Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 15:20:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472779.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_SRR3472779 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472779_1.fastq.gz SRR3472779_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 15:20:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472779.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,441,498
Mapped reads	20,232,233 / 98.98%
Unmapped reads	209,265 / 1.02%
Mapped paired reads	20,232,233 / 98.98%
Mapped reads, first in pair	10,164,085 / 49.72%
Mapped reads, second in pair	10,068,148 / 49.25%
Mapped reads, both in pair	20,095,218 / 98.31%
Mapped reads, singletons	137,015 / 0.67%
Secondary alignments	0
Supplementary alignments	68,621 / 0.34%
Read min/max/mean length	30 / 100 / 100.14
Duplicated reads (estimated)	13,443,313 / 65.76%
Duplication rate	48.46%
Clipped reads	1,431,673 / 7%

2.2. ACGT Content

Number/percentage of A's	559,487,477 / 28.02%
Number/percentage of C's	441,956,524 / 22.14%
Number/percentage of T's	555,660,712 / 27.83%
Number/percentage of G's	438,979,332 / 21.99%
Number/percentage of N's	381,774 / 0.02%

GC Percentage	44.12%

2.3. Coverage

Mean	0.645
Standard Deviation	23.1566

2.4. Mapping Quality

Mean Mapping Quality	55.13

2.5. Insert size

Mean	24,041.62
Standard Deviation	1,524,800.95
P25/Median/P75	190 / 267 / 357

2.6. Mismatches and indels

General error rate	0.67%
Mismatches	13,133,595
Insertions	119,394
Mapped reads with at least one insertion	0.58%
Deletions	111,688
Mapped reads with at least one deletion	0.54%
Homopolymer indels	45.62%

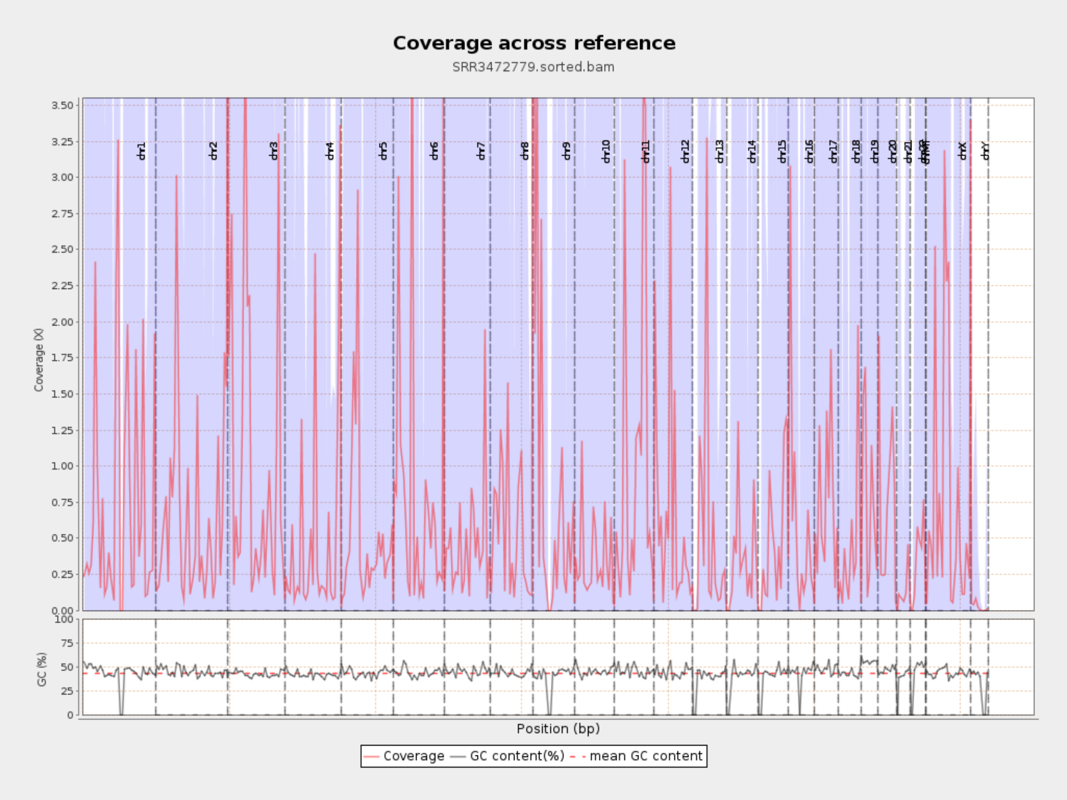
2.7. Chromosome stats

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

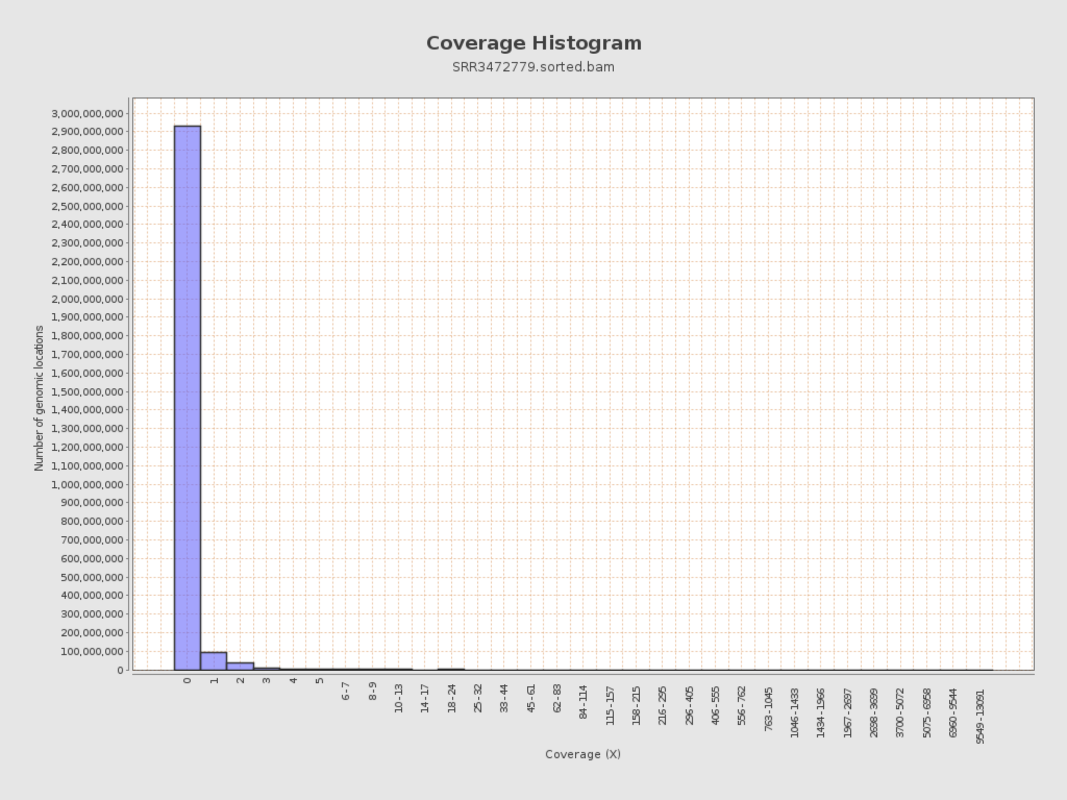
		bases	coverage	deviation
chr1	249250621	189585406	0.7606	28.5975
chr2	243199373	153932211	0.6329	23.3032
chr3	198022430	211054503	1.0658	23.1441
chr4	191154276	98165248	0.5135	24.0362
chr5	180915260	100372623	0.5548	18.5825
chr6	171115067	144938424	0.847	23.0808
chr7	159138663	73816238	0.4638	16.8159
chr8	146364022	76393678	0.5219	18.2052
chr9	141213431	118472812	0.839	19.6012
chr10	135534747	50240086	0.3707	15.5494
chr11	135006516	136439699	1.0106	43.0201
chr12	133851895	93230490	0.6965	22.9095
chr13	115169878	58822871	0.5107	24.0366
chr14	107349540	40002295	0.3726	11.1914
chr15	102531392	47649626	0.4647	14.1536
chr16	90354753	53411982	0.5911	16.3693
chr17	81195210	63191477	0.7783	19.1588
chr18	78077248	34951737	0.4477	16.1247
chr19	59128983	46499596	0.7864	23.3364
chr20	63025520	48427729	0.7684	26.2732
chr21	48129895	6875291	0.1428	4.3386
chr22	51304566	18454539	0.3597	9.8484
chrMT	16571	3294	0.1988	0.7113
chrX	155270560	130219794	0.8387	35.5901

chrY	59373566	1586441	0.0267	0.8192

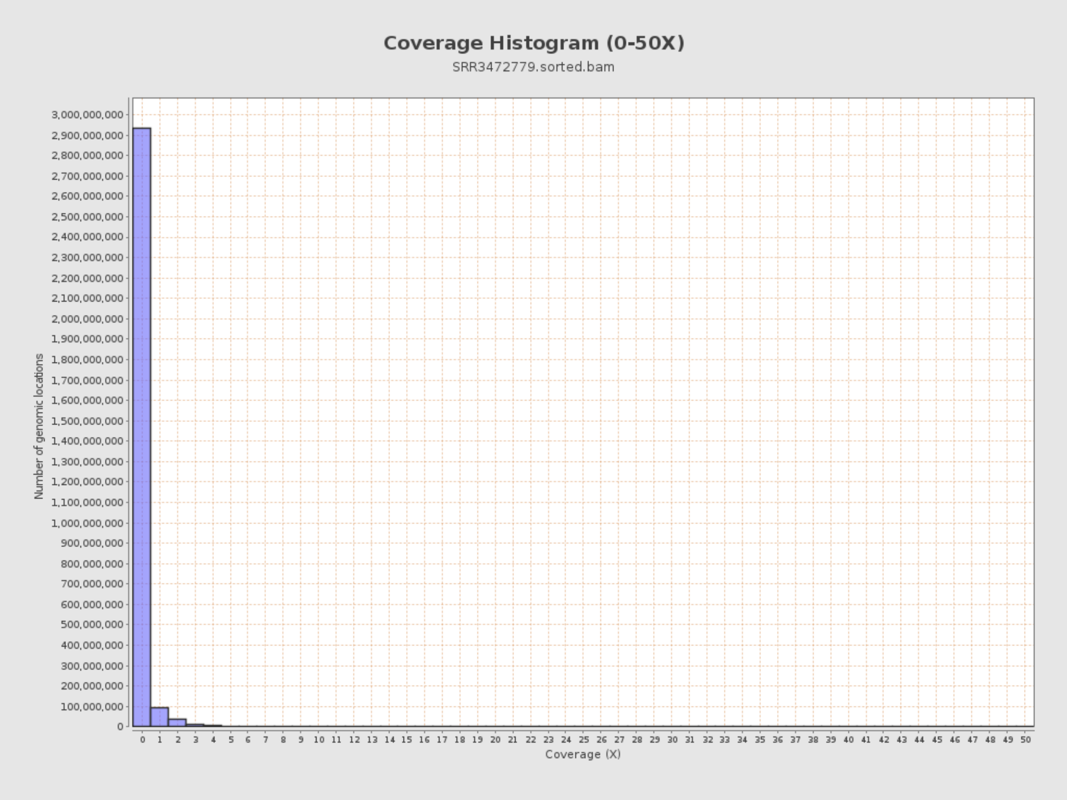
3. Results : Coverage across reference



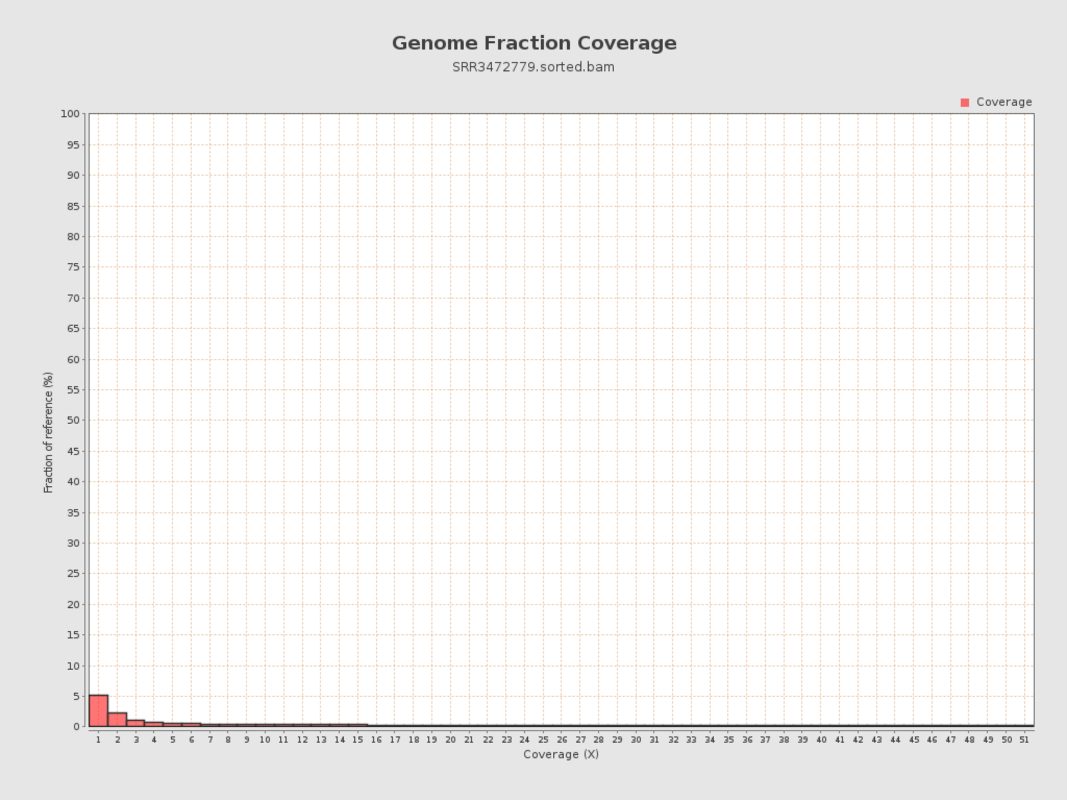
4. Results : Coverage Histogram



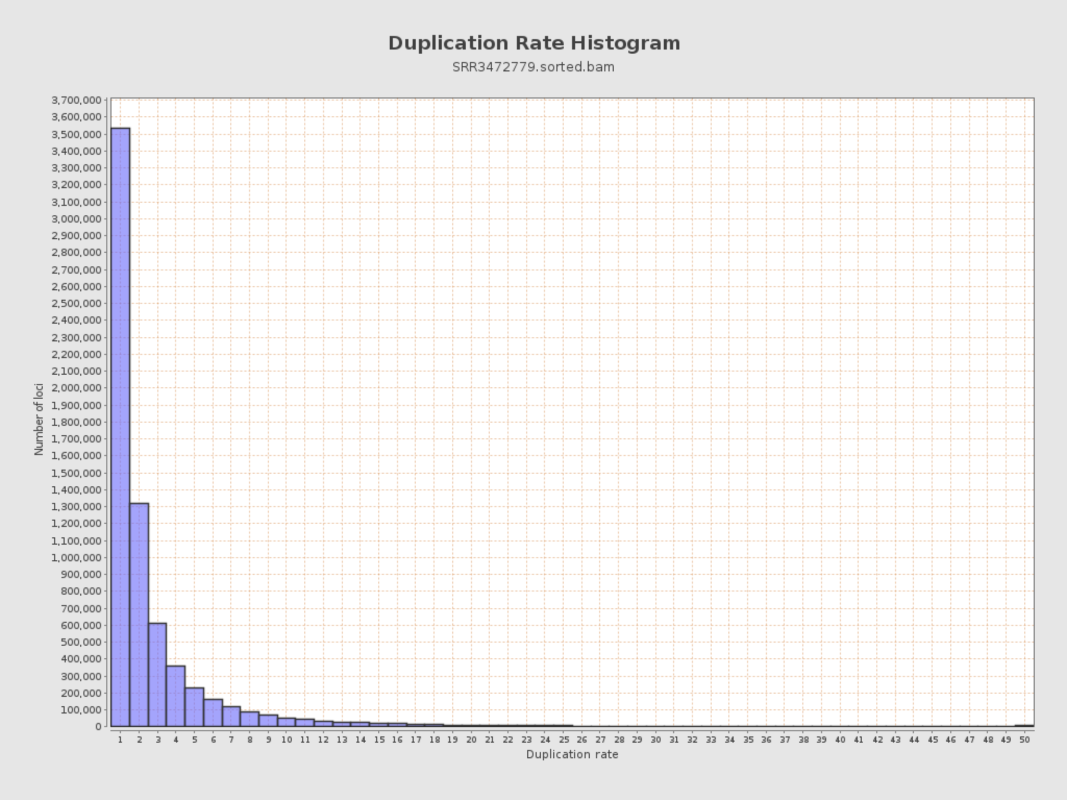
5. Results : Coverage Histogram (0-50X)



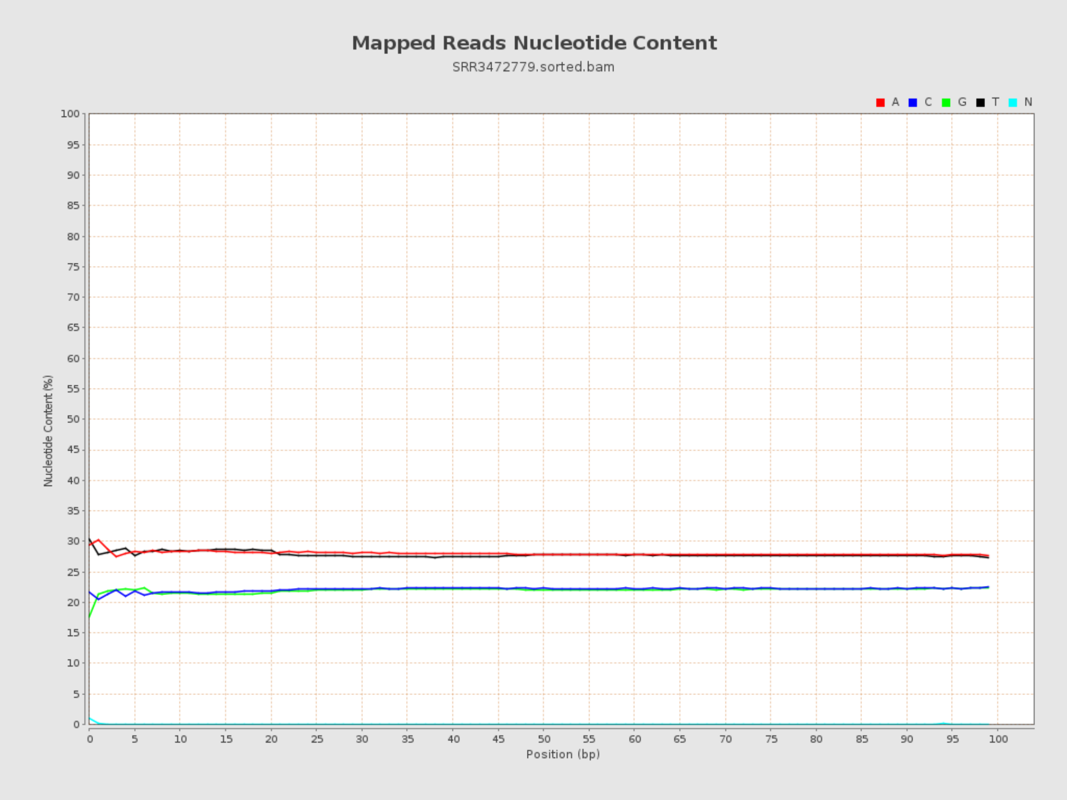
6. Results : Genome Fraction Coverage



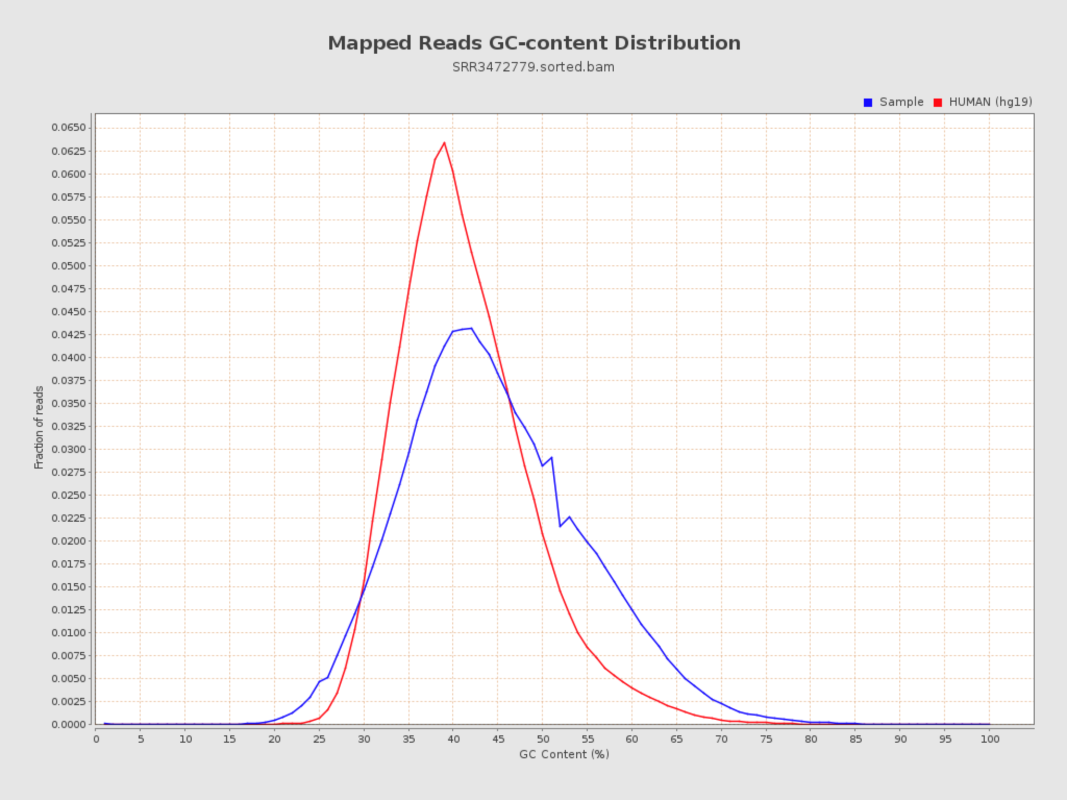
7. Results : Duplication Rate Histogram



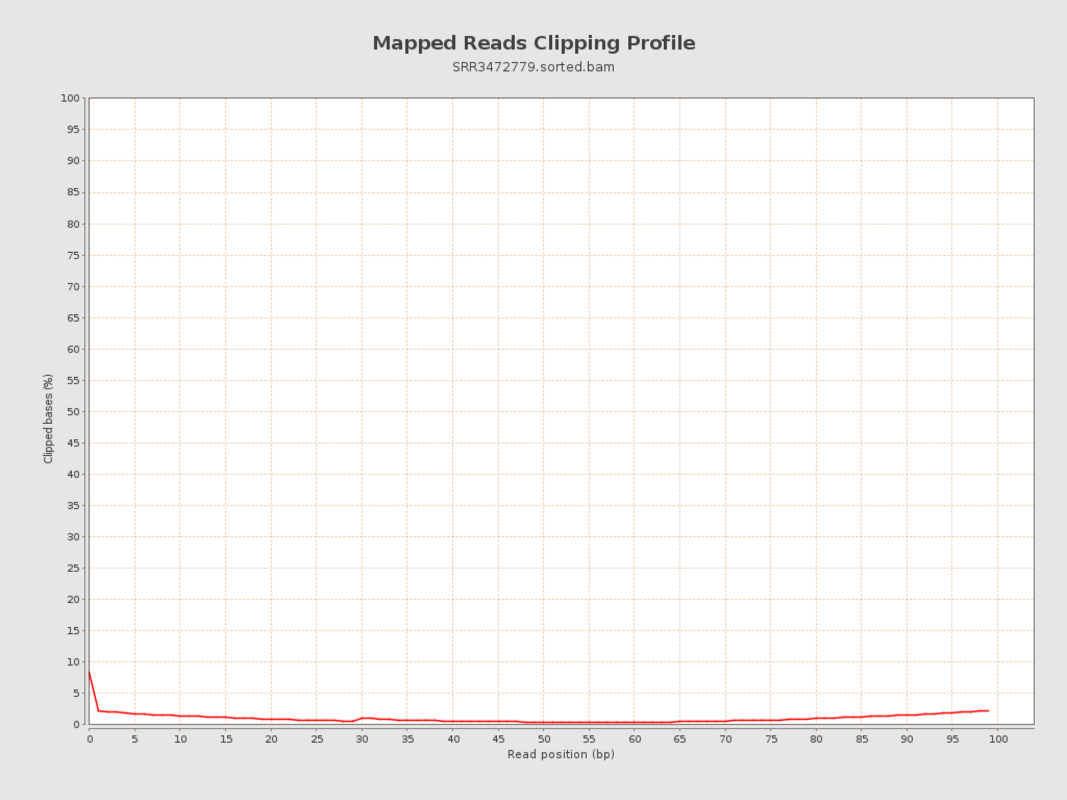
8. Results : Mapped Reads Nucleotide Content



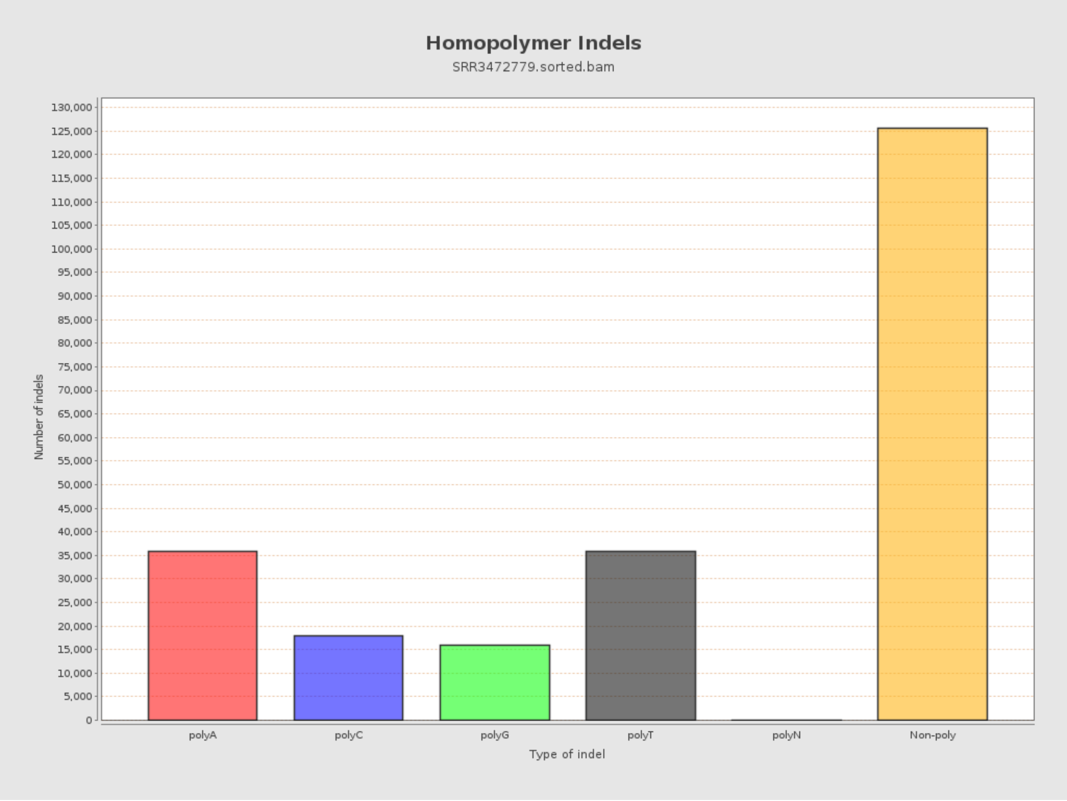
9. Results : Mapped Reads GC-content Distribution



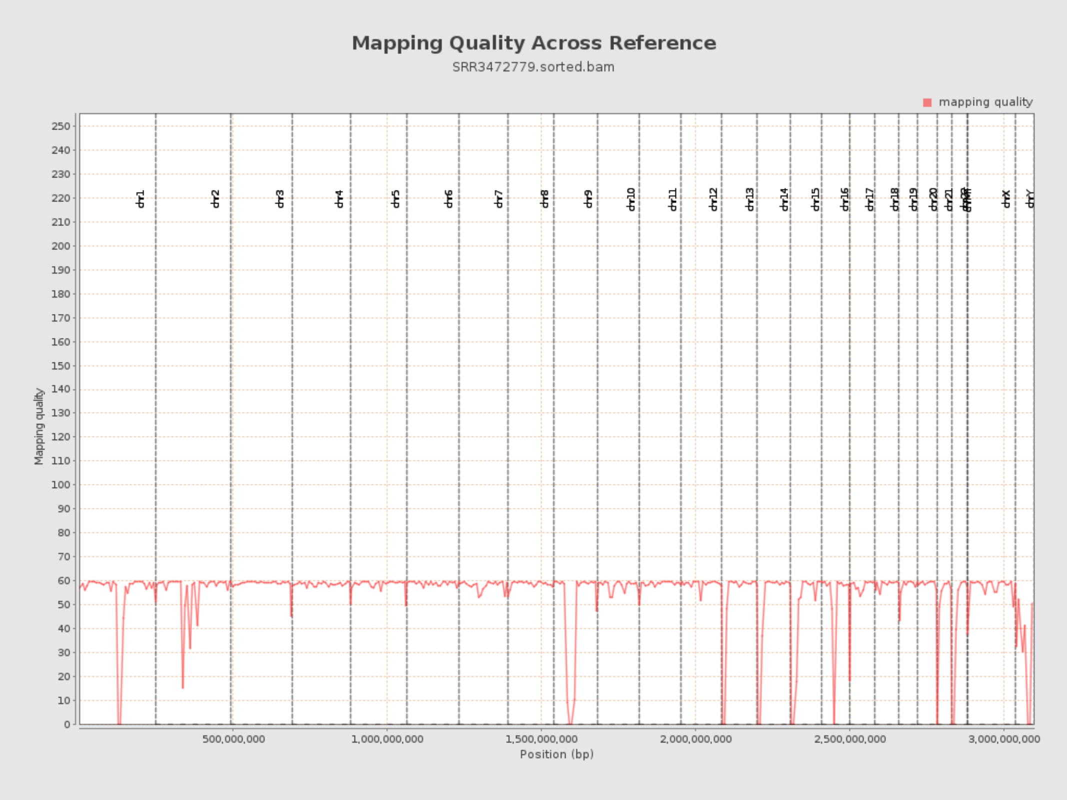
10. Results : Mapped Reads Clipping Profile



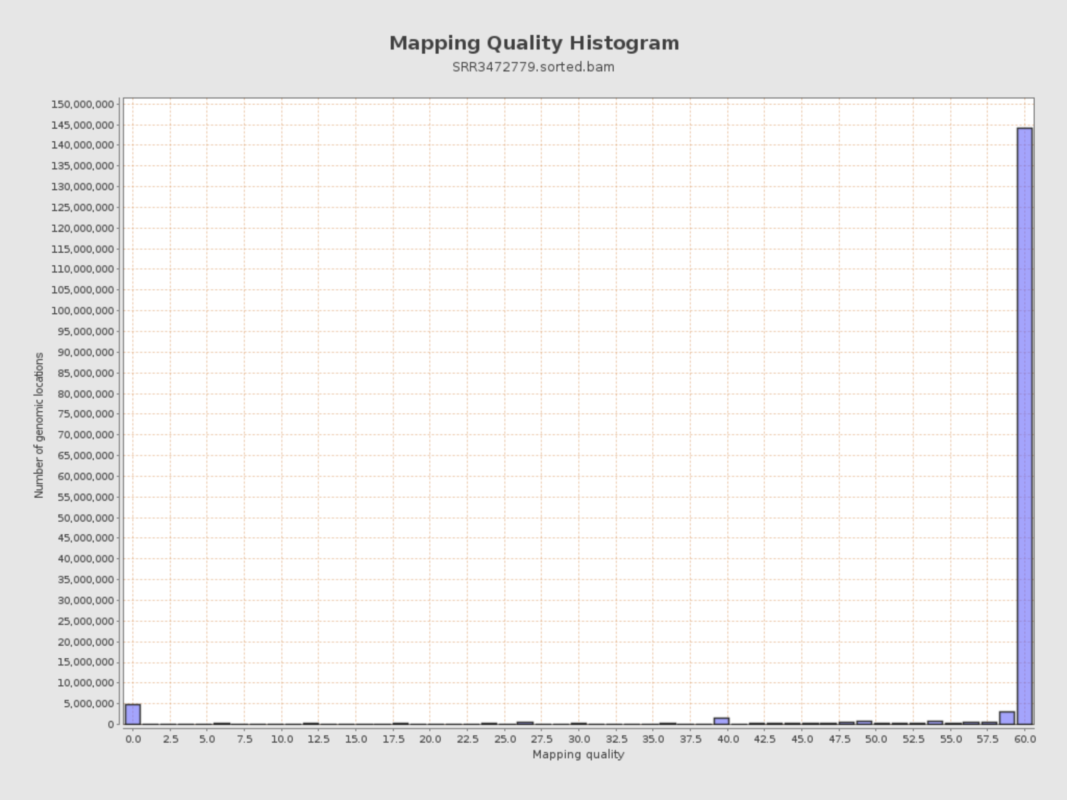
11. Results : Homopolymer Indels



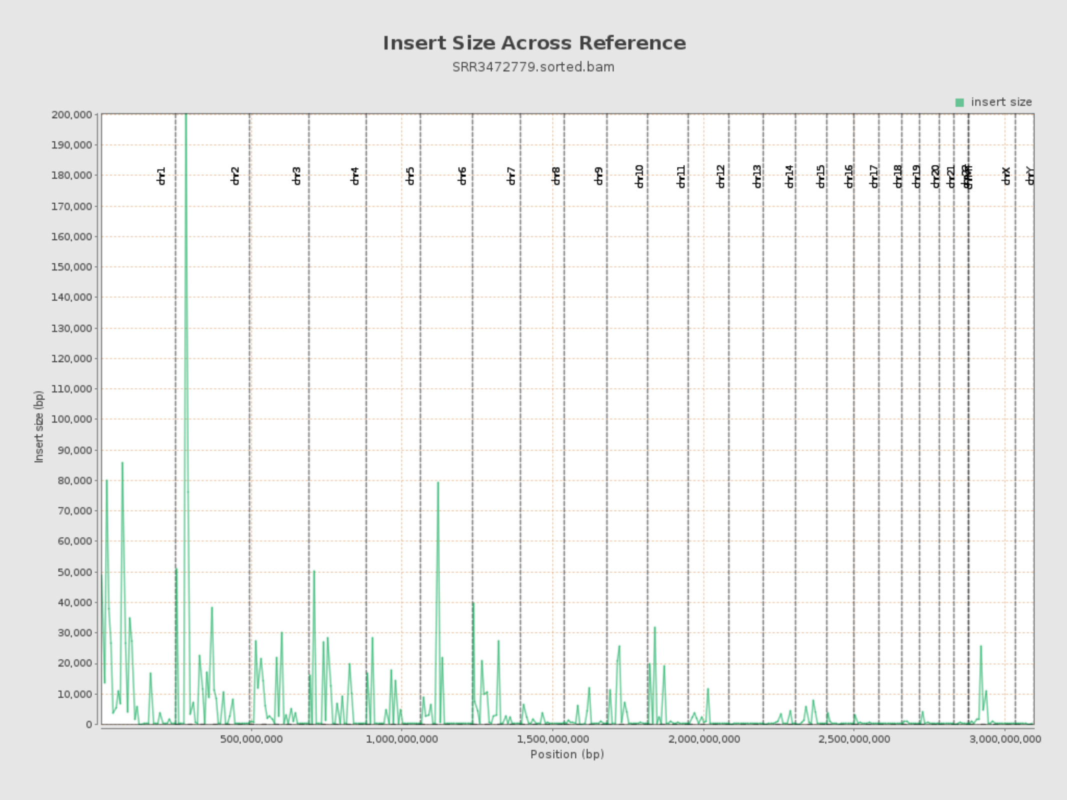
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram