

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 05:00:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472592.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_SRR3472592 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472592_1.fastq.gz SRR3472592_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 05:00:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472592.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,738,870
Mapped reads	7,111,888 / 91.9%
Unmapped reads	626,982 / 8.1%
Mapped paired reads	7,111,888 / 91.9%
Mapped reads, first in pair	3,585,186 / 46.33%
Mapped reads, second in pair	3,526,702 / 45.57%
Mapped reads, both in pair	6,946,998 / 89.77%
Mapped reads, singletons	164,890 / 2.13%
Secondary alignments	0
Supplementary alignments	204,130 / 2.64%
Read min/max/mean length	30 / 100 / 101.03
Duplicated reads (estimated)	1,065,054 / 13.76%
Duplication rate	13.07%
Clipped reads	5,440,724 / 70.3%

2.2. ACGT Content

Number/percentage of A's	149,790,841 / 25.95%
Number/percentage of C's	114,437,827 / 19.82%
Number/percentage of T's	172,798,004 / 29.93%
Number/percentage of G's	139,867,256 / 24.23%
Number/percentage of N's	357,669 / 0.06%

GC Percentage	44.05%
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2.3. Coverage

Mean	0.1866
Standard Deviation	1.8319

2.4. Mapping Quality

Mean Mapping Quality	50.32
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2.5. Insert size

Mean	216,237.95
Standard Deviation	4,463,025.42
P25/Median/P75	90 / 128 / 178

2.6. Mismatches and indels

General error rate	1.19%
Mismatches	6,768,865
Insertions	55,644
Mapped reads with at least one insertion	0.77%
Deletions	134,455
Mapped reads with at least one deletion	1.85%
Homopolymer indels	42.63%

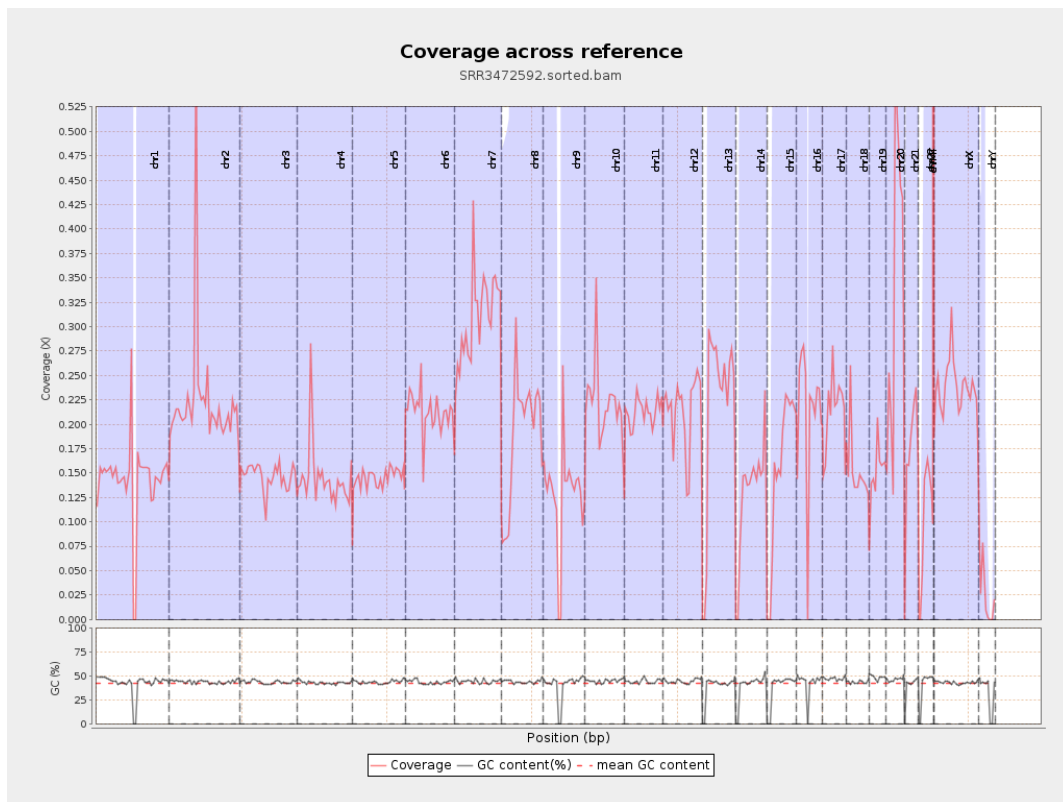
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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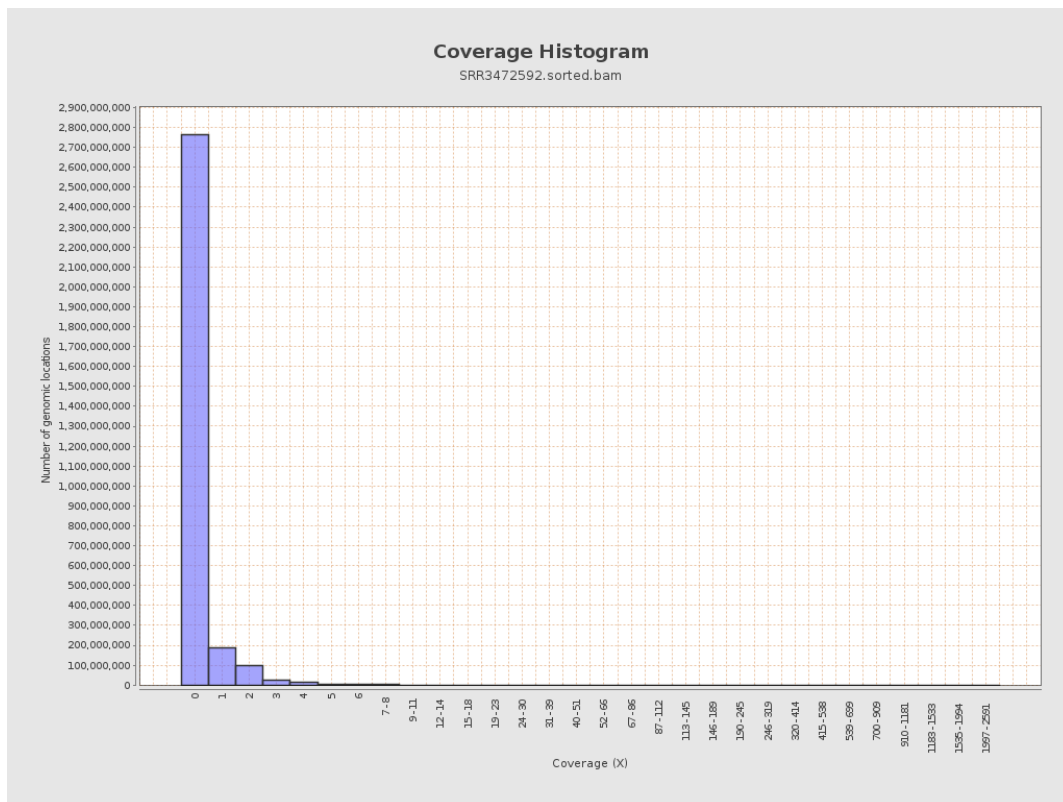
		bases	coverage	deviation
chr1	249250621	35533326	0.1426	2.3883
chr2	243199373	54458370	0.2239	2.8971
chr3	198022430	29028500	0.1466	0.5579
chr4	191154276	27504704	0.1439	0.9213
chr5	180915260	26289676	0.1453	0.5862
chr6	171115067	36310606	0.2122	1.0654
chr7	159138663	49488272	0.311	3.0764
chr8	146364022	27583091	0.1885	1.6016
chr9	141213431	17977657	0.1273	2.0192
chr10	135534747	30047050	0.2217	1.7631
chr11	135006516	28492419	0.211	1.6587
chr12	133851895	28532795	0.2132	0.7059
chr13	115169878	25024348	0.2173	0.707
chr14	107349540	13980174	0.1302	3.7996
chr15	102531392	15961533	0.1557	0.5922
chr16	90354753	19355123	0.2142	0.9995
chr17	81195210	17267221	0.2127	1.3924
chr18	78077248	12081257	0.1547	3.0615
chr19	59128983	9051135	0.1531	1.6398
chr20	63025520	21559057	0.3421	1.1714
chr21	48129895	8261626	0.1717	0.7701
chr22	51304566	5094060	0.0993	0.4701
chrMT	16571	126610	7.6405	5.6805
chrX	155270560	37058977	0.2387	1.0586

chrY	59373566	1435244	0.0242	0.7676
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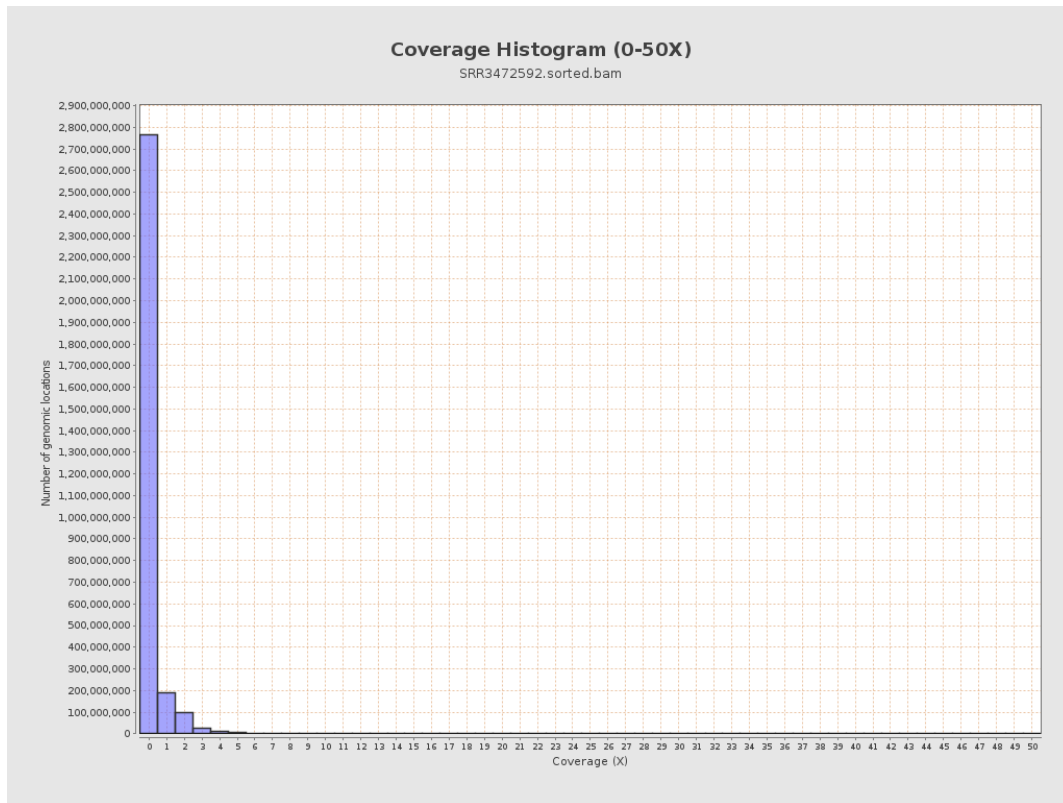
3. Results : Coverage across reference



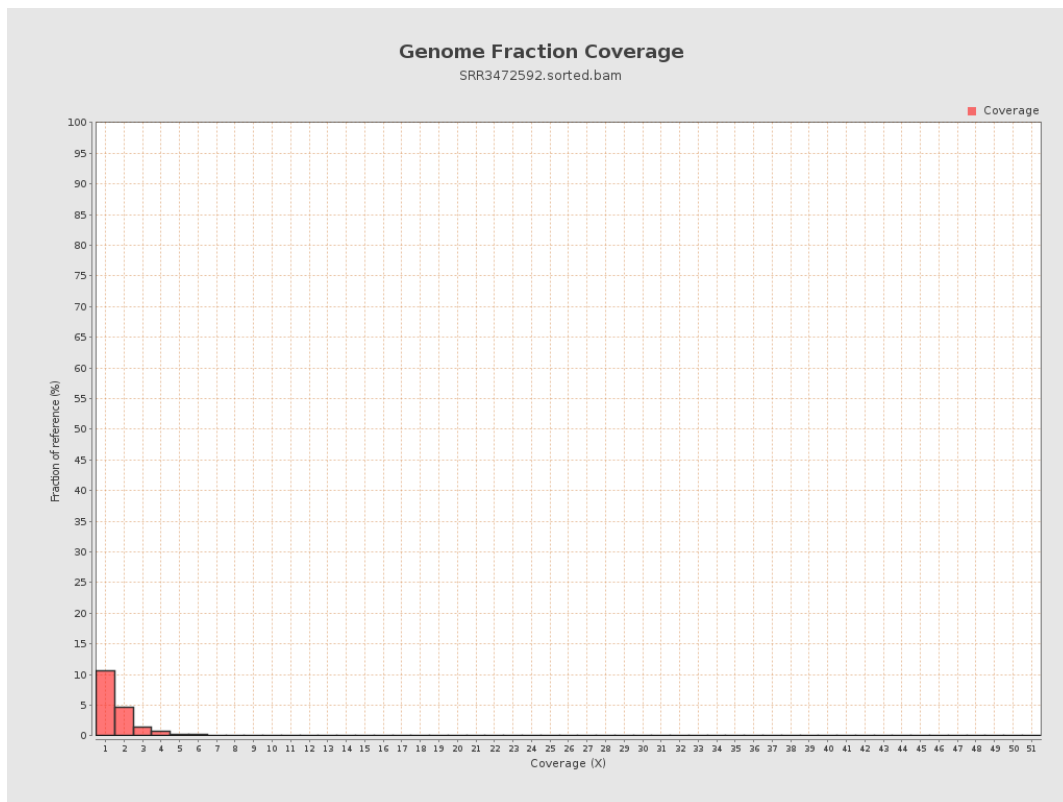
4. Results : Coverage Histogram



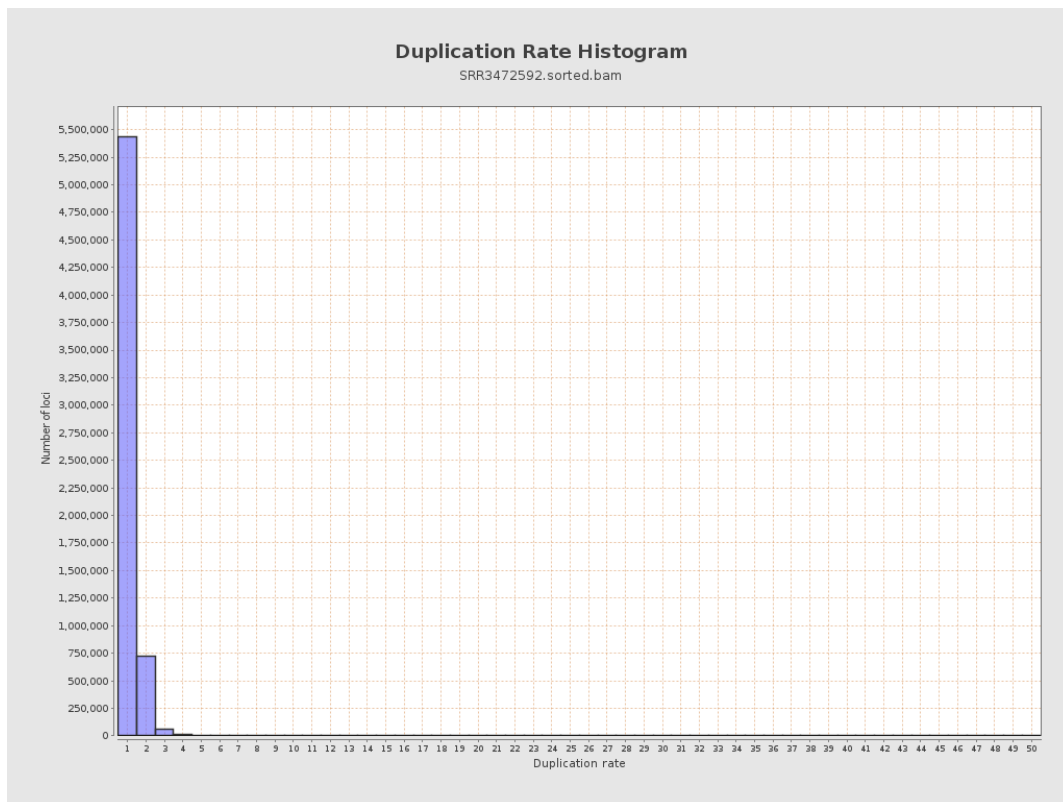
5. Results : Coverage Histogram (0-50X)



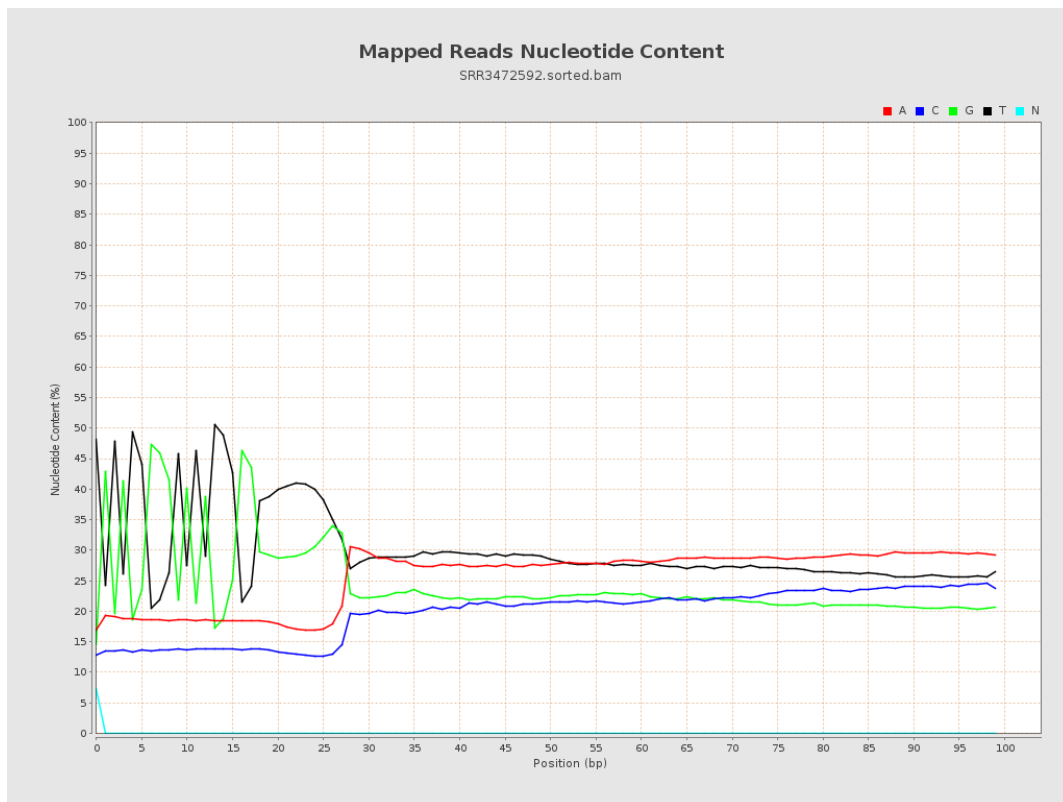
6. Results : Genome Fraction Coverage



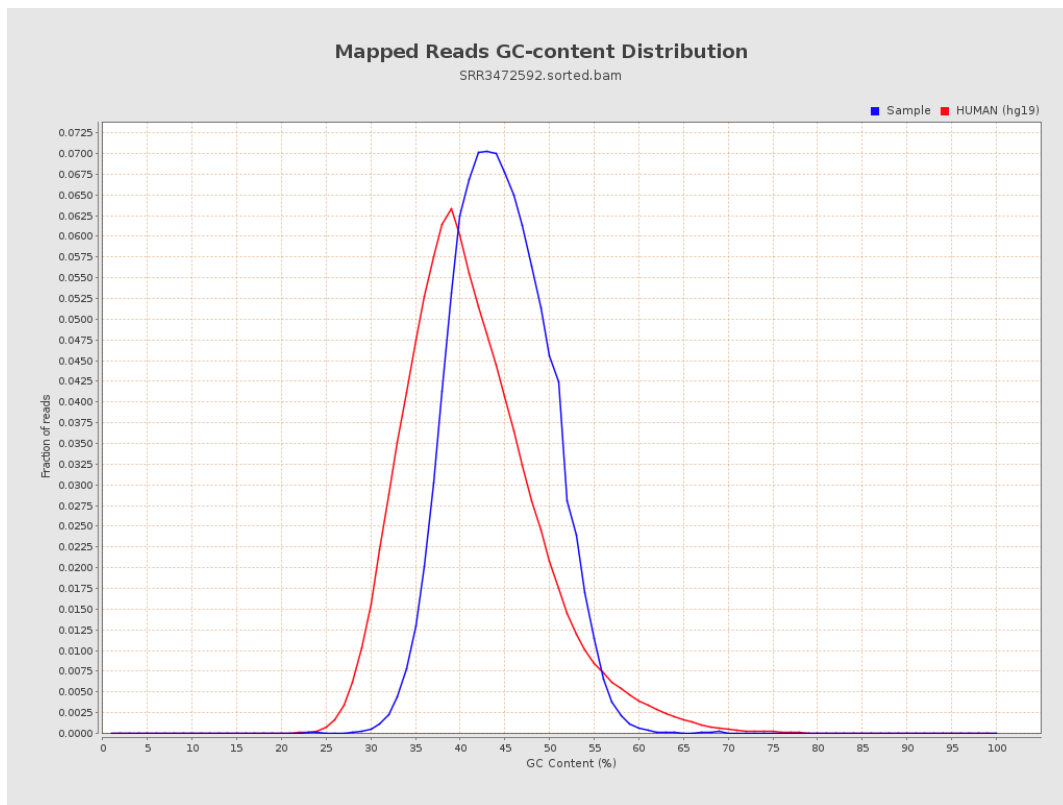
7. Results : Duplication Rate Histogram



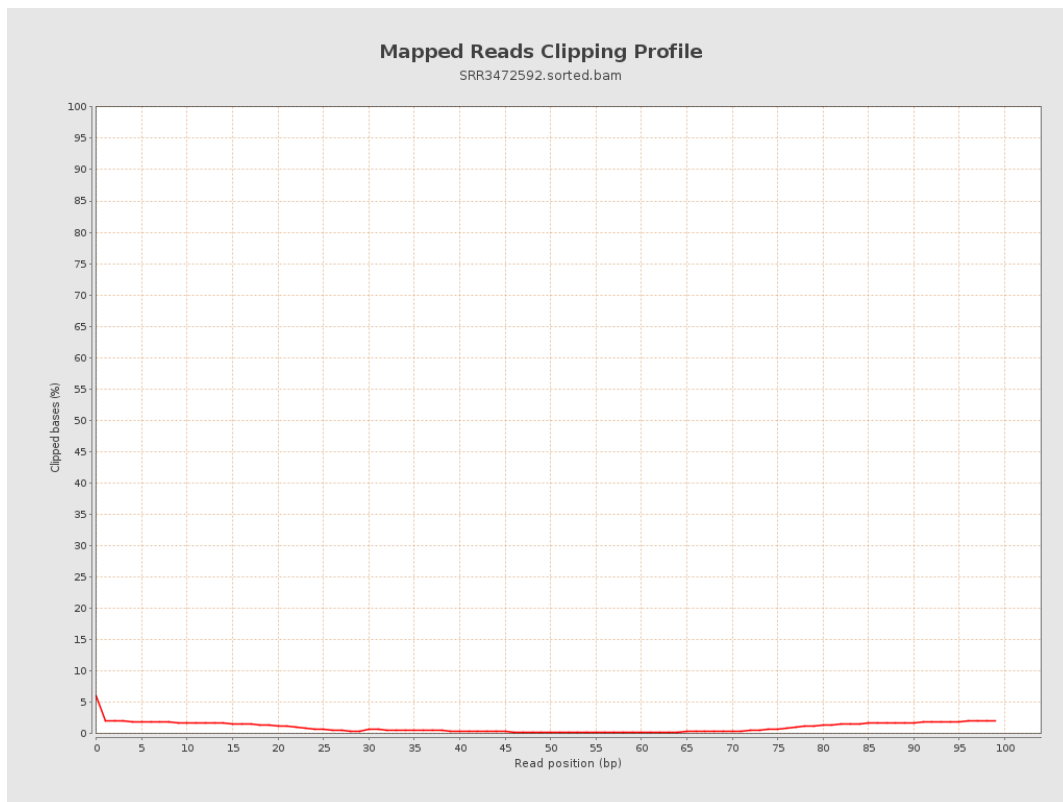
8. Results : Mapped Reads Nucleotide Content



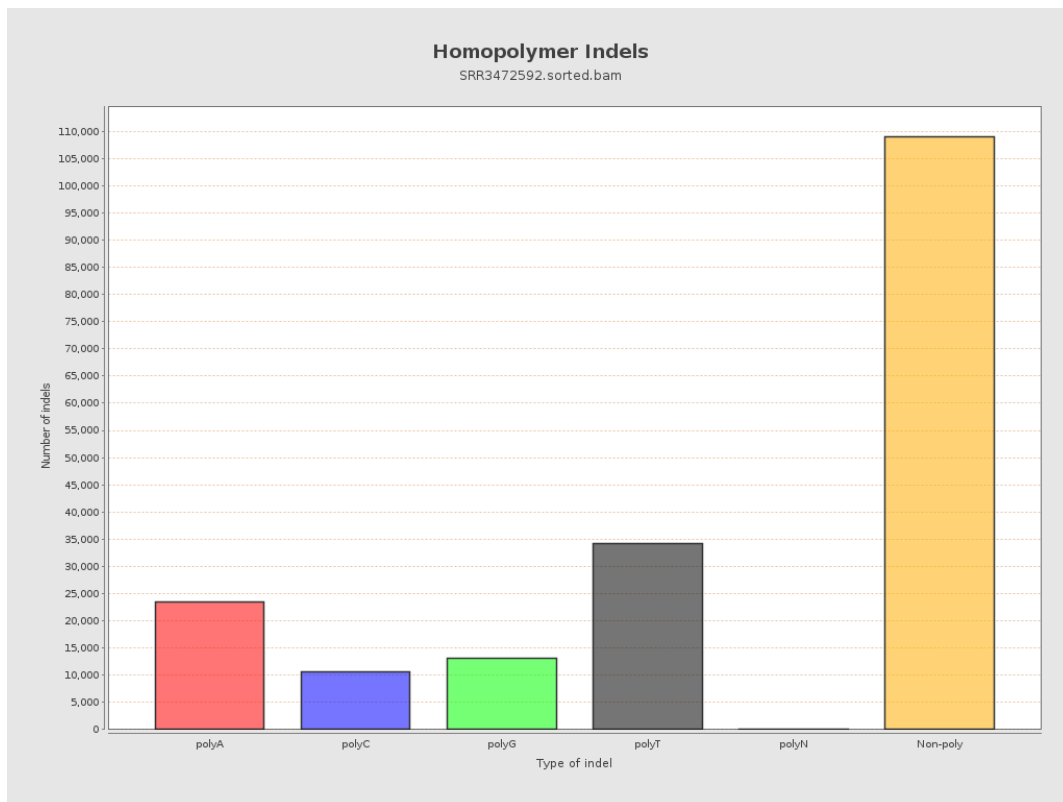
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



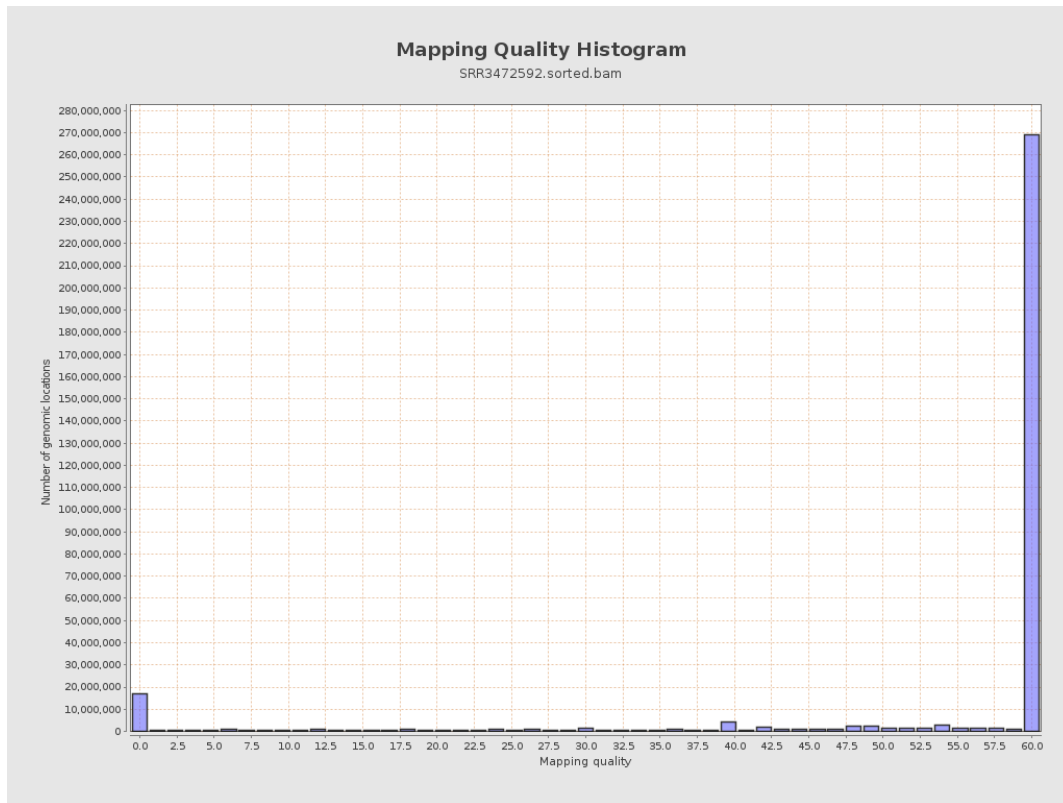
11. Results : Homopolymer Indels



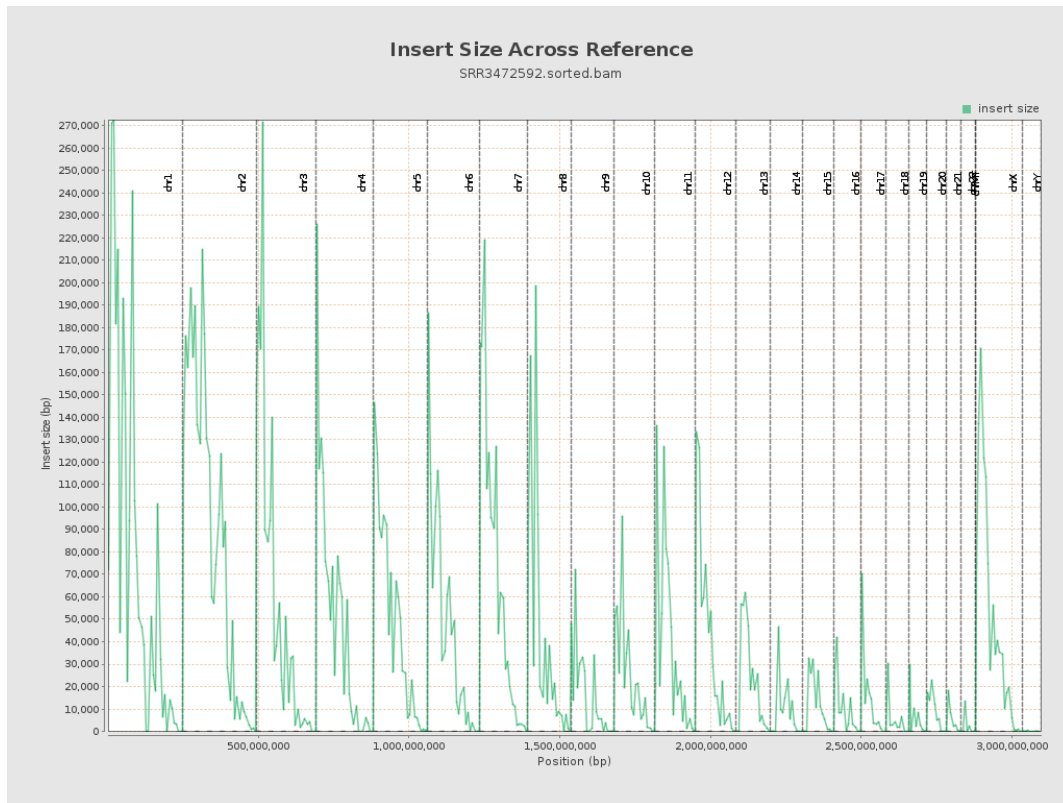
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

