

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 20:51:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236106.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_SRR6236106 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236106.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 20:51:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236106.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,527,609
Mapped reads	1,328,645 / 86.98%
Unmapped reads	198,964 / 13.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,880 / 0.58%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	72,114 / 4.72%
Duplication rate	4.6%
Clipped reads	648,945 / 42.48%

2.2. ACGT Content

Number/percentage of A's	23,387,609 / 26.95%
Number/percentage of C's	15,555,064 / 17.92%
Number/percentage of T's	28,047,880 / 32.32%
Number/percentage of G's	19,743,160 / 22.75%
Number/percentage of N's	46,954 / 0.05%
GC Percentage	40.68%

2.3. Coverage

Mean	0.028

Standard Deviation	0.2838
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2.4. Mapping Quality

Mean Mapping Quality	45.11
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2.5. Mismatches and indels

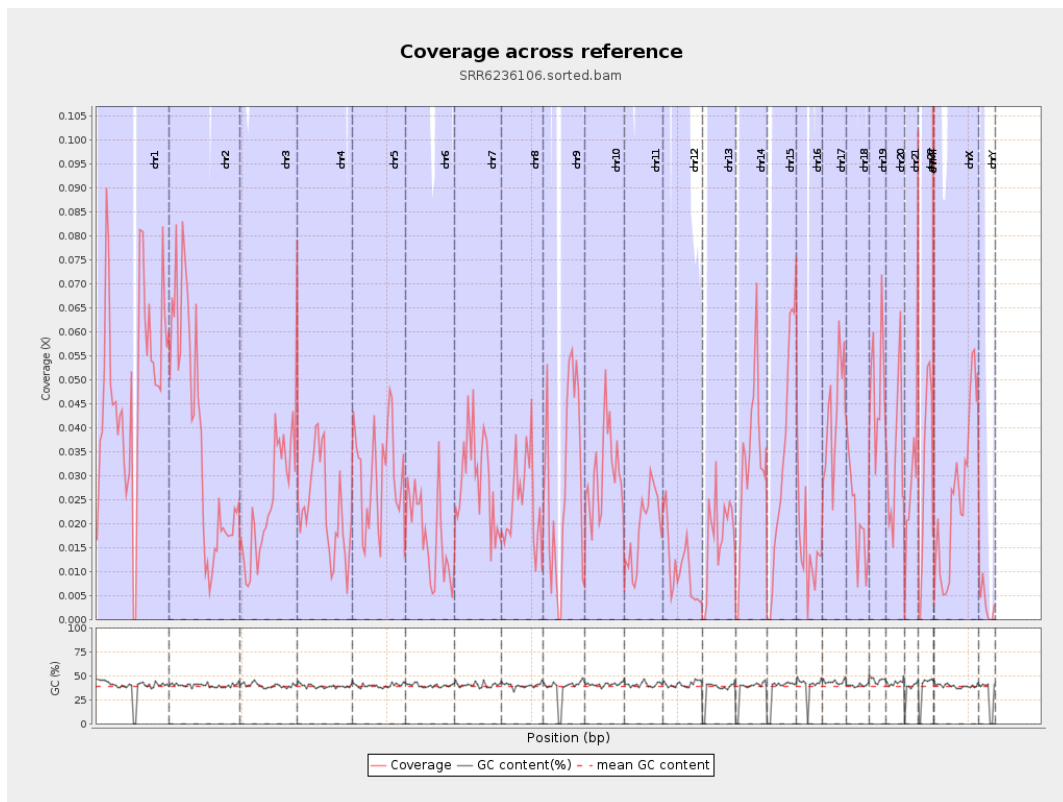
General error rate	0.83%
Mismatches	712,222
Insertions	6,173
Mapped reads with at least one insertion	0.46%
Deletions	26,604
Mapped reads with at least one deletion	1.98%
Homopolymer indels	46.57%

2.6. Chromosome stats

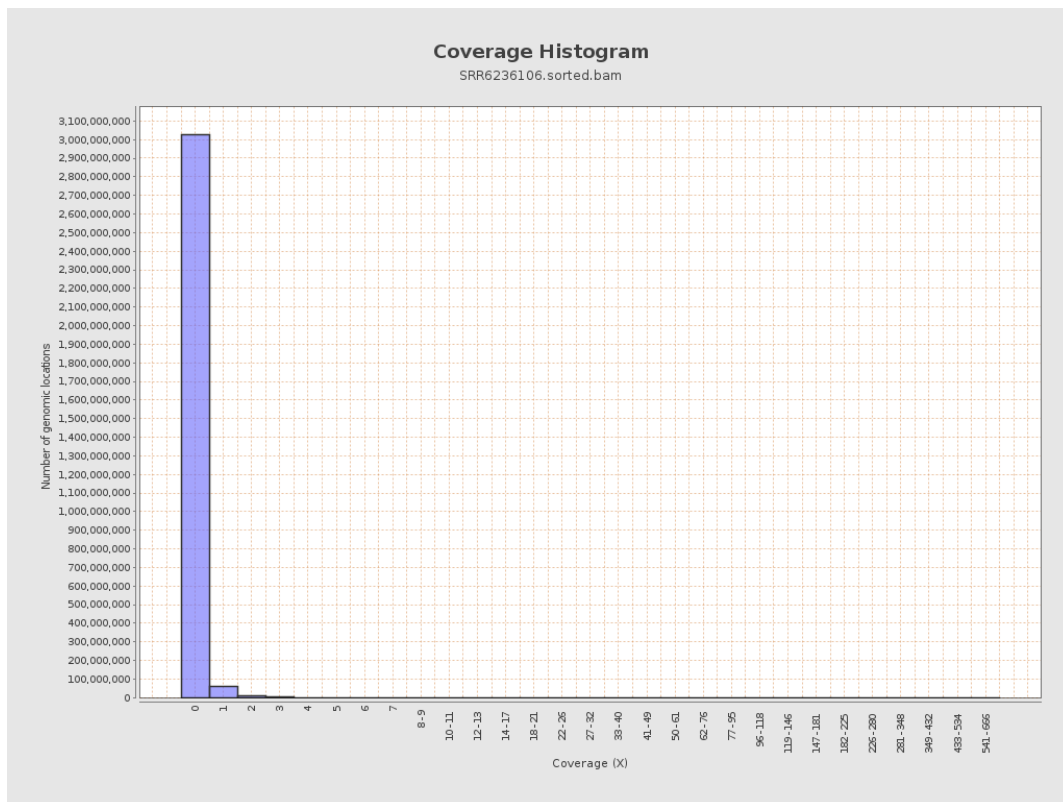
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	12183422	0.0489	0.5559
chr2	243199373	8957748	0.0368	0.3117
chr3	198022430	4832140	0.0244	0.1819
chr4	191154276	4409309	0.0231	0.1808
chr5	180915260	5452183	0.0301	0.2032
chr6	171115067	2959340	0.0173	0.1829
chr7	159138663	4640306	0.0292	0.3526

chr8	146364022	3530882	0.0241	0.4393
chr9	141213431	4088200	0.029	0.2403
chr10	135534747	4205424	0.031	0.232
chr11	135006516	2562811	0.019	0.1897
chr12	133851895	1435691	0.0107	0.1233
chr13	115169878	1993872	0.0173	0.153
chr14	107349540	3446877	0.0321	0.2138
chr15	102531392	3323730	0.0324	0.2137
chr16	90354753	1273289	0.0141	0.1487
chr17	81195210	3470569	0.0427	0.2541
chr18	78077248	1687273	0.0216	0.335
chr19	59128983	2840700	0.048	0.3666
chr20	63025520	2033411	0.0323	0.2109
chr21	48129895	1555543	0.0323	0.2162
chr22	51304566	1620123	0.0316	0.2073
chrMT	16571	155990	9.4134	6.4389
chrX	155270560	3984957	0.0257	0.1951
chrY	59373566	183430	0.0031	0.0786

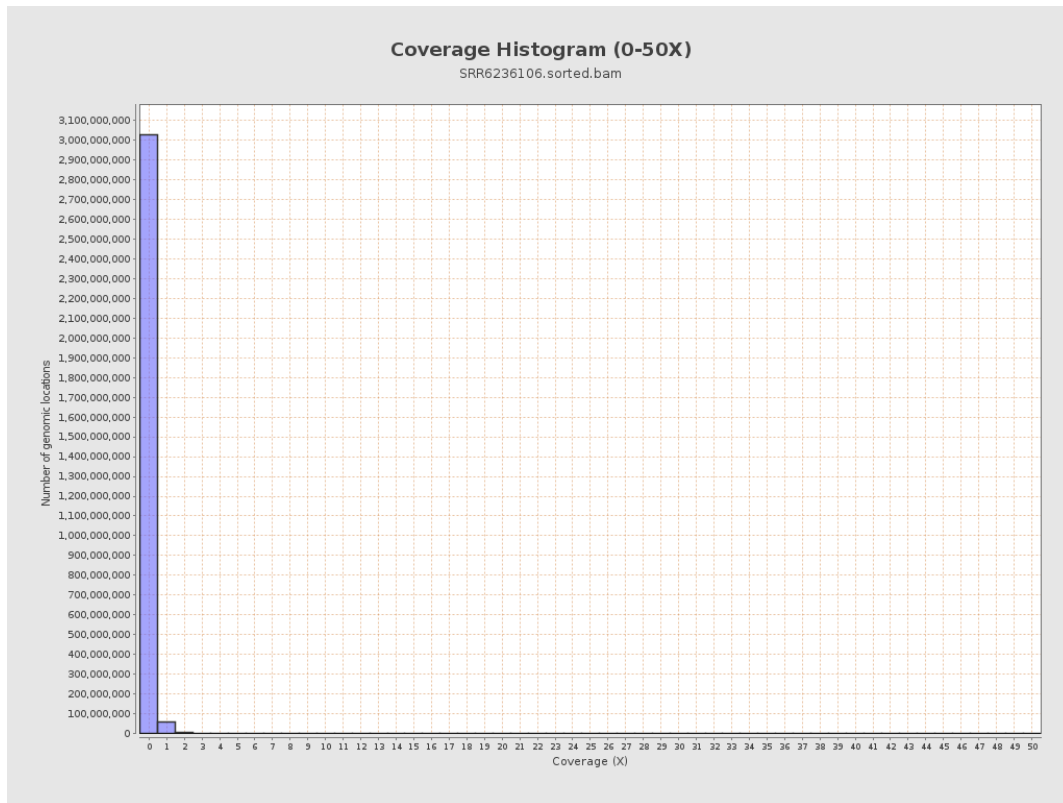
3. Results : Coverage across reference



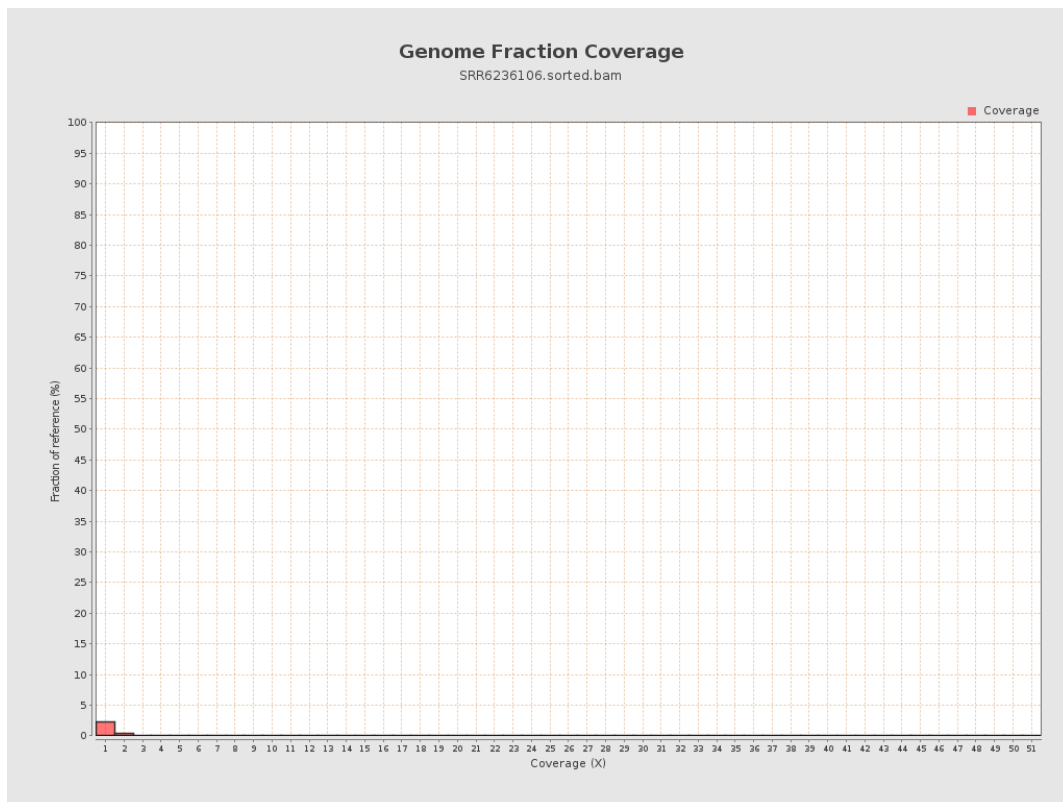
4. Results : Coverage Histogram



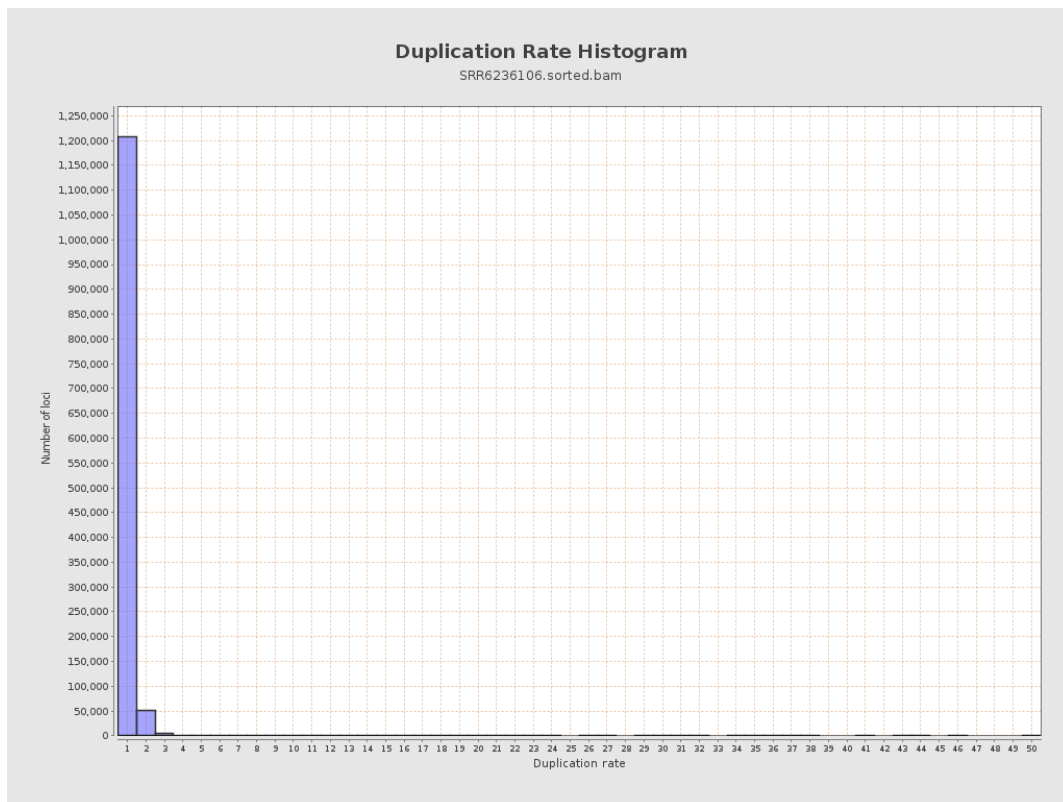
5. Results : Coverage Histogram (0-50X)



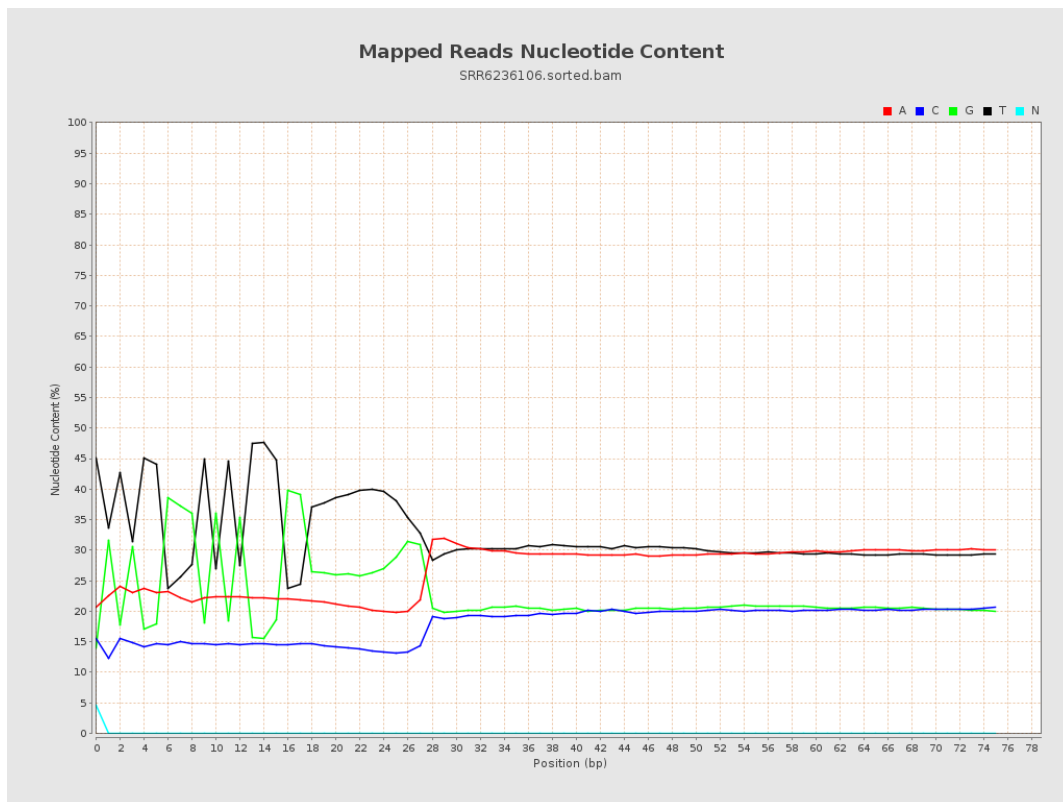
6. Results : Genome Fraction Coverage



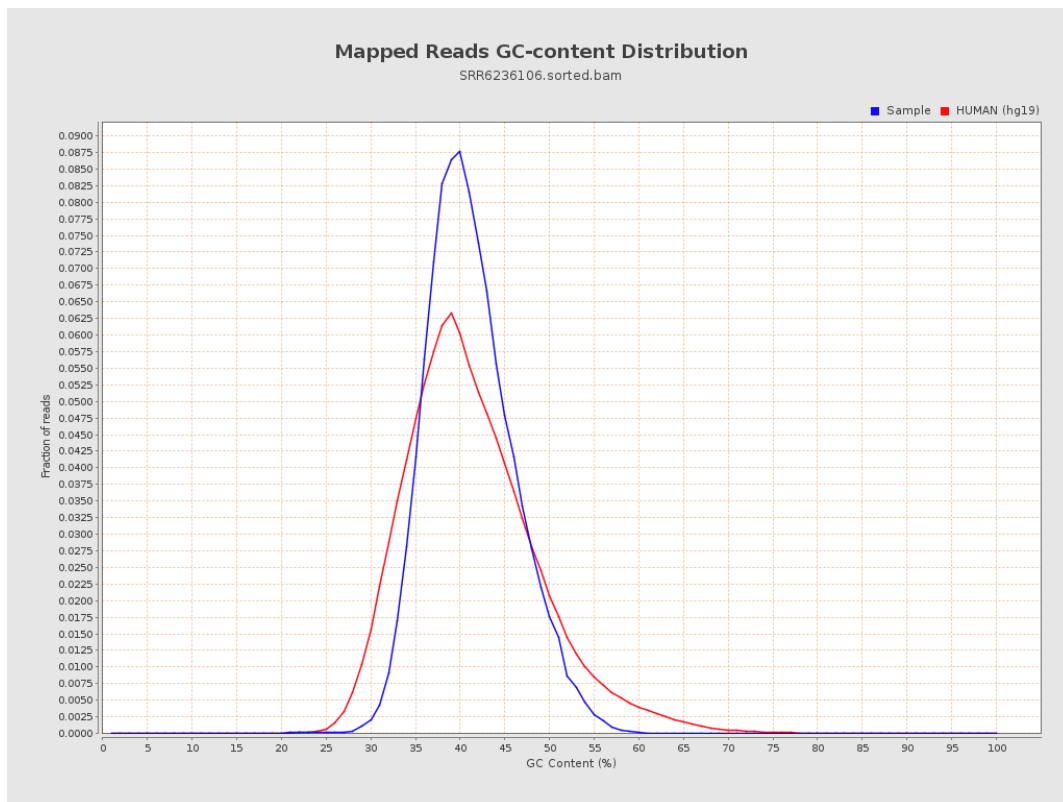
7. Results : Duplication Rate Histogram



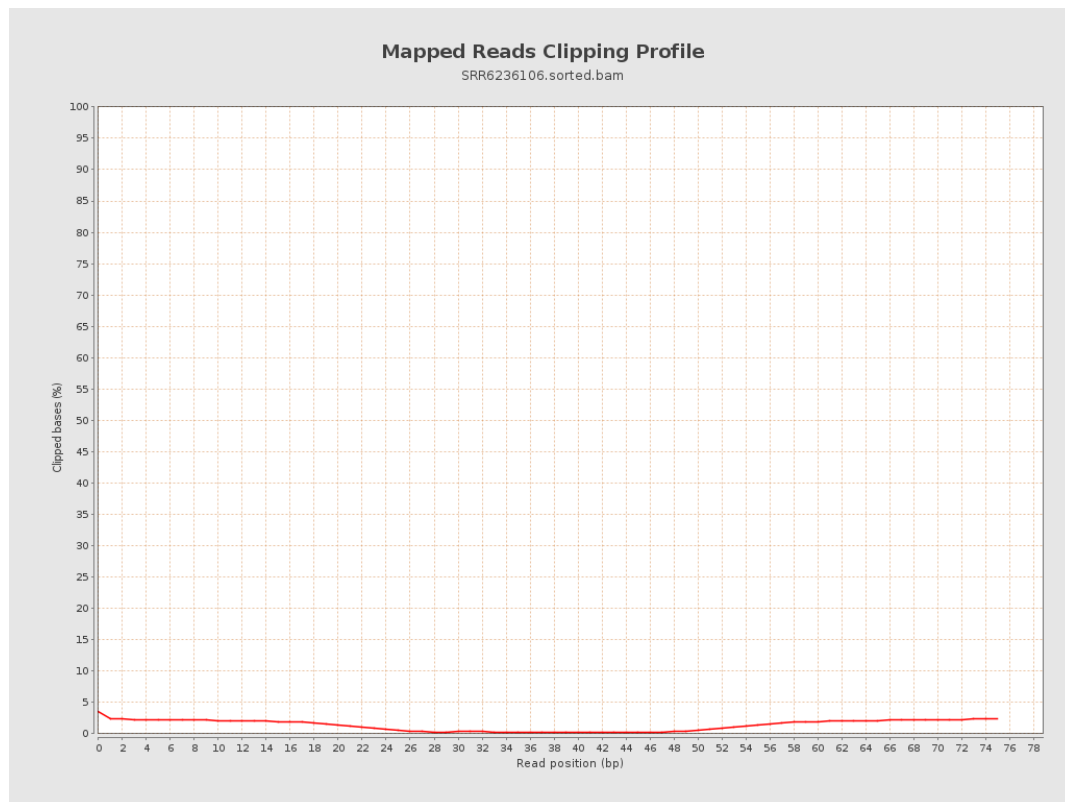
8. Results : Mapped Reads Nucleotide Content



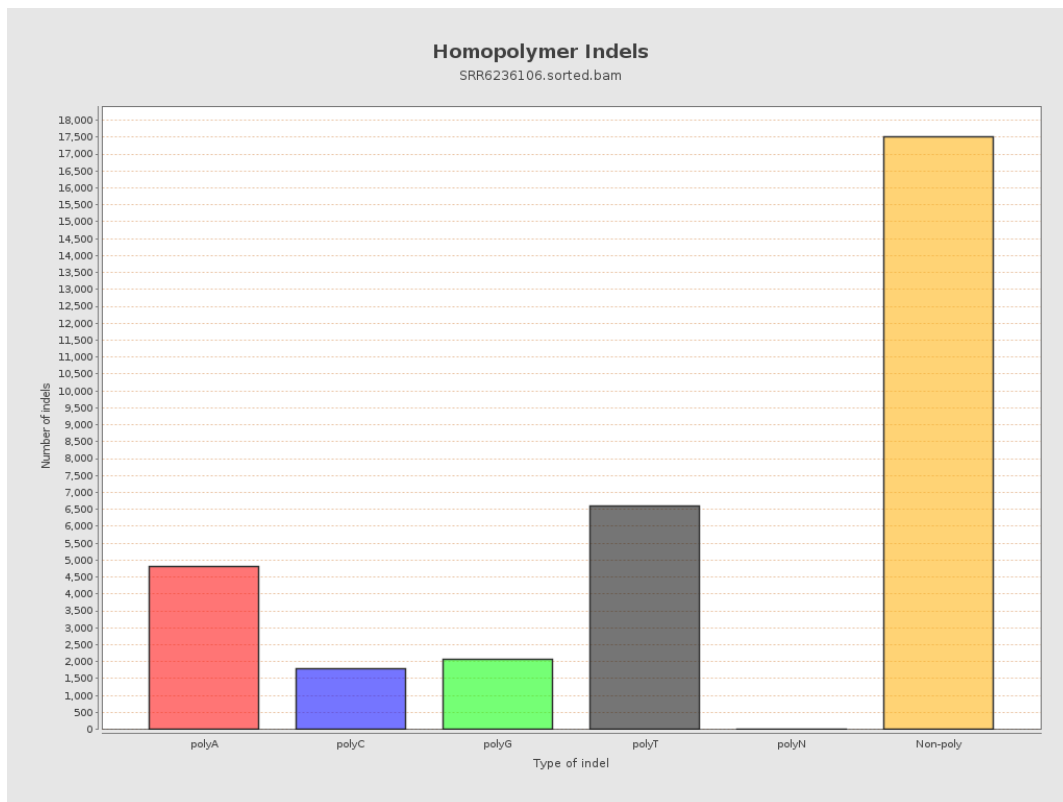
9. Results : Mapped Reads GC-content Distribution



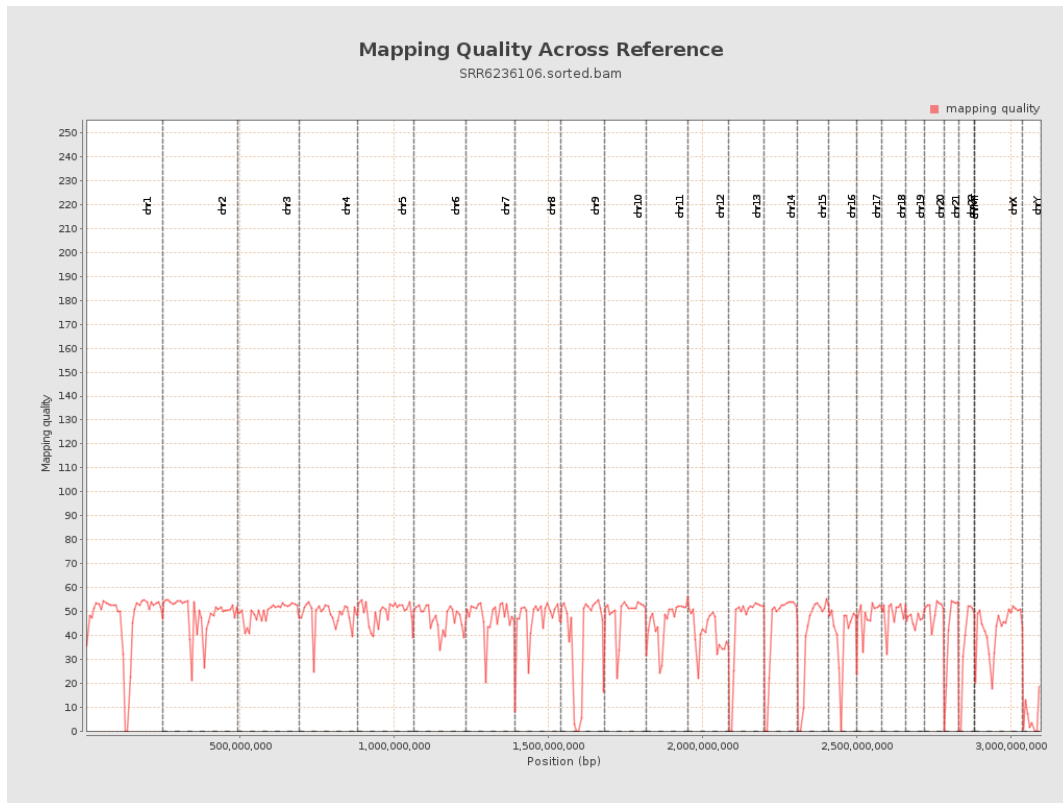
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

