

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/14 07:56:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695976.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_SRR1695976 /seu_share/home/tujing/220232460/reference/homo_bwa/hsa.fa SRR1695976.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.18-r1243-dirty)
Analysis date:	Sat Sep 14 07:56:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695976.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,888,066
Mapped reads	12,637,194 / 90.99%
Unmapped reads	1,250,872 / 9.01%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,590 / 0.13%
Read min/max/mean length	8 / 361 / 130.53
Duplicated reads (estimated)	2,911,593 / 20.96%
Duplication rate	19.45%
Clipped reads	3,179,887 / 22.9%

2.2. ACGT Content

Number/percentage of A's	464,465,093 / 27.35%
Number/percentage of C's	381,643,111 / 22.47%
Number/percentage of T's	464,944,043 / 27.38%
Number/percentage of G's	387,075,108 / 22.79%
Number/percentage of N's	0 / 0%
GC Percentage	45.27%

2.3. Coverage

Mean	0.5523

Standard Deviation	1.8967
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	52.02
----------------------	-------

2.5. Mismatches and indels

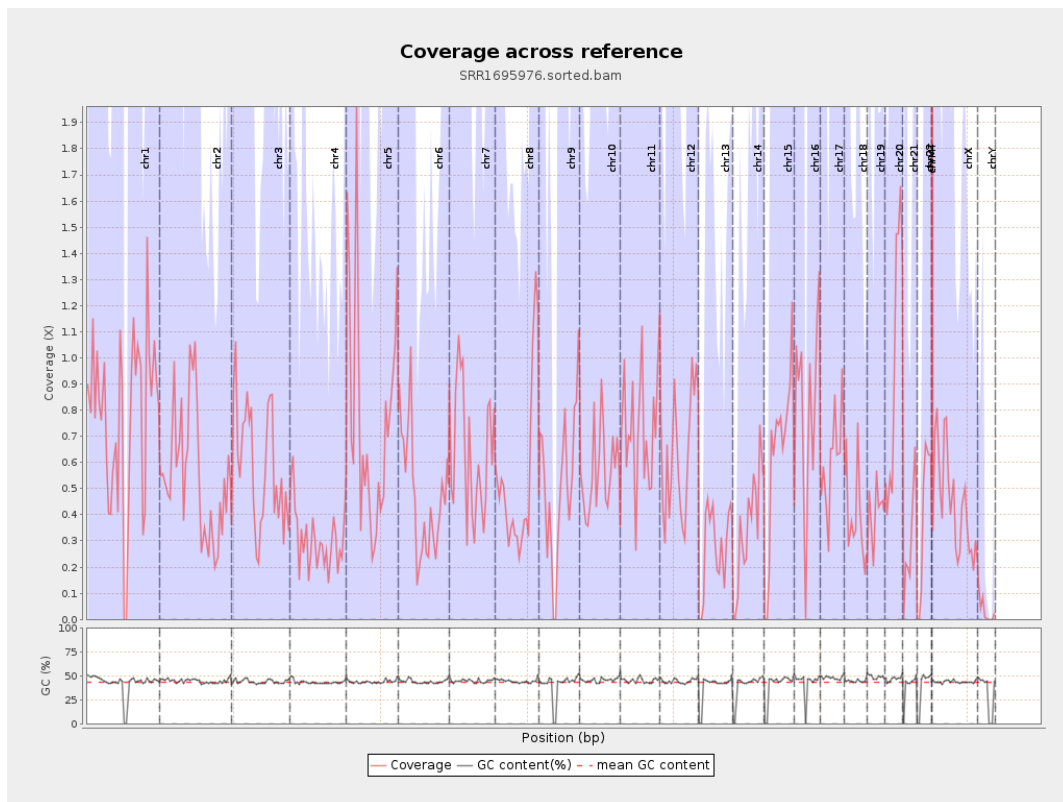
General error rate	1.98%
Mismatches	23,217,778
Insertions	9,593,523
Mapped reads with at least one insertion	45.97%
Deletions	10,328,359
Mapped reads with at least one deletion	50.16%
Homopolymer indels	36.68%

2.6. Chromosome stats

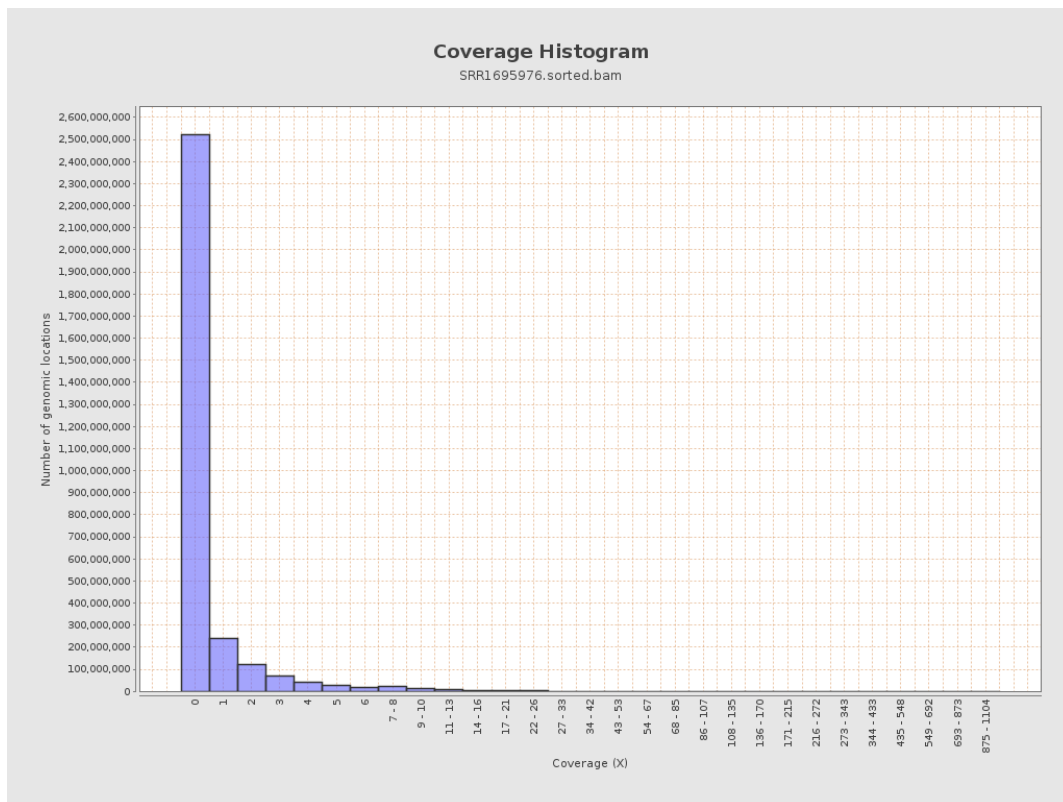
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	192987196	0.7743	2.5606
chr2	243199373	133785436	0.5501	1.9216
chr3	198022430	116393581	0.5878	1.7943
chr4	191154276	58410668	0.3056	1.3159
chr5	180915260	138281870	0.7643	2.3332
chr6	171115067	80580712	0.4709	1.5658
chr7	159138663	101712687	0.6391	1.9436

chr8	146364022	76919788	0.5255	1.7364
chr9	141213431	74094604	0.5247	1.8364
chr10	135534747	77377738	0.5709	1.799
chr11	135006516	96817427	0.7171	2.1166
chr12	133851895	84015615	0.6277	1.9049
chr13	115169878	31670313	0.275	1.1024
chr14	107349540	37275287	0.3472	1.2878
chr15	102531392	65171955	0.6356	2.0078
chr16	90354753	71797491	0.7946	2.4301
chr17	81195210	49956035	0.6153	1.9069
chr18	78077248	31323564	0.4012	1.6306
chr19	59128983	24243291	0.41	1.6091
chr20	63025520	61139243	0.9701	2.6898
chr21	48129895	15043435	0.3126	2.225
chr22	51304566	20528175	0.4001	1.4328
chrMT	16571	254906	15.3827	17.3678
chrX	155270560	67925802	0.4375	1.4691
chrY	59373566	1909331	0.0322	0.652

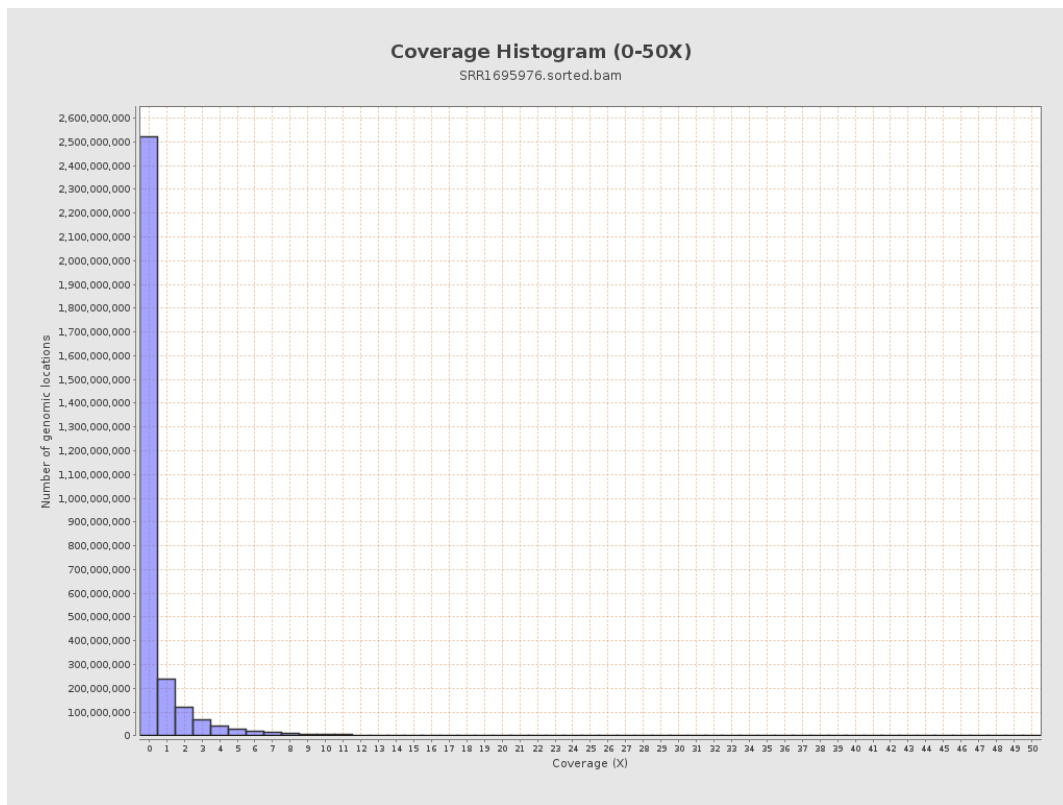
3. Results : Coverage across reference



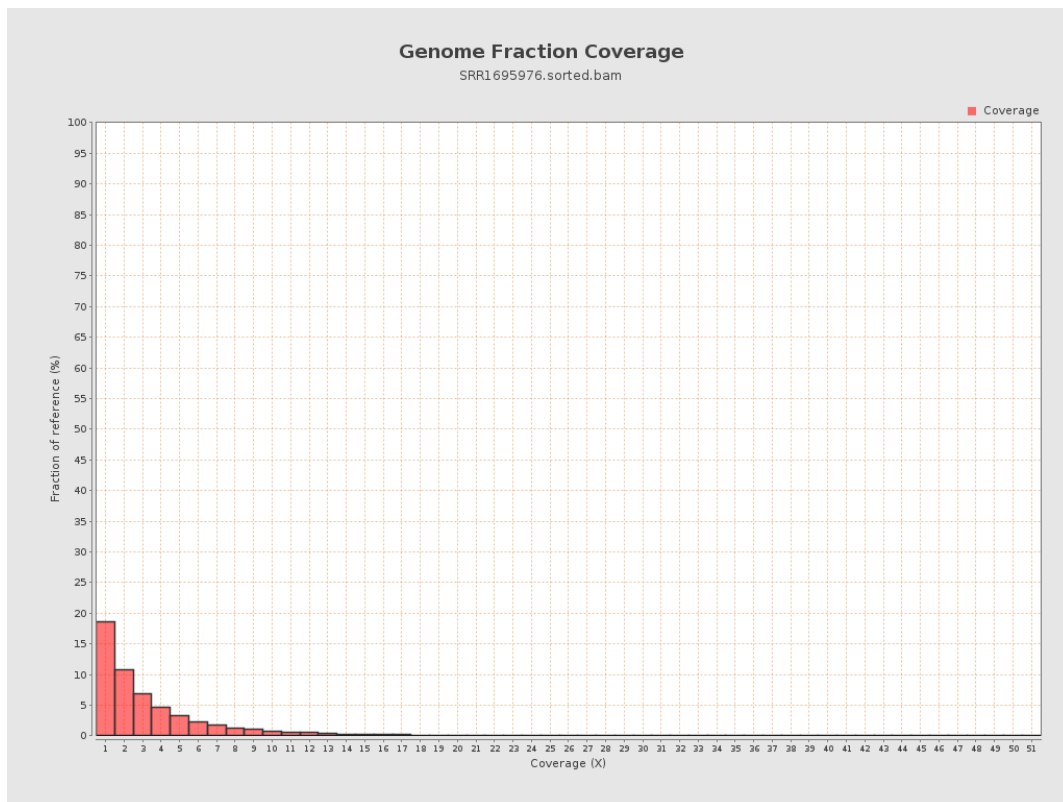
4. Results : Coverage Histogram



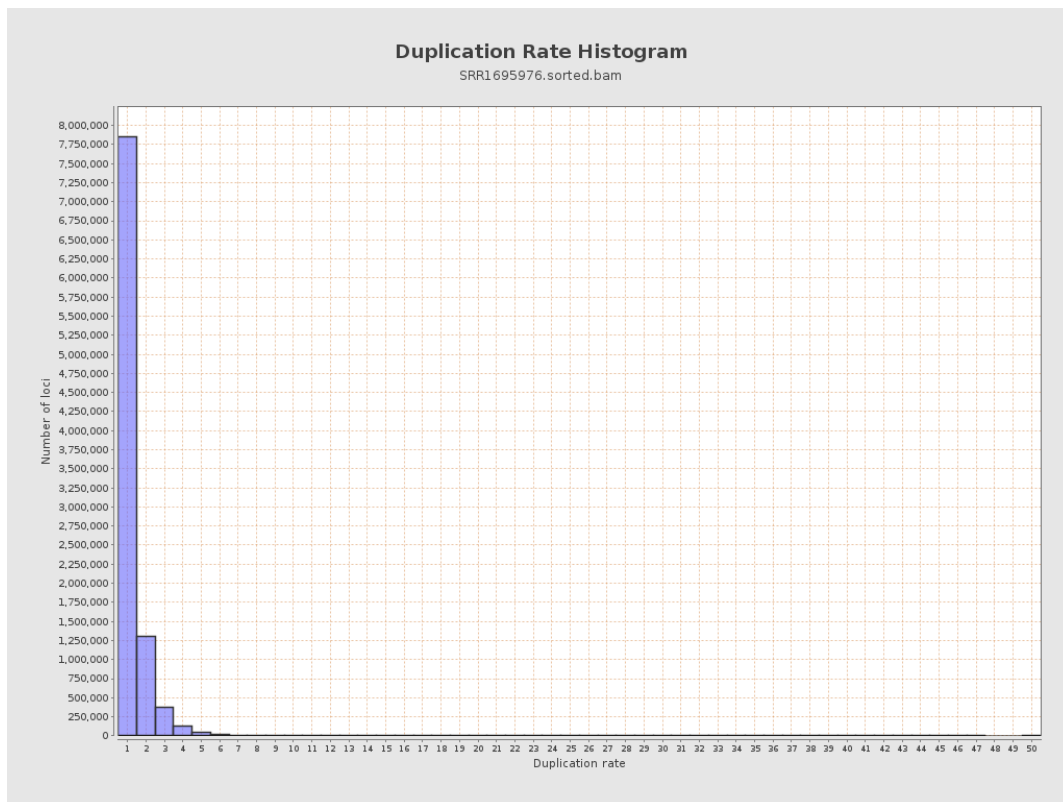
5. Results : Coverage Histogram (0-50X)



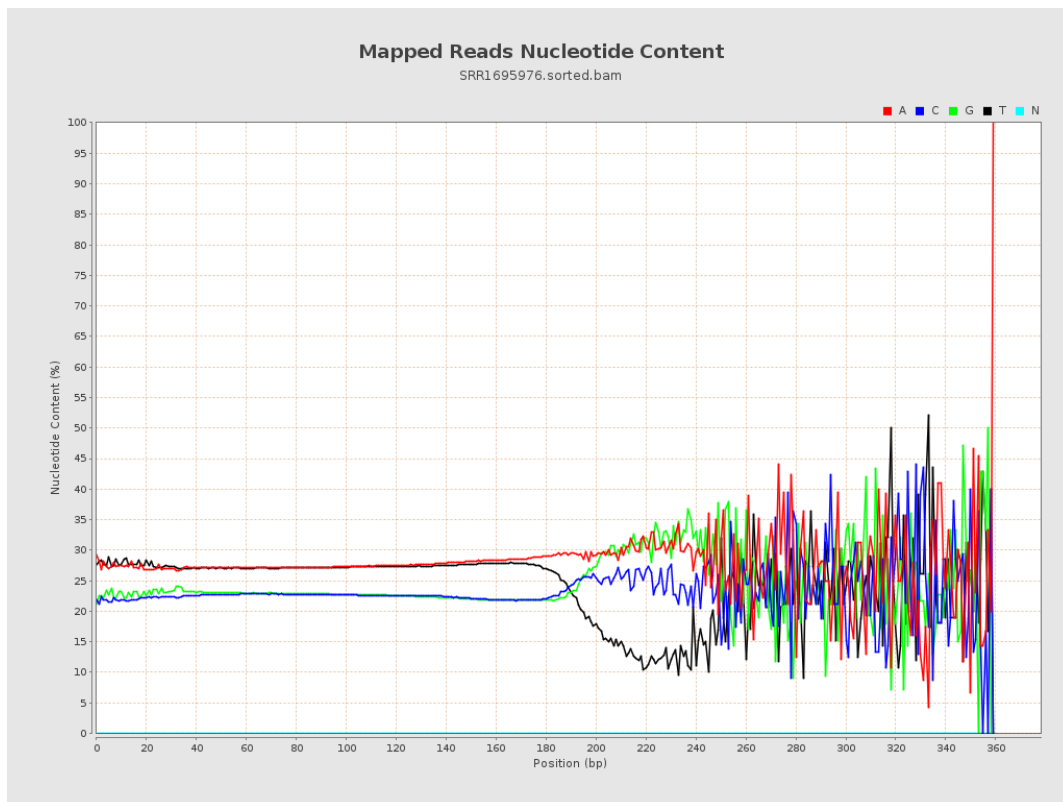
6. Results : Genome Fraction Coverage



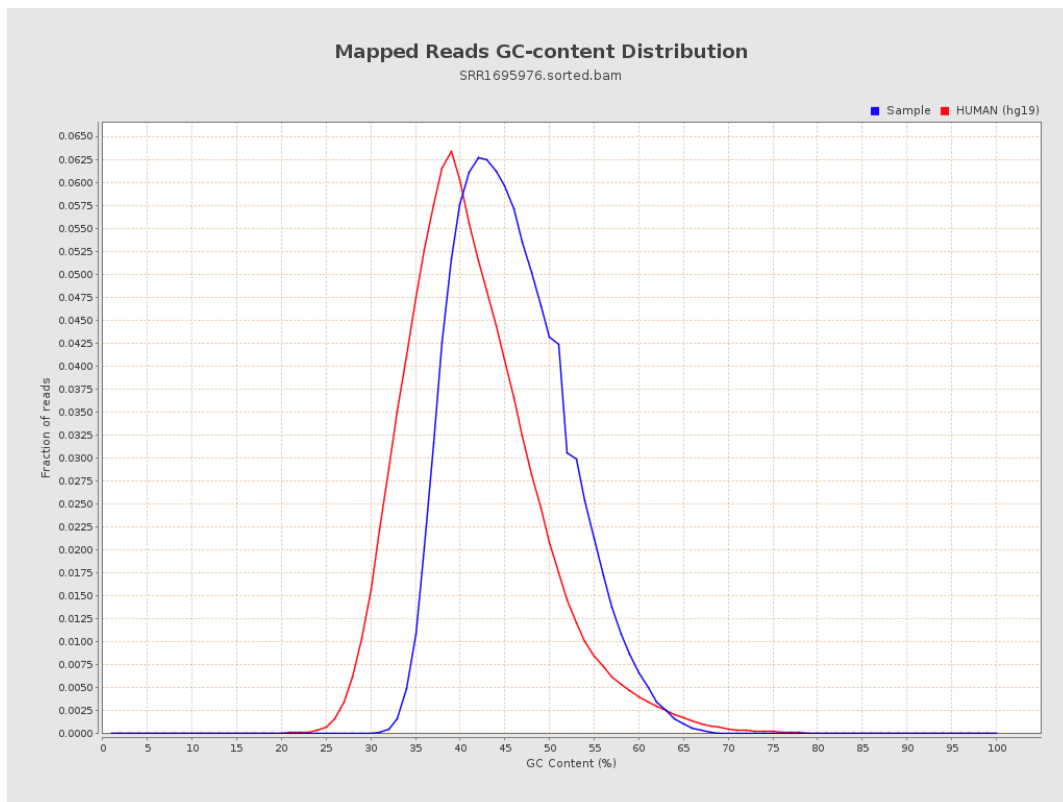
7. Results : Duplication Rate Histogram



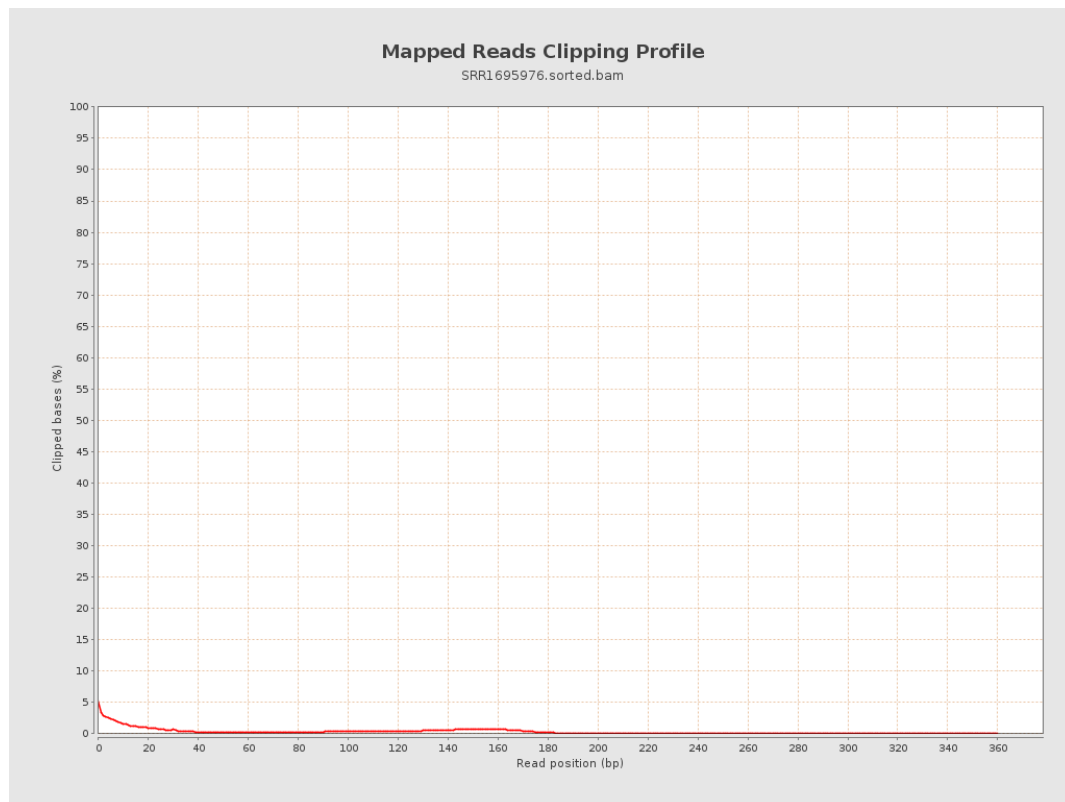
8. Results : Mapped Reads Nucleotide Content



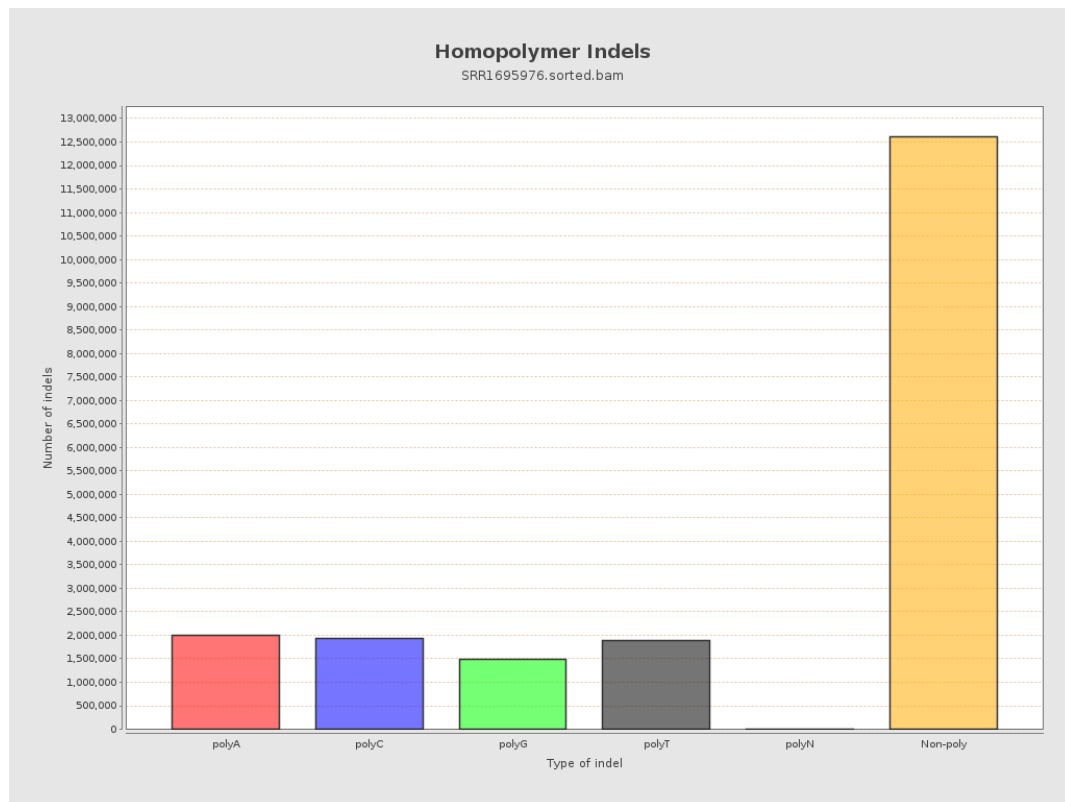
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

