Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.2-dev
2024/08/29 02:30:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975196.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_SRR975196 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975196_1.fastq.gz SRR975196_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 02:30:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975196.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	55,135,976
Mapped reads	54,991,588 / 99.74%
Unmapped reads	144,388 / 0.26%
Mapped paired reads	54,991,588 / 99.74%
Mapped reads, first in pair	27,491,326 / 49.86%
Mapped reads, second in pair	27,500,262 / 49.88%
Mapped reads, both in pair	54,906,892 / 99.58%
Mapped reads, singletons	84,696 / 0.15%
Secondary alignments	0
Supplementary alignments	146,836 / 0.27%
Read min/max/mean length	30 / 101 / 101.11
Duplicated reads (estimated)	37,158,637 / 67.39%
Duplication rate	48.09%
Clipped reads	32,071,453 / 58.17%

2.2. ACGT Content

Number/percentage of A's	1,394,638,988 / 26.93%
Number/percentage of C's	1,159,799,777 / 22.39%
Number/percentage of T's	1,398,774,717 / 27.01%
Number/percentage of G's	1,226,018,140 / 23.67%
Number/percentage of N's	267,817 / 0.01%

GC Percentage	46.06%

2.3. Coverage

Mean	1.6738
Standard Deviation	29.3006

2.4. Mapping Quality

Mean Mapping Quality	55.71

2.5. Insert size

Mean	178,720.36
Standard Deviation	4,155,018.9
P25/Median/P75	188 / 231 / 280

2.6. Mismatches and indels

General error rate	0.75%
Mismatches	37,883,254
Insertions	588,636
Mapped reads with at least one insertion	1.06%
Deletions	1,461,912
Mapped reads with at least one deletion	2.61%
Homopolymer indels	47.93%

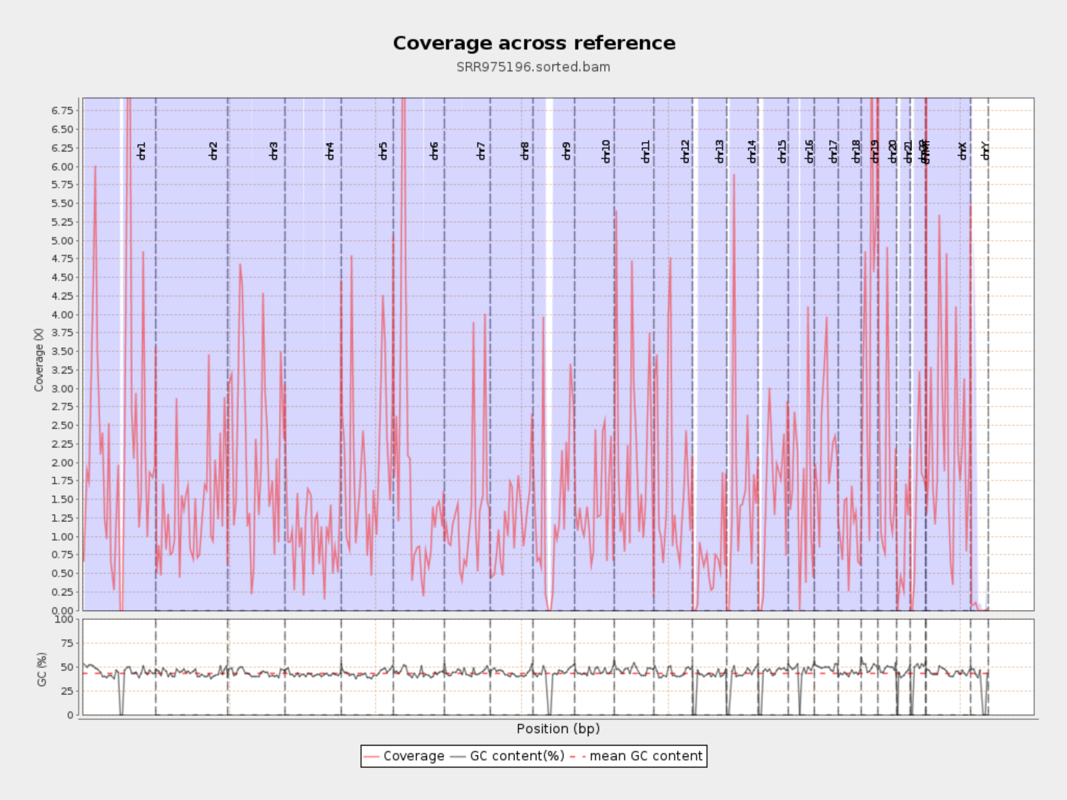
2.7. Chromosome stats

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

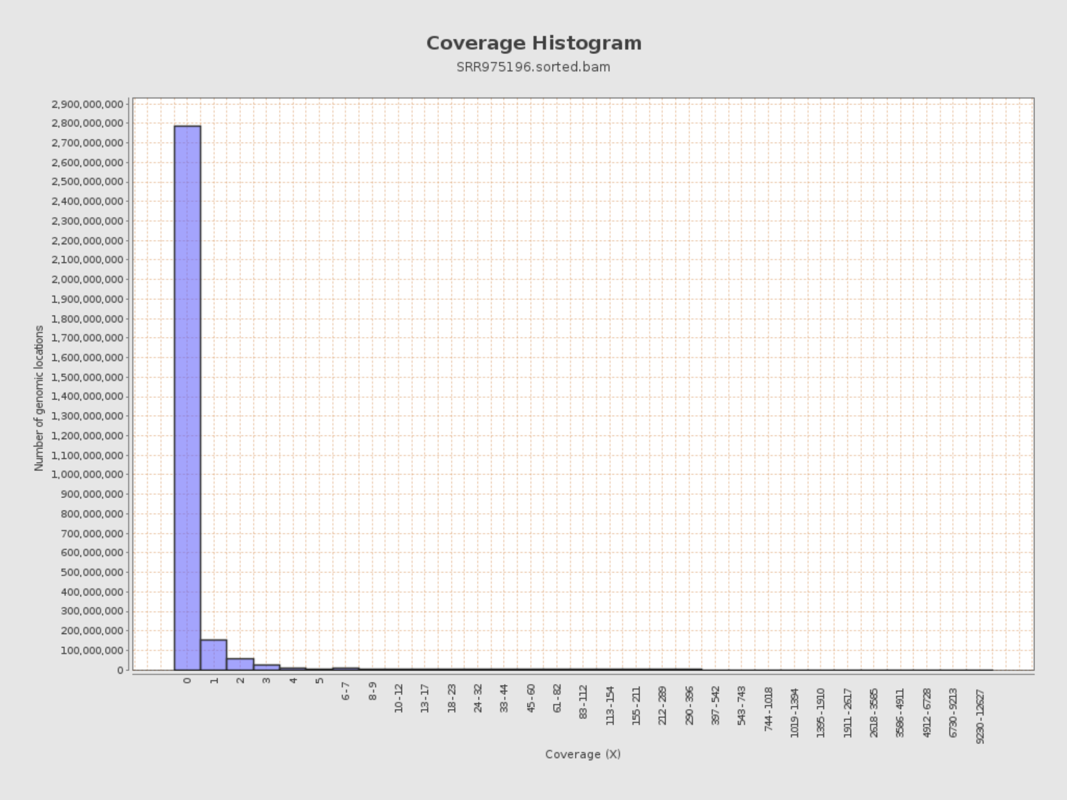
		bases	coverage	deviation
chr1	249250621	593423727	2.3808	37.251
chr2	243199373	331776977	1.3642	23.104
chr3	198022430	430448569	2.1737	31.6711
chr4	191154276	192116118	1.005	18.876
chr5	180915260	373985781	2.0672	33.1769
chr6	171115067	305539641	1.7856	32.9988
chr7	159138663	212888647	1.3378	24.1567
chr8	146364022	173850215	1.1878	20.9843
chr9	141213431	191714998	1.3576	24.4381
chr10	135534747	192268658	1.4186	24.6486
chr11	135006516	285682997	2.1161	32.1186
chr12	133851895	245224770	1.8321	28.1555
chr13	115169878	70298165	0.6104	17.7345
chr14	107349540	175416254	1.6341	26.7428
chr15	102531392	152032001	1.4828	24.3565
chr16	90354753	143929408	1.5929	26.3458
chr17	81195210	184164770	2.2682	36.2789
chr18	78077248	83113346	1.0645	25.2467
chr19	59128983	254194288	4.299	59.3991
chr20	63025520	112148268	1.7794	32.3506
chr21	48129895	41098489	0.8539	16.1808
chr22	51304566	77631856	1.5132	27.7886
chrMT	16571	455502	27.4879	34.1517
chrX	155270560	356152560	2.2938	39.2238

chrY	59373566	2037735	0.0343	2.2546

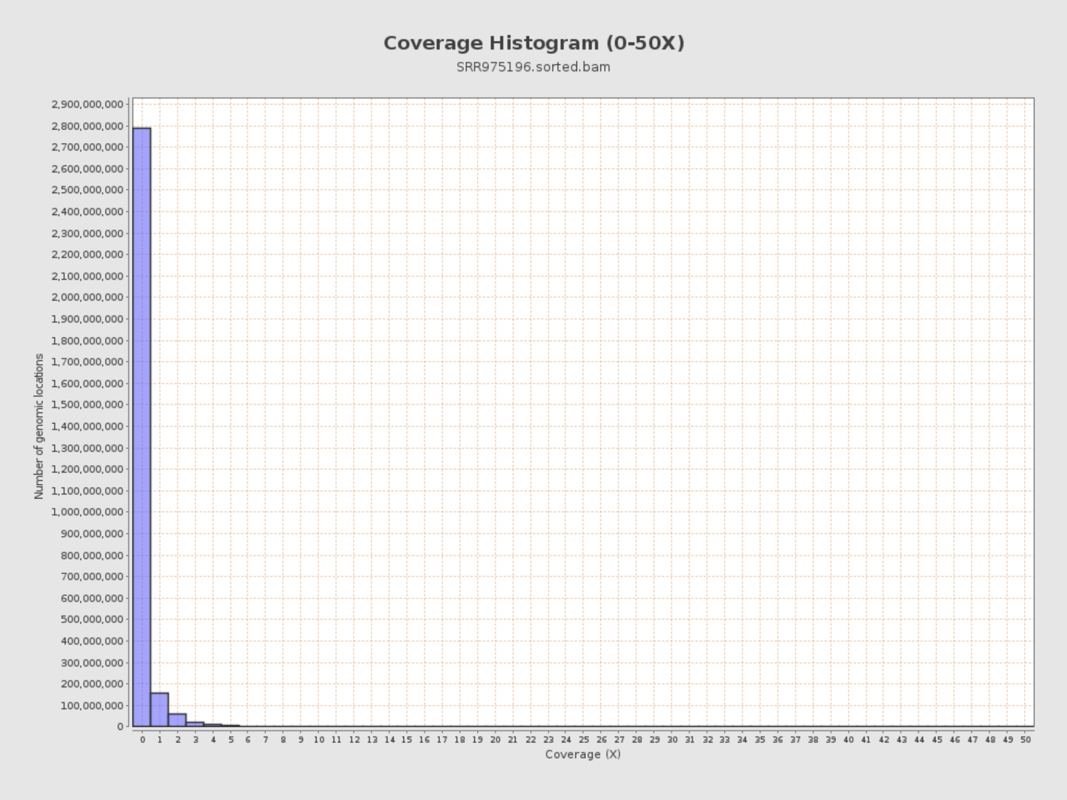
3. Results : Coverage across reference



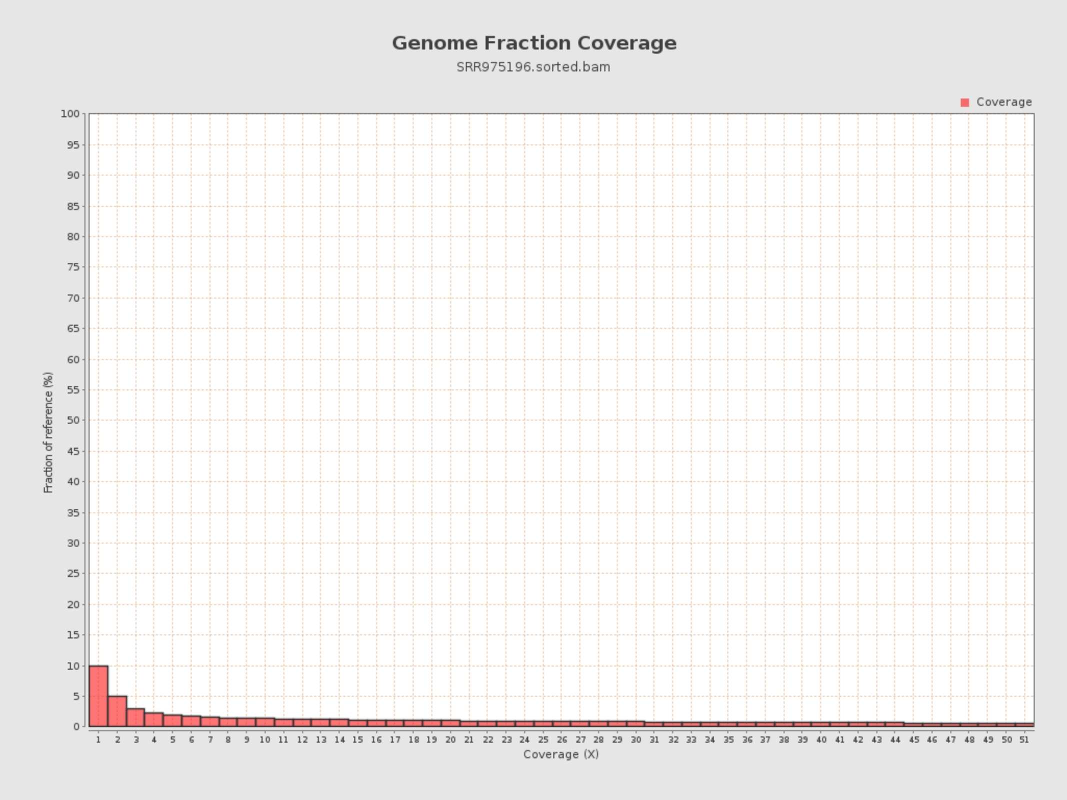
4. Results : Coverage Histogram



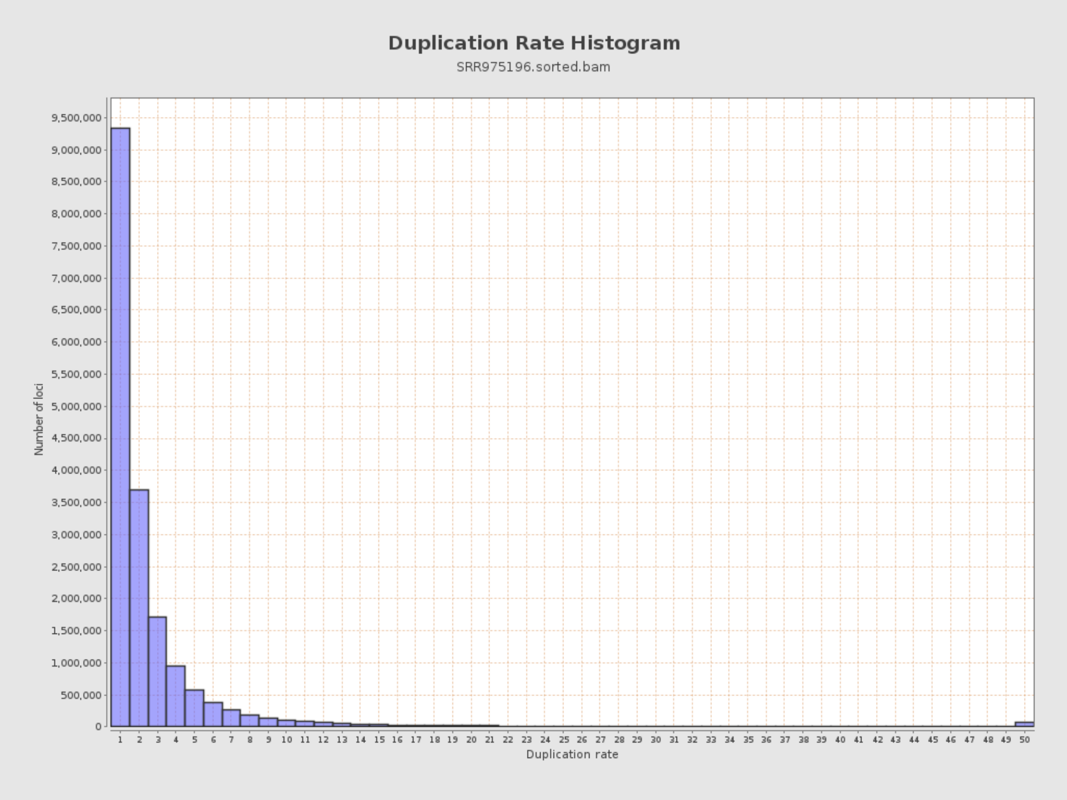
5. Results : Coverage Histogram (0-50X)



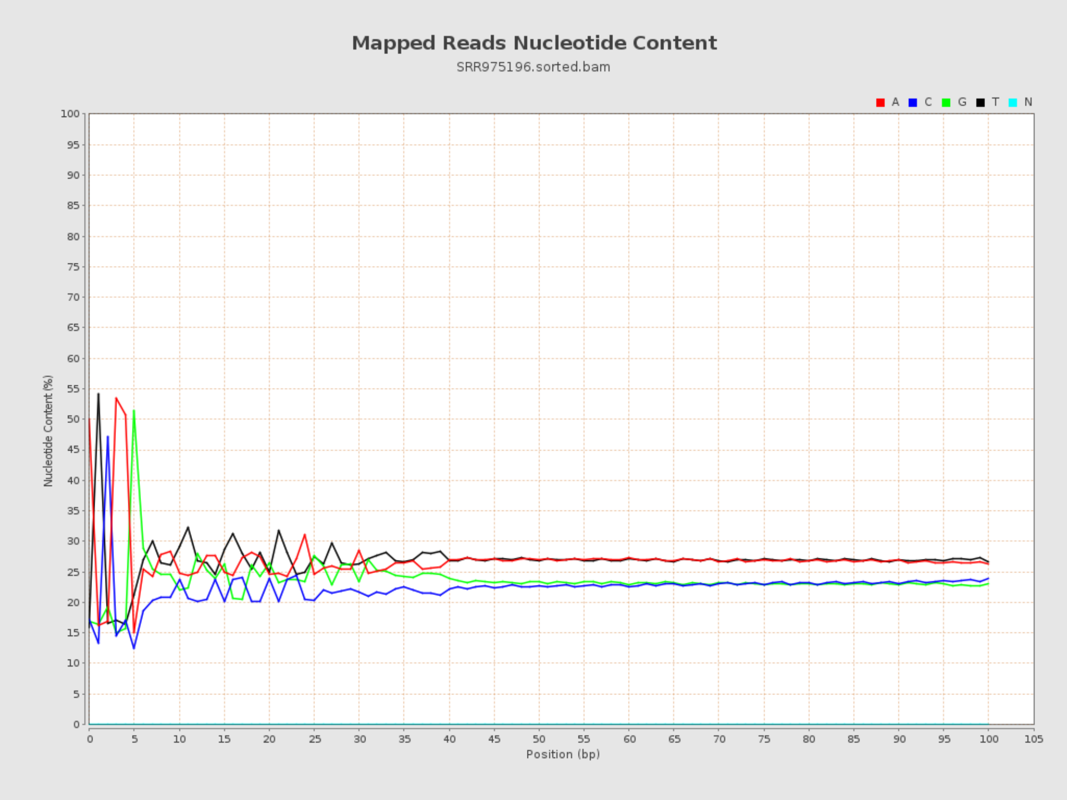
6. Results : Genome Fraction Coverage



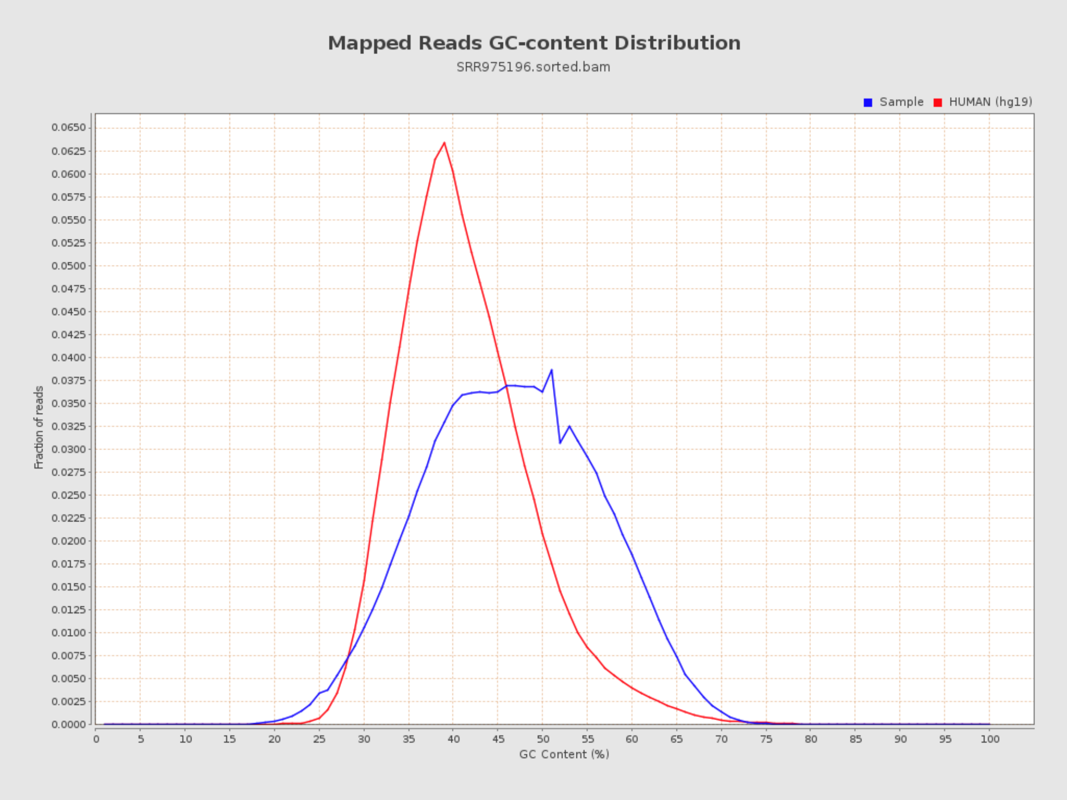
7. Results : Duplication Rate Histogram



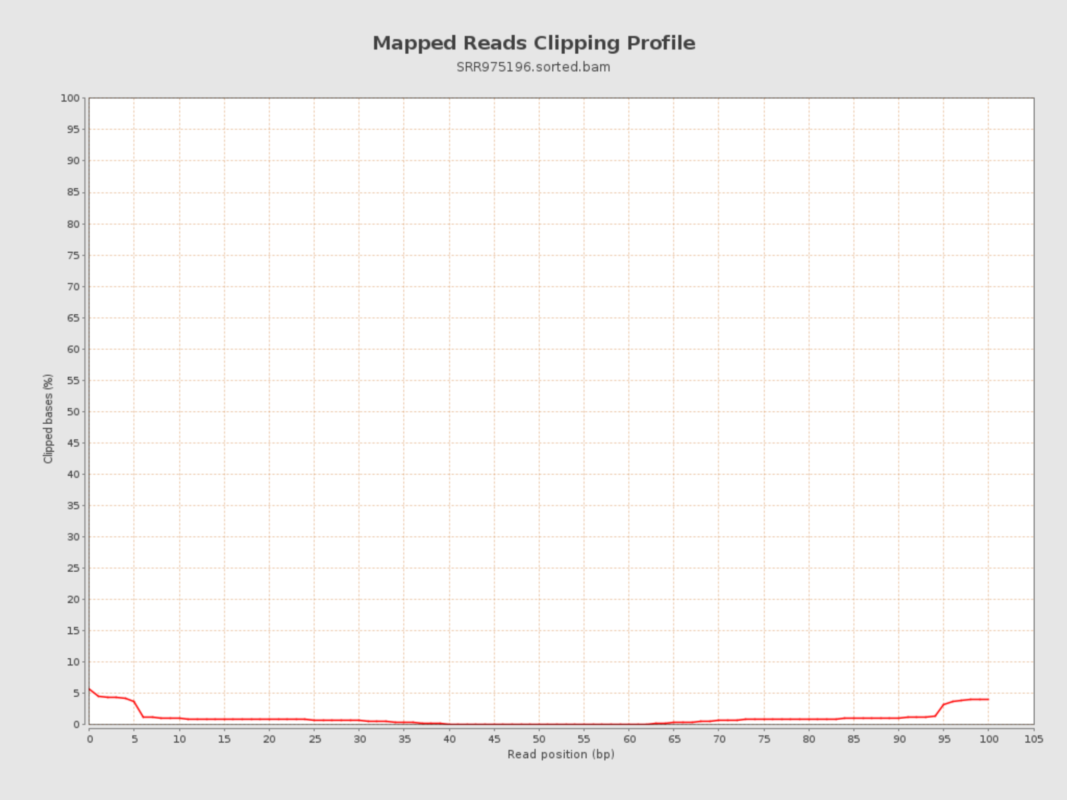
8. Results : Mapped Reads Nucleotide Content



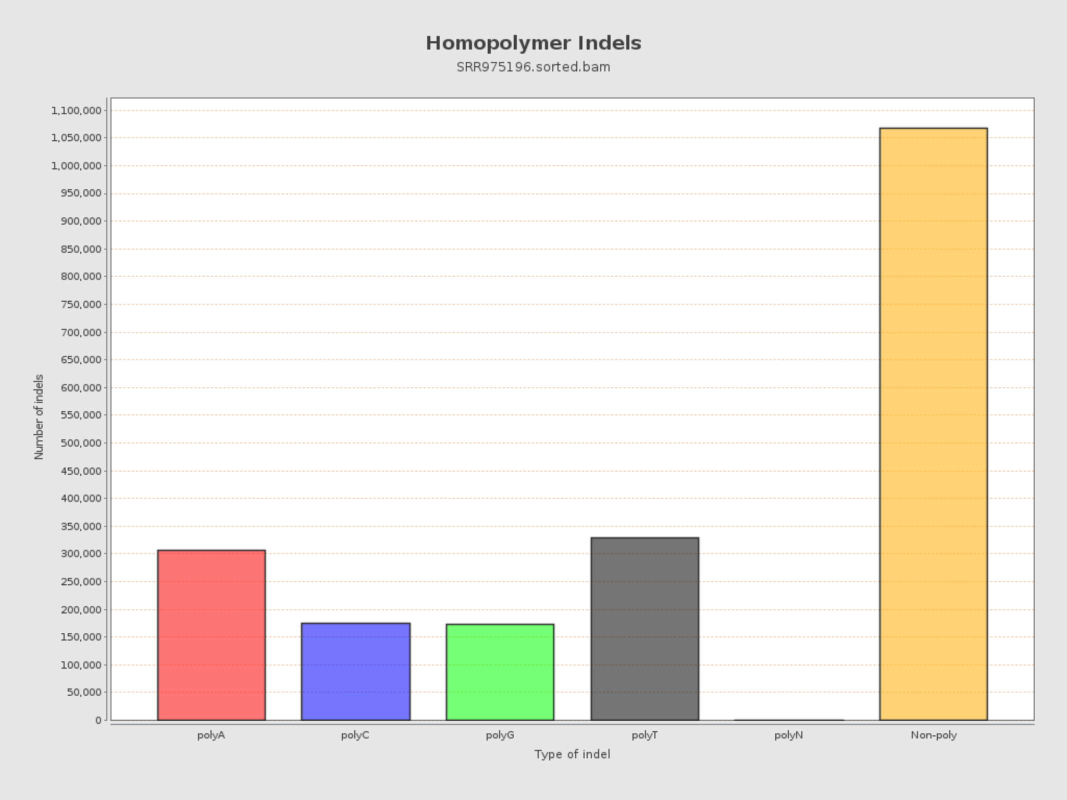
9. Results : Mapped Reads GC-content Distribution



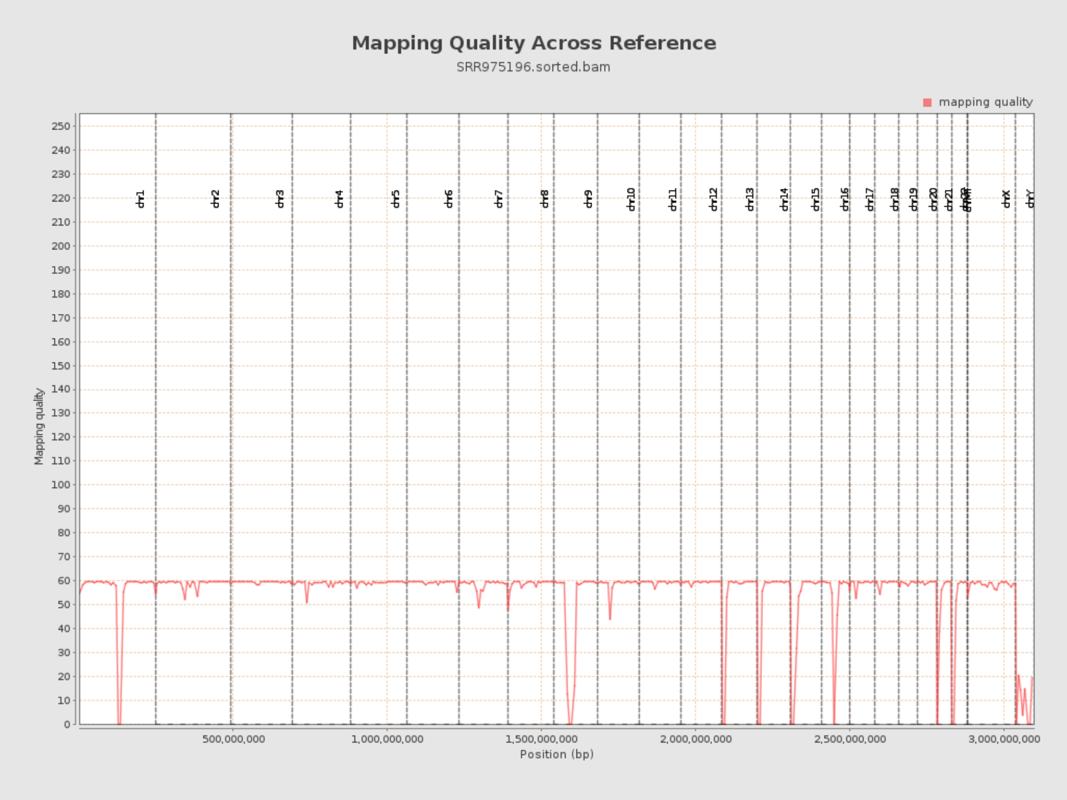
10. Results : Mapped Reads Clipping Profile



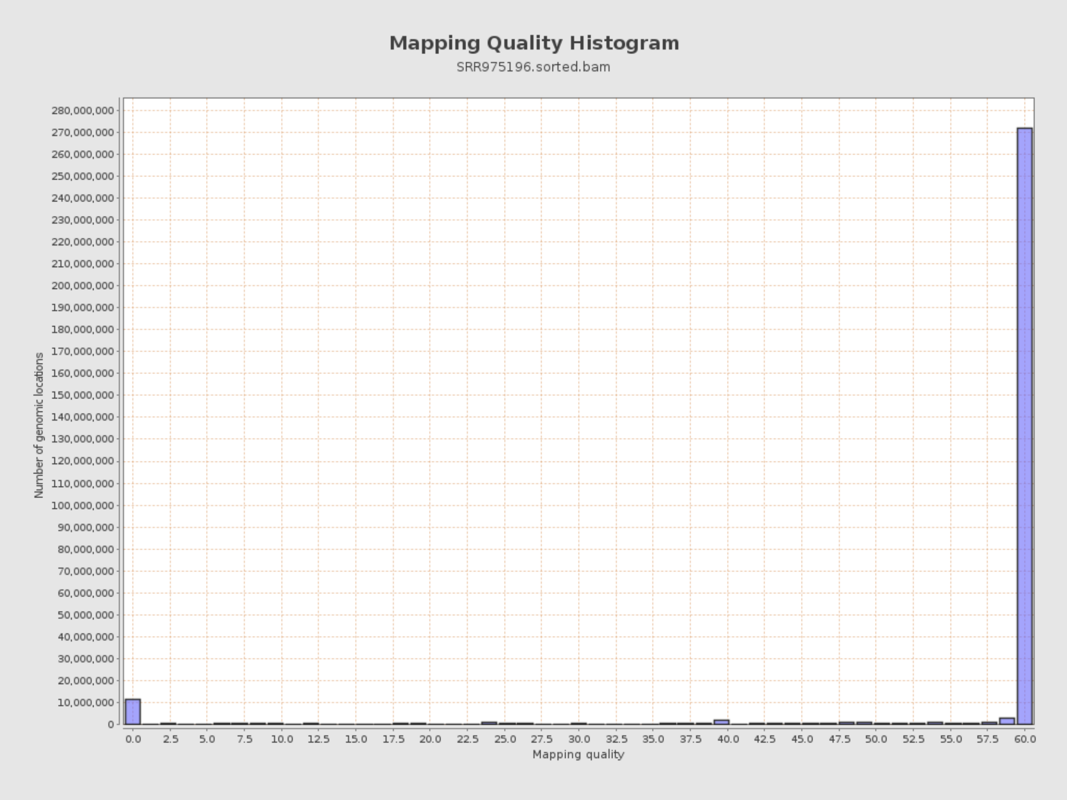
11. Results : Homopolymer Indels



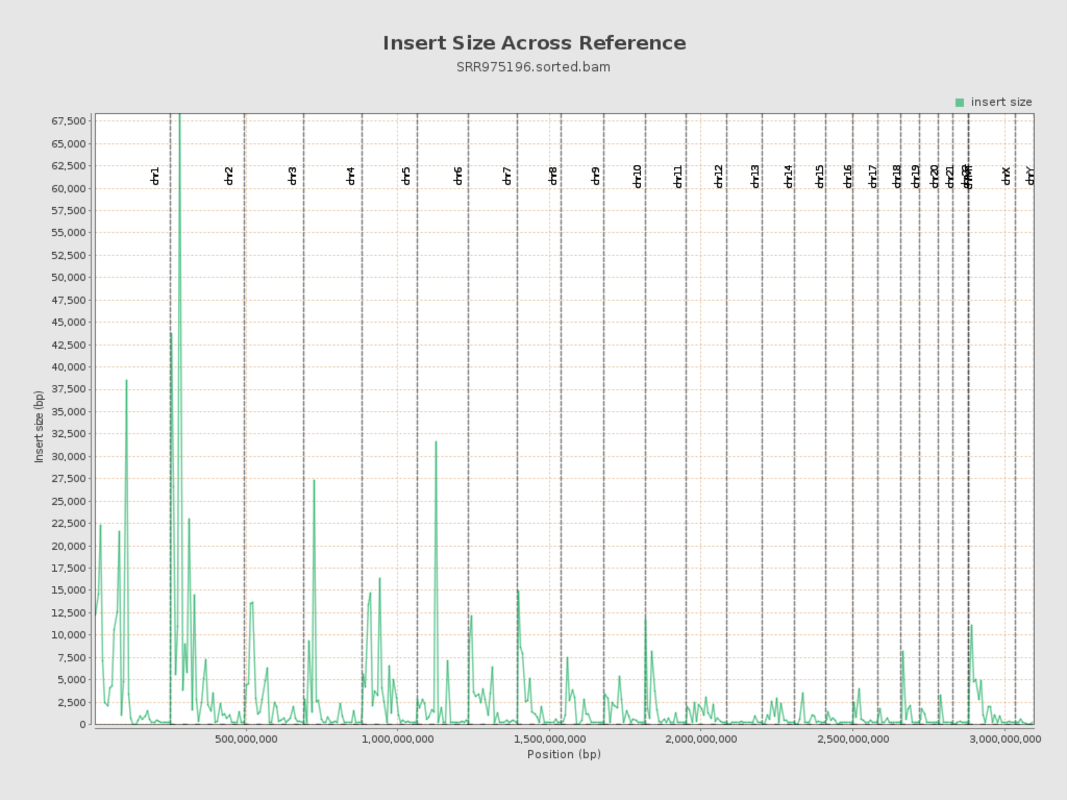
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram