Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 01:59:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975195.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_SRR975195 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975195_1.fastq.gz SRR975195_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 01:59:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975195.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,818,800
Mapped reads	5,632,585 / 96.8%
Unmapped reads	186,215 / 3.2%
Mapped paired reads	5,632,585 / 96.8%
Mapped reads, first in pair	2,817,818 / 48.43%
Mapped reads, second in pair	2,814,767 / 48.37%
Mapped reads, both in pair	5,584,870 / 95.98%
Mapped reads, singletons	47,715 / 0.82%
Secondary alignments	0
Supplementary alignments	82,228 / 1.41%
Read min/max/mean length	30 / 151 / 151.69
Duplicated reads (estimated)	1,181,207 / 20.3%
Duplication rate	18.3%
Clipped reads	4,086,247 / 70.22%

2.2. ACGT Content

Number/percentage of A's	224,733,769 / 29.54%
Number/percentage of C's	152,125,319 / 20%
Number/percentage of T's	224,598,968 / 29.52%
Number/percentage of G's	159,205,175 / 20.93%
Number/percentage of N's	77,882 / 0.01%

GC Percentage	40.92%

2.3. Coverage

Mean	0.2459
Standard Deviation	4.6843

2.4. Mapping Quality

Mean Mapping Quality	53.41

2.5. Insert size

Mean	104,755.88
Standard Deviation	3,094,971.58
P25/Median/P75	142 / 177 / 227

2.6. Mismatches and indels

General error rate	1.3%
Mismatches	9,500,992
Insertions	156,899
Mapped reads with at least one insertion	2.63%
Deletions	295,761
Mapped reads with at least one deletion	5.04%
Homopolymer indels	45.64%

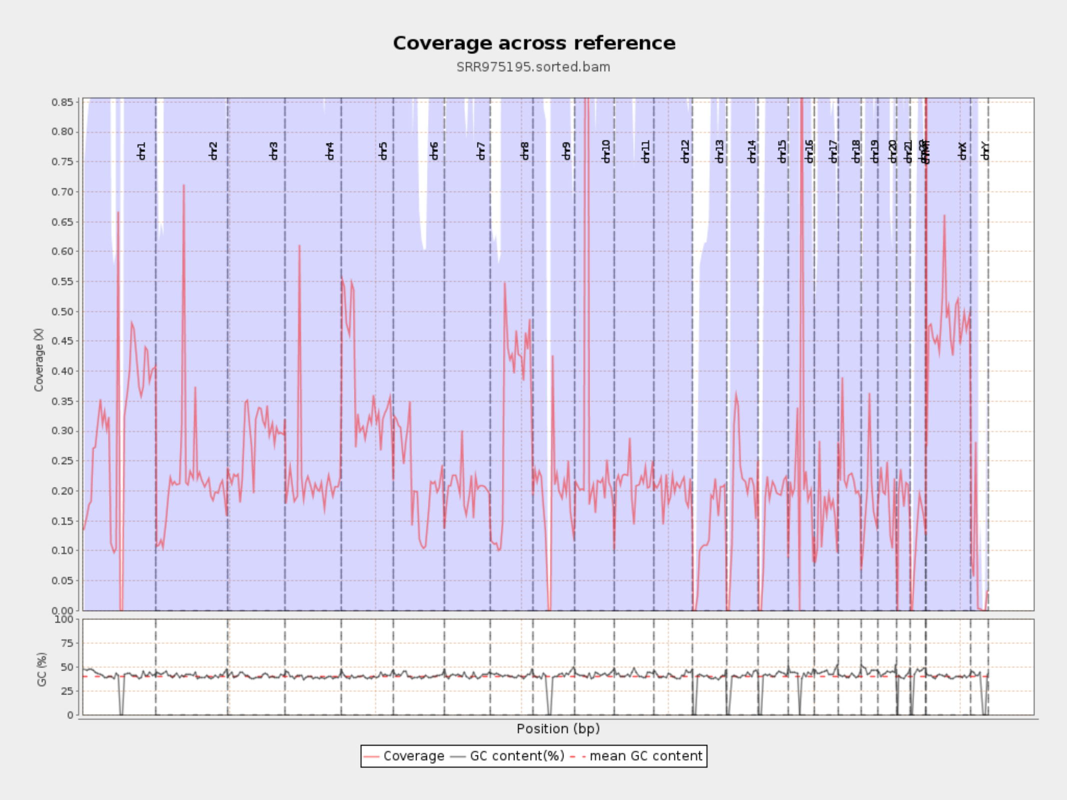
2.7. Chromosome stats

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

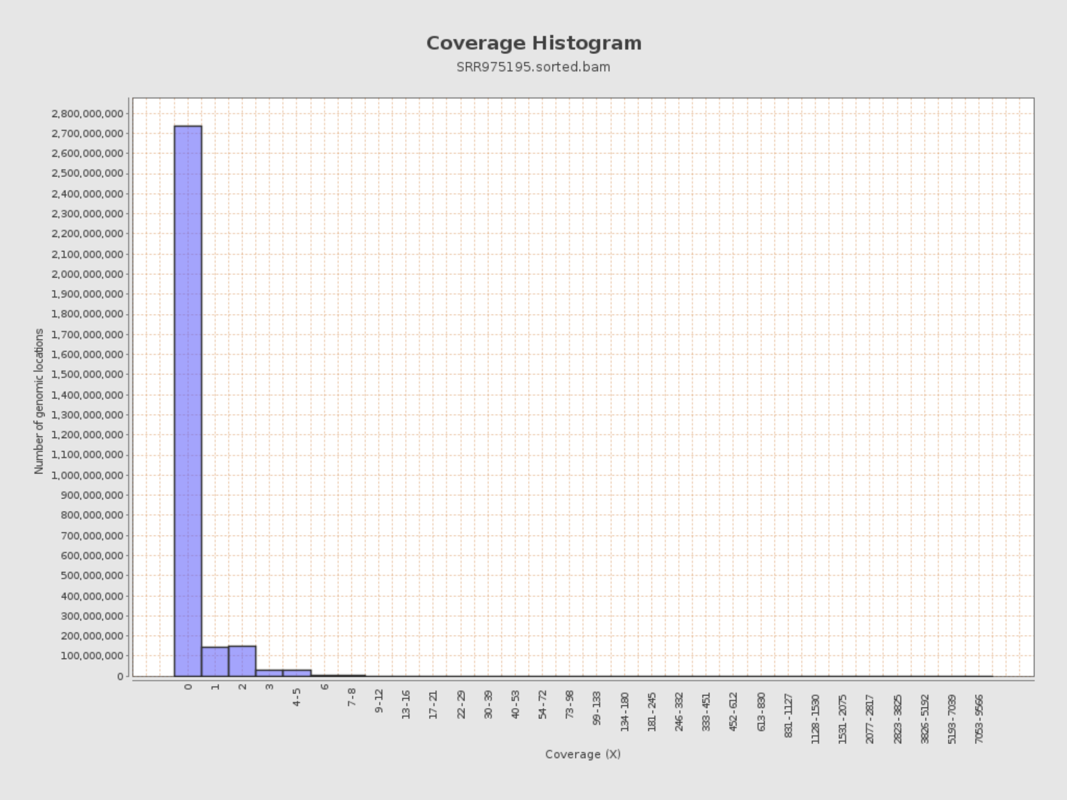
		bases	coverage	deviation
chr1	249250621	76206878	0.3057	5.8497
chr2	243199373	53429855	0.2197	3.4135
chr3	198022430	55744302	0.2815	1.0865
chr4	191154276	42365095	0.2216	2.6443
chr5	180915260	66144936	0.3656	0.9987
chr6	171115067	37650166	0.22	1.5941
chr7	159138663	32401343	0.2036	1.964
chr8	146364022	48630696	0.3323	1.5213
chr9	141213431	26826284	0.19	4.5734
chr10	135534747	42034843	0.3101	17.6262
chr11	135006516	29159188	0.216	2.1476
chr12	133851895	26954911	0.2014	0.7078
chr13	115169878	15341658	0.1332	0.5577
chr14	107349540	21928529	0.2043	0.763
chr15	102531392	16957766	0.1654	0.6285
chr16	90354753	23599563	0.2612	5.8345
chr17	81195210	12986392	0.1599	2.5392
chr18	78077248	18161007	0.2326	4.5502
chr19	59128983	10981229	0.1857	2.6994
chr20	63025520	11828167	0.1877	1.0474
chr21	48129895	8666614	0.1801	1.4974
chr22	51304566	6009736	0.1171	0.5584
chrMT	16571	148619	8.9686	5.6058
chrX	155270560	73834710	0.4755	1.8866

chrY	59373566	3338158	0.0562	4.3419

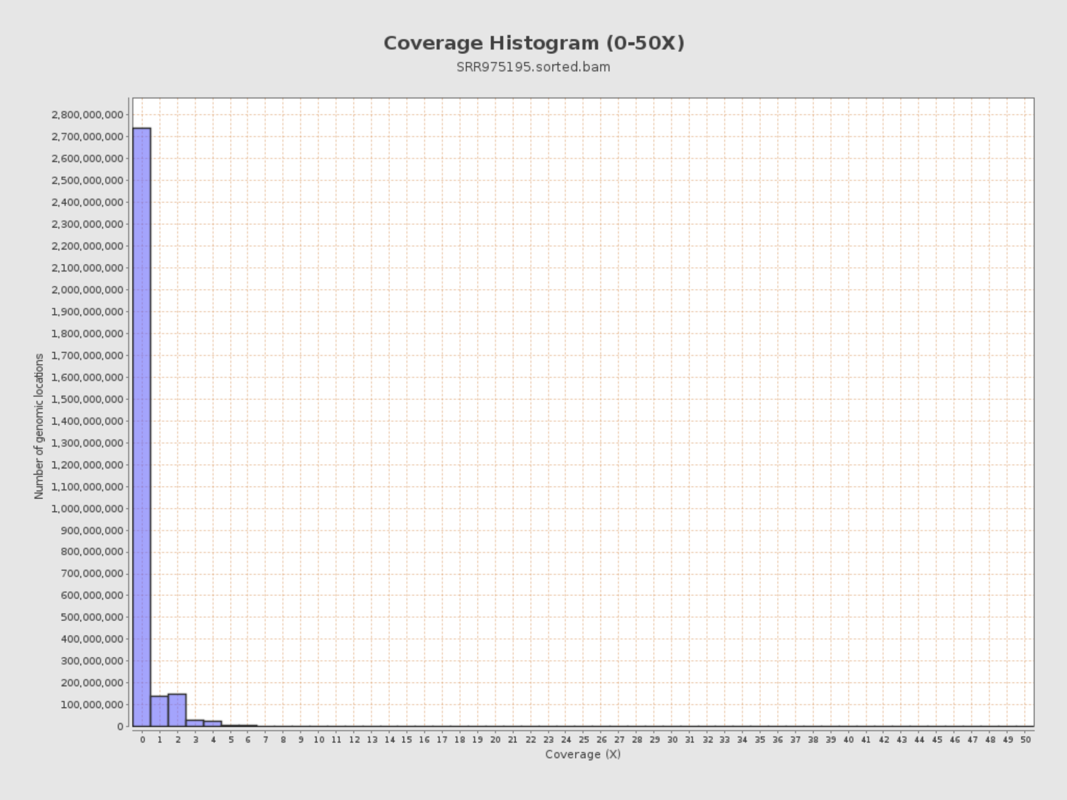
3. Results : Coverage across reference



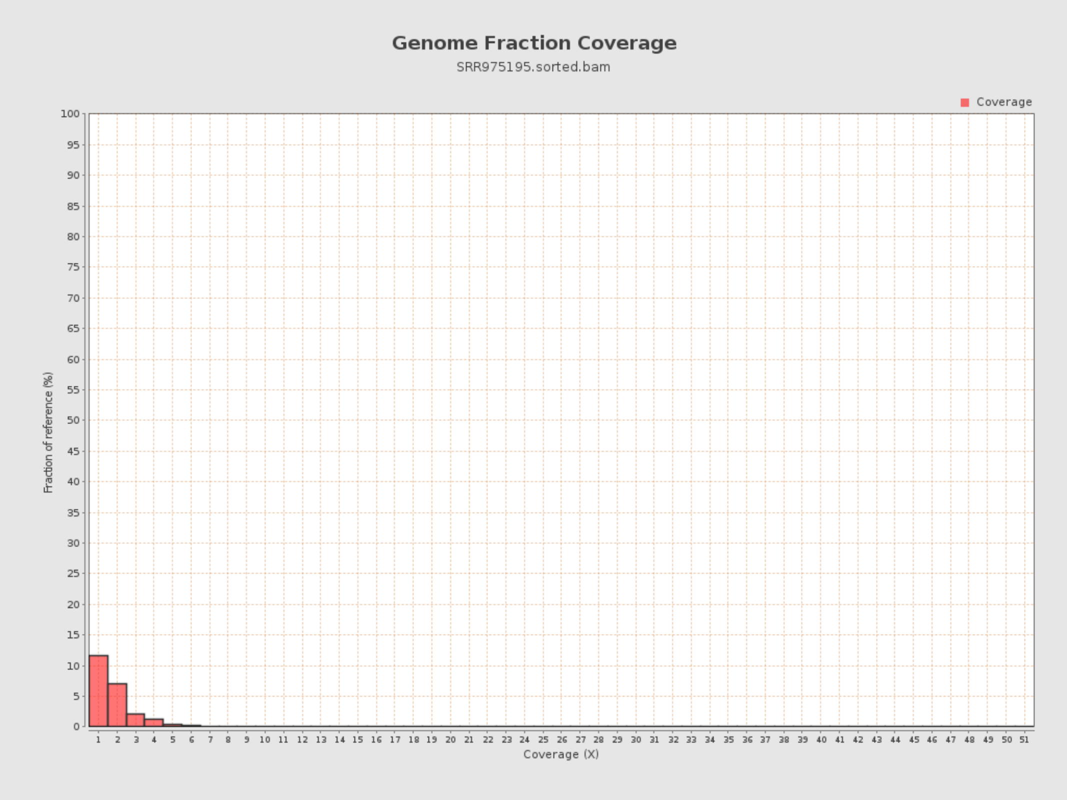
4. Results : Coverage Histogram



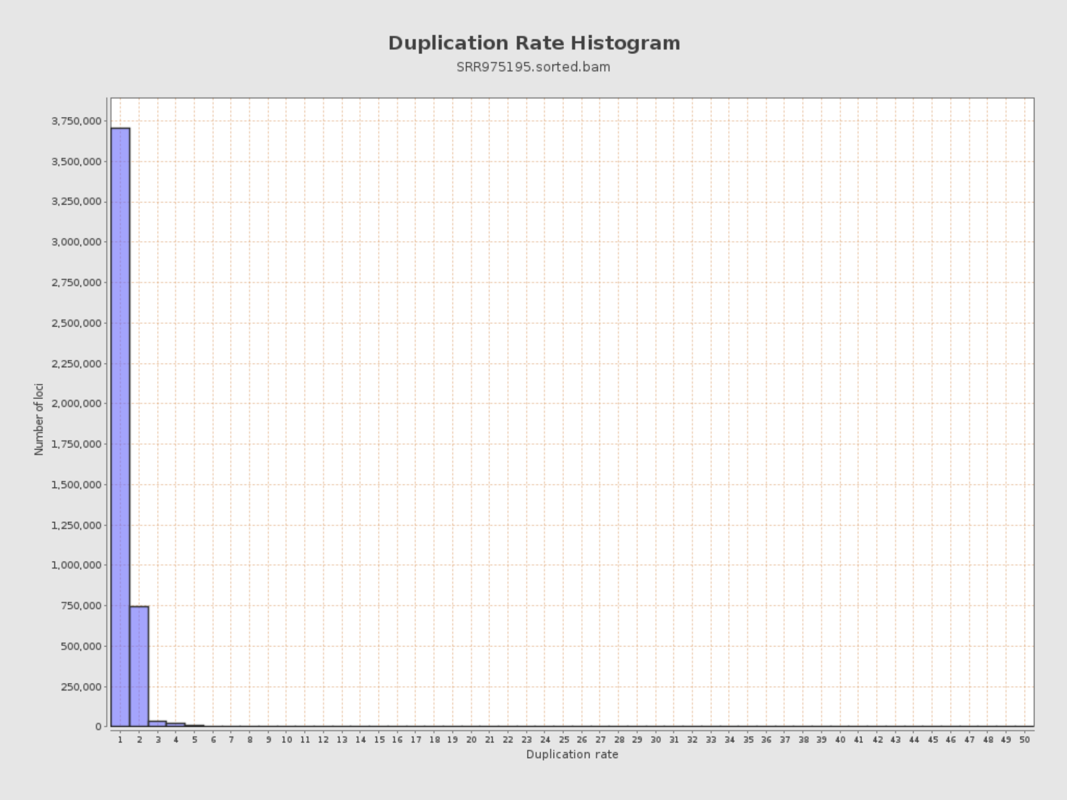
5. Results : Coverage Histogram (0-50X)



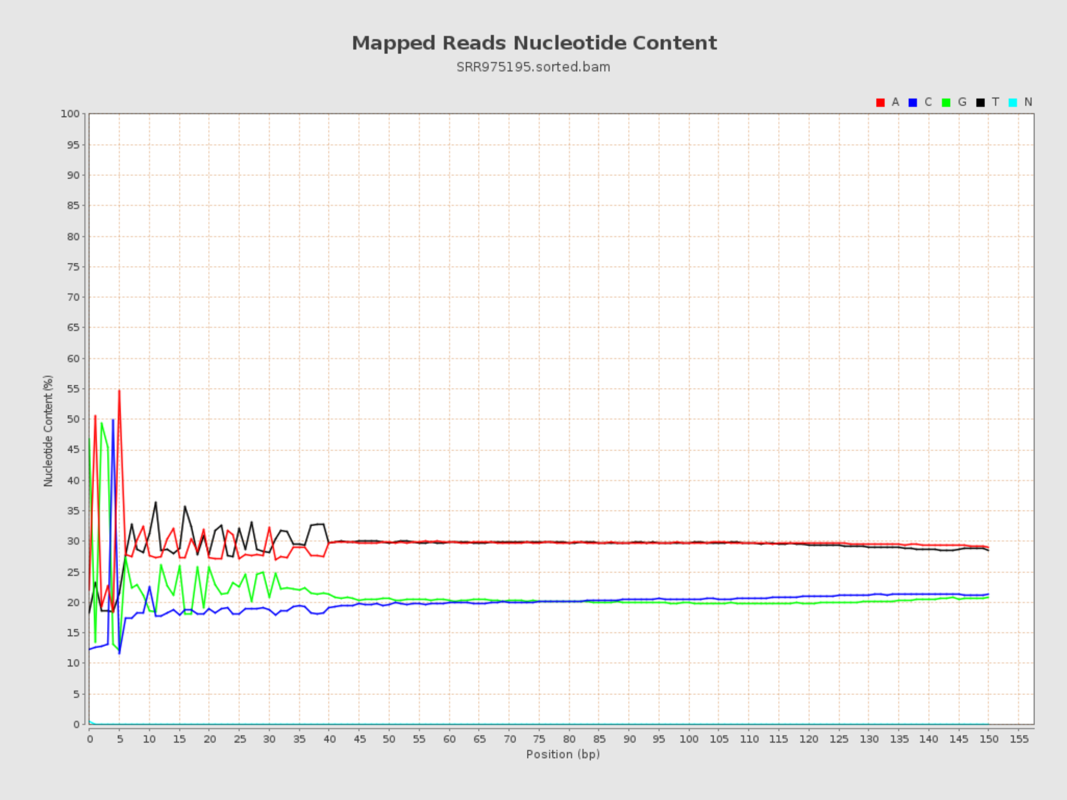
6. Results : Genome Fraction Coverage



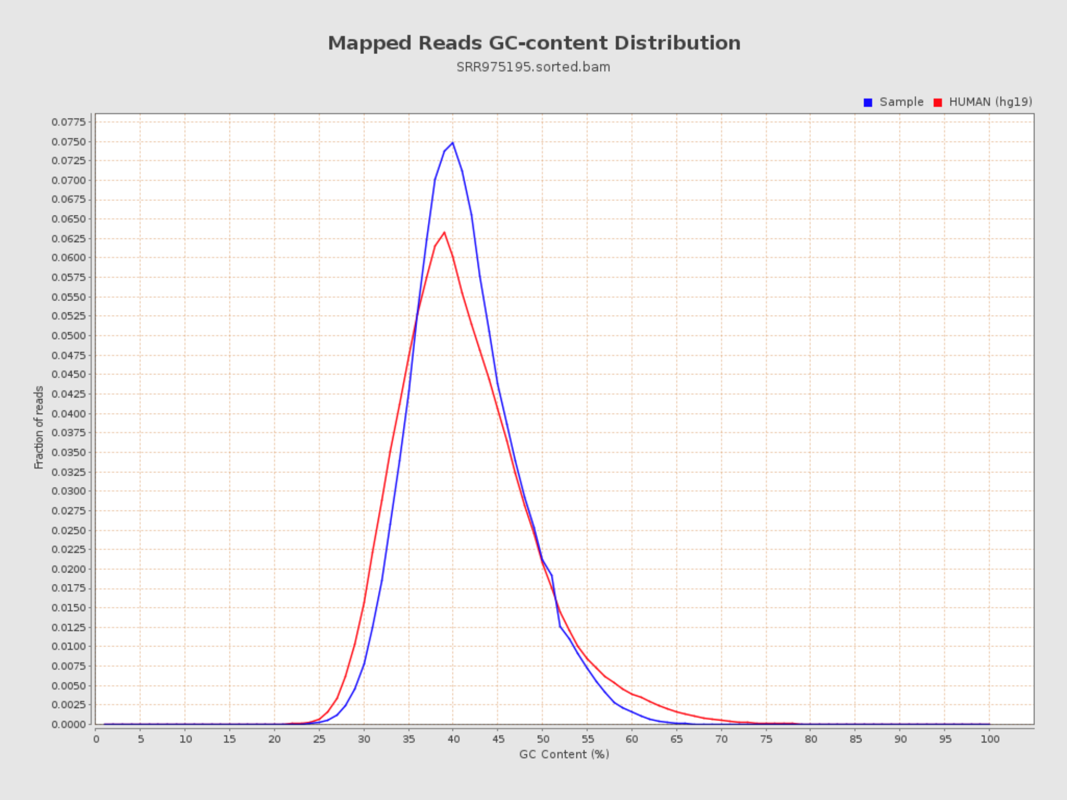
7. Results : Duplication Rate Histogram



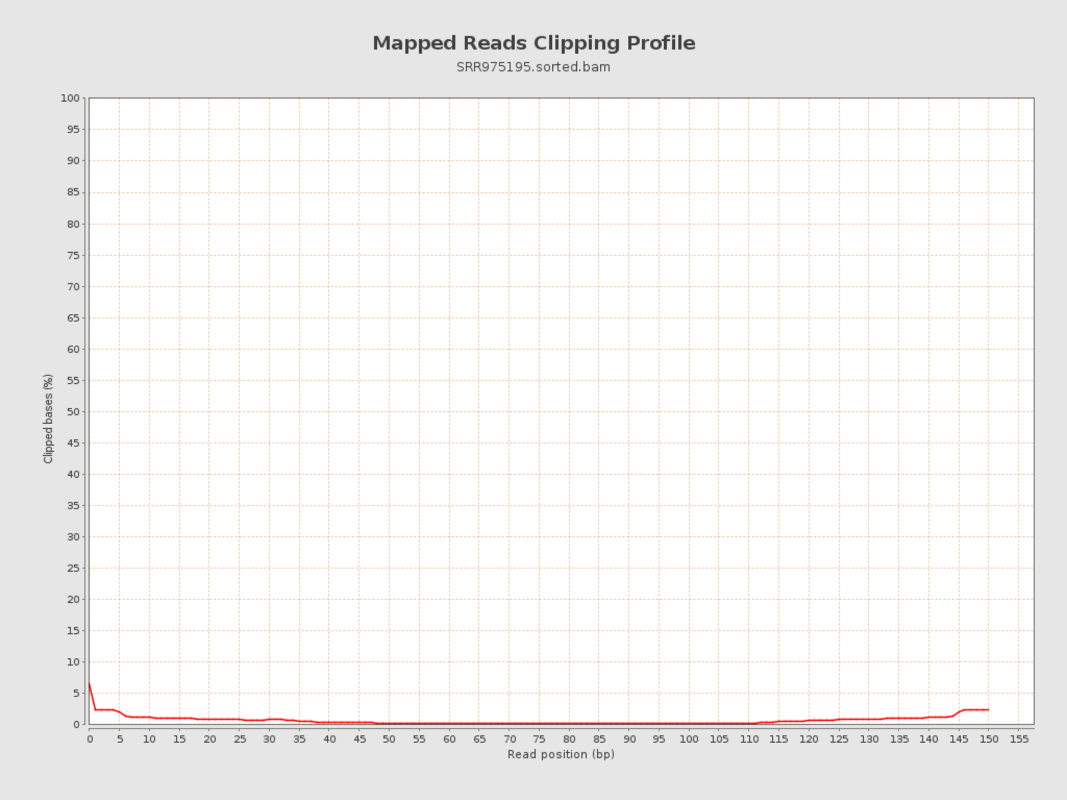
8. Results : Mapped Reads Nucleotide Content



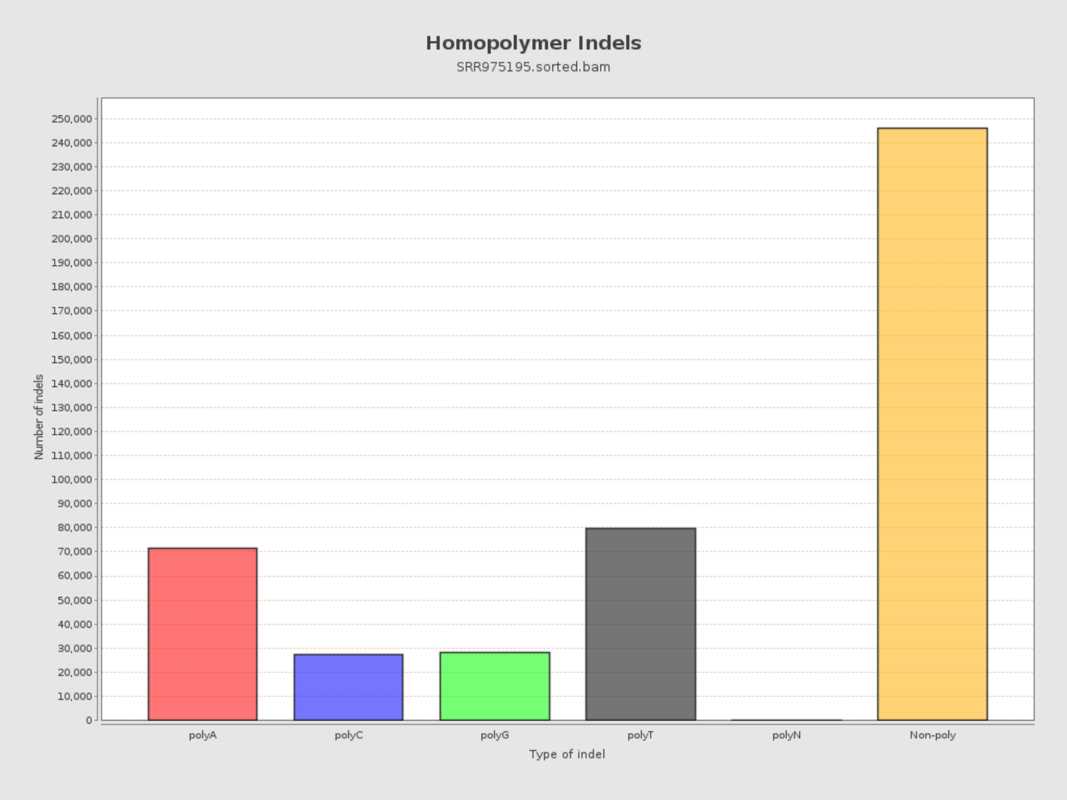
9. Results : Mapped Reads GC-content Distribution



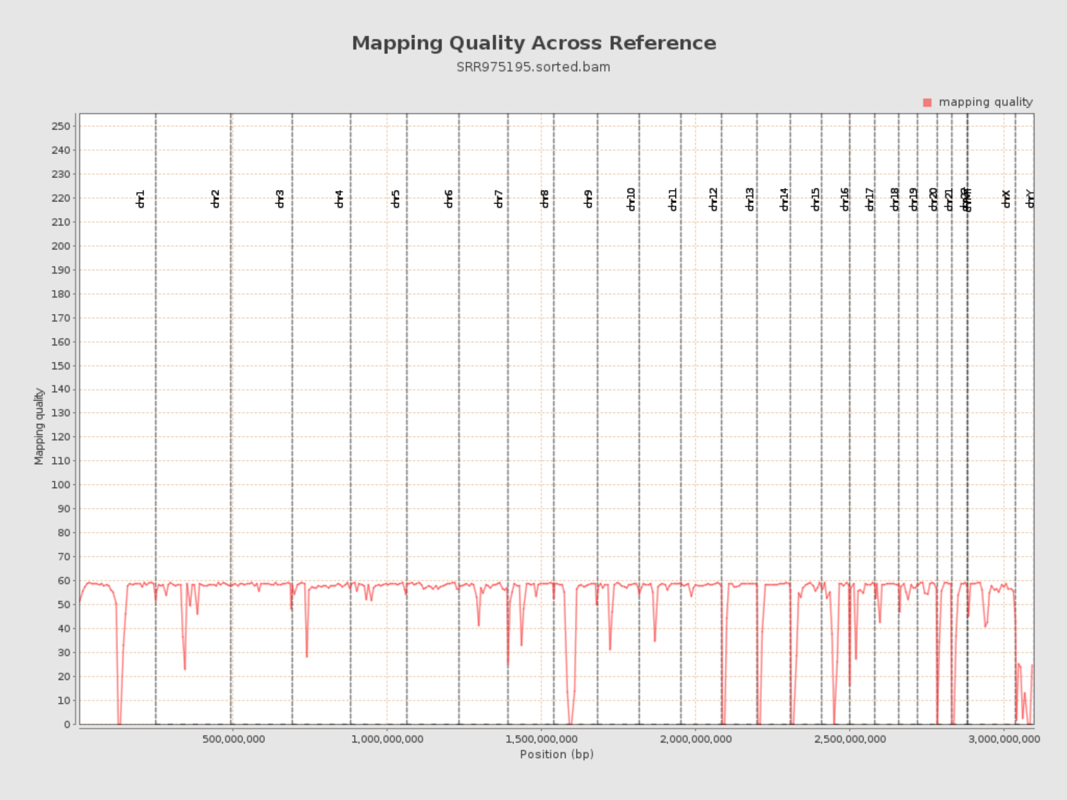
10. Results : Mapped Reads Clipping Profile



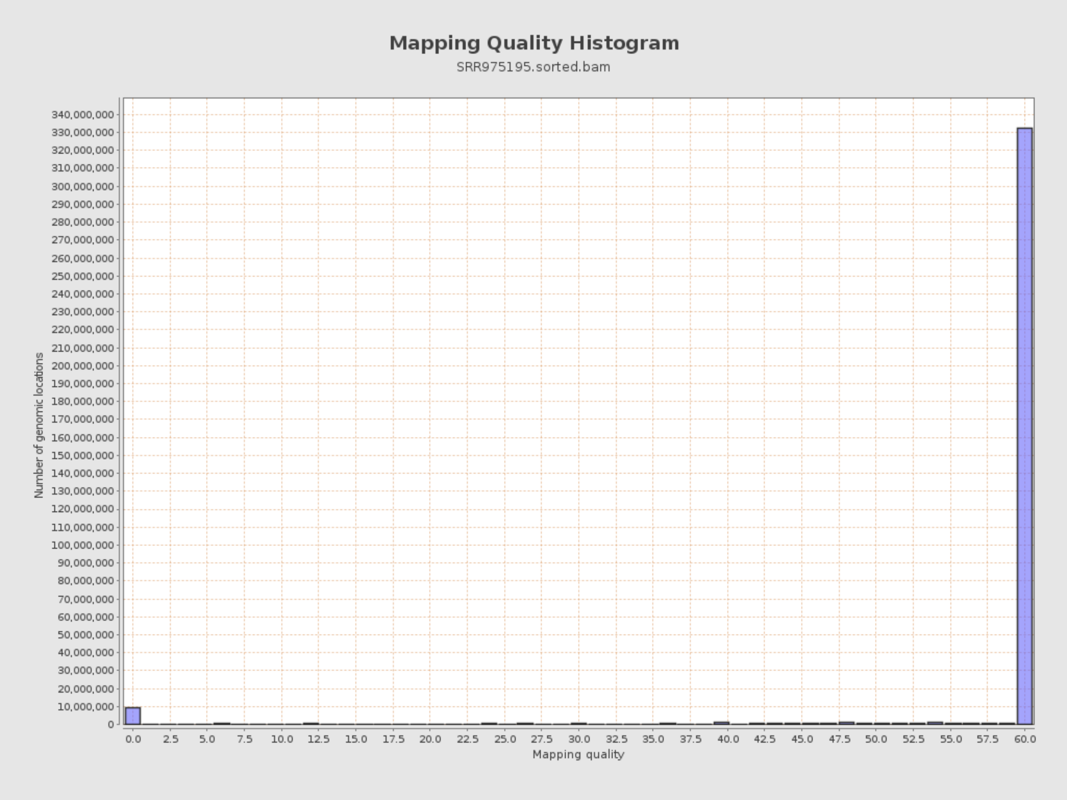
11. Results : Homopolymer Indels



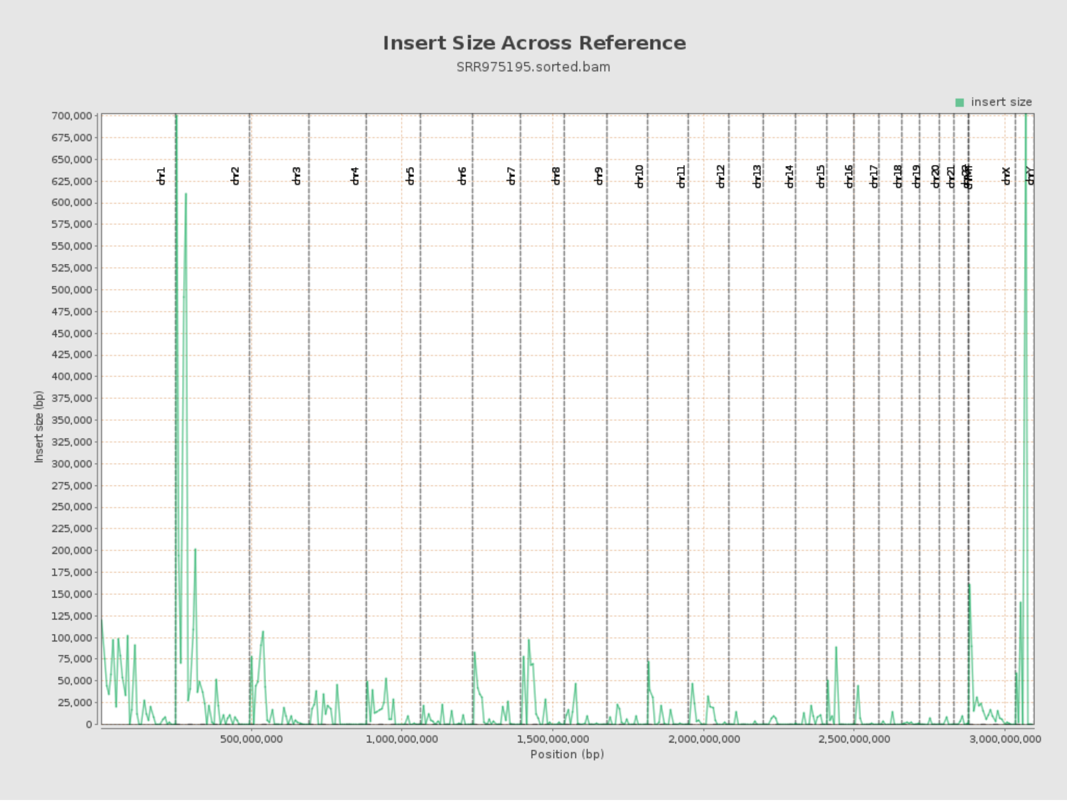
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram