

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 21:32:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013324.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_SRR6013324 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013324.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 21:32:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013324.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,953,849
Mapped reads	1,637,719 / 83.82%
Unmapped reads	316,130 / 16.18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,484 / 1.05%
Read min/max/mean length	30 / 76 / 76.37
Duplicated reads (estimated)	268,044 / 13.72%
Duplication rate	11.13%
Clipped reads	786,501 / 40.25%

2.2. ACGT Content

Number/percentage of A's	29,330,666 / 27.16%
Number/percentage of C's	20,782,478 / 19.24%
Number/percentage of T's	33,316,131 / 30.85%
Number/percentage of G's	24,559,921 / 22.74%
Number/percentage of N's	13,820 / 0.01%
GC Percentage	41.98%

2.3. Coverage

Mean	0.0349

Standard Deviation	0.4853
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2.4. Mapping Quality

Mean Mapping Quality	39.29
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2.5. Mismatches and indels

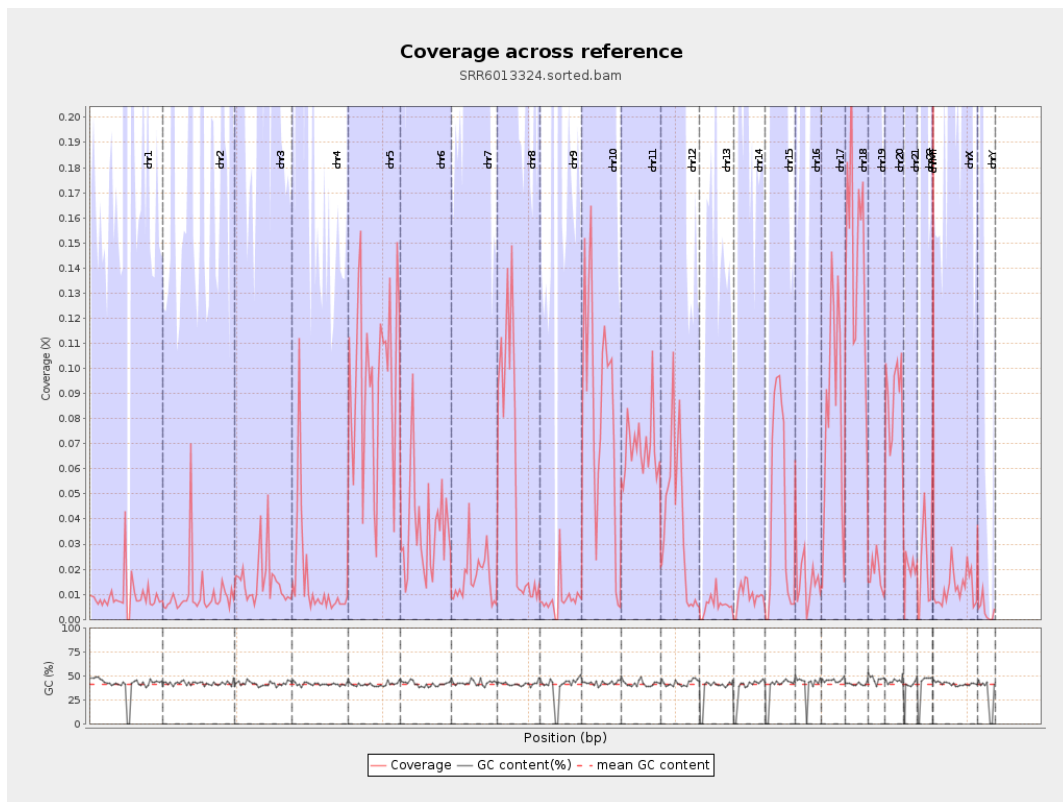
General error rate	0.8%
Mismatches	849,368
Insertions	8,056
Mapped reads with at least one insertion	0.49%
Deletions	28,690
Mapped reads with at least one deletion	1.73%
Homopolymer indels	45.08%

2.6. Chromosome stats

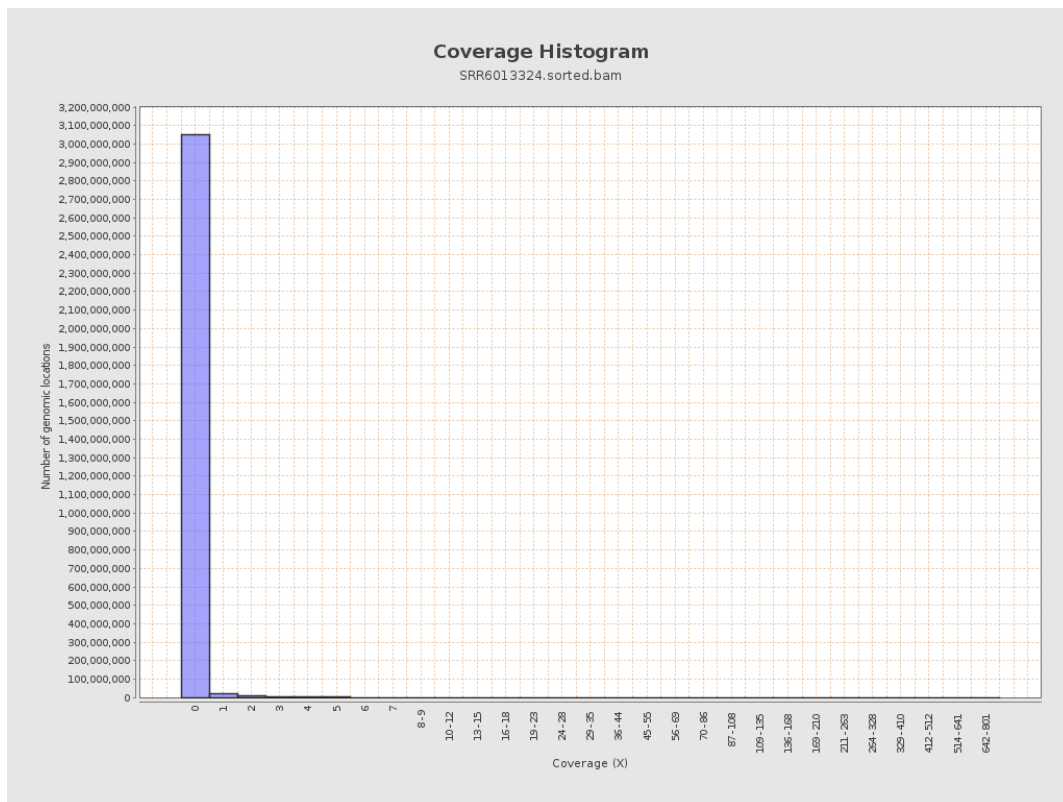
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	2227911	0.0089	0.5856
chr2	243199373	2401027	0.0099	0.6079
chr3	198022430	3064563	0.0155	0.2249
chr4	191154276	2960352	0.0155	0.2372
chr5	180915260	17192107	0.095	0.6201
chr6	171115067	6172812	0.0361	0.4045
chr7	159138663	2640205	0.0166	0.298

chr8	146364022	7691996	0.0526	0.6536
chr9	141213431	1155849	0.0082	0.3376
chr10	135534747	11290968	0.0833	0.7164
chr11	135006516	9246248	0.0685	0.6646
chr12	133851895	4976055	0.0372	0.3817
chr13	115169878	680378	0.0059	0.1378
chr14	107349540	1025322	0.0096	0.172
chr15	102531392	4479000	0.0437	0.4102
chr16	90354753	1482390	0.0164	0.2529
chr17	81195210	6844496	0.0843	0.624
chr18	78077248	11508509	0.1474	0.9292
chr19	59128983	1099713	0.0186	0.5912
chr20	63025520	5612475	0.0891	0.5997
chr21	48129895	965502	0.0201	0.2674
chr22	51304566	1080184	0.0211	0.2729
chrMT	16571	7871	0.475	0.9842
chrX	155270560	2028270	0.0131	0.2702
chrY	59373566	217827	0.0037	0.1295

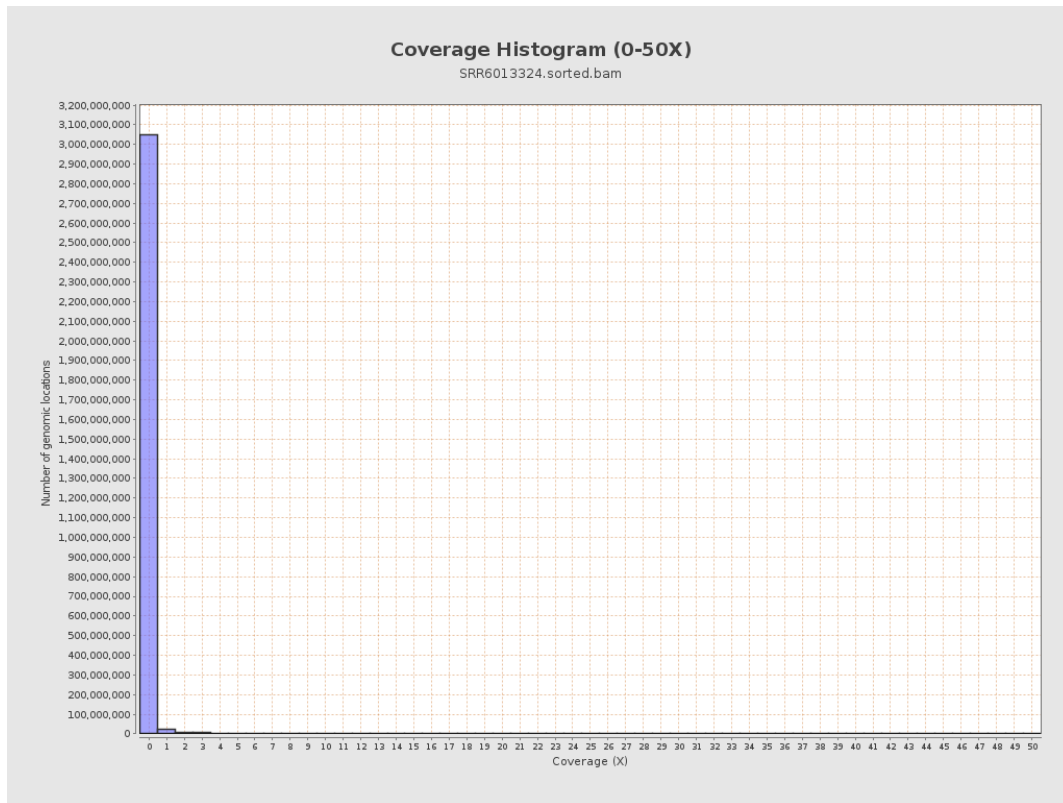
3. Results : Coverage across reference



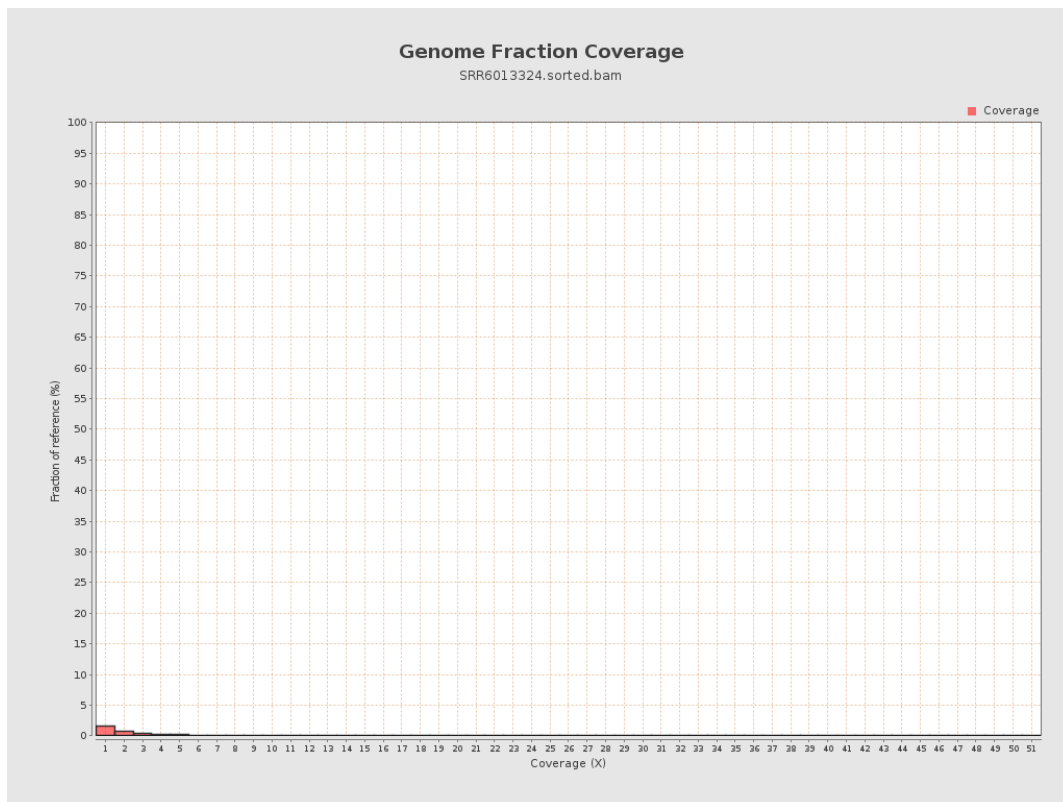
4. Results : Coverage Histogram



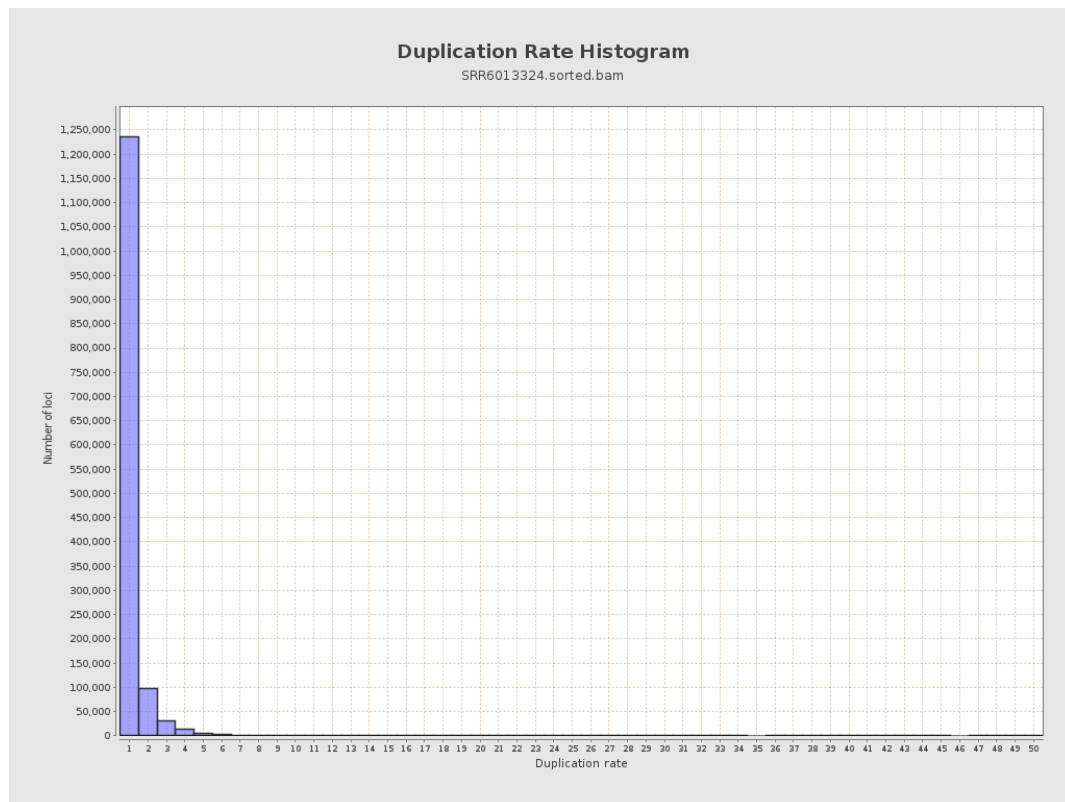
5. Results : Coverage Histogram (0-50X)



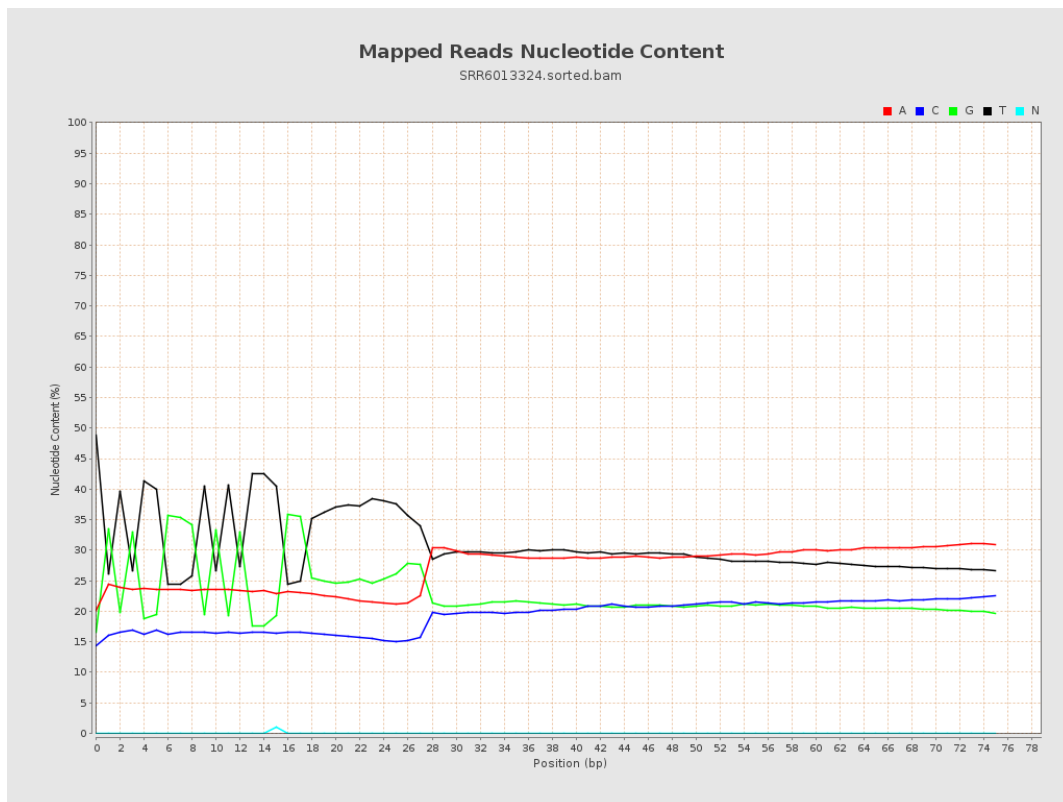
6. Results : Genome Fraction Coverage



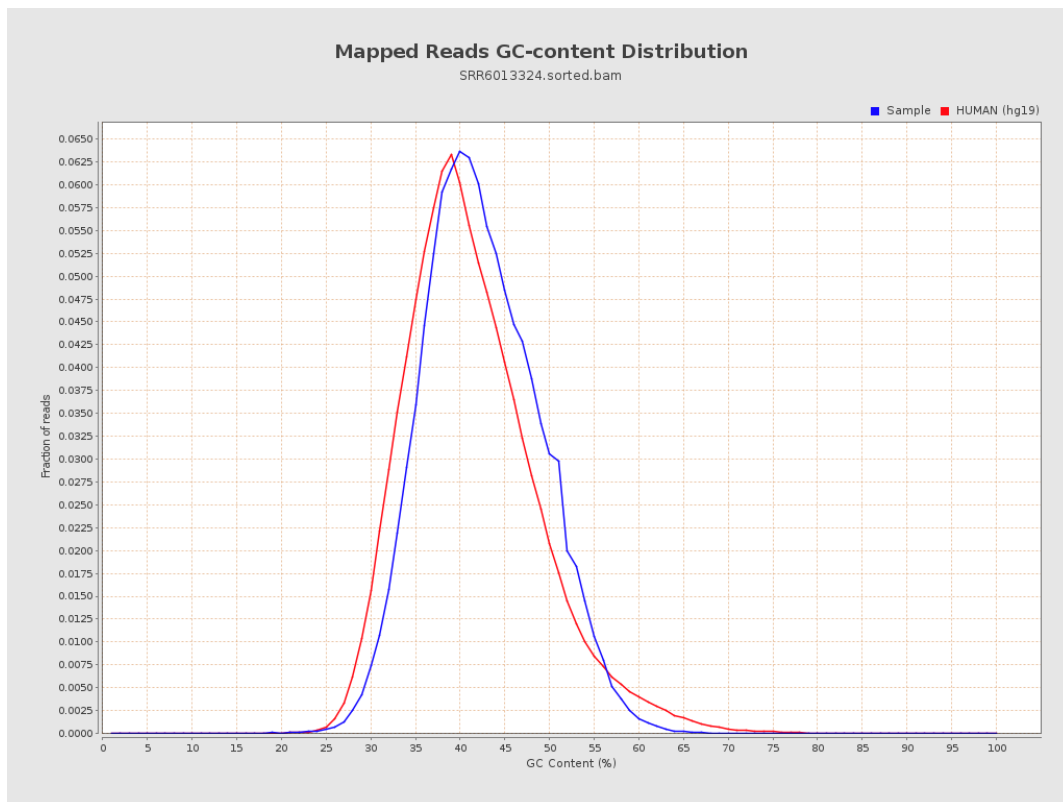
7. Results : Duplication Rate Histogram



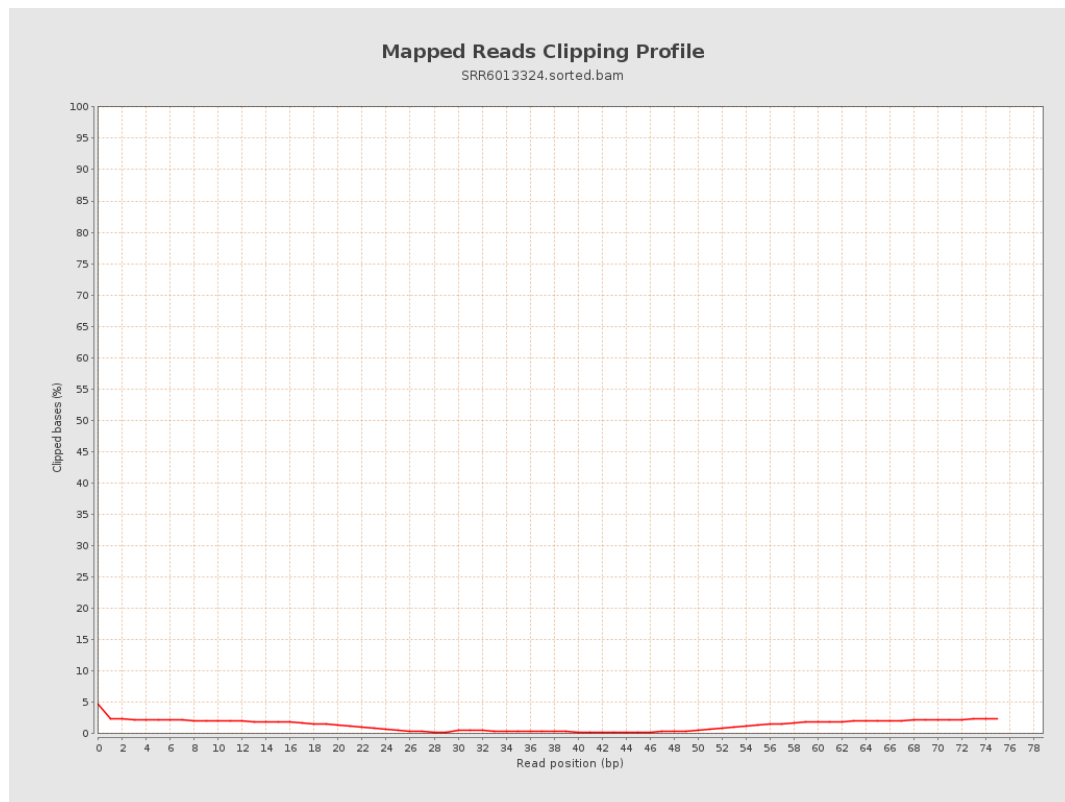
8. Results : Mapped Reads Nucleotide Content



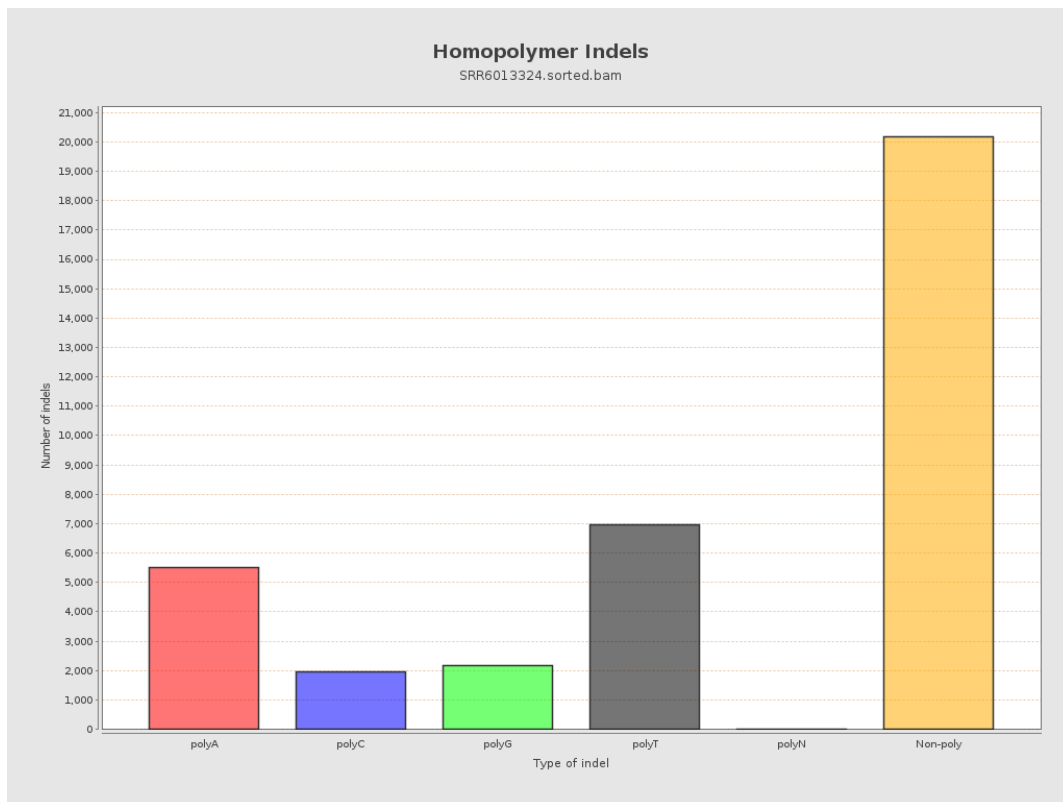
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

