Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 23:05:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524851.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_SRR10524851 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524851.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 23:05:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524851.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	400,709
Mapped reads	369,047 / 92.1%
Unmapped reads	31,662 / 7.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,447 / 0.61%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	5,287 / 1.32%
Duplication rate	1.04%
Clipped reads	371,292 / 92.66%

2.2. ACGT Content

Number/percentage of A's	5,538,421 / 25.52%
Number/percentage of C's	4,234,717 / 19.51%
Number/percentage of T's	6,718,300 / 30.95%
Number/percentage of G's	5,209,476 / 24%
Number/percentage of N's	3,020 / 0.01%
GC Percentage	43.51%

2.3. Coverage

Mean	0.007

Standard Deviation	0.1014

2.4. Mapping Quality

Mean Mapping Quality	44.47

2.5. Mismatches and indels

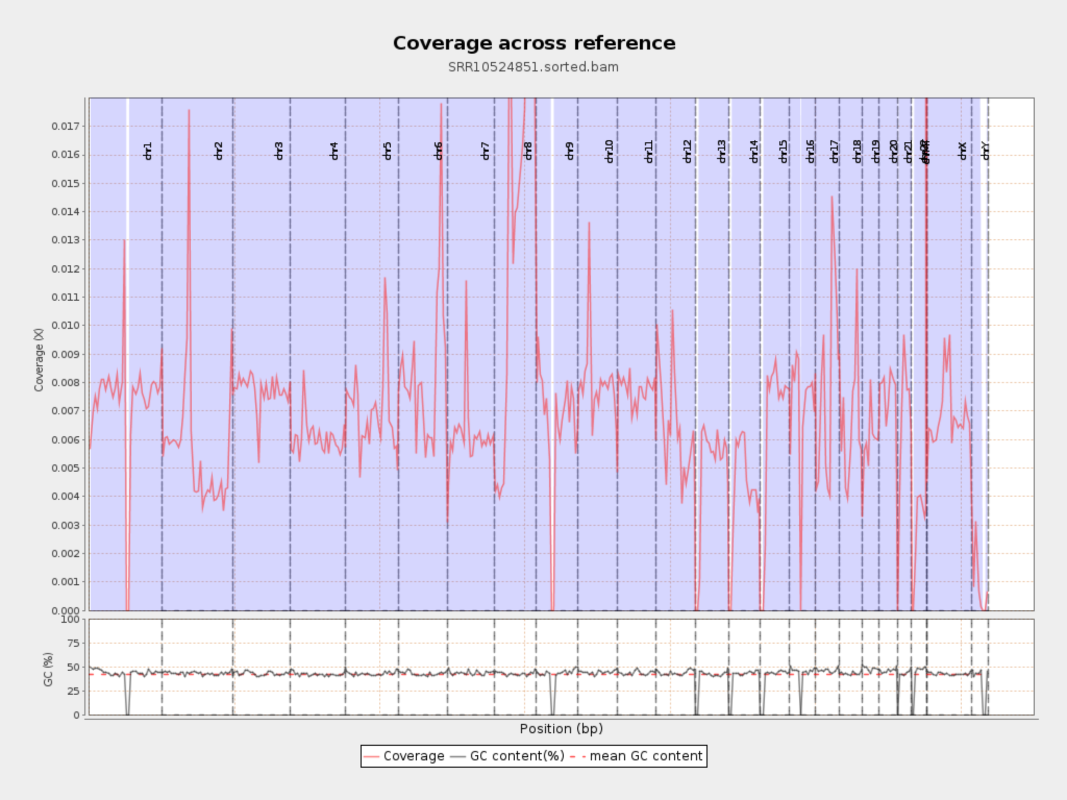
General error rate	0.49%
Mismatches	103,179
Insertions	1,254
Mapped reads with at least one insertion	0.34%
Deletions	3,957
Mapped reads with at least one deletion	1.07%
Homopolymer indels	44.96%

2.6. Chromosome stats

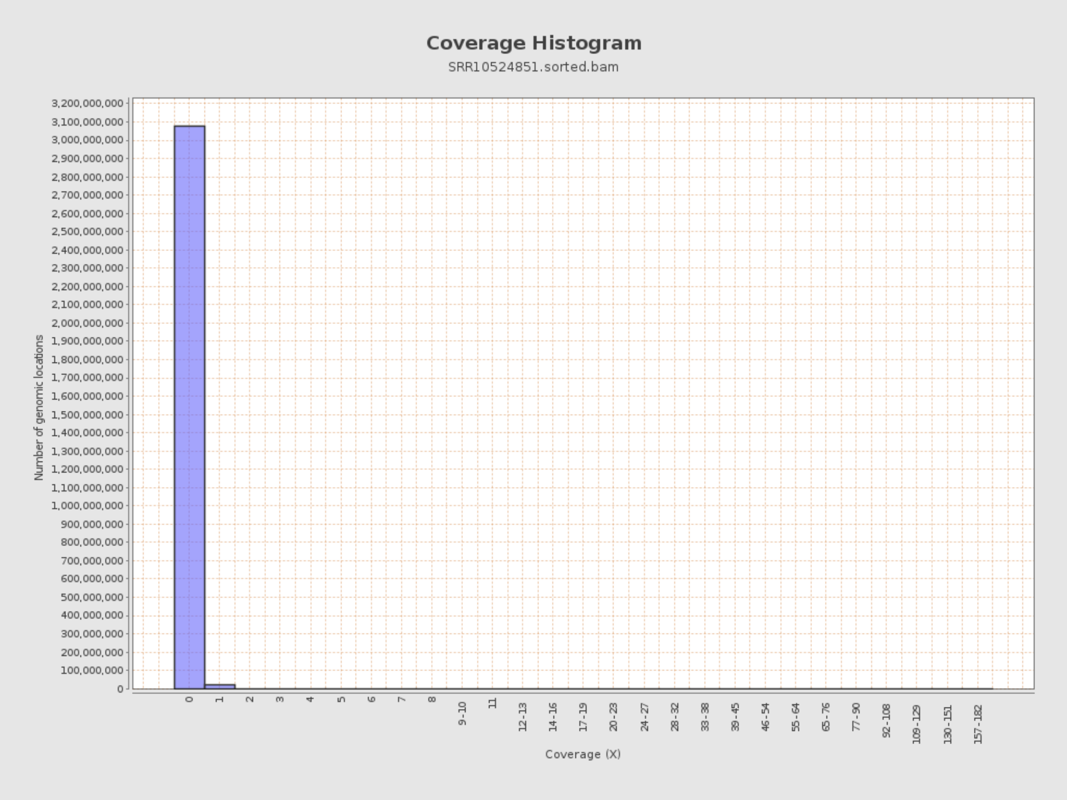
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1822727	0.0073	0.157
chr2	243199373	1396646	0.0057	0.1015
chr3	198022430	1523396	0.0077	0.0893
chr4	191154276	1157024	0.0061	0.0814
chr5	180915260	1284285	0.0071	0.0859
chr6	171115067	1415282	0.0083	0.0954
chr7	159138663	996993	0.0063	0.116

chr8	146364022	2319623	0.0158	0.1447
chr9	141213431	906411	0.0064	0.0928
chr10	135534747	1095545	0.0081	0.1031
chr11	135006516	1039278	0.0077	0.0986
chr12	133851895	871890	0.0065	0.083
chr13	115169878	557329	0.0048	0.0708
chr14	107349540	449932	0.0042	0.0672
chr15	102531392	657389	0.0064	0.0817
chr16	90354753	645044	0.0071	0.088
chr17	81195210	632674	0.0078	0.0935
chr18	78077248	530150	0.0068	0.1248
chr19	59128983	355528	0.006	0.1102
chr20	63025520	481334	0.0076	0.0892
chr21	48129895	313697	0.0065	0.0832
chr22	51304566	136981	0.0027	0.0525
chrMT	16571	3470	0.2094	0.486
chrX	155270560	1063070	0.0068	0.087
chrY	59373566	54527	0.0009	0.0377

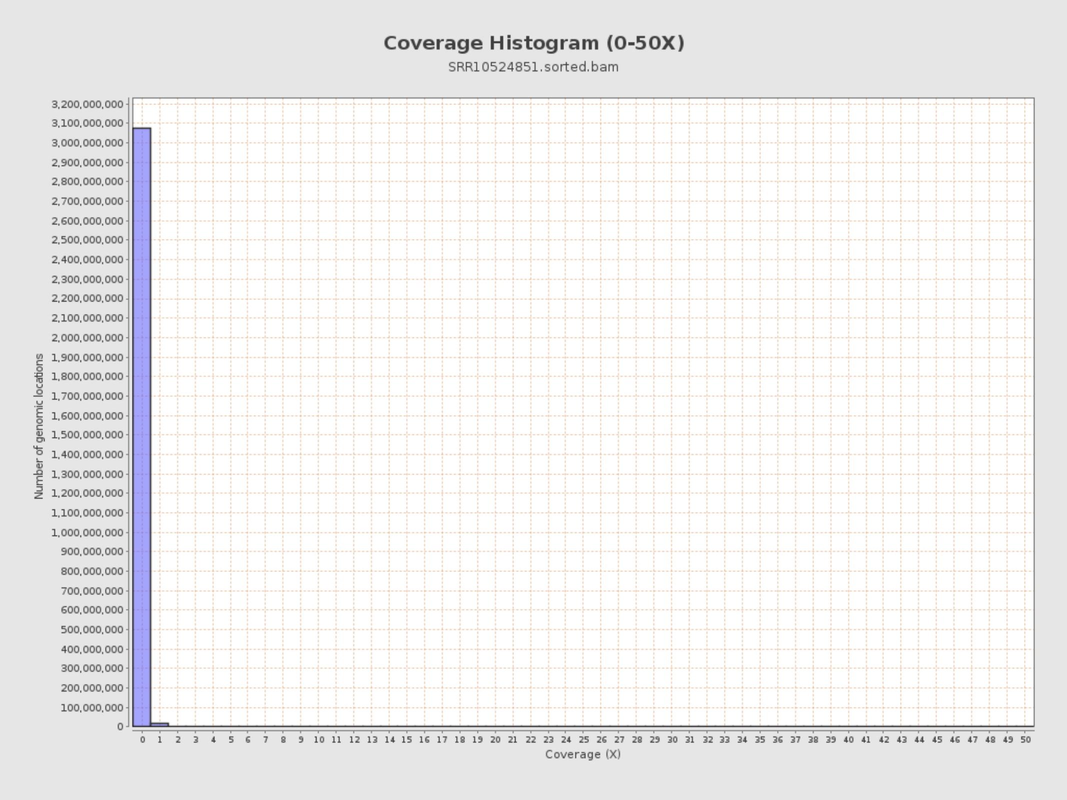
3. Results : Coverage across reference



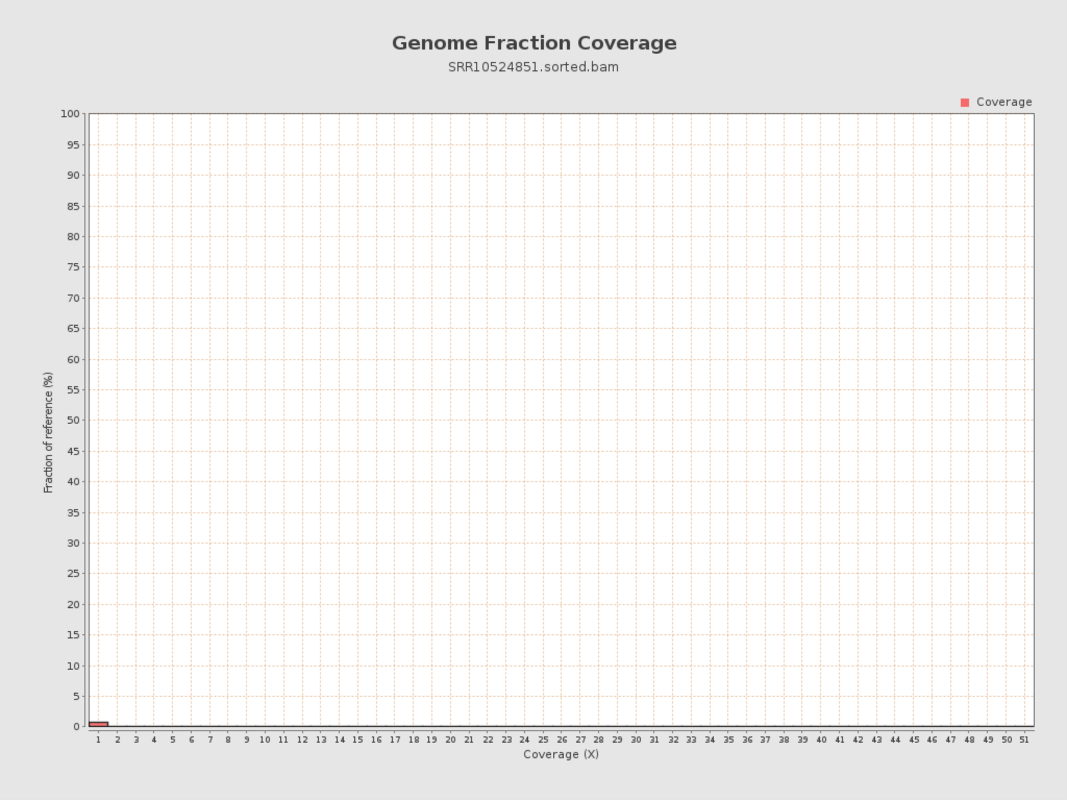
4. Results : Coverage Histogram



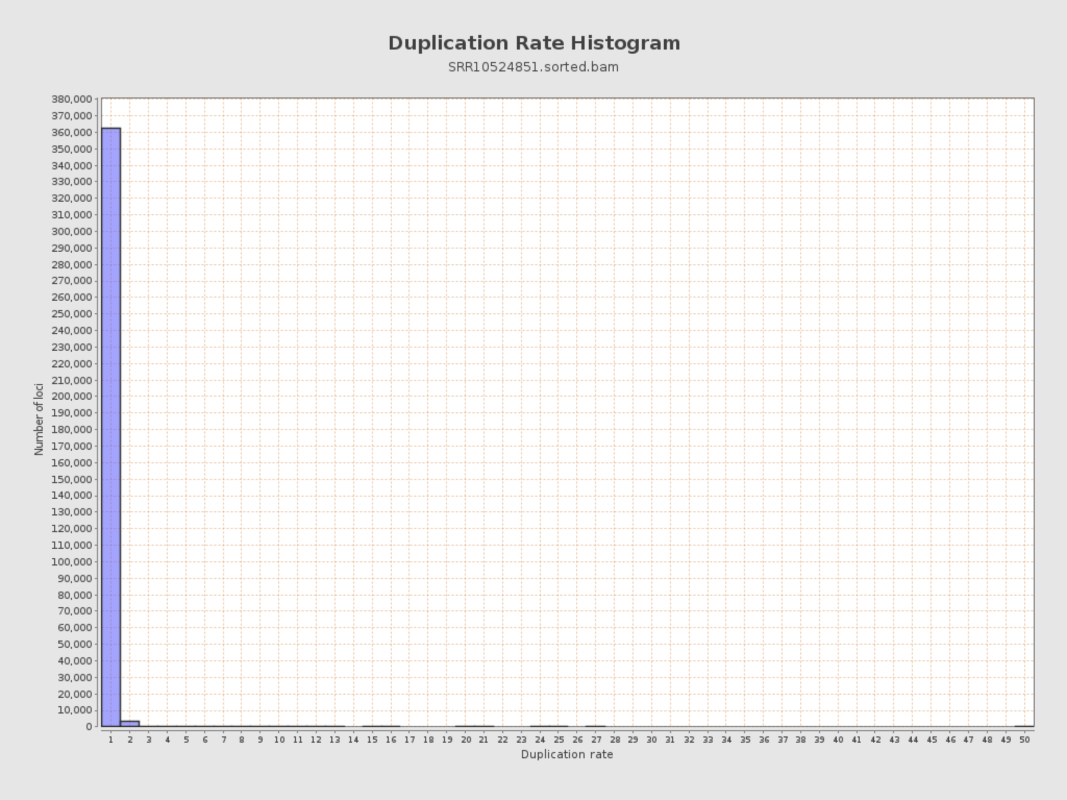
5. Results : Coverage Histogram (0-50X)



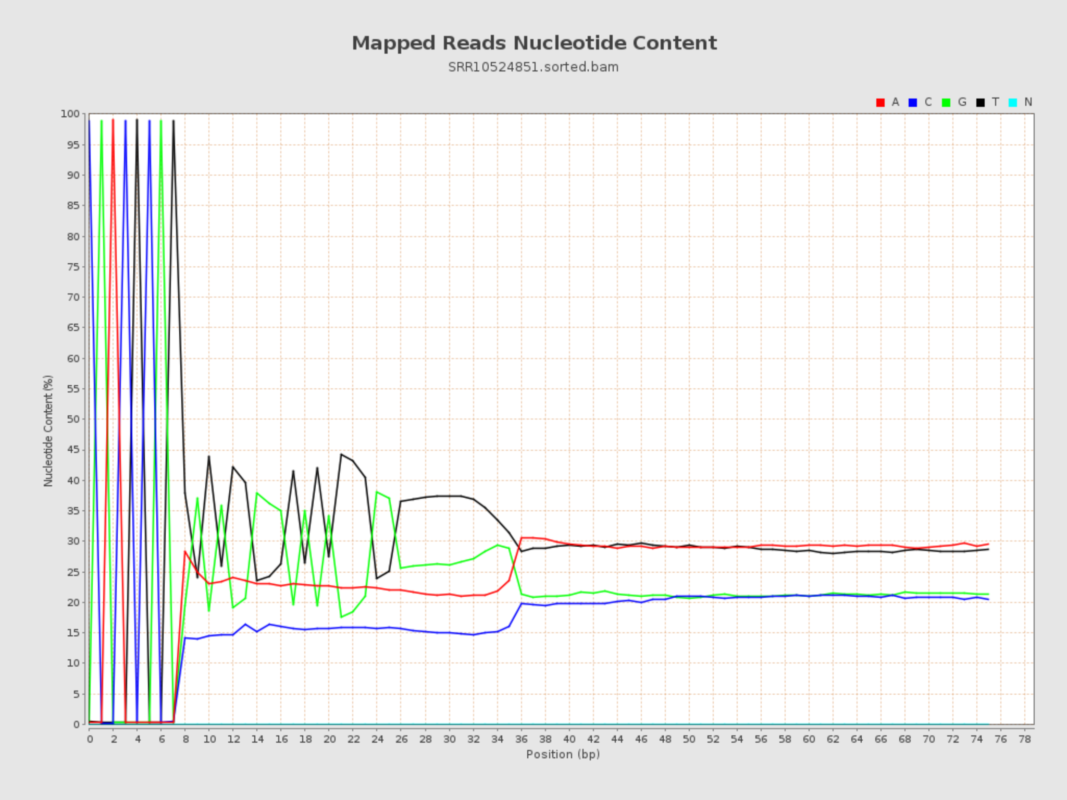
6. Results : Genome Fraction Coverage



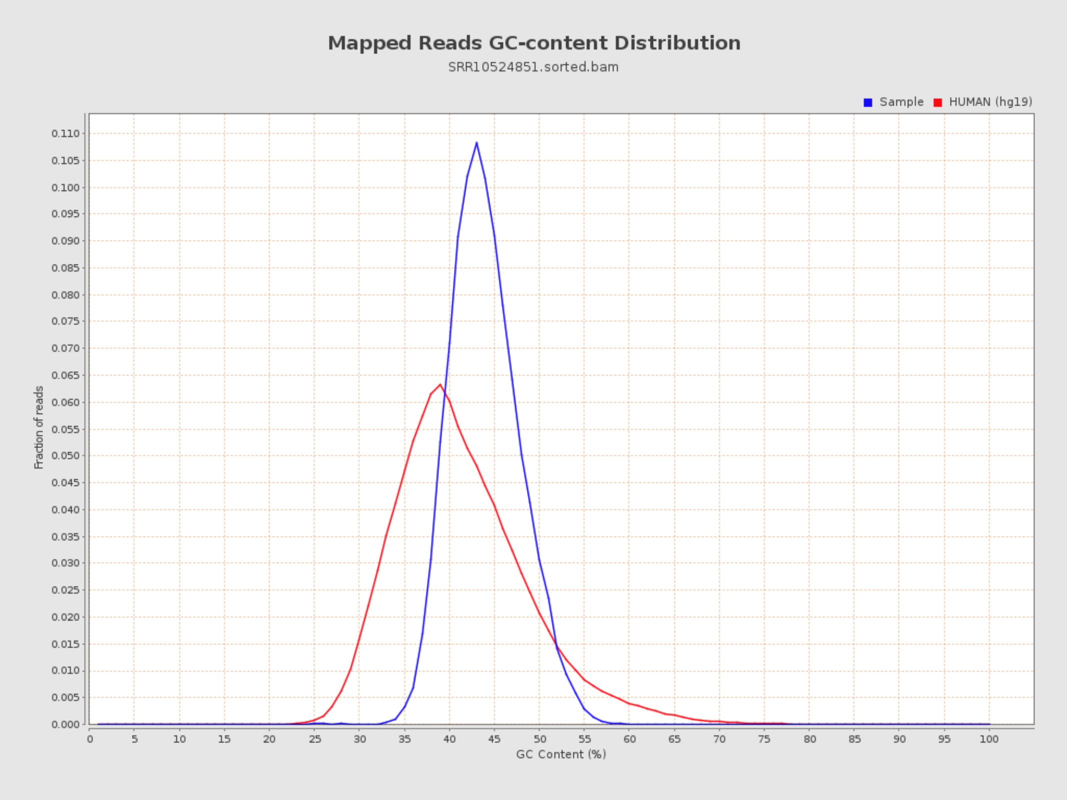
7. Results : Duplication Rate Histogram



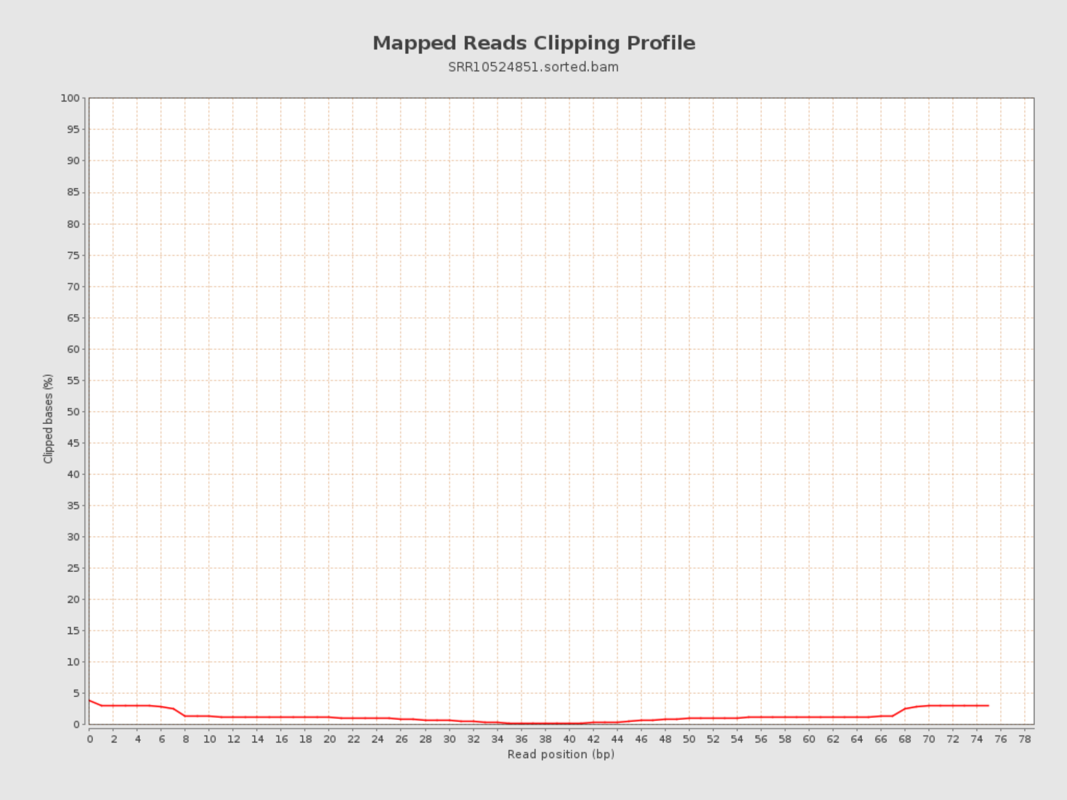
8. Results : Mapped Reads Nucleotide Content



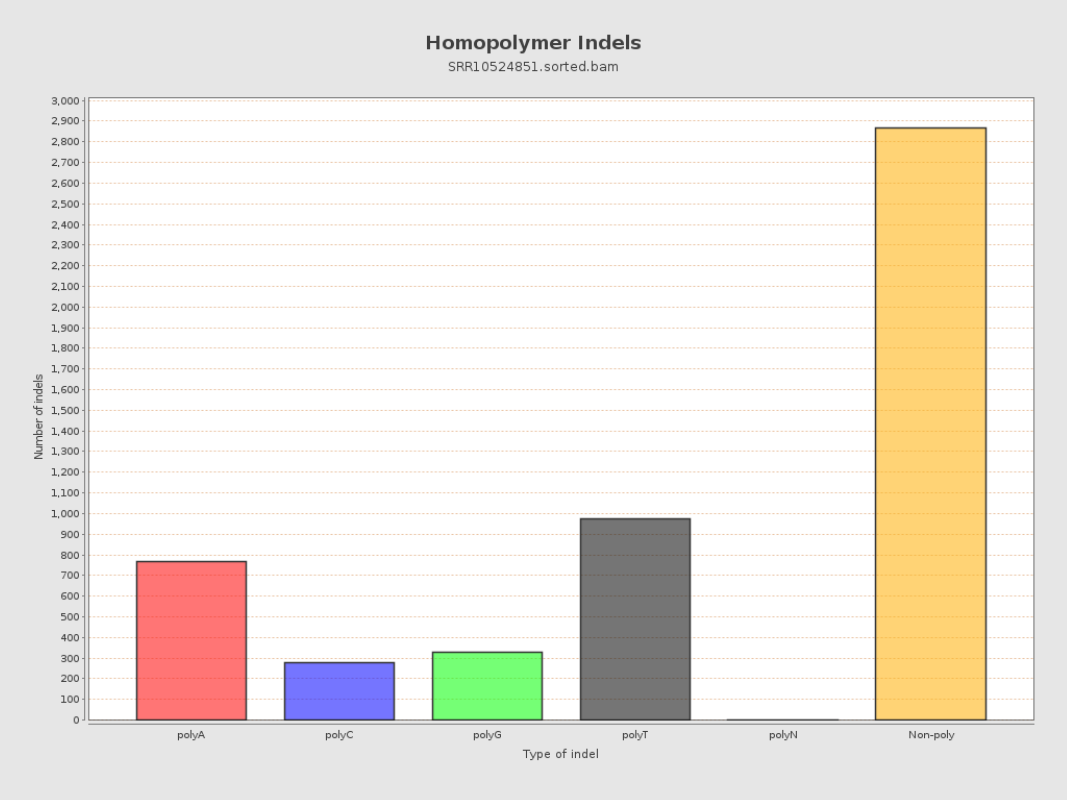
9. Results : Mapped Reads GC-content Distribution



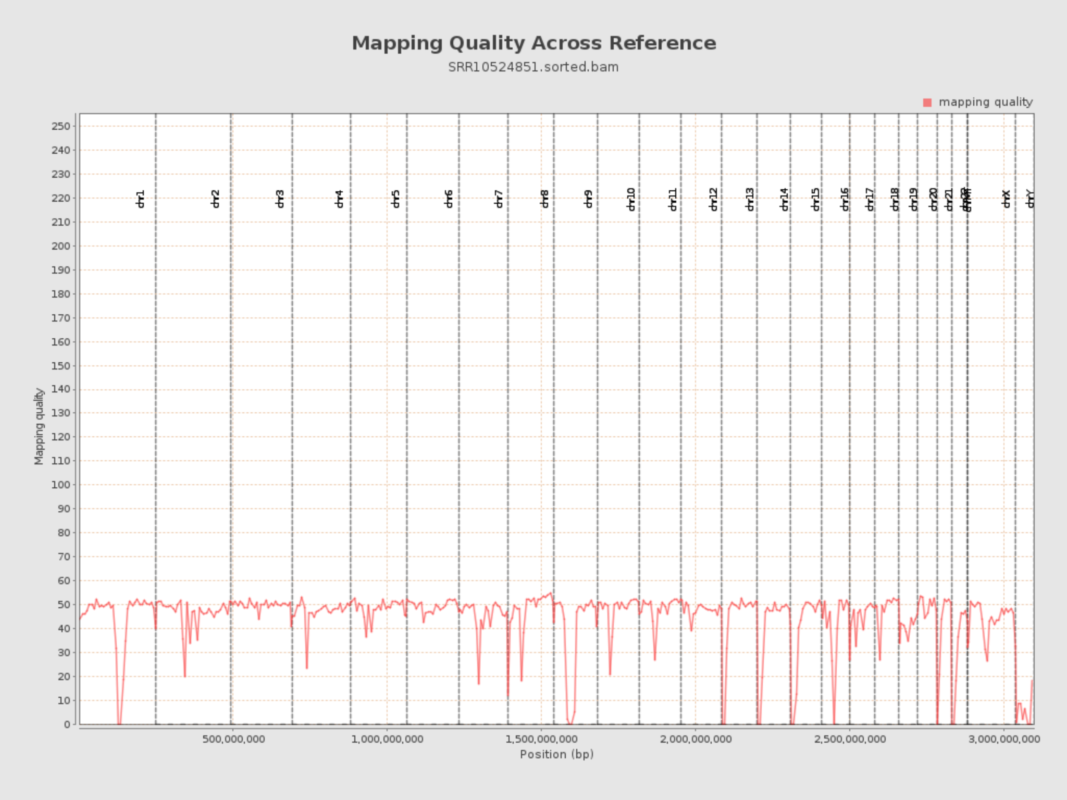
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram