Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/06 22:19:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975292.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_SRR975292 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975292_1.fastq.gz SRR975292_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 06 22:19:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975292.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,569,896
Mapped reads	5,523,525 / 99.17%
Unmapped reads	46,371 / 0.83%
Mapped paired reads	5,523,525 / 99.17%
Mapped reads, first in pair	2,760,927 / 49.57%
Mapped reads, second in pair	2,762,598 / 49.6%
Mapped reads, both in pair	5,505,558 / 98.84%
Mapped reads, singletons	17,967 / 0.32%
Secondary alignments	0
Supplementary alignments	30,625 / 0.55%
Read min/max/mean length	30 / 101 / 101.22
Duplicated reads (estimated)	297,624 / 5.34%
Duplication rate	2.88%
Clipped reads	3,326,317 / 59.72%

2.2. ACGT Content

Number/percentage of A's	149,399,045 / 29.18%
Number/percentage of C's	103,157,767 / 20.15%
Number/percentage of T's	151,400,732 / 29.57%
Number/percentage of G's	107,953,477 / 21.09%
Number/percentage of N's	13,713 / 0%

GC Percentage	41.24%

2.3. Coverage

Mean	0.1655
Standard Deviation	1.7481

2.4. Mapping Quality

Mean Mapping Quality	52.94

2.5. Insert size

Mean	85,121.49
Standard Deviation	2,798,393.76
P25/Median/P75	141 / 174 / 221

2.6. Mismatches and indels

General error rate	0.88%
Mismatches	4,320,170
Insertions	85,430
Mapped reads with at least one insertion	1.52%
Deletions	175,437
Mapped reads with at least one deletion	3.11%
Homopolymer indels	45.64%

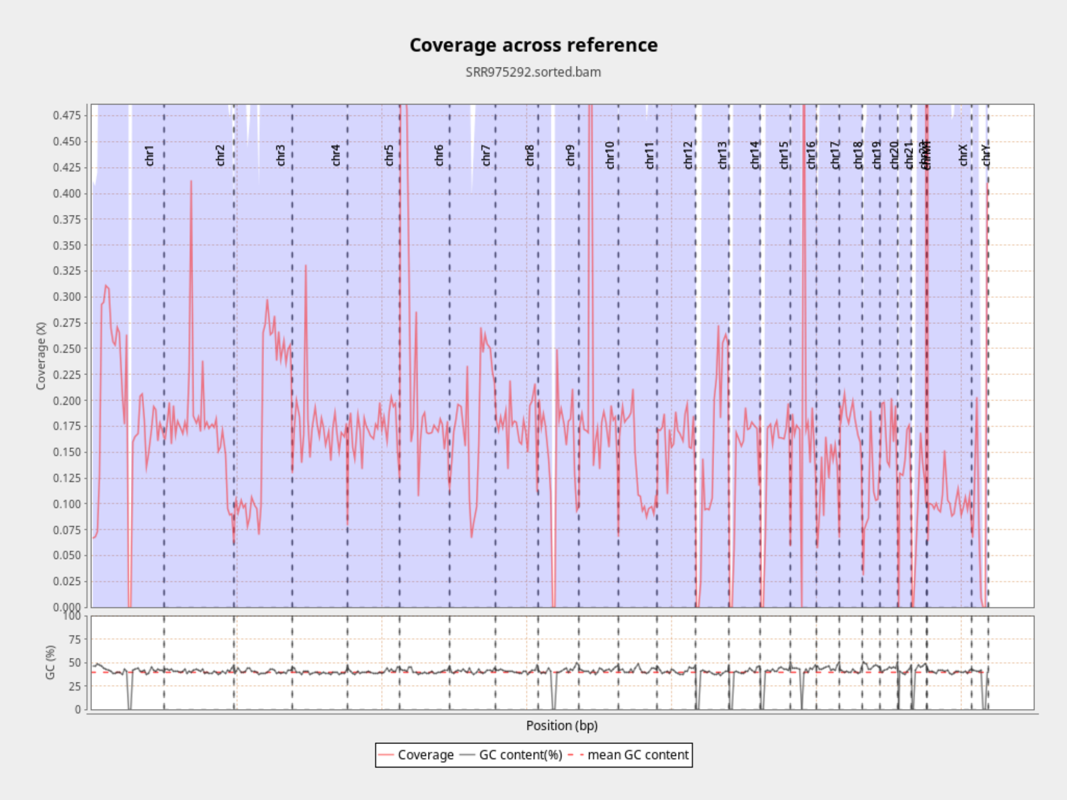
2.7. Chromosome stats

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

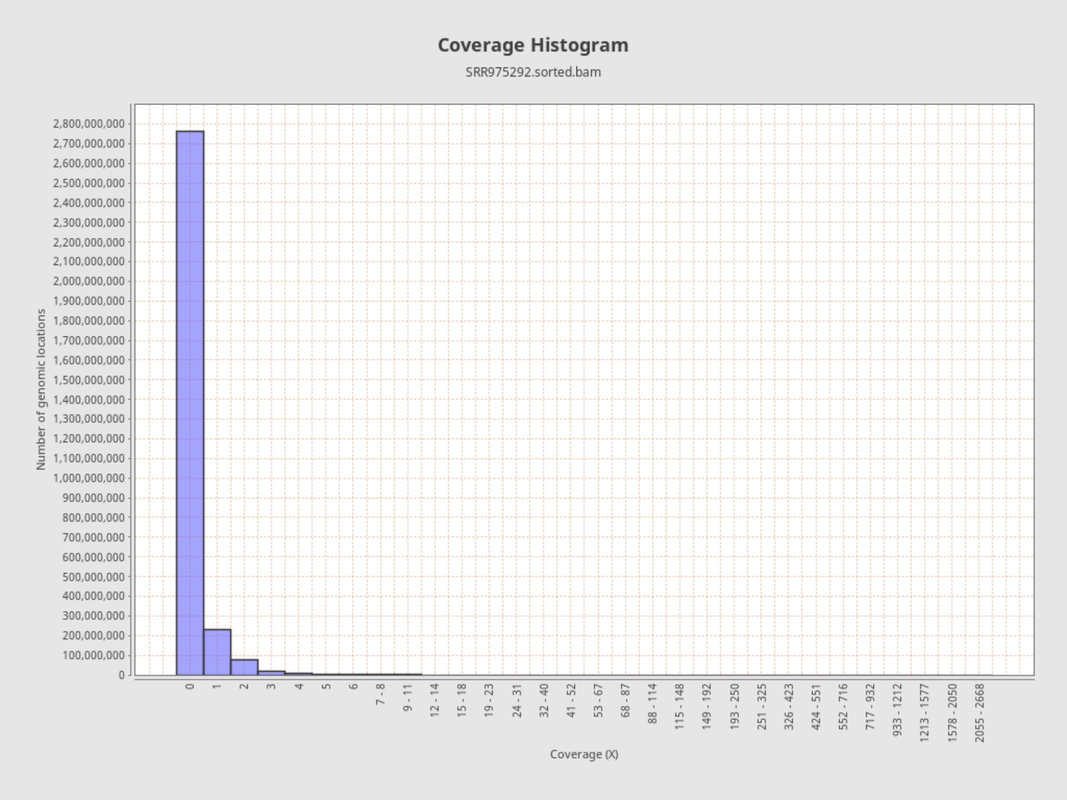
		bases	coverage	deviation
chr1	249250621	46222378	0.1854	1.6562
chr2	243199373	42465896	0.1746	1.6646
chr3	198022430	35603225	0.1798	0.6293
chr4	191154276	33522787	0.1754	1.1837
chr5	180915260	31338703	0.1732	0.5483
chr6	171115067	40675167	0.2377	1.3692
chr7	159138663	28976968	0.1821	1.6491
chr8	146364022	25701477	0.1756	0.7353
chr9	141213431	21472196	0.1521	2.1771
chr10	135534747	28184554	0.208	5.5199
chr11	135006516	18345593	0.1359	1.4547
chr12	133851895	22345122	0.1669	0.5429
chr13	115169878	17339583	0.1506	0.5145
chr14	107349540	14796644	0.1378	0.5437
chr15	102531392	14331223	0.1398	0.4951
chr16	90354753	16798041	0.1859	2.8028
chr17	81195210	10060674	0.1239	1.1988
chr18	78077248	14153805	0.1813	2.1164
chr19	59128983	6180955	0.1045	1.0218
chr20	63025520	10573953	0.1678	0.6056
chr21	48129895	6275183	0.1304	0.6845
chr22	51304566	4744921	0.0925	0.4103
chrMT	16571	102470	6.1837	6.9719
chrX	155270560	15558003	0.1002	0.681

chrY	59373566	6451891	0.1087	2.2045

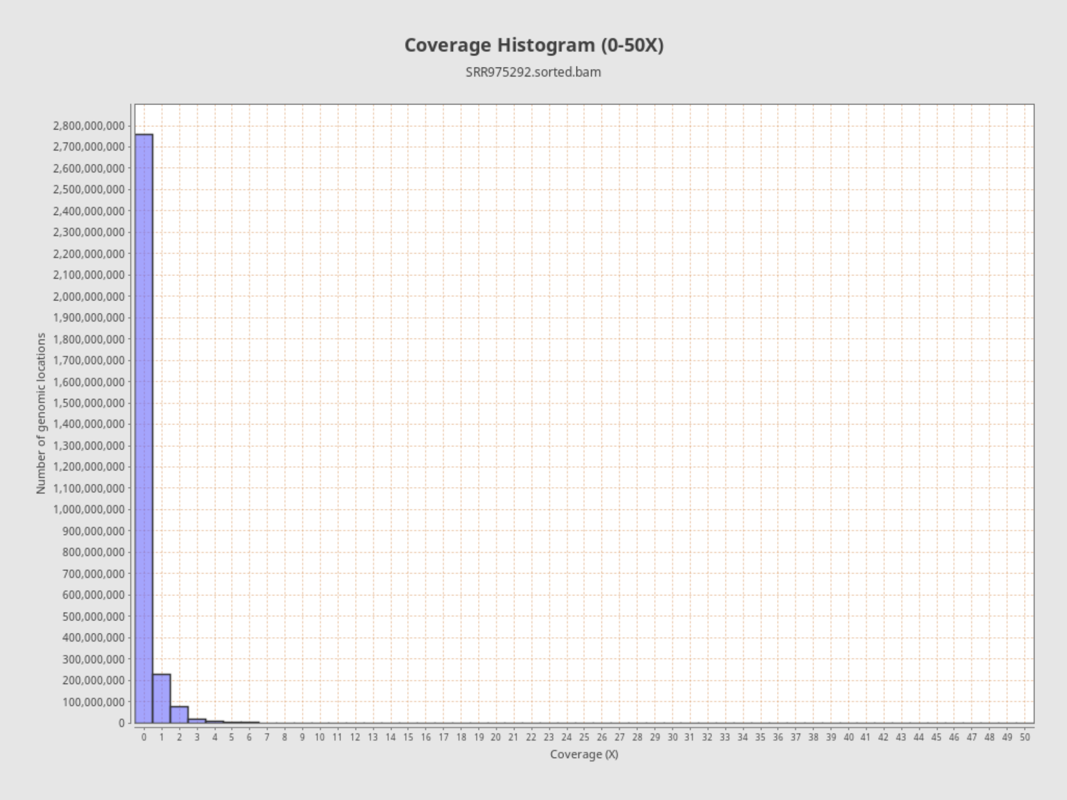
3. Results : Coverage across reference



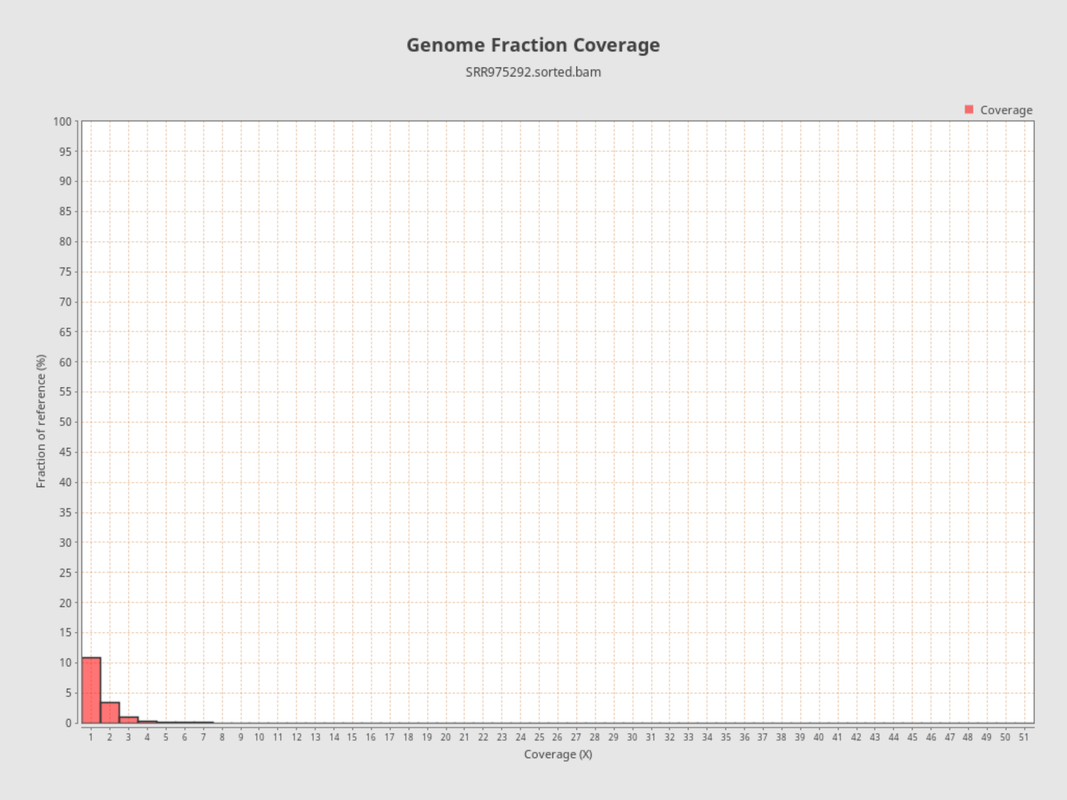
4. Results : Coverage Histogram



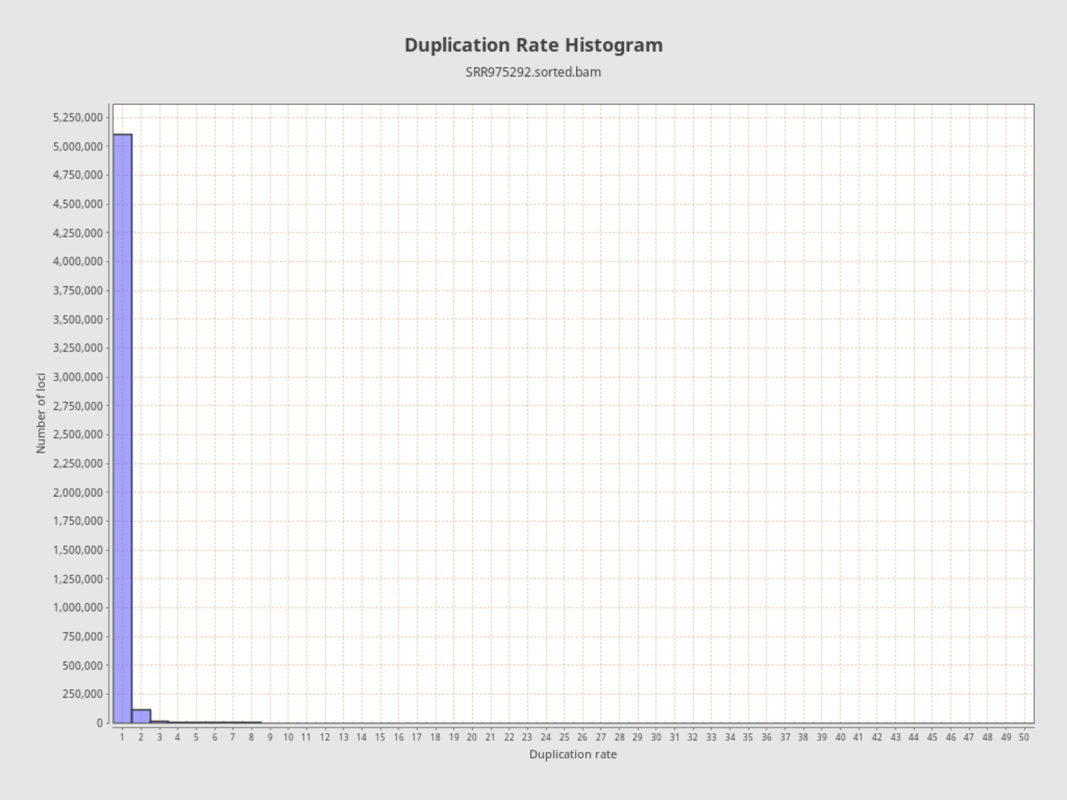
5. Results : Coverage Histogram (0-50X)



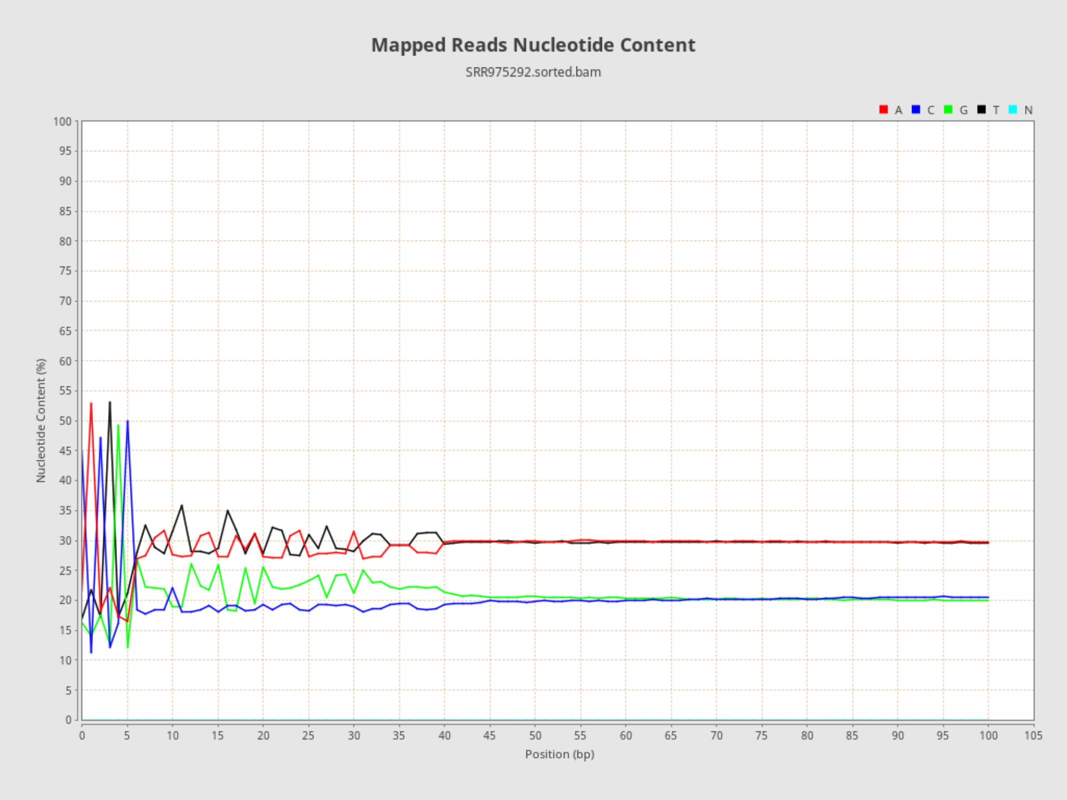
6. Results : Genome Fraction Coverage



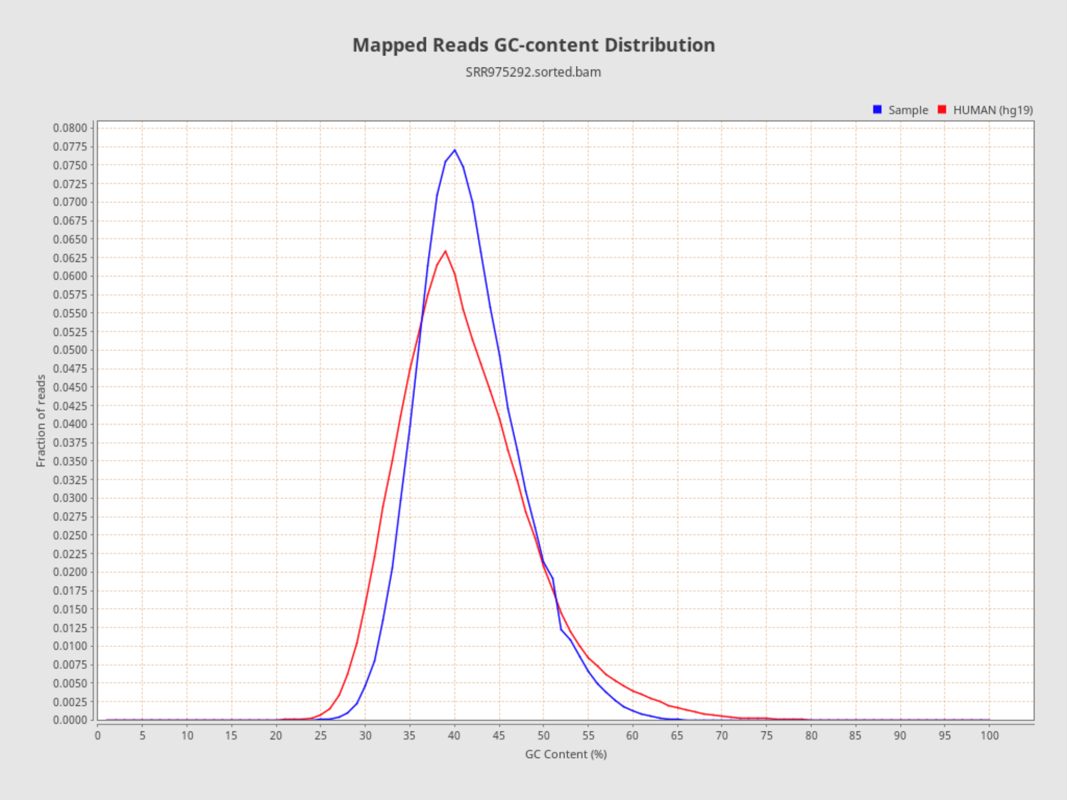
7. Results : Duplication Rate Histogram



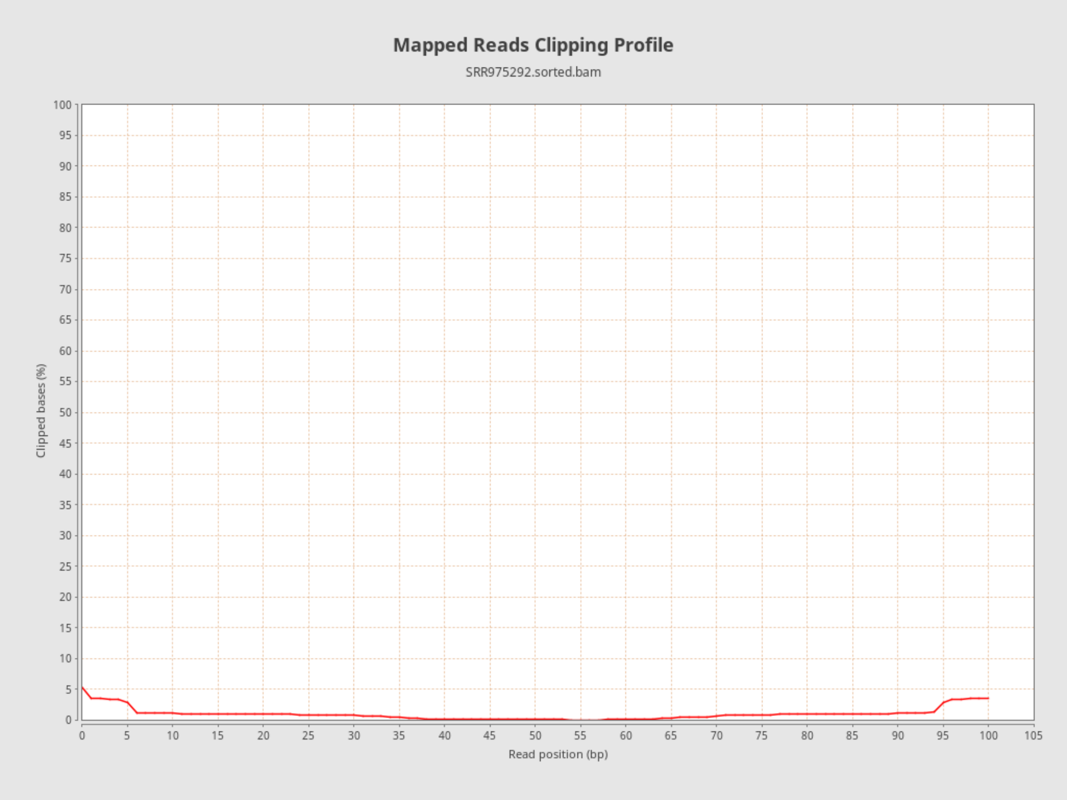
8. Results : Mapped Reads Nucleotide Content



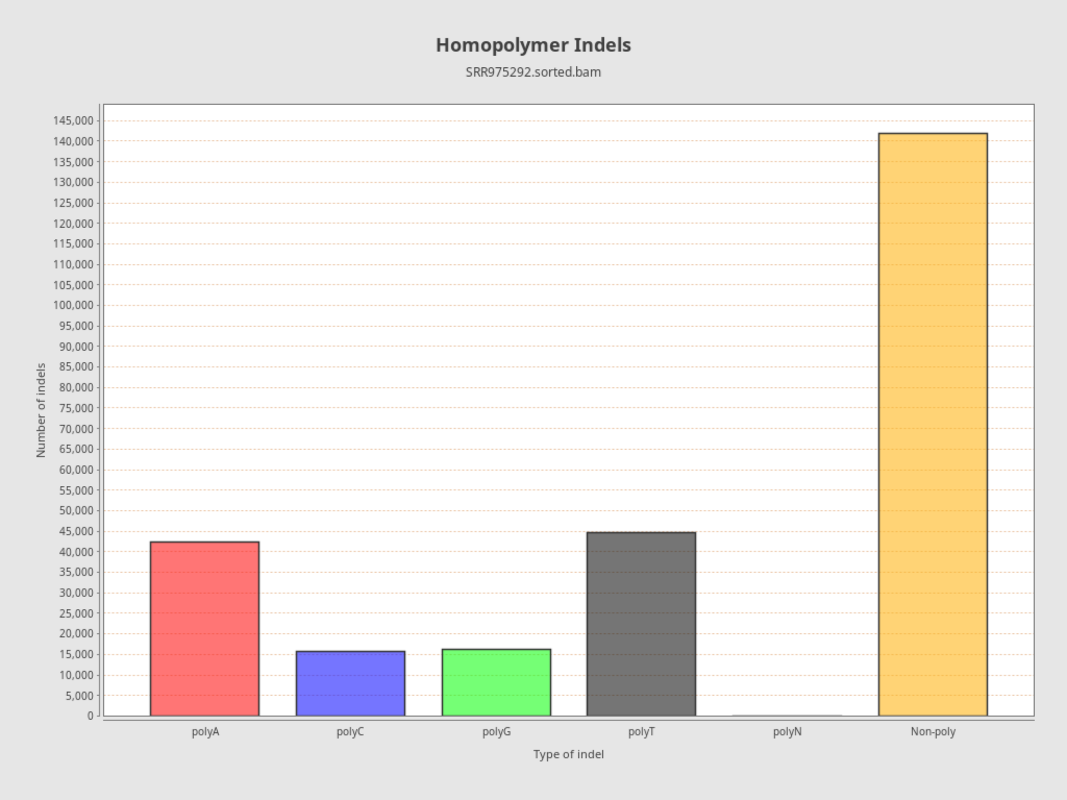
9. Results : Mapped Reads GC-content Distribution



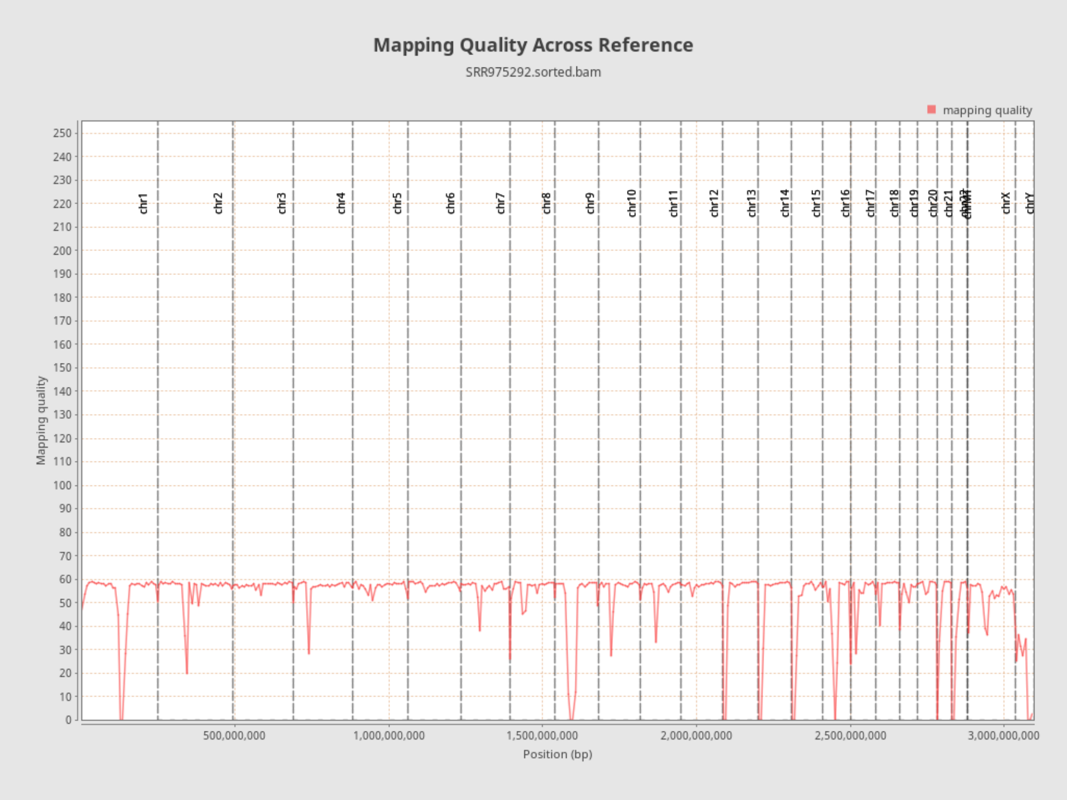
10. Results : Mapped Reads Clipping Profile



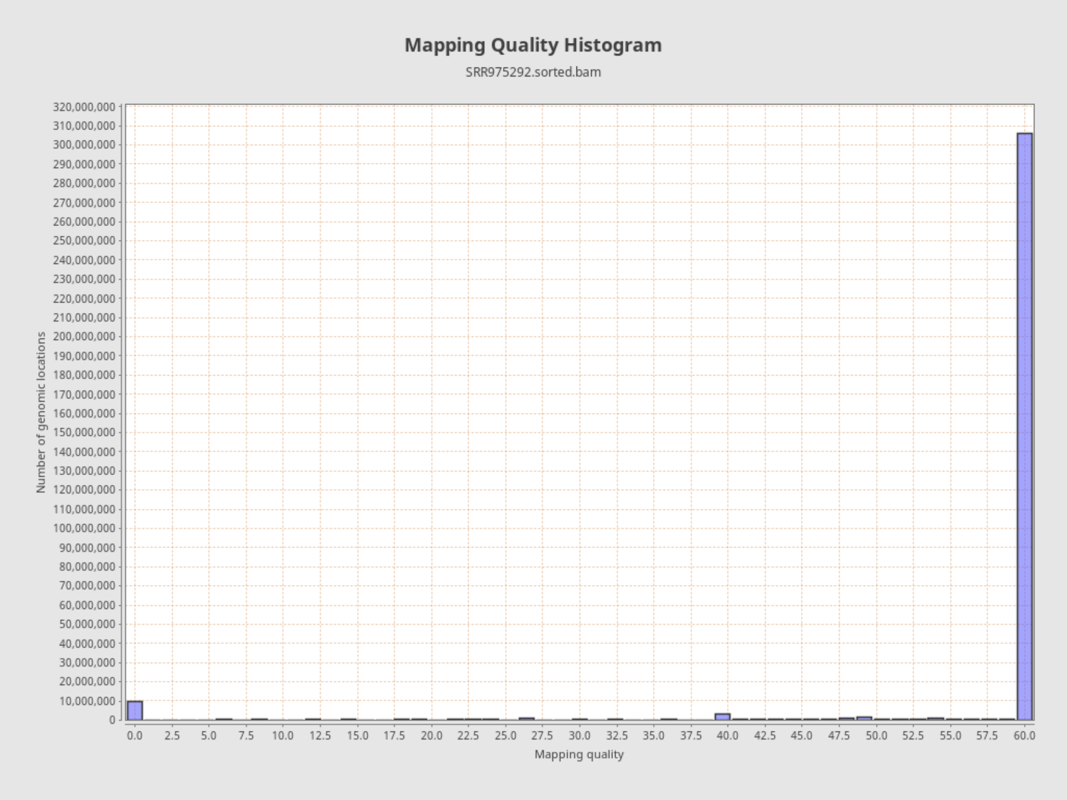
11. Results : Homopolymer Indels



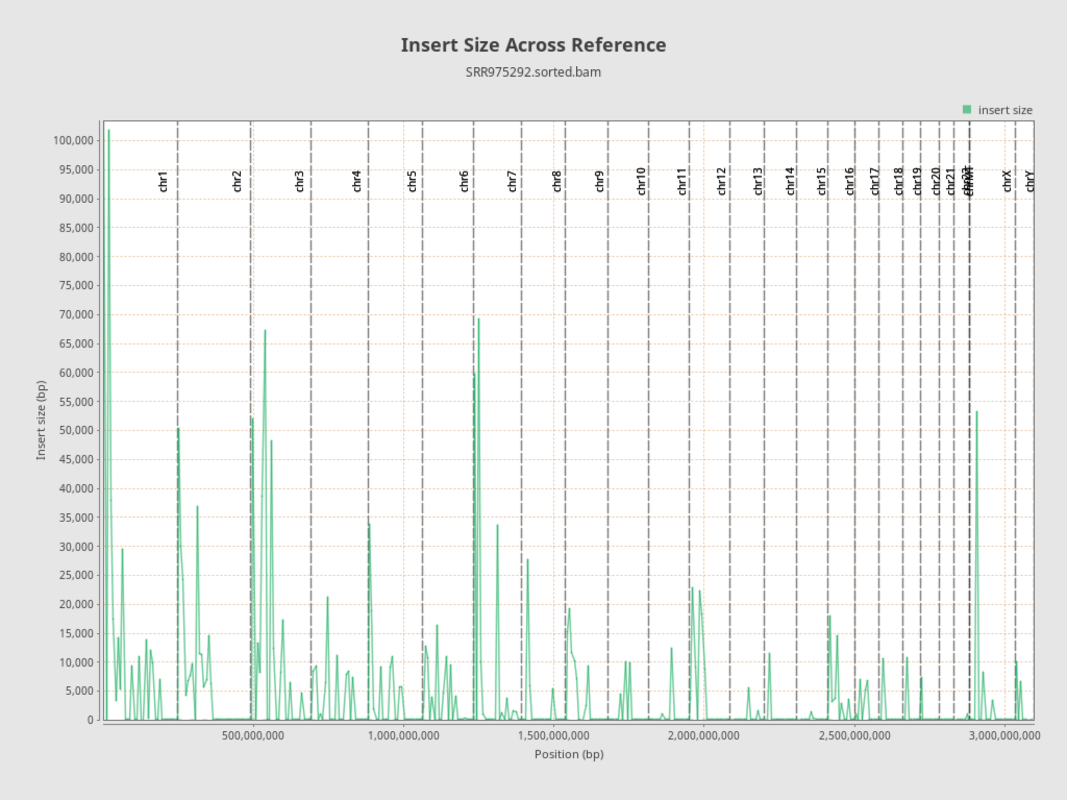
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram