Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 05:31:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524471.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_SRR10524471 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524471.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 05:31:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524471.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,427,309
Mapped reads	1,306,403 / 91.53%
Unmapped reads	120,906 / 8.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,985 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	48,669 / 3.41%
Duplication rate	2.8%
Clipped reads	1,305,612 / 91.47%

2.2. ACGT Content

Number/percentage of A's	19,443,609 / 25.6%
Number/percentage of C's	13,462,631 / 17.73%
Number/percentage of T's	23,709,505 / 31.22%
Number/percentage of G's	19,325,726 / 25.45%
Number/percentage of N's	1,606 / 0%
GC Percentage	43.17%

2.3. Coverage

Mean	0.0245

Standard Deviation	0.2393

2.4. Mapping Quality

Mean Mapping Quality	45.07

2.5. Mismatches and indels

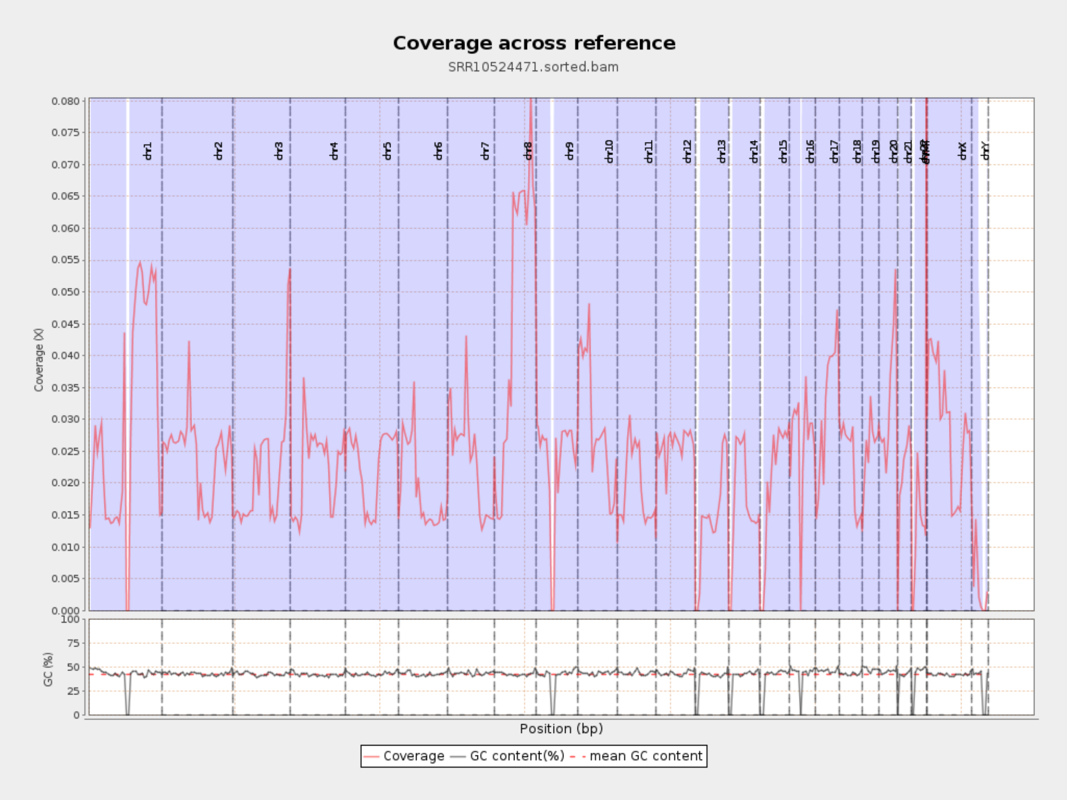
General error rate	0.48%
Mismatches	356,778
Insertions	4,896
Mapped reads with at least one insertion	0.37%
Deletions	14,427
Mapped reads with at least one deletion	1.1%
Homopolymer indels	41.9%

2.6. Chromosome stats

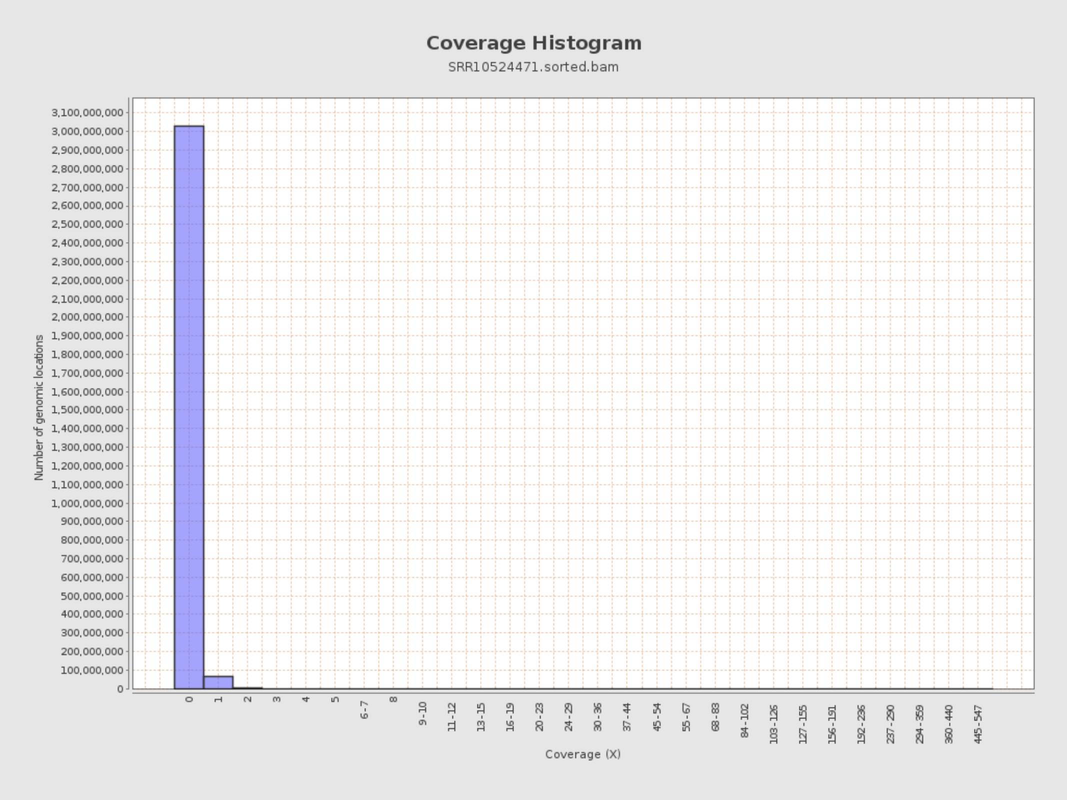
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7475152	0.03	0.43
chr2	243199373	5936017	0.0244	0.2588
chr3	198022430	4204839	0.0212	0.161
chr4	191154276	4289877	0.0224	0.1825
chr5	180915260	4188028	0.0231	0.1661
chr6	171115067	3251556	0.019	0.1905
chr7	159138663	3780588	0.0238	0.3092

chr8	146364022	6995868	0.0478	0.2676
chr9	141213431	3244554	0.023	0.2121
chr10	135534747	4001337	0.0295	0.2557
chr11	135006516	2618761	0.0194	0.2167
chr12	133851895	3501725	0.0262	0.1764
chr13	115169878	1689700	0.0147	0.1321
chr14	107349540	1812980	0.0169	0.1444
chr15	102531392	2044255	0.0199	0.1589
chr16	90354753	2396452	0.0265	0.1891
chr17	81195210	2654441	0.0327	0.2048
chr18	78077248	1803374	0.0231	0.348
chr19	59128983	1534294	0.0259	0.3145
chr20	63025520	2117327	0.0336	0.2014
chr21	48129895	1025499	0.0213	0.1686
chr22	51304566	603464	0.0118	0.1172
chrMT	16571	3524	0.2127	0.4794
chrX	155270560	4553481	0.0293	0.2036
chrY	59373566	240785	0.0041	0.1185

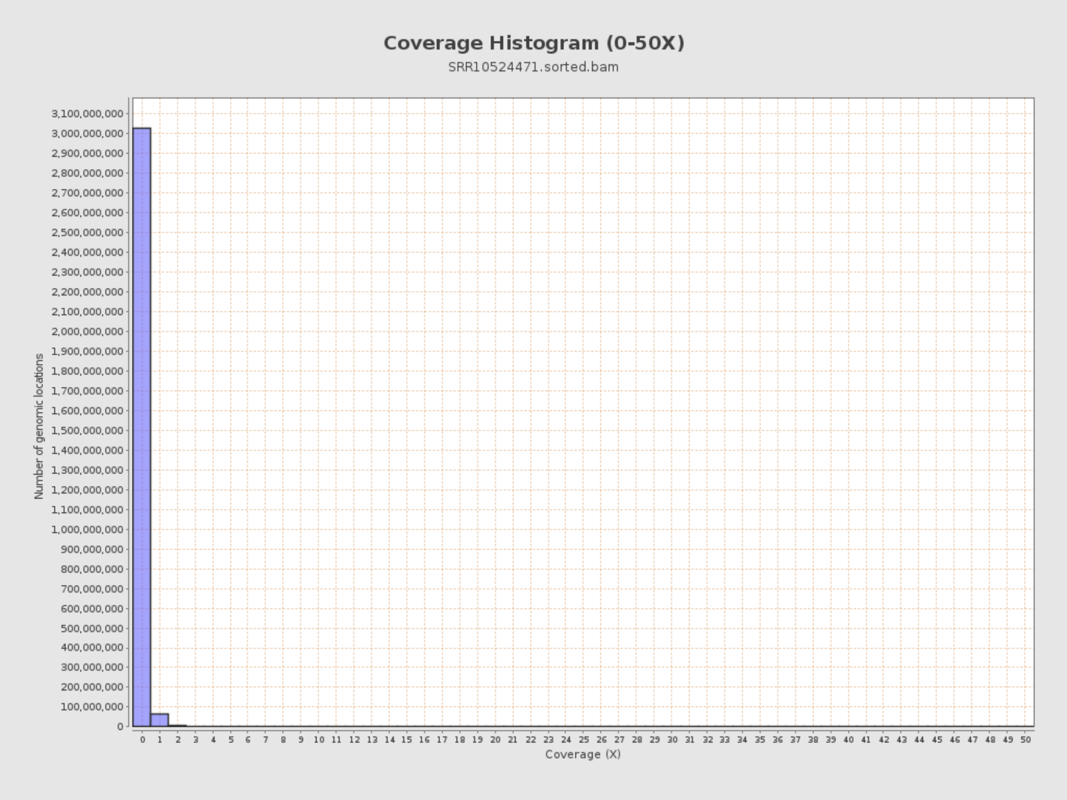
3. Results : Coverage across reference



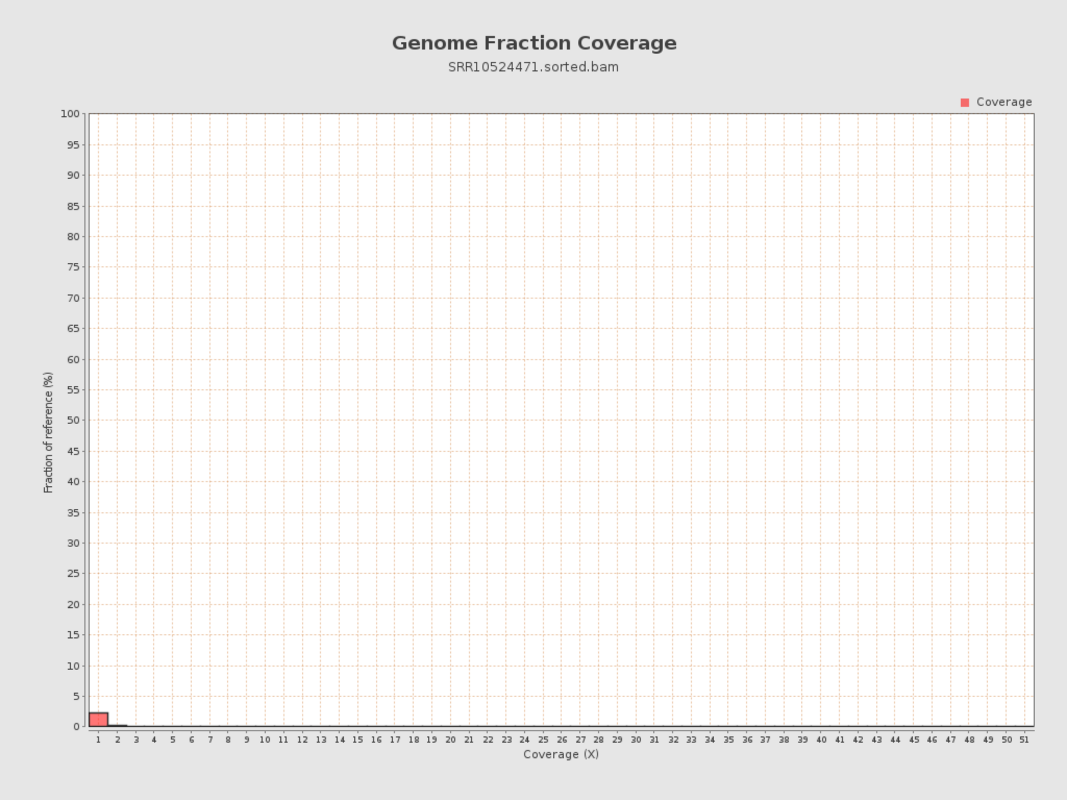
4. Results : Coverage Histogram



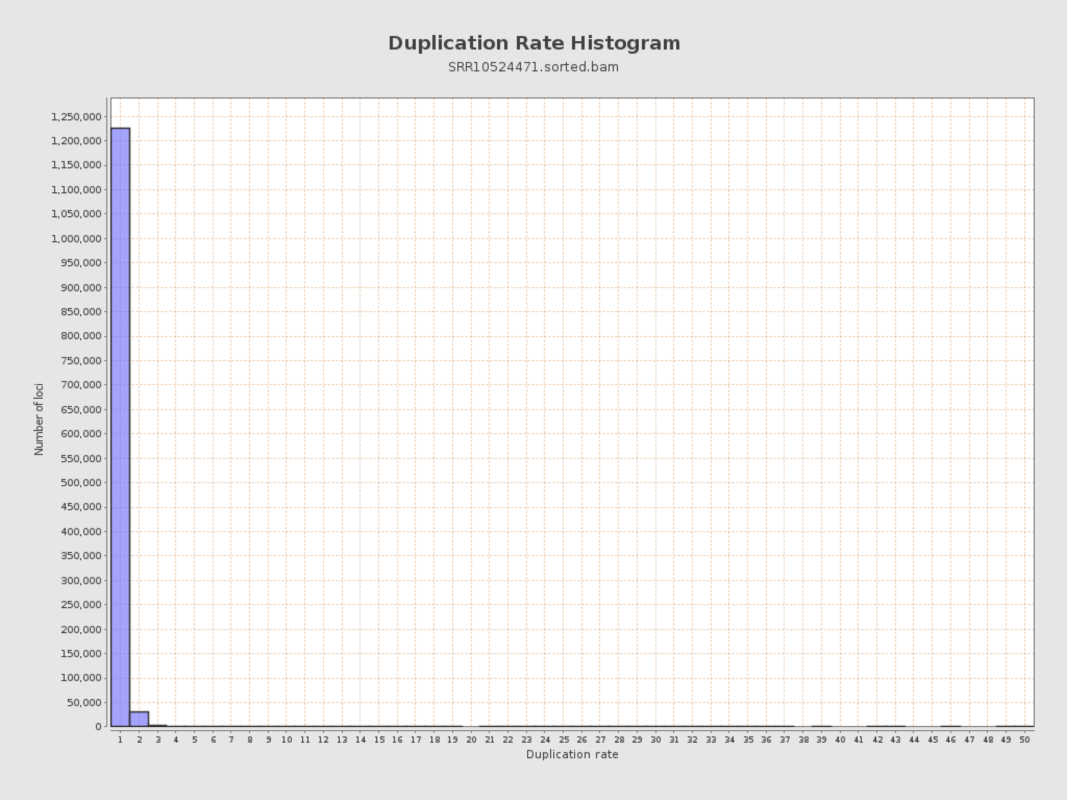
5. Results : Coverage Histogram (0-50X)



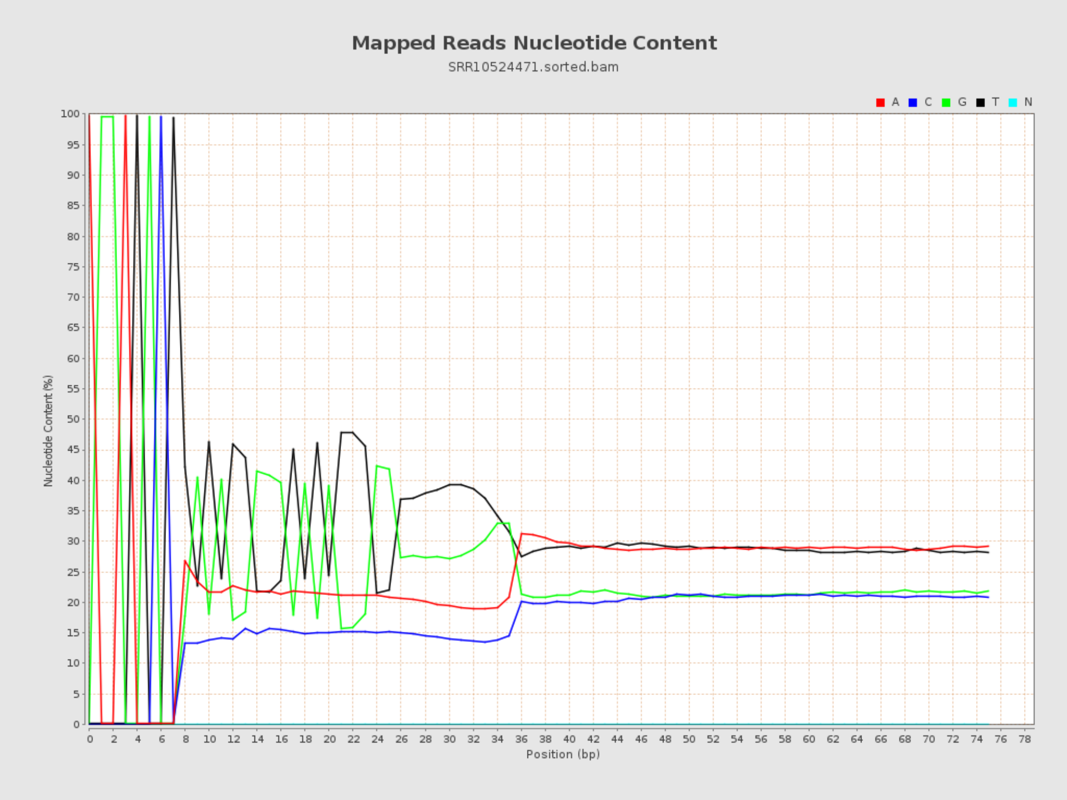
6. Results : Genome Fraction Coverage



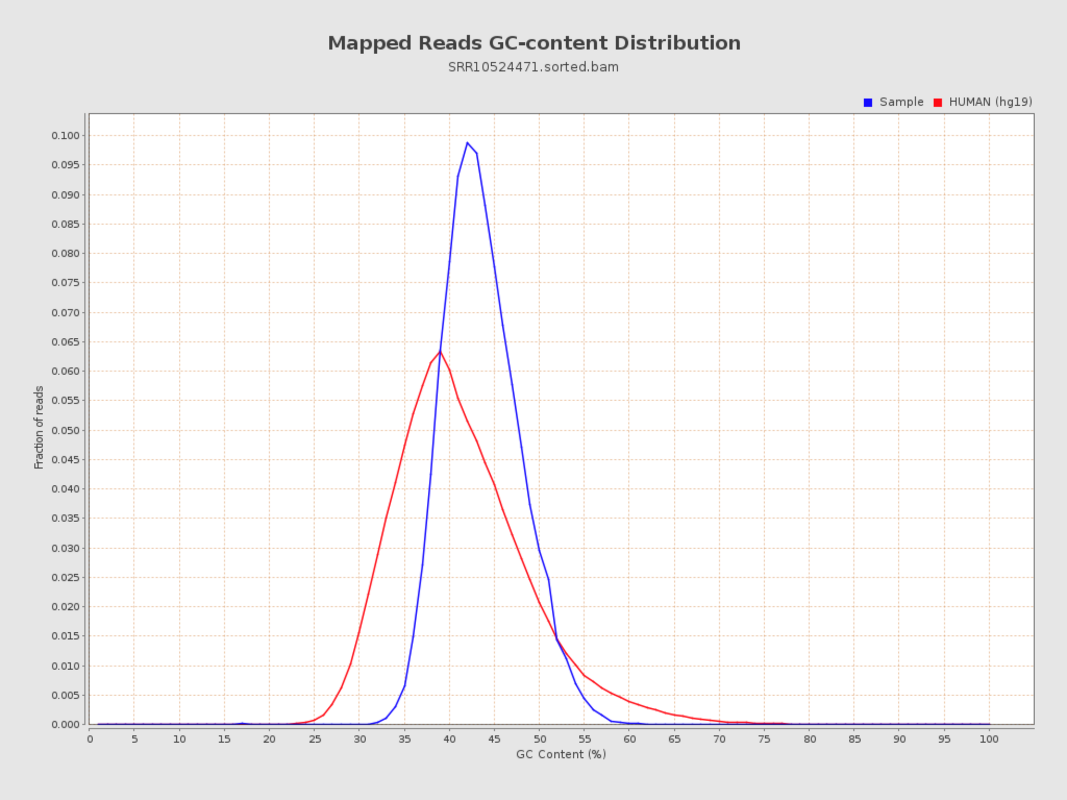
7. Results : Duplication Rate Histogram



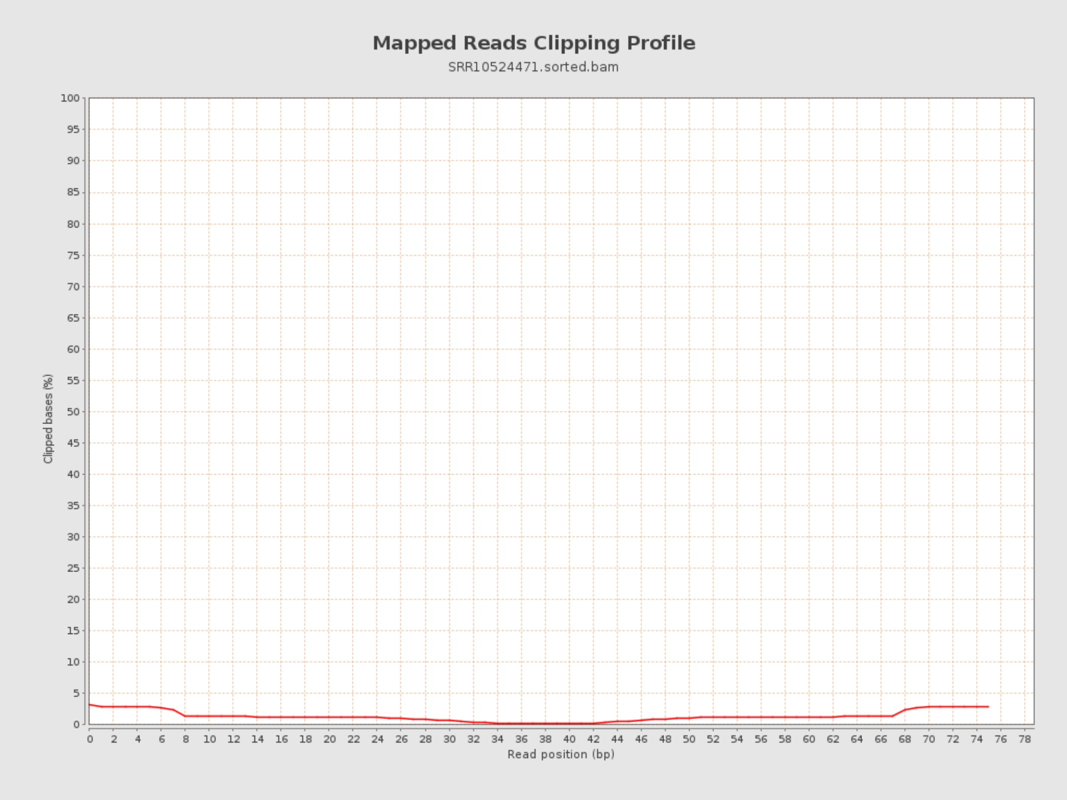
8. Results : Mapped Reads Nucleotide Content



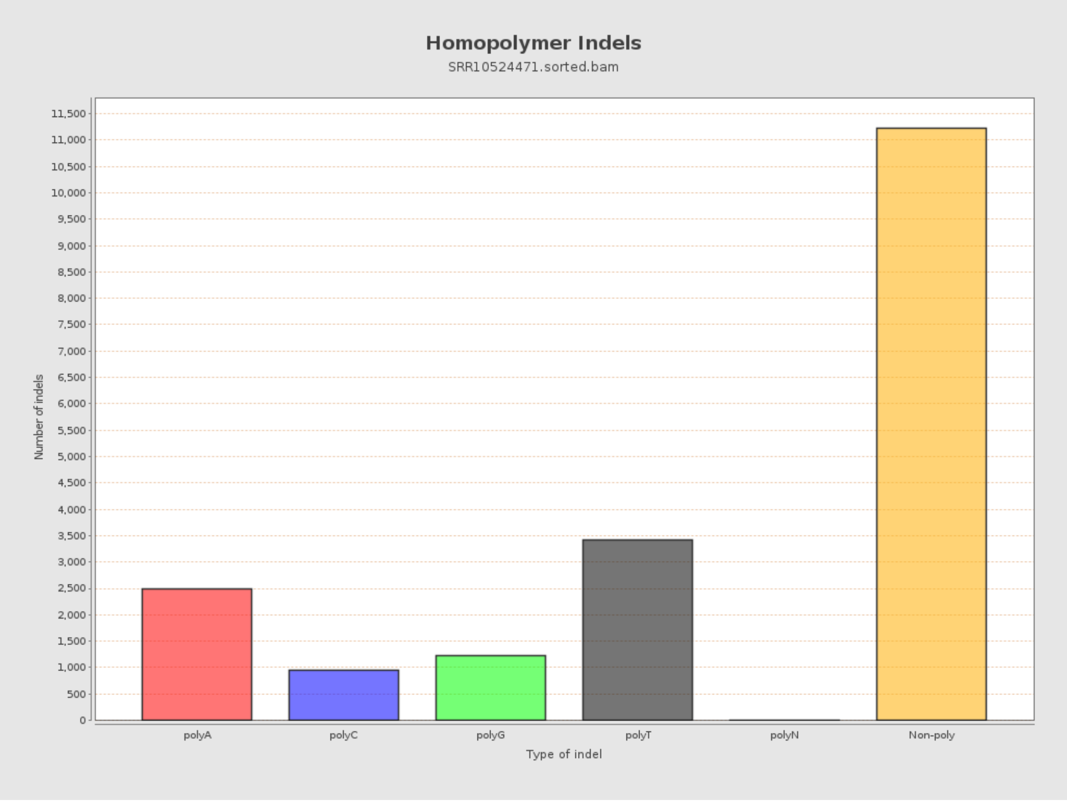
9. Results : Mapped Reads GC-content Distribution



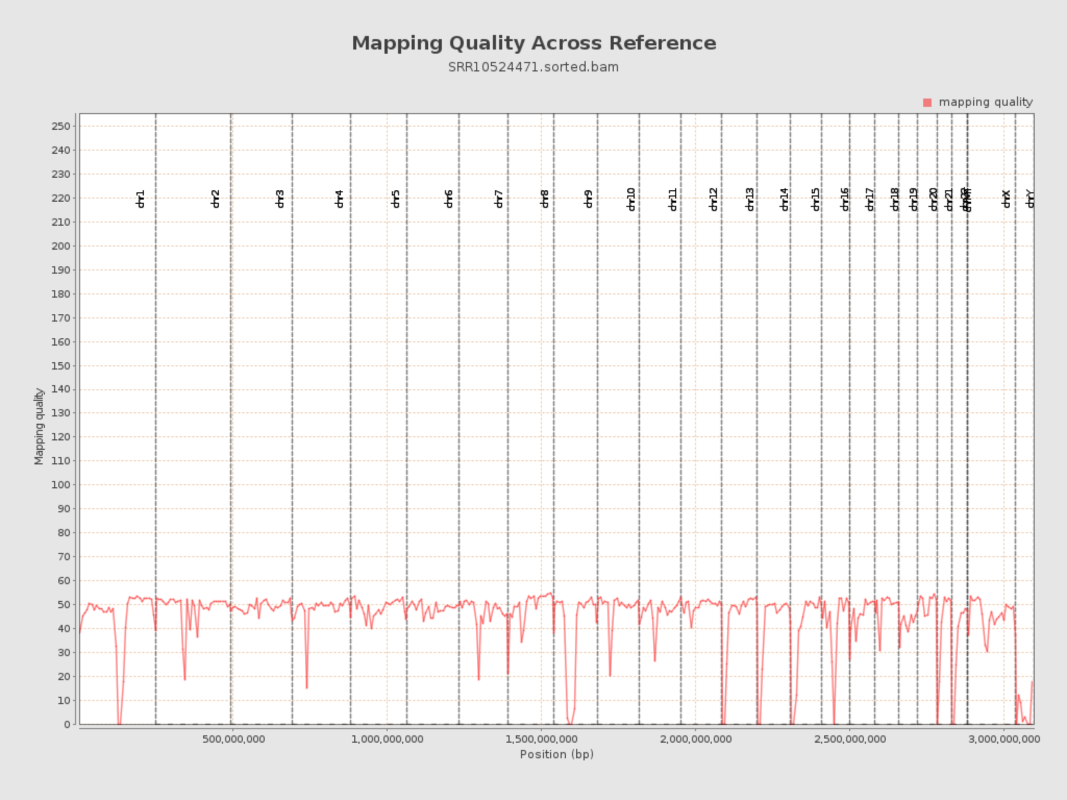
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram