Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/09 09:12:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617424.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_SRR617424 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617424_1.fastq.gz SRR617424_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 09 09:12:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617424.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	22,889,296
Mapped reads	18,624,634 / 81.37%
Unmapped reads	4,264,662 / 18.63%
Mapped paired reads	18,624,634 / 81.37%
Mapped reads, first in pair	10,113,370 / 44.18%
Mapped reads, second in pair	8,511,264 / 37.18%
Mapped reads, both in pair	16,819,904 / 73.48%
Mapped reads, singletons	1,804,730 / 7.88%
Secondary alignments	0
Supplementary alignments	262,239 / 1.15%
Read min/max/mean length	30 / 100 / 100.47
Duplicated reads (estimated)	565,762 / 2.47%
Duplication rate	2.76%
Clipped reads	3,343,528 / 14.61%

2.2. ACGT Content

Number/percentage of A's	539,630,090 / 29.93%
Number/percentage of C's	359,632,257 / 19.95%
Number/percentage of T's	534,874,173 / 29.67%
Number/percentage of G's	368,611,875 / 20.44%
Number/percentage of N's	197,889 / 0.01%

GC Percentage	40.39%

2.3. Coverage

Mean	0.5825
Standard Deviation	1.845

2.4. Mapping Quality

Mean Mapping Quality	53.3

2.5. Insert size

Mean	59,743.72
Standard Deviation	2,348,572.22
P25/Median/P75	166 / 202 / 257

2.6. Mismatches and indels

General error rate	1.82%
Mismatches	32,507,005
Insertions	151,085
Mapped reads with at least one insertion	0.8%
Deletions	174,229
Mapped reads with at least one deletion	0.92%
Homopolymer indels	43.46%

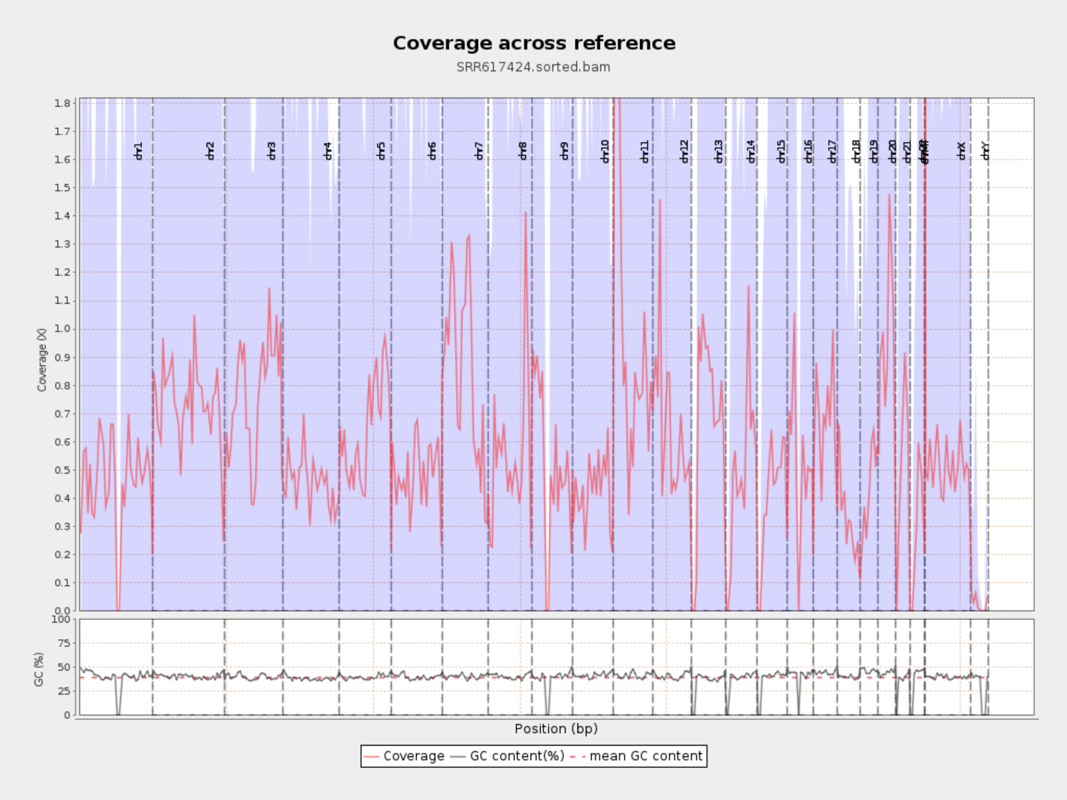
2.7. Chromosome stats

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

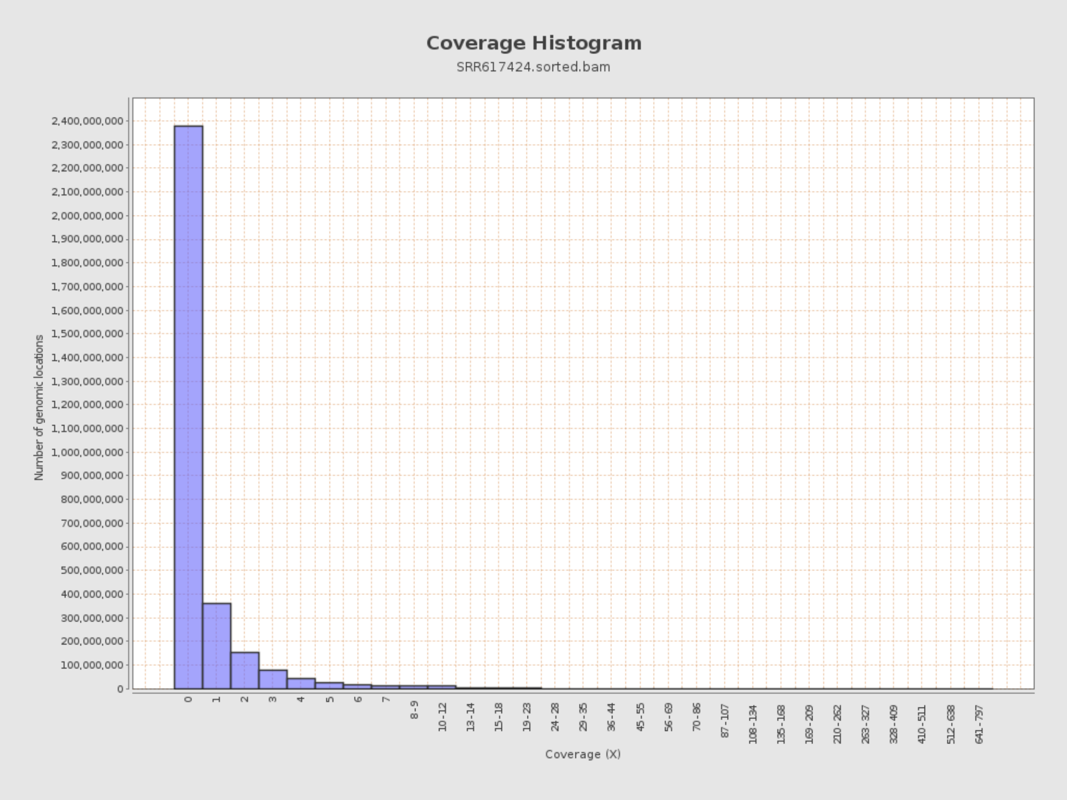
		bases	coverage	deviation
chr1	249250621	115674004	0.4641	1.7237
chr2	243199373	180034134	0.7403	1.9825
chr3	198022430	152606811	0.7707	2.1435
chr4	191154276	87809714	0.4594	1.4746
chr5	180915260	116032811	0.6414	1.8367
chr6	171115067	83577177	0.4884	1.6643
chr7	159138663	134978455	0.8482	2.0607
chr8	146364022	80182496	0.5478	2.0298
chr9	141213431	72149814	0.5109	1.6428
chr10	135534747	57686157	0.4256	1.5155
chr11	135006516	133233901	0.9869	2.4044
chr12	133851895	85937597	0.642	1.7768
chr13	115169878	78693272	0.6833	1.7842
chr14	107349540	52160755	0.4859	1.8003
chr15	102531392	41212800	0.402	1.5065
chr16	90354753	44859935	0.4965	2.0521
chr17	81195210	54608226	0.6726	2.2518
chr18	78077248	25953066	0.3324	1.2721
chr19	59128983	25090392	0.4243	1.4409
chr20	63025520	60533532	0.9605	2.8922
chr21	48129895	24714650	0.5135	1.6069
chr22	51304566	14278104	0.2783	1.2857
chrMT	16571	108347	6.5384	3.8672
chrX	155270560	79716172	0.5134	1.6378

chrY	59373566	1497904	0.0252	0.3855

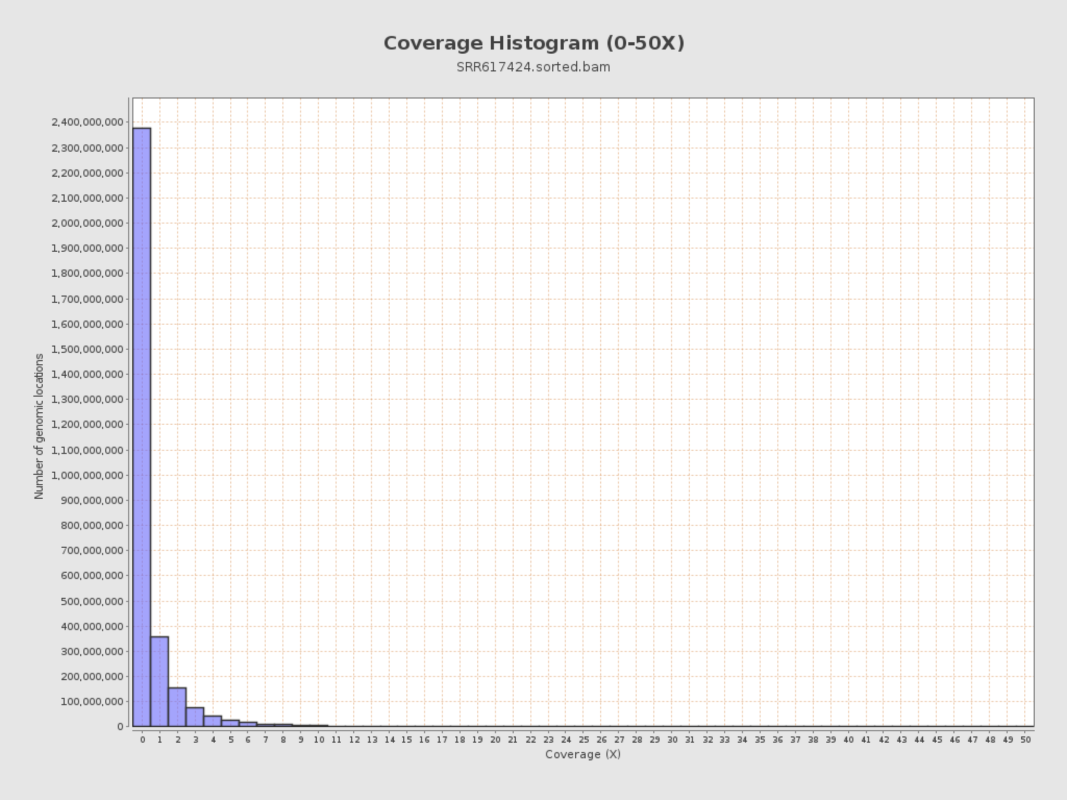
3. Results : Coverage across reference



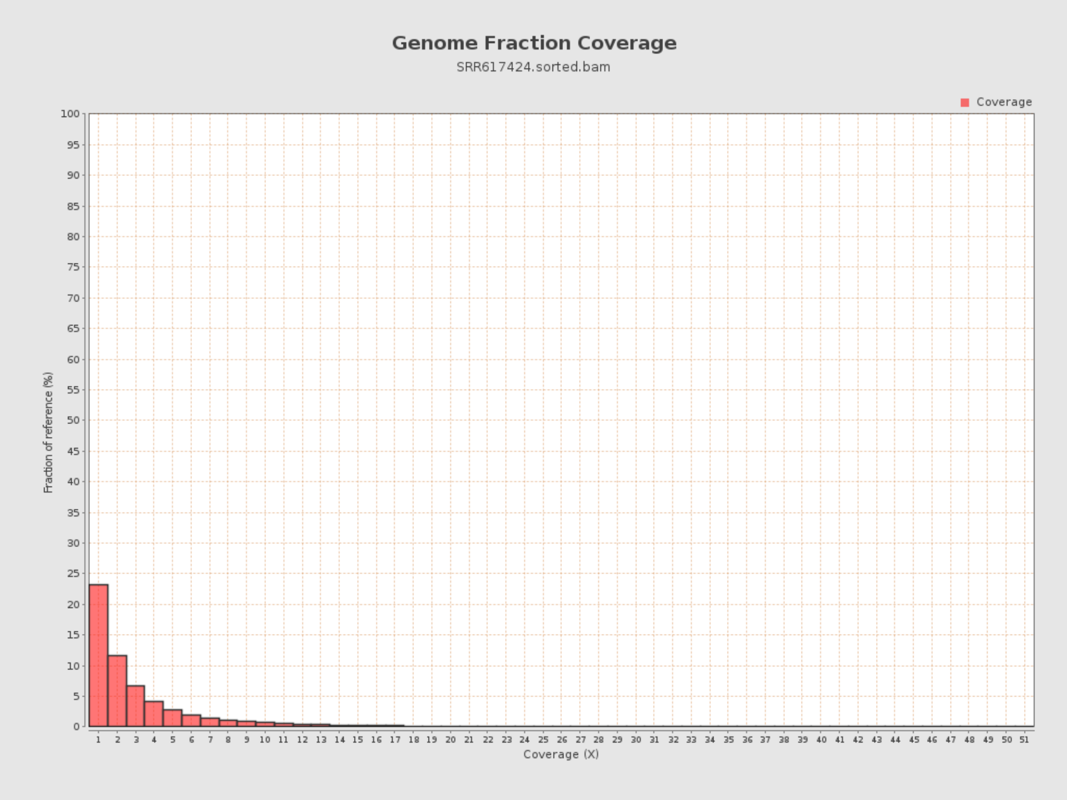
4. Results : Coverage Histogram



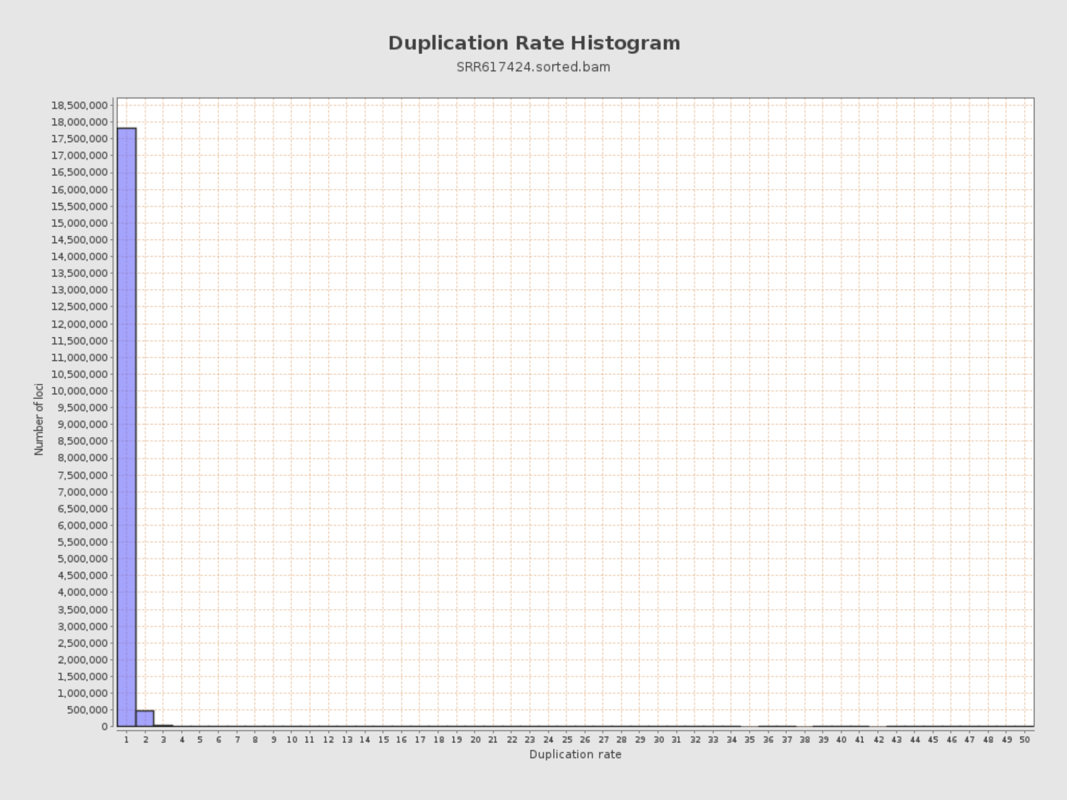
5. Results : Coverage Histogram (0-50X)



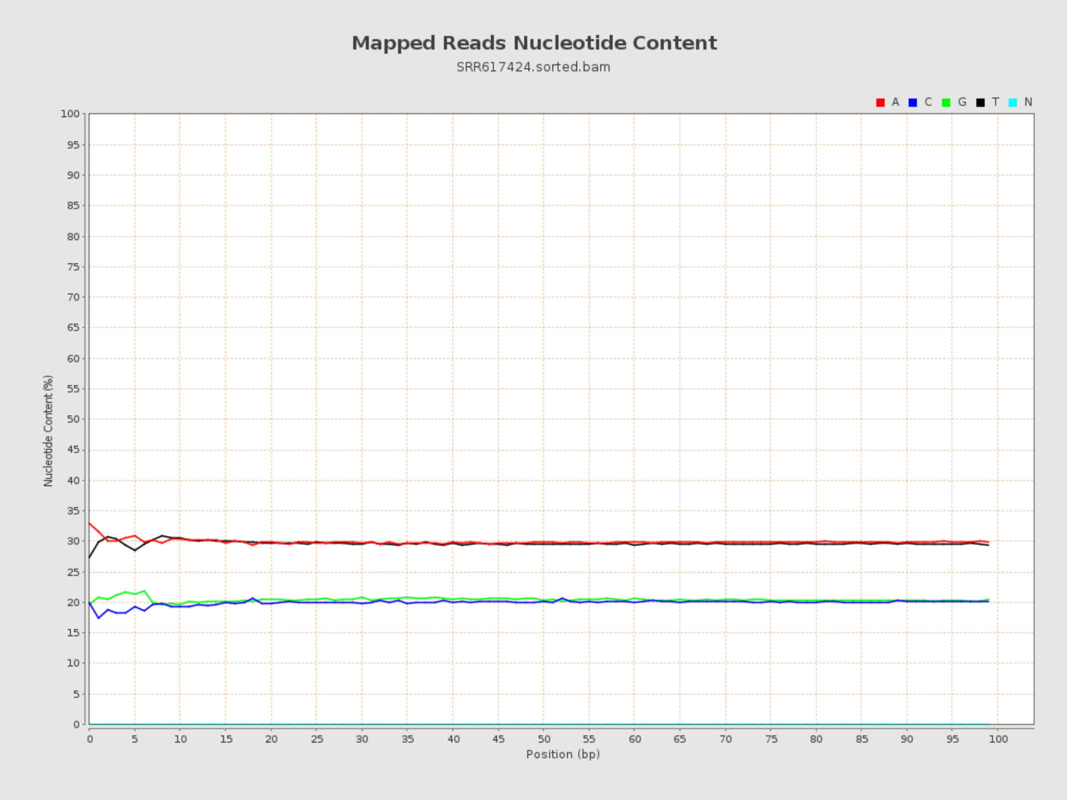
6. Results : Genome Fraction Coverage



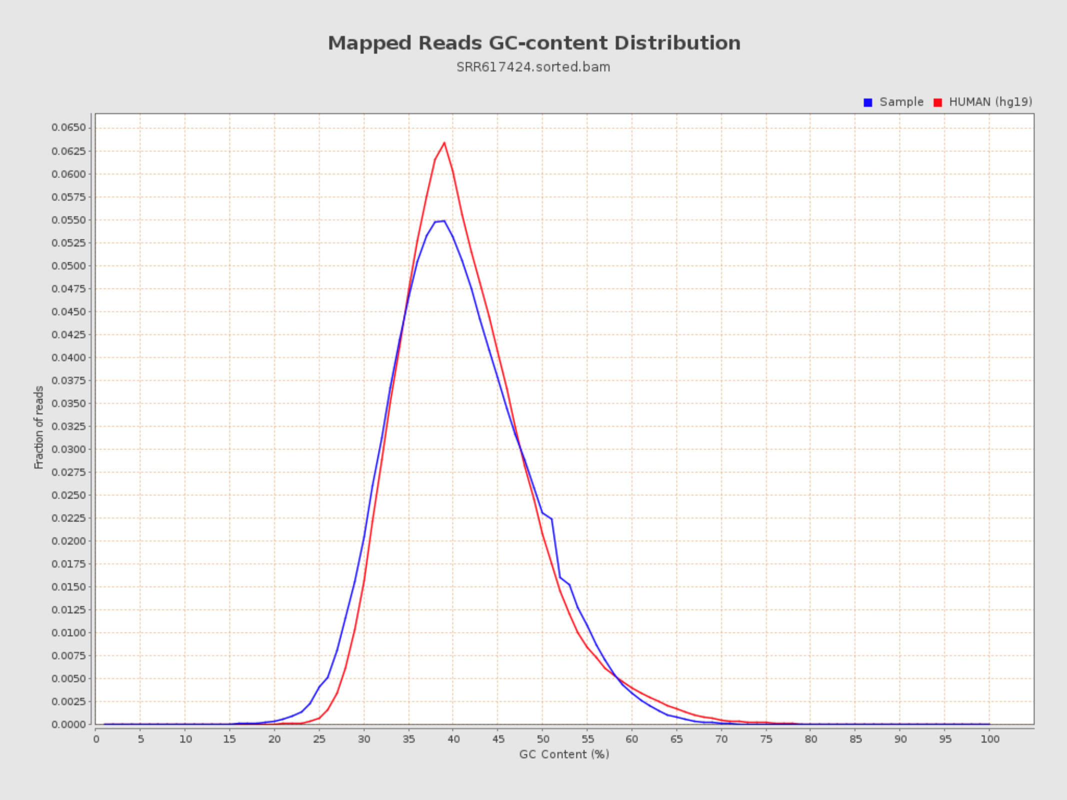
7. Results : Duplication Rate Histogram



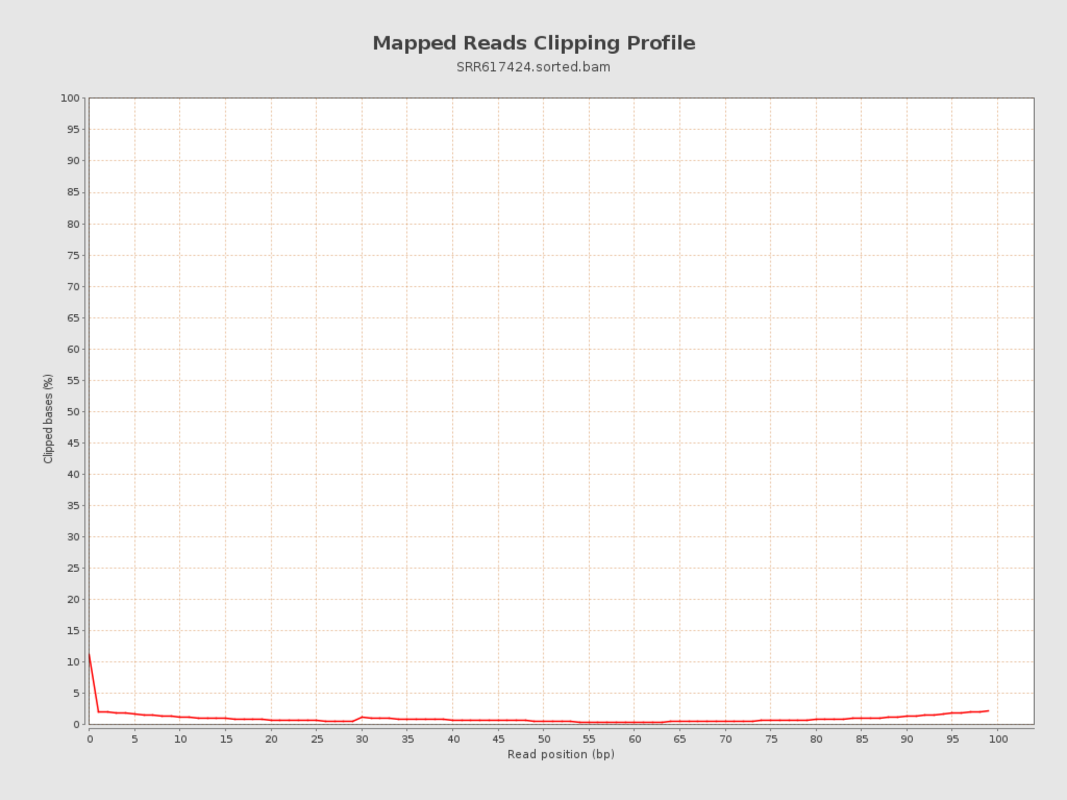
8. Results : Mapped Reads Nucleotide Content



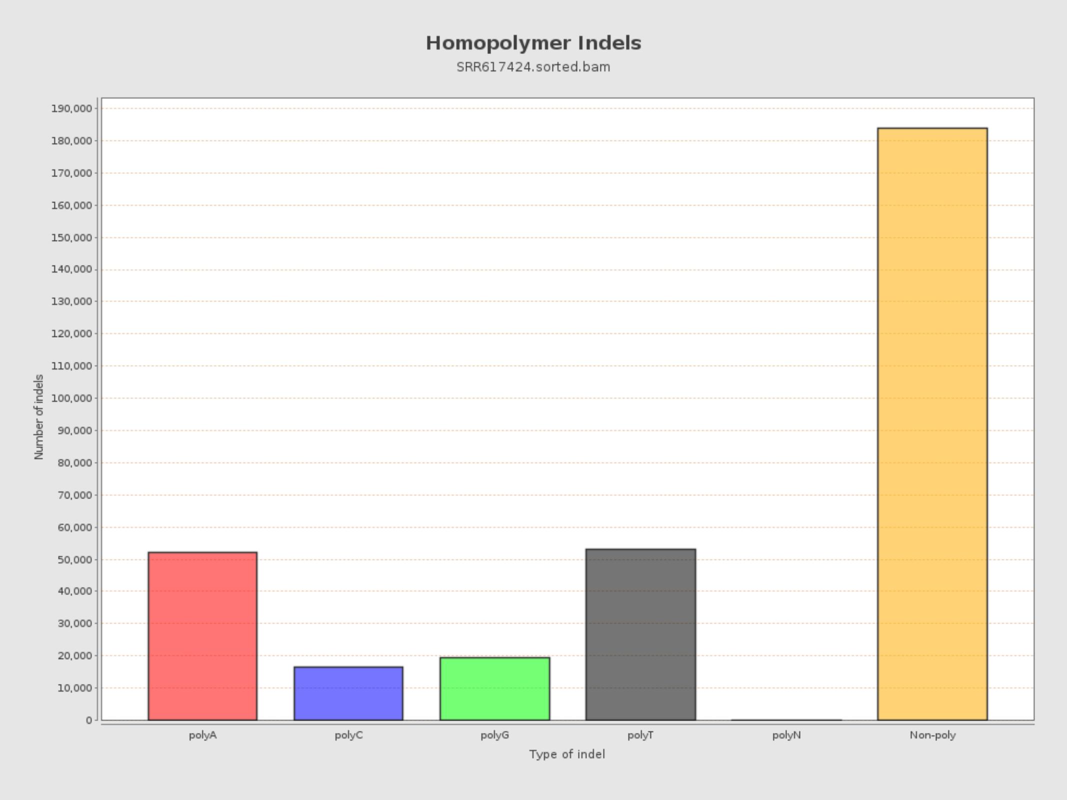
9. Results : Mapped Reads GC-content Distribution



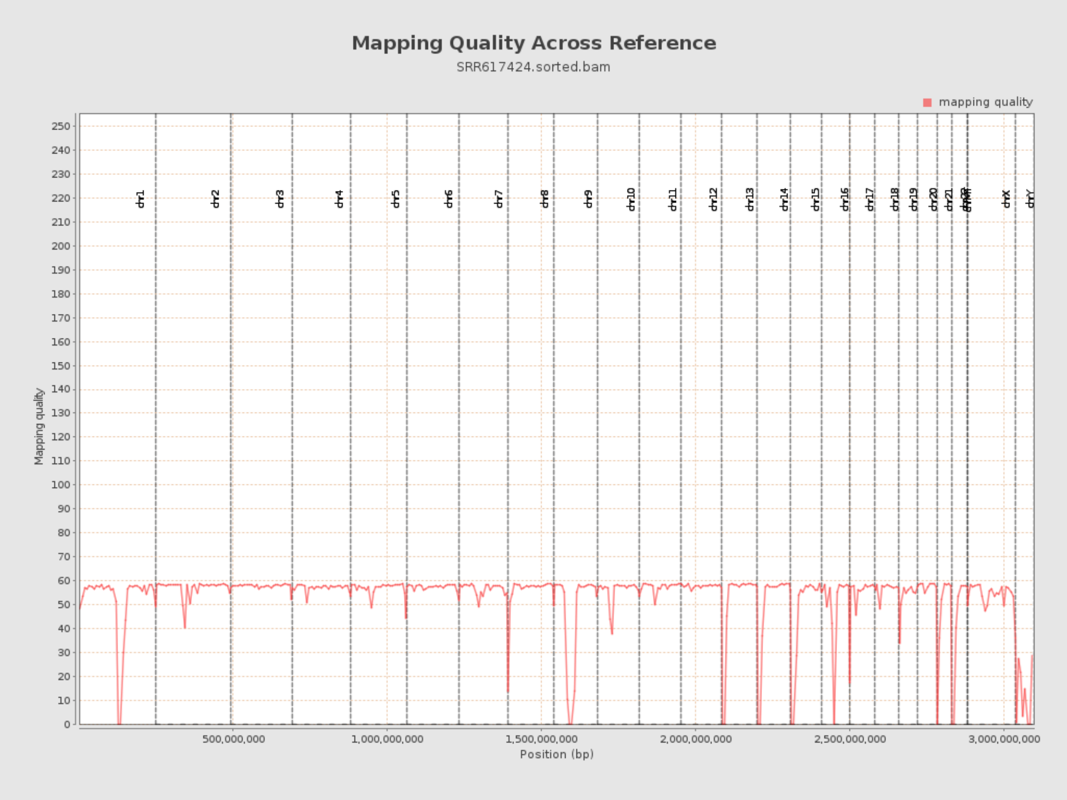
10. Results : Mapped Reads Clipping Profile



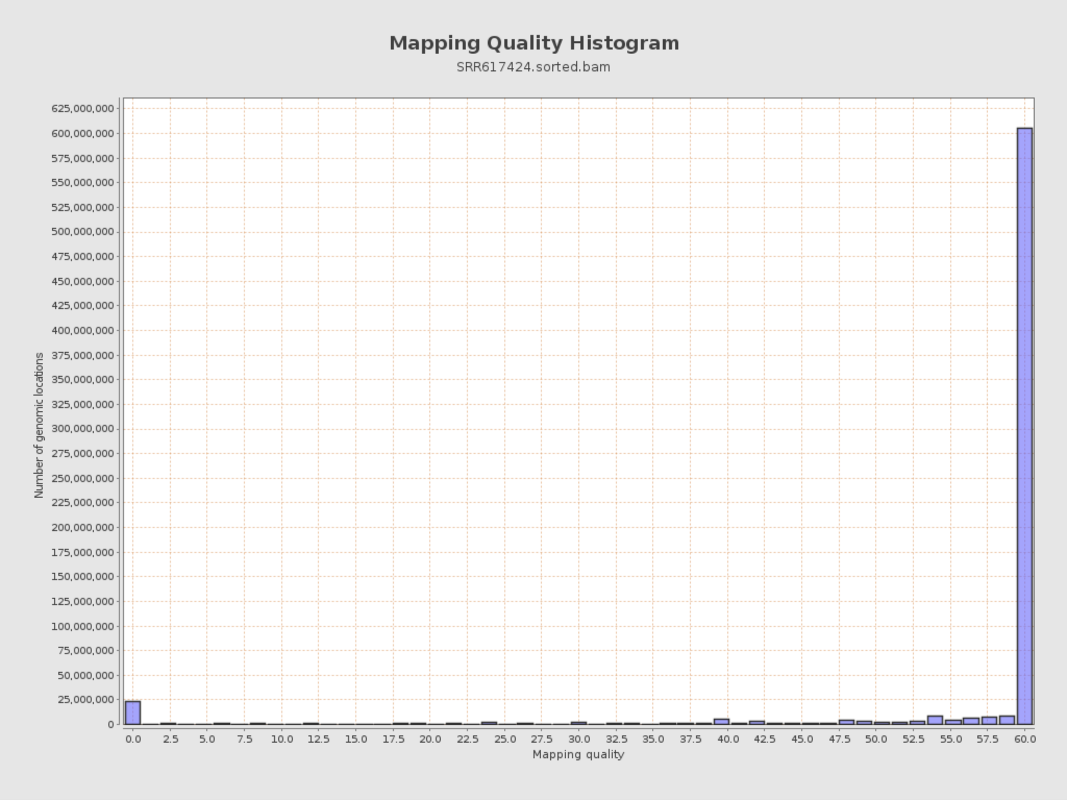
11. Results : Homopolymer Indels



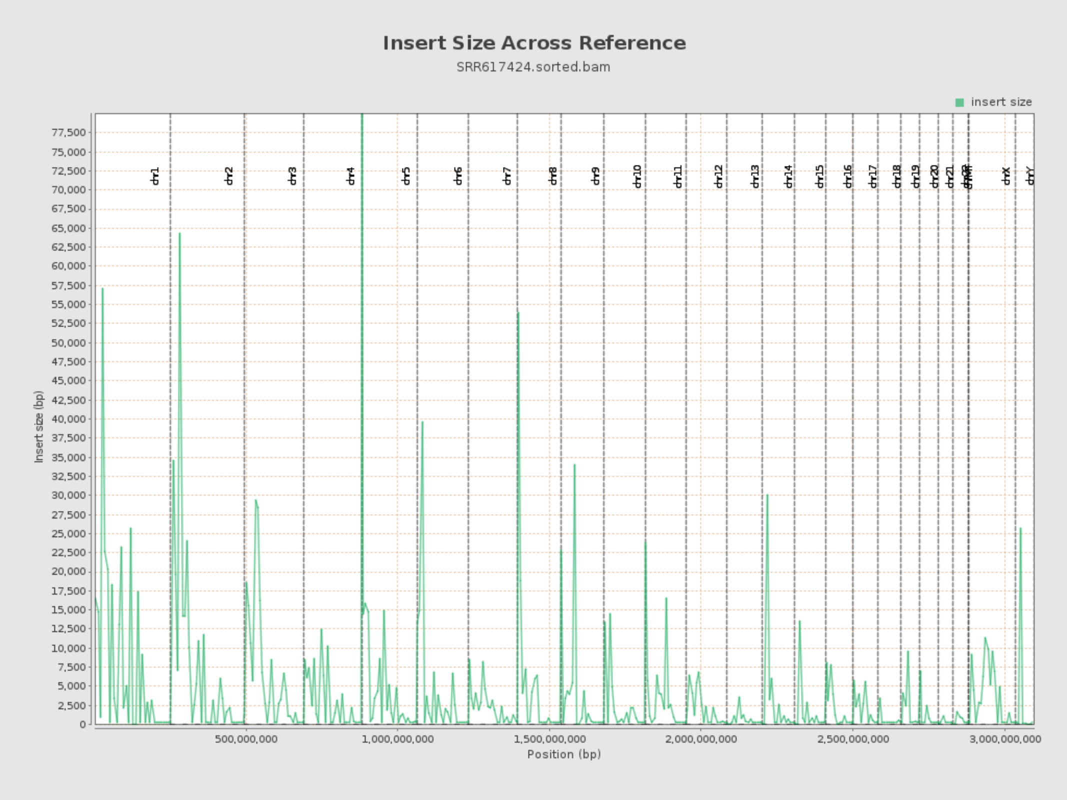
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram