

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 12:36:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238244.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_SRR6238244 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238244.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 12:36:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238244.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	874,858
Mapped reads	280,765 / 32.09%
Unmapped reads	594,093 / 67.91%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,729 / 0.31%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	41,514 / 4.75%
Duplication rate	8.65%
Clipped reads	178,826 / 20.44%

2.2. ACGT Content

Number/percentage of A's	4,771,300 / 27.75%
Number/percentage of C's	3,446,079 / 20.04%
Number/percentage of T's	5,145,779 / 29.93%
Number/percentage of G's	3,825,527 / 22.25%
Number/percentage of N's	3,508 / 0.02%
GC Percentage	42.3%

2.3. Coverage

Mean	0.0056

Standard Deviation	0.2349
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	42.7
----------------------	------

2.5. Mismatches and indels

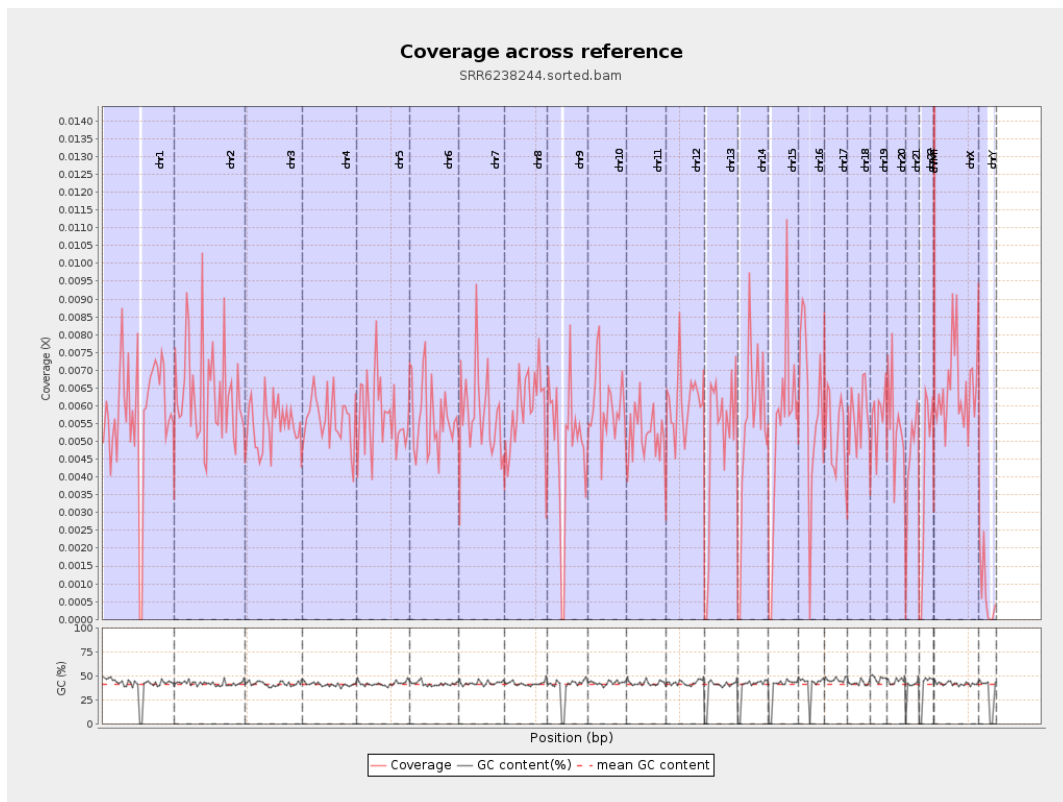
General error rate	1.07%
Mismatches	181,924
Insertions	1,530
Mapped reads with at least one insertion	0.54%
Deletions	4,577
Mapped reads with at least one deletion	1.61%
Homopolymer indels	44.8%

2.6. Chromosome stats

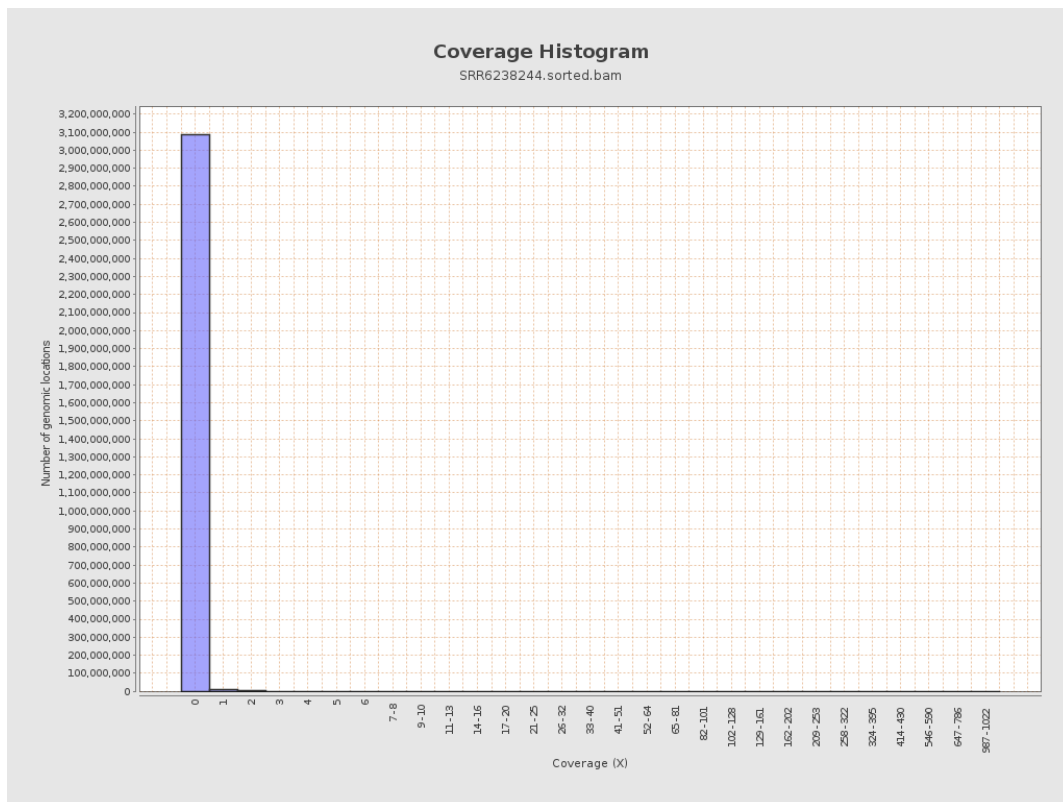
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	1427740	0.0057	0.2387
chr2	243199373	1540567	0.0063	0.3488
chr3	198022430	1083088	0.0055	0.1444
chr4	191154276	1080988	0.0057	0.1826
chr5	180915260	1039868	0.0057	0.1662
chr6	171115067	972109	0.0057	0.2205
chr7	159138663	917213	0.0058	0.1715

chr8	146364022	859339	0.0059	0.1668
chr9	141213431	687306	0.0049	0.141
chr10	135534747	810388	0.006	0.1502
chr11	135006516	702147	0.0052	0.1238
chr12	133851895	820620	0.0061	0.1674
chr13	115169878	575698	0.005	0.2127
chr14	107349540	580185	0.0054	0.4636
chr15	102531392	541837	0.0053	0.601
chr16	90354753	525807	0.0058	0.1436
chr17	81195210	414498	0.0051	0.144
chr18	78077248	448865	0.0057	0.1394
chr19	59128983	333776	0.0056	0.1332
chr20	63025520	345040	0.0055	0.126
chr21	48129895	223040	0.0046	0.1149
chr22	51304566	208738	0.0041	0.1057
chrMT	16571	3892	0.2349	1.4336
chrX	155270560	1013327	0.0065	0.2389
chrY	59373566	43473	0.0007	0.0578

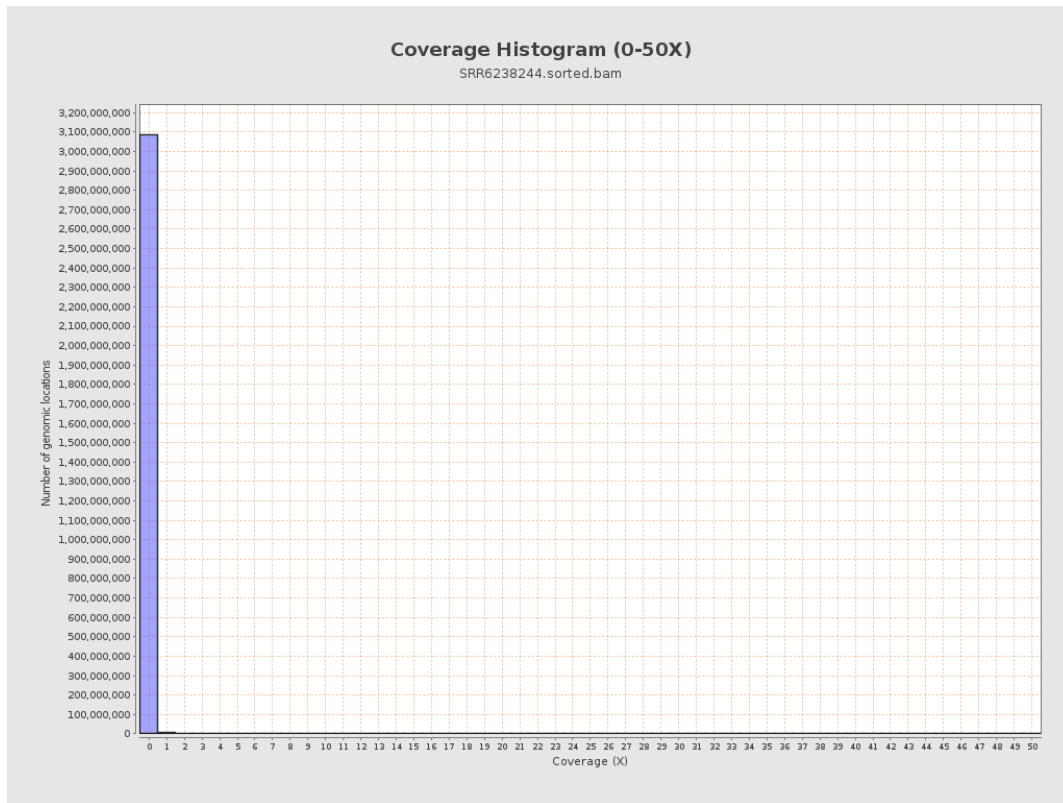
3. Results : Coverage across reference



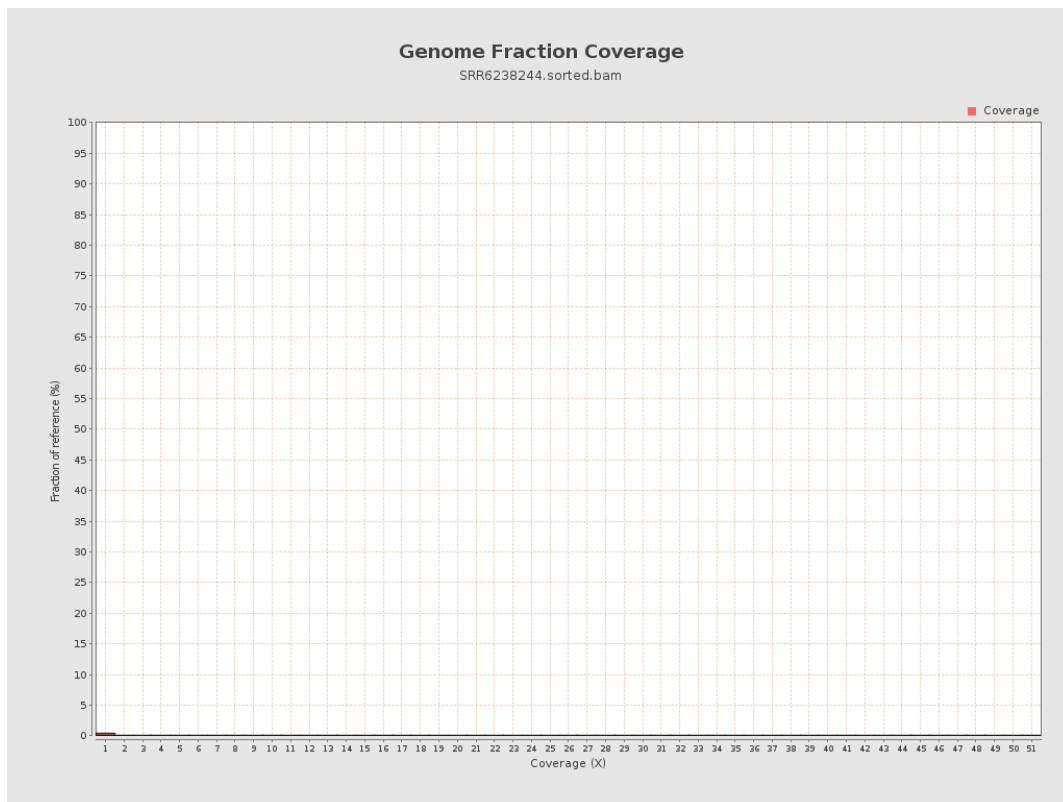
4. Results : Coverage Histogram



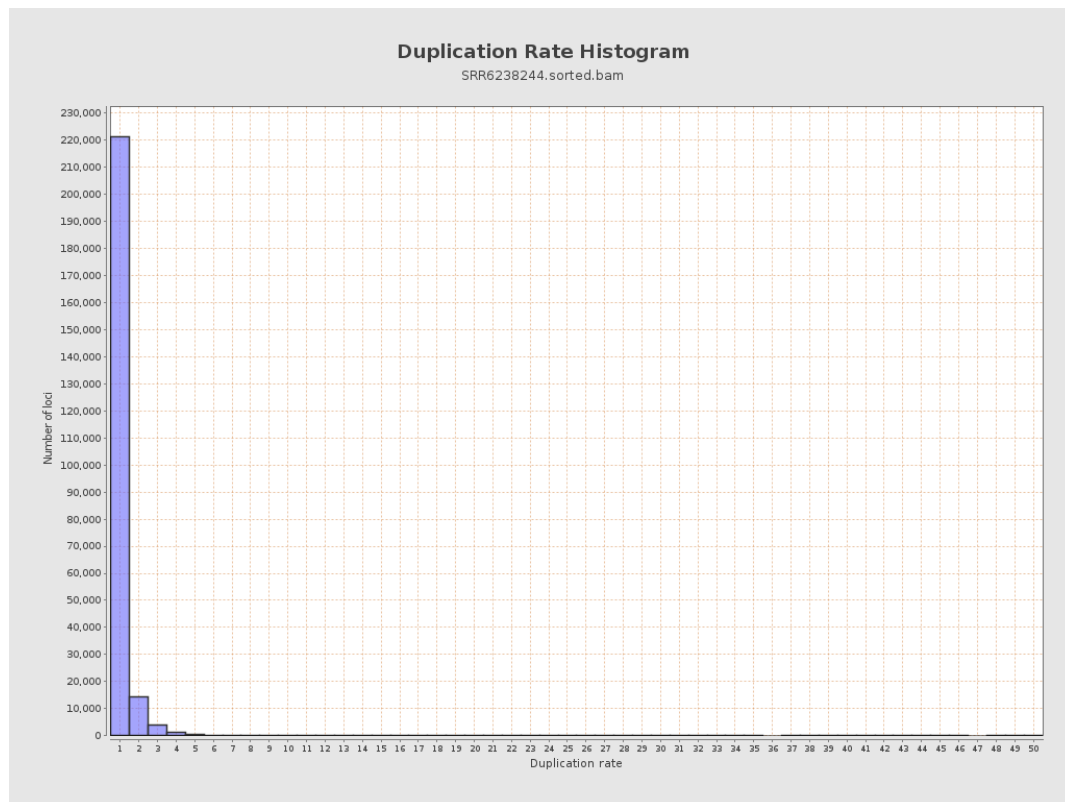
5. Results : Coverage Histogram (0-50X)



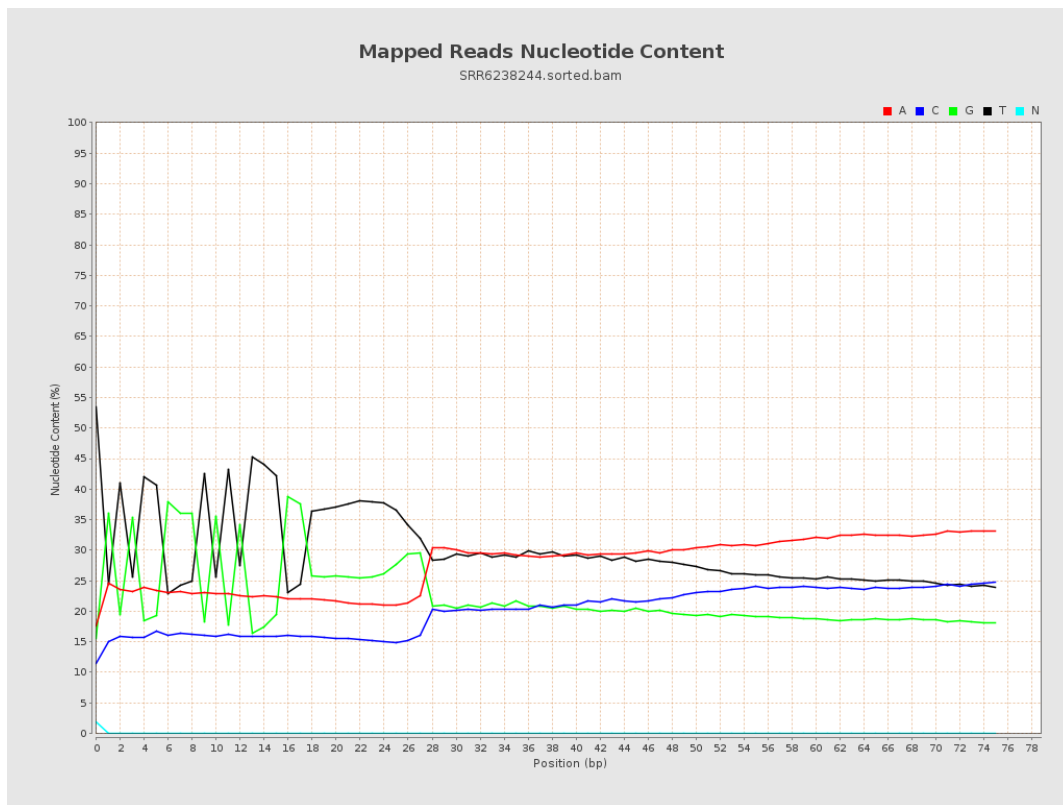
6. Results : Genome Fraction Coverage



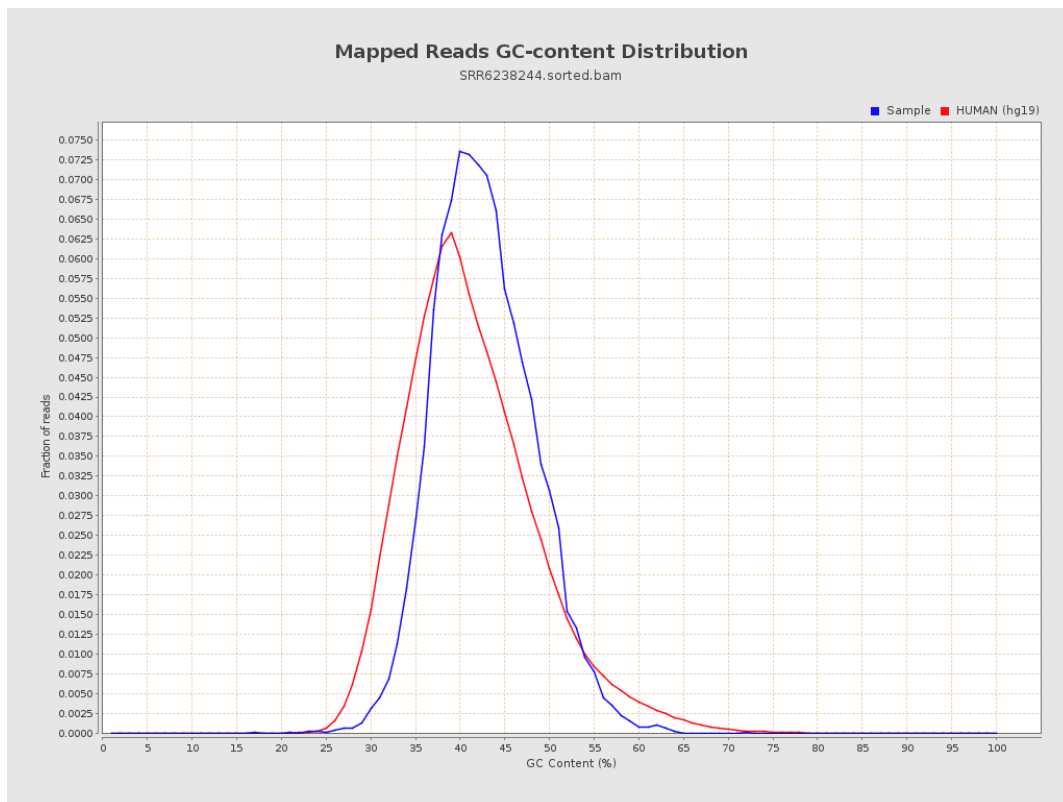
7. Results : Duplication Rate Histogram



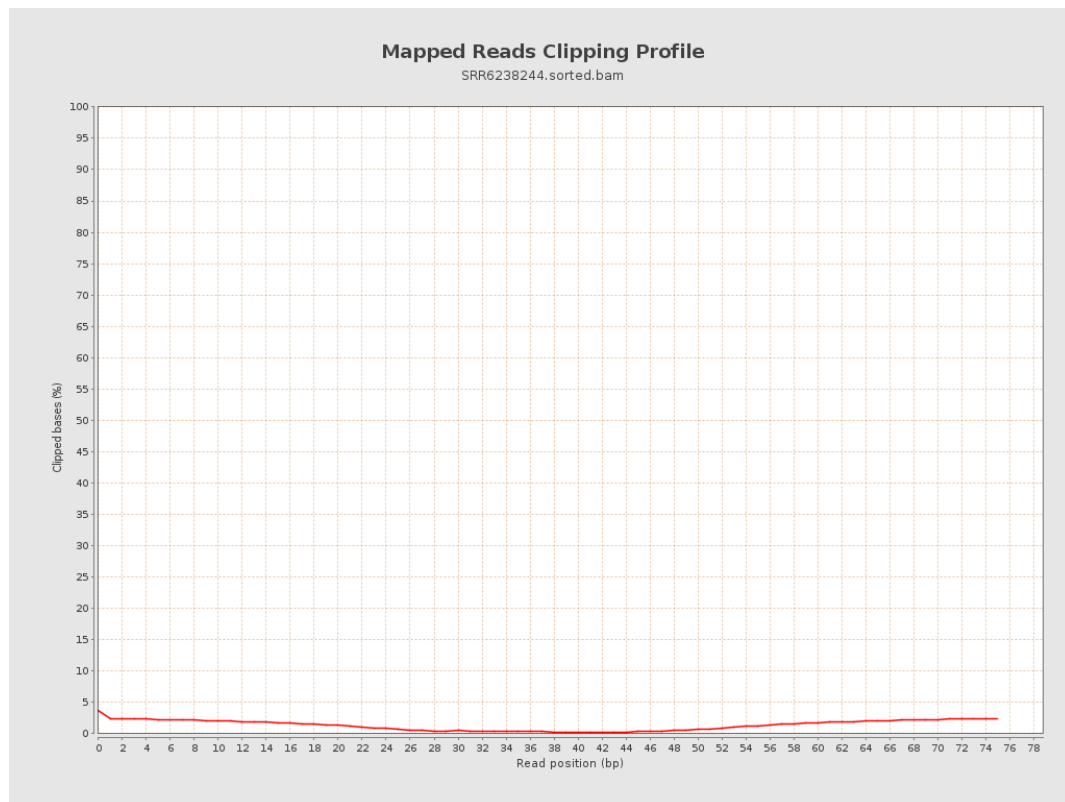
8. Results : Mapped Reads Nucleotide Content



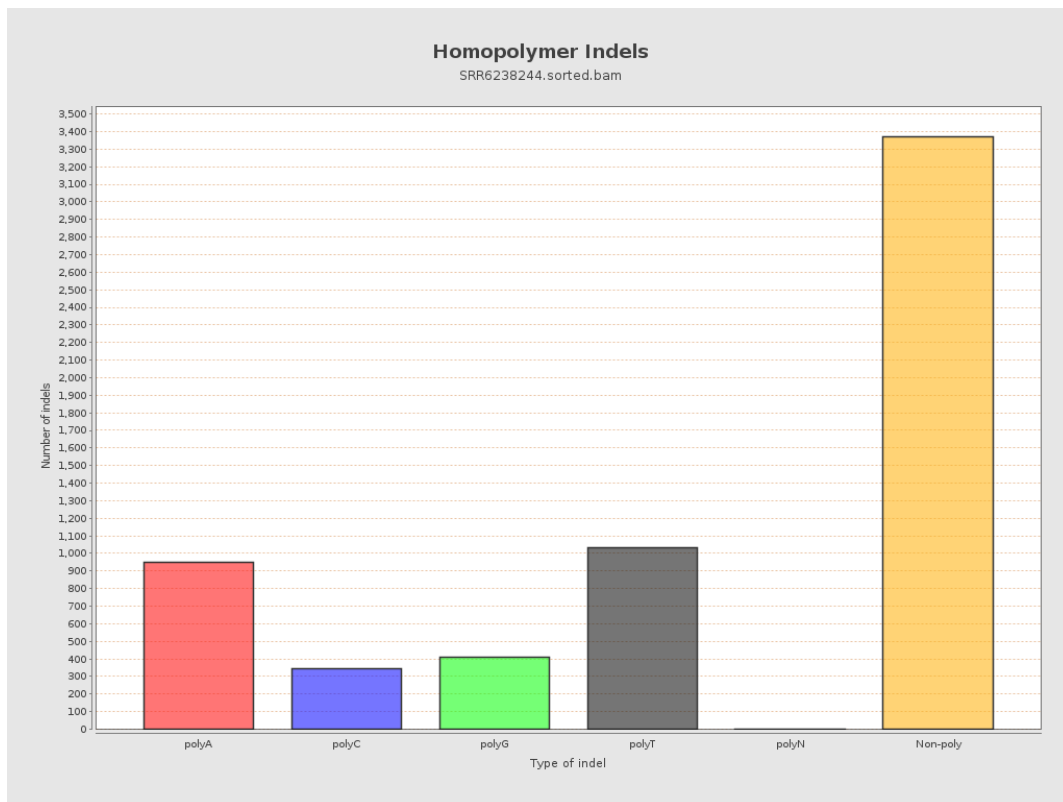
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

