Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/10 19:00:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617651.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_SRR617651 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617651_1.fastq.gz SRR617651_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 19:00:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617651.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,684,391 / 95.89%
Unmapped reads	1,315,609 / 4.11%
Mapped paired reads	30,684,391 / 95.89%
Mapped reads, first in pair	15,374,223 / 48.04%
Mapped reads, second in pair	15,310,168 / 47.84%
Mapped reads, both in pair	30,155,548 / 94.24%
Mapped reads, singletons	528,843 / 1.65%
Secondary alignments	0
Supplementary alignments	142,036 / 0.44%
Read min/max/mean length	30 / 100 / 100.18
Duplicated reads (estimated)	7,177,040 / 22.43%
Duplication rate	10.89%
Clipped reads	6,143,818 / 19.2%

2.2. ACGT Content

Number/percentage of A's	888,545,219 / 29.73%
Number/percentage of C's	596,868,801 / 19.97%
Number/percentage of T's	887,923,670 / 29.71%
Number/percentage of G's	613,265,822 / 20.52%
Number/percentage of N's	2,011,529 / 0.07%

GC Percentage	40.49%

2.3. Coverage

Mean	0.966
Standard Deviation	10.8823

2.4. Mapping Quality

Mean Mapping Quality	52.74

2.5. Insert size

Mean	31,069.54
Standard Deviation	1,608,422.44
P25/Median/P75	181 / 226 / 295

2.6. Mismatches and indels

General error rate	1.4%
Mismatches	40,984,779
Insertions	465,156
Mapped reads with at least one insertion	1.49%
Deletions	1,101,830
Mapped reads with at least one deletion	3.52%
Homopolymer indels	47.69%

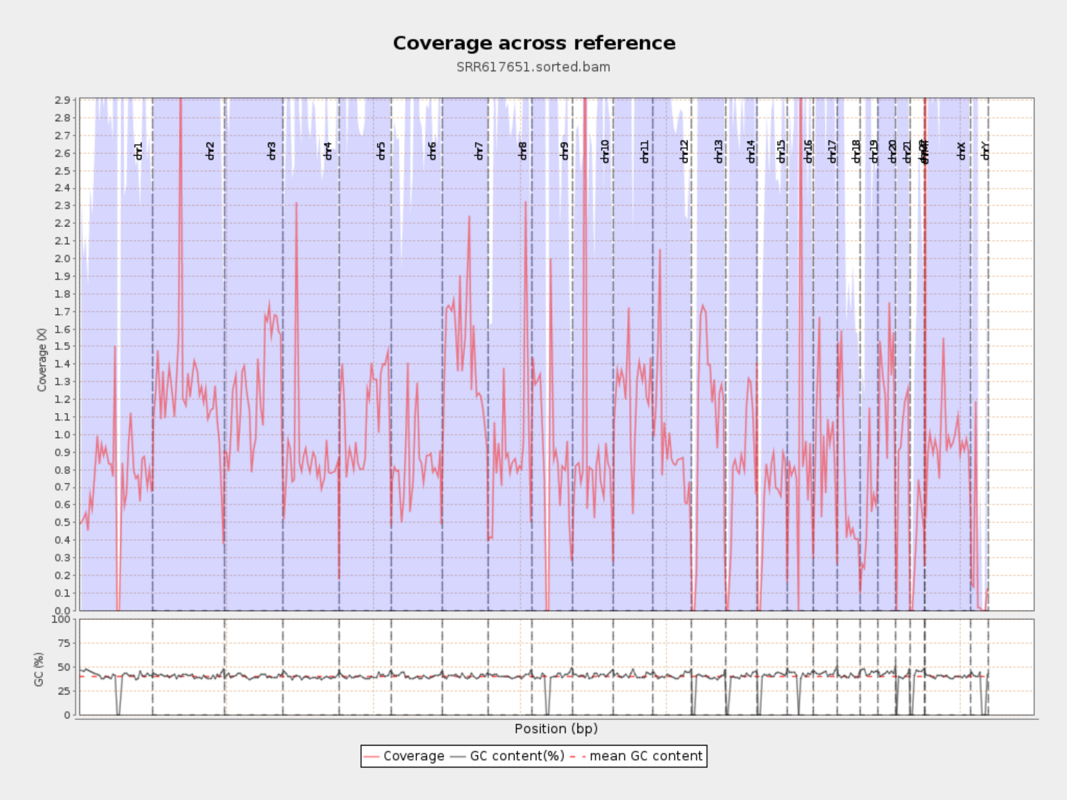
2.7. Chromosome stats

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

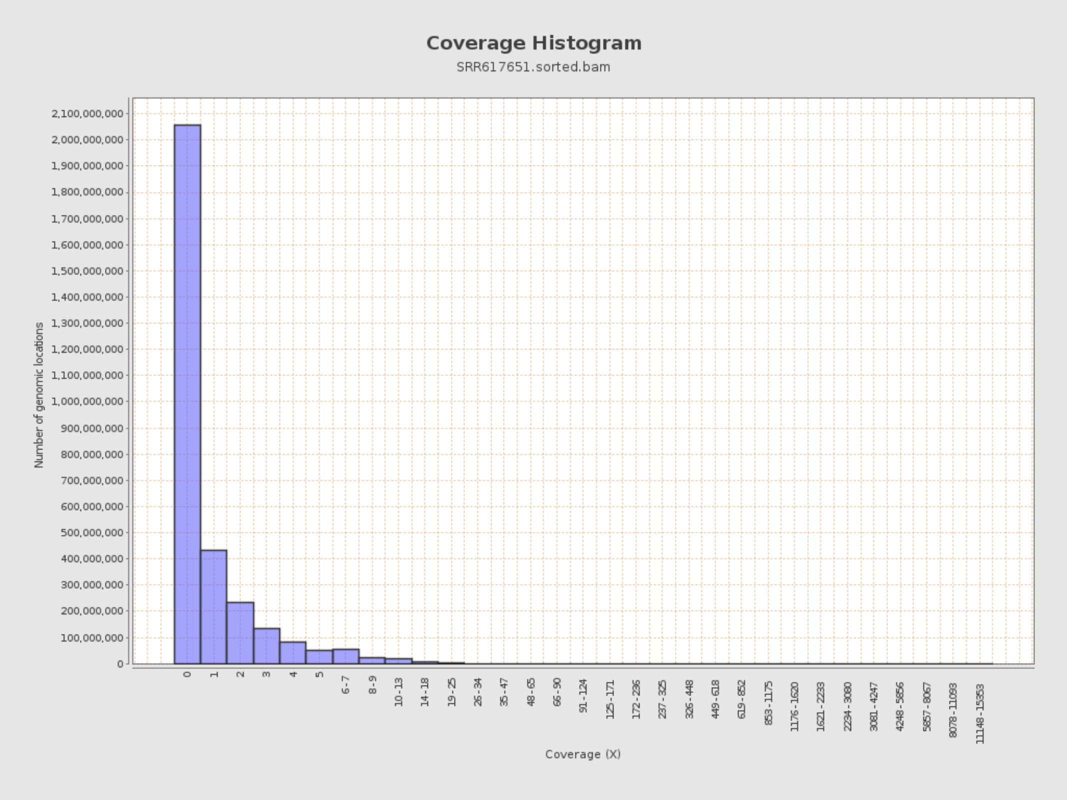
		bases	coverage	deviation
chr1	249250621	183357363	0.7356	10.4956
chr2	243199373	308196087	1.2673	12.4456
chr3	198022430	250650303	1.2658	2.5089
chr4	191154276	166989493	0.8736	8.7653
chr5	180915260	197972665	1.0943	2.3632
chr6	171115067	144648582	0.8453	5.8694
chr7	159138663	233864840	1.4696	13.4729
chr8	146364022	133007098	0.9087	4.1833
chr9	141213431	122750613	0.8693	21.3446
chr10	135534747	126756990	0.9352	21.9881
chr11	135006516	164501813	1.2185	12.2246
chr12	133851895	127647373	0.9536	2.1672
chr13	115169878	128916324	1.1194	2.3326
chr14	107349540	85375635	0.7953	2.4587
chr15	102531392	63952816	0.6237	1.5935
chr16	90354753	82836539	0.9168	17.0698
chr17	81195210	73949502	0.9108	13.1619
chr18	78077248	55206473	0.7071	18.6152
chr19	59128983	31799380	0.5378	6.2874
chr20	63025520	81179671	1.288	3.112
chr21	48129895	43742530	0.9088	4.4642
chr22	51304566	19273125	0.3757	1.2815
chrMT	16571	3204899	193.4041	137.0331
chrX	155270560	148502018	0.9564	4.4599

chrY	59373566	12159279	0.2048	18.0457

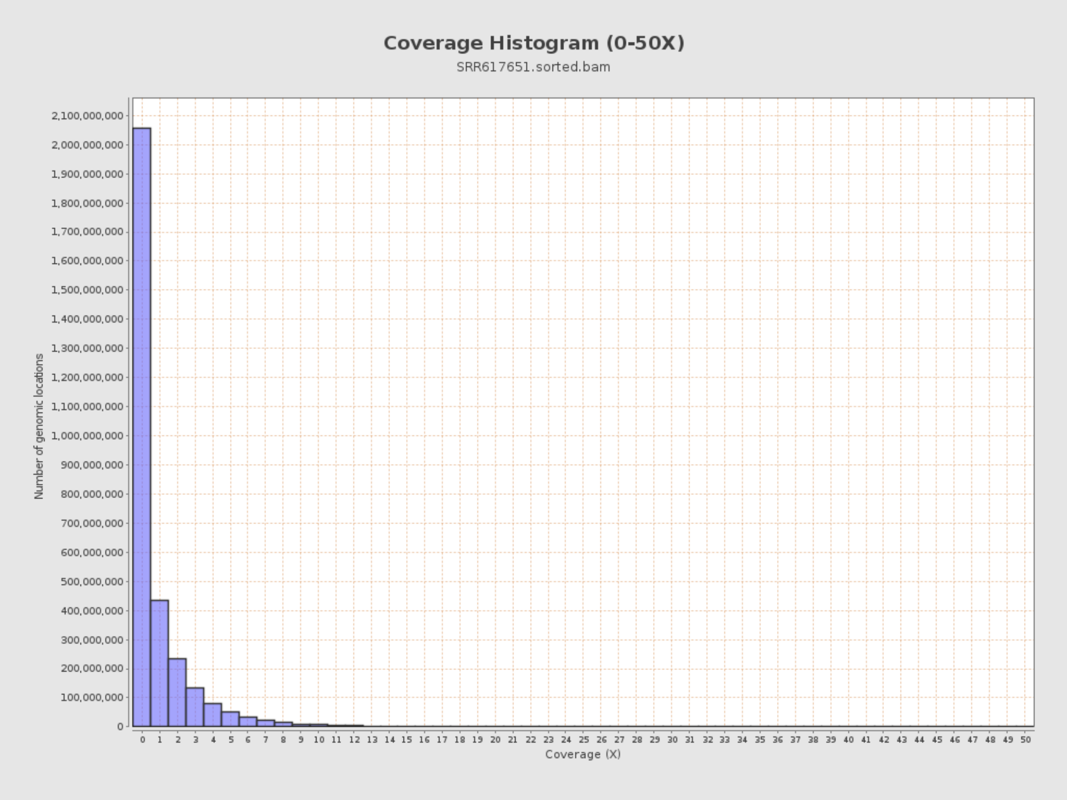
3. Results : Coverage across reference



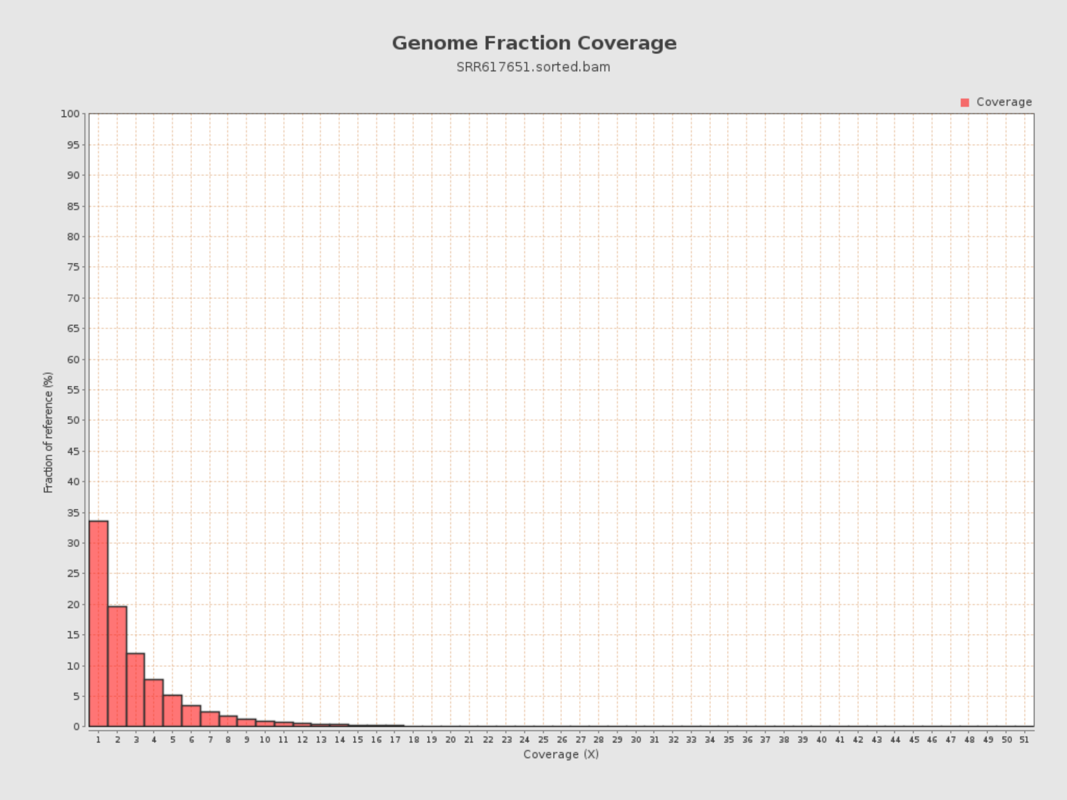
4. Results : Coverage Histogram



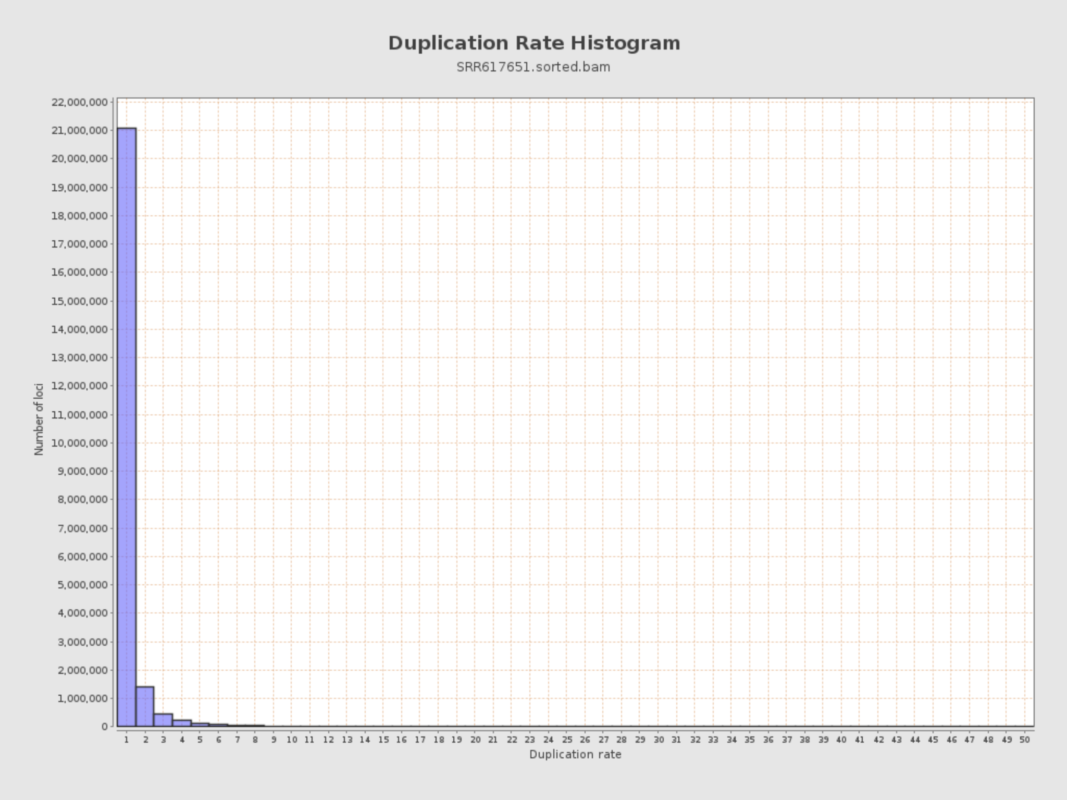
5. Results : Coverage Histogram (0-50X)



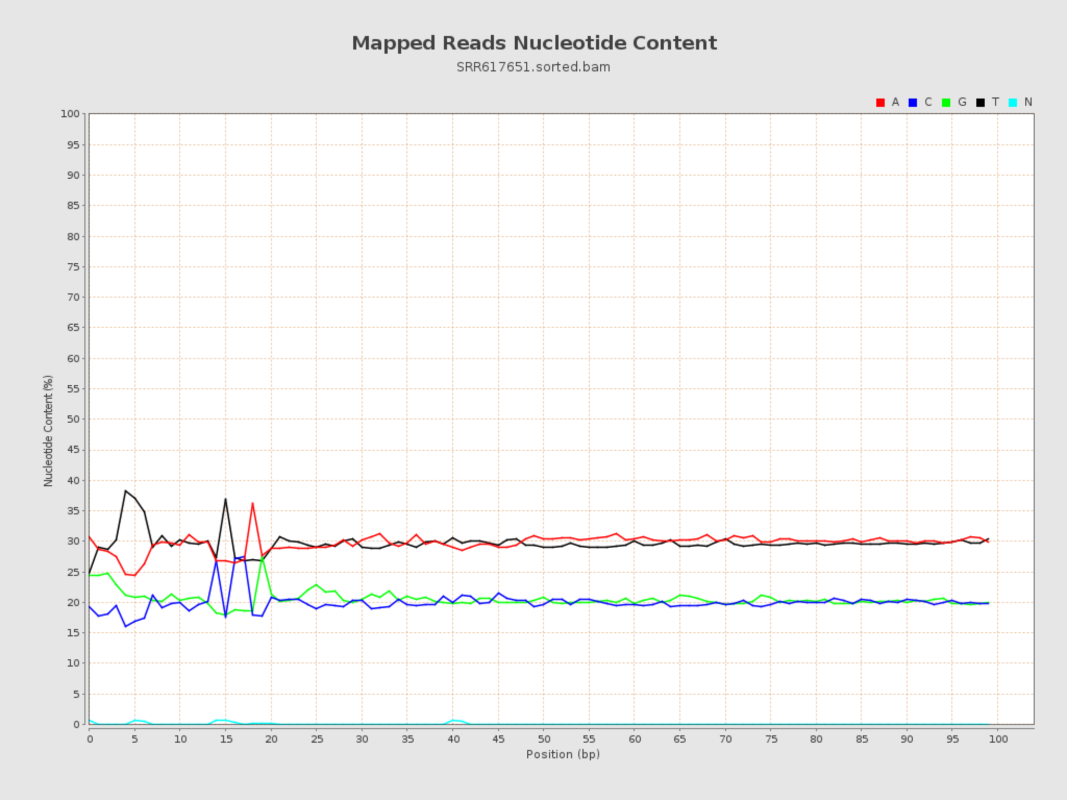
6. Results : Genome Fraction Coverage



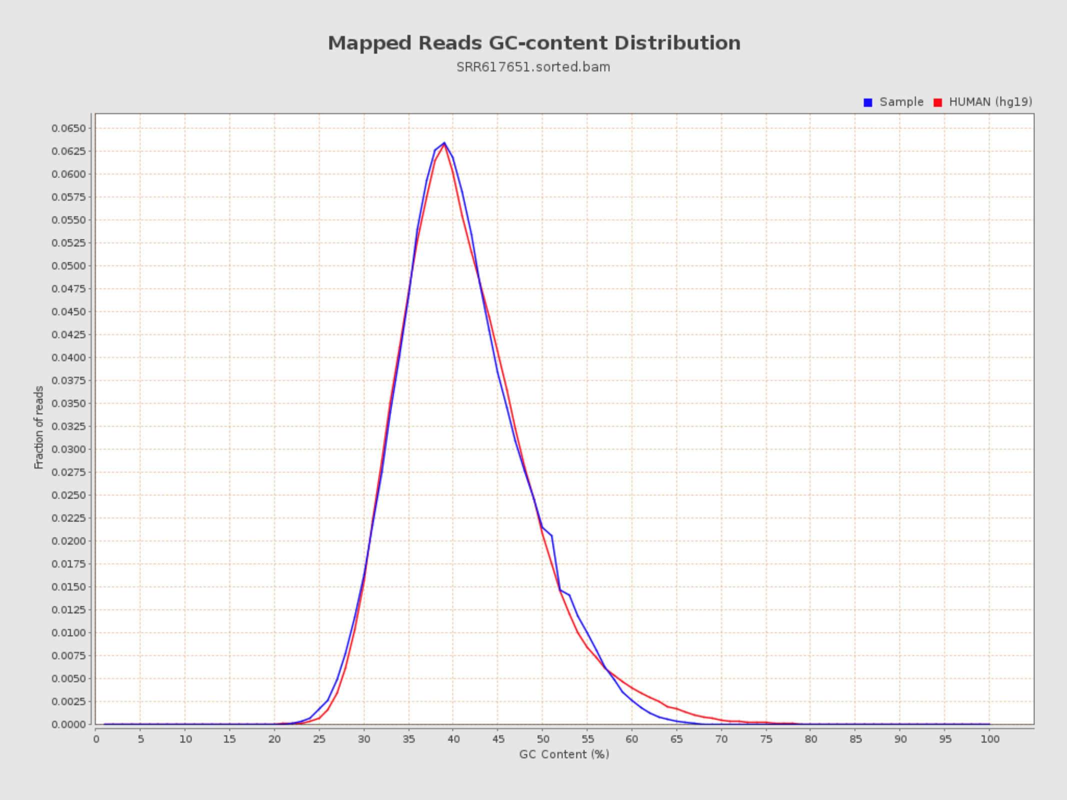
7. Results : Duplication Rate Histogram



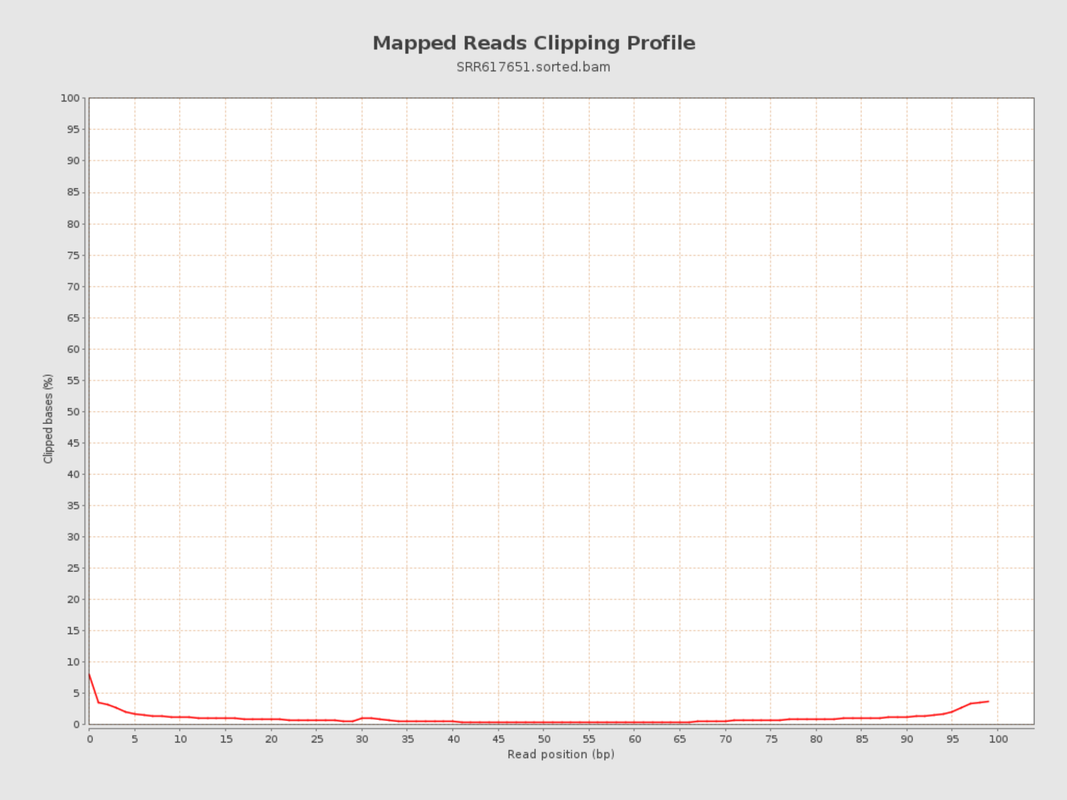
8. Results : Mapped Reads Nucleotide Content



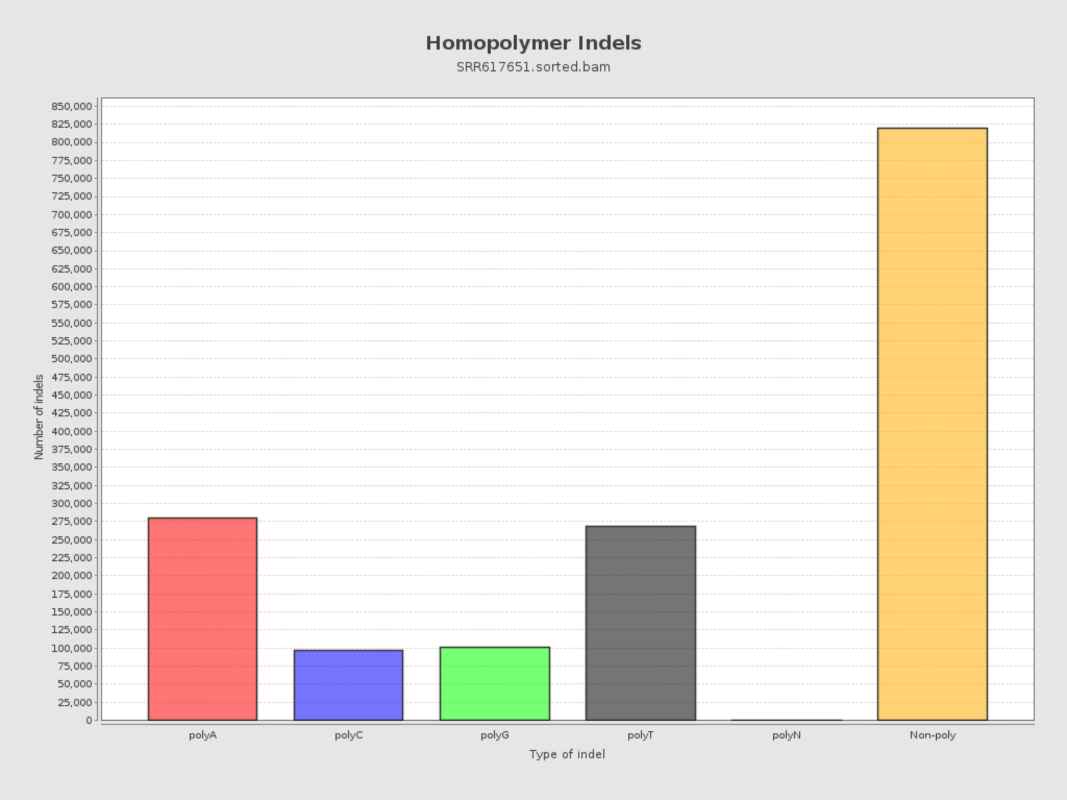
9. Results : Mapped Reads GC-content Distribution



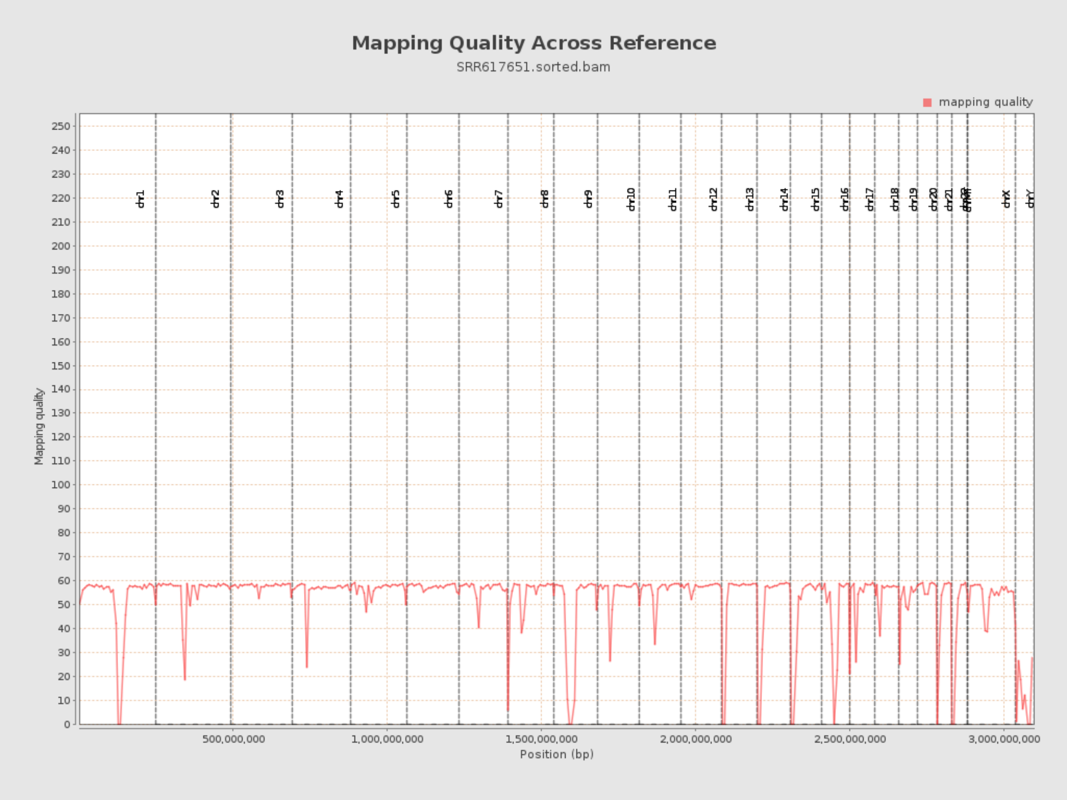
10. Results : Mapped Reads Clipping Profile



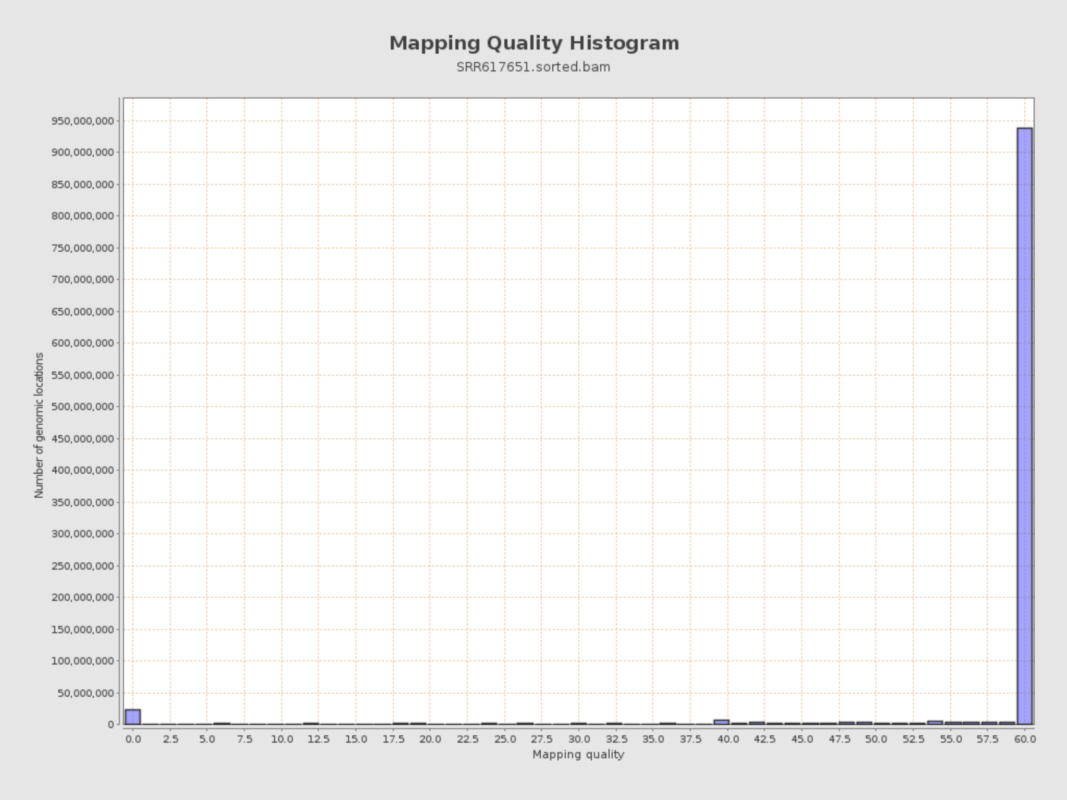
11. Results : Homopolymer Indels



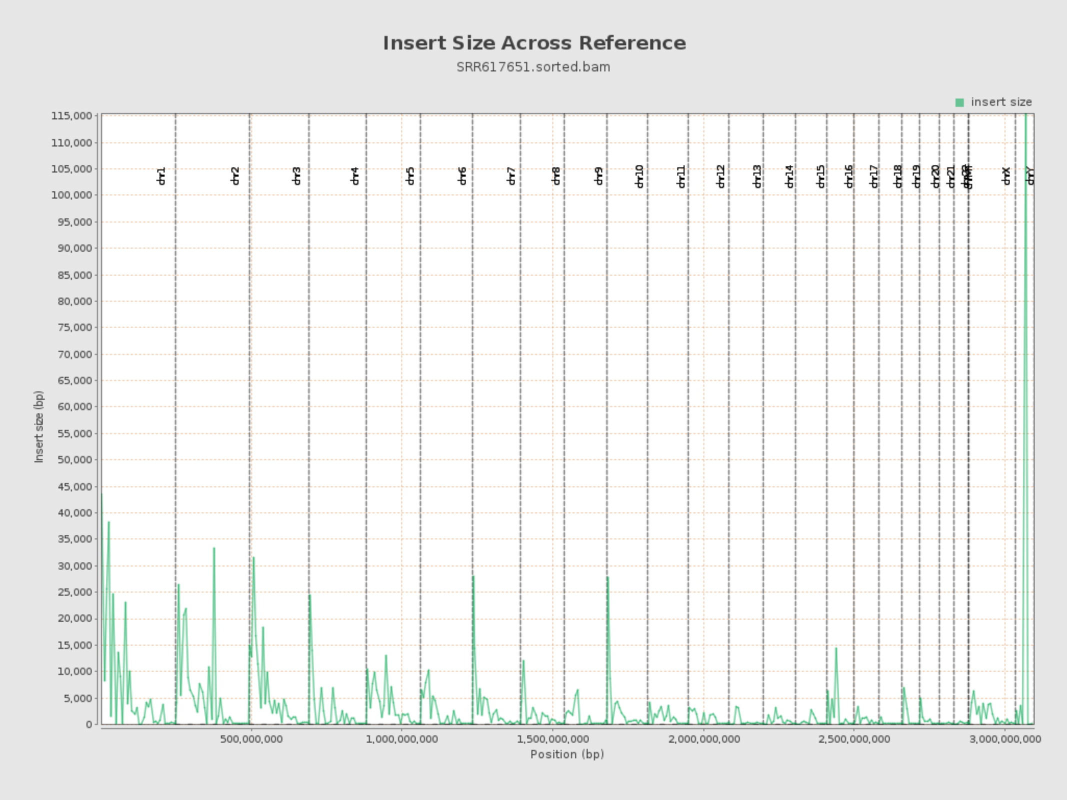
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram