Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 03:43:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472467.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_SRR3472467 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472467_1.fastq.gz SRR3472467_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 03:43:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472467.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	180,012
Mapped reads	178,375 / 99.09%
Unmapped reads	1,637 / 0.91%
Mapped paired reads	178,375 / 99.09%
Mapped reads, first in pair	89,459 / 49.7%
Mapped reads, second in pair	88,916 / 49.39%
Mapped reads, both in pair	177,374 / 98.53%
Mapped reads, singletons	1,001 / 0.56%
Secondary alignments	0
Supplementary alignments	722 / 0.4%
Read min/max/mean length	30 / 100 / 99.35
Duplicated reads (estimated)	35,807 / 19.89%
Duplication rate	20.27%
Clipped reads	12,242 / 6.8%

2.2. ACGT Content

Number/percentage of A's	4,780,121 / 27.33%
Number/percentage of C's	3,984,370 / 22.78%
Number/percentage of T's	4,778,742 / 27.32%
Number/percentage of G's	3,945,964 / 22.56%
Number/percentage of N's	2,304 / 0.01%

GC Percentage	45.34%

2.3. Coverage

Mean	0.0057
Standard Deviation	0.1972

2.4. Mapping Quality

Mean Mapping Quality	54.79

2.5. Insert size

Mean	19,575.75
Standard Deviation	1,410,835.57
P25/Median/P75	151 / 206 / 277

2.6. Mismatches and indels

General error rate	0.55%
Mismatches	93,823
Insertions	1,009
Mapped reads with at least one insertion	0.56%
Deletions	799
Mapped reads with at least one deletion	0.44%
Homopolymer indels	46.74%

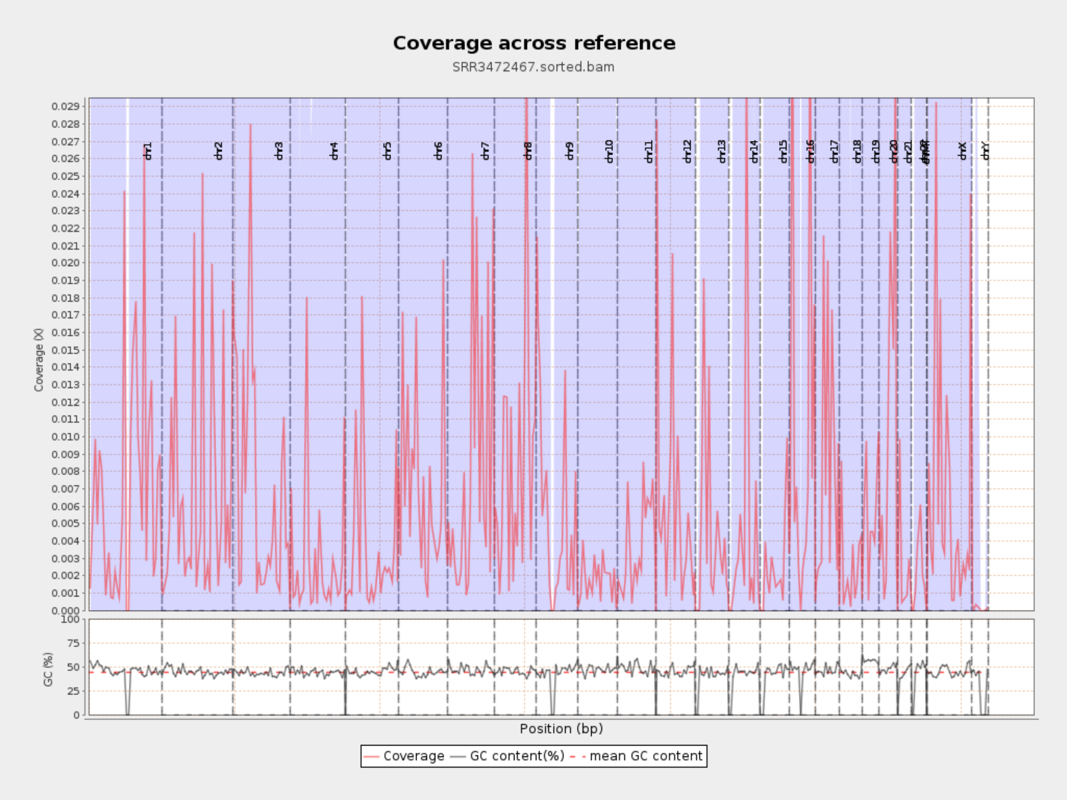
2.7. Chromosome stats

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

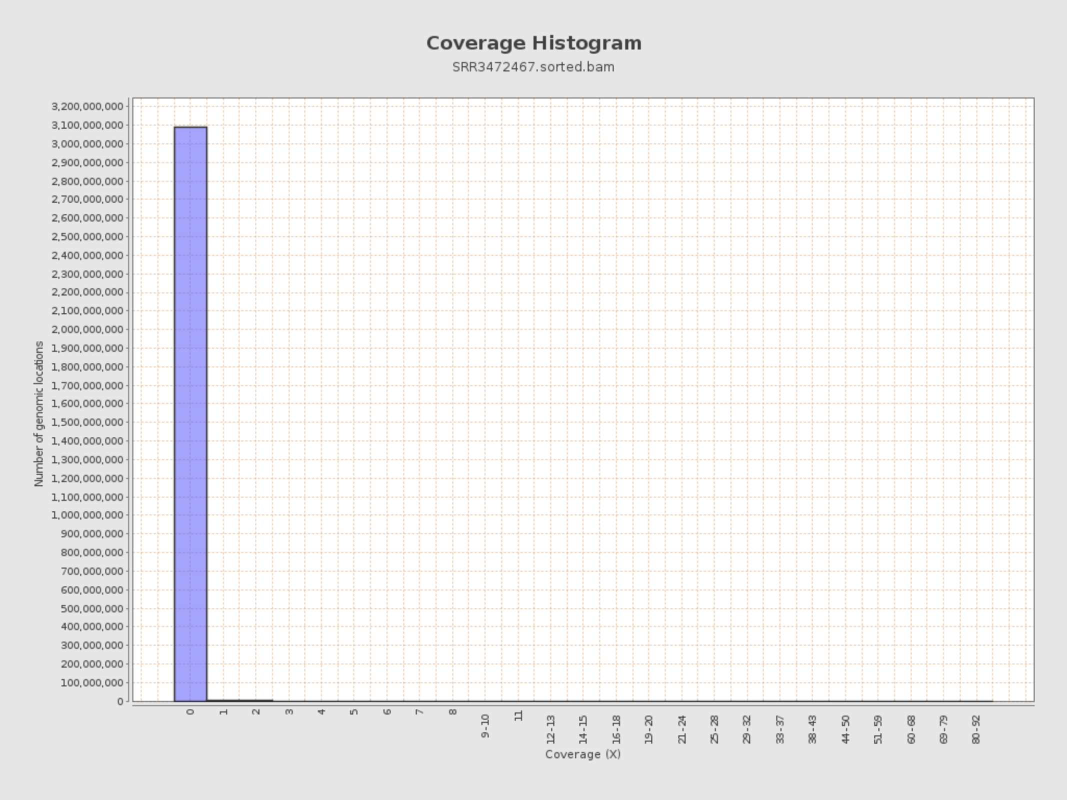
		bases	coverage	deviation
chr1	249250621	1742792	0.007	0.2164
chr2	243199373	1616112	0.0066	0.2301
chr3	198022430	1435179	0.0072	0.1936
chr4	191154276	530577	0.0028	0.1387
chr5	180915260	649294	0.0036	0.14
chr6	171115067	1230179	0.0072	0.1911
chr7	159138663	1308207	0.0082	0.2932
chr8	146364022	1245369	0.0085	0.2384
chr9	141213431	721740	0.0051	0.1781
chr10	135534747	247938	0.0018	0.0839
chr11	135006516	505322	0.0037	0.1487
chr12	133851895	859940	0.0064	0.1819
chr13	115169878	511317	0.0044	0.1645
chr14	107349540	474655	0.0044	0.2124
chr15	102531392	269083	0.0026	0.0979
chr16	90354753	1034878	0.0115	0.309
chr17	81195210	698649	0.0086	0.2353
chr18	78077248	190601	0.0024	0.0985
chr19	59128983	324711	0.0055	0.1629
chr20	63025520	720429	0.0114	0.3731
chr21	48129895	119207	0.0025	0.1877
chr22	51304566	111223	0.0022	0.0794
chrMT	16571	0	0	0
chrX	155270560	939183	0.006	0.1766

chrY	59373566	6772	0.0001	0.0168

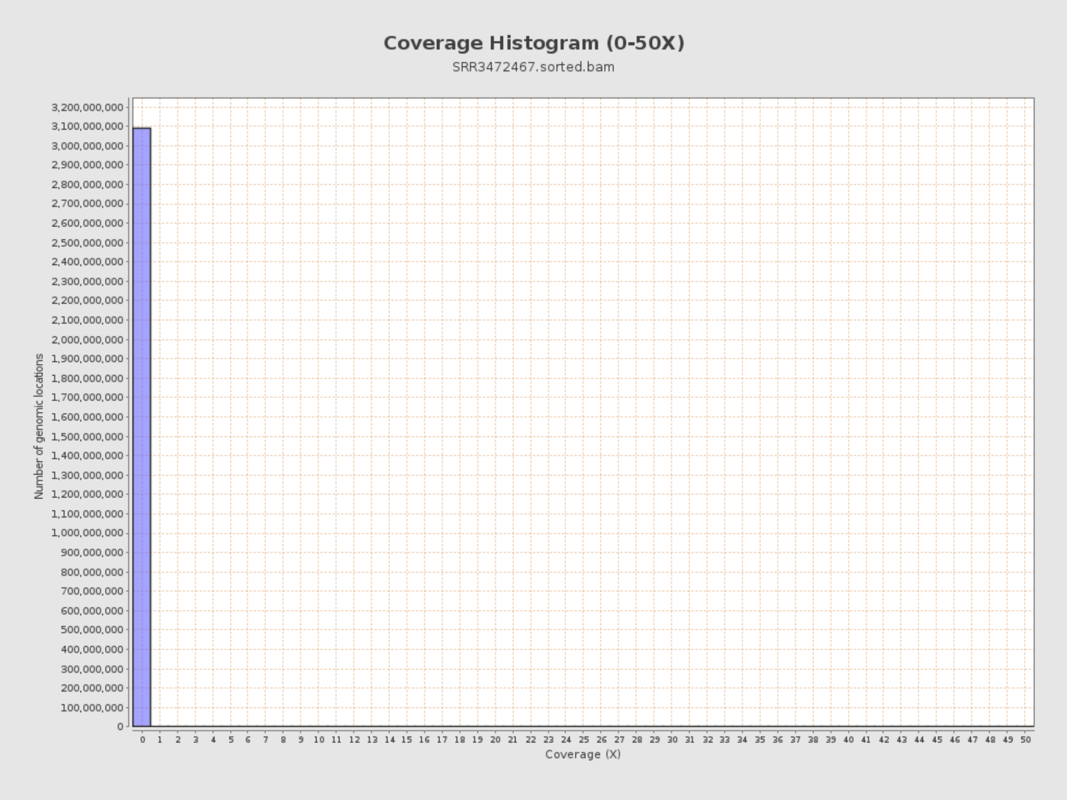
3. Results : Coverage across reference



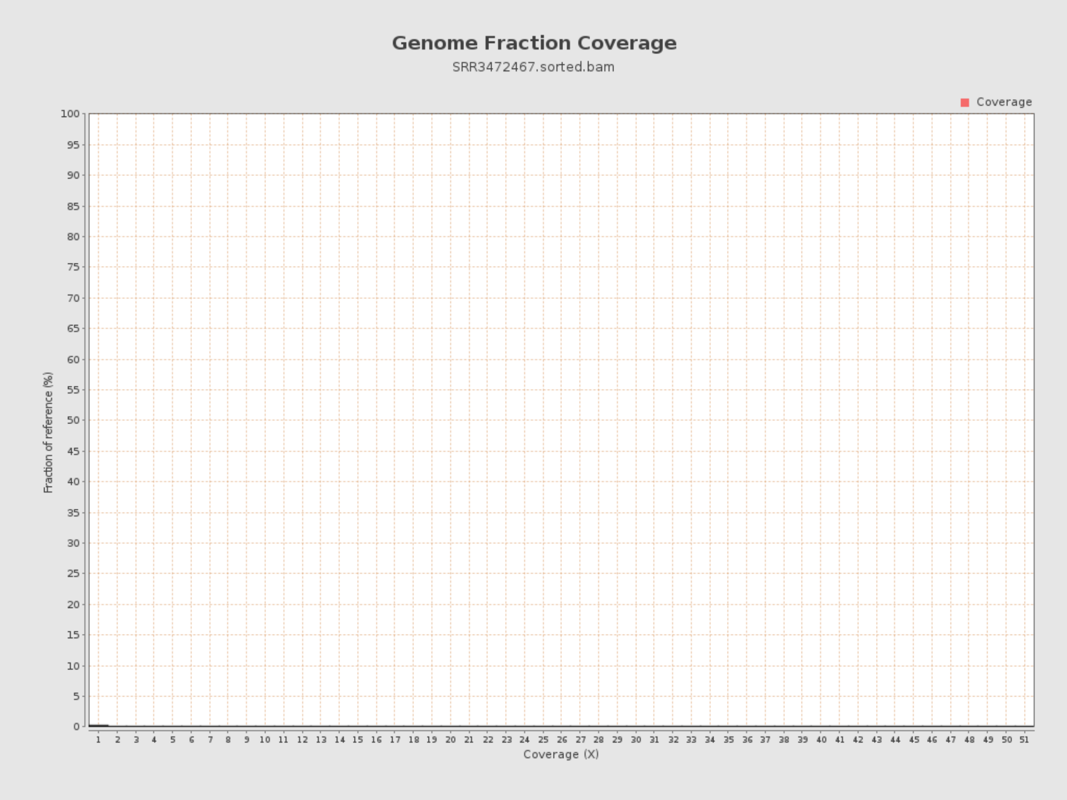
4. Results : Coverage Histogram



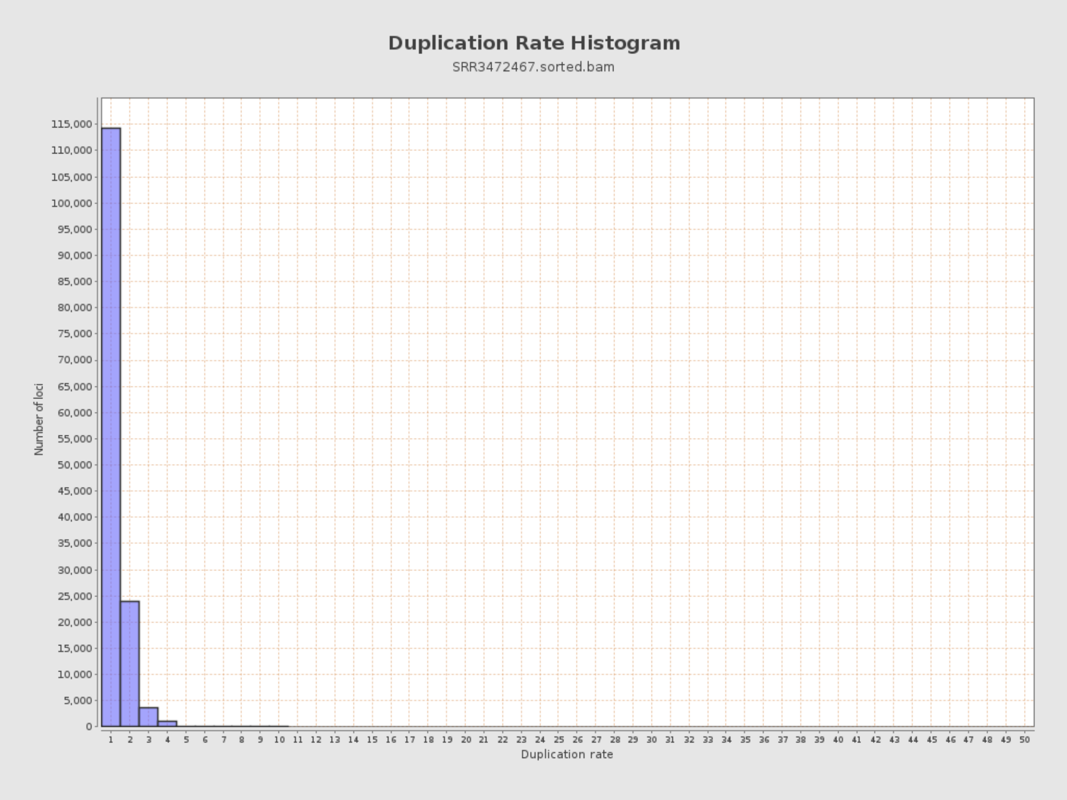
5. Results : Coverage Histogram (0-50X)



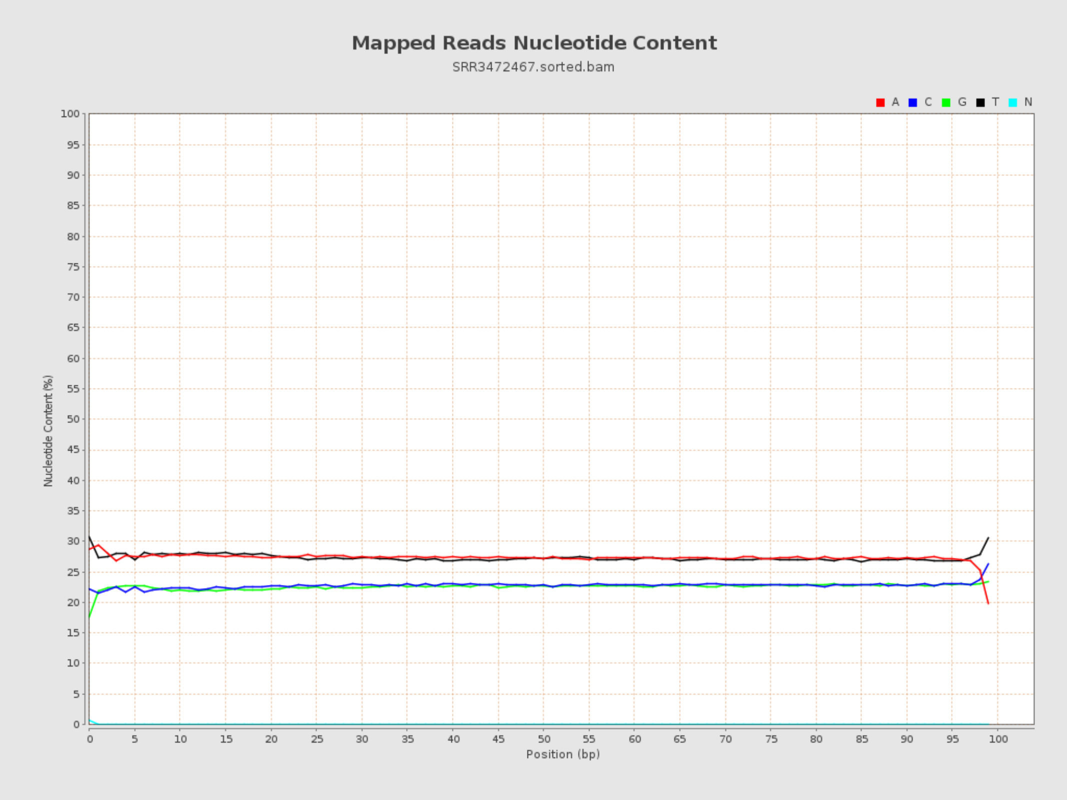
6. Results : Genome Fraction Coverage



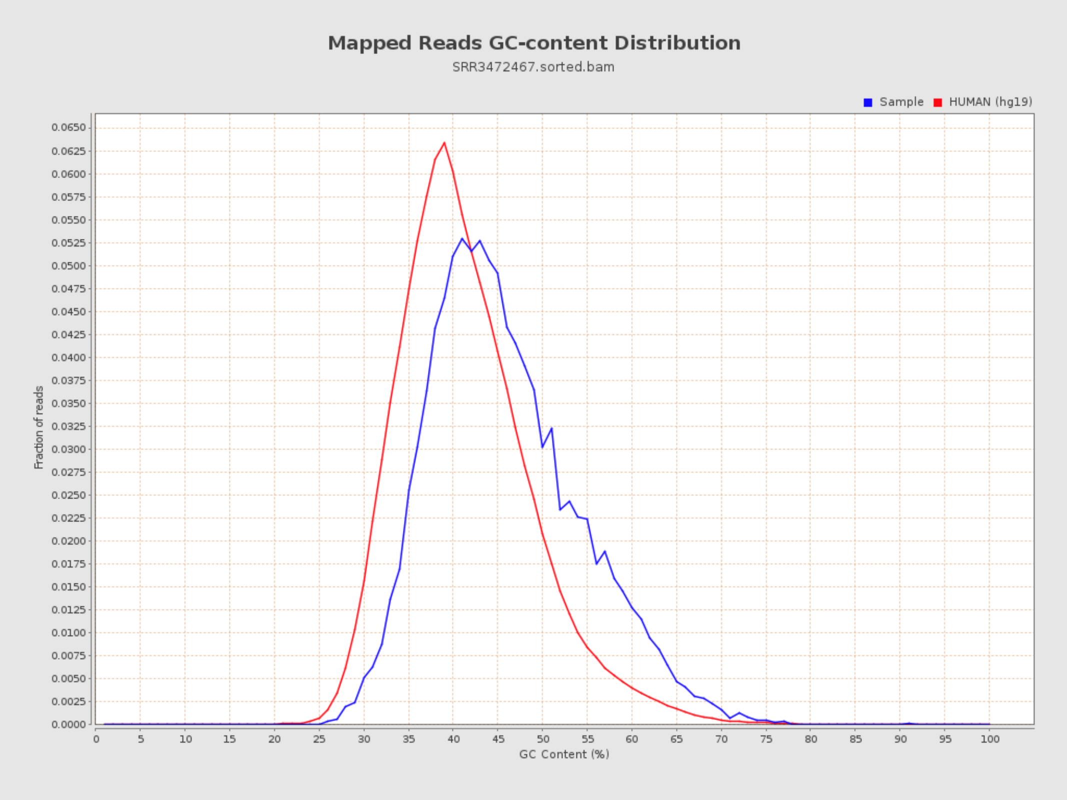
7. Results : Duplication Rate Histogram



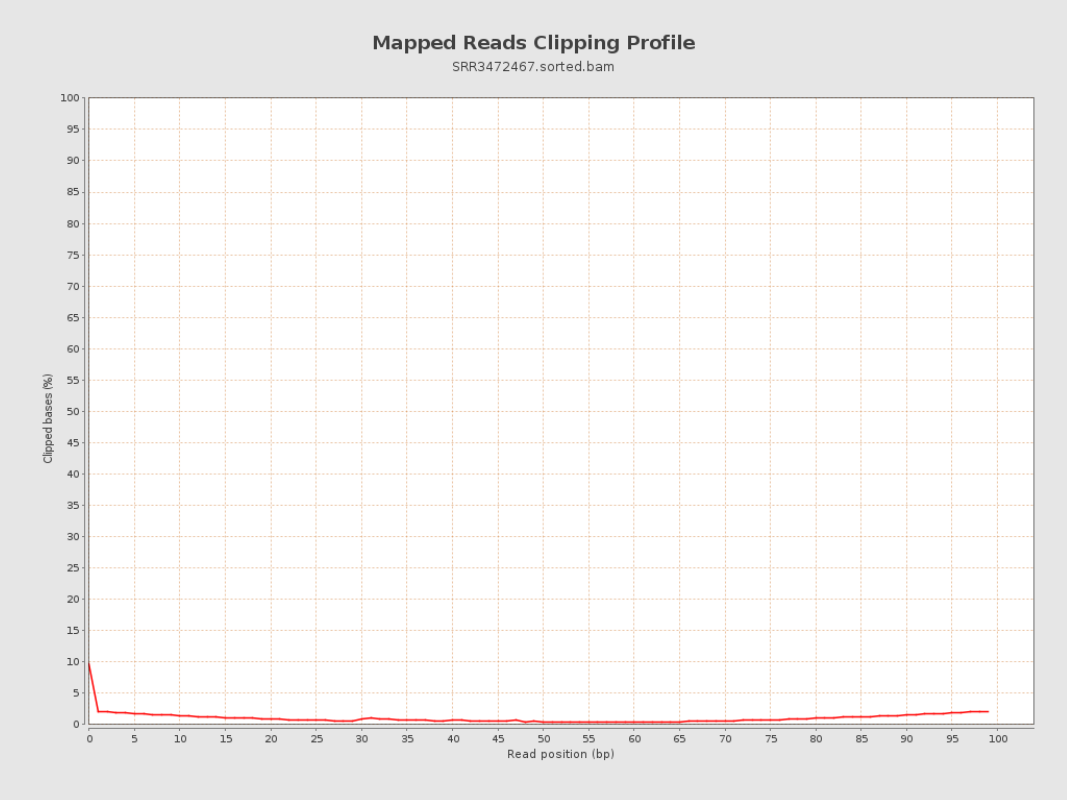
8. Results : Mapped Reads Nucleotide Content



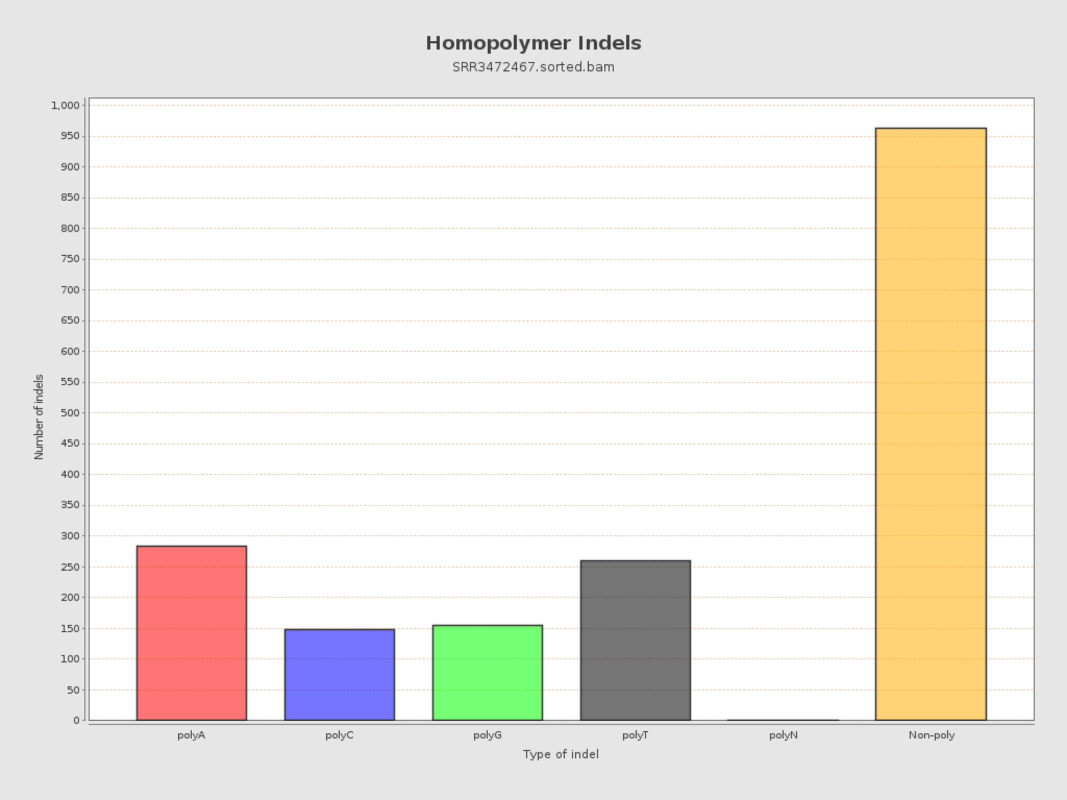
9. Results : Mapped Reads GC-content Distribution



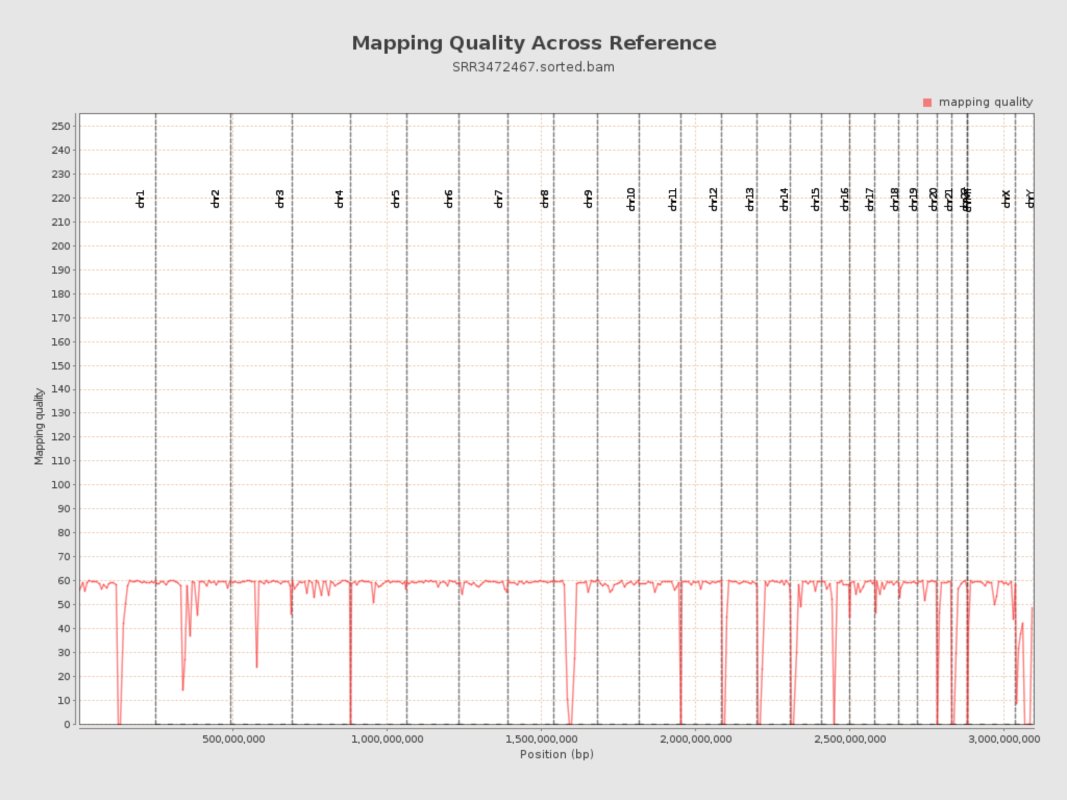
10. Results : Mapped Reads Clipping Profile



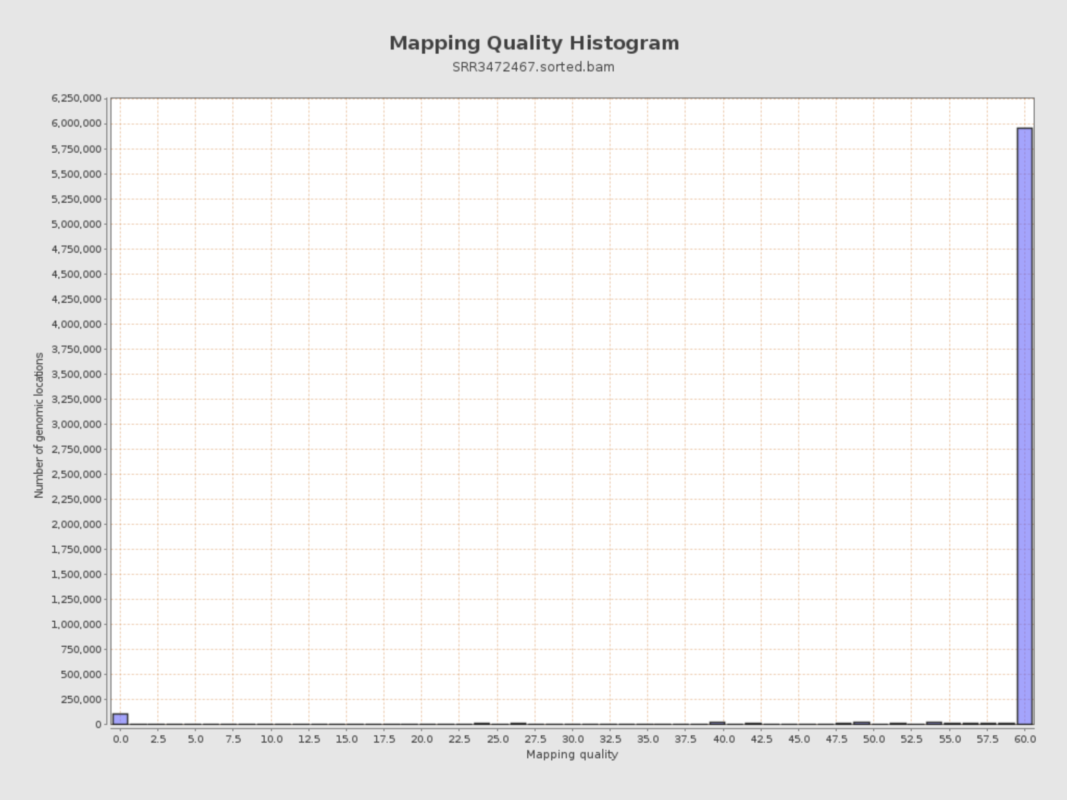
11. Results : Homopolymer Indels



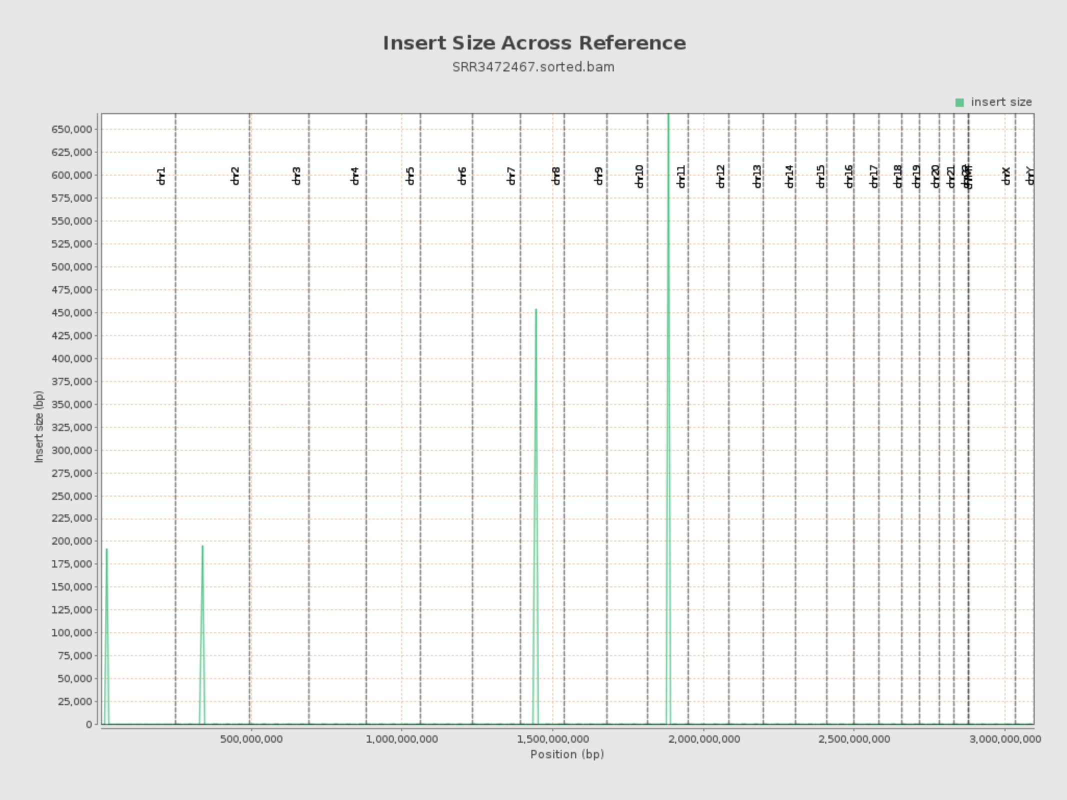
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram