Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 04:11:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975235.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_SRR975235 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975235_1.fastq.gz SRR975235_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 04:11:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975235.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,696,052
Mapped reads	3,658,966 / 99%
Unmapped reads	37,086 / 1%
Mapped paired reads	3,658,966 / 99%
Mapped reads, first in pair	1,828,622 / 49.48%
Mapped reads, second in pair	1,830,344 / 49.52%
Mapped reads, both in pair	3,645,860 / 98.64%
Mapped reads, singletons	13,106 / 0.35%
Secondary alignments	0
Supplementary alignments	38,018 / 1.03%
Read min/max/mean length	30 / 101 / 101.41
Duplicated reads (estimated)	203,992 / 5.52%
Duplication rate	3.37%
Clipped reads	2,206,248 / 59.69%

2.2. ACGT Content

Number/percentage of A's	98,490,037 / 28.77%
Number/percentage of C's	69,443,972 / 20.29%
Number/percentage of T's	101,059,866 / 29.52%
Number/percentage of G's	73,321,643 / 21.42%
Number/percentage of N's	4,394 / 0%

GC Percentage	41.71%

2.3. Coverage

Mean	0.1107
Standard Deviation	1.0648

2.4. Mapping Quality

Mean Mapping Quality	52.73

2.5. Insert size

Mean	138,383.15
Standard Deviation	3,550,960
P25/Median/P75	141 / 175 / 223

2.6. Mismatches and indels

General error rate	0.9%
Mismatches	2,937,189
Insertions	70,093
Mapped reads with at least one insertion	1.86%
Deletions	131,920
Mapped reads with at least one deletion	3.52%
Homopolymer indels	45.75%

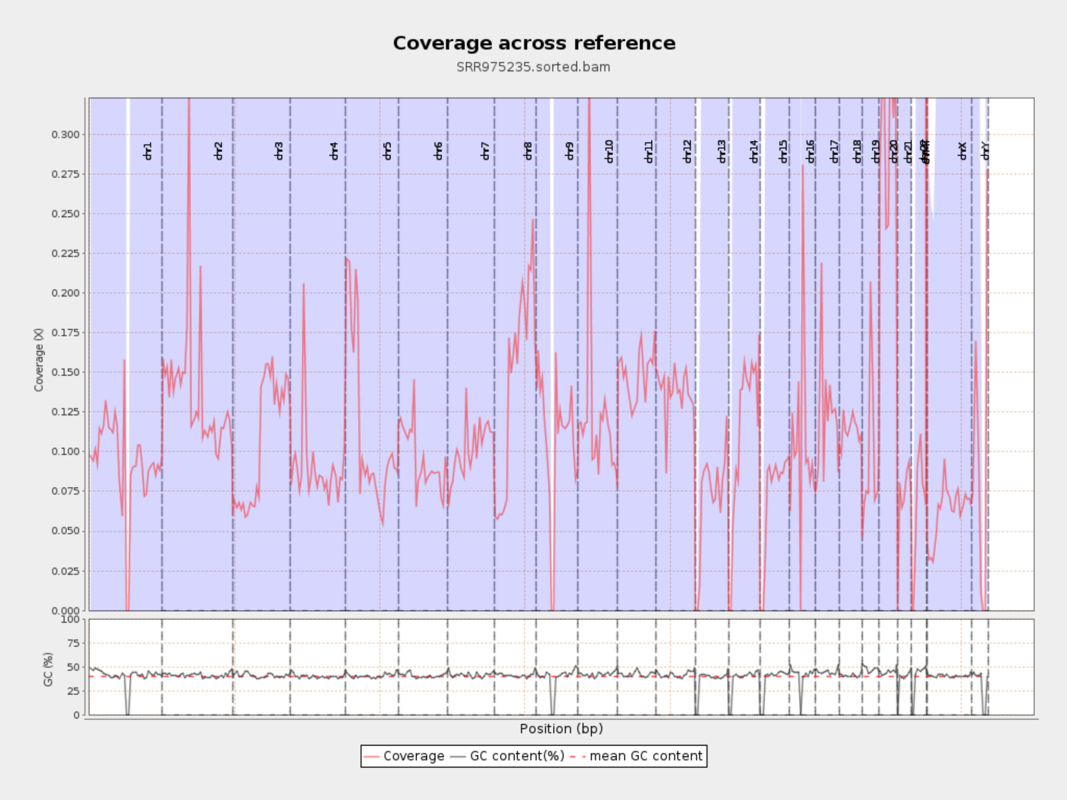
2.7. Chromosome stats

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

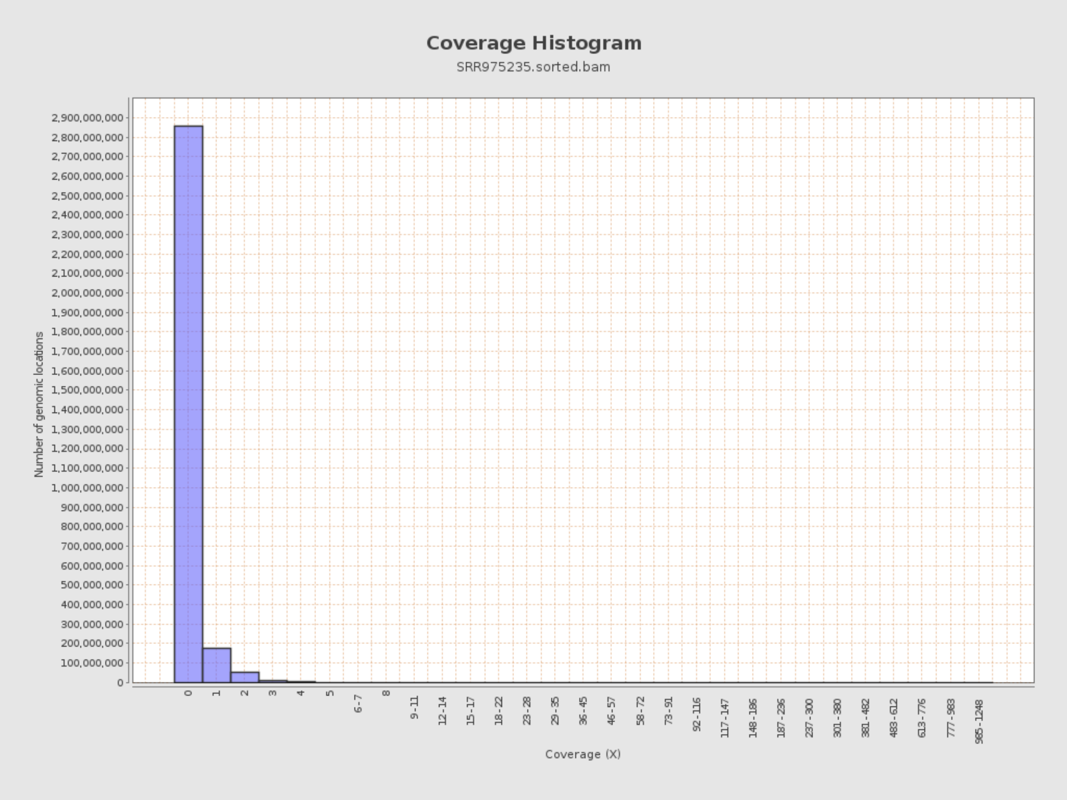
		bases	coverage	deviation
chr1	249250621	23326875	0.0936	1.3727
chr2	243199373	33664628	0.1384	1.6058
chr3	198022430	21080876	0.1065	0.4217
chr4	191154276	17103024	0.0895	0.8819
chr5	180915260	20344448	0.1125	0.4492
chr6	171115067	16353193	0.0956	0.5369
chr7	159138663	16261125	0.1022	0.9669
chr8	146364022	21423289	0.1464	0.6028
chr9	141213431	15254347	0.108	1.4714
chr10	135534747	16718619	0.1234	2.068
chr11	135006516	19927645	0.1476	0.8059
chr12	133851895	18392784	0.1374	0.4779
chr13	115169878	8129208	0.0706	0.33
chr14	107349540	11973121	0.1115	0.4637
chr15	102531392	7377237	0.072	0.3358
chr16	90354753	9509684	0.1052	1.4479
chr17	81195210	9953195	0.1226	1.8419
chr18	78077248	8892178	0.1139	1.3721
chr19	59128983	5915330	0.1	0.702
chr20	63025520	19044511	0.3022	0.7755
chr21	48129895	3416171	0.071	0.4707
chr22	51304566	3177808	0.0619	0.3417
chrMT	16571	170993	10.3188	5.2603
chrX	155270560	9741883	0.0627	0.408

chrY	59373566	5398745	0.0909	1.6563

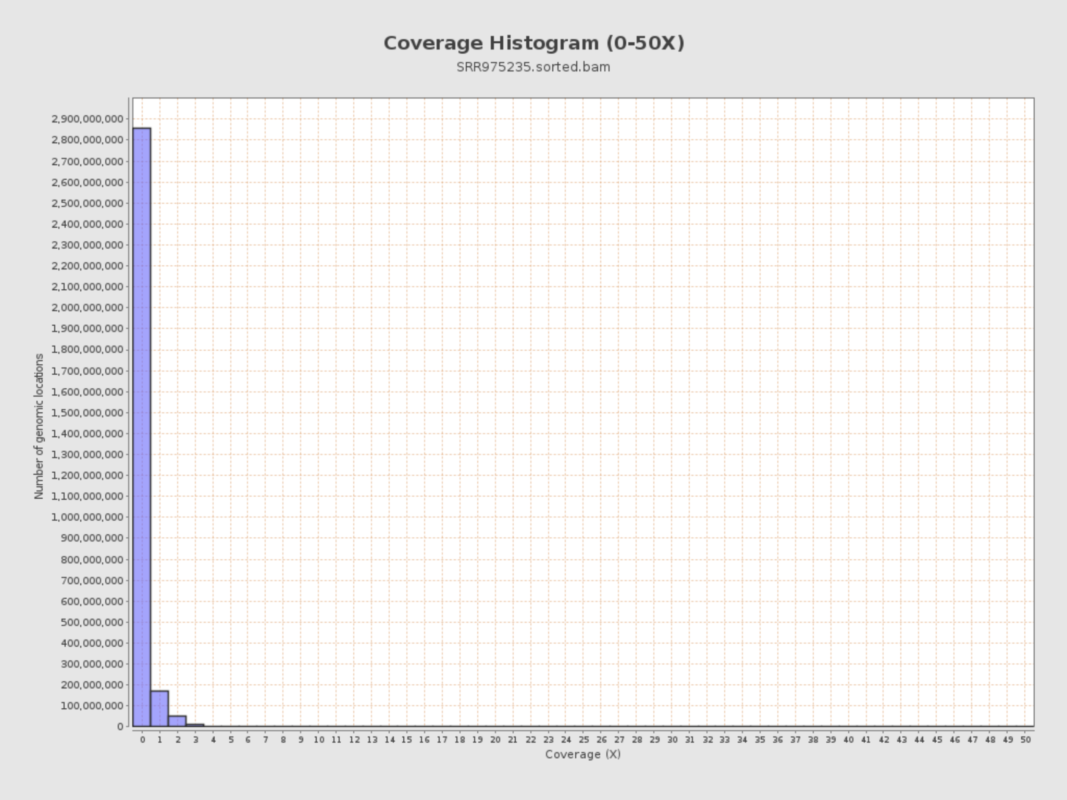
3. Results : Coverage across reference



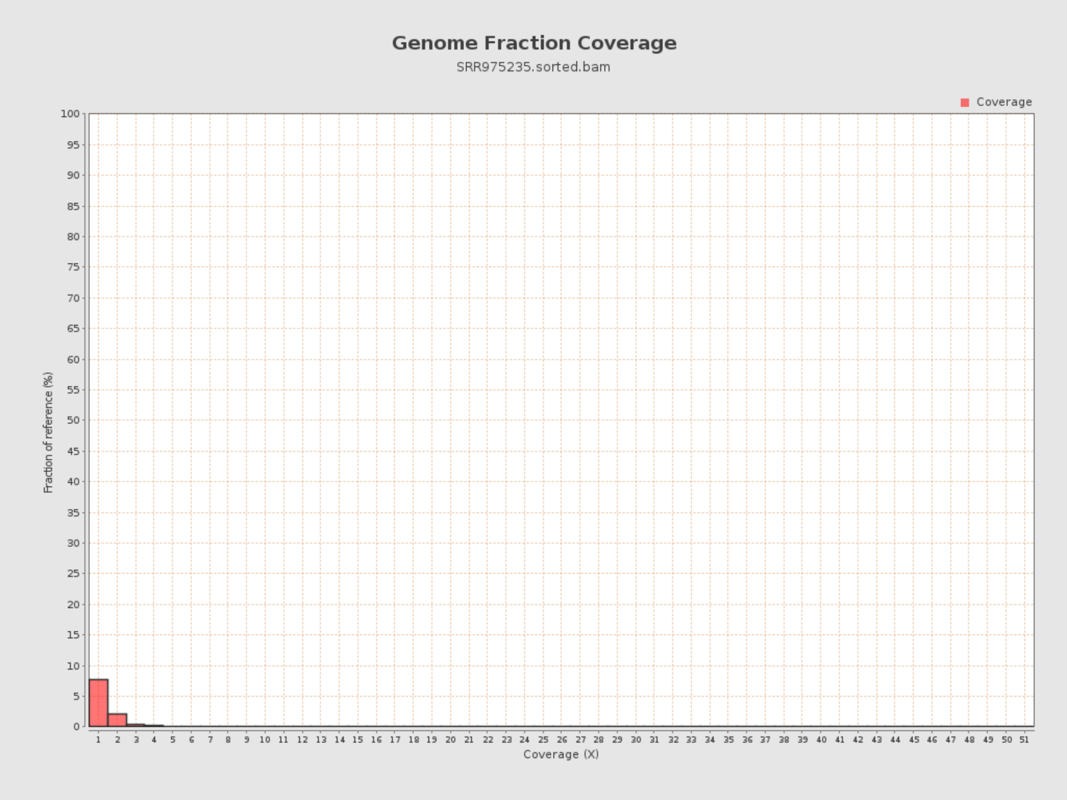
4. Results : Coverage Histogram



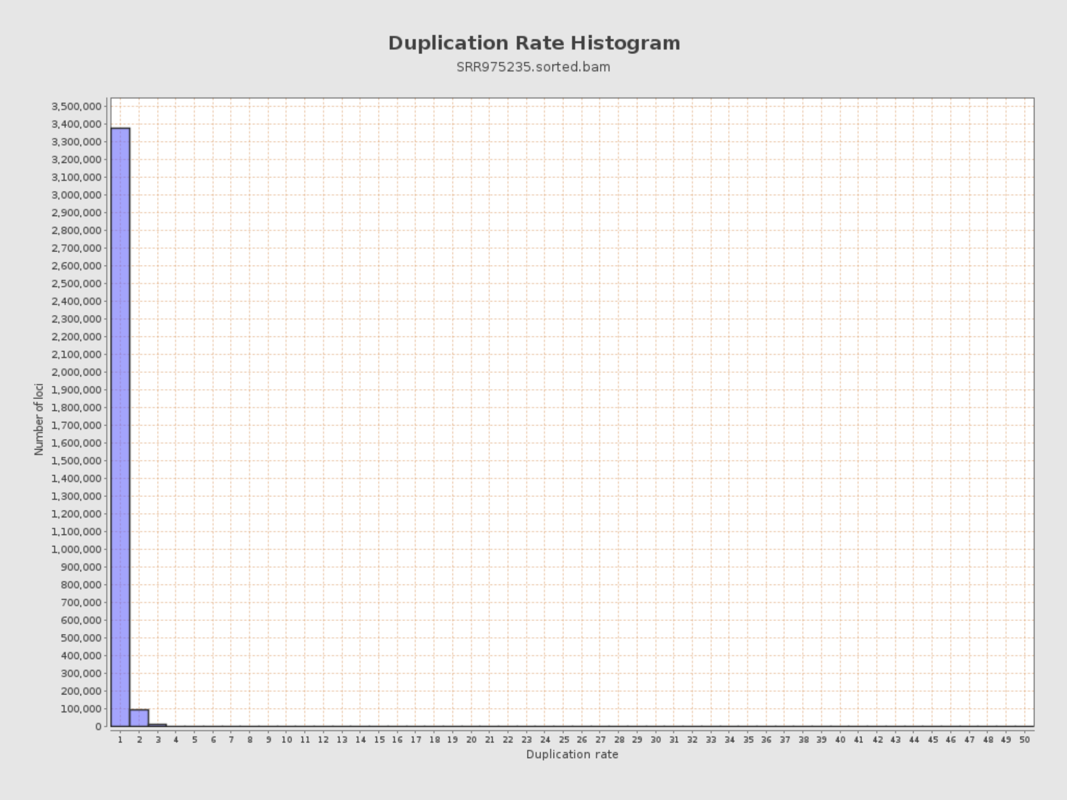
5. Results : Coverage Histogram (0-50X)



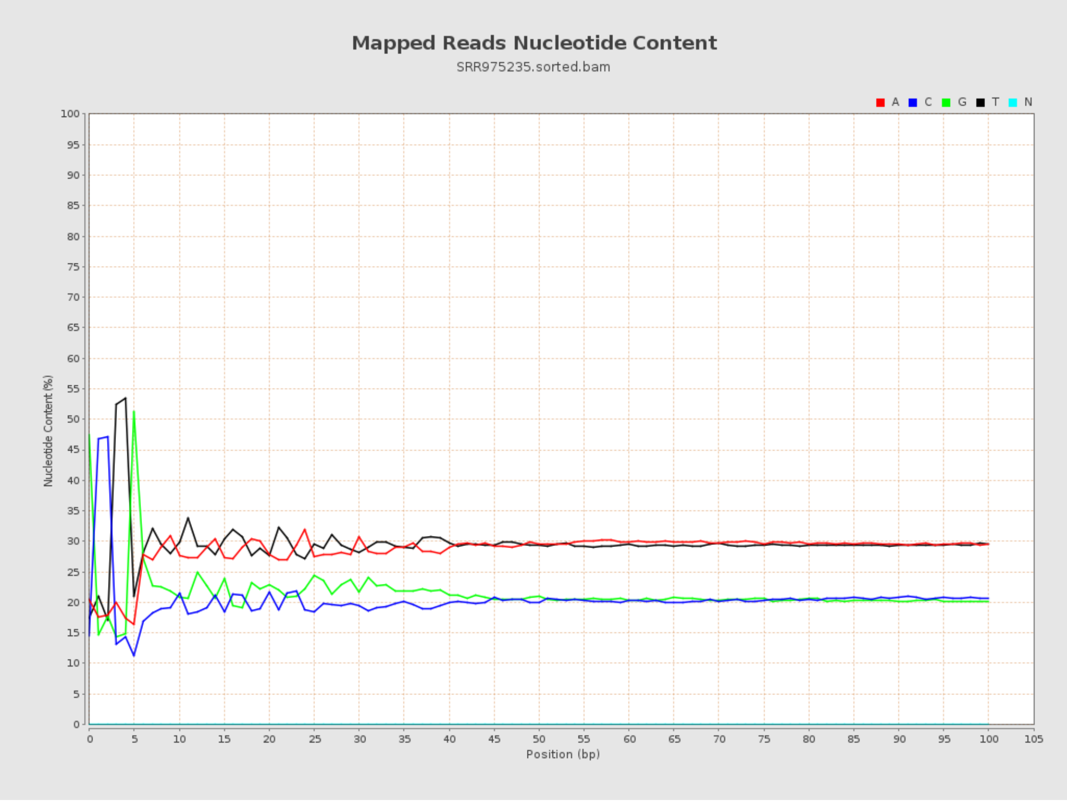
6. Results : Genome Fraction Coverage



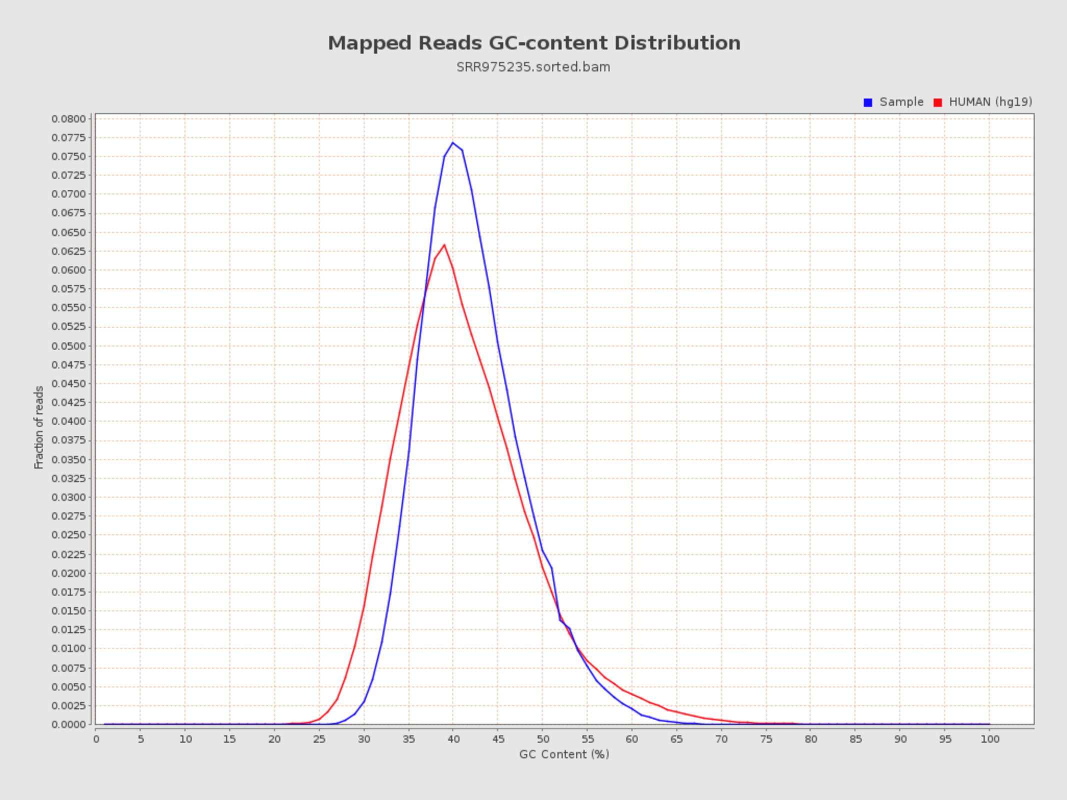
7. Results : Duplication Rate Histogram



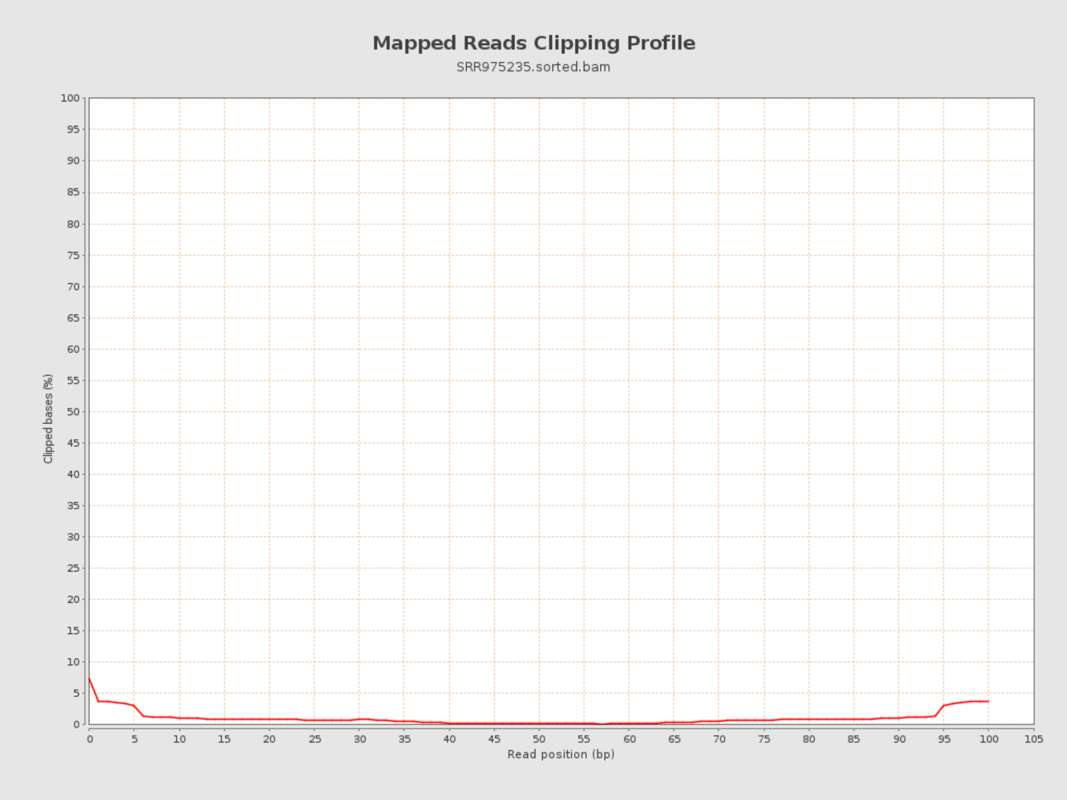
8. Results : Mapped Reads Nucleotide Content



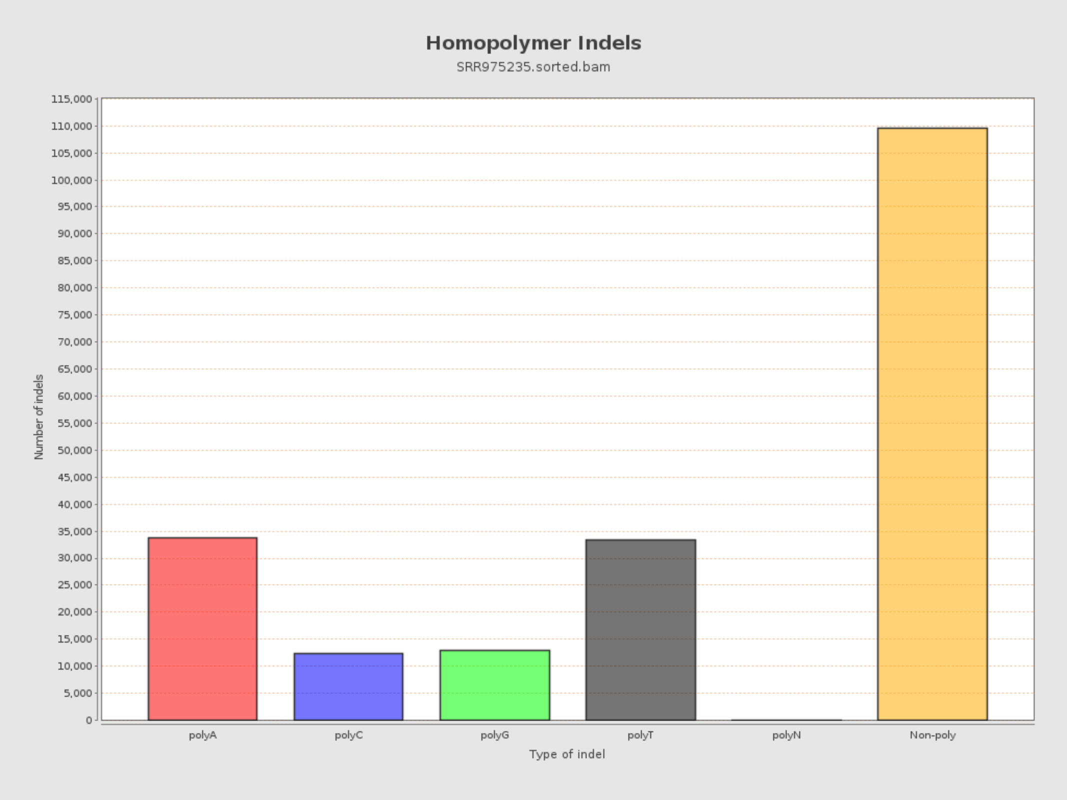
9. Results : Mapped Reads GC-content Distribution



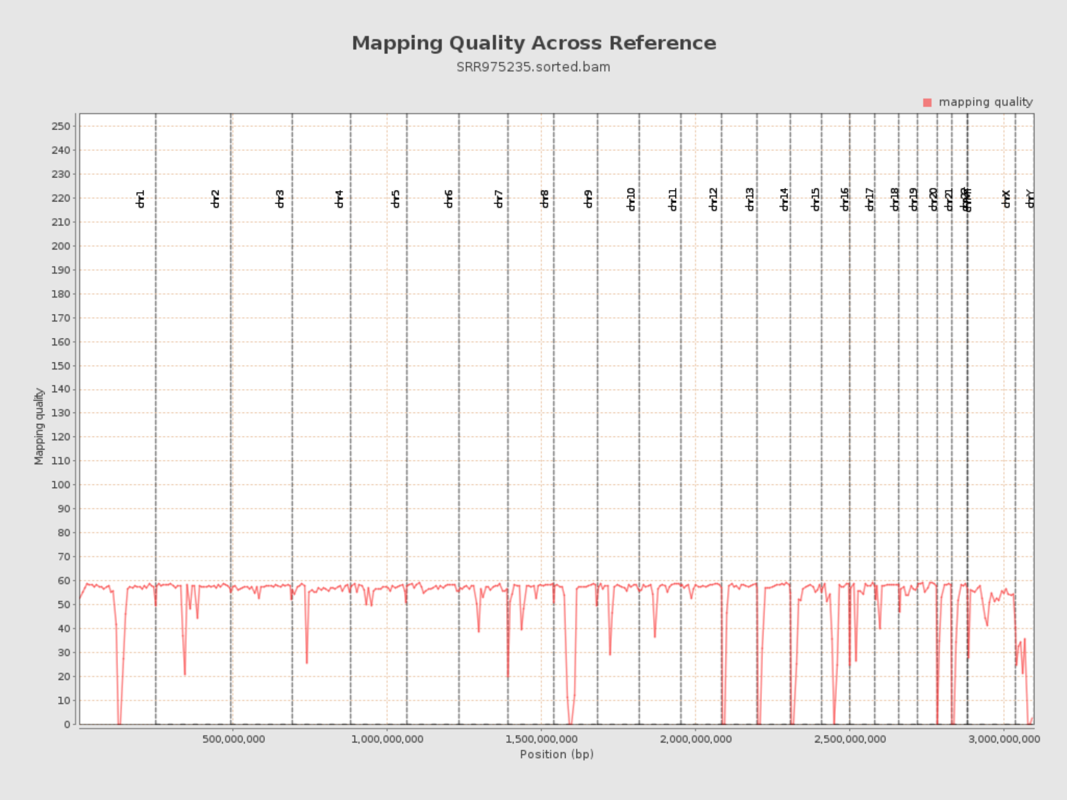
10. Results : Mapped Reads Clipping Profile



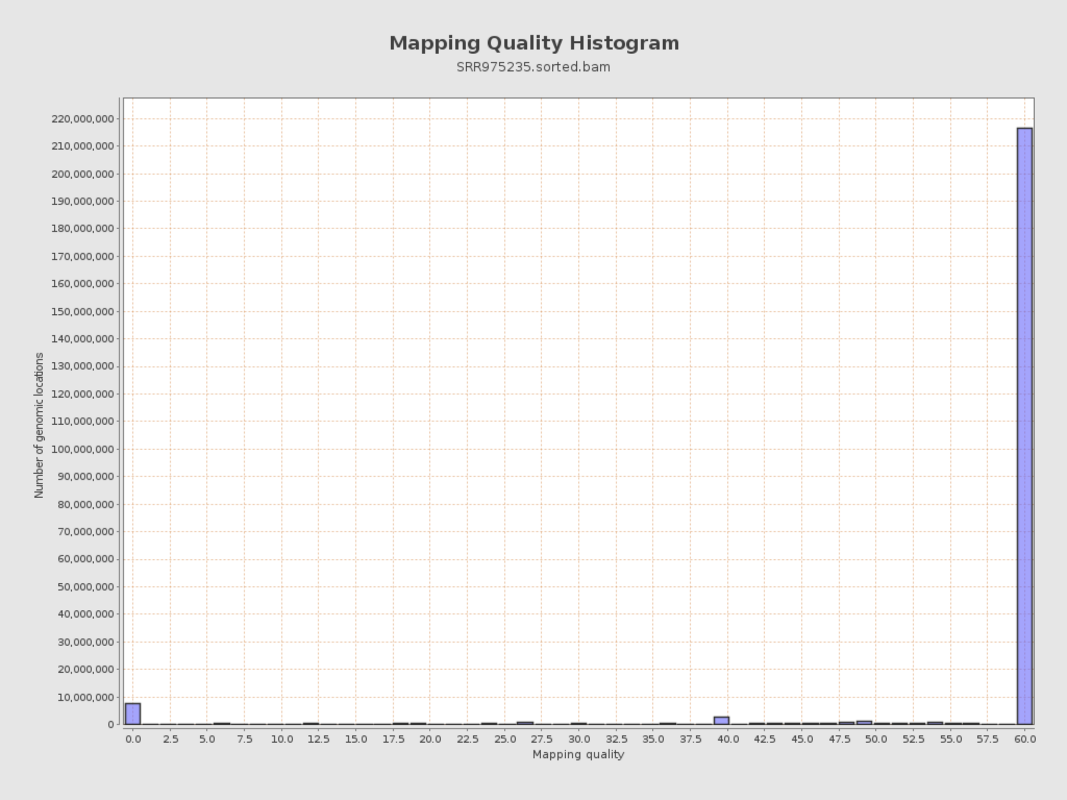
11. Results : Homopolymer Indels



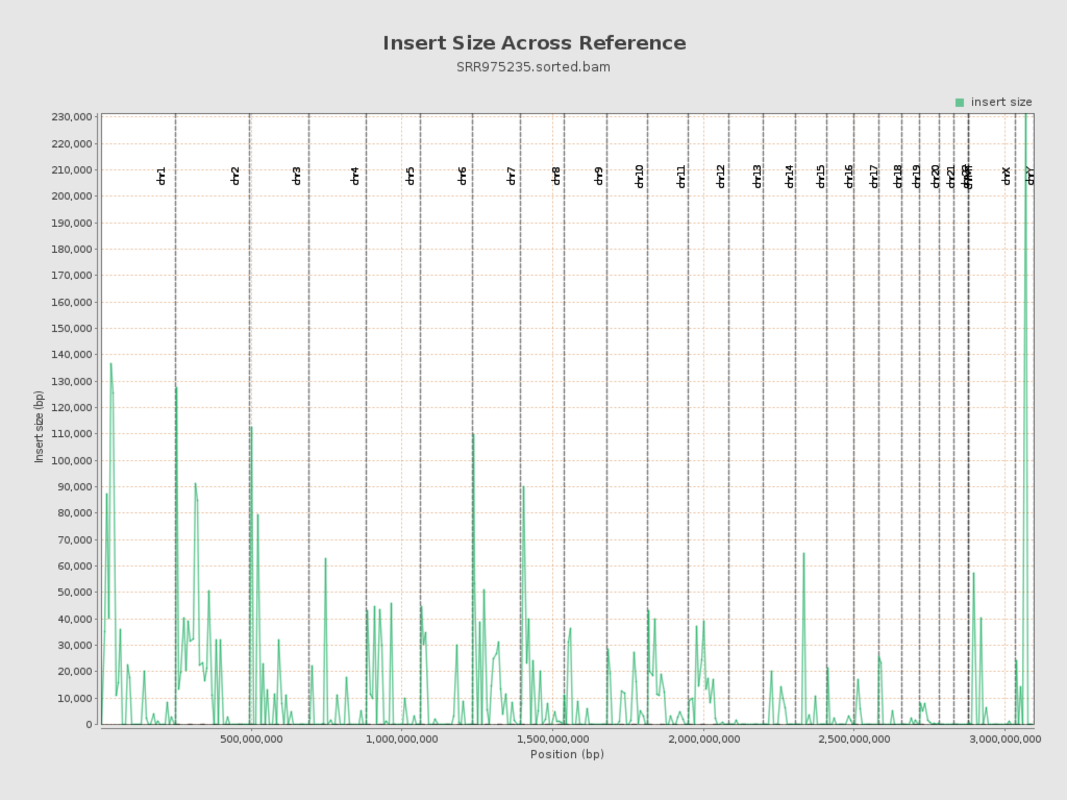
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram