Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 10:59:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472383.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_SRR3472383 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472383_1.fastq.gz SRR3472383_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 10:59:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472383.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,066,552
Mapped reads	17,925,621 / 99.22%
Unmapped reads	140,931 / 0.78%
Mapped paired reads	17,925,621 / 99.22%
Mapped reads, first in pair	8,984,729 / 49.73%
Mapped reads, second in pair	8,940,892 / 49.49%
Mapped reads, both in pair	17,850,846 / 98.81%
Mapped reads, singletons	74,775 / 0.41%
Secondary alignments	0
Supplementary alignments	65,699 / 0.36%
Read min/max/mean length	30 / 100 / 99.14
Duplicated reads (estimated)	11,186,053 / 61.92%
Duplication rate	47.71%
Clipped reads	1,395,065 / 7.72%

2.2. ACGT Content

Number/percentage of A's	471,422,100 / 26.93%
Number/percentage of C's	404,859,188 / 23.13%
Number/percentage of T's	472,077,387 / 26.97%
Number/percentage of G's	401,837,594 / 22.96%
Number/percentage of N's	218,933 / 0.01%

GC Percentage	46.09%

2.3. Coverage

Mean	0.5655
Standard Deviation	16.8673

2.4. Mapping Quality

Mean Mapping Quality	54.82

2.5. Insert size

Mean	16,017.91
Standard Deviation	1,252,930.18
P25/Median/P75	147 / 207 / 281

2.6. Mismatches and indels

General error rate	0.52%
Mismatches	8,904,221
Insertions	98,584
Mapped reads with at least one insertion	0.54%
Deletions	80,769
Mapped reads with at least one deletion	0.44%
Homopolymer indels	45.67%

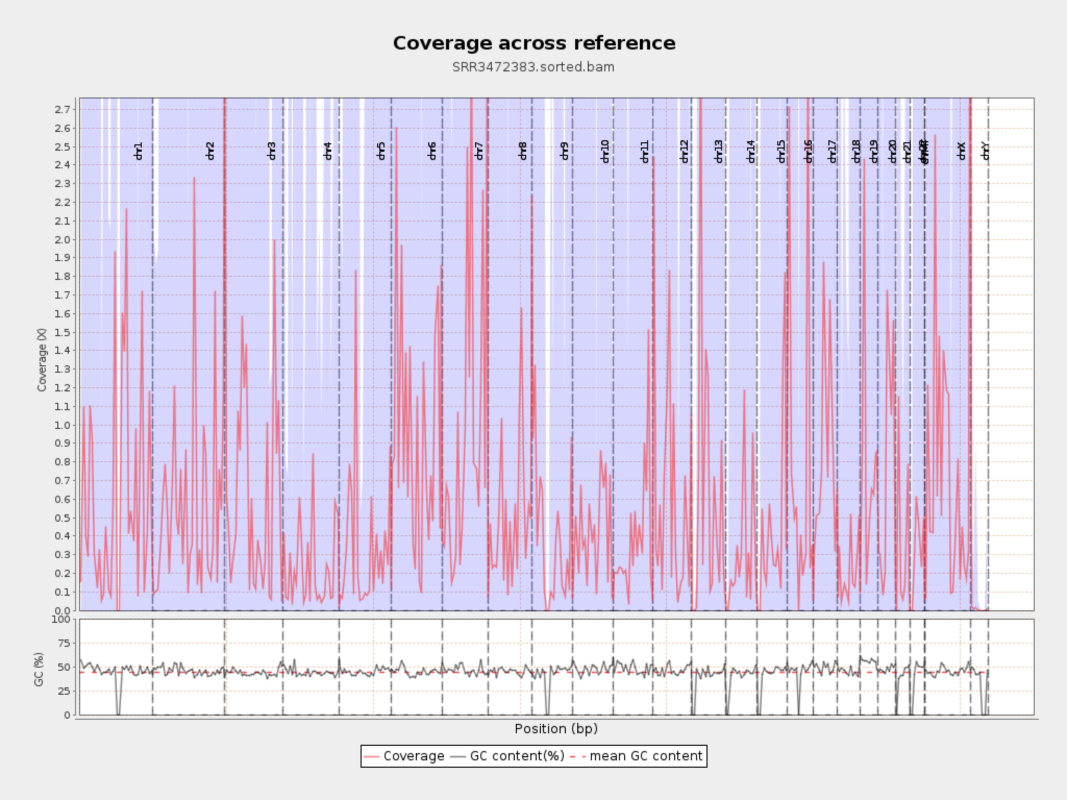
2.7. Chromosome stats

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

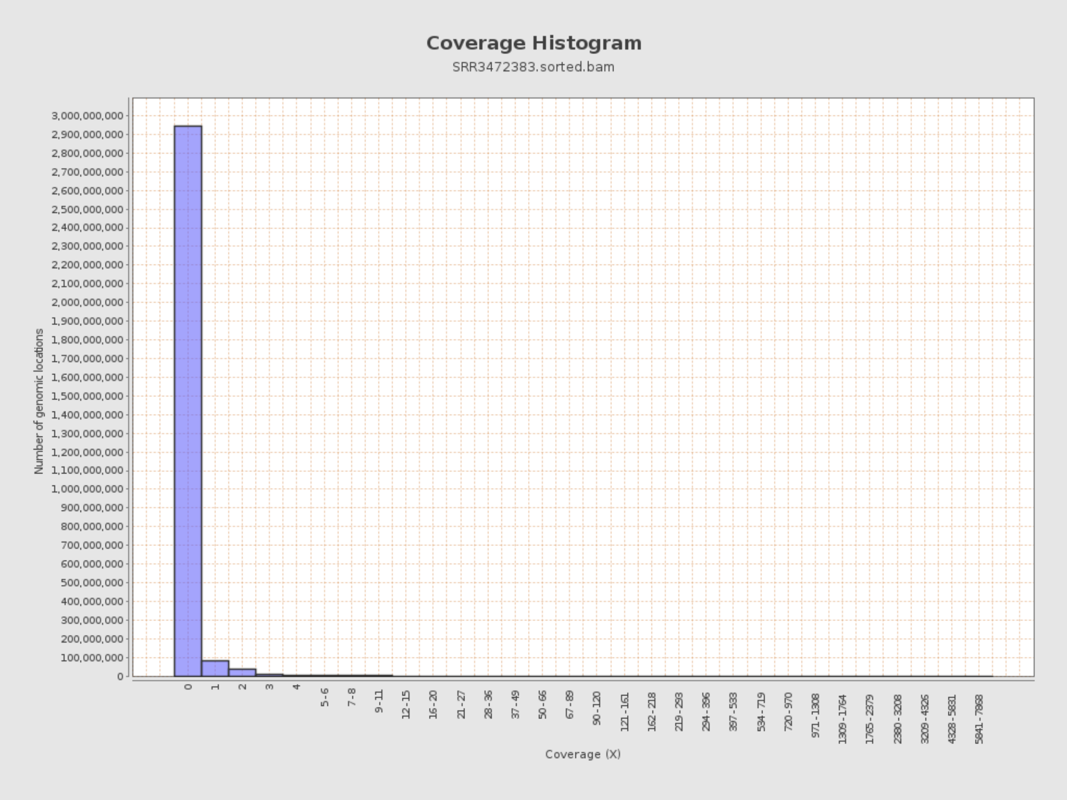
		bases	coverage	deviation
chr1	249250621	157714046	0.6328	18.8292
chr2	243199373	137137736	0.5639	16.3955
chr3	198022430	129022311	0.6516	17.5767
chr4	191154276	43297608	0.2265	8.6524
chr5	180915260	61723179	0.3412	12.2856
chr6	171115067	160420642	0.9375	22.3771
chr7	159138663	163728343	1.0288	27.6843
chr8	146364022	75218953	0.5139	14.3653
chr9	141213431	57004275	0.4037	9.8966
chr10	135534747	58322570	0.4303	14.5337
chr11	135006516	53901772	0.3993	12.3072
chr12	133851895	84284587	0.6297	14.0826
chr13	115169878	74469378	0.6466	23.8279
chr14	107349540	31258155	0.2912	9.6625
chr15	102531392	47143608	0.4598	17.6981
chr16	90354753	75644129	0.8372	19.4914
chr17	81195210	70997223	0.8744	18.0443
chr18	78077248	17094459	0.2189	6.9722
chr19	59128983	48699663	0.8236	16.5406
chr20	63025520	51057094	0.8101	22.0678
chr21	48129895	17839892	0.3707	21.6805
chr22	51304566	16282886	0.3174	9.0099
chrMT	16571	8492	0.5125	0.8344
chrX	155270560	117978100	0.7598	18.117

chrY	59373566	365120	0.0061	0.399

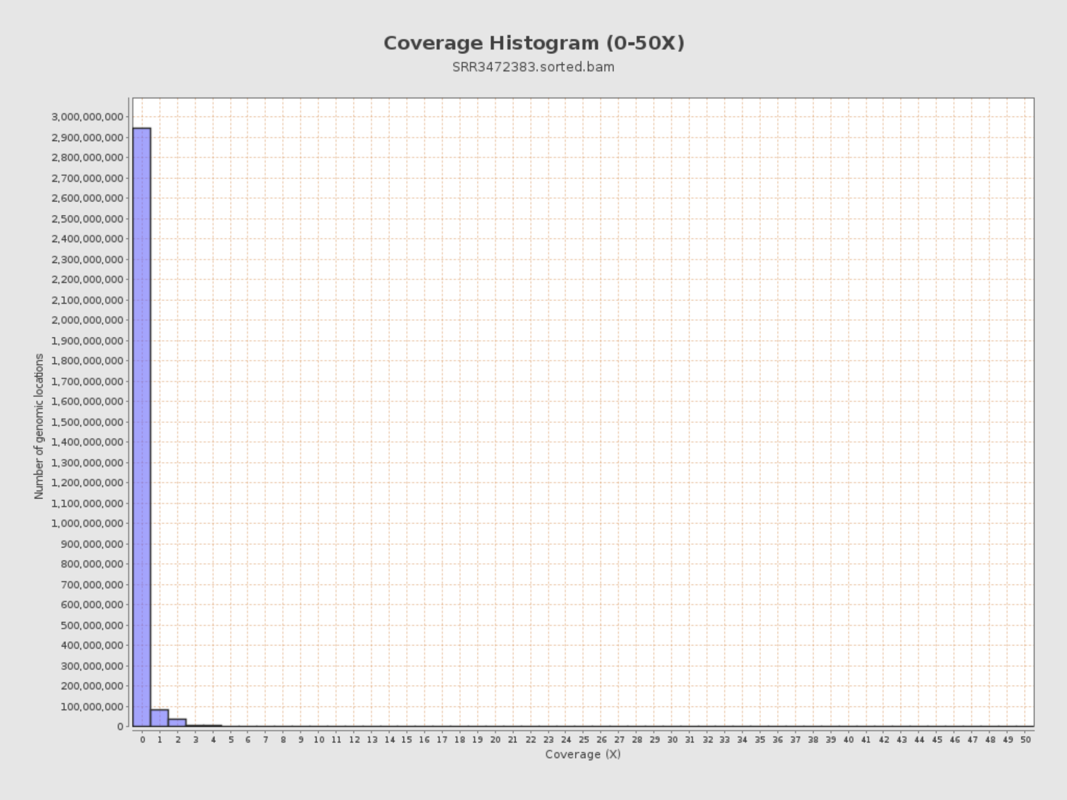
3. Results : Coverage across reference



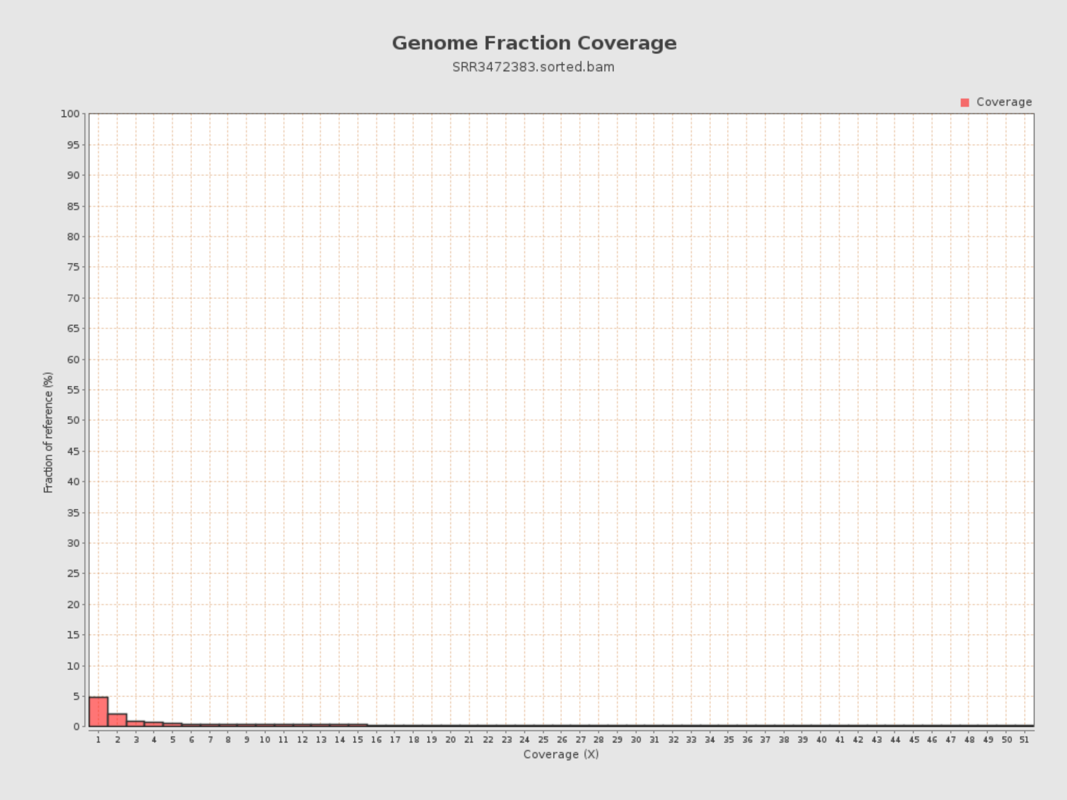
4. Results : Coverage Histogram



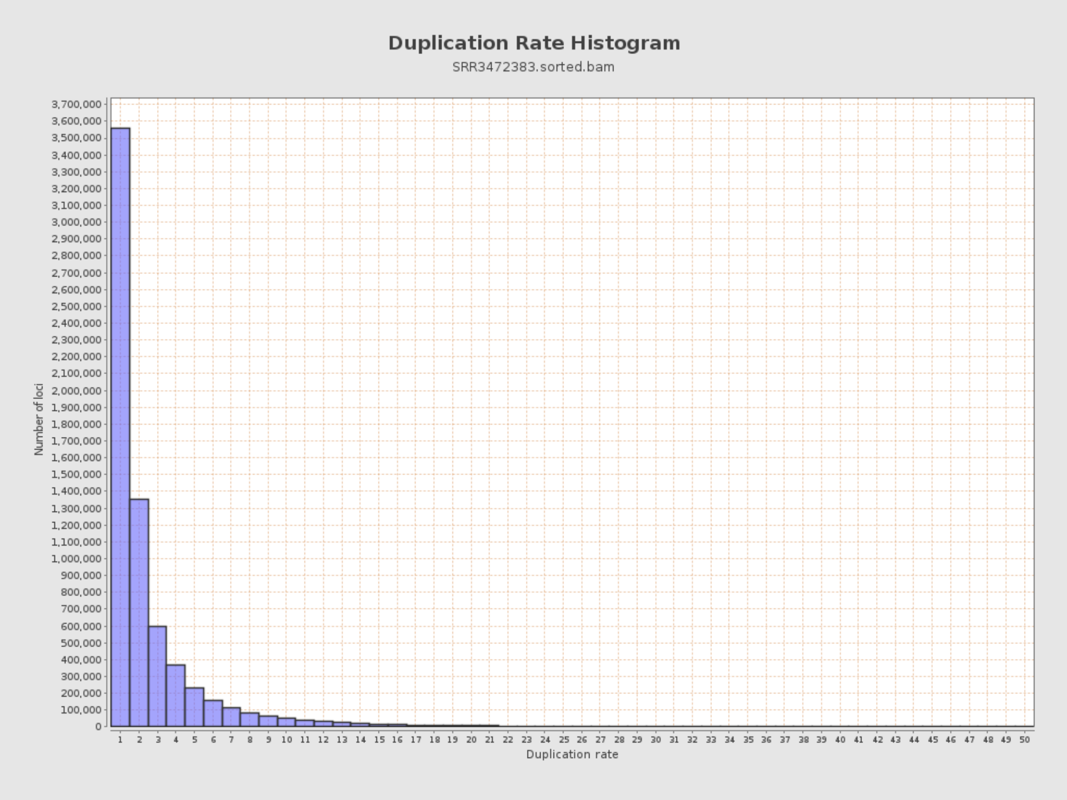
5. Results : Coverage Histogram (0-50X)



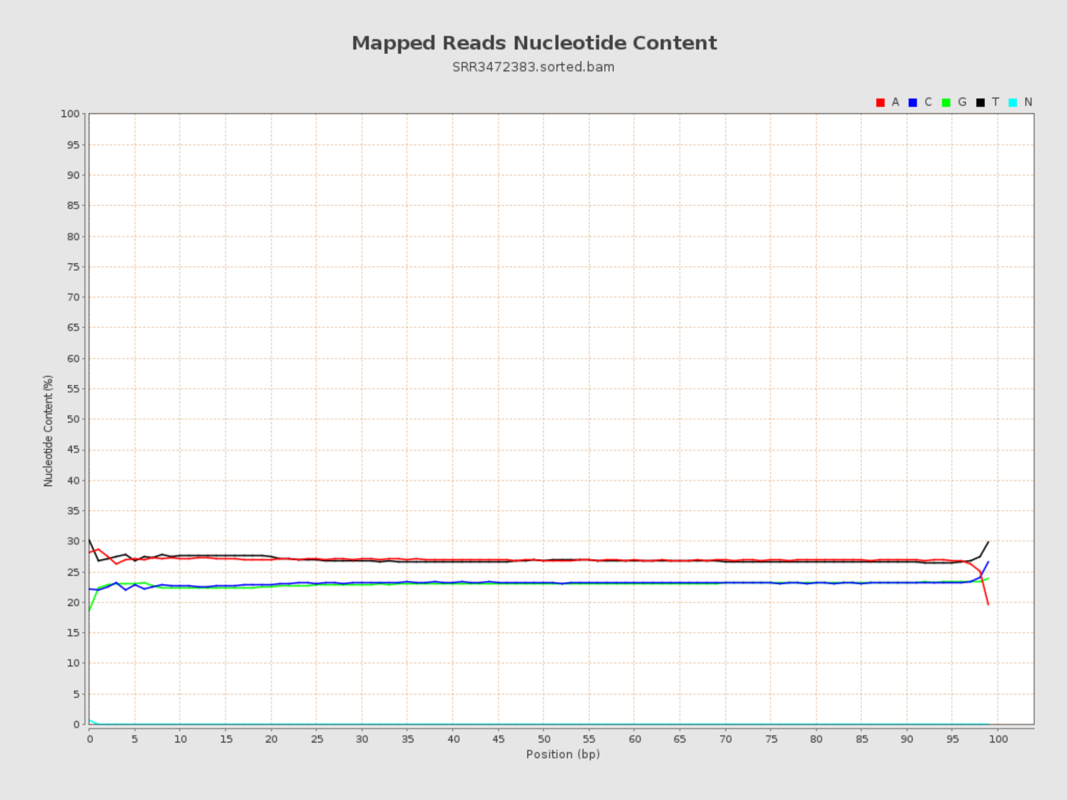
6. Results : Genome Fraction Coverage



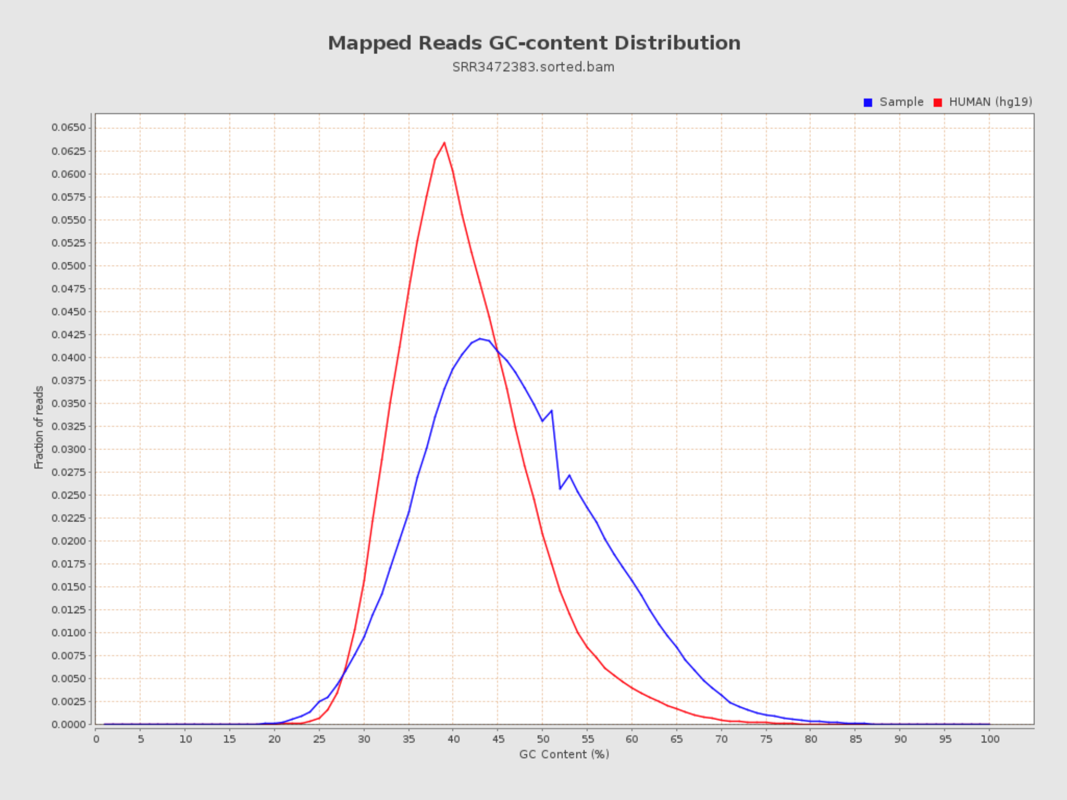
7. Results : Duplication Rate Histogram



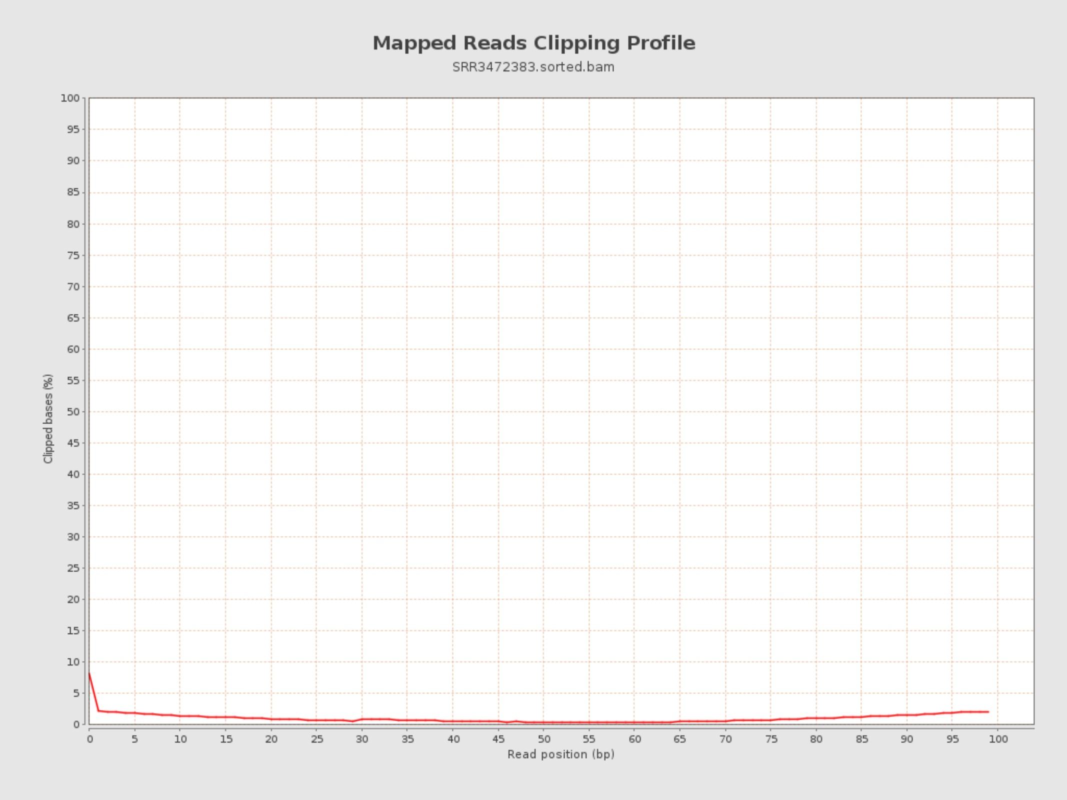
8. Results : Mapped Reads Nucleotide Content



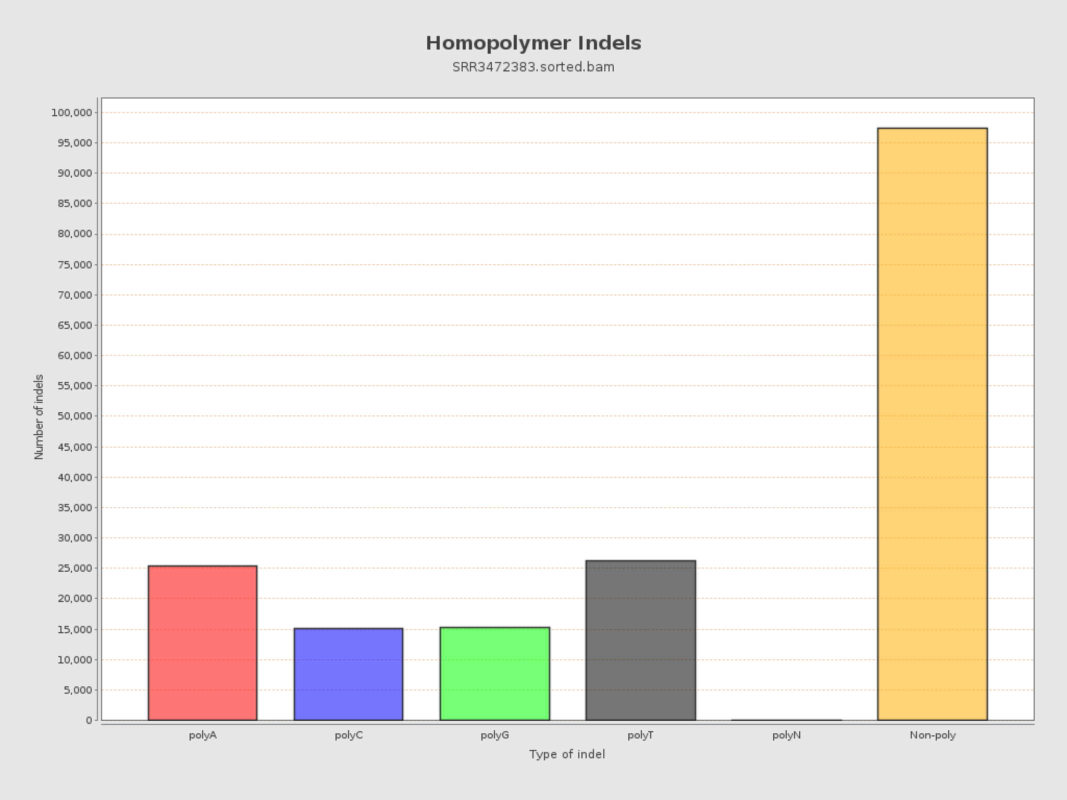
9. Results : Mapped Reads GC-content Distribution



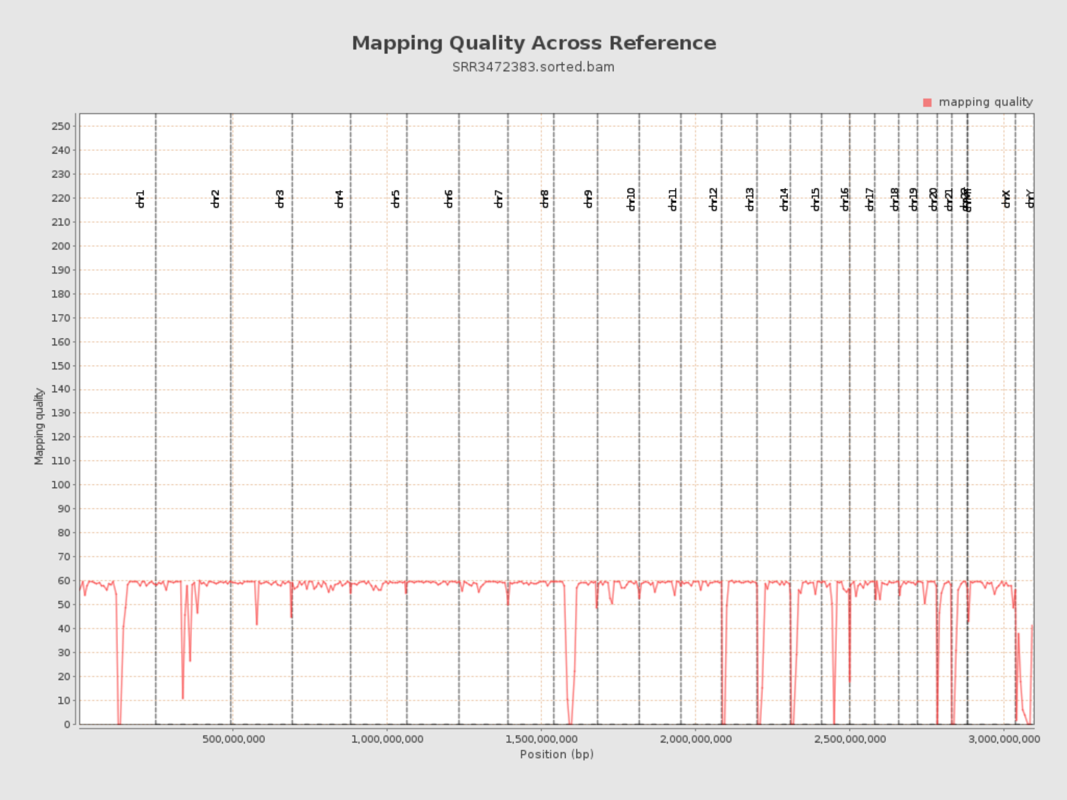
10. Results : Mapped Reads Clipping Profile



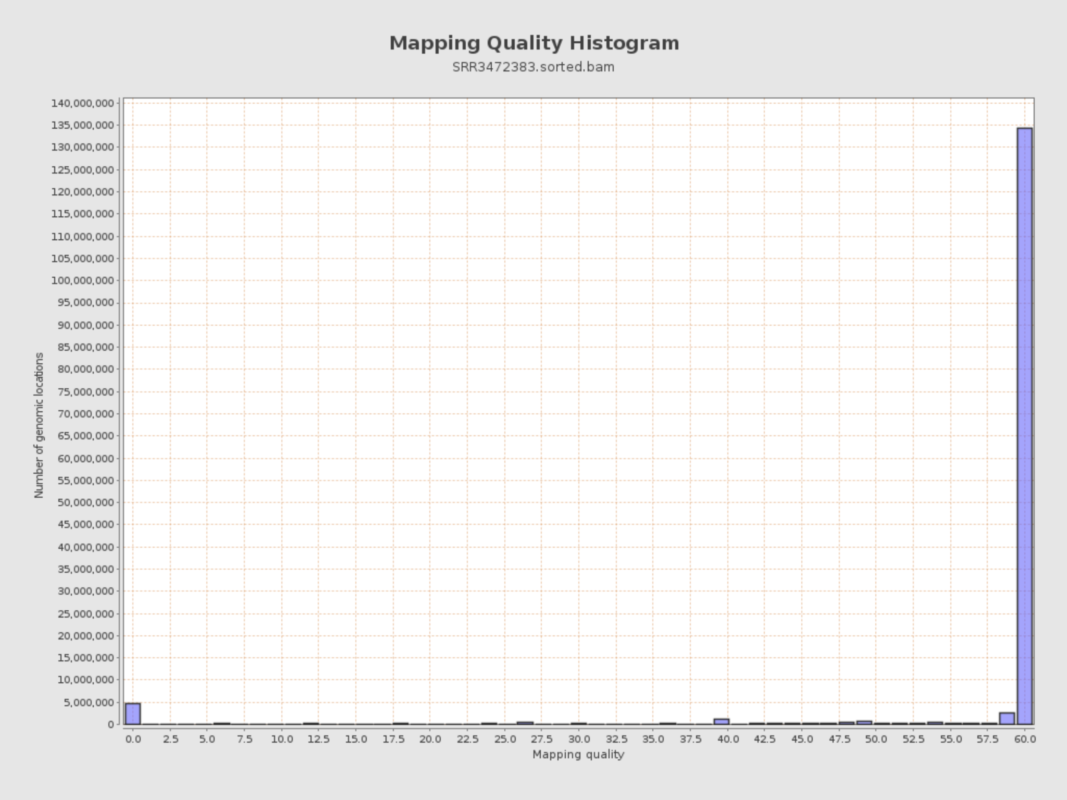
11. Results : Homopolymer Indels



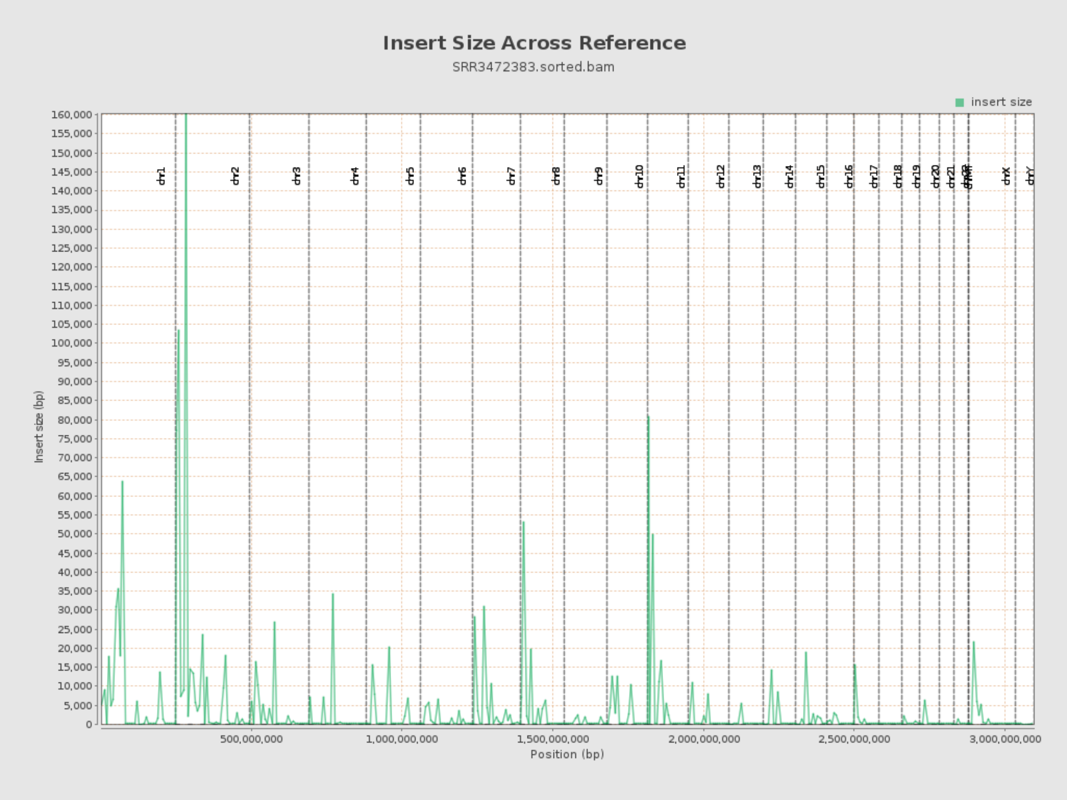
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram