Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 15:34:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975244.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_SRR975244 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975244_1.fastq.gz SRR975244_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 15:34:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975244.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	45,788,144
Mapped reads	45,632,338 / 99.66%
Unmapped reads	155,806 / 0.34%
Mapped paired reads	45,632,338 / 99.66%
Mapped reads, first in pair	22,808,171 / 49.81%
Mapped reads, second in pair	22,824,167 / 49.85%
Mapped reads, both in pair	45,552,484 / 99.49%
Mapped reads, singletons	79,854 / 0.17%
Secondary alignments	0
Supplementary alignments	255,920 / 0.56%
Read min/max/mean length	30 / 101 / 101.22
Duplicated reads (estimated)	27,220,350 / 59.45%
Duplication rate	40.74%
Clipped reads	28,309,599 / 61.83%

2.2. ACGT Content

Number/percentage of A's	1,097,784,911 / 26.38%
Number/percentage of C's	927,561,013 / 22.29%
Number/percentage of T's	1,109,578,576 / 26.66%
Number/percentage of G's	1,027,121,461 / 24.68%
Number/percentage of N's	165,887 / 0%

GC Percentage	46.96%

2.3. Coverage

Mean	1.3449
Standard Deviation	24.383

2.4. Mapping Quality

Mean Mapping Quality	55.29

2.5. Insert size

Mean	114,604.16
Standard Deviation	3,342,920.26
P25/Median/P75	144 / 181 / 229

2.6. Mismatches and indels

General error rate	0.66%
Mismatches	26,961,837
Insertions	367,803
Mapped reads with at least one insertion	0.79%
Deletions	866,861
Mapped reads with at least one deletion	1.87%
Homopolymer indels	48%

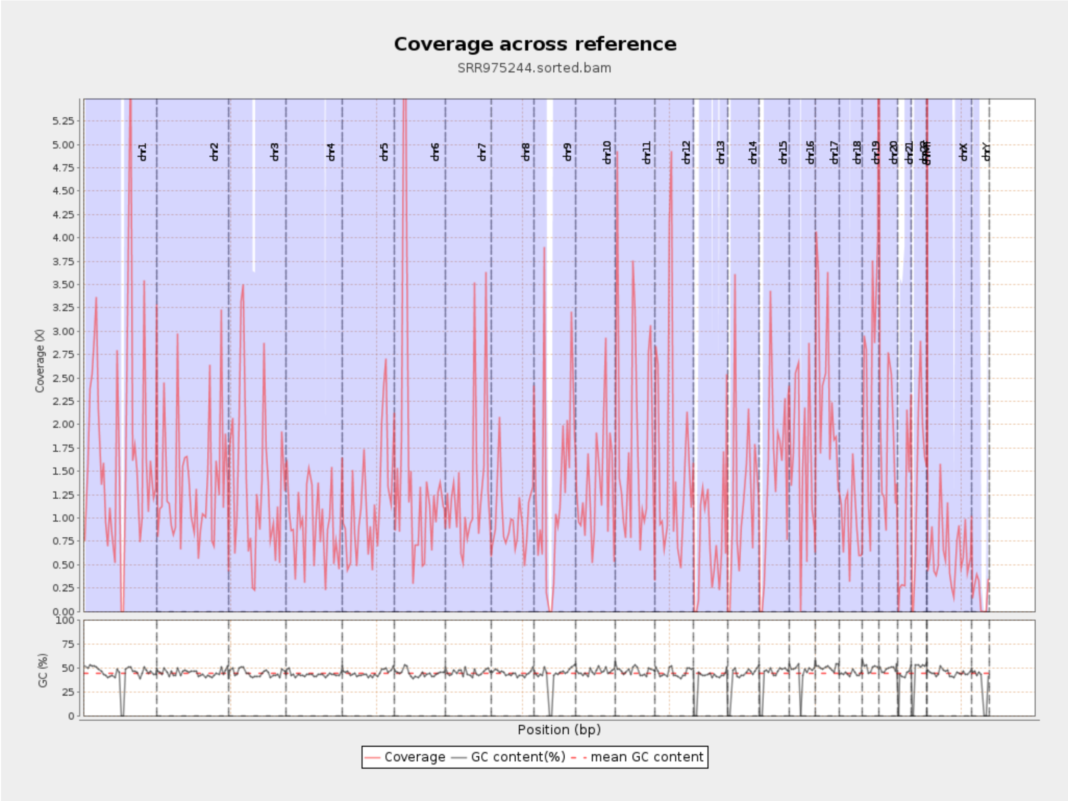
2.7. Chromosome stats

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

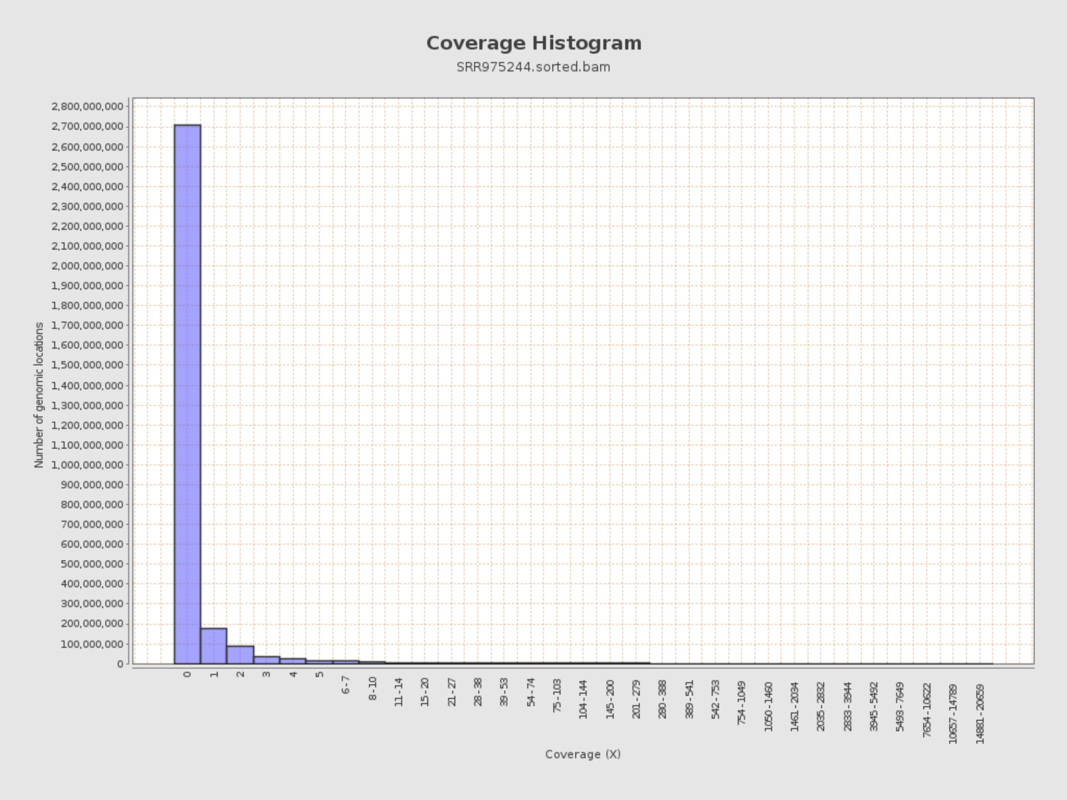
		bases	coverage	deviation
chr1	249250621	436417472	1.7509	30.5192
chr2	243199373	328500273	1.3507	24.0652
chr3	198022430	269288678	1.3599	22.7184
chr4	191154276	180918756	0.9465	17.5915
chr5	180915260	214632099	1.1864	21.9808
chr6	171115067	252489615	1.4756	25.8056
chr7	159138663	208583997	1.3107	27.105
chr8	146364022	147774004	1.0096	16.689
chr9	141213431	179320011	1.2699	23.3935
chr10	135534747	183793799	1.3561	24.0393
chr11	135006516	247805372	1.8355	29.7737
chr12	133851895	226324329	1.6909	25.4309
chr13	115169878	84433917	0.7331	16.5832
chr14	107349540	133188281	1.2407	22.0834
chr15	102531392	143769333	1.4022	23.737
chr16	90354753	146491574	1.6213	26.8656
chr17	81195210	201773184	2.485	39.0238
chr18	78077248	76970847	0.9858	17.7655
chr19	59128983	160348256	2.7118	37.8211
chr20	63025520	108357657	1.7193	27.5947
chr21	48129895	46003343	0.9558	24.8439
chr22	51304566	74554643	1.4532	25.361
chrMT	16571	285692	17.2405	17.691
chrX	155270560	100086620	0.6446	14.4677

chrY	59373566	11389721	0.1918	5.1162

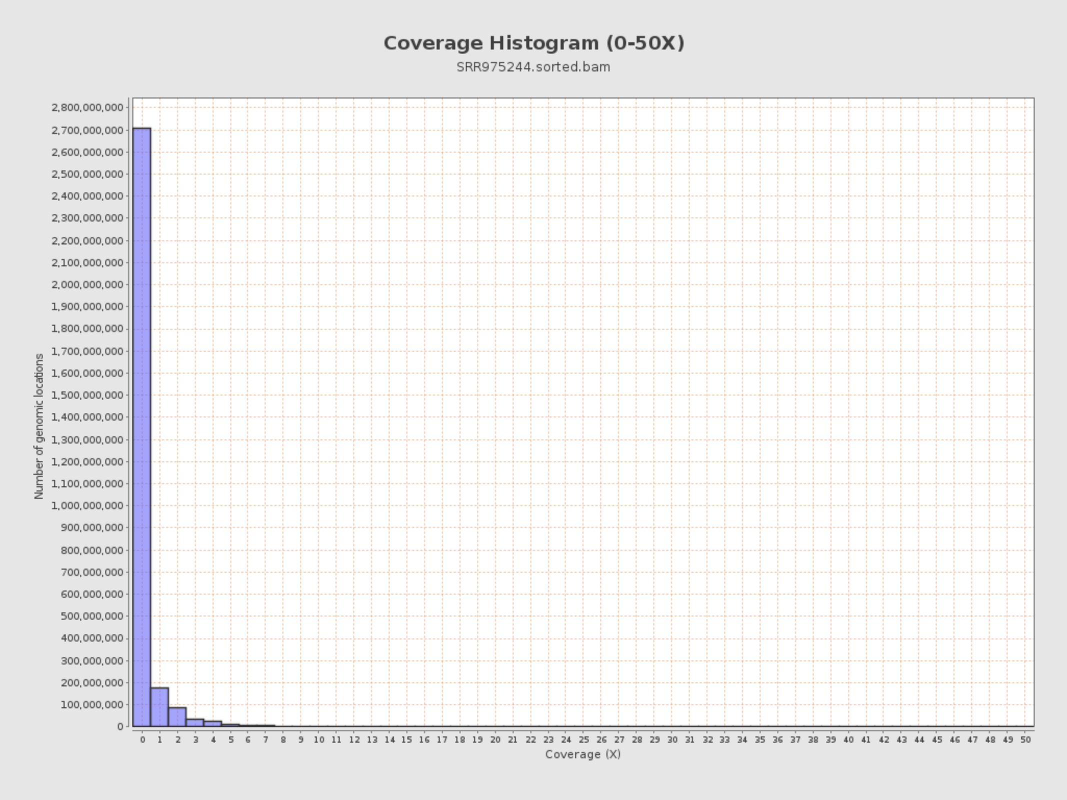
3. Results : Coverage across reference



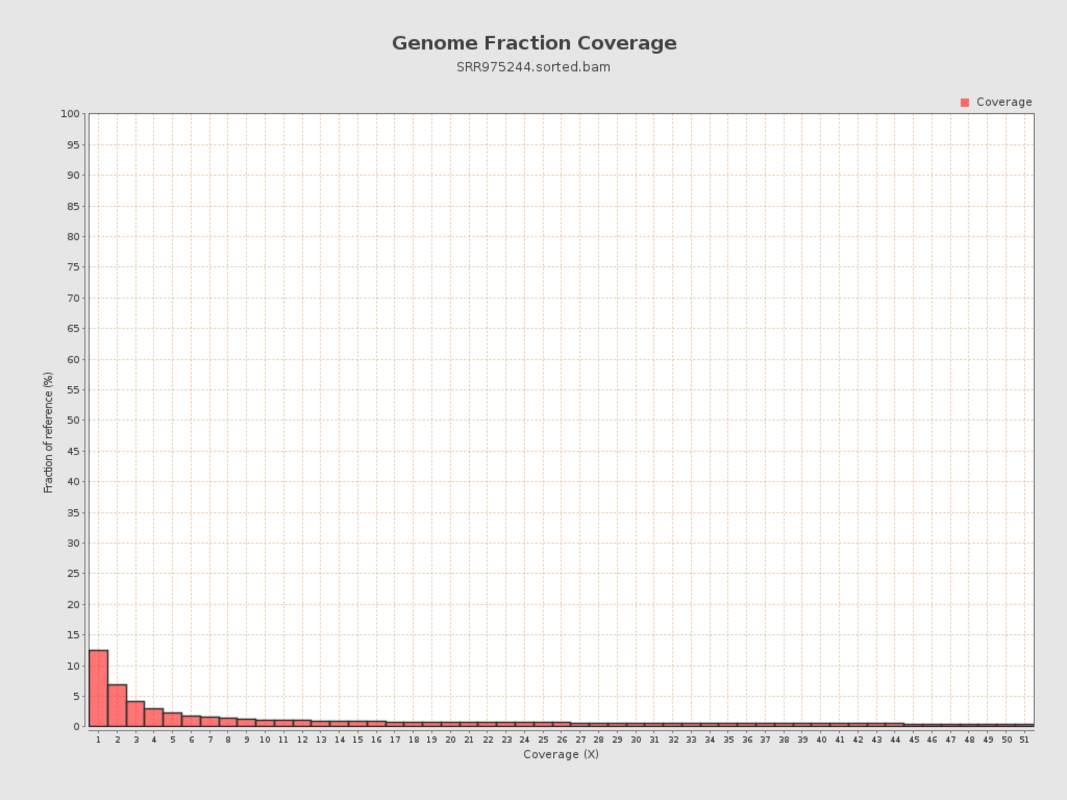
4. Results : Coverage Histogram



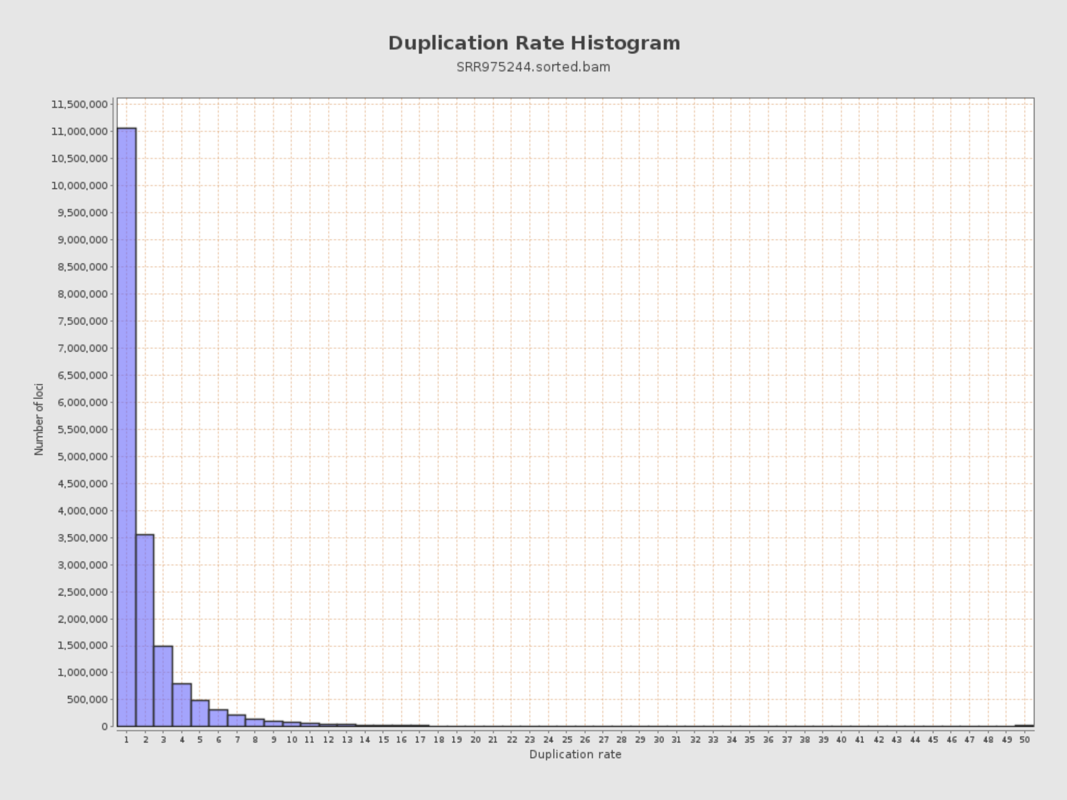
5. Results : Coverage Histogram (0-50X)



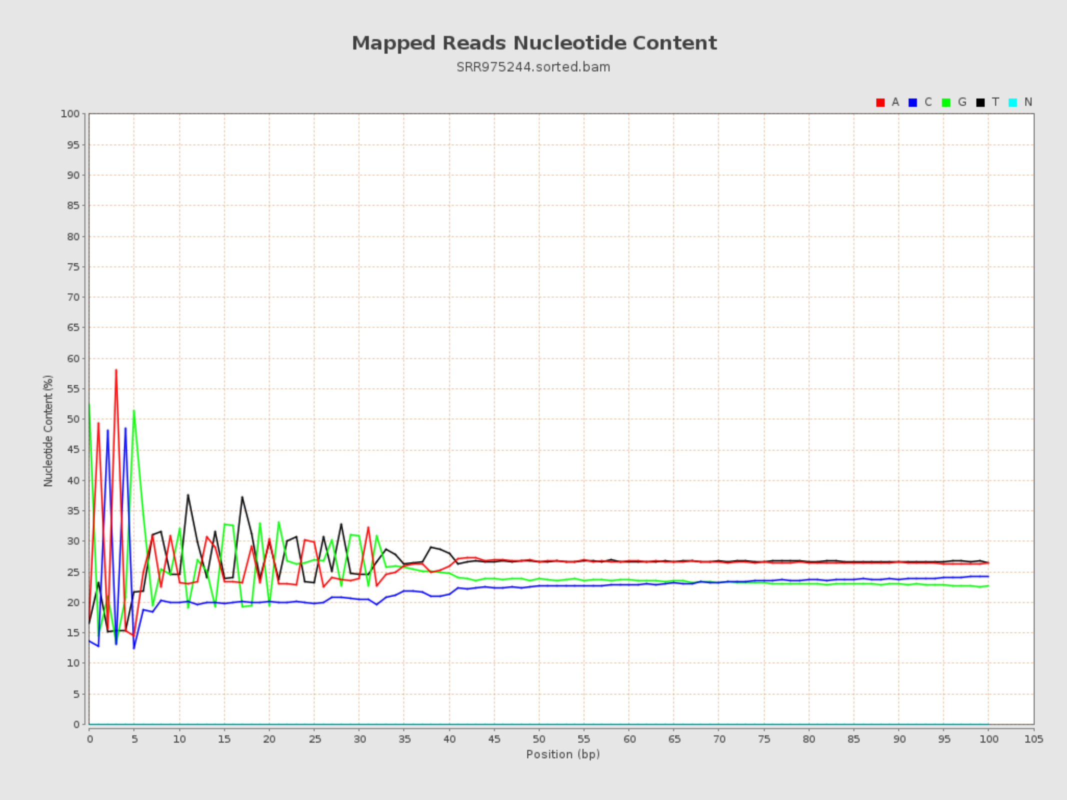
6. Results : Genome Fraction Coverage



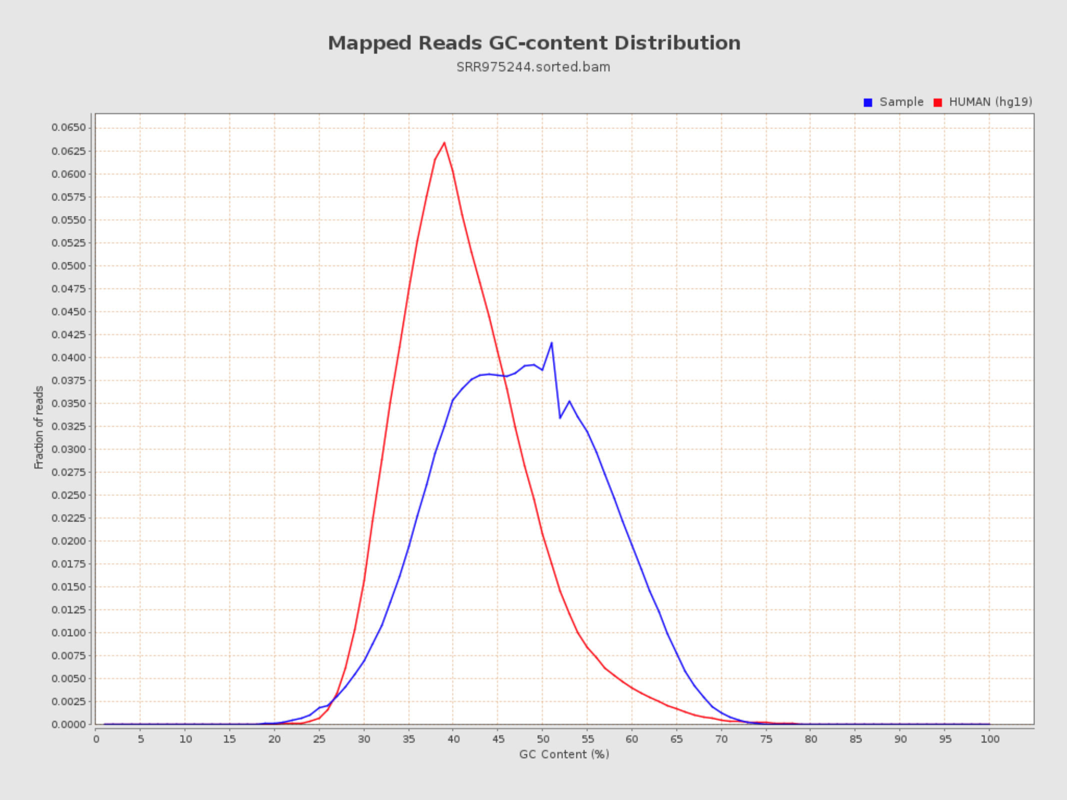
7. Results : Duplication Rate Histogram



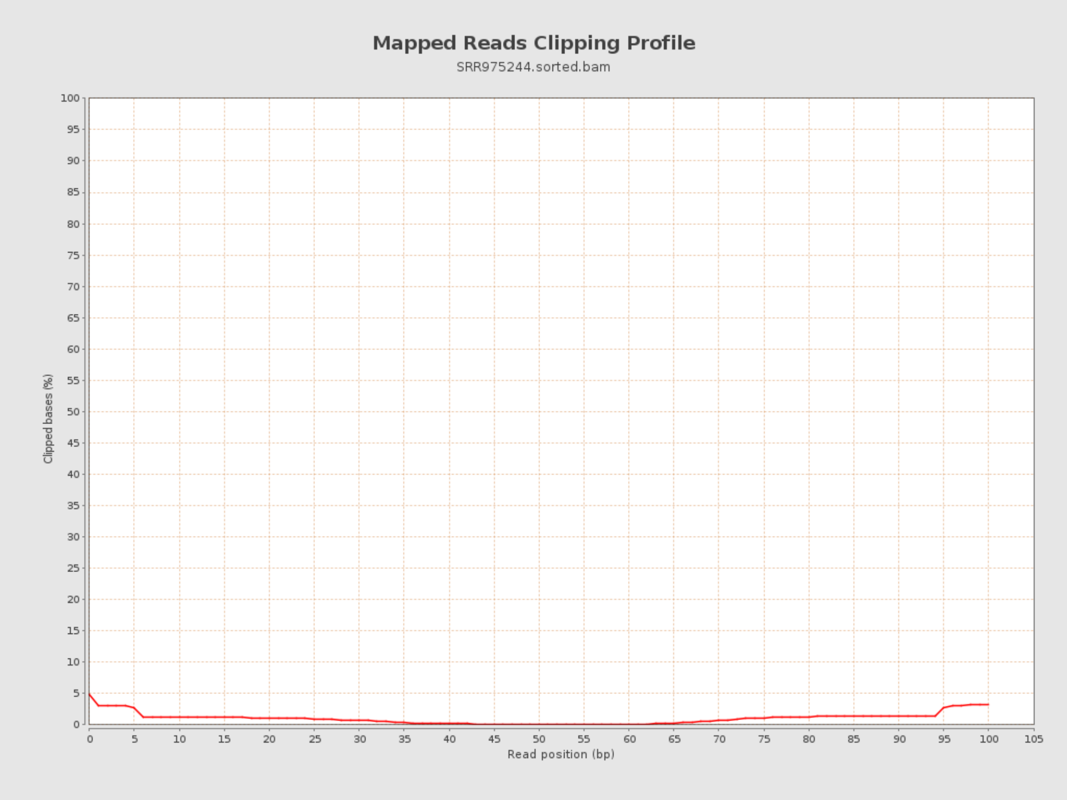
8. Results : Mapped Reads Nucleotide Content



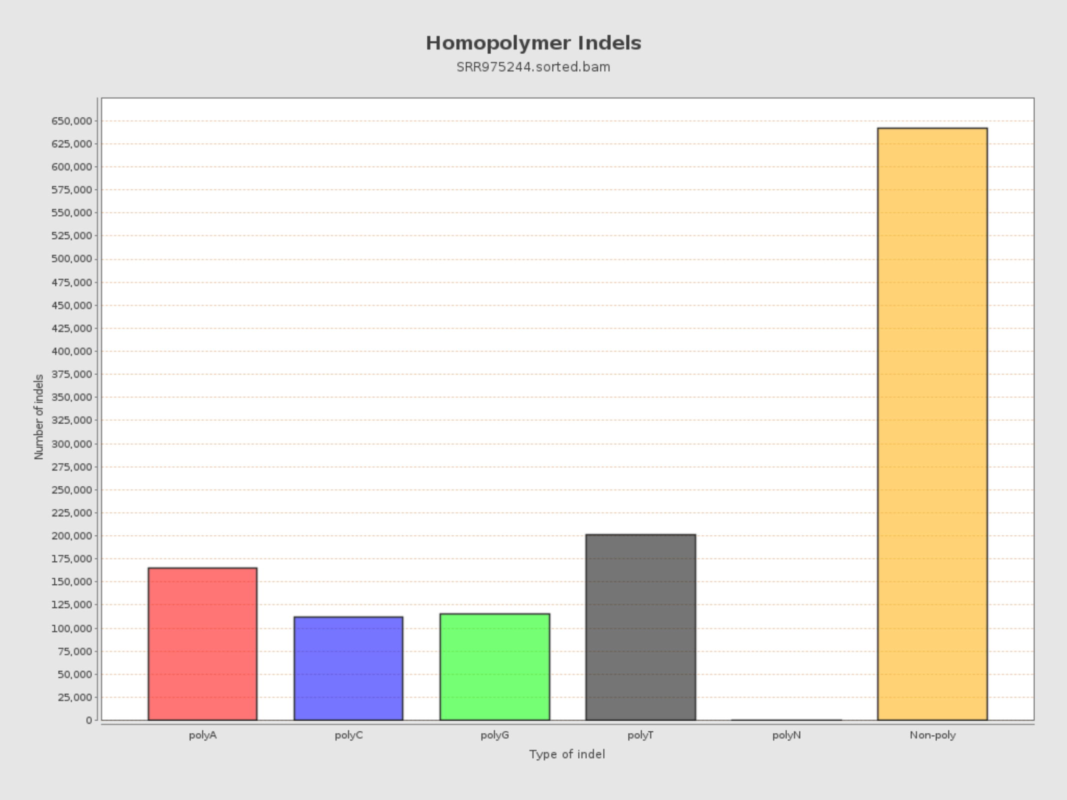
9. Results : Mapped Reads GC-content Distribution



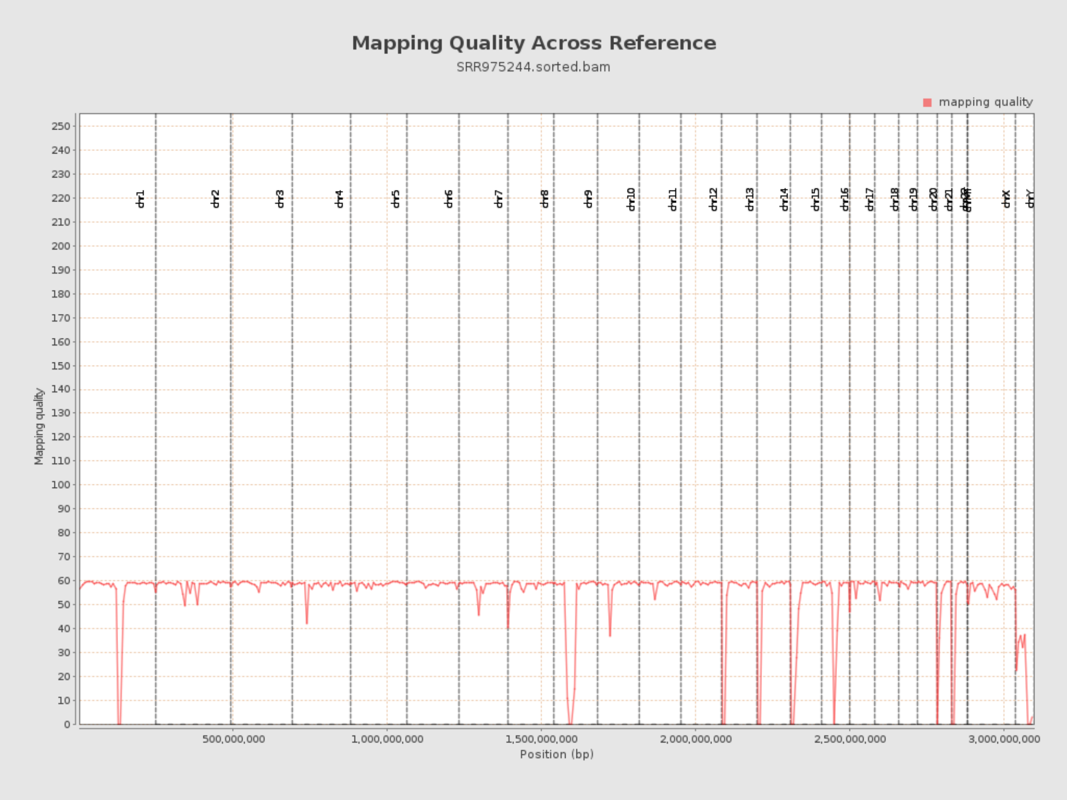
10. Results : Mapped Reads Clipping Profile



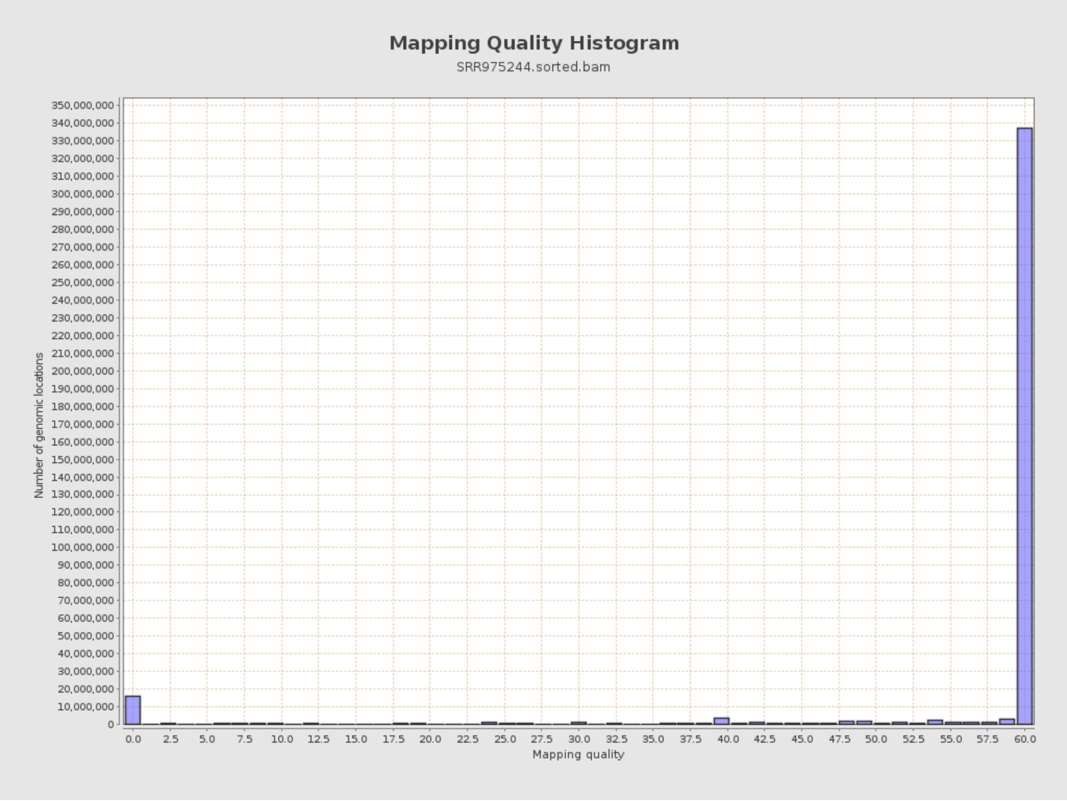
11. Results : Homopolymer Indels



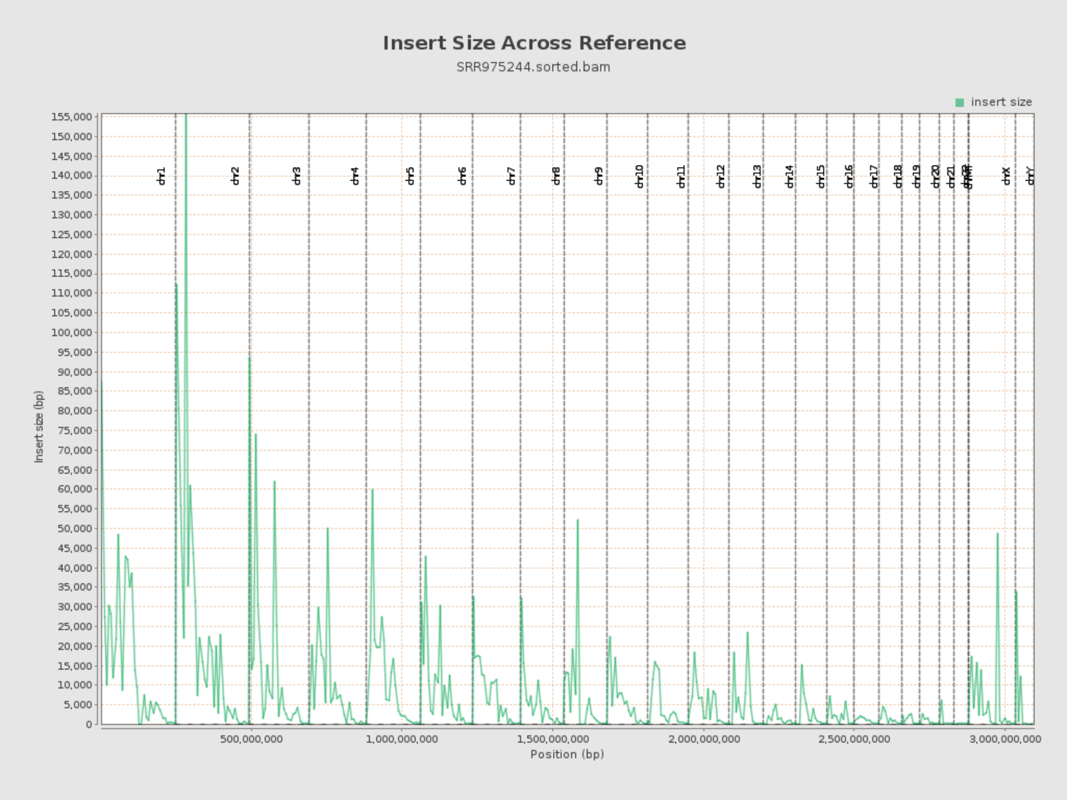
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram