.9634
chr11	135006516	80078173	0.5931	17.3532
chr12	133851895	128274890	0.9583	24.9884
chr13	115169878	45798712	0.3977	13.3464
chr14	107349540	62586392	0.583	16.9472
chr15	102531392	44068215	0.4298	12.2733
chr16	90354753	45412419	0.5026	12.4718
chr17	81195210	66482506	0.8188	17.3643
chr18	78077248	31739114	0.4065	16.2959
chr19	59128983	26527708	0.4486	12.0145
chr20	63025520	46010197	0.73	26.4176
chr21	48129895	7102563	0.1476	4.9653
chr22	51304566	17097253	0.3333	8.258
chrMT	16571	2065	0.1246	0.4897
chrX	155270560	78757149	0.5072	12.2937

chrY	59373566	2717666	0.0458	1.288
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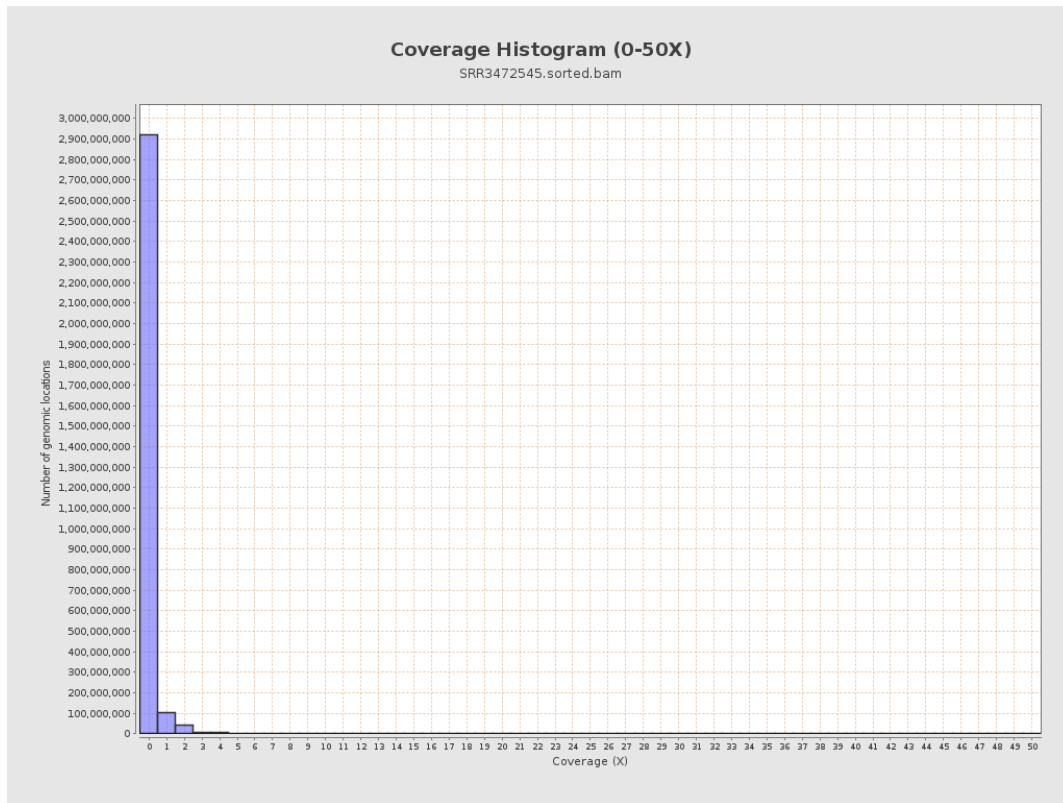
3. Results : Coverage across reference



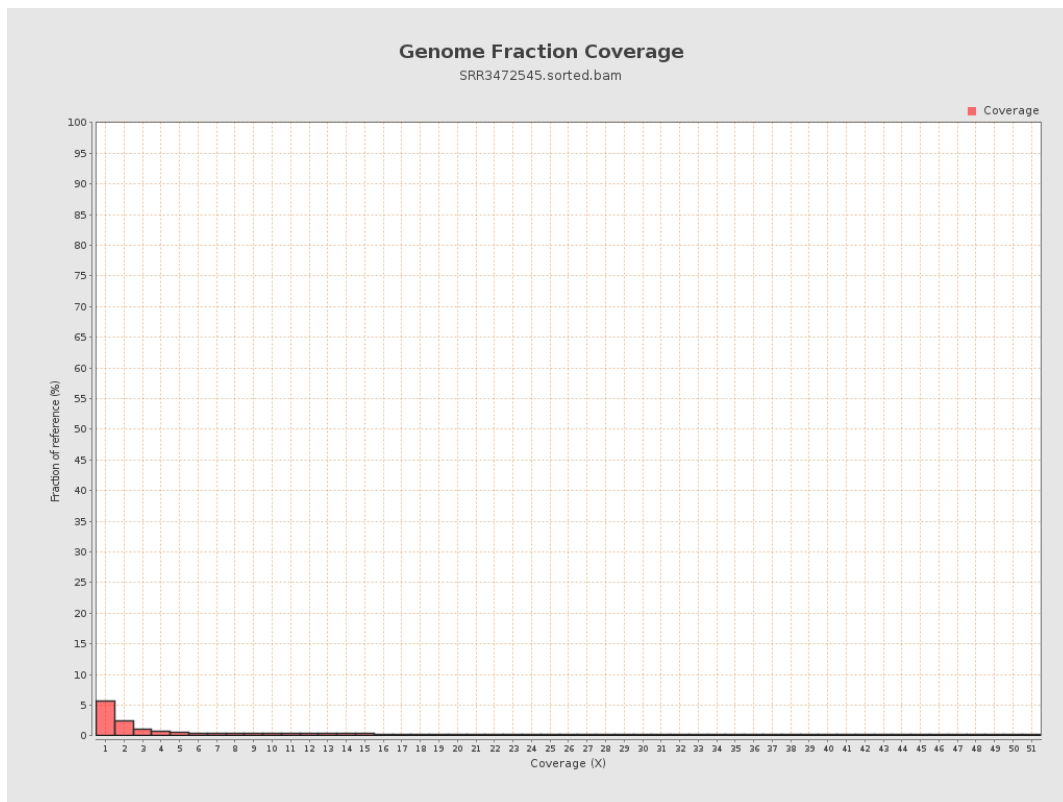
4. Results : Coverage Histogram



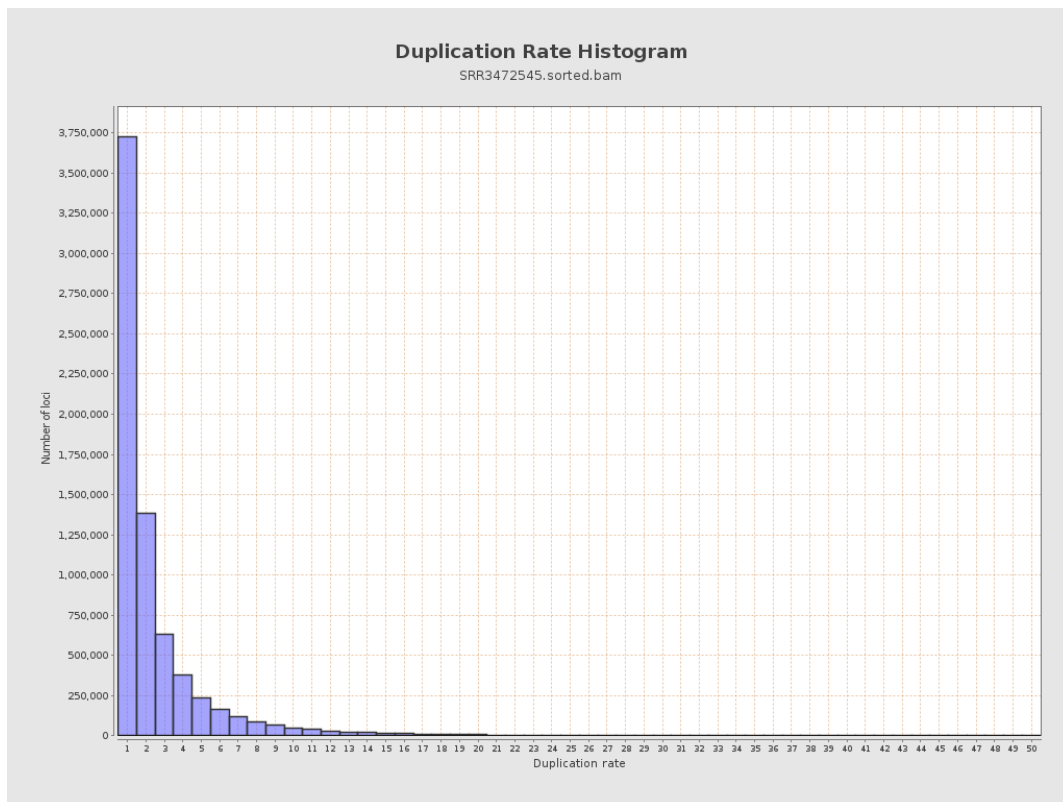
5. Results : Coverage Histogram (0-50X)



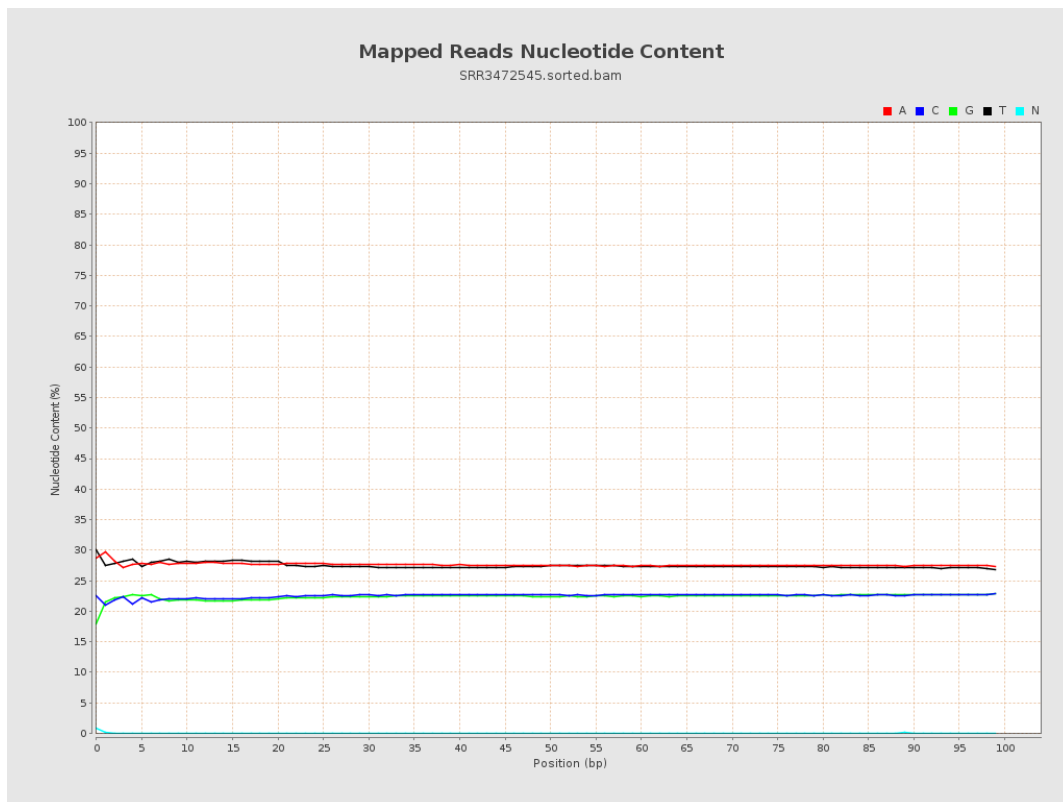
6. Results : Genome Fraction Coverage



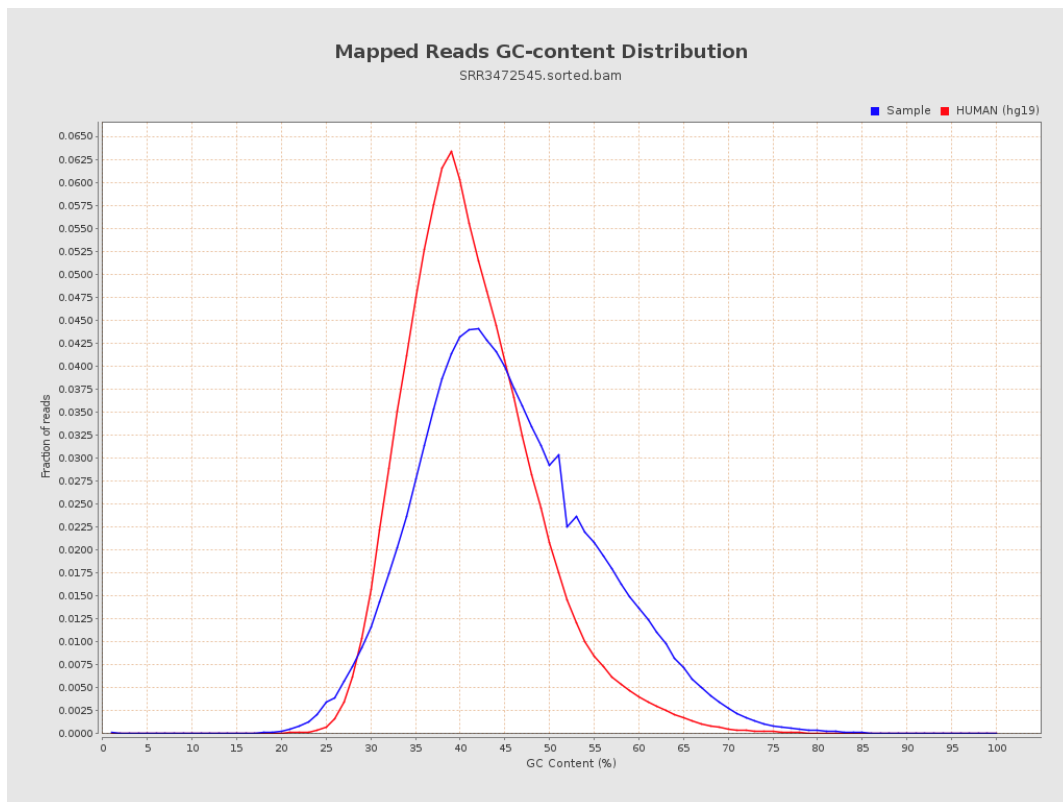
7. Results : Duplication Rate Histogram



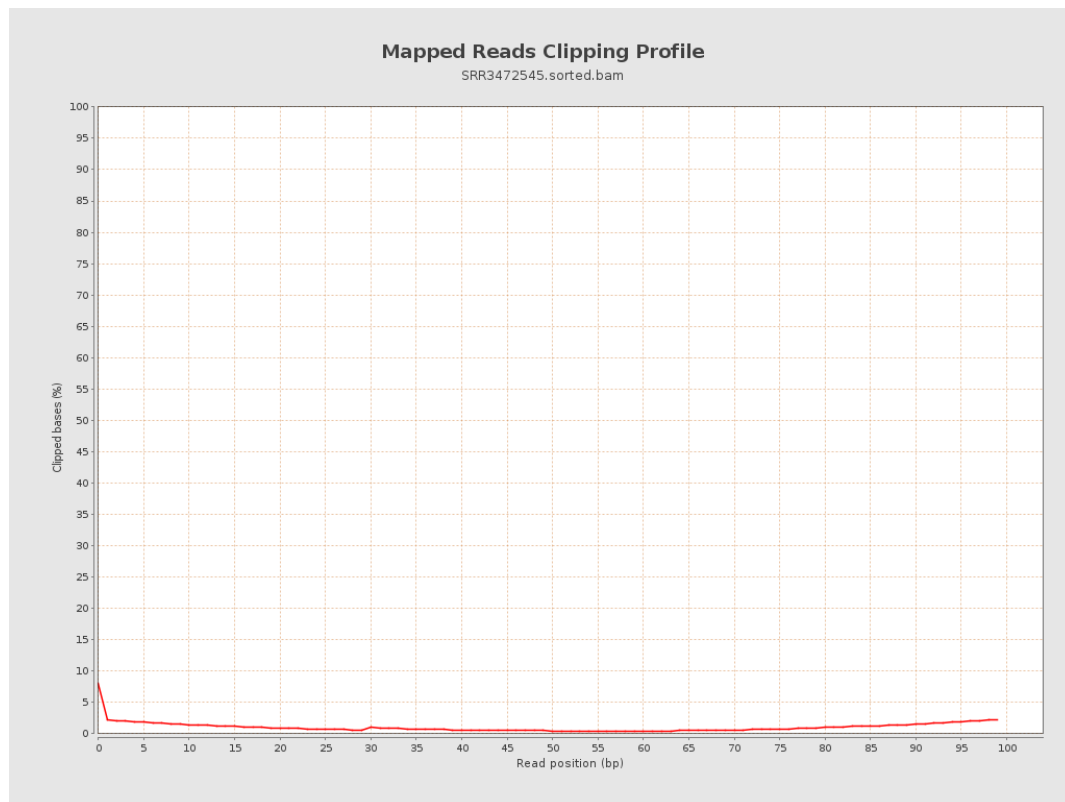
8. Results : Mapped Reads Nucleotide Content



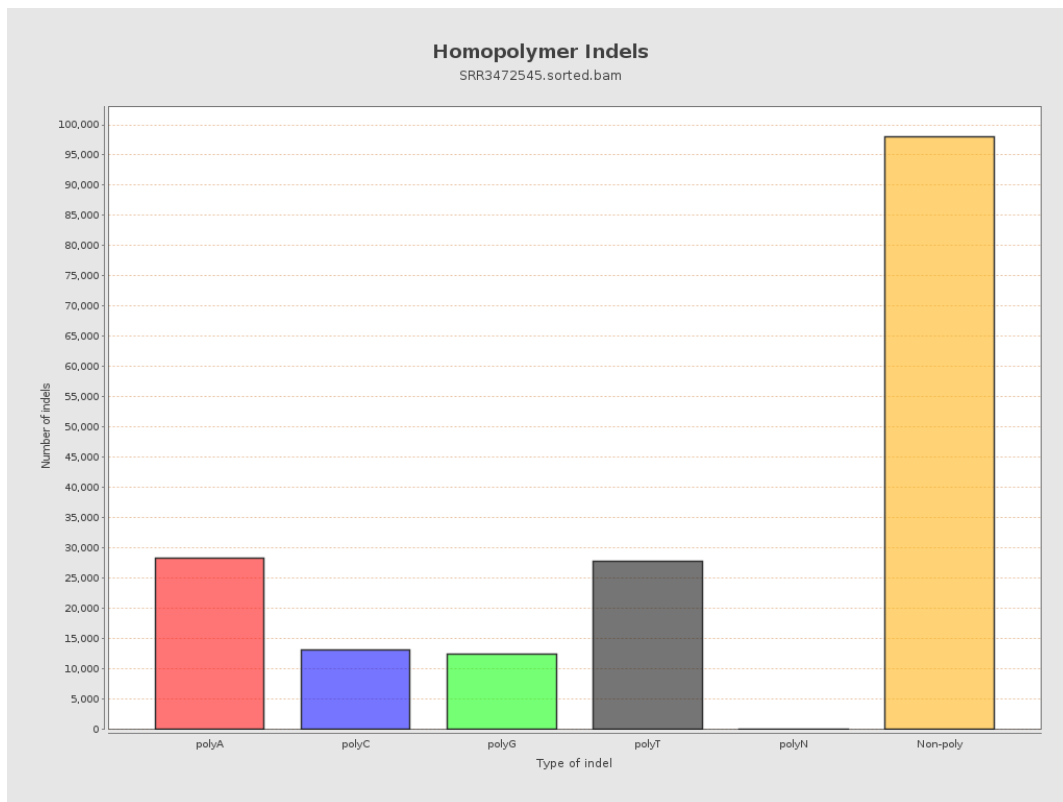
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



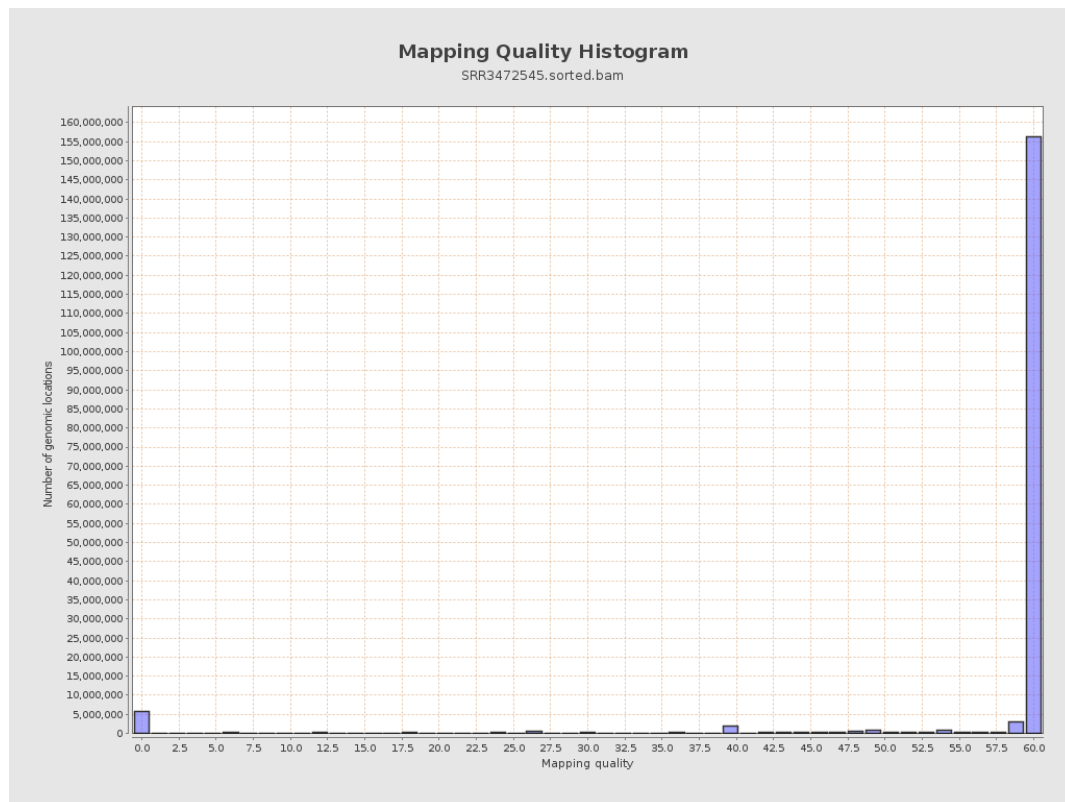
11. Results : Homopolymer Indels



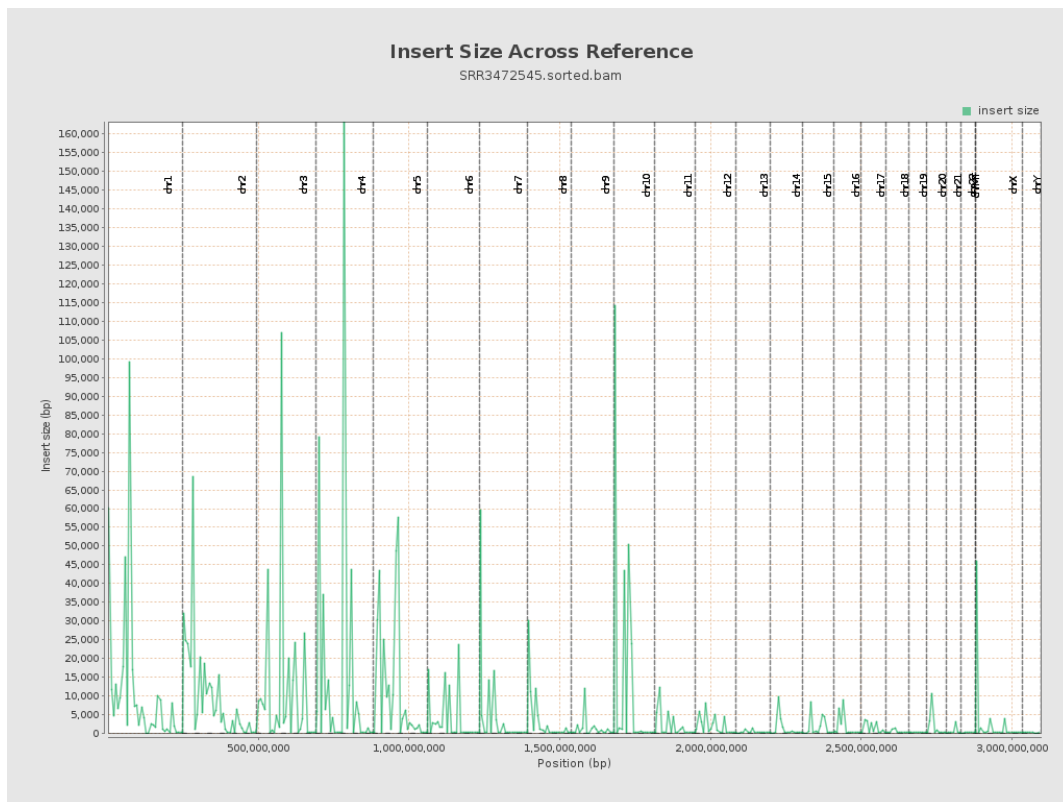
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

