Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 11:20:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472491.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_SRR3472491 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472491_1.fastq.gz SRR3472491_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 11:20:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472491.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,261,606
Mapped reads	15,040,497 / 98.55%
Unmapped reads	221,109 / 1.45%
Mapped paired reads	15,040,497 / 98.55%
Mapped reads, first in pair	7,528,188 / 49.33%
Mapped reads, second in pair	7,512,309 / 49.22%
Mapped reads, both in pair	14,916,314 / 97.74%
Mapped reads, singletons	124,183 / 0.81%
Secondary alignments	0
Supplementary alignments	71,009 / 0.47%
Read min/max/mean length	30 / 100 / 100.19
Duplicated reads (estimated)	9,144,328 / 59.92%
Duplication rate	44.72%
Clipped reads	1,519,198 / 9.95%

2.2. ACGT Content

Number/percentage of A's	415,683,330 / 28.17%
Number/percentage of C's	329,098,507 / 22.3%
Number/percentage of T's	405,434,999 / 27.47%
Number/percentage of G's	325,233,713 / 22.04%
Number/percentage of N's	224,212 / 0.02%

GC Percentage	44.34%

2.3. Coverage

Mean	0.4767
Standard Deviation	16.0871

2.4. Mapping Quality

Mean Mapping Quality	54.98

2.5. Insert size

Mean	38,921.26
Standard Deviation	1,942,516.75
P25/Median/P75	168 / 235 / 316

2.6. Mismatches and indels

General error rate	0.86%
Mismatches	12,573,275
Insertions	77,066
Mapped reads with at least one insertion	0.51%
Deletions	71,556
Mapped reads with at least one deletion	0.47%
Homopolymer indels	44.75%

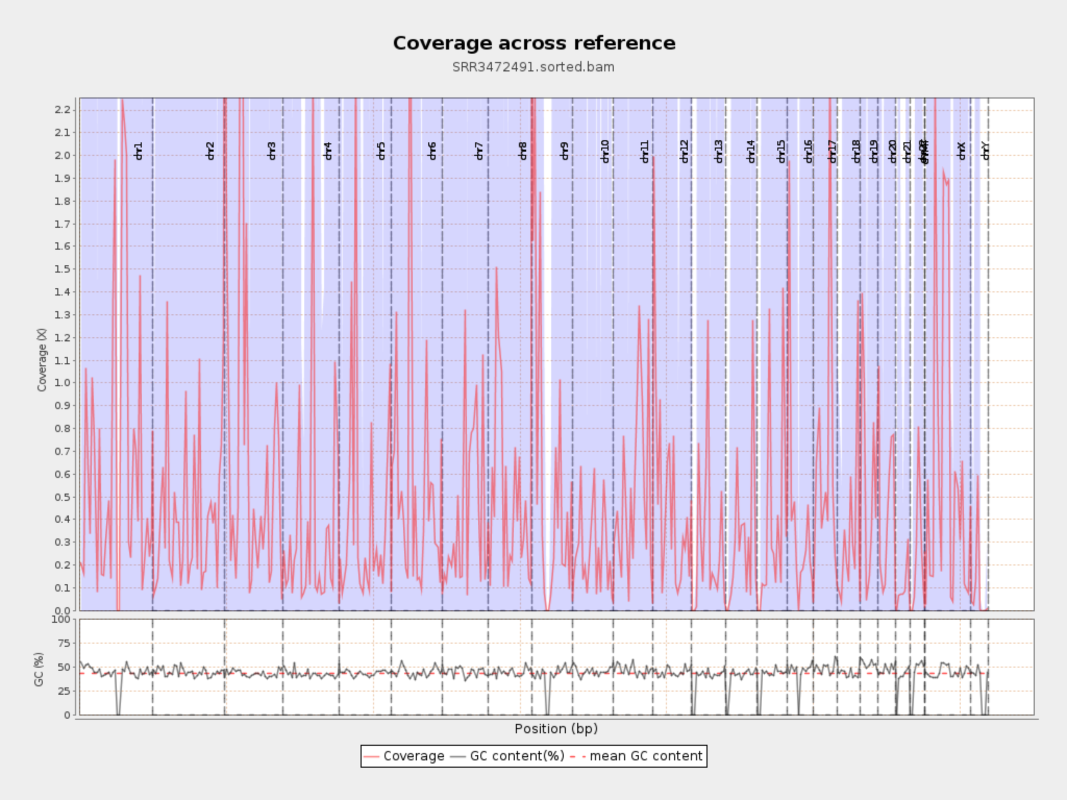
2.7. Chromosome stats

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

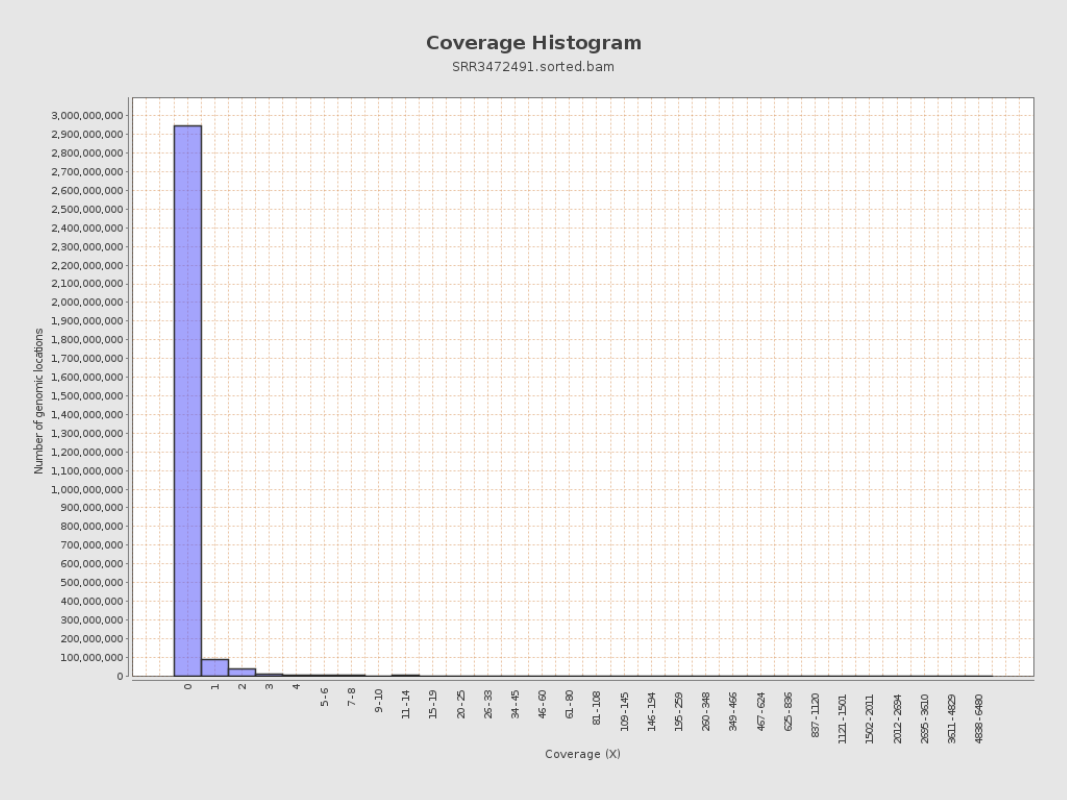
		bases	coverage	deviation
chr1	249250621	165680363	0.6647	19.9097
chr2	243199373	100173721	0.4119	13.4162
chr3	198022430	155601255	0.7858	18.0319
chr4	191154276	67117583	0.3511	14.907
chr5	180915260	79795262	0.4411	16.4104
chr6	171115067	97172353	0.5679	16.7271
chr7	159138663	67459478	0.4239	16.093
chr8	146364022	72001439	0.4919	18.5525
chr9	141213431	84445749	0.598	14.2467
chr10	135534747	36432390	0.2688	10.487
chr11	135006516	71979505	0.5332	14.8766
chr12	133851895	67181950	0.5019	14.4105
chr13	115169878	34719729	0.3015	12.3603
chr14	107349540	32061940	0.2987	9.628
chr15	102531392	39658710	0.3868	16.2237
chr16	90354753	36527147	0.4043	9.9987
chr17	81195210	51791089	0.6379	14.6731
chr18	78077248	26628861	0.3411	13.0982
chr19	59128983	34088056	0.5765	18.7795
chr20	63025520	28784523	0.4567	14.1276
chr21	48129895	5122218	0.1064	2.9599
chr22	51304566	11604655	0.2262	6.5088
chrMT	16571	4270	0.2577	0.8492
chrX	155270560	103730915	0.6681	28.6701

chrY	59373566	6082866	0.1025	8.3102

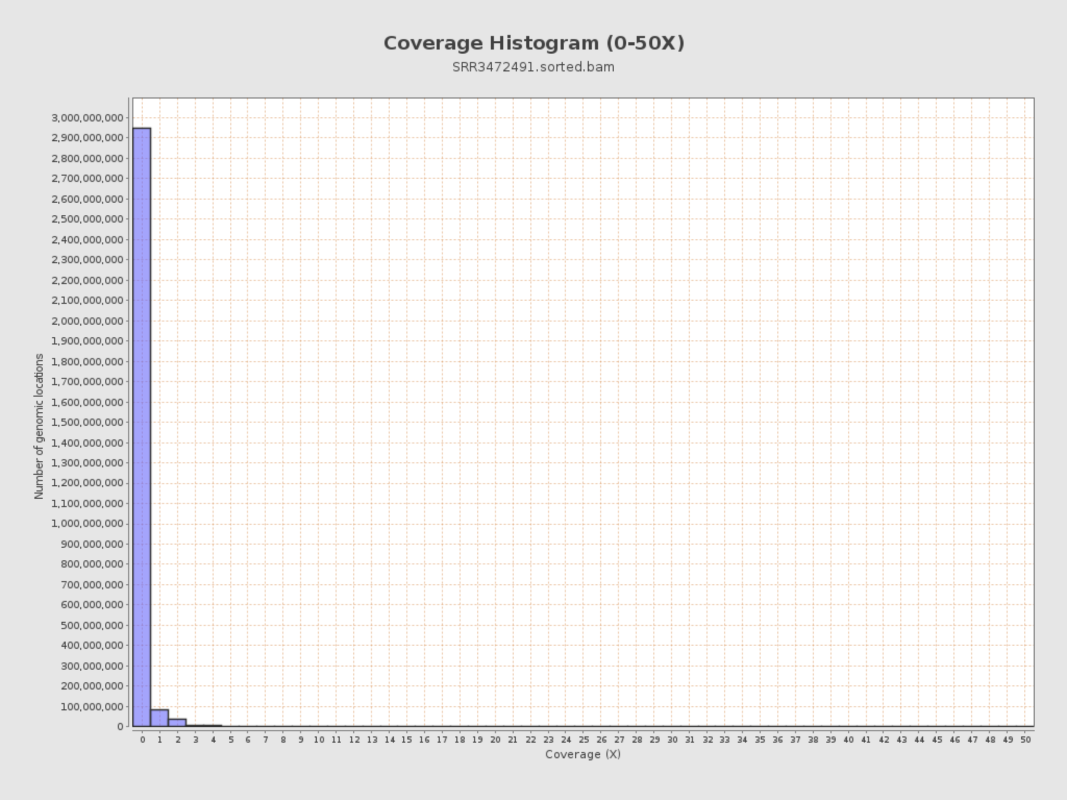
3. Results : Coverage across reference



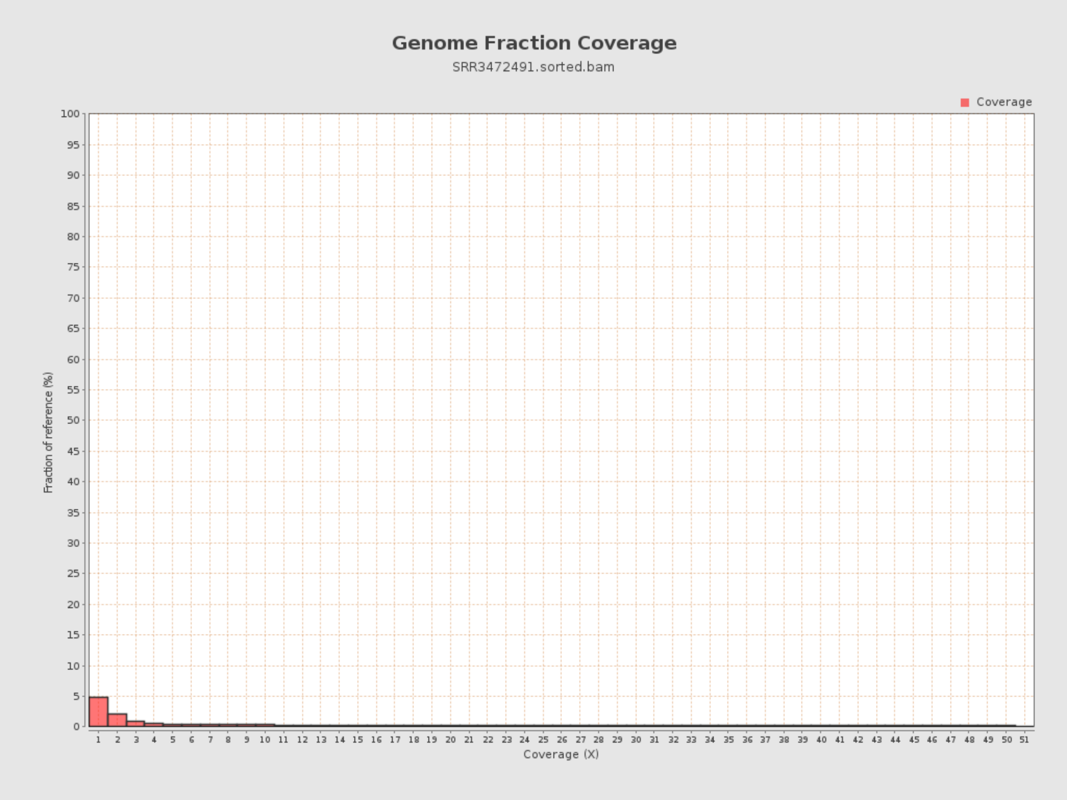
4. Results : Coverage Histogram



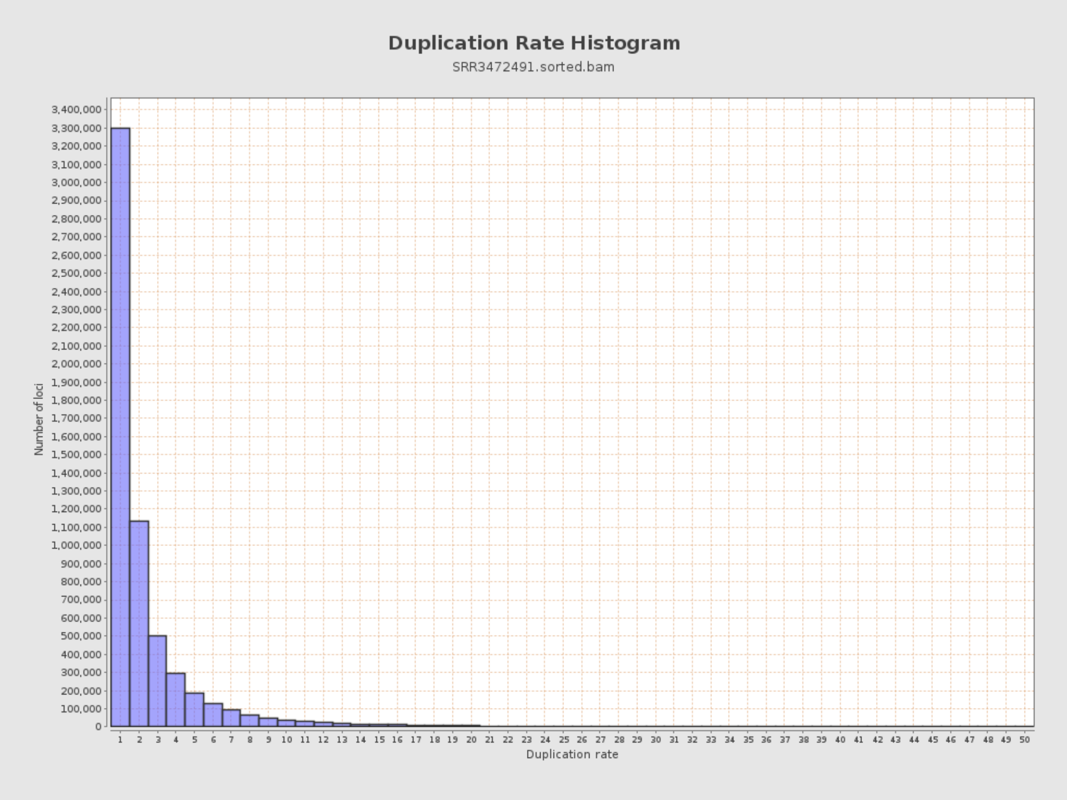
5. Results : Coverage Histogram (0-50X)



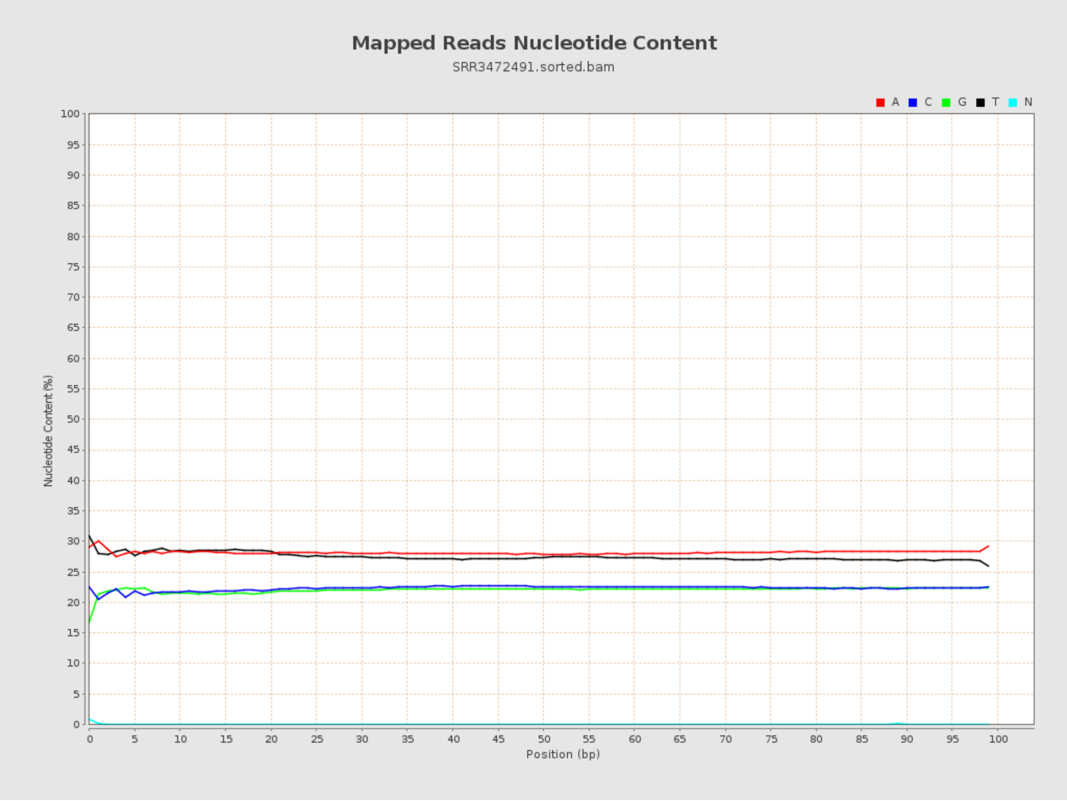
6. Results : Genome Fraction Coverage



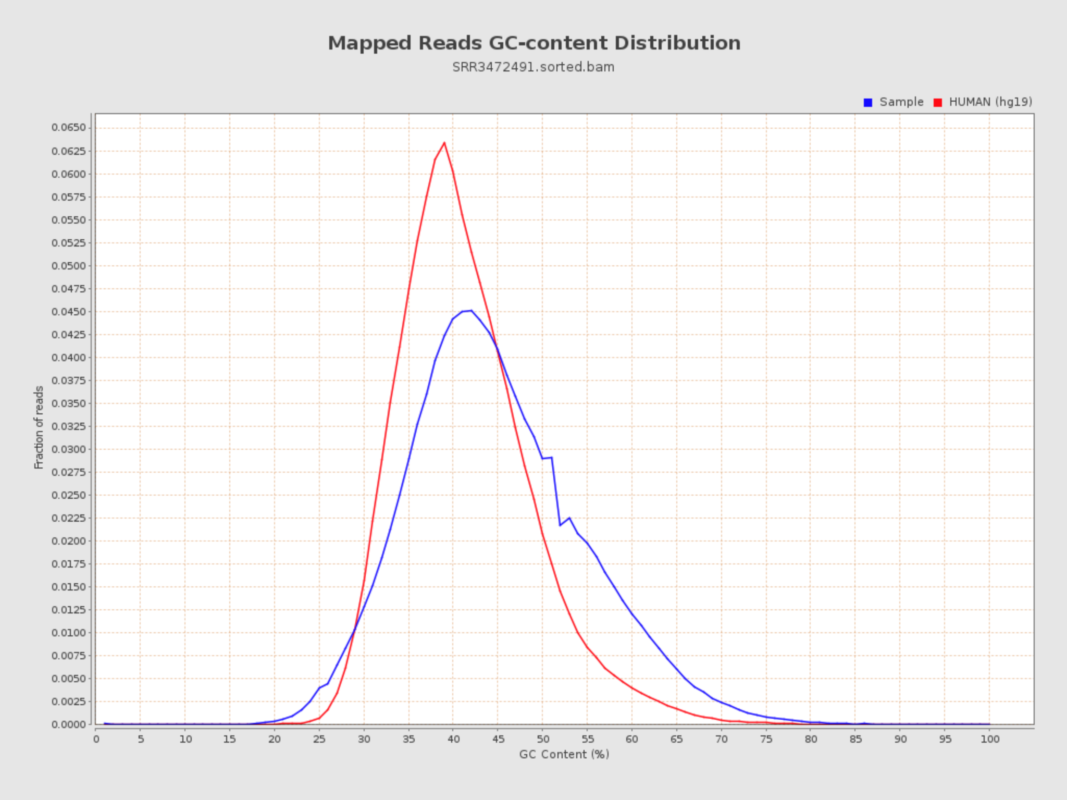
7. Results : Duplication Rate Histogram



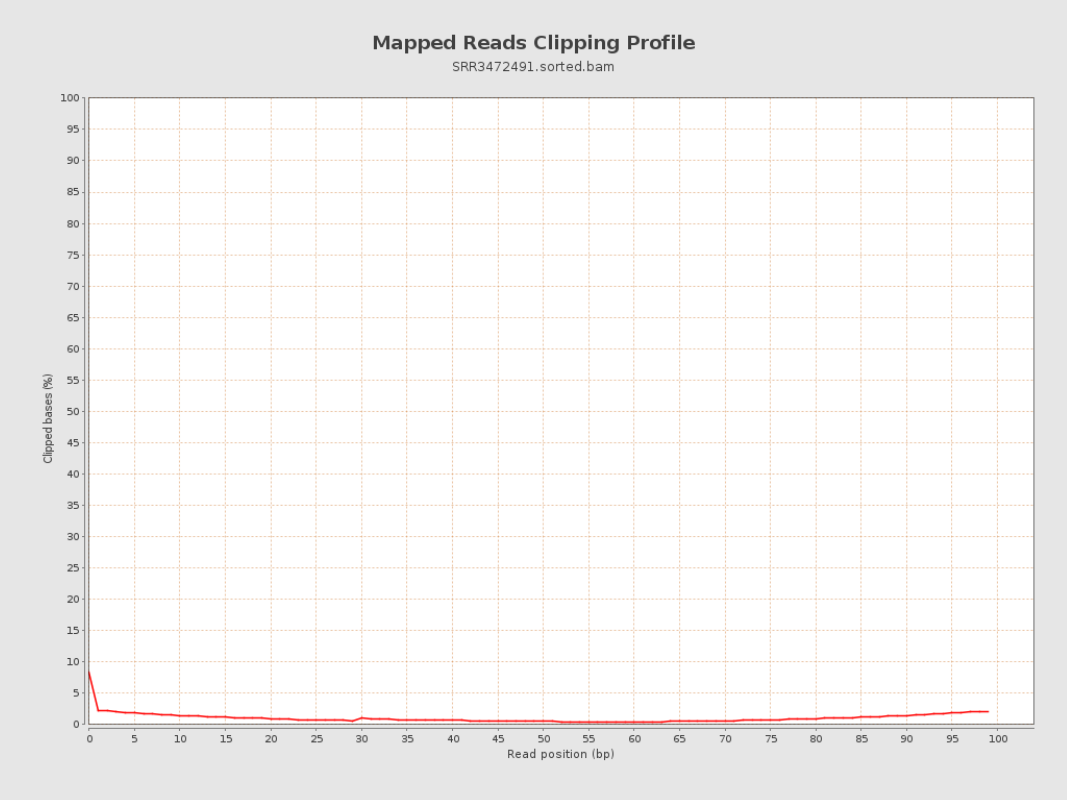
8. Results : Mapped Reads Nucleotide Content



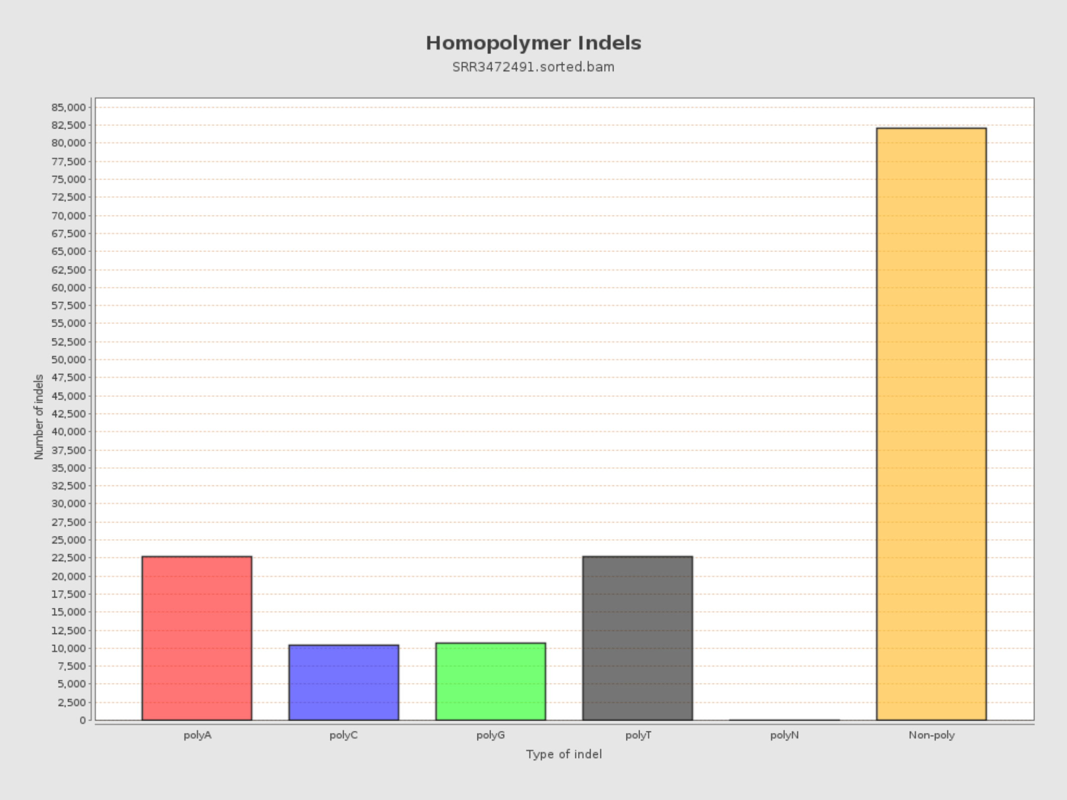
9. Results : Mapped Reads GC-content Distribution



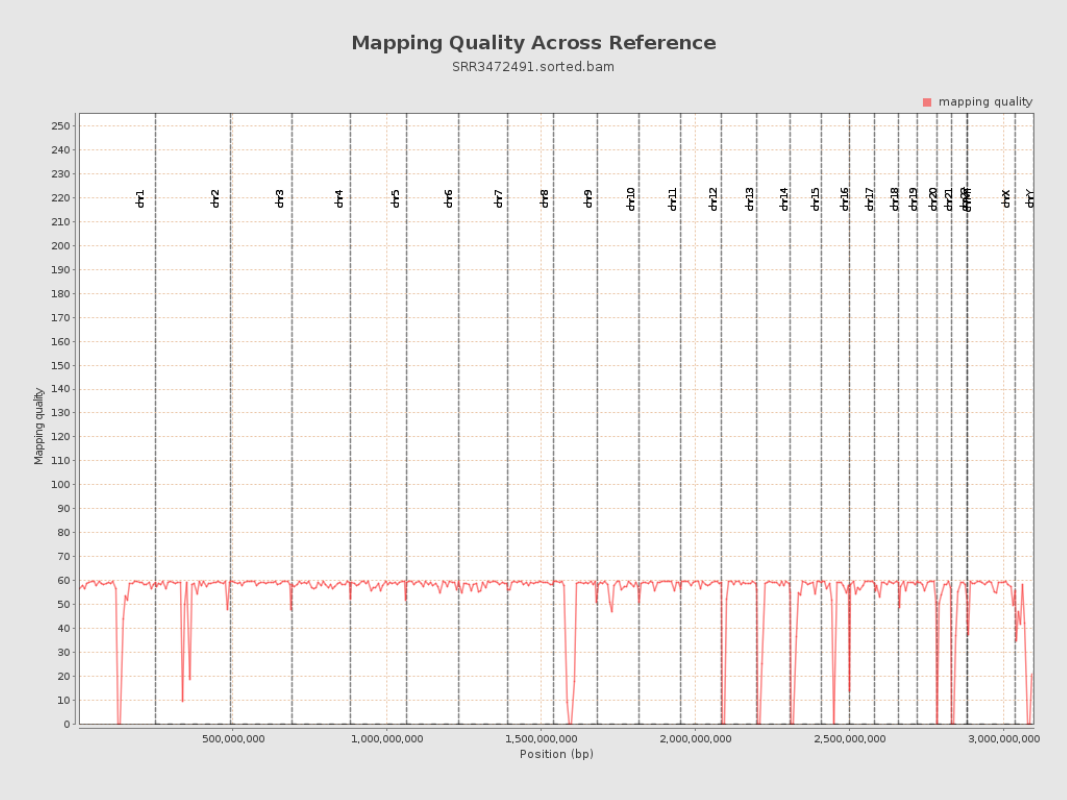
10. Results : Mapped Reads Clipping Profile



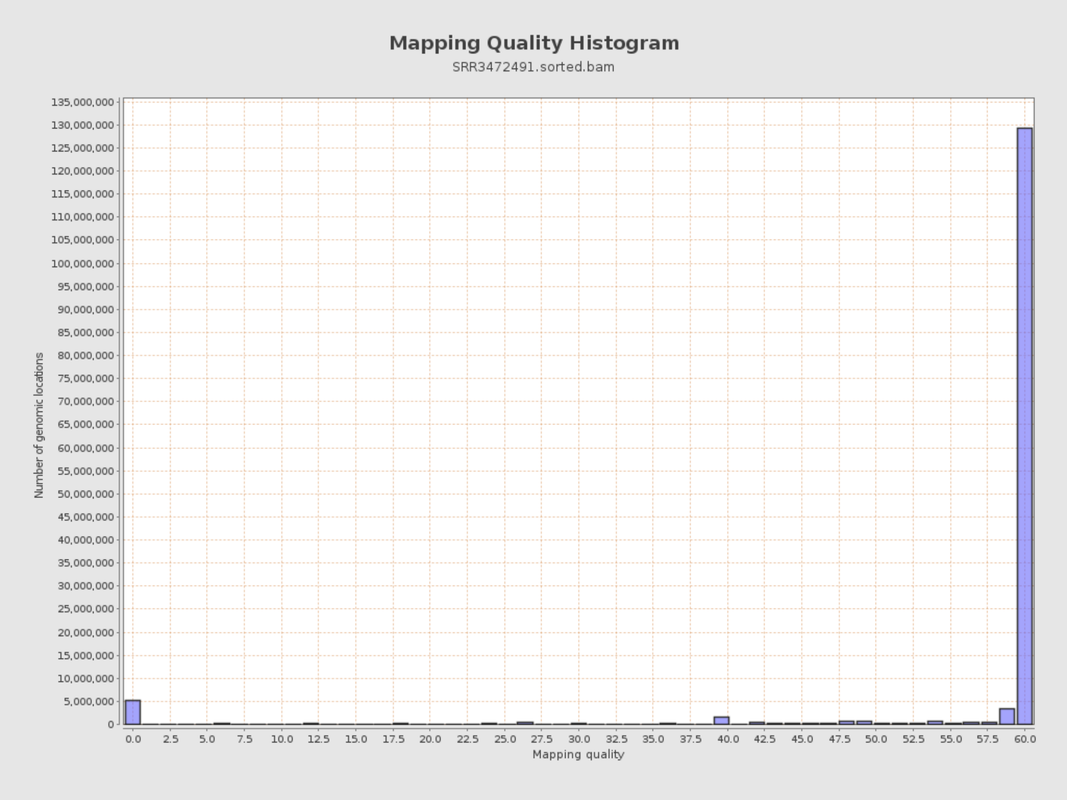
11. Results : Homopolymer Indels



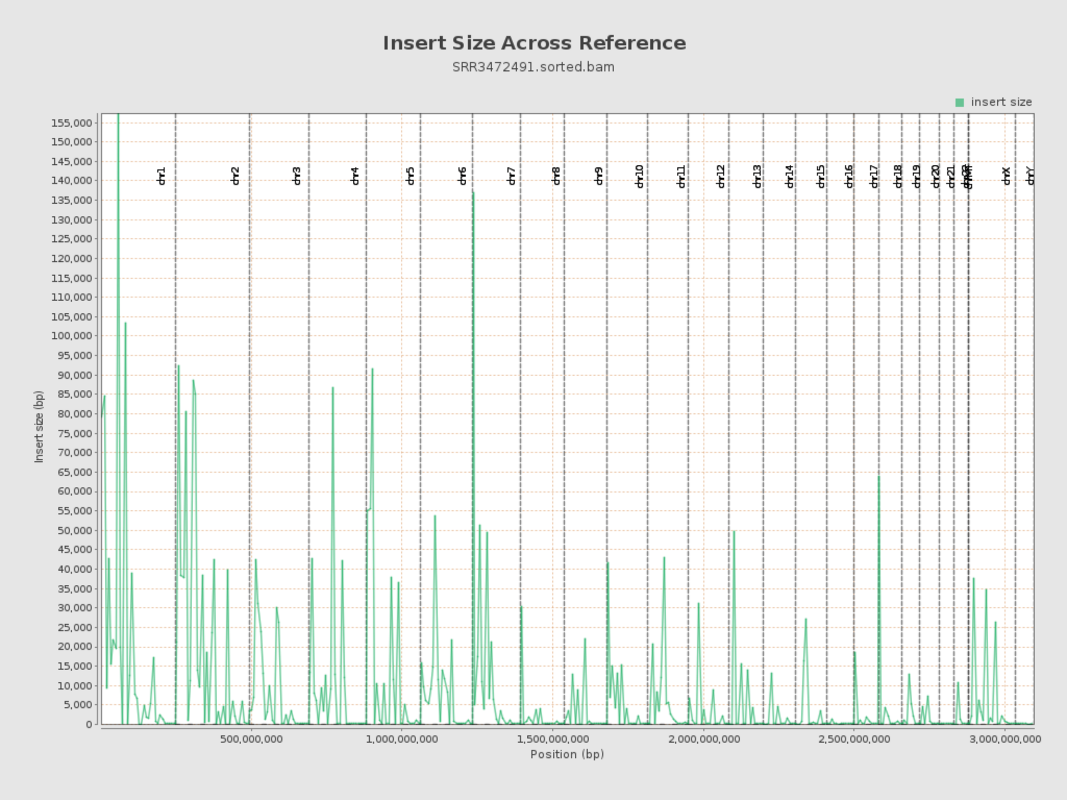
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram