Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 18:19:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472636.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_SRR3472636 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472636_1.fastq.gz SRR3472636_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 18:19:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472636.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,872,540
Mapped reads	13,765,028 / 99.23%
Unmapped reads	107,512 / 0.77%
Mapped paired reads	13,765,028 / 99.23%
Mapped reads, first in pair	6,900,344 / 49.74%
Mapped reads, second in pair	6,864,684 / 49.48%
Mapped reads, both in pair	13,692,904 / 98.71%
Mapped reads, singletons	72,124 / 0.52%
Secondary alignments	0
Supplementary alignments	67,364 / 0.49%
Read min/max/mean length	30 / 101 / 99.69
Duplicated reads (estimated)	9,094,072 / 65.55%
Duplication rate	48.16%
Clipped reads	934,611 / 6.74%

2.2. ACGT Content

Number/percentage of A's	363,493,921 / 26.84%
Number/percentage of C's	315,228,206 / 23.28%
Number/percentage of T's	364,543,743 / 26.92%
Number/percentage of G's	310,731,528 / 22.95%
Number/percentage of N's	247,109 / 0.02%

GC Percentage	46.22%

2.3. Coverage

Mean	0.4375
Standard Deviation	19.1518

2.4. Mapping Quality

Mean Mapping Quality	54.8

2.5. Insert size

Mean	21,576.05
Standard Deviation	1,445,607.34
P25/Median/P75	158 / 217 / 288

2.6. Mismatches and indels

General error rate	0.62%
Mismatches	8,261,380
Insertions	77,312
Mapped reads with at least one insertion	0.56%
Deletions	67,917
Mapped reads with at least one deletion	0.48%
Homopolymer indels	44.88%

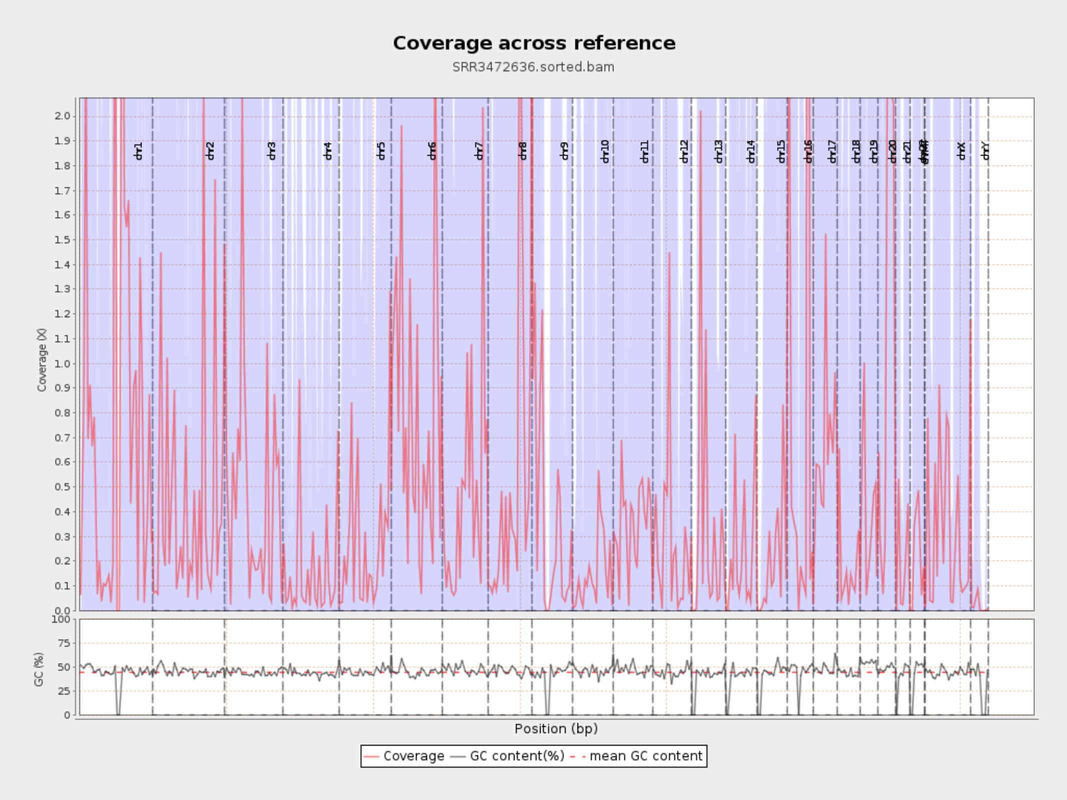
2.7. Chromosome stats

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

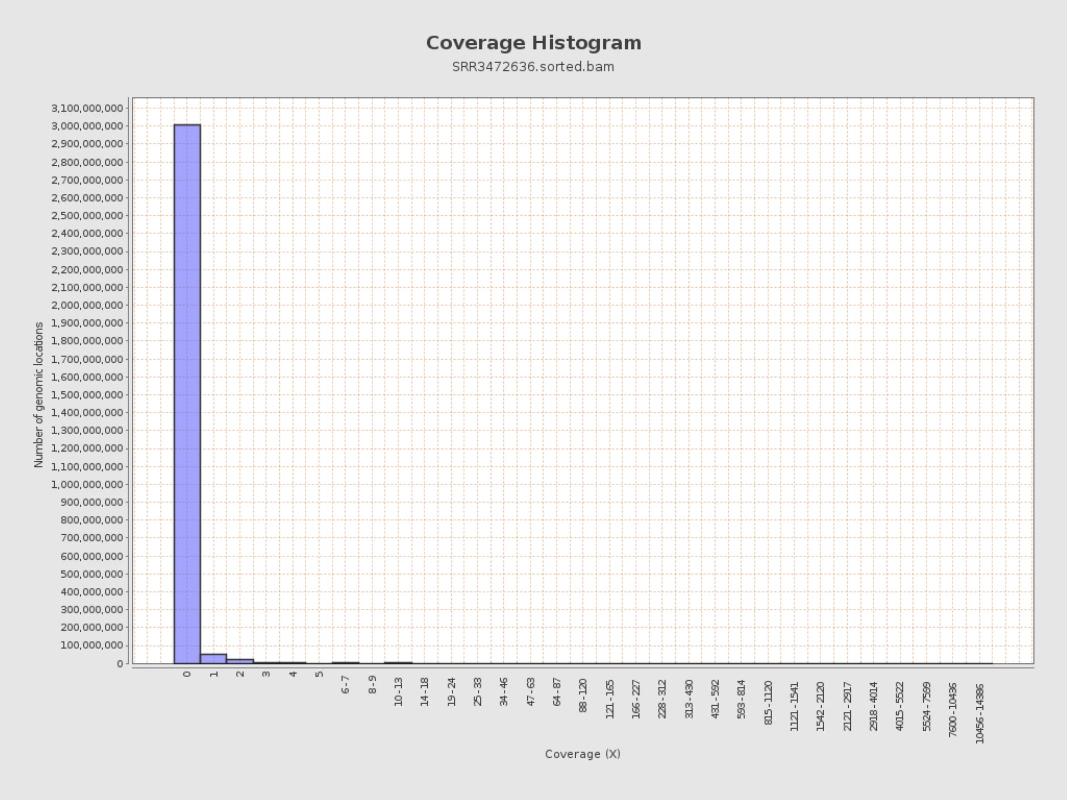
		bases	coverage	deviation
chr1	249250621	194448866	0.7801	32.6225
chr2	243199373	106509242	0.438	16.5577
chr3	198022430	96385380	0.4867	14.8442
chr4	191154276	29473930	0.1542	9.0135
chr5	180915260	51529589	0.2848	16.3371
chr6	171115067	135244722	0.7904	24.3494
chr7	159138663	76851967	0.4829	24.0807
chr8	146364022	81628597	0.5577	20.1793
chr9	141213431	54816305	0.3882	10.7936
chr10	135534747	20515549	0.1514	11.4626
chr11	135006516	48049486	0.3559	15.5693
chr12	133851895	37428741	0.2796	10.985
chr13	115169878	40066267	0.3479	12.8295
chr14	107349540	25048966	0.2333	13.3907
chr15	102531392	21320497	0.2079	8.8582
chr16	90354753	84960000	0.9403	40.0427
chr17	81195210	54833515	0.6753	22.2796
chr18	78077248	14206847	0.182	7.2557
chr19	59128983	25481193	0.4309	12.2864
chr20	63025520	82879148	1.315	35.2256
chr21	48129895	9730013	0.2022	10.687
chr22	51304566	11561881	0.2254	10.377
chrMT	16571	2996	0.1808	0.5422
chrX	155270560	50111462	0.3227	12.83

chrY	59373566	1323023	0.0223	1.6462

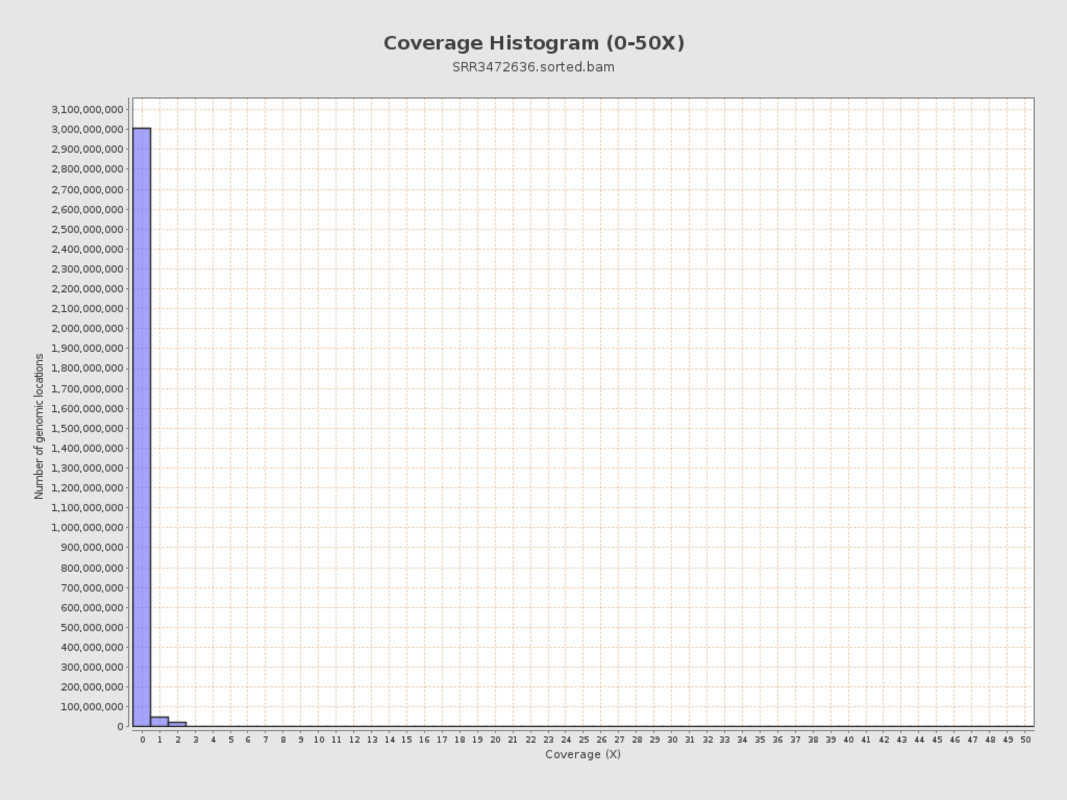
3. Results : Coverage across reference



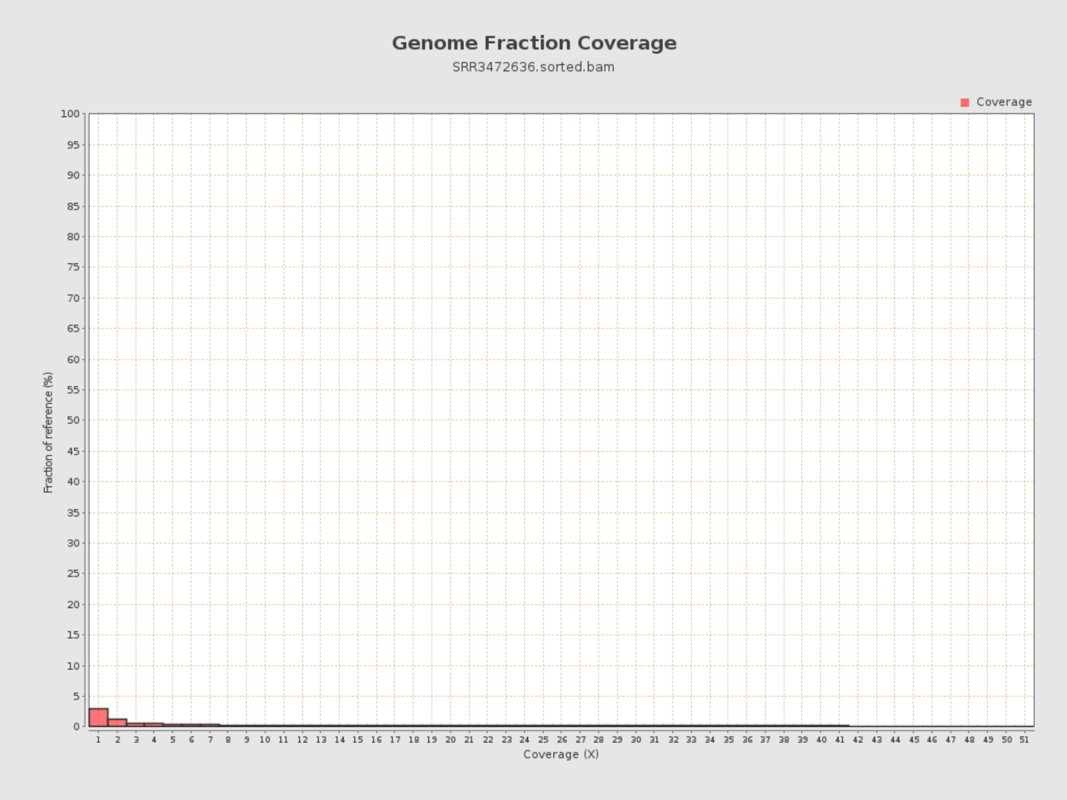
4. Results : Coverage Histogram



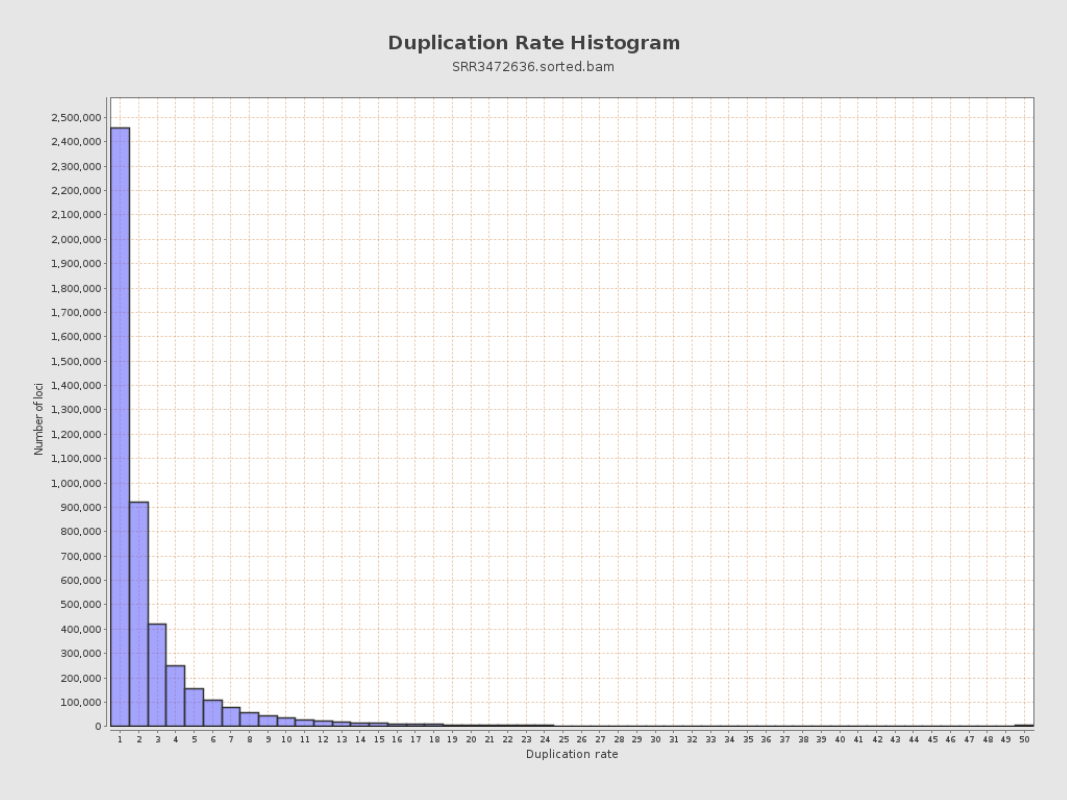
5. Results : Coverage Histogram (0-50X)



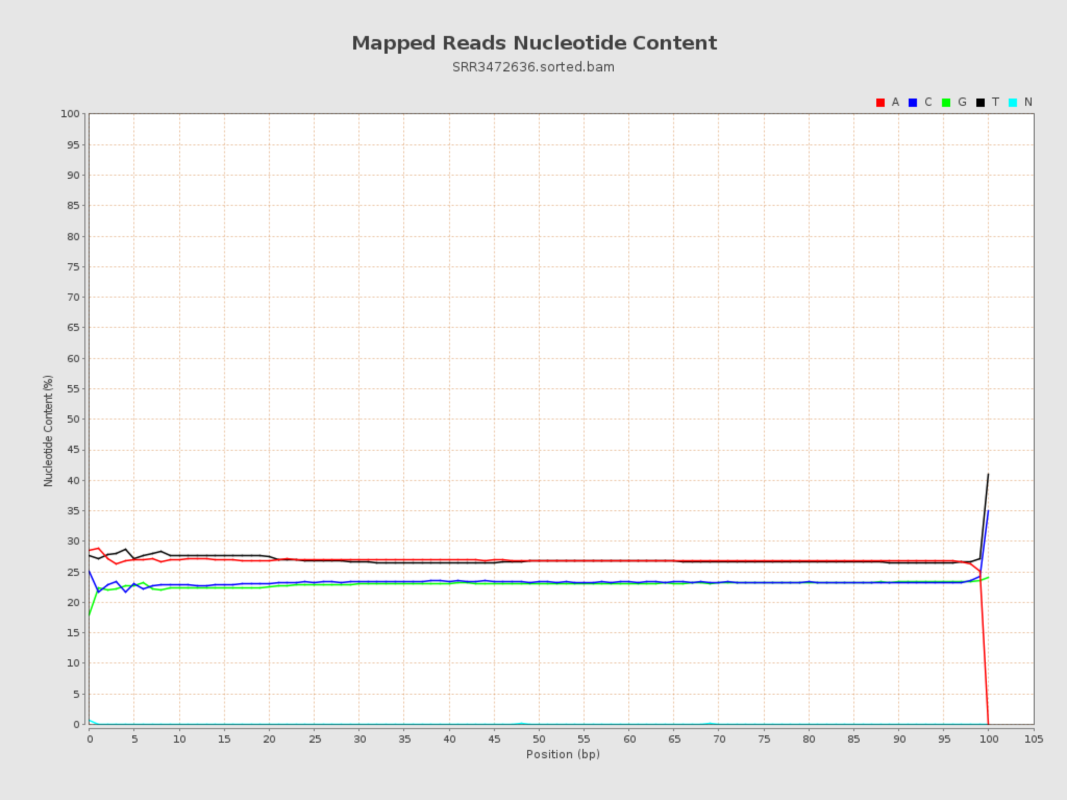
6. Results : Genome Fraction Coverage



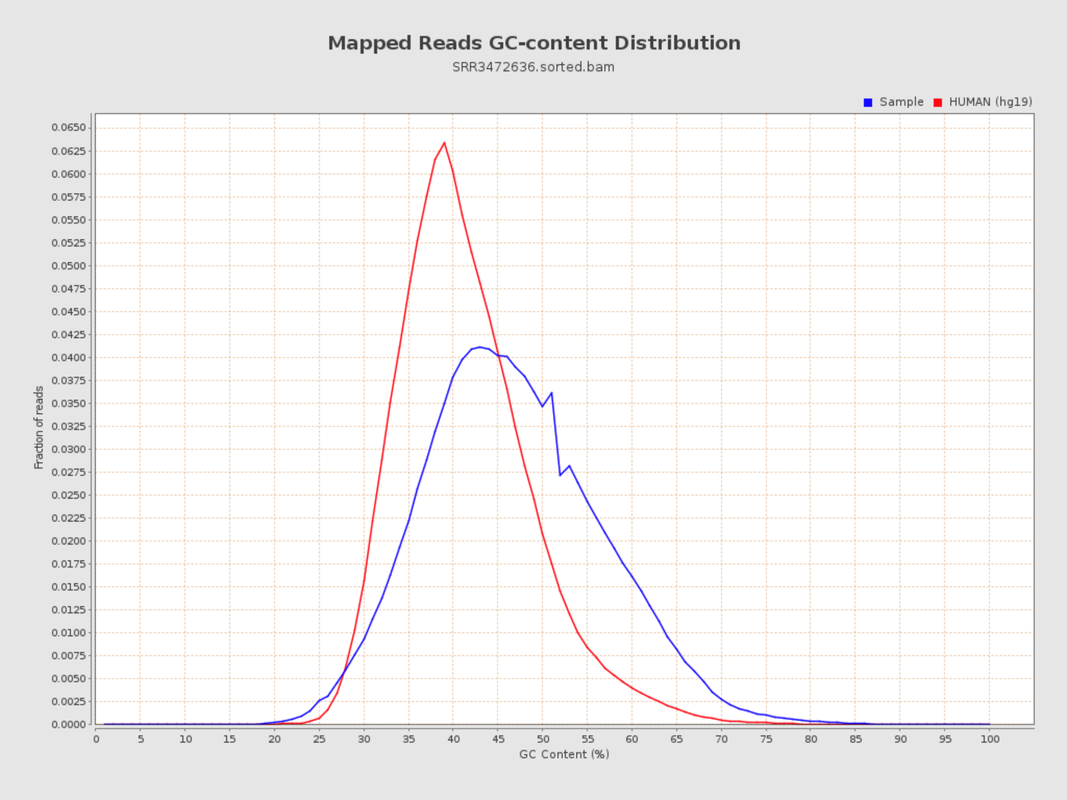
7. Results : Duplication Rate Histogram



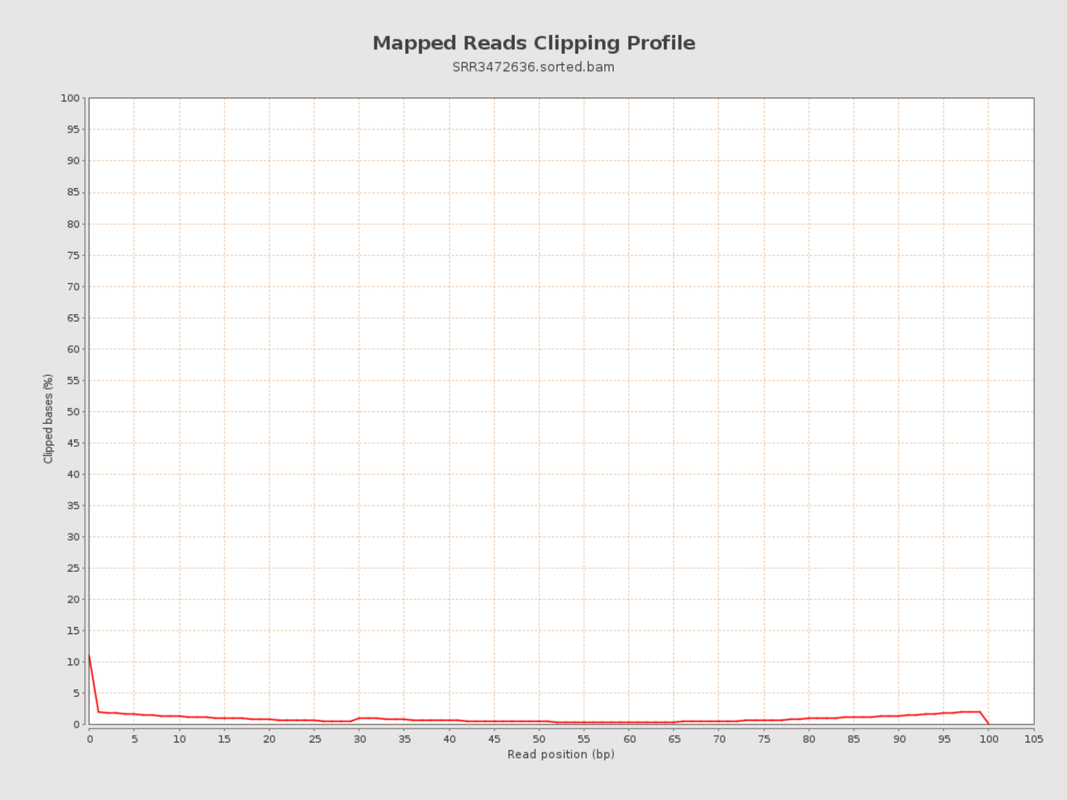
8. Results : Mapped Reads Nucleotide Content



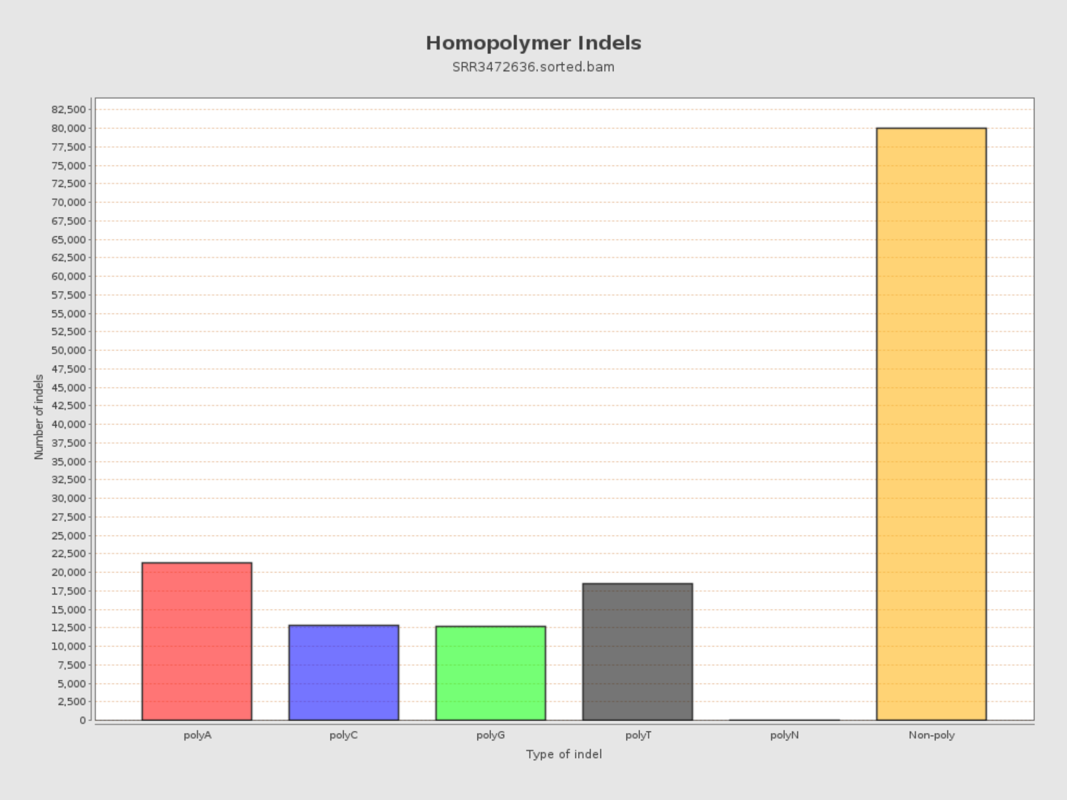
9. Results : Mapped Reads GC-content Distribution



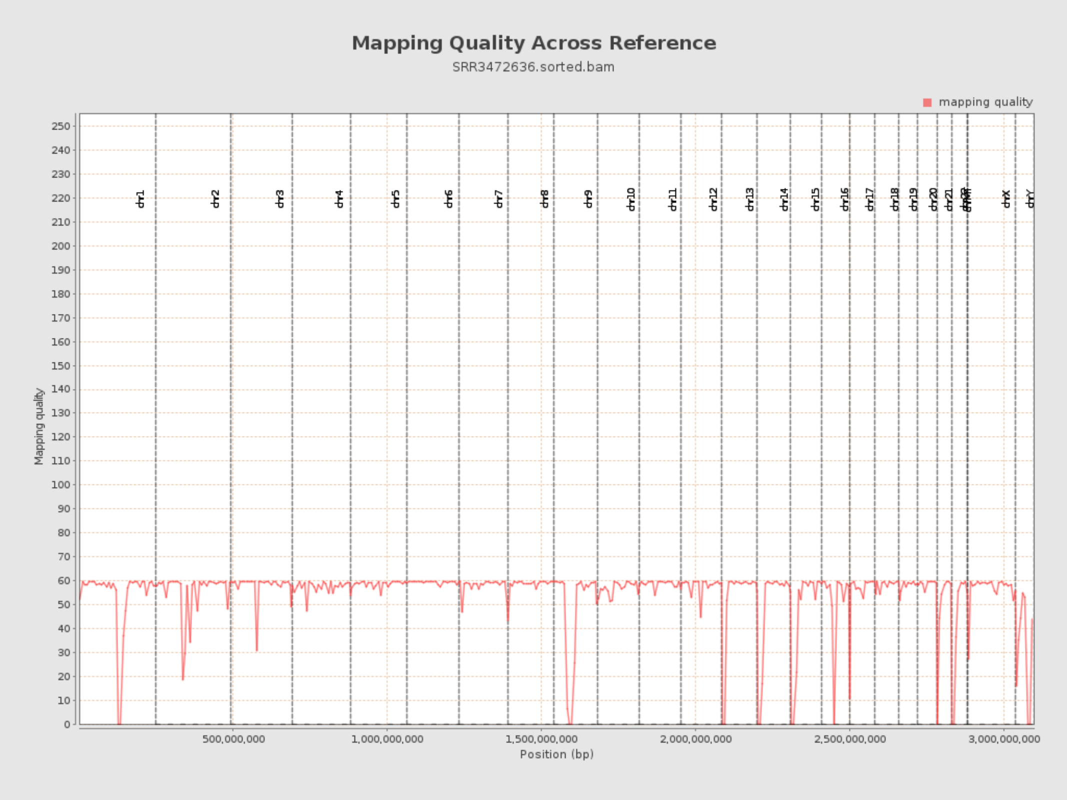
10. Results : Mapped Reads Clipping Profile



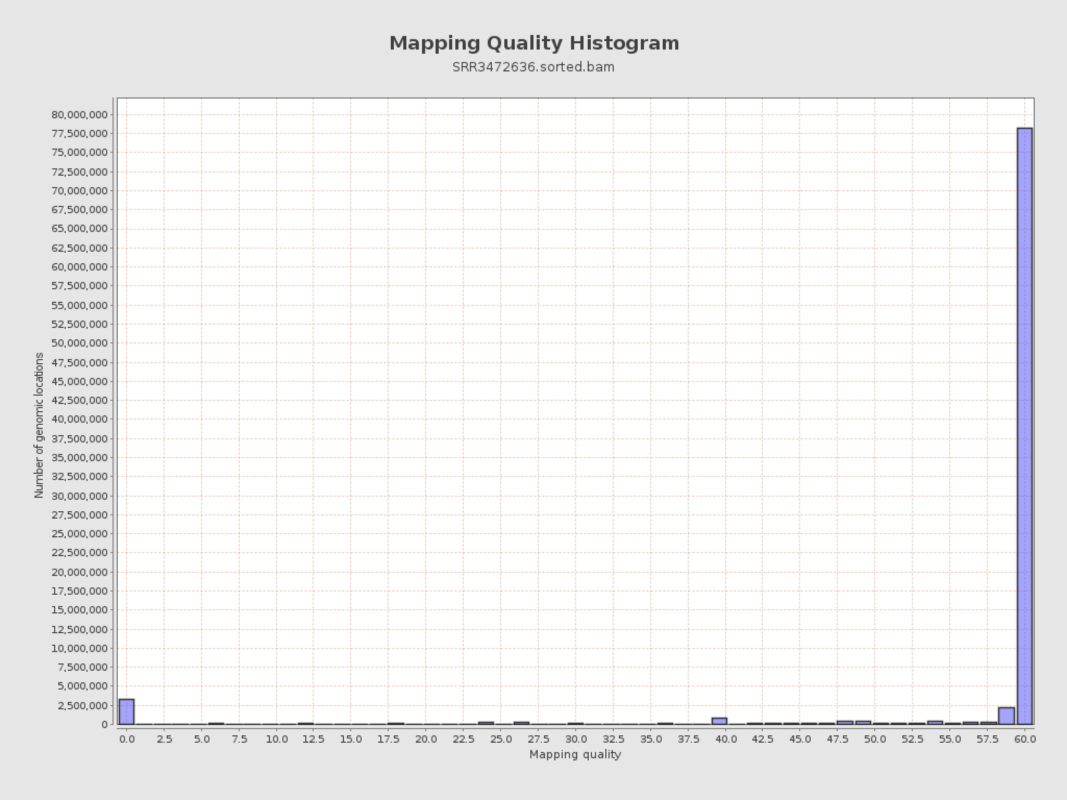
11. Results : Homopolymer Indels



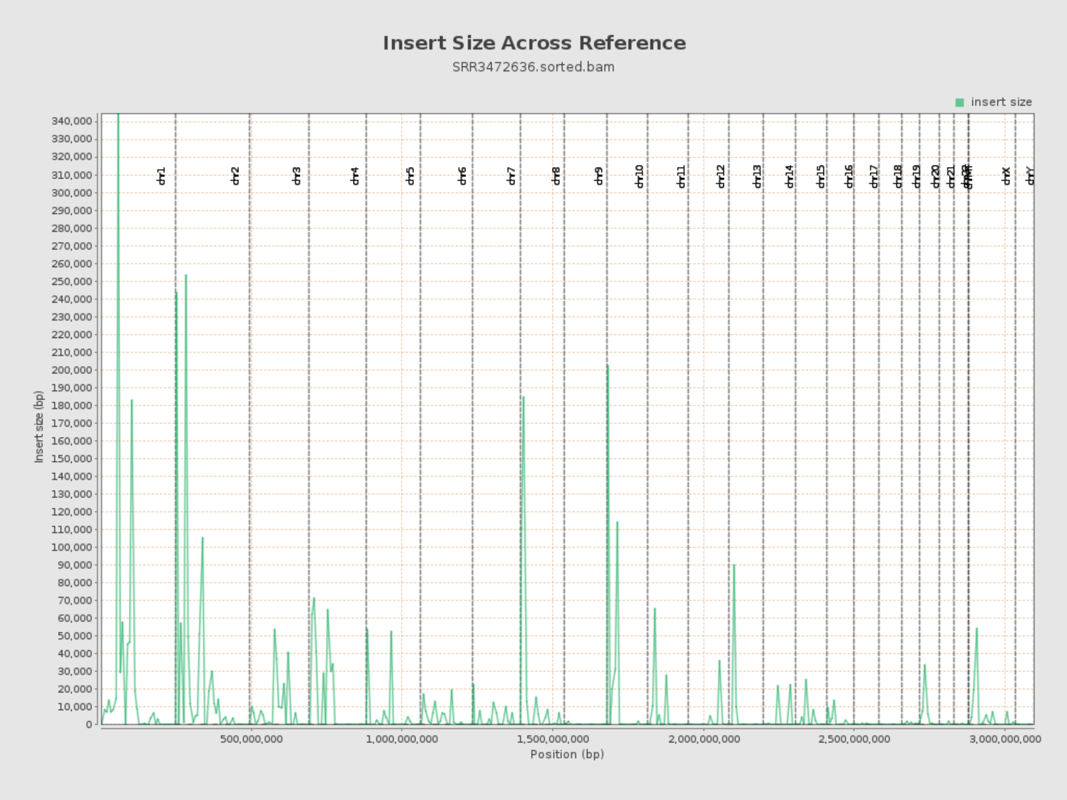
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram