Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 12:23:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472426.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_SRR3472426 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472426_1.fastq.gz SRR3472426_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 12:23:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472426.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,440,822
Mapped reads	17,232,196 / 98.8%
Unmapped reads	208,626 / 1.2%
Mapped paired reads	17,232,196 / 98.8%
Mapped reads, first in pair	8,643,182 / 49.56%
Mapped reads, second in pair	8,589,014 / 49.25%
Mapped reads, both in pair	17,130,896 / 98.22%
Mapped reads, singletons	101,300 / 0.58%
Secondary alignments	0
Supplementary alignments	66,915 / 0.38%
Read min/max/mean length	30 / 100 / 99.19
Duplicated reads (estimated)	10,958,700 / 62.83%
Duplication rate	47.07%
Clipped reads	1,258,048 / 7.21%

2.2. ACGT Content

Number/percentage of A's	455,037,352 / 26.98%
Number/percentage of C's	389,495,952 / 23.09%
Number/percentage of T's	456,017,099 / 27.03%
Number/percentage of G's	386,074,033 / 22.89%
Number/percentage of N's	209,597 / 0.01%

GC Percentage	45.98%

2.3. Coverage

Mean	0.545
Standard Deviation	18.258

2.4. Mapping Quality

Mean Mapping Quality	54.77

2.5. Insert size

Mean	20,189.64
Standard Deviation	1,396,708.67
P25/Median/P75	149 / 204 / 273

2.6. Mismatches and indels

General error rate	0.54%
Mismatches	9,001,569
Insertions	100,180
Mapped reads with at least one insertion	0.58%
Deletions	80,580
Mapped reads with at least one deletion	0.46%
Homopolymer indels	46.2%

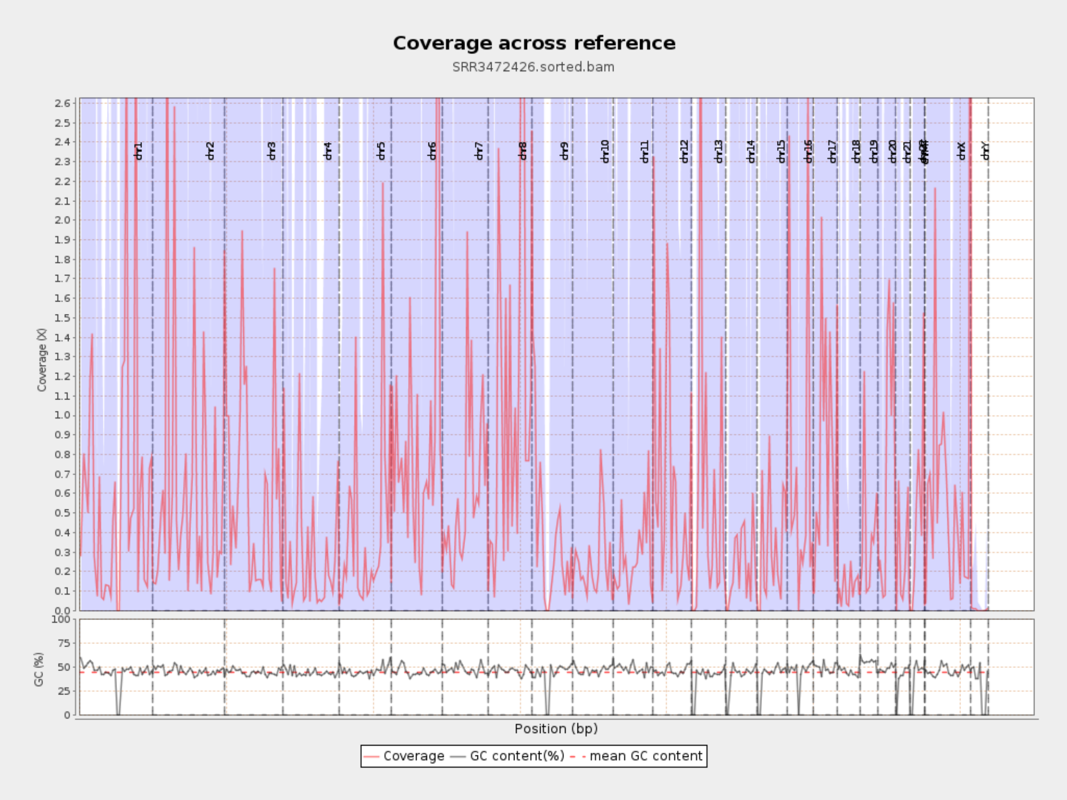
2.7. Chromosome stats

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

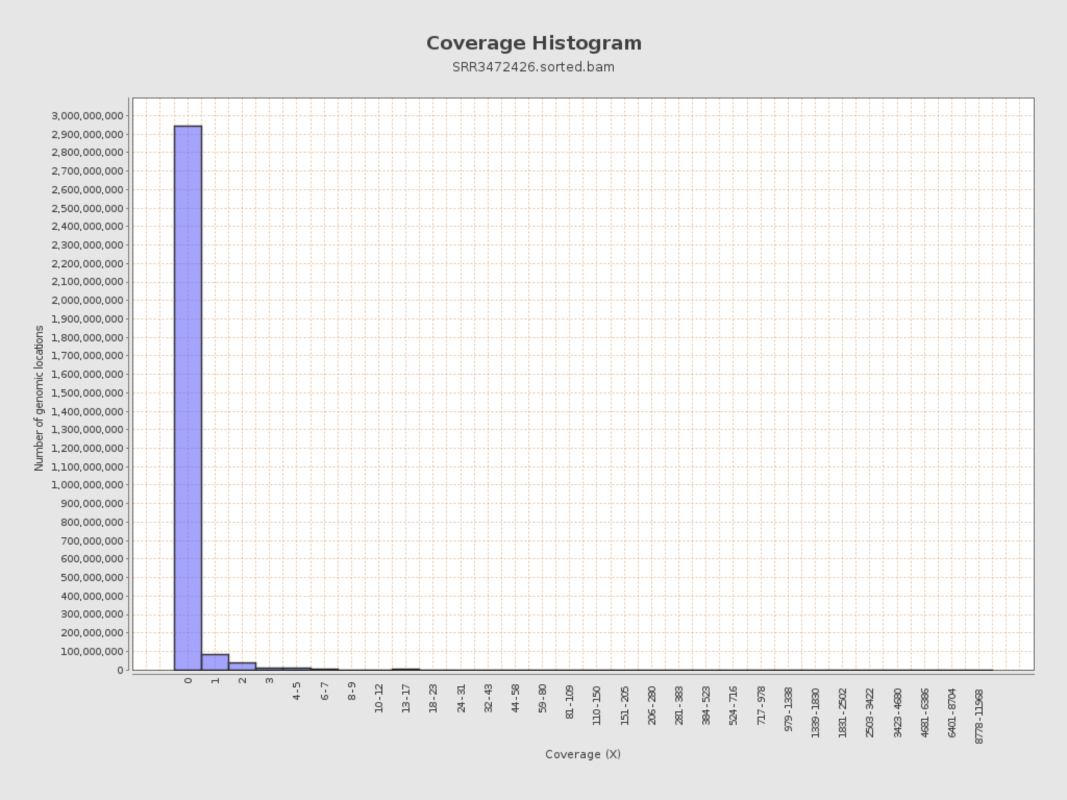
		bases	coverage	deviation
chr1	249250621	162208380	0.6508	21.1735
chr2	243199373	155388721	0.6389	26.1897
chr3	198022430	122819577	0.6202	14.9495
chr4	191154276	51796437	0.271	9.8282
chr5	180915260	75430510	0.4169	17.5409
chr6	171115067	149513264	0.8738	21.389
chr7	159138663	100439511	0.6311	19.0937
chr8	146364022	169542300	1.1584	33.4644
chr9	141213431	55706261	0.3945	10.9914
chr10	135534747	32836961	0.2423	10.0715
chr11	135006516	38380208	0.2843	9.473
chr12	133851895	90436837	0.6756	16.9861
chr13	115169878	70914798	0.6157	21.8096
chr14	107349540	23993739	0.2235	6.3645
chr15	102531392	33231194	0.3241	13.4855
chr16	90354753	68602065	0.7593	18.0715
chr17	81195210	68617474	0.8451	20.6266
chr18	78077248	8995955	0.1152	5.7289
chr19	59128983	24309823	0.4111	10.2115
chr20	63025520	49433002	0.7843	18.5001
chr21	48129895	13080055	0.2718	11.4432
chr22	51304566	26763873	0.5217	19.3929
chrMT	16571	4676	0.2822	0.6013
chrX	155270560	94293771	0.6073	18.8805

chrY	59373566	282146	0.0048	0.2553

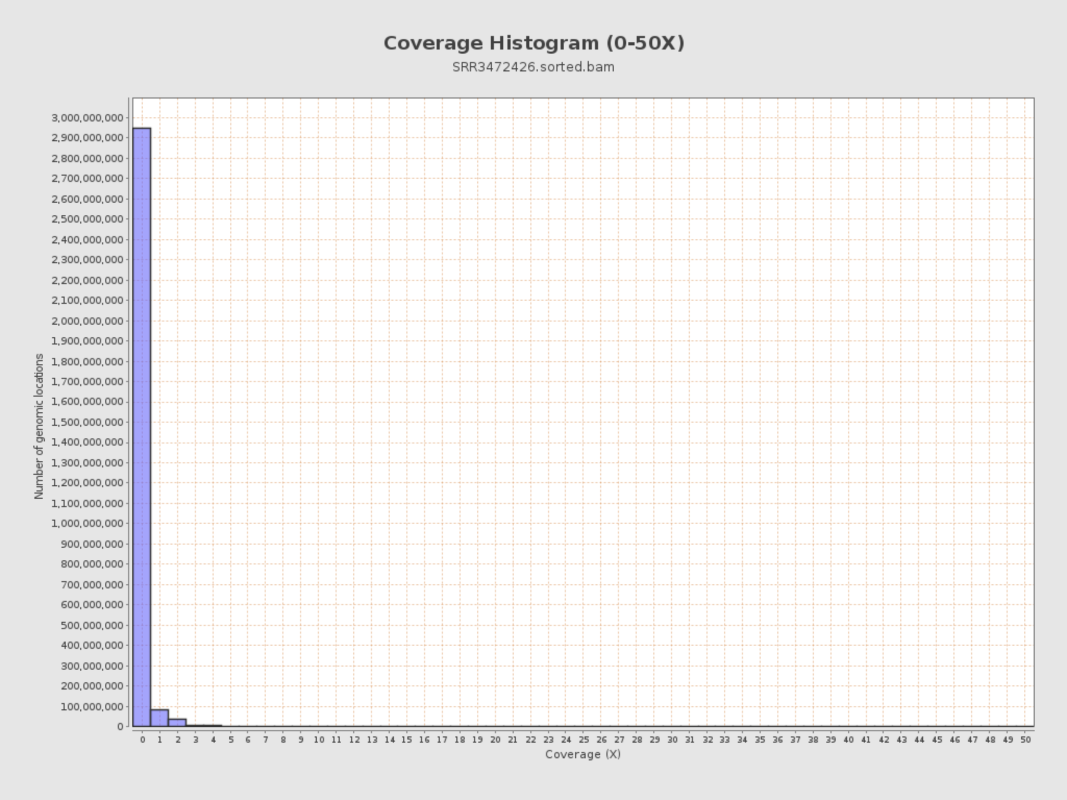
3. Results : Coverage across reference



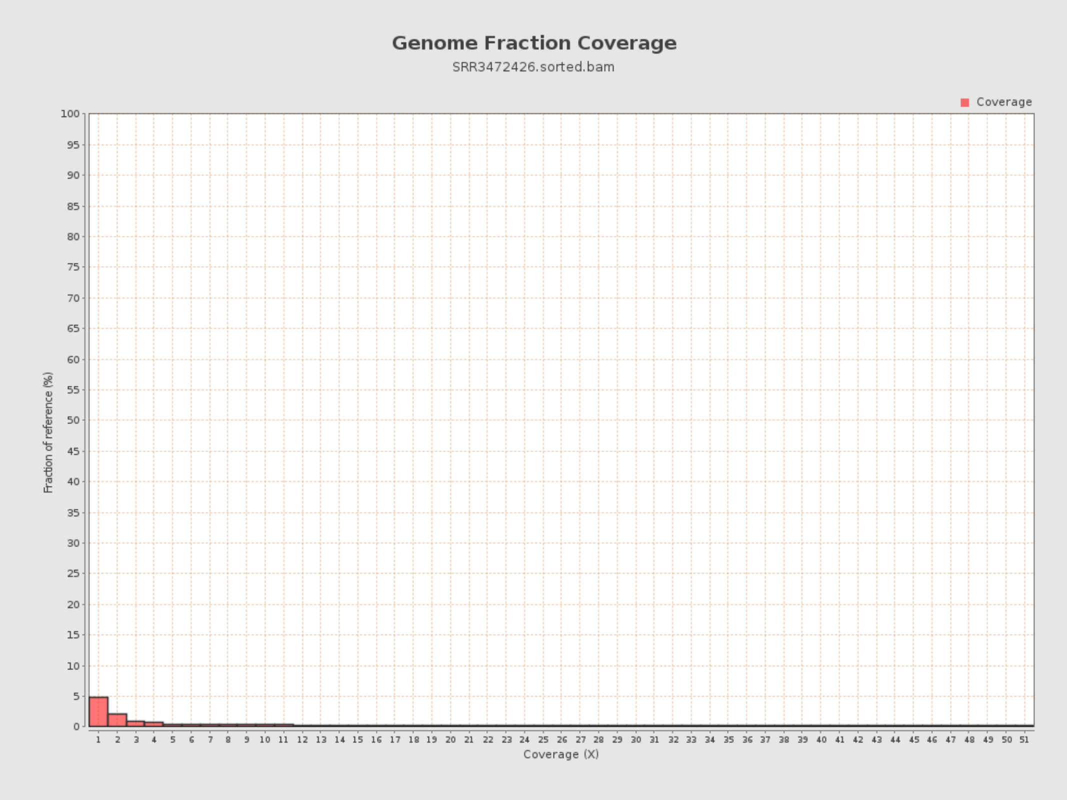
4. Results : Coverage Histogram



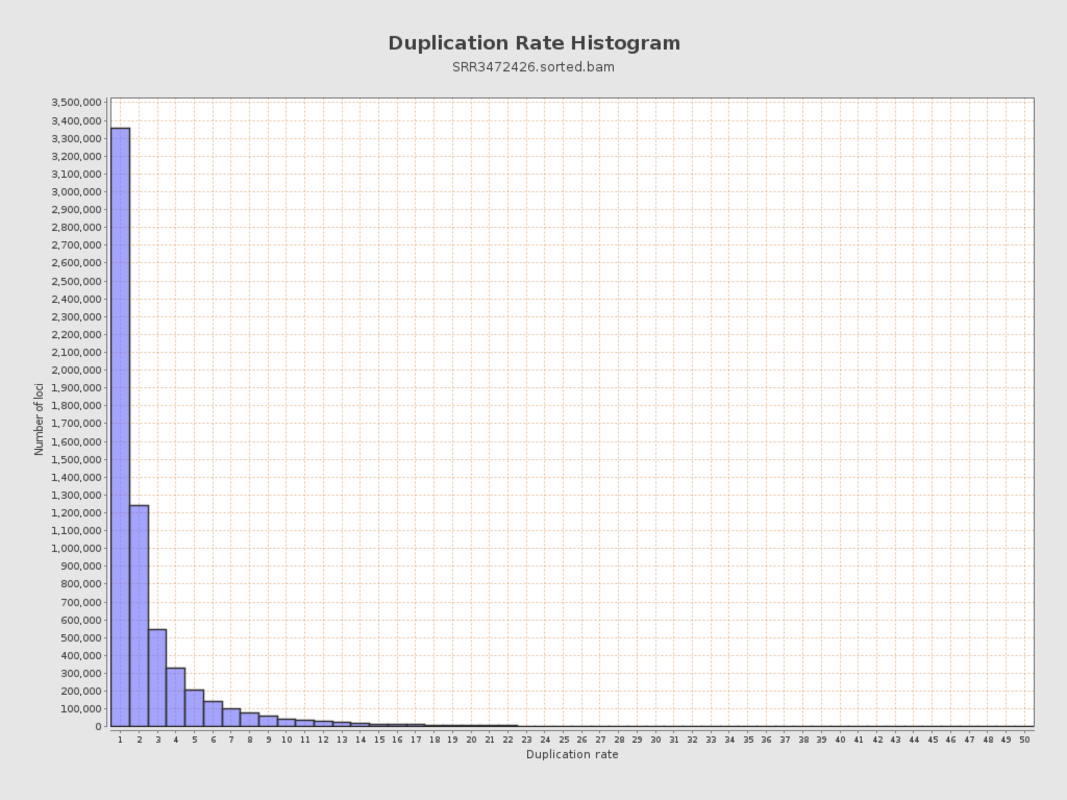
5. Results : Coverage Histogram (0-50X)



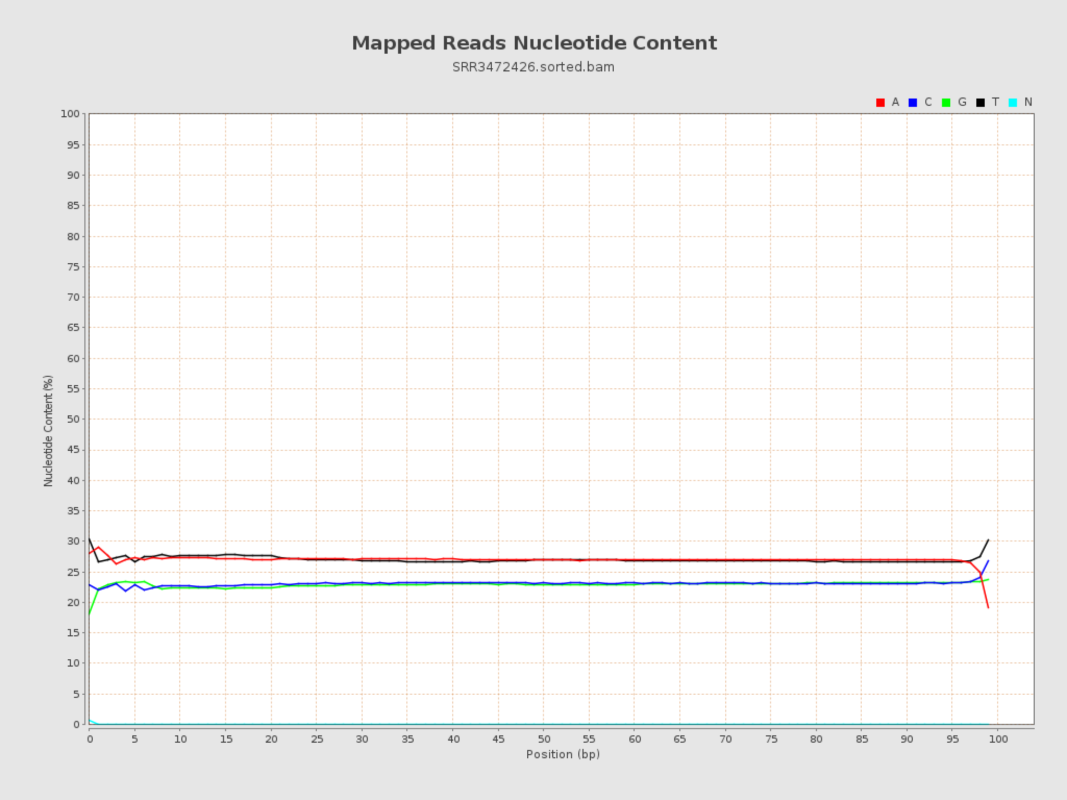
6. Results : Genome Fraction Coverage



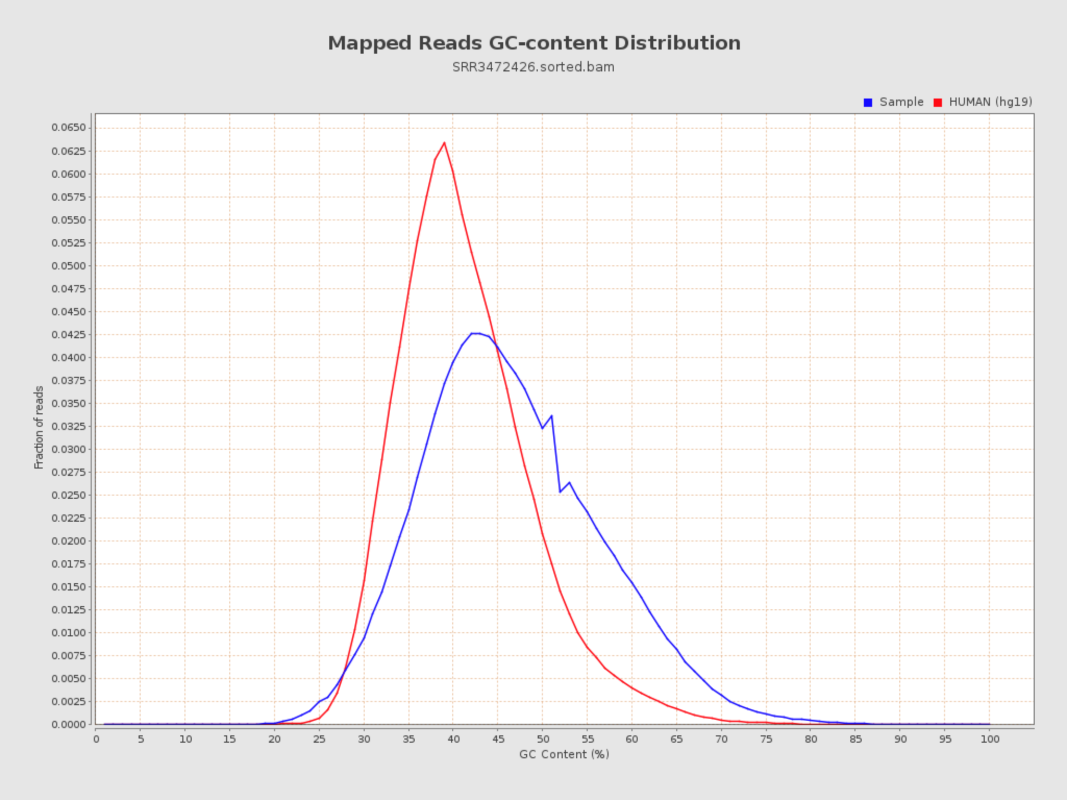
7. Results : Duplication Rate Histogram



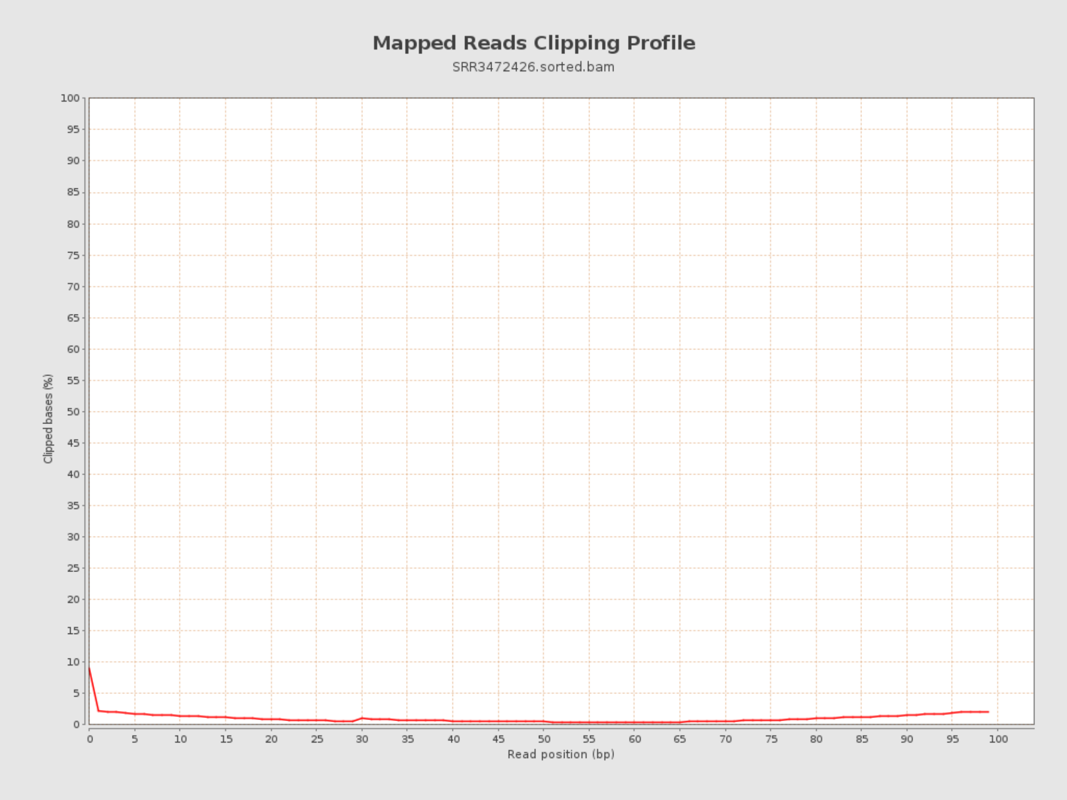
8. Results : Mapped Reads Nucleotide Content



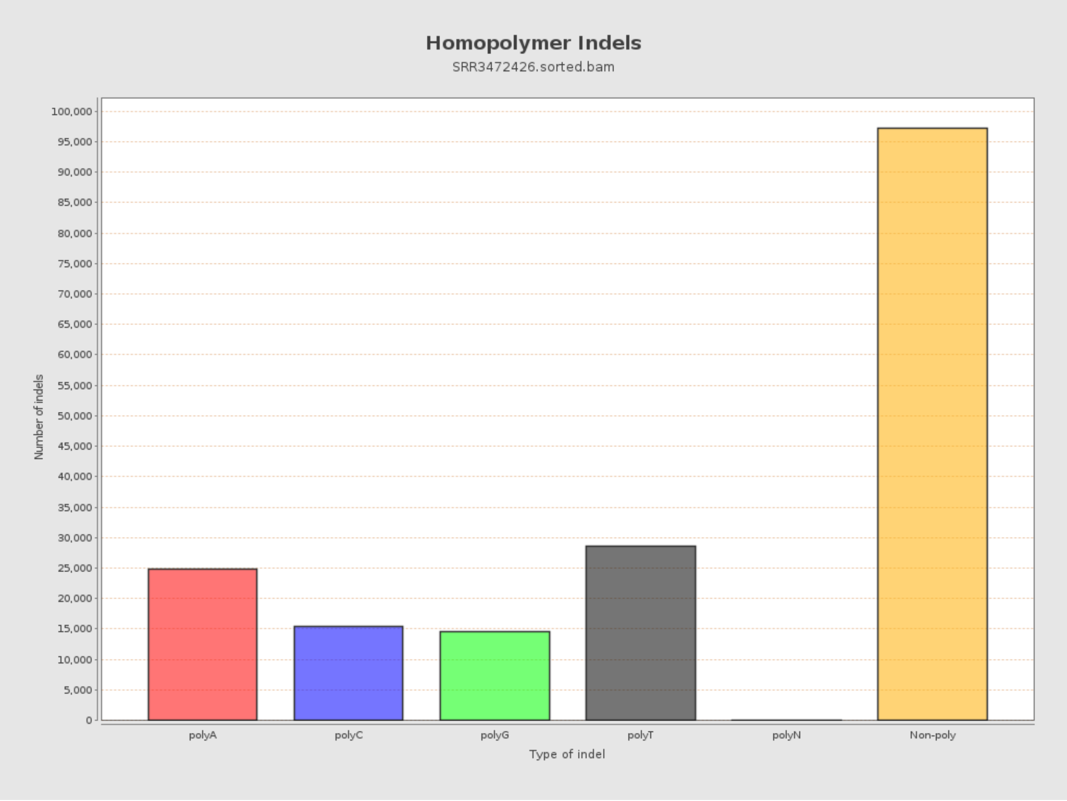
9. Results : Mapped Reads GC-content Distribution



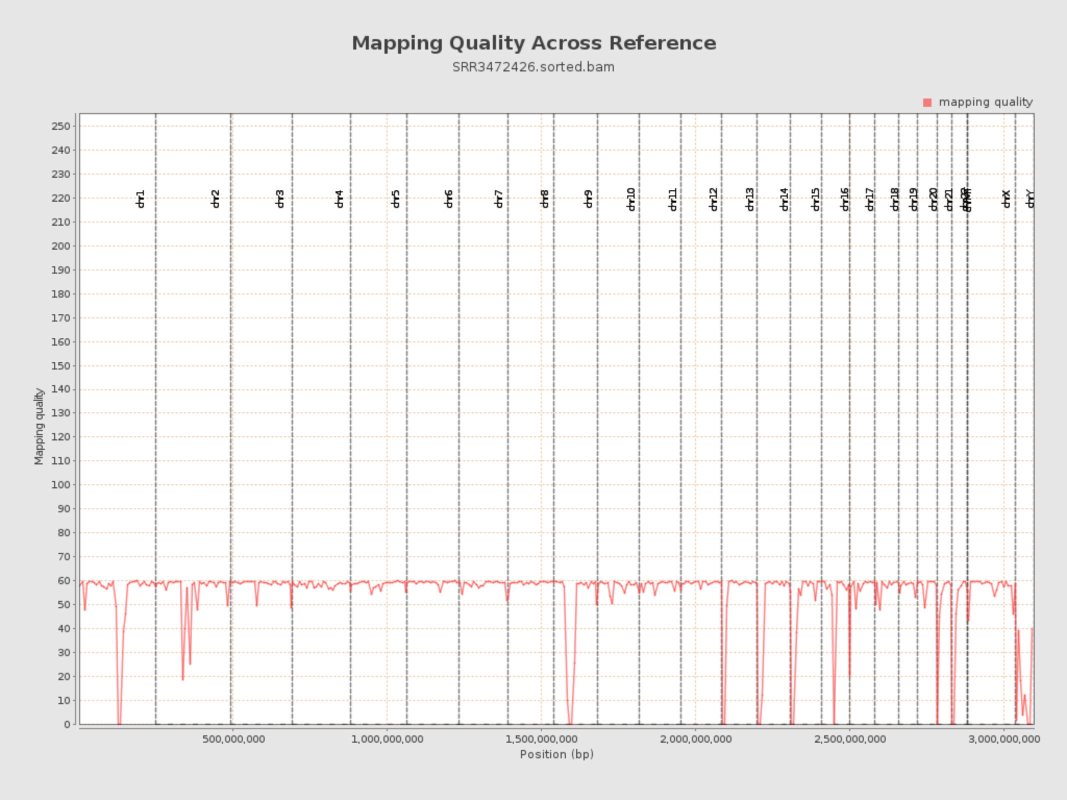
10. Results : Mapped Reads Clipping Profile



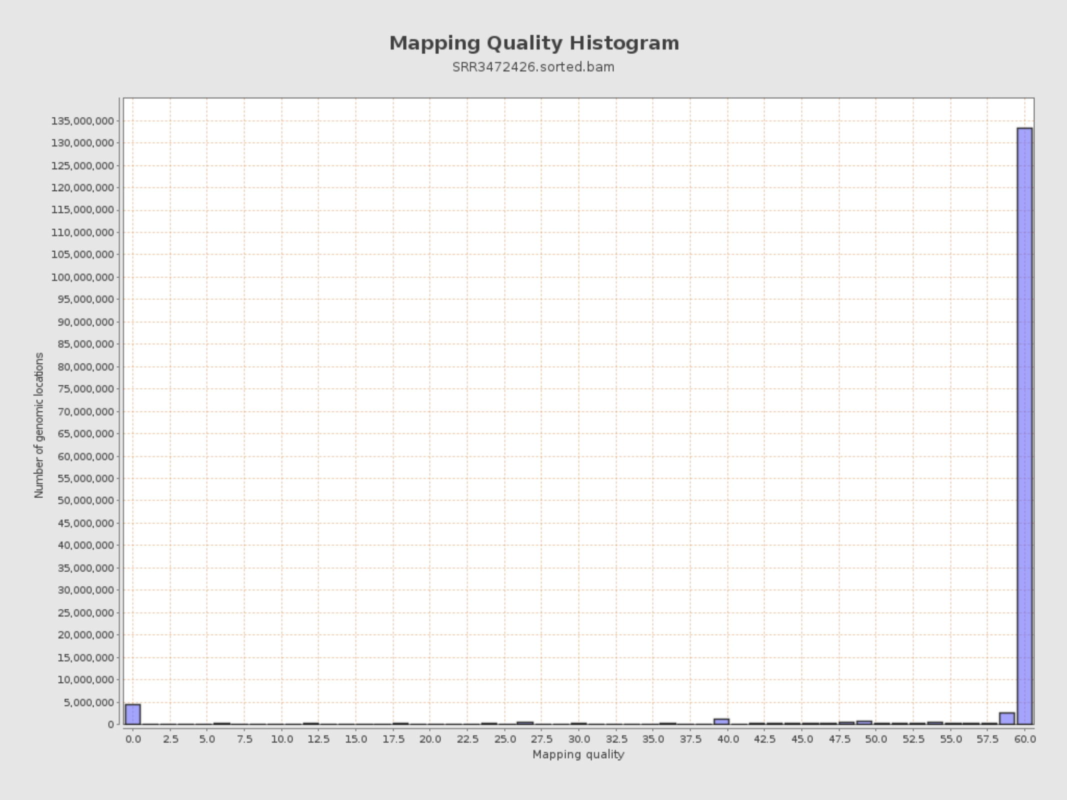
11. Results : Homopolymer Indels



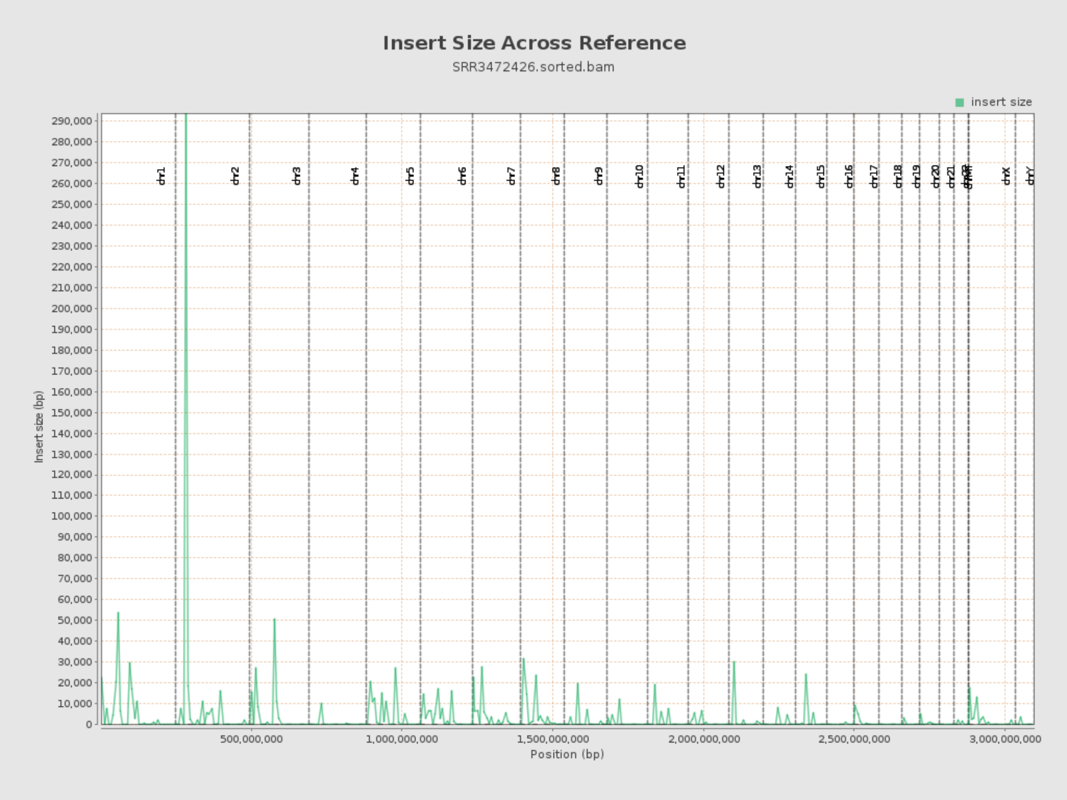
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram