Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 15:19:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472707.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_SRR3472707 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472707_1.fastq.gz SRR3472707_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 15:19:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472707.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,959,194
Mapped reads	16,802,825 / 99.08%
Unmapped reads	156,369 / 0.92%
Mapped paired reads	16,802,825 / 99.08%
Mapped reads, first in pair	8,428,954 / 49.7%
Mapped reads, second in pair	8,373,871 / 49.38%
Mapped reads, both in pair	16,709,062 / 98.53%
Mapped reads, singletons	93,763 / 0.55%
Secondary alignments	0
Supplementary alignments	58,093 / 0.34%
Read min/max/mean length	30 / 100 / 100.14
Duplicated reads (estimated)	10,402,175 / 61.34%
Duplication rate	47.63%
Clipped reads	1,391,238 / 8.2%

2.2. ACGT Content

Number/percentage of A's	458,853,286 / 27.75%
Number/percentage of C's	370,525,508 / 22.4%
Number/percentage of T's	456,378,830 / 27.6%
Number/percentage of G's	367,713,698 / 22.23%
Number/percentage of N's	321,451 / 0.02%

GC Percentage	44.64%

2.3. Coverage

Mean	0.5343
Standard Deviation	16.3403

2.4. Mapping Quality

Mean Mapping Quality	55.18

2.5. Insert size

Mean	24,090.51
Standard Deviation	1,547,673.6
P25/Median/P75	172 / 242 / 327

2.6. Mismatches and indels

General error rate	0.62%
Mismatches	10,112,440
Insertions	95,839
Mapped reads with at least one insertion	0.56%
Deletions	92,397
Mapped reads with at least one deletion	0.54%
Homopolymer indels	46.65%

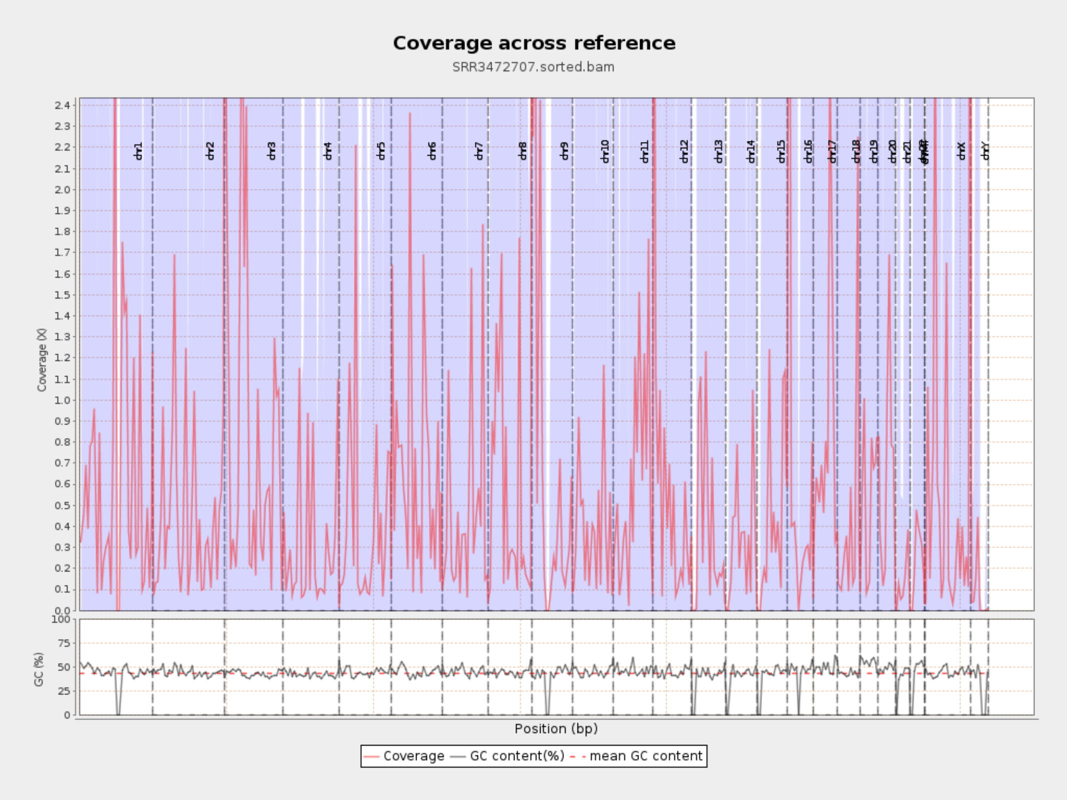
2.7. Chromosome stats

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

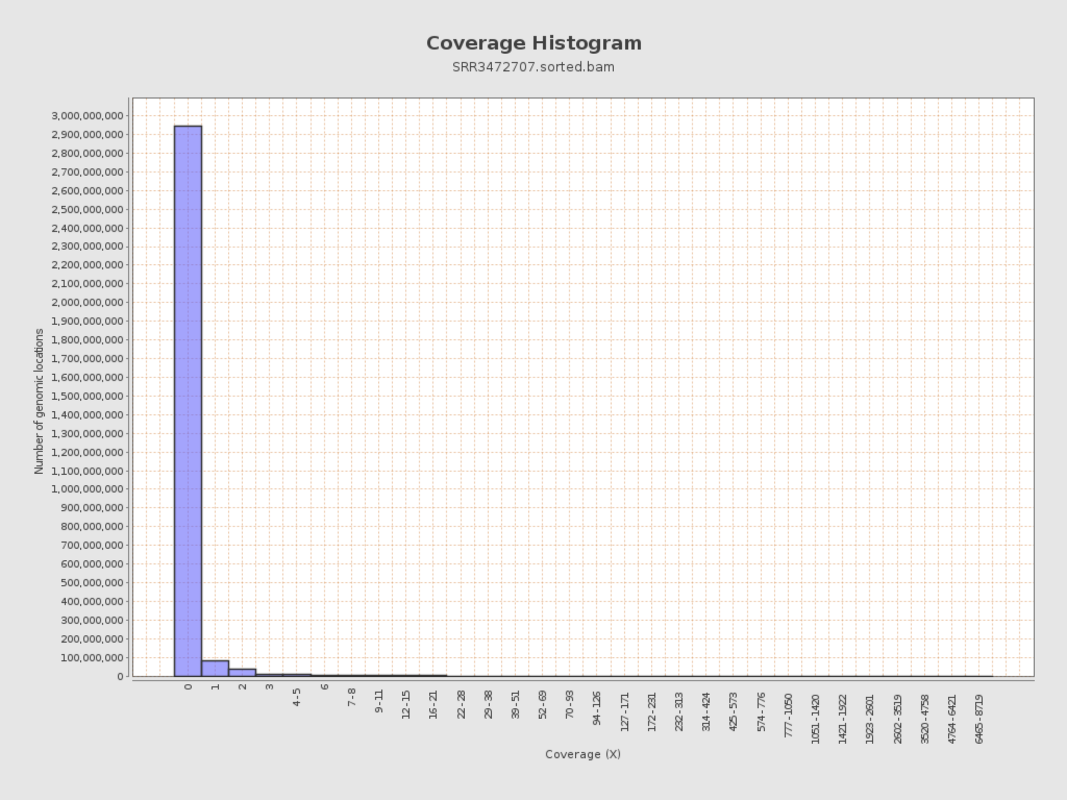
		bases	coverage	deviation
chr1	249250621	156660624	0.6285	19.8086
chr2	243199373	107713954	0.4429	14.3713
chr3	198022430	182193072	0.9201	20.0004
chr4	191154276	58087558	0.3039	9.7901
chr5	180915260	75070668	0.4149	12.6893
chr6	171115067	115011444	0.6721	17.0092
chr7	159138663	75130298	0.4721	15.9522
chr8	146364022	81433419	0.5564	19.1001
chr9	141213431	103418893	0.7324	18.3876
chr10	135534747	52581228	0.388	14.0122
chr11	135006516	85526438	0.6335	18.4994
chr12	133851895	84484805	0.6312	22.5499
chr13	115169878	44527737	0.3866	13.5406
chr14	107349540	35400074	0.3298	10.2724
chr15	102531392	44394819	0.433	14.248
chr16	90354753	62622836	0.6931	18.071
chr17	81195210	66311668	0.8167	18.9548
chr18	78077248	33430893	0.4282	16.7736
chr19	59128983	33093492	0.5597	13.2384
chr20	63025520	43170186	0.685	20.0785
chr21	48129895	6733607	0.1399	4.9512
chr22	51304566	12026788	0.2344	5.1486
chrMT	16571	4977	0.3003	0.9376
chrX	155270560	89818254	0.5785	17.0906

chrY	59373566	5168236	0.087	6.0647

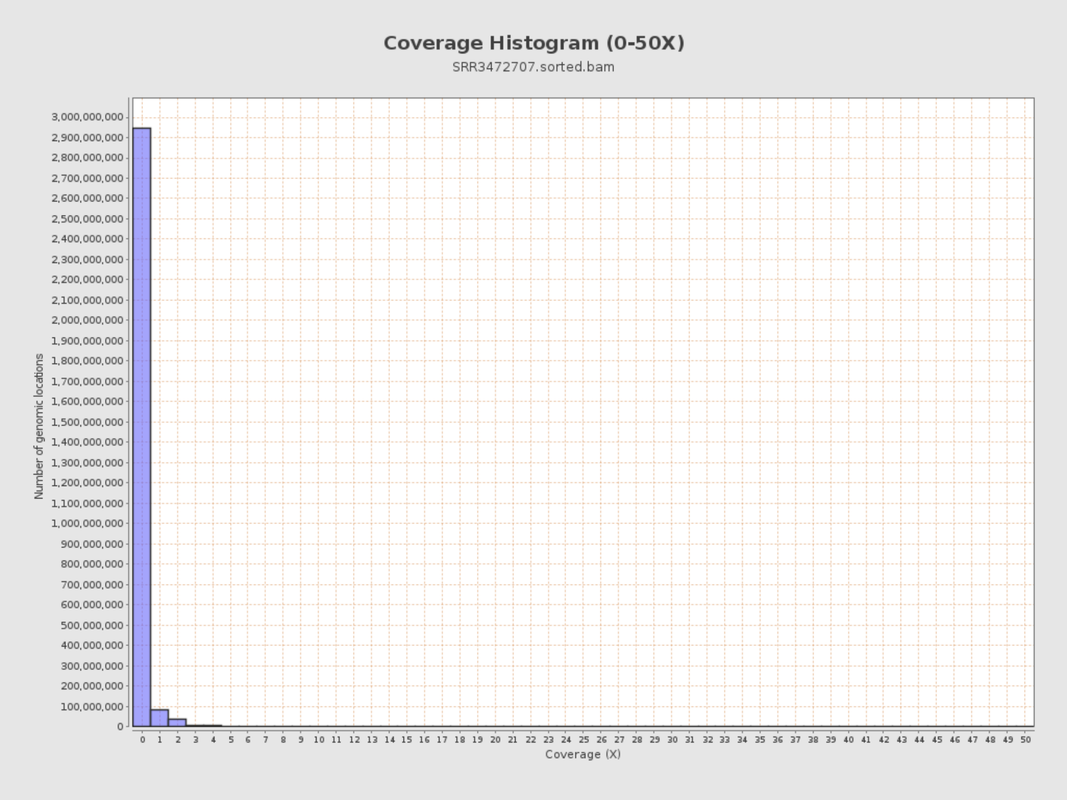
3. Results : Coverage across reference



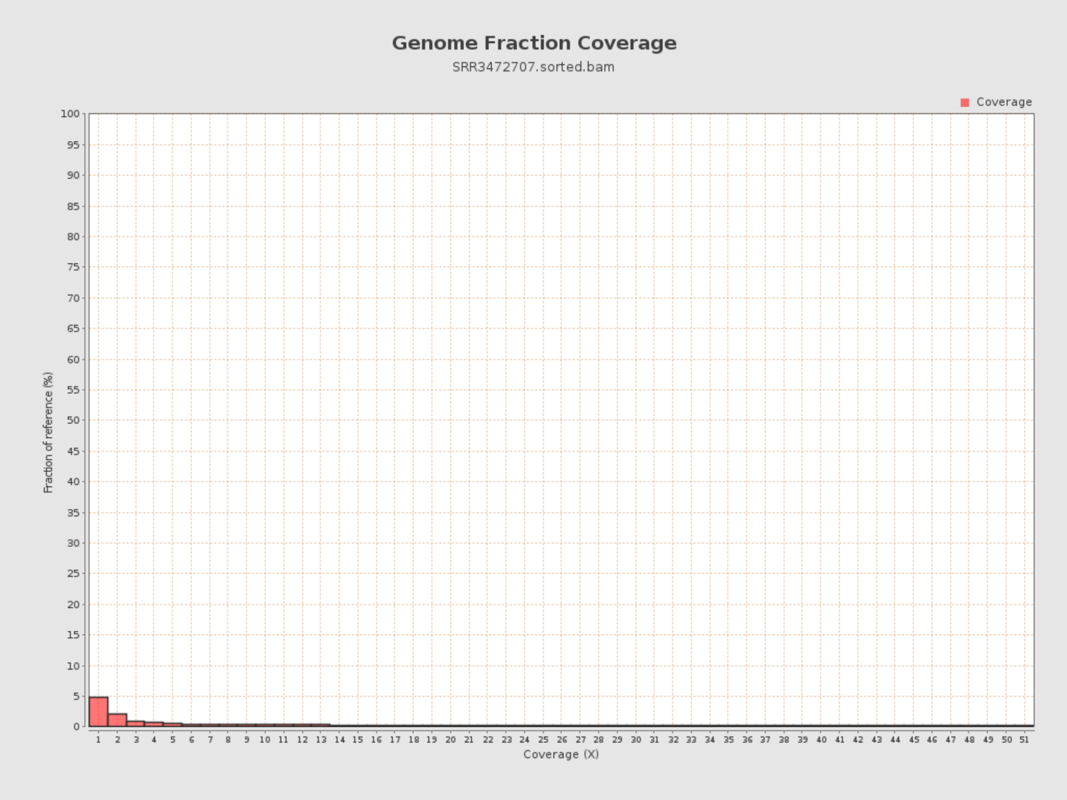
4. Results : Coverage Histogram



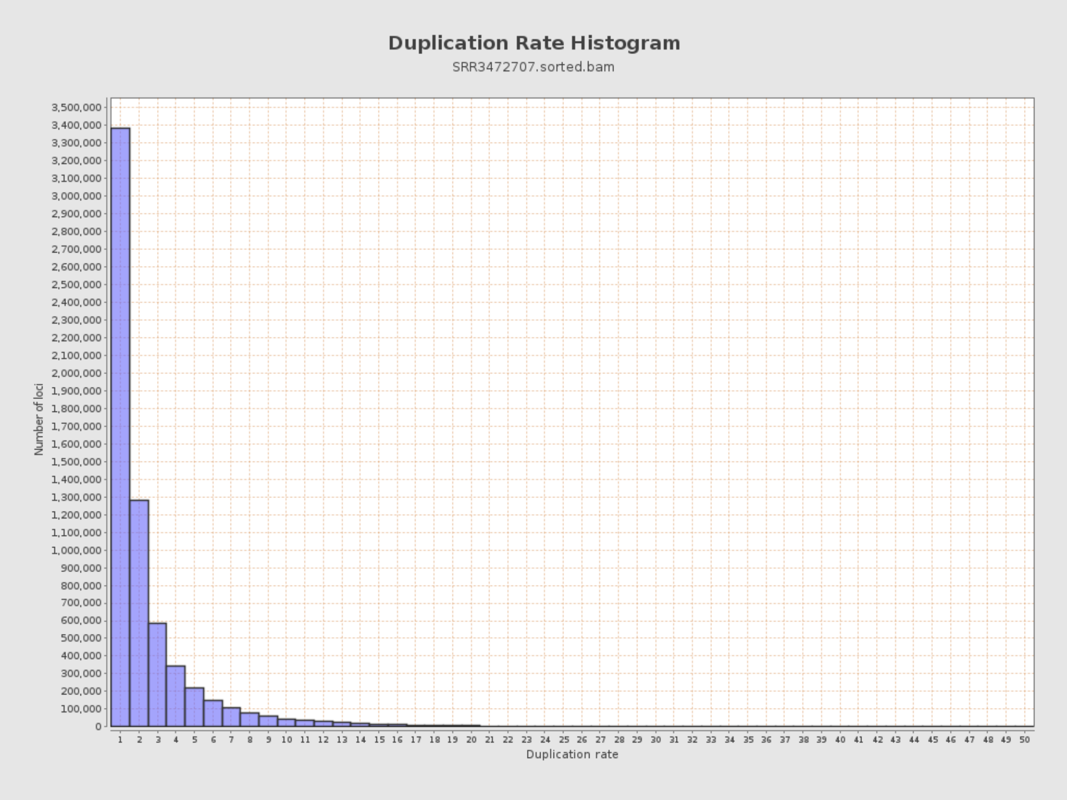
5. Results : Coverage Histogram (0-50X)



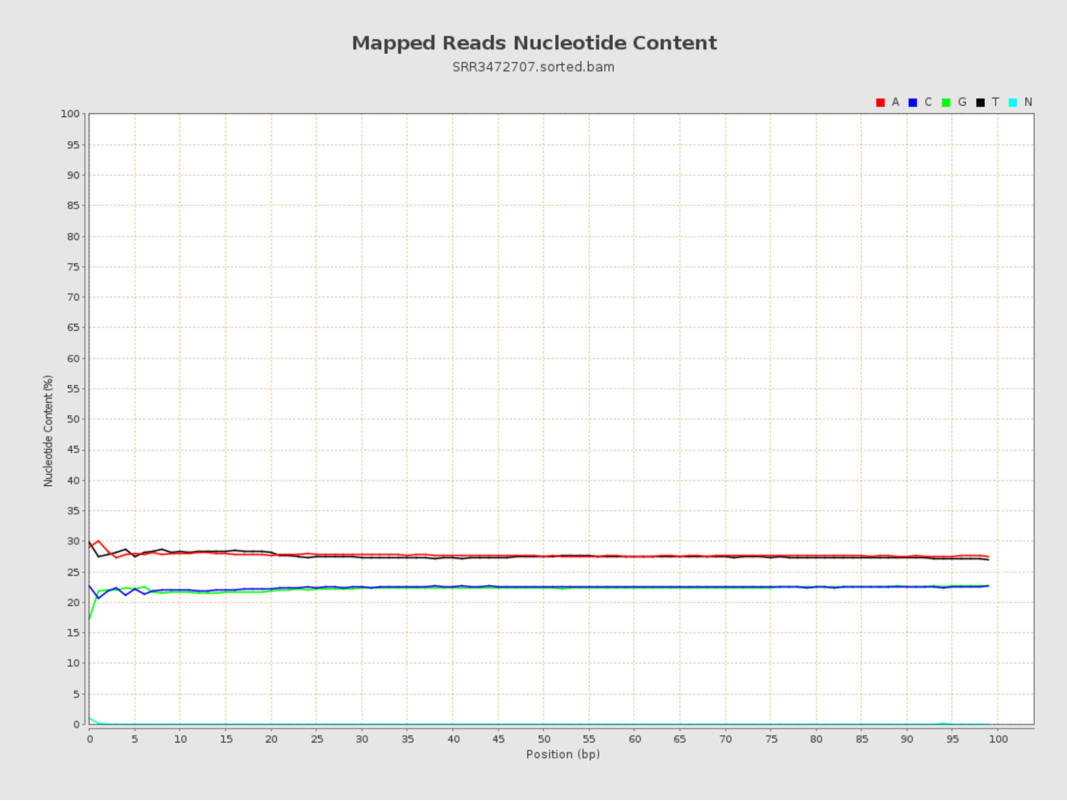
6. Results : Genome Fraction Coverage



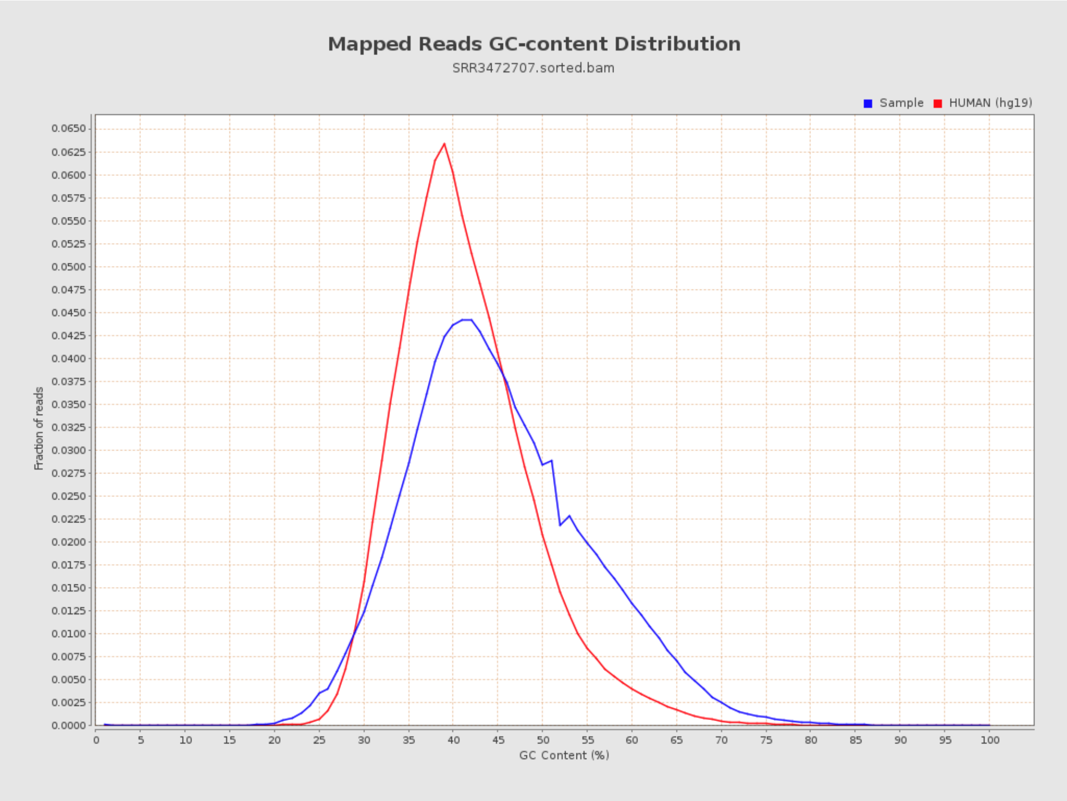
7. Results : Duplication Rate Histogram



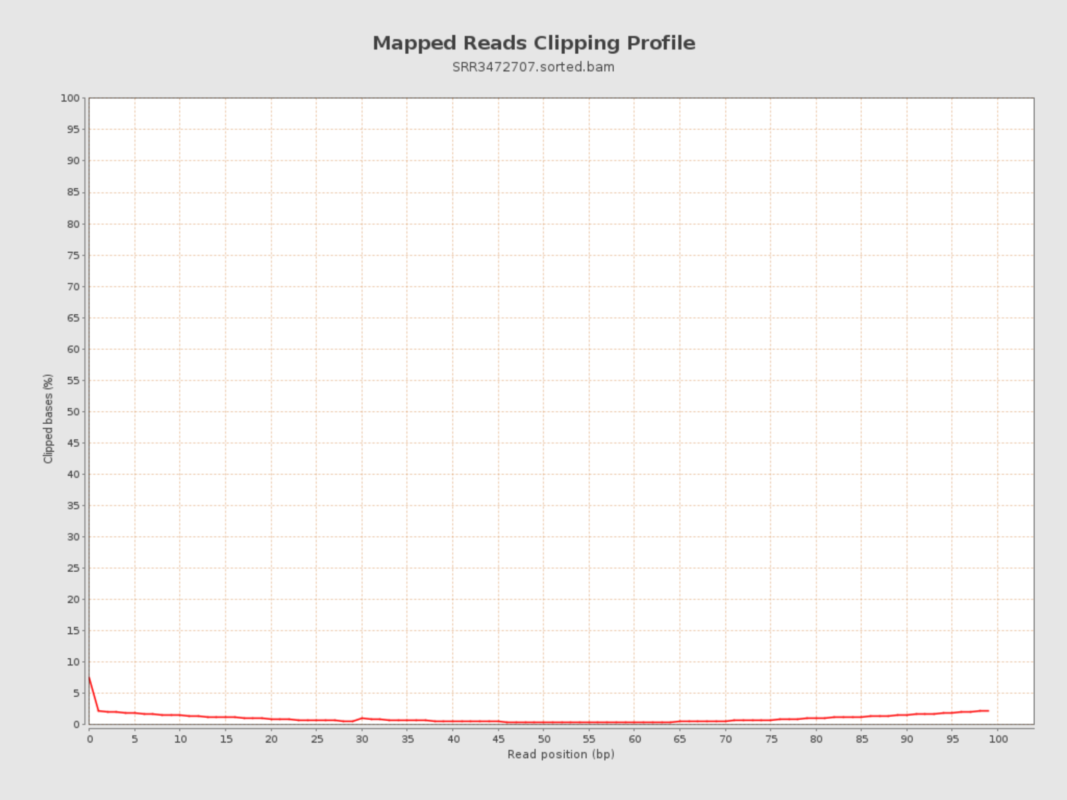
8. Results : Mapped Reads Nucleotide Content



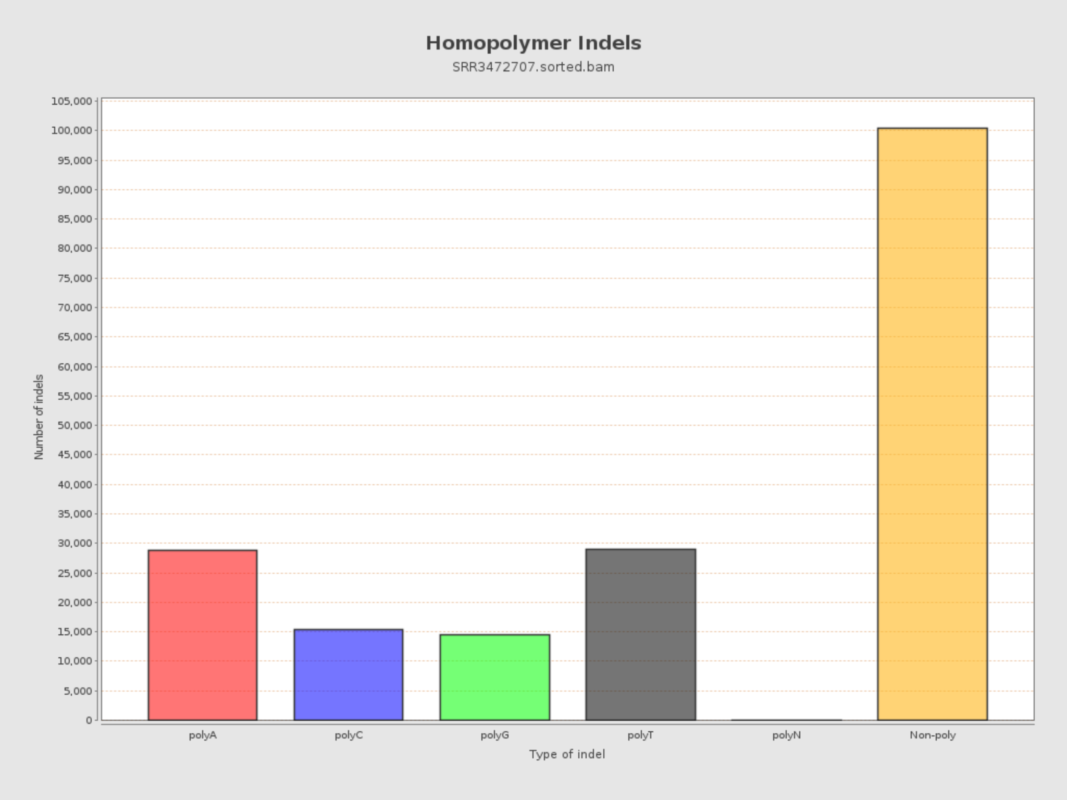
9. Results : Mapped Reads GC-content Distribution



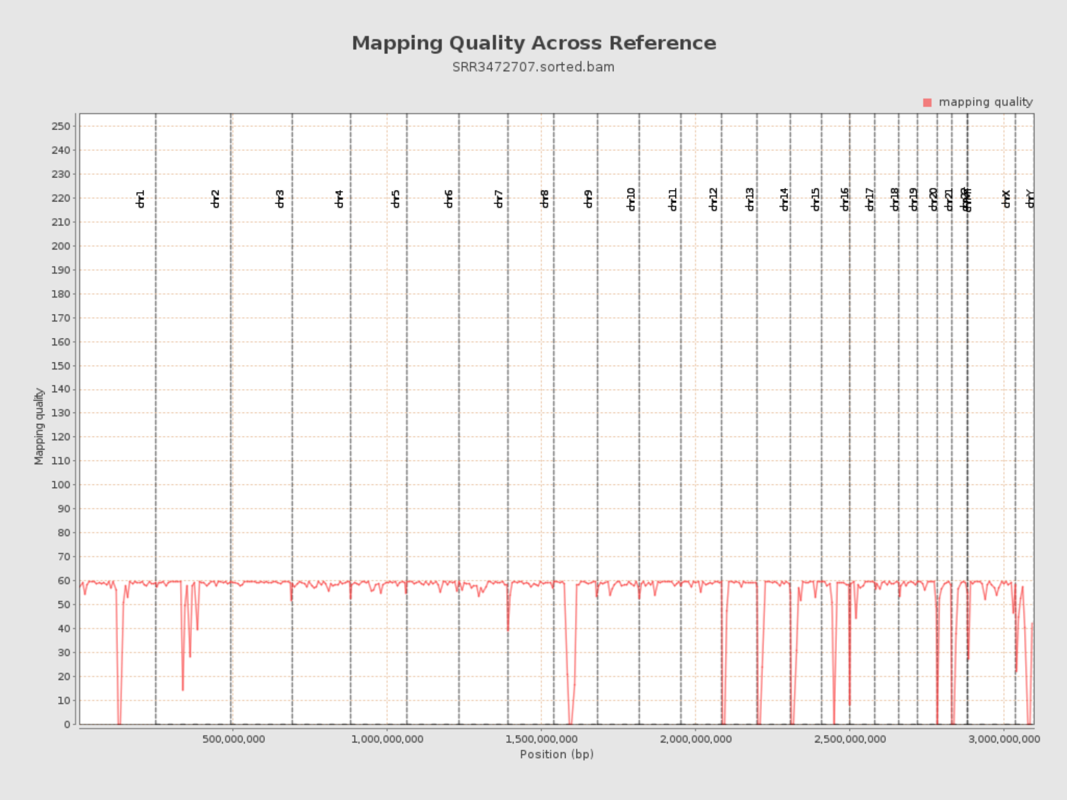
10. Results : Mapped Reads Clipping Profile



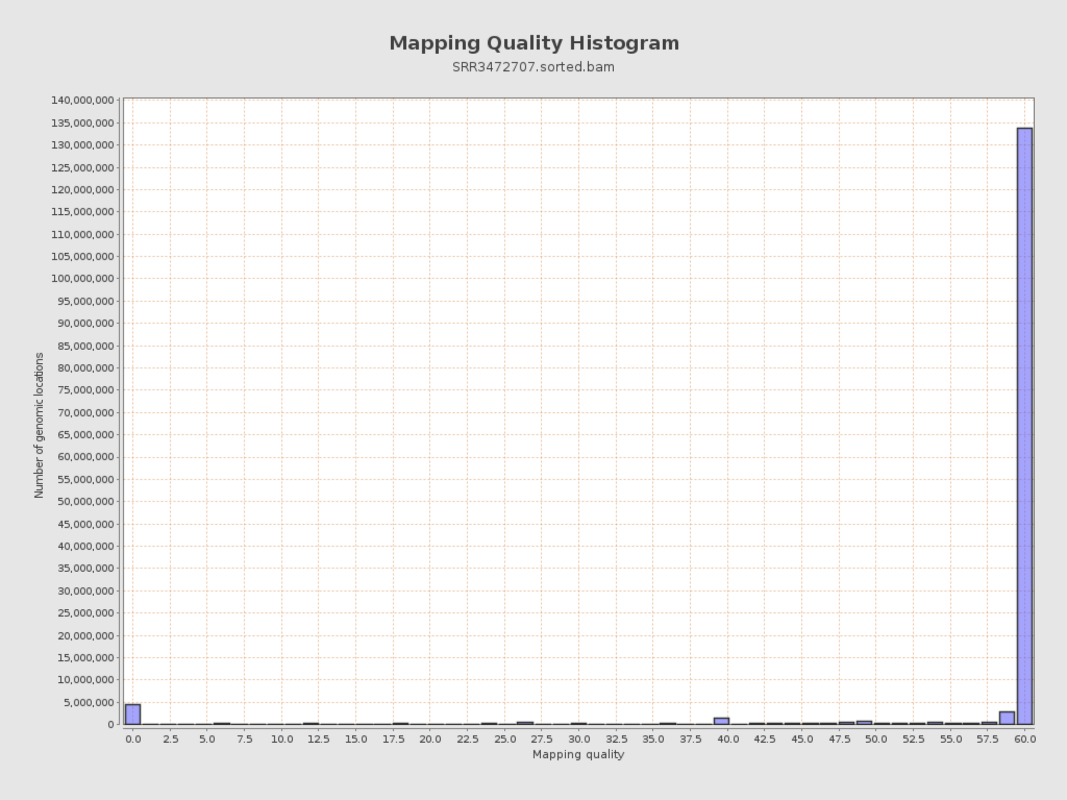
11. Results : Homopolymer Indels



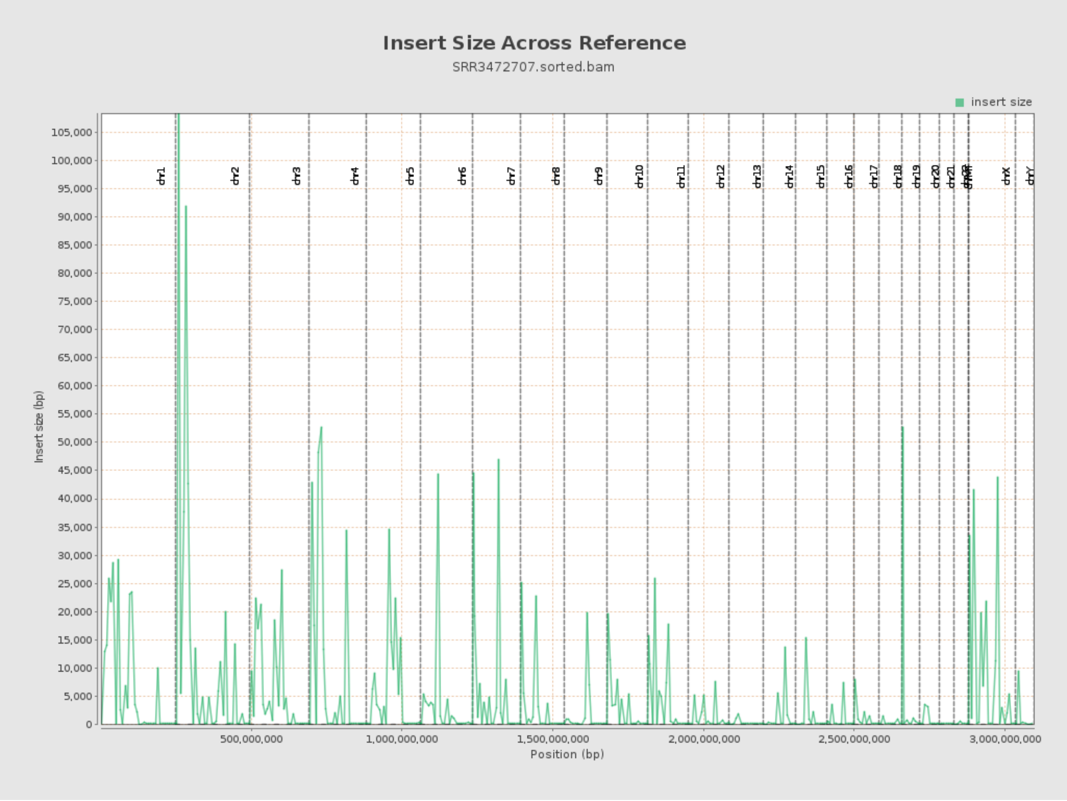
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram