Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/01 03:42:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472800.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_SRR3472800 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472800_1.fastq.gz SRR3472800_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 01 03:42:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472800.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	114,517,230
Mapped reads	113,969,470 / 99.52%
Unmapped reads	547,760 / 0.48%
Mapped paired reads	113,969,470 / 99.52%
Mapped reads, first in pair	57,169,951 / 49.92%
Mapped reads, second in pair	56,799,519 / 49.6%
Mapped reads, both in pair	113,557,246 / 99.16%
Mapped reads, singletons	412,224 / 0.36%
Secondary alignments	0
Supplementary alignments	87,098 / 0.08%
Read min/max/mean length	30 / 100 / 100.03
Duplicated reads (estimated)	59,322,312 / 51.8%
Duplication rate	47.68%
Clipped reads	5,541,362 / 4.84%

2.2. ACGT Content

Number/percentage of A's	3,177,344,093 / 28.14%
Number/percentage of C's	2,465,803,054 / 21.84%
Number/percentage of T's	3,222,864,420 / 28.55%
Number/percentage of G's	2,422,531,123 / 21.46%
Number/percentage of N's	1,127,979 / 0.01%

GC Percentage	43.3%

2.3. Coverage

Mean	3.6474
Standard Deviation	26.1279

2.4. Mapping Quality

Mean Mapping Quality	53.66

2.5. Insert size

Mean	13,745.4
Standard Deviation	1,158,902.36
P25/Median/P75	182 / 241 / 314

2.6. Mismatches and indels

General error rate	0.42%
Mismatches	46,709,797
Insertions	507,412
Mapped reads with at least one insertion	0.44%
Deletions	601,993
Mapped reads with at least one deletion	0.52%
Homopolymer indels	45.79%

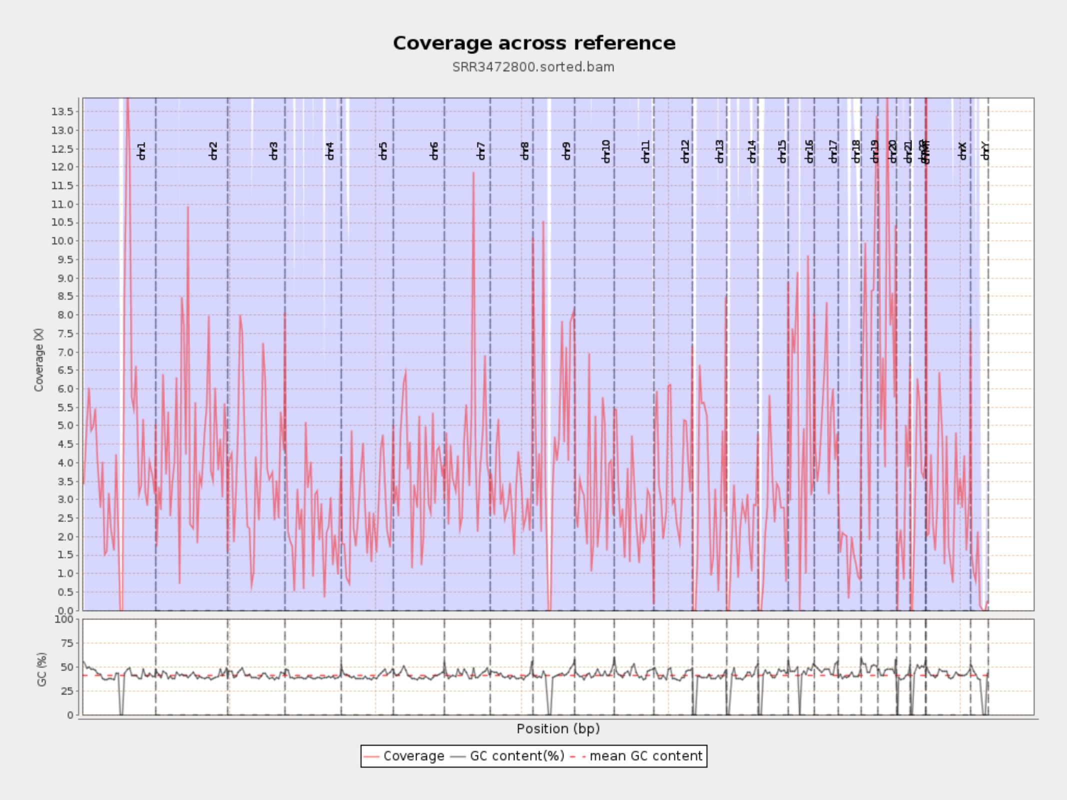
2.7. Chromosome stats

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

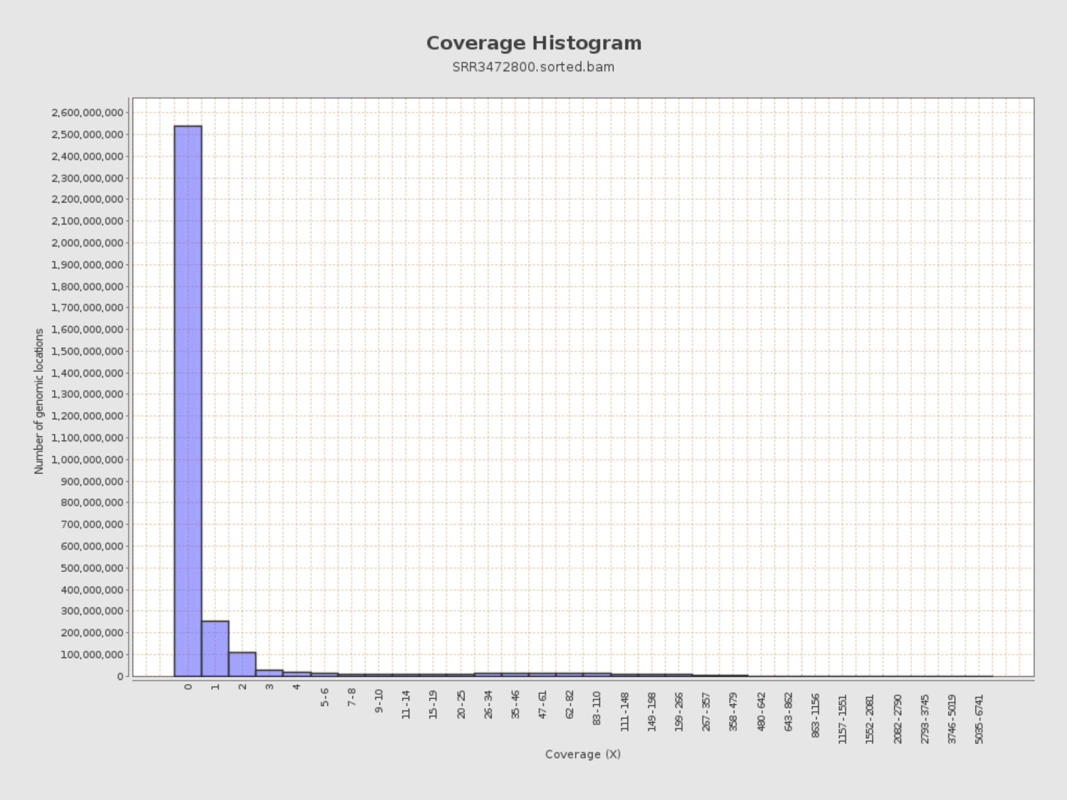
		bases	coverage	deviation
chr1	249250621	1082634458	4.3436	29.0727
chr2	243199373	1101458512	4.529	32.6262
chr3	198022430	770526387	3.8911	26.4132
chr4	191154276	452458915	2.367	18.4426
chr5	180915260	480707166	2.6571	19.3166
chr6	171115067	637215146	3.7239	25.9115
chr7	159138663	689734167	4.3342	31.5797
chr8	146364022	460367293	3.1454	23.8517
chr9	141213431	674964212	4.7797	34.5552
chr10	135534747	449412219	3.3158	23.4424
chr11	135006516	377846640	2.7987	17.3221
chr12	133851895	518865858	3.8764	23.0815
chr13	115169878	355907293	3.0903	26.9745
chr14	107349540	219070725	2.0407	14.8454
chr15	102531392	243727824	2.3771	15.4868
chr16	90354753	450473492	4.9856	31.5442
chr17	81195210	409469882	5.043	24.3802
chr18	78077248	121712662	1.5589	12.6355
chr19	59128983	468913282	7.9303	34.482
chr20	63025520	499640901	7.9276	48.5069
chr21	48129895	138256470	2.8726	25.1976
chr22	51304566	172204820	3.3565	21.2625
chrMT	16571	1836449	110.8231	306.6346
chrX	155270560	471492408	3.0366	24.4142

chrY	59373566	42196448	0.7107	10.6956

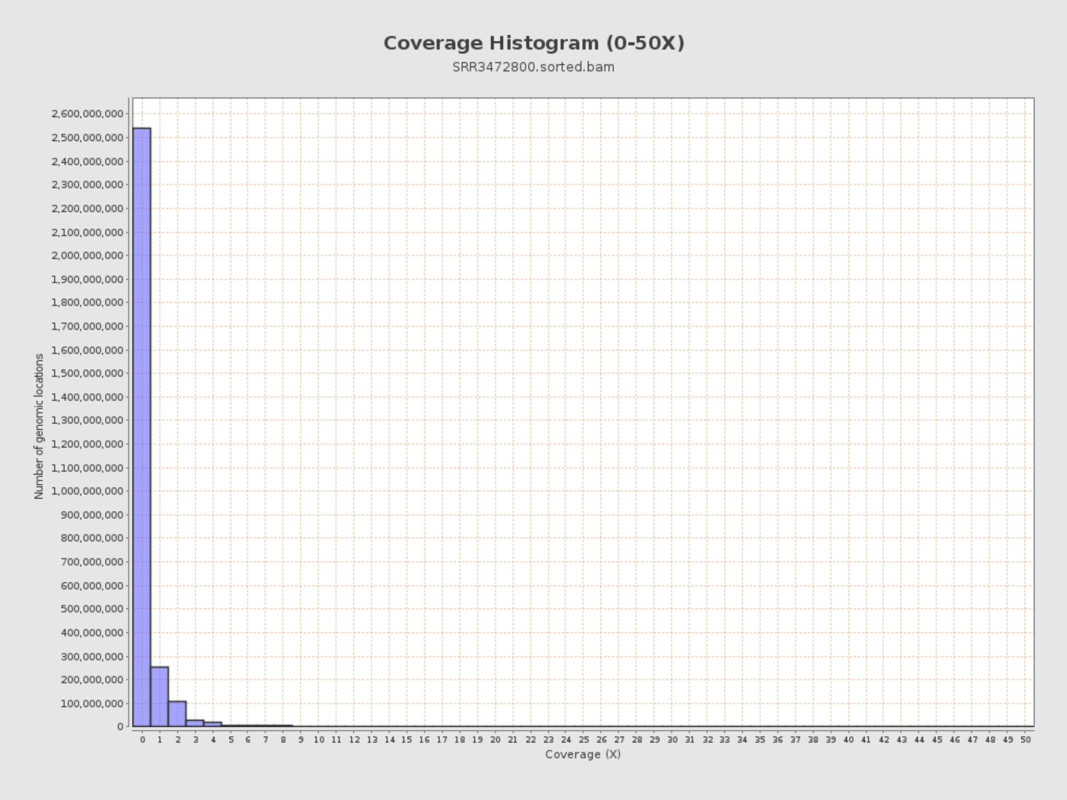
3. Results : Coverage across reference



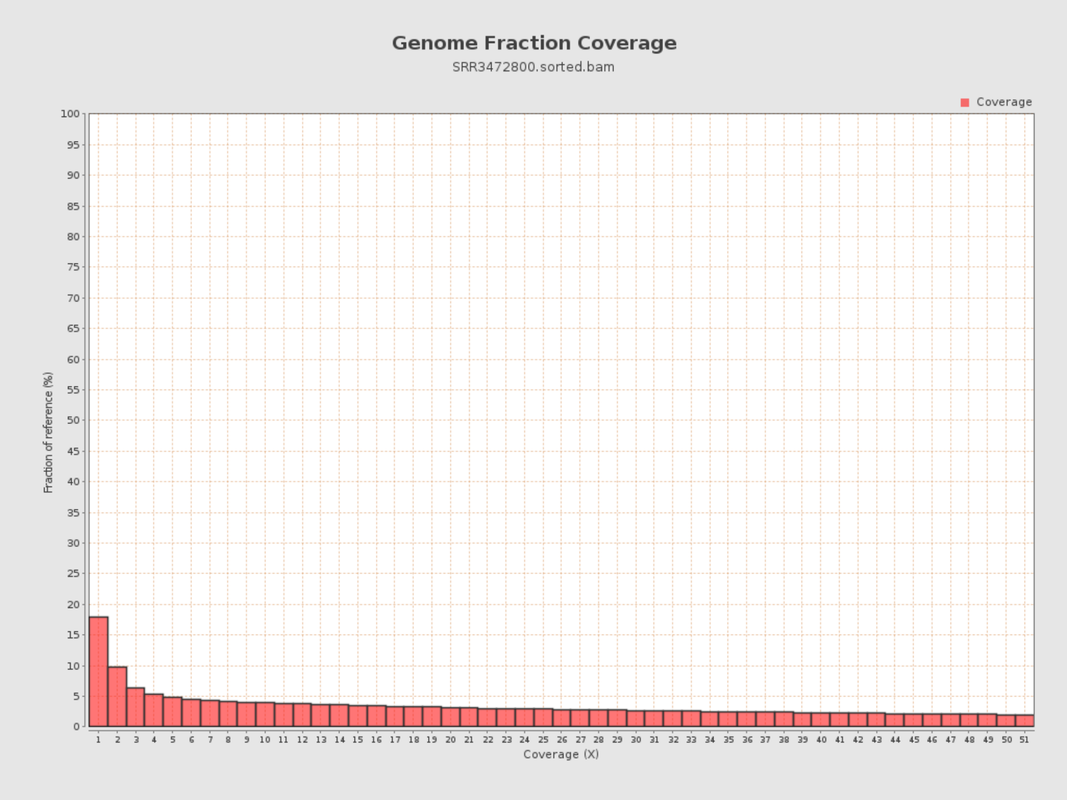
4. Results : Coverage Histogram



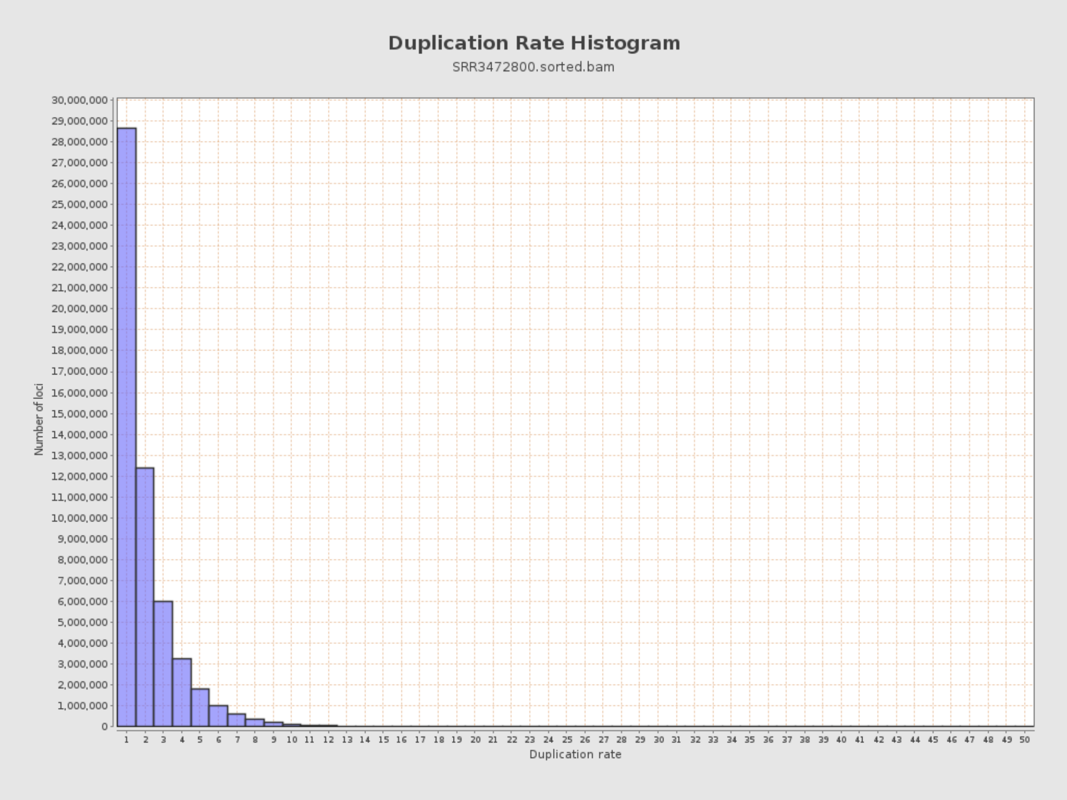
5. Results : Coverage Histogram (0-50X)



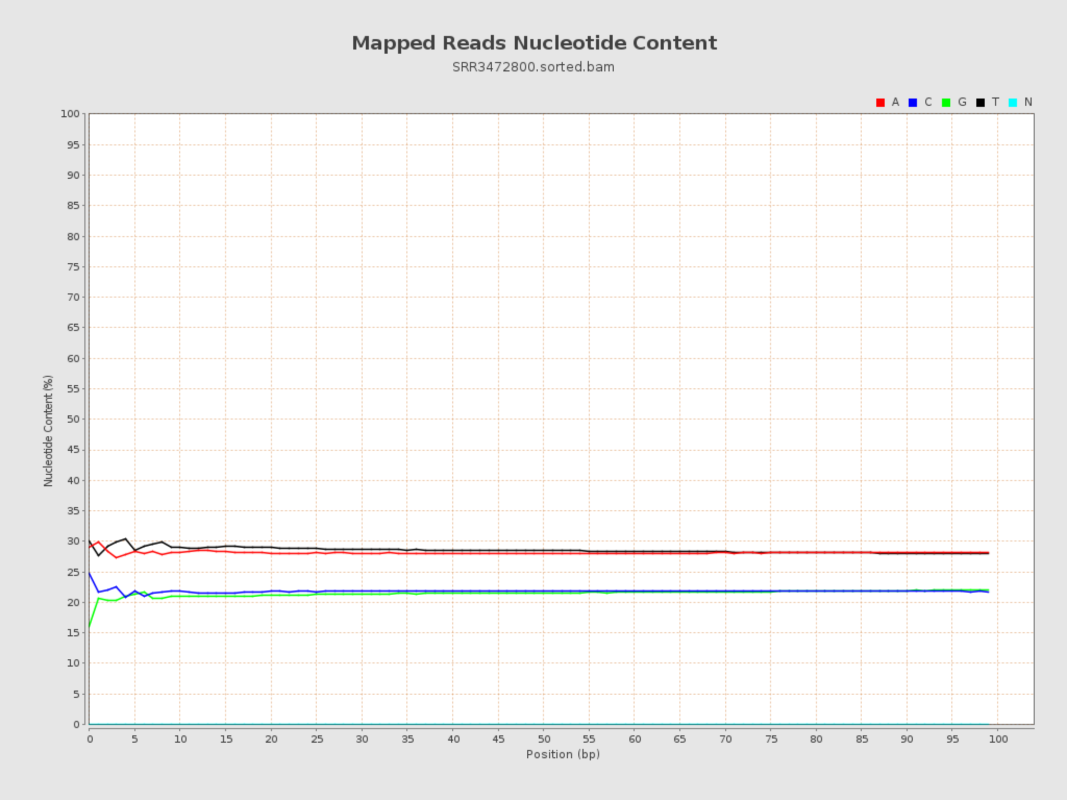
6. Results : Genome Fraction Coverage



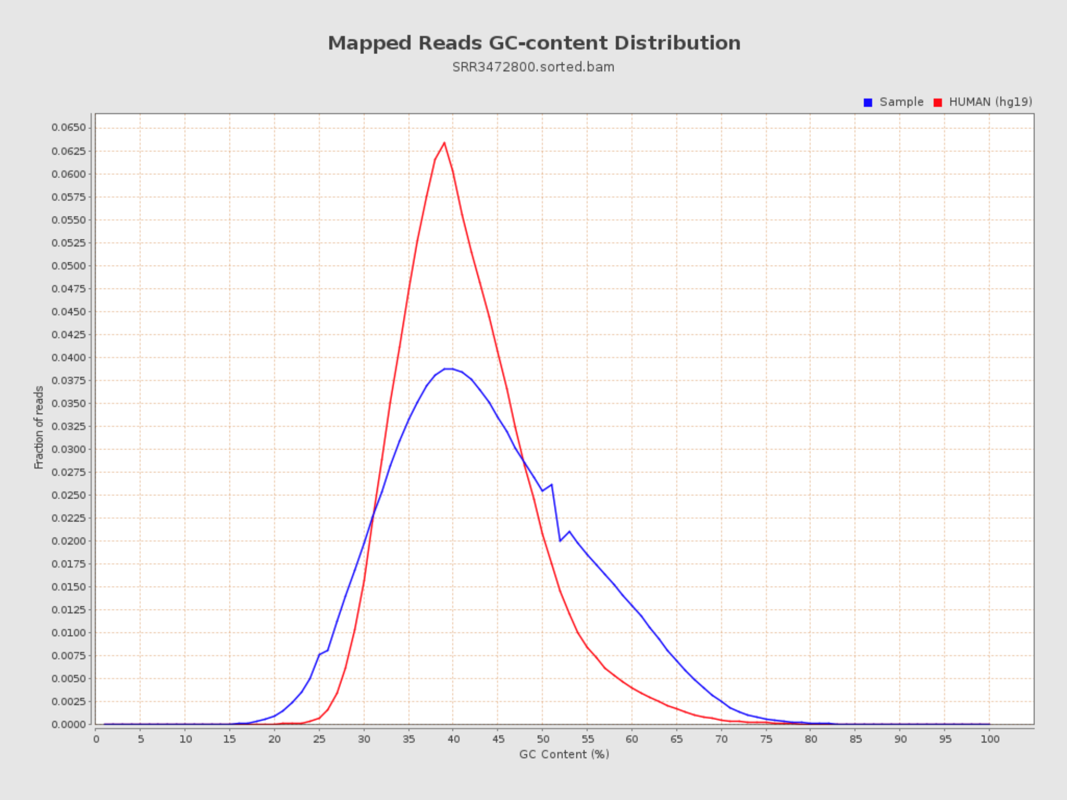
7. Results : Duplication Rate Histogram



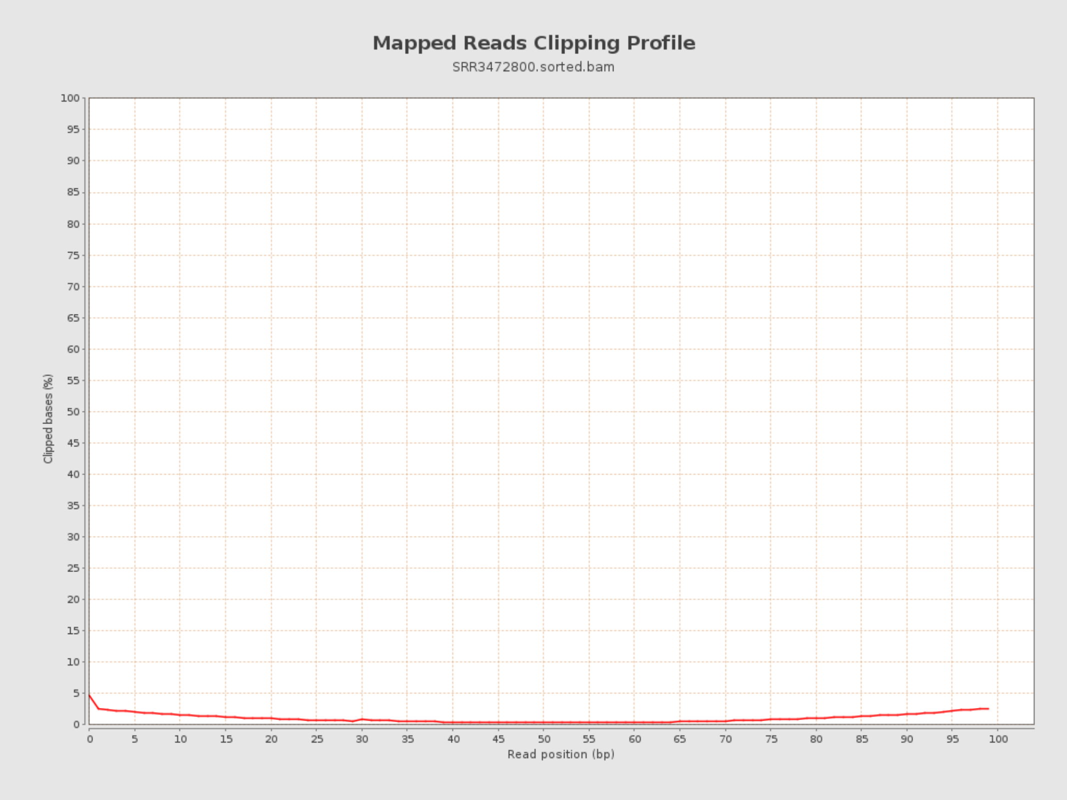
8. Results : Mapped Reads Nucleotide Content



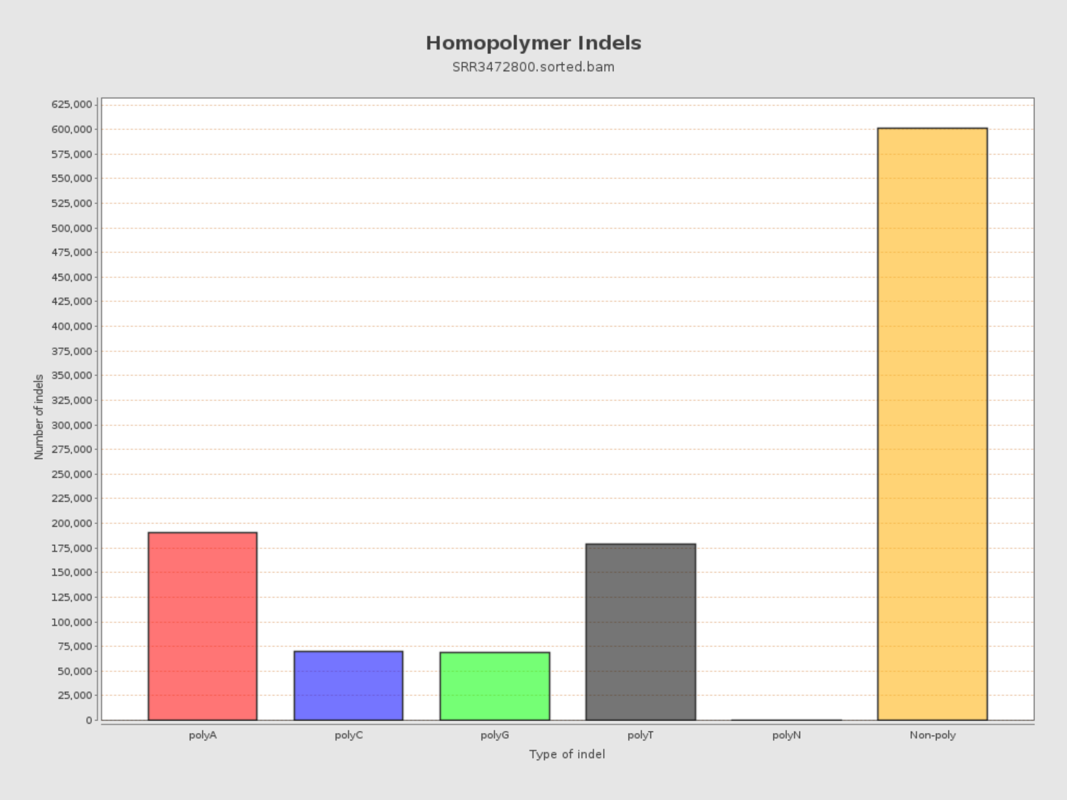
9. Results : Mapped Reads GC-content Distribution



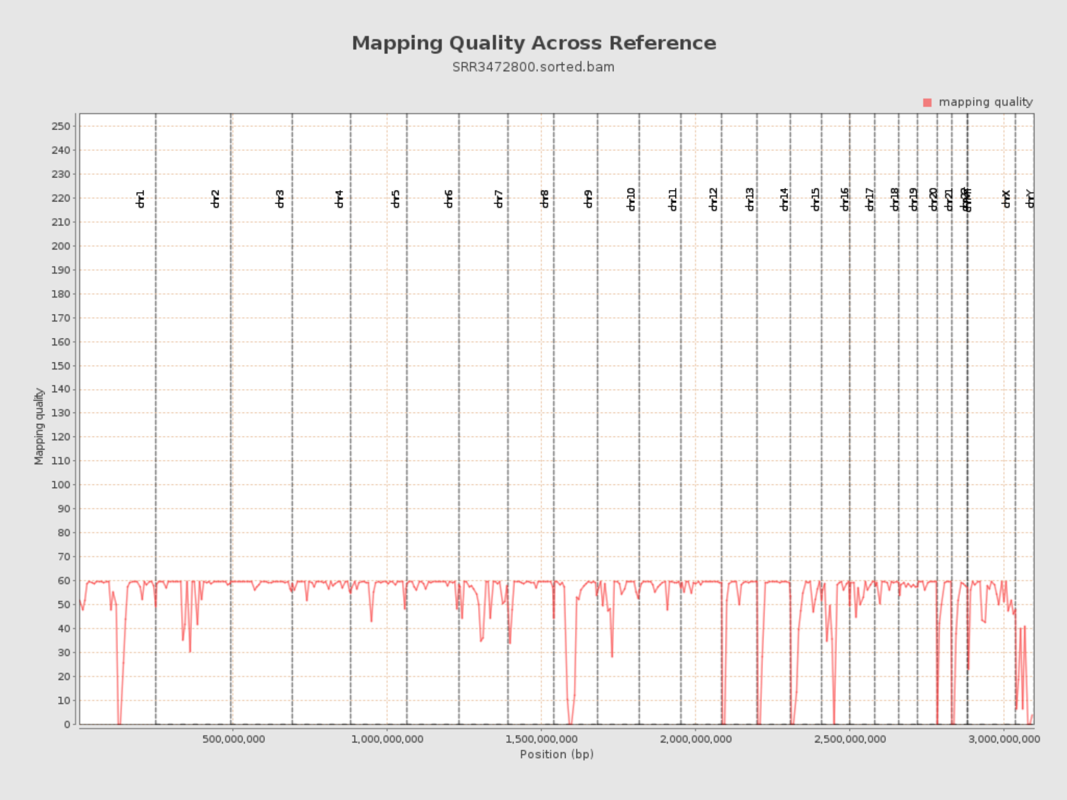
10. Results : Mapped Reads Clipping Profile



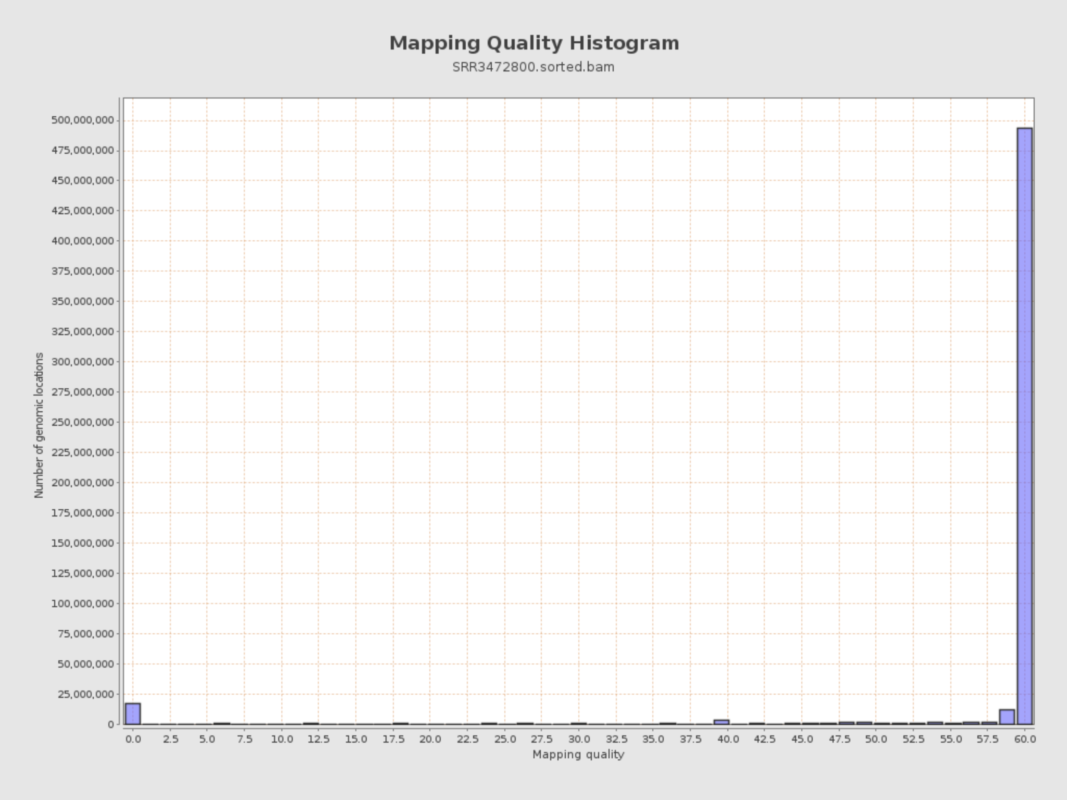
11. Results : Homopolymer Indels



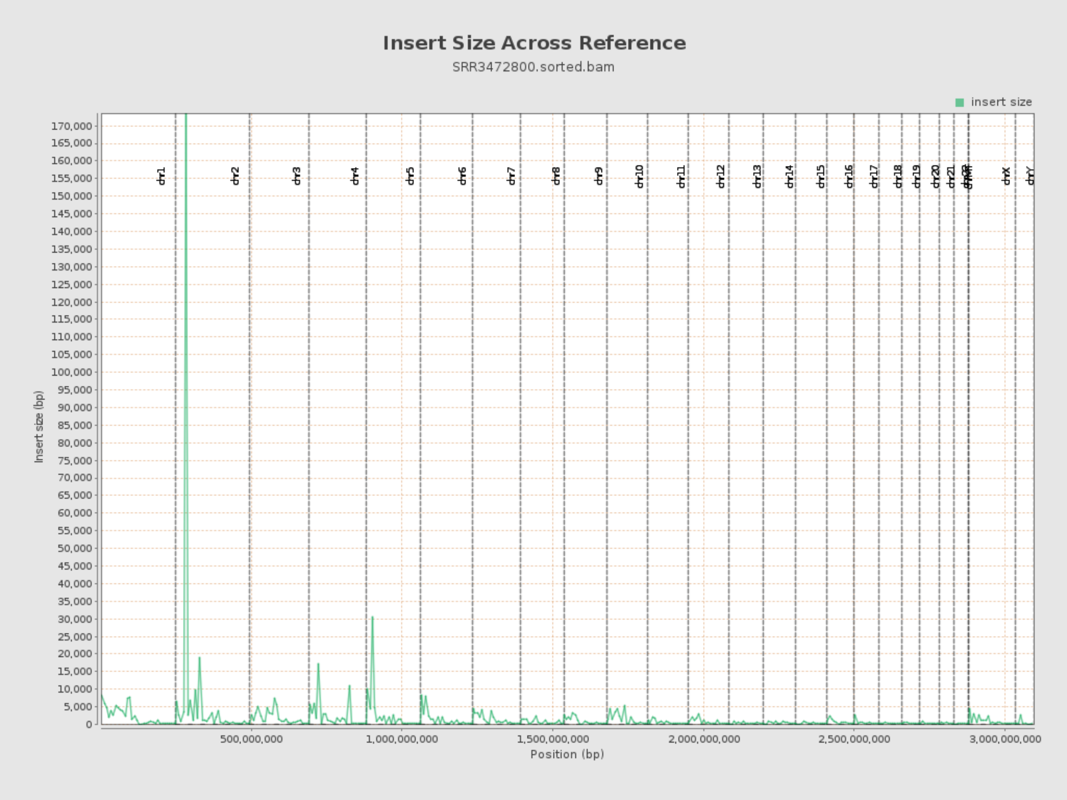
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram