Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 01:57:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472740.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_SRR3472740 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472740_1.fastq.gz SRR3472740_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 01:57:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472740.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,245,516
Mapped reads	15,088,646 / 98.97%
Unmapped reads	156,870 / 1.03%
Mapped paired reads	15,088,646 / 98.97%
Mapped reads, first in pair	7,574,372 / 49.68%
Mapped reads, second in pair	7,514,274 / 49.29%
Mapped reads, both in pair	14,994,196 / 98.35%
Mapped reads, singletons	94,450 / 0.62%
Secondary alignments	0
Supplementary alignments	56,625 / 0.37%
Read min/max/mean length	30 / 100 / 100.15
Duplicated reads (estimated)	9,216,507 / 60.45%
Duplication rate	46.36%
Clipped reads	1,100,063 / 7.22%

2.2. ACGT Content

Number/percentage of A's	413,037,172 / 27.75%
Number/percentage of C's	333,270,165 / 22.39%
Number/percentage of T's	410,024,577 / 27.55%
Number/percentage of G's	331,720,688 / 22.29%
Number/percentage of N's	287,313 / 0.02%

GC Percentage	44.68%

2.3. Coverage

Mean	0.4808
Standard Deviation	16.2607

2.4. Mapping Quality

Mean Mapping Quality	55.07

2.5. Insert size

Mean	24,400.12
Standard Deviation	1,541,783.25
P25/Median/P75	182 / 253 / 339

2.6. Mismatches and indels

General error rate	0.63%
Mismatches	9,196,302
Insertions	90,385
Mapped reads with at least one insertion	0.59%
Deletions	85,757
Mapped reads with at least one deletion	0.56%
Homopolymer indels	46.14%

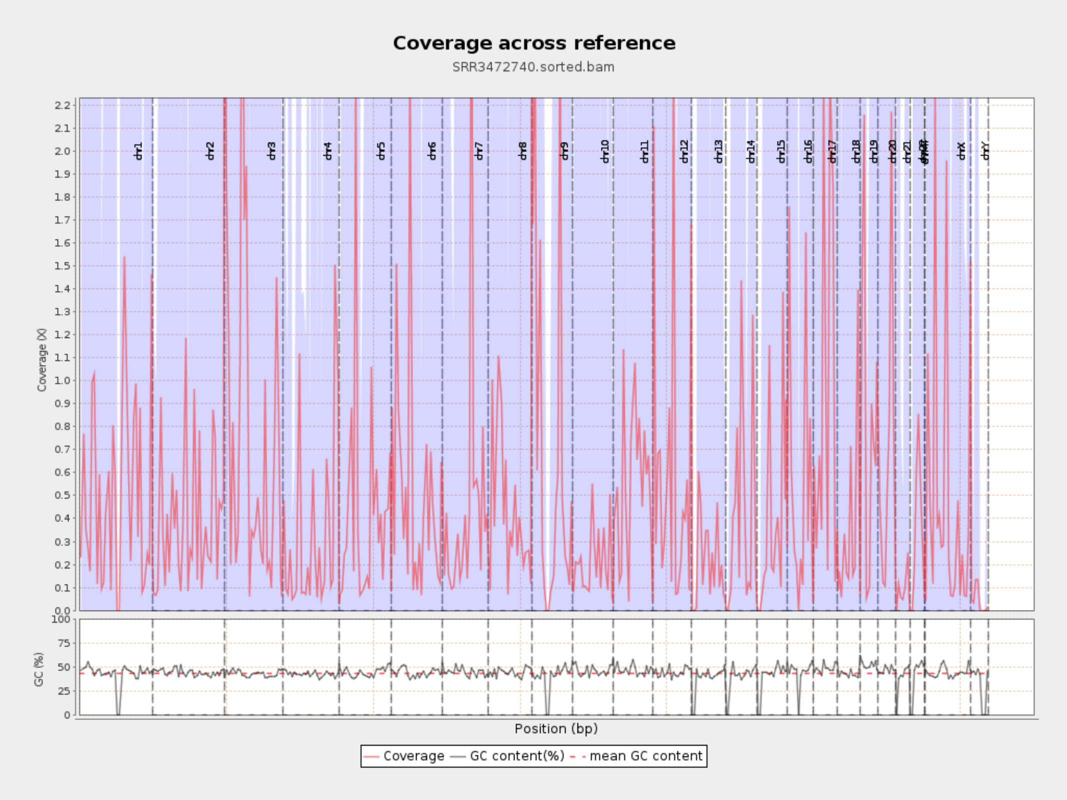
2.7. Chromosome stats

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

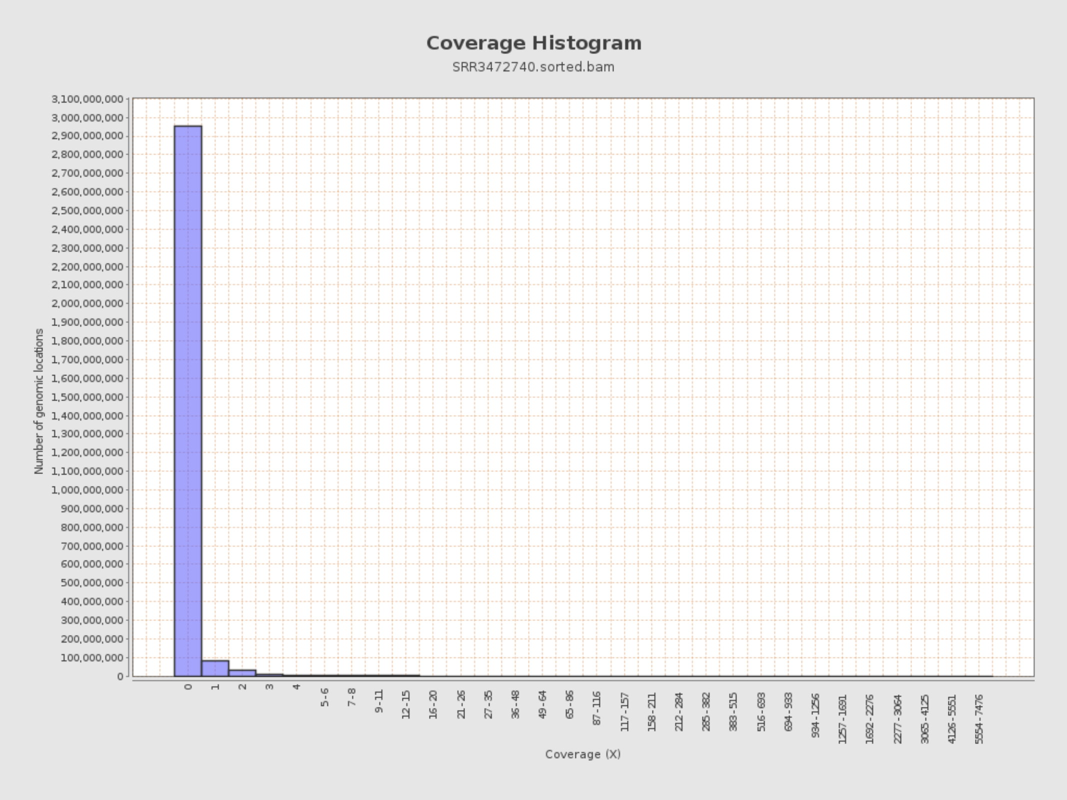
		bases	coverage	deviation
chr1	249250621	130032561	0.5217	15.2576
chr2	243199373	93338399	0.3838	11.7158
chr3	198022430	160861042	0.8123	18.2771
chr4	191154276	60241543	0.3151	13.2005
chr5	180915260	78384552	0.4333	13.6708
chr6	171115067	88321612	0.5162	13.7916
chr7	159138663	75097697	0.4719	15.594
chr8	146364022	63987654	0.4372	12.4426
chr9	141213431	97373066	0.6895	22.4957
chr10	135534747	28751212	0.2121	7.0917
chr11	135006516	77691387	0.5755	17.8291
chr12	133851895	82249633	0.6145	18.4799
chr13	115169878	24596948	0.2136	6.9738
chr14	107349540	43261204	0.403	15.9672
chr15	102531392	38544767	0.3759	17.4618
chr16	90354753	49012616	0.5424	22.0188
chr17	81195210	76675889	0.9443	28.6308
chr18	78077248	28598543	0.3663	11.1054
chr19	59128983	49376204	0.8351	25.0452
chr20	63025520	43867286	0.696	33.4334
chr21	48129895	4747254	0.0986	4.1064
chr22	51304566	17056994	0.3325	7.7232
chrMT	16571	5252	0.3169	1.1205
chrX	155270560	73761066	0.475	15.4739

chrY	59373566	2717426	0.0458	1.4358

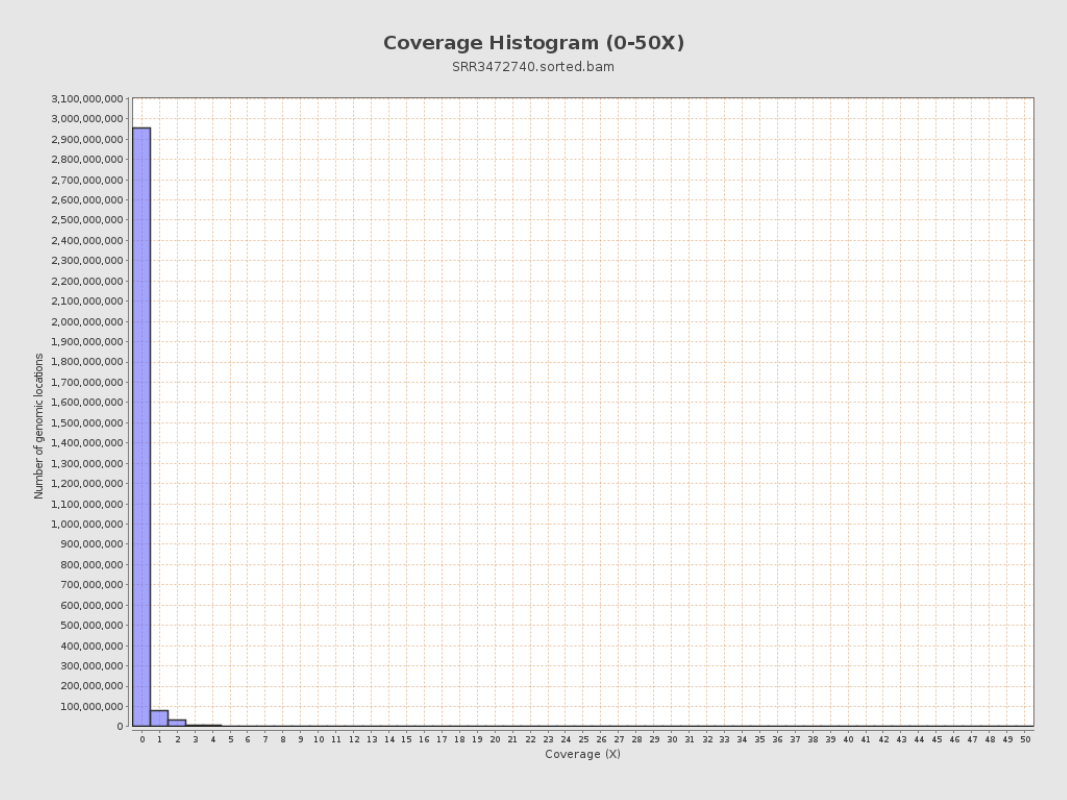
3. Results : Coverage across reference



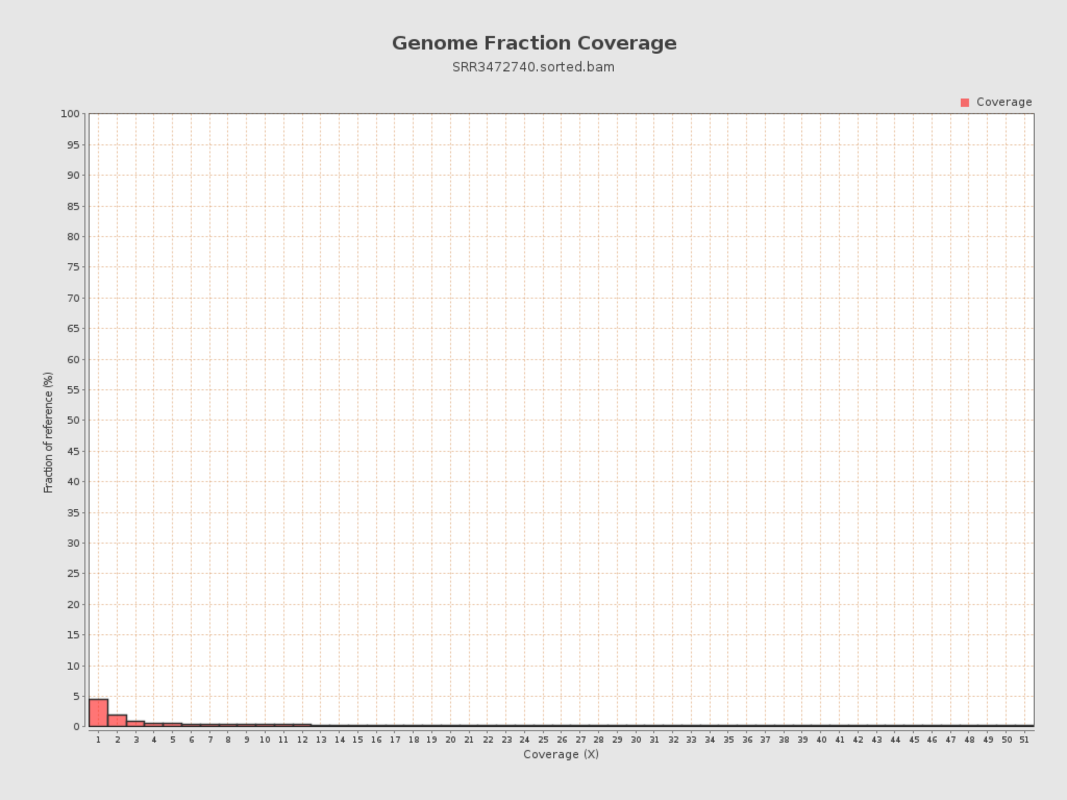
4. Results : Coverage Histogram



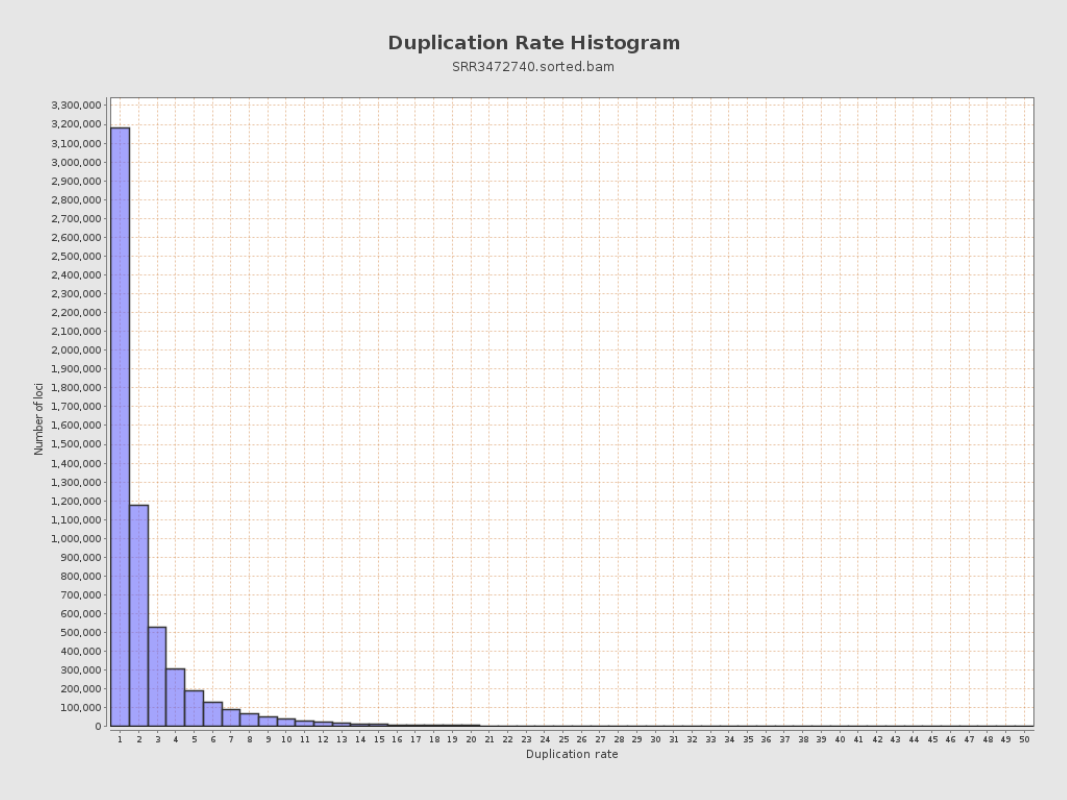
5. Results : Coverage Histogram (0-50X)



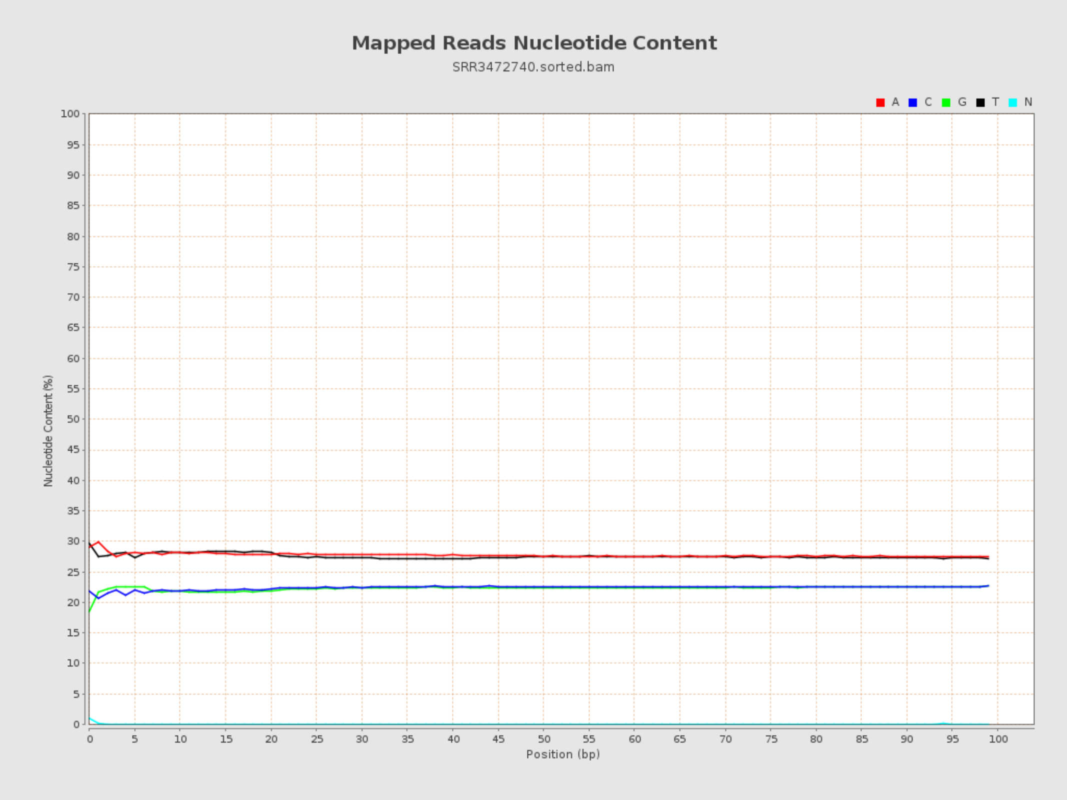
6. Results : Genome Fraction Coverage



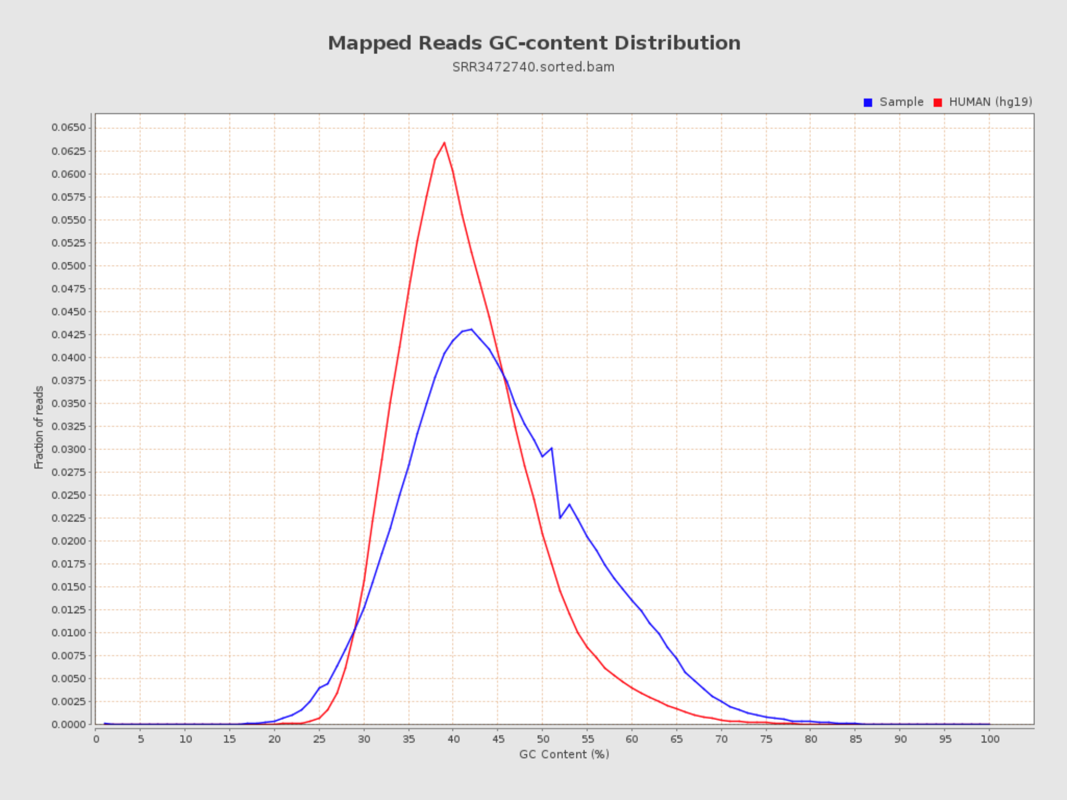
7. Results : Duplication Rate Histogram



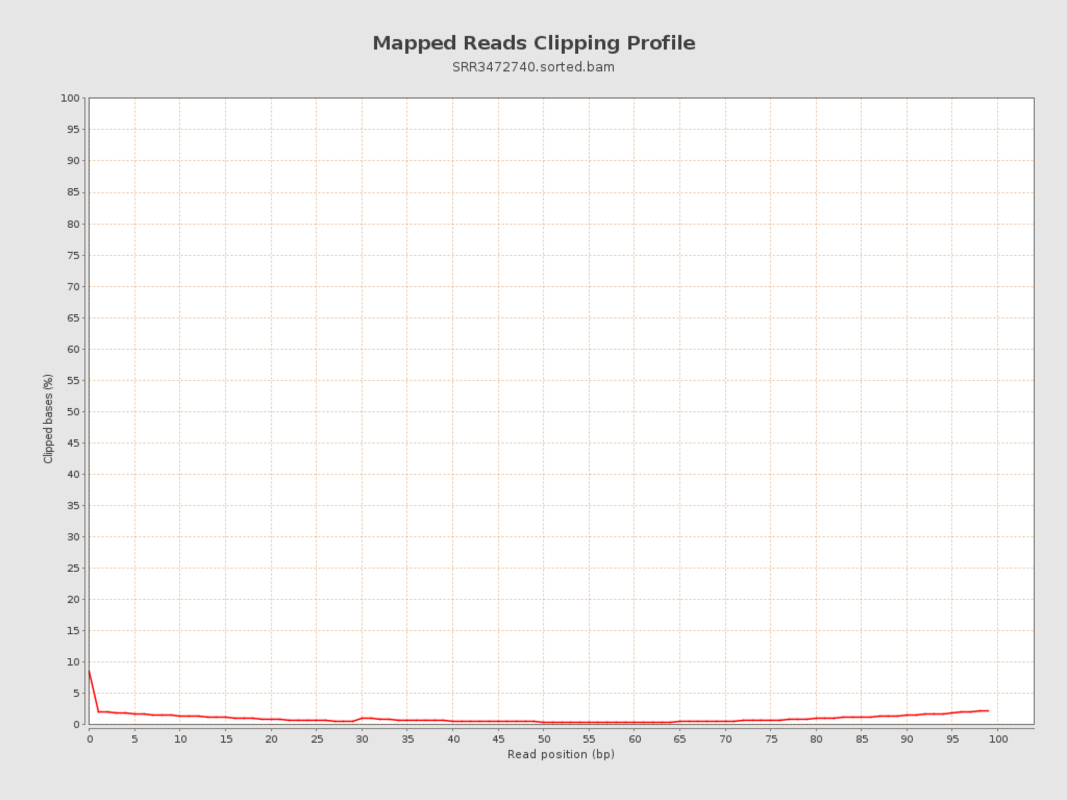
8. Results : Mapped Reads Nucleotide Content



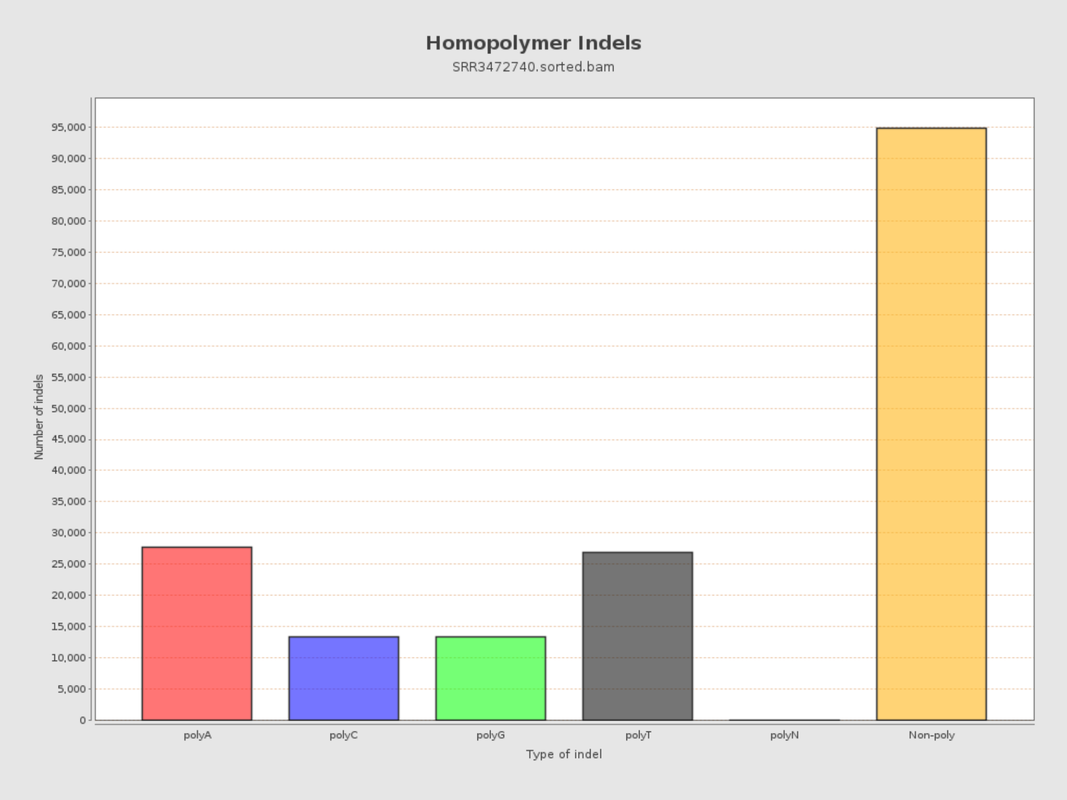
9. Results : Mapped Reads GC-content Distribution



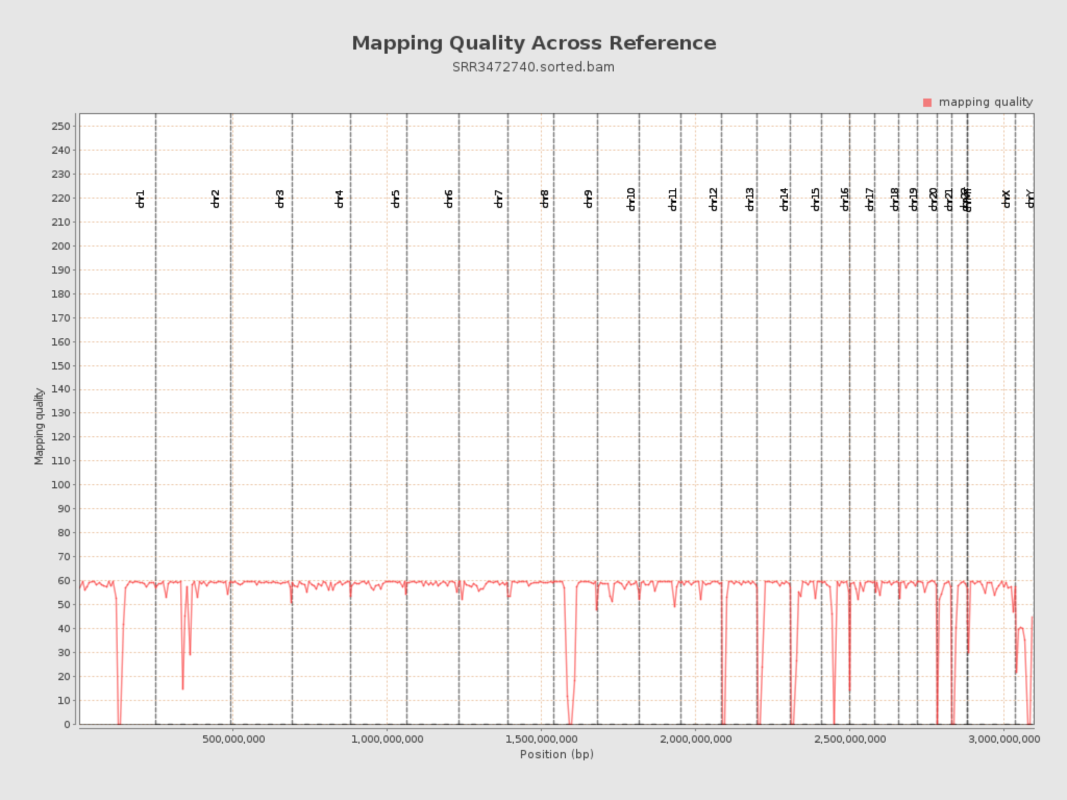
10. Results : Mapped Reads Clipping Profile



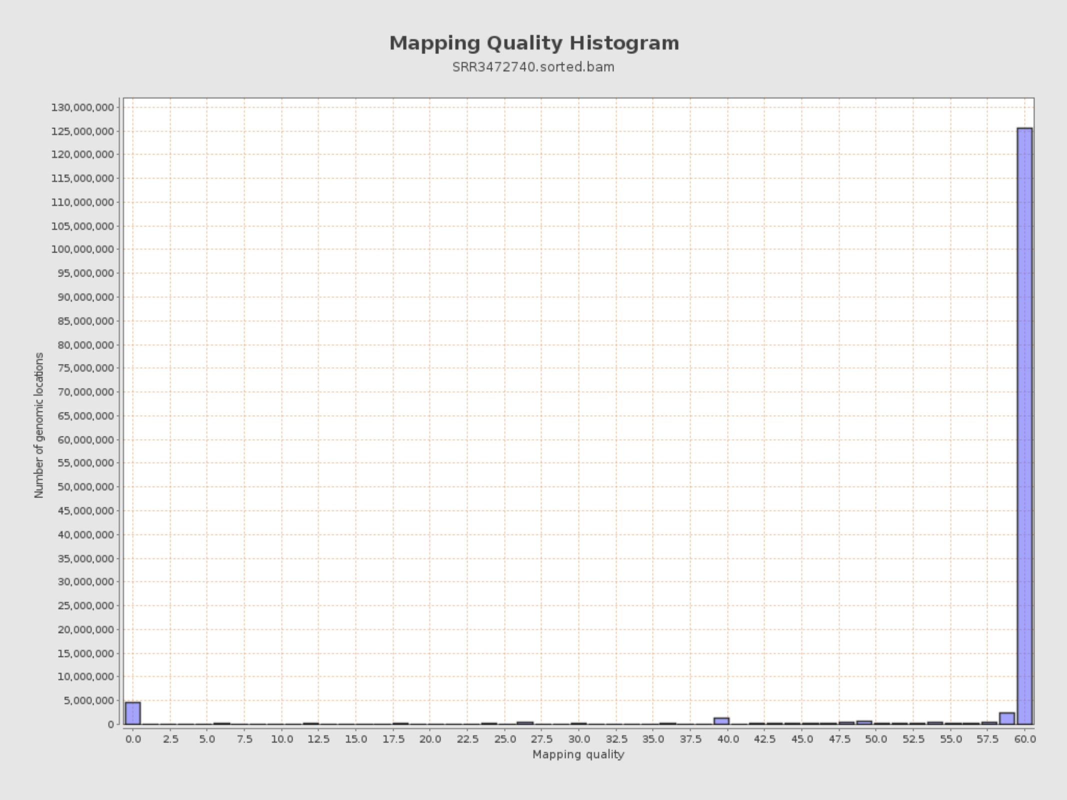
11. Results : Homopolymer Indels



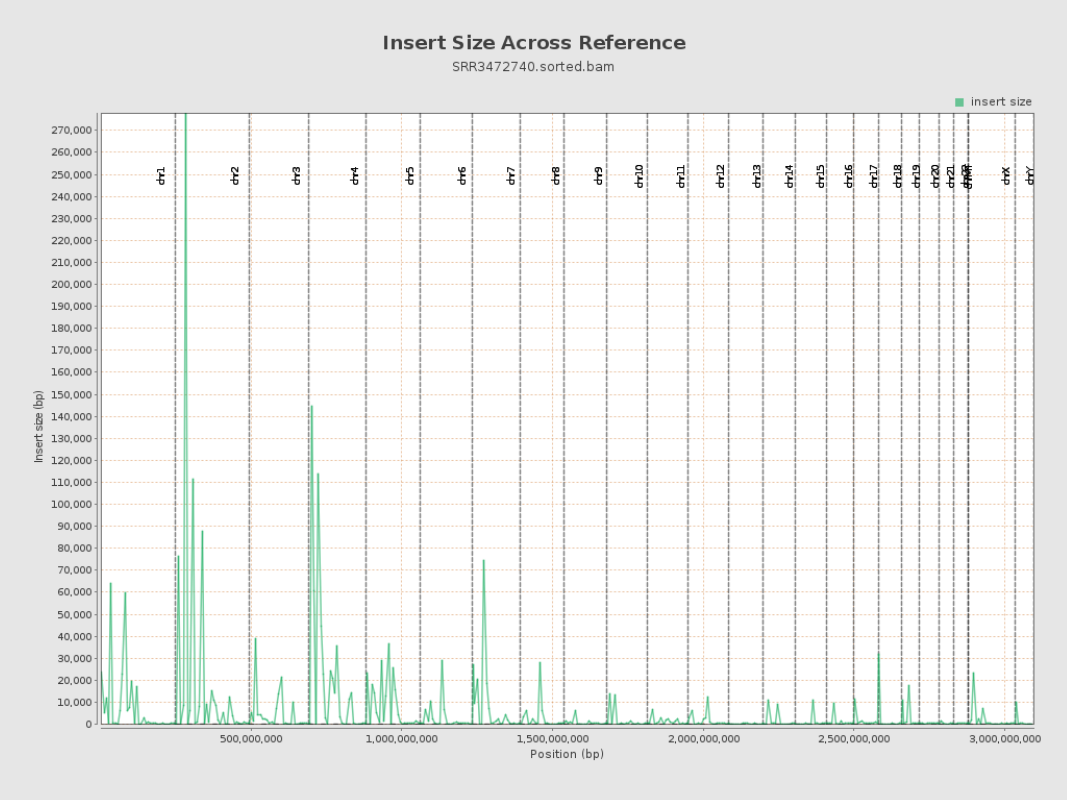
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram