

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/14 08:56:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695985.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_SRR1695985 /seu_share/home/tujing/220232460/reference/homo_bwa/hsa.fa SRR1695985.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.18-r1243-dirty)
Analysis date:	Sat Sep 14 08:56:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695985.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,991,054
Mapped reads	9,876,862 / 89.86%
Unmapped reads	1,114,192 / 10.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,407 / 0.13%
Read min/max/mean length	8 / 359 / 128.19
Duplicated reads (estimated)	1,895,784 / 17.25%
Duplication rate	16.36%
Clipped reads	2,577,477 / 23.45%

2.2. ACGT Content

Number/percentage of A's	373,978,072 / 28.46%
Number/percentage of C's	280,572,769 / 21.35%
Number/percentage of T's	370,059,888 / 28.16%
Number/percentage of G's	289,352,913 / 22.02%
Number/percentage of N's	0 / 0%
GC Percentage	43.37%

2.3. Coverage

Mean	0.4276

Standard Deviation	1.4174
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2.4. Mapping Quality

Mean Mapping Quality	52.05
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2.5. Mismatches and indels

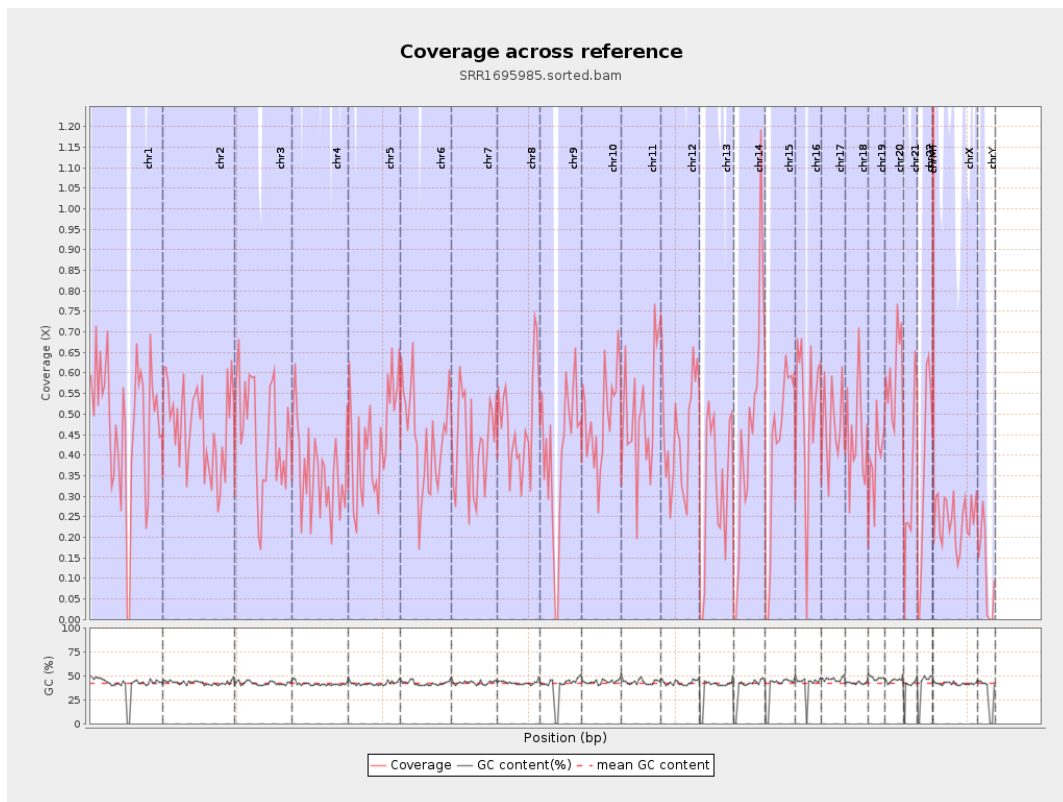
General error rate	2.09%
Mismatches	18,879,815
Insertions	7,831,840
Mapped reads with at least one insertion	47.97%
Deletions	8,652,982
Mapped reads with at least one deletion	51.58%
Homopolymer indels	37.21%

2.6. Chromosome stats

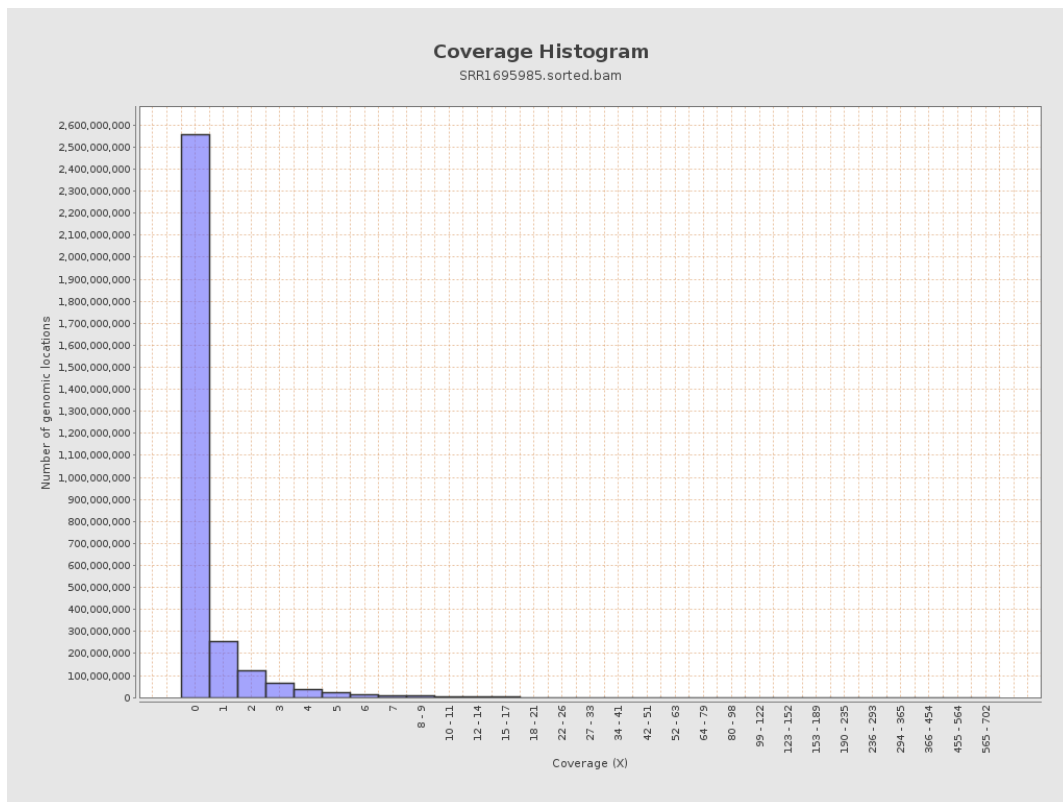
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	117944267	0.4732	1.5963
chr2	243199373	113965987	0.4686	1.6376
chr3	198022430	88891361	0.4489	1.3439
chr4	191154276	69067089	0.3613	1.2863
chr5	180915260	79162253	0.4376	1.3282
chr6	171115067	75108040	0.4389	1.3338
chr7	159138663	67641272	0.425	1.3162

chr8	146364022	70022870	0.4784	1.4457
chr9	141213431	56699762	0.4015	1.442
chr10	135534747	66446763	0.4903	1.479
chr11	135006516	67568296	0.5005	1.498
chr12	133851895	61000464	0.4557	1.3706
chr13	115169878	36837799	0.3199	1.1396
chr14	107349540	49853780	0.4644	1.504
chr15	102531392	43392192	0.4232	1.3437
chr16	90354753	45517891	0.5038	1.6991
chr17	81195210	38626110	0.4757	1.4612
chr18	78077248	34654888	0.4439	1.5916
chr19	59128983	23169243	0.3918	1.3572
chr20	63025520	37772299	0.5993	1.6585
chr21	48129895	16422290	0.3412	1.755
chr22	51304566	19093566	0.3722	1.2884
chrMT	16571	141195	8.5206	9.4411
chrX	155270560	37527643	0.2417	0.8863
chrY	59373566	7076407	0.1192	0.8176

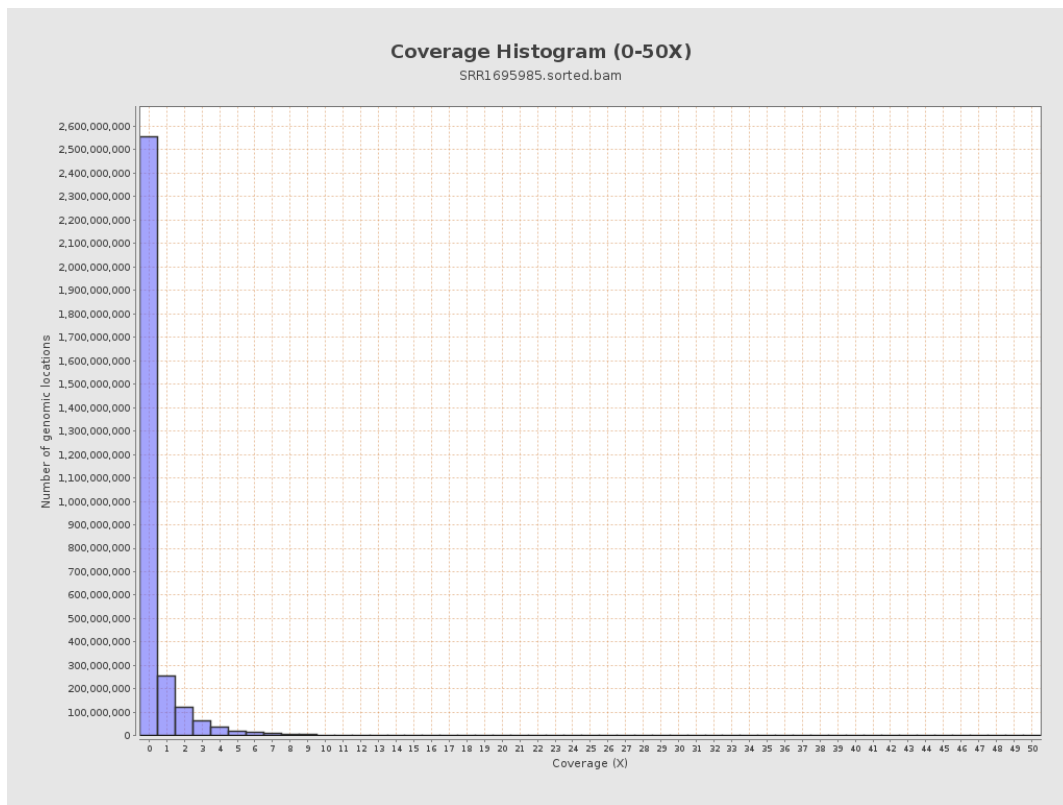
3. Results : Coverage across reference



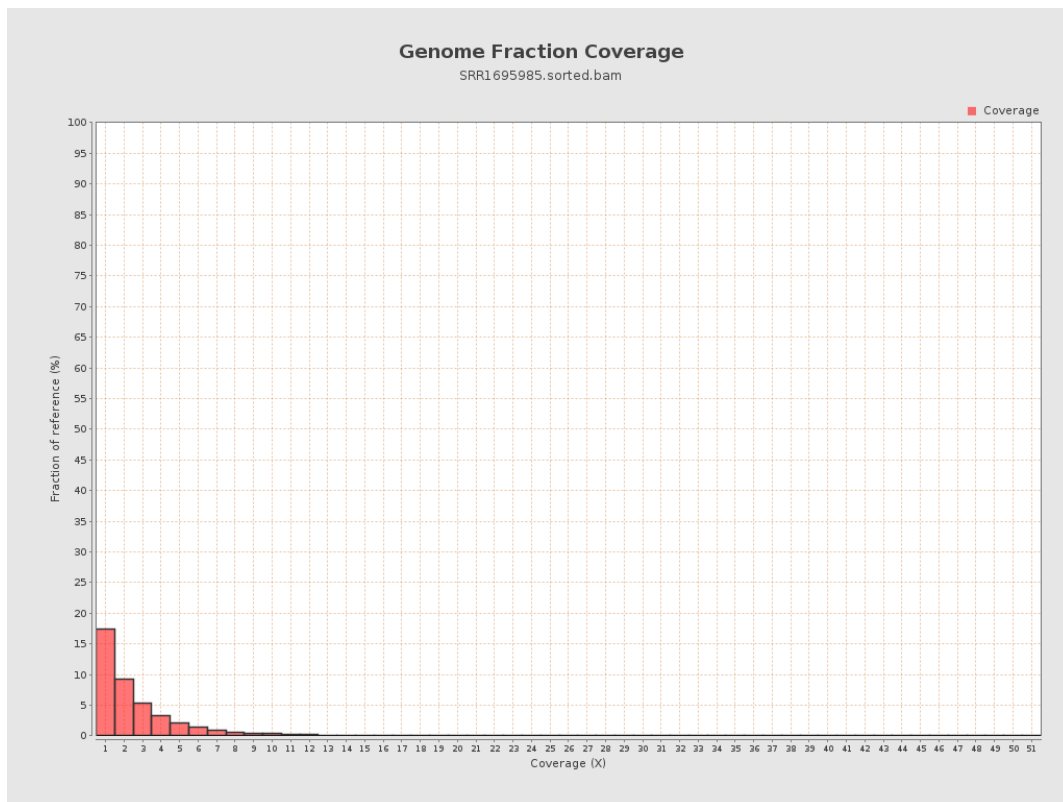
4. Results : Coverage Histogram



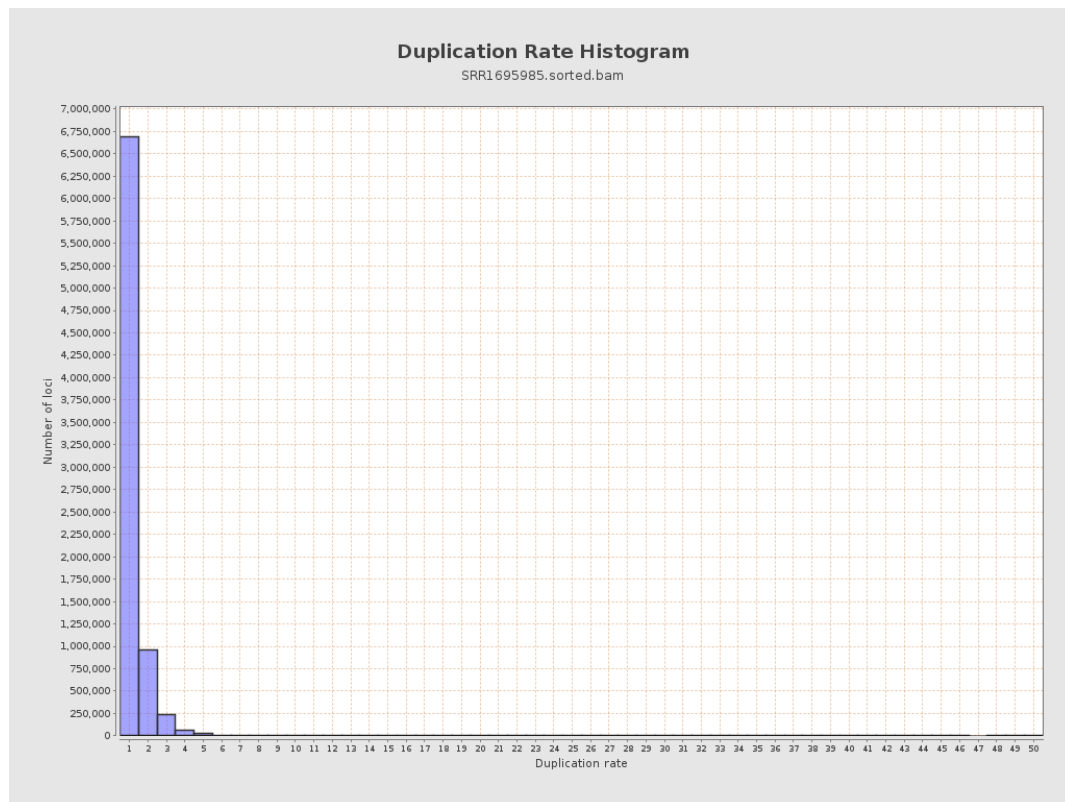
5. Results : Coverage Histogram (0-50X)



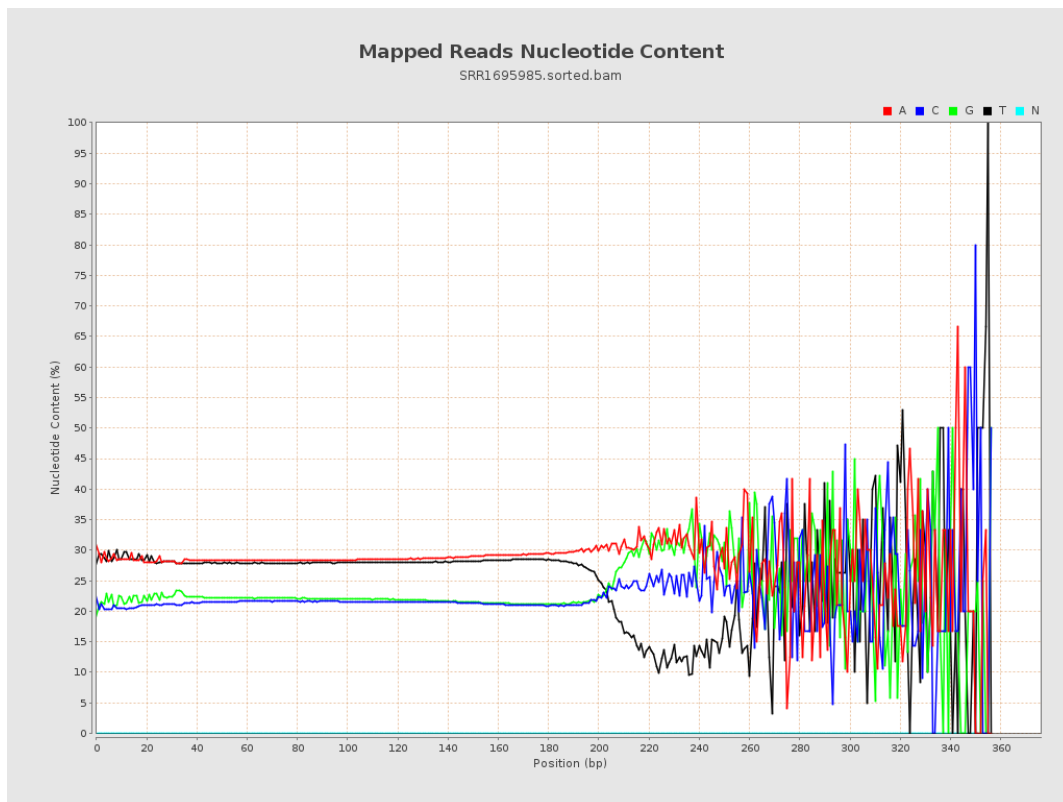
6. Results : Genome Fraction Coverage



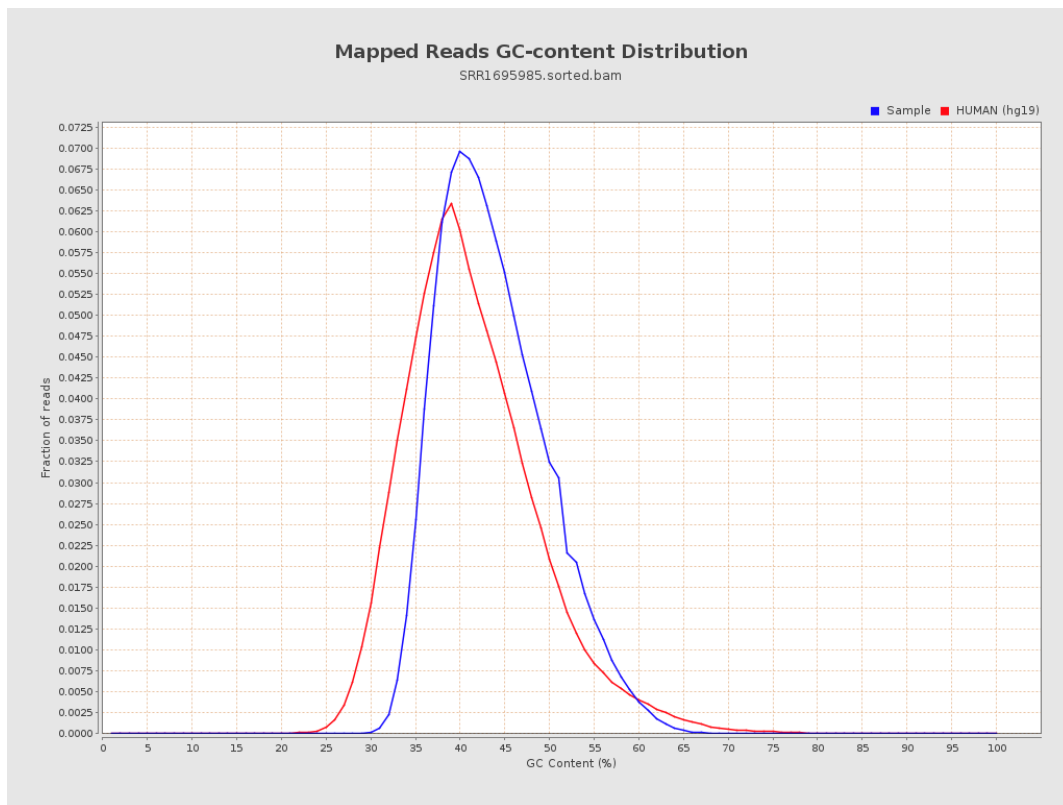
7. Results : Duplication Rate Histogram



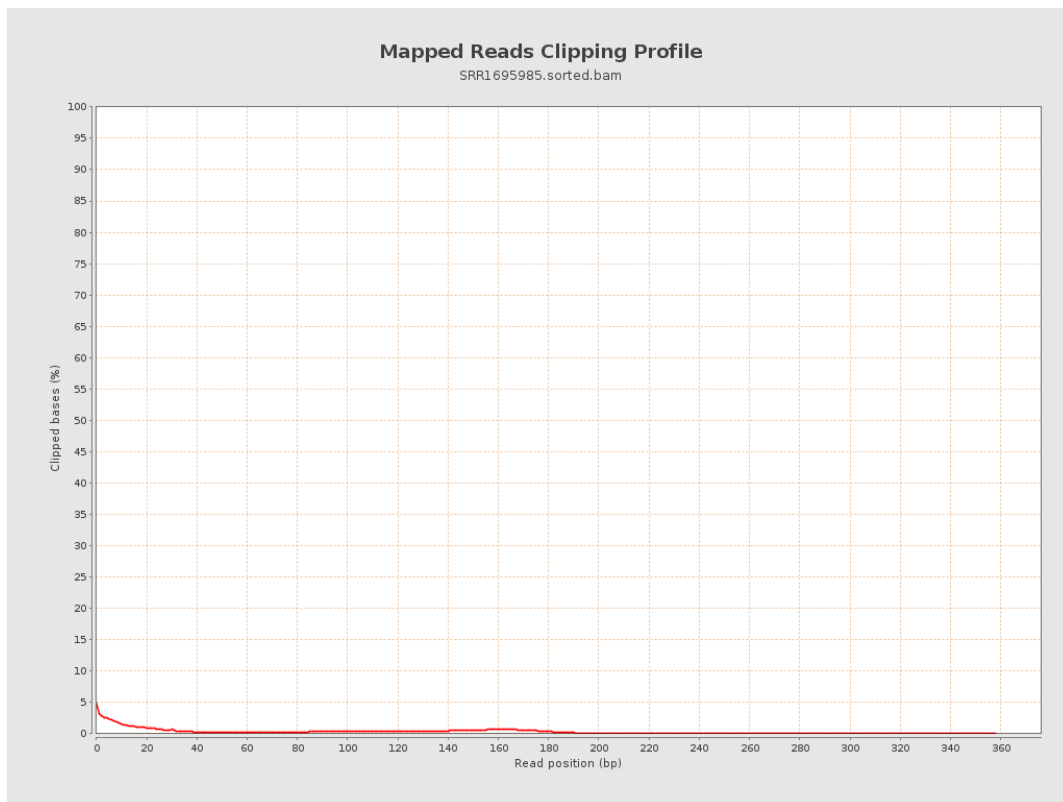
8. Results : Mapped Reads Nucleotide Content



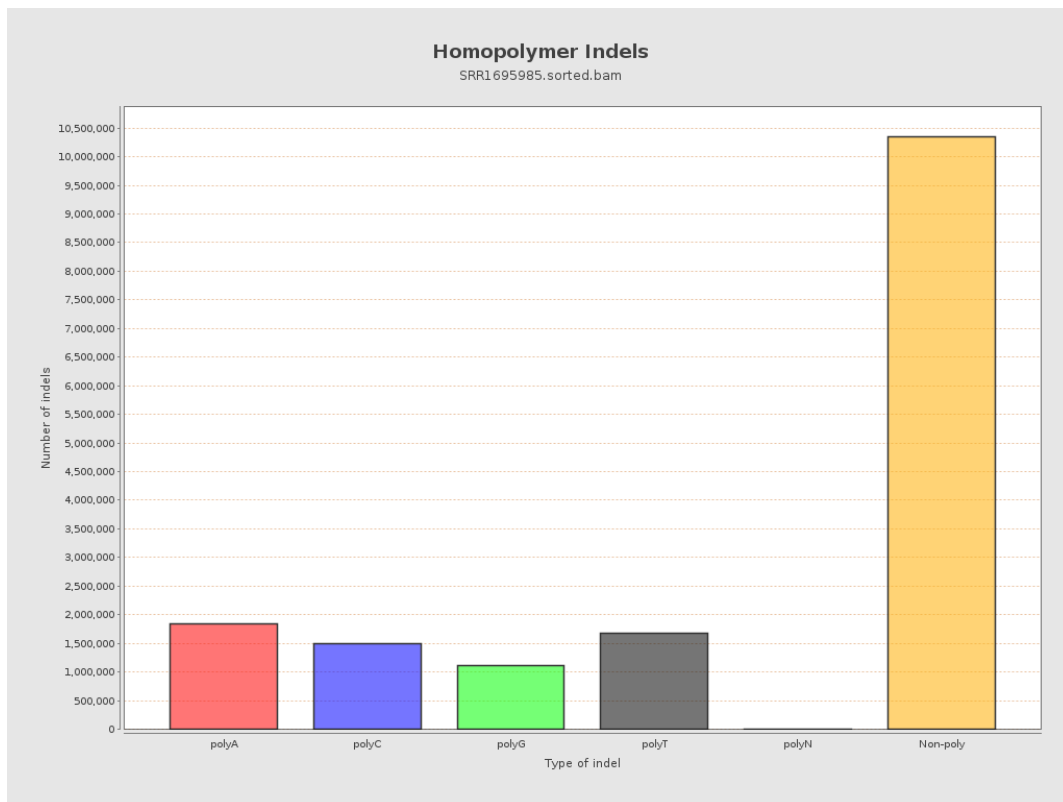
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

