Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 21:02:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084978.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_SRR3084978 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084978.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 21:02:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084978.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,478
Mapped reads	833 / 23.95%
Unmapped reads	2,645 / 76.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	1 / 0.03%
Duplication rate	0.12%
Clipped reads	289 / 8.31%

2.2. ACGT Content

Number/percentage of A's	17,005 / 29.46%
Number/percentage of C's	10,618 / 18.4%
Number/percentage of T's	17,982 / 31.15%
Number/percentage of G's	12,104 / 20.97%
Number/percentage of N's	11 / 0.02%
GC Percentage	39.37%

2.3. Coverage

Mean	0

Standard Deviation	0.0043

2.4. Mapping Quality

Mean Mapping Quality	39.6

2.5. Mismatches and indels

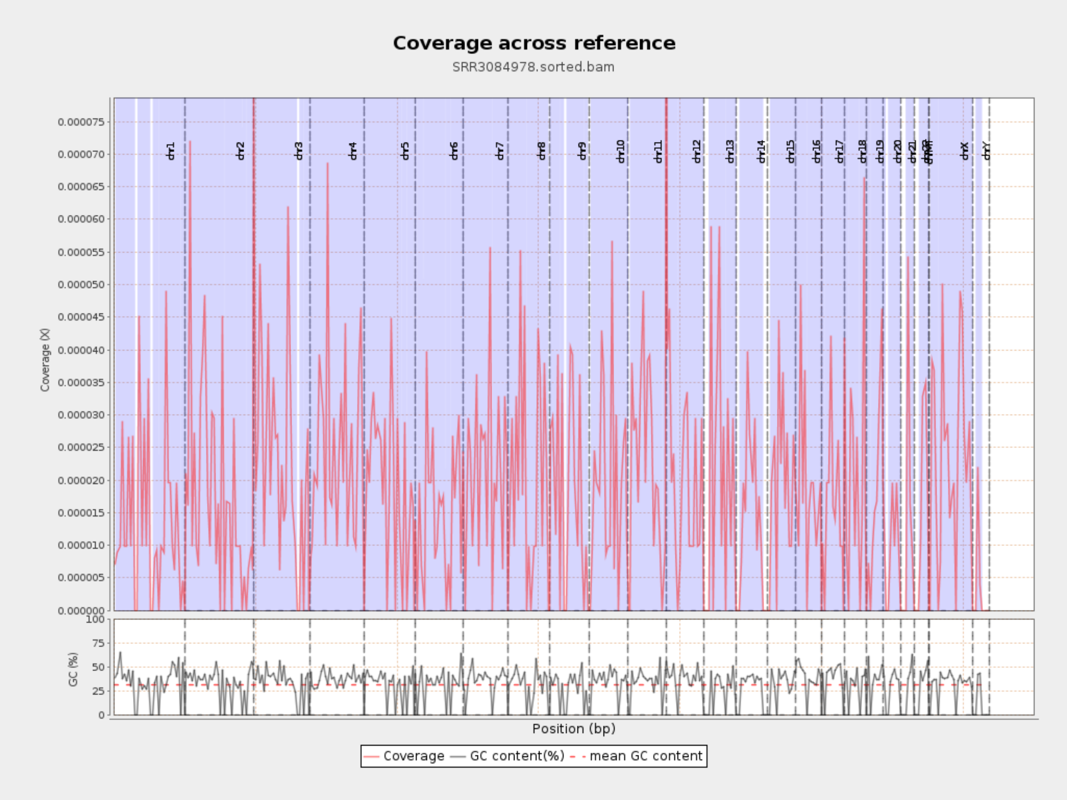
General error rate	0.75%
Mismatches	434
Insertions	2
Mapped reads with at least one insertion	0.24%
Deletions	18
Mapped reads with at least one deletion	2.16%
Homopolymer indels	35%

2.6. Chromosome stats

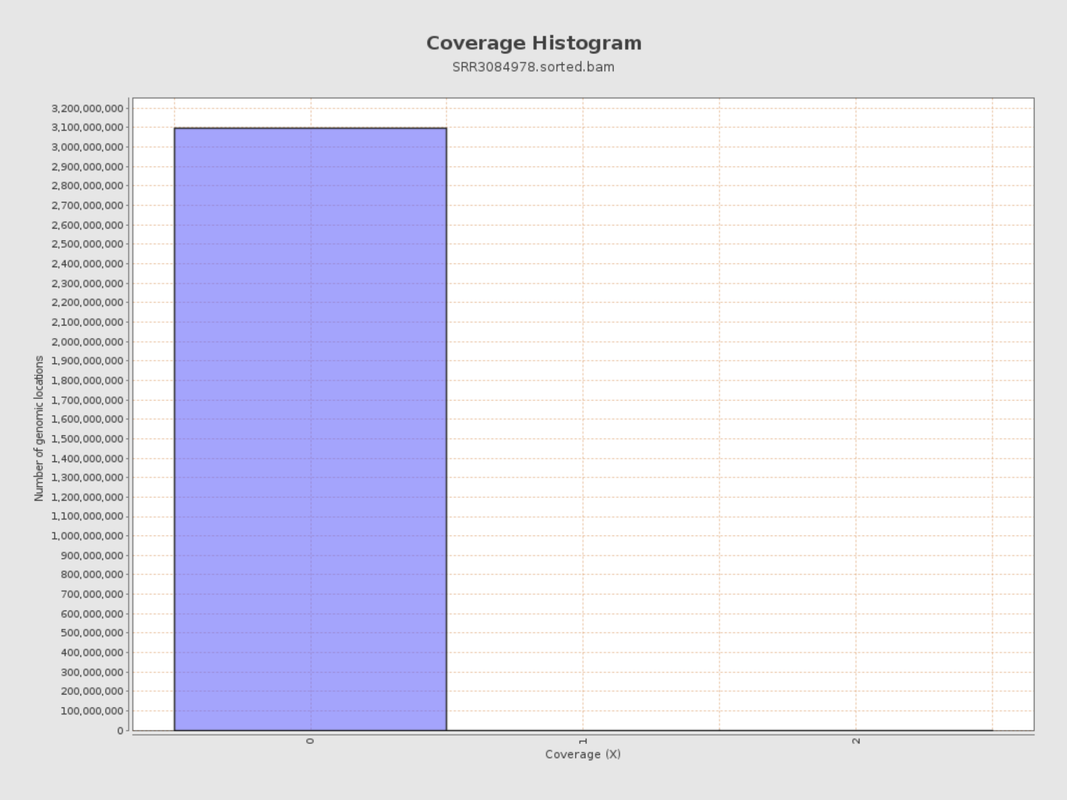
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3422	0	0.0038
chr2	243199373	4276	0	0.0043
chr3	198022430	4680	0	0.0049
chr4	191154276	4712	0	0.005
chr5	180915260	3482	0	0.0044
chr6	171115067	2586	0	0.0039
chr7	159138663	3377	0	0.0046

chr8	146364022	3081	0	0.0046
chr9	141213431	2549	0	0.0042
chr10	135534747	2746	0	0.0045
chr11	135006516	3073	0	0.0048
chr12	133851895	2590	0	0.0044
chr13	115169878	2325	0	0.0045
chr14	107349540	1509	0	0.0037
chr15	102531392	1909	0	0.0043
chr16	90354753	1720	0	0.0044
chr17	81195210	1293	0	0.004
chr18	78077248	1703	0	0.0047
chr19	59128983	1009	0	0.0041
chr20	63025520	608	0	0.0031
chr21	48129895	618	0	0.0036
chr22	51304566	722	0	0.0038
chrMT	16571	0	0	0
chrX	155270560	3571	0	0.0048
chrY	59373566	201	0	0.0018

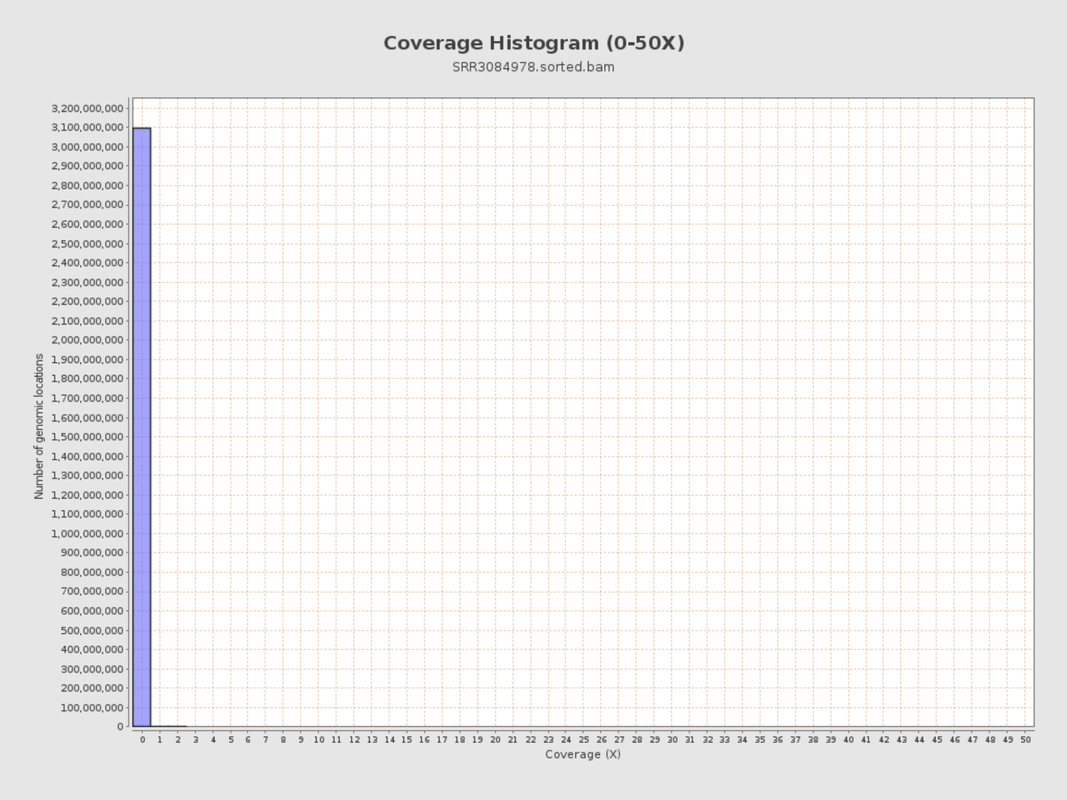
3. Results : Coverage across reference



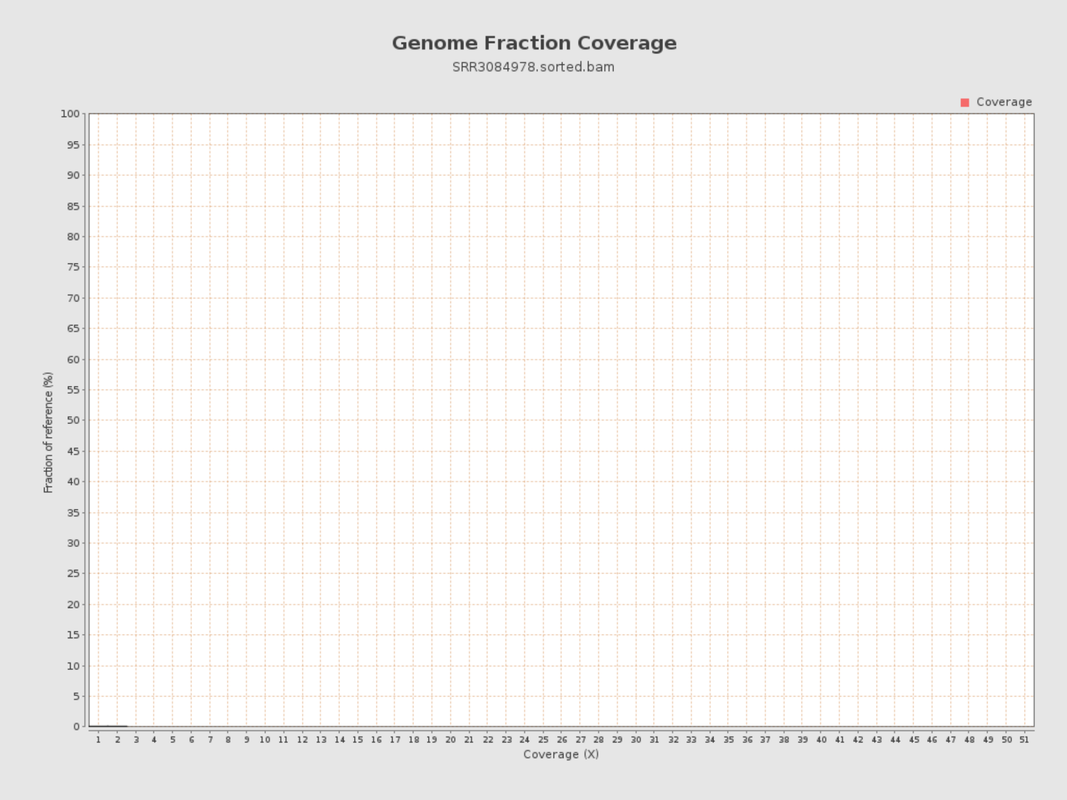
4. Results : Coverage Histogram



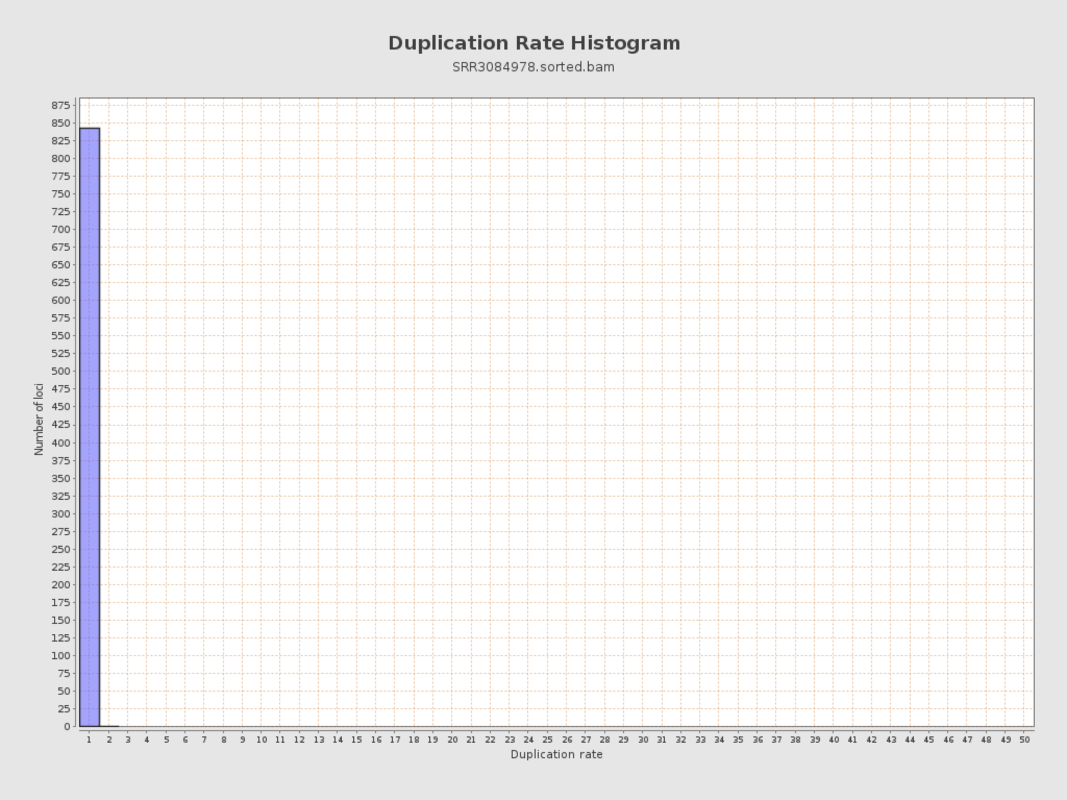
5. Results : Coverage Histogram (0-50X)



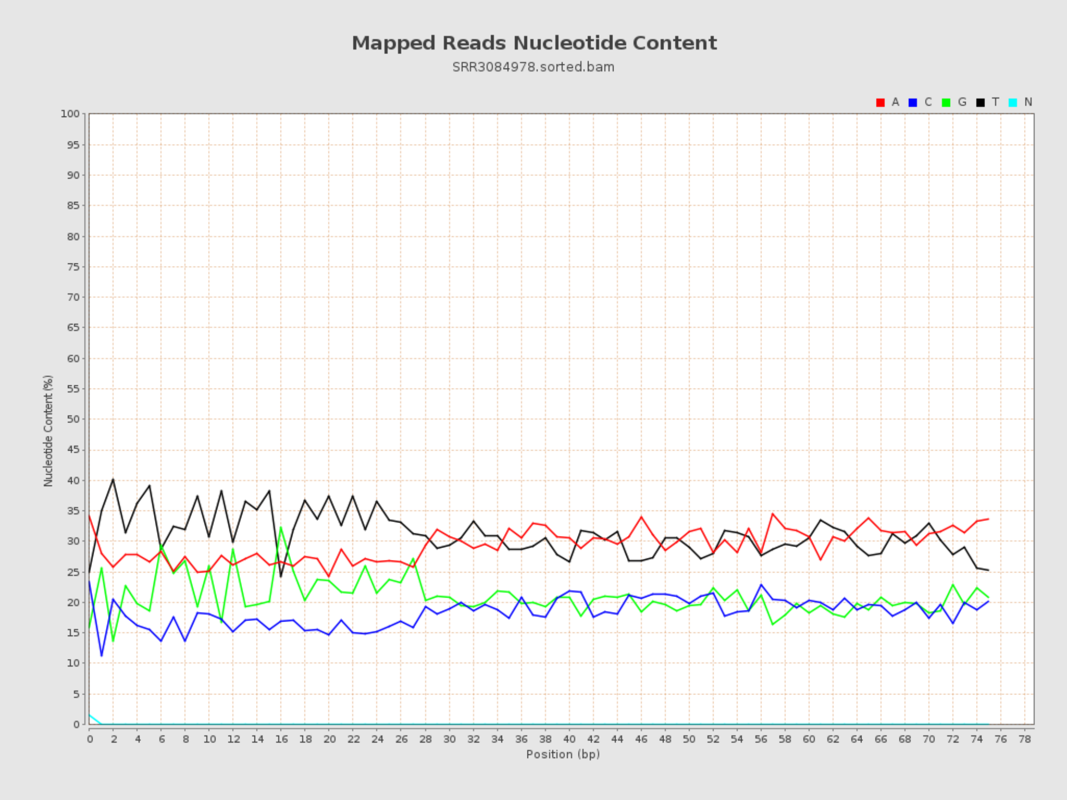
6. Results : Genome Fraction Coverage



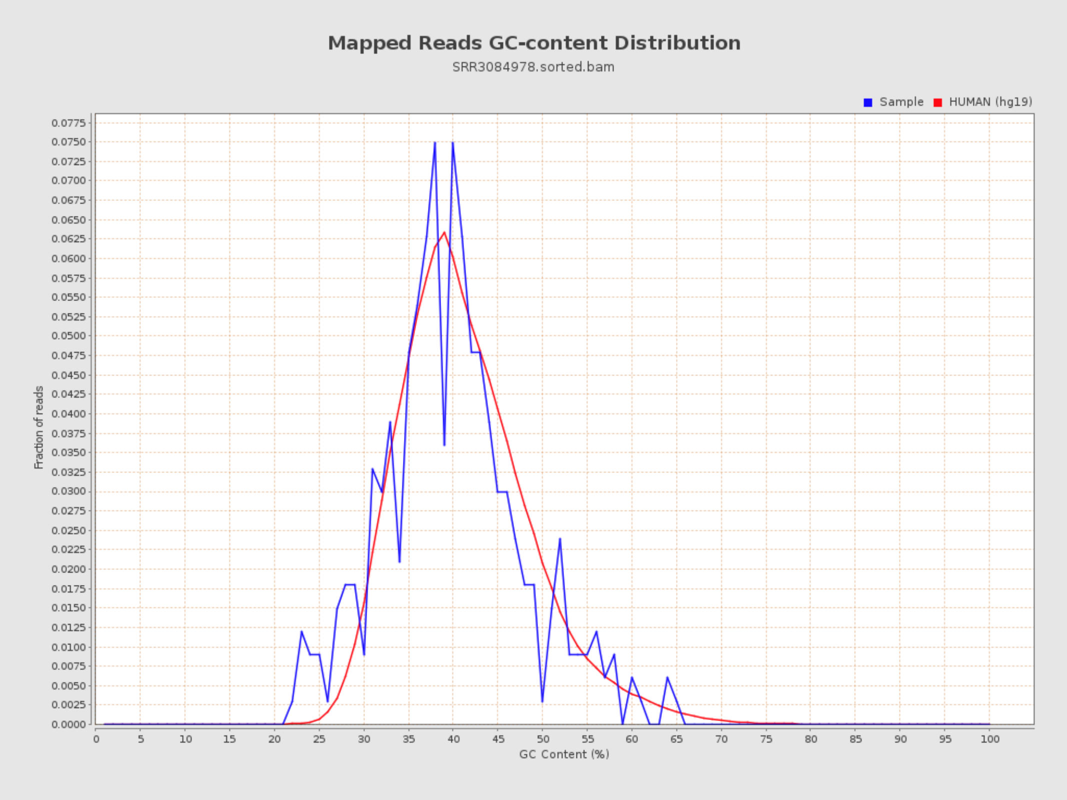
7. Results : Duplication Rate Histogram



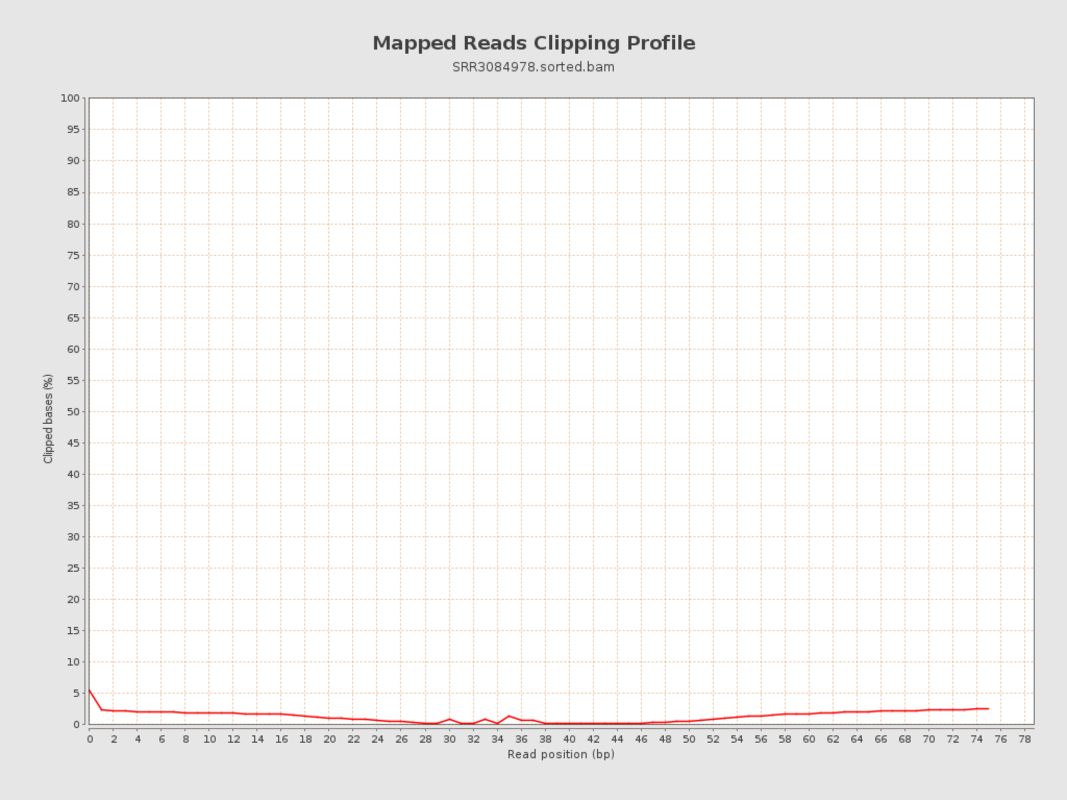
8. Results : Mapped Reads Nucleotide Content



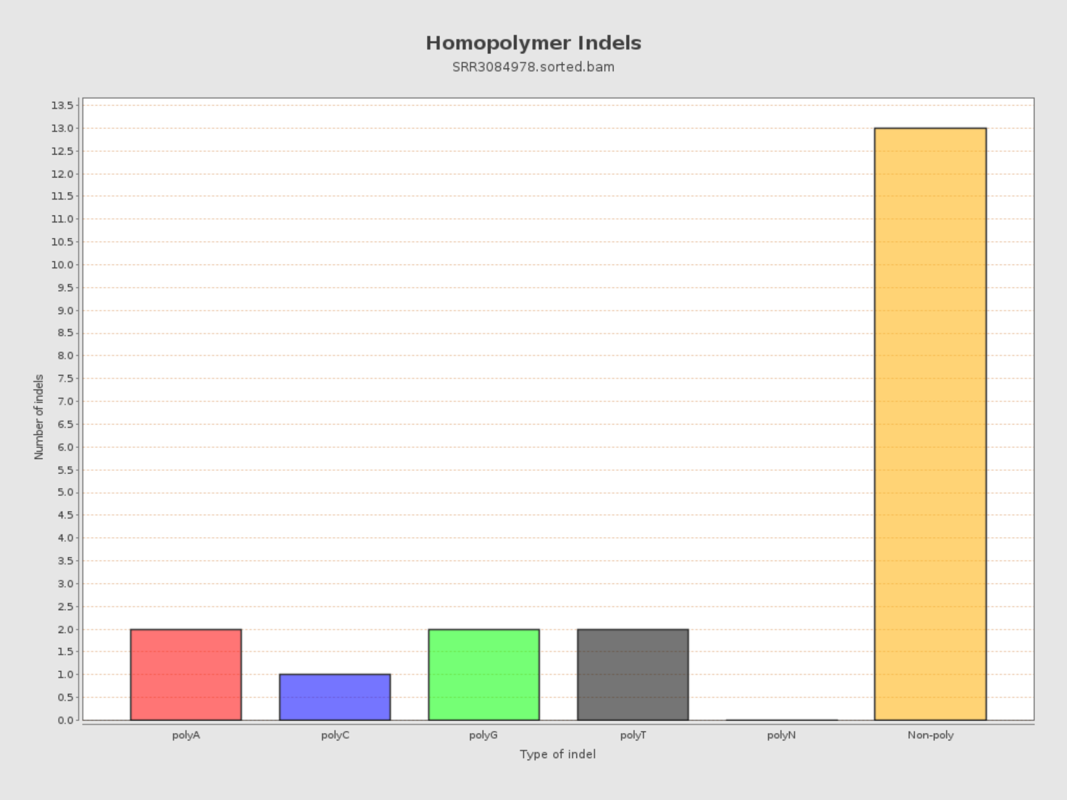
9. Results : Mapped Reads GC-content Distribution



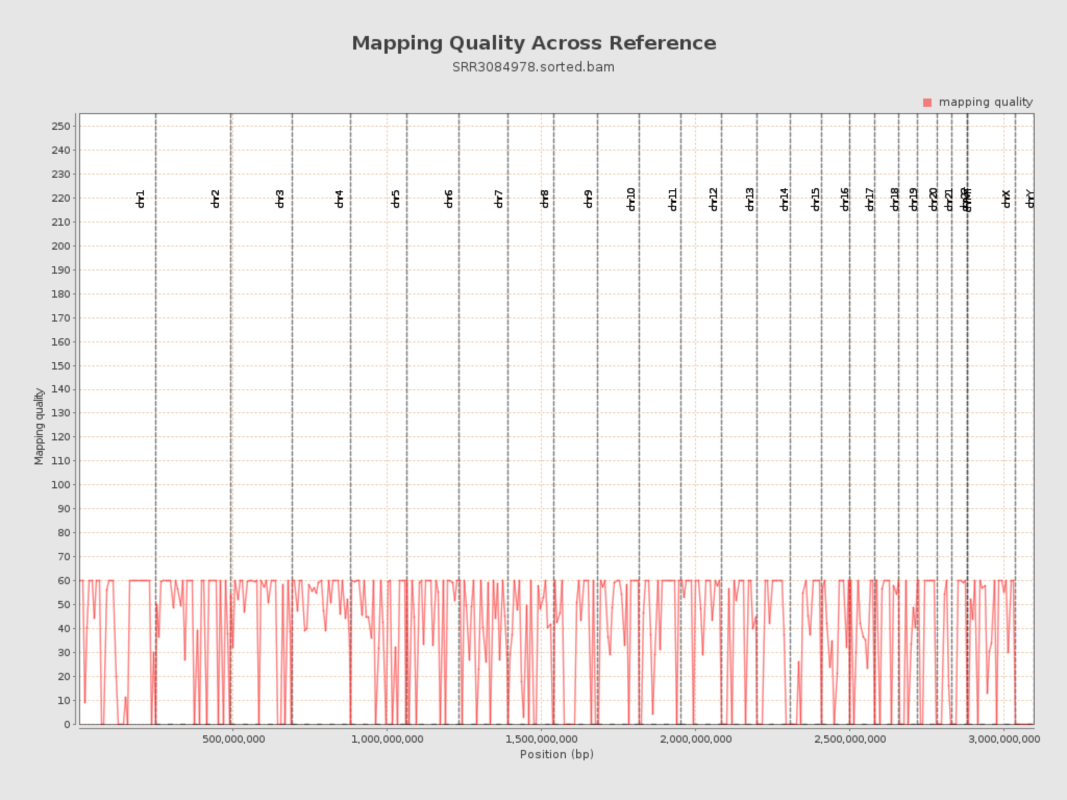
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram