

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 15:21:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013195.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR6013195 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013195.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 15:21:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013195.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,237,176
Mapped reads	1,951,097 / 87.21%
Unmapped reads	286,079 / 12.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,897 / 0.62%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	85,519 / 3.82%
Duplication rate	3.46%
Clipped reads	870,512 / 38.91%

2.2. ACGT Content

Number/percentage of A's	35,870,343 / 27.71%
Number/percentage of C's	23,638,226 / 18.26%
Number/percentage of T's	41,307,220 / 31.91%
Number/percentage of G's	28,611,261 / 22.11%
Number/percentage of N's	1,875 / 0%
GC Percentage	40.37%

2.3. Coverage

Mean	0.0418

Standard Deviation	0.3758
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2.4. Mapping Quality

Mean Mapping Quality	46.57
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2.5. Mismatches and indels

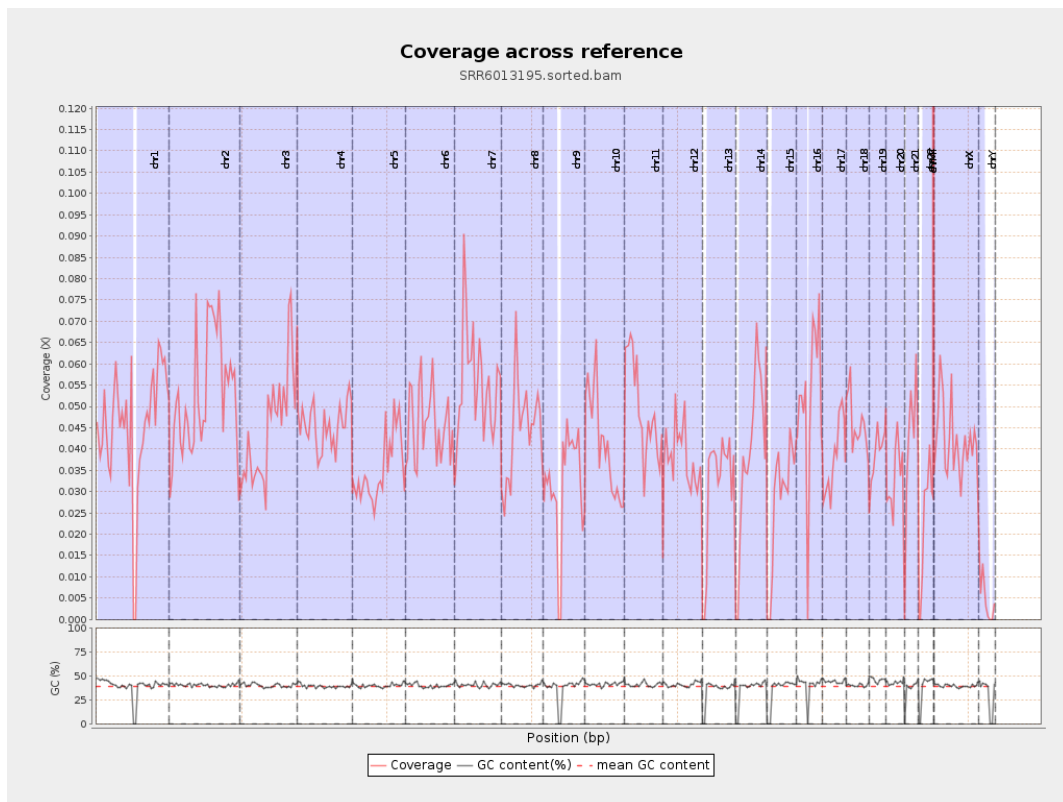
General error rate	0.71%
Mismatches	902,905
Insertions	8,830
Mapped reads with at least one insertion	0.45%
Deletions	30,398
Mapped reads with at least one deletion	1.54%
Homopolymer indels	47.49%

2.6. Chromosome stats

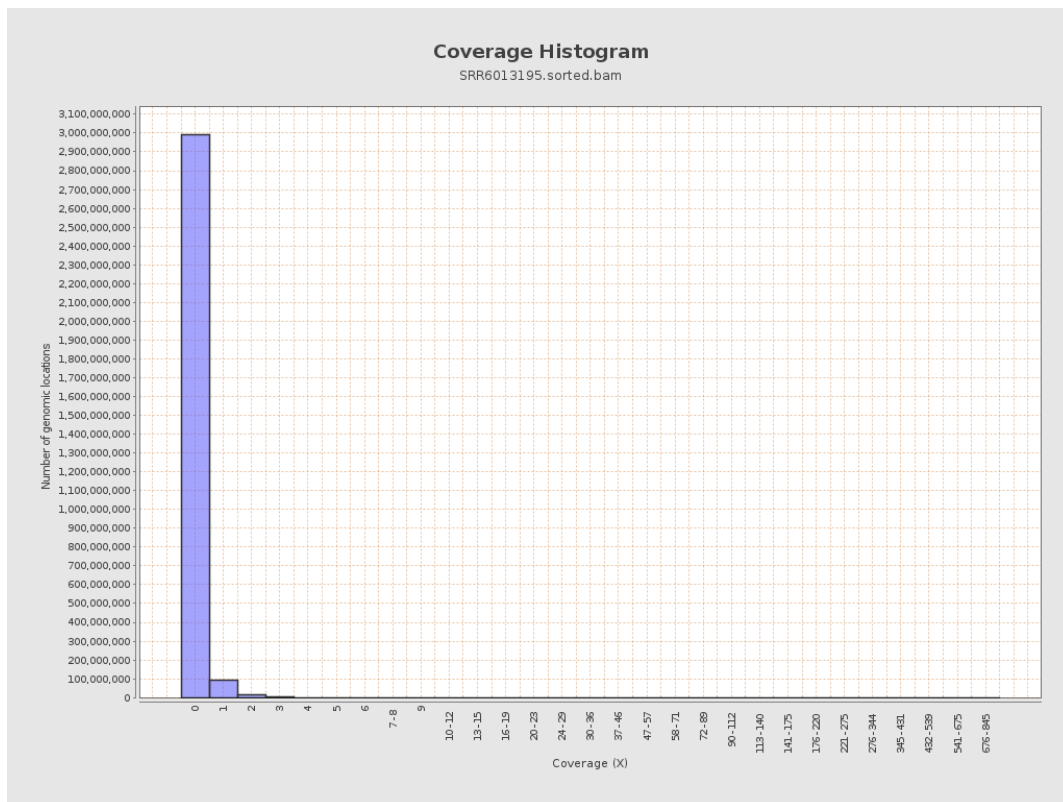
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	11324579	0.0454	0.7365
chr2	243199373	12873722	0.0529	0.4305
chr3	198022430	8898121	0.0449	0.2501
chr4	191154276	8665206	0.0453	0.2559
chr5	180915260	6362791	0.0352	0.2212
chr6	171115067	7822694	0.0457	0.3215
chr7	159138663	8912820	0.056	0.5032

chr8	146364022	6516054	0.0445	0.4277
chr9	141213431	4471856	0.0317	0.305
chr10	135534747	5603587	0.0413	0.3321
chr11	135006516	6601844	0.0489	0.367
chr12	133851895	5095788	0.0381	0.2331
chr13	115169878	3571657	0.031	0.2073
chr14	107349540	4178212	0.0389	0.2389
chr15	102531392	2908321	0.0284	0.2027
chr16	90354753	4666928	0.0517	0.2775
chr17	81195210	3064640	0.0377	0.2541
chr18	78077248	3609356	0.0462	0.5498
chr19	59128983	2326696	0.0393	0.4832
chr20	63025520	2060323	0.0327	0.219
chr21	48129895	1998725	0.0415	0.2482
chr22	51304566	1163501	0.0227	0.1733
chrMT	16571	20617	1.2442	1.3191
chrX	155270560	6487296	0.0418	0.2712
chrY	59373566	276599	0.0047	0.1068

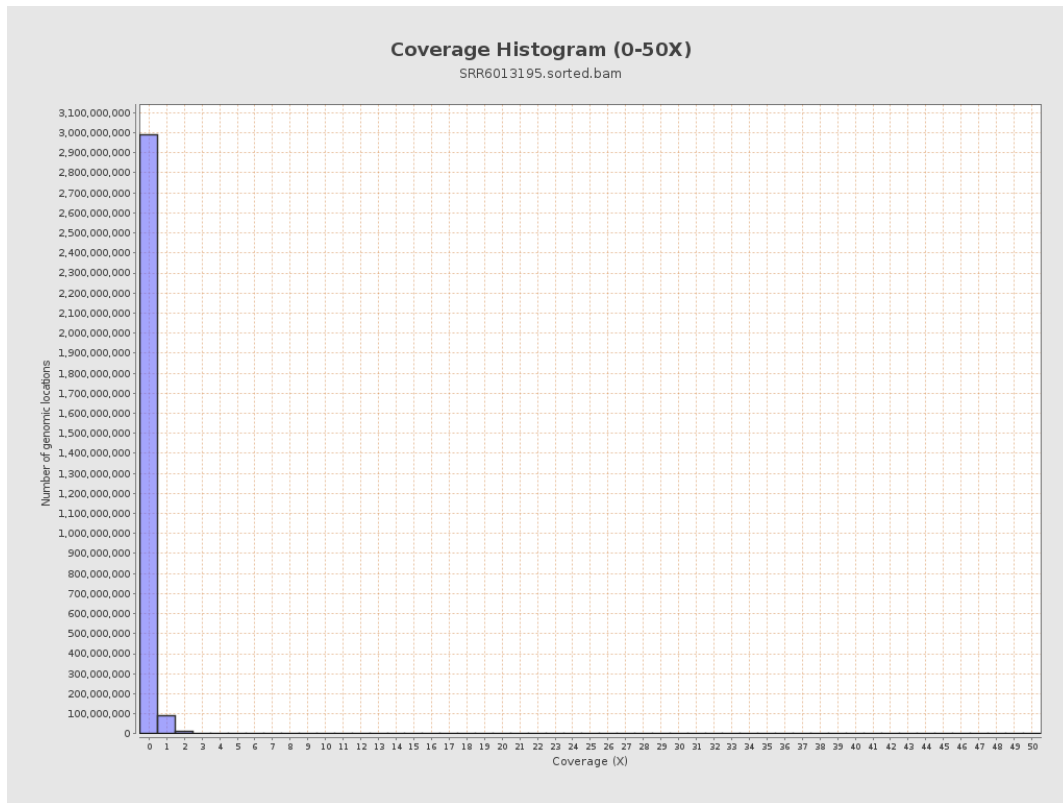
3. Results : Coverage across reference



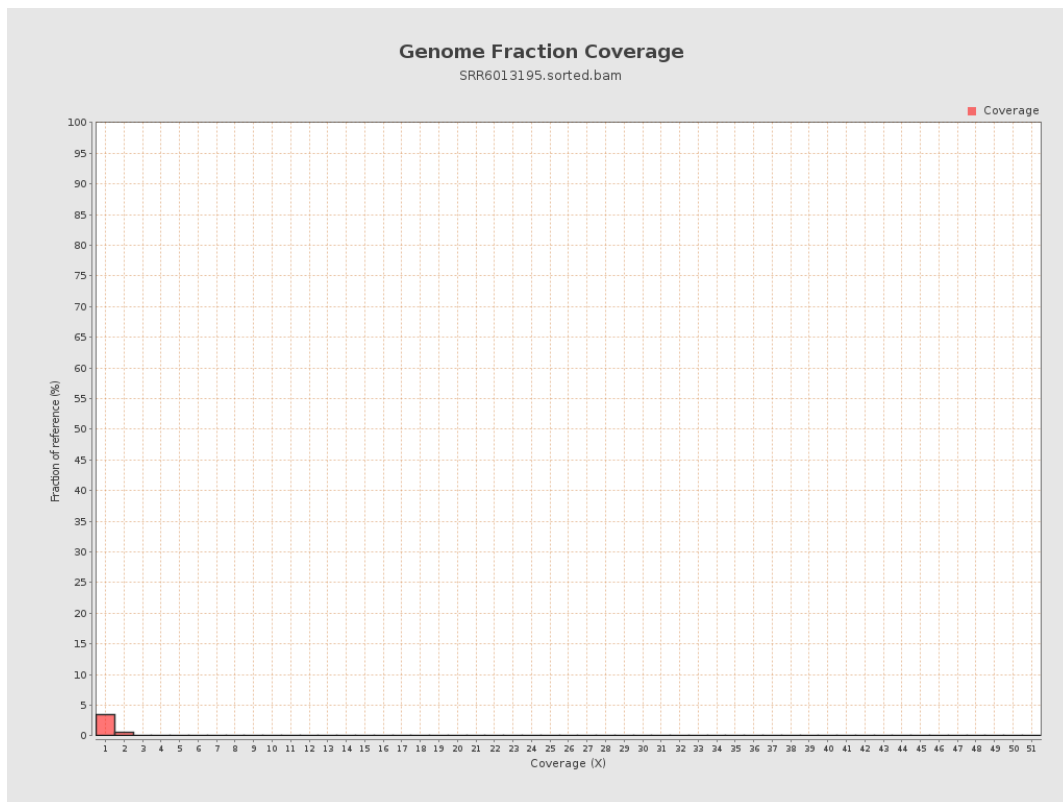
4. Results : Coverage Histogram



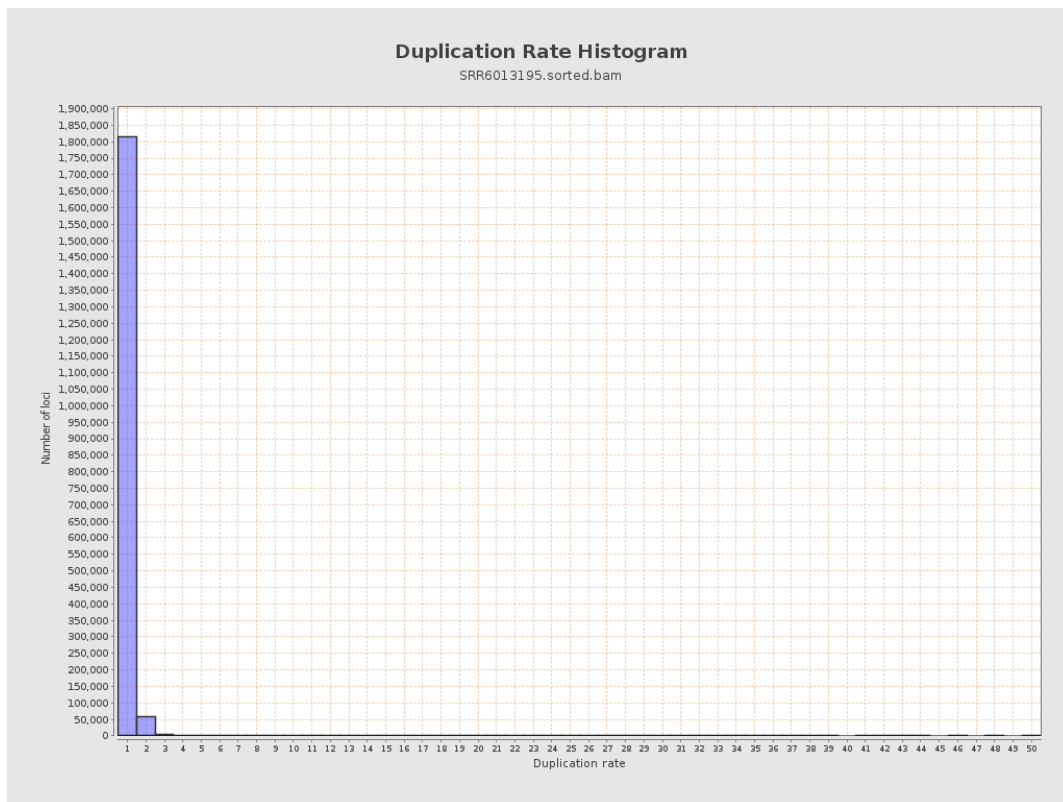
5. Results : Coverage Histogram (0-50X)



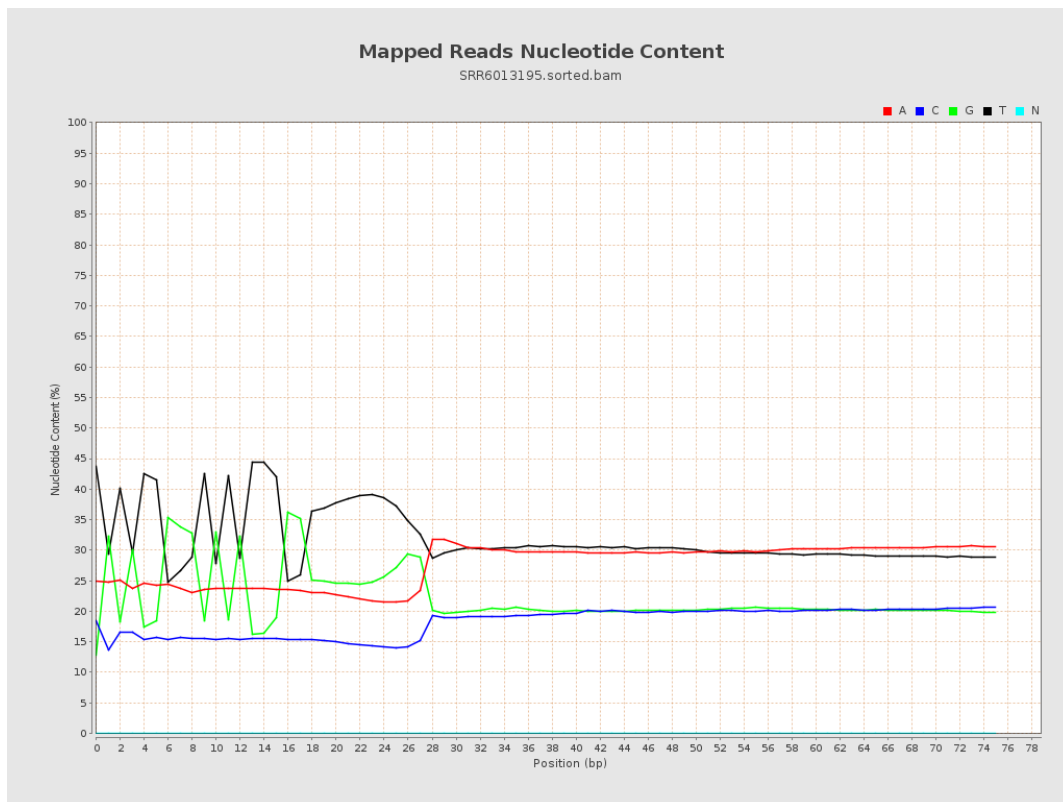
6. Results : Genome Fraction Coverage



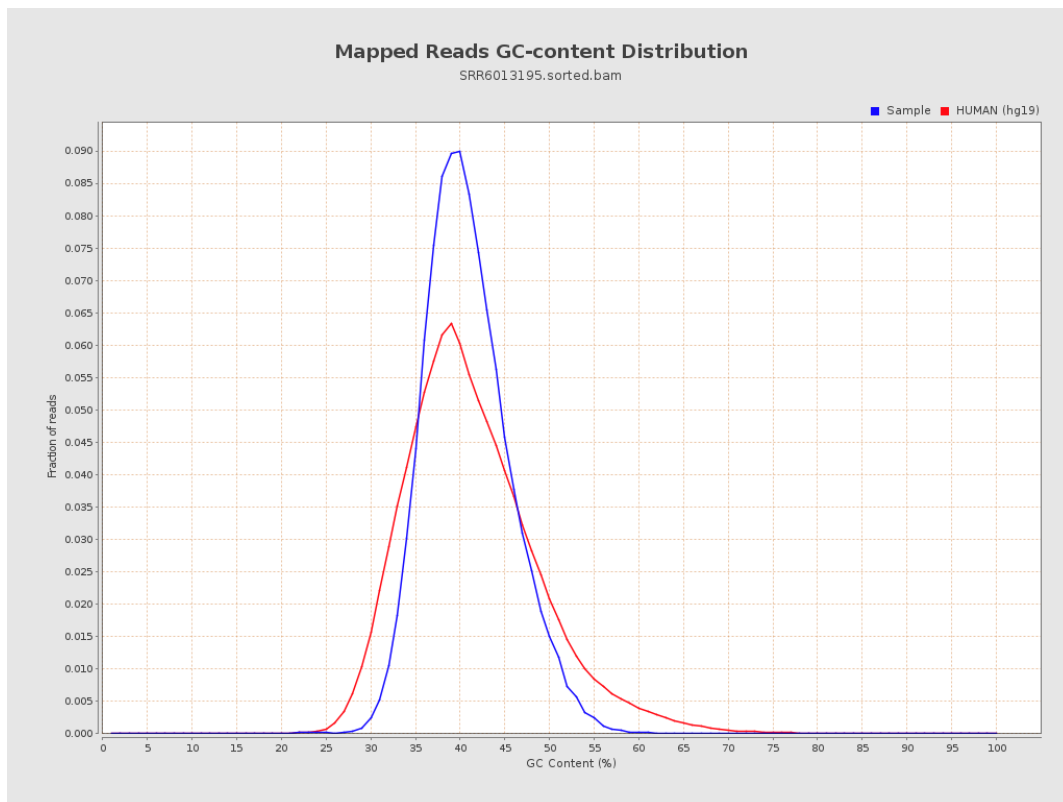
7. Results : Duplication Rate Histogram



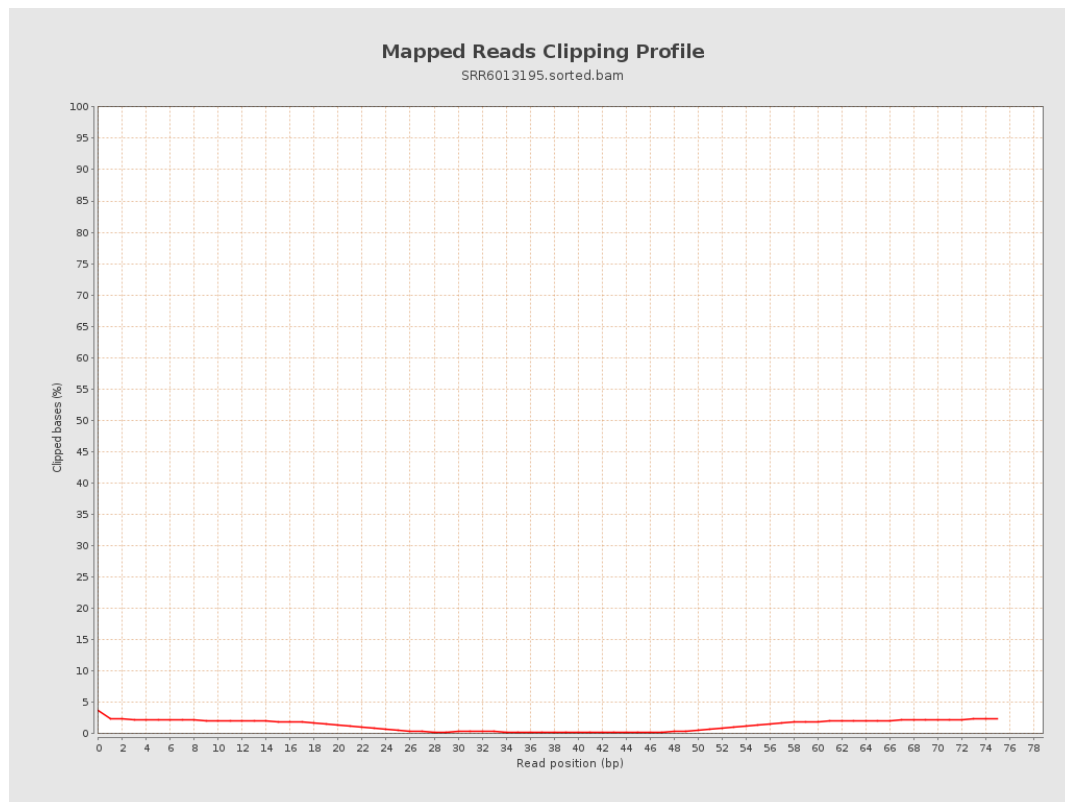
8. Results : Mapped Reads Nucleotide Content



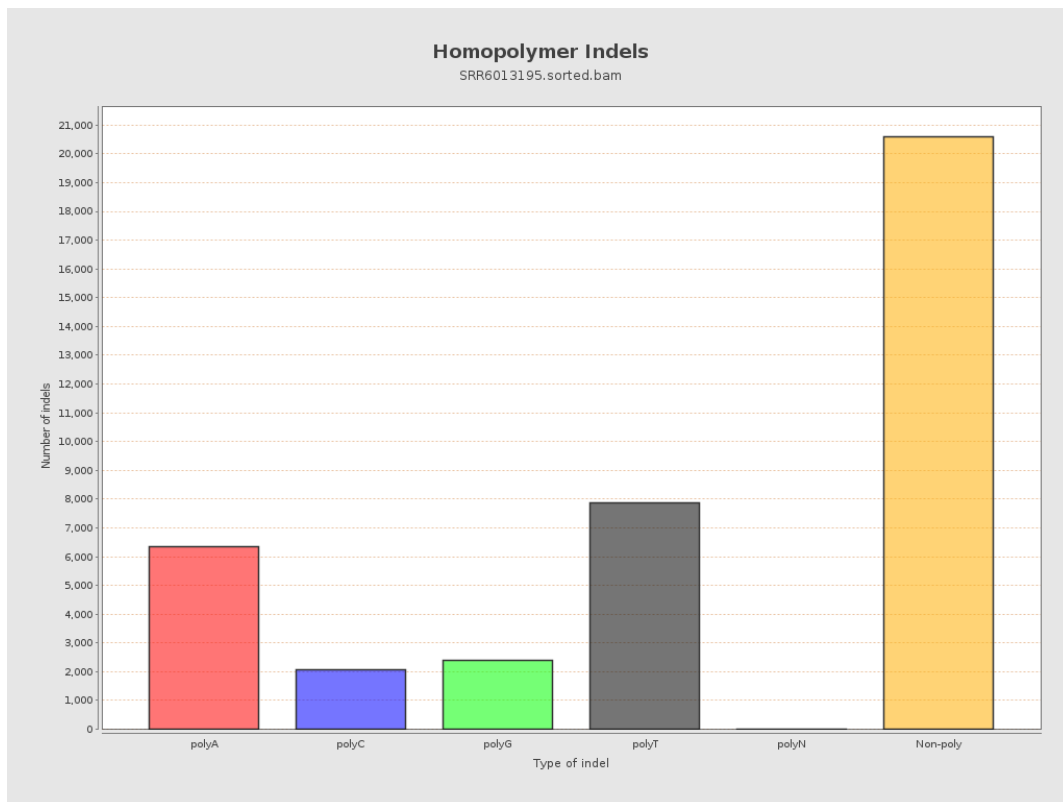
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

