

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 21:27:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230396.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_SRR6230396 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230396.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 21:27:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230396.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,779,672
Mapped reads	2,470,278 / 88.87%
Unmapped reads	309,394 / 11.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,867 / 0.71%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	96,048 / 3.46%
Duplication rate	2.66%
Clipped reads	1,344,631 / 48.37%

2.2. ACGT Content

Number/percentage of A's	43,846,148 / 27.62%
Number/percentage of C's	28,944,760 / 18.23%
Number/percentage of T's	49,210,377 / 31%
Number/percentage of G's	36,701,400 / 23.12%
Number/percentage of N's	61,487 / 0.04%
GC Percentage	41.35%

2.3. Coverage

Mean	0.0513

Standard Deviation	0.4874
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2.4. Mapping Quality

Mean Mapping Quality	43.63
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2.5. Mismatches and indels

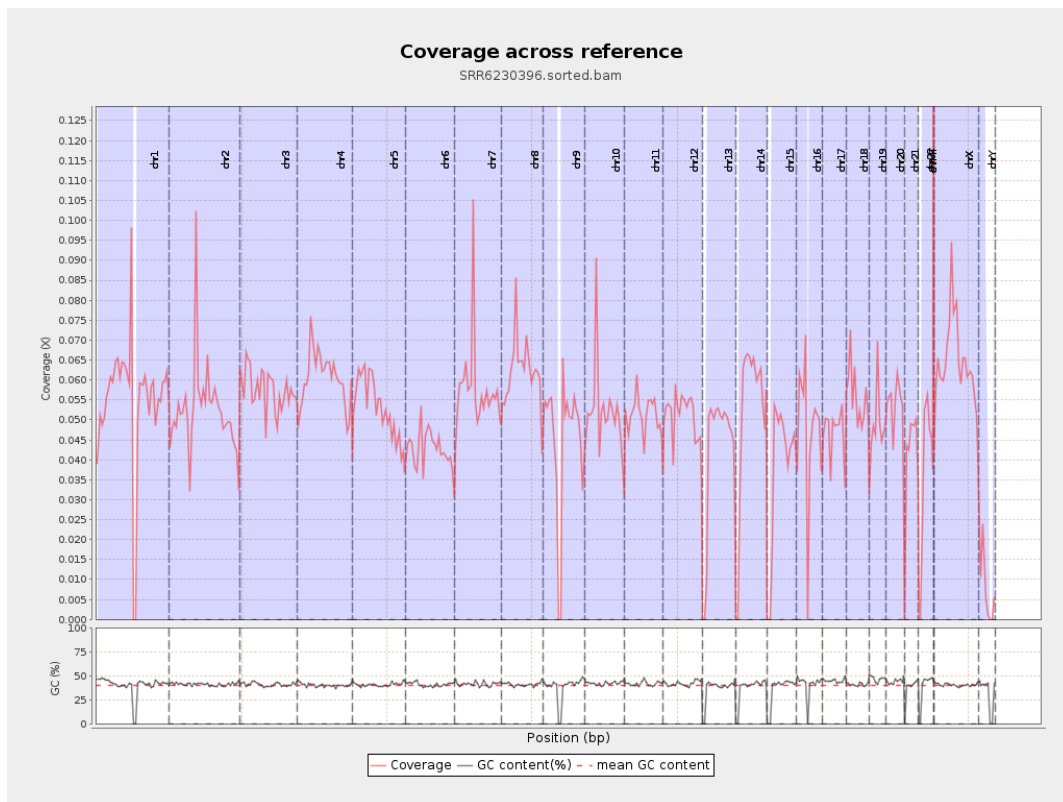
General error rate	0.87%
Mismatches	1,357,586
Insertions	13,225
Mapped reads with at least one insertion	0.53%
Deletions	44,413
Mapped reads with at least one deletion	1.78%
Homopolymer indels	45.35%

2.6. Chromosome stats

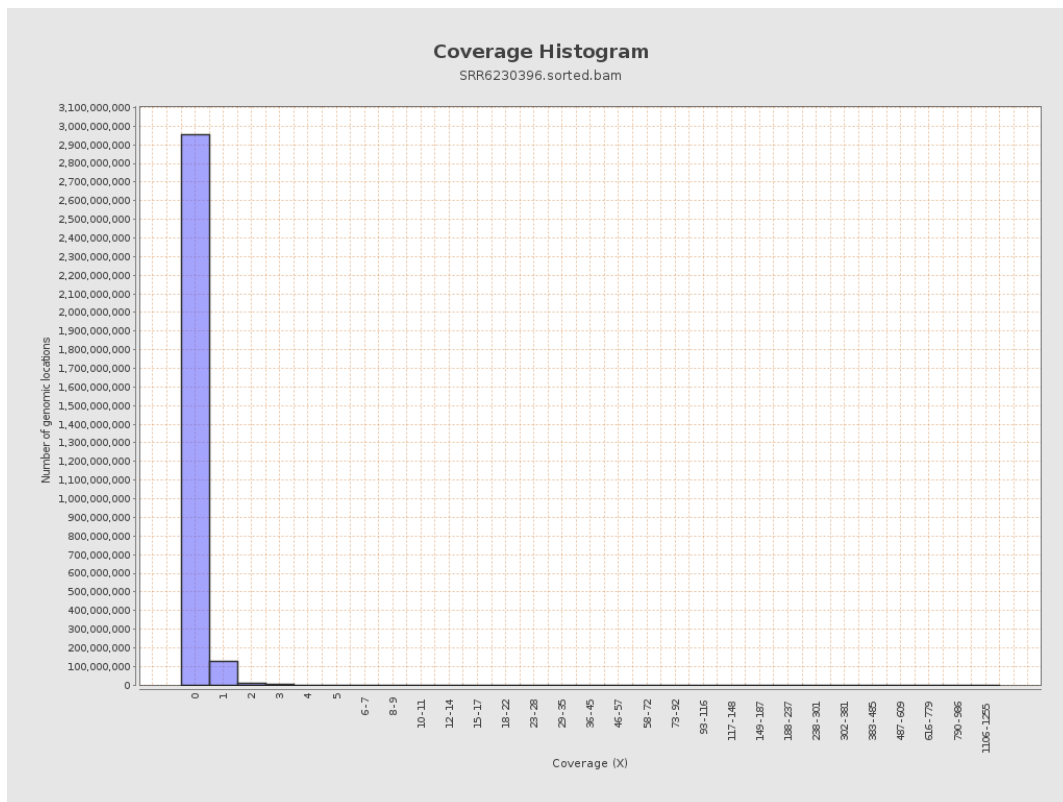
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	13695548	0.0549	0.9704
chr2	243199373	12736194	0.0524	0.5745
chr3	198022430	11380909	0.0575	0.2641
chr4	191154276	11531080	0.0603	0.2954
chr5	180915260	9593005	0.053	0.256
chr6	171115067	7304812	0.0427	0.2758
chr7	159138663	9210525	0.0579	0.7075

chr8	146364022	9067065	0.0619	0.5803
chr9	141213431	6354053	0.045	0.4655
chr10	135534747	7065341	0.0521	0.4316
chr11	135006516	6873761	0.0509	0.4073
chr12	133851895	6833294	0.0511	0.2568
chr13	115169878	4793466	0.0416	0.2231
chr14	107349540	5539945	0.0516	0.2767
chr15	102531392	3907363	0.0381	0.2403
chr16	90354753	4303765	0.0476	0.3017
chr17	81195210	3760927	0.0463	0.2567
chr18	78077248	4368809	0.056	0.8963
chr19	59128983	2908271	0.0492	0.6362
chr20	63025520	3355752	0.0532	0.2751
chr21	48129895	1977998	0.0411	0.2451
chr22	51304566	1806214	0.0352	0.2047
chrMT	16571	3558	0.2147	0.4539
chrX	155270560	9992665	0.0644	0.3324
chrY	59373566	473409	0.008	0.1659

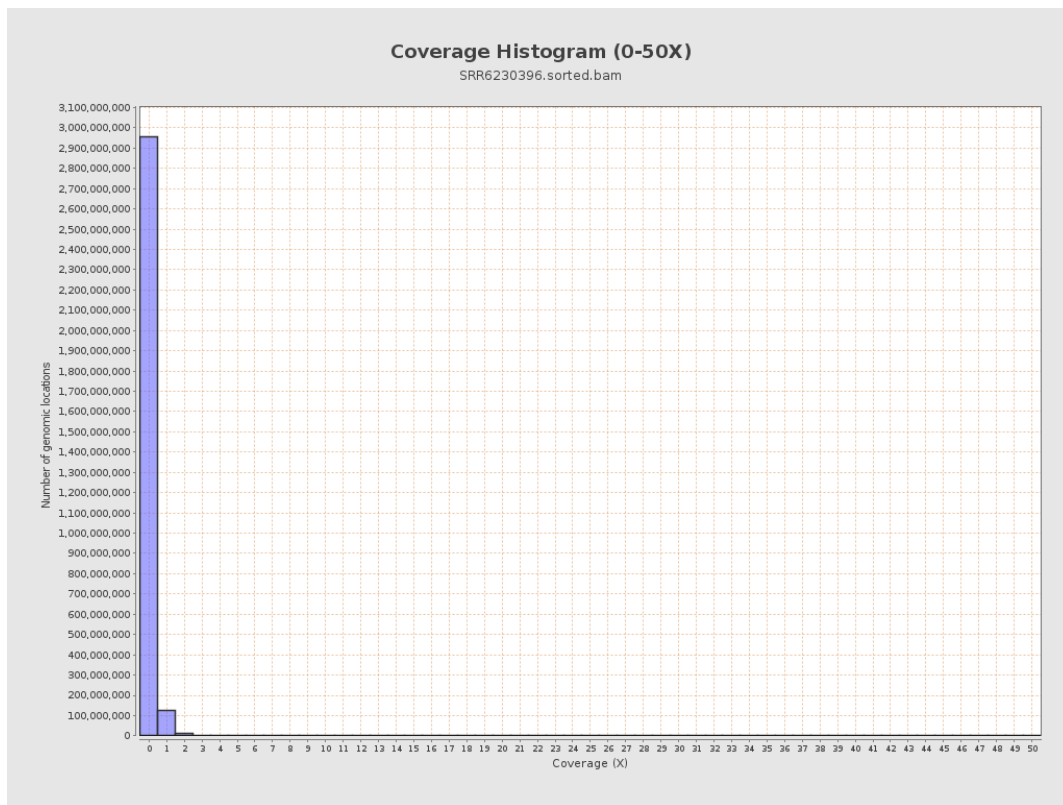
3. Results : Coverage across reference



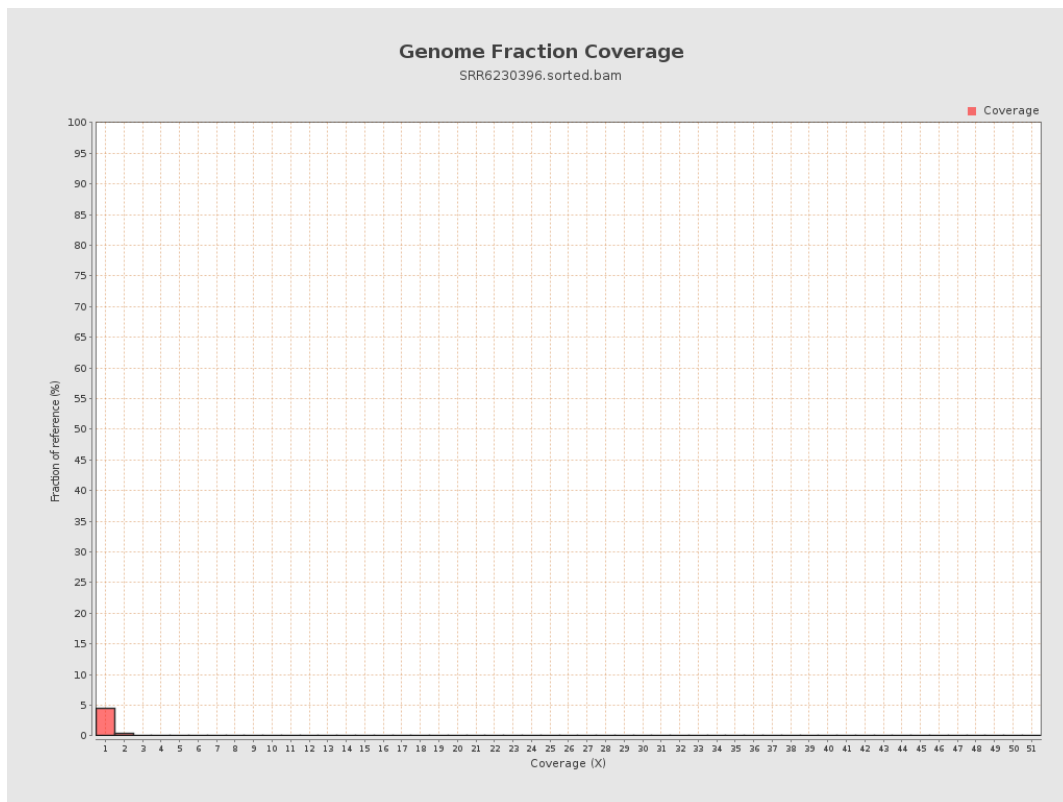
4. Results : Coverage Histogram



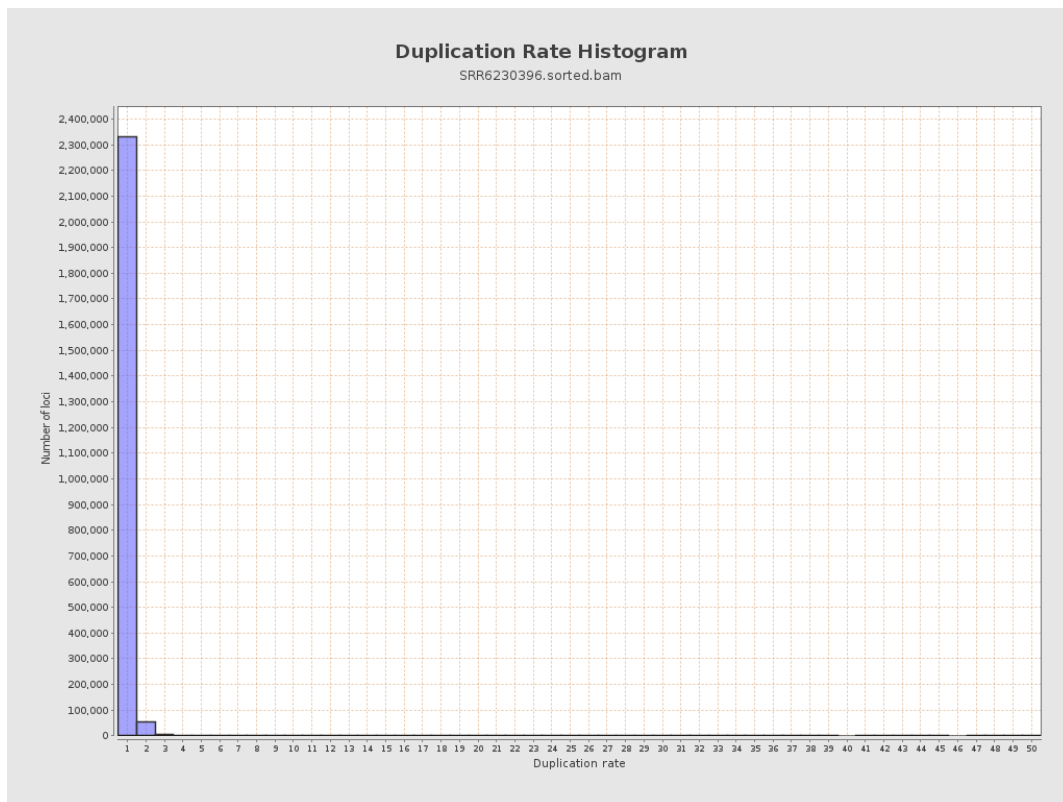
5. Results : Coverage Histogram (0-50X)



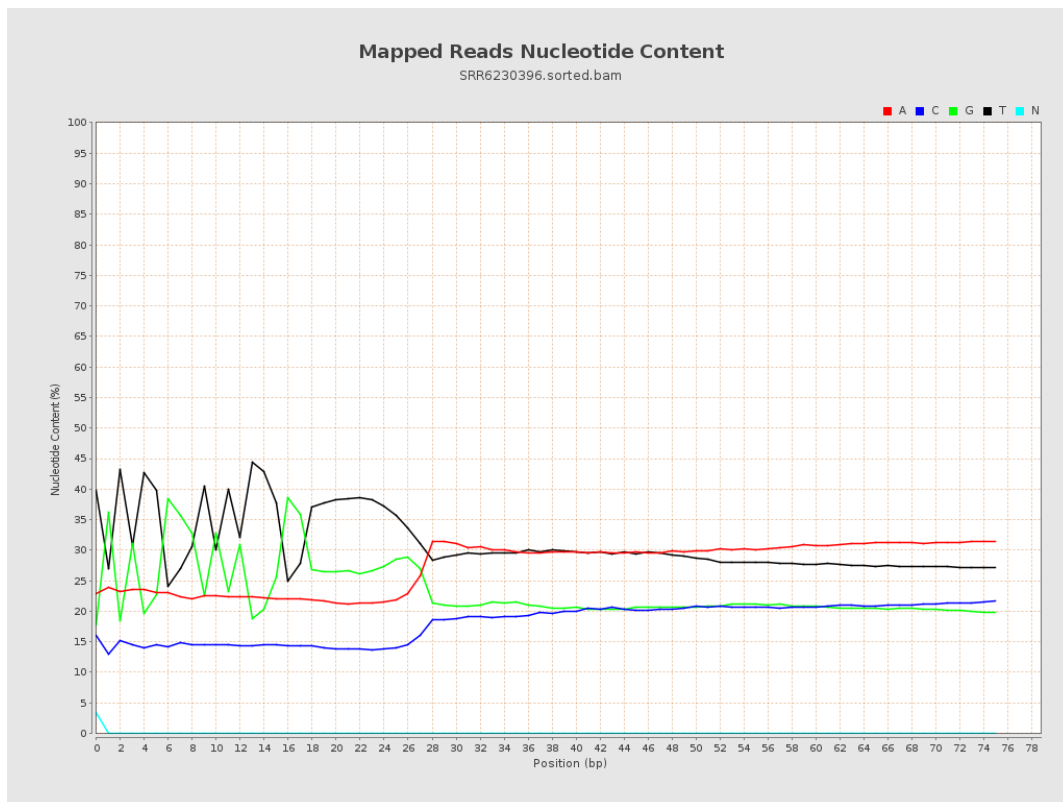
6. Results : Genome Fraction Coverage



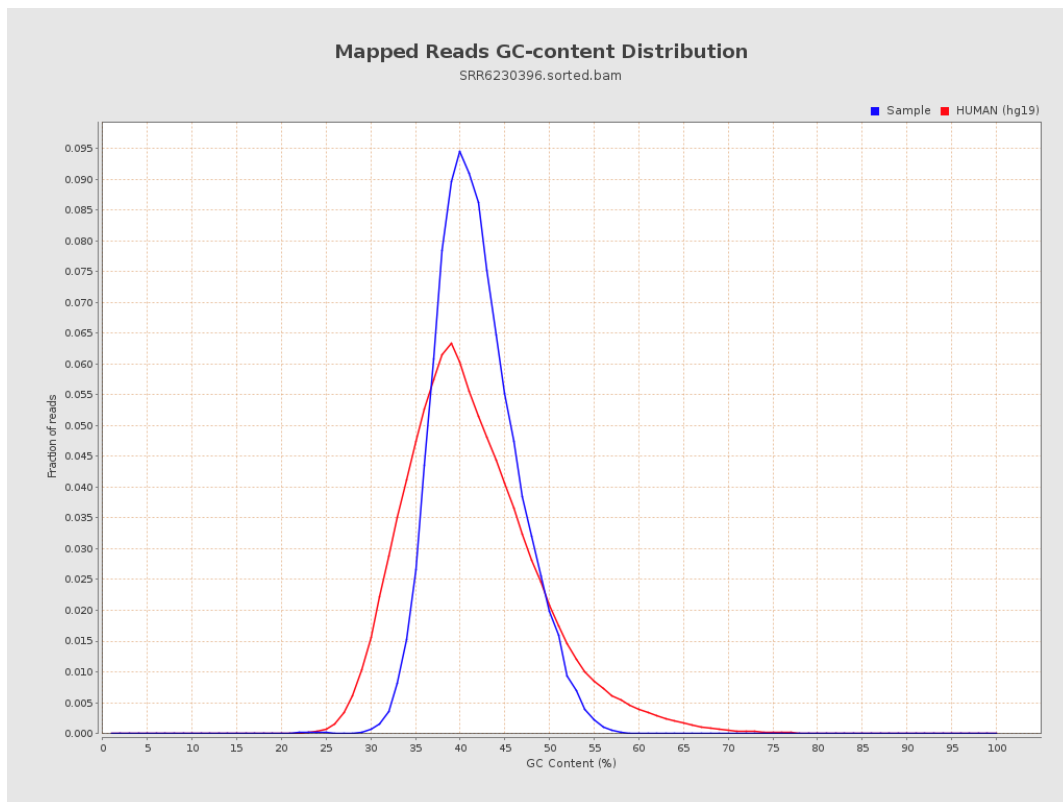
7. Results : Duplication Rate Histogram



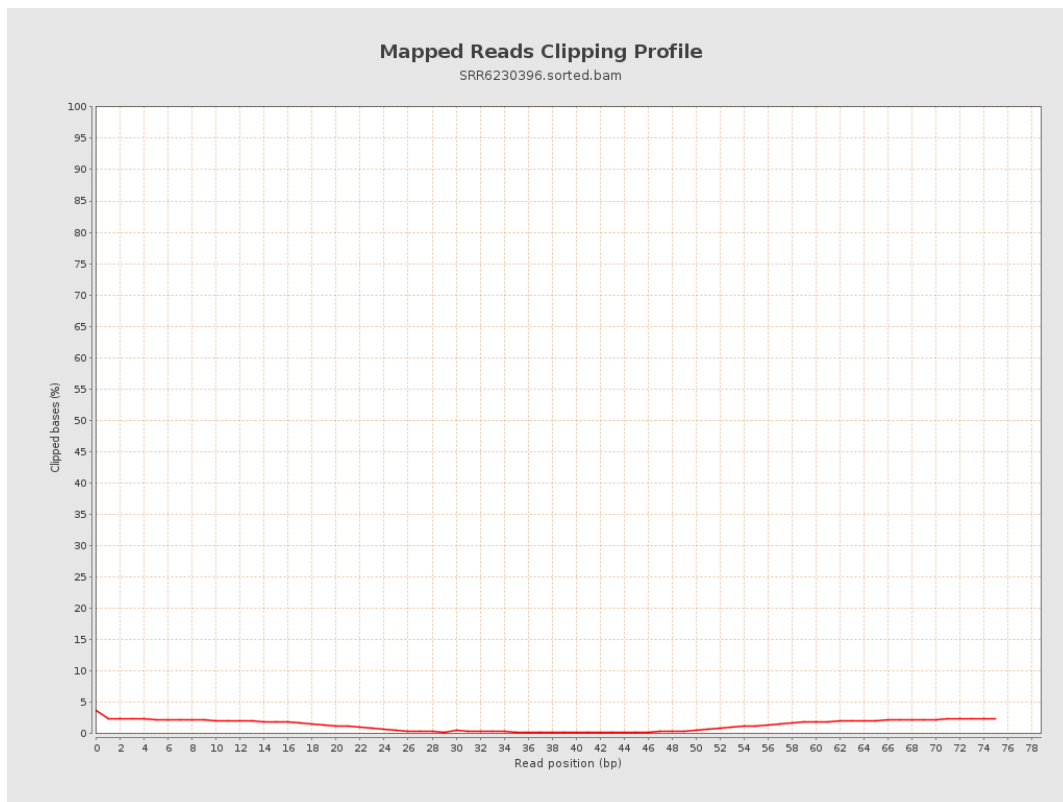
8. Results : Mapped Reads Nucleotide Content



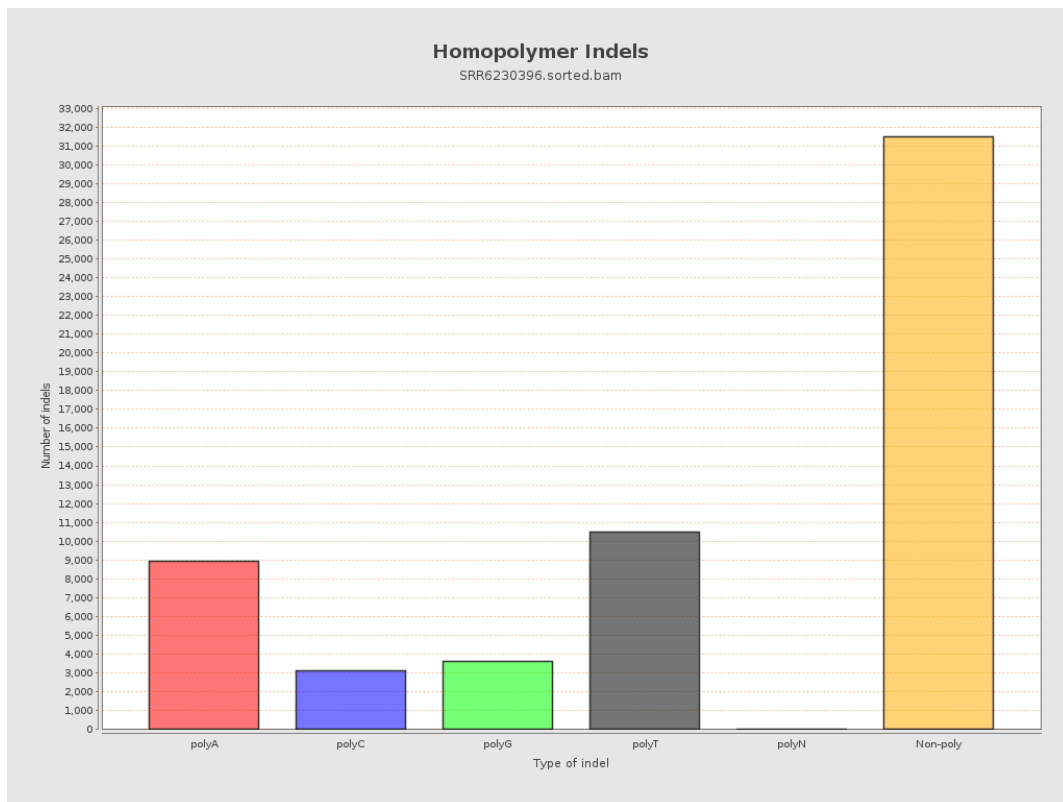
9. Results : Mapped Reads GC-content Distribution



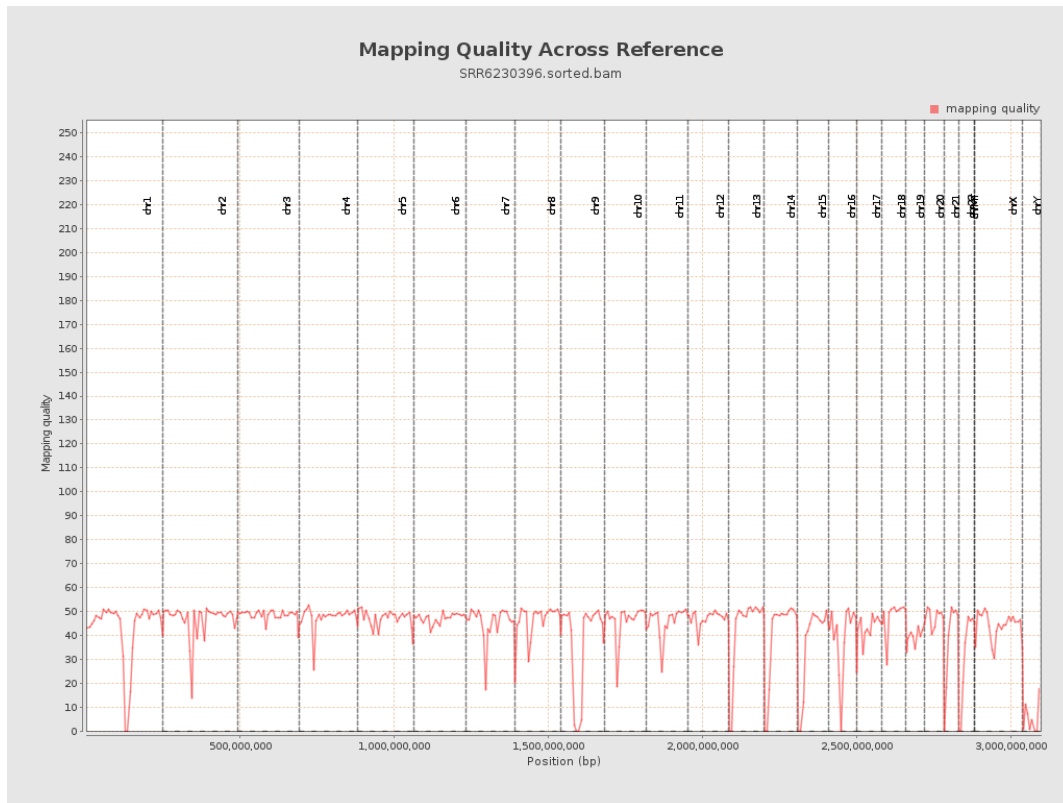
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

