Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/09 20:31:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617495.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_SRR617495 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617495_1.fastq.gz SRR617495_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 09 20:31:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617495.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,752,029 / 96.1%
Unmapped reads	1,247,971 / 3.9%
Mapped paired reads	30,752,029 / 96.1%
Mapped reads, first in pair	15,402,744 / 48.13%
Mapped reads, second in pair	15,349,285 / 47.97%
Mapped reads, both in pair	30,330,272 / 94.78%
Mapped reads, singletons	421,757 / 1.32%
Secondary alignments	0
Supplementary alignments	138,256 / 0.43%
Read min/max/mean length	30 / 100 / 100.17
Duplicated reads (estimated)	6,404,063 / 20.01%
Duplication rate	10.05%
Clipped reads	5,733,715 / 17.92%

2.2. ACGT Content

Number/percentage of A's	887,153,804 / 29.49%
Number/percentage of C's	608,474,750 / 20.23%
Number/percentage of T's	887,146,771 / 29.49%
Number/percentage of G's	623,745,442 / 20.73%
Number/percentage of N's	1,899,549 / 0.06%

GC Percentage	40.96%

2.3. Coverage

Mean	0.9724
Standard Deviation	9.85

2.4. Mapping Quality

Mean Mapping Quality	52.82

2.5. Insert size

Mean	29,812.93
Standard Deviation	1,595,436.92
P25/Median/P75	176 / 223 / 296

2.6. Mismatches and indels

General error rate	1.19%
Mismatches	35,031,932
Insertions	446,748
Mapped reads with at least one insertion	1.42%
Deletions	1,050,498
Mapped reads with at least one deletion	3.34%
Homopolymer indels	47.5%

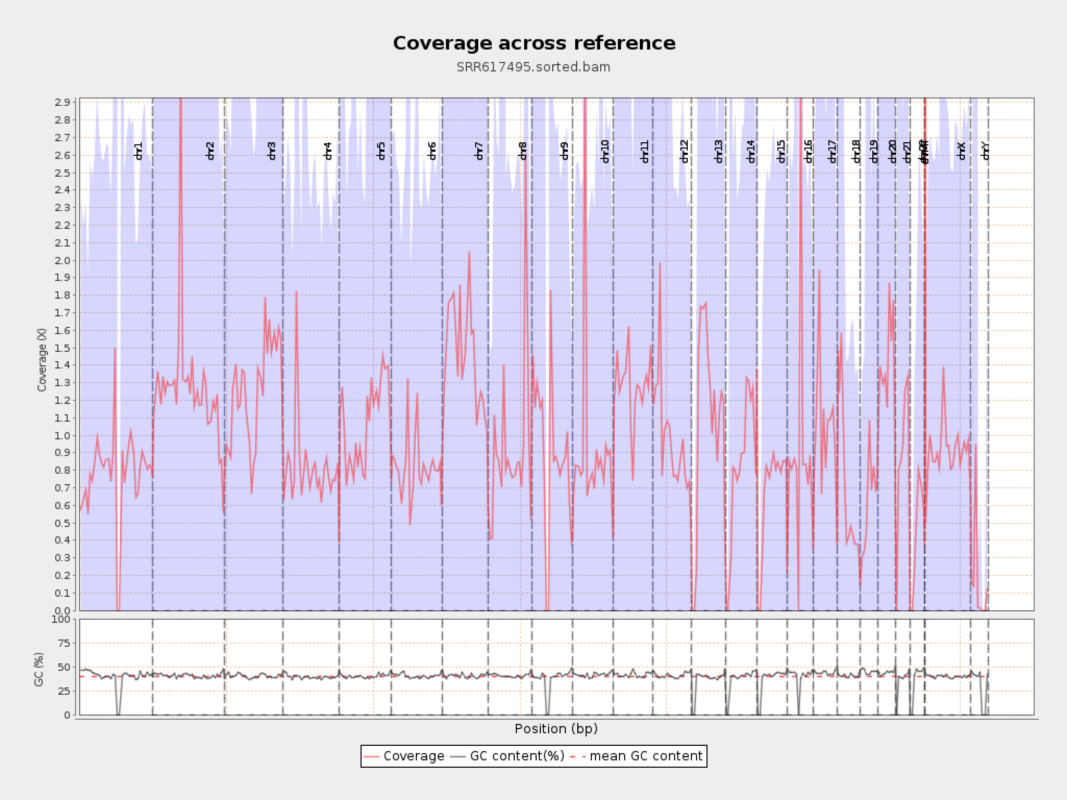
2.7. Chromosome stats

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

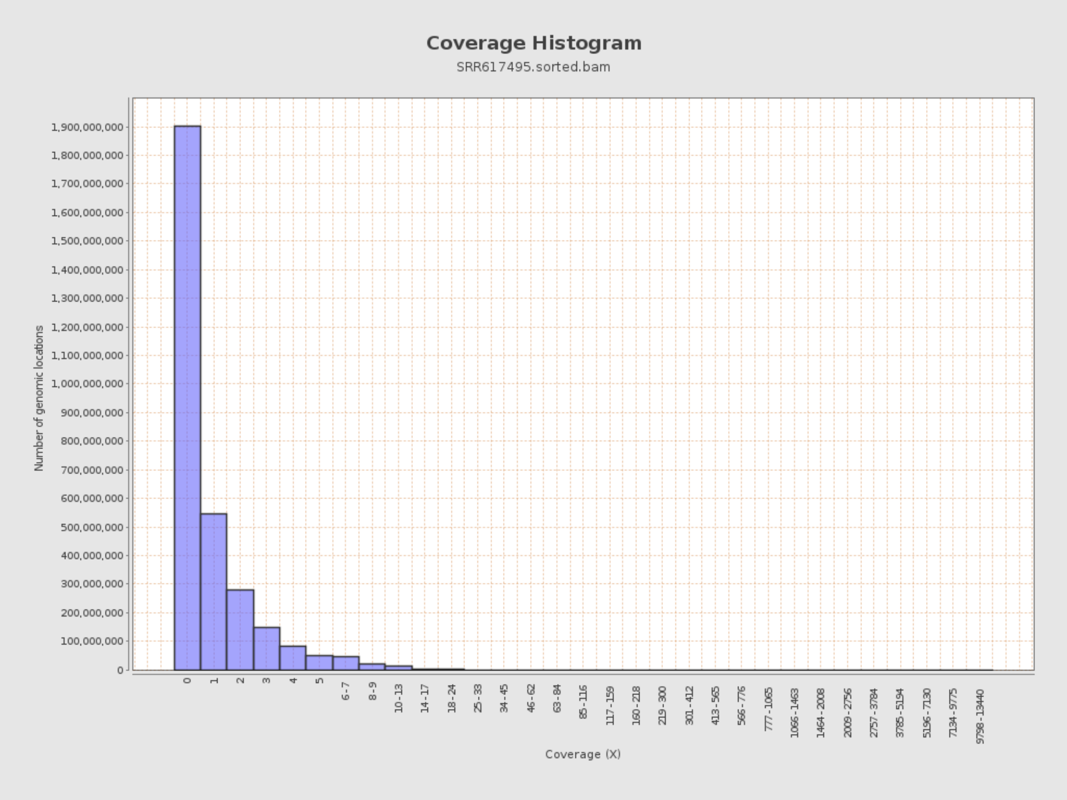
		bases	coverage	deviation
chr1	249250621	193923879	0.778	9.5802
chr2	243199373	311104841	1.2792	11.6556
chr3	198022430	248526570	1.255	2.2625
chr4	191154276	155491136	0.8134	6.3103
chr5	180915260	193420639	1.0691	2.1013
chr6	171115067	141762543	0.8285	5.4608
chr7	159138663	232178165	1.459	13.1858
chr8	146364022	133729285	0.9137	3.838
chr9	141213431	124775702	0.8836	18.8074
chr10	135534747	127529732	0.9409	18.9734
chr11	135006516	169780350	1.2576	12.8743
chr12	133851895	131599627	0.9832	2.0077
chr13	115169878	127766379	1.1094	2.1365
chr14	107349540	87582289	0.8159	2.2302
chr15	102531392	67831796	0.6616	1.4572
chr16	90354753	81017449	0.8967	14.9066
chr17	81195210	84231563	1.0374	13.8822
chr18	78077248	53821596	0.6893	17.2504
chr19	59128983	35782313	0.6052	5.9899
chr20	63025520	88701854	1.4074	2.8128
chr21	48129895	43228212	0.8982	3.8726
chr22	51304566	22585852	0.4402	1.2529
chrMT	16571	2107998	127.2101	93.5589
chrX	155270560	141292243	0.91	4.114

chrY	59373566	10441686	0.1759	13.9328

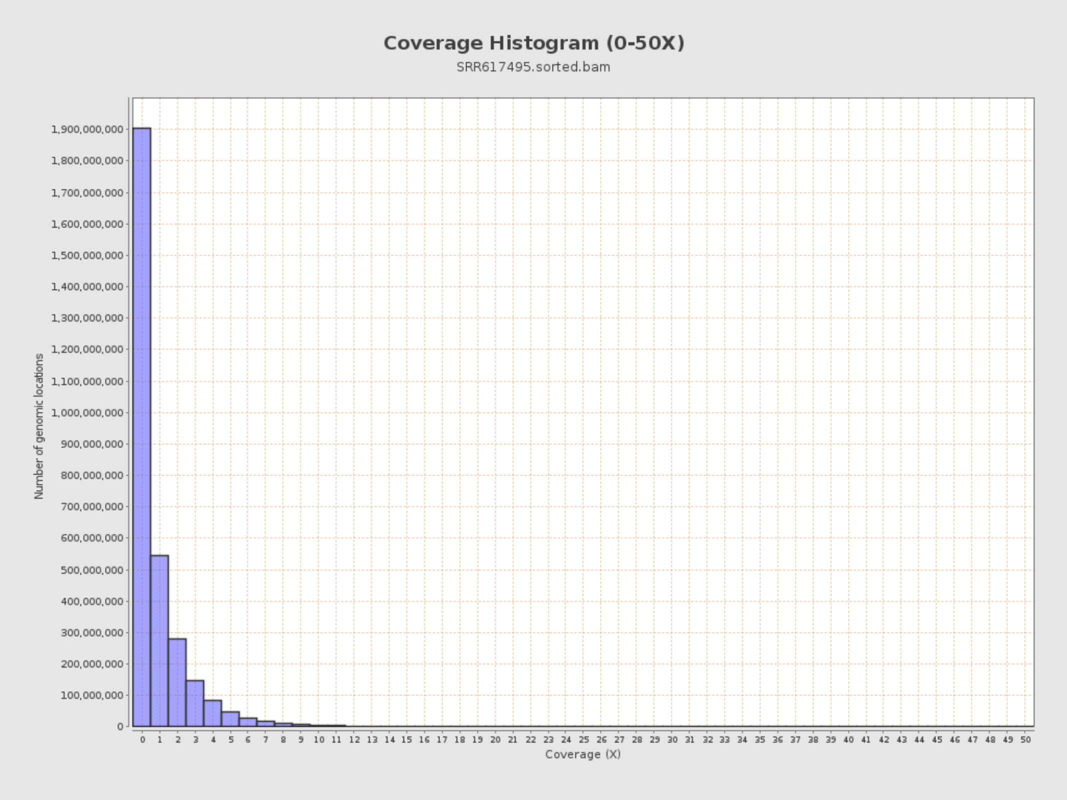
3. Results : Coverage across reference



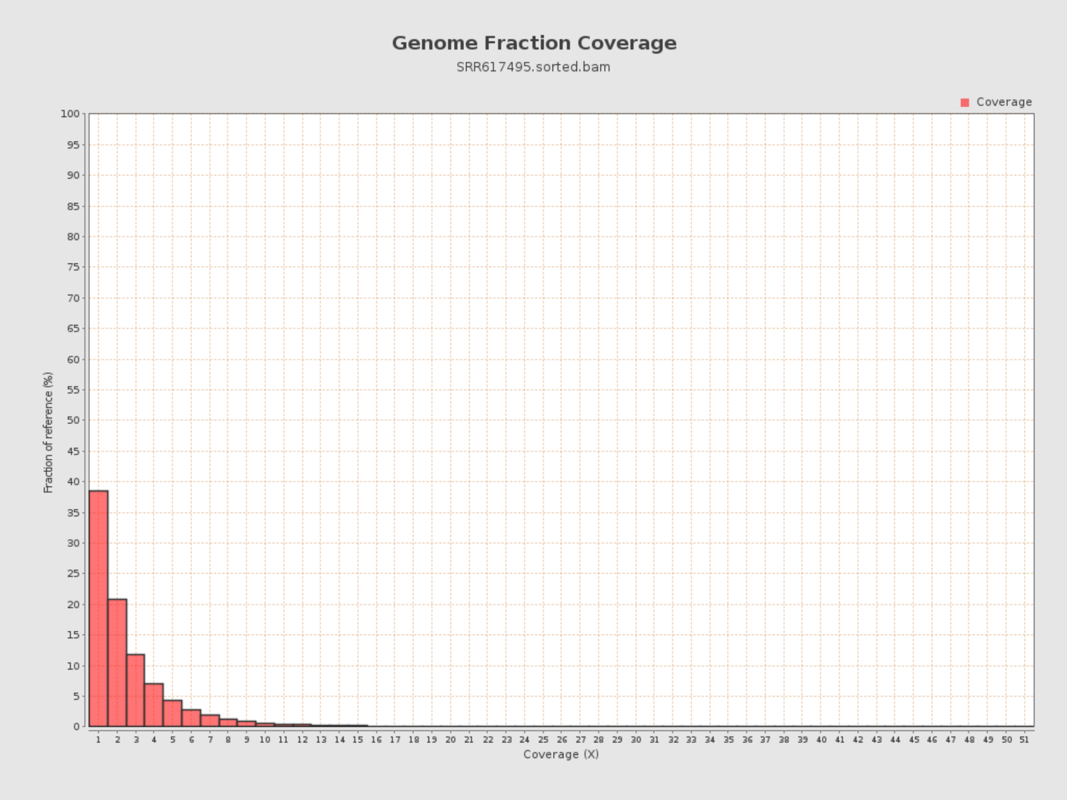
4. Results : Coverage Histogram



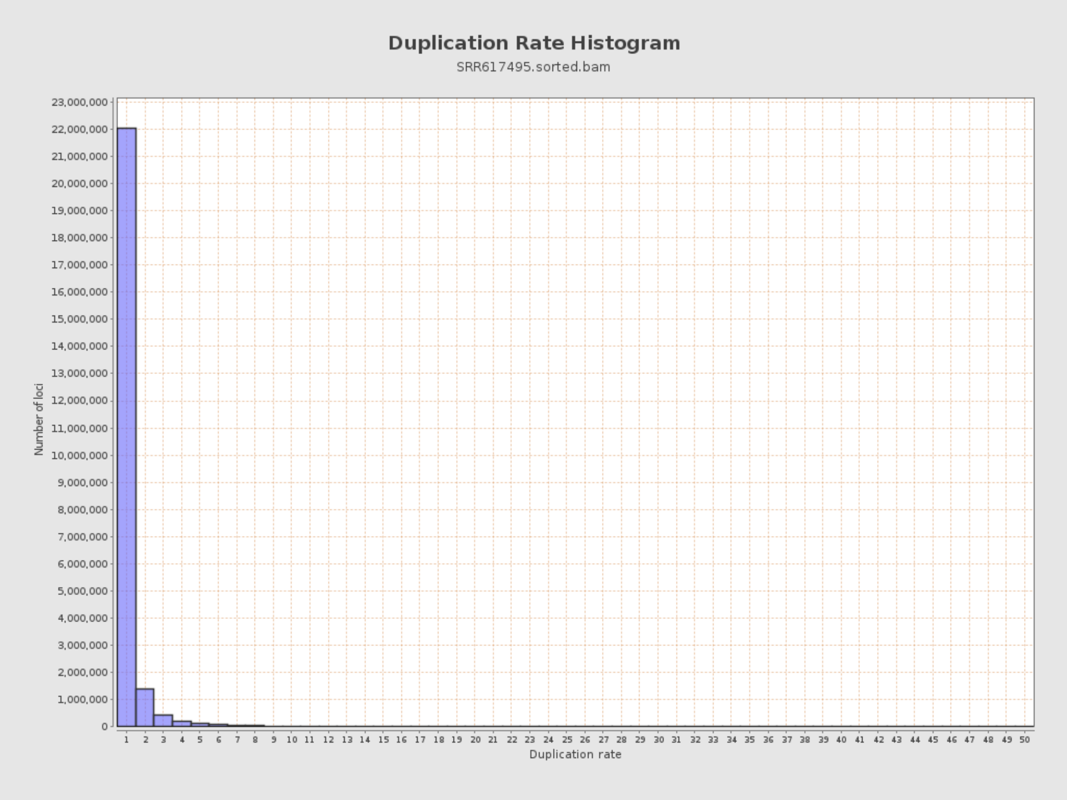
5. Results : Coverage Histogram (0-50X)



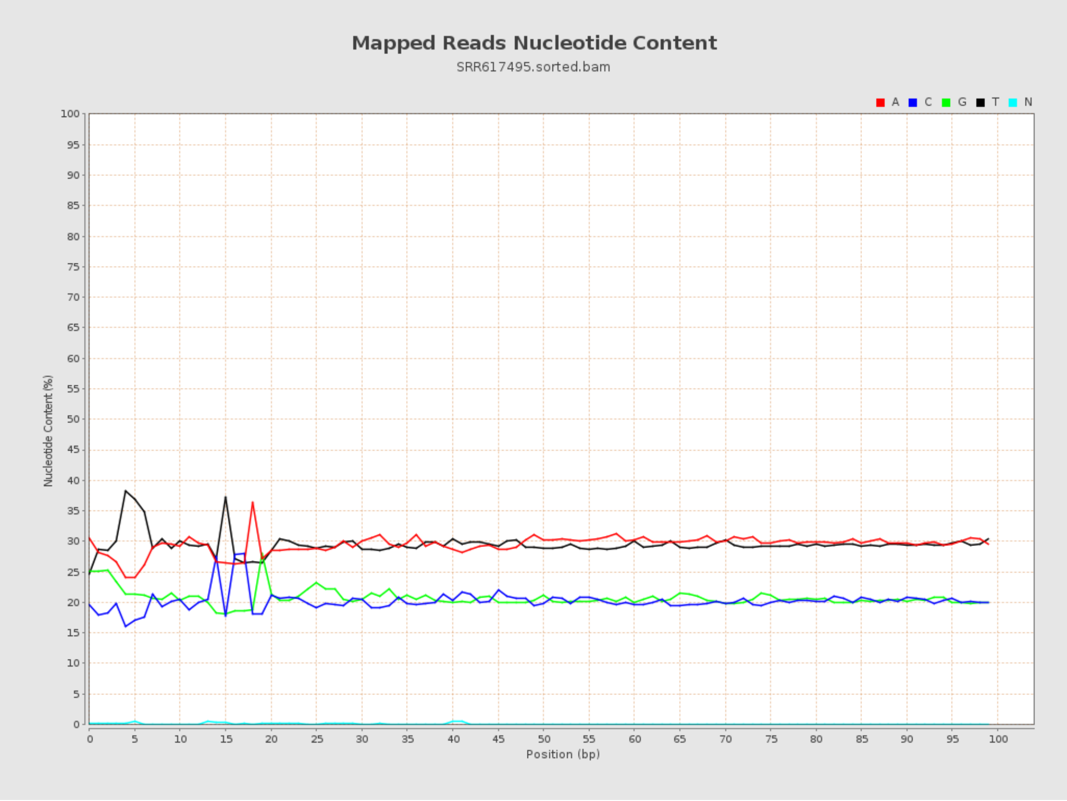
6. Results : Genome Fraction Coverage



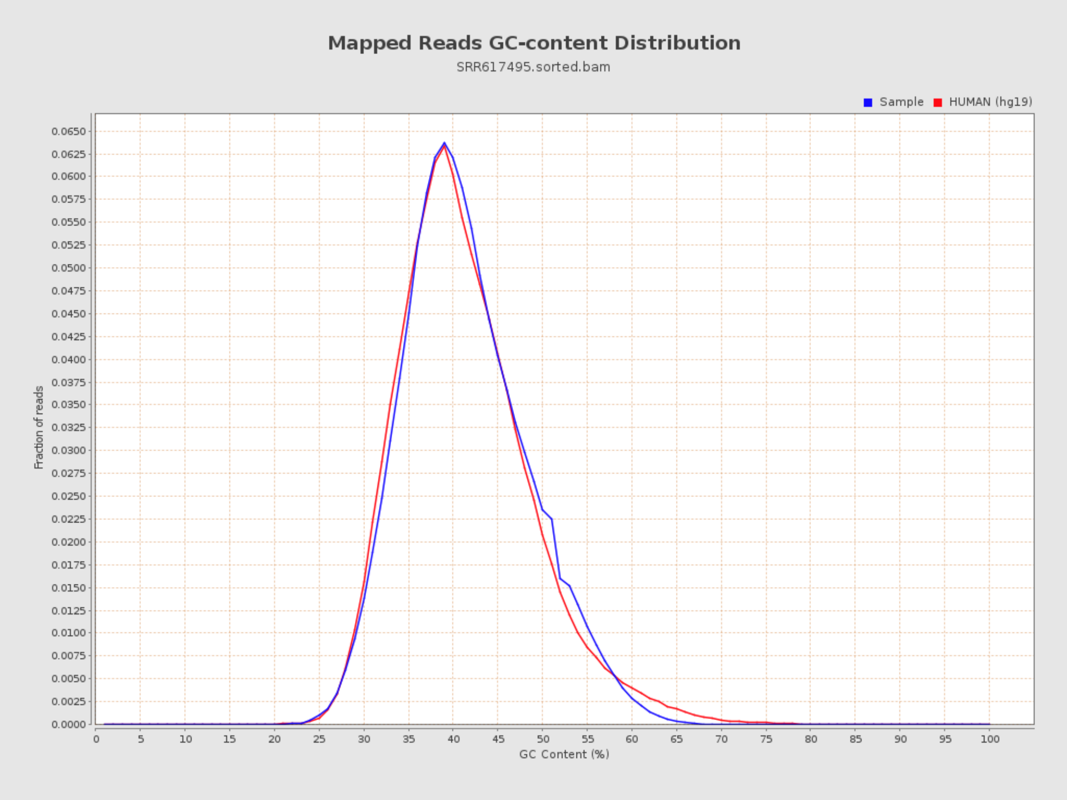
7. Results : Duplication Rate Histogram



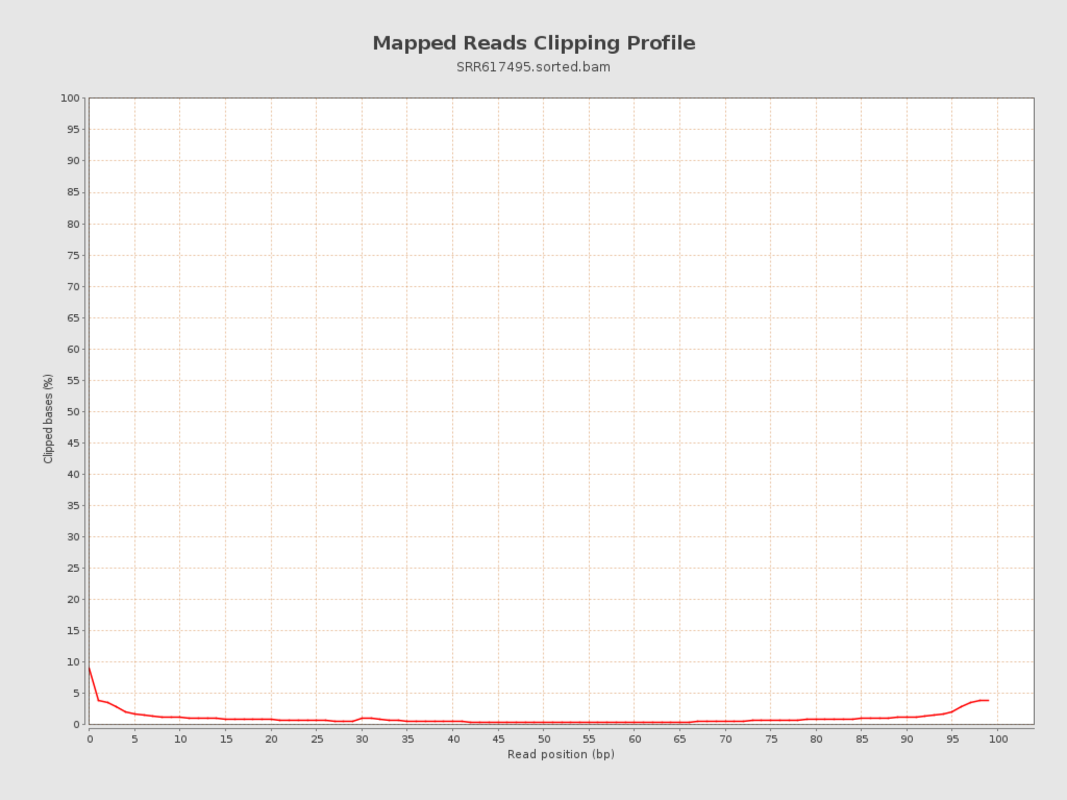
8. Results : Mapped Reads Nucleotide Content



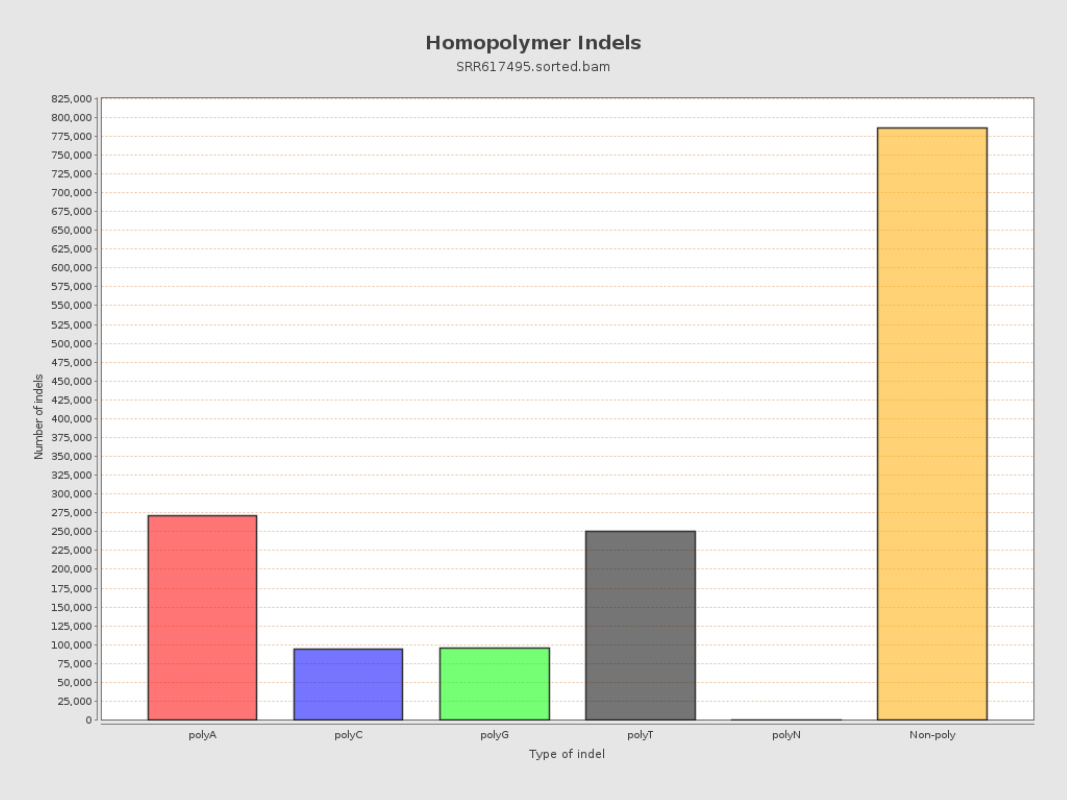
9. Results : Mapped Reads GC-content Distribution



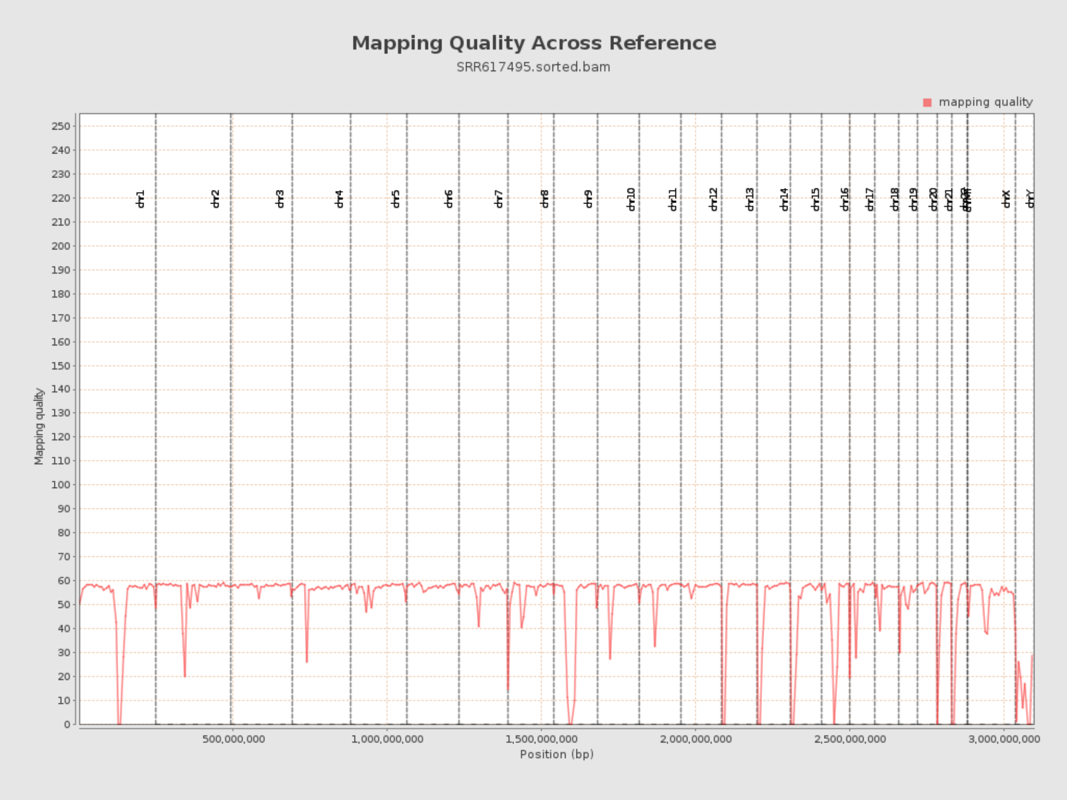
10. Results : Mapped Reads Clipping Profile



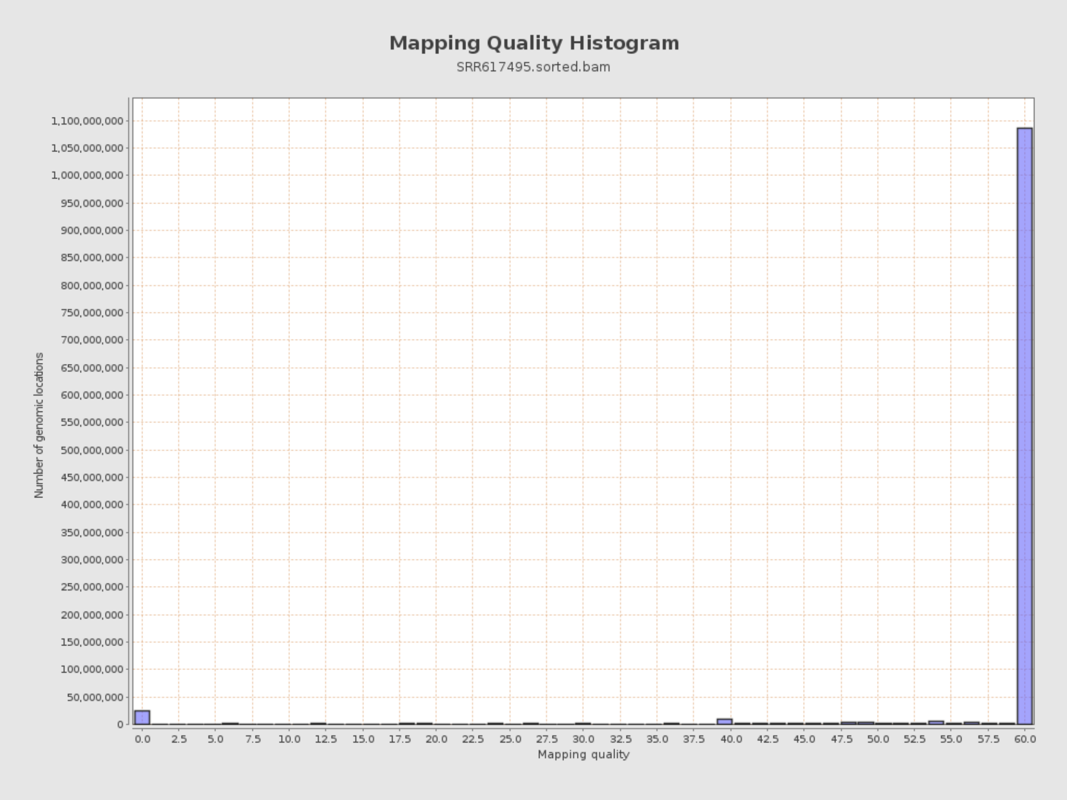
11. Results : Homopolymer Indels



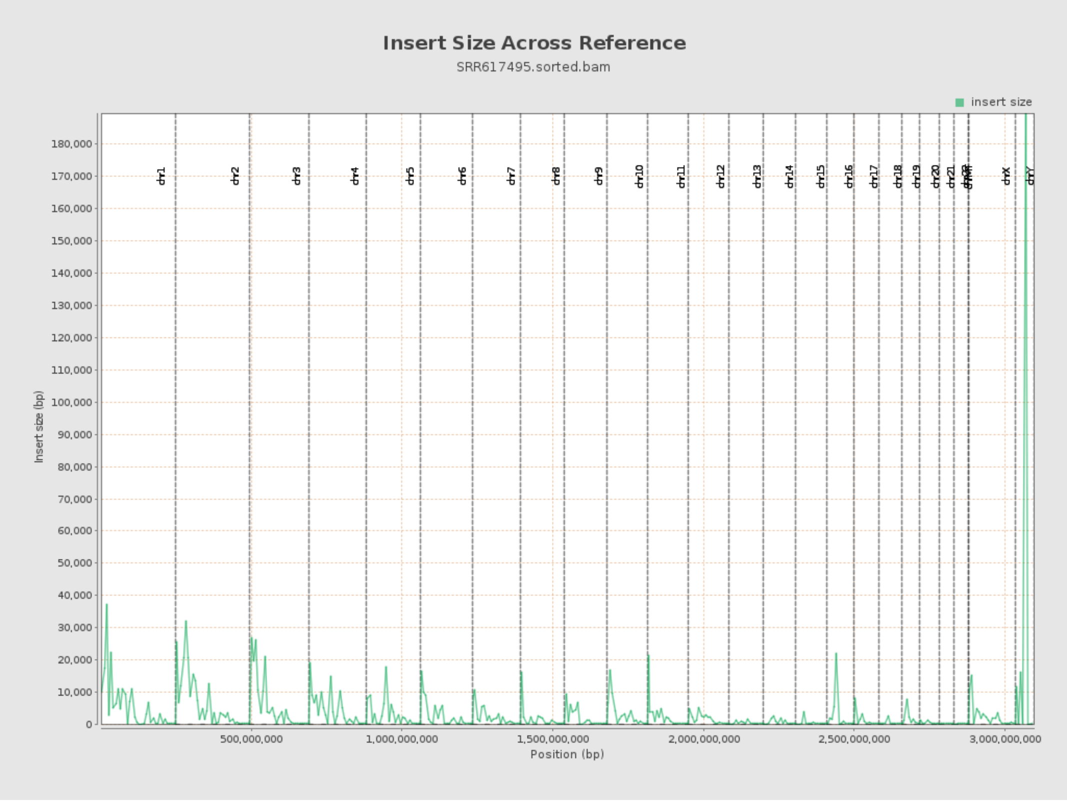
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram