

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/12 10:49:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695914.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/seu_share/home/tujing/220232460/software/bwa-0.7.18/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR1695914 /seu_share/home/tujing/220232460/reference/homo_bwa/hsa.fa SRR1695914.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.18-r1243-dirty)
Analysis date:	Thu Sep 12 10:49:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695914.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,694,076
Mapped reads	13,410,902 / 91.27%
Unmapped reads	1,283,174 / 8.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,996 / 0.14%
Read min/max/mean length	8 / 360 / 127.87
Duplicated reads (estimated)	3,228,524 / 21.97%
Duplication rate	20.47%
Clipped reads	3,202,282 / 21.79%

2.2. ACGT Content

Number/percentage of A's	482,552,418 / 27.34%
Number/percentage of C's	397,146,635 / 22.5%
Number/percentage of T's	480,801,175 / 27.24%
Number/percentage of G's	404,356,182 / 22.91%
Number/percentage of N's	0 / 0%
GC Percentage	45.41%

2.3. Coverage

Mean	0.5737

Standard Deviation	1.9397
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	51.92
----------------------	-------

2.5. Mismatches and indels

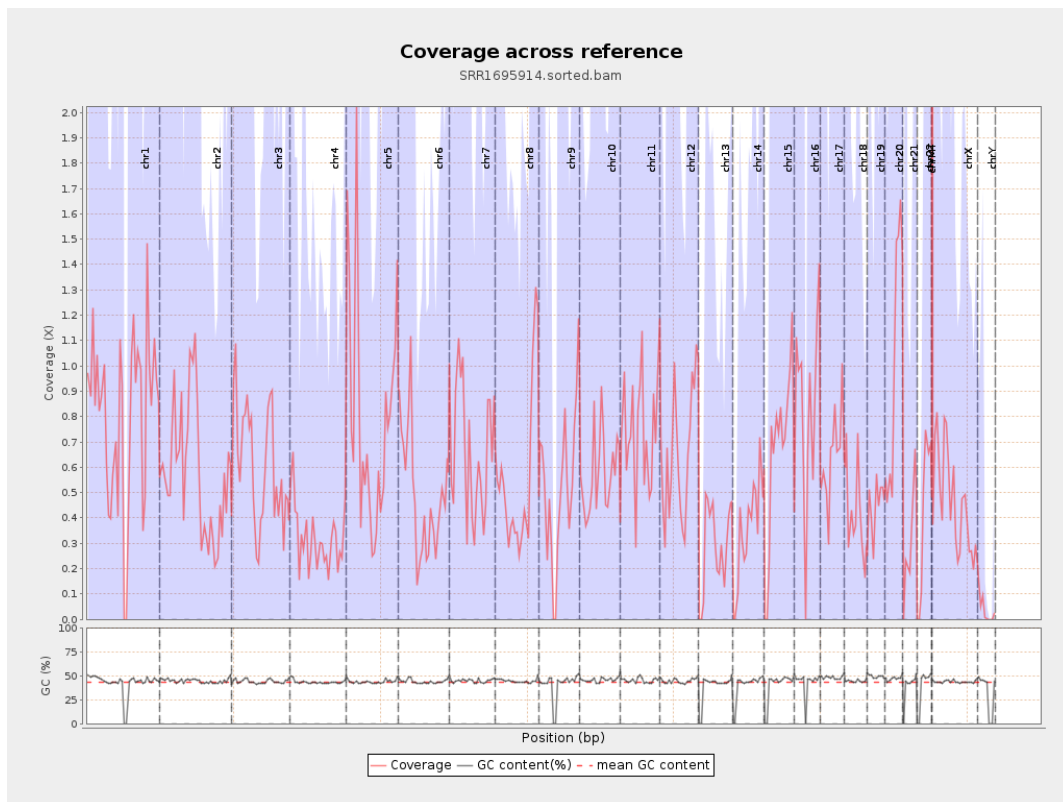
General error rate	1.94%
Mismatches	23,826,531
Insertions	9,540,297
Mapped reads with at least one insertion	43.86%
Deletions	10,118,072
Mapped reads with at least one deletion	47.91%
Homopolymer indels	37.23%

2.6. Chromosome stats

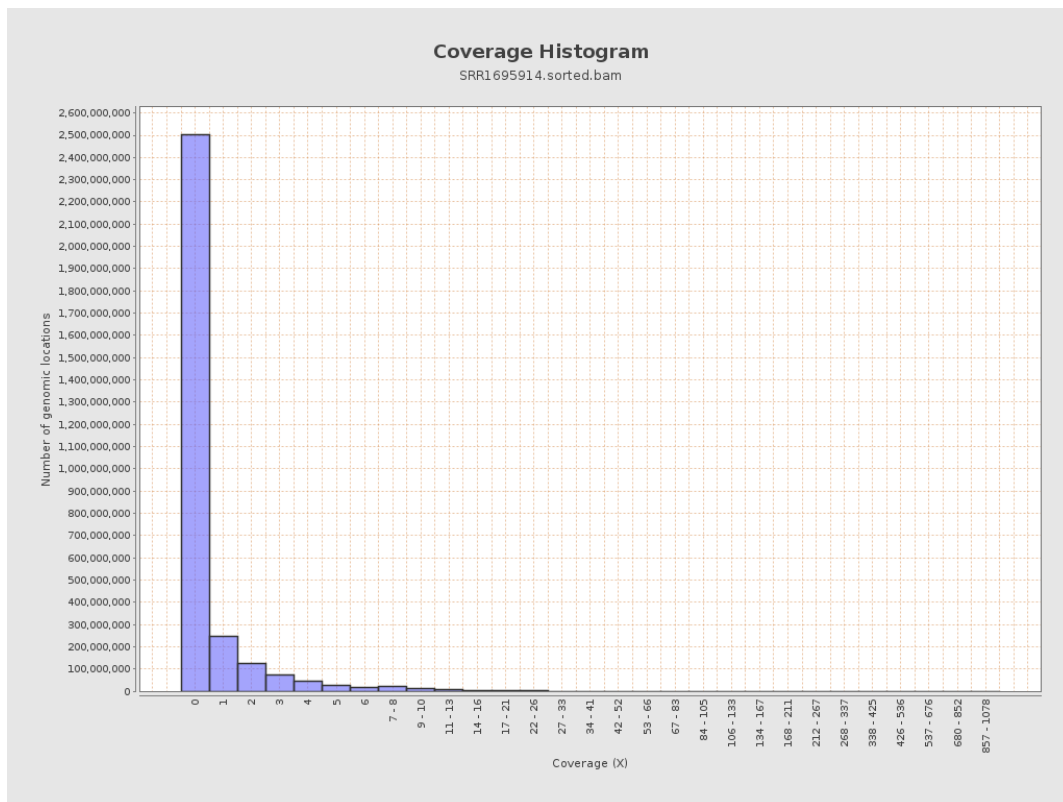
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	200041227	0.8026	2.5849
chr2	243199373	140752896	0.5788	2.0283
chr3	198022430	120512811	0.6086	1.8395
chr4	191154276	60775608	0.3179	1.2972
chr5	180915260	144930622	0.8011	2.3867
chr6	171115067	83590133	0.4885	1.5783
chr7	159138663	105935653	0.6657	1.982

chr8	146364022	79765634	0.545	1.7643
chr9	141213431	74954884	0.5308	1.8541
chr10	135534747	78512709	0.5793	1.8177
chr11	135006516	99017759	0.7334	2.1495
chr12	133851895	86905993	0.6493	1.9438
chr13	115169878	33137040	0.2877	1.1212
chr14	107349540	37511787	0.3494	1.2737
chr15	102531392	68425630	0.6674	2.0814
chr16	90354753	74872228	0.8286	2.6405
chr17	81195210	52567946	0.6474	1.948
chr18	78077248	32912346	0.4215	1.6905
chr19	59128983	26633859	0.4504	1.6857
chr20	63025520	63284840	1.0041	2.7446
chr21	48129895	15685066	0.3259	2.1078
chr22	51304566	22078227	0.4303	1.5101
chrMT	16571	253794	15.3156	17.4686
chrX	155270560	70882217	0.4565	1.499
chrY	59373566	2175501	0.0366	0.7477

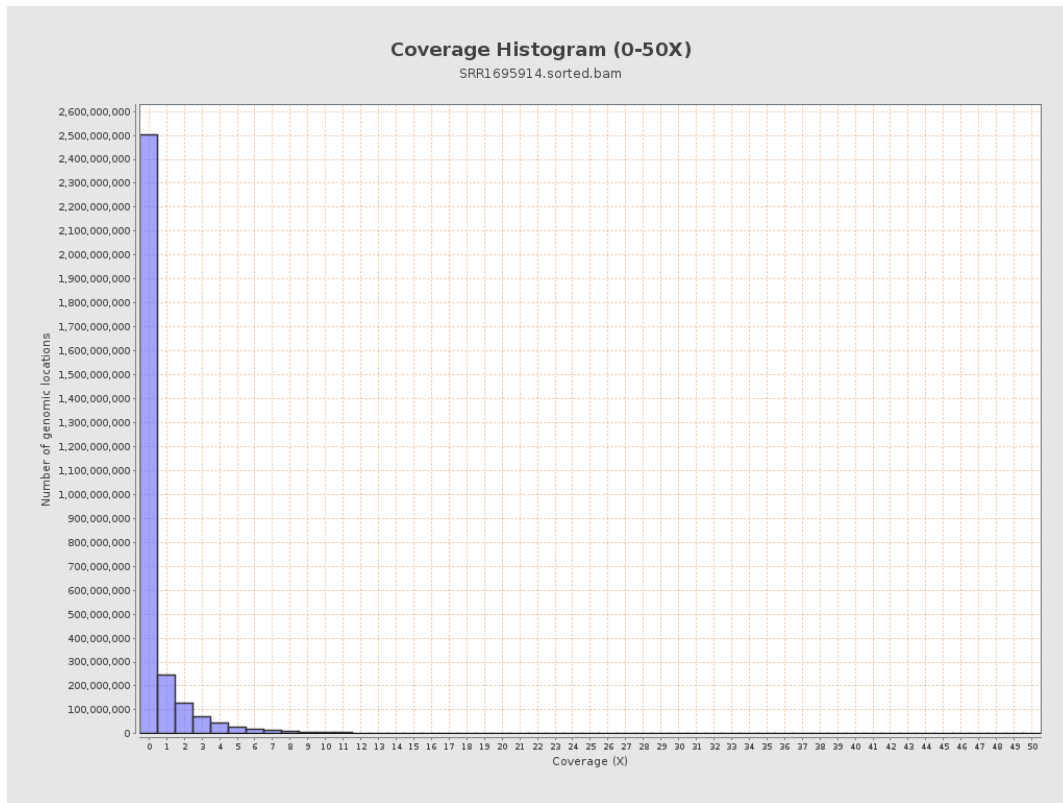
3. Results : Coverage across reference



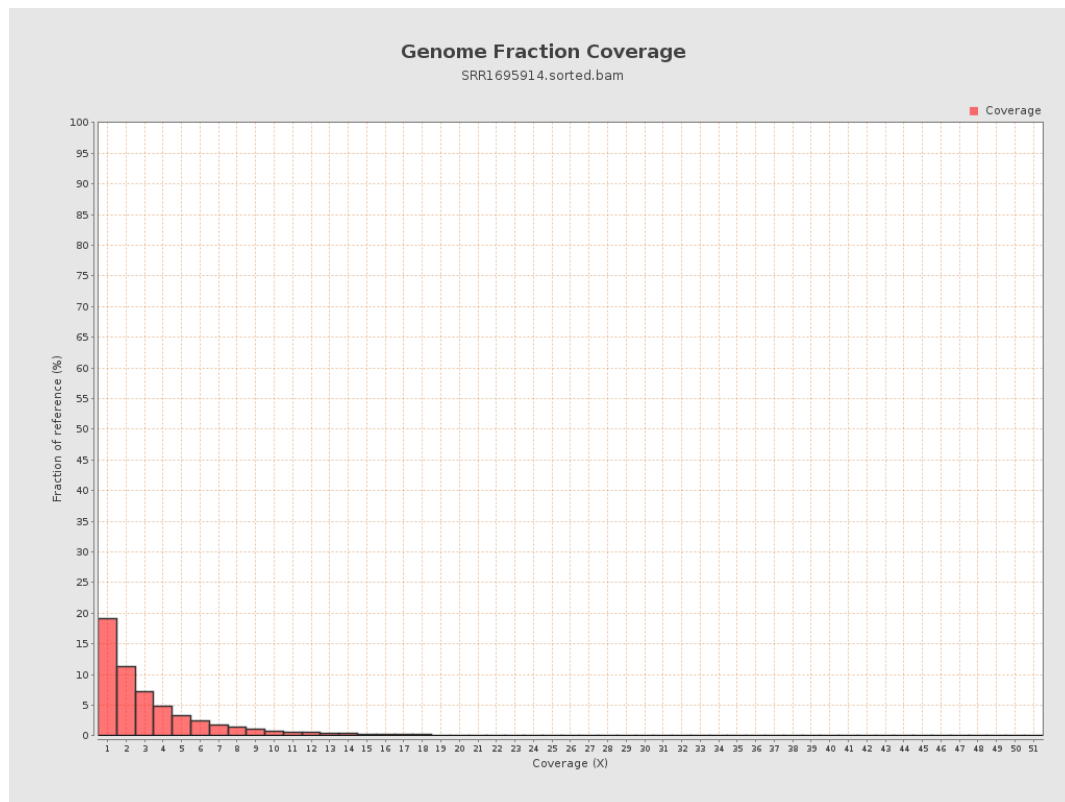
4. Results : Coverage Histogram



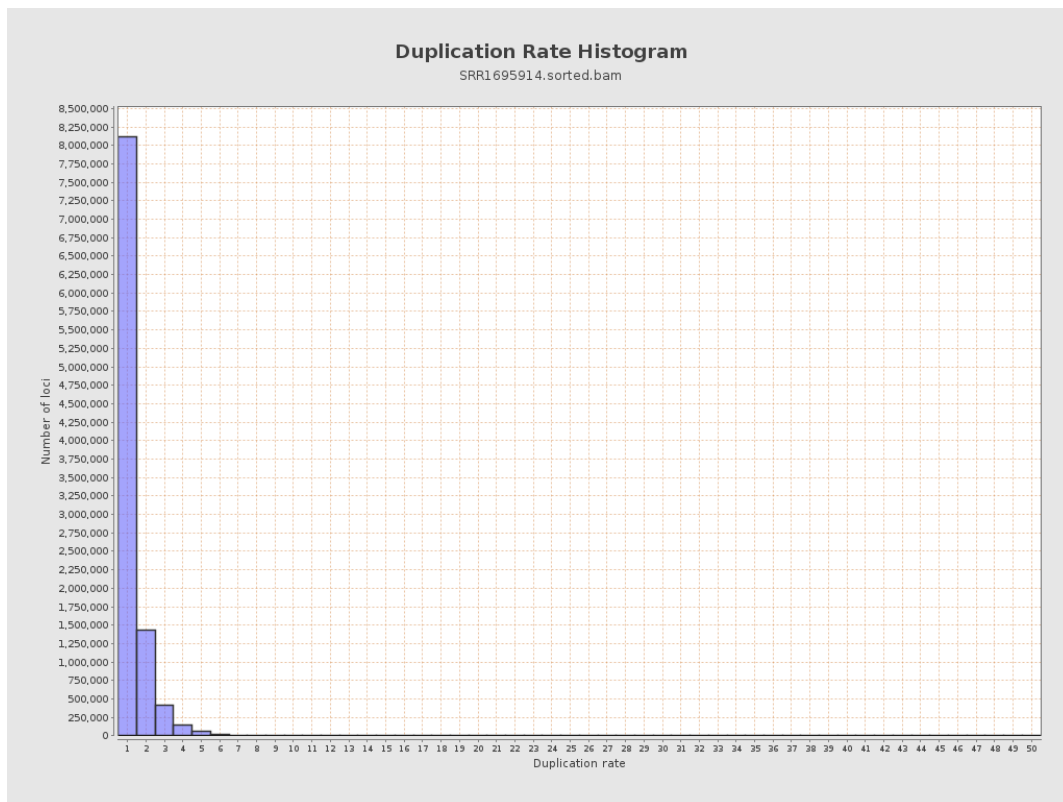
5. Results : Coverage Histogram (0-50X)



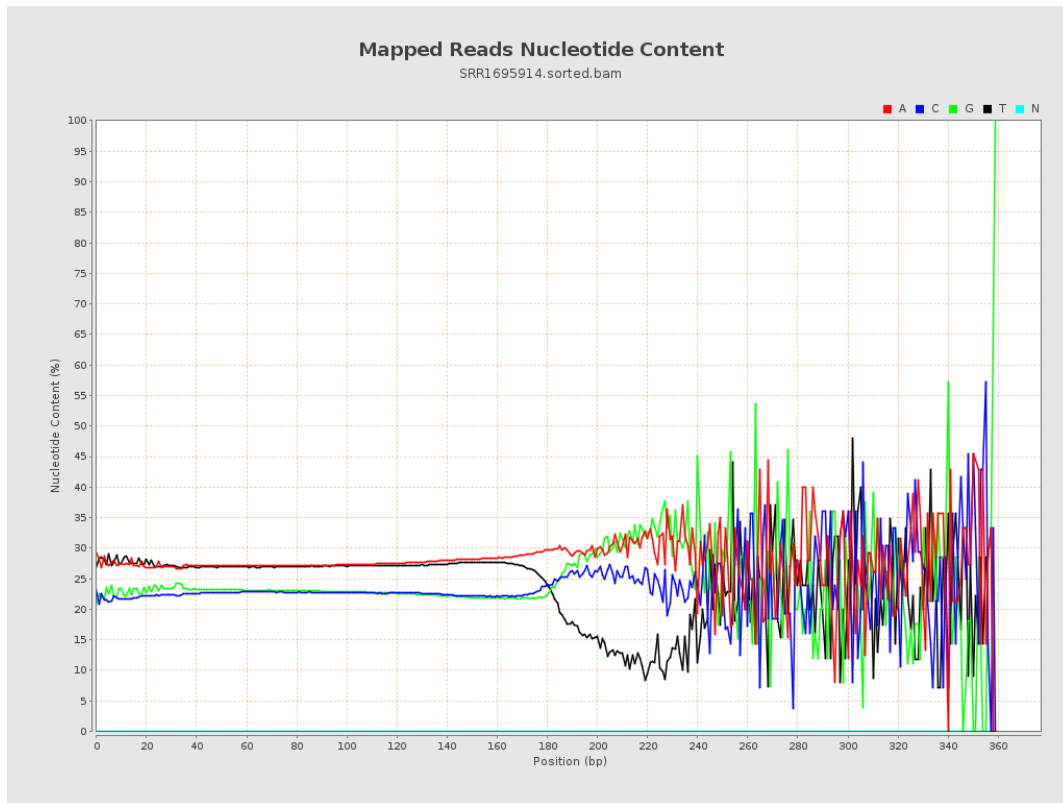
6. Results : Genome Fraction Coverage



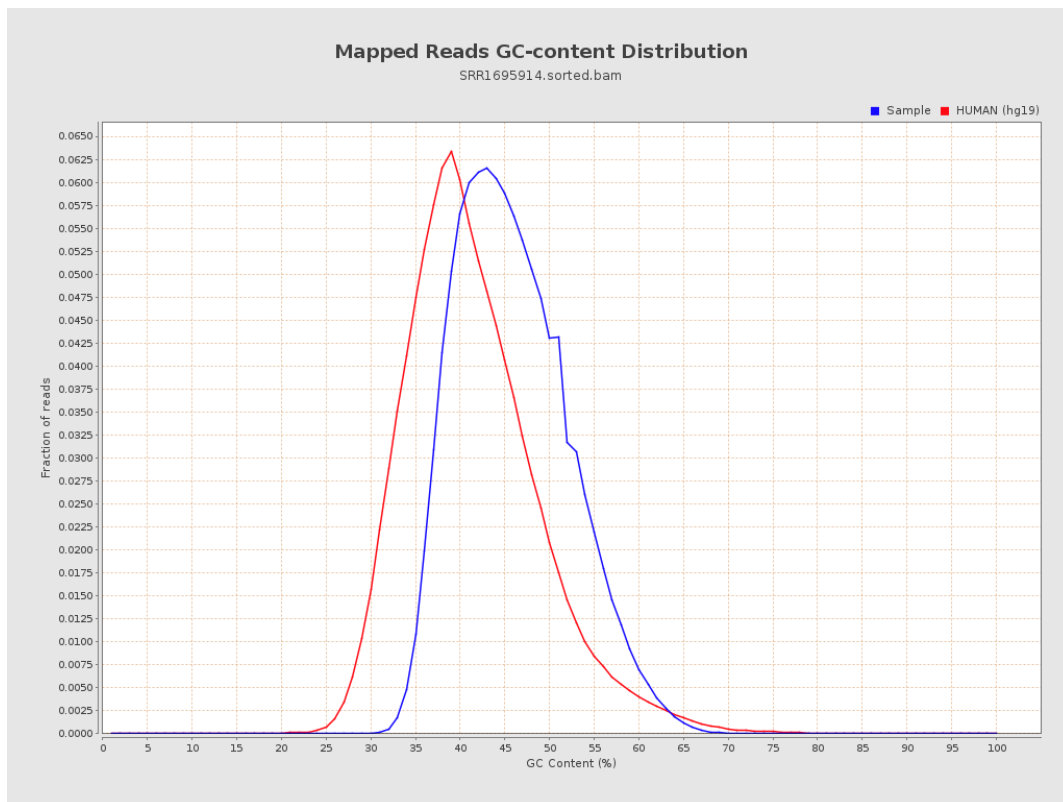
7. Results : Duplication Rate Histogram



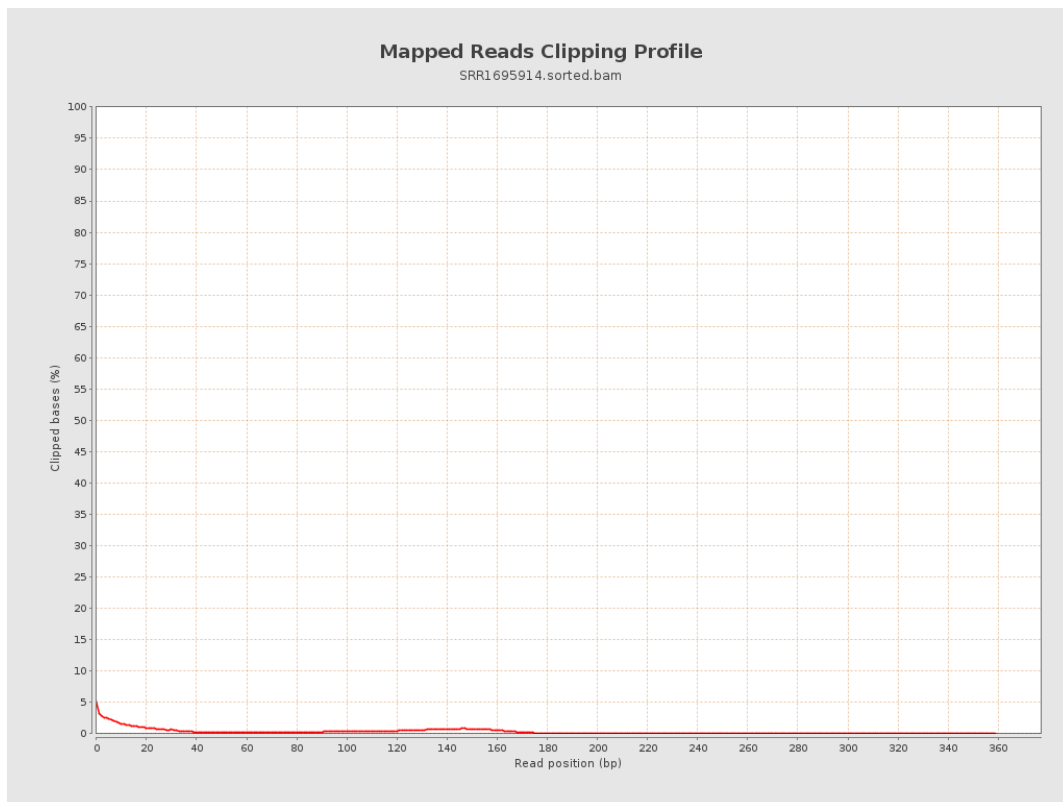
8. Results : Mapped Reads Nucleotide Content



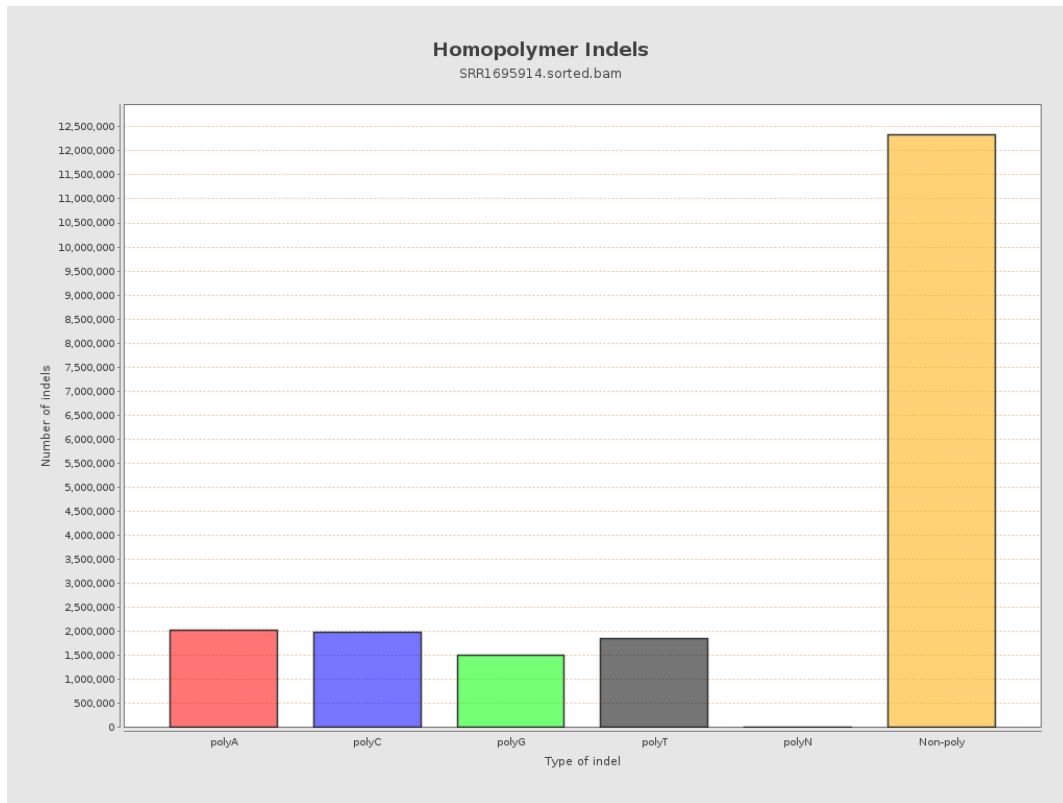
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

