Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 17:58:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081042.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_SRR3081042 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081042.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 17:58:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081042.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,684
Mapped reads	1,132 / 24.17%
Unmapped reads	3,552 / 75.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3 / 0.06%
Read min/max/mean length	30 / 76 / 76.02
Duplicated reads (estimated)	0 / 0%
Duplication rate	0%
Clipped reads	594 / 12.68%

2.2. ACGT Content

Number/percentage of A's	20,723 / 28.85%
Number/percentage of C's	13,411 / 18.67%
Number/percentage of T's	21,921 / 30.52%
Number/percentage of G's	15,770 / 21.96%
Number/percentage of N's	0 / 0%
GC Percentage	40.63%

2.3. Coverage

Mean	0

Standard Deviation	0.0048

2.4. Mapping Quality

Mean Mapping Quality	40.59

2.5. Mismatches and indels

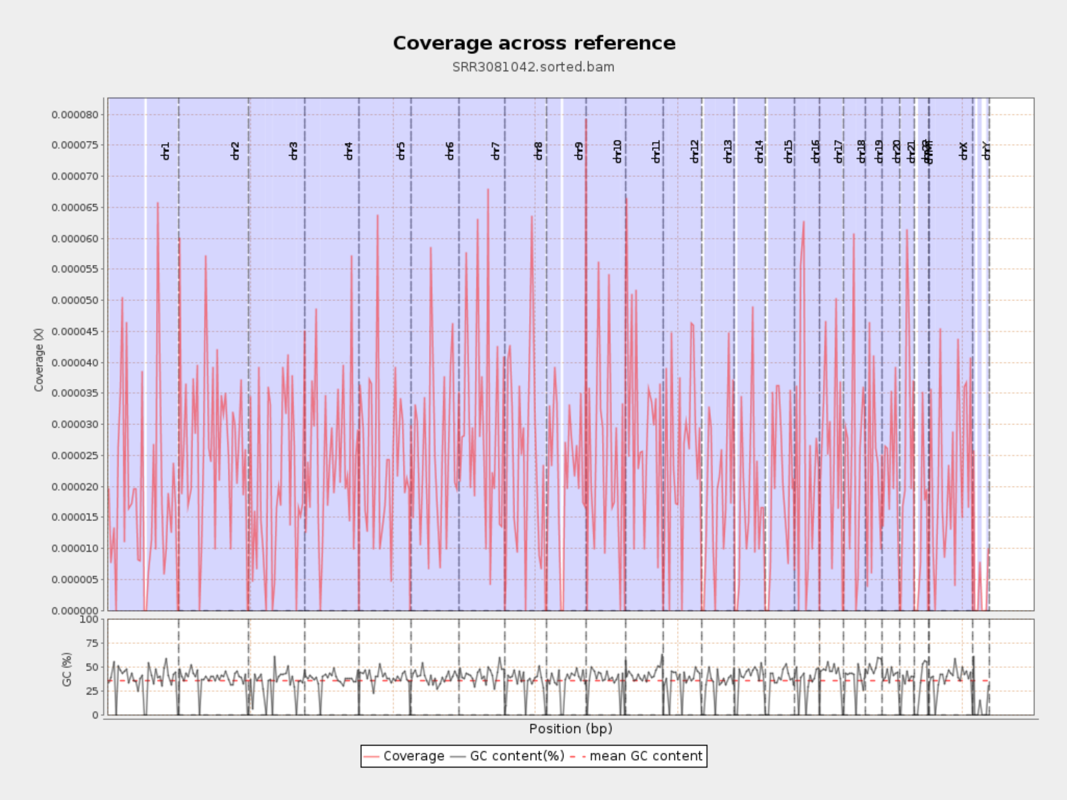
General error rate	0.86%
Mismatches	602
Insertions	5
Mapped reads with at least one insertion	0.44%
Deletions	19
Mapped reads with at least one deletion	1.68%
Homopolymer indels	37.5%

2.6. Chromosome stats

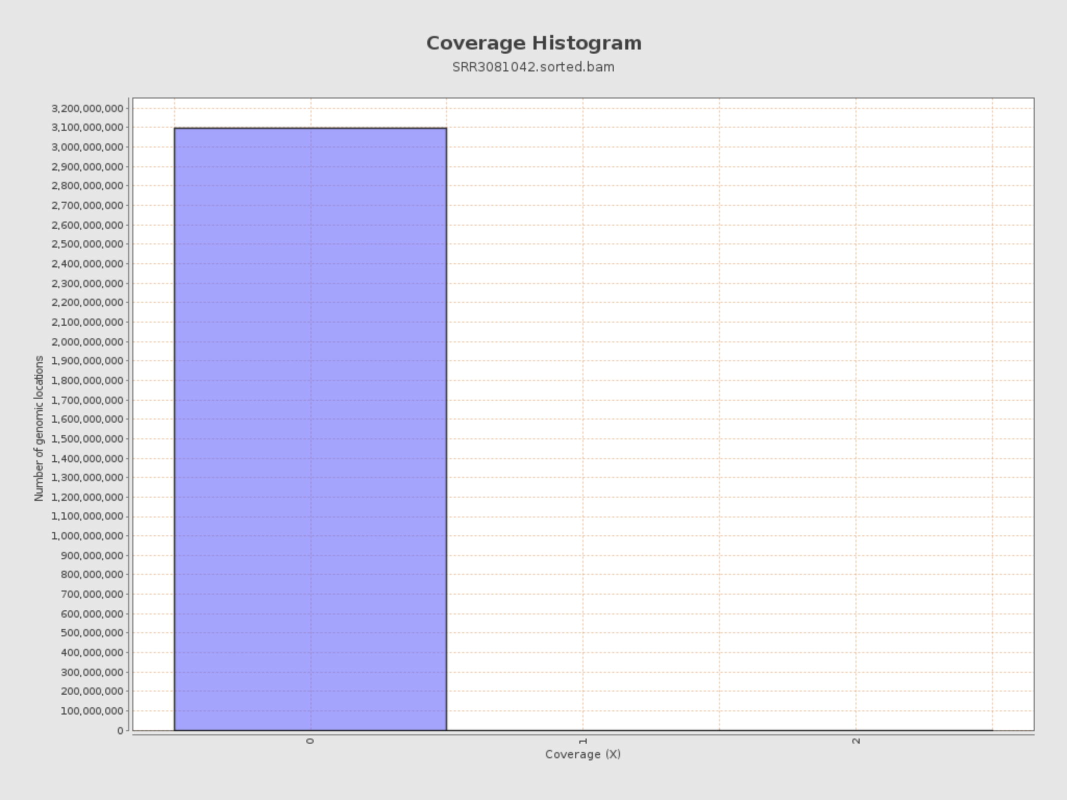
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4665	0	0.0043
chr2	243199373	6624	0	0.0052
chr3	198022430	3885	0	0.0044
chr4	191154276	4717	0	0.005
chr5	180915260	4428	0	0.0049
chr6	171115067	4477	0	0.0051
chr7	159138663	4806	0	0.0055

chr8	146364022	3542	0	0.0049
chr9	141213431	3180	0	0.0047
chr10	135534747	3201	0	0.0049
chr11	135006516	4012	0	0.0054
chr12	133851895	3419	0	0.0051
chr13	115169878	2174	0	0.0043
chr14	107349540	1852	0	0.0042
chr15	102531392	2074	0	0.0045
chr16	90354753	2109	0	0.0048
chr17	81195210	2251	0	0.0053
chr18	78077248	1880	0	0.0049
chr19	59128983	1338	0	0.0048
chr20	63025520	1455	0	0.0048
chr21	48129895	1446	0	0.0055
chr22	51304566	621	0	0.0035
chrMT	16571	0	0	0
chrX	155270560	3429	0	0.0047
chrY	59373566	271	0	0.0021

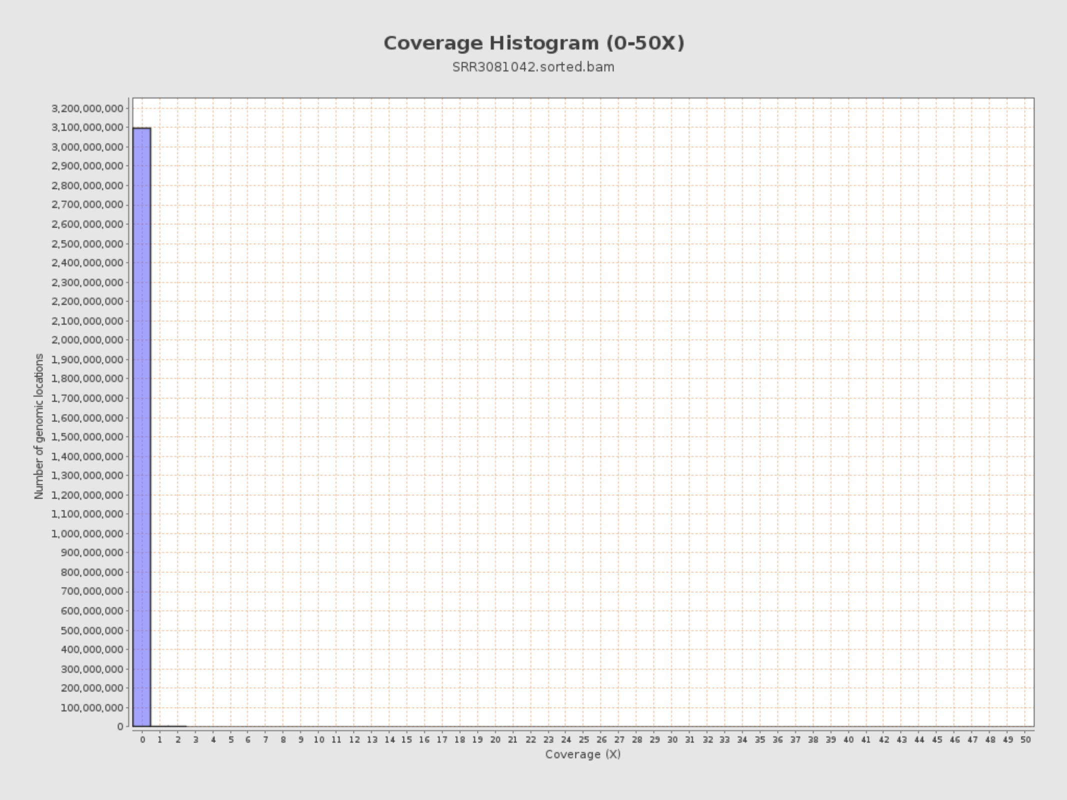
3. Results : Coverage across reference



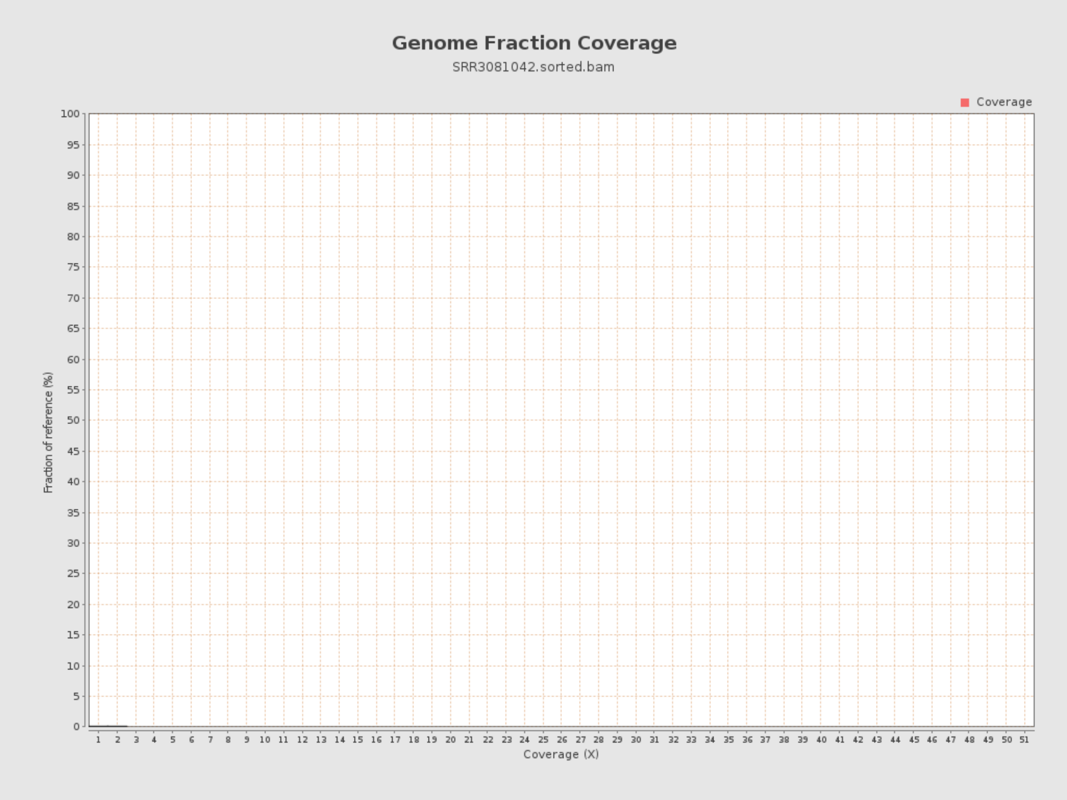
4. Results : Coverage Histogram



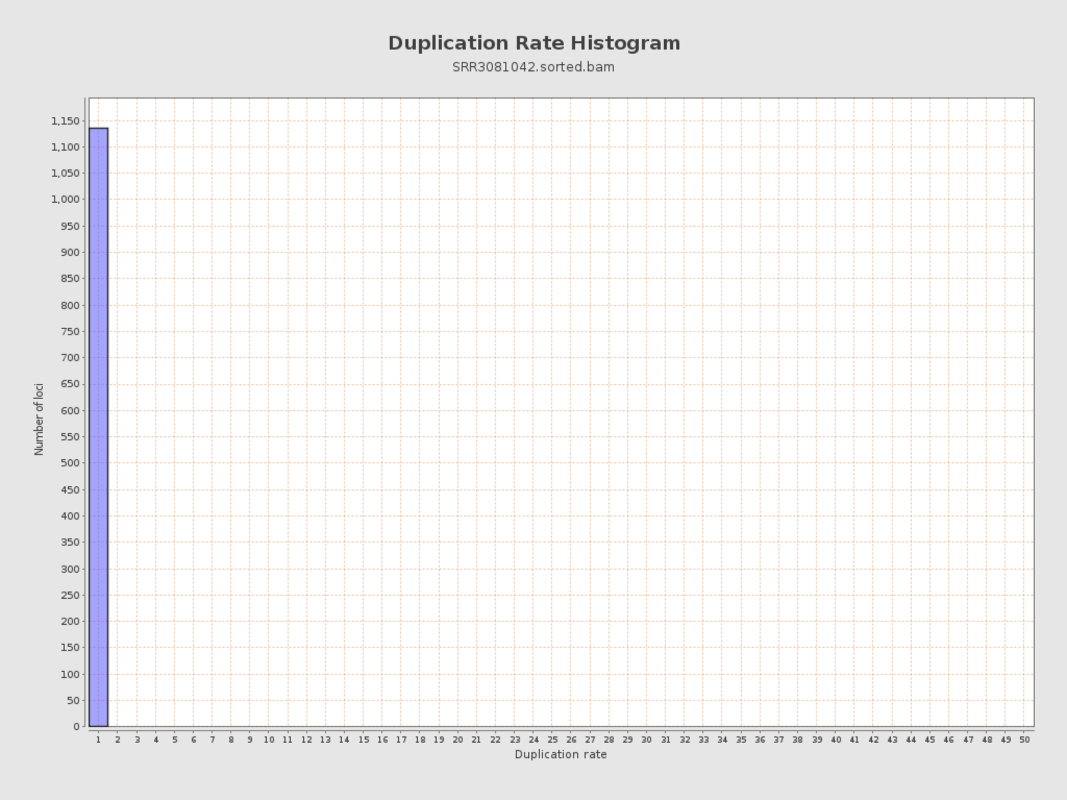
5. Results : Coverage Histogram (0-50X)



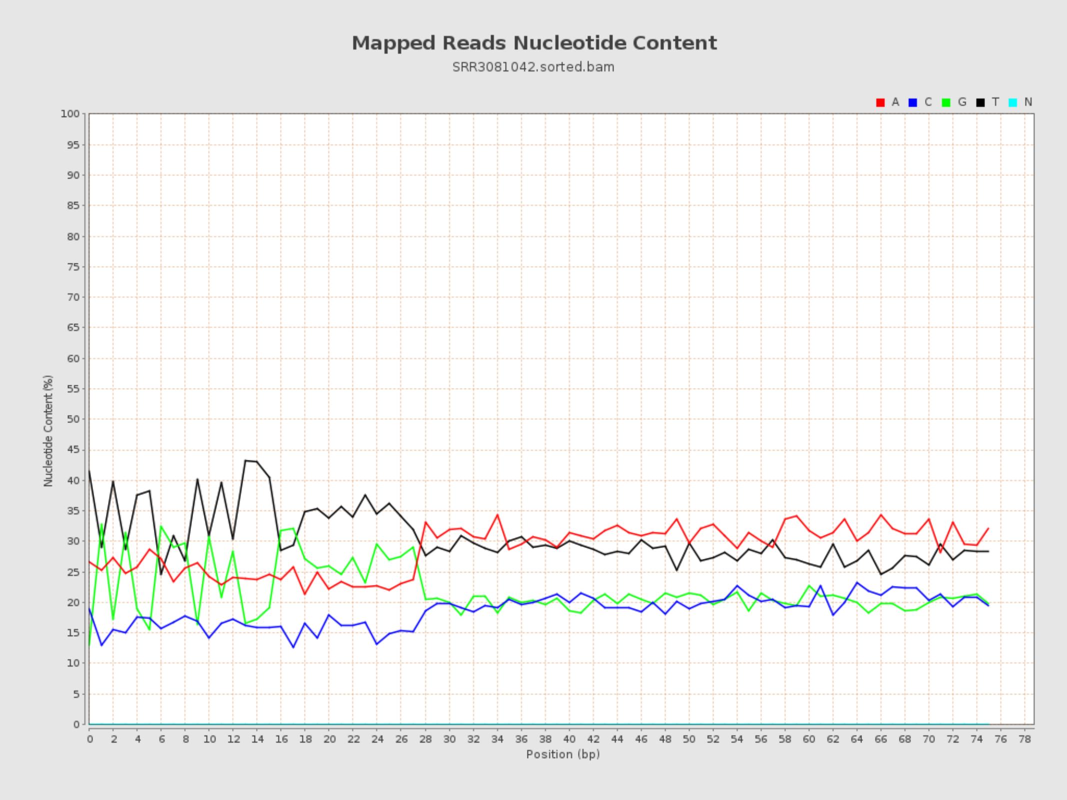
6. Results : Genome Fraction Coverage



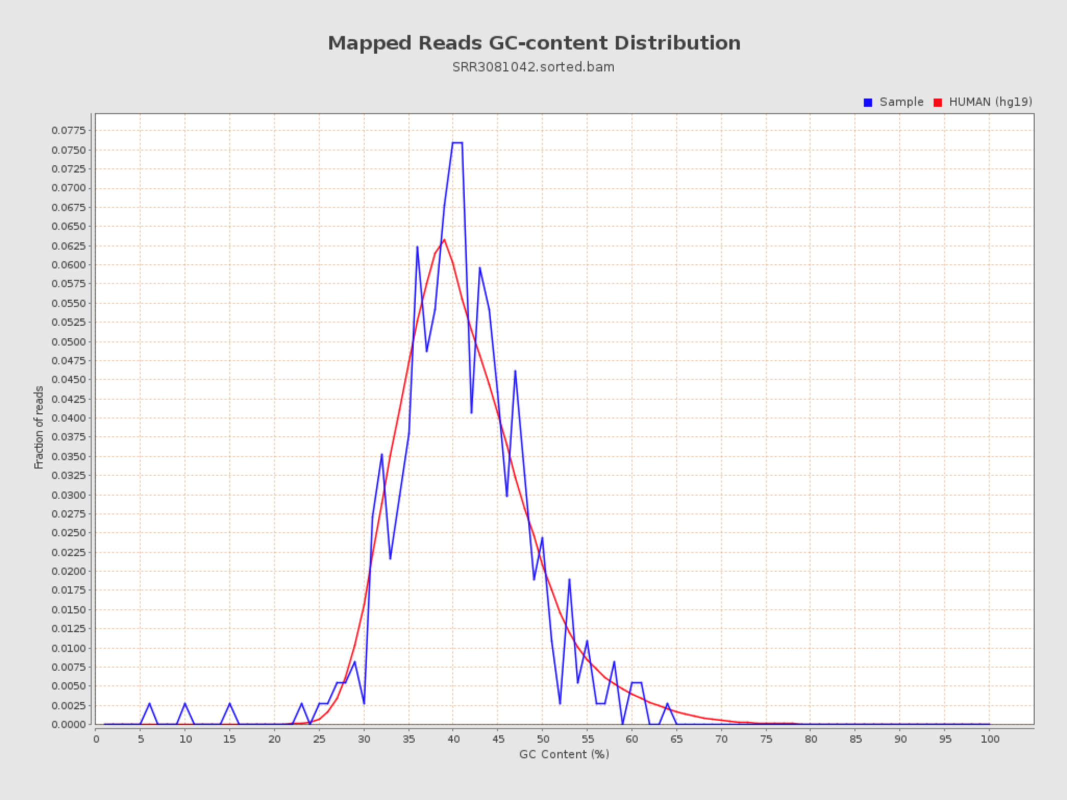
7. Results : Duplication Rate Histogram



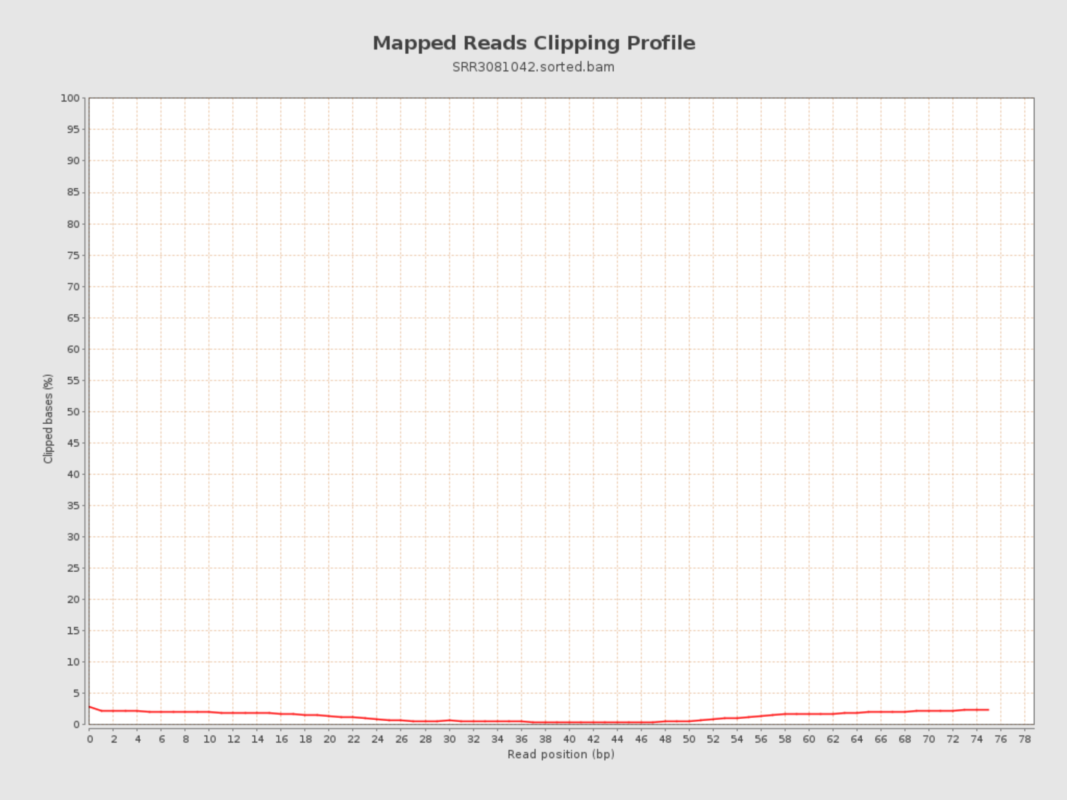
8. Results : Mapped Reads Nucleotide Content



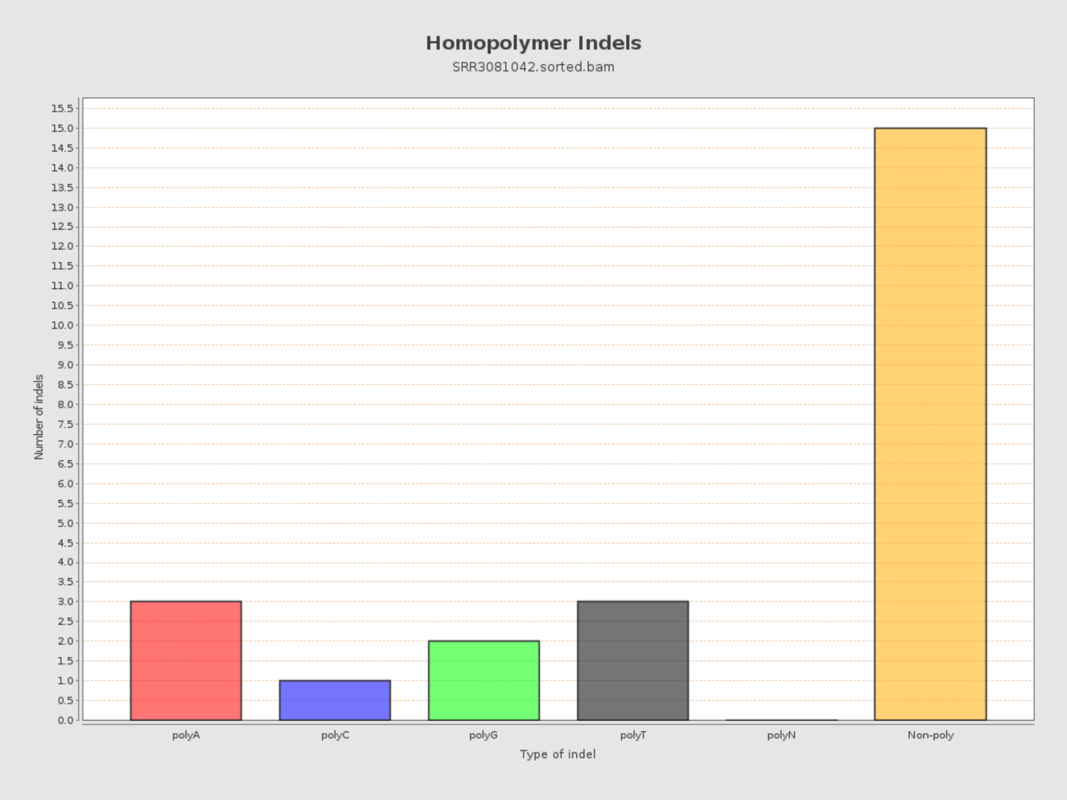
9. Results : Mapped Reads GC-content Distribution



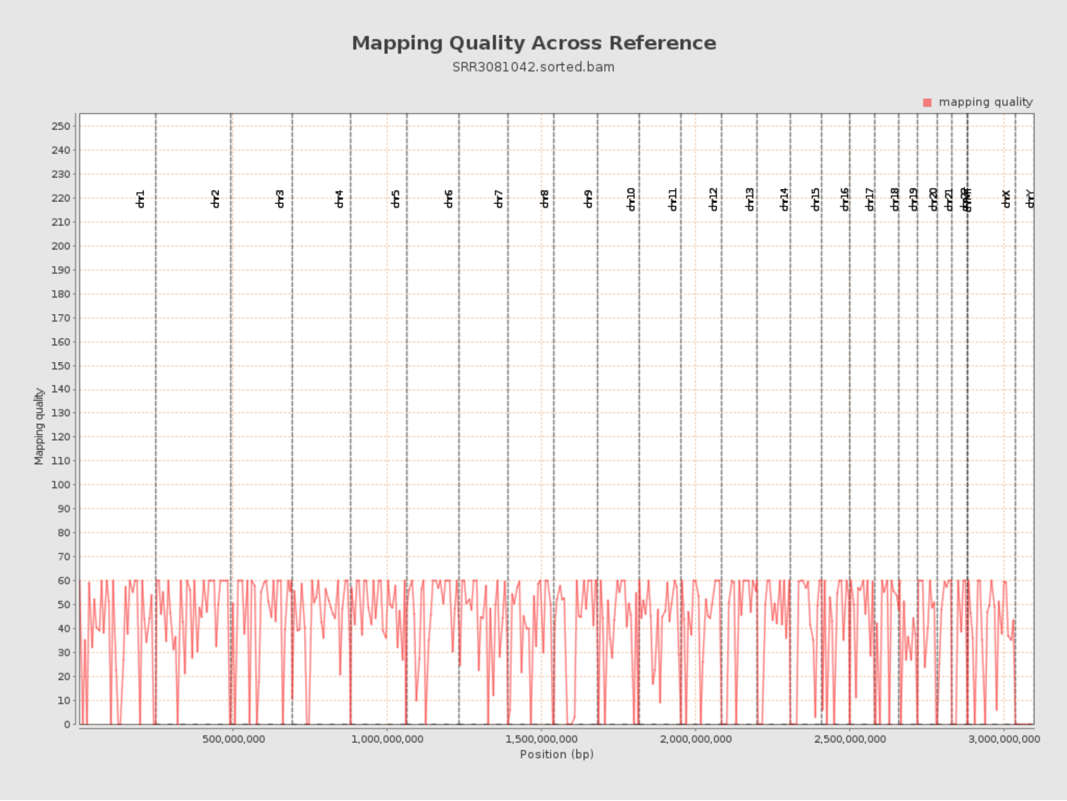
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram