Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 20:18:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524778.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_SRR10524778 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524778.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 20:18:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524778.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,467,652
Mapped reads	2,231,613 / 90.43%
Unmapped reads	236,039 / 9.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,948 / 0.4%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	99,750 / 4.04%
Duplication rate	3.24%
Clipped reads	2,236,638 / 90.64%

2.2. ACGT Content

Number/percentage of A's	32,267,227 / 25.46%
Number/percentage of C's	22,214,303 / 17.53%
Number/percentage of T's	42,433,218 / 33.48%
Number/percentage of G's	29,812,748 / 23.52%
Number/percentage of N's	2,627 / 0%
GC Percentage	41.05%

2.3. Coverage

Mean	0.041

Standard Deviation	0.398

2.4. Mapping Quality

Mean Mapping Quality	44.74

2.5. Mismatches and indels

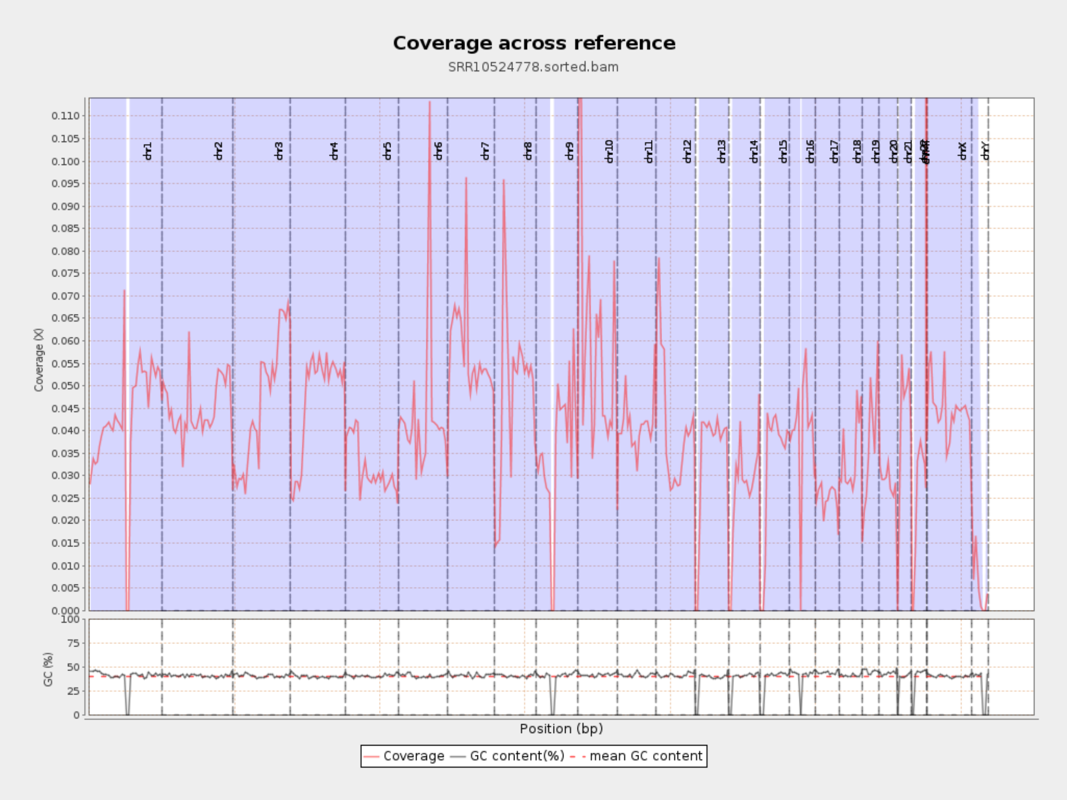
General error rate	0.52%
Mismatches	642,593
Insertions	9,140
Mapped reads with at least one insertion	0.41%
Deletions	25,052
Mapped reads with at least one deletion	1.11%
Homopolymer indels	43.56%

2.6. Chromosome stats

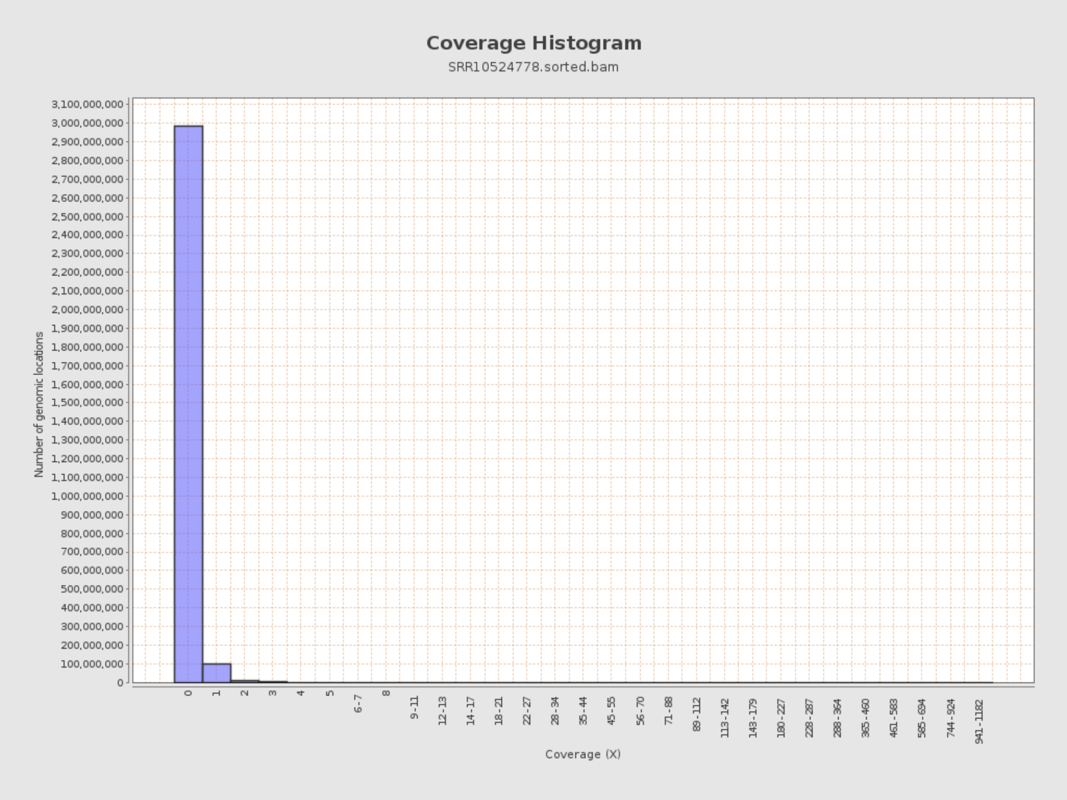
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10685407	0.0429	0.7194
chr2	243199373	10999251	0.0452	0.5373
chr3	198022430	9162825	0.0463	0.2447
chr4	191154276	9008754	0.0471	0.252
chr5	180915260	5754355	0.0318	0.2
chr6	171115067	7550021	0.0441	0.2776
chr7	159138663	9239860	0.0581	0.7698

chr8	146364022	7003590	0.0479	0.3613
chr9	141213431	5004554	0.0354	0.2804
chr10	135534747	8230998	0.0607	0.4212
chr11	135006516	5568261	0.0412	0.2923
chr12	133851895	5493983	0.041	0.2295
chr13	115169878	3956995	0.0344	0.2093
chr14	107349540	2818336	0.0263	0.1892
chr15	102531392	3302874	0.0322	0.2153
chr16	90354753	3586300	0.0397	0.2503
chr17	81195210	2010058	0.0248	0.1833
chr18	78077248	2681141	0.0343	0.525
chr19	59128983	2243008	0.0379	0.5116
chr20	63025520	1794130	0.0285	0.1934
chr21	48129895	2014254	0.0419	0.2347
chr22	51304566	1224959	0.0239	0.1718
chrMT	16571	131715	7.9485	5.042
chrX	155270560	6964893	0.0449	0.2684
chrY	59373566	338889	0.0057	0.129

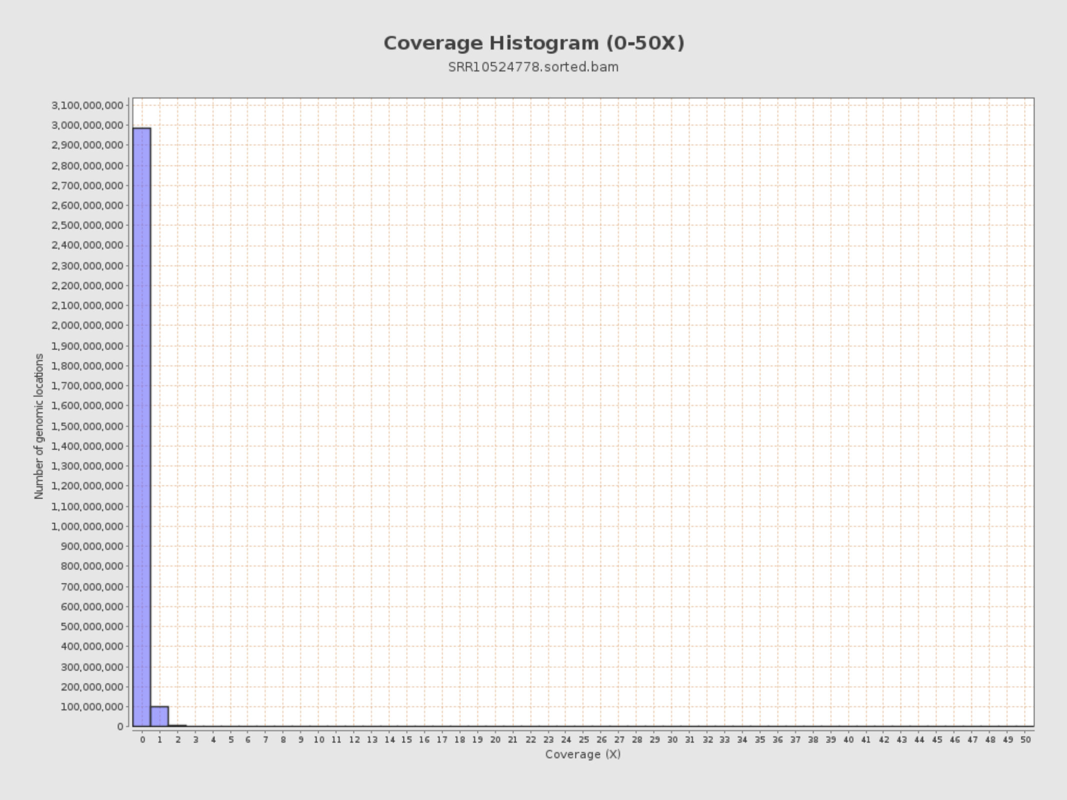
3. Results : Coverage across reference



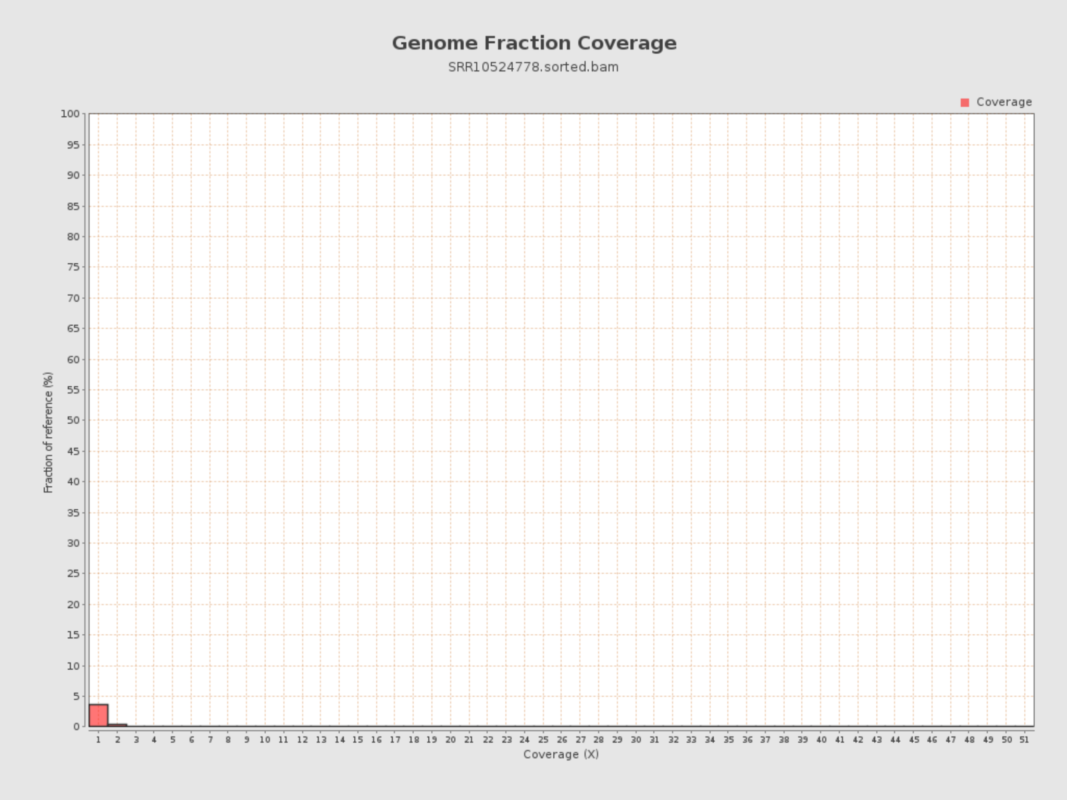
4. Results : Coverage Histogram



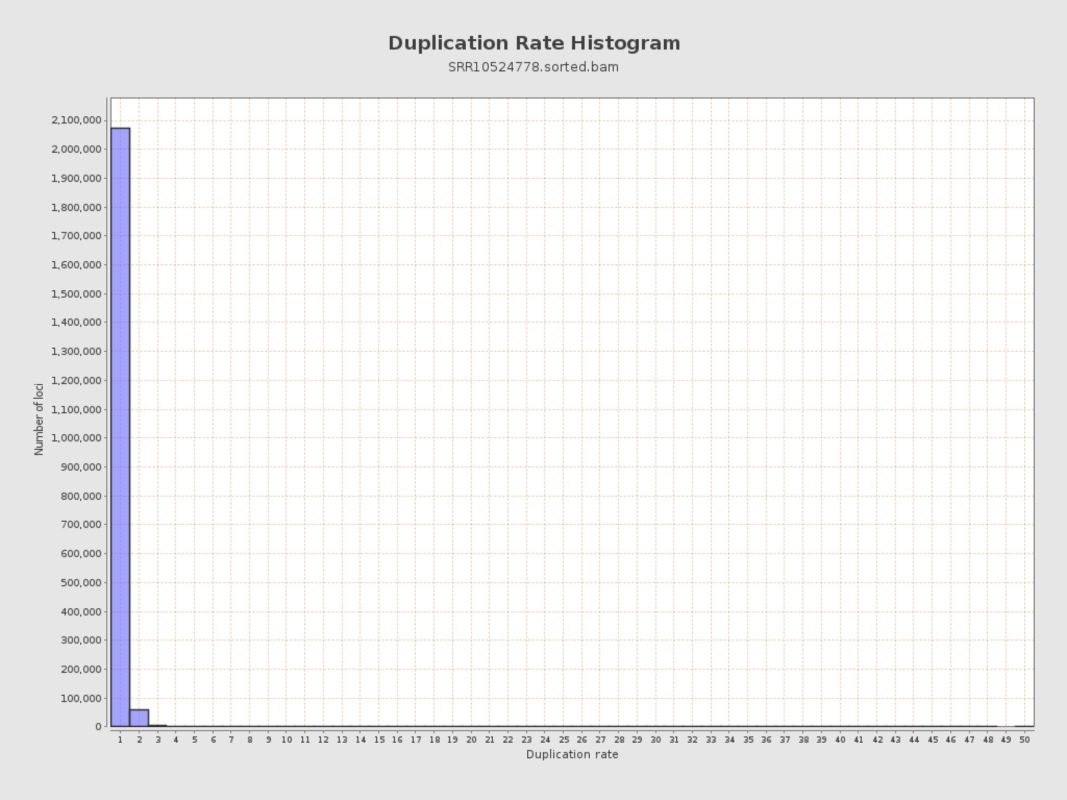
5. Results : Coverage Histogram (0-50X)



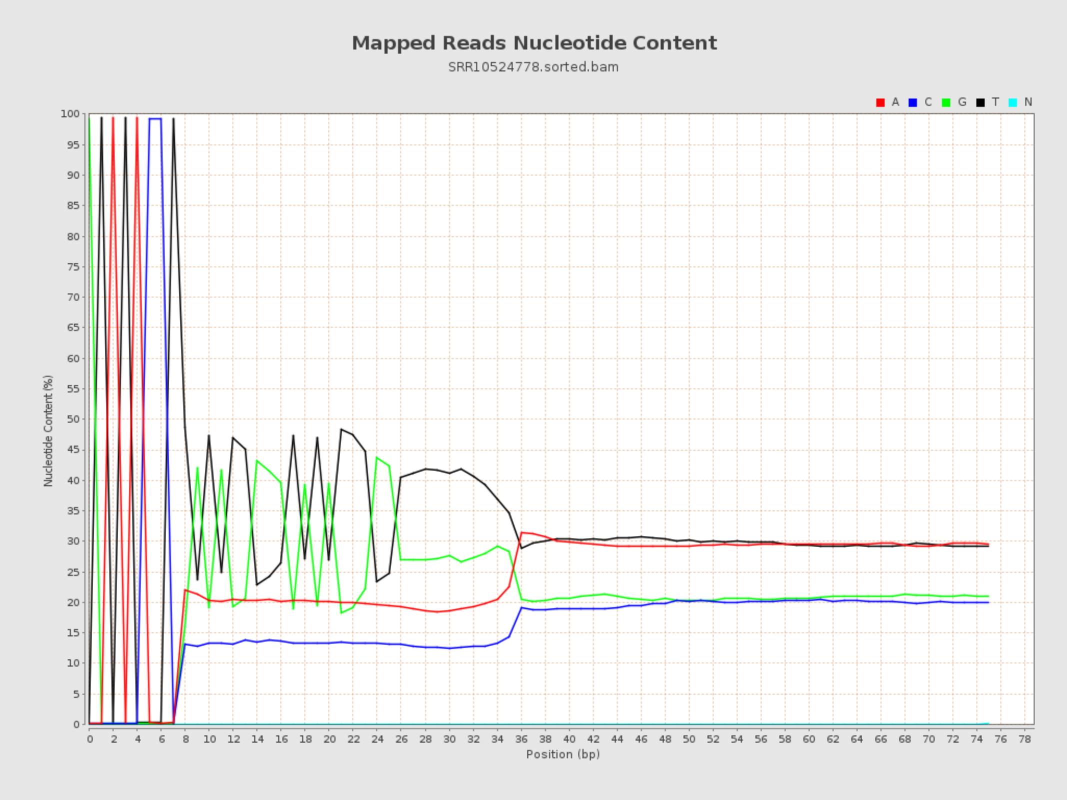
6. Results : Genome Fraction Coverage



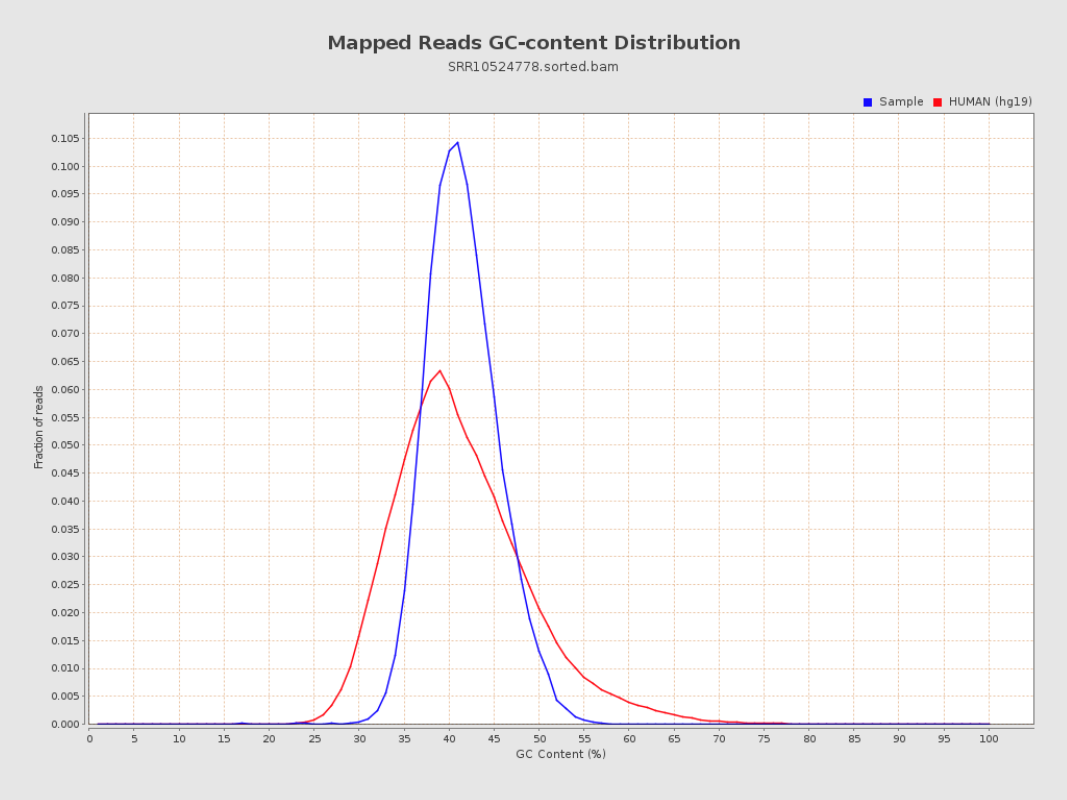
7. Results : Duplication Rate Histogram



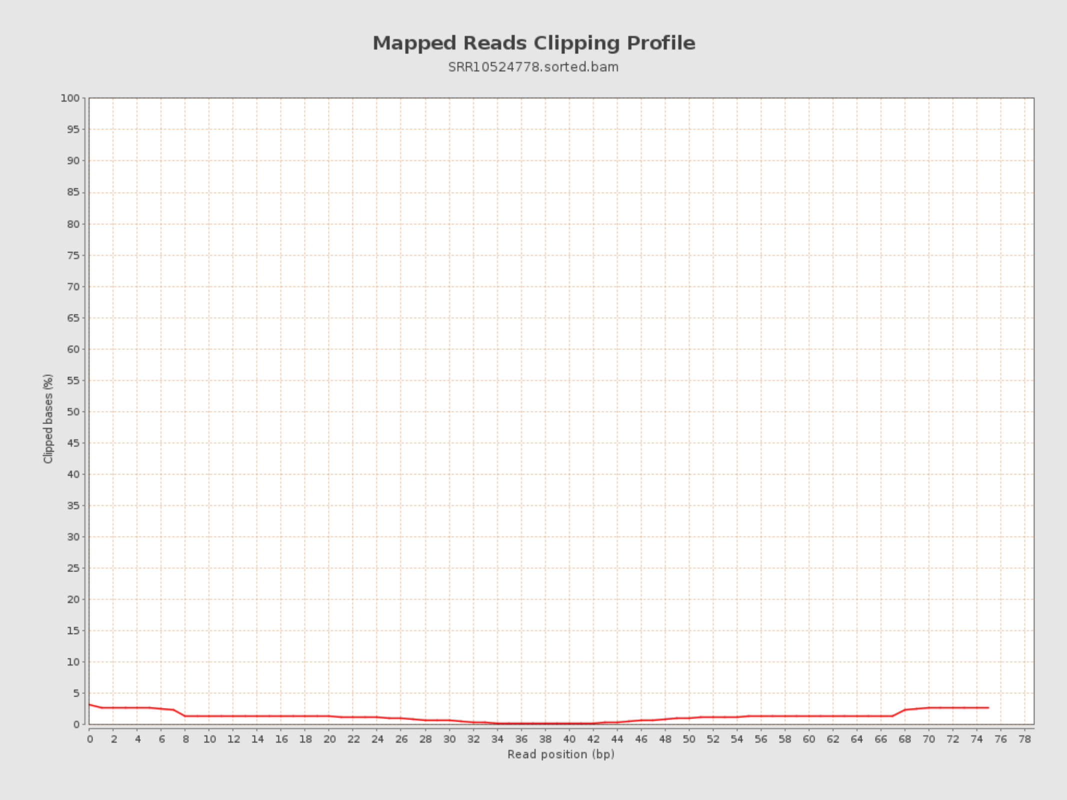
8. Results : Mapped Reads Nucleotide Content



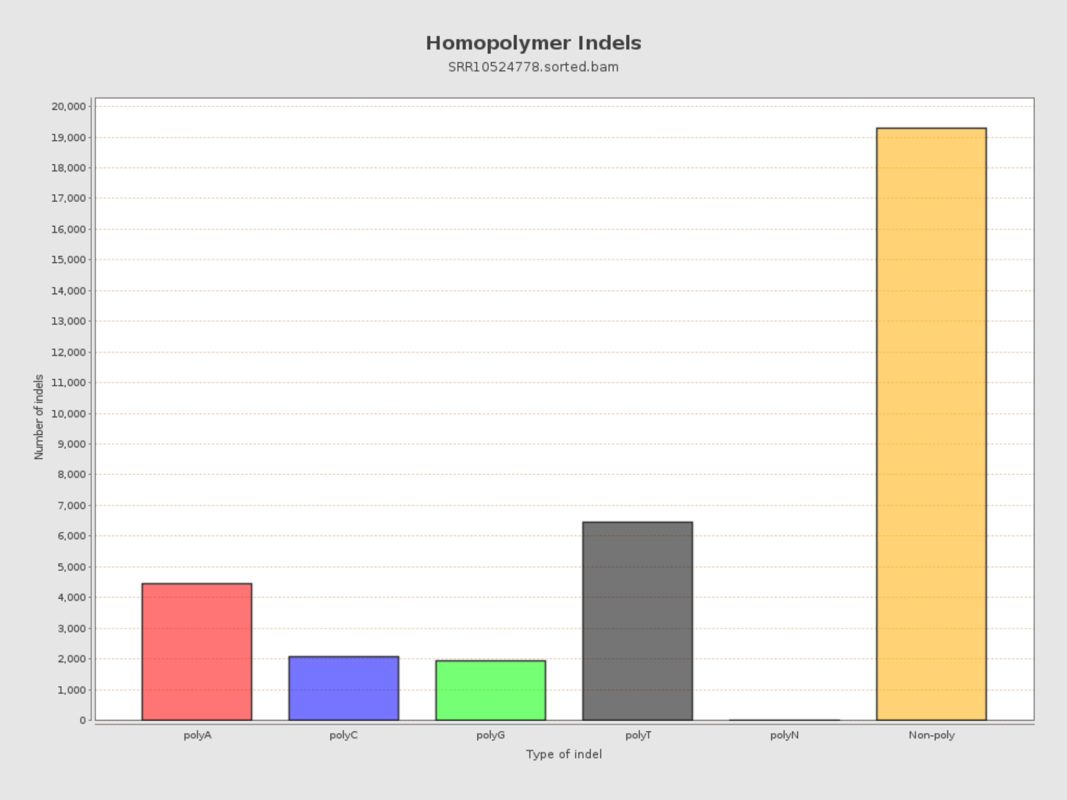
9. Results : Mapped Reads GC-content Distribution



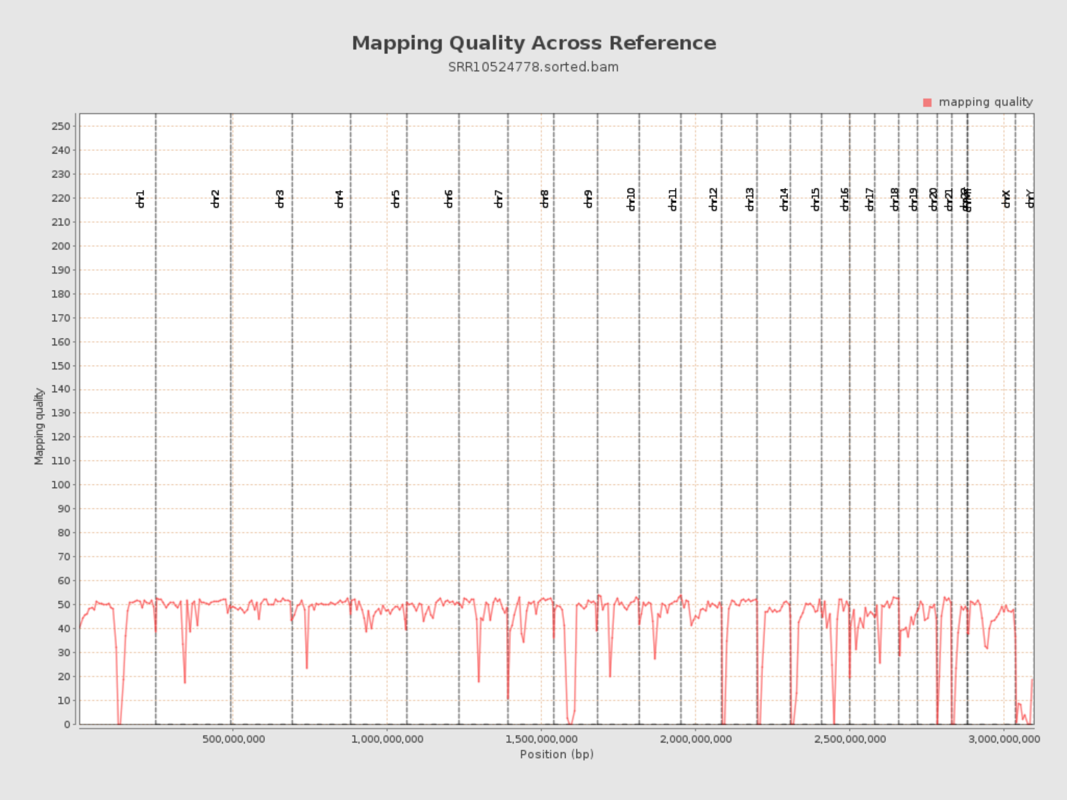
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram