Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 14:40:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524645.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_SRR10524645 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524645.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 14:40:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524645.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	950,662
Mapped reads	880,712 / 92.64%
Unmapped reads	69,950 / 7.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,790 / 0.4%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	42,194 / 4.44%
Duplication rate	3.85%
Clipped reads	881,880 / 92.76%

2.2. ACGT Content

Number/percentage of A's	12,901,322 / 24.9%
Number/percentage of C's	8,965,484 / 17.31%
Number/percentage of T's	16,530,843 / 31.91%
Number/percentage of G's	13,407,024 / 25.88%
Number/percentage of N's	351 / 0%
GC Percentage	43.19%

2.3. Coverage

Mean	0.0167

Standard Deviation	0.1825

2.4. Mapping Quality

Mean Mapping Quality	45.23

2.5. Mismatches and indels

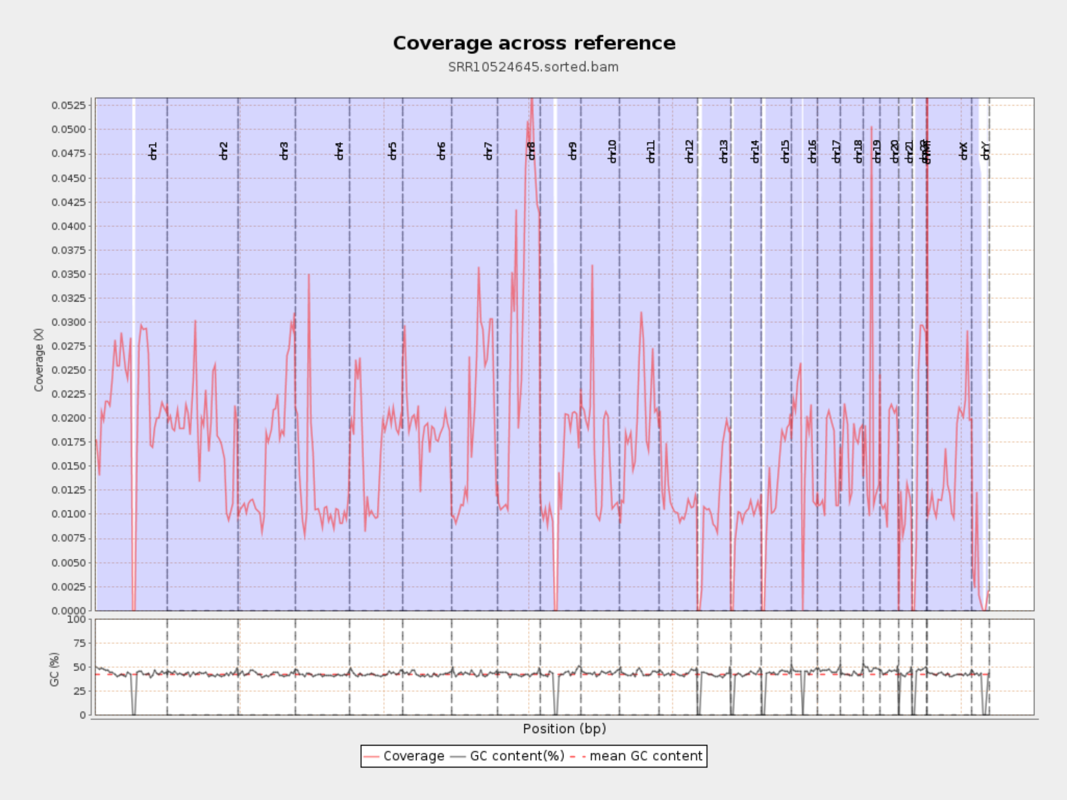
General error rate	0.51%
Mismatches	254,053
Insertions	3,669
Mapped reads with at least one insertion	0.42%
Deletions	9,863
Mapped reads with at least one deletion	1.11%
Homopolymer indels	44.18%

2.6. Chromosome stats

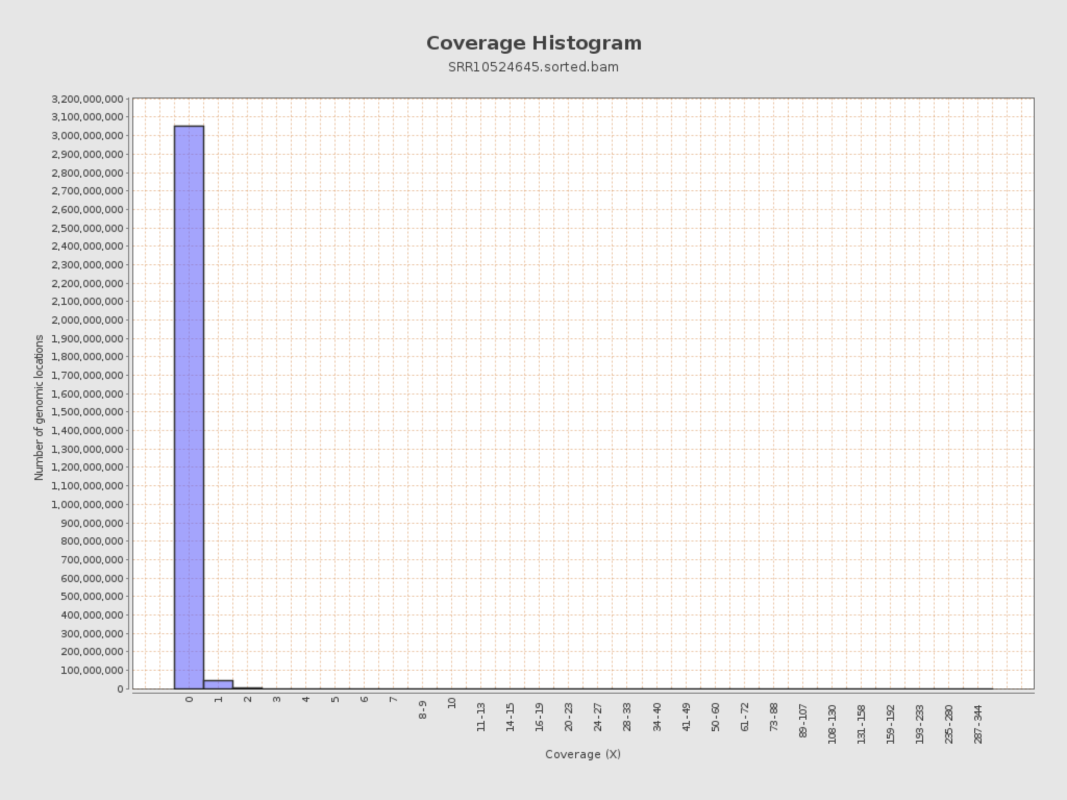
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5366840	0.0215	0.2902
chr2	243199373	4577255	0.0188	0.212
chr3	198022430	3275035	0.0165	0.1412
chr4	191154276	2385971	0.0125	0.1553
chr5	180915260	3125823	0.0173	0.1446
chr6	171115067	3319627	0.0194	0.1569
chr7	159138663	3171321	0.0199	0.2141

chr8	146364022	4558148	0.0311	0.2654
chr9	141213431	1876329	0.0133	0.1475
chr10	135534747	2298854	0.017	0.2112
chr11	135006516	2651370	0.0196	0.1706
chr12	133851895	1571673	0.0117	0.1206
chr13	115169878	1249704	0.0109	0.1155
chr14	107349540	951206	0.0089	0.1067
chr15	102531392	1286681	0.0125	0.1225
chr16	90354753	1553099	0.0172	0.1477
chr17	81195210	1181730	0.0146	0.1367
chr18	78077248	1338365	0.0171	0.2271
chr19	59128983	1077058	0.0182	0.2174
chr20	63025520	1006265	0.016	0.1423
chr21	48129895	468326	0.0097	0.1295
chr22	51304566	981425	0.0191	0.1543
chrMT	16571	3712	0.224	0.5297
chrX	155270560	2374483	0.0153	0.1428
chrY	59373566	171247	0.0029	0.1237

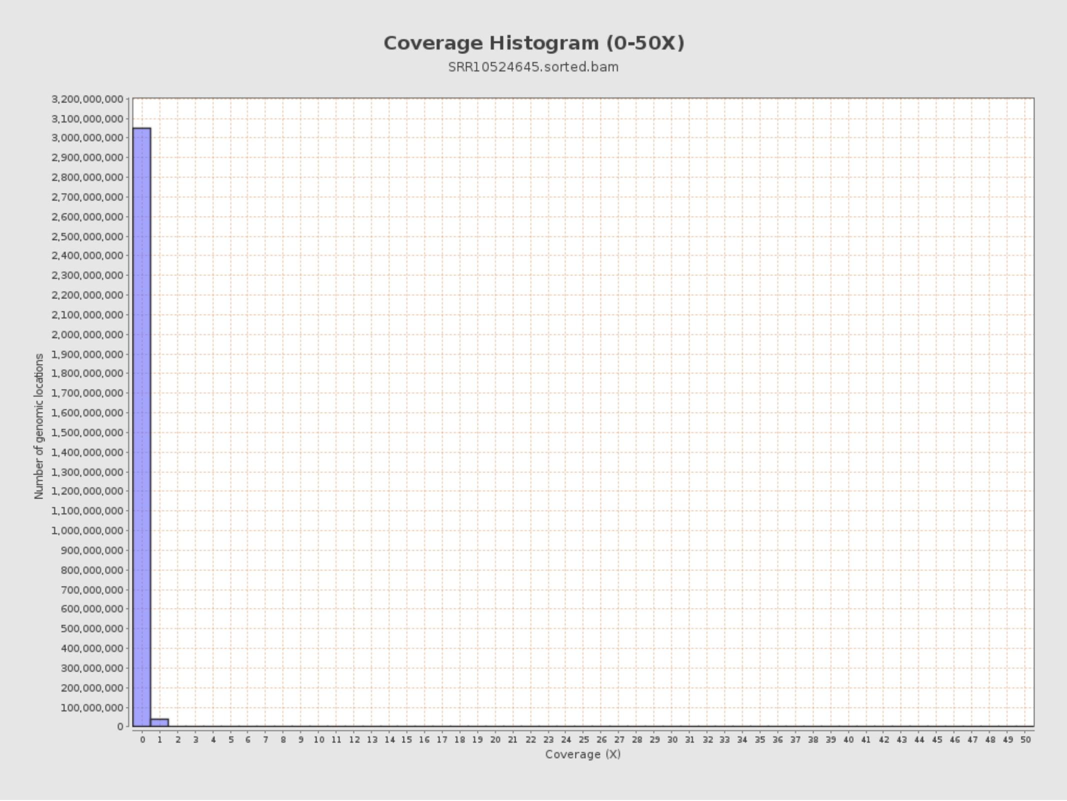
3. Results : Coverage across reference



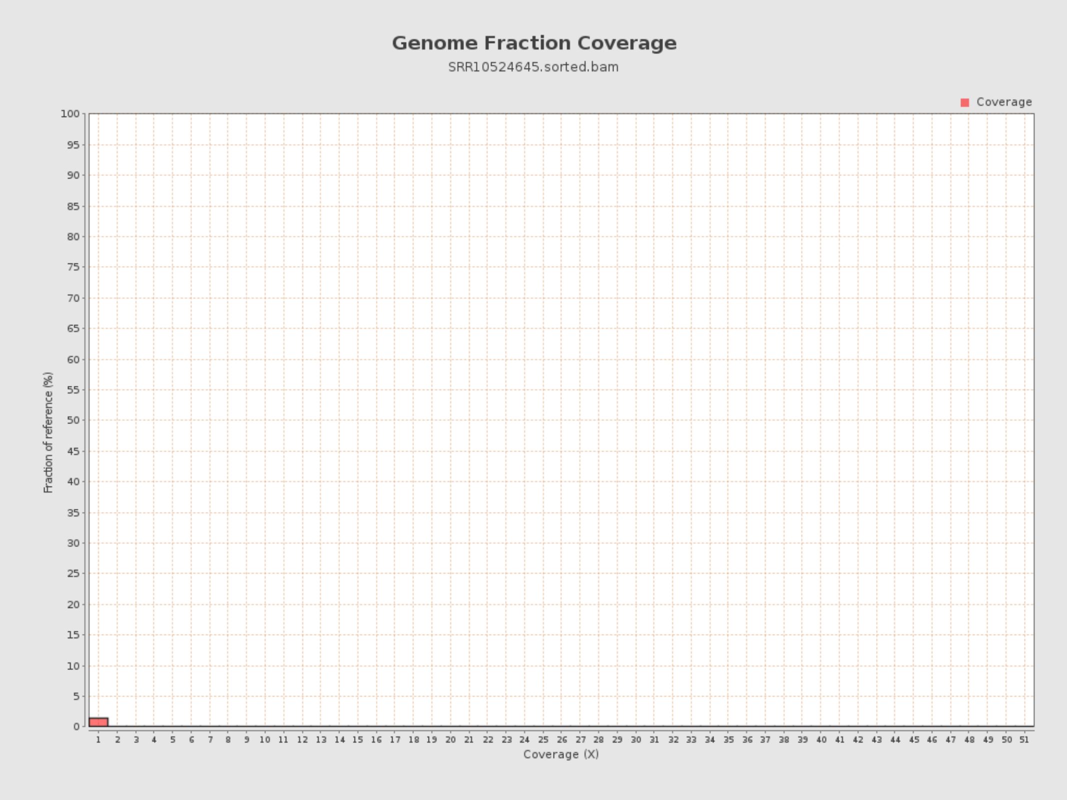
4. Results : Coverage Histogram



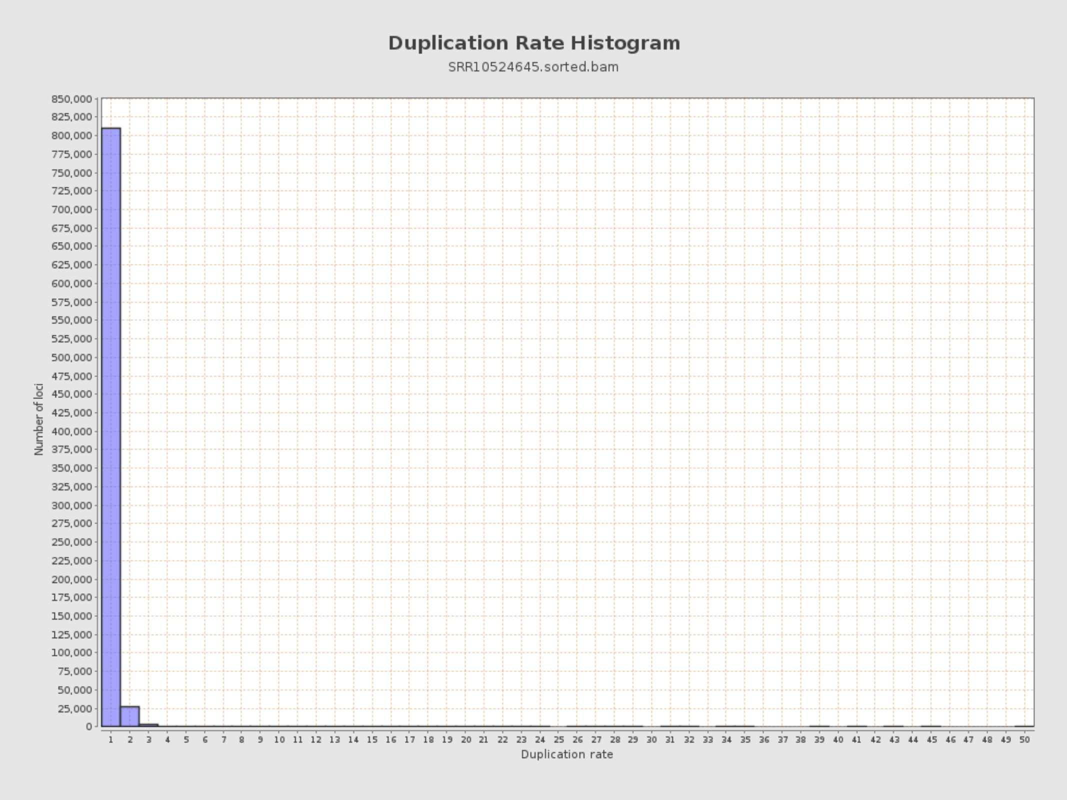
5. Results : Coverage Histogram (0-50X)



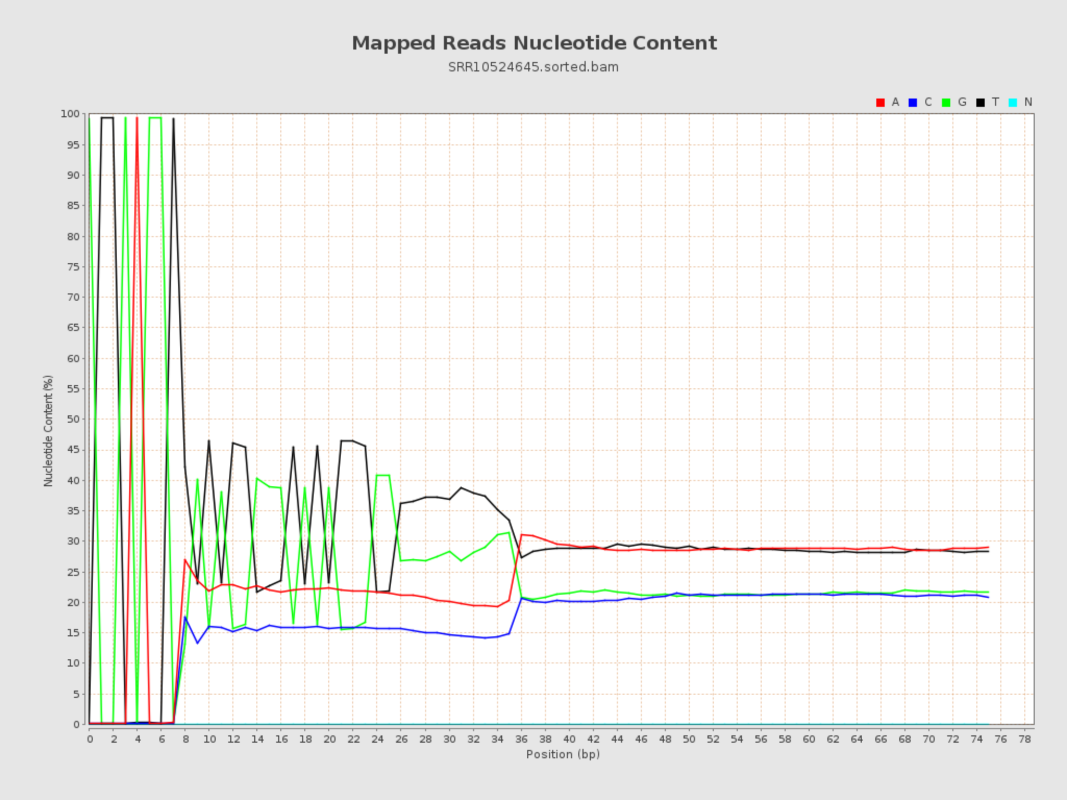
6. Results : Genome Fraction Coverage



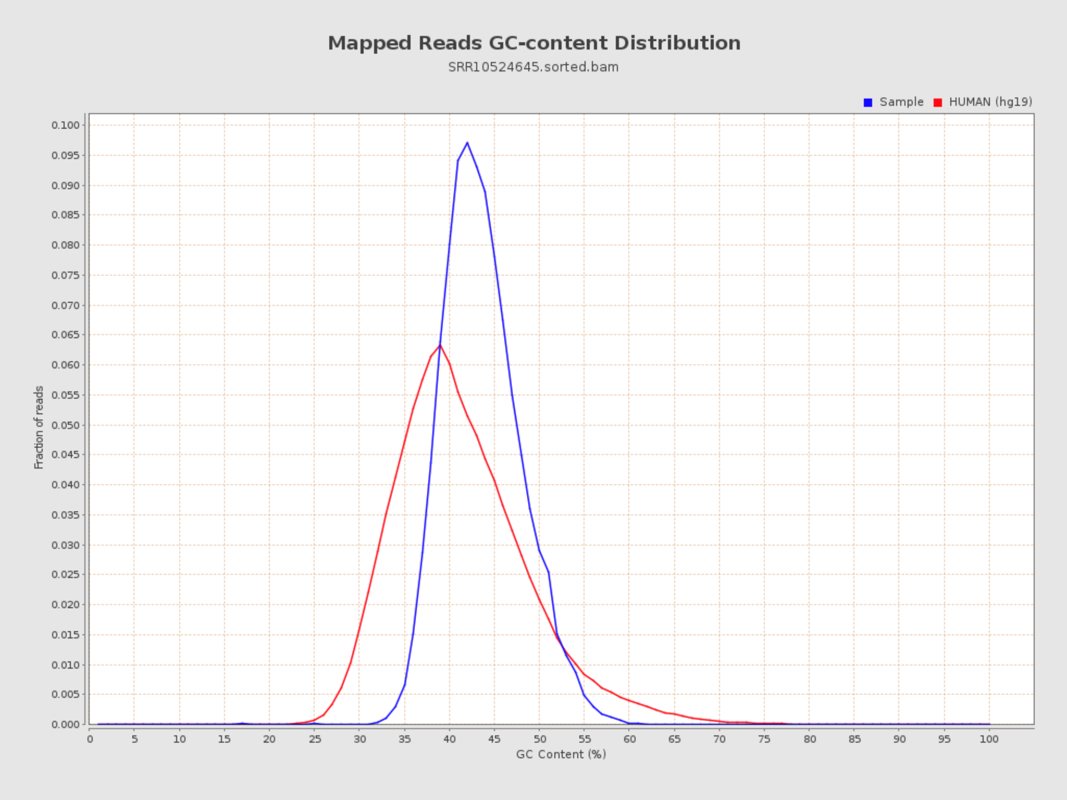
7. Results : Duplication Rate Histogram



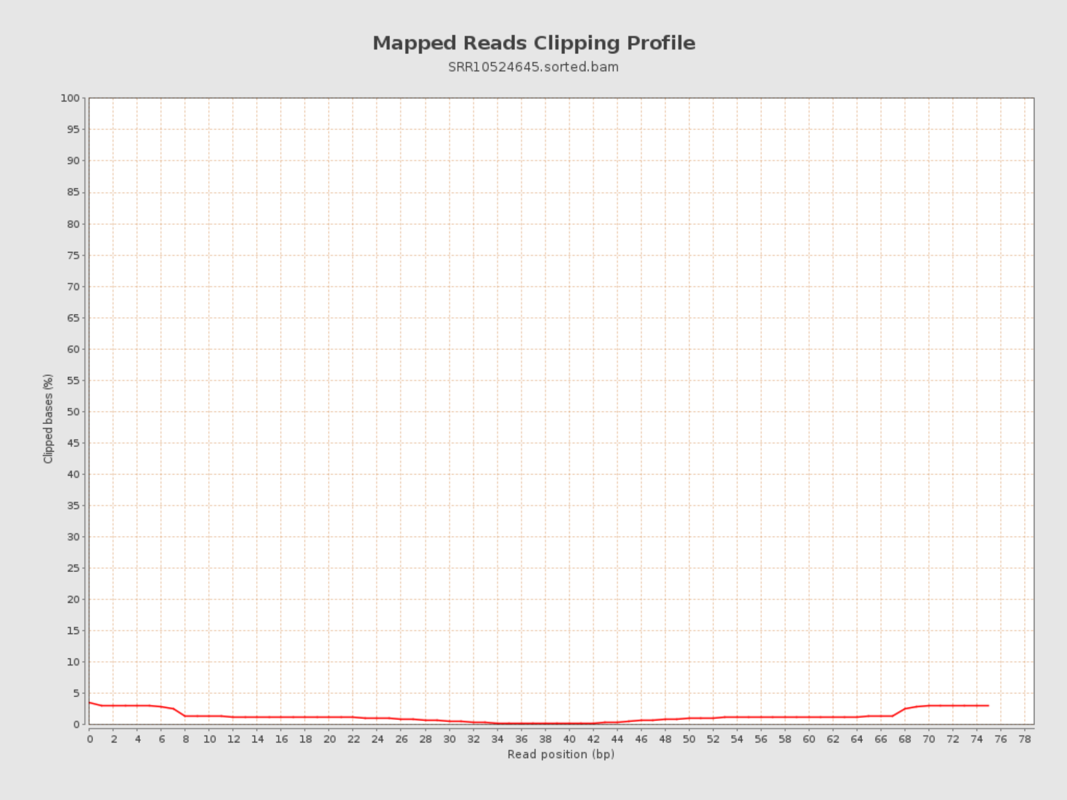
8. Results : Mapped Reads Nucleotide Content



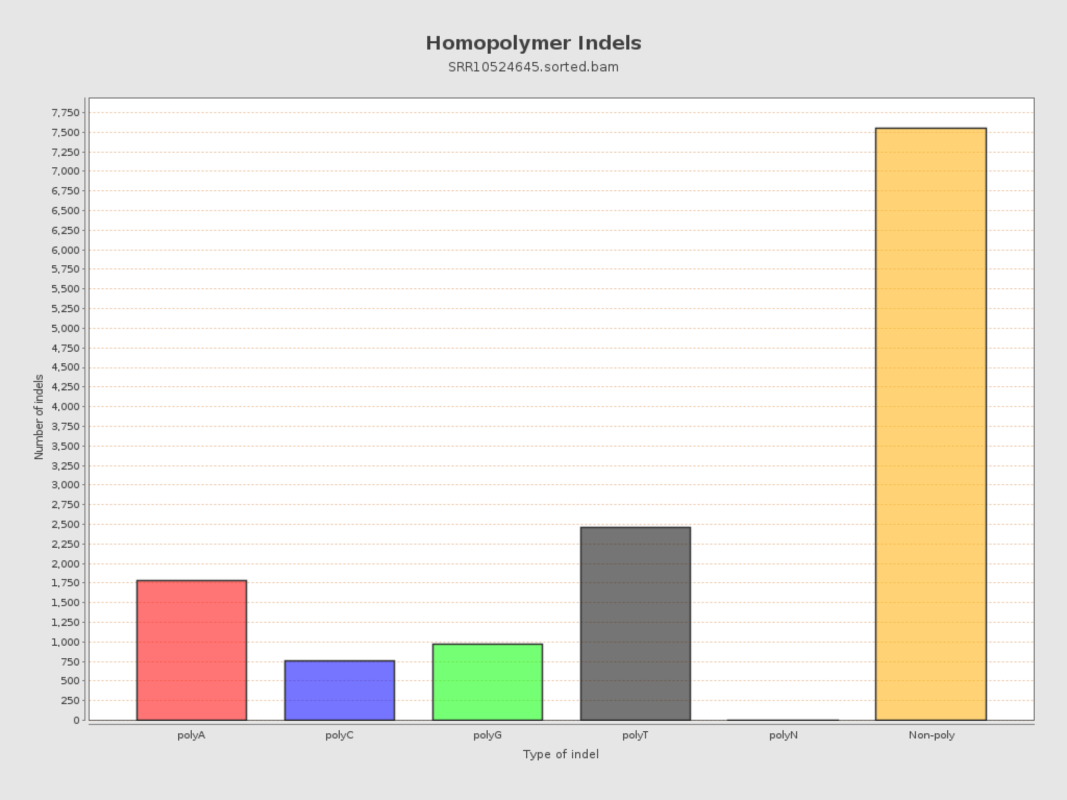
9. Results : Mapped Reads GC-content Distribution



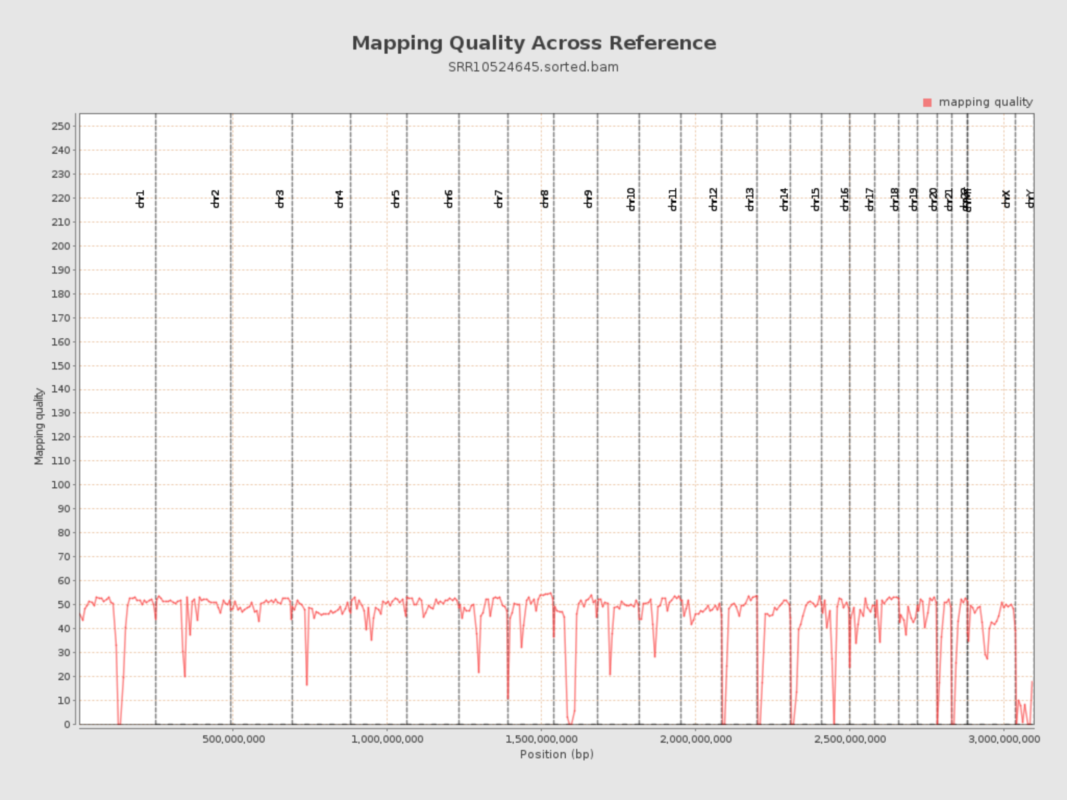
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram