Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 20:33:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472522.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_SRR3472522 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472522_1.fastq.gz SRR3472522_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 20:33:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472522.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,207,746
Mapped reads	14,054,167 / 98.92%
Unmapped reads	153,579 / 1.08%
Mapped paired reads	14,054,167 / 98.92%
Mapped reads, first in pair	7,050,782 / 49.63%
Mapped reads, second in pair	7,003,385 / 49.29%
Mapped reads, both in pair	13,969,904 / 98.33%
Mapped reads, singletons	84,263 / 0.59%
Secondary alignments	0
Supplementary alignments	66,829 / 0.47%
Read min/max/mean length	30 / 100 / 100.19
Duplicated reads (estimated)	9,163,351 / 64.5%
Duplication rate	42.66%
Clipped reads	1,143,930 / 8.05%

2.2. ACGT Content

Number/percentage of A's	395,573,057 / 28.57%
Number/percentage of C's	298,414,339 / 21.56%
Number/percentage of T's	393,466,021 / 28.42%
Number/percentage of G's	296,692,340 / 21.43%
Number/percentage of N's	213,282 / 0.02%

GC Percentage	42.99%

2.3. Coverage

Mean	0.4472
Standard Deviation	23.1186

2.4. Mapping Quality

Mean Mapping Quality	54.8

2.5. Insert size

Mean	25,923.3
Standard Deviation	1,576,785.33
P25/Median/P75	171 / 239 / 326

2.6. Mismatches and indels

General error rate	0.62%
Mismatches	8,379,249
Insertions	75,439
Mapped reads with at least one insertion	0.53%
Deletions	74,983
Mapped reads with at least one deletion	0.53%
Homopolymer indels	45.86%

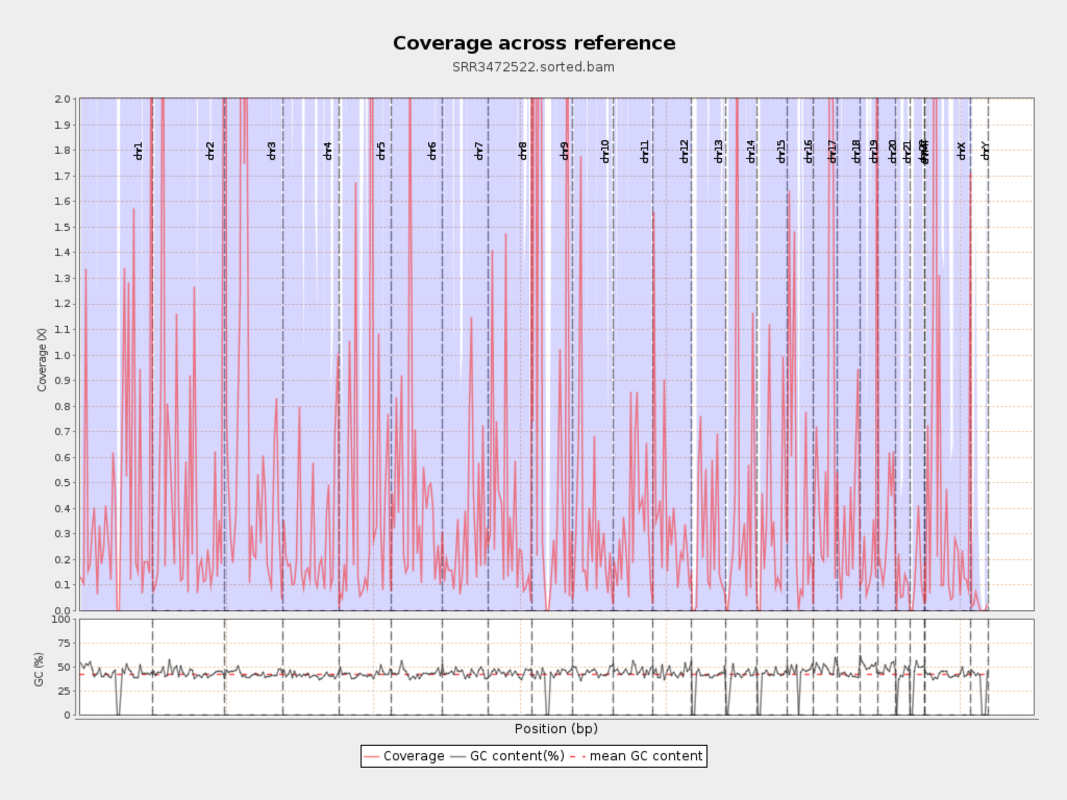
2.7. Chromosome stats

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

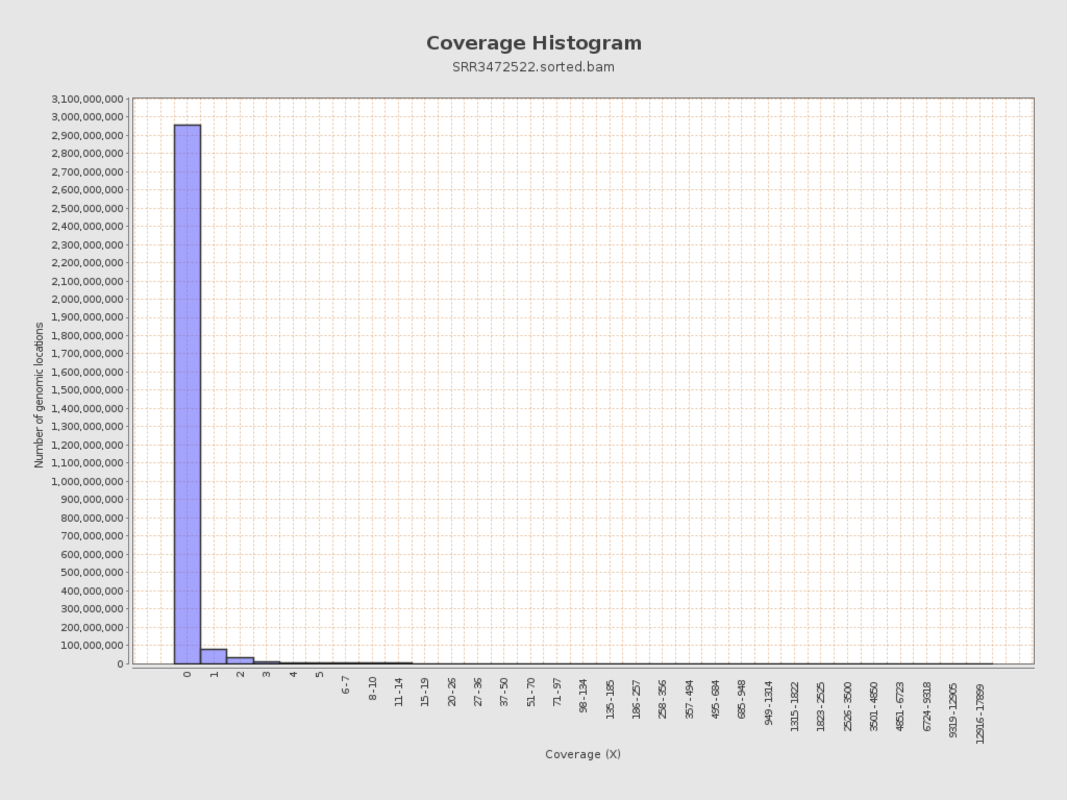
		bases	**coverage**	**deviation**
chr1	249250621	122163797	0.4901	22.653
chr2	243199373	116983430	0.481	35.4048
chr3	198022430	165111392	0.8338	25.4556
chr4	191154276	51671370	0.2703	8.7942
chr5	180915260	92161650	0.5094	28.6631
chr6	171115067	78163948	0.4568	14.1329
chr7	159138663	51297252	0.3223	10.1019
chr8	146364022	56499686	0.386	15.5384
chr9	141213431	131336860	0.9301	50.346
chr10	135534747	45397104	0.3349	21.6605
chr11	135006516	47871609	0.3546	17.0637
chr12	133851895	49304557	0.3684	14.798
chr13	115169878	31742751	0.2756	11.9608
chr14	107349540	48348049	0.4504	20.8043
chr15	102531392	36262860	0.3537	15.8052
chr16	90354753	42468146	0.47	21.564
chr17	81195210	60141364	0.7407	33.9119
chr18	78077248	26787882	0.3431	13.4025
chr19	59128983	15078729	0.255	9.5608
chr20	63025520	20740761	0.3291	13.6556
chr21	48129895	4638663	0.0964	6.7076
chr22	51304566	6704624	0.1307	4.706
chrMT	16571	3116	0.188	0.4988
chrX	155270560	82345638	0.5303	24.8096

chrY	59373566	1309644	0.0221	0.9447

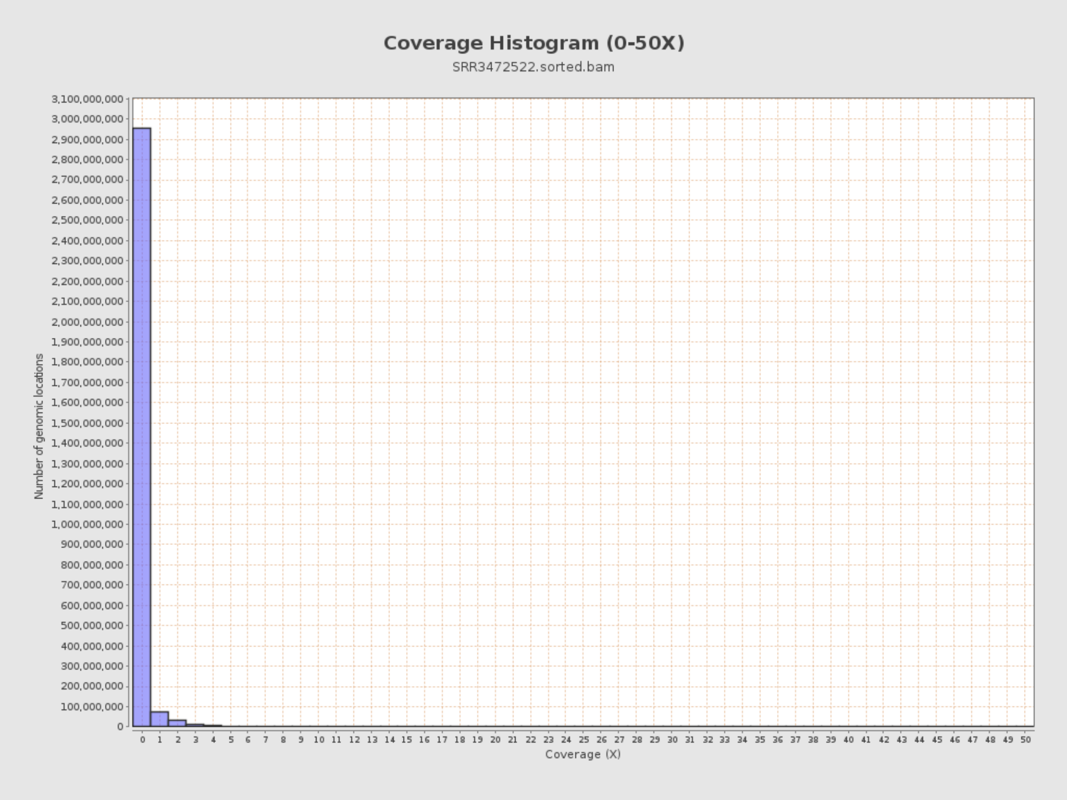
3. Results : Coverage across reference



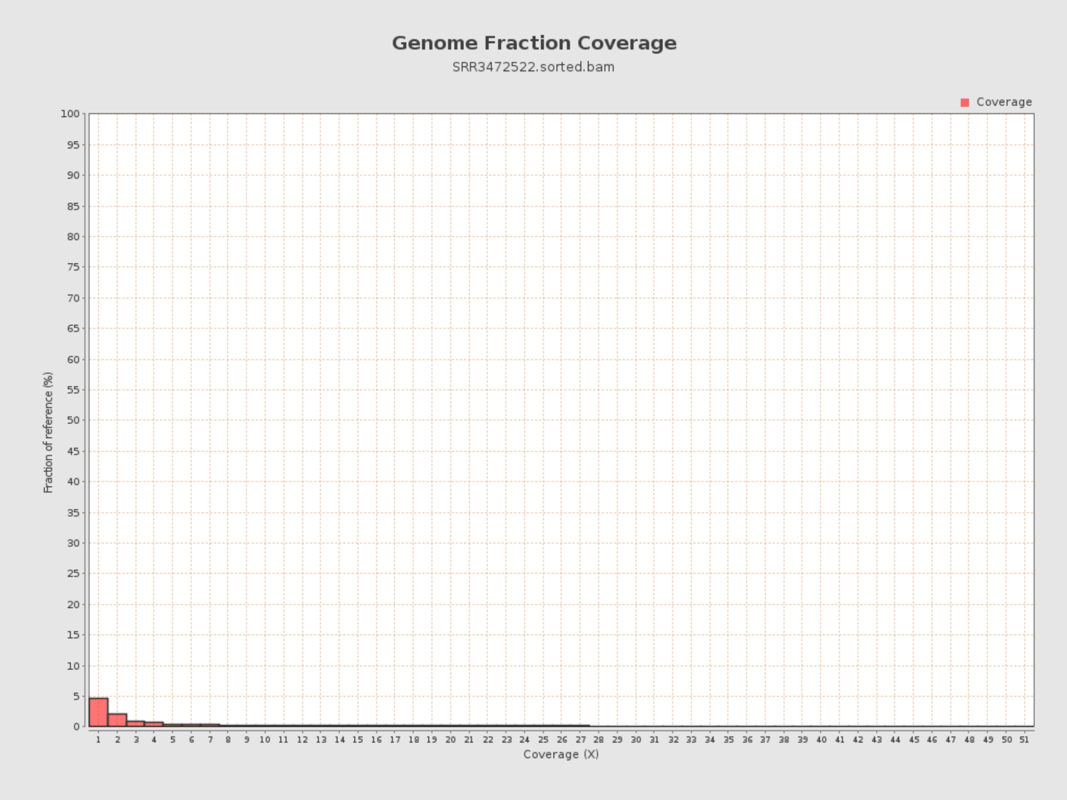
4. Results : Coverage Histogram



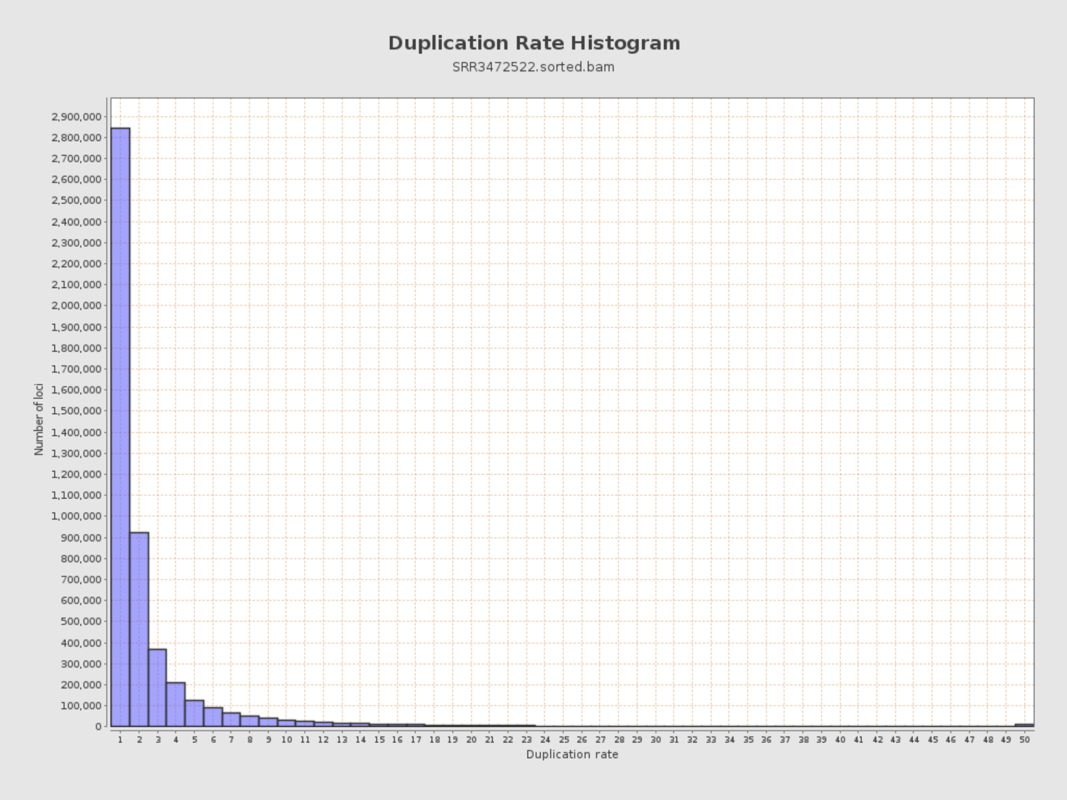
5. Results : Coverage Histogram (0-50X)



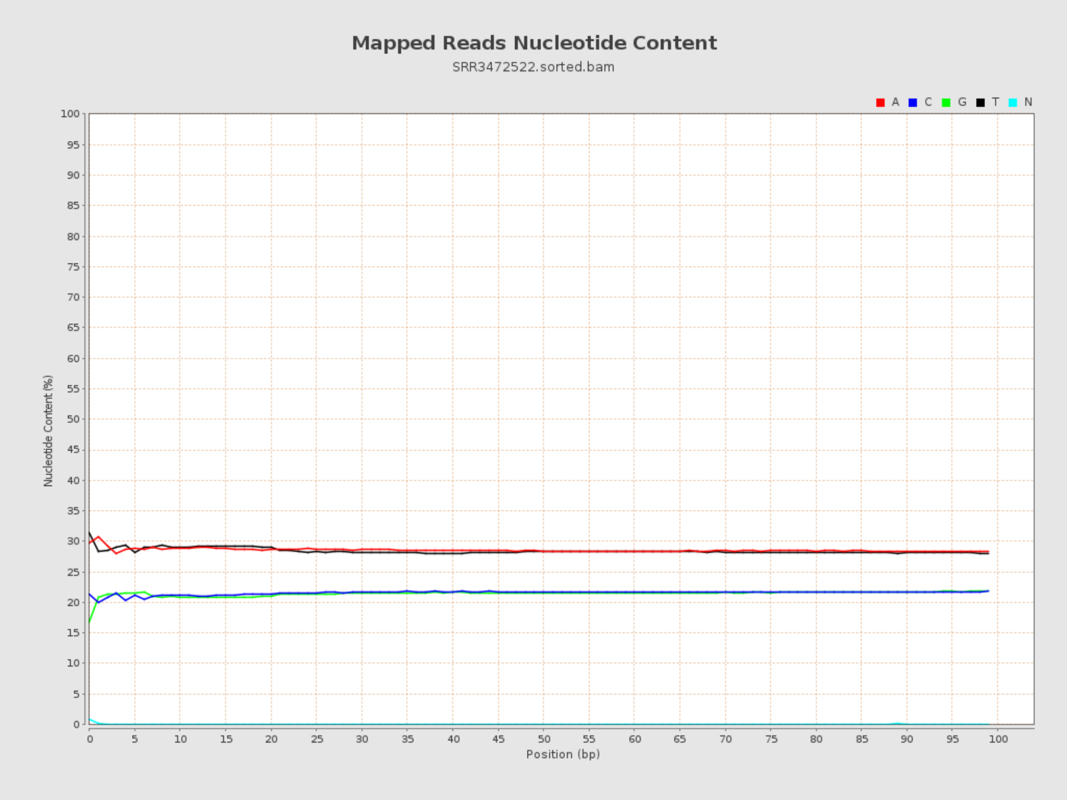
6. Results : Genome Fraction Coverage



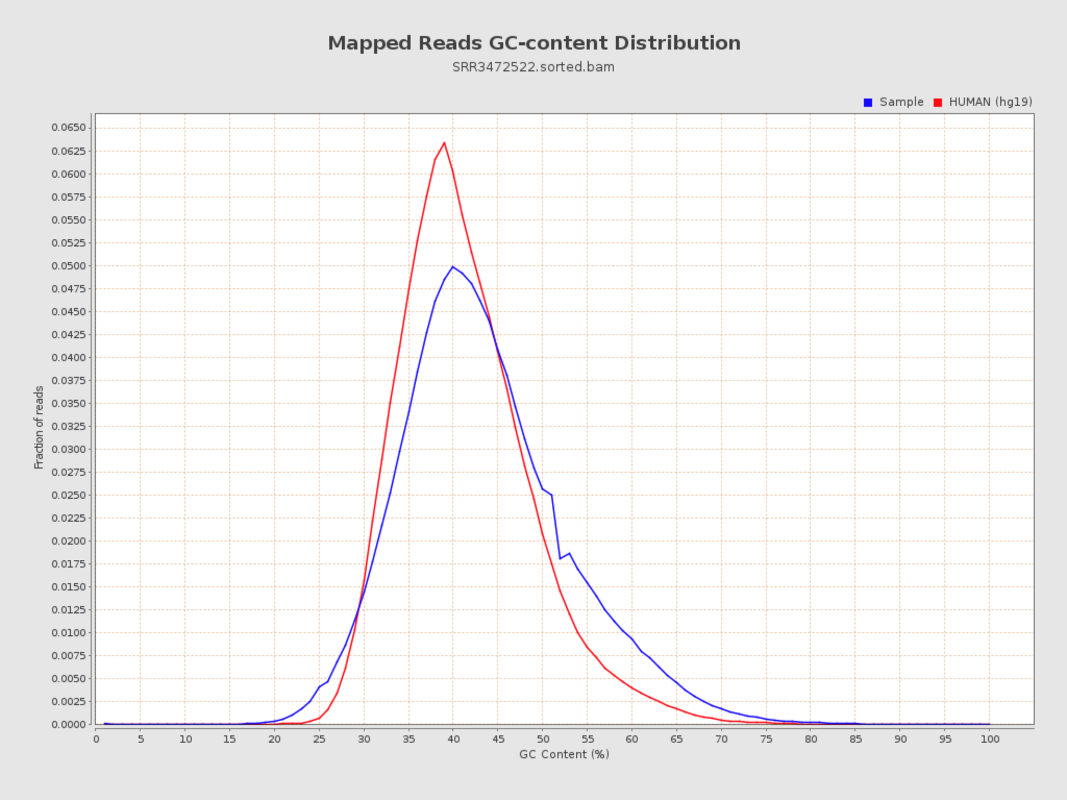
7. Results : Duplication Rate Histogram



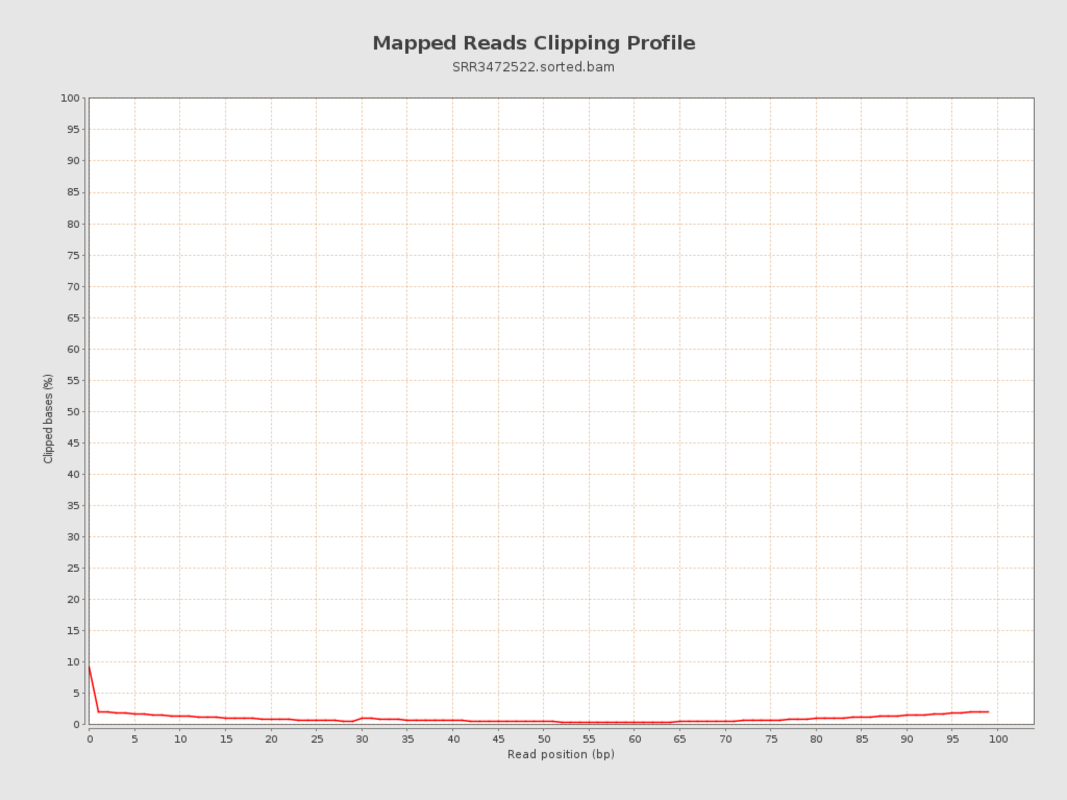
8. Results : Mapped Reads Nucleotide Content



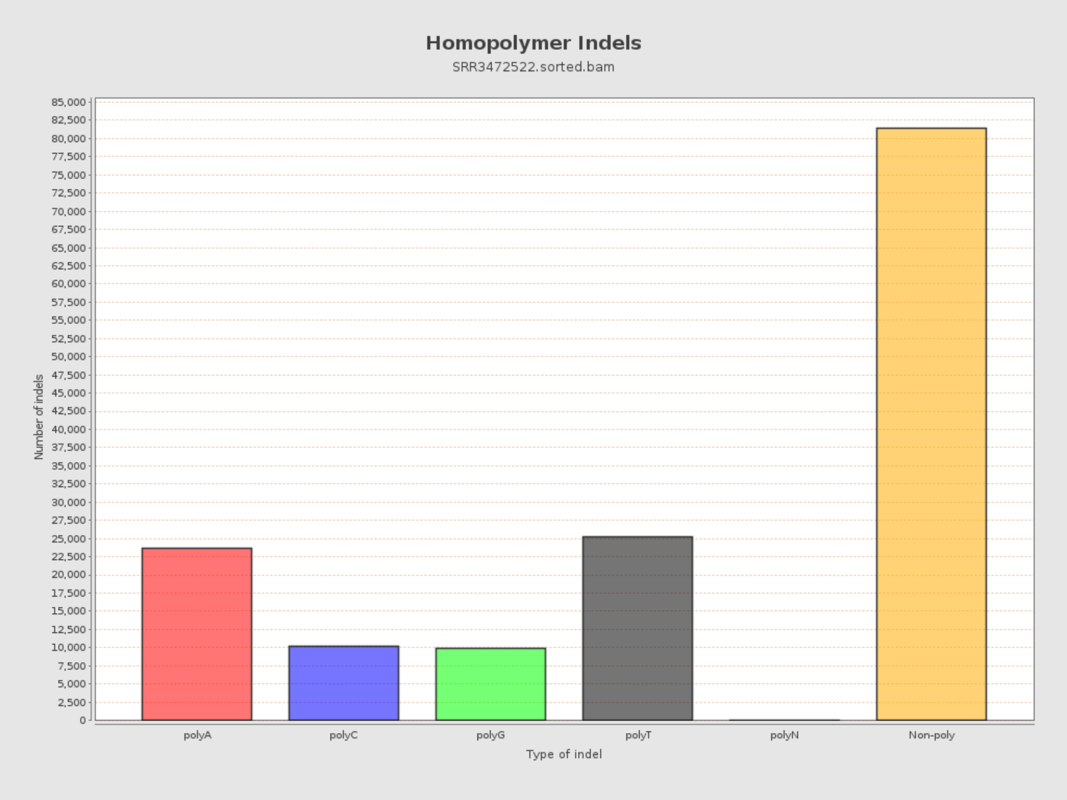
9. Results : Mapped Reads GC-content Distribution



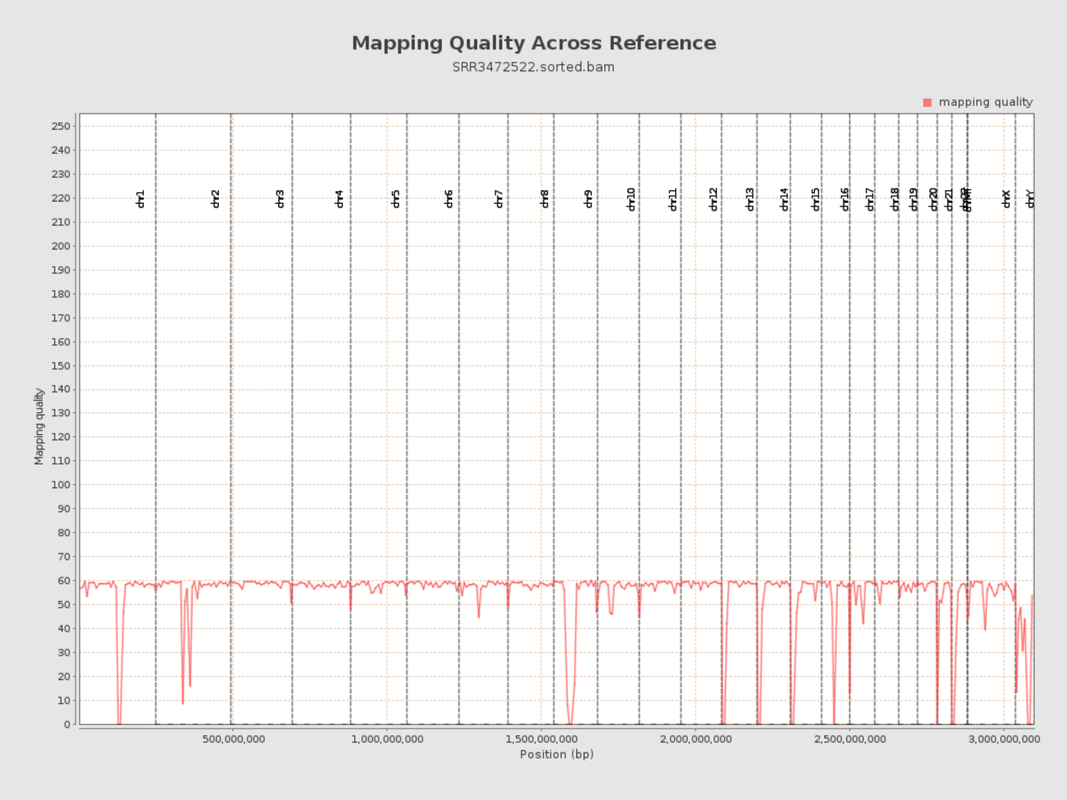
10. Results : Mapped Reads Clipping Profile



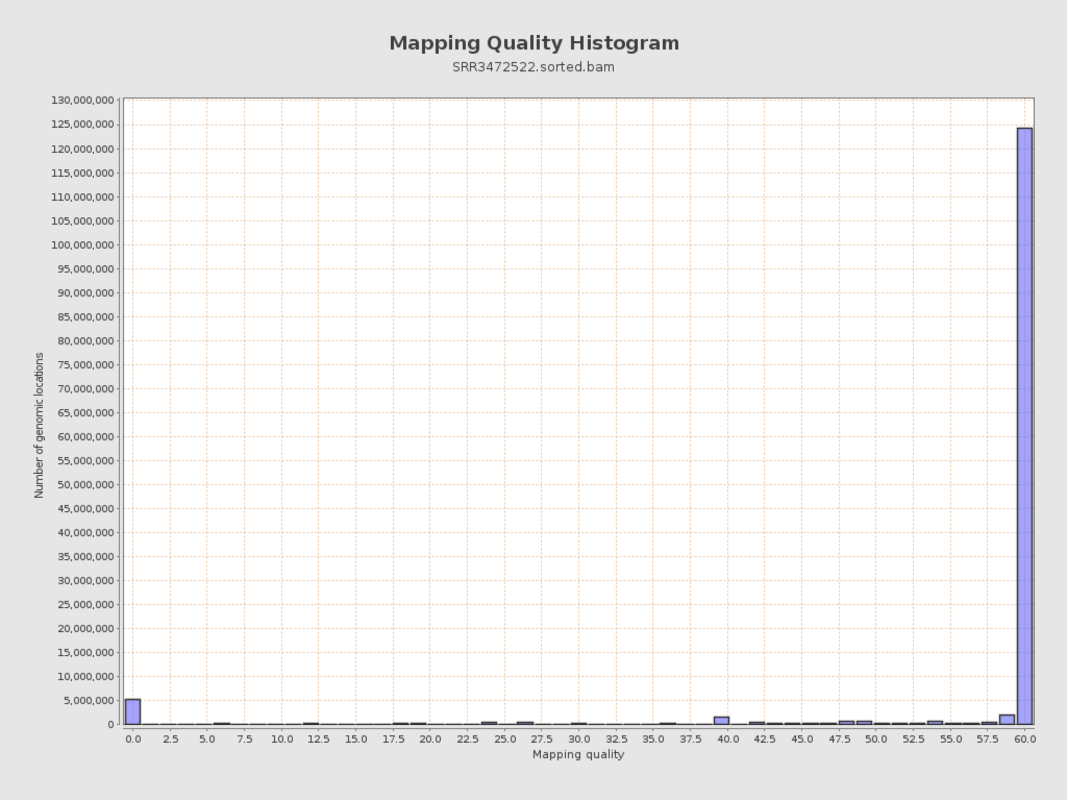
11. Results : Homopolymer Indels



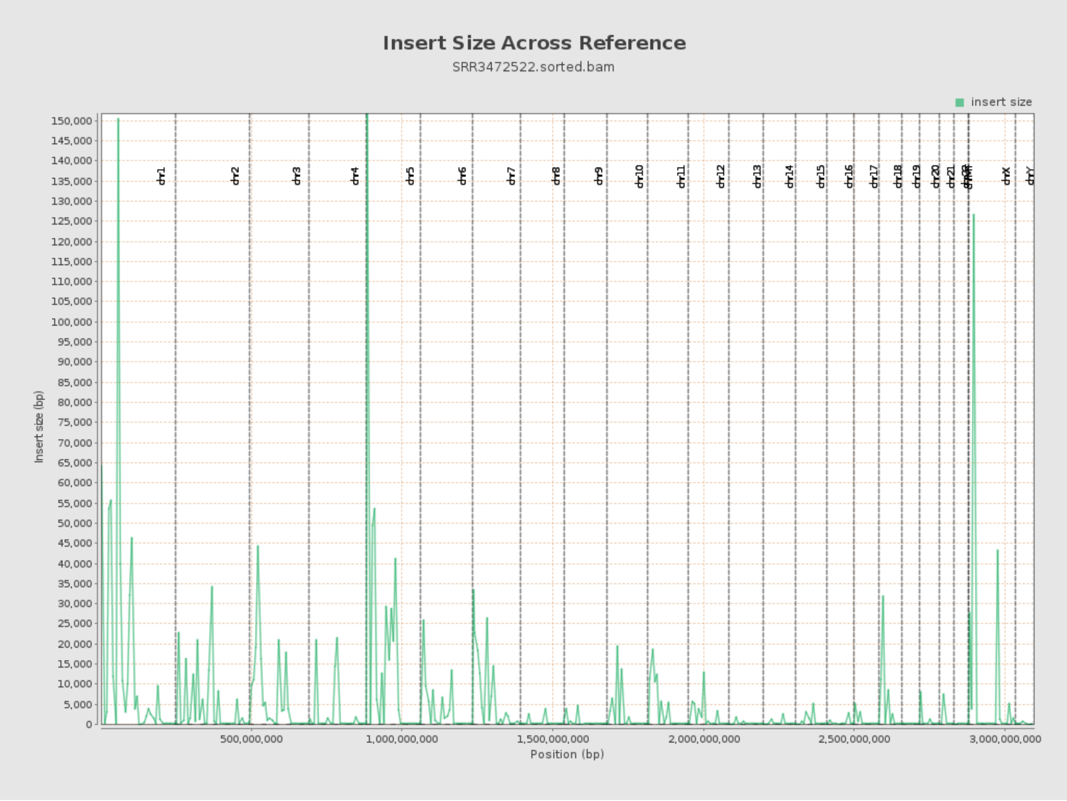
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram