Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/11 09:58:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617670.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_SRR617670 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617670_1.fastq.gz SRR617670_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Oct 11 09:58:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617670.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	29,536,755 / 92.3%
Unmapped reads	2,463,245 / 7.7%
Mapped paired reads	29,536,755 / 92.3%
Mapped reads, first in pair	14,979,571 / 46.81%
Mapped reads, second in pair	14,557,184 / 45.49%
Mapped reads, both in pair	28,682,340 / 89.63%
Mapped reads, singletons	854,415 / 2.67%
Secondary alignments	0
Supplementary alignments	167,602 / 0.52%
Read min/max/mean length	30 / 100 / 100.21
Duplicated reads (estimated)	6,649,257 / 20.78%
Duplication rate	10.53%
Clipped reads	6,707,427 / 20.96%

2.2. ACGT Content

Number/percentage of A's	848,891,870 / 29.82%
Number/percentage of C's	564,648,397 / 19.84%
Number/percentage of T's	846,779,777 / 29.75%
Number/percentage of G's	581,092,443 / 20.42%
Number/percentage of N's	4,878,362 / 0.17%

GC Percentage	40.25%

2.3. Coverage

Mean	0.92
Standard Deviation	10.2605

2.4. Mapping Quality

Mean Mapping Quality	52.46

2.5. Insert size

Mean	43,116.02
Standard Deviation	1,924,622.17
P25/Median/P75	178 / 220 / 285

2.6. Mismatches and indels

General error rate	1.66%
Mismatches	46,420,590
Insertions	444,720
Mapped reads with at least one insertion	1.48%
Deletions	1,035,923
Mapped reads with at least one deletion	3.43%
Homopolymer indels	47.54%

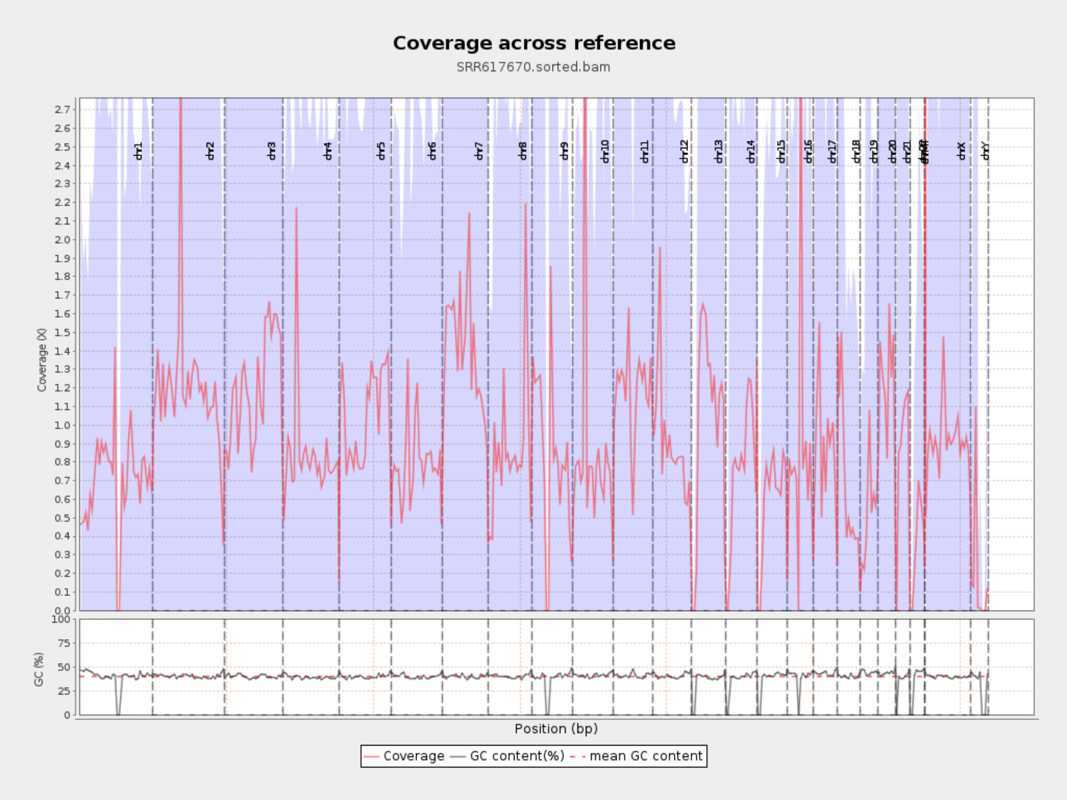
2.7. Chromosome stats

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

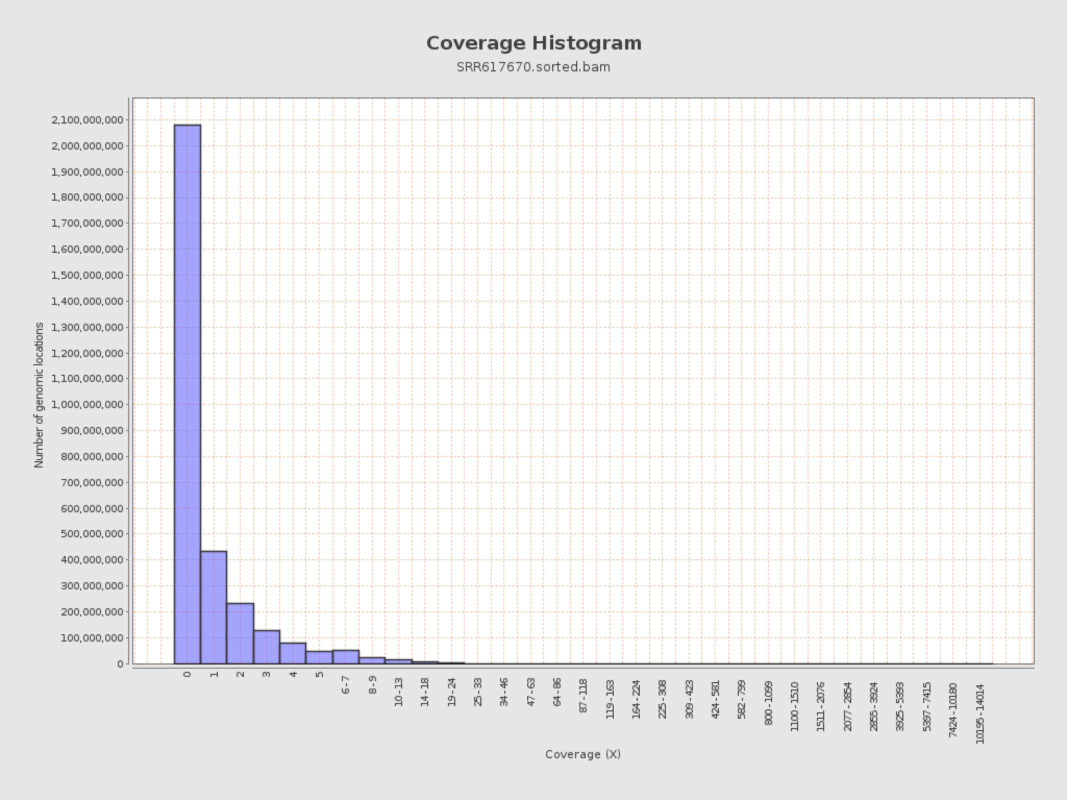
		bases	coverage	deviation
chr1	249250621	174405908	0.6997	9.9776
chr2	243199373	294469086	1.2108	11.6896
chr3	198022430	239008097	1.207	2.4446
chr4	191154276	159692672	0.8354	7.9747
chr5	180915260	188494543	1.0419	2.2815
chr6	171115067	138213618	0.8077	5.6203
chr7	159138663	223157574	1.4023	13.1665
chr8	146364022	126652016	0.8653	4.024
chr9	141213431	116626732	0.8259	19.558
chr10	135534747	120416202	0.8885	20.9539
chr11	135006516	156249492	1.1573	11.5336
chr12	133851895	121581919	0.9083	2.2356
chr13	115169878	122495551	1.0636	2.2832
chr14	107349540	81416623	0.7584	2.4481
chr15	102531392	61003617	0.595	1.7599
chr16	90354753	79099916	0.8754	16.463
chr17	81195210	69631714	0.8576	12.302
chr18	78077248	52581986	0.6735	17.7013
chr19	59128983	30016405	0.5076	5.7978
chr20	63025520	76616858	1.2156	2.9594
chr21	48129895	41561078	0.8635	4.1555
chr22	51304566	18238834	0.3555	1.268
chrMT	16571	3015757	181.99	127.8366
chrX	155270560	141939750	0.9141	4.2449

chrY	59373566	11414593	0.1923	16.4212

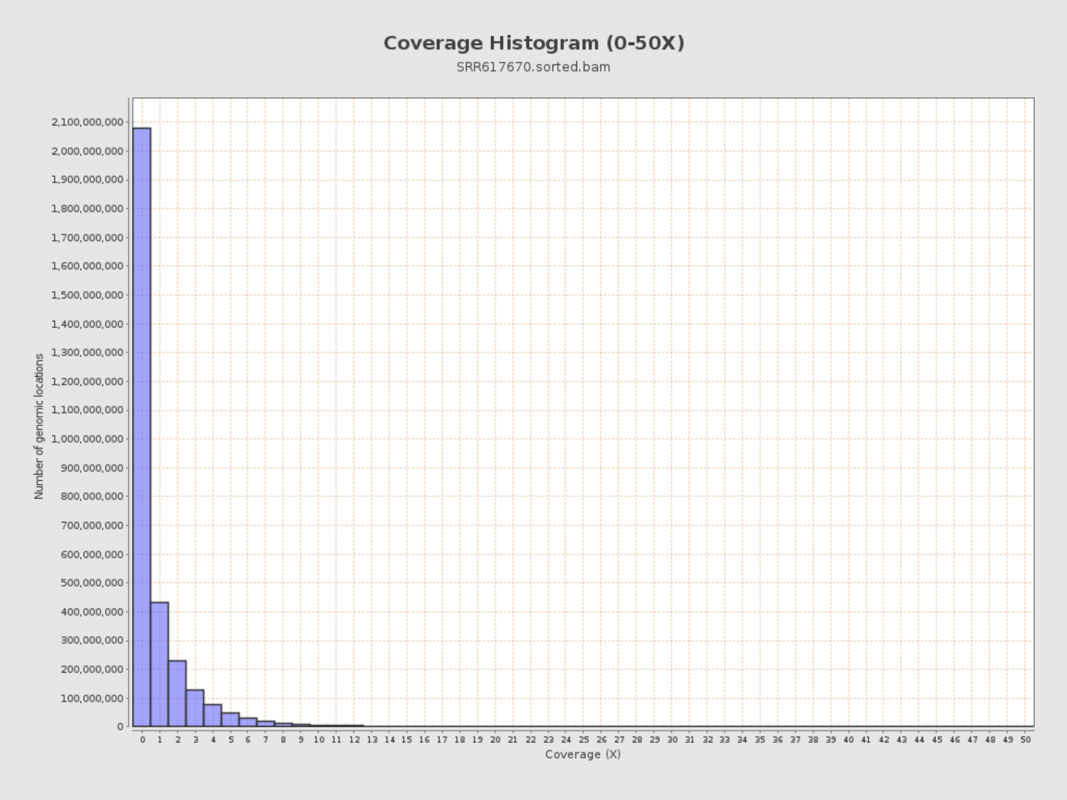
3. Results : Coverage across reference



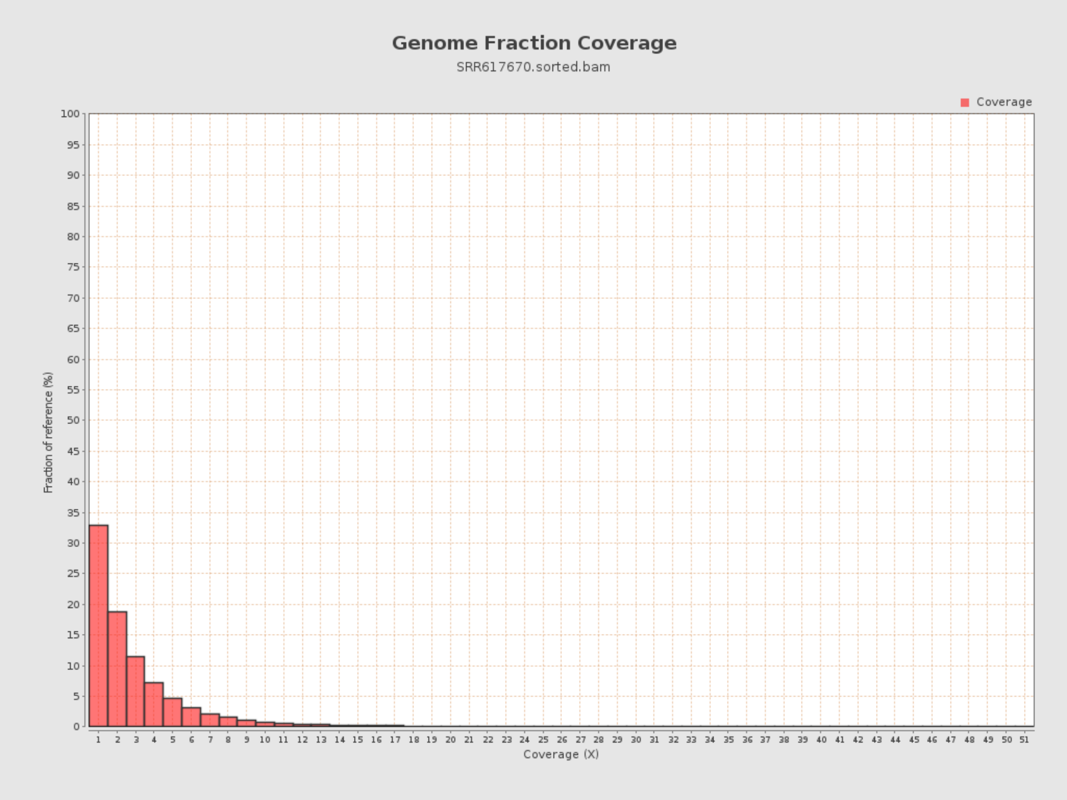
4. Results : Coverage Histogram



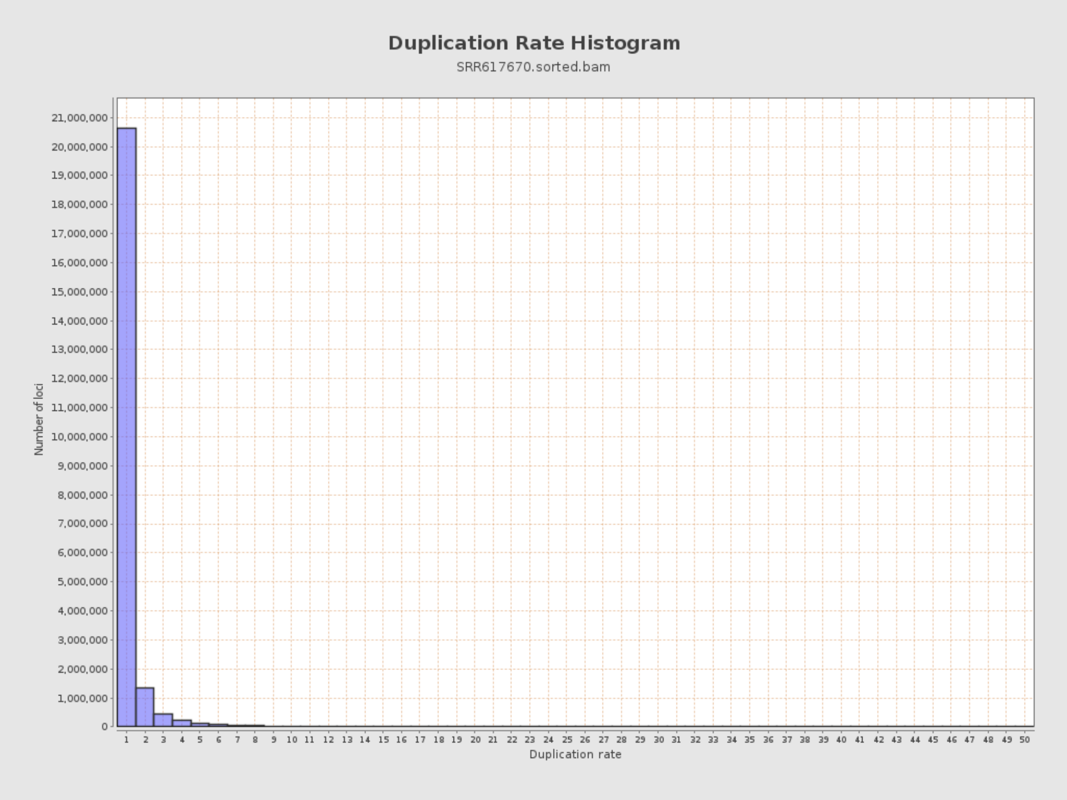
5. Results : Coverage Histogram (0-50X)



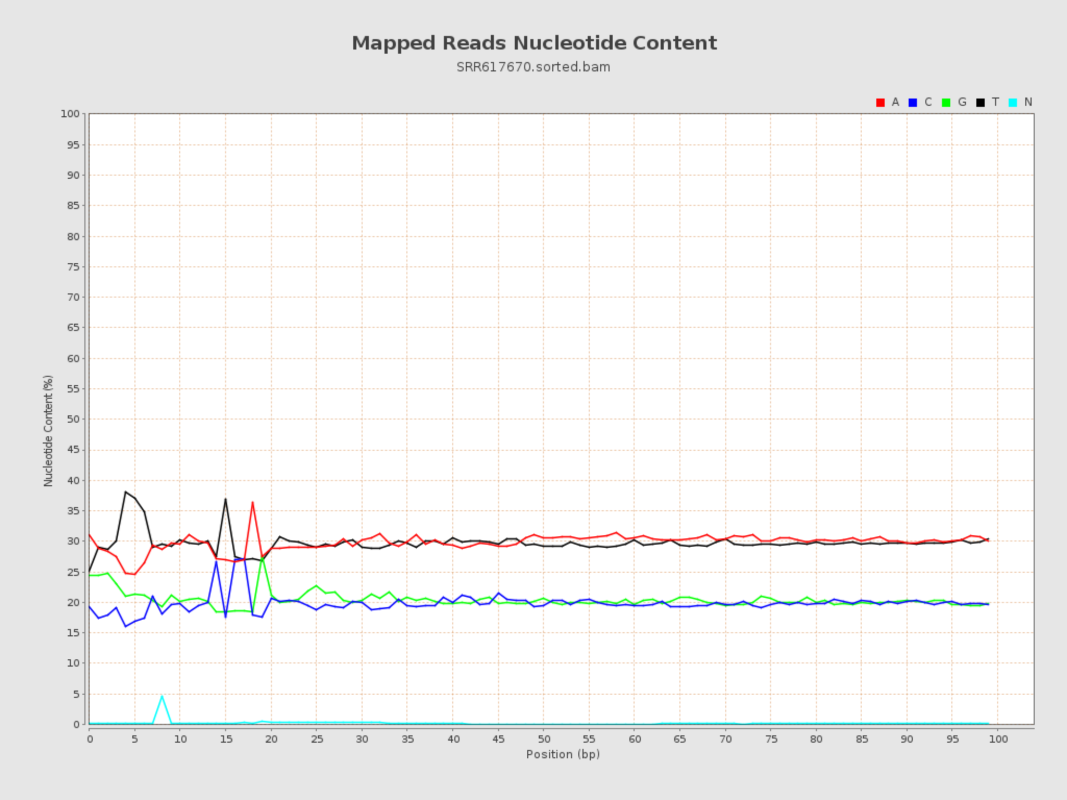
6. Results : Genome Fraction Coverage



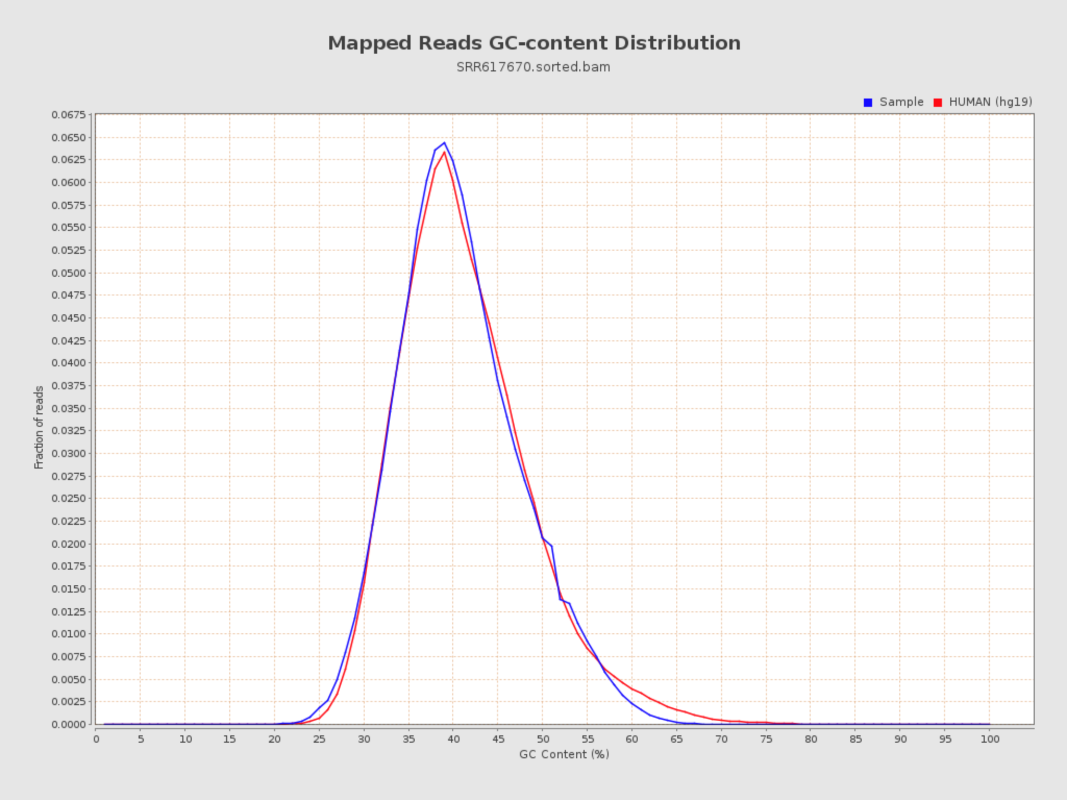
7. Results : Duplication Rate Histogram



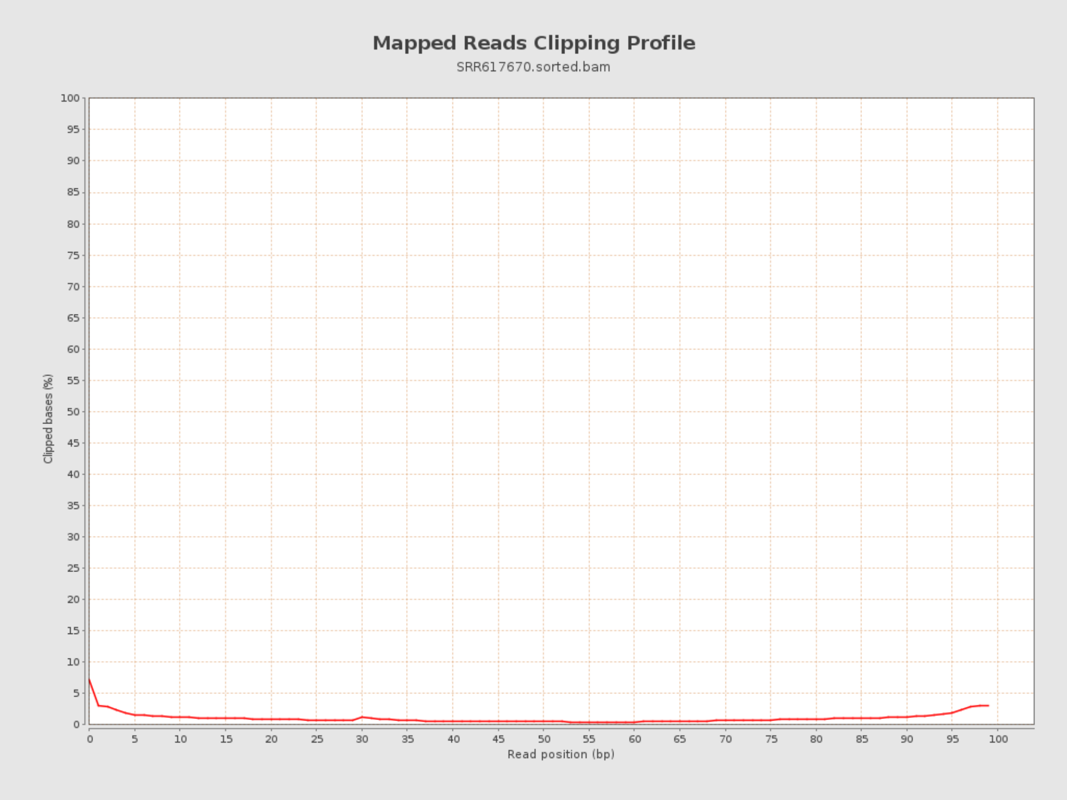
8. Results : Mapped Reads Nucleotide Content



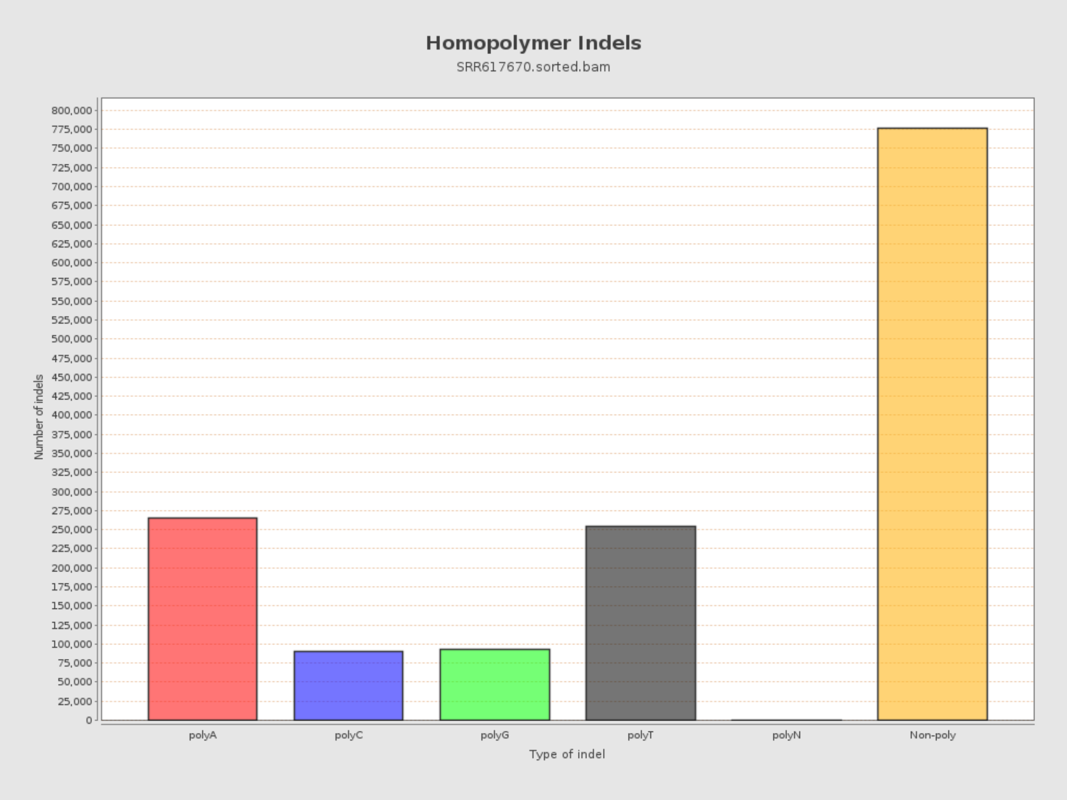
9. Results : Mapped Reads GC-content Distribution



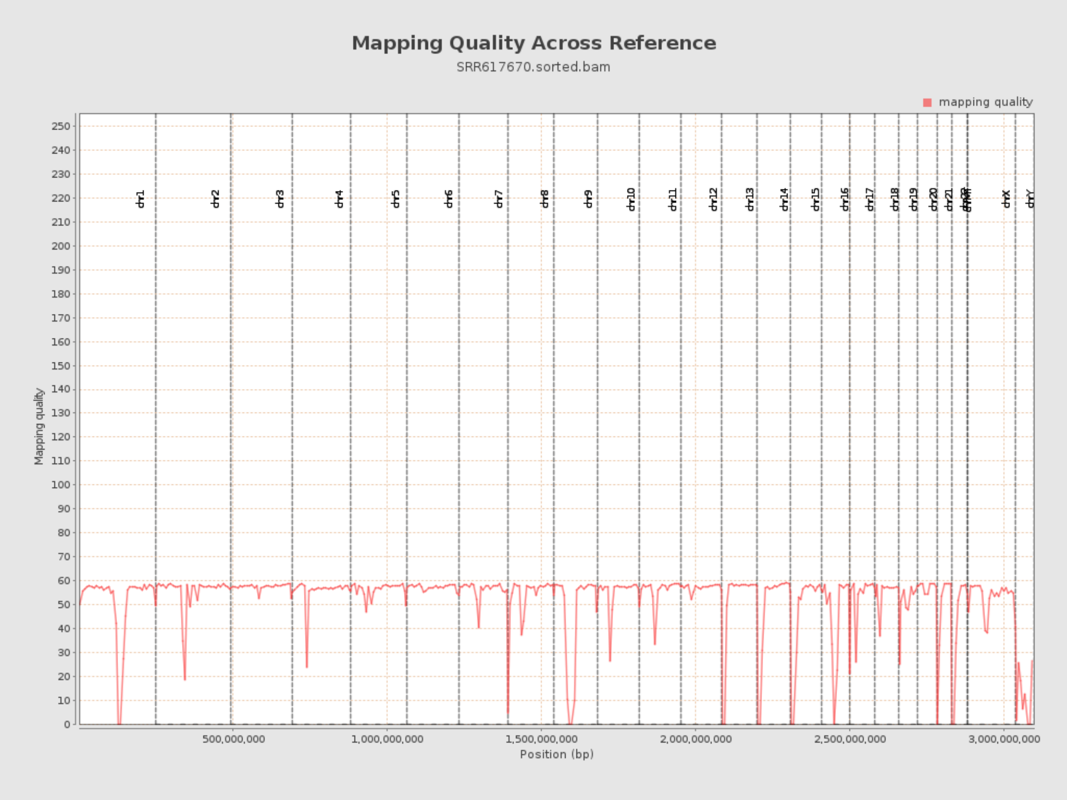
10. Results : Mapped Reads Clipping Profile



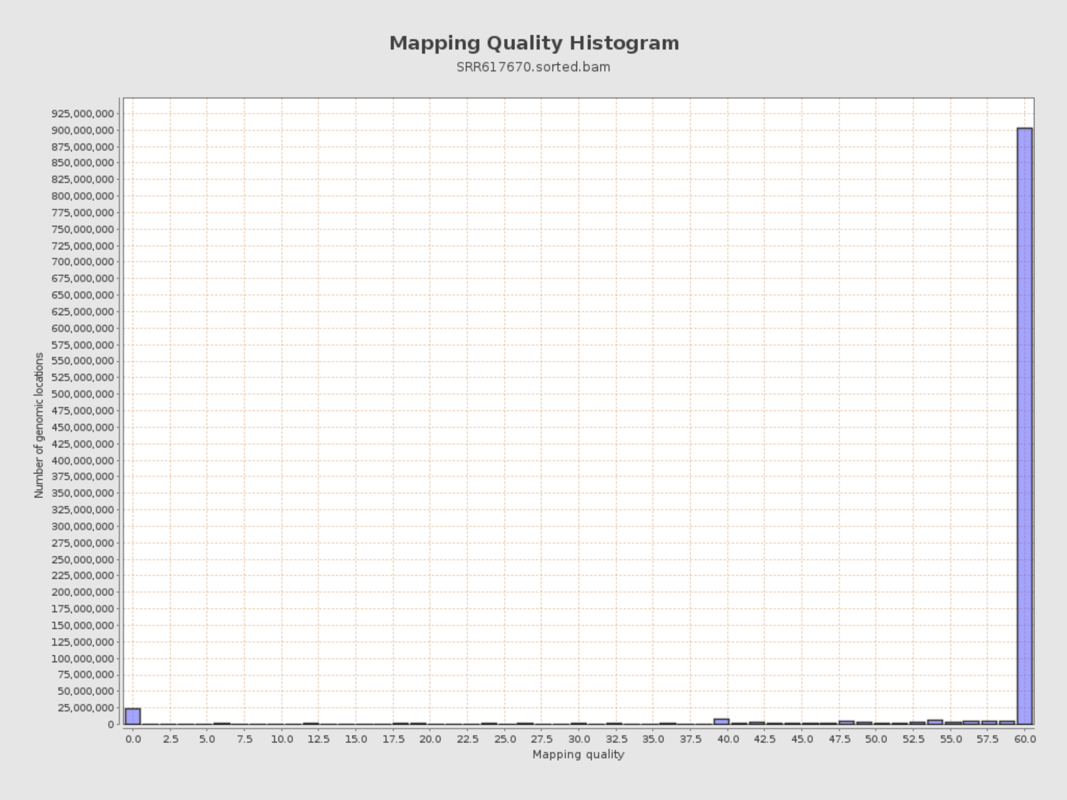
11. Results : Homopolymer Indels



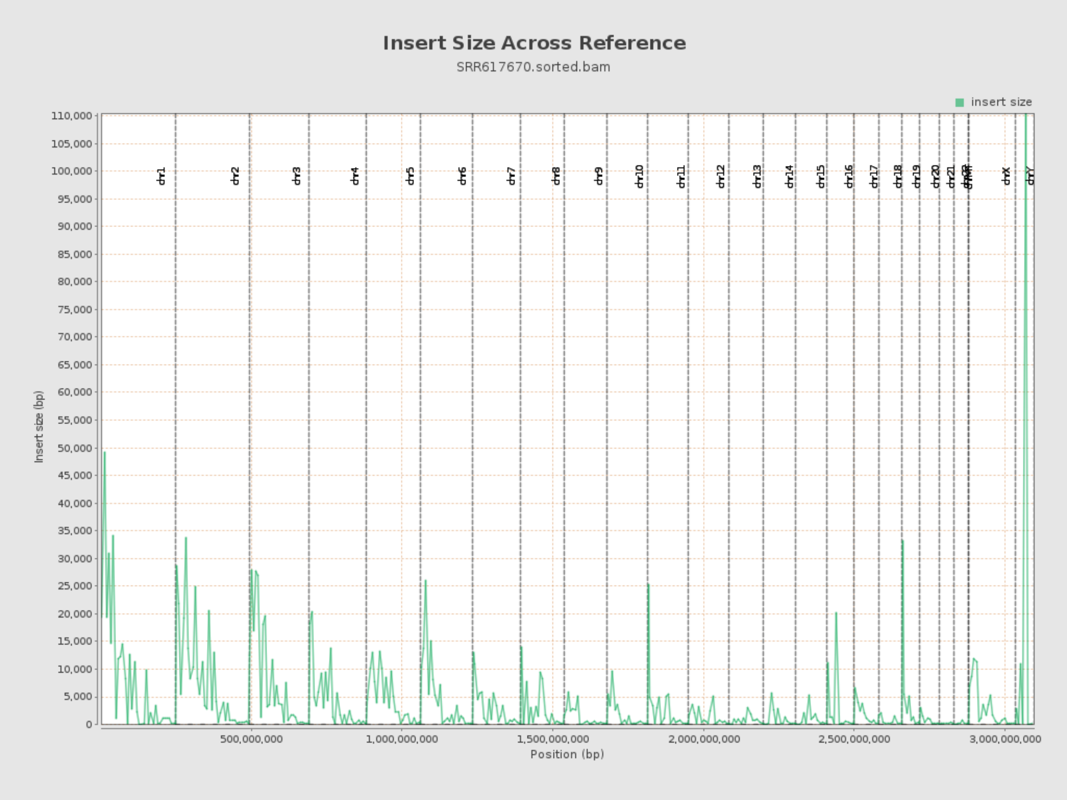
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram