Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 11:53:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124972.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_SRR3124972 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124972_1.fastq.gz SRR3124972_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 11:53:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124972.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,299,298
Mapped reads	2,258,264 / 98.22%
Unmapped reads	41,034 / 1.78%
Mapped paired reads	2,258,264 / 98.22%
Mapped reads, first in pair	1,136,128 / 49.41%
Mapped reads, second in pair	1,122,136 / 48.8%
Mapped reads, both in pair	2,242,274 / 97.52%
Mapped reads, singletons	15,990 / 0.7%
Secondary alignments	0
Supplementary alignments	44,758 / 1.95%
Read min/max/mean length	30 / 151 / 151.95
Duplicated reads (estimated)	321,157 / 13.97%
Duplication rate	12.82%
Clipped reads	1,520,791 / 66.14%

2.2. ACGT Content

Number/percentage of A's	83,891,932 / 29%
Number/percentage of C's	56,485,608 / 19.52%
Number/percentage of T's	85,752,864 / 29.64%
Number/percentage of G's	63,180,060 / 21.84%
Number/percentage of N's	2,123 / 0%

GC Percentage	41.36%

2.3. Coverage

Mean	0.0935
Standard Deviation	1.0232

2.4. Mapping Quality

Mean Mapping Quality	53.5

2.5. Insert size

Mean	89,642.73
Standard Deviation	2,850,733.97
P25/Median/P75	136 / 186 / 255

2.6. Mismatches and indels

General error rate	1.04%
Mismatches	2,839,266
Insertions	60,096
Mapped reads with at least one insertion	2.49%
Deletions	122,679
Mapped reads with at least one deletion	5.2%
Homopolymer indels	46.26%

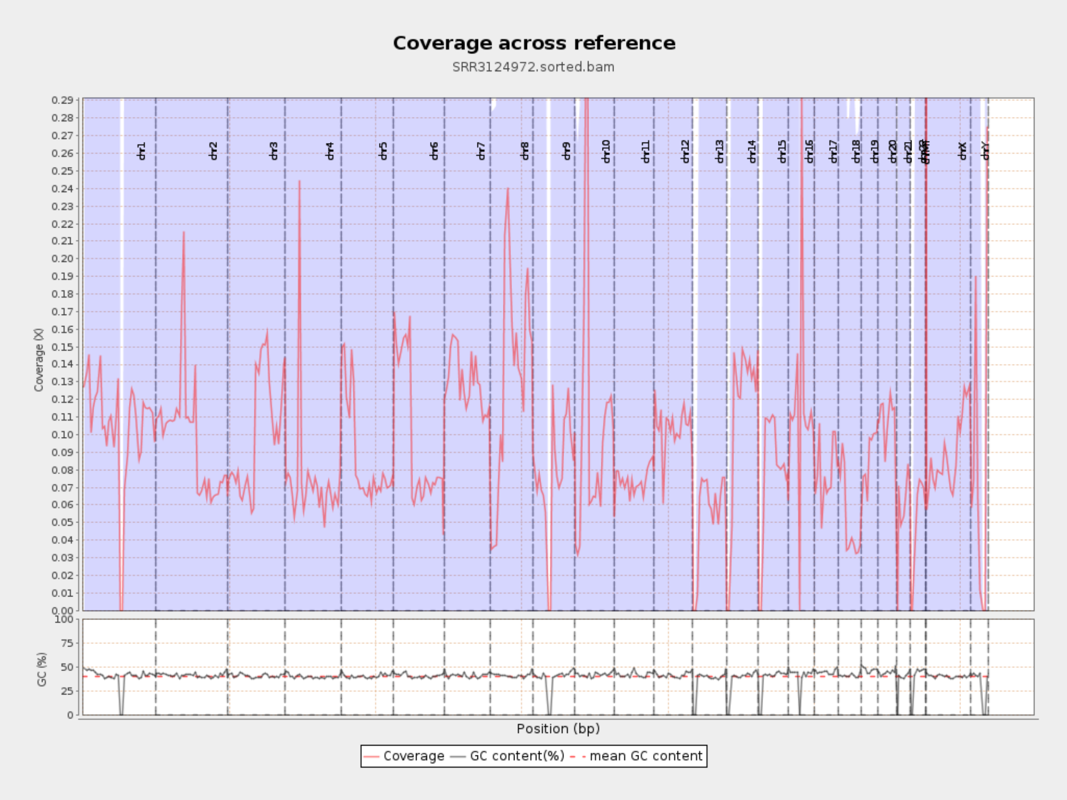
2.7. Chromosome stats

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

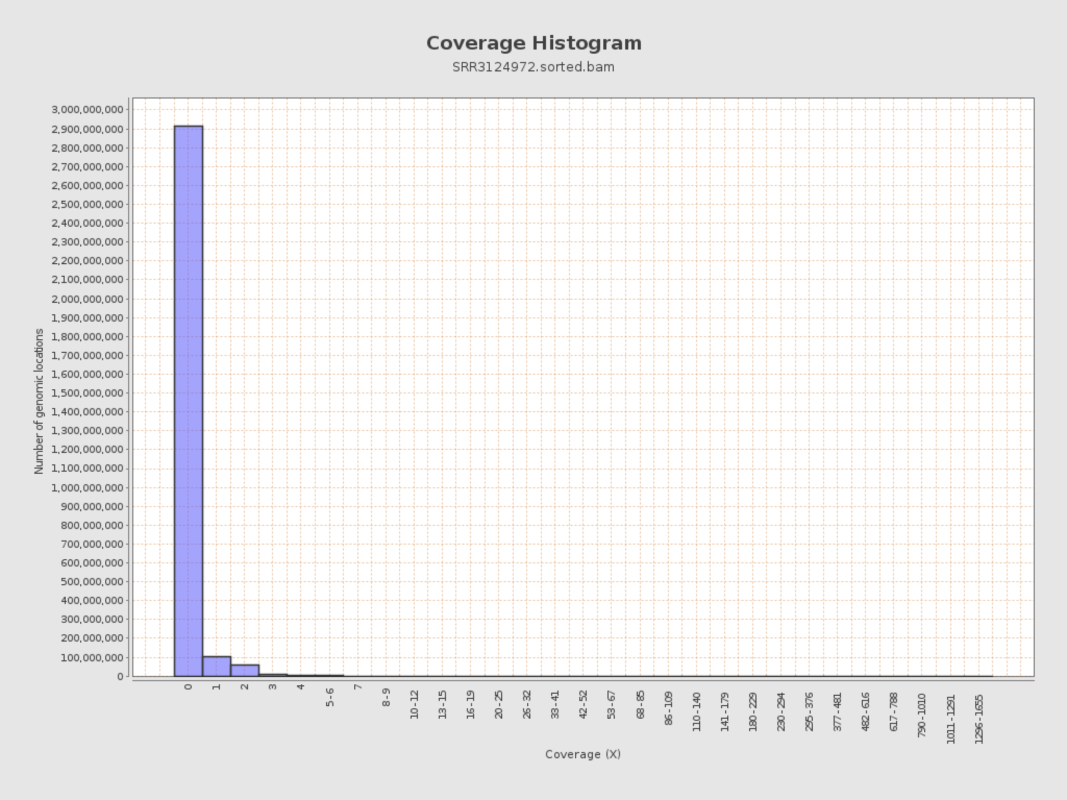
		bases	coverage	deviation
chr1	249250621	26109427	0.1048	0.7547
chr2	243199373	23850308	0.0981	1.1226
chr3	198022430	19814450	0.1001	0.4363
chr4	191154276	14277423	0.0747	1.3495
chr5	180915260	15852247	0.0876	0.4035
chr6	171115067	16933449	0.099	0.5454
chr7	159138663	20768653	0.1305	0.9072
chr8	146364022	19597454	0.1339	0.5784
chr9	141213431	10943516	0.0775	1.1
chr10	135534747	14034970	0.1036	2.865
chr11	135006516	9949432	0.0737	0.4633
chr12	133851895	13989234	0.1045	0.439
chr13	115169878	6285947	0.0546	0.3088
chr14	107349540	12027987	0.112	0.4705
chr15	102531392	7898167	0.077	0.3807
chr16	90354753	10451730	0.1157	1.5648
chr17	81195210	6374214	0.0785	0.8329
chr18	78077248	4120364	0.0528	1.0037
chr19	59128983	5127931	0.0867	0.5067
chr20	63025520	6860223	0.1088	0.6403
chr21	48129895	2842904	0.0591	0.7357
chr22	51304566	2520922	0.0491	0.3102
chrMT	16571	18956	1.1439	1.4963
chrX	155270560	13861563	0.0893	0.4453

chrY	59373566	5053952	0.0851	2.2424

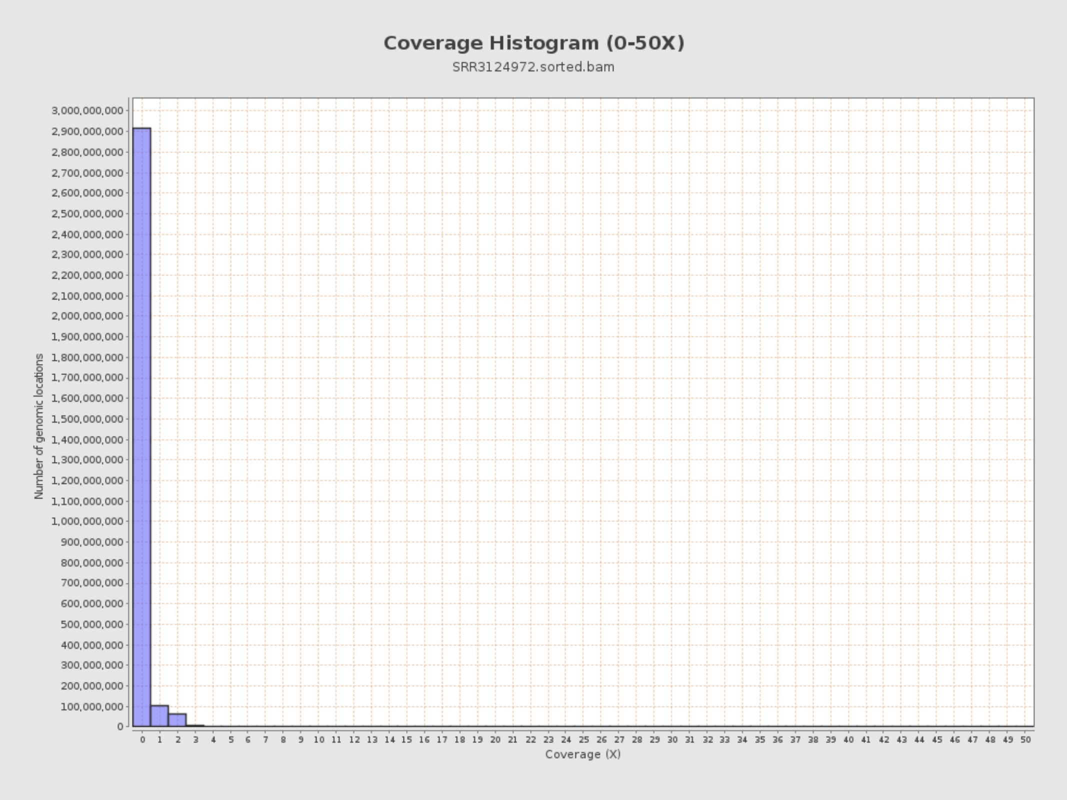
3. Results : Coverage across reference



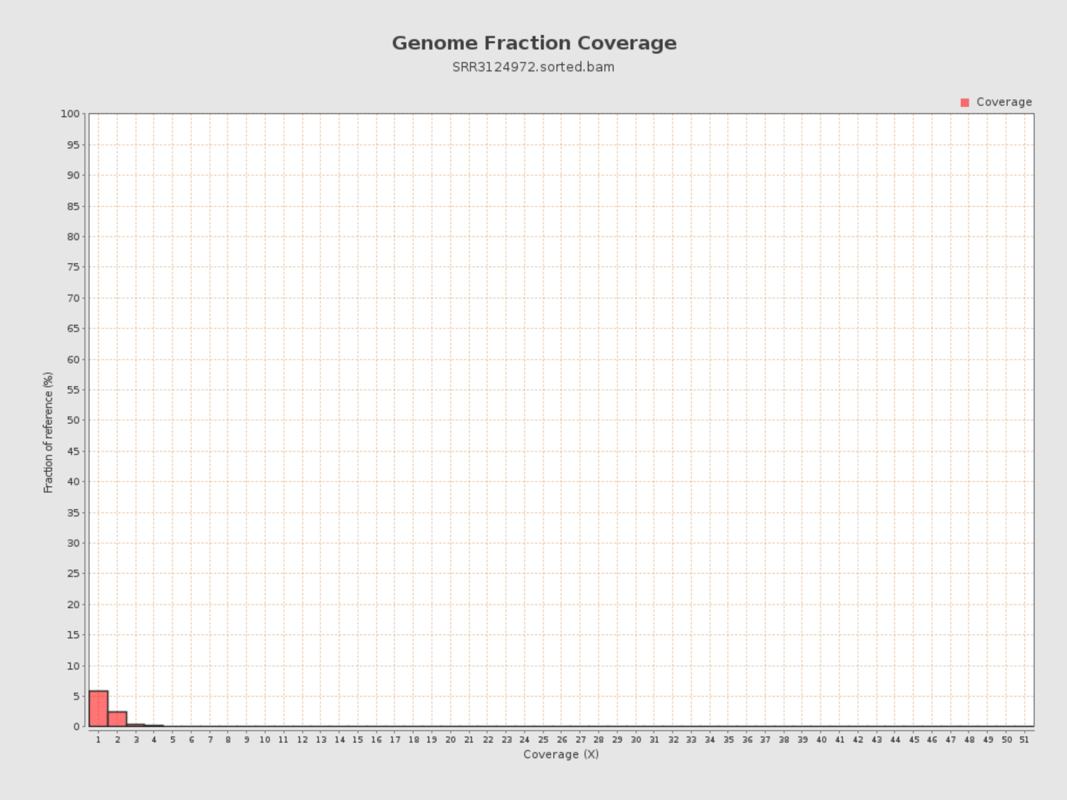
4. Results : Coverage Histogram



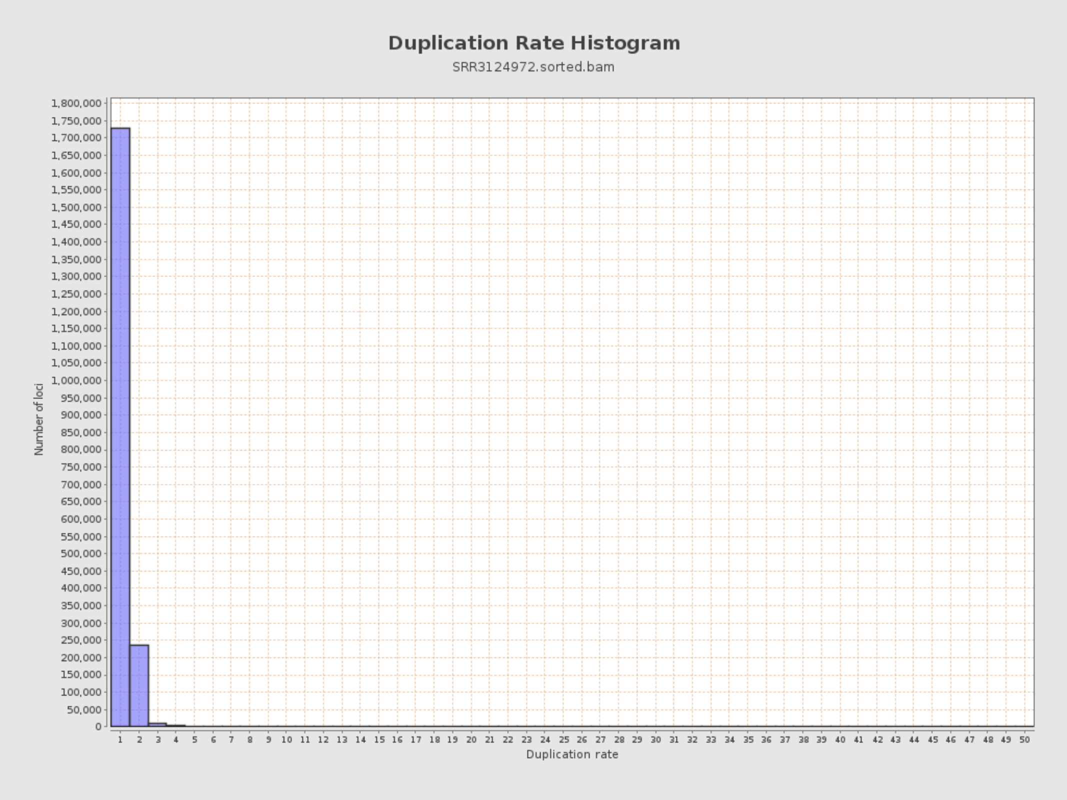
5. Results : Coverage Histogram (0-50X)



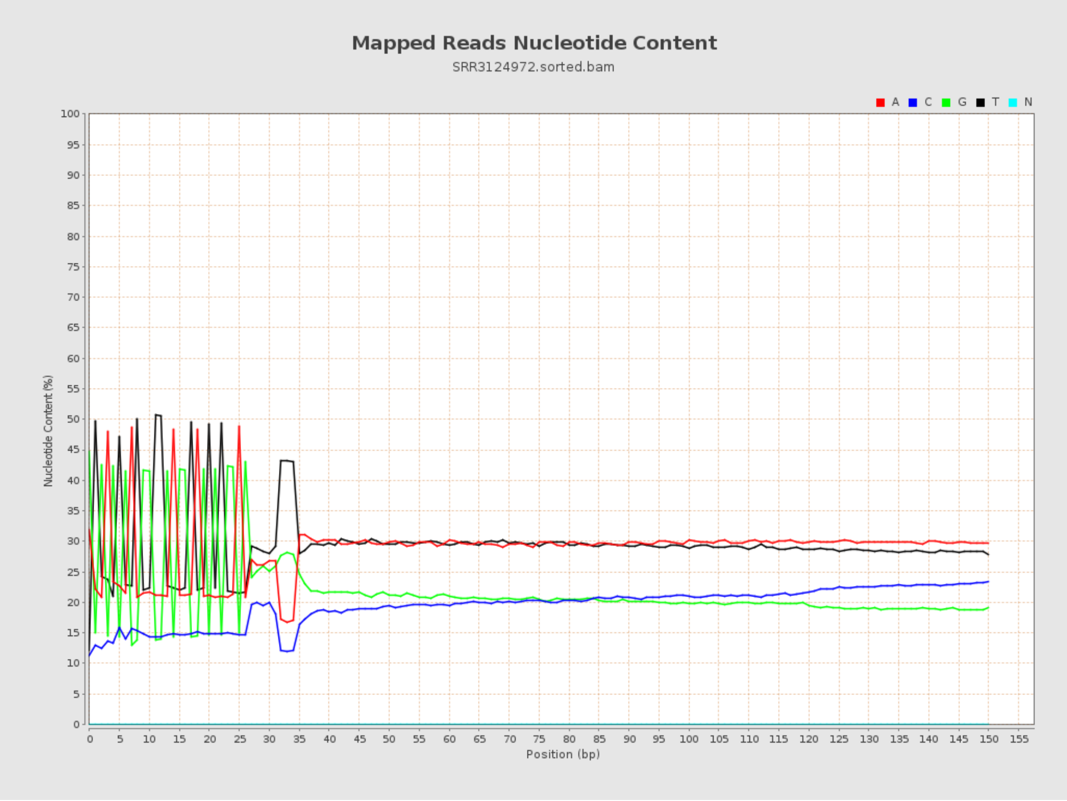
6. Results : Genome Fraction Coverage



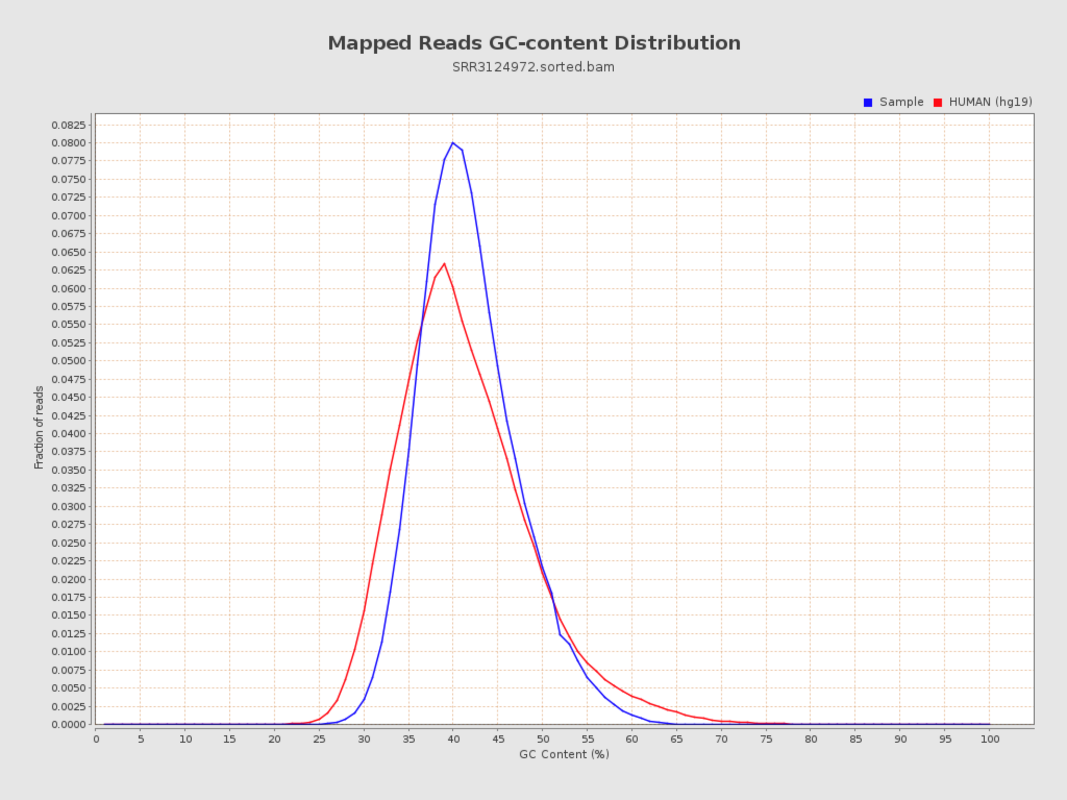
7. Results : Duplication Rate Histogram



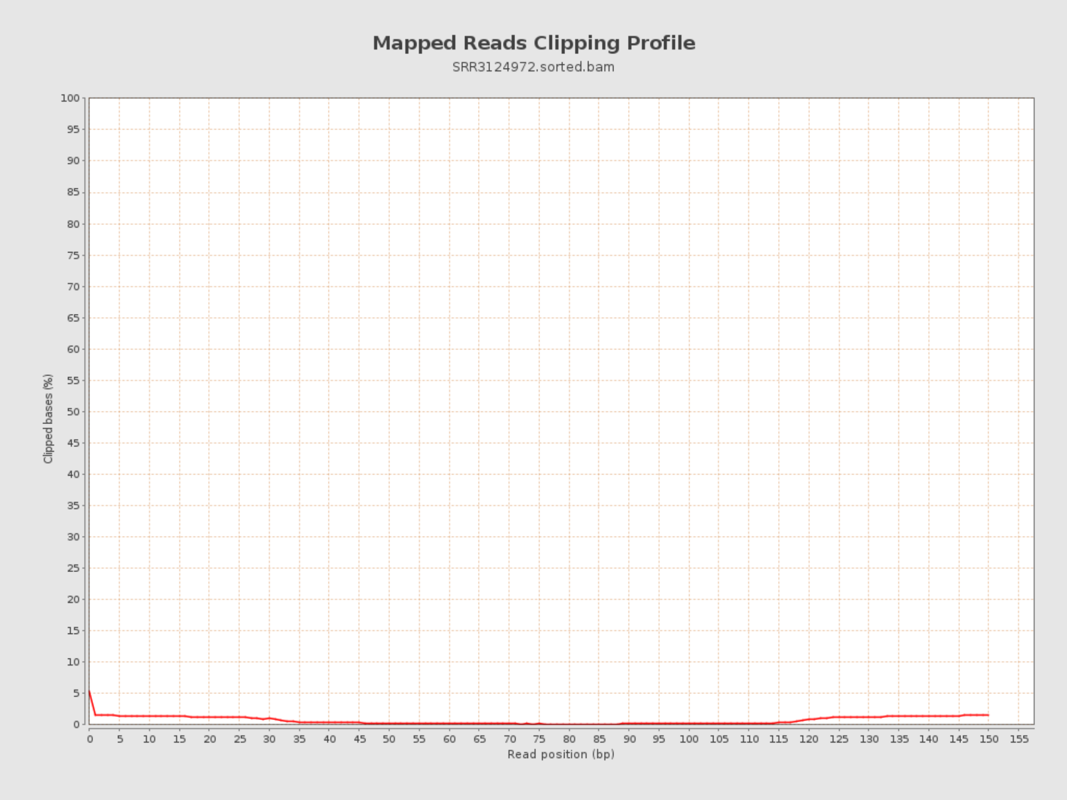
8. Results : Mapped Reads Nucleotide Content



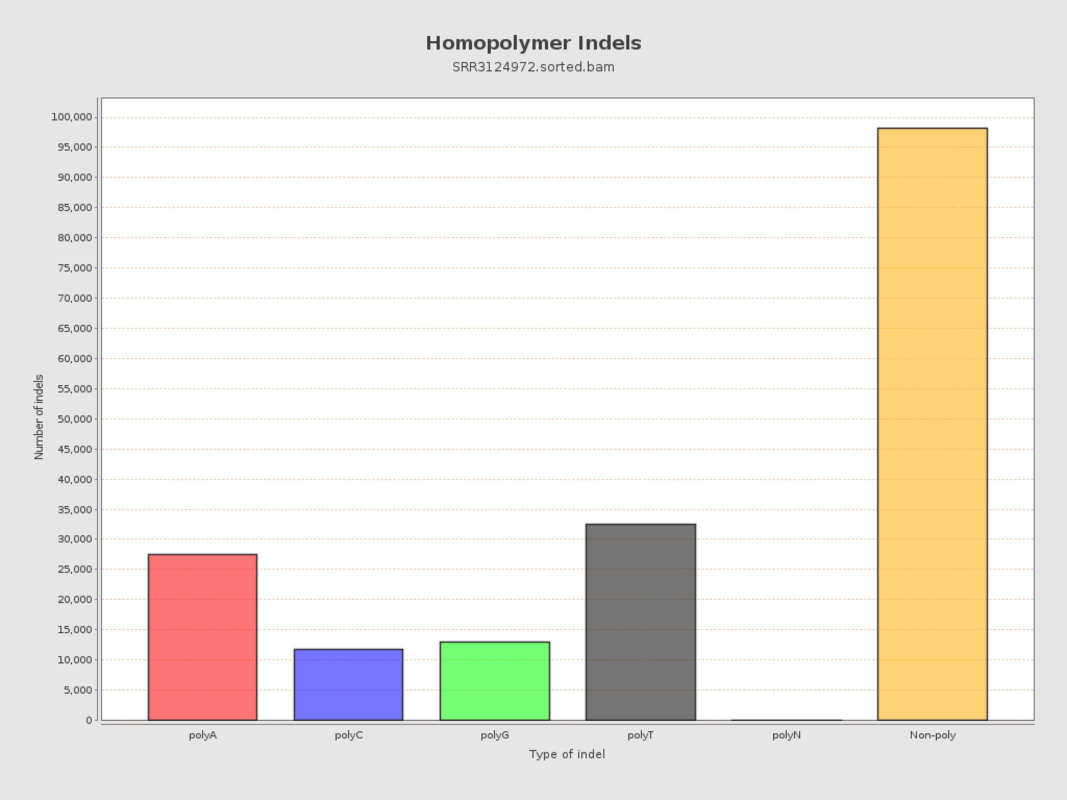
9. Results : Mapped Reads GC-content Distribution



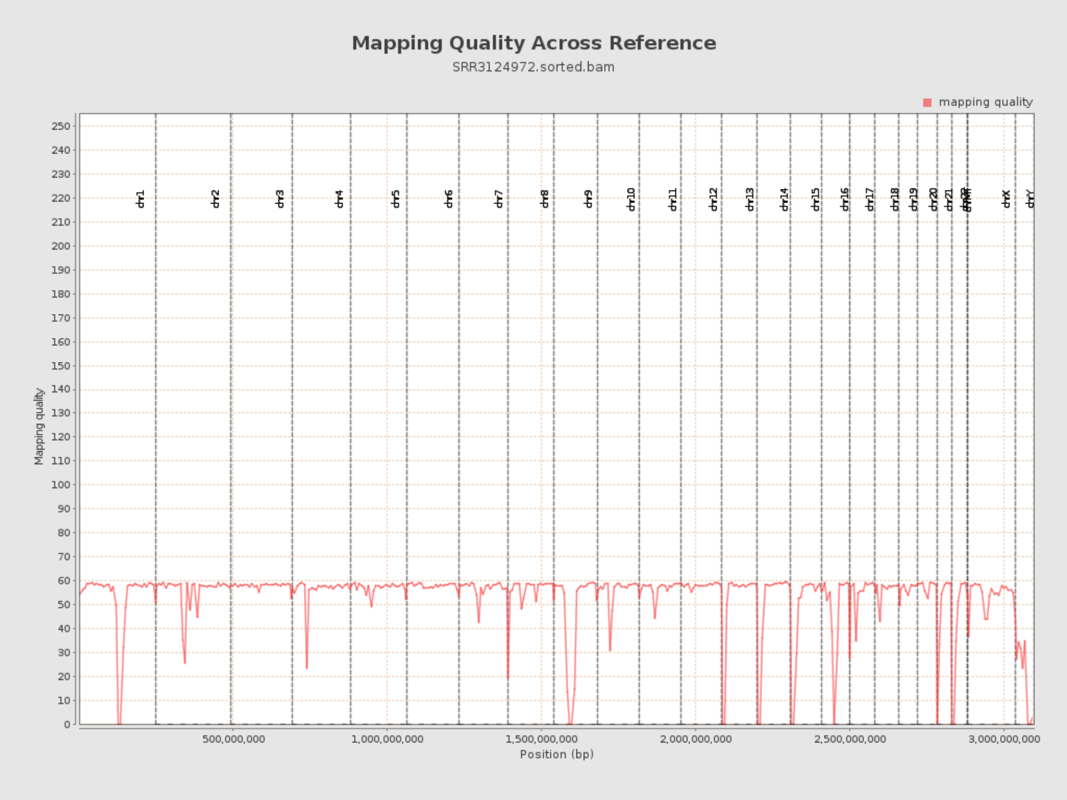
10. Results : Mapped Reads Clipping Profile



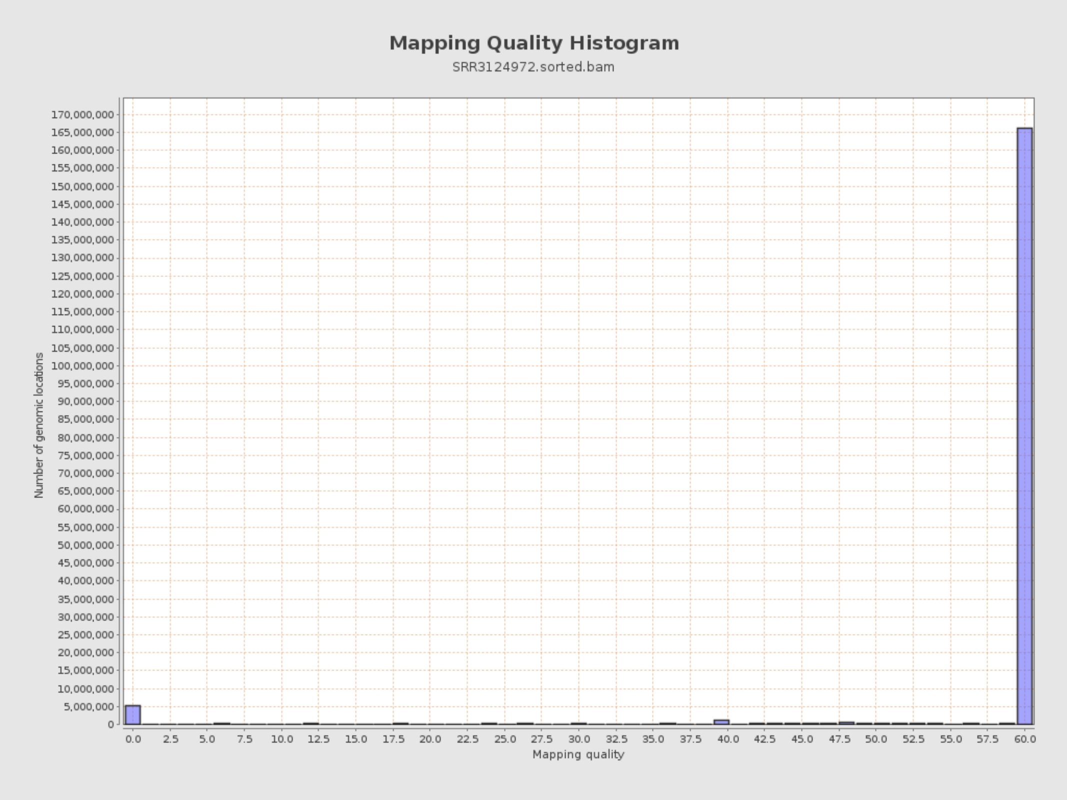
11. Results : Homopolymer Indels



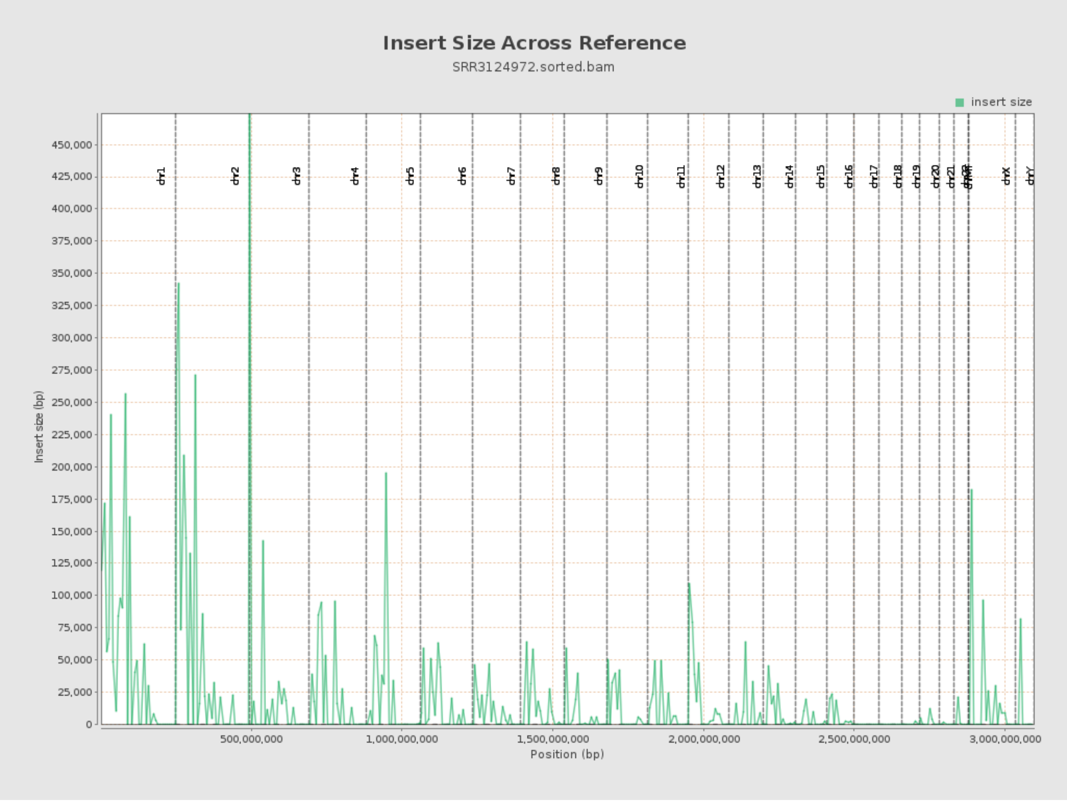
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram