Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/09 23:08:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617498.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_SRR617498 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617498_1.fastq.gz SRR617498_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 09 23:08:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617498.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,555,524 / 95.49%
Unmapped reads	1,444,476 / 4.51%
Mapped paired reads	30,555,524 / 95.49%
Mapped reads, first in pair	15,353,013 / 47.98%
Mapped reads, second in pair	15,202,511 / 47.51%
Mapped reads, both in pair	30,111,242 / 94.1%
Mapped reads, singletons	444,282 / 1.39%
Secondary alignments	0
Supplementary alignments	137,497 / 0.43%
Read min/max/mean length	30 / 100 / 100.17
Duplicated reads (estimated)	6,273,493 / 19.6%
Duplication rate	9.91%
Clipped reads	5,913,817 / 18.48%

2.2. ACGT Content

Number/percentage of A's	879,803,816 / 29.51%
Number/percentage of C's	602,841,557 / 20.22%
Number/percentage of T's	879,168,411 / 29.49%
Number/percentage of G's	617,601,538 / 20.71%
Number/percentage of N's	2,017,261 / 0.07%

GC Percentage	40.93%

2.3. Coverage

Mean	0.9637
Standard Deviation	9.7568

2.4. Mapping Quality

Mean Mapping Quality	52.79

2.5. Insert size

Mean	30,464.84
Standard Deviation	1,614,683.32
P25/Median/P75	173 / 219 / 289

2.6. Mismatches and indels

General error rate	1.27%
Mismatches	36,927,411
Insertions	441,811
Mapped reads with at least one insertion	1.42%
Deletions	1,036,220
Mapped reads with at least one deletion	3.32%
Homopolymer indels	47.4%

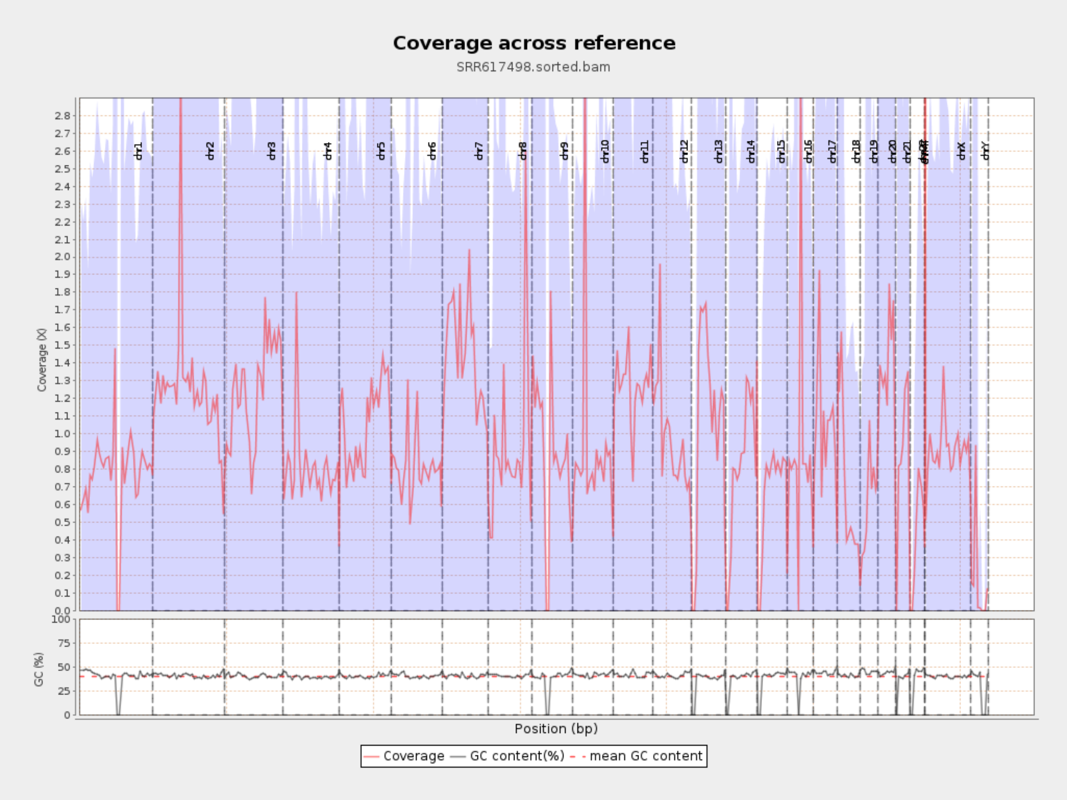
2.7. Chromosome stats

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

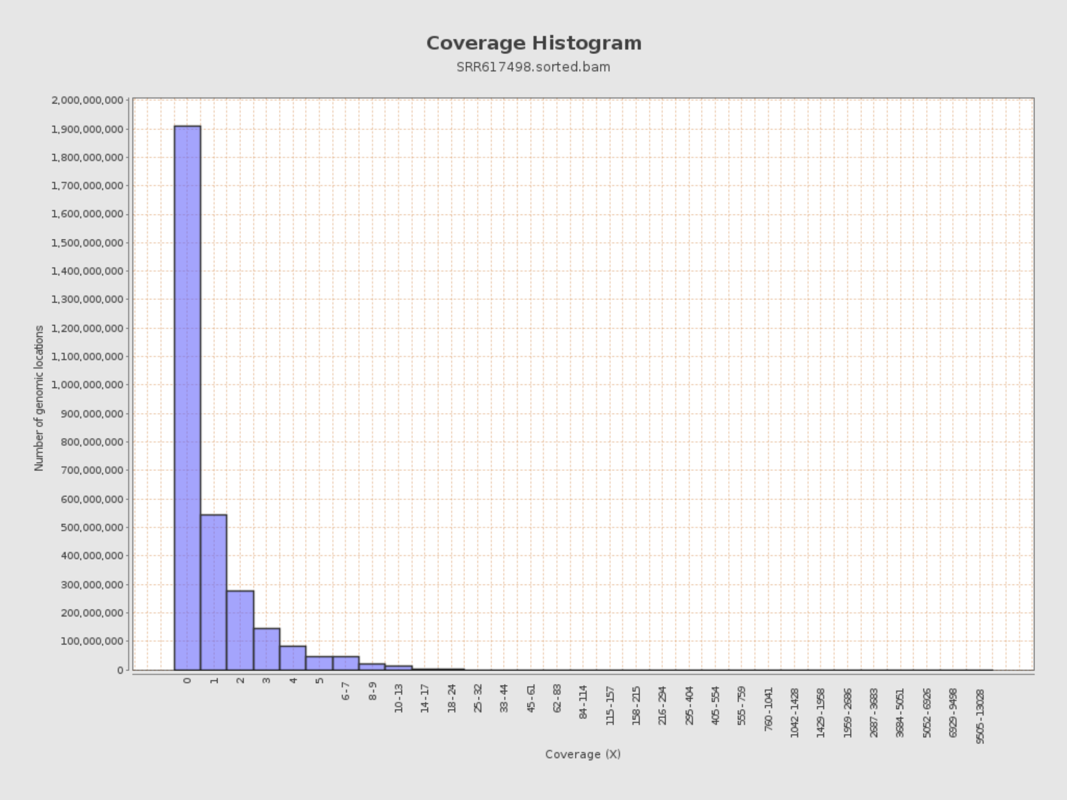
		bases	coverage	deviation
chr1	249250621	192280497	0.7714	9.5424
chr2	243199373	308153643	1.2671	11.5345
chr3	198022430	246380763	1.2442	2.2434
chr4	191154276	154198627	0.8067	6.173
chr5	180915260	190677987	1.054	2.0818
chr6	171115067	140301667	0.8199	5.4311
chr7	159138663	230252159	1.4469	13.1917
chr8	146364022	132655822	0.9063	3.8863
chr9	141213431	123323824	0.8733	18.4258
chr10	135534747	126232860	0.9314	18.6868
chr11	135006516	168413986	1.2475	12.6444
chr12	133851895	130371638	0.974	1.9949
chr13	115169878	126564124	1.0989	2.128
chr14	107349540	86602339	0.8067	2.2149
chr15	102531392	67275439	0.6561	1.4524
chr16	90354753	80764211	0.8939	15.058
chr17	81195210	83352821	1.0266	13.8337
chr18	78077248	53471747	0.6849	17.1257
chr19	59128983	35581450	0.6018	5.8913
chr20	63025520	88049659	1.397	2.7696
chr21	48129895	43071333	0.8949	3.8404
chr22	51304566	22354098	0.4357	1.251
chrMT	16571	2107929	127.2059	95.804
chrX	155270560	140437929	0.9045	4.1638

chrY	59373566	10320189	0.1738	13.8667

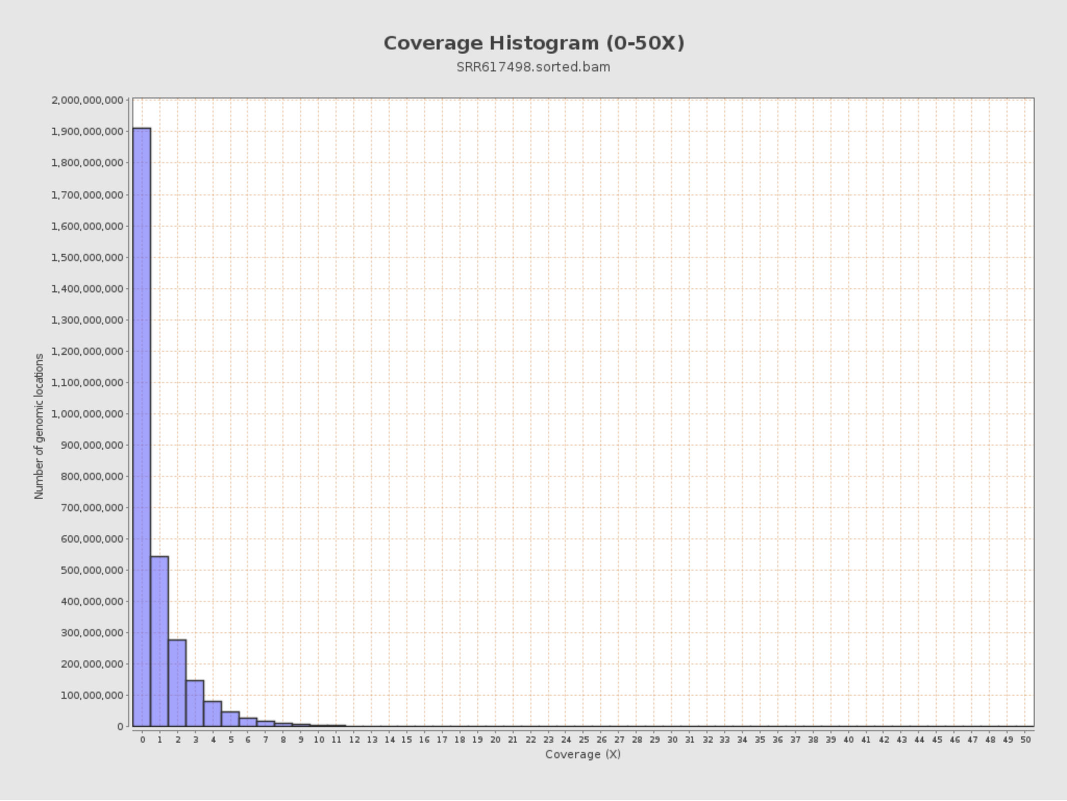
3. Results : Coverage across reference



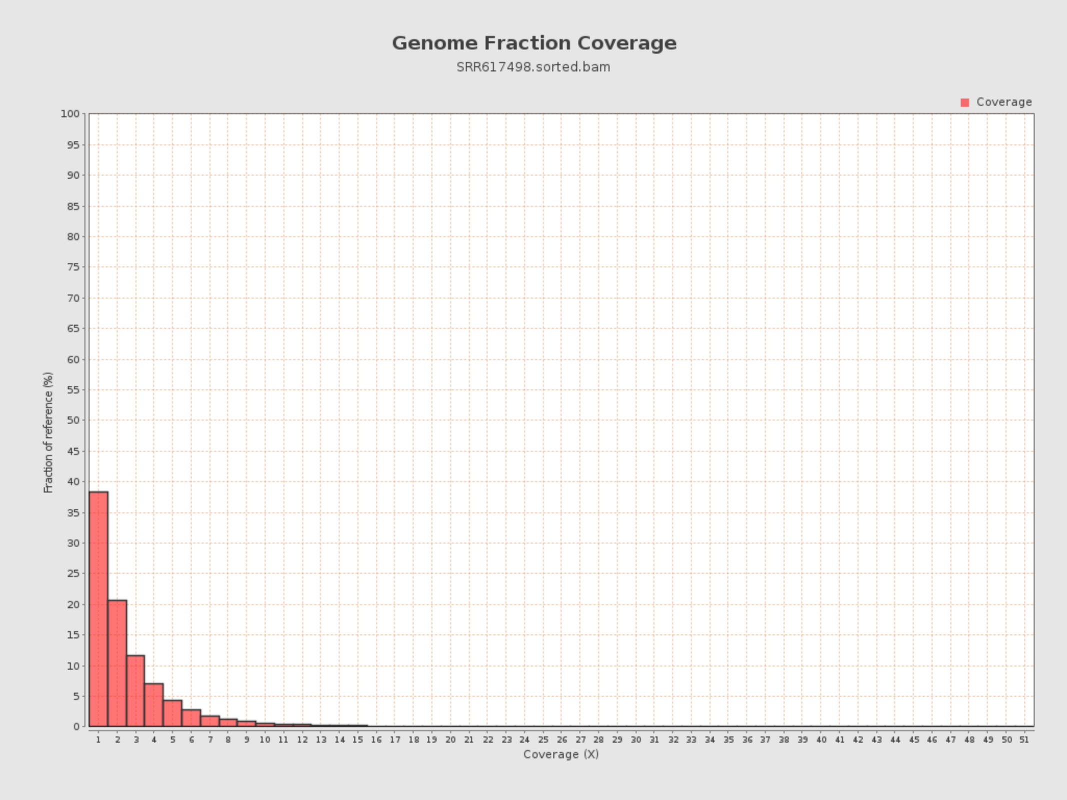
4. Results : Coverage Histogram



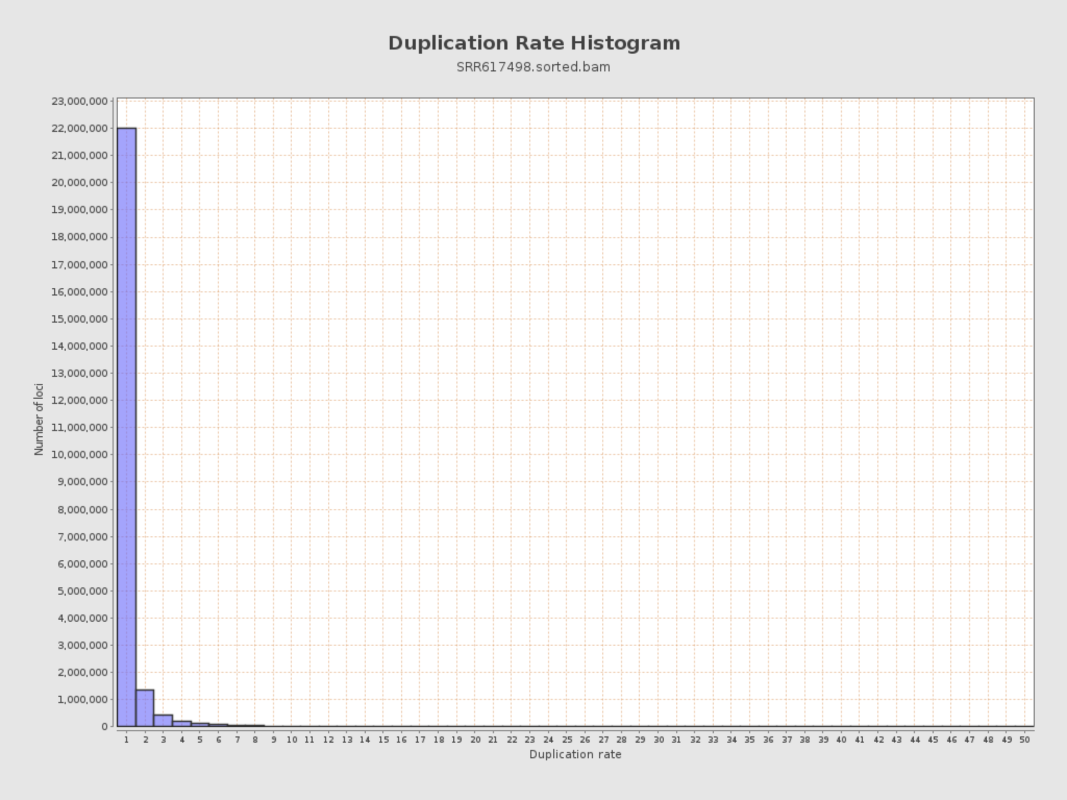
5. Results : Coverage Histogram (0-50X)



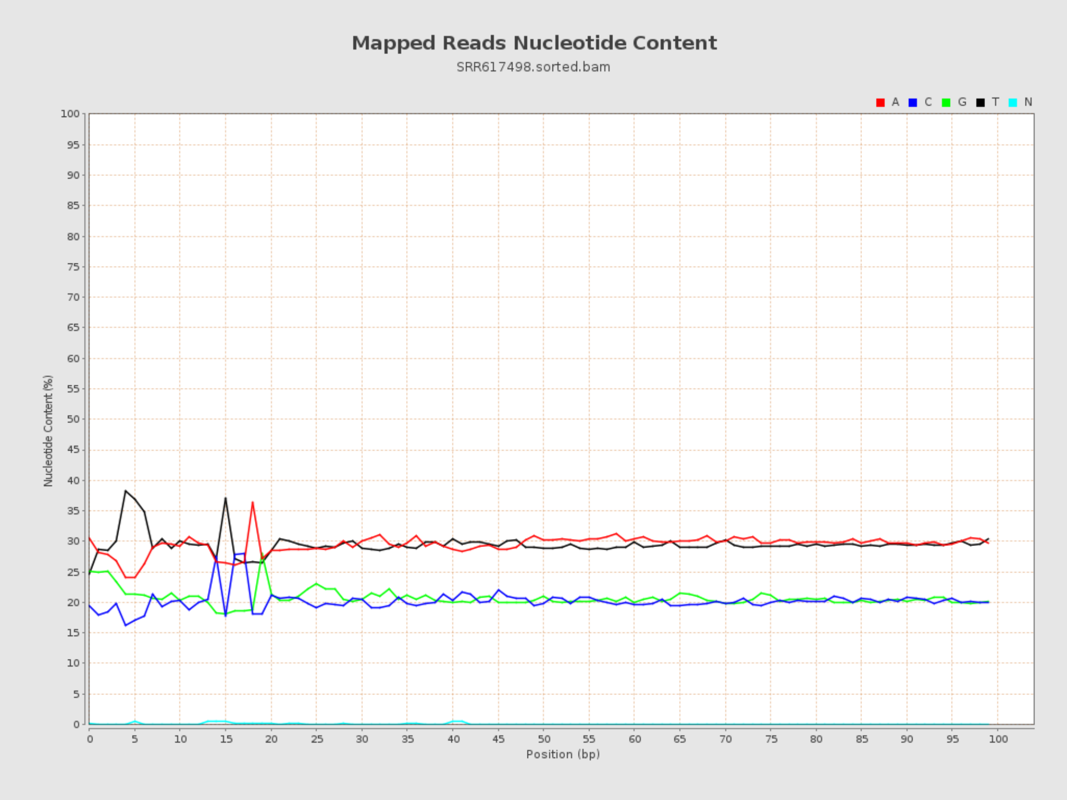
6. Results : Genome Fraction Coverage



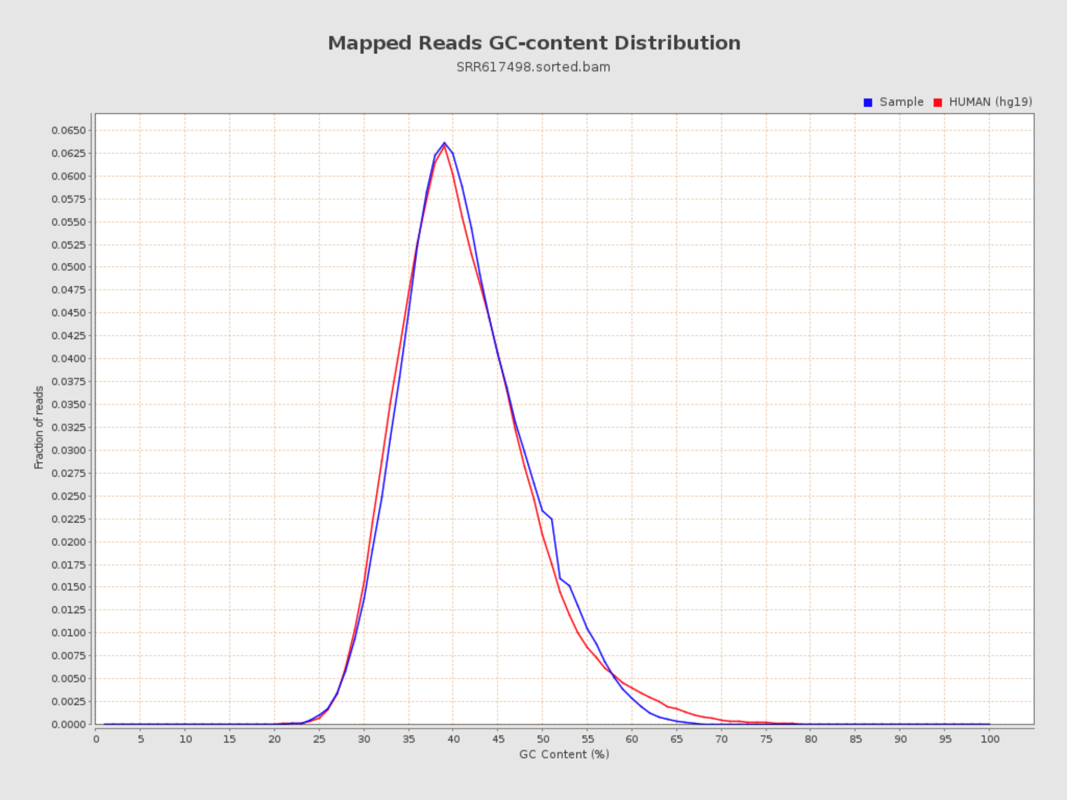
7. Results : Duplication Rate Histogram



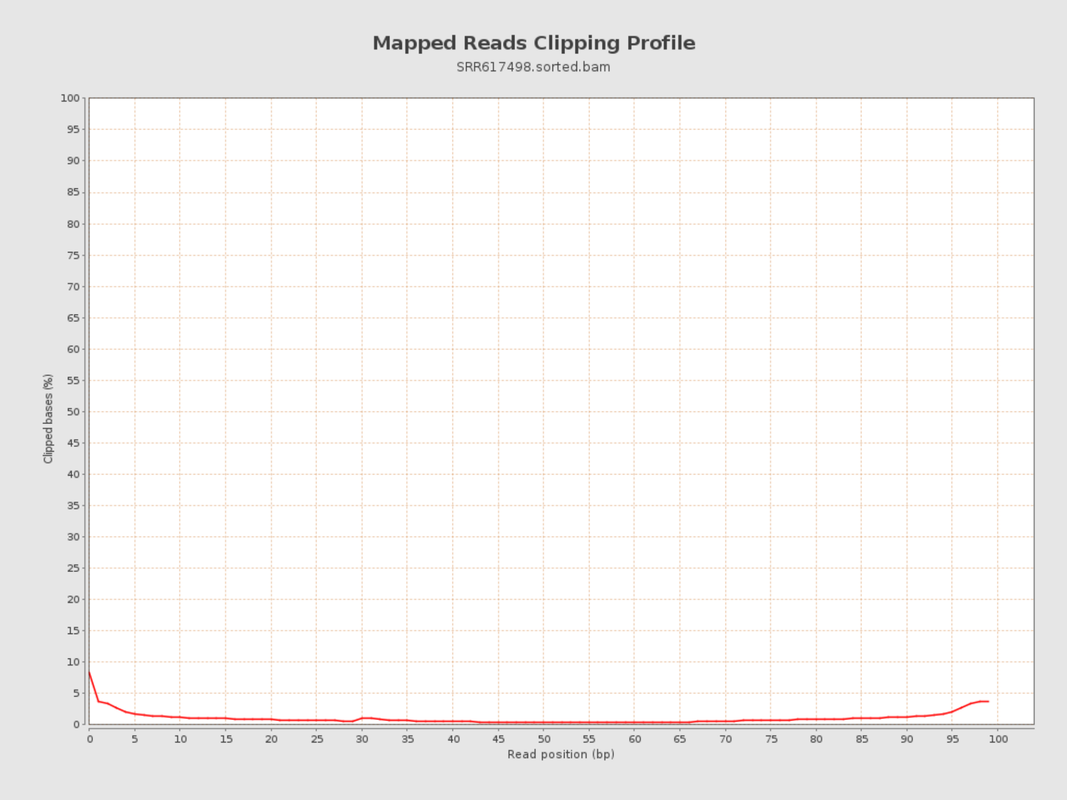
8. Results : Mapped Reads Nucleotide Content



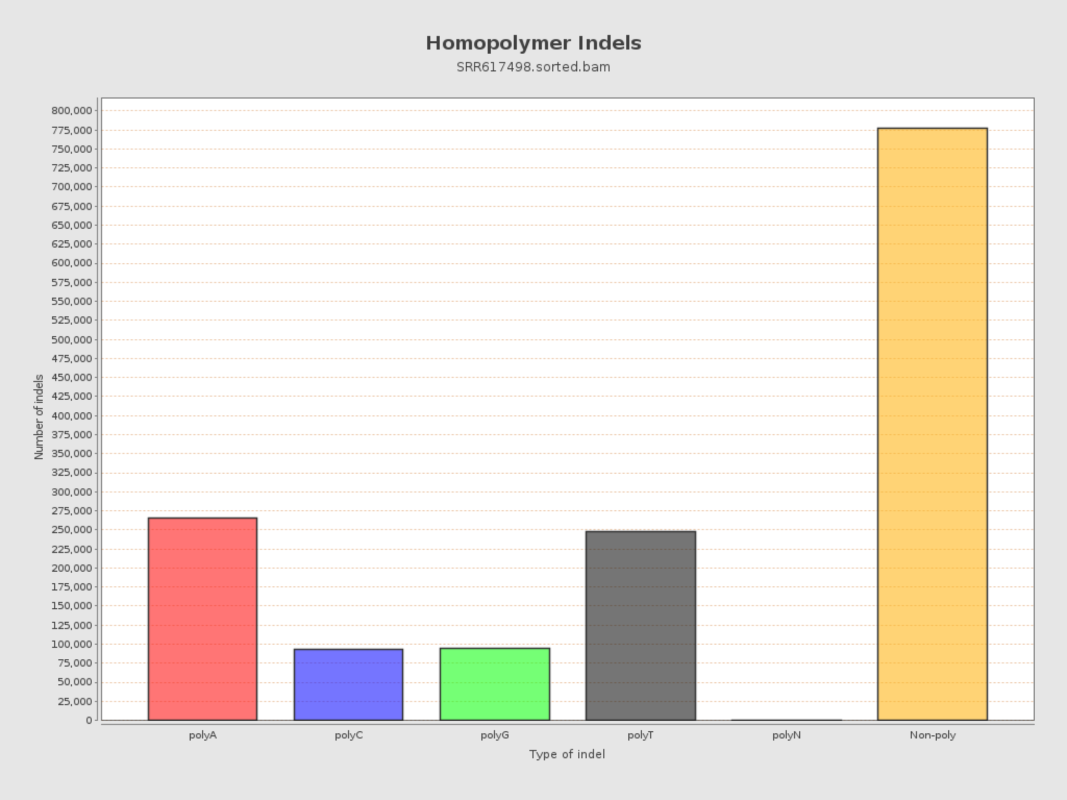
9. Results : Mapped Reads GC-content Distribution



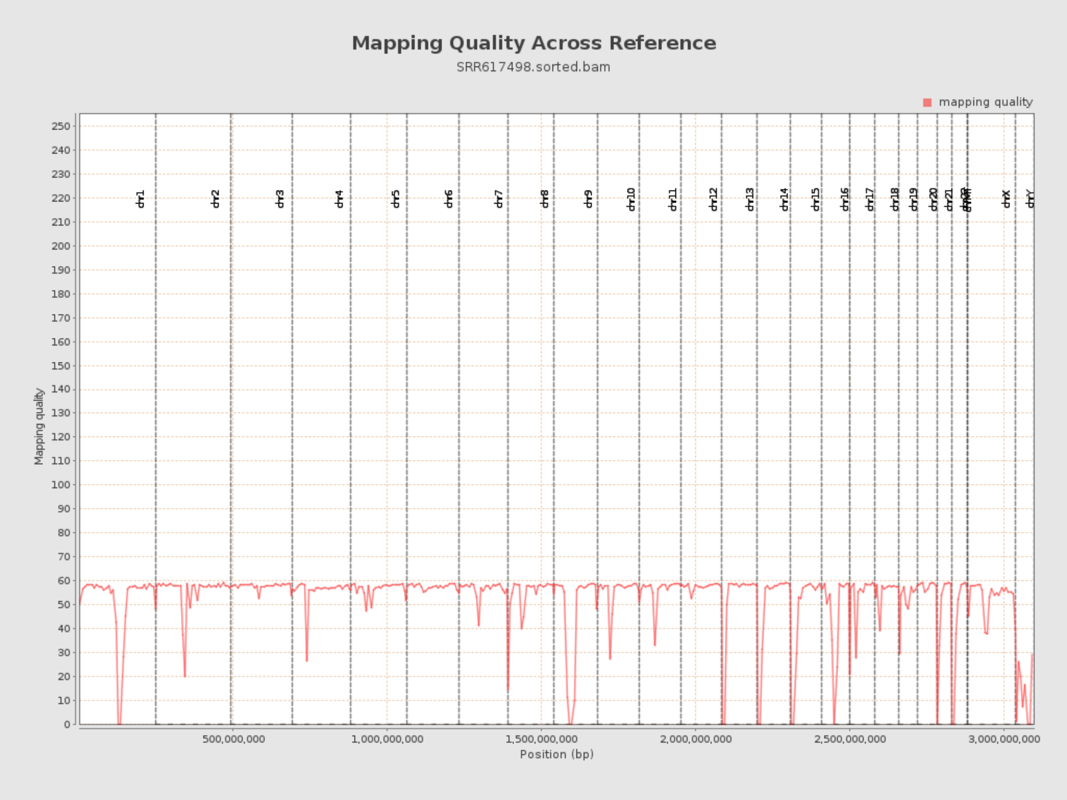
10. Results : Mapped Reads Clipping Profile



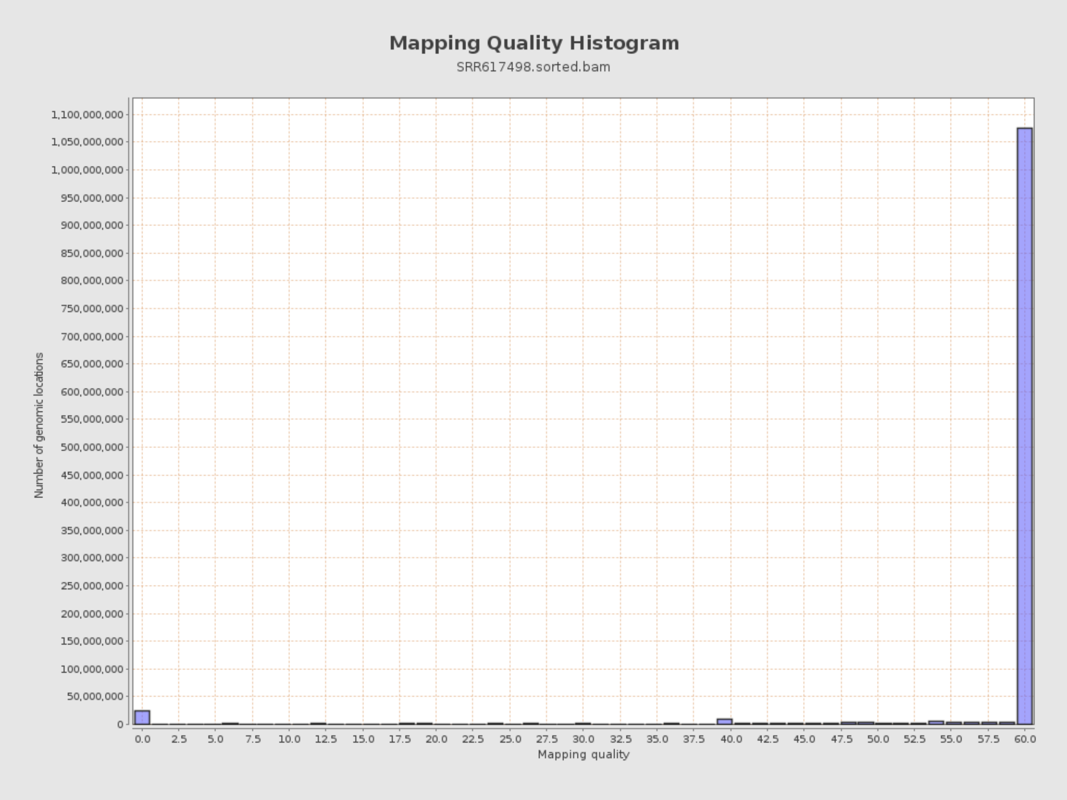
11. Results : Homopolymer Indels



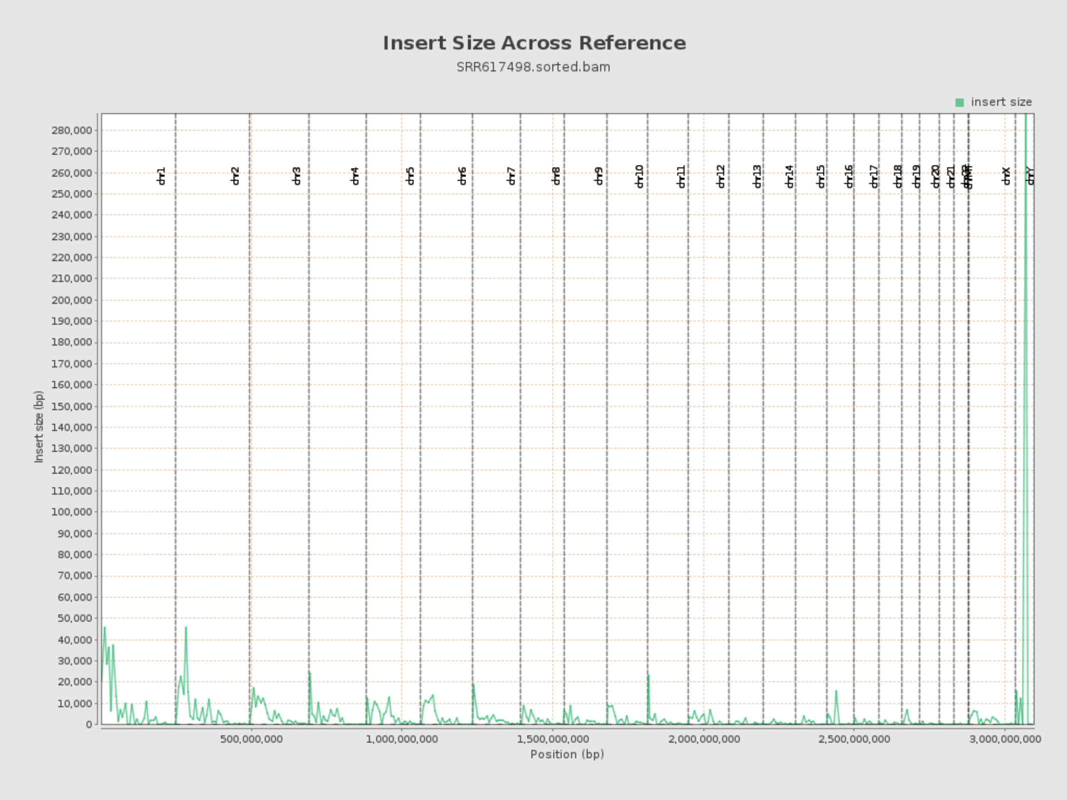
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram