

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/14 09:23:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695989.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_SRR1695989 /seu_share/home/tujing/220232460/reference/homo_bwa/hsa.fa SRR1695989.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.18-r1243-dirty)
Analysis date:	Sat Sep 14 09:23:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695989.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,758,276
Mapped reads	13,457,012 / 91.18%
Unmapped reads	1,301,264 / 8.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	221,025 / 1.5%
Read min/max/mean length	8 / 358 / 142.7
Duplicated reads (estimated)	2,994,880 / 20.29%
Duplication rate	19.03%
Clipped reads	3,442,340 / 23.32%

2.2. ACGT Content

Number/percentage of A's	566,737,185 / 28.52%
Number/percentage of C's	426,571,337 / 21.47%
Number/percentage of T's	563,991,828 / 28.39%
Number/percentage of G's	429,592,328 / 21.62%
Number/percentage of N's	0 / 0%
GC Percentage	43.09%

2.3. Coverage

Mean	0.6463

Standard Deviation	1.7498
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	51.98
----------------------	-------

2.5. Mismatches and indels

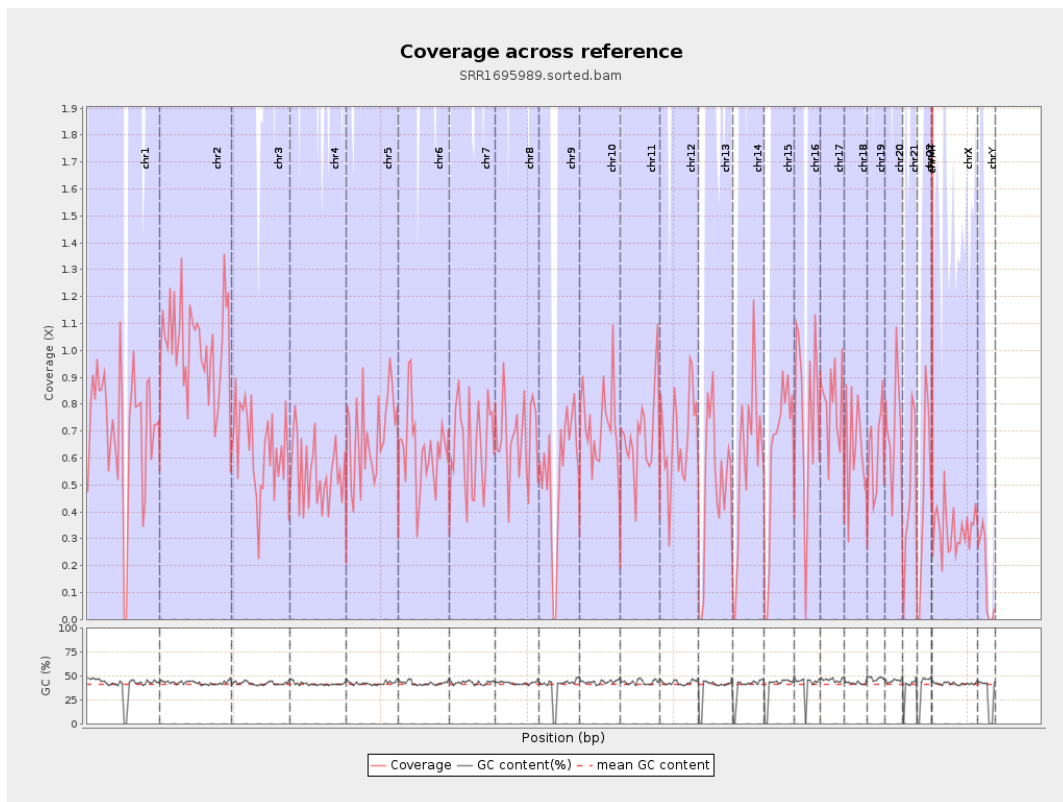
General error rate	1.65%
Mismatches	21,028,217
Insertions	10,951,248
Mapped reads with at least one insertion	45.99%
Deletions	12,483,851
Mapped reads with at least one deletion	52.57%
Homopolymer indels	37.61%

2.6. Chromosome stats

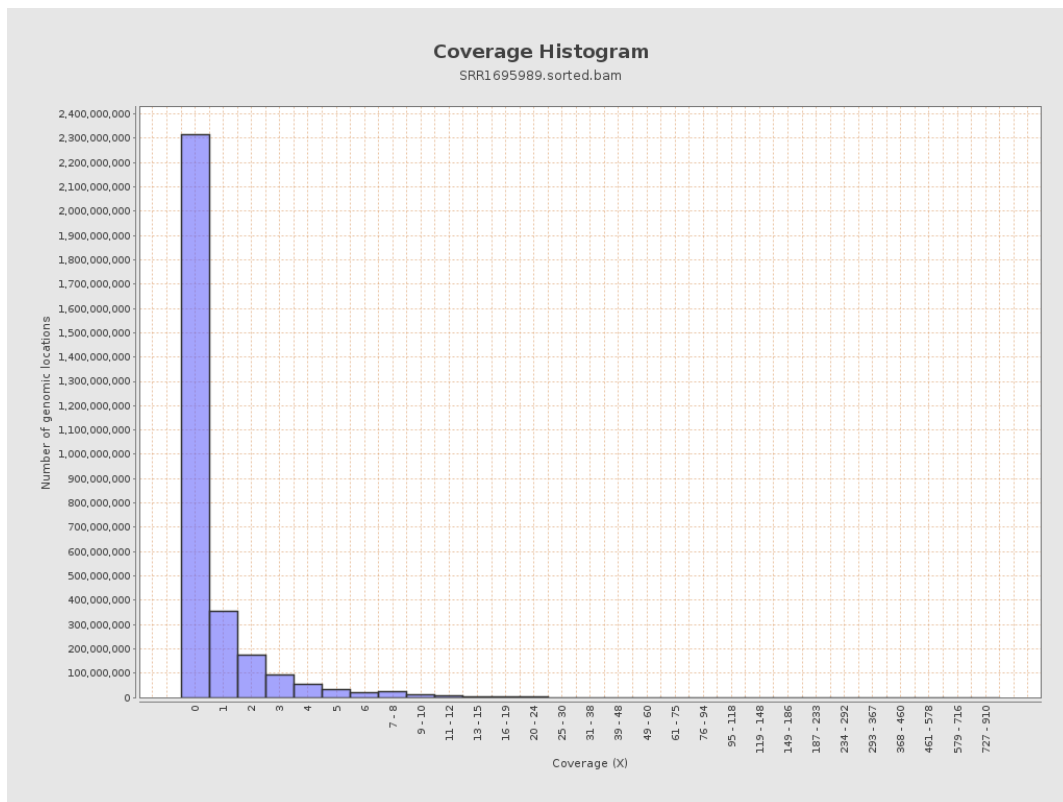
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	176695348	0.7089	2.0007
chr2	243199373	248060541	1.02	2.1782
chr3	198022430	125330217	0.6329	1.5846
chr4	191154276	105321380	0.551	1.5193
chr5	180915260	123467862	0.6825	1.7879
chr6	171115067	108048659	0.6314	1.6867
chr7	159138663	102081604	0.6415	1.651

chr8	146364022	98807640	0.6751	1.6494
chr9	141213431	76056669	0.5386	1.5401
chr10	135534747	98279729	0.7251	1.9427
chr11	135006516	92630732	0.6861	1.7308
chr12	133851895	90485316	0.676	1.6642
chr13	115169878	56995858	0.4949	1.4596
chr14	107349540	64702008	0.6027	1.6453
chr15	102531392	63048146	0.6149	1.7179
chr16	90354753	66268364	0.7334	2.0104
chr17	81195210	63732413	0.7849	2.1189
chr18	78077248	50755132	0.6501	1.8424
chr19	59128983	37703462	0.6376	1.9566
chr20	63025520	44770351	0.7104	1.8302
chr21	48129895	22495995	0.4674	1.5637
chr22	51304566	23094883	0.4502	1.463
chrMT	16571	692364	41.7817	26.5191
chrX	155270560	51680768	0.3328	1.1362
chrY	59373566	9566337	0.1611	0.9608

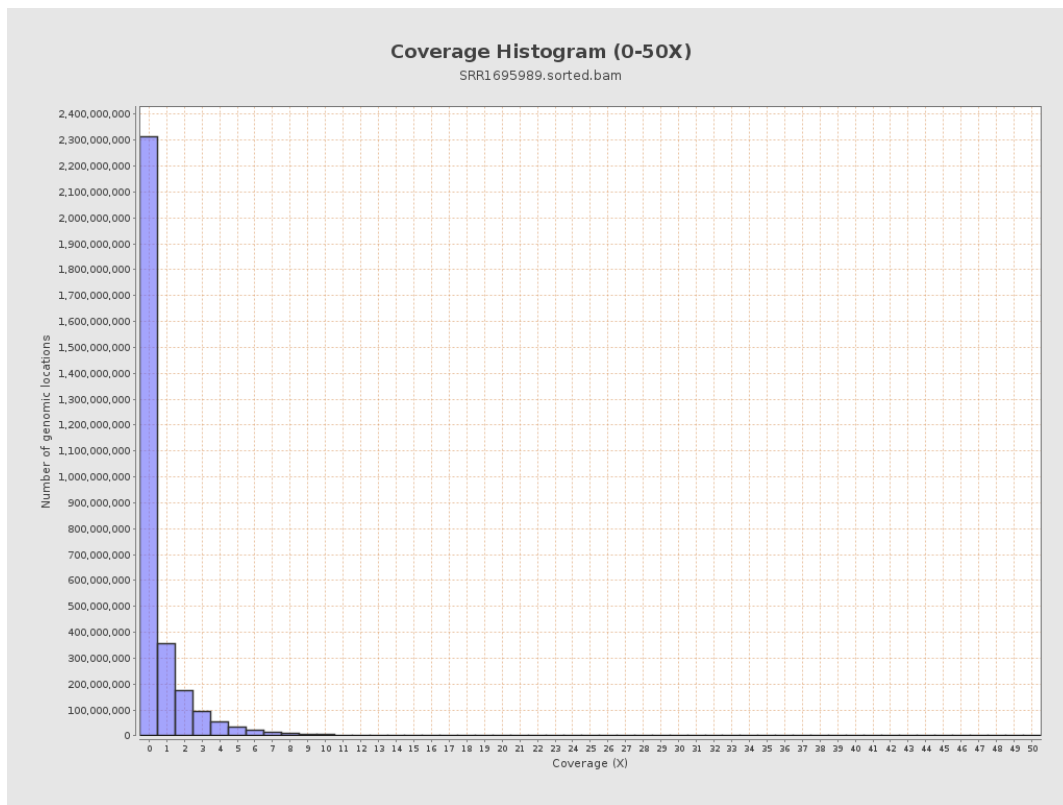
3. Results : Coverage across reference



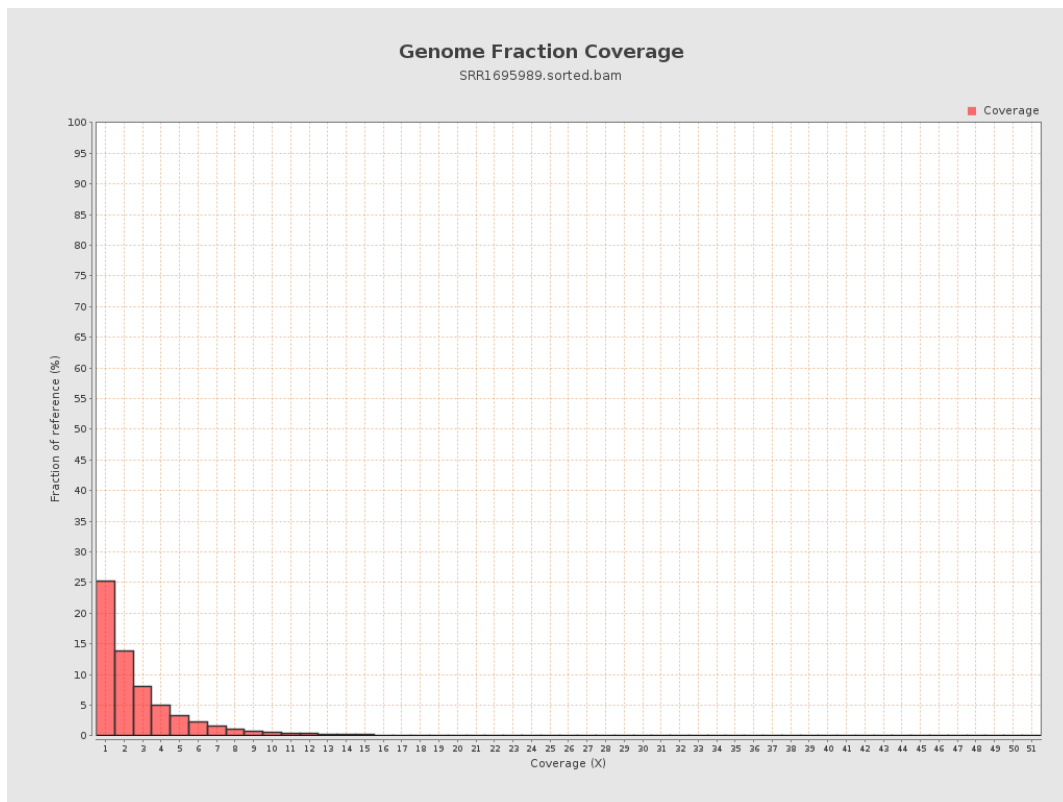
4. Results : Coverage Histogram



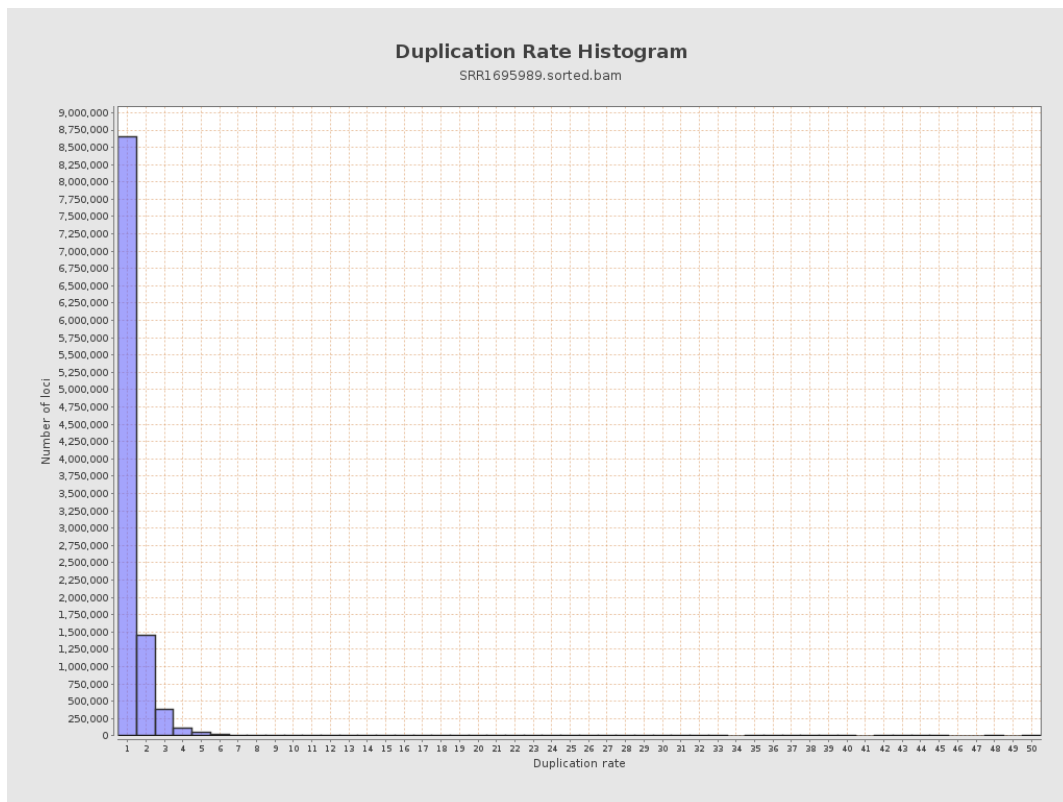
5. Results : Coverage Histogram (0-50X)



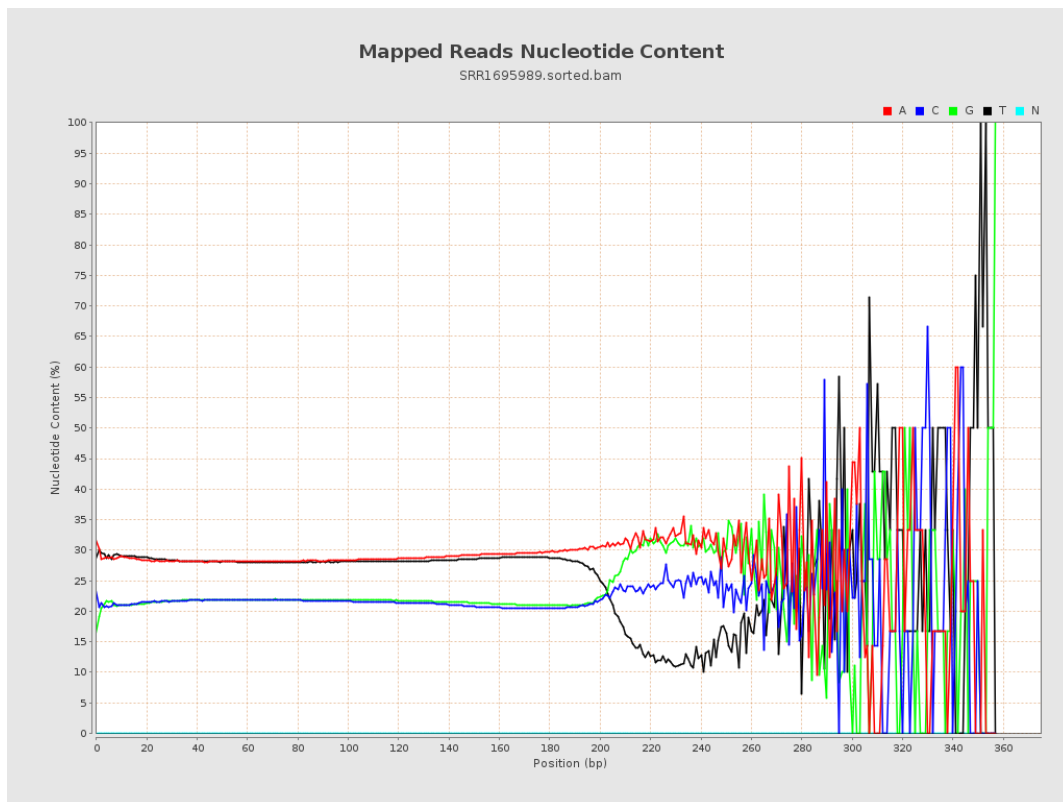
6. Results : Genome Fraction Coverage



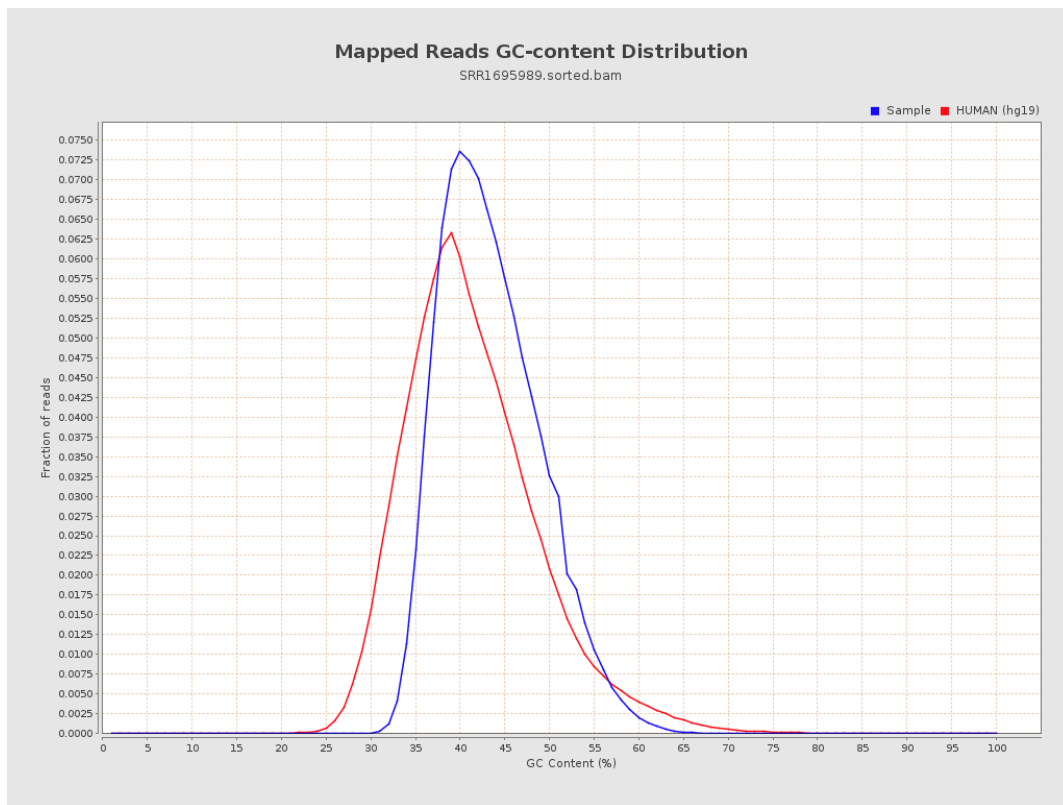
7. Results : Duplication Rate Histogram



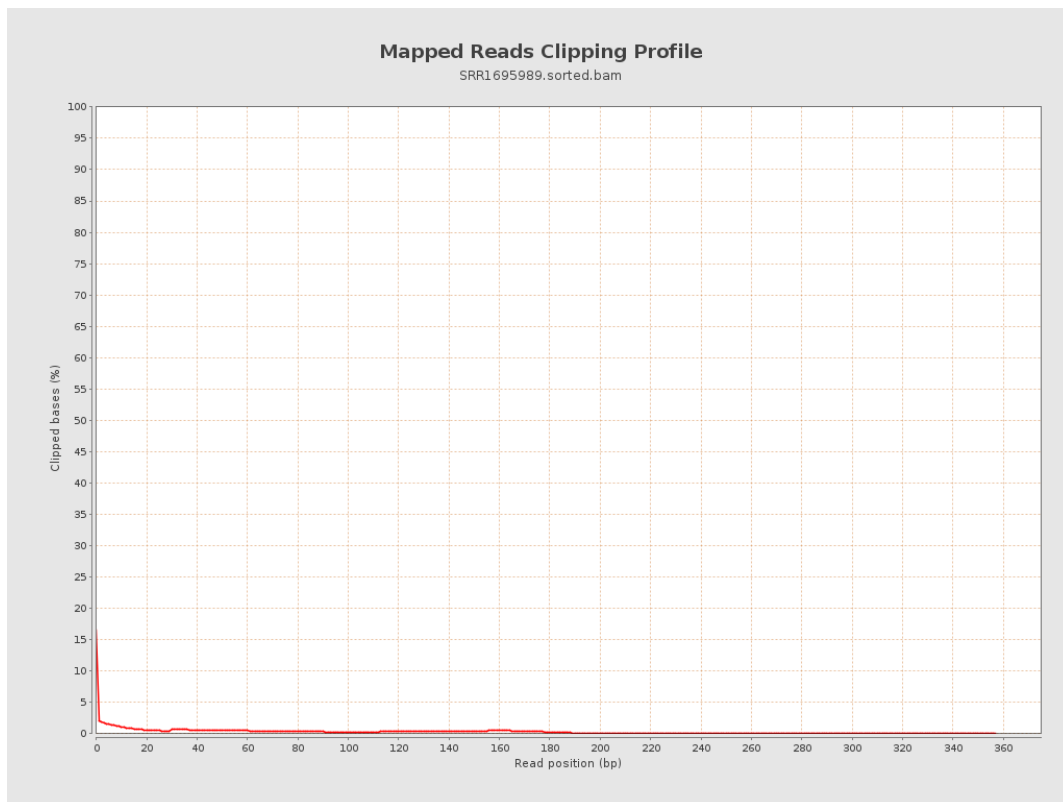
8. Results : Mapped Reads Nucleotide Content



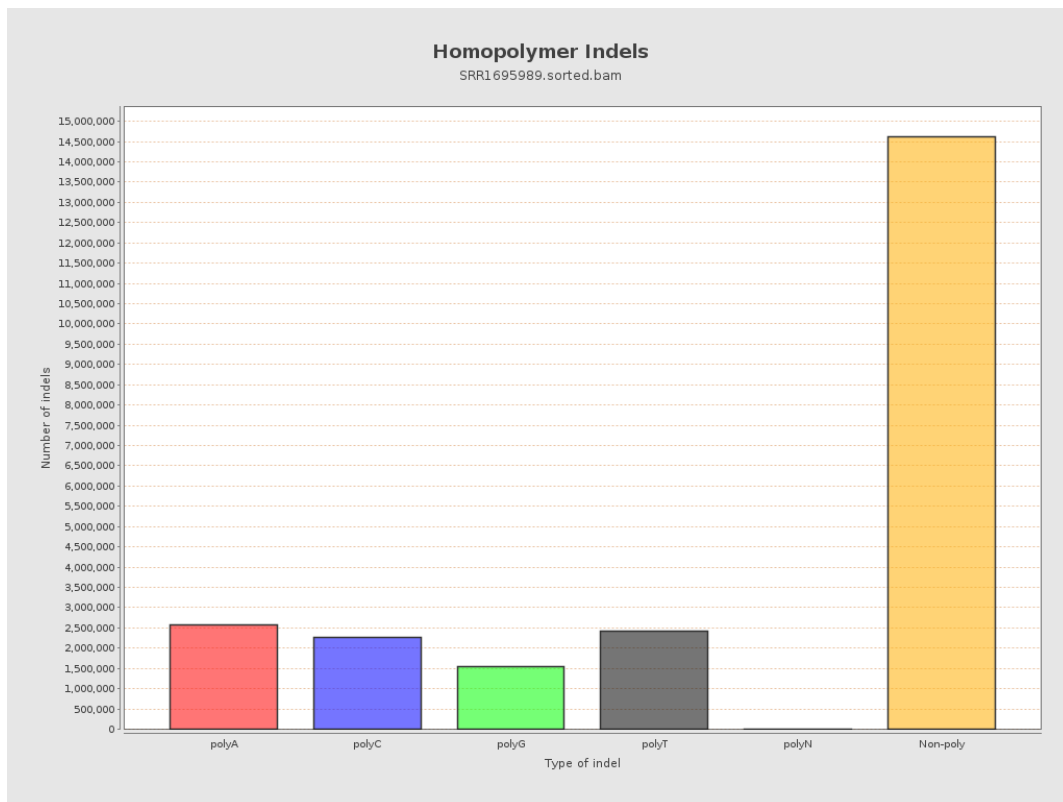
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

