Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 16:42:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975246.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_SRR975246 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975246_1.fastq.gz SRR975246_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 16:42:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975246.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	48,835,124
Mapped reads	48,775,985 / 99.88%
Unmapped reads	59,139 / 0.12%
Mapped paired reads	48,775,985 / 99.88%
Mapped reads, first in pair	24,391,671 / 49.95%
Mapped reads, second in pair	24,384,314 / 49.93%
Mapped reads, both in pair	48,756,644 / 99.84%
Mapped reads, singletons	19,341 / 0.04%
Secondary alignments	0
Supplementary alignments	279,117 / 0.57%
Read min/max/mean length	30 / 101 / 101.23
Duplicated reads (estimated)	22,499,697 / 46.07%
Duplication rate	41.19%
Clipped reads	24,928,976 / 51.05%

2.2. ACGT Content

Number/percentage of A's	1,132,661,557 / 23.72%
Number/percentage of C's	1,258,935,341 / 26.37%
Number/percentage of T's	1,140,457,461 / 23.89%
Number/percentage of G's	1,242,218,256 / 26.02%
Number/percentage of N's	190,039 / 0%

GC Percentage	52.39%

2.3. Coverage

Mean	1.5424
Standard Deviation	15.4131

2.4. Mapping Quality

Mean Mapping Quality	56.48

2.5. Insert size

Mean	57,519.6
Standard Deviation	2,361,097.46
P25/Median/P75	139 / 164 / 200

2.6. Mismatches and indels

General error rate	0.24%
Mismatches	10,904,609
Insertions	344,025
Mapped reads with at least one insertion	0.7%
Deletions	218,929
Mapped reads with at least one deletion	0.44%
Homopolymer indels	32.19%

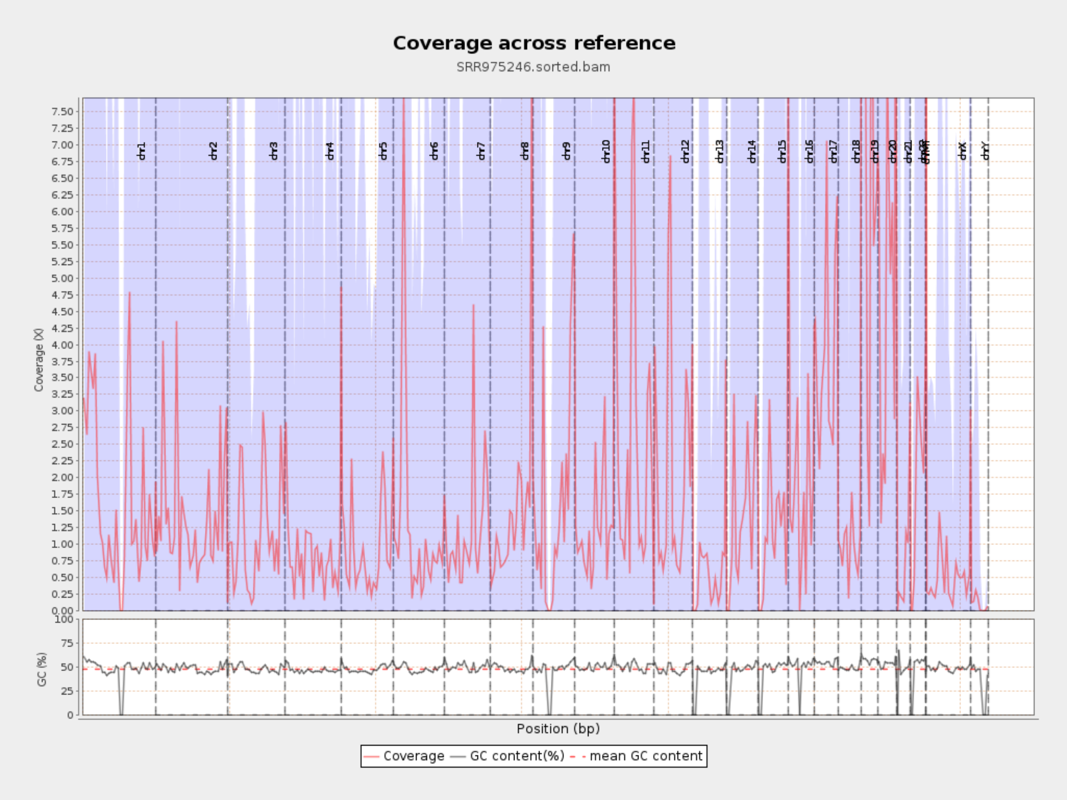
2.7. Chromosome stats

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

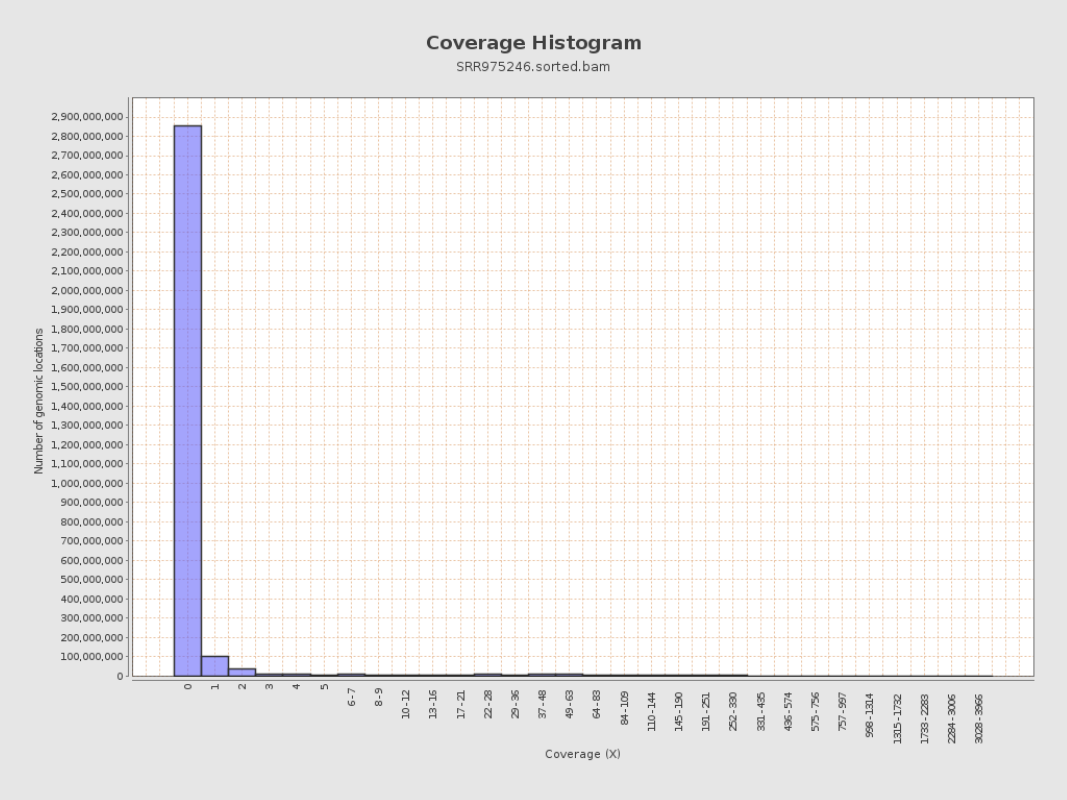
		bases	coverage	deviation
chr1	249250621	408357149	1.6383	14.1622
chr2	243199373	342505587	1.4083	13.9396
chr3	198022430	226853346	1.1456	11.3001
chr4	191154276	152104932	0.7957	9.1088
chr5	180915260	176011632	0.9729	10.5555
chr6	171115067	213266981	1.2463	12.8128
chr7	159138663	195782169	1.2303	12.237
chr8	146364022	224015724	1.5305	17.7322
chr9	141213431	222203401	1.5735	15.3068
chr10	135534747	165308681	1.2197	12.2049
chr11	135006516	356680837	2.642	21.4795
chr12	133851895	294916061	2.2033	19.0288
chr13	115169878	61355565	0.5327	7.0264
chr14	107349540	156408281	1.457	14.0917
chr15	102531392	114057427	1.1124	10.0082
chr16	90354753	171852904	1.902	15.0706
chr17	81195210	313051218	3.8555	24.7628
chr18	78077248	72881091	0.9334	11.1279
chr19	59128983	396759687	6.7101	37.3252
chr20	63025520	288379430	4.5756	37.4696
chr21	48129895	37191494	0.7727	11.0956
chr22	51304566	97586639	1.9021	14.9874
chrMT	16571	700203	42.2547	55.4065
chrX	155270560	80655735	0.5195	5.9049

chrY	59373566	6057970	0.102	2.1803

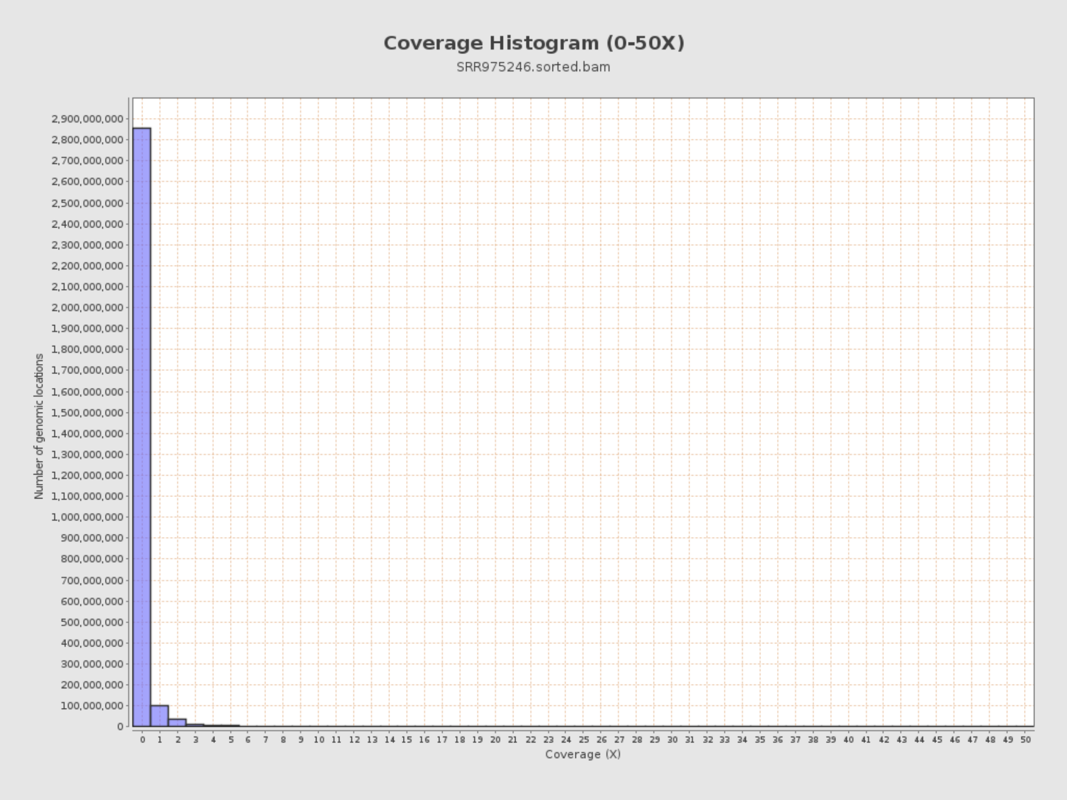
3. Results : Coverage across reference



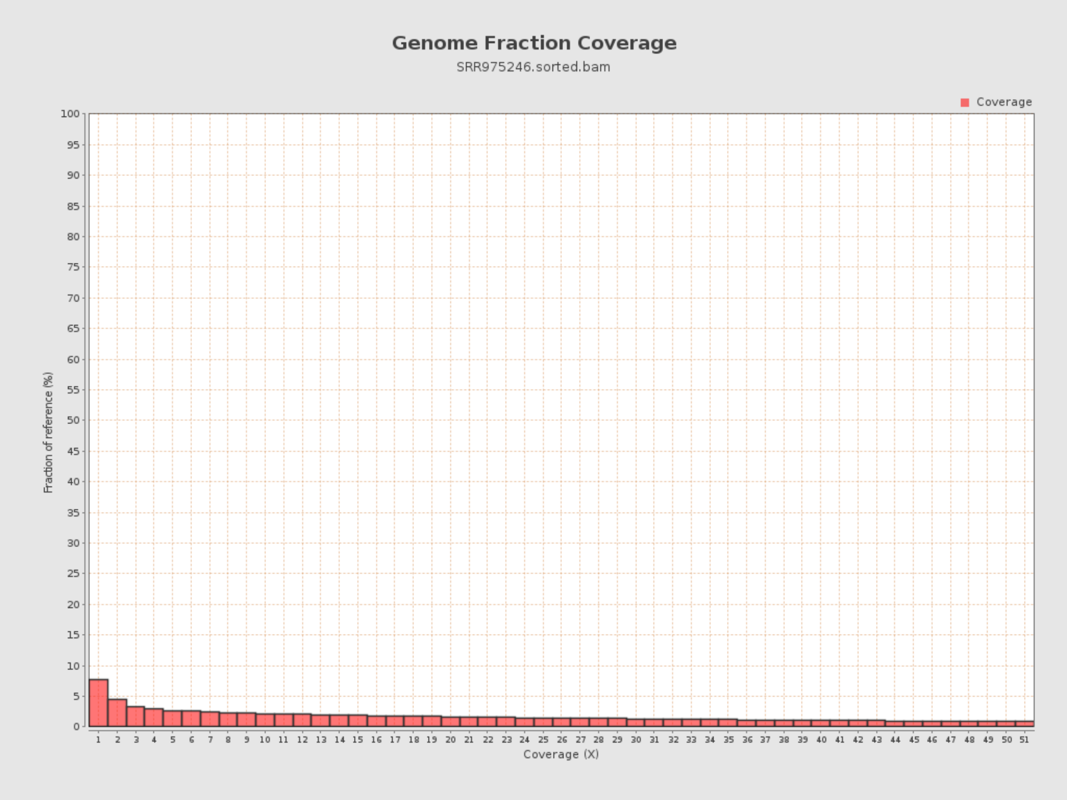
4. Results : Coverage Histogram



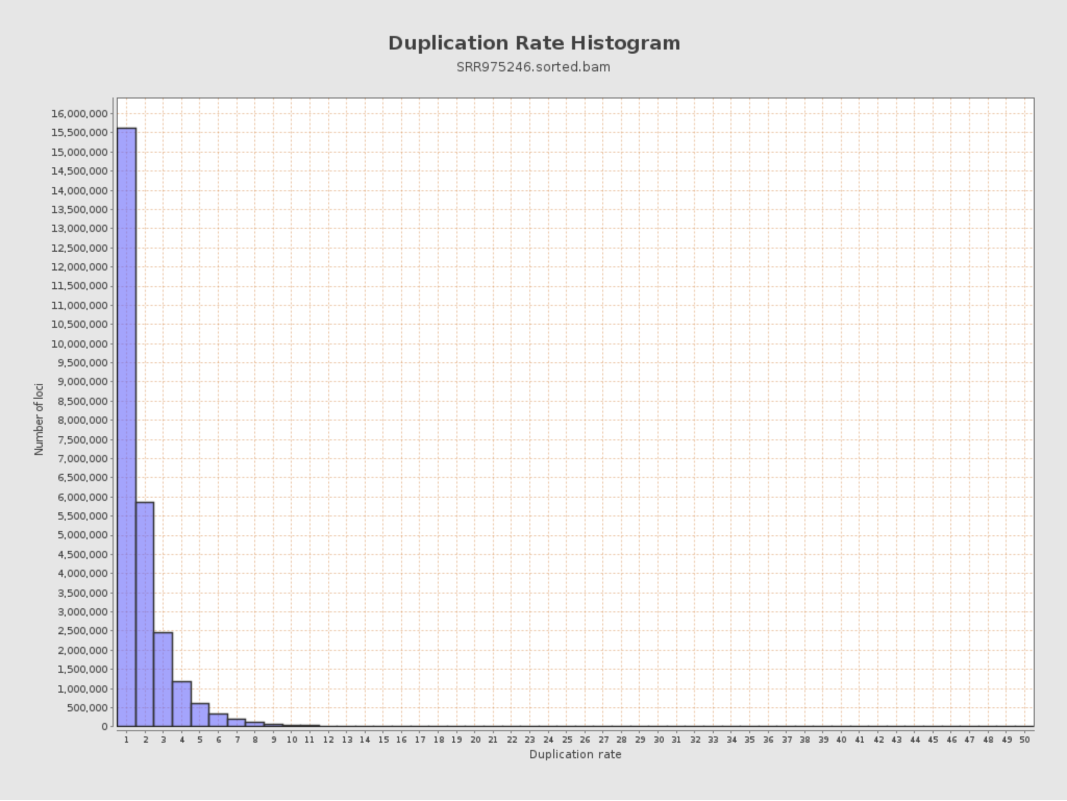
5. Results : Coverage Histogram (0-50X)



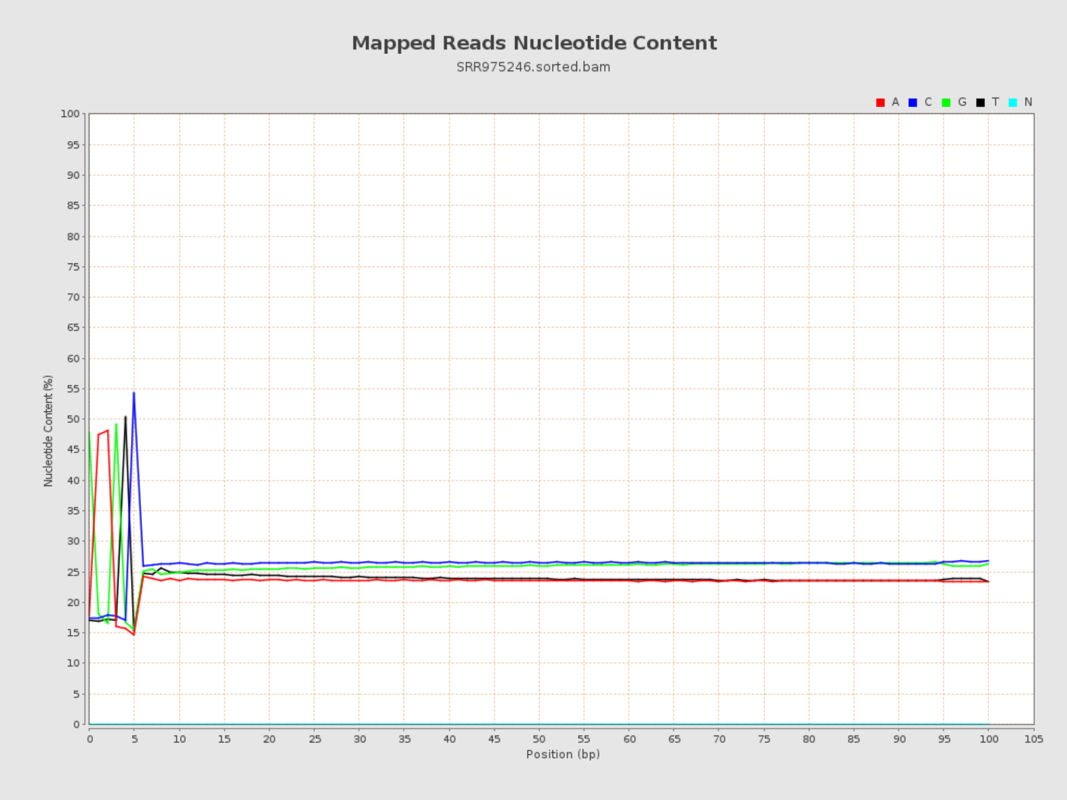
6. Results : Genome Fraction Coverage



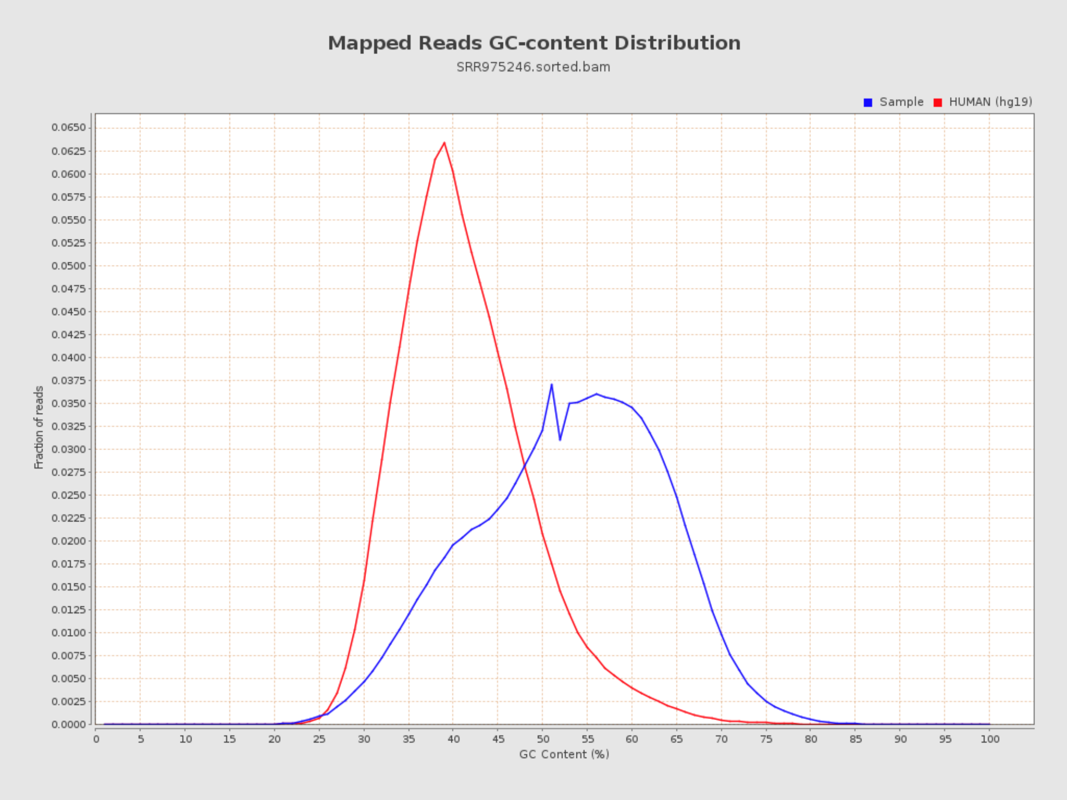
7. Results : Duplication Rate Histogram



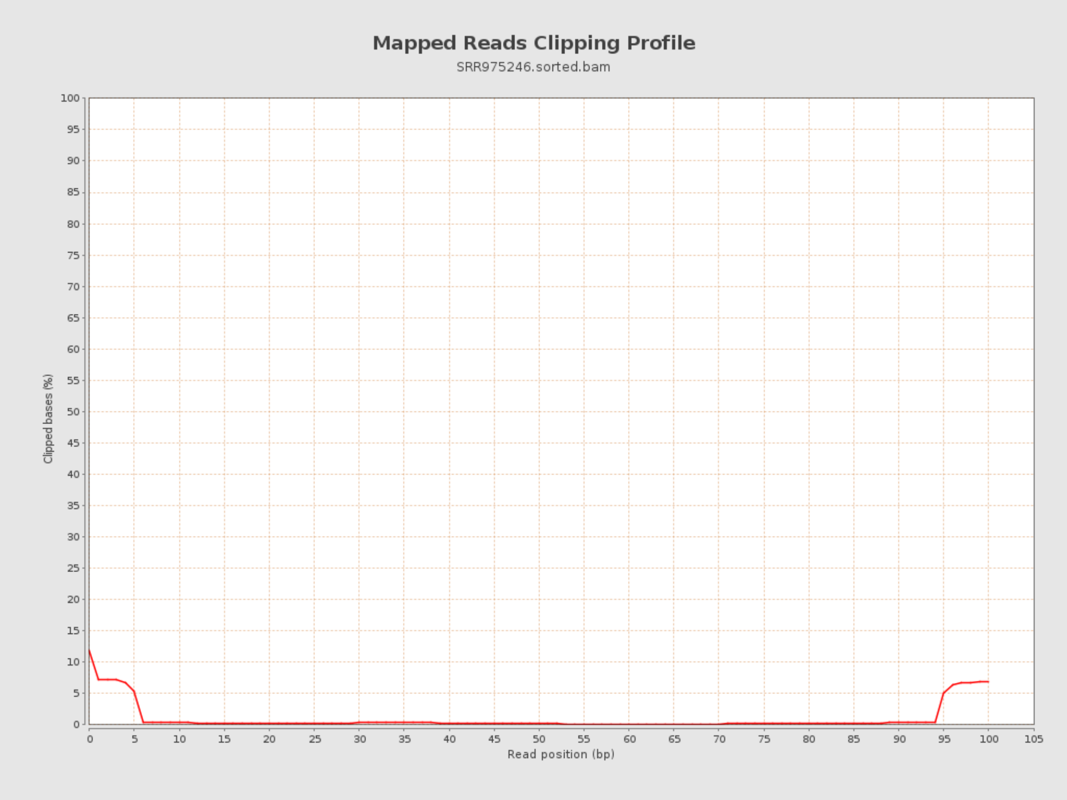
8. Results : Mapped Reads Nucleotide Content



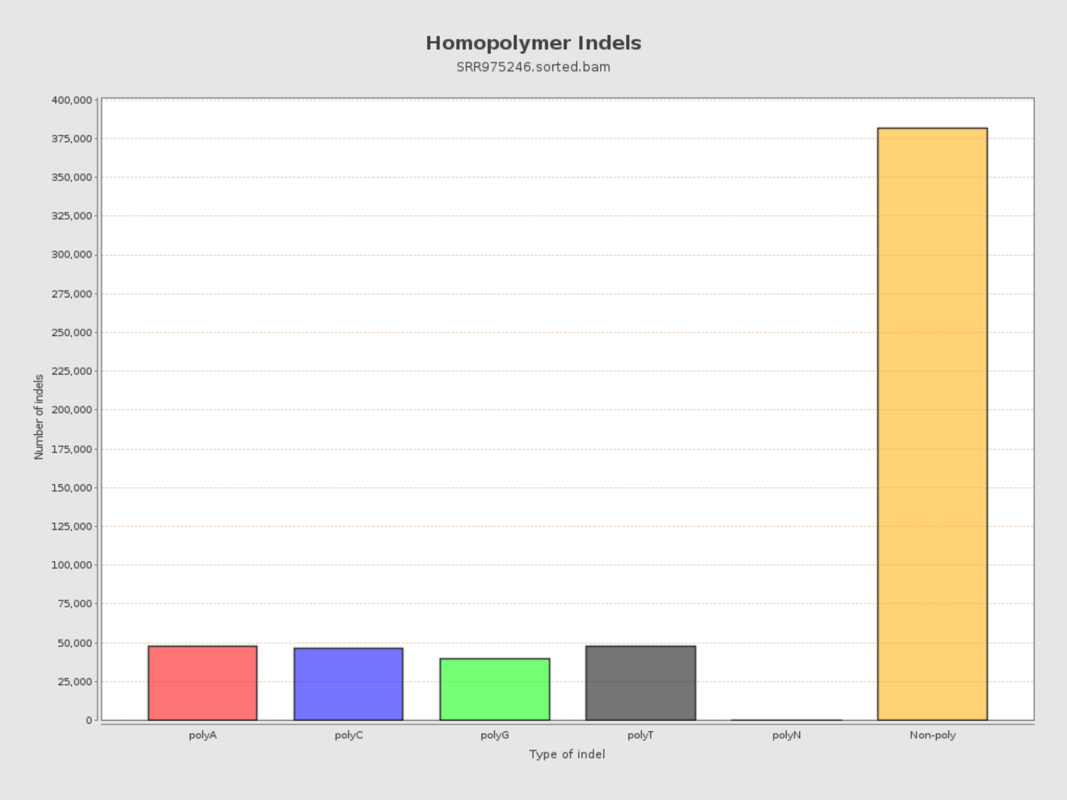
9. Results : Mapped Reads GC-content Distribution



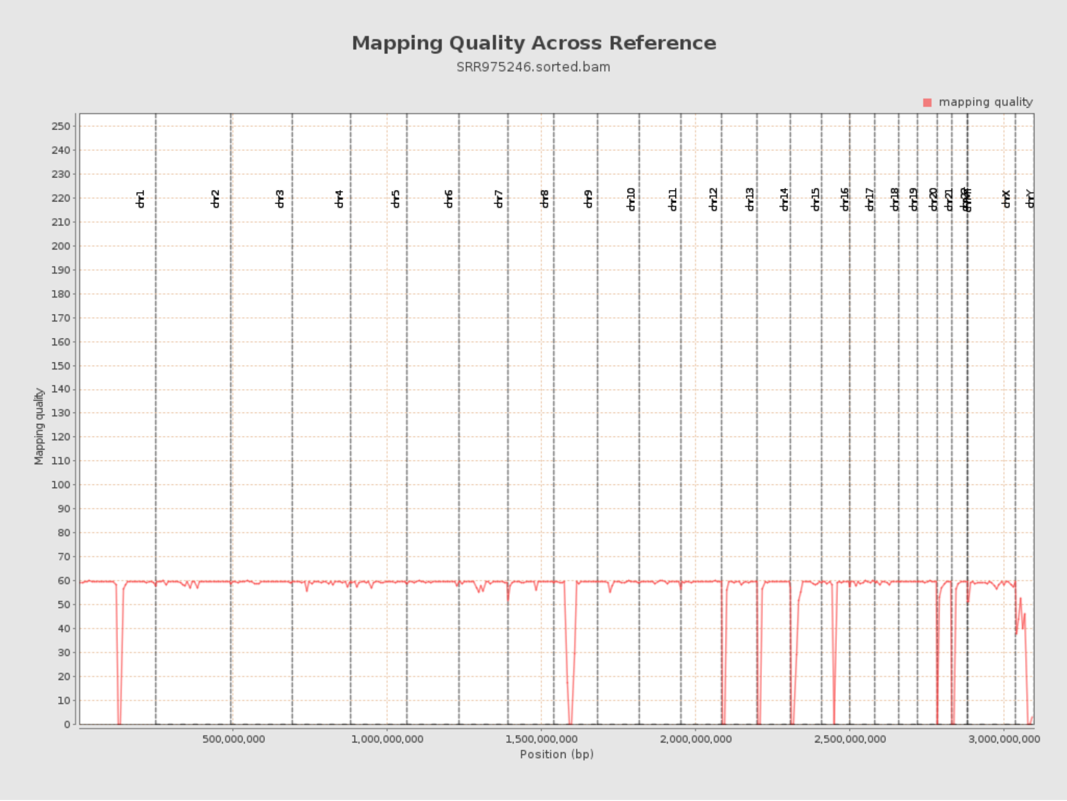
10. Results : Mapped Reads Clipping Profile



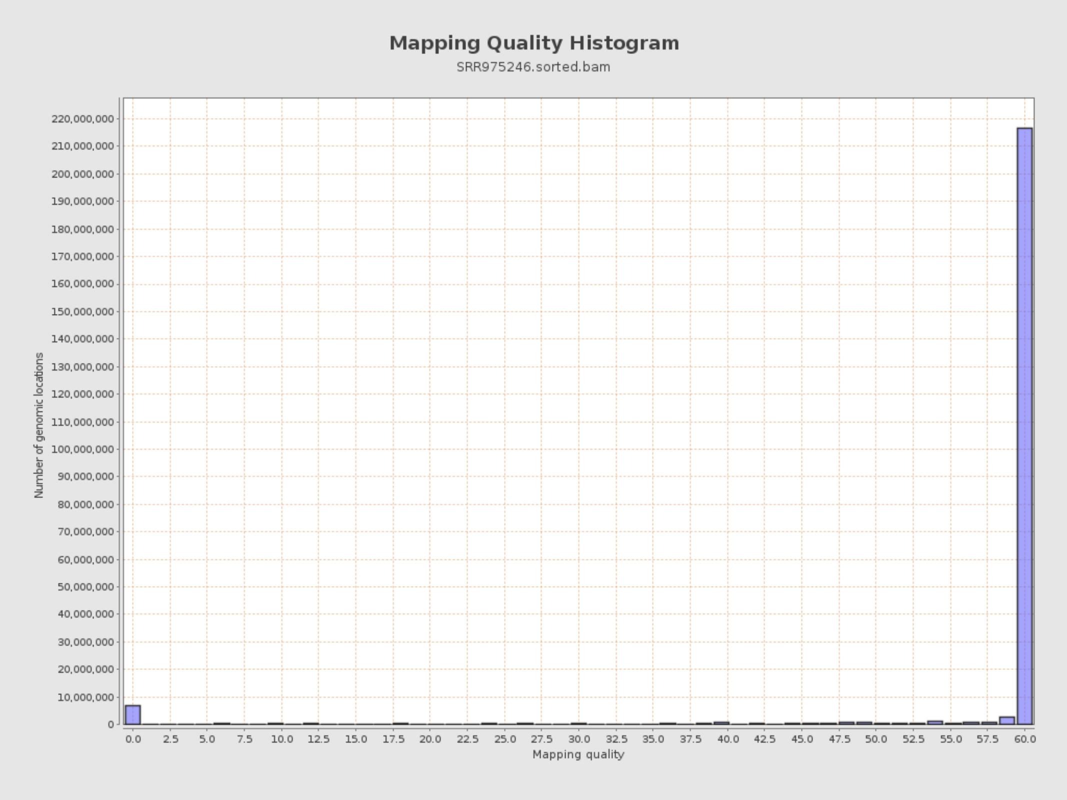
11. Results : Homopolymer Indels



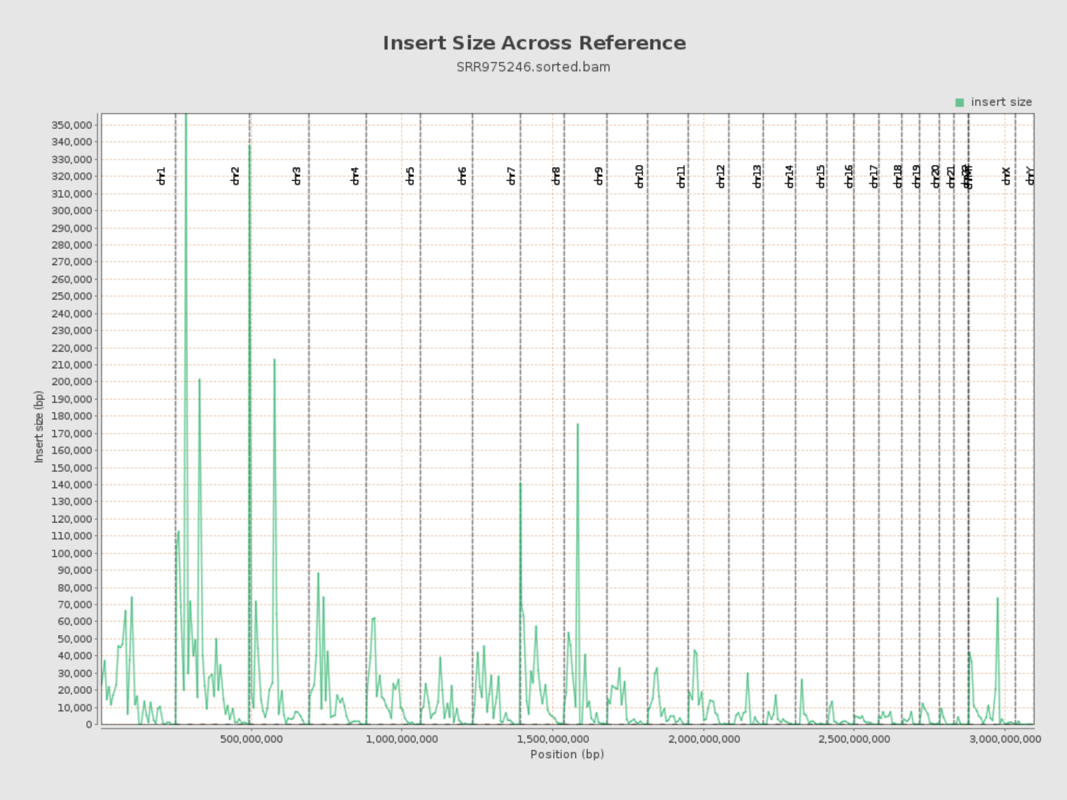
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram