Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 14:24:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472433.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_SRR3472433 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472433_1.fastq.gz SRR3472433_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 14:24:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472433.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,310,598
Mapped reads	15,167,674 / 99.07%
Unmapped reads	142,924 / 0.93%
Mapped paired reads	15,167,674 / 99.07%
Mapped reads, first in pair	7,606,178 / 49.68%
Mapped reads, second in pair	7,561,496 / 49.39%
Mapped reads, both in pair	15,087,326 / 98.54%
Mapped reads, singletons	80,348 / 0.52%
Secondary alignments	0
Supplementary alignments	59,772 / 0.39%
Read min/max/mean length	30 / 100 / 99.15
Duplicated reads (estimated)	9,181,254 / 59.97%
Duplication rate	45.78%
Clipped reads	1,096,244 / 7.16%

2.2. ACGT Content

Number/percentage of A's	408,028,639 / 27.51%
Number/percentage of C's	334,477,741 / 22.55%
Number/percentage of T's	408,798,667 / 27.56%
Number/percentage of G's	331,843,920 / 22.37%
Number/percentage of N's	179,739 / 0.01%

GC Percentage	44.92%

2.3. Coverage

Mean	0.4792
Standard Deviation	15.4187

2.4. Mapping Quality

Mean Mapping Quality	54.81

2.5. Insert size

Mean	19,193.88
Standard Deviation	1,355,694.44
P25/Median/P75	152 / 214 / 290

2.6. Mismatches and indels

General error rate	0.55%
Mismatches	8,003,725
Insertions	97,501
Mapped reads with at least one insertion	0.64%
Deletions	80,813
Mapped reads with at least one deletion	0.52%
Homopolymer indels	45.92%

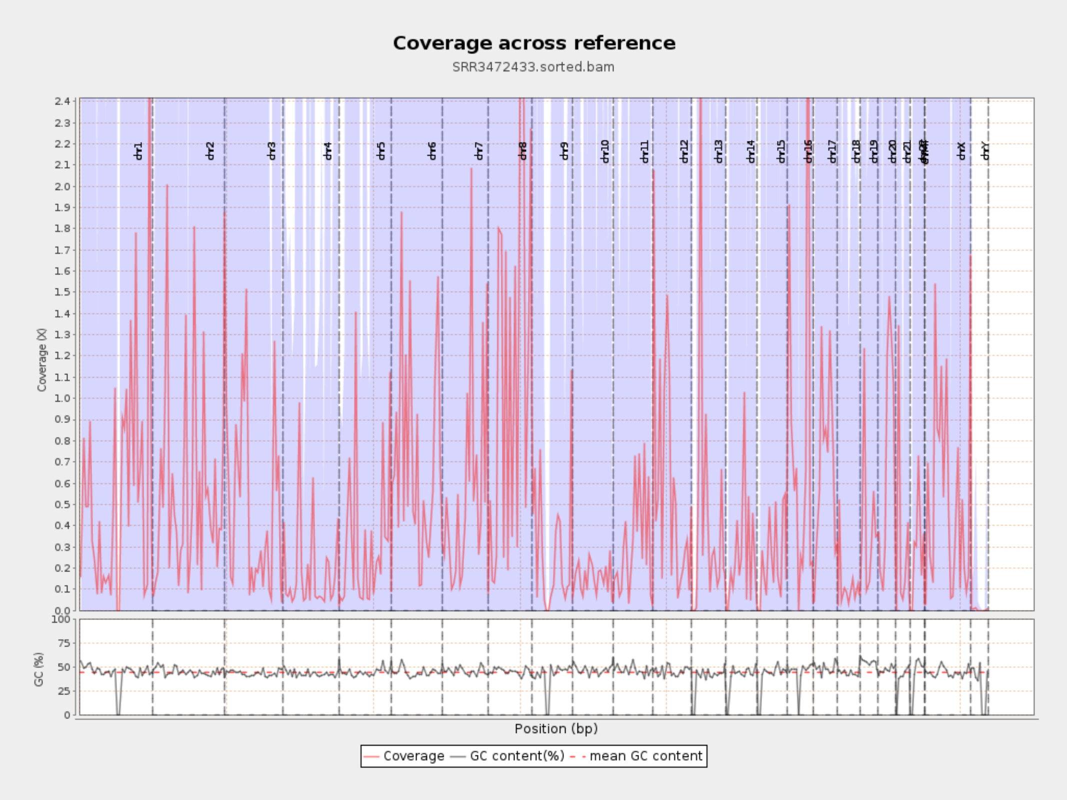
2.7. Chromosome stats

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

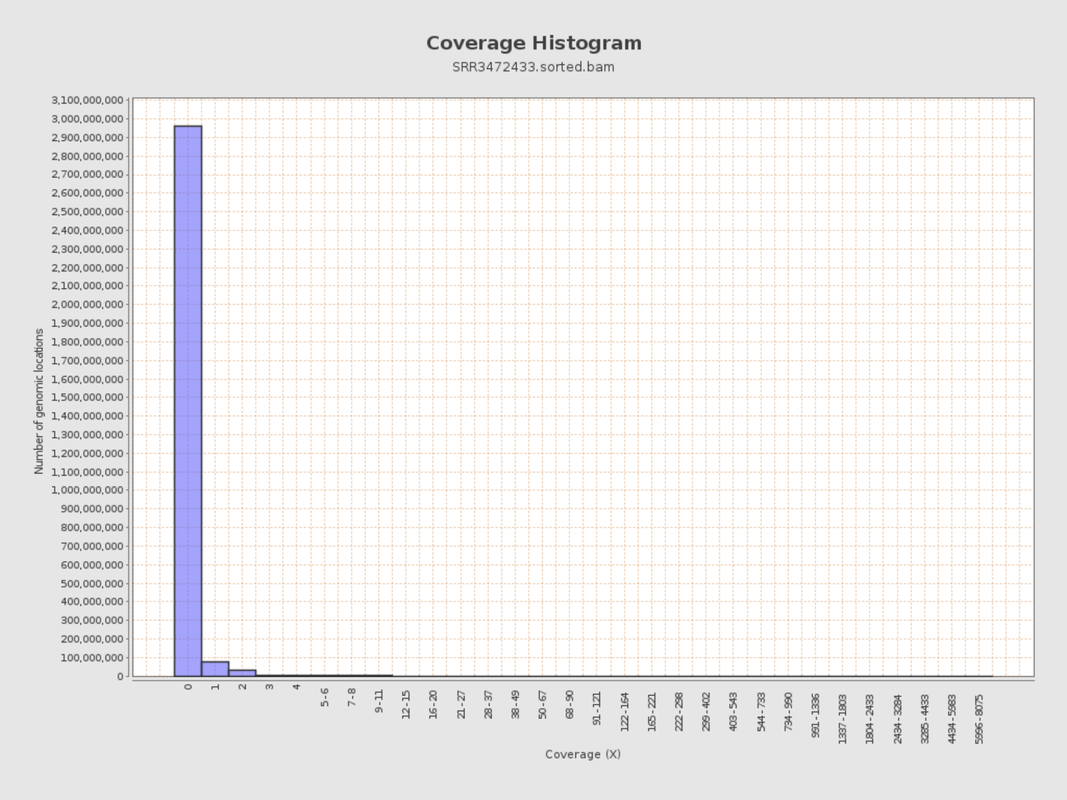
		bases	coverage	deviation
chr1	249250621	142900216	0.5733	18.3716
chr2	243199373	134709506	0.5539	18.3242
chr3	198022430	100556599	0.5078	11.8587
chr4	191154276	34163272	0.1787	5.852
chr5	180915260	59361620	0.3281	10.7735
chr6	171115067	120494081	0.7042	16.8201
chr7	159138663	93030232	0.5846	15.3415
chr8	146364022	181227262	1.2382	32.5359
chr9	141213431	41523956	0.2941	8.2484
chr10	135534747	21179024	0.1563	4.3405
chr11	135006516	43107217	0.3193	9.6495
chr12	133851895	80845000	0.604	14.704
chr13	115169878	52829302	0.4587	14.1521
chr14	107349540	27753840	0.2585	9.7771
chr15	102531392	25204277	0.2458	9.0119
chr16	90354753	75287603	0.8332	25.4666
chr17	81195210	55719168	0.6862	15.6737
chr18	78077248	9939765	0.1273	3.9938
chr19	59128983	24933886	0.4217	8.4571
chr20	63025520	46606839	0.7395	19.1382
chr21	48129895	16052113	0.3335	21.4593
chr22	51304566	14652491	0.2856	10.008
chrMT	16571	2980	0.1798	0.5183
chrX	155270560	81169434	0.5228	16.8386

chrY	59373566	269865	0.0045	0.3923

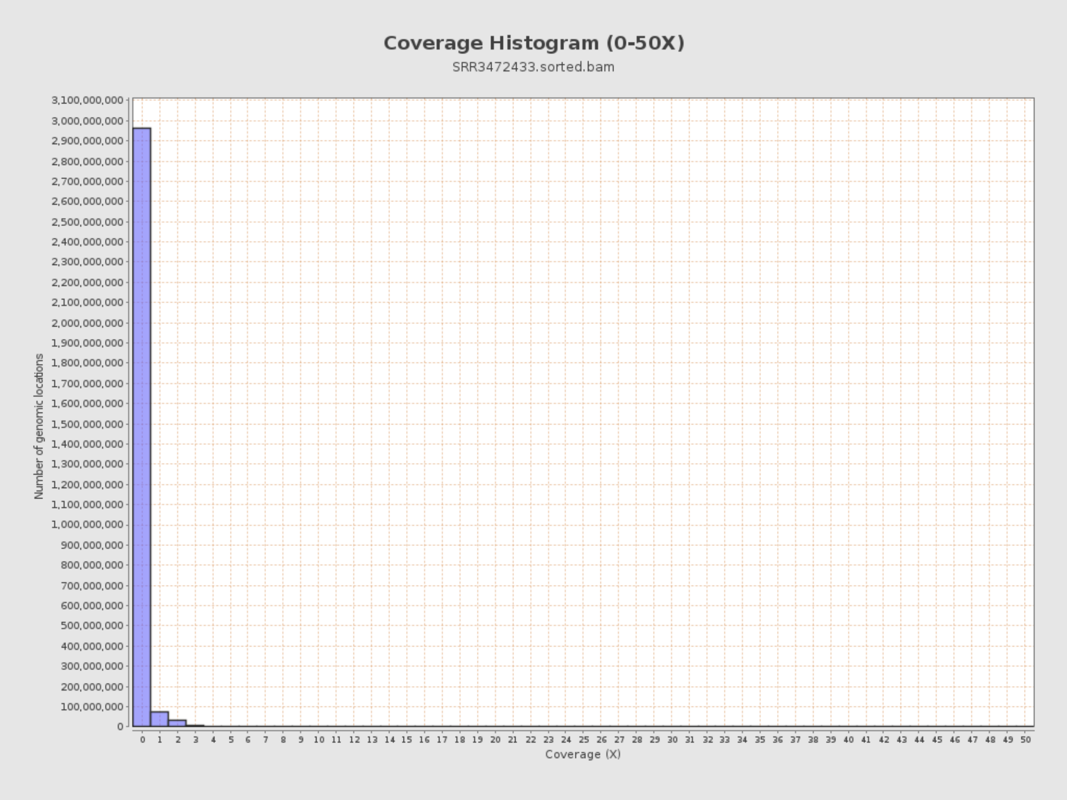
3. Results : Coverage across reference



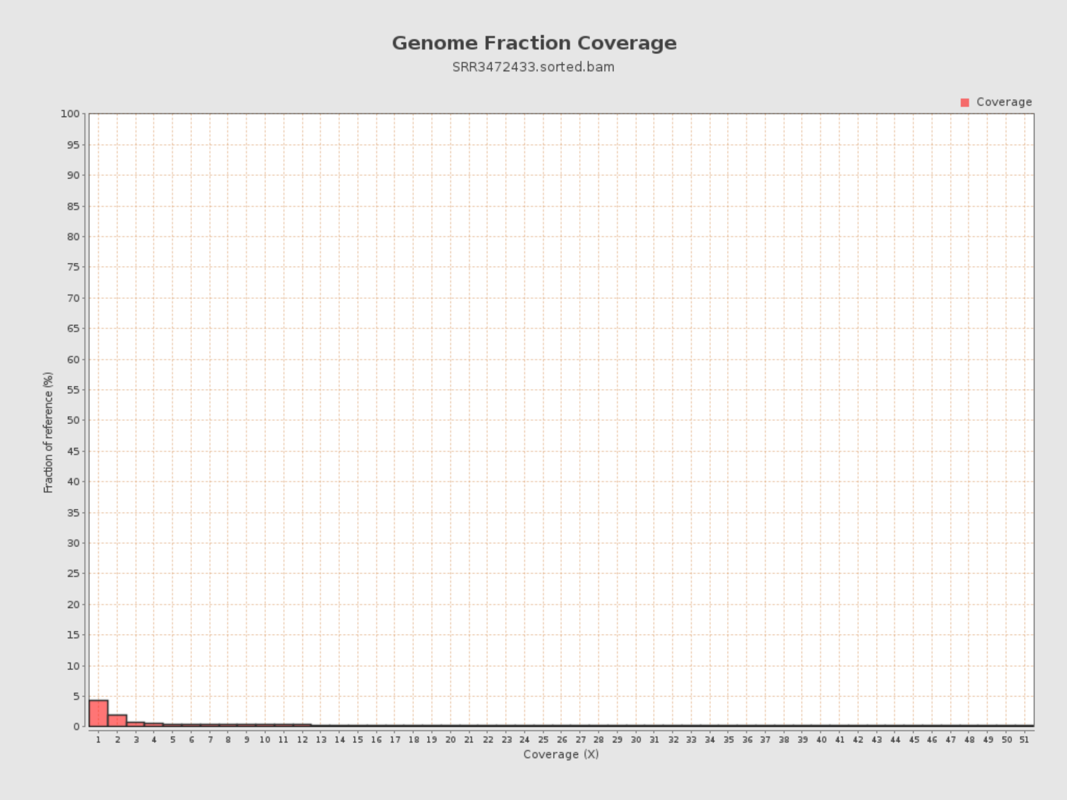
4. Results : Coverage Histogram



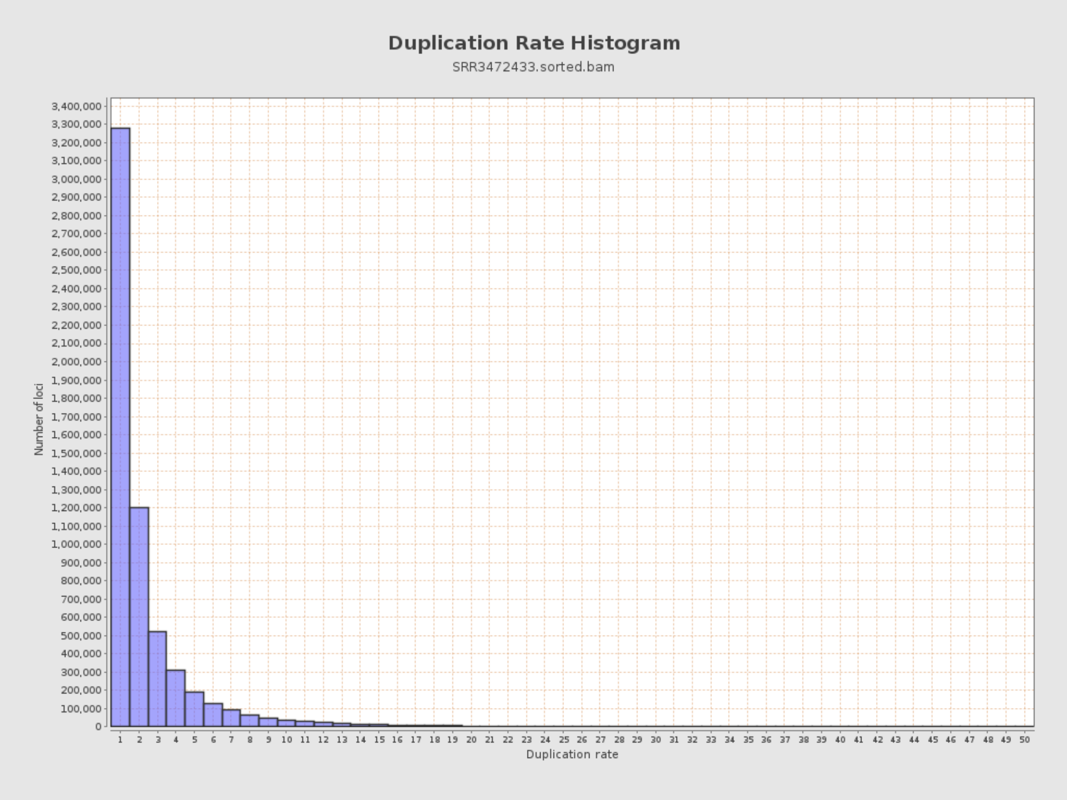
5. Results : Coverage Histogram (0-50X)



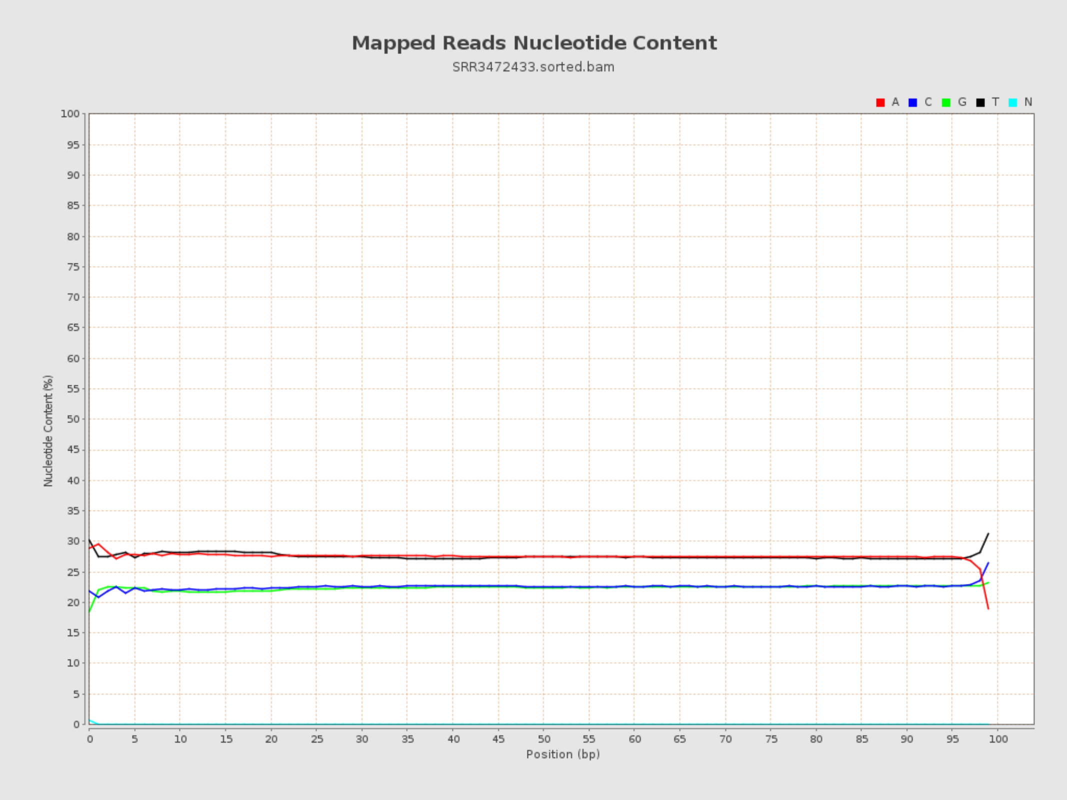
6. Results : Genome Fraction Coverage



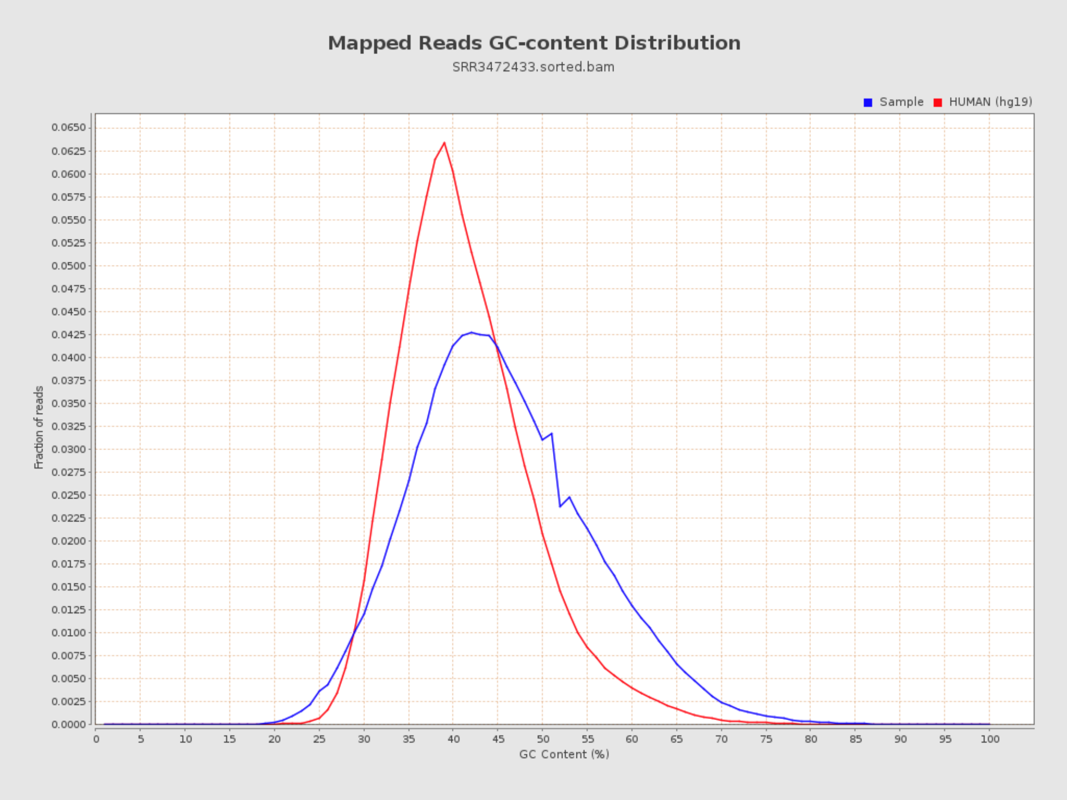
7. Results : Duplication Rate Histogram



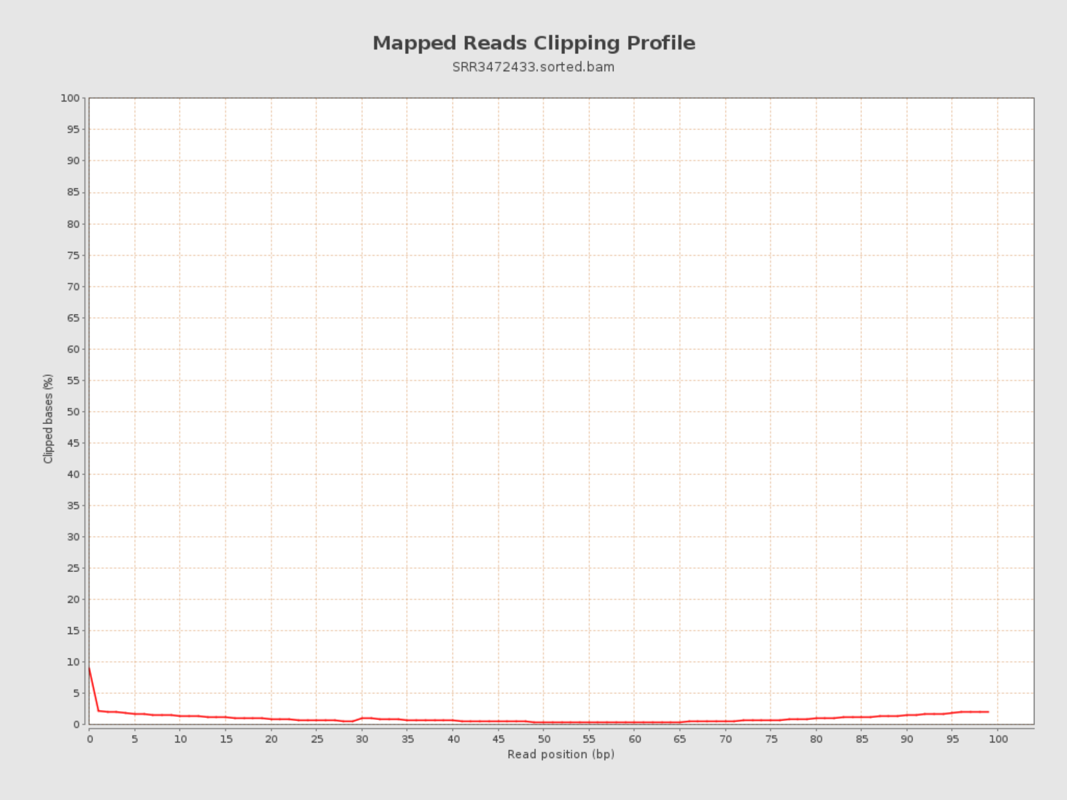
8. Results : Mapped Reads Nucleotide Content



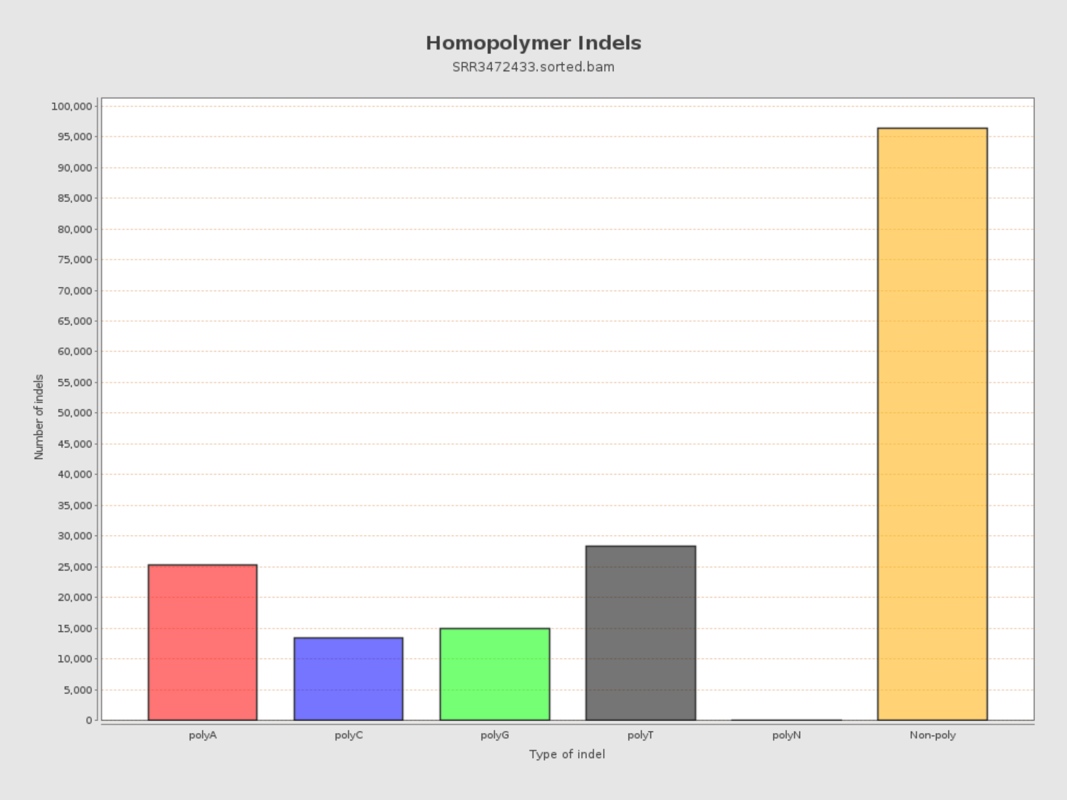
9. Results : Mapped Reads GC-content Distribution



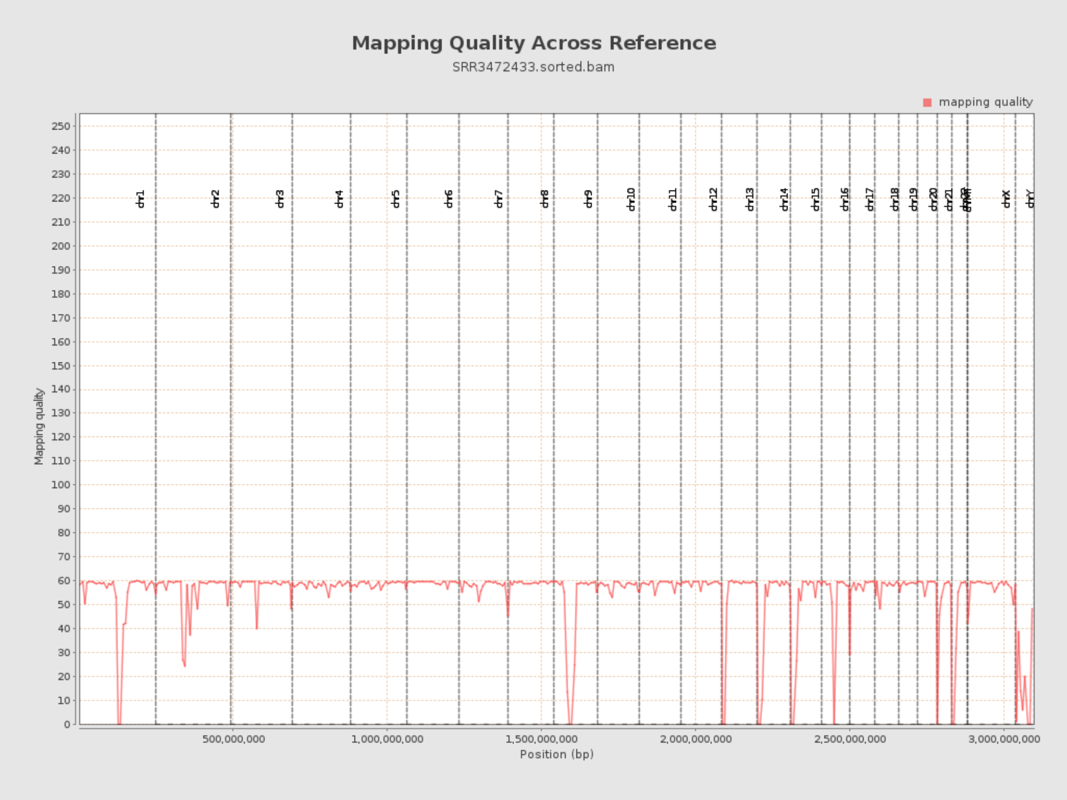
10. Results : Mapped Reads Clipping Profile



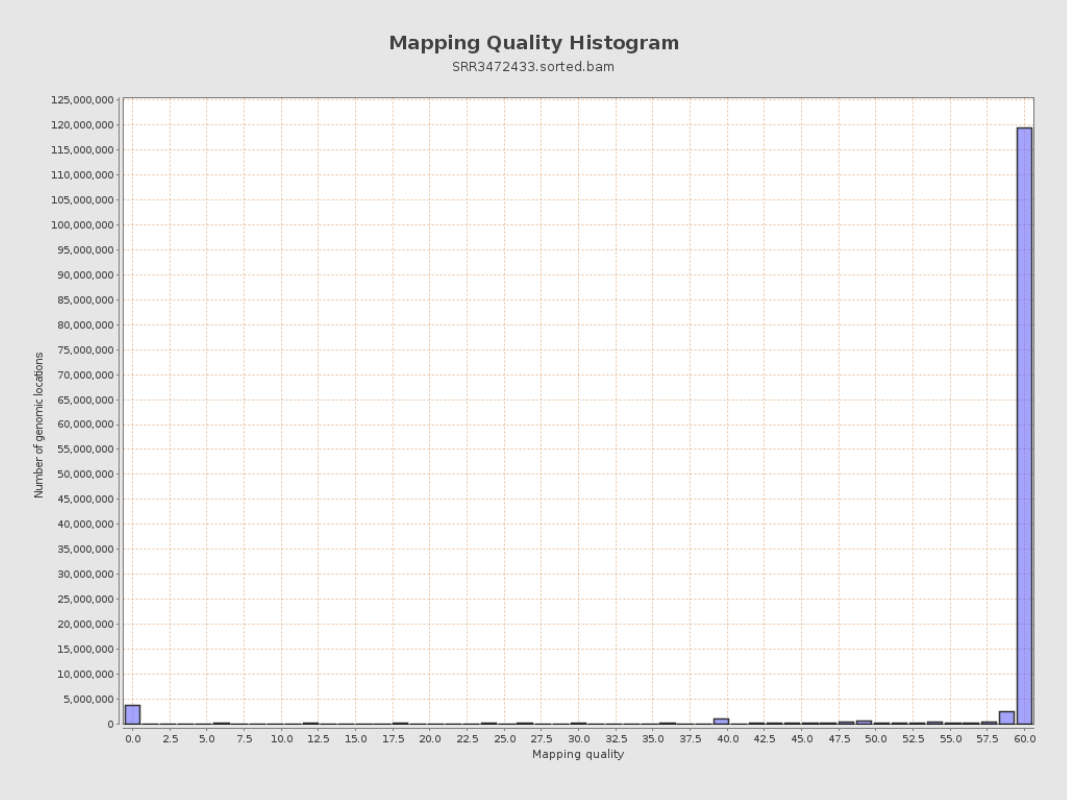
11. Results : Homopolymer Indels



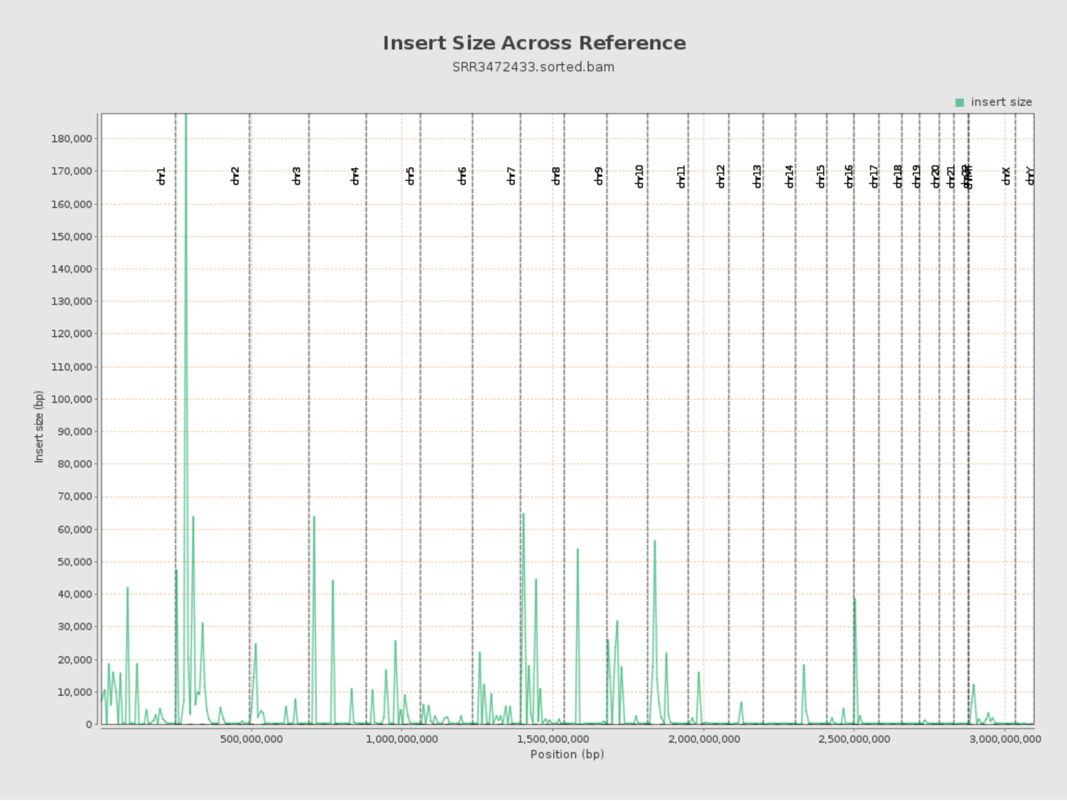
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram