

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 00:14:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238642.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_SRR6238642 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238642.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 00:14:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238642.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,070,518
Mapped reads	2,742,190 / 89.31%
Unmapped reads	328,328 / 10.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,368 / 0.83%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	675,107 / 21.99%
Duplication rate	18.08%
Clipped reads	1,791,163 / 58.33%

2.2. ACGT Content

Number/percentage of A's	41,075,555 / 24.48%
Number/percentage of C's	29,647,502 / 17.67%
Number/percentage of T's	56,371,392 / 33.59%
Number/percentage of G's	40,709,438 / 24.26%
Number/percentage of N's	8,180 / 0%
GC Percentage	41.93%

2.3. Coverage

Mean	0.0542

Standard Deviation	0.8505
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2.4. Mapping Quality

Mean Mapping Quality	41.33
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2.5. Mismatches and indels

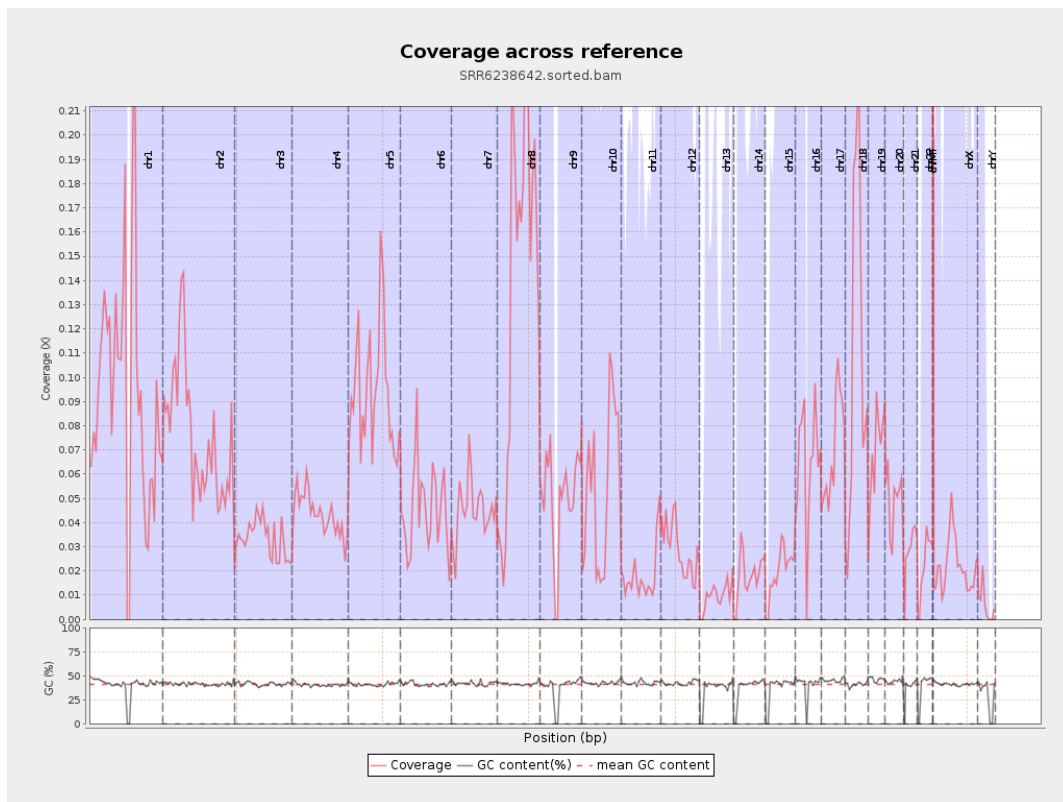
General error rate	0.63%
Mismatches	1,032,914
Insertions	11,008
Mapped reads with at least one insertion	0.4%
Deletions	49,332
Mapped reads with at least one deletion	1.78%
Homopolymer indels	40.18%

2.6. Chromosome stats

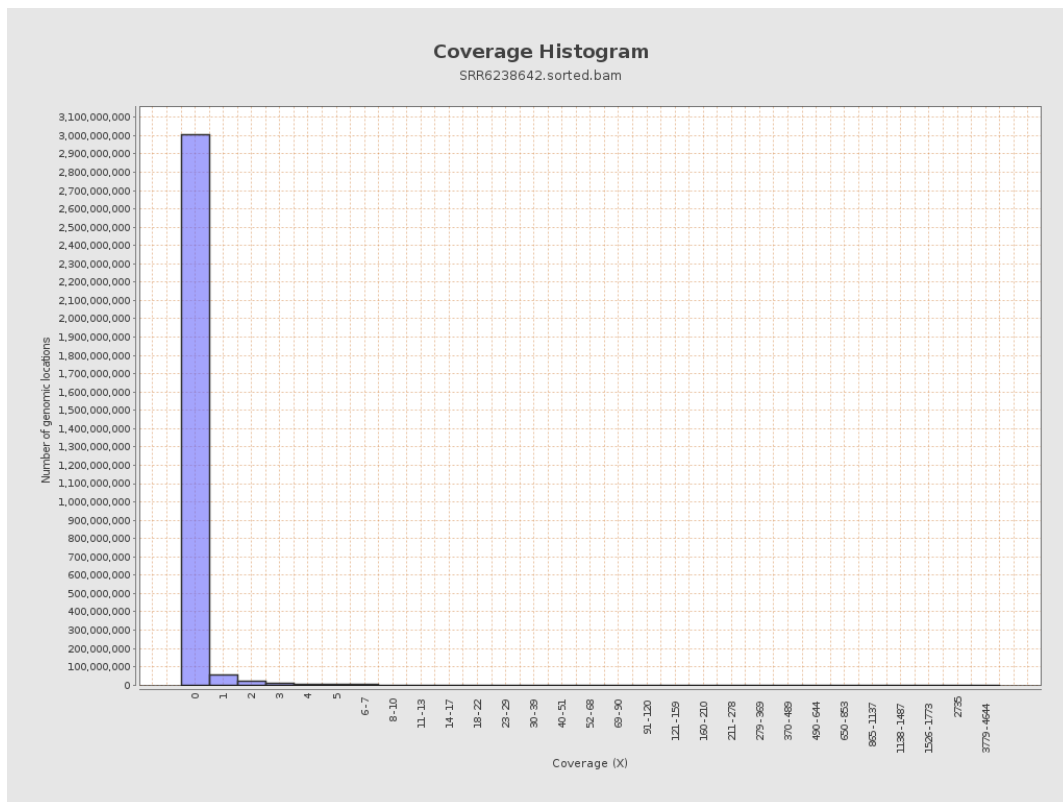
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	23126208	0.0928	1.4769
chr2	243199373	18543994	0.0763	2.0404
chr3	198022430	6604390	0.0334	0.3156
chr4	191154276	8339169	0.0436	0.3576
chr5	180915260	16821902	0.093	0.5257
chr6	171115067	7752583	0.0453	0.7189
chr7	159138663	7211800	0.0453	0.6032

chr8	146364022	20102023	0.1373	0.7549
chr9	141213431	7105734	0.0503	0.481
chr10	135534747	7423672	0.0548	0.4915
chr11	135006516	2429179	0.018	0.236
chr12	133851895	3877820	0.029	0.3071
chr13	115169878	1109356	0.0096	0.3498
chr14	107349540	1935127	0.018	0.2657
chr15	102531392	1980891	0.0193	0.383
chr16	90354753	5724346	0.0634	0.4663
chr17	81195210	5802759	0.0715	0.4782
chr18	78077248	8404715	0.1076	1.0996
chr19	59128983	4143601	0.0701	1.0732
chr20	63025520	3098231	0.0492	0.3874
chr21	48129895	1396574	0.029	0.3104
chr22	51304566	1149859	0.0224	0.2504
chrMT	16571	20262	1.2227	1.9029
chrX	155270560	3420798	0.022	0.2633
chrY	59373566	371570	0.0063	0.2892

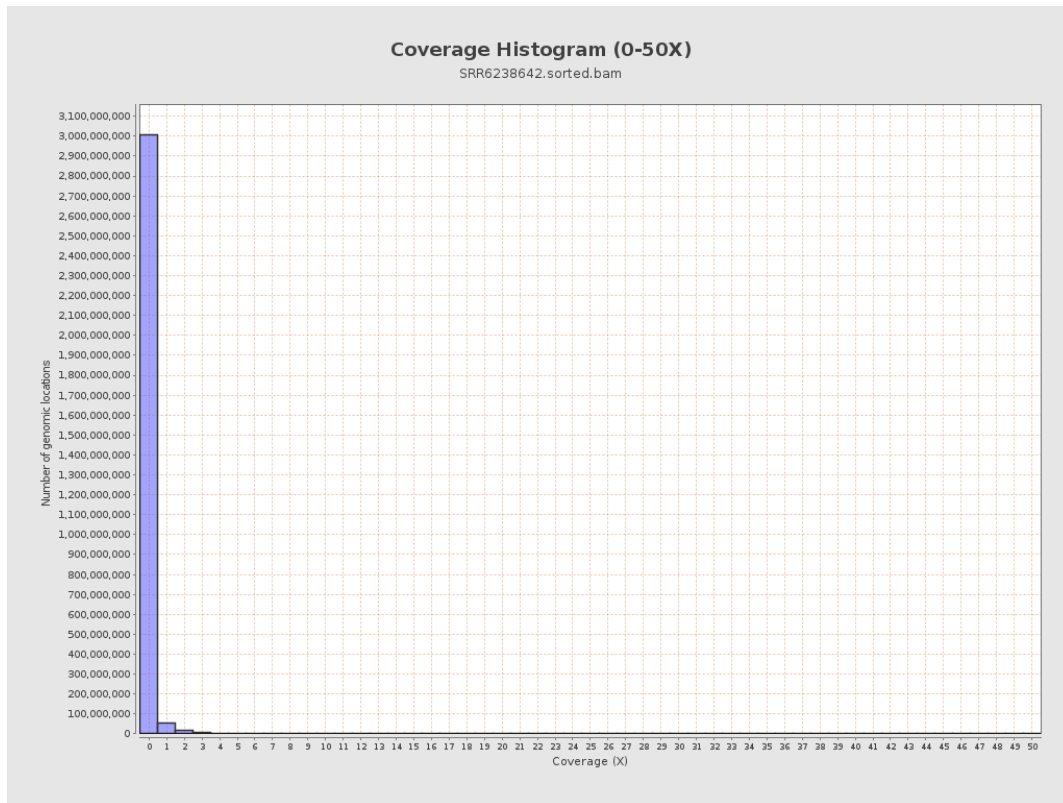
3. Results : Coverage across reference



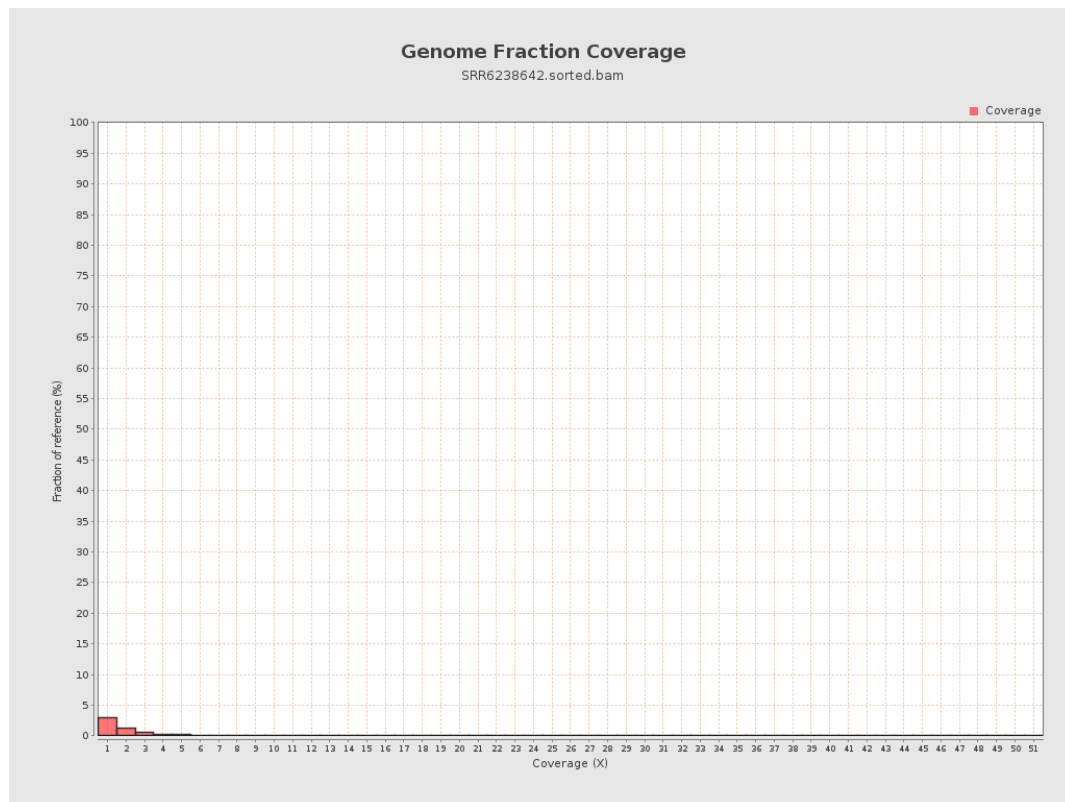
4. Results : Coverage Histogram



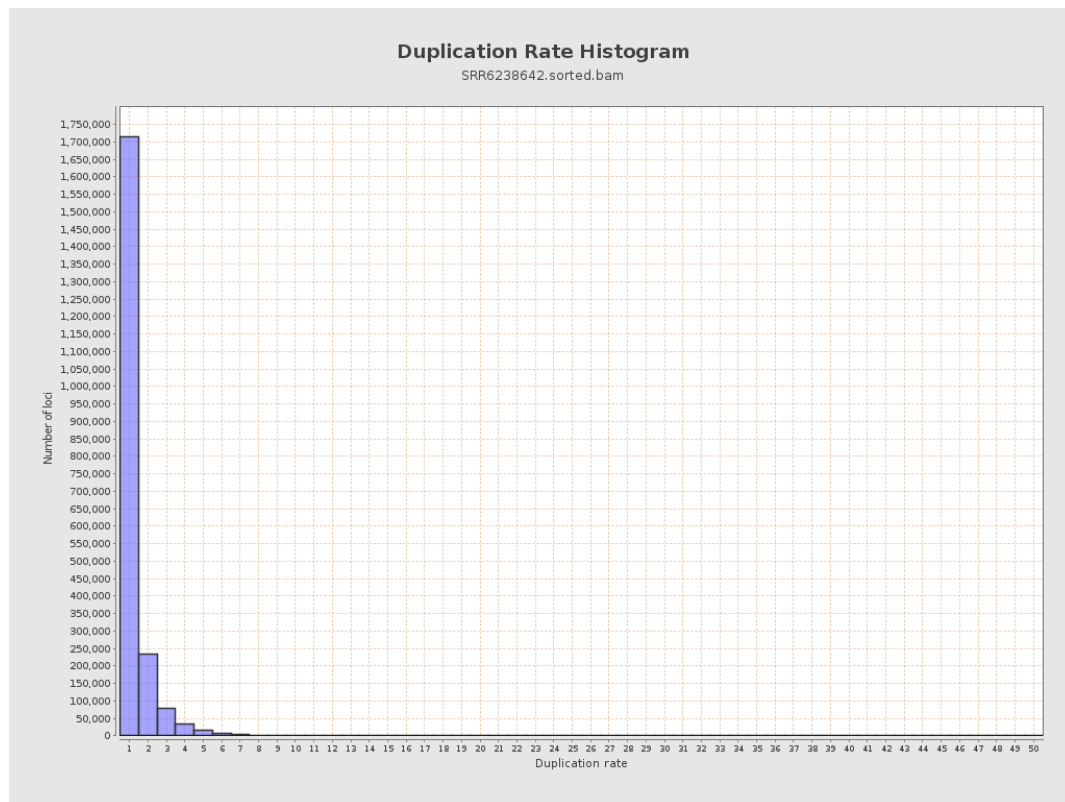
5. Results : Coverage Histogram (0-50X)



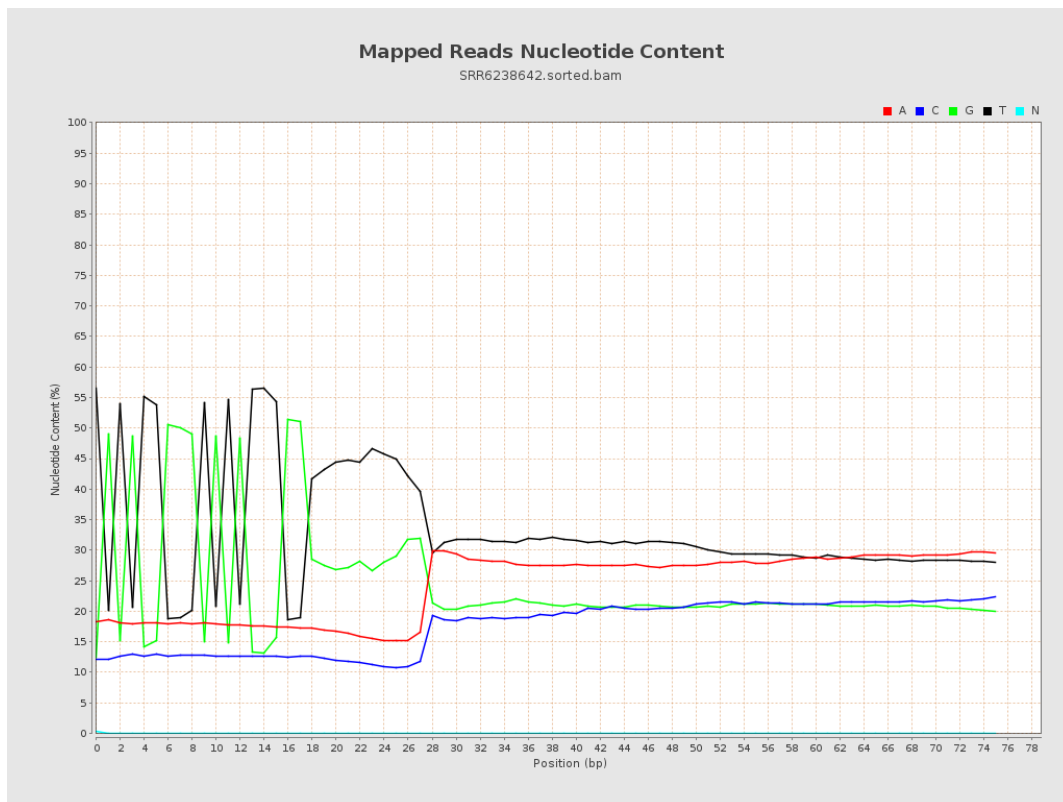
6. Results : Genome Fraction Coverage



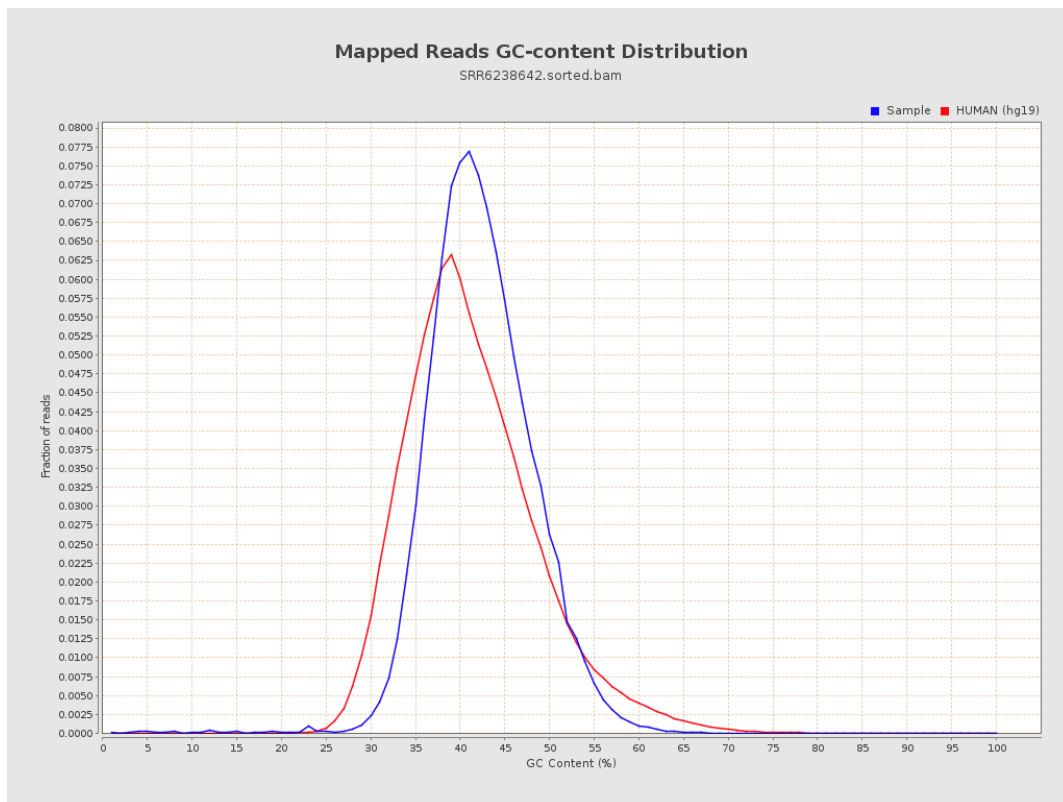
7. Results : Duplication Rate Histogram



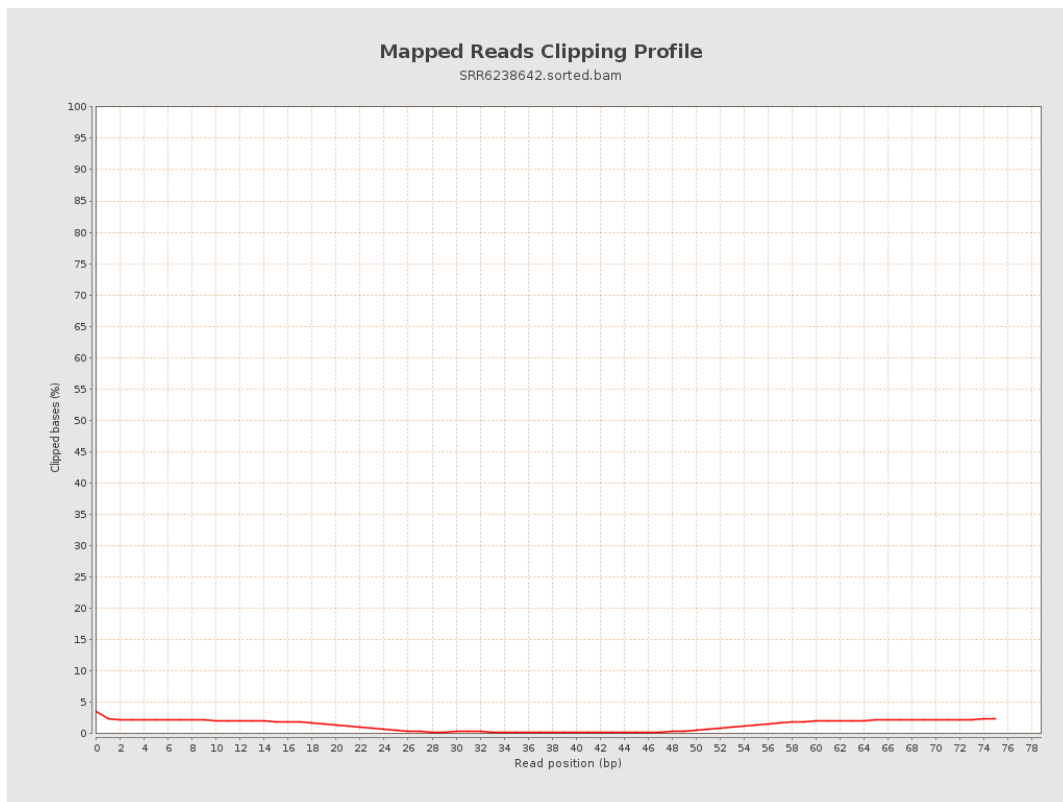
8. Results : Mapped Reads Nucleotide Content



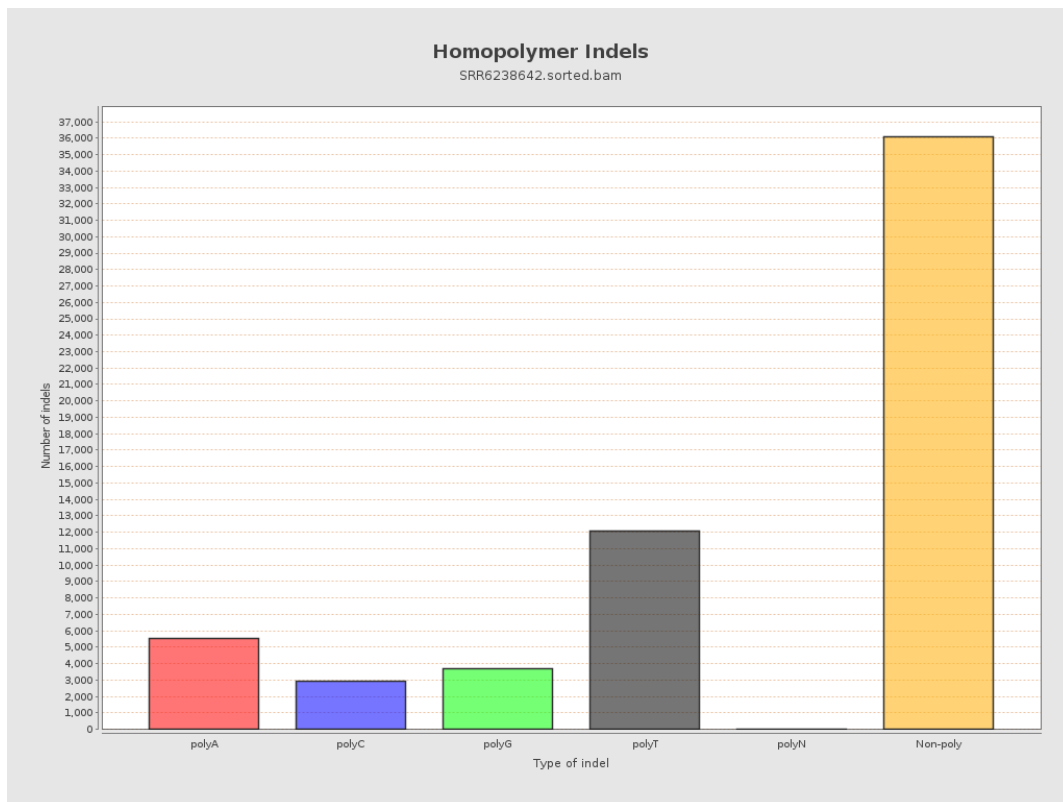
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

