Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 15:42:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472780.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_SRR3472780 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472780_1.fastq.gz SRR3472780_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 15:42:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472780.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,298,080
Mapped reads	15,129,284 / 98.9%
Unmapped reads	168,796 / 1.1%
Mapped paired reads	15,129,284 / 98.9%
Mapped reads, first in pair	7,597,589 / 49.66%
Mapped reads, second in pair	7,531,695 / 49.23%
Mapped reads, both in pair	15,029,062 / 98.24%
Mapped reads, singletons	100,222 / 0.66%
Secondary alignments	0
Supplementary alignments	51,214 / 0.33%
Read min/max/mean length	30 / 100 / 100.14
Duplicated reads (estimated)	9,194,552 / 60.1%
Duplication rate	46.59%
Clipped reads	1,173,514 / 7.67%

2.2. ACGT Content

Number/percentage of A's	412,173,336 / 27.66%
Number/percentage of C's	335,323,625 / 22.5%
Number/percentage of T's	408,682,954 / 27.42%
Number/percentage of G's	333,800,642 / 22.4%
Number/percentage of N's	283,854 / 0.02%

GC Percentage	44.9%

2.3. Coverage

Mean	0.4815
Standard Deviation	15.5635

2.4. Mapping Quality

Mean Mapping Quality	55.22

2.5. Insert size

Mean	26,586.88
Standard Deviation	1,611,907.32
P25/Median/P75	182 / 256 / 343

2.6. Mismatches and indels

General error rate	0.67%
Mismatches	9,870,127
Insertions	91,262
Mapped reads with at least one insertion	0.6%
Deletions	91,509
Mapped reads with at least one deletion	0.6%
Homopolymer indels	45.56%

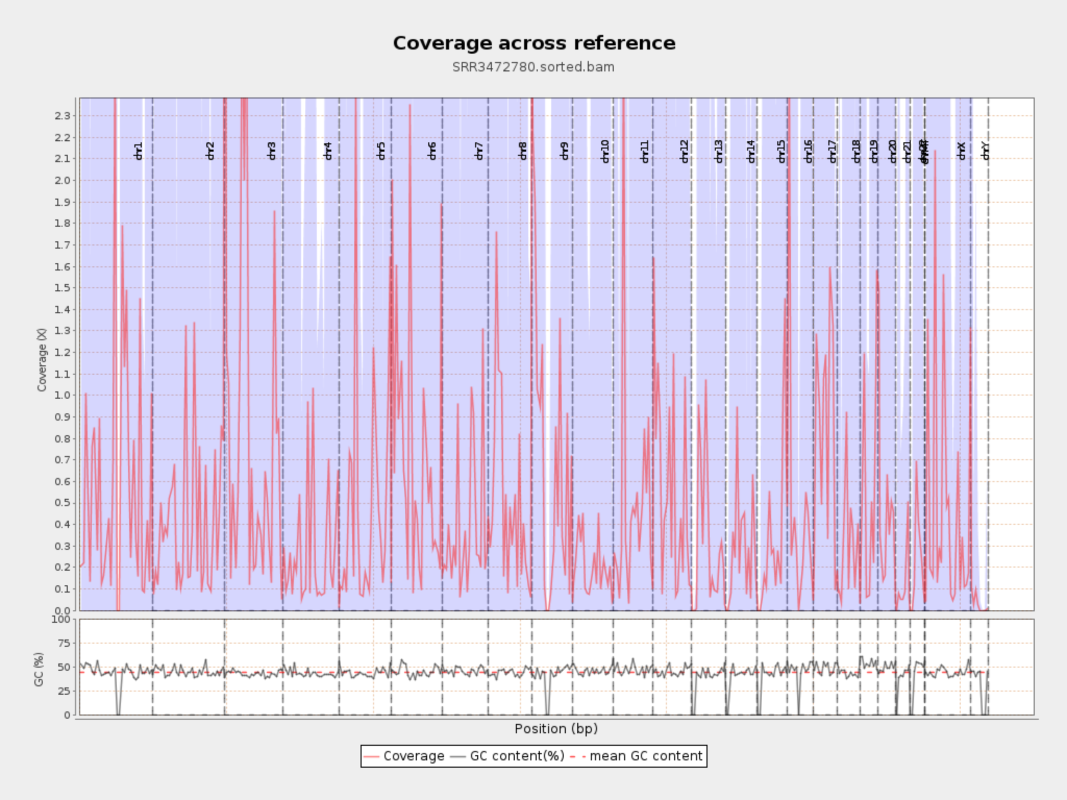
2.7. Chromosome stats

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

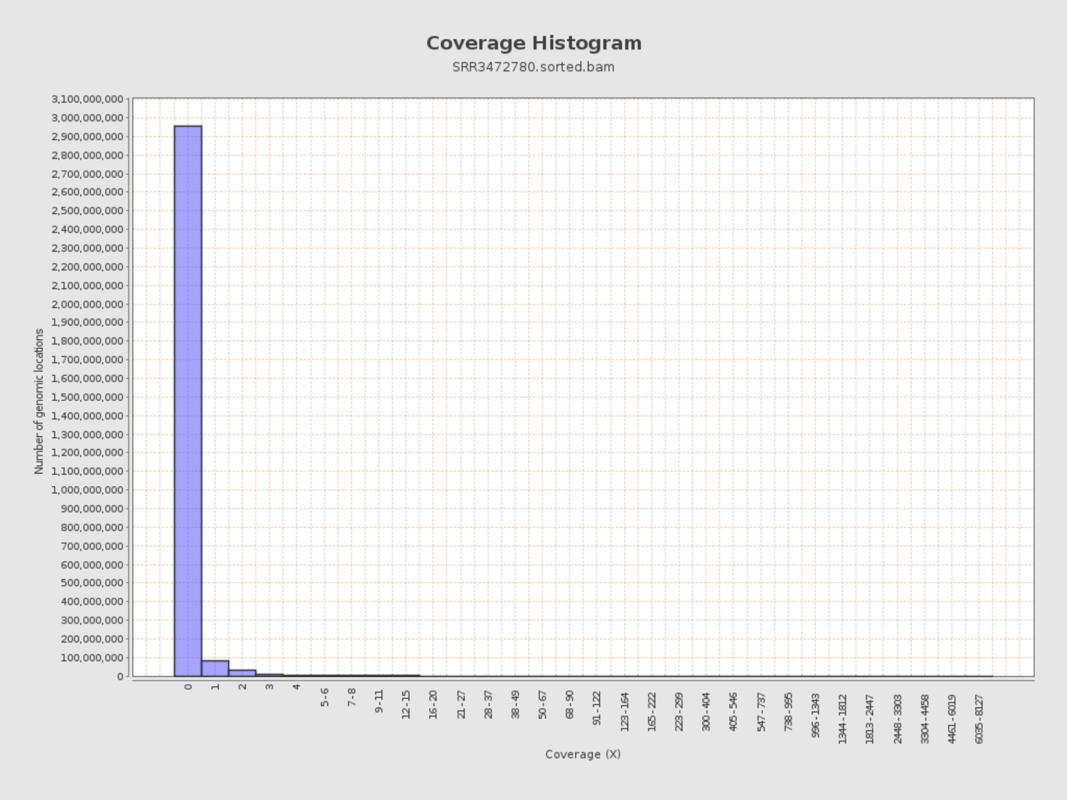
		bases	coverage	deviation
chr1	249250621	149296343	0.599	19.6907
chr2	243199373	99550141	0.4093	12.7019
chr3	198022430	172941872	0.8733	20.217
chr4	191154276	53103795	0.2778	10.6188
chr5	180915260	91388587	0.5051	17.3989
chr6	171115067	119736468	0.6997	18.1438
chr7	159138663	61478181	0.3863	11.4842
chr8	146364022	73470089	0.502	16.7037
chr9	141213431	100694326	0.7131	20.1376
chr10	135534747	28686942	0.2117	6.119
chr11	135006516	70421137	0.5216	20.9812
chr12	133851895	78053419	0.5831	16.3552
chr13	115169878	37421104	0.3249	12.7957
chr14	107349540	30284129	0.2821	8.5301
chr15	102531392	36095705	0.352	11.8858
chr16	90354753	43399507	0.4803	13.2126
chr17	81195210	67091544	0.8263	19.6524
chr18	78077248	24734669	0.3168	11.9008
chr19	59128983	31686679	0.5359	15.2243
chr20	63025520	28683897	0.4551	14.5705
chr21	48129895	6292812	0.1307	5.5239
chr22	51304566	12100514	0.2359	9.9195
chrMT	16571	4179	0.2522	0.7318
chrX	155270560	72093091	0.4643	17.5129

chrY	59373566	1801357	0.0303	2.2529

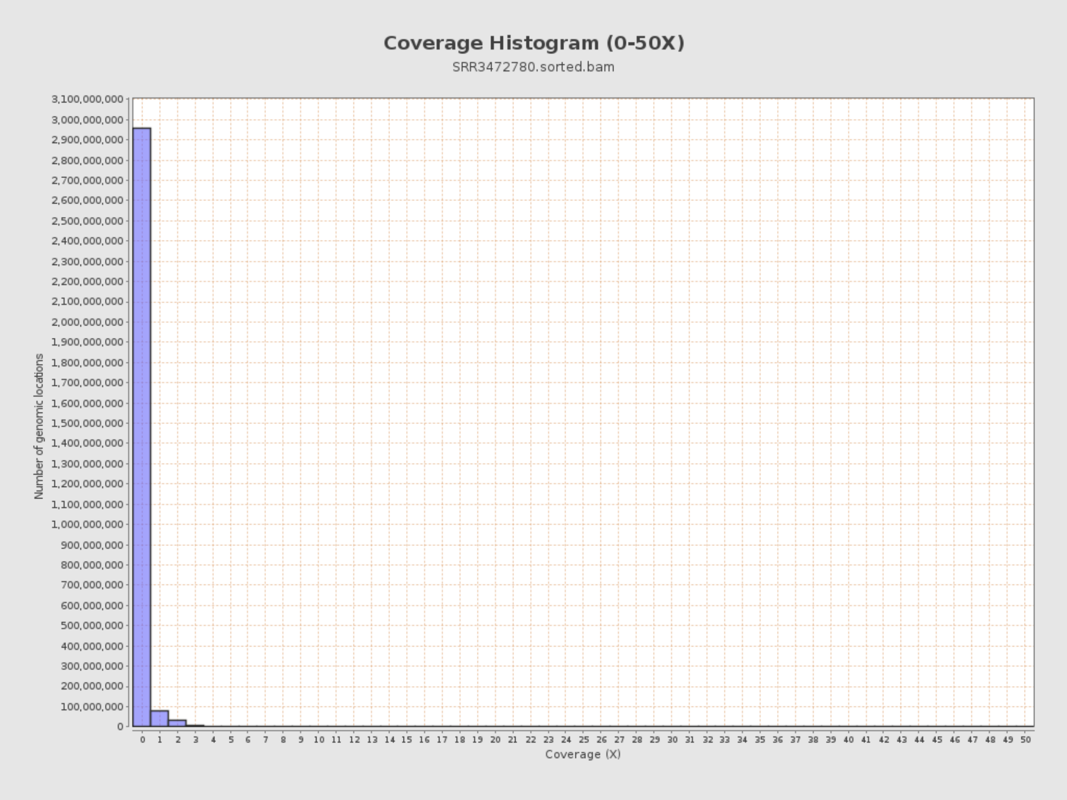
3. Results : Coverage across reference



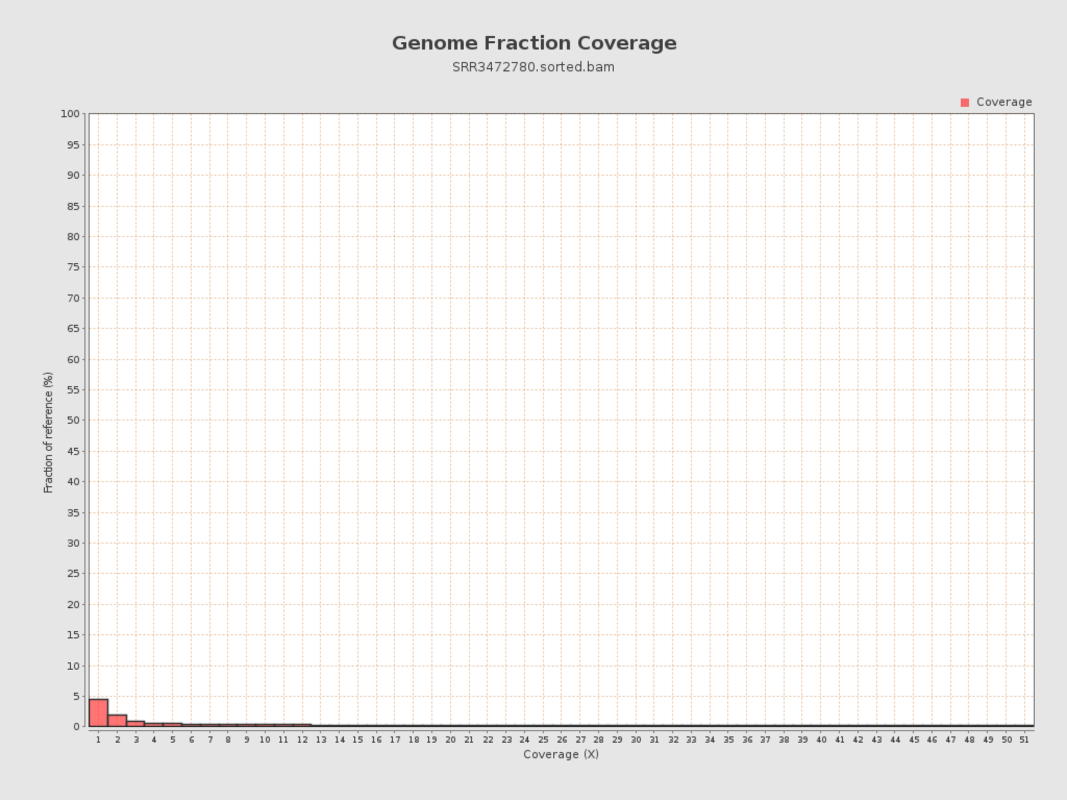
4. Results : Coverage Histogram



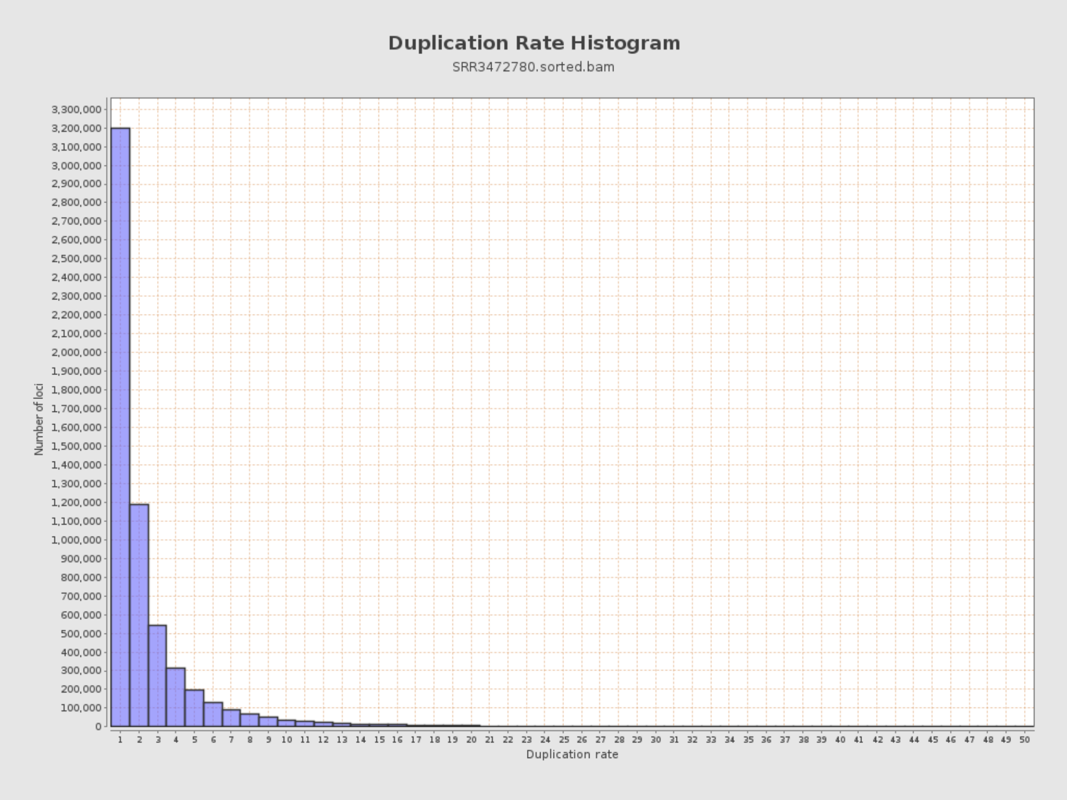
5. Results : Coverage Histogram (0-50X)



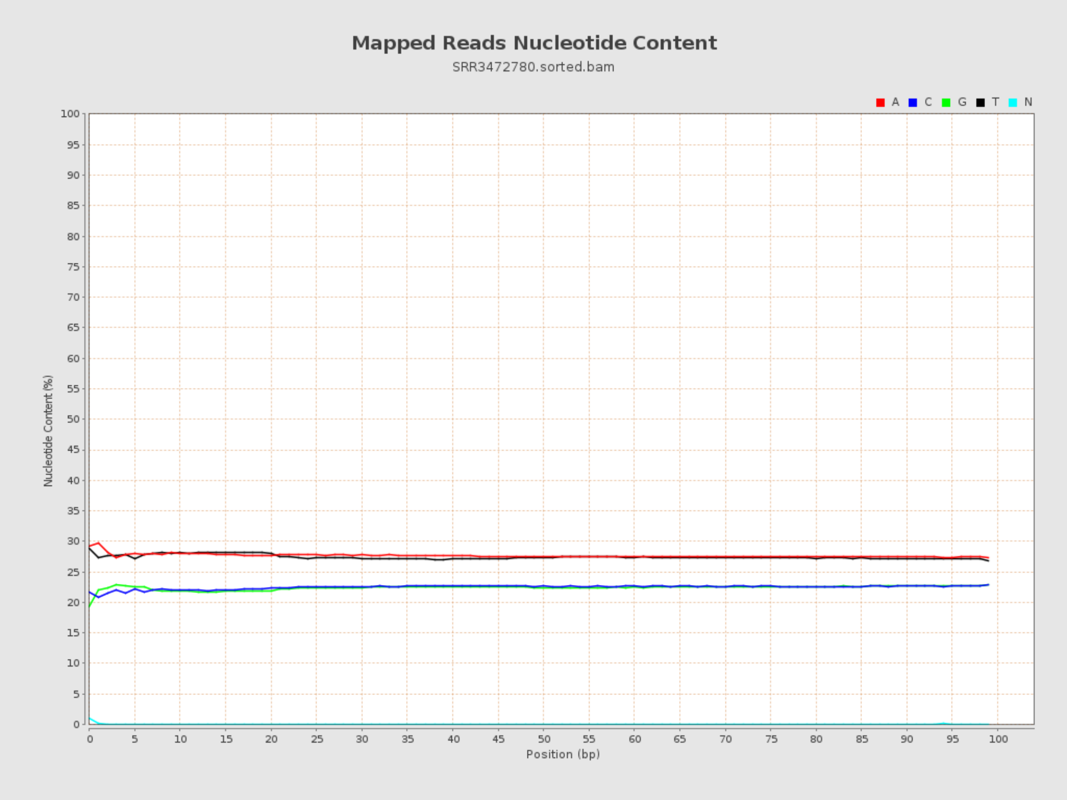
6. Results : Genome Fraction Coverage



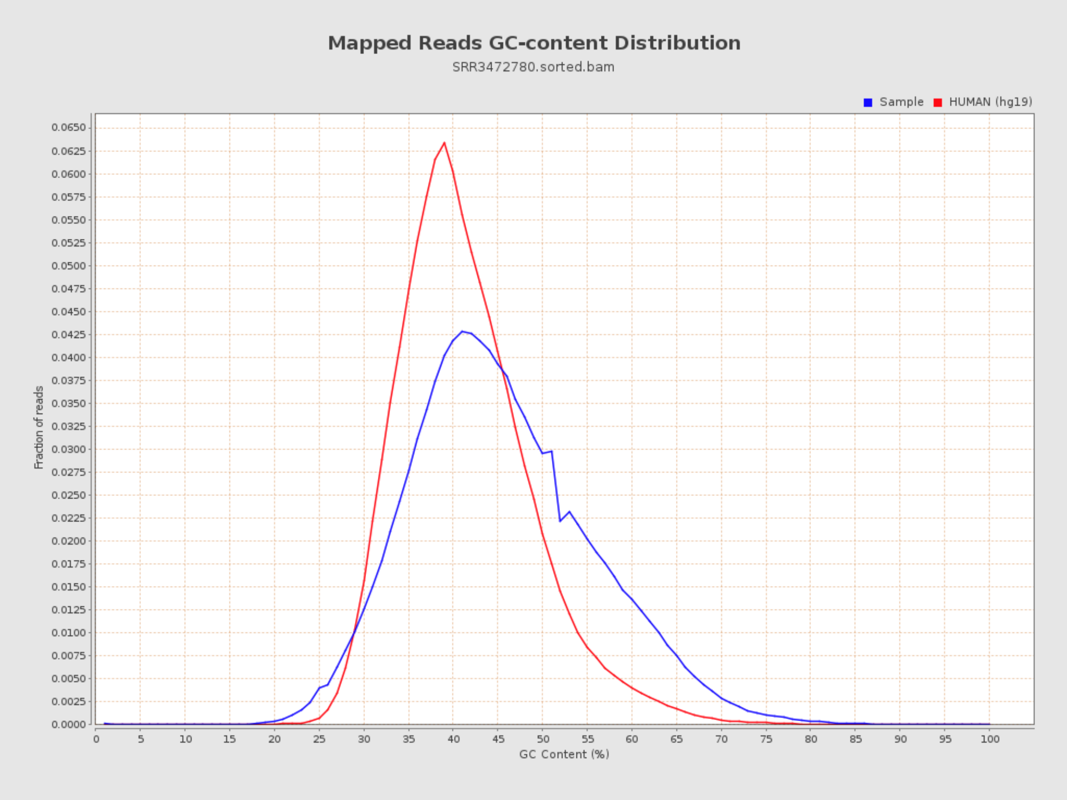
7. Results : Duplication Rate Histogram



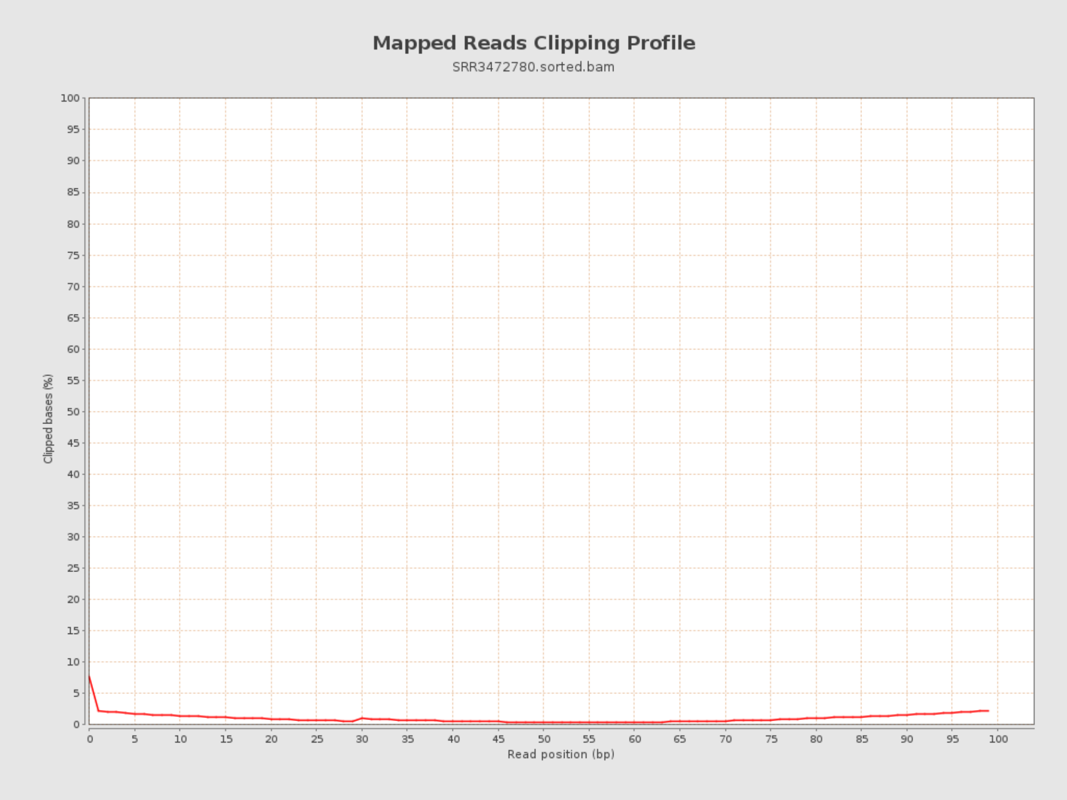
8. Results : Mapped Reads Nucleotide Content



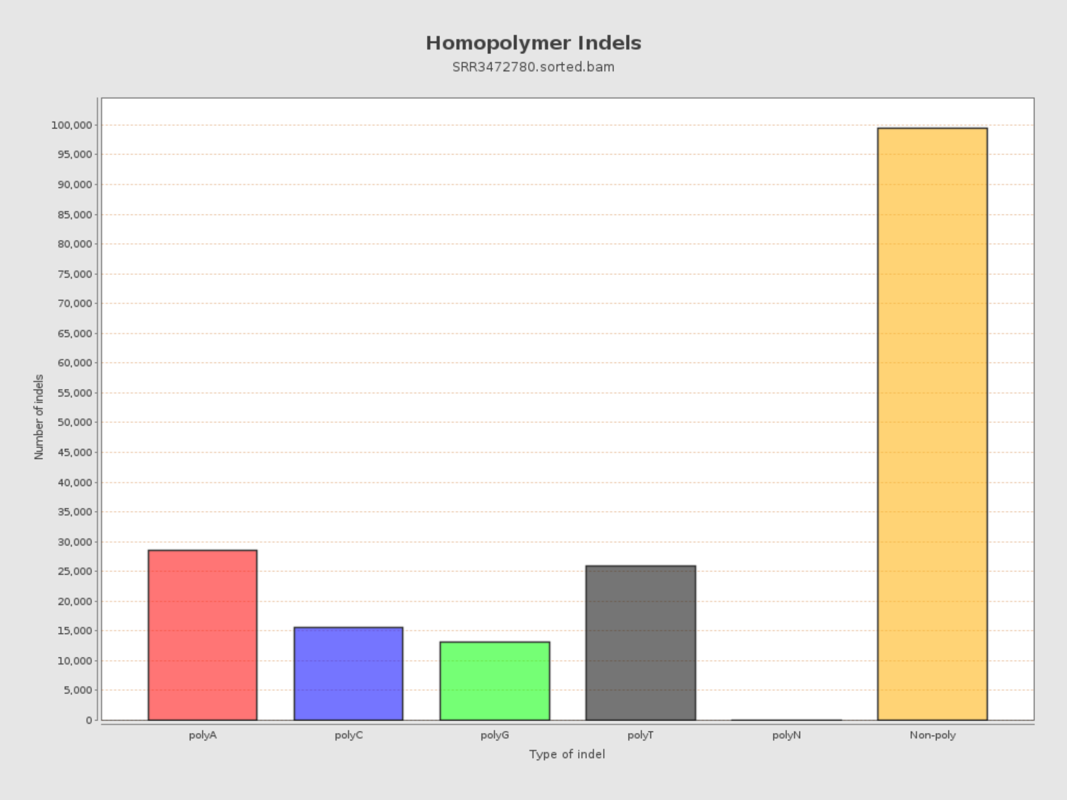
9. Results : Mapped Reads GC-content Distribution



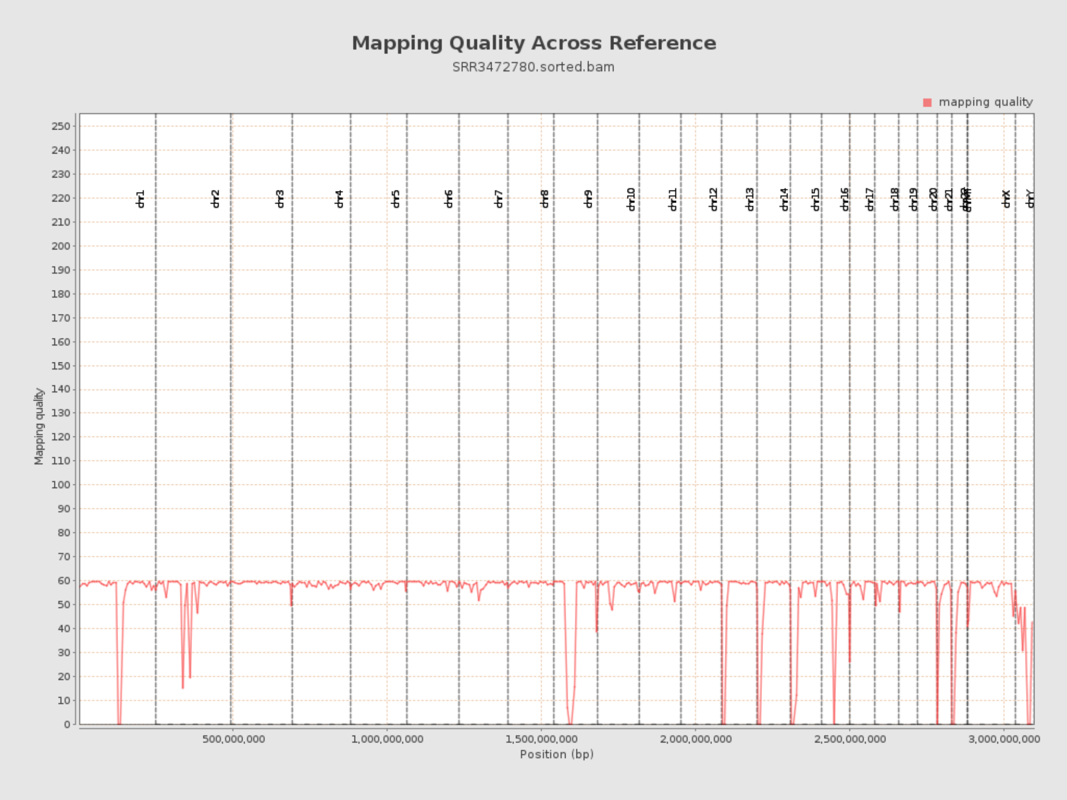
10. Results : Mapped Reads Clipping Profile



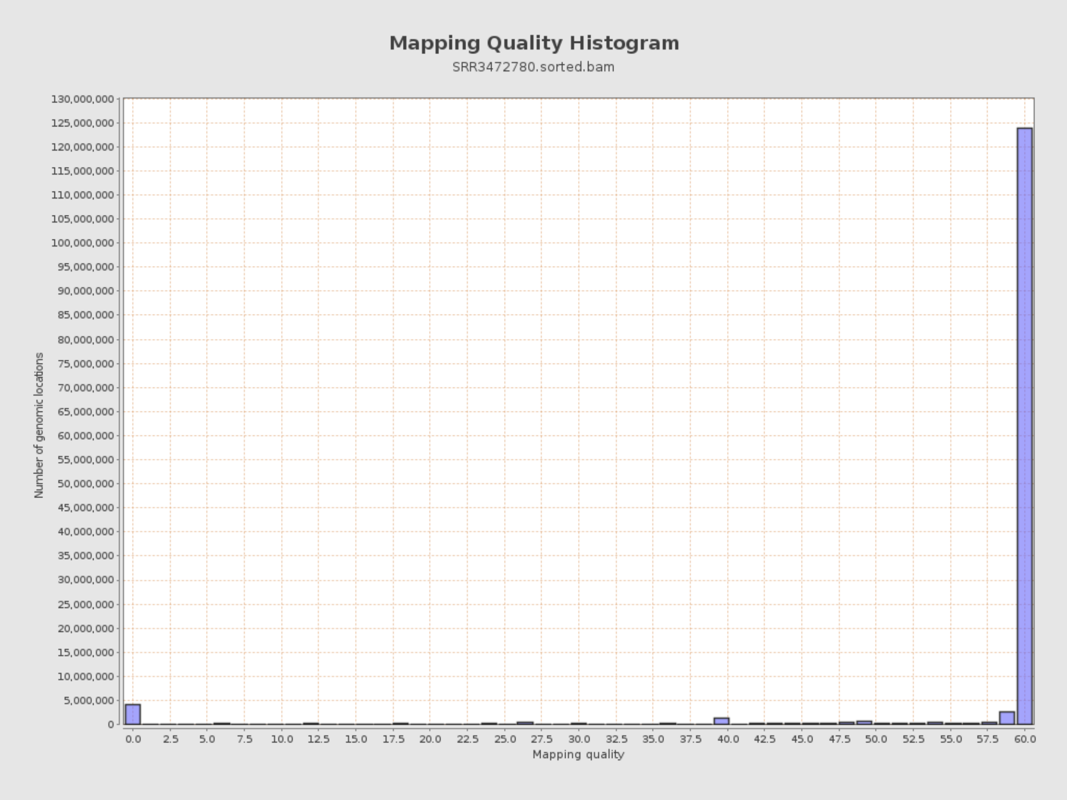
11. Results : Homopolymer Indels



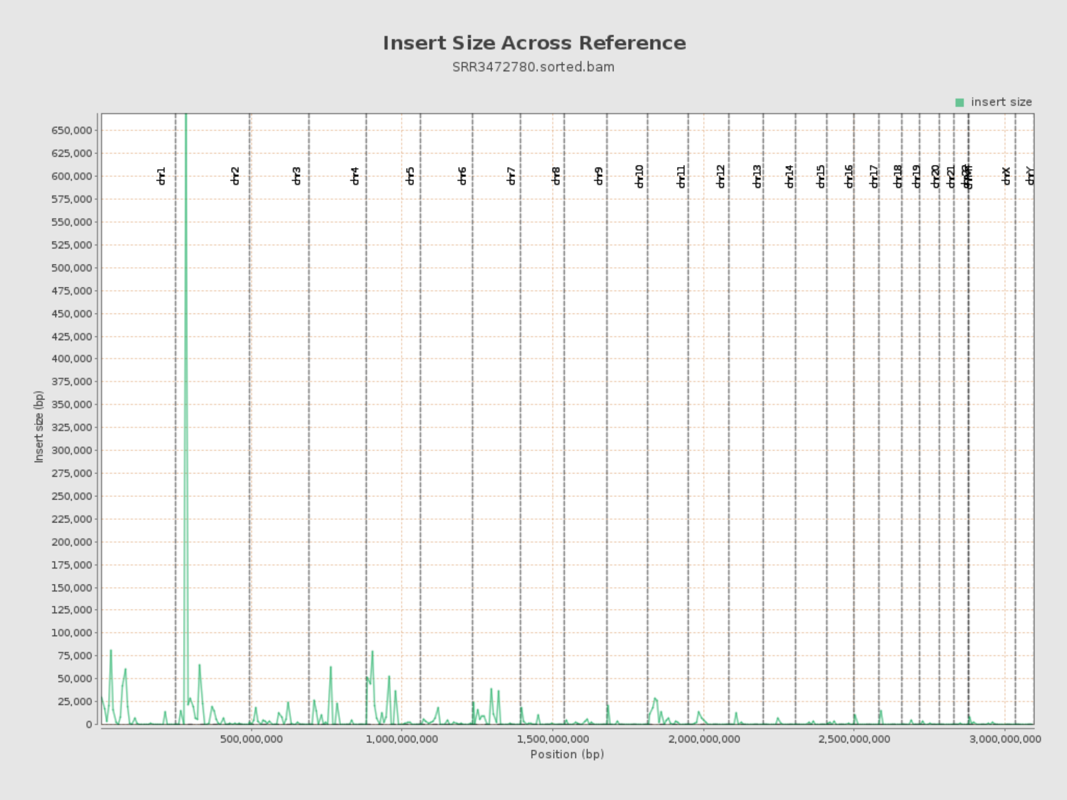
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram