Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/07 11:34:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617367.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_SRR617367 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617367_1.fastq.gz SRR617367_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Oct 07 11:34:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617367.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	28,140,411 / 87.94%
Unmapped reads	3,859,589 / 12.06%
Mapped paired reads	28,140,411 / 87.94%
Mapped reads, first in pair	14,399,829 / 45%
Mapped reads, second in pair	13,740,582 / 42.94%
Mapped reads, both in pair	27,057,286 / 84.55%
Mapped reads, singletons	1,083,125 / 3.38%
Secondary alignments	0
Supplementary alignments	86,699 / 0.27%
Read min/max/mean length	30 / 100 / 100.1
Duplicated reads (estimated)	1,419,834 / 4.44%
Duplication rate	1.5%
Clipped reads	3,303,382 / 10.32%

2.2. ACGT Content

Number/percentage of A's	829,089,694 / 30.32%
Number/percentage of C's	541,838,820 / 19.82%
Number/percentage of T's	817,337,065 / 29.9%
Number/percentage of G's	544,685,900 / 19.92%
Number/percentage of N's	1,065,128 / 0.04%

GC Percentage	39.74%

2.3. Coverage

Mean	0.8834
Standard Deviation	8.6484

2.4. Mapping Quality

Mean Mapping Quality	53.11

2.5. Insert size

Mean	66,271.56
Standard Deviation	2,458,779.59
P25/Median/P75	170 / 210 / 271

2.6. Mismatches and indels

General error rate	1.65%
Mismatches	44,405,099
Insertions	278,922
Mapped reads with at least one insertion	0.96%
Deletions	328,779
Mapped reads with at least one deletion	1.13%
Homopolymer indels	40.63%

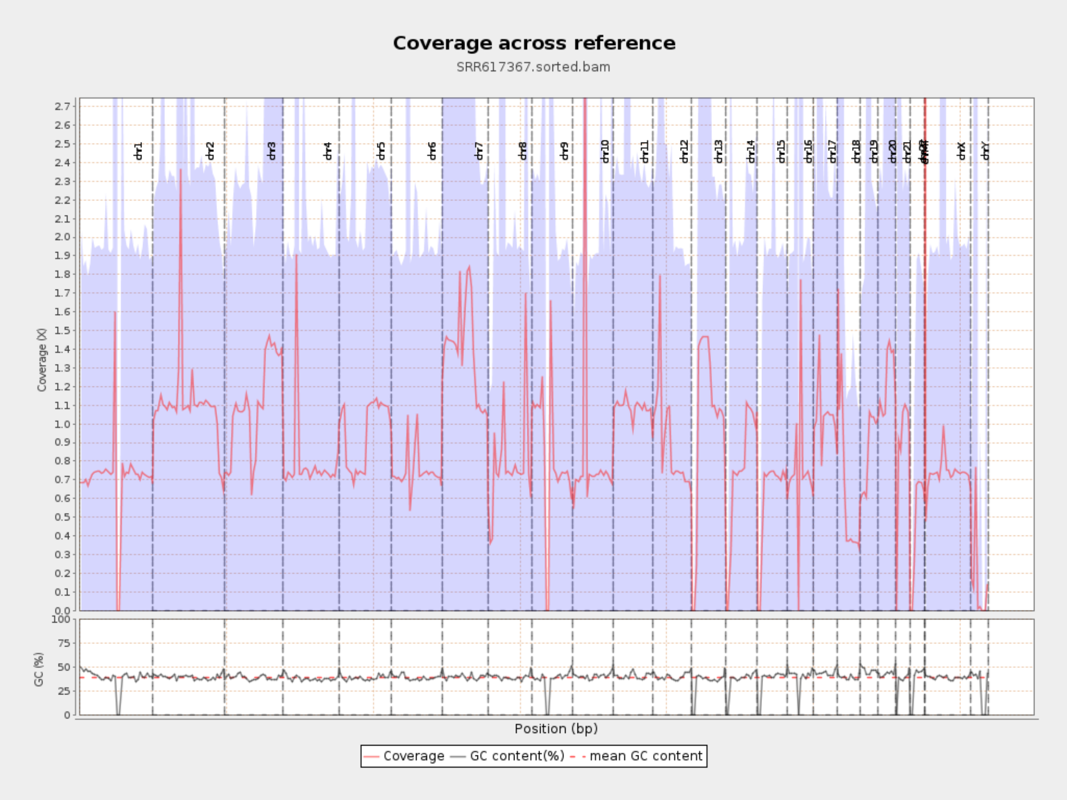
2.7. Chromosome stats

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

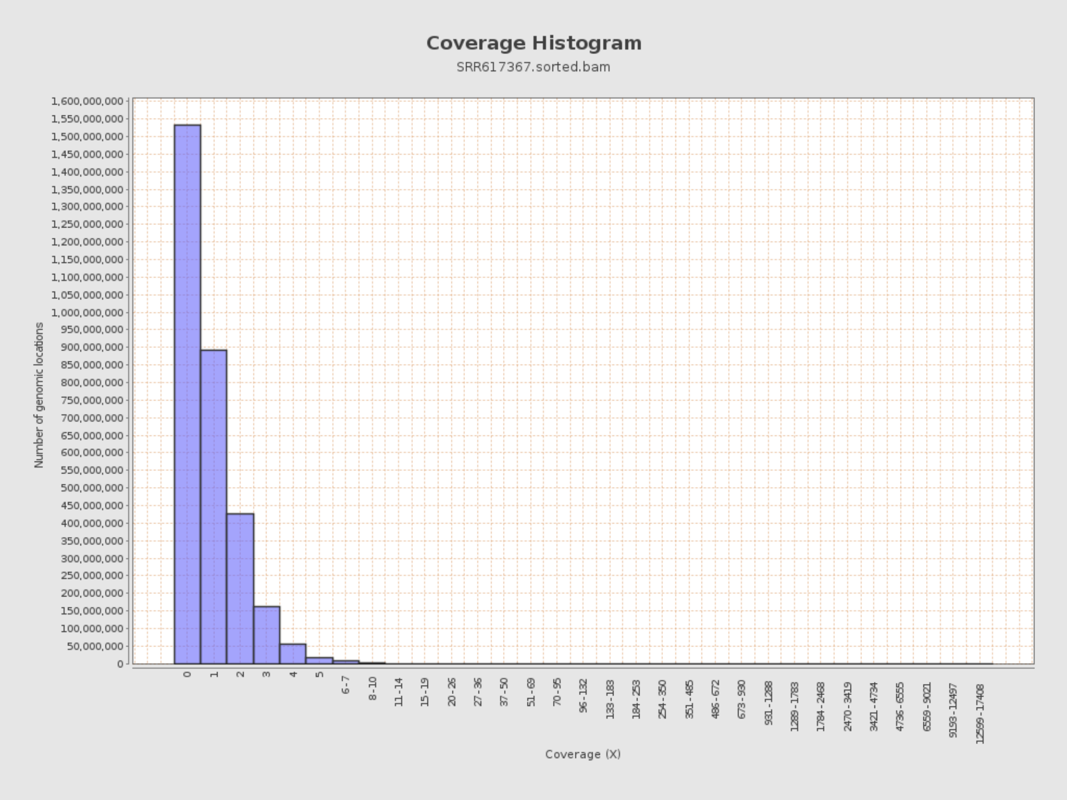
		bases	coverage	deviation
chr1	249250621	177247596	0.7111	17.8727
chr2	243199373	270332342	1.1116	7.7414
chr3	198022430	218149280	1.1016	1.439
chr4	191154276	150054144	0.785	7.8005
chr5	180915260	172380610	0.9528	1.3797
chr6	171115067	128674313	0.752	3.4269
chr7	159138663	222118552	1.3958	10.0104
chr8	146364022	115207346	0.7871	6.4691
chr9	141213431	114776180	0.8128	12.4267
chr10	135534747	114764323	0.8468	17.9927
chr11	135006516	146577982	1.0857	4.8144
chr12	133851895	120887789	0.9031	1.3084
chr13	115169878	119699795	1.0393	1.2718
chr14	107349540	79237376	0.7381	1.3022
chr15	102531392	61622062	0.601	1.0831
chr16	90354753	68466279	0.7577	7.355
chr17	81195210	84343097	1.0388	6.1753
chr18	78077248	49232481	0.6306	13.2156
chr19	59128983	50294026	0.8506	8.7632
chr20	63025520	77970425	1.2371	2.1472
chr21	48129895	43443502	0.9026	2.8636
chr22	51304566	24046722	0.4687	0.8811
chrMT	16571	1846347	111.4204	20.3752
chrX	155270560	114399477	0.7368	2.6984

chrY	59373566	9028653	0.1521	7.0658

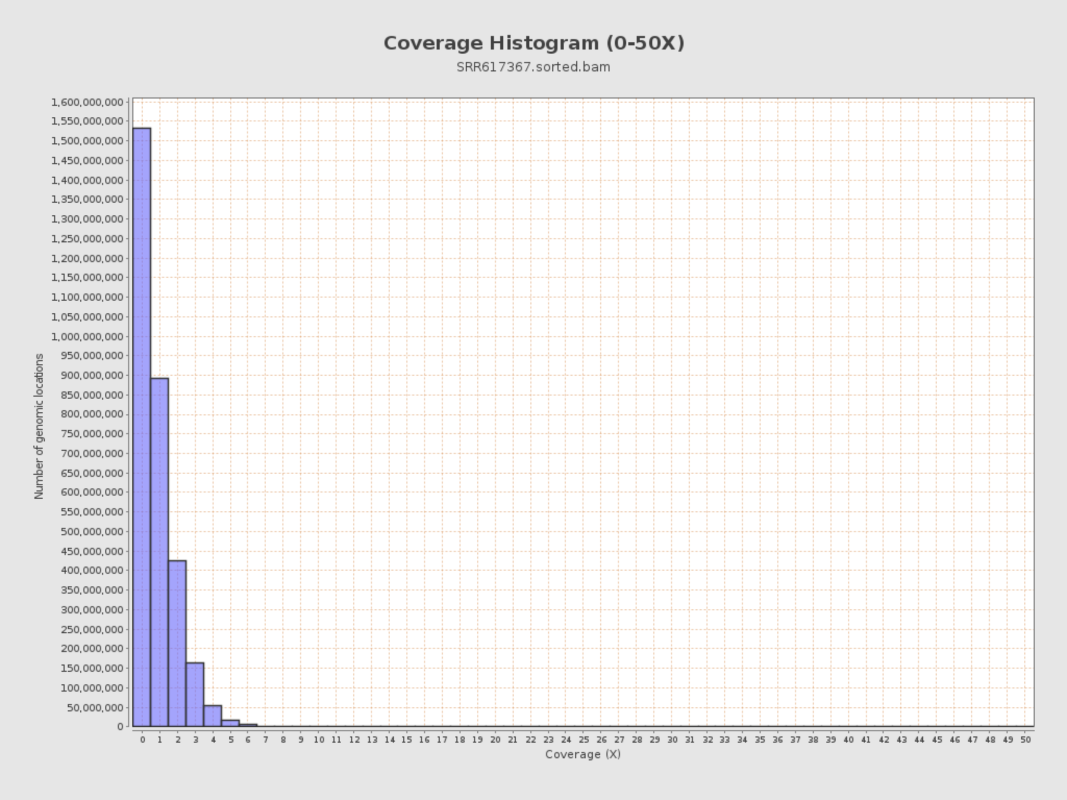
3. Results : Coverage across reference



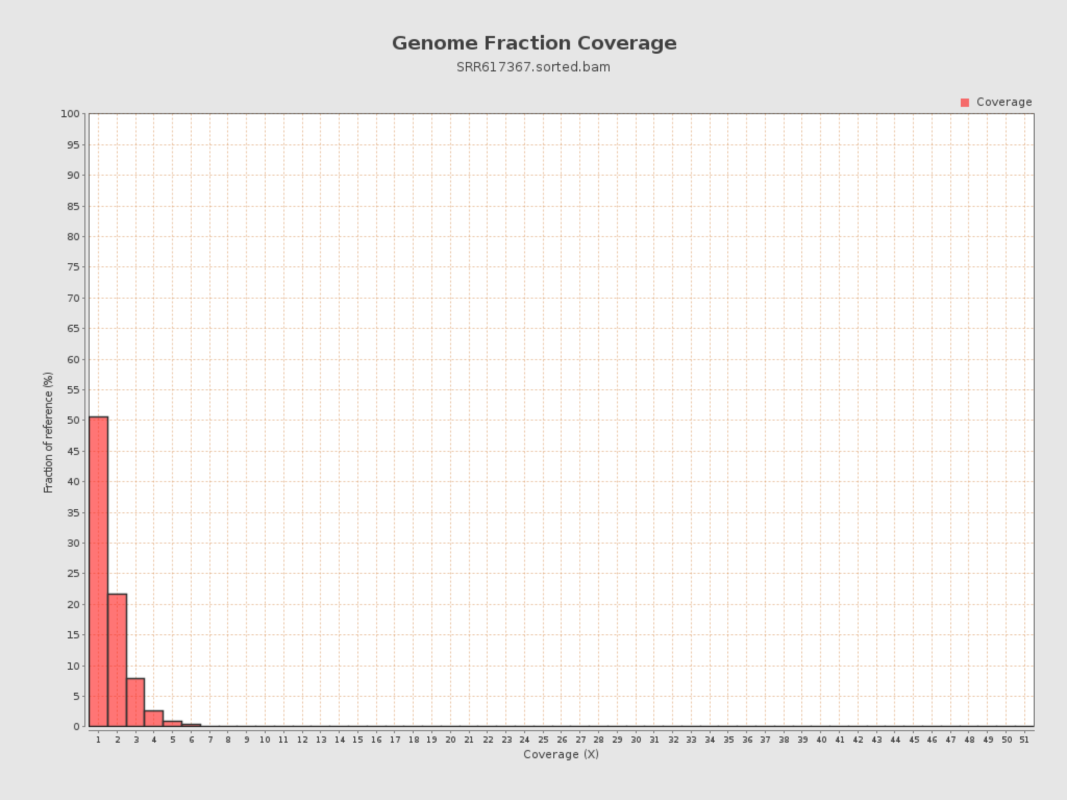
4. Results : Coverage Histogram



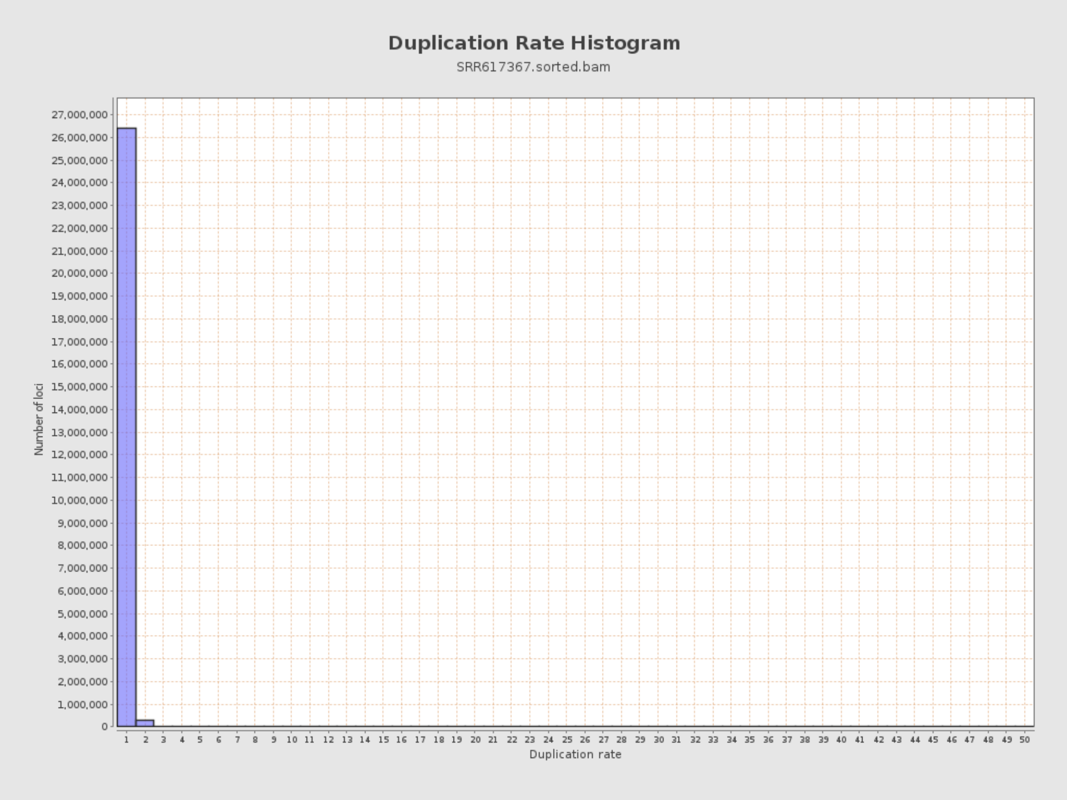
5. Results : Coverage Histogram (0-50X)



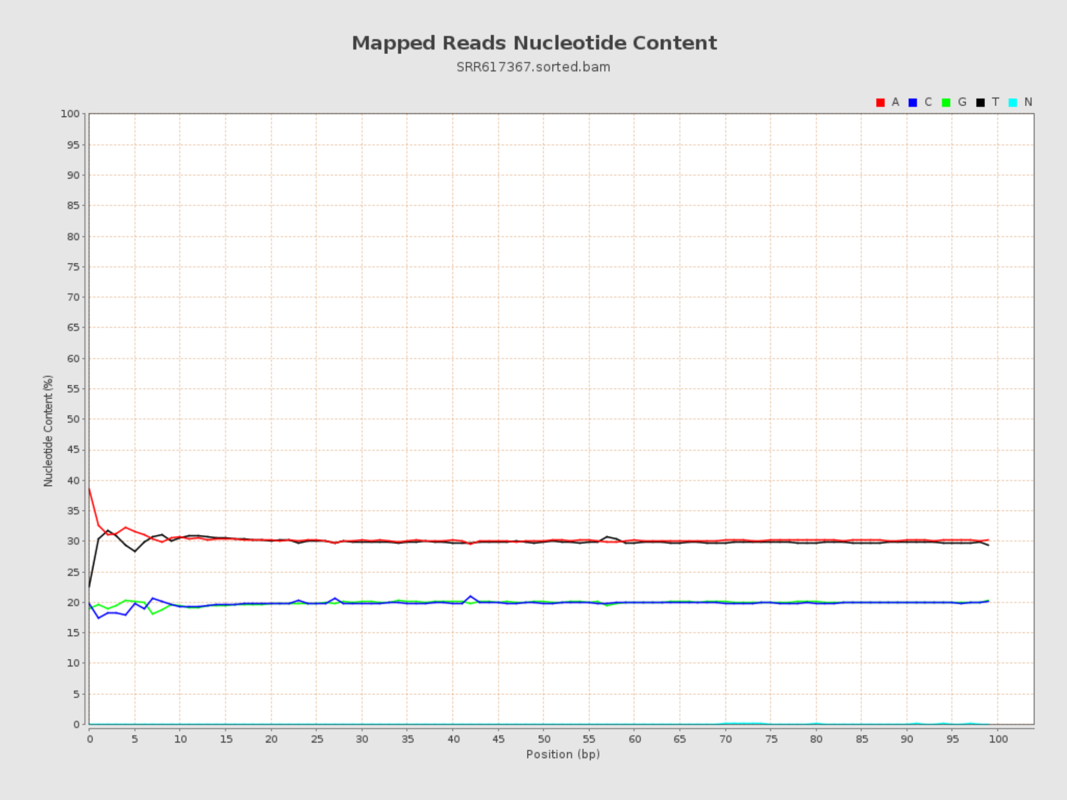
6. Results : Genome Fraction Coverage



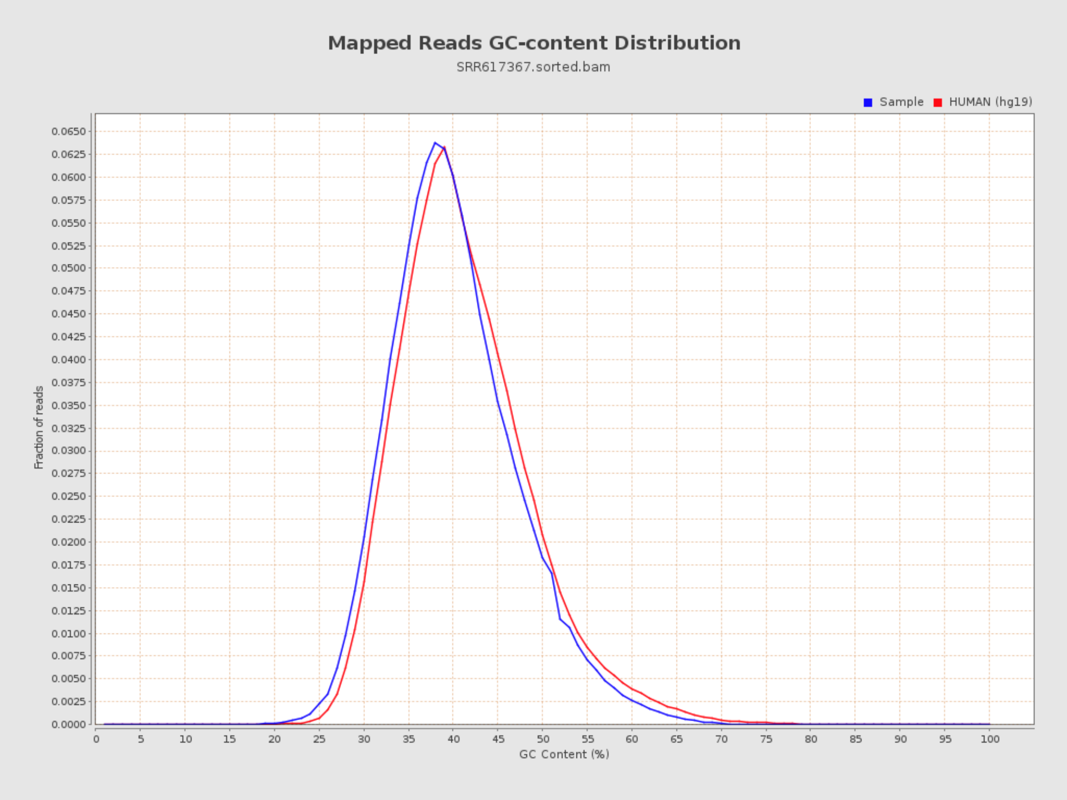
7. Results : Duplication Rate Histogram



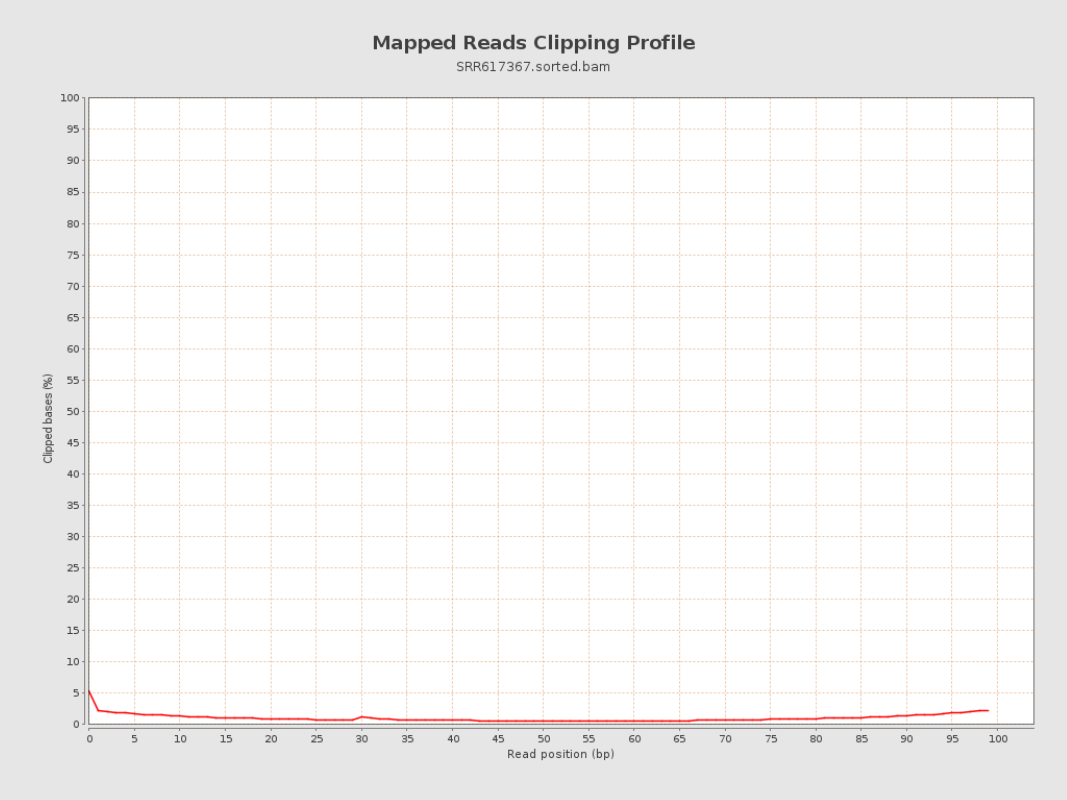
8. Results : Mapped Reads Nucleotide Content



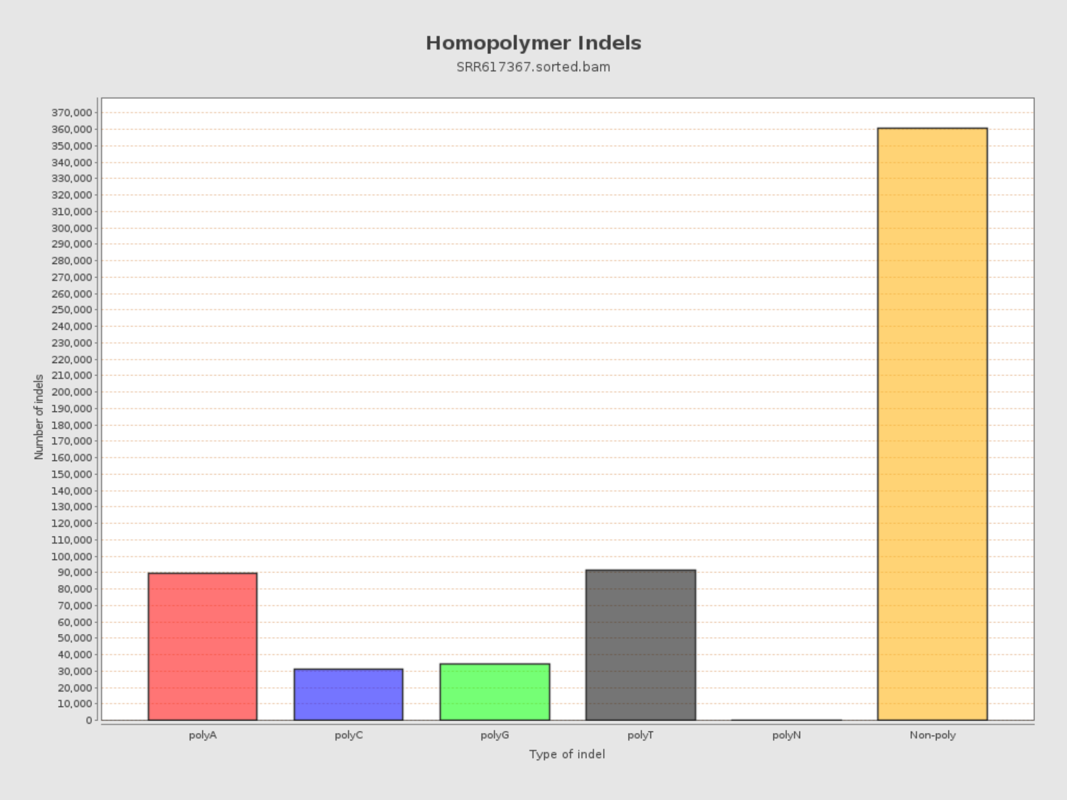
9. Results : Mapped Reads GC-content Distribution



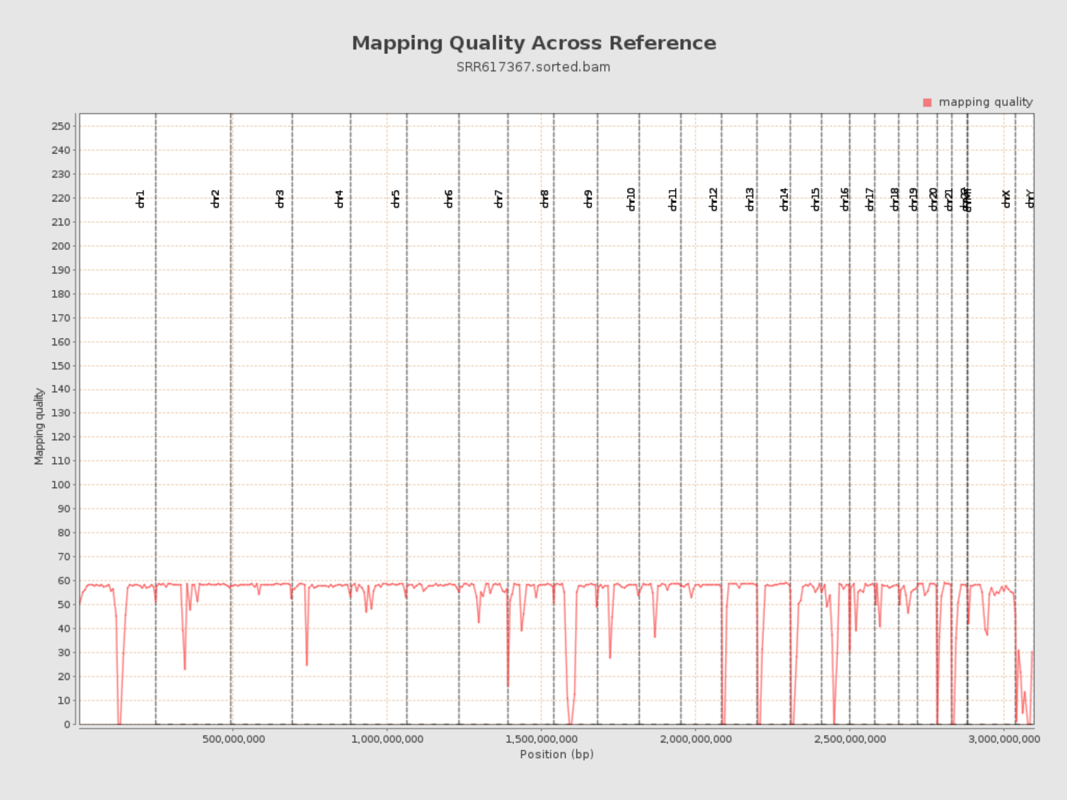
10. Results : Mapped Reads Clipping Profile



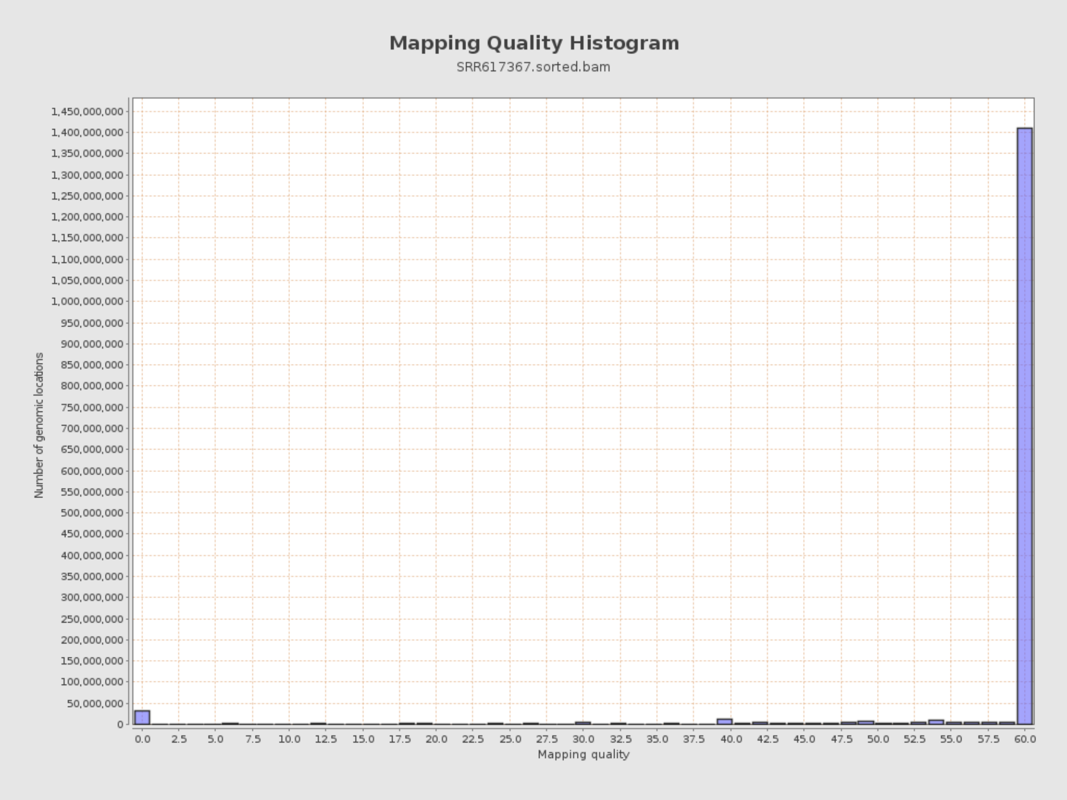
11. Results : Homopolymer Indels



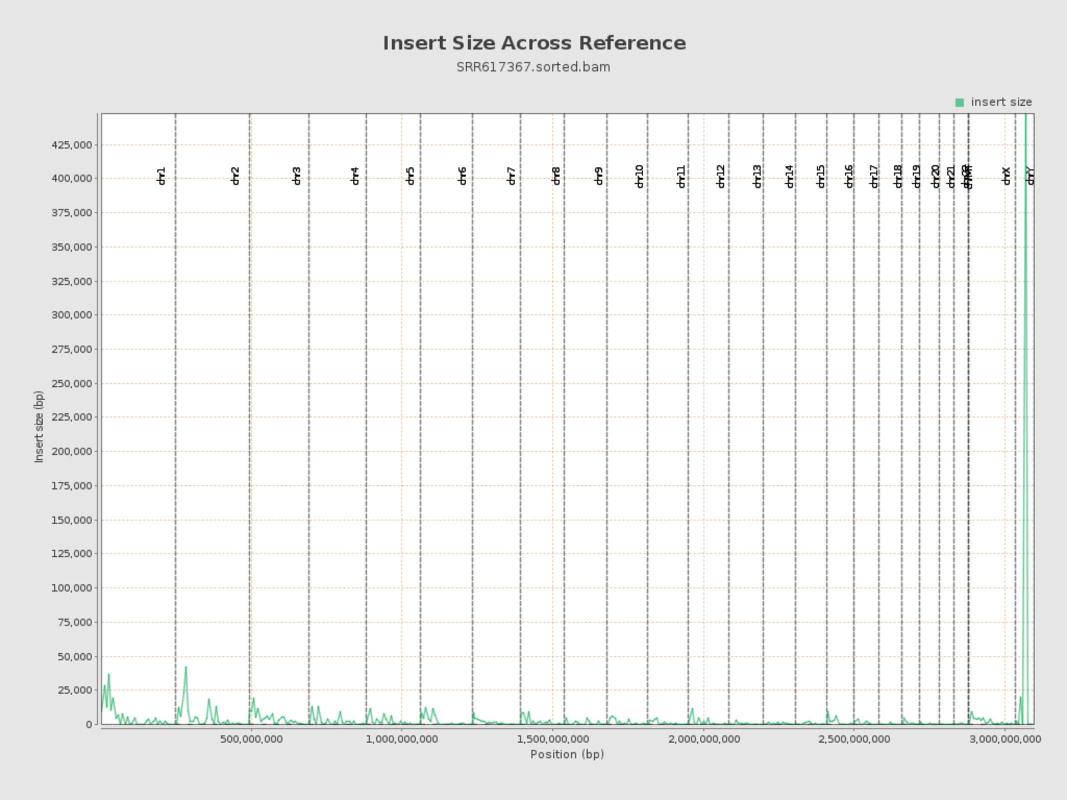
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram