Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 18:34:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082894.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_SRR3082894 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082894.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 18:34:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082894.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,599,924
Mapped reads	3,003,854 / 83.44%
Unmapped reads	596,070 / 16.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,484 / 0.62%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	154,651 / 4.3%
Duplication rate	4.25%
Clipped reads	1,238,488 / 34.4%

2.2. ACGT Content

Number/percentage of A's	57,666,468 / 28.35%
Number/percentage of C's	36,525,632 / 17.96%
Number/percentage of T's	66,559,644 / 32.73%
Number/percentage of G's	42,627,813 / 20.96%
Number/percentage of N's	11,000 / 0.01%
GC Percentage	38.92%

2.3. Coverage

Mean	0.0657

Standard Deviation	0.4673

2.4. Mapping Quality

Mean Mapping Quality	47.23

2.5. Mismatches and indels

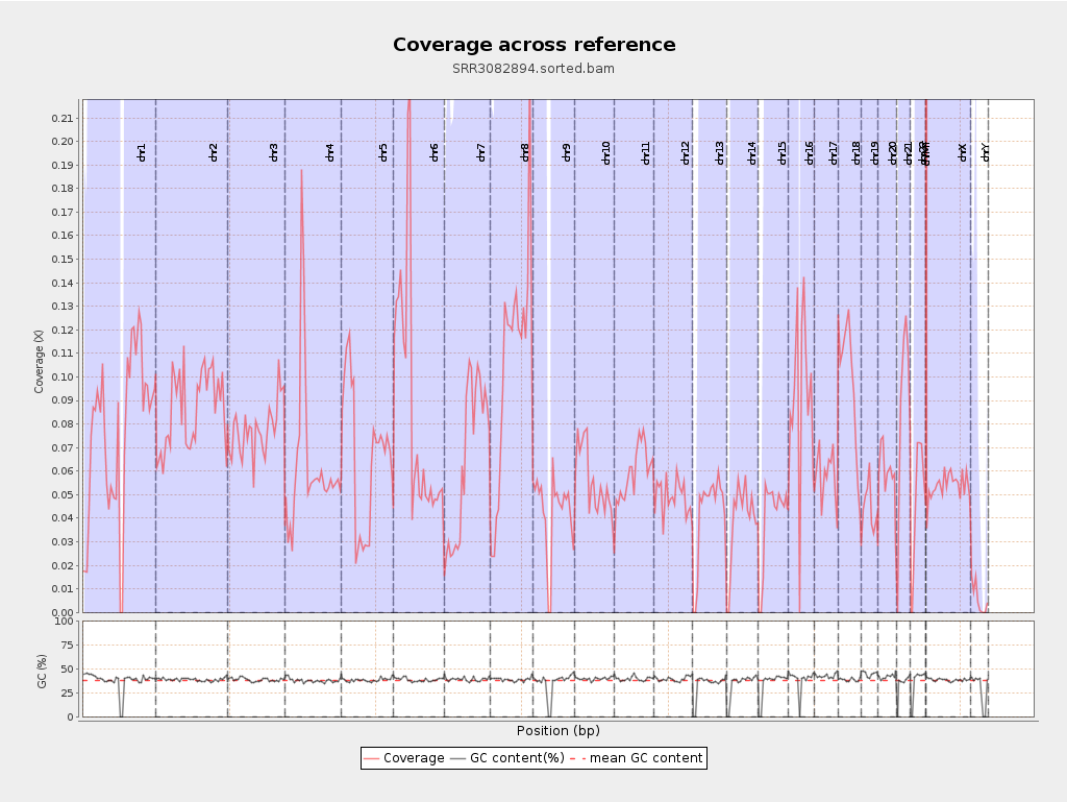
General error rate	0.9%
Mismatches	1,797,857
Insertions	16,558
Mapped reads with at least one insertion	0.55%
Deletions	44,378
Mapped reads with at least one deletion	1.46%
Homopolymer indels	47.91%

2.6. Chromosome stats

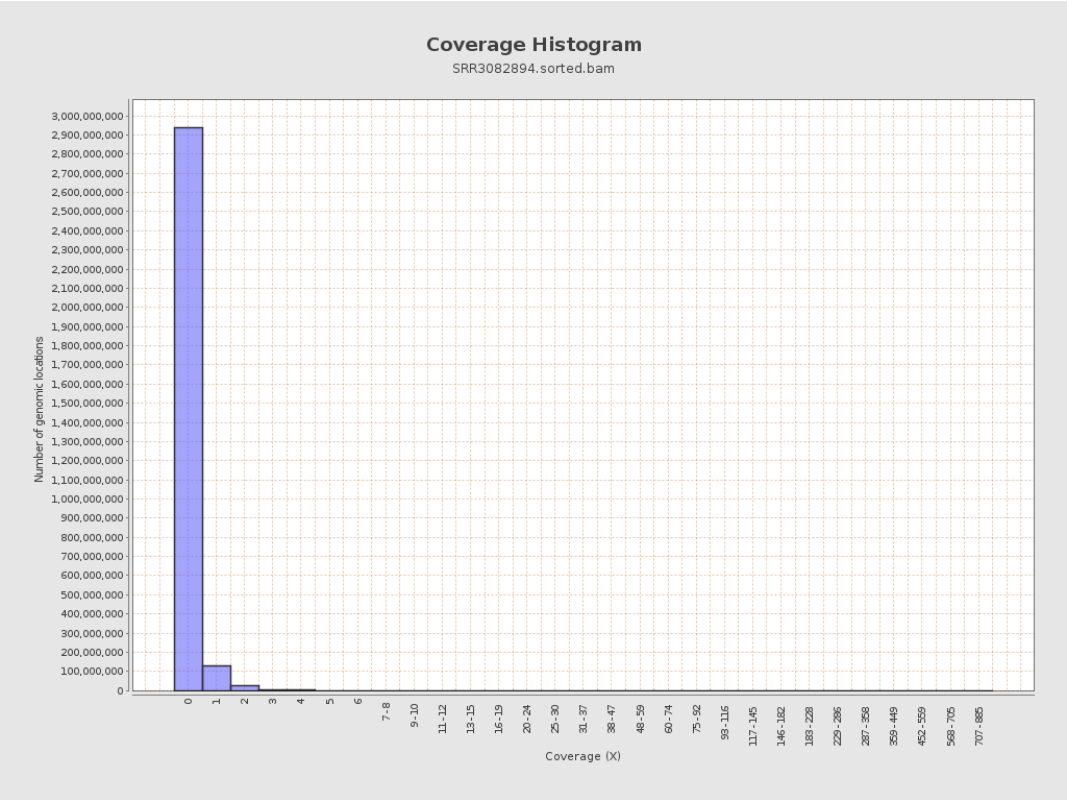
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	19136849	0.0768	0.8271
chr2	243199373	21068479	0.0866	0.5743
chr3	198022430	15314694	0.0773	0.337
chr4	191154276	12171586	0.0637	0.3145
chr5	180915260	11782203	0.0651	0.3141
chr6	171115067	14574342	0.0852	0.4769
chr7	159138663	10319158	0.0648	0.4175

chr8	146364022	15520410	0.106	0.6781
chr9	141213431	6041155	0.0428	0.42
chr10	135534747	7565109	0.0558	0.3792
chr11	135006516	8026023	0.0594	0.371
chr12	133851895	6535268	0.0488	0.2757
chr13	115169878	4829186	0.0419	0.2465
chr14	107349540	4256028	0.0396	0.2738
chr15	102531392	4023319	0.0392	0.2379
chr16	90354753	8082046	0.0894	0.4058
chr17	81195210	4803742	0.0592	0.3523
chr18	78077248	7655303	0.098	0.8631
chr19	59128983	2627583	0.0444	0.584
chr20	63025520	3802623	0.0603	0.3114
chr21	48129895	4132497	0.0859	0.3676
chr22	51304566	2434210	0.0474	0.2588
chrMT	16571	106174	6.4072	4.6689
chrX	155270560	8322079	0.0536	0.3171
chrY	59373566	336532	0.0057	0.1123

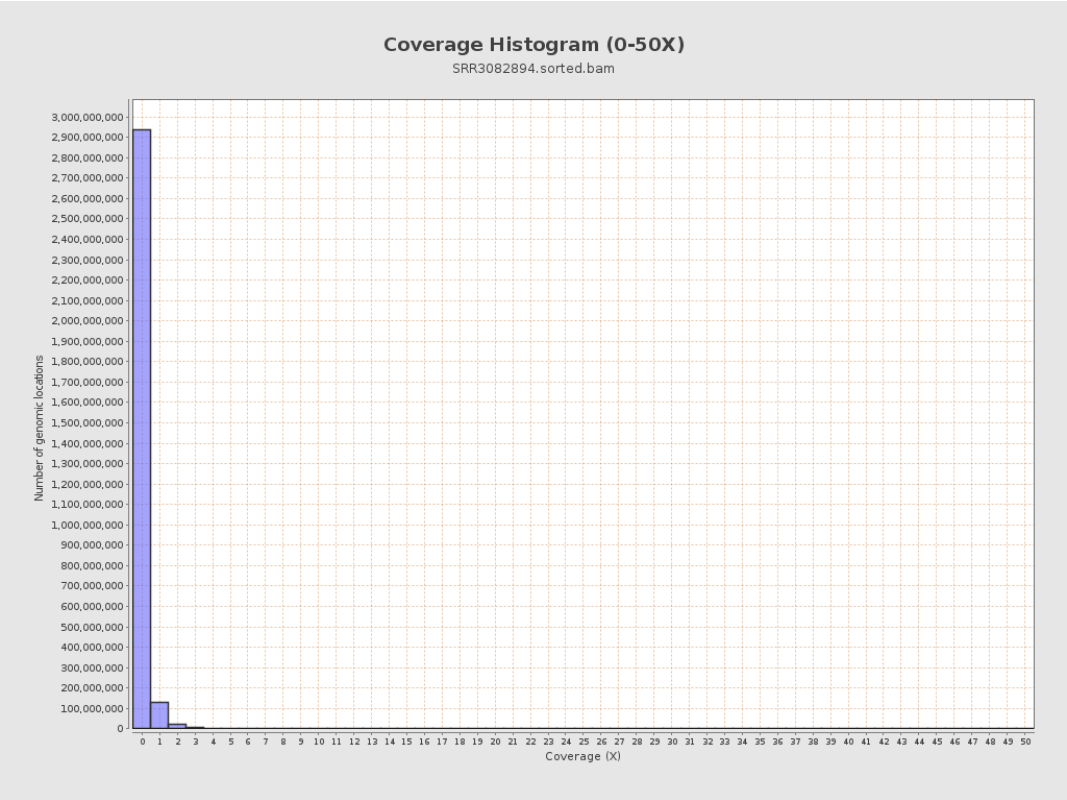
3. Results : Coverage across reference



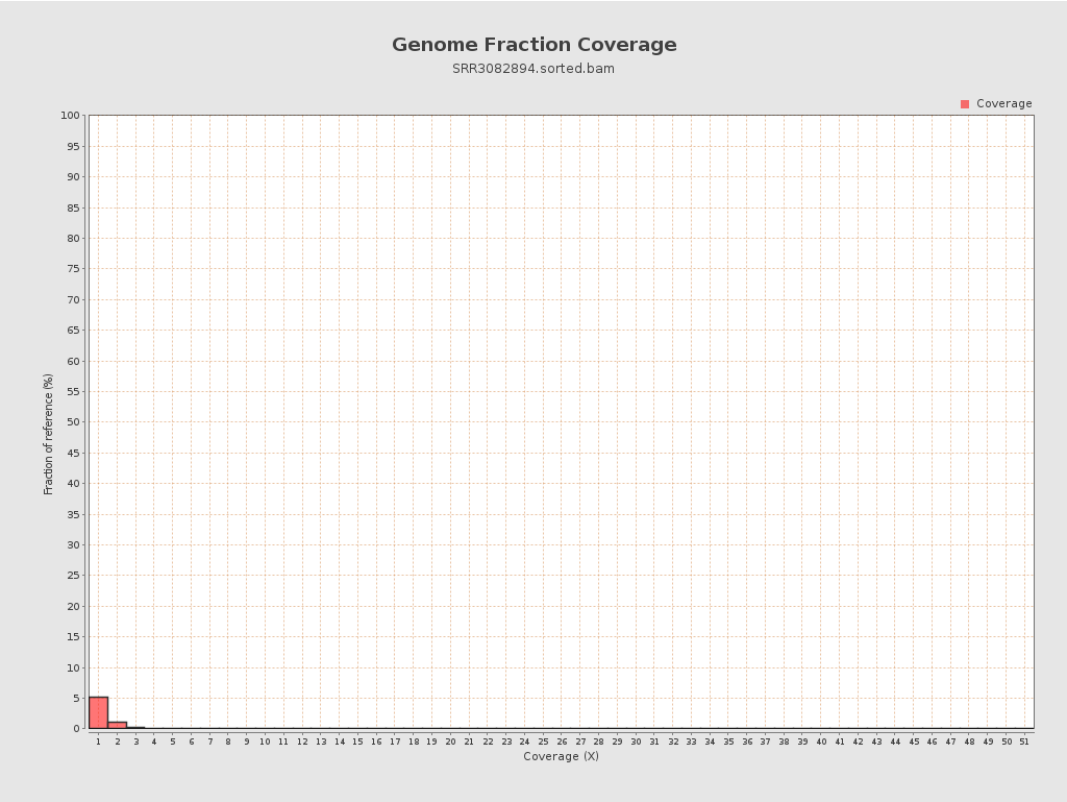
4. Results : Coverage Histogram



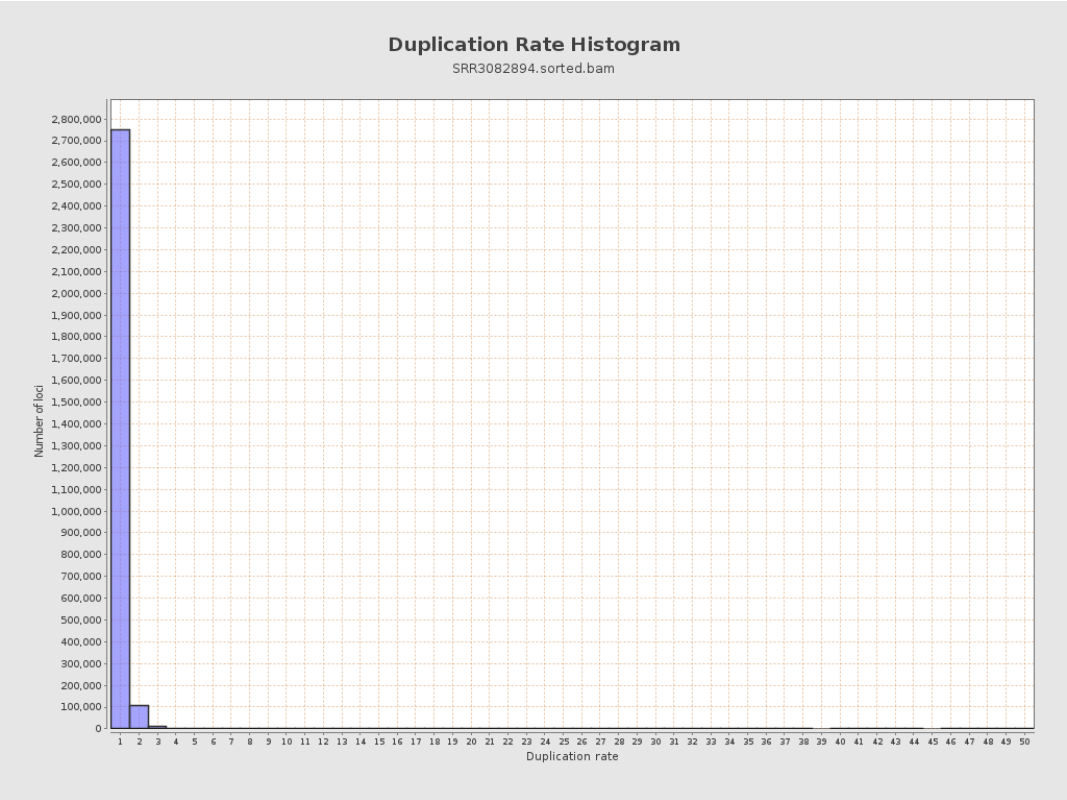
5. Results : Coverage Histogram (0-50X)



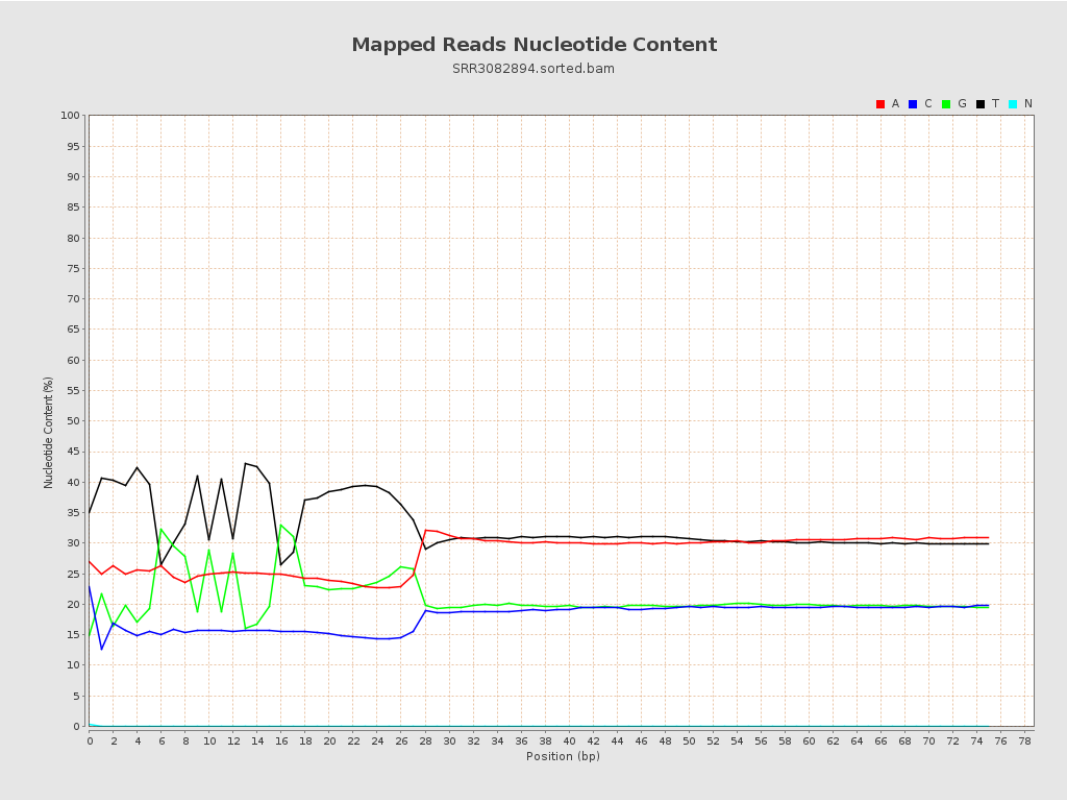
6. Results : Genome Fraction Coverage



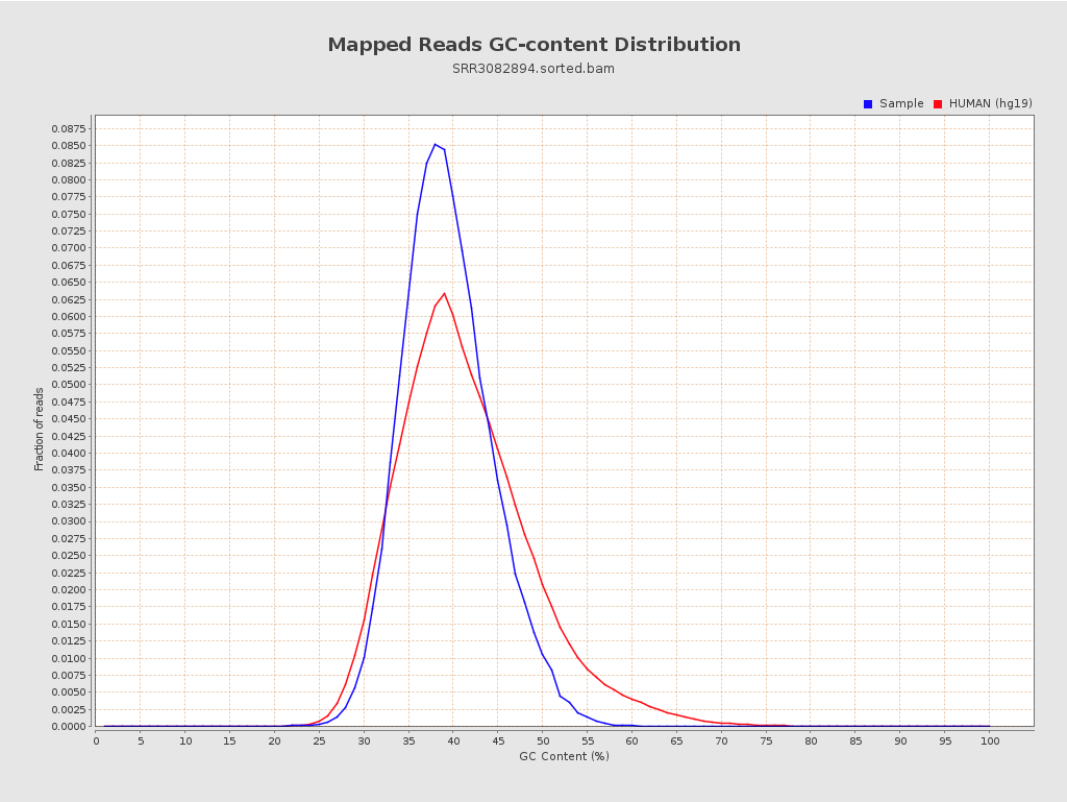
7. Results : Duplication Rate Histogram



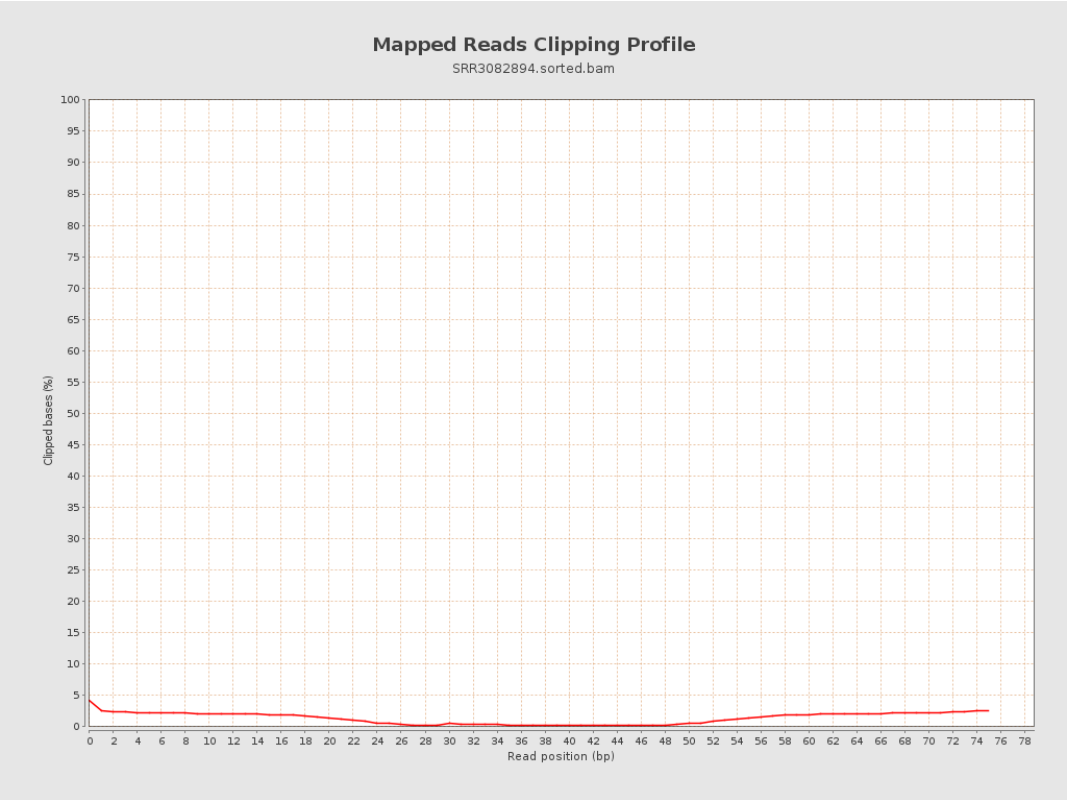
8. Results : Mapped Reads Nucleotide Content



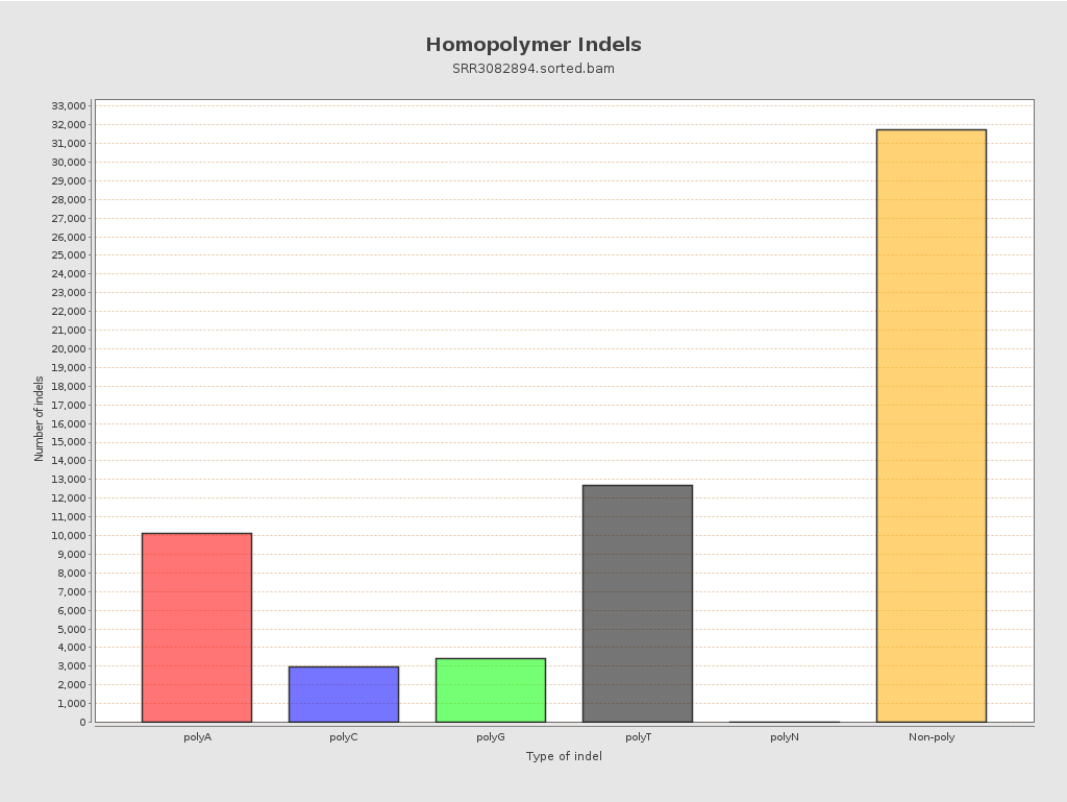
9. Results : Mapped Reads GC-content Distribution



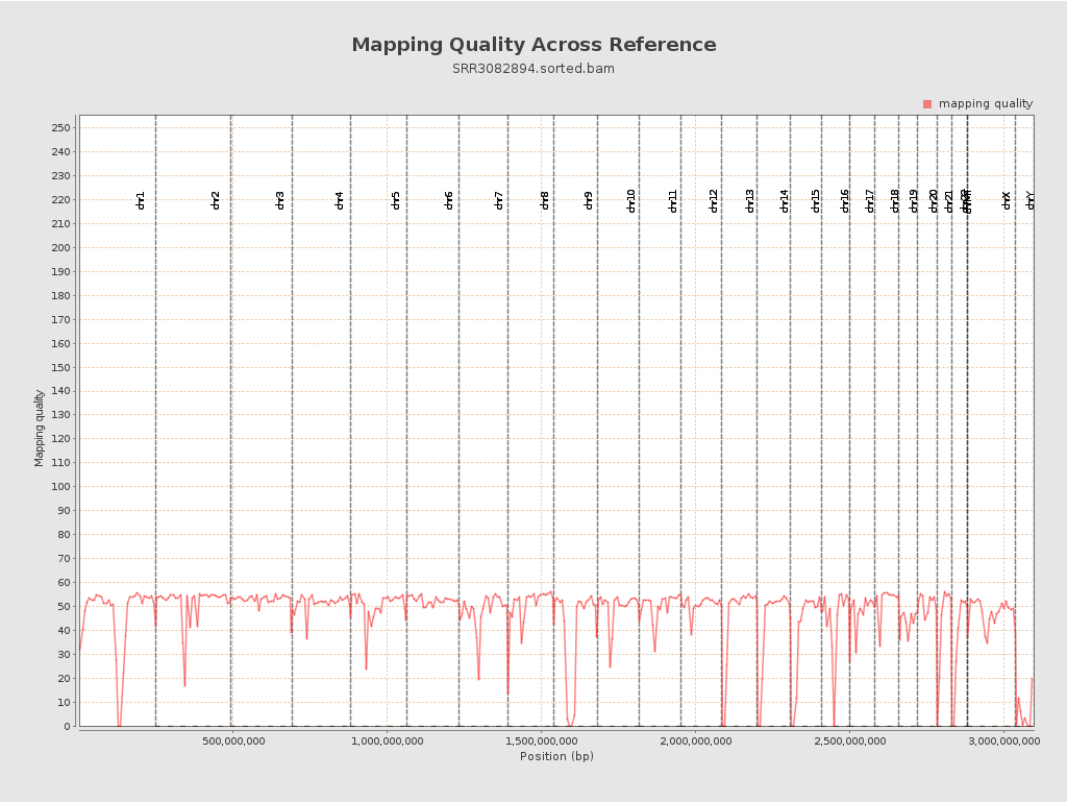
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram