Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 09:40:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975239.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_SRR975239 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975239_1.fastq.gz SRR975239_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 09:40:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975239.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,409,852
Mapped reads	2,387,376 / 99.07%
Unmapped reads	22,476 / 0.93%
Mapped paired reads	2,387,376 / 99.07%
Mapped reads, first in pair	1,193,350 / 49.52%
Mapped reads, second in pair	1,194,026 / 49.55%
Mapped reads, both in pair	2,379,376 / 98.74%
Mapped reads, singletons	8,000 / 0.33%
Secondary alignments	0
Supplementary alignments	9,918 / 0.41%
Read min/max/mean length	30 / 101 / 101.16
Duplicated reads (estimated)	76,285 / 3.17%
Duplication rate	1.94%
Clipped reads	1,457,135 / 60.47%

2.2. ACGT Content

Number/percentage of A's	63,517,823 / 29.11%
Number/percentage of C's	42,130,577 / 19.31%
Number/percentage of T's	65,599,957 / 30.06%
Number/percentage of G's	46,953,124 / 21.52%
Number/percentage of N's	2,826 / 0%

GC Percentage	40.83%

2.3. Coverage

Mean	0.0705
Standard Deviation	0.6084

2.4. Mapping Quality

Mean Mapping Quality	52.86

2.5. Insert size

Mean	53,291.24
Standard Deviation	2,218,162.67
P25/Median/P75	140 / 173 / 217

2.6. Mismatches and indels

General error rate	0.77%
Mismatches	1,607,718
Insertions	35,493
Mapped reads with at least one insertion	1.45%
Deletions	71,074
Mapped reads with at least one deletion	2.91%
Homopolymer indels	45.54%

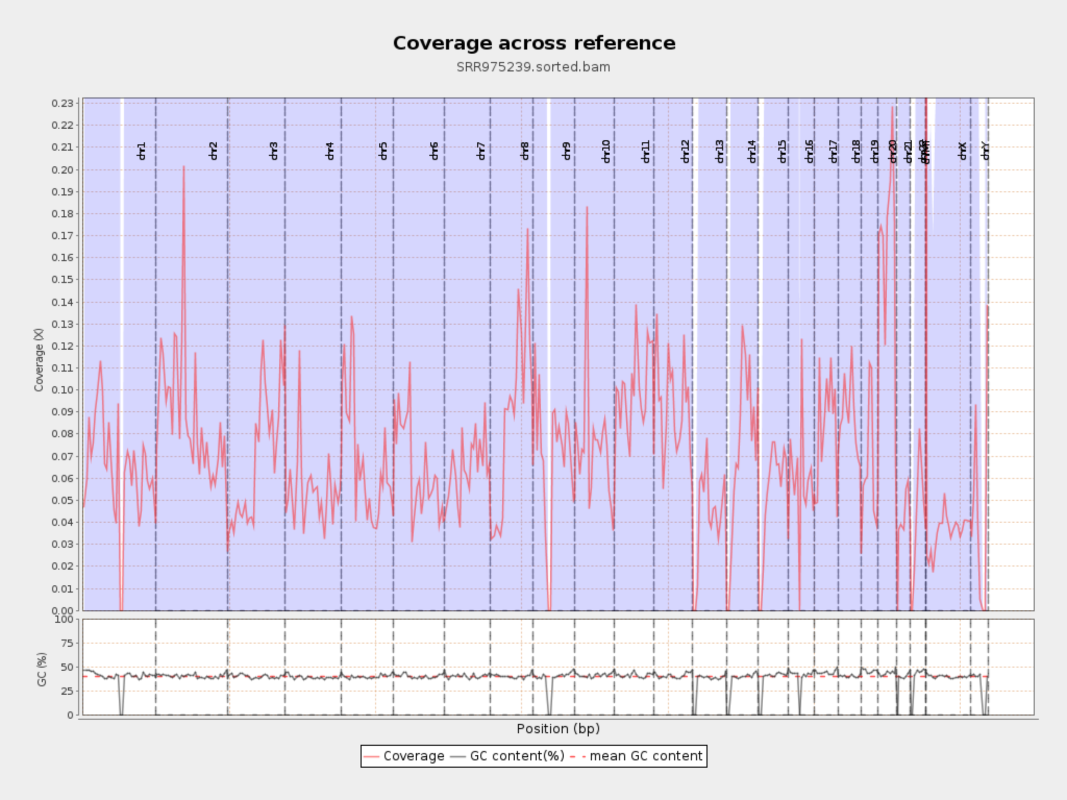
2.7. Chromosome stats

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

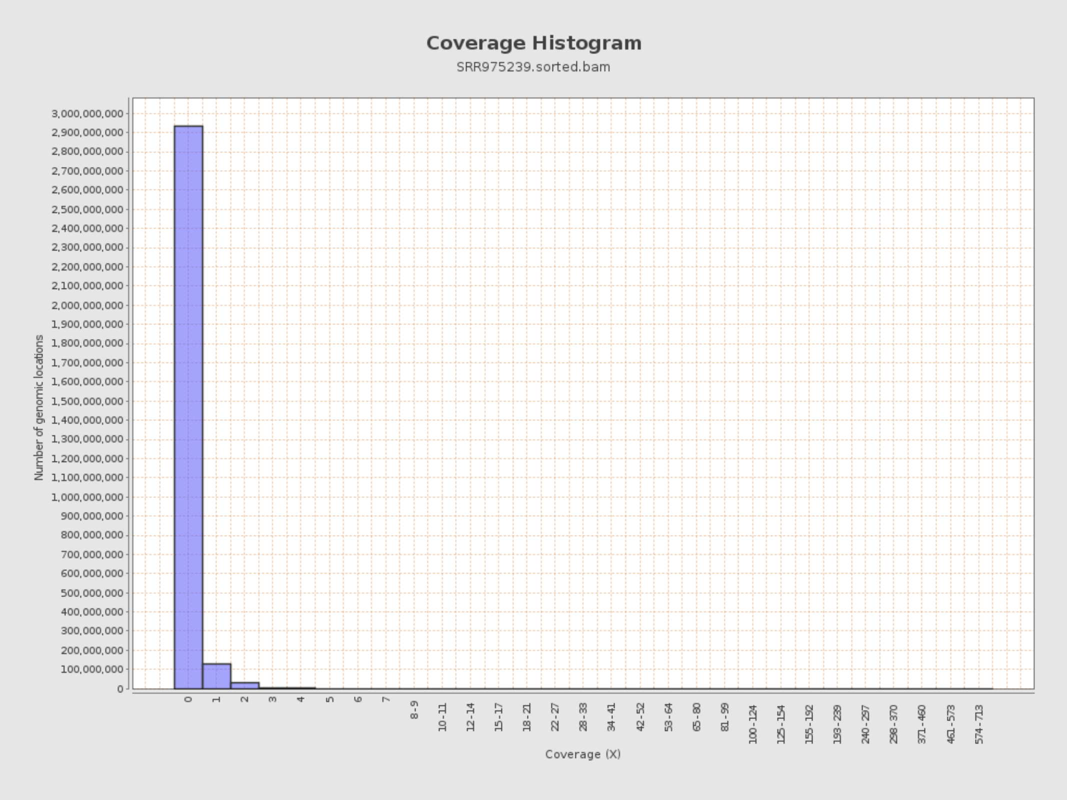
		bases	coverage	deviation
chr1	249250621	15950777	0.064	0.728
chr2	243199373	21532085	0.0885	0.9667
chr3	198022430	13544852	0.0684	0.3185
chr4	191154276	10416259	0.0545	0.539
chr5	180915260	12307385	0.068	0.3202
chr6	171115067	11158057	0.0652	0.3741
chr7	159138663	10262358	0.0645	0.6227
chr8	146364022	12922036	0.0883	0.43
chr9	141213431	9796801	0.0694	0.888
chr10	135534747	10210576	0.0753	0.9911
chr11	135006516	13512735	0.1001	0.5131
chr12	133851895	12612313	0.0942	0.3749
chr13	115169878	4885849	0.0424	0.245
chr14	107349540	7833431	0.073	0.3447
chr15	102531392	5274962	0.0514	0.2703
chr16	90354753	5261039	0.0582	0.6856
chr17	81195210	6872621	0.0846	0.9045
chr18	78077248	6873980	0.088	0.8044
chr19	59128983	3927341	0.0664	0.4301
chr20	63025520	10802453	0.1714	0.5324
chr21	48129895	1950820	0.0405	0.2866
chr22	51304566	2176464	0.0424	0.2676
chrMT	16571	21118	1.2744	1.3505
chrX	155270560	5522650	0.0356	0.2798

chrY	59373566	2702293	0.0455	0.8608

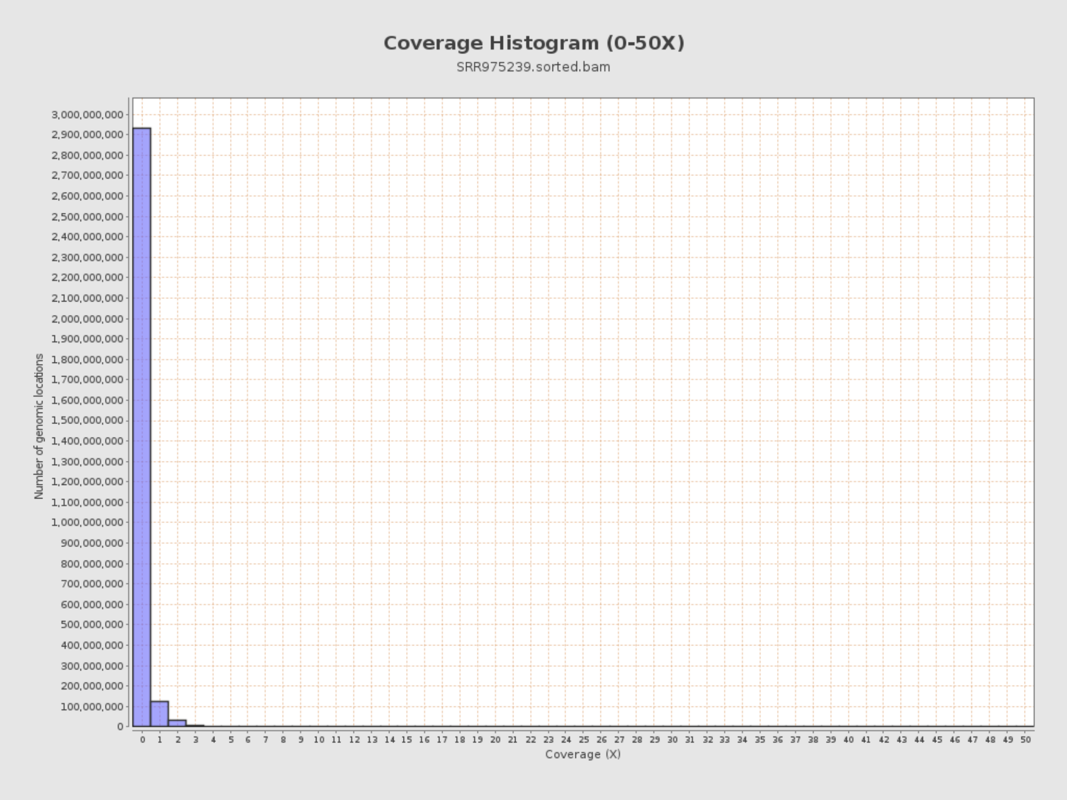
3. Results : Coverage across reference



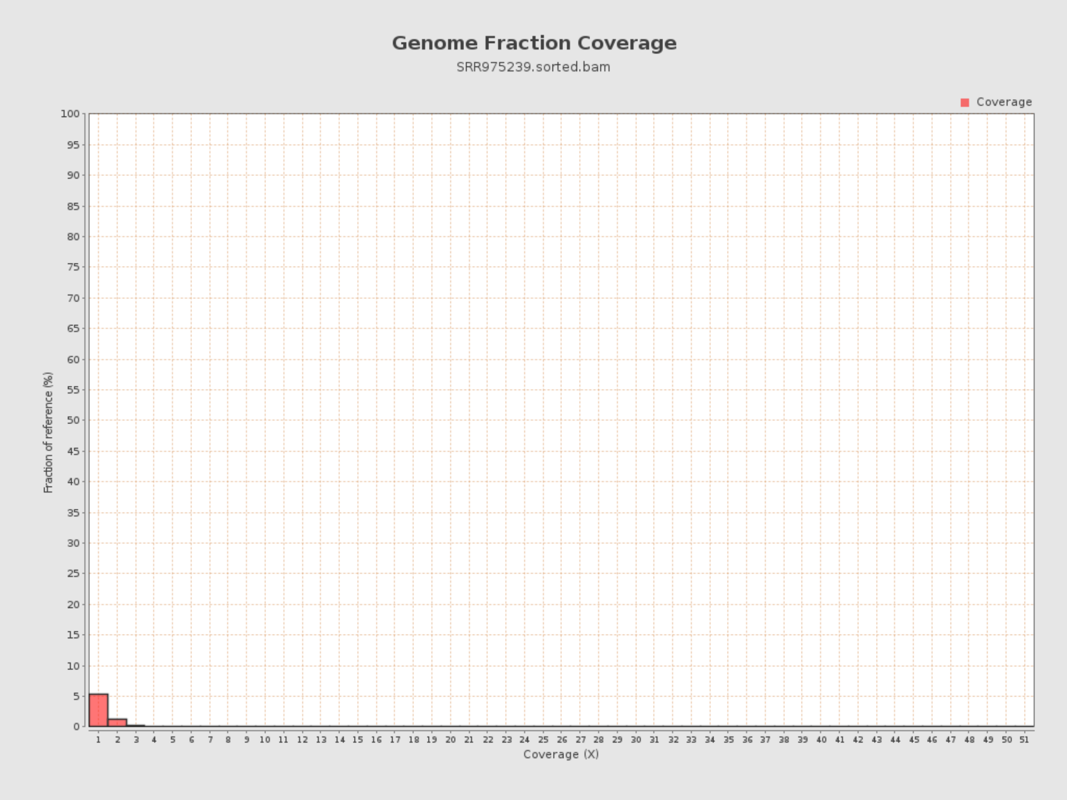
4. Results : Coverage Histogram



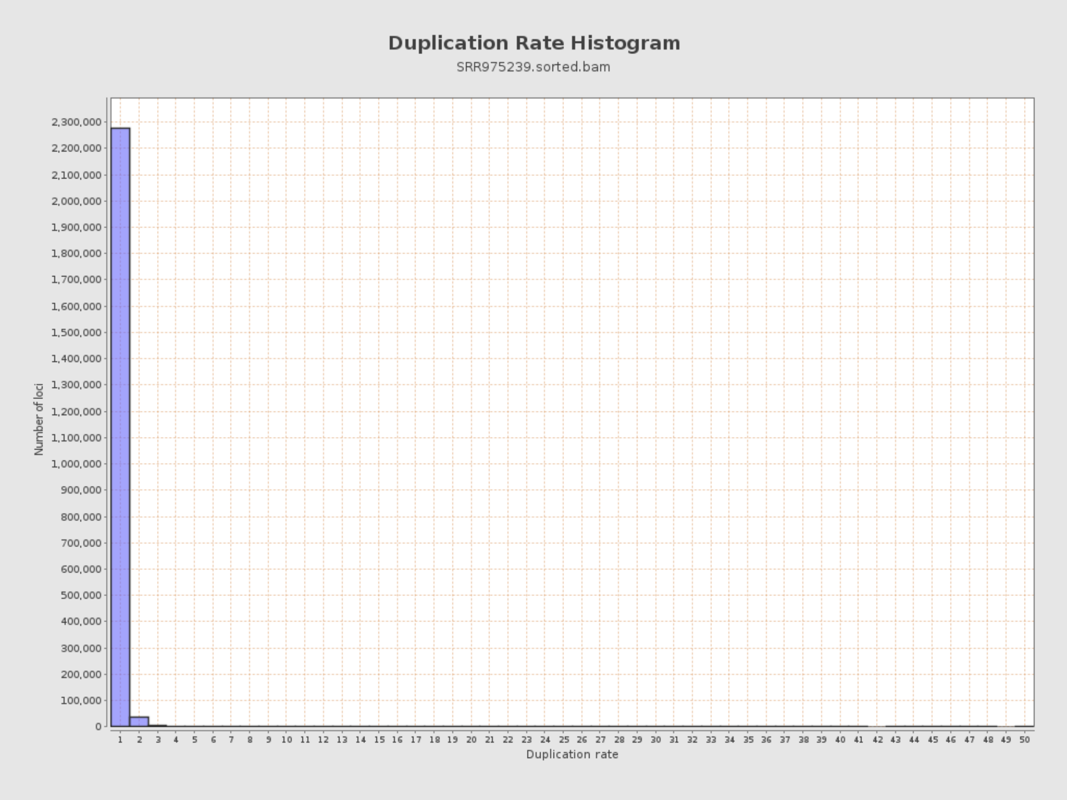
5. Results : Coverage Histogram (0-50X)



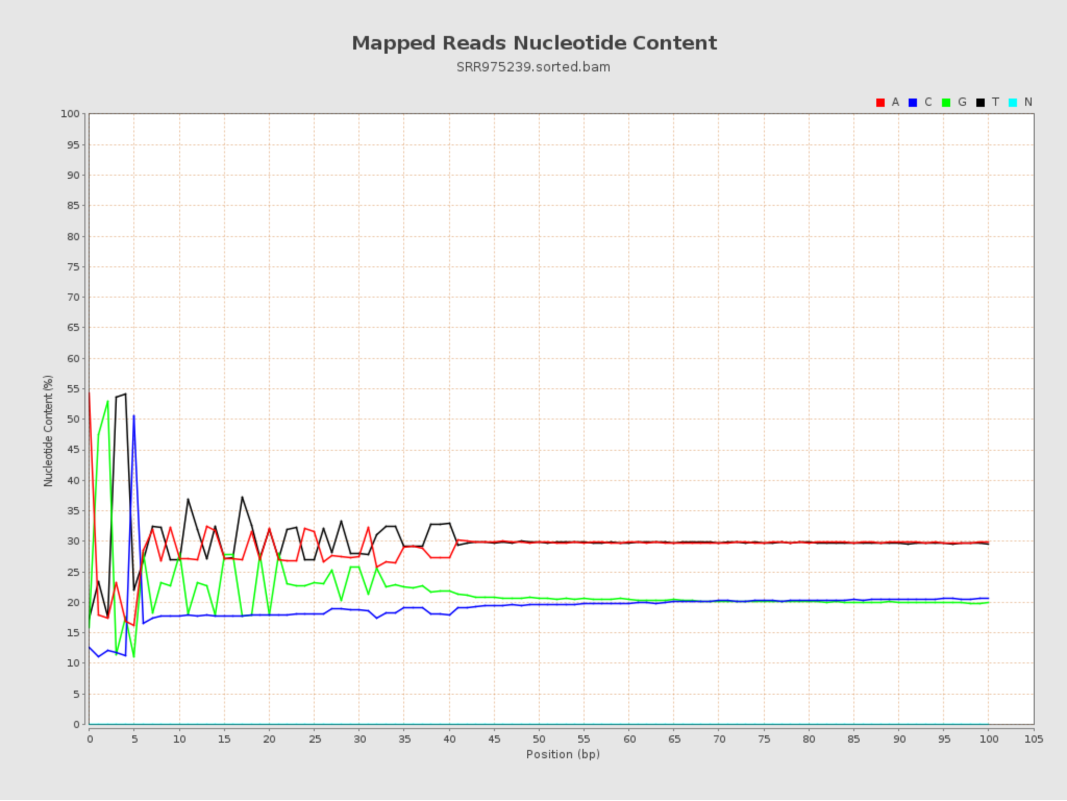
6. Results : Genome Fraction Coverage



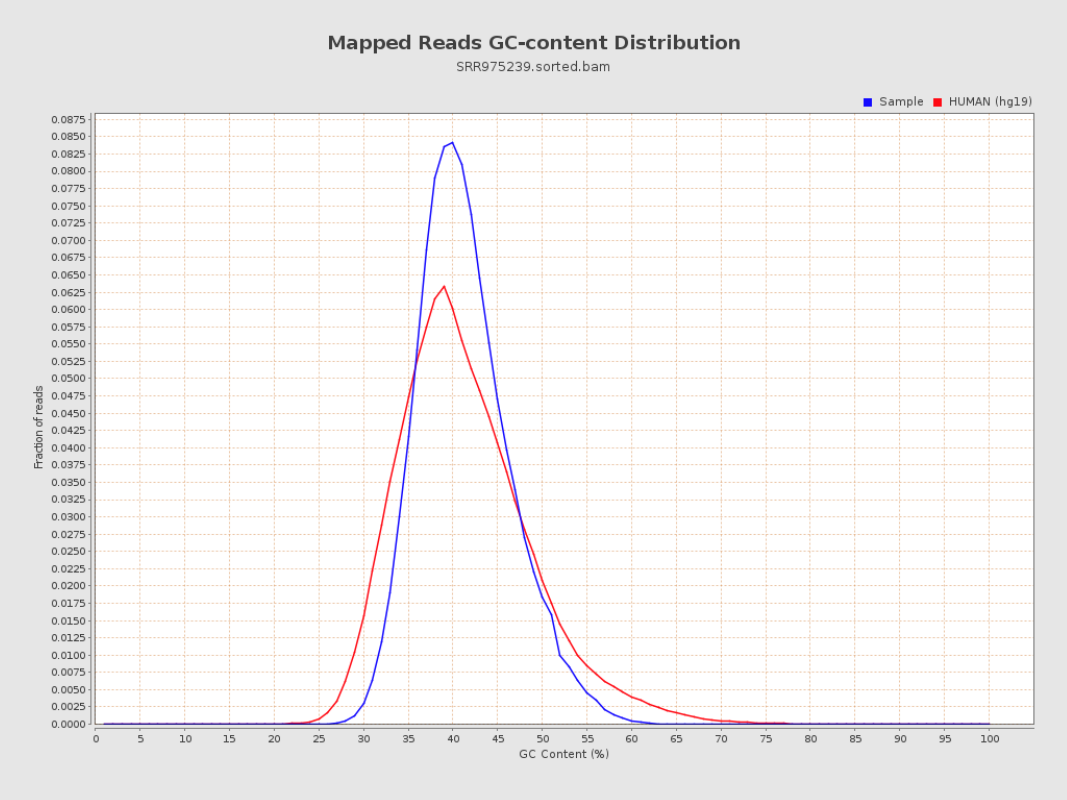
7. Results : Duplication Rate Histogram



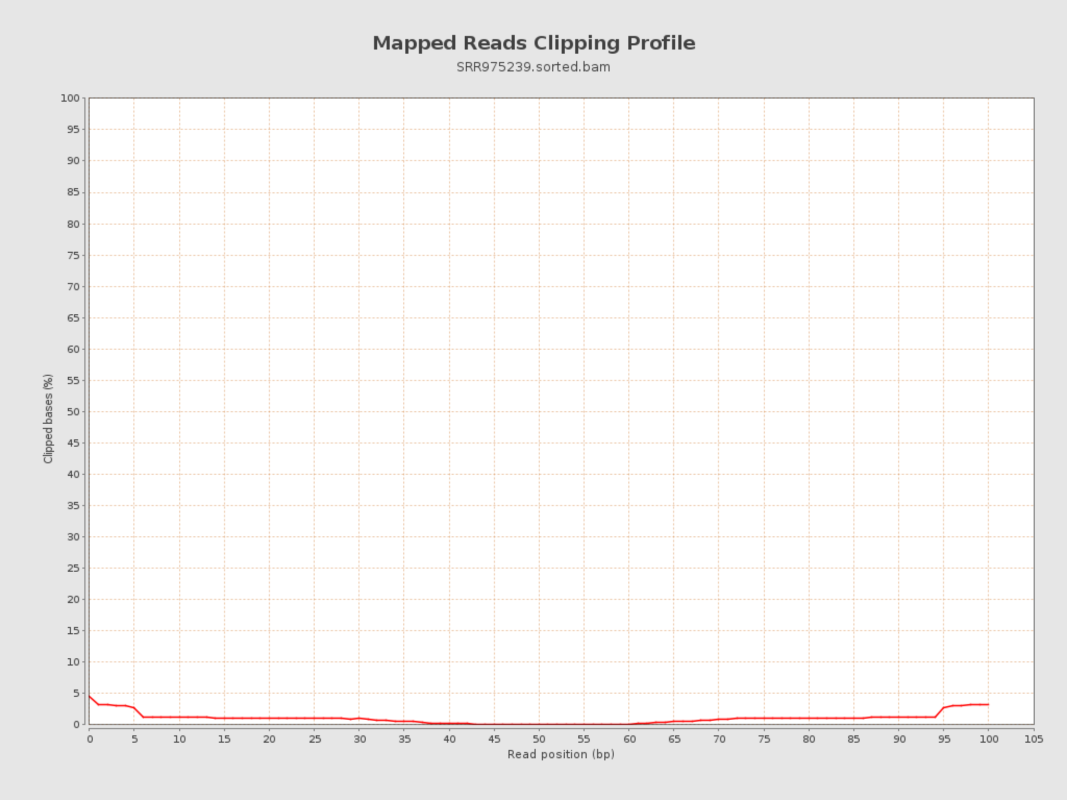
8. Results : Mapped Reads Nucleotide Content



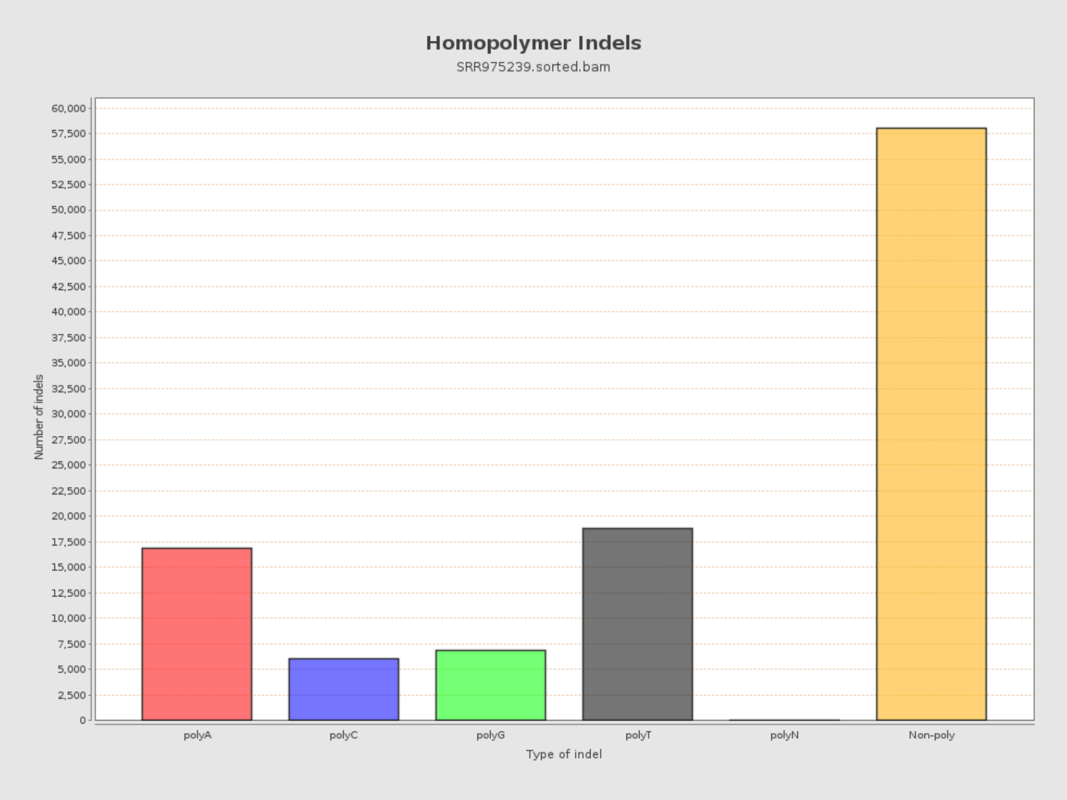
9. Results : Mapped Reads GC-content Distribution



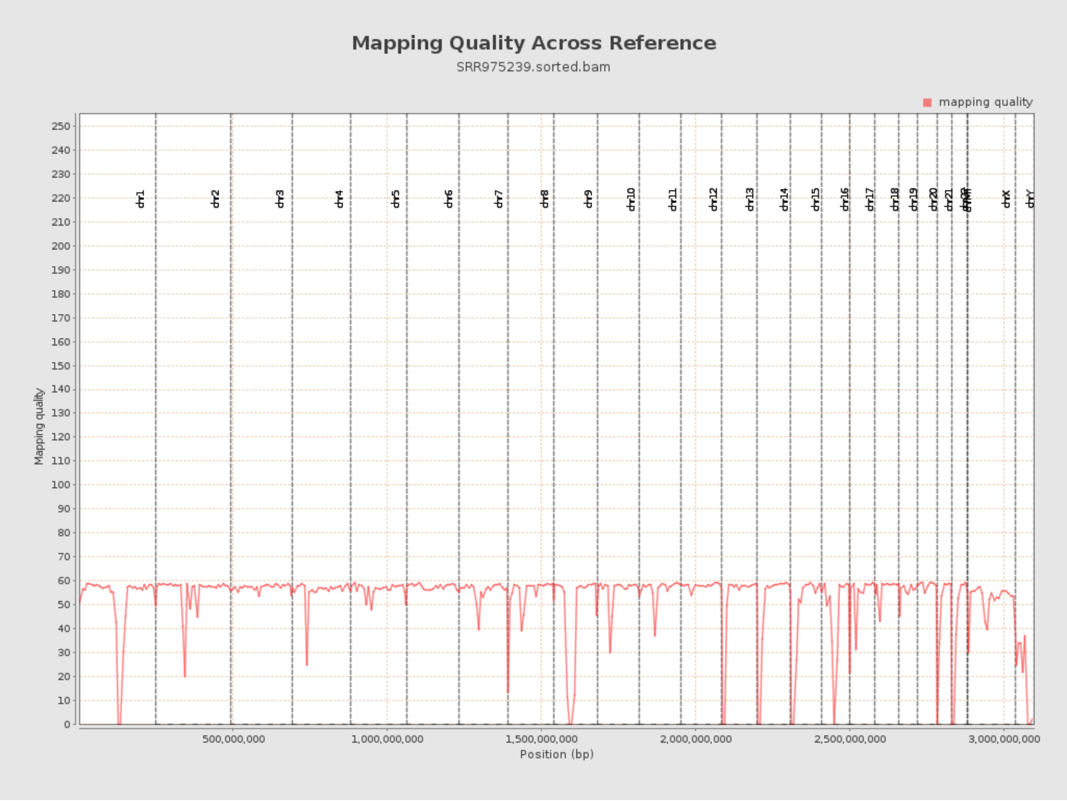
10. Results : Mapped Reads Clipping Profile



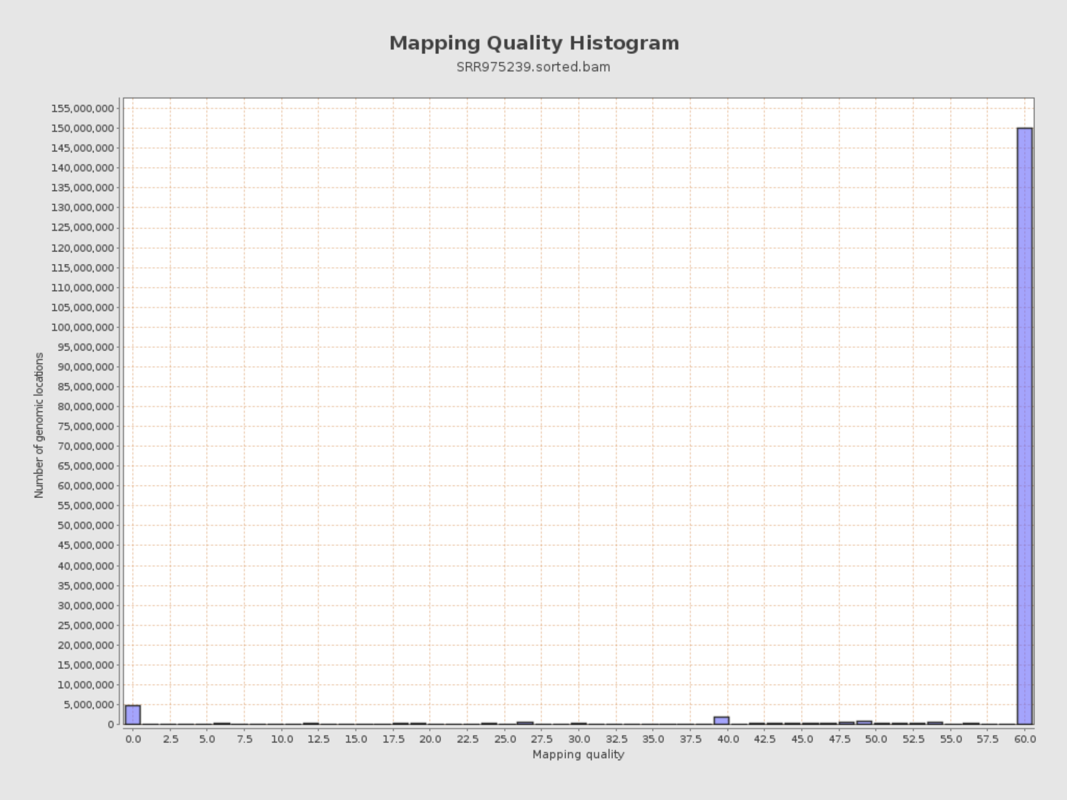
11. Results : Homopolymer Indels



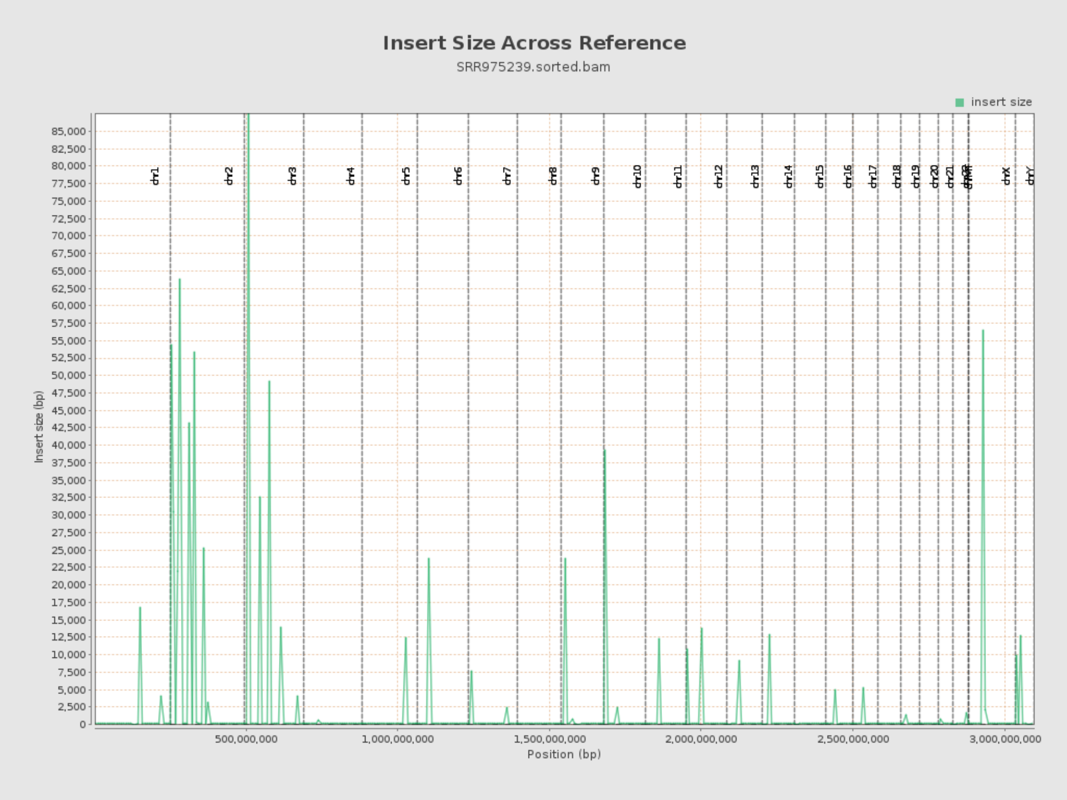
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram