Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/10 15:56:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617647.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_SRR617647 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617647_1.fastq.gz SRR617647_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 15:56:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617647.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,191,074 / 94.35%
Unmapped reads	1,808,926 / 5.65%
Mapped paired reads	30,191,074 / 94.35%
Mapped reads, first in pair	15,160,210 / 47.38%
Mapped reads, second in pair	15,030,864 / 46.97%
Mapped reads, both in pair	29,659,108 / 92.68%
Mapped reads, singletons	531,966 / 1.66%
Secondary alignments	0
Supplementary alignments	143,380 / 0.45%
Read min/max/mean length	30 / 100 / 100.18
Duplicated reads (estimated)	6,904,238 / 21.58%
Duplication rate	10.66%
Clipped reads	6,332,736 / 19.79%

2.2. ACGT Content

Number/percentage of A's	873,424,345 / 29.8%
Number/percentage of C's	583,905,399 / 19.93%
Number/percentage of T's	871,389,493 / 29.74%
Number/percentage of G's	599,664,772 / 20.46%
Number/percentage of N's	2,095,634 / 0.07%

GC Percentage	40.39%

2.3. Coverage

Mean	0.9472
Standard Deviation	10.6891

2.4. Mapping Quality

Mean Mapping Quality	52.66

2.5. Insert size

Mean	32,667.98
Standard Deviation	1,659,122.61
P25/Median/P75	179 / 222 / 287

2.6. Mismatches and indels

General error rate	1.53%
Mismatches	43,879,061
Insertions	454,846
Mapped reads with at least one insertion	1.48%
Deletions	1,071,812
Mapped reads with at least one deletion	3.48%
Homopolymer indels	47.71%

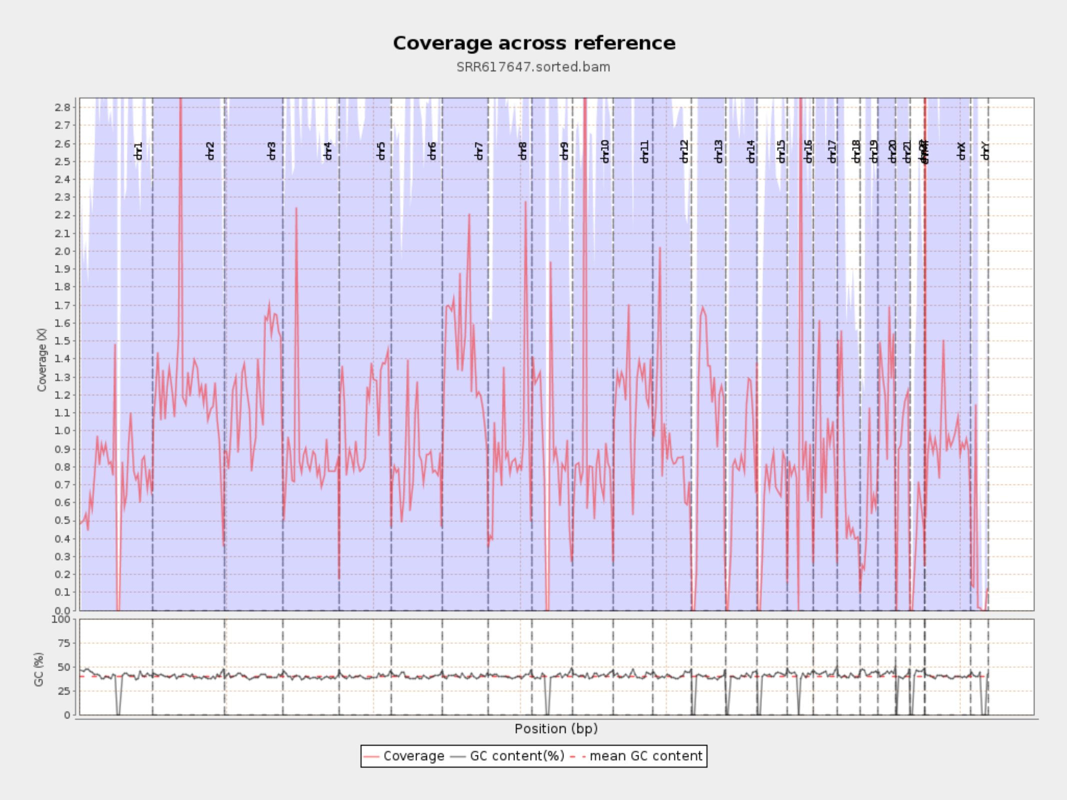
2.7. Chromosome stats

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

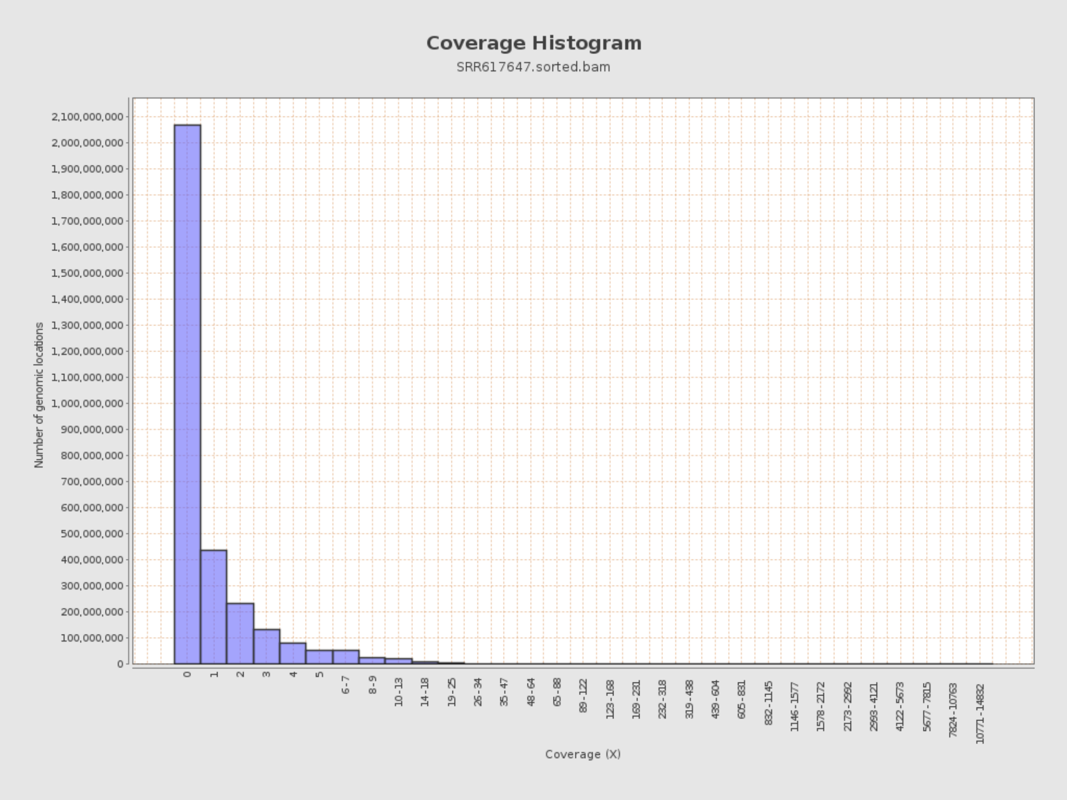
		bases	coverage	deviation
chr1	249250621	179623565	0.7207	10.2438
chr2	243199373	302967772	1.2458	12.2533
chr3	198022430	246076915	1.2427	2.4672
chr4	191154276	164034127	0.8581	8.413
chr5	180915260	193977151	1.0722	2.3223
chr6	171115067	142116573	0.8305	5.7859
chr7	159138663	229472261	1.442	13.497
chr8	146364022	130658149	0.8927	4.1741
chr9	141213431	120527263	0.8535	20.6893
chr10	135534747	124363137	0.9176	21.8076
chr11	135006516	161150022	1.1936	12.048
chr12	133851895	125206992	0.9354	2.1394
chr13	115169878	125991414	1.094	2.2879
chr14	107349540	83920614	0.7818	2.4694
chr15	102531392	62481340	0.6094	1.5706
chr16	90354753	81250090	0.8992	16.9095
chr17	81195210	72080938	0.8877	12.8262
chr18	78077248	54227983	0.6945	18.3697
chr19	59128983	30909324	0.5227	6.1464
chr20	63025520	78942132	1.2525	3.0471
chr21	48129895	42916636	0.8917	4.3721
chr22	51304566	18714777	0.3648	1.2678
chrMT	16571	3098020	186.9543	132.0081
chrX	155270560	145782042	0.9389	4.3068

chrY	59373566	11763666	0.1981	17.477

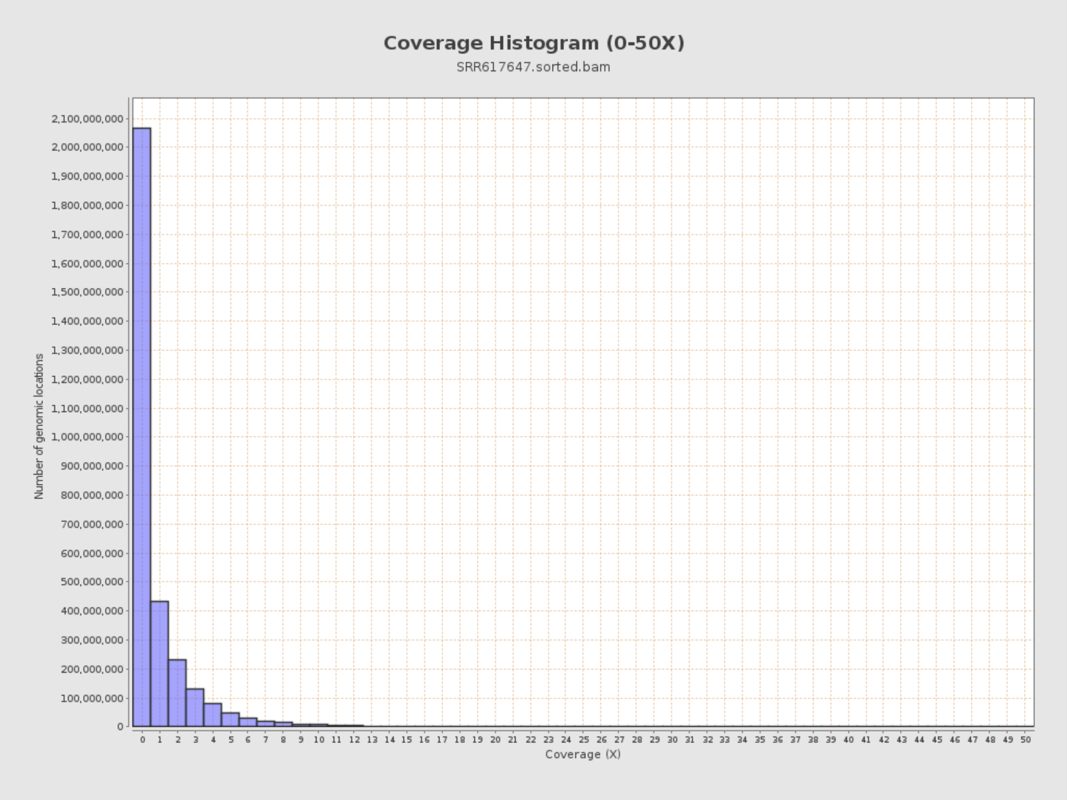
3. Results : Coverage across reference



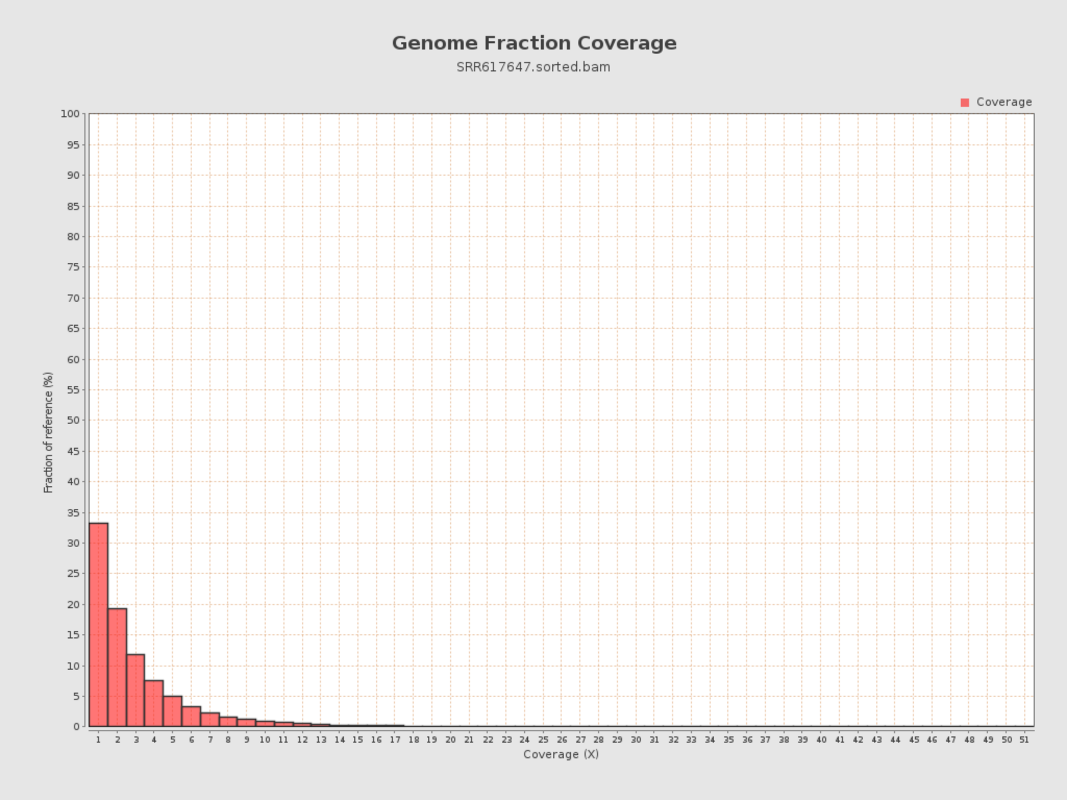
4. Results : Coverage Histogram



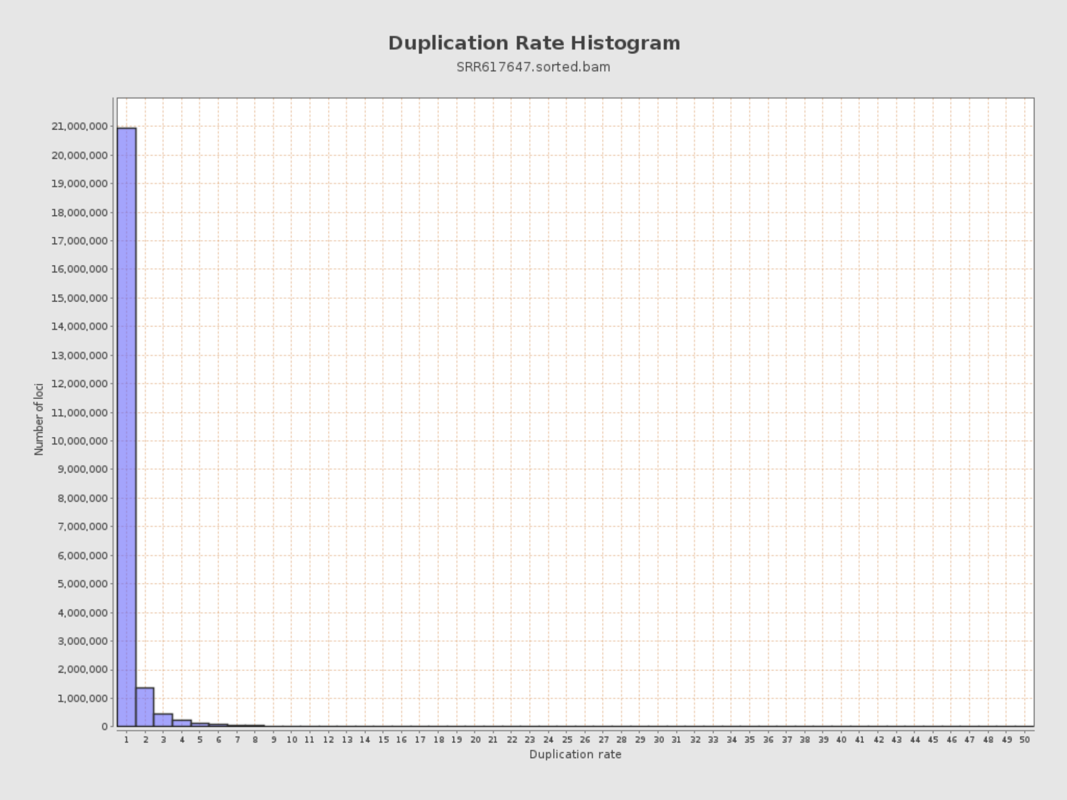
5. Results : Coverage Histogram (0-50X)



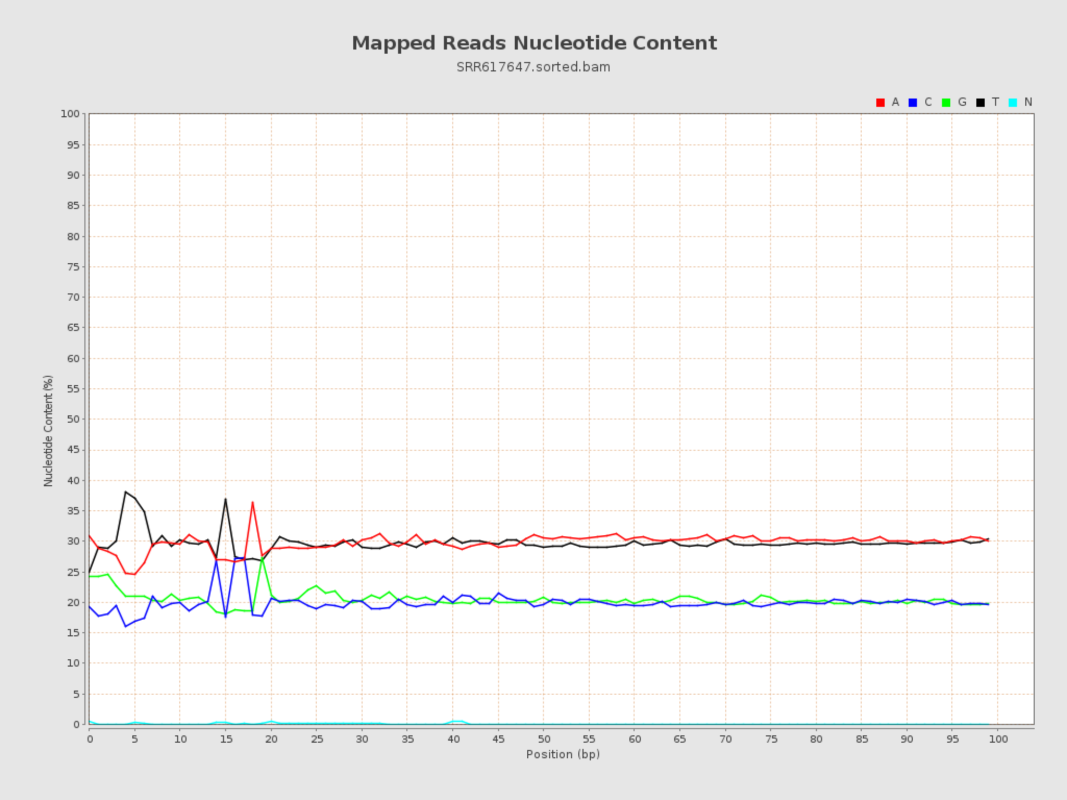
6. Results : Genome Fraction Coverage



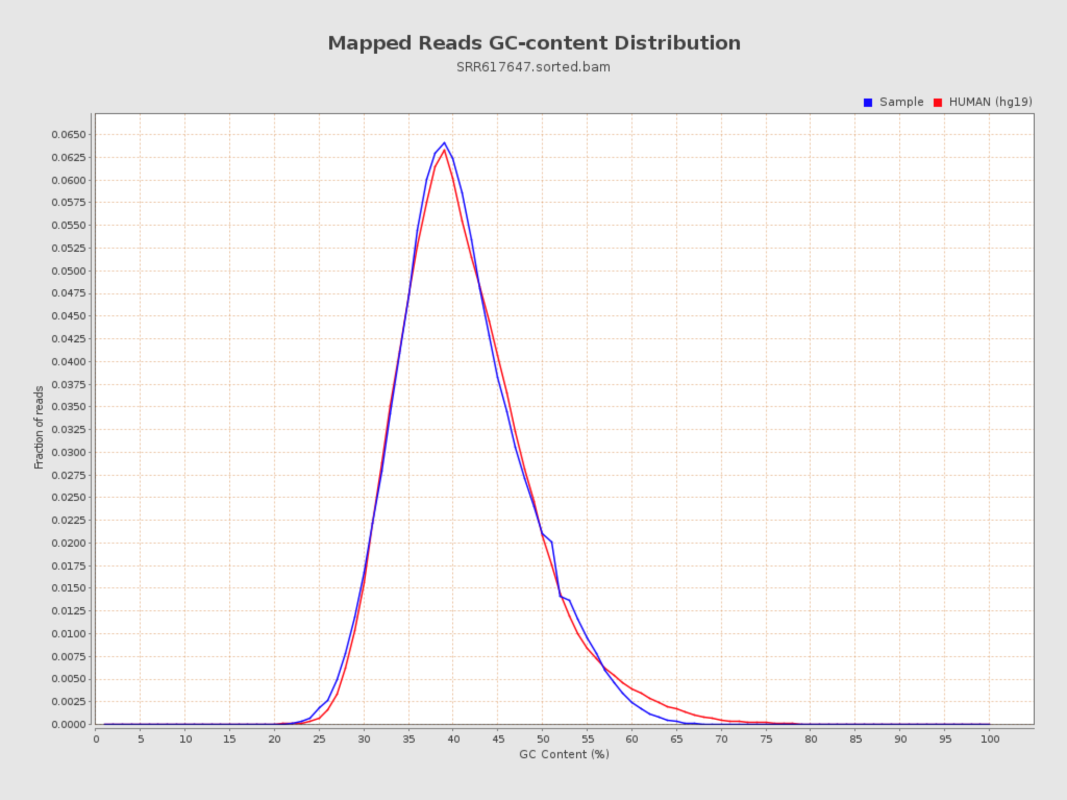
7. Results : Duplication Rate Histogram



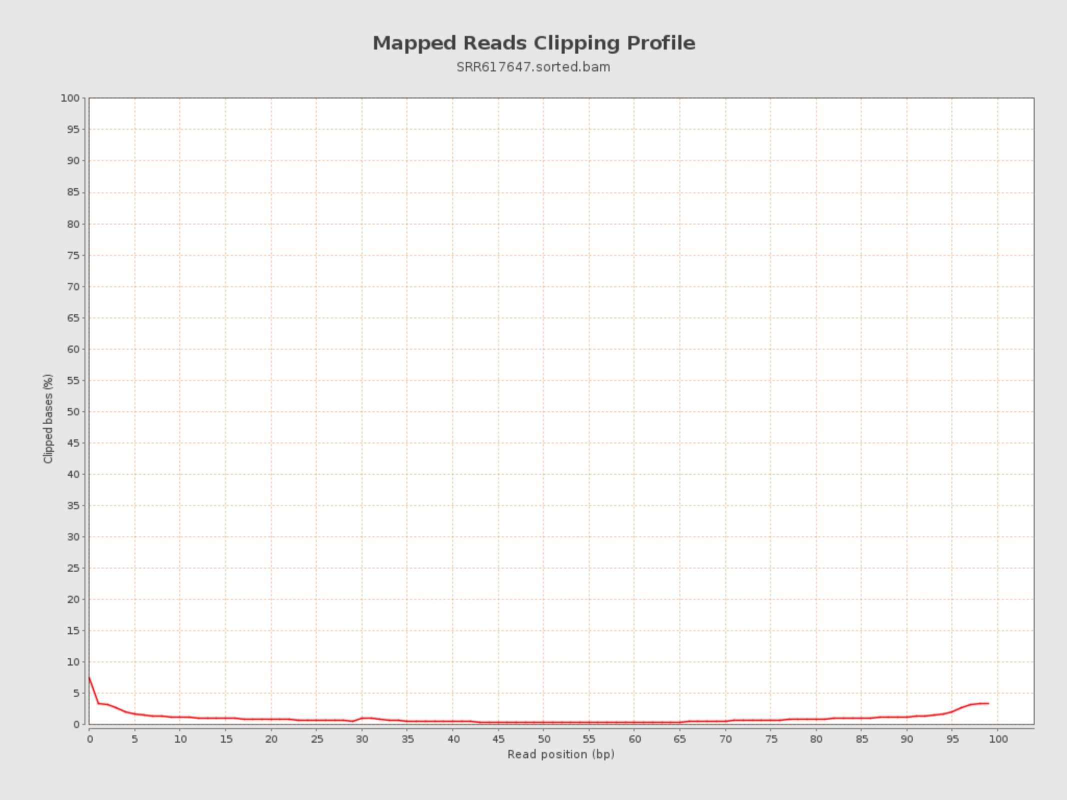
8. Results : Mapped Reads Nucleotide Content



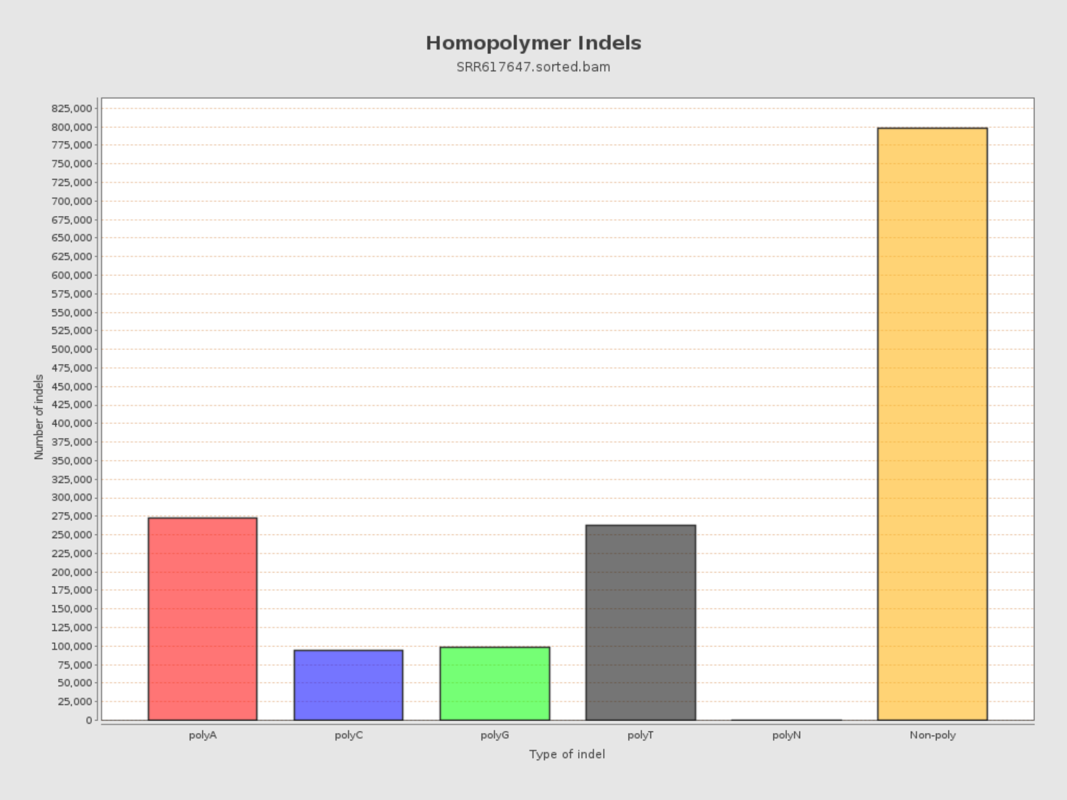
9. Results : Mapped Reads GC-content Distribution



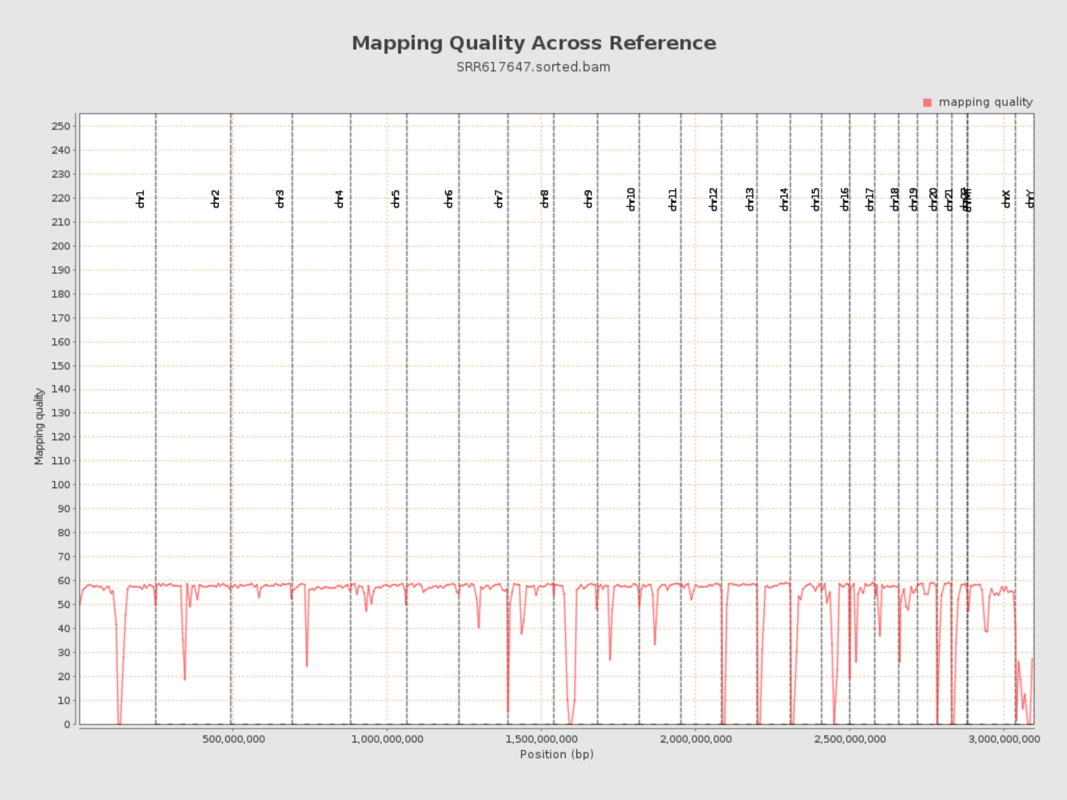
10. Results : Mapped Reads Clipping Profile



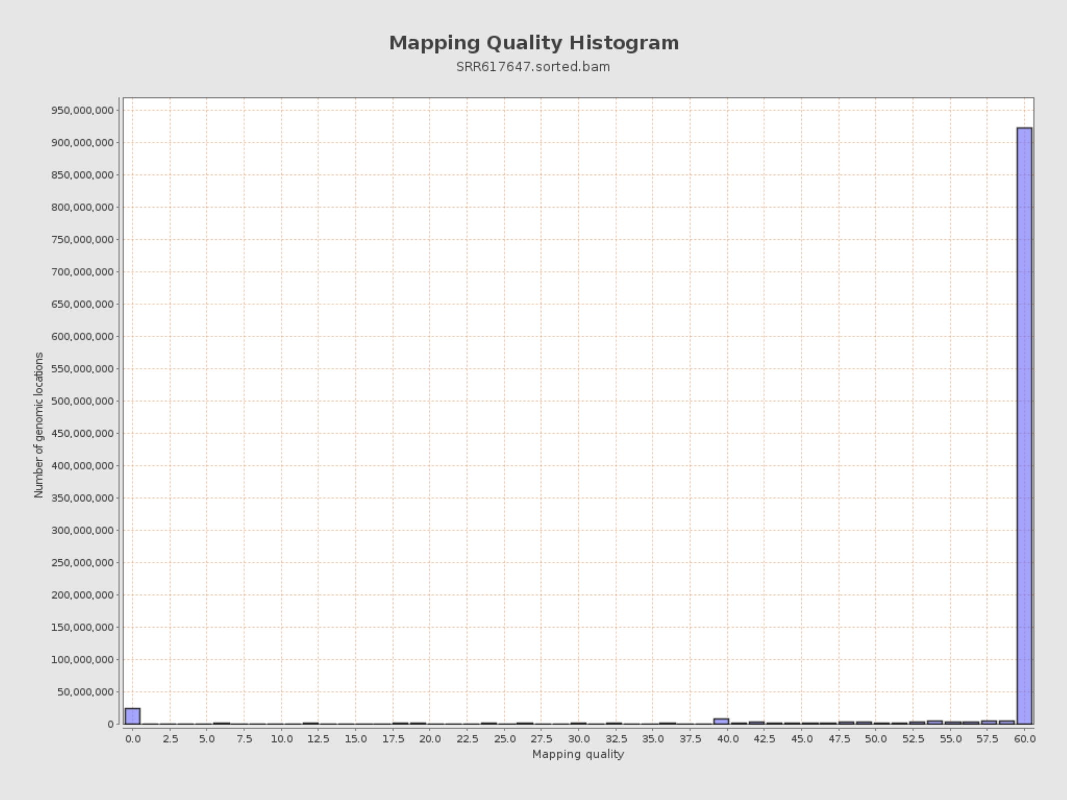
11. Results : Homopolymer Indels



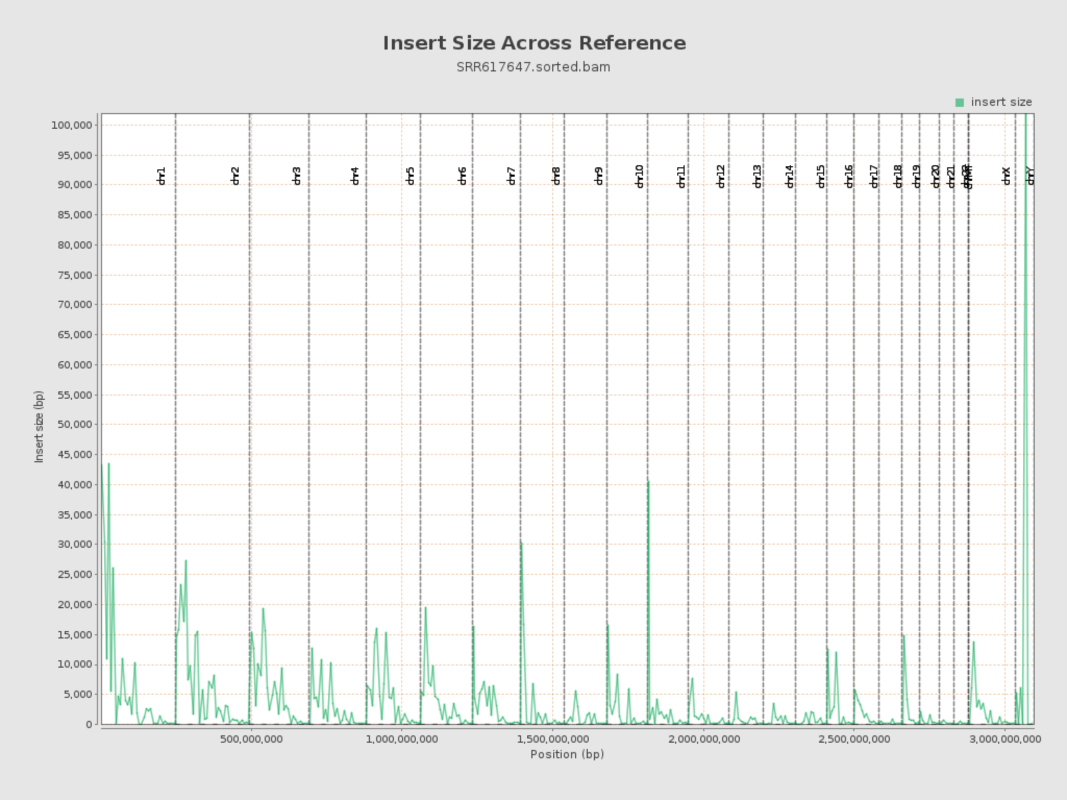
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram