

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 00:12:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472572.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_SRR3472572 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472572_1.fastq.gz SRR3472572_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 00:12:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472572.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,304,564
Mapped reads	6,717,702 / 91.97%
Unmapped reads	586,862 / 8.03%
Mapped paired reads	6,717,702 / 91.97%
Mapped reads, first in pair	3,384,502 / 46.33%
Mapped reads, second in pair	3,333,200 / 45.63%
Mapped reads, both in pair	6,563,194 / 89.85%
Mapped reads, singletons	154,508 / 2.12%
Secondary alignments	0
Supplementary alignments	228,067 / 3.12%
Read min/max/mean length	30 / 100 / 101.21
Duplicated reads (estimated)	1,059,107 / 14.5%
Duplication rate	14.04%
Clipped reads	5,249,373 / 71.86%

2.2. ACGT Content

Number/percentage of A's	139,495,373 / 25.77%
Number/percentage of C's	109,525,504 / 20.24%
Number/percentage of T's	159,688,582 / 29.51%
Number/percentage of G's	132,154,779 / 24.42%
Number/percentage of N's	359,131 / 0.07%

GC Percentage	44.65%
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2.3. Coverage

Mean	0.1749
Standard Deviation	1.696

2.4. Mapping Quality

Mean Mapping Quality	50.21
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2.5. Insert size

Mean	243,226.94
Standard Deviation	4,769,818.83
P25/Median/P75	86 / 122 / 169

2.6. Mismatches and indels

General error rate	1.21%
Mismatches	6,425,268
Insertions	52,629
Mapped reads with at least one insertion	0.77%
Deletions	122,392
Mapped reads with at least one deletion	1.78%
Homopolymer indels	42.06%

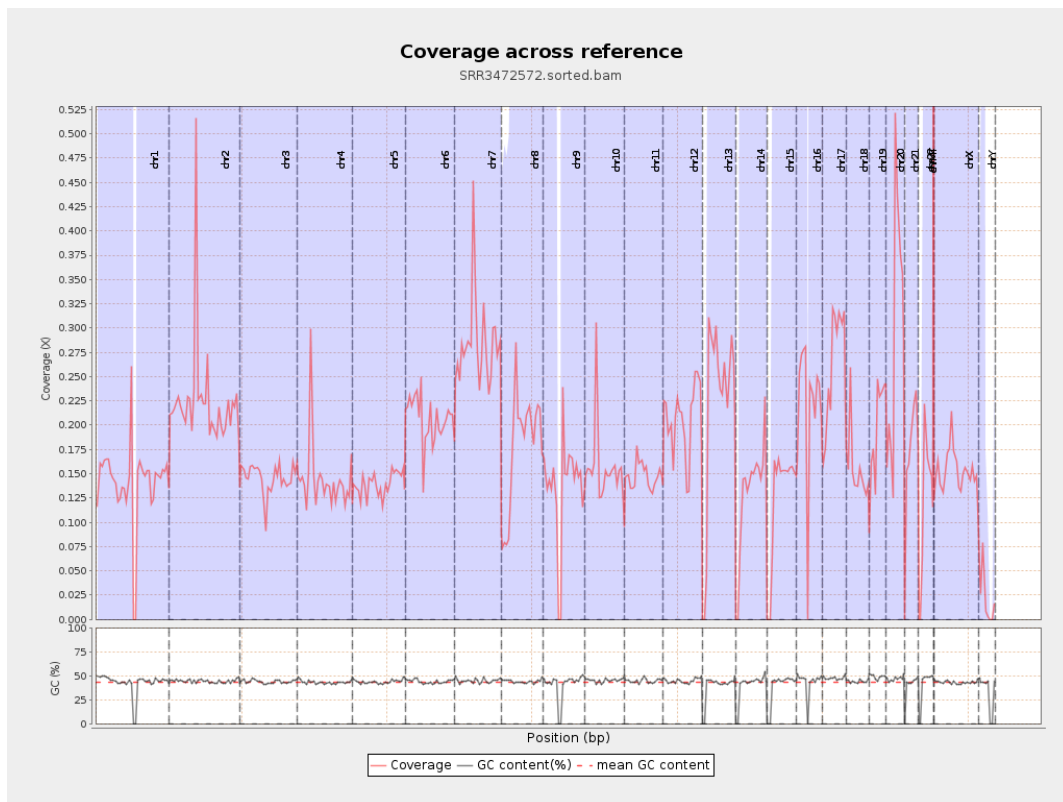
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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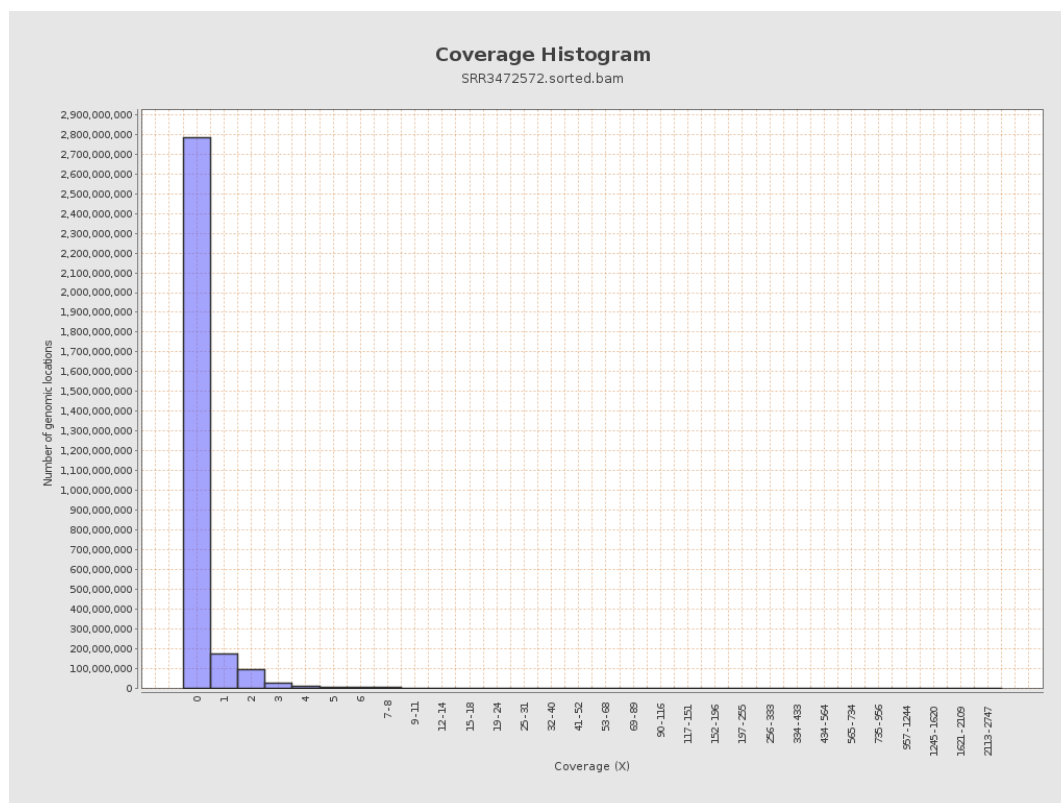
		bases	coverage	deviation
chr1	249250621	34965534	0.1403	2.2069
chr2	243199373	54644130	0.2247	2.3608
chr3	198022430	28783217	0.1454	0.5521
chr4	191154276	27403437	0.1434	0.9828
chr5	180915260	25274864	0.1397	0.5731
chr6	171115067	35331395	0.2065	0.9457
chr7	159138663	45334702	0.2849	3.1898
chr8	146364022	25979972	0.1775	1.5331
chr9	141213431	19094895	0.1352	1.7868
chr10	135534747	21104661	0.1557	1.6267
chr11	135006516	19759831	0.1464	1.2793
chr12	133851895	27535639	0.2057	0.6835
chr13	115169878	25615792	0.2224	0.7158
chr14	107349540	13971446	0.1301	3.4375
chr15	102531392	12990928	0.1267	0.5244
chr16	90354753	19959838	0.2209	1.0385
chr17	81195210	21471796	0.2644	1.4367
chr18	78077248	12201059	0.1563	3.1642
chr19	59128983	11747745	0.1987	1.6278
chr20	63025520	18783815	0.298	1.0509
chr21	48129895	8285072	0.1721	0.7815
chr22	51304566	6088807	0.1187	0.5129
chrMT	16571	17502	1.0562	4.0461
chrX	155270560	23819622	0.1534	0.8124

chrY	59373566	1289964	0.0217	0.8085
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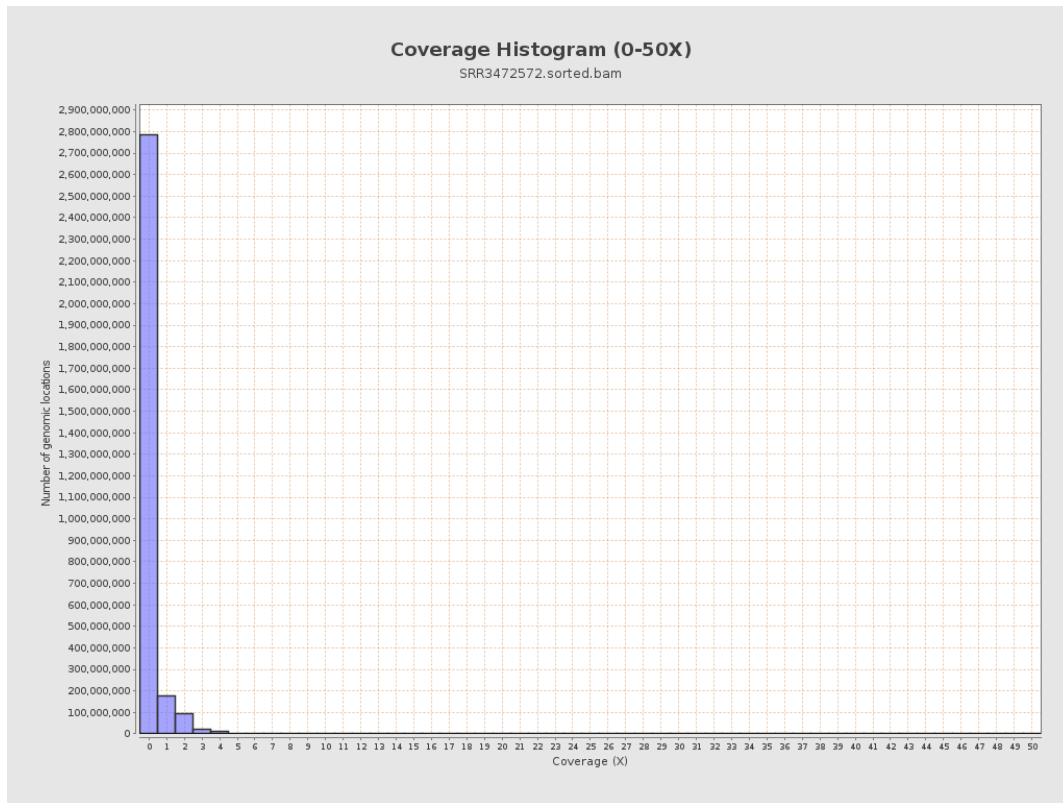
3. Results : Coverage across reference



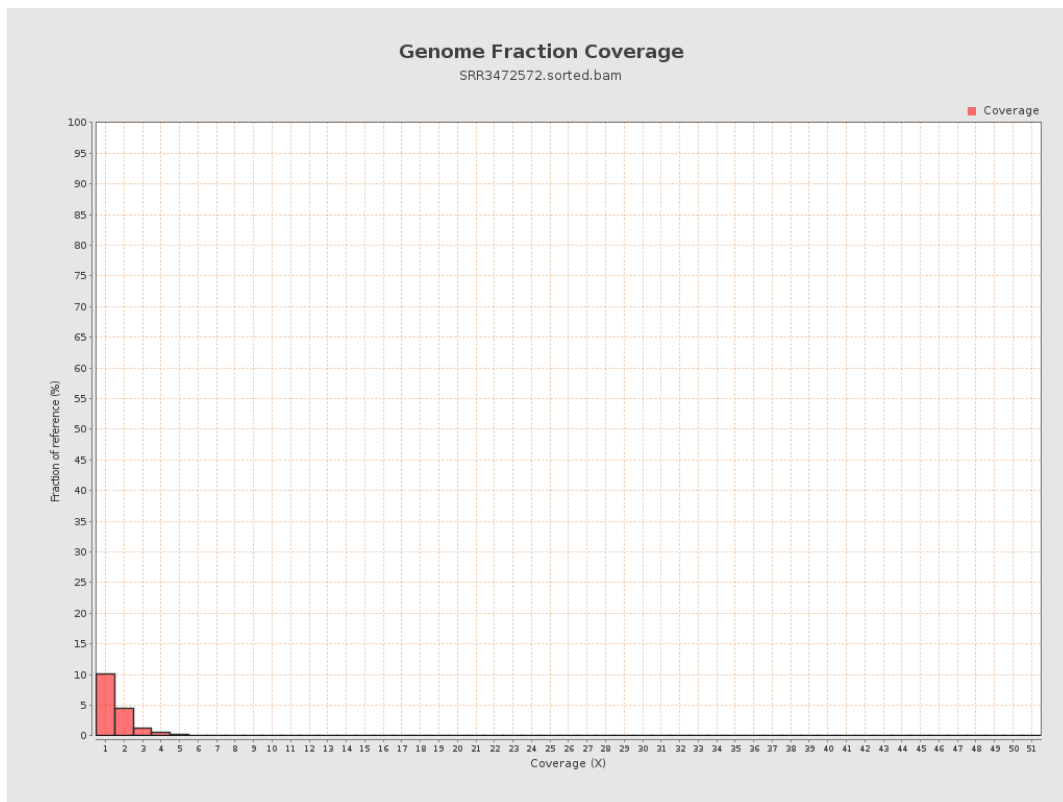
4. Results : Coverage Histogram



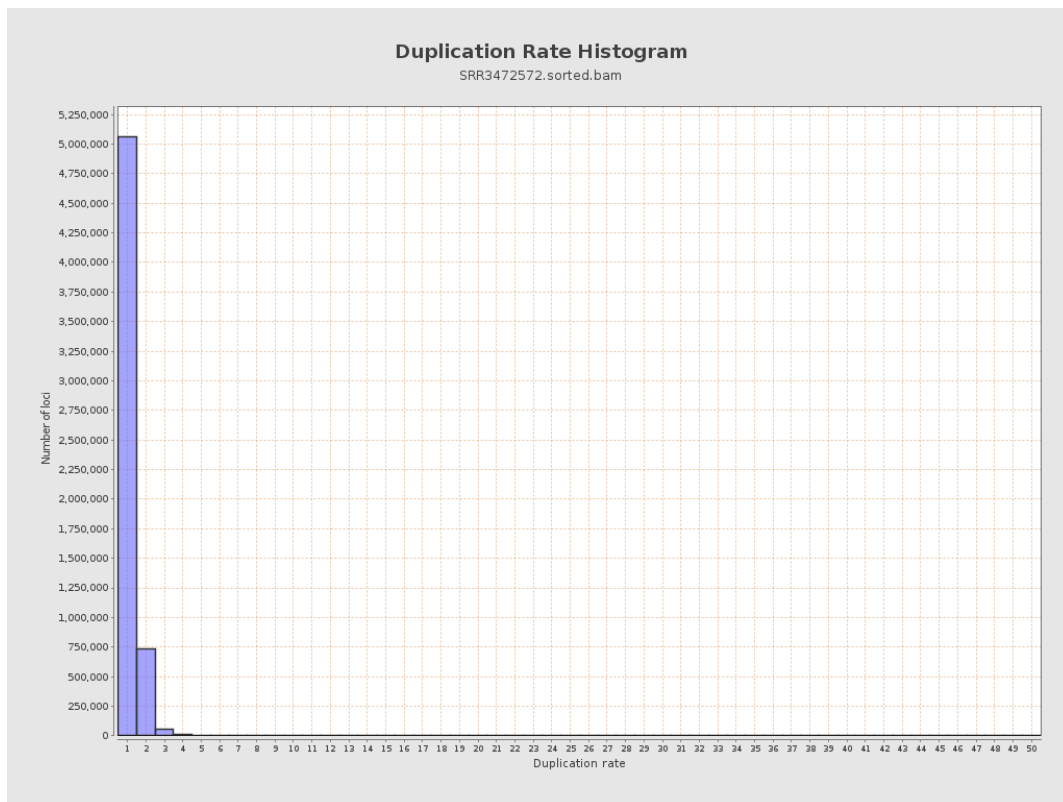
5. Results : Coverage Histogram (0-50X)



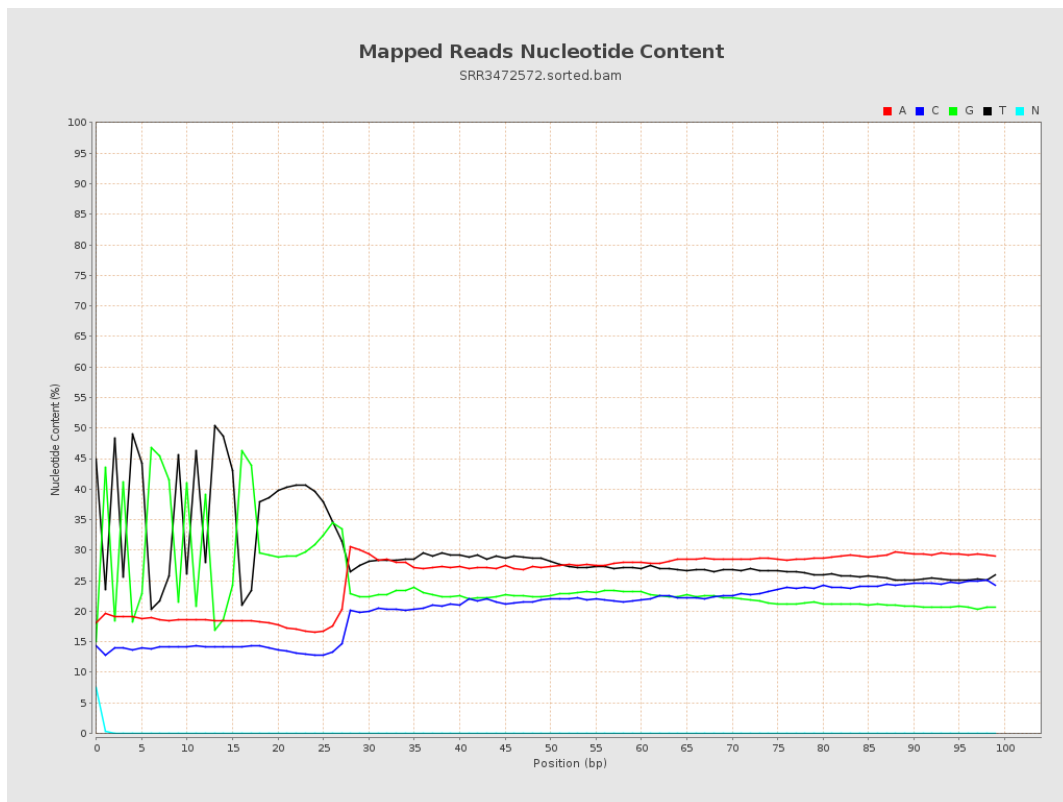
6. Results : Genome Fraction Coverage



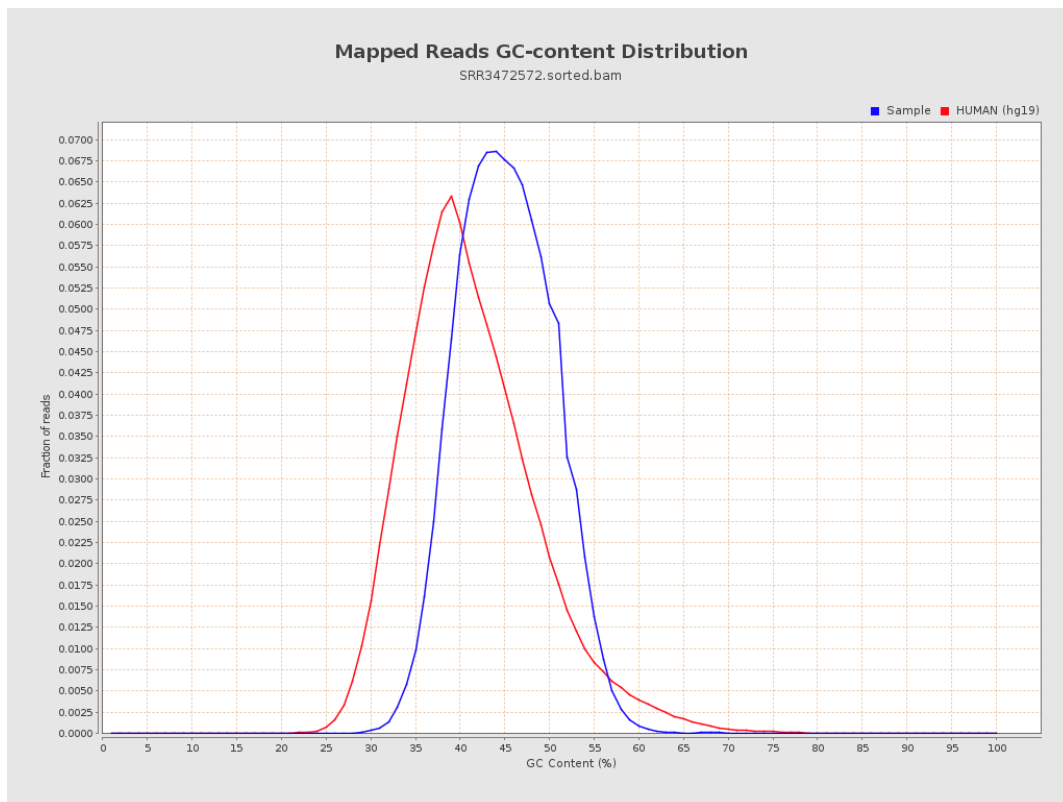
7. Results : Duplication Rate Histogram



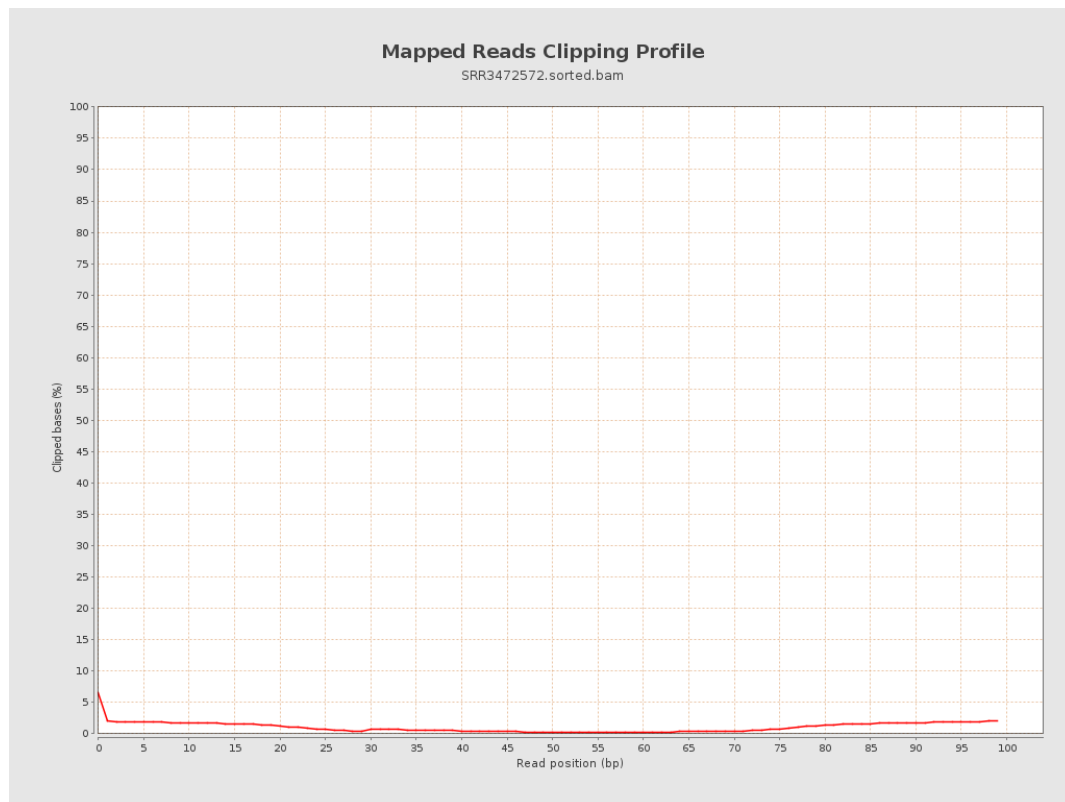
8. Results : Mapped Reads Nucleotide Content



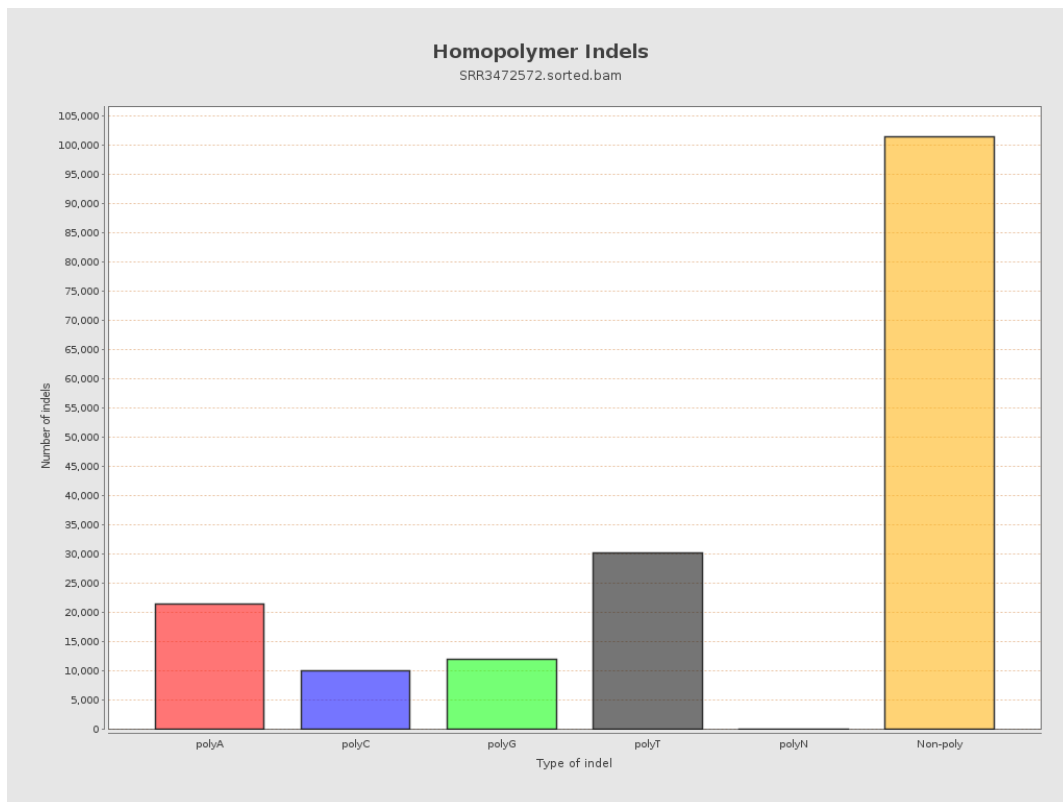
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



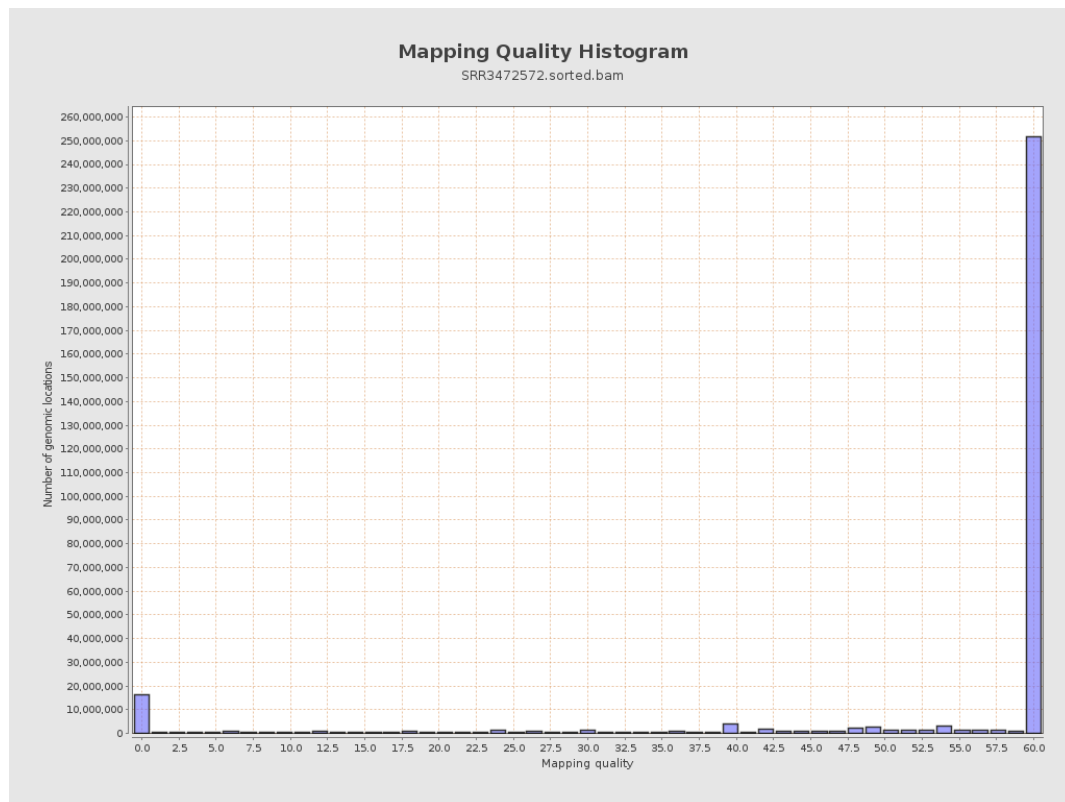
11. Results : Homopolymer Indels



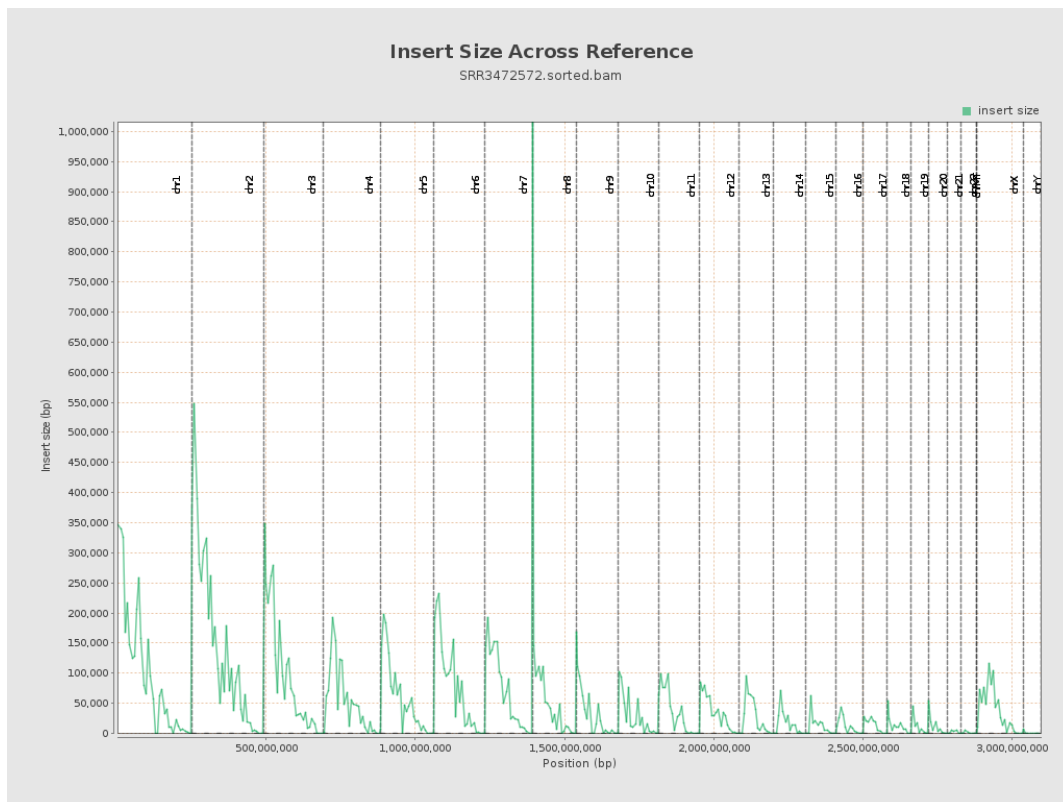
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

