Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 06:35:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472476.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_SRR3472476 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472476_1.fastq.gz SRR3472476_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 06:34:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472476.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,313,242
Mapped reads	9,180,840 / 98.58%
Unmapped reads	132,402 / 1.42%
Mapped paired reads	9,180,840 / 98.58%
Mapped reads, first in pair	4,611,271 / 49.51%
Mapped reads, second in pair	4,569,569 / 49.07%
Mapped reads, both in pair	9,114,212 / 97.86%
Mapped reads, singletons	66,628 / 0.72%
Secondary alignments	0
Supplementary alignments	34,874 / 0.37%
Read min/max/mean length	30 / 100 / 100.15
Duplicated reads (estimated)	5,250,993 / 56.38%
Duplication rate	43.97%
Clipped reads	1,080,520 / 11.6%

2.2. ACGT Content

Number/percentage of A's	237,266,695 / 26.47%
Number/percentage of C's	212,359,197 / 23.69%
Number/percentage of T's	235,352,838 / 26.26%
Number/percentage of G's	211,104,955 / 23.55%
Number/percentage of N's	139,680 / 0.02%

GC Percentage	47.25%

2.3. Coverage

Mean	0.2895
Standard Deviation	11.1889

2.4. Mapping Quality

Mean Mapping Quality	55.1

2.5. Insert size

Mean	25,604.17
Standard Deviation	1,586,934.29
P25/Median/P75	143 / 201 / 273

2.6. Mismatches and indels

General error rate	0.61%
Mismatches	5,378,544
Insertions	45,816
Mapped reads with at least one insertion	0.49%
Deletions	39,041
Mapped reads with at least one deletion	0.42%
Homopolymer indels	43.07%

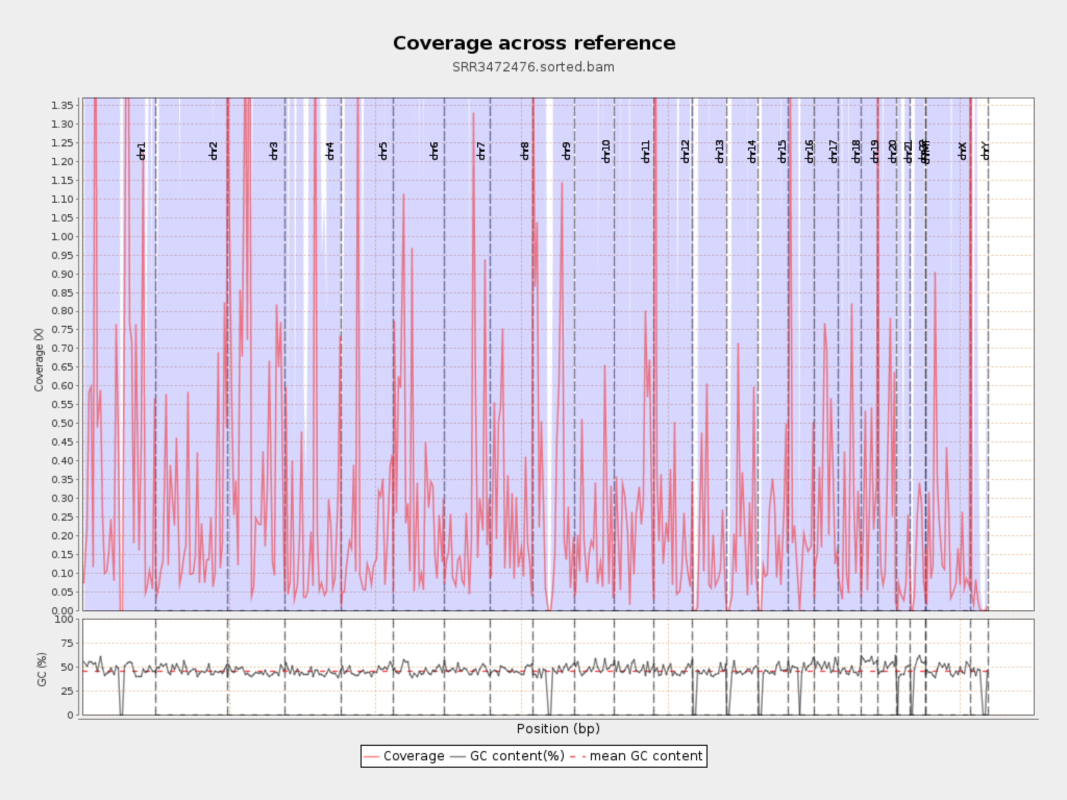
2.7. Chromosome stats

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

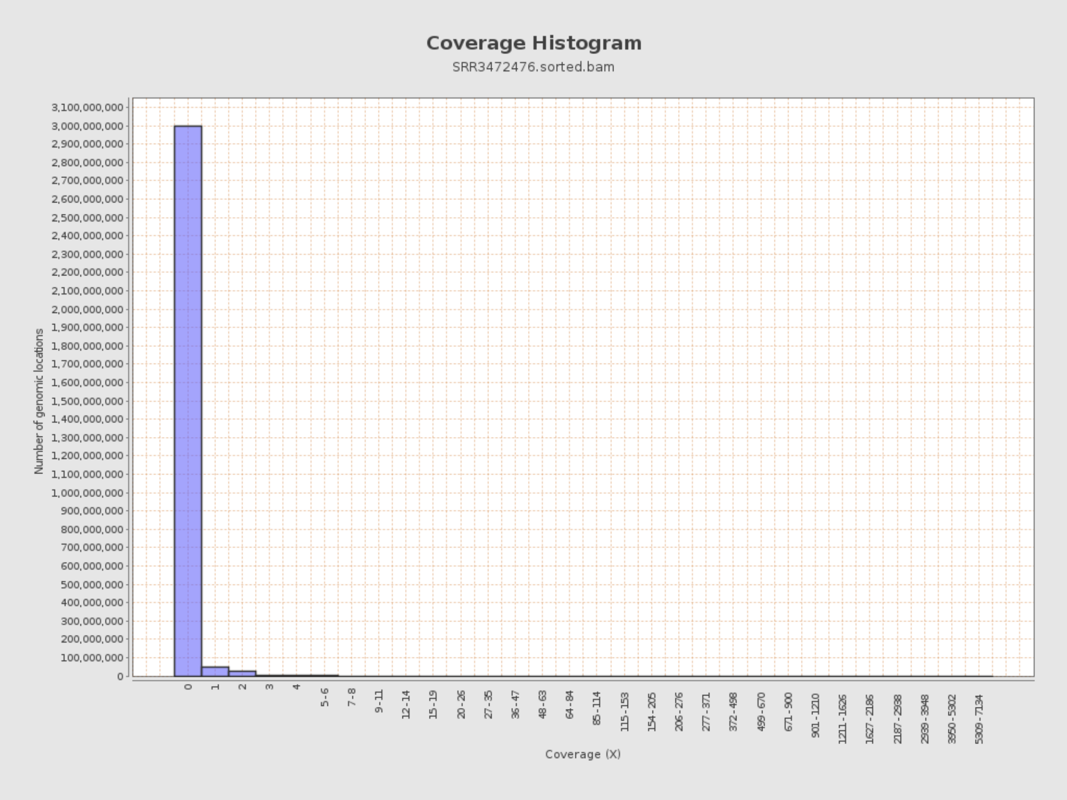
		bases	**coverage**	**deviation**
chr1	249250621	115006688	0.4614	20.8277
chr2	243199373	57631267	0.237	8.9437
chr3	198022430	110078954	0.5559	14.4107
chr4	191154276	46564850	0.2436	11.0856
chr5	180915260	41514766	0.2295	7.5
chr6	171115067	57982765	0.3389	10.1618
chr7	159138663	43563211	0.2737	12.9829
chr8	146364022	39134024	0.2674	10.0629
chr9	141213431	49930501	0.3536	10.9235
chr10	135534747	28119685	0.2075	9.3509
chr11	135006516	39540942	0.2929	9.7522
chr12	133851895	44227292	0.3304	11.5092
chr13	115169878	18580734	0.1613	6.5161
chr14	107349540	22384637	0.2085	9.0306
chr15	102531392	18643764	0.1818	5.7349
chr16	90354753	26660583	0.2951	8.4538
chr17	81195210	28270024	0.3482	10.2576
chr18	78077248	18196438	0.2331	11.0342
chr19	59128983	20204020	0.3417	9.9486
chr20	63025520	19713701	0.3128	9.9187
chr21	48129895	4084349	0.0849	3.77
chr22	51304566	7807719	0.1522	5.4007
chrMT	16571	2751	0.166	0.5599
chrX	155270560	37172964	0.2394	8.3216

chrY	59373566	1301157	0.0219	0.9787

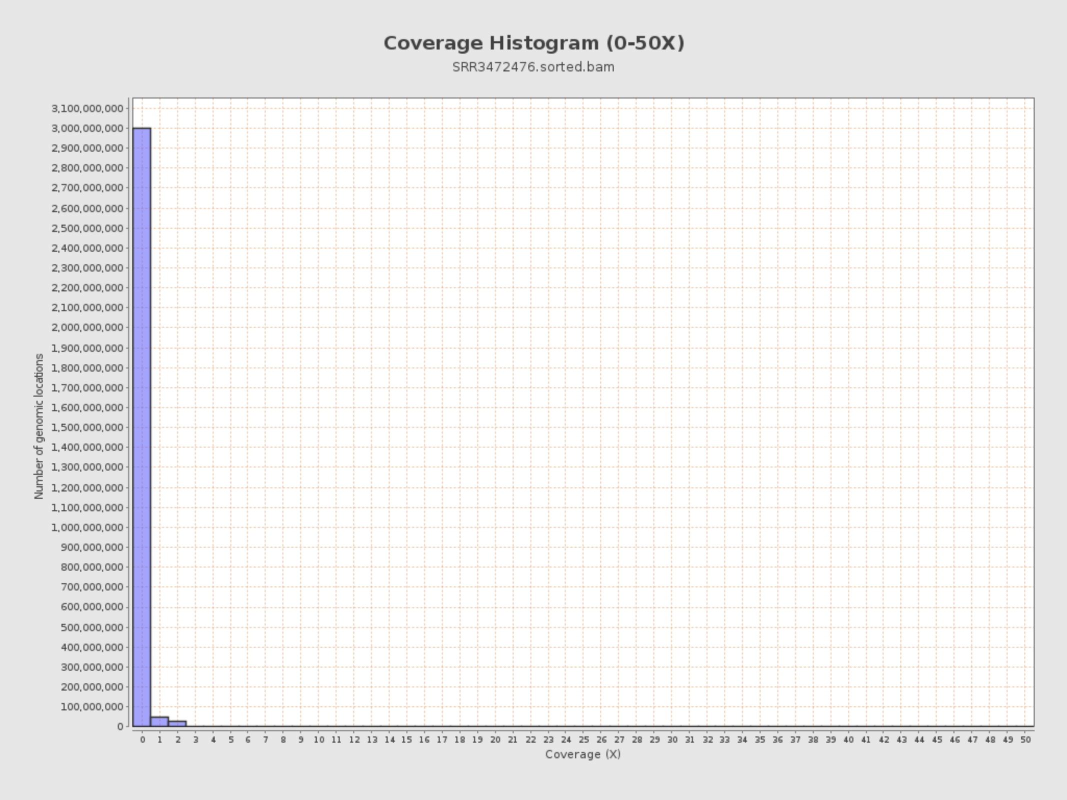
3. Results : Coverage across reference



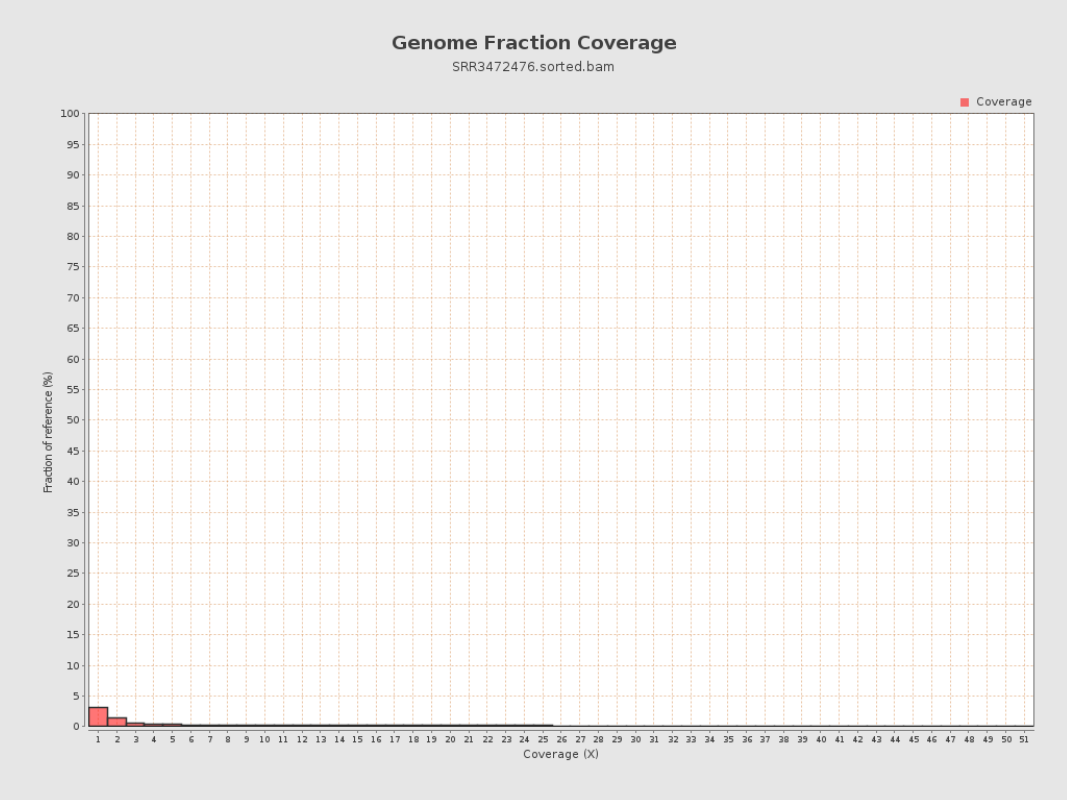
4. Results : Coverage Histogram



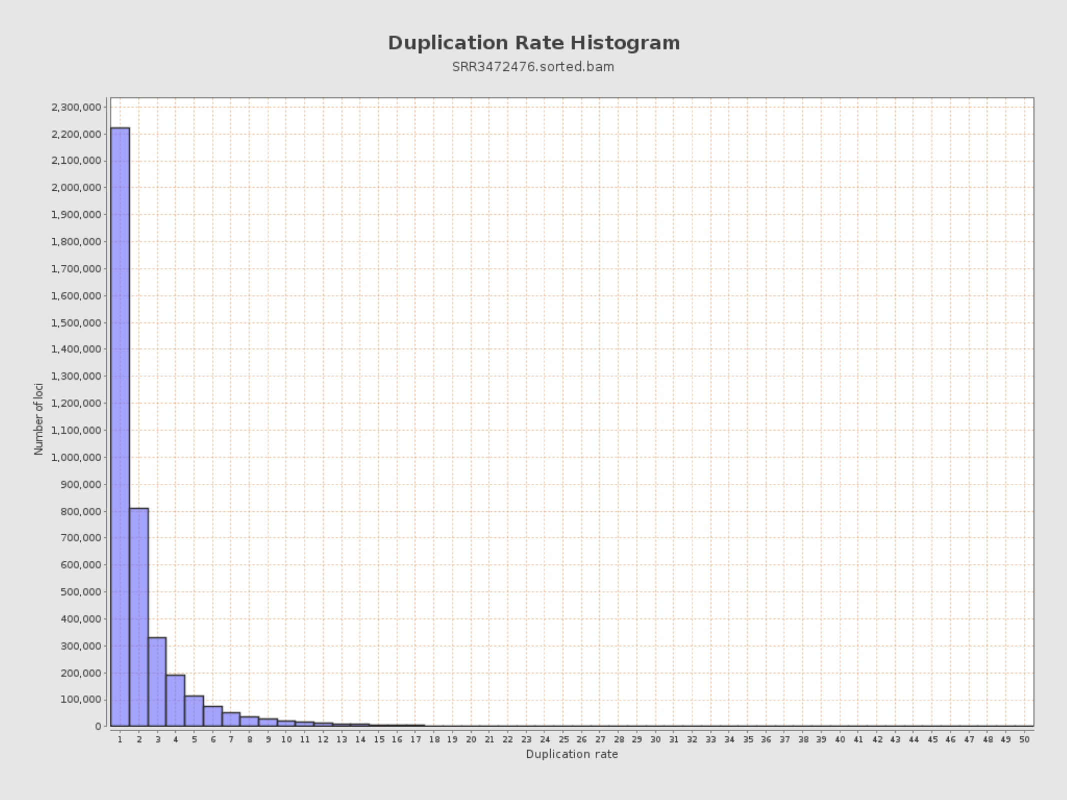
5. Results : Coverage Histogram (0-50X)



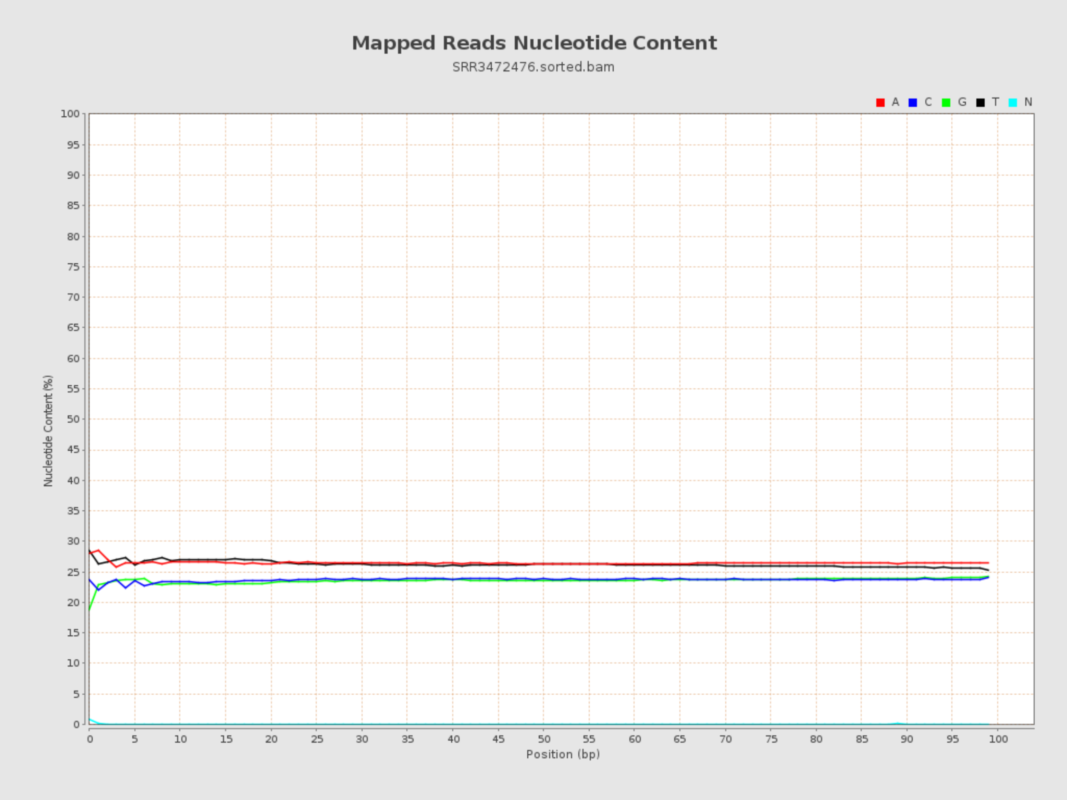
6. Results : Genome Fraction Coverage



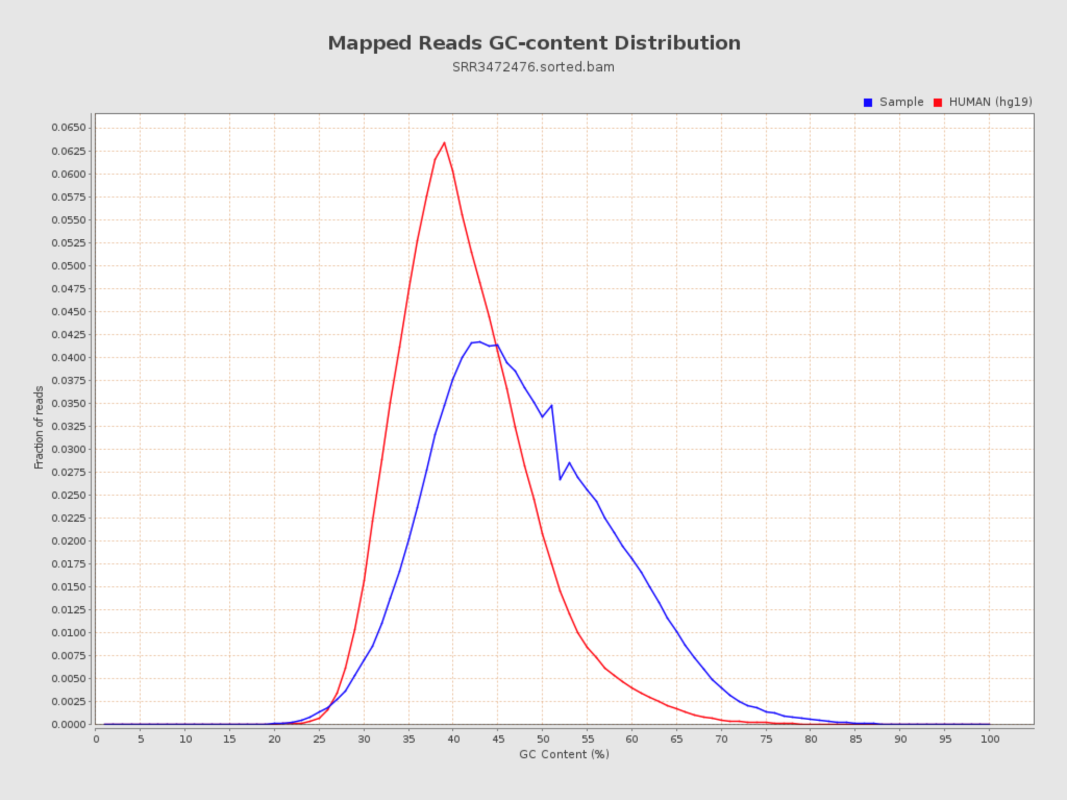
7. Results : Duplication Rate Histogram



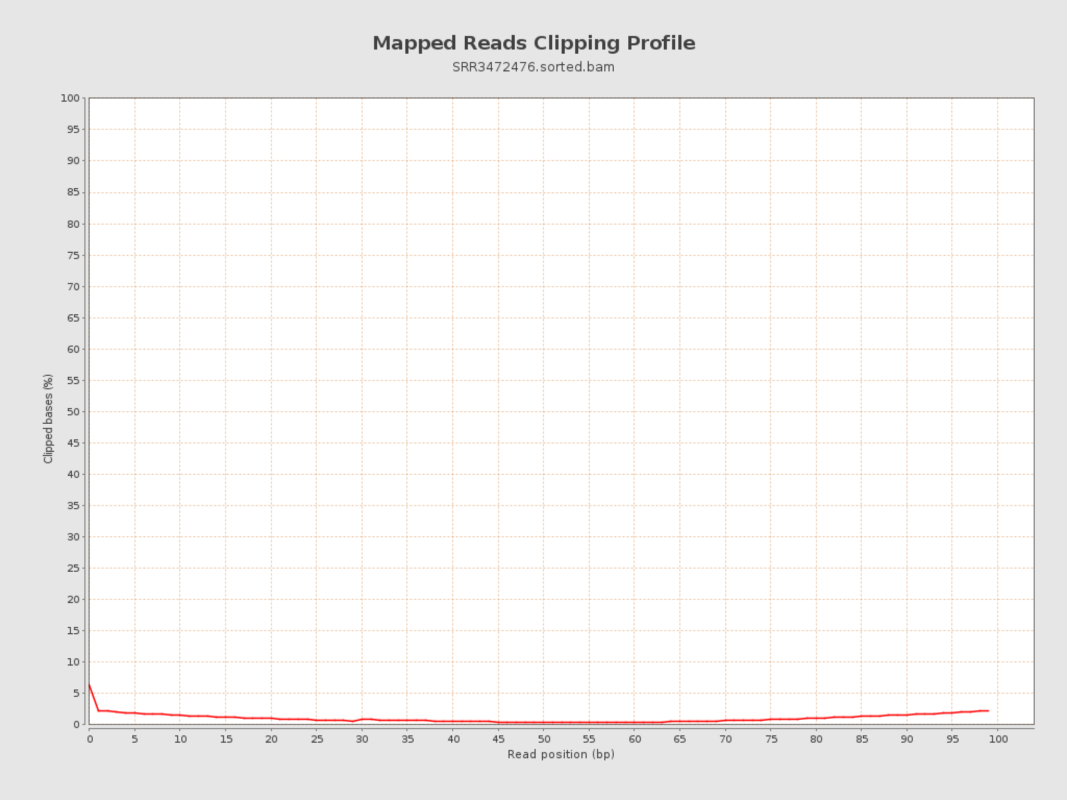
8. Results : Mapped Reads Nucleotide Content



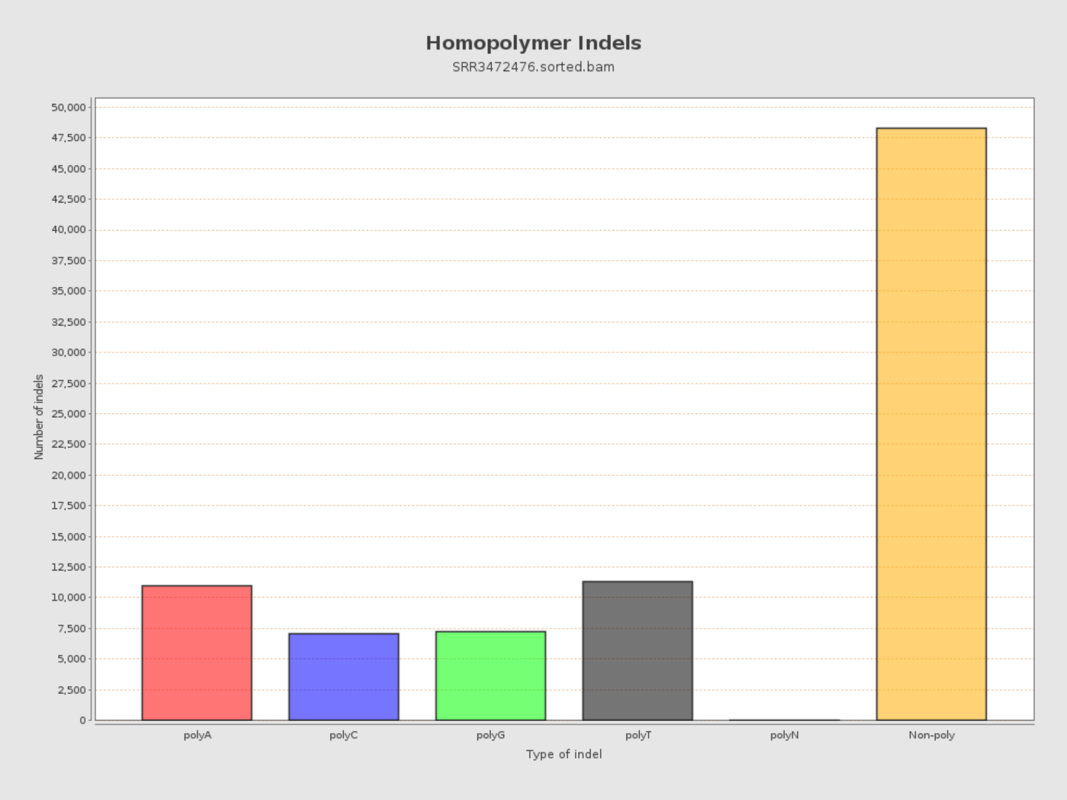
9. Results : Mapped Reads GC-content Distribution



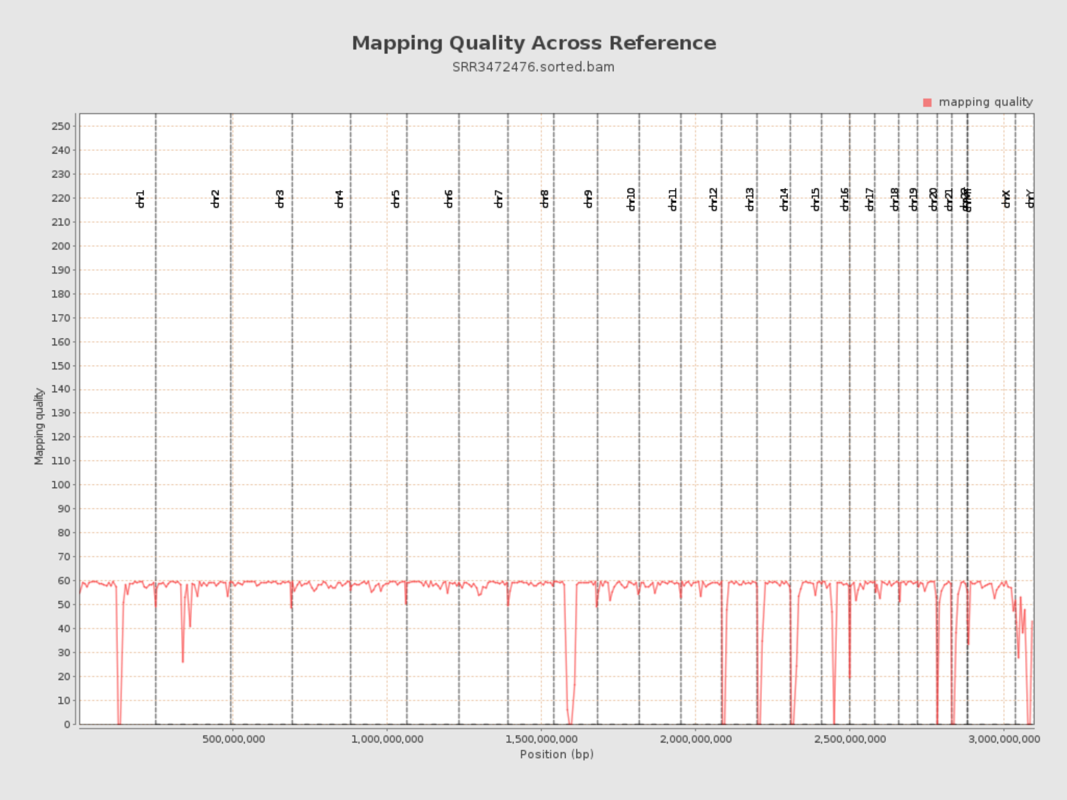
10. Results : Mapped Reads Clipping Profile



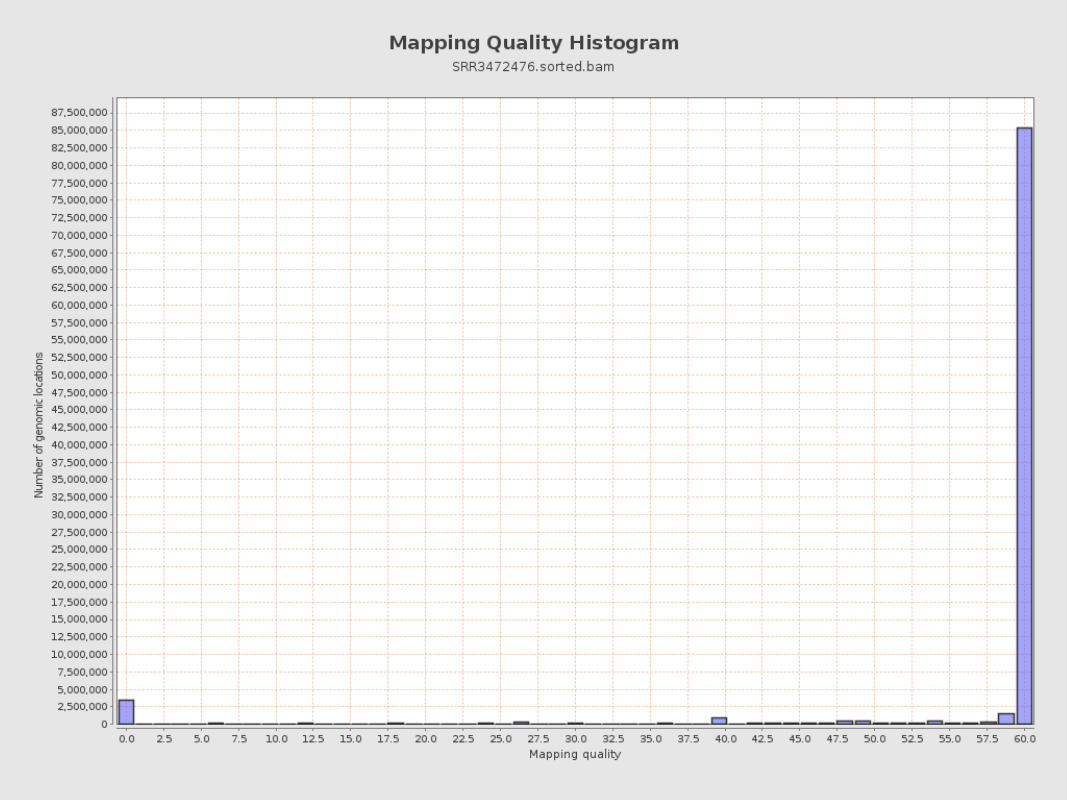
11. Results : Homopolymer Indels



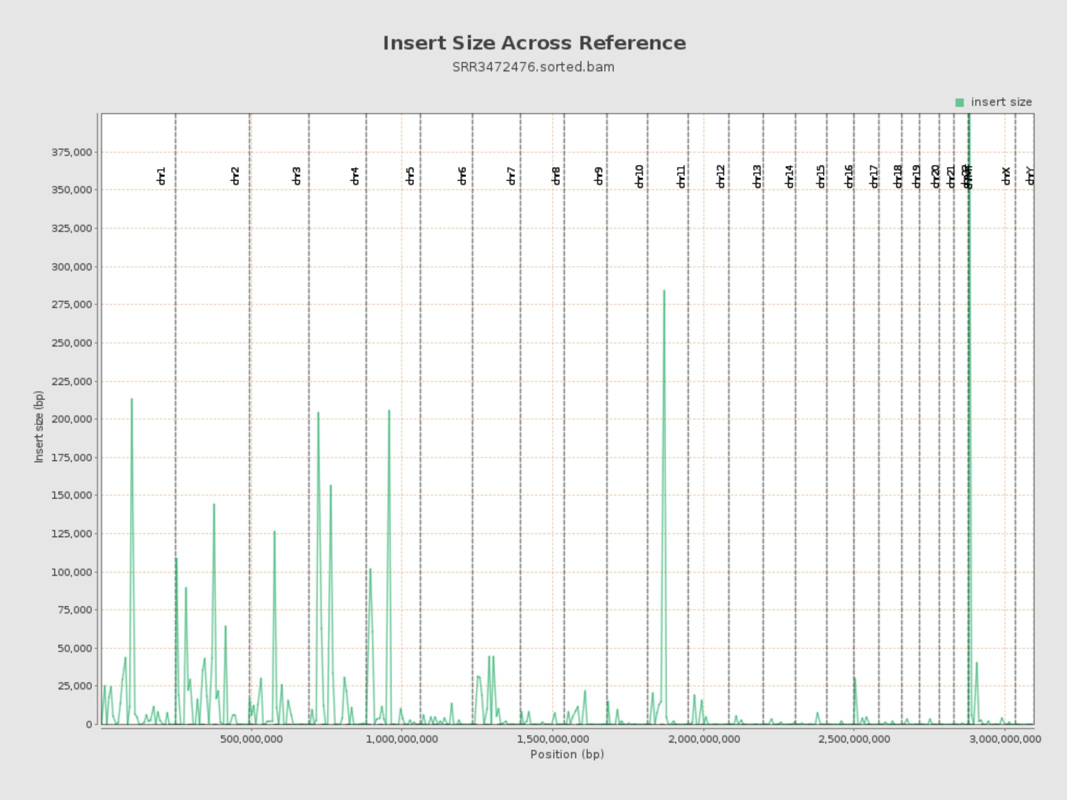
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram