Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 06:49:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472477.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_SRR3472477 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472477_1.fastq.gz SRR3472477_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 06:49:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472477.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,652,046
Mapped reads	17,456,531 / 98.89%
Unmapped reads	195,515 / 1.11%
Mapped paired reads	17,456,531 / 98.89%
Mapped reads, first in pair	8,757,599 / 49.61%
Mapped reads, second in pair	8,698,932 / 49.28%
Mapped reads, both in pair	17,348,026 / 98.28%
Mapped reads, singletons	108,505 / 0.61%
Secondary alignments	0
Supplementary alignments	72,561 / 0.41%
Read min/max/mean length	30 / 100 / 100.17
Duplicated reads (estimated)	11,061,964 / 62.67%
Duplication rate	45.74%
Clipped reads	1,496,973 / 8.48%

2.2. ACGT Content

Number/percentage of A's	482,254,864 / 28.09%
Number/percentage of C's	378,532,684 / 22.05%
Number/percentage of T's	479,686,892 / 27.94%
Number/percentage of G's	376,031,702 / 21.9%
Number/percentage of N's	267,994 / 0.02%

GC Percentage	43.95%

2.3. Coverage

Mean	0.5546
Standard Deviation	19.0938

2.4. Mapping Quality

Mean Mapping Quality	55.1

2.5. Insert size

Mean	33,969.24
Standard Deviation	1,815,126.29
P25/Median/P75	171 / 241 / 325

2.6. Mismatches and indels

General error rate	0.62%
Mismatches	10,518,399
Insertions	95,411
Mapped reads with at least one insertion	0.54%
Deletions	92,090
Mapped reads with at least one deletion	0.52%
Homopolymer indels	45.44%

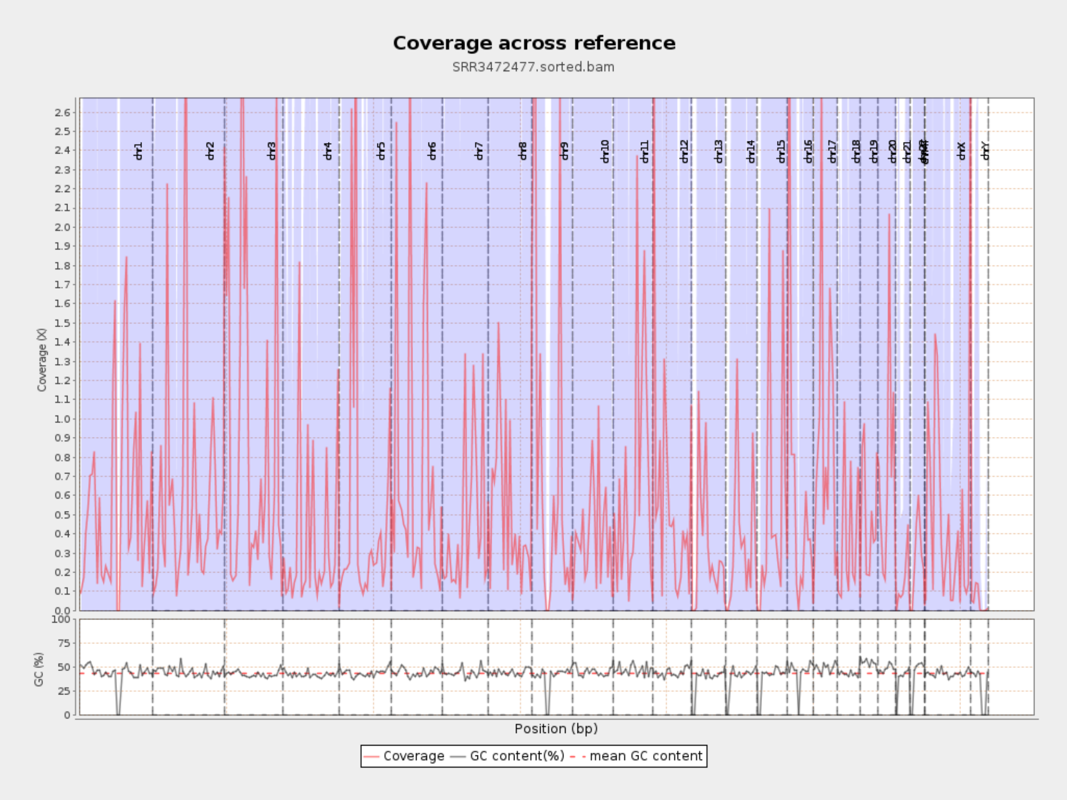
2.7. Chromosome stats

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

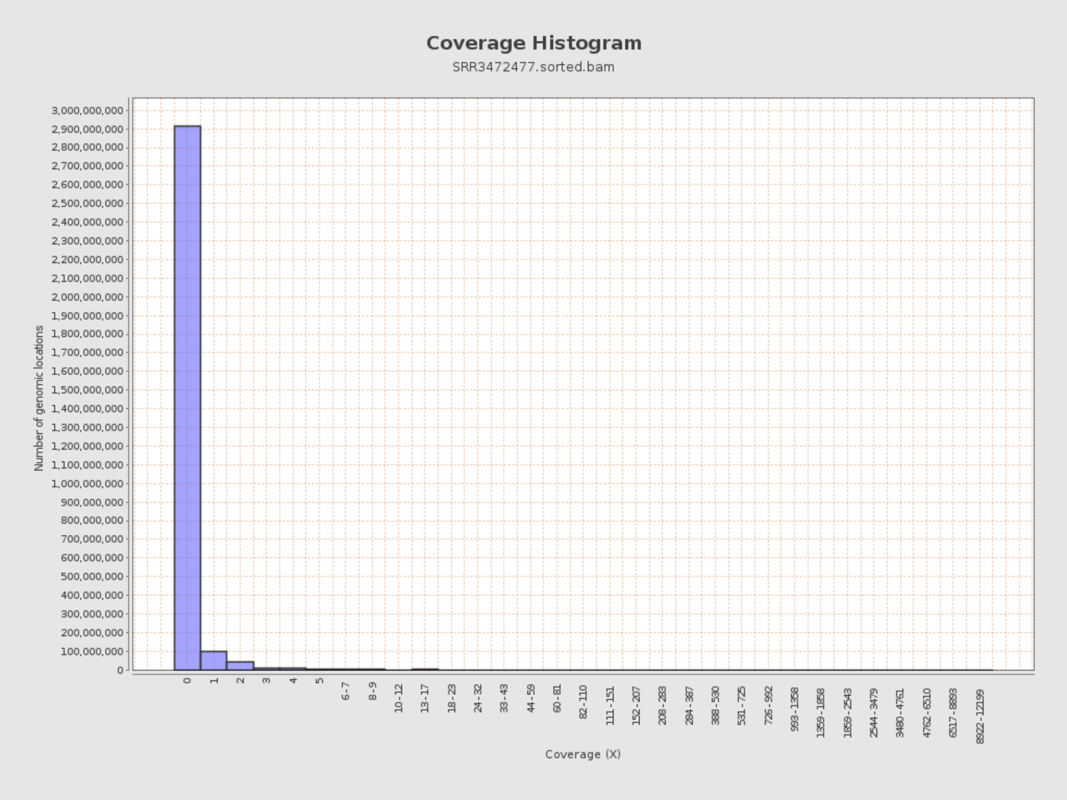
		bases	coverage	deviation
chr1	249250621	145431916	0.5835	18.8629
chr2	243199373	145015271	0.5963	22.5823
chr3	198022430	186288069	0.9407	23.7981
chr4	191154276	67932282	0.3554	13.3468
chr5	180915260	99459263	0.5498	18.828
chr6	171115067	124175434	0.7257	22.309
chr7	159138663	69710597	0.438	13.8341
chr8	146364022	72859685	0.4978	20.6696
chr9	141213431	110771426	0.7844	23.3139
chr10	135534747	55341496	0.4083	13.953
chr11	135006516	93311868	0.6912	27.7569
chr12	133851895	80377378	0.6005	18.3934
chr13	115169878	37906501	0.3291	13.2133
chr14	107349540	39463174	0.3676	11.3146
chr15	102531392	54066892	0.5273	17.4897
chr16	90354753	55748597	0.617	16.8574
chr17	81195210	74650726	0.9194	30.4242
chr18	78077248	30222261	0.3871	18.0258
chr19	59128983	28654091	0.4846	13.0683
chr20	63025520	46944116	0.7448	22.1878
chr21	48129895	7097099	0.1475	4.2385
chr22	51304566	13717054	0.2674	8.0245
chrMT	16571	2886	0.1742	0.6021
chrX	155270560	74991342	0.483	15.6503

chrY	59373566	2871643	0.0484	1.4032

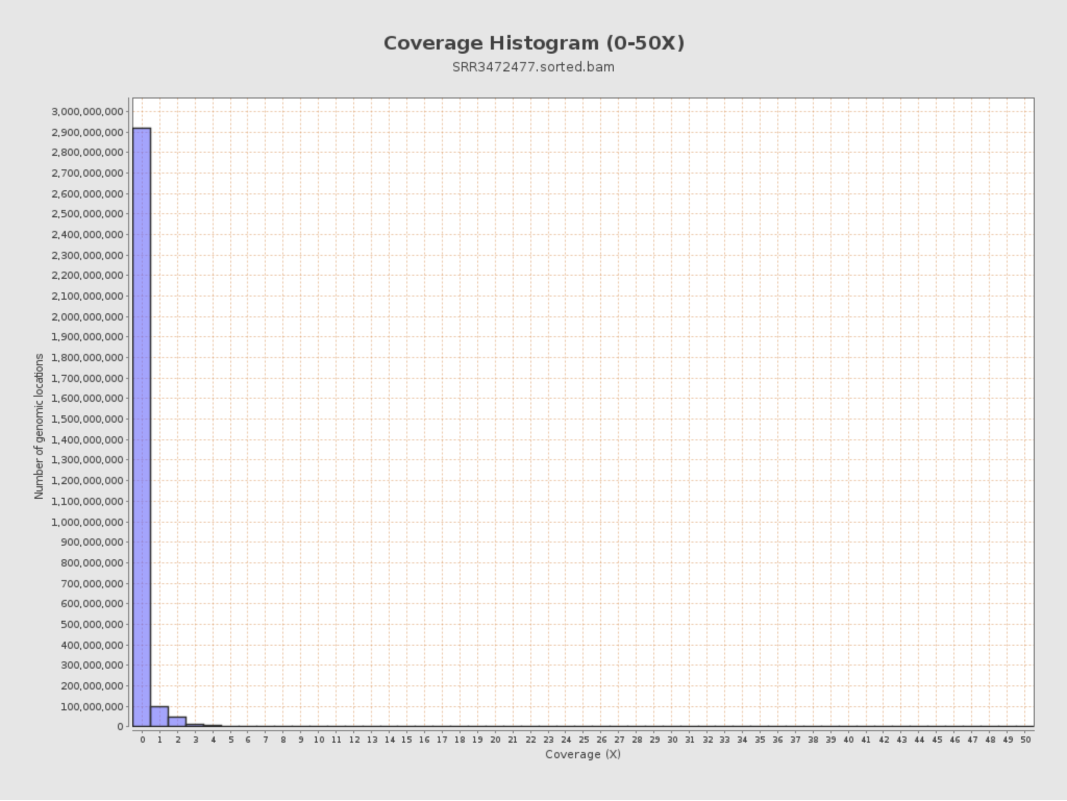
3. Results : Coverage across reference



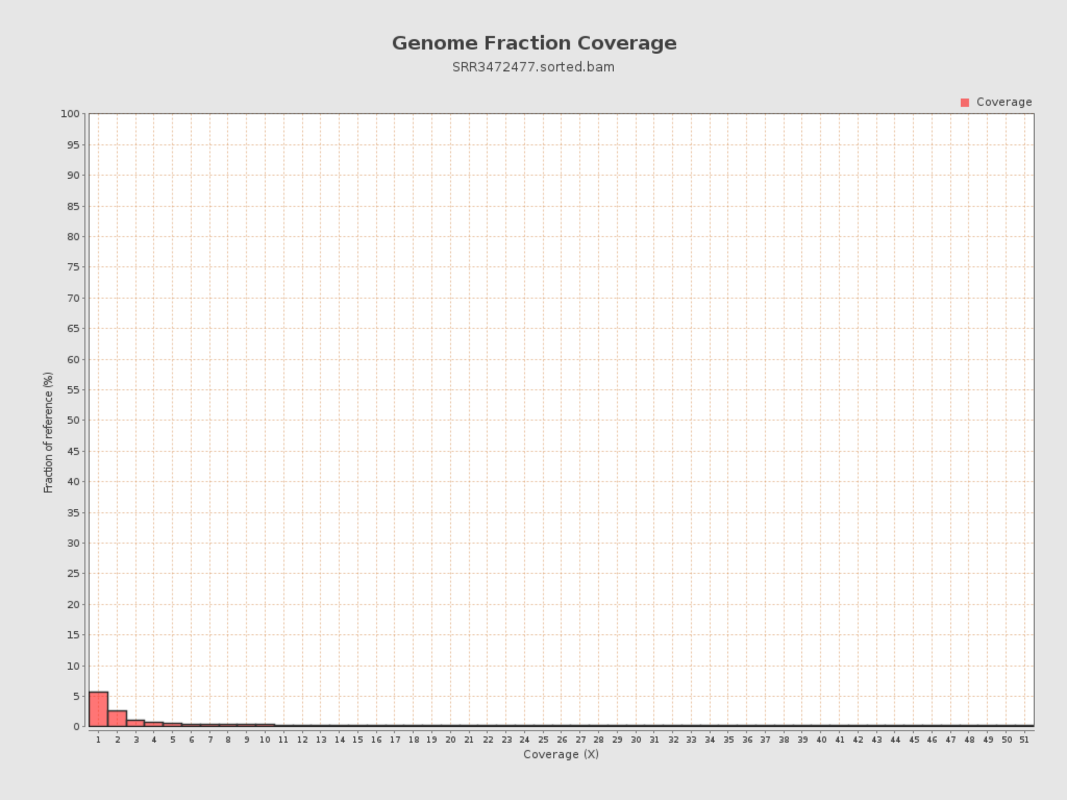
4. Results : Coverage Histogram



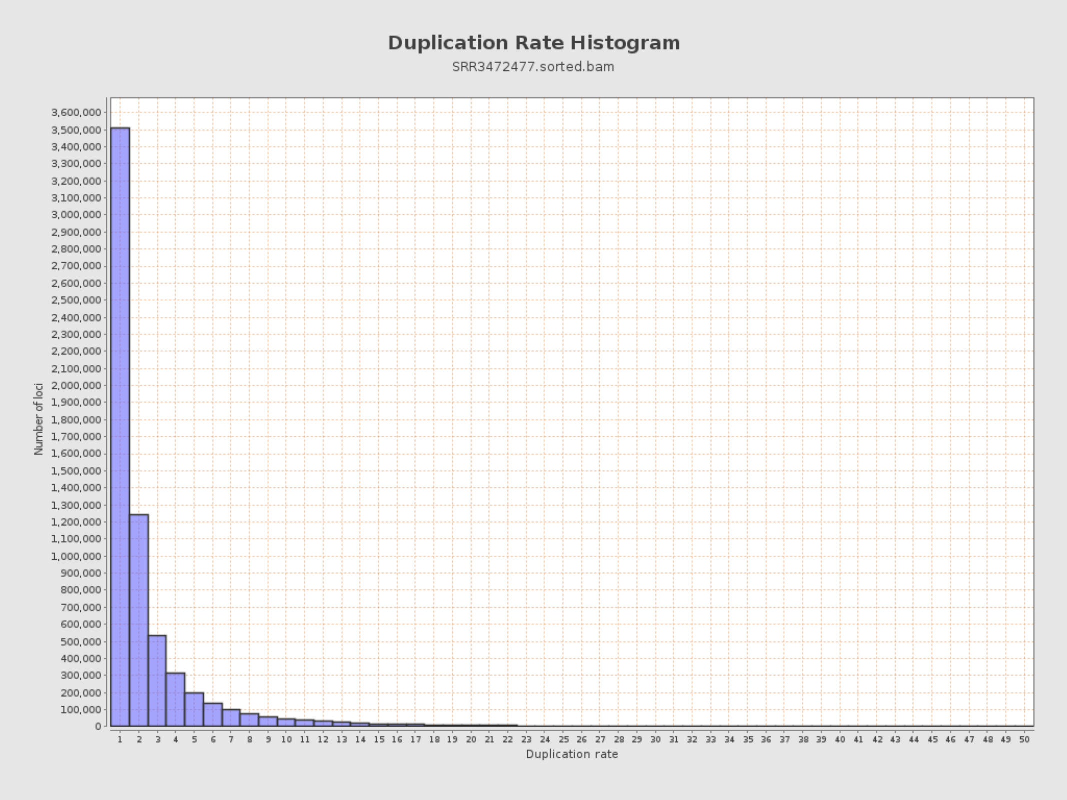
5. Results : Coverage Histogram (0-50X)



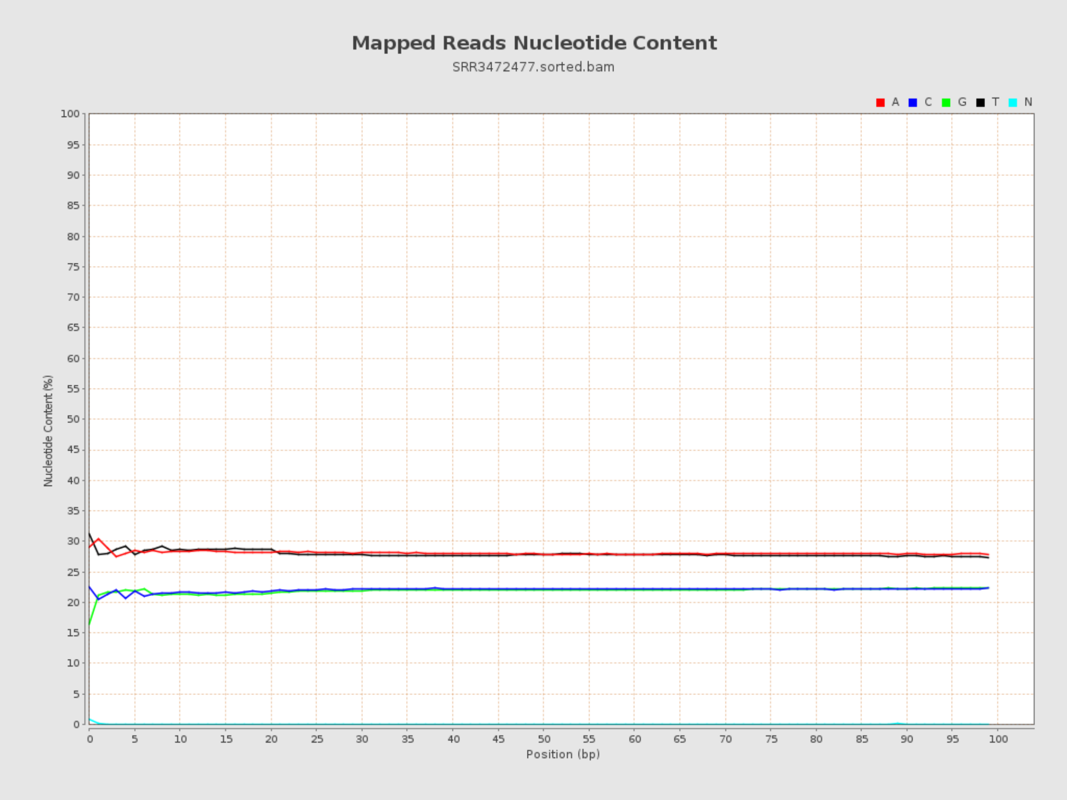
6. Results : Genome Fraction Coverage



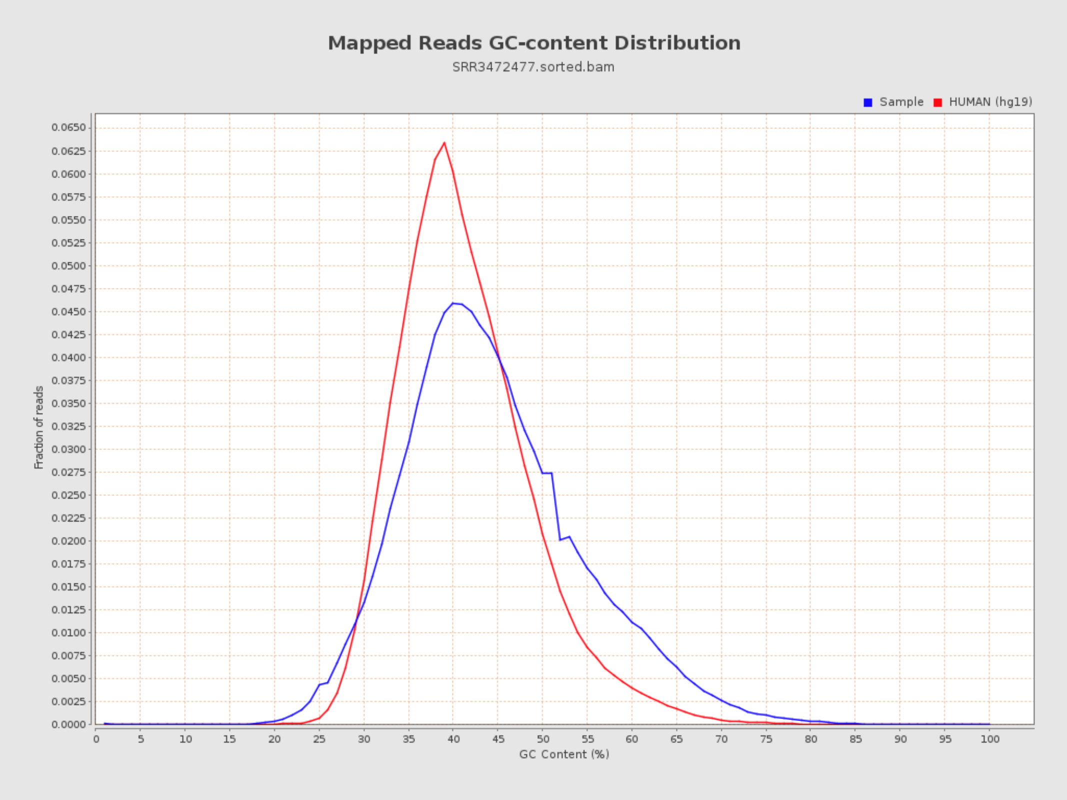
7. Results : Duplication Rate Histogram



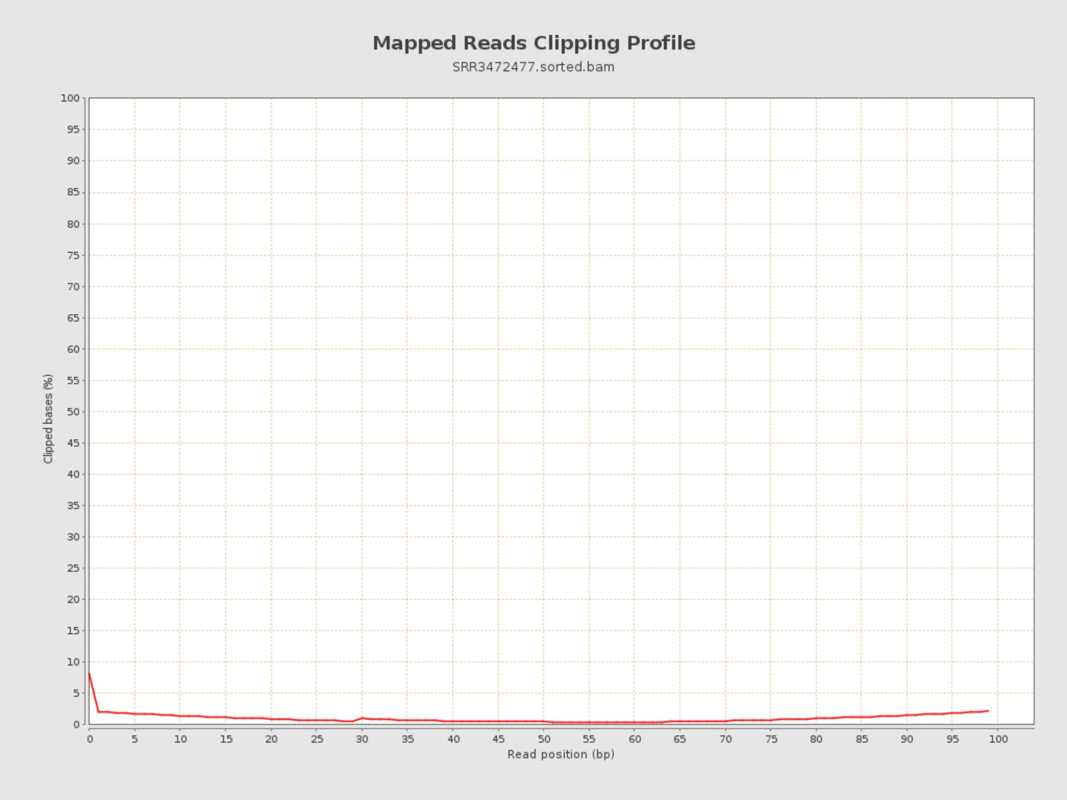
8. Results : Mapped Reads Nucleotide Content



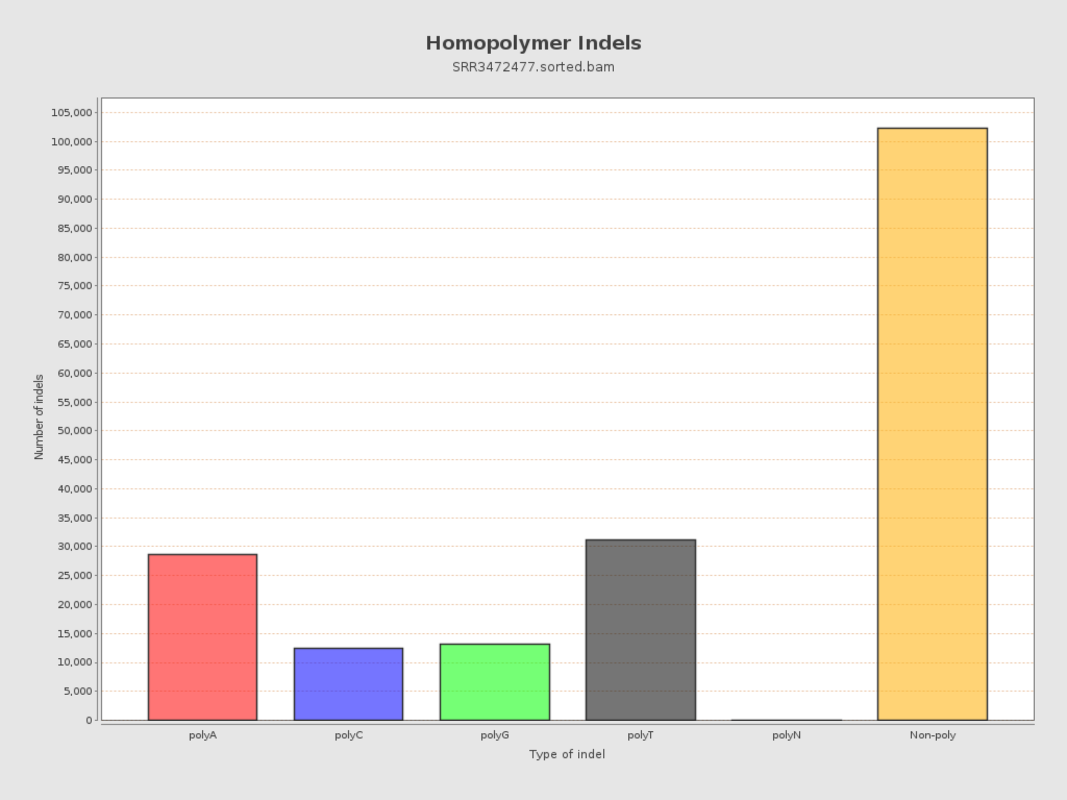
9. Results : Mapped Reads GC-content Distribution



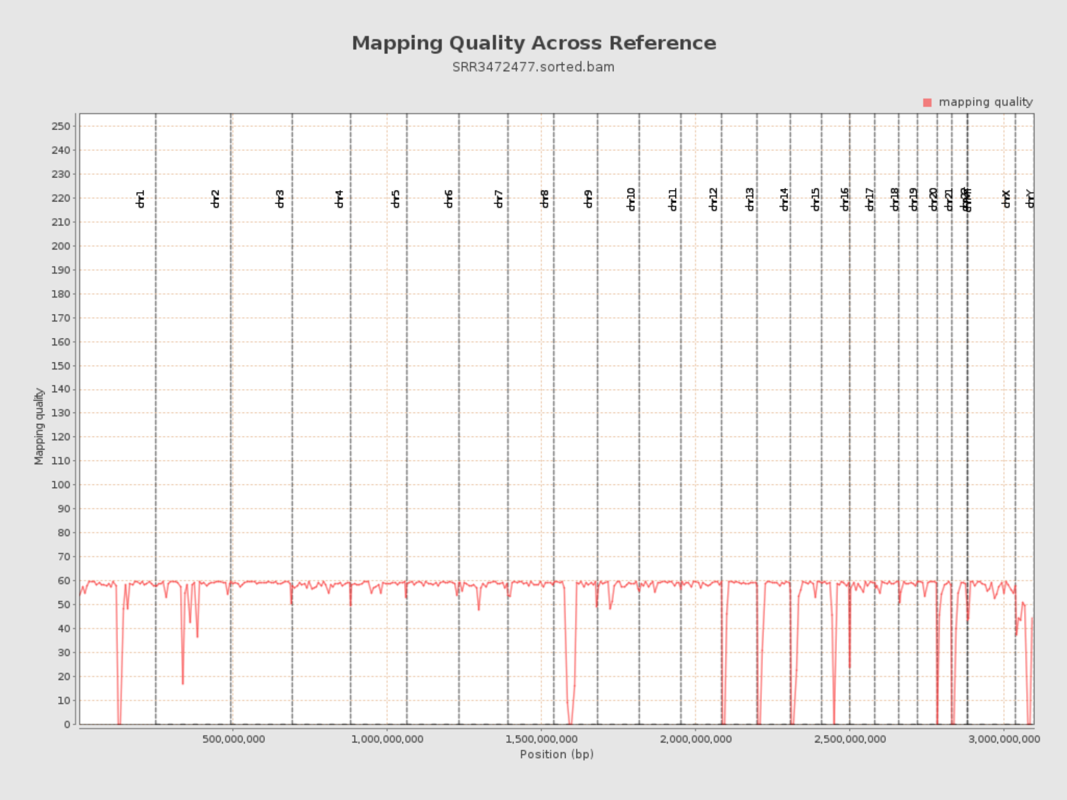
10. Results : Mapped Reads Clipping Profile



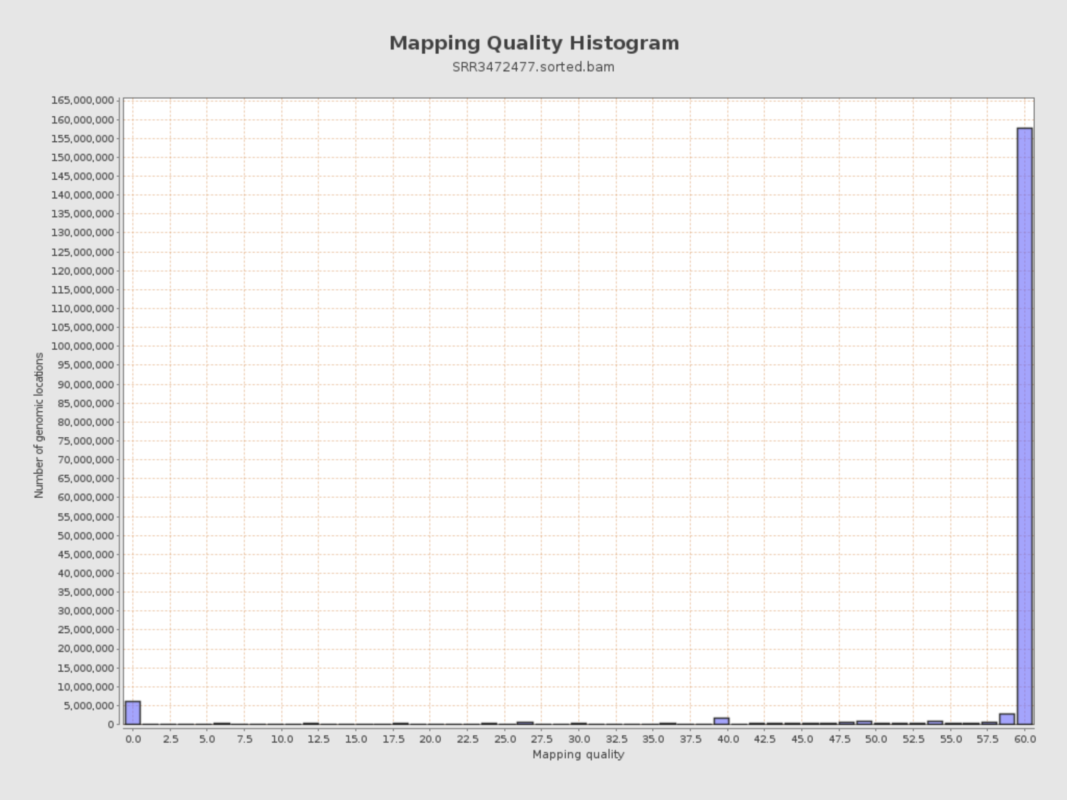
11. Results : Homopolymer Indels



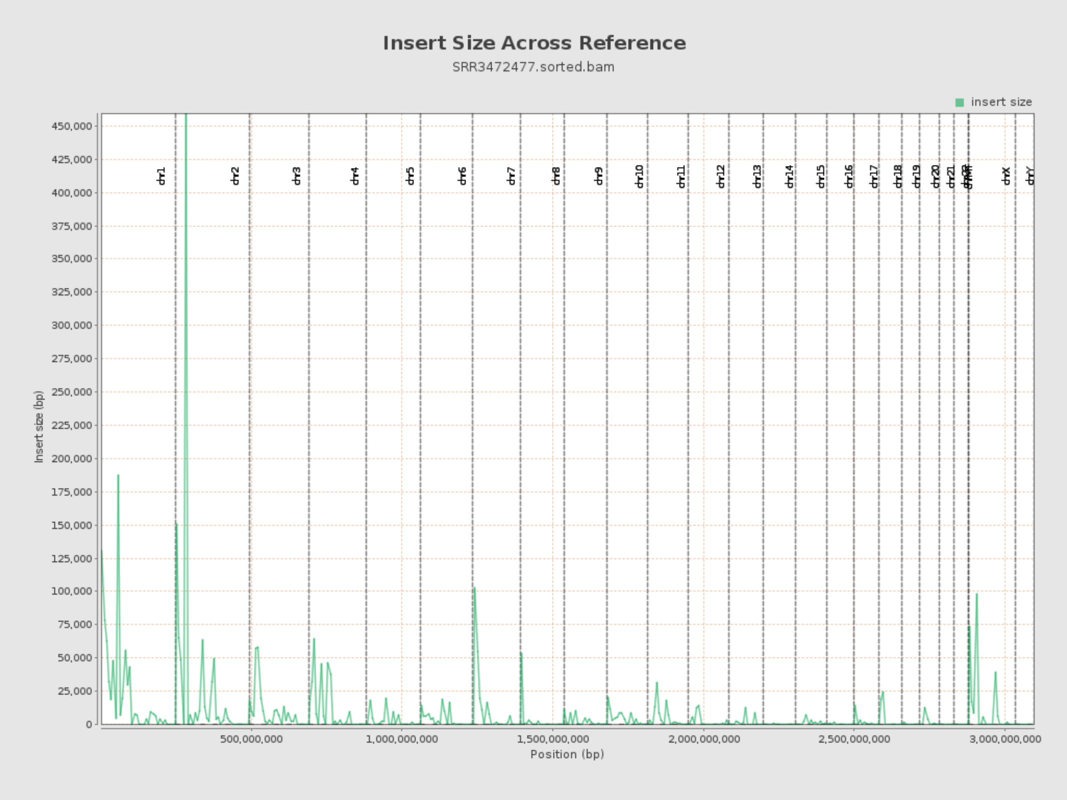
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram