Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 19:33:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975223.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_SRR975223 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975223_1.fastq.gz SRR975223_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 19:33:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975223.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,011,662
Mapped reads	3,974,776 / 99.08%
Unmapped reads	36,886 / 0.92%
Mapped paired reads	3,974,776 / 99.08%
Mapped reads, first in pair	1,995,583 / 49.74%
Mapped reads, second in pair	1,979,193 / 49.34%
Mapped reads, both in pair	3,955,718 / 98.61%
Mapped reads, singletons	19,058 / 0.48%
Secondary alignments	0
Supplementary alignments	49,757 / 1.24%
Read min/max/mean length	30 / 151 / 151.62
Duplicated reads (estimated)	537,448 / 13.4%
Duplication rate	12.3%
Clipped reads	1,604,955 / 40.01%

2.2. ACGT Content

Number/percentage of A's	166,557,825 / 29.46%
Number/percentage of C's	115,116,600 / 20.36%
Number/percentage of T's	164,799,625 / 29.15%
Number/percentage of G's	118,860,369 / 21.02%
Number/percentage of N's	52,781 / 0.01%

GC Percentage	41.38%

2.3. Coverage

Mean	0.1828
Standard Deviation	1.9944

2.4. Mapping Quality

Mean Mapping Quality	53.9

2.5. Insert size

Mean	92,642.95
Standard Deviation	2,962,998.7
P25/Median/P75	144 / 173 / 215

2.6. Mismatches and indels

General error rate	0.94%
Mismatches	5,092,810
Insertions	96,409
Mapped reads with at least one insertion	2.32%
Deletions	214,734
Mapped reads with at least one deletion	5.21%
Homopolymer indels	48.91%

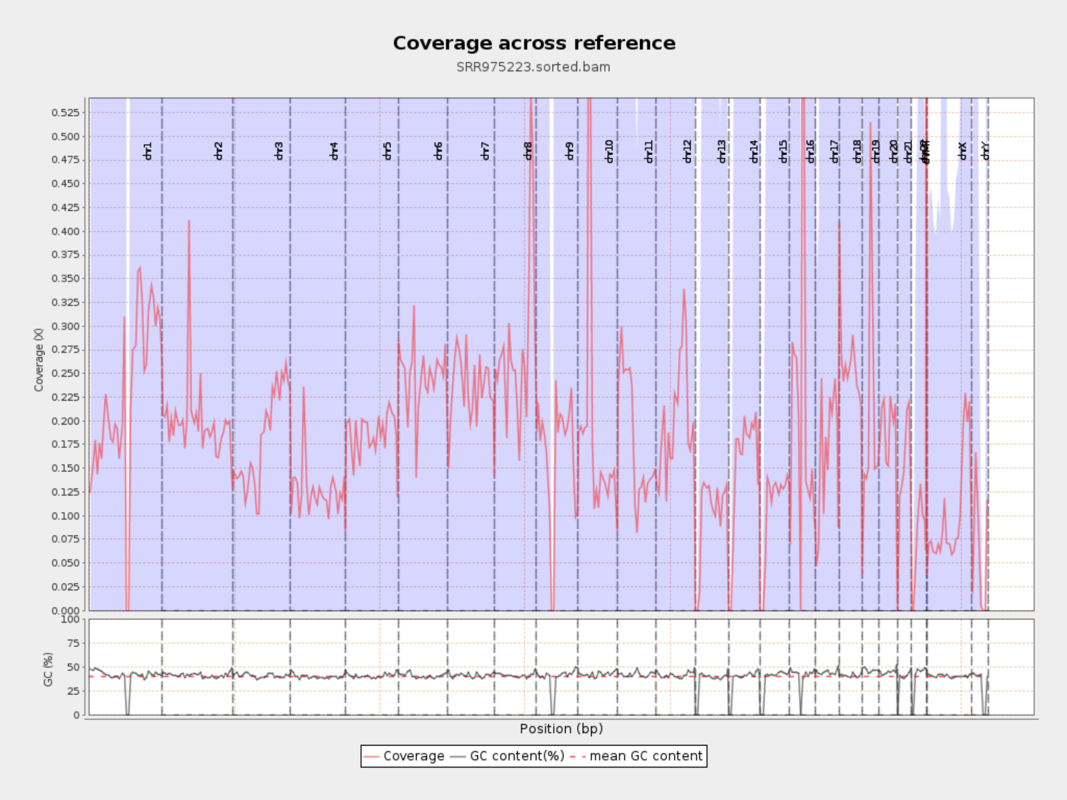
2.7. Chromosome stats

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

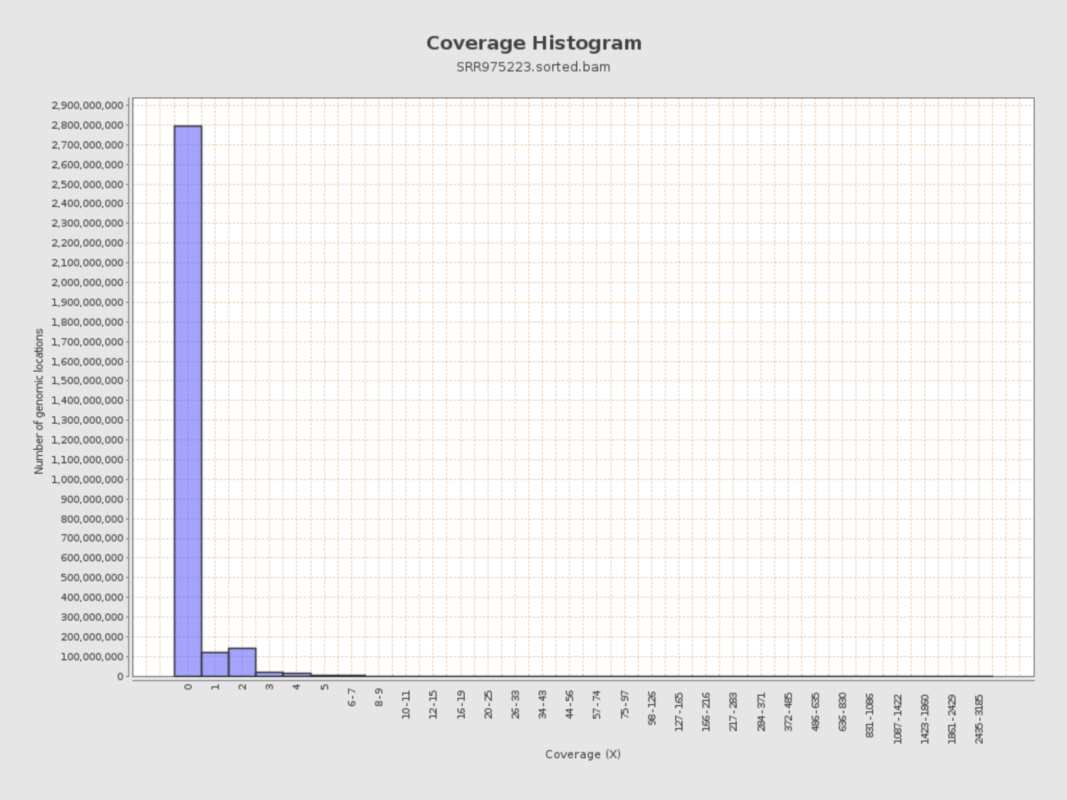
		bases	coverage	deviation
chr1	249250621	56294094	0.2259	2.118
chr2	243199373	48675446	0.2001	1.7696
chr3	198022430	35621315	0.1799	0.6505
chr4	191154276	24087865	0.126	0.9724
chr5	180915260	33693399	0.1862	0.6206
chr6	171115067	42345112	0.2475	1.088
chr7	159138663	37888862	0.2381	2.2323
chr8	146364022	40881236	0.2793	0.9443
chr9	141213431	23271208	0.1648	2.1185
chr10	135534747	25612590	0.189	5.8463
chr11	135006516	24025189	0.178	1.973
chr12	133851895	27026994	0.2019	0.6487
chr13	115169878	11395018	0.0989	0.4367
chr14	107349540	16155594	0.1505	0.5613
chr15	102531392	10890017	0.1062	0.4577
chr16	90354753	19787896	0.219	4.5089
chr17	81195210	13229707	0.1629	2.4048
chr18	78077248	20332006	0.2604	2.078
chr19	59128983	12725764	0.2152	1.4663
chr20	63025520	12004452	0.1905	0.7037
chr21	48129895	6884499	0.143	0.7762
chr22	51304566	3710697	0.0723	0.3881
chrMT	16571	34427	2.0775	2.255
chrX	155270560	15740992	0.1014	0.6998

chrY	59373566	3463674	0.0583	1.4477

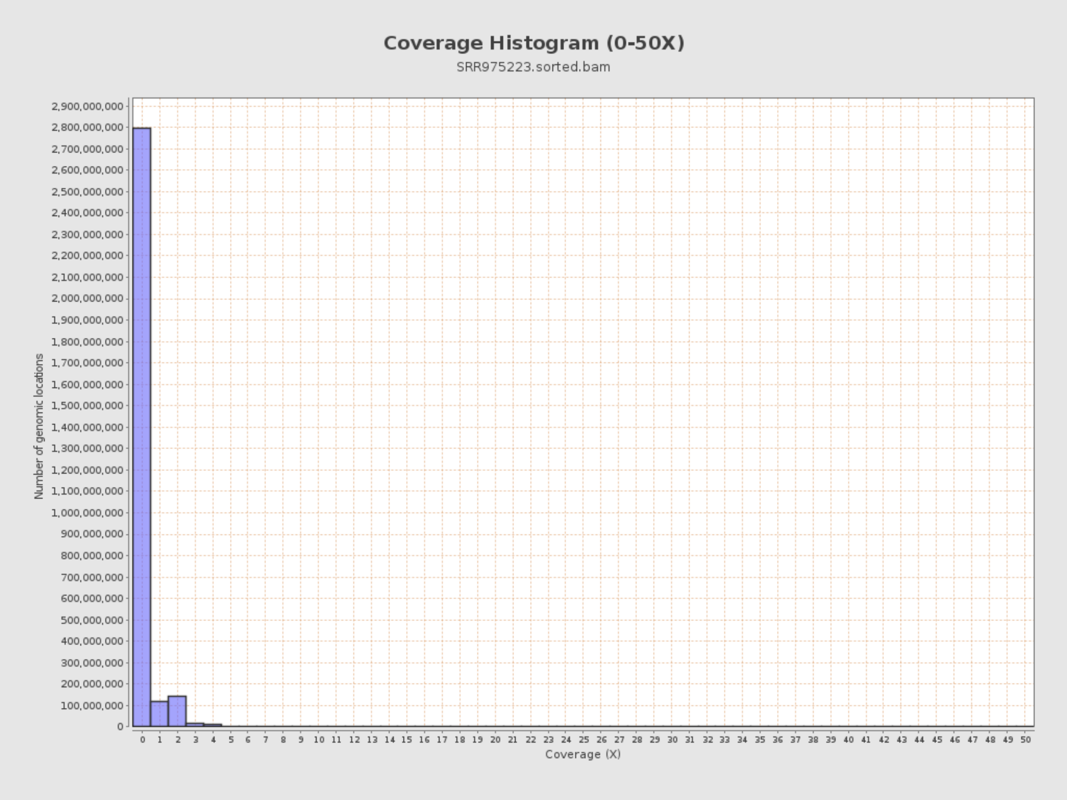
3. Results : Coverage across reference



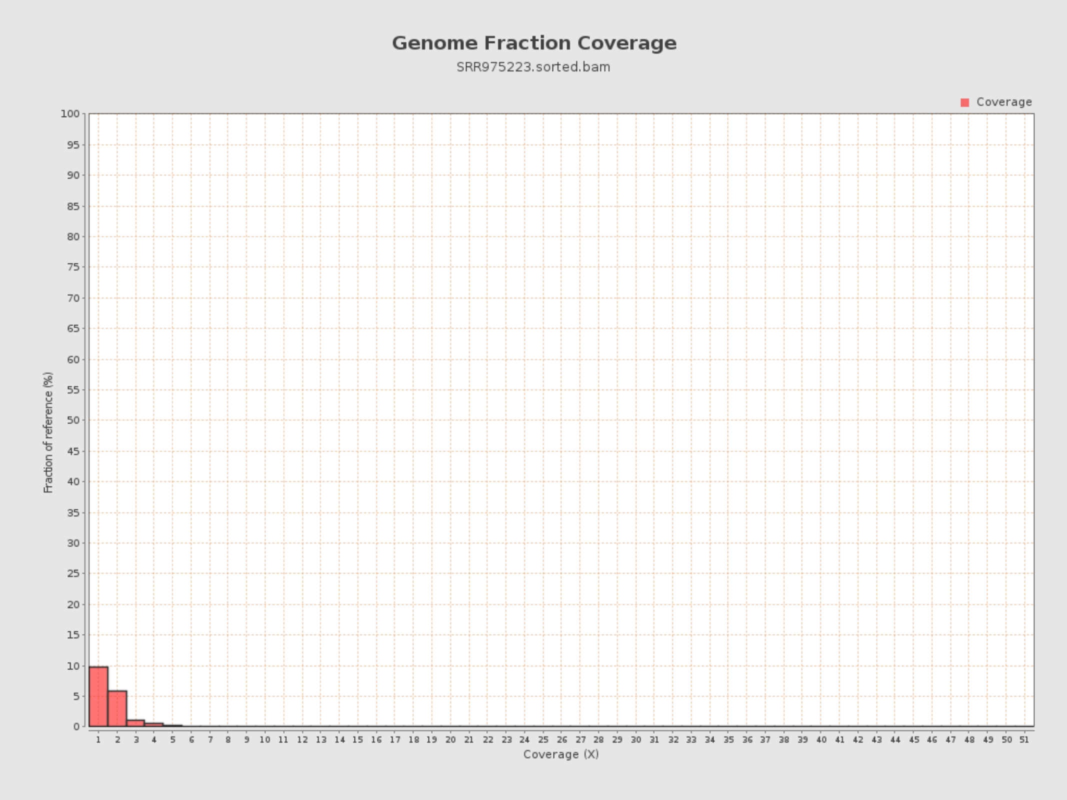
4. Results : Coverage Histogram



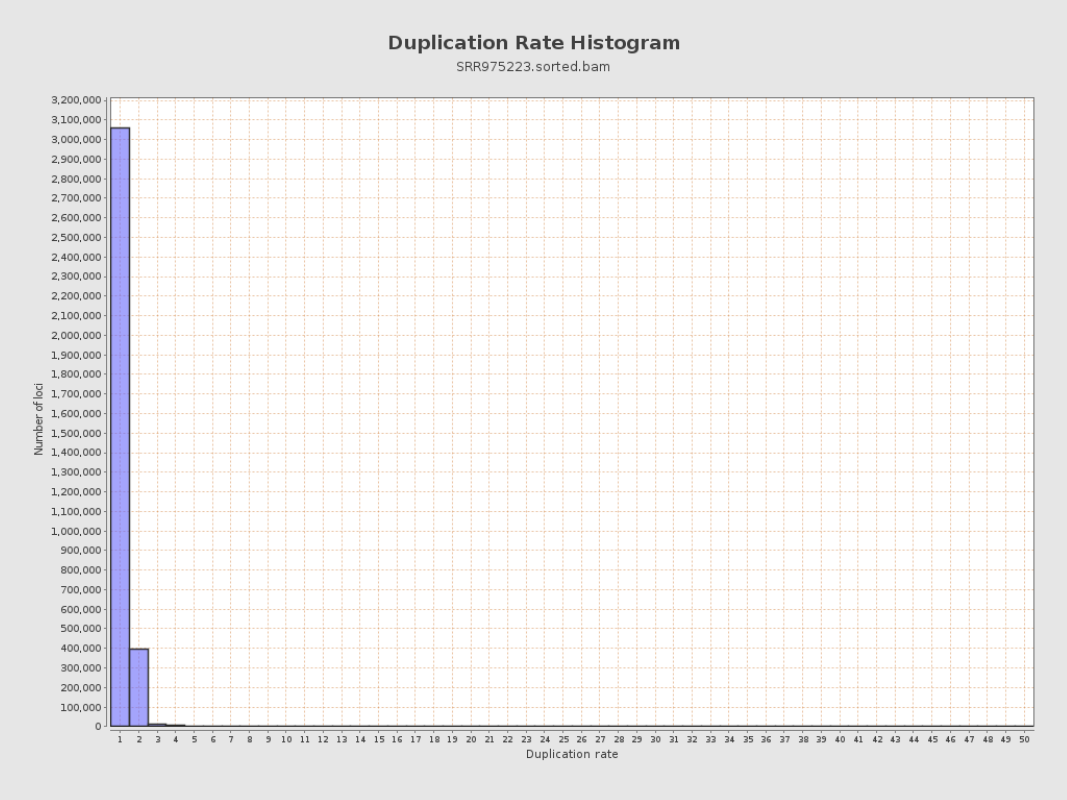
5. Results : Coverage Histogram (0-50X)



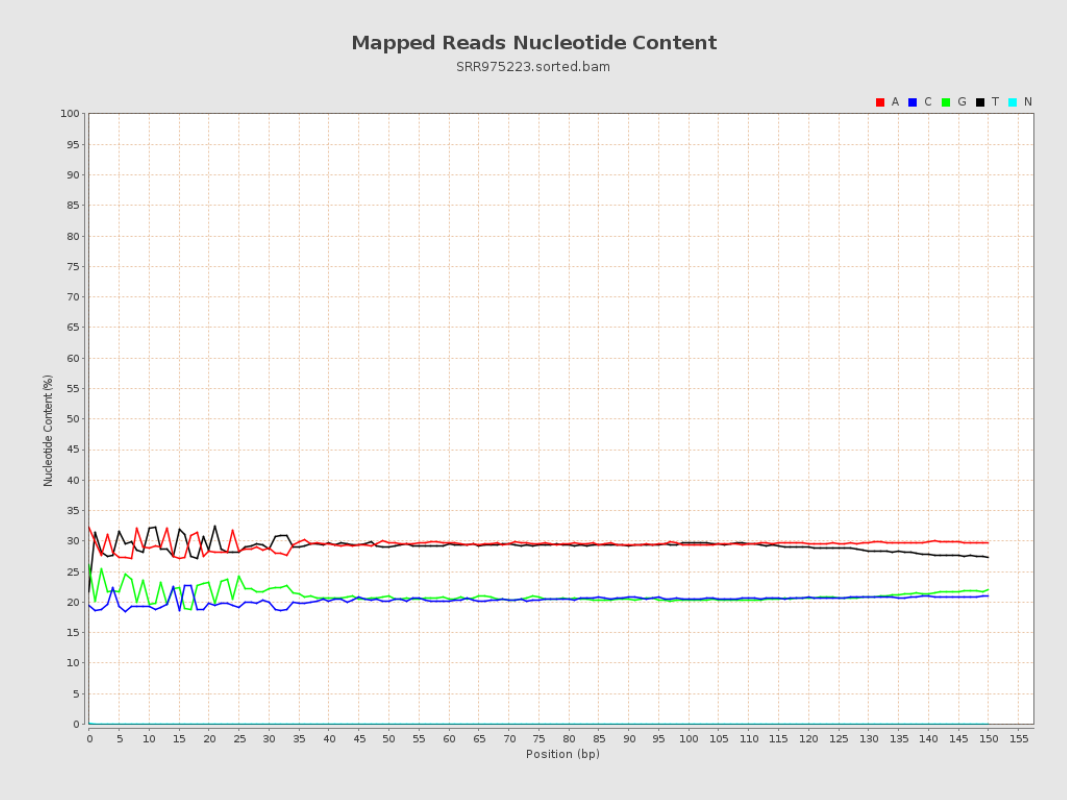
6. Results : Genome Fraction Coverage



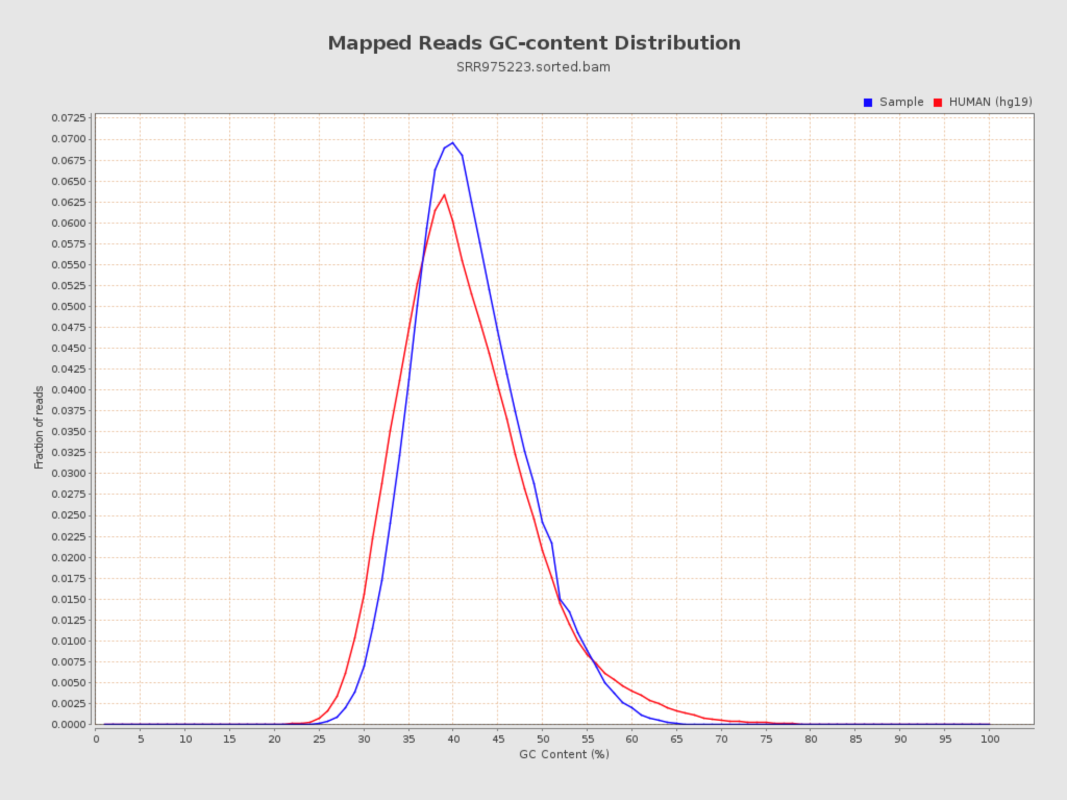
7. Results : Duplication Rate Histogram



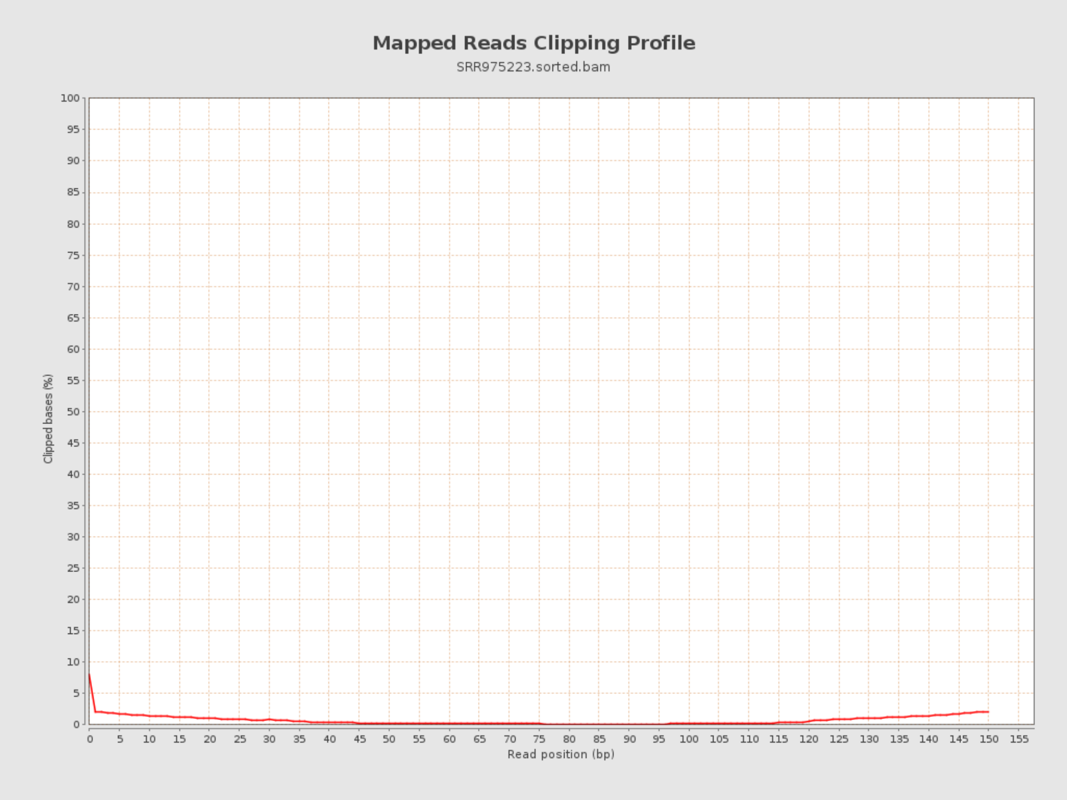
8. Results : Mapped Reads Nucleotide Content



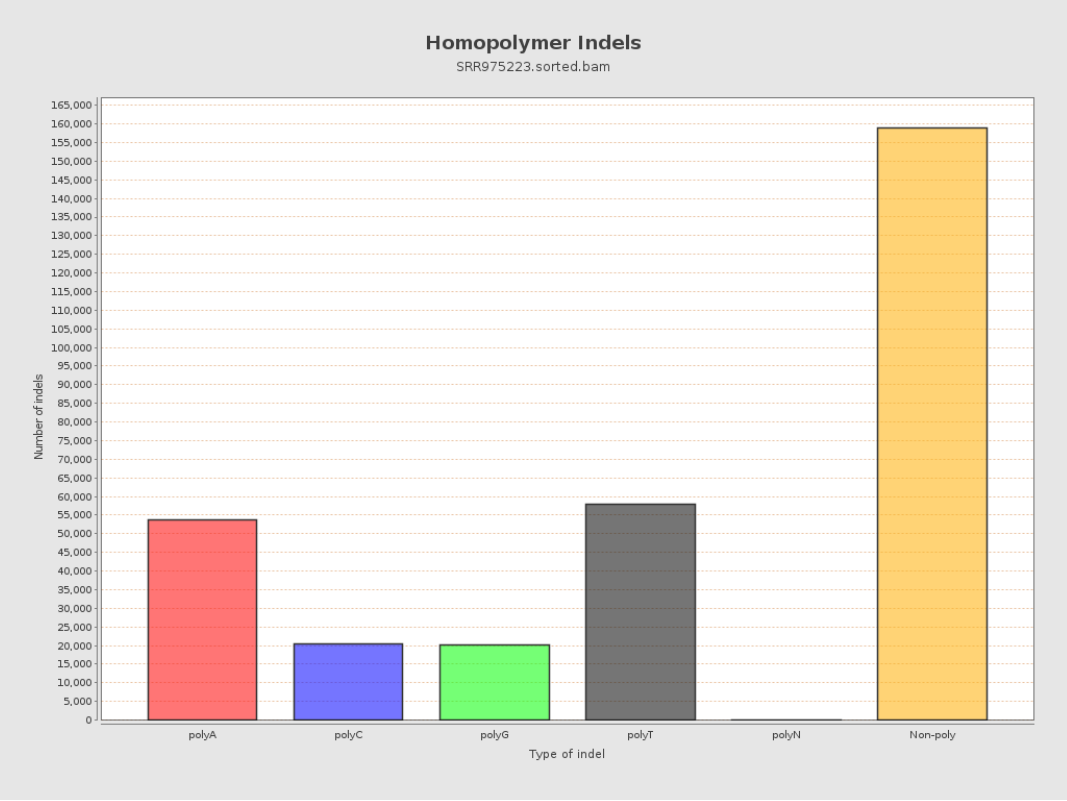
9. Results : Mapped Reads GC-content Distribution



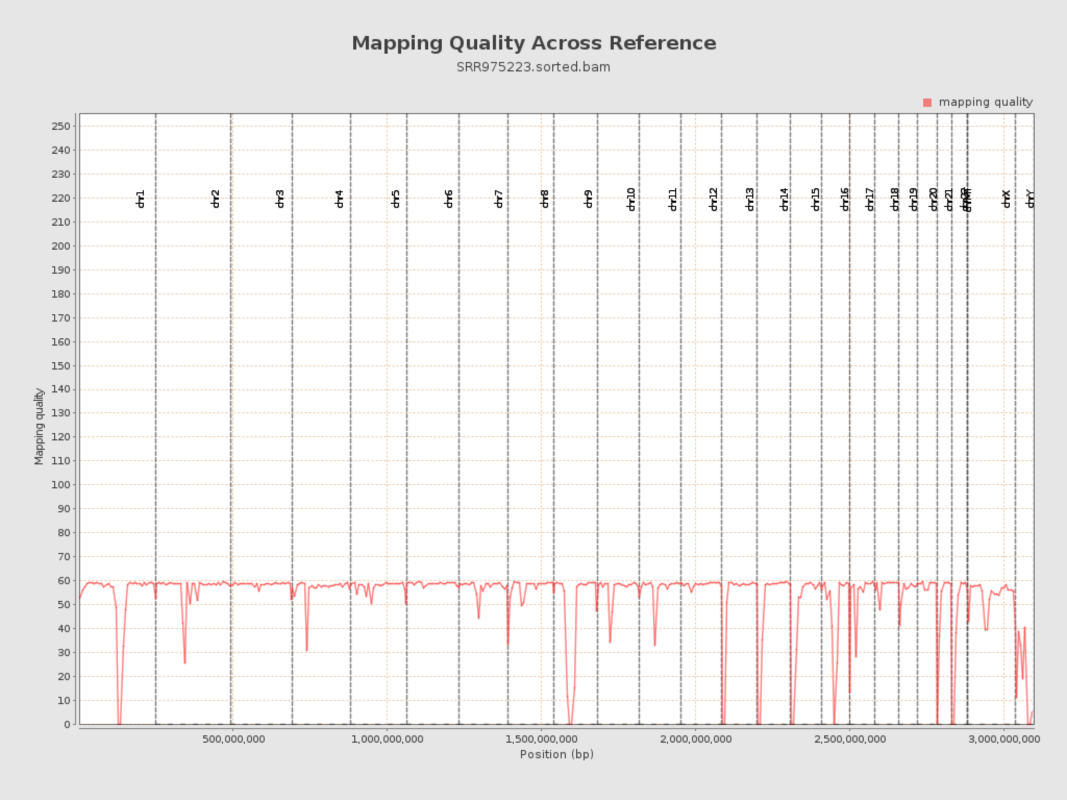
10. Results : Mapped Reads Clipping Profile



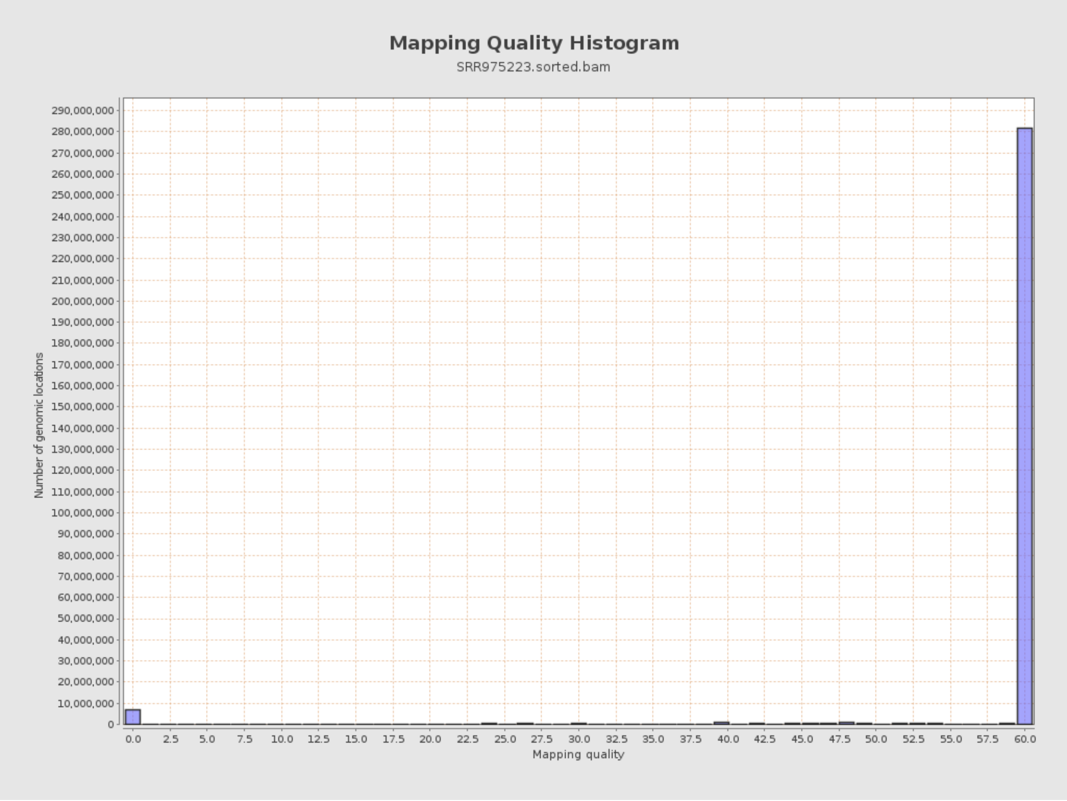
11. Results : Homopolymer Indels



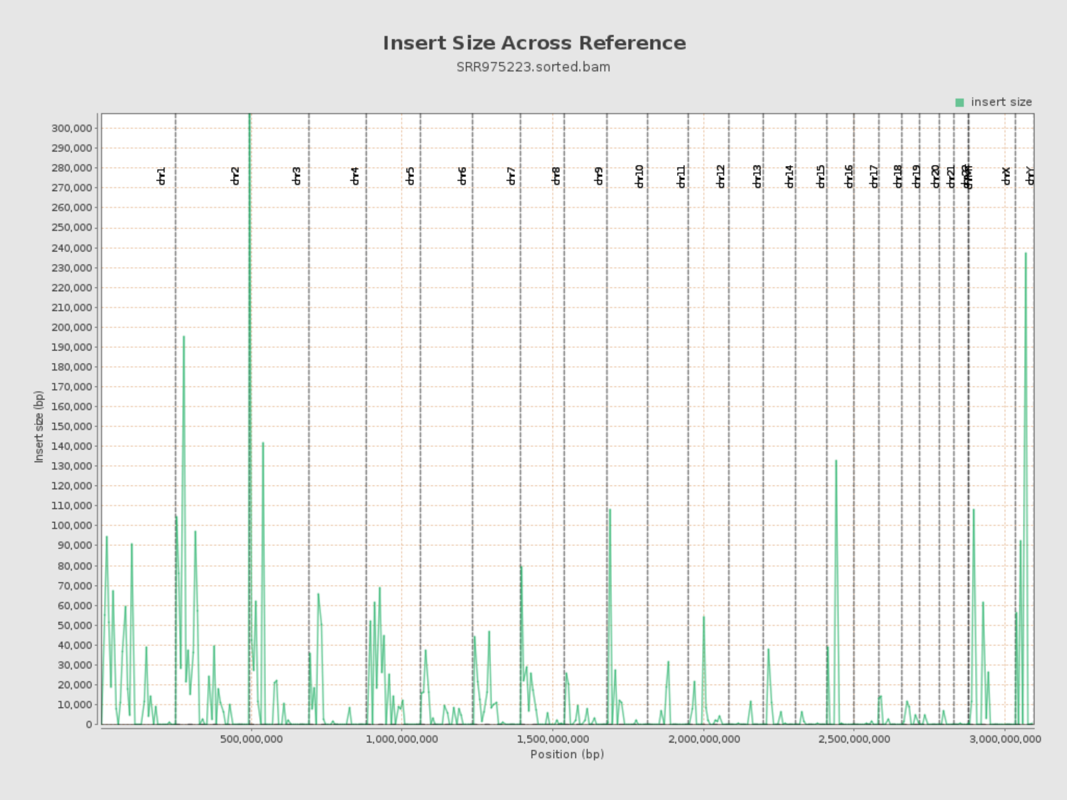
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram