Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 10:38:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524555.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_SRR10524555 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524555.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 10:38:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524555.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	915,763
Mapped reads	841,416 / 91.88%
Unmapped reads	74,347 / 8.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,001 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	15,547 / 1.7%
Duplication rate	1.32%
Clipped reads	842,168 / 91.96%

2.2. ACGT Content

Number/percentage of A's	11,970,386 / 24.56%
Number/percentage of C's	8,834,348 / 18.13%
Number/percentage of T's	15,791,726 / 32.4%
Number/percentage of G's	12,138,309 / 24.91%
Number/percentage of N's	1,450 / 0%
GC Percentage	43.03%

2.3. Coverage

Mean	0.0157

Standard Deviation	0.1613

2.4. Mapping Quality

Mean Mapping Quality	45.28

2.5. Mismatches and indels

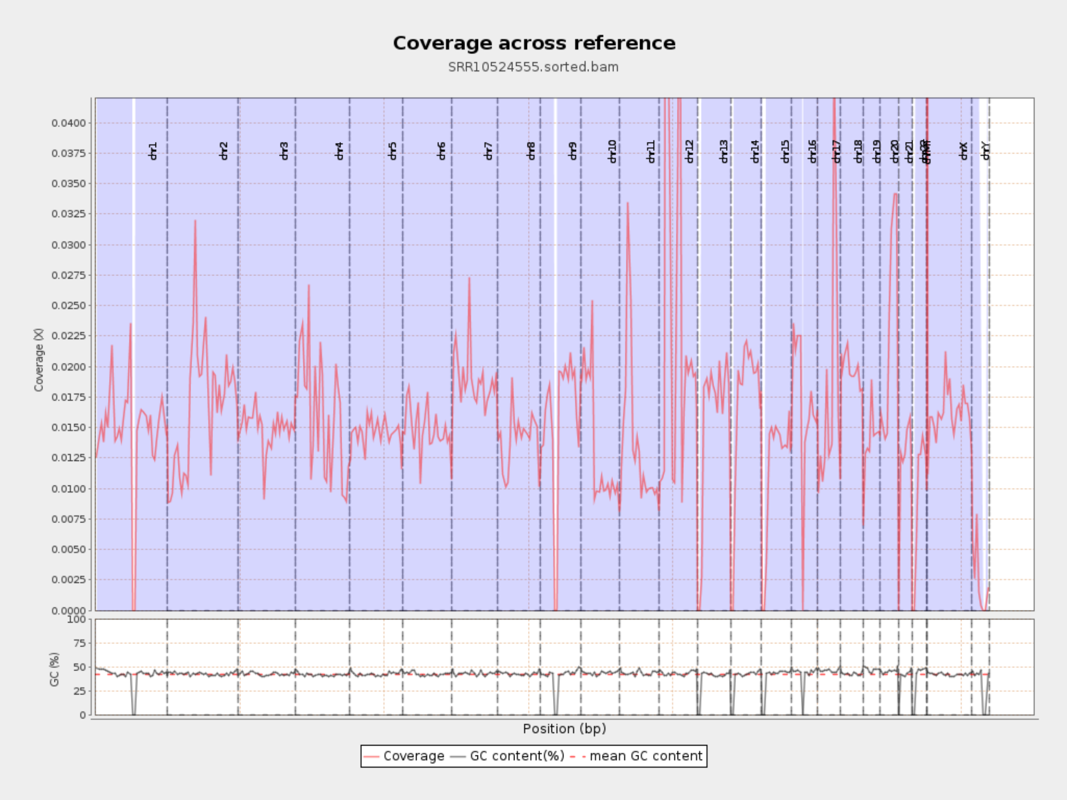
General error rate	0.49%
Mismatches	234,420
Insertions	3,258
Mapped reads with at least one insertion	0.38%
Deletions	7,480
Mapped reads with at least one deletion	0.88%
Homopolymer indels	41.37%

2.6. Chromosome stats

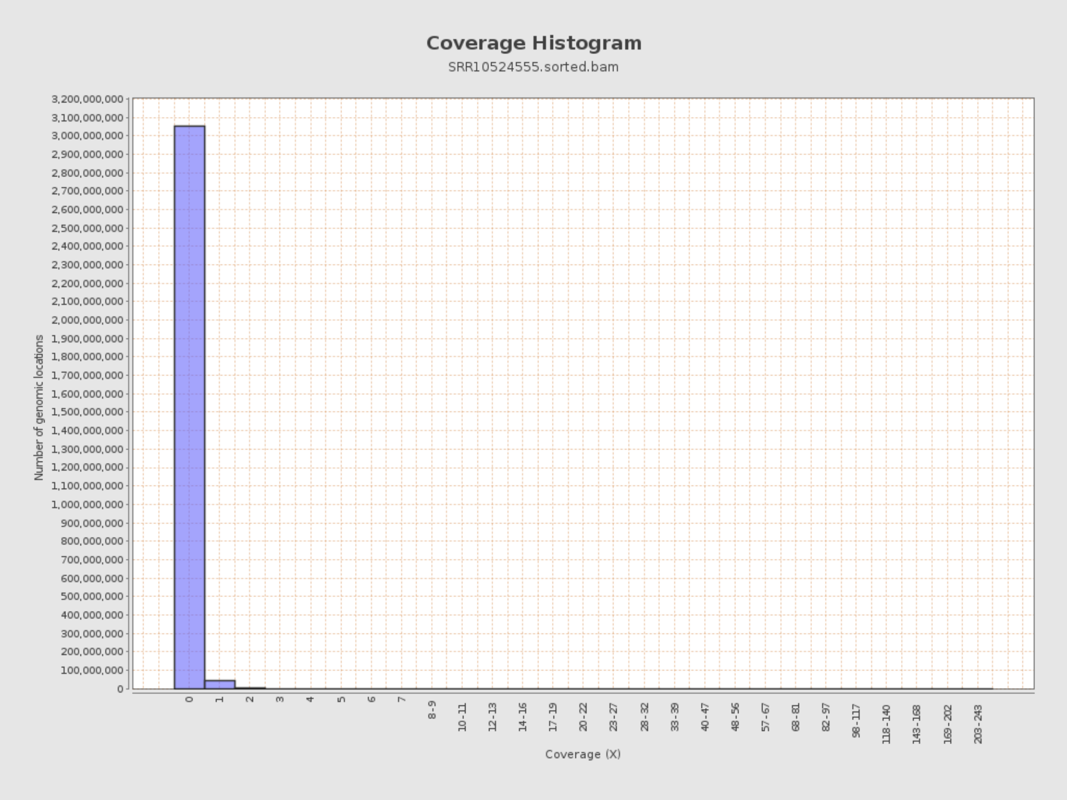
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3667143	0.0147	0.2342
chr2	243199373	4084180	0.0168	0.1789
chr3	198022430	2956819	0.0149	0.1271
chr4	191154276	3063875	0.016	0.1405
chr5	180915260	2661395	0.0147	0.1272
chr6	171115067	2535443	0.0148	0.1328
chr7	159138663	3033261	0.0191	0.2001

chr8	146364022	2064168	0.0141	0.1506
chr9	141213431	2196205	0.0156	0.1607
chr10	135534747	1829014	0.0135	0.1575
chr11	135006516	1863187	0.0138	0.1375
chr12	133851895	3499108	0.0261	0.1791
chr13	115169878	1767685	0.0153	0.1287
chr14	107349540	1783136	0.0166	0.1394
chr15	102531392	1186551	0.0116	0.1118
chr16	90354753	1494703	0.0165	0.1404
chr17	81195210	1488873	0.0183	0.1434
chr18	78077248	1540818	0.0197	0.2621
chr19	59128983	837428	0.0142	0.1894
chr20	63025520	1456307	0.0231	0.1613
chr21	48129895	592382	0.0123	0.124
chr22	51304566	470316	0.0092	0.0993
chrMT	16571	9577	0.5779	0.8154
chrX	155270560	2527259	0.0163	0.1431
chrY	59373566	139960	0.0024	0.0662

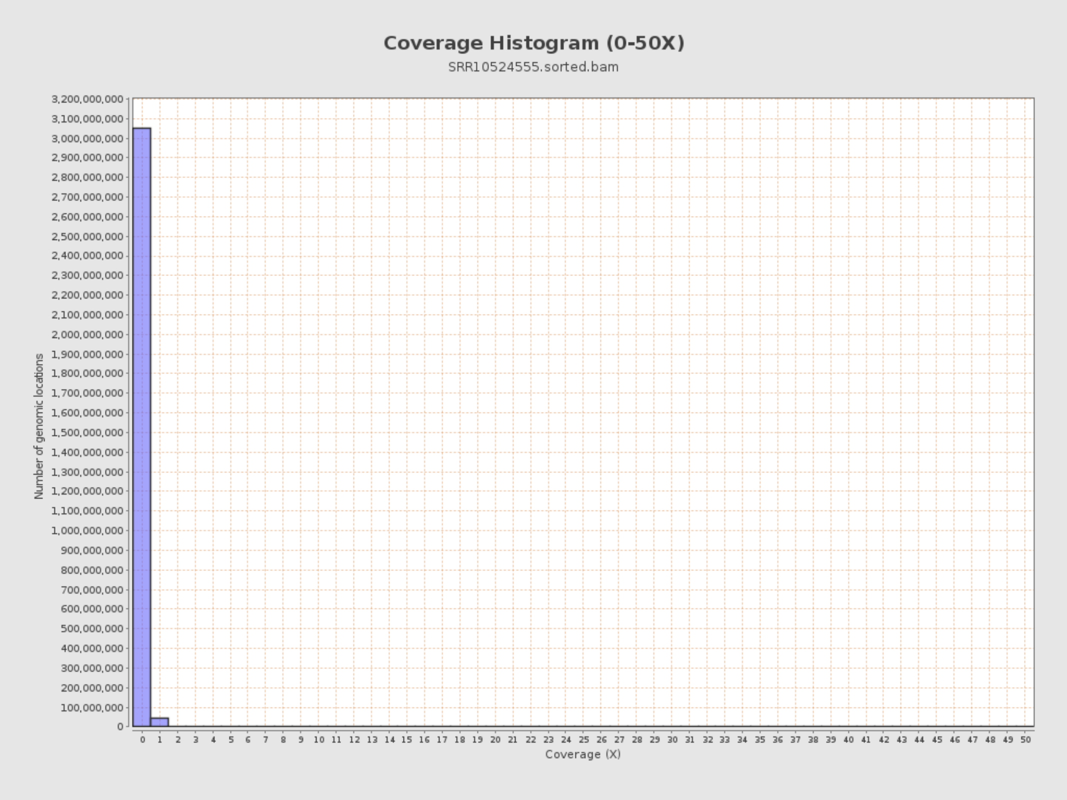
3. Results : Coverage across reference



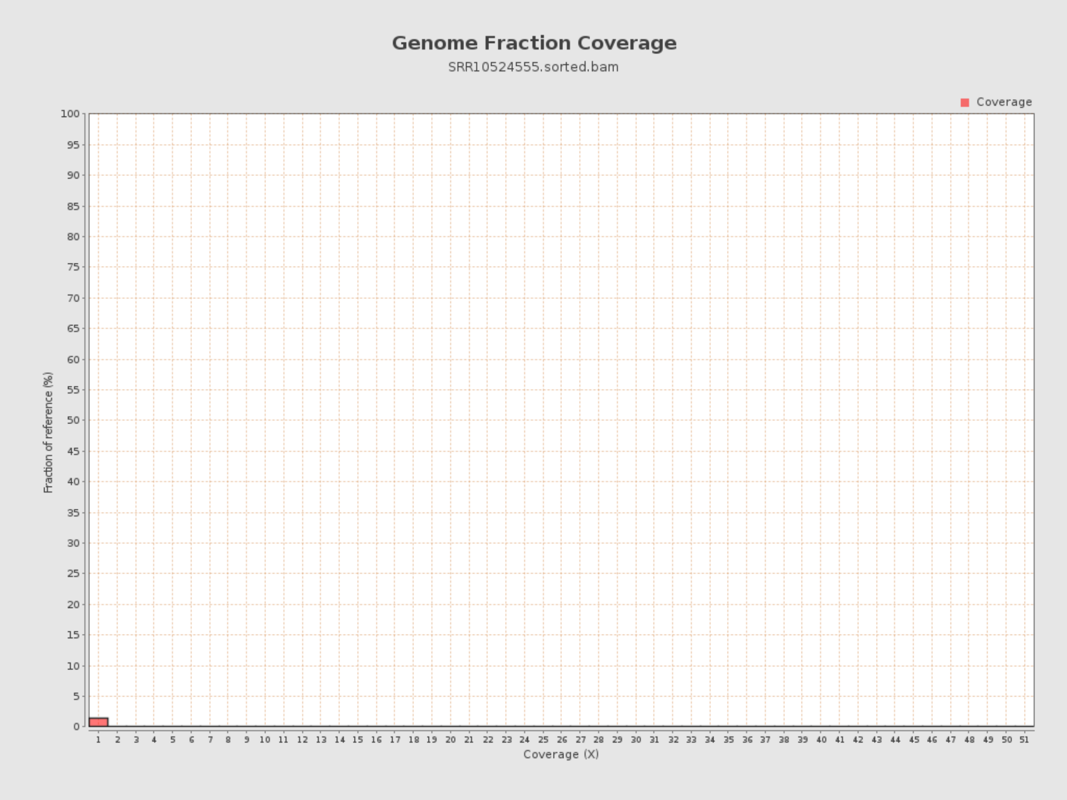
4. Results : Coverage Histogram



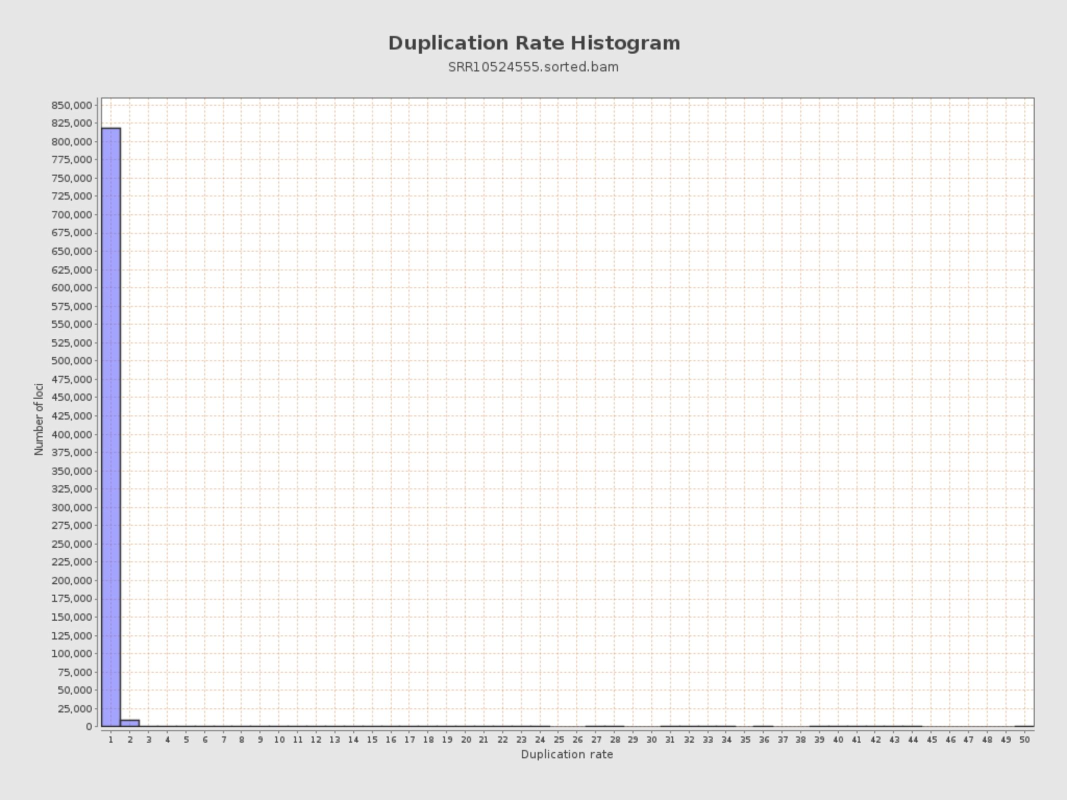
5. Results : Coverage Histogram (0-50X)



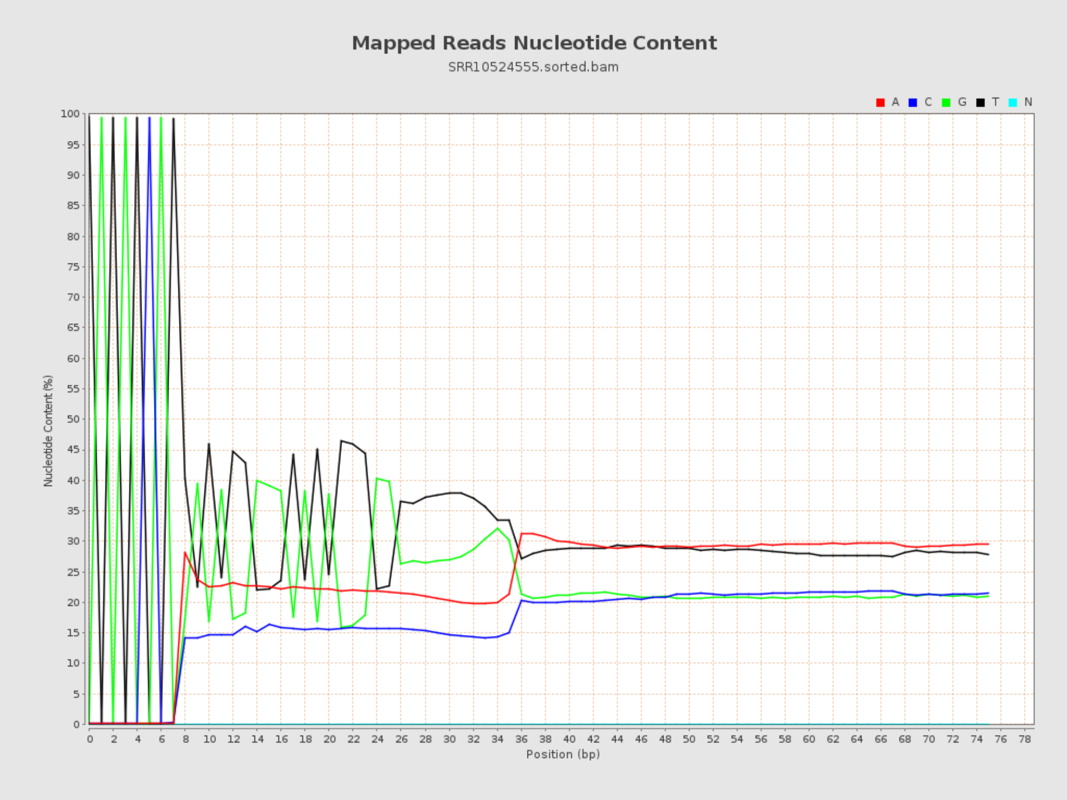
6. Results : Genome Fraction Coverage



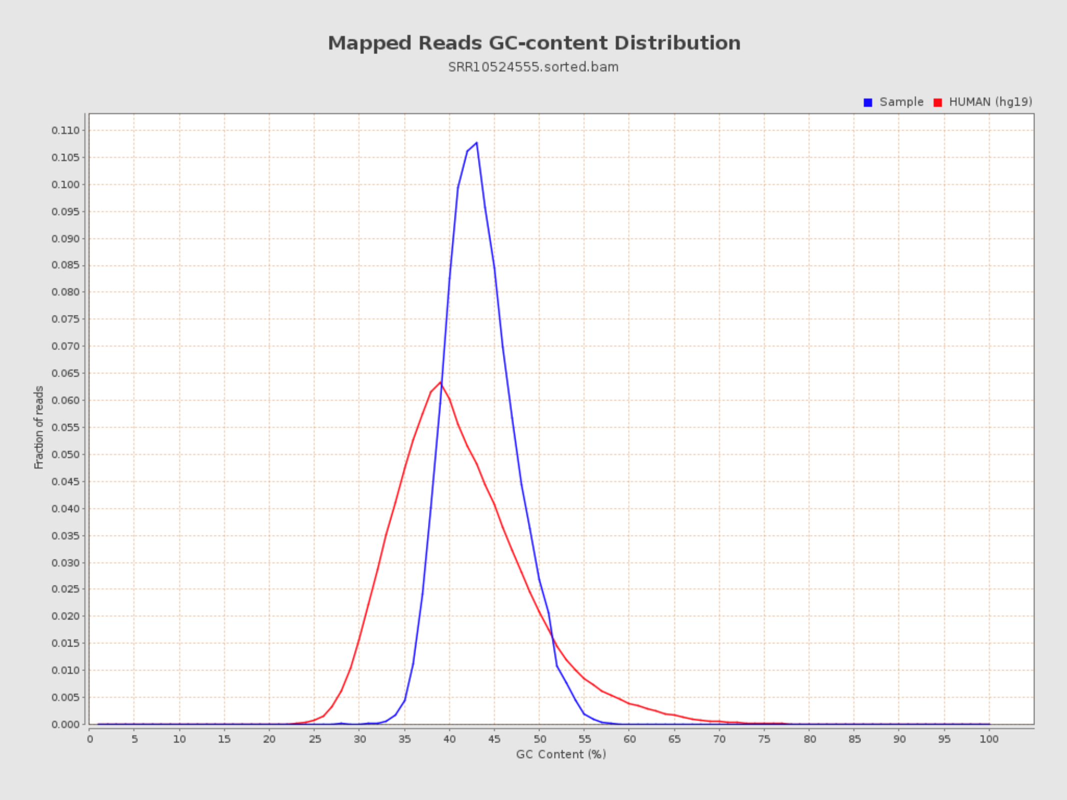
7. Results : Duplication Rate Histogram



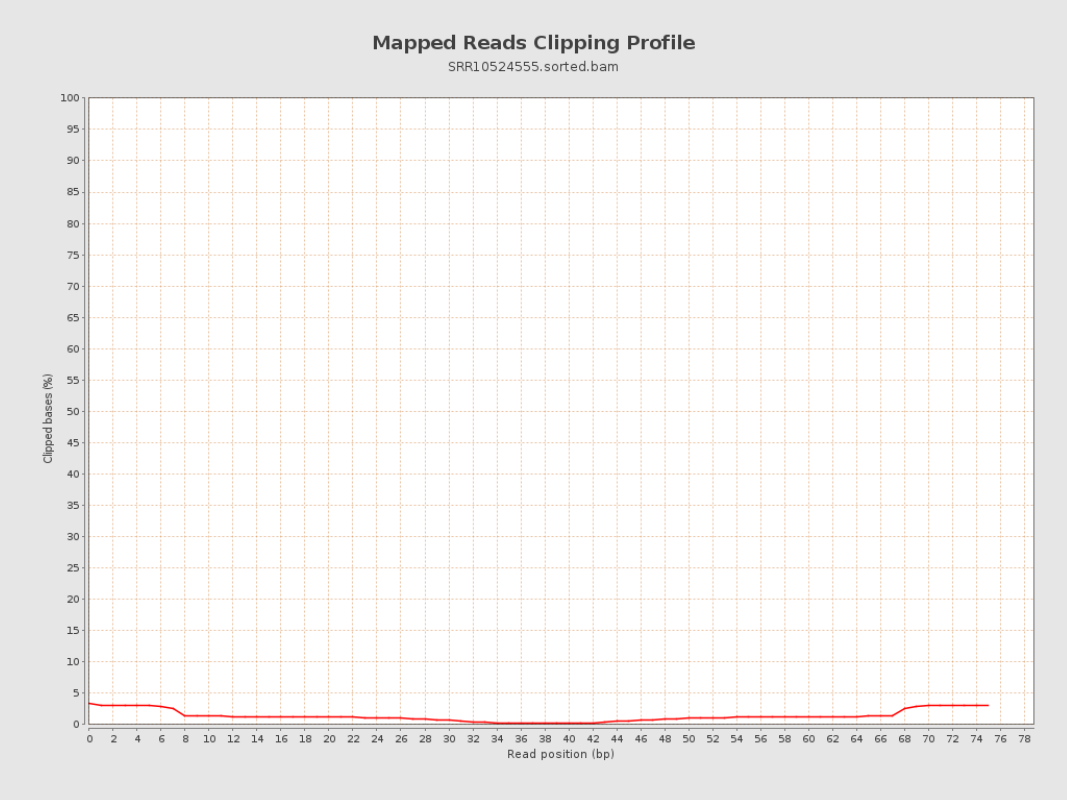
8. Results : Mapped Reads Nucleotide Content



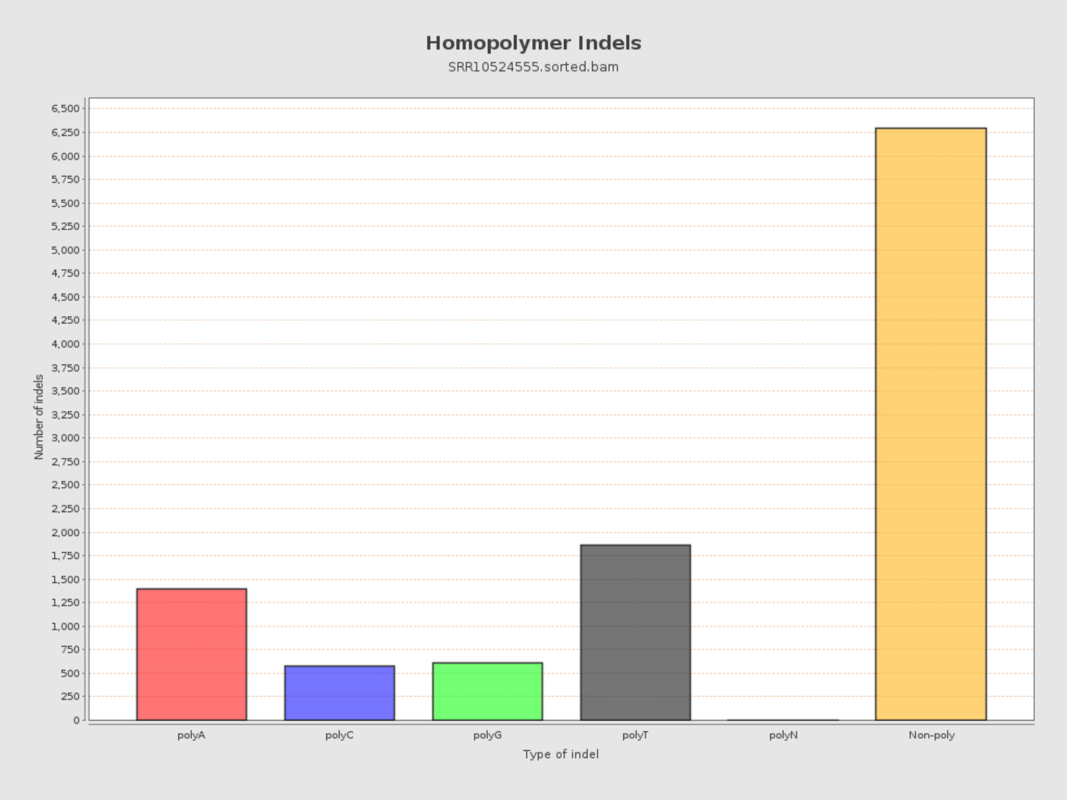
9. Results : Mapped Reads GC-content Distribution



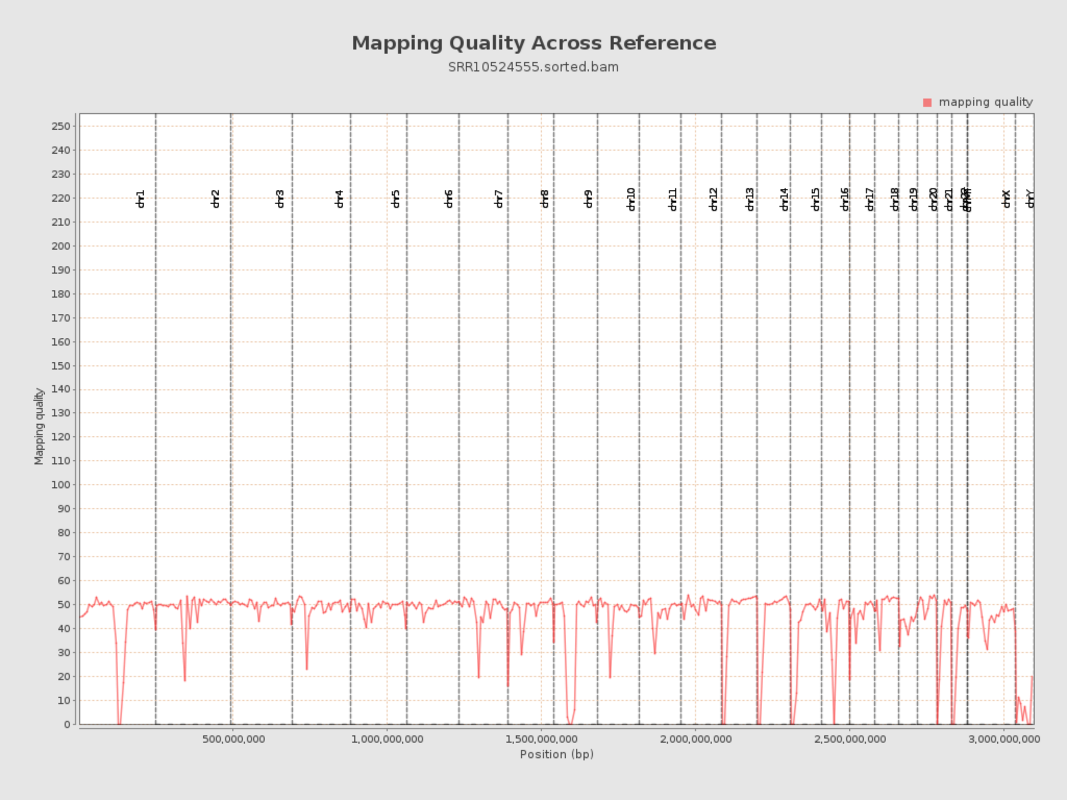
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram