Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 06:33:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975237.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_SRR975237 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975237_1.fastq.gz SRR975237_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 06:33:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975237.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,128,310
Mapped reads	4,085,385 / 98.96%
Unmapped reads	42,925 / 1.04%
Mapped paired reads	4,085,385 / 98.96%
Mapped reads, first in pair	2,042,201 / 49.47%
Mapped reads, second in pair	2,043,184 / 49.49%
Mapped reads, both in pair	4,071,566 / 98.63%
Mapped reads, singletons	13,819 / 0.33%
Secondary alignments	0
Supplementary alignments	33,549 / 0.81%
Read min/max/mean length	30 / 101 / 101.32
Duplicated reads (estimated)	232,038 / 5.62%
Duplication rate	3.39%
Clipped reads	2,492,795 / 60.38%

2.2. ACGT Content

Number/percentage of A's	112,536,093 / 29.29%
Number/percentage of C's	78,116,000 / 20.33%
Number/percentage of T's	113,565,112 / 29.56%
Number/percentage of G's	79,927,702 / 20.81%
Number/percentage of N's	5,365 / 0%

GC Percentage	41.14%

2.3. Coverage

Mean	0.1242
Standard Deviation	1.1821

2.4. Mapping Quality

Mean Mapping Quality	52.79

2.5. Insert size

Mean	111,099.94
Standard Deviation	3,214,888.98
P25/Median/P75	142 / 177 / 226

2.6. Mismatches and indels

General error rate	0.89%
Mismatches	3,252,156
Insertions	76,559
Mapped reads with at least one insertion	1.82%
Deletions	147,000
Mapped reads with at least one deletion	3.52%
Homopolymer indels	46.06%

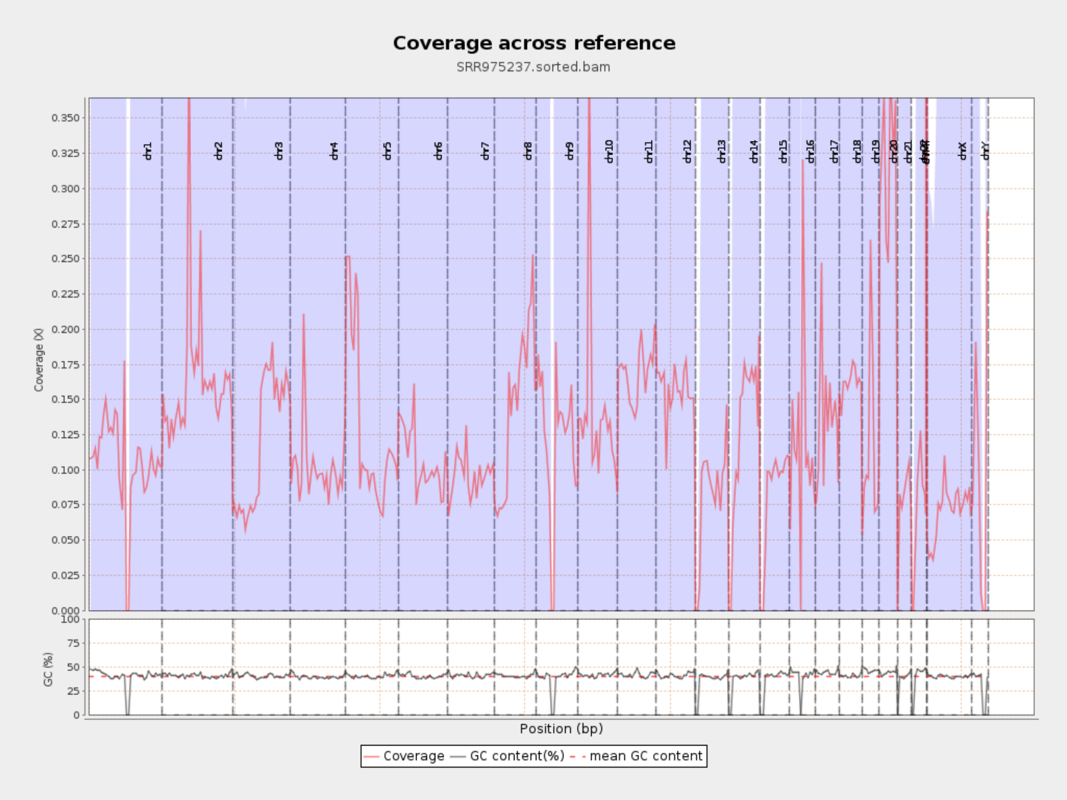
2.7. Chromosome stats

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

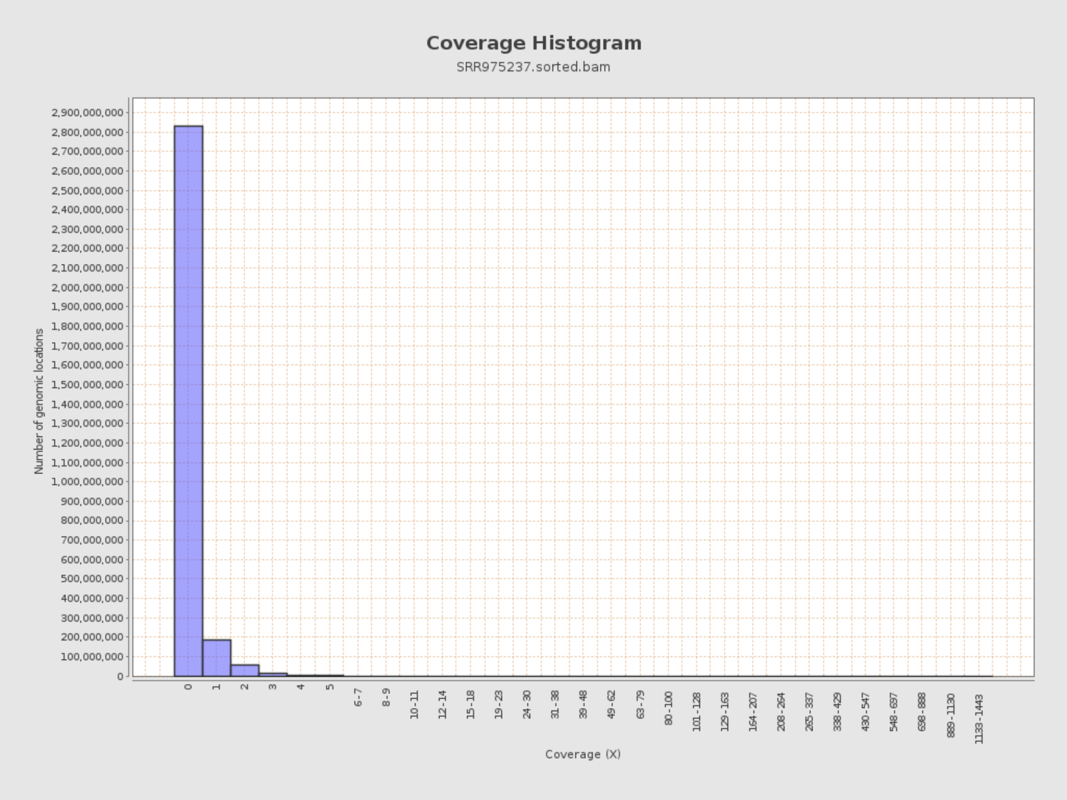
		bases	coverage	deviation
chr1	249250621	26326324	0.1056	1.5779
chr2	243199373	40153819	0.1651	1.7868
chr3	198022430	23689280	0.1196	0.4542
chr4	191154276	19265305	0.1008	0.907
chr5	180915260	23152875	0.128	0.4806
chr6	171115067	18354568	0.1073	0.5845
chr7	159138663	15316632	0.0962	0.8821
chr8	146364022	21384746	0.1461	0.6132
chr9	141213431	17214822	0.1219	1.6962
chr10	135534747	19001769	0.1402	2.327
chr11	135006516	22643135	0.1677	0.9283
chr12	133851895	20900170	0.1561	0.5138
chr13	115169878	9408188	0.0817	0.3579
chr14	107349540	13393767	0.1248	0.4972
chr15	102531392	8428902	0.0822	0.3625
chr16	90354753	10683159	0.1182	1.6511
chr17	81195210	11040789	0.136	2.129
chr18	78077248	12672900	0.1623	1.5516
chr19	59128983	7143368	0.1208	0.7656
chr20	63025520	19983569	0.3171	0.8078
chr21	48129895	3759296	0.0781	0.4662
chr22	51304566	3514984	0.0685	0.3703
chrMT	16571	95205	5.7453	4.1229
chrX	155270560	11061594	0.0712	0.453

chrY	59373566	5817233	0.098	1.7026

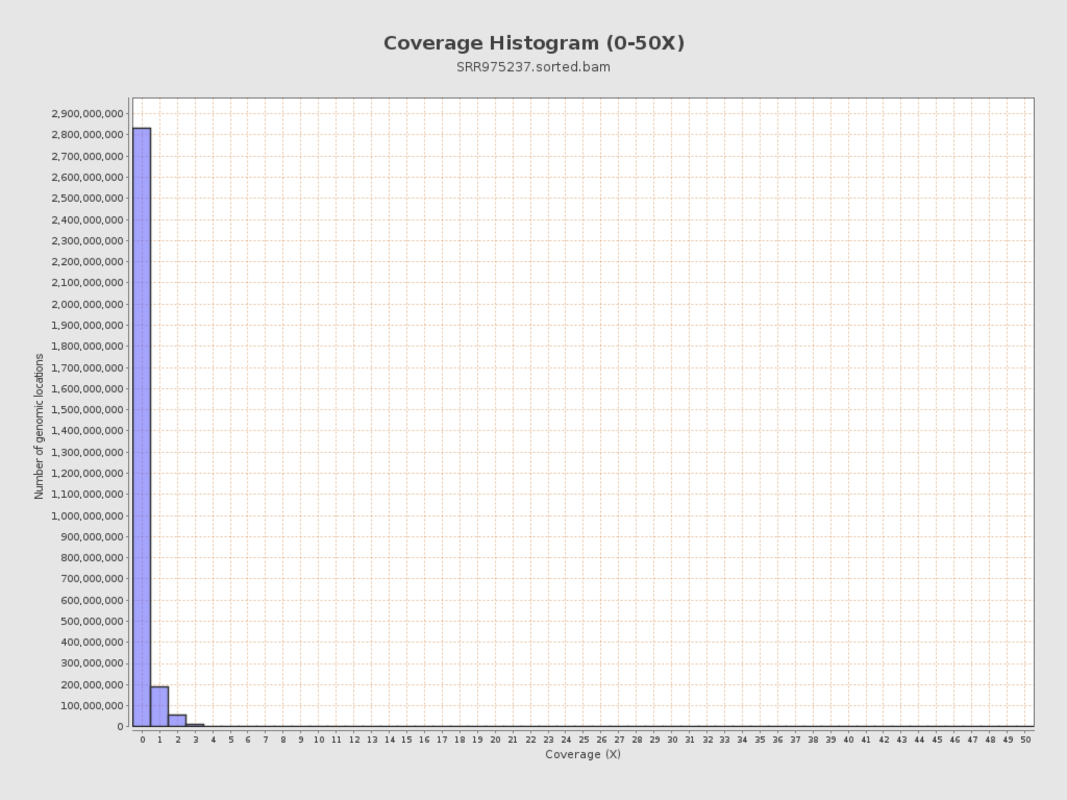
3. Results : Coverage across reference



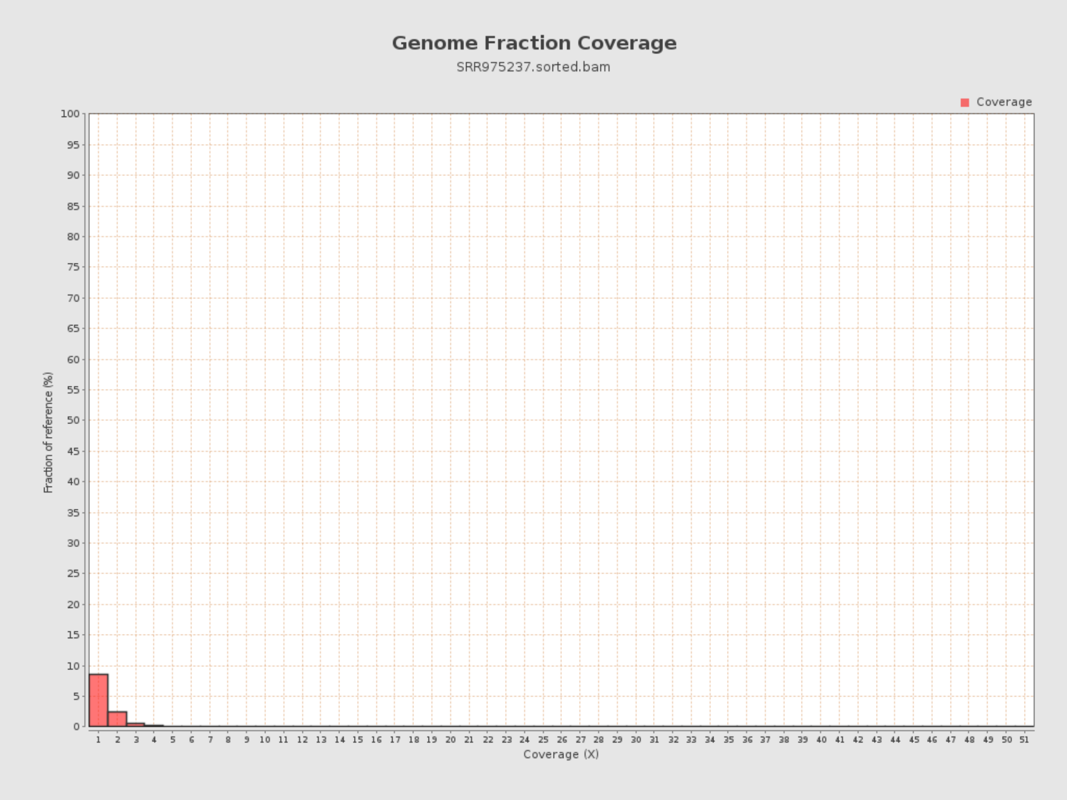
4. Results : Coverage Histogram



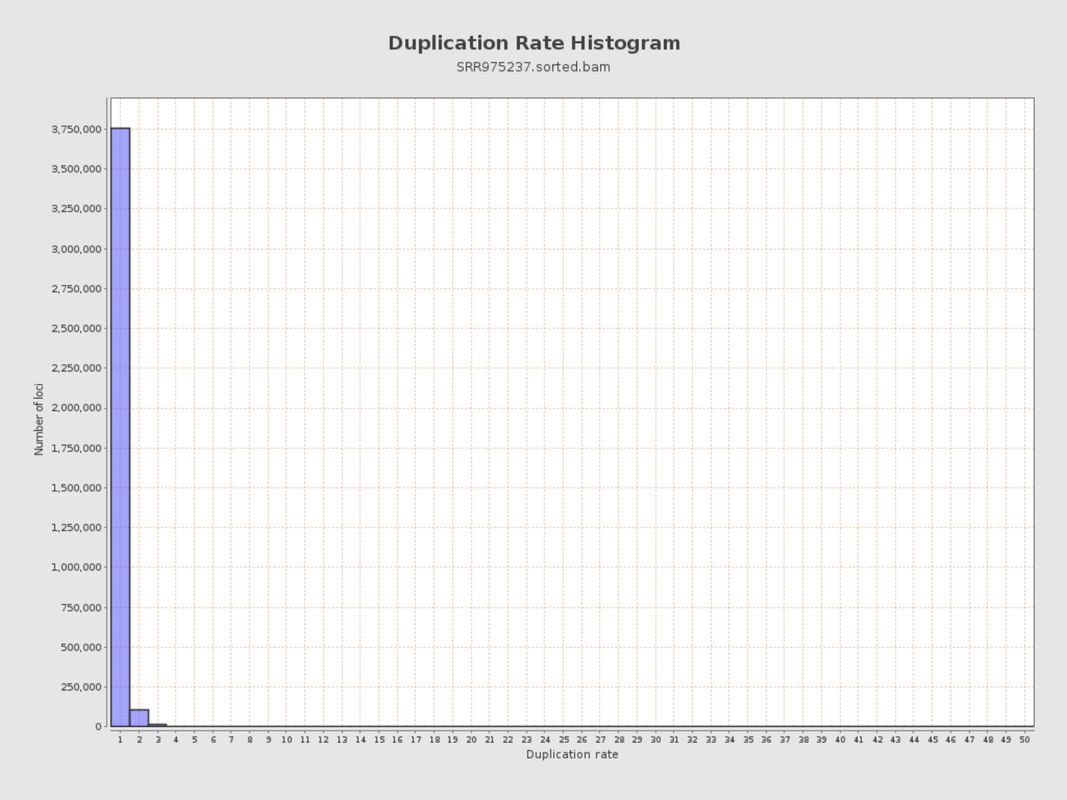
5. Results : Coverage Histogram (0-50X)



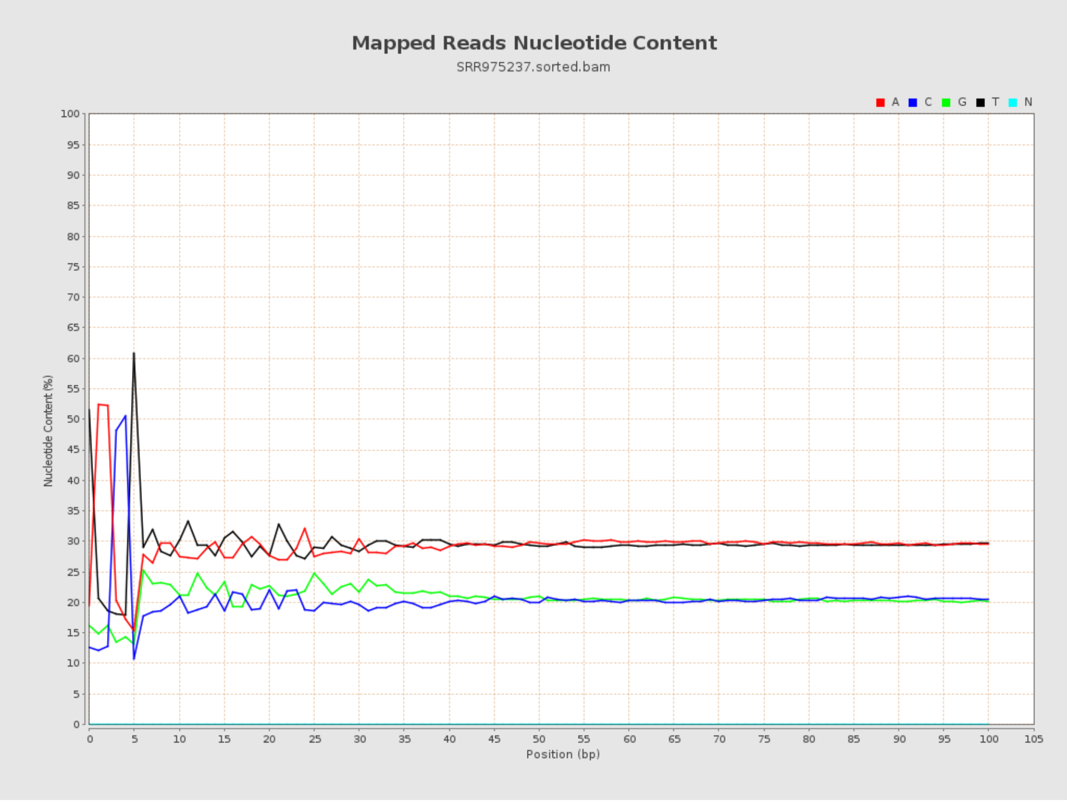
6. Results : Genome Fraction Coverage



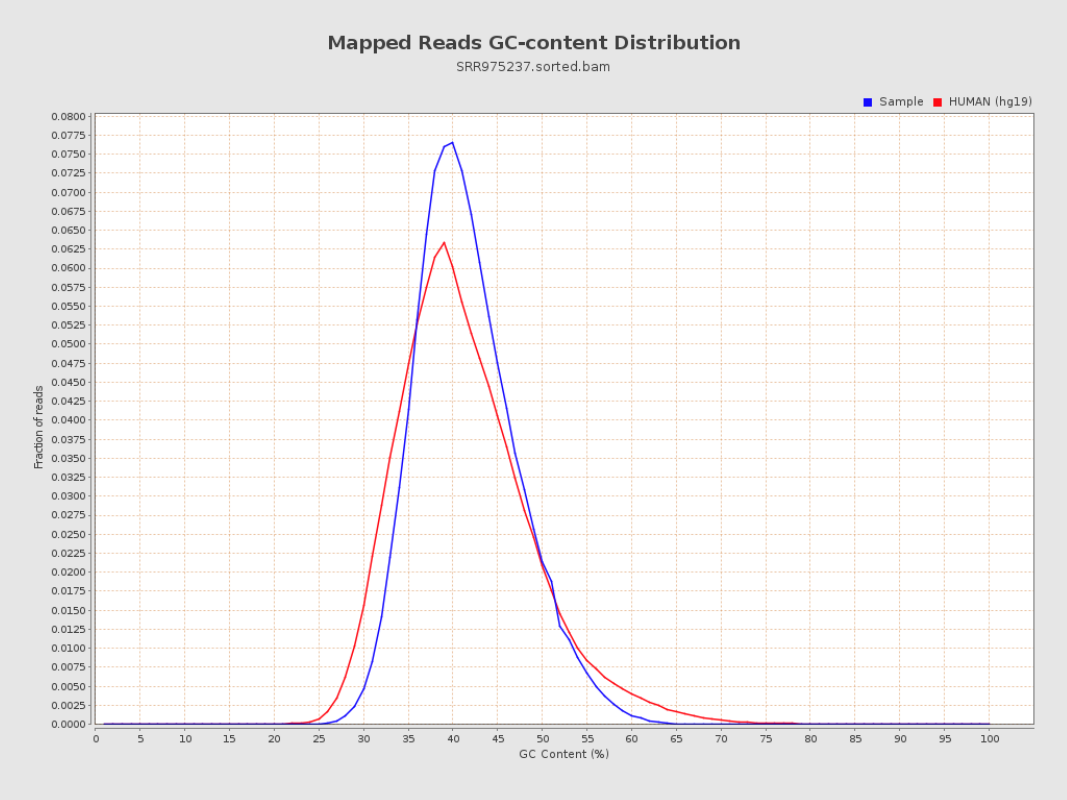
7. Results : Duplication Rate Histogram



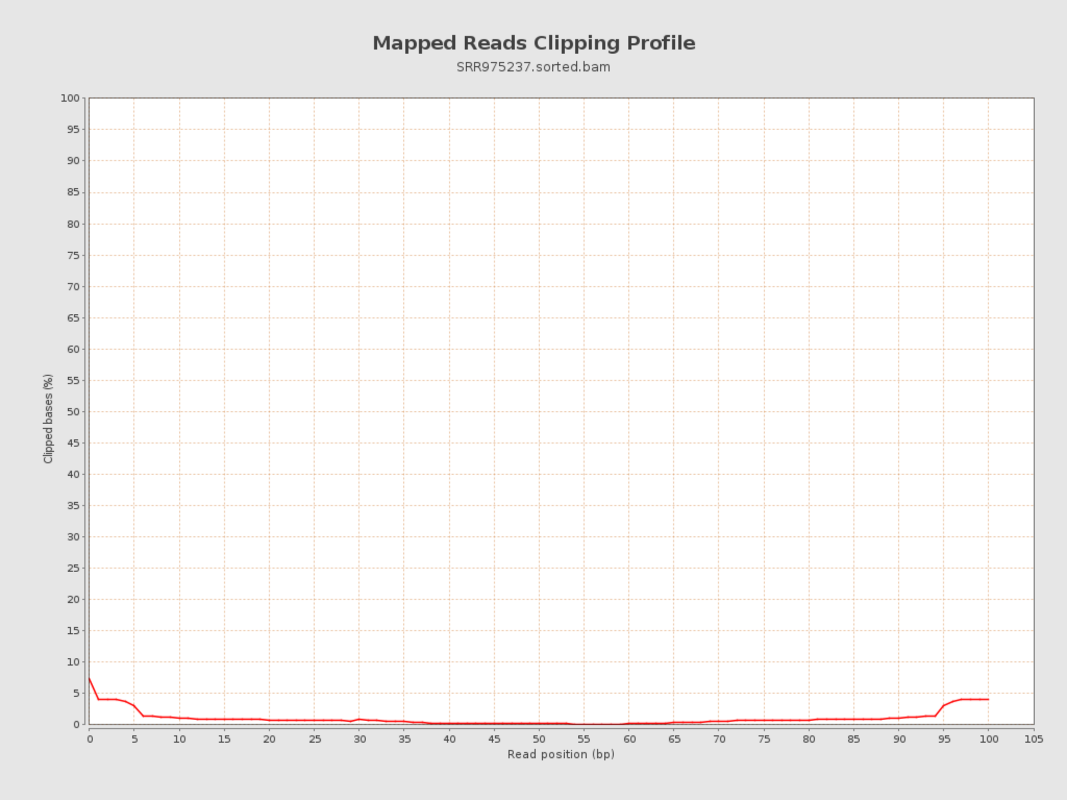
8. Results : Mapped Reads Nucleotide Content



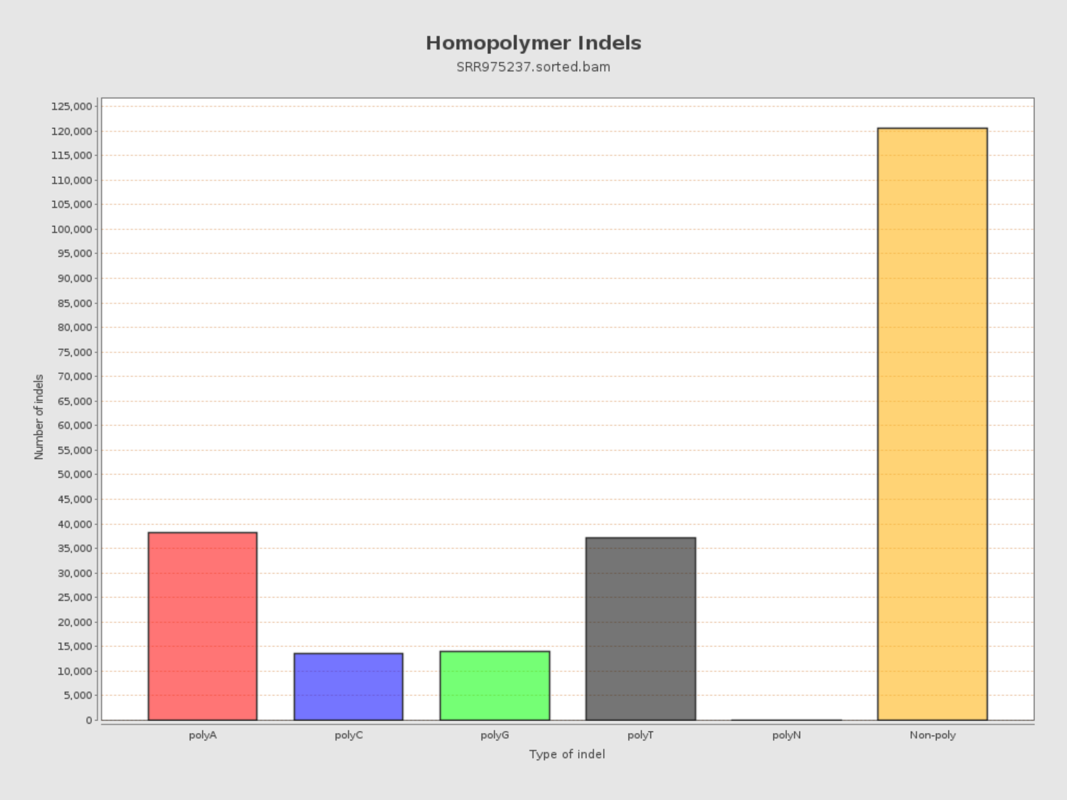
9. Results : Mapped Reads GC-content Distribution



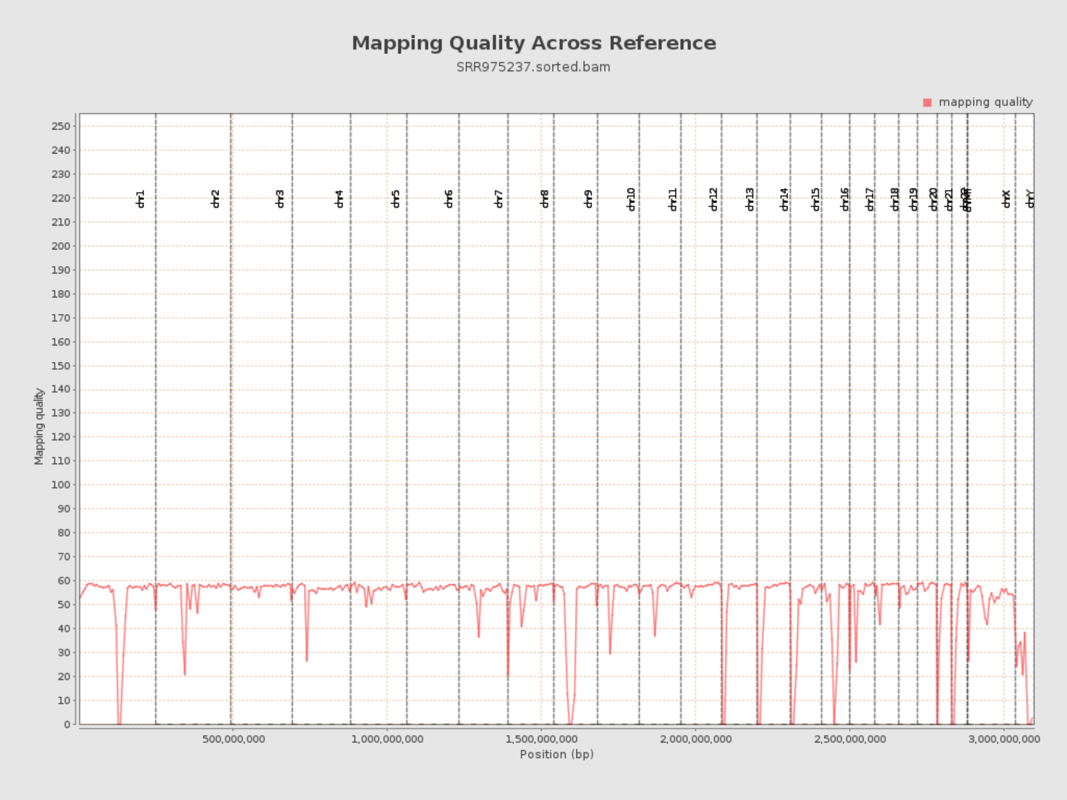
10. Results : Mapped Reads Clipping Profile



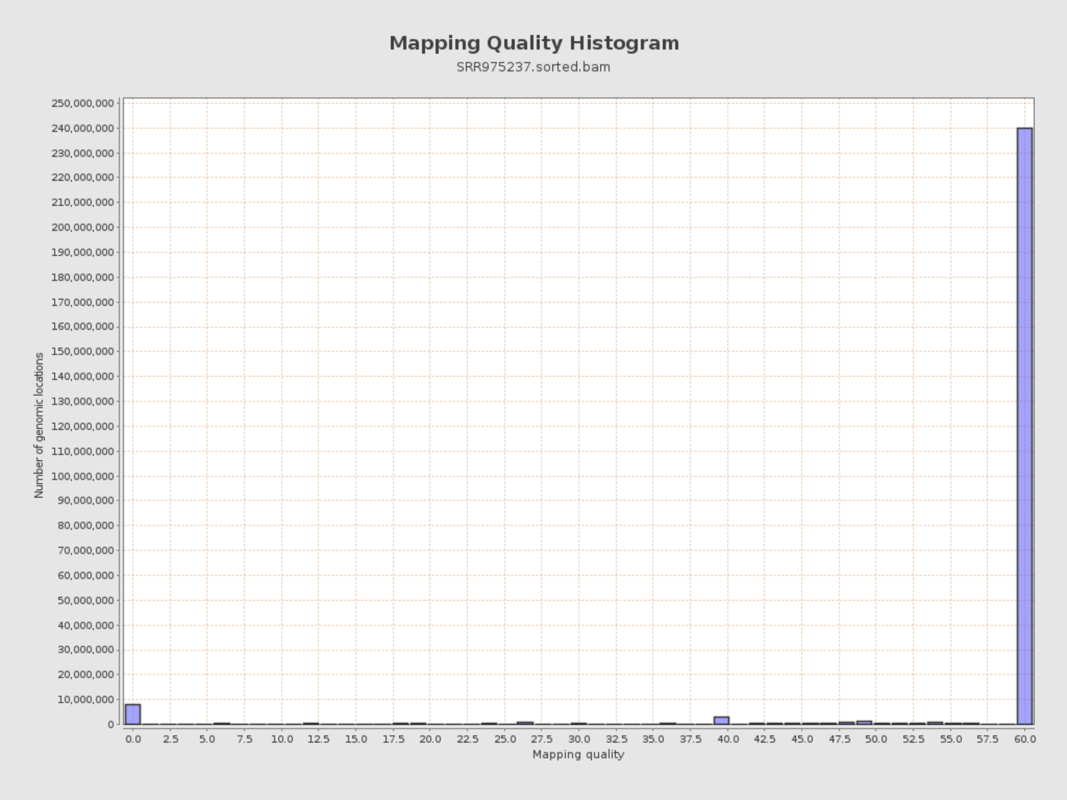
11. Results : Homopolymer Indels



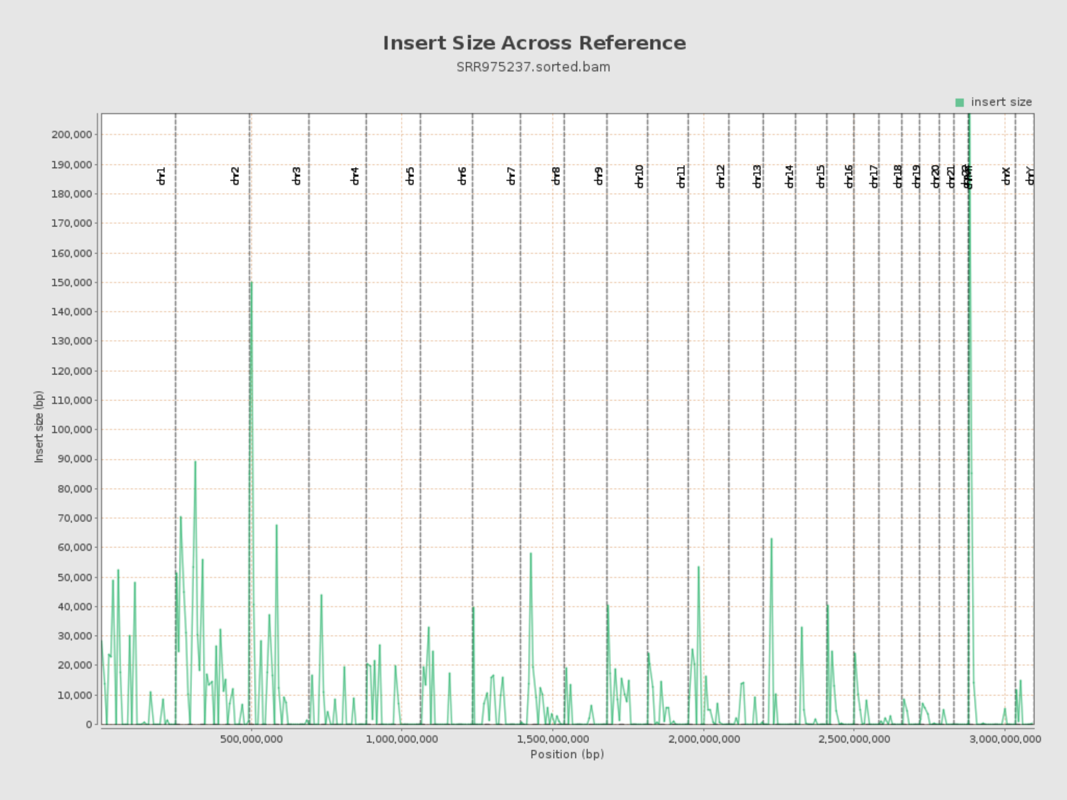
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram