Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 13:15:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975242.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_SRR975242 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975242_1.fastq.gz SRR975242_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 13:15:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975242.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	50,026,366
Mapped reads	49,962,959 / 99.87%
Unmapped reads	63,407 / 0.13%
Mapped paired reads	49,962,959 / 99.87%
Mapped reads, first in pair	24,985,054 / 49.94%
Mapped reads, second in pair	24,977,905 / 49.93%
Mapped reads, both in pair	49,925,910 / 99.8%
Mapped reads, singletons	37,049 / 0.07%
Secondary alignments	0
Supplementary alignments	128,500 / 0.26%
Read min/max/mean length	30 / 101 / 101.1
Duplicated reads (estimated)	21,351,556 / 42.68%
Duplication rate	40.94%
Clipped reads	25,168,005 / 50.31%

2.2. ACGT Content

Number/percentage of A's	1,282,679,713 / 26.22%
Number/percentage of C's	1,168,382,613 / 23.88%
Number/percentage of T's	1,296,929,062 / 26.51%
Number/percentage of G's	1,144,667,913 / 23.39%
Number/percentage of N's	138,105 / 0%

GC Percentage	47.27%

2.3. Coverage

Mean	1.5807
Standard Deviation	12.2417

2.4. Mapping Quality

Mean Mapping Quality	56.37

2.5. Insert size

Mean	151,995.19
Standard Deviation	3,857,291.19
P25/Median/P75	191 / 232 / 279

2.6. Mismatches and indels

General error rate	0.37%
Mismatches	17,542,650
Insertions	375,683
Mapped reads with at least one insertion	0.74%
Deletions	274,750
Mapped reads with at least one deletion	0.54%
Homopolymer indels	33.88%

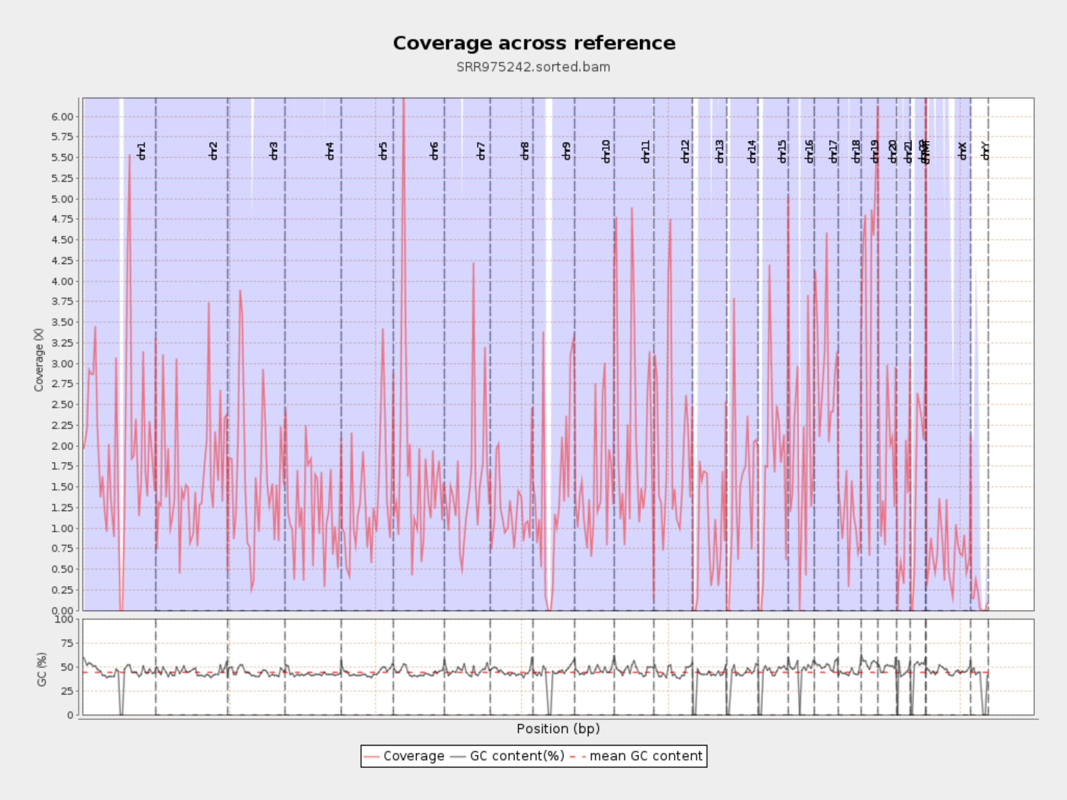
2.7. Chromosome stats

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

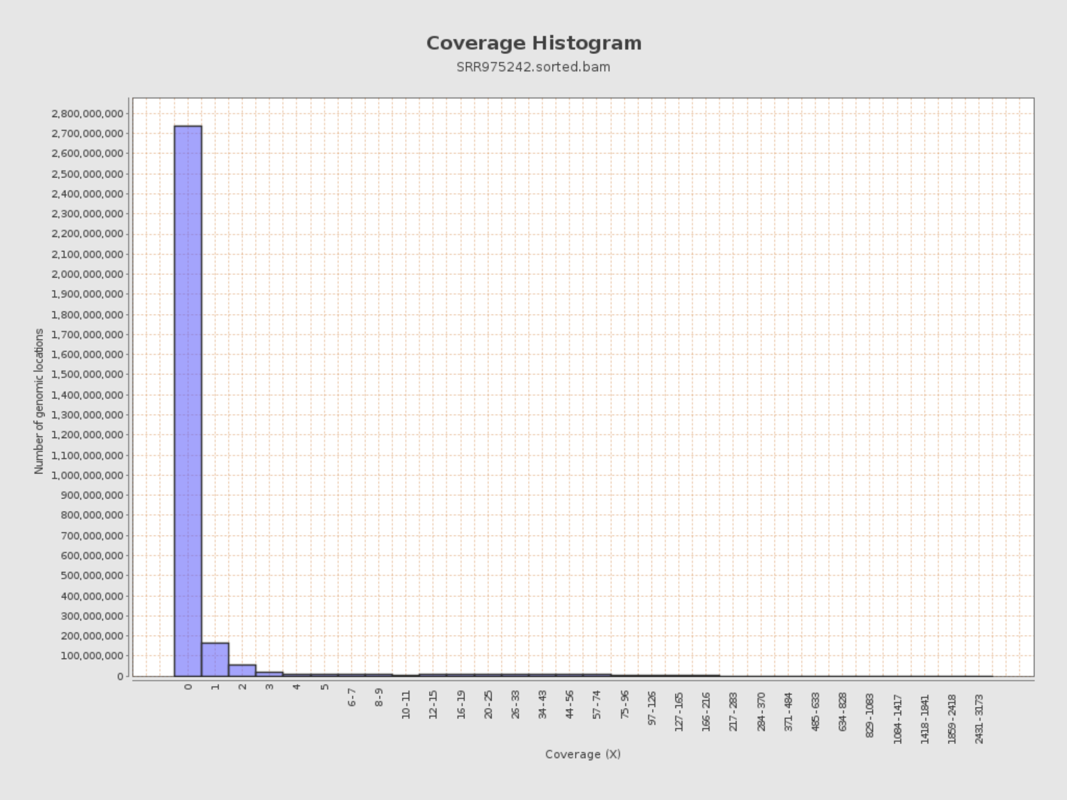
		bases	coverage	deviation
chr1	249250621	500197074	2.0068	14.2524
chr2	243199373	394270203	1.6212	12.3934
chr3	198022430	314193805	1.5867	12.1598
chr4	191154276	231668268	1.2119	11.1182
chr5	180915260	248985394	1.3763	11.3016
chr6	171115067	288472588	1.6858	13.4351
chr7	159138663	244777164	1.5381	12.6415
chr8	146364022	179941040	1.2294	10.3009
chr9	141213431	194763681	1.3792	11.1971
chr10	135534747	204134798	1.5061	11.772
chr11	135006516	293553161	2.1744	15.1593
chr12	133851895	270954102	2.0243	13.9489
chr13	115169878	106493957	0.9247	9.5583
chr14	107349540	160878752	1.4986	11.9499
chr15	102531392	170991276	1.6677	12.6404
chr16	90354753	168944606	1.8698	12.5862
chr17	81195210	241568328	2.9752	16.3577
chr18	78077248	84744759	1.0854	9.913
chr19	59128983	228909813	3.8714	18.0415
chr20	63025520	112089668	1.7785	12.5909
chr21	48129895	51731953	1.0748	10.5552
chr22	51304566	83771007	1.6328	11.0411
chrMT	16571	221611	13.3734	23.5659
chrX	155270560	109717202	0.7066	6.4586

chrY	59373566	7438718	0.1253	2.0074

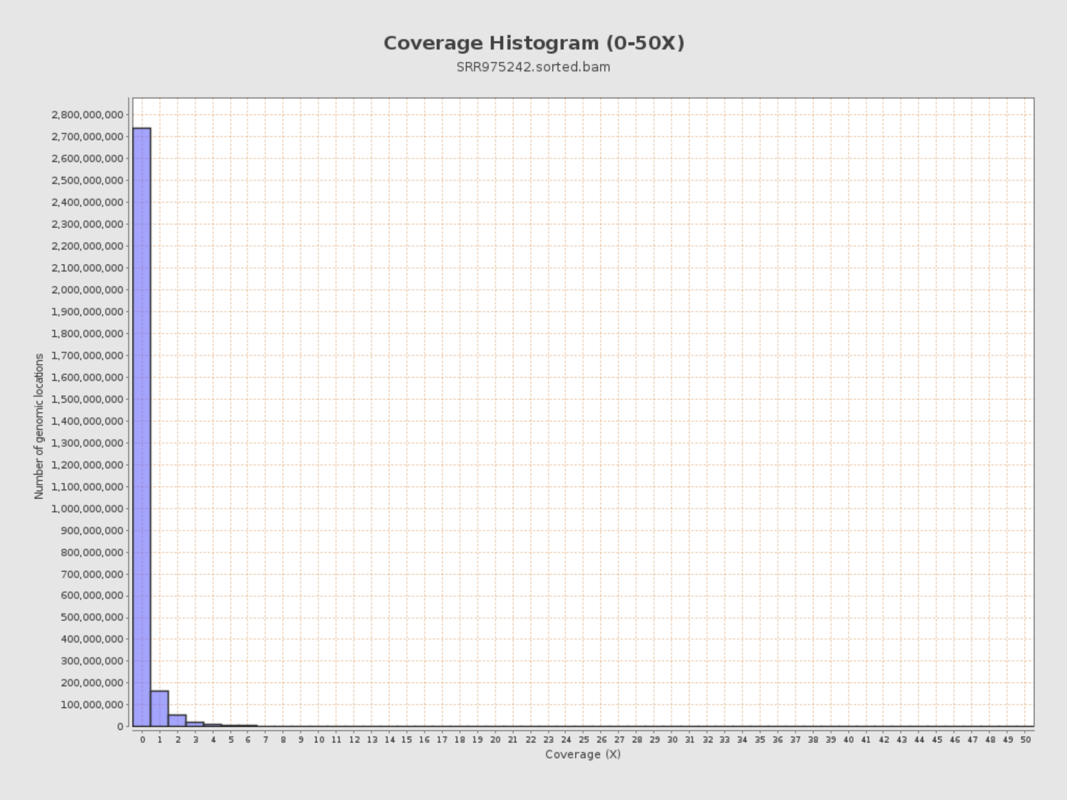
3. Results : Coverage across reference



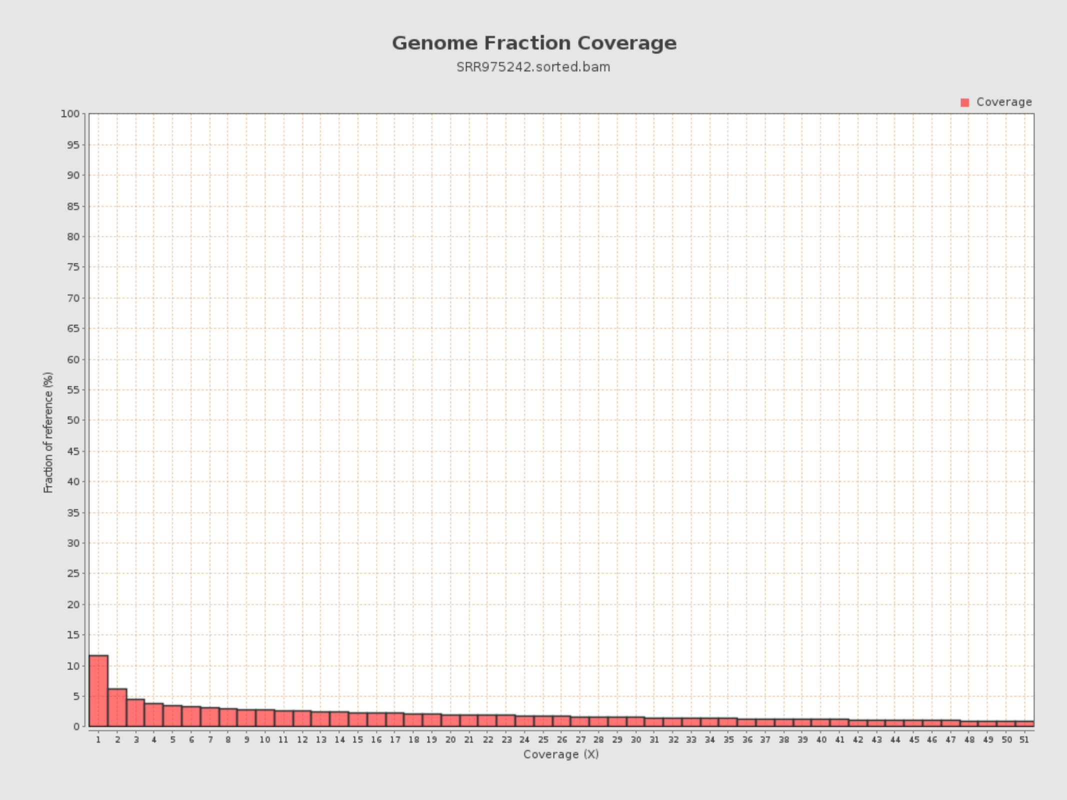
4. Results : Coverage Histogram



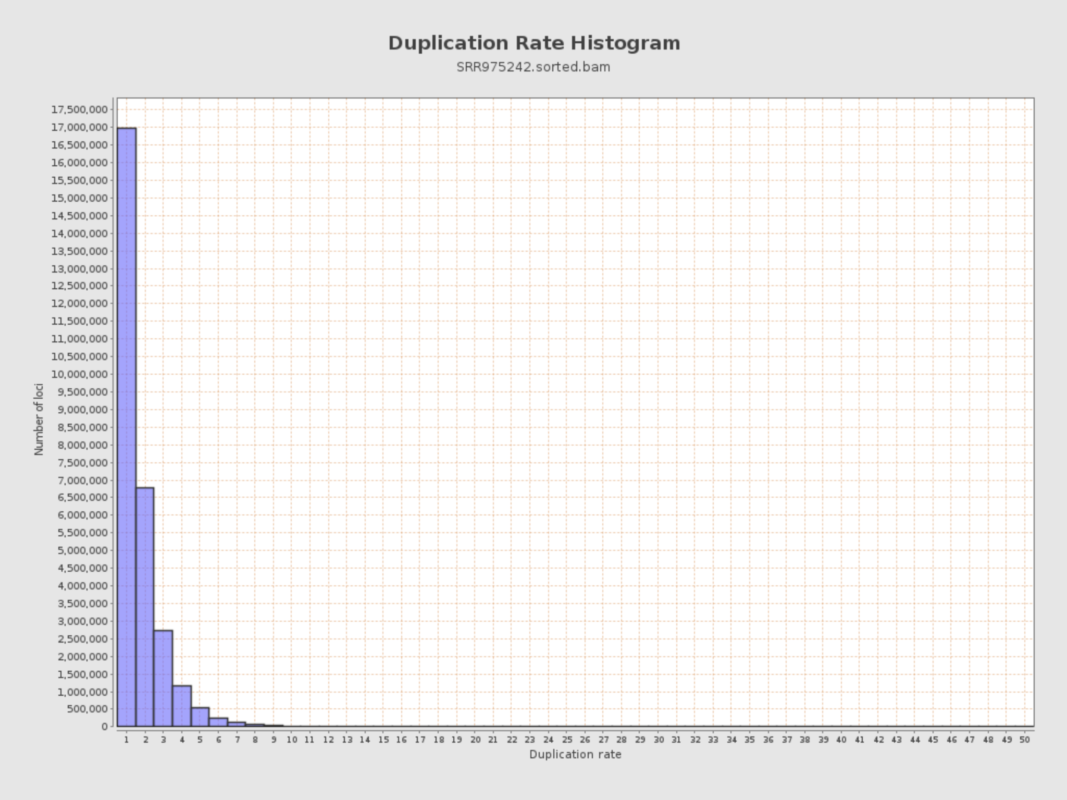
5. Results : Coverage Histogram (0-50X)



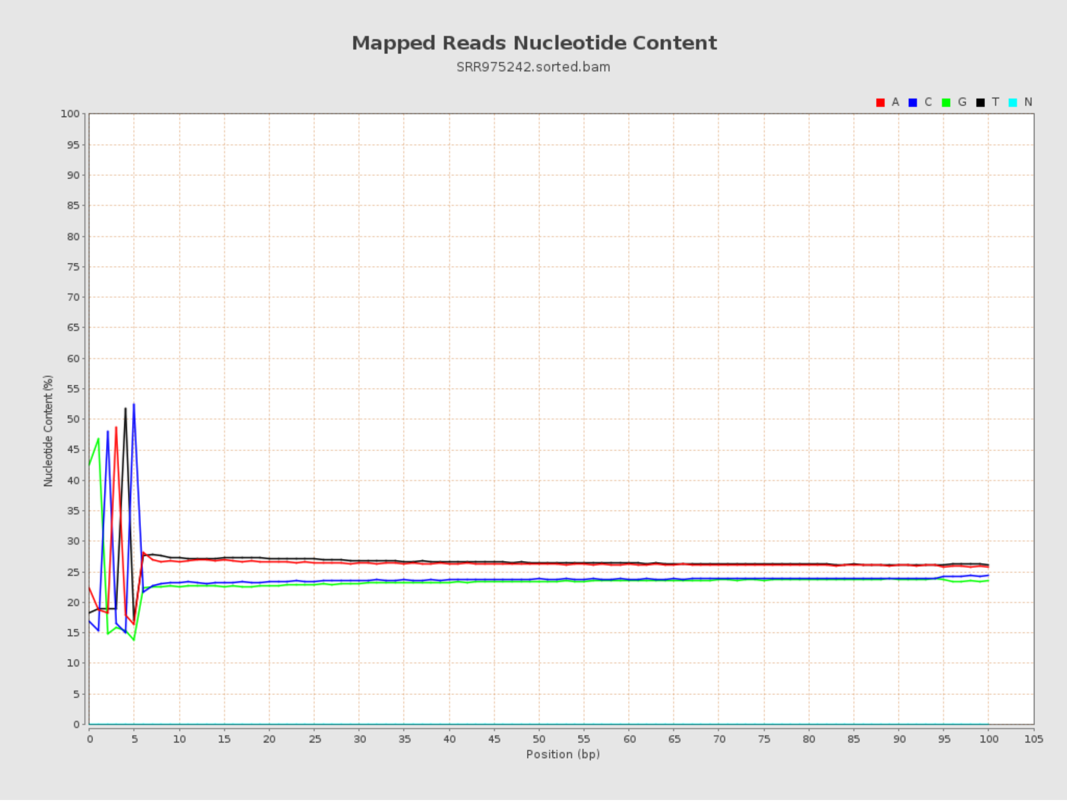
6. Results : Genome Fraction Coverage



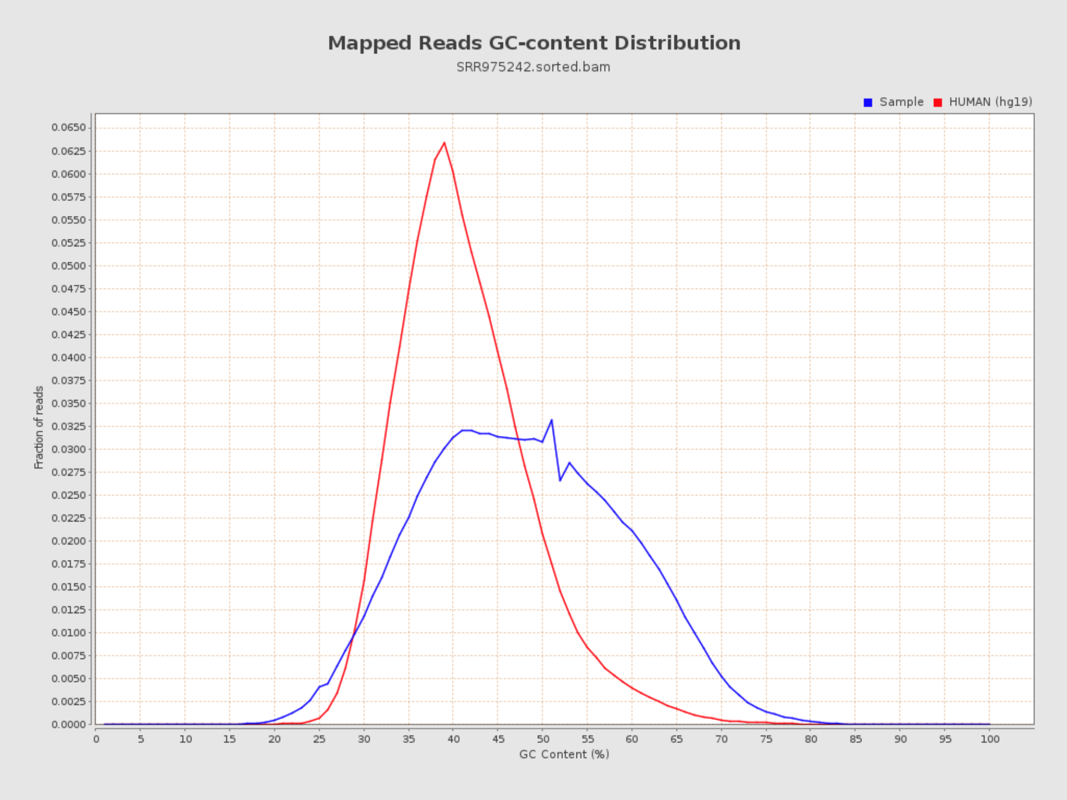
7. Results : Duplication Rate Histogram



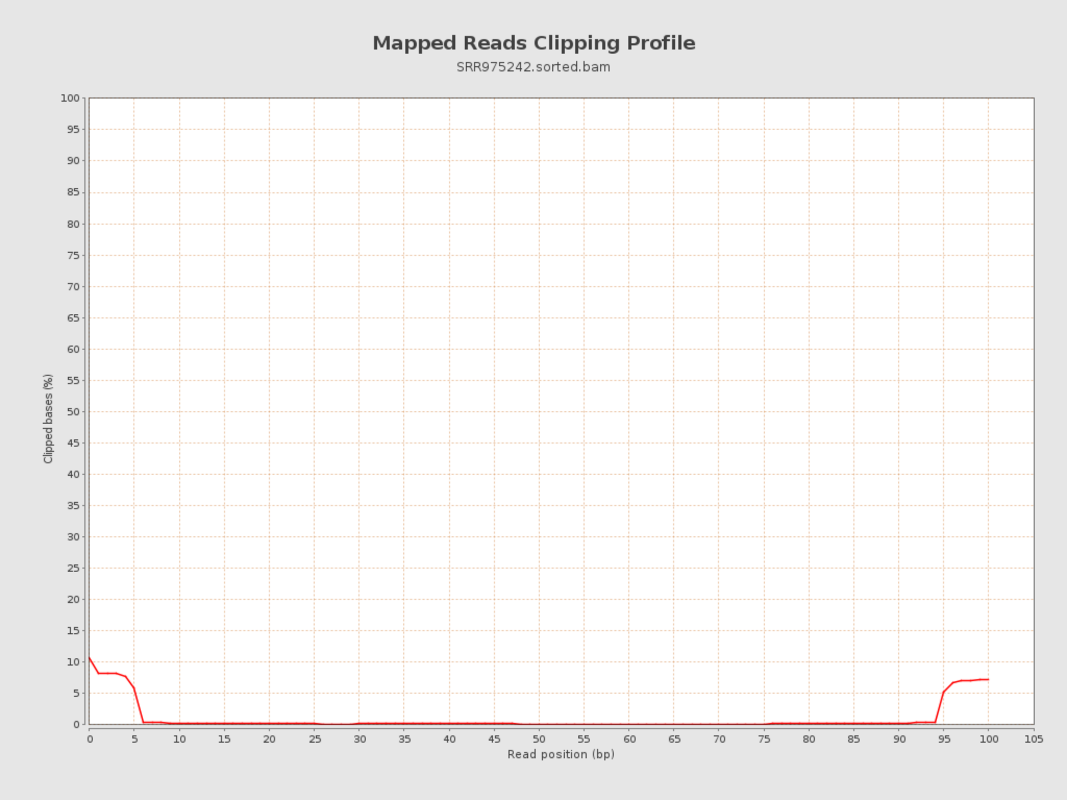
8. Results : Mapped Reads Nucleotide Content



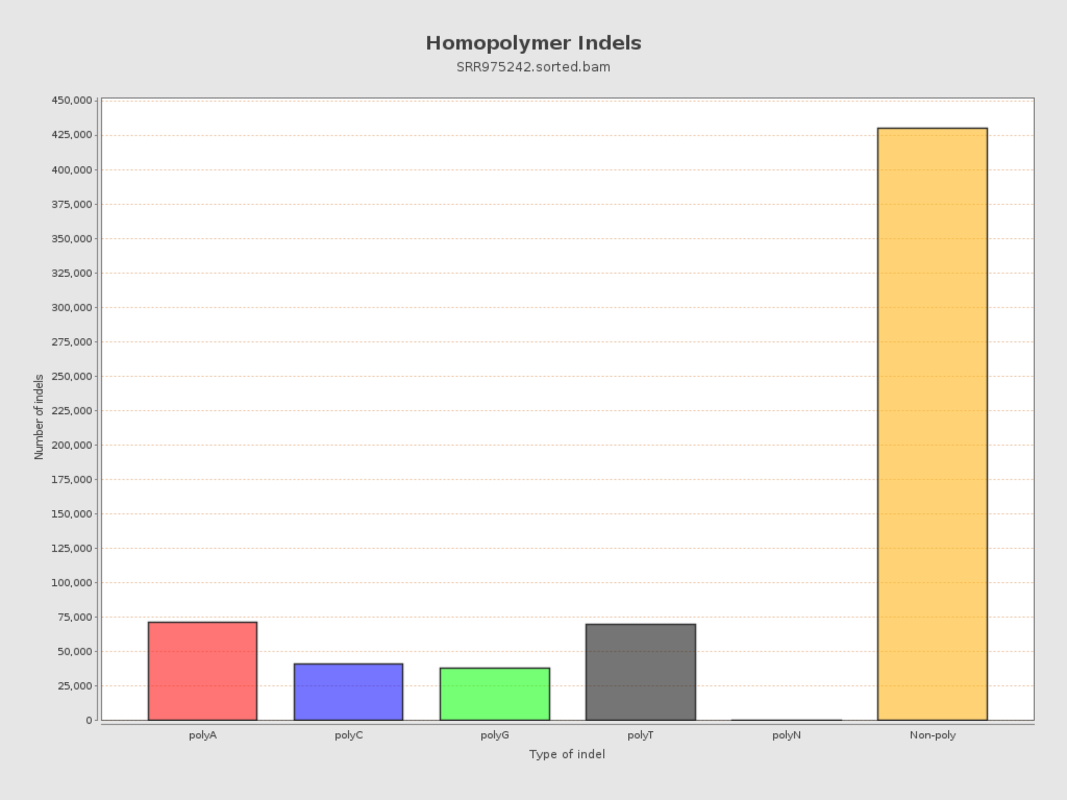
9. Results : Mapped Reads GC-content Distribution



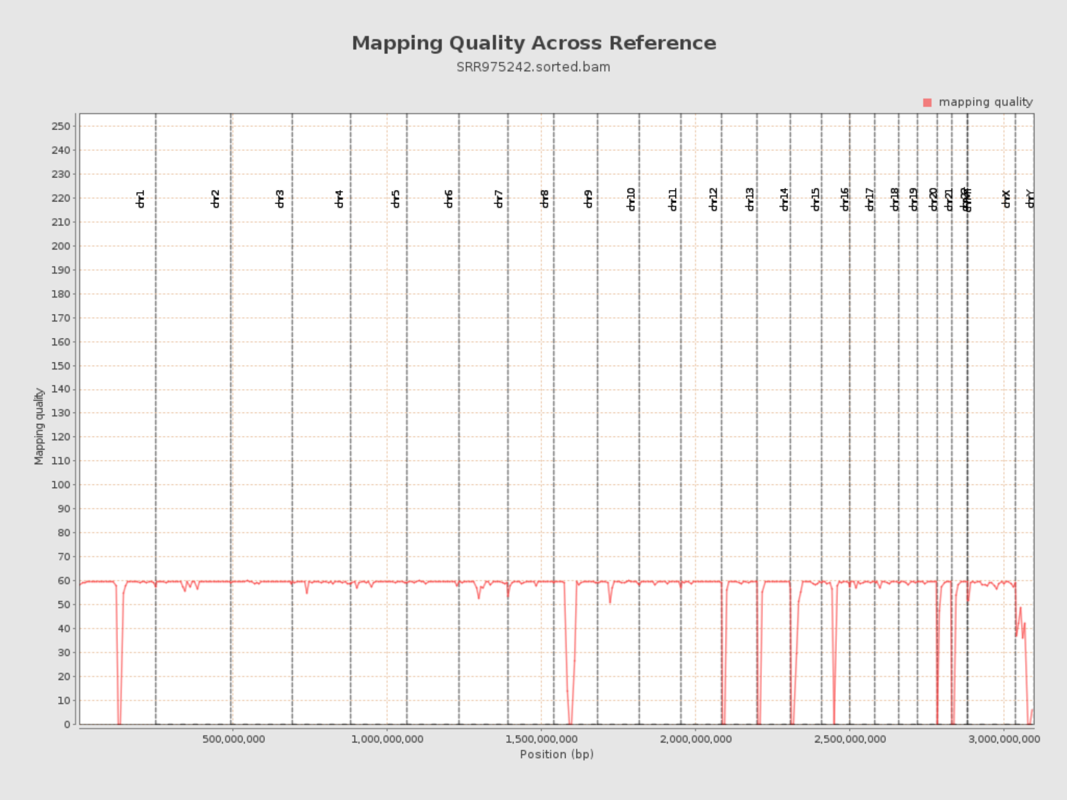
10. Results : Mapped Reads Clipping Profile



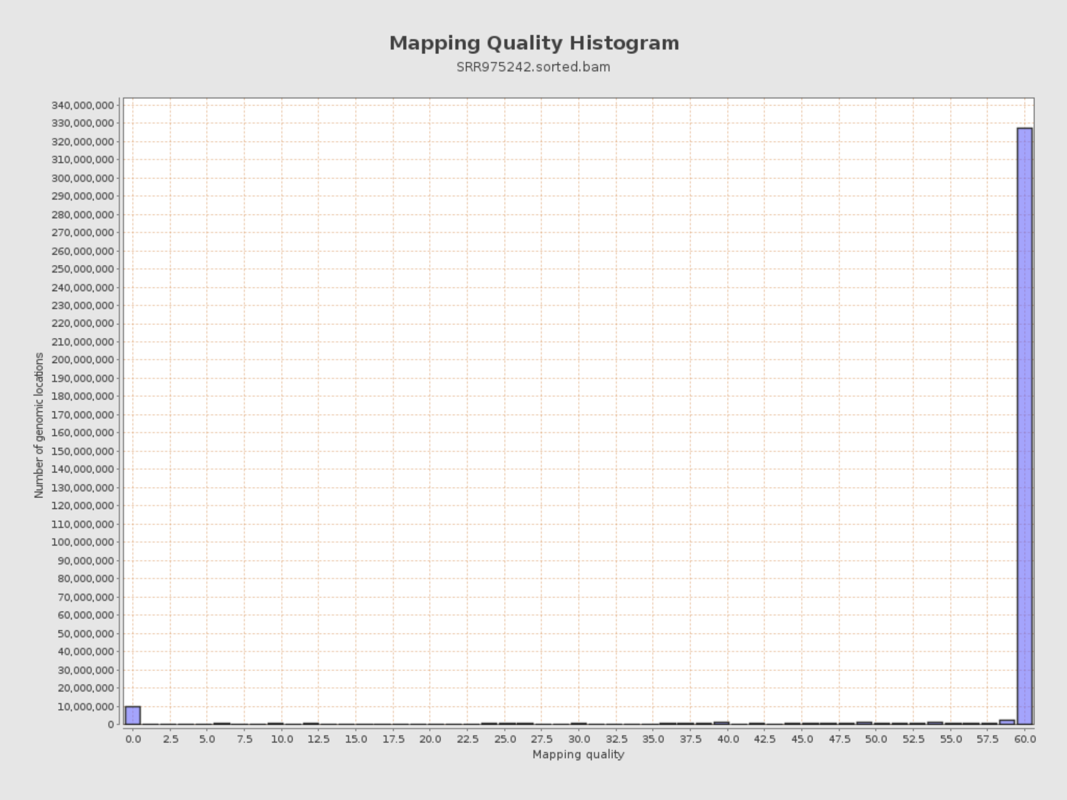
11. Results : Homopolymer Indels



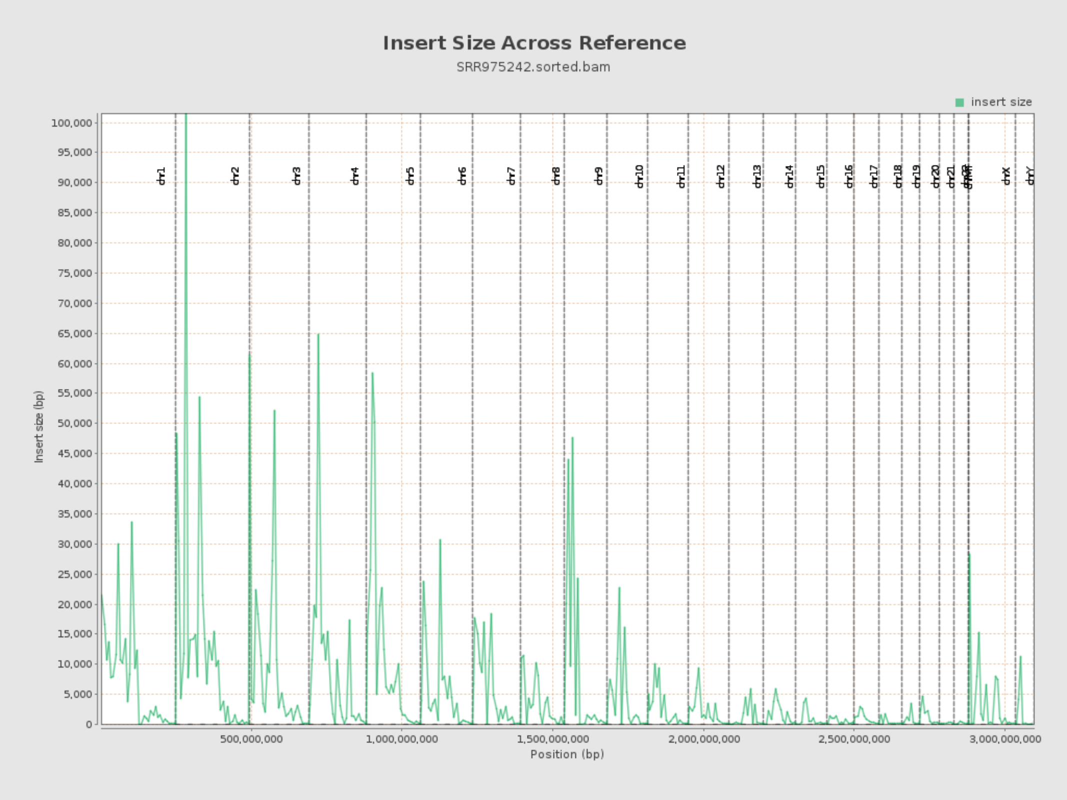
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram