

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/14 08:45:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695983.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_SRR1695983 /seu_share/home/tujing/220232460/reference/homo_bwa/hsa.fa SRR1695983.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.18-r1243-dirty)
Analysis date:	Sat Sep 14 08:45:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695983.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,426,334
Mapped reads	11,282,656 / 90.8%
Unmapped reads	1,143,678 / 9.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	170,957 / 1.38%
Read min/max/mean length	8 / 359 / 126.59
Duplicated reads (estimated)	2,232,500 / 17.97%
Duplication rate	16.8%
Clipped reads	2,723,054 / 21.91%

2.2. ACGT Content

Number/percentage of A's	429,309,713 / 28.92%
Number/percentage of C's	314,268,649 / 21.17%
Number/percentage of T's	421,269,898 / 28.38%
Number/percentage of G's	319,741,330 / 21.54%
Number/percentage of N's	0 / 0%
GC Percentage	42.71%

2.3. Coverage

Mean	0.4828

Standard Deviation	1.462
--------------------	-------

2.4. Mapping Quality

Mean Mapping Quality	51.08
----------------------	-------

2.5. Mismatches and indels

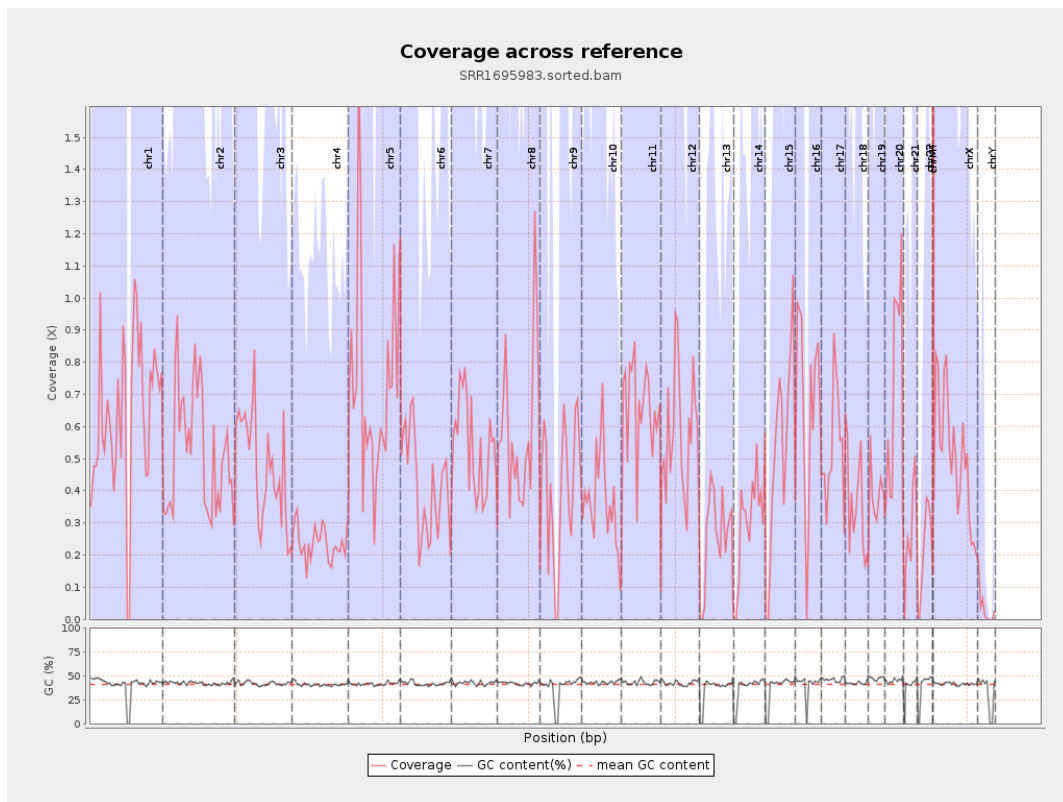
General error rate	1.68%
Mismatches	15,585,995
Insertions	8,510,108
Mapped reads with at least one insertion	46.05%
Deletions	9,096,027
Mapped reads with at least one deletion	48.68%
Homopolymer indels	37.06%

2.6. Chromosome stats

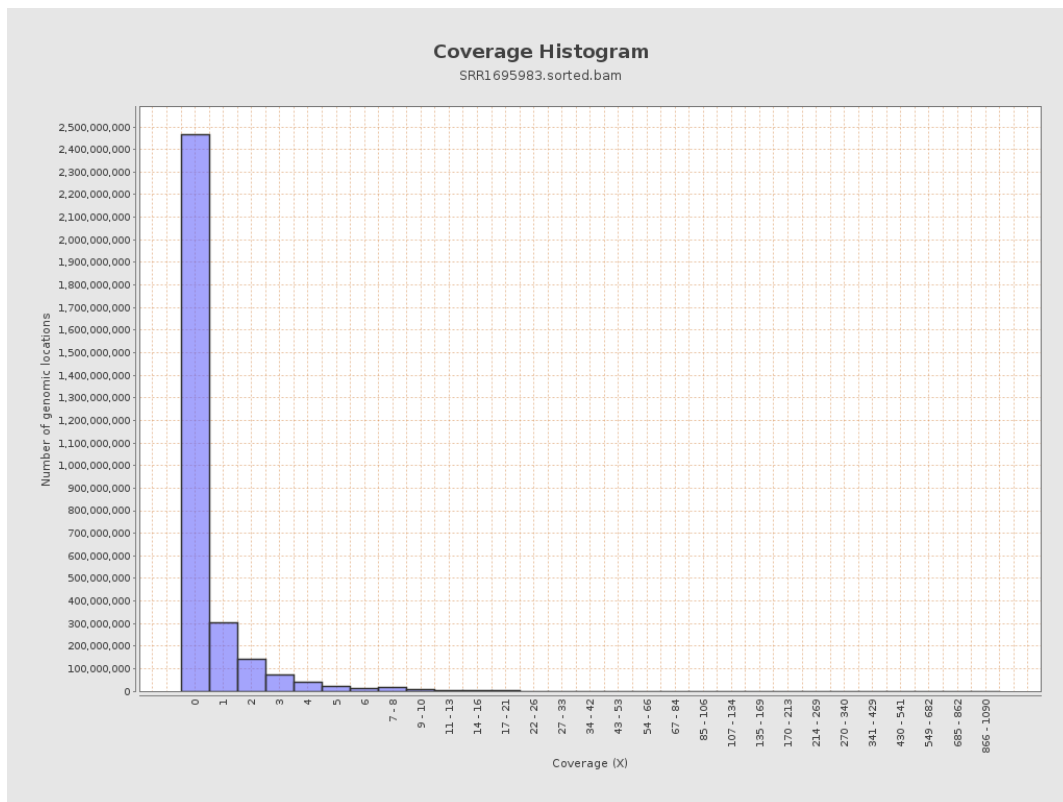
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	158323694	0.6352	1.9628
chr2	243199373	127159086	0.5229	1.4581
chr3	198022430	93369592	0.4715	1.3451
chr4	191154276	45640292	0.2388	0.8745
chr5	180915260	133576362	0.7383	1.7578
chr6	171115067	70598487	0.4126	1.2738
chr7	159138663	85569010	0.5377	1.4215

chr8	146364022	87677321	0.599	1.6456
chr9	141213431	57436970	0.4067	1.2927
chr10	135534747	51136982	0.3773	1.3169
chr11	135006516	87675884	0.6494	1.6827
chr12	133851895	78499010	0.5865	1.5285
chr13	115169878	29702980	0.2579	0.9202
chr14	107349540	32516055	0.3029	1.052
chr15	102531392	53163184	0.5185	1.4557
chr16	90354753	58506492	0.6475	1.7154
chr17	81195210	44513314	0.5482	1.5751
chr18	78077248	27919961	0.3576	1.4303
chr19	59128983	22639263	0.3829	1.5836
chr20	63025520	45184381	0.7169	1.7964
chr21	48129895	12978063	0.2696	1.0885
chr22	51304566	11227461	0.2188	0.8698
chrMT	16571	215333	12.9946	7.3488
chrX	155270560	77480598	0.499	1.4104
chrY	59373566	1967018	0.0331	0.5797

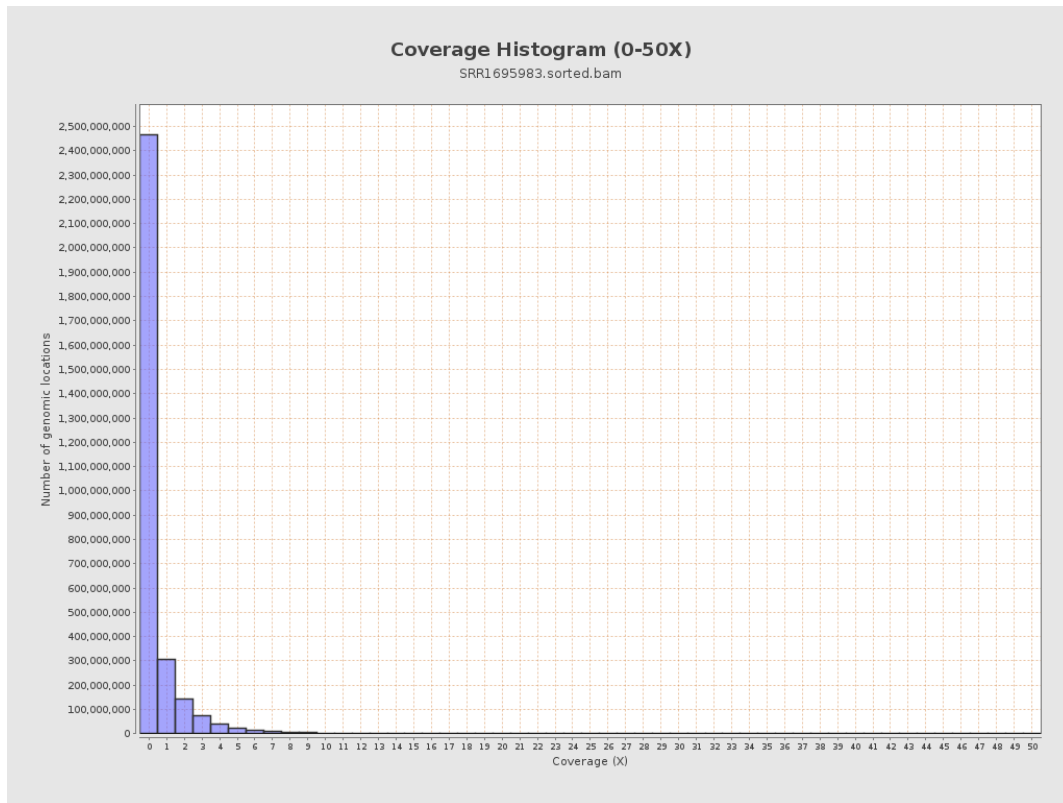
3. Results : Coverage across reference



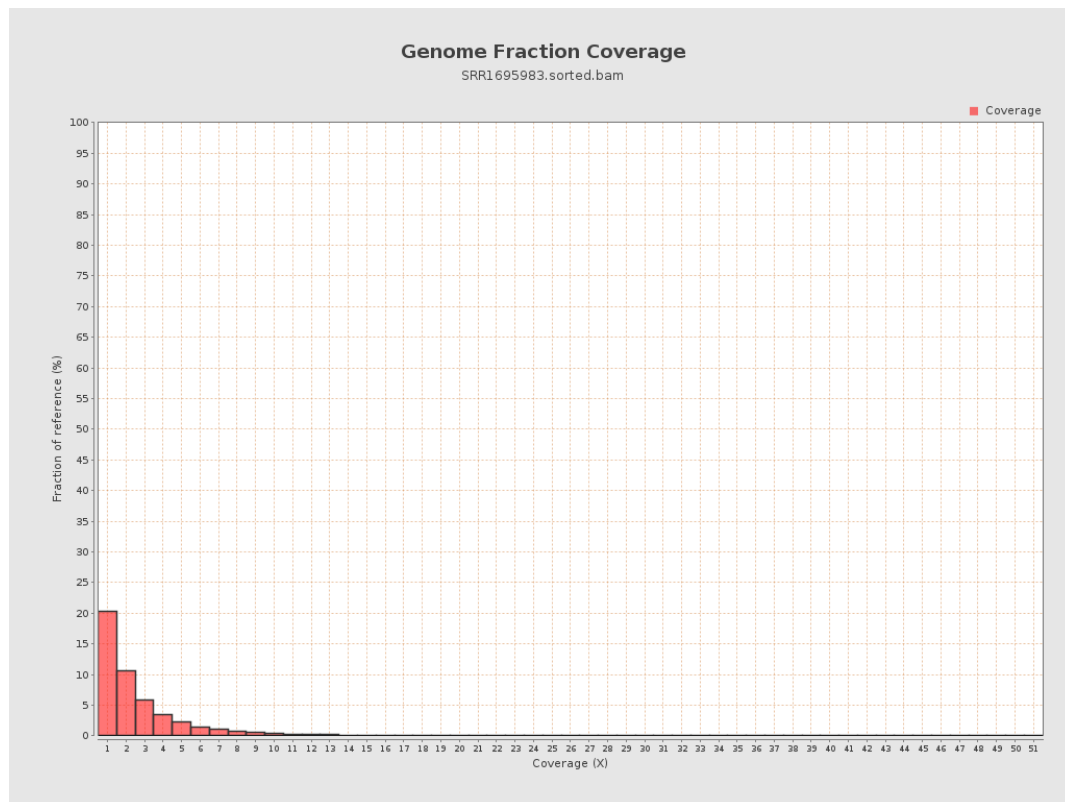
4. Results : Coverage Histogram



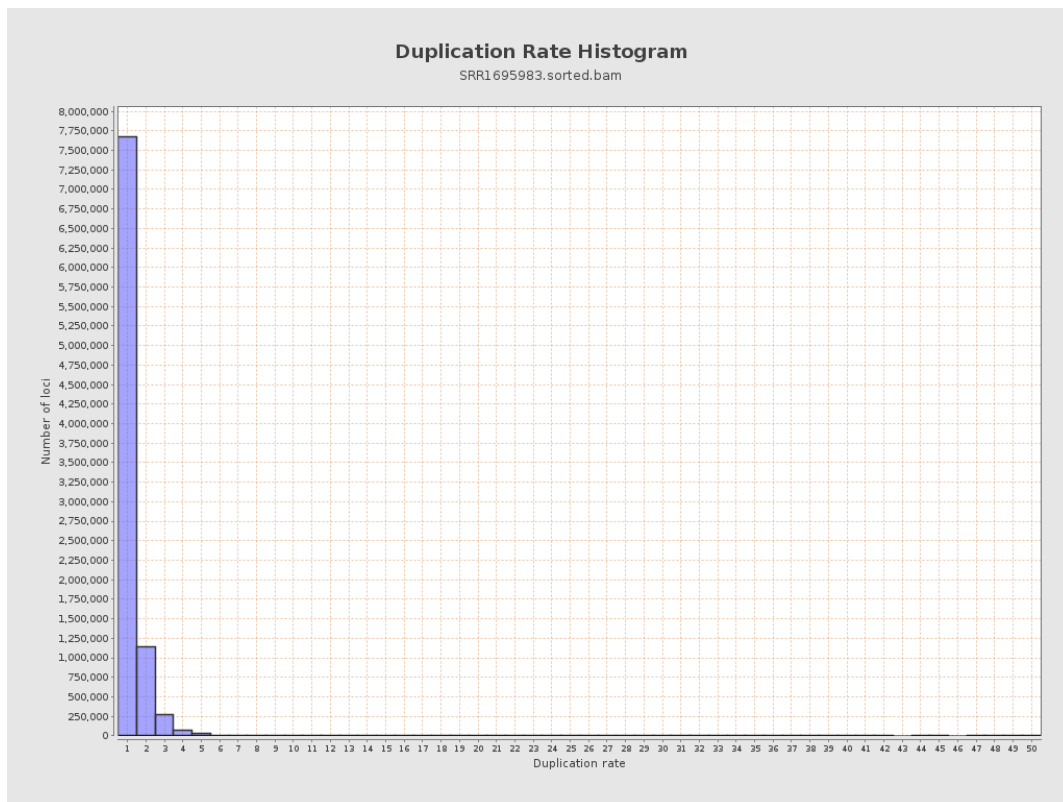
5. Results : Coverage Histogram (0-50X)



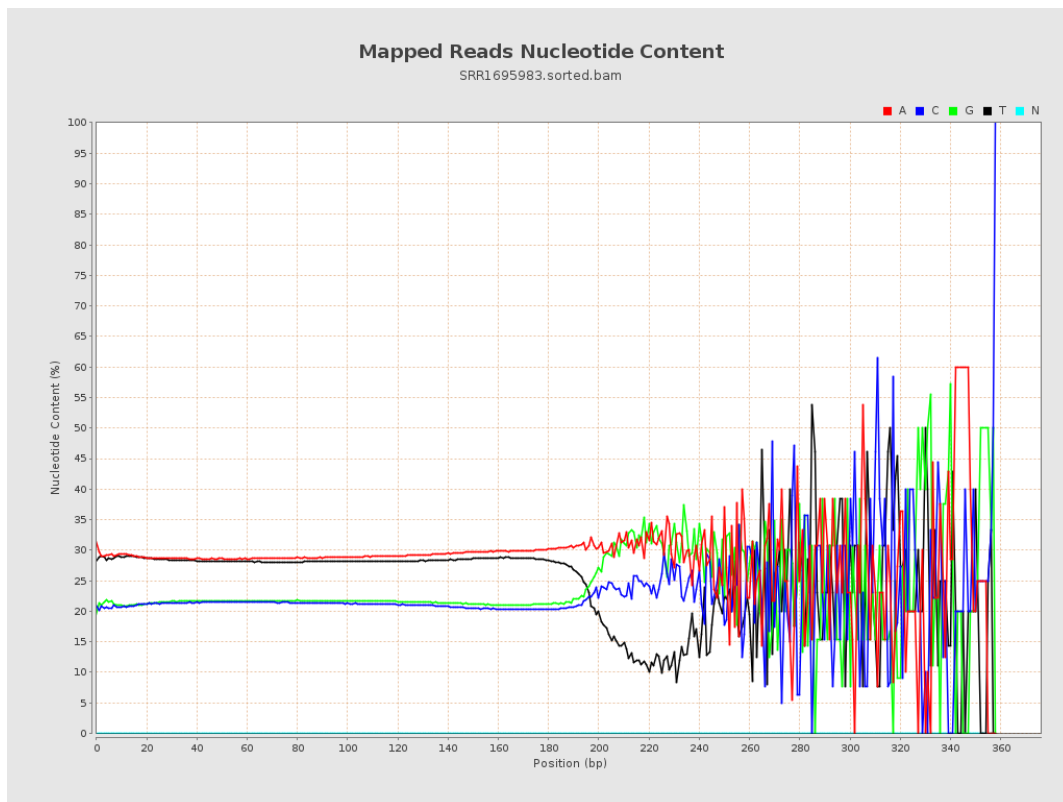
6. Results : Genome Fraction Coverage



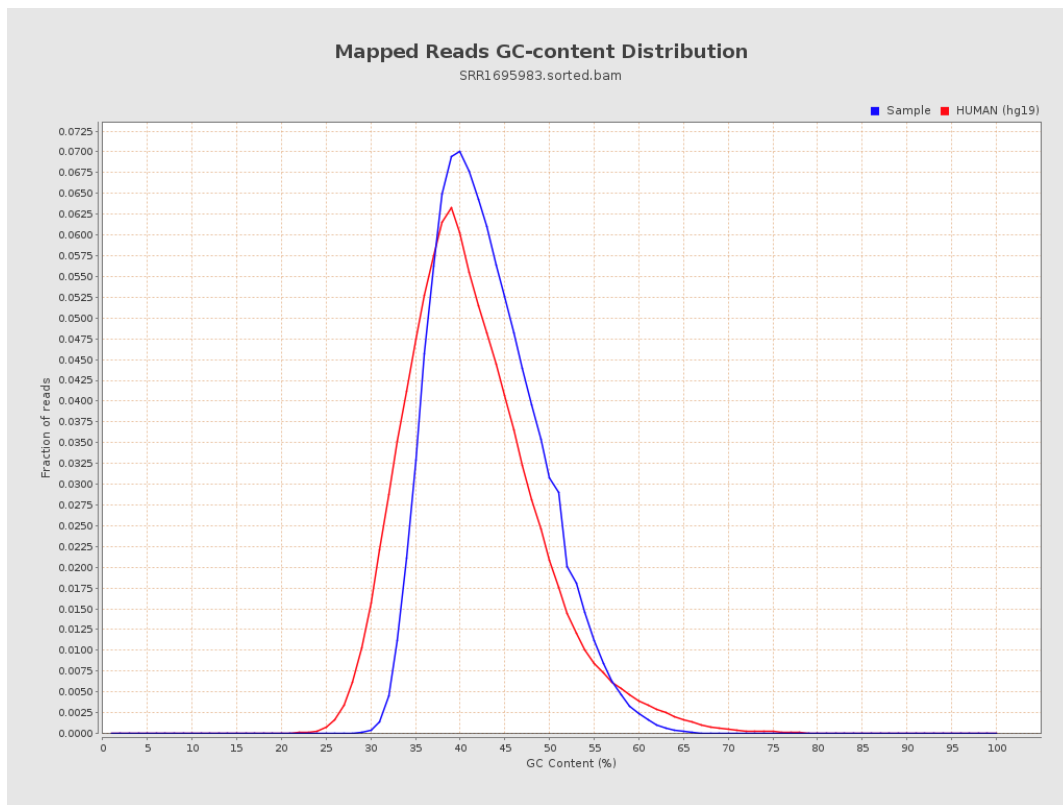
7. Results : Duplication Rate Histogram



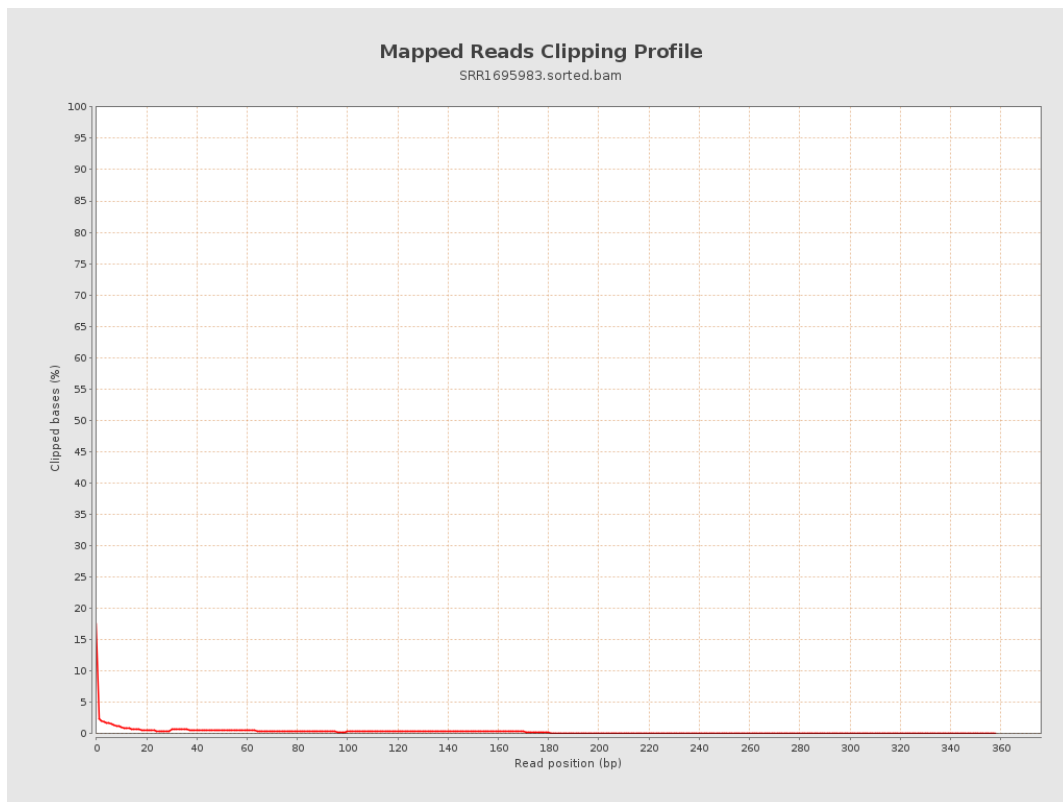
8. Results : Mapped Reads Nucleotide Content



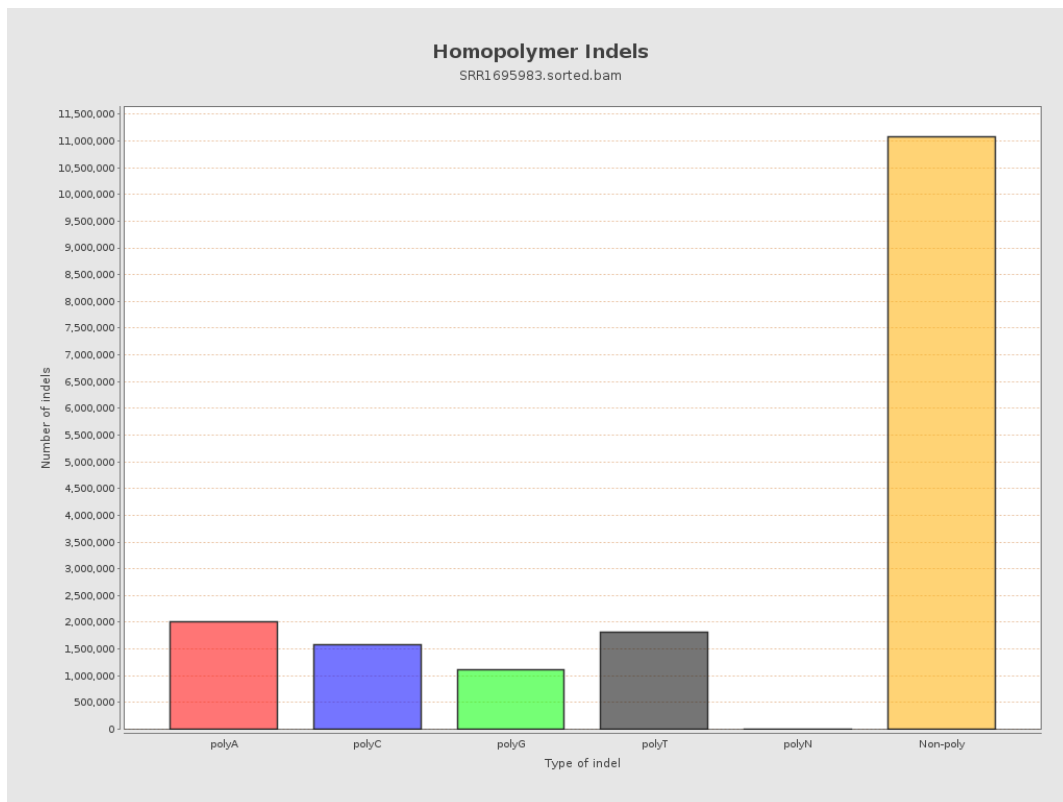
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

