Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 17:29:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472633.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_SRR3472633 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472633_1.fastq.gz SRR3472633_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 17:29:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472633.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,266,132
Mapped reads	19,121,657 / 99.25%
Unmapped reads	144,475 / 0.75%
Mapped paired reads	19,121,657 / 99.25%
Mapped reads, first in pair	9,586,877 / 49.76%
Mapped reads, second in pair	9,534,780 / 49.49%
Mapped reads, both in pair	19,021,256 / 98.73%
Mapped reads, singletons	100,401 / 0.52%
Secondary alignments	0
Supplementary alignments	86,829 / 0.45%
Read min/max/mean length	30 / 101 / 99.76
Duplicated reads (estimated)	13,212,232 / 68.58%
Duplication rate	51.13%
Clipped reads	1,241,757 / 6.45%

2.2. ACGT Content

Number/percentage of A's	506,051,605 / 26.86%
Number/percentage of C's	437,742,461 / 23.23%
Number/percentage of T's	507,357,811 / 26.93%
Number/percentage of G's	432,488,027 / 22.96%
Number/percentage of N's	349,247 / 0.02%

GC Percentage	46.19%

2.3. Coverage

Mean	0.6087
Standard Deviation	23.7736

2.4. Mapping Quality

Mean Mapping Quality	54.87

2.5. Insert size

Mean	19,167.9
Standard Deviation	1,374,414.09
P25/Median/P75	160 / 220 / 291

2.6. Mismatches and indels

General error rate	0.63%
Mismatches	11,573,910
Insertions	111,267
Mapped reads with at least one insertion	0.58%
Deletions	97,808
Mapped reads with at least one deletion	0.5%
Homopolymer indels	47.67%

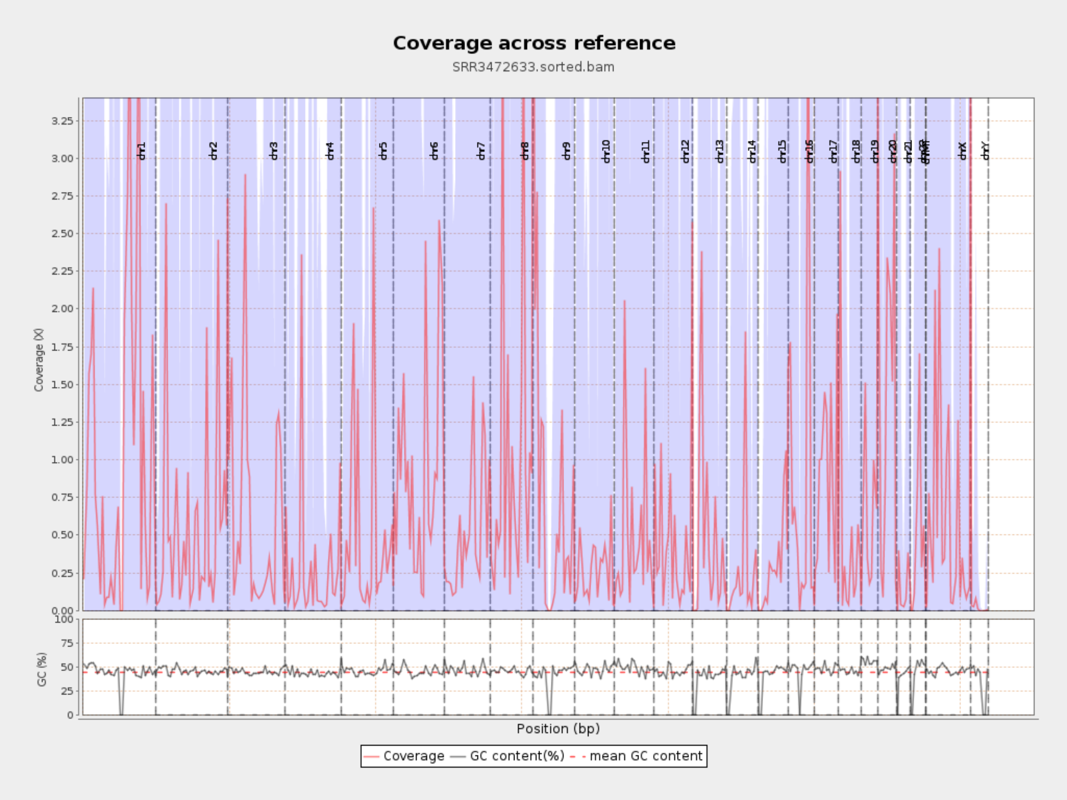
2.7. Chromosome stats

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

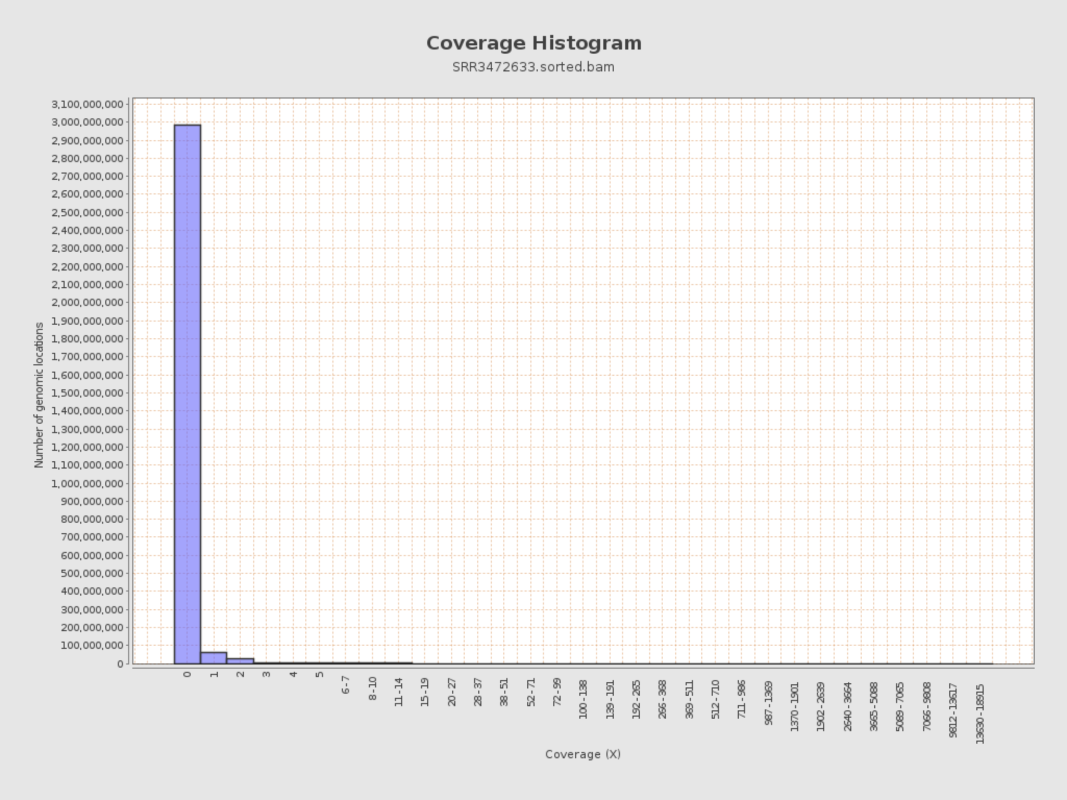
		bases	**coverage**	**deviation**
chr1	249250621	257807079	1.0343	31.5294
chr2	243199373	131821430	0.542	30.1641
chr3	198022430	124891790	0.6307	17.8427
chr4	191154276	55419997	0.2899	13.5089
chr5	180915260	90854867	0.5022	22.4942
chr6	171115067	157623721	0.9212	30.6343
chr7	159138663	84161495	0.5289	18.3403
chr8	146364022	148641649	1.0156	37.7623
chr9	141213431	97607764	0.6912	19.5725
chr10	135534747	38050883	0.2807	11.236
chr11	135006516	64836820	0.4802	20.563
chr12	133851895	57948010	0.4329	13.4884
chr13	115169878	56138549	0.4874	20.2932
chr14	107349540	27937837	0.2603	15.079
chr15	102531392	31022688	0.3026	11.2402
chr16	90354753	75786106	0.8388	28.7192
chr17	81195210	70315240	0.866	21.3722
chr18	78077248	38532218	0.4935	28.9328
chr19	59128983	43359101	0.7333	20.8814
chr20	63025520	92013363	1.4599	45.9386
chr21	48129895	7943895	0.1651	6.6568
chr22	51304566	27070943	0.5277	18.3208
chrMT	16571	1133	0.0684	0.2657
chrX	155270560	103314166	0.6654	22.0404

chrY	59373566	1123696	0.0189	0.9462

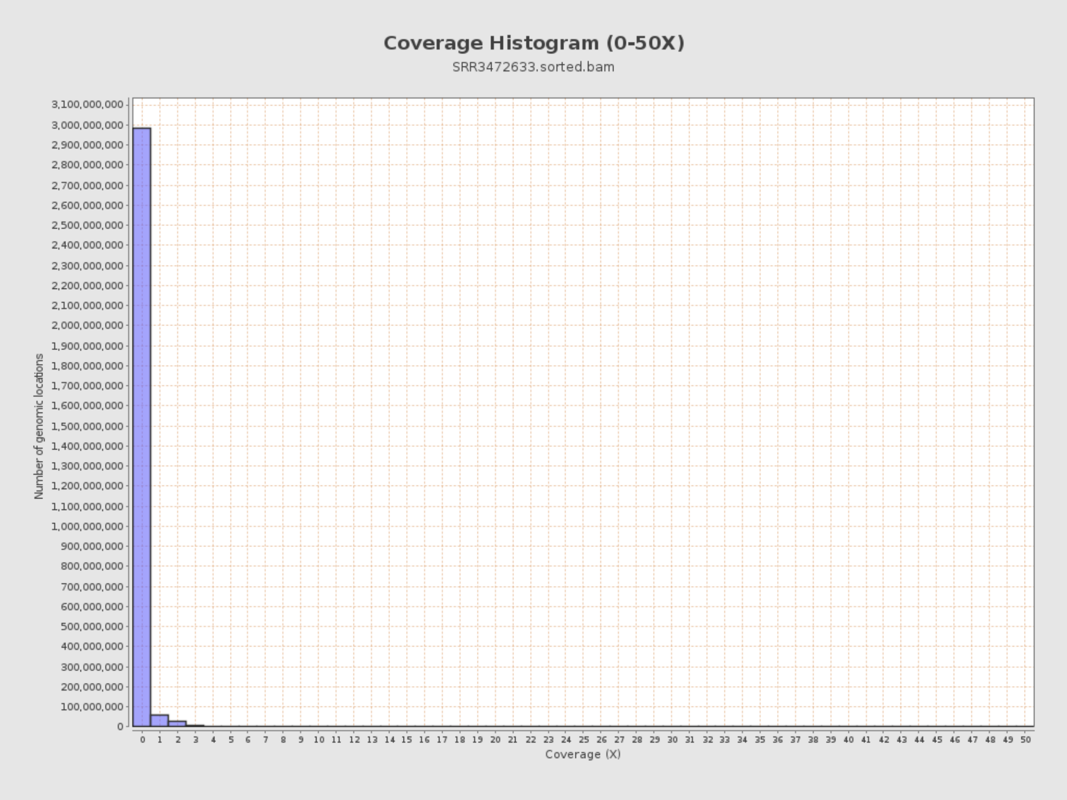
3. Results : Coverage across reference



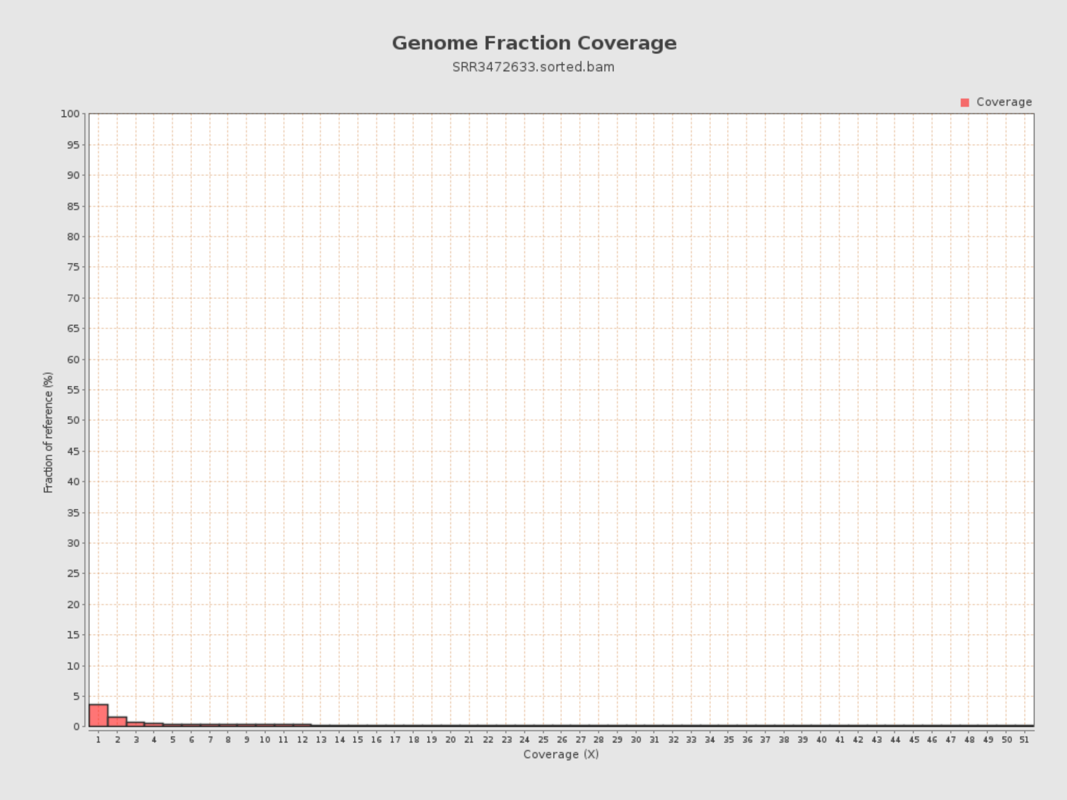
4. Results : Coverage Histogram



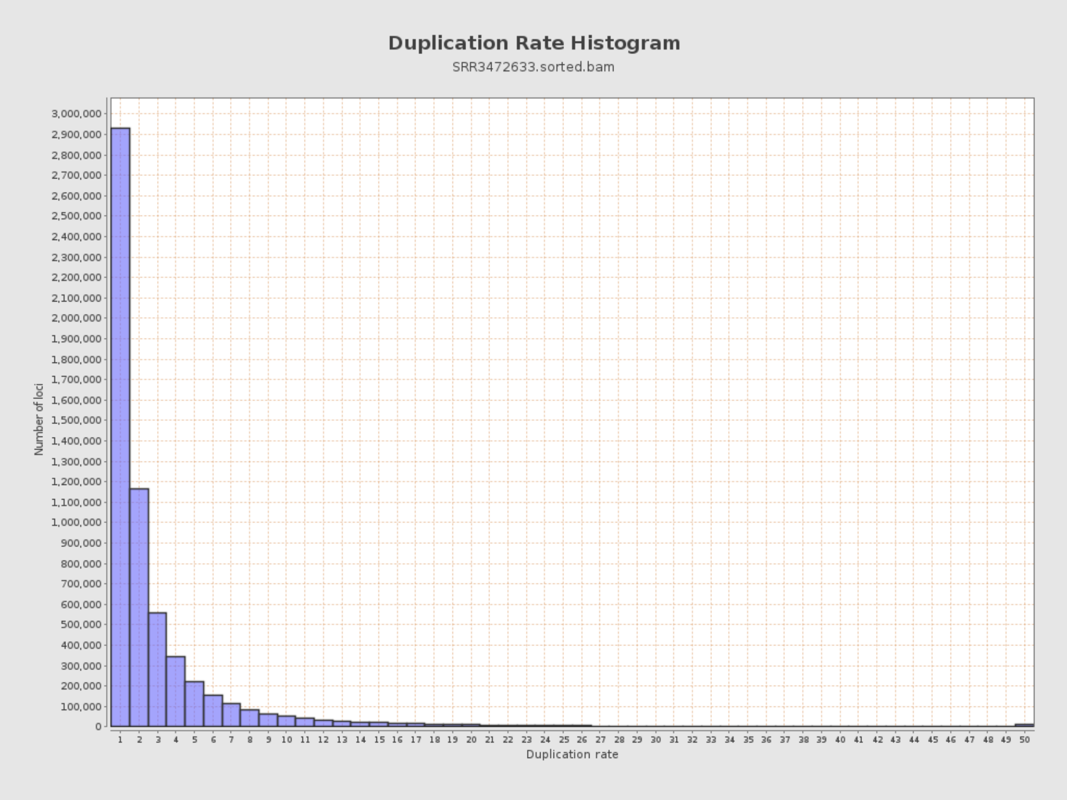
5. Results : Coverage Histogram (0-50X)



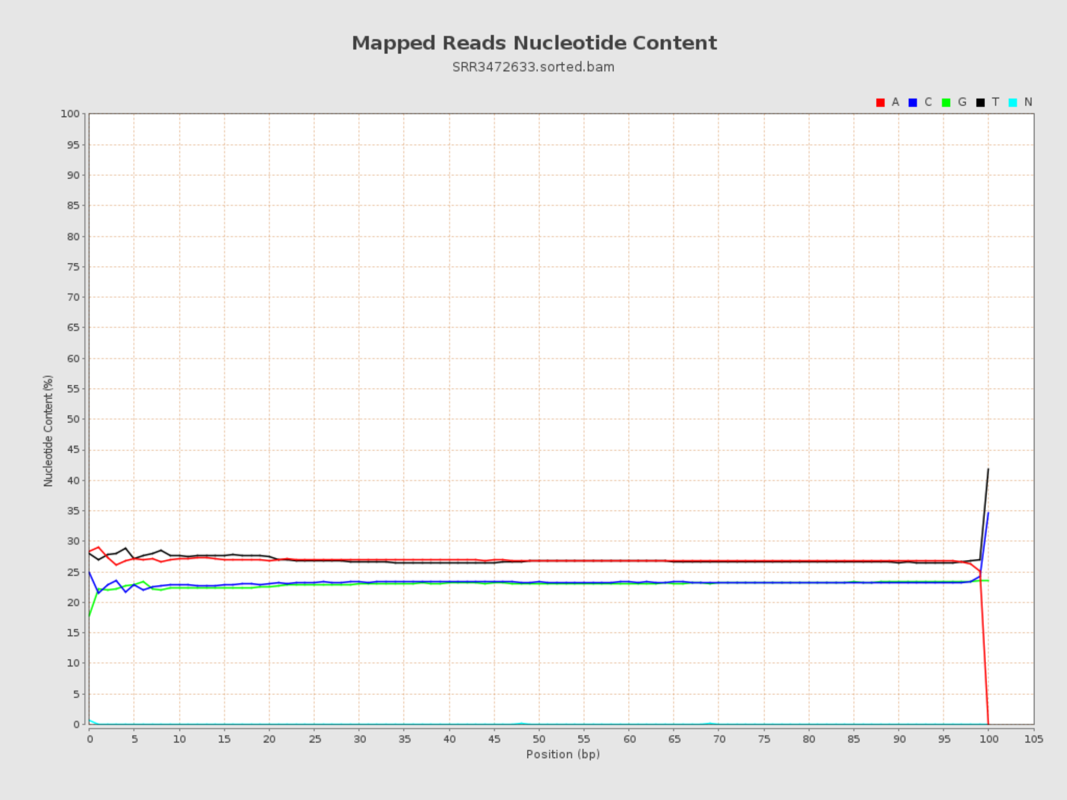
6. Results : Genome Fraction Coverage



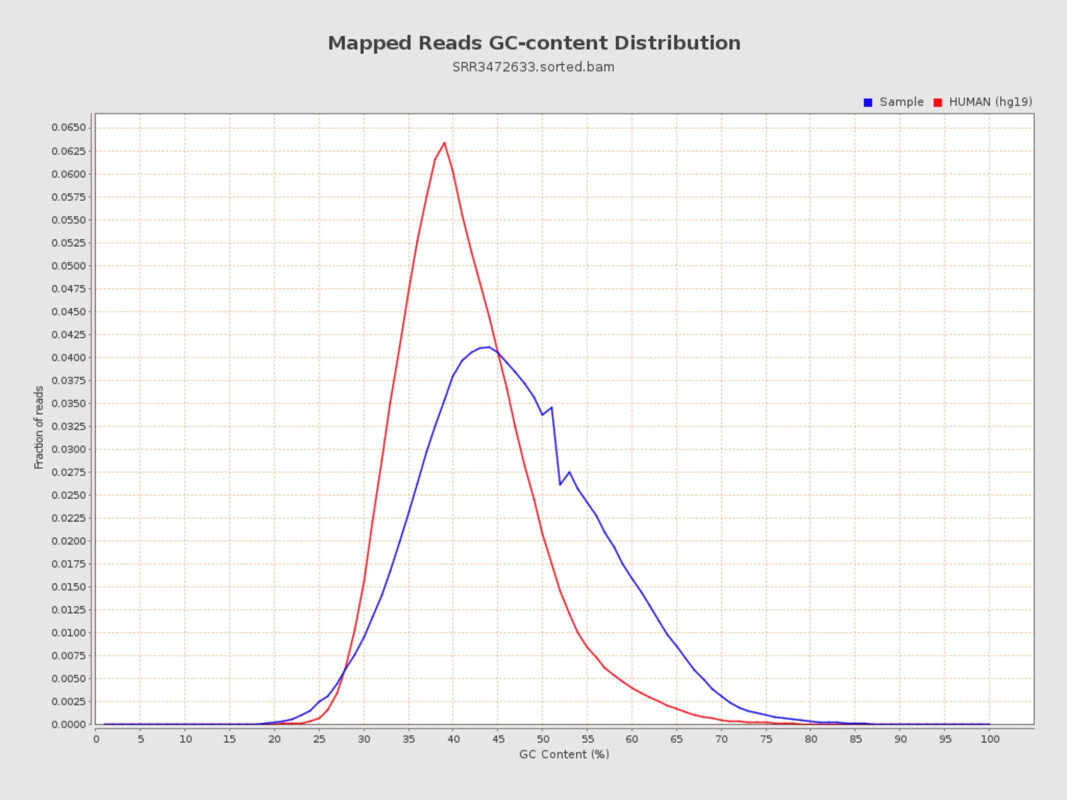
7. Results : Duplication Rate Histogram



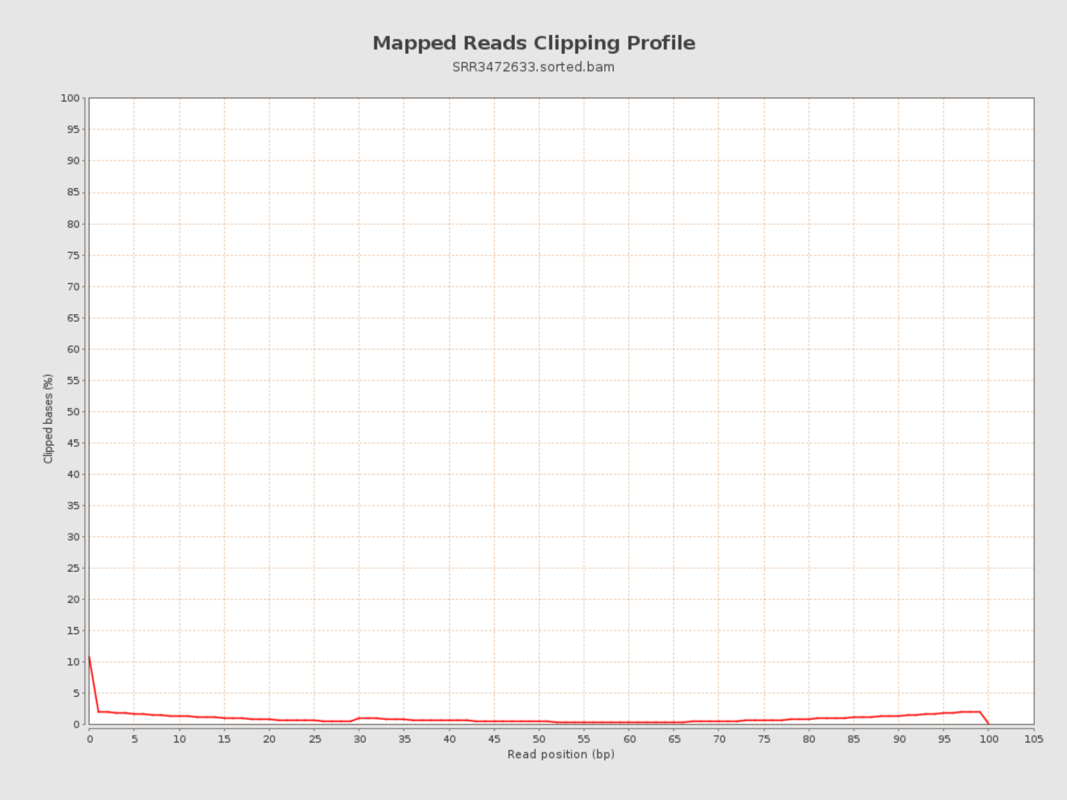
8. Results : Mapped Reads Nucleotide Content



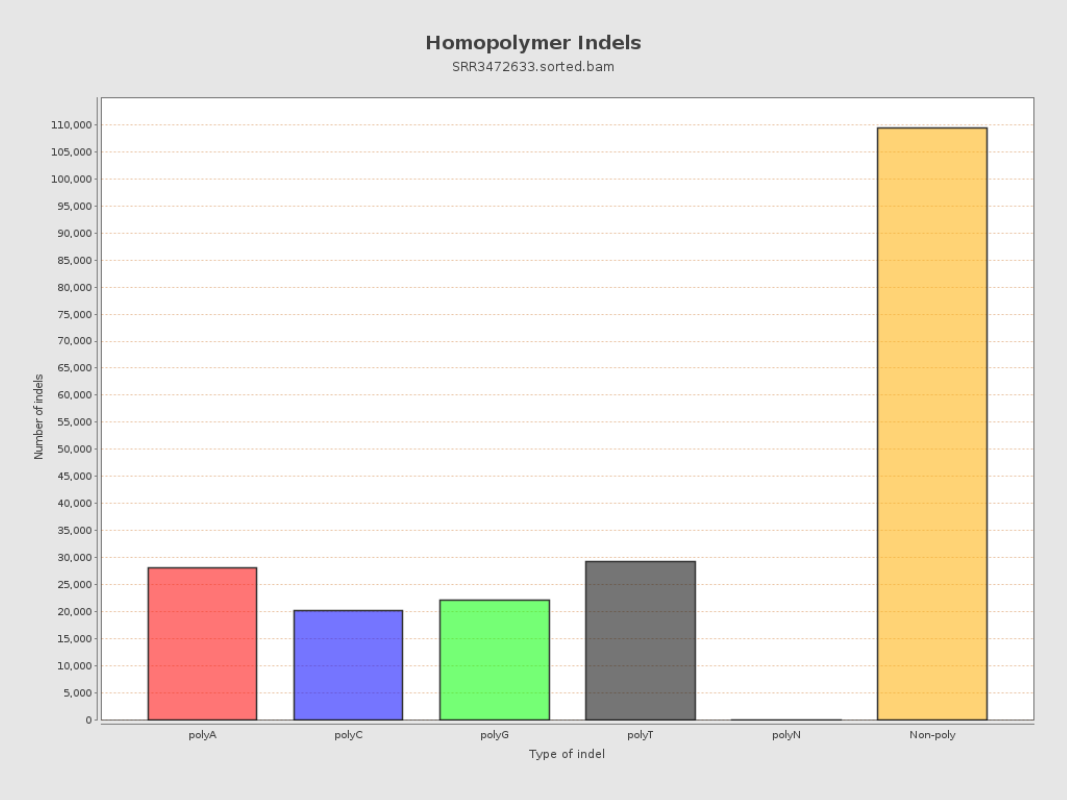
9. Results : Mapped Reads GC-content Distribution



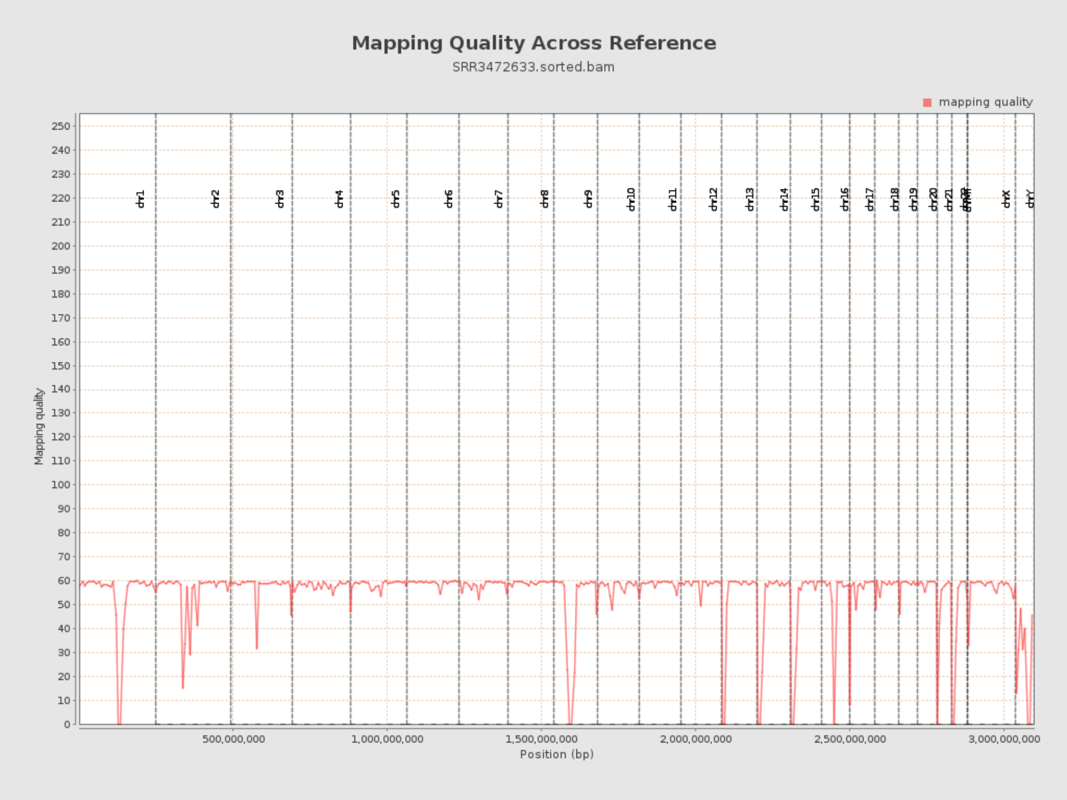
10. Results : Mapped Reads Clipping Profile



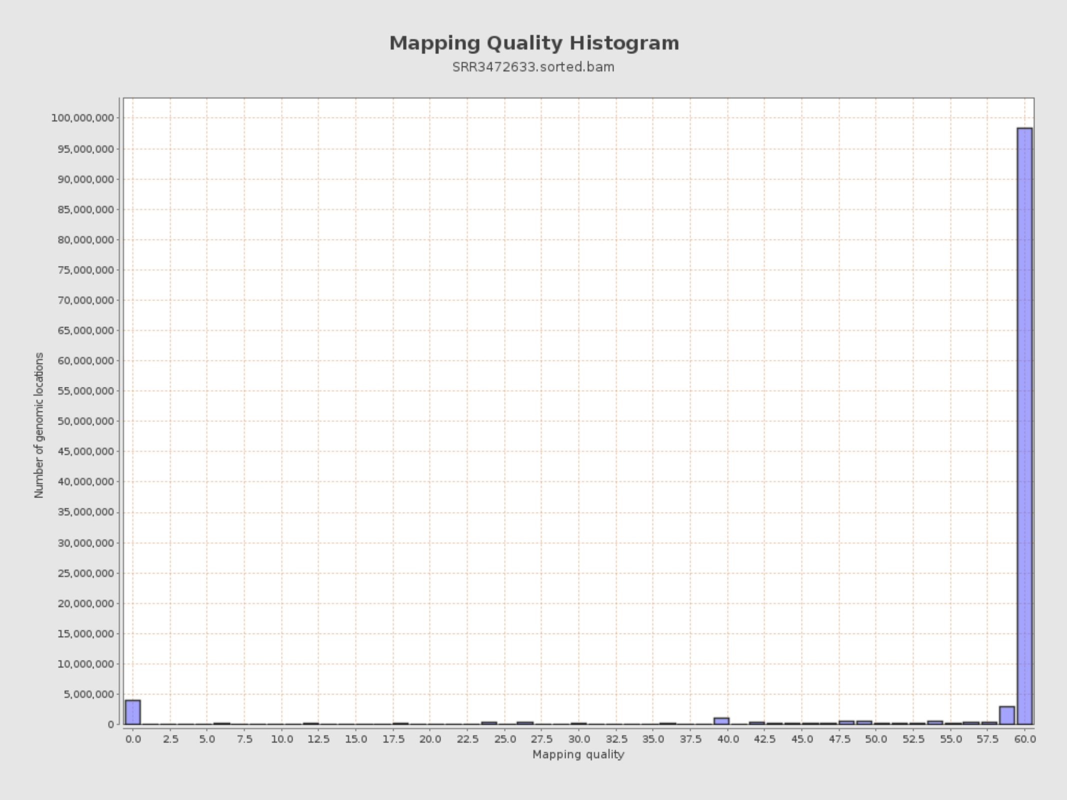
11. Results : Homopolymer Indels



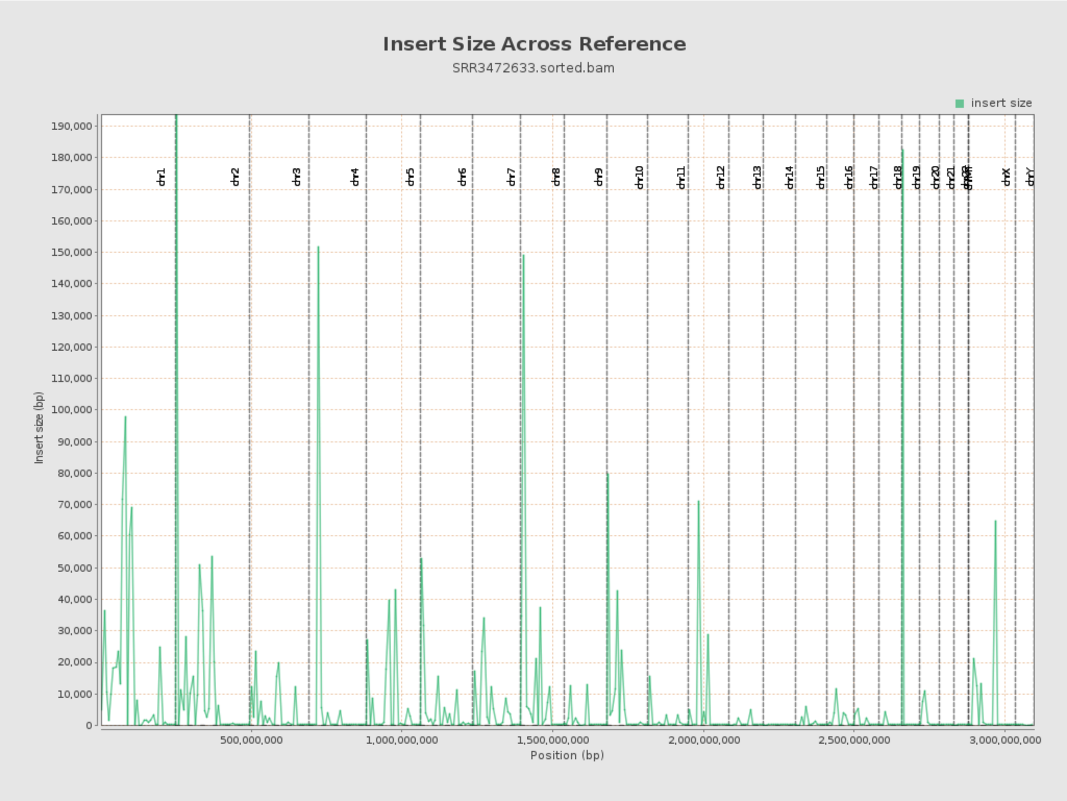
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram