

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/14 08:50:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695984.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_SRR1695984 /seu_share/home/tujing/220232460/reference/homo_bwa/hsa.fa SRR1695984.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.18-r1243-dirty)
Analysis date:	Sat Sep 14 08:50:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695984.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,898,304
Mapped reads	9,577,964 / 87.88%
Unmapped reads	1,320,340 / 12.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,541 / 0.23%
Read min/max/mean length	8 / 360 / 124.45
Duplicated reads (estimated)	1,824,954 / 16.75%
Duplication rate	16.25%
Clipped reads	3,002,255 / 27.55%

2.2. ACGT Content

Number/percentage of A's	348,679,897 / 28.15%
Number/percentage of C's	267,701,143 / 21.61%
Number/percentage of T's	342,995,861 / 27.69%
Number/percentage of G's	279,341,229 / 22.55%
Number/percentage of N's	0 / 0%
GC Percentage	44.16%

2.3. Coverage

Mean	0.4033

Standard Deviation	1.4311
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2.4. Mapping Quality

Mean Mapping Quality	51.96
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2.5. Mismatches and indels

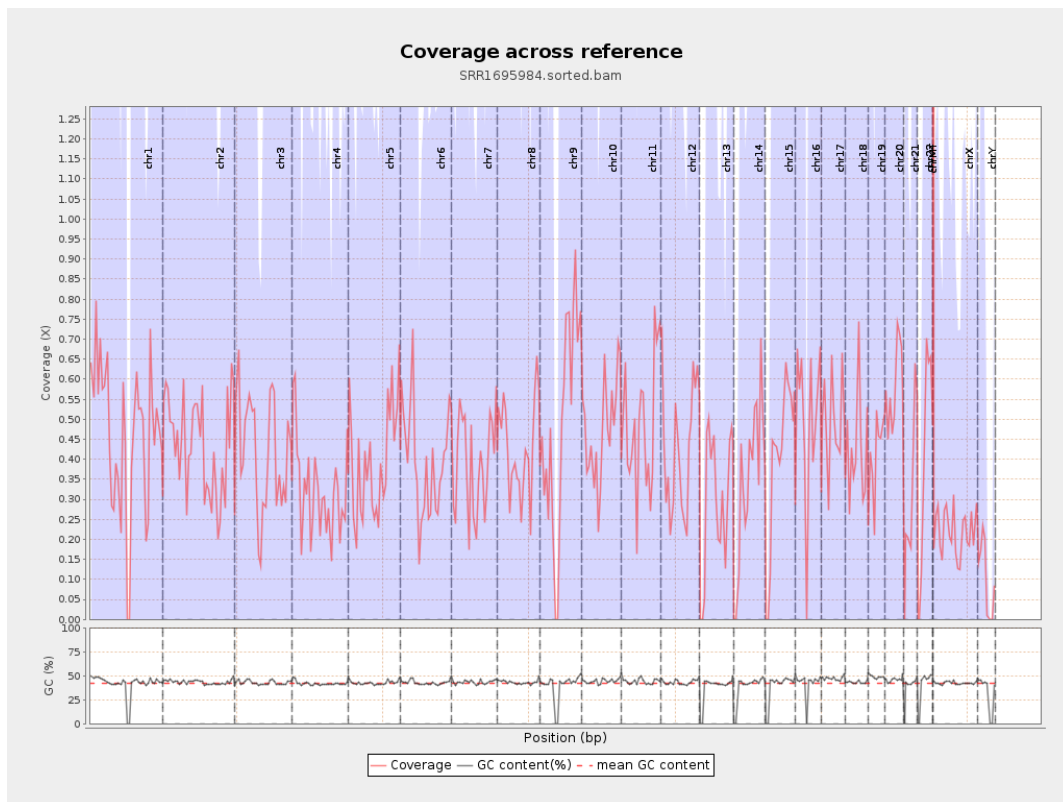
General error rate	2.1%
Mismatches	18,400,493
Insertions	6,969,898
Mapped reads with at least one insertion	45.2%
Deletions	8,783,284
Mapped reads with at least one deletion	53.08%
Homopolymer indels	37.48%

2.6. Chromosome stats

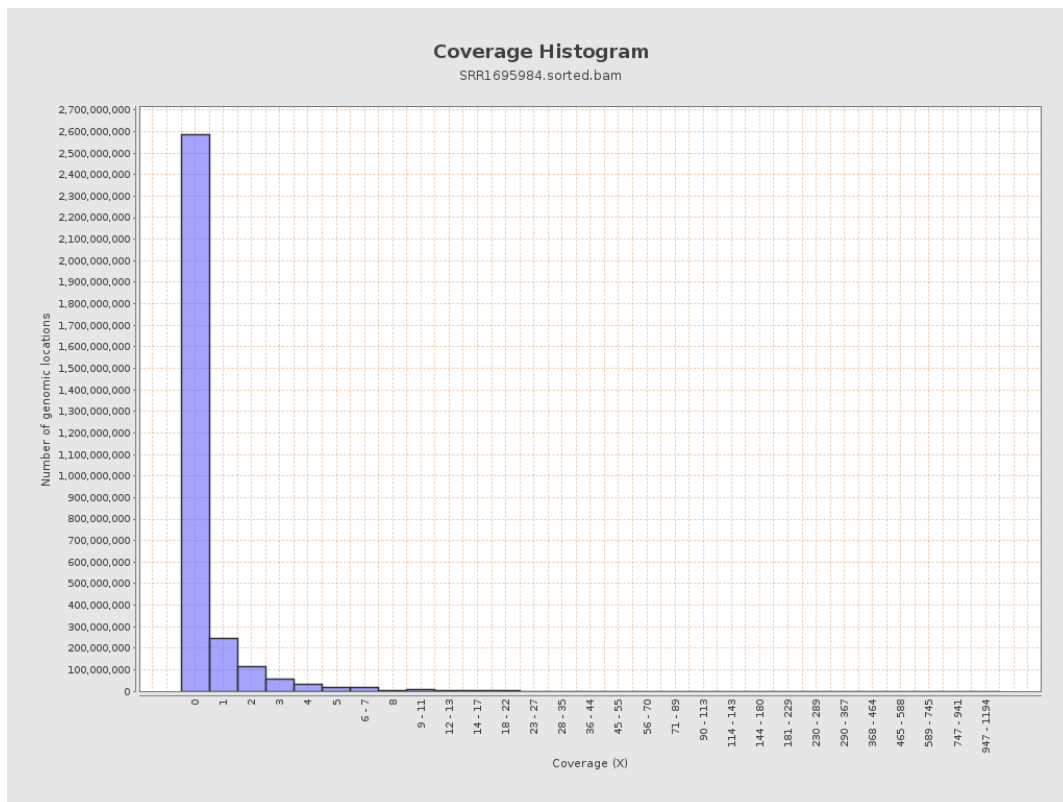
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	114148266	0.458	1.5962
chr2	243199373	105937697	0.4356	1.6485
chr3	198022430	81923568	0.4137	1.3276
chr4	191154276	61103559	0.3197	1.271
chr5	180915260	71776445	0.3967	1.2915
chr6	171115067	67236871	0.3929	1.2831
chr7	159138663	61805910	0.3884	1.2854

chr8	146364022	62202965	0.425	1.3807
chr9	141213431	68404936	0.4844	1.642
chr10	135534747	63738381	0.4703	1.5176
chr11	135006516	65017201	0.4816	1.5314
chr12	133851895	57281751	0.4279	1.3953
chr13	115169878	33720754	0.2928	1.1102
chr14	107349540	37831405	0.3524	1.2256
chr15	102531392	40911239	0.399	1.3397
chr16	90354753	44289772	0.4902	2.0084
chr17	81195210	40263934	0.4959	1.5441
chr18	78077248	32765081	0.4196	1.4637
chr19	59128983	24415988	0.4129	1.4018
chr20	63025520	36903762	0.5855	1.6943
chr21	48129895	15422342	0.3204	1.972
chr22	51304566	20779901	0.405	1.39
chrMT	16571	437631	26.4095	25.4804
chrX	155270560	34039084	0.2192	0.8496
chrY	59373566	6145773	0.1035	0.8256

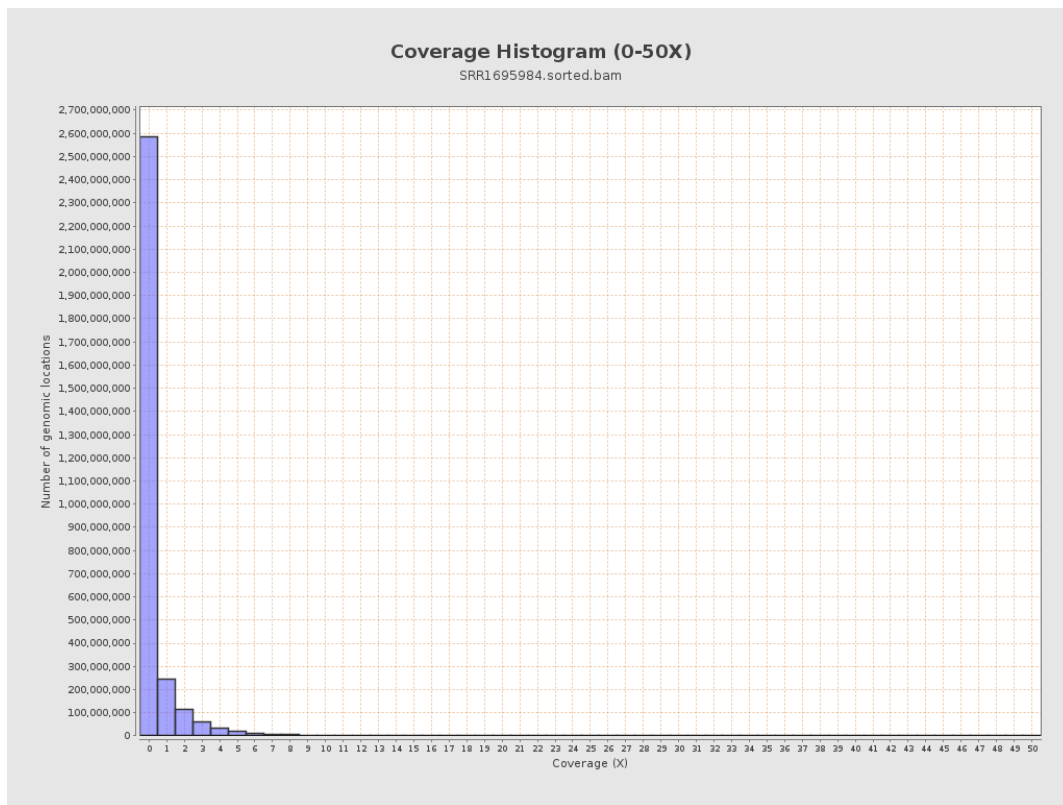
3. Results : Coverage across reference



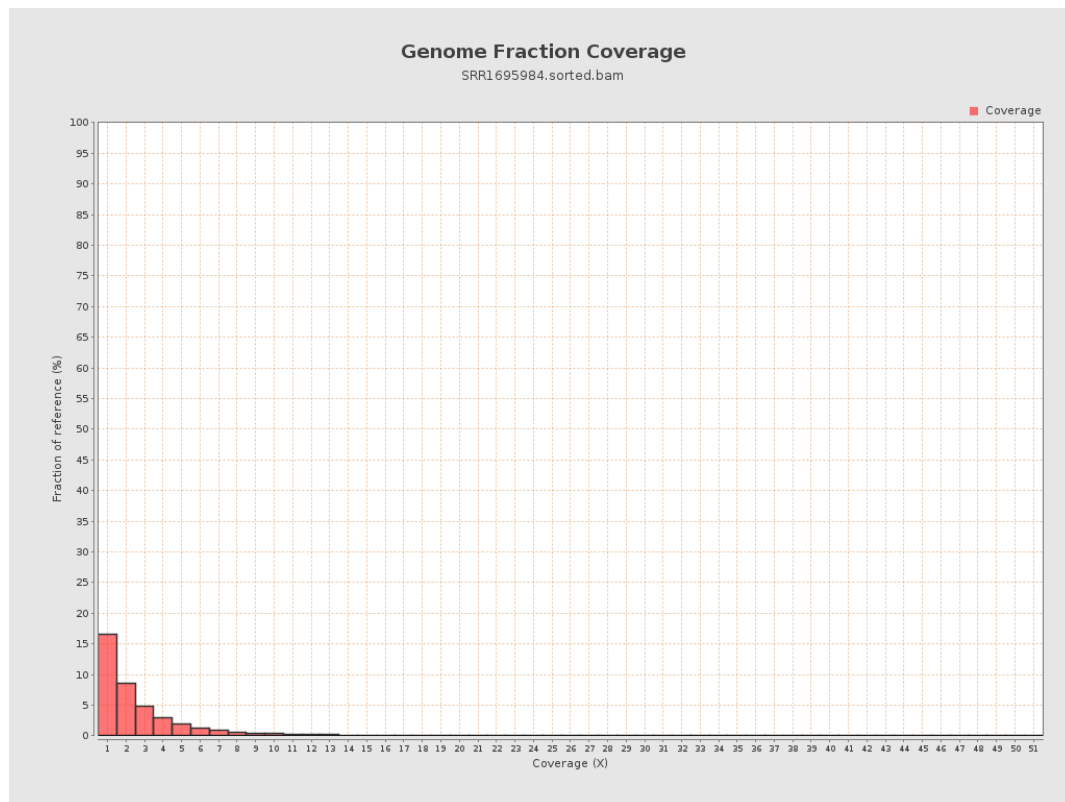
4. Results : Coverage Histogram



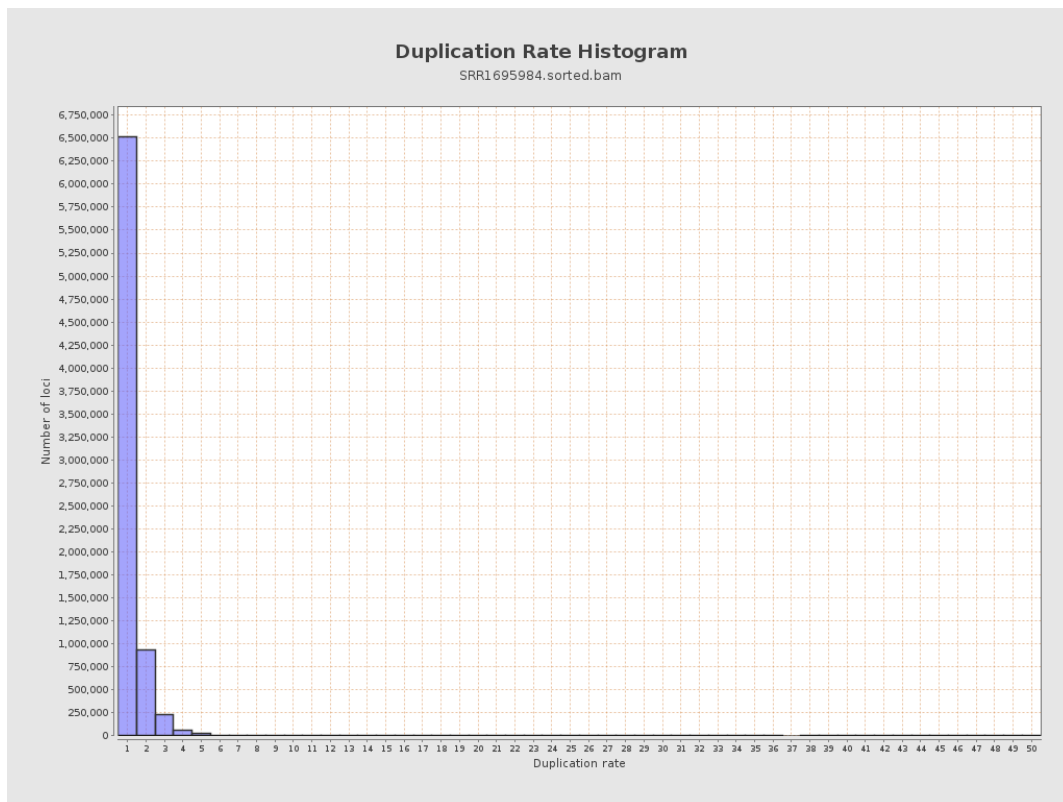
5. Results : Coverage Histogram (0-50X)



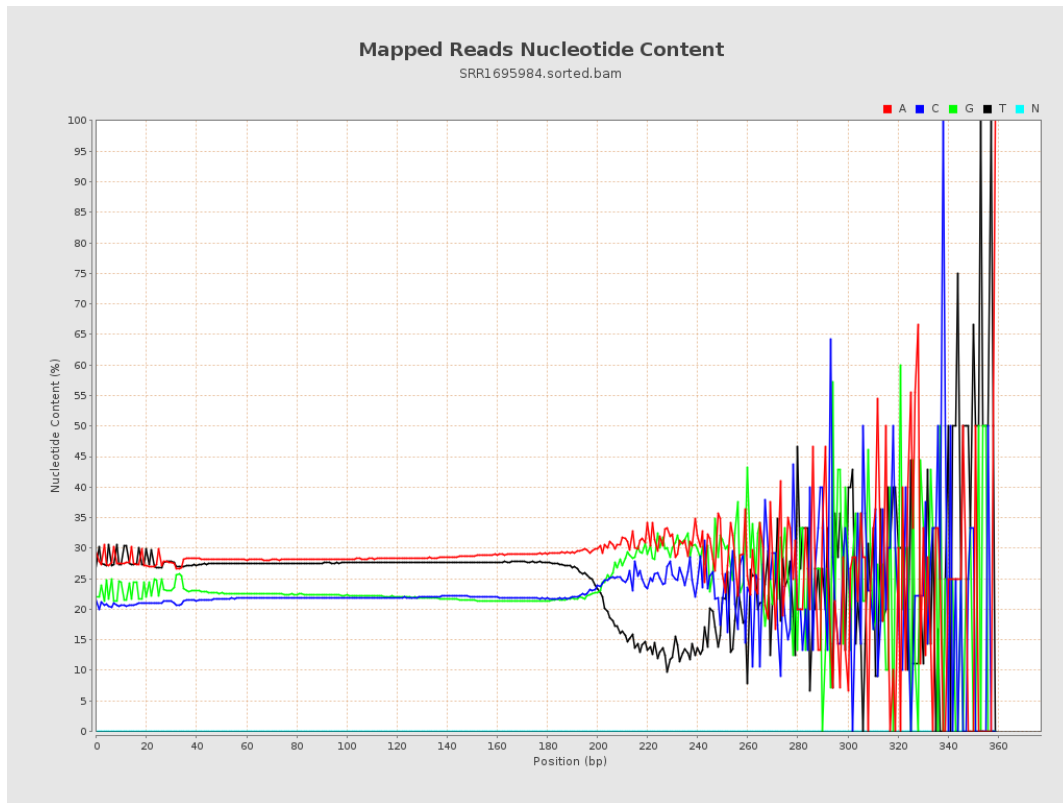
6. Results : Genome Fraction Coverage



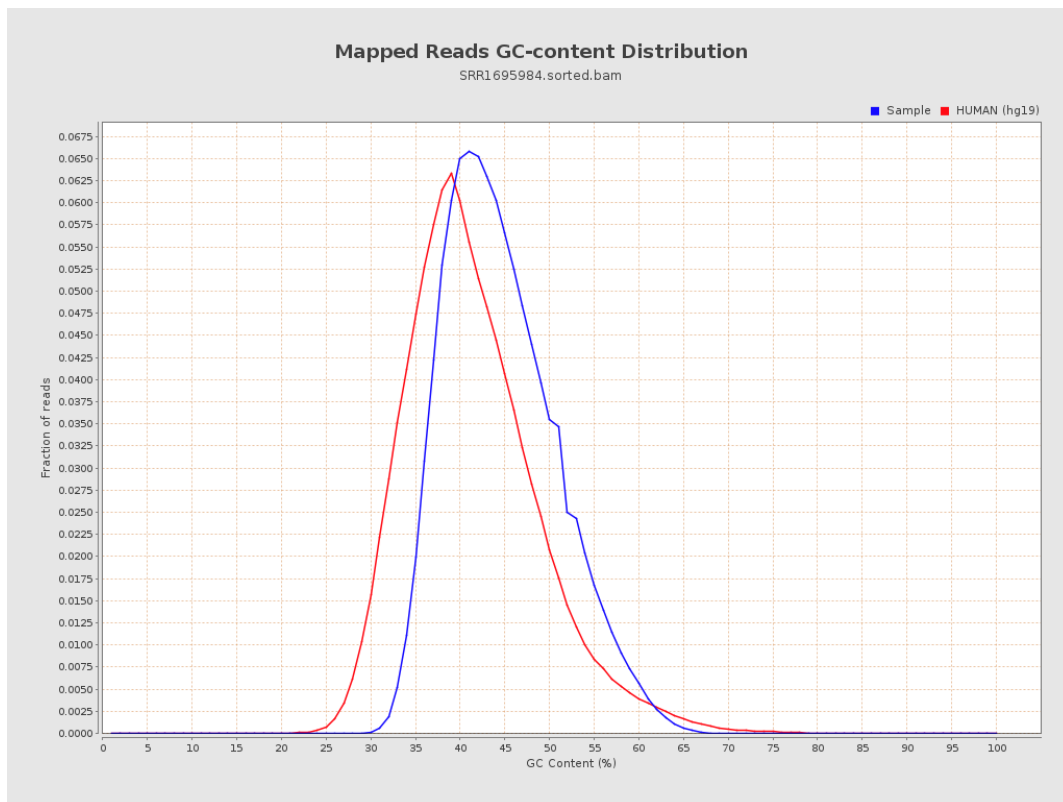
7. Results : Duplication Rate Histogram



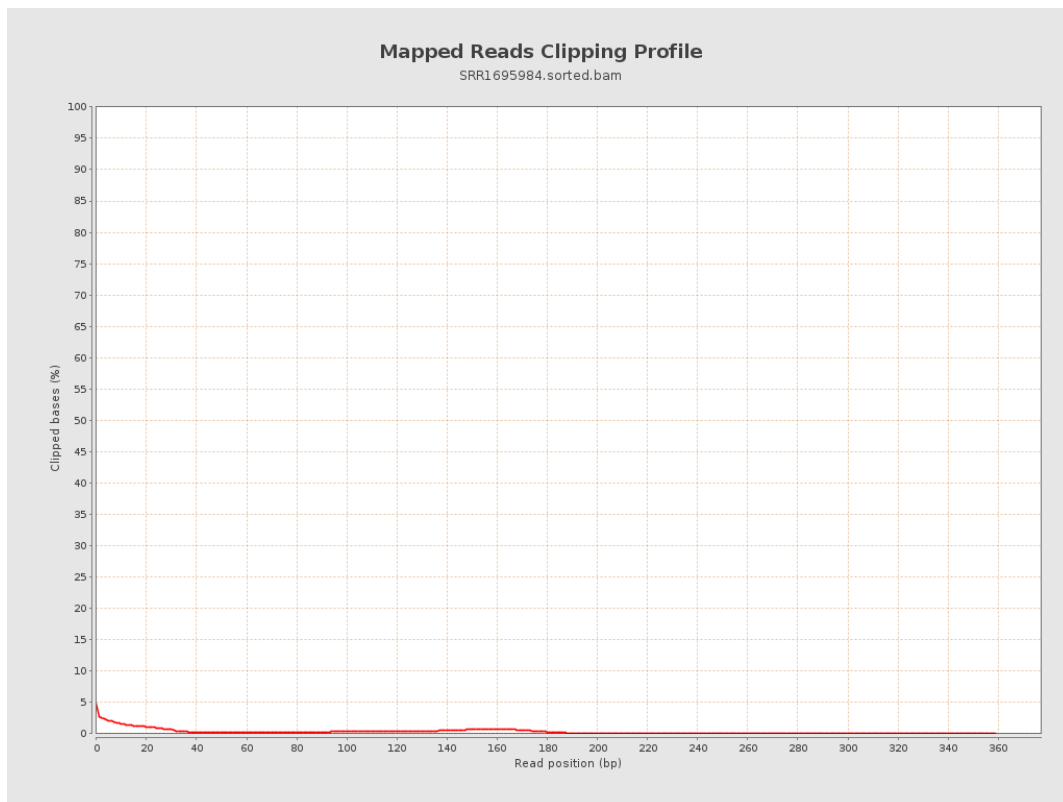
8. Results : Mapped Reads Nucleotide Content



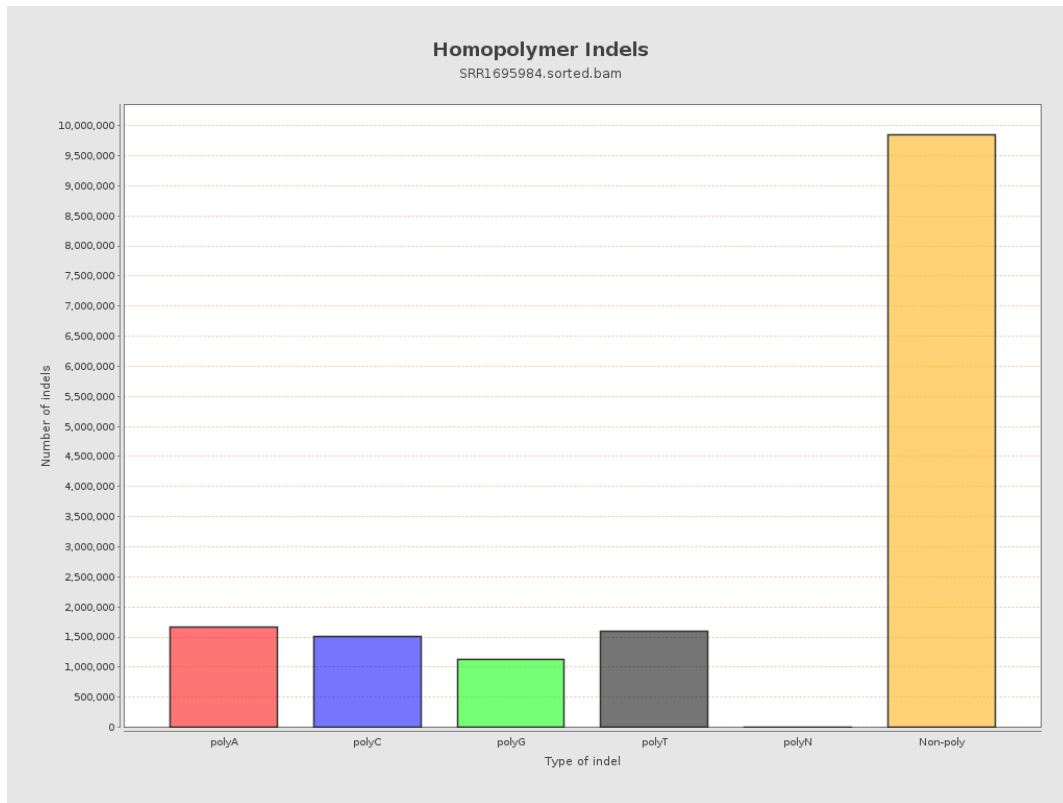
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

