

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 17:56:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2971308.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_SRR2971308 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2971308.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 17:56:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2971308.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,330,949
Mapped reads	6,134,910 / 83.69%
Unmapped reads	1,196,039 / 16.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	340,960 / 4.65%
Duplication rate	4.52%
Clipped reads	647,861 / 8.84%

2.2. ACGT Content

Number/percentage of A's	70,200,505 / 29.05%
Number/percentage of C's	49,243,472 / 20.38%
Number/percentage of T's	71,831,489 / 29.73%
Number/percentage of G's	50,326,398 / 20.83%
Number/percentage of N's	13,470 / 0.01%
GC Percentage	41.21%

2.3. Coverage

Mean	0.0781
Standard Deviation	0.577

2.4. Mapping Quality

Mean Mapping Quality	40.17
----------------------	-------

2.5. Mismatches and indels

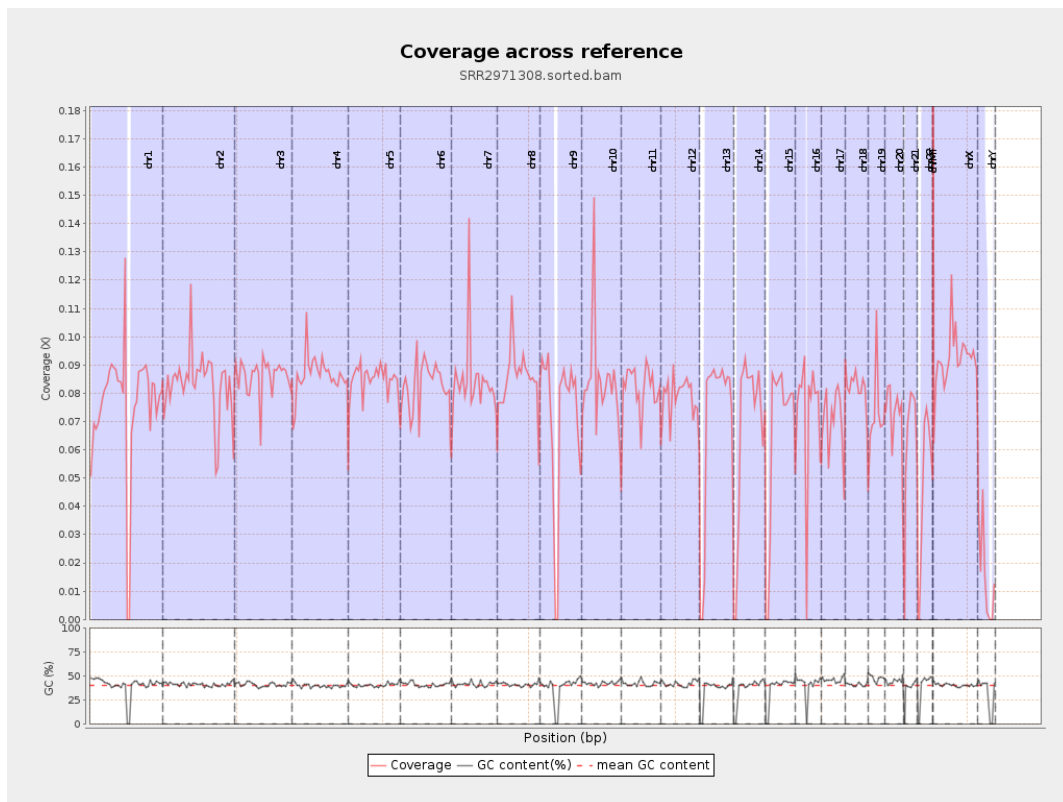
General error rate	0.31%
Mismatches	736,521
Insertions	9,072
Mapped reads with at least one insertion	0.15%
Deletions	19,256
Mapped reads with at least one deletion	0.31%
Homopolymer indels	39.36%

2.6. Chromosome stats

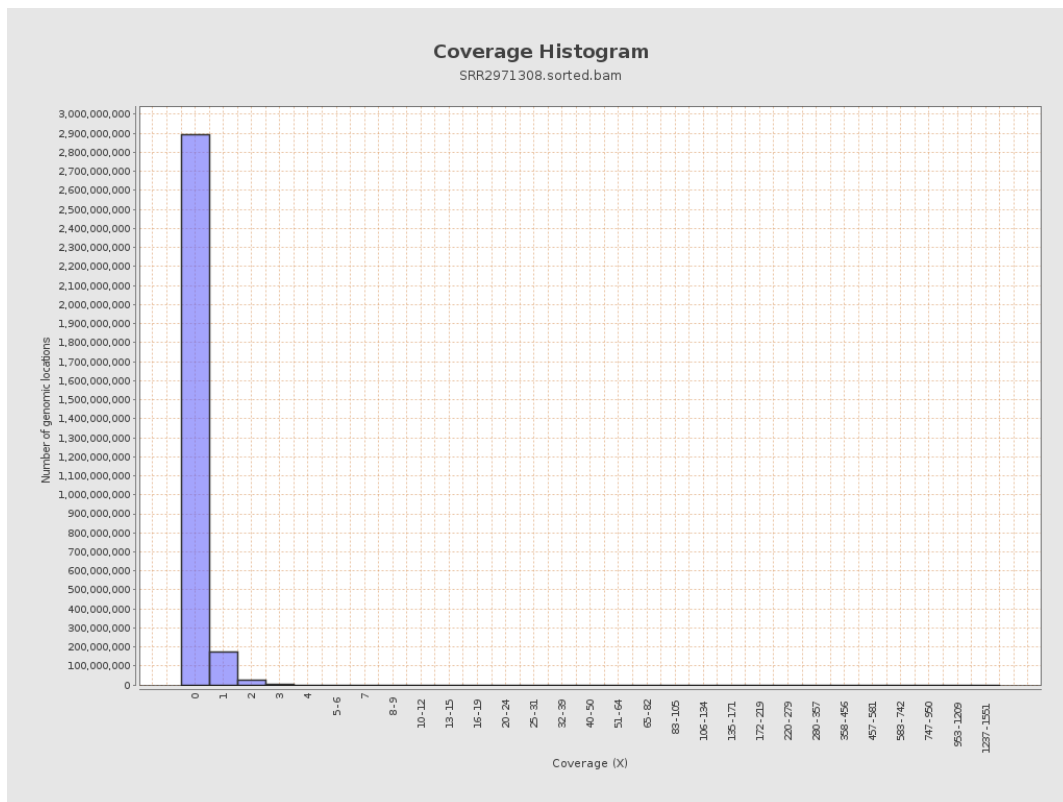
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	18935021	0.076	1.0878
chr2	243199373	20150503	0.0829	0.5004
chr3	198022430	17035069	0.086	0.3396
chr4	191154276	16531747	0.0865	0.3694
chr5	180915260	15296572	0.0846	0.3398
chr6	171115067	14219703	0.0831	0.3859
chr7	159138663	13388196	0.0841	0.826
chr8	146364022	12483061	0.0853	0.8612

chr9	141213431	10156025	0.0719	0.5128
chr10	135534747	11385146	0.084	0.6291
chr11	135006516	11010765	0.0816	0.4551
chr12	133851895	10519740	0.0786	0.337
chr13	115169878	8087722	0.0702	0.3015
chr14	107349540	7348067	0.0684	0.3794
chr15	102531392	6753130	0.0659	0.2932
chr16	90354753	6468051	0.0716	0.3863
chr17	81195210	5780960	0.0712	0.353
chr18	78077248	6441465	0.0825	0.9018
chr19	59128983	4343180	0.0735	1.0043
chr20	63025520	4604291	0.0731	0.3258
chr21	48129895	3039169	0.0631	0.3495
chr22	51304566	2429268	0.0473	0.2581
chrMT	16571	8152	0.4919	0.8718
chrX	155270560	14307848	0.0921	0.4185
chrY	59373566	916173	0.0154	0.2316

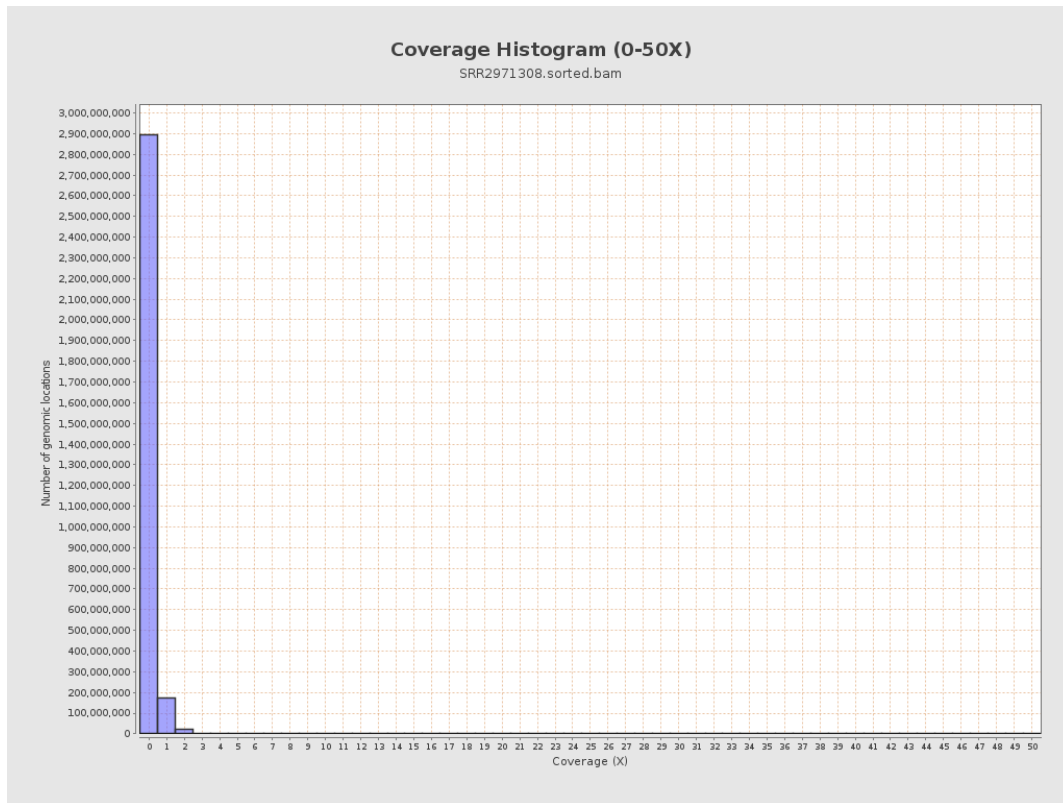
3. Results : Coverage across reference



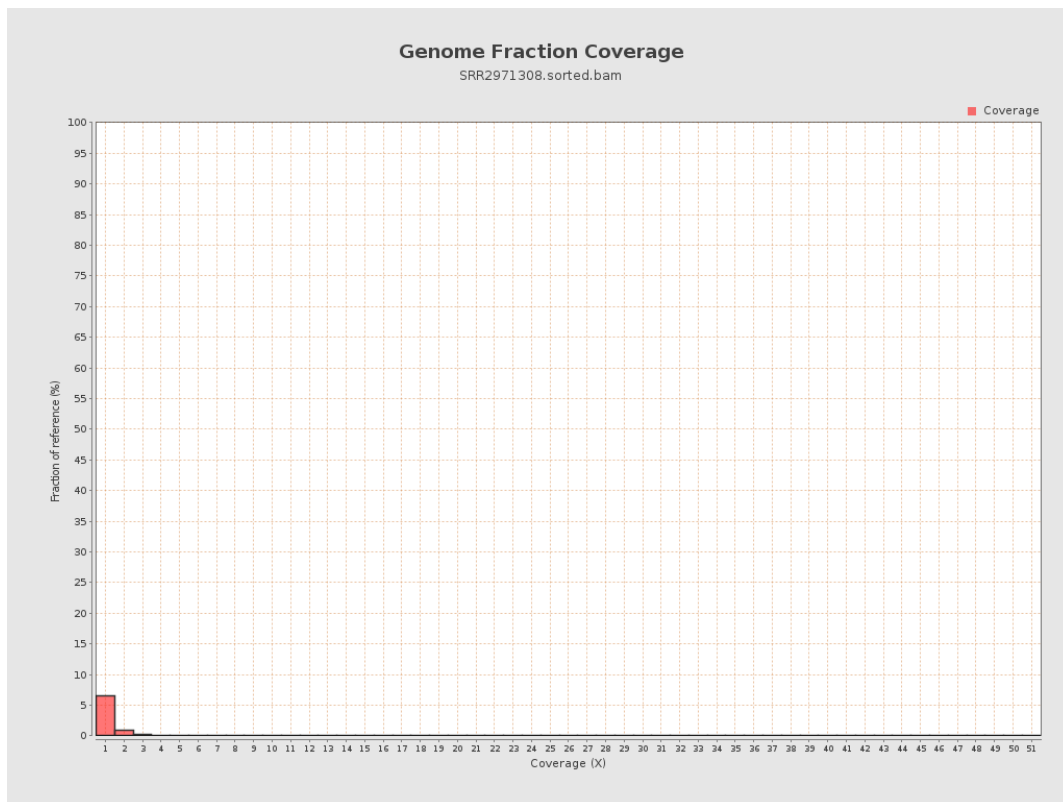
4. Results : Coverage Histogram



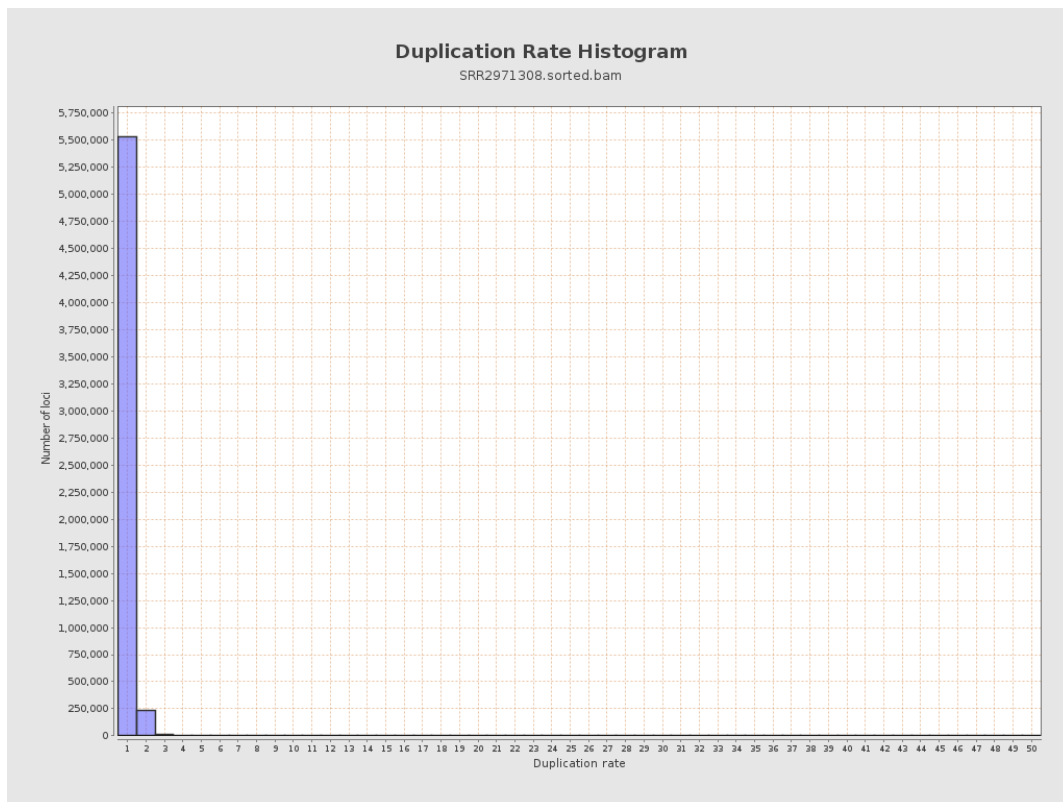
5. Results : Coverage Histogram (0-50X)



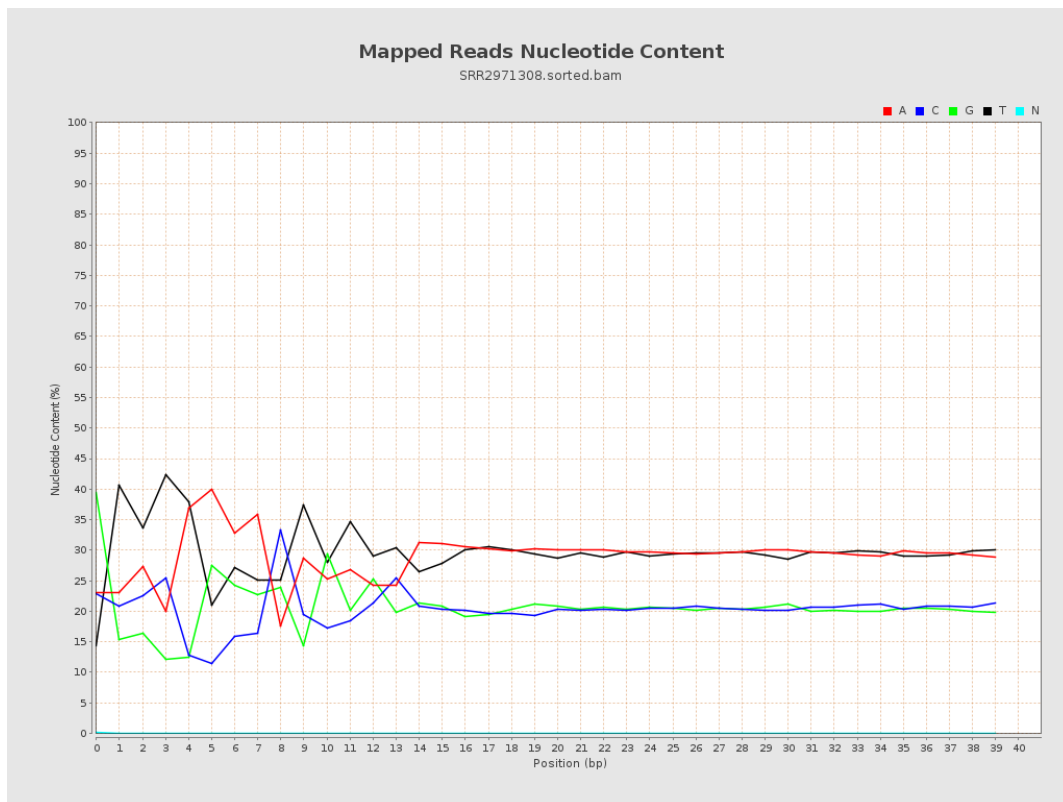
6. Results : Genome Fraction Coverage



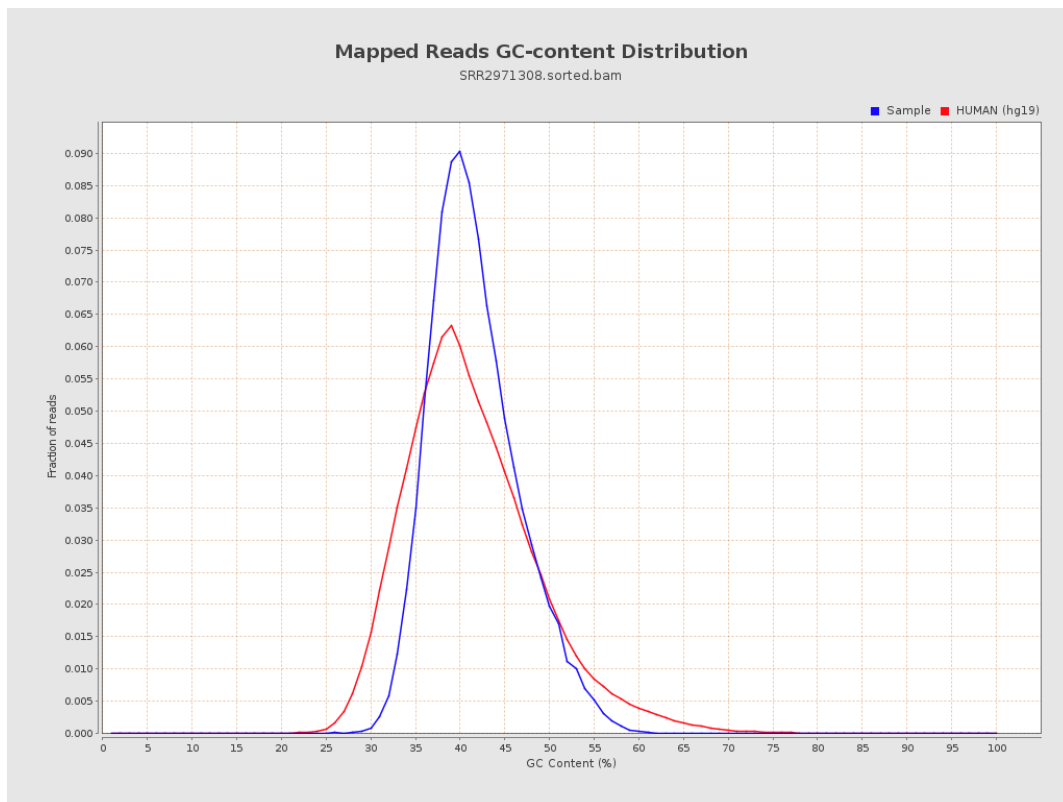
7. Results : Duplication Rate Histogram



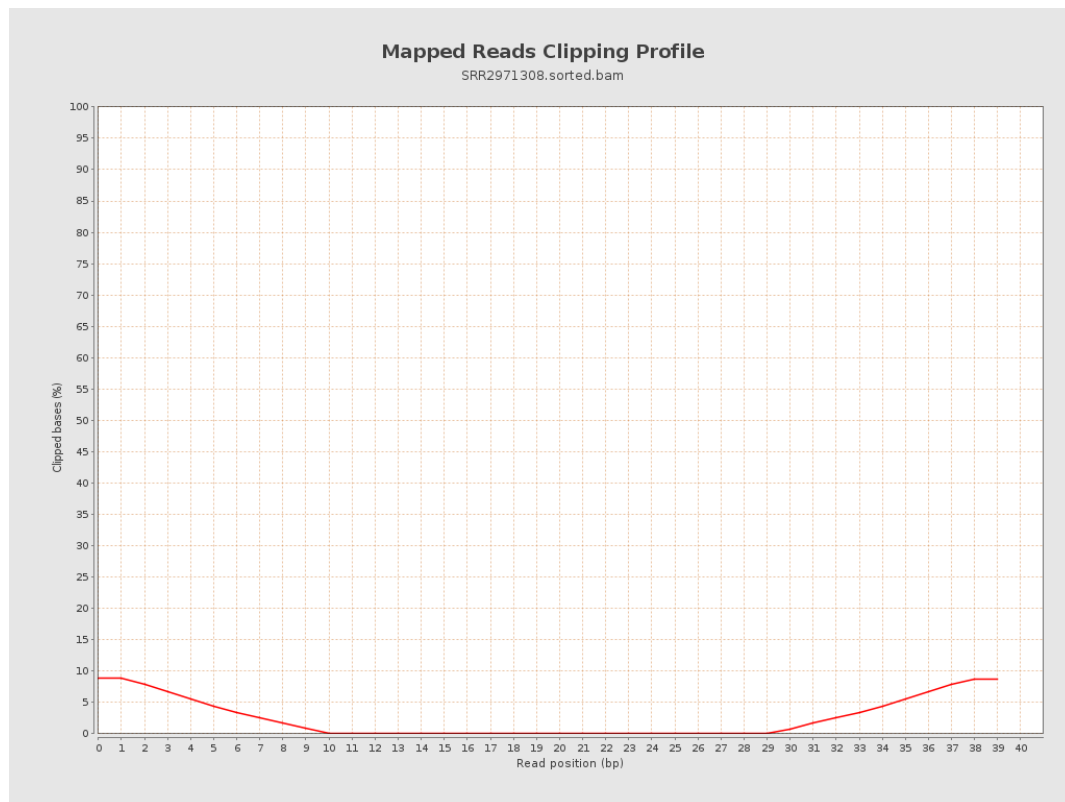
8. Results : Mapped Reads Nucleotide Content



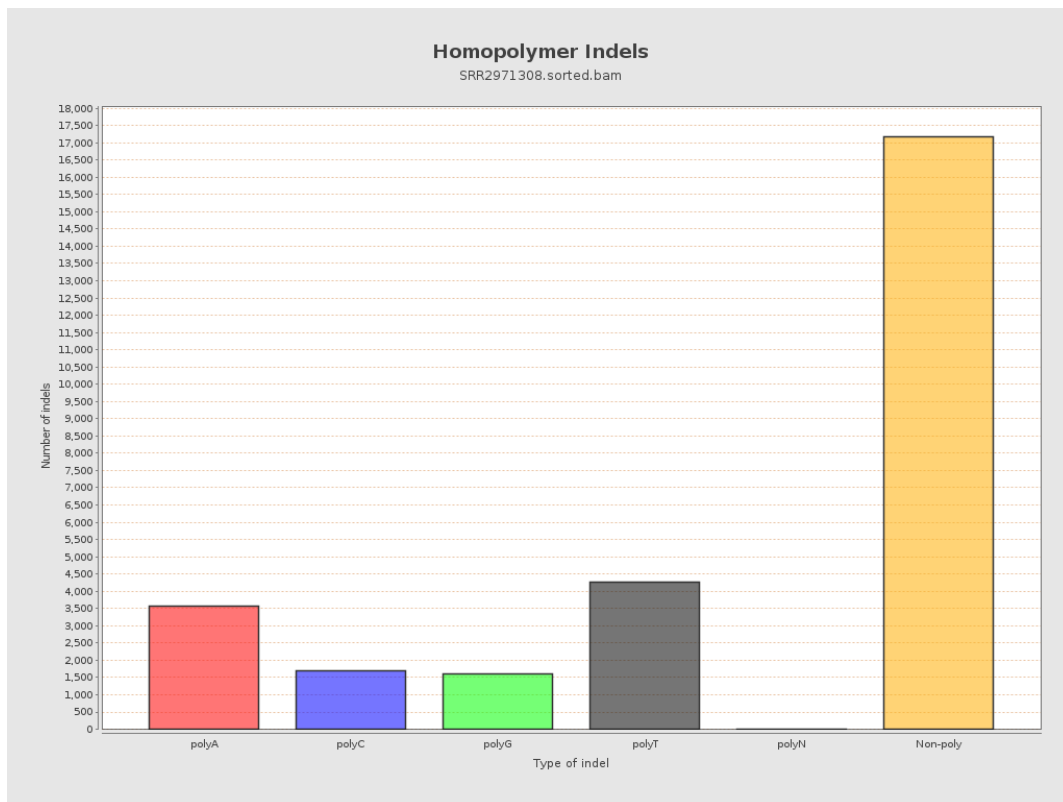
9. Results : Mapped Reads GC-content Distribution



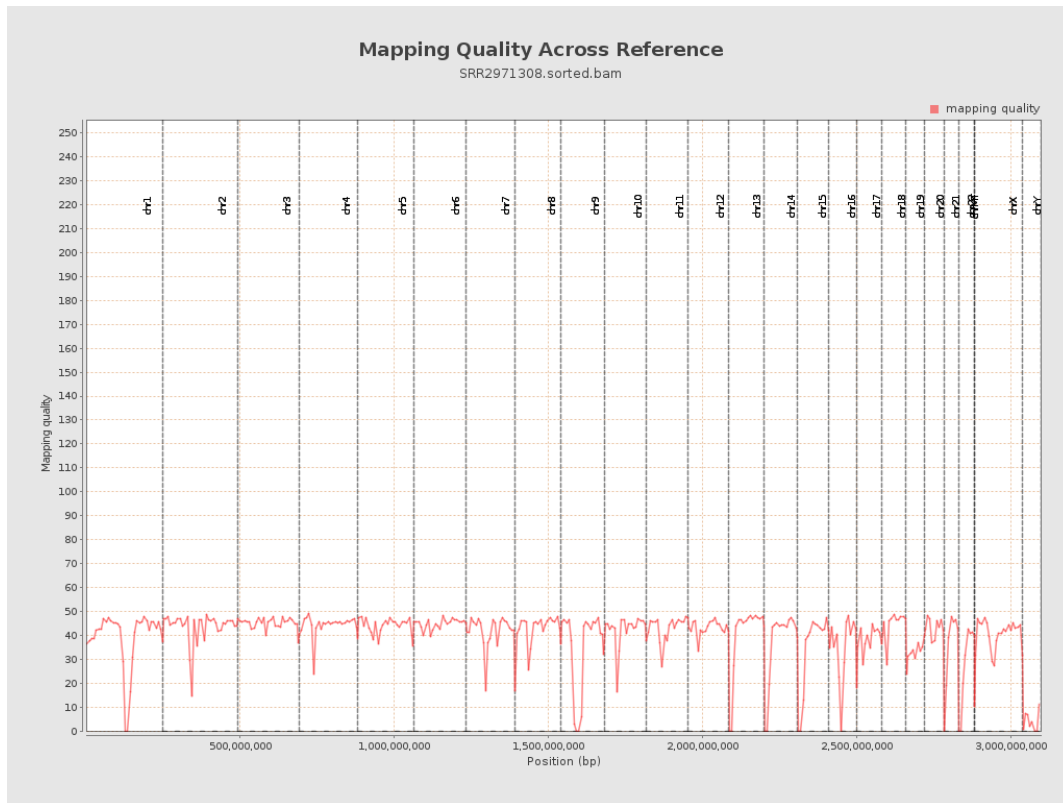
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

