Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/07 04:15:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617359.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_SRR617359 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617359_1.fastq.gz SRR617359_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Oct 07 04:15:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617359.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	27,730,009 / 86.66%
Unmapped reads	4,269,991 / 13.34%
Mapped paired reads	27,730,009 / 86.66%
Mapped reads, first in pair	14,390,366 / 44.97%
Mapped reads, second in pair	13,339,643 / 41.69%
Mapped reads, both in pair	26,318,536 / 82.25%
Mapped reads, singletons	1,411,473 / 4.41%
Secondary alignments	0
Supplementary alignments	60,720 / 0.19%
Read min/max/mean length	30 / 100 / 100.08
Duplicated reads (estimated)	1,342,328 / 4.19%
Duplication rate	1.44%
Clipped reads	3,493,619 / 10.92%

2.2. ACGT Content

Number/percentage of A's	815,416,571 / 30.35%
Number/percentage of C's	533,398,425 / 19.85%
Number/percentage of T's	804,846,169 / 29.96%
Number/percentage of G's	532,173,801 / 19.81%
Number/percentage of N's	750,439 / 0.03%

GC Percentage	39.66%

2.3. Coverage

Mean	0.8681
Standard Deviation	8.4118

2.4. Mapping Quality

Mean Mapping Quality	53.08

2.5. Insert size

Mean	51,192.17
Standard Deviation	2,157,253.04
P25/Median/P75	168 / 208 / 269

2.6. Mismatches and indels

General error rate	1.77%
Mismatches	46,905,960
Insertions	274,988
Mapped reads with at least one insertion	0.96%
Deletions	325,912
Mapped reads with at least one deletion	1.14%
Homopolymer indels	40.51%

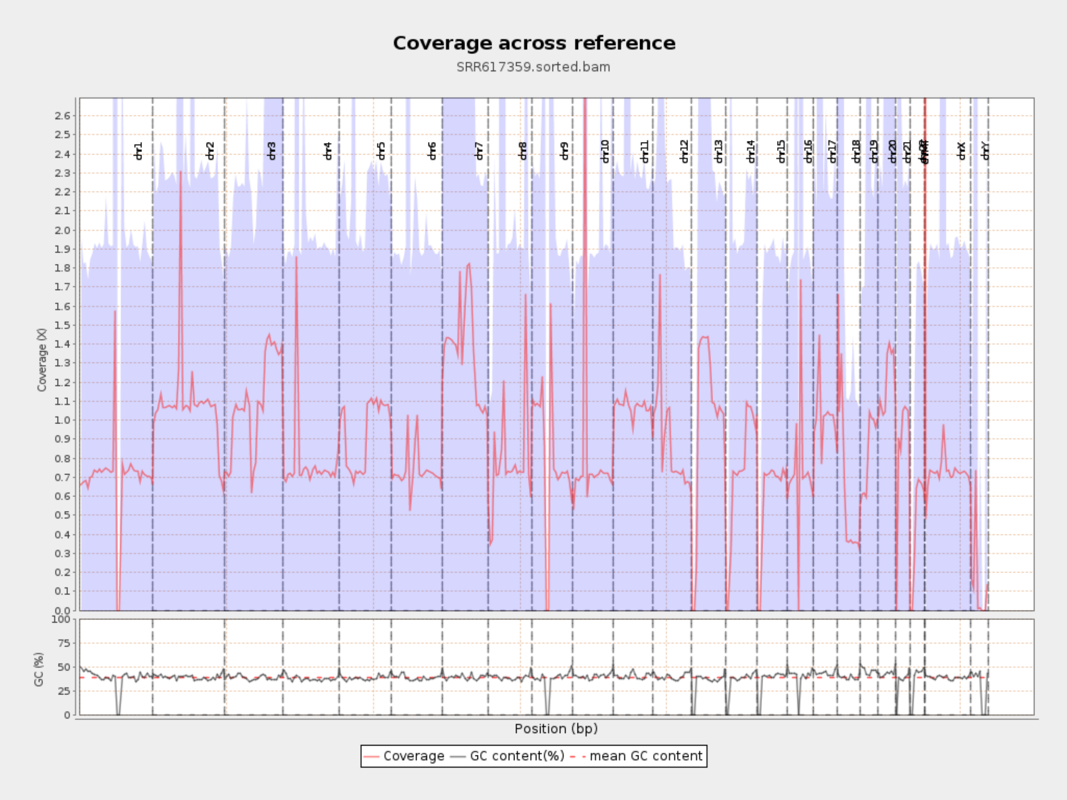
2.7. Chromosome stats

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

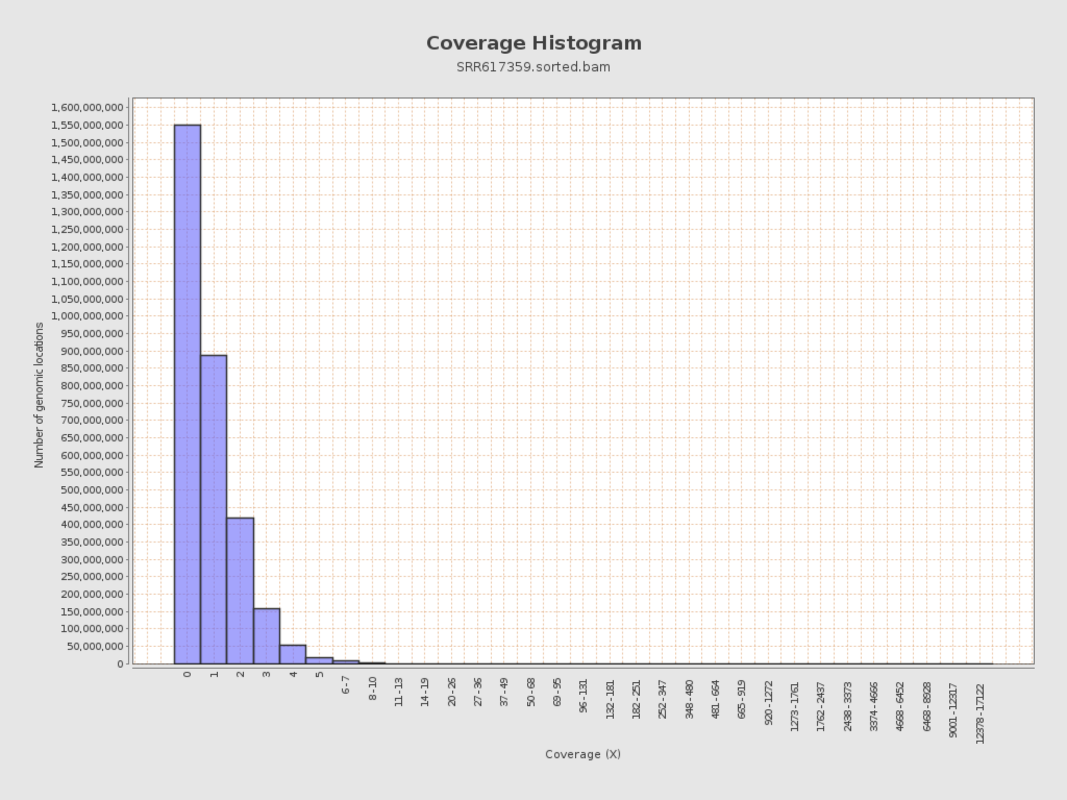
		bases	coverage	deviation
chr1	249250621	174521841	0.7002	17.4644
chr2	243199373	264962550	1.0895	7.4616
chr3	198022430	214937560	1.0854	1.4021
chr4	191154276	147529877	0.7718	7.4916
chr5	180915260	169659358	0.9378	1.355
chr6	171115067	126676206	0.7403	3.322
chr7	159138663	218705481	1.3743	9.7964
chr8	146364022	113303182	0.7741	6.3827
chr9	141213431	112853133	0.7992	12.0978
chr10	135534747	112491203	0.83	17.3659
chr11	135006516	144276545	1.0687	4.7294
chr12	133851895	118890042	0.8882	1.2698
chr13	115169878	117831817	1.0231	1.2209
chr14	107349540	77675355	0.7236	1.2861
chr15	102531392	60597980	0.591	0.9248
chr16	90354753	66977445	0.7413	7.2037
chr17	81195210	82584903	1.0171	6.1257
chr18	78077248	47996088	0.6147	12.795
chr19	59128983	49006117	0.8288	8.5732
chr20	63025520	76330447	1.2111	2.0935
chr21	48129895	42764025	0.8885	2.7469
chr22	51304566	23488141	0.4578	0.8469
chrMT	16571	1813964	109.4662	21.2872
chrX	155270560	112696524	0.7258	2.6407

chrY	59373566	8786138	0.148	6.7675

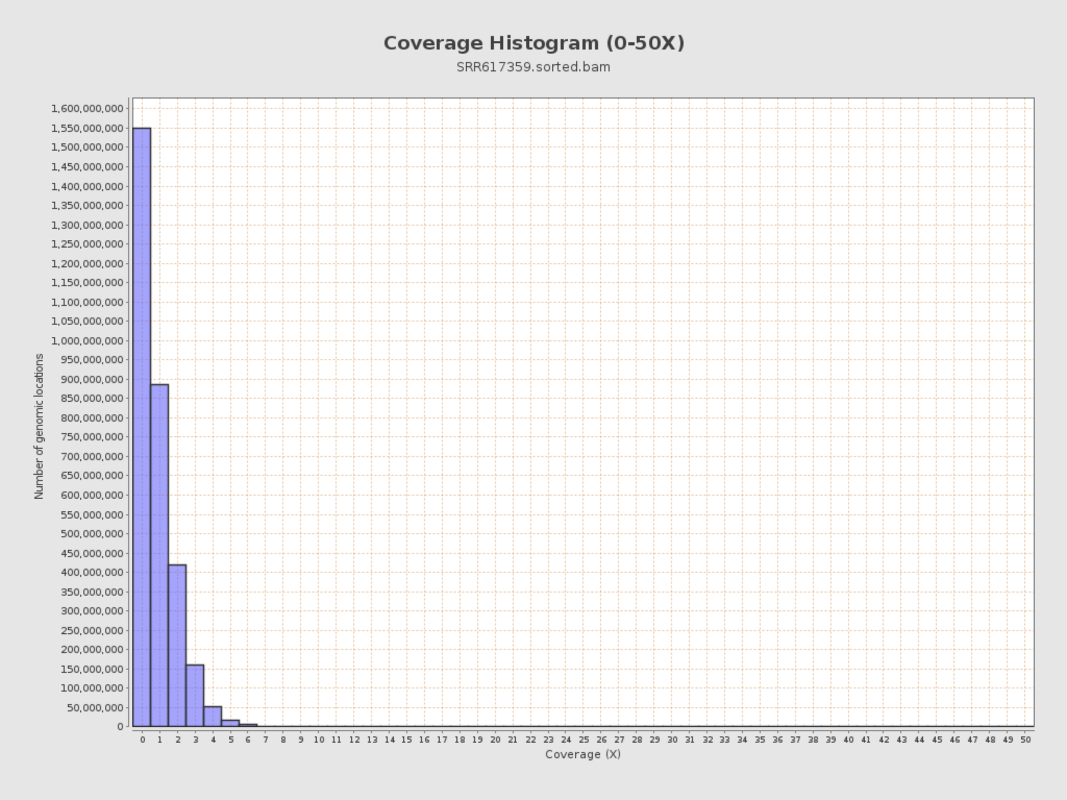
3. Results : Coverage across reference



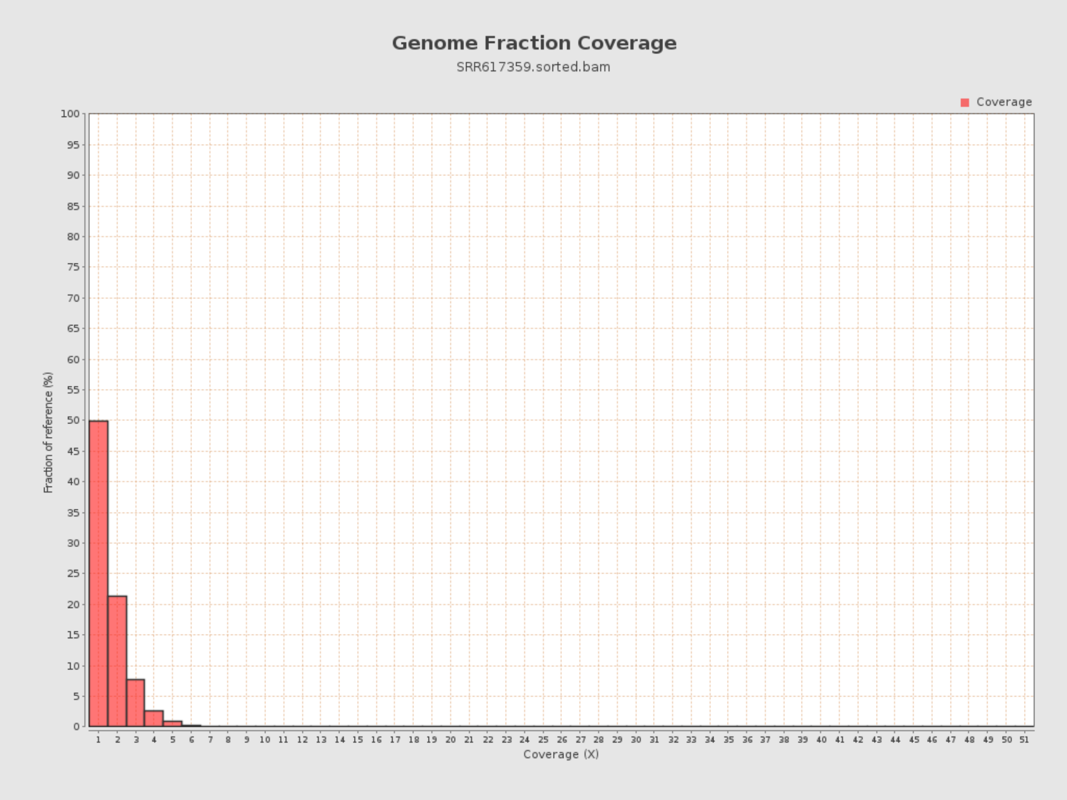
4. Results : Coverage Histogram



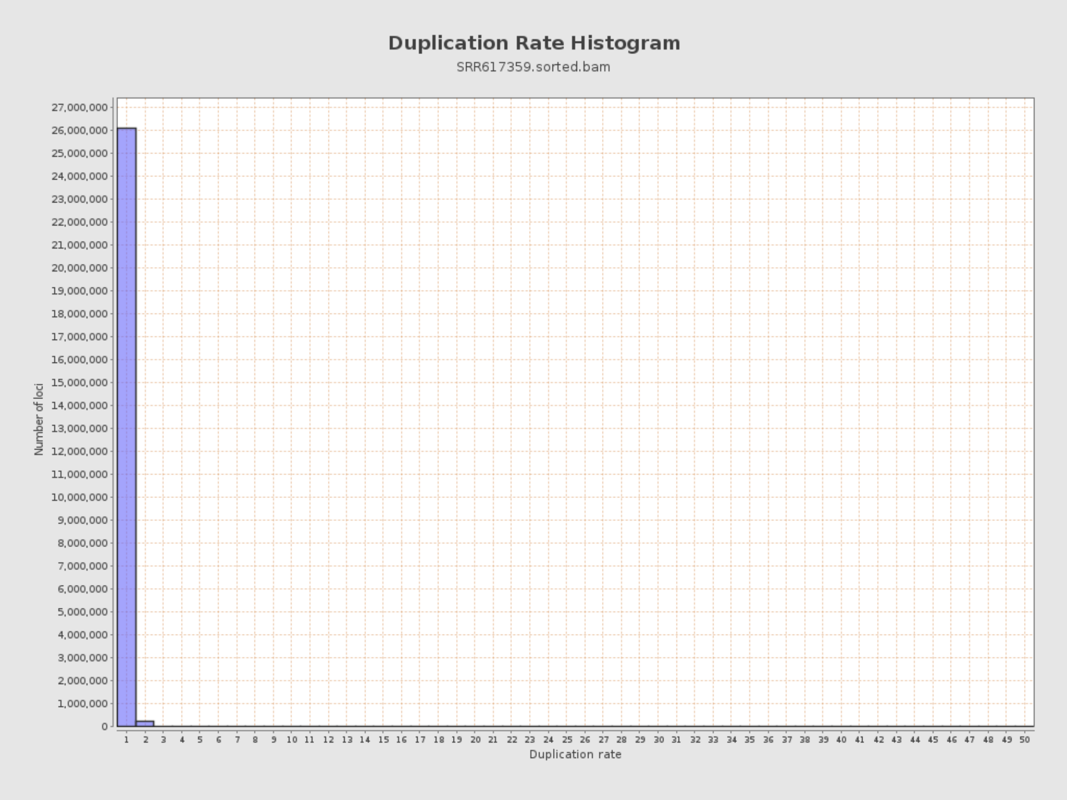
5. Results : Coverage Histogram (0-50X)



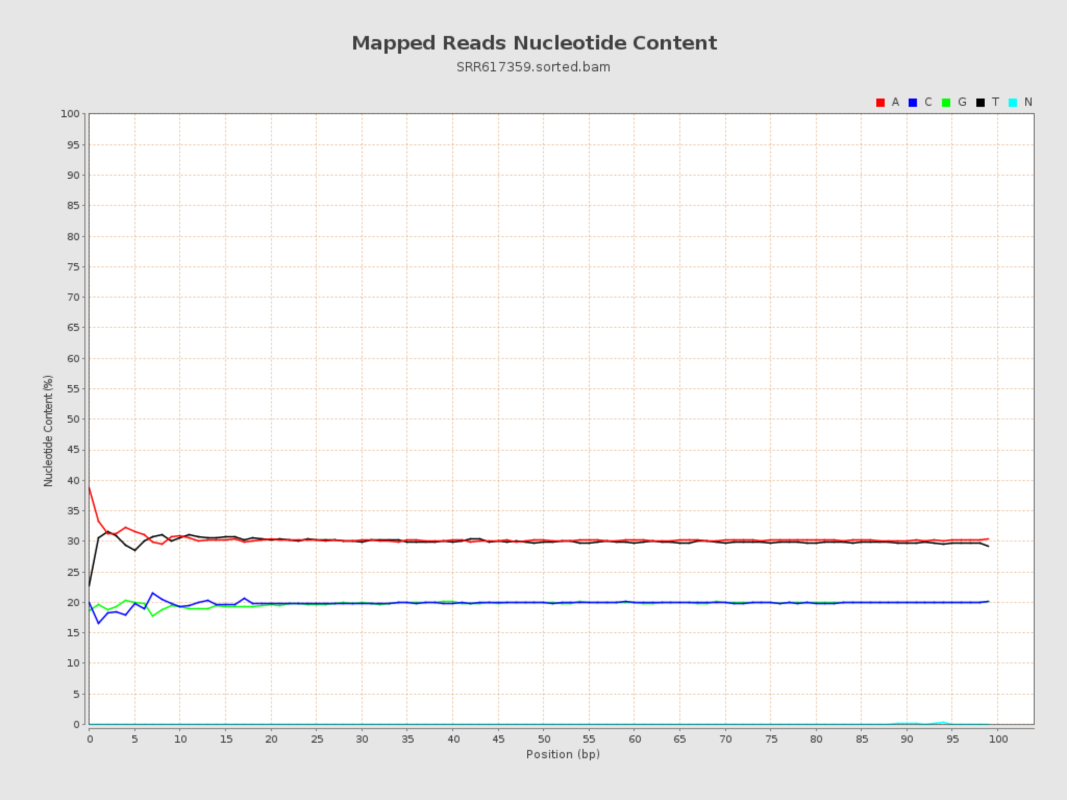
6. Results : Genome Fraction Coverage



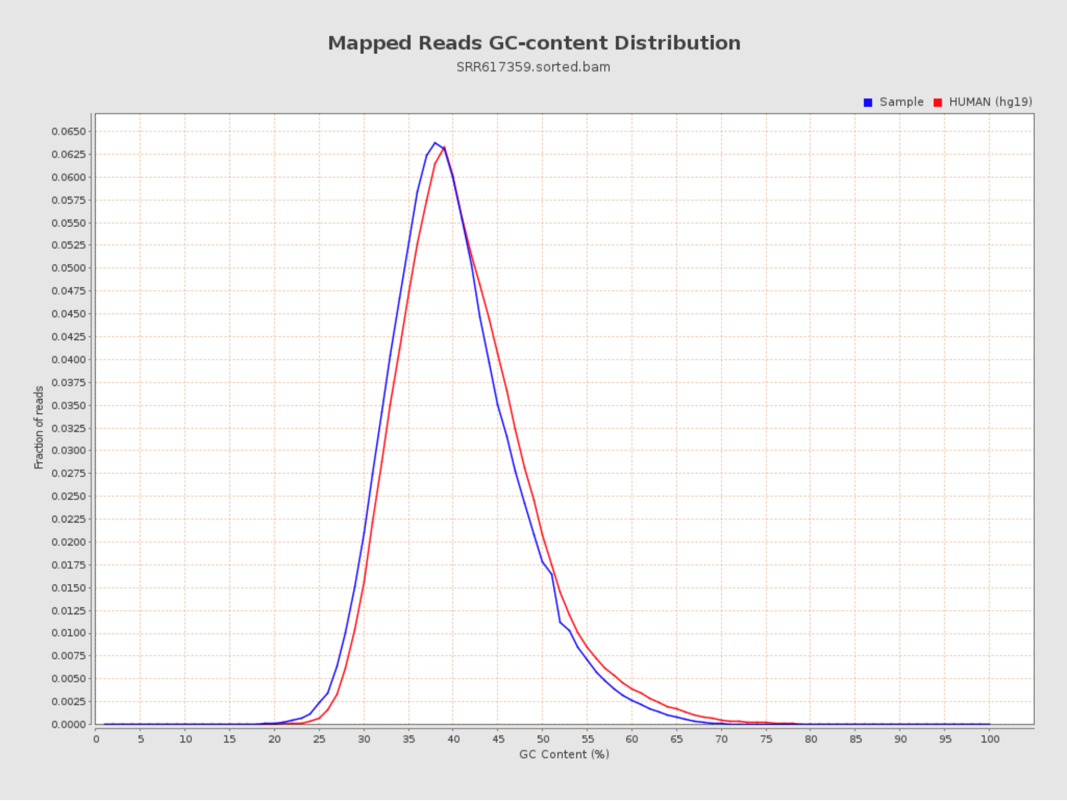
7. Results : Duplication Rate Histogram



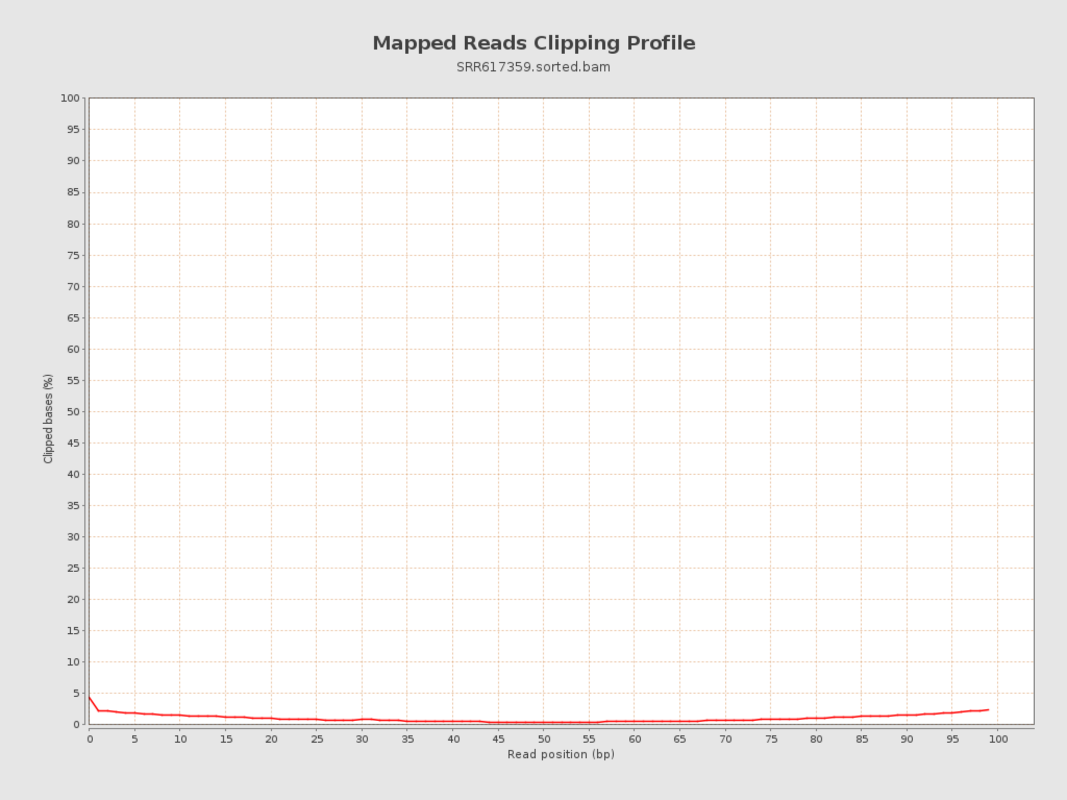
8. Results : Mapped Reads Nucleotide Content



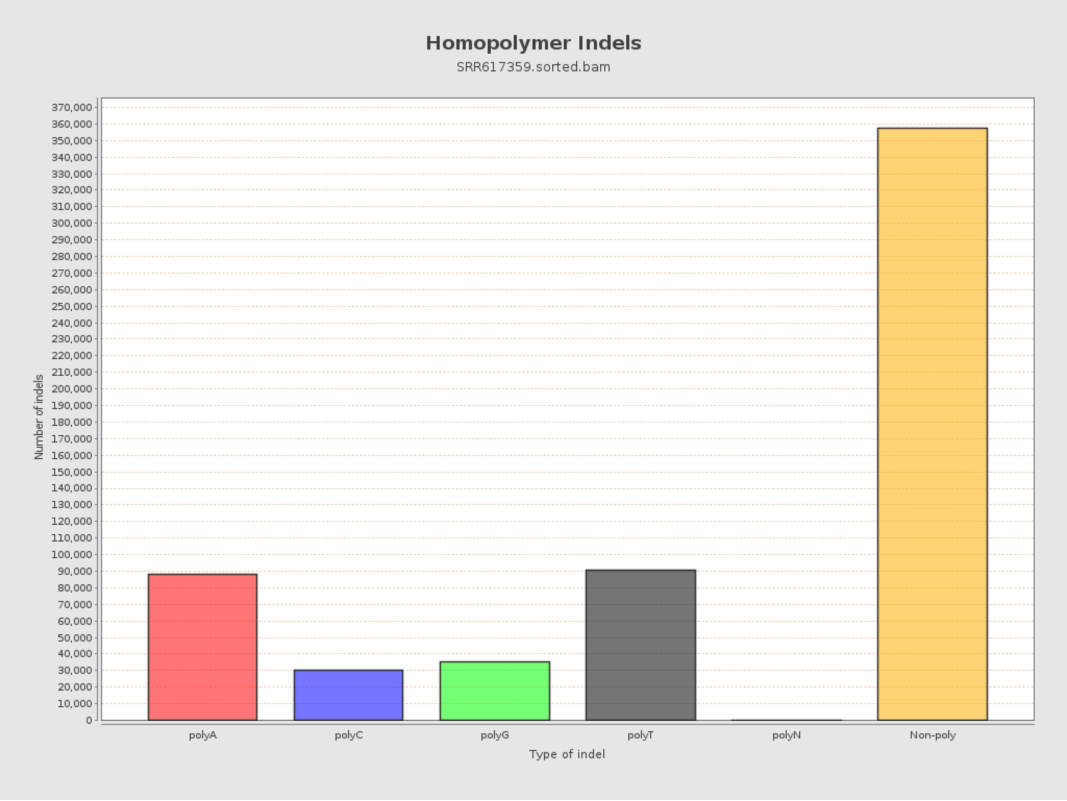
9. Results : Mapped Reads GC-content Distribution



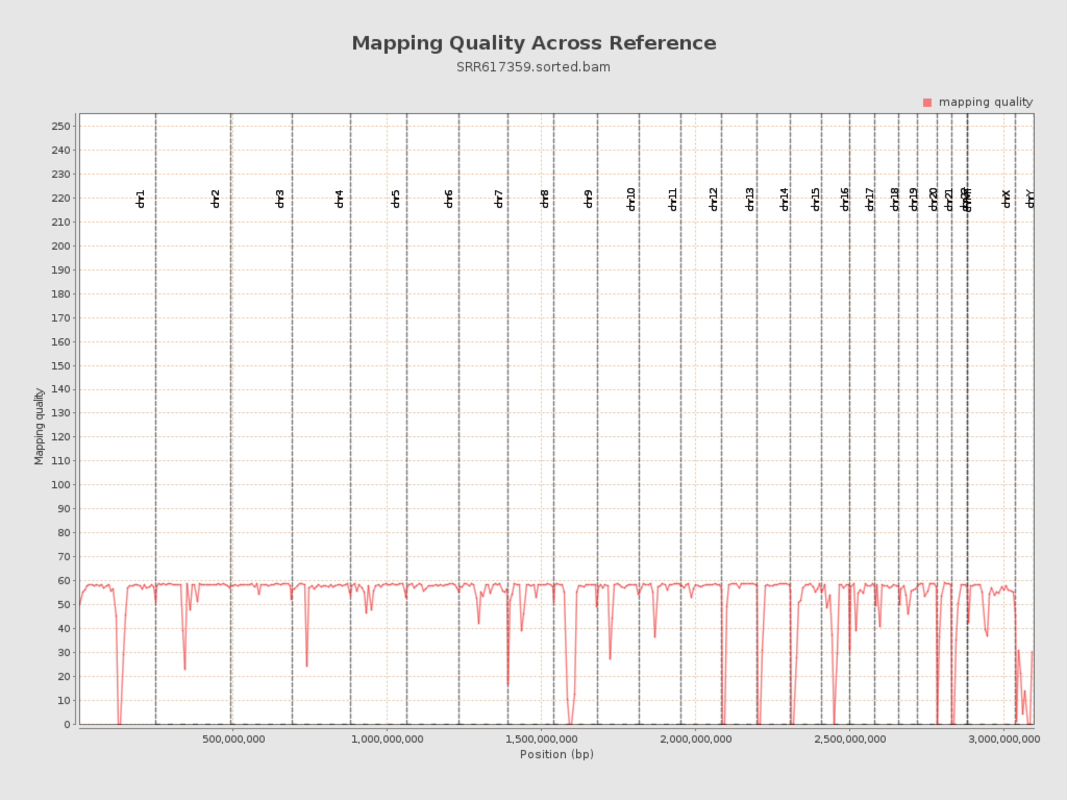
10. Results : Mapped Reads Clipping Profile



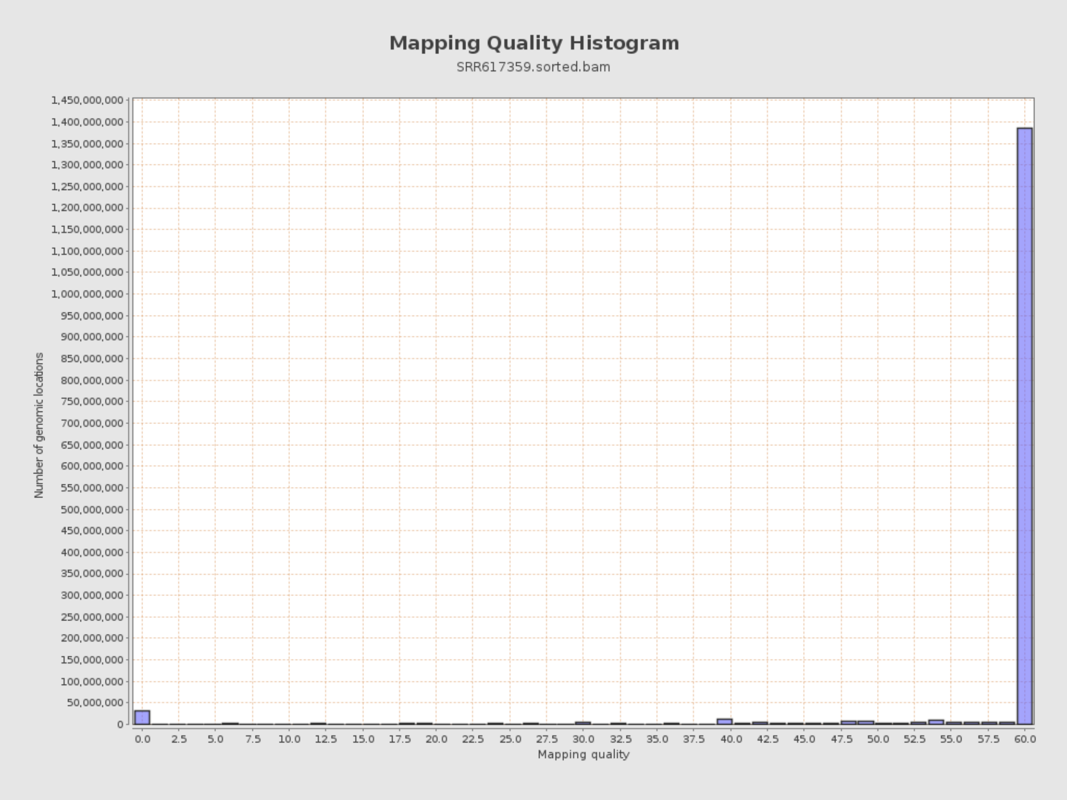
11. Results : Homopolymer Indels



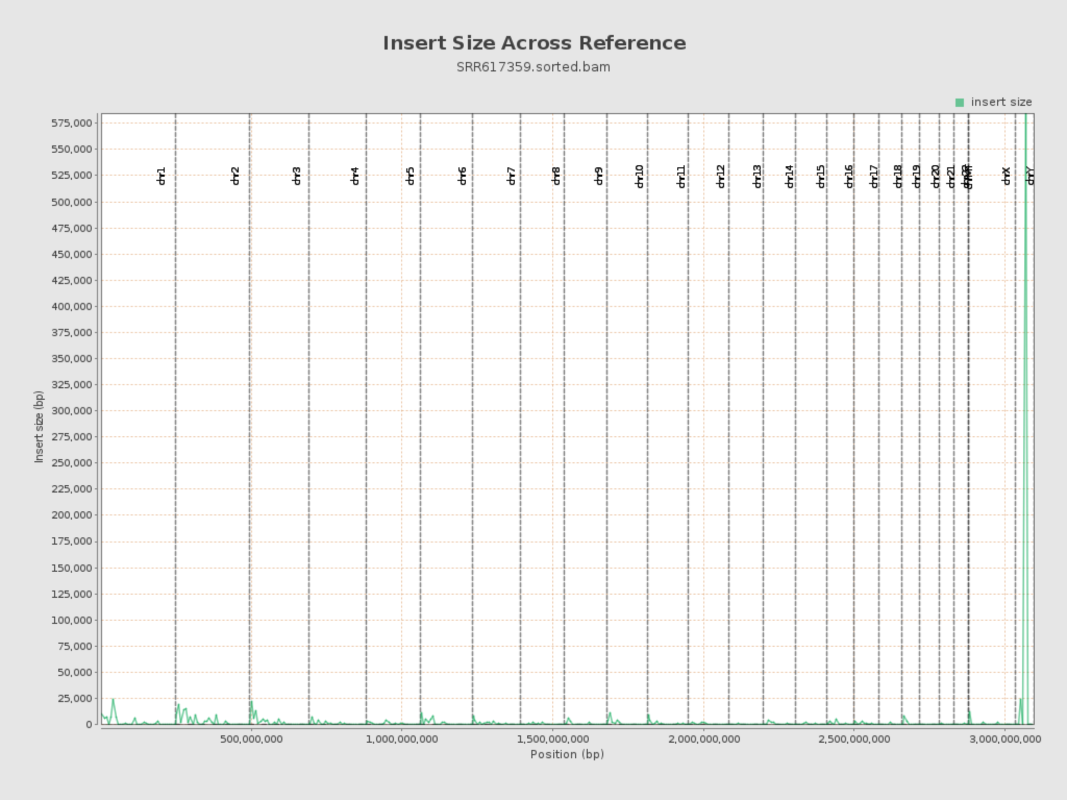
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram