Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 05:18:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975236.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_SRR975236 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975236_1.fastq.gz SRR975236_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 05:17:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975236.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	46,252,408
Mapped reads	46,160,775 / 99.8%
Unmapped reads	91,633 / 0.2%
Mapped paired reads	46,160,775 / 99.8%
Mapped reads, first in pair	23,084,630 / 49.91%
Mapped reads, second in pair	23,076,145 / 49.89%
Mapped reads, both in pair	46,096,502 / 99.66%
Mapped reads, singletons	64,273 / 0.14%
Secondary alignments	0
Supplementary alignments	174,807 / 0.38%
Read min/max/mean length	30 / 101 / 101.15
Duplicated reads (estimated)	30,382,245 / 65.69%
Duplication rate	45.59%
Clipped reads	27,472,743 / 59.4%

2.2. ACGT Content

Number/percentage of A's	1,157,104,580 / 26.4%
Number/percentage of C's	1,008,296,691 / 23.01%
Number/percentage of T's	1,181,635,239 / 26.96%
Number/percentage of G's	1,035,123,900 / 23.62%
Number/percentage of N's	123,645 / 0%

GC Percentage	46.63%

2.3. Coverage

Mean	1.4162
Standard Deviation	23.3491

2.4. Mapping Quality

Mean Mapping Quality	56.1

2.5. Insert size

Mean	158,423.89
Standard Deviation	3,921,275.68
P25/Median/P75	192 / 236 / 286

2.6. Mismatches and indels

General error rate	0.74%
Mismatches	31,794,956
Insertions	447,280
Mapped reads with at least one insertion	0.95%
Deletions	1,198,796
Mapped reads with at least one deletion	2.55%
Homopolymer indels	48.03%

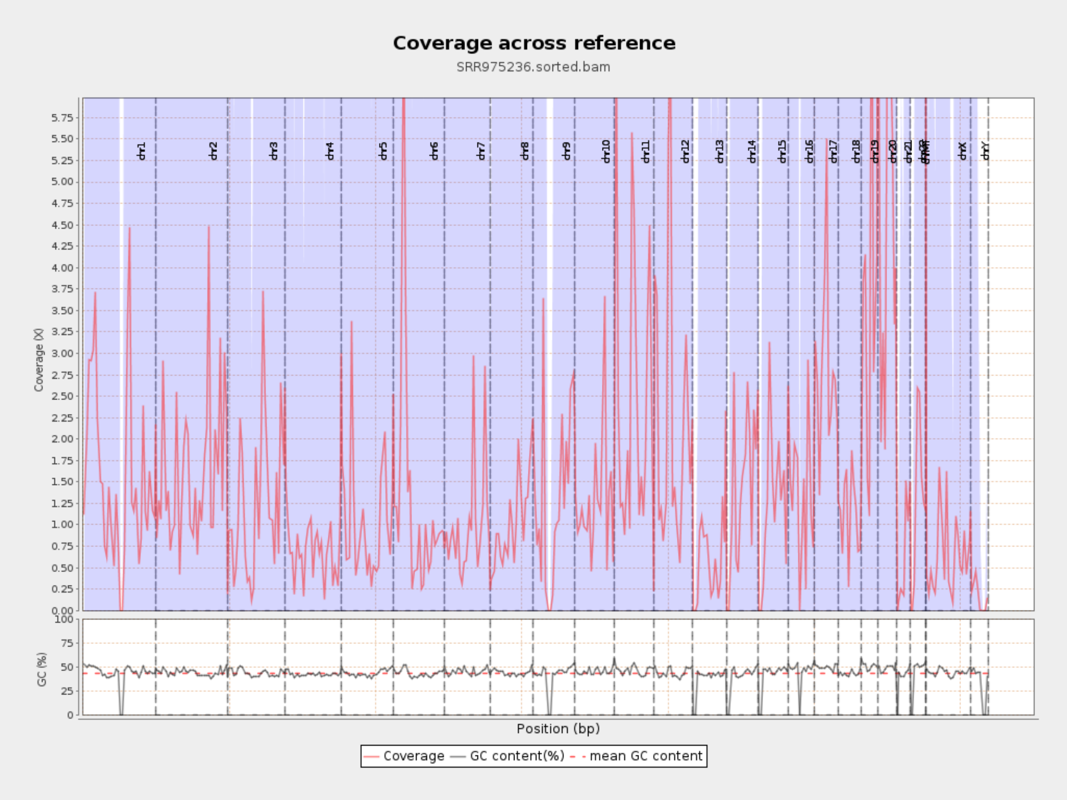
2.7. Chromosome stats

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

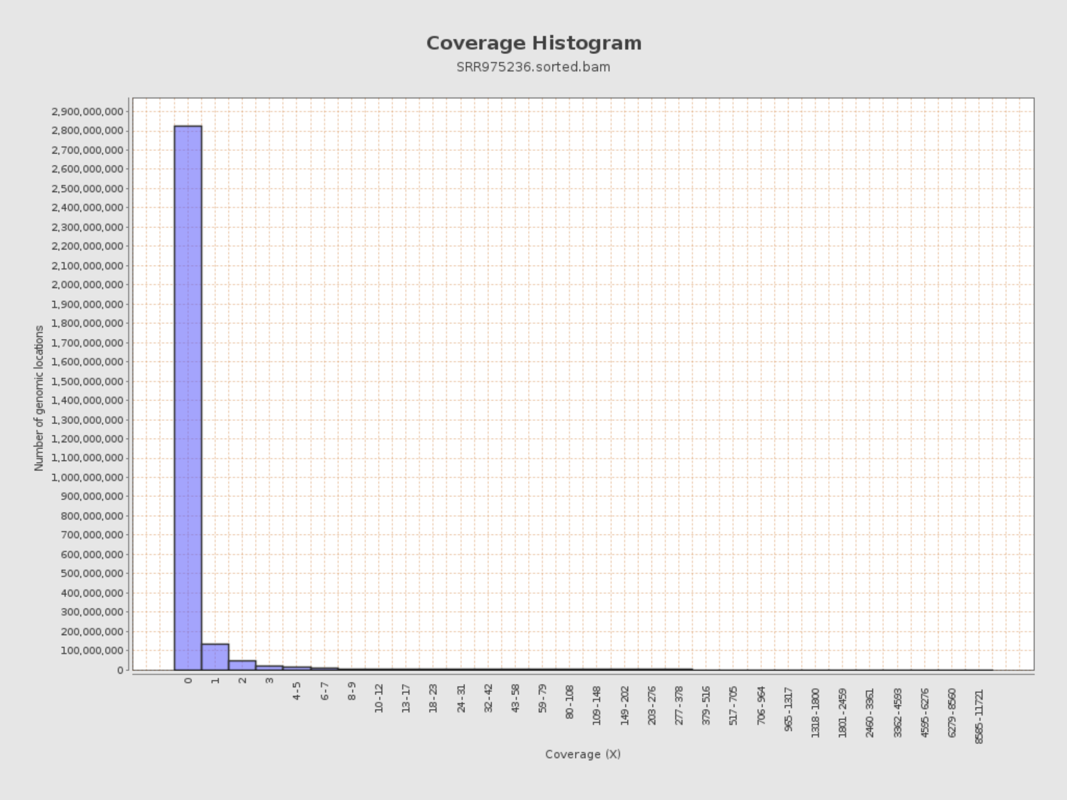
		bases	coverage	deviation
chr1	249250621	387728344	1.5556	22.4812
chr2	243199373	392622023	1.6144	23.4483
chr3	198022430	246426169	1.2444	20.0541
chr4	191154276	132328976	0.6923	13.3298
chr5	180915260	195279229	1.0794	18.4141
chr6	171115067	218780591	1.2786	22.2162
chr7	159138663	160531879	1.0088	19.4166
chr8	146364022	150234887	1.0264	17.5382
chr9	141213431	180148849	1.2757	20.664
chr10	135534747	179861787	1.3271	22.6941
chr11	135006516	341659946	2.5307	34.7992
chr12	133851895	308464238	2.3045	31.4156
chr13	115169878	66630128	0.5785	11.3946
chr14	107349540	151199333	1.4085	21.6354
chr15	102531392	121531590	1.1853	20.167
chr16	90354753	119640461	1.3241	19.8734
chr17	81195210	233277777	2.873	33.9816
chr18	78077248	89019581	1.1401	18.8901
chr19	59128983	227540580	3.8482	45.8643
chr20	63025520	273960773	4.3468	54.4846
chr21	48129895	31382906	0.652	12.7739
chr22	51304566	66408694	1.2944	19.3842
chrMT	16571	106705	6.4393	10.9114
chrX	155270560	98846929	0.6366	14.1662

chrY	59373566	10418422	0.1755	5.9348

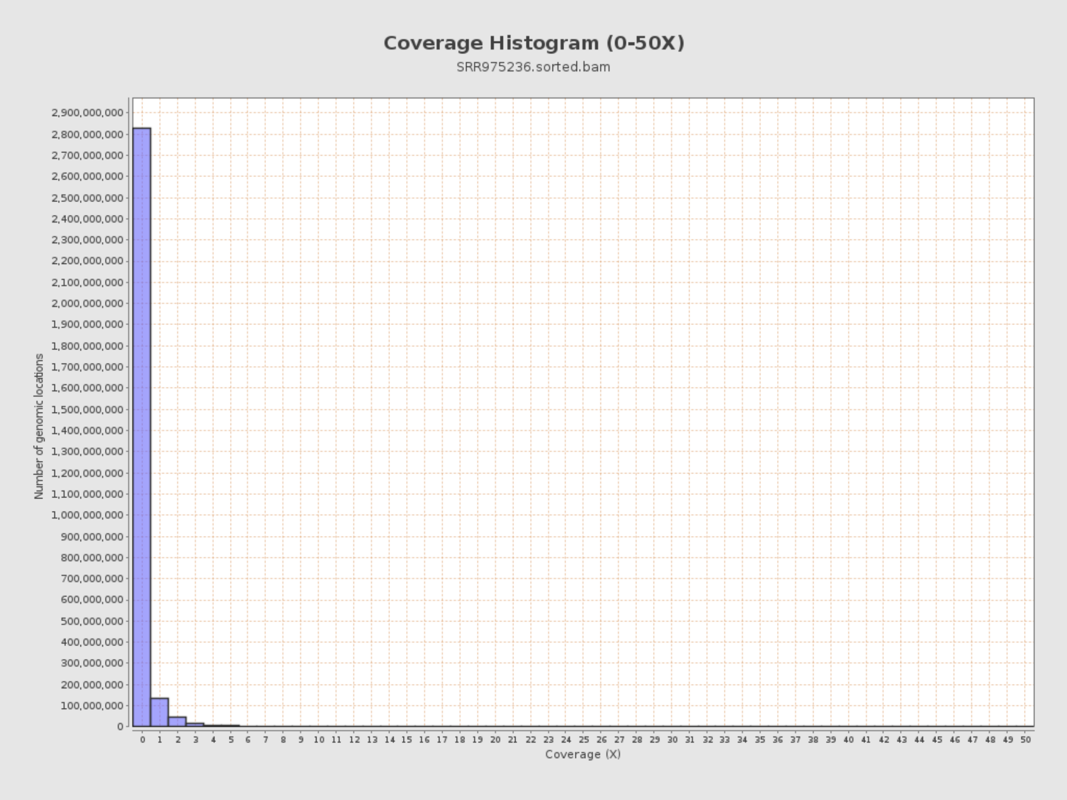
3. Results : Coverage across reference



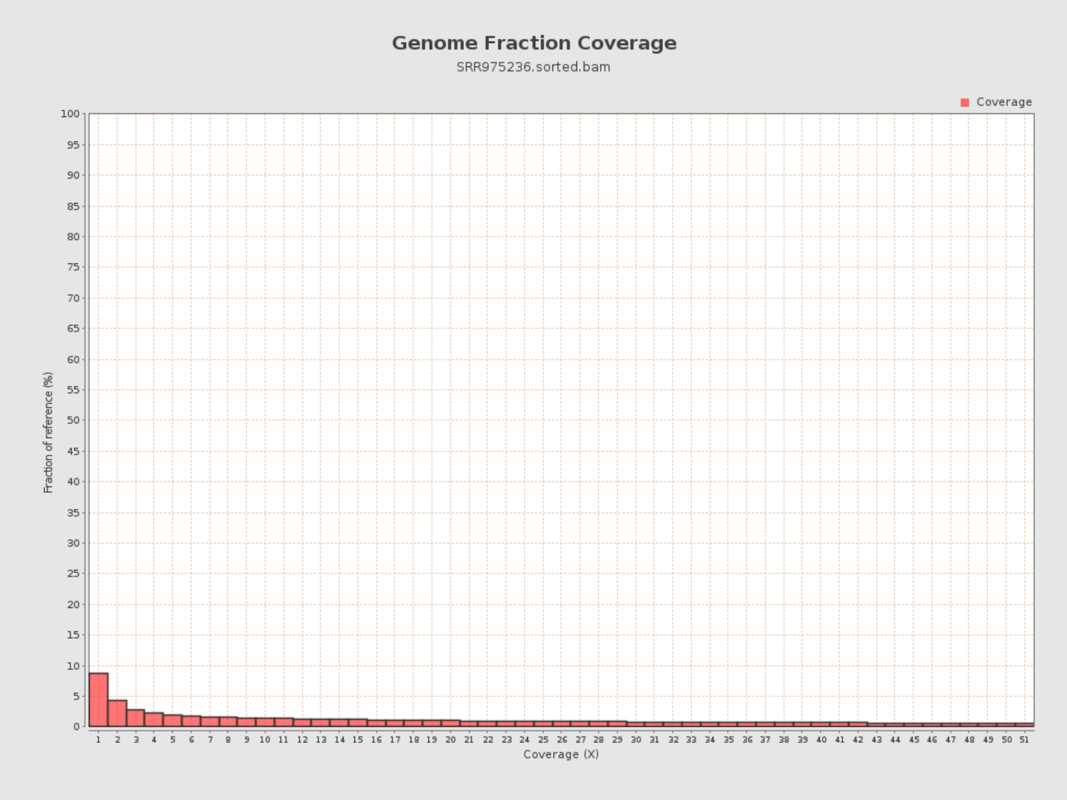
4. Results : Coverage Histogram



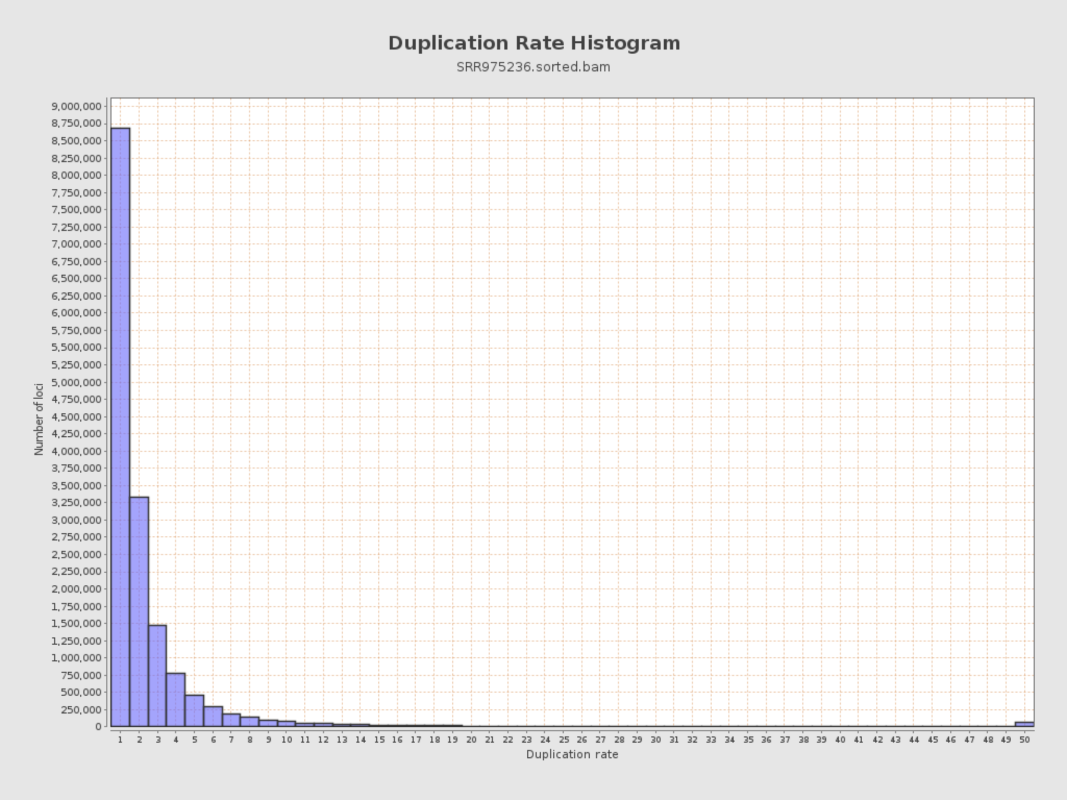
5. Results : Coverage Histogram (0-50X)



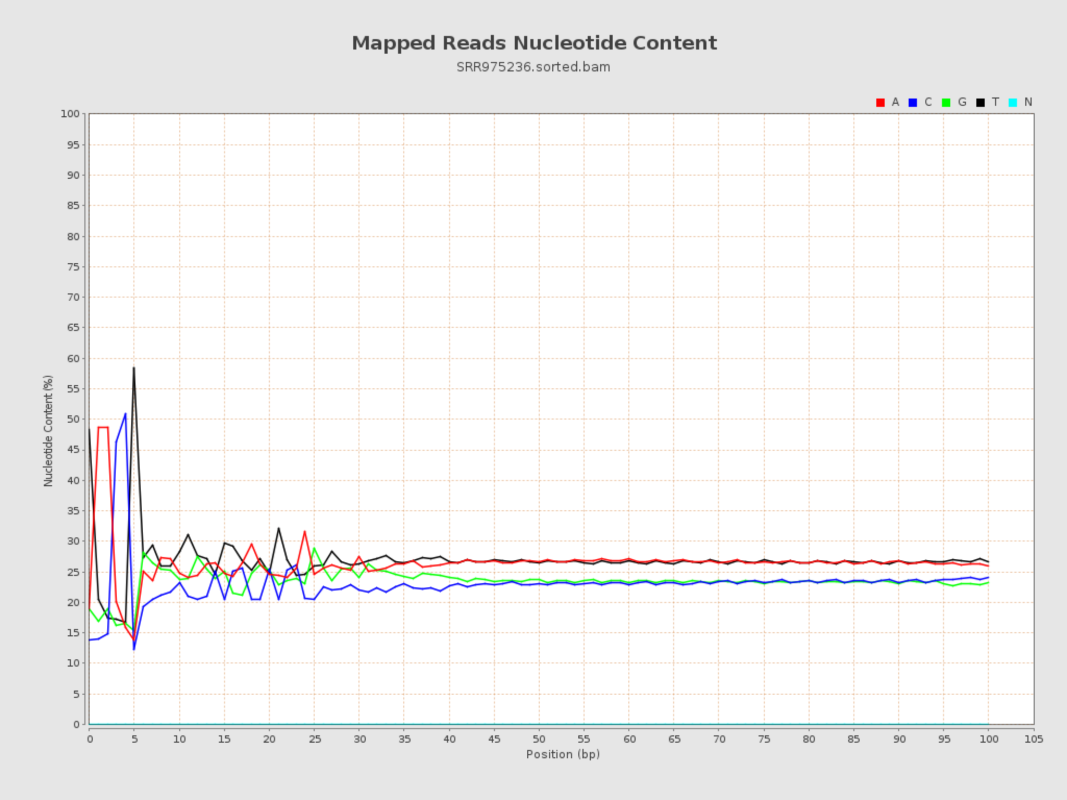
6. Results : Genome Fraction Coverage



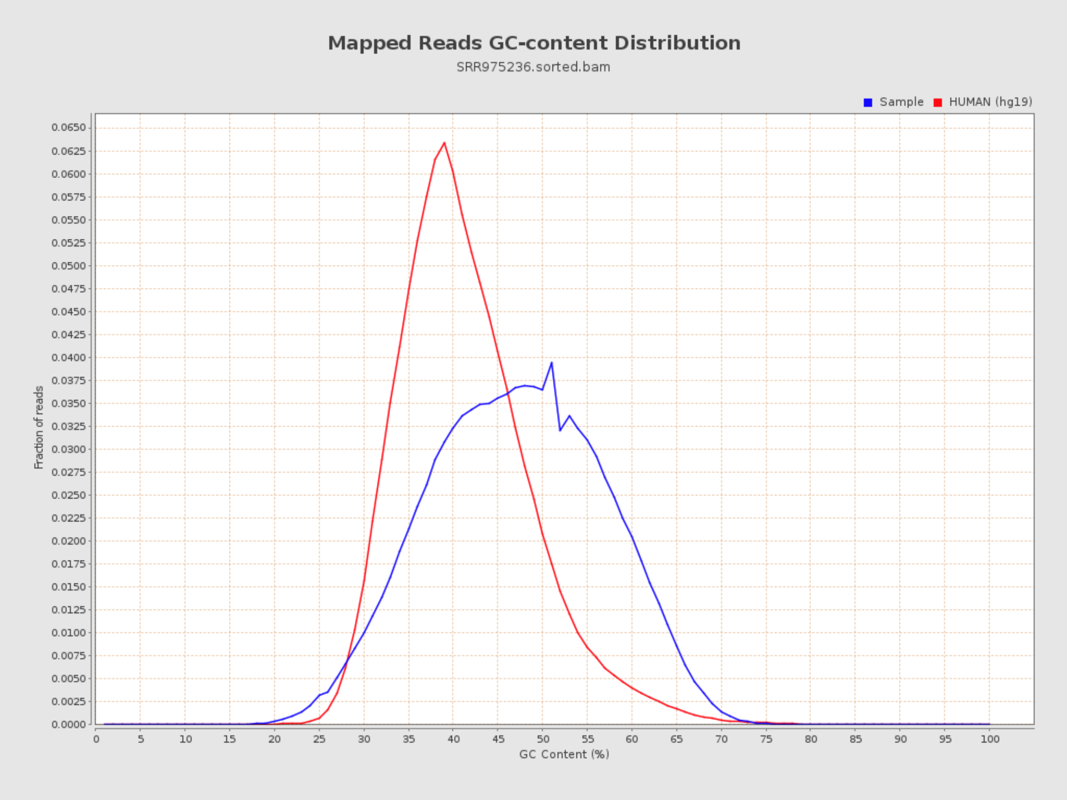
7. Results : Duplication Rate Histogram



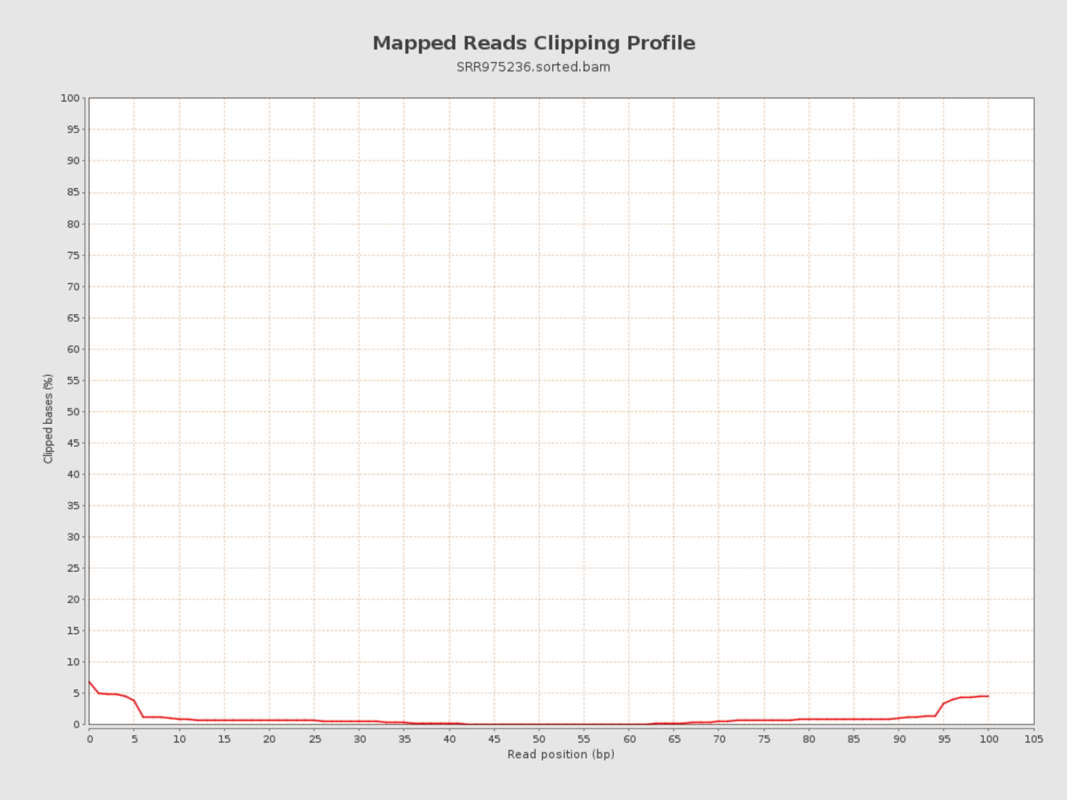
8. Results : Mapped Reads Nucleotide Content



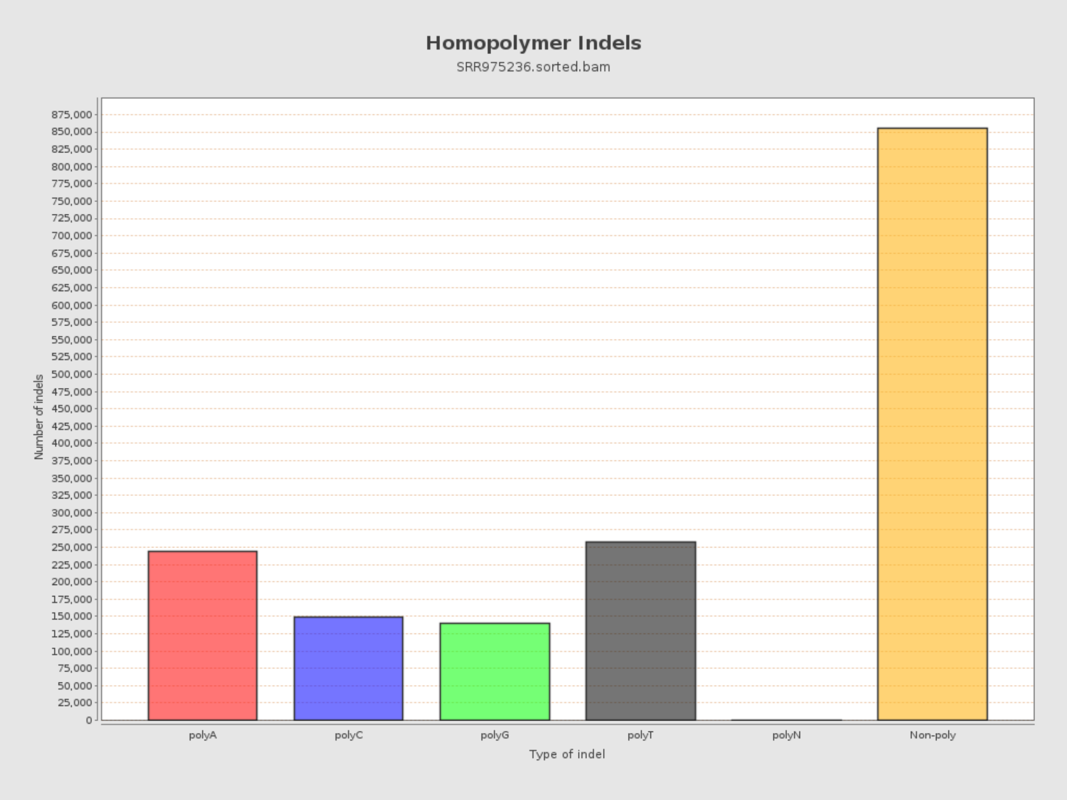
9. Results : Mapped Reads GC-content Distribution



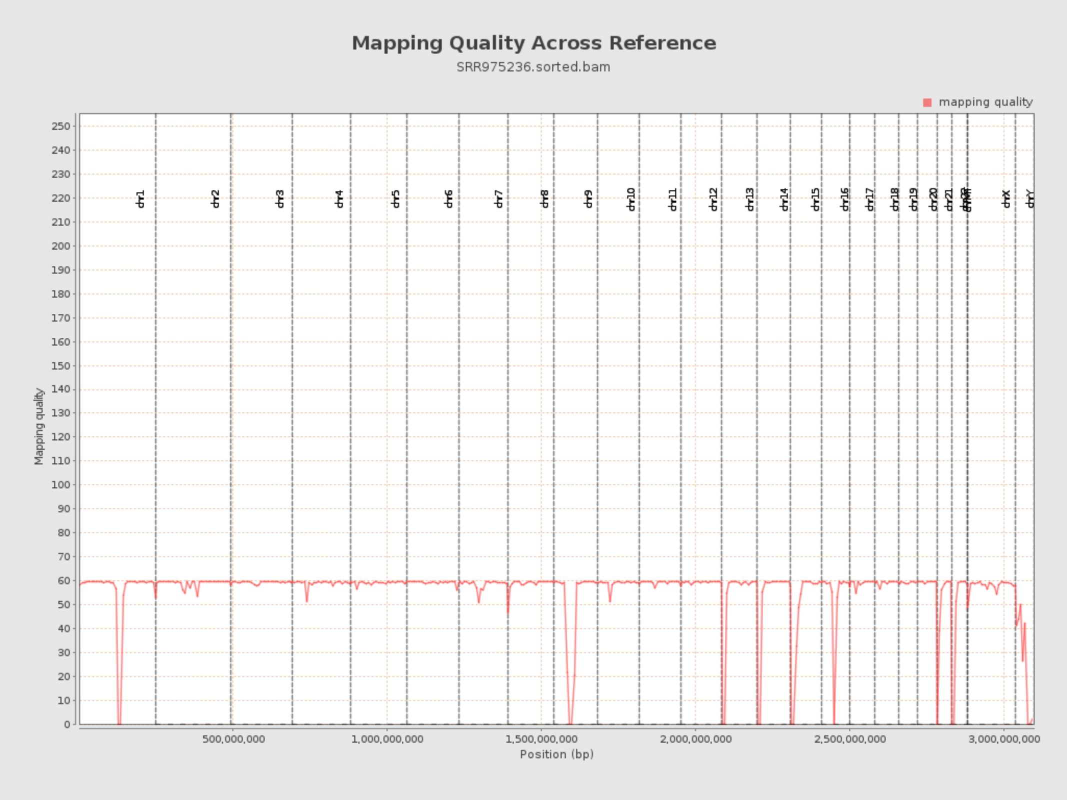
10. Results : Mapped Reads Clipping Profile



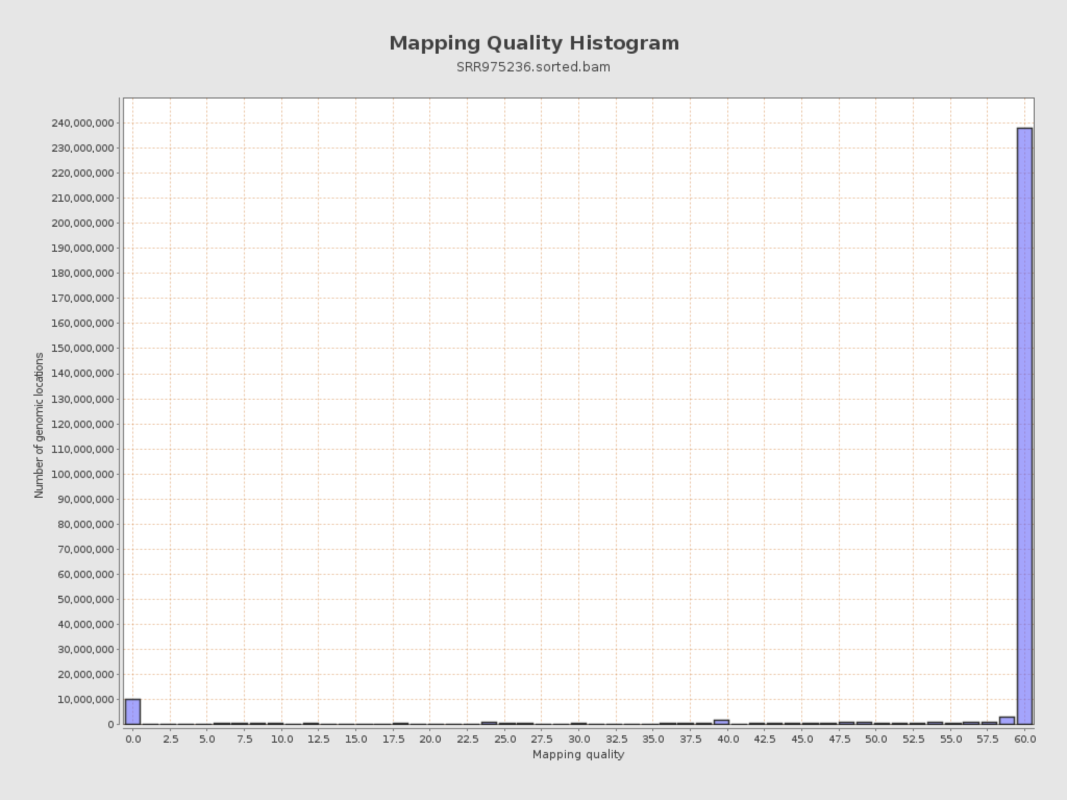
11. Results : Homopolymer Indels



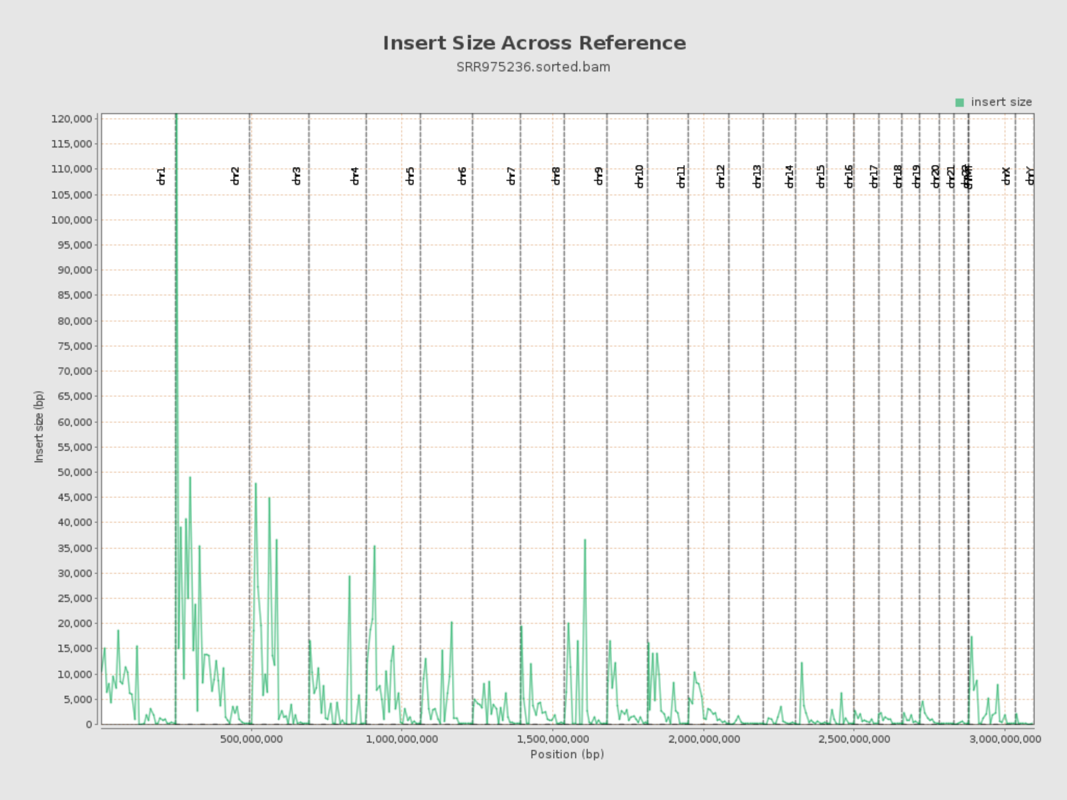
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram