Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 10:15:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472382.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_SRR3472382 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472382_1.fastq.gz SRR3472382_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 10:15:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472382.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,766,942
Mapped reads	19,555,461 / 98.93%
Unmapped reads	211,481 / 1.07%
Mapped paired reads	19,555,461 / 98.93%
Mapped reads, first in pair	9,807,170 / 49.61%
Mapped reads, second in pair	9,748,291 / 49.32%
Mapped reads, both in pair	19,445,640 / 98.37%
Mapped reads, singletons	109,821 / 0.56%
Secondary alignments	0
Supplementary alignments	72,780 / 0.37%
Read min/max/mean length	30 / 100 / 99.27
Duplicated reads (estimated)	12,484,689 / 63.16%
Duplication rate	47.66%
Clipped reads	1,419,714 / 7.18%

2.2. ACGT Content

Number/percentage of A's	516,681,740 / 26.98%
Number/percentage of C's	442,501,991 / 23.11%
Number/percentage of T's	517,620,610 / 27.03%
Number/percentage of G's	437,800,254 / 22.86%
Number/percentage of N's	237,412 / 0.01%

GC Percentage	45.97%

2.3. Coverage

Mean	0.6186
Standard Deviation	19.3997

2.4. Mapping Quality

Mean Mapping Quality	54.83

2.5. Insert size

Mean	18,545.38
Standard Deviation	1,373,904.92
P25/Median/P75	152 / 211 / 284

2.6. Mismatches and indels

General error rate	0.56%
Mismatches	10,586,331
Insertions	110,125
Mapped reads with at least one insertion	0.56%
Deletions	95,901
Mapped reads with at least one deletion	0.48%
Homopolymer indels	44.27%

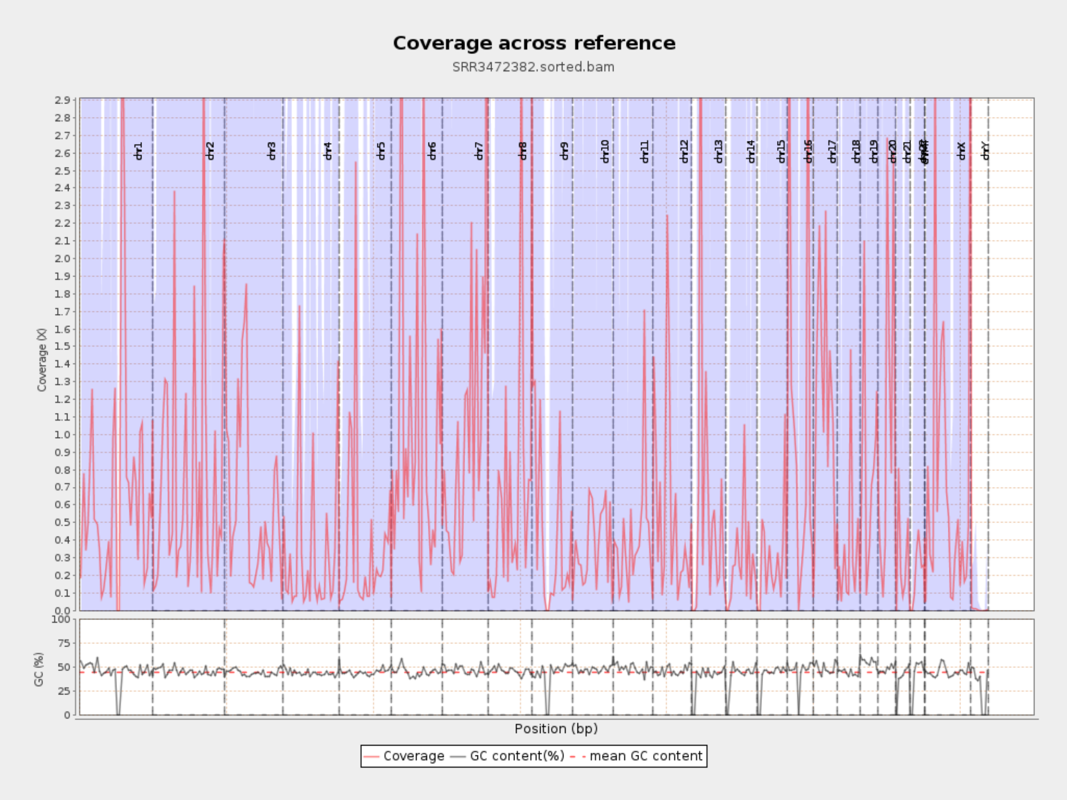
2.7. Chromosome stats

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

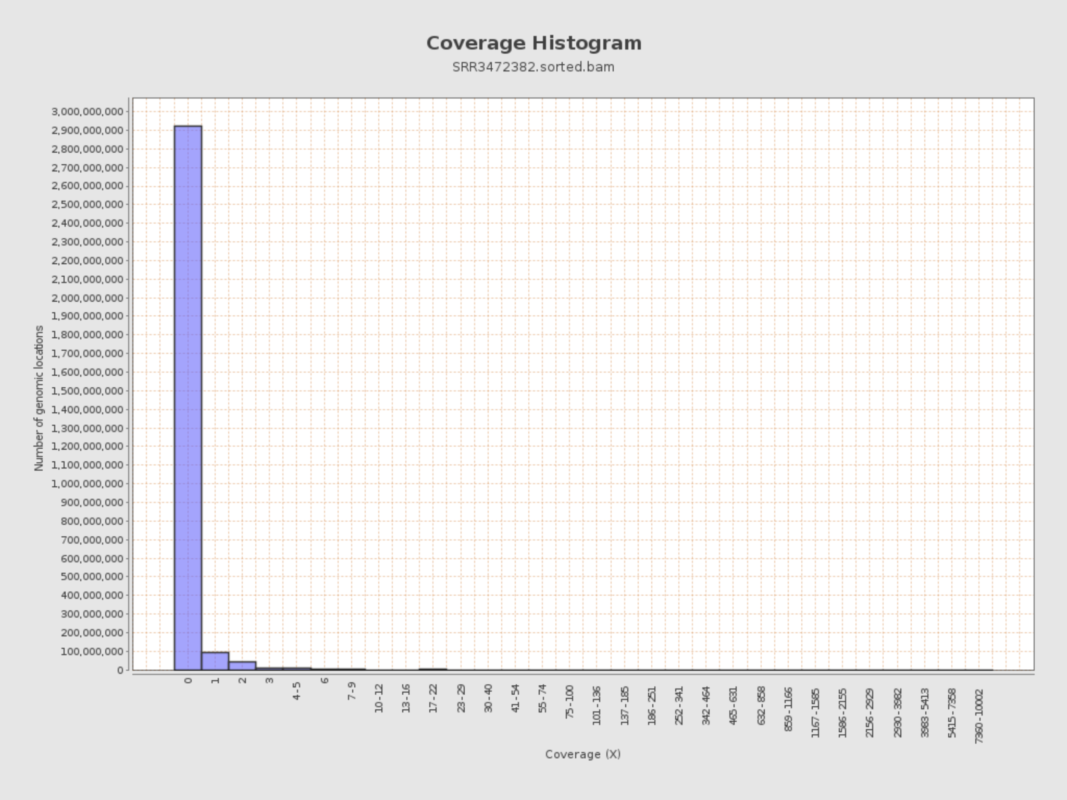
		bases	coverage	deviation
chr1	249250621	171468992	0.6879	19.9585
chr2	243199373	180398930	0.7418	21.7386
chr3	198022430	128627424	0.6496	13.9514
chr4	191154276	60253667	0.3152	11.5279
chr5	180915260	68911469	0.3809	13.2565
chr6	171115067	174933448	1.0223	34.1455
chr7	159138663	173904264	1.0928	30.0594
chr8	146364022	98124741	0.6704	19.3489
chr9	141213431	64096745	0.4539	10.6322
chr10	135534747	50099077	0.3696	10.3111
chr11	135006516	56650858	0.4196	12.6538
chr12	133851895	77044579	0.5756	15.591
chr13	115169878	74796922	0.6494	23.9463
chr14	107349540	28544382	0.2659	7.9151
chr15	102531392	30381440	0.2963	9.7047
chr16	90354753	99228724	1.0982	26.4589
chr17	81195210	96138530	1.184	27.5351
chr18	78077248	26936257	0.345	14.8432
chr19	59128983	49273355	0.8333	16.9009
chr20	63025520	68343392	1.0844	29.8427
chr21	48129895	14042484	0.2918	13.6203
chr22	51304566	10755372	0.2096	5.0908
chrMT	16571	6849	0.4133	0.7639
chrX	155270560	111839265	0.7203	20.3839

chrY	59373566	291513	0.0049	0.2612

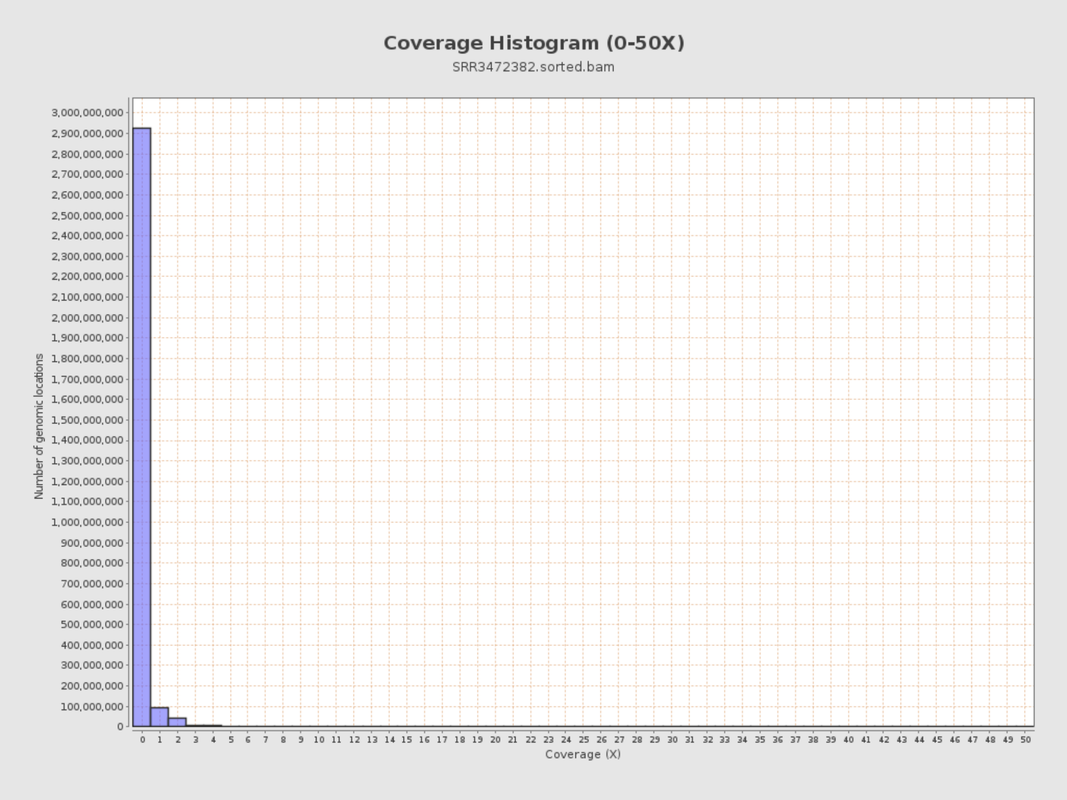
3. Results : Coverage across reference



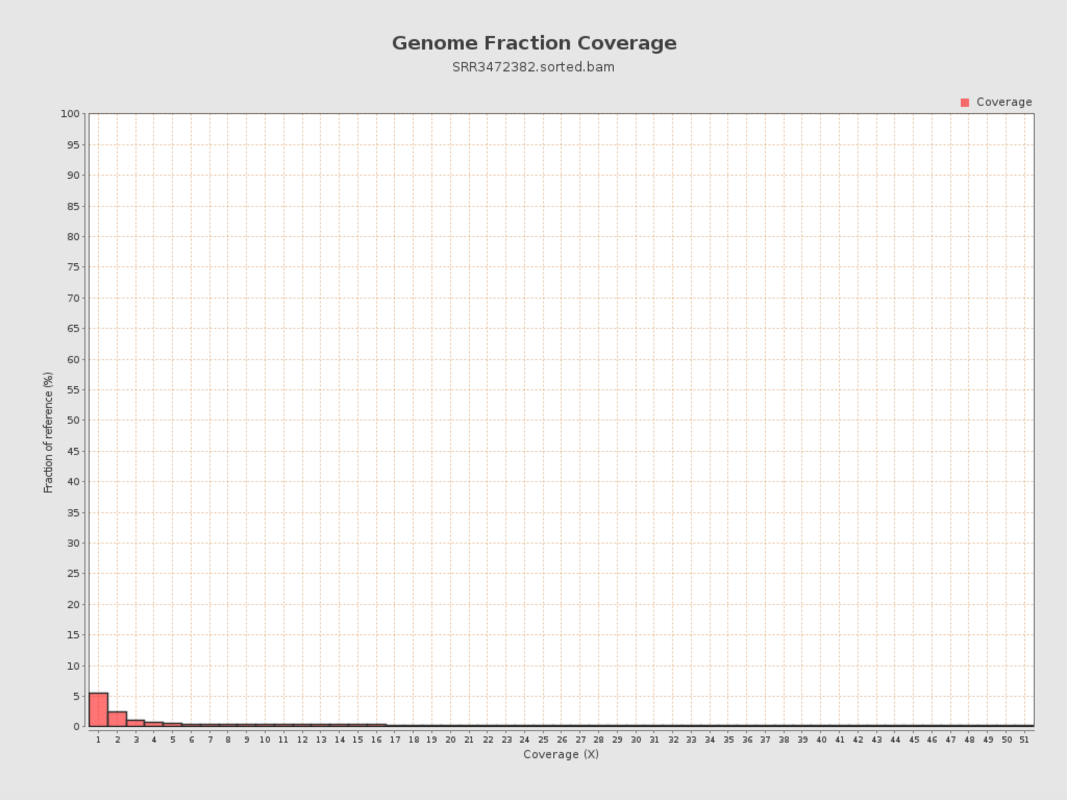
4. Results : Coverage Histogram



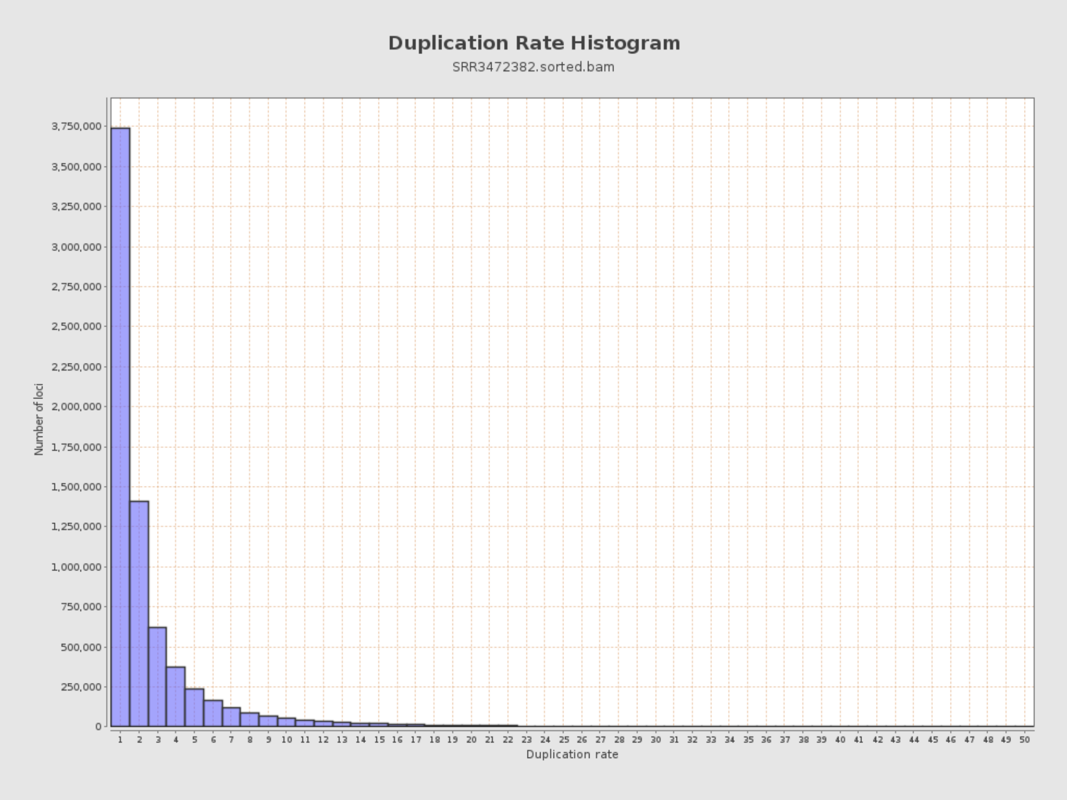
5. Results : Coverage Histogram (0-50X)



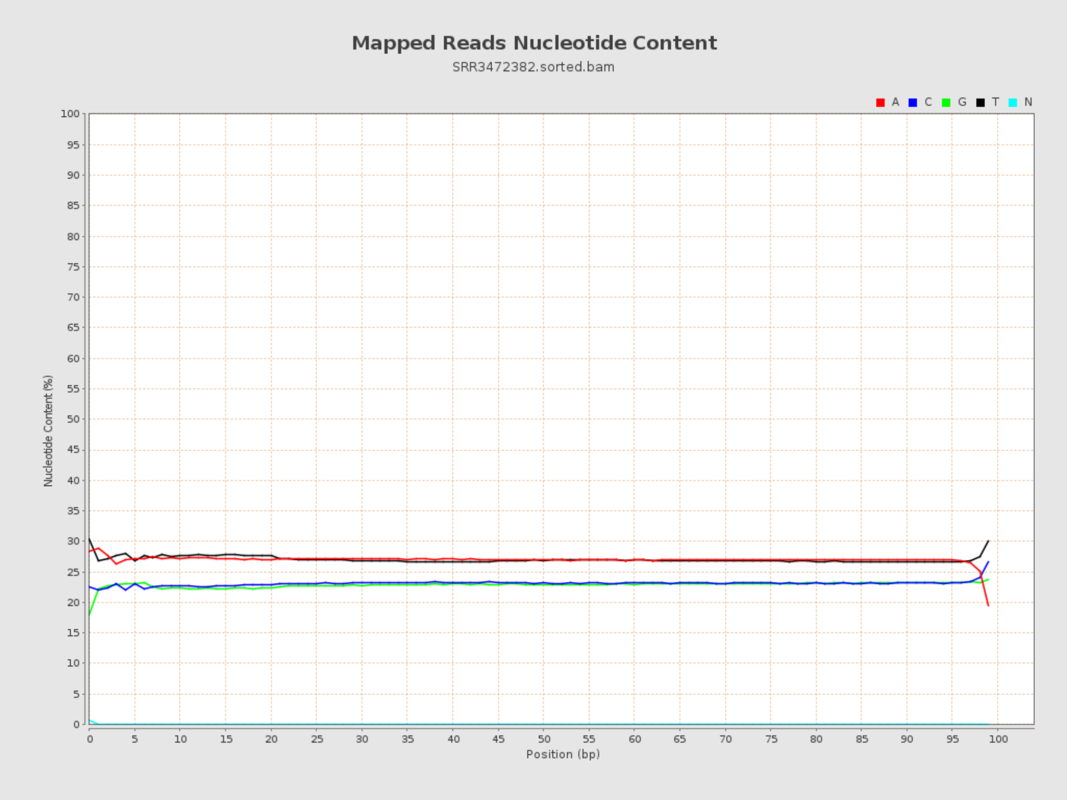
6. Results : Genome Fraction Coverage



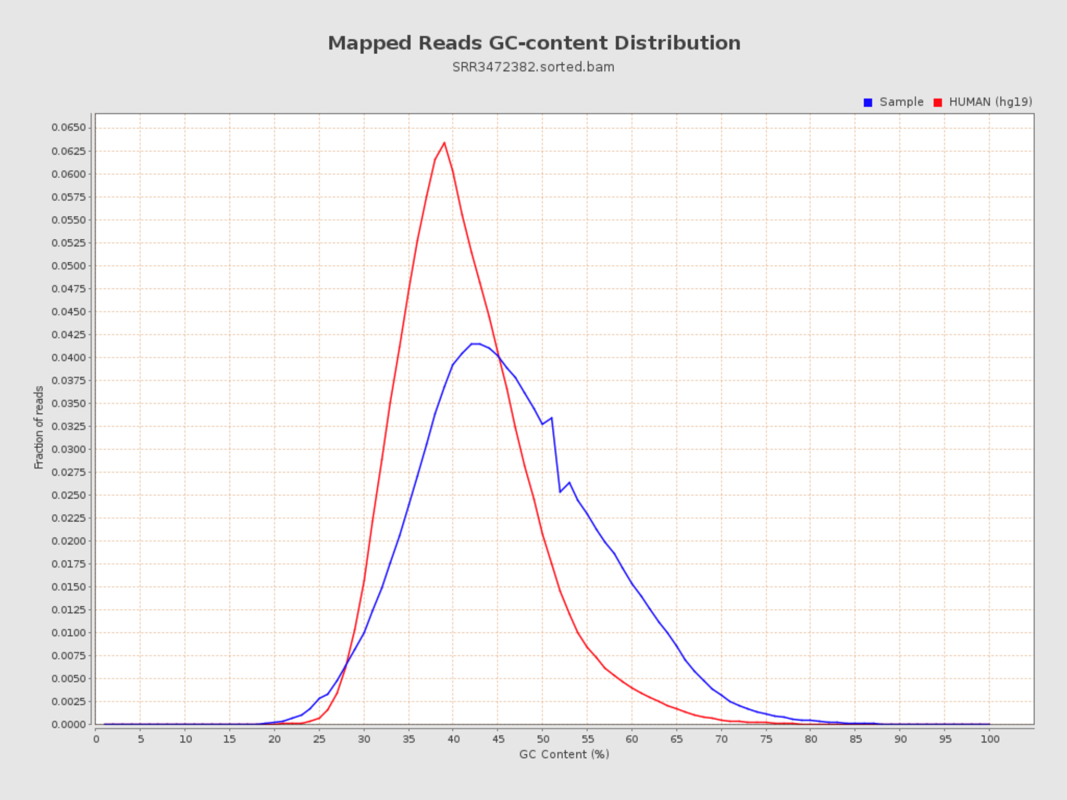
7. Results : Duplication Rate Histogram



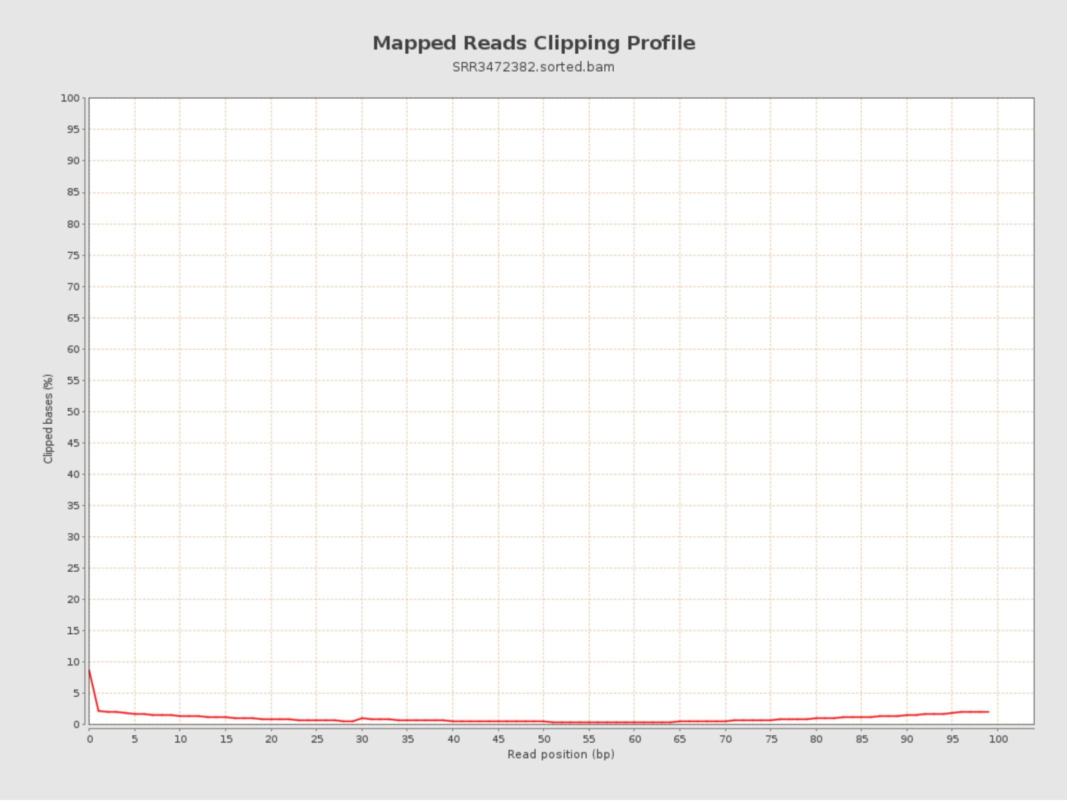
8. Results : Mapped Reads Nucleotide Content



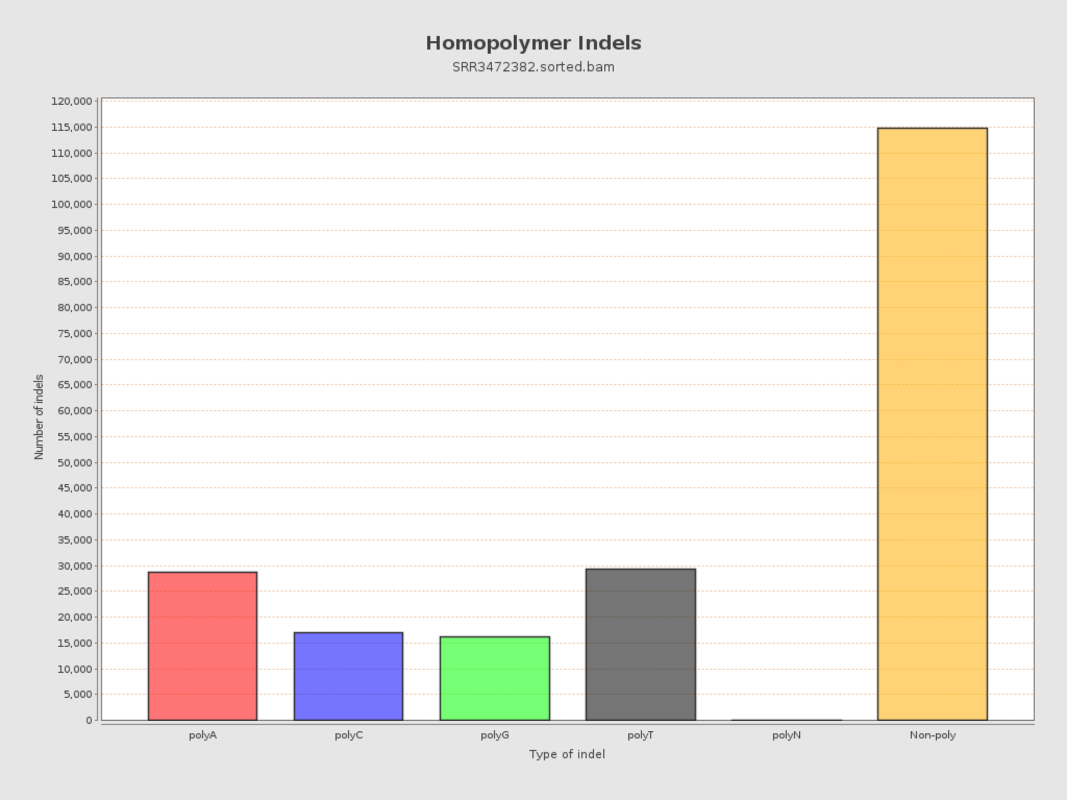
9. Results : Mapped Reads GC-content Distribution



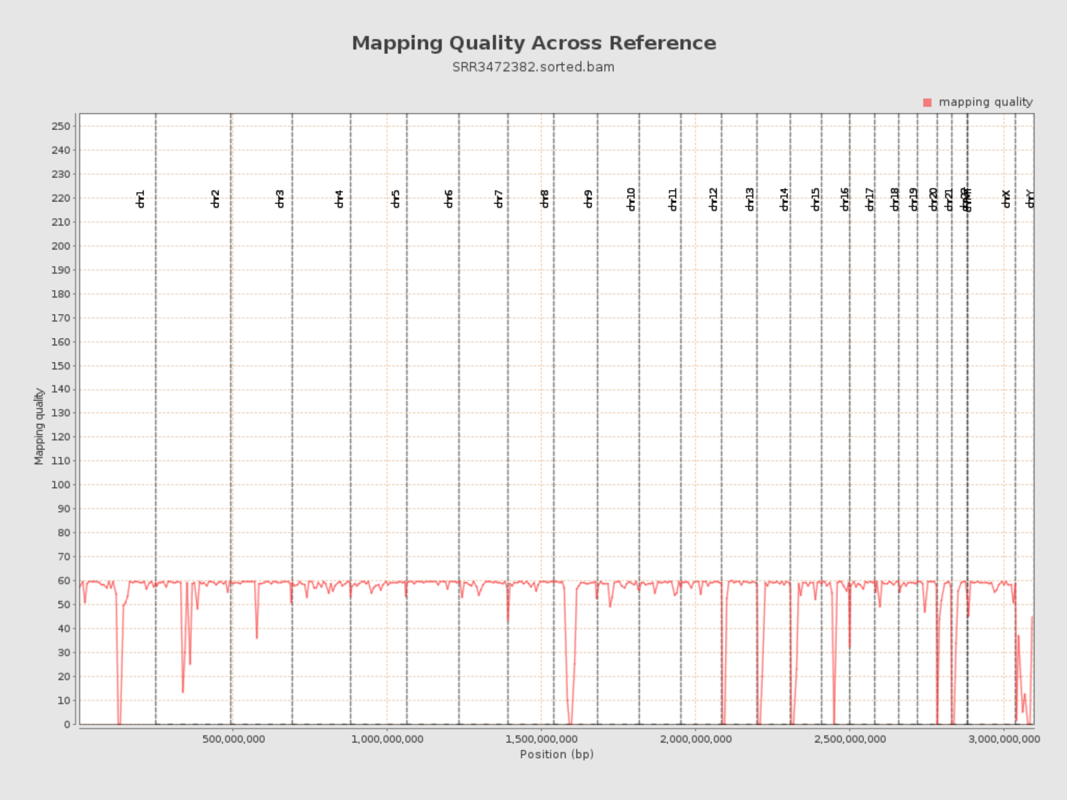
10. Results : Mapped Reads Clipping Profile



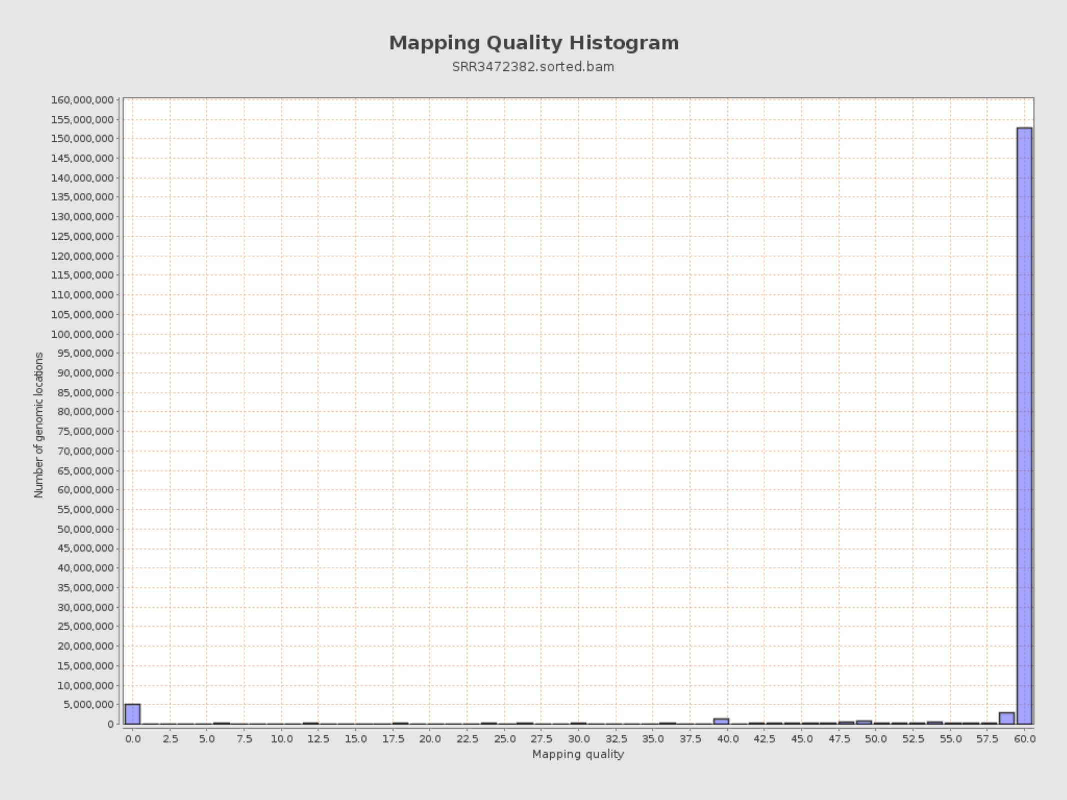
11. Results : Homopolymer Indels



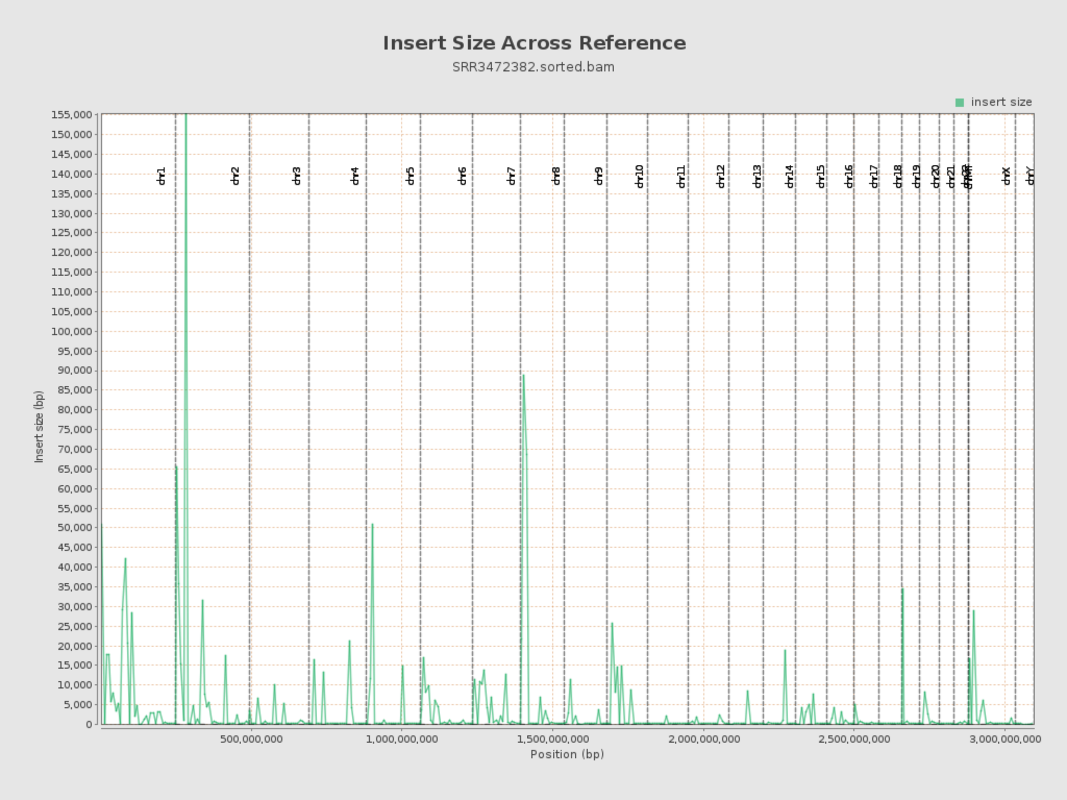
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram