

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 12:40:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10251080.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_SRR10251080 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10251080.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 12:40:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10251080.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,940,513
Mapped reads	3,737,877 / 94.86%
Unmapped reads	202,636 / 5.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	31,680 / 0.8%
Read min/max/mean length	30 / 80 / 80.29
Duplicated reads (estimated)	758,433 / 19.25%
Duplication rate	17.7%
Clipped reads	549,539 / 13.95%

2.2. ACGT Content

Number/percentage of A's	84,863,573 / 29.32%
Number/percentage of C's	57,759,586 / 19.96%
Number/percentage of T's	85,595,248 / 29.58%
Number/percentage of G's	61,175,561 / 21.14%
Number/percentage of N's	2,429 / 0%
GC Percentage	41.1%

2.3. Coverage

Mean	0.0935

Standard Deviation	1.0849
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2.4. Mapping Quality

Mean Mapping Quality	47.97
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2.5. Mismatches and indels

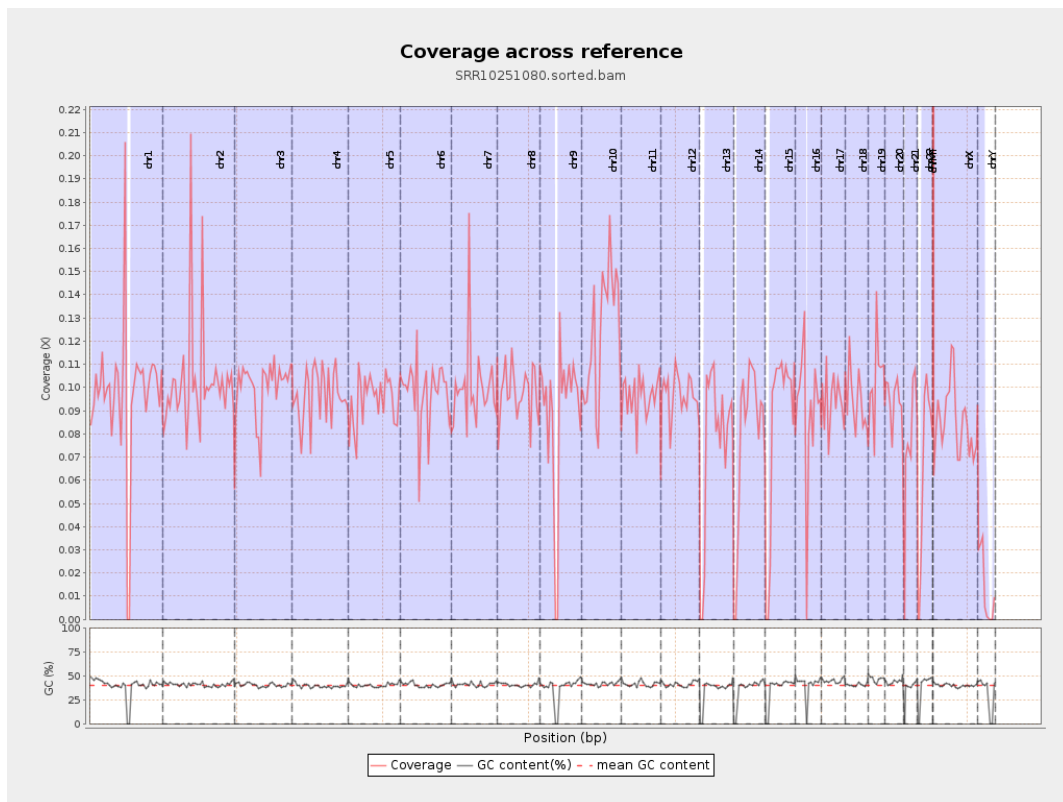
General error rate	0.64%
Mismatches	1,764,999
Insertions	37,310
Mapped reads with at least one insertion	0.98%
Deletions	110,288
Mapped reads with at least one deletion	2.9%
Homopolymer indels	44.78%

2.6. Chromosome stats

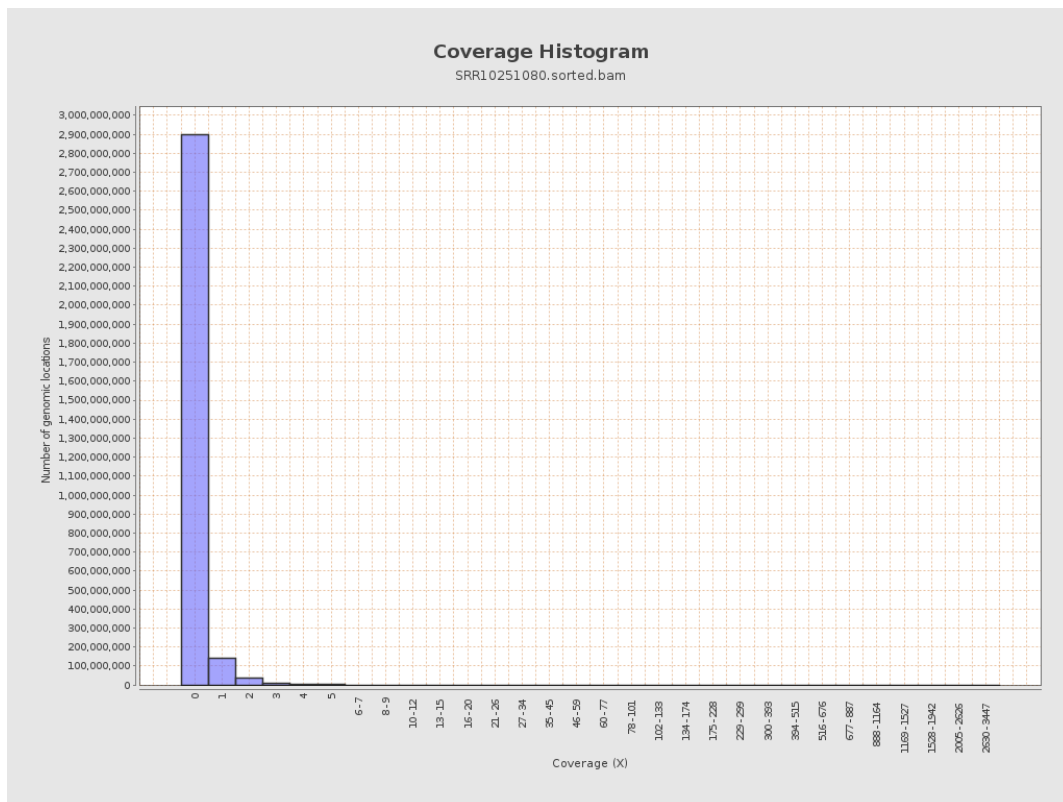
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	24275645	0.0974	2.3664
chr2	243199373	25077097	0.1031	1.4602
chr3	198022430	19780320	0.0999	0.4321
chr4	191154276	18486874	0.0967	0.5037
chr5	180915260	17231413	0.0952	0.4456
chr6	171115067	16680982	0.0975	0.5516
chr7	159138663	15926996	0.1001	1.4924

chr8	146364022	14227033	0.0972	0.7045
chr9	141213431	12528943	0.0887	1.1449
chr10	135534747	16788702	0.1239	1.0292
chr11	135006516	12995528	0.0963	0.6494
chr12	133851895	13070613	0.0976	0.4491
chr13	115169878	8768435	0.0761	0.3702
chr14	107349540	8649095	0.0806	0.6821
chr15	102531392	8477019	0.0827	0.395
chr16	90354753	8034077	0.0889	0.8689
chr17	81195210	7703256	0.0949	0.552
chr18	78077248	7398190	0.0948	1.3323
chr19	59128983	6110907	0.1033	2.0841
chr20	63025520	5910738	0.0938	0.4782
chr21	48129895	3730984	0.0775	0.4249
chr22	51304566	3395524	0.0662	0.3779
chrMT	16571	305941	18.4624	10.9266
chrX	155270560	13228750	0.0852	0.5185
chrY	59373566	810501	0.0137	1.0525

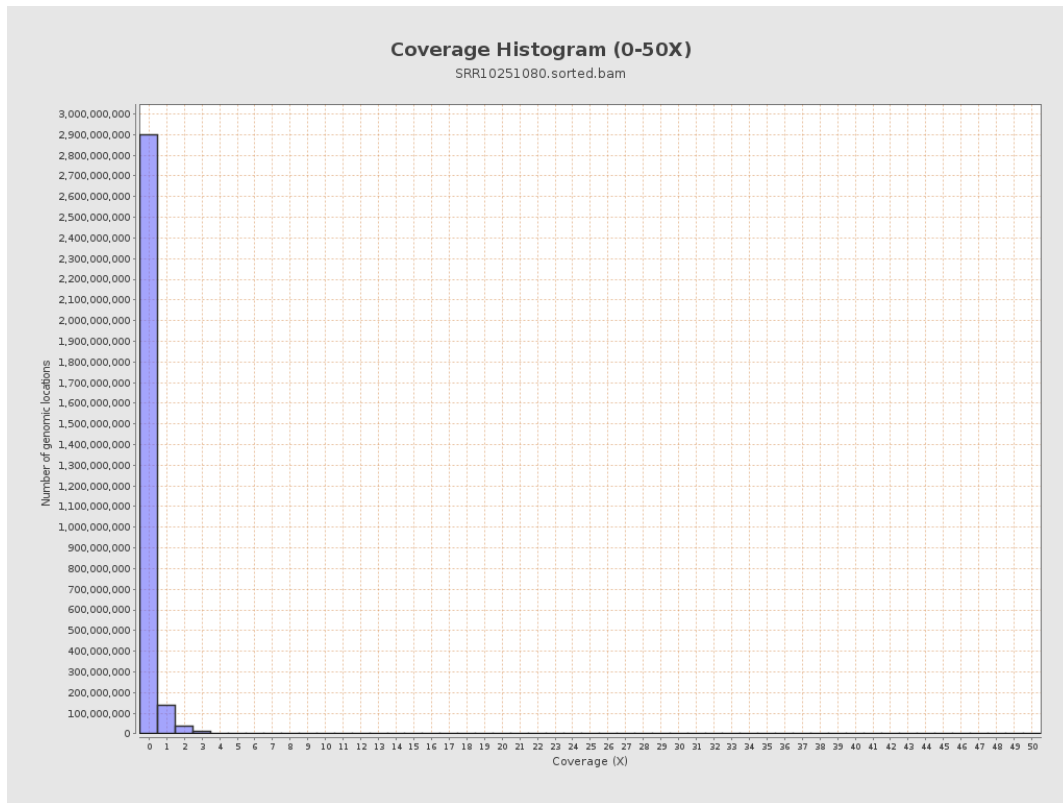
3. Results : Coverage across reference



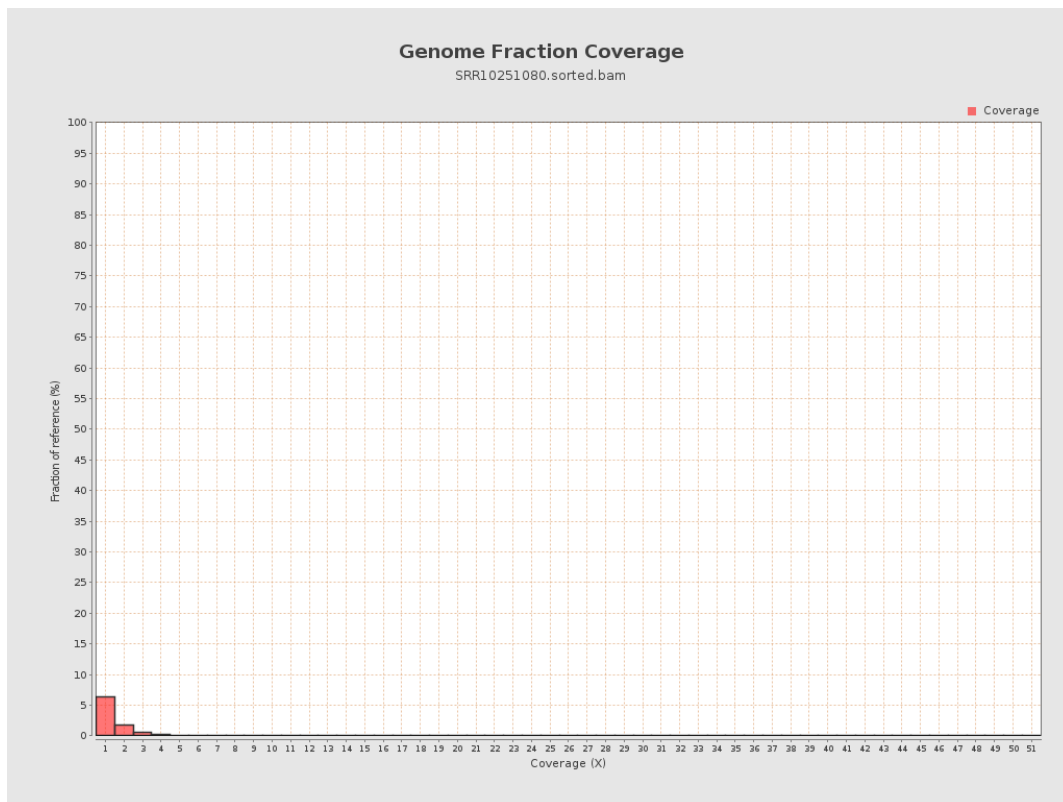
4. Results : Coverage Histogram



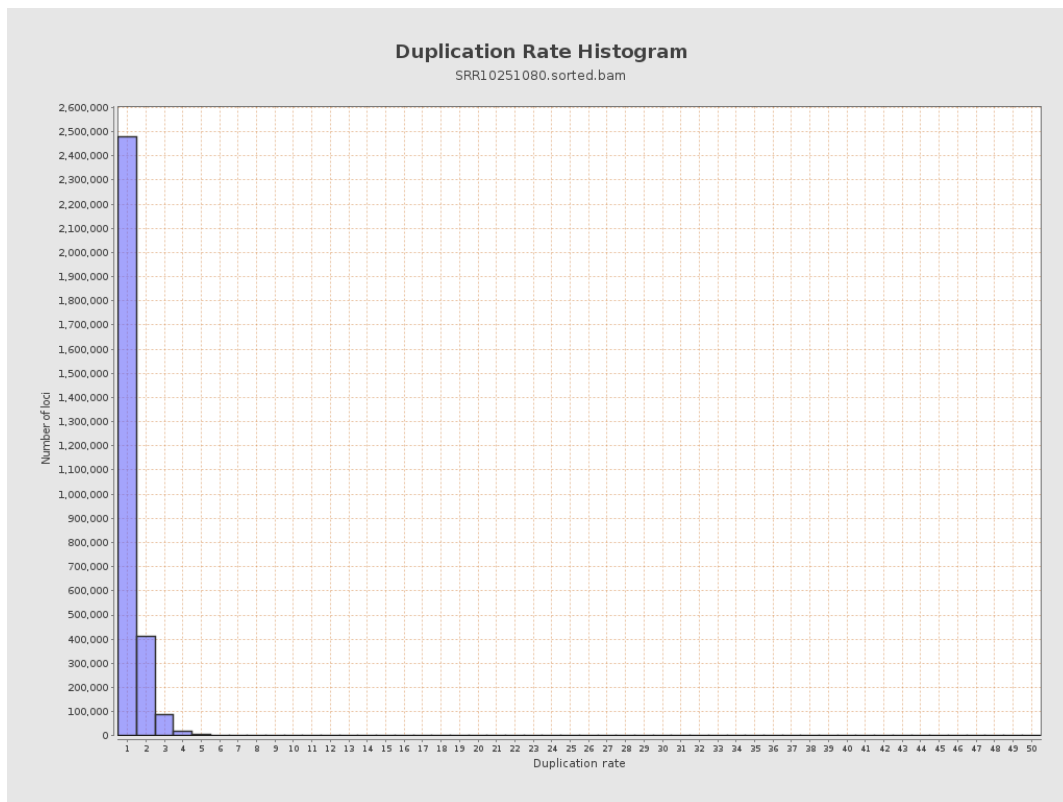
5. Results : Coverage Histogram (0-50X)



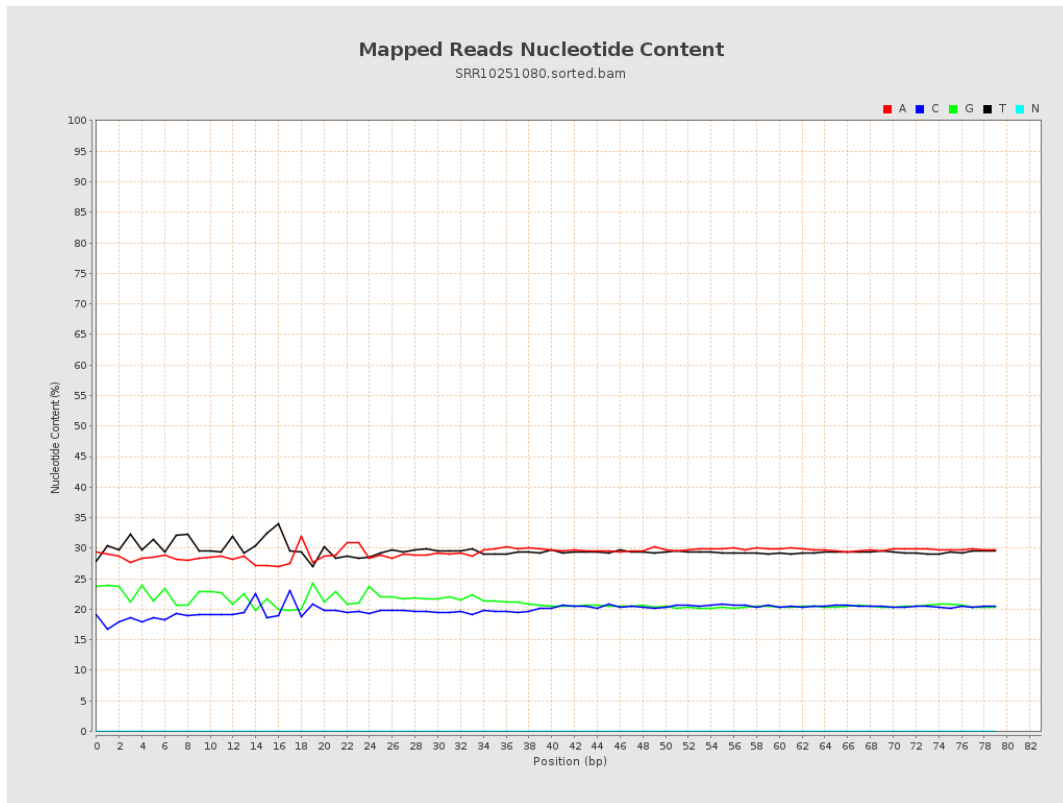
6. Results : Genome Fraction Coverage



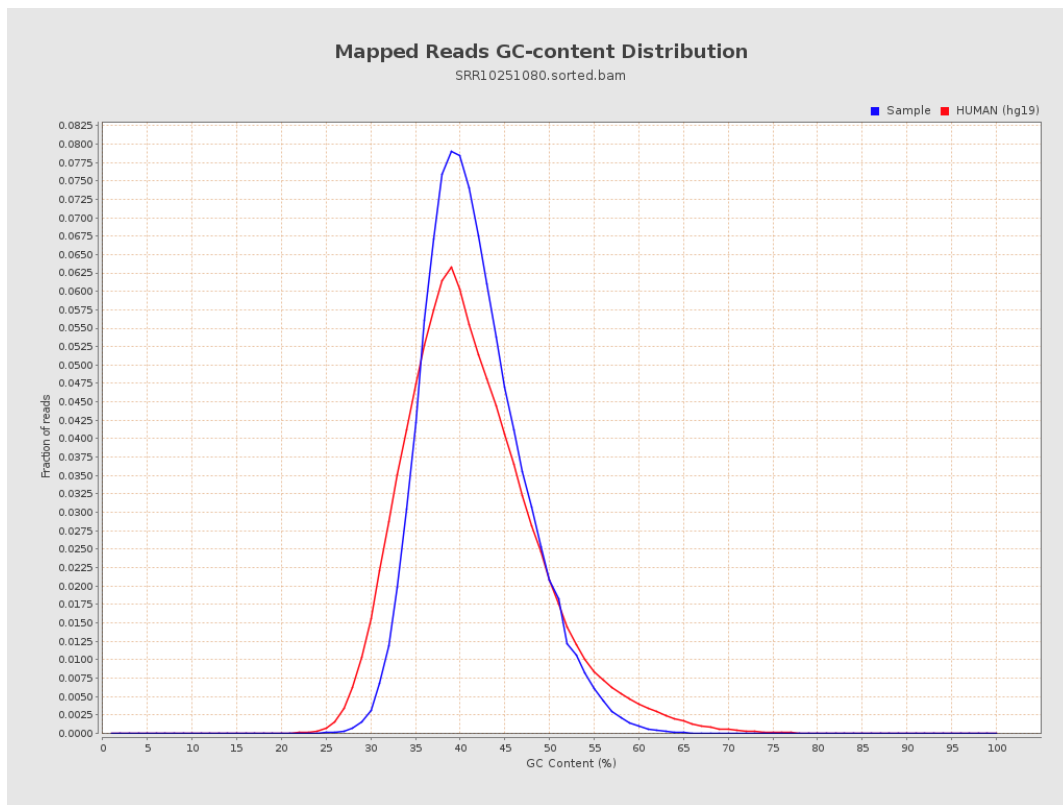
7. Results : Duplication Rate Histogram



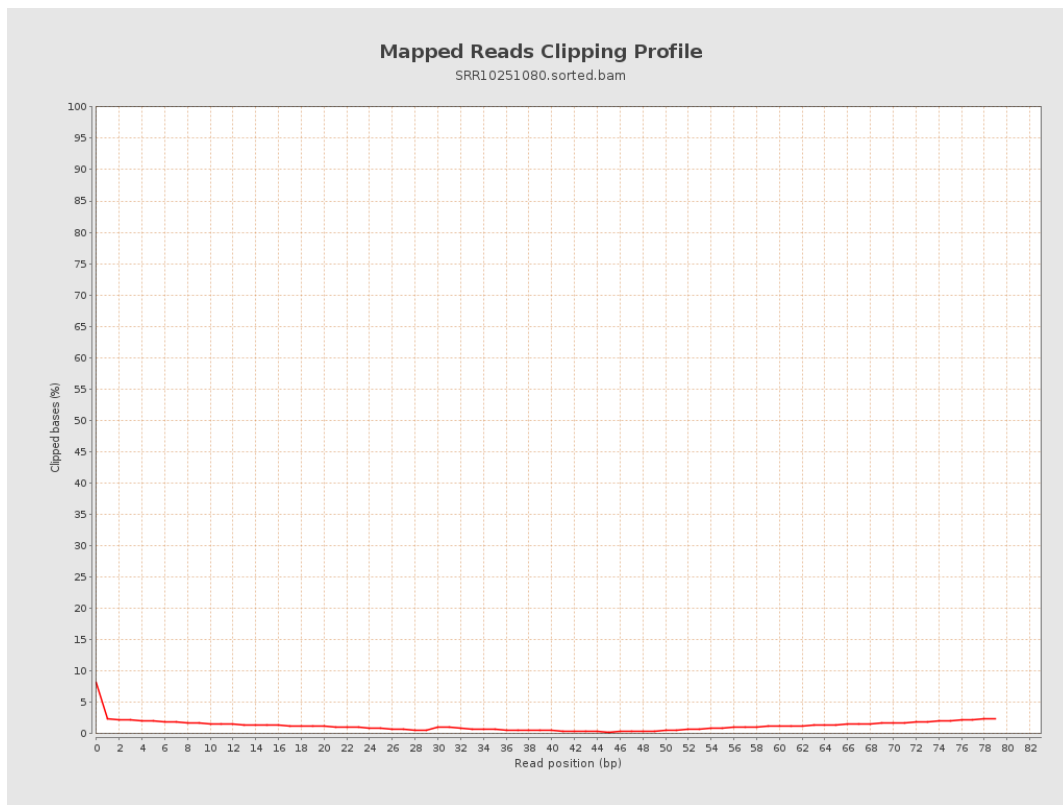
8. Results : Mapped Reads Nucleotide Content



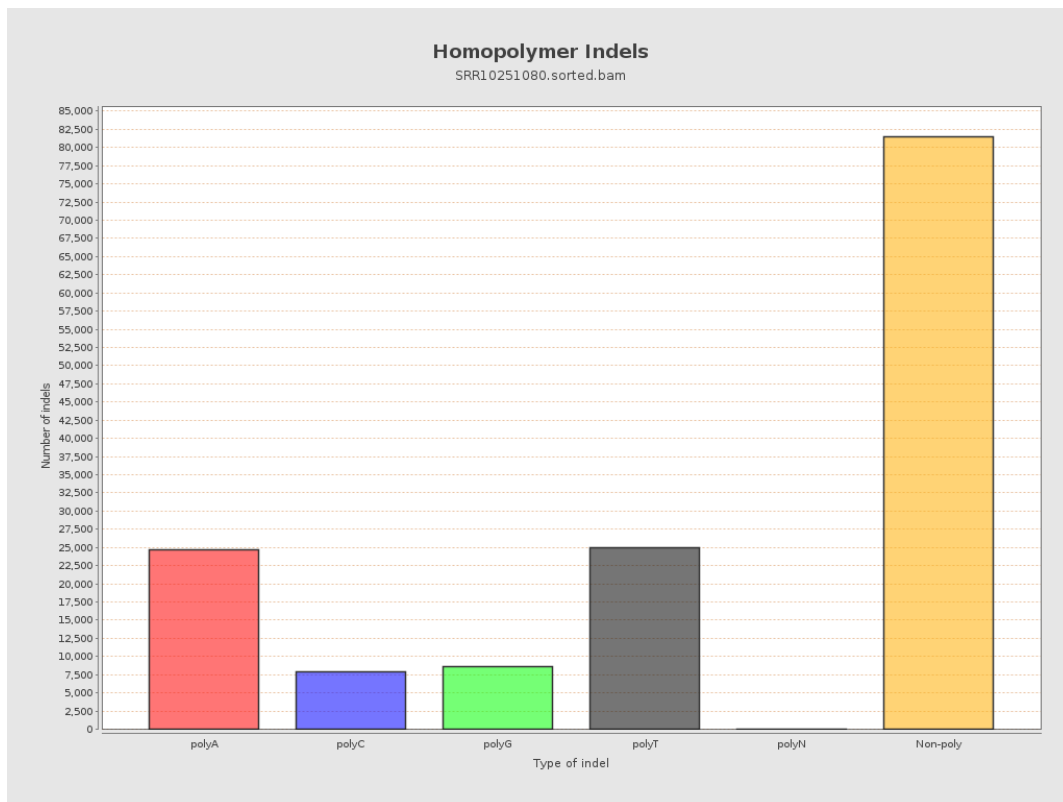
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

