Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/10 22:16:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617655.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_SRR617655 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617655_1.fastq.gz SRR617655_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 22:16:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617655.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	29,599,207 / 92.5%
Unmapped reads	2,400,793 / 7.5%
Mapped paired reads	29,599,207 / 92.5%
Mapped reads, first in pair	14,989,383 / 46.84%
Mapped reads, second in pair	14,609,824 / 45.66%
Mapped reads, both in pair	28,783,088 / 89.95%
Mapped reads, singletons	816,119 / 2.55%
Secondary alignments	0
Supplementary alignments	169,915 / 0.53%
Read min/max/mean length	30 / 100 / 100.21
Duplicated reads (estimated)	6,659,310 / 20.81%
Duplication rate	10.54%
Clipped reads	6,809,582 / 21.28%

2.2. ACGT Content

Number/percentage of A's	849,523,247 / 29.81%
Number/percentage of C's	565,575,380 / 19.85%
Number/percentage of T's	847,230,443 / 29.73%
Number/percentage of G's	582,979,598 / 20.46%
Number/percentage of N's	4,258,410 / 0.15%

GC Percentage	40.31%

2.3. Coverage

Mean	0.921
Standard Deviation	10.1778

2.4. Mapping Quality

Mean Mapping Quality	52.46

2.5. Insert size

Mean	47,575.37
Standard Deviation	2,051,282.44
P25/Median/P75	178 / 221 / 286

2.6. Mismatches and indels

General error rate	1.66%
Mismatches	46,471,543
Insertions	445,655
Mapped reads with at least one insertion	1.48%
Deletions	1,038,346
Mapped reads with at least one deletion	3.44%
Homopolymer indels	47.53%

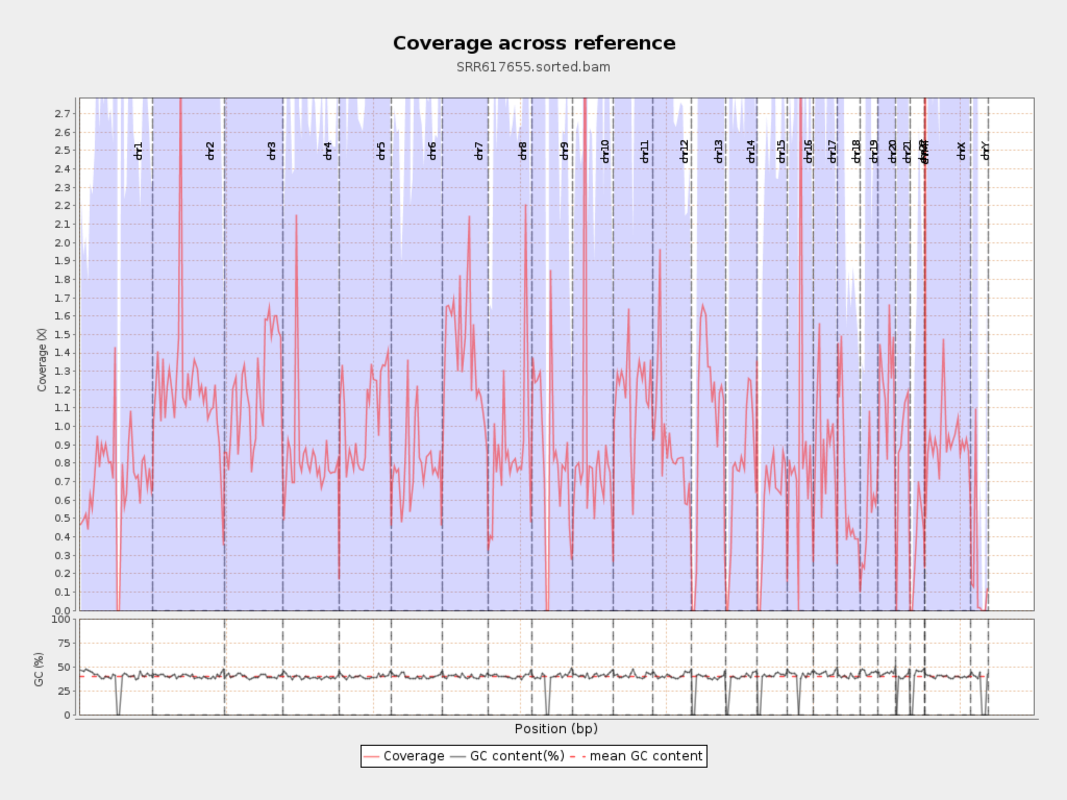
2.7. Chromosome stats

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

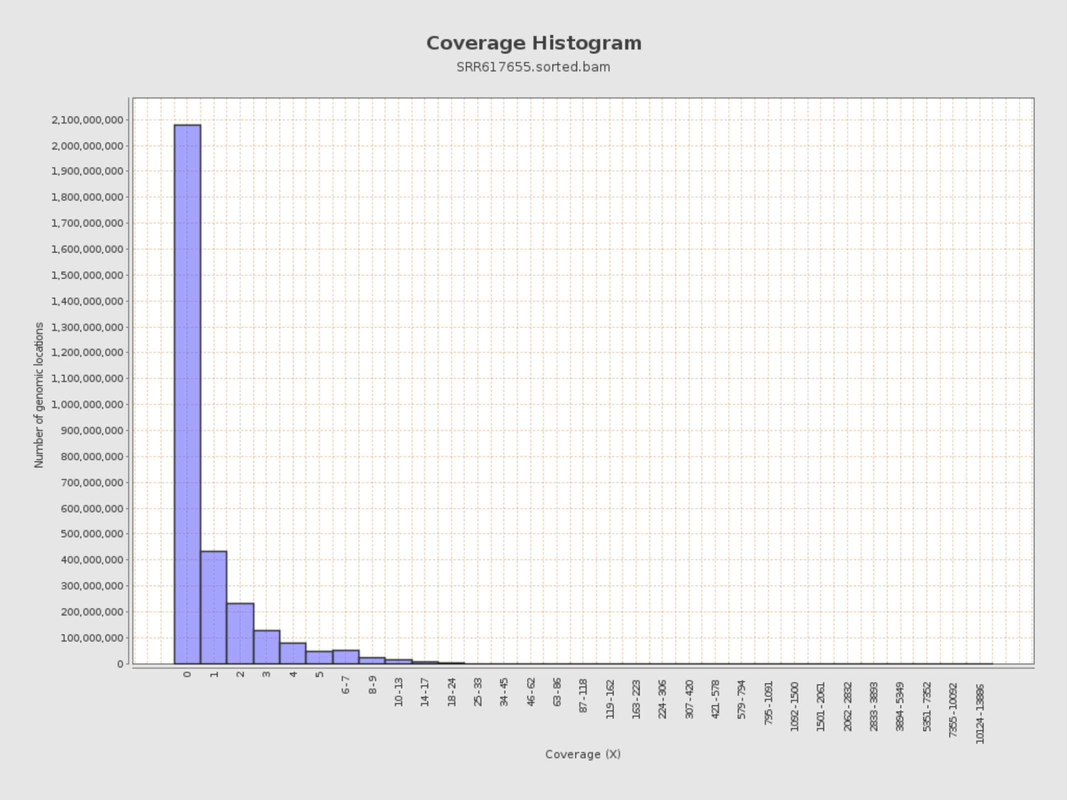
		bases	coverage	deviation
chr1	249250621	175002653	0.7021	9.9551
chr2	243199373	294771571	1.2121	11.7446
chr3	198022430	239173865	1.2078	2.4337
chr4	191154276	159329926	0.8335	7.8254
chr5	180915260	188698979	1.043	2.2913
chr6	171115067	138261761	0.808	5.7145
chr7	159138663	223278711	1.403	12.9867
chr8	146364022	126791114	0.8663	3.9594
chr9	141213431	116909021	0.8279	19.211
chr10	135534747	120632952	0.8901	20.7629
chr11	135006516	156943140	1.1625	11.6282
chr12	133851895	121734134	0.9095	2.1952
chr13	115169878	122777898	1.0661	2.2821
chr14	107349540	81393600	0.7582	2.4149
chr15	102531392	61025650	0.5952	1.7498
chr16	90354753	79193999	0.8765	16.3277
chr17	81195210	69938499	0.8614	12.1805
chr18	78077248	52400931	0.6711	17.4826
chr19	59128983	30204227	0.5108	5.8084
chr20	63025520	76745712	1.2177	2.9491
chr21	48129895	41527888	0.8628	4.1187
chr22	51304566	18163819	0.354	1.2451
chrMT	16571	3024644	182.5263	128.02
chrX	155270560	141969867	0.9143	4.2434

chrY	59373566	11386464	0.1918	16.2366

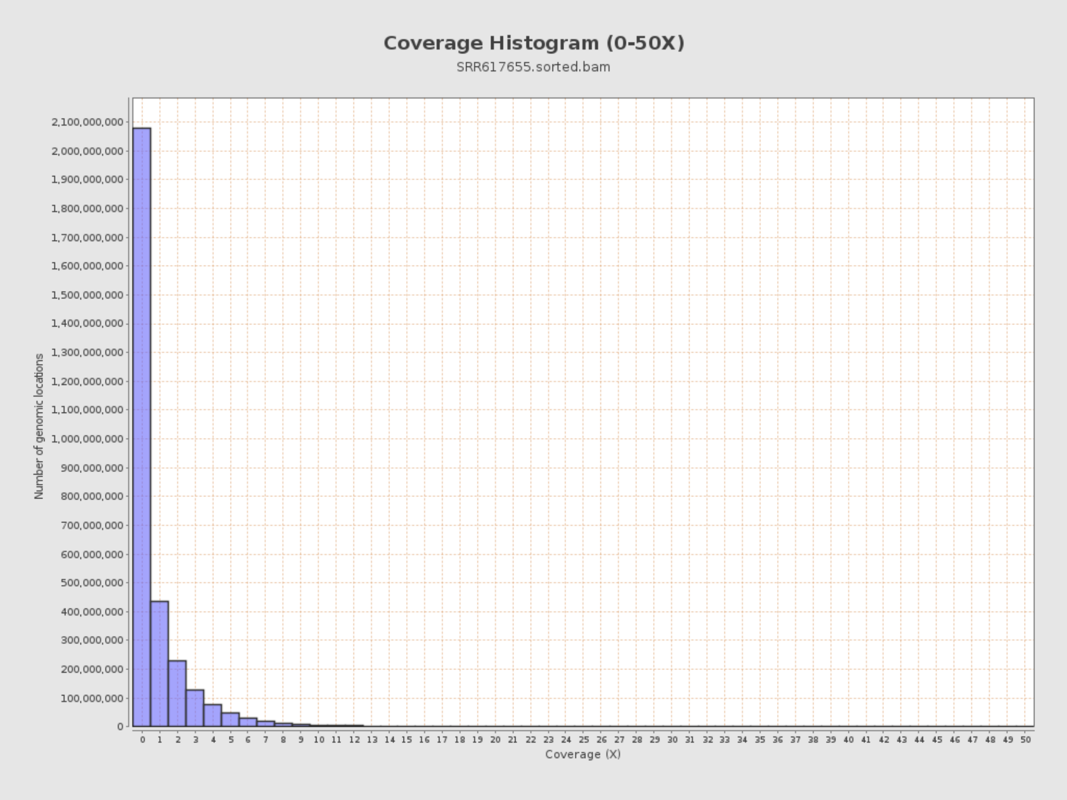
3. Results : Coverage across reference



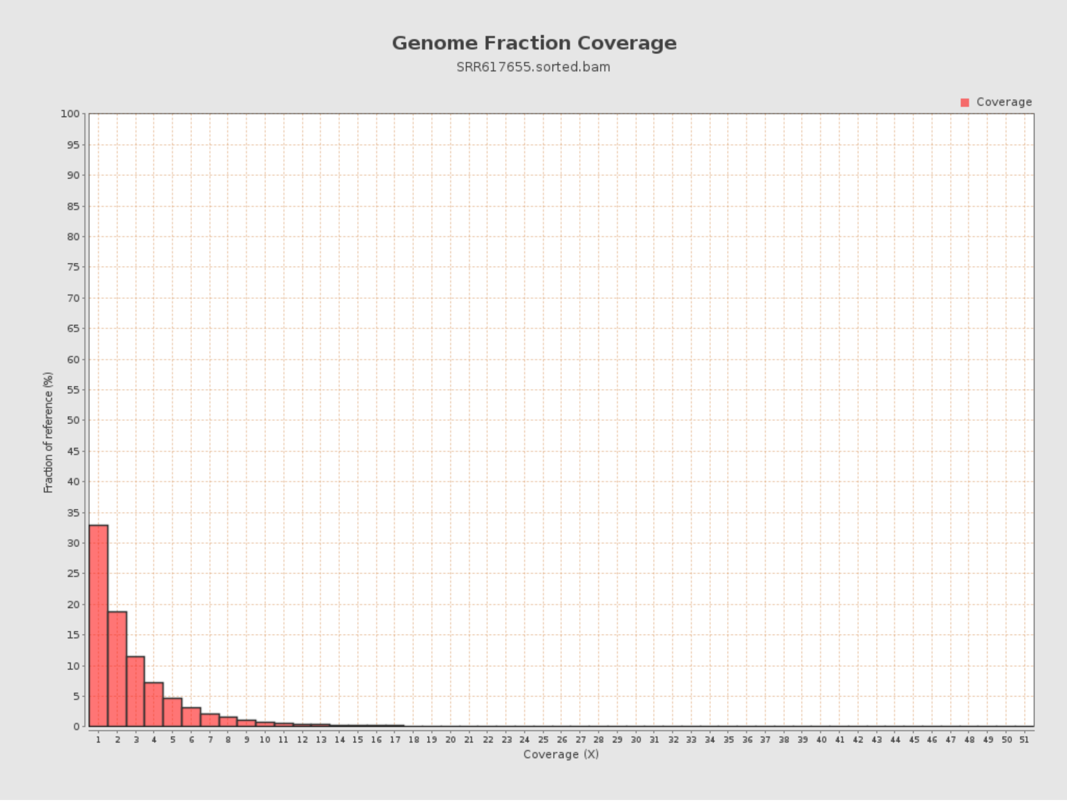
4. Results : Coverage Histogram



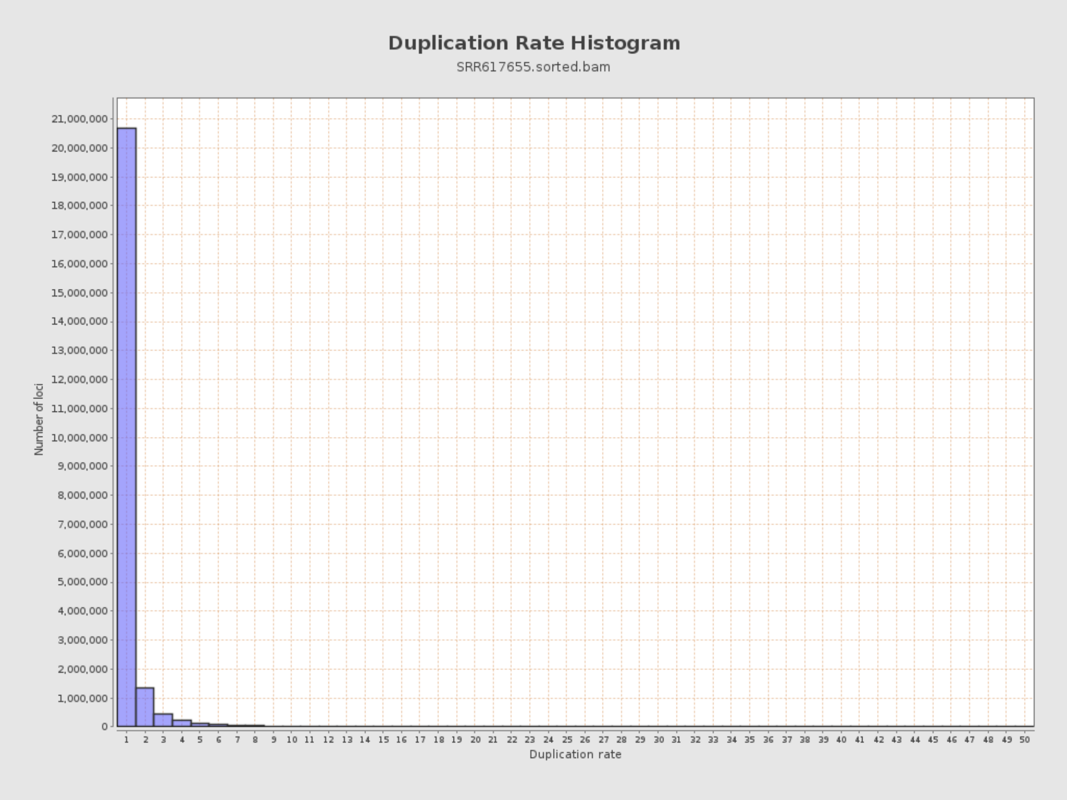
5. Results : Coverage Histogram (0-50X)



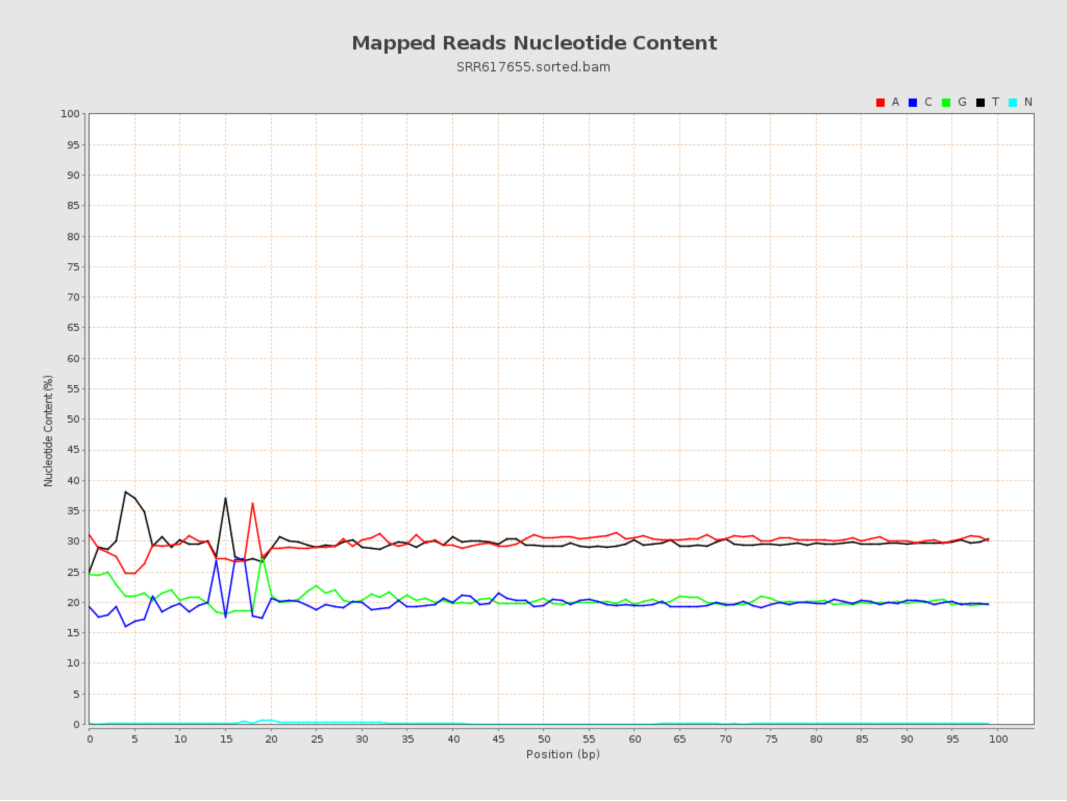
6. Results : Genome Fraction Coverage



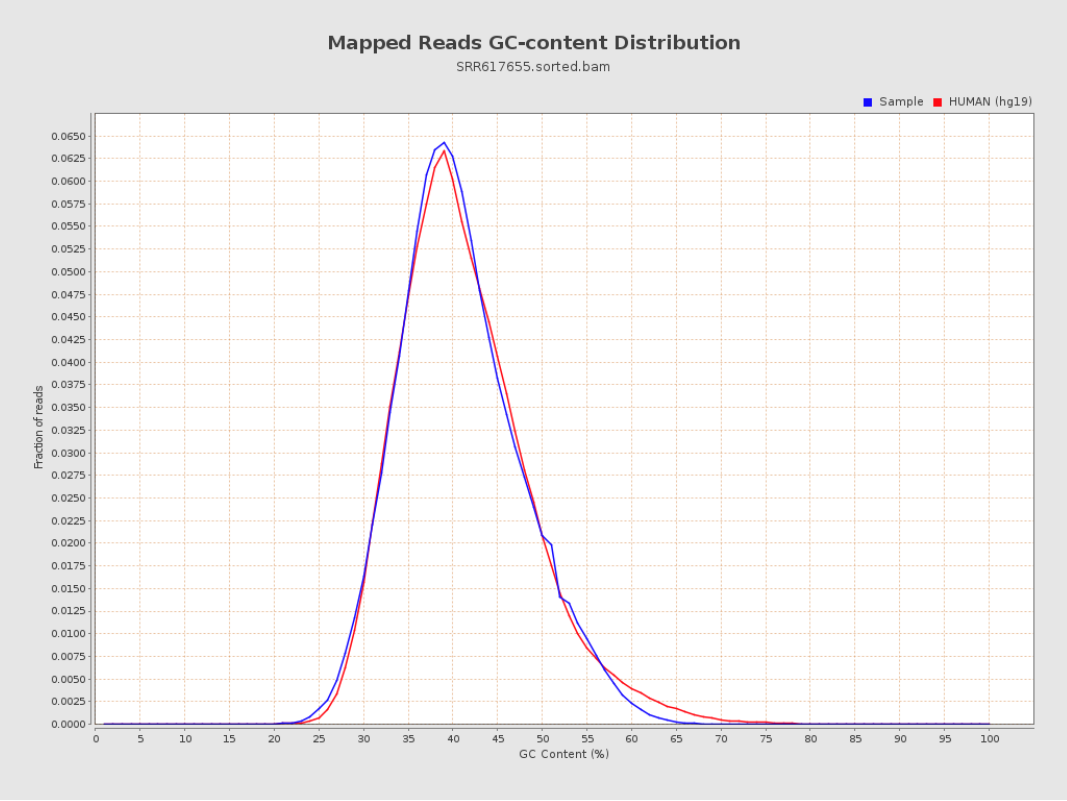
7. Results : Duplication Rate Histogram



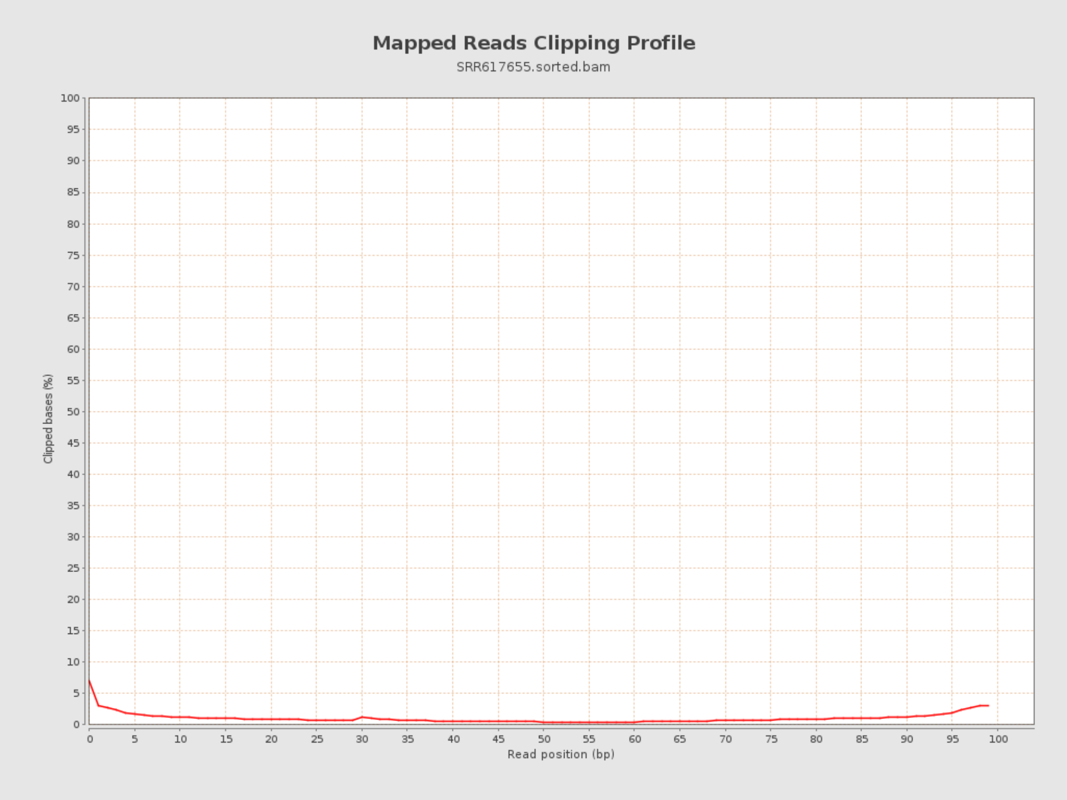
8. Results : Mapped Reads Nucleotide Content



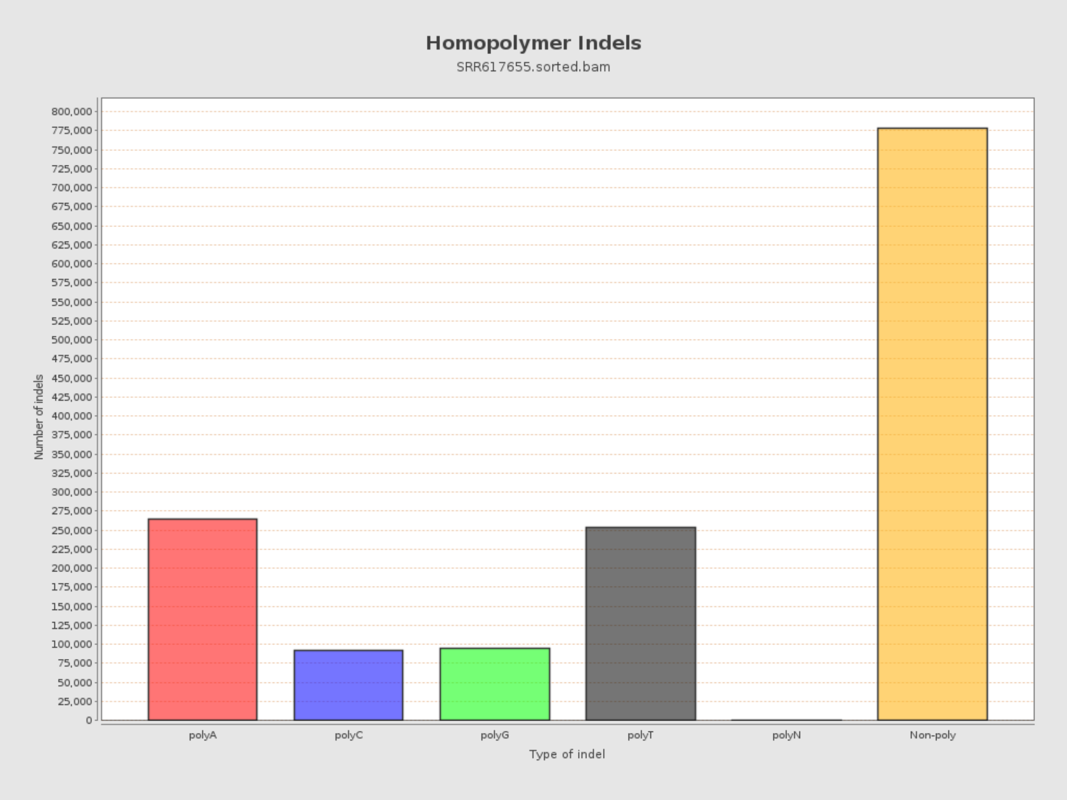
9. Results : Mapped Reads GC-content Distribution



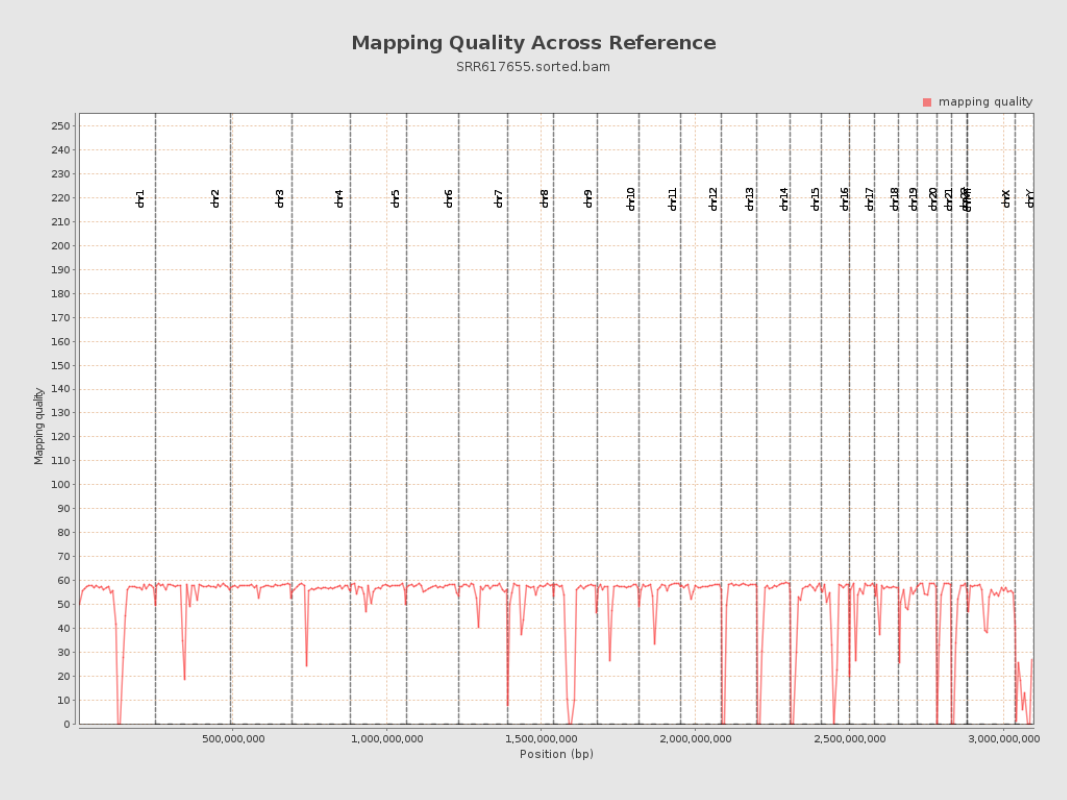
10. Results : Mapped Reads Clipping Profile



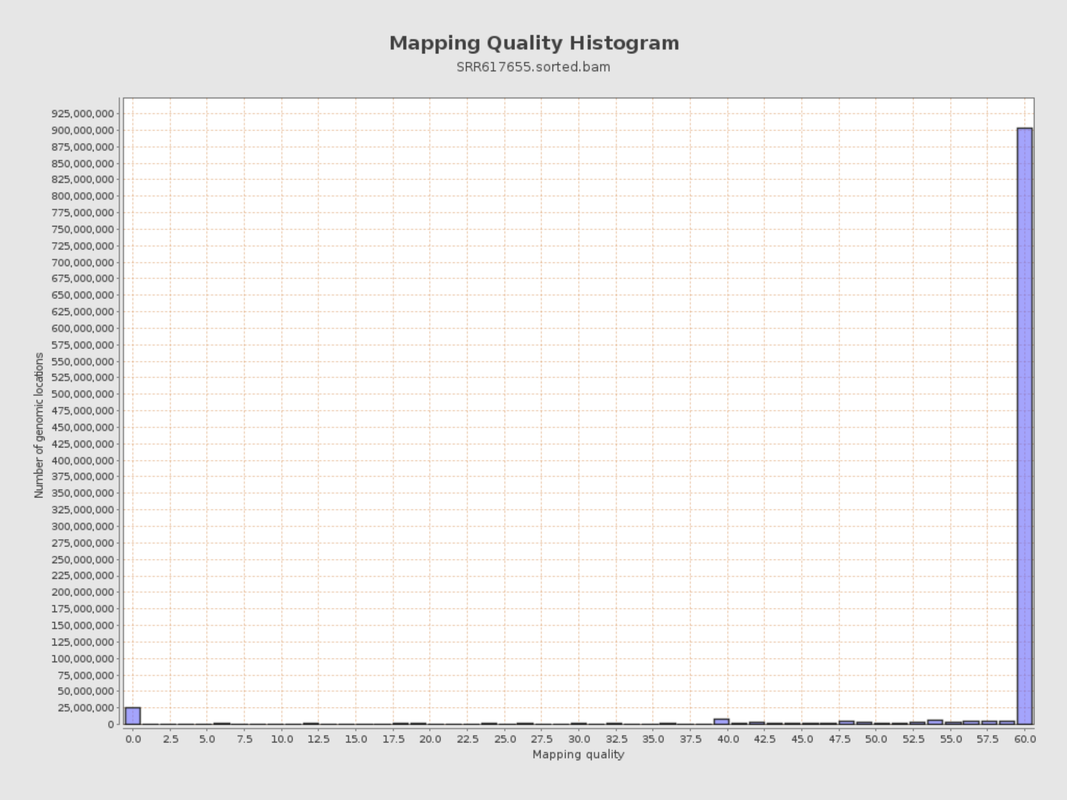
11. Results : Homopolymer Indels



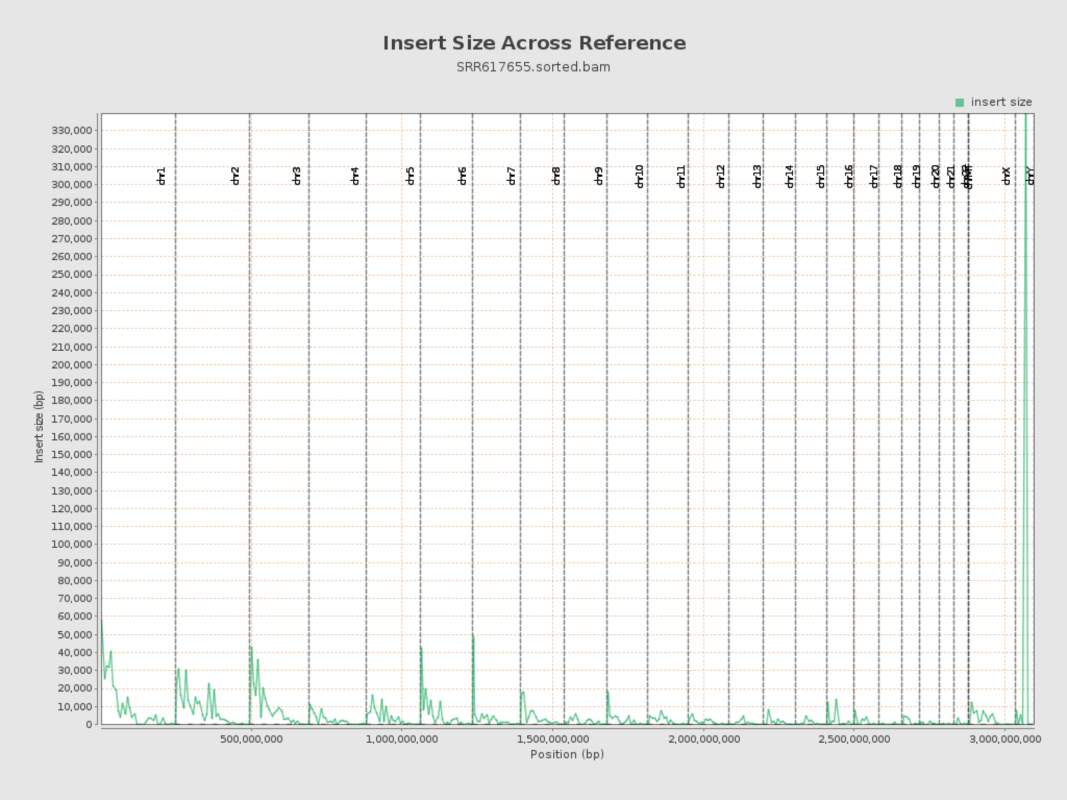
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram