

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 19:00:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230353.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_SRR6230353 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230353.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 19:00:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230353.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,394,515
Mapped reads	1,954,919 / 81.64%
Unmapped reads	439,596 / 18.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,869 / 0.37%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	86,124 / 3.6%
Duplication rate	3.58%
Clipped reads	969,470 / 40.49%

2.2. ACGT Content

Number/percentage of A's	34,948,555 / 27.39%
Number/percentage of C's	21,595,975 / 16.93%
Number/percentage of T's	43,853,104 / 34.37%
Number/percentage of G's	26,930,748 / 21.11%
Number/percentage of N's	244,855 / 0.19%
GC Percentage	38.04%

2.3. Coverage

Mean	0.0412

Standard Deviation	0.339
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2.4. Mapping Quality

Mean Mapping Quality	47.75
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2.5. Mismatches and indels

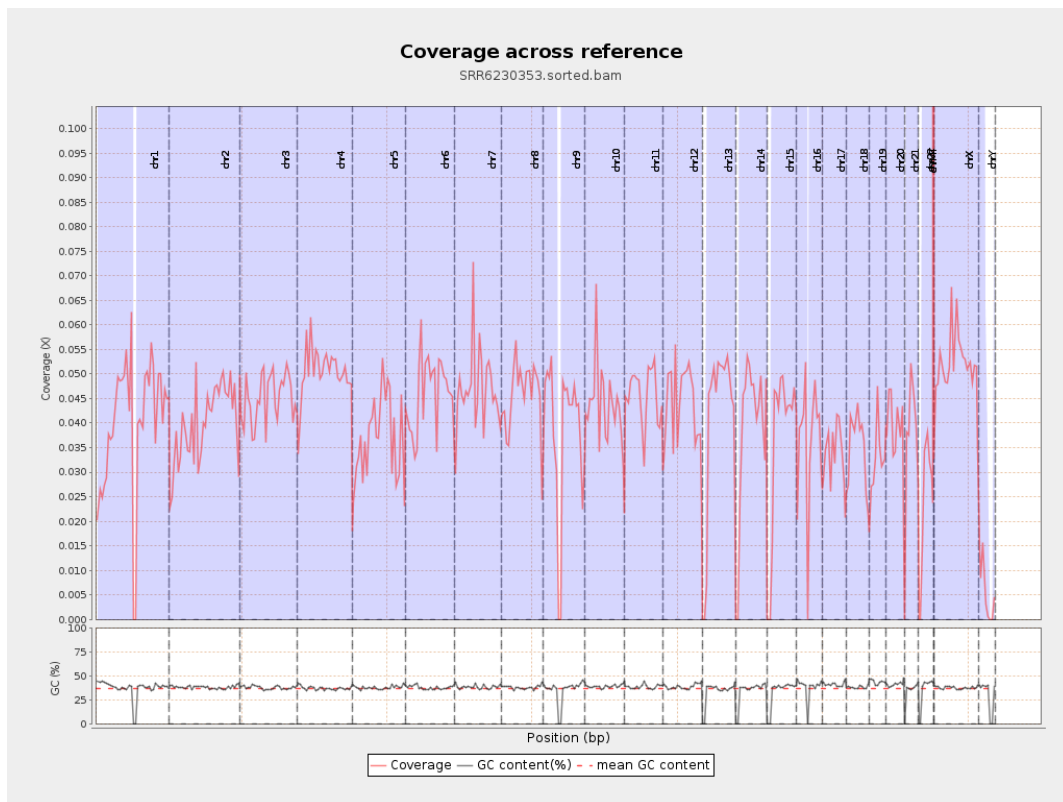
General error rate	1.11%
Mismatches	1,394,112
Insertions	11,247
Mapped reads with at least one insertion	0.57%
Deletions	34,137
Mapped reads with at least one deletion	1.73%
Homopolymer indels	48.45%

2.6. Chromosome stats

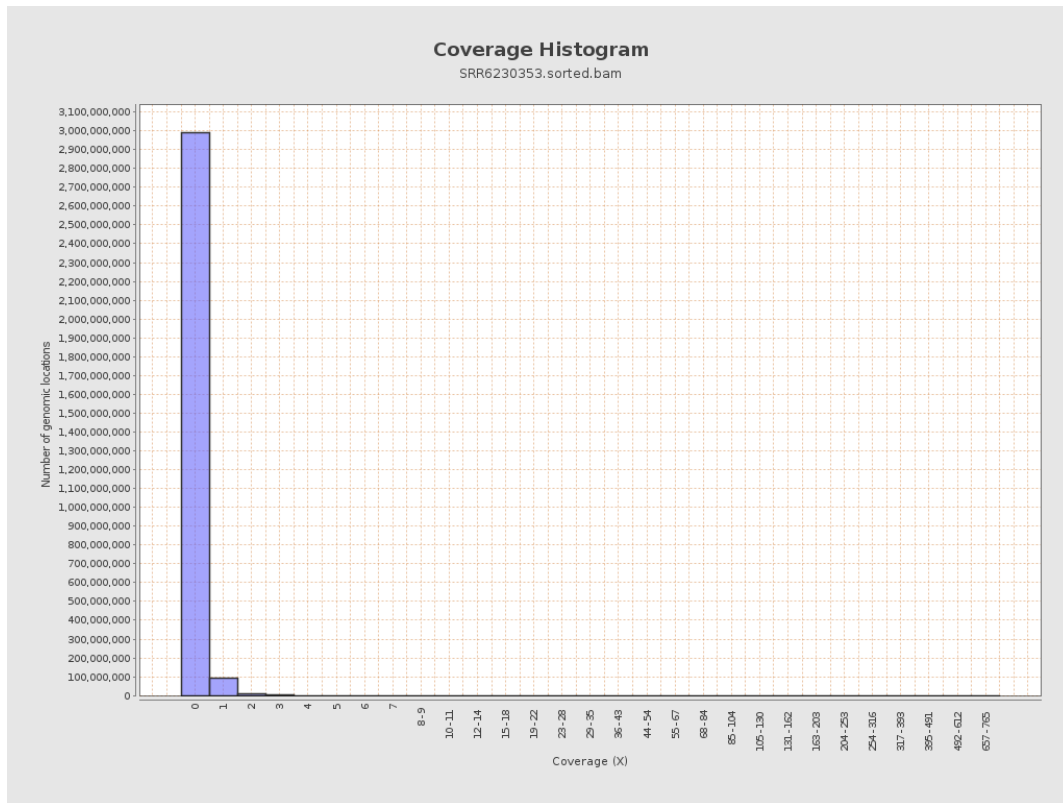
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10008117	0.0402	0.5072
chr2	243199373	9722936	0.04	0.3227
chr3	198022430	8954152	0.0452	0.2445
chr4	191154276	9660403	0.0505	0.2694
chr5	180915260	6748488	0.0373	0.2218
chr6	171115067	7857765	0.0459	0.3031
chr7	159138663	7514359	0.0472	0.5026

chr8	146364022	6685433	0.0457	0.5359
chr9	141213431	5423744	0.0384	0.3411
chr10	135534747	5948758	0.0439	0.339
chr11	135006516	6100766	0.0452	0.3322
chr12	133851895	5873667	0.0439	0.245
chr13	115169878	4668688	0.0405	0.2305
chr14	107349540	4110417	0.0383	0.2377
chr15	102531392	3756195	0.0366	0.2184
chr16	90354753	3280622	0.0363	0.2453
chr17	81195210	2724560	0.0336	0.2243
chr18	78077248	2762056	0.0354	0.5465
chr19	59128983	1946969	0.0329	0.3503
chr20	63025520	2484250	0.0394	0.2355
chr21	48129895	1783704	0.0371	0.2409
chr22	51304566	1198889	0.0234	0.1727
chrMT	16571	30515	1.8415	2.0571
chrX	155270560	8059319	0.0519	0.2866
chrY	59373566	323288	0.0054	0.1207

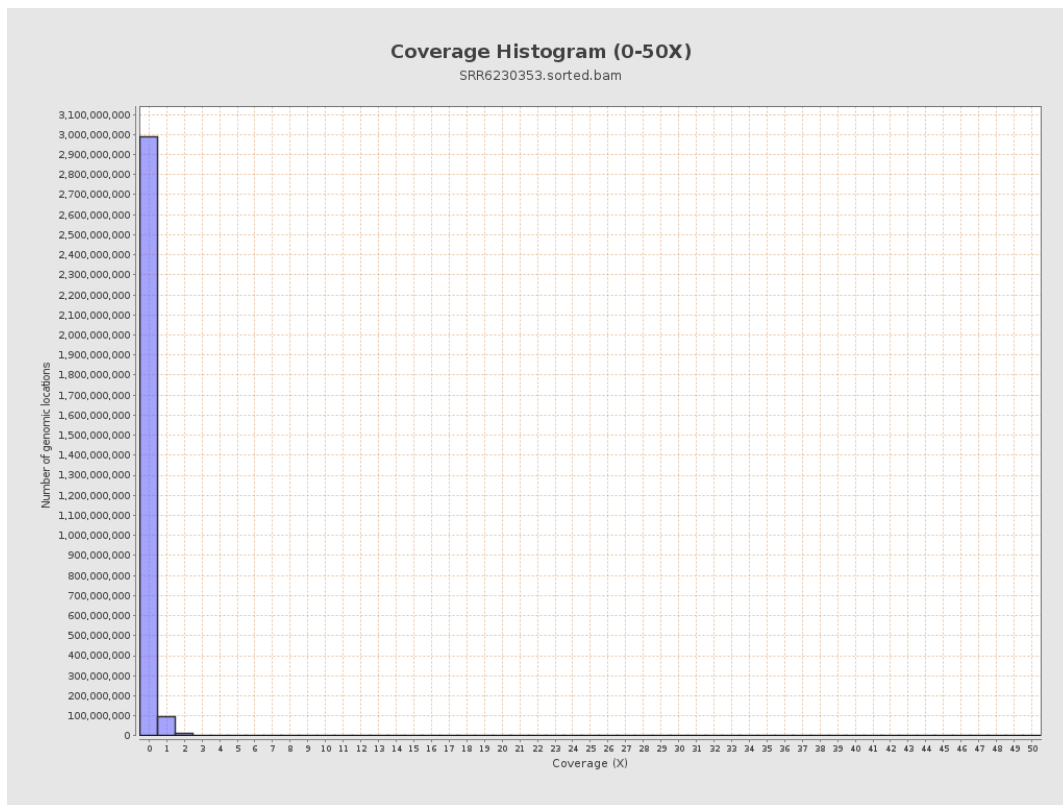
3. Results : Coverage across reference



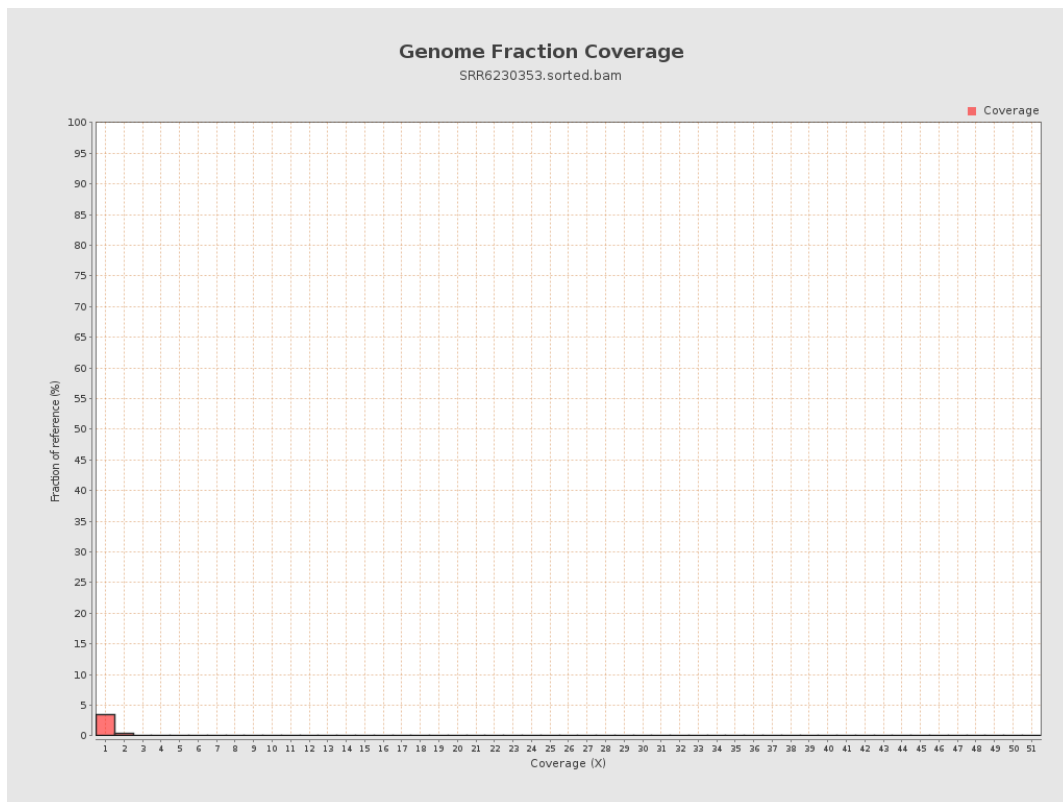
4. Results : Coverage Histogram



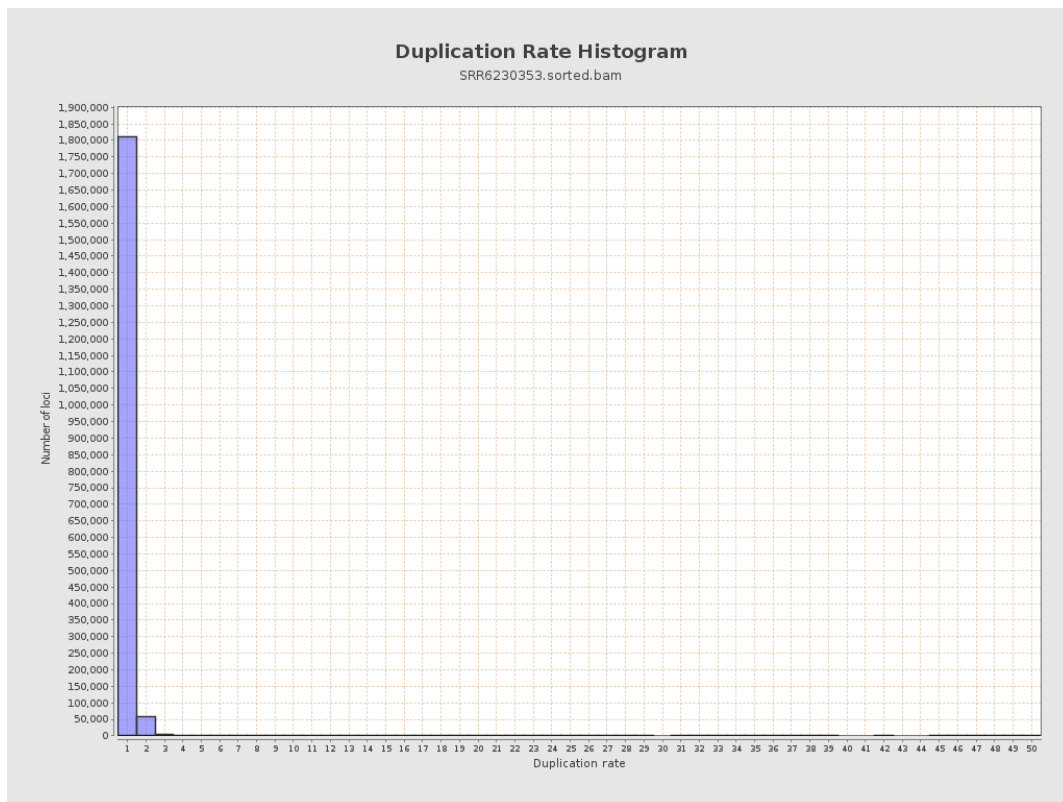
5. Results : Coverage Histogram (0-50X)



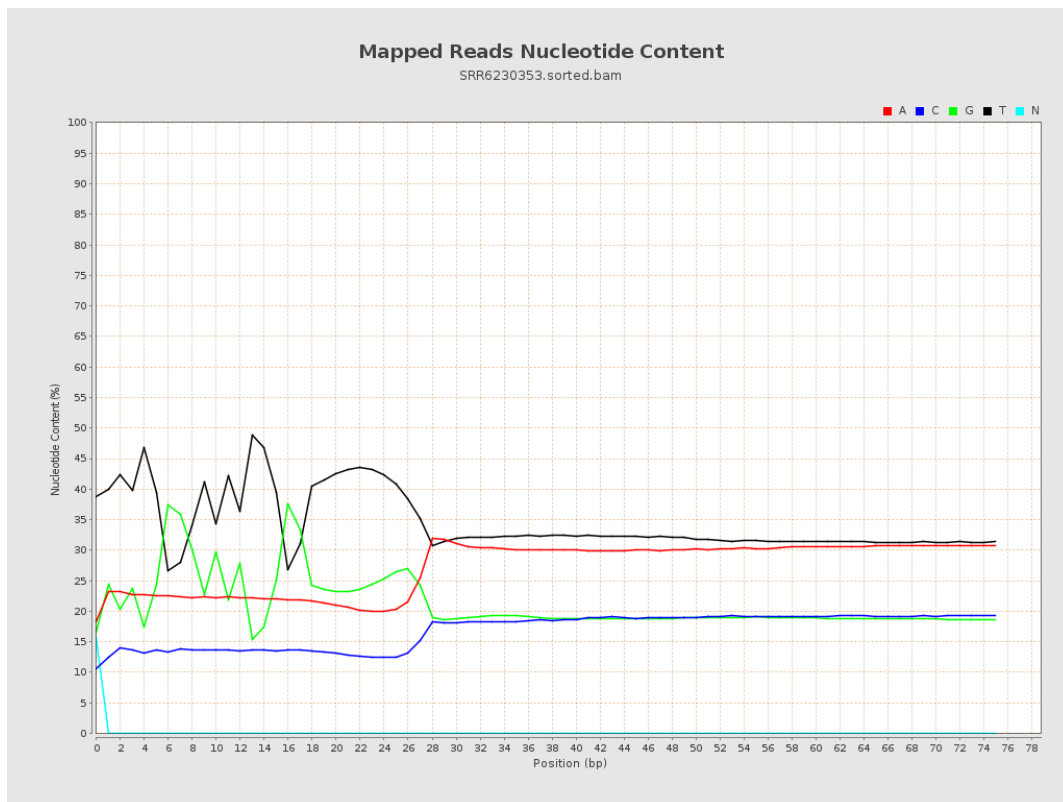
6. Results : Genome Fraction Coverage



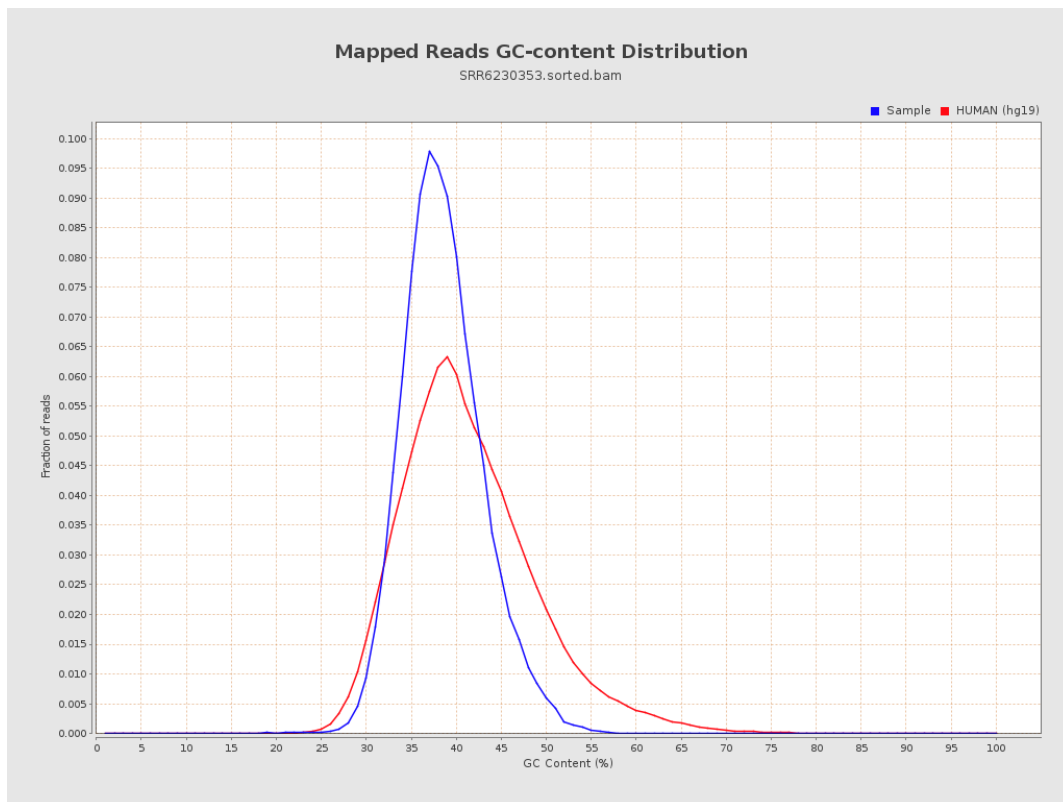
7. Results : Duplication Rate Histogram



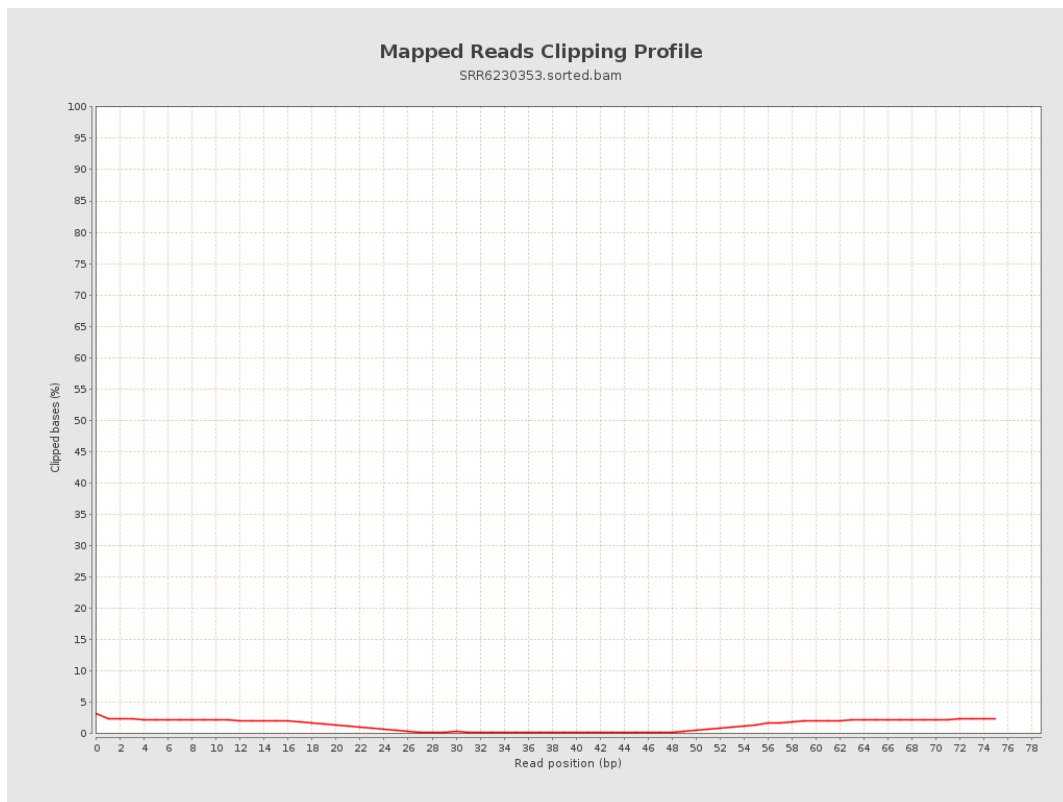
8. Results : Mapped Reads Nucleotide Content



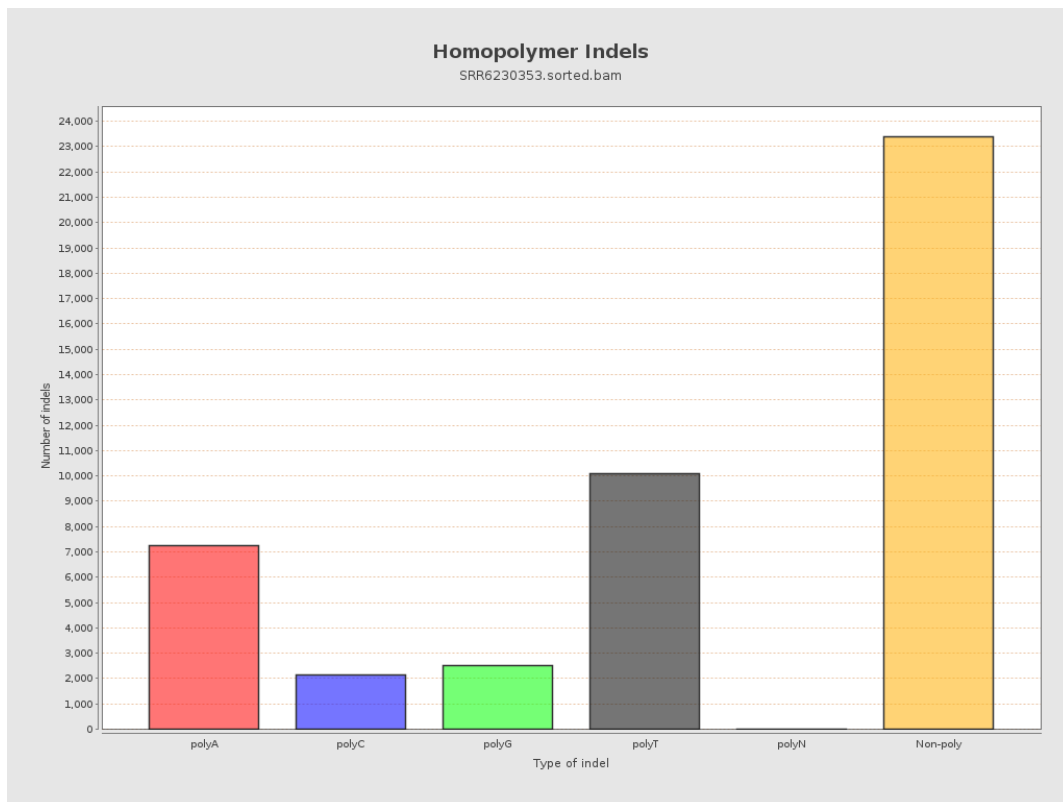
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

