Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 20:41:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472645.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_SRR3472645 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472645_1.fastq.gz SRR3472645_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 20:41:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472645.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,587,844
Mapped reads	8,530,565 / 99.33%
Unmapped reads	57,279 / 0.67%
Mapped paired reads	8,530,565 / 99.33%
Mapped reads, first in pair	4,271,577 / 49.74%
Mapped reads, second in pair	4,258,988 / 49.59%
Mapped reads, both in pair	8,491,818 / 98.88%
Mapped reads, singletons	38,747 / 0.45%
Secondary alignments	0
Supplementary alignments	43,177 / 0.5%
Read min/max/mean length	30 / 101 / 99.48
Duplicated reads (estimated)	5,480,643 / 63.82%
Duplication rate	42.62%
Clipped reads	525,350 / 6.12%

2.2. ACGT Content

Number/percentage of A's	226,611,392 / 27.03%
Number/percentage of C's	194,128,393 / 23.15%
Number/percentage of T's	226,350,563 / 26.99%
Number/percentage of G's	191,296,154 / 22.81%
Number/percentage of N's	109,767 / 0.01%

GC Percentage	45.97%

2.3. Coverage

Mean	0.2709
Standard Deviation	15.1599

2.4. Mapping Quality

Mean Mapping Quality	54.59

2.5. Insert size

Mean	17,957.46
Standard Deviation	1,337,754.26
P25/Median/P75	151 / 206 / 274

2.6. Mismatches and indels

General error rate	0.8%
Mismatches	6,622,390
Insertions	58,895
Mapped reads with at least one insertion	0.68%
Deletions	56,509
Mapped reads with at least one deletion	0.6%
Homopolymer indels	43.61%

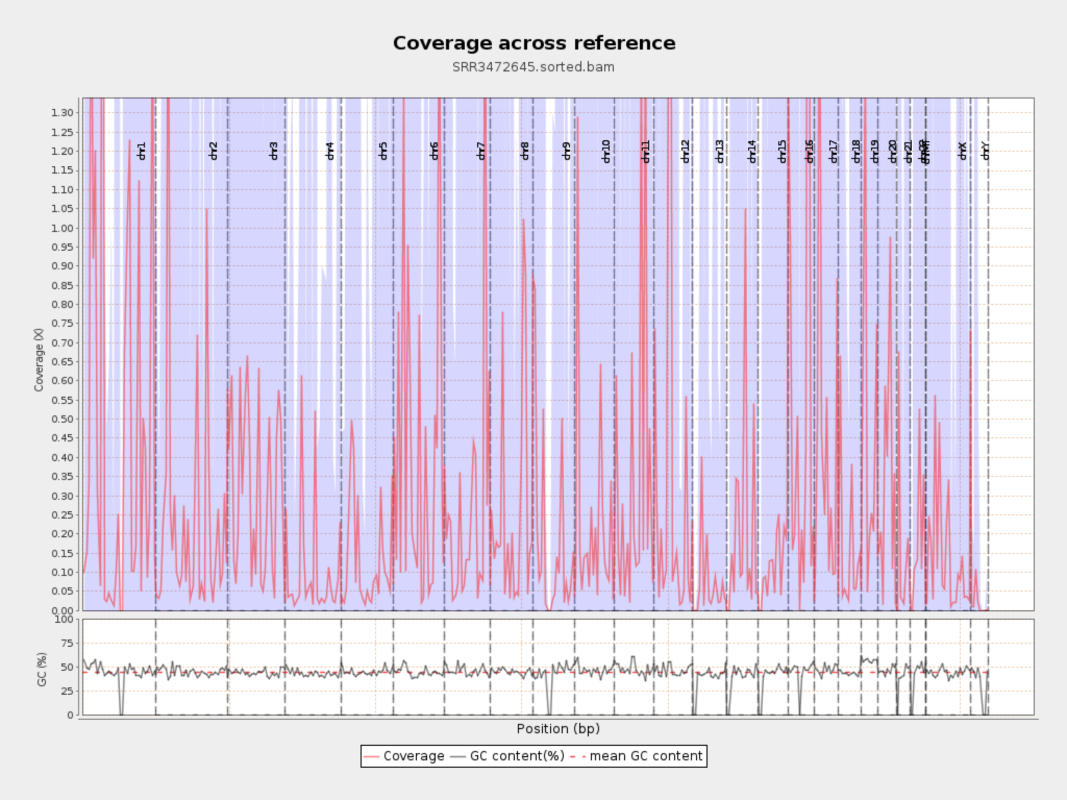
2.7. Chromosome stats

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

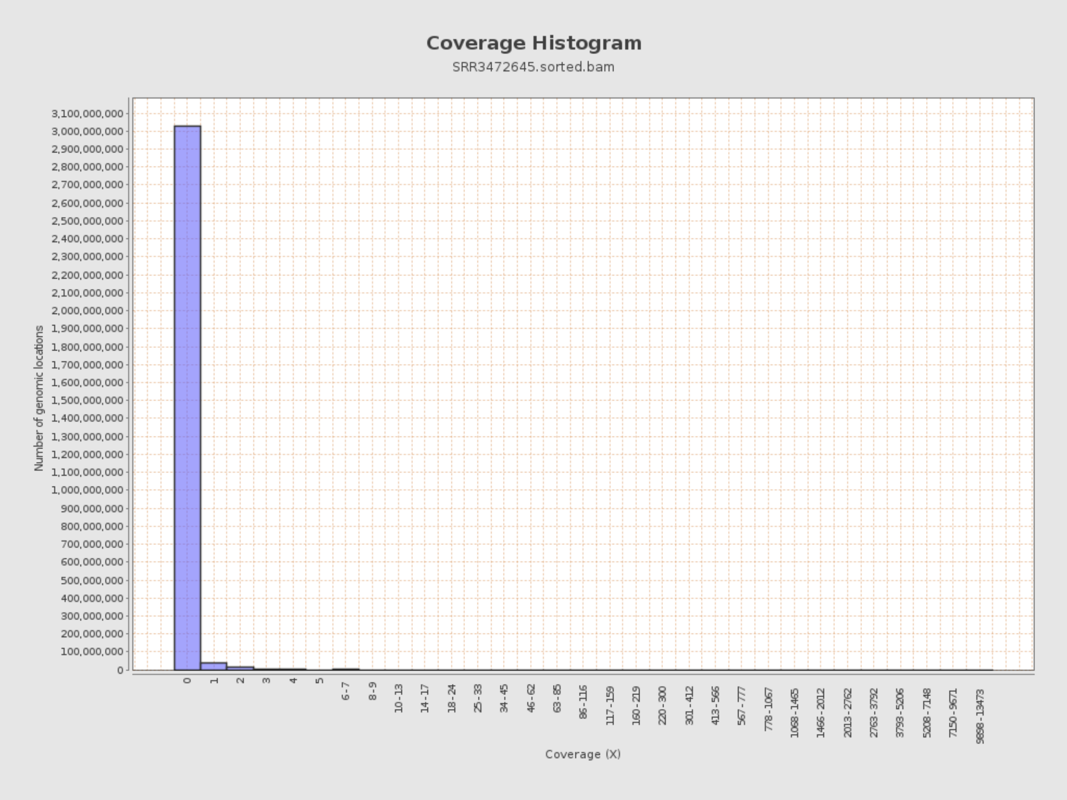
		bases	coverage	deviation
chr1	249250621	124726223	0.5004	27.0775
chr2	243199373	61350123	0.2523	17.7628
chr3	198022430	62521998	0.3157	12.365
chr4	191154276	19788945	0.1035	6.1897
chr5	180915260	24990709	0.1381	7.4254
chr6	171115067	71974197	0.4206	16.5497
chr7	159138663	46111977	0.2898	18.1666
chr8	146364022	38266681	0.2614	12.7504
chr9	141213431	23521401	0.1666	10.0744
chr10	135534747	31641632	0.2335	16.3962
chr11	135006516	50282519	0.3724	17.1276
chr12	133851895	48838140	0.3649	14.1626
chr13	115169878	7873643	0.0684	3.4894
chr14	107349540	22486765	0.2095	8.7877
chr15	102531392	11808114	0.1152	4.7292
chr16	90354753	51092838	0.5655	21.3885
chr17	81195210	36664228	0.4516	22.5991
chr18	78077248	12045278	0.1543	8.0868
chr19	59128983	28663139	0.4848	15.6608
chr20	63025520	21491242	0.341	23.1349
chr21	48129895	8192407	0.1702	12.9074
chr22	51304566	9566096	0.1865	7.8339
chrMT	16571	1104	0.0666	0.3047
chrX	155270560	23547672	0.1517	5.3414

chrY	59373566	1177854	0.0198	1.9215

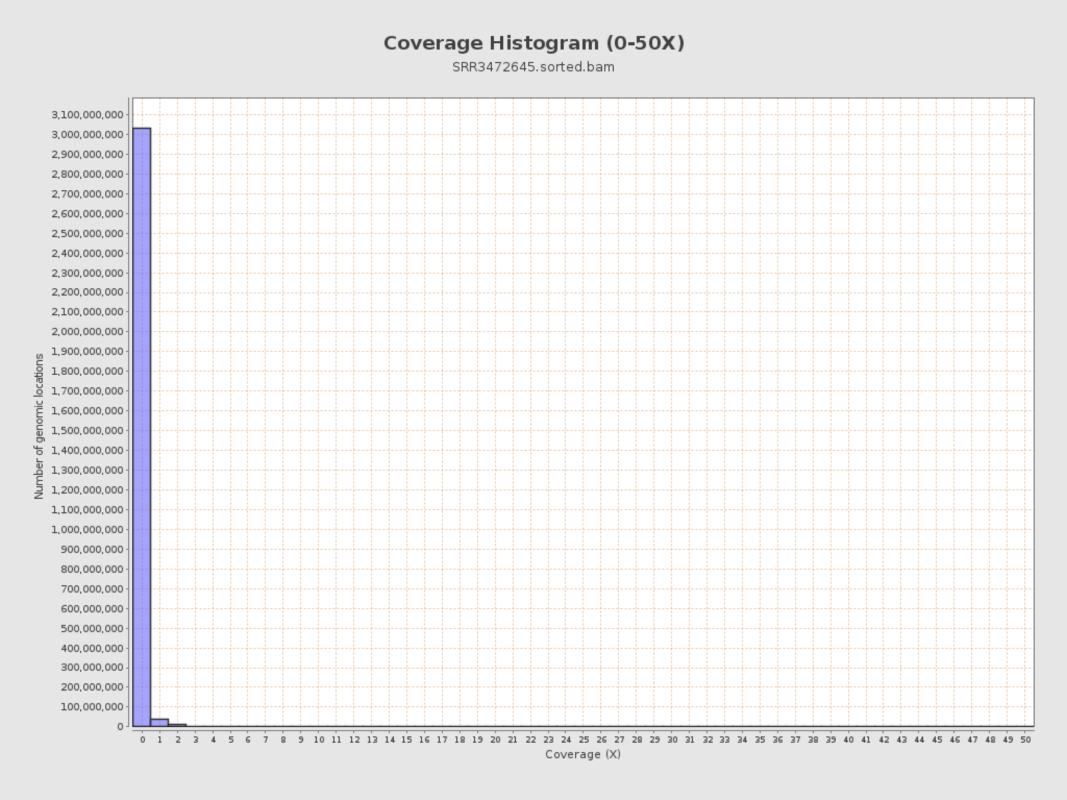
3. Results : Coverage across reference



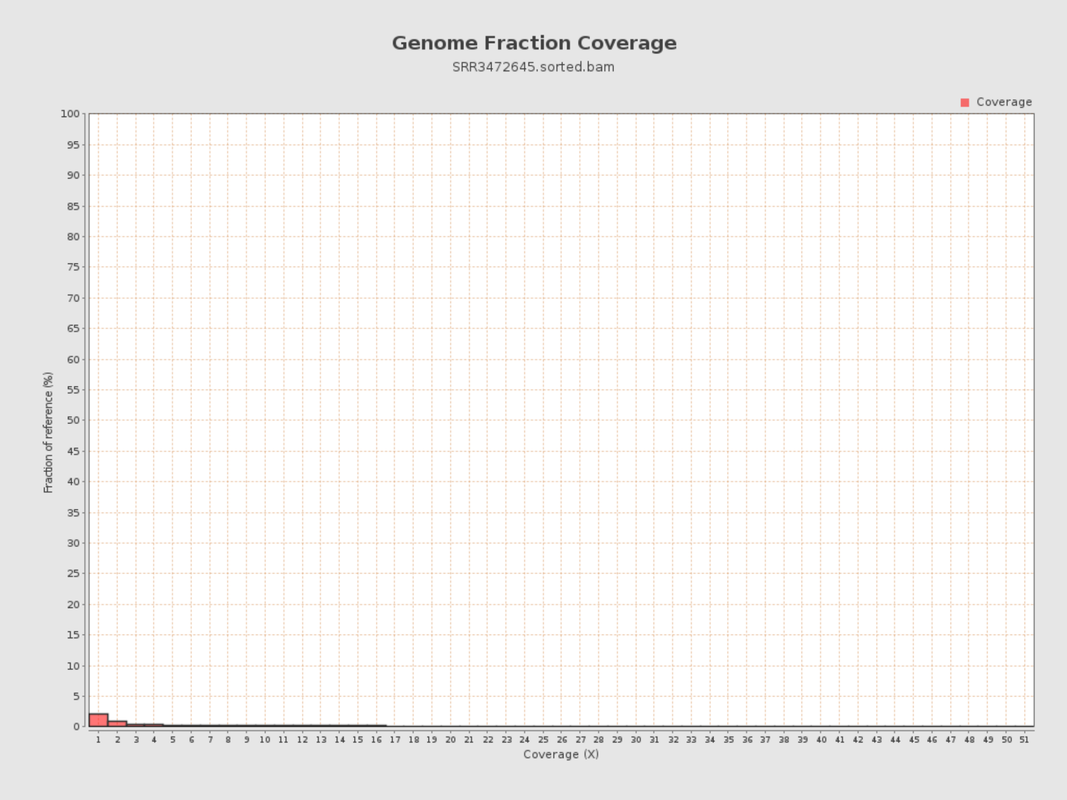
4. Results : Coverage Histogram



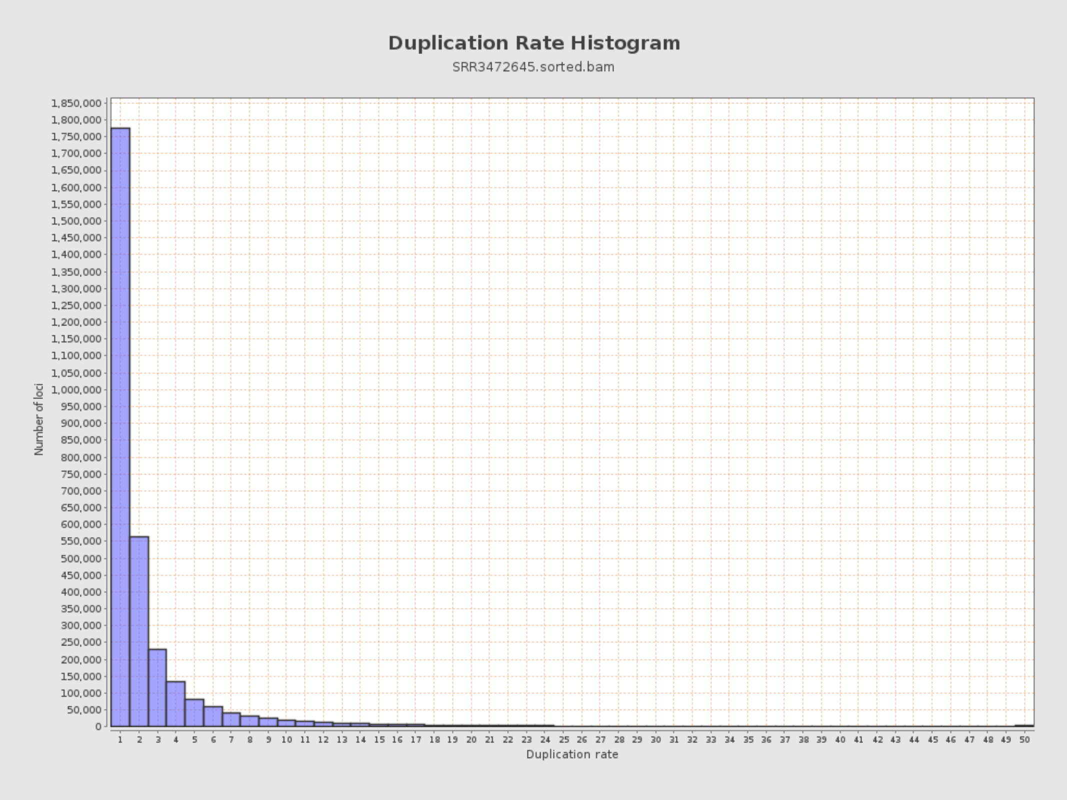
5. Results : Coverage Histogram (0-50X)



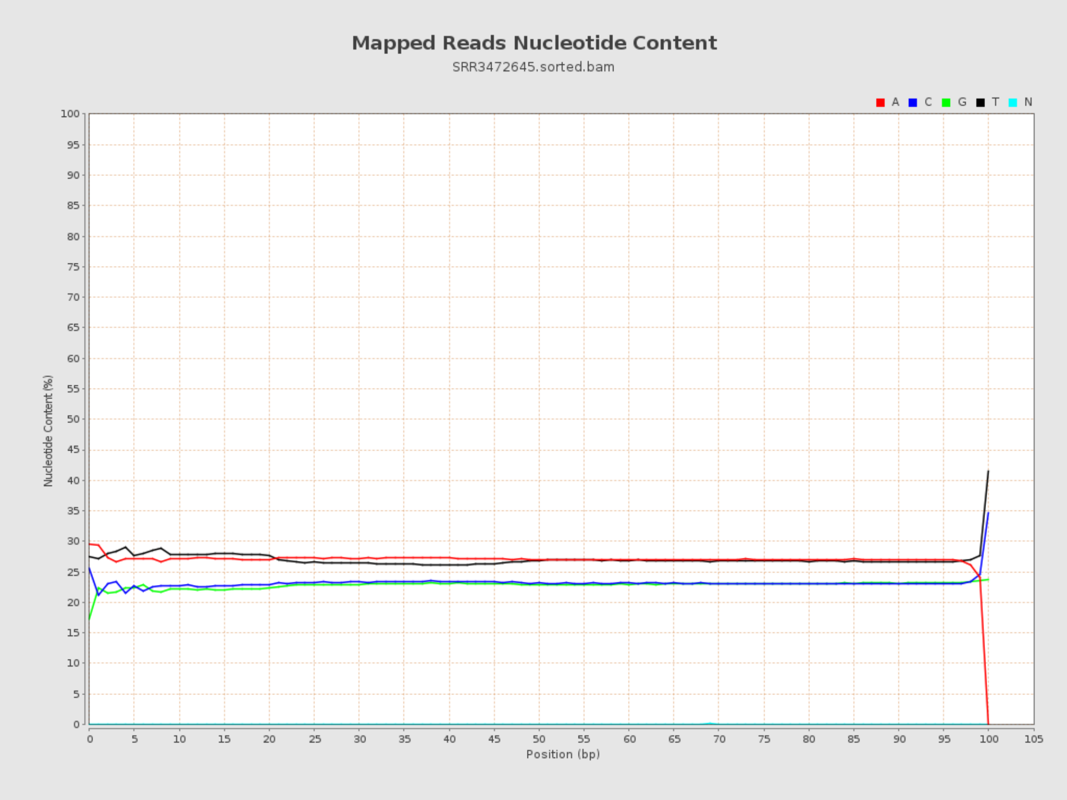
6. Results : Genome Fraction Coverage



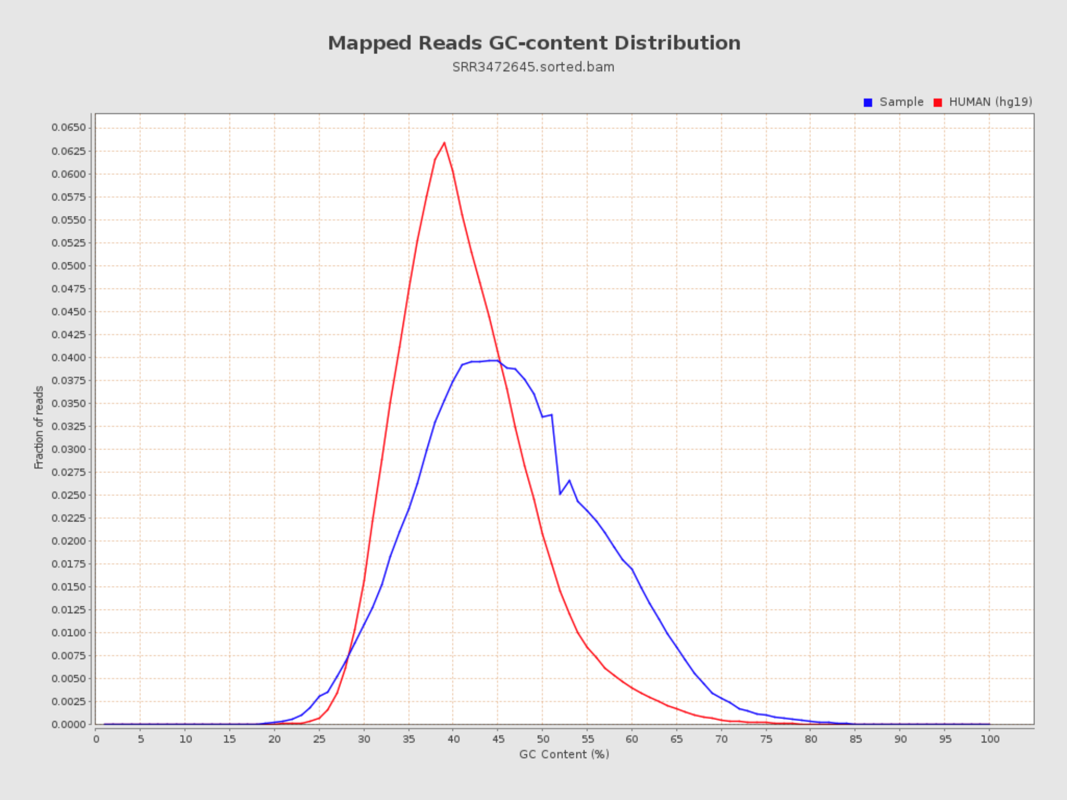
7. Results : Duplication Rate Histogram



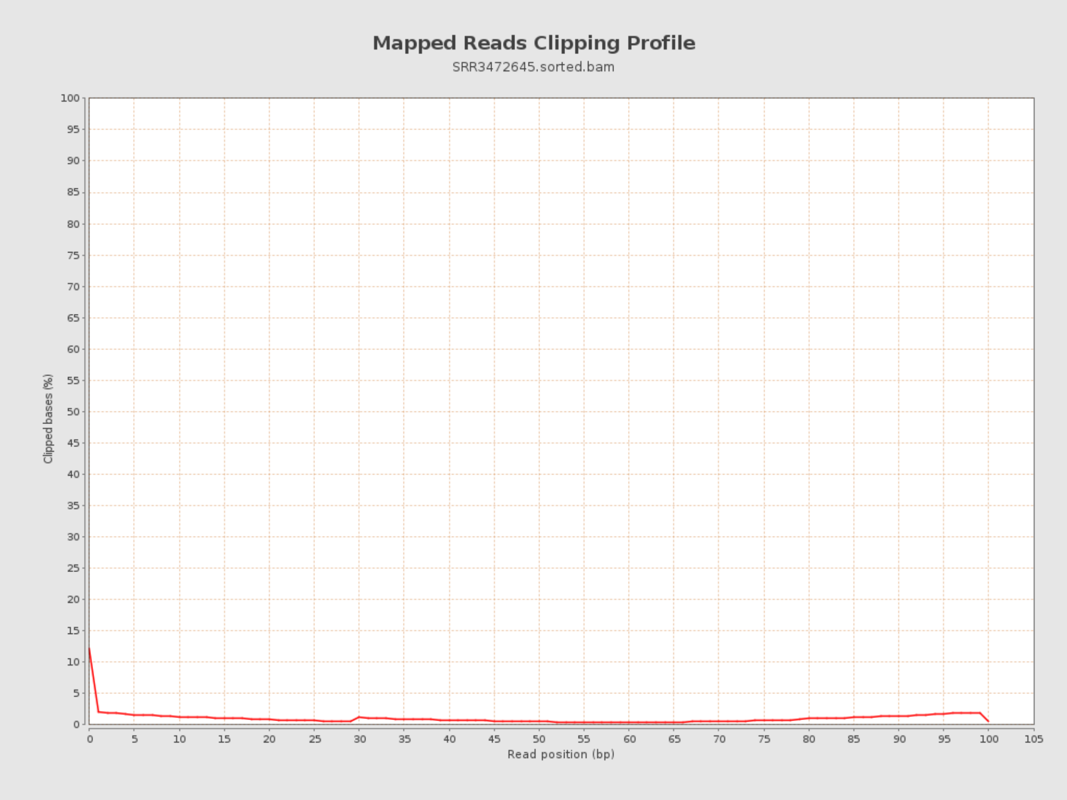
8. Results : Mapped Reads Nucleotide Content



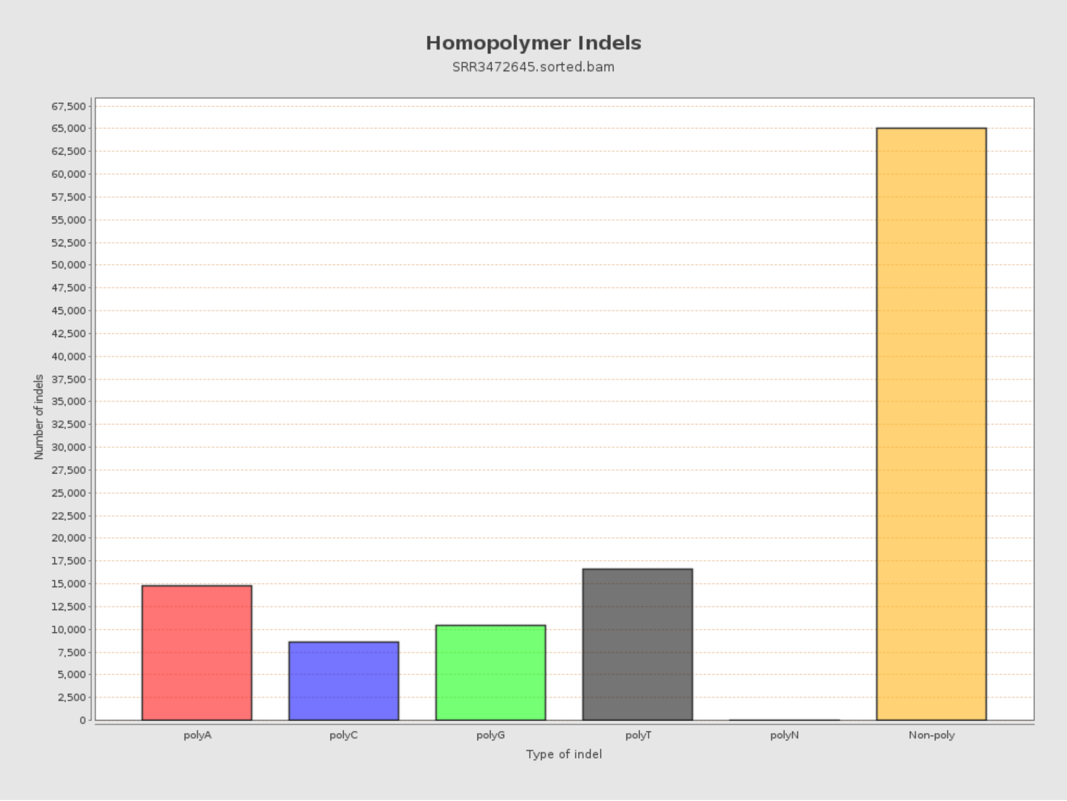
9. Results : Mapped Reads GC-content Distribution



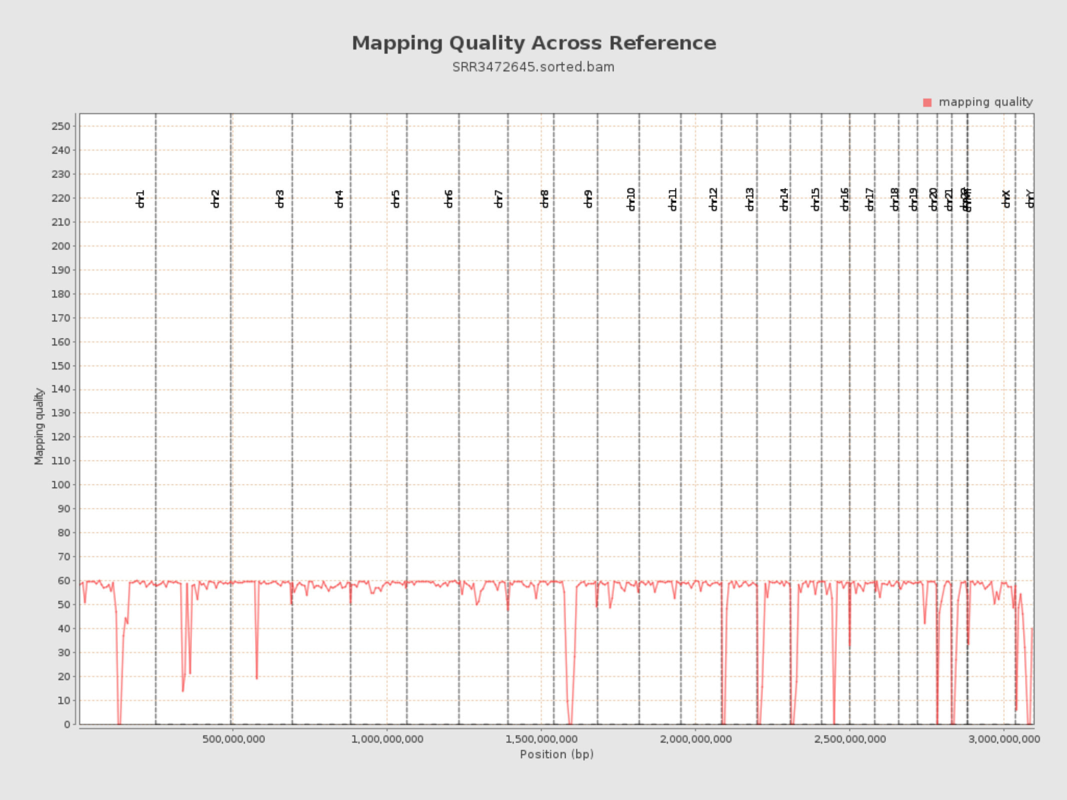
10. Results : Mapped Reads Clipping Profile



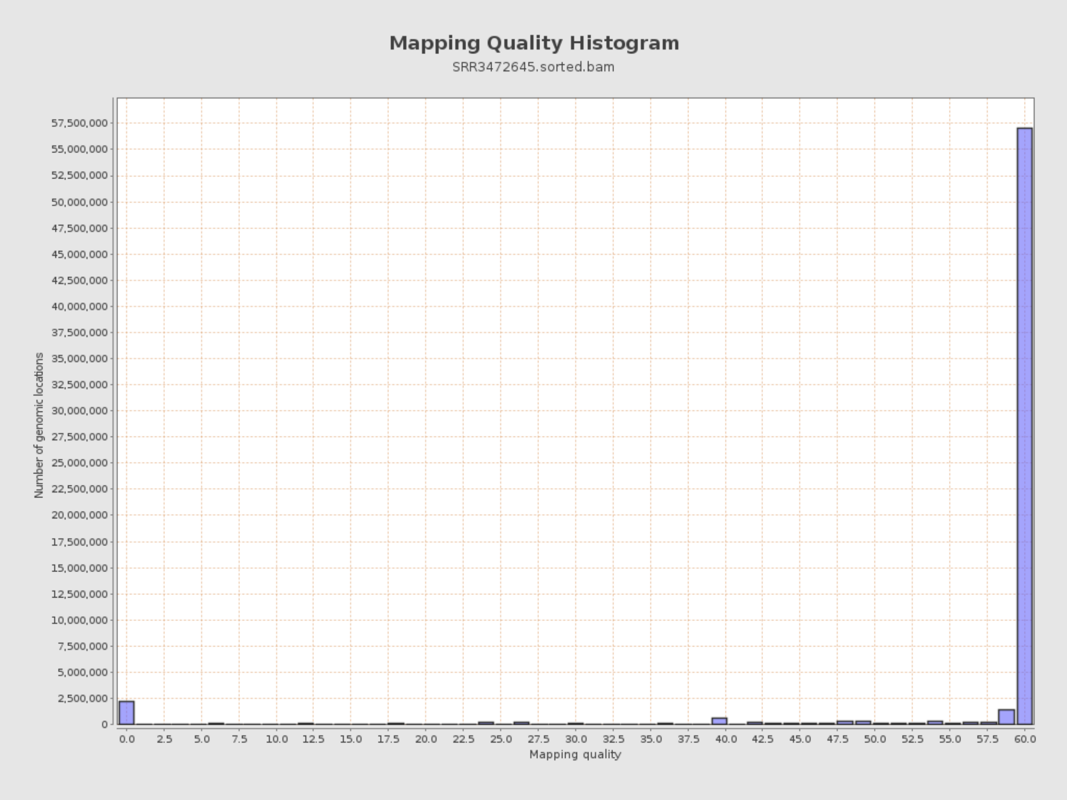
11. Results : Homopolymer Indels



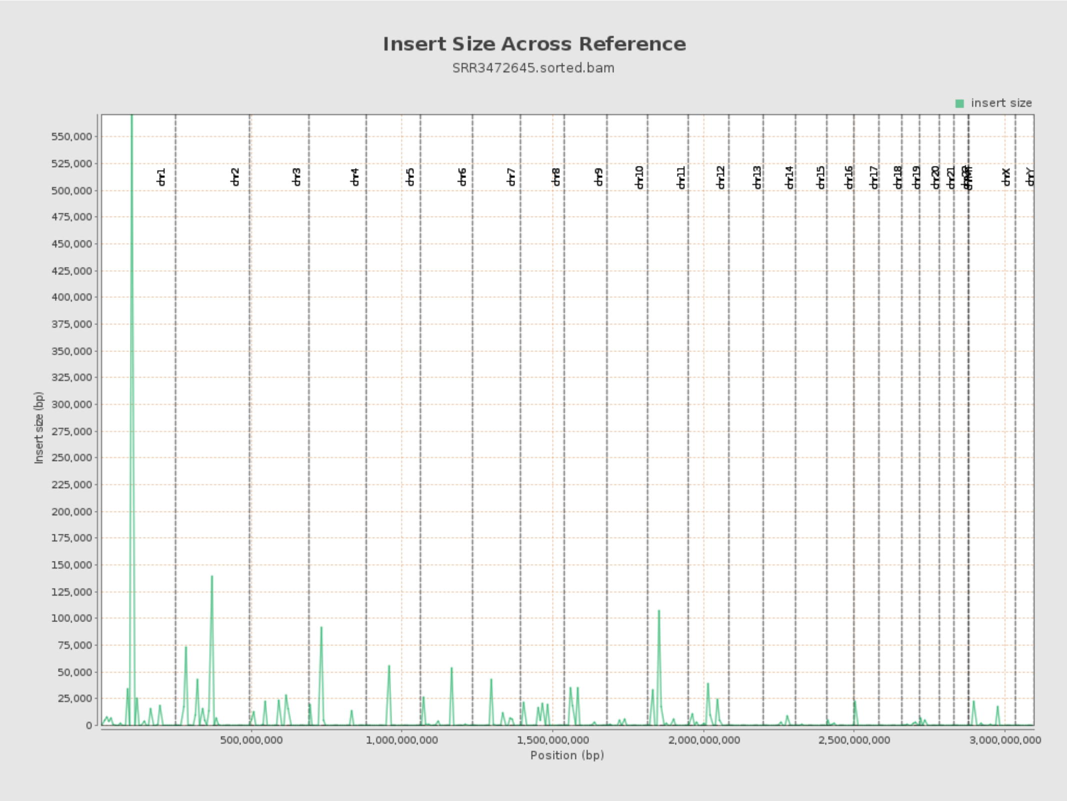
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram