Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 22:50:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472655.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_SRR3472655 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472655_1.fastq.gz SRR3472655_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 22:50:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472655.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	21,369,974
Mapped reads	21,168,363 / 99.06%
Unmapped reads	201,611 / 0.94%
Mapped paired reads	21,168,363 / 99.06%
Mapped reads, first in pair	10,609,049 / 49.64%
Mapped reads, second in pair	10,559,314 / 49.41%
Mapped reads, both in pair	21,038,050 / 98.45%
Mapped reads, singletons	130,313 / 0.61%
Secondary alignments	0
Supplementary alignments	139,289 / 0.65%
Read min/max/mean length	30 / 101 / 99.88
Duplicated reads (estimated)	15,594,652 / 72.97%
Duplication rate	49.79%
Clipped reads	1,594,118 / 7.46%

2.2. ACGT Content

Number/percentage of A's	560,744,750 / 26.92%
Number/percentage of C's	483,853,468 / 23.23%
Number/percentage of T's	561,034,701 / 26.93%
Number/percentage of G's	477,042,108 / 22.9%
Number/percentage of N's	396,003 / 0.02%

GC Percentage	46.13%

2.3. Coverage

Mean	0.673
Standard Deviation	34.5842

2.4. Mapping Quality

Mean Mapping Quality	54.61

2.5. Insert size

Mean	23,197.24
Standard Deviation	1,561,661.36
P25/Median/P75	162 / 220 / 290

2.6. Mismatches and indels

General error rate	0.66%
Mismatches	13,491,682
Insertions	139,312
Mapped reads with at least one insertion	0.65%
Deletions	107,207
Mapped reads with at least one deletion	0.5%
Homopolymer indels	47.5%

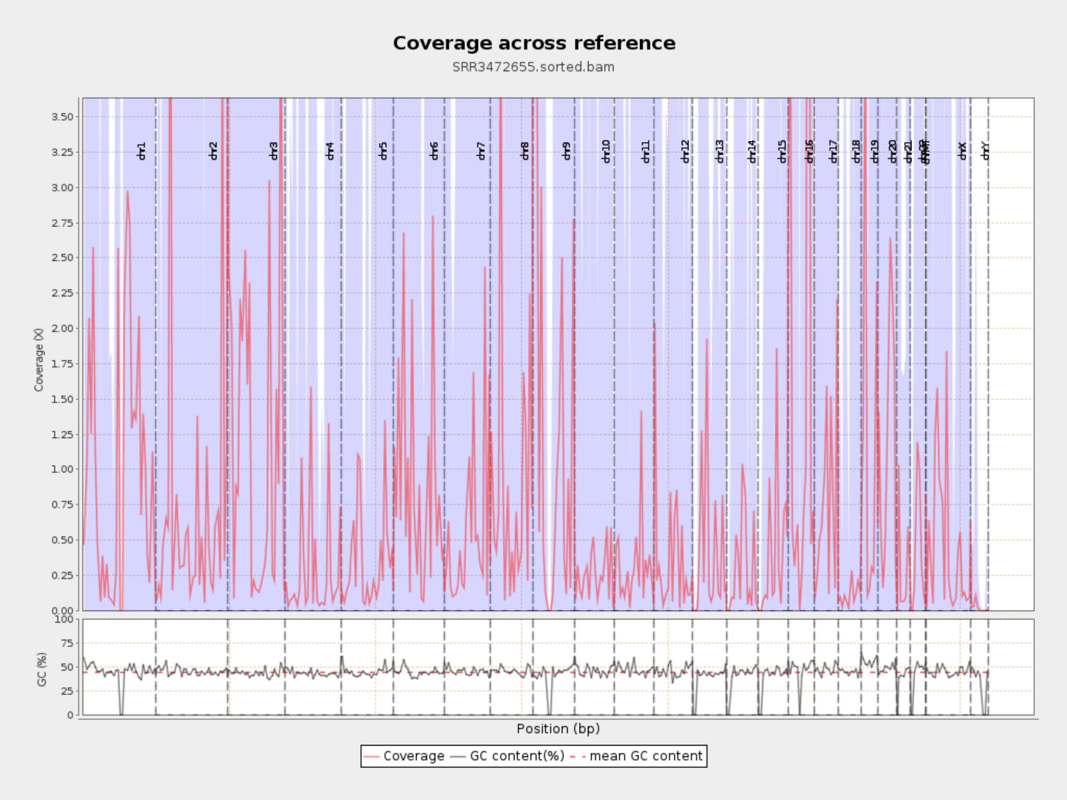
2.7. Chromosome stats

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

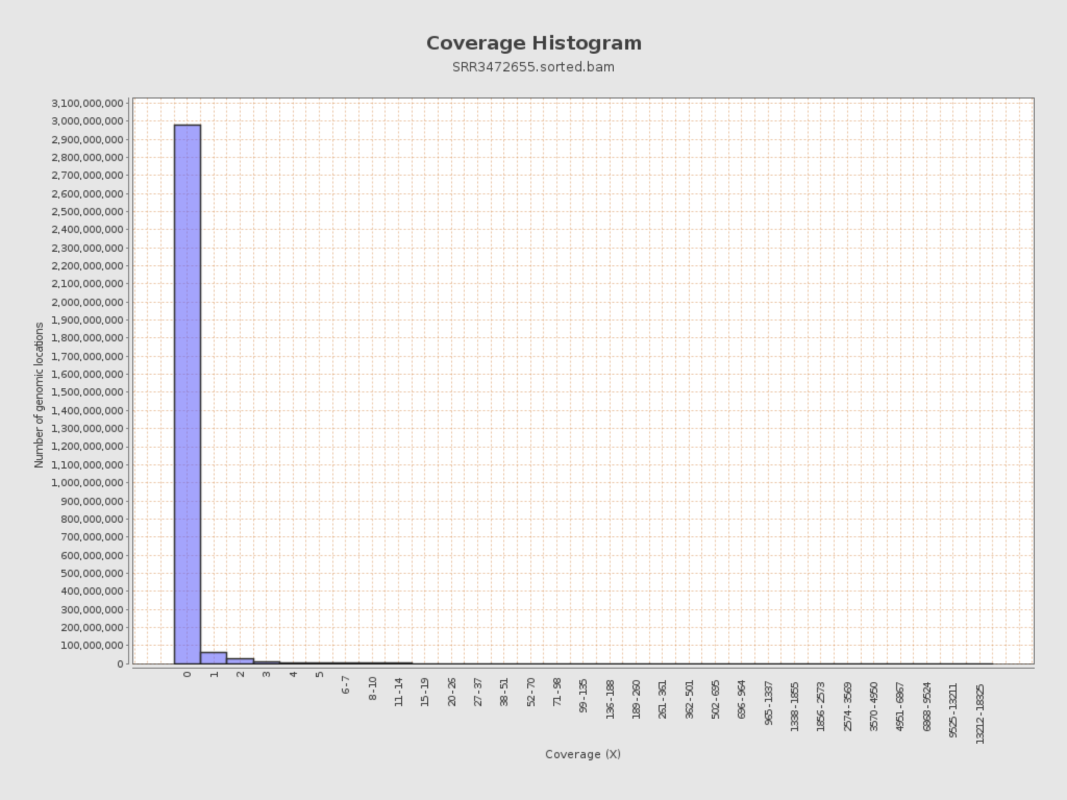
		bases	coverage	deviation
chr1	249250621	249672793	1.0017	38.533
chr2	243199373	176161876	0.7244	46.9834
chr3	198022430	239492057	1.2094	50.3235
chr4	191154276	56641455	0.2963	19.953
chr5	180915260	64052584	0.354	17.3952
chr6	171115067	156056273	0.912	44.8293
chr7	159138663	93557514	0.5879	24.949
chr8	146364022	135694292	0.9271	43.2906
chr9	141213431	175439144	1.2424	38.1896
chr10	135534747	35809931	0.2642	16.368
chr11	135006516	42624001	0.3157	24.6388
chr12	133851895	50767880	0.3793	21.2317
chr13	115169878	48307494	0.4194	16.6261
chr14	107349540	31447012	0.2929	16.1437
chr15	102531392	41063707	0.4005	32.8804
chr16	90354753	153752470	1.7017	67.3107
chr17	81195210	60512684	0.7453	28.9709
chr18	78077248	8589938	0.11	5.9914
chr19	59128983	72493983	1.226	53.8811
chr20	63025520	78787356	1.2501	38.2152
chr21	48129895	15633610	0.3248	20.4327
chr22	51304566	21742715	0.4238	18.9231
chrMT	16571	13660	0.8243	1.1852
chrX	155270560	73630634	0.4742	26.3606

chrY	59373566	1389102	0.0234	1.0918

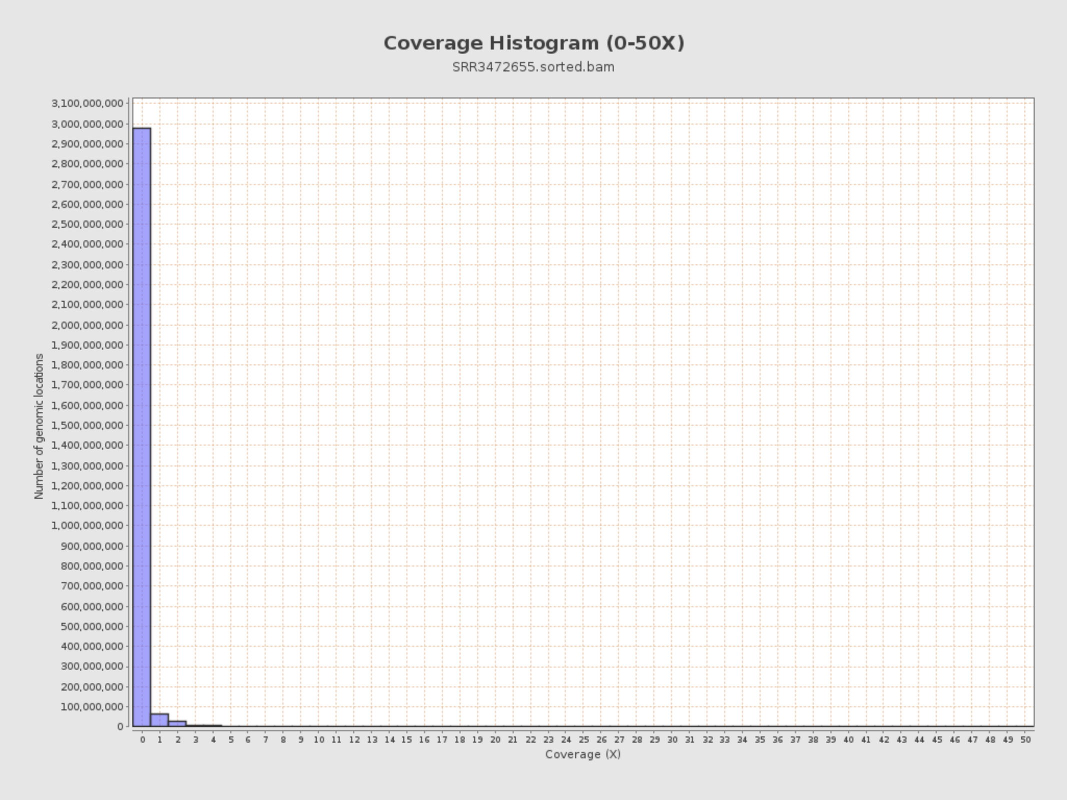
3. Results : Coverage across reference



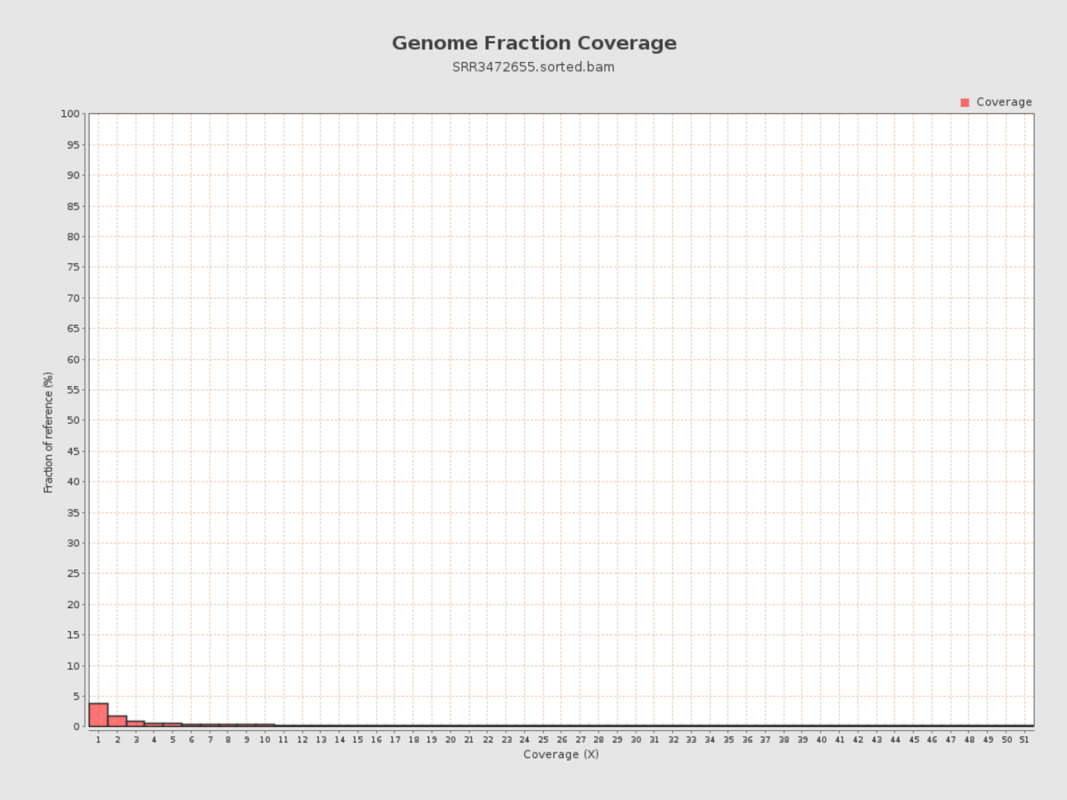
4. Results : Coverage Histogram



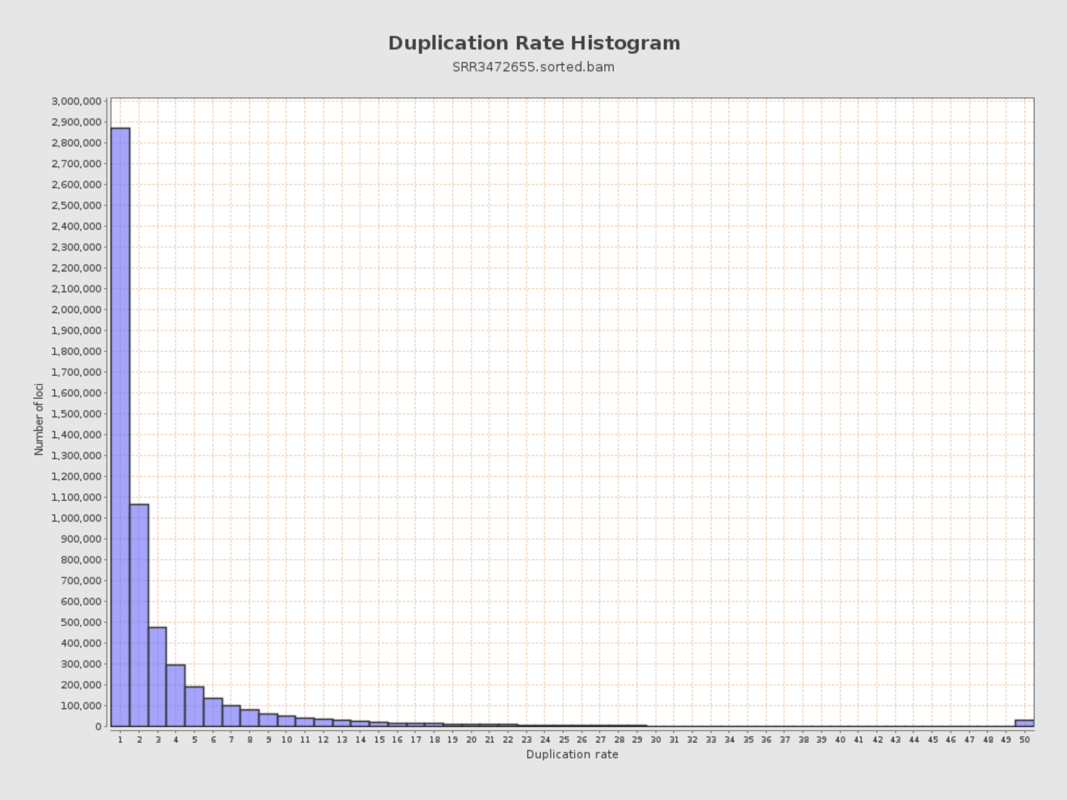
5. Results : Coverage Histogram (0-50X)



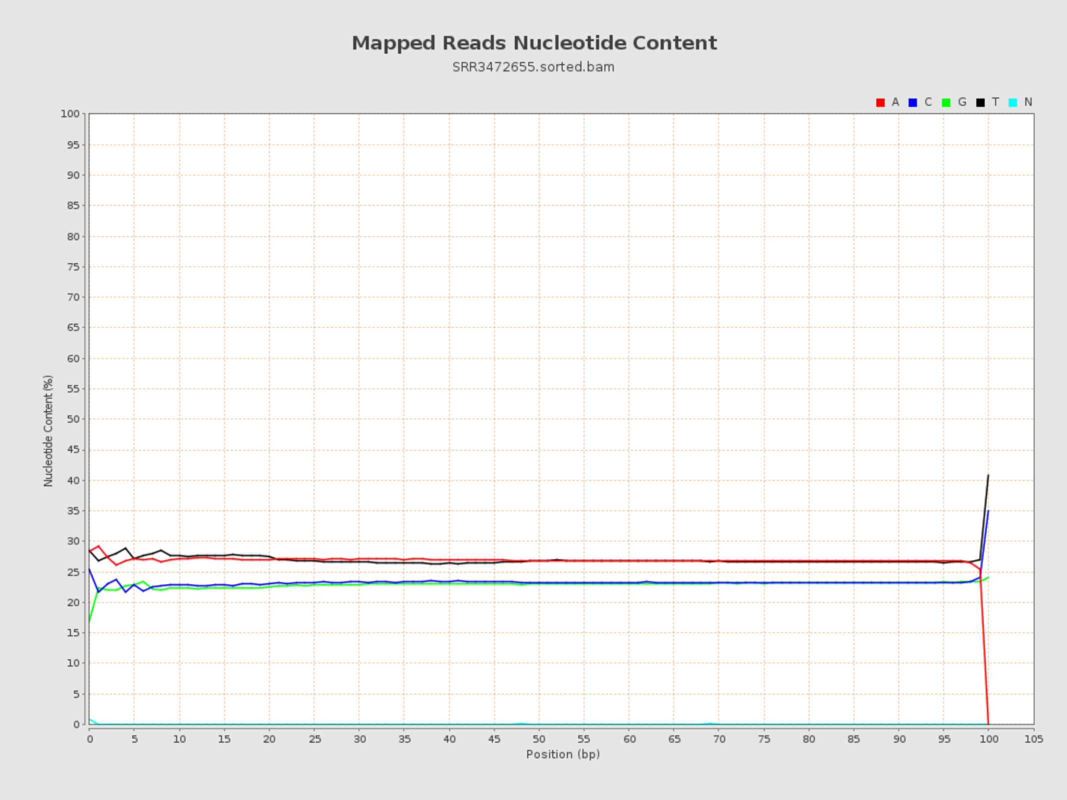
6. Results : Genome Fraction Coverage



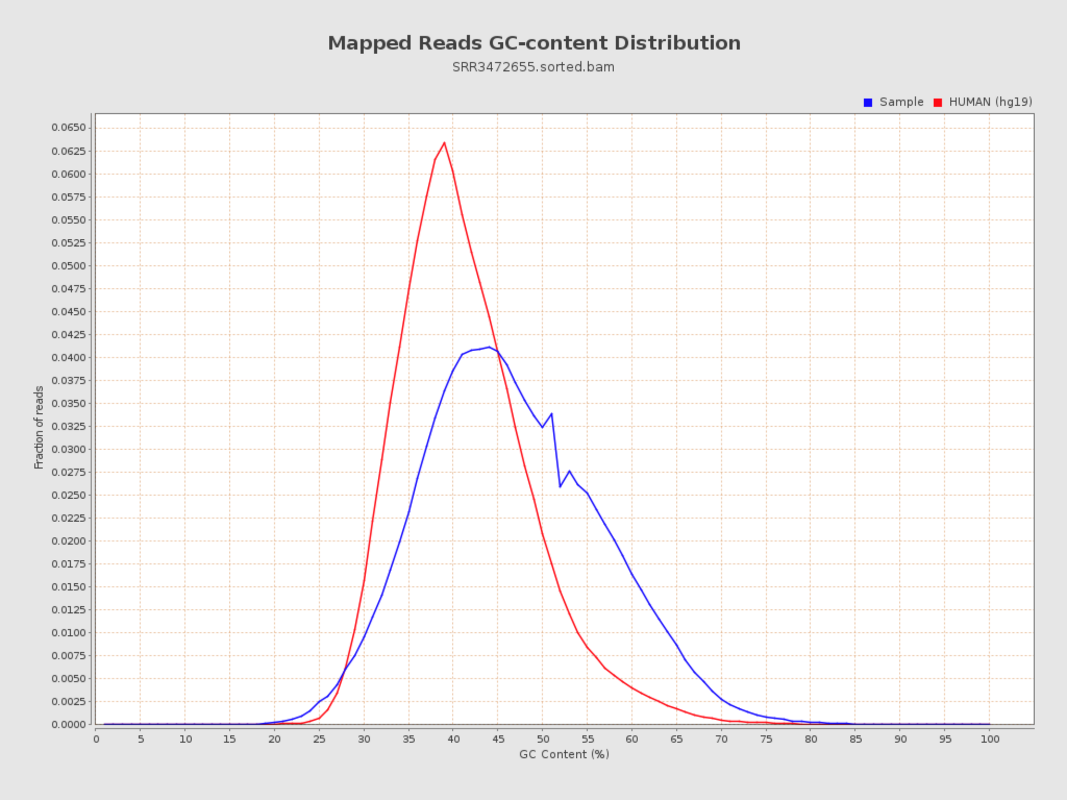
7. Results : Duplication Rate Histogram



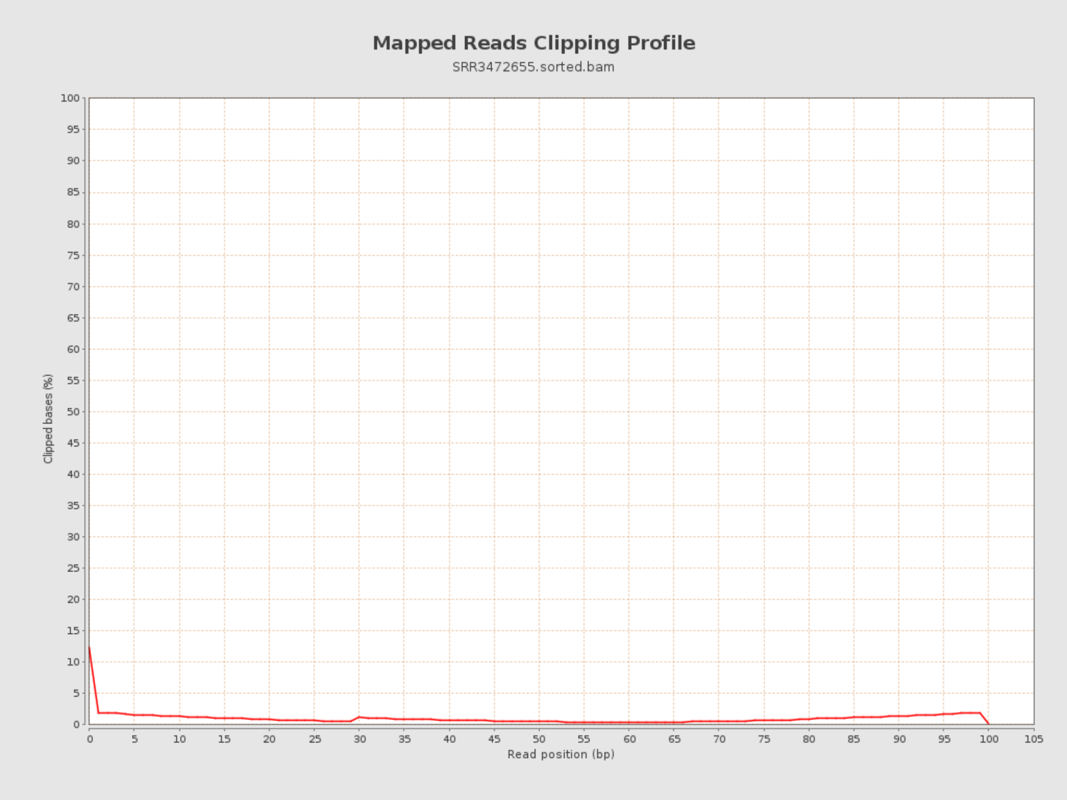
8. Results : Mapped Reads Nucleotide Content



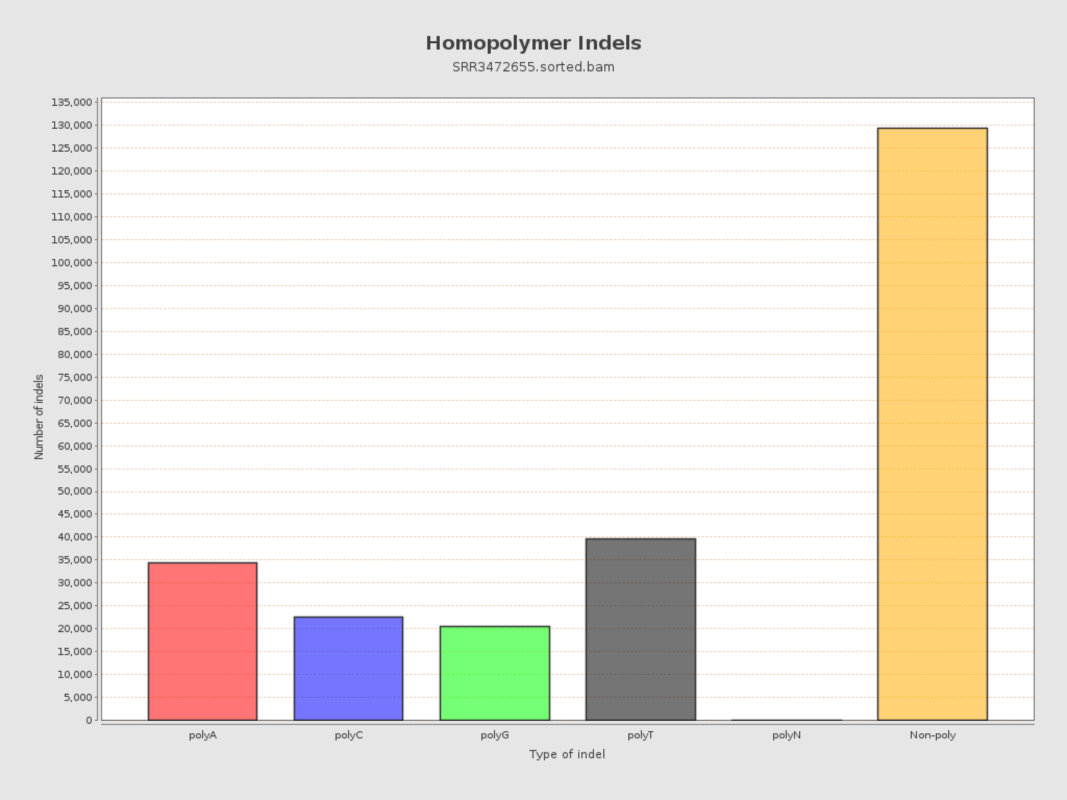
9. Results : Mapped Reads GC-content Distribution



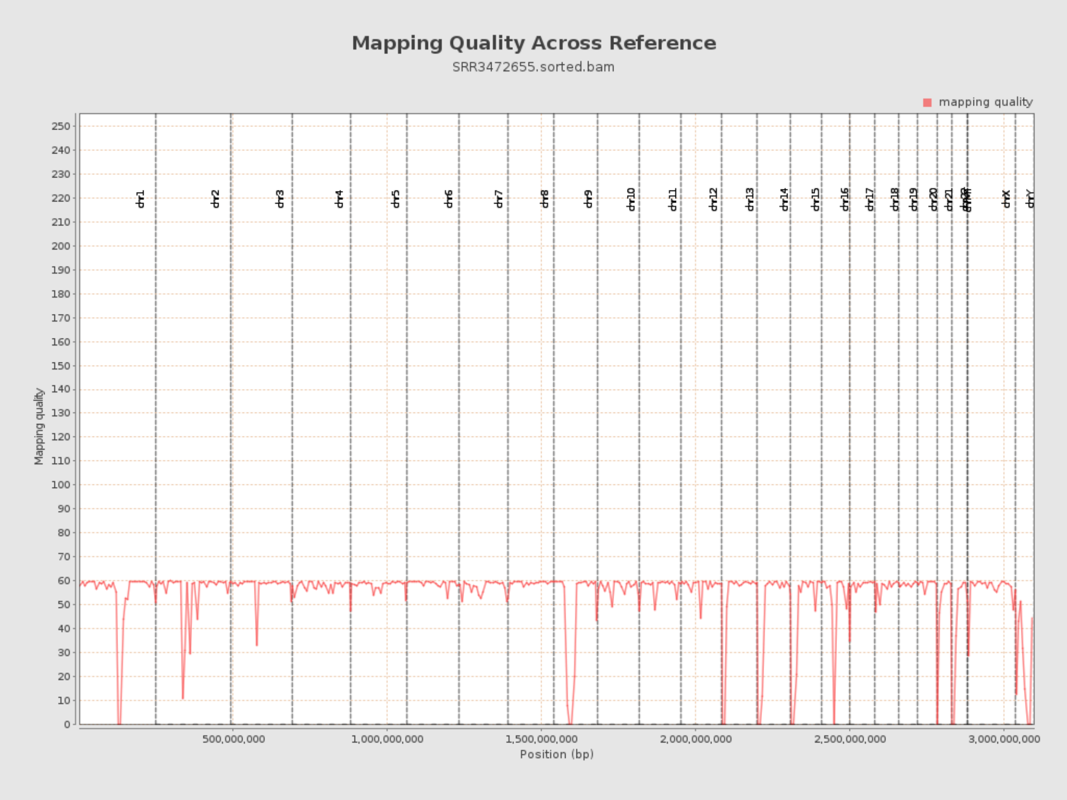
10. Results : Mapped Reads Clipping Profile



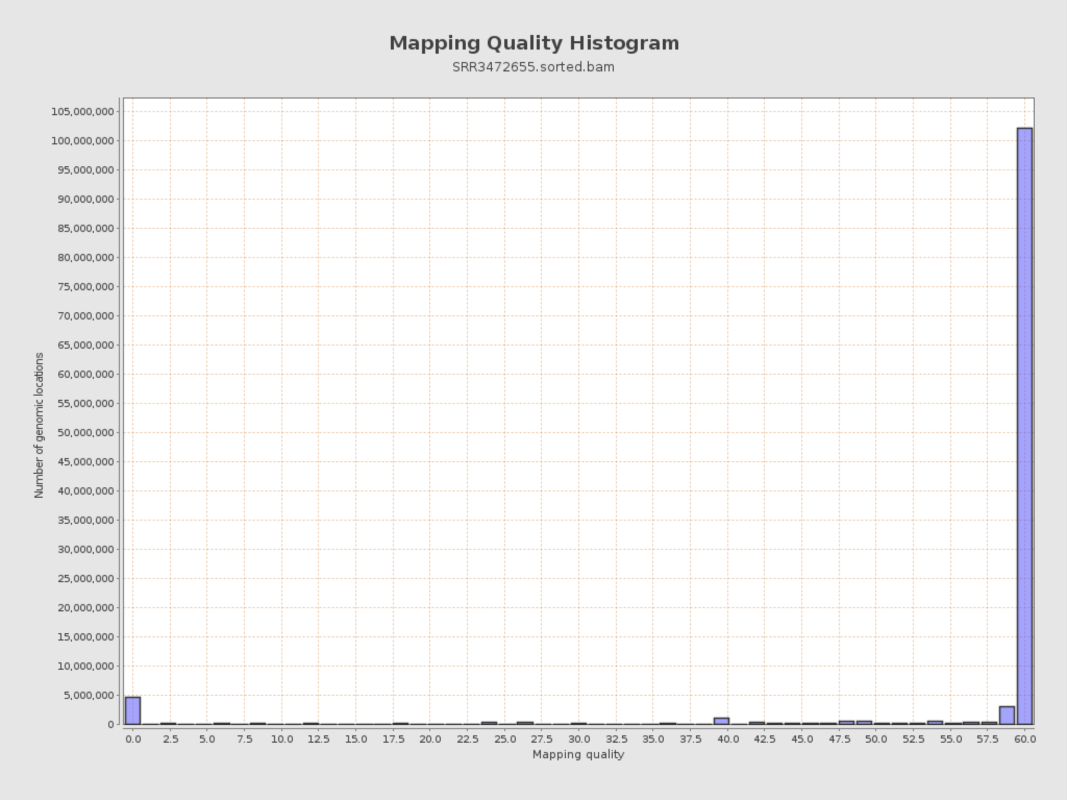
11. Results : Homopolymer Indels



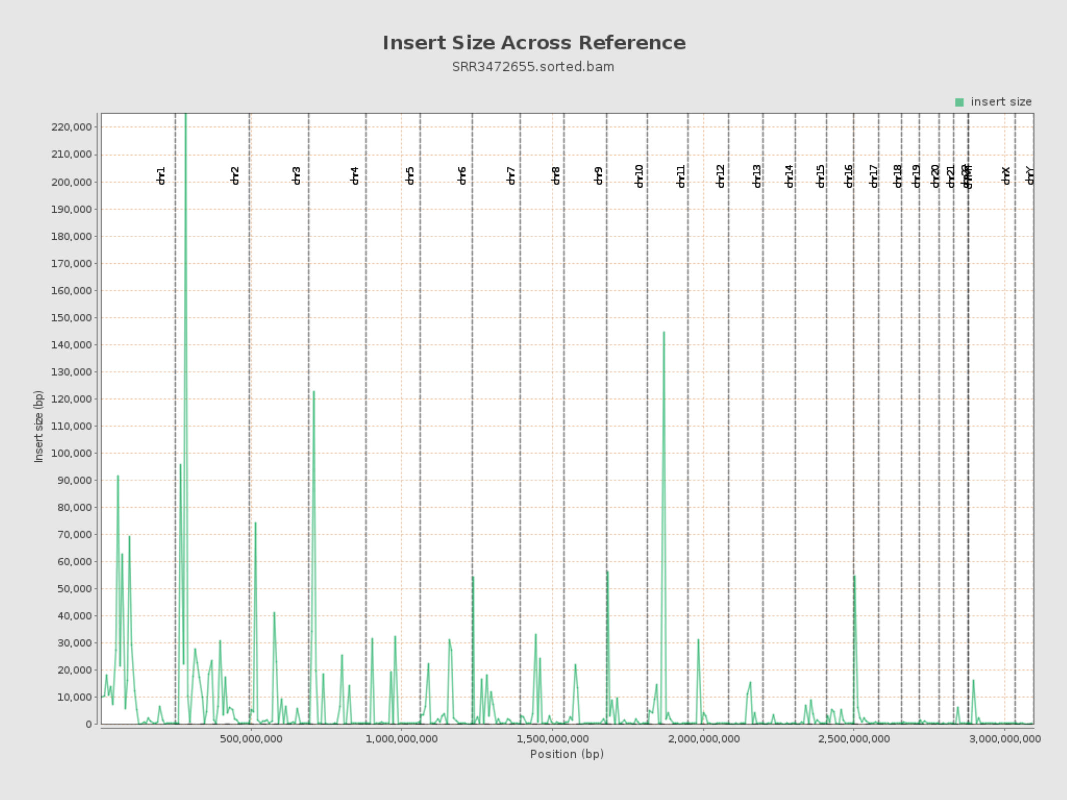
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram