Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 06:05:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472378.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_SRR3472378 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472378_1.fastq.gz SRR3472378_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 06:05:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472378.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,203,194
Mapped reads	19,038,462 / 99.14%
Unmapped reads	164,732 / 0.86%
Mapped paired reads	19,038,462 / 99.14%
Mapped reads, first in pair	9,556,396 / 49.76%
Mapped reads, second in pair	9,482,066 / 49.38%
Mapped reads, both in pair	18,927,200 / 98.56%
Mapped reads, singletons	111,262 / 0.58%
Secondary alignments	0
Supplementary alignments	71,084 / 0.37%
Read min/max/mean length	30 / 100 / 99.39
Duplicated reads (estimated)	11,889,296 / 61.91%
Duplication rate	47.75%
Clipped reads	1,300,445 / 6.77%

2.2. ACGT Content

Number/percentage of A's	506,589,205 / 27.13%
Number/percentage of C's	428,210,233 / 22.93%
Number/percentage of T's	507,560,556 / 27.18%
Number/percentage of G's	424,488,561 / 22.74%
Number/percentage of N's	230,444 / 0.01%

GC Percentage	45.67%

2.3. Coverage

Mean	0.6032
Standard Deviation	17.5208

2.4. Mapping Quality

Mean Mapping Quality	54.85

2.5. Insert size

Mean	17,269.51
Standard Deviation	1,274,467.86
P25/Median/P75	155 / 215 / 290

2.6. Mismatches and indels

General error rate	0.54%
Mismatches	9,958,885
Insertions	109,692
Mapped reads with at least one insertion	0.57%
Deletions	90,349
Mapped reads with at least one deletion	0.47%
Homopolymer indels	45.44%

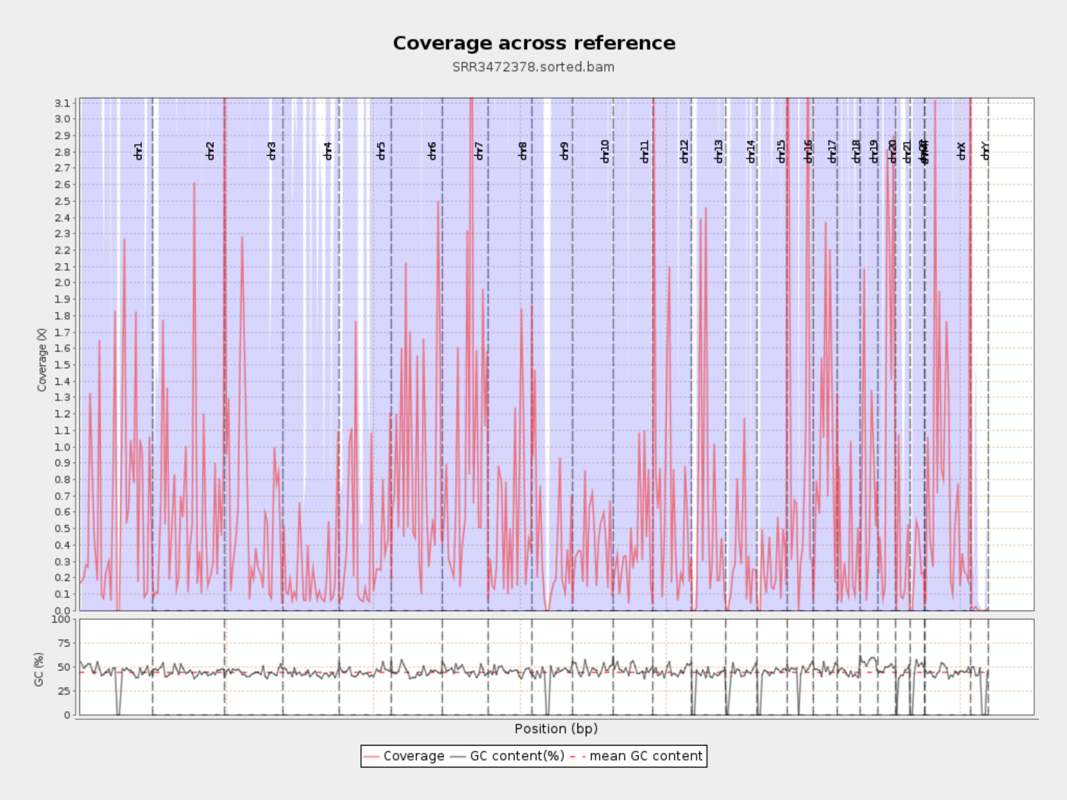
2.7. Chromosome stats

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

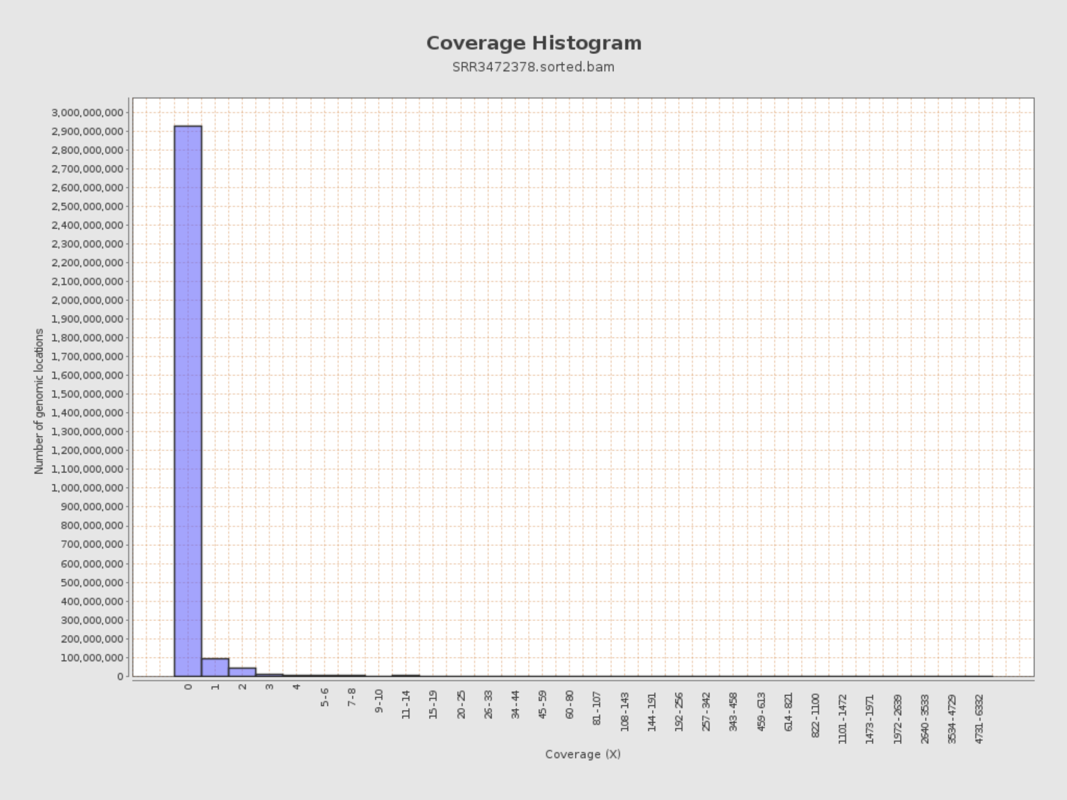
		bases	**coverage**	**deviation**
chr1	249250621	162999820	0.654	17.9242
chr2	243199373	142311524	0.5852	16.9435
chr3	198022430	133541865	0.6744	13.8572
chr4	191154276	41890475	0.2191	7.2861
chr5	180915260	78200284	0.4322	14.1098
chr6	171115067	156413408	0.9141	21.6205
chr7	159138663	171073223	1.075	29.4126
chr8	146364022	80276863	0.5485	16.3102
chr9	141213431	57272676	0.4056	9.0326
chr10	135534747	56018659	0.4133	11.4191
chr11	135006516	54682678	0.405	12.5995
chr12	133851895	101295209	0.7568	16.9354
chr13	115169878	71751976	0.623	20.7276
chr14	107349540	33038623	0.3078	8.7204
chr15	102531392	25604086	0.2497	7.1899
chr16	90354753	99738320	1.1039	29.3055
chr17	81195210	87541428	1.0782	23.3081
chr18	78077248	26177488	0.3353	11.8907
chr19	59128983	51577417	0.8723	20.0444
chr20	63025520	80405251	1.2758	35.4361
chr21	48129895	15059678	0.3129	18.2015
chr22	51304566	13398599	0.2612	6.5906
chrMT	16571	3172	0.1914	0.5172
chrX	155270560	126577743	0.8152	18.5749

chrY	59373566	440281	0.0074	0.655

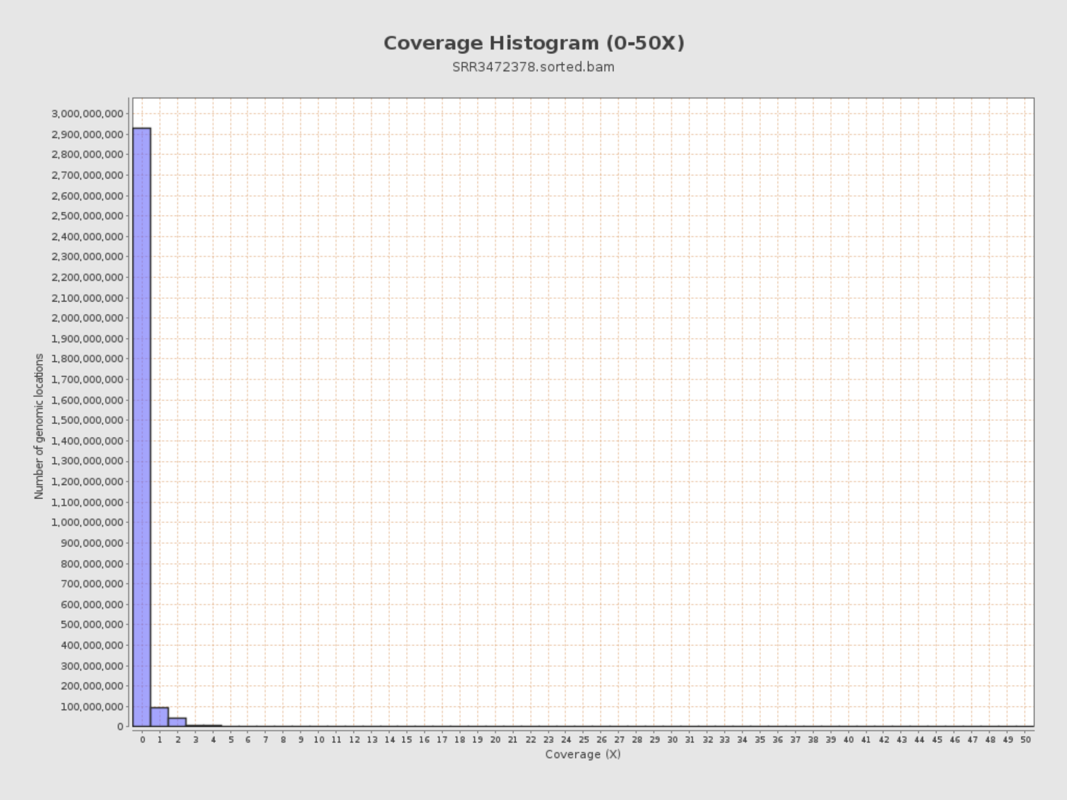
3. Results : Coverage across reference



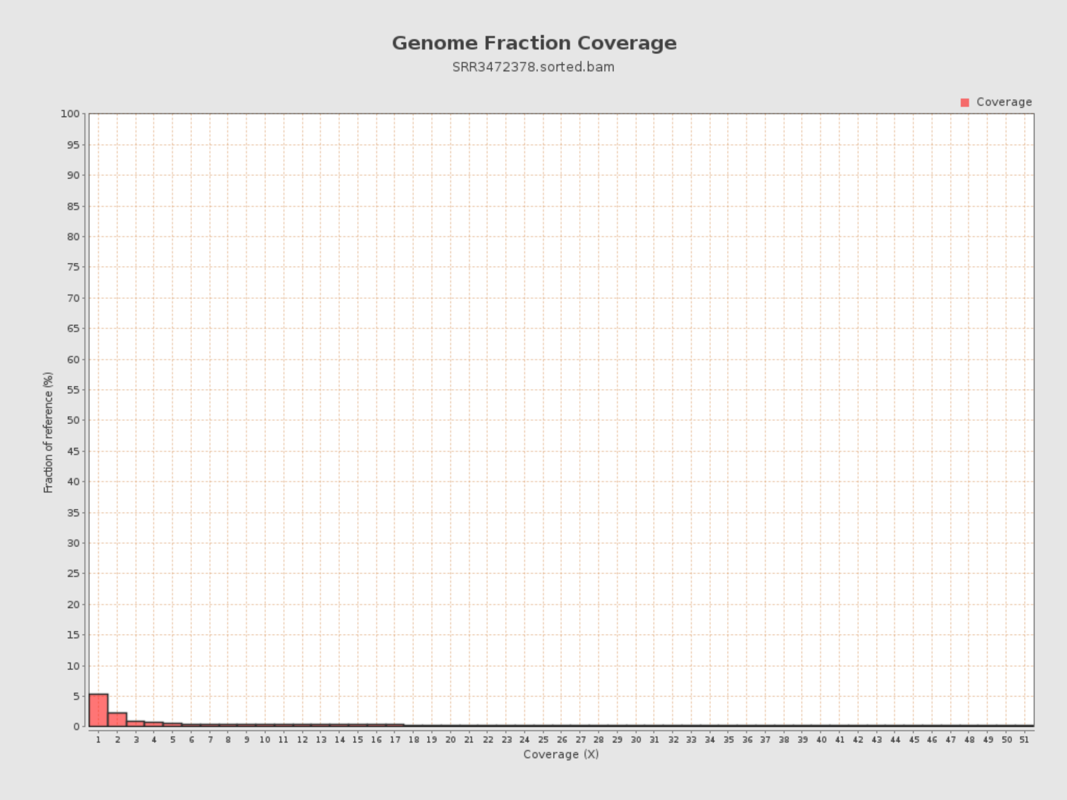
4. Results : Coverage Histogram



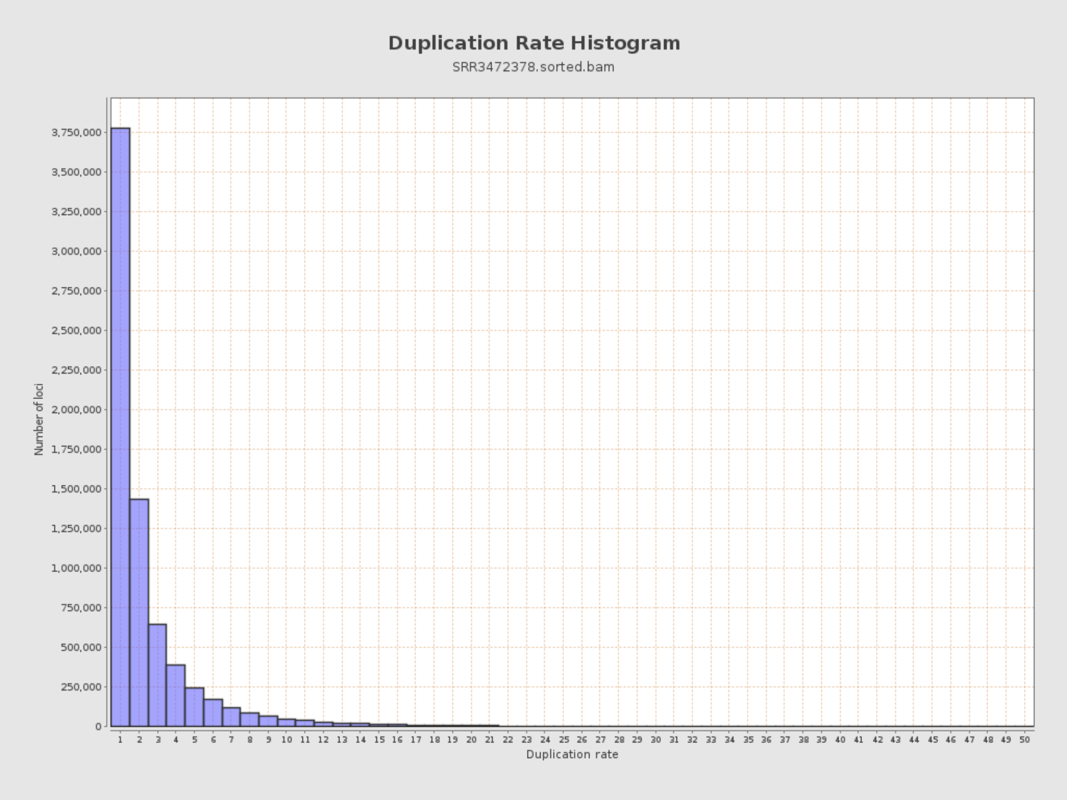
5. Results : Coverage Histogram (0-50X)



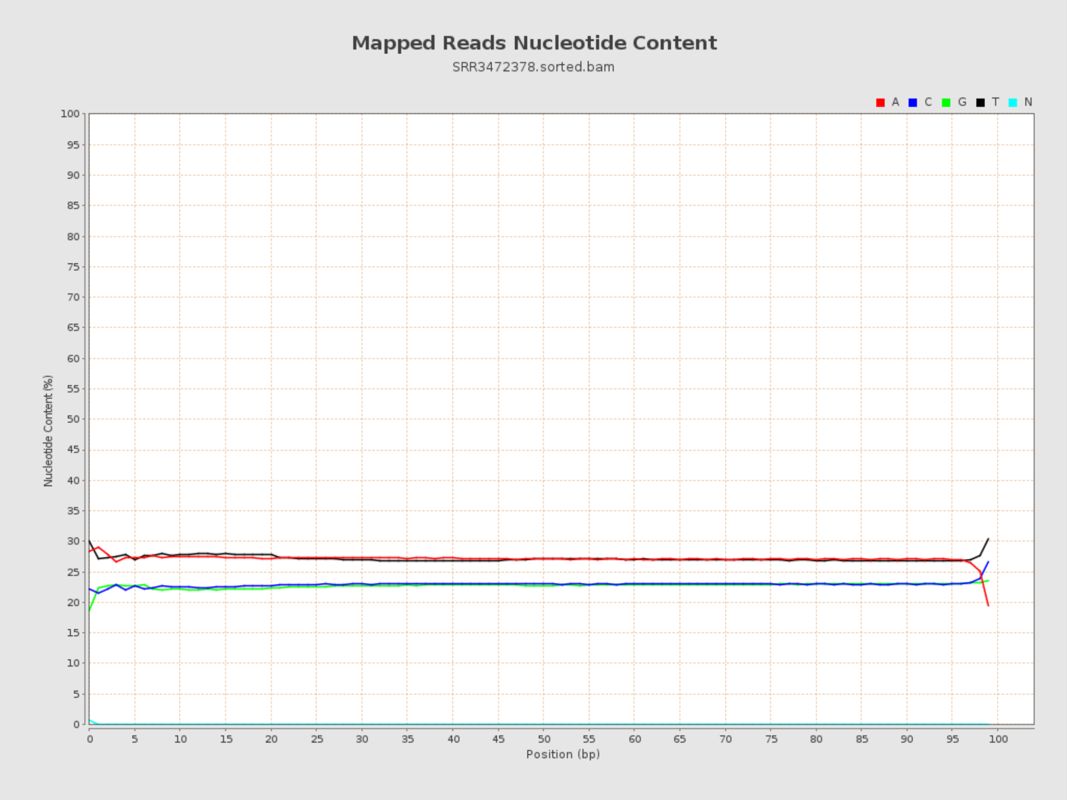
6. Results : Genome Fraction Coverage



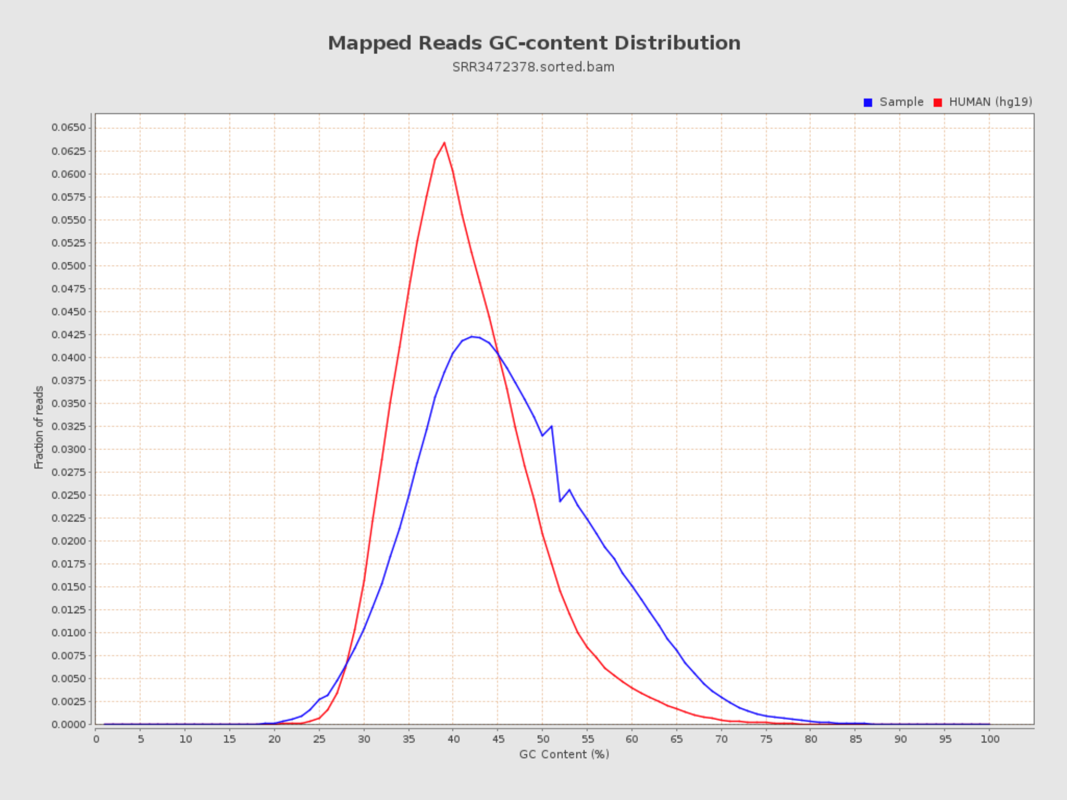
7. Results : Duplication Rate Histogram



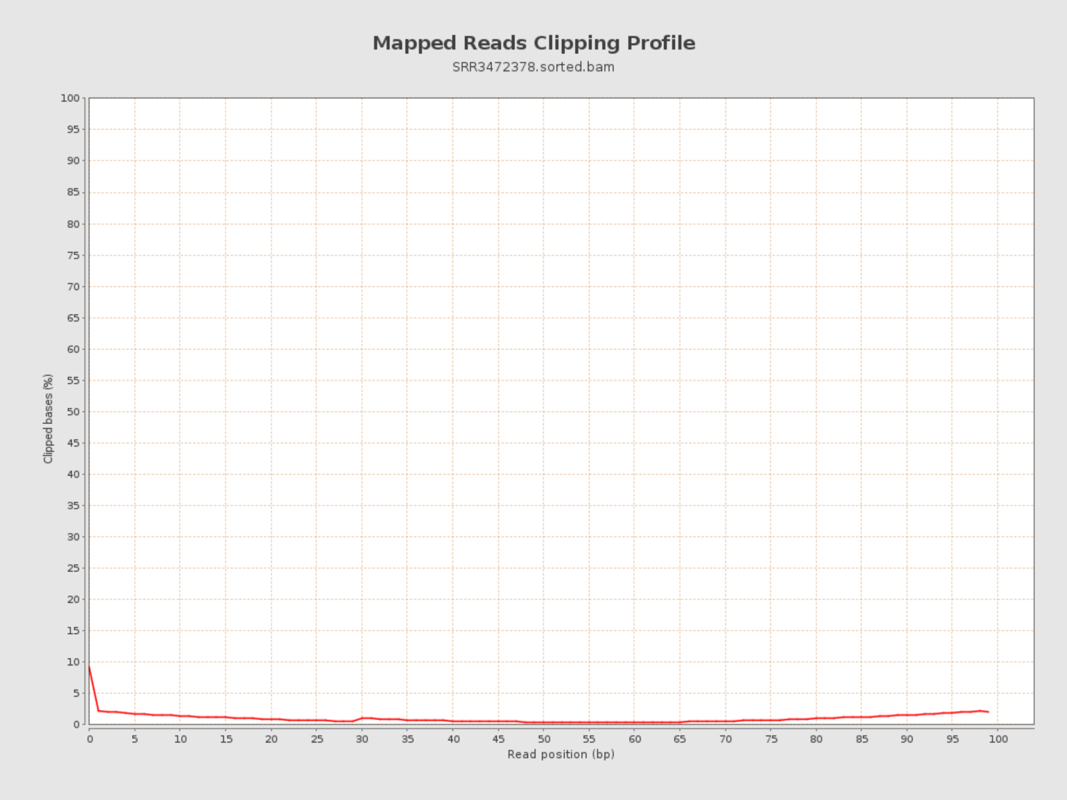
8. Results : Mapped Reads Nucleotide Content



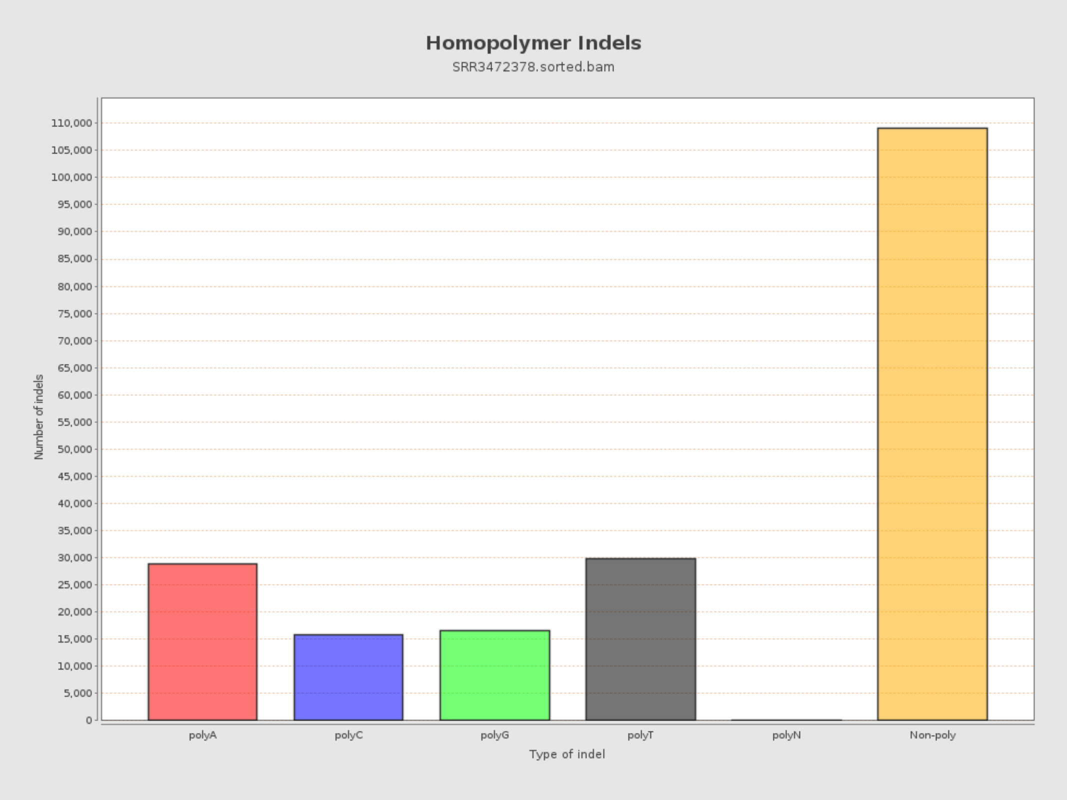
9. Results : Mapped Reads GC-content Distribution



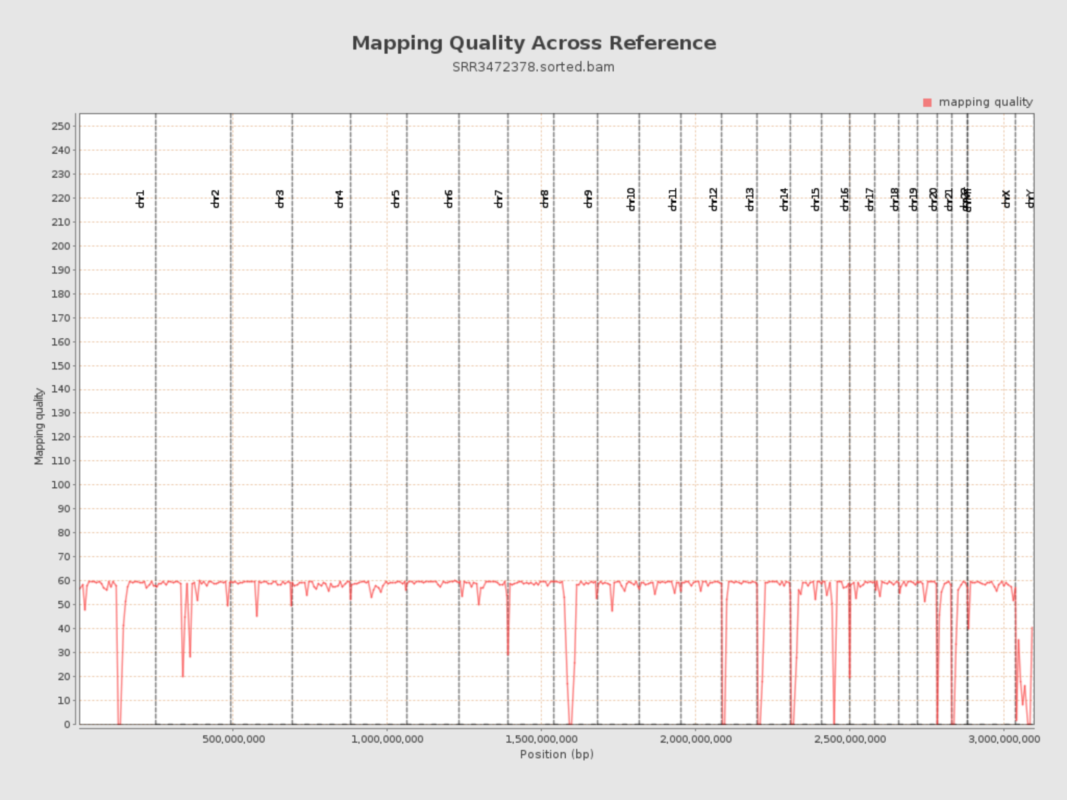
10. Results : Mapped Reads Clipping Profile



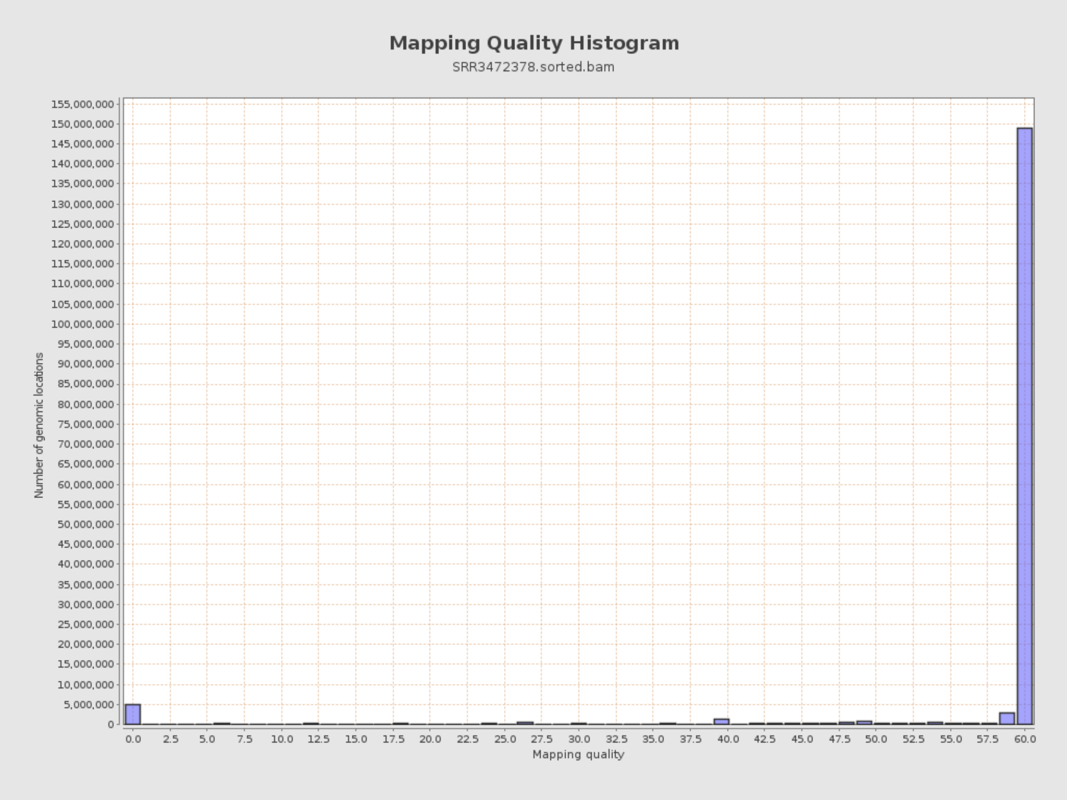
11. Results : Homopolymer Indels



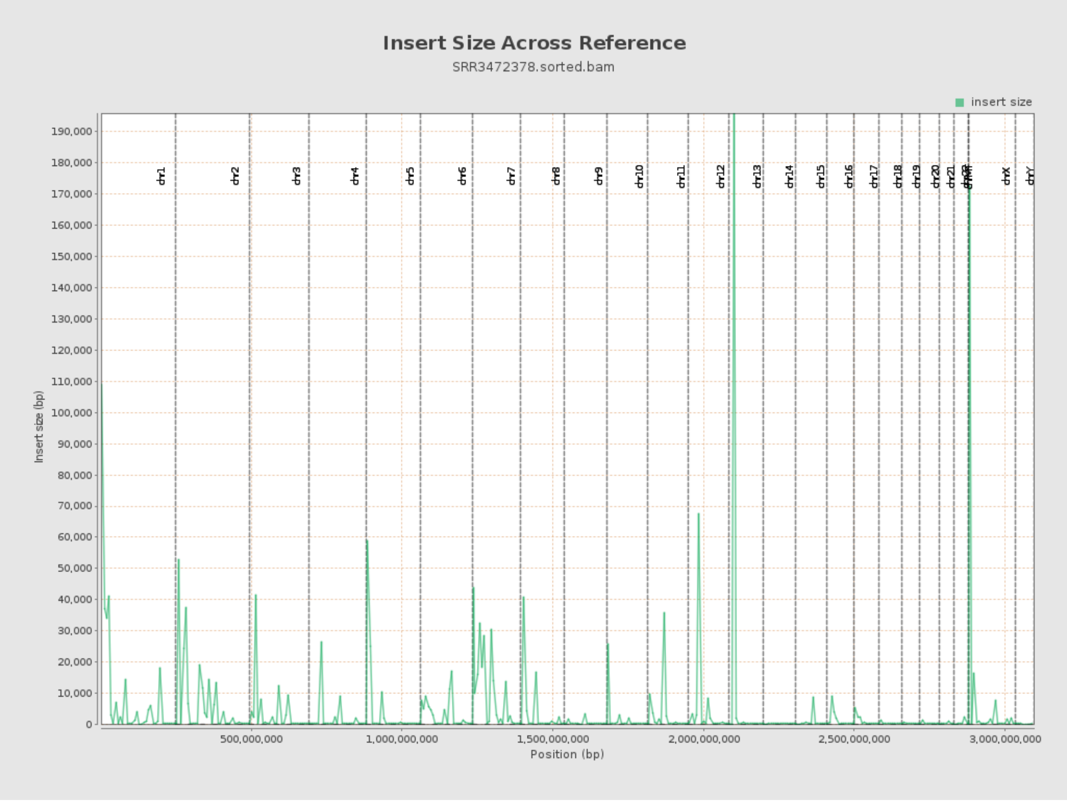
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram