Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 15:38:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472708.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_SRR3472708 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472708_1.fastq.gz SRR3472708_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 15:38:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472708.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,524,482
Mapped reads	15,166,450 / 97.69%
Unmapped reads	358,032 / 2.31%
Mapped paired reads	15,166,450 / 97.69%
Mapped reads, first in pair	7,618,106 / 49.07%
Mapped reads, second in pair	7,548,344 / 48.62%
Mapped reads, both in pair	15,065,060 / 97.04%
Mapped reads, singletons	101,390 / 0.65%
Secondary alignments	0
Supplementary alignments	49,403 / 0.32%
Read min/max/mean length	30 / 100 / 100.13
Duplicated reads (estimated)	9,091,697 / 58.56%
Duplication rate	46.43%
Clipped reads	1,137,364 / 7.33%

2.2. ACGT Content

Number/percentage of A's	414,793,693 / 27.74%
Number/percentage of C's	334,953,049 / 22.4%
Number/percentage of T's	412,055,240 / 27.55%
Number/percentage of G's	333,423,911 / 22.29%
Number/percentage of N's	287,169 / 0.02%

GC Percentage	44.69%

2.3. Coverage

Mean	0.4832
Standard Deviation	14.6425

2.4. Mapping Quality

Mean Mapping Quality	55.26

2.5. Insert size

Mean	24,200.67
Standard Deviation	1,489,437.22
P25/Median/P75	178 / 248 / 333

2.6. Mismatches and indels

General error rate	0.66%
Mismatches	9,660,589
Insertions	90,667
Mapped reads with at least one insertion	0.59%
Deletions	86,505
Mapped reads with at least one deletion	0.56%
Homopolymer indels	44.81%

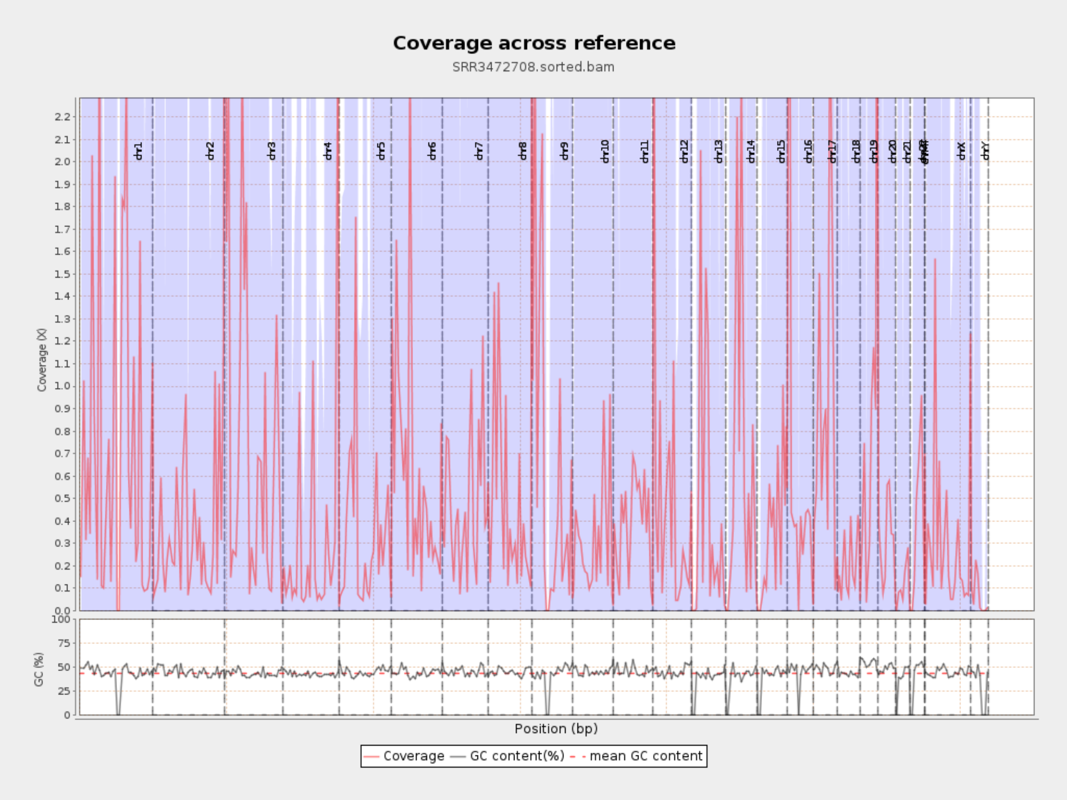
2.7. Chromosome stats

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

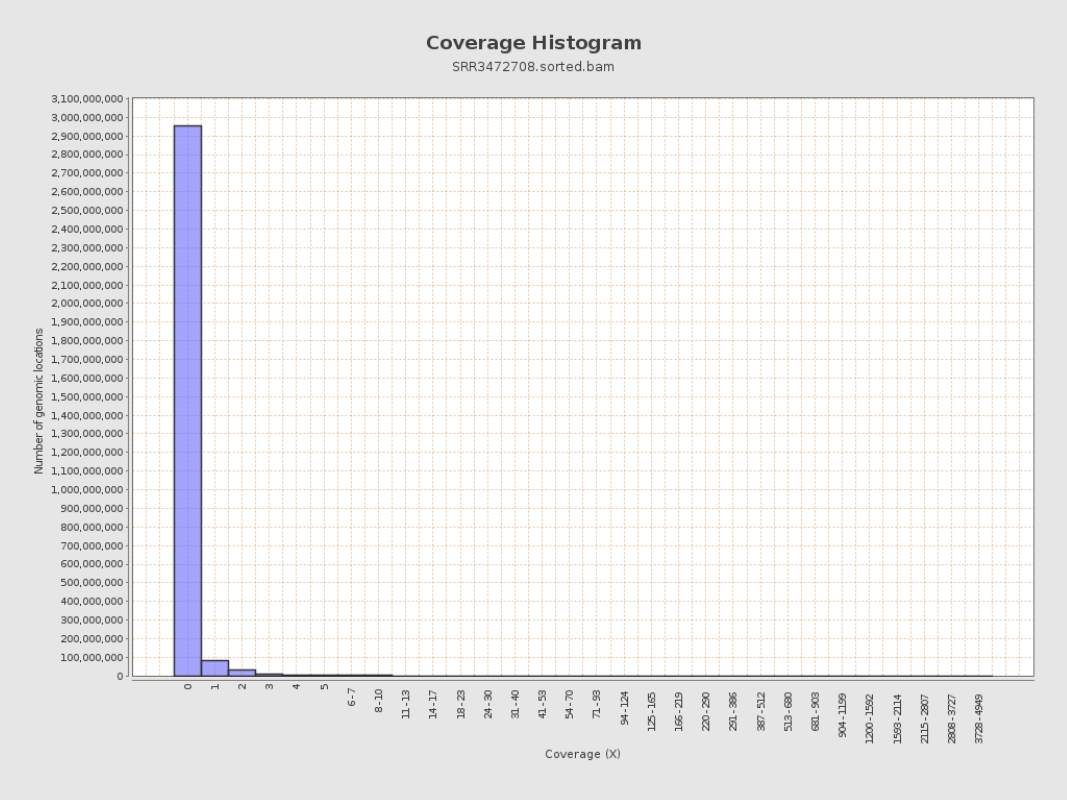
		bases	coverage	deviation
chr1	249250621	187231338	0.7512	23.3169
chr2	243199373	83285472	0.3425	11.7781
chr3	198022430	160893532	0.8125	16.5733
chr4	191154276	58076865	0.3038	11.9949
chr5	180915260	60863624	0.3364	10.6411
chr6	171115067	104293775	0.6095	13.8216
chr7	159138663	75851776	0.4766	14.3355
chr8	146364022	66597625	0.455	12.0599
chr9	141213431	92220286	0.6531	16.5957
chr10	135534747	43933530	0.3241	10.2132
chr11	135006516	54297447	0.4022	11.2659
chr12	133851895	66257813	0.495	16.8257
chr13	115169878	52381018	0.4548	17.1795
chr14	107349540	71325561	0.6644	20.2266
chr15	102531392	34627497	0.3377	10.4906
chr16	90354753	59019730	0.6532	15.4812
chr17	81195210	72466127	0.8925	20.2605
chr18	78077248	16424771	0.2104	7.5617
chr19	59128983	41450505	0.701	21.518
chr20	63025520	20385431	0.3234	8.3126
chr21	48129895	5589147	0.1161	4.4193
chr22	51304566	19584718	0.3817	11.1322
chrMT	16571	11611	0.7007	2.1546
chrX	155270560	44729876	0.2881	7.4972

chrY	59373566	3943317	0.0664	3.7483

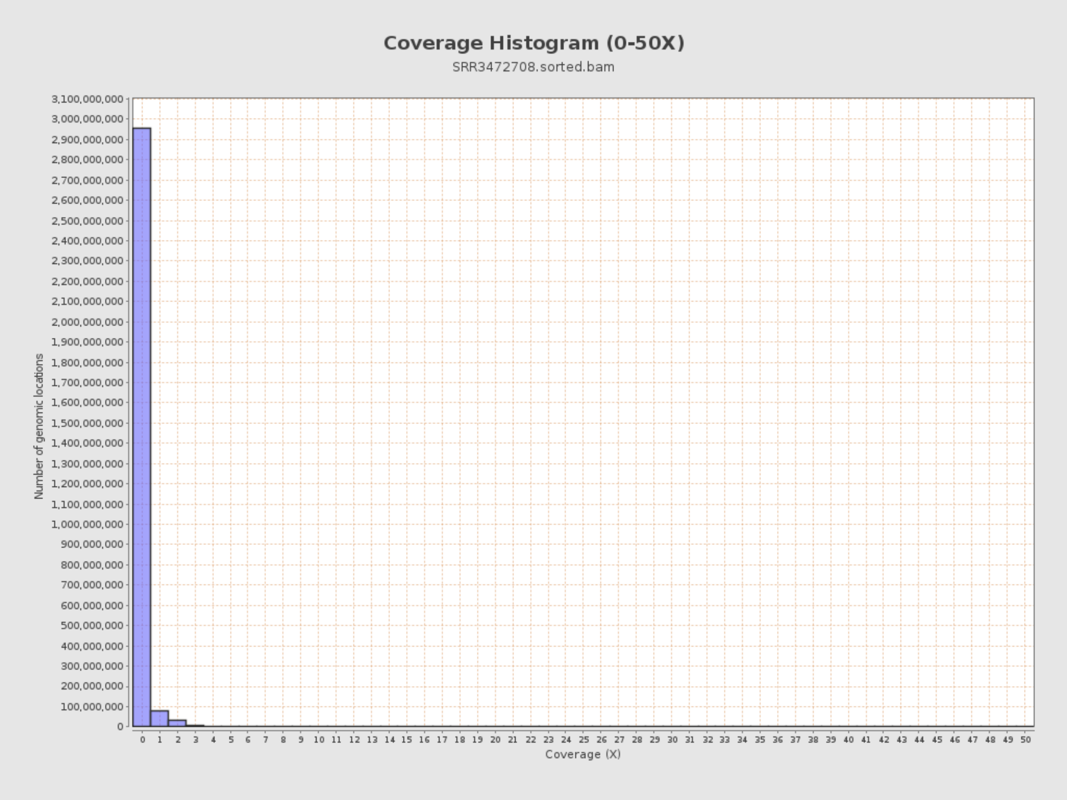
3. Results : Coverage across reference



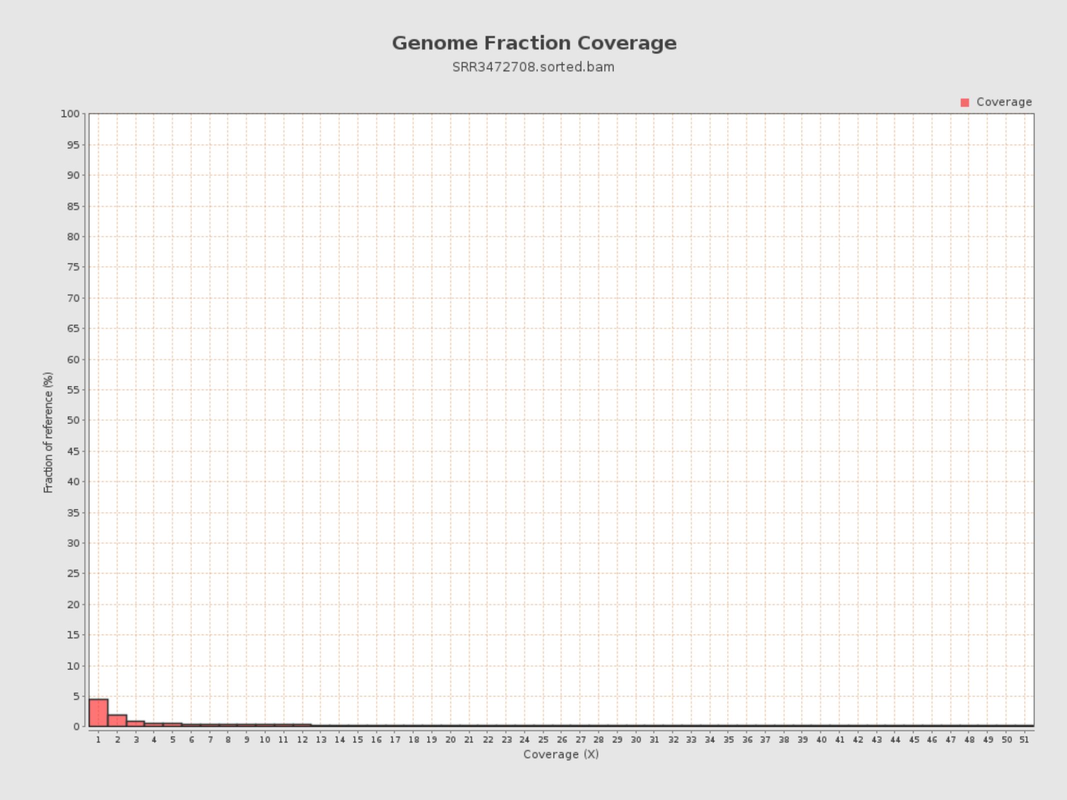
4. Results : Coverage Histogram



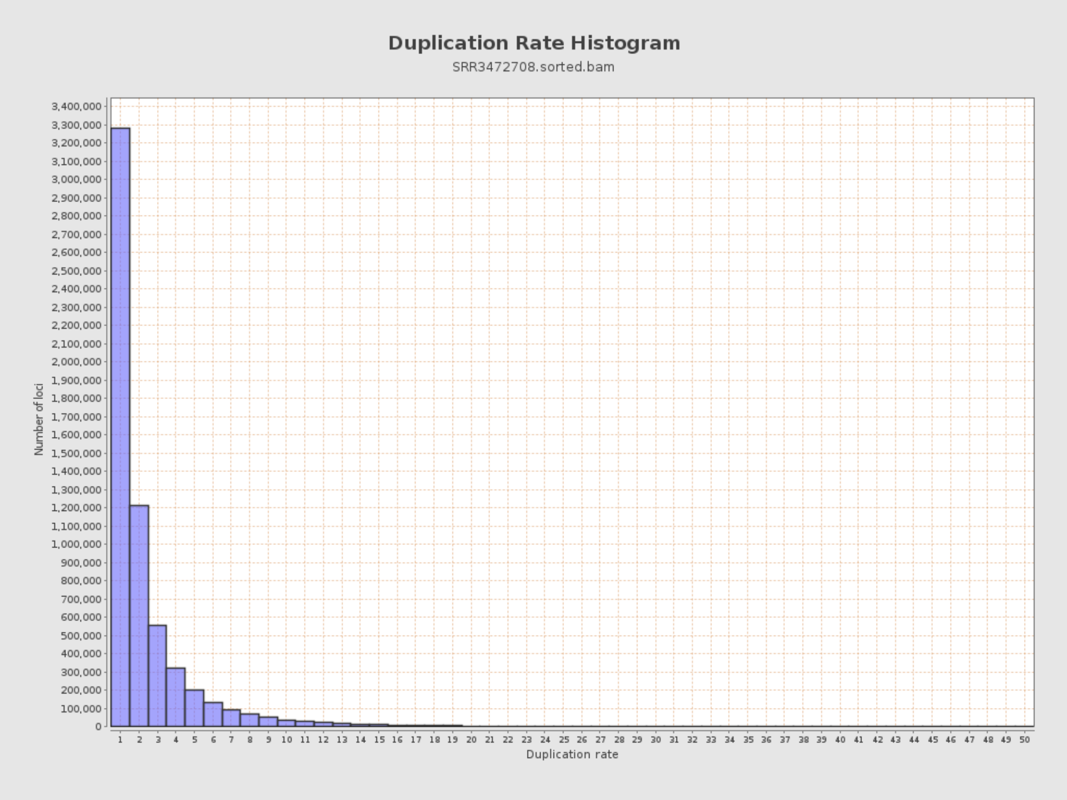
5. Results : Coverage Histogram (0-50X)



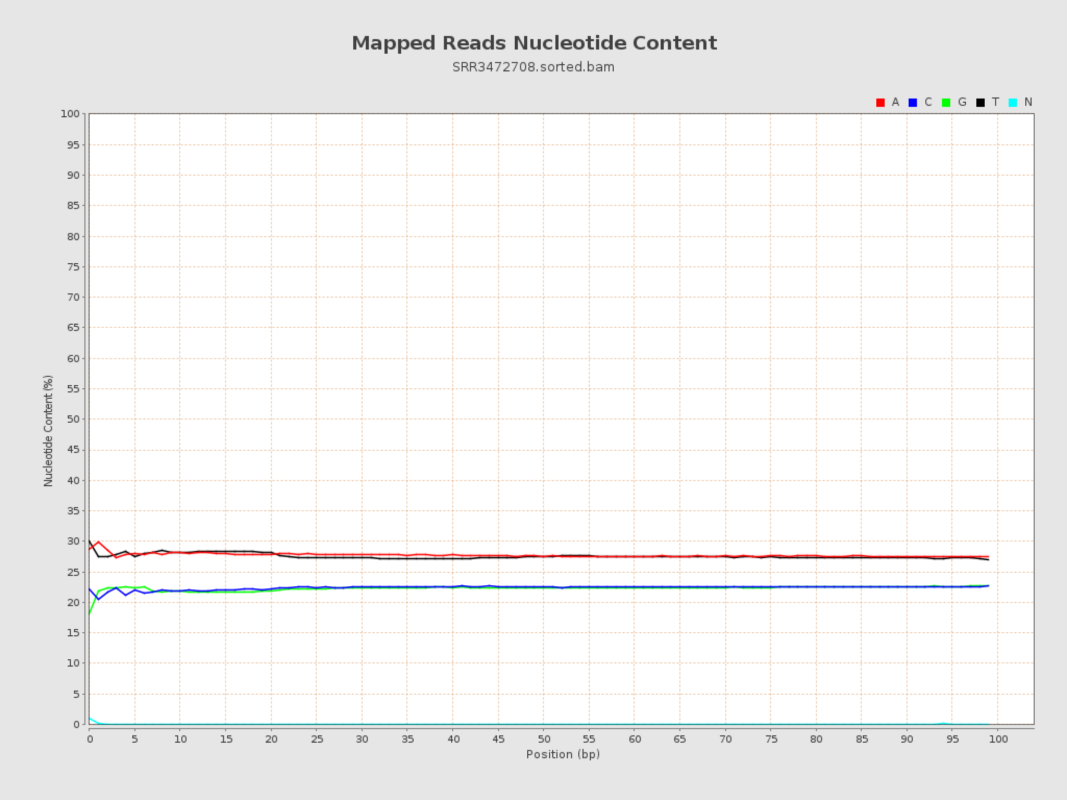
6. Results : Genome Fraction Coverage



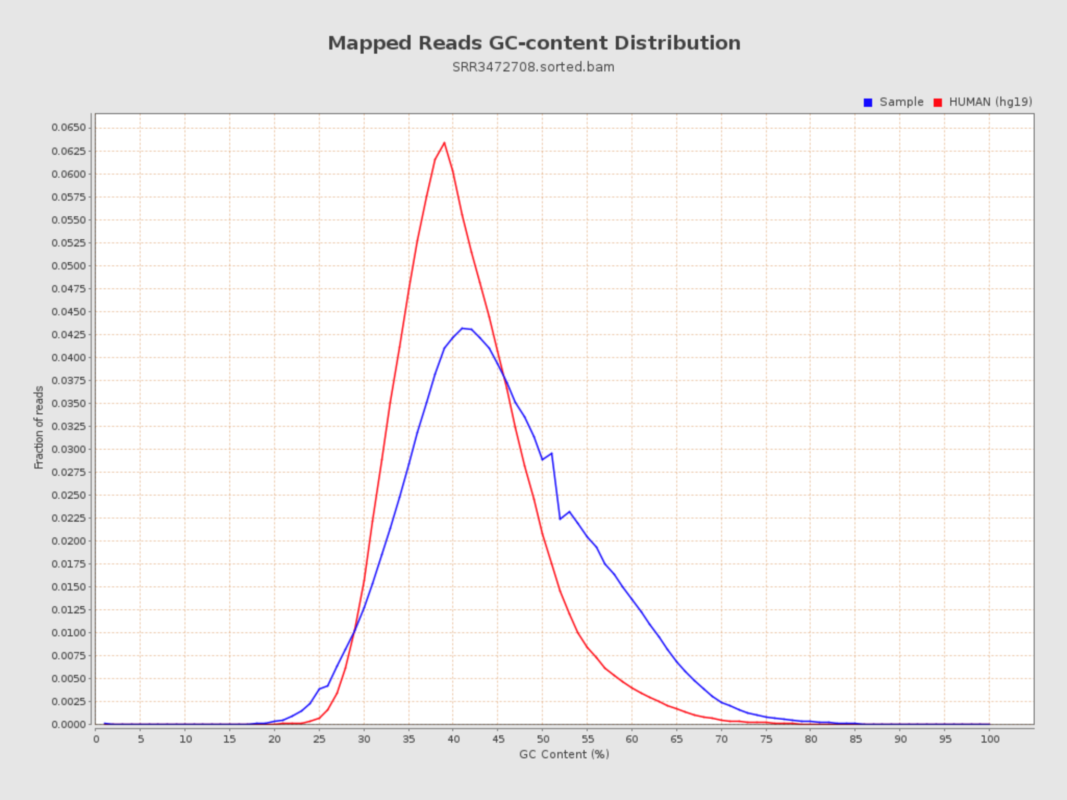
7. Results : Duplication Rate Histogram



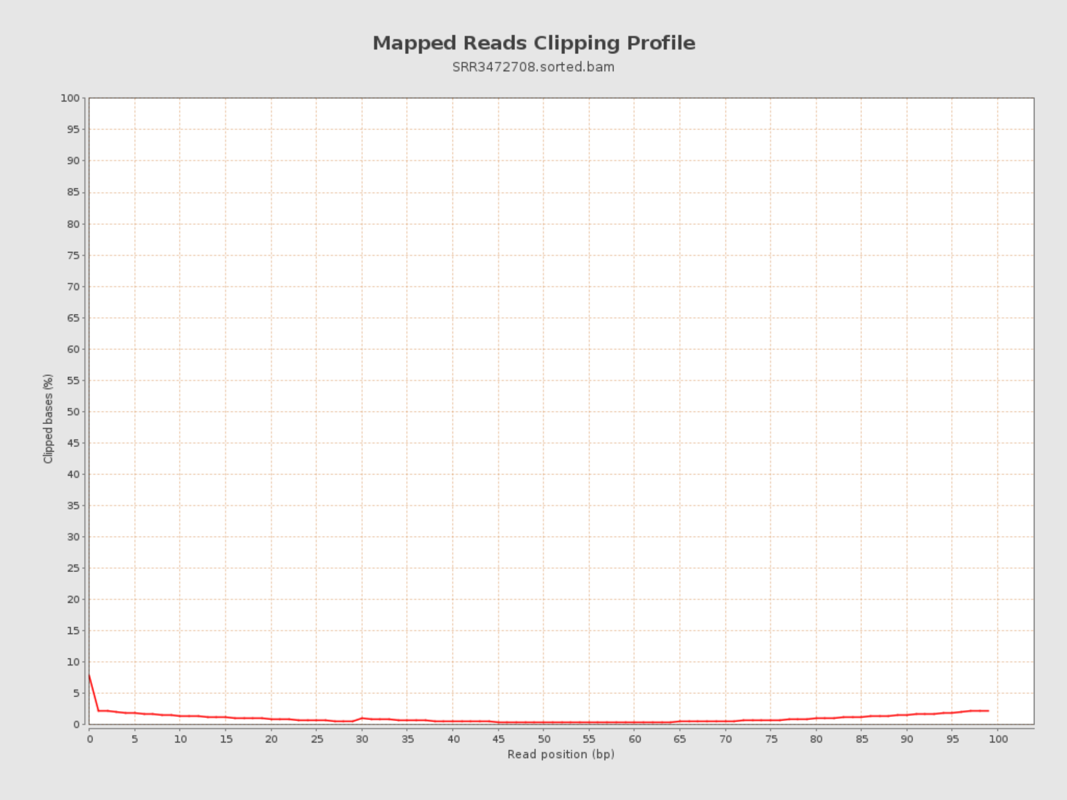
8. Results : Mapped Reads Nucleotide Content



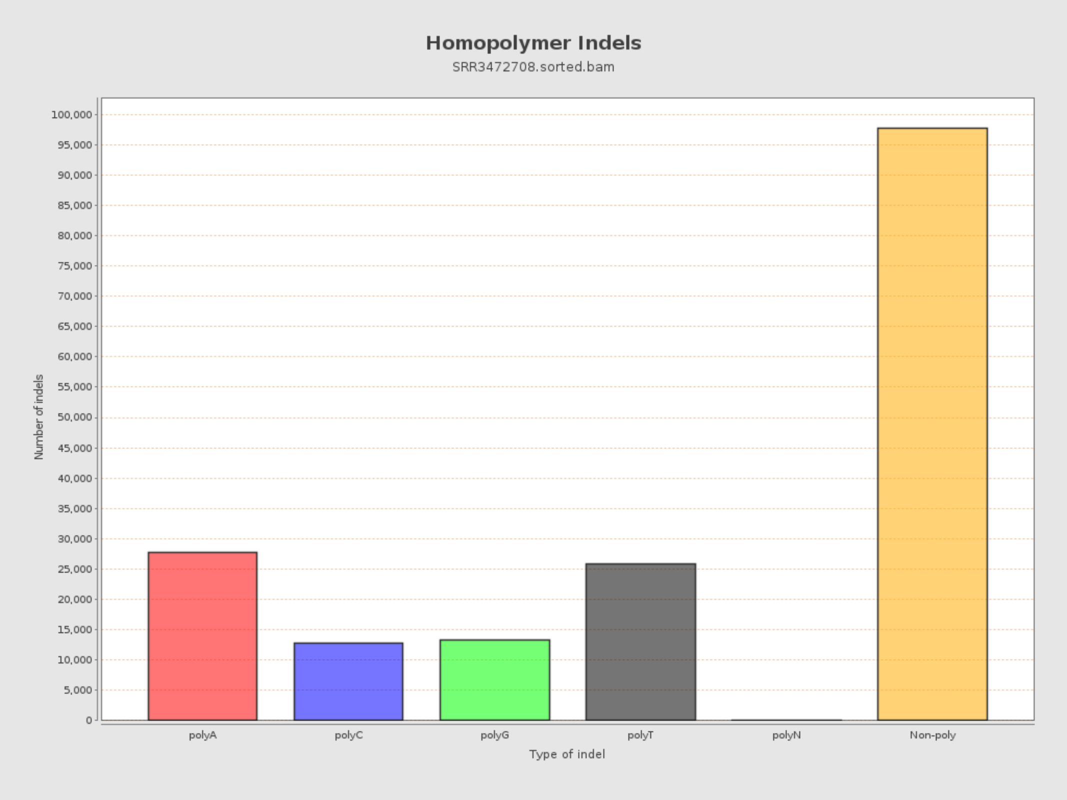
9. Results : Mapped Reads GC-content Distribution



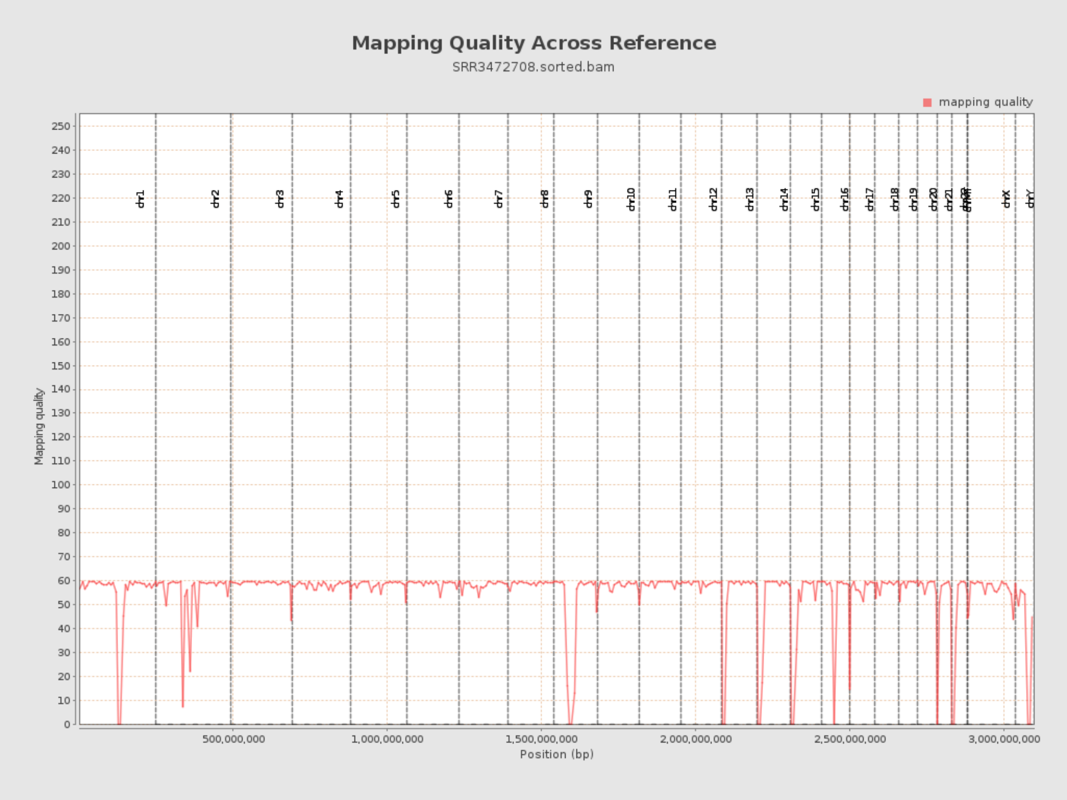
10. Results : Mapped Reads Clipping Profile



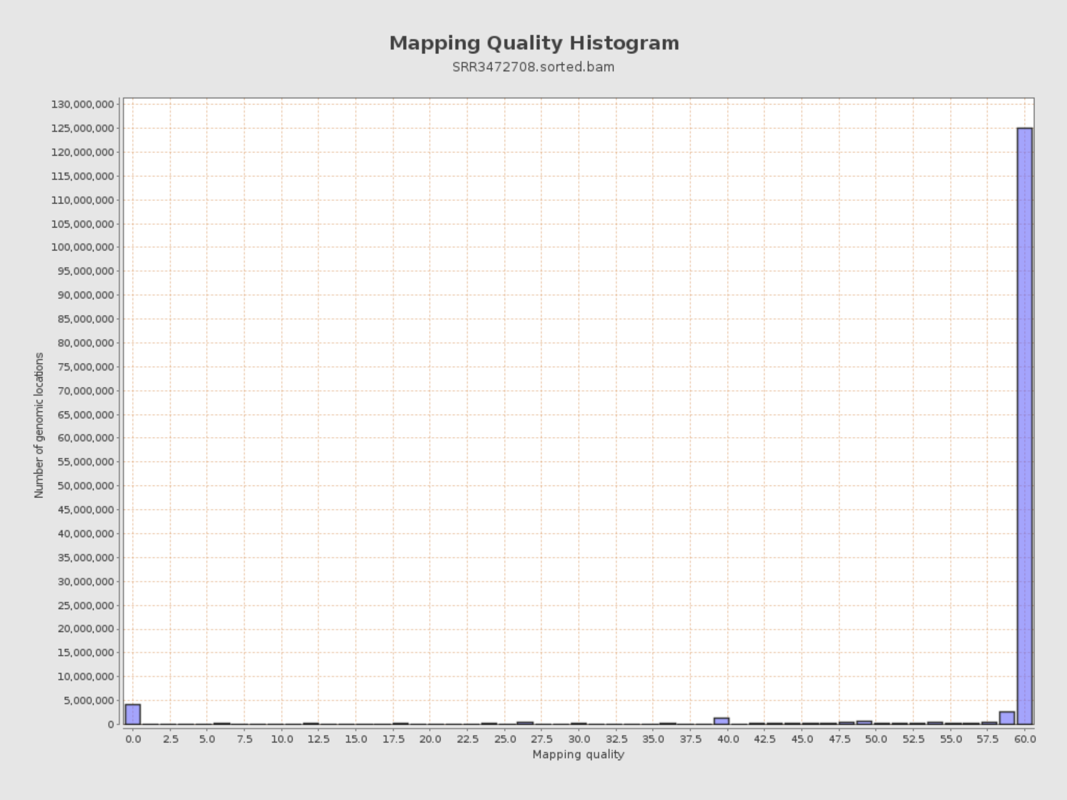
11. Results : Homopolymer Indels



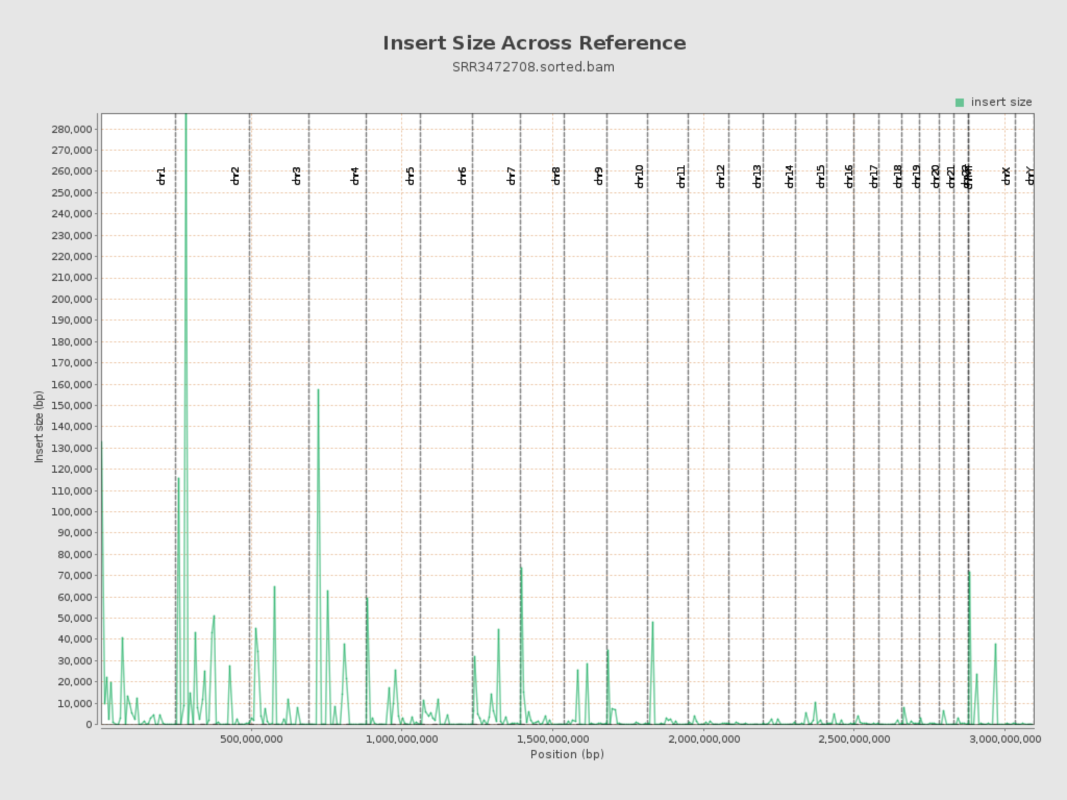
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram