Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 16:16:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975245.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_SRR975245 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975245_1.fastq.gz SRR975245_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 16:16:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975245.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,421,750
Mapped reads	2,397,672 / 99.01%
Unmapped reads	24,078 / 0.99%
Mapped paired reads	2,397,672 / 99.01%
Mapped reads, first in pair	1,198,352 / 49.48%
Mapped reads, second in pair	1,199,320 / 49.52%
Mapped reads, both in pair	2,387,740 / 98.6%
Mapped reads, singletons	9,932 / 0.41%
Secondary alignments	0
Supplementary alignments	24,795 / 1.02%
Read min/max/mean length	30 / 101 / 101.4
Duplicated reads (estimated)	152,348 / 6.29%
Duplication rate	3.46%
Clipped reads	1,508,835 / 62.3%

2.2. ACGT Content

Number/percentage of A's	63,898,144 / 29.27%
Number/percentage of C's	42,893,481 / 19.65%
Number/percentage of T's	63,947,102 / 29.29%
Number/percentage of G's	47,547,506 / 21.78%
Number/percentage of N's	3,028 / 0%

GC Percentage	41.43%

2.3. Coverage

Mean	0.0706
Standard Deviation	1.1113

2.4. Mapping Quality

Mean Mapping Quality	52.12

2.5. Insert size

Mean	157,444.05
Standard Deviation	3,876,619.21
P25/Median/P75	137 / 169 / 214

2.6. Mismatches and indels

General error rate	0.89%
Mismatches	1,840,163
Insertions	37,610
Mapped reads with at least one insertion	1.51%
Deletions	68,619
Mapped reads with at least one deletion	2.79%
Homopolymer indels	44.16%

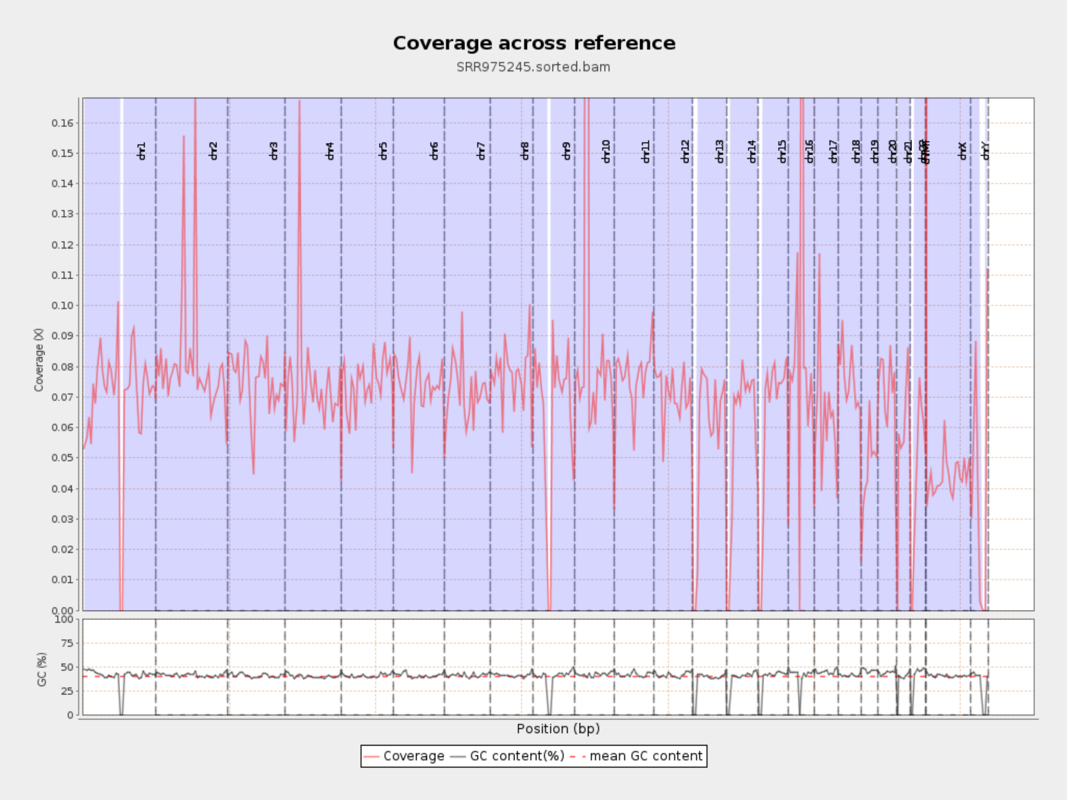
2.7. Chromosome stats

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

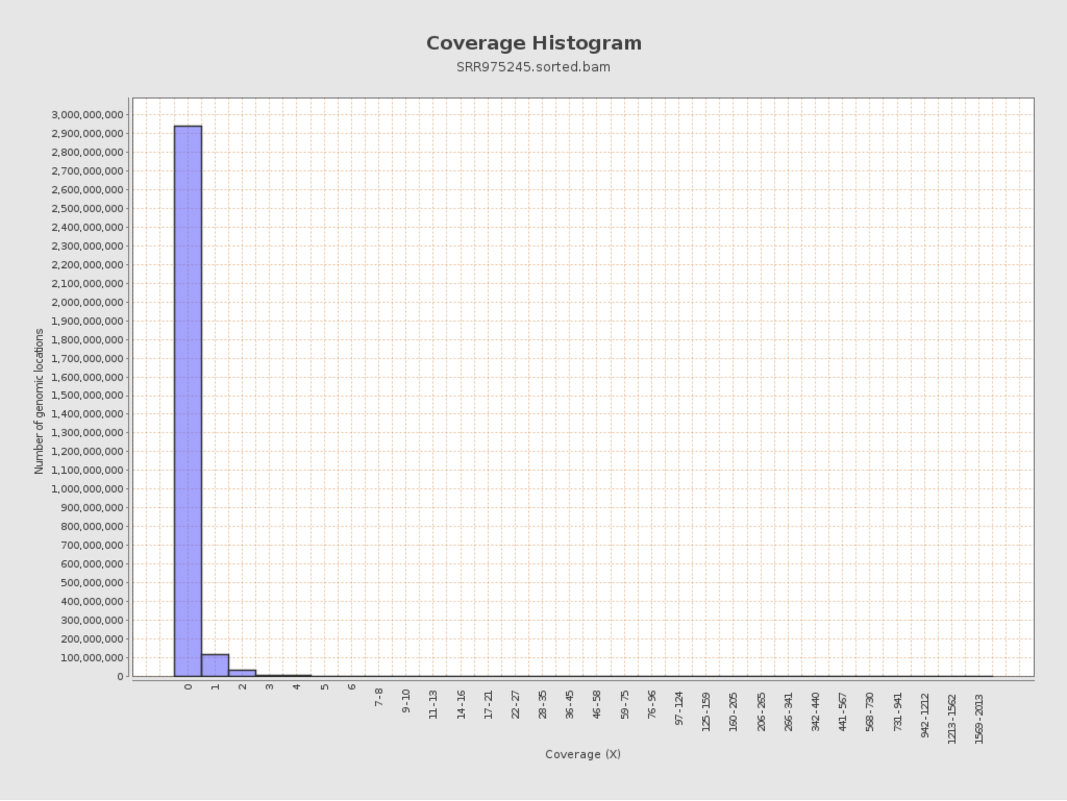
		bases	coverage	deviation
chr1	249250621	17290260	0.0694	0.5742
chr2	243199373	20019208	0.0823	1.3562
chr3	198022430	14881000	0.0751	0.4351
chr4	191154276	14333999	0.075	0.7033
chr5	180915260	13497919	0.0746	0.3763
chr6	171115067	12705241	0.0742	0.4063
chr7	159138663	11398080	0.0716	0.7893
chr8	146364022	11314957	0.0773	0.3898
chr9	141213431	9160862	0.0649	0.9319
chr10	135534747	13240399	0.0977	4.0088
chr11	135006516	10337458	0.0766	0.5479
chr12	133851895	9538122	0.0713	0.3414
chr13	115169878	6565016	0.057	0.3024
chr14	107349540	6324161	0.0589	0.3771
chr15	102531392	6310199	0.0615	0.312
chr16	90354753	8383468	0.0928	1.8874
chr17	81195210	5285545	0.0651	0.8751
chr18	78077248	5978804	0.0766	0.9931
chr19	59128983	2813594	0.0476	0.3766
chr20	63025520	4627475	0.0734	0.3882
chr21	48129895	2767125	0.0575	0.3997
chr22	51304566	2286961	0.0446	0.3227
chrMT	16571	49685	2.9983	2.3916
chrX	155270560	6819341	0.0439	0.3199

chrY	59373566	2492613	0.042	1.1968

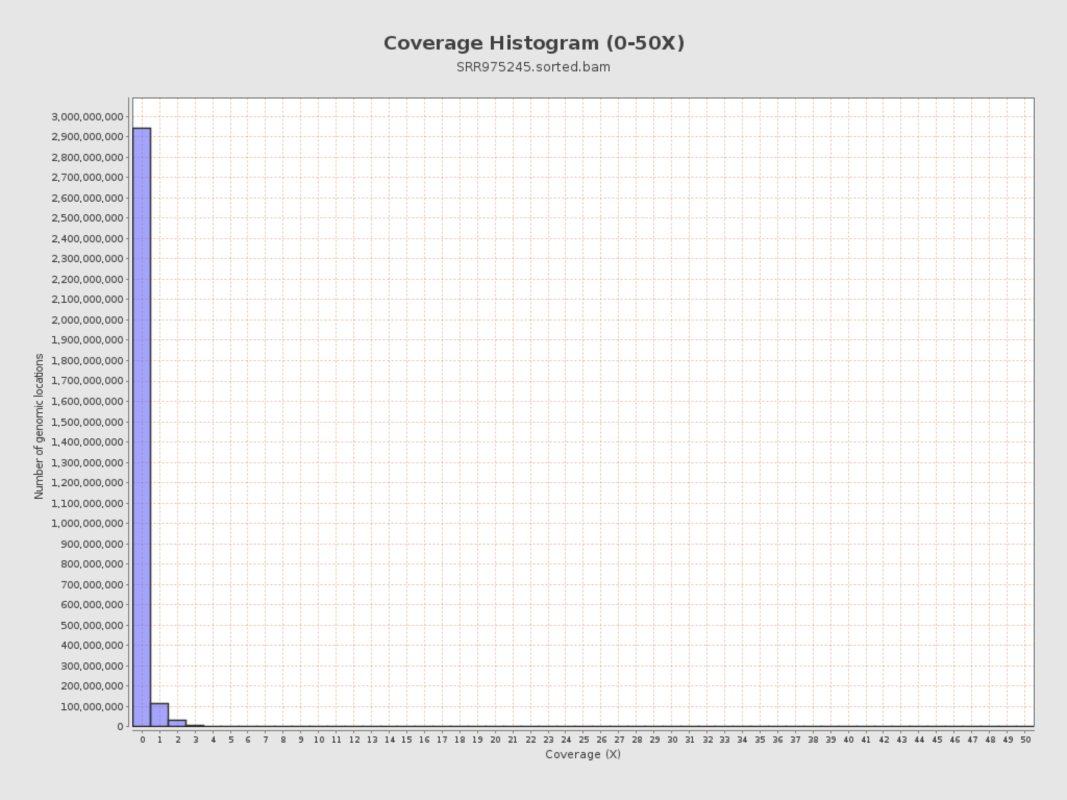
3. Results : Coverage across reference



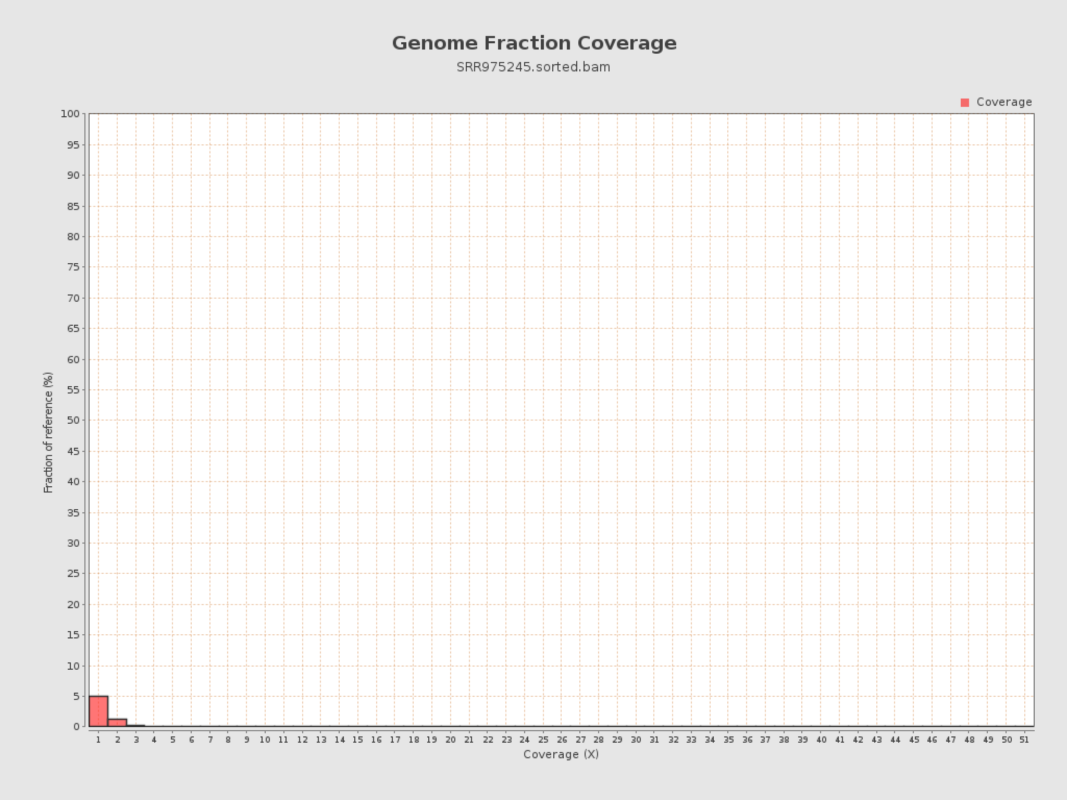
4. Results : Coverage Histogram



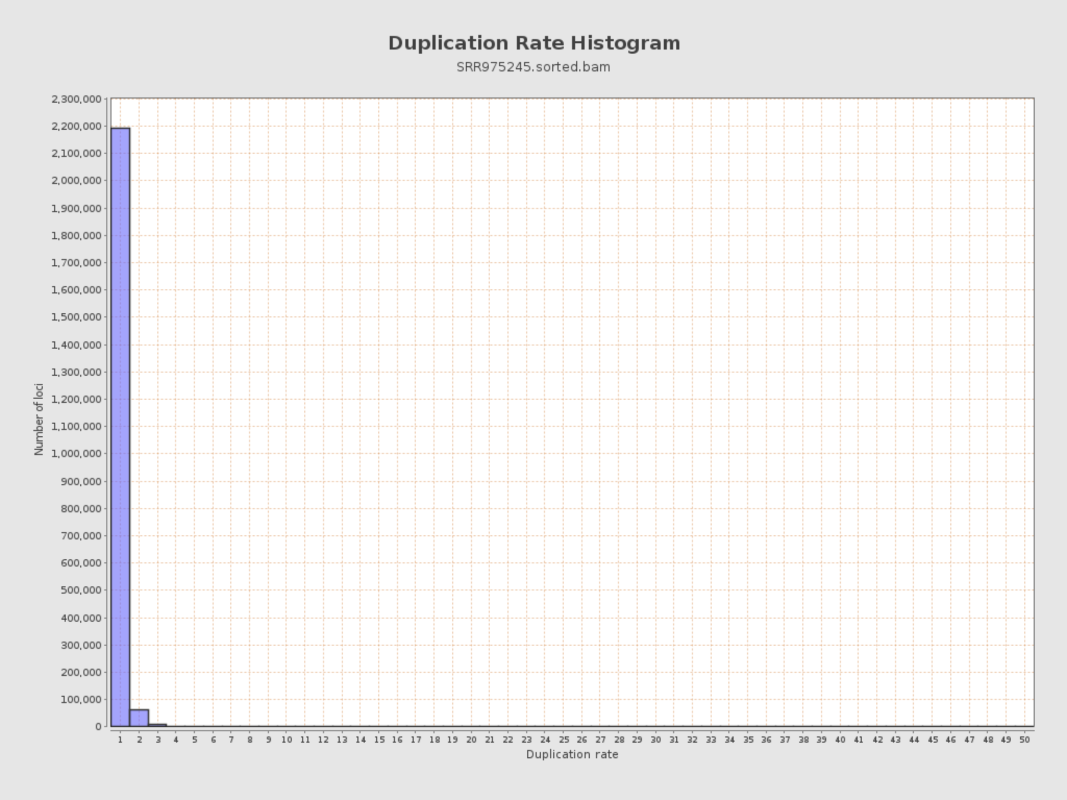
5. Results : Coverage Histogram (0-50X)



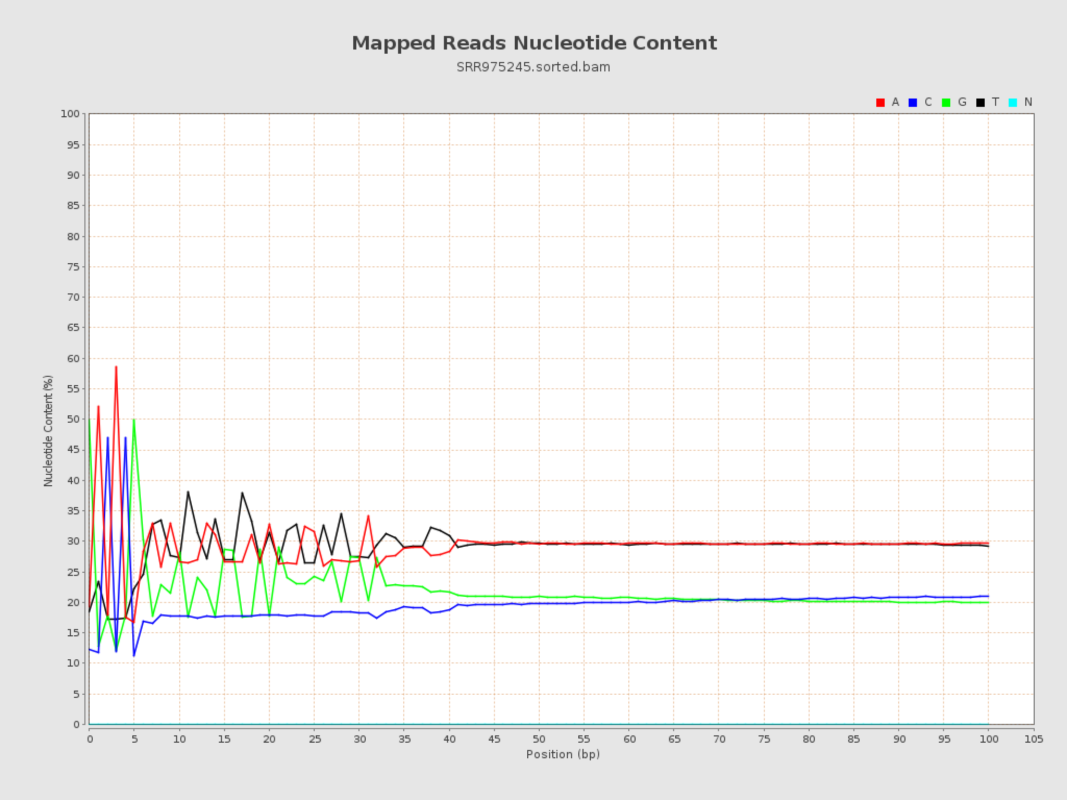
6. Results : Genome Fraction Coverage



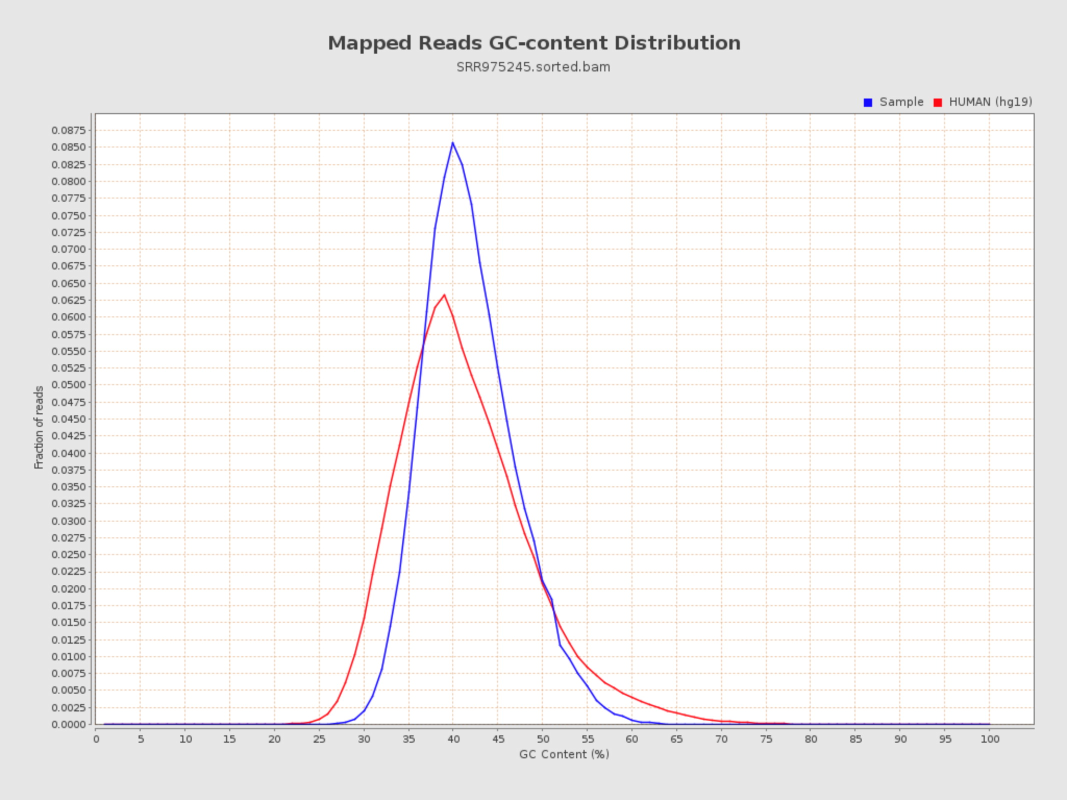
7. Results : Duplication Rate Histogram



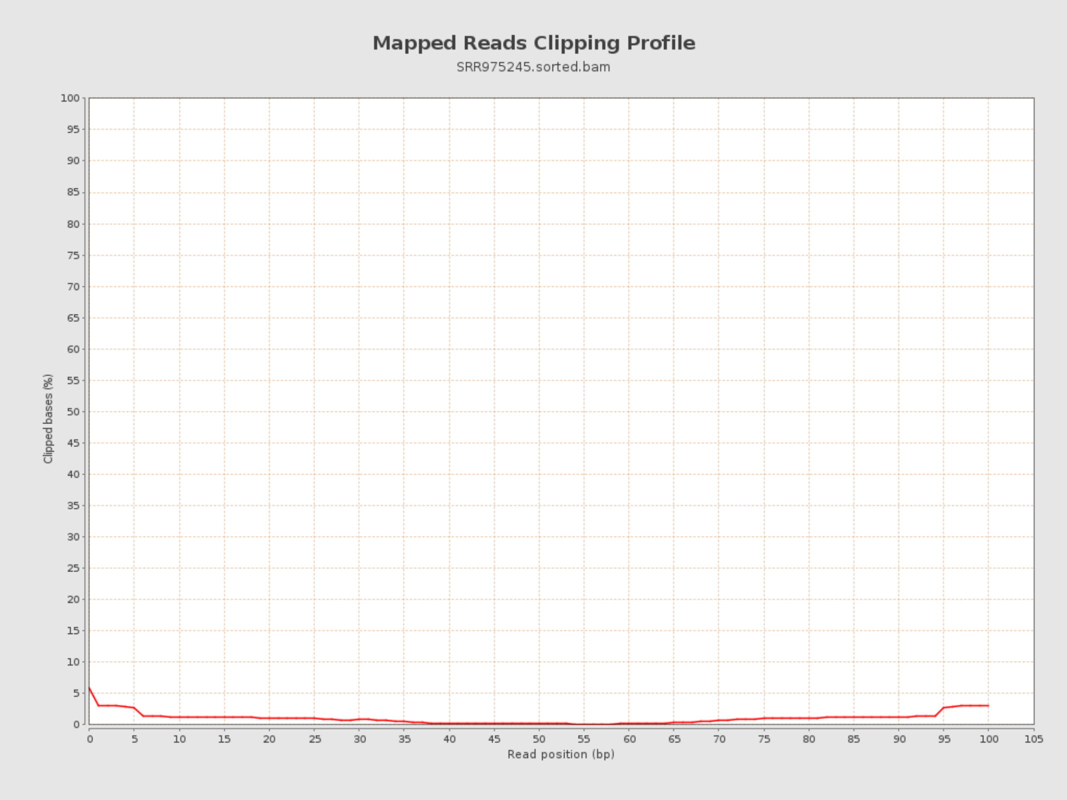
8. Results : Mapped Reads Nucleotide Content



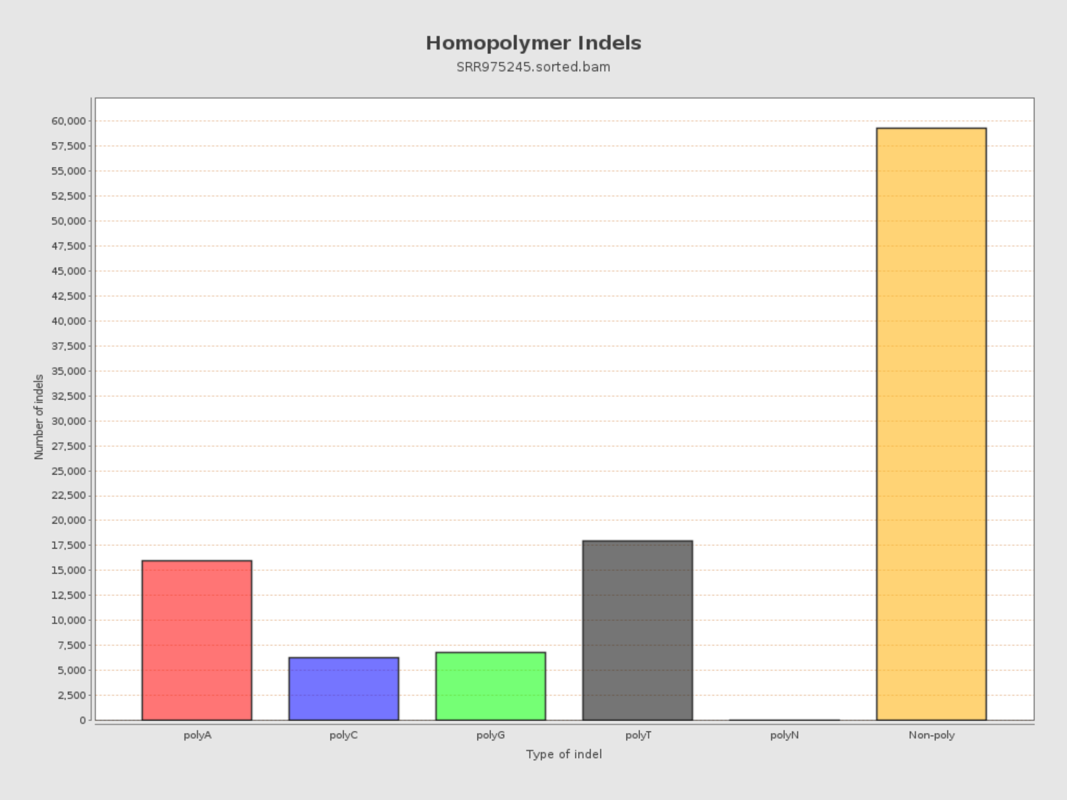
9. Results : Mapped Reads GC-content Distribution



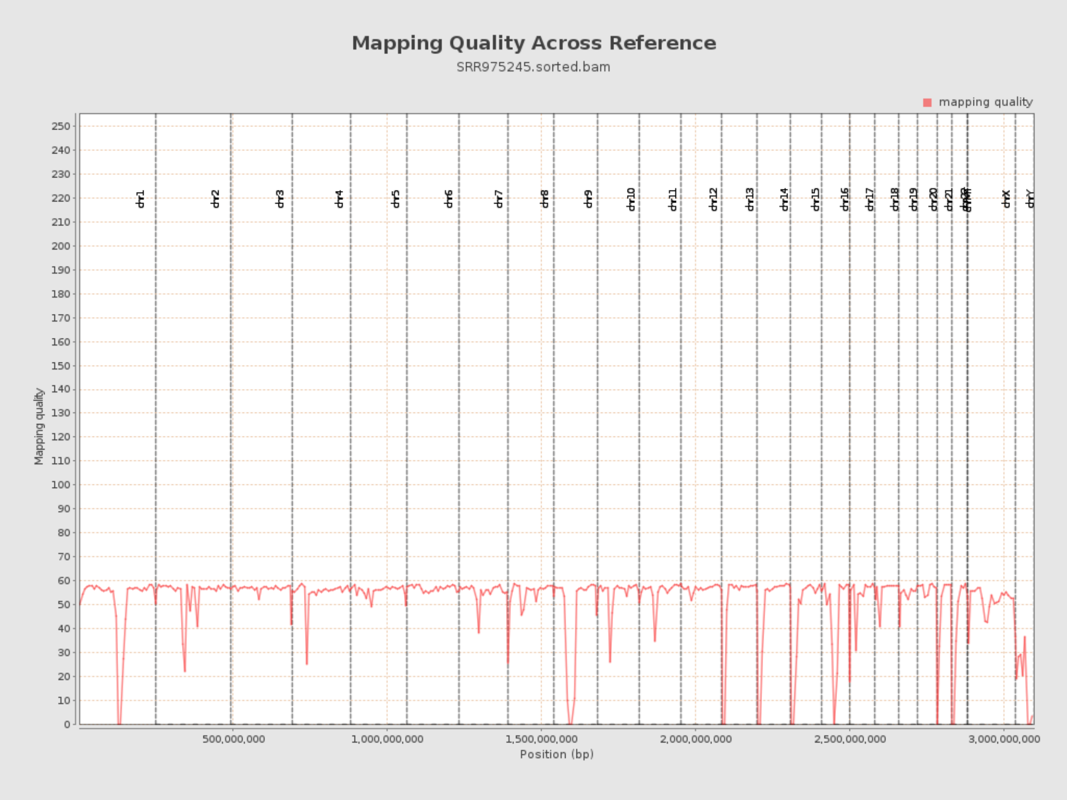
10. Results : Mapped Reads Clipping Profile



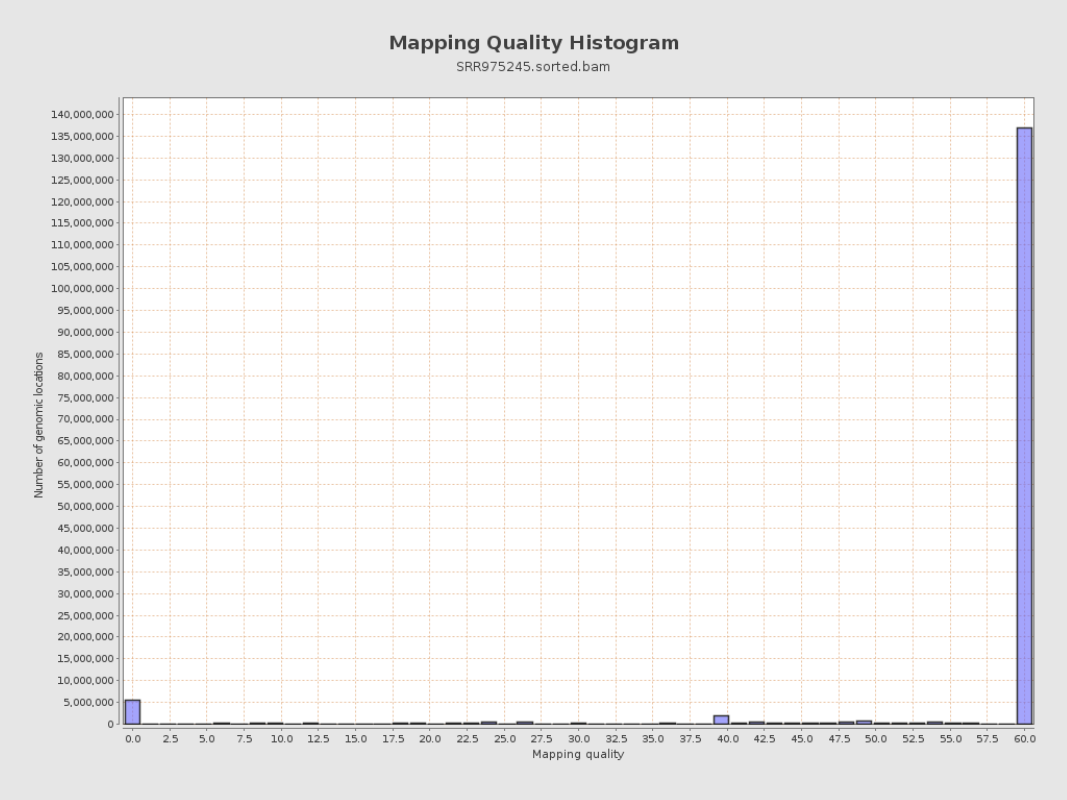
11. Results : Homopolymer Indels



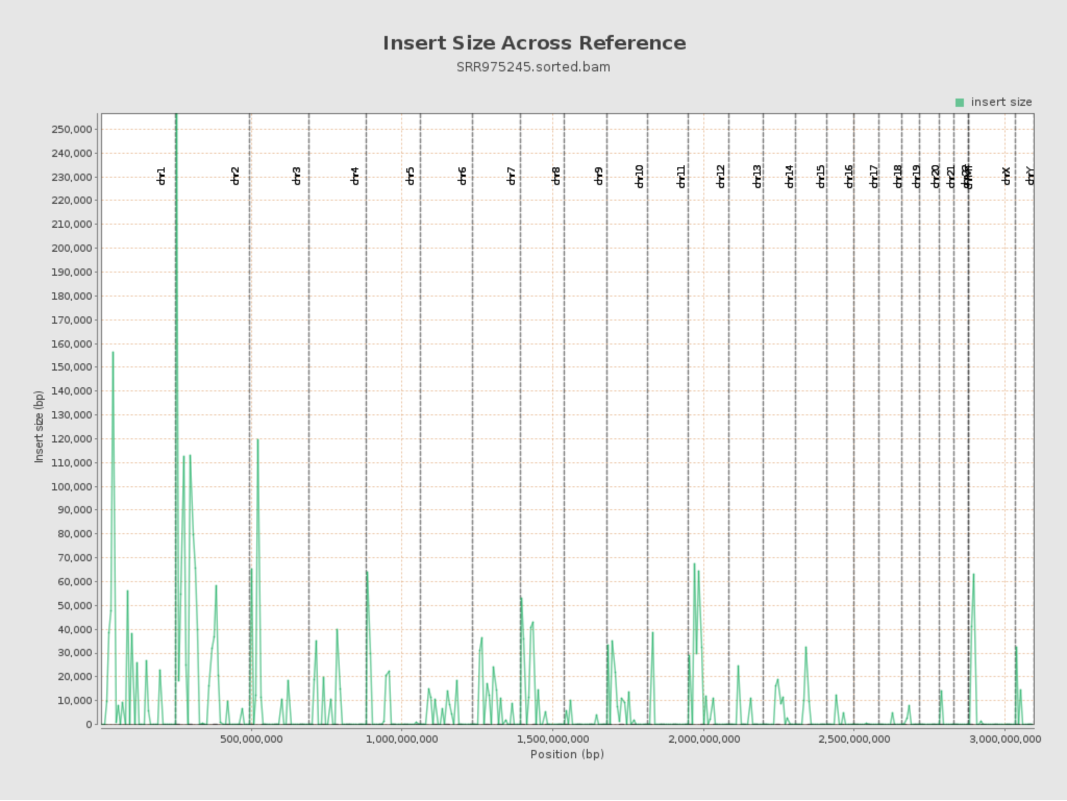
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram