Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 09:50:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524951.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_SRR10524951 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524951.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 09:50:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524951.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	968,497
Mapped reads	895,992 / 92.51%
Unmapped reads	72,505 / 7.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,220 / 0.23%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	20,151 / 2.08%
Duplication rate	1.58%
Clipped reads	895,405 / 92.45%

2.2. ACGT Content

Number/percentage of A's	13,874,301 / 26.54%
Number/percentage of C's	9,672,204 / 18.5%
Number/percentage of T's	15,808,285 / 30.24%
Number/percentage of G's	12,927,325 / 24.73%
Number/percentage of N's	726 / 0%
GC Percentage	43.23%

2.3. Coverage

Mean	0.0169

Standard Deviation	0.1776

2.4. Mapping Quality

Mean Mapping Quality	44.5

2.5. Mismatches and indels

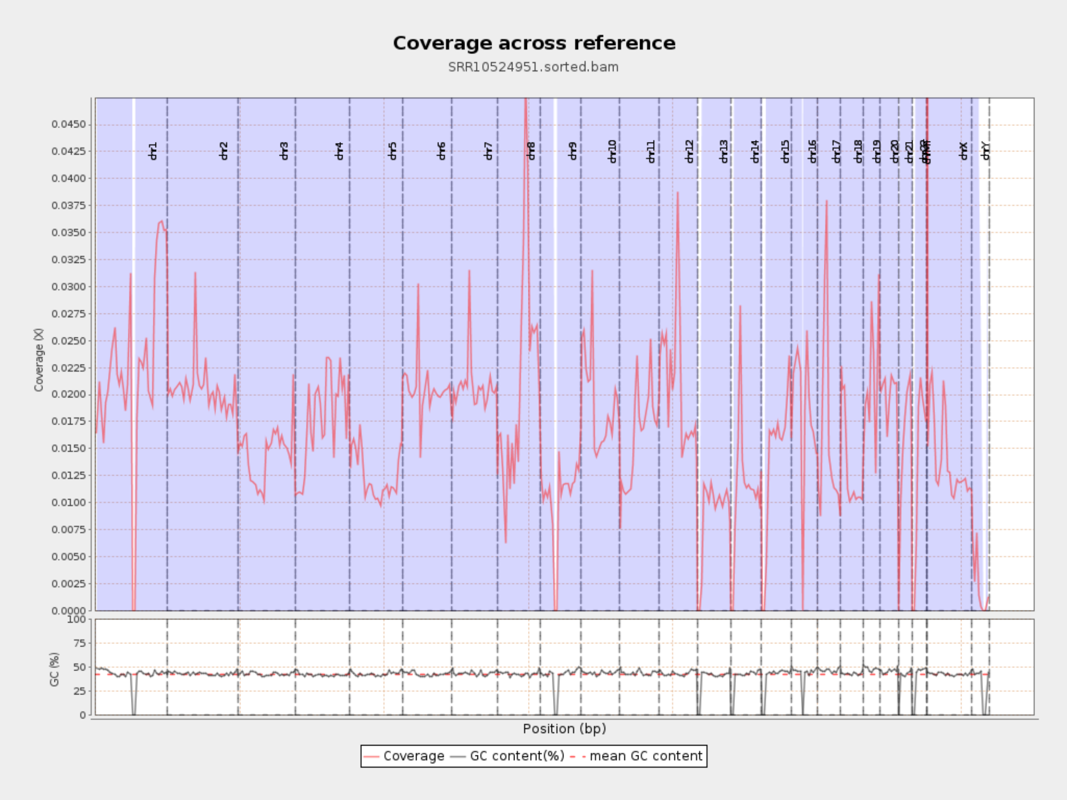
General error rate	0.51%
Mismatches	258,120
Insertions	3,823
Mapped reads with at least one insertion	0.42%
Deletions	10,075
Mapped reads with at least one deletion	1.12%
Homopolymer indels	41.29%

2.6. Chromosome stats

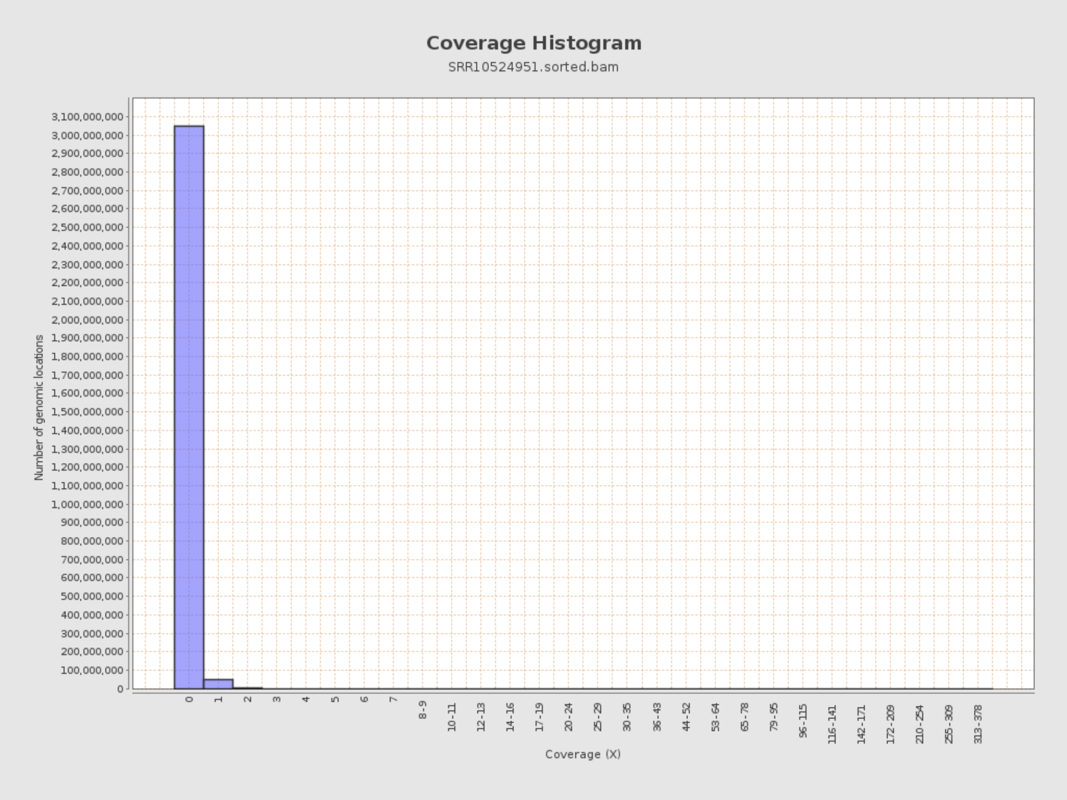
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5612285	0.0225	0.3092
chr2	243199373	4991764	0.0205	0.2054
chr3	198022430	2884700	0.0146	0.1271
chr4	191154276	3401752	0.0178	0.1467
chr5	180915260	2258083	0.0125	0.118
chr6	171115067	3517153	0.0206	0.1833
chr7	159138663	3319058	0.0209	0.2418

chr8	146364022	3176158	0.0217	0.1789
chr9	141213431	1466182	0.0104	0.1351
chr10	135534747	2625523	0.0194	0.1757
chr11	135006516	2212326	0.0164	0.1671
chr12	133851895	2827744	0.0211	0.1531
chr13	115169878	1018899	0.0088	0.0989
chr14	107349540	1206731	0.0112	0.114
chr15	102531392	1453216	0.0142	0.128
chr16	90354753	1663283	0.0184	0.1466
chr17	81195210	1340921	0.0165	0.1599
chr18	78077248	1023911	0.0131	0.2074
chr19	59128983	1269481	0.0215	0.2068
chr20	63025520	1255585	0.0199	0.1481
chr21	48129895	747108	0.0155	0.1333
chr22	51304566	687400	0.0134	0.1205
chrMT	16571	10073	0.6079	0.8359
chrX	155270560	2194742	0.0141	0.1364
chrY	59373566	136068	0.0023	0.0639

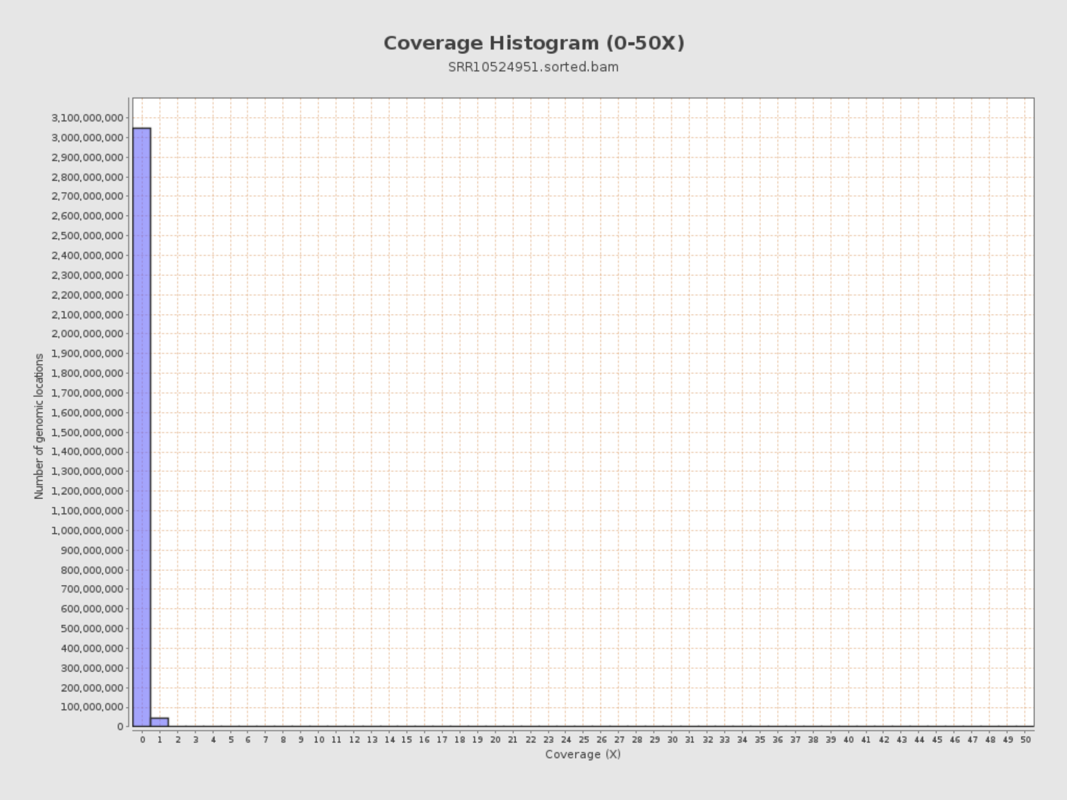
3. Results : Coverage across reference



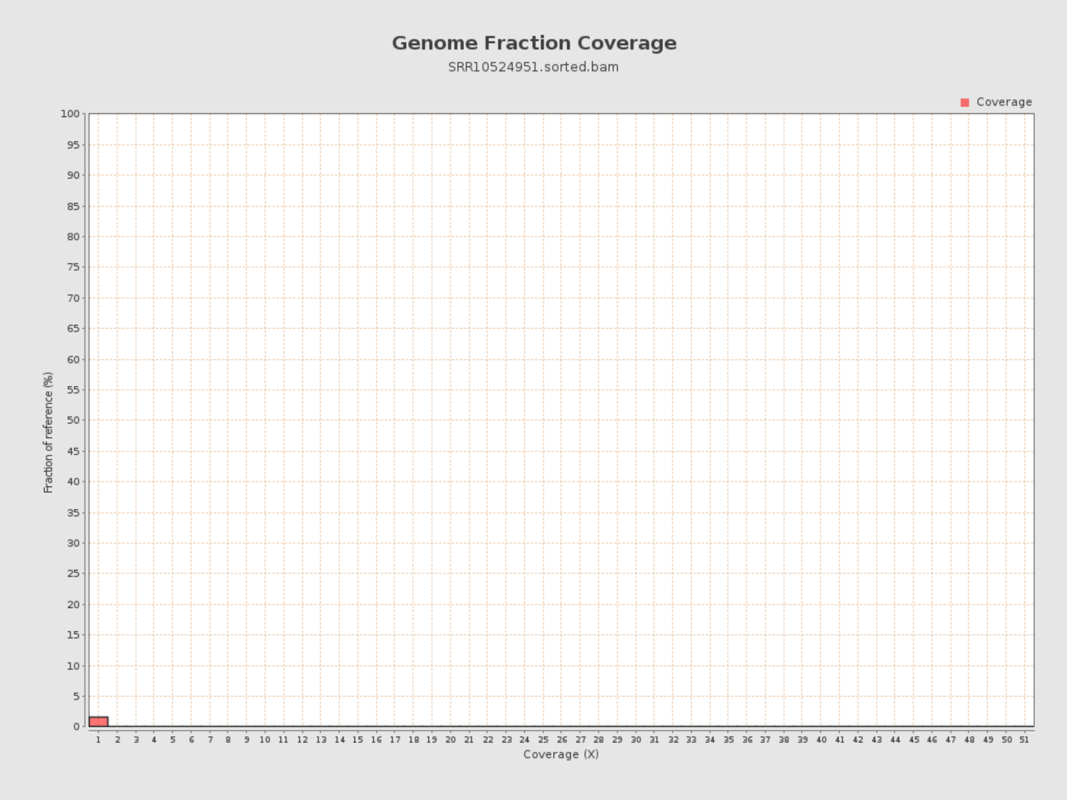
4. Results : Coverage Histogram



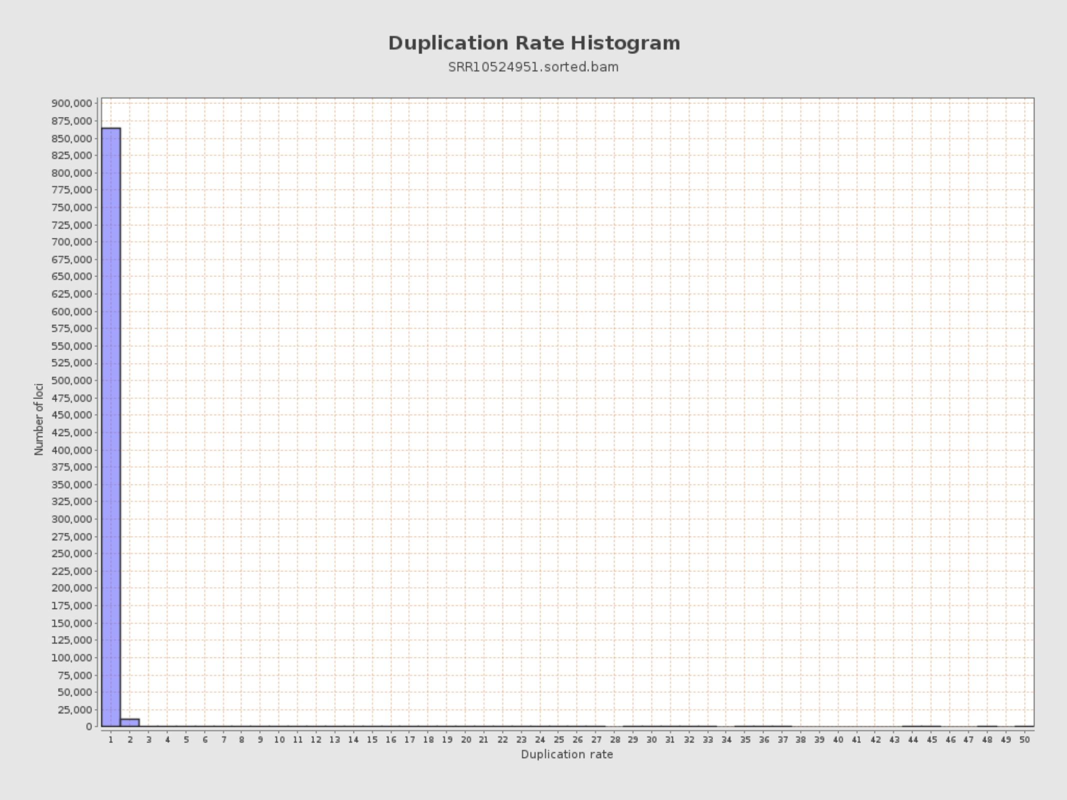
5. Results : Coverage Histogram (0-50X)



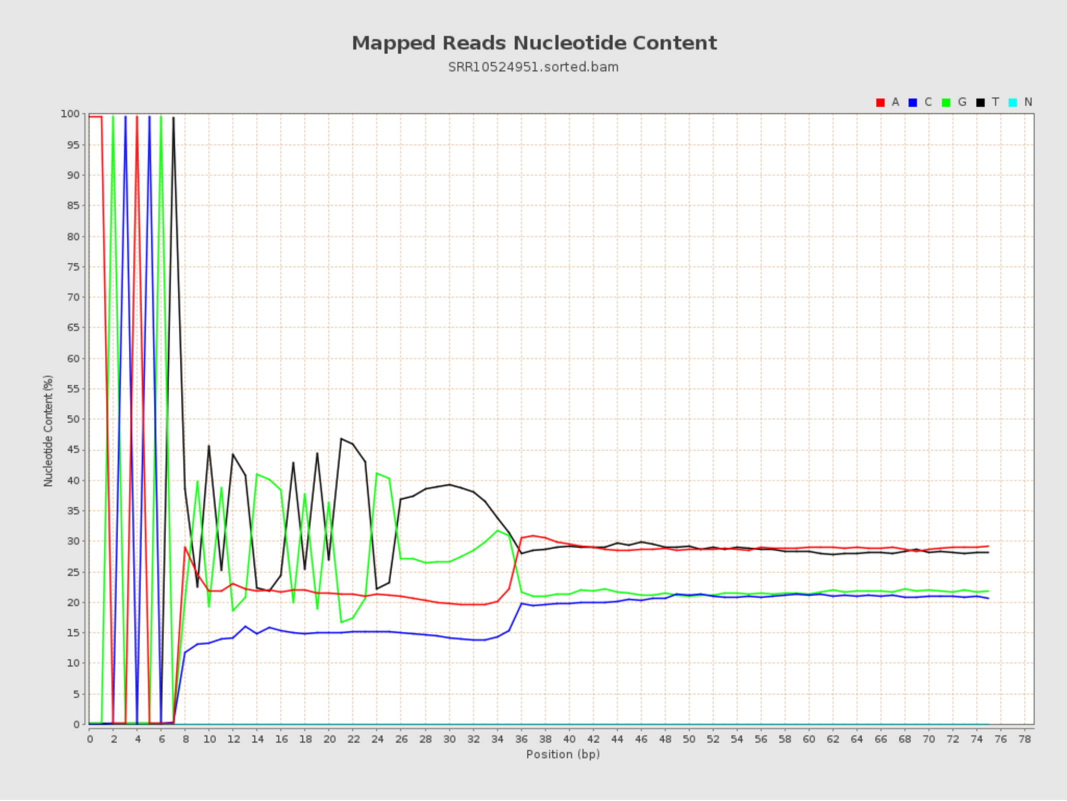
6. Results : Genome Fraction Coverage



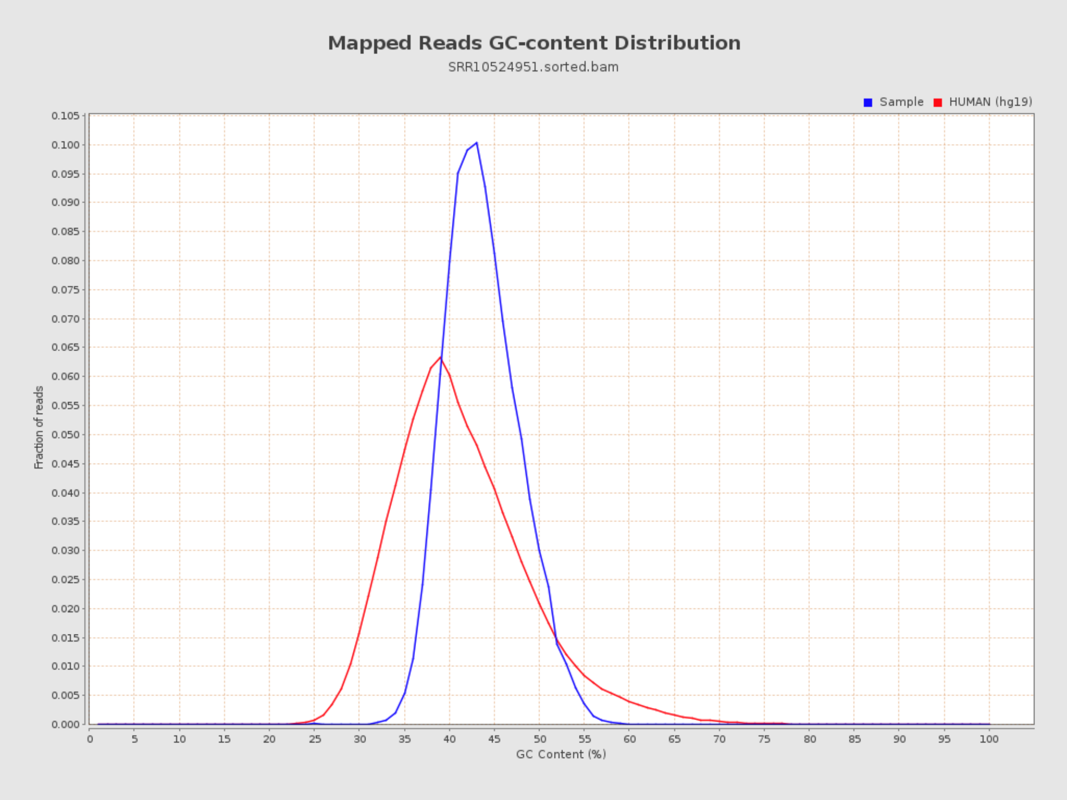
7. Results : Duplication Rate Histogram



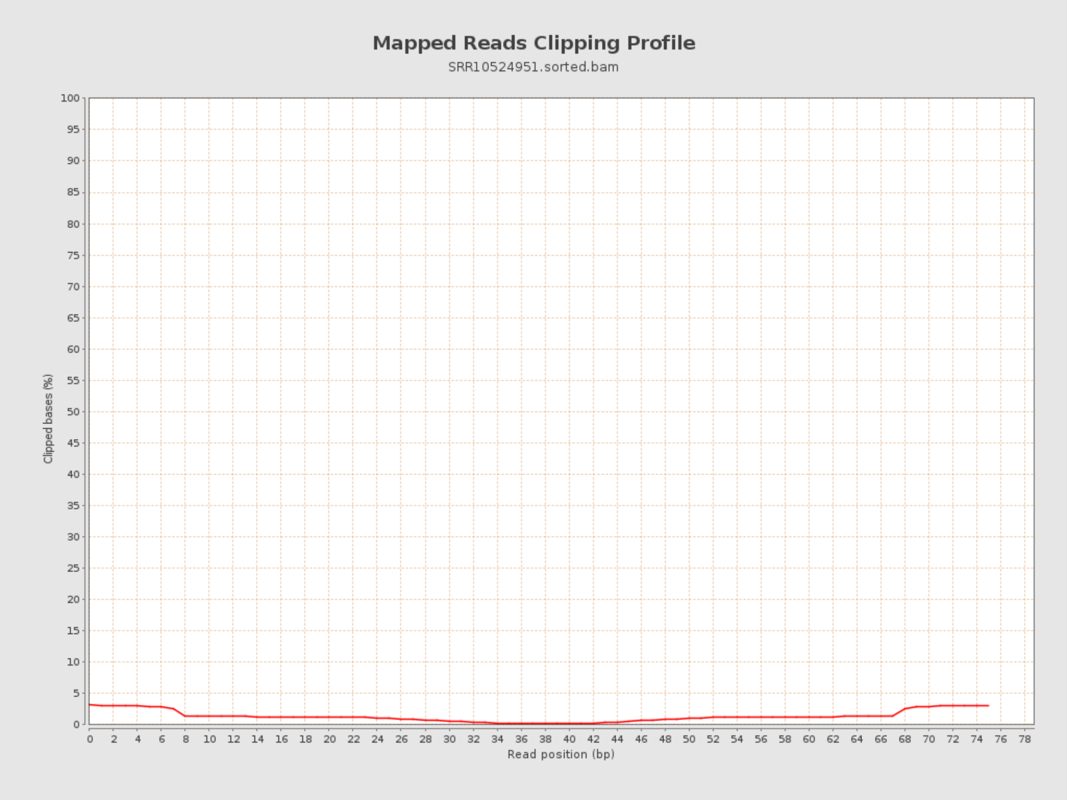
8. Results : Mapped Reads Nucleotide Content



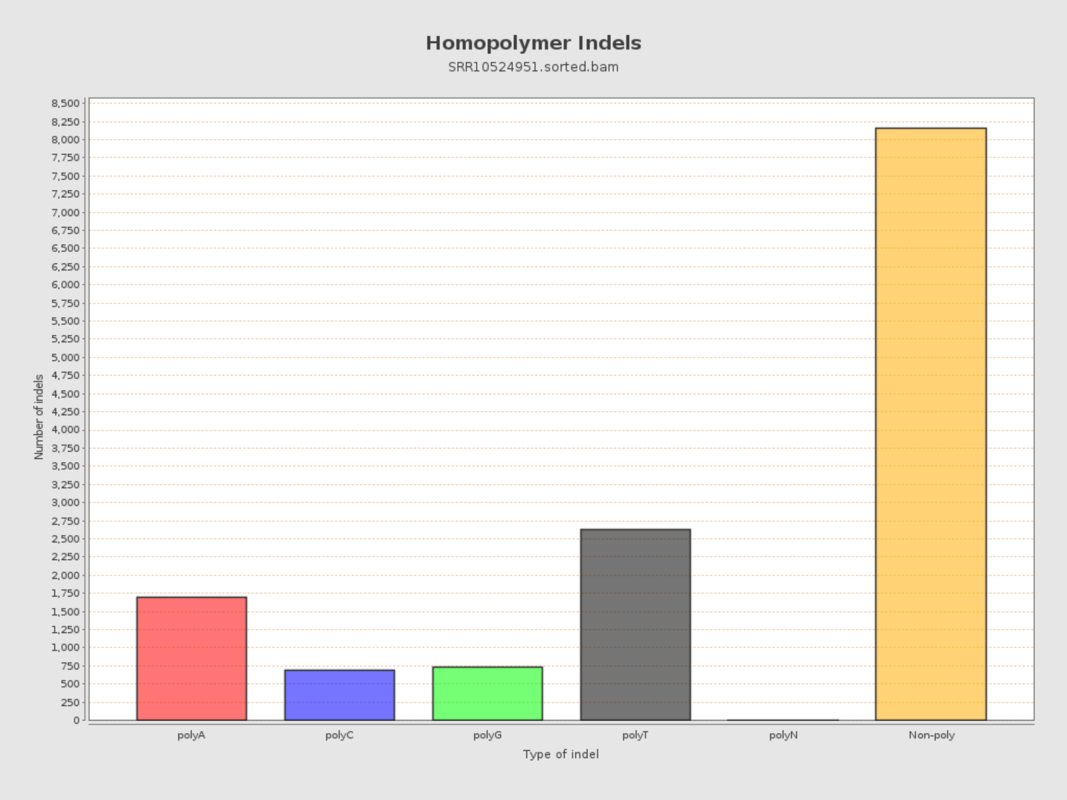
9. Results : Mapped Reads GC-content Distribution



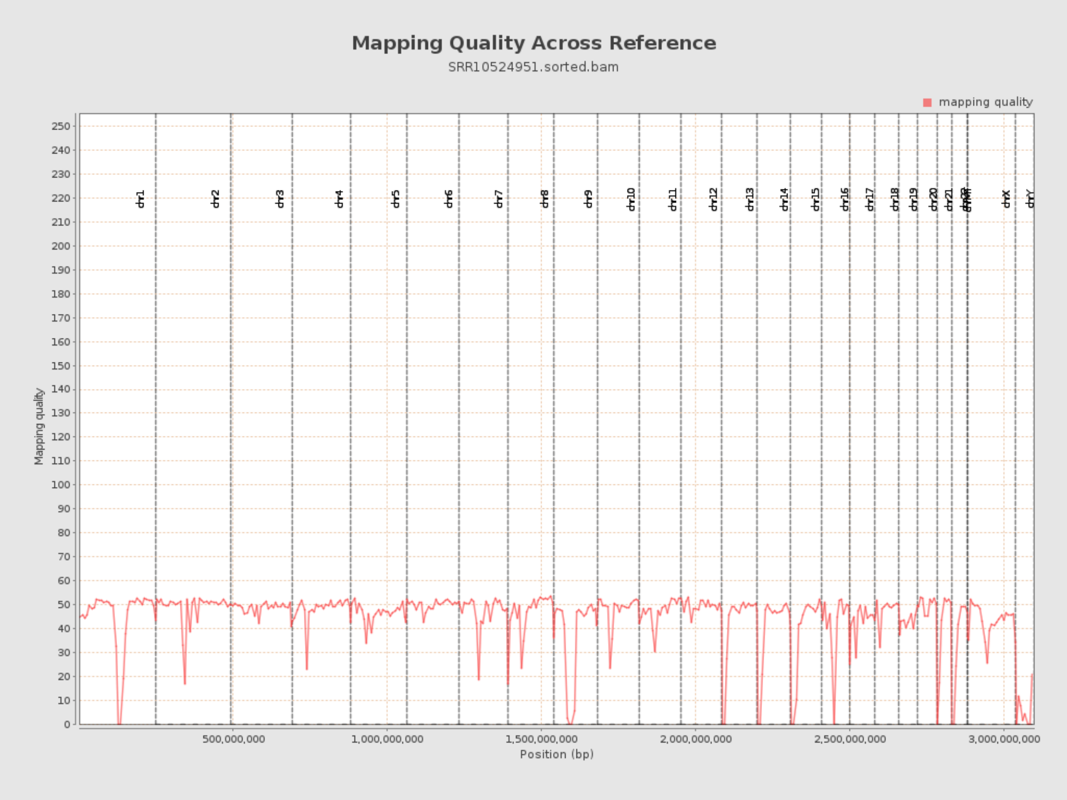
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram