

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 11:39:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238067.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_SRR6238067 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238067.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 11:39:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238067.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,675,794
Mapped reads	1,546,478 / 92.28%
Unmapped reads	129,316 / 7.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,732 / 0.7%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	53,010 / 3.16%
Duplication rate	2.49%
Clipped reads	595,997 / 35.57%

2.2. ACGT Content

Number/percentage of A's	29,178,697 / 27.91%
Number/percentage of C's	19,361,930 / 18.52%
Number/percentage of T's	33,195,236 / 31.76%
Number/percentage of G's	22,781,342 / 21.79%
Number/percentage of N's	13,689 / 0.01%
GC Percentage	40.32%

2.3. Coverage

Mean	0.0338

Standard Deviation	0.3493
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2.4. Mapping Quality

Mean Mapping Quality	46.68
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2.5. Mismatches and indels

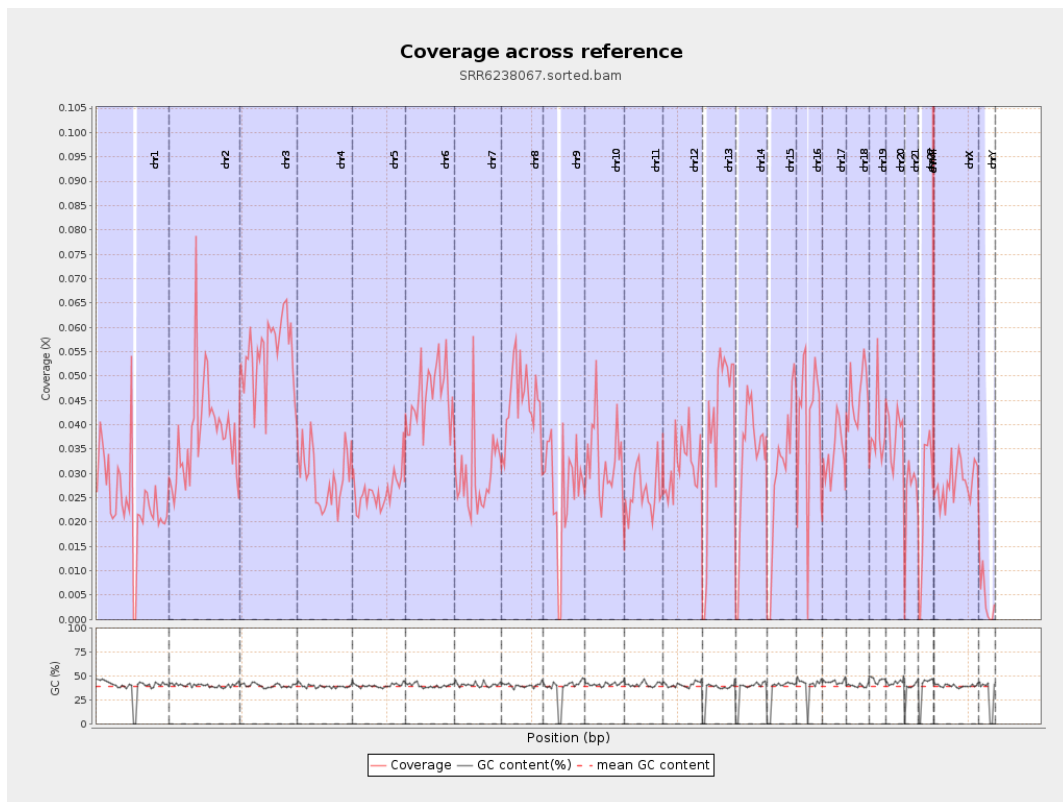
General error rate	0.74%
Mismatches	755,504
Insertions	7,444
Mapped reads with at least one insertion	0.48%
Deletions	25,605
Mapped reads with at least one deletion	1.64%
Homopolymer indels	47.27%

2.6. Chromosome stats

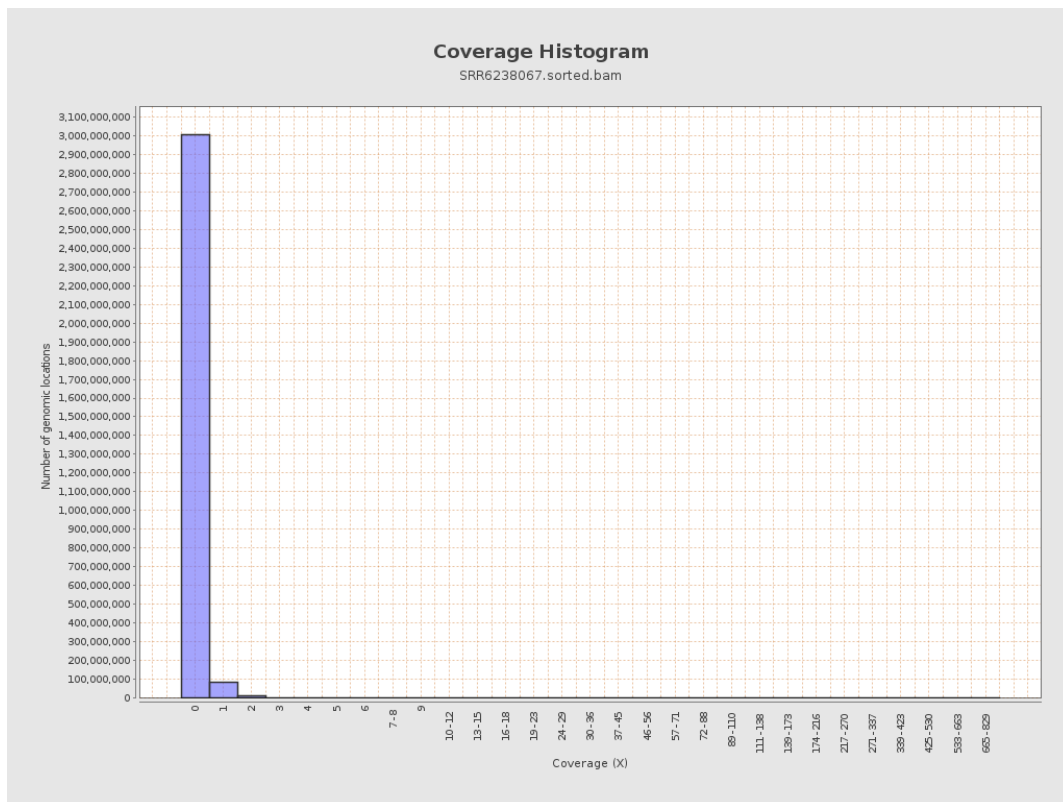
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6076726	0.0244	0.6816
chr2	243199373	9295040	0.0382	0.371
chr3	198022430	10859308	0.0548	0.2607
chr4	191154276	5552862	0.029	0.1973
chr5	180915260	4776029	0.0264	0.1829
chr6	171115067	7869946	0.046	0.283
chr7	159138663	4698889	0.0295	0.399

chr8	146364022	6498383	0.0444	0.5618
chr9	141213431	3756804	0.0266	0.3117
chr10	135534747	4426294	0.0327	0.3066
chr11	135006516	3493694	0.0259	0.2348
chr12	133851895	4263521	0.0319	0.204
chr13	115169878	4500599	0.0391	0.2195
chr14	107349540	3512698	0.0327	0.2161
chr15	102531392	3088920	0.0301	0.1935
chr16	90354753	3658174	0.0405	0.2529
chr17	81195210	2758123	0.034	0.2205
chr18	78077248	3619373	0.0464	0.5931
chr19	59128983	2293944	0.0388	0.4298
chr20	63025520	2377323	0.0377	0.2216
chr21	48129895	1237696	0.0257	0.1935
chr22	51304566	1261279	0.0246	0.1729
chrMT	16571	44088	2.6606	2.2529
chrX	155270560	4404656	0.0284	0.2087
chrY	59373566	252161	0.0042	0.1054

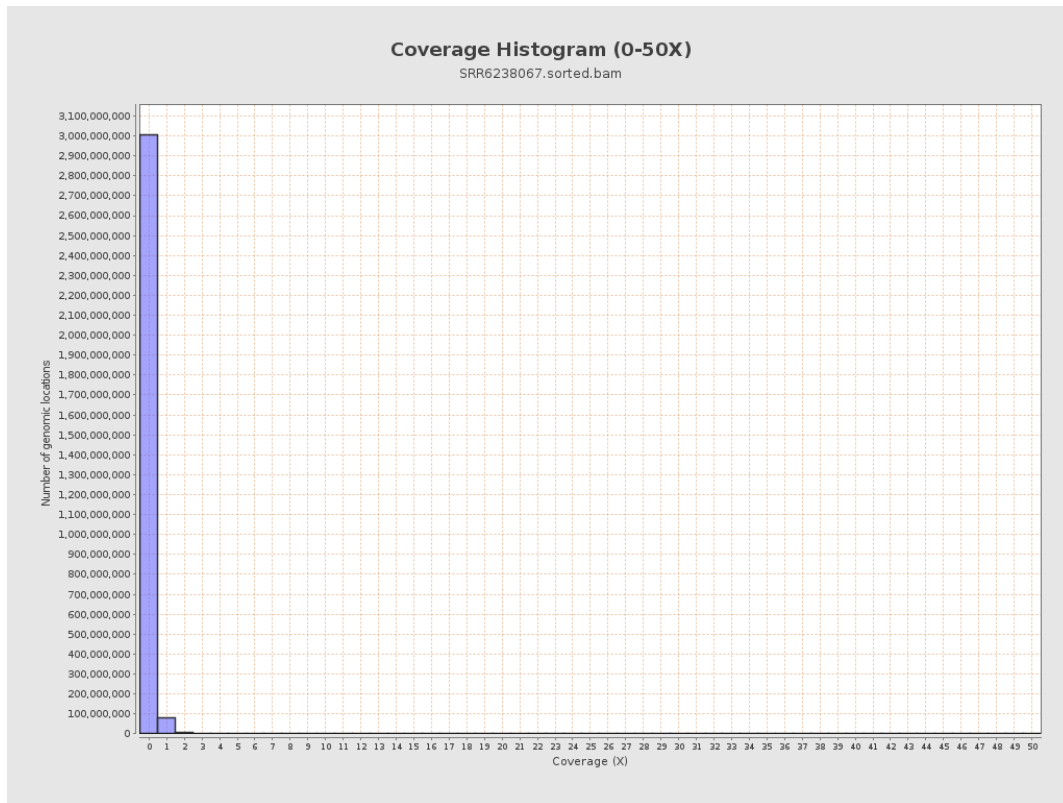
3. Results : Coverage across reference



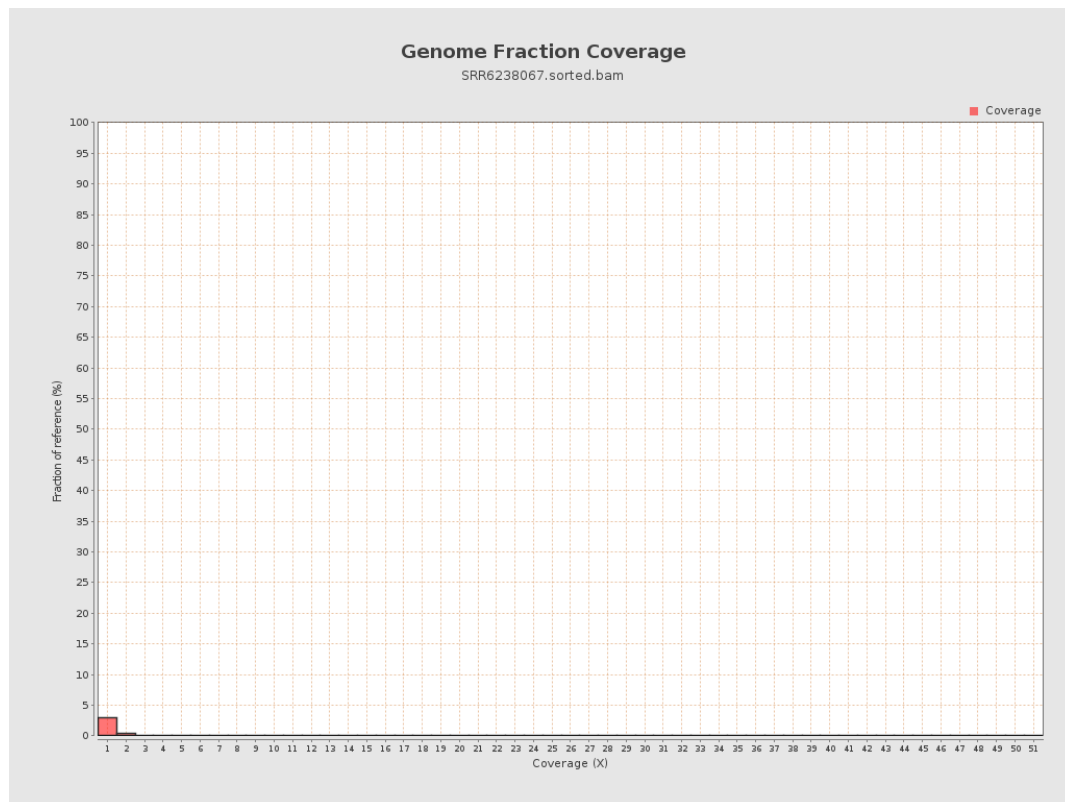
4. Results : Coverage Histogram



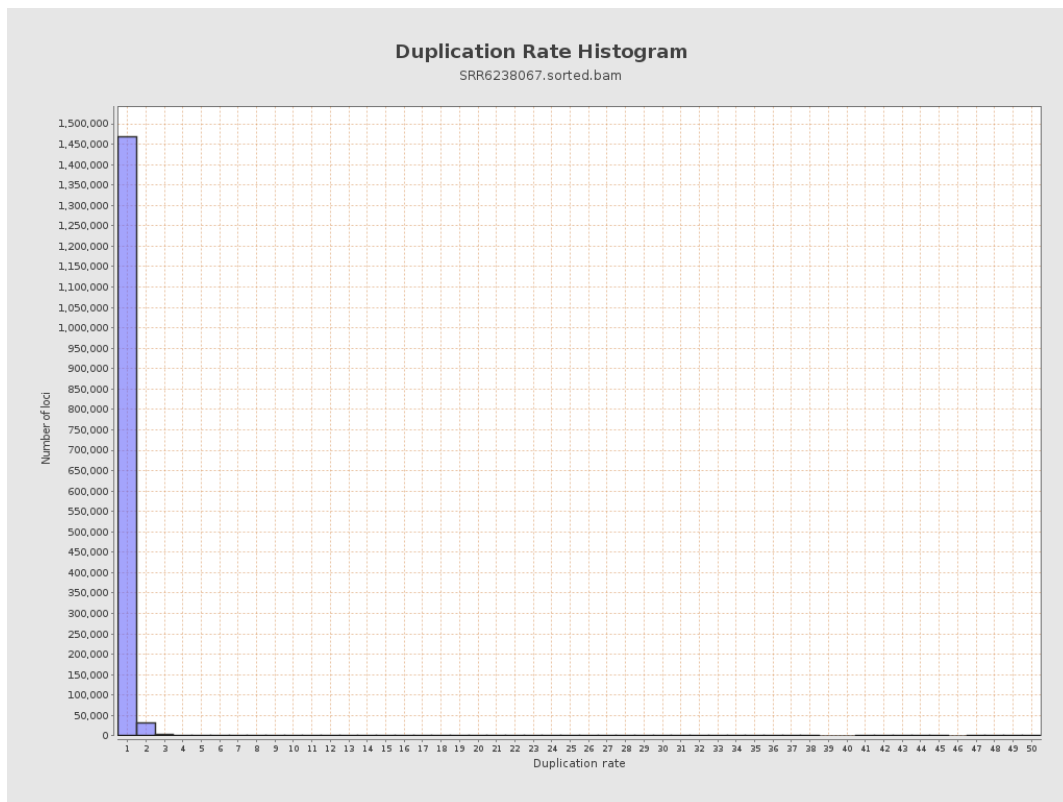
5. Results : Coverage Histogram (0-50X)



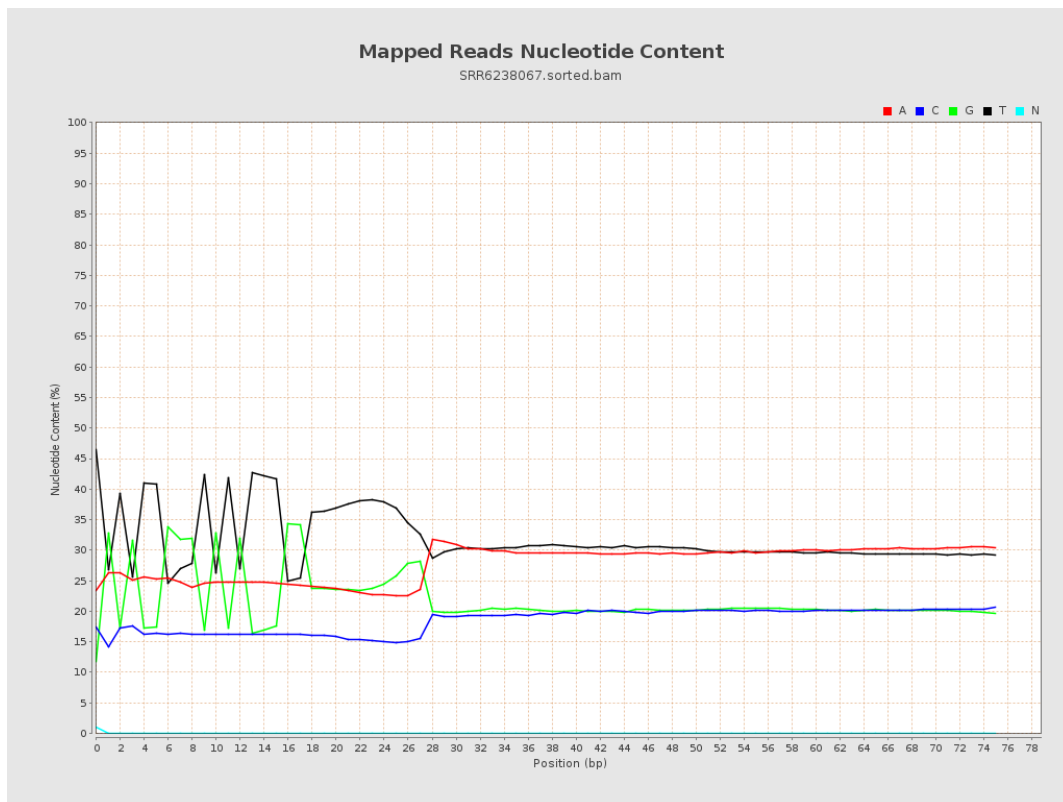
6. Results : Genome Fraction Coverage



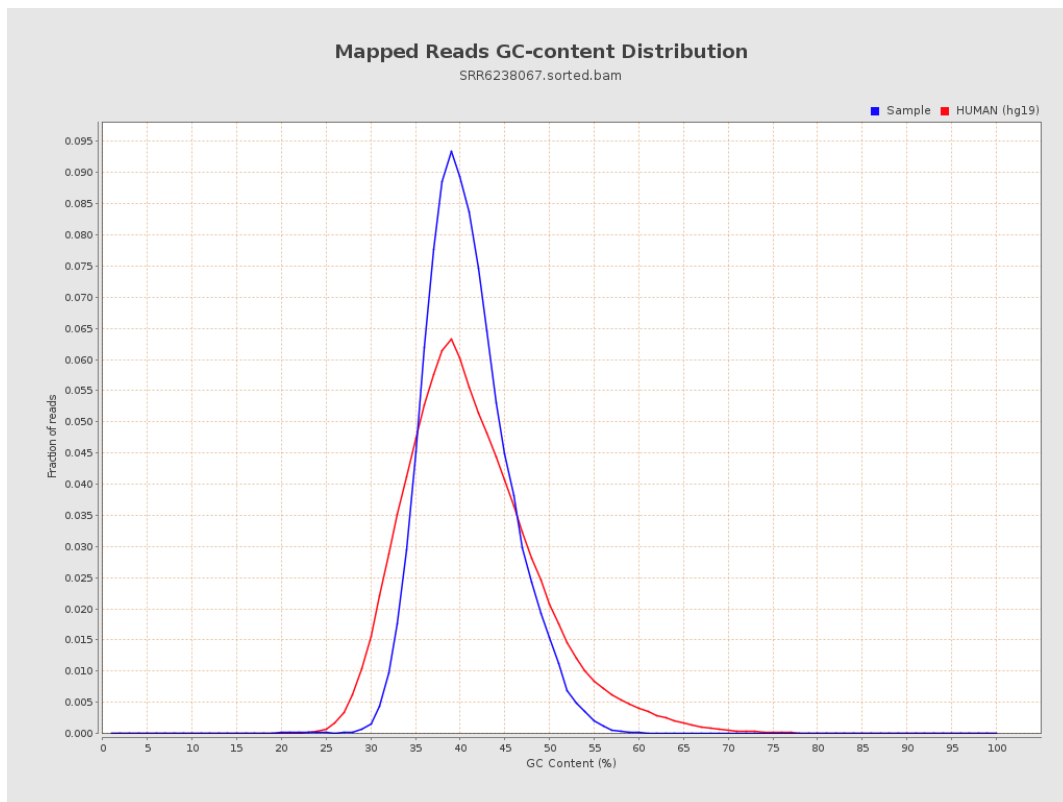
7. Results : Duplication Rate Histogram



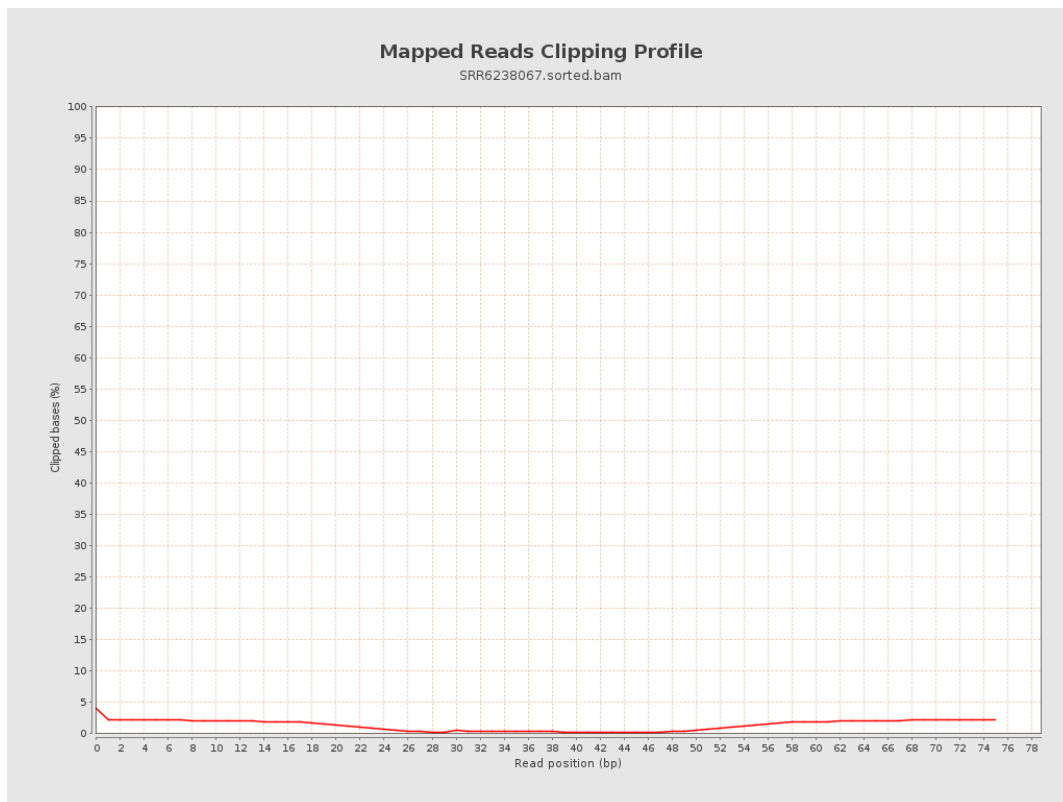
8. Results : Mapped Reads Nucleotide Content



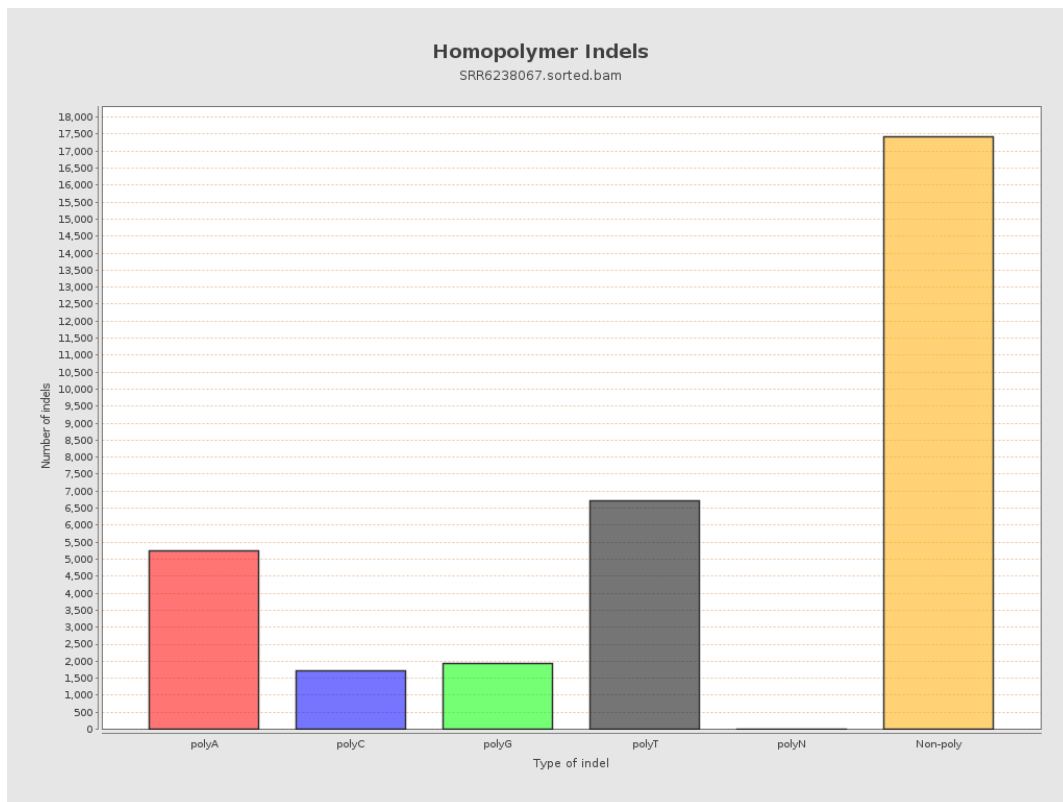
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

