Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 18:06:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472635.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_SRR3472635 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472635_1.fastq.gz SRR3472635_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 18:06:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472635.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,731,340
Mapped reads	15,608,224 / 99.22%
Unmapped reads	123,116 / 0.78%
Mapped paired reads	15,608,224 / 99.22%
Mapped reads, first in pair	7,825,702 / 49.75%
Mapped reads, second in pair	7,782,522 / 49.47%
Mapped reads, both in pair	15,524,904 / 98.69%
Mapped reads, singletons	83,320 / 0.53%
Secondary alignments	0
Supplementary alignments	76,582 / 0.49%
Read min/max/mean length	30 / 101 / 99.69
Duplicated reads (estimated)	10,660,943 / 67.77%
Duplication rate	49.78%
Clipped reads	1,045,580 / 6.65%

2.2. ACGT Content

Number/percentage of A's	417,573,383 / 27.19%
Number/percentage of C's	351,290,138 / 22.88%
Number/percentage of T's	419,202,033 / 27.3%
Number/percentage of G's	347,280,439 / 22.61%
Number/percentage of N's	280,040 / 0.02%

GC Percentage	45.49%

2.3. Coverage

Mean	0.4961
Standard Deviation	22.1627

2.4. Mapping Quality

Mean Mapping Quality	54.71

2.5. Insert size

Mean	24,424.75
Standard Deviation	1,468,756.18
P25/Median/P75	156 / 213 / 284

2.6. Mismatches and indels

General error rate	0.62%
Mismatches	9,360,862
Insertions	94,325
Mapped reads with at least one insertion	0.6%
Deletions	83,224
Mapped reads with at least one deletion	0.52%
Homopolymer indels	46.08%

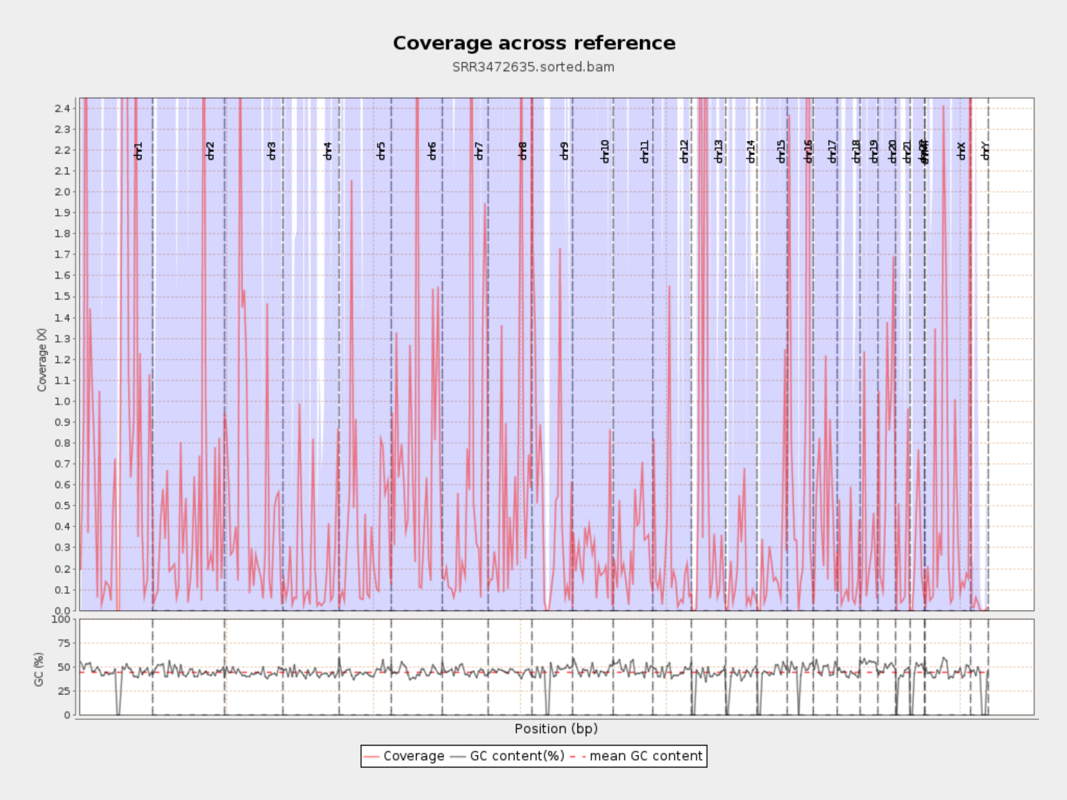
2.7. Chromosome stats

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

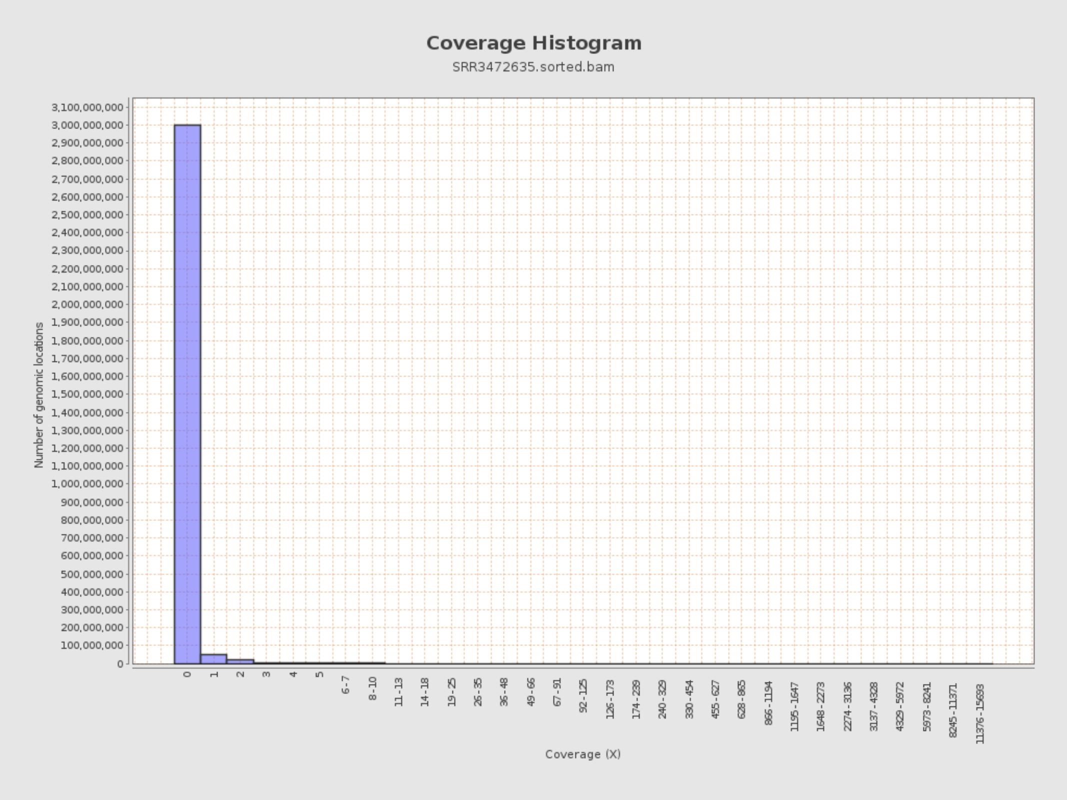
		bases	coverage	deviation
chr1	249250621	243139419	0.9755	33.4838
chr2	243199373	108558557	0.4464	19.556
chr3	198022430	115242184	0.582	17.1397
chr4	191154276	41116425	0.2151	11.6401
chr5	180915260	72344952	0.3999	16.5802
chr6	171115067	134332674	0.785	27.7016
chr7	159138663	98949042	0.6218	27.1648
chr8	146364022	86857746	0.5934	20.1374
chr9	141213431	76893669	0.5445	15.8475
chr10	135534747	36317826	0.268	14.639
chr11	135006516	40214865	0.2979	12.6467
chr12	133851895	34281344	0.2561	12.8215
chr13	115169878	85674858	0.7439	41.9675
chr14	107349540	18481631	0.1722	7.3482
chr15	102531392	26678737	0.2602	13.7386
chr16	90354753	87606705	0.9696	39.3315
chr17	81195210	39136291	0.482	14.319
chr18	78077248	14731985	0.1887	8.8724
chr19	59128983	20339390	0.344	11.1702
chr20	63025520	50908564	0.8077	20.8928
chr21	48129895	13043009	0.271	13.1381
chr22	51304566	13036104	0.2541	8.8284
chrMT	16571	3262	0.1968	0.4919
chrX	155270560	76855458	0.495	32.1077

chrY	59373566	1080761	0.0182	1.0164

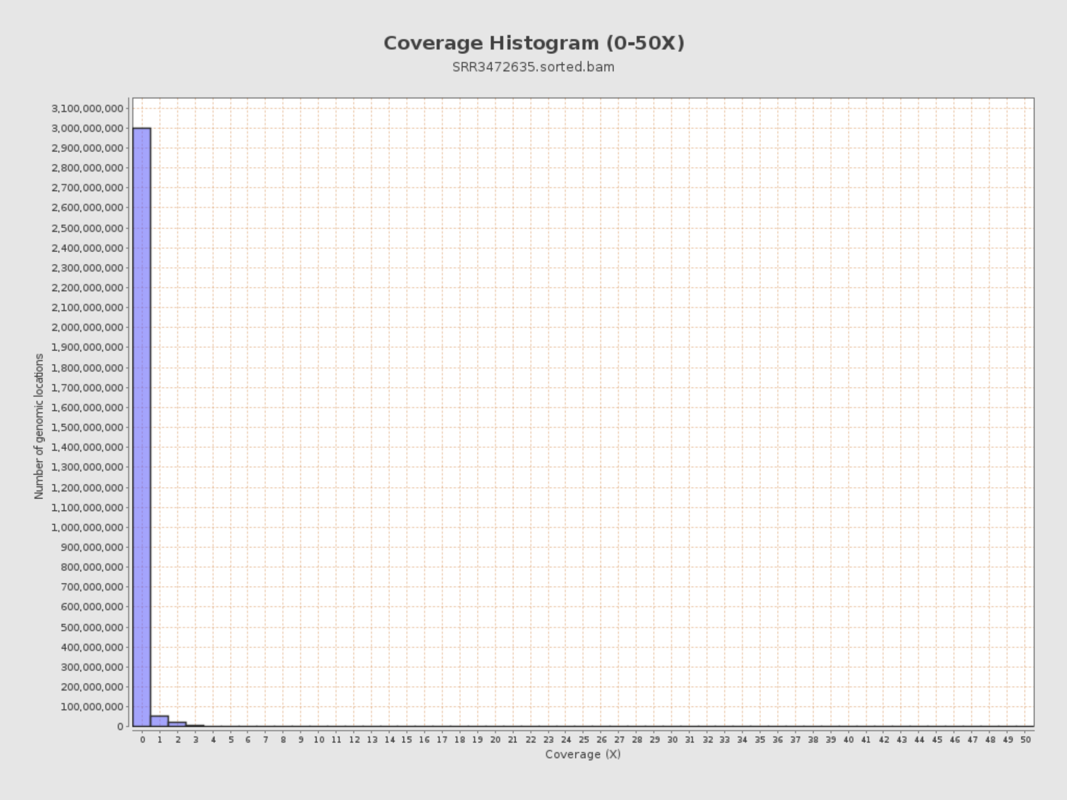
3. Results : Coverage across reference



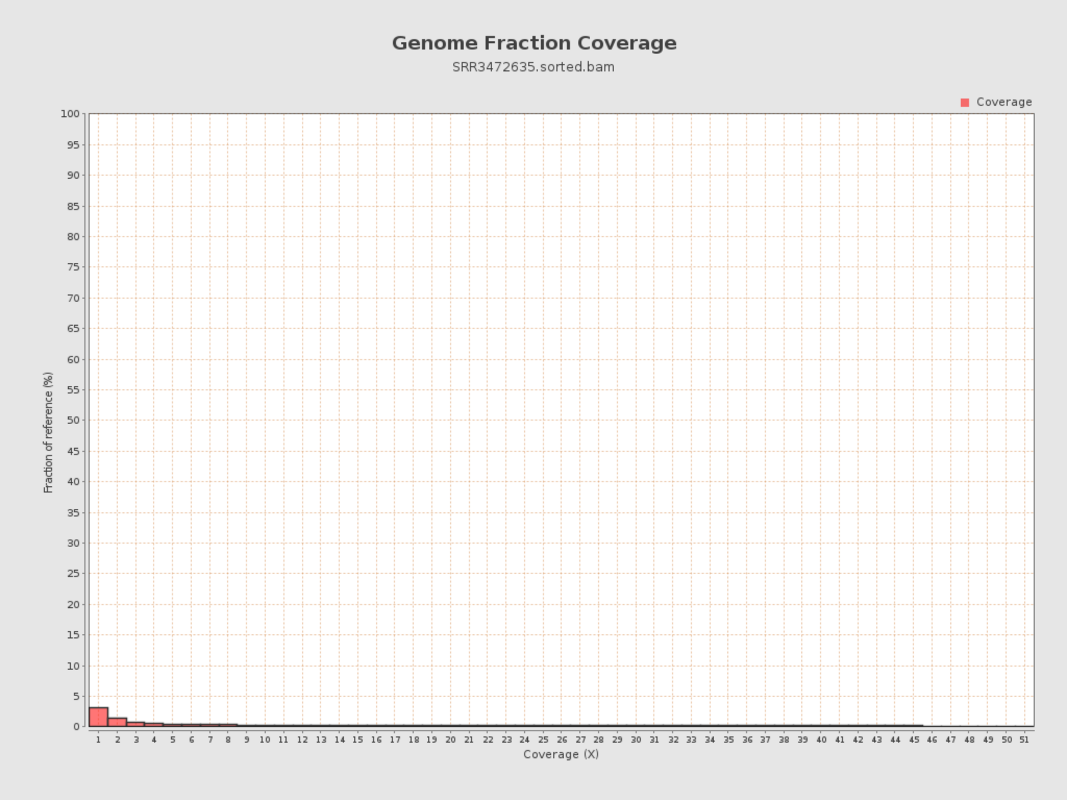
4. Results : Coverage Histogram



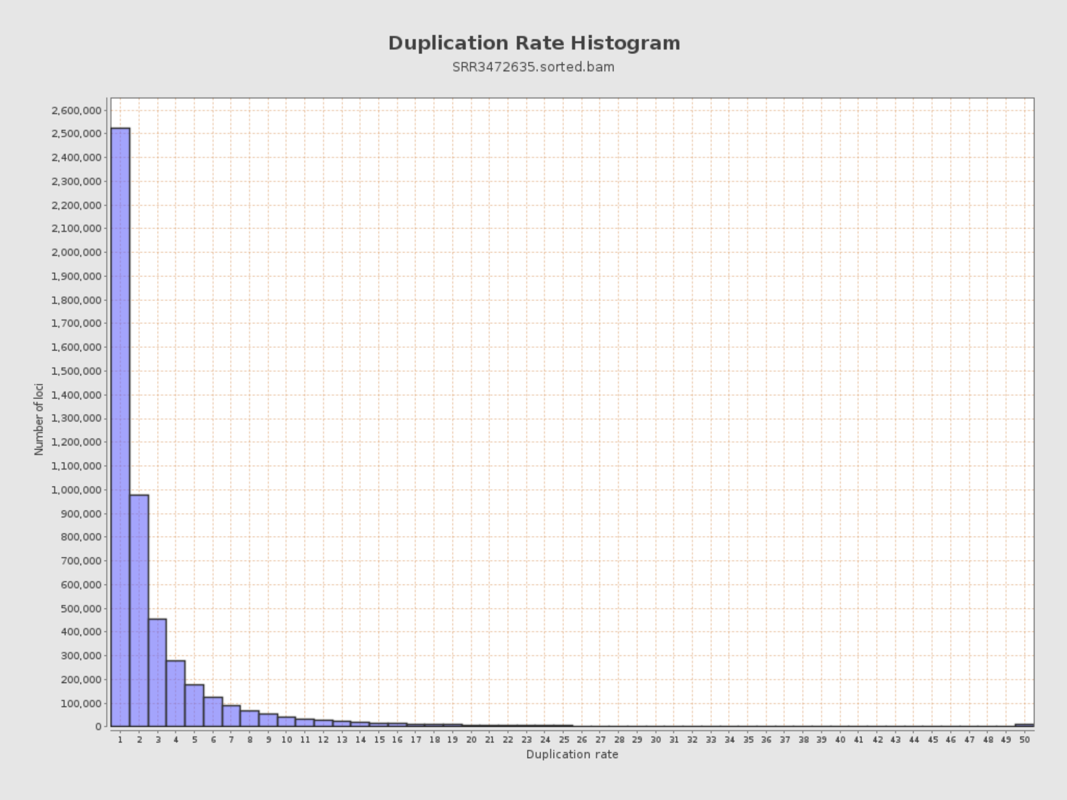
5. Results : Coverage Histogram (0-50X)



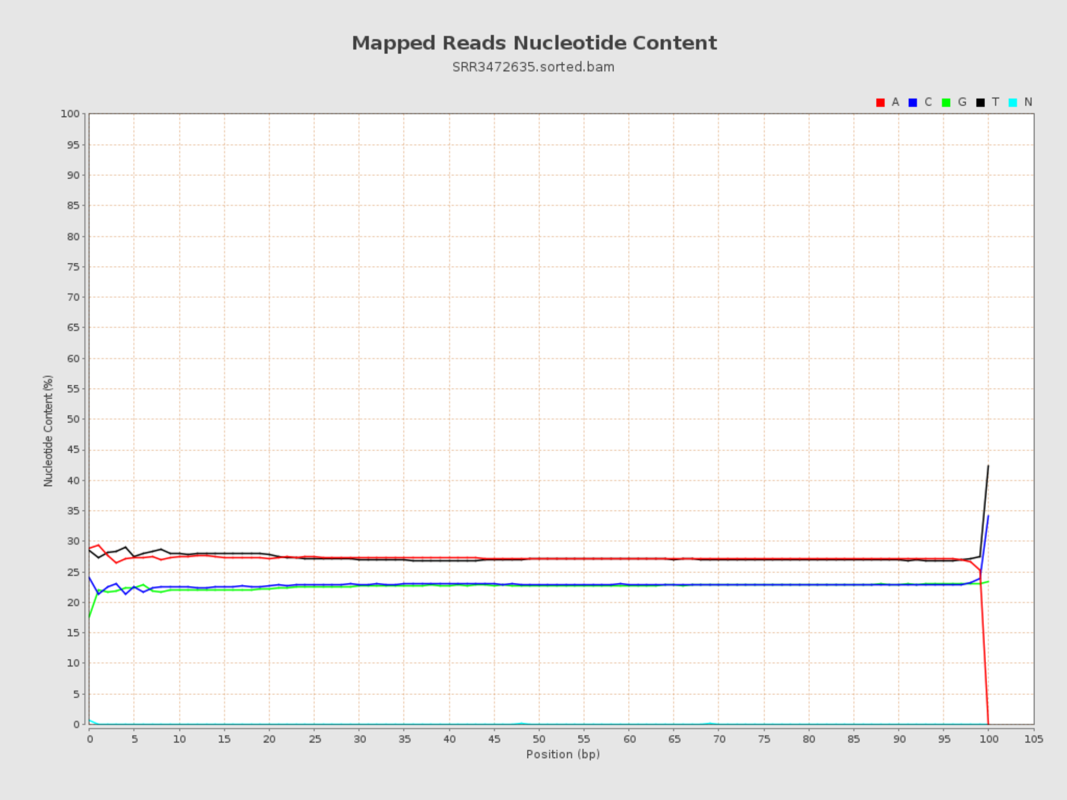
6. Results : Genome Fraction Coverage



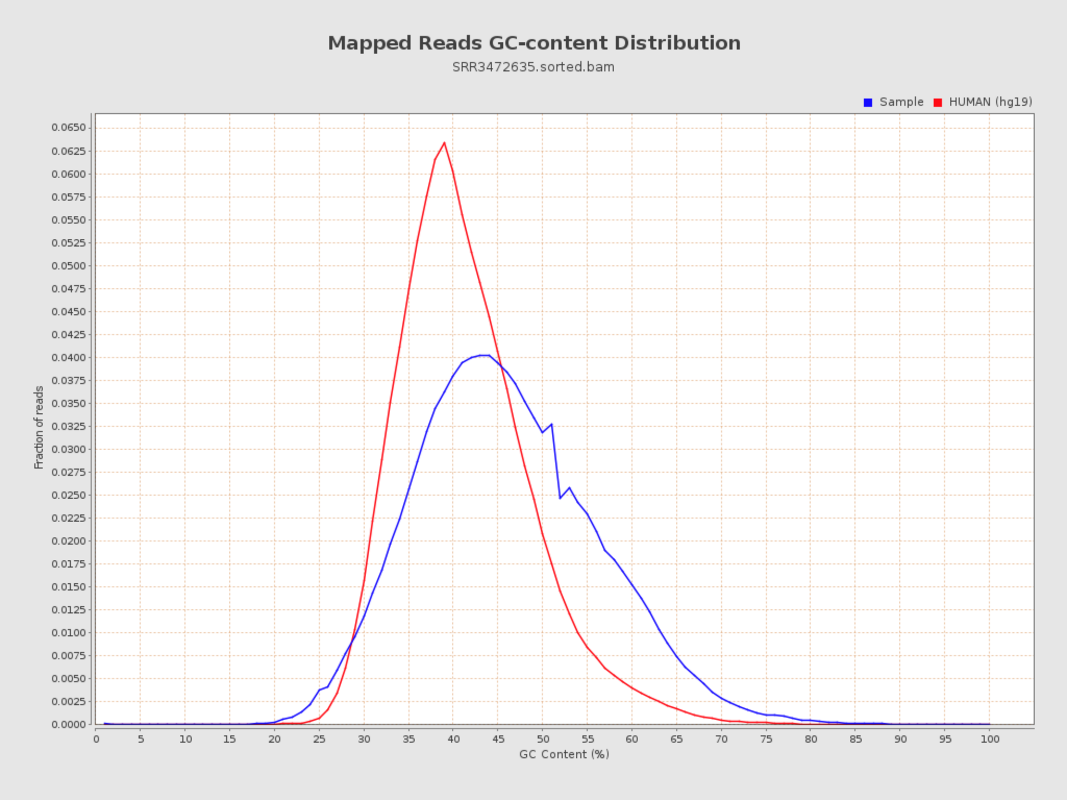
7. Results : Duplication Rate Histogram



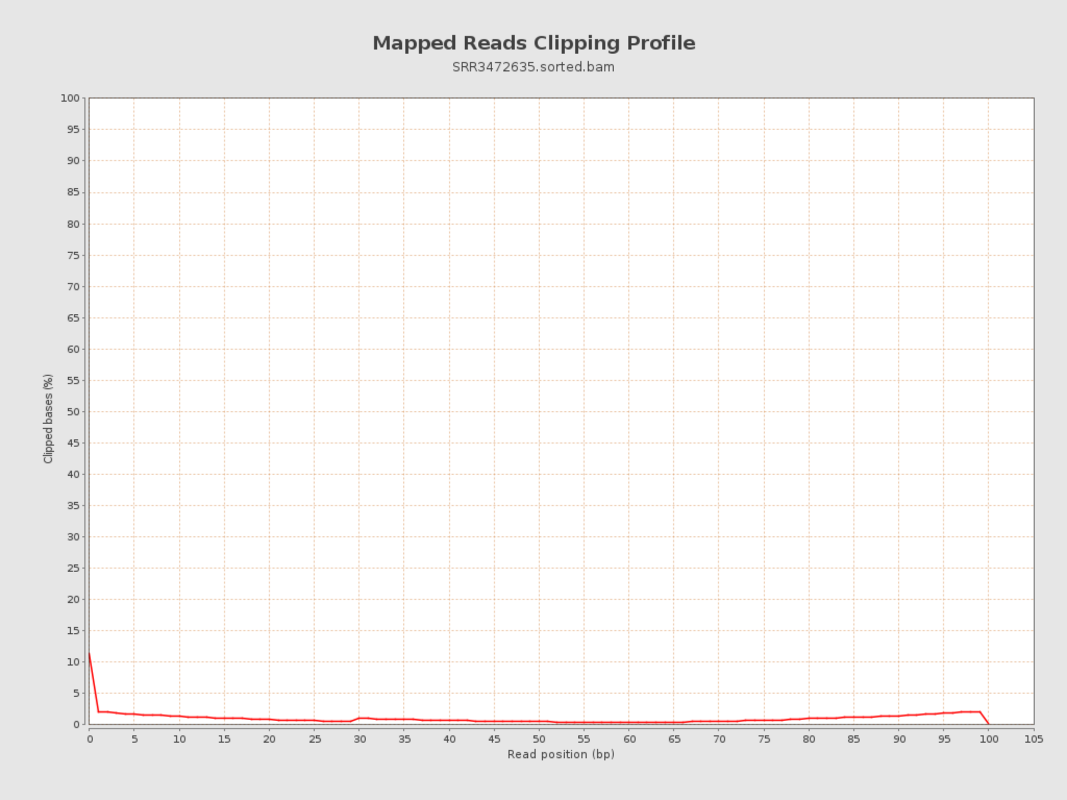
8. Results : Mapped Reads Nucleotide Content



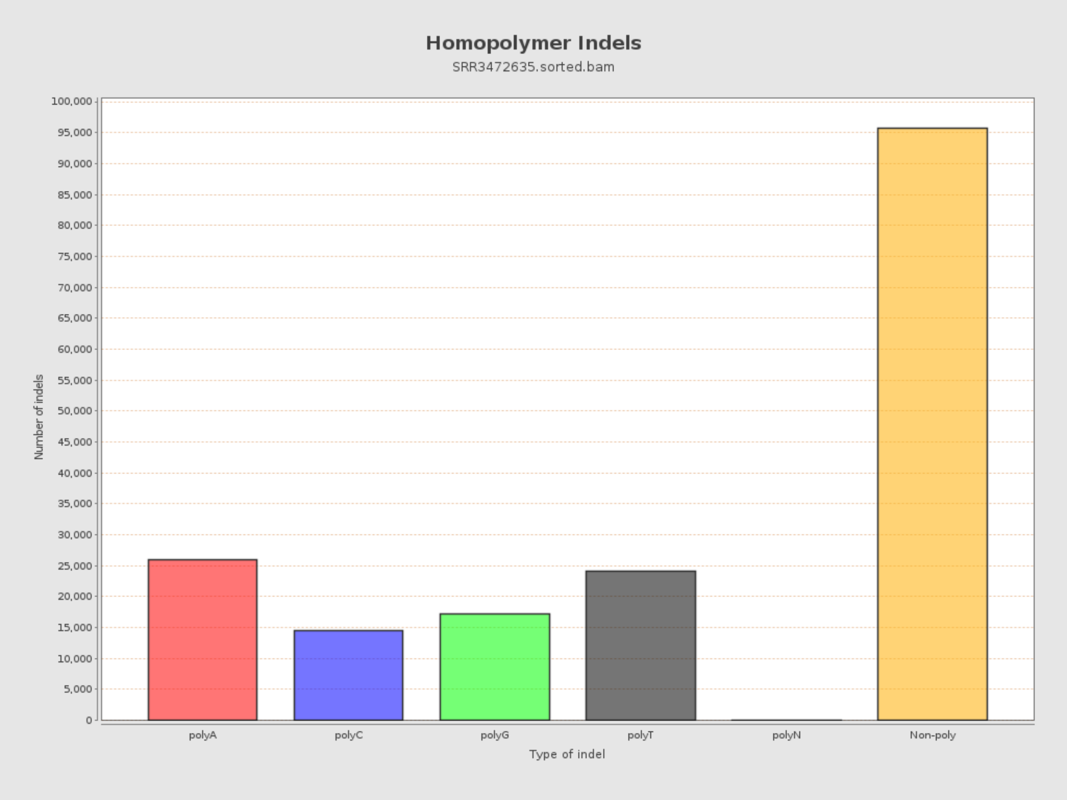
9. Results : Mapped Reads GC-content Distribution



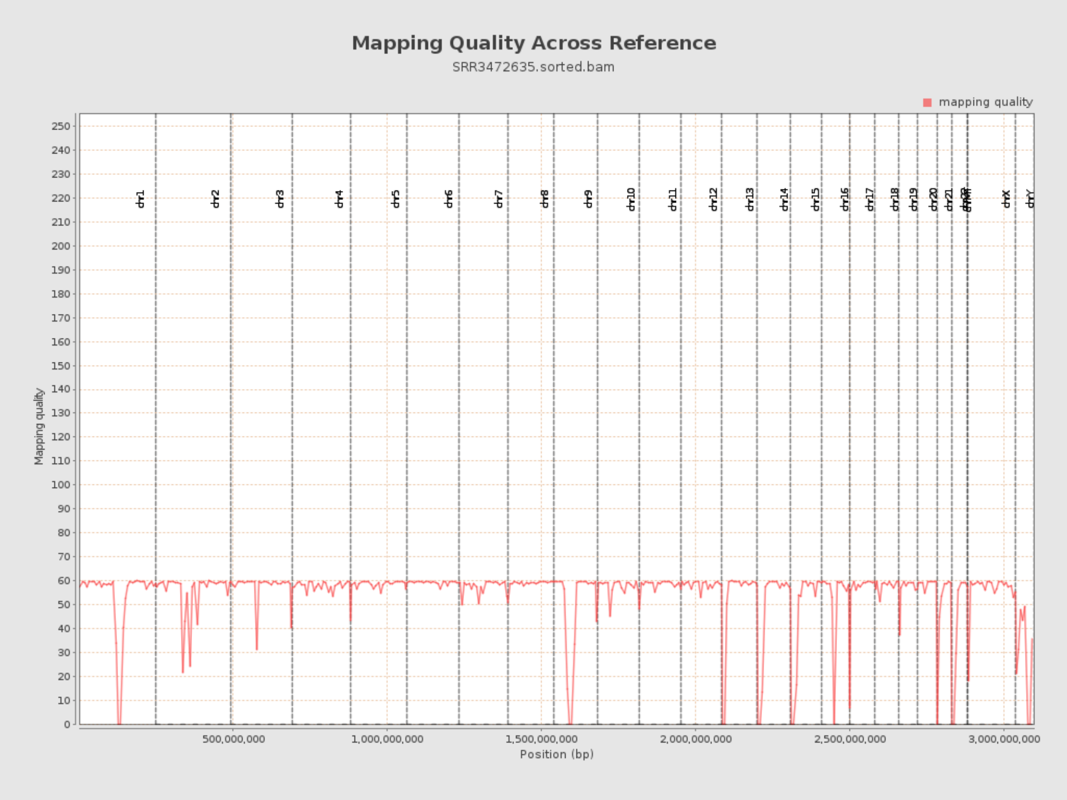
10. Results : Mapped Reads Clipping Profile



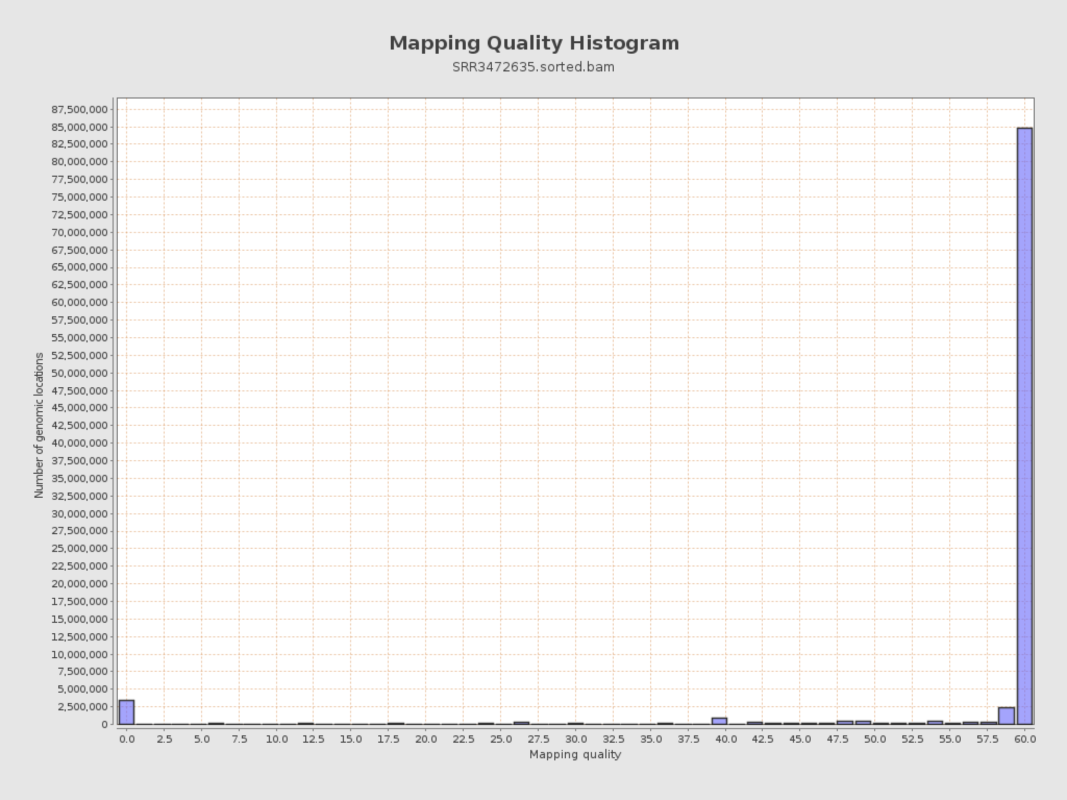
11. Results : Homopolymer Indels



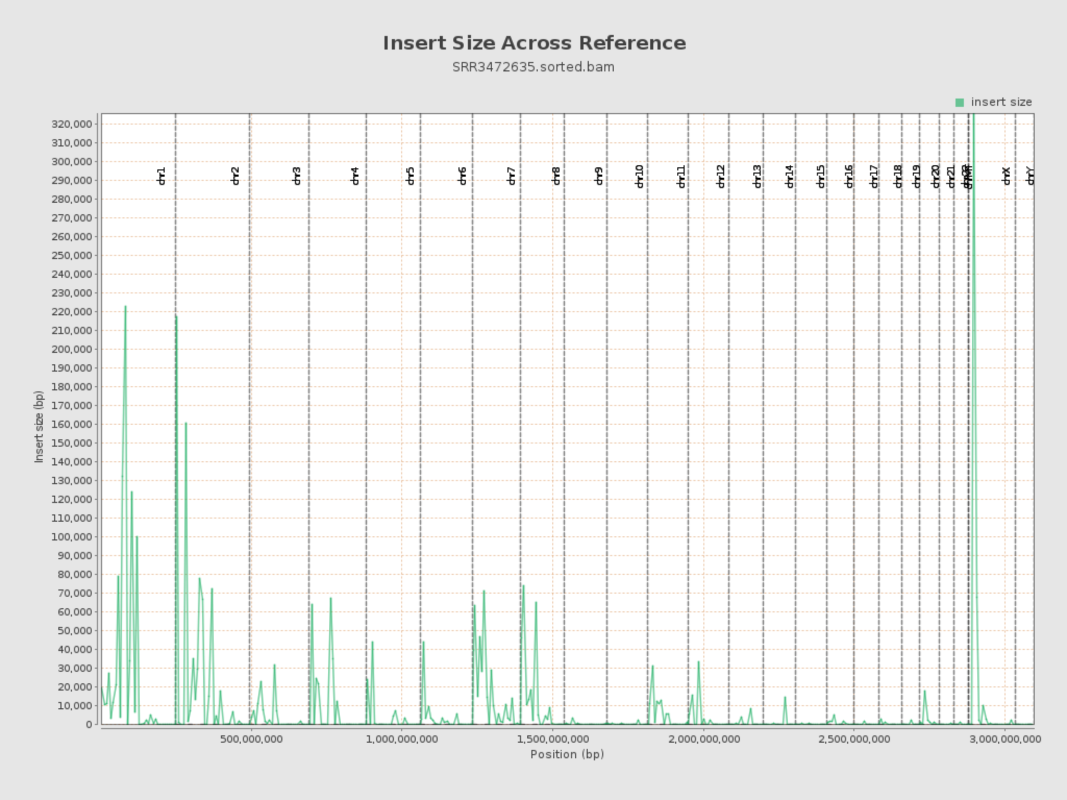
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram