

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 00:39:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472456.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_SRR3472456 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472456_1.fastq.gz SRR3472456_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 00:39:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472456.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,814,174
Mapped reads	13,696,436 / 99.15%
Unmapped reads	117,738 / 0.85%
Mapped paired reads	13,696,436 / 99.15%
Mapped reads, first in pair	6,865,801 / 49.7%
Mapped reads, second in pair	6,830,635 / 49.45%
Mapped reads, both in pair	13,642,230 / 98.76%
Mapped reads, singletons	54,206 / 0.39%
Secondary alignments	0
Supplementary alignments	44,032 / 0.32%
Read min/max/mean length	30 / 100 / 98.95
Duplicated reads (estimated)	8,288,299 / 60%
Duplication rate	47.99%
Clipped reads	1,019,304 / 7.38%

2.2. ACGT Content

Number/percentage of A's	350,650,818 / 26.24%
Number/percentage of C's	317,952,719 / 23.79%
Number/percentage of T's	352,320,684 / 26.36%
Number/percentage of G's	315,290,312 / 23.59%
Number/percentage of N's	183,494 / 0.01%

GC Percentage	47.38%
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2.3. Coverage

Mean	0.4317
Standard Deviation	13.4701

2.4. Mapping Quality

Mean Mapping Quality	55.17
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2.5. Insert size

Mean	15,659.69
Standard Deviation	1,251,331.12
P25/Median/P75	140 / 193 / 259

2.6. Mismatches and indels

General error rate	0.44%
Mismatches	5,762,624
Insertions	75,277
Mapped reads with at least one insertion	0.55%
Deletions	62,539
Mapped reads with at least one deletion	0.45%
Homopolymer indels	44.85%

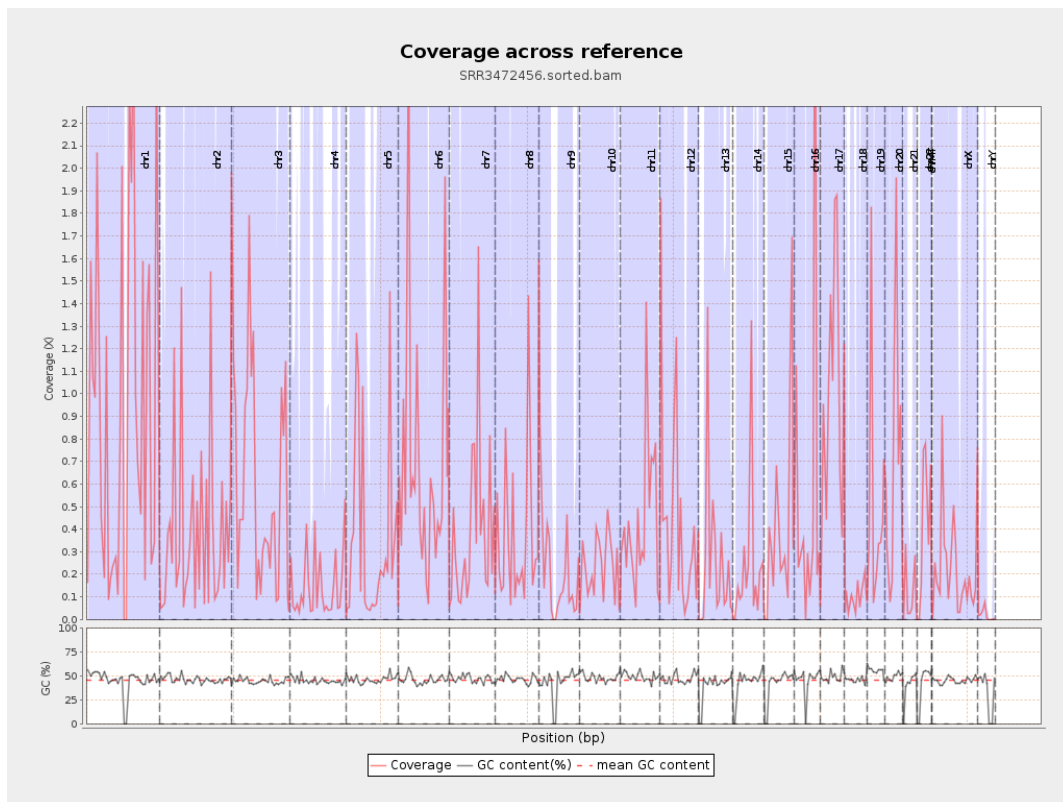
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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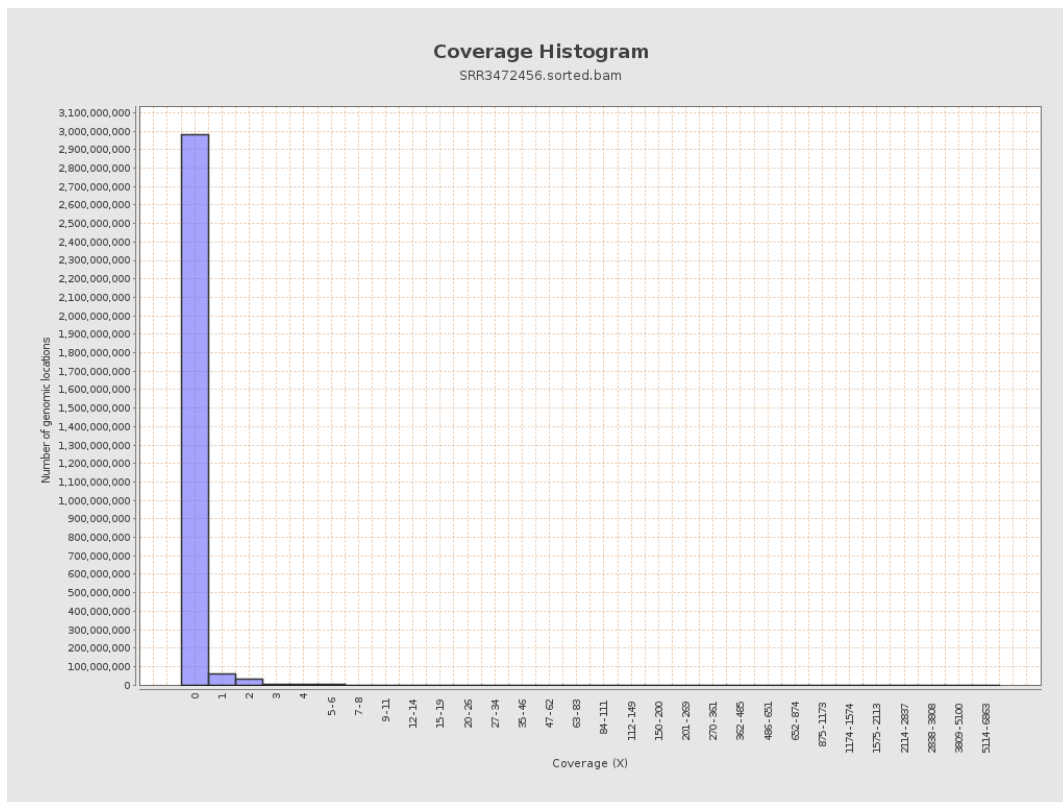
		bases	coverage	deviation
chr1	249250621	238943507	0.9586	23.3853
chr2	243199373	94523249	0.3887	13.8867
chr3	198022430	122825826	0.6203	14.1934
chr4	191154276	27566382	0.1442	5.0459
chr5	180915260	64165539	0.3547	13.0753
chr6	171115067	115586057	0.6755	17.1722
chr7	159138663	62175109	0.3907	11.9648
chr8	146364022	53945537	0.3686	11.0033
chr9	141213431	30980215	0.2194	6.2961
chr10	135534747	31655132	0.2336	7.5693
chr11	135006516	58364377	0.4323	12.1978
chr12	133851895	59040582	0.4411	10.2209
chr13	115169878	29110090	0.2528	7.8215
chr14	107349540	23945883	0.2231	7.1551
chr15	102531392	44422590	0.4333	14.9096
chr16	90354753	53045248	0.5871	19.4247
chr17	81195210	81647364	1.0056	25.5829
chr18	78077248	7946175	0.1018	3.0122
chr19	59128983	29305903	0.4956	9.9762
chr20	63025520	45258899	0.7181	17.6903
chr21	48129895	5844629	0.1214	6.6085
chr22	51304566	21053305	0.4104	11.1724
chrMT	16571	664	0.0401	0.2216
chrX	155270560	34033680	0.2192	6.5947

chrY	59373566	1169833	0.0197	1.0869
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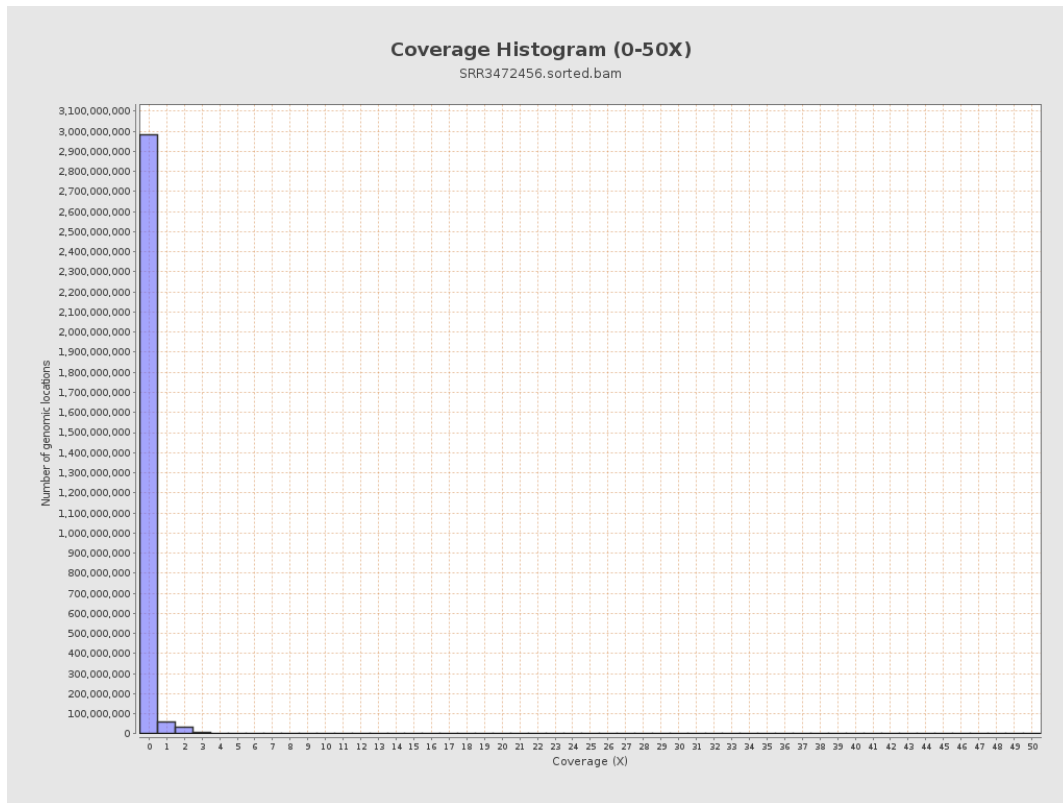
3. Results : Coverage across reference



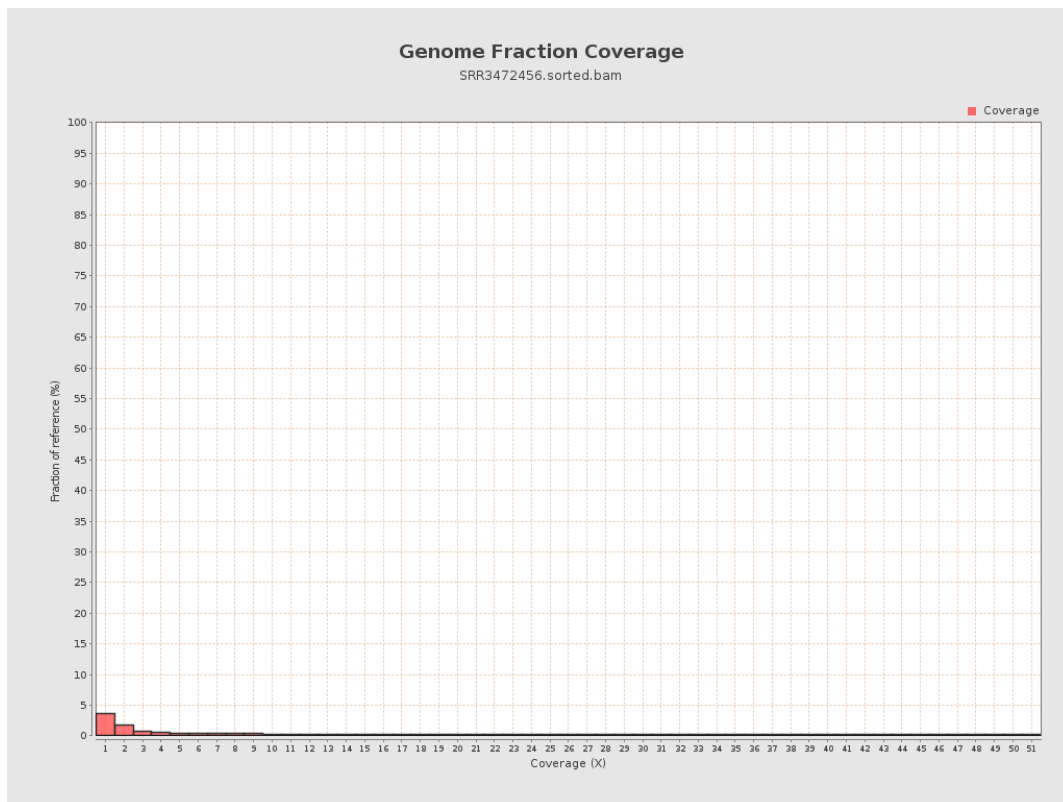
4. Results : Coverage Histogram



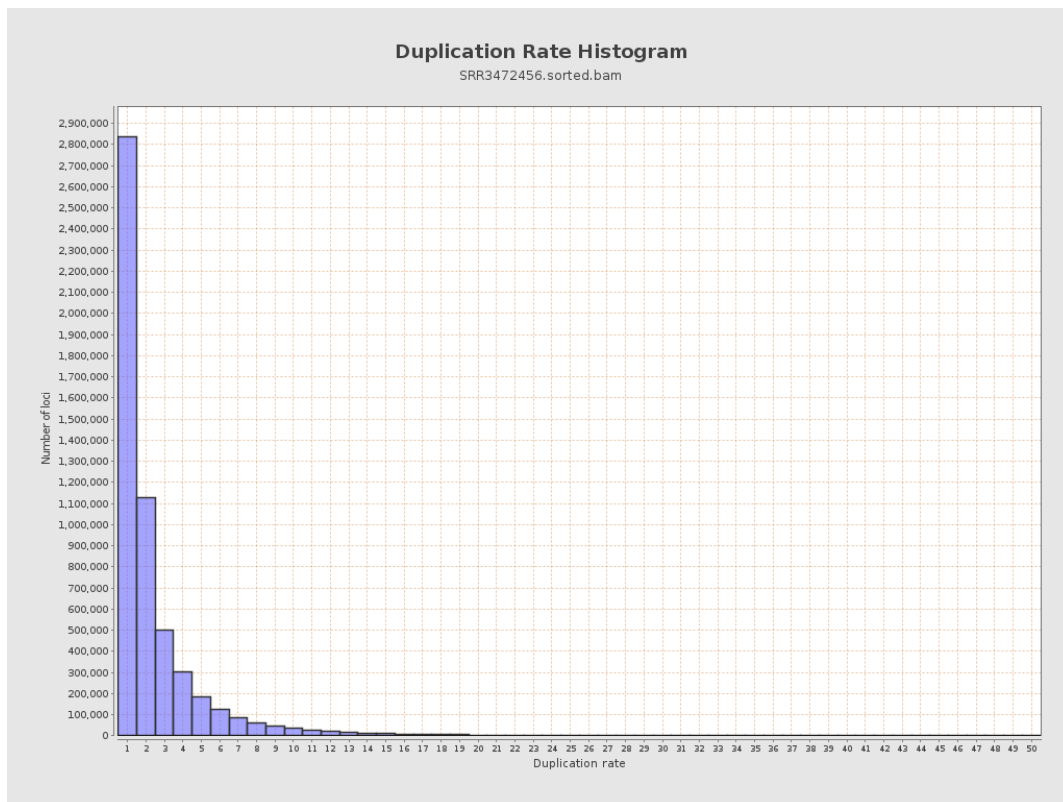
5. Results : Coverage Histogram (0-50X)



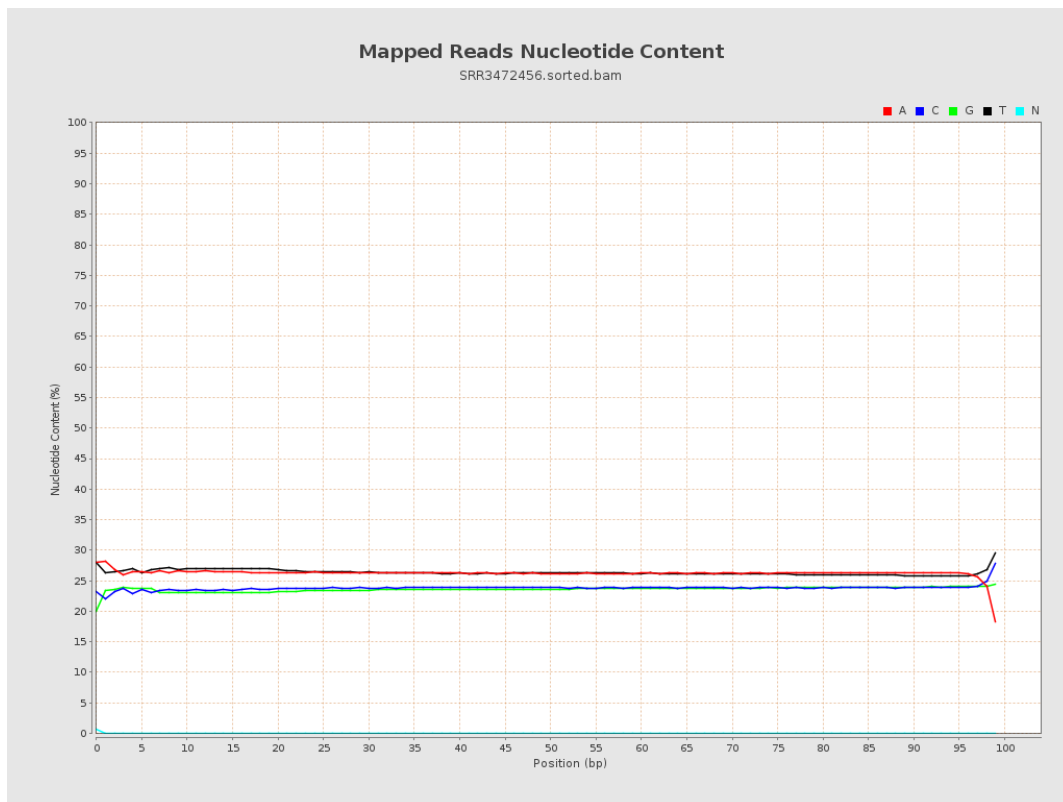
6. Results : Genome Fraction Coverage



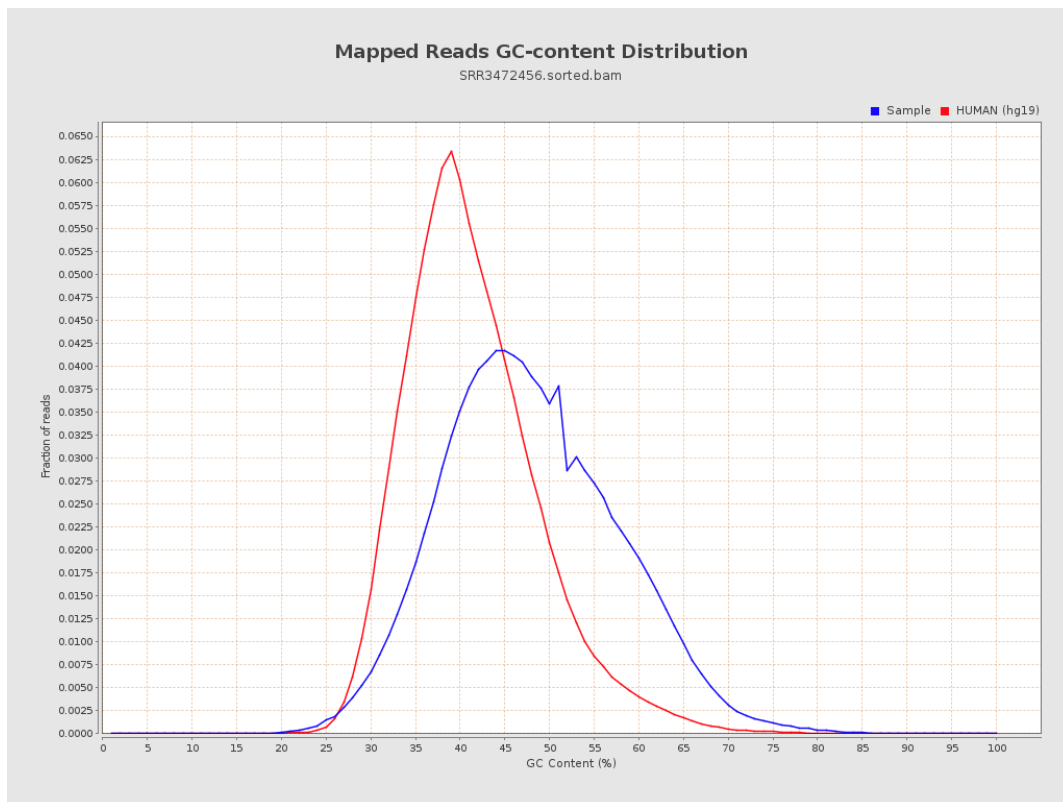
7. Results : Duplication Rate Histogram



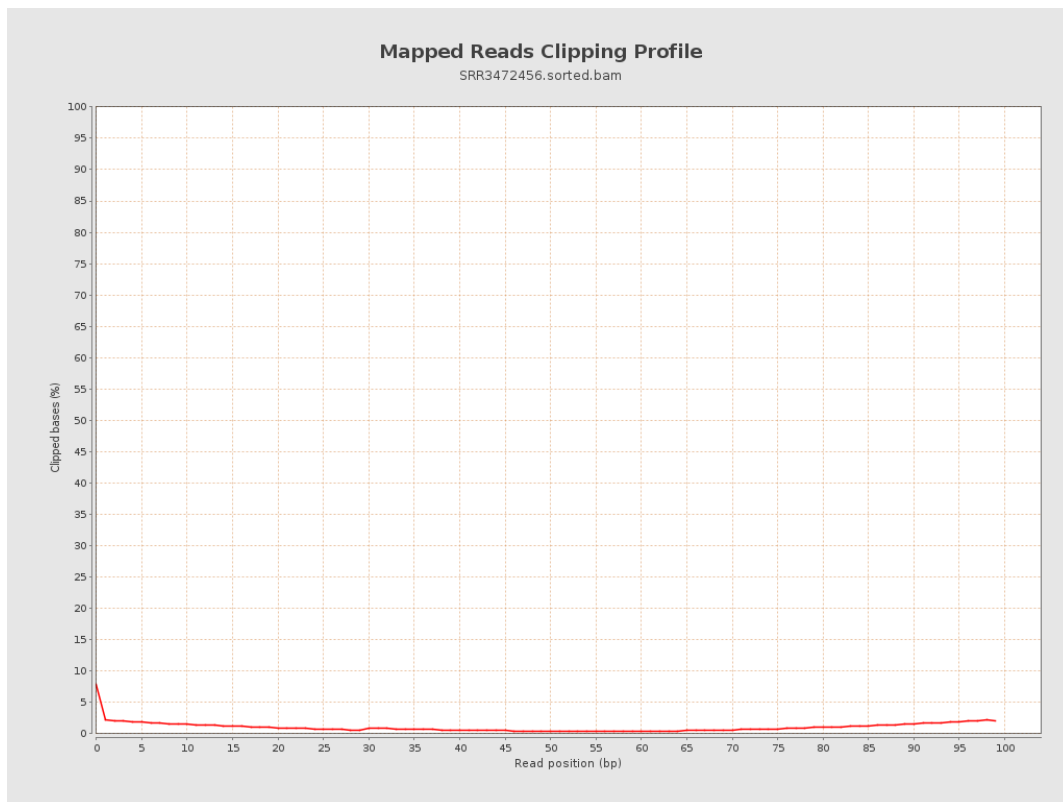
8. Results : Mapped Reads Nucleotide Content



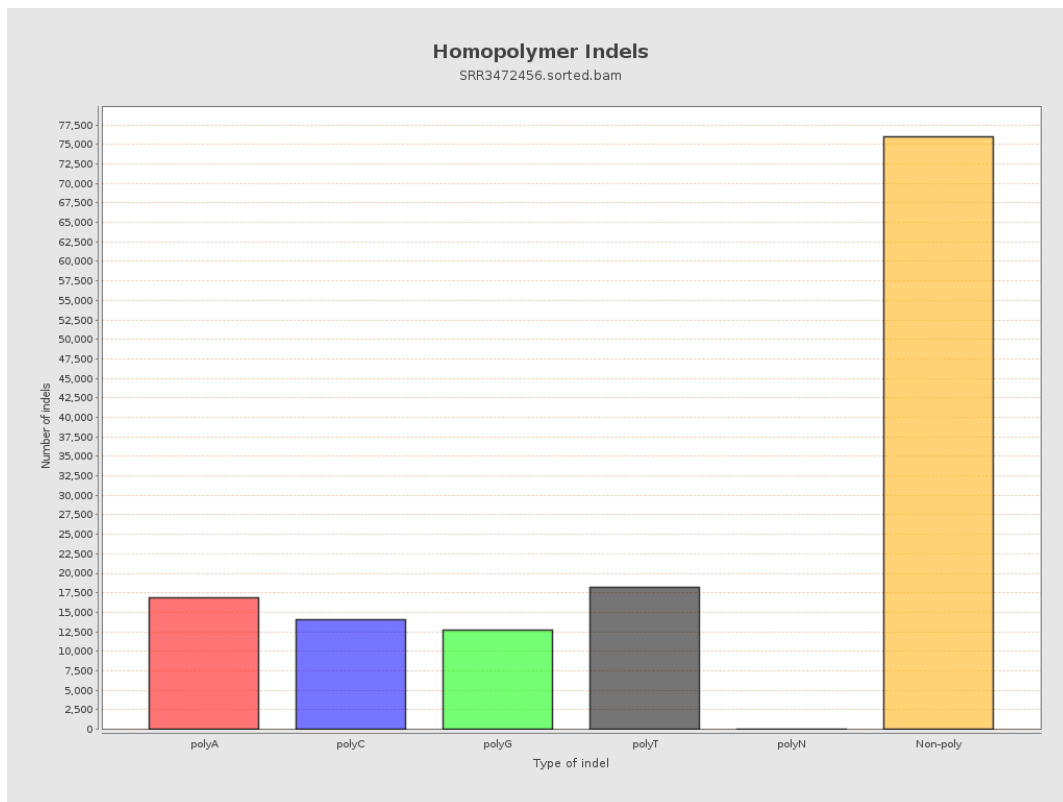
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



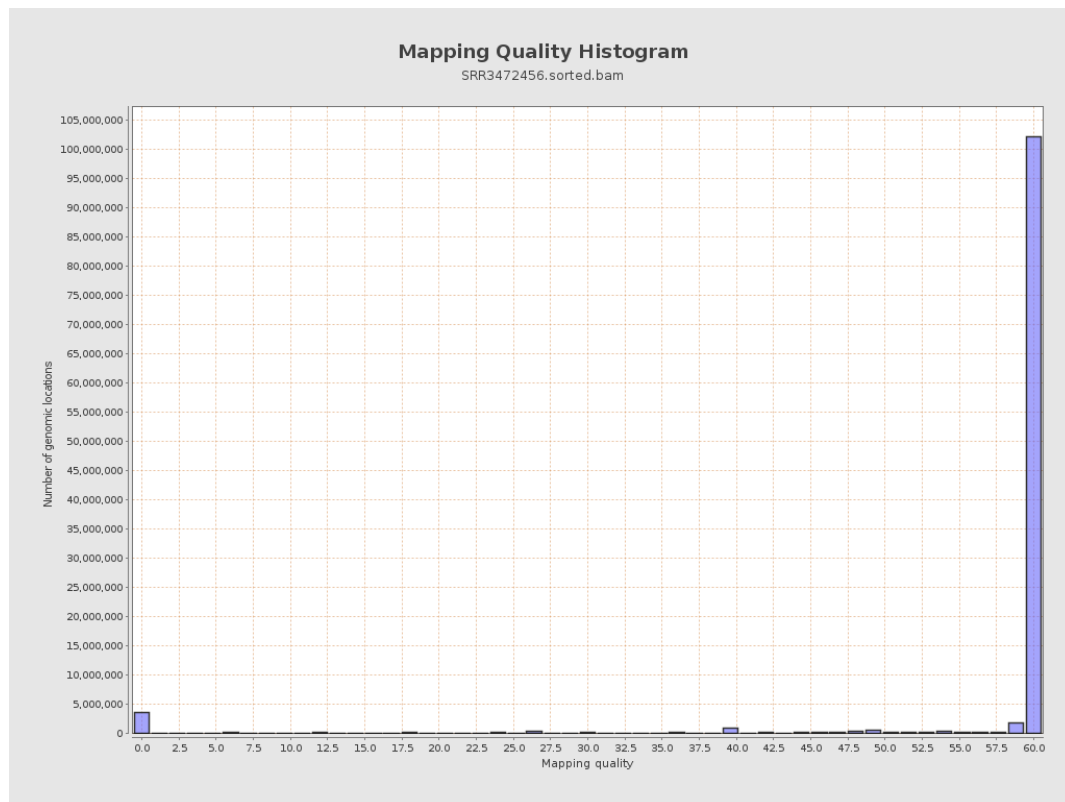
11. Results : Homopolymer Indels



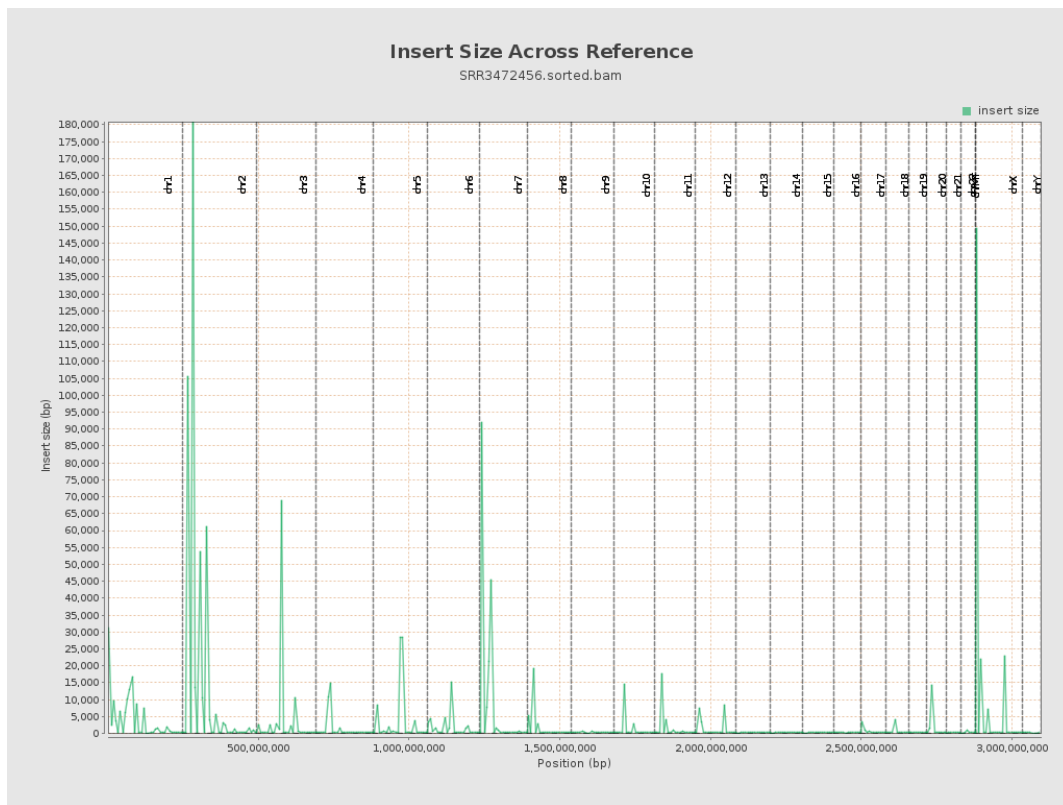
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

