Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 17:47:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617401.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_SRR617401 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617401_1.fastq.gz SRR617401_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 17:47:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617401.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	28,157,403 / 87.99%
Unmapped reads	3,842,597 / 12.01%
Mapped paired reads	28,157,403 / 87.99%
Mapped reads, first in pair	14,301,843 / 44.69%
Mapped reads, second in pair	13,855,560 / 43.3%
Mapped reads, both in pair	27,308,818 / 85.34%
Mapped reads, singletons	848,585 / 2.65%
Secondary alignments	0
Supplementary alignments	427,197 / 1.33%
Read min/max/mean length	30 / 100 / 100.55
Duplicated reads (estimated)	1,243,324 / 3.89%
Duplication rate	3.97%
Clipped reads	3,568,344 / 11.15%

2.2. ACGT Content

Number/percentage of A's	826,322,836 / 29.98%
Number/percentage of C's	550,566,789 / 19.97%
Number/percentage of T's	816,118,230 / 29.61%
Number/percentage of G's	563,391,873 / 20.44%
Number/percentage of N's	254,944 / 0.01%

GC Percentage	40.41%

2.3. Coverage

Mean	0.8907
Standard Deviation	2.7391

2.4. Mapping Quality

Mean Mapping Quality	53.68

2.5. Insert size

Mean	58,139.13
Standard Deviation	2,313,421.78
P25/Median/P75	168 / 205 / 262

2.6. Mismatches and indels

General error rate	1.43%
Mismatches	38,838,011
Insertions	248,465
Mapped reads with at least one insertion	0.87%
Deletions	266,949
Mapped reads with at least one deletion	0.93%
Homopolymer indels	43.74%

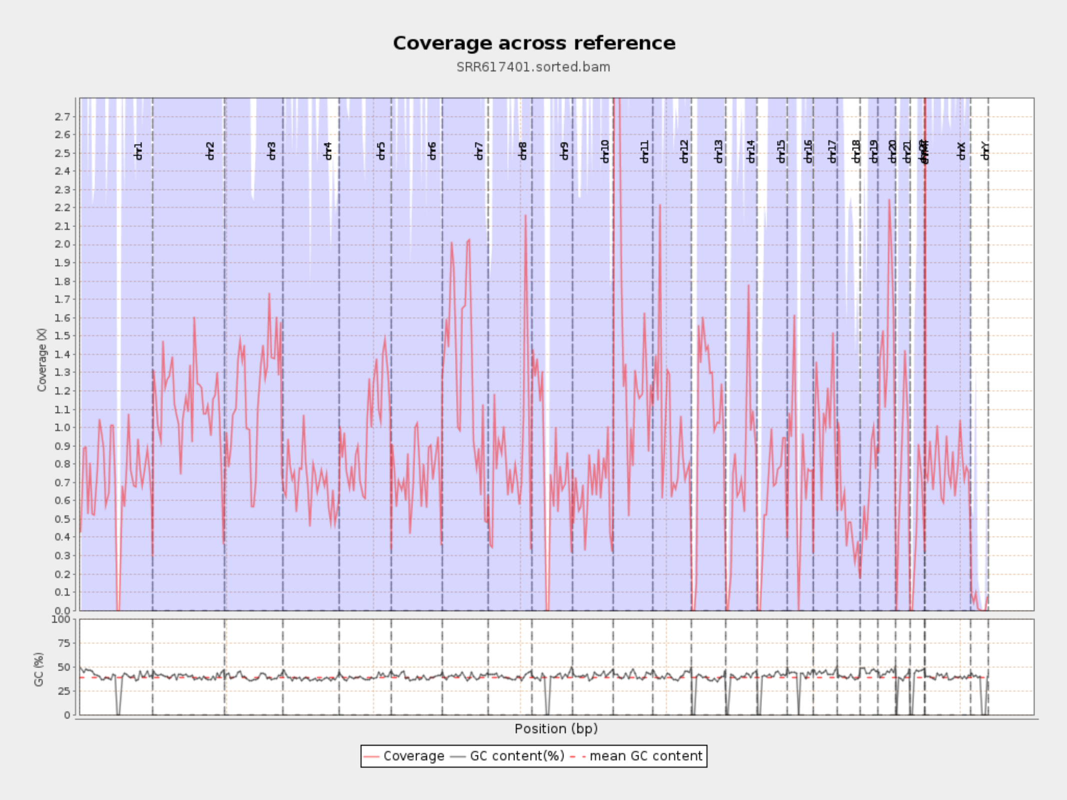
2.7. Chromosome stats

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

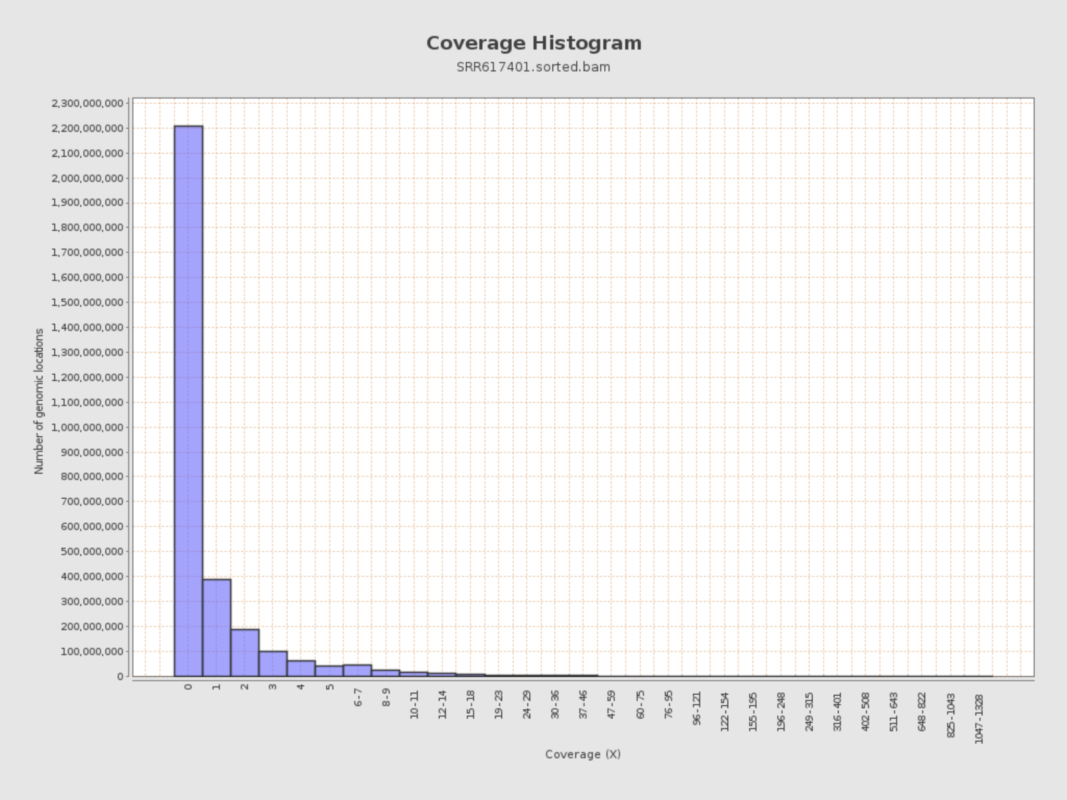
		bases	coverage	deviation
chr1	249250621	177364429	0.7116	2.5706
chr2	243199373	275156769	1.1314	2.9174
chr3	198022430	233446381	1.1789	3.1851
chr4	191154276	133503684	0.6984	2.1548
chr5	180915260	176984183	0.9783	2.7006
chr6	171115067	126956616	0.7419	2.4403
chr7	159138663	206870507	1.2999	3.0419
chr8	146364022	122280272	0.8355	3.0291
chr9	141213431	110307918	0.7811	2.4489
chr10	135534747	88226551	0.651	2.2569
chr11	135006516	204203749	1.5125	3.5723
chr12	133851895	131342313	0.9813	2.6292
chr13	115169878	120030836	1.0422	2.6039
chr14	107349540	79807993	0.7434	2.699
chr15	102531392	63164941	0.6161	2.24
chr16	90354753	68567755	0.7589	3.0744
chr17	81195210	83891985	1.0332	3.4555
chr18	78077248	39666110	0.508	1.875
chr19	59128983	38735869	0.6551	2.155
chr20	63025520	93230229	1.4792	4.3504
chr21	48129895	37902911	0.7875	2.3587
chr22	51304566	21927900	0.4274	1.926
chrMT	16571	167099	10.0838	5.1611
chrX	155270560	121301677	0.7812	2.4079

chrY	59373566	2212425	0.0373	0.5883

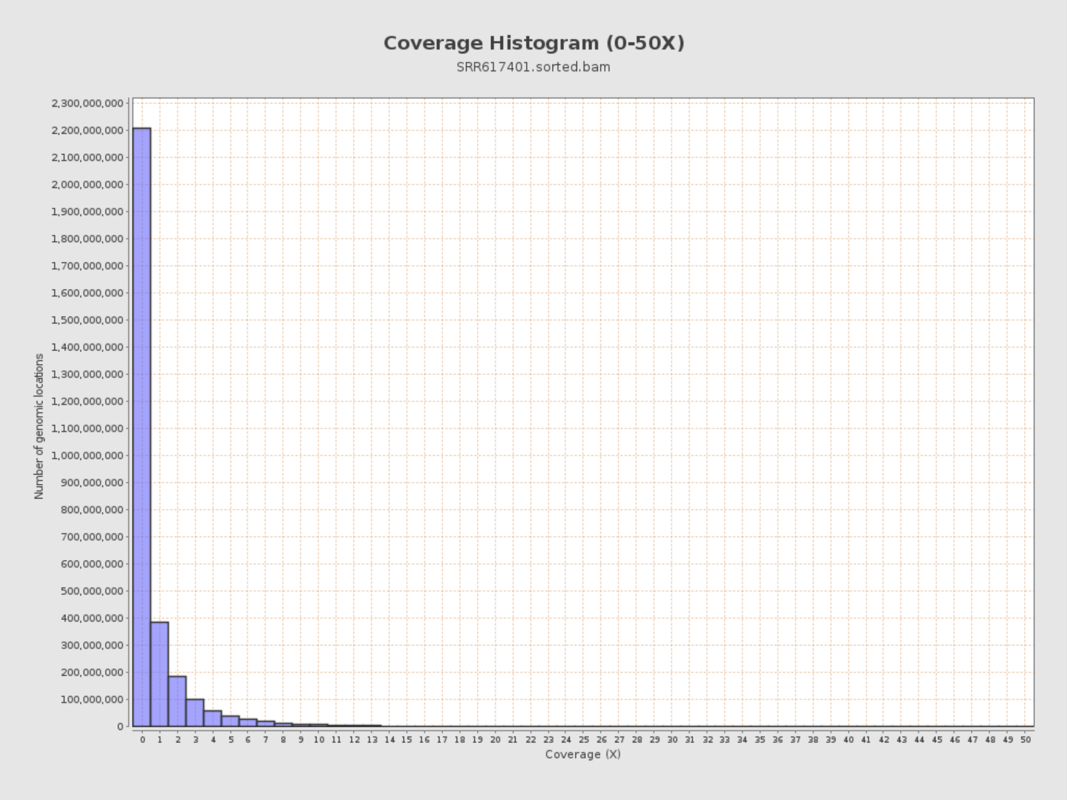
3. Results : Coverage across reference



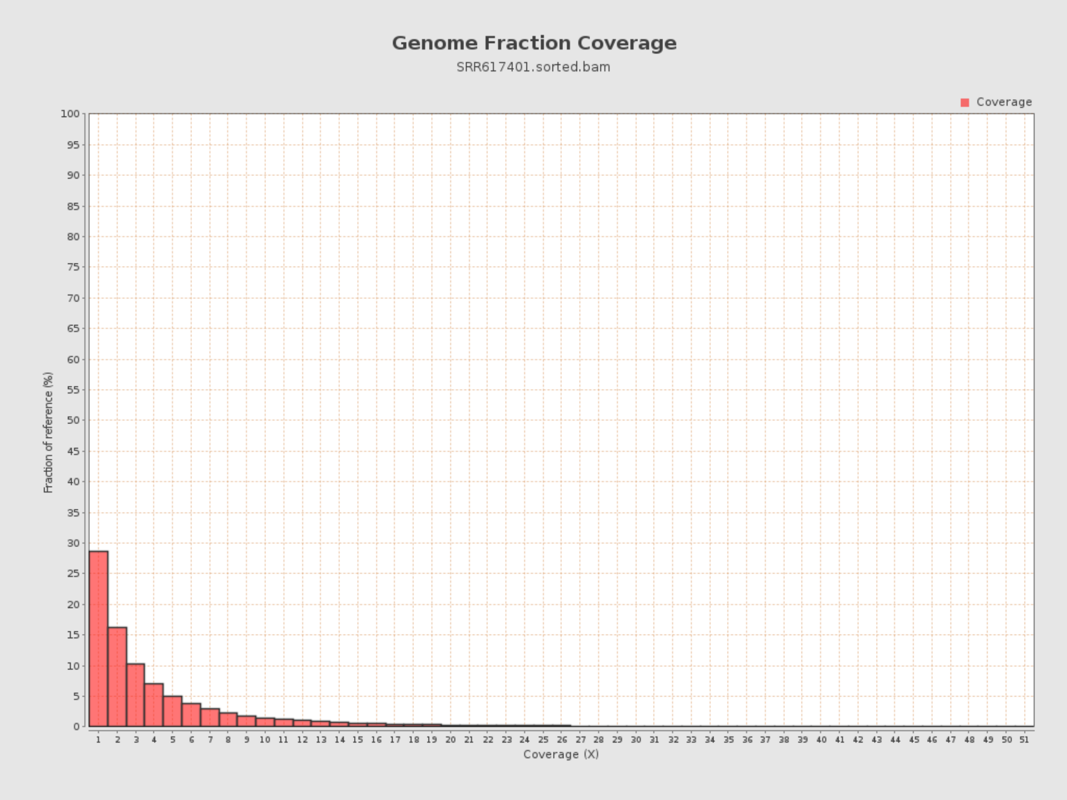
4. Results : Coverage Histogram



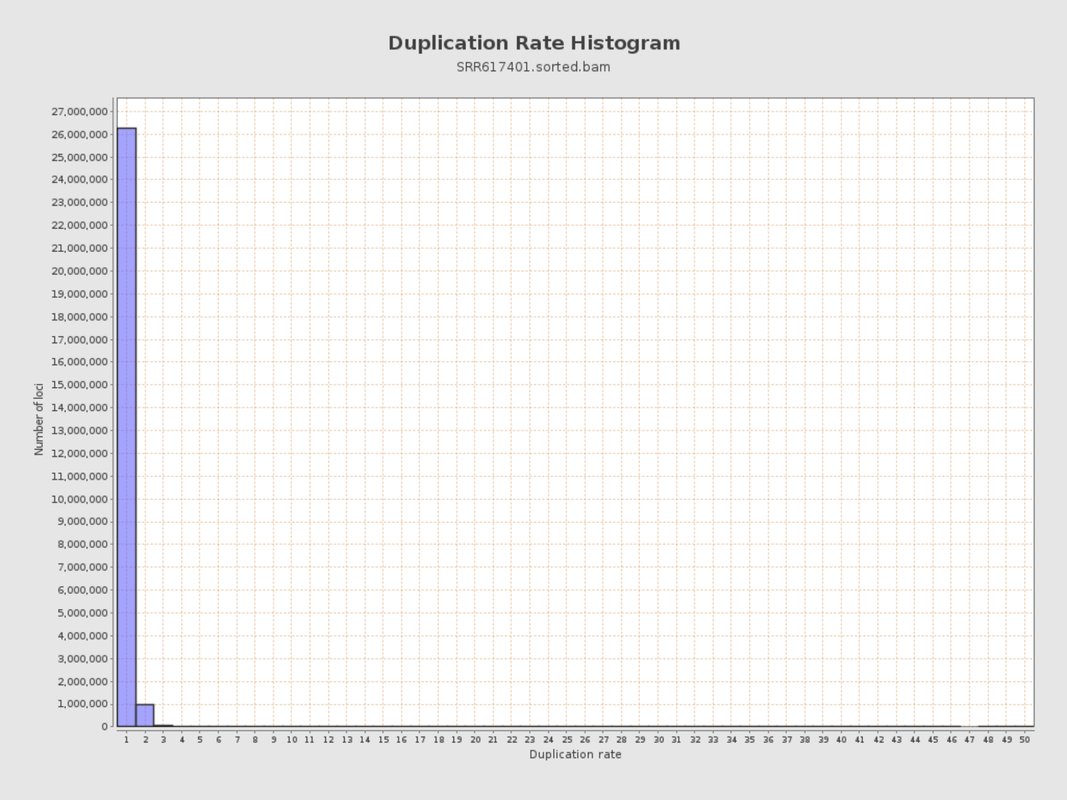
5. Results : Coverage Histogram (0-50X)



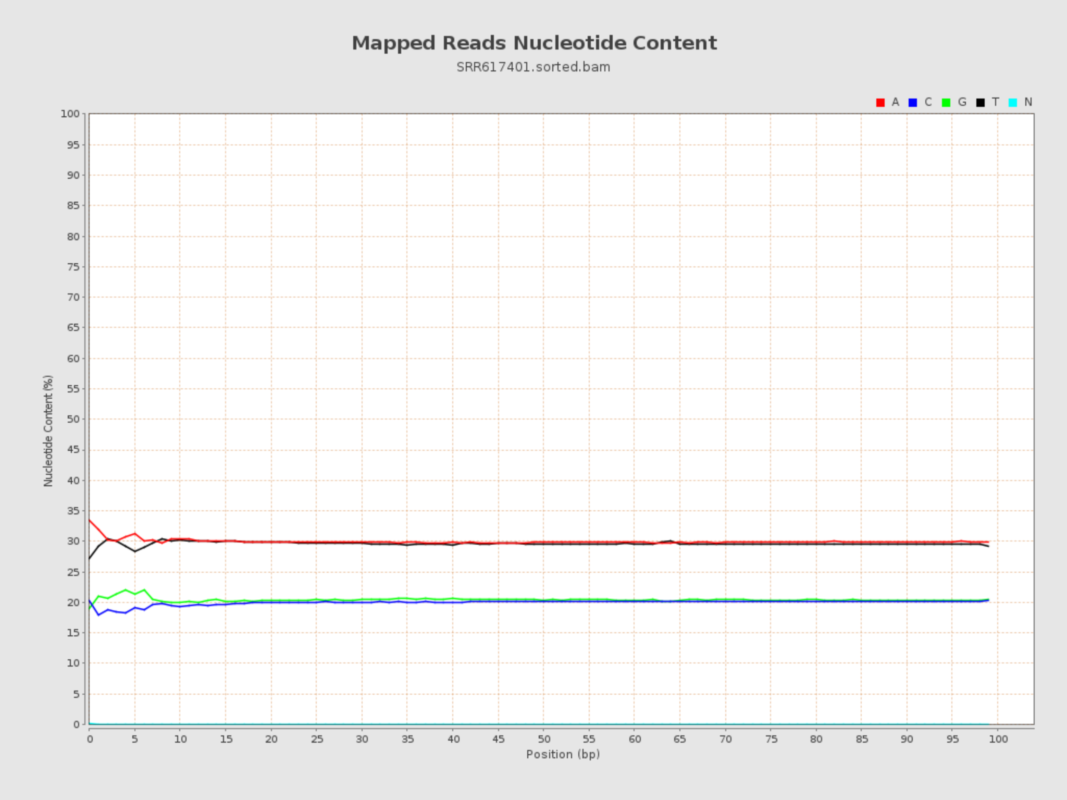
6. Results : Genome Fraction Coverage



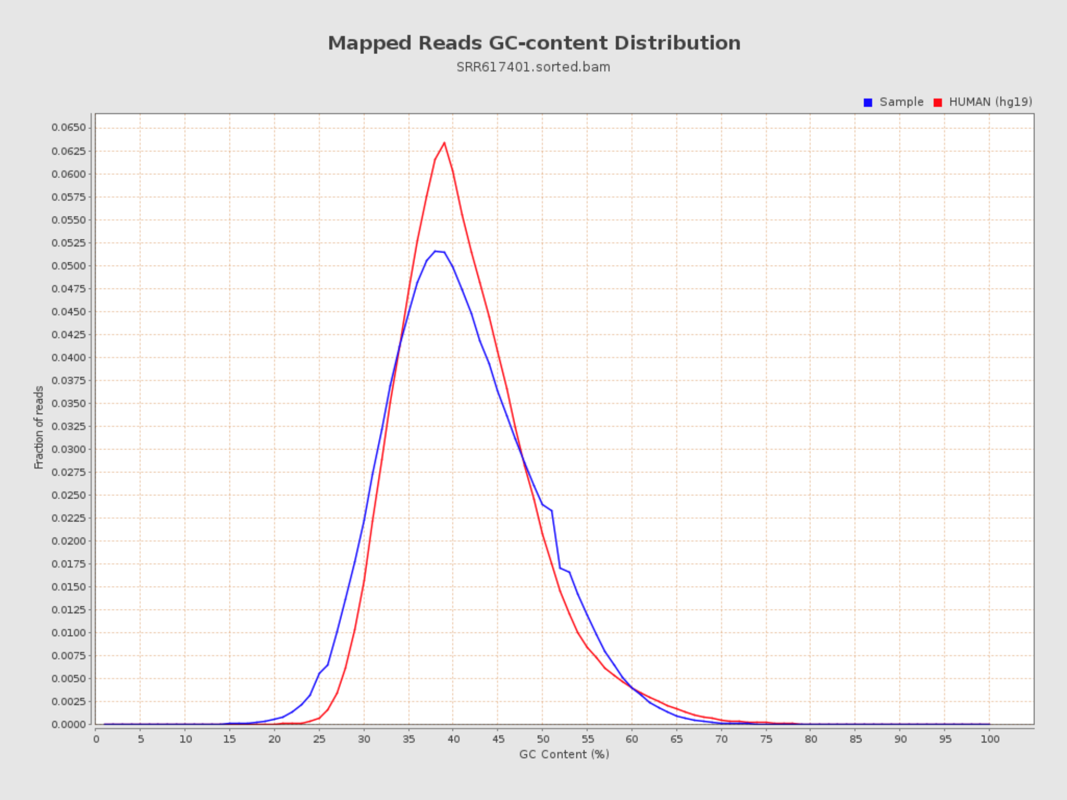
7. Results : Duplication Rate Histogram



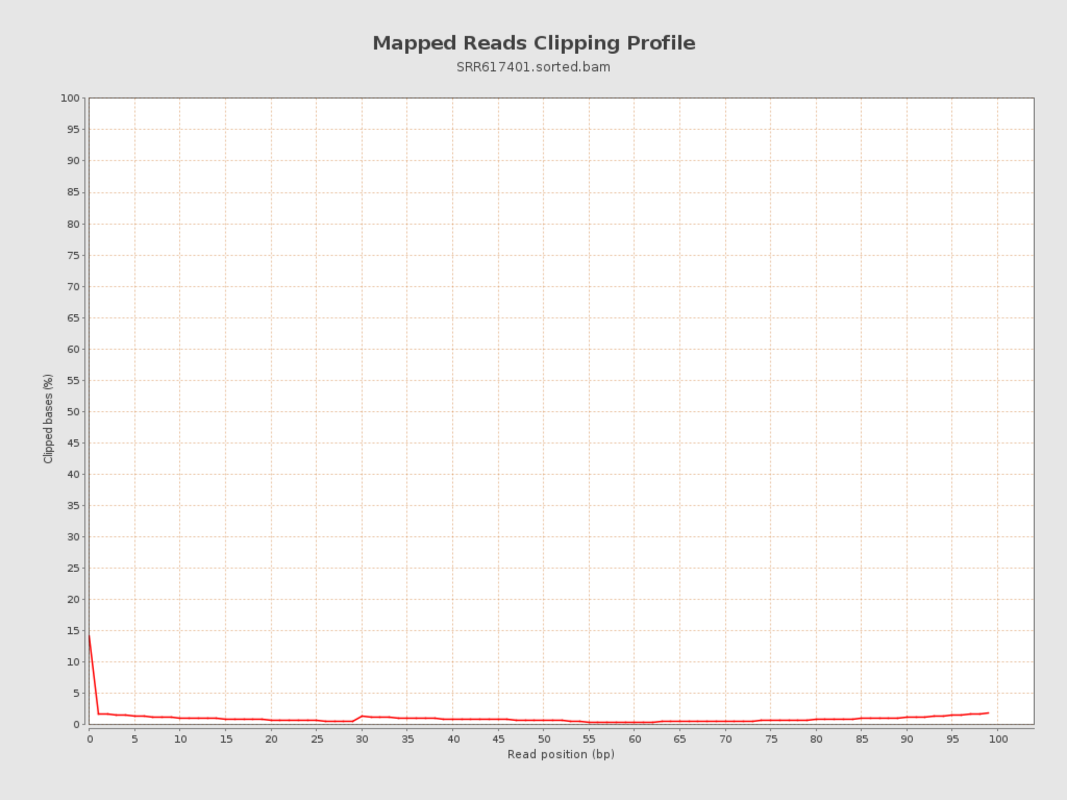
8. Results : Mapped Reads Nucleotide Content



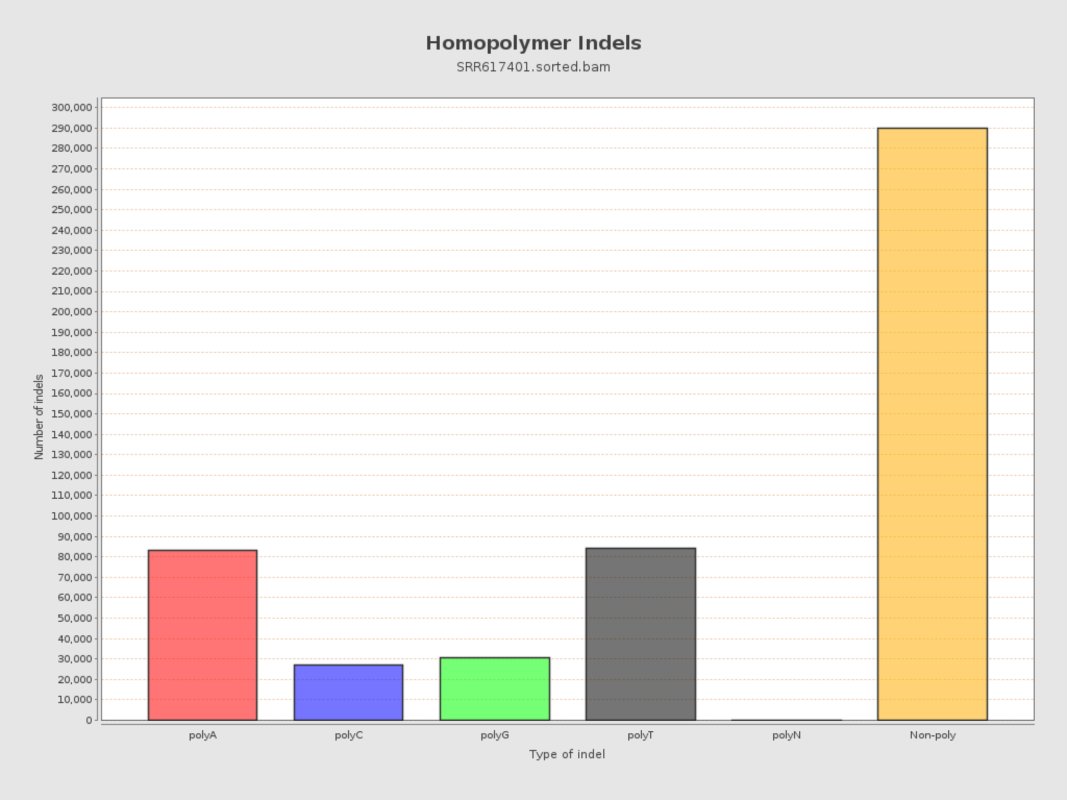
9. Results : Mapped Reads GC-content Distribution



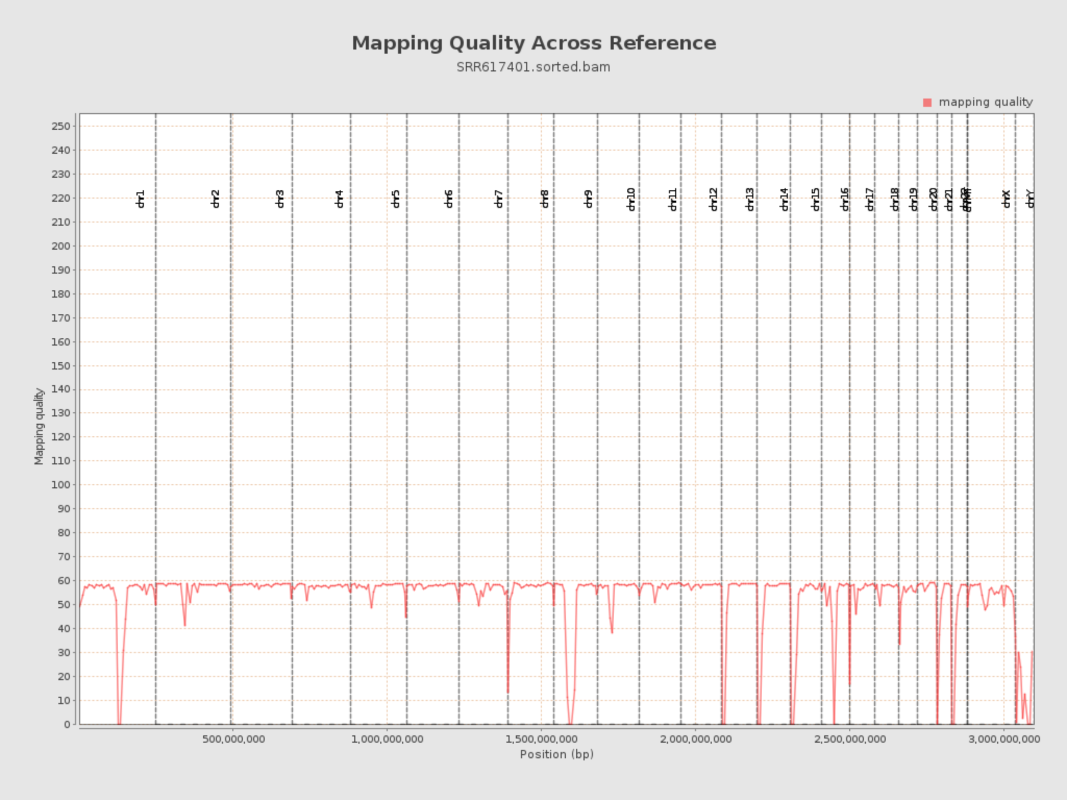
10. Results : Mapped Reads Clipping Profile



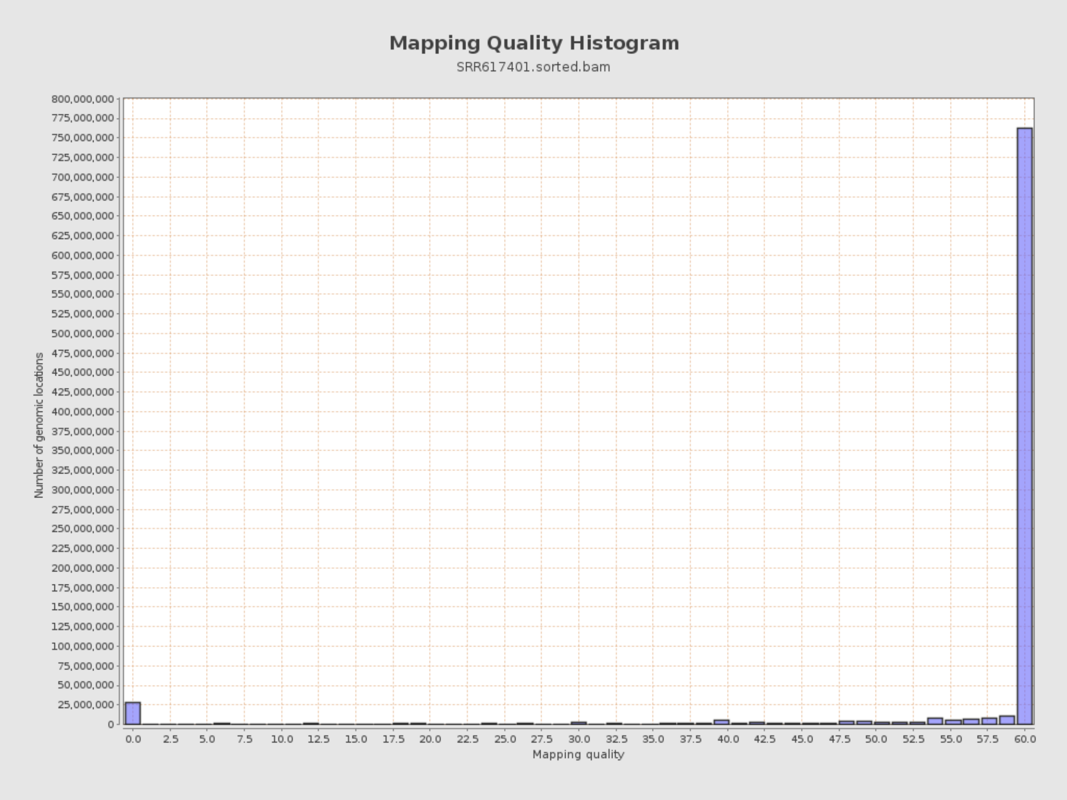
11. Results : Homopolymer Indels



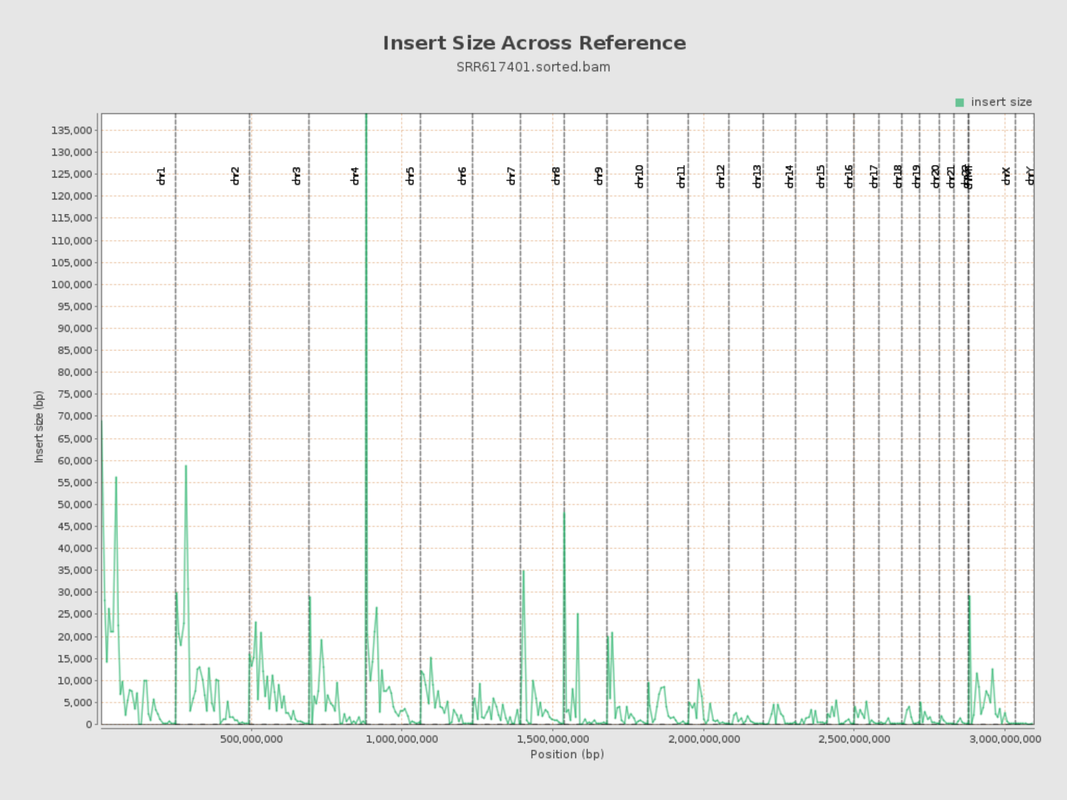
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram