Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 15:56:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472507.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_SRR3472507 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472507_1.fastq.gz SRR3472507_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 15:56:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472507.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,773,196
Mapped reads	16,530,807 / 98.55%
Unmapped reads	242,389 / 1.45%
Mapped paired reads	16,530,807 / 98.55%
Mapped reads, first in pair	8,294,628 / 49.45%
Mapped reads, second in pair	8,236,179 / 49.1%
Mapped reads, both in pair	16,415,120 / 97.87%
Mapped reads, singletons	115,687 / 0.69%
Secondary alignments	0
Supplementary alignments	60,180 / 0.36%
Read min/max/mean length	30 / 100 / 100.15
Duplicated reads (estimated)	10,310,724 / 61.47%
Duplication rate	45.95%
Clipped reads	1,301,966 / 7.76%

2.2. ACGT Content

Number/percentage of A's	460,480,346 / 28.3%
Number/percentage of C's	355,724,721 / 21.86%
Number/percentage of T's	457,605,896 / 28.12%
Number/percentage of G's	352,997,266 / 21.7%
Number/percentage of N's	250,998 / 0.02%

GC Percentage	43.56%

2.3. Coverage

Mean	0.5257
Standard Deviation	17.862

2.4. Mapping Quality

Mean Mapping Quality	55.04

2.5. Insert size

Mean	26,112.16
Standard Deviation	1,580,745.77
P25/Median/P75	177 / 247 / 334

2.6. Mismatches and indels

General error rate	0.65%
Mismatches	10,334,621
Insertions	94,439
Mapped reads with at least one insertion	0.57%
Deletions	89,406
Mapped reads with at least one deletion	0.53%
Homopolymer indels	46.14%

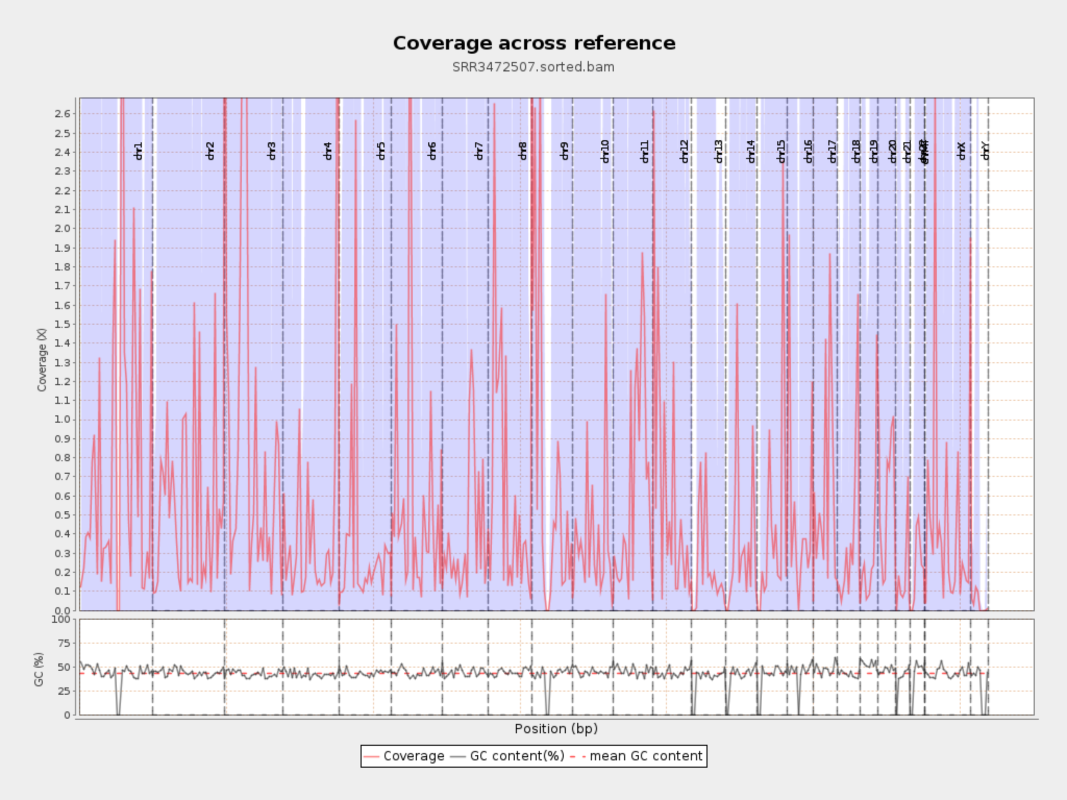
2.7. Chromosome stats

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

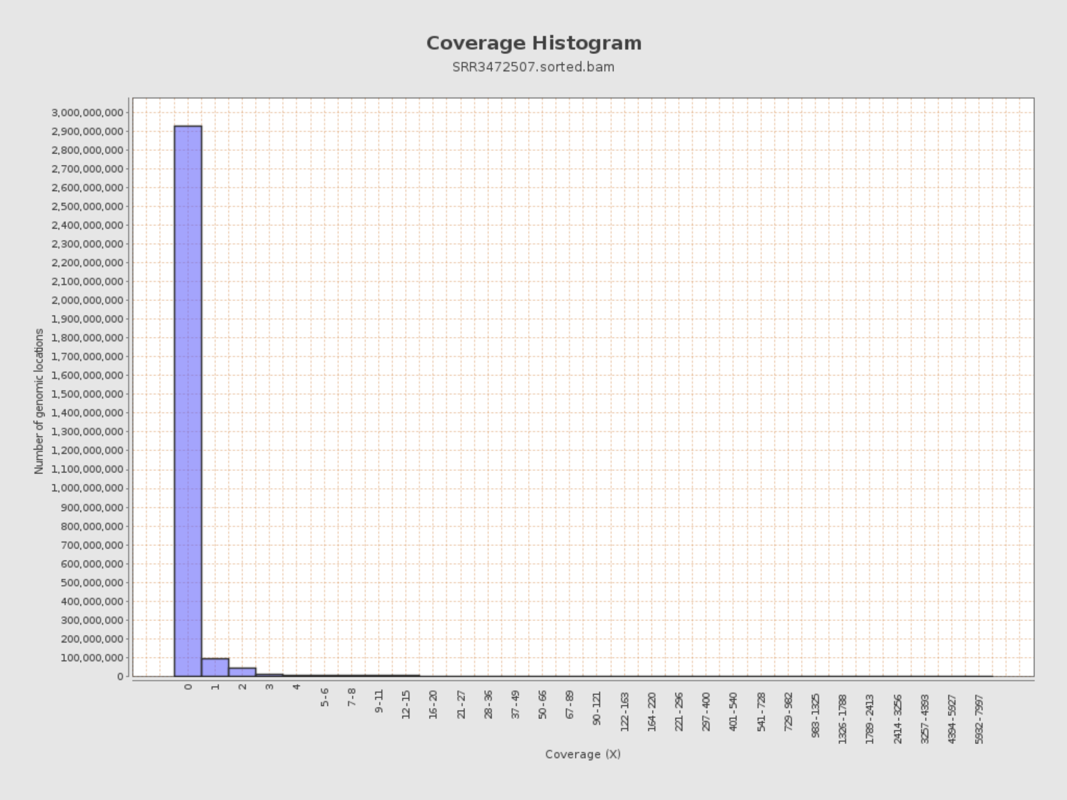
		bases	coverage	deviation
chr1	249250621	192632005	0.7728	24.1652
chr2	243199373	128280789	0.5275	19.5246
chr3	198022430	187679399	0.9478	21.7015
chr4	191154276	85885710	0.4493	18.4947
chr5	180915260	62416090	0.345	10.0574
chr6	171115067	100089716	0.5849	18.129
chr7	159138663	65186587	0.4096	14.7912
chr8	146364022	90365042	0.6174	21.8342
chr9	141213431	97412560	0.6898	17.652
chr10	135534747	52905993	0.3904	15.9195
chr11	135006516	90171815	0.6679	23.9208
chr12	133851895	84208511	0.6291	23.1741
chr13	115169878	26736378	0.2321	8.1117
chr14	107349540	38380980	0.3575	14.1672
chr15	102531392	47264131	0.461	16.228
chr16	90354753	46345506	0.5129	14.7987
chr17	81195210	51227705	0.6309	17.373
chr18	78077248	29789769	0.3815	16.5152
chr19	59128983	16615708	0.281	7.8369
chr20	63025520	39030739	0.6193	18.7829
chr21	48129895	9144833	0.19	8.207
chr22	51304566	11329208	0.2208	7.1608
chrMT	16571	2836	0.1711	0.6047
chrX	155270560	71772460	0.4622	14.009

chrY	59373566	2395476	0.0403	1.4085

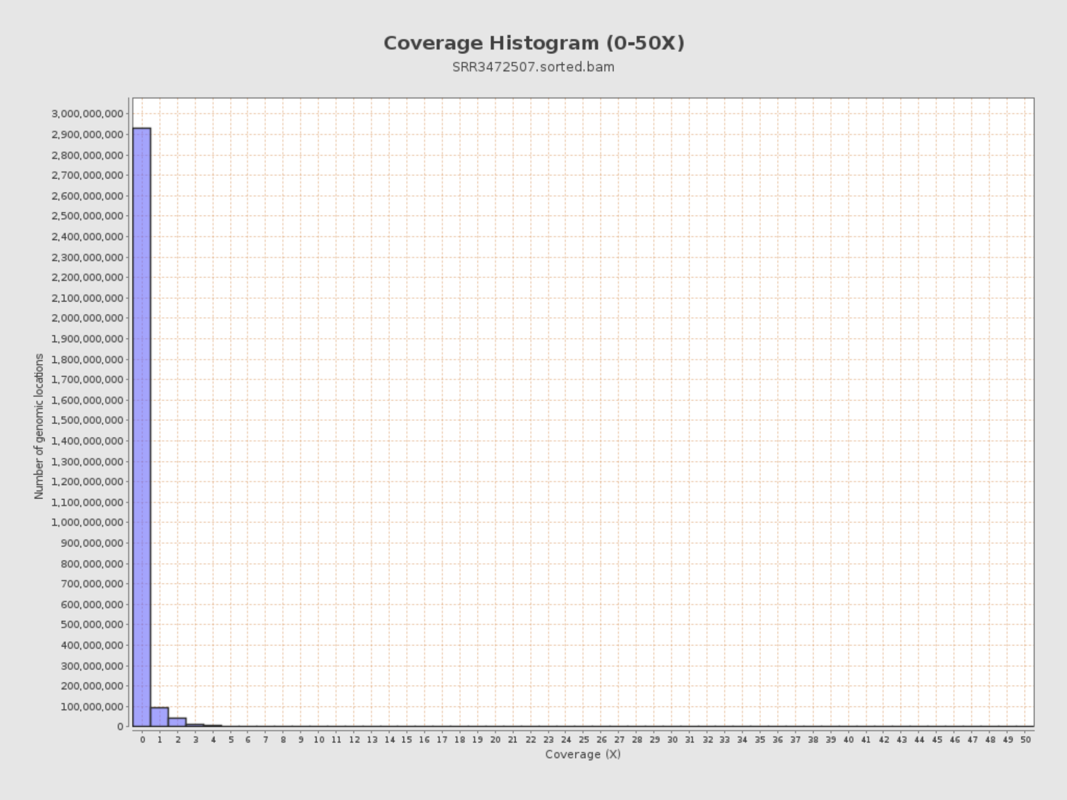
3. Results : Coverage across reference



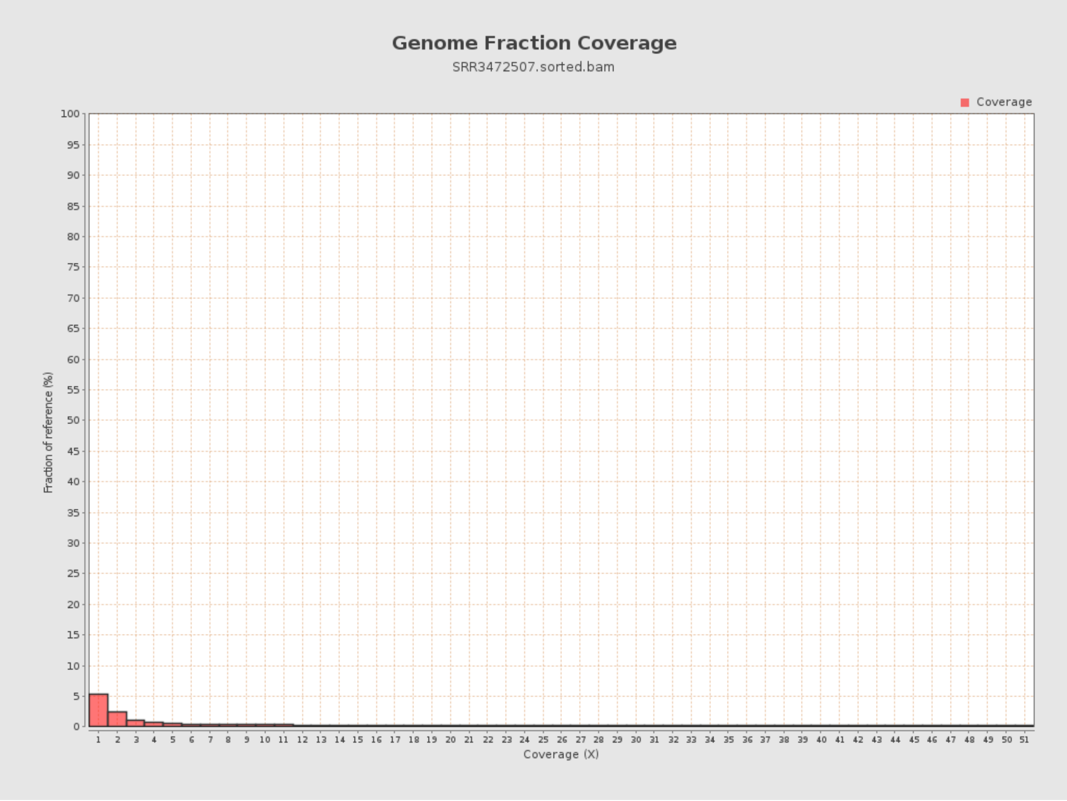
4. Results : Coverage Histogram



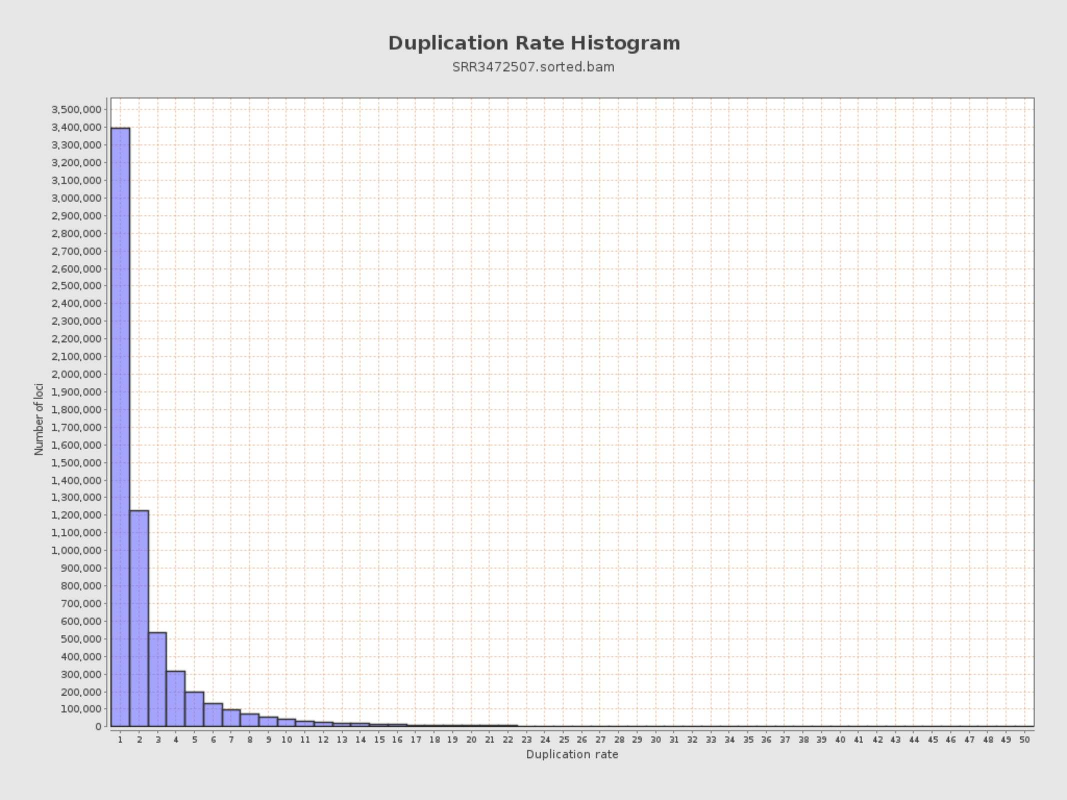
5. Results : Coverage Histogram (0-50X)



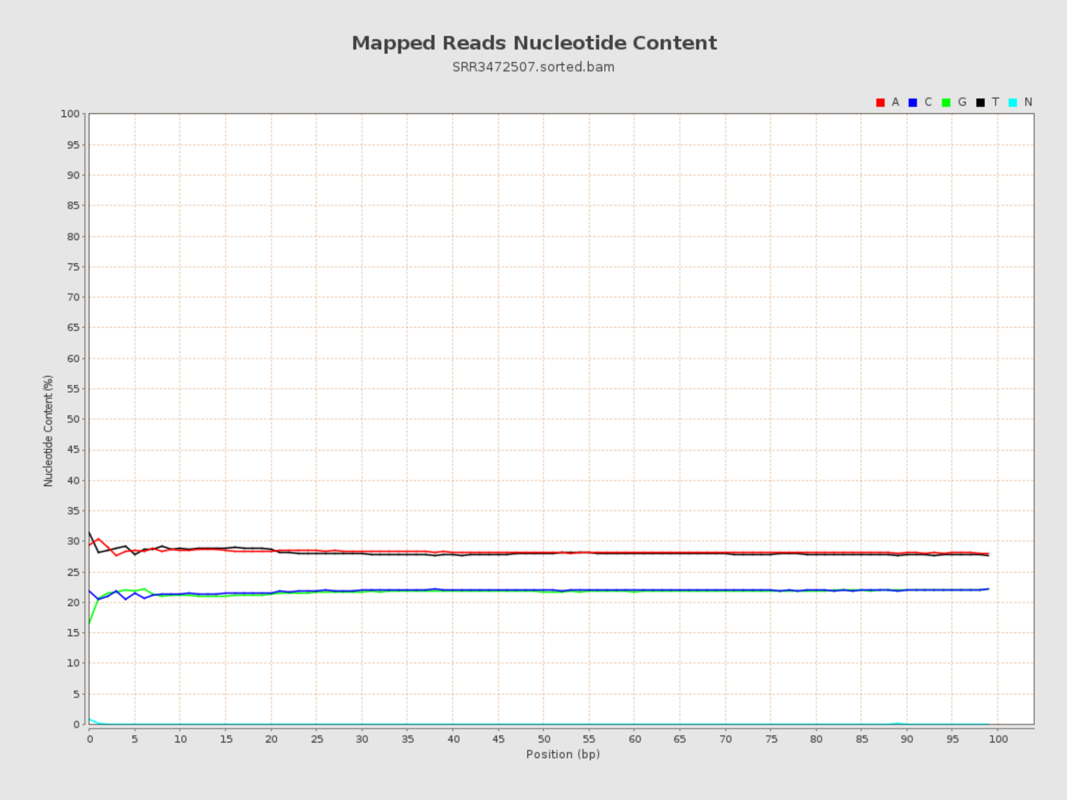
6. Results : Genome Fraction Coverage



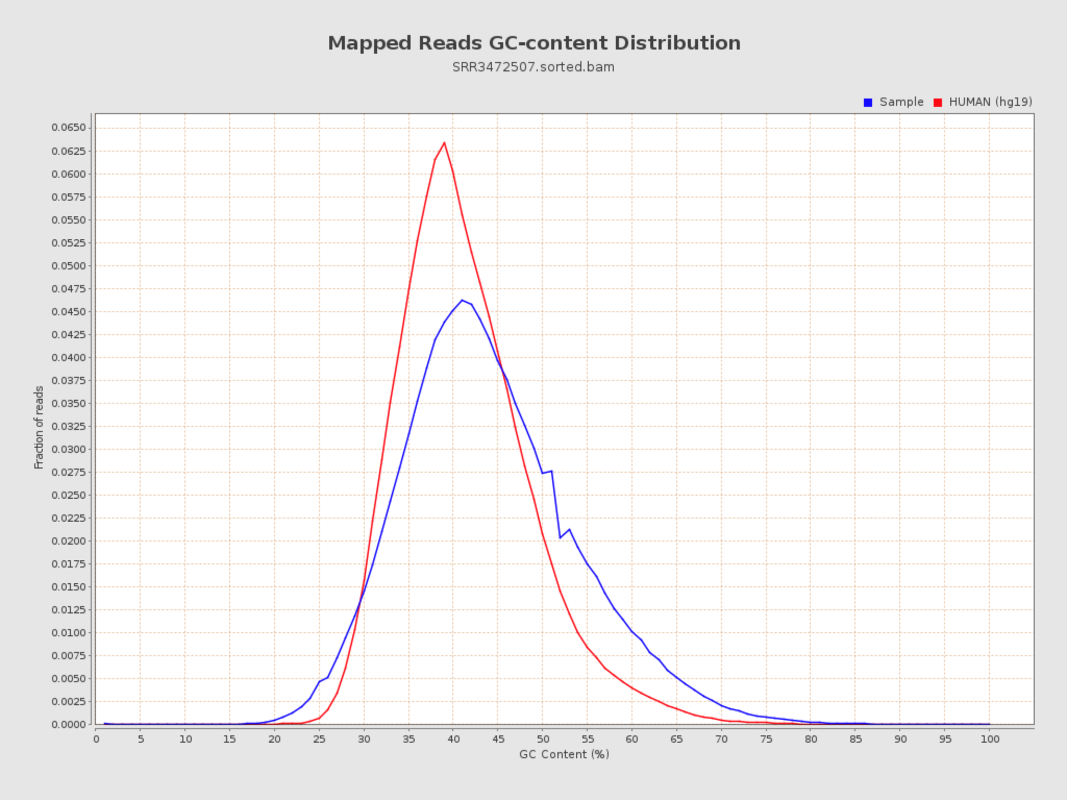
7. Results : Duplication Rate Histogram



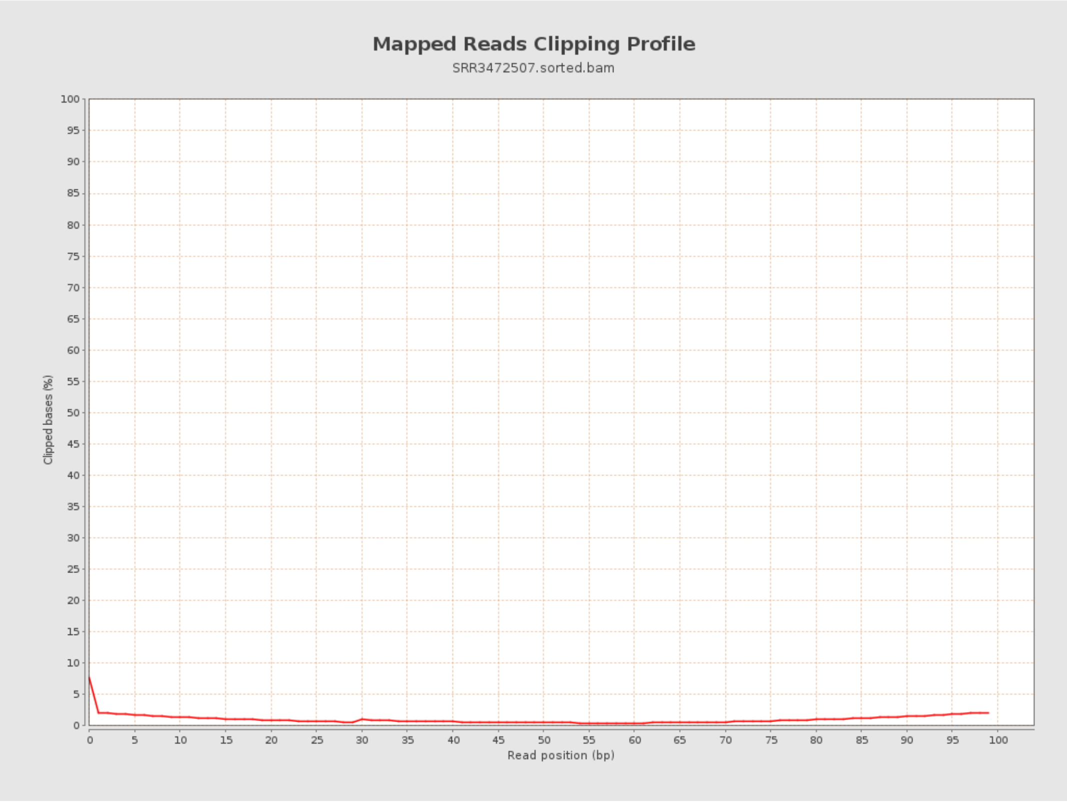
8. Results : Mapped Reads Nucleotide Content



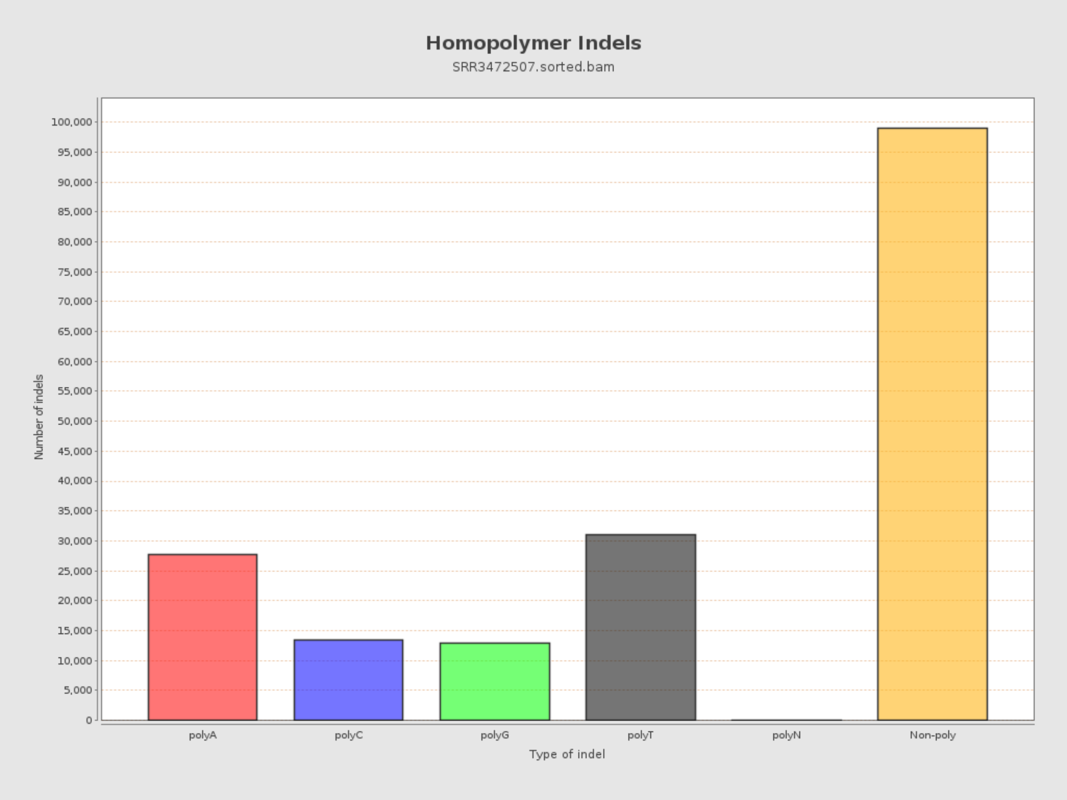
9. Results : Mapped Reads GC-content Distribution



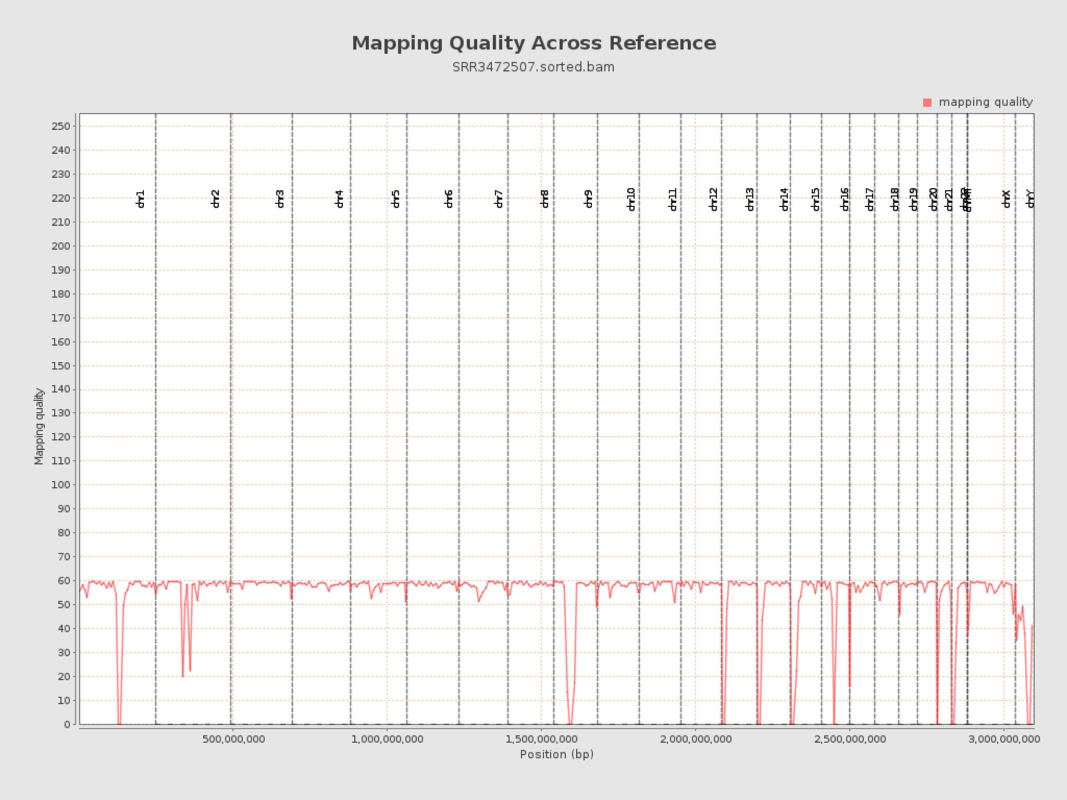
10. Results : Mapped Reads Clipping Profile



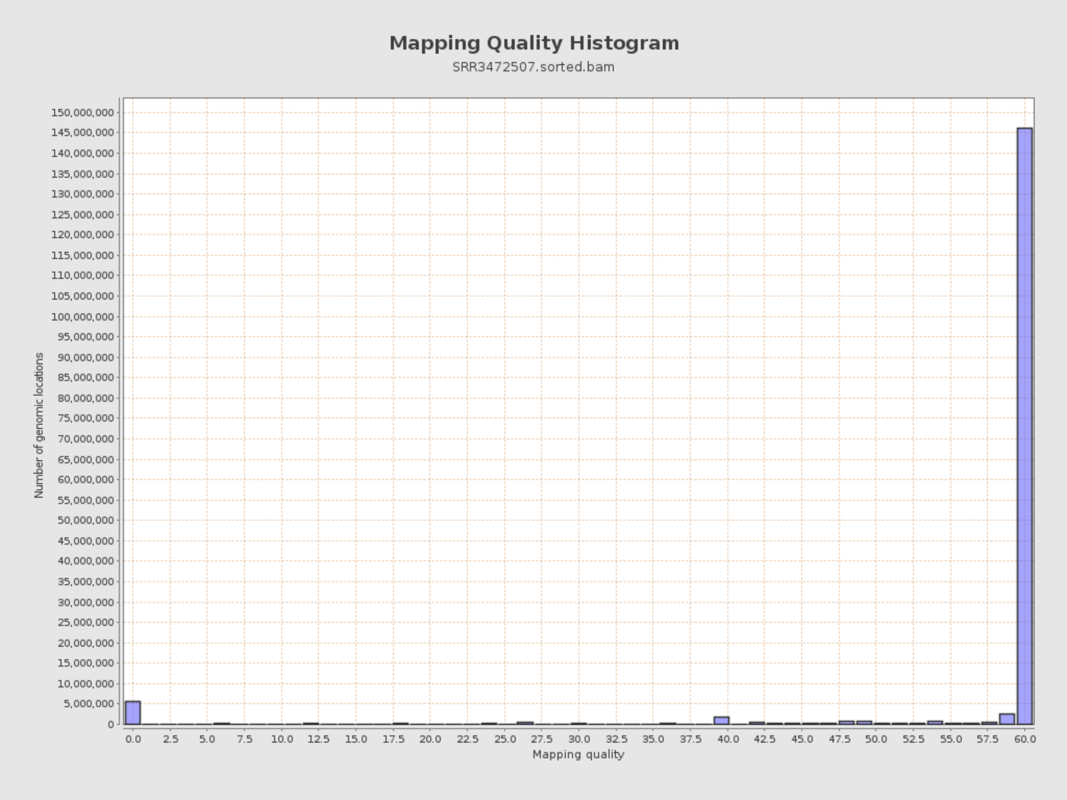
11. Results : Homopolymer Indels



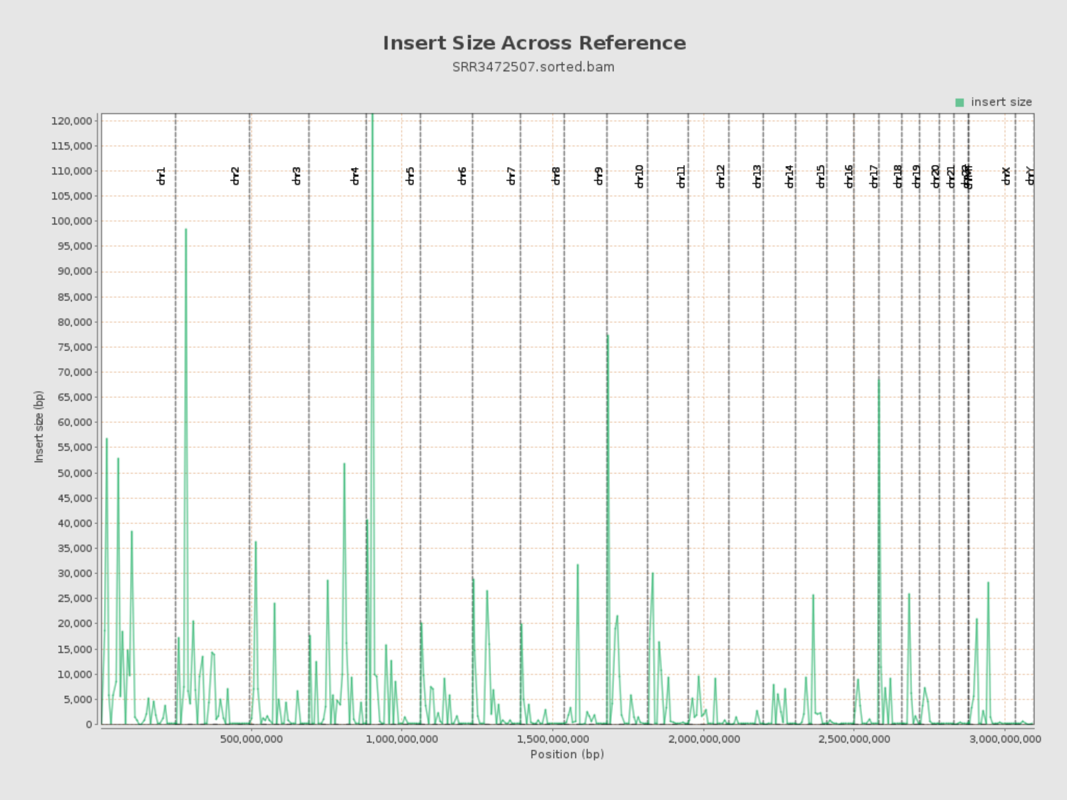
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram