Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/11 05:39:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617664.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_SRR617664 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617664_1.fastq.gz SRR617664_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Oct 11 05:39:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617664.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,512,494 / 95.35%
Unmapped reads	1,487,506 / 4.65%
Mapped paired reads	30,512,494 / 95.35%
Mapped reads, first in pair	15,327,514 / 47.9%
Mapped reads, second in pair	15,184,980 / 47.45%
Mapped reads, both in pair	29,948,862 / 93.59%
Mapped reads, singletons	563,632 / 1.76%
Secondary alignments	0
Supplementary alignments	144,215 / 0.45%
Read min/max/mean length	30 / 100 / 100.18
Duplicated reads (estimated)	7,050,574 / 22.03%
Duplication rate	10.78%
Clipped reads	6,293,539 / 19.67%

2.2. ACGT Content

Number/percentage of A's	882,343,183 / 29.76%
Number/percentage of C's	591,417,955 / 19.95%
Number/percentage of T's	881,090,042 / 29.72%
Number/percentage of G's	607,879,079 / 20.51%
Number/percentage of N's	1,715,636 / 0.06%

GC Percentage	40.46%

2.3. Coverage

Mean	0.9582
Standard Deviation	10.7546

2.4. Mapping Quality

Mean Mapping Quality	52.71

2.5. Insert size

Mean	31,799.31
Standard Deviation	1,635,581.43
P25/Median/P75	180 / 224 / 291

2.6. Mismatches and indels

General error rate	1.46%
Mismatches	42,363,616
Insertions	463,184
Mapped reads with at least one insertion	1.49%
Deletions	1,090,864
Mapped reads with at least one deletion	3.5%
Homopolymer indels	47.7%

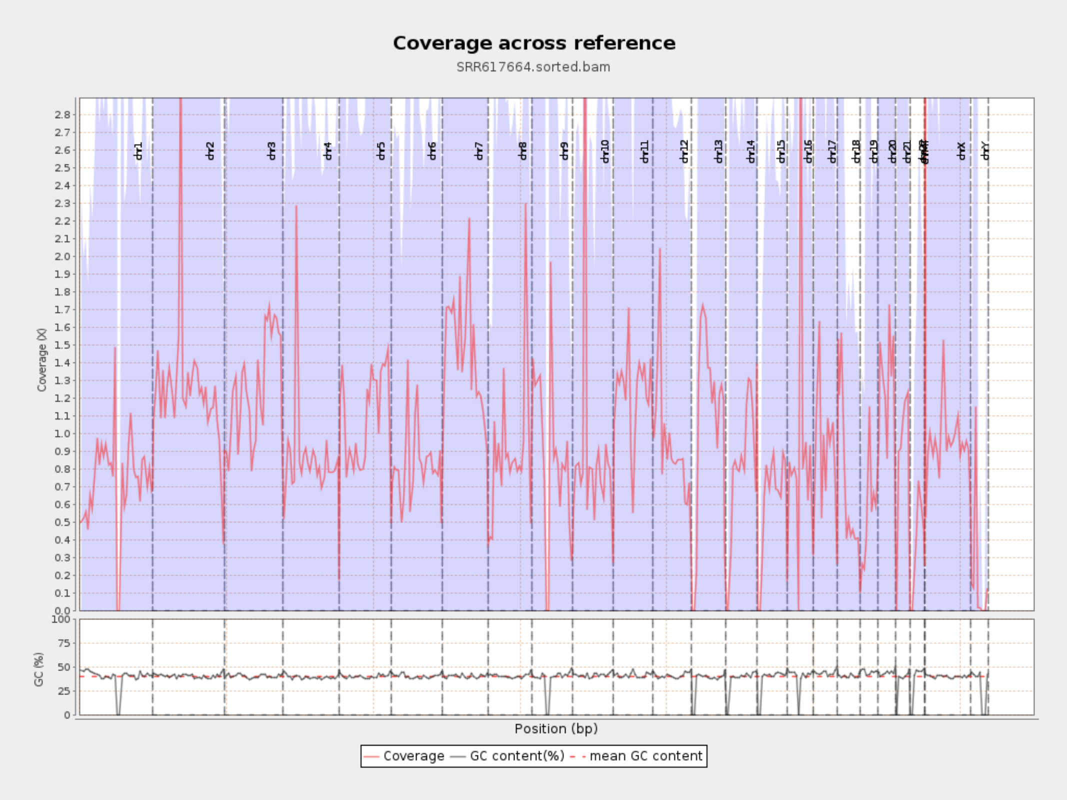
2.7. Chromosome stats

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

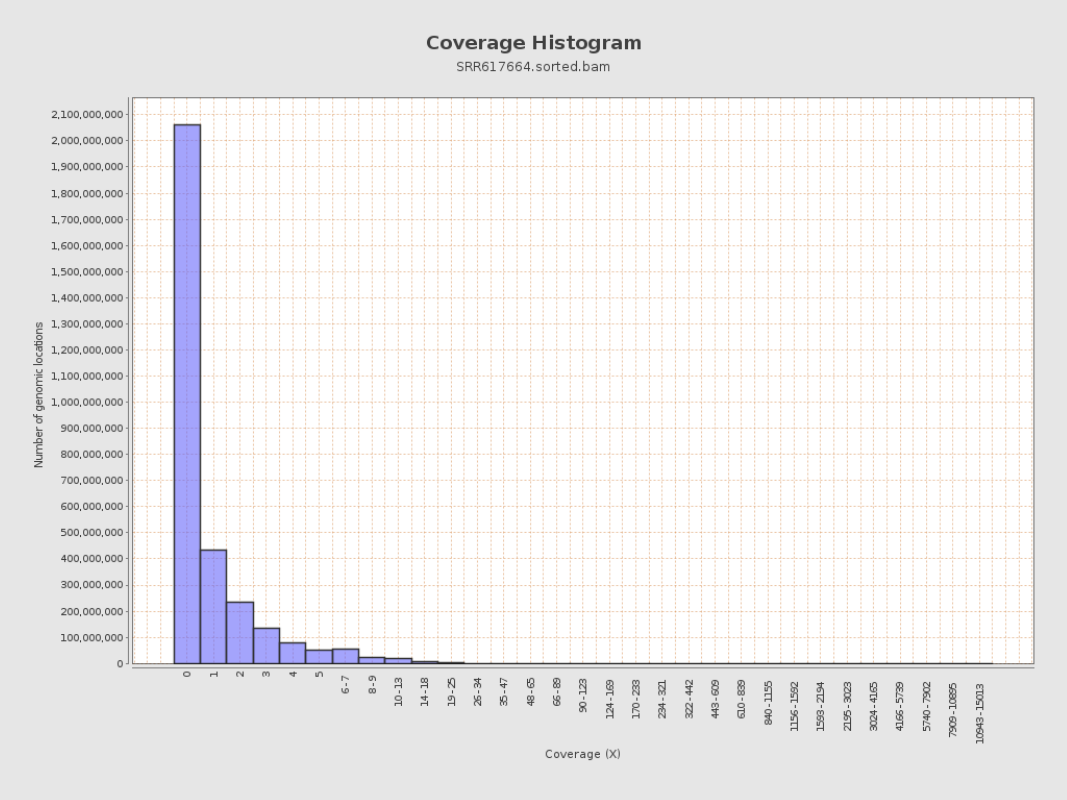
		bases	coverage	deviation
chr1	249250621	182061915	0.7304	10.3845
chr2	243199373	306746362	1.2613	12.3388
chr3	198022430	248670856	1.2558	2.5015
chr4	191154276	165822310	0.8675	8.509
chr5	180915260	196352090	1.0853	2.3491
chr6	171115067	143590202	0.8391	5.8963
chr7	159138663	231907305	1.4573	13.4403
chr8	146364022	132024766	0.902	4.1514
chr9	141213431	121759723	0.8622	20.9929
chr10	135534747	125581621	0.9266	21.8528
chr11	135006516	162920340	1.2068	12.1761
chr12	133851895	126601592	0.9458	2.1614
chr13	115169878	127334811	1.1056	2.3029
chr14	107349540	84877245	0.7907	2.5051
chr15	102531392	63255503	0.6169	1.581
chr16	90354753	82060037	0.9082	16.9675
chr17	81195210	73231382	0.9019	12.7375
chr18	78077248	54861178	0.7027	18.4015
chr19	59128983	31611455	0.5346	6.2938
chr20	63025520	80291168	1.2739	3.0703
chr21	48129895	43165225	0.8968	4.4195
chr22	51304566	19075511	0.3718	1.2834
chrMT	16571	3151973	190.2102	131.0398
chrX	155270560	147451240	0.9496	4.3189

chrY	59373566	11849879	0.1996	17.486

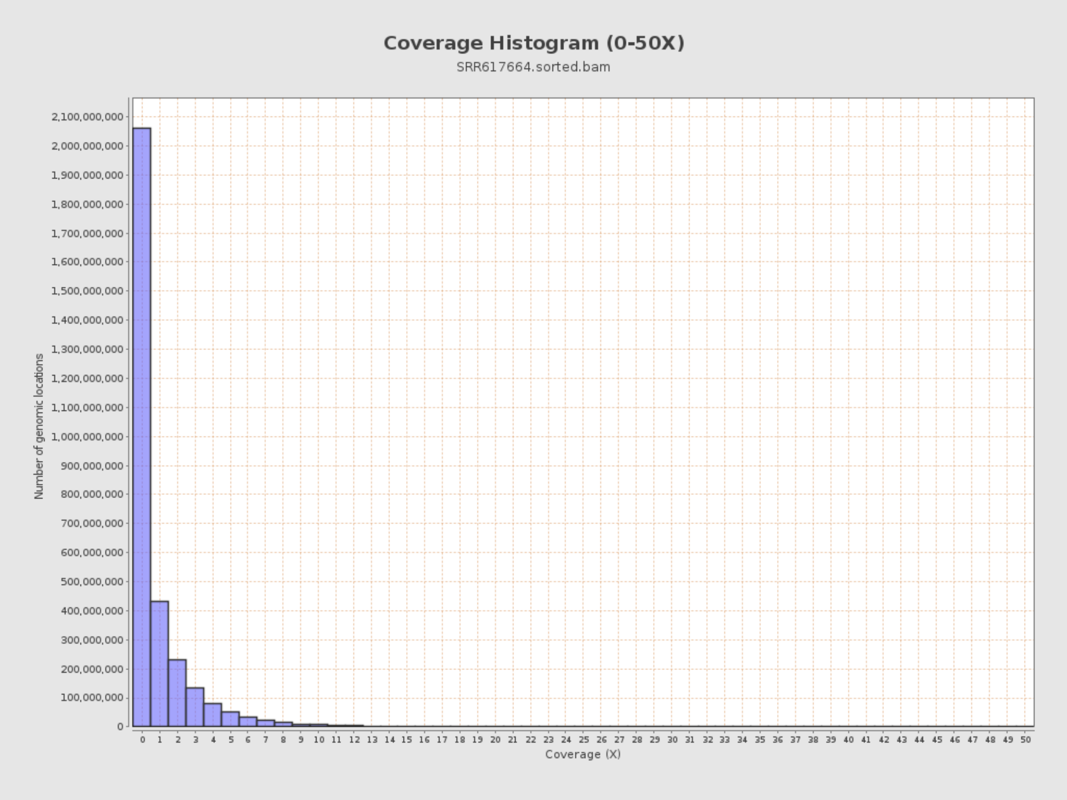
3. Results : Coverage across reference



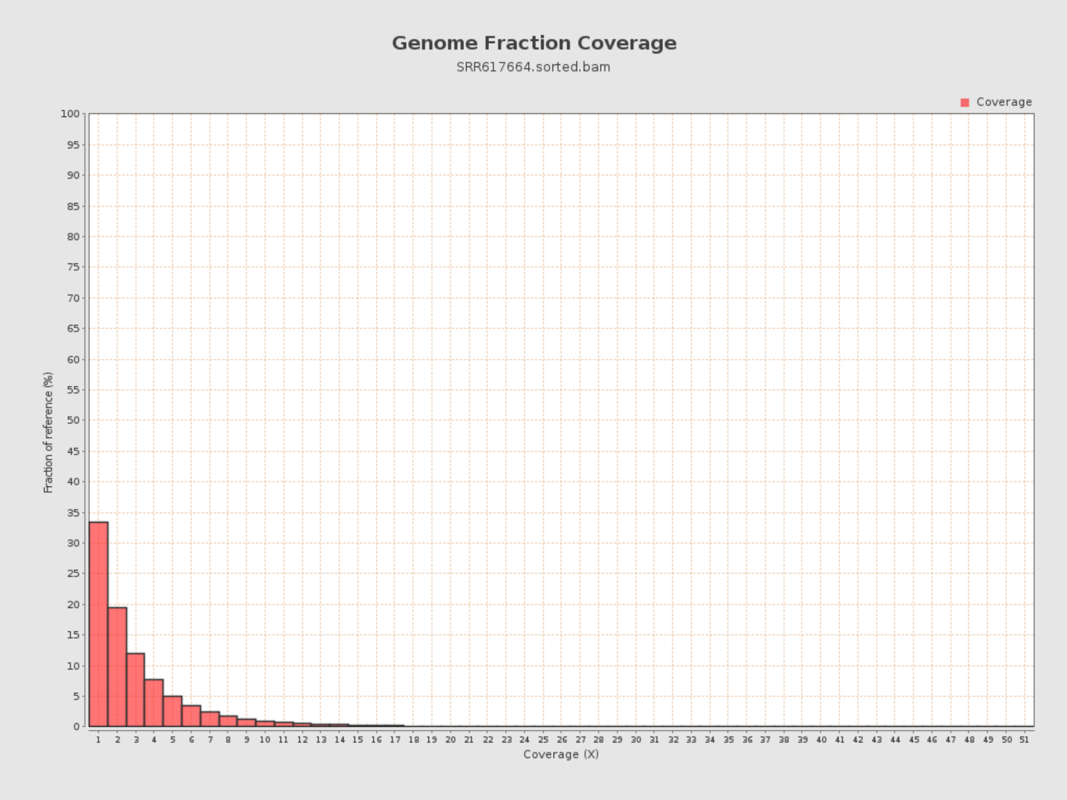
4. Results : Coverage Histogram



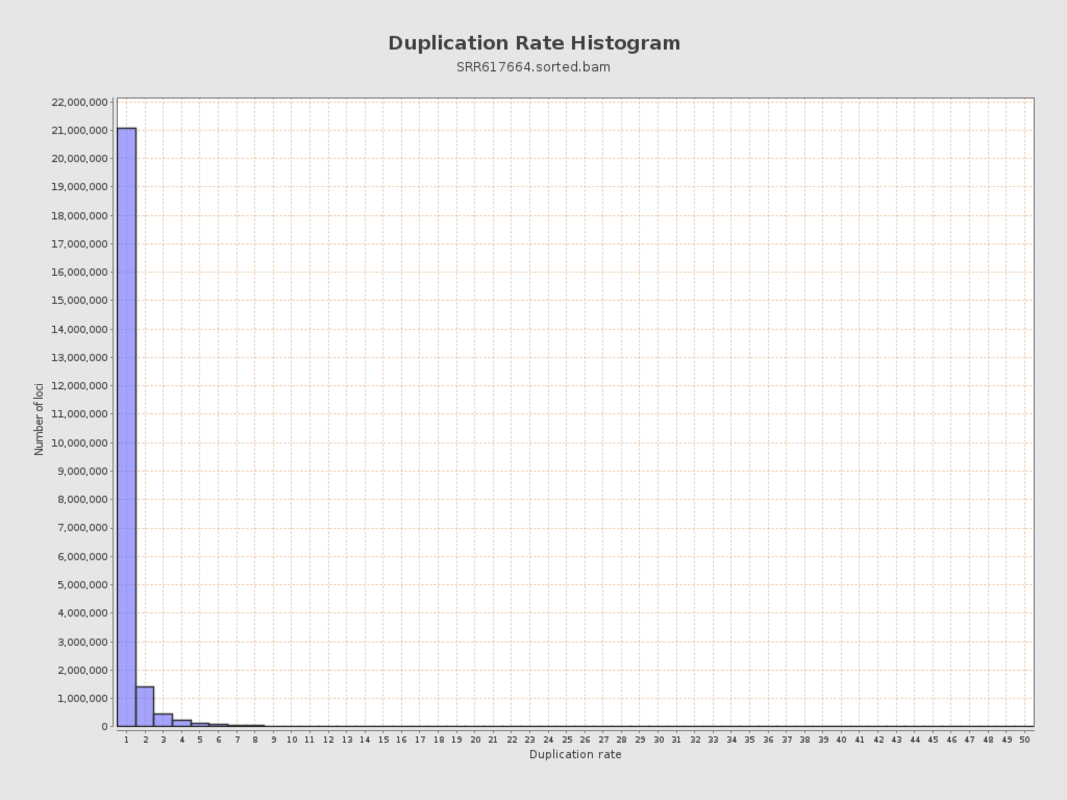
5. Results : Coverage Histogram (0-50X)



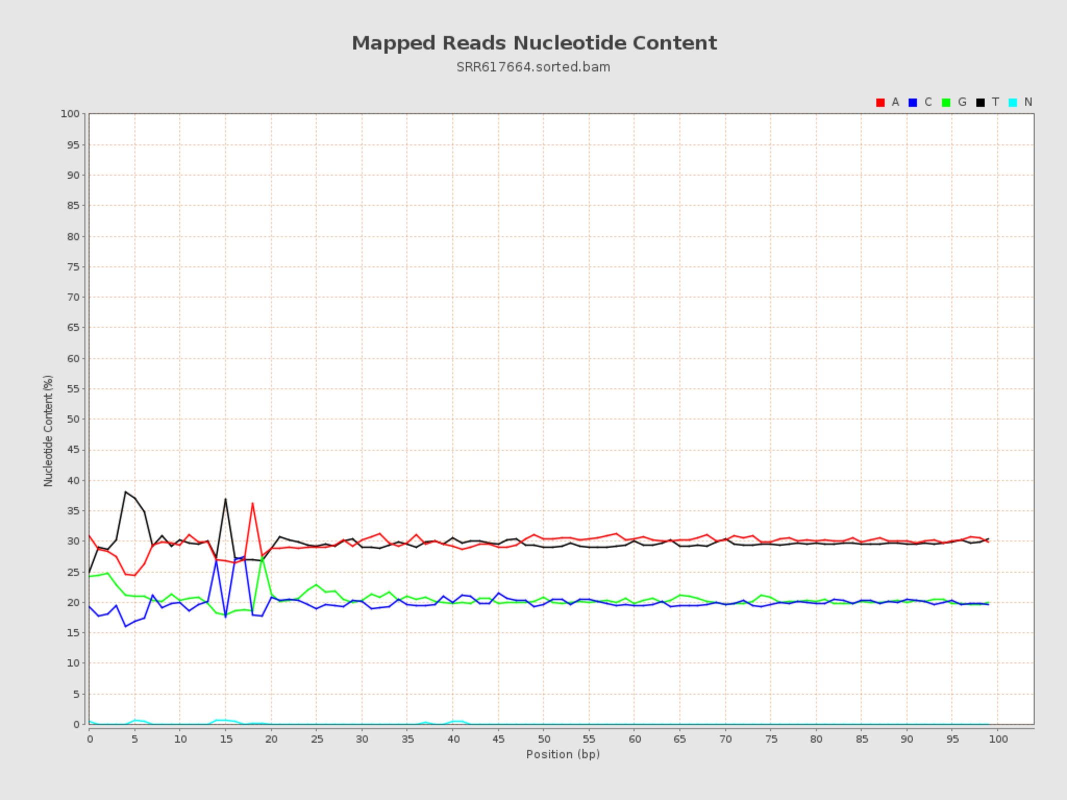
6. Results : Genome Fraction Coverage



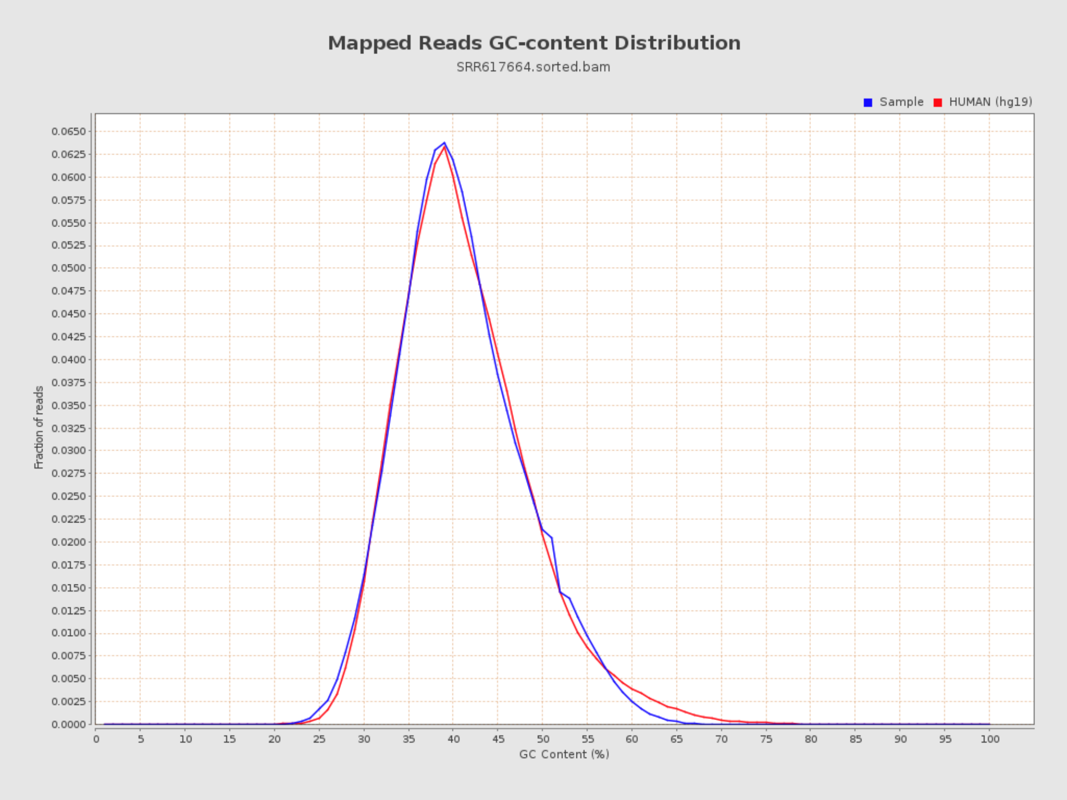
7. Results : Duplication Rate Histogram



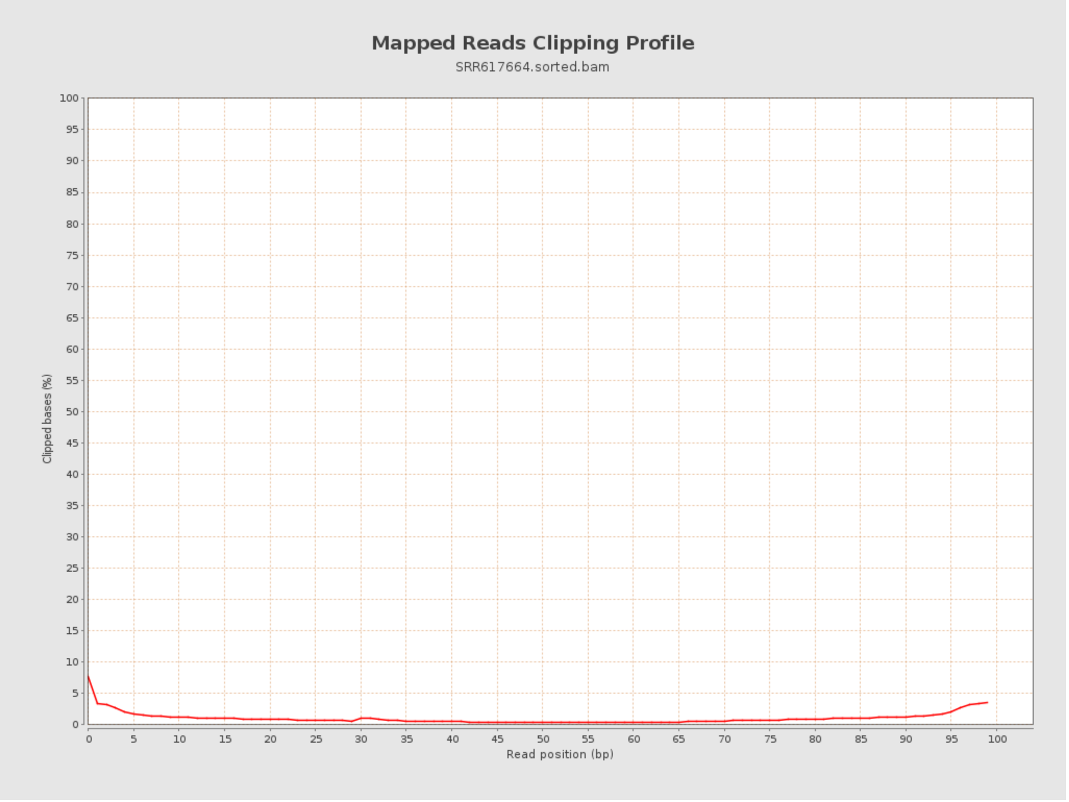
8. Results : Mapped Reads Nucleotide Content



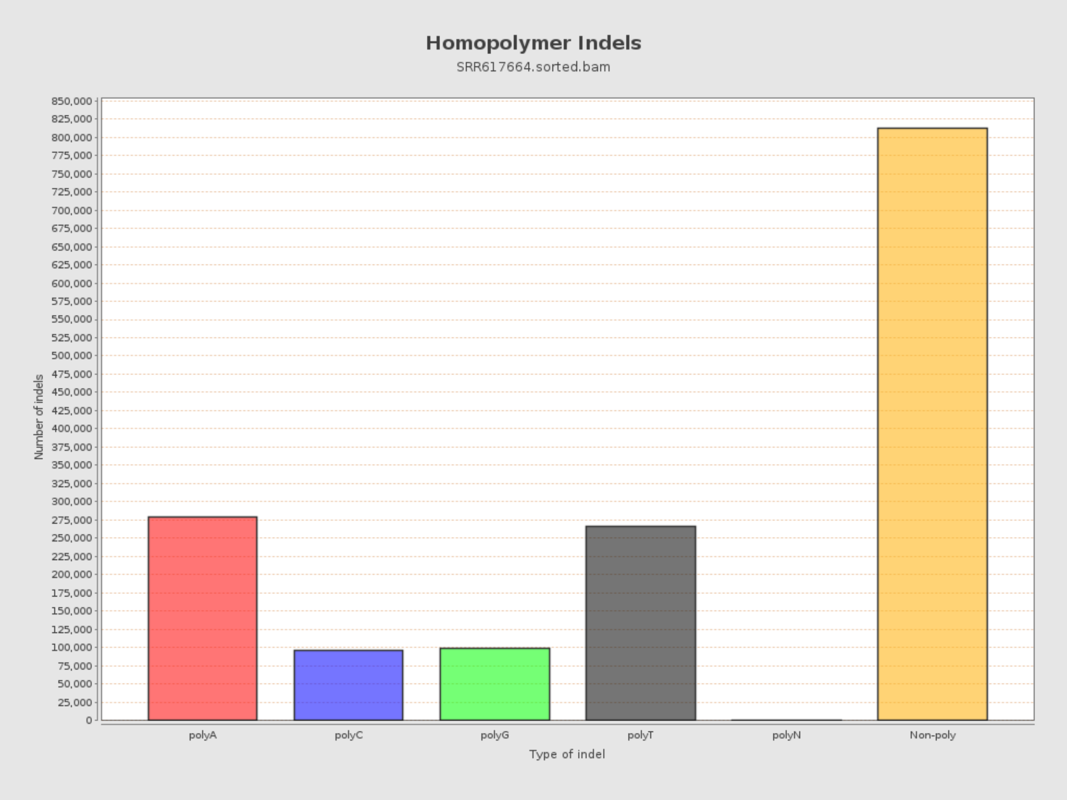
9. Results : Mapped Reads GC-content Distribution



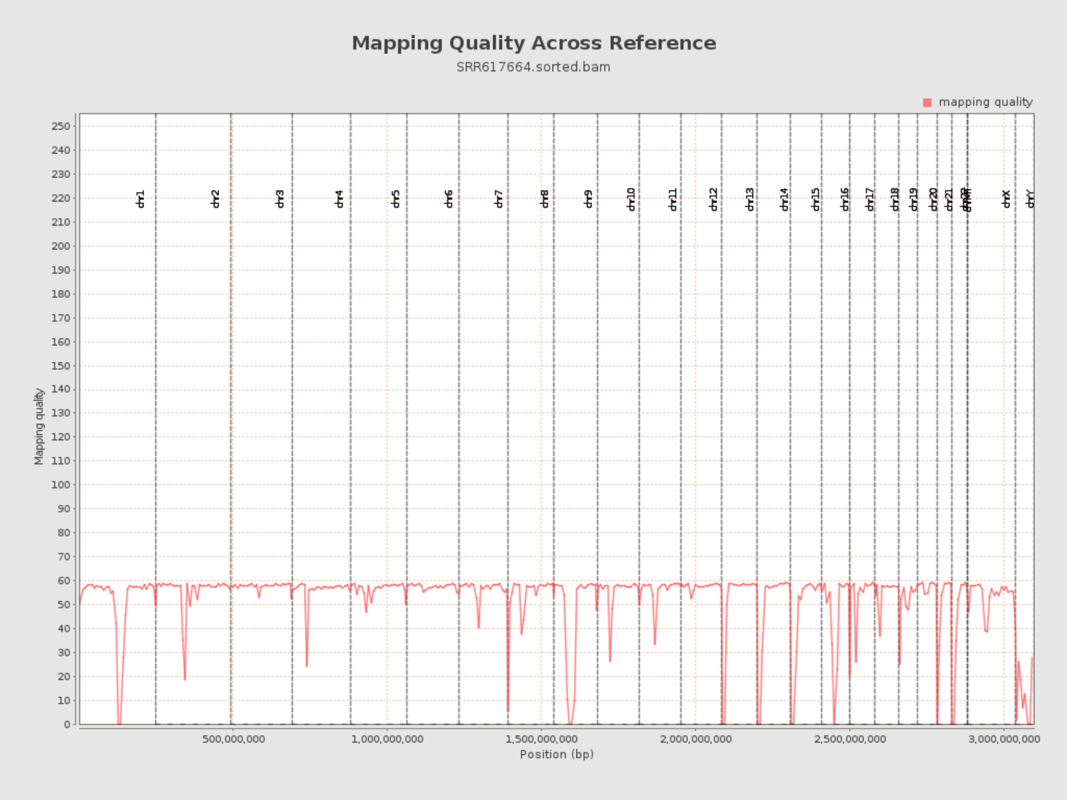
10. Results : Mapped Reads Clipping Profile



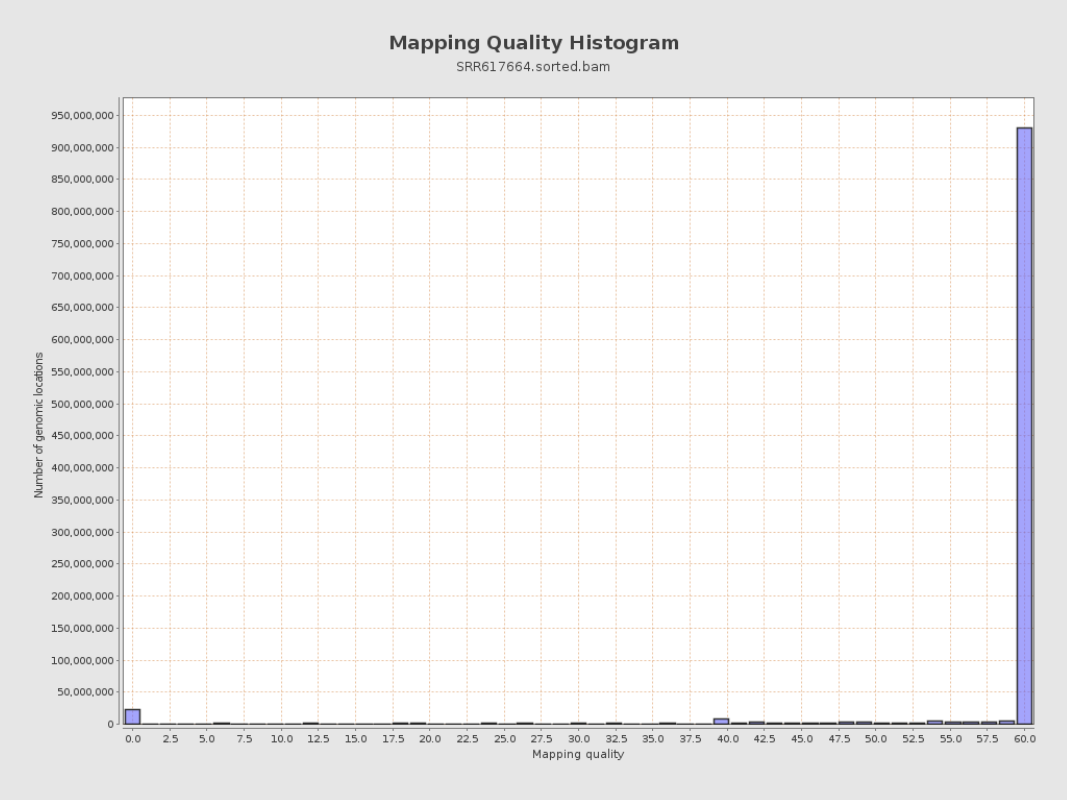
11. Results : Homopolymer Indels



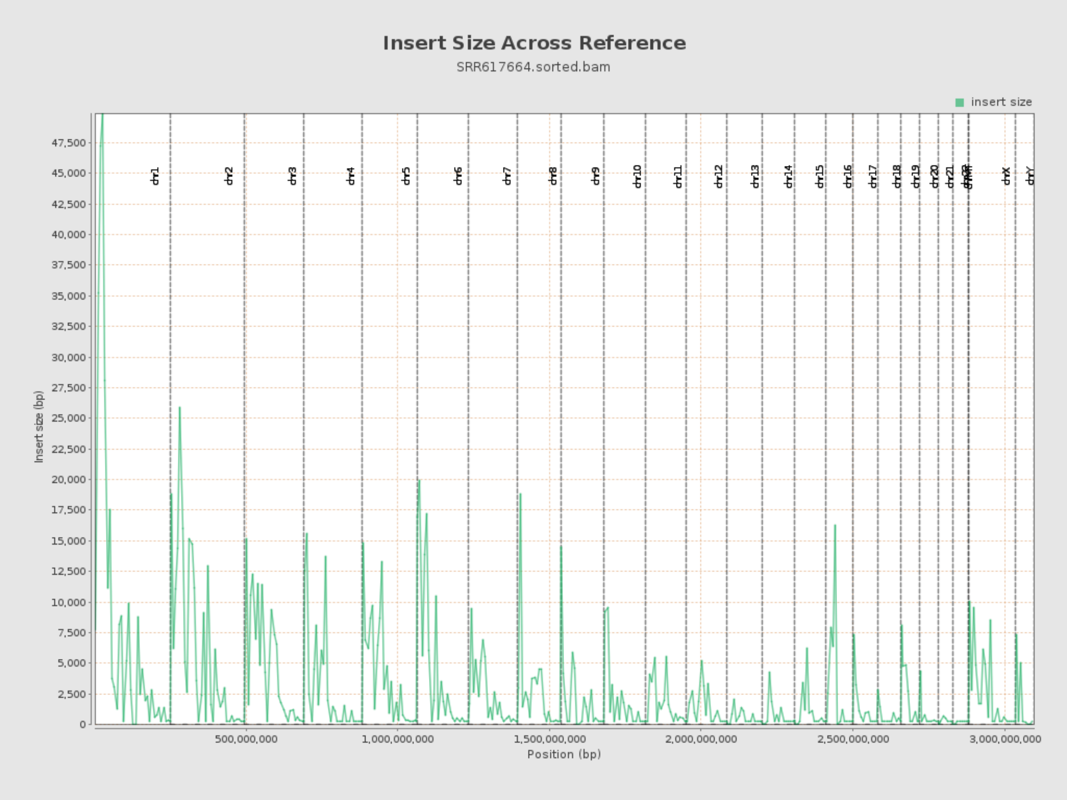
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram