

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 03:44:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081229.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_SRR3081229 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081229.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 03:44:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081229.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,390,511
Mapped reads	2,119,901 / 88.68%
Unmapped reads	270,610 / 11.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,318 / 1.1%
Read min/max/mean length	30 / 76 / 76.38
Duplicated reads (estimated)	107,905 / 4.51%
Duplication rate	4.28%
Clipped reads	1,127,991 / 47.19%

2.2. ACGT Content

Number/percentage of A's	39,494,696 / 28.55%
Number/percentage of C's	26,983,908 / 19.5%
Number/percentage of T's	42,125,872 / 30.45%
Number/percentage of G's	29,729,668 / 21.49%
Number/percentage of N's	17,318 / 0.01%
GC Percentage	40.99%

2.3. Coverage

Mean	0.0447

Standard Deviation	0.3333
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2.4. Mapping Quality

Mean Mapping Quality	45.13
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2.5. Mismatches and indels

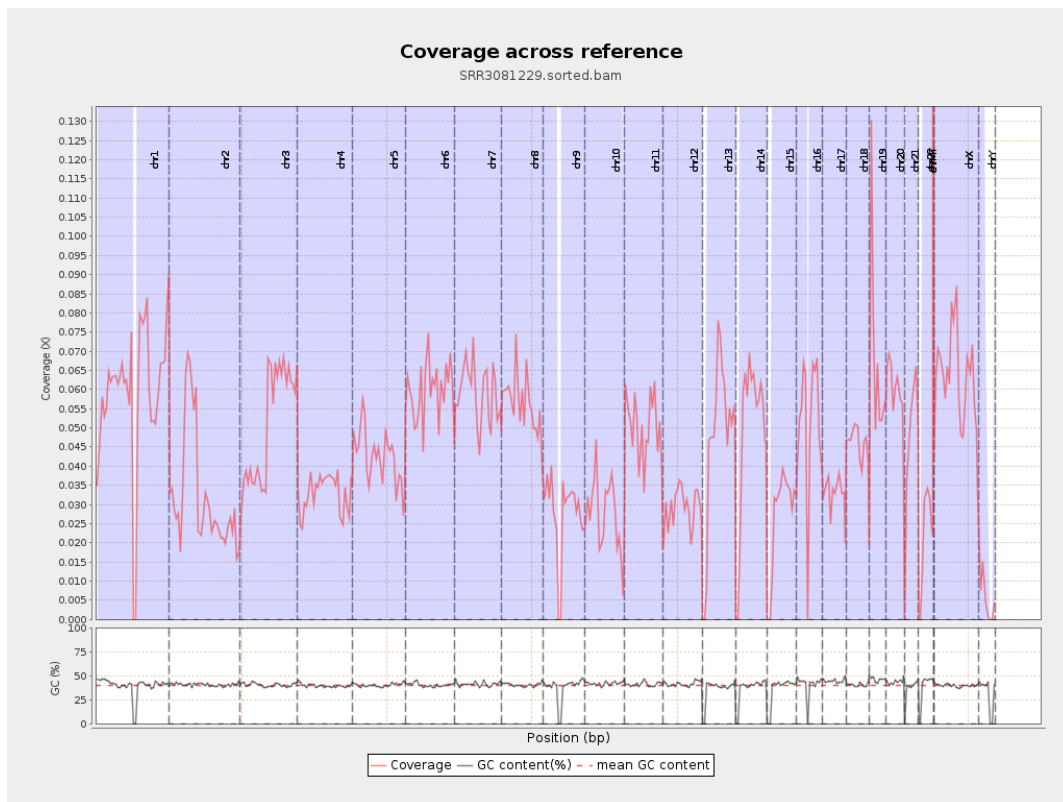
General error rate	0.91%
Mismatches	1,235,182
Insertions	10,386
Mapped reads with at least one insertion	0.49%
Deletions	31,375
Mapped reads with at least one deletion	1.46%
Homopolymer indels	47.53%

2.6. Chromosome stats

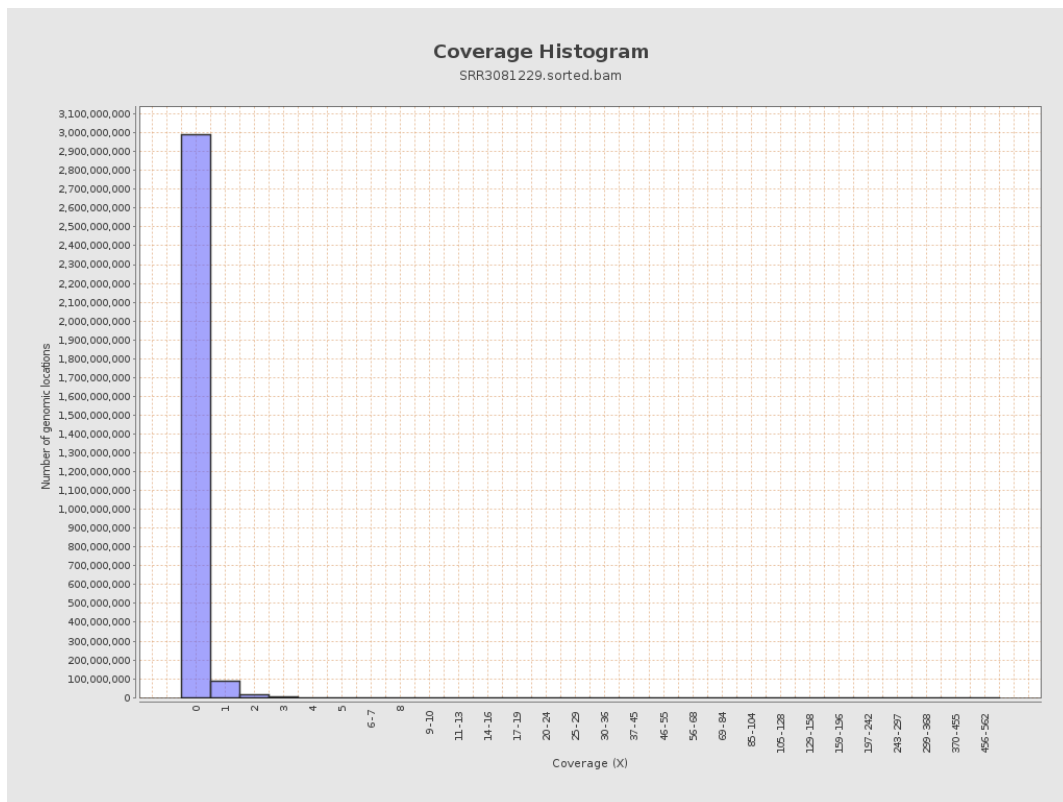
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	14698717	0.059	0.543
chr2	243199373	7928264	0.0326	0.3526
chr3	198022430	9896981	0.05	0.2787
chr4	191154276	6313323	0.033	0.2261
chr5	180915260	7719350	0.0427	0.2555
chr6	171115067	10211114	0.0597	0.3299
chr7	159138663	9410194	0.0591	0.4724

chr8	146364022	8265204	0.0565	0.4
chr9	141213431	3918864	0.0278	0.2518
chr10	135534747	3736304	0.0276	0.2784
chr11	135006516	6668344	0.0494	0.311
chr12	133851895	3913117	0.0292	0.2115
chr13	115169878	5460351	0.0474	0.2714
chr14	107349540	5279323	0.0492	0.2792
chr15	102531392	2782254	0.0271	0.2121
chr16	90354753	4647537	0.0514	0.2871
chr17	81195210	2671471	0.0329	0.2324
chr18	78077248	3605841	0.0462	0.4026
chr19	59128983	3931814	0.0665	0.4447
chr20	63025520	3798219	0.0603	0.3086
chr21	48129895	2279839	0.0474	0.2778
chr22	51304566	1082837	0.0211	0.178
chrMT	16571	79664	4.8074	3.7283
chrX	155270560	9772271	0.0629	0.3249
chrY	59373566	332376	0.0056	0.1046

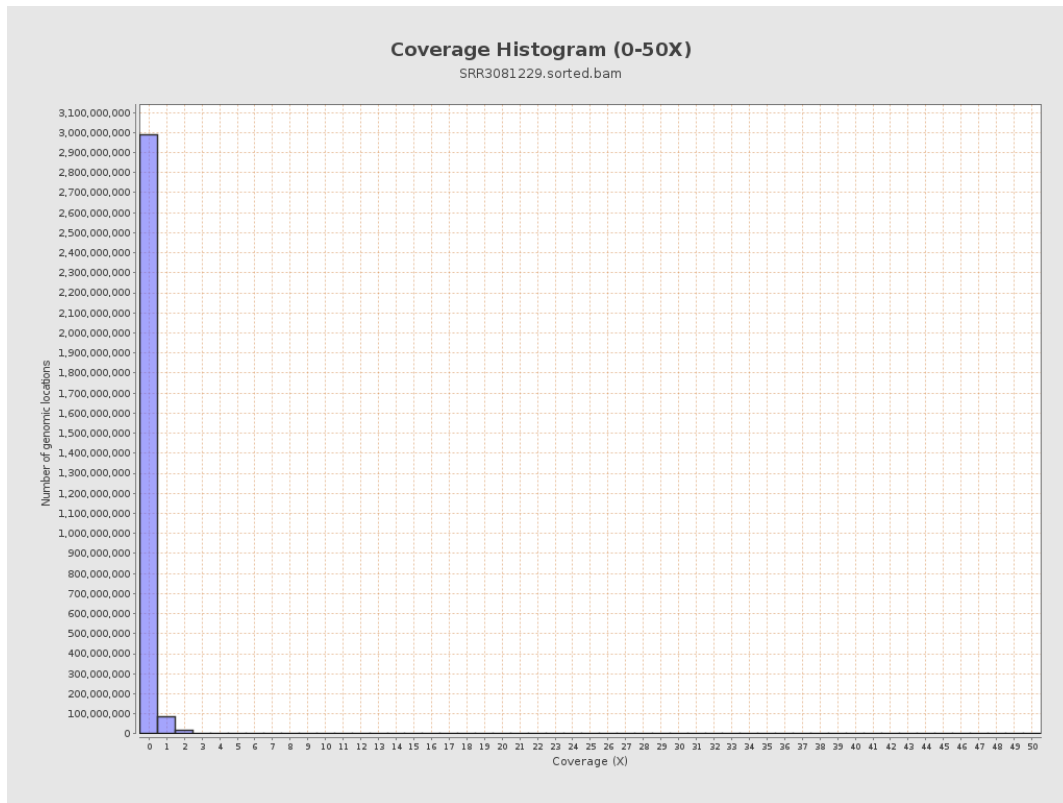
3. Results : Coverage across reference



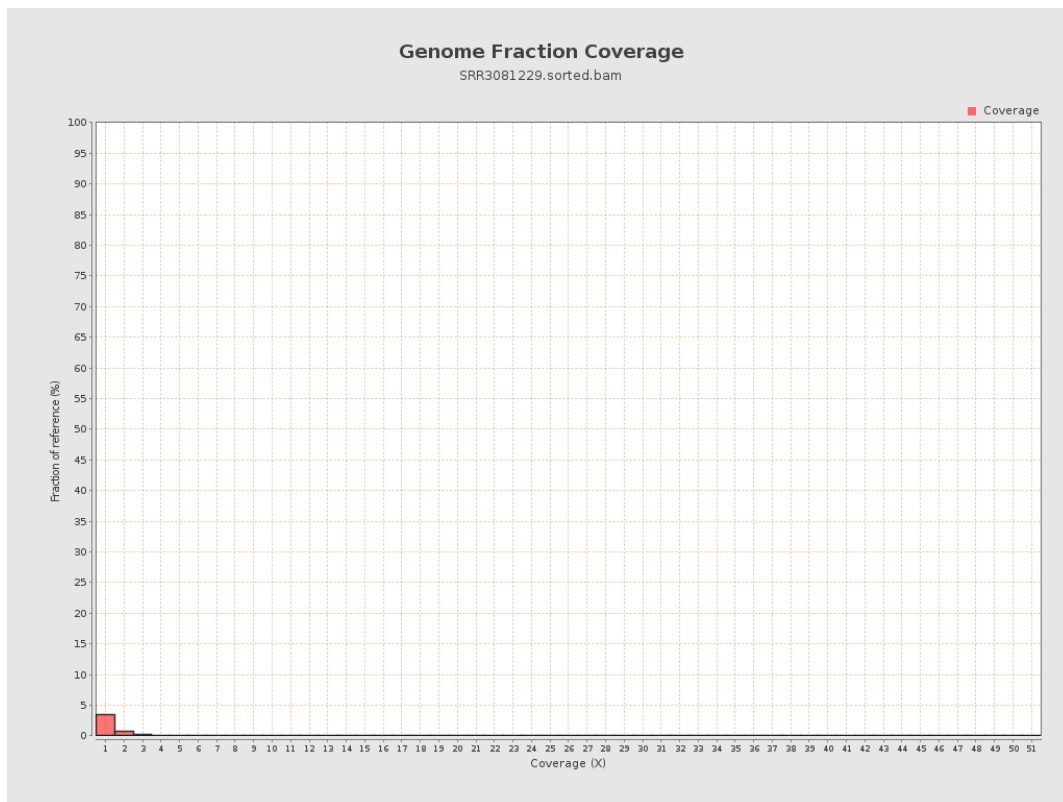
4. Results : Coverage Histogram



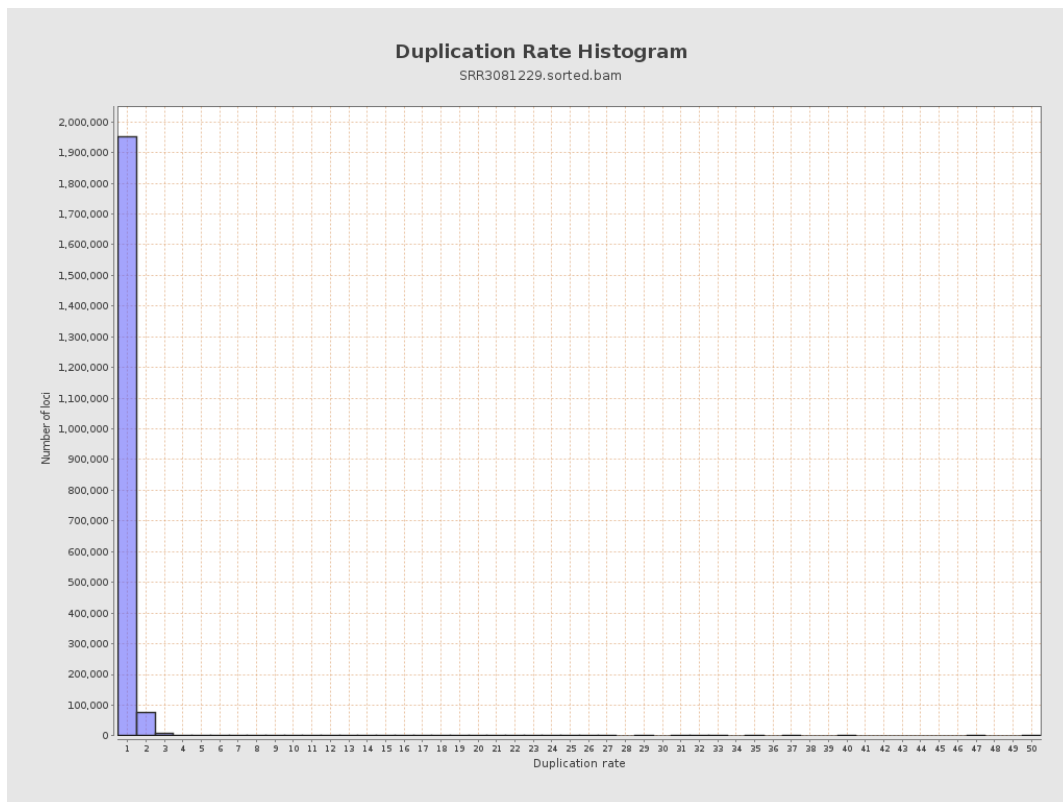
5. Results : Coverage Histogram (0-50X)



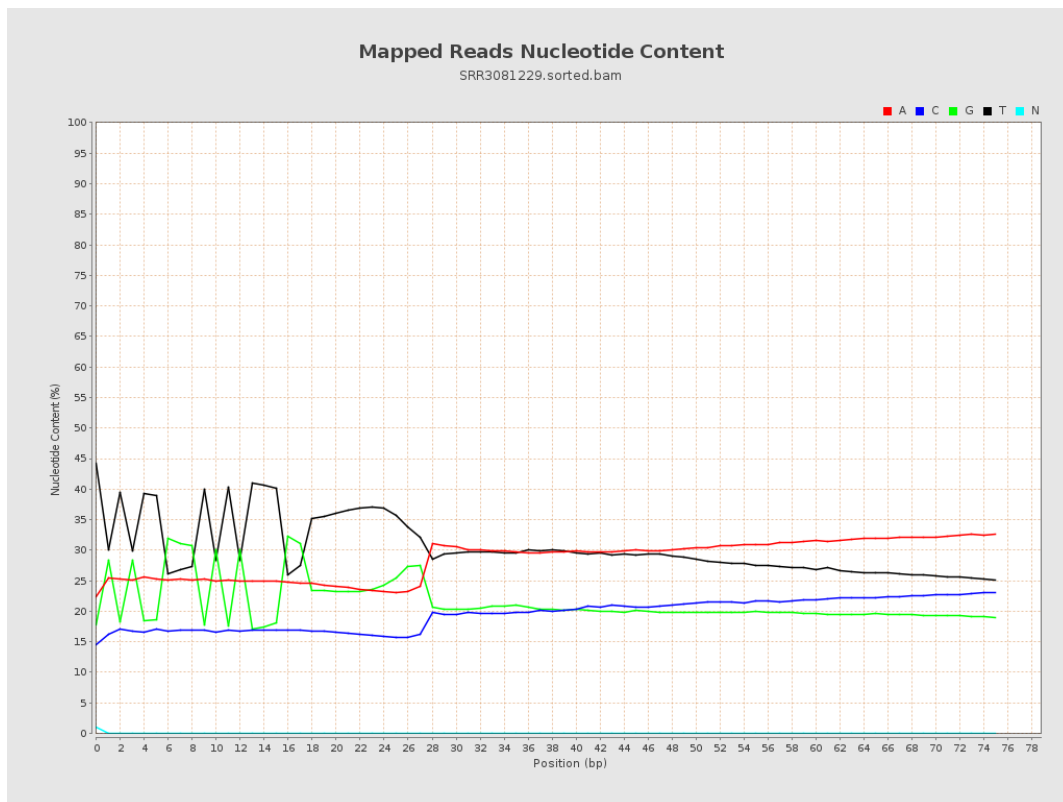
6. Results : Genome Fraction Coverage



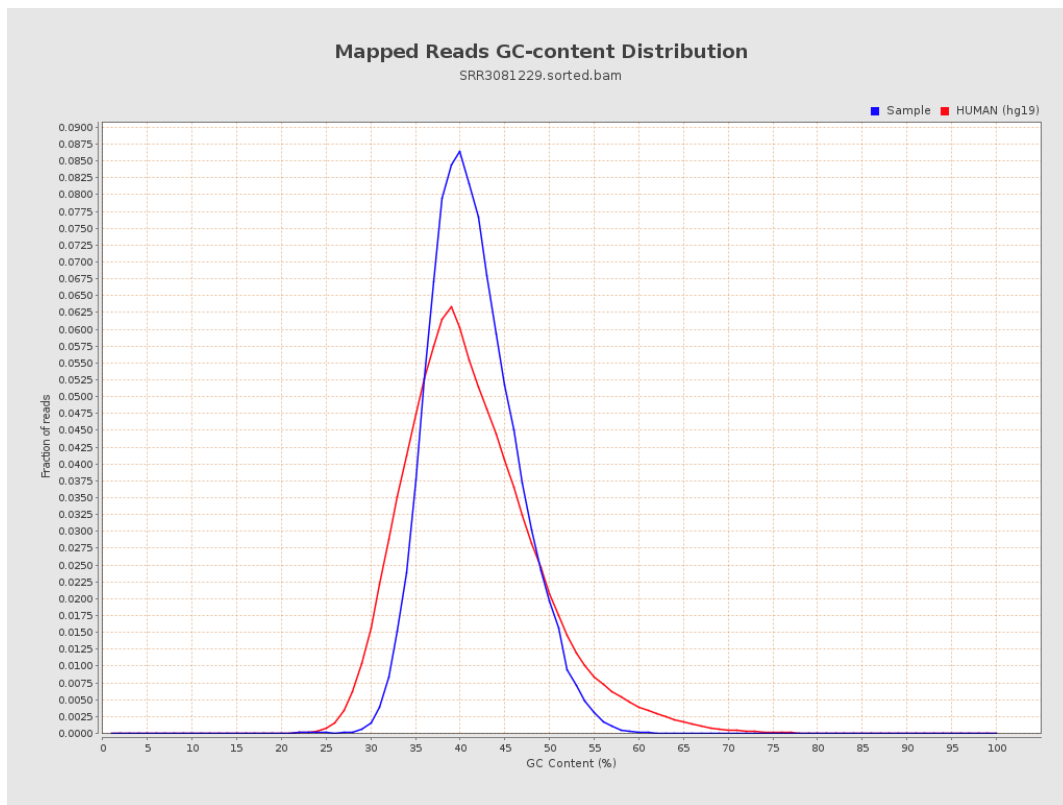
7. Results : Duplication Rate Histogram



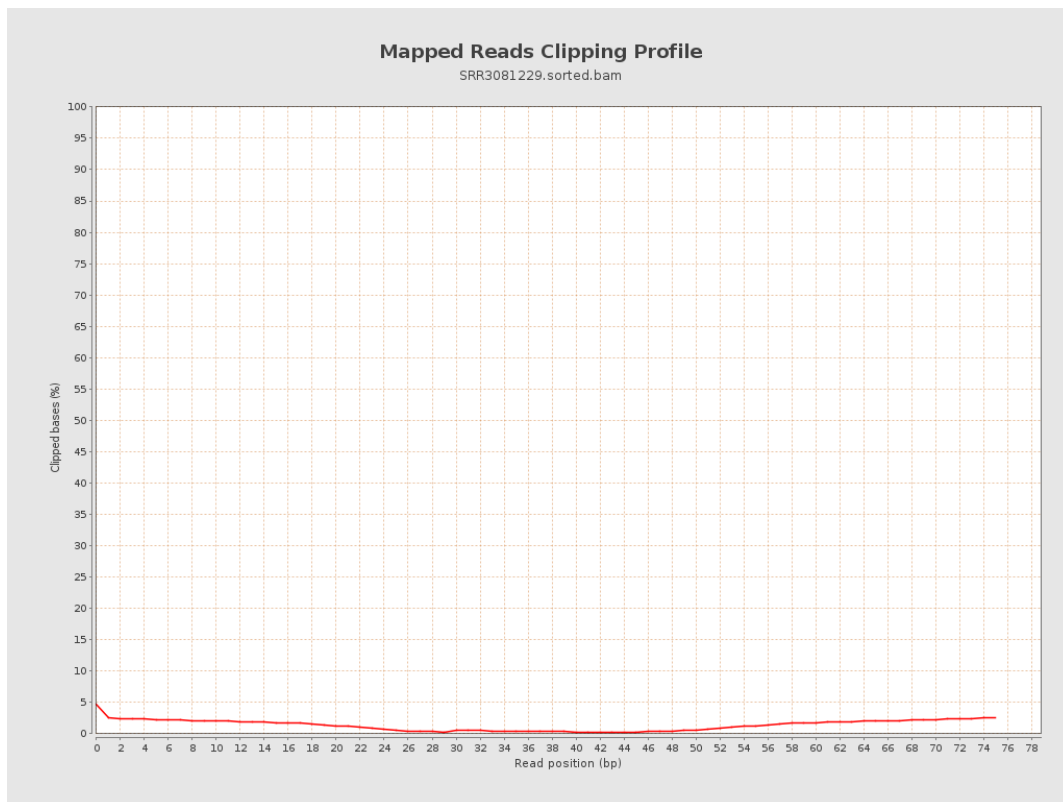
8. Results : Mapped Reads Nucleotide Content



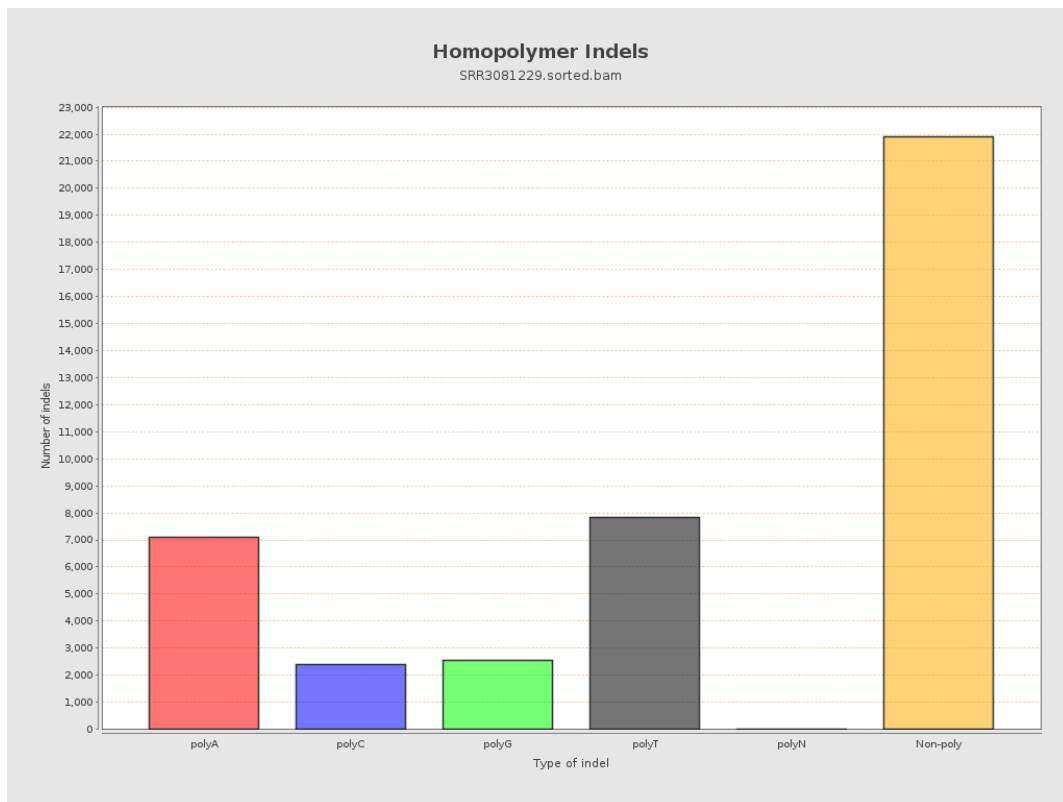
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

