

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 02:20:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472741.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_SRR3472741 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472741_1.fastq.gz SRR3472741_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 02:20:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472741.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,611,164
Mapped reads	19,432,207 / 99.09%
Unmapped reads	178,957 / 0.91%
Mapped paired reads	19,432,207 / 99.09%
Mapped reads, first in pair	9,749,106 / 49.71%
Mapped reads, second in pair	9,683,101 / 49.38%
Mapped reads, both in pair	19,322,998 / 98.53%
Mapped reads, singletons	109,209 / 0.56%
Secondary alignments	0
Supplementary alignments	69,229 / 0.35%
Read min/max/mean length	30 / 100 / 100.14
Duplicated reads (estimated)	12,793,218 / 65.23%
Duplication rate	46.97%
Clipped reads	1,475,117 / 7.52%

2.2. ACGT Content

Number/percentage of A's	522,456,563 / 27.27%
Number/percentage of C's	437,381,680 / 22.83%
Number/percentage of T's	518,424,261 / 27.06%
Number/percentage of G's	436,917,901 / 22.81%
Number/percentage of N's	370,375 / 0.02%

GC Percentage	45.64%
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2.3. Coverage

Mean	0.6189
Standard Deviation	25.8315

2.4. Mapping Quality

Mean Mapping Quality	55.19
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2.5. Insert size

Mean	22,195.54
Standard Deviation	1,466,618.45
P25/Median/P75	180 / 251 / 335

2.6. Mismatches and indels

General error rate	0.63%
Mismatches	11,834,476
Insertions	118,929
Mapped reads with at least one insertion	0.6%
Deletions	99,745
Mapped reads with at least one deletion	0.51%
Homopolymer indels	45.19%

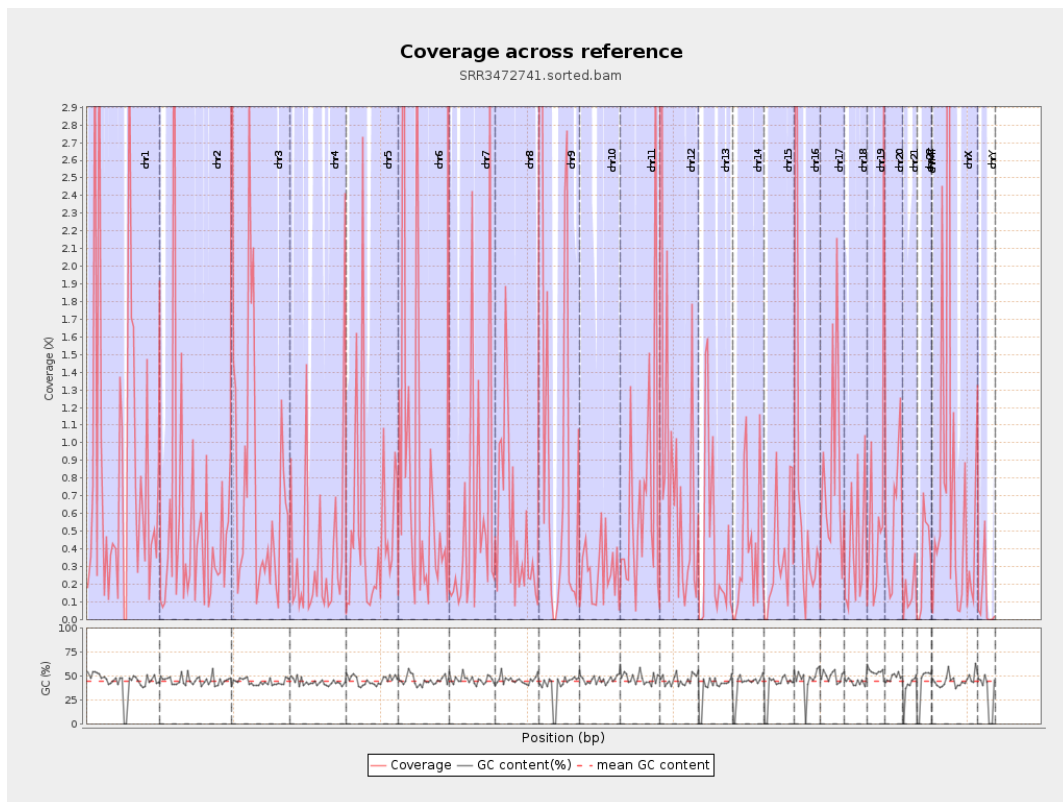
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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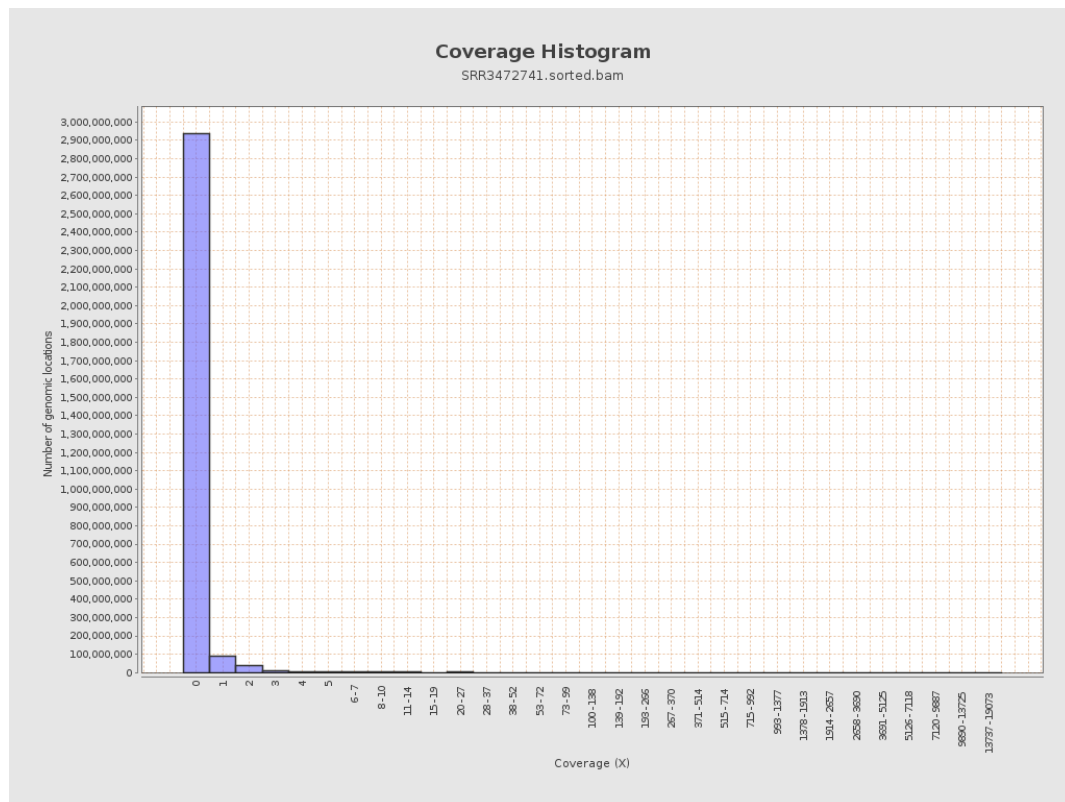
		bases	coverage	deviation
chr1	249250621	217175334	0.8713	33.8743
chr2	243199373	129802799	0.5337	25.3142
chr3	198022430	155031809	0.7829	15.8914
chr4	191154276	70521359	0.3689	13.9119
chr5	180915260	93291085	0.5157	15.4537
chr6	171115067	154106748	0.9006	31.429
chr7	159138663	91817798	0.577	19.6005
chr8	146364022	75417425	0.5153	16.992
chr9	141213431	143503528	1.0162	35.4786
chr10	135534747	36895268	0.2722	9.7811
chr11	135006516	94045902	0.6966	26.9752
chr12	133851895	135036648	1.0089	36.7599
chr13	115169878	46745893	0.4059	18.3494
chr14	107349540	42393186	0.3949	14.4613
chr15	102531392	36023881	0.3513	11.1488
chr16	90354753	66730893	0.7385	21.8742
chr17	81195210	67286575	0.8287	20.8749
chr18	78077248	31197710	0.3996	14.2516
chr19	59128983	32102804	0.5429	13.7101
chr20	63025520	36961717	0.5865	18.5088
chr21	48129895	7401829	0.1538	7.5494
chr22	51304566	17154144	0.3344	9.1978
chrMT	16571	2641	0.1594	0.5349
chrX	155270560	128414833	0.827	58.9646

chrY	59373566	6745208	0.1136	7.2036
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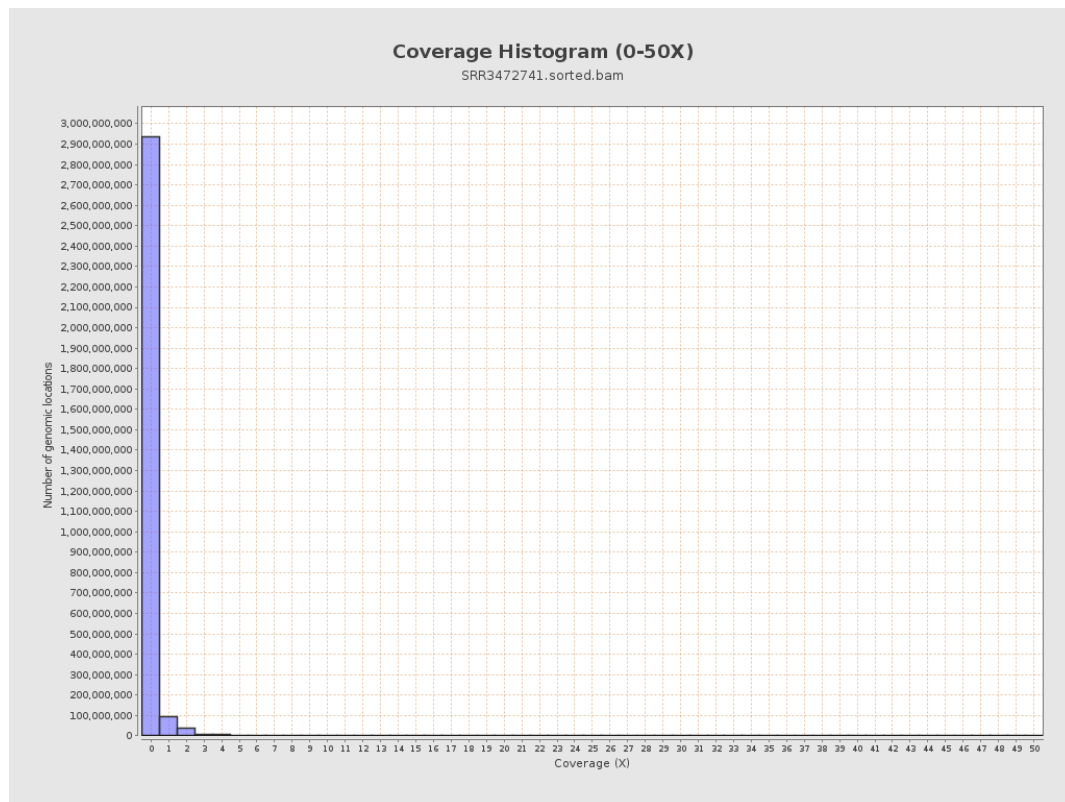
3. Results : Coverage across reference



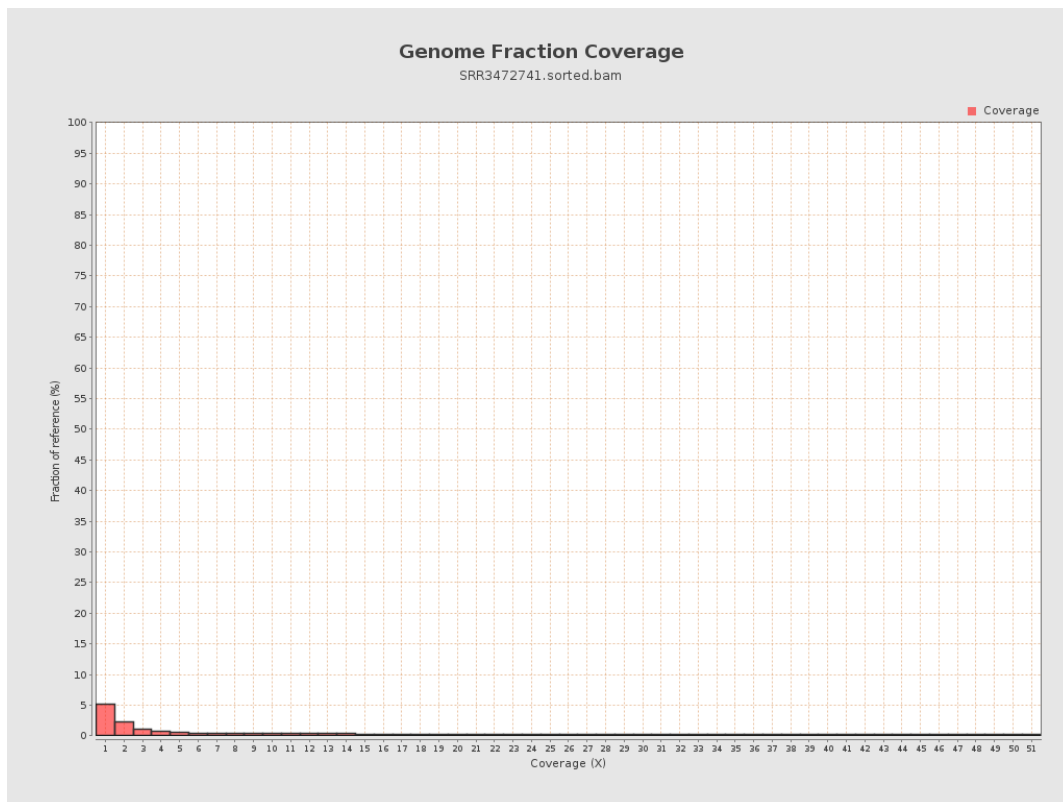
4. Results : Coverage Histogram



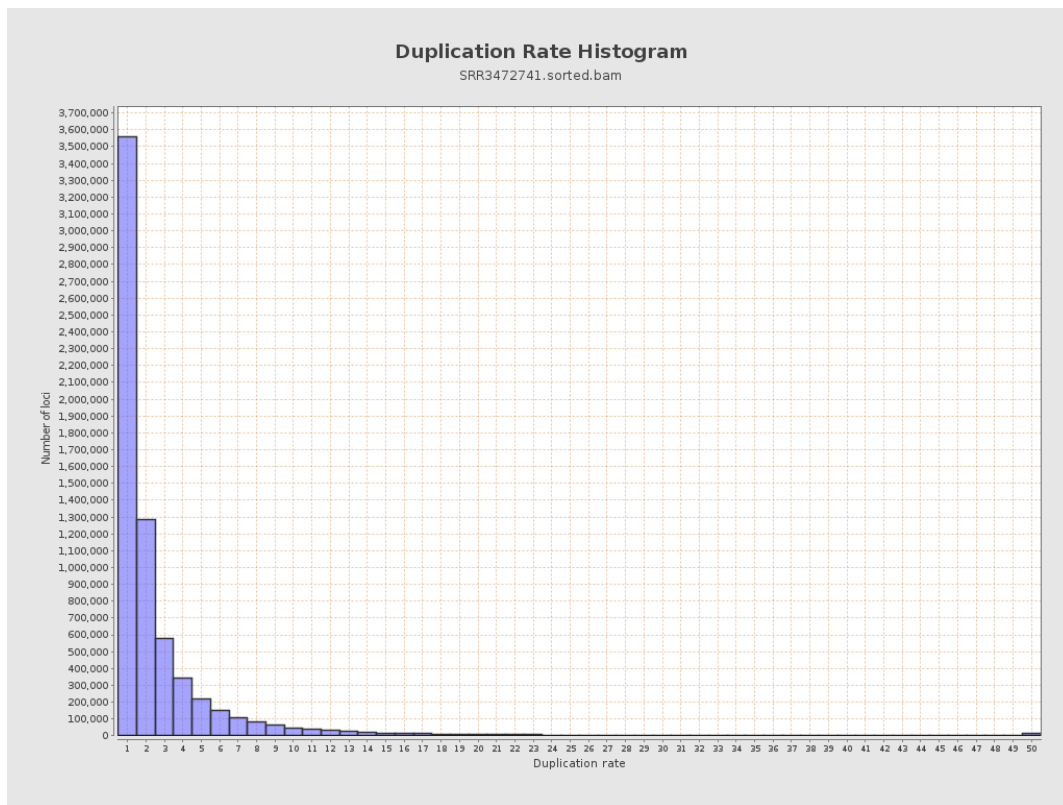
5. Results : Coverage Histogram (0-50X)



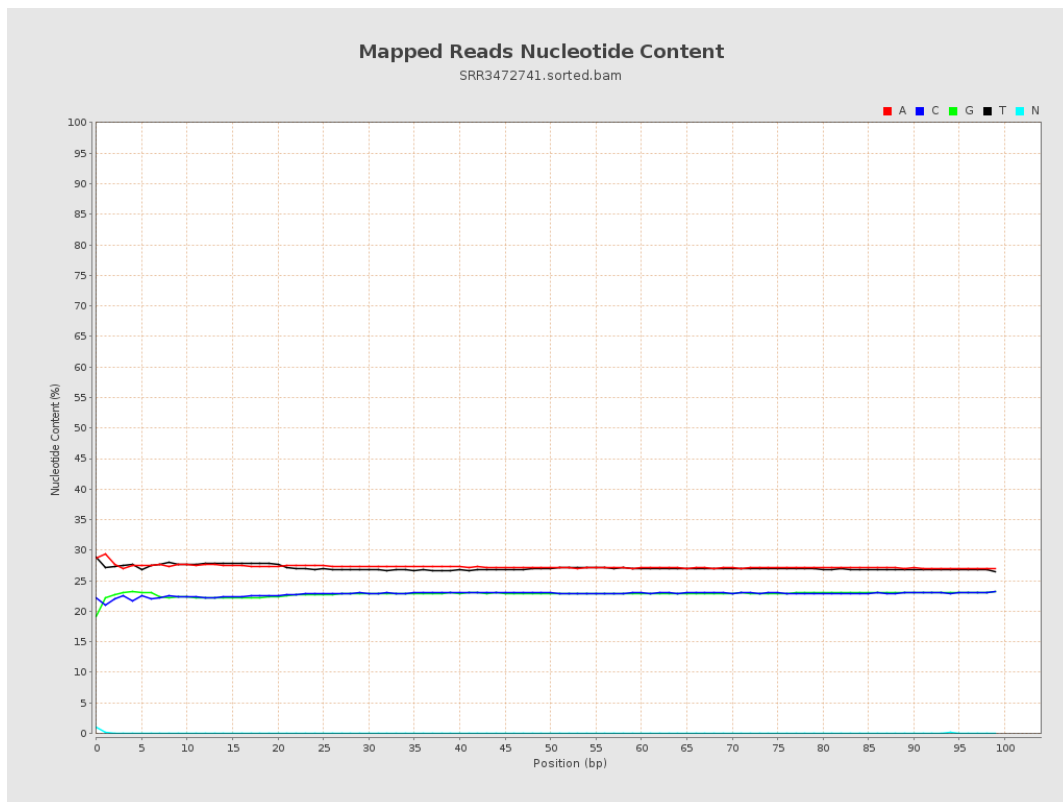
6. Results : Genome Fraction Coverage



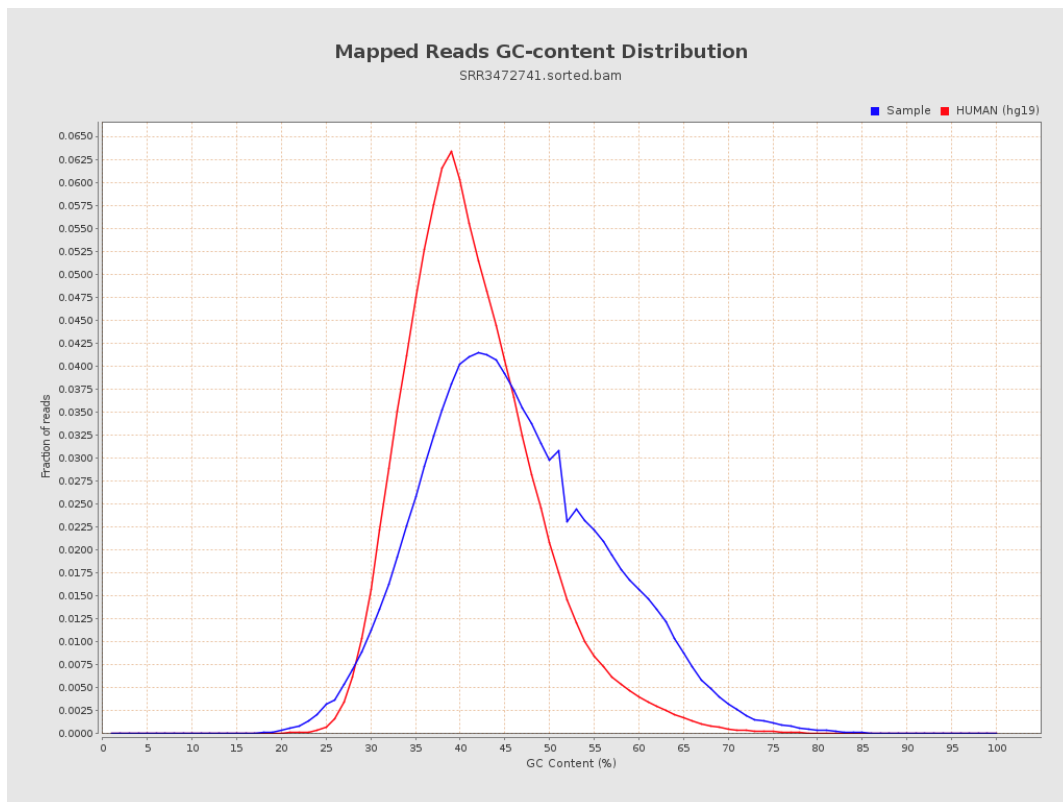
7. Results : Duplication Rate Histogram



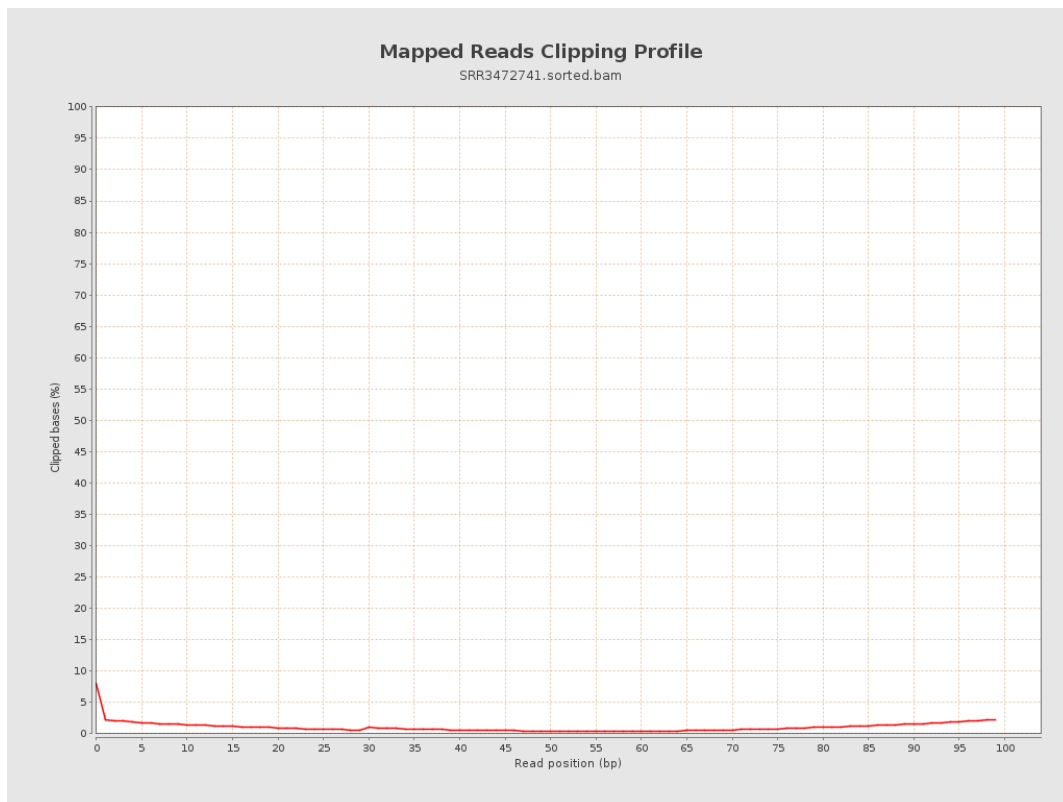
8. Results : Mapped Reads Nucleotide Content



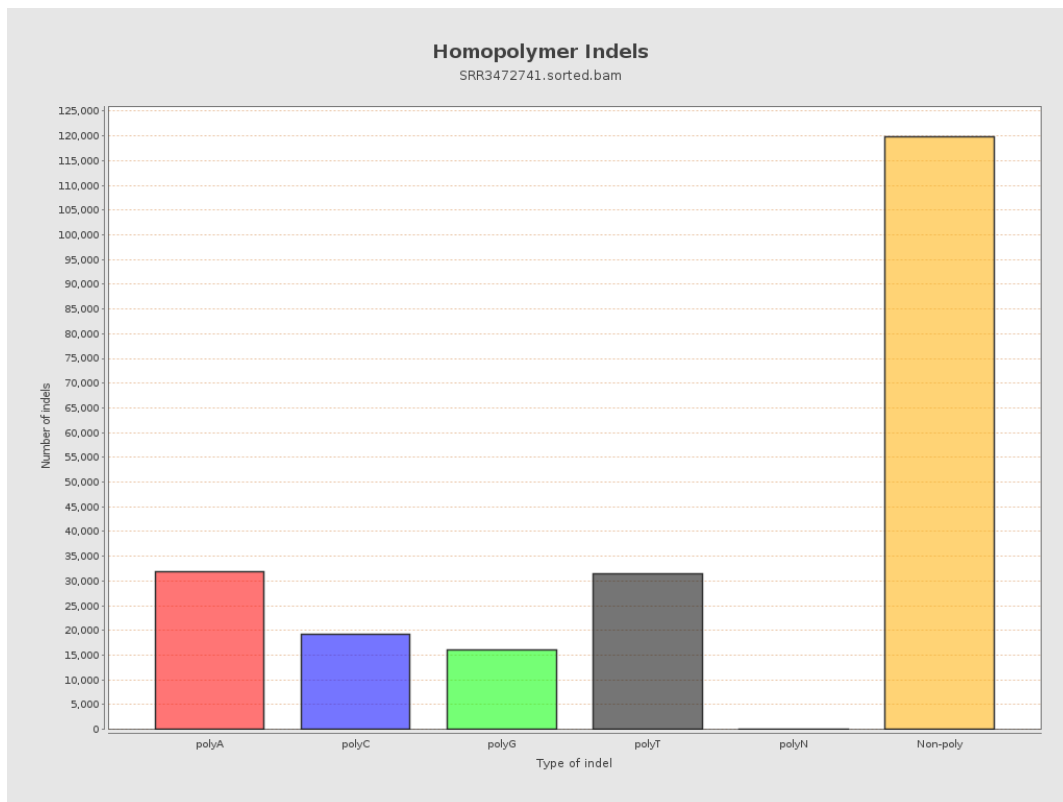
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



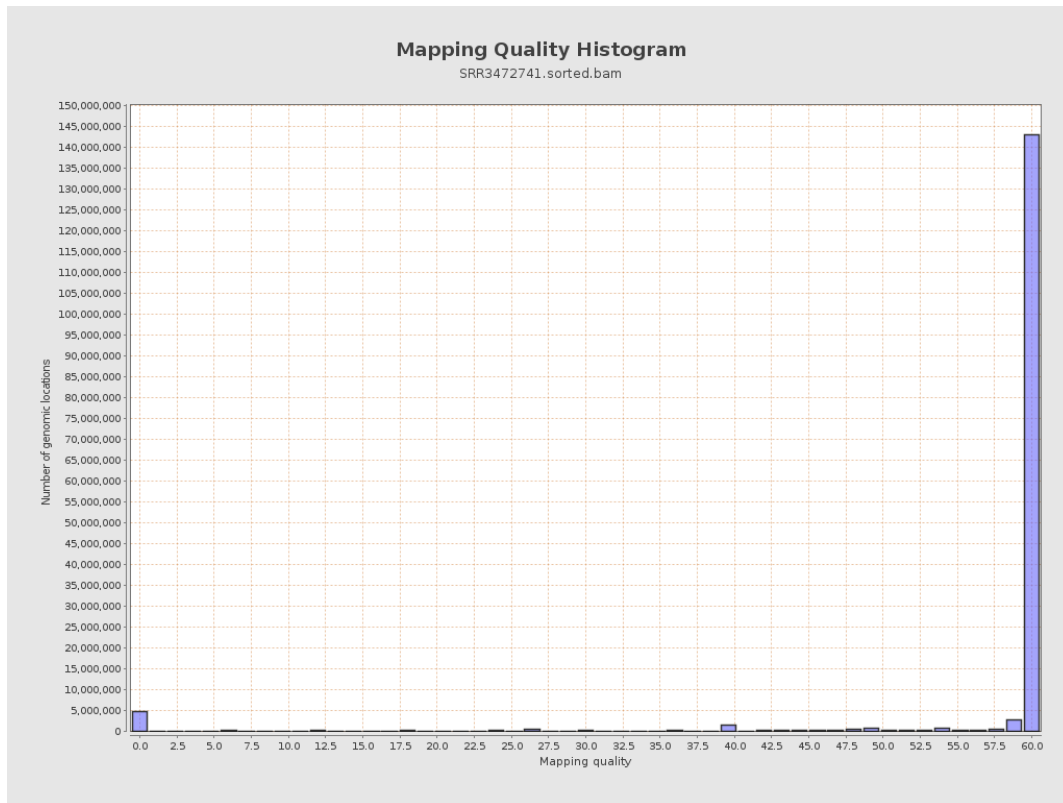
11. Results : Homopolymer Indels



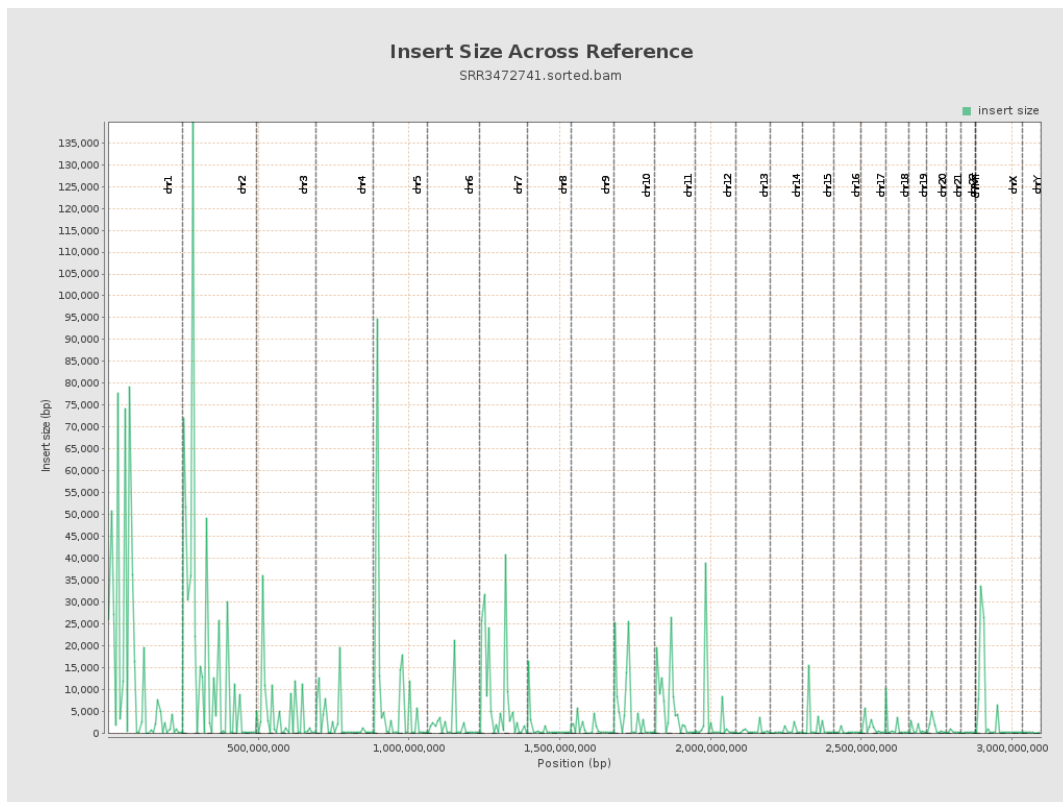
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

