Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 01:25:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472459.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_SRR3472459 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472459_1.fastq.gz SRR3472459_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 01:25:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472459.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,684,186
Mapped reads	17,524,810 / 99.1%
Unmapped reads	159,376 / 0.9%
Mapped paired reads	17,524,810 / 99.1%
Mapped reads, first in pair	8,778,246 / 49.64%
Mapped reads, second in pair	8,746,564 / 49.46%
Mapped reads, both in pair	17,441,432 / 98.63%
Mapped reads, singletons	83,378 / 0.47%
Secondary alignments	0
Supplementary alignments	62,749 / 0.35%
Read min/max/mean length	30 / 100 / 99.34
Duplicated reads (estimated)	11,078,497 / 62.65%
Duplication rate	48.12%
Clipped reads	1,394,969 / 7.89%

2.2. ACGT Content

Number/percentage of A's	462,335,921 / 26.97%
Number/percentage of C's	396,070,205 / 23.1%
Number/percentage of T's	462,026,354 / 26.95%
Number/percentage of G's	393,616,115 / 22.96%
Number/percentage of N's	221,740 / 0.01%

GC Percentage	46.07%

2.3. Coverage

Mean	0.5538
Standard Deviation	17.4866

2.4. Mapping Quality

Mean Mapping Quality	55.14

2.5. Insert size

Mean	18,413.22
Standard Deviation	1,350,543.66
P25/Median/P75	143 / 197 / 265

2.6. Mismatches and indels

General error rate	0.55%
Mismatches	9,237,486
Insertions	99,609
Mapped reads with at least one insertion	0.56%
Deletions	87,426
Mapped reads with at least one deletion	0.49%
Homopolymer indels	45.76%

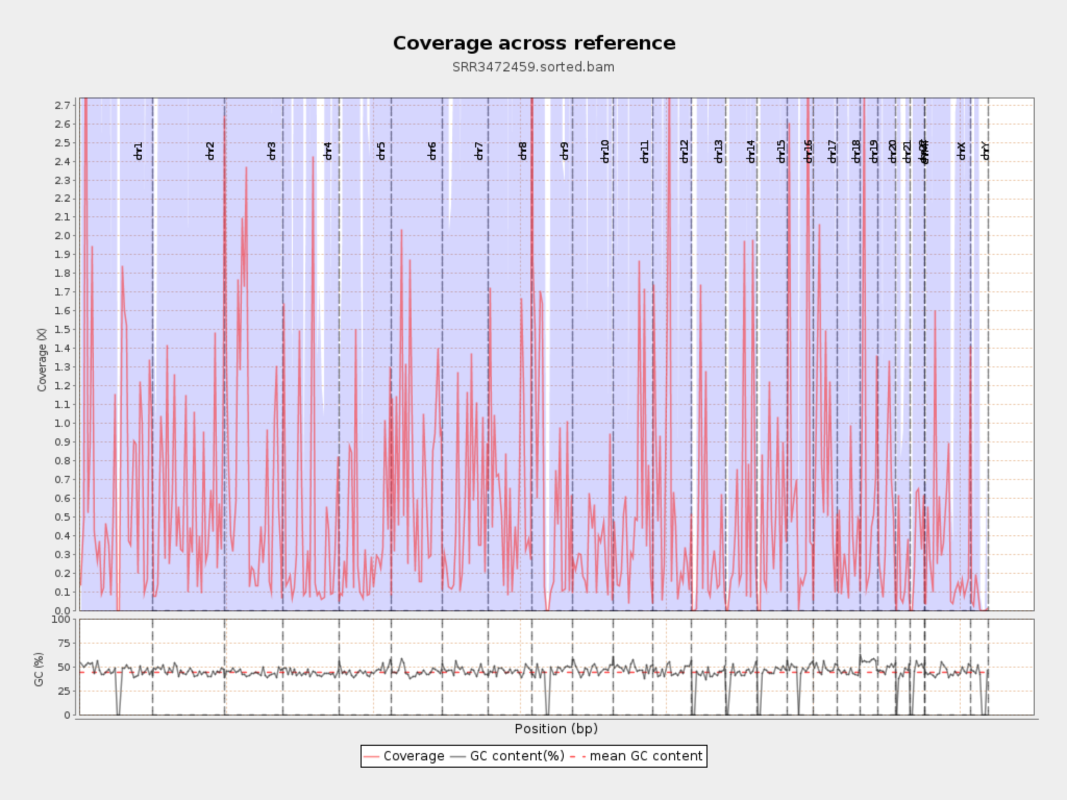
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard

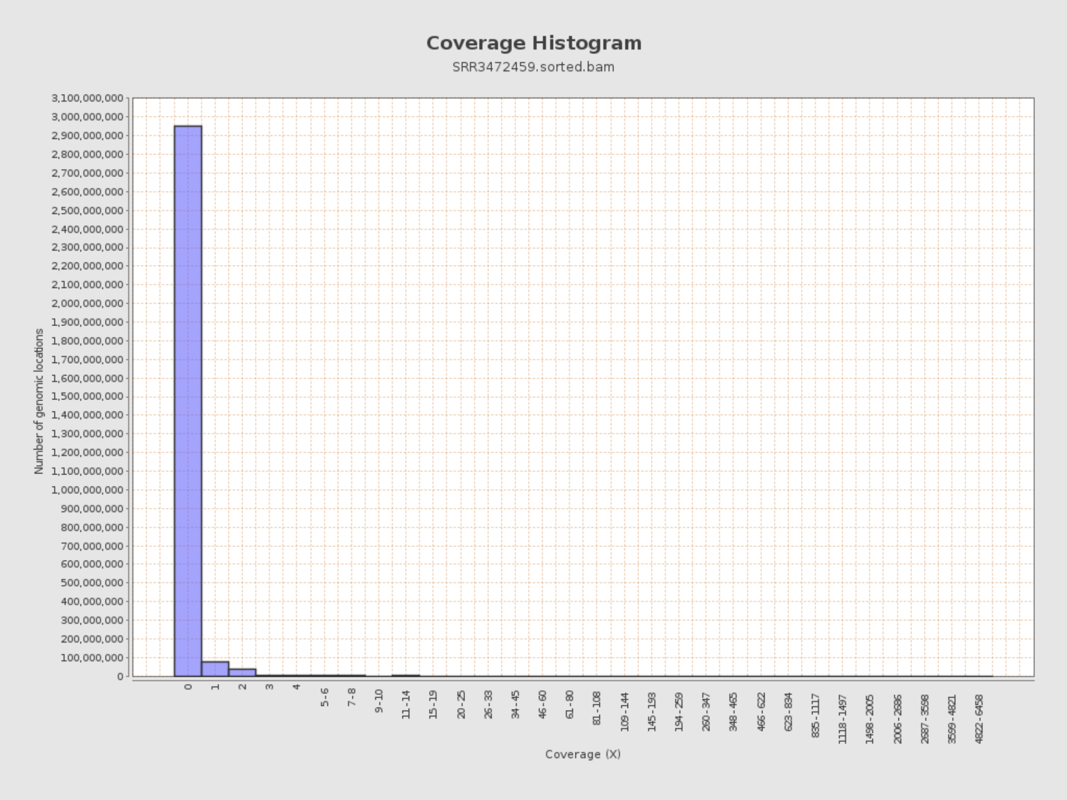
		bases	coverage	deviation
chr1	249250621	187940950	0.754	24.3138
chr2	243199373	132762921	0.5459	17.3816
chr3	198022430	154531884	0.7804	17.0099
chr4	191154276	78075113	0.4084	19.5931
chr5	180915260	70594226	0.3902	13.375
chr6	171115067	132985870	0.7772	21.2031
chr7	159138663	83979135	0.5277	16.6874
chr8	146364022	94327316	0.6445	17.8733
chr9	141213431	96137126	0.6808	18.6555
chr10	135534747	44373534	0.3274	11.2866
chr11	135006516	70335005	0.521	16.091
chr12	133851895	87698418	0.6552	16.8663
chr13	115169878	43186963	0.375	13.877
chr14	107349540	53895143	0.5021	20.2557
chr15	102531392	48213147	0.4702	15.2455
chr16	90354753	73000438	0.8079	21.0725
chr17	81195210	67432400	0.8305	23.3149
chr18	78077248	27770704	0.3557	12.9151
chr19	59128983	48593227	0.8218	18.9472
chr20	63025520	32783865	0.5202	16.2336
chr21	48129895	9735405	0.2023	11.9789
chr22	51304566	18849425	0.3674	10.035
chrMT	16571	2570	0.1551	0.4975
chrX	155270560	54396510	0.3503	10.5882

chrY	59373566	2894571	0.0488	3.0038

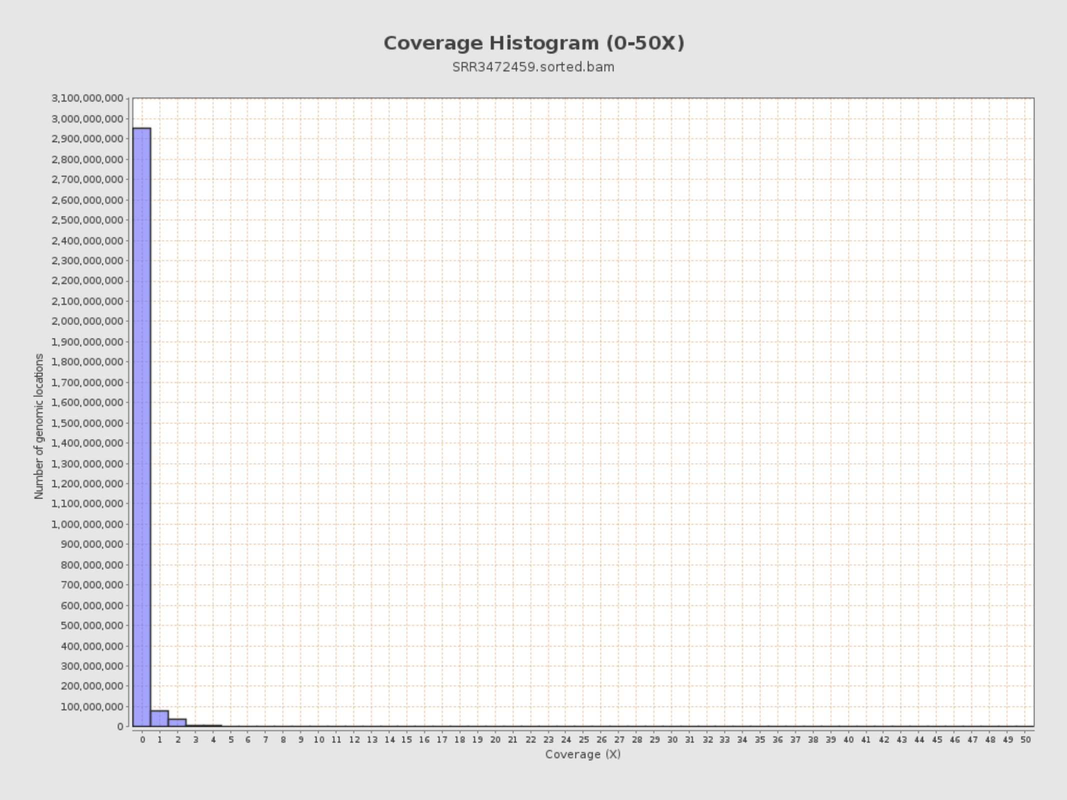
3. Results : Coverage across reference



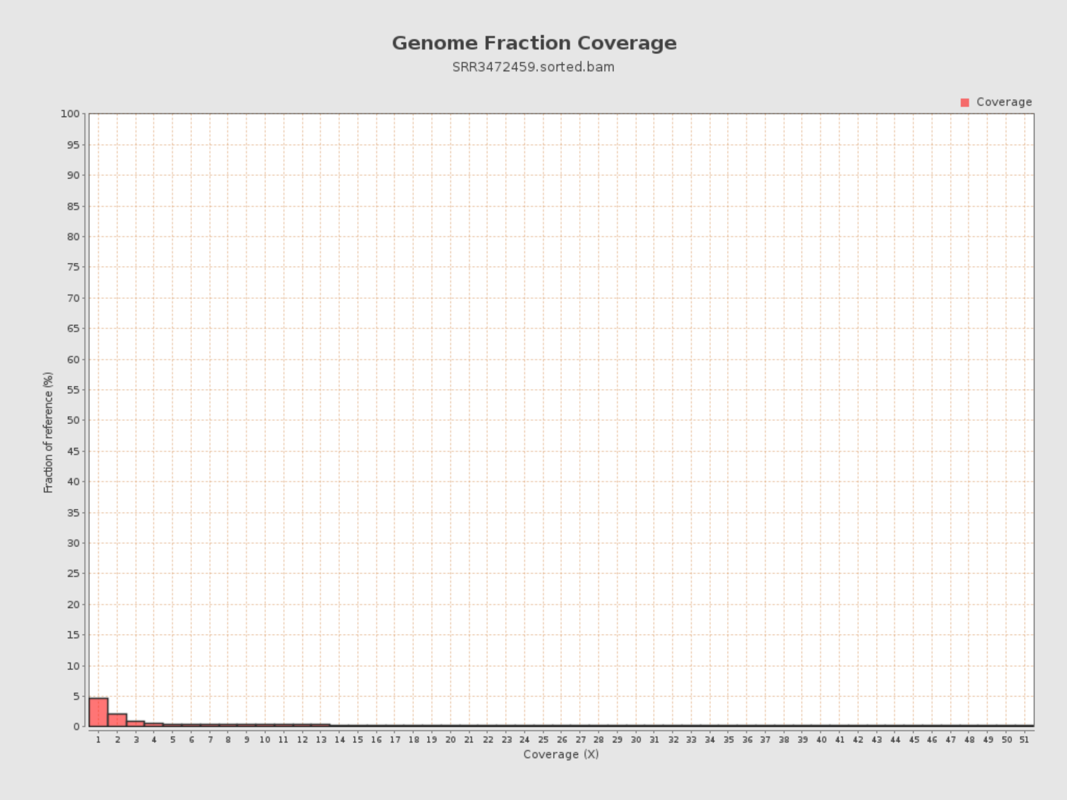
4. Results : Coverage Histogram



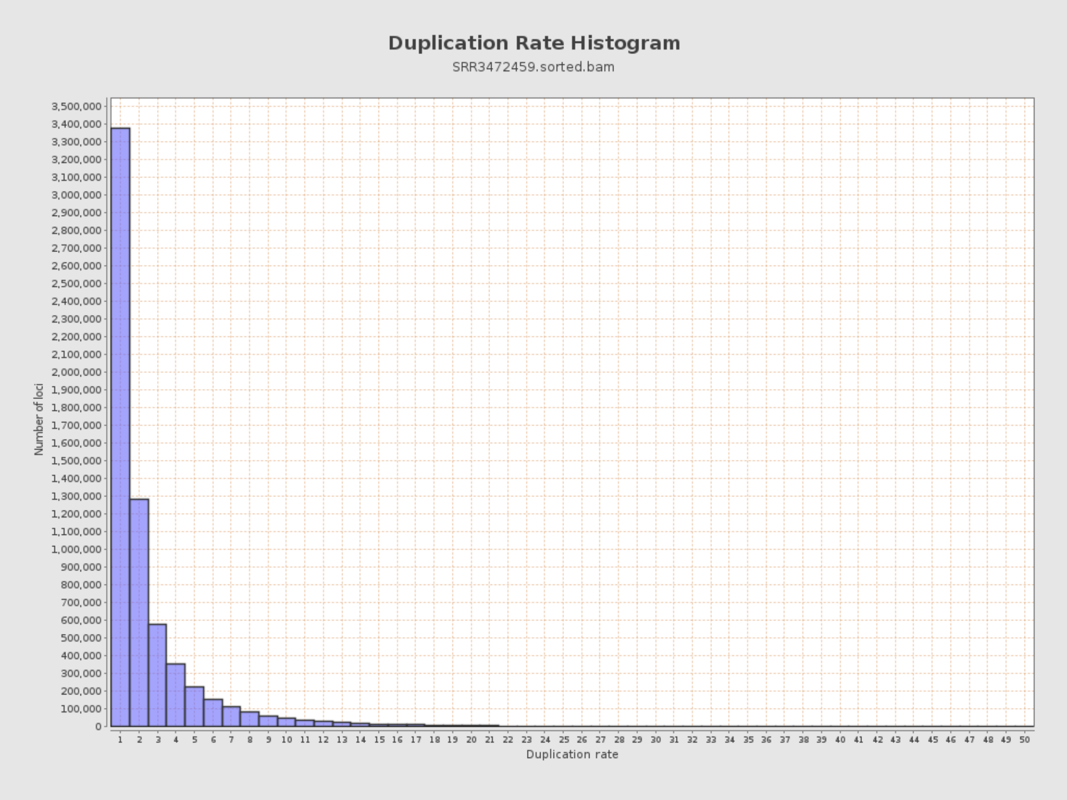
5. Results : Coverage Histogram (0-50X)



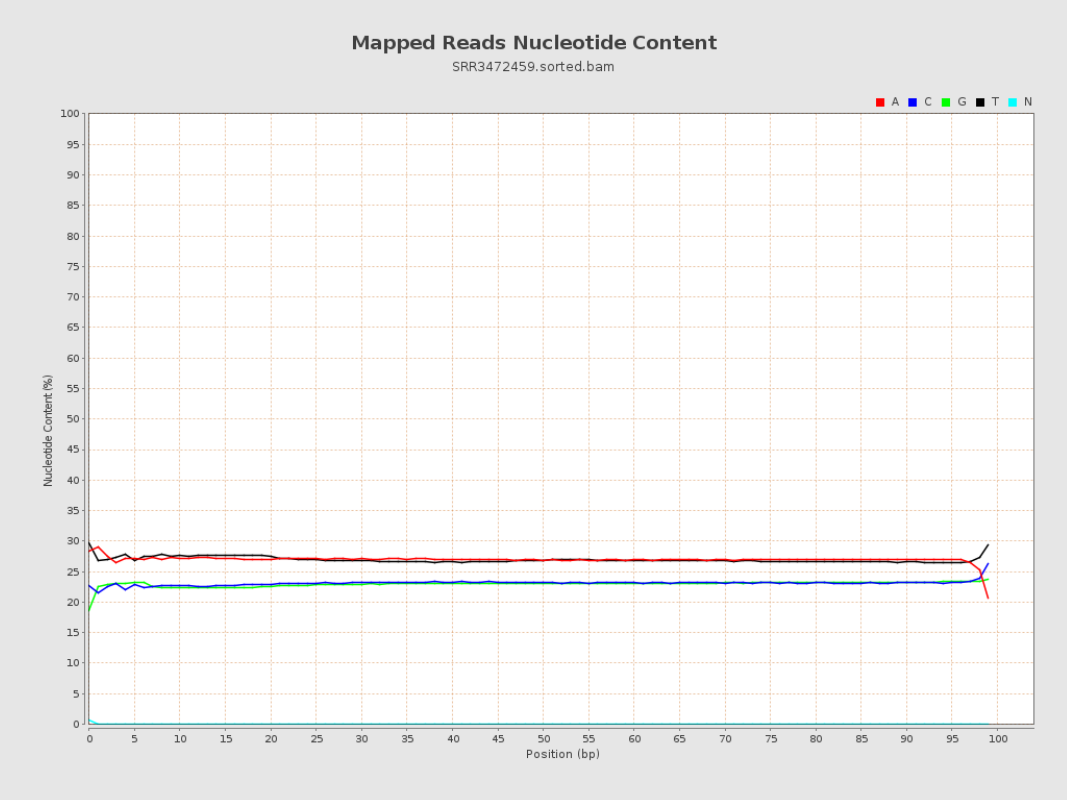
6. Results : Genome Fraction Coverage



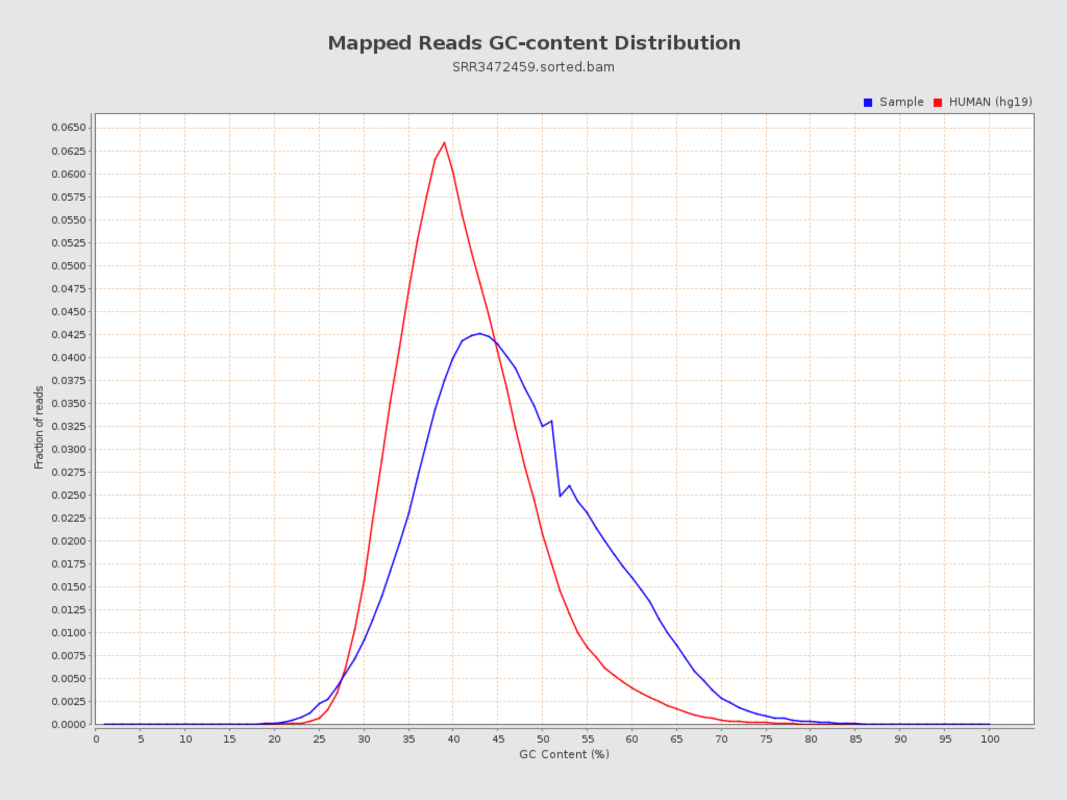
7. Results : Duplication Rate Histogram



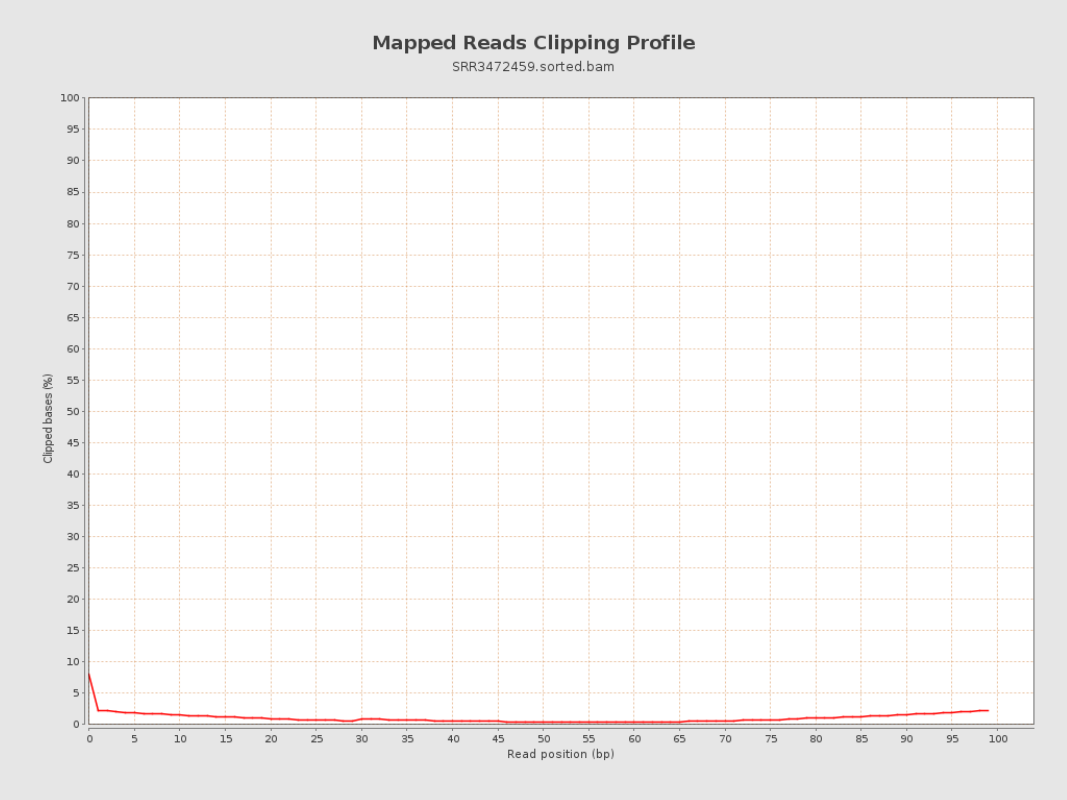
8. Results : Mapped Reads Nucleotide Content



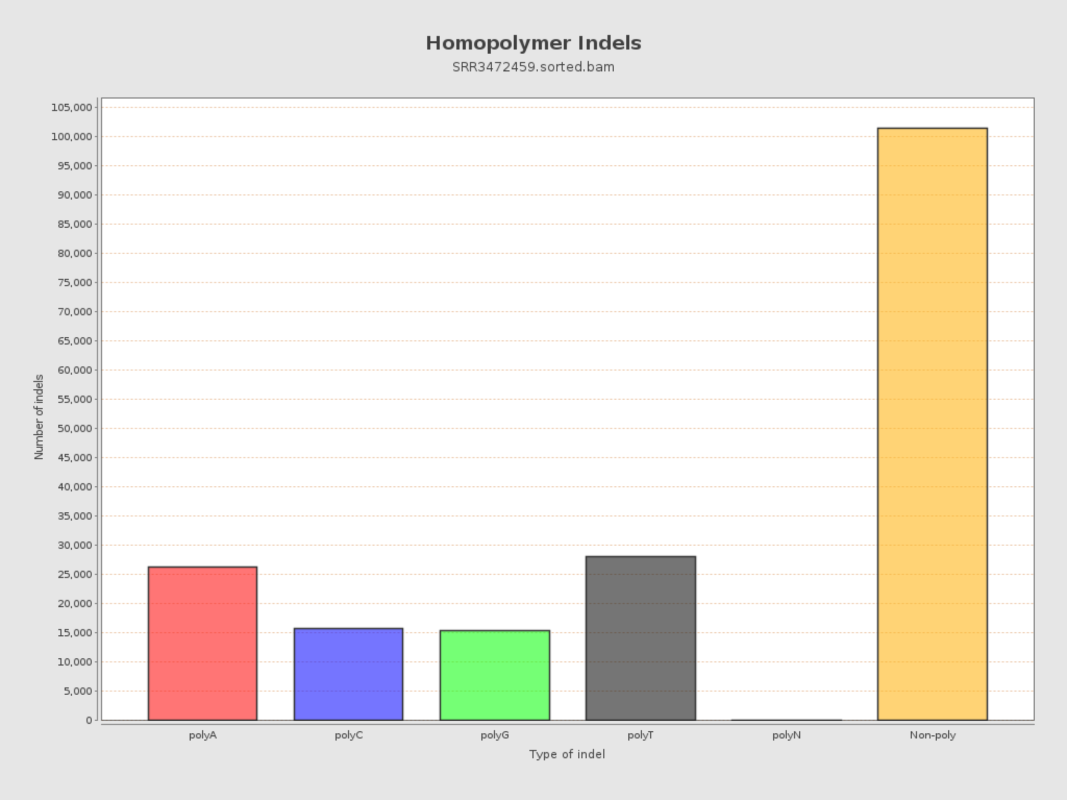
9. Results : Mapped Reads GC-content Distribution



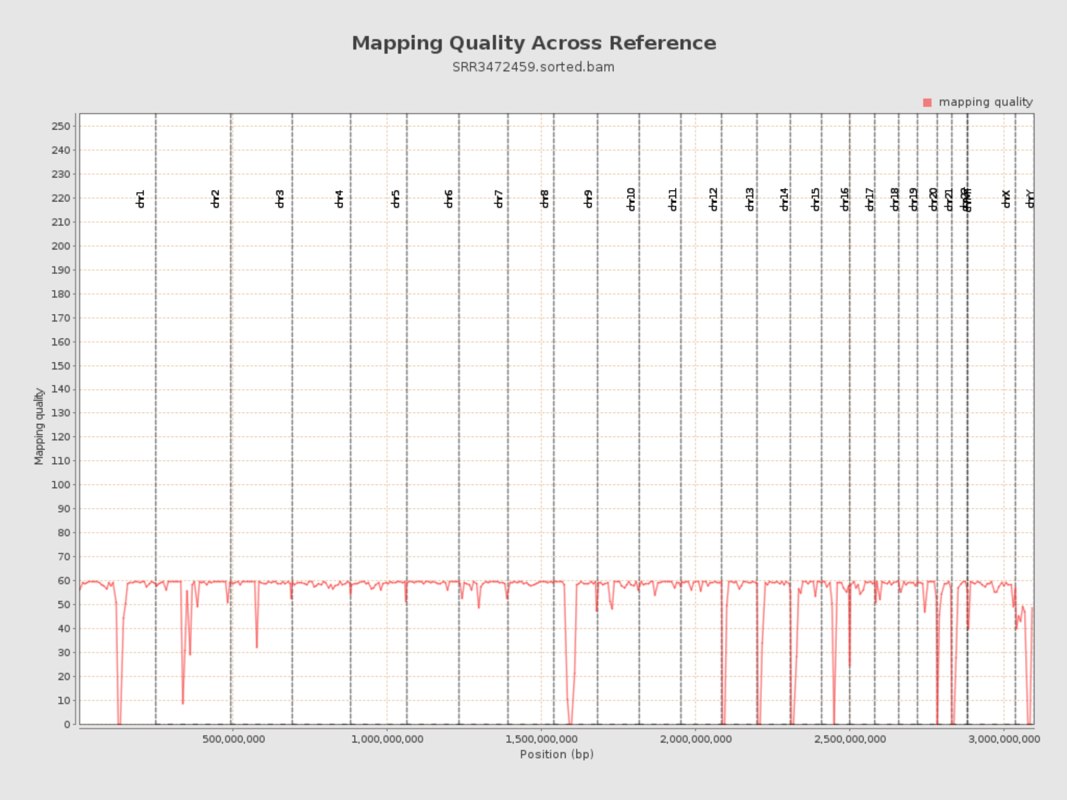
10. Results : Mapped Reads Clipping Profile



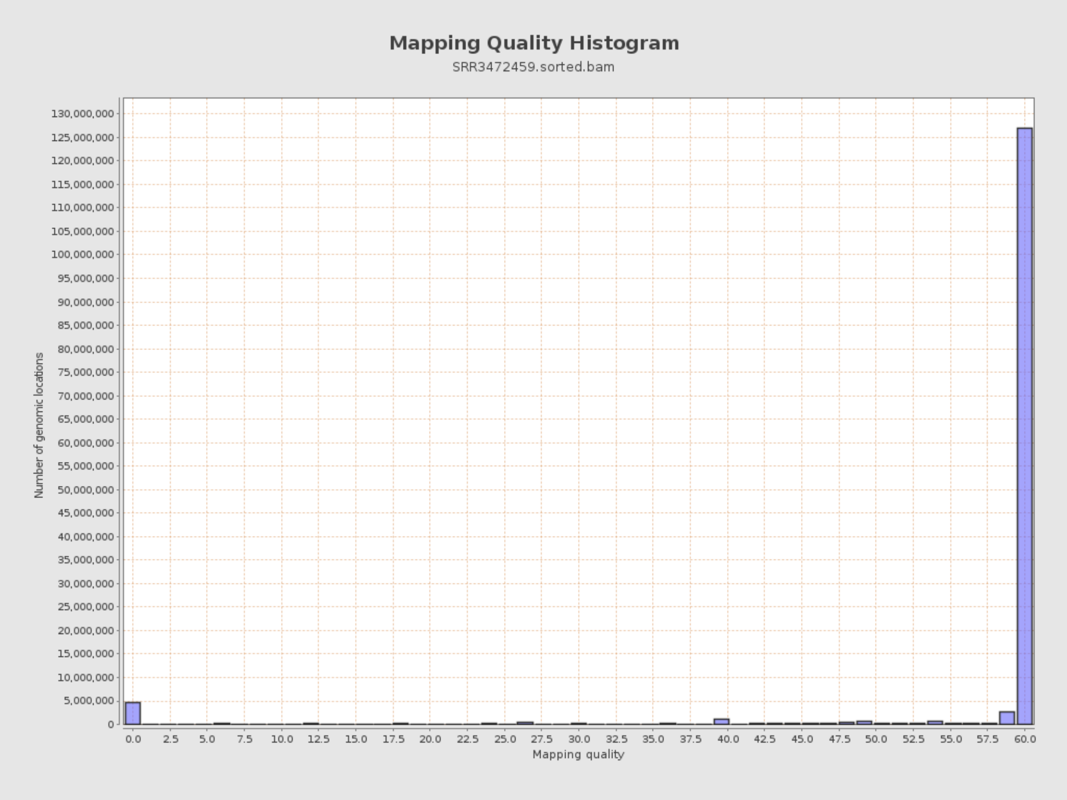
11. Results : Homopolymer Indels



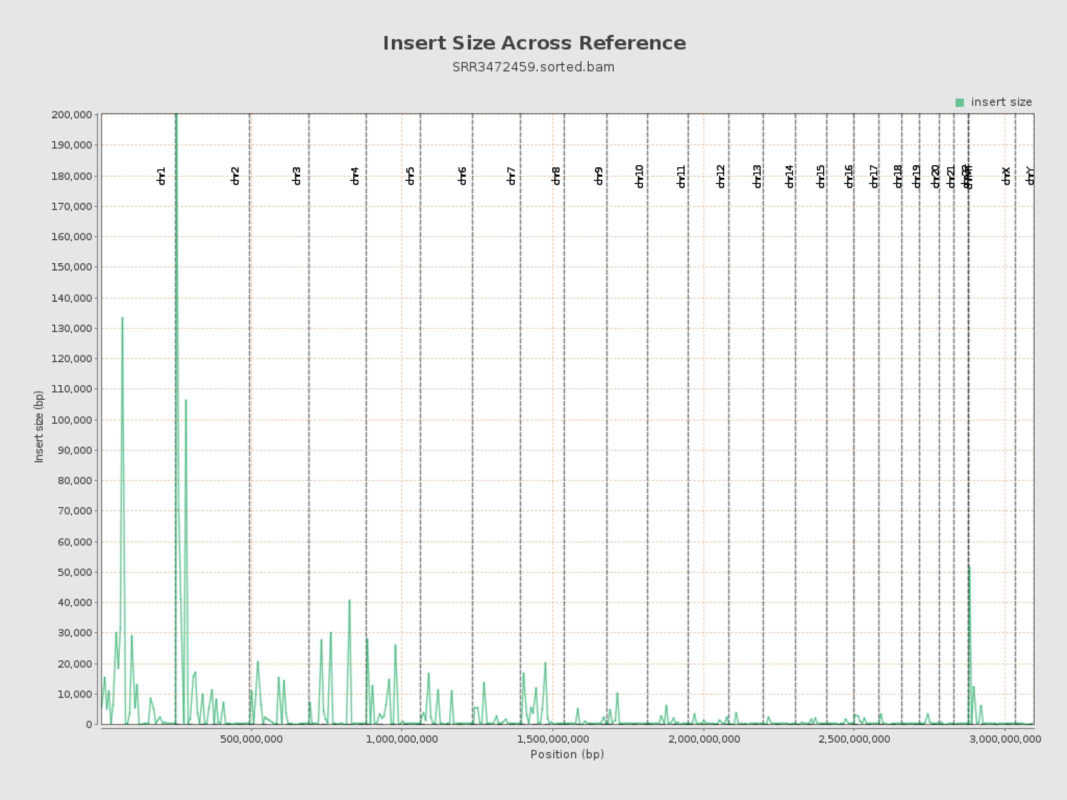
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram