Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 10:49:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975240.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_SRR975240 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975240_1.fastq.gz SRR975240_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 10:49:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975240.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	47,450,380
Mapped reads	47,295,238 / 99.67%
Unmapped reads	155,142 / 0.33%
Mapped paired reads	47,295,238 / 99.67%
Mapped reads, first in pair	23,647,590 / 49.84%
Mapped reads, second in pair	23,647,648 / 49.84%
Mapped reads, both in pair	47,229,156 / 99.53%
Mapped reads, singletons	66,082 / 0.14%
Secondary alignments	0
Supplementary alignments	105,122 / 0.22%
Read min/max/mean length	30 / 101 / 101.09
Duplicated reads (estimated)	25,354,010 / 53.43%
Duplication rate	39.24%
Clipped reads	30,229,925 / 63.71%

2.2. ACGT Content

Number/percentage of A's	1,139,355,180 / 26.44%
Number/percentage of C's	922,072,863 / 21.4%
Number/percentage of T's	1,217,194,423 / 28.25%
Number/percentage of G's	1,030,331,825 / 23.91%
Number/percentage of N's	182,307 / 0%

GC Percentage	45.31%

2.3. Coverage

Mean	1.3925
Standard Deviation	19.4044

2.4. Mapping Quality

Mean Mapping Quality	55.75

2.5. Insert size

Mean	33,901.79
Standard Deviation	1,806,873.91
P25/Median/P75	146 / 183 / 232

2.6. Mismatches and indels

General error rate	0.63%
Mismatches	26,229,877
Insertions	443,790
Mapped reads with at least one insertion	0.93%
Deletions	991,368
Mapped reads with at least one deletion	2.07%
Homopolymer indels	46.28%

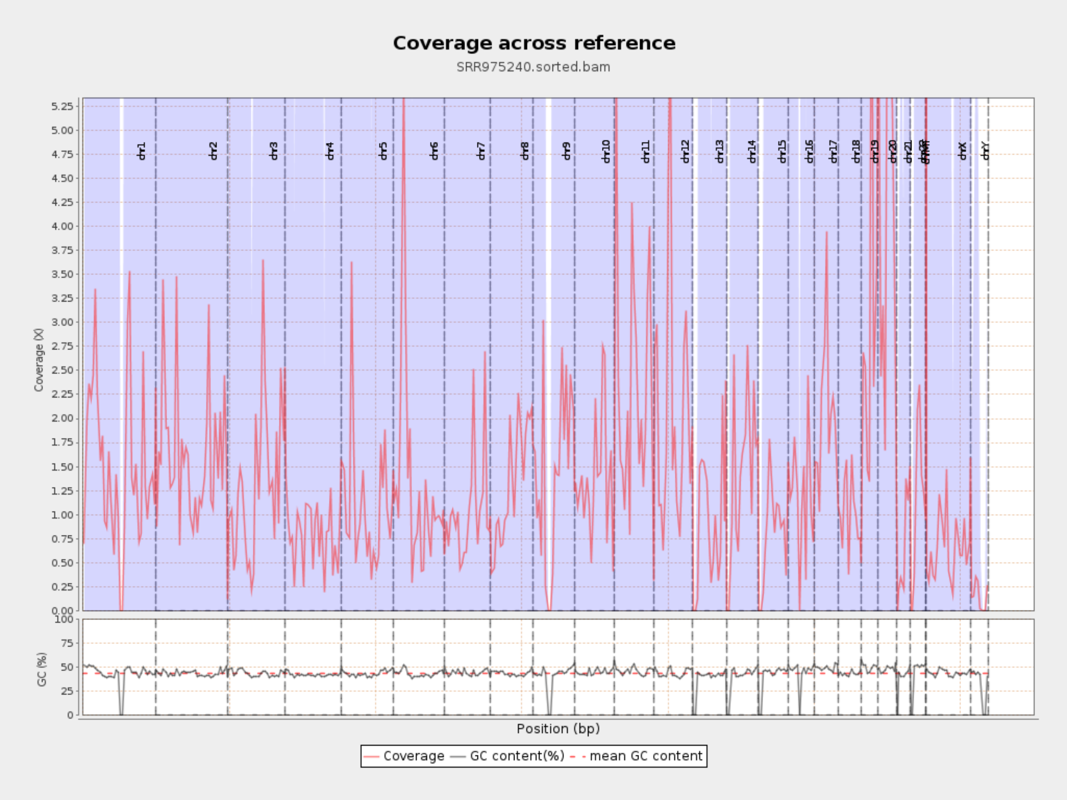
2.7. Chromosome stats

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

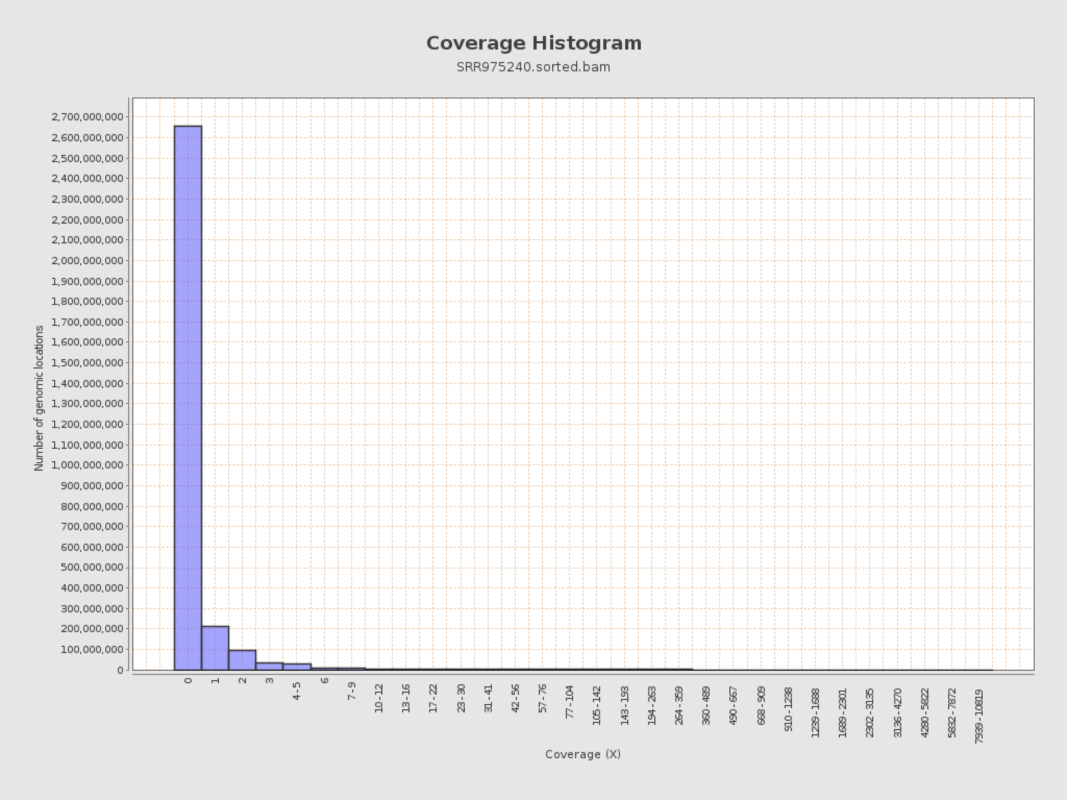
		bases	coverage	deviation
chr1	249250621	375656210	1.5071	18.2935
chr2	243199373	393887866	1.6196	19.9817
chr3	198022430	257647007	1.3011	17.7355
chr4	191154276	151929419	0.7948	12.1632
chr5	180915260	203004005	1.1221	16.0693
chr6	171115067	225489264	1.3178	17.8097
chr7	159138663	166296280	1.045	15.0538
chr8	146364022	196005640	1.3392	18.8764
chr9	141213431	199681697	1.414	18.3759
chr10	135534747	189038014	1.3948	18.2399
chr11	135006516	320598095	2.3747	26.9841
chr12	133851895	289760567	2.1648	26.5997
chr13	115169878	103431067	0.8981	15.5641
chr14	107349540	154232772	1.4367	17.9309
chr15	102531392	79847028	0.7788	11.6526
chr16	90354753	104860317	1.1605	14.7936
chr17	81195210	168030099	2.0695	22.6741
chr18	78077248	80570997	1.0319	15.3391
chr19	59128983	184669123	3.1232	39.1184
chr20	63025520	261300539	4.1459	46.1779
chr21	48129895	33028028	0.6862	10.8266
chr22	51304566	59577911	1.1613	15.2537
chrMT	16571	353888	21.3559	25.7376
chrX	155270560	102464512	0.6599	11.0386

chrY	59373566	9259412	0.156	3.2653

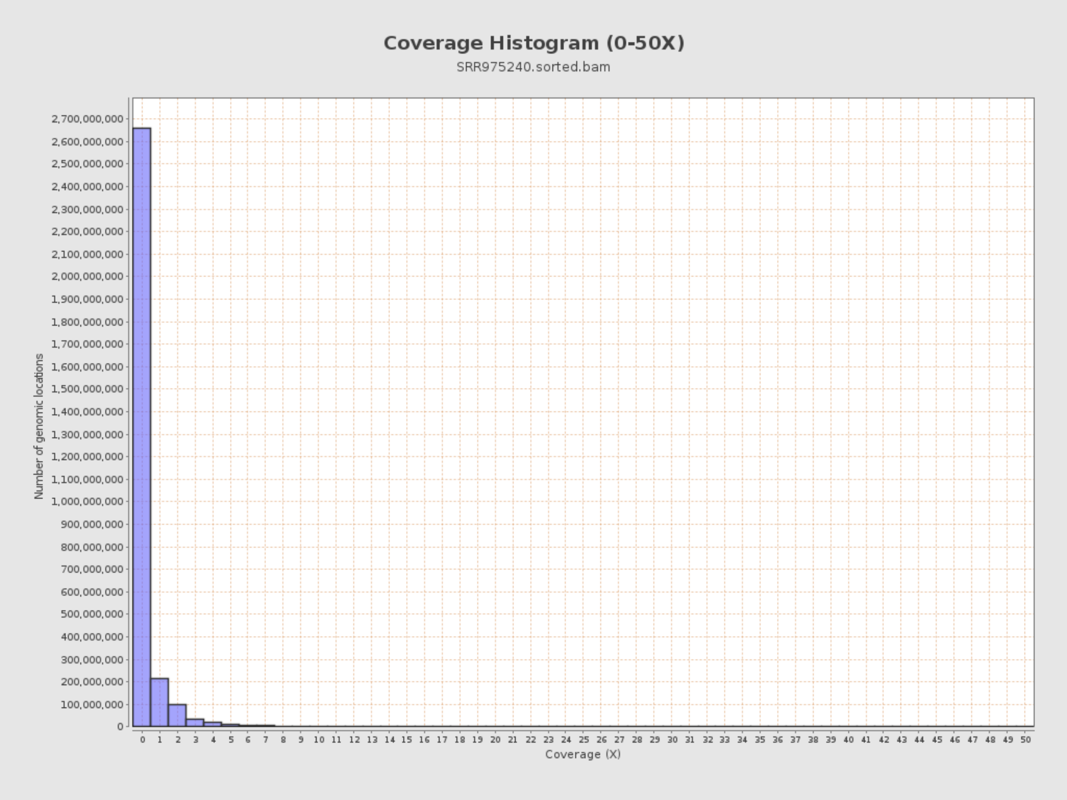
3. Results : Coverage across reference



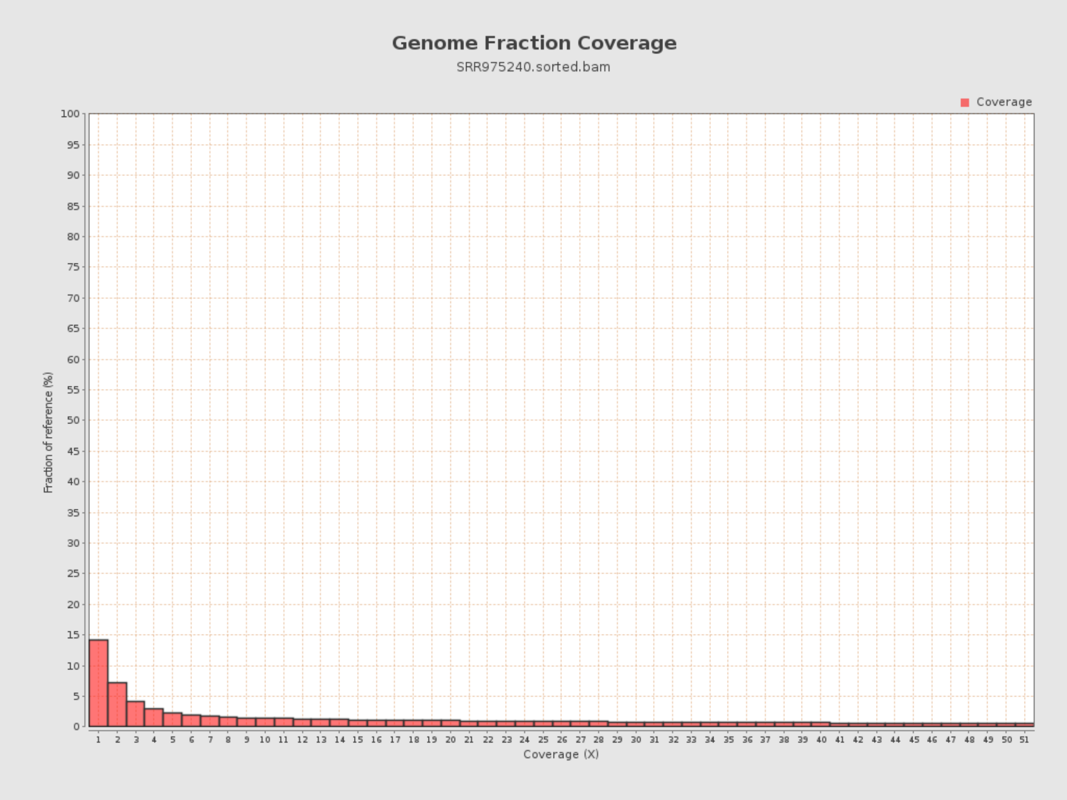
4. Results : Coverage Histogram



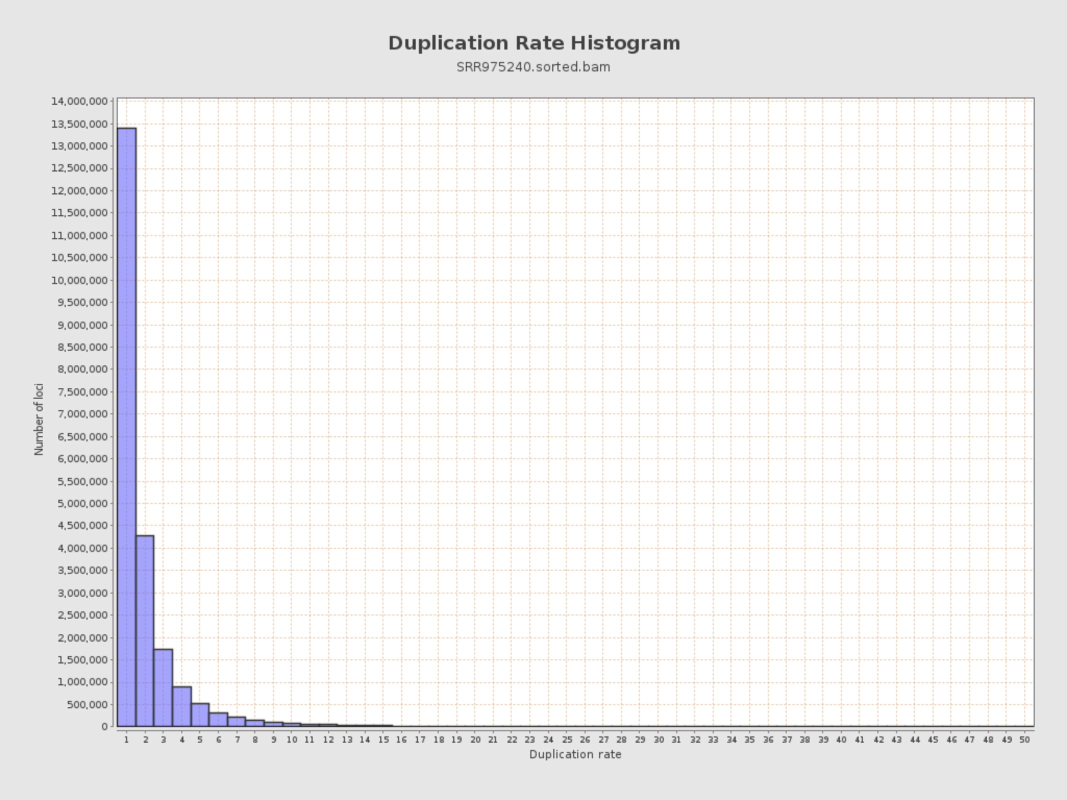
5. Results : Coverage Histogram (0-50X)



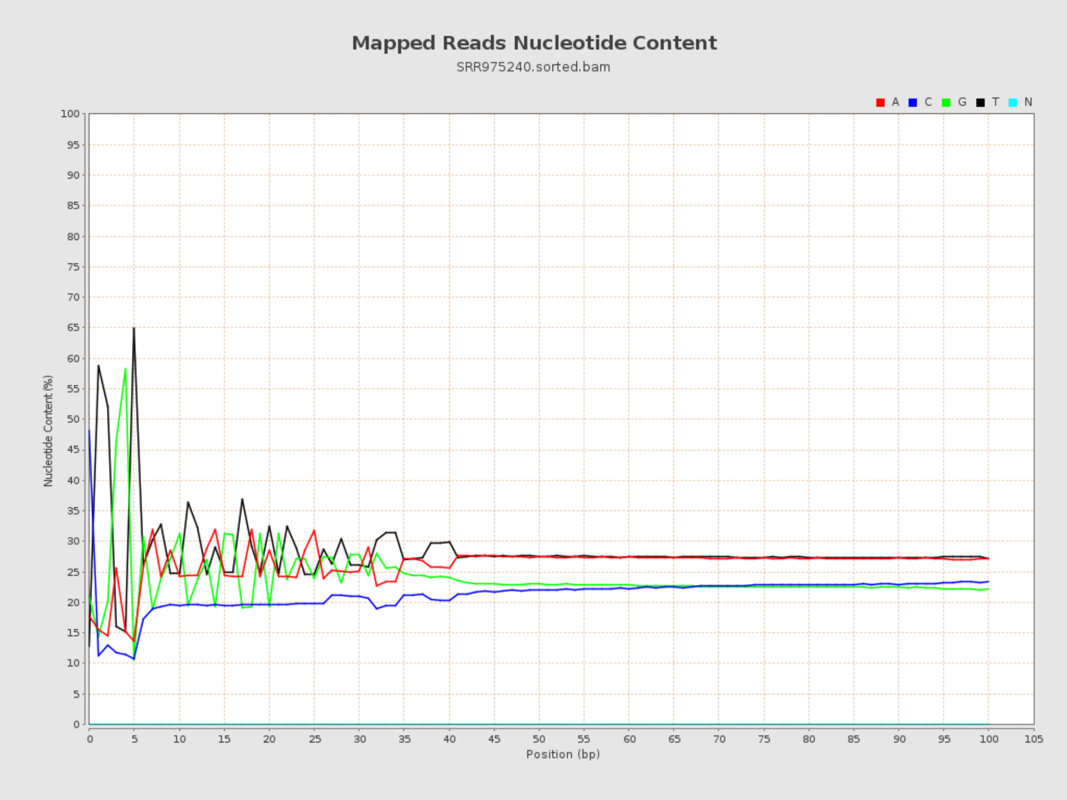
6. Results : Genome Fraction Coverage



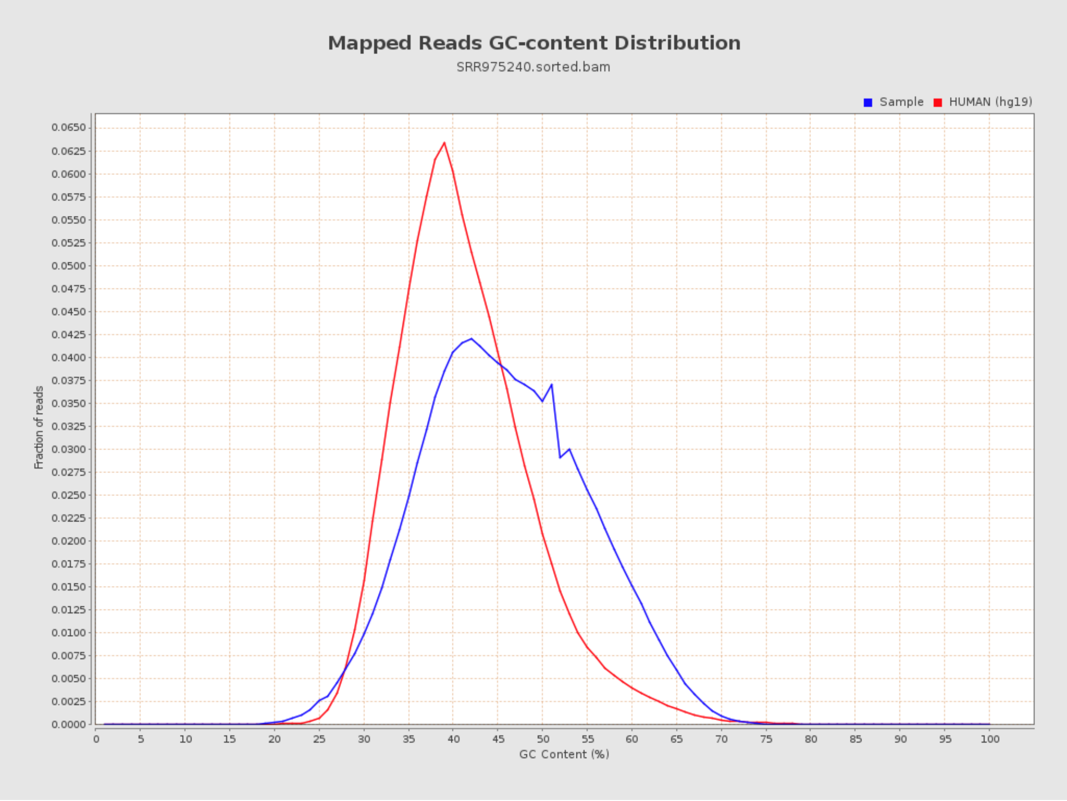
7. Results : Duplication Rate Histogram



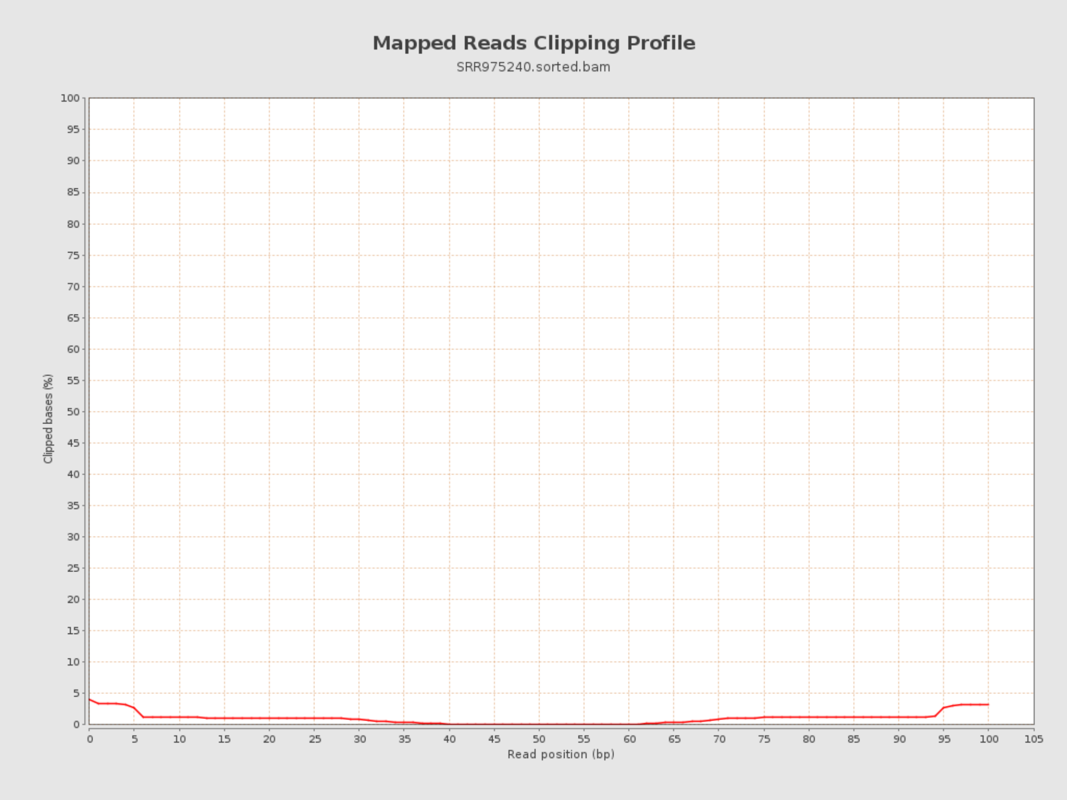
8. Results : Mapped Reads Nucleotide Content



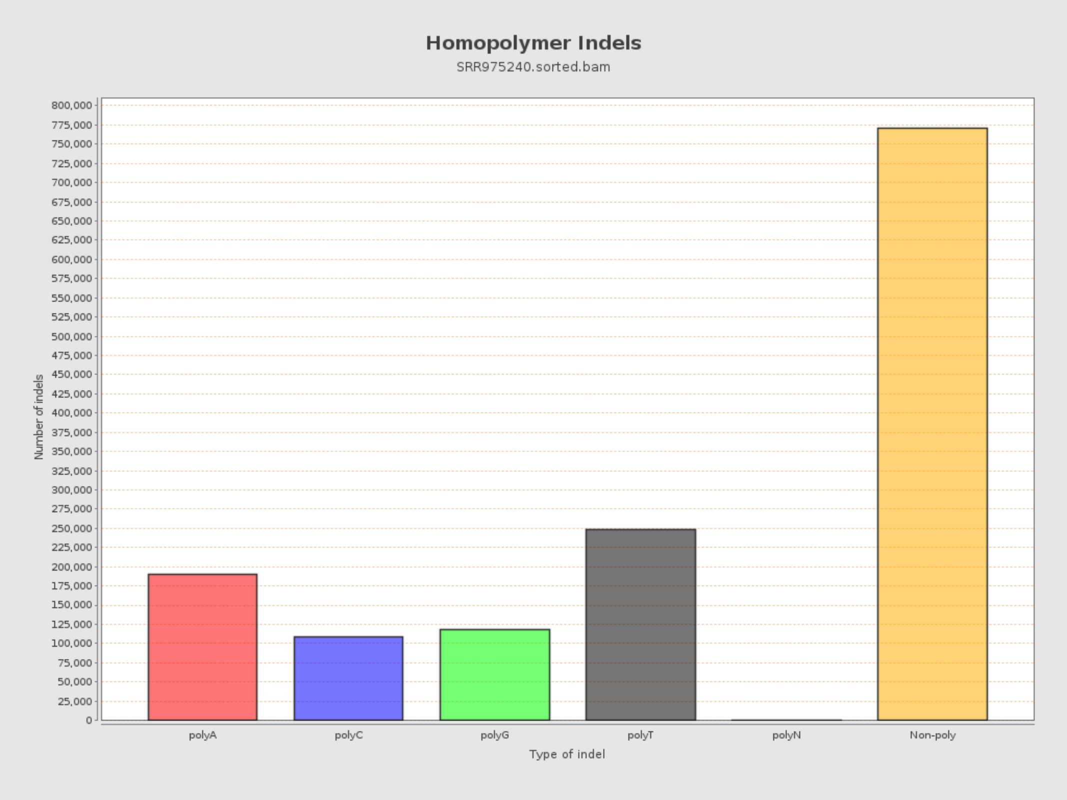
9. Results : Mapped Reads GC-content Distribution



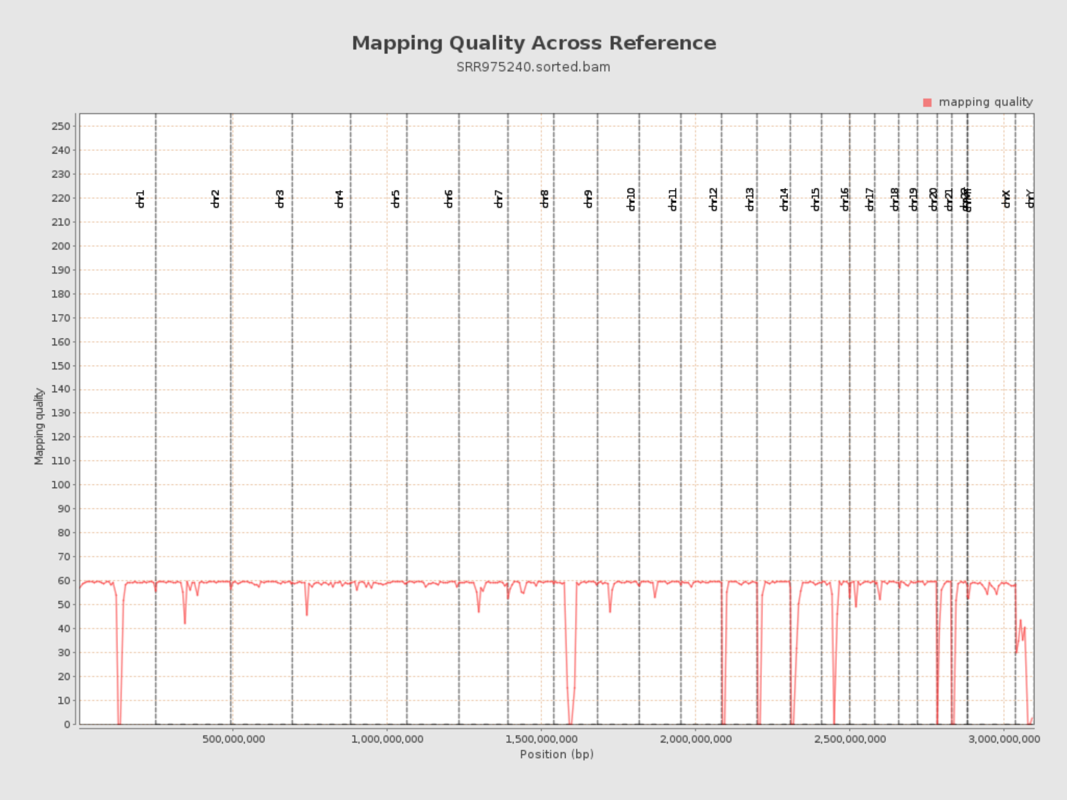
10. Results : Mapped Reads Clipping Profile



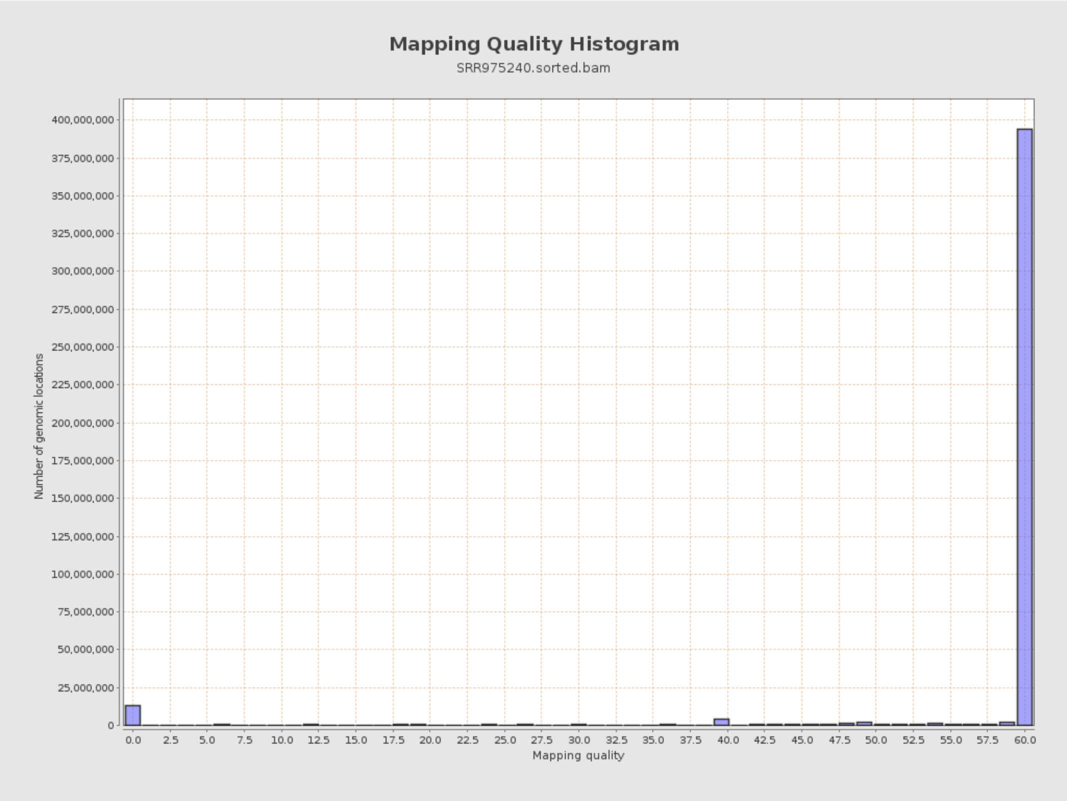
11. Results : Homopolymer Indels



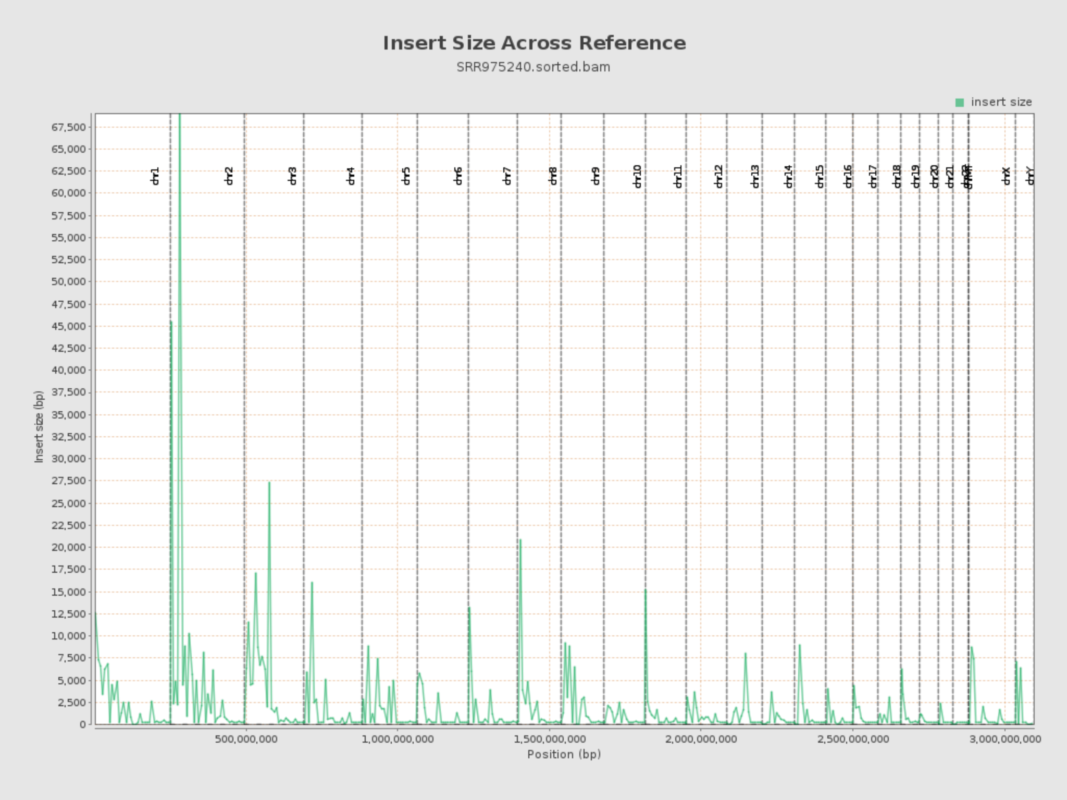
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram