Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 10:58:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524964.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_SRR10524964 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524964.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 10:58:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524964.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,056,297
Mapped reads	981,824 / 92.95%
Unmapped reads	74,473 / 7.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,617 / 0.25%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	22,946 / 2.17%
Duplication rate	1.63%
Clipped reads	981,882 / 92.96%

2.2. ACGT Content

Number/percentage of A's	14,424,242 / 25.06%
Number/percentage of C's	10,718,788 / 18.62%
Number/percentage of T's	18,341,596 / 31.87%
Number/percentage of G's	14,067,724 / 24.44%
Number/percentage of N's	696 / 0%
GC Percentage	43.07%

2.3. Coverage

Mean	0.0186

Standard Deviation	0.191

2.4. Mapping Quality

Mean Mapping Quality	44.51

2.5. Mismatches and indels

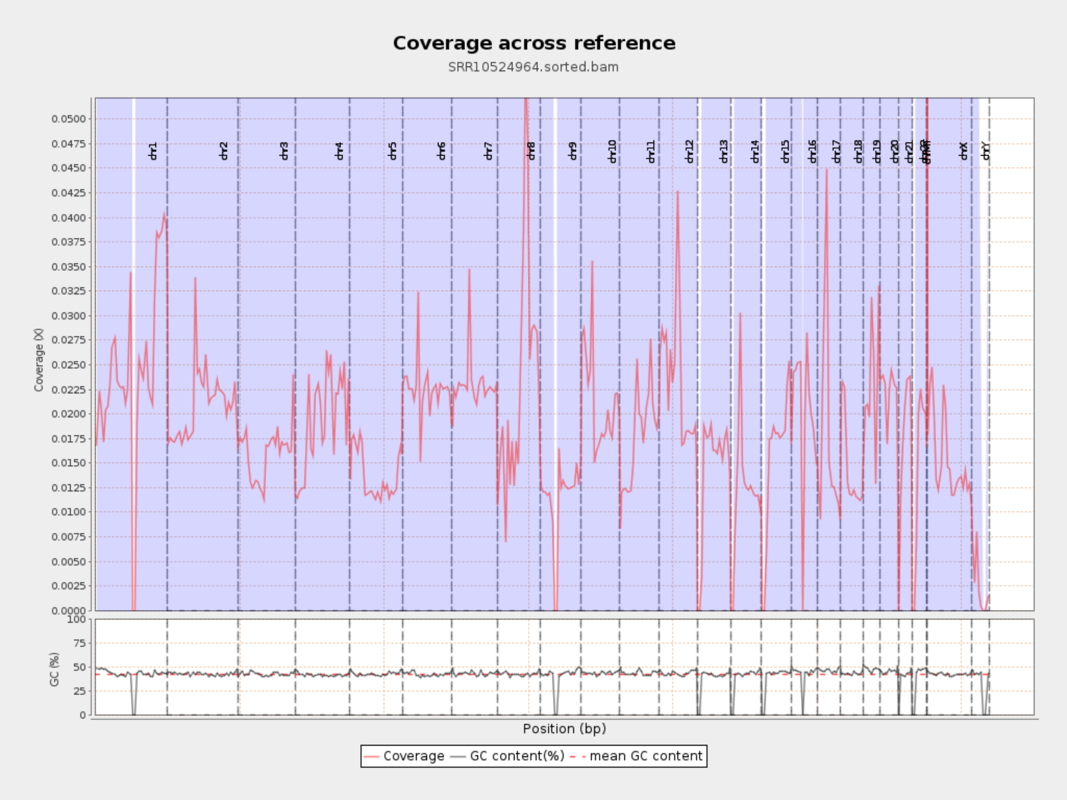
General error rate	0.5%
Mismatches	279,933
Insertions	3,681
Mapped reads with at least one insertion	0.37%
Deletions	11,119
Mapped reads with at least one deletion	1.12%
Homopolymer indels	41.95%

2.6. Chromosome stats

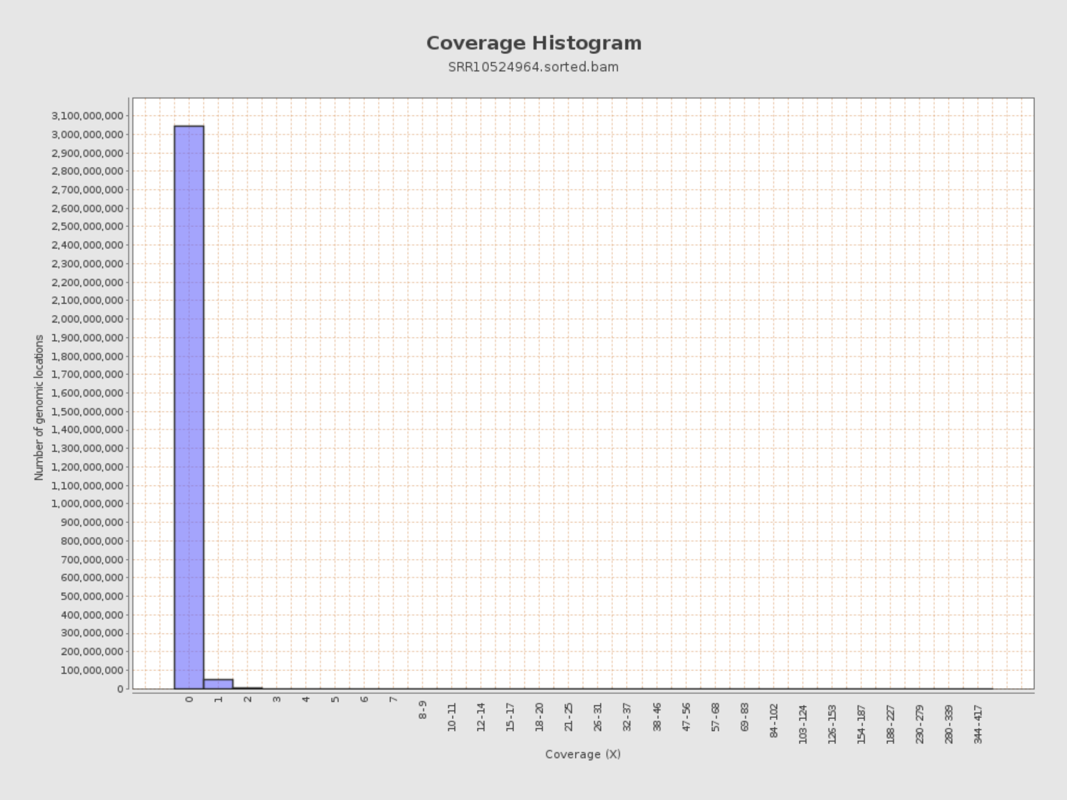
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6072832	0.0244	0.3374
chr2	243199373	5086823	0.0209	0.2139
chr3	198022430	3181399	0.0161	0.1349
chr4	191154276	3719656	0.0195	0.1538
chr5	180915260	2490953	0.0138	0.1247
chr6	171115067	3860609	0.0226	0.2
chr7	159138663	3676525	0.0231	0.2573

chr8	146364022	3490892	0.0239	0.1949
chr9	141213431	1595478	0.0113	0.1475
chr10	135534747	2920262	0.0215	0.1915
chr11	135006516	2414763	0.0179	0.1728
chr12	133851895	3167762	0.0237	0.1627
chr13	115169878	1649265	0.0143	0.1273
chr14	107349540	1299589	0.0121	0.1178
chr15	102531392	1597298	0.0156	0.1391
chr16	90354753	1814393	0.0201	0.1547
chr17	81195210	1478758	0.0182	0.177
chr18	78077248	1135323	0.0145	0.222
chr19	59128983	1374351	0.0232	0.2233
chr20	63025520	1394334	0.0221	0.1582
chr21	48129895	844188	0.0175	0.1424
chr22	51304566	730666	0.0142	0.1243
chrMT	16571	4254	0.2567	0.5568
chrX	155270560	2423056	0.0156	0.1472
chrY	59373566	148852	0.0025	0.0689

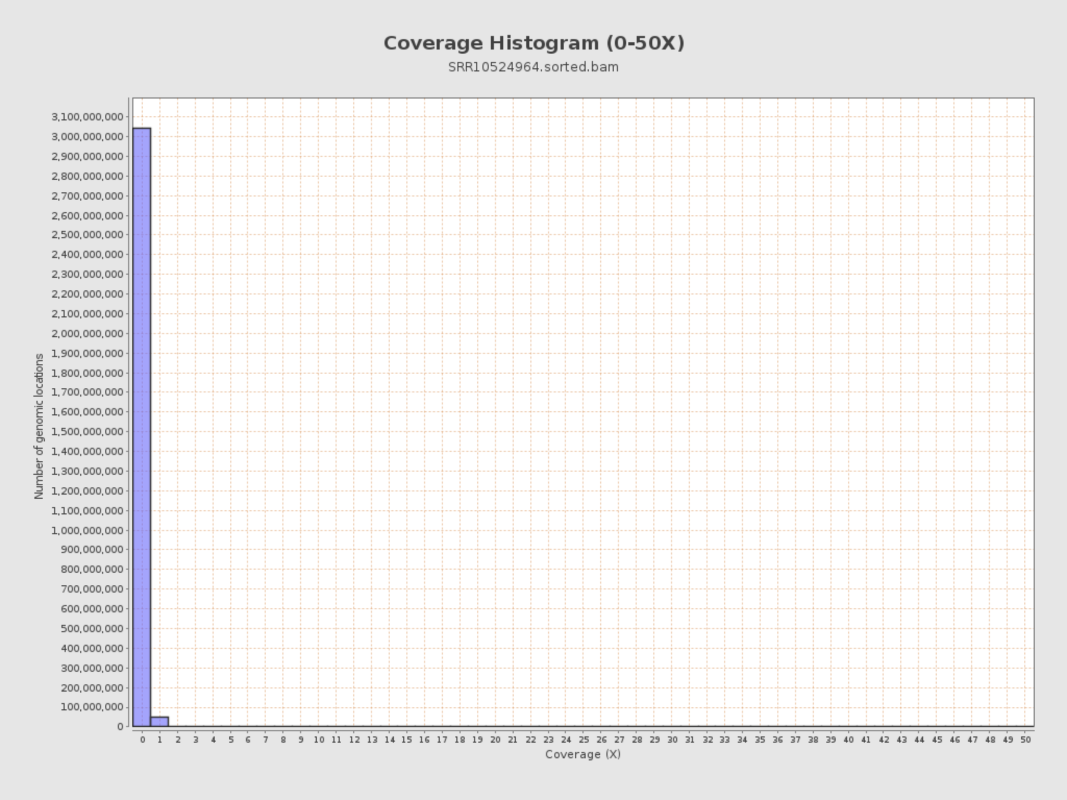
3. Results : Coverage across reference



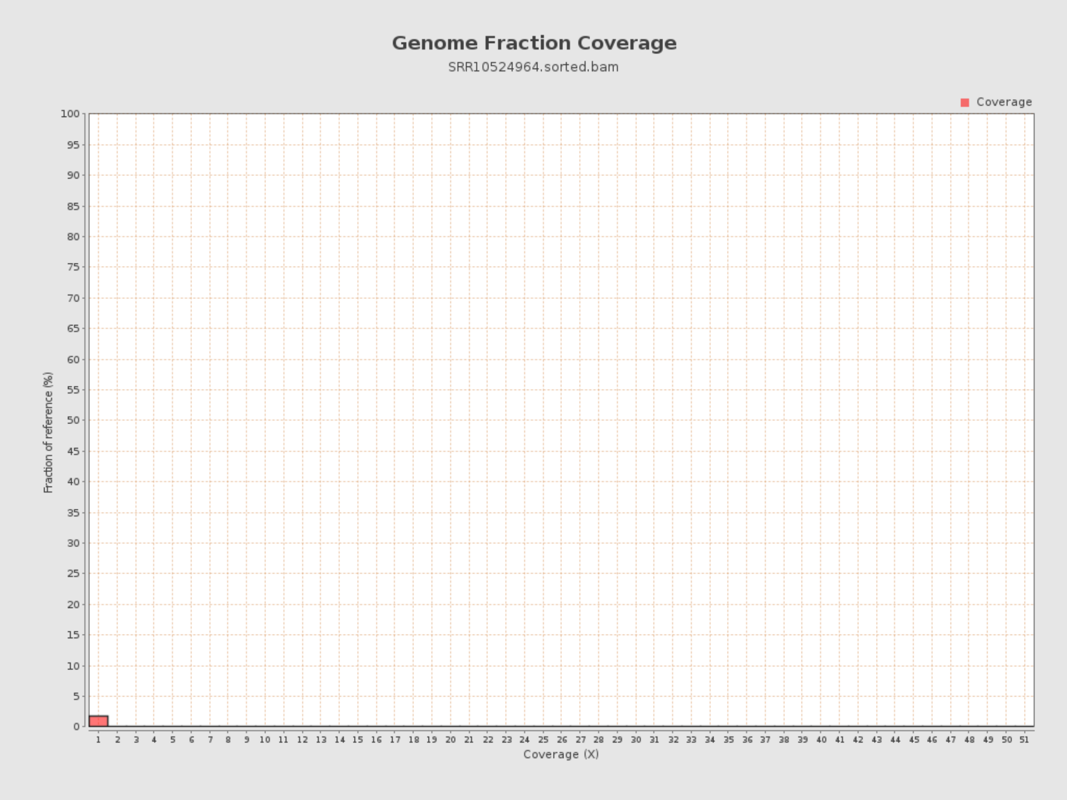
4. Results : Coverage Histogram



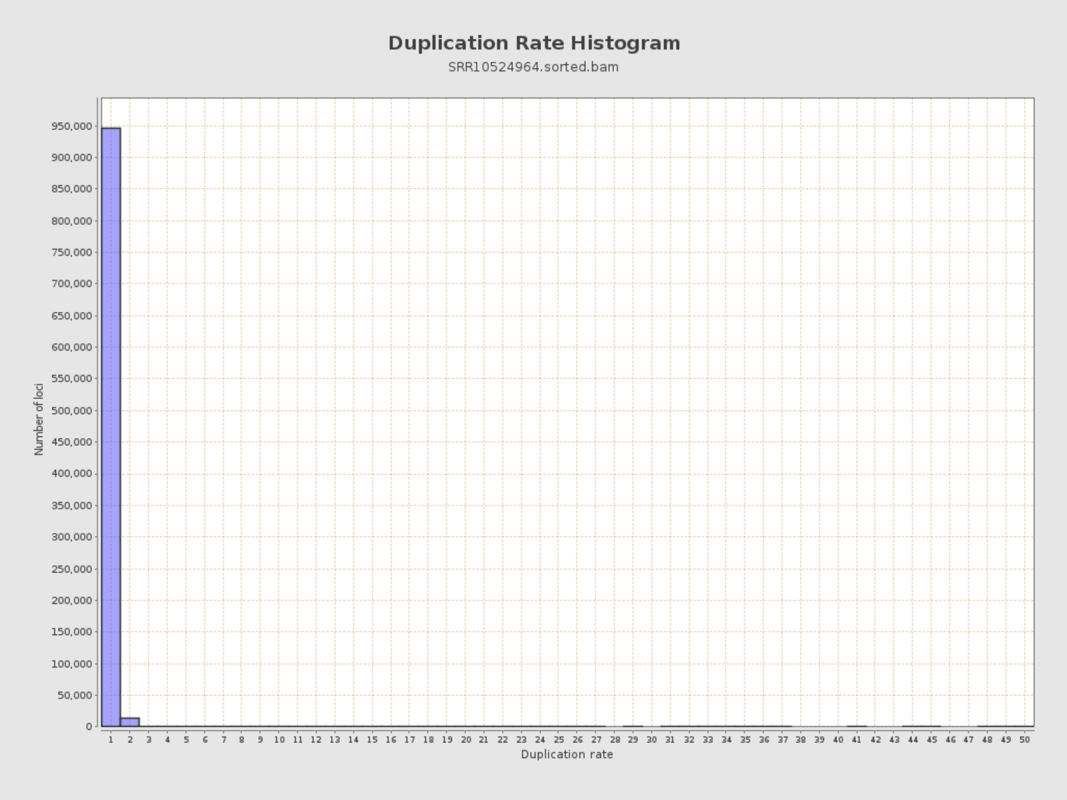
5. Results : Coverage Histogram (0-50X)



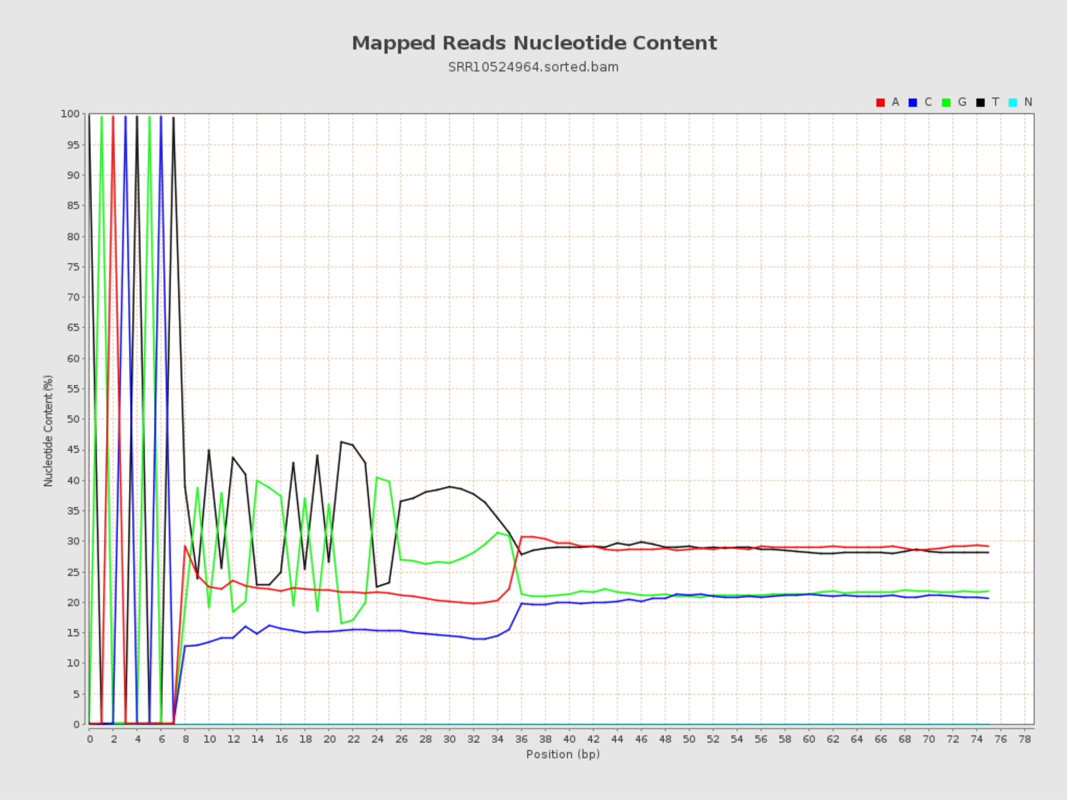
6. Results : Genome Fraction Coverage



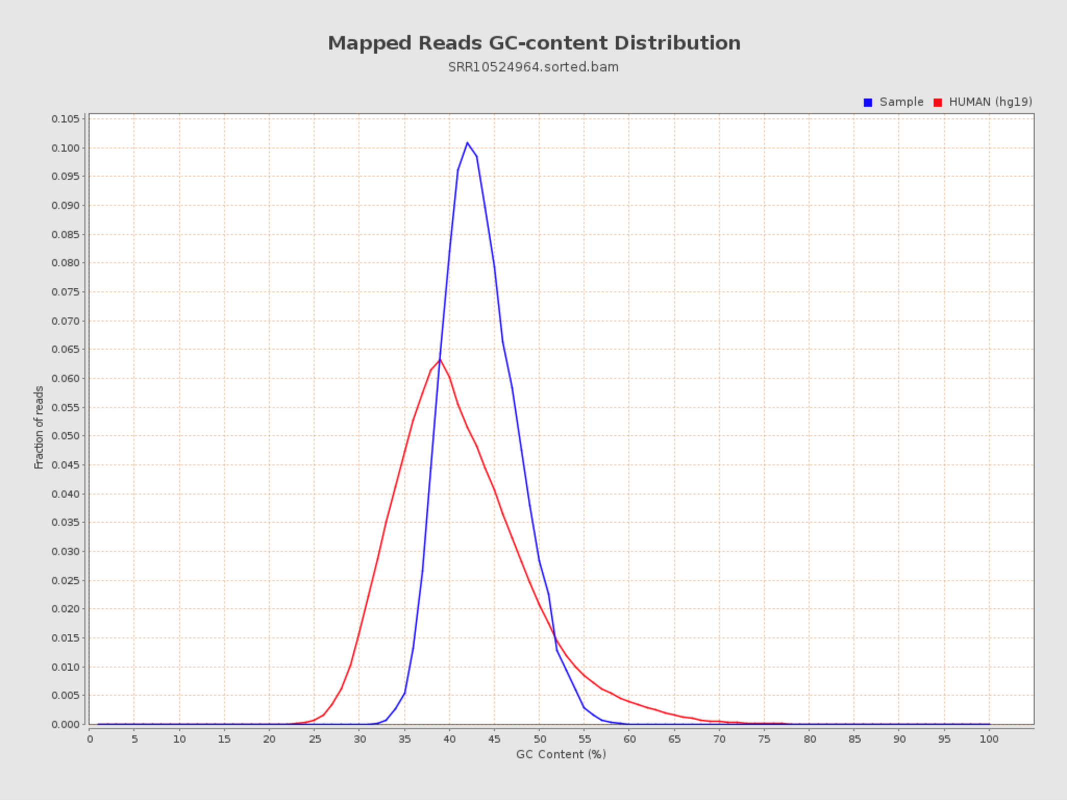
7. Results : Duplication Rate Histogram



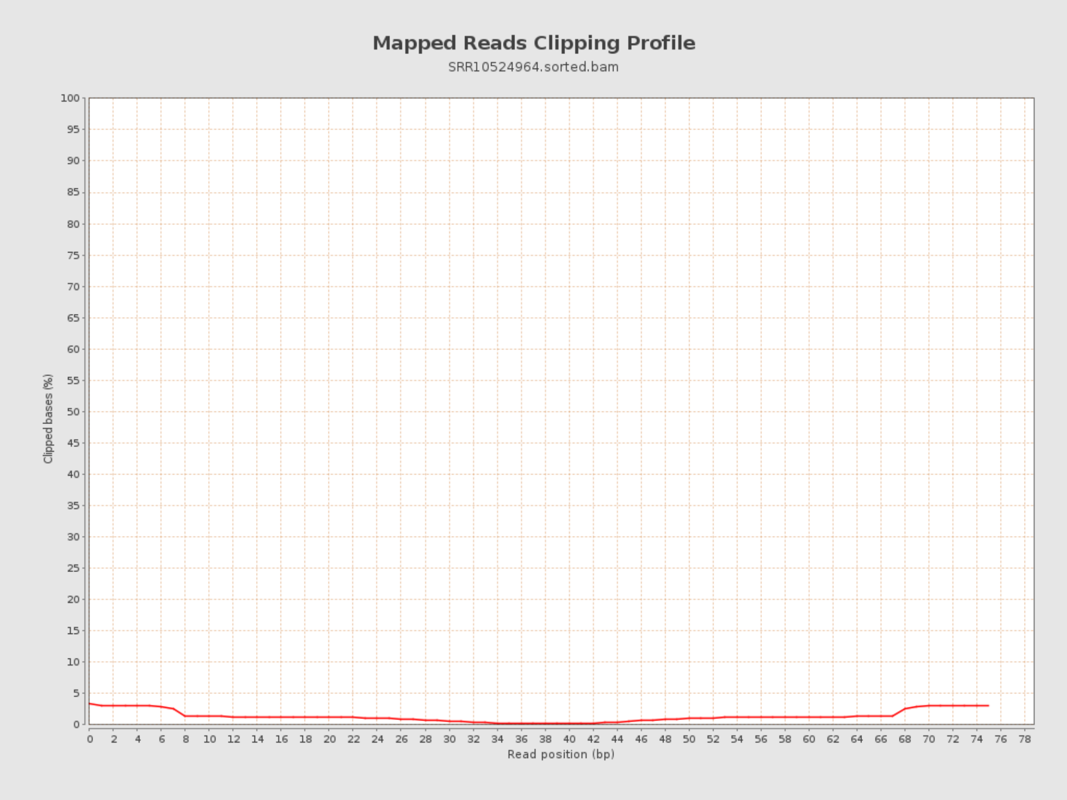
8. Results : Mapped Reads Nucleotide Content



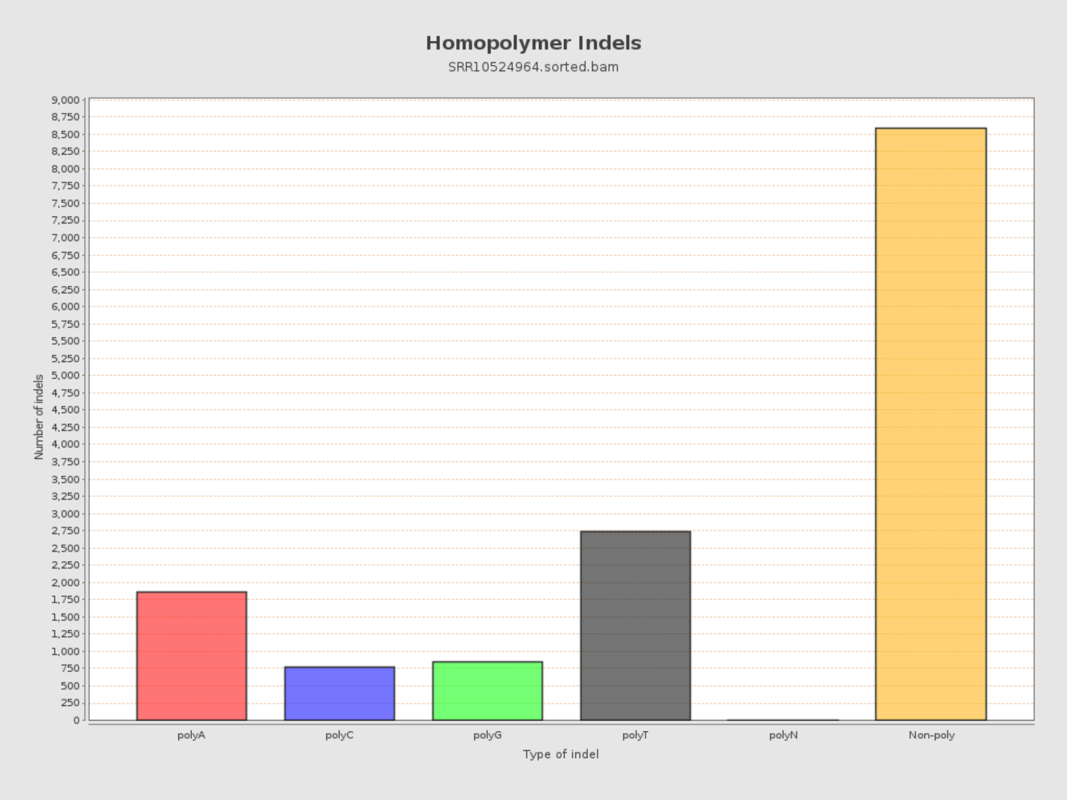
9. Results : Mapped Reads GC-content Distribution



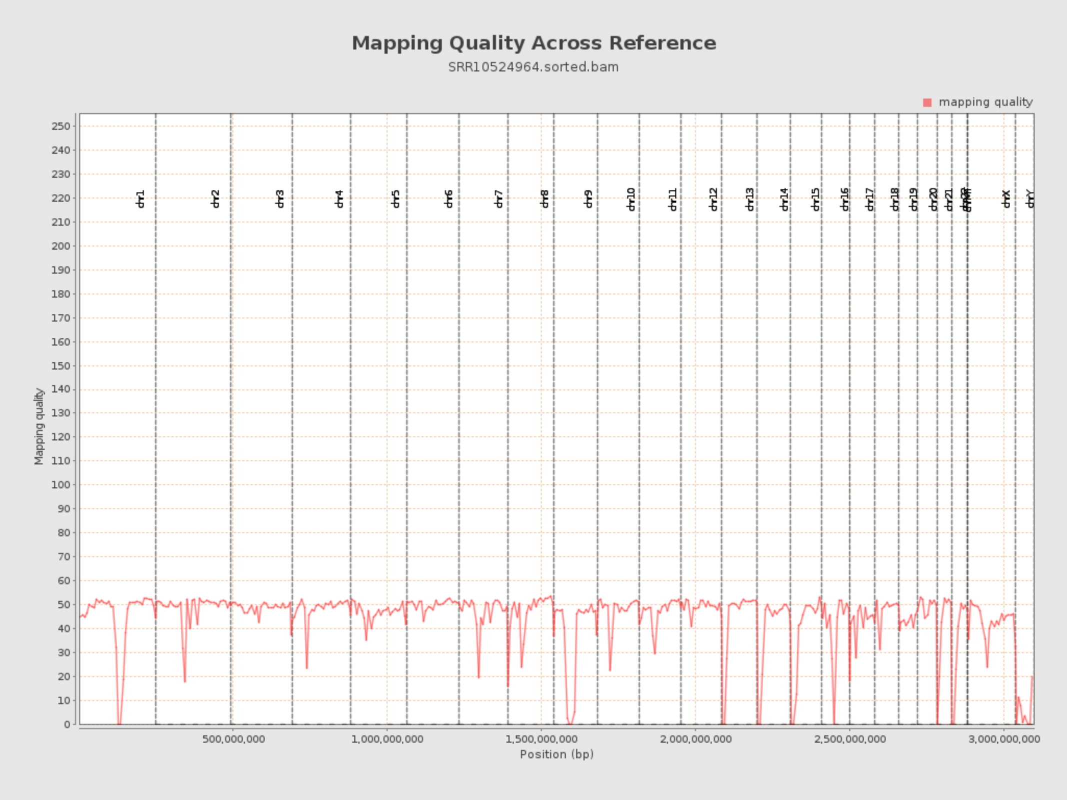
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram