Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 19:14:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472517.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_SRR3472517 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472517_1.fastq.gz SRR3472517_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 19:14:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472517.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,398,428
Mapped reads	16,242,854 / 99.05%
Unmapped reads	155,574 / 0.95%
Mapped paired reads	16,242,854 / 99.05%
Mapped reads, first in pair	8,141,194 / 49.65%
Mapped reads, second in pair	8,101,660 / 49.41%
Mapped reads, both in pair	16,162,800 / 98.56%
Mapped reads, singletons	80,054 / 0.49%
Secondary alignments	0
Supplementary alignments	68,014 / 0.41%
Read min/max/mean length	30 / 100 / 100.17
Duplicated reads (estimated)	10,192,754 / 62.16%
Duplication rate	46.11%
Clipped reads	1,490,109 / 9.09%

2.2. ACGT Content

Number/percentage of A's	434,122,642 / 27.19%
Number/percentage of C's	366,534,419 / 22.96%
Number/percentage of T's	431,374,354 / 27.02%
Number/percentage of G's	364,084,459 / 22.81%
Number/percentage of N's	248,451 / 0.02%

GC Percentage	45.77%

2.3. Coverage

Mean	0.5157
Standard Deviation	19.0209

2.4. Mapping Quality

Mean Mapping Quality	55.04

2.5. Insert size

Mean	32,717.44
Standard Deviation	1,790,256
P25/Median/P75	159 / 223 / 302

2.6. Mismatches and indels

General error rate	0.58%
Mismatches	9,020,417
Insertions	85,046
Mapped reads with at least one insertion	0.52%
Deletions	76,577
Mapped reads with at least one deletion	0.47%
Homopolymer indels	44.78%

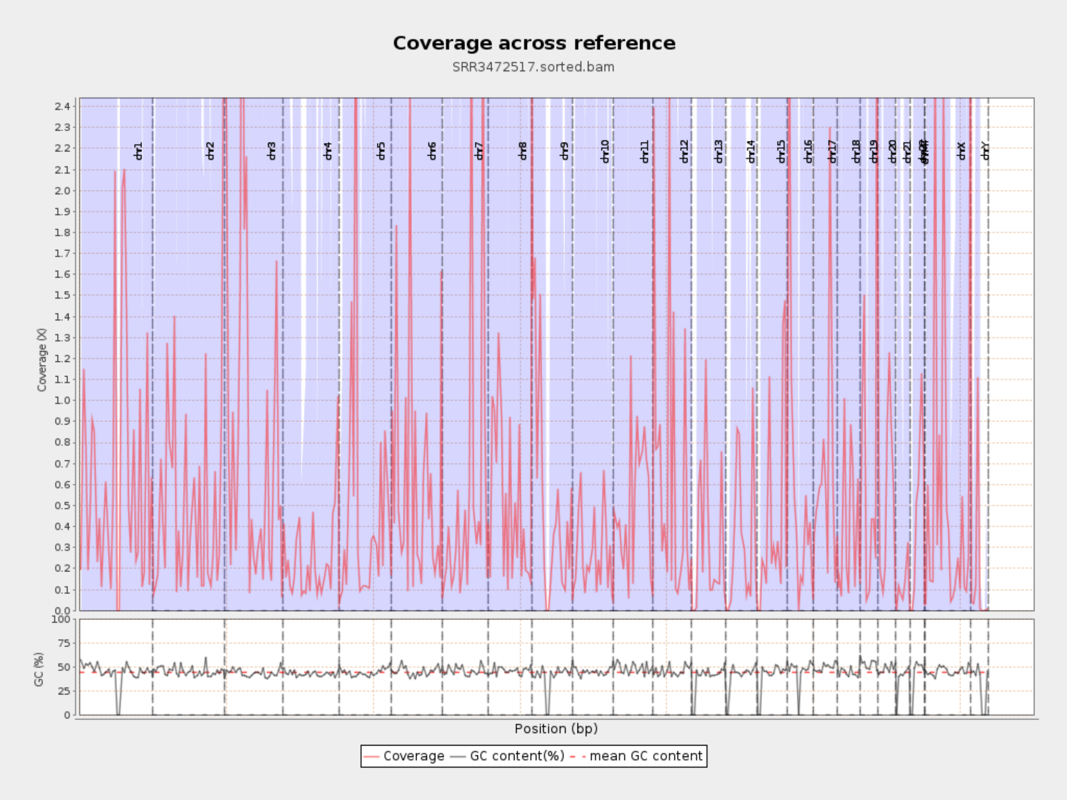
2.7. Chromosome stats

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

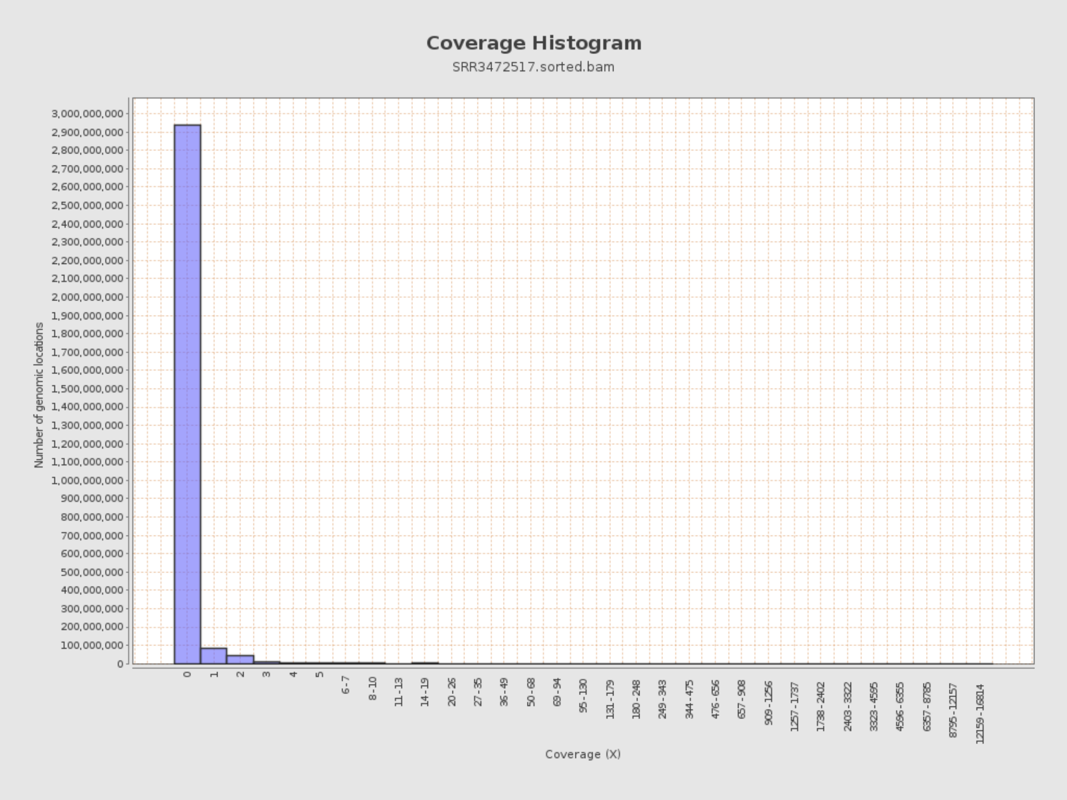
		bases	coverage	deviation
chr1	249250621	158976197	0.6378	26.0369
chr2	243199373	121644439	0.5002	17.6693
chr3	198022430	180239827	0.9102	21.2026
chr4	191154276	46505585	0.2433	9.3577
chr5	180915260	89818037	0.4965	16.6725
chr6	171115067	104743229	0.6121	17.6435
chr7	159138663	92284713	0.5799	26.4781
chr8	146364022	74928887	0.5119	18.3522
chr9	141213431	75233999	0.5328	13.121
chr10	135534747	37835797	0.2792	10.2565
chr11	135006516	69480486	0.5146	16.9739
chr12	133851895	93270053	0.6968	29.2318
chr13	115169878	36889576	0.3203	12.2188
chr14	107349540	35434755	0.3301	12.1832
chr15	102531392	45009476	0.439	14.1243
chr16	90354753	53202607	0.5888	15.5542
chr17	81195210	52685426	0.6489	20.2259
chr18	78077248	31361873	0.4017	17.3443
chr19	59128983	36008033	0.609	16.2452
chr20	63025520	35351315	0.5609	18.2833
chr21	48129895	5897122	0.1225	4.5016
chr22	51304566	23962523	0.4671	17.9865
chrMT	16571	1269	0.0766	0.2952
chrX	155270560	85650737	0.5516	26.3318

chrY	59373566	10127006	0.1706	17.8604

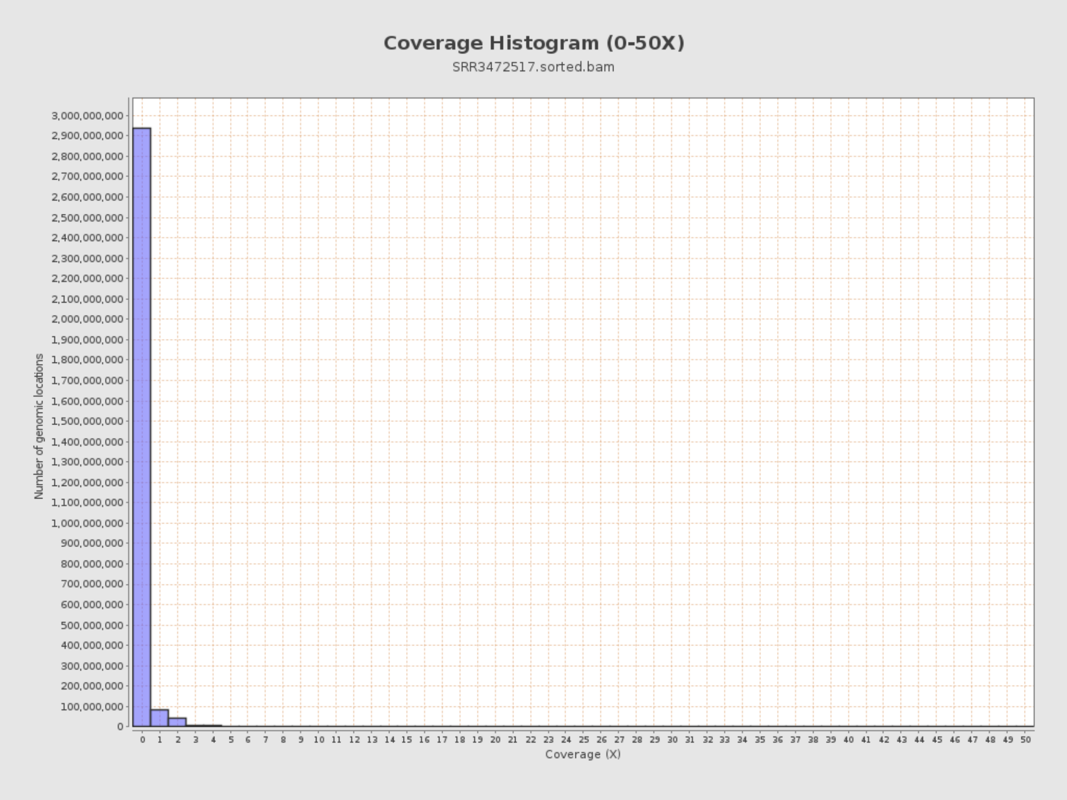
3. Results : Coverage across reference



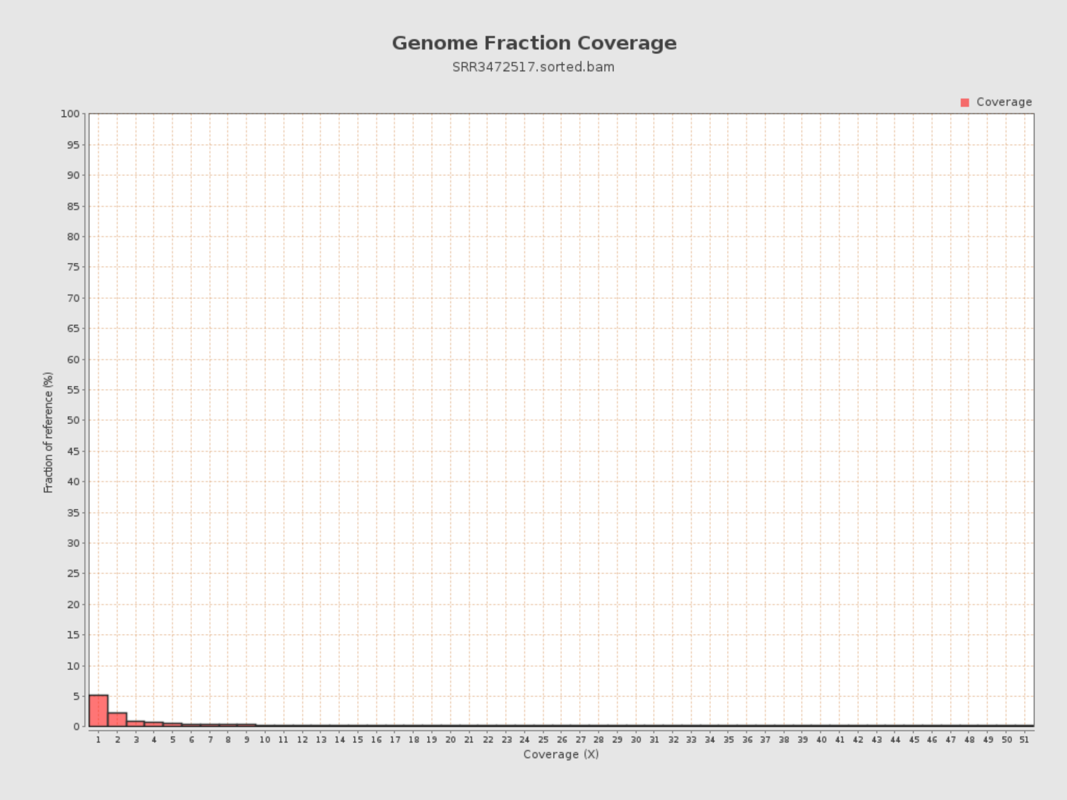
4. Results : Coverage Histogram



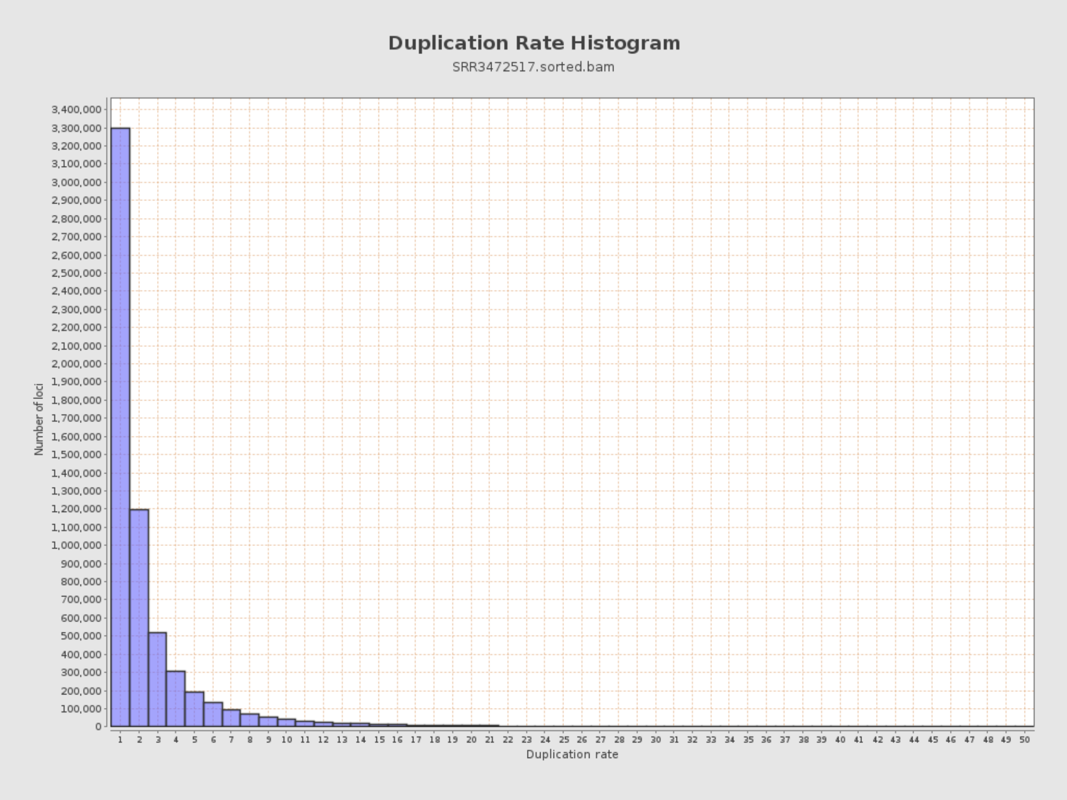
5. Results : Coverage Histogram (0-50X)



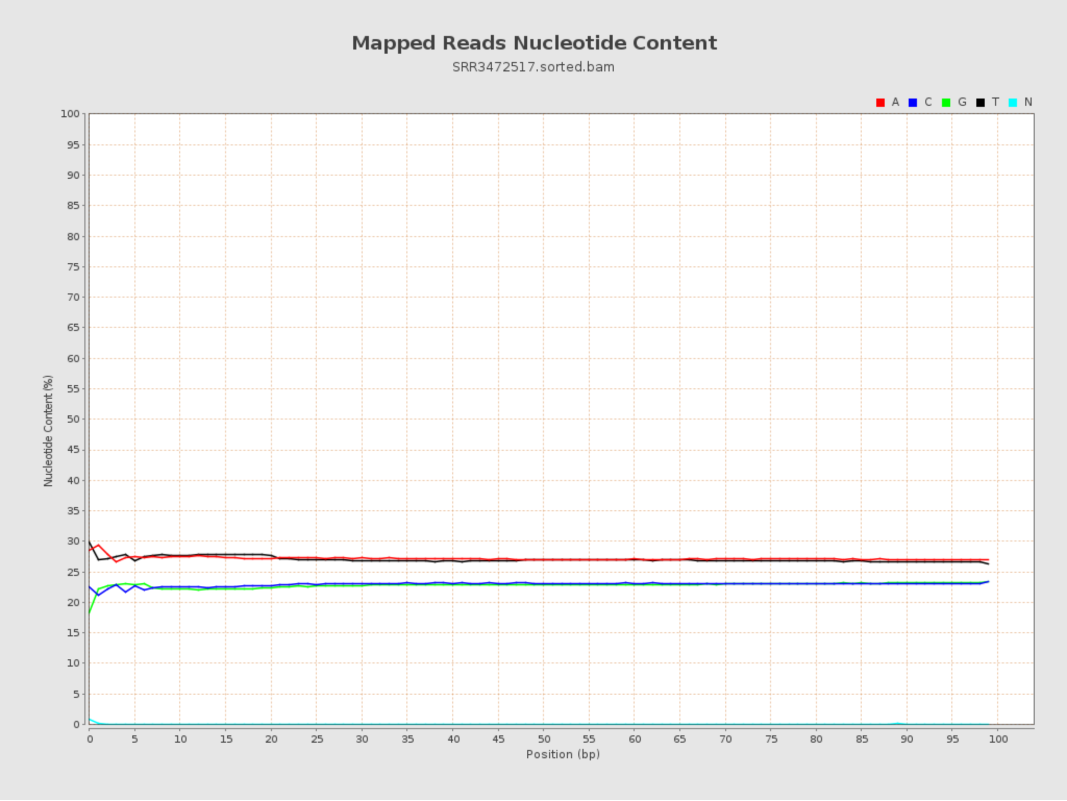
6. Results : Genome Fraction Coverage



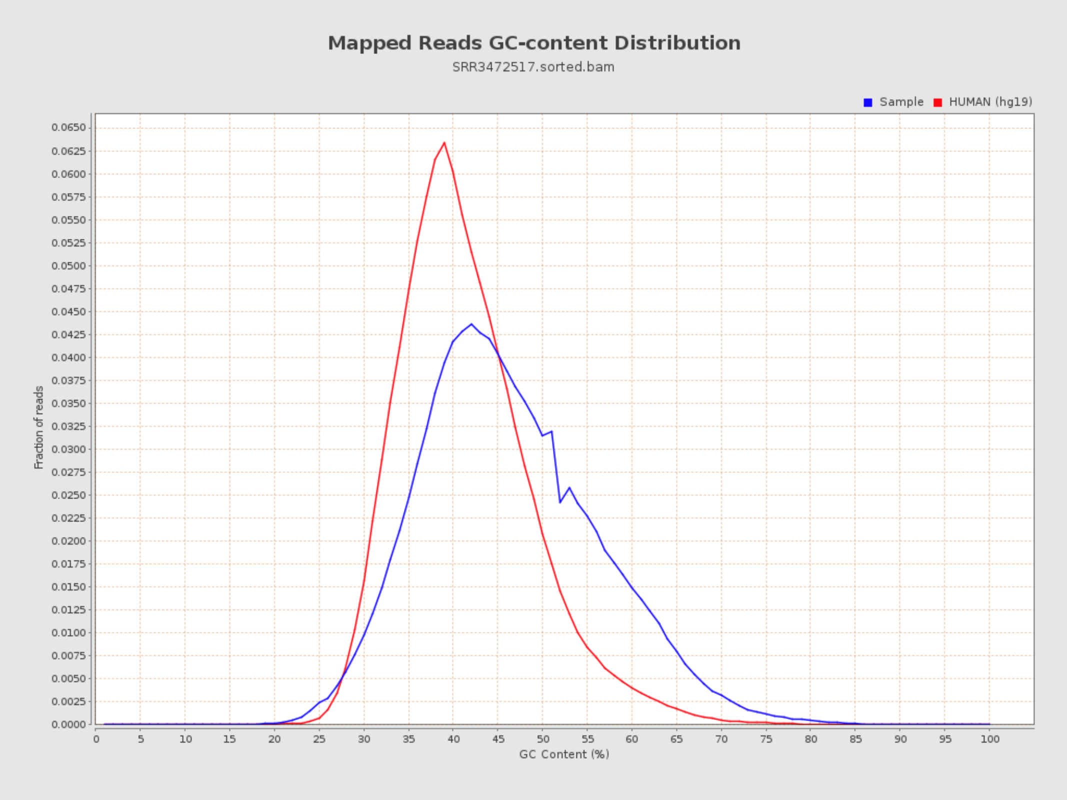
7. Results : Duplication Rate Histogram



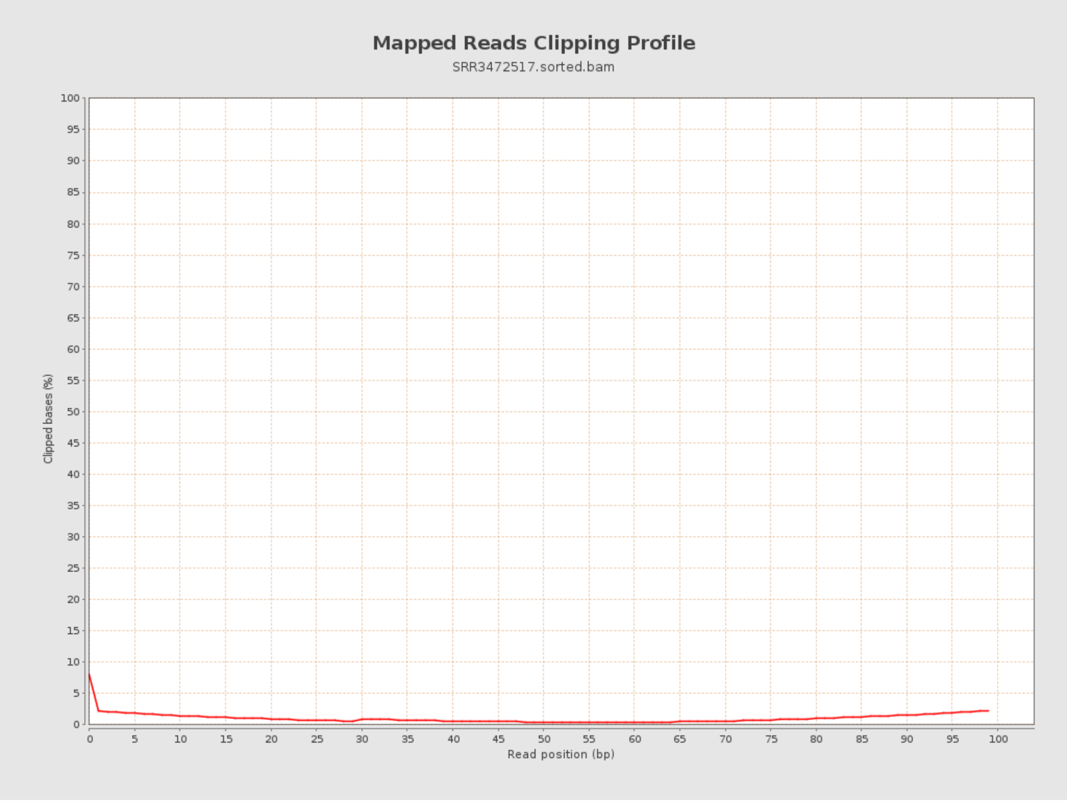
8. Results : Mapped Reads Nucleotide Content



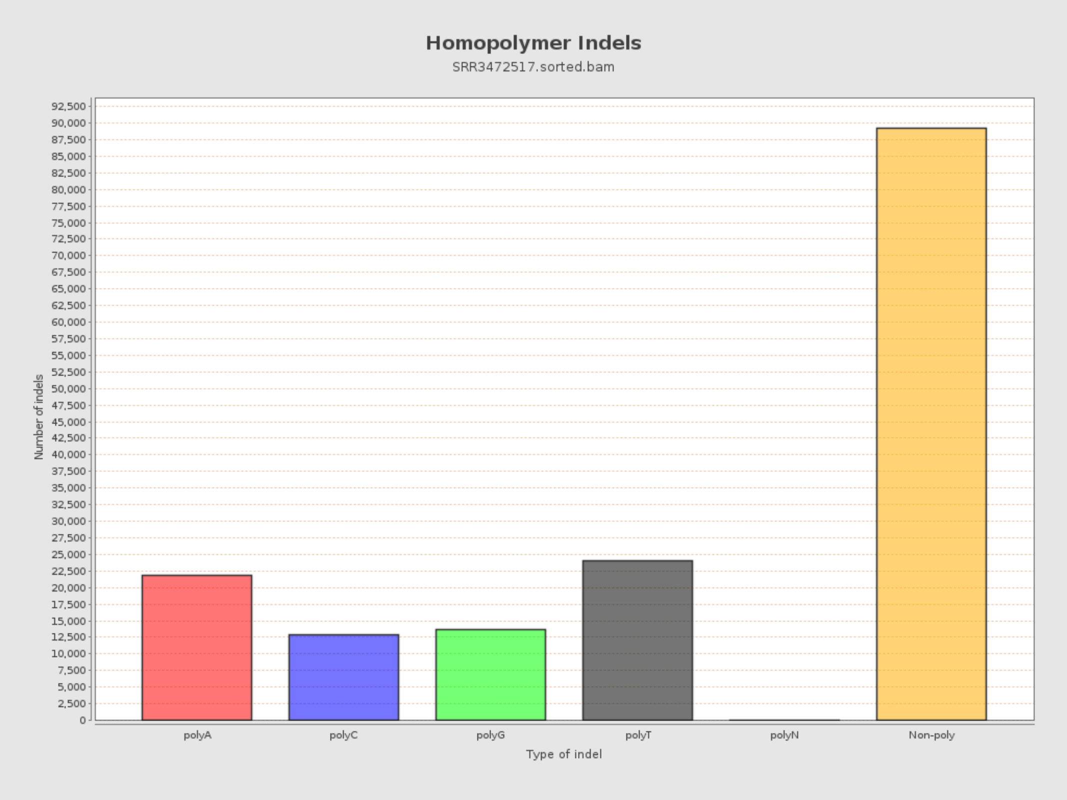
9. Results : Mapped Reads GC-content Distribution



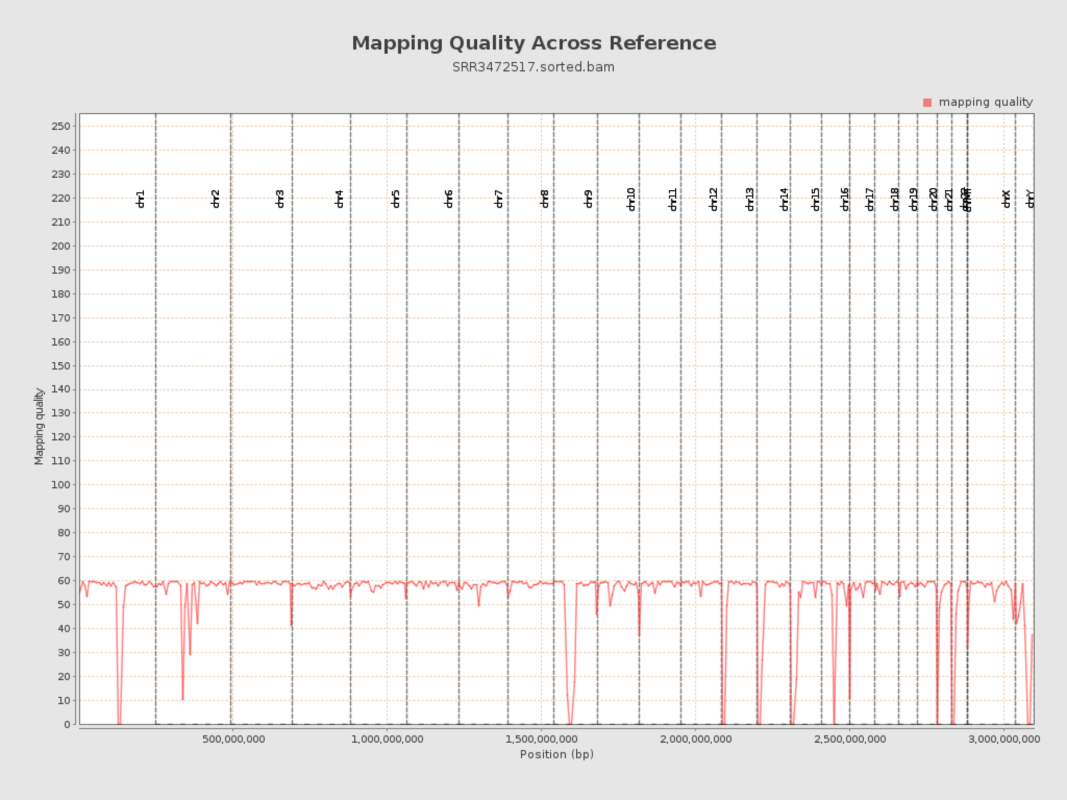
10. Results : Mapped Reads Clipping Profile



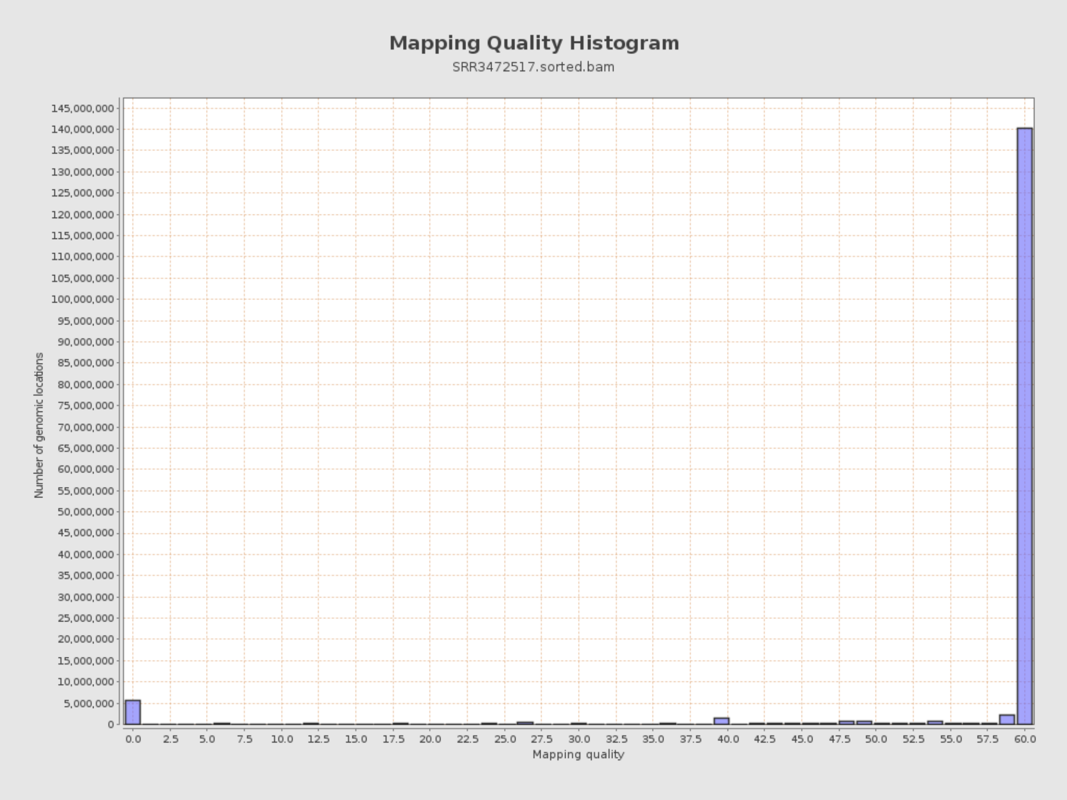
11. Results : Homopolymer Indels



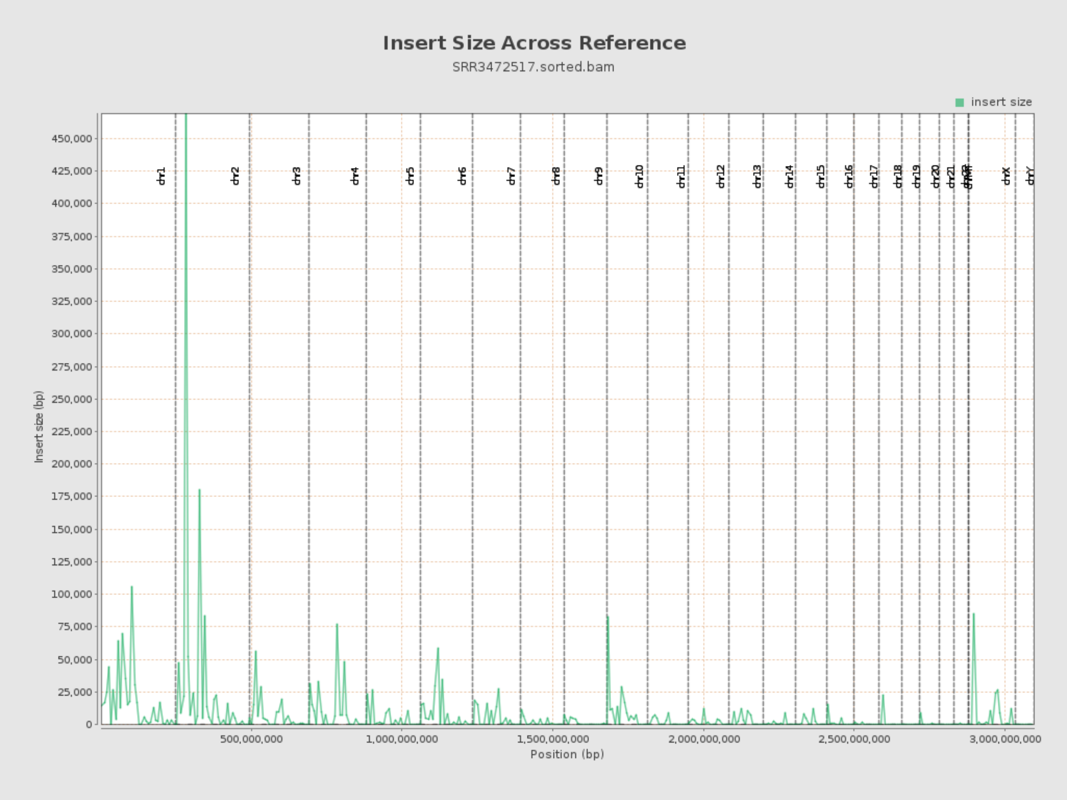
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram