

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 08:01:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231852.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_SRR6231852 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231852.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 08:01:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231852.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,453,371
Mapped reads	3,019,470 / 87.44%
Unmapped reads	433,901 / 12.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,561 / 0.83%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	507,277 / 14.69%
Duplication rate	13.33%
Clipped reads	1,730,773 / 50.12%

2.2. ACGT Content

Number/percentage of A's	48,865,326 / 25.49%
Number/percentage of C's	34,526,861 / 18.01%
Number/percentage of T's	62,702,594 / 32.71%
Number/percentage of G's	45,517,960 / 23.75%
Number/percentage of N's	73,019 / 0.04%
GC Percentage	41.76%

2.3. Coverage

Mean	0.0619

Standard Deviation	0.7169
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2.4. Mapping Quality

Mean Mapping Quality	44.23
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2.5. Mismatches and indels

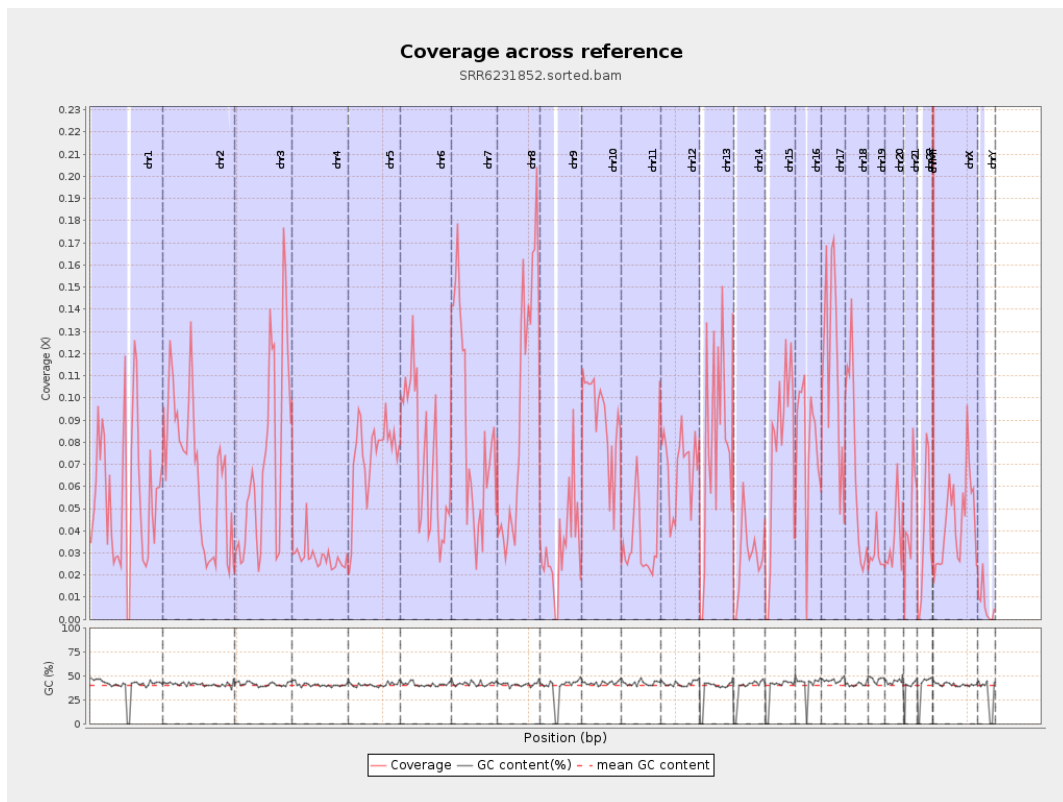
General error rate	0.66%
Mismatches	1,241,179
Insertions	12,151
Mapped reads with at least one insertion	0.4%
Deletions	42,080
Mapped reads with at least one deletion	1.38%
Homopolymer indels	43.19%

2.6. Chromosome stats

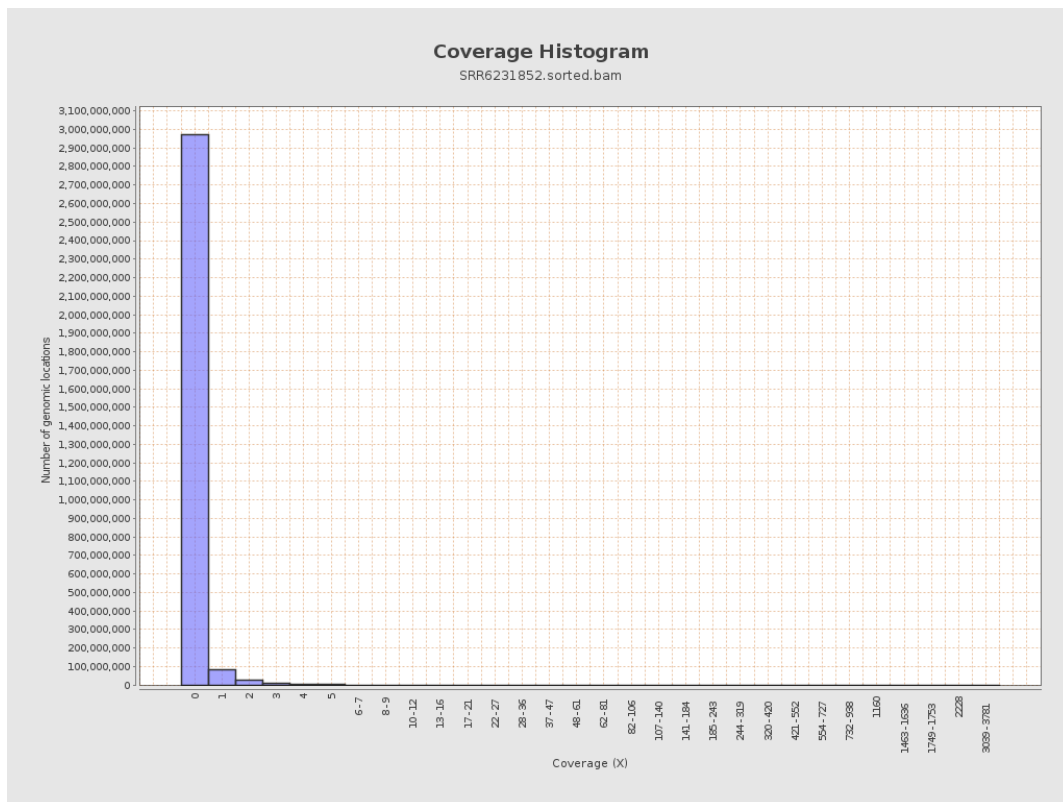
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	13939123	0.0559	0.8108
chr2	243199373	16111395	0.0662	1.7569
chr3	198022430	14057926	0.071	0.3931
chr4	191154276	5401693	0.0283	0.2775
chr5	180915260	13431849	0.0742	0.4027
chr6	171115067	12425997	0.0726	0.6199
chr7	159138663	13451498	0.0845	0.5558

chr8	146364022	13820031	0.0944	0.6937
chr9	141213431	4622989	0.0327	0.4074
chr10	135534747	12340458	0.0911	0.5555
chr11	135006516	5037195	0.0373	0.563
chr12	133851895	9217815	0.0689	0.3807
chr13	115169878	8865543	0.077	0.4601
chr14	107349540	3062586	0.0285	0.2773
chr15	102531392	7811534	0.0762	0.426
chr16	90354753	7127010	0.0789	0.4401
chr17	81195210	9489271	0.1169	0.5905
chr18	78077248	5499813	0.0704	1.1432
chr19	59128983	1746576	0.0295	0.6555
chr20	63025520	2283163	0.0362	0.3398
chr21	48129895	2263930	0.047	0.3245
chr22	51304566	1978917	0.0386	0.2788
chrMT	16571	516526	31.1705	20.9374
chrX	155270560	6849562	0.0441	0.3675
chrY	59373566	405275	0.0068	0.1947

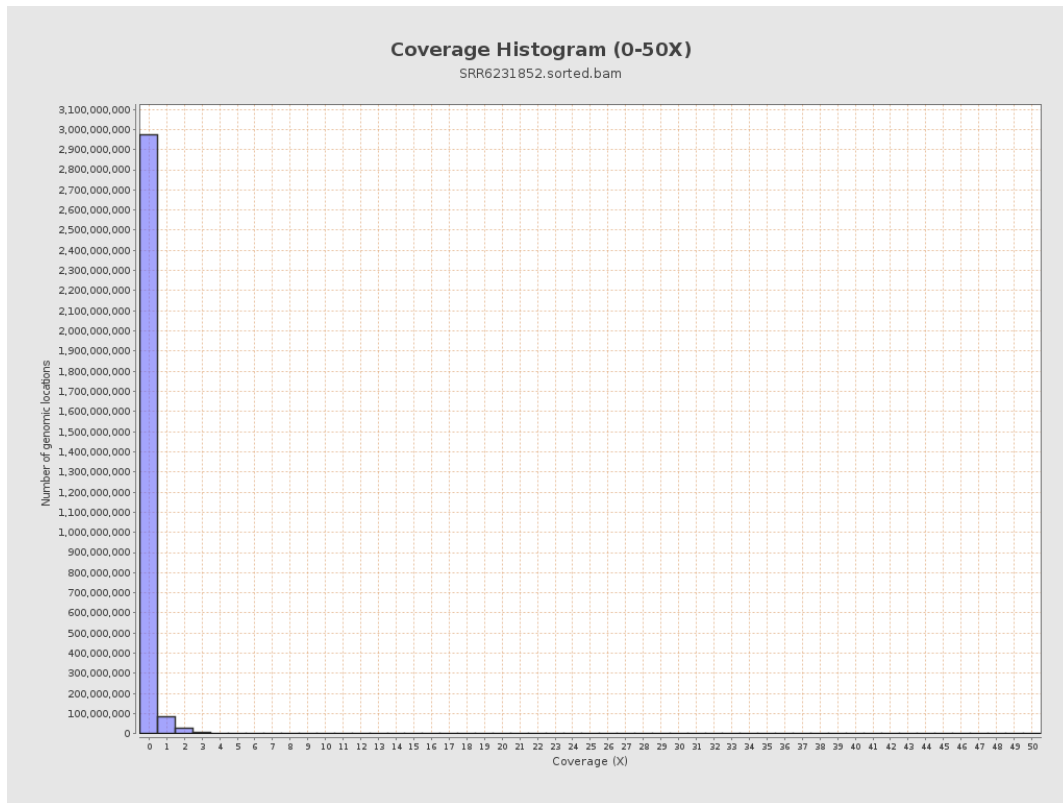
3. Results : Coverage across reference



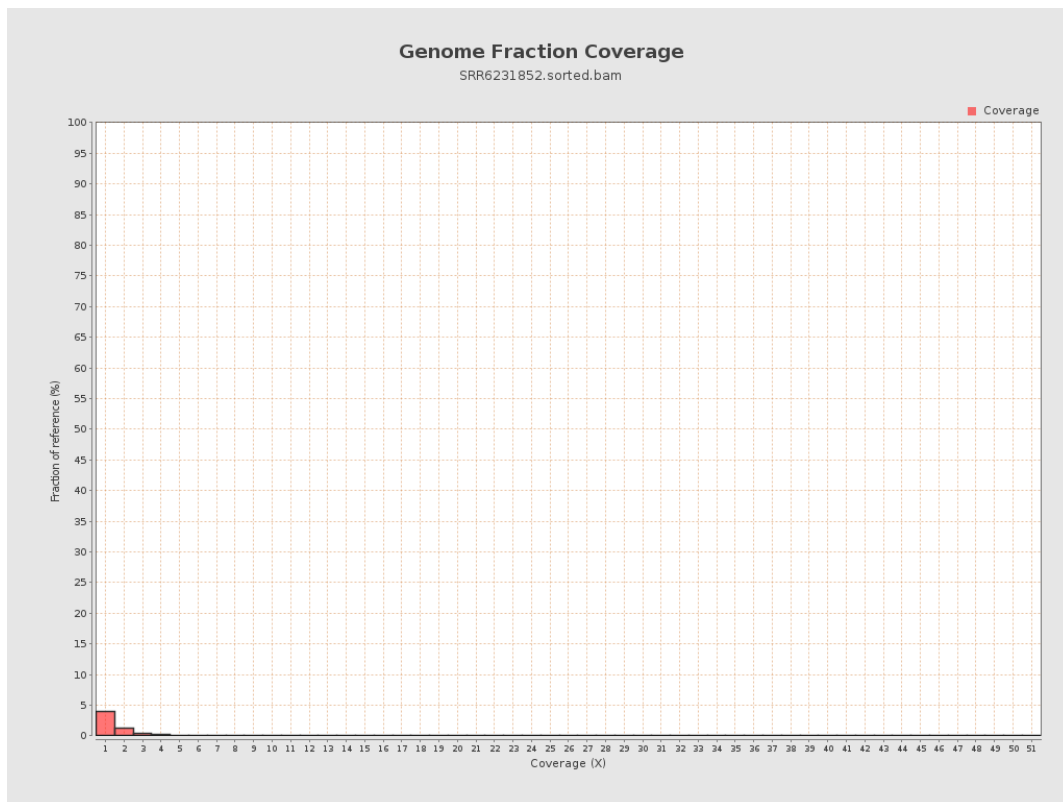
4. Results : Coverage Histogram



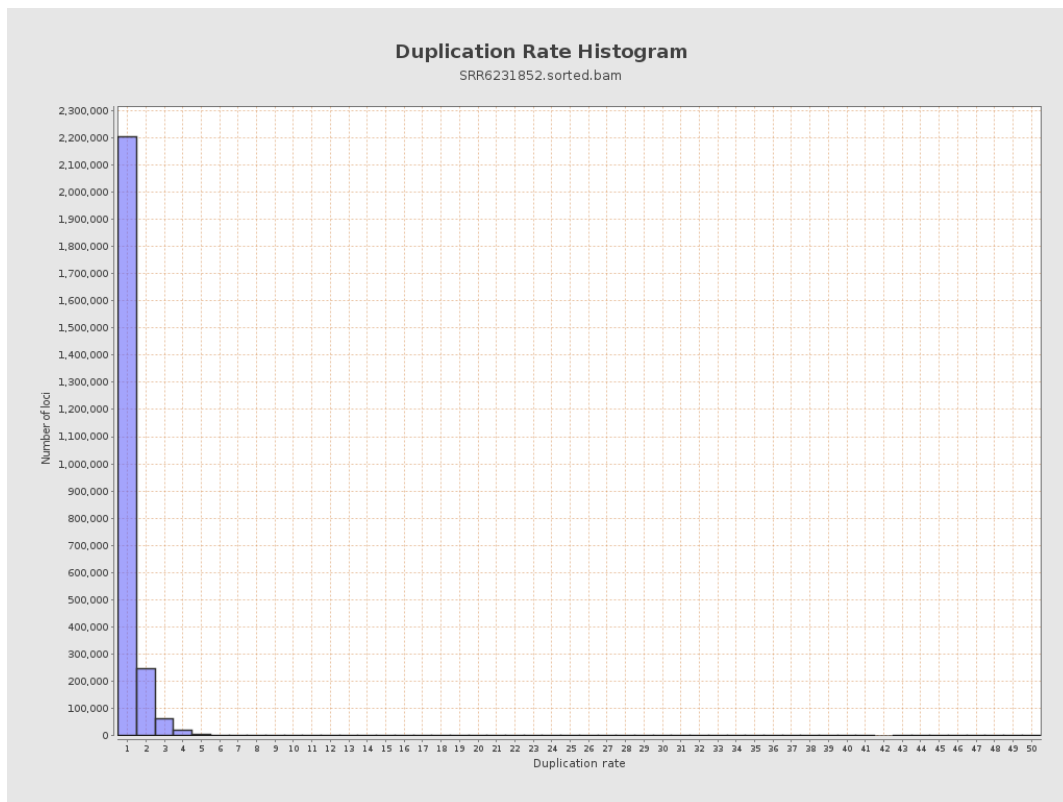
5. Results : Coverage Histogram (0-50X)



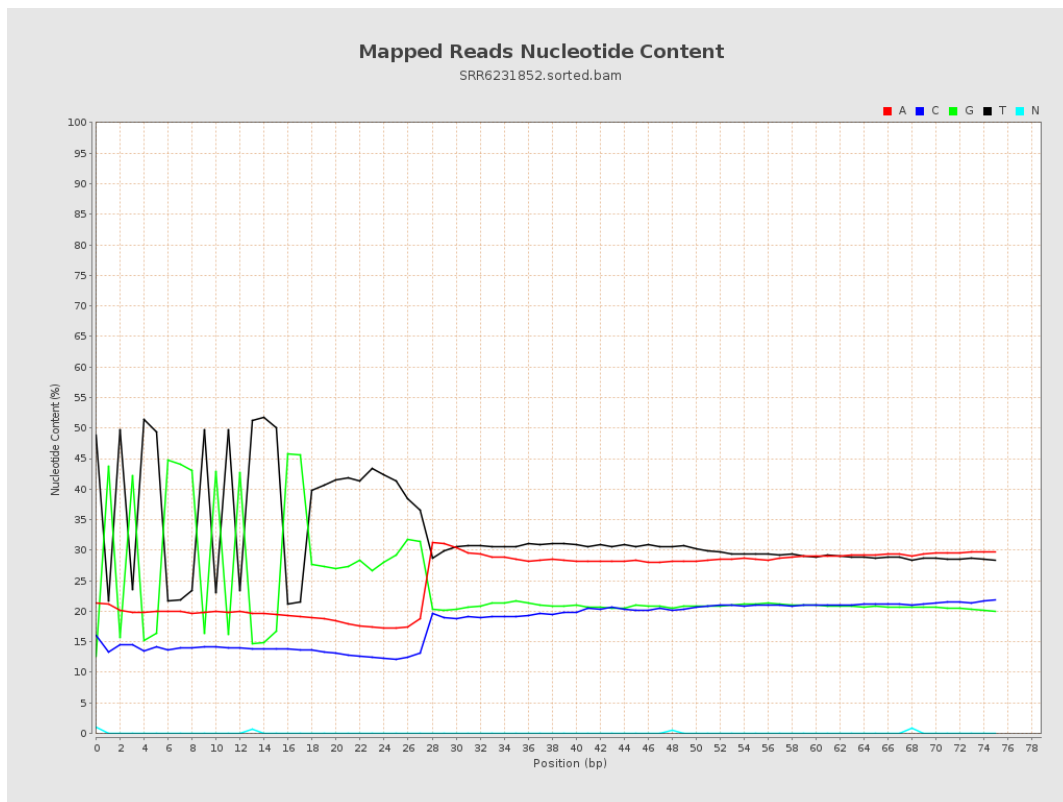
6. Results : Genome Fraction Coverage



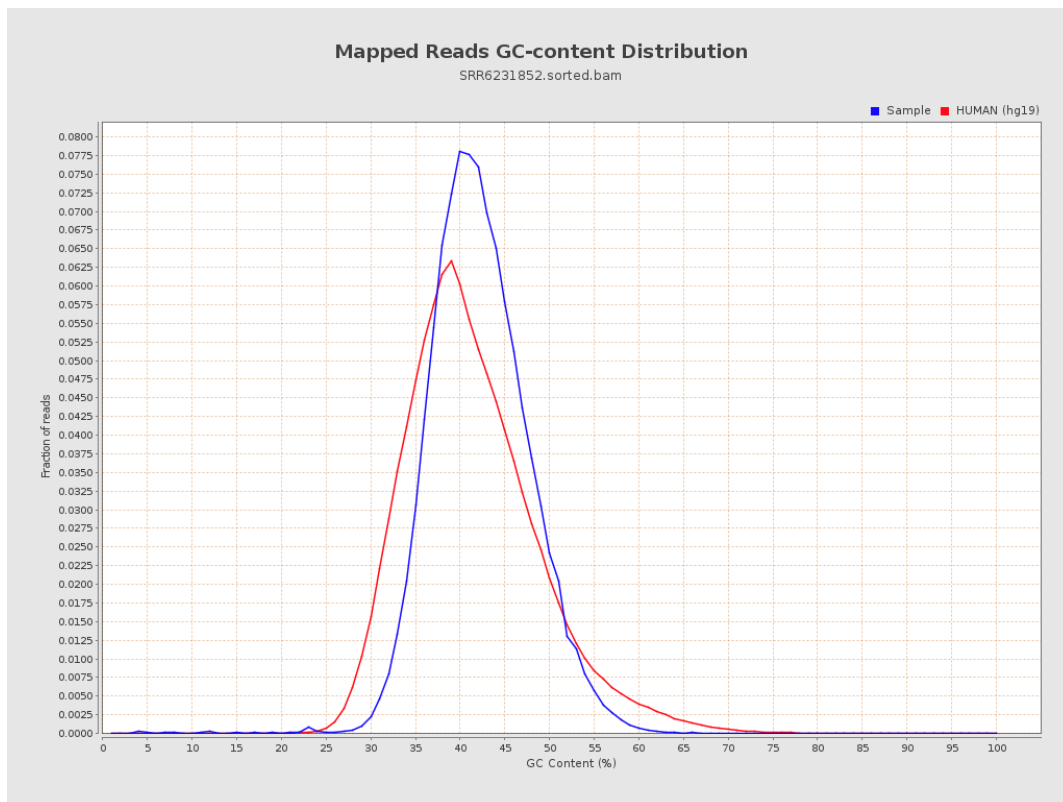
7. Results : Duplication Rate Histogram



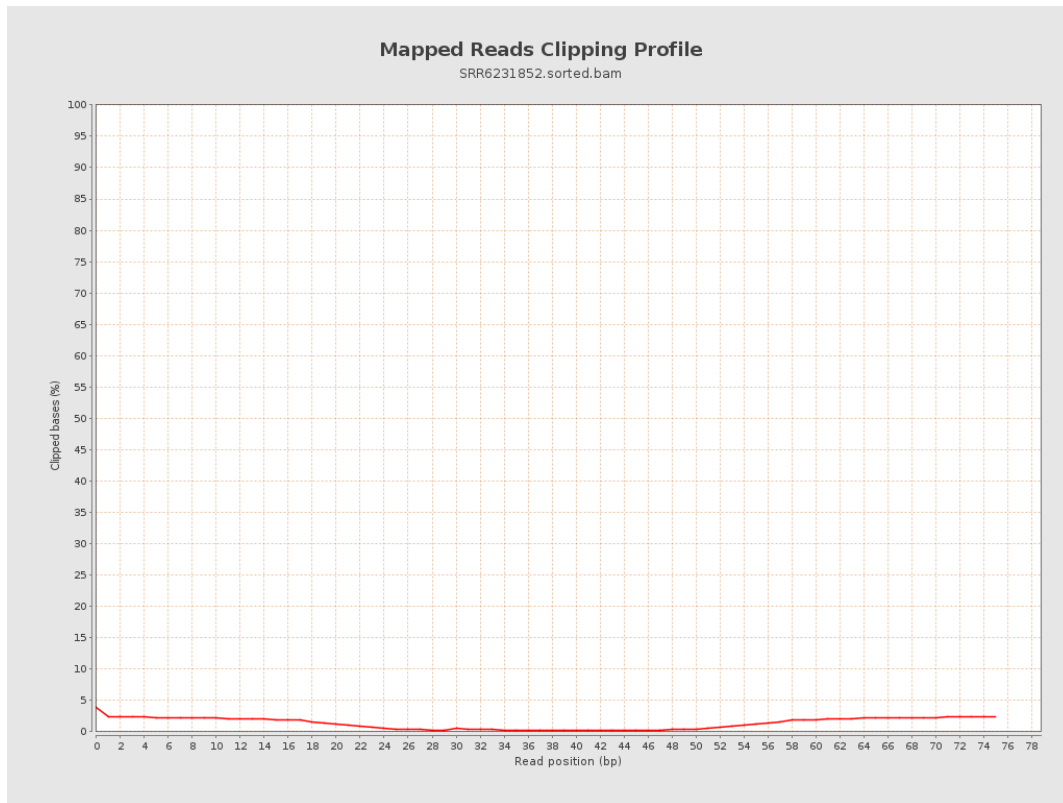
8. Results : Mapped Reads Nucleotide Content



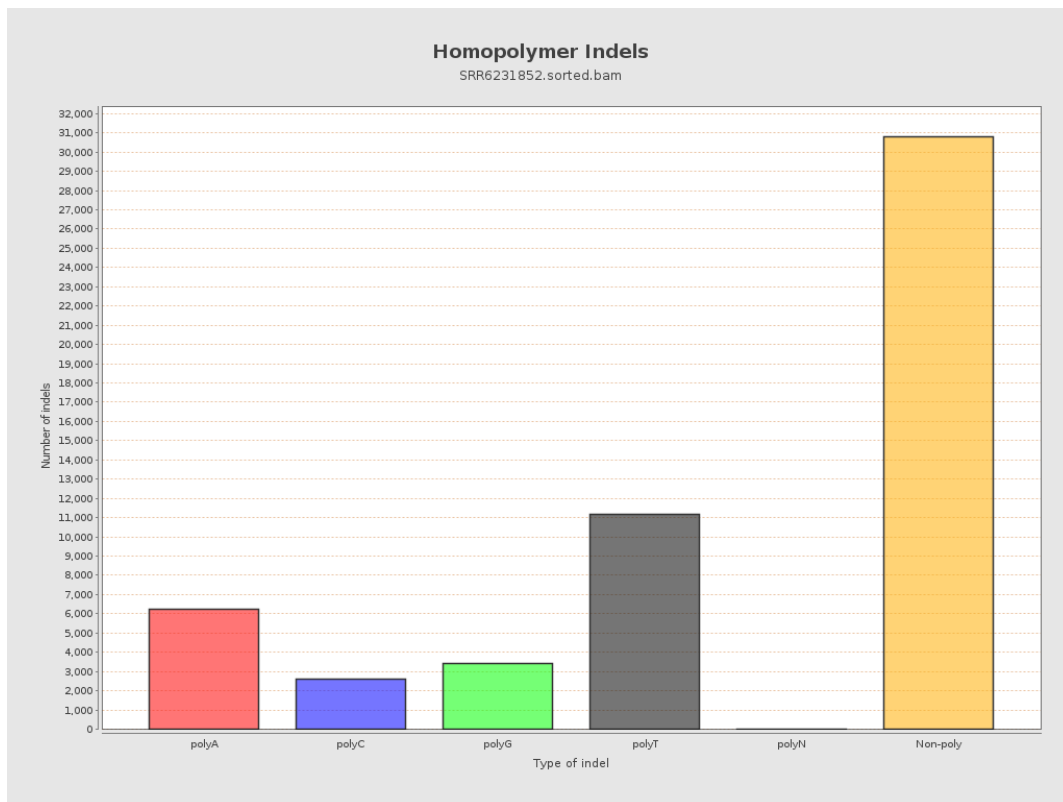
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

