Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 05:40:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472750.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_SRR3472750 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472750_1.fastq.gz SRR3472750_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 05:40:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472750.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,963,470
Mapped reads	12,807,986 / 98.8%
Unmapped reads	155,484 / 1.2%
Mapped paired reads	12,807,986 / 98.8%
Mapped reads, first in pair	6,431,535 / 49.61%
Mapped reads, second in pair	6,376,451 / 49.19%
Mapped reads, both in pair	12,725,288 / 98.16%
Mapped reads, singletons	82,698 / 0.64%
Secondary alignments	0
Supplementary alignments	41,422 / 0.32%
Read min/max/mean length	30 / 100 / 100.13
Duplicated reads (estimated)	7,902,756 / 60.96%
Duplication rate	47.03%
Clipped reads	959,202 / 7.4%

2.2. ACGT Content

Number/percentage of A's	351,553,456 / 27.84%
Number/percentage of C's	281,824,333 / 22.32%
Number/percentage of T's	349,689,357 / 27.69%
Number/percentage of G's	279,437,647 / 22.13%
Number/percentage of N's	241,984 / 0.02%

GC Percentage	44.45%

2.3. Coverage

Mean	0.408
Standard Deviation	15.1022

2.4. Mapping Quality

Mean Mapping Quality	55.11

2.5. Insert size

Mean	22,833.3
Standard Deviation	1,453,204.86
P25/Median/P75	182 / 255 / 344

2.6. Mismatches and indels

General error rate	0.67%
Mismatches	8,315,511
Insertions	80,643
Mapped reads with at least one insertion	0.62%
Deletions	71,451
Mapped reads with at least one deletion	0.55%
Homopolymer indels	44.88%

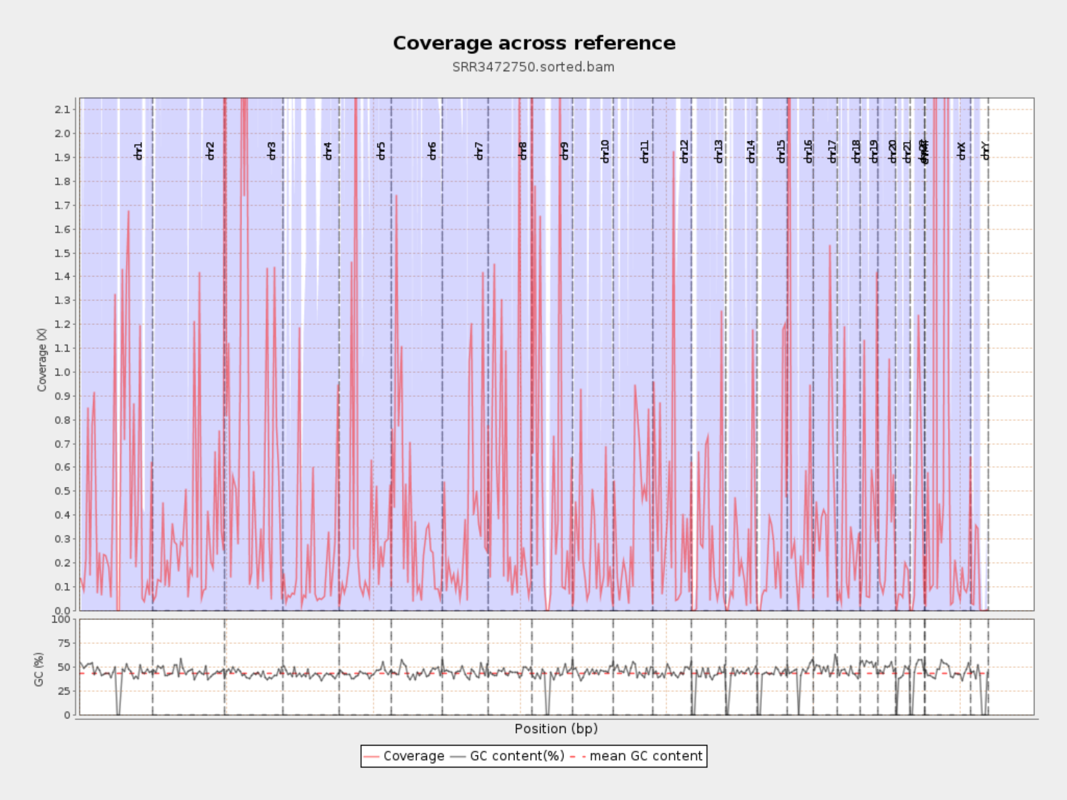
2.7. Chromosome stats

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

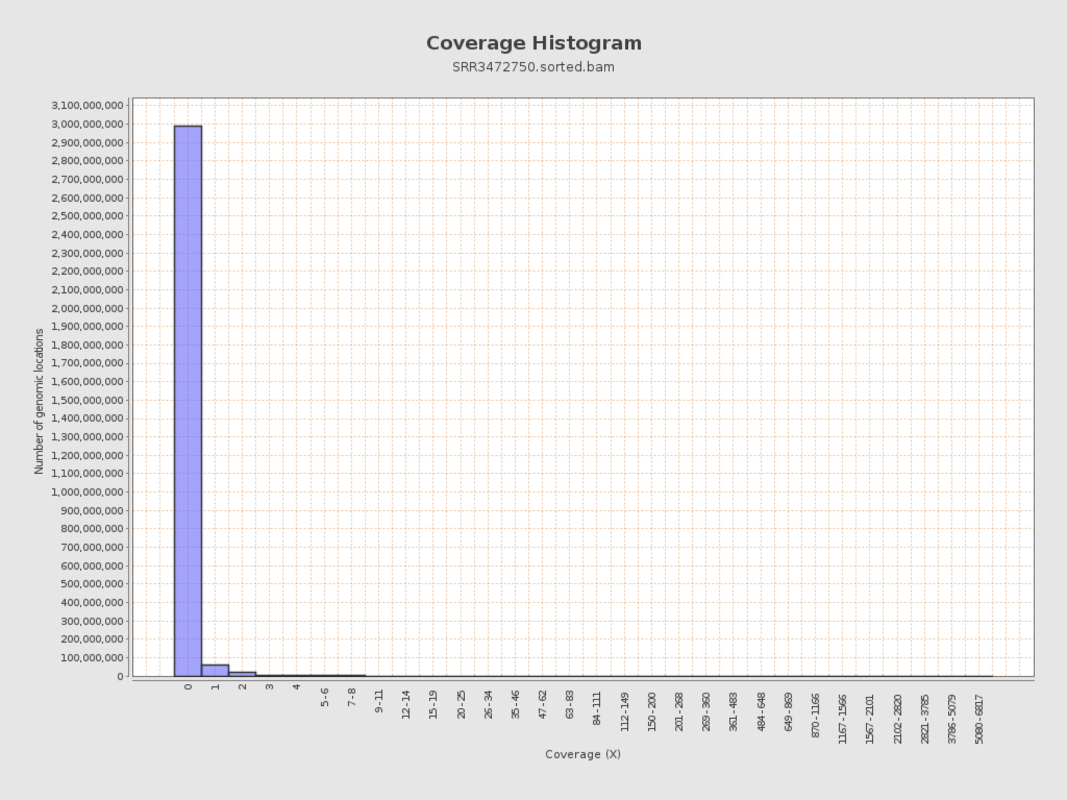
		bases	coverage	deviation
chr1	249250621	116579741	0.4677	18.393
chr2	243199373	75172809	0.3091	11.4201
chr3	198022430	156957689	0.7926	17.7608
chr4	191154276	38690189	0.2024	7.0964
chr5	180915260	68854144	0.3806	12.6418
chr6	171115067	65525624	0.3829	12.1551
chr7	159138663	60337325	0.3791	13.9726
chr8	146364022	75149968	0.5134	17.6083
chr9	141213431	79053887	0.5598	20.2462
chr10	135534747	35573530	0.2625	12.335
chr11	135006516	51376839	0.3806	12.2714
chr12	133851895	56563871	0.4226	13.8209
chr13	115169878	36073239	0.3132	13.9034
chr14	107349540	24882378	0.2318	12.2581
chr15	102531392	32766817	0.3196	10.4262
chr16	90354753	48780189	0.5399	13.7886
chr17	81195210	37059433	0.4564	14.8877
chr18	78077248	21286825	0.2726	15.0253
chr19	59128983	24299764	0.411	12.339
chr20	63025520	22593309	0.3585	10.0812
chr21	48129895	4703714	0.0977	3.5963
chr22	51304566	20125598	0.3923	15.3914
chrMT	16571	3799	0.2293	0.7
chrX	155270560	104684609	0.6742	28.954

chrY	59373566	5831424	0.0982	5.9464

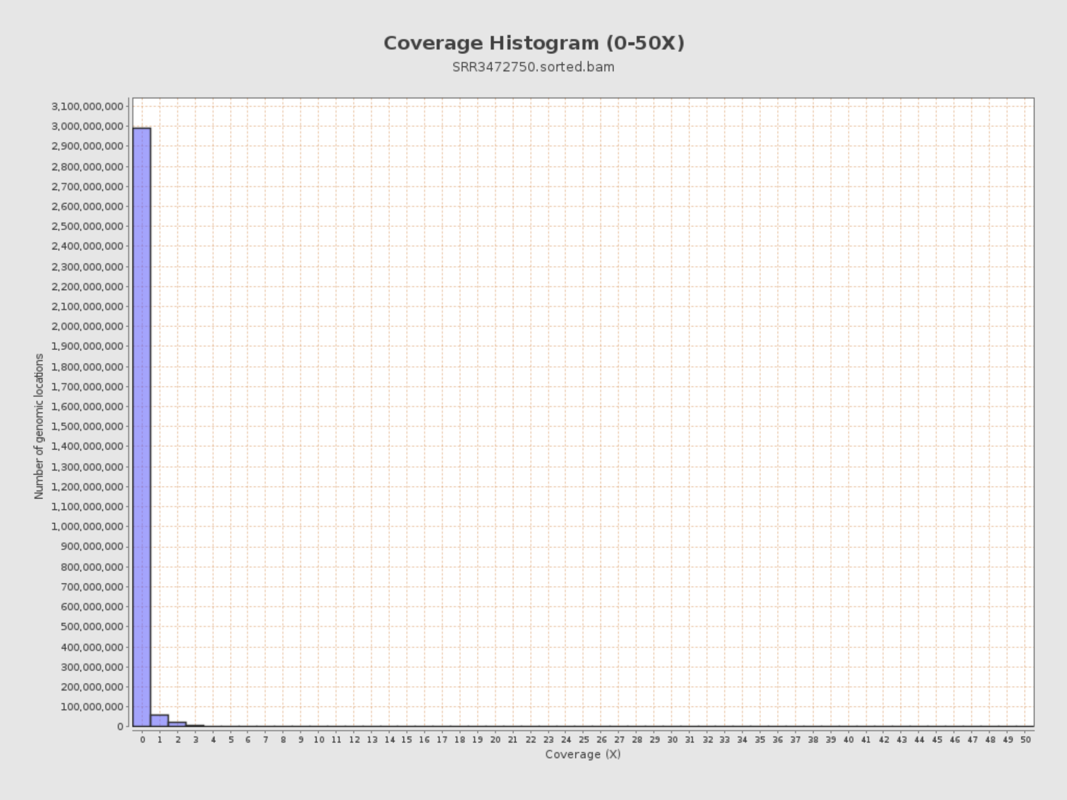
3. Results : Coverage across reference



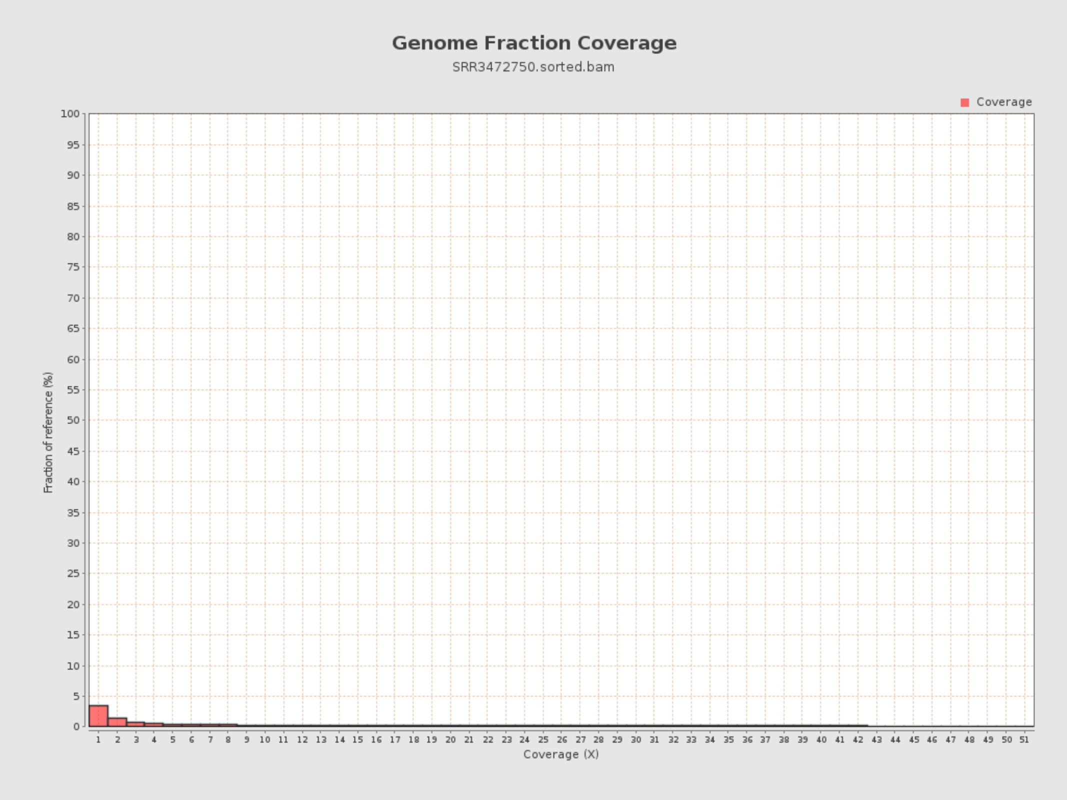
4. Results : Coverage Histogram



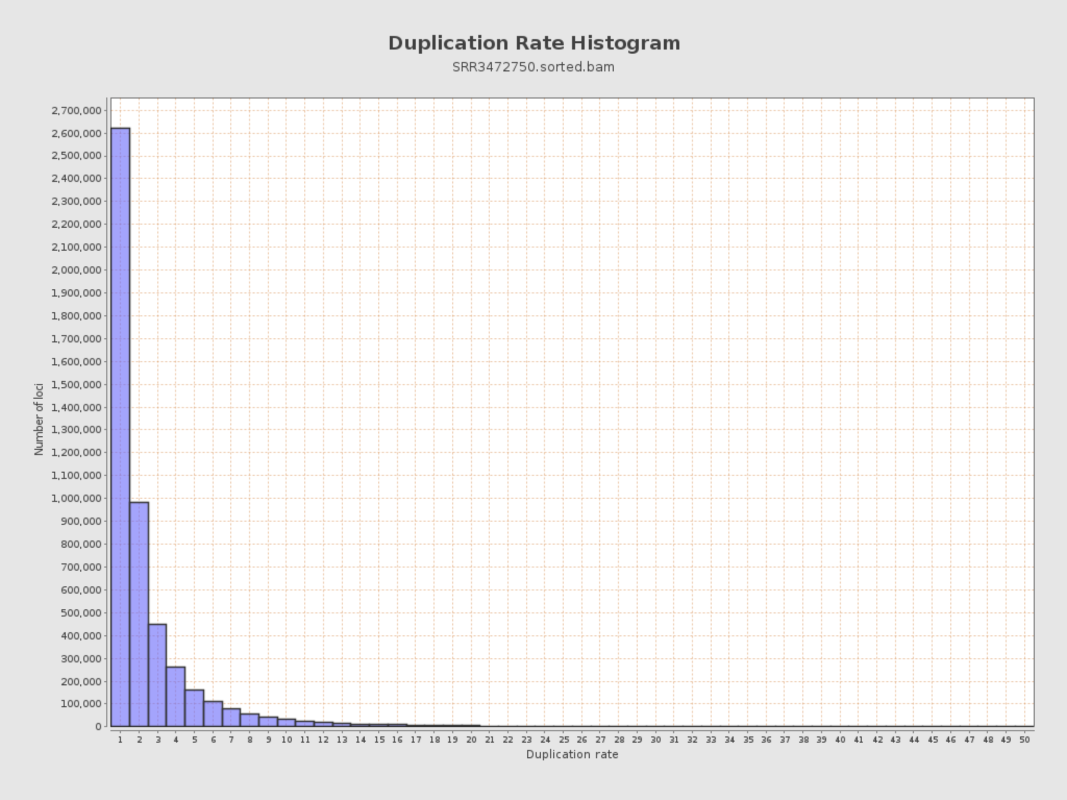
5. Results : Coverage Histogram (0-50X)



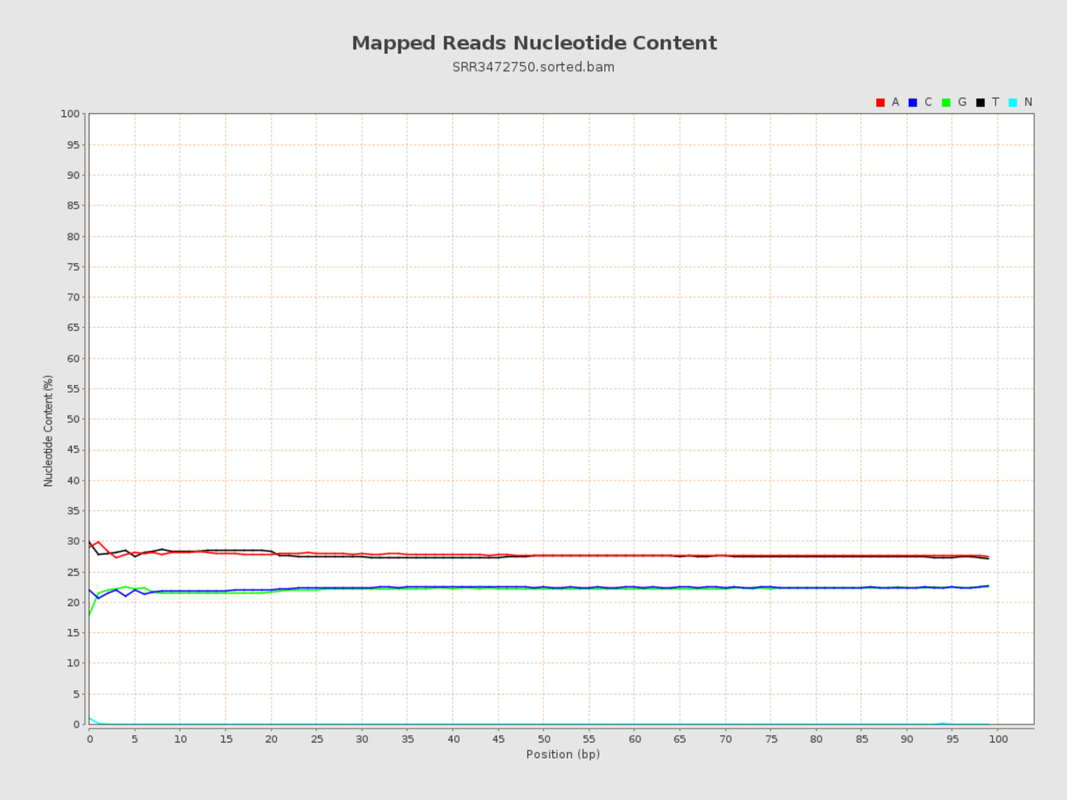
6. Results : Genome Fraction Coverage



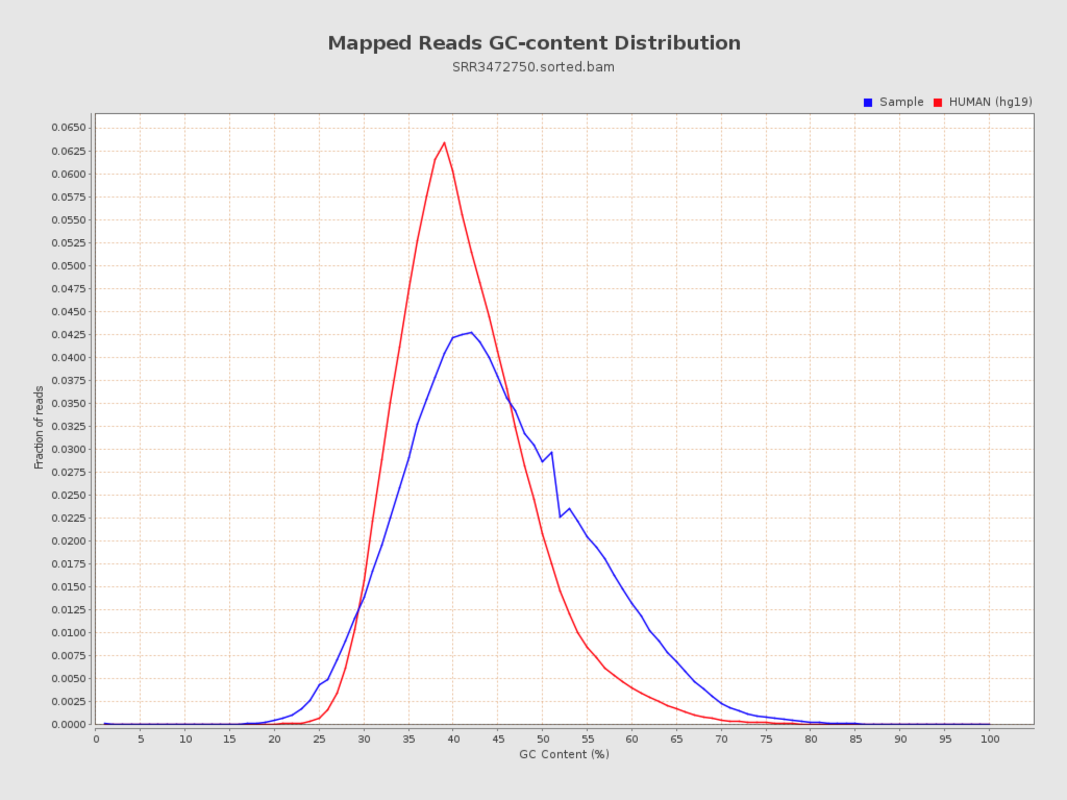
7. Results : Duplication Rate Histogram



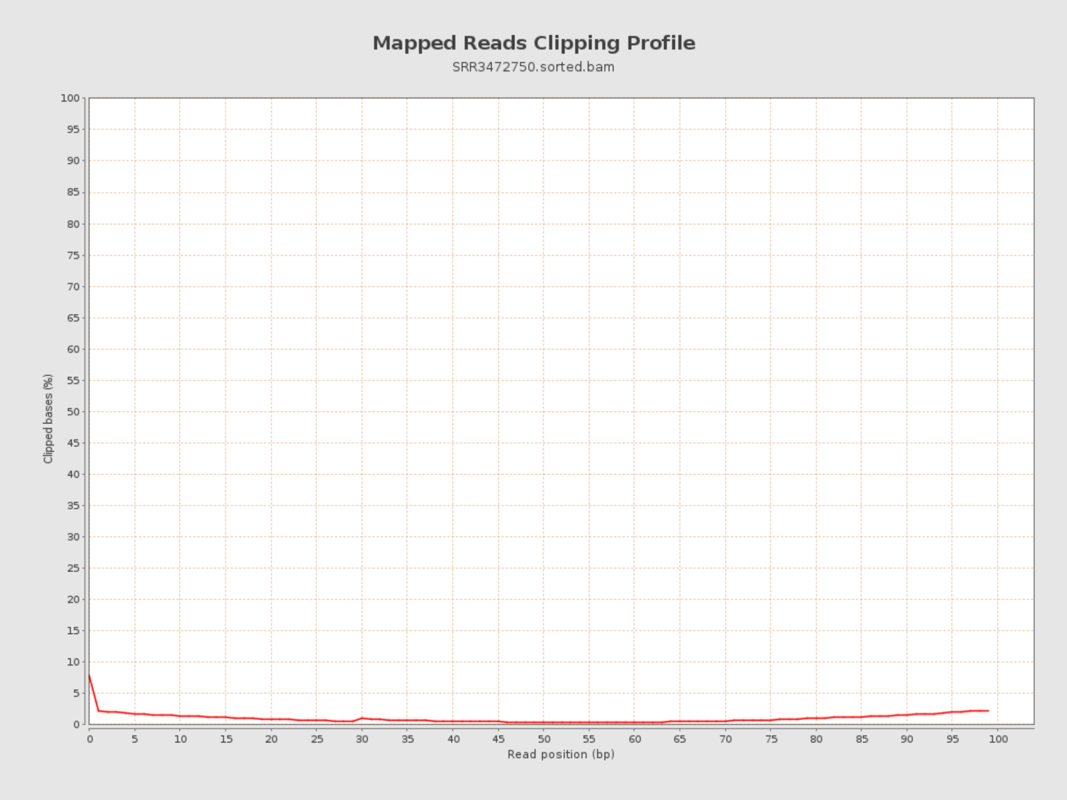
8. Results : Mapped Reads Nucleotide Content



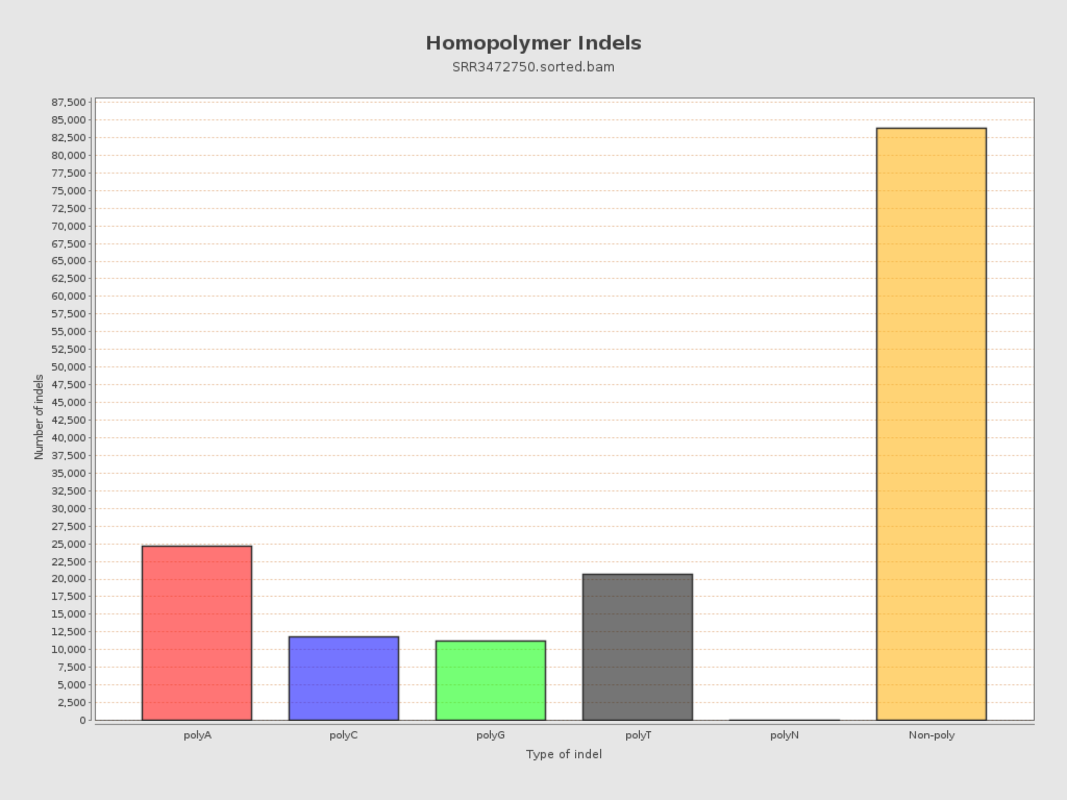
9. Results : Mapped Reads GC-content Distribution



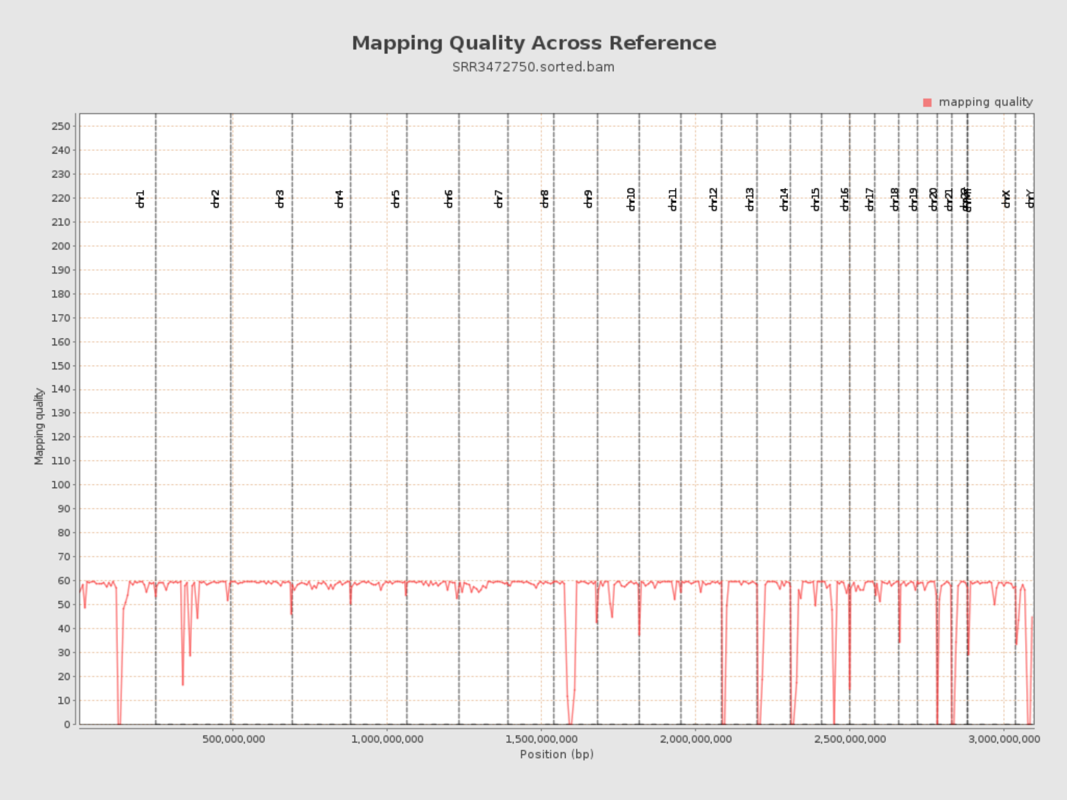
10. Results : Mapped Reads Clipping Profile



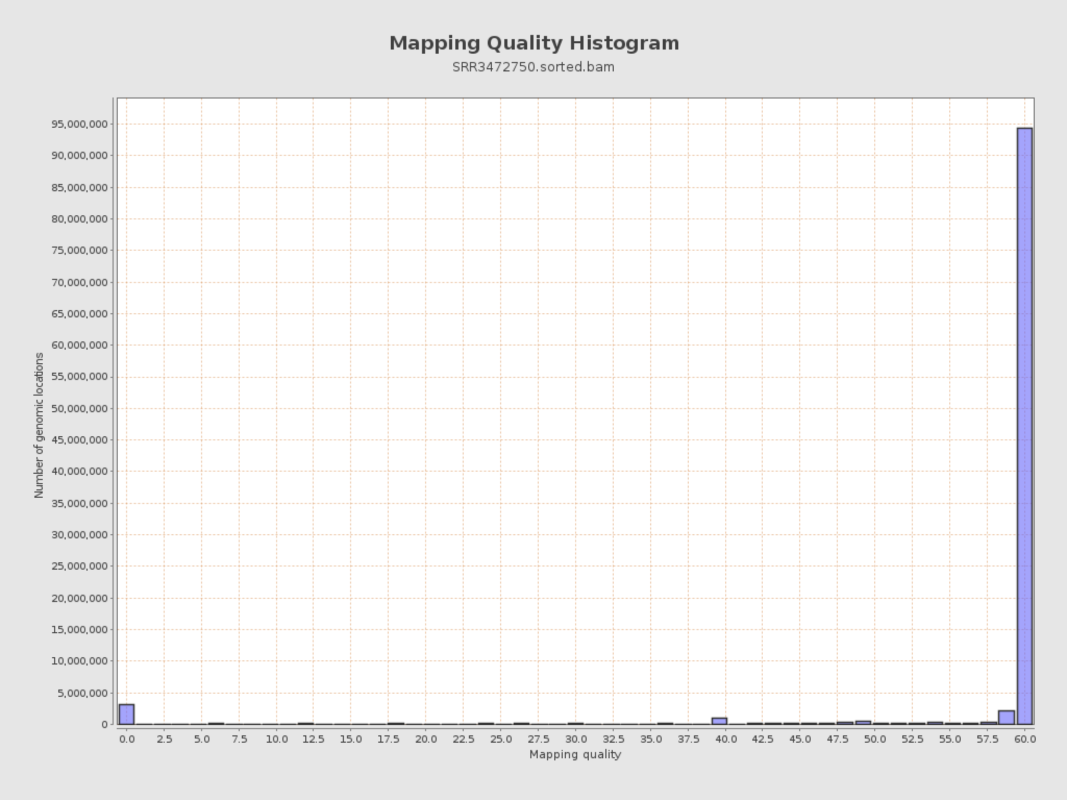
11. Results : Homopolymer Indels



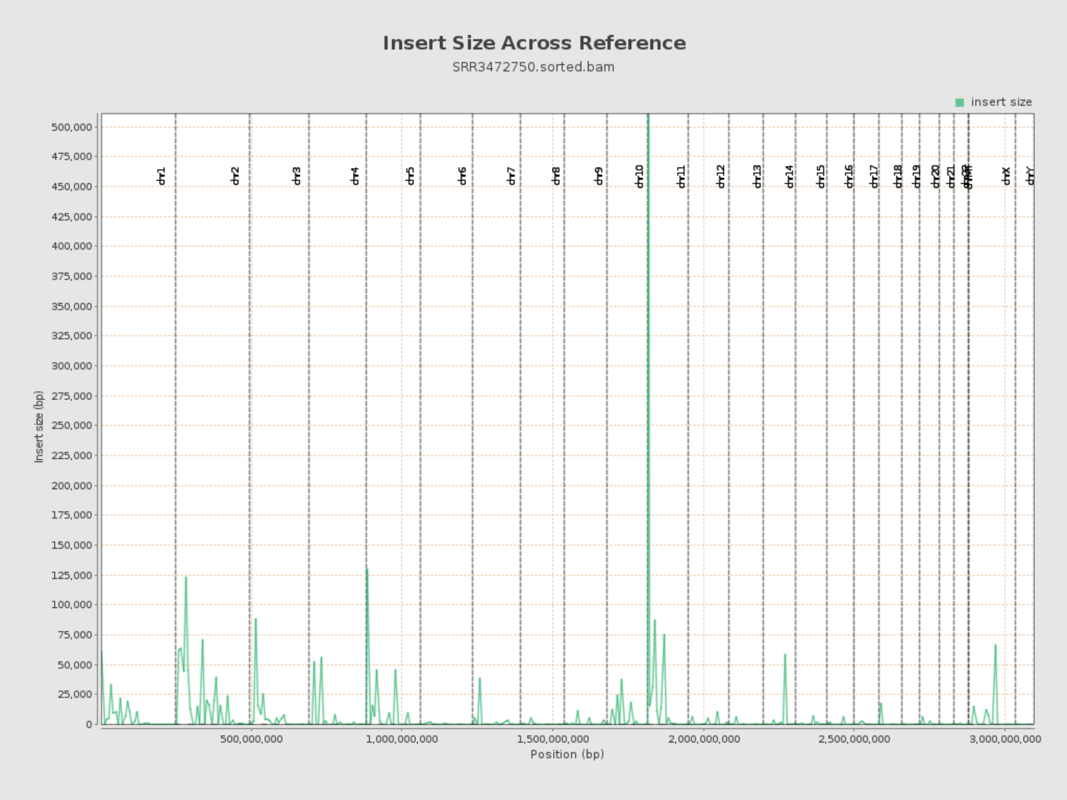
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram