Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 19:58:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617404.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_SRR617404 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617404_1.fastq.gz SRR617404_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 19:58:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617404.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	27,309,618 / 85.34%
Unmapped reads	4,690,382 / 14.66%
Mapped paired reads	27,309,618 / 85.34%
Mapped reads, first in pair	14,327,833 / 44.77%
Mapped reads, second in pair	12,981,785 / 40.57%
Mapped reads, both in pair	25,608,472 / 80.03%
Mapped reads, singletons	1,701,146 / 5.32%
Secondary alignments	0
Supplementary alignments	391,298 / 1.22%
Read min/max/mean length	30 / 100 / 100.5
Duplicated reads (estimated)	1,145,404 / 3.58%
Duplication rate	3.81%
Clipped reads	4,205,794 / 13.14%

2.2. ACGT Content

Number/percentage of A's	793,920,855 / 29.88%
Number/percentage of C's	532,962,606 / 20.06%
Number/percentage of T's	785,463,656 / 29.57%
Number/percentage of G's	543,712,139 / 20.47%
Number/percentage of N's	646,364 / 0.02%

GC Percentage	40.53%

2.3. Coverage

Mean	0.8584
Standard Deviation	2.6327

2.4. Mapping Quality

Mean Mapping Quality	53.53

2.5. Insert size

Mean	53,933.07
Standard Deviation	2,208,737.99
P25/Median/P75	167 / 204 / 261

2.6. Mismatches and indels

General error rate	1.61%
Mismatches	41,599,665
Insertions	846,212
Mapped reads with at least one insertion	3.07%
Deletions	256,162
Mapped reads with at least one deletion	0.92%
Homopolymer indels	30.74%

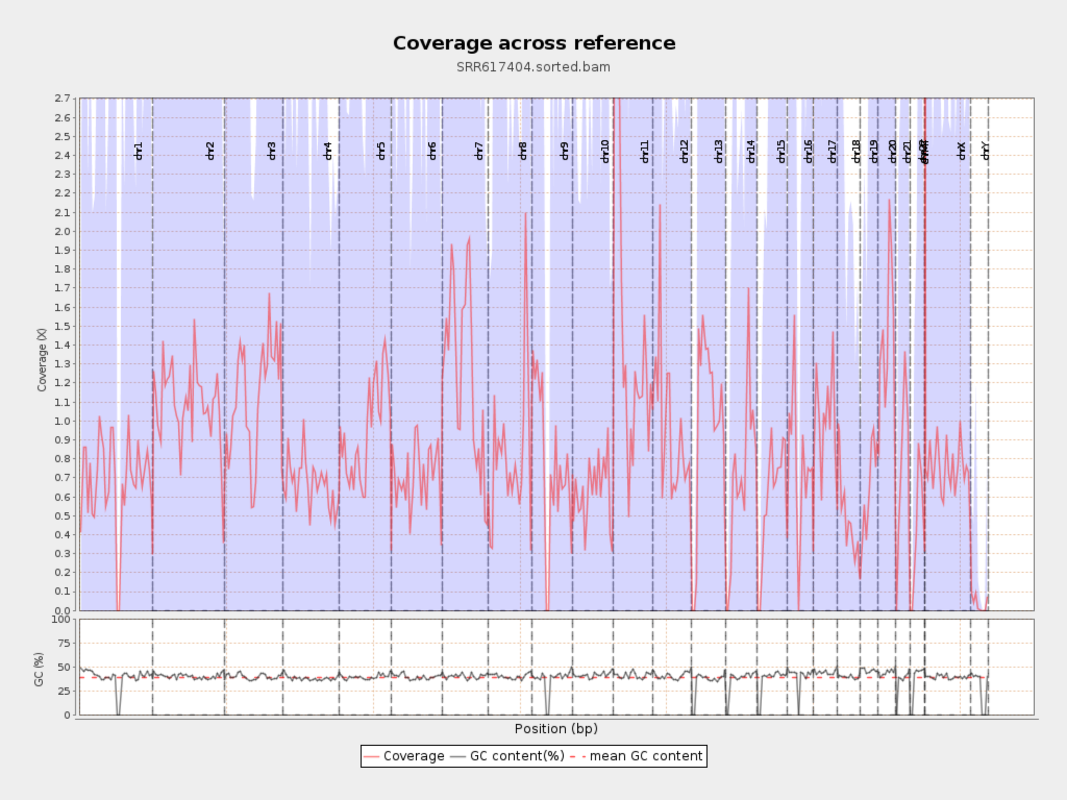
2.7. Chromosome stats

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

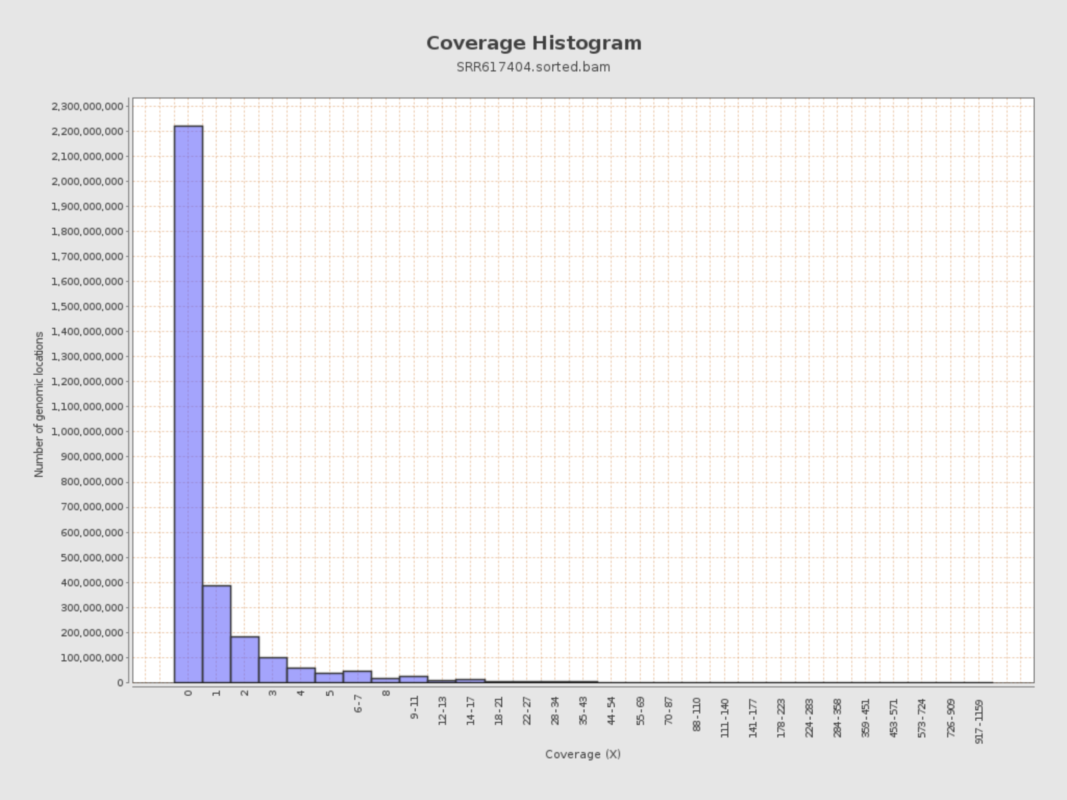
		bases	**coverage**	**deviation**
chr1	249250621	171101073	0.6865	2.472
chr2	243199373	265465068	1.0916	2.7923
chr3	198022430	224832564	1.1354	3.0684
chr4	191154276	128600108	0.6728	2.0781
chr5	180915260	170618815	0.9431	2.6013
chr6	171115067	122231388	0.7143	2.3559
chr7	159138663	198979124	1.2504	2.9281
chr8	146364022	117870950	0.8053	2.9116
chr9	141213431	106294721	0.7527	2.3358
chr10	135534747	84945607	0.6267	2.1589
chr11	135006516	196677668	1.4568	3.4475
chr12	133851895	126336368	0.9439	2.5208
chr13	115169878	115575568	1.0035	2.5102
chr14	107349540	76890078	0.7163	2.5922
chr15	102531392	60721135	0.5922	2.1369
chr16	90354753	66457405	0.7355	2.9605
chr17	81195210	81126685	0.9992	3.2607
chr18	78077248	38214817	0.4894	1.8079
chr19	59128983	37548428	0.635	2.0856
chr20	63025520	89688333	1.423	4.2098
chr21	48129895	36498117	0.7583	2.2879
chr22	51304566	21208544	0.4134	1.8618
chrMT	16571	158535	9.567	4.7777
chrX	155270560	117105859	0.7542	2.3158

chrY	59373566	2128221	0.0358	0.526

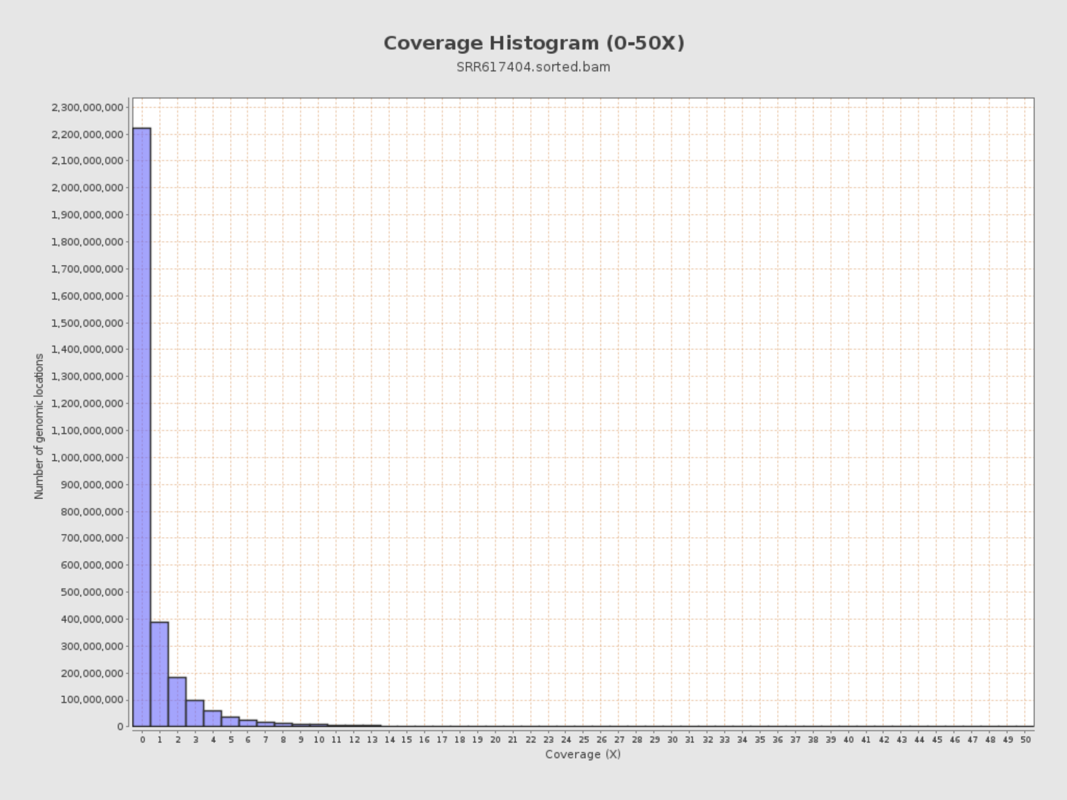
3. Results : Coverage across reference



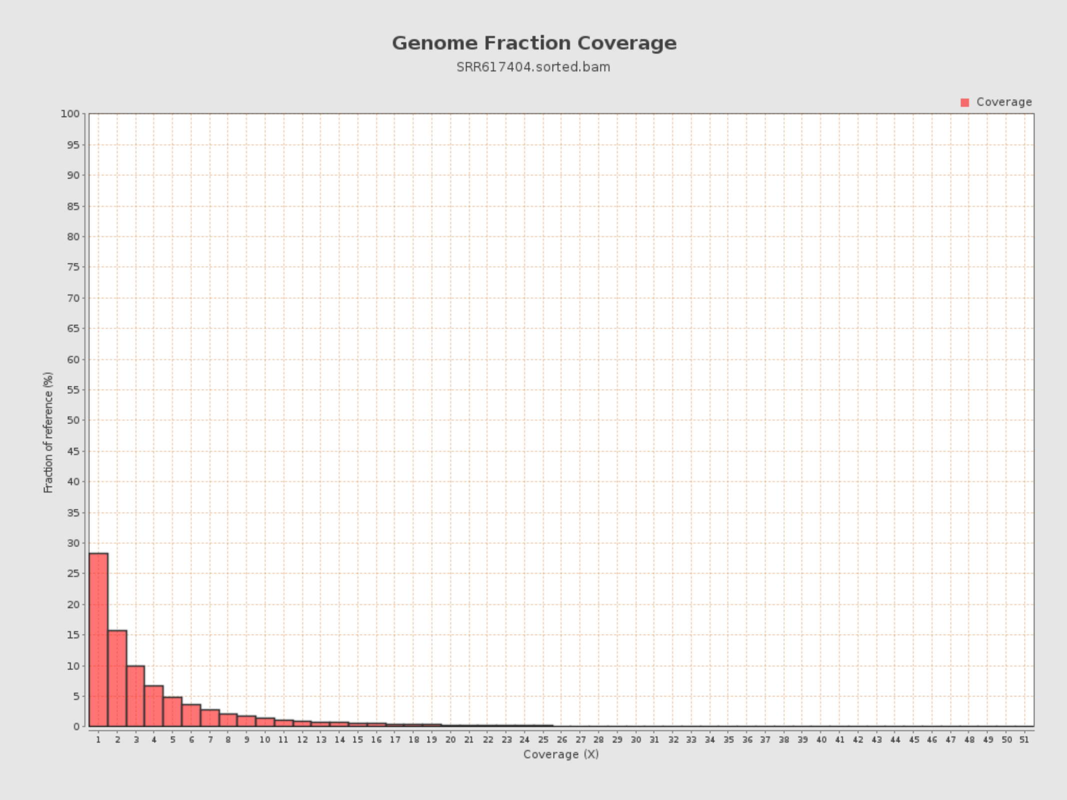
4. Results : Coverage Histogram



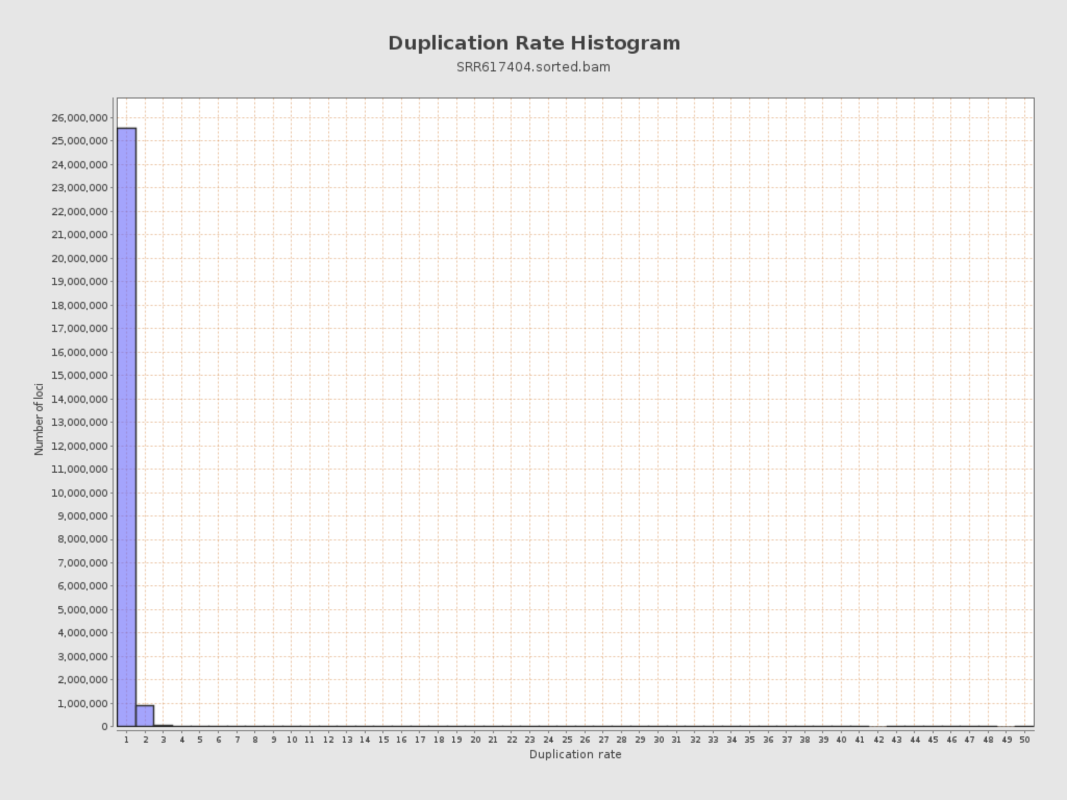
5. Results : Coverage Histogram (0-50X)



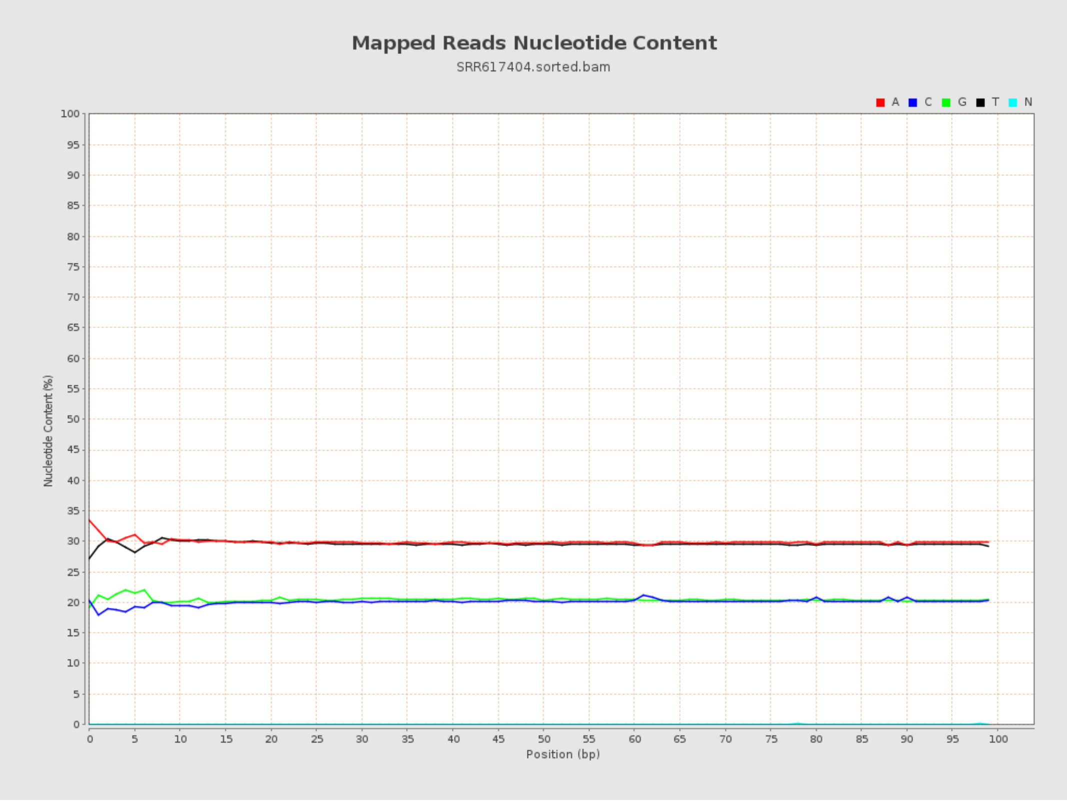
6. Results : Genome Fraction Coverage



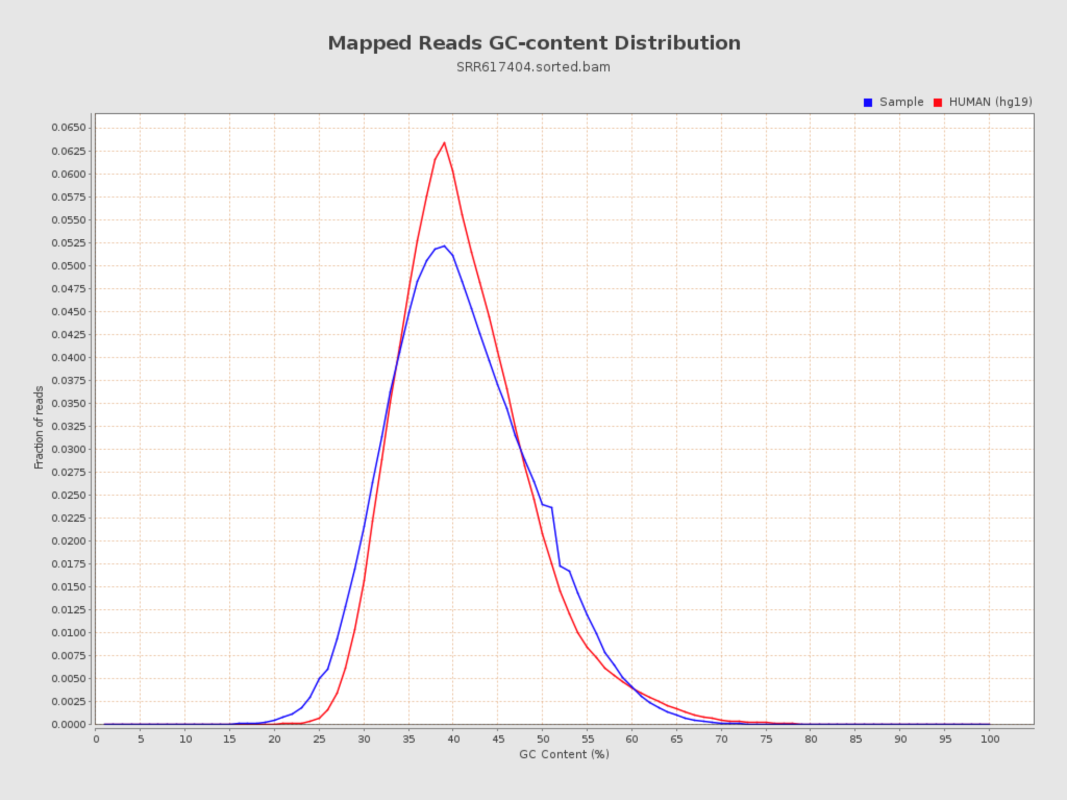
7. Results : Duplication Rate Histogram



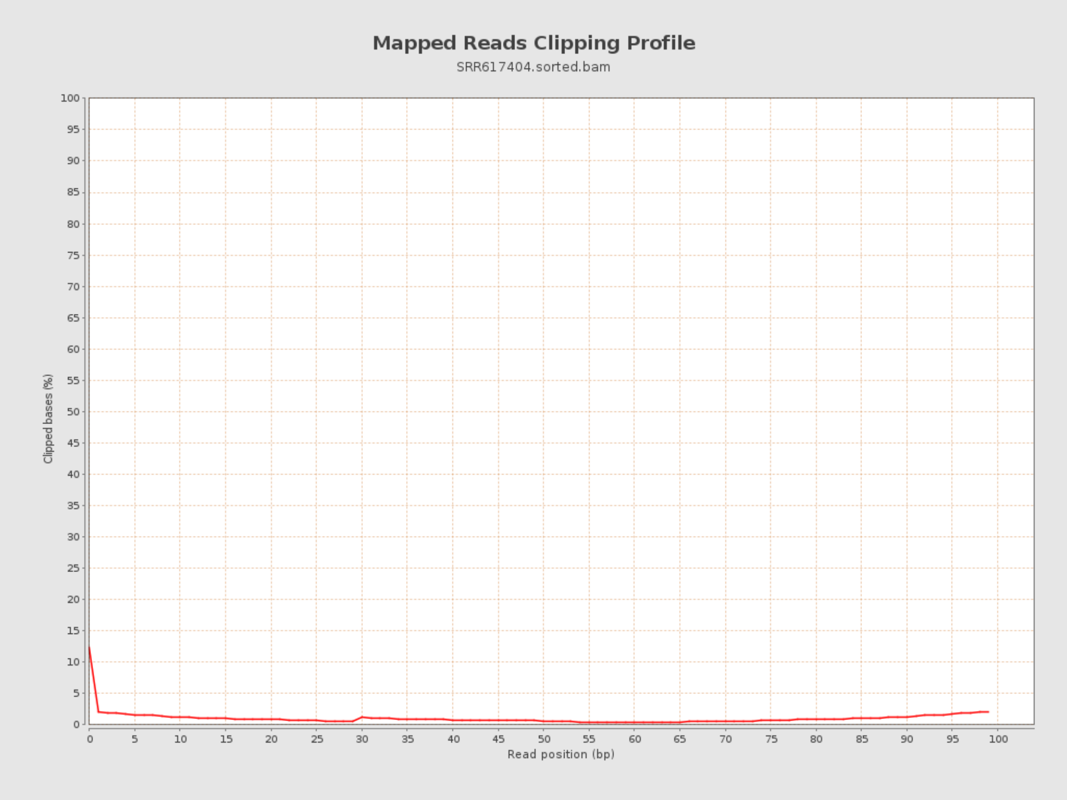
8. Results : Mapped Reads Nucleotide Content



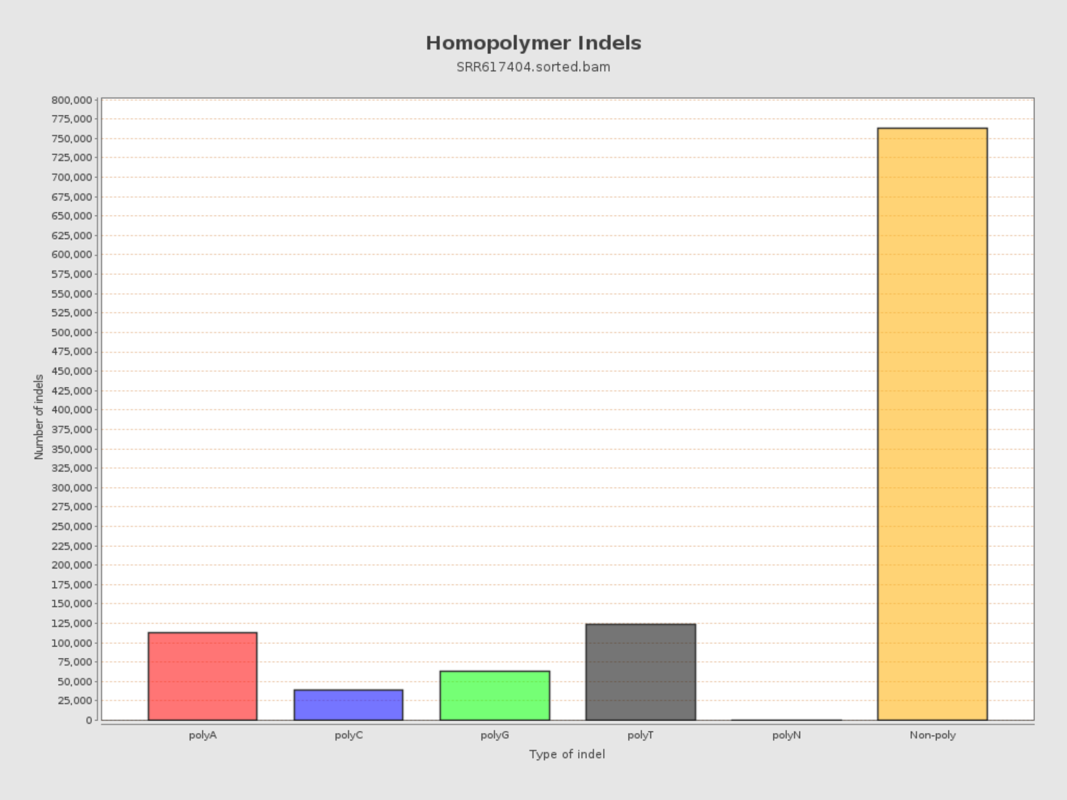
9. Results : Mapped Reads GC-content Distribution



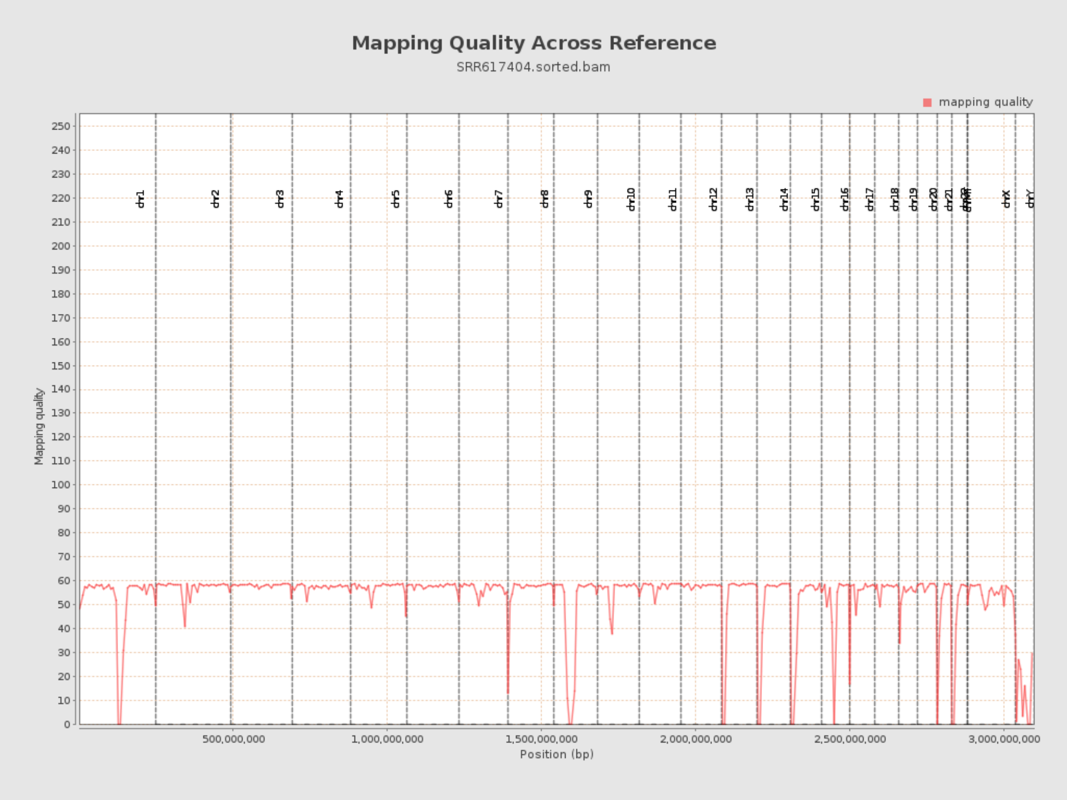
10. Results : Mapped Reads Clipping Profile



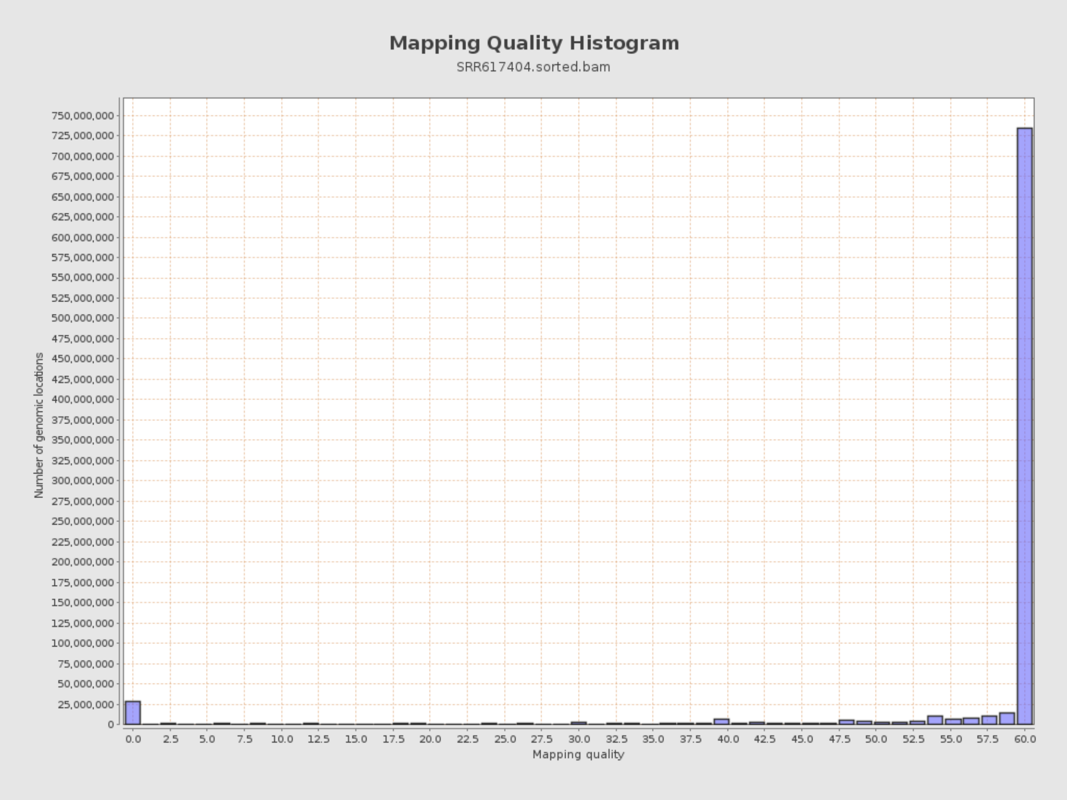
11. Results : Homopolymer Indels



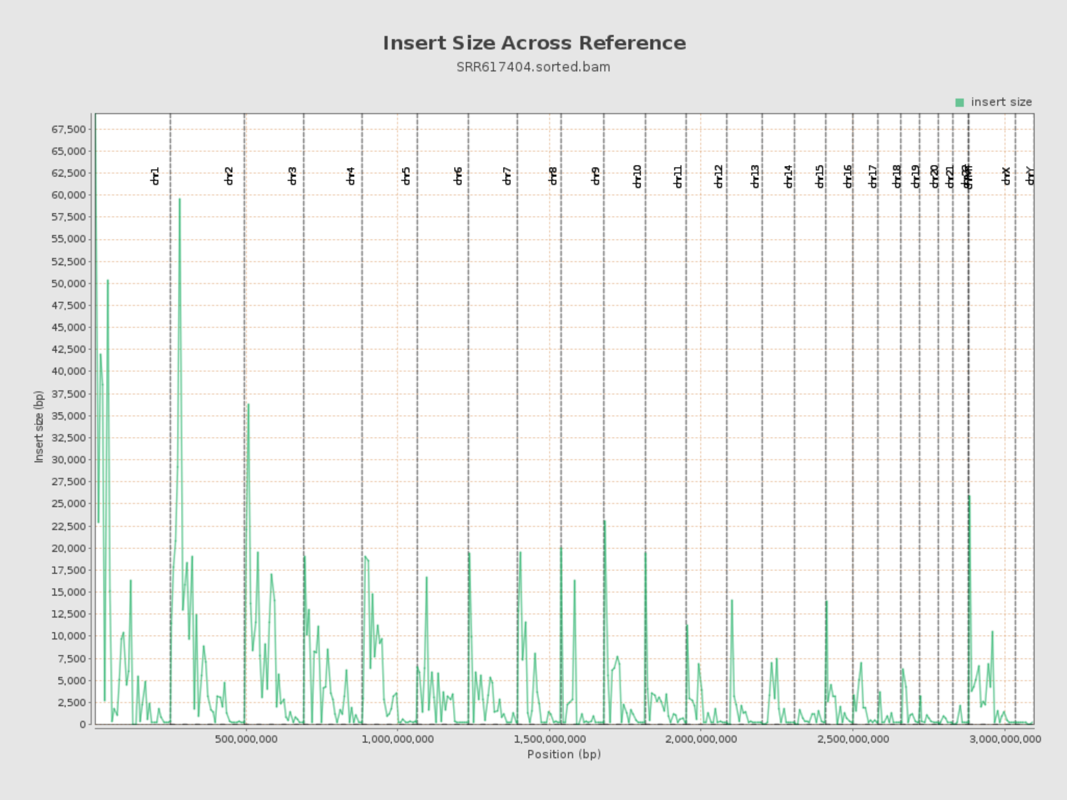
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram