

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 02:02:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2971324.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_SRR2971324 /home/luna/Desktop/database/homo_hsa/hsa.fa SRR2971324.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 02:02:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2971324.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	88,952,985
Mapped reads	67,167,897 / 75.51%
Unmapped reads	21,785,088 / 24.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	9,917,200 / 11.15%
Duplication rate	10.8%
Clipped reads	5,506,105 / 6.19%

2.2. ACGT Content

Number/percentage of A's	768,289,787 / 28.92%
Number/percentage of C's	563,775,012 / 21.22%
Number/percentage of T's	760,529,498 / 28.63%
Number/percentage of G's	563,474,858 / 21.21%
Number/percentage of N's	139,228 / 0.01%
GC Percentage	42.44%

2.3. Coverage

Mean	0.8581
Standard Deviation	7.3508

2.4. Mapping Quality

Mean Mapping Quality	39.07
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2.5. Mismatches and indels

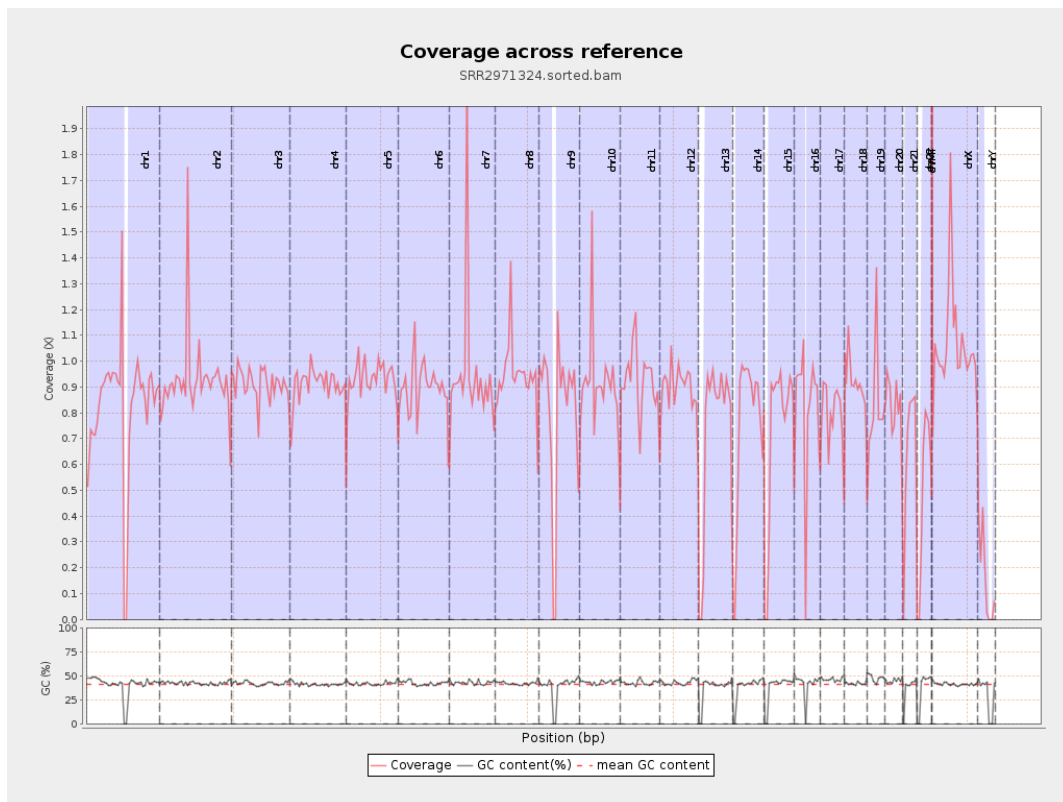
General error rate	0.33%
Mismatches	8,586,349
Insertions	90,002
Mapped reads with at least one insertion	0.13%
Deletions	191,183
Mapped reads with at least one deletion	0.28%
Homopolymer indels	39.29%

2.6. Chromosome stats

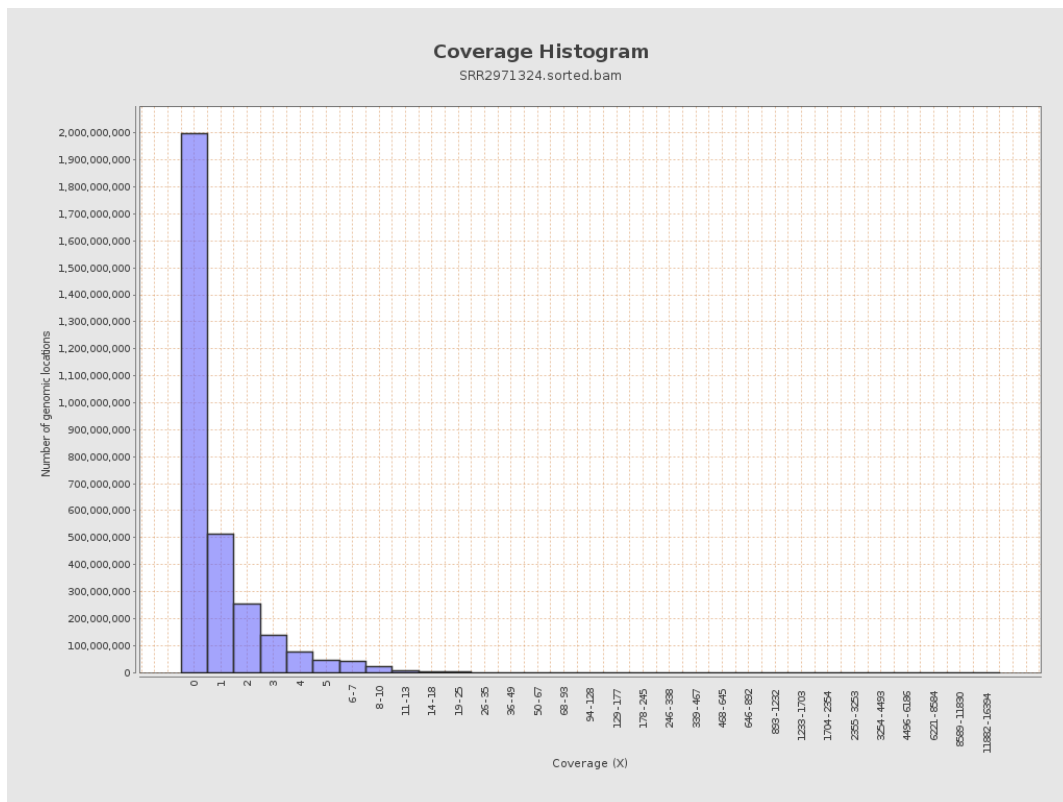
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	206276363	0.8276	12.3334
chr2	243199373	225481787	0.9271	7.5126
chr3	198022430	180758326	0.9128	2.1559
chr4	191154276	174184643	0.9112	2.1698
chr5	180915260	167884103	0.928	2.4156
chr6	171115067	154646875	0.9038	3.4023
chr7	159138663	150251157	0.9442	14.2025
chr8	146364022	138269237	0.9447	5.6261

chr9	141213431	111097524	0.7867	8.0605
chr10	135534747	124634555	0.9196	6.4798
chr11	135006516	123822742	0.9172	9.249
chr12	133851895	120174554	0.8978	2.7573
chr13	115169878	84664177	0.7351	1.6361
chr14	107349540	80541928	0.7503	5.8101
chr15	102531392	73947493	0.7212	1.8879
chr16	90354753	72199068	0.7991	4.1406
chr17	81195210	63832093	0.7862	3.5867
chr18	78077248	71564058	0.9166	17.4577
chr19	59128983	48444075	0.8193	13.1899
chr20	63025520	51913169	0.8237	2.48
chr21	48129895	32116819	0.6673	3.3334
chr22	51304566	25350324	0.4941	2.1911
chrMT	16571	71983	4.3439	5.0669
chrX	155270560	164772522	1.0612	5.2458
chrY	59373566	9551789	0.1609	1.5325

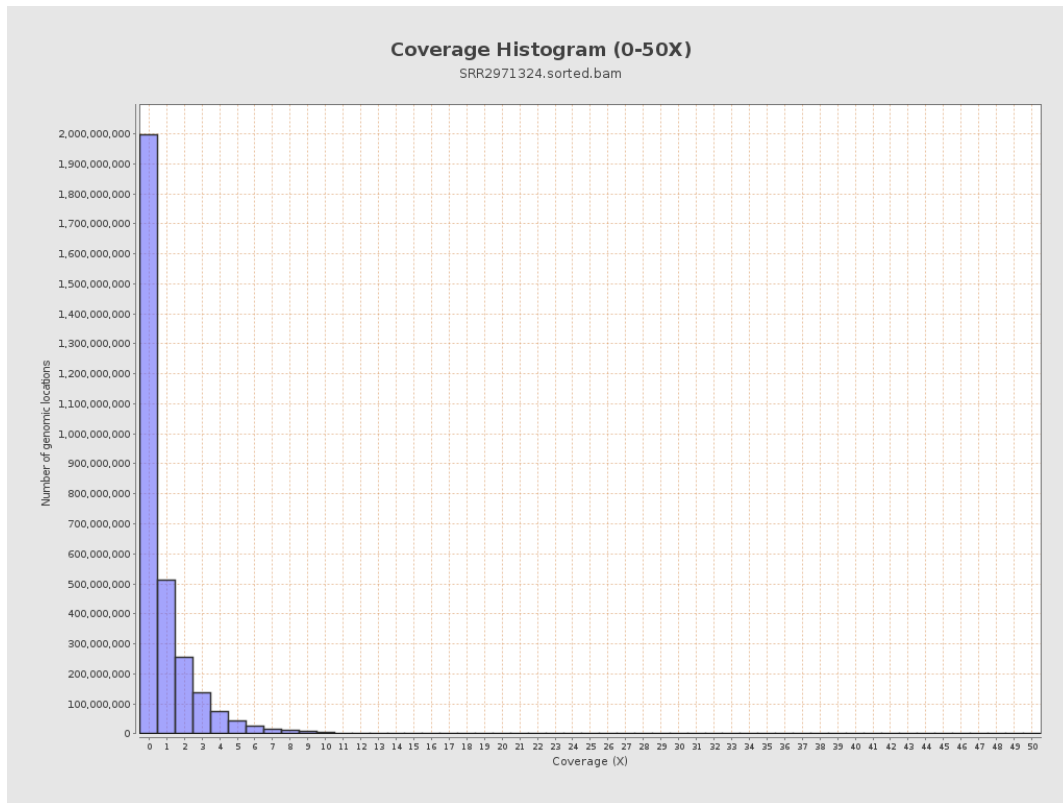
3. Results : Coverage across reference



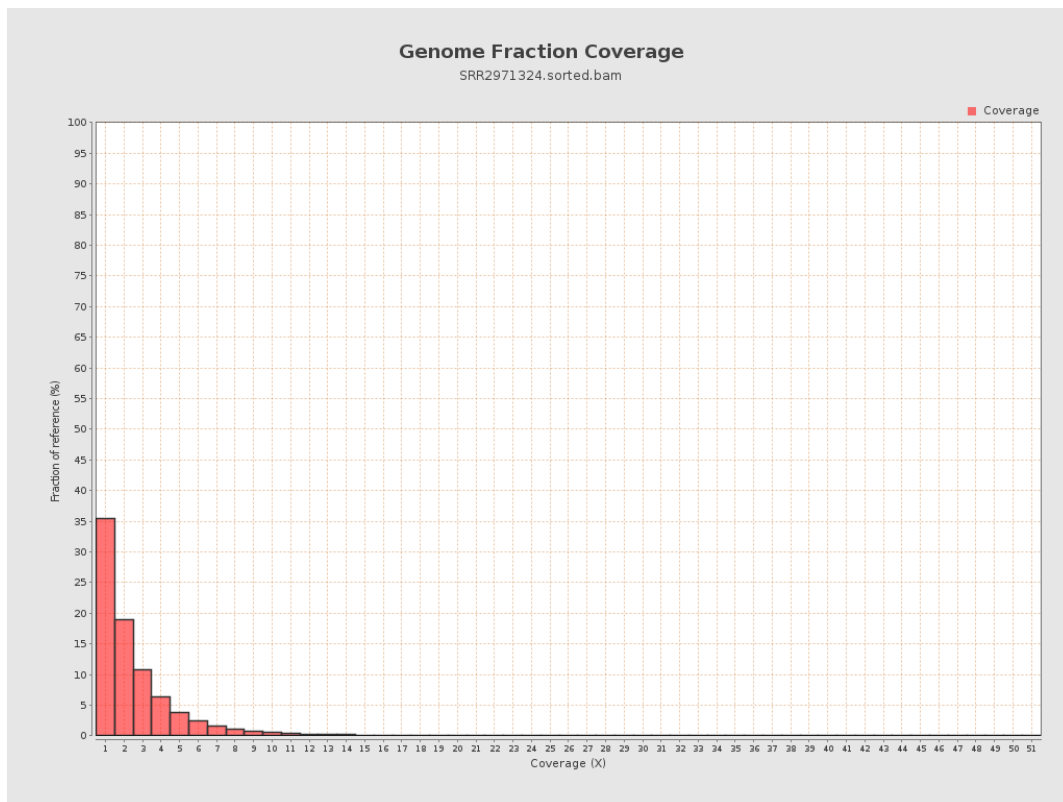
4. Results : Coverage Histogram



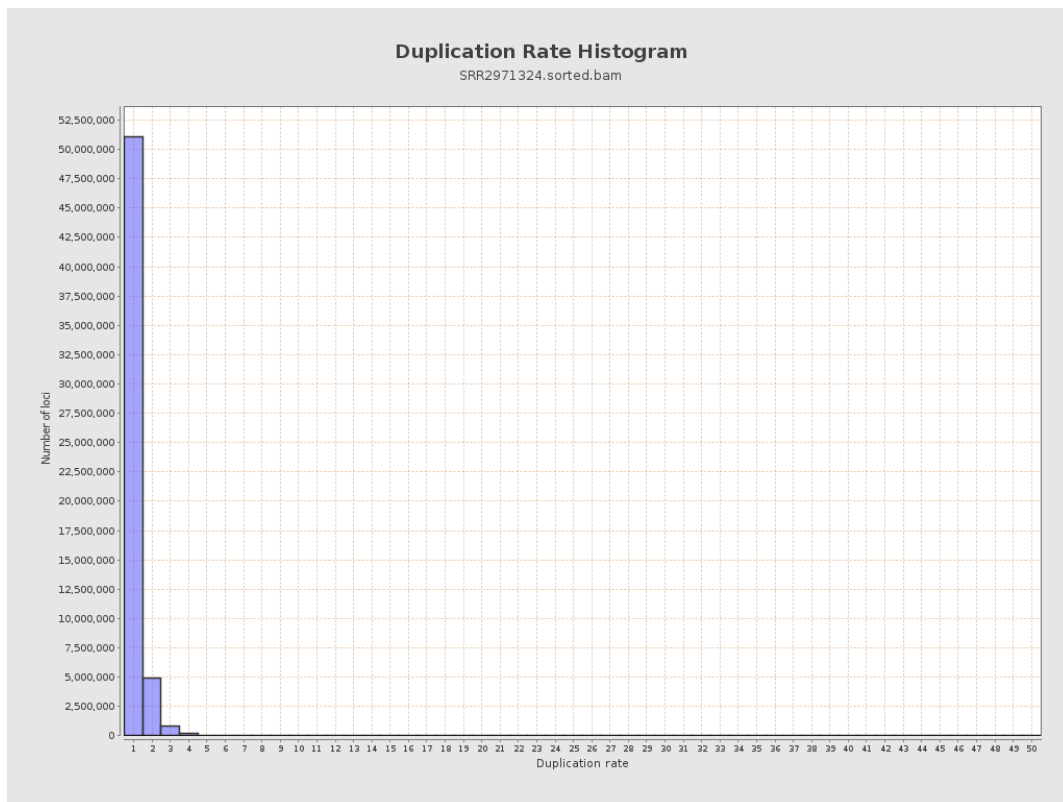
5. Results : Coverage Histogram (0-50X)



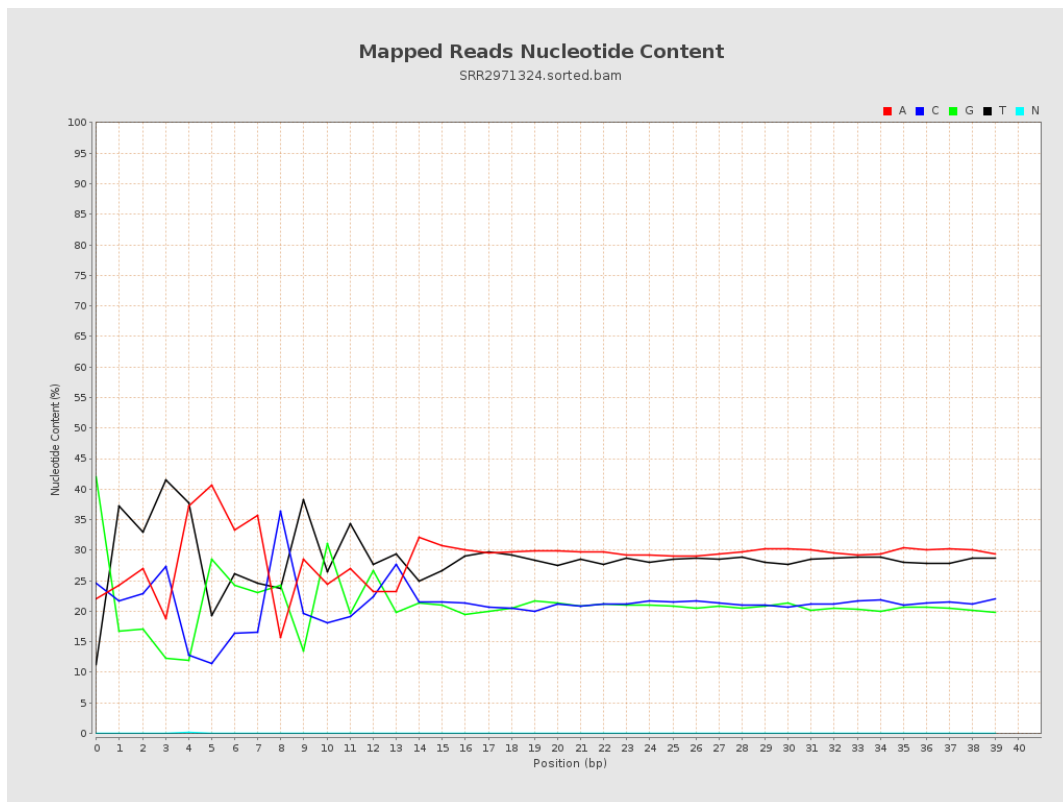
6. Results : Genome Fraction Coverage



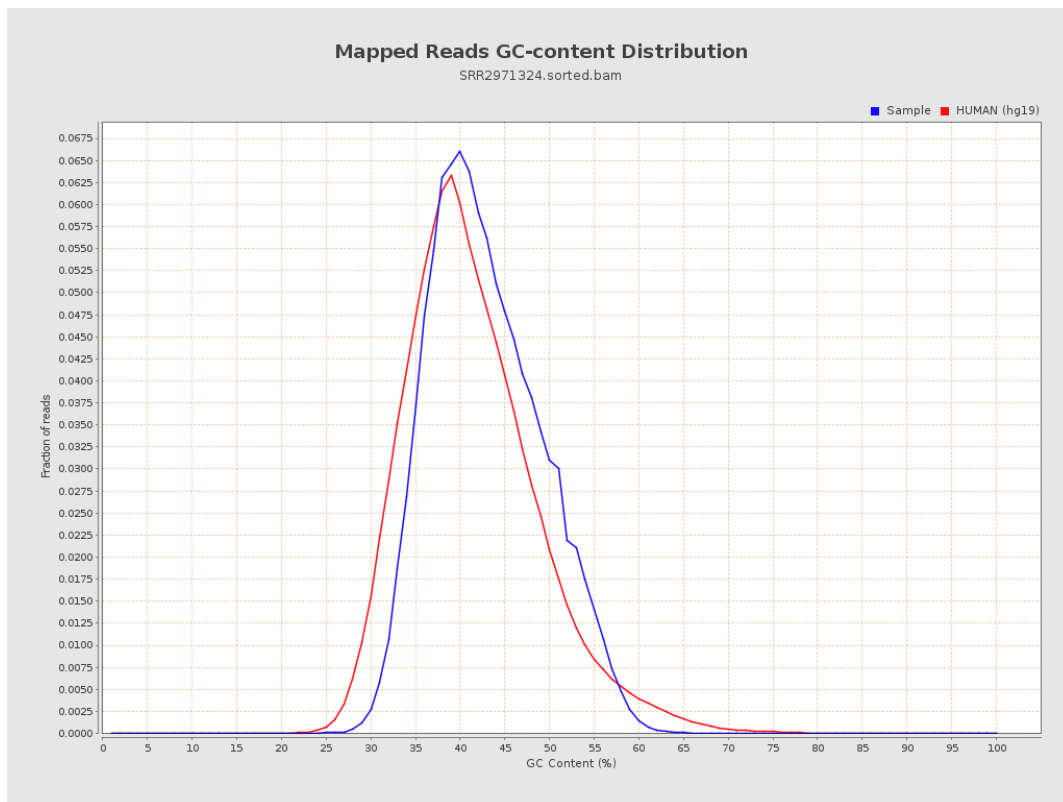
7. Results : Duplication Rate Histogram



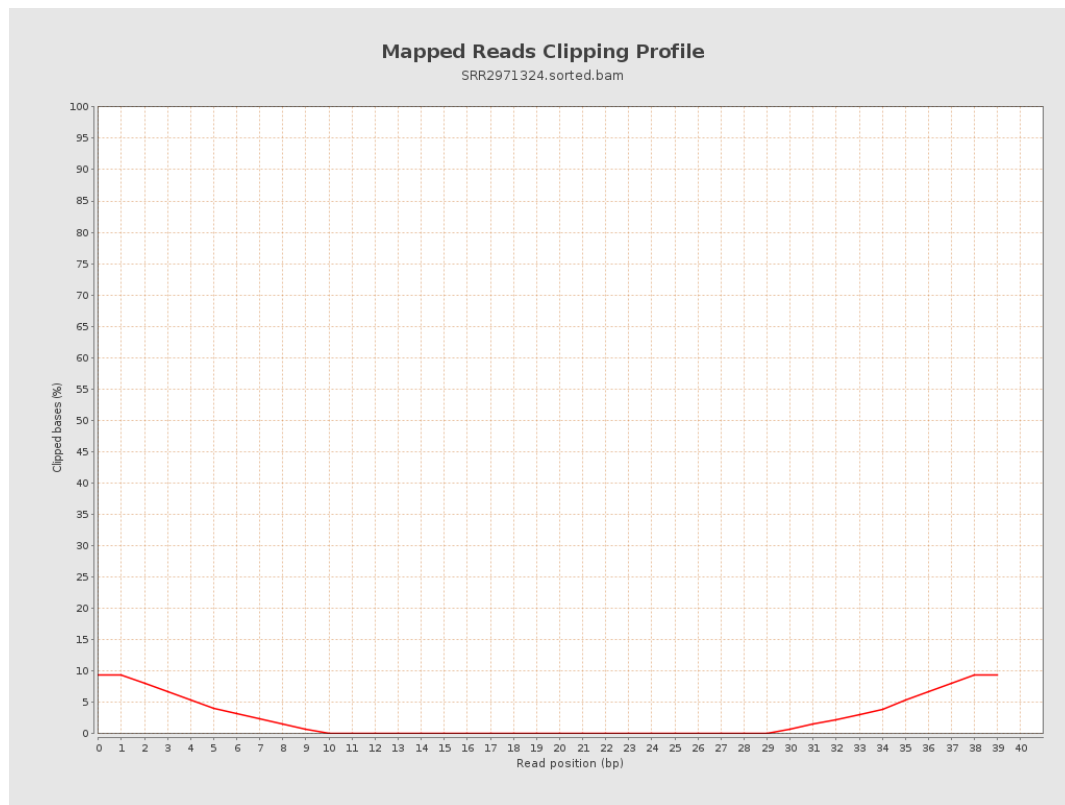
8. Results : Mapped Reads Nucleotide Content



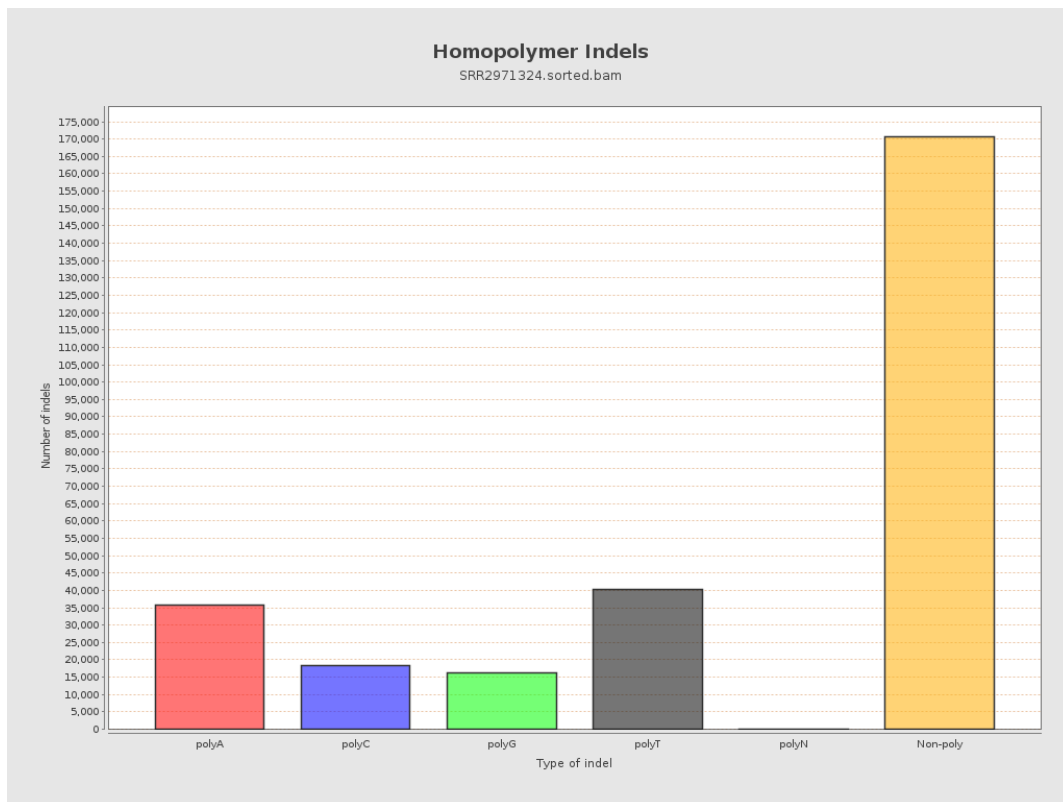
9. Results : Mapped Reads GC-content Distribution



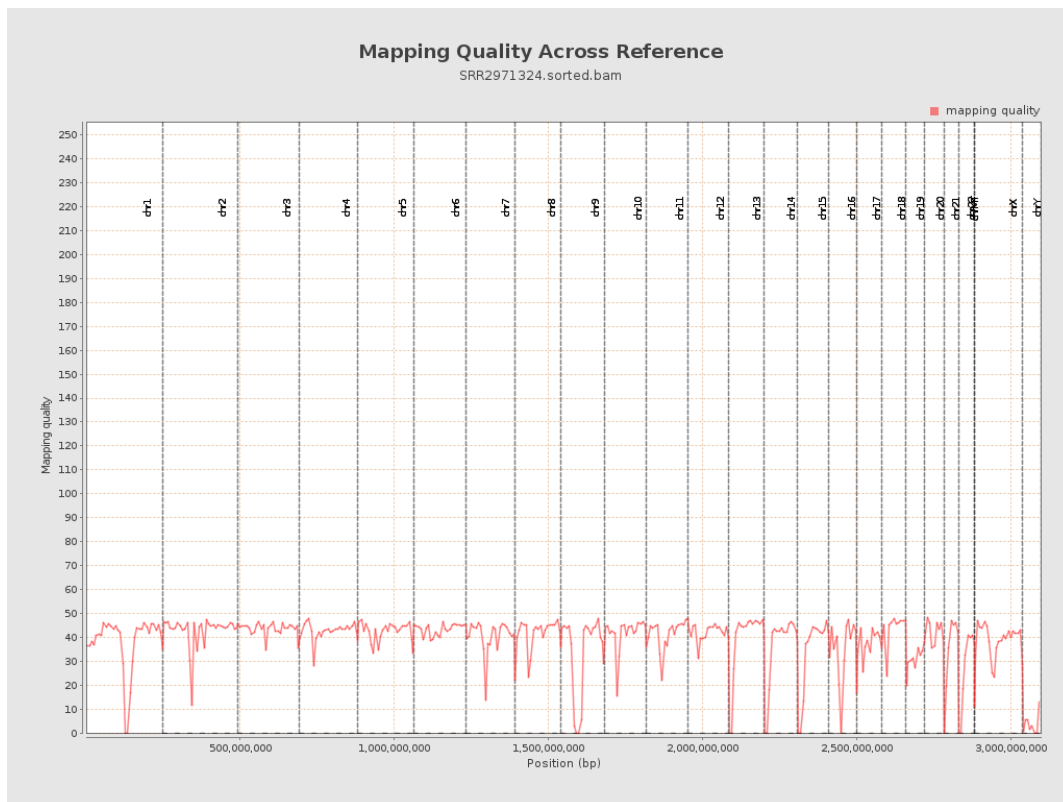
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

