Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 12:51:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472697.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_SRR3472697 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472697_1.fastq.gz SRR3472697_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 12:51:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472697.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,563,114
Mapped reads	13,458,345 / 99.23%
Unmapped reads	104,769 / 0.77%
Mapped paired reads	13,458,345 / 99.23%
Mapped reads, first in pair	6,756,645 / 49.82%
Mapped reads, second in pair	6,701,700 / 49.41%
Mapped reads, both in pair	13,396,714 / 98.77%
Mapped reads, singletons	61,631 / 0.45%
Secondary alignments	0
Supplementary alignments	91,466 / 0.67%
Read min/max/mean length	30 / 101 / 99.59
Duplicated reads (estimated)	9,760,754 / 71.97%
Duplication rate	47.63%
Clipped reads	876,015 / 6.46%

2.2. ACGT Content

Number/percentage of A's	359,330,740 / 27.13%
Number/percentage of C's	301,938,796 / 22.8%
Number/percentage of T's	364,641,778 / 27.53%
Number/percentage of G's	298,097,048 / 22.51%
Number/percentage of N's	310,271 / 0.02%

GC Percentage	45.31%

2.3. Coverage

Mean	0.4279
Standard Deviation	30.0823

2.4. Mapping Quality

Mean Mapping Quality	54.3

2.5. Insert size

Mean	24,118.8
Standard Deviation	1,553,915.65
P25/Median/P75	154 / 211 / 279

2.6. Mismatches and indels

General error rate	0.43%
Mismatches	5,486,434
Insertions	90,539
Mapped reads with at least one insertion	0.67%
Deletions	85,032
Mapped reads with at least one deletion	0.62%
Homopolymer indels	47.3%

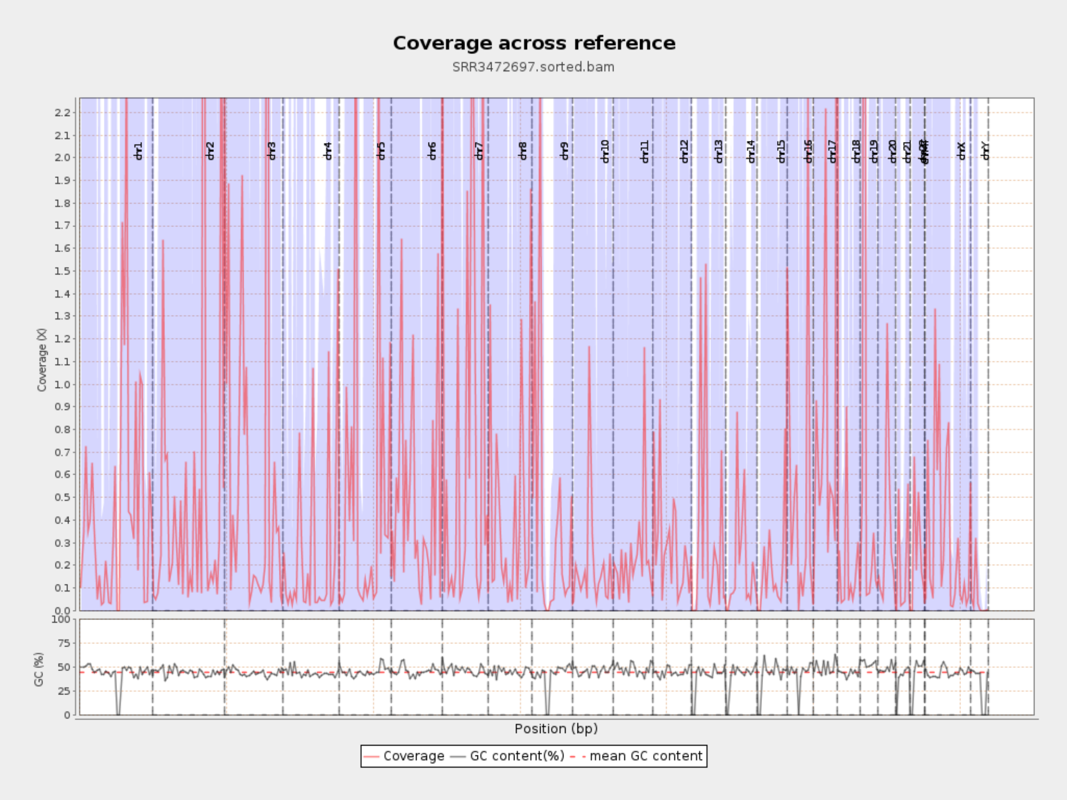
2.7. Chromosome stats

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

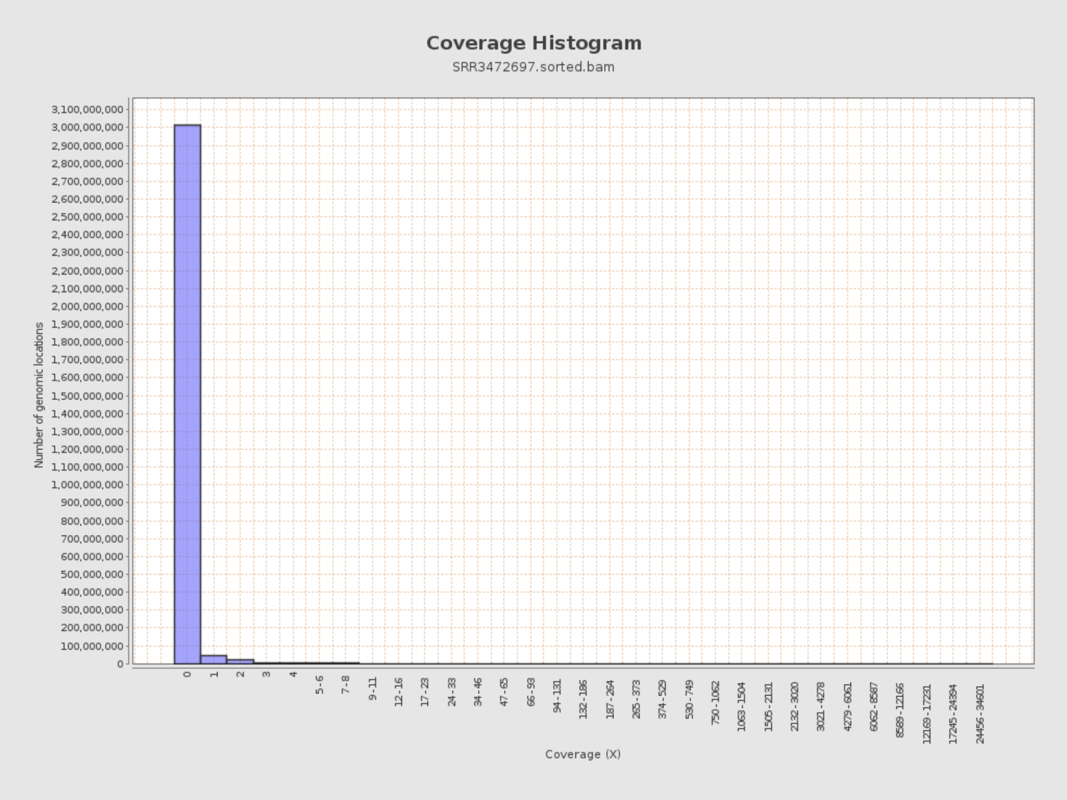
		bases	coverage	deviation
chr1	249250621	118864407	0.4769	19.1996
chr2	243199373	135875196	0.5587	47.8151
chr3	198022430	137095693	0.6923	55.6103
chr4	191154276	46892313	0.2453	16.6922
chr5	180915260	97393632	0.5383	32.6001
chr6	171115067	80226517	0.4688	21.0548
chr7	159138663	120762058	0.7588	52.9012
chr8	146364022	66113572	0.4517	24.6867
chr9	141213431	54872439	0.3886	17.7438
chr10	135534747	26119032	0.1927	18.0212
chr11	135006516	32947242	0.244	16.2554
chr12	133851895	39612059	0.2959	16.6767
chr13	115169878	38820923	0.3371	21.4439
chr14	107349540	21248032	0.1979	9.7924
chr15	102531392	18619745	0.1816	9.1667
chr16	90354753	48602944	0.5379	24.3852
chr17	81195210	75289041	0.9273	34.6363
chr18	78077248	15501451	0.1985	16.3779
chr19	59128983	48601204	0.822	50.1005
chr20	63025520	22665352	0.3596	17.0332
chr21	48129895	9532754	0.1981	10.9977
chr22	51304566	12880769	0.2511	28.8122
chrMT	16571	4577	0.2762	0.7088
chrX	155270560	52797579	0.34	19.4001

chrY	59373566	3176604	0.0535	10.2159

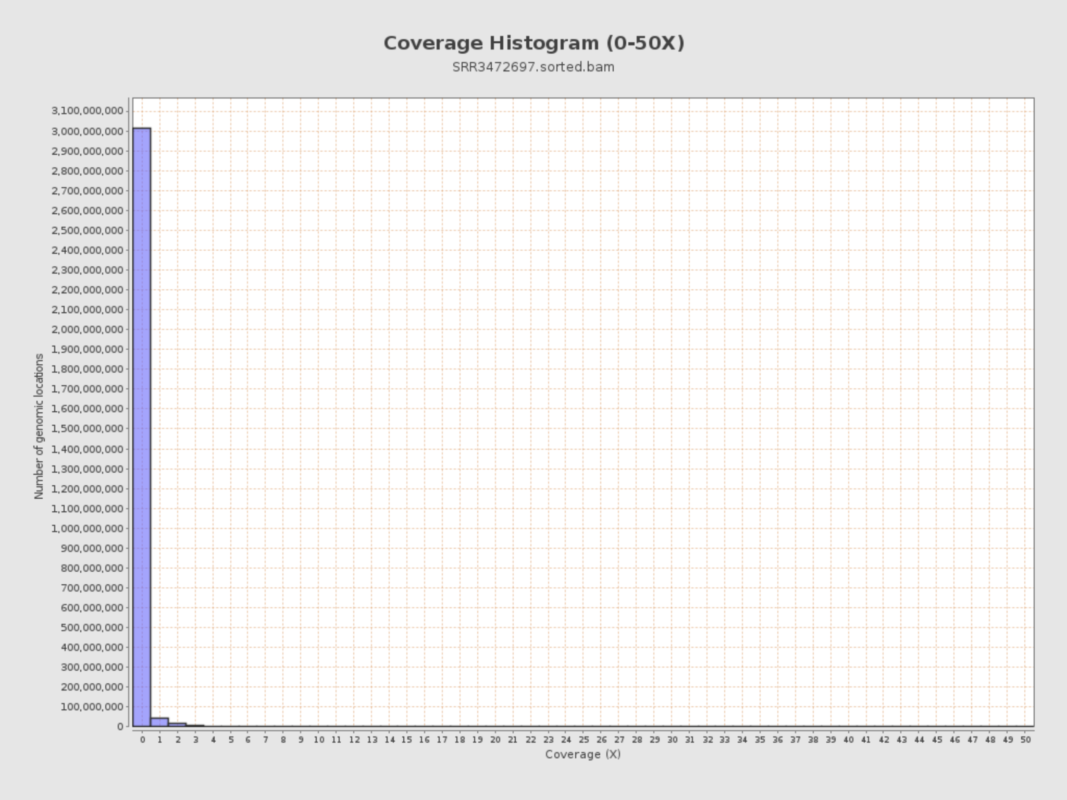
3. Results : Coverage across reference



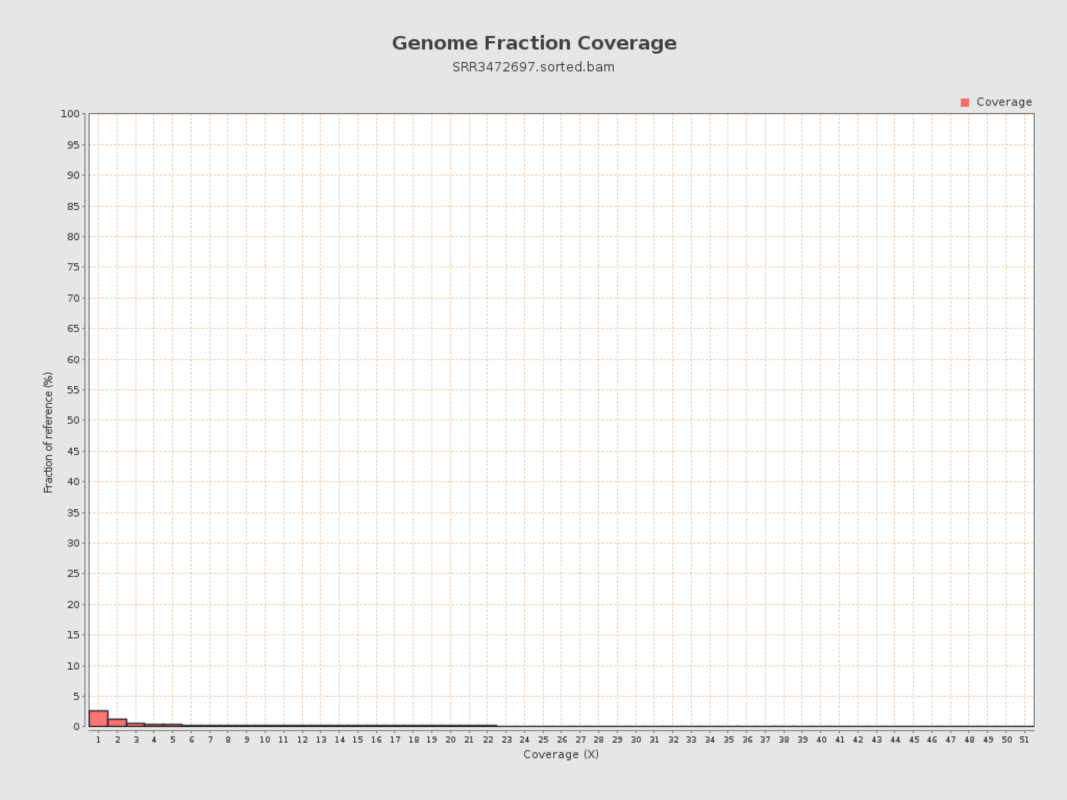
4. Results : Coverage Histogram



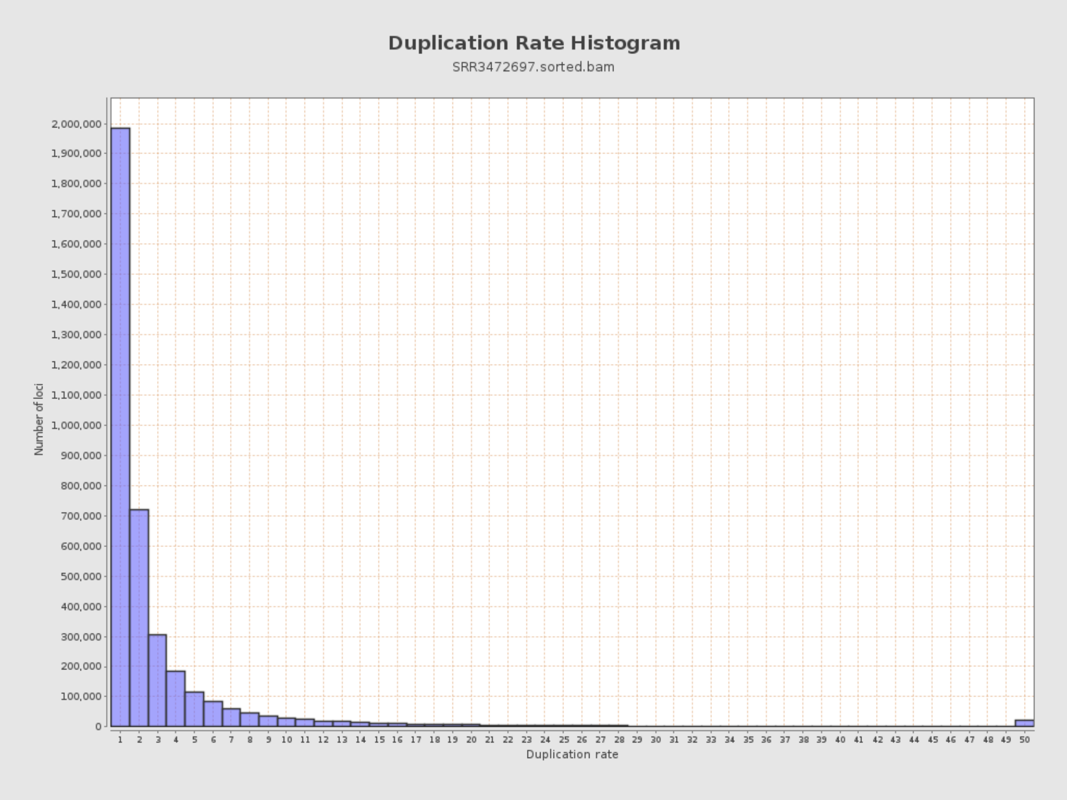
5. Results : Coverage Histogram (0-50X)



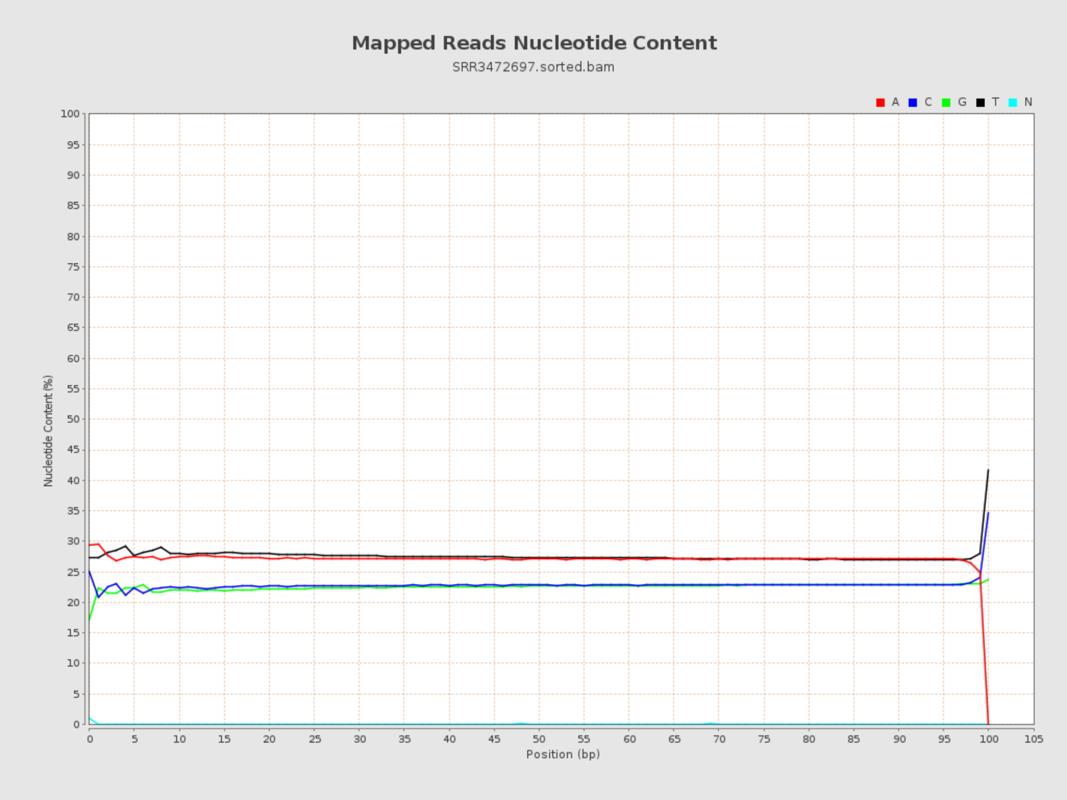
6. Results : Genome Fraction Coverage



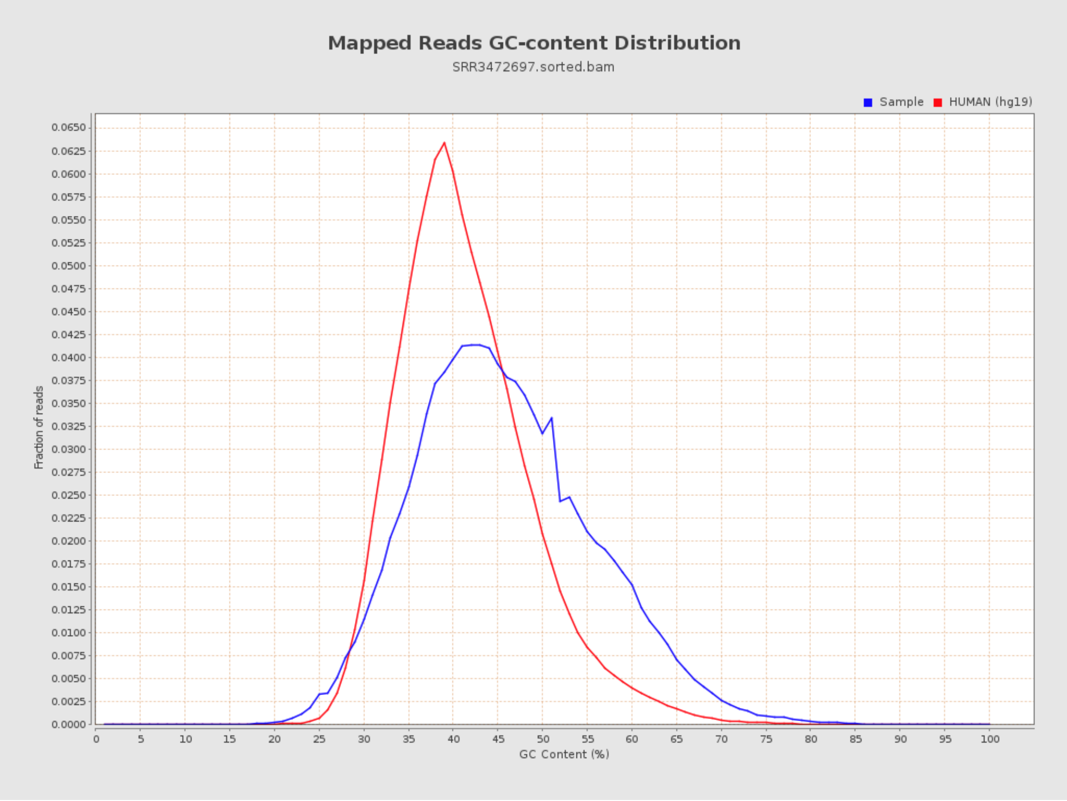
7. Results : Duplication Rate Histogram



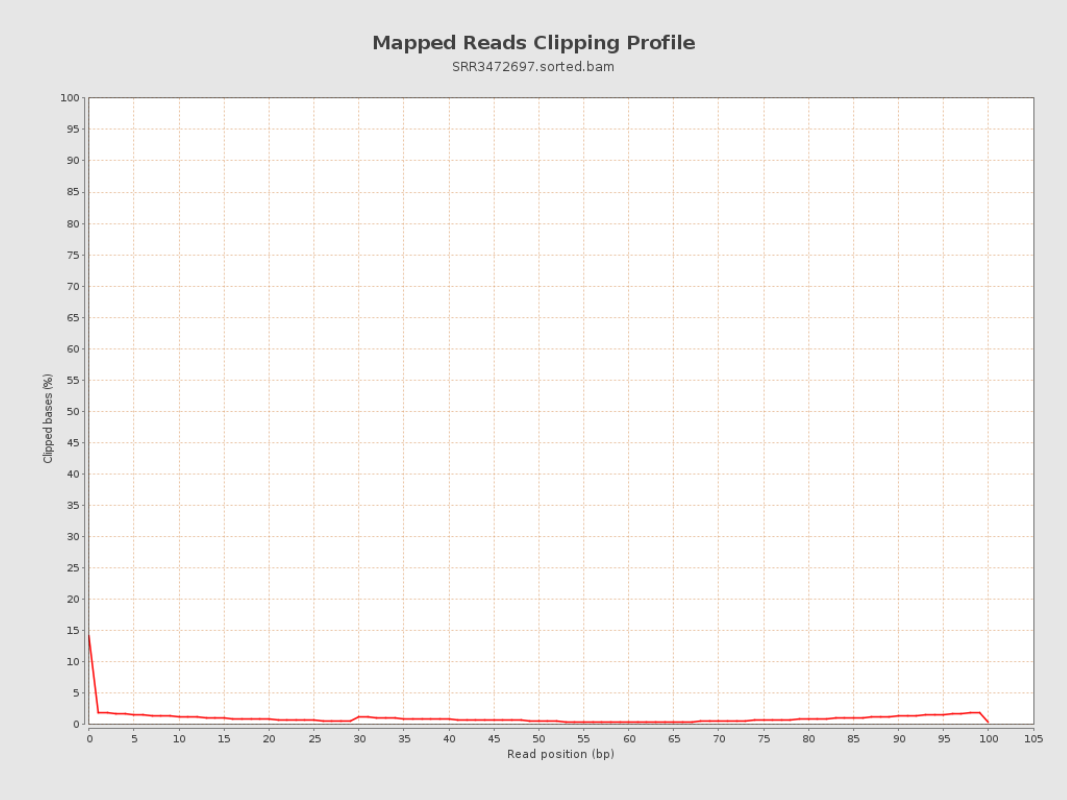
8. Results : Mapped Reads Nucleotide Content



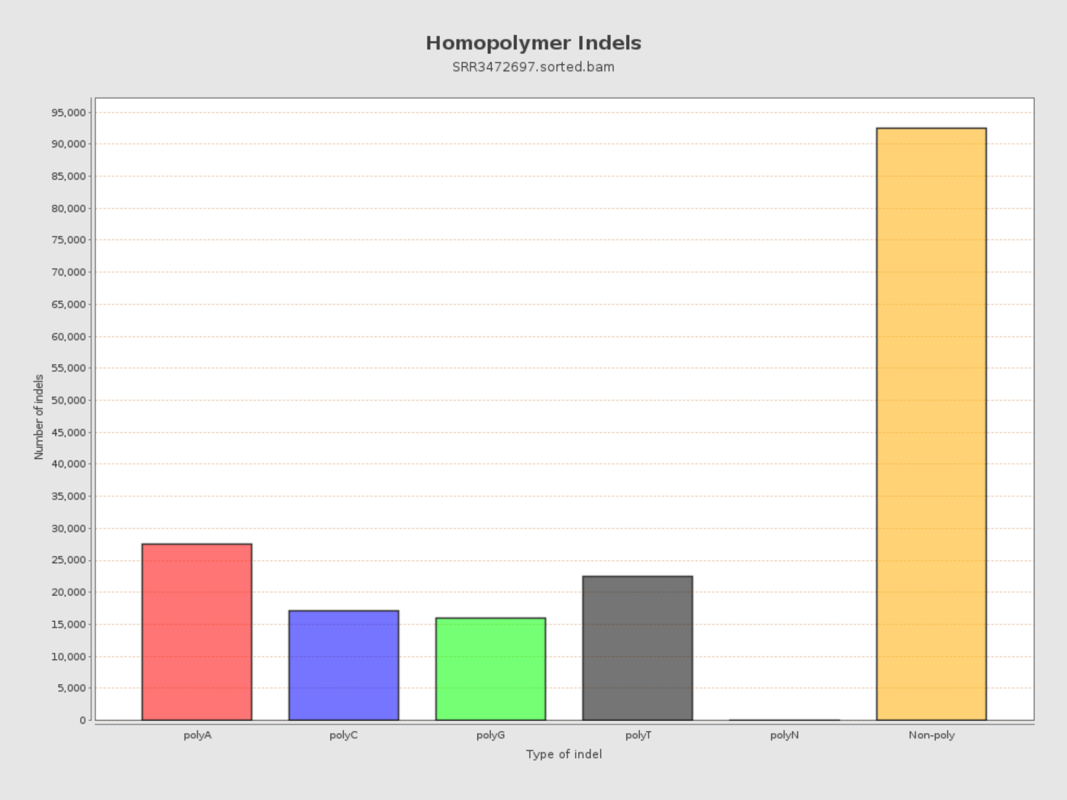
9. Results : Mapped Reads GC-content Distribution



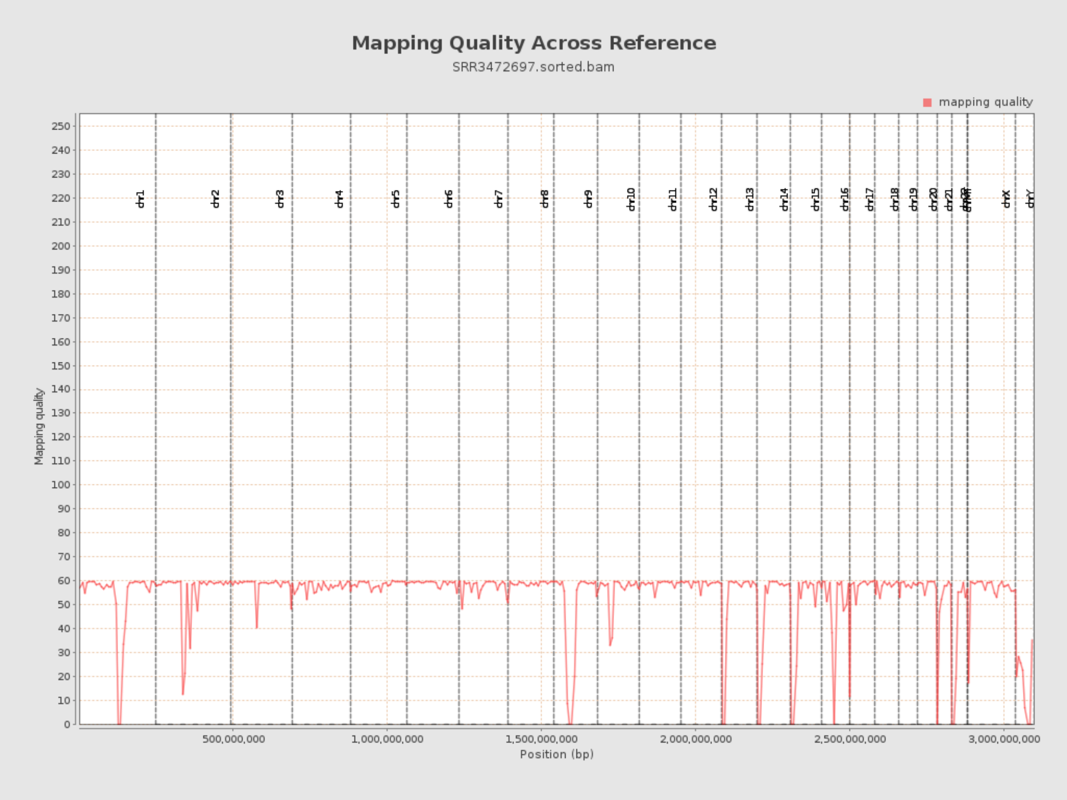
10. Results : Mapped Reads Clipping Profile



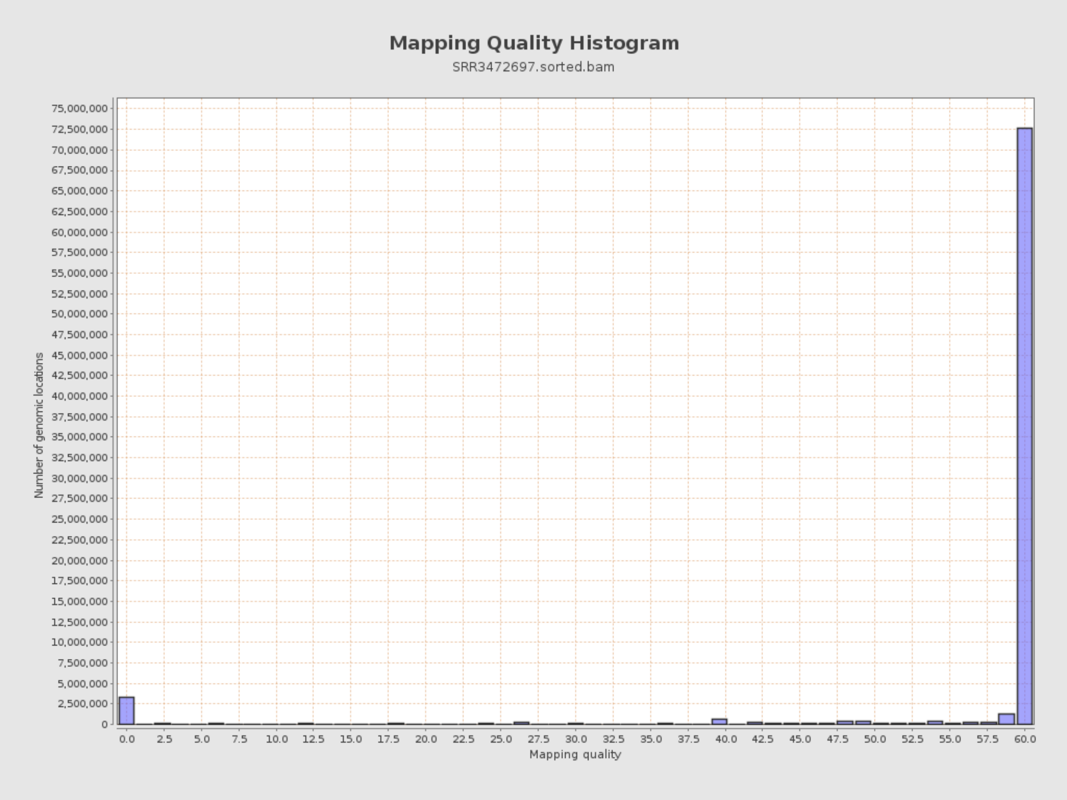
11. Results : Homopolymer Indels



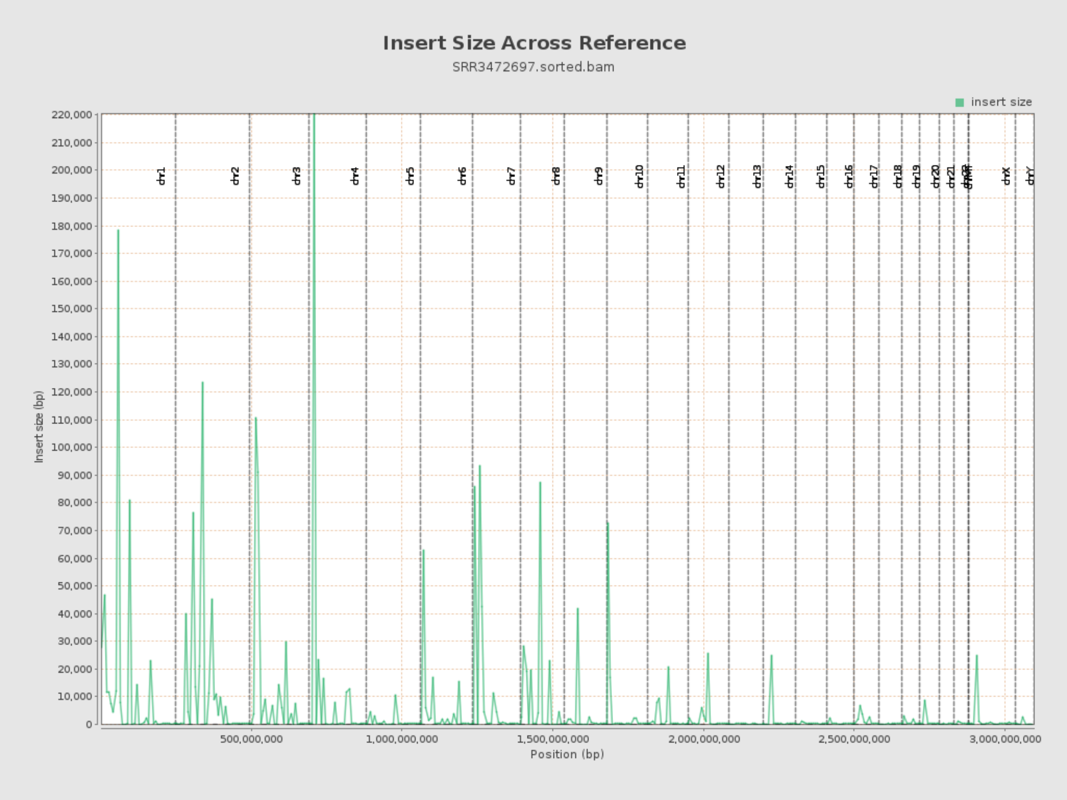
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram