Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 20:03:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472722.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_SRR3472722 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472722_1.fastq.gz SRR3472722_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 20:03:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472722.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,967,574
Mapped reads	13,742,769 / 98.39%
Unmapped reads	224,805 / 1.61%
Mapped paired reads	13,742,769 / 98.39%
Mapped reads, first in pair	6,917,508 / 49.53%
Mapped reads, second in pair	6,825,261 / 48.87%
Mapped reads, both in pair	13,615,244 / 97.48%
Mapped reads, singletons	127,525 / 0.91%
Secondary alignments	0
Supplementary alignments	52,112 / 0.37%
Read min/max/mean length	30 / 100 / 100.15
Duplicated reads (estimated)	8,247,628 / 59.05%
Duplication rate	46.05%
Clipped reads	1,157,433 / 8.29%

2.2. ACGT Content

Number/percentage of A's	374,767,594 / 27.72%
Number/percentage of C's	303,165,798 / 22.42%
Number/percentage of T's	371,626,698 / 27.49%
Number/percentage of G's	302,171,829 / 22.35%
Number/percentage of N's	260,018 / 0.02%

GC Percentage	44.77%

2.3. Coverage

Mean	0.4368
Standard Deviation	14.5223

2.4. Mapping Quality

Mean Mapping Quality	55.26

2.5. Insert size

Mean	26,807.52
Standard Deviation	1,625,597.5
P25/Median/P75	174 / 246 / 333

2.6. Mismatches and indels

General error rate	0.66%
Mismatches	8,700,699
Insertions	81,278
Mapped reads with at least one insertion	0.59%
Deletions	75,043
Mapped reads with at least one deletion	0.54%
Homopolymer indels	45.76%

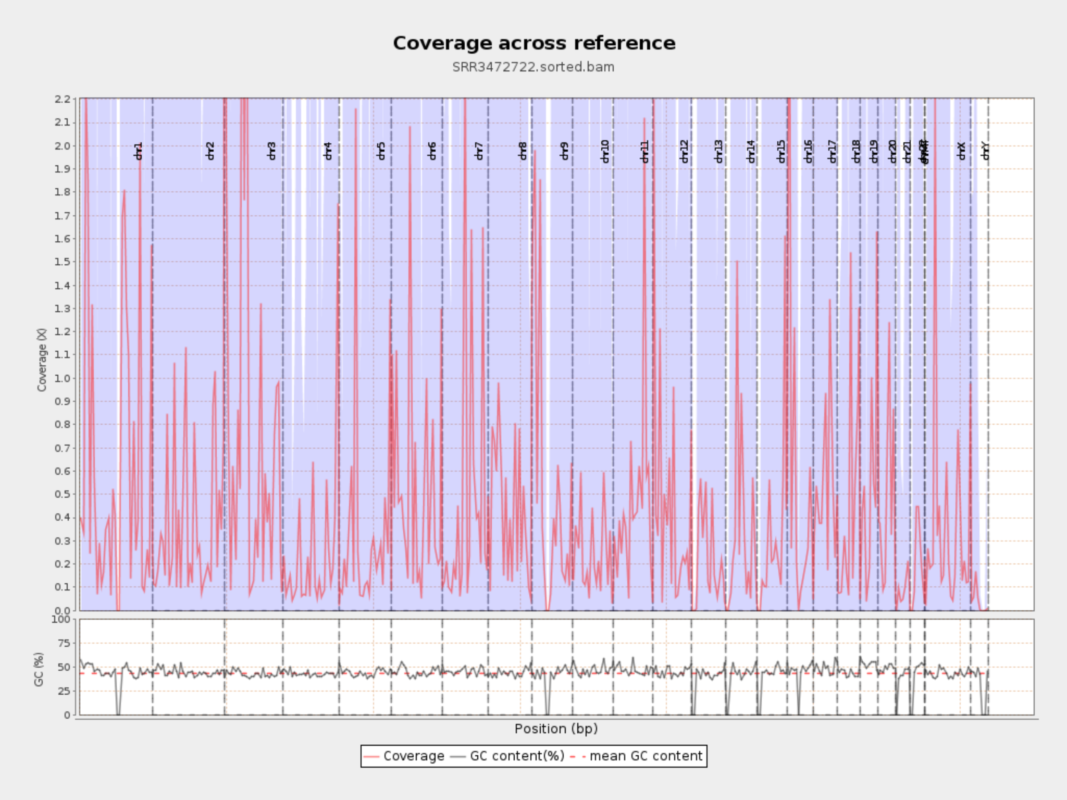
2.7. Chromosome stats

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

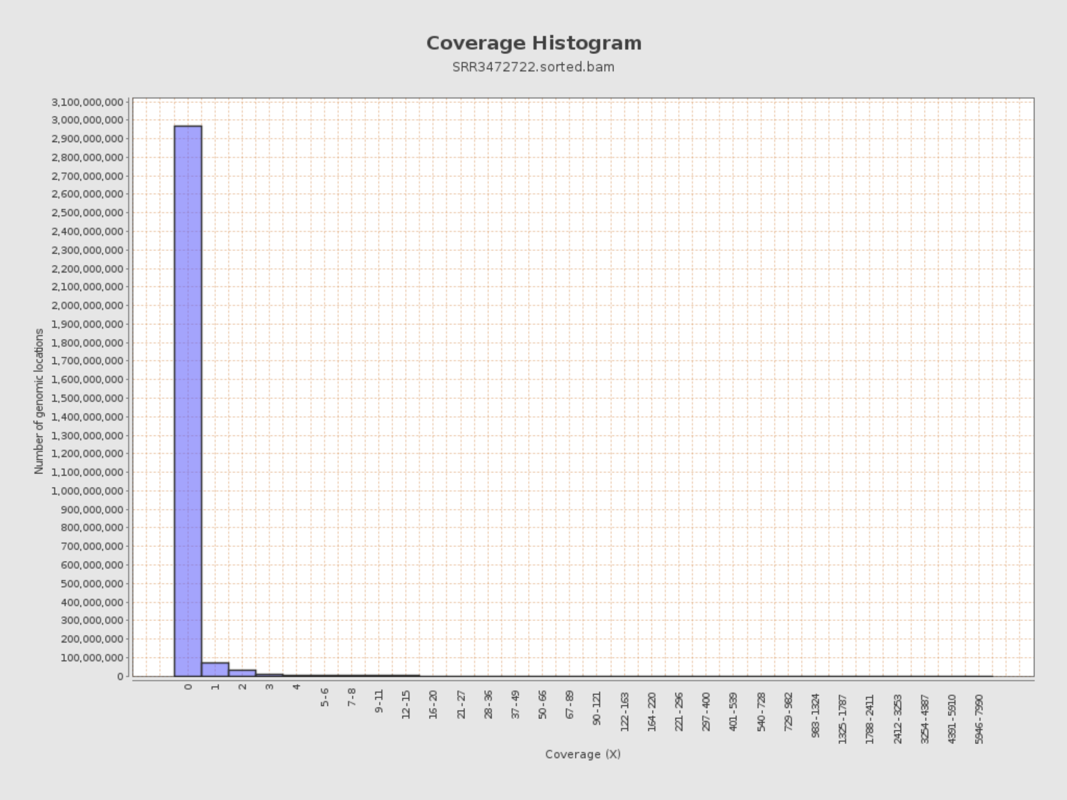
		bases	coverage	deviation
chr1	249250621	163355340	0.6554	20.4461
chr2	243199373	88854866	0.3654	12.172
chr3	198022430	170120847	0.8591	20.4918
chr4	191154276	45662333	0.2389	9.6605
chr5	180915260	61785545	0.3415	11.1683
chr6	171115067	88882471	0.5194	13.5295
chr7	159138663	74758814	0.4698	19.0445
chr8	146364022	62800691	0.4291	14.4832
chr9	141213431	75495920	0.5346	13.0256
chr10	135534747	32872349	0.2425	8.6649
chr11	135006516	65821452	0.4875	21.013
chr12	133851895	61768901	0.4615	12.5783
chr13	115169878	25608515	0.2224	8.0579
chr14	107349540	35784700	0.3333	11.1235
chr15	102531392	33196691	0.3238	11.1325
chr16	90354753	53314354	0.5901	15.9705
chr17	81195210	44387762	0.5467	11.9553
chr18	78077248	36240383	0.4642	18.0752
chr19	59128983	28195138	0.4768	17.9998
chr20	63025520	31064425	0.4929	16.5538
chr21	48129895	4553830	0.0946	3.176
chr22	51304566	9641729	0.1879	5.6781
chrMT	16571	3627	0.2189	0.7051
chrX	155270560	55545670	0.3577	11.9038

chrY	59373566	2469564	0.0416	1.4804

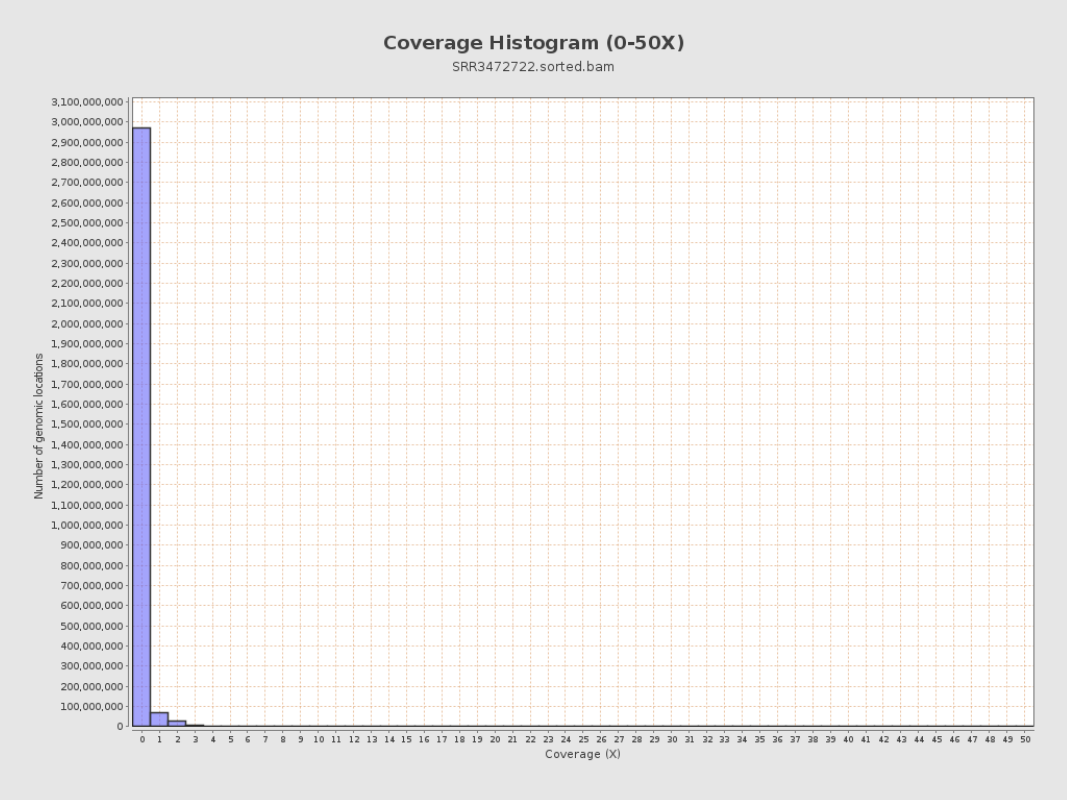
3. Results : Coverage across reference



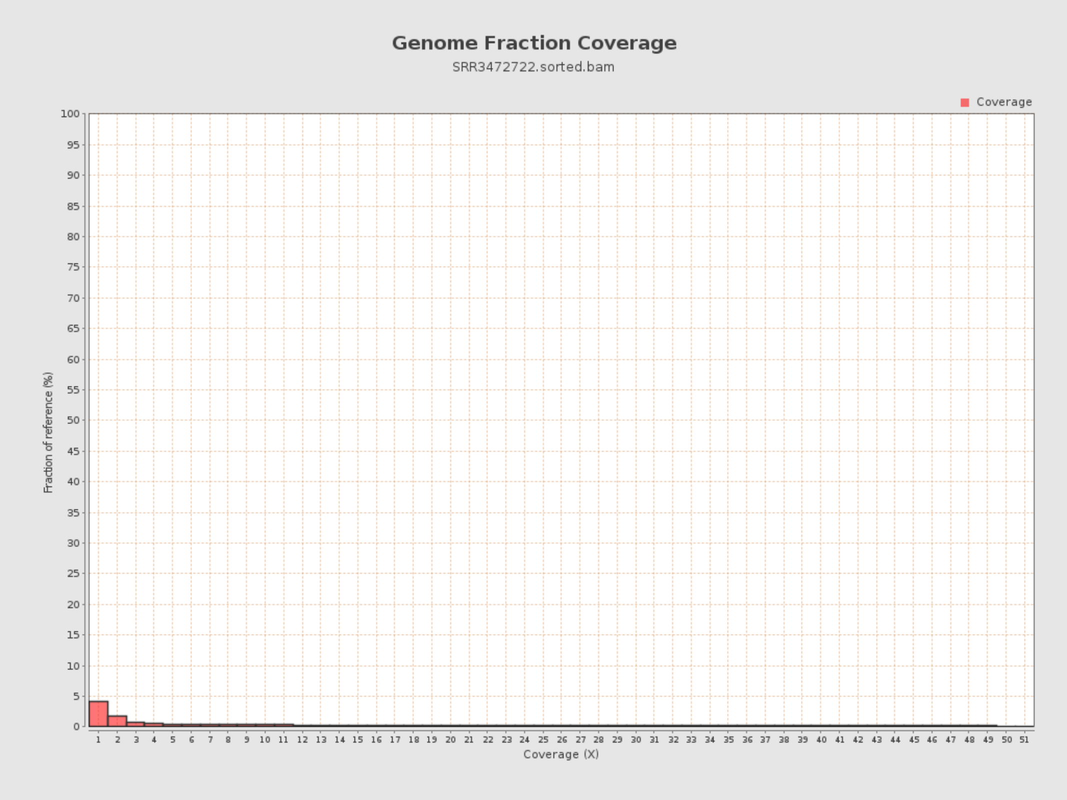
4. Results : Coverage Histogram



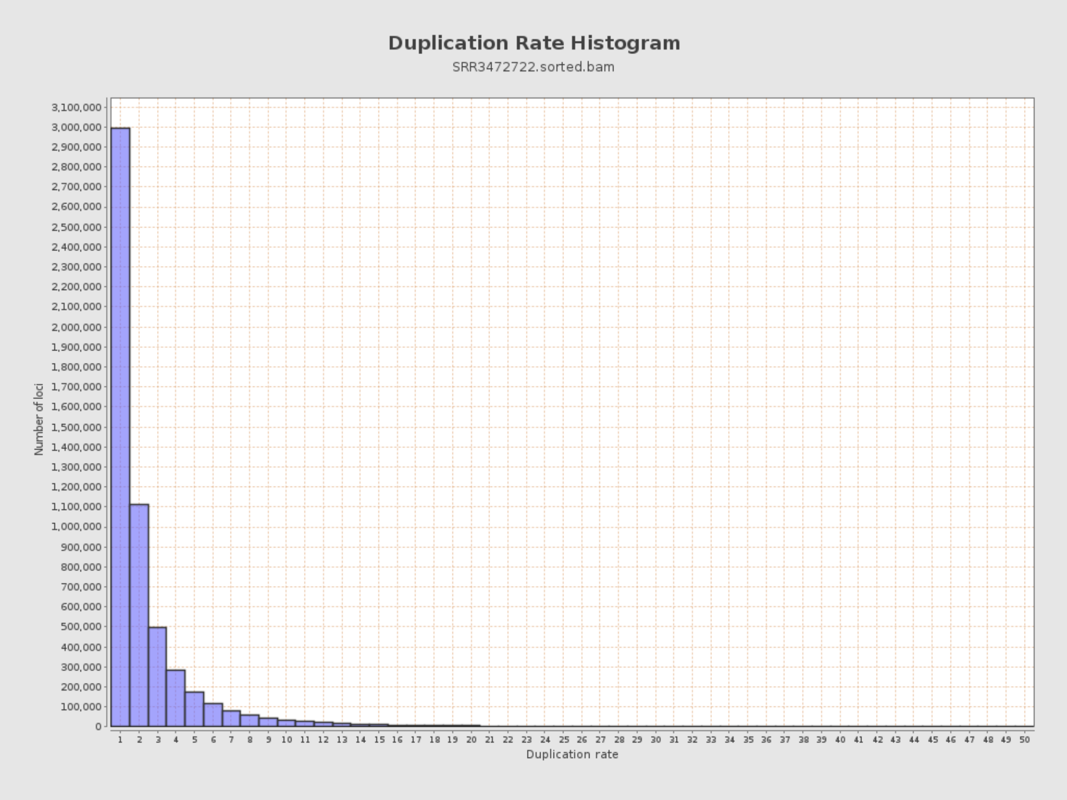
5. Results : Coverage Histogram (0-50X)



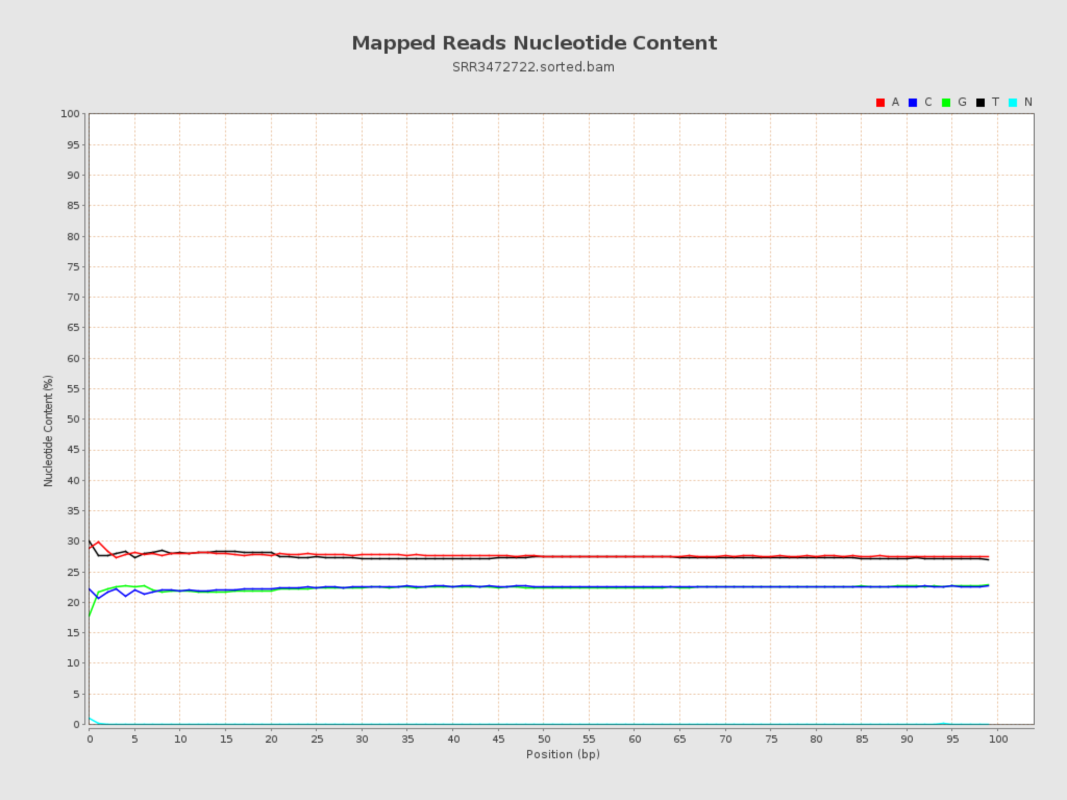
6. Results : Genome Fraction Coverage



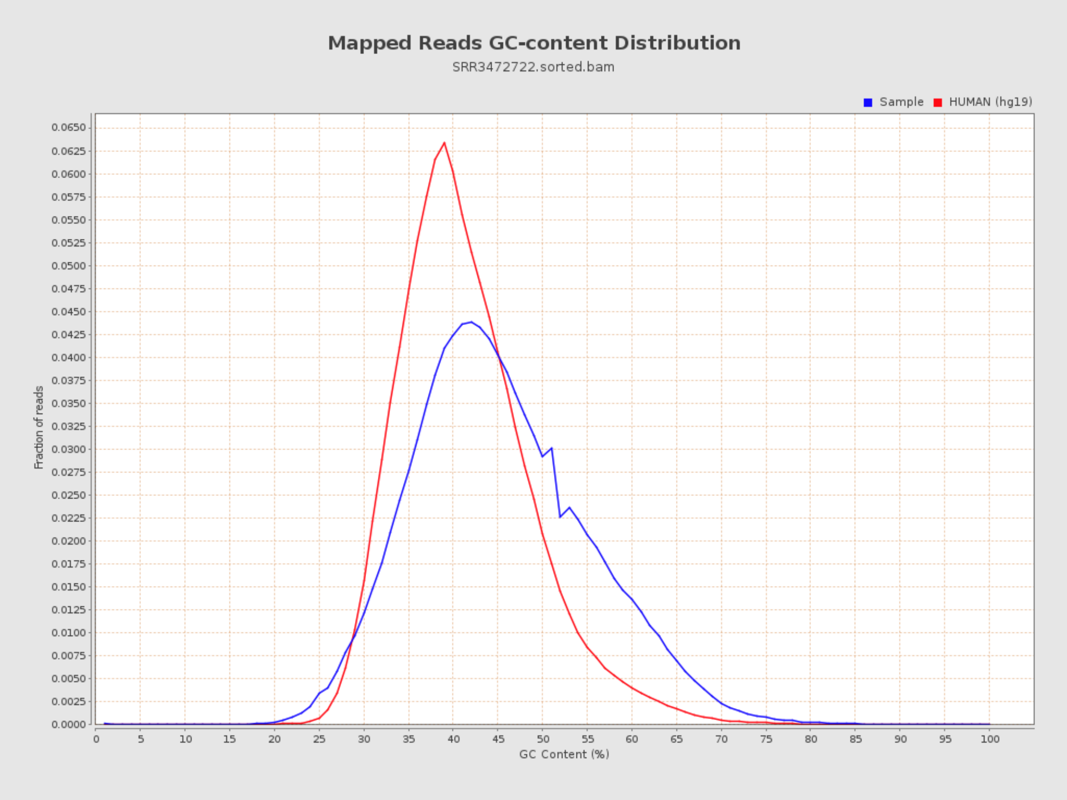
7. Results : Duplication Rate Histogram



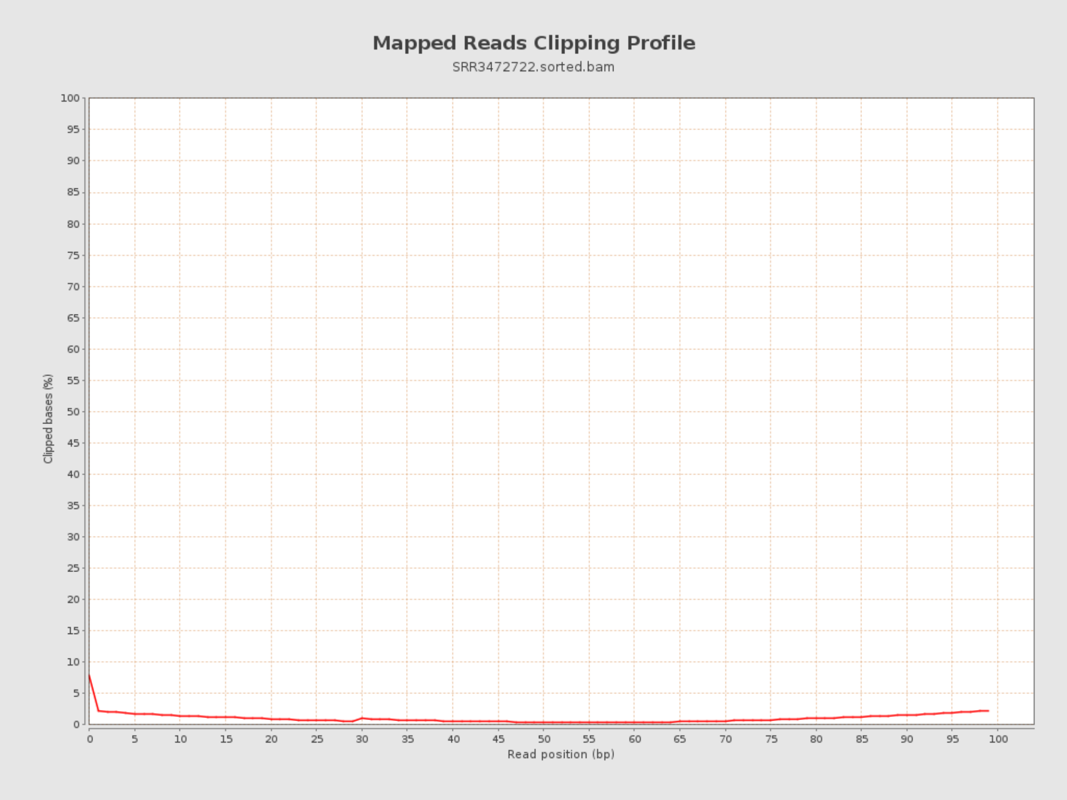
8. Results : Mapped Reads Nucleotide Content



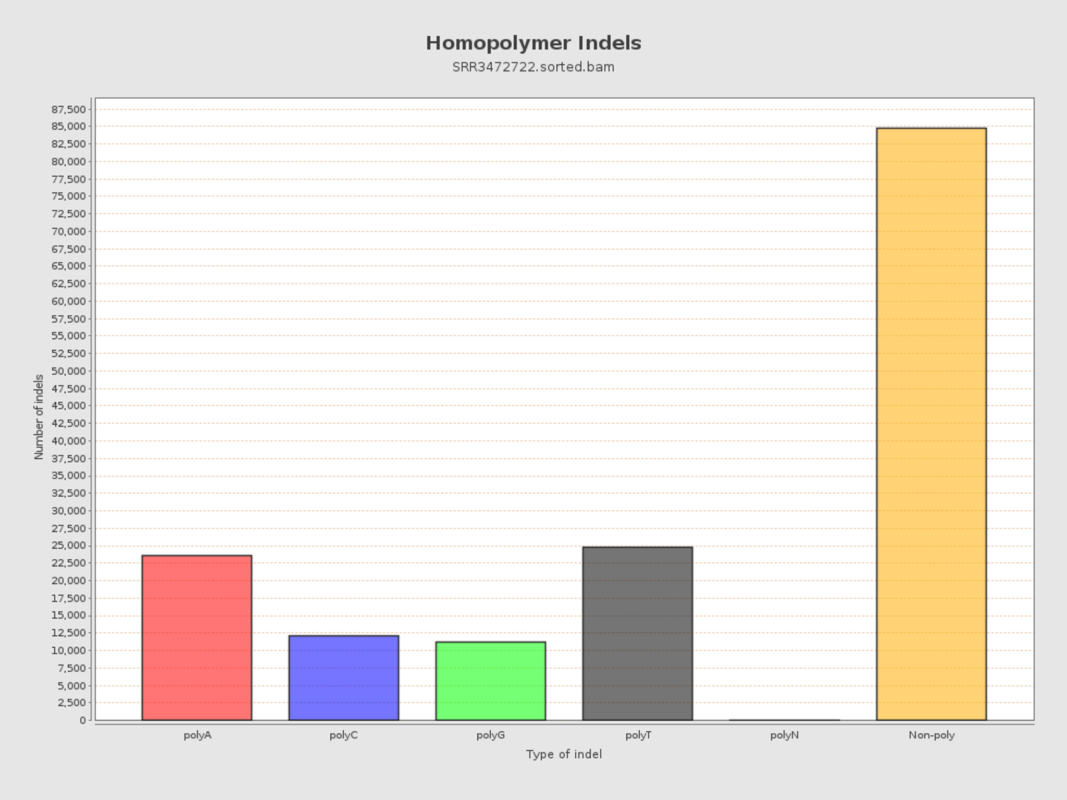
9. Results : Mapped Reads GC-content Distribution



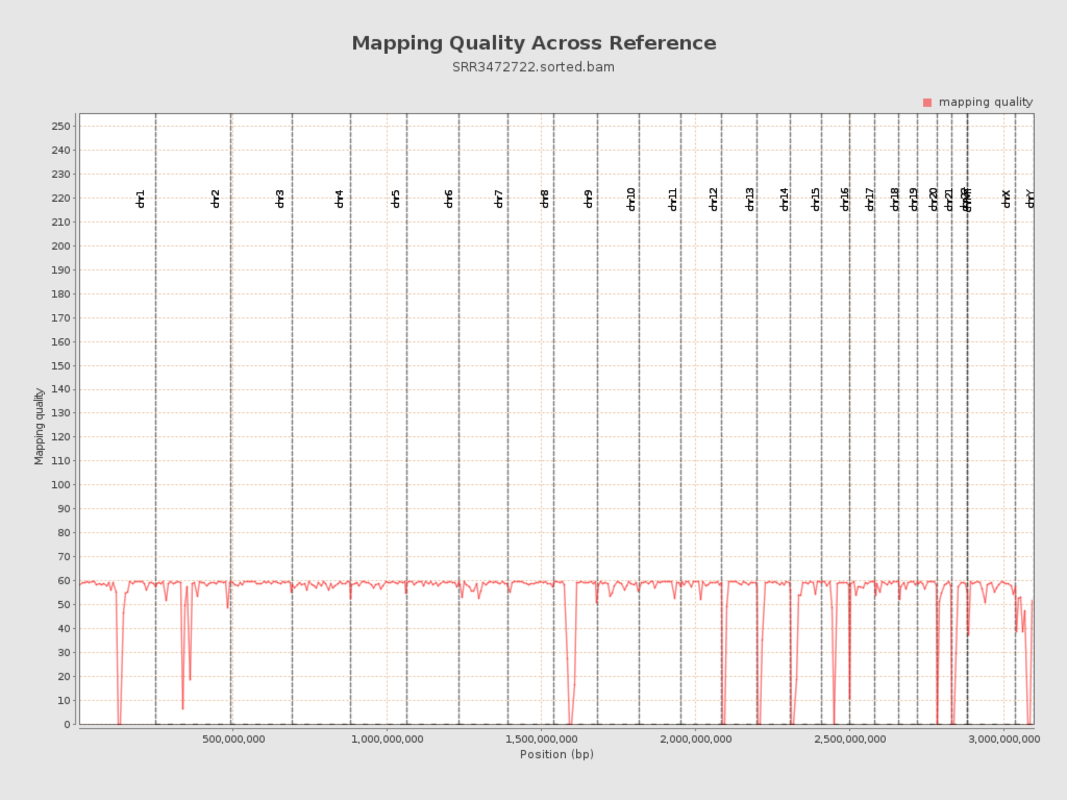
10. Results : Mapped Reads Clipping Profile



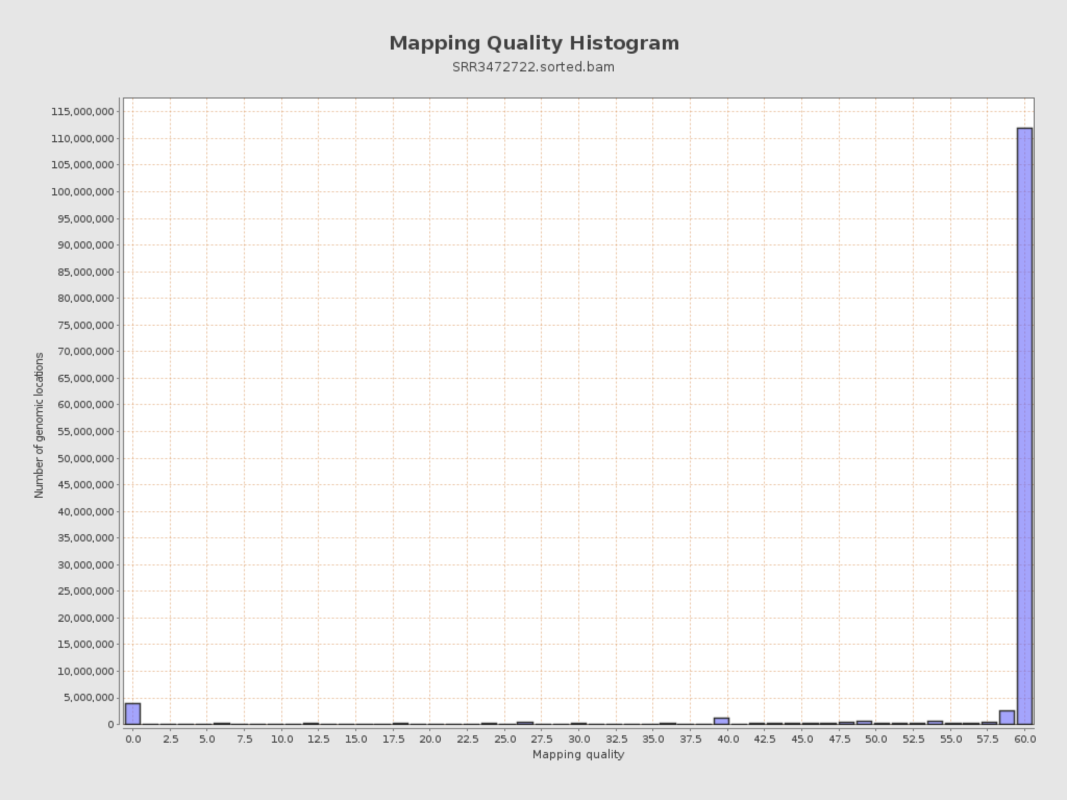
11. Results : Homopolymer Indels



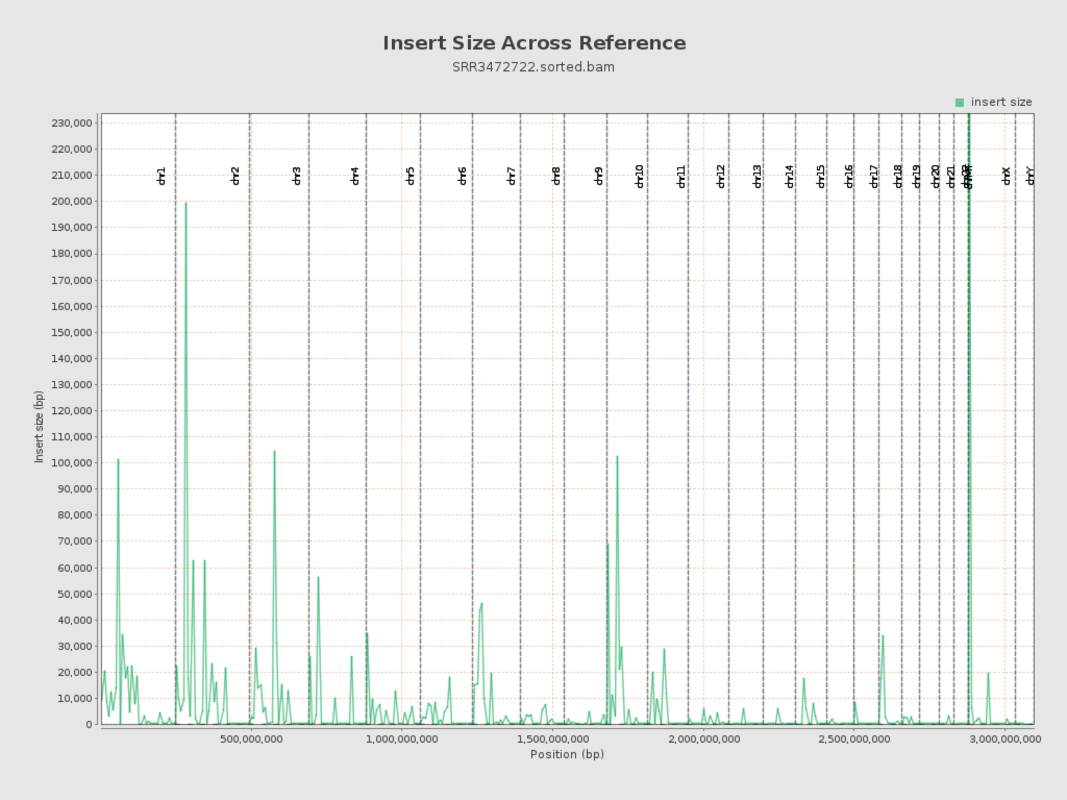
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram