Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/07 03:17:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617358.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_SRR617358 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617358_1.fastq.gz SRR617358_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Oct 07 03:17:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617358.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,101,589 / 94.07%
Unmapped reads	1,898,411 / 5.93%
Mapped paired reads	30,101,589 / 94.07%
Mapped reads, first in pair	15,131,234 / 47.29%
Mapped reads, second in pair	14,970,355 / 46.78%
Mapped reads, both in pair	29,605,852 / 92.52%
Mapped reads, singletons	495,737 / 1.55%
Secondary alignments	0
Supplementary alignments	65,858 / 0.21%
Read min/max/mean length	30 / 100 / 100.08
Duplicated reads (estimated)	1,551,738 / 4.85%
Duplication rate	1.48%
Clipped reads	2,383,351 / 7.45%

2.2. ACGT Content

Number/percentage of A's	895,808,290 / 30.3%
Number/percentage of C's	587,103,032 / 19.86%
Number/percentage of T's	883,302,317 / 29.88%
Number/percentage of G's	589,019,870 / 19.93%
Number/percentage of N's	752,857 / 0.03%

GC Percentage	39.79%

2.3. Coverage

Mean	0.9552
Standard Deviation	9.7527

2.4. Mapping Quality

Mean Mapping Quality	53.47

2.5. Insert size

Mean	51,559.26
Standard Deviation	2,164,816.34
P25/Median/P75	171 / 211 / 273

2.6. Mismatches and indels

General error rate	1.15%
Mismatches	33,054,858
Insertions	296,368
Mapped reads with at least one insertion	0.95%
Deletions	361,563
Mapped reads with at least one deletion	1.16%
Homopolymer indels	41.16%

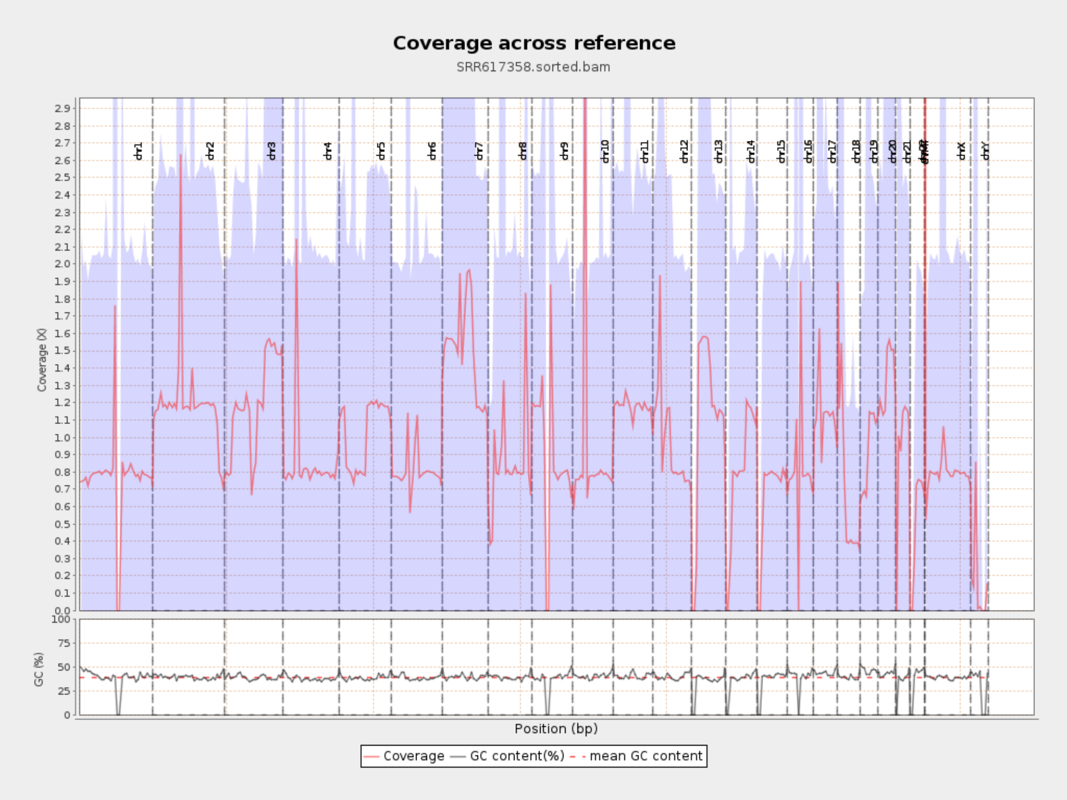
2.7. Chromosome stats

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

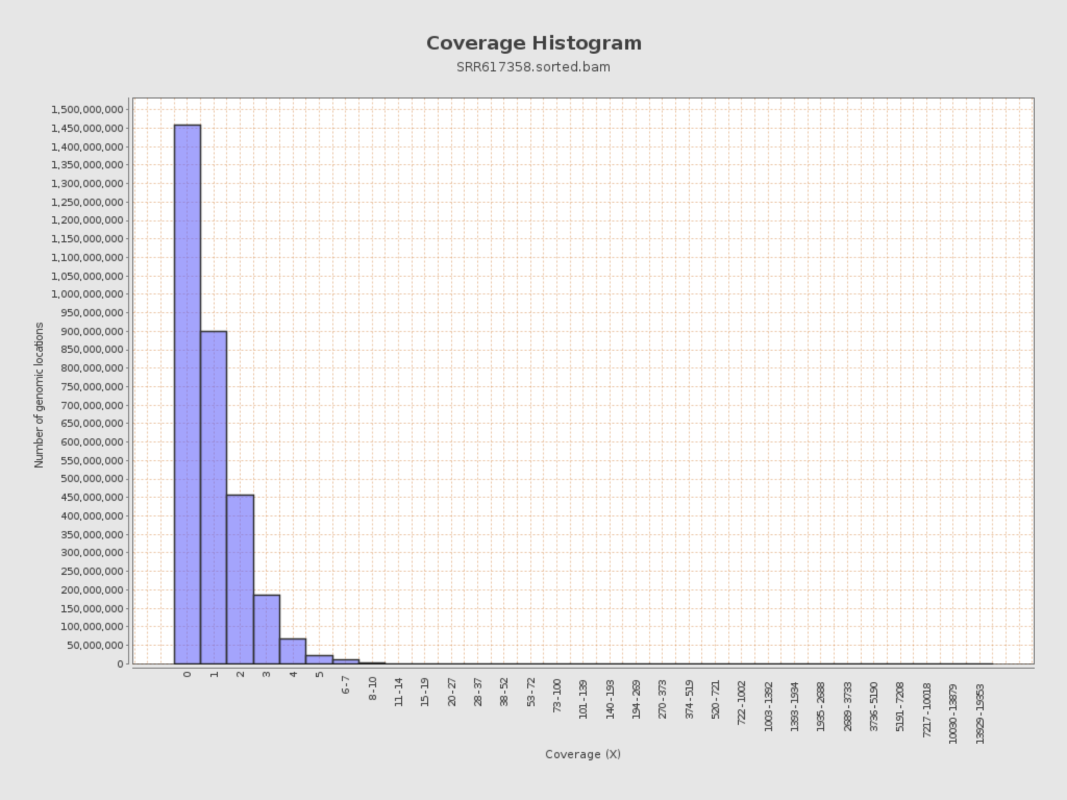
		bases	coverage	deviation
chr1	249250621	191772241	0.7694	19.8136
chr2	243199373	292595673	1.2031	8.7802
chr3	198022430	235257666	1.188	1.465
chr4	191154276	162090609	0.848	9.2924
chr5	180915260	185696325	1.0264	1.4609
chr6	171115067	138840082	0.8114	3.6901
chr7	159138663	239640581	1.5059	10.8194
chr8	146364022	124742565	0.8523	7.6662
chr9	141213431	124634798	0.8826	14.8351
chr10	135534747	124438334	0.9181	20.237
chr11	135006516	158665789	1.1752	5.496
chr12	133851895	130514747	0.9751	1.3671
chr13	115169878	128839772	1.1187	1.2908
chr14	107349540	85590057	0.7973	1.3594
chr15	102531392	66497481	0.6486	0.9751
chr16	90354753	74233395	0.8216	7.9282
chr17	81195210	91866840	1.1314	7.0723
chr18	78077248	53476348	0.6849	15.1146
chr19	59128983	54516982	0.922	9.4476
chr20	63025520	84675447	1.3435	2.4573
chr21	48129895	46979083	0.9761	3.1506
chr22	51304566	26105498	0.5088	0.9123
chrMT	16571	1968321	118.7811	20.9186
chrX	155270560	123117194	0.7929	2.9755

chrY	59373566	10100257	0.1701	8.2268

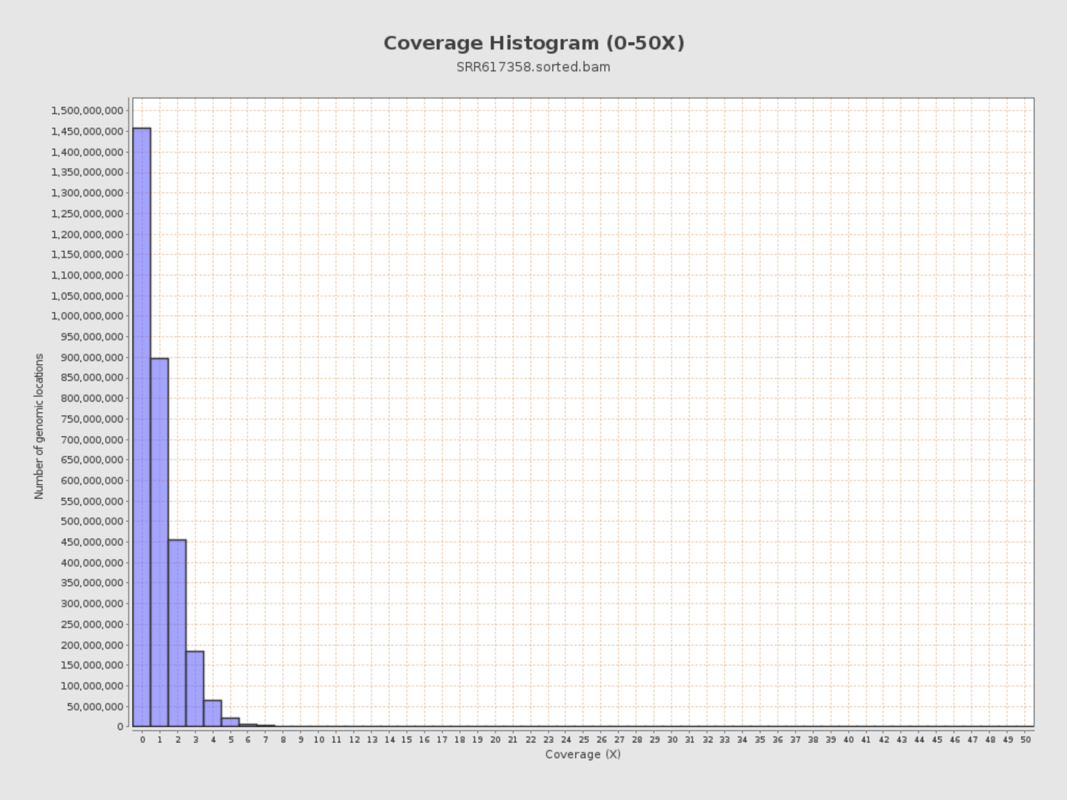
3. Results : Coverage across reference



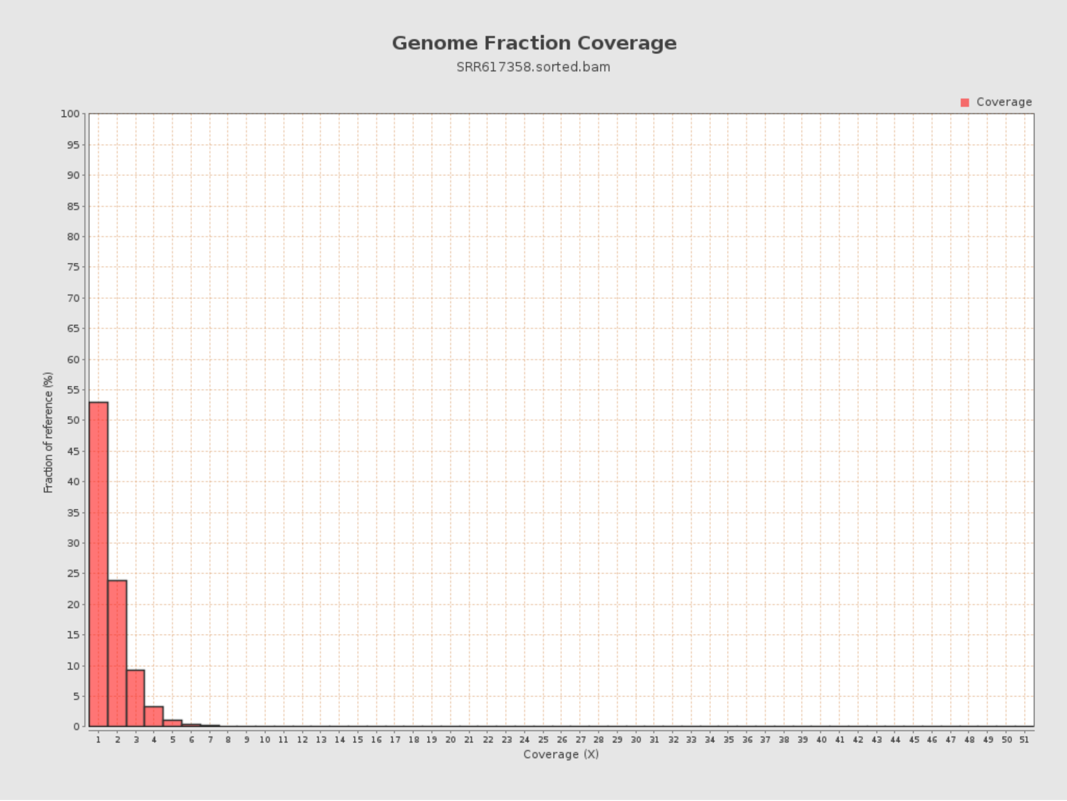
4. Results : Coverage Histogram



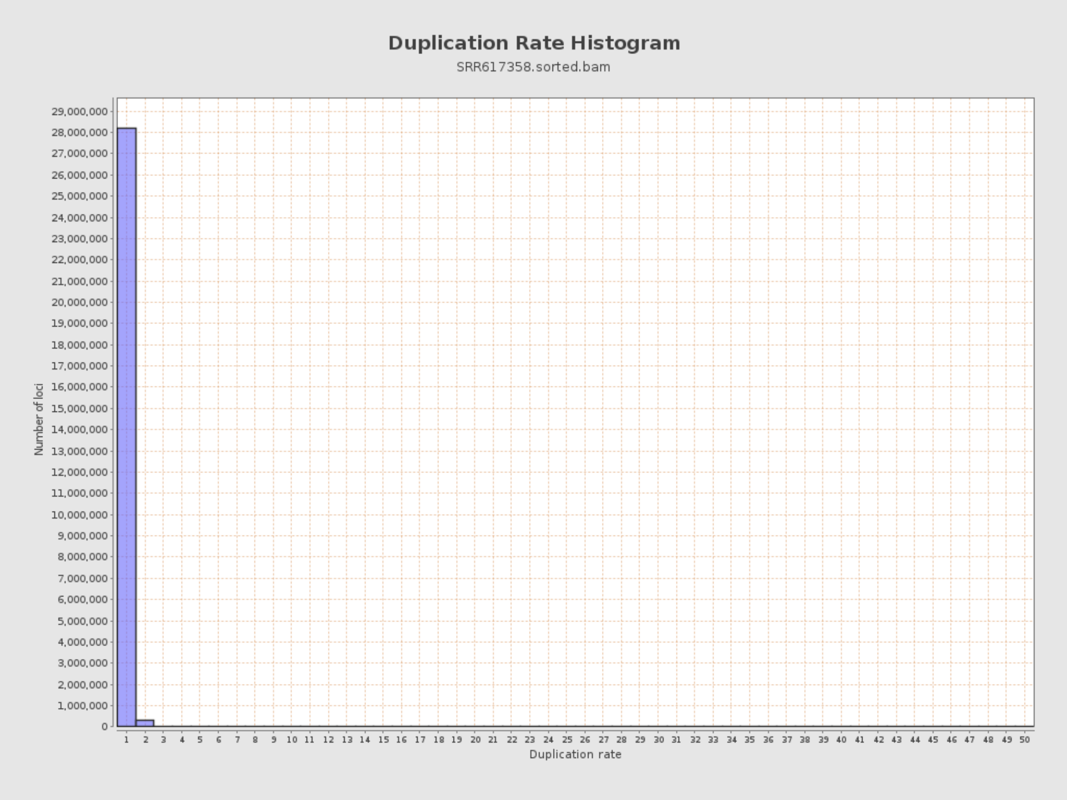
5. Results : Coverage Histogram (0-50X)



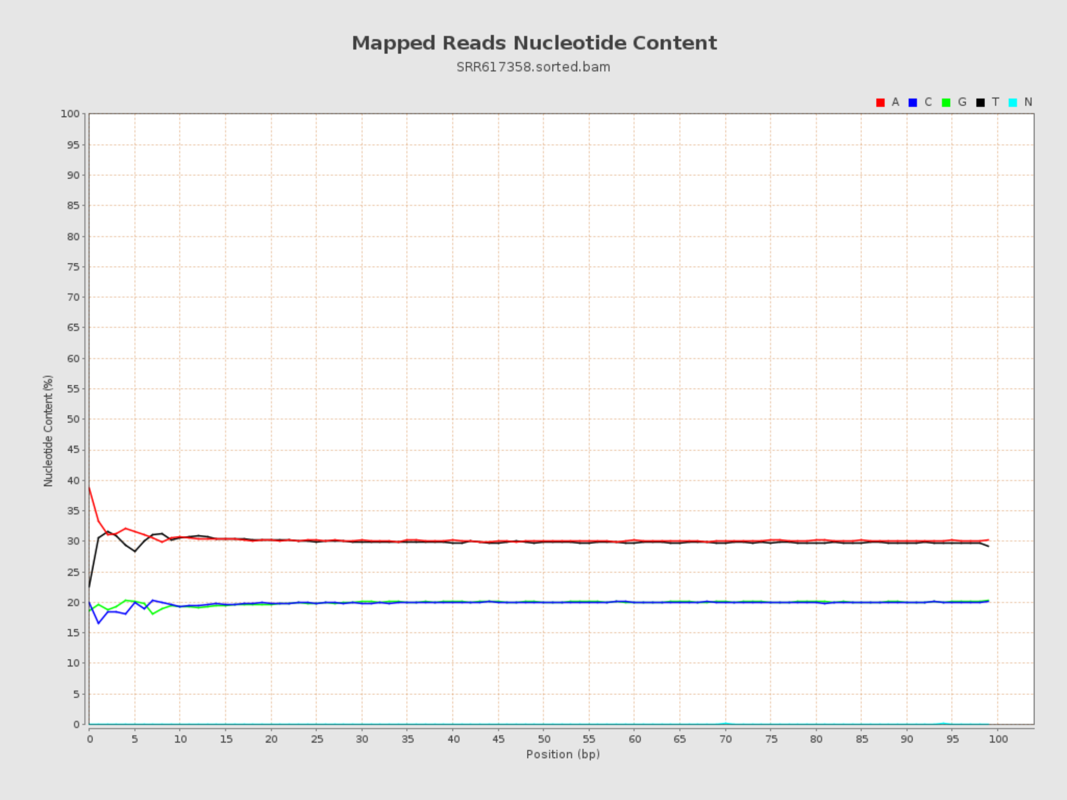
6. Results : Genome Fraction Coverage



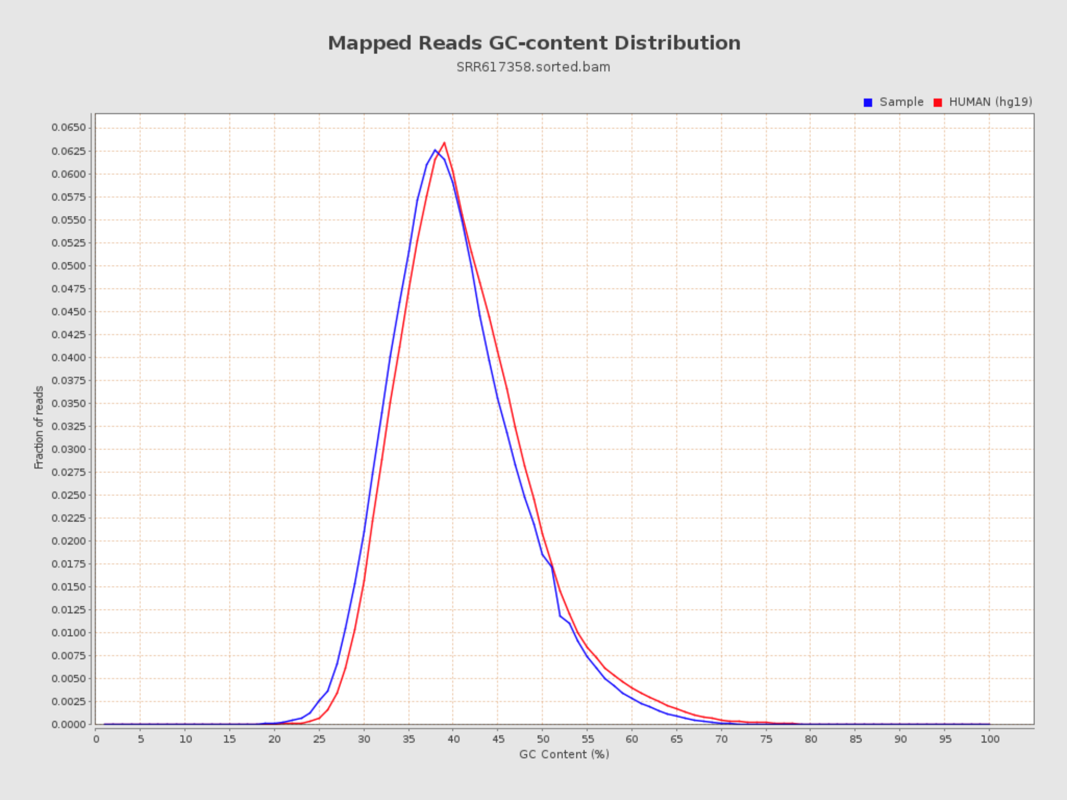
7. Results : Duplication Rate Histogram



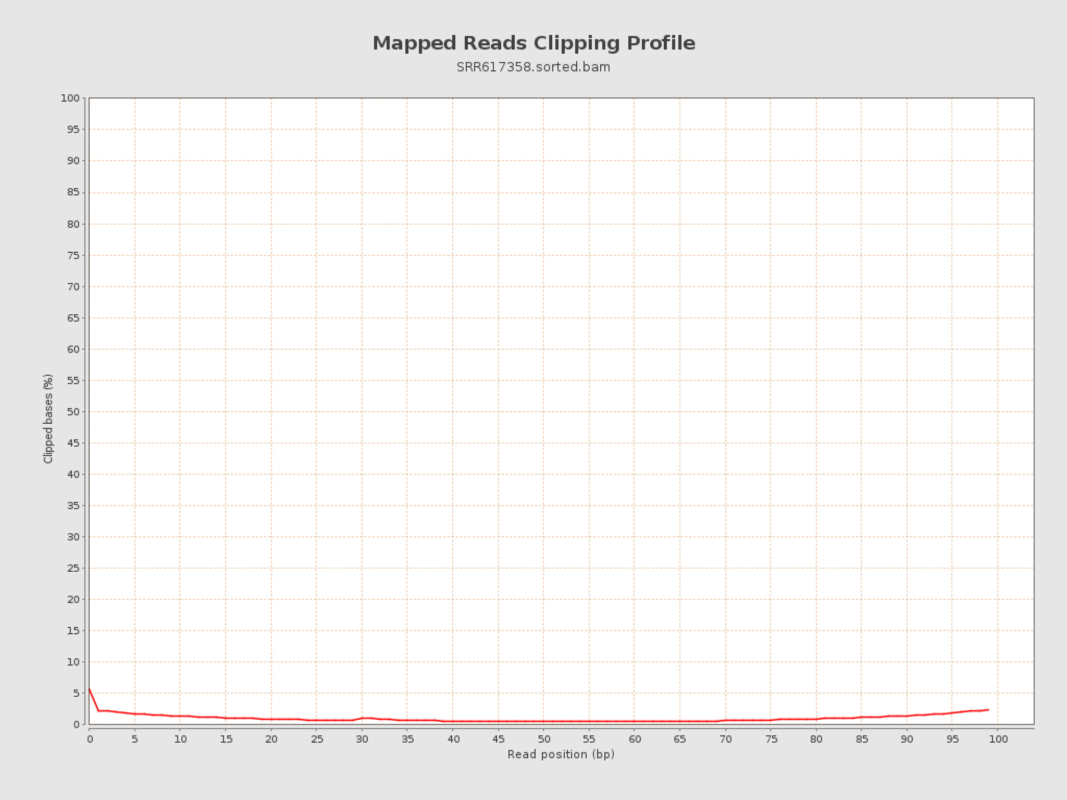
8. Results : Mapped Reads Nucleotide Content



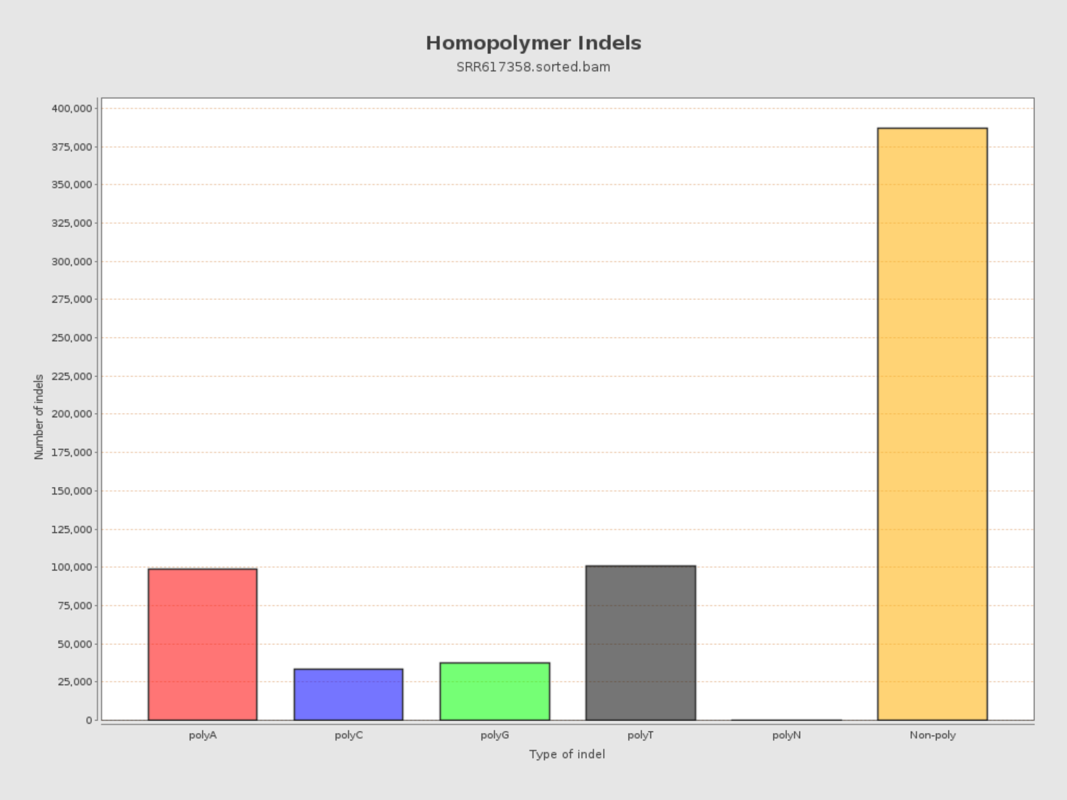
9. Results : Mapped Reads GC-content Distribution



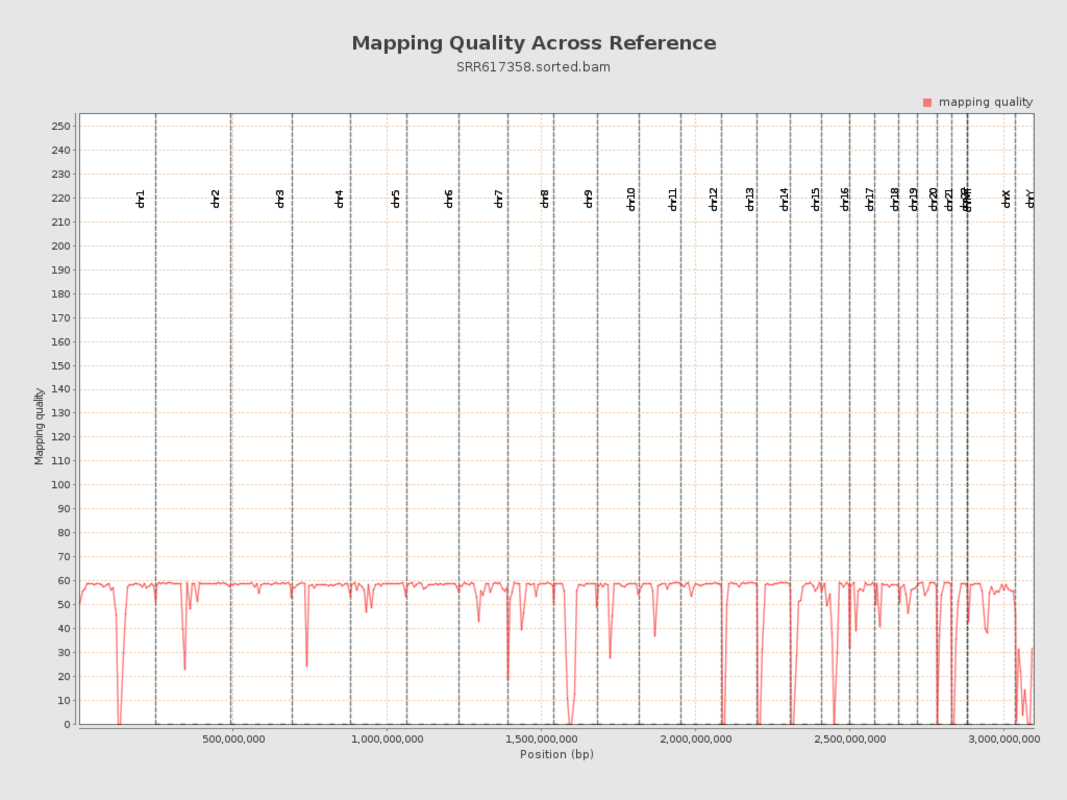
10. Results : Mapped Reads Clipping Profile



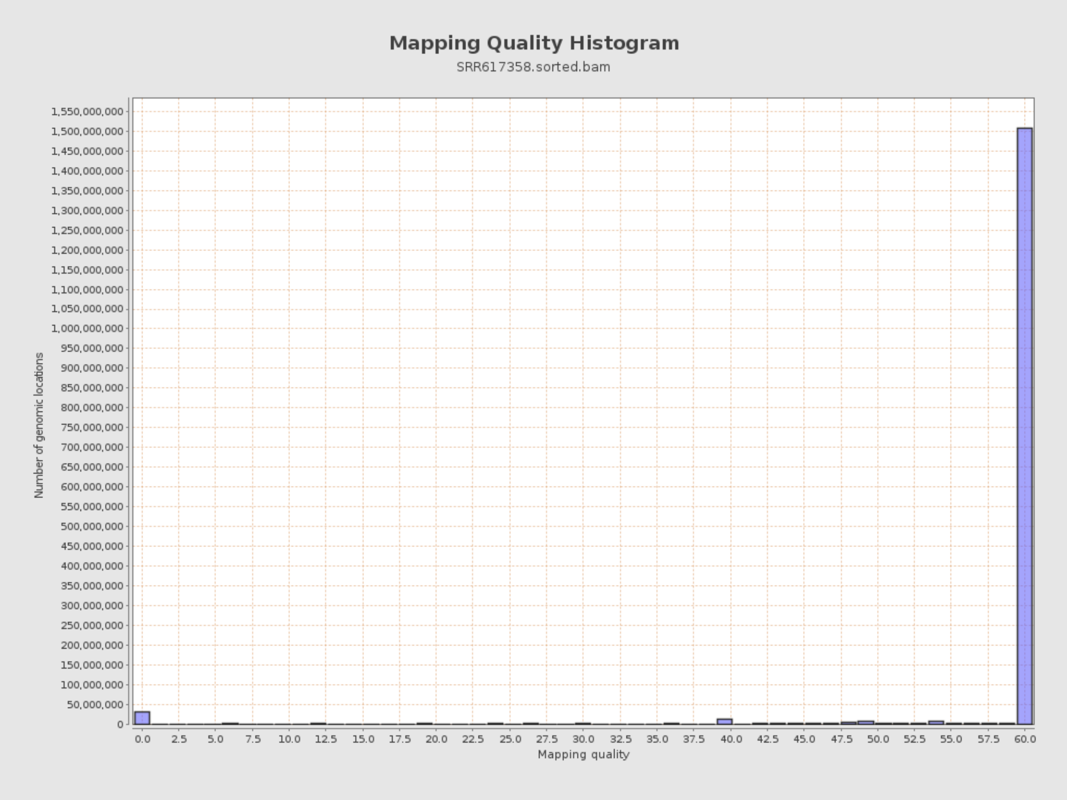
11. Results : Homopolymer Indels



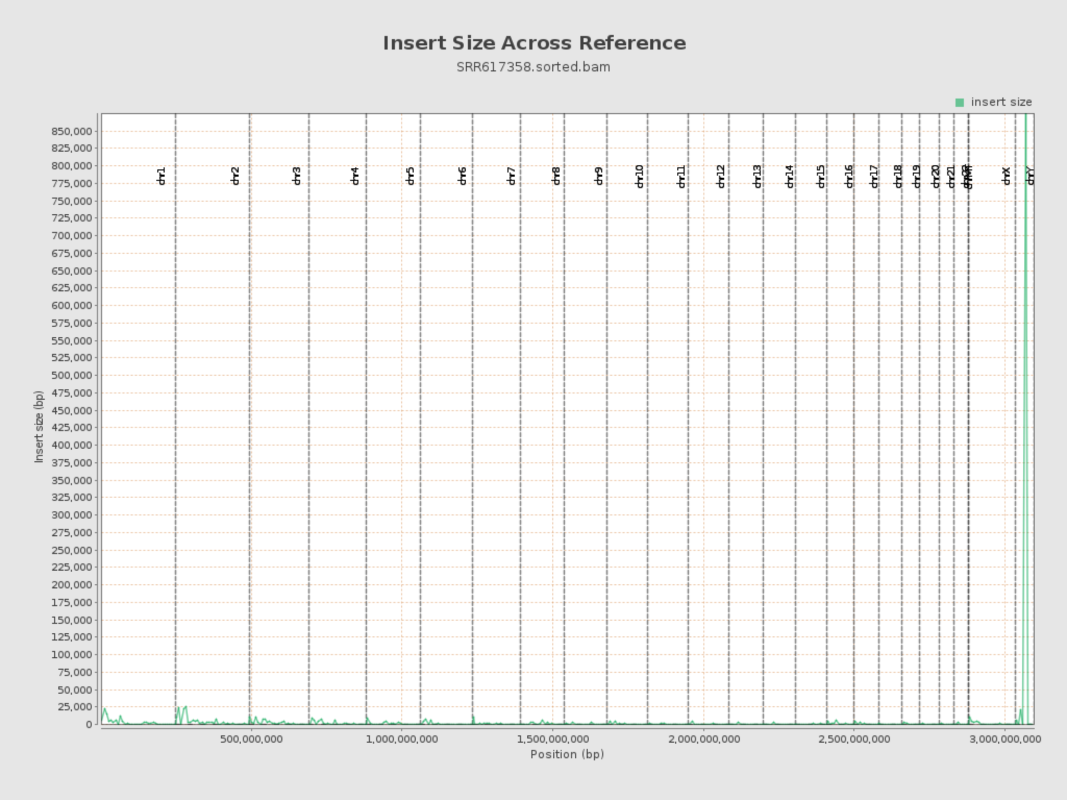
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram