Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 18:29:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472717.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_SRR3472717 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472717_1.fastq.gz SRR3472717_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 18:29:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472717.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,407,296
Mapped reads	17,170,728 / 98.64%
Unmapped reads	236,568 / 1.36%
Mapped paired reads	17,170,728 / 98.64%
Mapped reads, first in pair	8,628,210 / 49.57%
Mapped reads, second in pair	8,542,518 / 49.07%
Mapped reads, both in pair	17,044,884 / 97.92%
Mapped reads, singletons	125,844 / 0.72%
Secondary alignments	0
Supplementary alignments	62,538 / 0.36%
Read min/max/mean length	30 / 100 / 100.15
Duplicated reads (estimated)	10,719,494 / 61.58%
Duplication rate	46.8%
Clipped reads	1,473,436 / 8.46%

2.2. ACGT Content

Number/percentage of A's	467,993,812 / 27.72%
Number/percentage of C's	379,179,108 / 22.46%
Number/percentage of T's	464,568,708 / 27.51%
Number/percentage of G's	376,499,132 / 22.3%
Number/percentage of N's	326,924 / 0.02%

GC Percentage	44.75%

2.3. Coverage

Mean	0.5455
Standard Deviation	17.7463

2.4. Mapping Quality

Mean Mapping Quality	55.11

2.5. Insert size

Mean	25,473.16
Standard Deviation	1,593,380.26
P25/Median/P75	171 / 242 / 328

2.6. Mismatches and indels

General error rate	0.65%
Mismatches	10,805,940
Insertions	102,955
Mapped reads with at least one insertion	0.59%
Deletions	96,740
Mapped reads with at least one deletion	0.56%
Homopolymer indels	45.91%

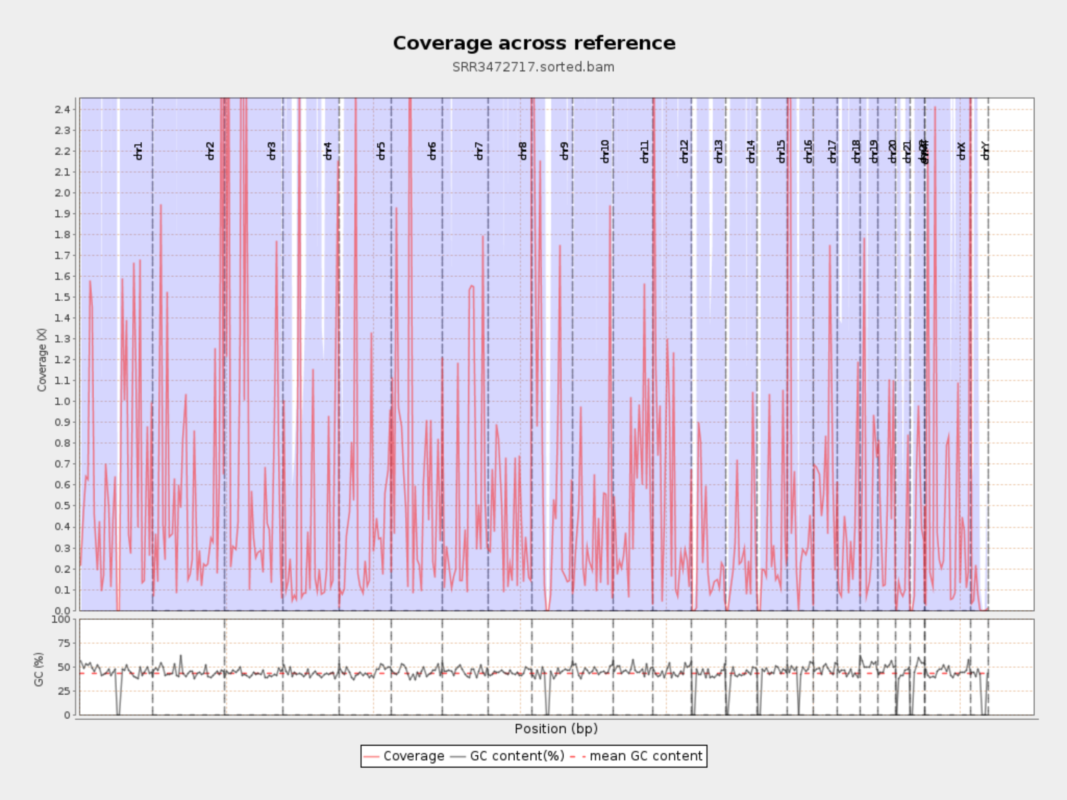
2.7. Chromosome stats

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

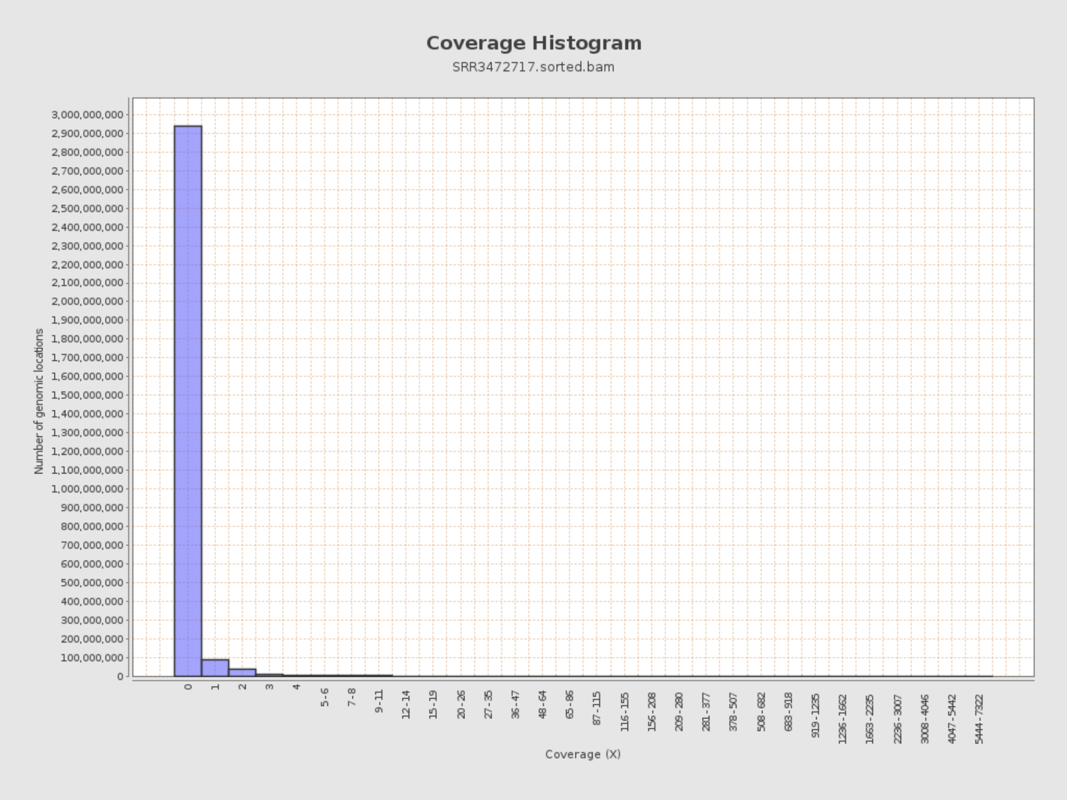
		bases	coverage	deviation
chr1	249250621	160505962	0.644	17.9426
chr2	243199373	136366274	0.5607	23.6684
chr3	198022430	185525729	0.9369	20.5822
chr4	191154276	83502865	0.4368	17.7133
chr5	180915260	85780106	0.4741	15.3717
chr6	171115067	120121906	0.702	20.0793
chr7	159138663	93987792	0.5906	21.3782
chr8	146364022	59322850	0.4053	10.8246
chr9	141213431	111773598	0.7915	21.1058
chr10	135534747	57580844	0.4248	20.43
chr11	135006516	77351143	0.5729	20.3624
chr12	133851895	85950404	0.6421	17.6802
chr13	115169878	28976650	0.2516	8.0842
chr14	107349540	29338925	0.2733	12.9658
chr15	102531392	31099995	0.3033	10.0156
chr16	90354753	69793853	0.7724	22.3263
chr17	81195210	54860924	0.6757	15.7972
chr18	78077248	26480588	0.3392	10.306
chr19	59128983	37369602	0.632	16.5435
chr20	63025520	34960612	0.5547	13.7993
chr21	48129895	10239181	0.2127	9.423
chr22	51304566	19020301	0.3707	11.9458
chrMT	16571	8345	0.5036	1.7175
chrX	155270560	85915591	0.5533	17.2169

chrY	59373566	2970992	0.05	2.2633

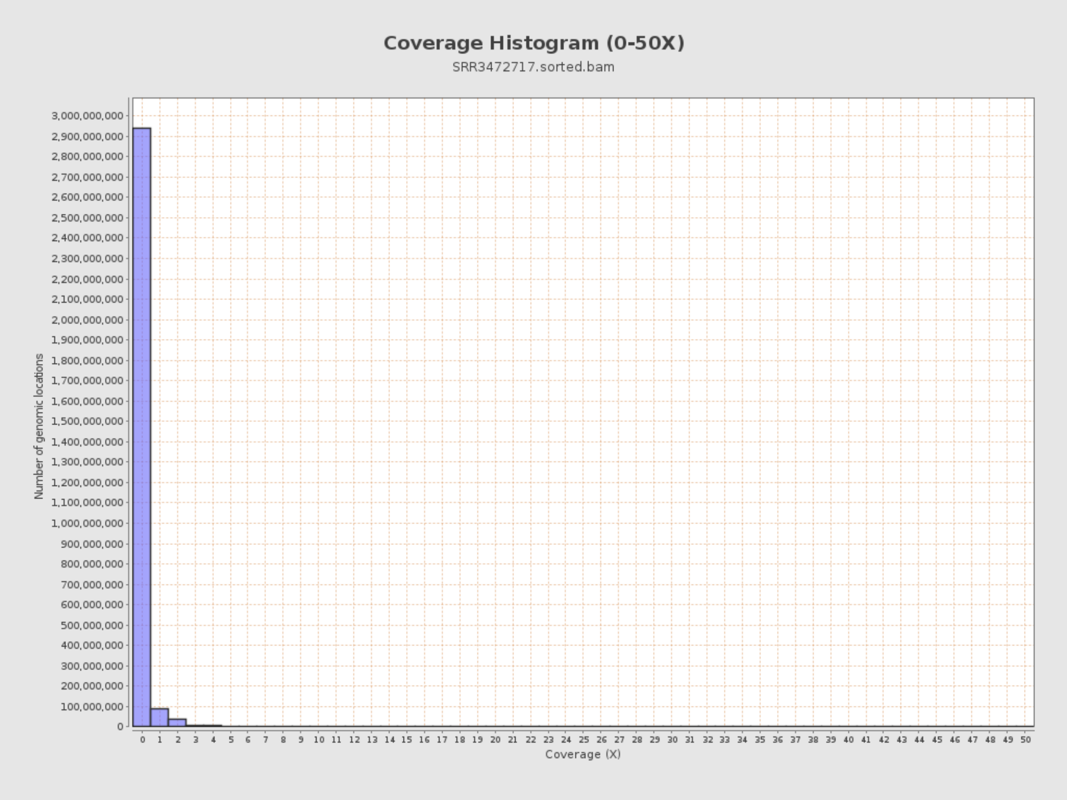
3. Results : Coverage across reference



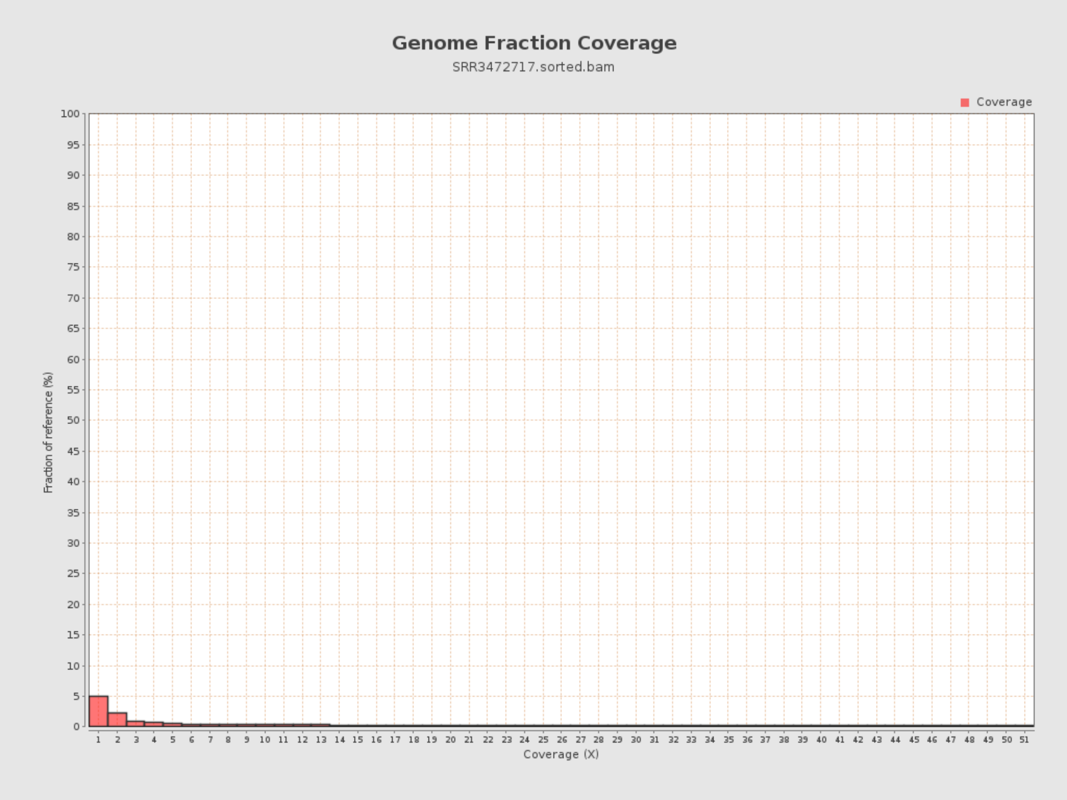
4. Results : Coverage Histogram



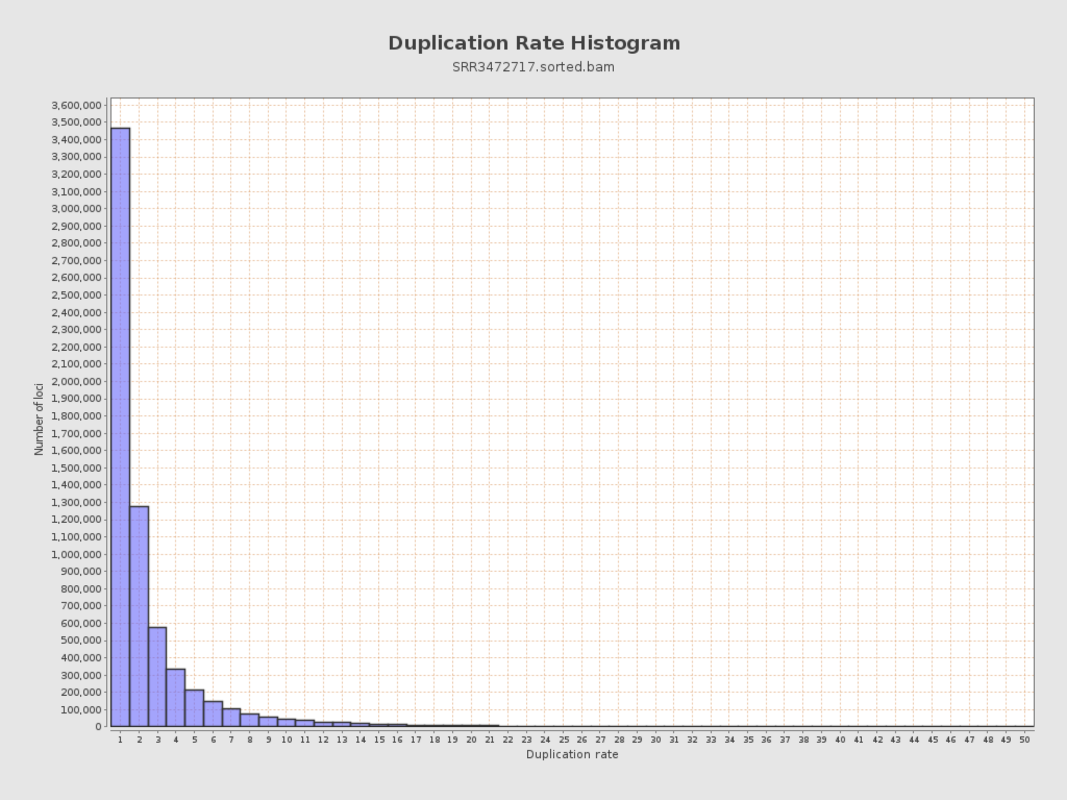
5. Results : Coverage Histogram (0-50X)



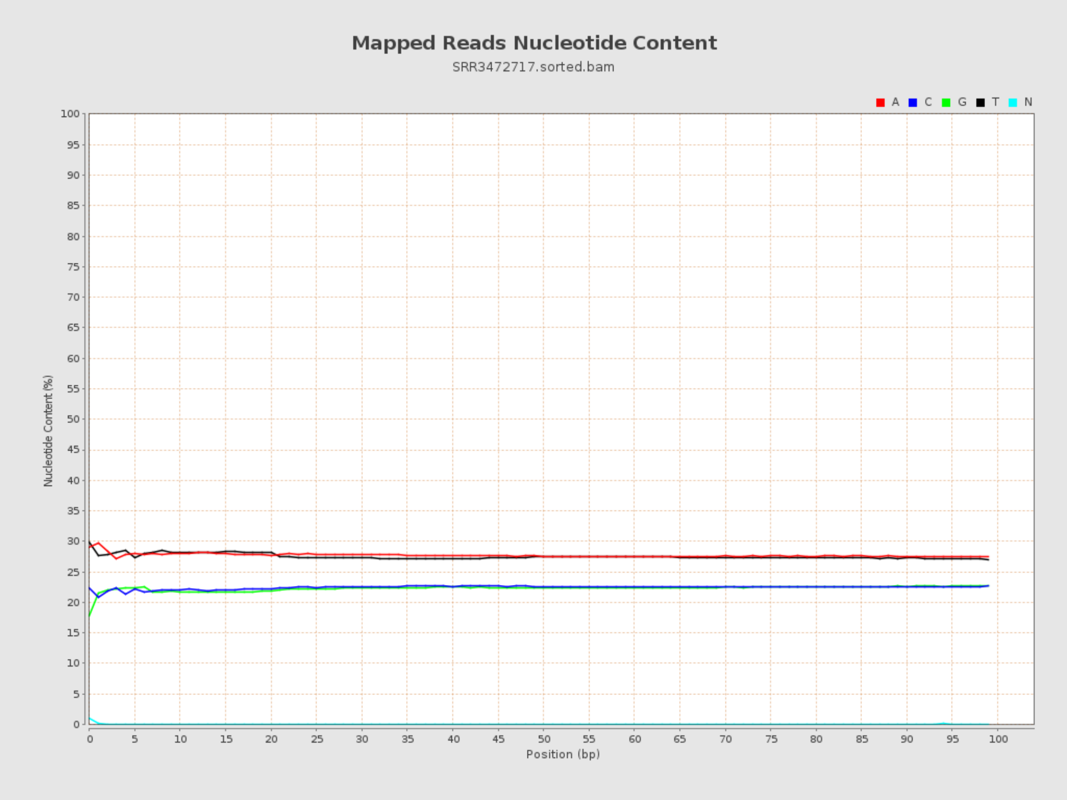
6. Results : Genome Fraction Coverage



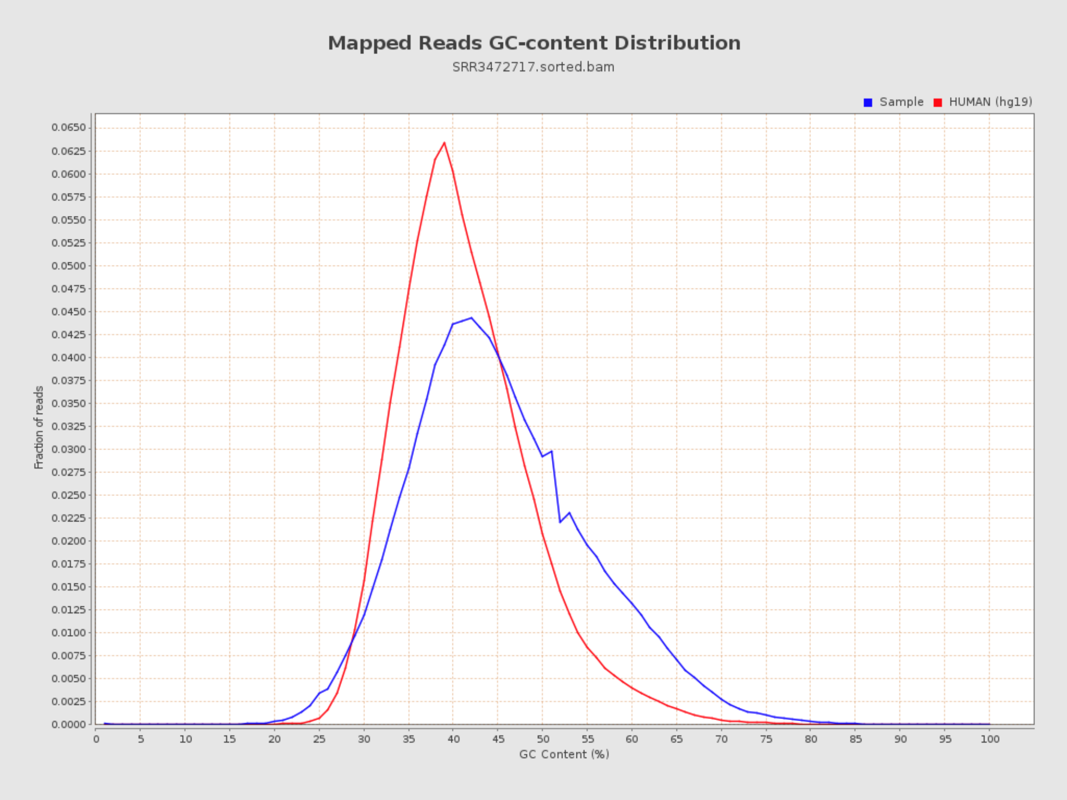
7. Results : Duplication Rate Histogram



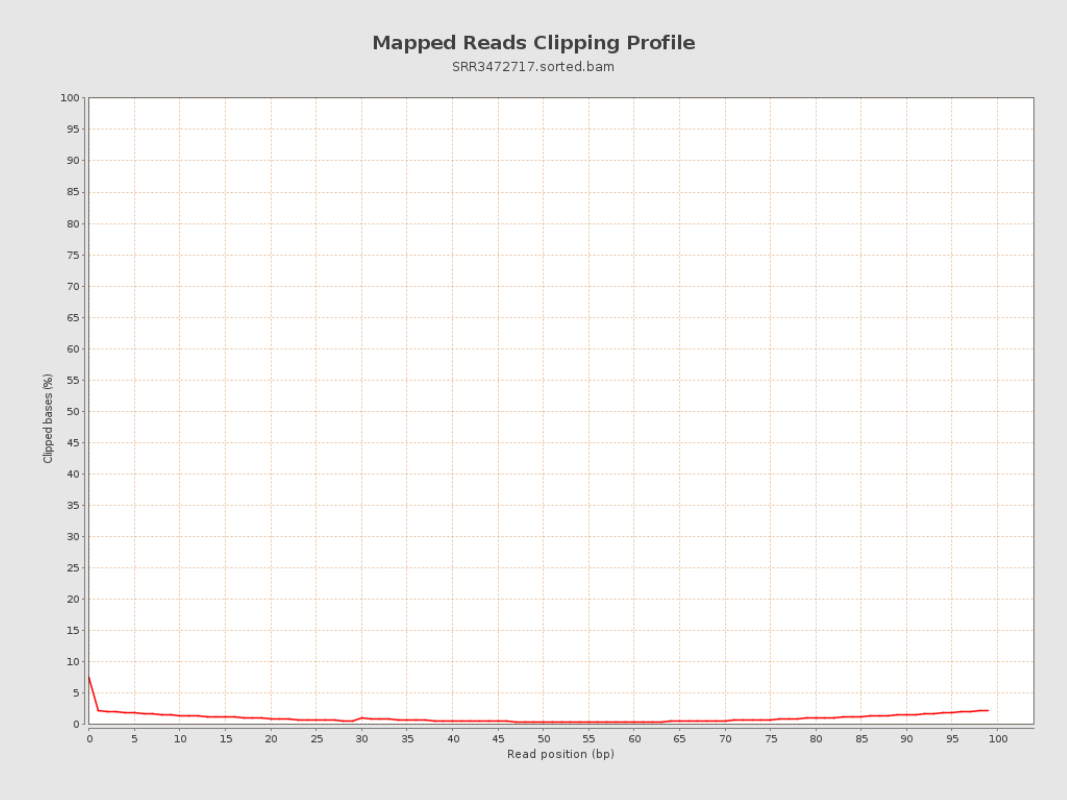
8. Results : Mapped Reads Nucleotide Content



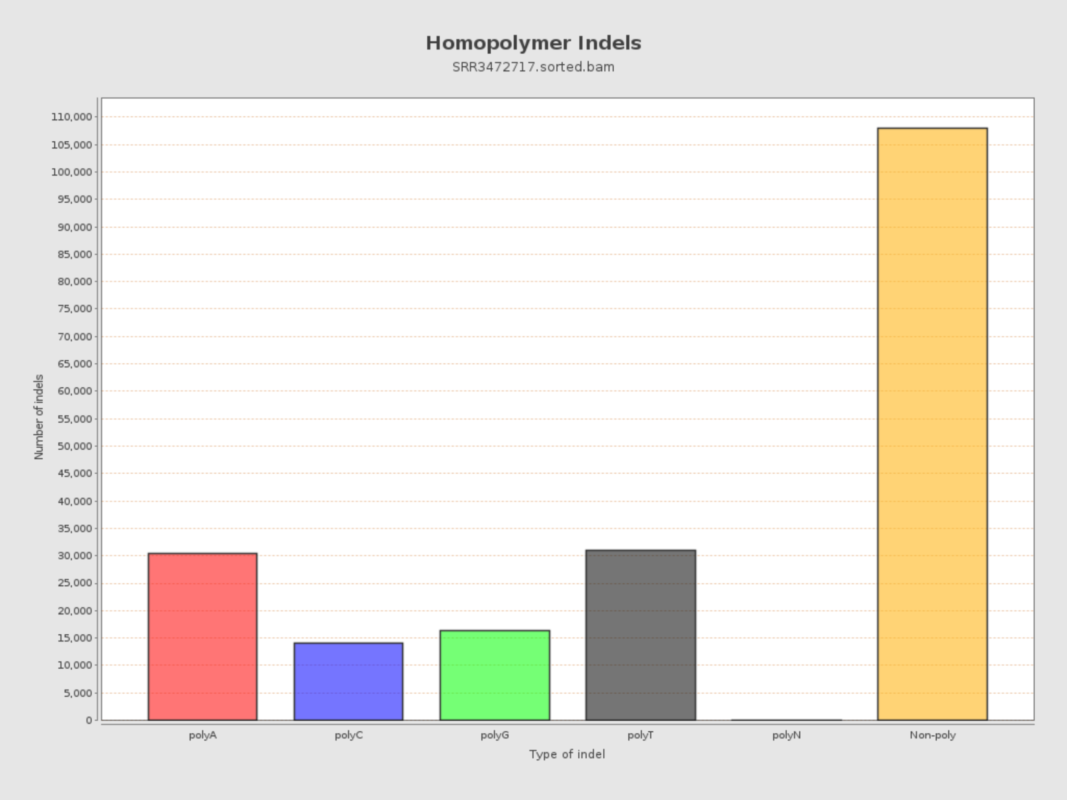
9. Results : Mapped Reads GC-content Distribution



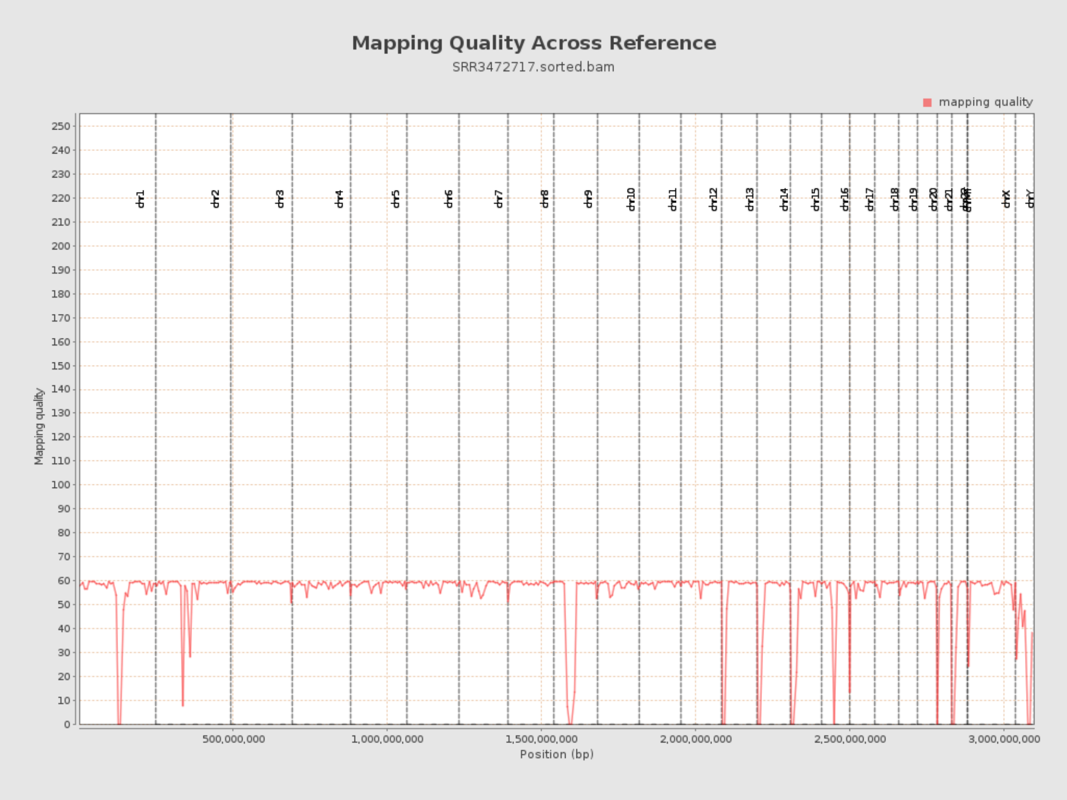
10. Results : Mapped Reads Clipping Profile



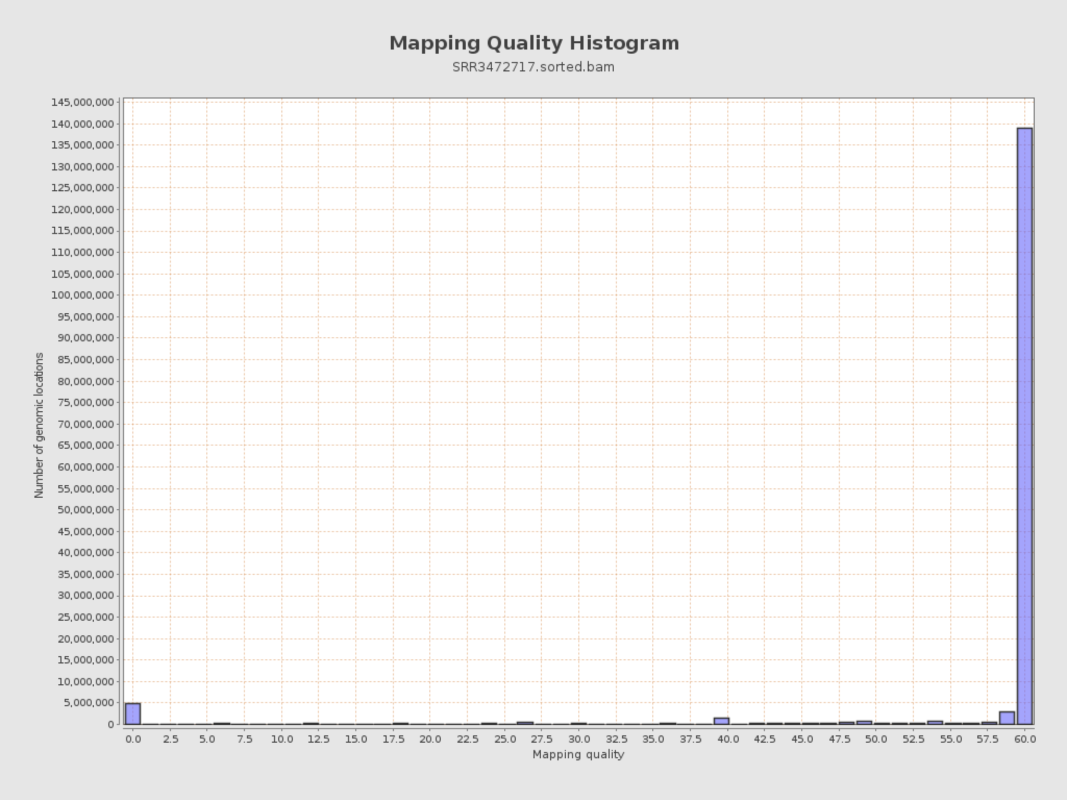
11. Results : Homopolymer Indels



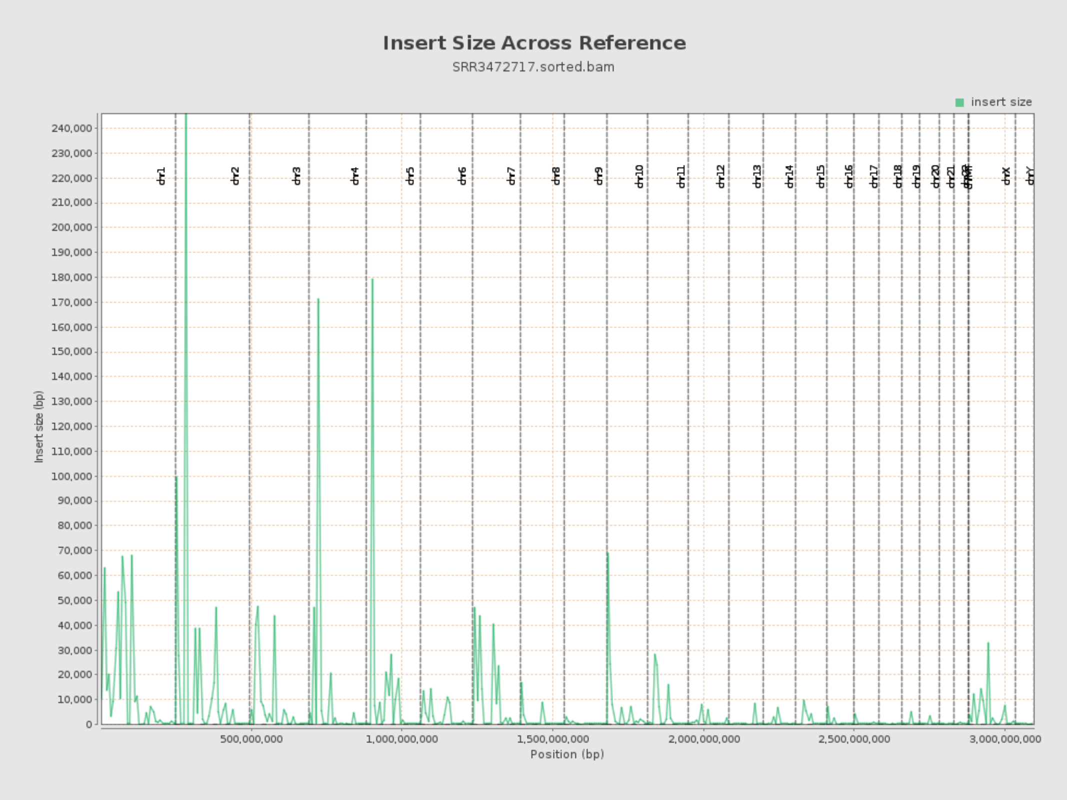
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram