Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 22:30:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472730.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_SRR3472730 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472730_1.fastq.gz SRR3472730_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 22:30:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472730.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,666,100
Mapped reads	13,546,704 / 99.13%
Unmapped reads	119,396 / 0.87%
Mapped paired reads	13,546,704 / 99.13%
Mapped reads, first in pair	6,795,162 / 49.72%
Mapped reads, second in pair	6,751,542 / 49.4%
Mapped reads, both in pair	13,475,638 / 98.61%
Mapped reads, singletons	71,066 / 0.52%
Secondary alignments	0
Supplementary alignments	66,506 / 0.49%
Read min/max/mean length	30 / 100 / 100.2
Duplicated reads (estimated)	8,215,625 / 60.12%
Duplication rate	46.31%
Clipped reads	1,040,998 / 7.62%

2.2. ACGT Content

Number/percentage of A's	363,378,387 / 27.18%
Number/percentage of C's	307,290,095 / 22.98%
Number/percentage of T's	361,715,568 / 27.05%
Number/percentage of G's	304,442,079 / 22.77%
Number/percentage of N's	259,030 / 0.02%

GC Percentage	45.75%

2.3. Coverage

Mean	0.432
Standard Deviation	14.3764

2.4. Mapping Quality

Mean Mapping Quality	55.19

2.5. Insert size

Mean	29,375.3
Standard Deviation	1,655,215.08
P25/Median/P75	166 / 227 / 306

2.6. Mismatches and indels

General error rate	0.6%
Mismatches	7,891,581
Insertions	78,417
Mapped reads with at least one insertion	0.57%
Deletions	70,376
Mapped reads with at least one deletion	0.51%
Homopolymer indels	44.34%

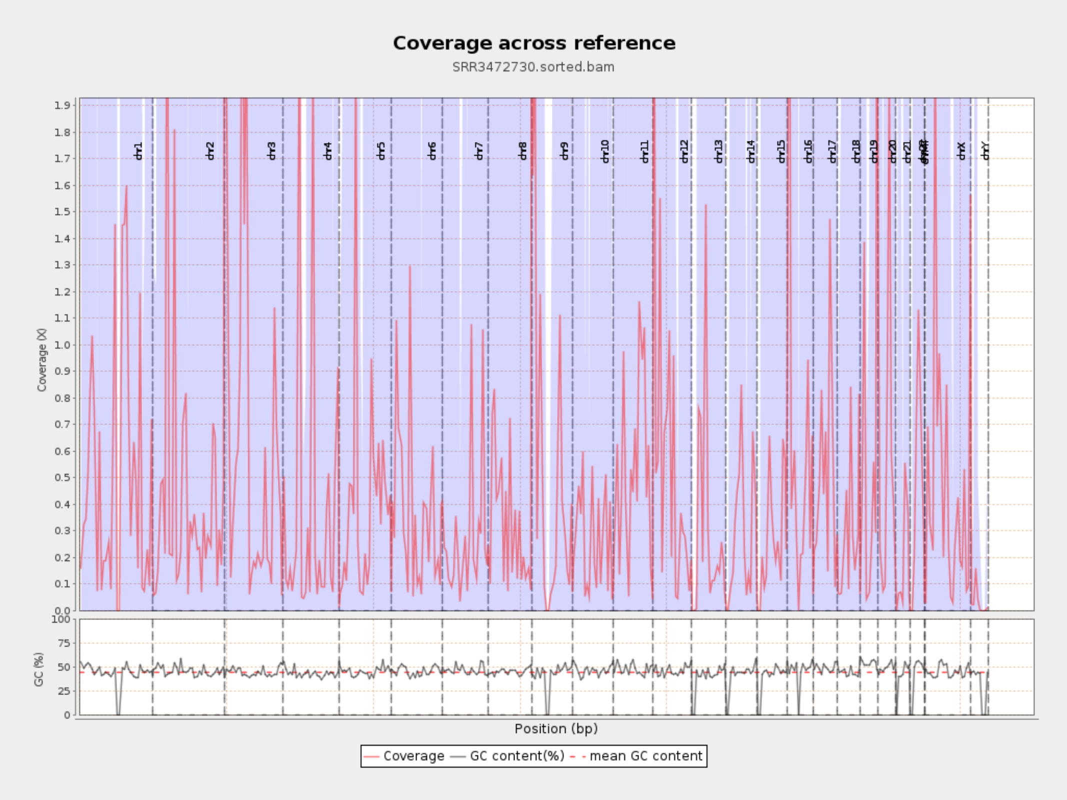
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

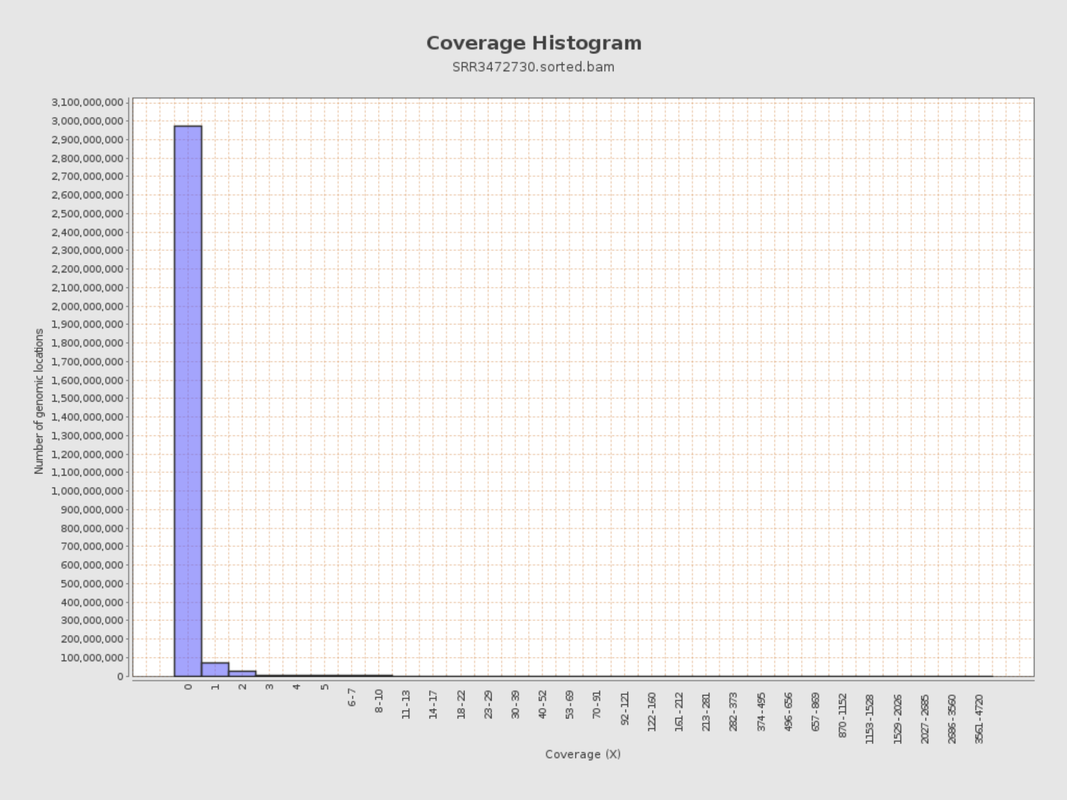
		bases	coverage	deviation
chr1	249250621	130643753	0.5241	15.0171
chr2	243199373	105390491	0.4334	20.8195
chr3	198022430	138359740	0.6987	15.493
chr4	191154276	72051347	0.3769	15.8474
chr5	180915260	74498672	0.4118	13.5904
chr6	171115067	63070167	0.3686	11.3668
chr7	159138663	45426582	0.2855	9.1438
chr8	146364022	47702455	0.3259	9.9832
chr9	141213431	76930884	0.5448	14.086
chr10	135534747	37216491	0.2746	9.2012
chr11	135006516	72392766	0.5362	16.6567
chr12	133851895	81088438	0.6058	17.1984
chr13	115169878	35404858	0.3074	11.1634
chr14	107349540	30437160	0.2835	10.2301
chr15	102531392	27771306	0.2709	7.2243
chr16	90354753	58867365	0.6515	19.2023
chr17	81195210	41454561	0.5106	12.0259
chr18	78077248	23479993	0.3007	11.0893
chr19	59128983	29243875	0.4946	14.4595
chr20	63025520	38898028	0.6172	21.2037
chr21	48129895	8648895	0.1797	12.3145
chr22	51304566	23105319	0.4504	13.7734
chrMT	16571	2193	0.1323	0.4111
chrX	155270560	73210741	0.4715	15.875

chrY	59373566	1958017	0.033	1.722

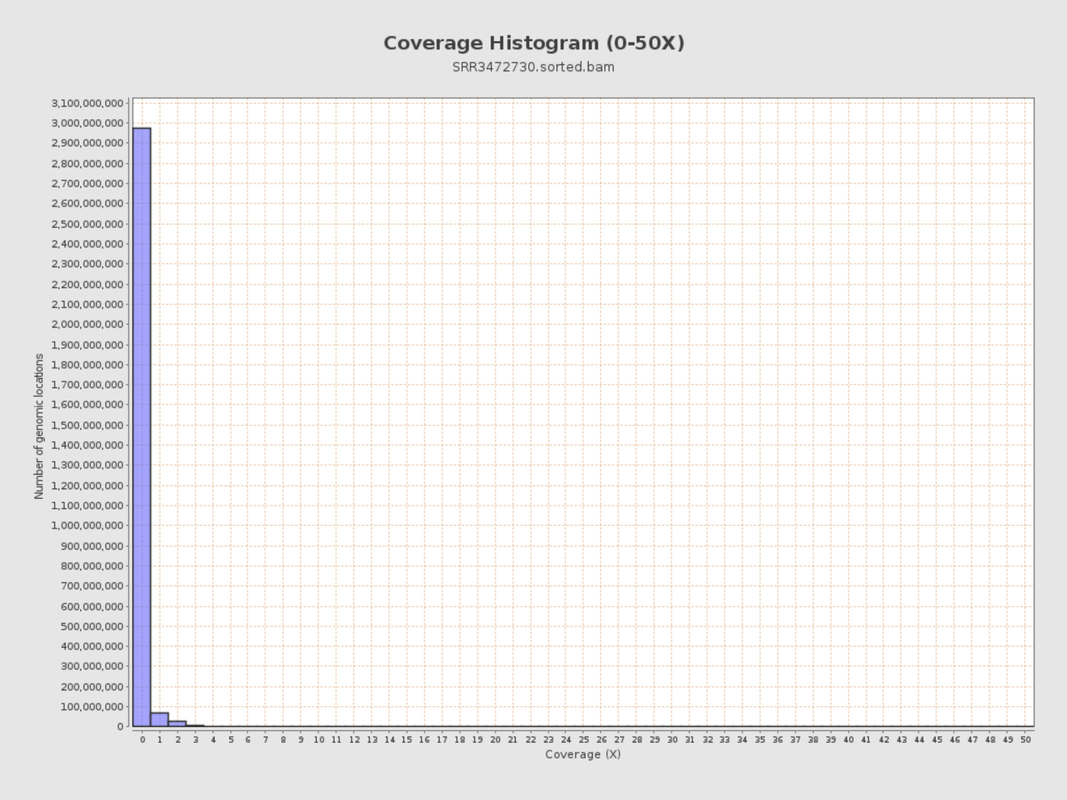
3. Results : Coverage across reference



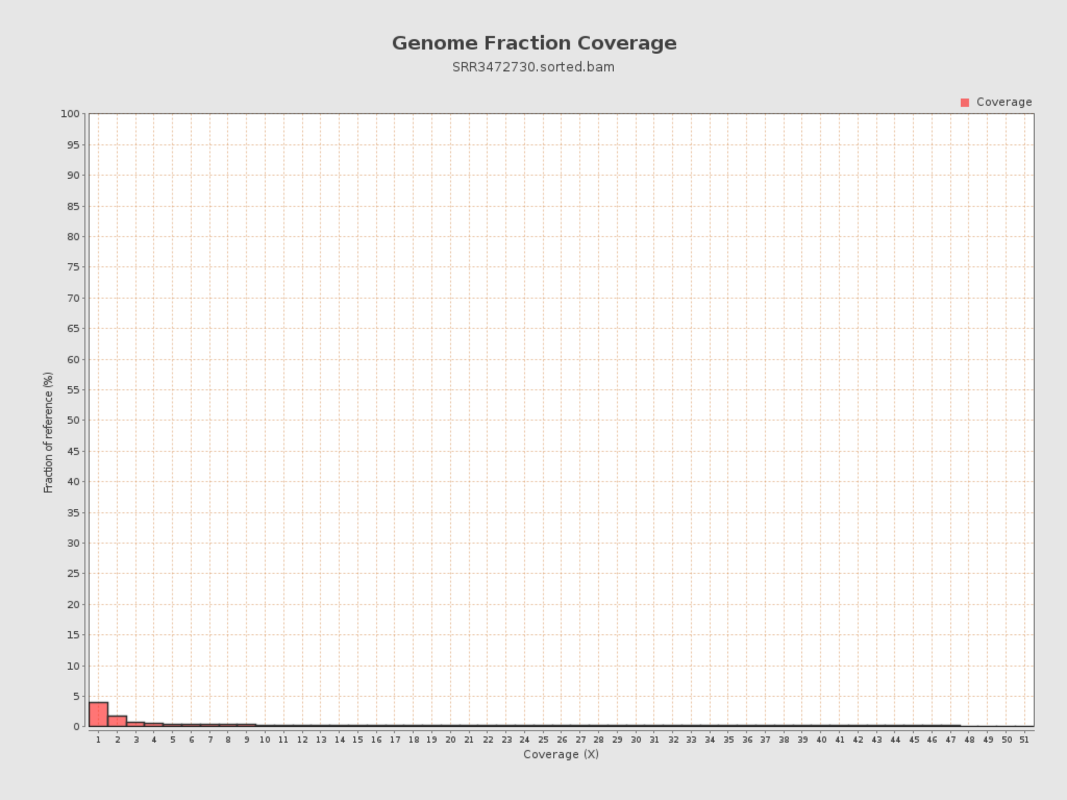
4. Results : Coverage Histogram



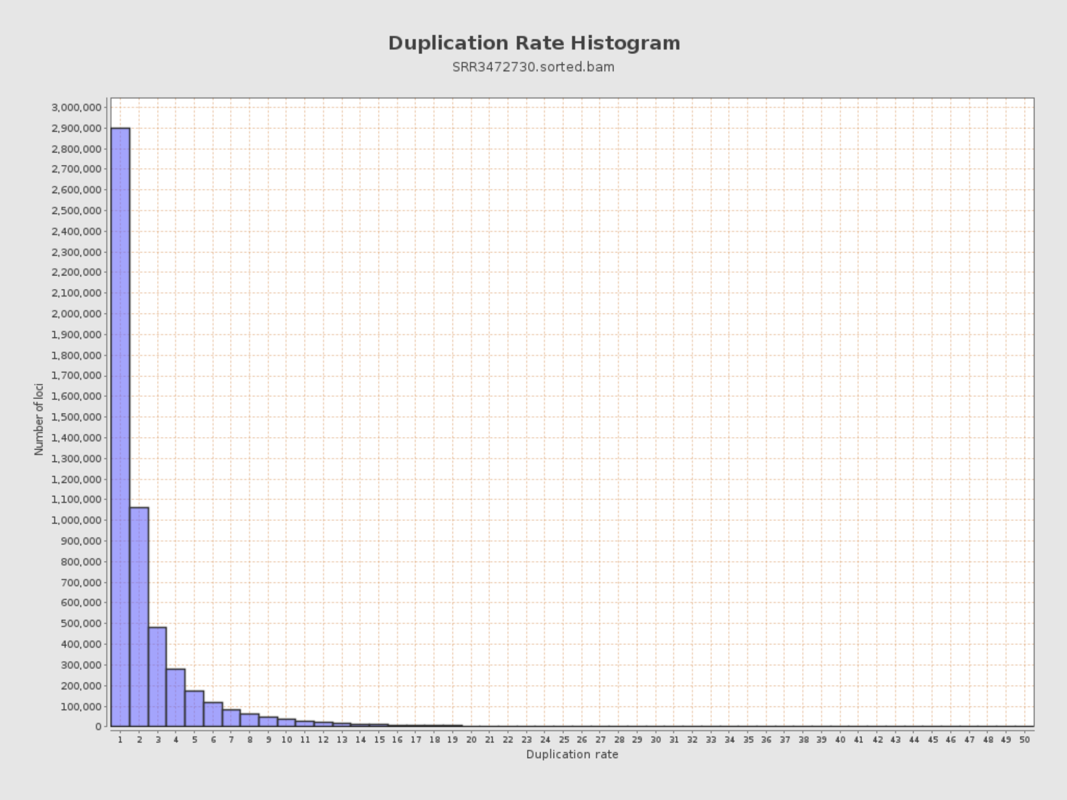
5. Results : Coverage Histogram (0-50X)



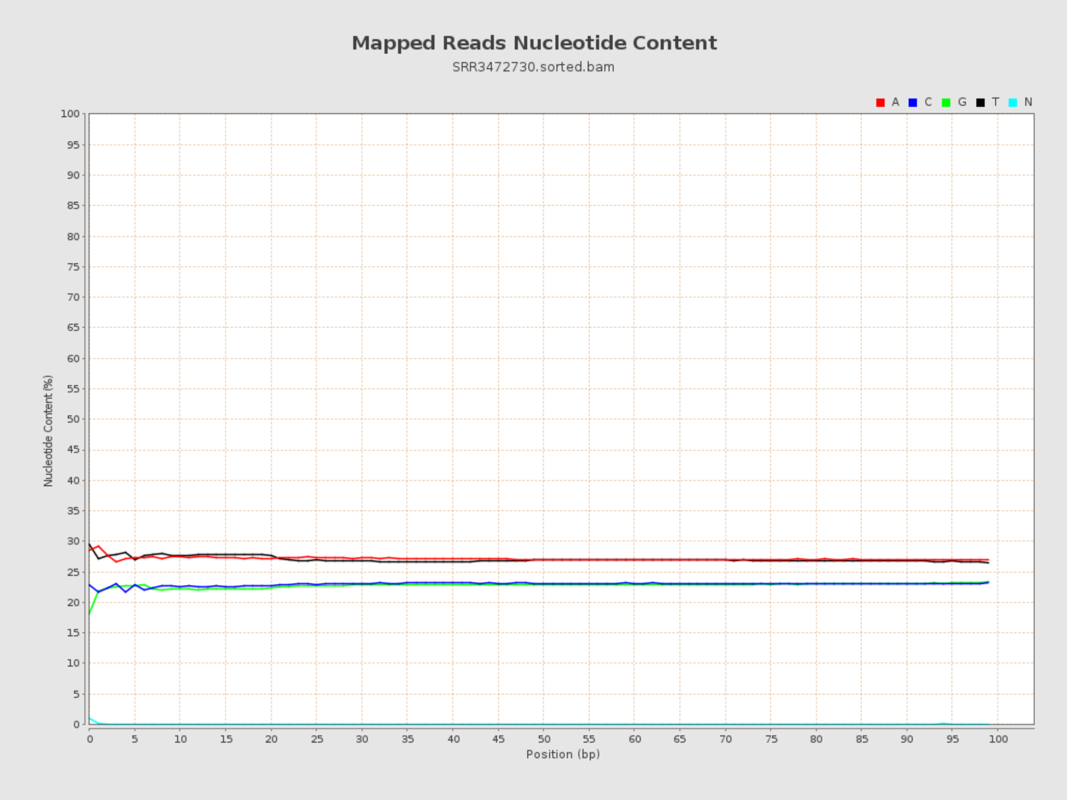
6. Results : Genome Fraction Coverage



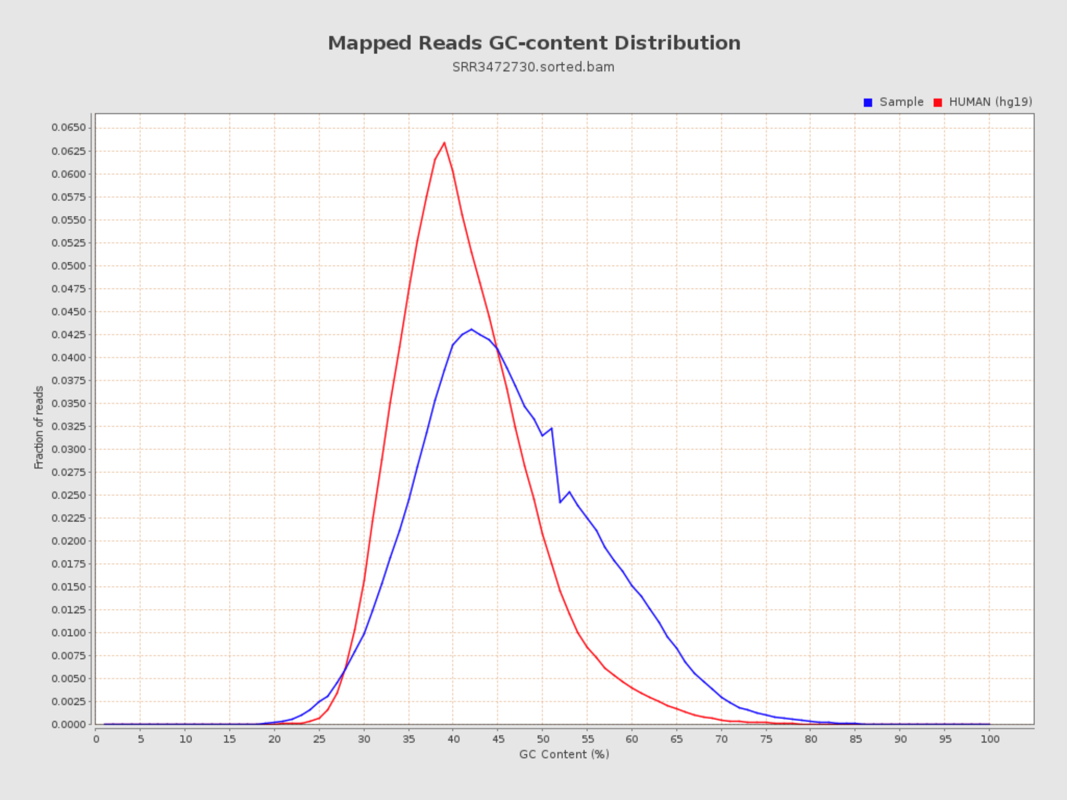
7. Results : Duplication Rate Histogram



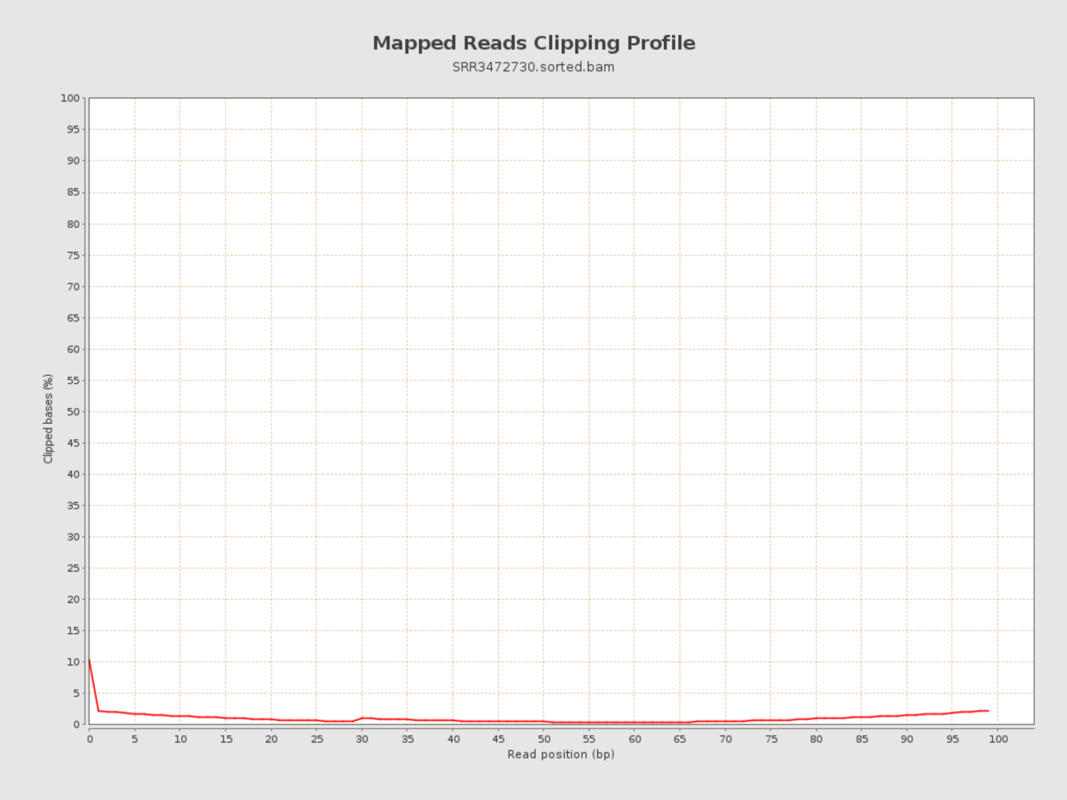
8. Results : Mapped Reads Nucleotide Content



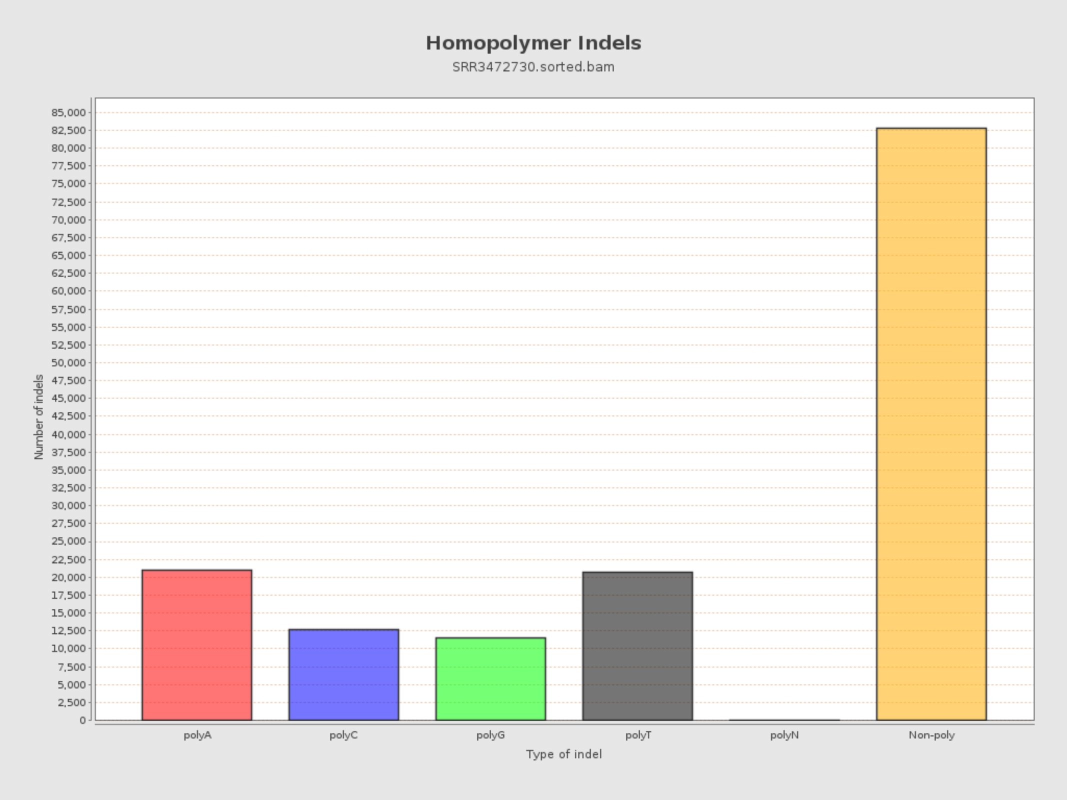
9. Results : Mapped Reads GC-content Distribution



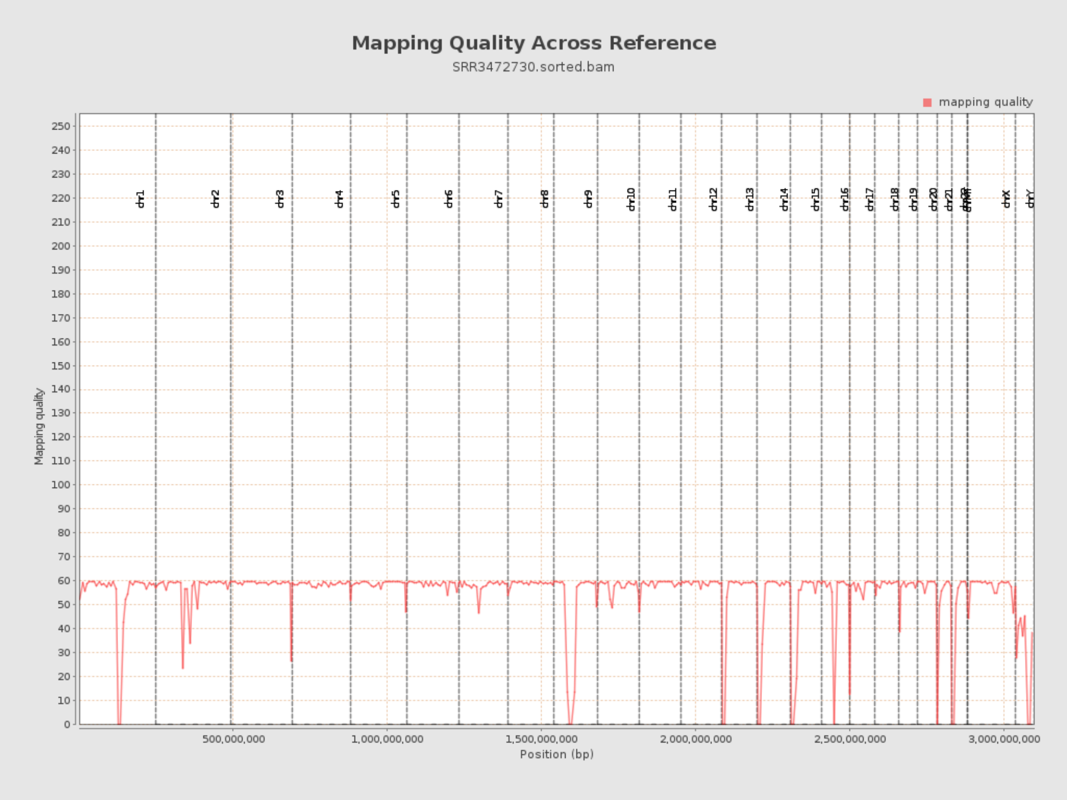
10. Results : Mapped Reads Clipping Profile



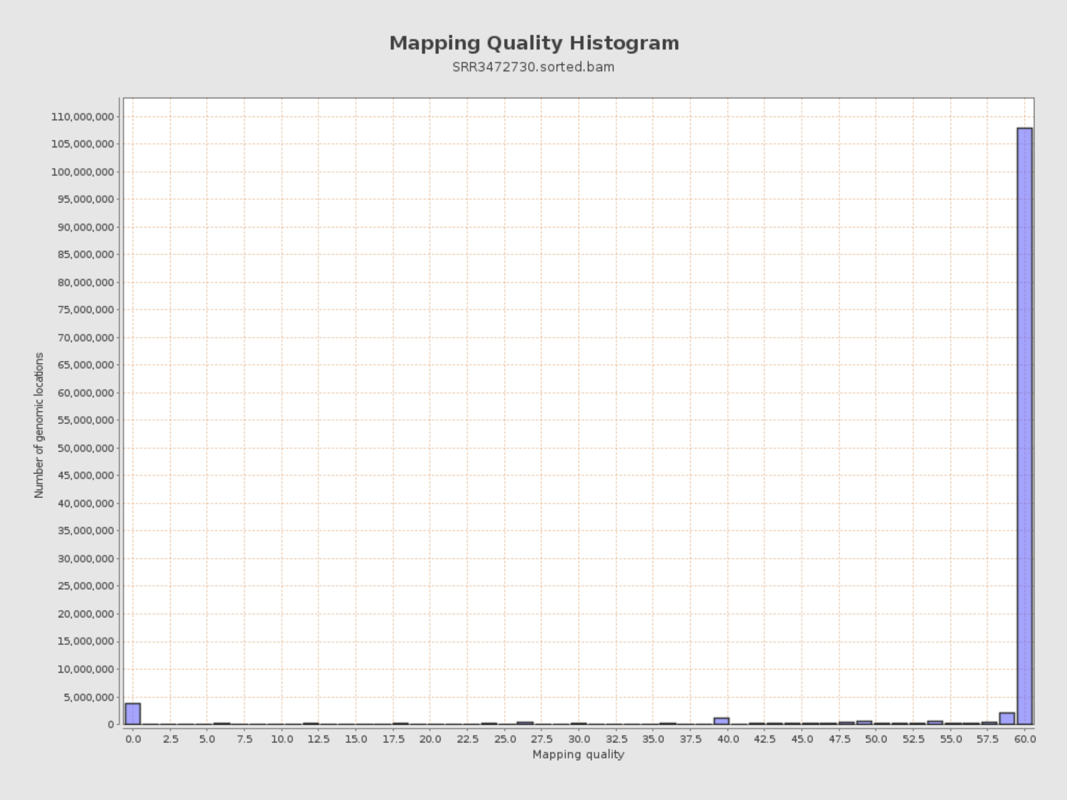
11. Results : Homopolymer Indels



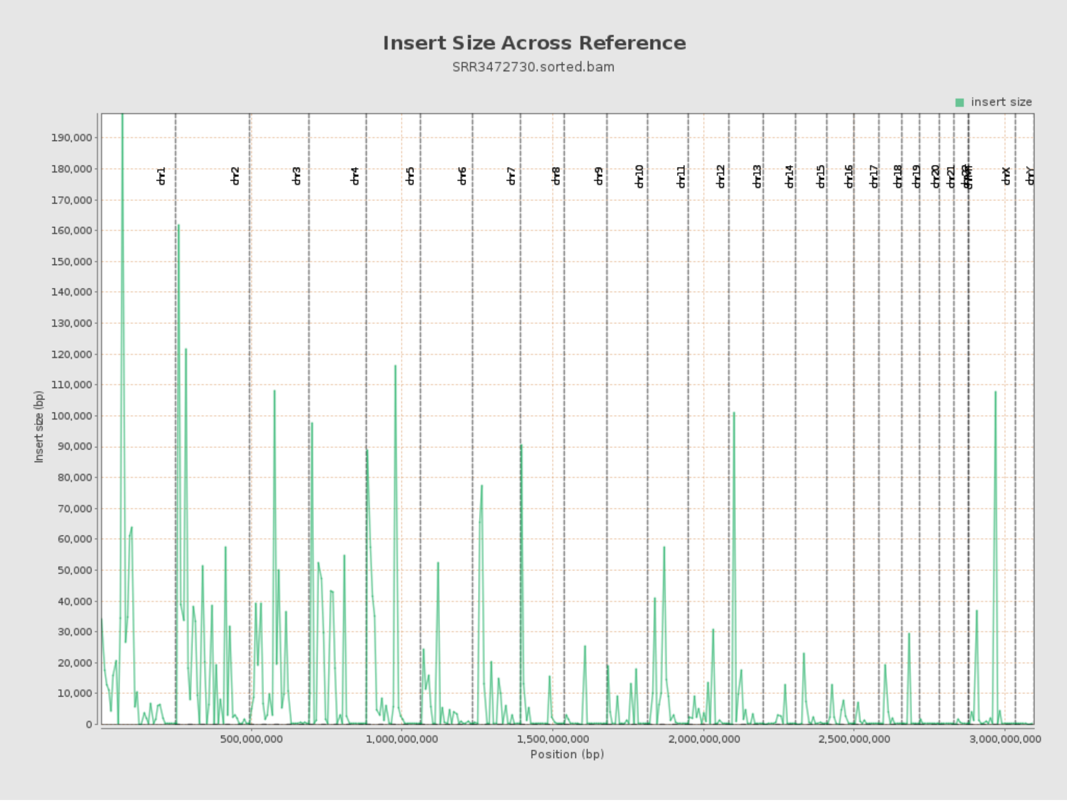
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram