

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 22:24:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975227.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_SRR975227 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975227_1.fastq.gz SRR975227_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 22:24:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975227.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,434,046
Mapped reads	3,400,047 / 99.01%
Unmapped reads	33,999 / 0.99%
Mapped paired reads	3,400,047 / 99.01%
Mapped reads, first in pair	1,699,823 / 49.5%
Mapped reads, second in pair	1,700,224 / 49.51%
Mapped reads, both in pair	3,391,344 / 98.76%
Mapped reads, singletons	8,703 / 0.25%
Secondary alignments	0
Supplementary alignments	34,717 / 1.01%
Read min/max/mean length	30 / 101 / 101.42
Duplicated reads (estimated)	103,711 / 3.02%
Duplication rate	1.39%
Clipped reads	1,812,275 / 52.77%

2.2. ACGT Content

Number/percentage of A's	97,513,619 / 29.51%
Number/percentage of C's	65,995,818 / 19.97%
Number/percentage of T's	99,325,881 / 30.05%
Number/percentage of G's	67,645,195 / 20.47%
Number/percentage of N's	4,366 / 0%

GC Percentage	40.44%
---------------	--------

2.3. Coverage

Mean	0.1068
Standard Deviation	1.1861

2.4. Mapping Quality

Mean Mapping Quality	53.41
----------------------	-------

2.5. Insert size

Mean	137,462.5
Standard Deviation	3,512,000.94
P25/Median/P75	146 / 177 / 222

2.6. Mismatches and indels

General error rate	0.52%
Mismatches	1,643,086
Insertions	36,178
Mapped reads with at least one insertion	1.03%
Deletions	41,585
Mapped reads with at least one deletion	1.19%
Homopolymer indels	40.34%

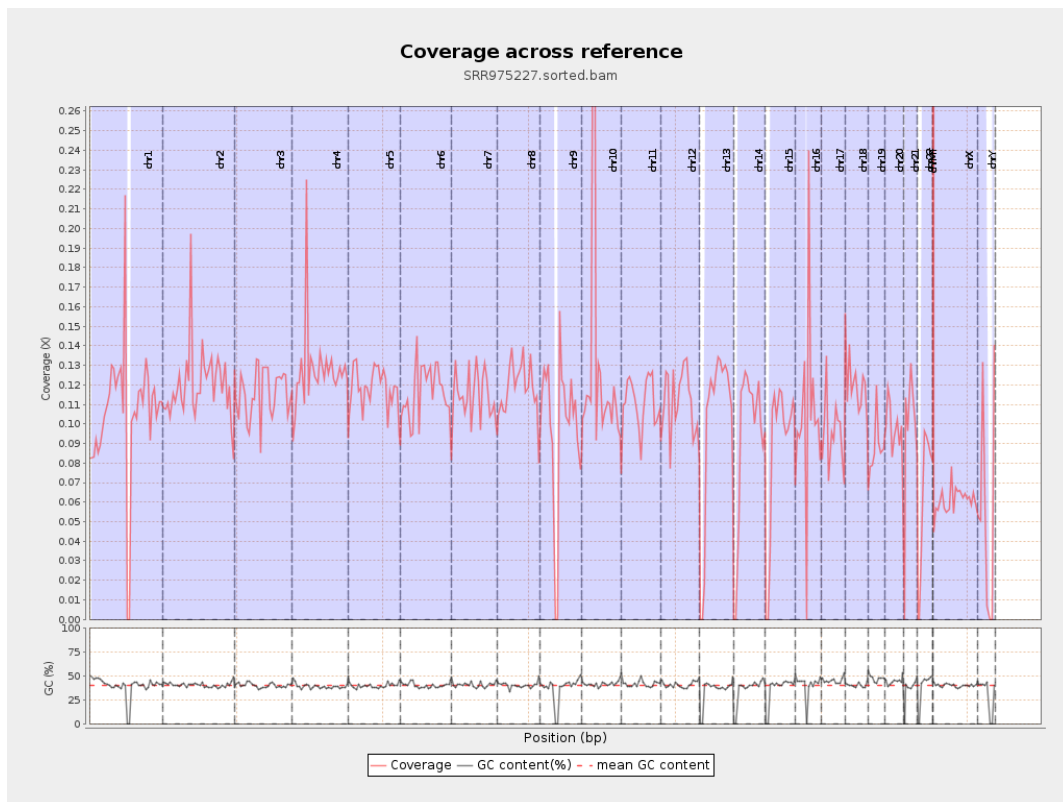
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
------	--------	--------	------	----------

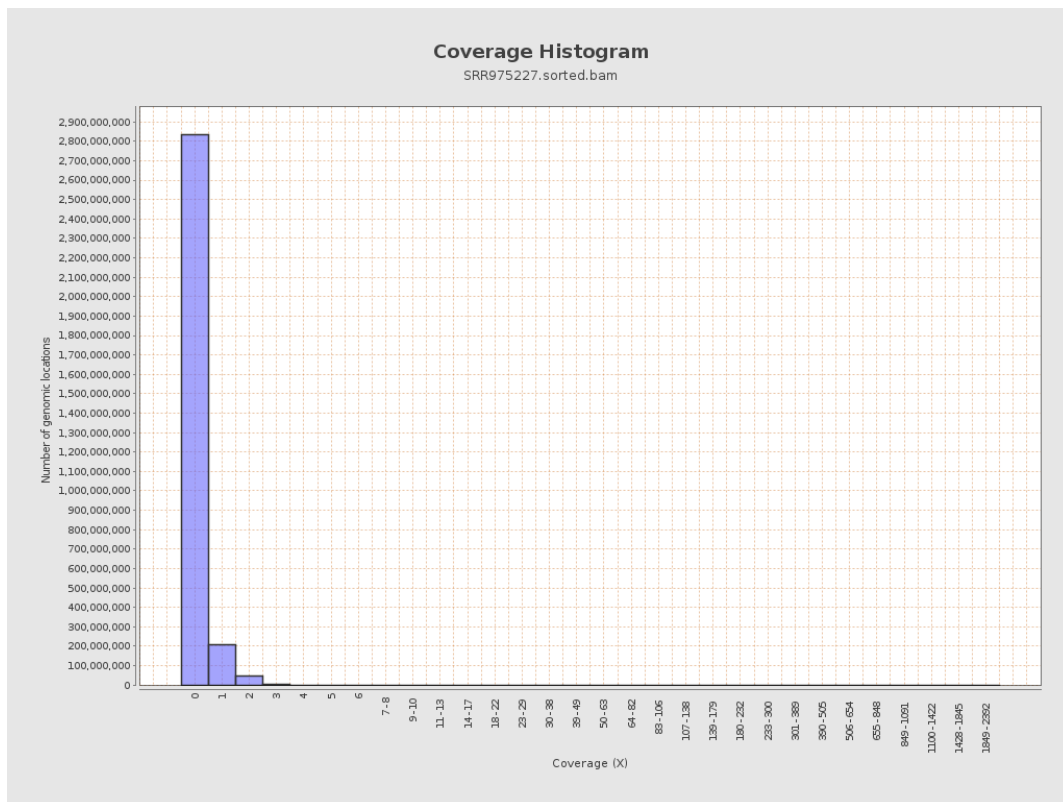
		bases	coverage	deviation
chr1	249250621	26298956	0.1055	2.4632
chr2	243199373	29211553	0.1201	0.7575
chr3	198022430	22943717	0.1159	0.413
chr4	191154276	24419765	0.1277	0.9553
chr5	180915260	21296136	0.1177	0.3943
chr6	171115067	19974595	0.1167	0.4739
chr7	159138663	18148427	0.114	0.7693
chr8	146364022	17343831	0.1185	1.7022
chr9	141213431	14111159	0.0999	1.149
chr10	135534747	17362183	0.1281	2.8868
chr11	135006516	14972457	0.1109	0.5694
chr12	133851895	14860108	0.111	0.3829
chr13	115169878	11612024	0.1008	0.3625
chr14	107349540	10081042	0.0939	0.3553
chr15	102531392	8870466	0.0865	0.3352
chr16	90354753	9409963	0.1041	1.0498
chr17	81195210	7788241	0.0959	0.6698
chr18	78077248	9378888	0.1201	1.3053
chr19	59128983	5224907	0.0884	1.2109
chr20	63025520	6184091	0.0981	0.4131
chr21	48129895	4718722	0.098	0.5699
chr22	51304566	3244021	0.0632	0.4859
chrMT	16571	365083	22.0314	6.3054
chrX	155270560	9459942	0.0609	0.3627

chrY	59373566	3304824	0.0557	1.0611
------	----------	---------	--------	--------

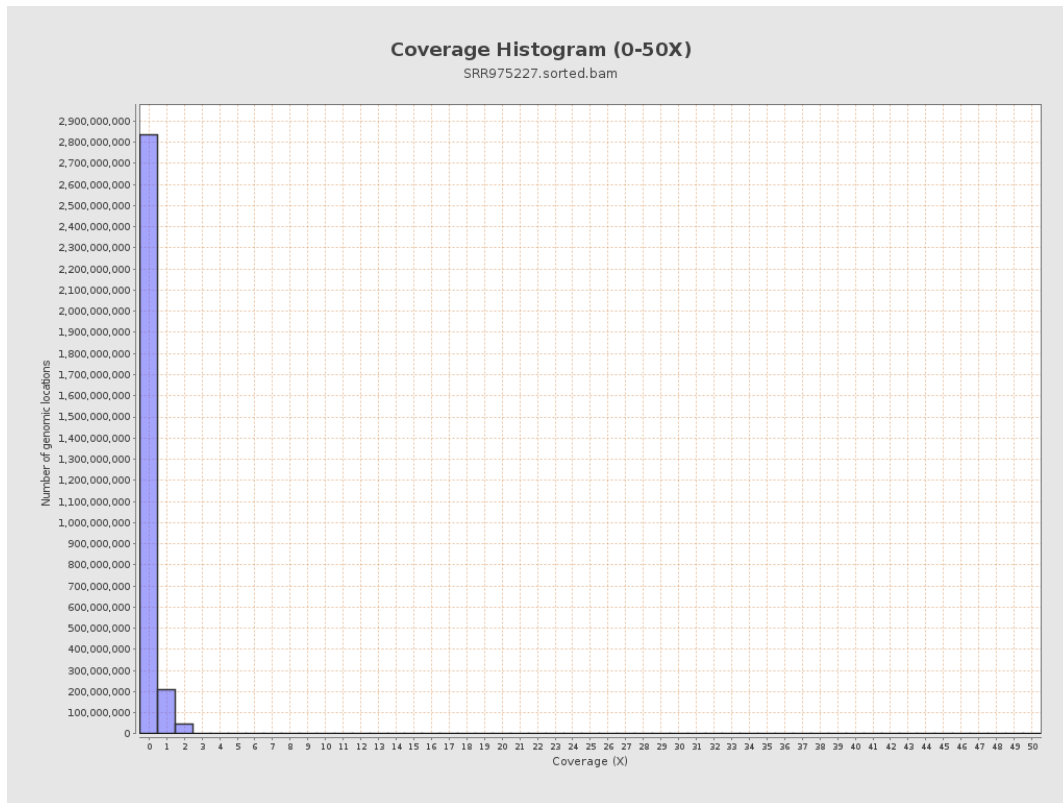
3. Results : Coverage across reference



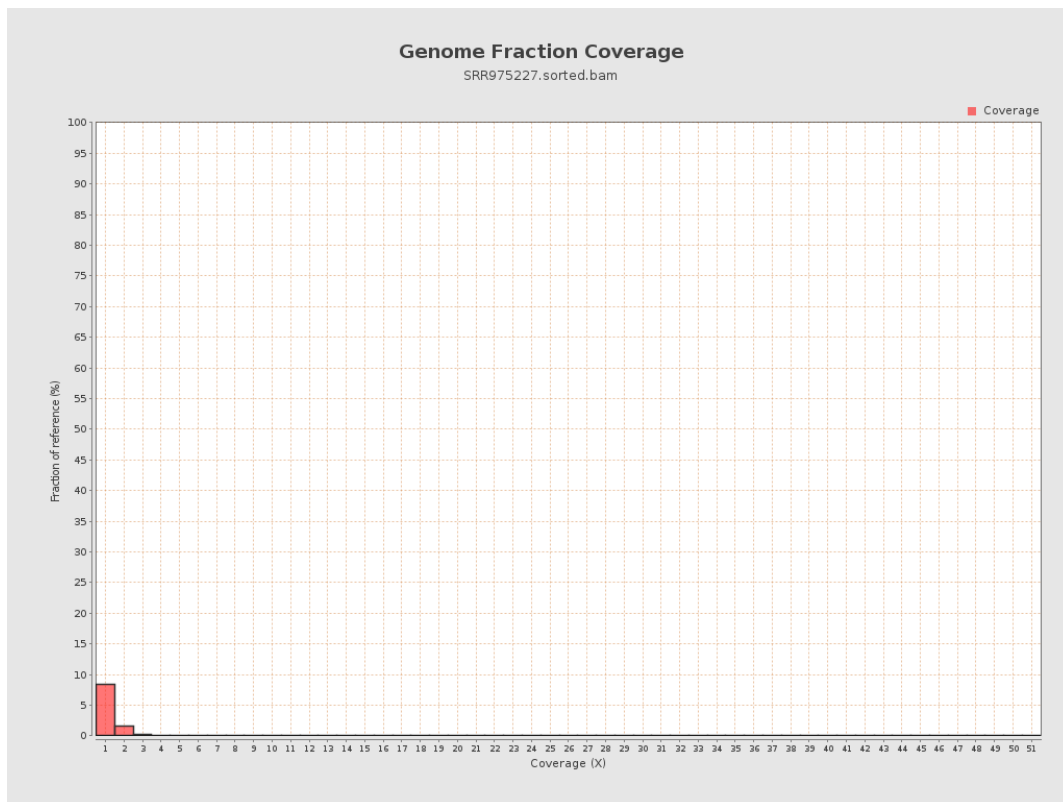
4. Results : Coverage Histogram



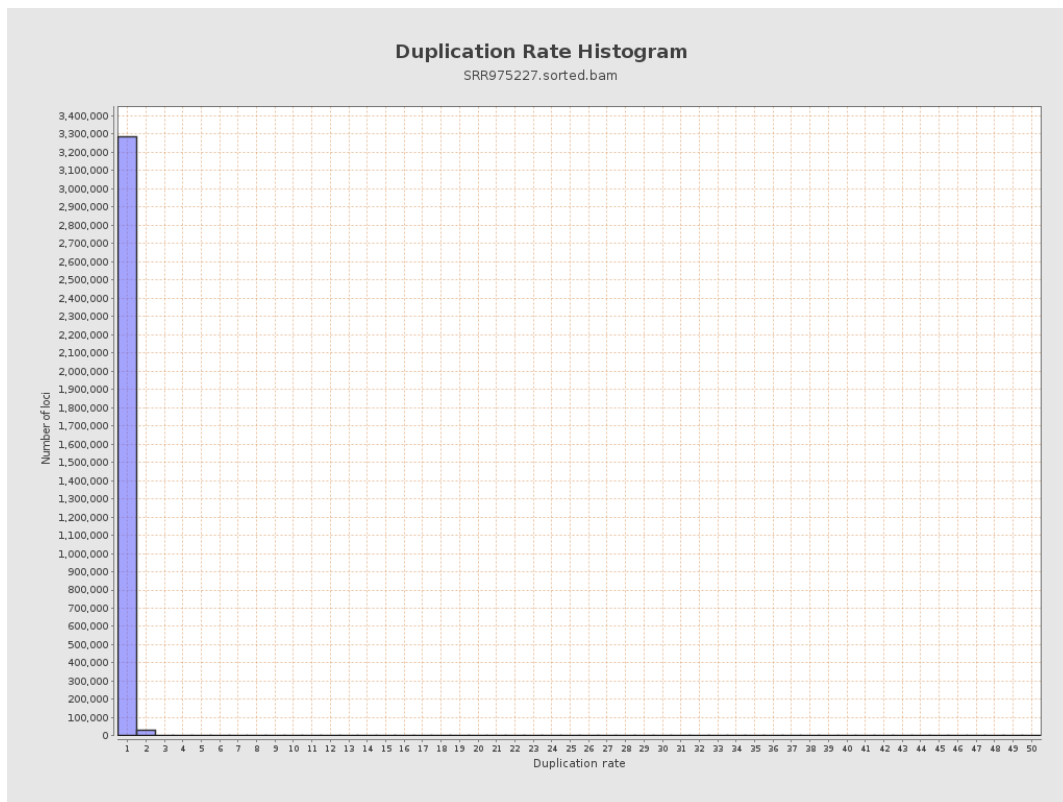
5. Results : Coverage Histogram (0-50X)



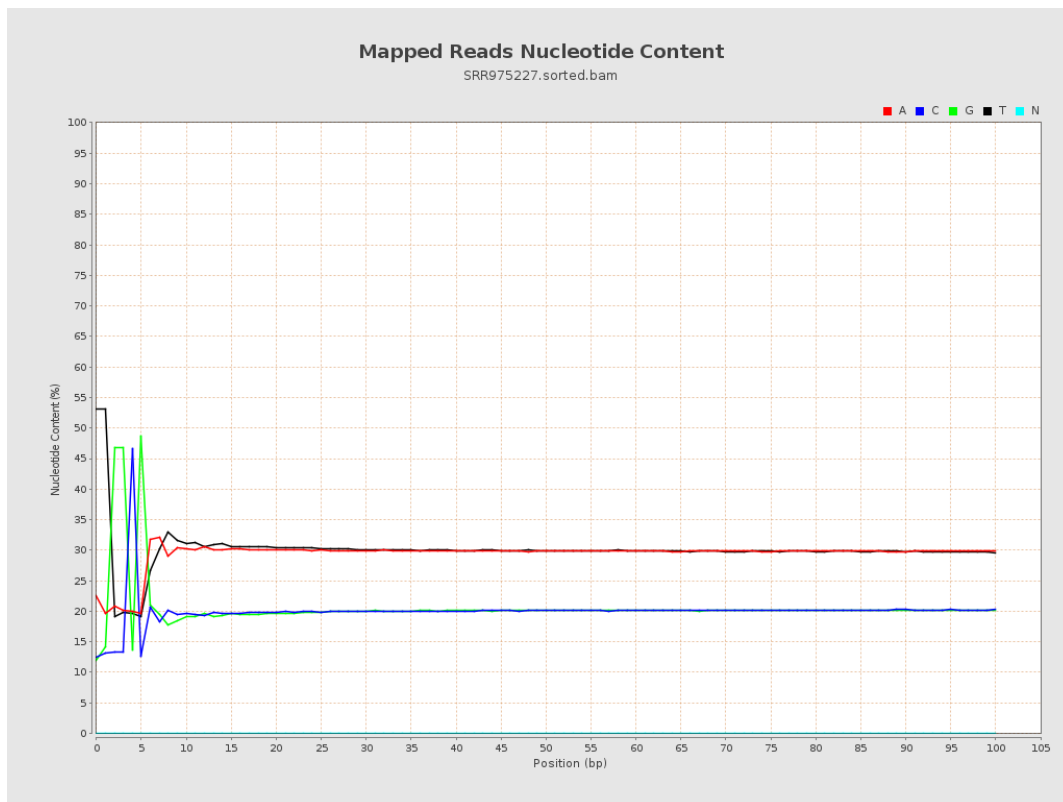
6. Results : Genome Fraction Coverage



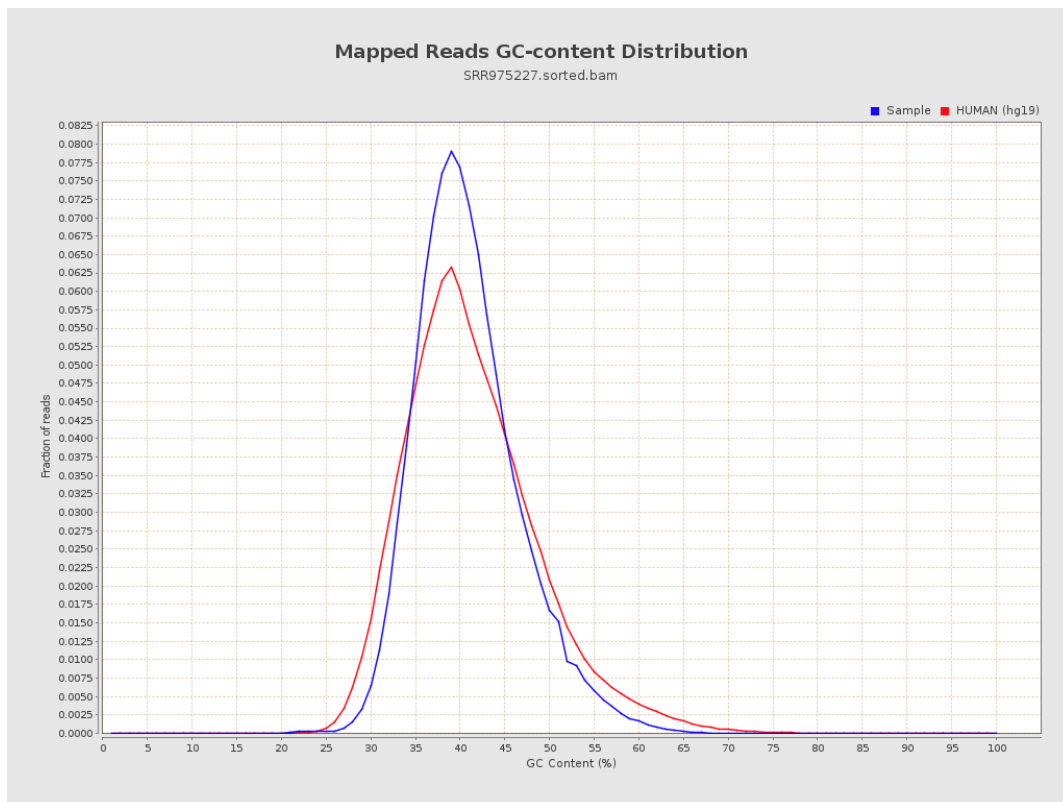
7. Results : Duplication Rate Histogram



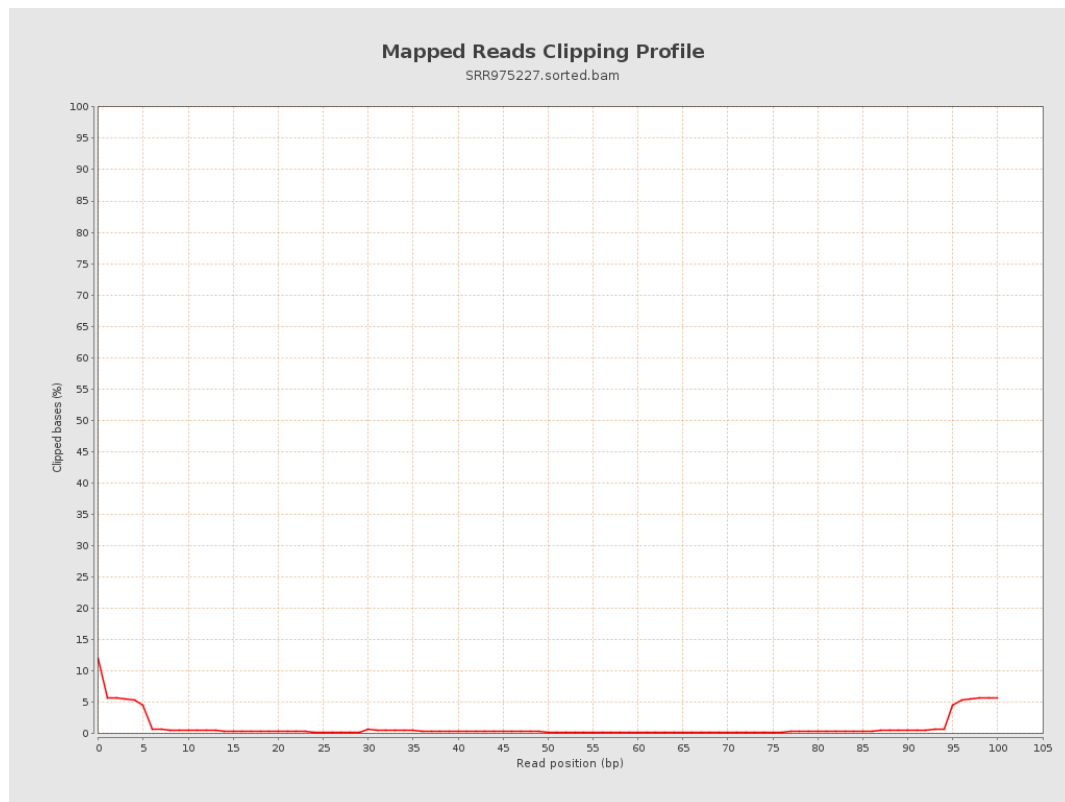
8. Results : Mapped Reads Nucleotide Content



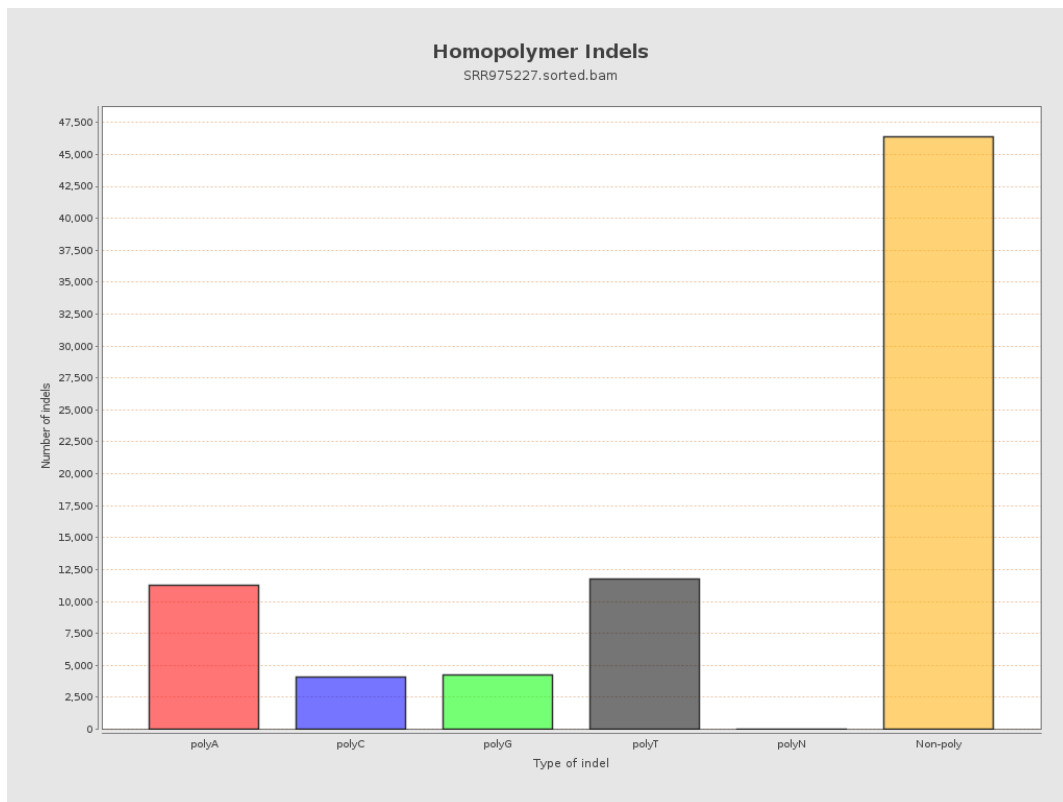
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



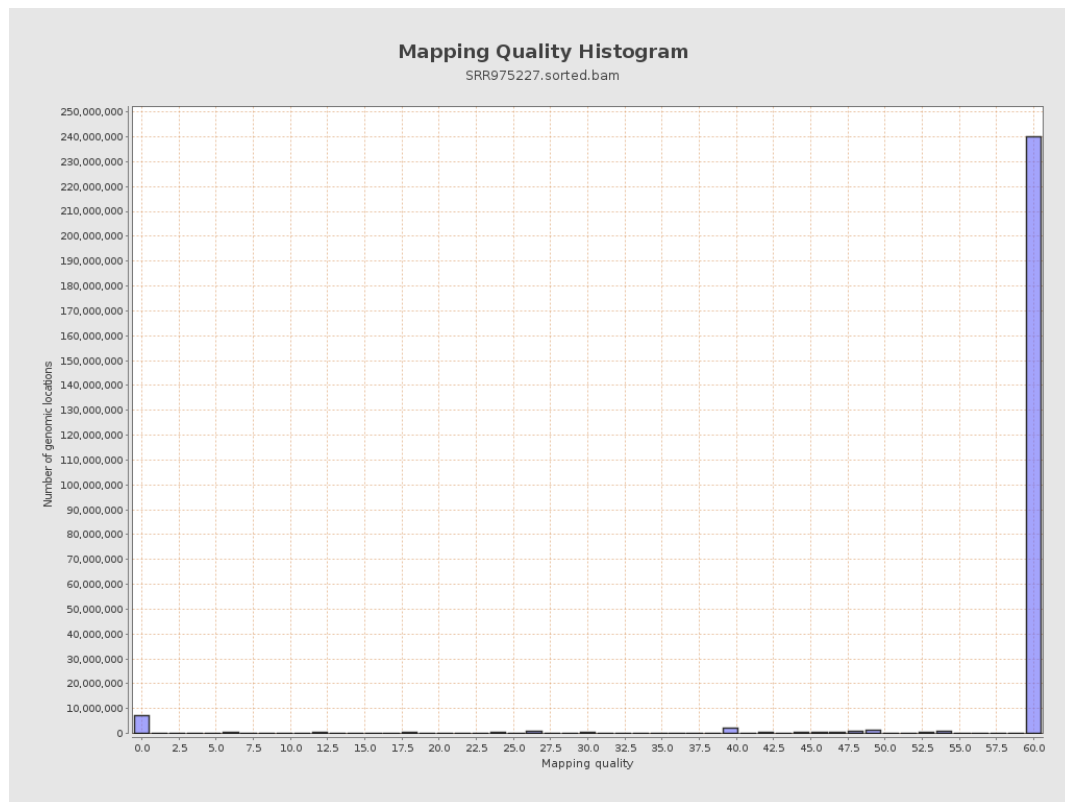
11. Results : Homopolymer Indels



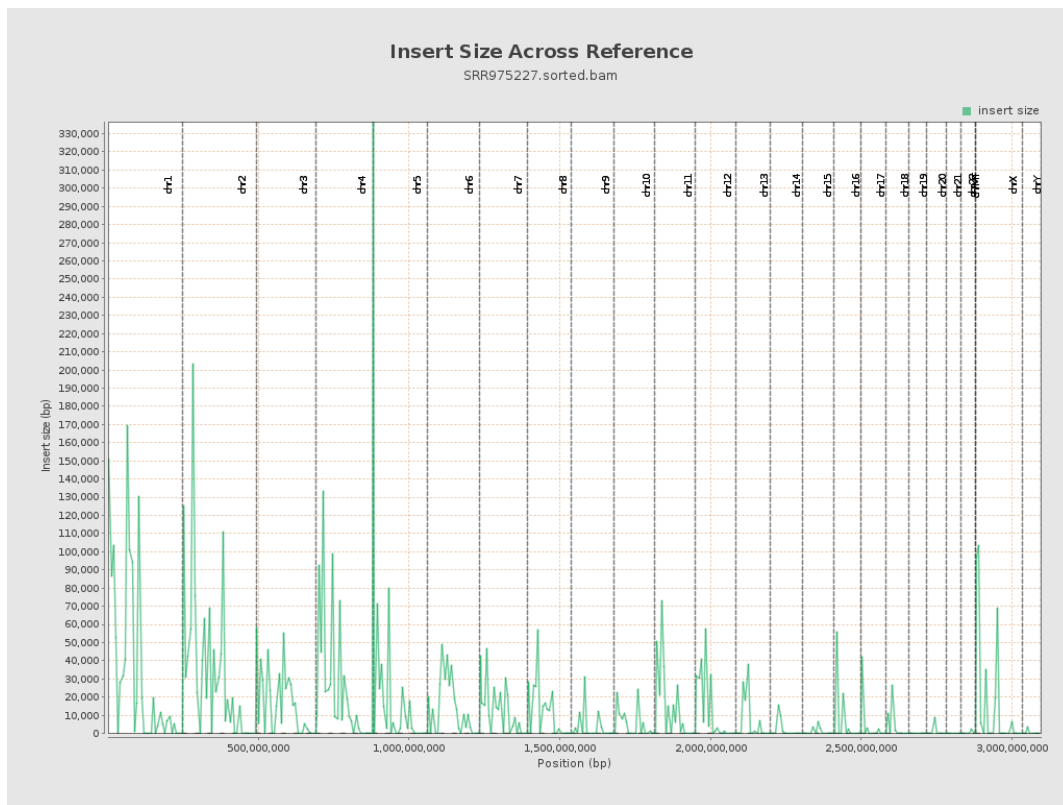
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

