Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 00:02:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524350.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_SRR10524350 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524350.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 00:02:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524350.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	546,677
Mapped reads	488,733 / 89.4%
Unmapped reads	57,944 / 10.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,984 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	9,983 / 1.83%
Duplication rate	1.47%
Clipped reads	489,363 / 89.52%

2.2. ACGT Content

Number/percentage of A's	7,215,589 / 25.31%
Number/percentage of C's	5,159,246 / 18.1%
Number/percentage of T's	8,890,773 / 31.19%
Number/percentage of G's	7,239,772 / 25.39%
Number/percentage of N's	3,898 / 0.01%
GC Percentage	43.49%

2.3. Coverage

Mean	0.0092

Standard Deviation	0.1229

2.4. Mapping Quality

Mean Mapping Quality	44.72

2.5. Mismatches and indels

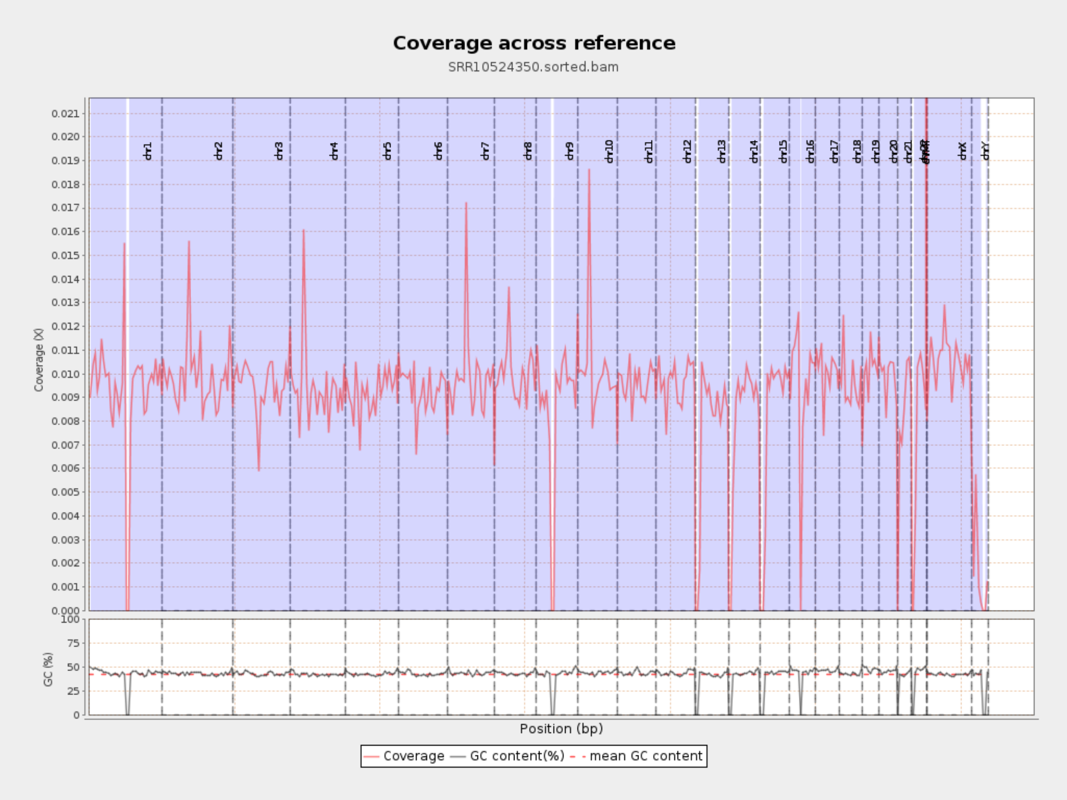
General error rate	0.54%
Mismatches	149,601
Insertions	1,863
Mapped reads with at least one insertion	0.38%
Deletions	5,245
Mapped reads with at least one deletion	1.07%
Homopolymer indels	43.64%

2.6. Chromosome stats

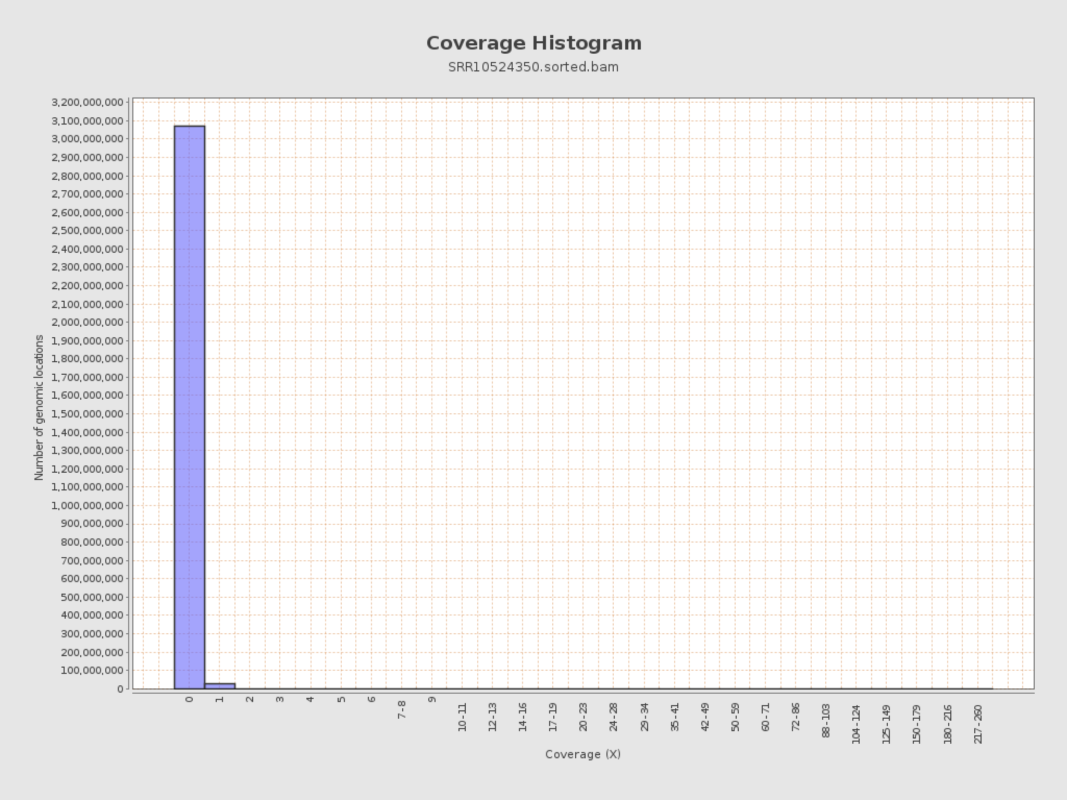
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2298749	0.0092	0.191
chr2	243199373	2421488	0.01	0.1491
chr3	198022430	1880170	0.0095	0.1016
chr4	191154276	1785746	0.0093	0.1048
chr5	180915260	1666195	0.0092	0.099
chr6	171115067	1599051	0.0093	0.1032
chr7	159138663	1579027	0.0099	0.1514

chr8	146364022	1464146	0.01	0.1179
chr9	141213431	1191358	0.0084	0.1066
chr10	135534747	1374767	0.0101	0.125
chr11	135006516	1292165	0.0096	0.117
chr12	133851895	1295015	0.0097	0.1022
chr13	115169878	867723	0.0075	0.0899
chr14	107349540	849033	0.0079	0.0939
chr15	102531392	817455	0.008	0.0925
chr16	90354753	855858	0.0095	0.1049
chr17	81195210	817641	0.0101	0.1068
chr18	78077248	752795	0.0096	0.1763
chr19	59128983	600509	0.0102	0.1389
chr20	63025520	621537	0.0099	0.1036
chr21	48129895	387949	0.0081	0.0985
chr22	51304566	361139	0.007	0.0869
chrMT	16571	6246	0.3769	0.6967
chrX	155270560	1635301	0.0105	0.1116
chrY	59373566	96467	0.0016	0.0546

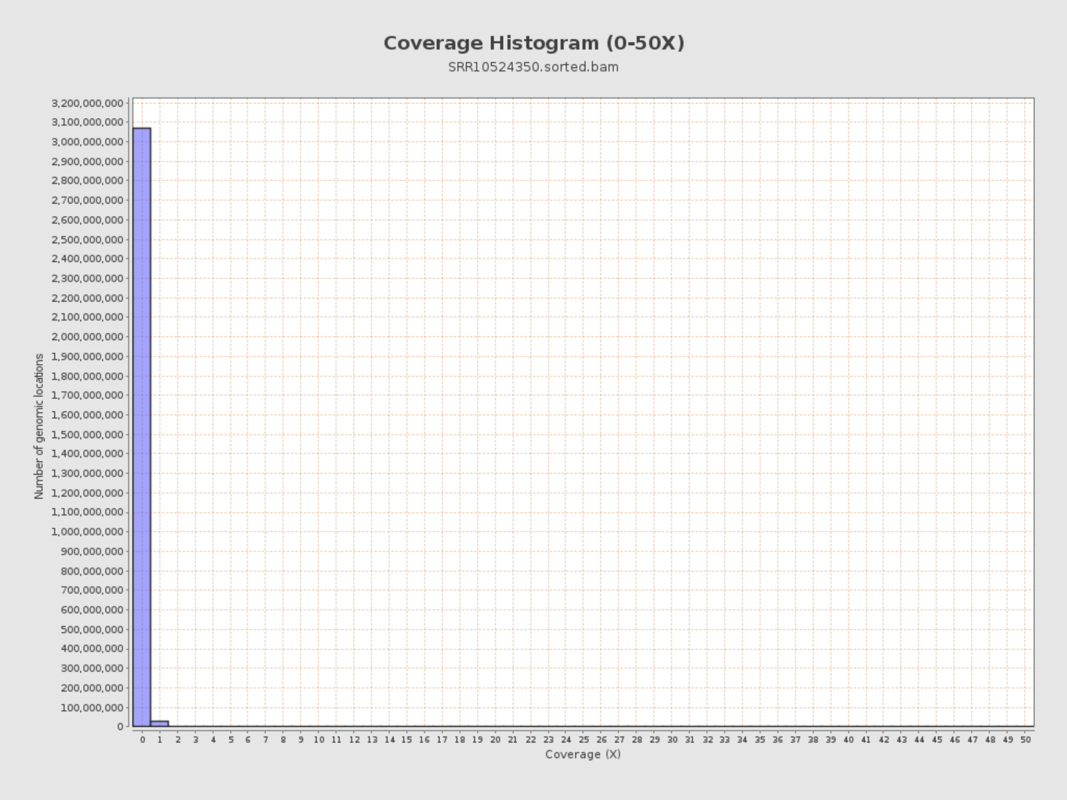
3. Results : Coverage across reference



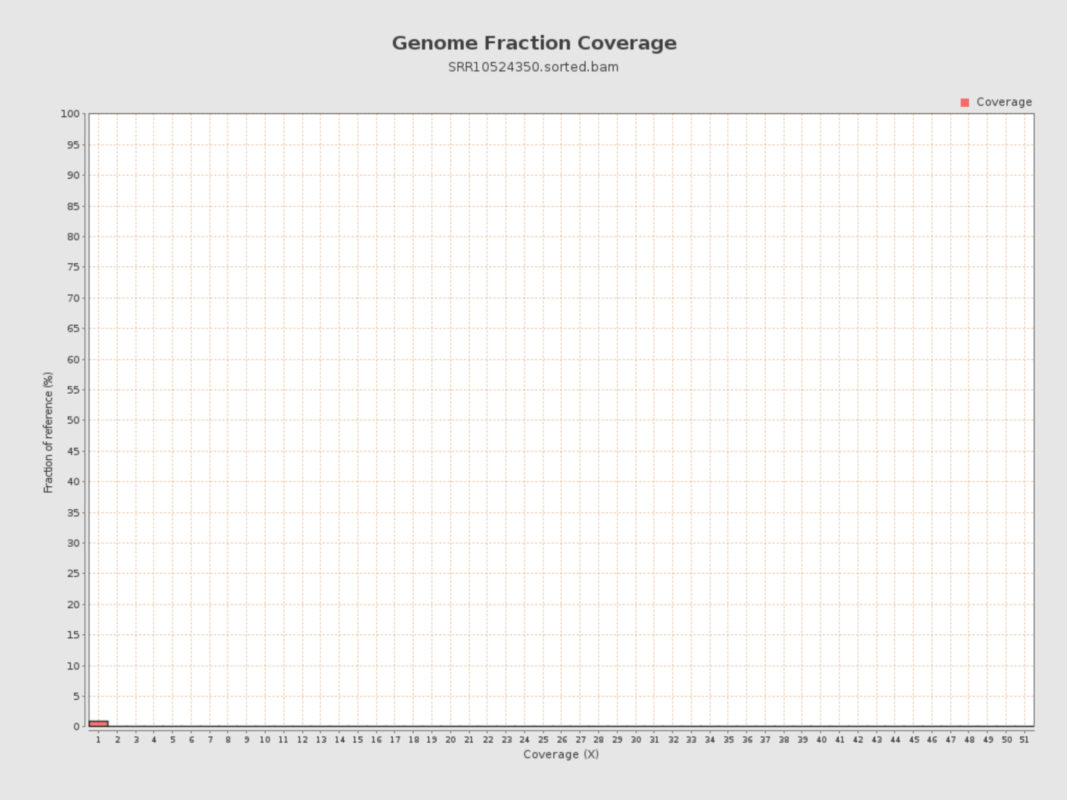
4. Results : Coverage Histogram



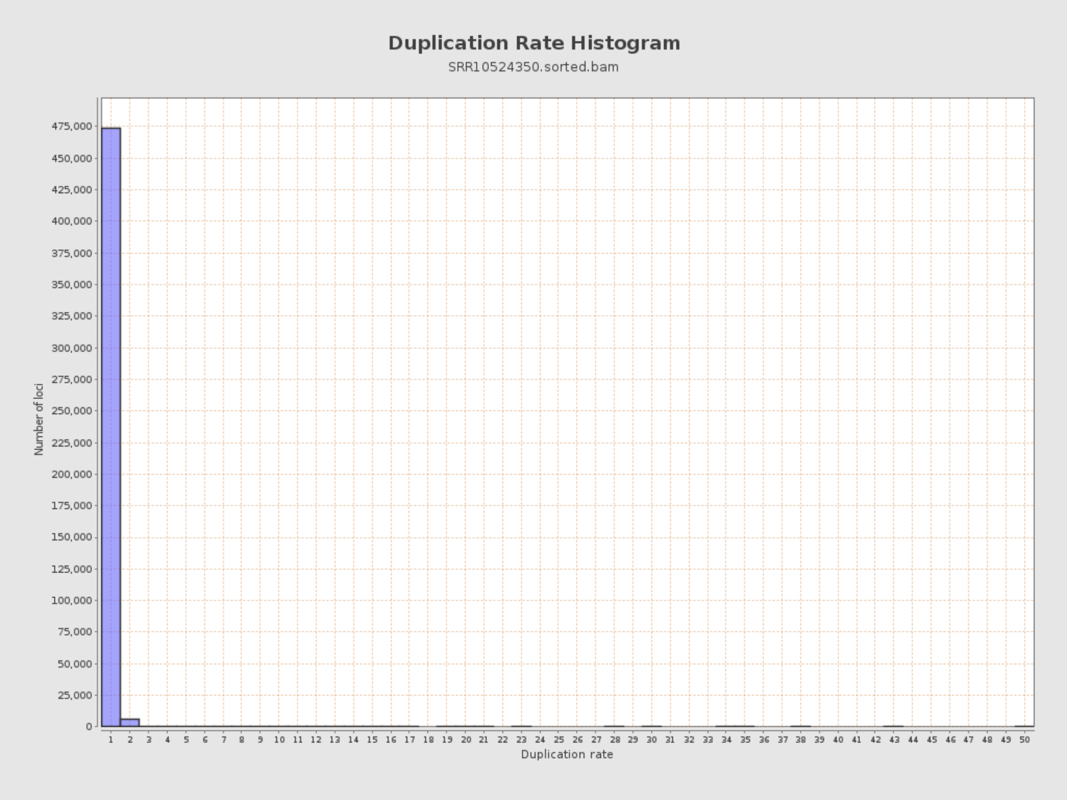
5. Results : Coverage Histogram (0-50X)



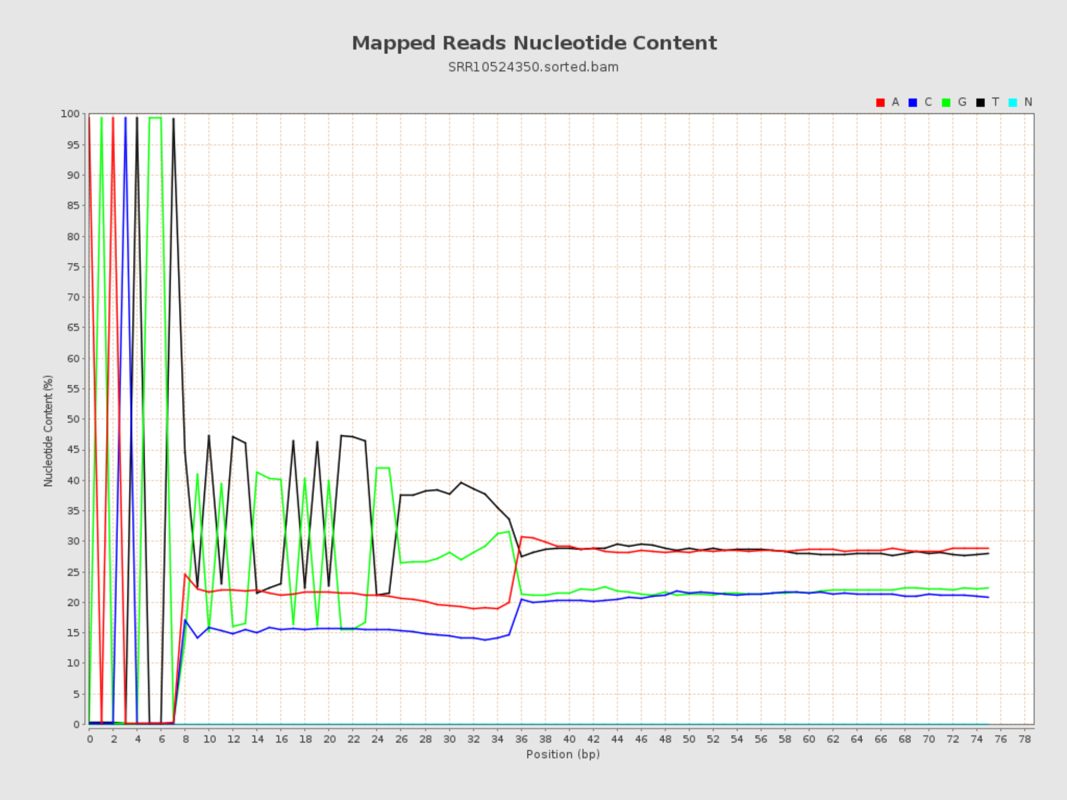
6. Results : Genome Fraction Coverage



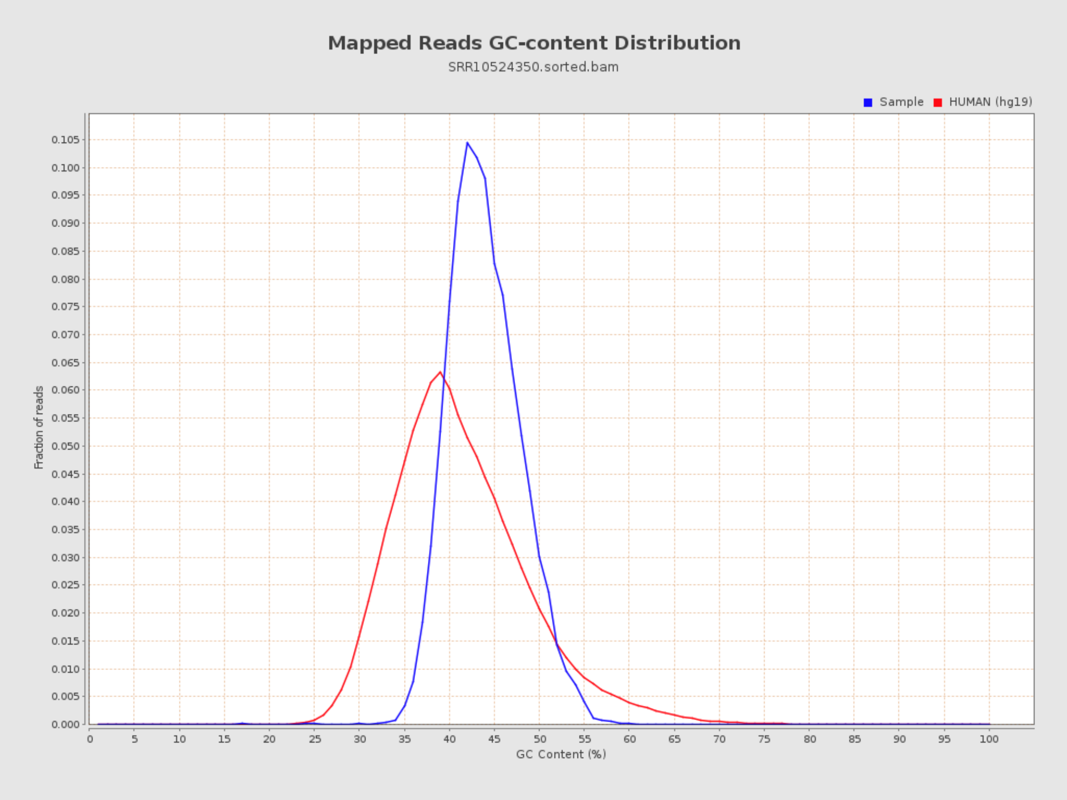
7. Results : Duplication Rate Histogram



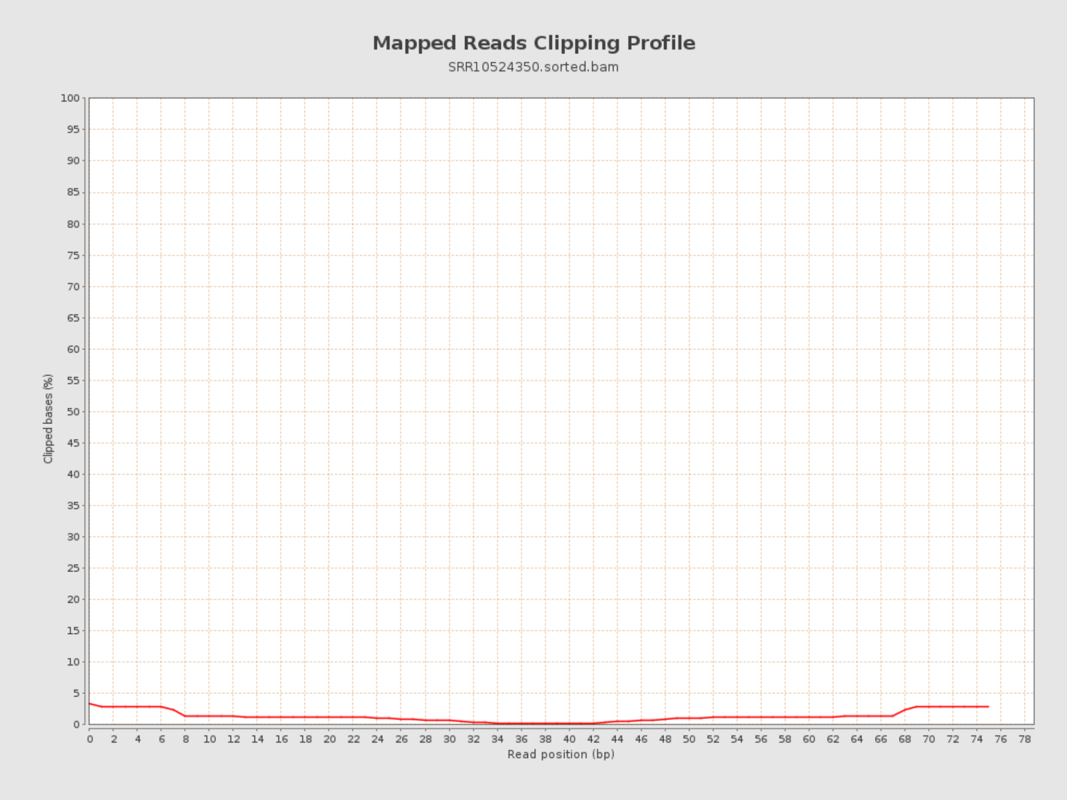
8. Results : Mapped Reads Nucleotide Content



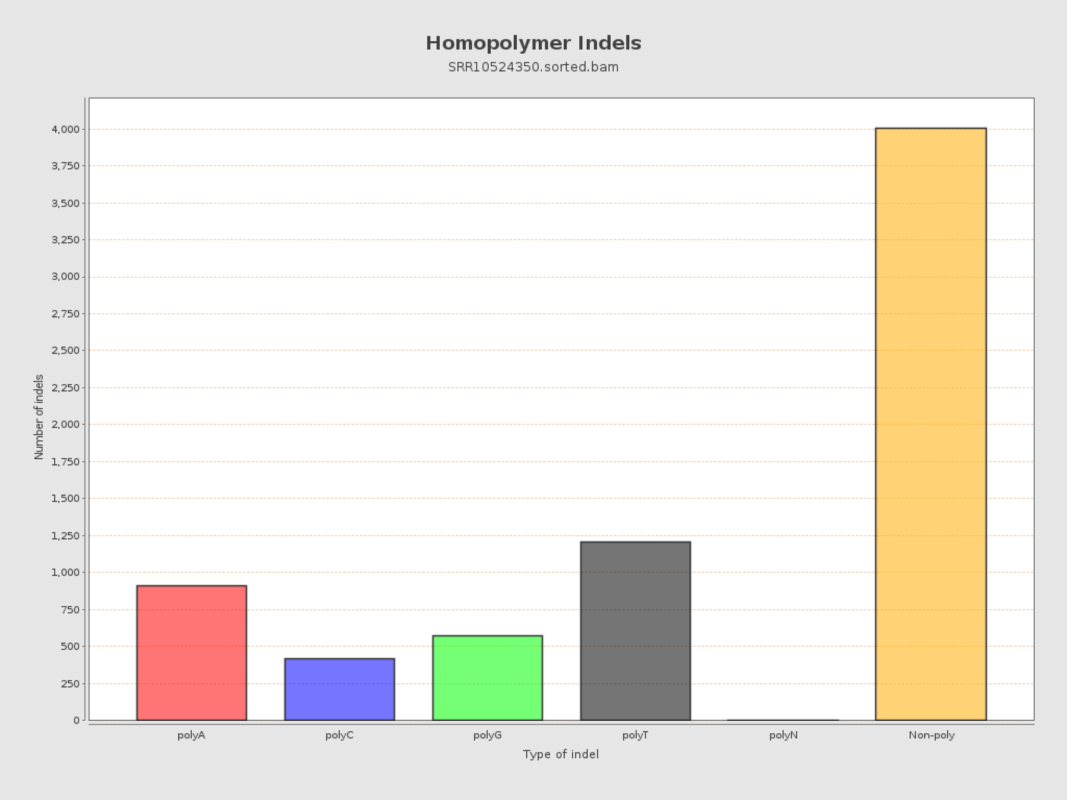
9. Results : Mapped Reads GC-content Distribution



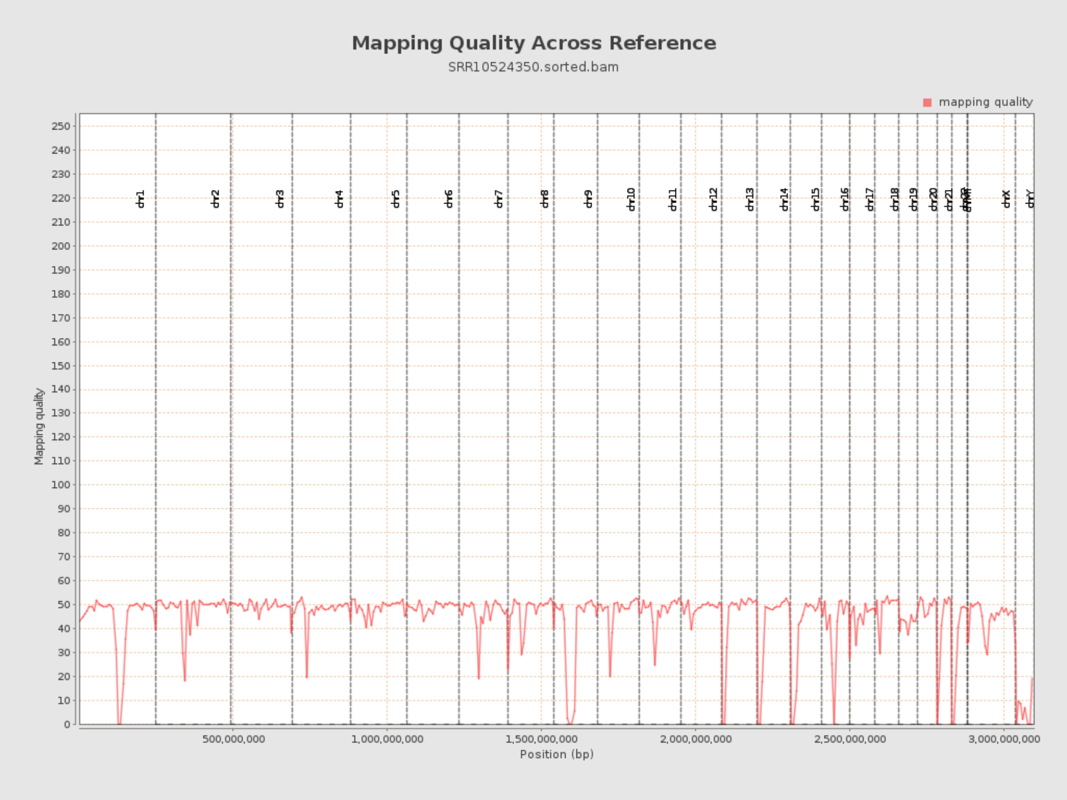
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram