

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 07:09:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472379.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_SRR3472379 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472379_1.fastq.gz SRR3472379_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 07:09:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472379.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,931,070
Mapped reads	19,780,116 / 99.24%
Unmapped reads	150,954 / 0.76%
Mapped paired reads	19,780,116 / 99.24%
Mapped reads, first in pair	9,915,468 / 49.75%
Mapped reads, second in pair	9,864,648 / 49.49%
Mapped reads, both in pair	19,694,640 / 98.81%
Mapped reads, singletons	85,476 / 0.43%
Secondary alignments	0
Supplementary alignments	73,272 / 0.37%
Read min/max/mean length	30 / 100 / 99.46
Duplicated reads (estimated)	12,598,597 / 63.21%
Duplication rate	48.11%
Clipped reads	1,292,897 / 6.49%

2.2. ACGT Content

Number/percentage of A's	515,652,370 / 26.53%
Number/percentage of C's	457,739,527 / 23.55%
Number/percentage of T's	516,099,550 / 26.55%
Number/percentage of G's	453,808,301 / 23.35%
Number/percentage of N's	242,272 / 0.01%

GC Percentage	46.9%
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2.3. Coverage

Mean	0.6279
Standard Deviation	19.4074

2.4. Mapping Quality

Mean Mapping Quality	54.93
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2.5. Insert size

Mean	18,375.87
Standard Deviation	1,333,264.06
P25/Median/P75	156 / 214 / 287

2.6. Mismatches and indels

General error rate	0.54%
Mismatches	10,247,288
Insertions	113,998
Mapped reads with at least one insertion	0.57%
Deletions	95,799
Mapped reads with at least one deletion	0.47%
Homopolymer indels	44.83%

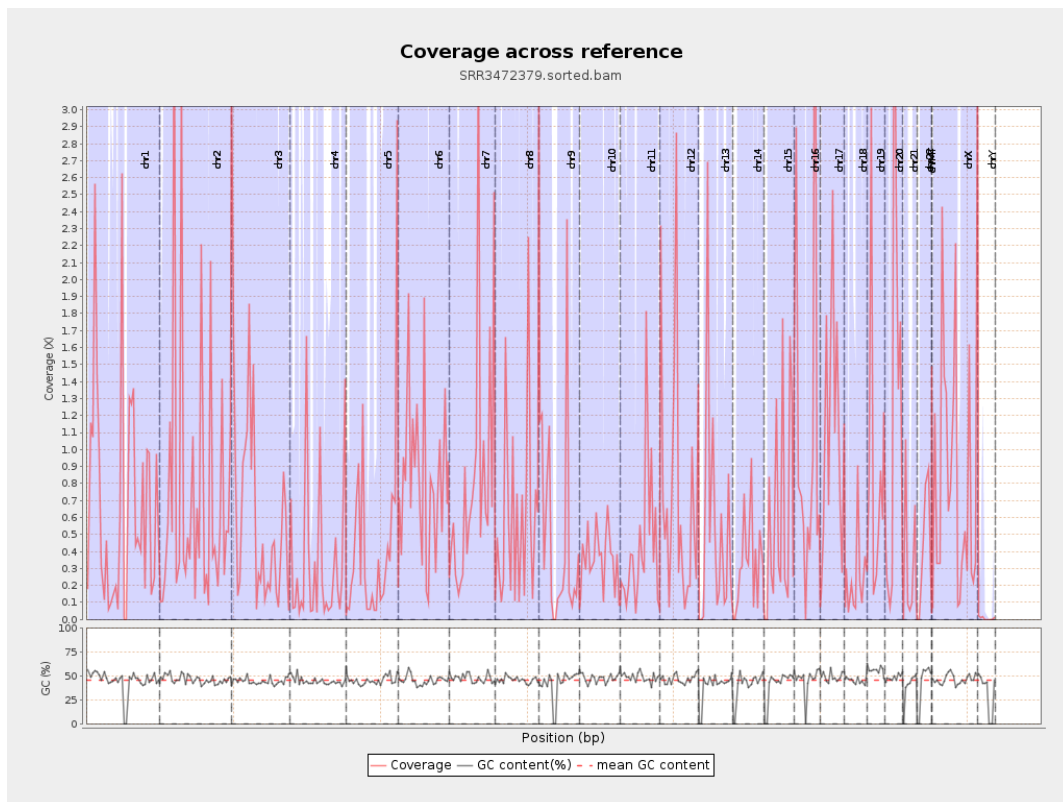
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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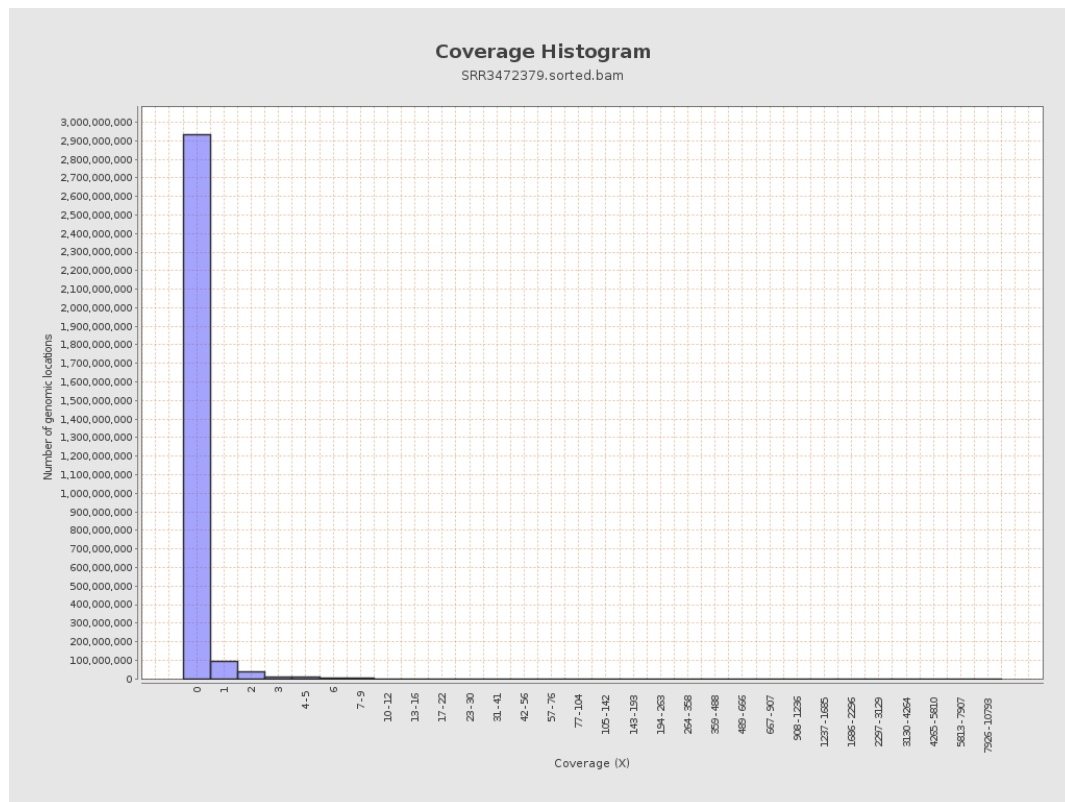
		bases	coverage	deviation
chr1	249250621	172629737	0.6926	21.1851
chr2	243199373	183866148	0.756	28.7464
chr3	198022430	125474316	0.6336	14.4238
chr4	191154276	60903467	0.3186	11.9907
chr5	180915260	80778806	0.4465	18.7084
chr6	171115067	141362347	0.8261	17.1189
chr7	159138663	134755657	0.8468	20.9409
chr8	146364022	89166044	0.6092	17.3669
chr9	141213431	71531911	0.5066	15.7112
chr10	135534747	48886258	0.3607	10.3868
chr11	135006516	56714389	0.4201	14.1964
chr12	133851895	99309770	0.7419	20.2014
chr13	115169878	61865141	0.5372	15.8937
chr14	107349540	34847870	0.3246	9.3673
chr15	102531392	64135436	0.6255	27.1526
chr16	90354753	105265281	1.165	29.0751
chr17	81195210	90436669	1.1138	25.4916
chr18	78077248	19711742	0.2525	9.6766
chr19	59128983	51668741	0.8738	18.1373
chr20	63025520	82534112	1.3095	31.4249
chr21	48129895	15786332	0.328	17.4558
chr22	51304566	20653270	0.4026	9.6742
chrMT	16571	24707	1.491	1.5116
chrX	155270560	131028746	0.8439	21.8046

chrY	59373566	433061	0.0073	0.5135
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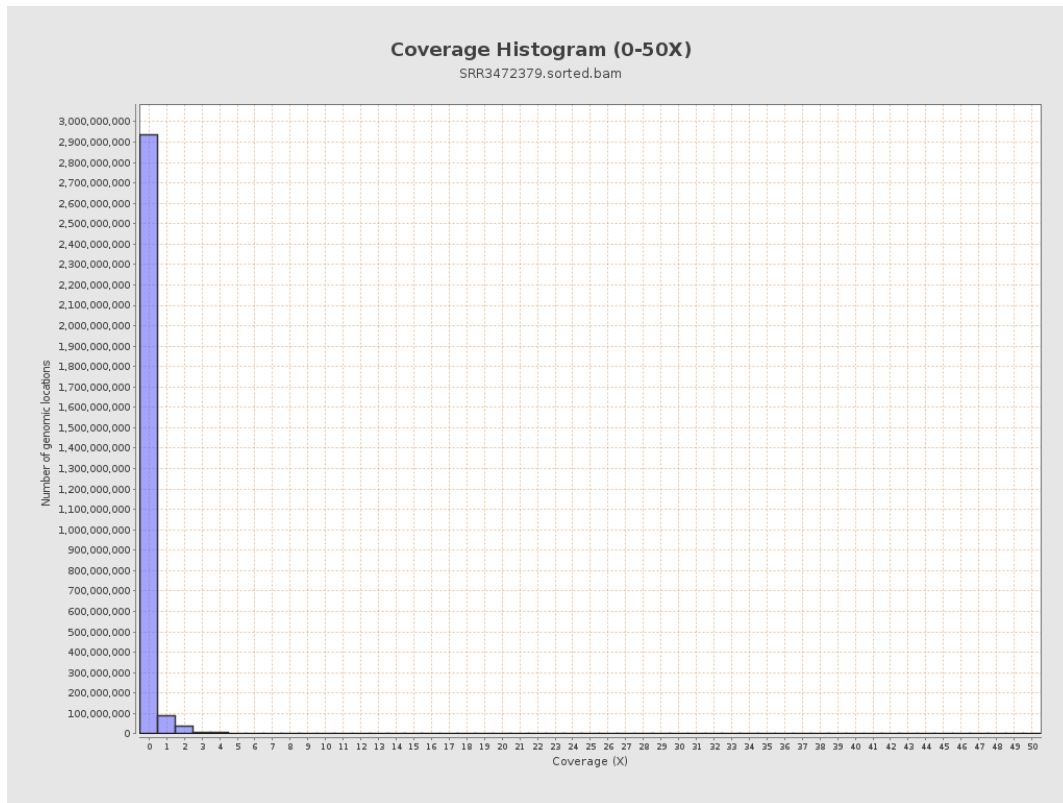
3. Results : Coverage across reference



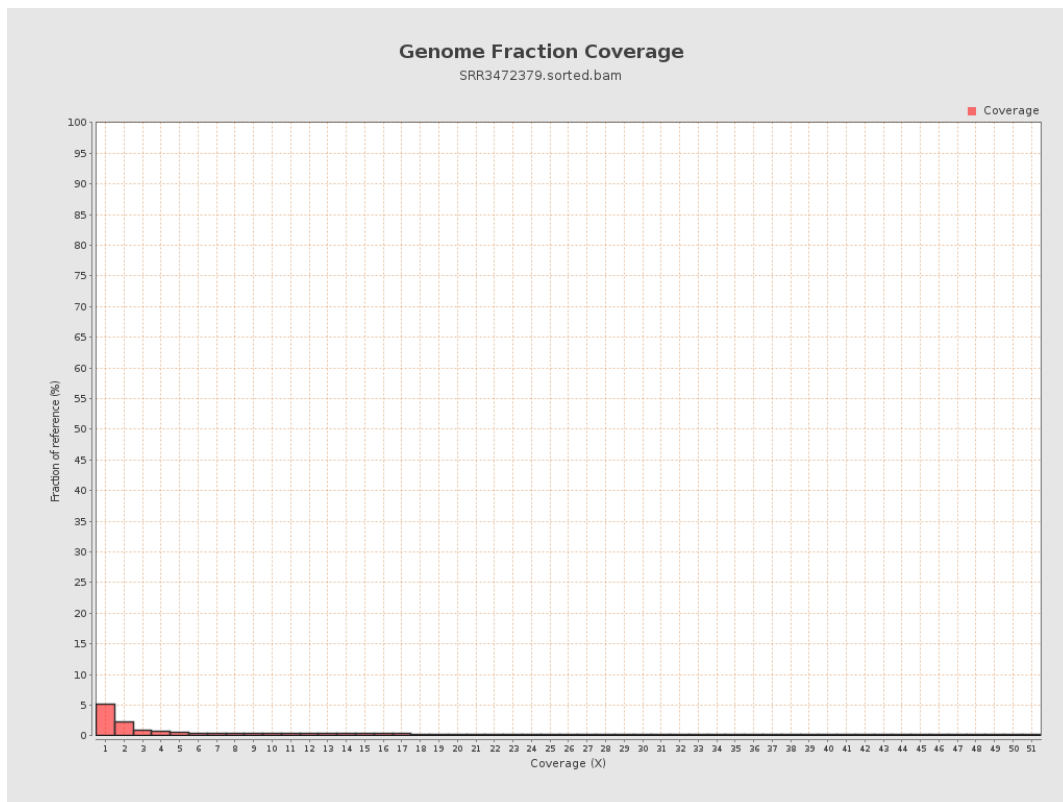
4. Results : Coverage Histogram



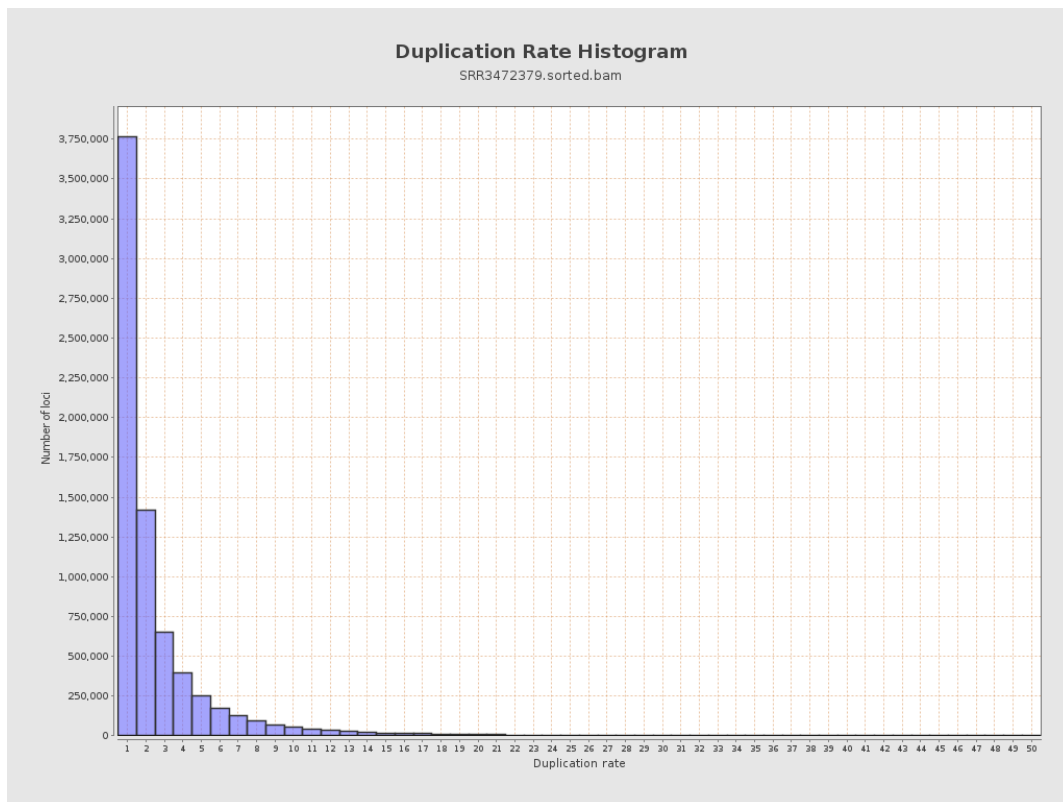
5. Results : Coverage Histogram (0-50X)



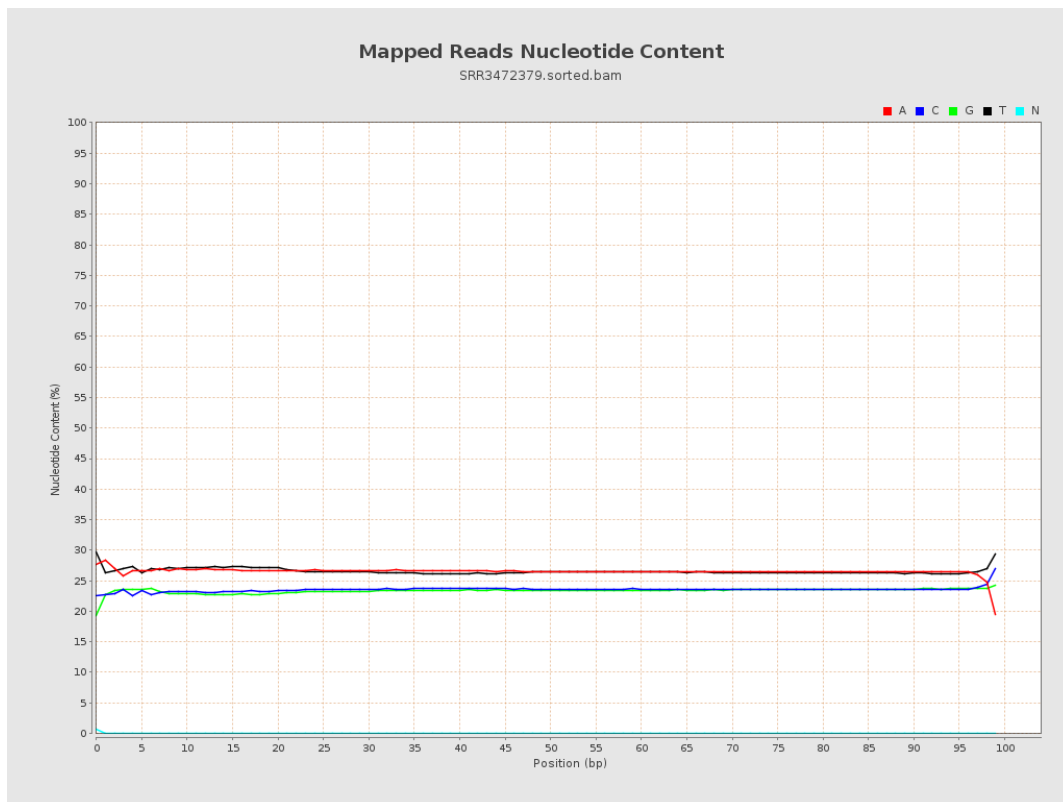
6. Results : Genome Fraction Coverage



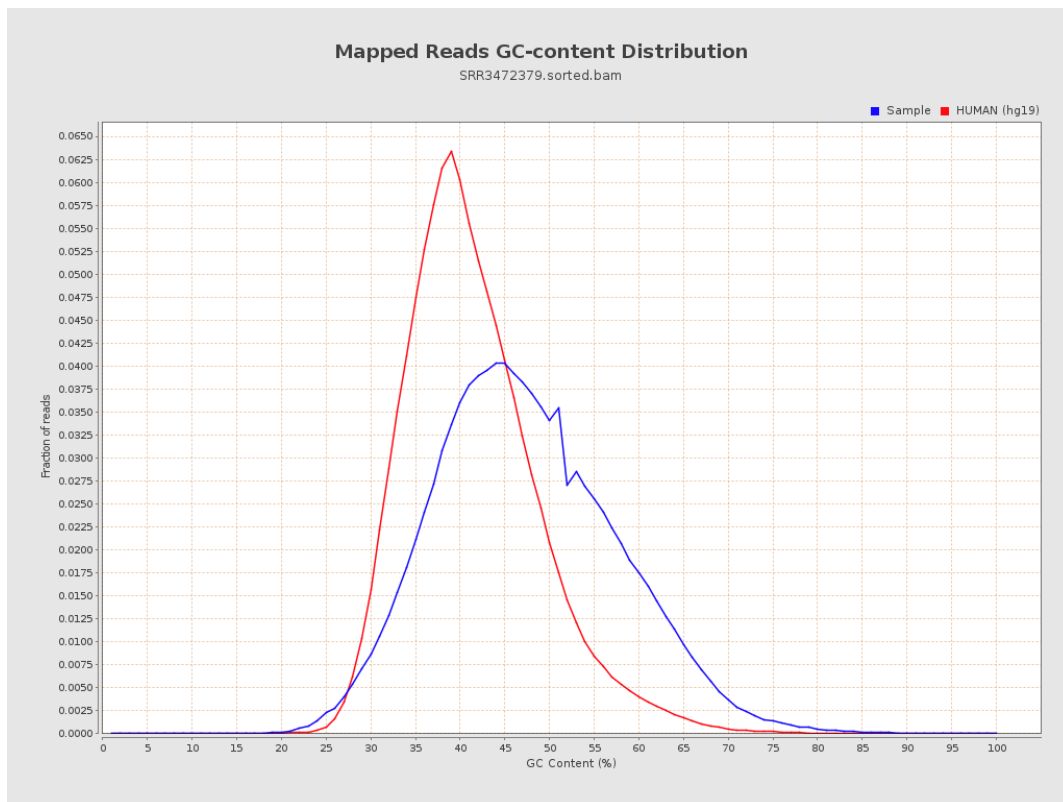
7. Results : Duplication Rate Histogram



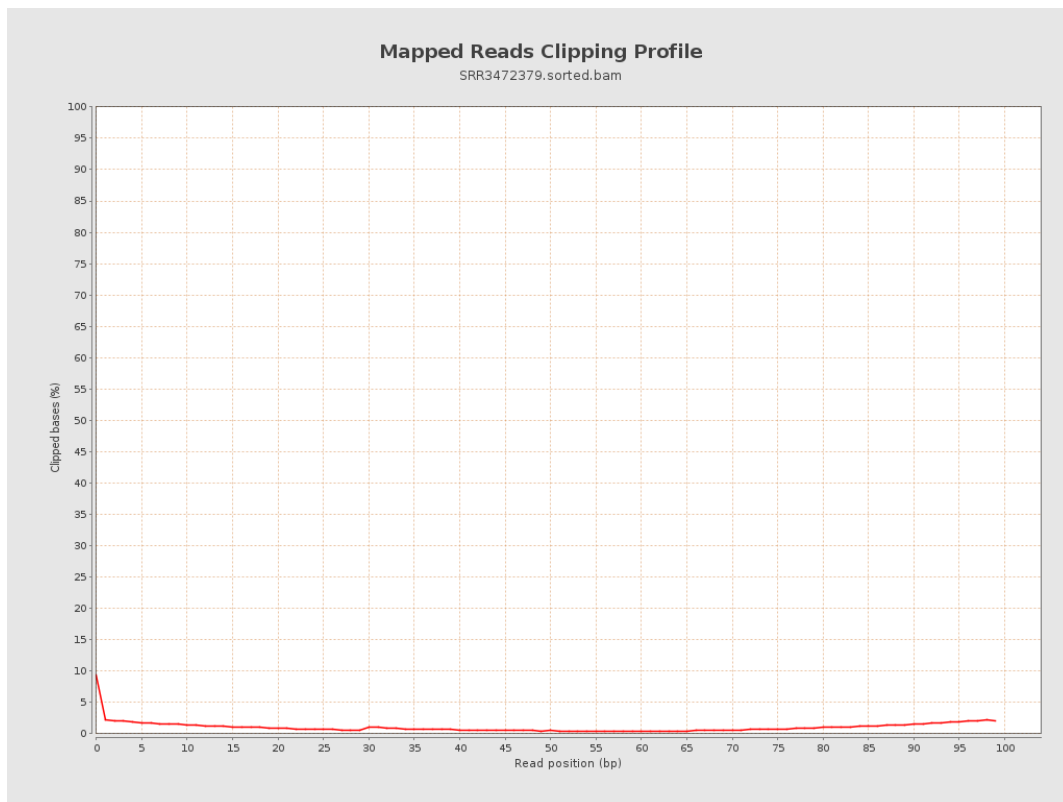
8. Results : Mapped Reads Nucleotide Content



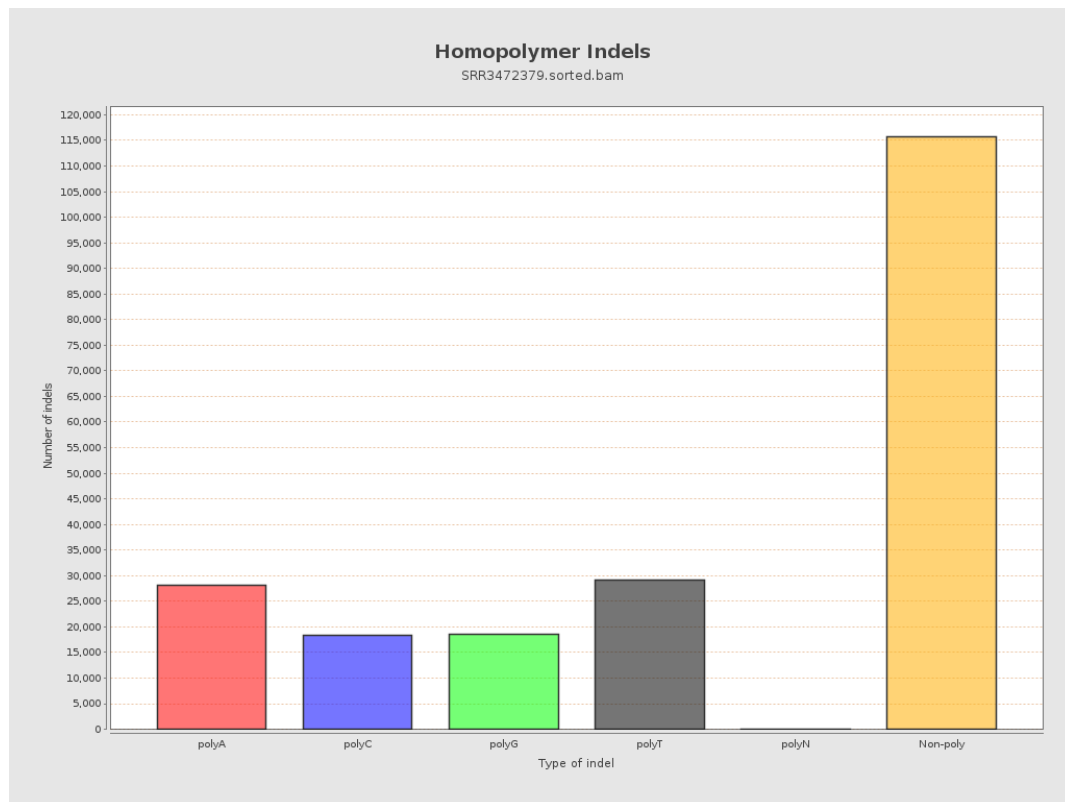
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



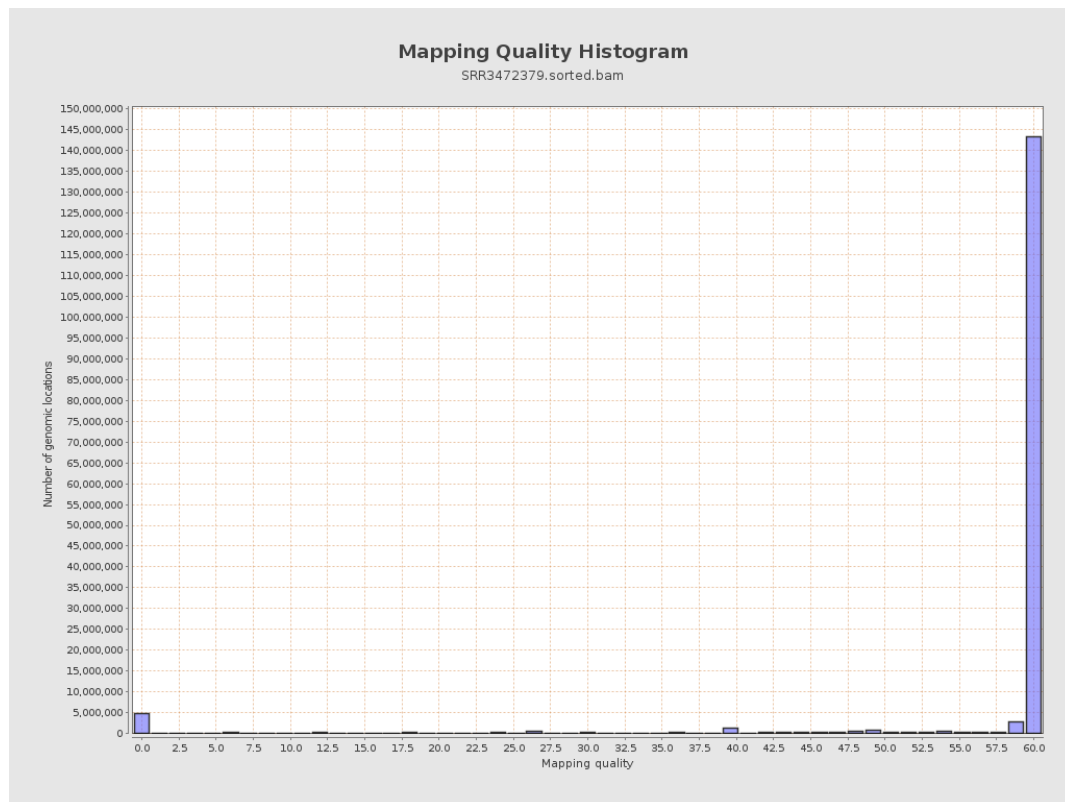
11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



15. Results : Insert Size Histogram

