Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 15:04:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472435.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_SRR3472435 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472435_1.fastq.gz SRR3472435_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 15:04:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472435.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,539,316
Mapped reads	15,373,067 / 98.93%
Unmapped reads	166,249 / 1.07%
Mapped paired reads	15,373,067 / 98.93%
Mapped reads, first in pair	7,714,040 / 49.64%
Mapped reads, second in pair	7,659,027 / 49.29%
Mapped reads, both in pair	15,282,146 / 98.35%
Mapped reads, singletons	90,921 / 0.59%
Secondary alignments	0
Supplementary alignments	60,525 / 0.39%
Read min/max/mean length	30 / 100 / 99.3
Duplicated reads (estimated)	9,400,973 / 60.5%
Duplication rate	46.5%
Clipped reads	1,079,873 / 6.95%

2.2. ACGT Content

Number/percentage of A's	414,595,773 / 27.53%
Number/percentage of C's	339,473,521 / 22.54%
Number/percentage of T's	415,324,881 / 27.58%
Number/percentage of G's	336,414,990 / 22.34%
Number/percentage of N's	187,746 / 0.01%

GC Percentage	44.88%

2.3. Coverage

Mean	0.4865
Standard Deviation	15.9014

2.4. Mapping Quality

Mean Mapping Quality	54.76

2.5. Insert size

Mean	18,031.33
Standard Deviation	1,335,342.99
P25/Median/P75	158 / 220 / 297

2.6. Mismatches and indels

General error rate	0.57%
Mismatches	8,423,059
Insertions	97,299
Mapped reads with at least one insertion	0.63%
Deletions	72,805
Mapped reads with at least one deletion	0.47%
Homopolymer indels	46.72%

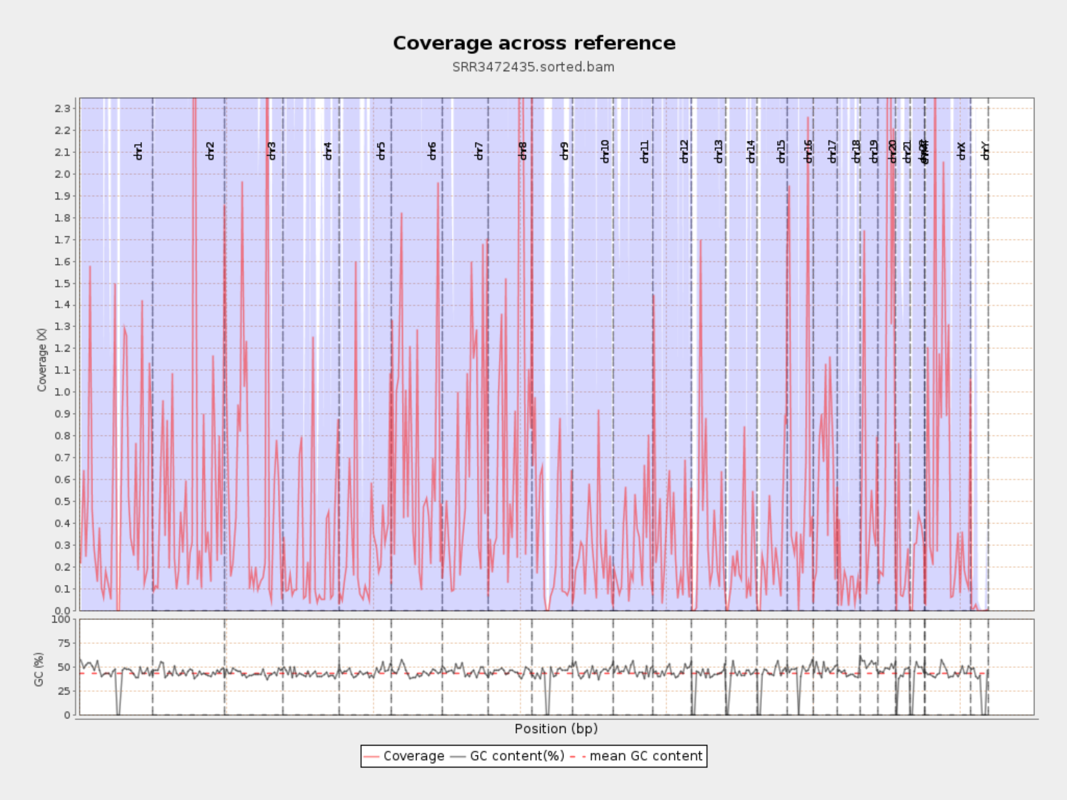
2.7. Chromosome stats

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

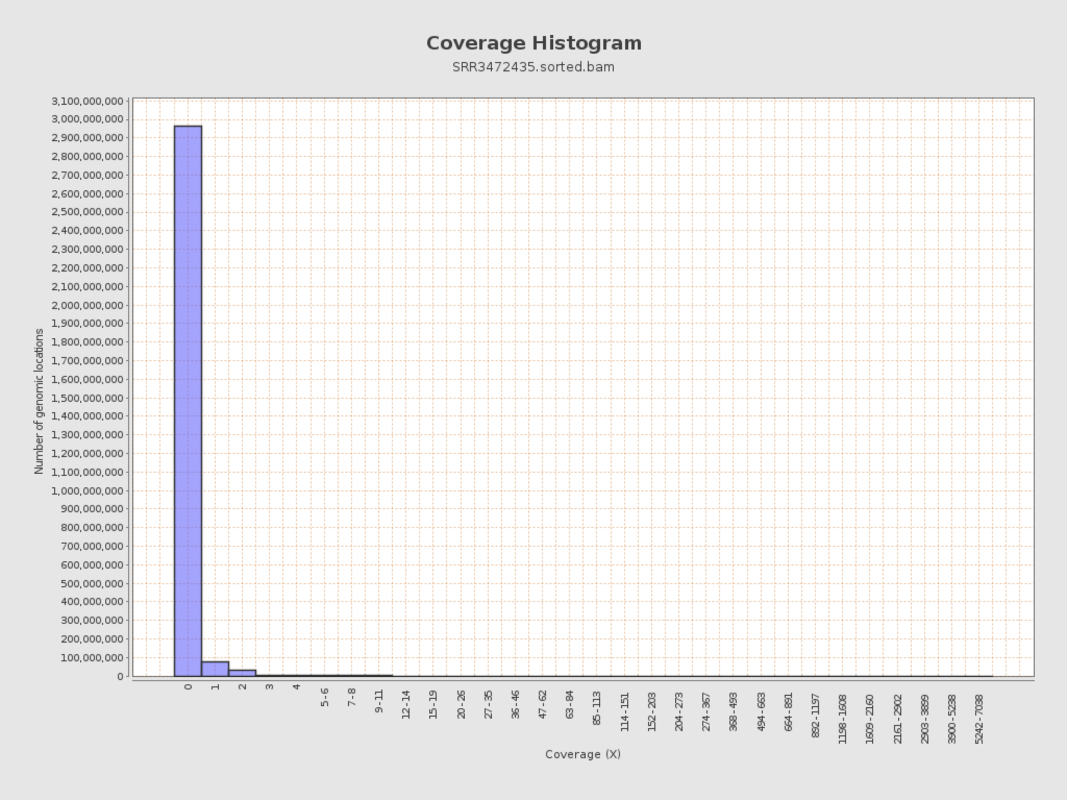
		bases	coverage	deviation
chr1	249250621	131612127	0.528	15.8643
chr2	243199373	130754170	0.5376	18.9562
chr3	198022430	122060814	0.6164	19.8428
chr4	191154276	50950013	0.2665	12.7778
chr5	180915260	60069443	0.332	9.5198
chr6	171115067	120124050	0.702	14.8009
chr7	159138663	105946578	0.6658	21.2693
chr8	146364022	136342596	0.9315	23.2154
chr9	141213431	48852772	0.3459	8.6035
chr10	135534747	36424854	0.2687	11.6283
chr11	135006516	39849245	0.2952	8.7047
chr12	133851895	48271468	0.3606	9.559
chr13	115169878	44520206	0.3866	11.7019
chr14	107349540	22326337	0.208	6.0009
chr15	102531392	29274717	0.2855	9.9527
chr16	90354753	63293427	0.7005	19.3181
chr17	81195210	50310086	0.6196	12.4818
chr18	78077248	10394802	0.1331	4.4721
chr19	59128983	33448784	0.5657	10.9966
chr20	63025520	97133450	1.5412	41.9392
chr21	48129895	10436291	0.2168	12.1056
chr22	51304566	13602770	0.2651	8.7441
chrMT	16571	4860	0.2933	0.7228
chrX	155270560	99811286	0.6428	19.7411

chrY	59373566	350710	0.0059	0.8624

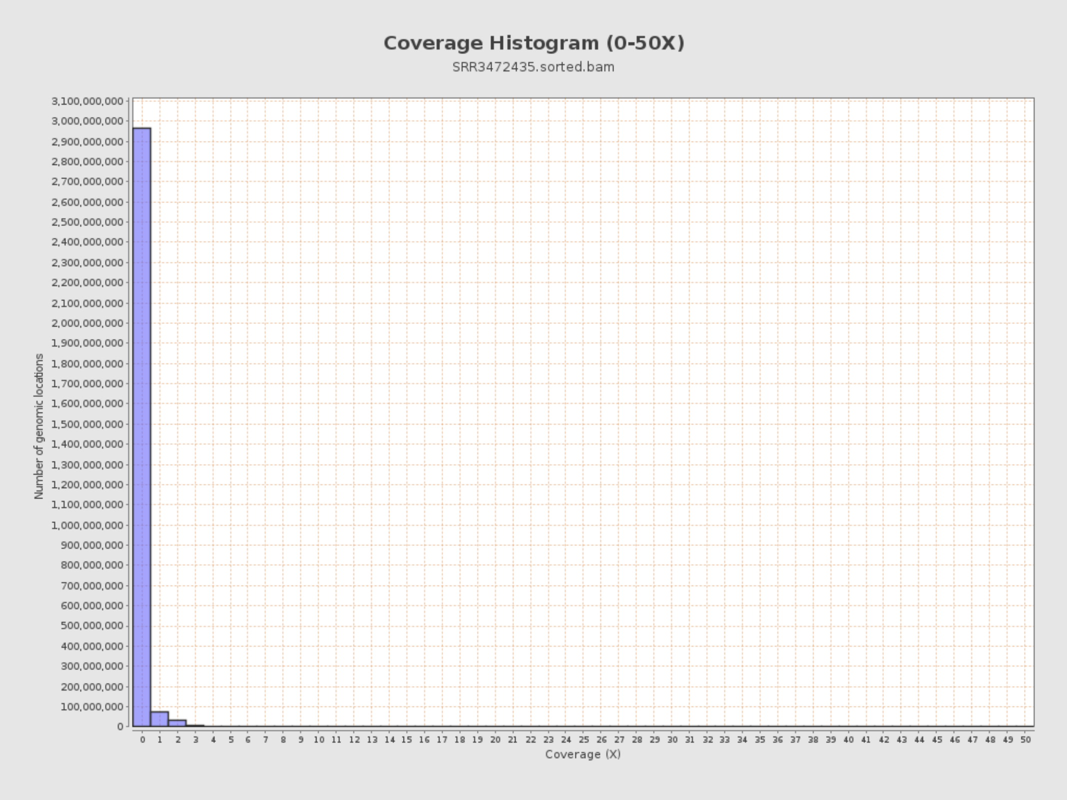
3. Results : Coverage across reference



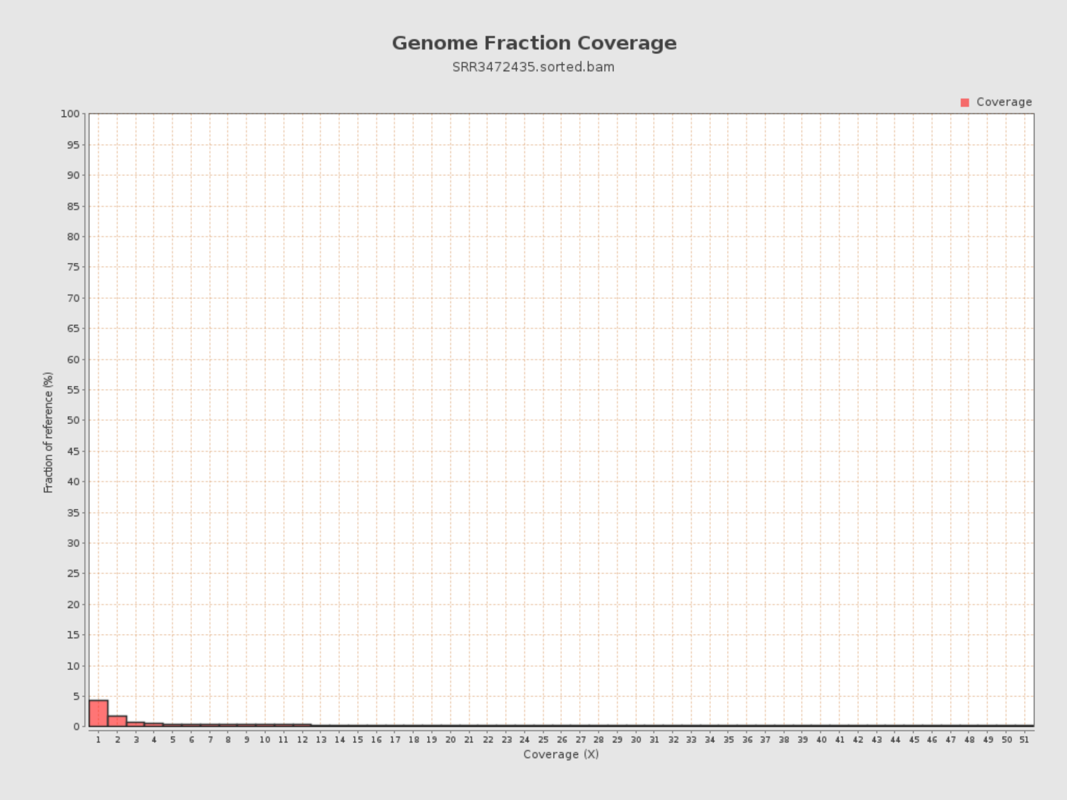
4. Results : Coverage Histogram



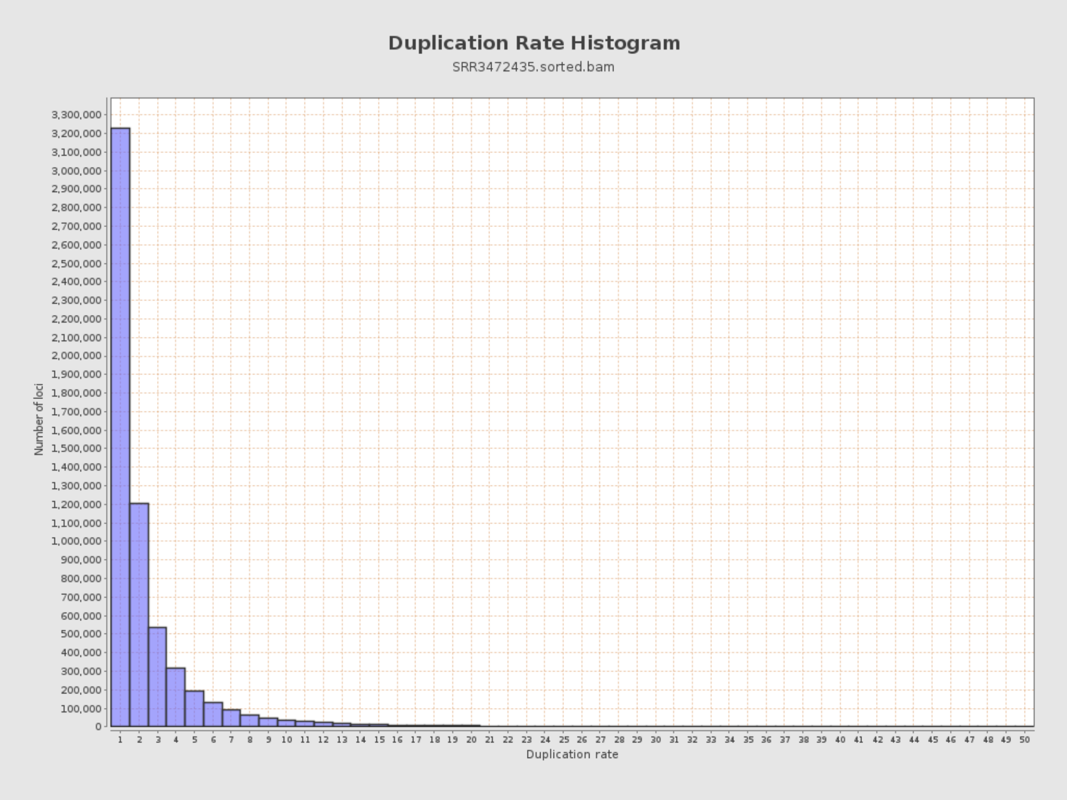
5. Results : Coverage Histogram (0-50X)



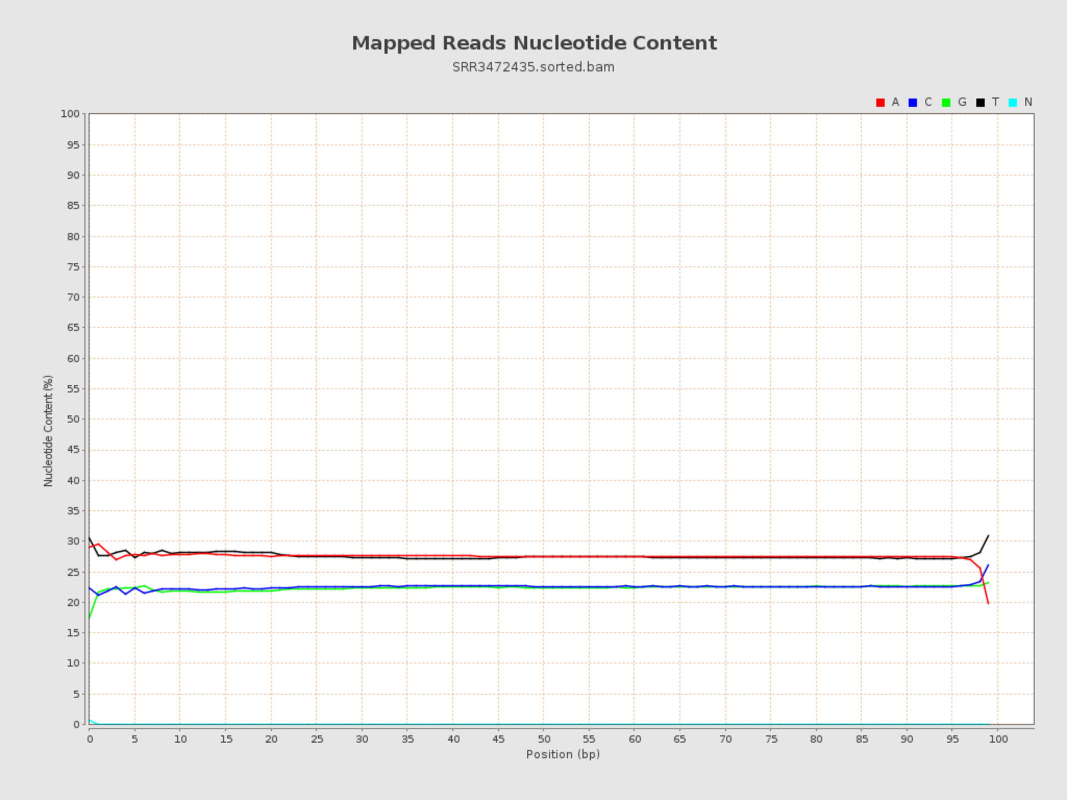
6. Results : Genome Fraction Coverage



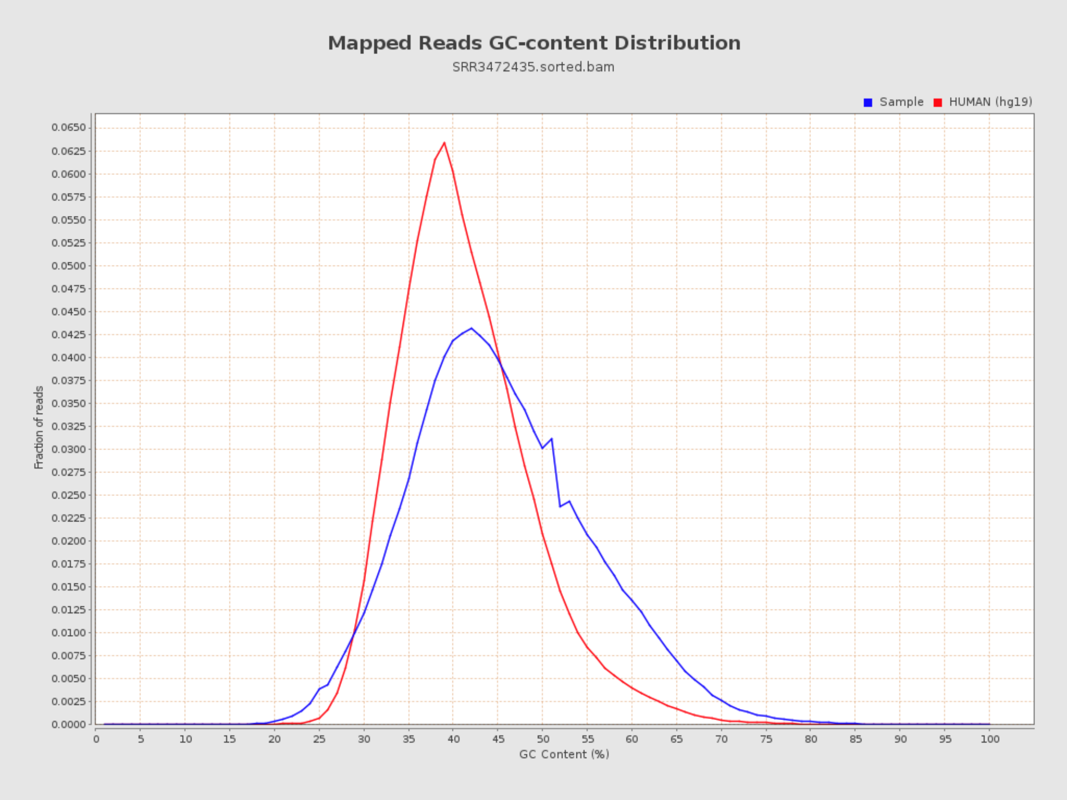
7. Results : Duplication Rate Histogram



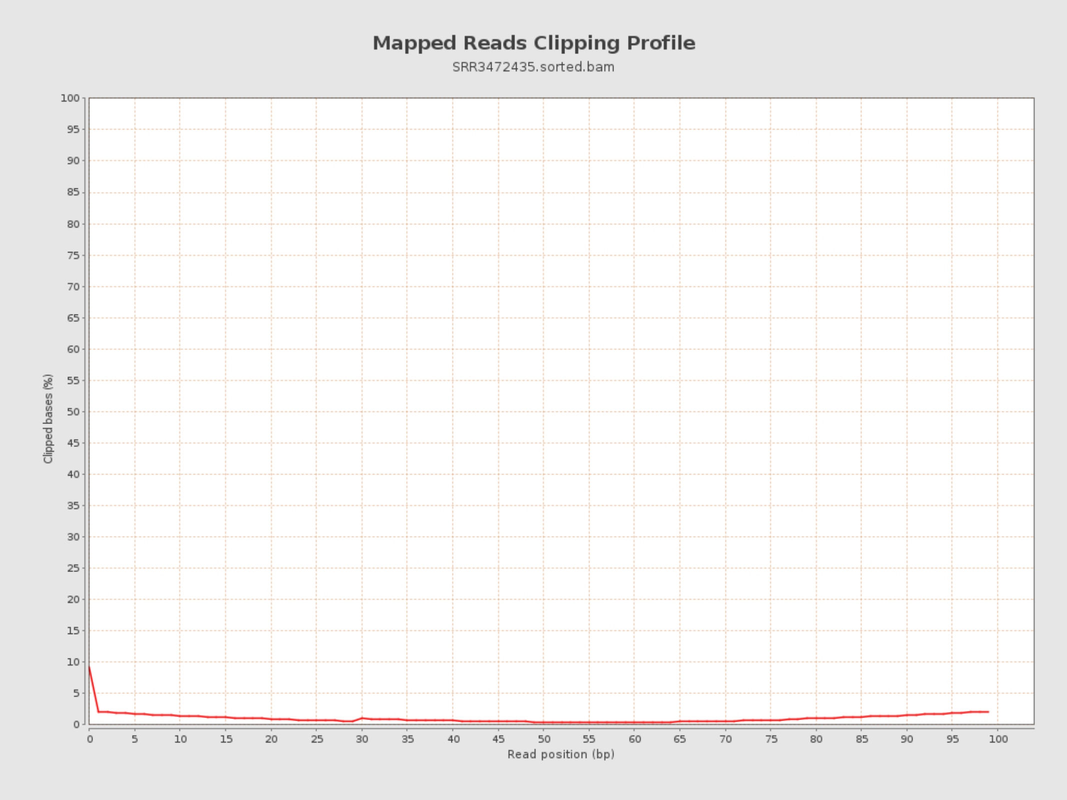
8. Results : Mapped Reads Nucleotide Content



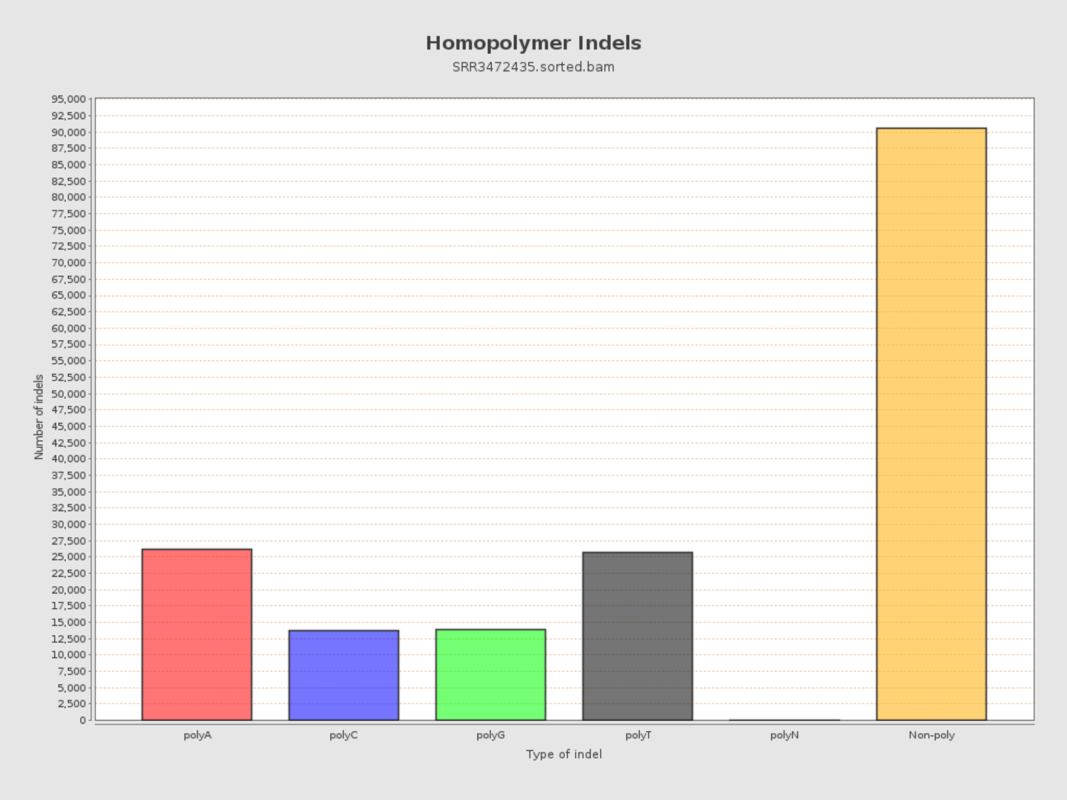
9. Results : Mapped Reads GC-content Distribution



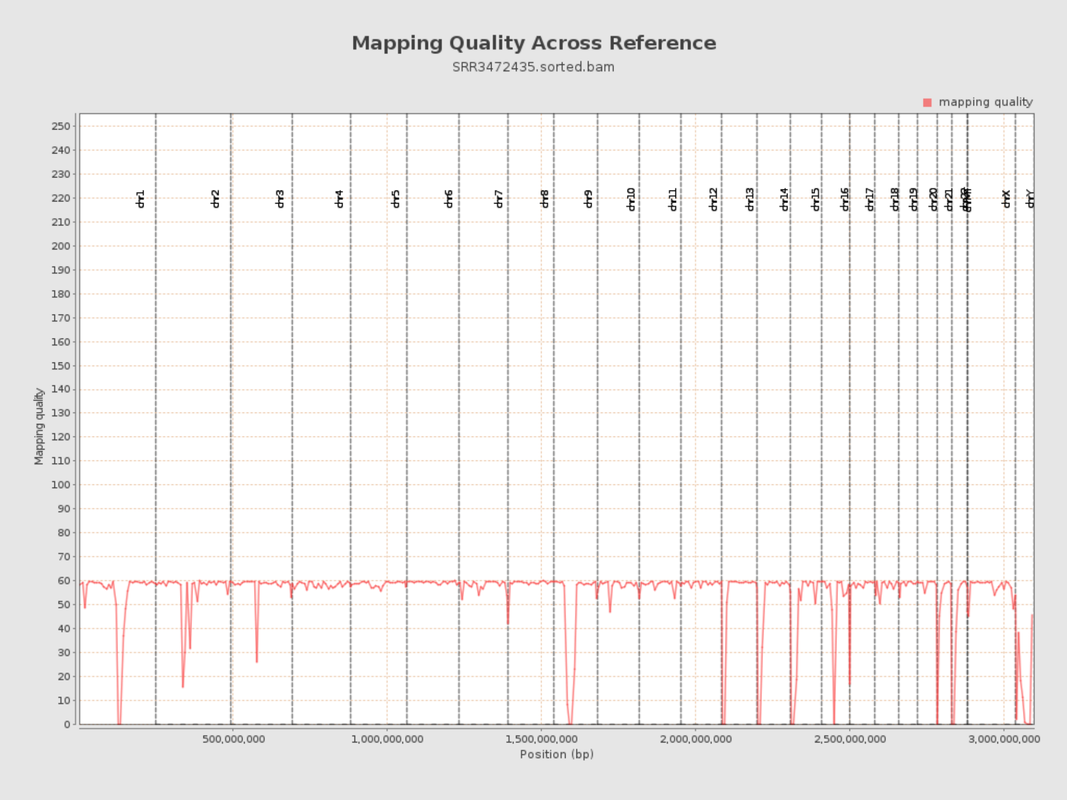
10. Results : Mapped Reads Clipping Profile



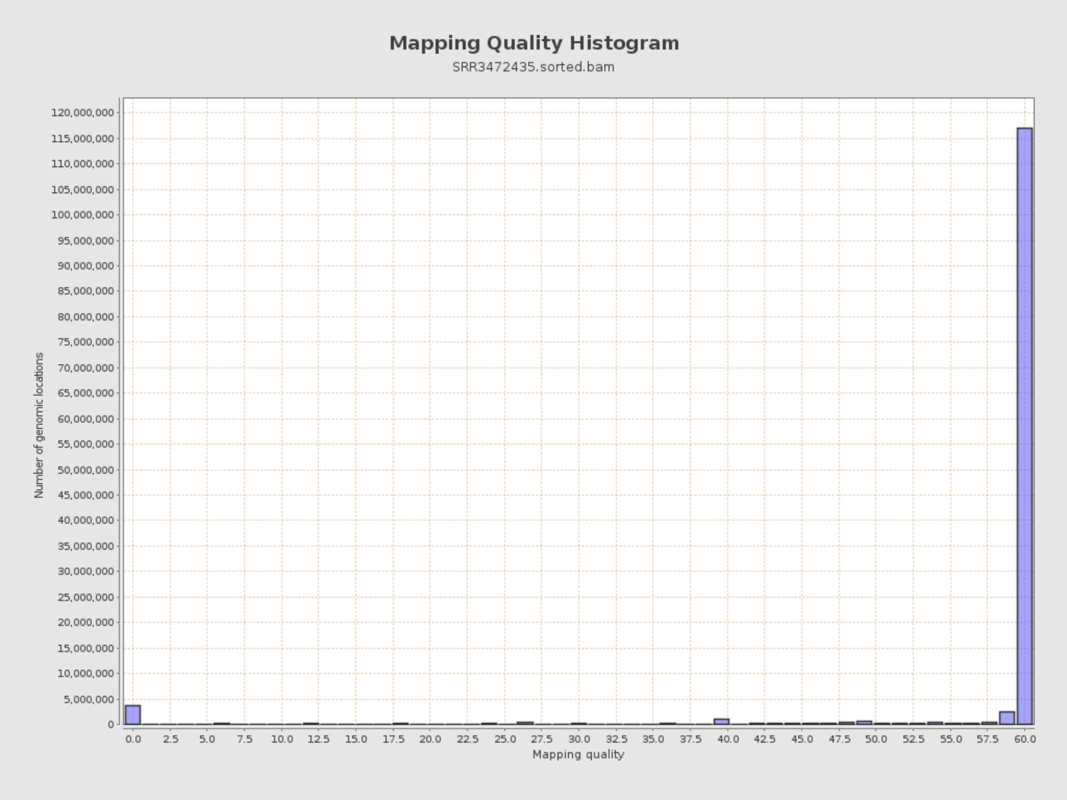
11. Results : Homopolymer Indels



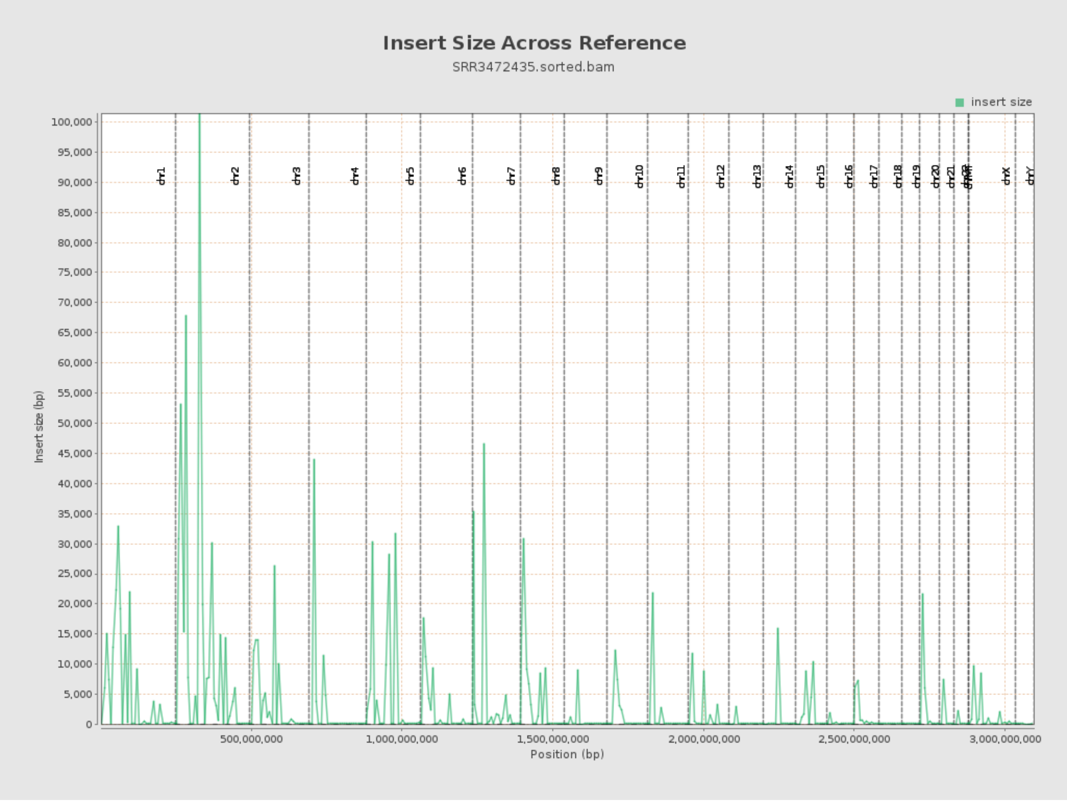
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram