

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 02:32:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472541.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_SRR3472541 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472541_1.fastq.gz SRR3472541_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 02:32:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472541.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,420,880
Mapped reads	8,304,399 / 98.62%
Unmapped reads	116,481 / 1.38%
Mapped paired reads	8,304,399 / 98.62%
Mapped reads, first in pair	4,162,049 / 49.43%
Mapped reads, second in pair	4,142,350 / 49.19%
Mapped reads, both in pair	8,250,178 / 97.97%
Mapped reads, singletons	54,221 / 0.64%
Secondary alignments	0
Supplementary alignments	33,390 / 0.4%
Read min/max/mean length	30 / 100 / 100.16
Duplicated reads (estimated)	4,639,109 / 55.09%
Duplication rate	43.52%
Clipped reads	708,435 / 8.41%

2.2. ACGT Content

Number/percentage of A's	222,934,995 / 27.31%
Number/percentage of C's	186,605,577 / 22.86%
Number/percentage of T's	221,533,463 / 27.14%
Number/percentage of G's	185,092,507 / 22.67%
Number/percentage of N's	127,188 / 0.02%

GC Percentage	45.53%
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2.3. Coverage

Mean	0.2637
Standard Deviation	9.8464

2.4. Mapping Quality

Mean Mapping Quality	55.12
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2.5. Insert size

Mean	29,031.7
Standard Deviation	1,660,761.35
P25/Median/P75	161 / 222 / 300

2.6. Mismatches and indels

General error rate	0.57%
Mismatches	4,539,791
Insertions	43,252
Mapped reads with at least one insertion	0.52%
Deletions	42,200
Mapped reads with at least one deletion	0.5%
Homopolymer indels	42.52%

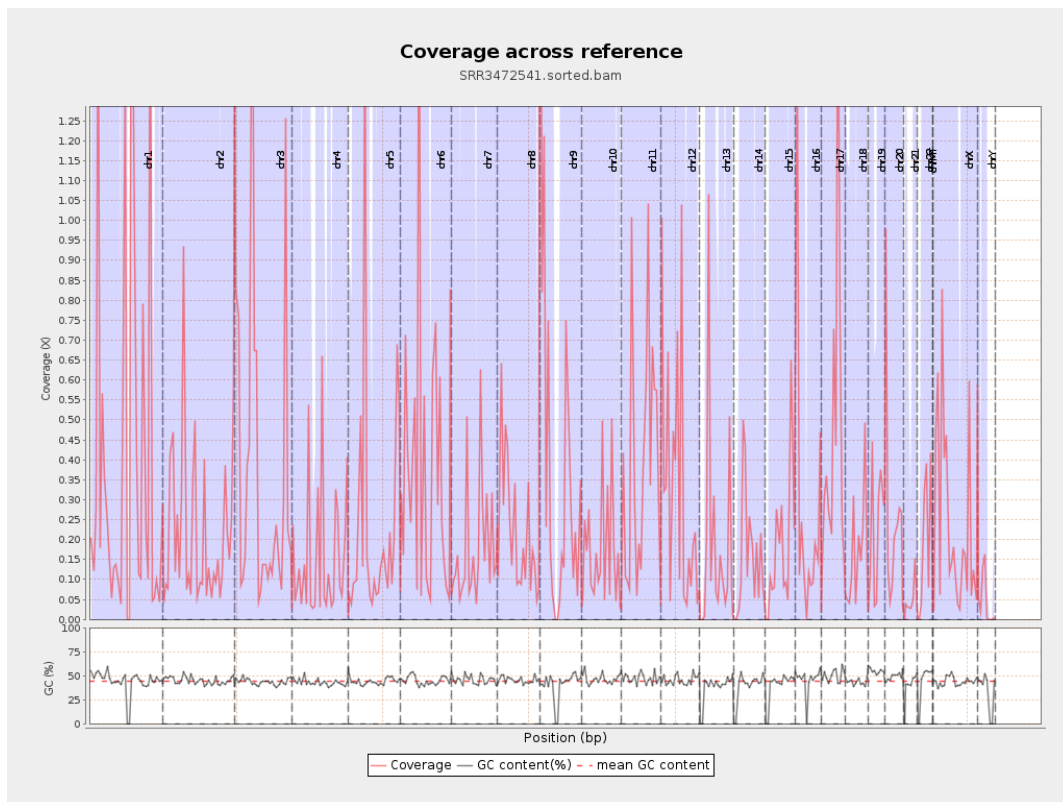
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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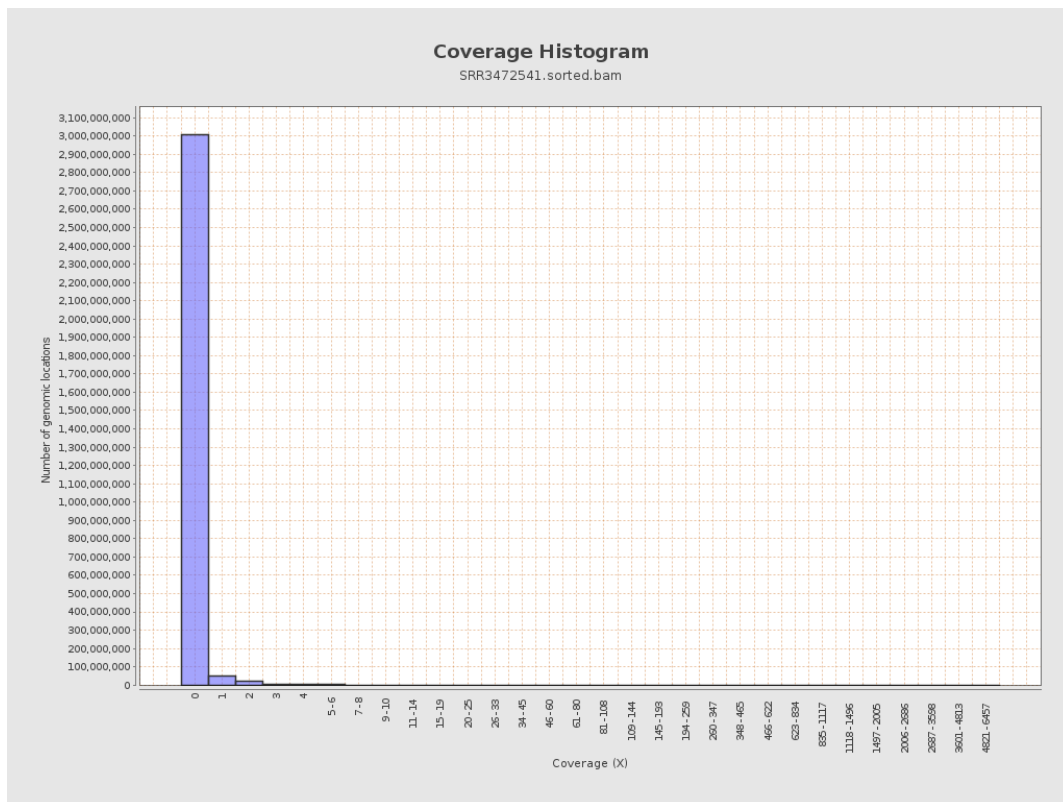
		bases	coverage	deviation
chr1	249250621	101735844	0.4082	15.7355
chr2	243199373	51797505	0.213	7.748
chr3	198022430	75682702	0.3822	10.4561
chr4	191154276	30303782	0.1585	6.5327
chr5	180915260	42846299	0.2368	7.8504
chr6	171115067	66704355	0.3898	13.2875
chr7	159138663	28426748	0.1786	5.3785
chr8	146364022	31666109	0.2164	7.1894
chr9	141213431	47824802	0.3387	9.7424
chr10	135534747	24195455	0.1785	7.4906
chr11	135006516	51921391	0.3846	14.8317
chr12	133851895	45149800	0.3373	10.6825
chr13	115169878	21600410	0.1876	9.5118
chr14	107349540	17014393	0.1585	7.0227
chr15	102531392	18332651	0.1788	5.542
chr16	90354753	26025377	0.288	10.8313
chr17	81195210	40539033	0.4993	14.0843
chr18	78077248	13446275	0.1722	6.6619
chr19	59128983	13070454	0.221	5.7696
chr20	63025520	15267517	0.2422	11.5572
chr21	48129895	2404465	0.05	1.5145
chr22	51304566	9733418	0.1897	7.0711
chrMT	16571	1175	0.0709	0.3134
chrX	155270560	37960523	0.2445	8.7557

chrY	59373566	2743159	0.0462	2.7989
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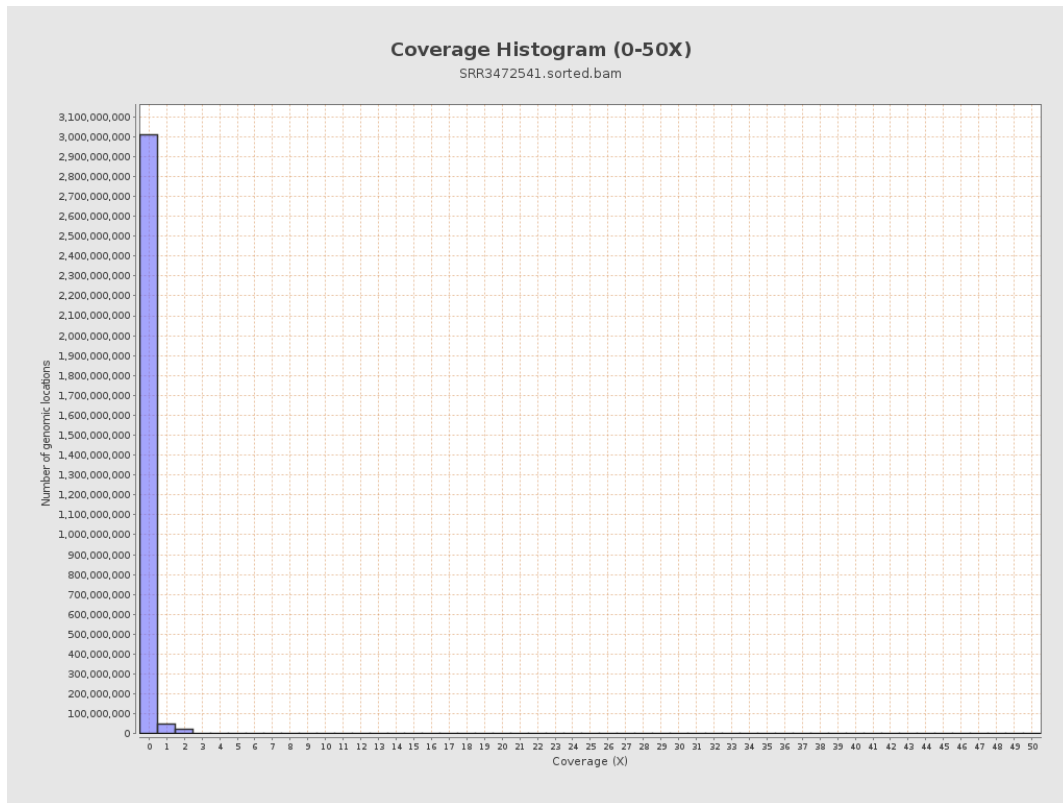
3. Results : Coverage across reference



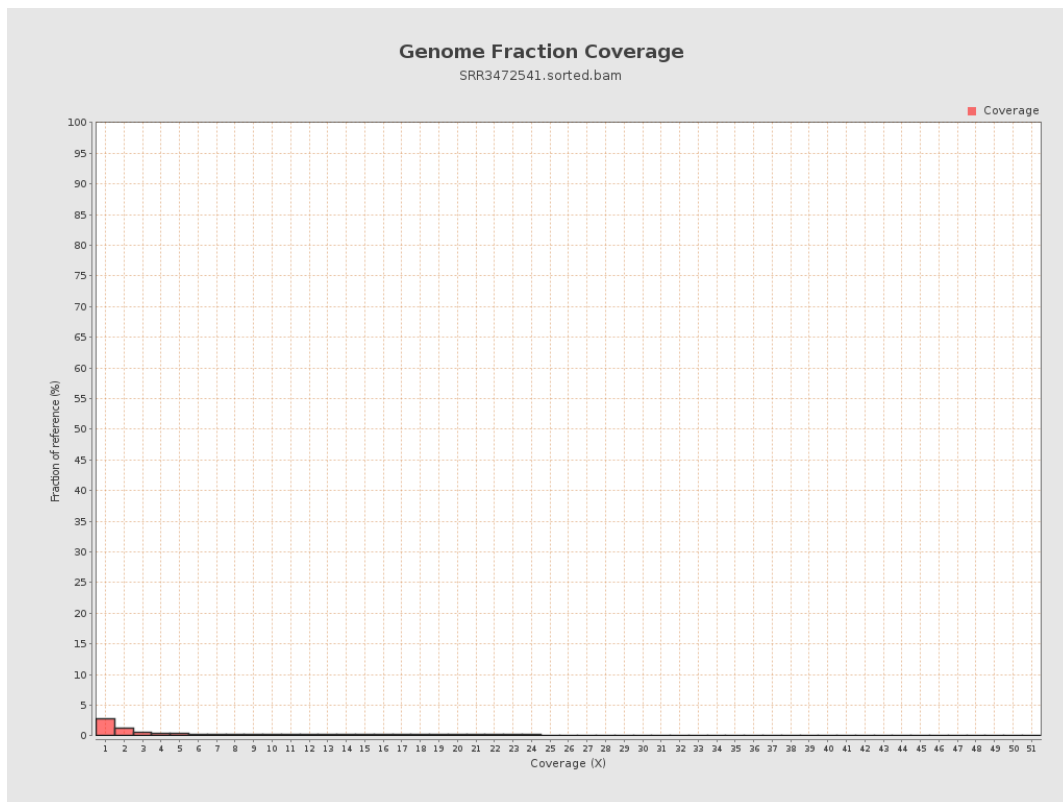
4. Results : Coverage Histogram



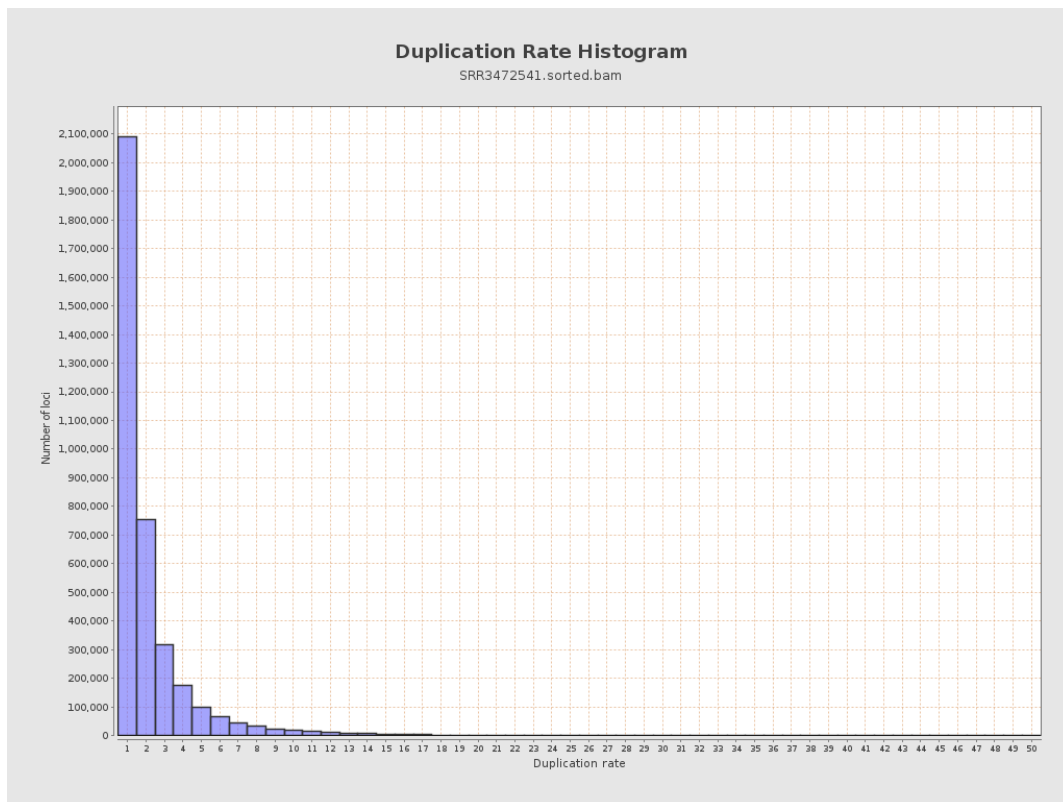
5. Results : Coverage Histogram (0-50X)



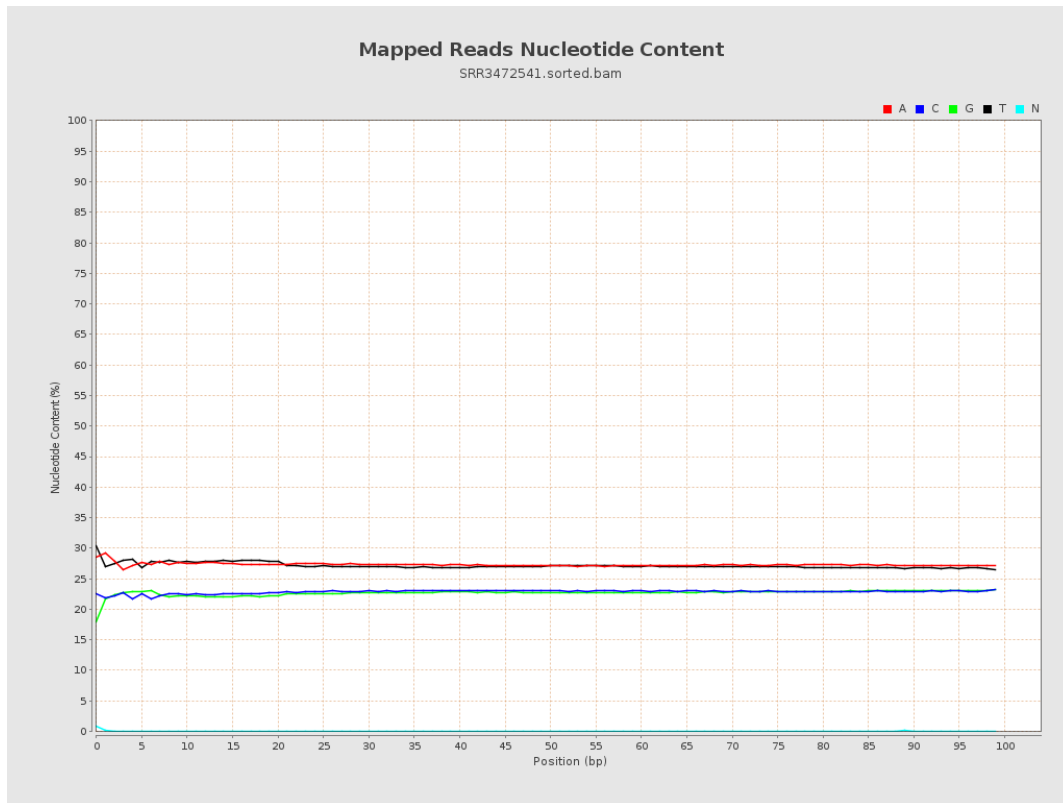
6. Results : Genome Fraction Coverage



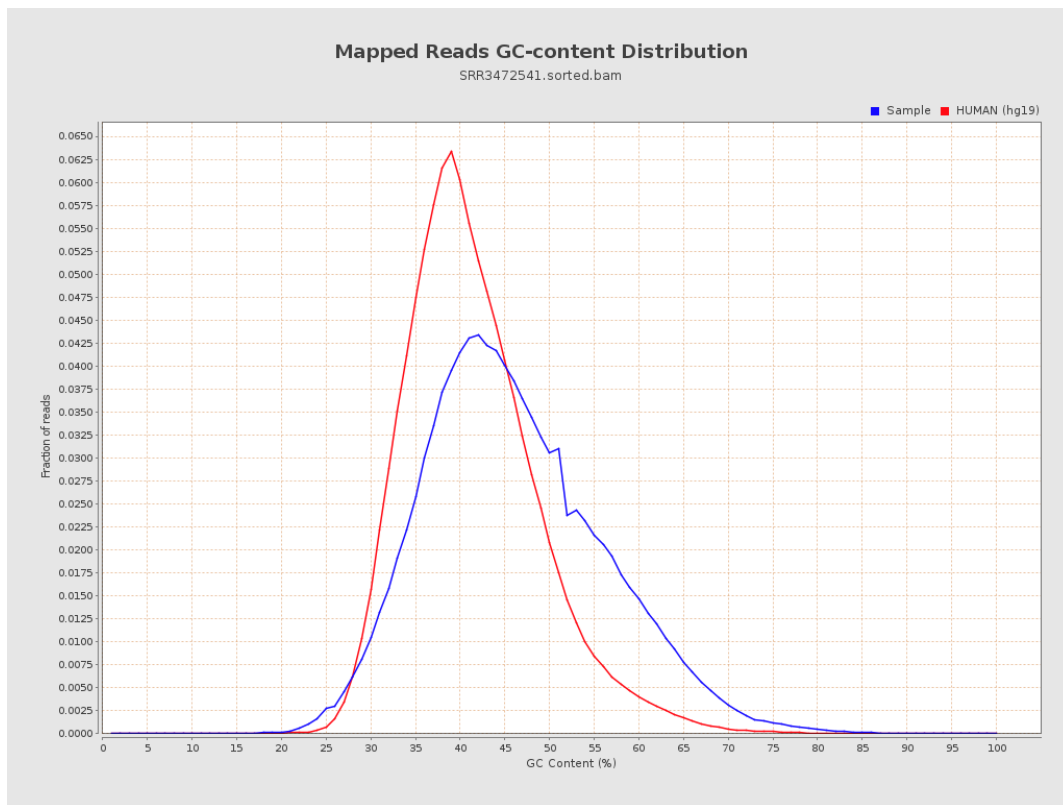
7. Results : Duplication Rate Histogram



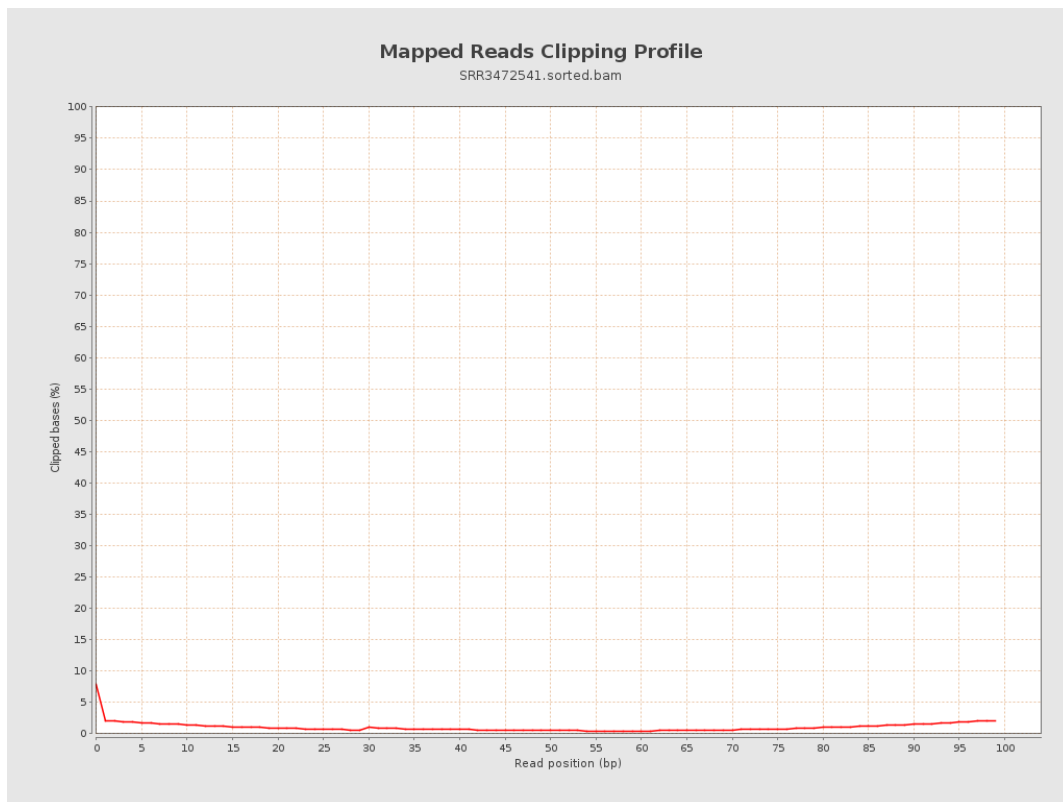
8. Results : Mapped Reads Nucleotide Content



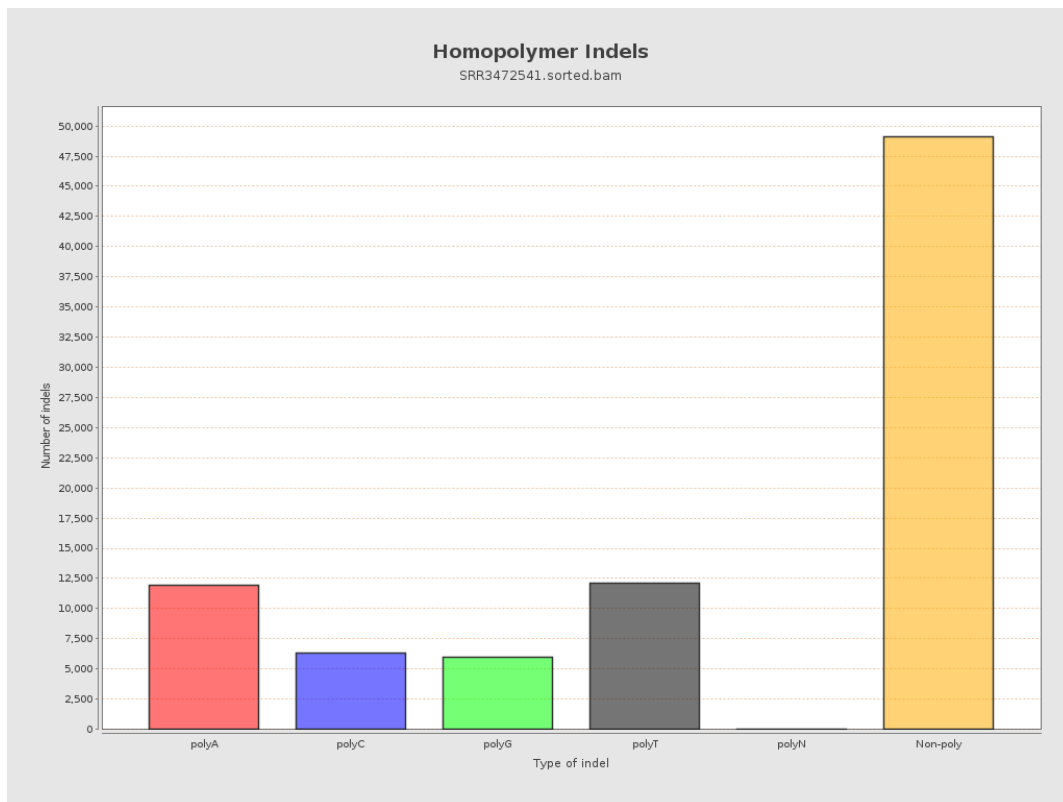
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



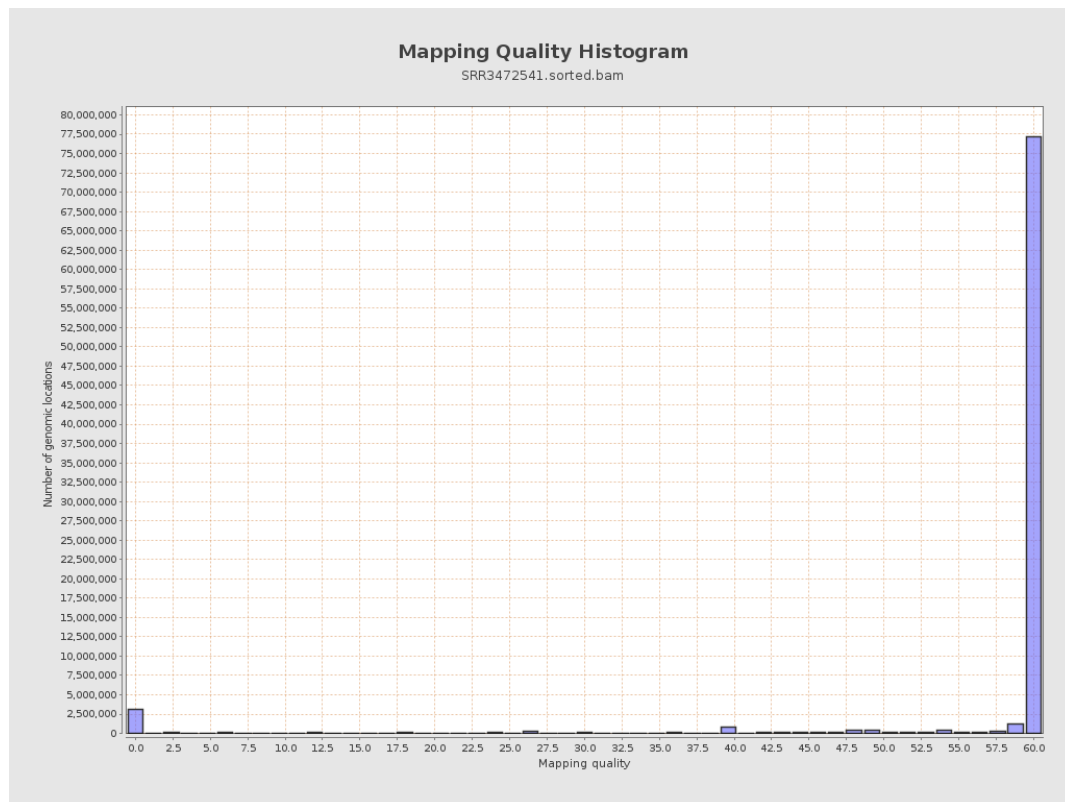
11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



15. Results : Insert Size Histogram

