

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 22:21:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013341.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_SRR6013341 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013341.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 22:21:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013341.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,677,191
Mapped reads	1,486,779 / 88.65%
Unmapped reads	190,412 / 11.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,742 / 0.7%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	64,342 / 3.84%
Duplication rate	3.53%
Clipped reads	690,713 / 41.18%

2.2. ACGT Content

Number/percentage of A's	26,687,925 / 27.14%
Number/percentage of C's	18,844,934 / 19.17%
Number/percentage of T's	30,434,475 / 30.95%
Number/percentage of G's	22,334,381 / 22.71%
Number/percentage of N's	25,171 / 0.03%
GC Percentage	41.88%

2.3. Coverage

Mean	0.0318

Standard Deviation	0.2852
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2.4. Mapping Quality

Mean Mapping Quality	46.09
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2.5. Mismatches and indels

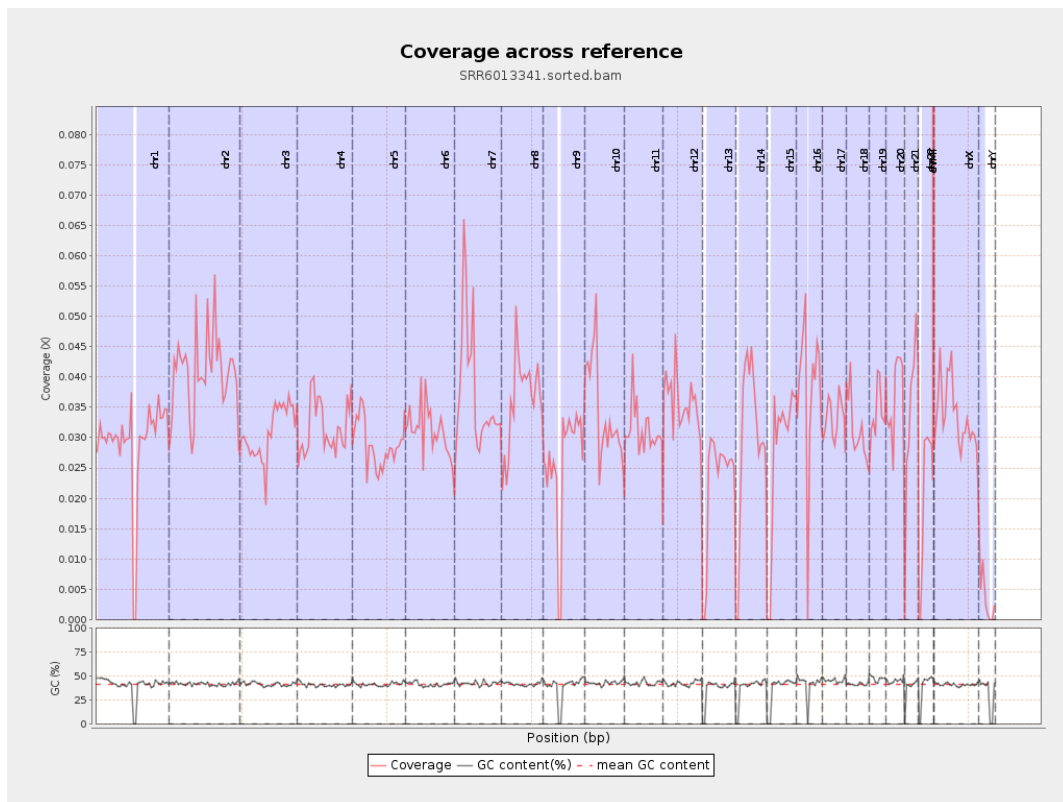
General error rate	0.82%
Mismatches	790,869
Insertions	6,592
Mapped reads with at least one insertion	0.44%
Deletions	26,891
Mapped reads with at least one deletion	1.79%
Homopolymer indels	45.42%

2.6. Chromosome stats

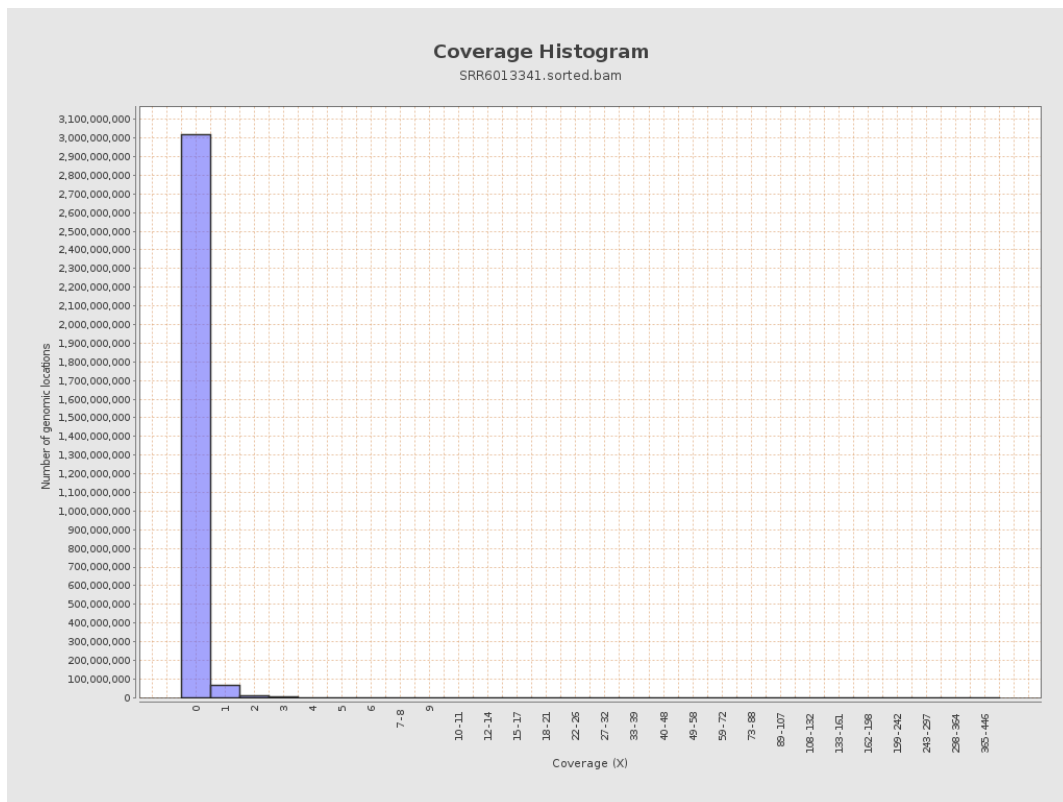
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7282305	0.0292	0.4095
chr2	243199373	9922425	0.0408	0.3453
chr3	198022430	6110225	0.0309	0.2079
chr4	191154276	6043558	0.0316	0.2152
chr5	180915260	5204292	0.0288	0.2032
chr6	171115067	5314649	0.0311	0.2471
chr7	159138663	5990391	0.0376	0.4177

chr8	146364022	5307535	0.0363	0.2749
chr9	141213431	3643061	0.0258	0.2633
chr10	135534747	4665238	0.0344	0.3045
chr11	135006516	4209628	0.0312	0.249
chr12	133851895	4797145	0.0358	0.2265
chr13	115169878	2561219	0.0222	0.1792
chr14	107349540	3227040	0.0301	0.2173
chr15	102531392	2847891	0.0278	0.1967
chr16	90354753	3428295	0.0379	0.2572
chr17	81195210	2668221	0.0329	0.2317
chr18	78077248	2451383	0.0314	0.4637
chr19	59128983	2031018	0.0343	0.3511
chr20	63025520	2287748	0.0363	0.2303
chr21	48129895	1644921	0.0342	0.23
chr22	51304566	1036583	0.0202	0.1679
chrMT	16571	261147	15.7593	9.717
chrX	155270560	5224159	0.0336	0.2334
chrY	59373566	213631	0.0036	0.0911

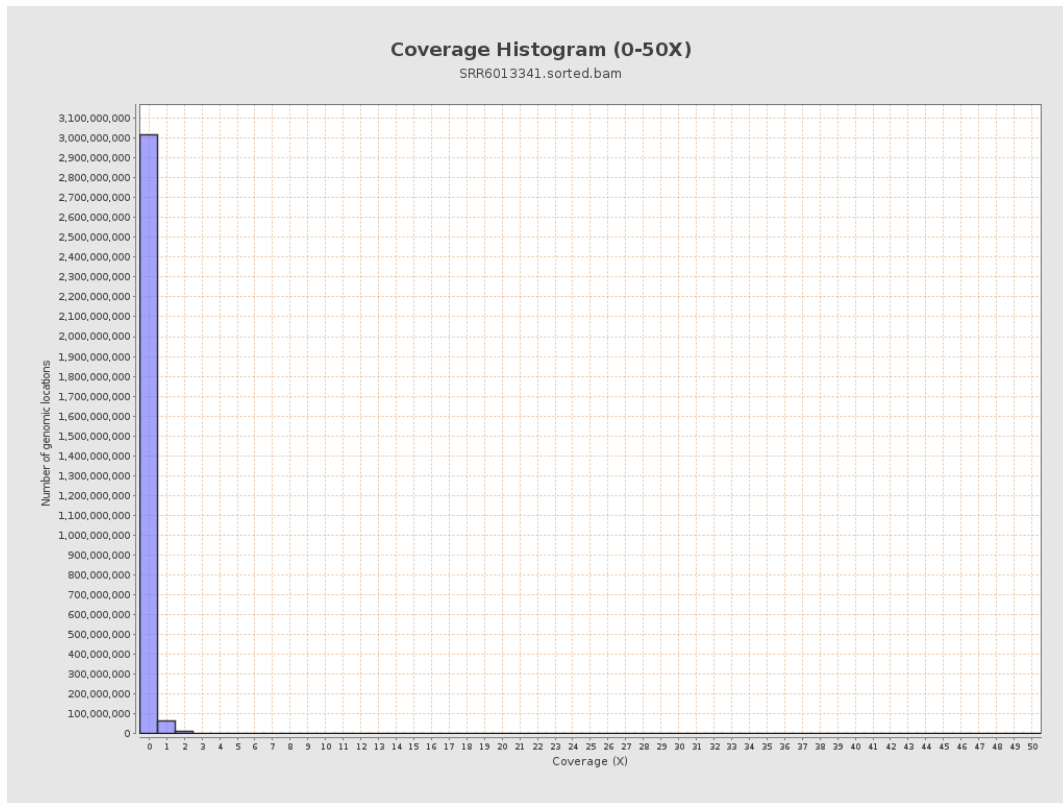
3. Results : Coverage across reference



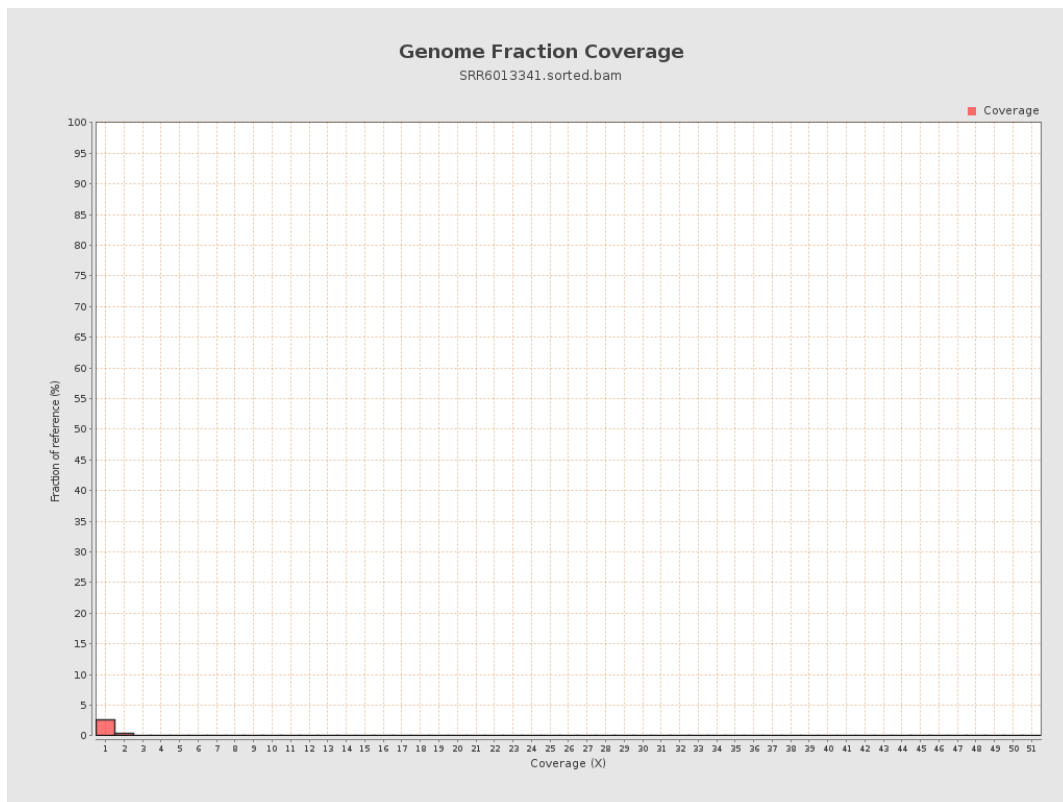
4. Results : Coverage Histogram



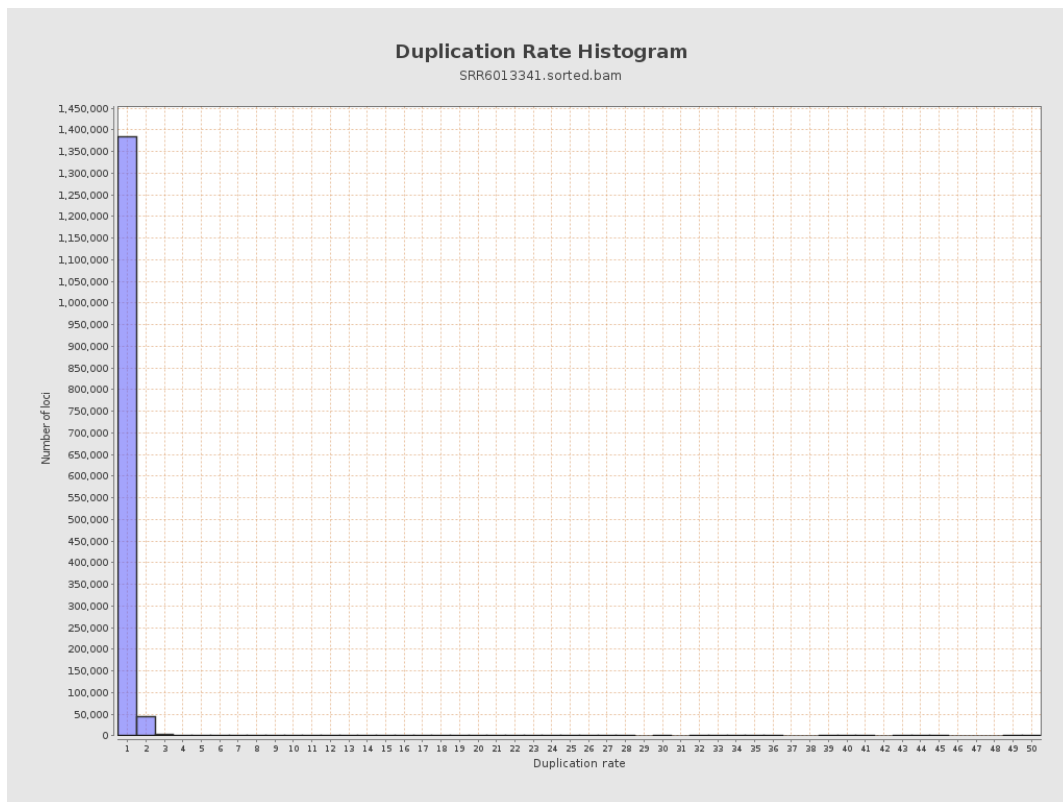
5. Results : Coverage Histogram (0-50X)



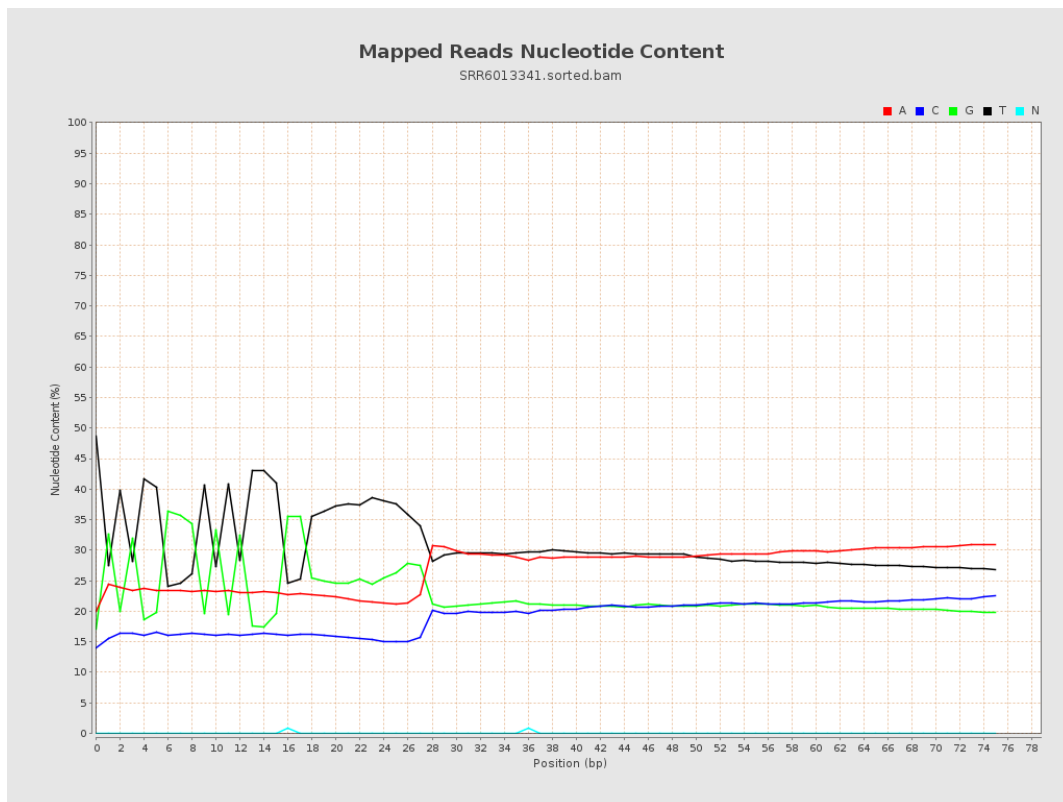
6. Results : Genome Fraction Coverage



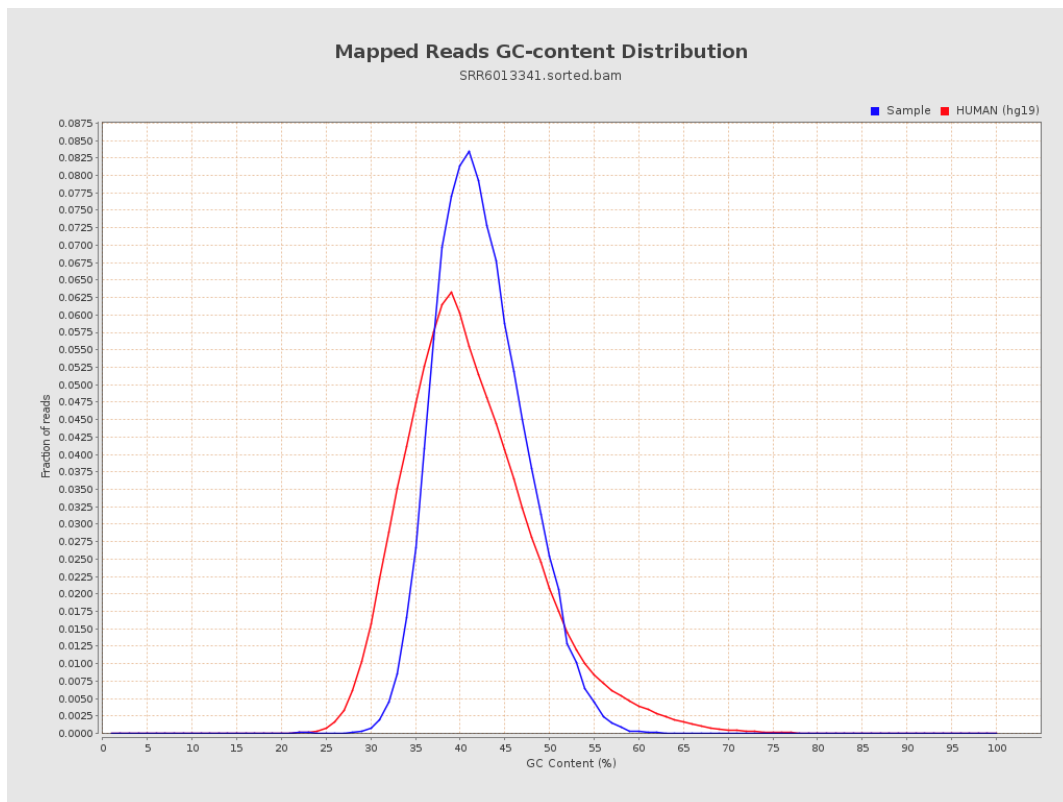
7. Results : Duplication Rate Histogram



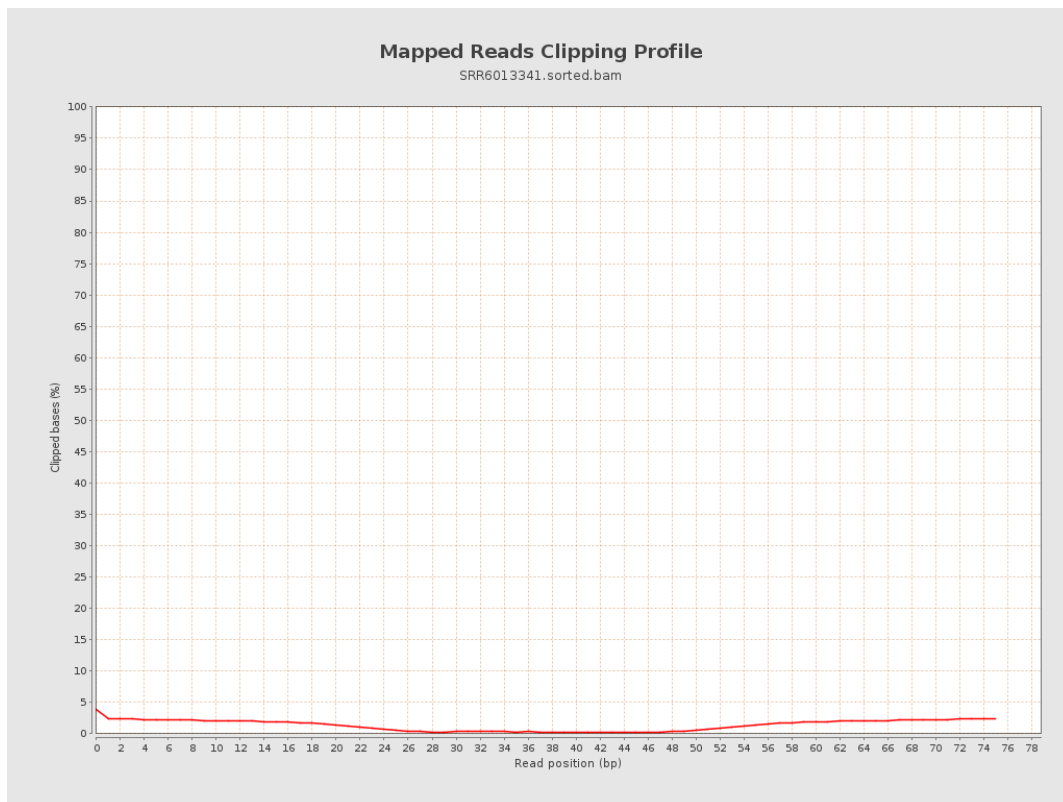
8. Results : Mapped Reads Nucleotide Content



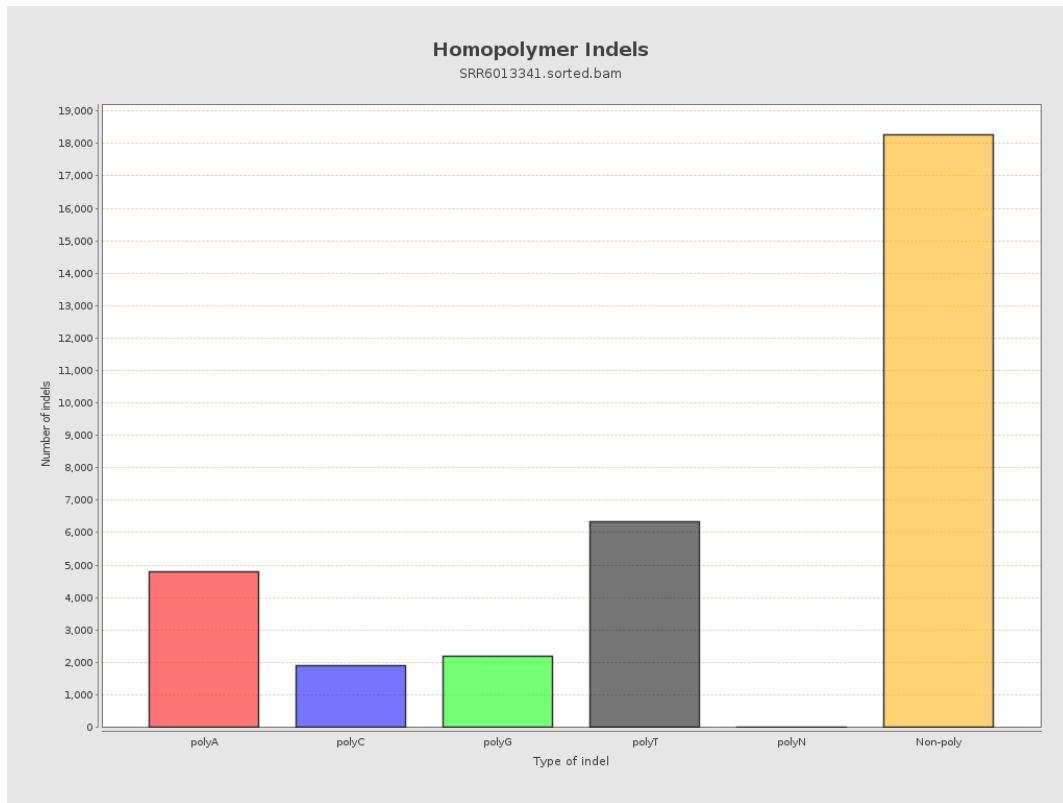
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

