Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/01 05:43:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472801.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_SRR3472801 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472801_1.fastq.gz SRR3472801_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 01 05:43:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472801.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	114,678,784
Mapped reads	114,175,897 / 99.56%
Unmapped reads	502,887 / 0.44%
Mapped paired reads	114,175,897 / 99.56%
Mapped reads, first in pair	57,257,320 / 49.93%
Mapped reads, second in pair	56,918,577 / 49.63%
Mapped reads, both in pair	113,795,946 / 99.23%
Mapped reads, singletons	379,951 / 0.33%
Secondary alignments	0
Supplementary alignments	94,248 / 0.08%
Read min/max/mean length	30 / 100 / 100.03
Duplicated reads (estimated)	59,033,121 / 51.48%
Duplication rate	48.16%
Clipped reads	4,699,290 / 4.1%

2.2. ACGT Content

Number/percentage of A's	3,191,394,172 / 28.17%
Number/percentage of C's	2,466,425,700 / 21.77%
Number/percentage of T's	3,243,316,863 / 28.63%
Number/percentage of G's	2,426,656,583 / 21.42%
Number/percentage of N's	1,165,444 / 0.01%

GC Percentage	43.19%

2.3. Coverage

Mean	3.66
Standard Deviation	25.2172

2.4. Mapping Quality

Mean Mapping Quality	53.69

2.5. Insert size

Mean	14,786.04
Standard Deviation	1,205,681.52
P25/Median/P75	189 / 246 / 318

2.6. Mismatches and indels

General error rate	0.42%
Mismatches	46,957,779
Insertions	506,806
Mapped reads with at least one insertion	0.44%
Deletions	600,576
Mapped reads with at least one deletion	0.52%
Homopolymer indels	46.15%

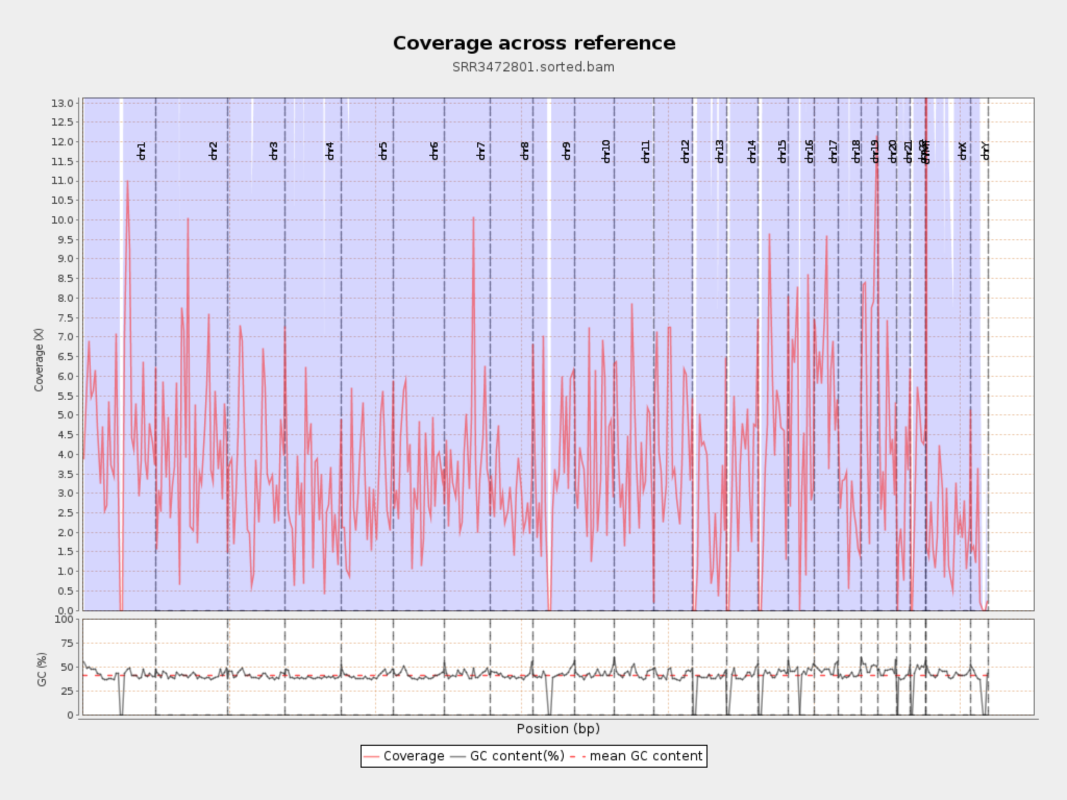
2.7. Chromosome stats

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

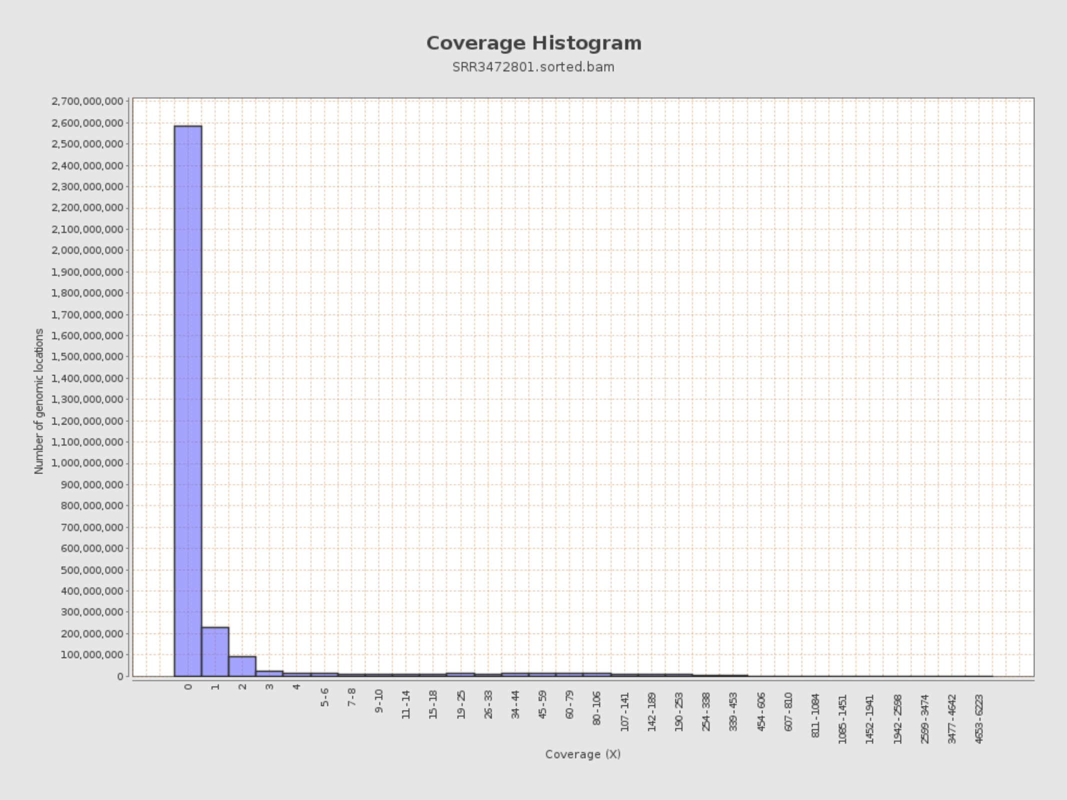
		bases	coverage	deviation
chr1	249250621	1162649034	4.6646	29.9454
chr2	243199373	1030155763	4.2358	30.3972
chr3	198022430	705838102	3.5644	24.0972
chr4	191154276	540913339	2.8297	21.9981
chr5	180915260	564406763	3.1197	22.6789
chr6	171115067	586475127	3.4274	23.883
chr7	159138663	621872725	3.9077	27.481
chr8	146364022	419990775	2.8695	21.8487
chr9	141213431	495251936	3.5071	25.386
chr10	135534747	520652296	3.8415	26.8032
chr11	135006516	538416580	3.9881	24.075
chr12	133851895	604512009	4.5163	26.5842
chr13	115169878	270685145	2.3503	20.5851
chr14	107349540	359509809	3.349	23.9463
chr15	102531392	408566136	3.9848	25.3477
chr16	90354753	407970523	4.5152	28.5413
chr17	81195210	515296977	6.3464	30.0381
chr18	78077248	201871869	2.5855	20.5652
chr19	59128983	430149849	7.2748	31.3424
chr20	63025520	258933452	4.1084	25.4883
chr21	48129895	129673293	2.6942	23.7792
chr22	51304566	176186281	3.4341	22.2123
chrMT	16571	2231736	134.6772	381.6118
chrX	155270560	316215340	2.0365	16.4082

chrY	59373566	61944780	1.0433	16.104

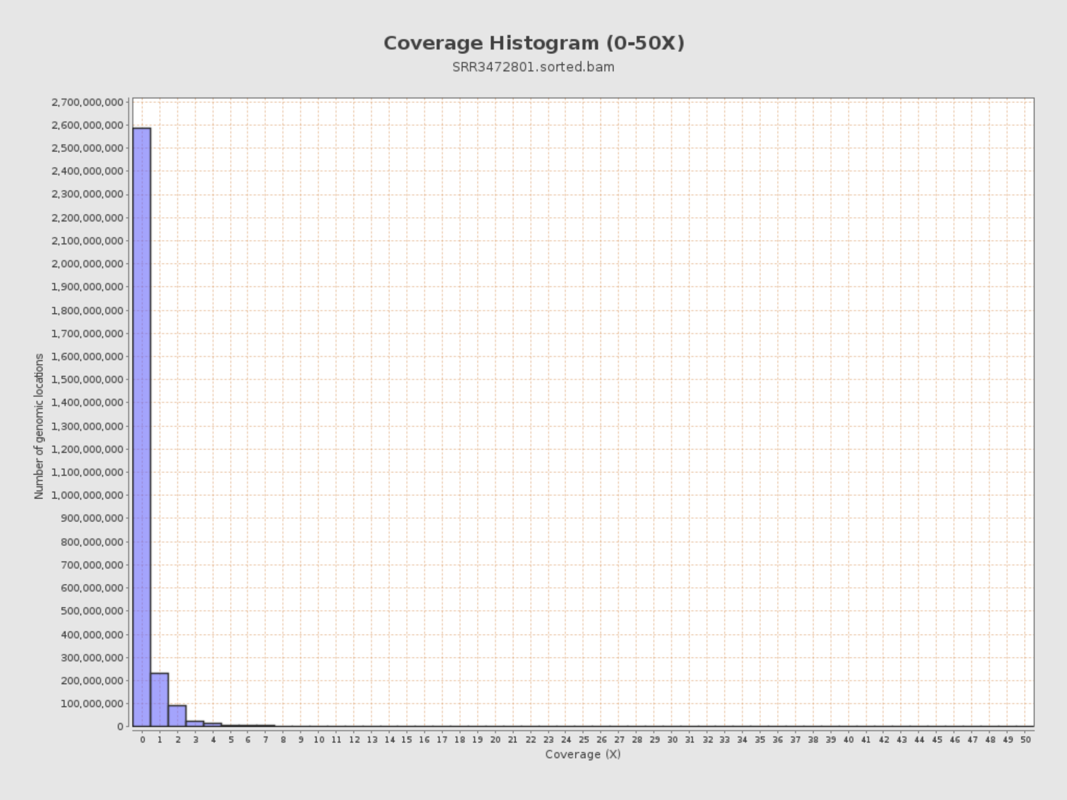
3. Results : Coverage across reference



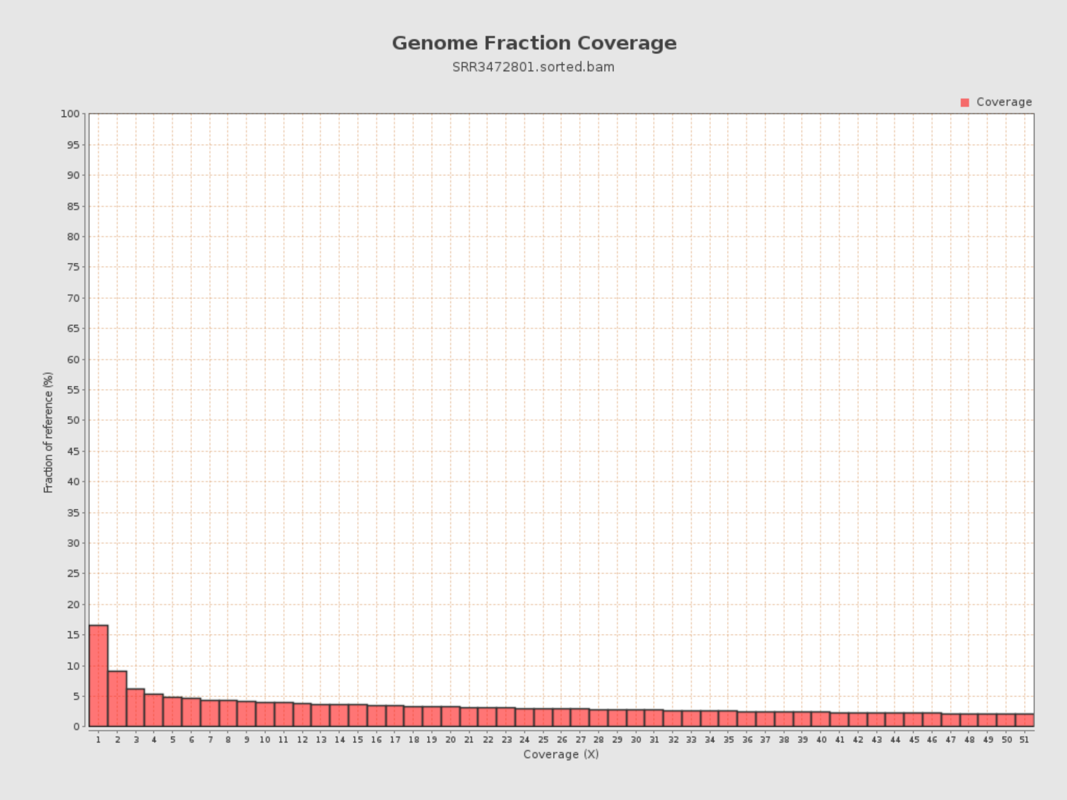
4. Results : Coverage Histogram



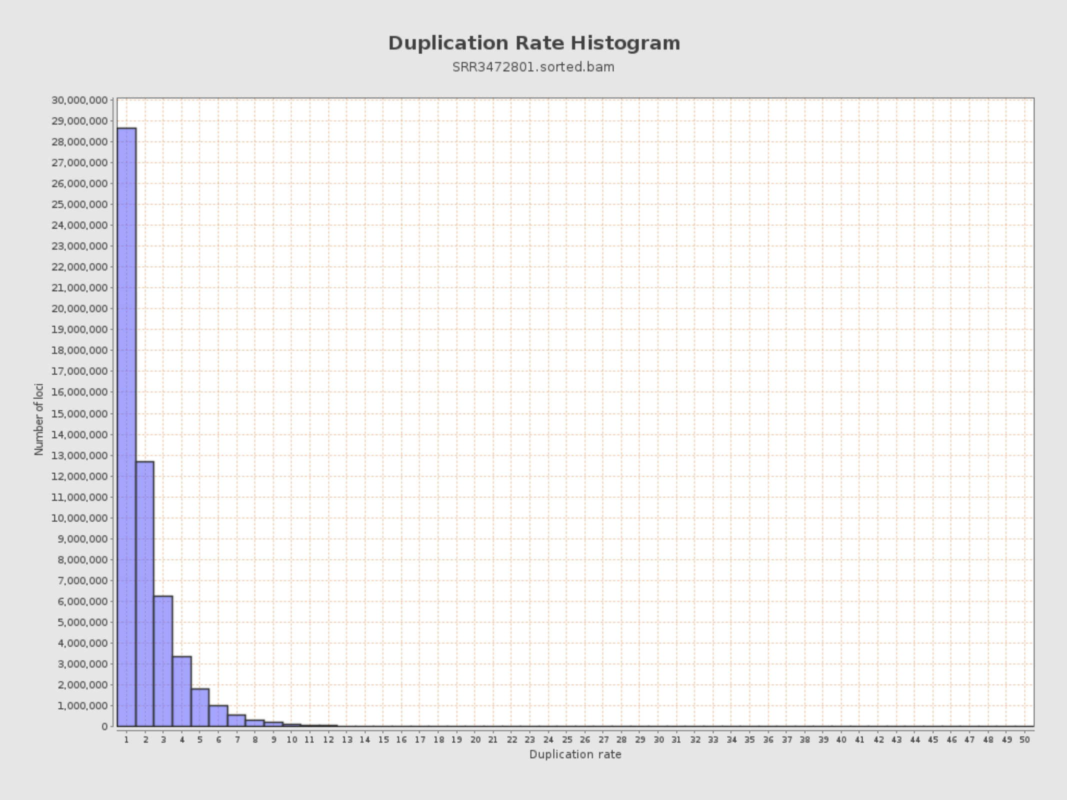
5. Results : Coverage Histogram (0-50X)



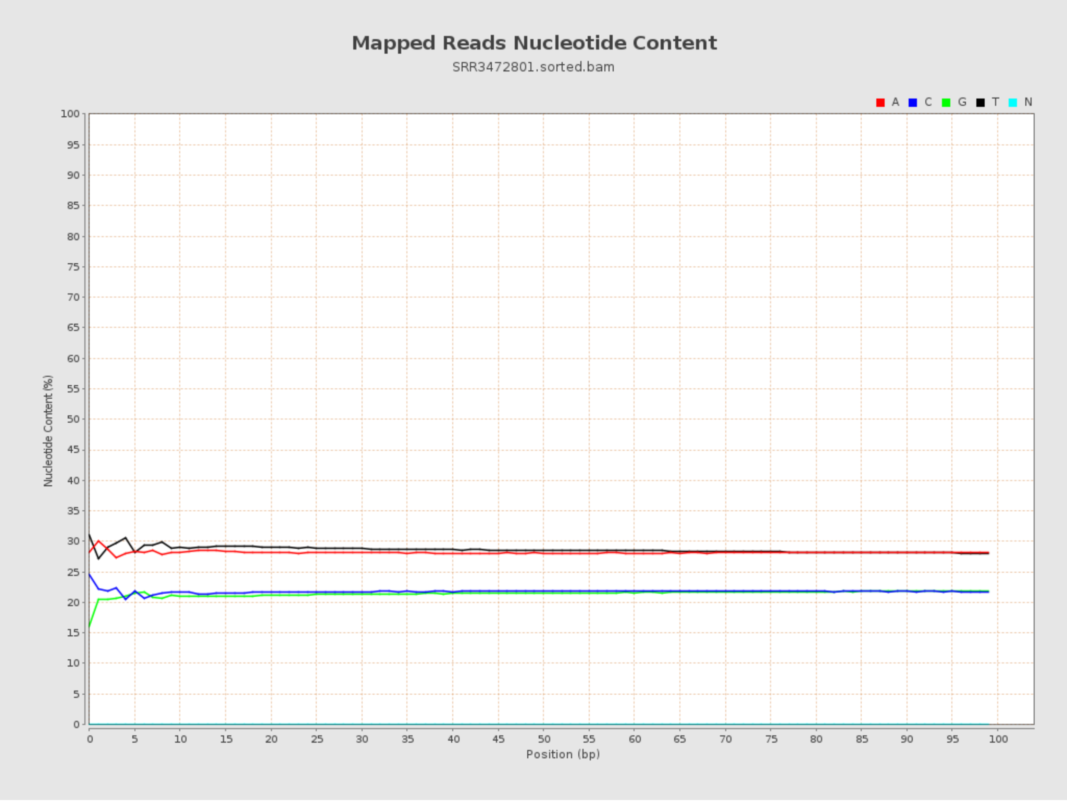
6. Results : Genome Fraction Coverage



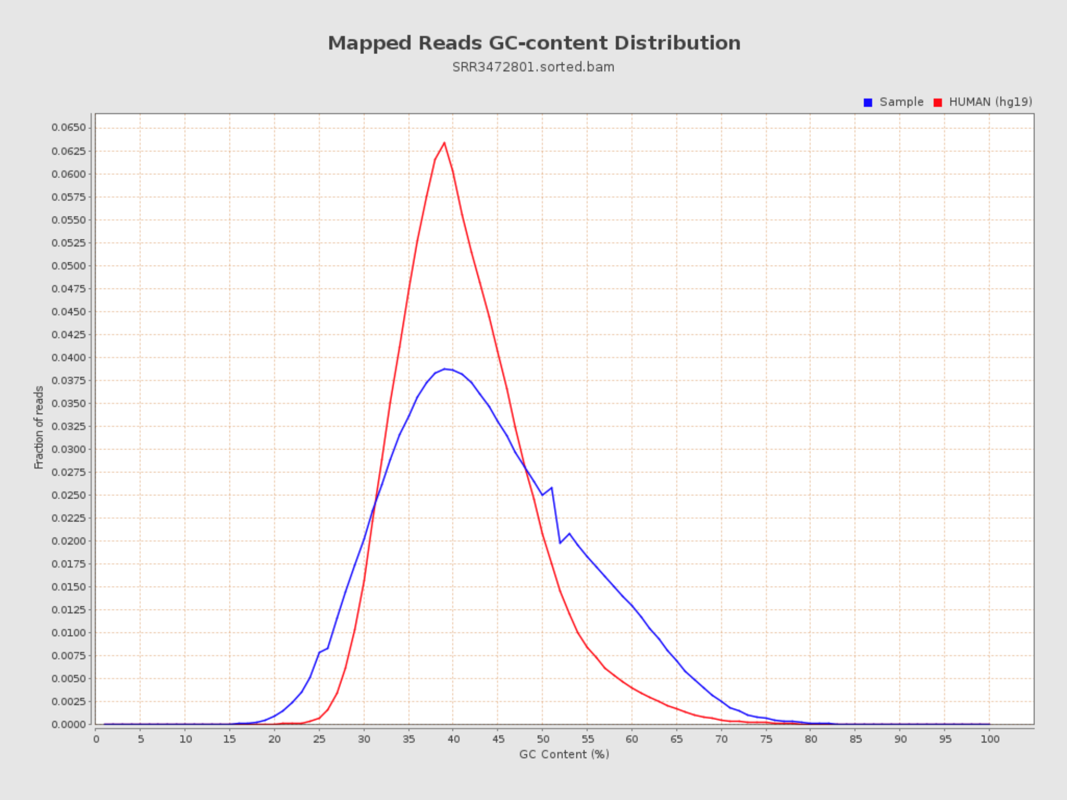
7. Results : Duplication Rate Histogram



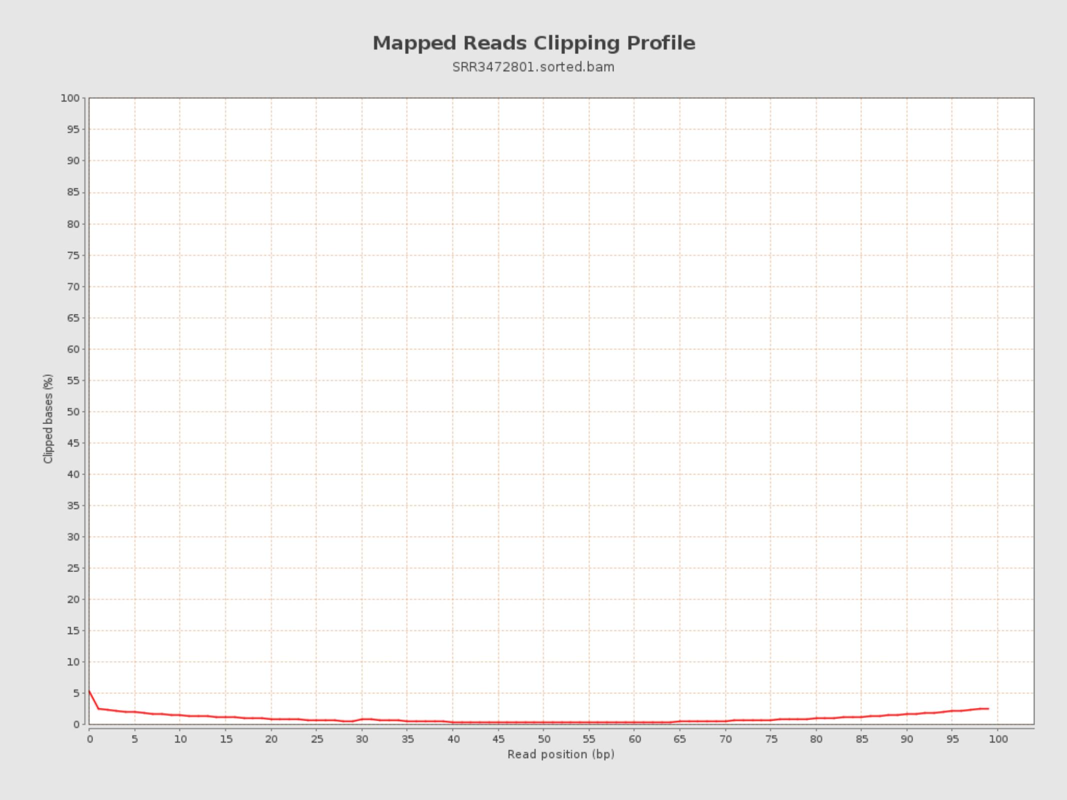
8. Results : Mapped Reads Nucleotide Content



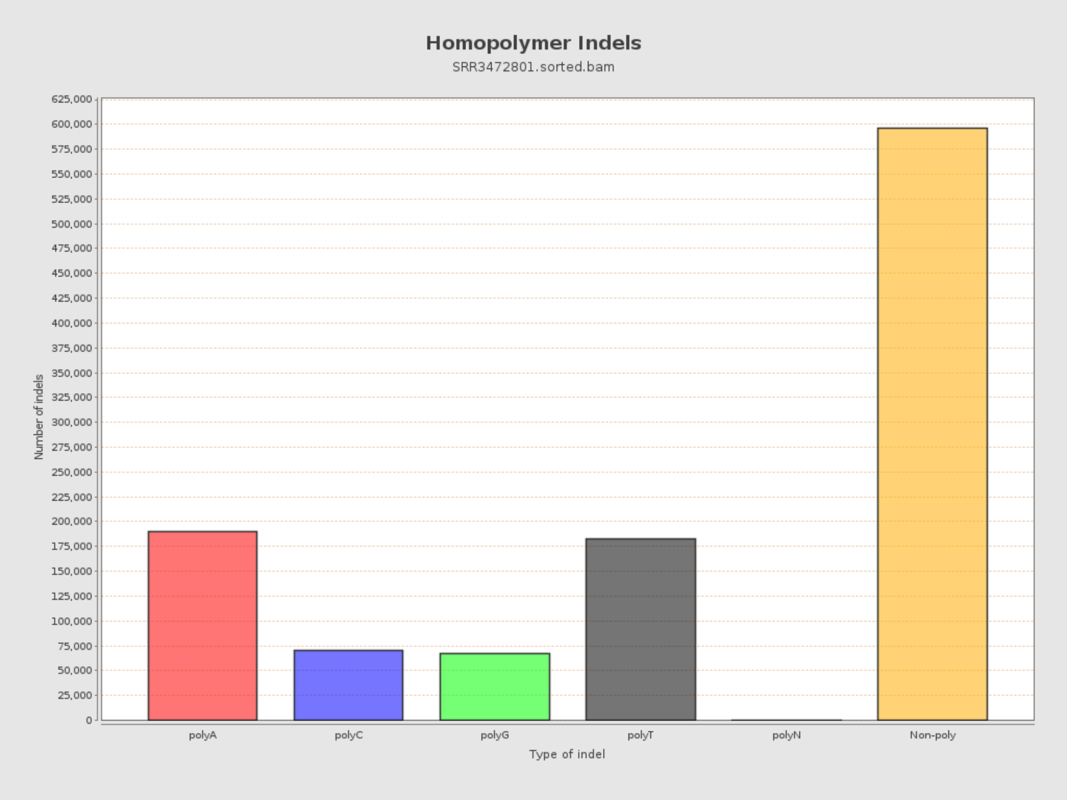
9. Results : Mapped Reads GC-content Distribution



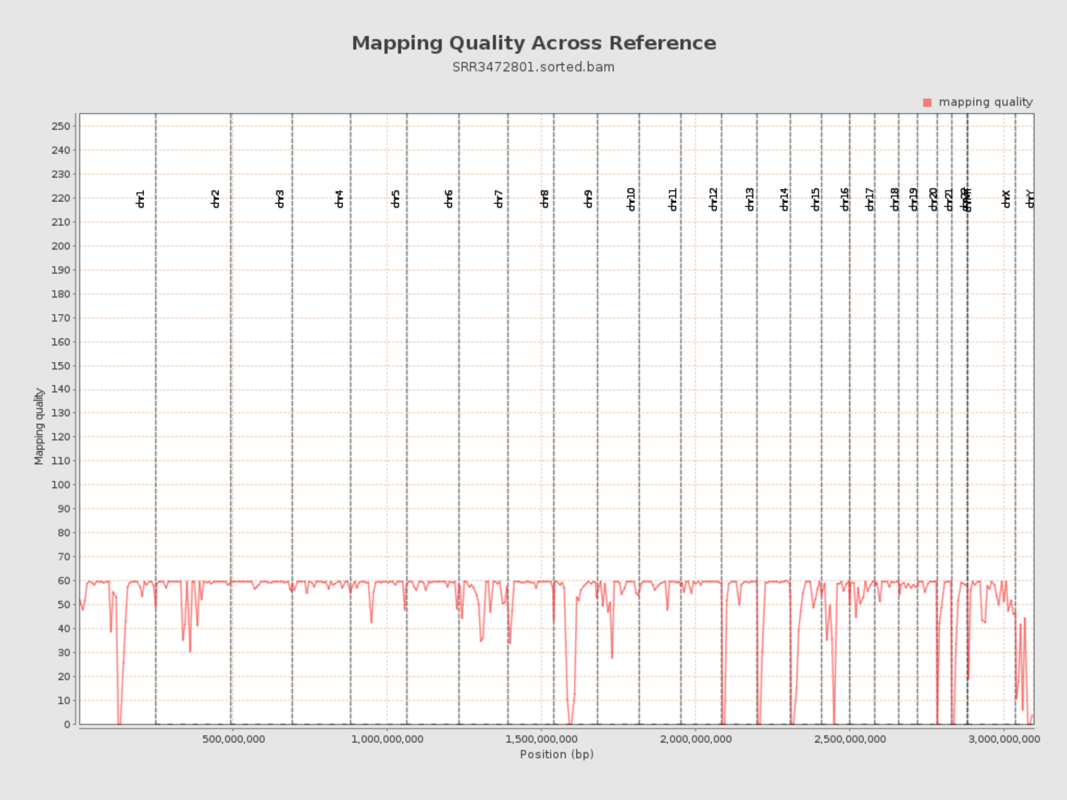
10. Results : Mapped Reads Clipping Profile



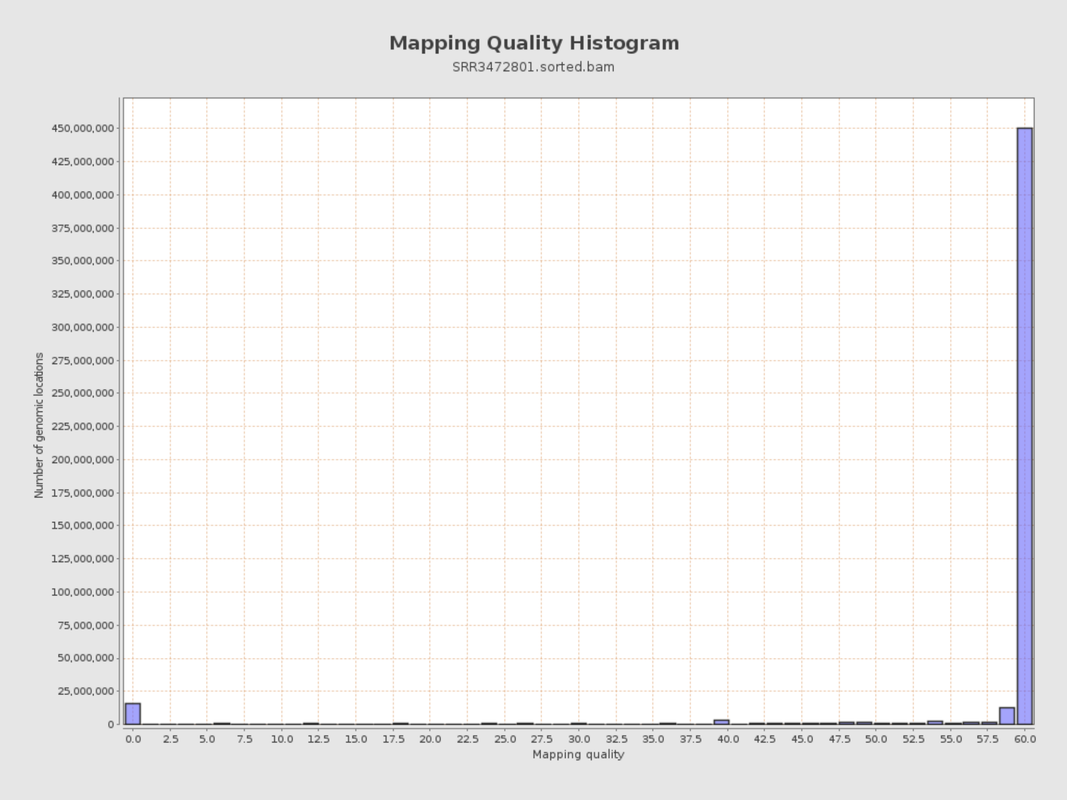
11. Results : Homopolymer Indels



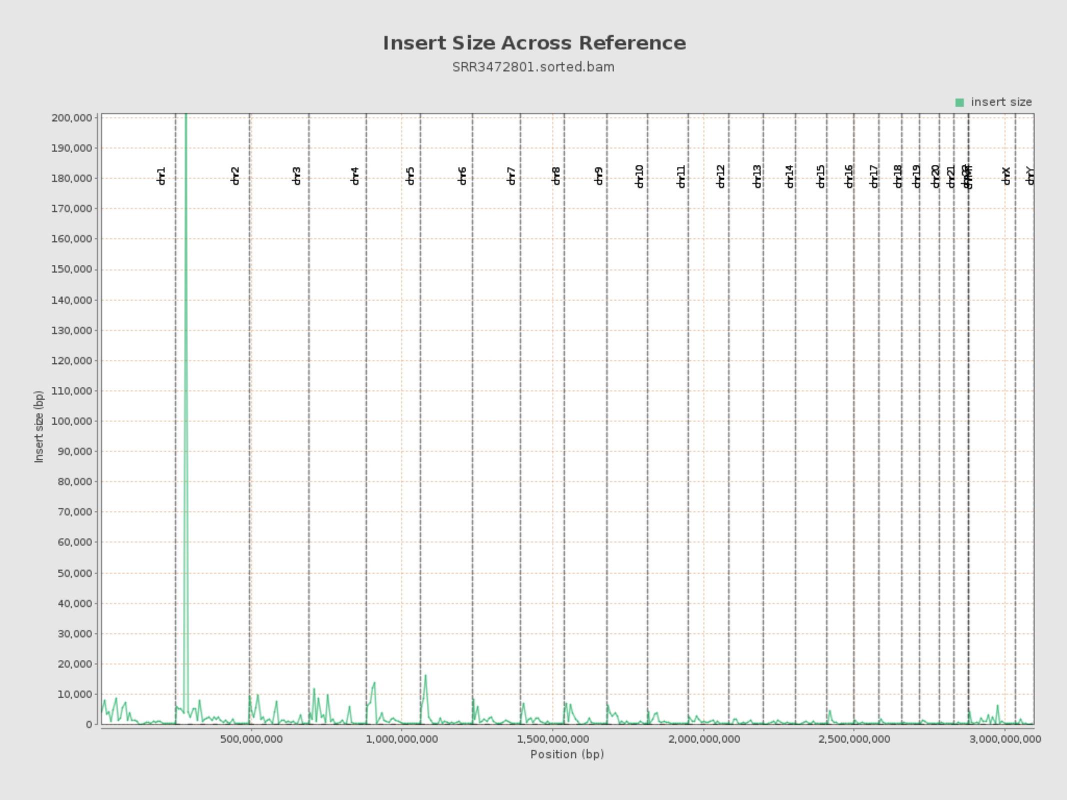
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram