Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 13:00:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472428.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_SRR3472428 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472428_1.fastq.gz SRR3472428_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 13:00:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472428.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	21,789,822
Mapped reads	21,621,072 / 99.23%
Unmapped reads	168,750 / 0.77%
Mapped paired reads	21,621,072 / 99.23%
Mapped reads, first in pair	10,836,763 / 49.73%
Mapped reads, second in pair	10,784,309 / 49.49%
Mapped reads, both in pair	21,527,980 / 98.8%
Mapped reads, singletons	93,092 / 0.43%
Secondary alignments	0
Supplementary alignments	85,108 / 0.39%
Read min/max/mean length	30 / 100 / 99.26
Duplicated reads (estimated)	14,651,119 / 67.24%
Duplication rate	48.56%
Clipped reads	1,421,034 / 6.52%

2.2. ACGT Content

Number/percentage of A's	580,153,190 / 27.36%
Number/percentage of C's	480,267,715 / 22.65%
Number/percentage of T's	583,130,520 / 27.5%
Number/percentage of G's	476,435,274 / 22.47%
Number/percentage of N's	261,101 / 0.01%

GC Percentage	45.12%

2.3. Coverage

Mean	0.685
Standard Deviation	24.0551

2.4. Mapping Quality

Mean Mapping Quality	54.67

2.5. Insert size

Mean	16,568.13
Standard Deviation	1,296,536.97
P25/Median/P75	149 / 203 / 270

2.6. Mismatches and indels

General error rate	0.51%
Mismatches	10,585,012
Insertions	139,866
Mapped reads with at least one insertion	0.64%
Deletions	106,338
Mapped reads with at least one deletion	0.48%
Homopolymer indels	46.37%

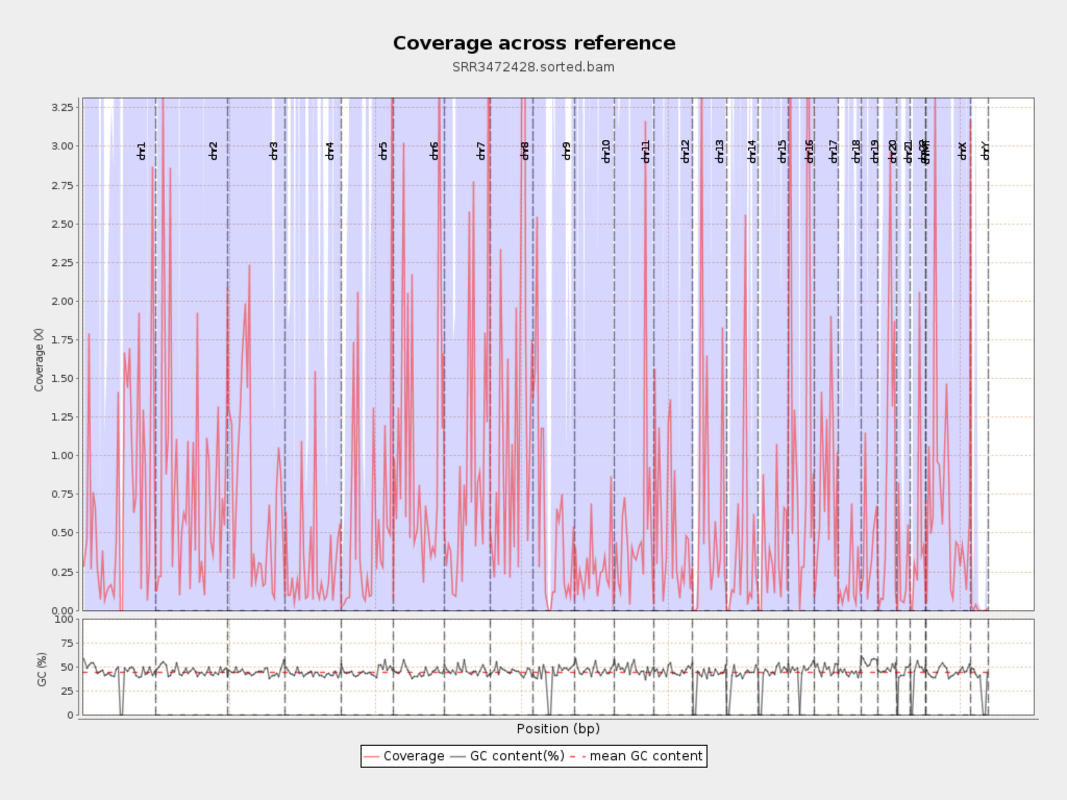
2.7. Chromosome stats

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

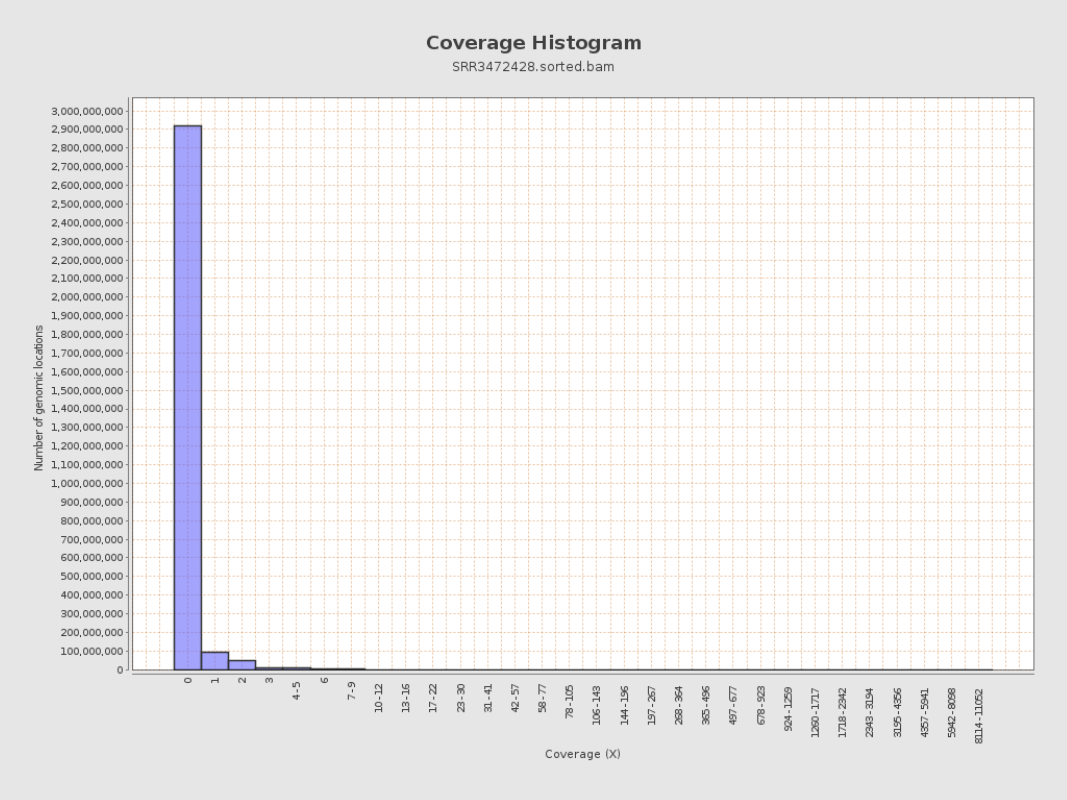
		bases	coverage	deviation
chr1	249250621	177685905	0.7129	21.6205
chr2	243199373	194871799	0.8013	27.6145
chr3	198022430	153137769	0.7733	20.3016
chr4	191154276	58350114	0.3053	12.38
chr5	180915260	116087703	0.6417	30.8528
chr6	171115067	174410190	1.0193	26.0413
chr7	159138663	165742980	1.0415	34.0336
chr8	146364022	209969693	1.4346	45.5944
chr9	141213431	79662897	0.5641	18.0515
chr10	135534747	38113082	0.2812	10.5956
chr11	135006516	73641572	0.5455	21.5659
chr12	133851895	74459695	0.5563	13.0221
chr13	115169878	81408490	0.7069	31.2604
chr14	107349540	42995280	0.4005	14.0028
chr15	102531392	38639783	0.3769	15.0339
chr16	90354753	114954883	1.2723	33.216
chr17	81195210	67062429	0.8259	20.1073
chr18	78077248	14257359	0.1826	8.2476
chr19	59128983	25463257	0.4306	9.6793
chr20	63025520	61104056	0.9695	28.4156
chr21	48129895	13109417	0.2724	14.5584
chr22	51304566	25842043	0.5037	27.8312
chrMT	16571	11907	0.7185	1.1975
chrX	155270560	118931169	0.766	18.5634

chrY	59373566	575055	0.0097	1.2665

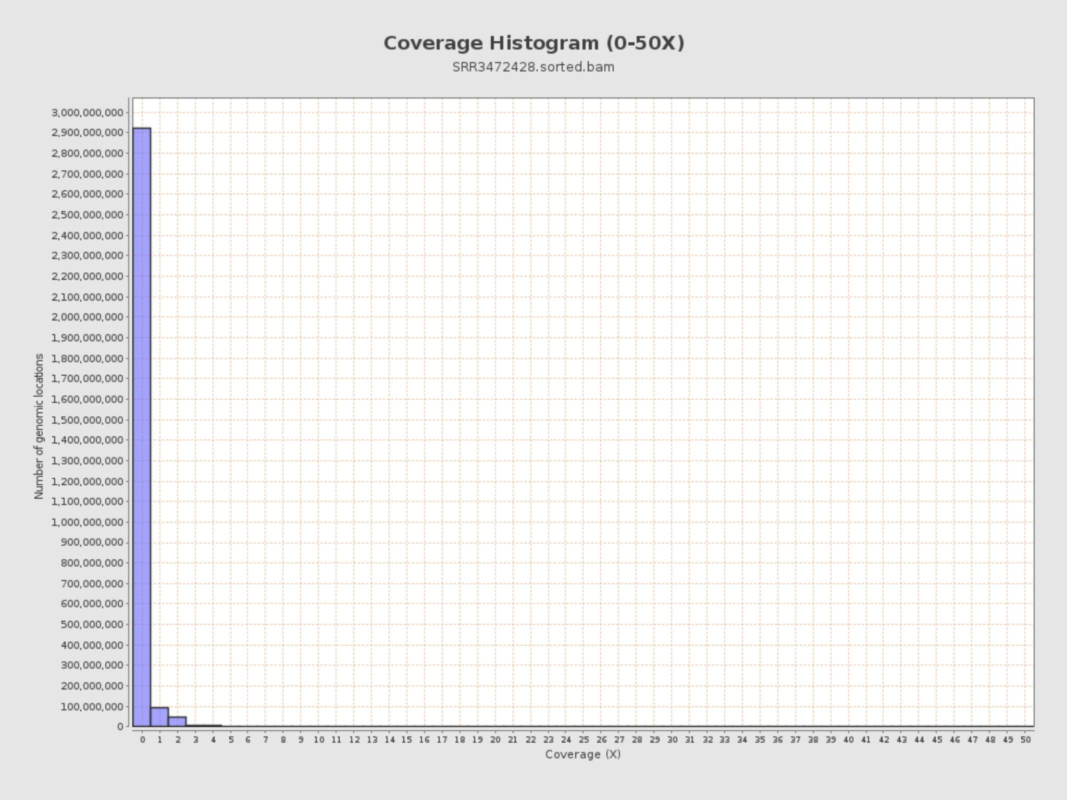
3. Results : Coverage across reference



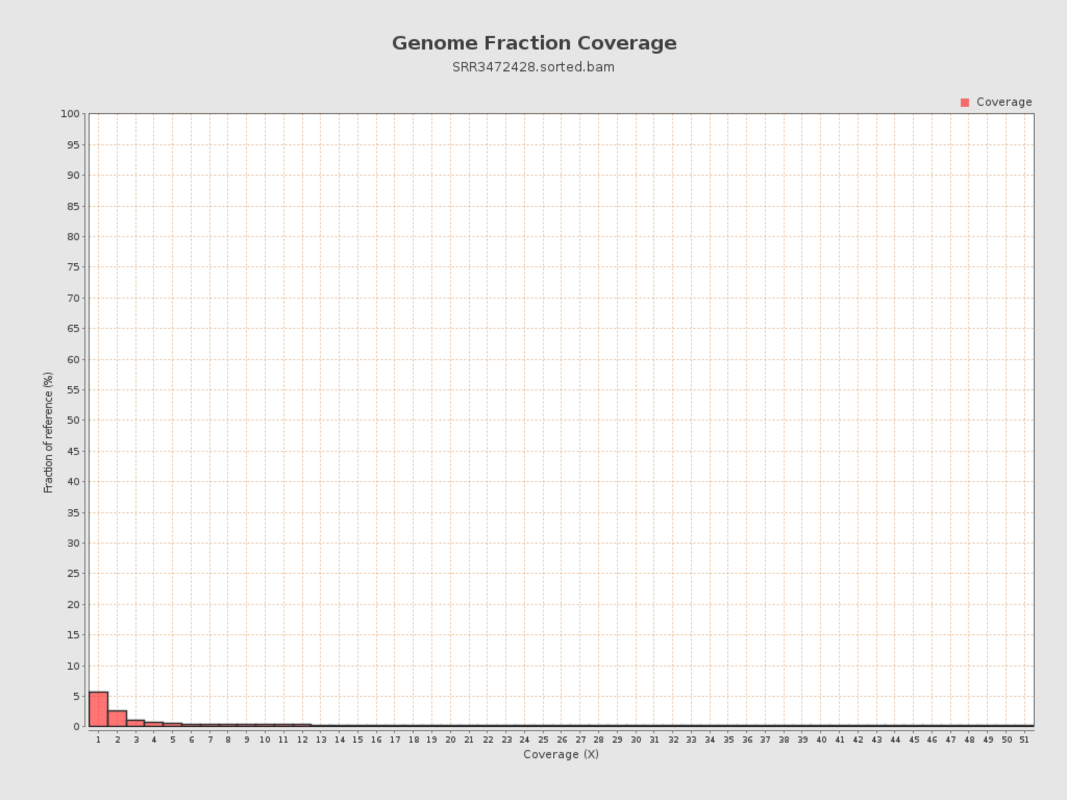
4. Results : Coverage Histogram



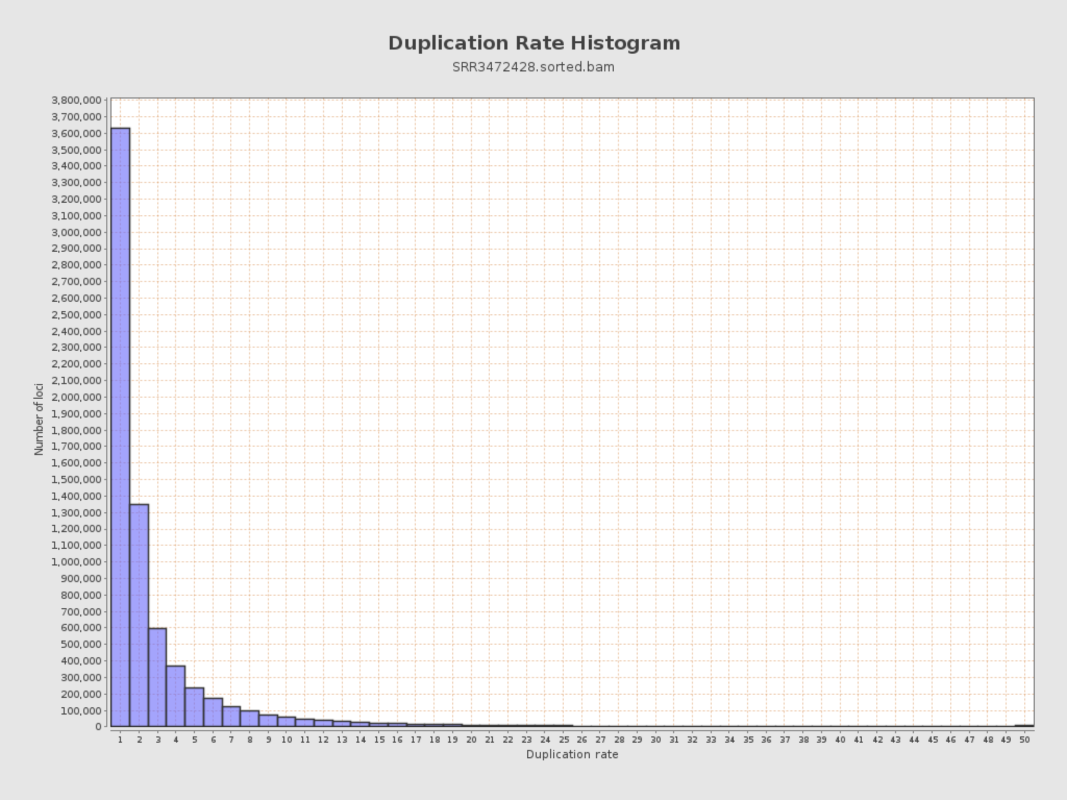
5. Results : Coverage Histogram (0-50X)



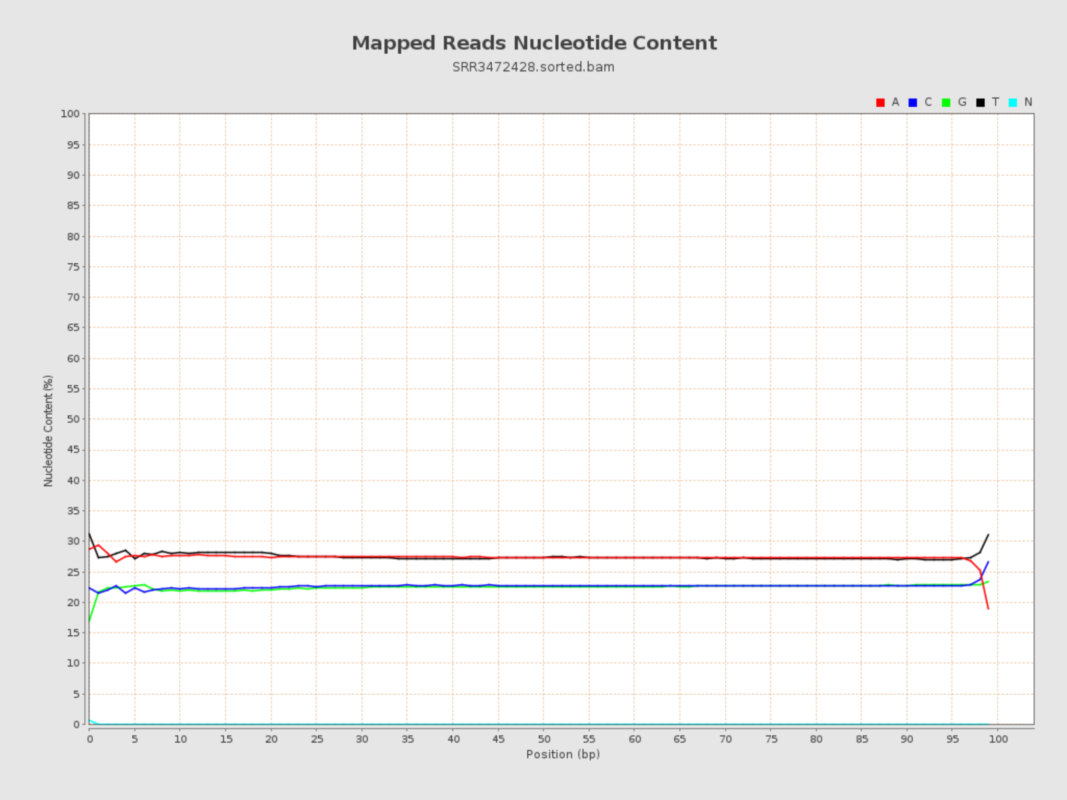
6. Results : Genome Fraction Coverage



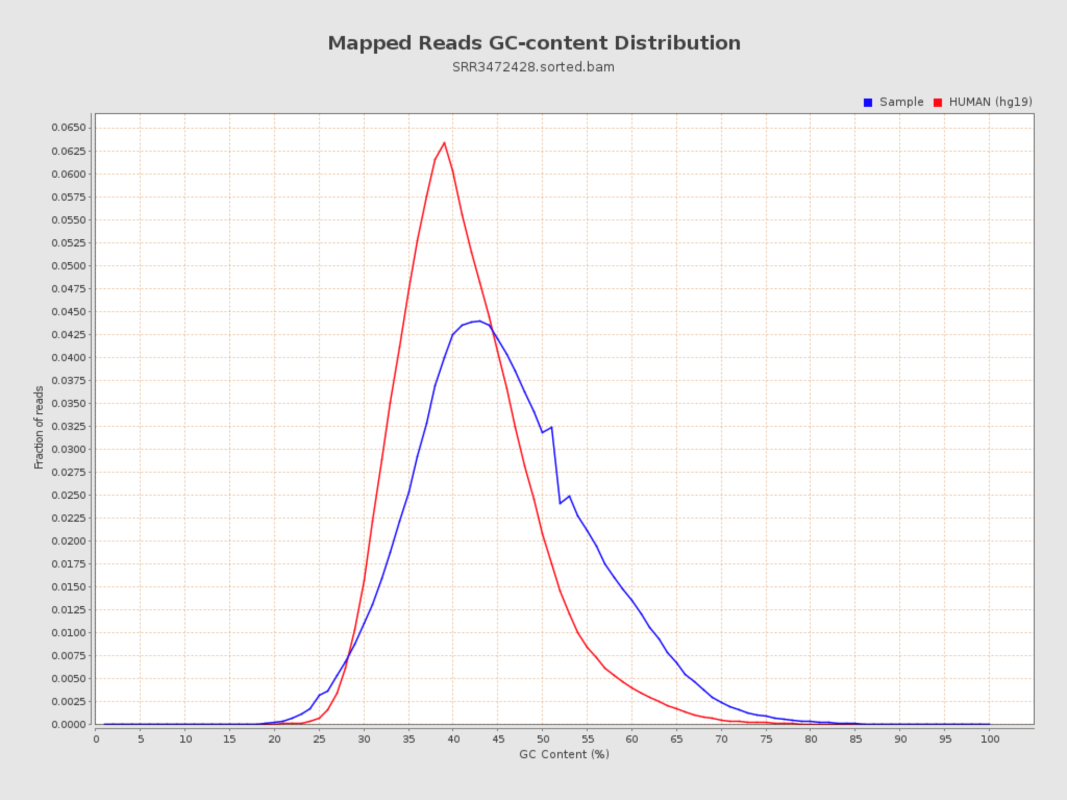
7. Results : Duplication Rate Histogram



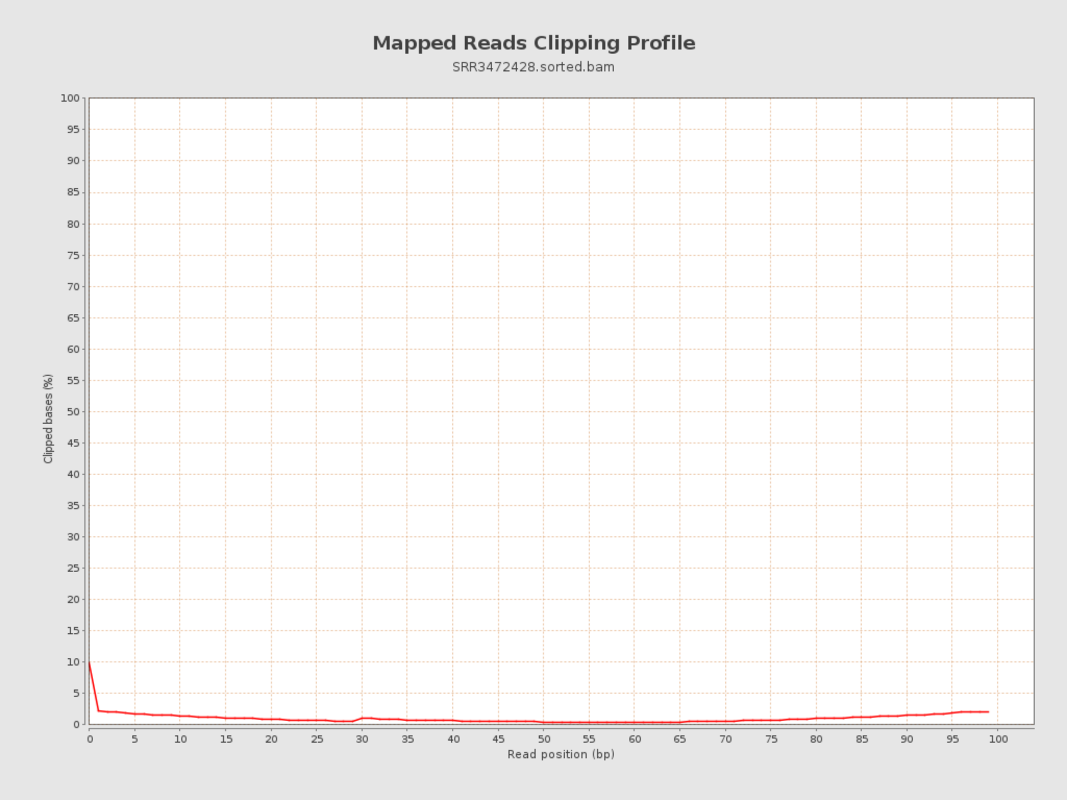
8. Results : Mapped Reads Nucleotide Content



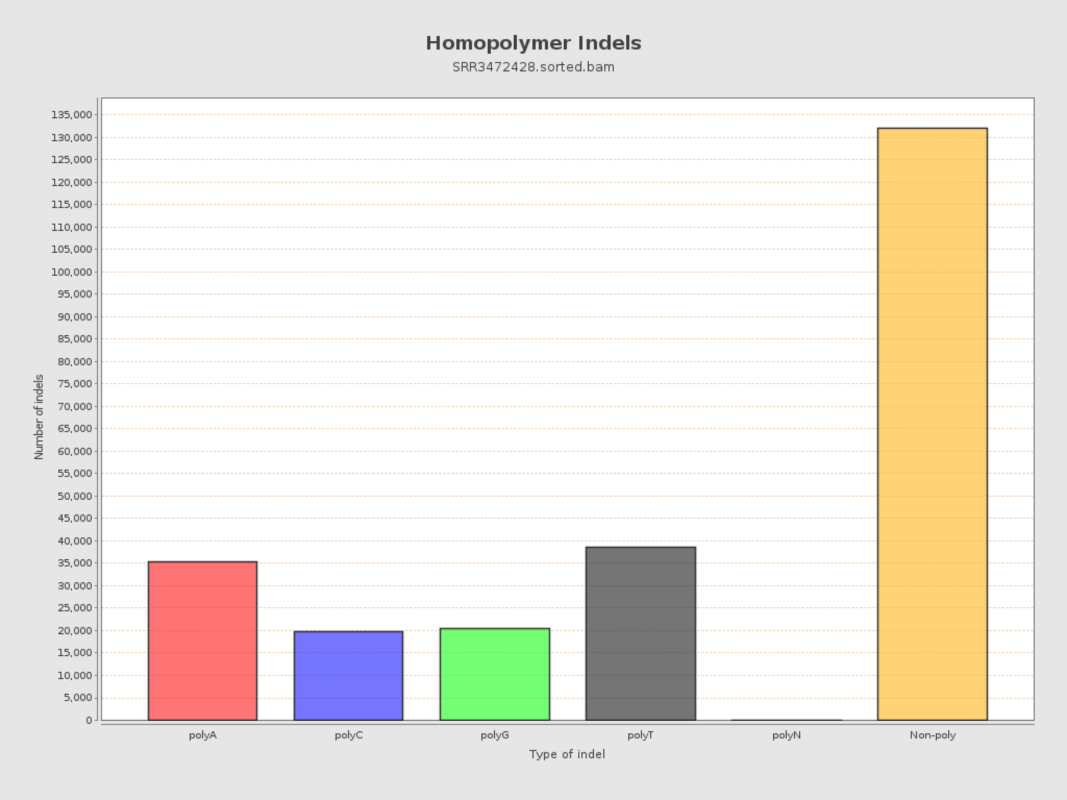
9. Results : Mapped Reads GC-content Distribution



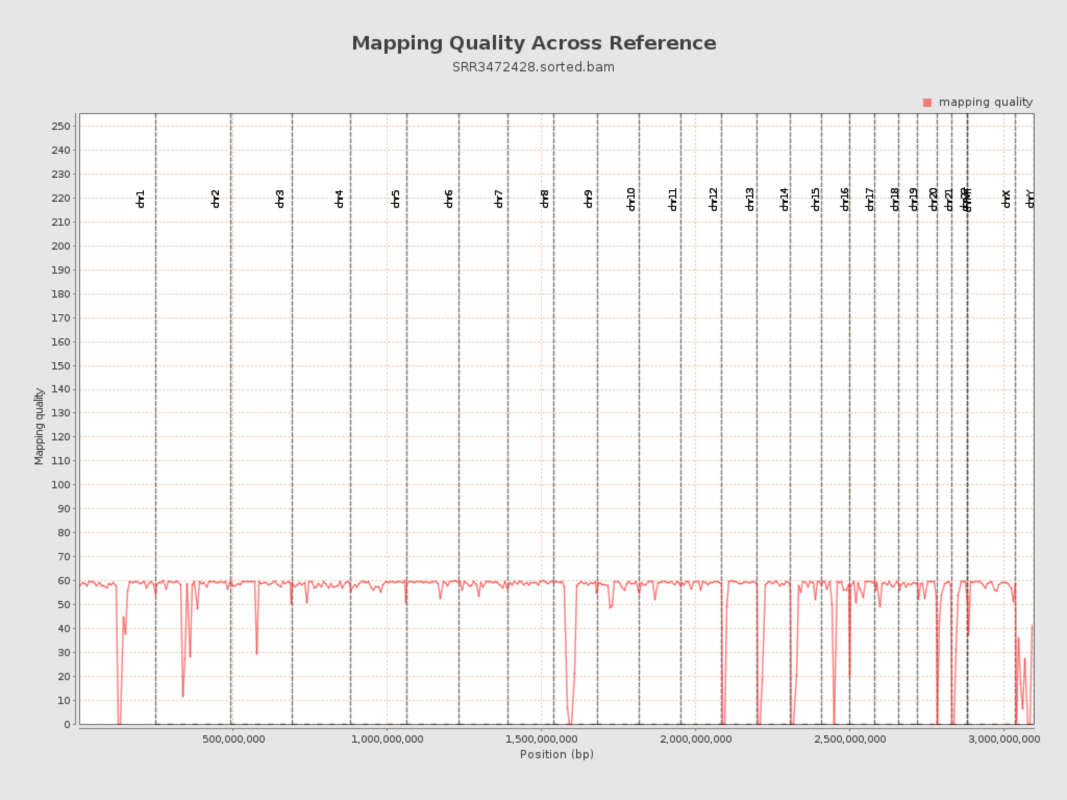
10. Results : Mapped Reads Clipping Profile



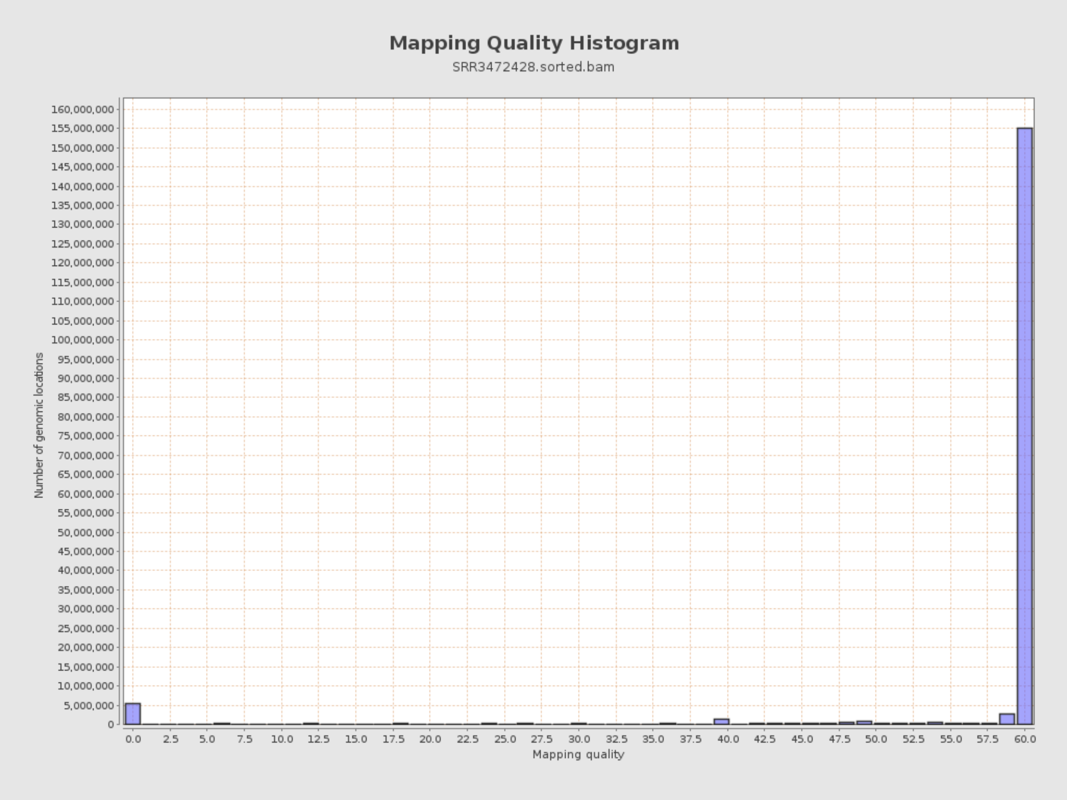
11. Results : Homopolymer Indels



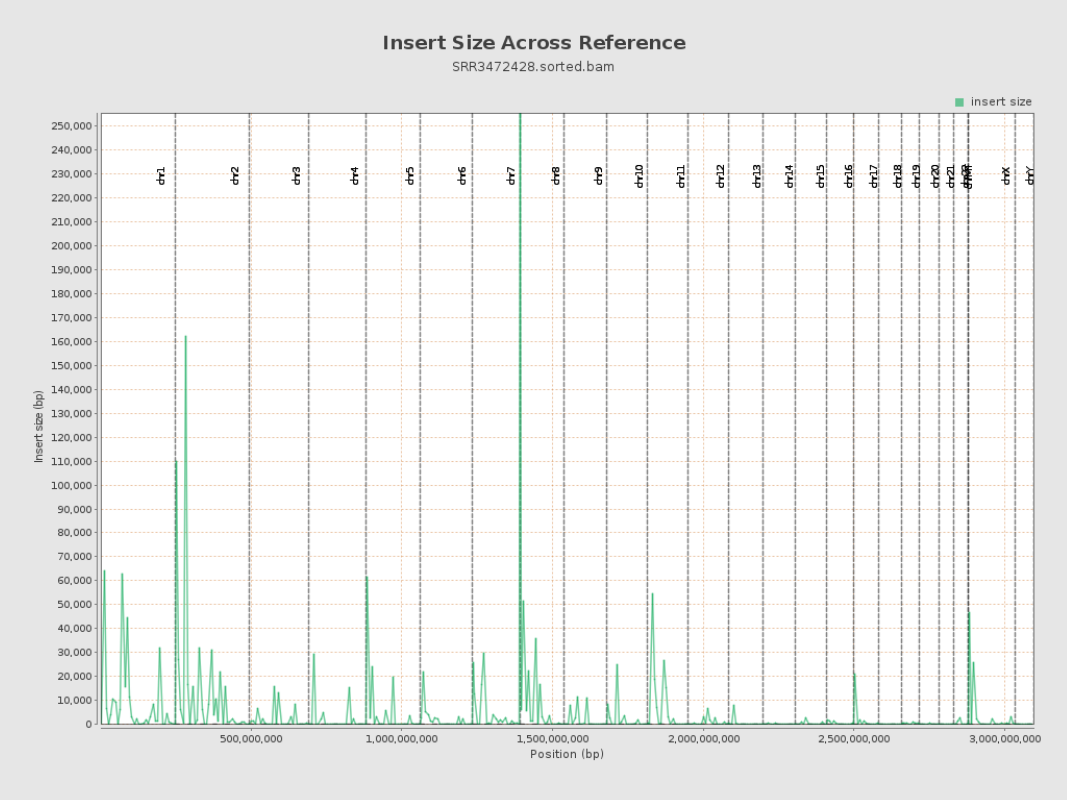
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram