Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 11:38:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472769.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_SRR3472769 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472769_1.fastq.gz SRR3472769_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 11:38:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472769.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,852,902
Mapped reads	12,726,198 / 99.01%
Unmapped reads	126,704 / 0.99%
Mapped paired reads	12,726,198 / 99.01%
Mapped reads, first in pair	6,386,768 / 49.69%
Mapped reads, second in pair	6,339,430 / 49.32%
Mapped reads, both in pair	12,649,002 / 98.41%
Mapped reads, singletons	77,196 / 0.6%
Secondary alignments	0
Supplementary alignments	73,626 / 0.57%
Read min/max/mean length	30 / 100 / 100.23
Duplicated reads (estimated)	7,683,519 / 59.78%
Duplication rate	45.61%
Clipped reads	1,162,157 / 9.04%

2.2. ACGT Content

Number/percentage of A's	337,503,052 / 26.96%
Number/percentage of C's	290,339,627 / 23.19%
Number/percentage of T's	336,061,070 / 26.84%
Number/percentage of G's	287,715,522 / 22.98%
Number/percentage of N's	243,880 / 0.02%

GC Percentage	46.18%

2.3. Coverage

Mean	0.4044
Standard Deviation	14.9423

2.4. Mapping Quality

Mean Mapping Quality	55.14

2.5. Insert size

Mean	39,323.54
Standard Deviation	1,954,230.22
P25/Median/P75	163 / 228 / 307

2.6. Mismatches and indels

General error rate	0.59%
Mismatches	7,236,064
Insertions	69,130
Mapped reads with at least one insertion	0.54%
Deletions	67,051
Mapped reads with at least one deletion	0.52%
Homopolymer indels	44.95%

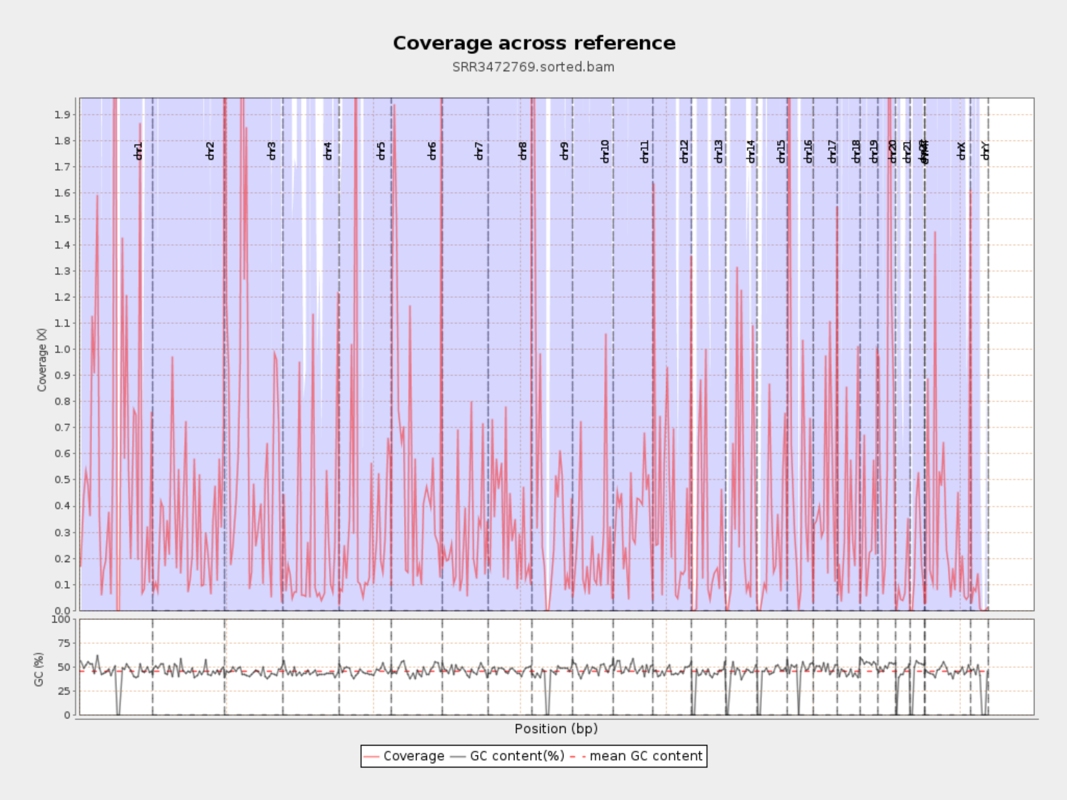
2.7. Chromosome stats

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

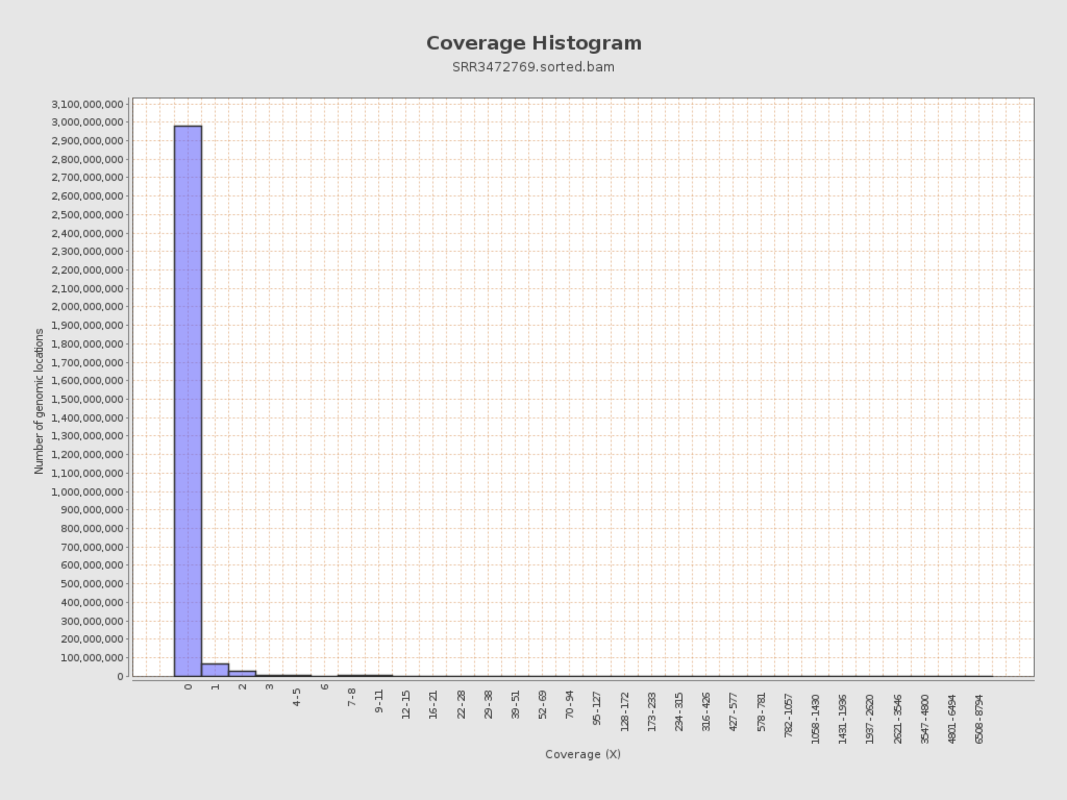
		bases	coverage	deviation
chr1	249250621	154358293	0.6193	25.8286
chr2	243199373	76225656	0.3134	9.4727
chr3	198022430	137516912	0.6945	15.5914
chr4	191154276	47631889	0.2492	10.6624
chr5	180915260	67875069	0.3752	11.9332
chr6	171115067	99153983	0.5795	20.7546
chr7	159138663	45899270	0.2884	9.24
chr8	146364022	48942461	0.3344	11.1283
chr9	141213431	73286662	0.519	16.1491
chr10	135534747	34051061	0.2512	11.5158
chr11	135006516	48414468	0.3586	11.8502
chr12	133851895	56610081	0.4229	13.2391
chr13	115169878	30394549	0.2639	10.419
chr14	107349540	43497517	0.4052	14.8141
chr15	102531392	28843366	0.2813	10.4328
chr16	90354753	47564633	0.5264	16.5858
chr17	81195210	40826241	0.5028	12.6002
chr18	78077248	29955406	0.3837	14.5754
chr19	59128983	19095644	0.3229	7.9665
chr20	63025520	53682790	0.8518	35.0964
chr21	48129895	5123797	0.1065	4.2679
chr22	51304566	10416273	0.203	6.4229
chrMT	16571	1630	0.0984	0.4241
chrX	155270560	50048593	0.3223	10.9058

chrY	59373566	2612318	0.044	2.3292

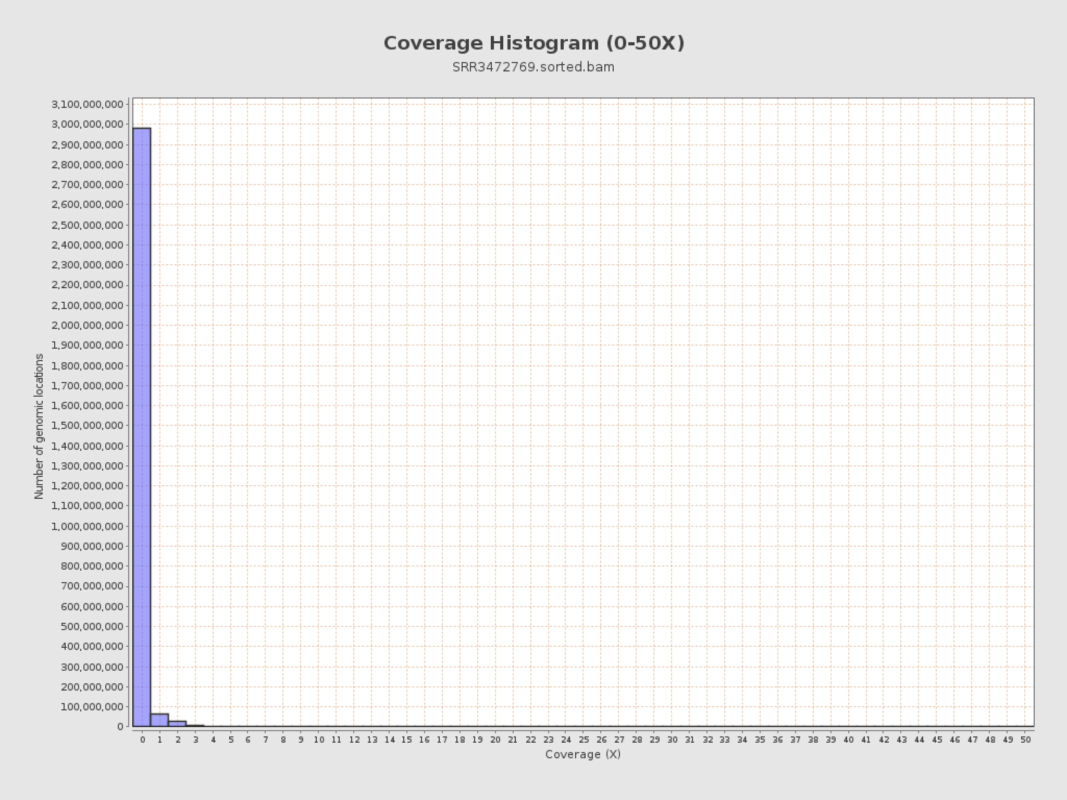
3. Results : Coverage across reference



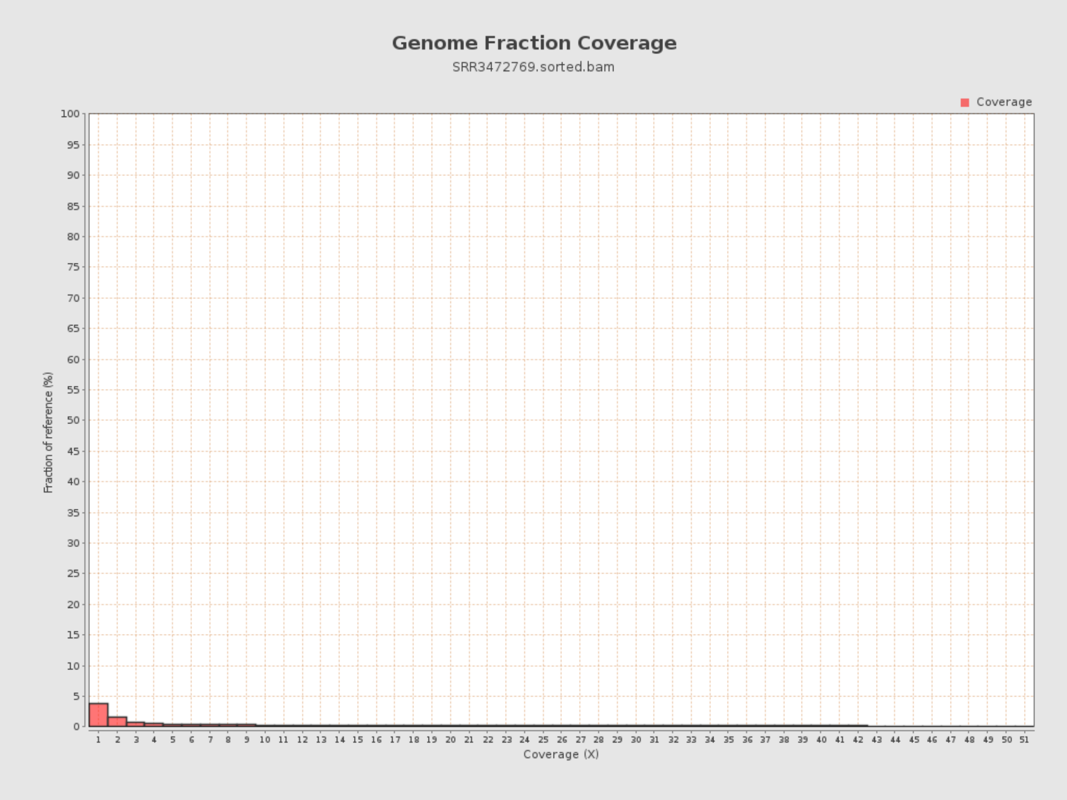
4. Results : Coverage Histogram



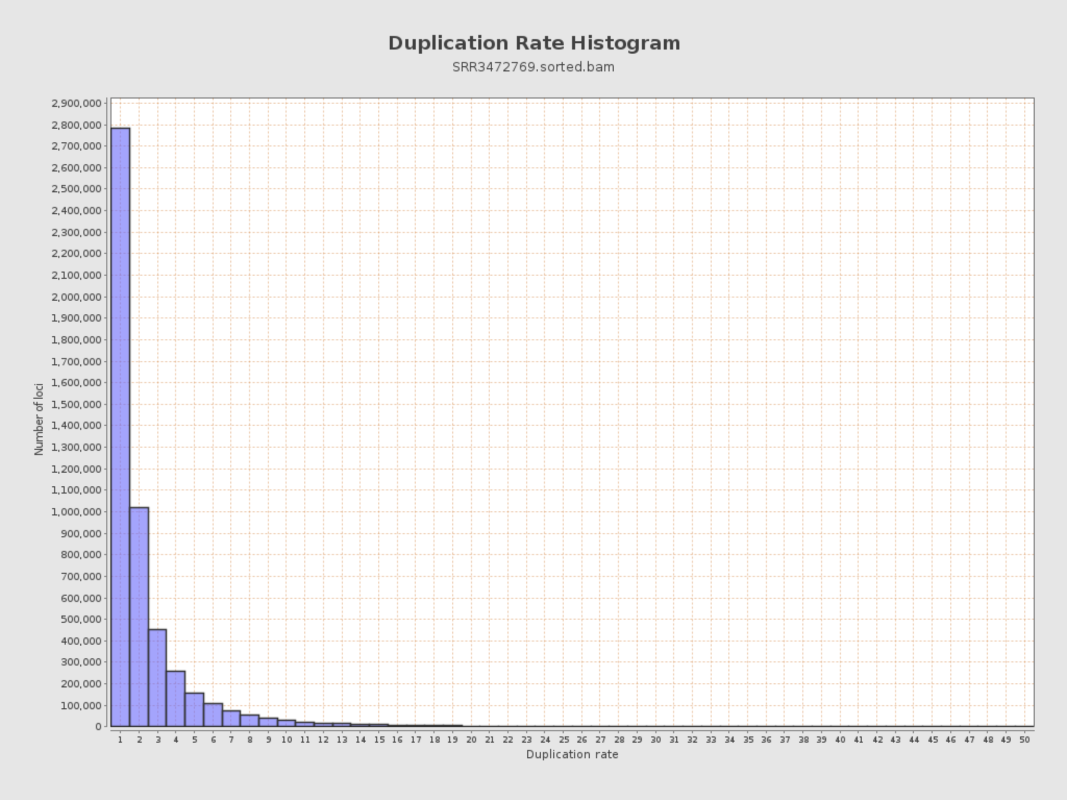
5. Results : Coverage Histogram (0-50X)



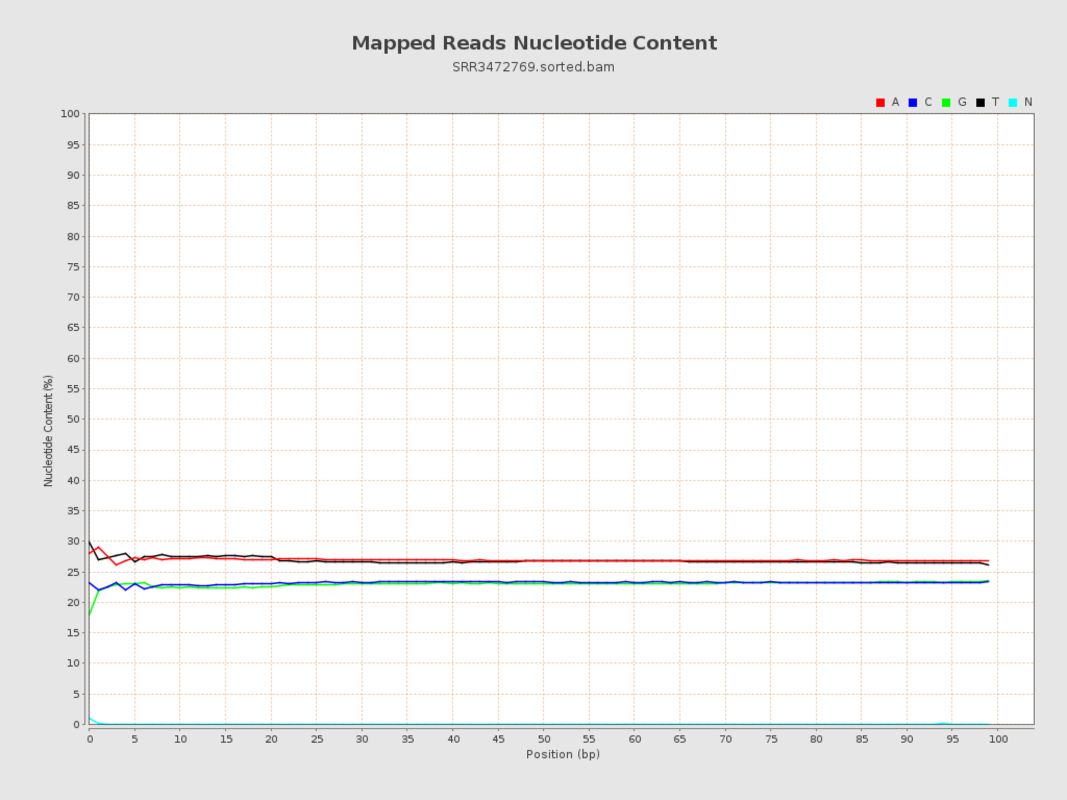
6. Results : Genome Fraction Coverage



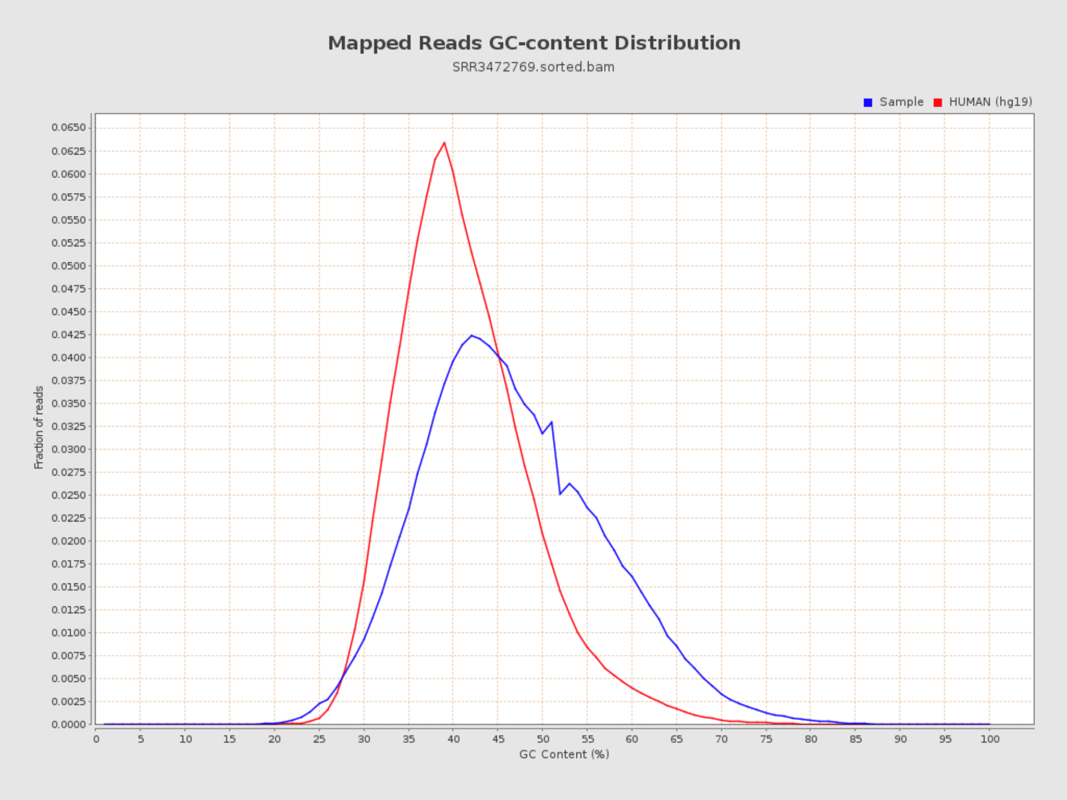
7. Results : Duplication Rate Histogram



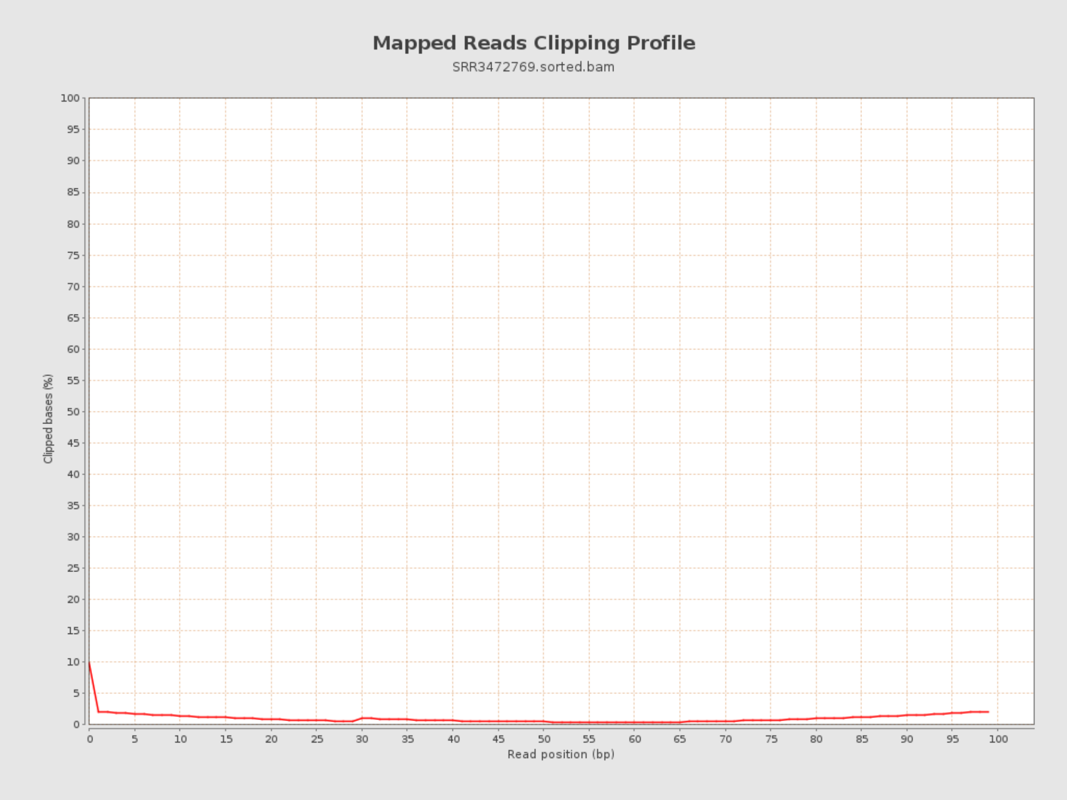
8. Results : Mapped Reads Nucleotide Content



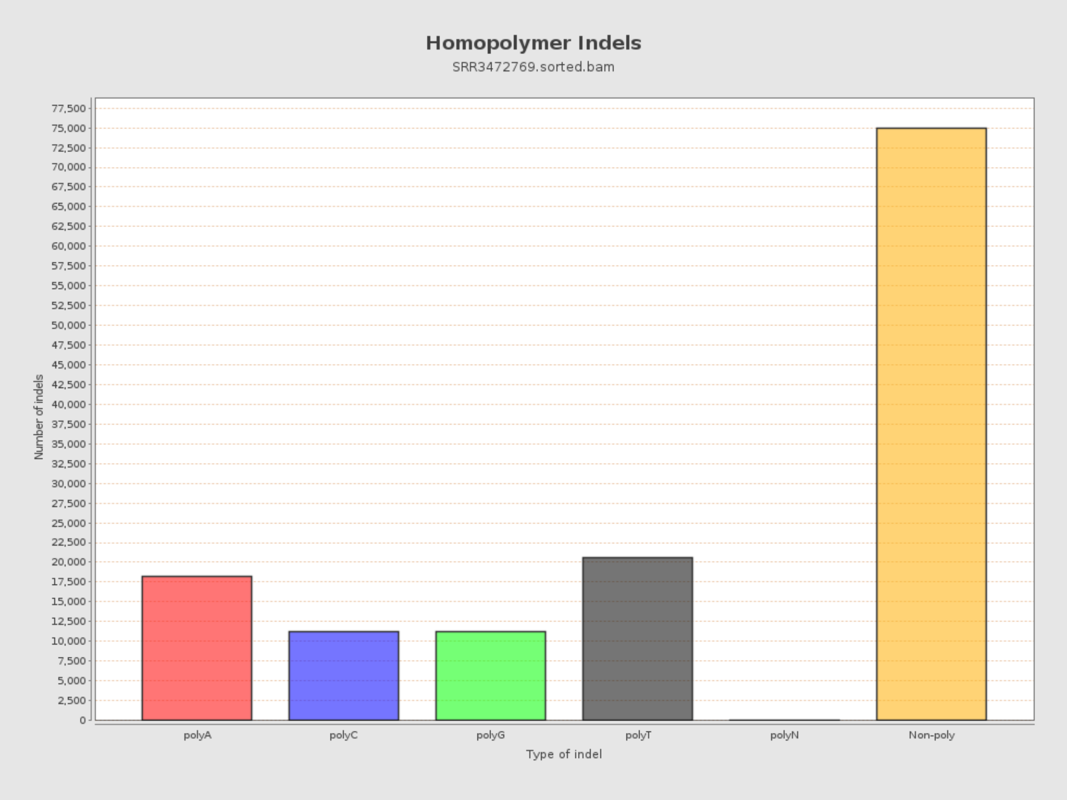
9. Results : Mapped Reads GC-content Distribution



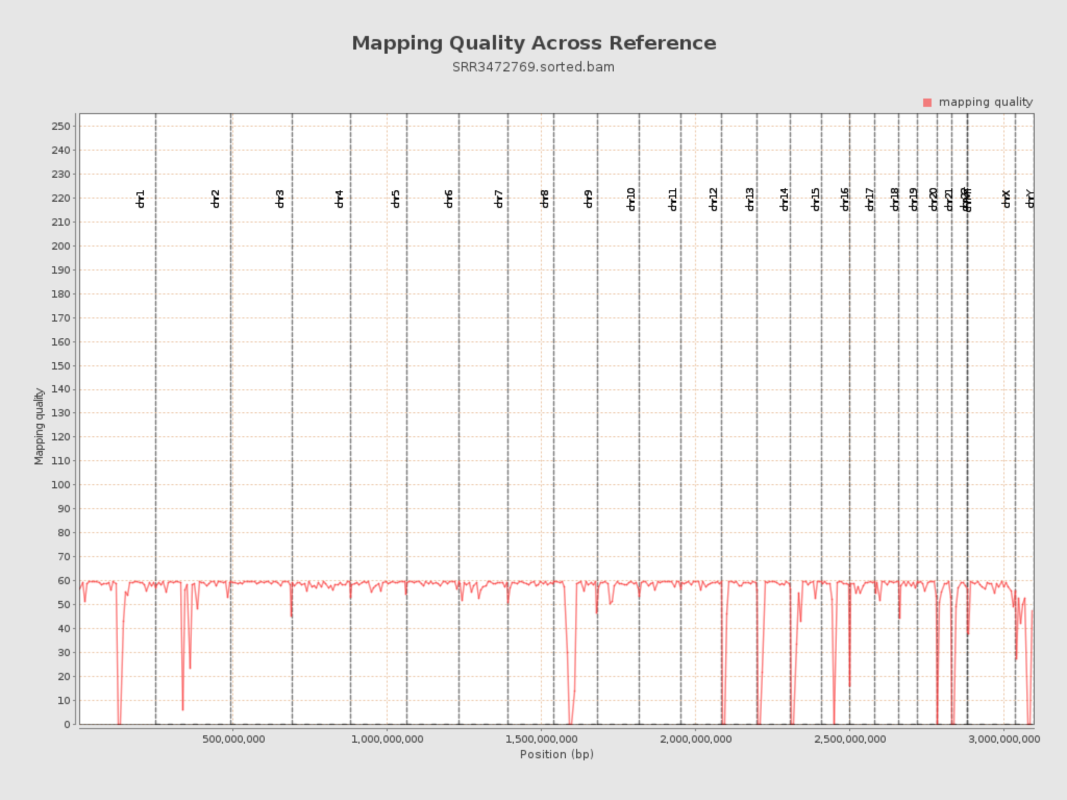
10. Results : Mapped Reads Clipping Profile



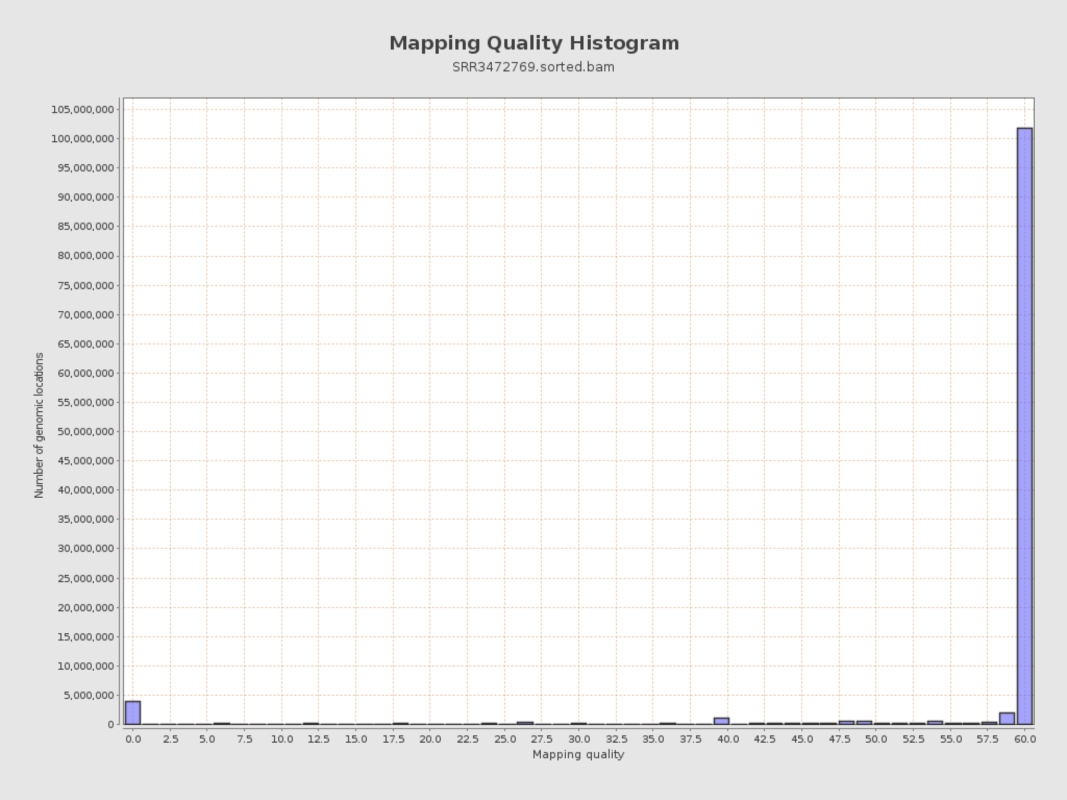
11. Results : Homopolymer Indels



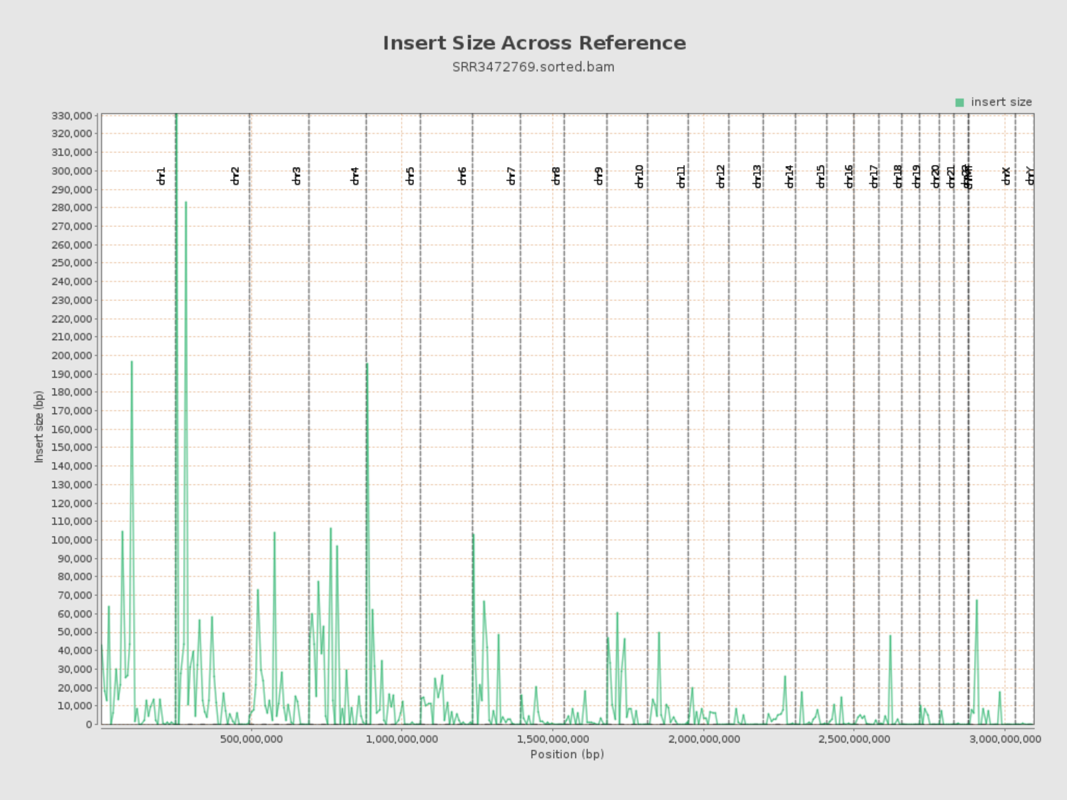
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram