Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/09 22:18:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617497.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_SRR617497 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617497_1.fastq.gz SRR617497_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 09 22:17:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617497.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,773,423 / 96.17%
Unmapped reads	1,226,577 / 3.83%
Mapped paired reads	30,773,423 / 96.17%
Mapped reads, first in pair	15,438,476 / 48.25%
Mapped reads, second in pair	15,334,947 / 47.92%
Mapped reads, both in pair	30,398,404 / 95%
Mapped reads, singletons	375,019 / 1.17%
Secondary alignments	0
Supplementary alignments	139,975 / 0.44%
Read min/max/mean length	30 / 100 / 100.18
Duplicated reads (estimated)	6,406,481 / 20.02%
Duplication rate	10.05%
Clipped reads	5,763,300 / 18.01%

2.2. ACGT Content

Number/percentage of A's	886,912,707 / 29.47%
Number/percentage of C's	608,927,461 / 20.23%
Number/percentage of T's	887,097,173 / 29.48%
Number/percentage of G's	624,562,641 / 20.75%
Number/percentage of N's	1,852,931 / 0.06%

GC Percentage	40.99%

2.3. Coverage

Mean	0.9727
Standard Deviation	9.7999

2.4. Mapping Quality

Mean Mapping Quality	52.83

2.5. Insert size

Mean	29,888.32
Standard Deviation	1,604,412.91
P25/Median/P75	176 / 223 / 296

2.6. Mismatches and indels

General error rate	1.19%
Mismatches	34,771,984
Insertions	446,933
Mapped reads with at least one insertion	1.42%
Deletions	1,051,671
Mapped reads with at least one deletion	3.35%
Homopolymer indels	47.54%

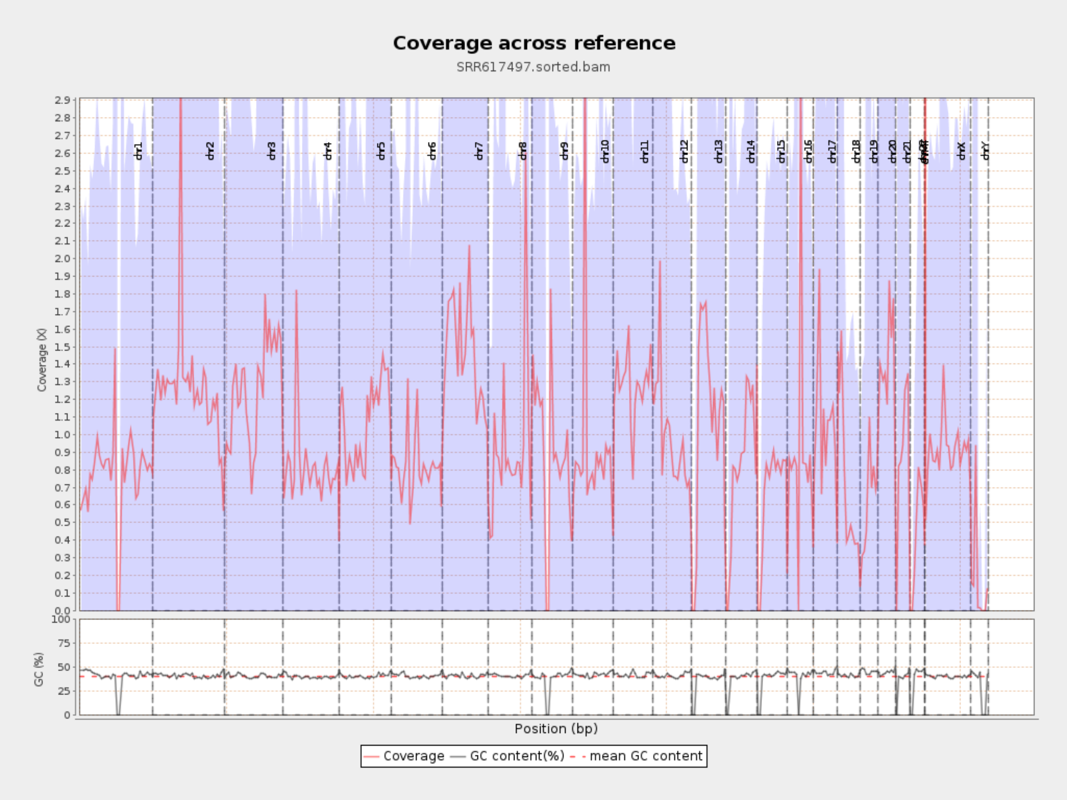
2.7. Chromosome stats

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

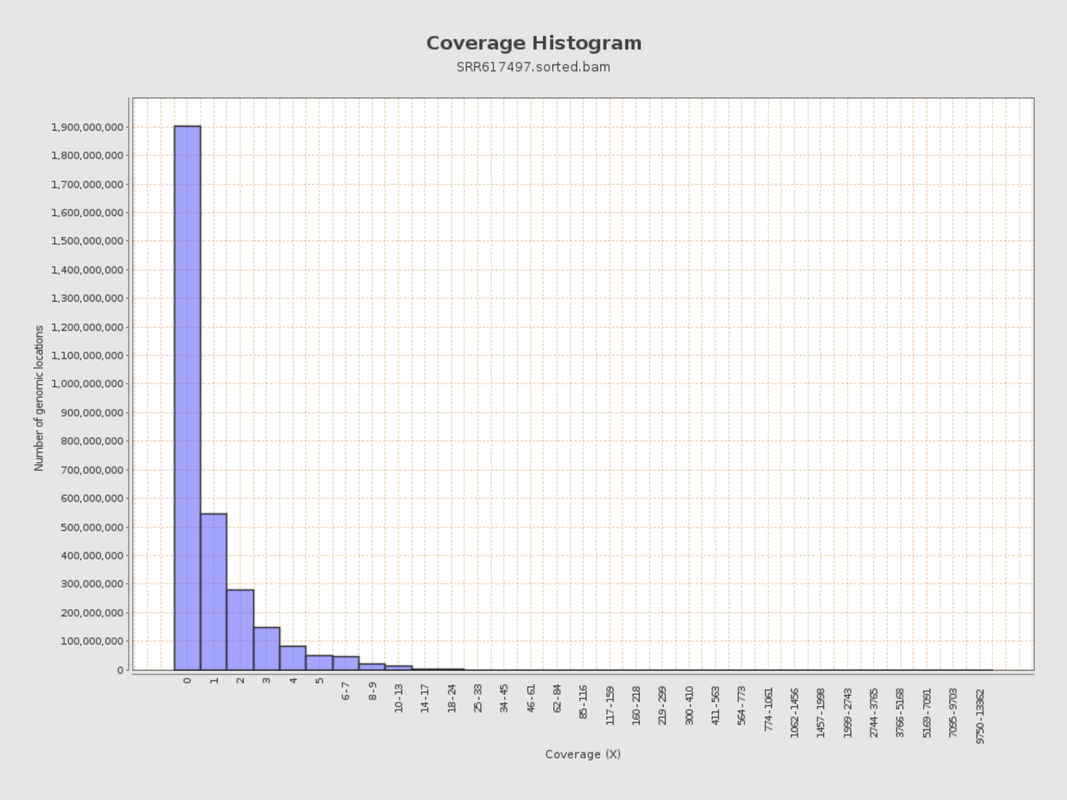
		bases	coverage	deviation
chr1	249250621	193316648	0.7756	9.3724
chr2	243199373	311455730	1.2807	11.6695
chr3	198022430	248724187	1.256	2.2523
chr4	191154276	155652059	0.8143	6.2958
chr5	180915260	192868586	1.0661	2.0985
chr6	171115067	141527436	0.8271	5.5091
chr7	159138663	232579337	1.4615	13.224
chr8	146364022	133924918	0.915	3.8944
chr9	141213431	124788922	0.8837	18.6414
chr10	135534747	127531819	0.941	18.7963
chr11	135006516	169846387	1.2581	12.747
chr12	133851895	131417578	0.9818	2.0027
chr13	115169878	127692075	1.1087	2.1401
chr14	107349540	87582879	0.8159	2.2179
chr15	102531392	67995799	0.6632	1.4636
chr16	90354753	81209517	0.8988	14.9216
chr17	81195210	84271362	1.0379	13.85
chr18	78077248	53945359	0.6909	17.1756
chr19	59128983	35954000	0.6081	5.8847
chr20	63025520	89228283	1.4157	2.807
chr21	48129895	43365560	0.901	3.8806
chr22	51304566	22574238	0.44	1.2591
chrMT	16571	2151509	129.8358	93.0508
chrX	155270560	141162010	0.9091	4.1815

chrY	59373566	10380990	0.1748	13.9482

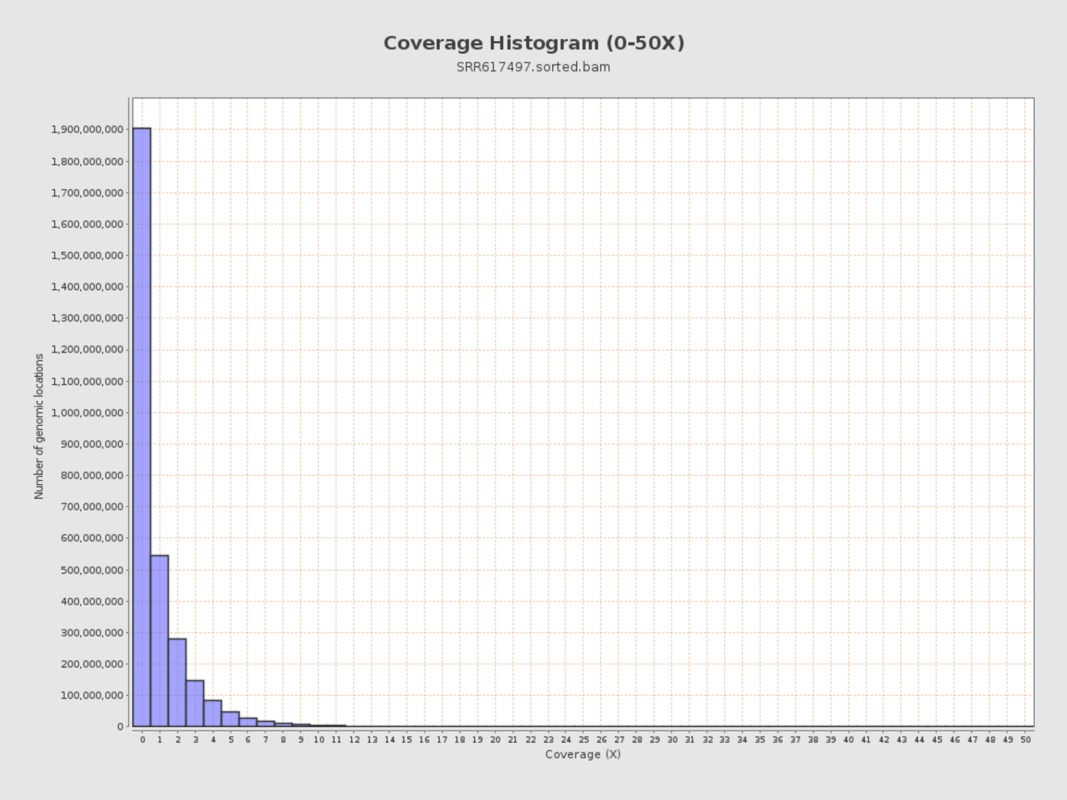
3. Results : Coverage across reference



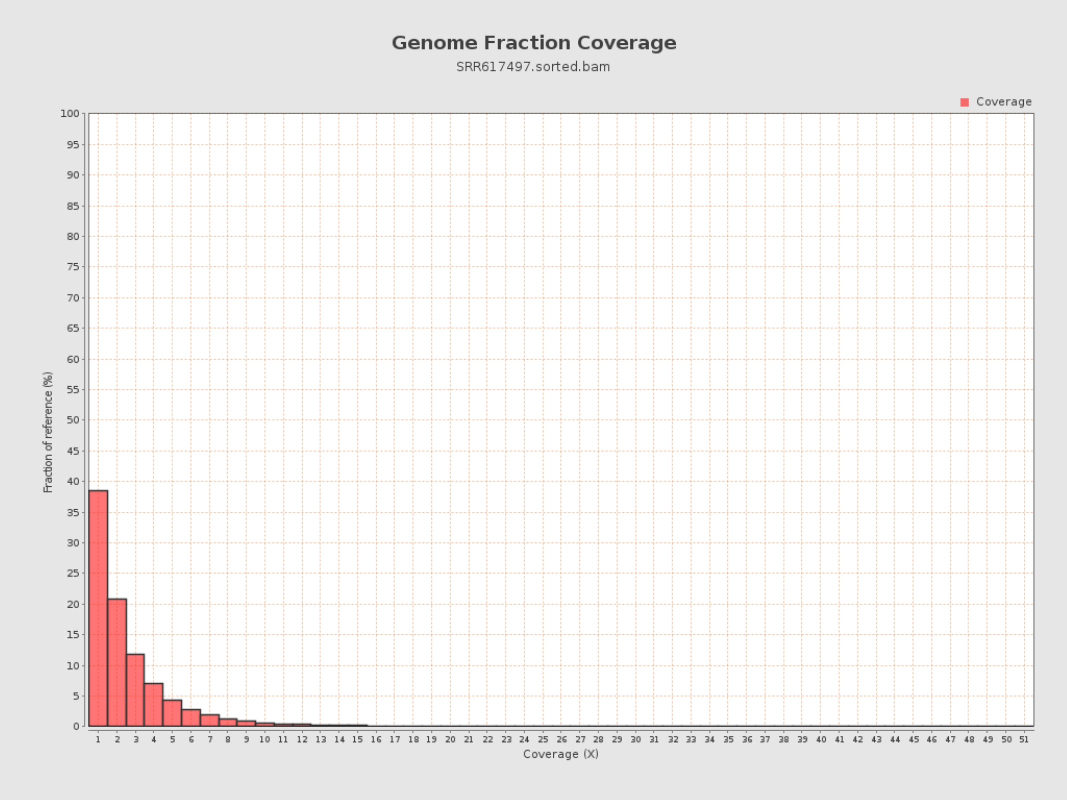
4. Results : Coverage Histogram



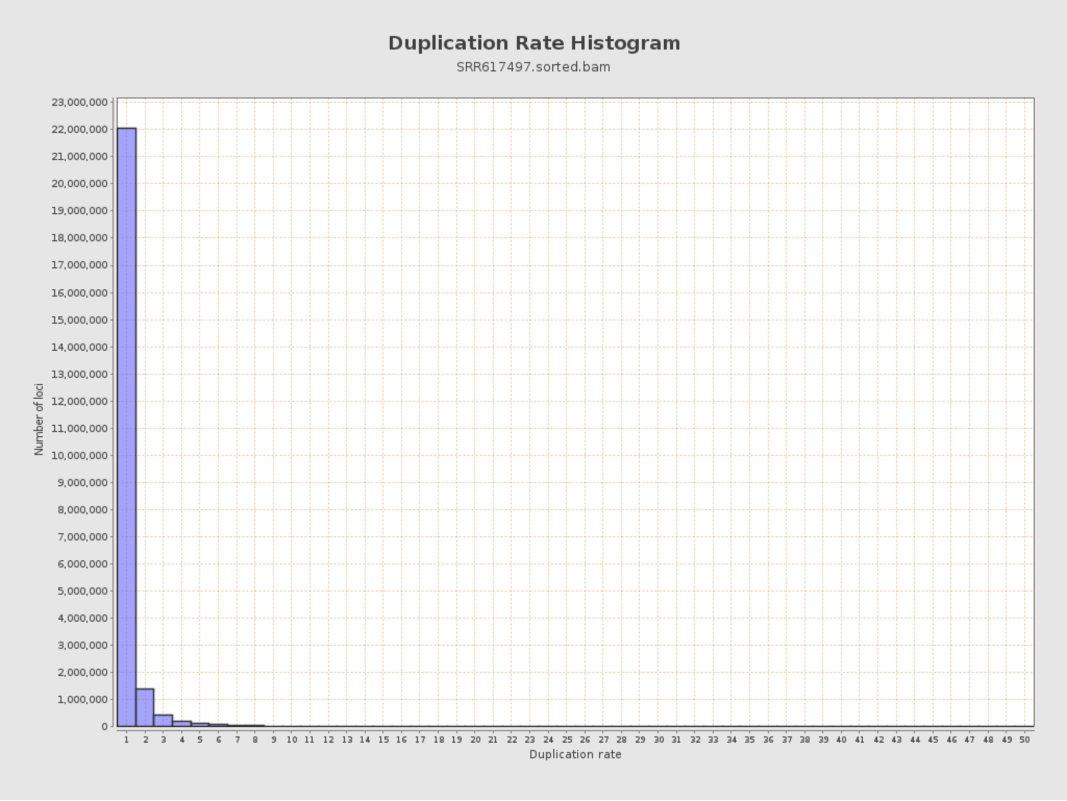
5. Results : Coverage Histogram (0-50X)



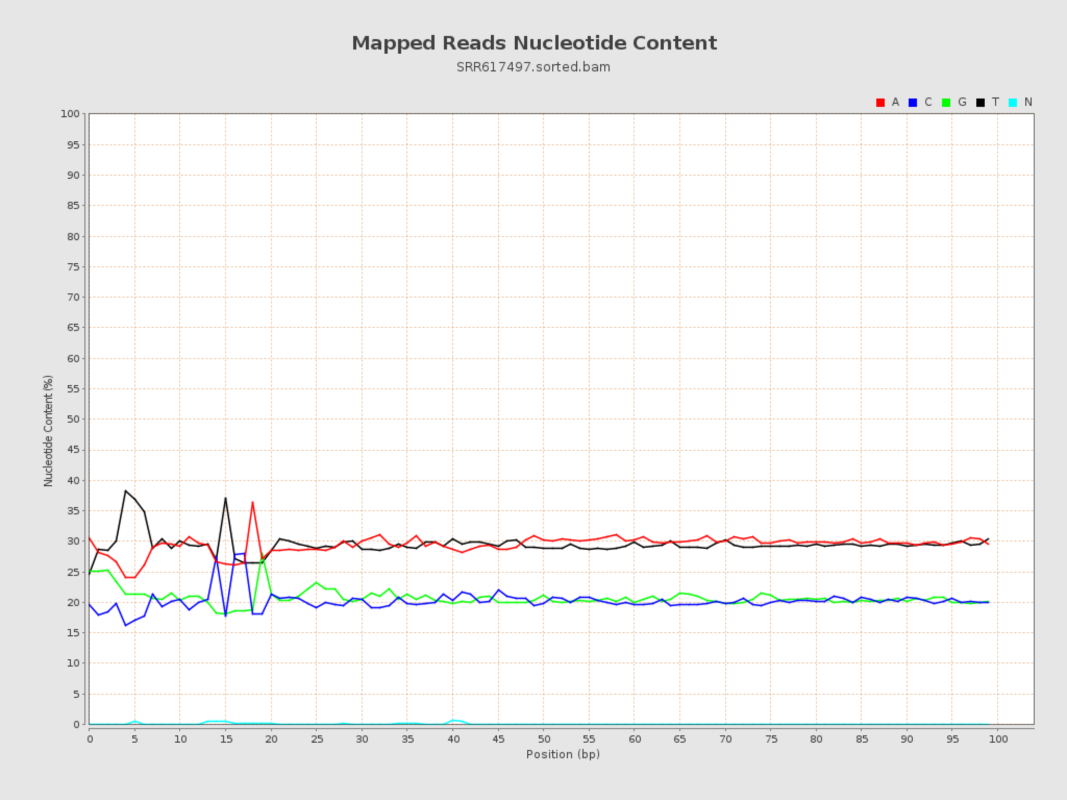
6. Results : Genome Fraction Coverage



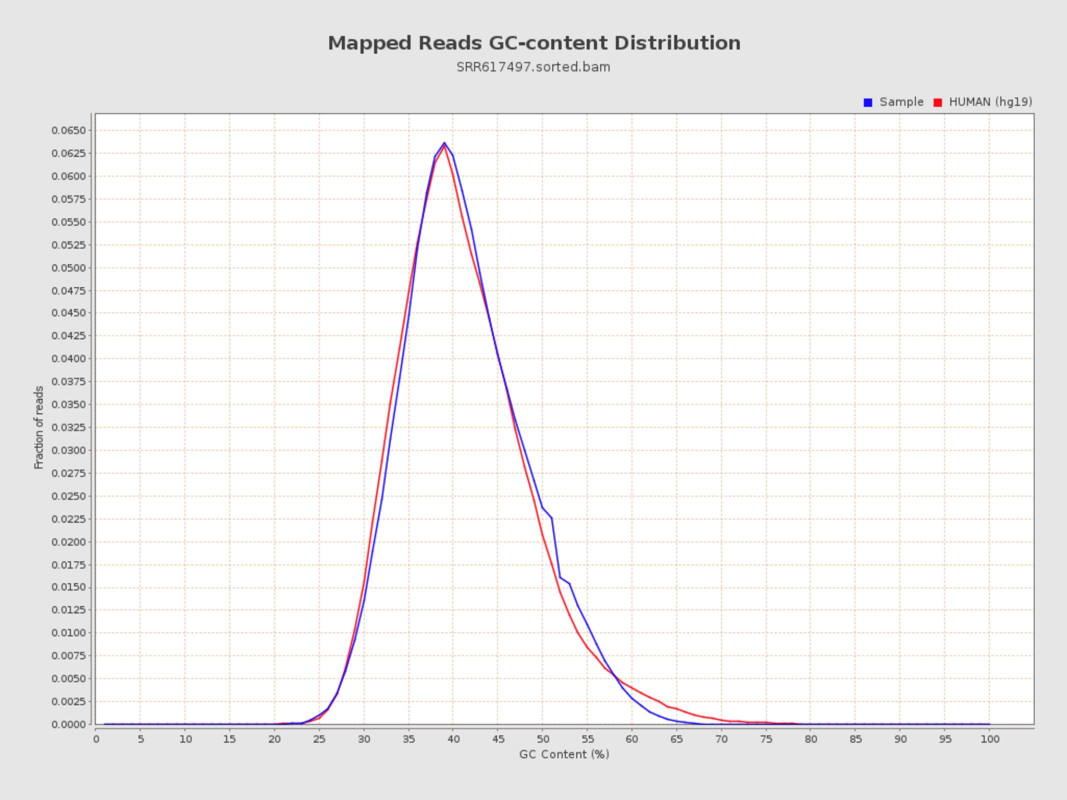
7. Results : Duplication Rate Histogram



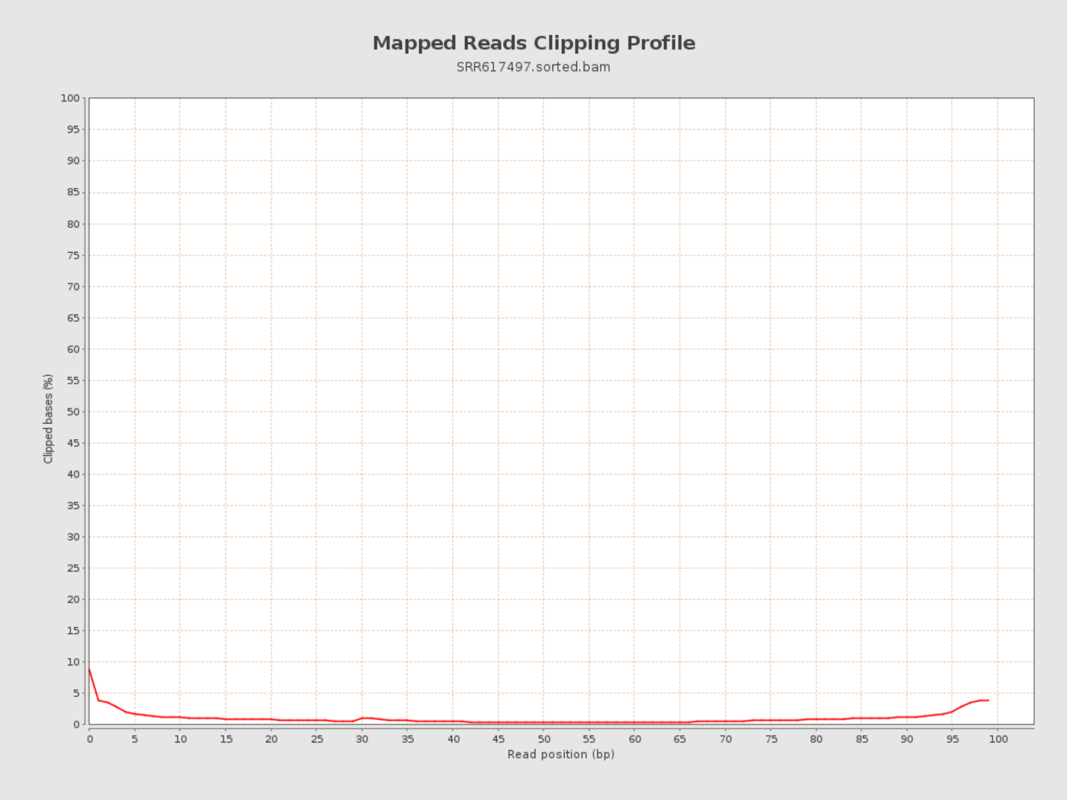
8. Results : Mapped Reads Nucleotide Content



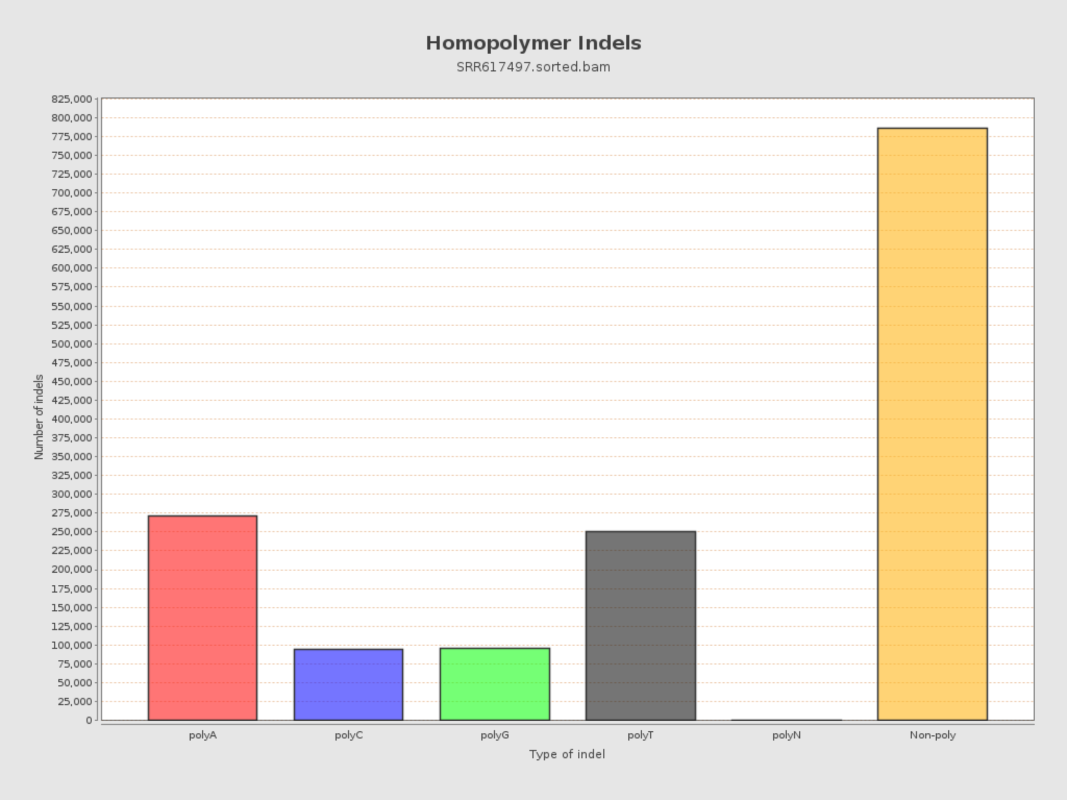
9. Results : Mapped Reads GC-content Distribution



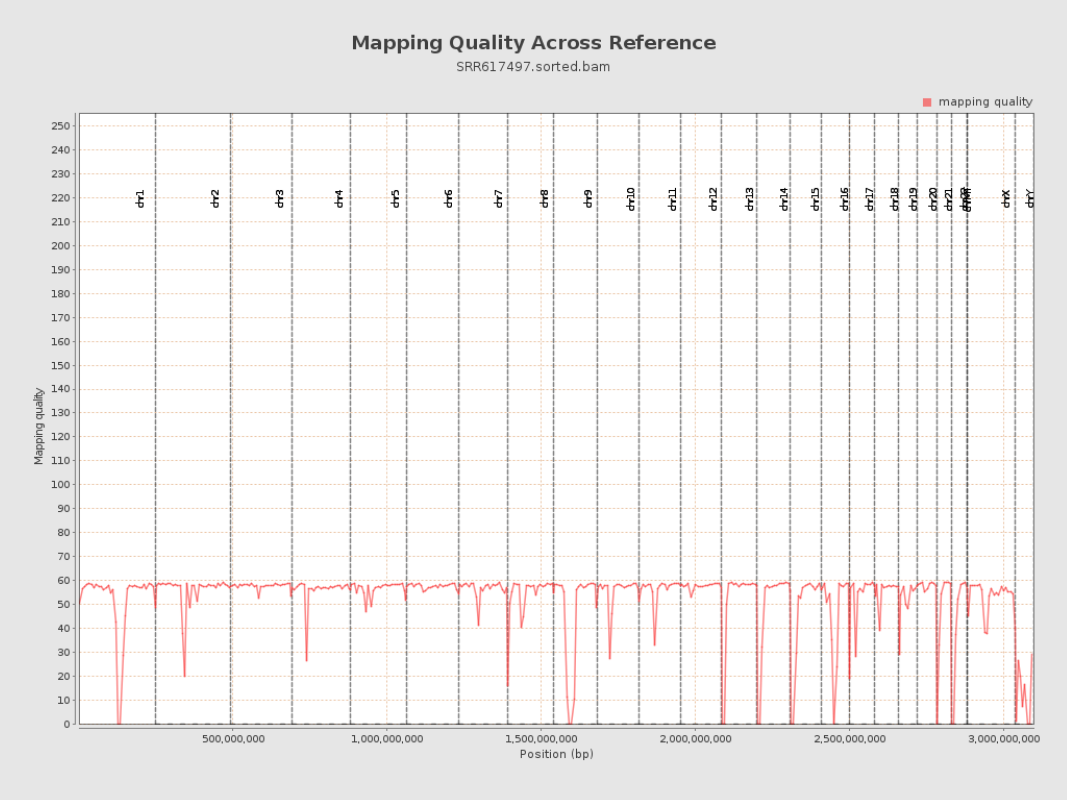
10. Results : Mapped Reads Clipping Profile



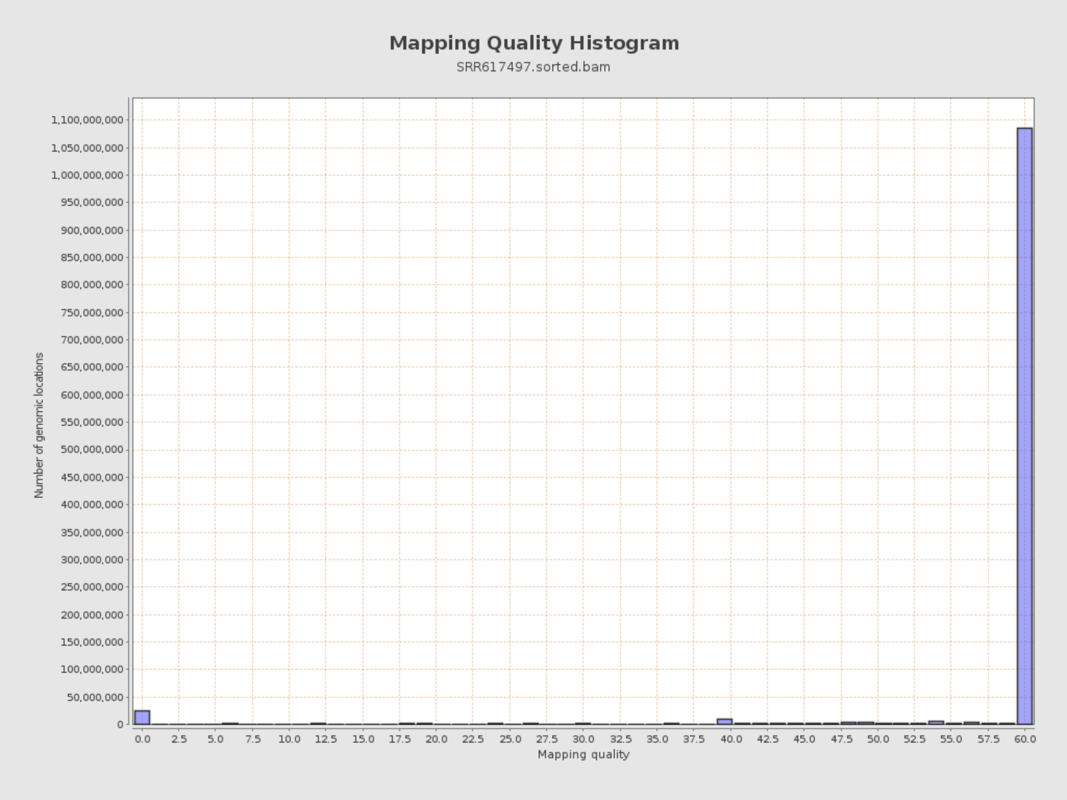
11. Results : Homopolymer Indels



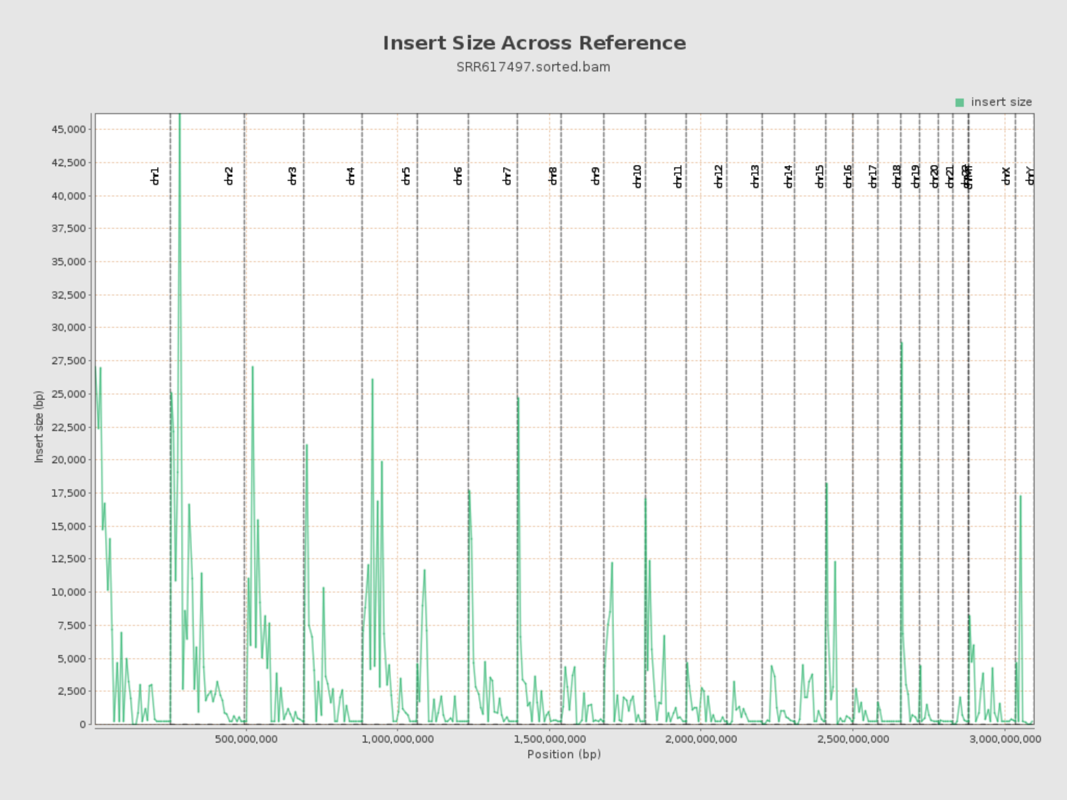
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram