Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 18:23:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472514.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_SRR3472514 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472514_1.fastq.gz SRR3472514_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 18:23:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472514.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,402,232
Mapped reads	18,215,788 / 98.99%
Unmapped reads	186,444 / 1.01%
Mapped paired reads	18,215,788 / 98.99%
Mapped reads, first in pair	9,132,352 / 49.63%
Mapped reads, second in pair	9,083,436 / 49.36%
Mapped reads, both in pair	18,119,362 / 98.46%
Mapped reads, singletons	96,426 / 0.52%
Secondary alignments	0
Supplementary alignments	75,330 / 0.41%
Read min/max/mean length	30 / 100 / 100.17
Duplicated reads (estimated)	11,480,715 / 62.39%
Duplication rate	46.45%
Clipped reads	1,650,020 / 8.97%

2.2. ACGT Content

Number/percentage of A's	494,217,246 / 27.61%
Number/percentage of C's	403,766,712 / 22.55%
Number/percentage of T's	490,653,158 / 27.41%
Number/percentage of G's	401,376,871 / 22.42%
Number/percentage of N's	278,542 / 0.02%

GC Percentage	44.97%

2.3. Coverage

Mean	0.5784
Standard Deviation	18.8869

2.4. Mapping Quality

Mean Mapping Quality	55.25

2.5. Insert size

Mean	29,060.15
Standard Deviation	1,675,873.52
P25/Median/P75	161 / 224 / 303

2.6. Mismatches and indels

General error rate	0.6%
Mismatches	10,449,706
Insertions	99,238
Mapped reads with at least one insertion	0.54%
Deletions	94,433
Mapped reads with at least one deletion	0.51%
Homopolymer indels	46.09%

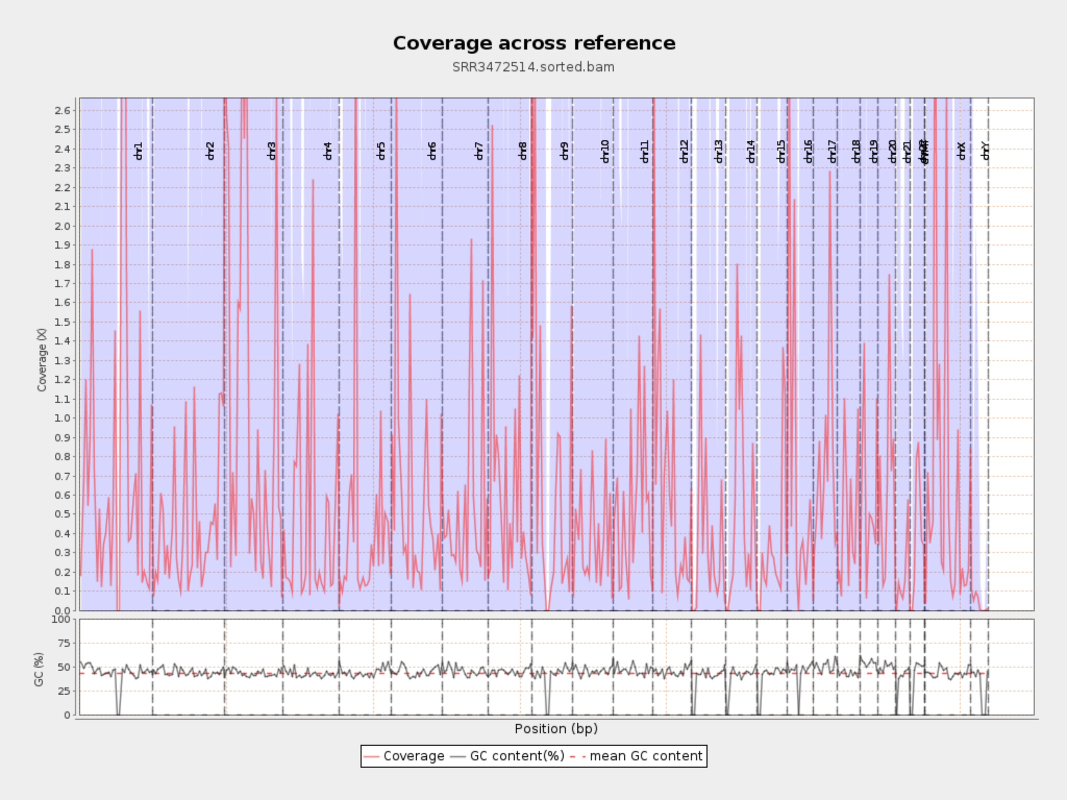
2.7. Chromosome stats

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

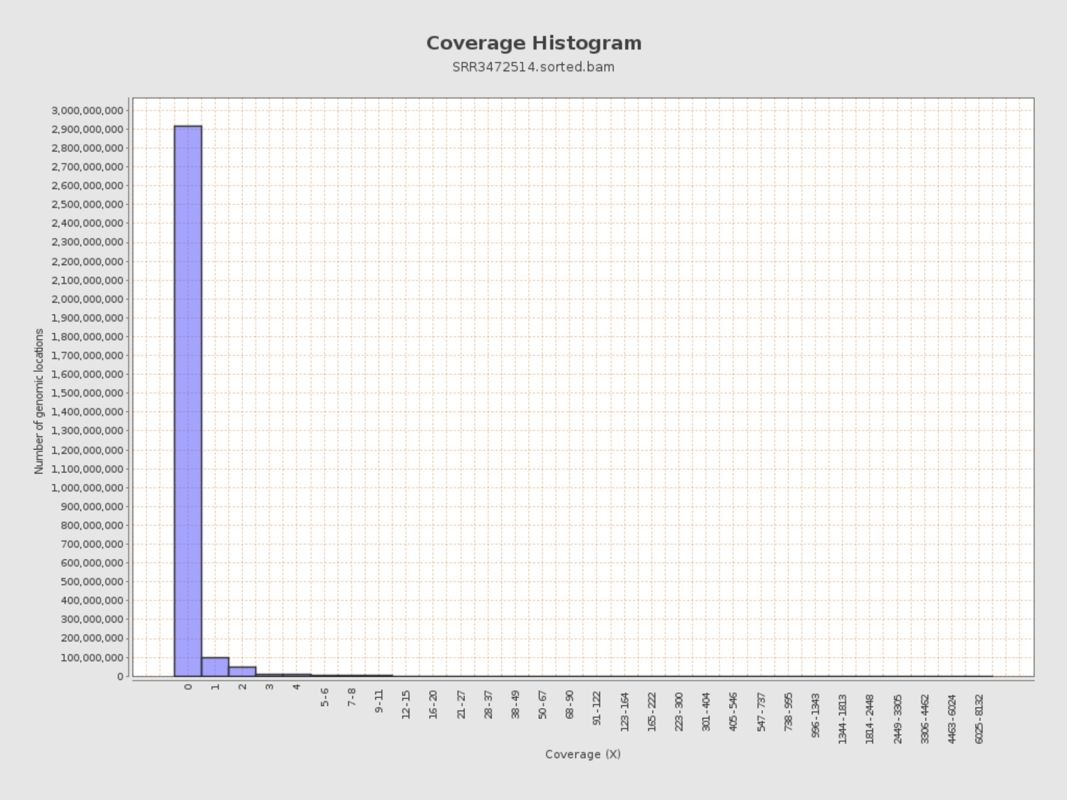
		bases	coverage	deviation
chr1	249250621	200145099	0.803	27.6938
chr2	243199373	104836548	0.4311	13.1814
chr3	198022430	224565812	1.134	26.4499
chr4	191154276	88245677	0.4616	17.652
chr5	180915260	79749328	0.4408	15.4936
chr6	171115067	100150538	0.5853	16.0096
chr7	159138663	87296985	0.5486	16.829
chr8	146364022	87475605	0.5977	18.9118
chr9	141213431	94930794	0.6723	17.3519
chr10	135534747	50959248	0.376	12.4781
chr11	135006516	72582115	0.5376	15.599
chr12	133851895	93609944	0.6994	23.2591
chr13	115169878	41791533	0.3629	14.8059
chr14	107349540	55239620	0.5146	16.9947
chr15	102531392	36305181	0.3541	10.1567
chr16	90354753	62225420	0.6887	23.0622
chr17	81195210	61407017	0.7563	18.9444
chr18	78077248	37275460	0.4774	18.2201
chr19	59128983	34003620	0.5751	15.723
chr20	63025520	41636711	0.6606	22.319
chr21	48129895	8584097	0.1784	6.8619
chr22	51304566	19639600	0.3828	9.9332
chrMT	16571	4539	0.2739	0.8028
chrX	155270560	105477045	0.6793	24.8073

chrY	59373566	2392827	0.0403	1.7932

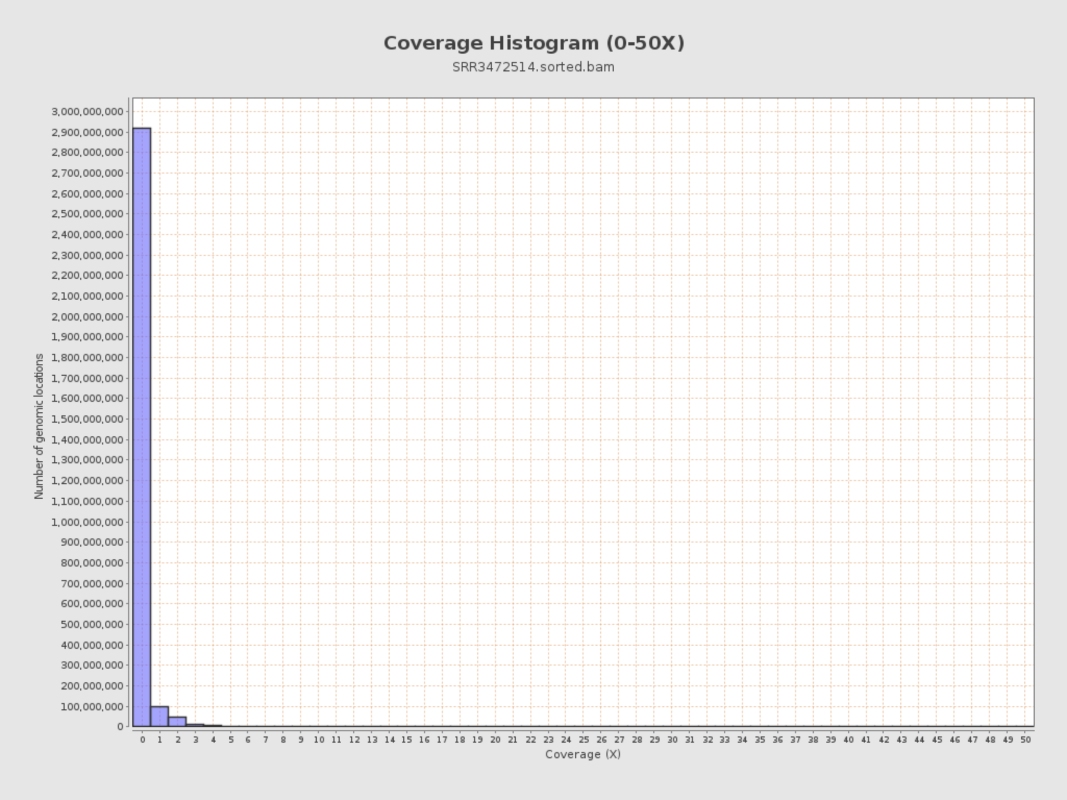
3. Results : Coverage across reference



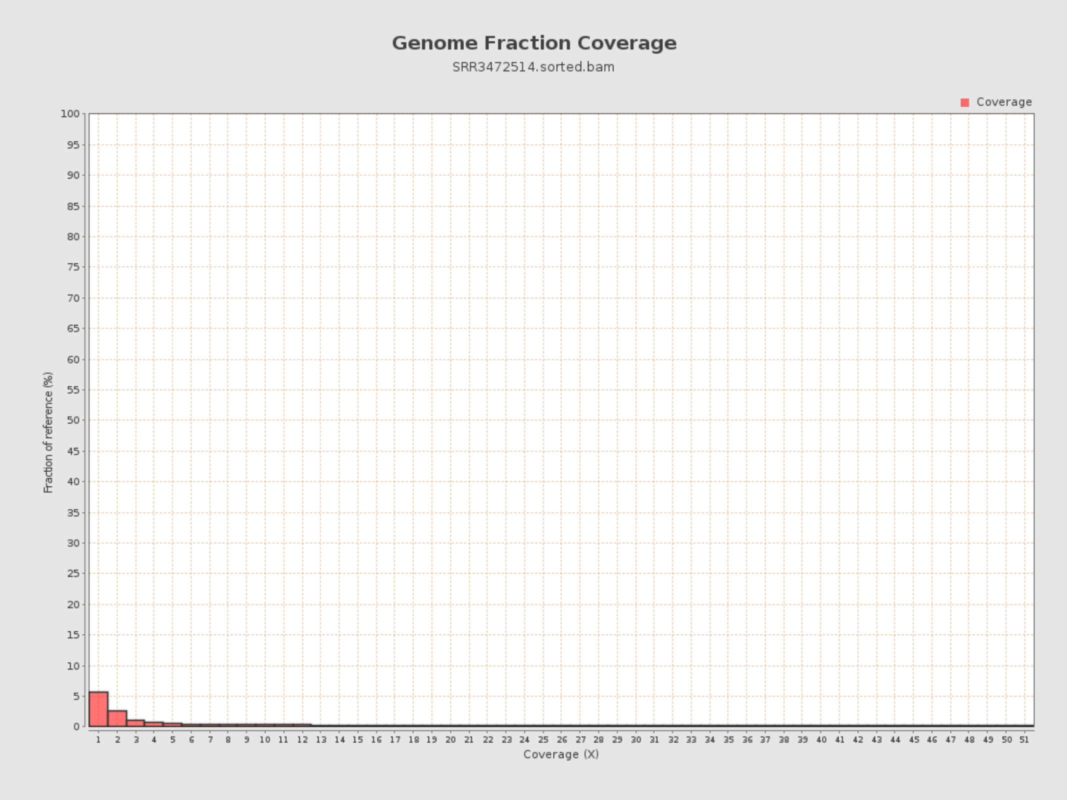
4. Results : Coverage Histogram



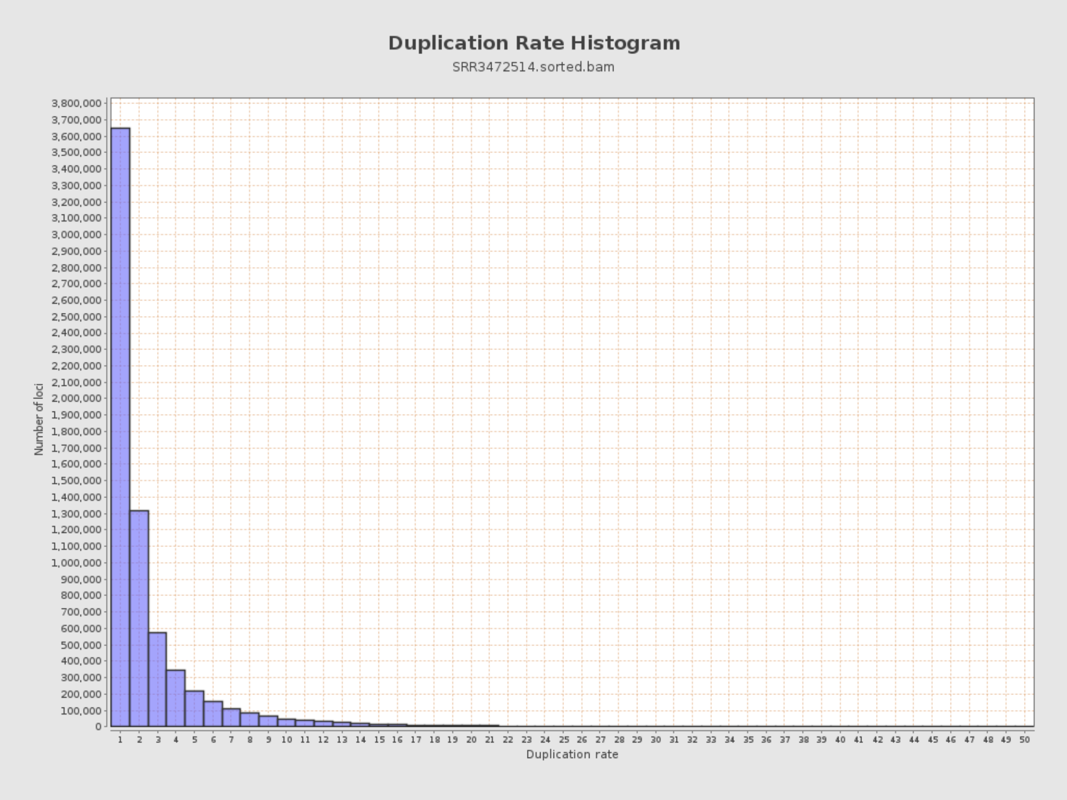
5. Results : Coverage Histogram (0-50X)



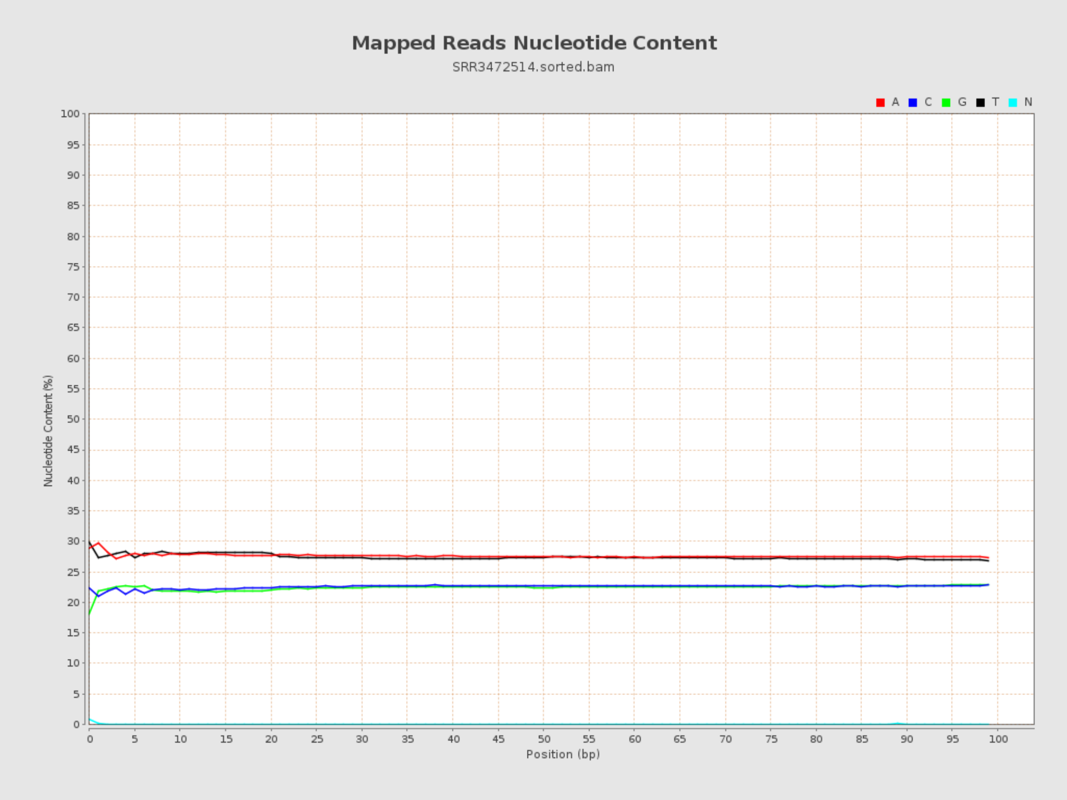
6. Results : Genome Fraction Coverage



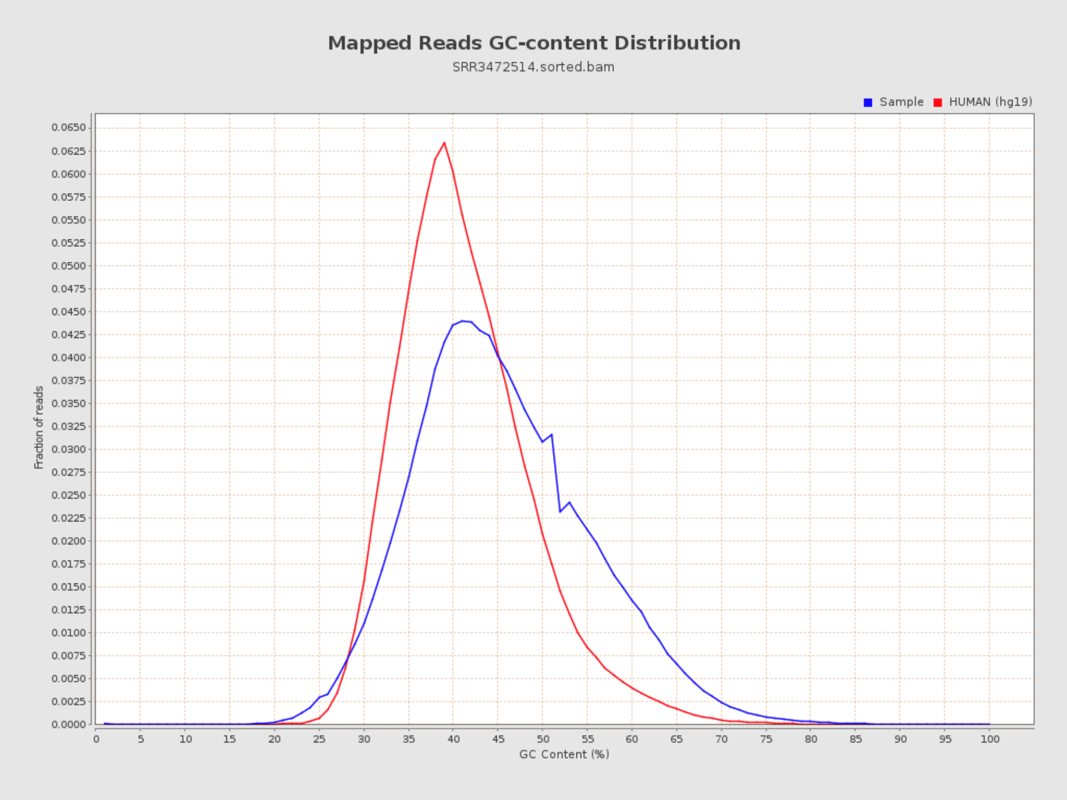
7. Results : Duplication Rate Histogram



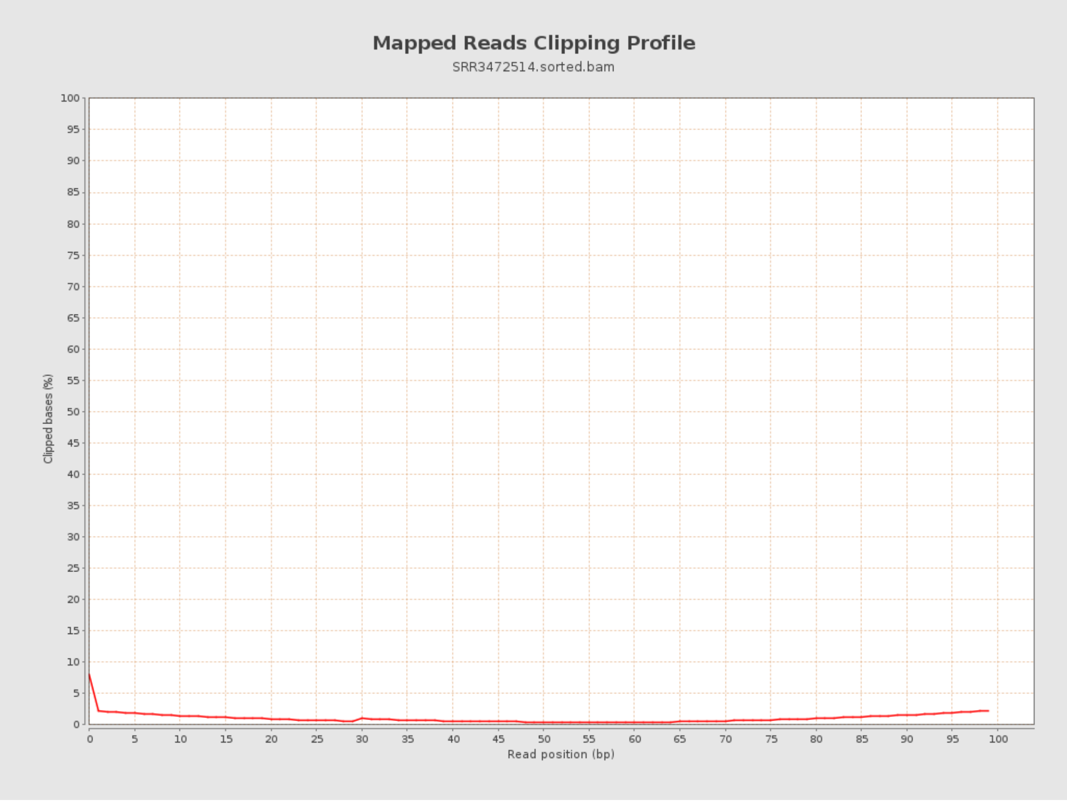
8. Results : Mapped Reads Nucleotide Content



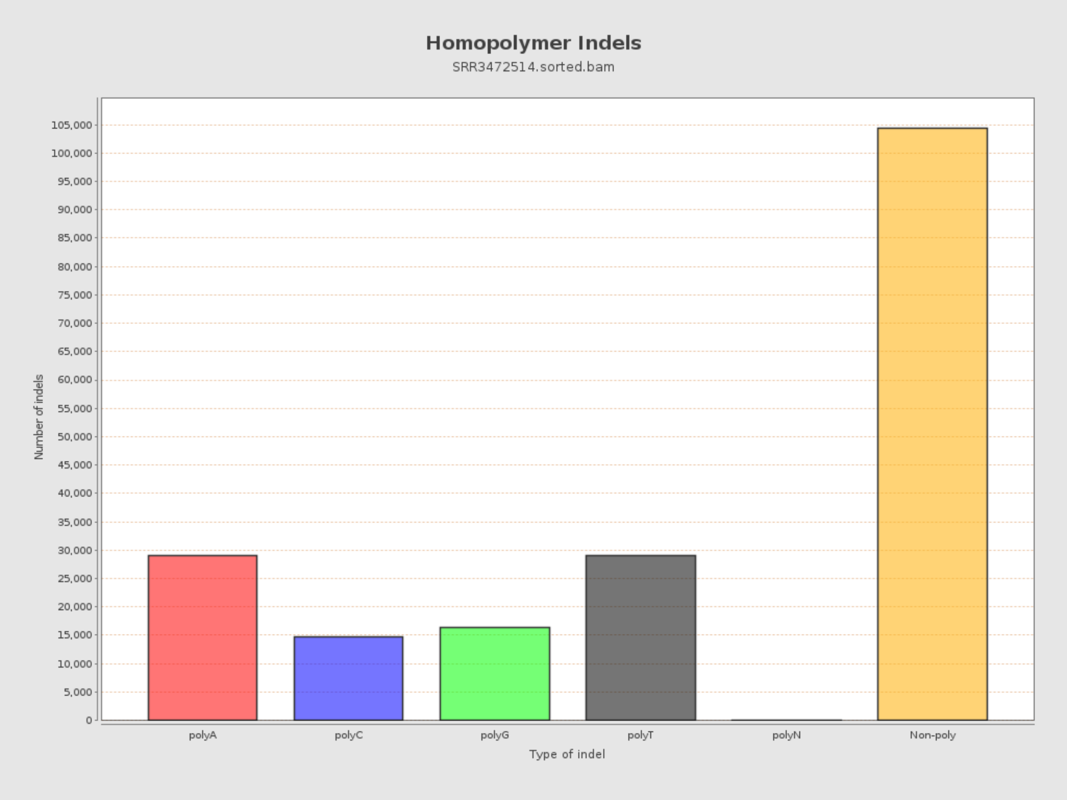
9. Results : Mapped Reads GC-content Distribution



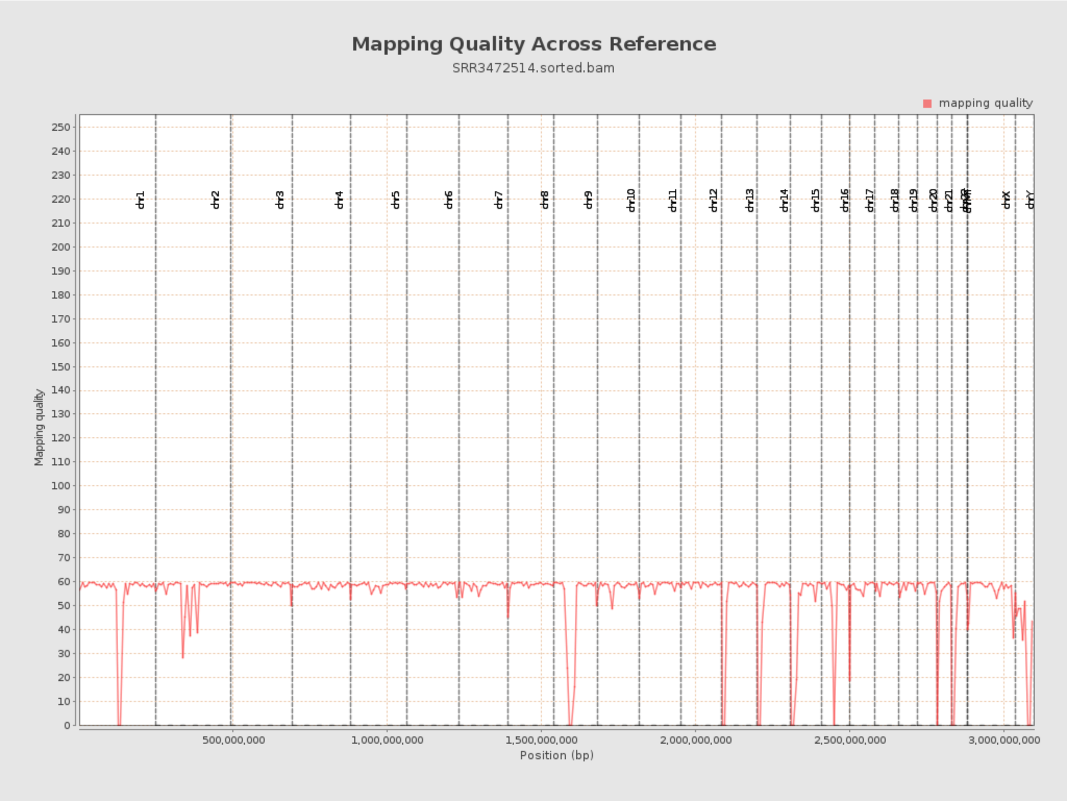
10. Results : Mapped Reads Clipping Profile



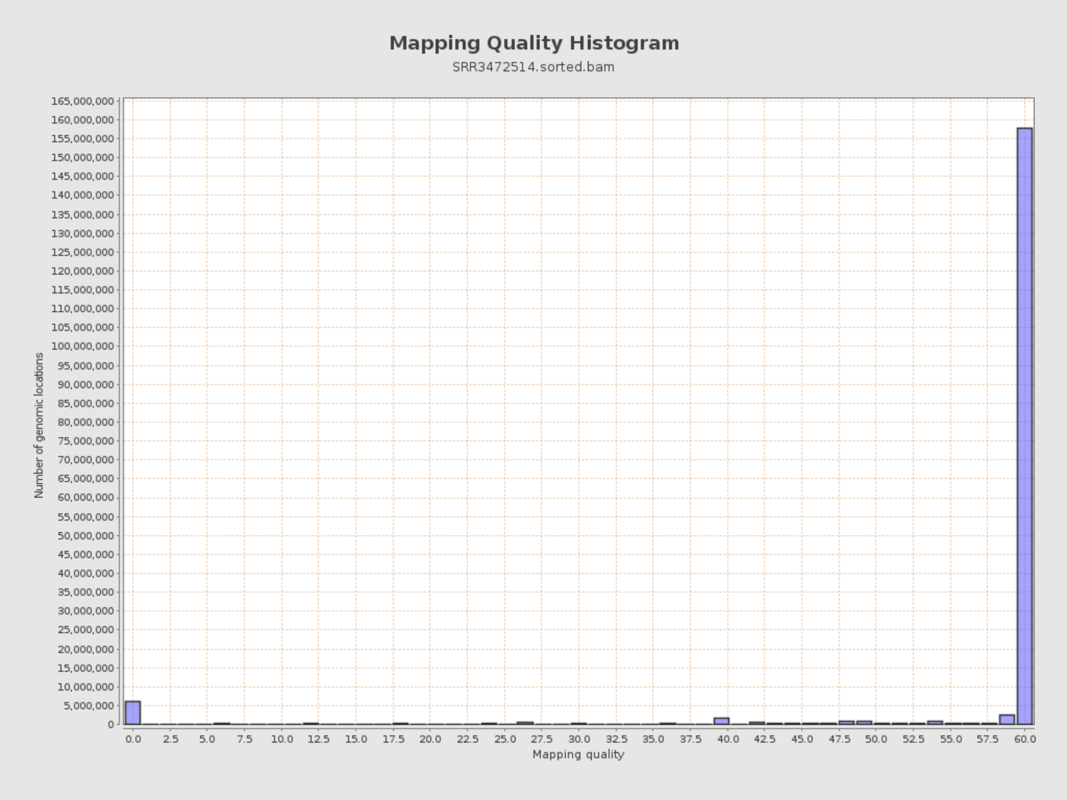
11. Results : Homopolymer Indels



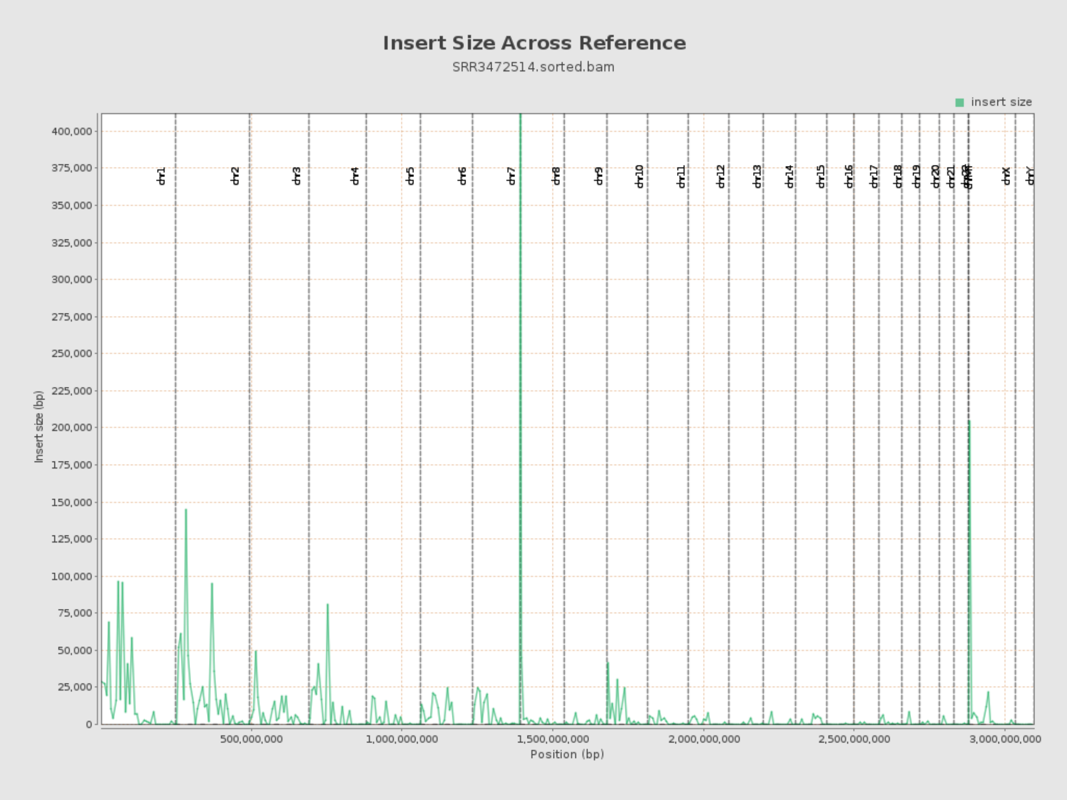
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram