Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 02:50:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472464.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_SRR3472464 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472464_1.fastq.gz SRR3472464_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 02:50:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472464.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,170,982
Mapped reads	14,027,537 / 98.99%
Unmapped reads	143,445 / 1.01%
Mapped paired reads	14,027,537 / 98.99%
Mapped reads, first in pair	7,030,481 / 49.61%
Mapped reads, second in pair	6,997,056 / 49.38%
Mapped reads, both in pair	13,953,508 / 98.47%
Mapped reads, singletons	74,029 / 0.52%
Secondary alignments	0
Supplementary alignments	52,190 / 0.37%
Read min/max/mean length	30 / 100 / 99.35
Duplicated reads (estimated)	8,337,531 / 58.84%
Duplication rate	45.85%
Clipped reads	978,928 / 6.91%

2.2. ACGT Content

Number/percentage of A's	375,517,617 / 27.3%
Number/percentage of C's	313,228,299 / 22.77%
Number/percentage of T's	375,440,761 / 27.29%
Number/percentage of G's	311,222,068 / 22.62%
Number/percentage of N's	172,668 / 0.01%

GC Percentage	45.4%

2.3. Coverage

Mean	0.4444
Standard Deviation	14.0128

2.4. Mapping Quality

Mean Mapping Quality	55.08

2.5. Insert size

Mean	18,005.62
Standard Deviation	1,314,410.71
P25/Median/P75	152 / 209 / 279

2.6. Mismatches and indels

General error rate	0.56%
Mismatches	7,592,755
Insertions	80,202
Mapped reads with at least one insertion	0.57%
Deletions	68,297
Mapped reads with at least one deletion	0.48%
Homopolymer indels	46.55%

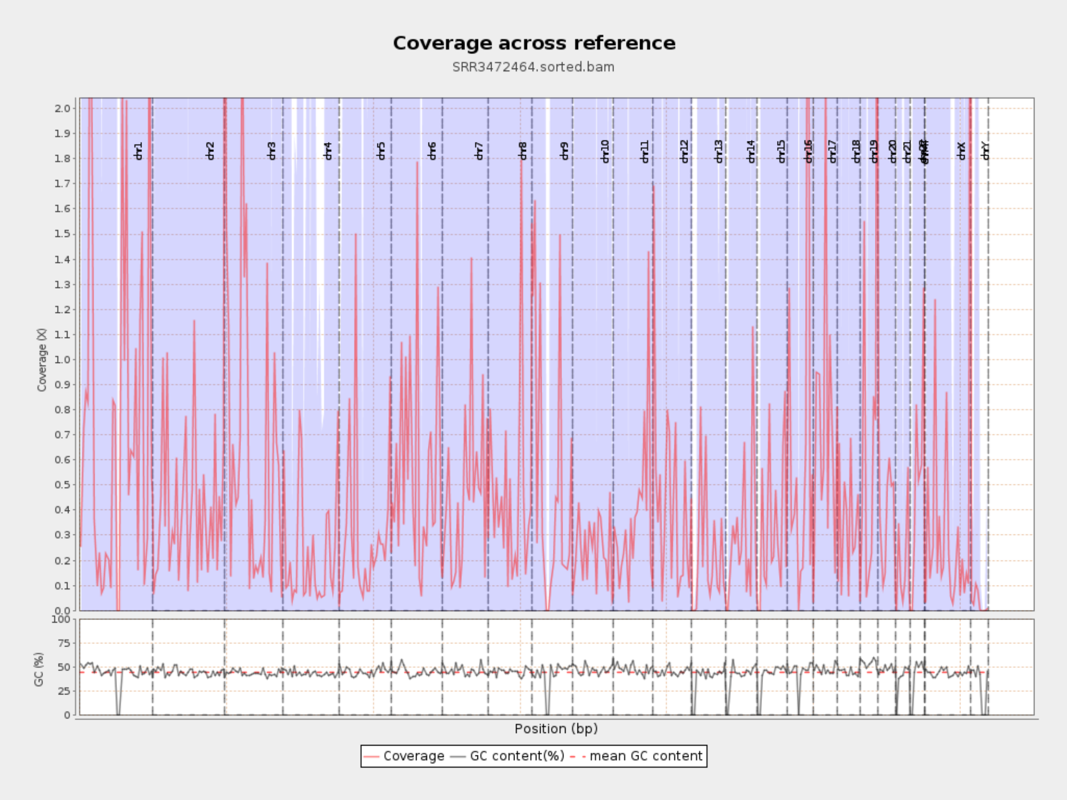
2.7. Chromosome stats

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

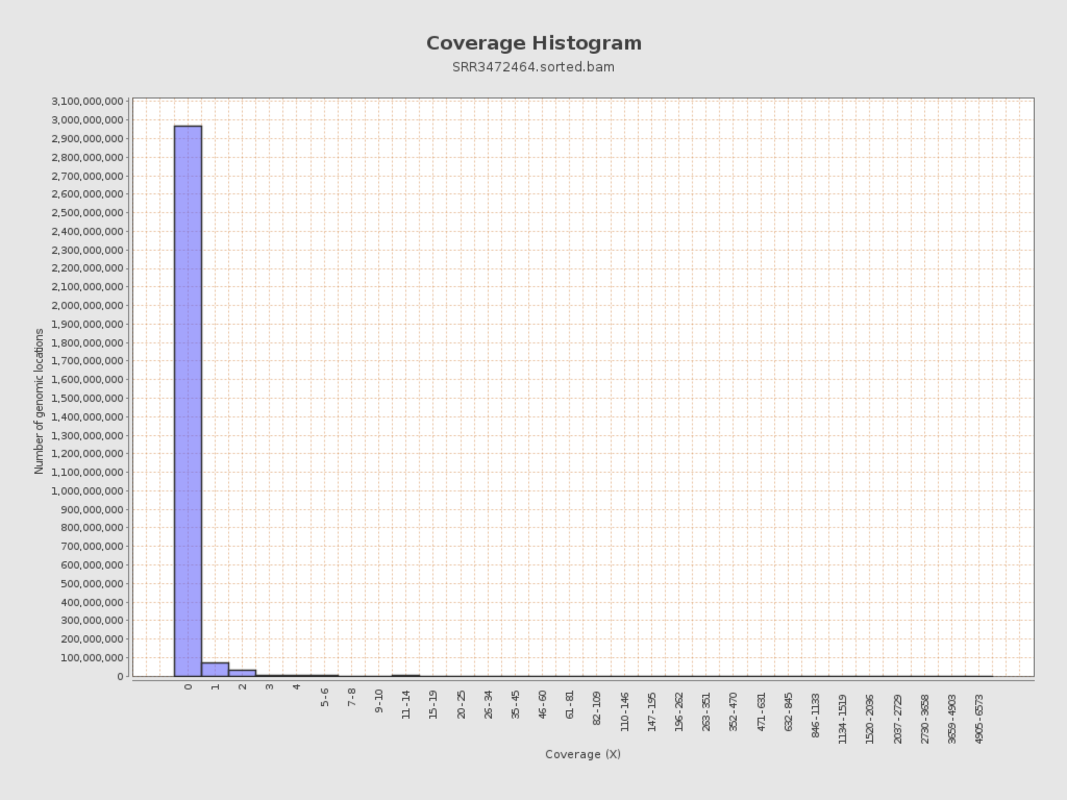
		bases	coverage	deviation
chr1	249250621	192092788	0.7707	23.347
chr2	243199373	98252977	0.404	13.467
chr3	198022430	134978733	0.6816	16.4916
chr4	191154276	43595793	0.2281	7.4184
chr5	180915260	56092267	0.31	9.3705
chr6	171115067	99213985	0.5798	14.9697
chr7	159138663	73538543	0.4621	12.8495
chr8	146364022	68917954	0.4709	12.1077
chr9	141213431	71361901	0.5053	13.9359
chr10	135534747	33219261	0.2451	7.1907
chr11	135006516	50693197	0.3755	11.7964
chr12	133851895	58646125	0.4381	12.469
chr13	115169878	25657409	0.2228	7.2338
chr14	107349540	30505845	0.2842	14.9194
chr15	102531392	34700366	0.3384	9.9322
chr16	90354753	63970404	0.708	22.605
chr17	81195210	61099413	0.7525	19.4117
chr18	78077248	27786013	0.3559	11.3855
chr19	59128983	37259702	0.6301	17.3261
chr20	63025520	25067686	0.3977	11.9056
chr21	48129895	9401083	0.1953	9.6967
chr22	51304566	26979560	0.5259	15.5322
chrMT	16571	1514	0.0914	0.3776
chrX	155270560	50801071	0.3272	10.4027

chrY	59373566	1911539	0.0322	1.4043

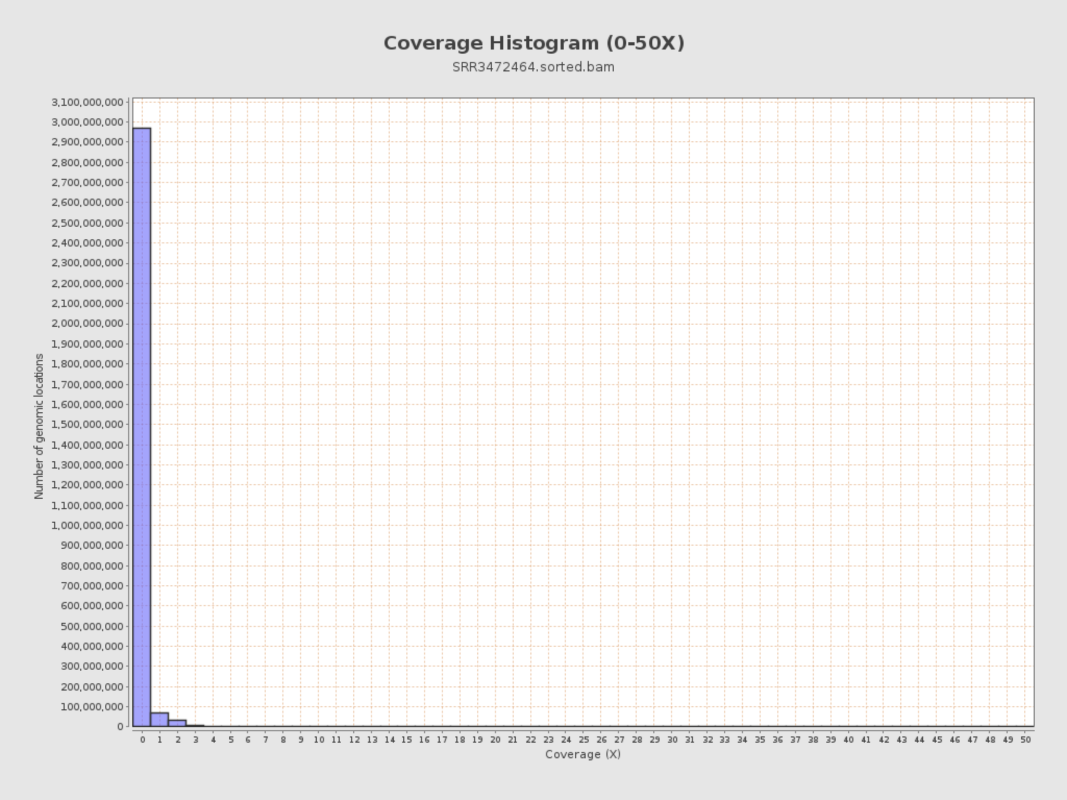
3. Results : Coverage across reference



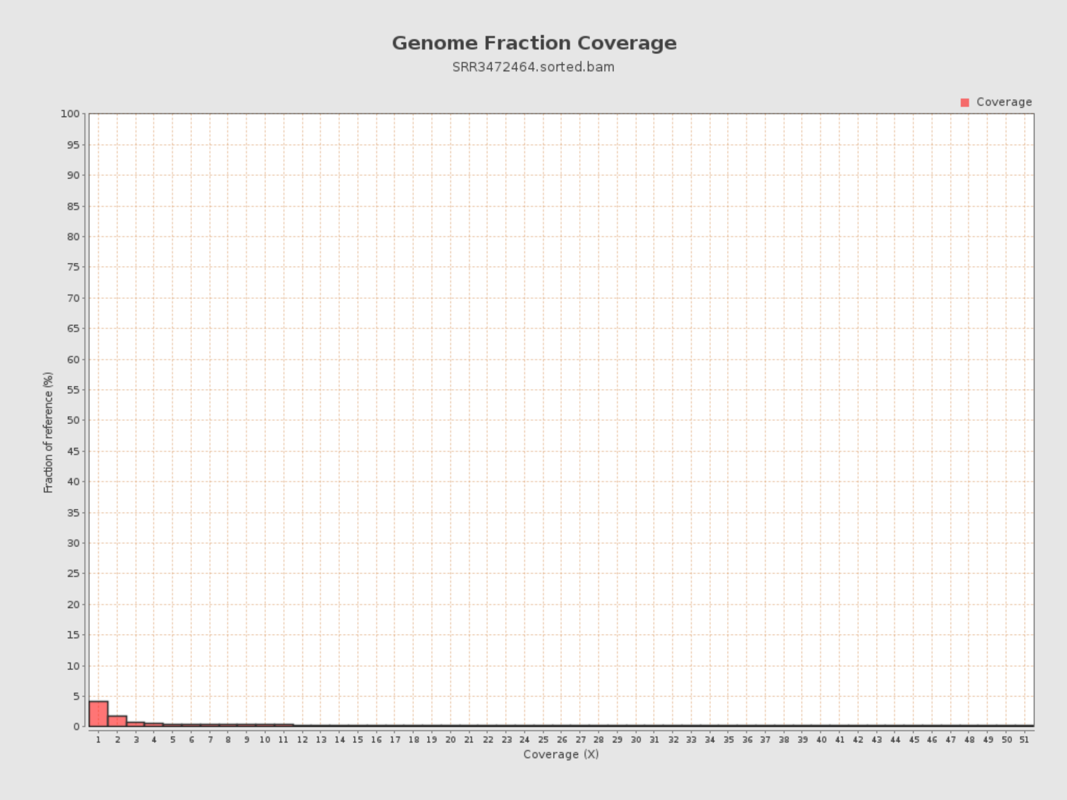
4. Results : Coverage Histogram



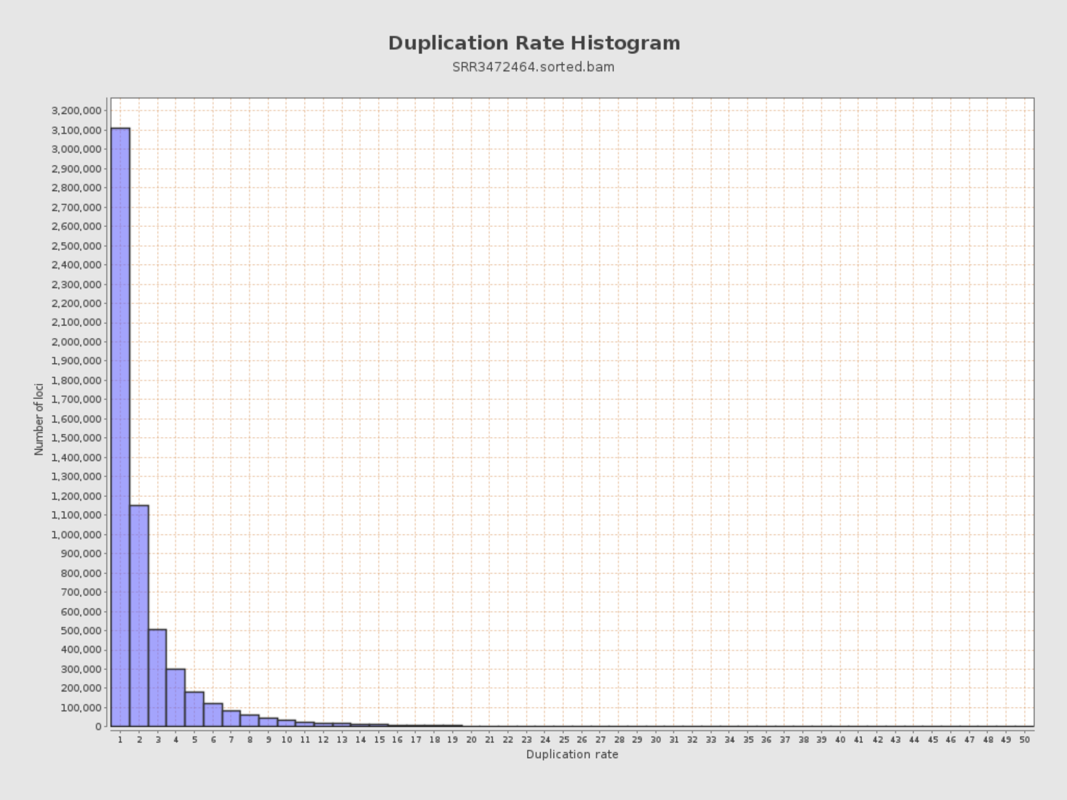
5. Results : Coverage Histogram (0-50X)



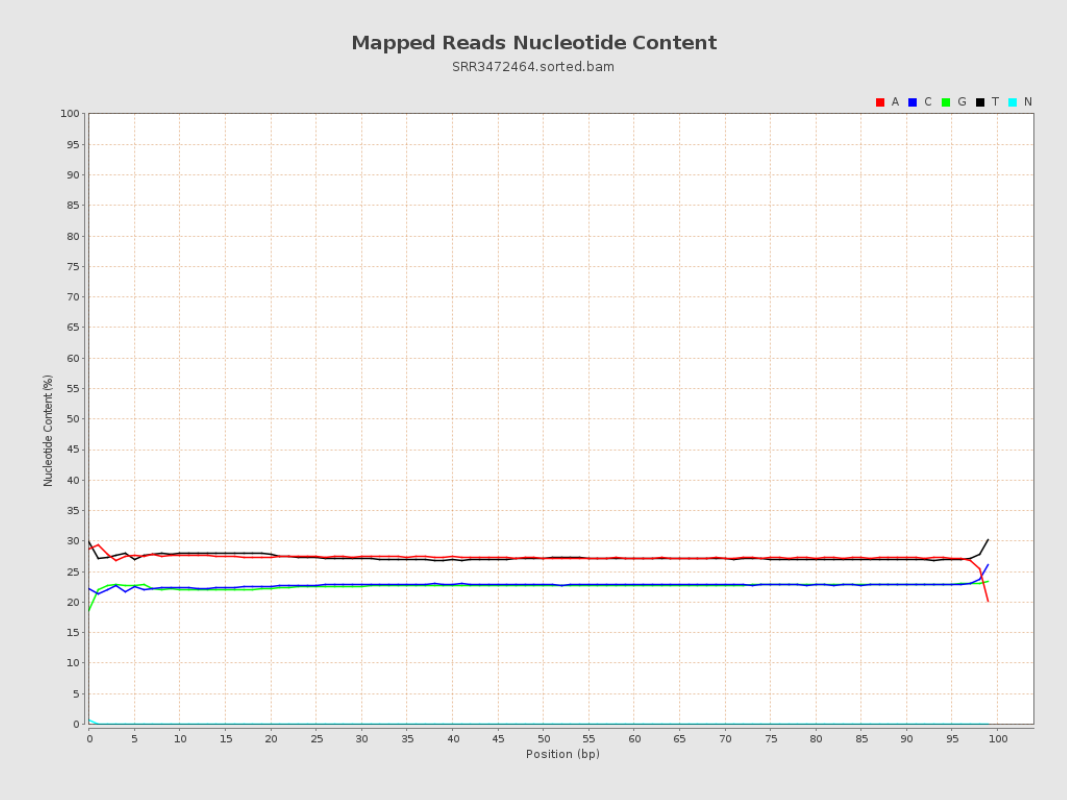
6. Results : Genome Fraction Coverage



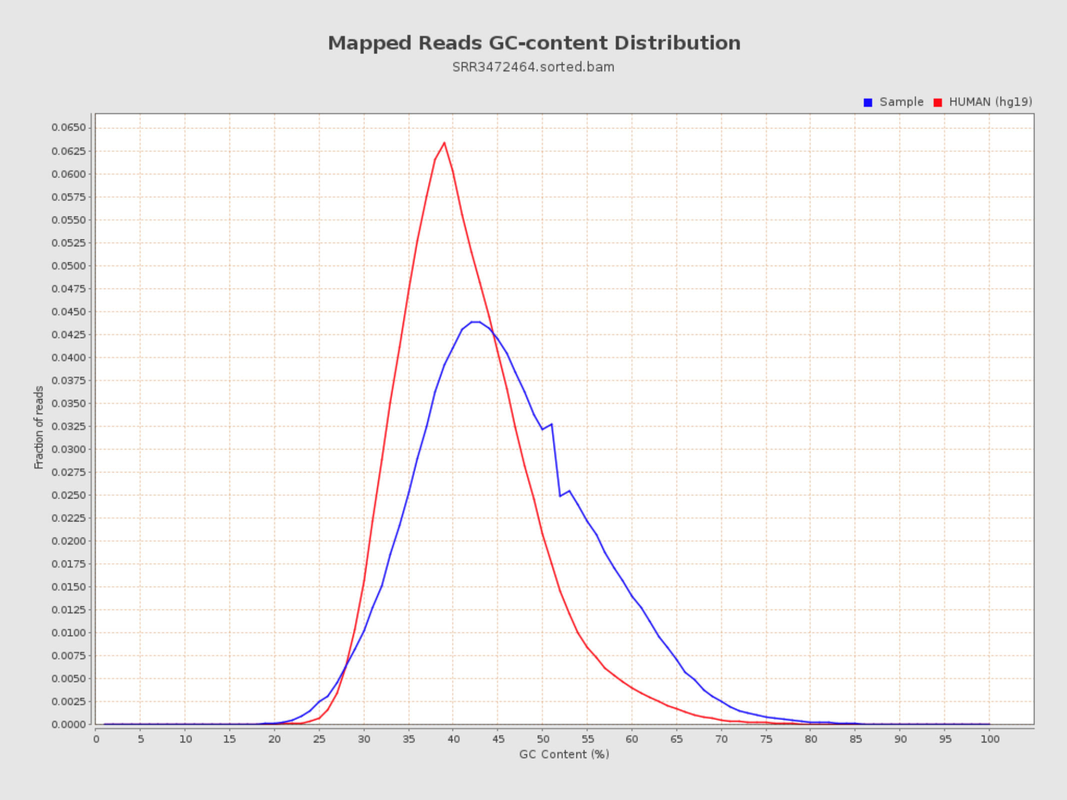
7. Results : Duplication Rate Histogram



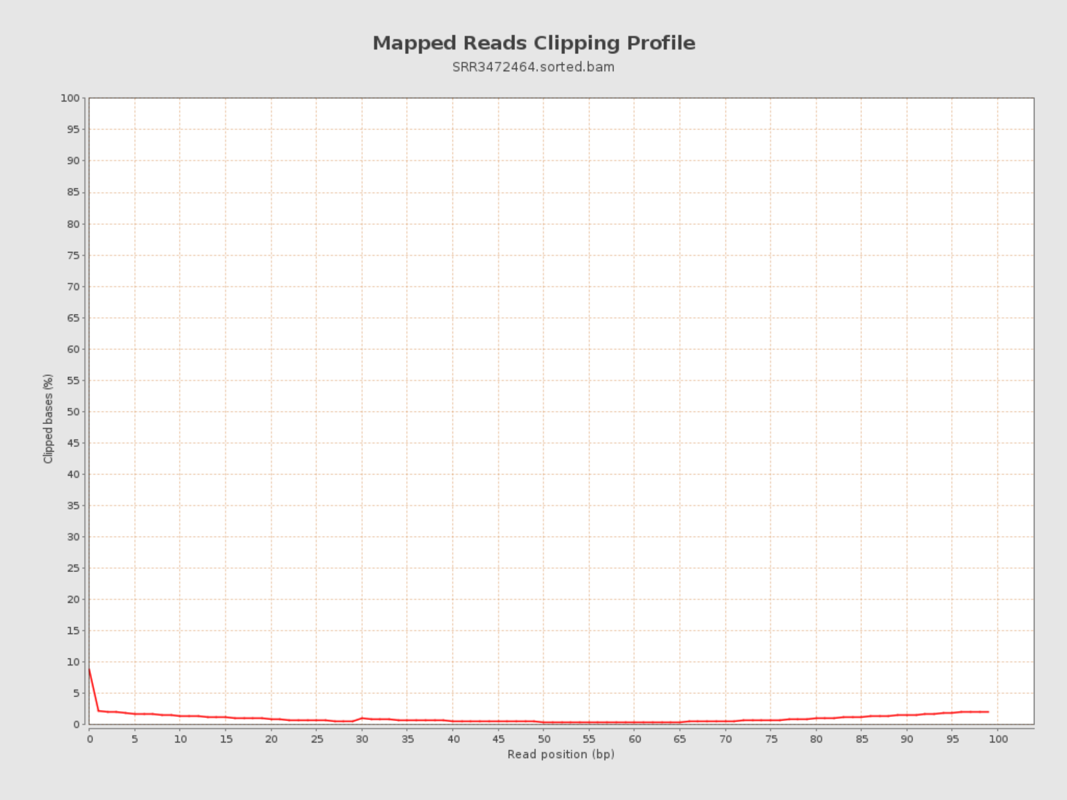
8. Results : Mapped Reads Nucleotide Content



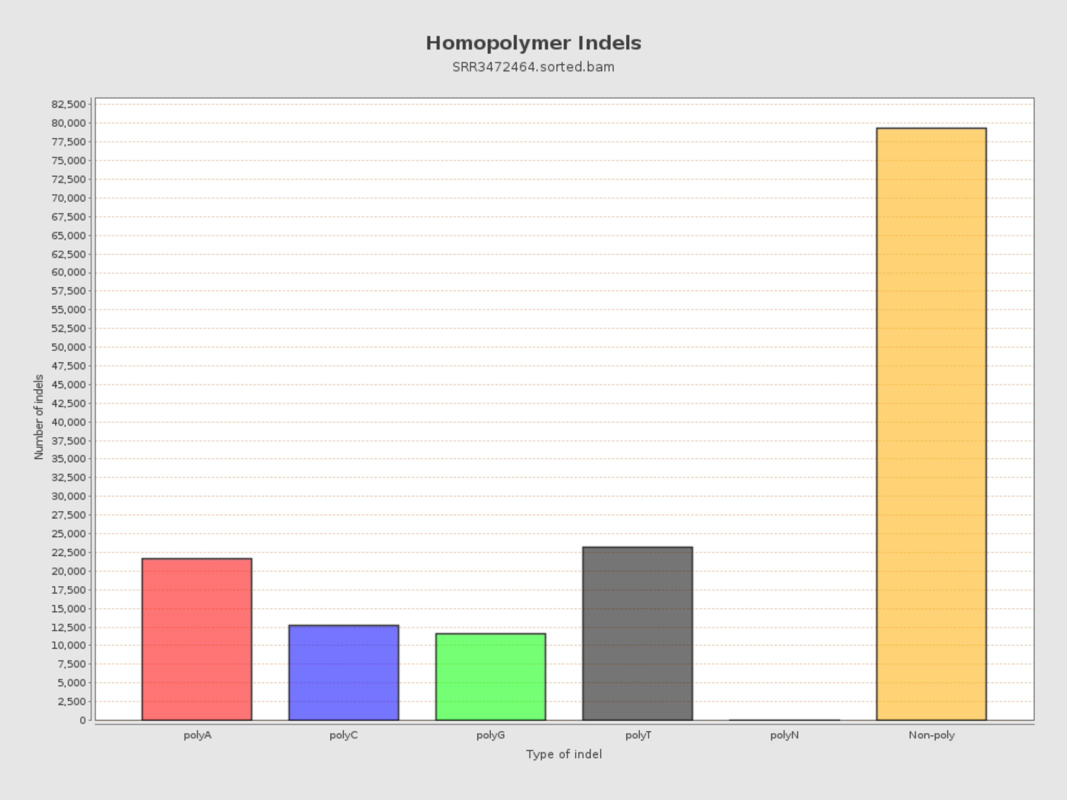
9. Results : Mapped Reads GC-content Distribution



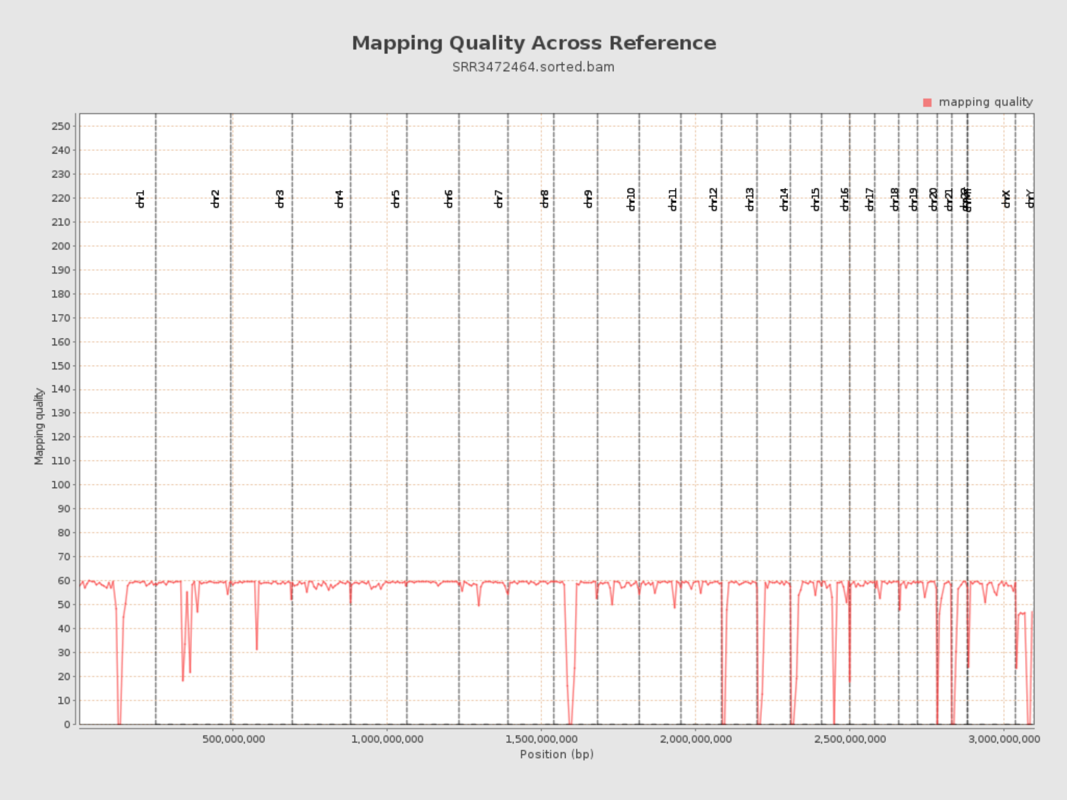
10. Results : Mapped Reads Clipping Profile



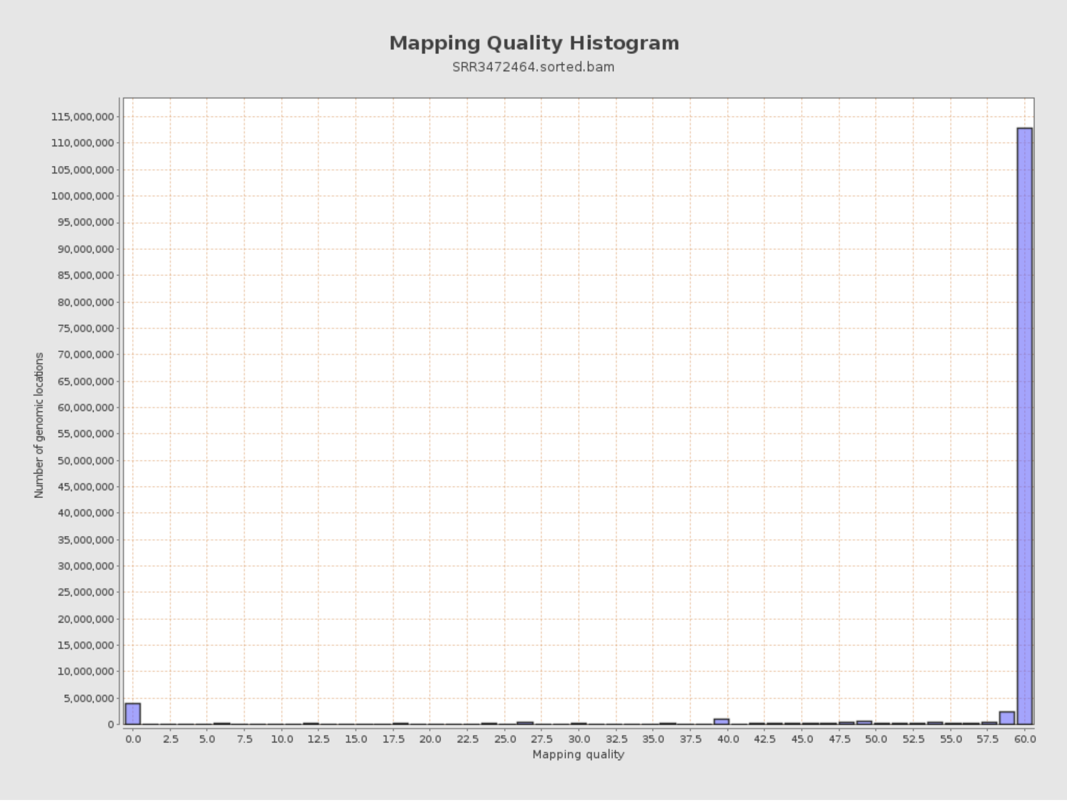
11. Results : Homopolymer Indels



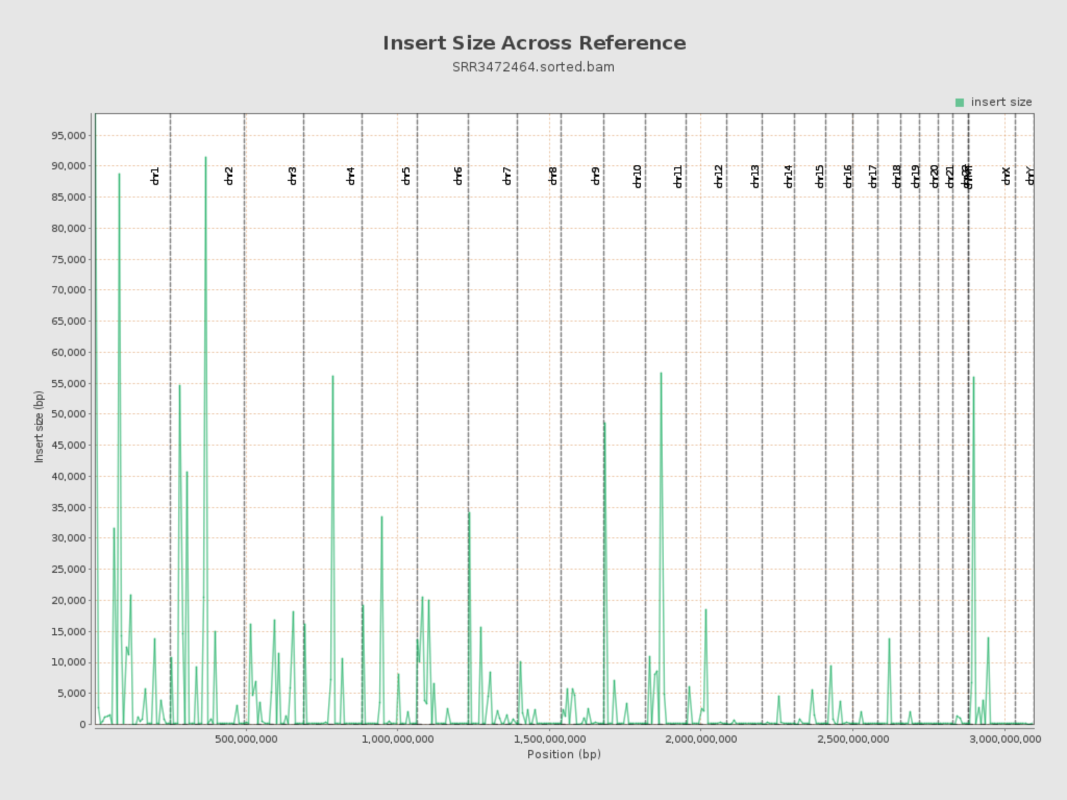
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram