Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 06:51:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081734.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_SRR3081734 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081734.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 06:51:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081734.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,676,105
Mapped reads	2,436,148 / 91.03%
Unmapped reads	239,957 / 8.97%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,417 / 0.58%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	95,536 / 3.57%
Duplication rate	2.85%
Clipped reads	1,051,971 / 39.31%

2.2. ACGT Content

Number/percentage of A's	44,514,531 / 27.27%
Number/percentage of C's	31,816,223 / 19.49%
Number/percentage of T's	49,349,494 / 30.23%
Number/percentage of G's	37,569,196 / 23.01%
Number/percentage of N's	1,840 / 0%
GC Percentage	42.5%

2.3. Coverage

Mean	0.0528

Standard Deviation	0.4436

2.4. Mapping Quality

Mean Mapping Quality	44.16

2.5. Mismatches and indels

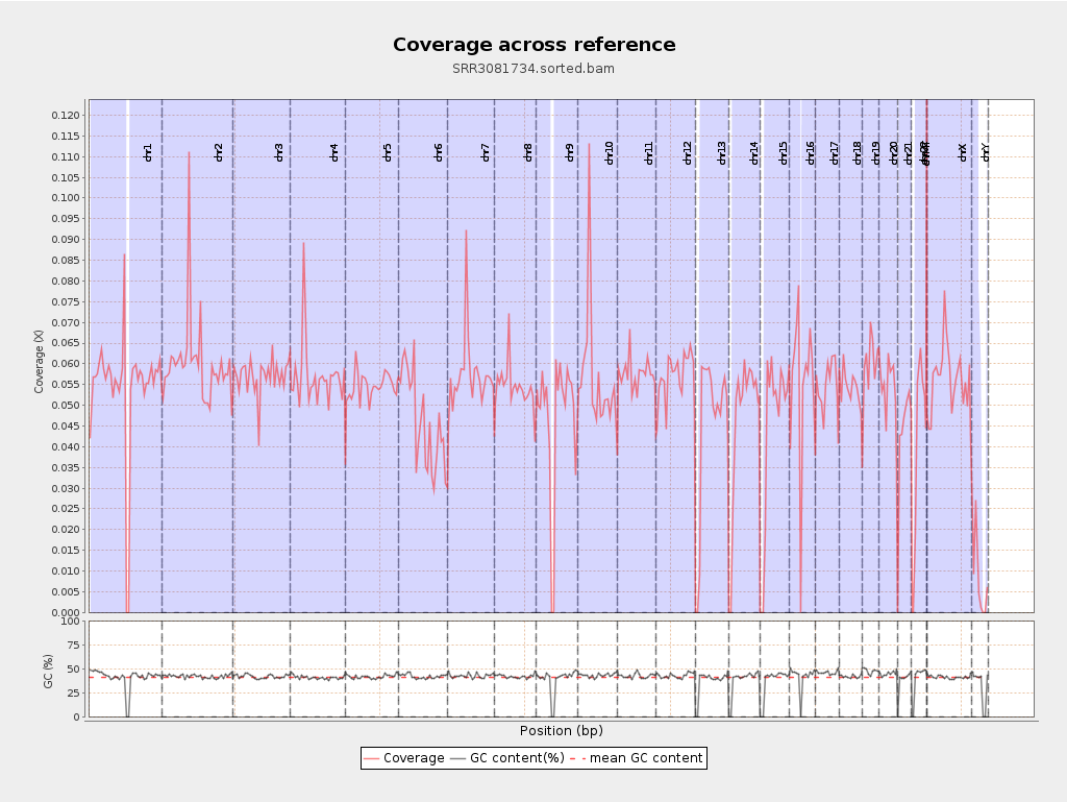
General error rate	0.85%
Mismatches	1,362,932
Insertions	12,504
Mapped reads with at least one insertion	0.51%
Deletions	34,279
Mapped reads with at least one deletion	1.39%
Homopolymer indels	45.7%

2.6. Chromosome stats

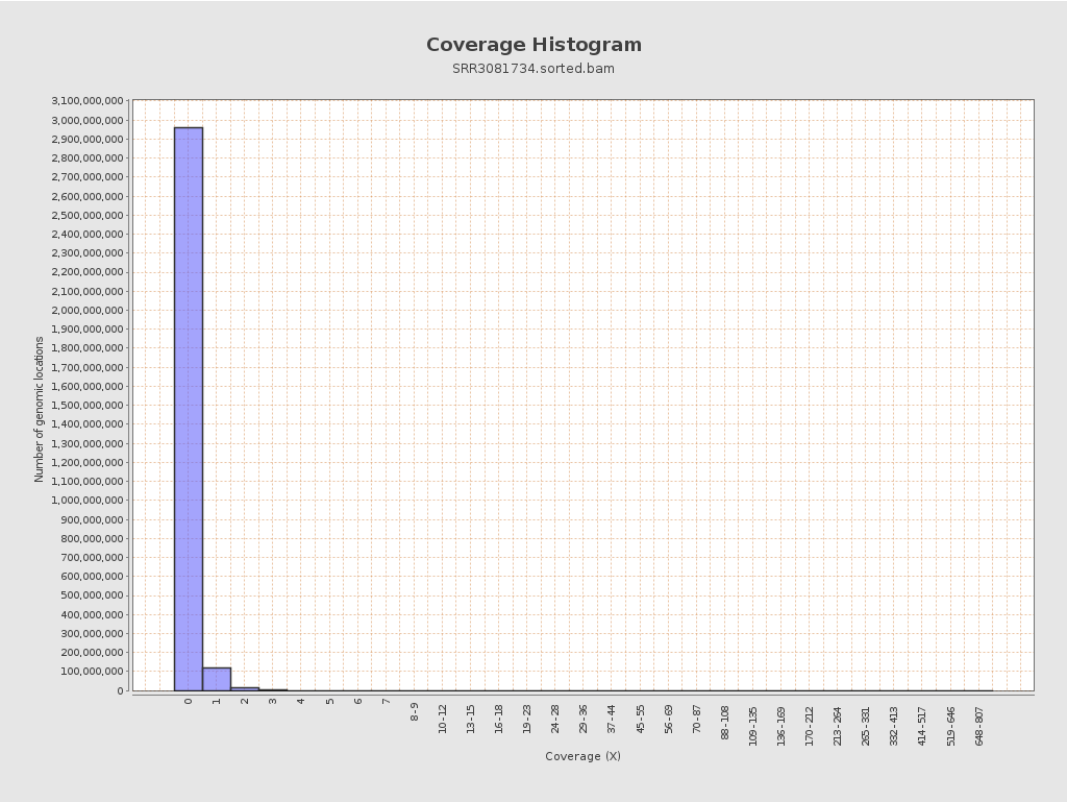
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	13489186	0.0541	0.7537
chr2	243199373	14600933	0.06	0.5963
chr3	198022430	11270688	0.0569	0.2782
chr4	191154276	10847990	0.0567	0.3228
chr5	180915260	9880775	0.0546	0.2684
chr6	171115067	7896427	0.0461	0.3034
chr7	159138663	9146085	0.0575	0.6073

chr8	146364022	7947884	0.0543	0.4536
chr9	141213431	6568393	0.0465	0.4186
chr10	135534747	7630731	0.0563	0.555
chr11	135006516	7731850	0.0573	0.403
chr12	133851895	7642612	0.0571	0.2747
chr13	115169878	5183404	0.045	0.2413
chr14	107349540	4929530	0.0459	0.2593
chr15	102531392	4587046	0.0447	0.2491
chr16	90354753	4995406	0.0553	0.3226
chr17	81195210	4422782	0.0545	0.2886
chr18	78077248	4260684	0.0546	0.7286
chr19	59128983	3574315	0.0604	0.6068
chr20	63025520	3417516	0.0542	0.2803
chr21	48129895	2073664	0.0431	0.2832
chr22	51304566	1993679	0.0389	0.225
chrMT	16571	2101	0.1268	0.3789
chrX	155270560	8730635	0.0562	0.3134
chrY	59373566	488360	0.0082	0.2355

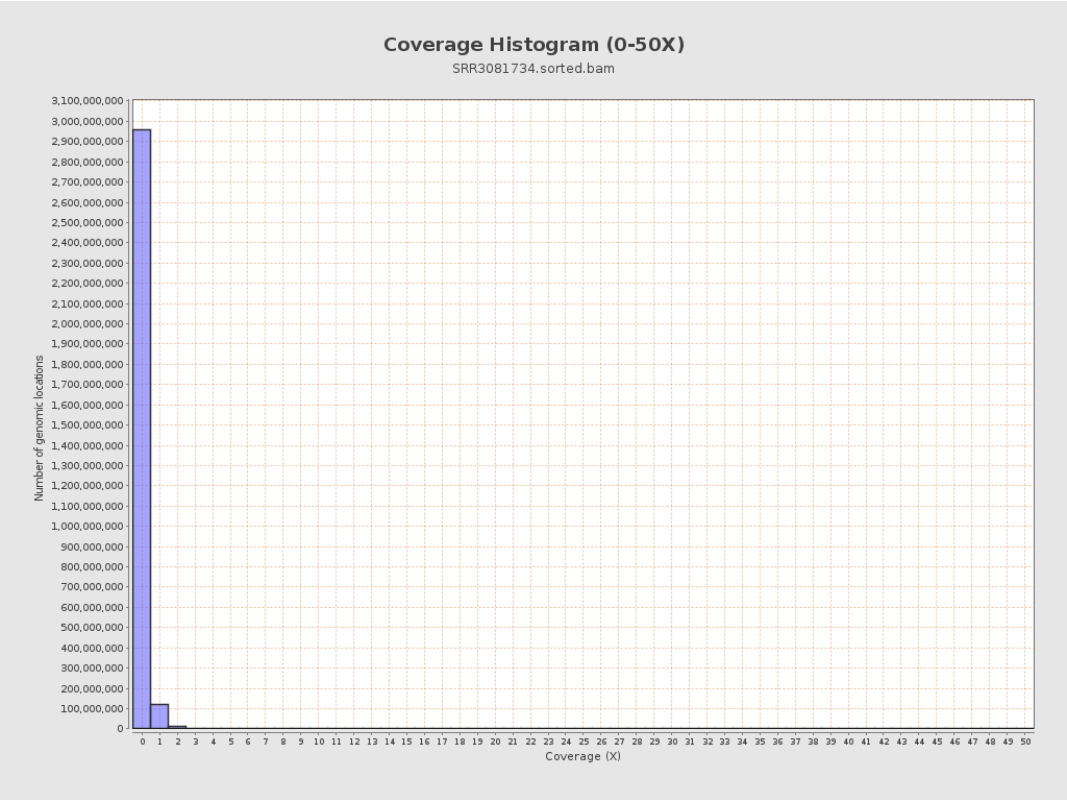
3. Results : Coverage across reference



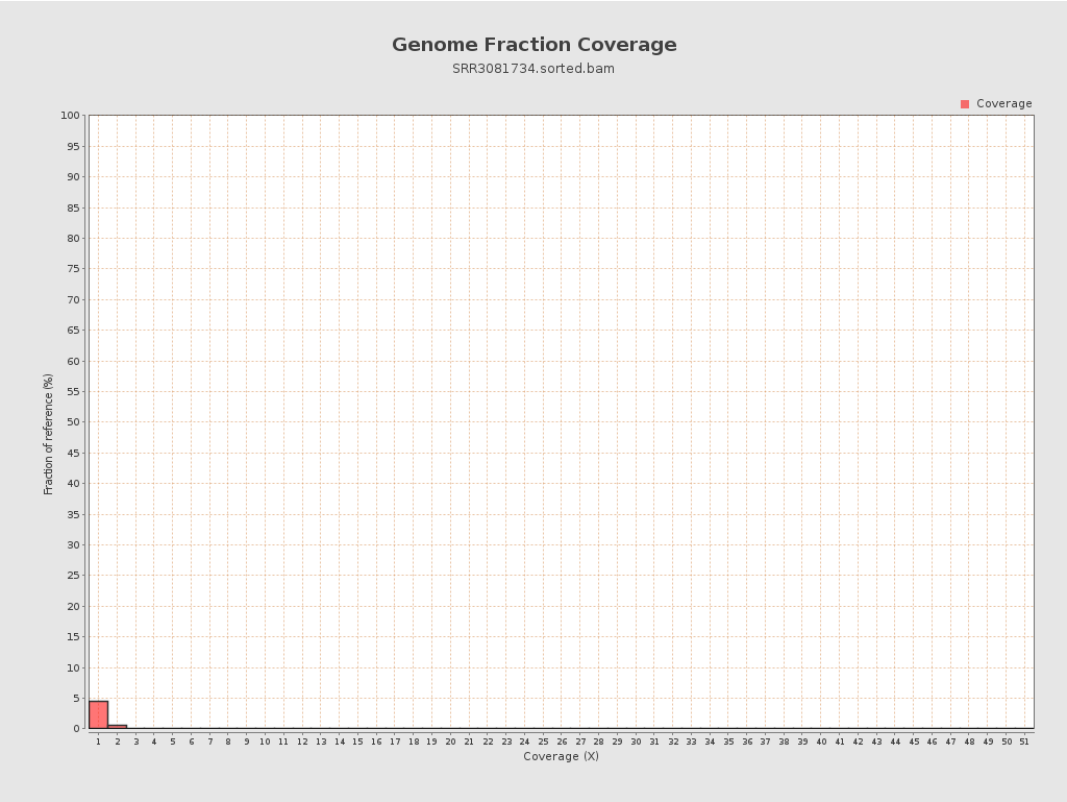
4. Results : Coverage Histogram



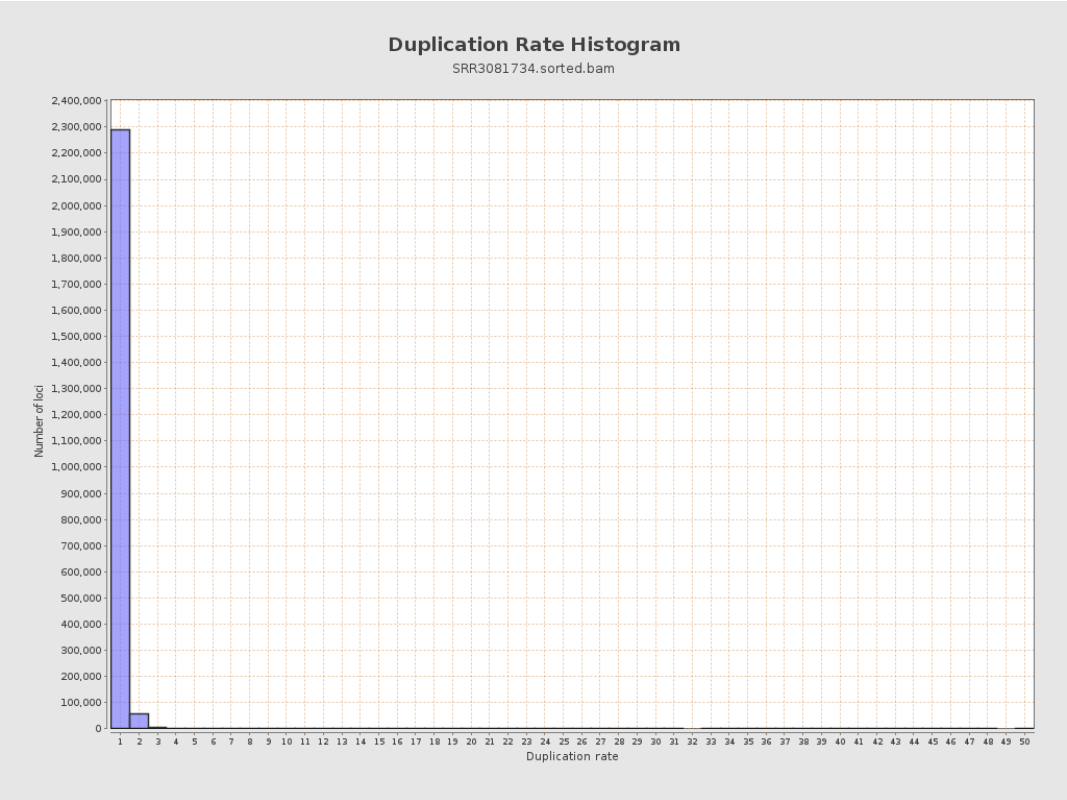
5. Results : Coverage Histogram (0-50X)



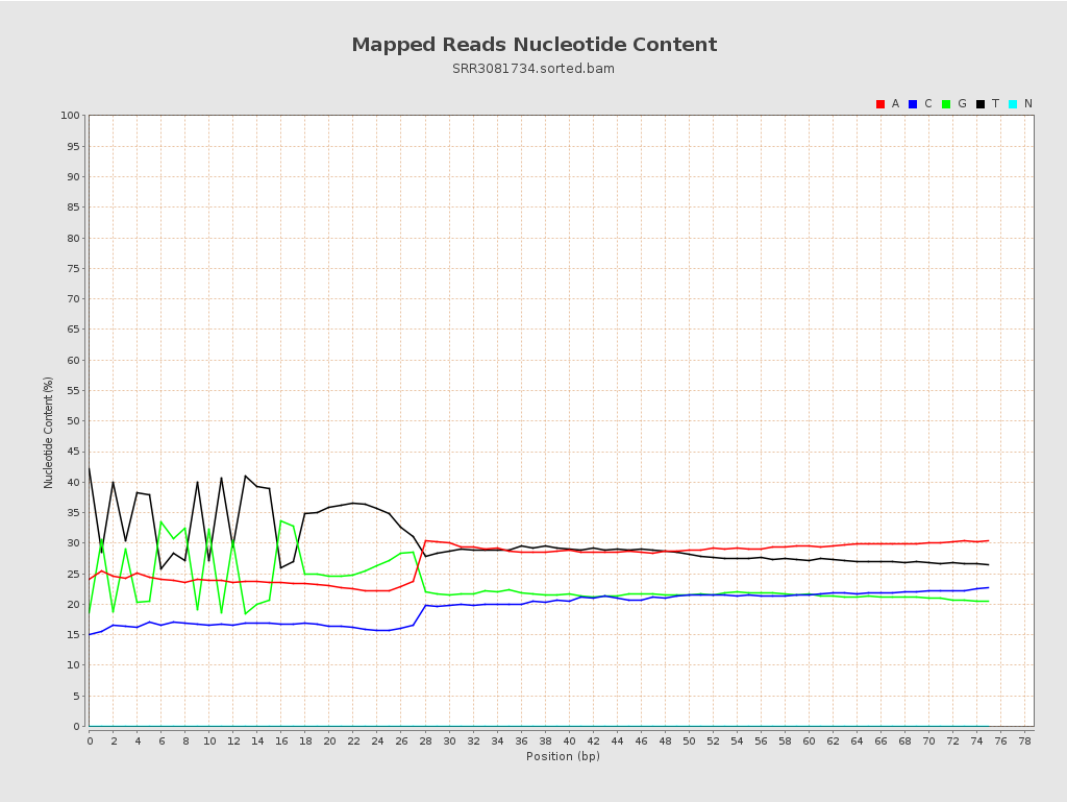
6. Results : Genome Fraction Coverage



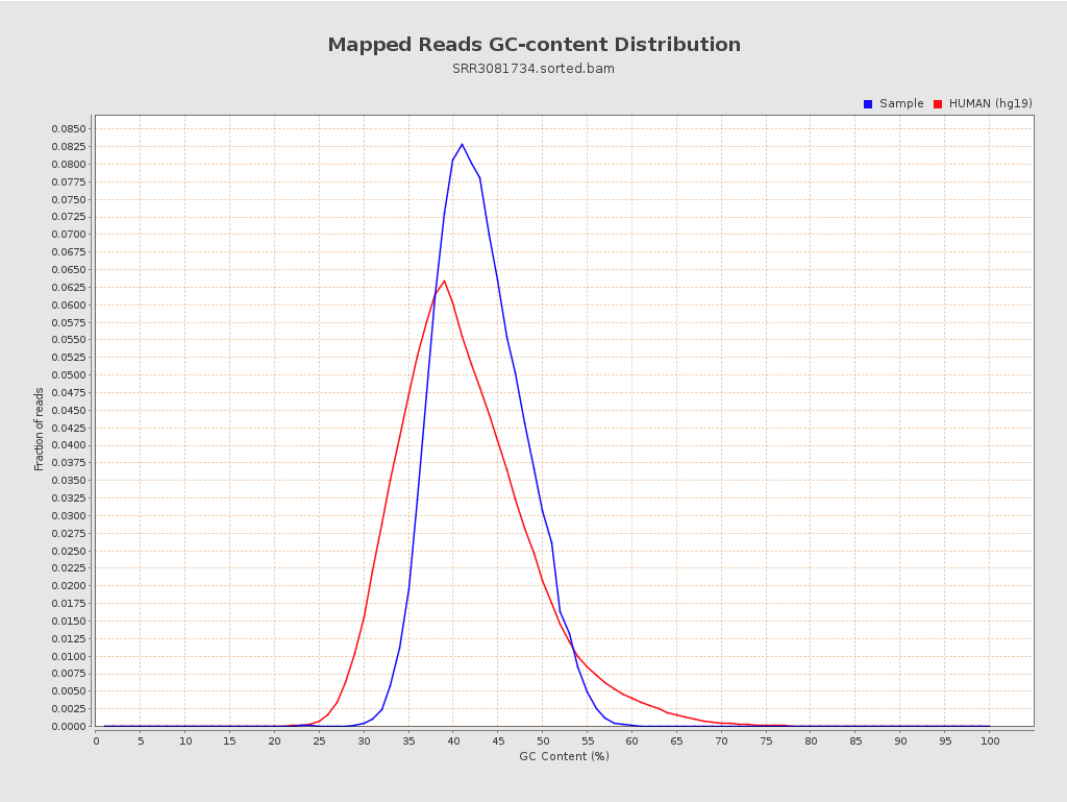
7. Results : Duplication Rate Histogram



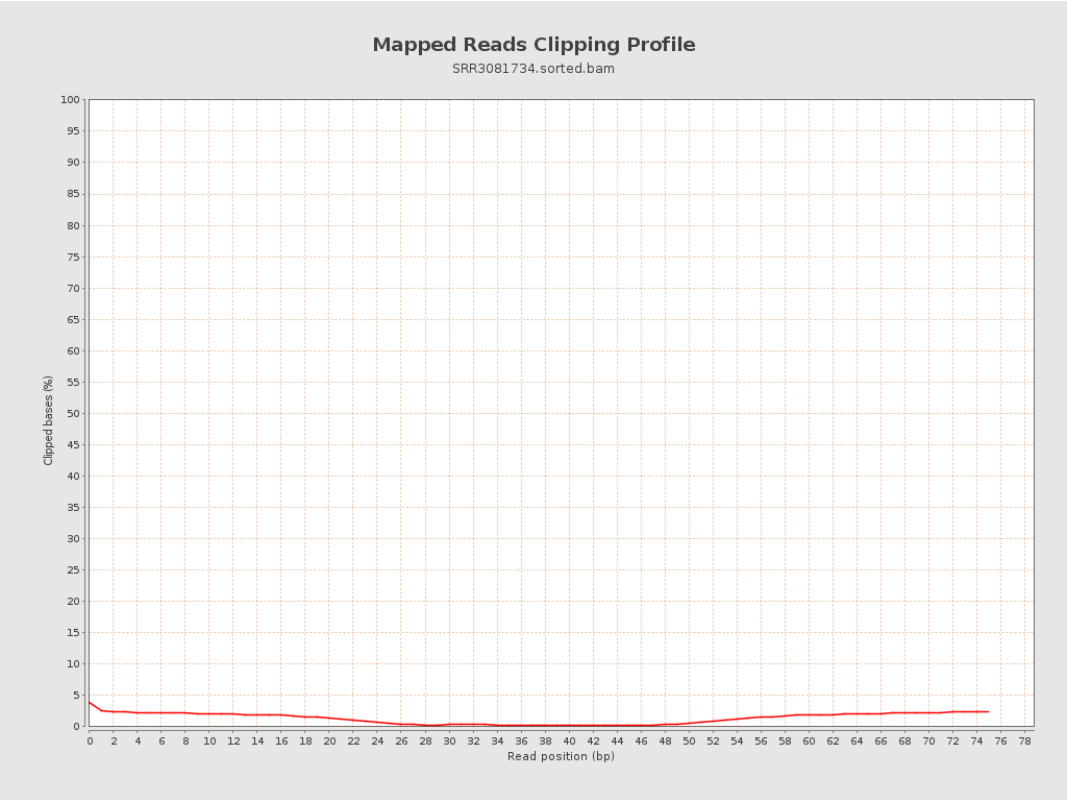
8. Results : Mapped Reads Nucleotide Content



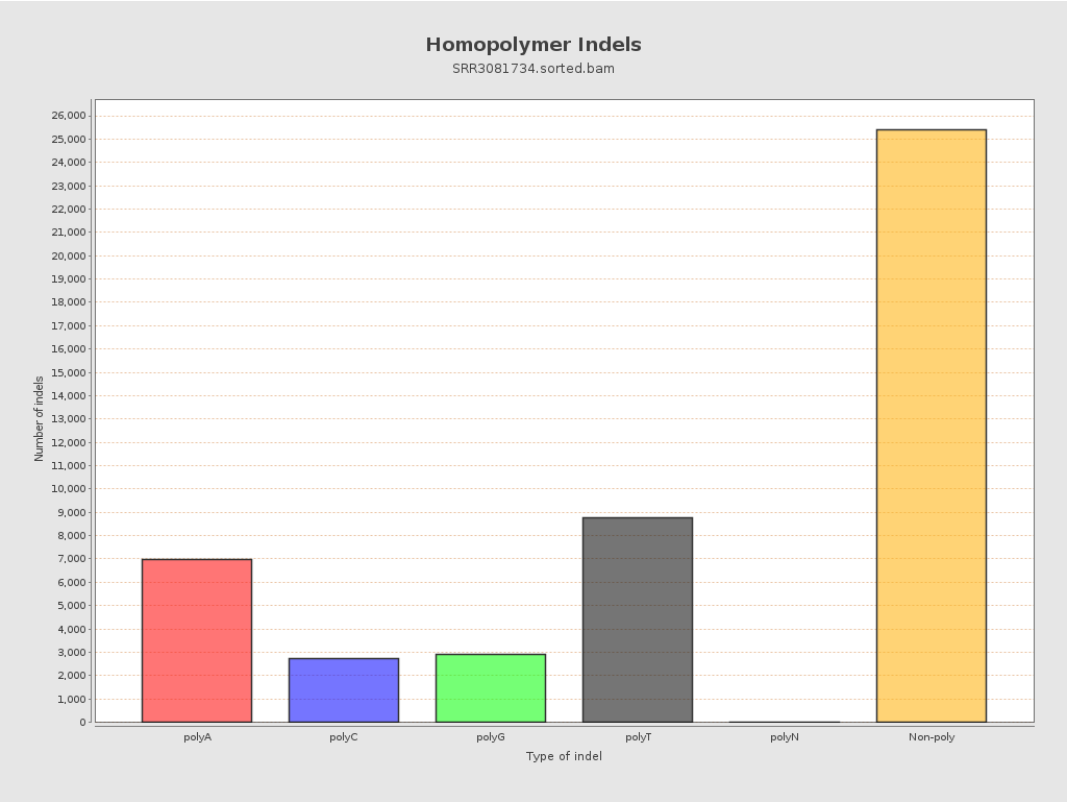
9. Results : Mapped Reads GC-content Distribution



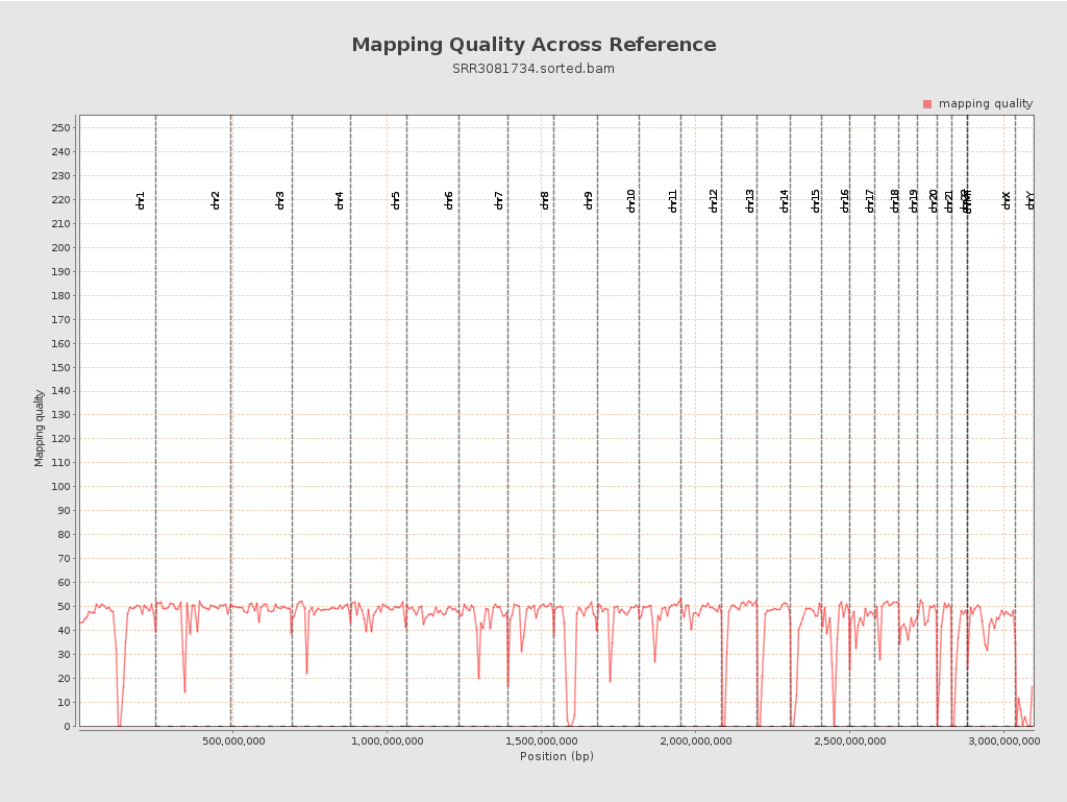
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram