Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 18:48:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472794.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_SRR3472794 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472794_1.fastq.gz SRR3472794_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 18:48:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472794.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,387,760
Mapped reads	15,215,885 / 98.88%
Unmapped reads	171,875 / 1.12%
Mapped paired reads	15,215,885 / 98.88%
Mapped reads, first in pair	7,632,501 / 49.6%
Mapped reads, second in pair	7,583,384 / 49.28%
Mapped reads, both in pair	15,131,320 / 98.33%
Mapped reads, singletons	84,565 / 0.55%
Secondary alignments	0
Supplementary alignments	53,568 / 0.35%
Read min/max/mean length	30 / 100 / 100.14
Duplicated reads (estimated)	10,082,852 / 65.53%
Duplication rate	46.95%
Clipped reads	1,315,753 / 8.55%

2.2. ACGT Content

Number/percentage of A's	416,553,565 / 27.84%
Number/percentage of C's	333,899,752 / 22.31%
Number/percentage of T's	413,540,613 / 27.63%
Number/percentage of G's	332,163,208 / 22.2%
Number/percentage of N's	289,088 / 0.02%

GC Percentage	44.51%

2.3. Coverage

Mean	0.4835
Standard Deviation	19.8656

2.4. Mapping Quality

Mean Mapping Quality	54.7

2.5. Insert size

Mean	27,217.14
Standard Deviation	1,611,359.34
P25/Median/P75	165 / 232 / 315

2.6. Mismatches and indels

General error rate	0.61%
Mismatches	8,912,388
Insertions	83,416
Mapped reads with at least one insertion	0.54%
Deletions	81,992
Mapped reads with at least one deletion	0.53%
Homopolymer indels	44.33%

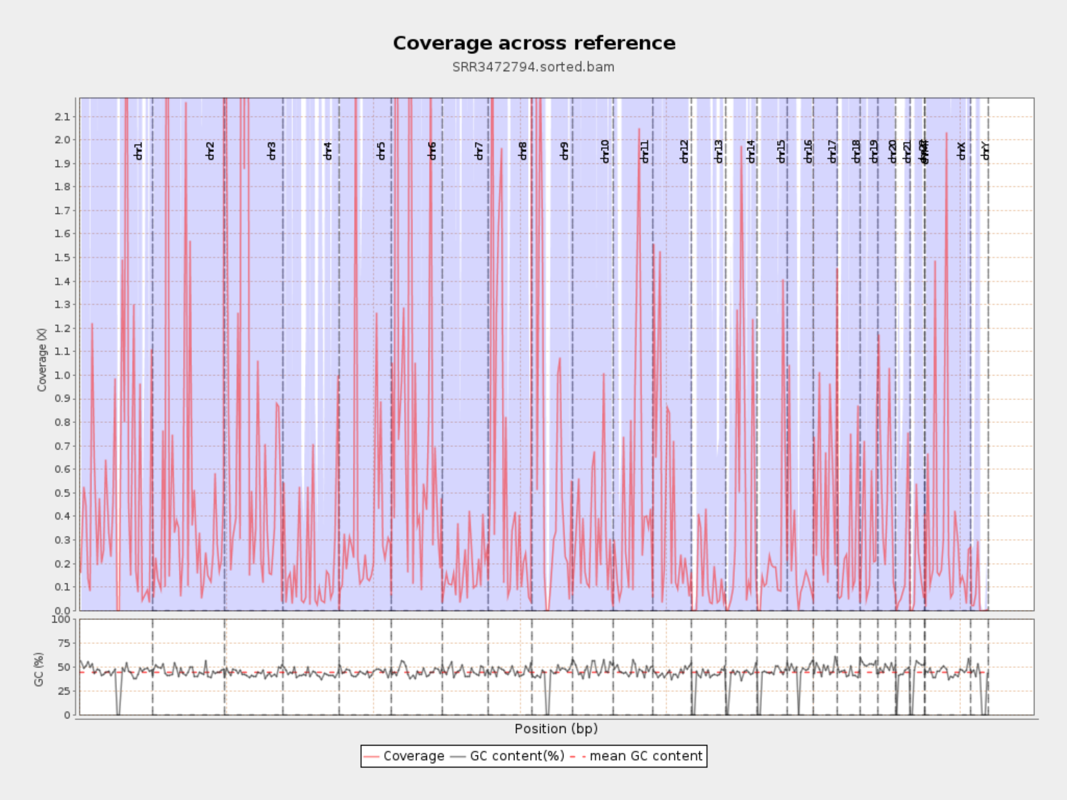
2.7. Chromosome stats

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

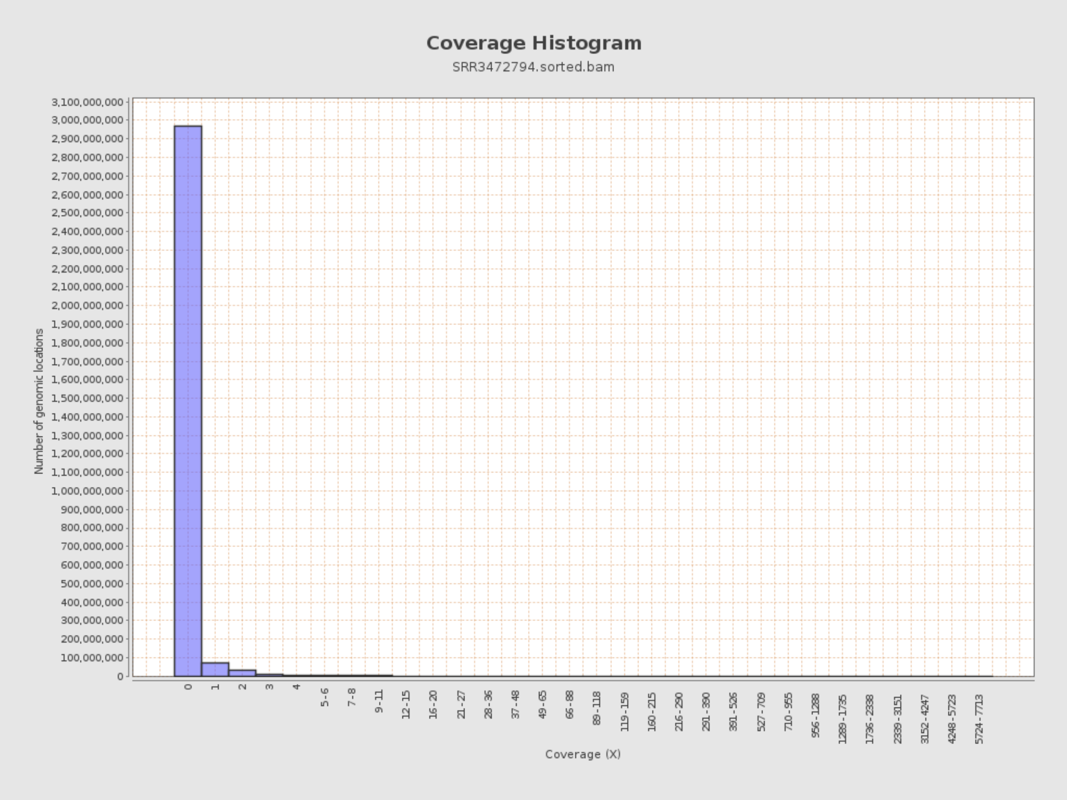
		bases	coverage	deviation
chr1	249250621	133321934	0.5349	20.3225
chr2	243199373	122805147	0.505	26.1987
chr3	198022430	231881409	1.171	32.9104
chr4	191154276	37662123	0.197	9.6159
chr5	180915260	69529124	0.3843	14.23
chr6	171115067	163844260	0.9575	31.981
chr7	159138663	28163466	0.177	6.1243
chr8	146364022	90801542	0.6204	28.0114
chr9	141213431	134402794	0.9518	29.5295
chr10	135534747	43337913	0.3198	13.4788
chr11	135006516	68628733	0.5083	20.7448
chr12	133851895	65853321	0.492	16.5525
chr13	115169878	14540654	0.1263	5.7268
chr14	107349540	52436213	0.4885	17.1918
chr15	102531392	27854348	0.2717	12.9498
chr16	90354753	19680725	0.2178	7.2221
chr17	81195210	43571633	0.5366	14.9672
chr18	78077248	20033206	0.2566	12.1416
chr19	59128983	19130778	0.3235	8.689
chr20	63025520	33700577	0.5347	18.1775
chr21	48129895	9788483	0.2034	8.6665
chr22	51304566	7763508	0.1513	11.5041
chrMT	16571	6810	0.411	1.2466
chrX	155270560	54792868	0.3529	11.476

chrY	59373566	3106043	0.0523	4.4274

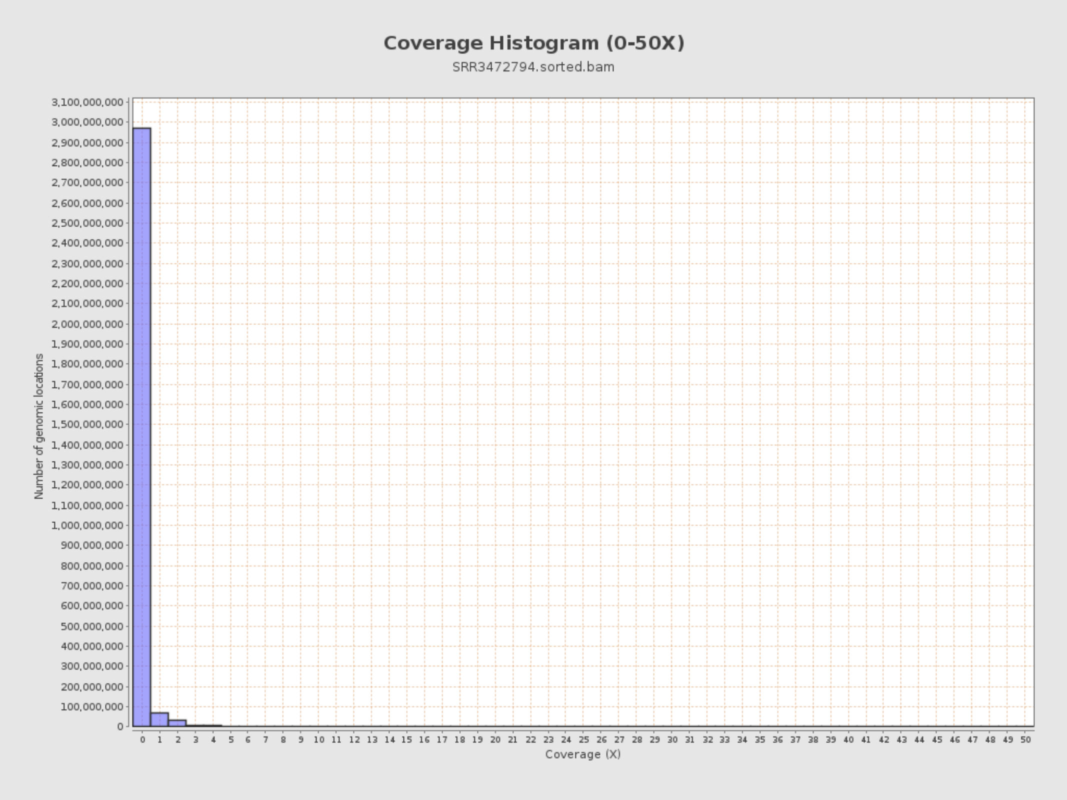
3. Results : Coverage across reference



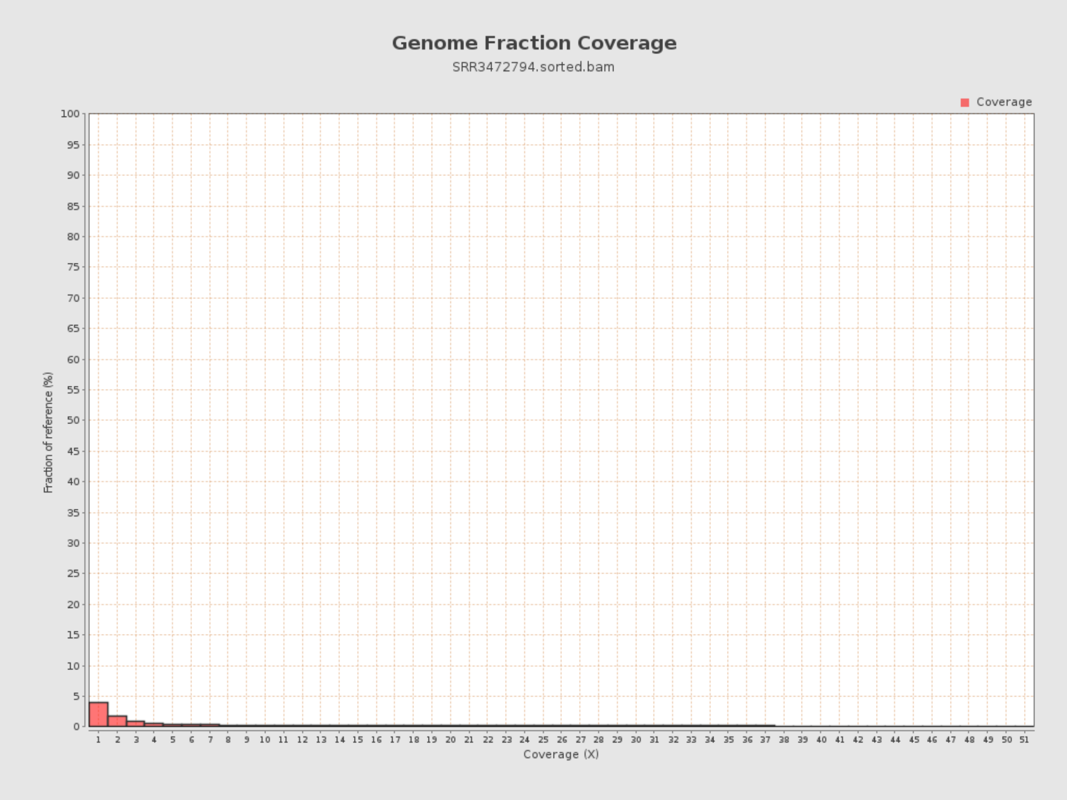
4. Results : Coverage Histogram



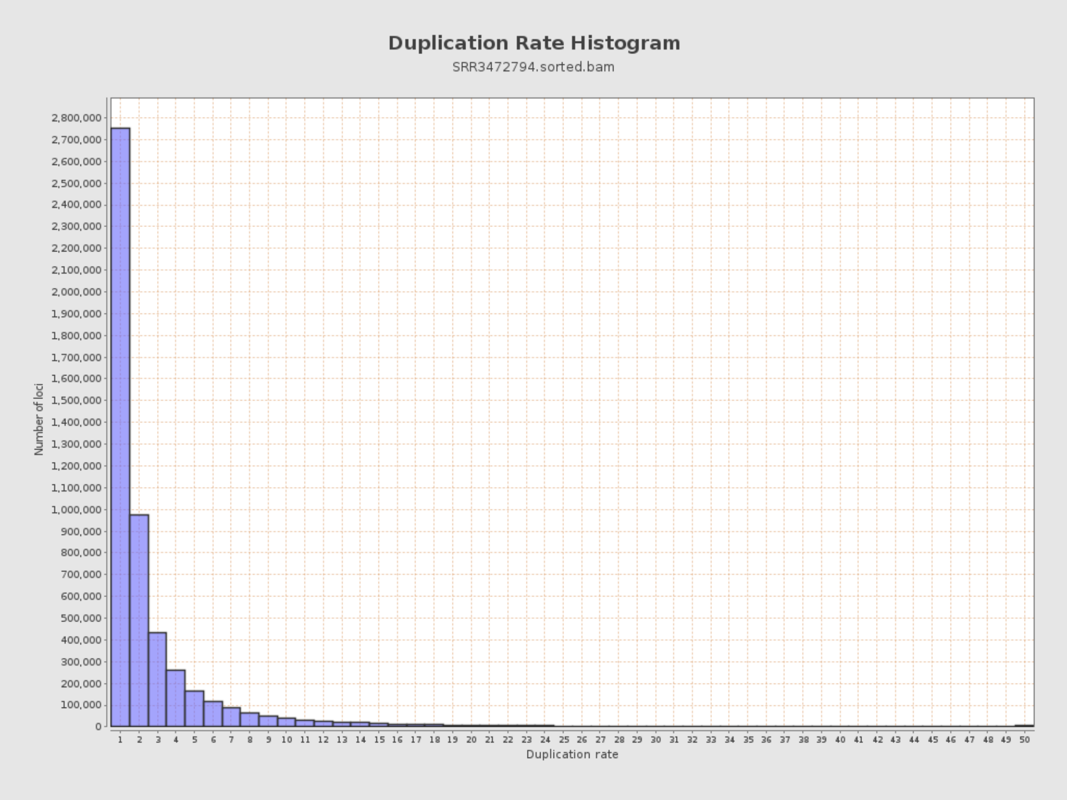
5. Results : Coverage Histogram (0-50X)



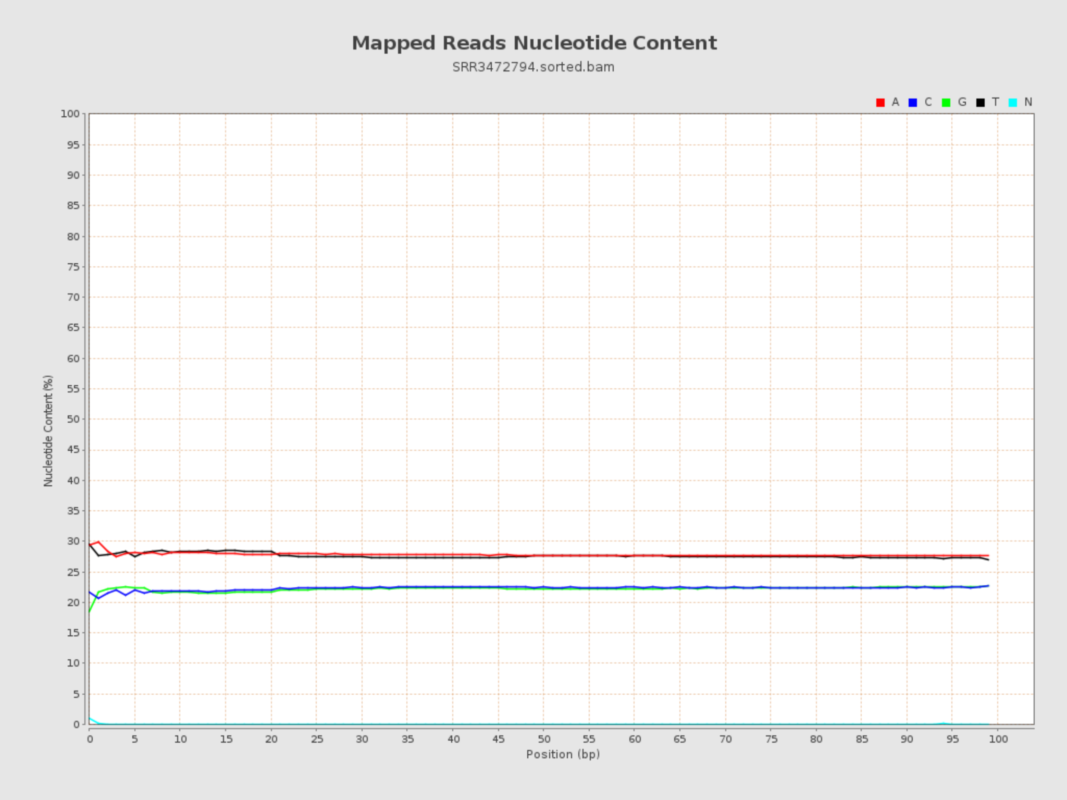
6. Results : Genome Fraction Coverage



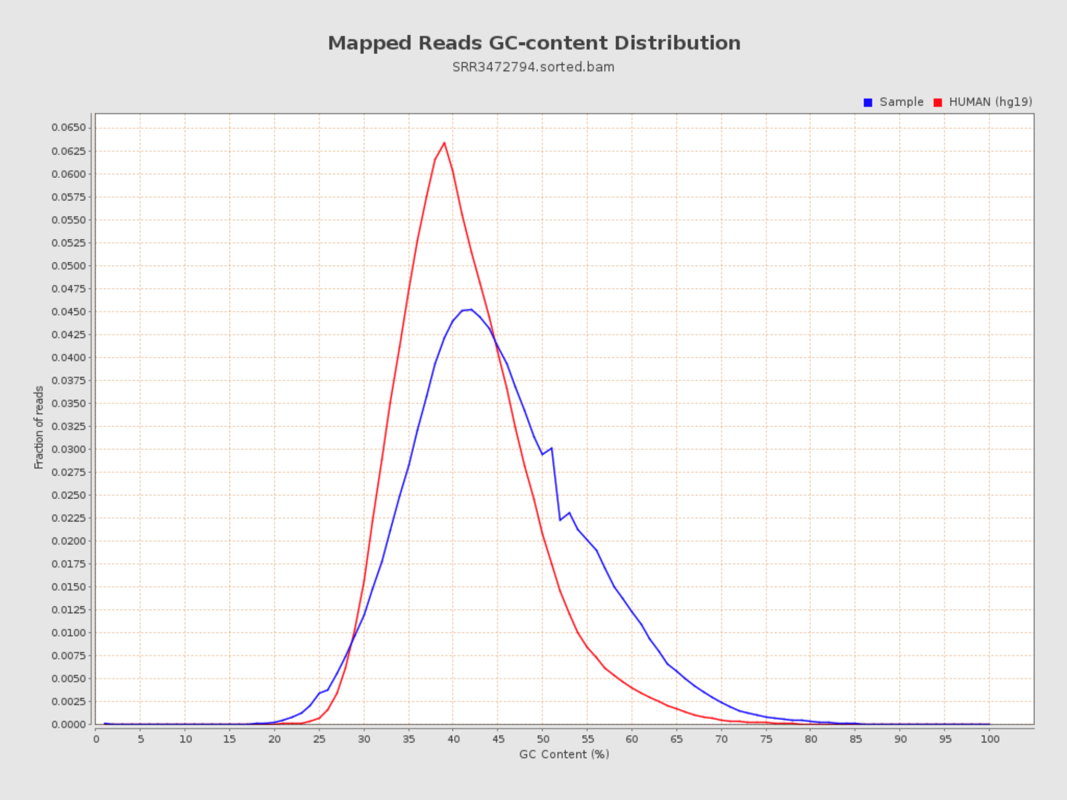
7. Results : Duplication Rate Histogram



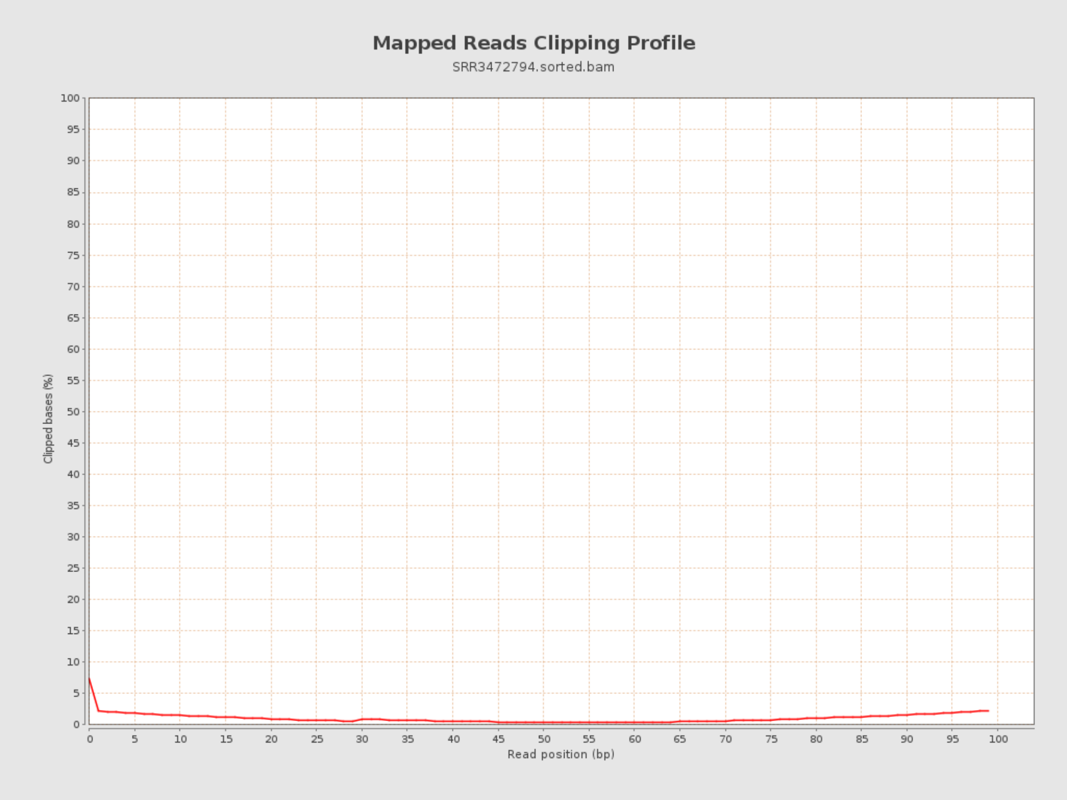
8. Results : Mapped Reads Nucleotide Content



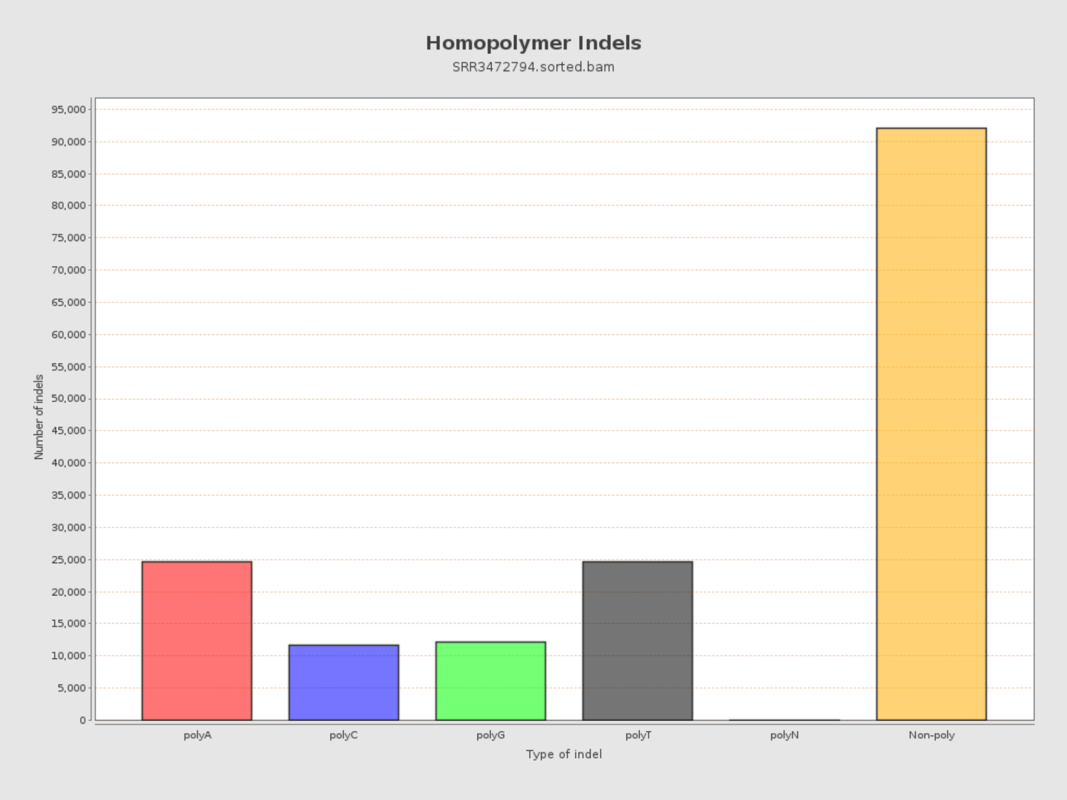
9. Results : Mapped Reads GC-content Distribution



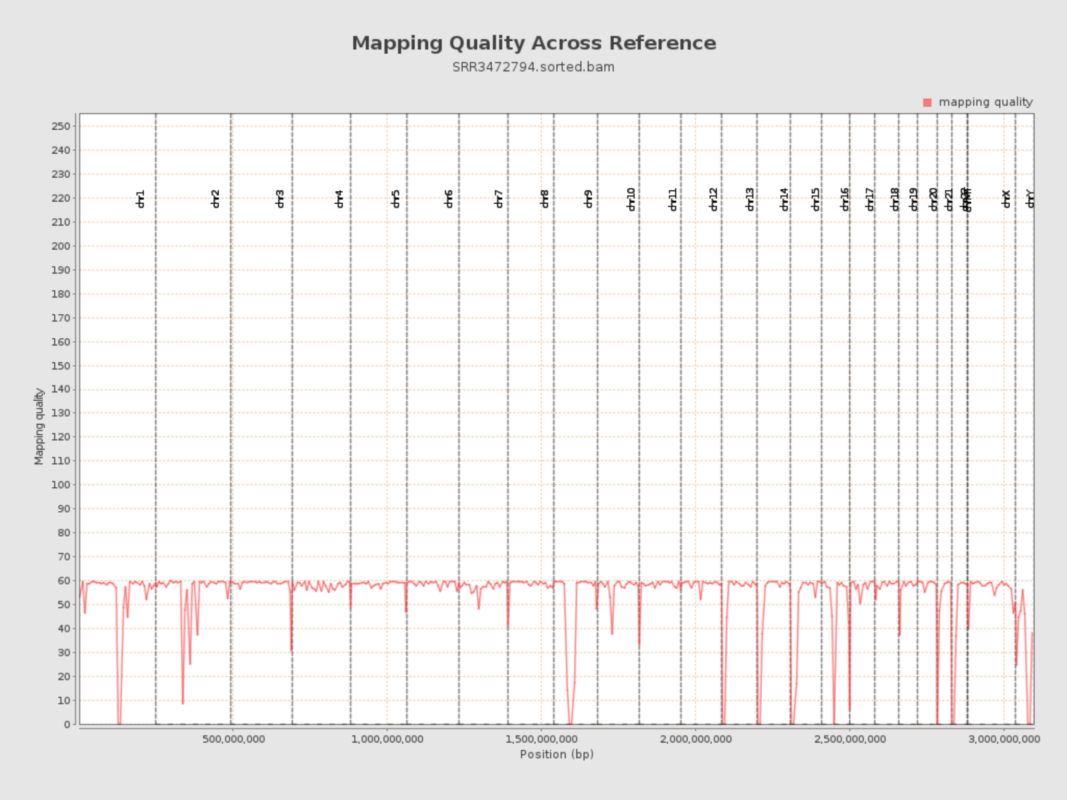
10. Results : Mapped Reads Clipping Profile



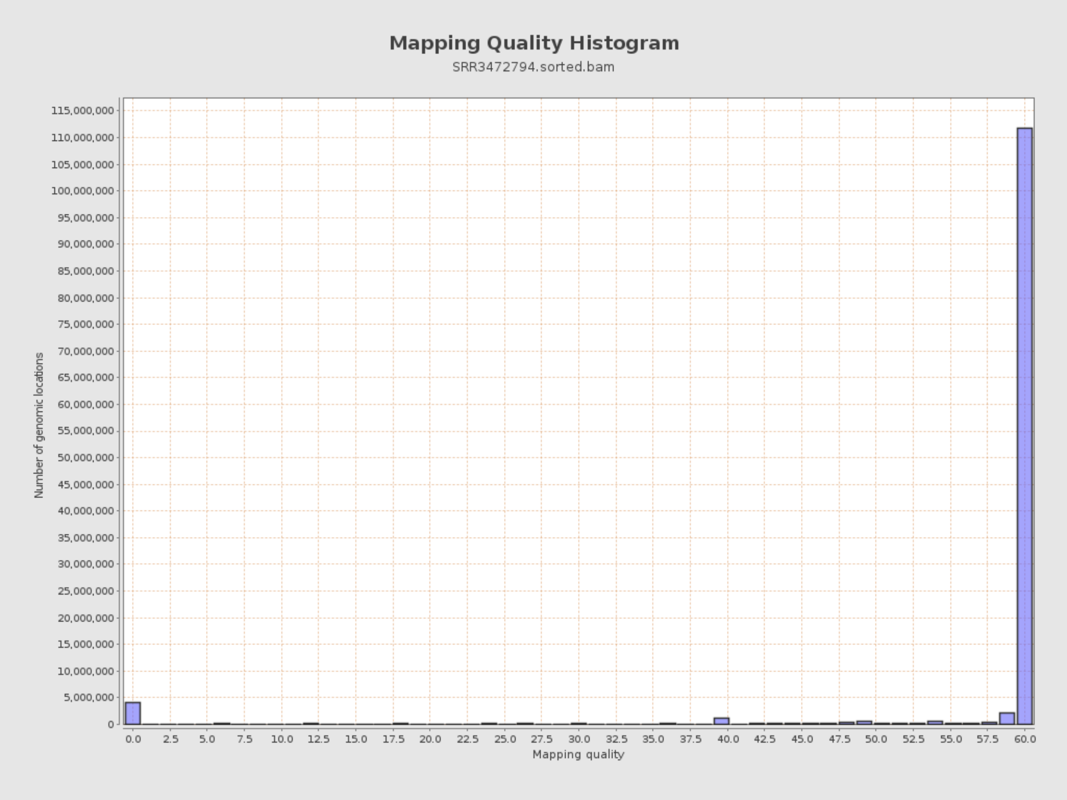
11. Results : Homopolymer Indels



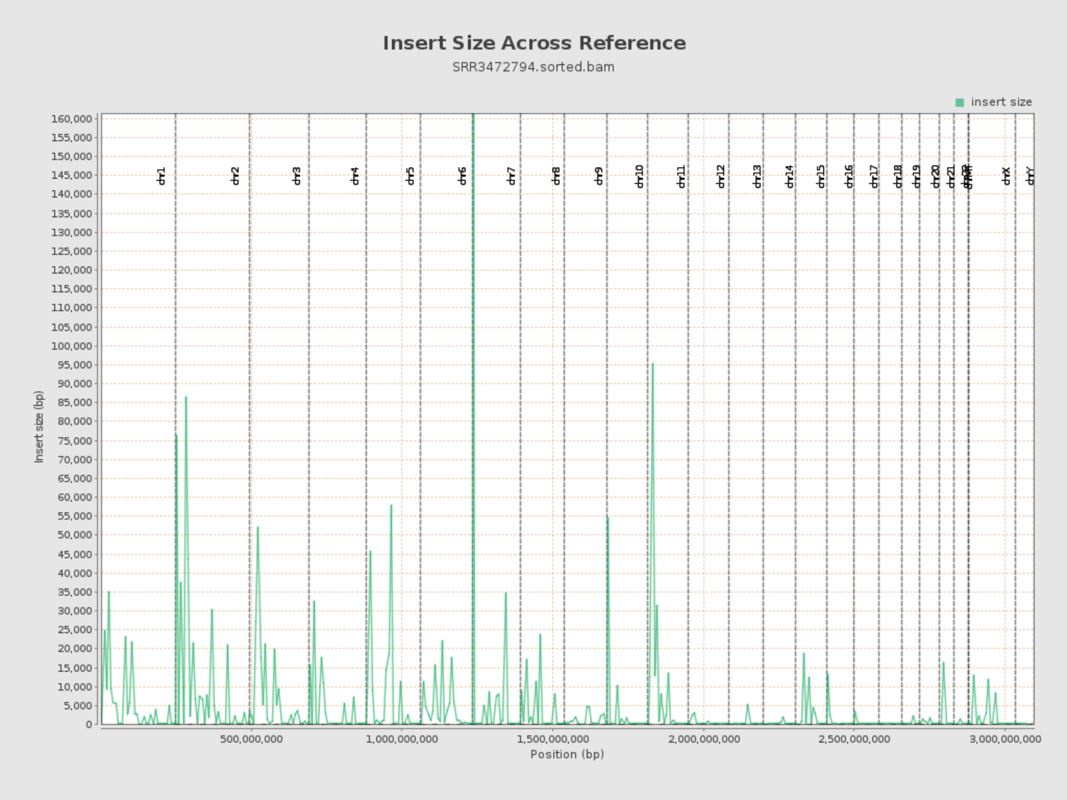
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram