Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 01:58:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524398.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_SRR10524398 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524398.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 01:58:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524398.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,022,390
Mapped reads	949,739 / 92.89%
Unmapped reads	72,651 / 7.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,154 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	28,497 / 2.79%
Duplication rate	2.27%
Clipped reads	950,752 / 92.99%

2.2. ACGT Content

Number/percentage of A's	13,323,697 / 23.96%
Number/percentage of C's	11,361,938 / 20.43%
Number/percentage of T's	17,767,529 / 31.95%
Number/percentage of G's	13,157,275 / 23.66%
Number/percentage of N's	7,284 / 0.01%
GC Percentage	44.09%

2.3. Coverage

Mean	0.018

Standard Deviation	0.1983

2.4. Mapping Quality

Mean Mapping Quality	45.72

2.5. Mismatches and indels

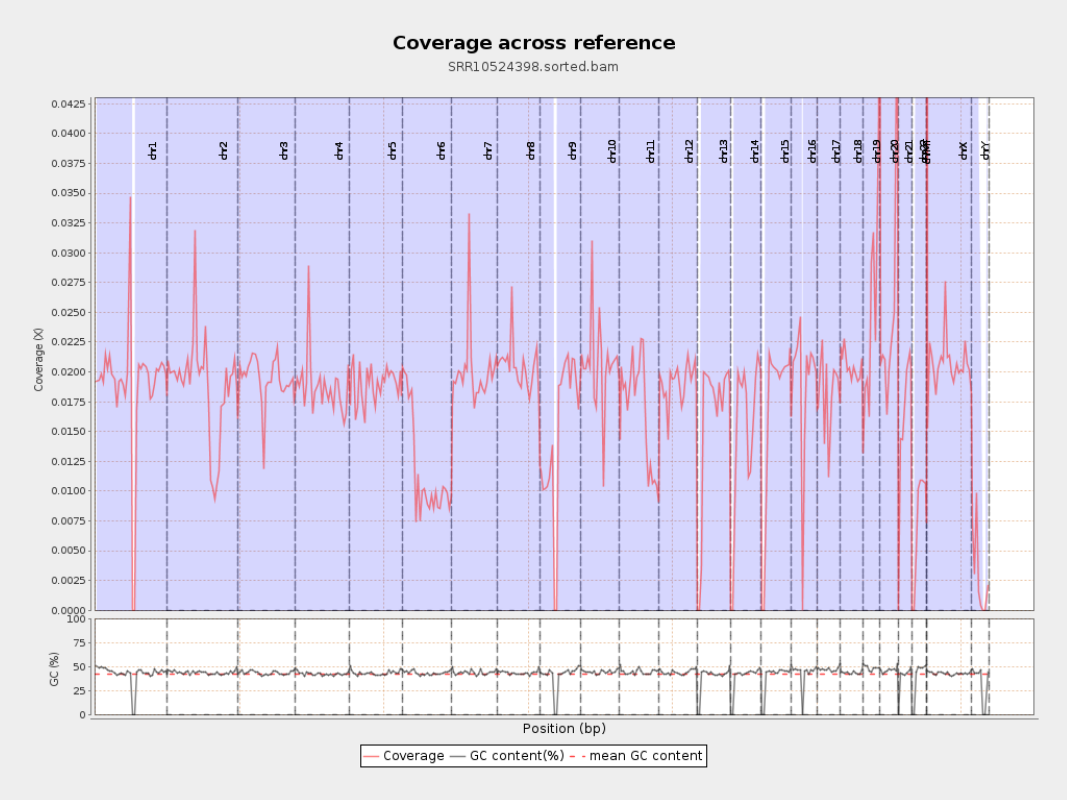
General error rate	0.5%
Mismatches	270,455
Insertions	4,125
Mapped reads with at least one insertion	0.43%
Deletions	10,231
Mapped reads with at least one deletion	1.07%
Homopolymer indels	42.59%

2.6. Chromosome stats

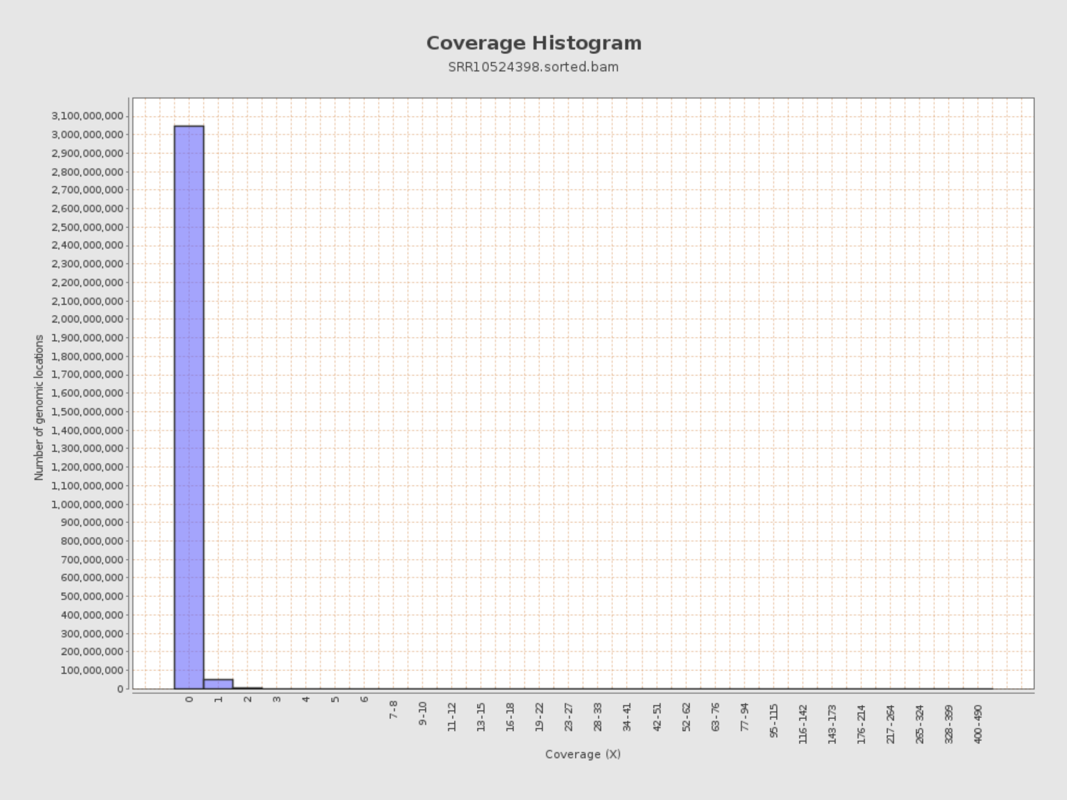
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4687273	0.0188	0.3912
chr2	243199373	4562736	0.0188	0.2093
chr3	198022430	3846293	0.0194	0.1468
chr4	191154276	3589615	0.0188	0.1562
chr5	180915260	3443736	0.019	0.1457
chr6	171115067	1992920	0.0116	0.1197
chr7	159138663	3191999	0.0201	0.2617

chr8	146364022	2991321	0.0204	0.1791
chr9	141213431	2073458	0.0147	0.1522
chr10	135534747	2793964	0.0206	0.1844
chr11	135006516	2278492	0.0169	0.1689
chr12	133851895	2551648	0.0191	0.1505
chr13	115169878	1814542	0.0158	0.1327
chr14	107349540	1608863	0.015	0.1326
chr15	102531392	1710033	0.0167	0.1365
chr16	90354753	1689889	0.0187	0.1484
chr17	81195210	1485119	0.0183	0.1506
chr18	78077248	1595061	0.0204	0.2583
chr19	59128983	1562058	0.0264	0.277
chr20	63025520	1614313	0.0256	0.1736
chr21	48129895	779323	0.0162	0.1432
chr22	51304566	381329	0.0074	0.0907
chrMT	16571	8472	0.5113	0.7857
chrX	155270560	3212306	0.0207	0.1642
chrY	59373566	169329	0.0029	0.0832

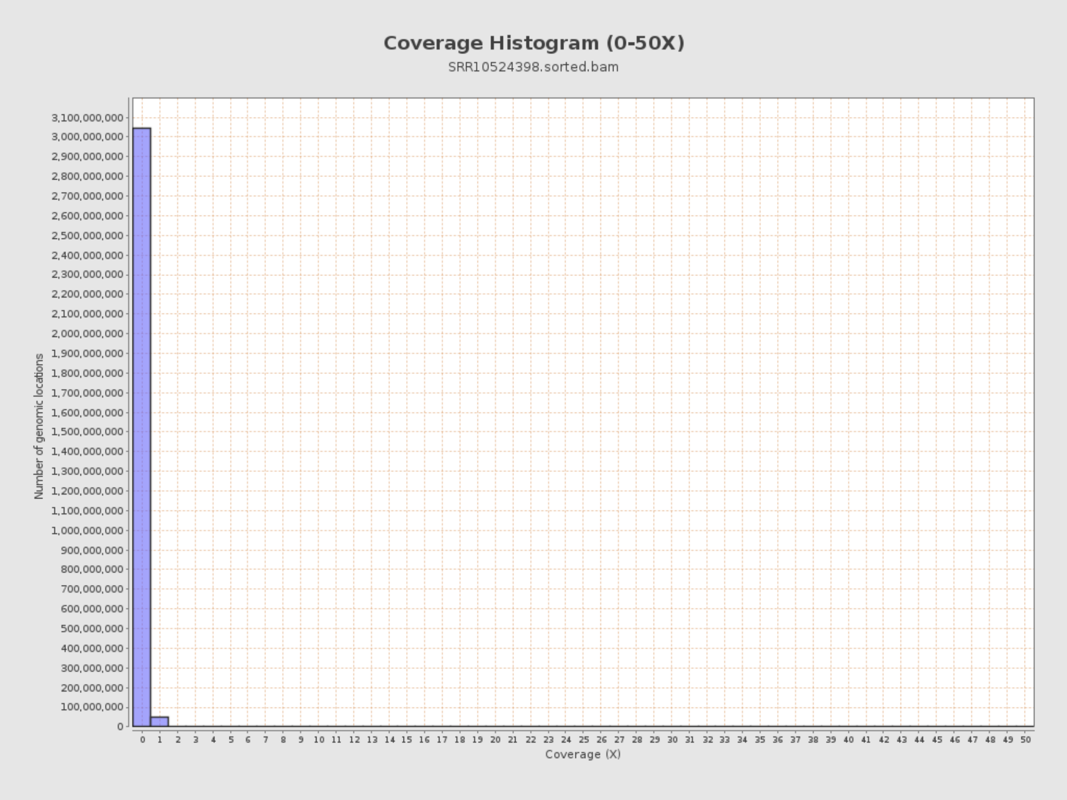
3. Results : Coverage across reference



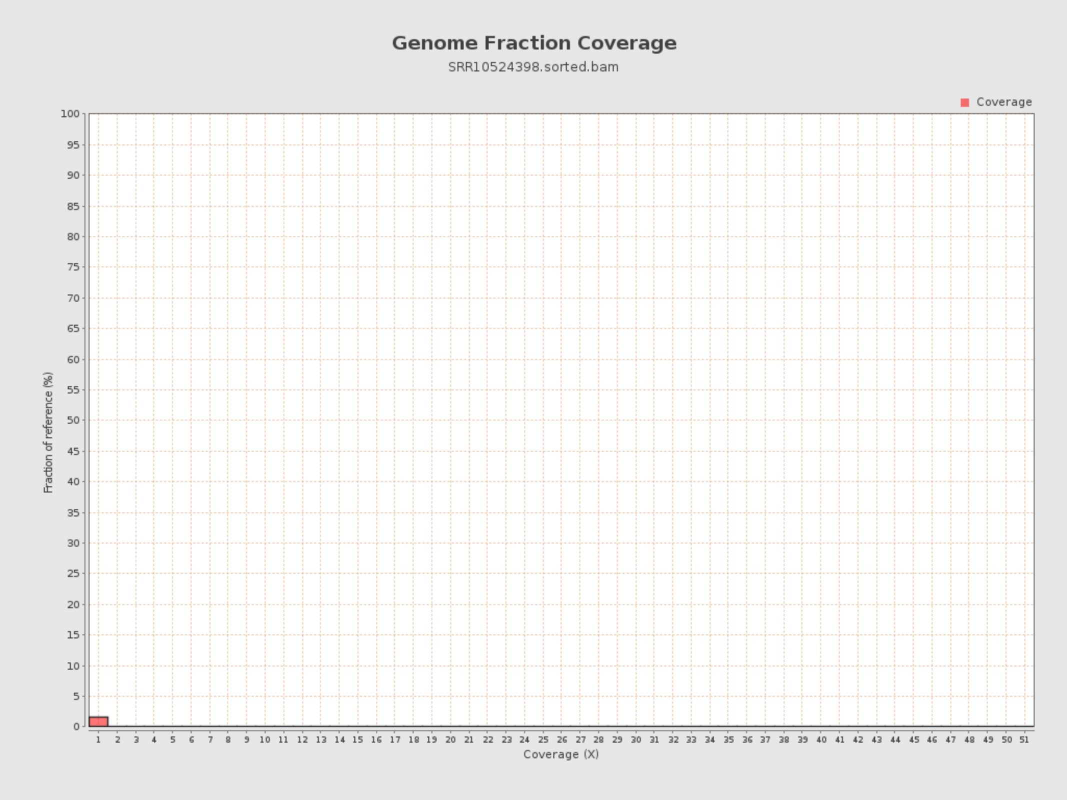
4. Results : Coverage Histogram



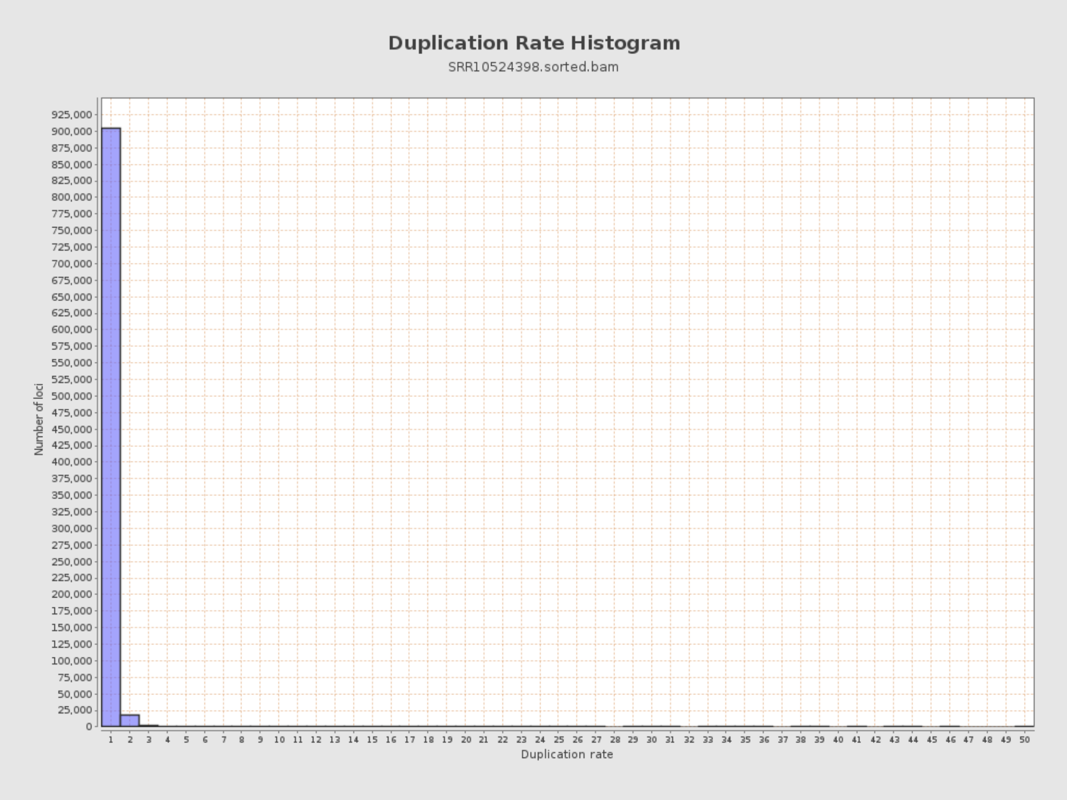
5. Results : Coverage Histogram (0-50X)



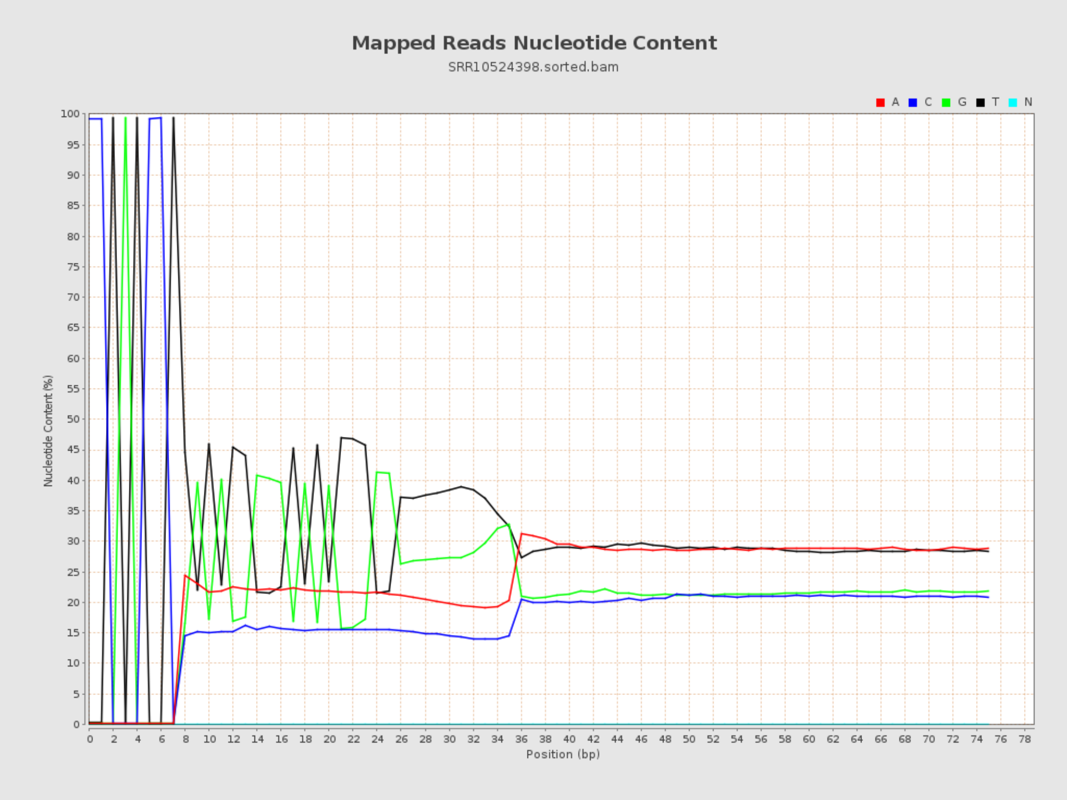
6. Results : Genome Fraction Coverage



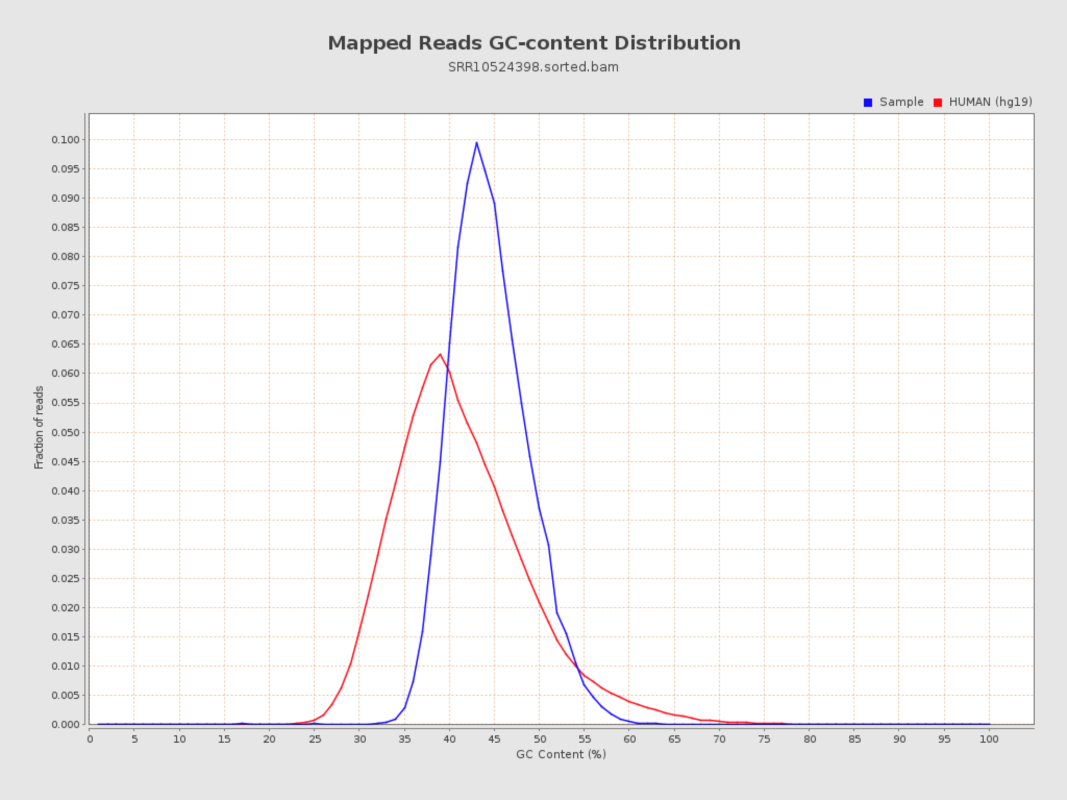
7. Results : Duplication Rate Histogram



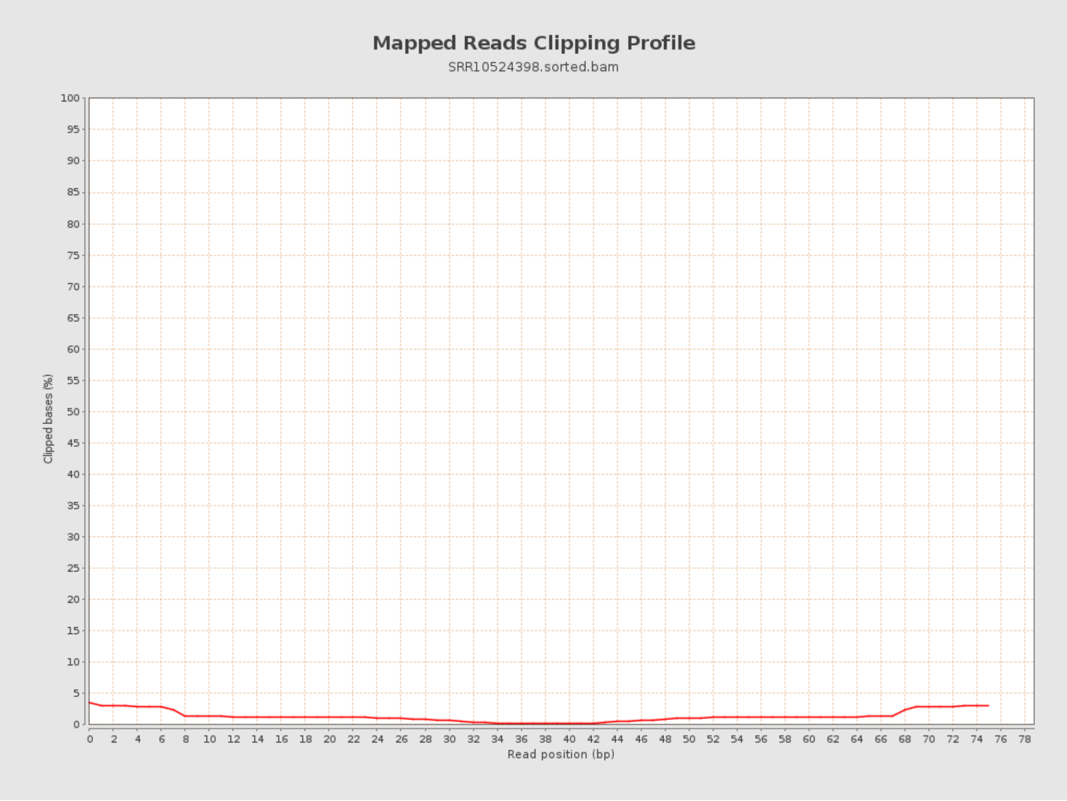
8. Results : Mapped Reads Nucleotide Content



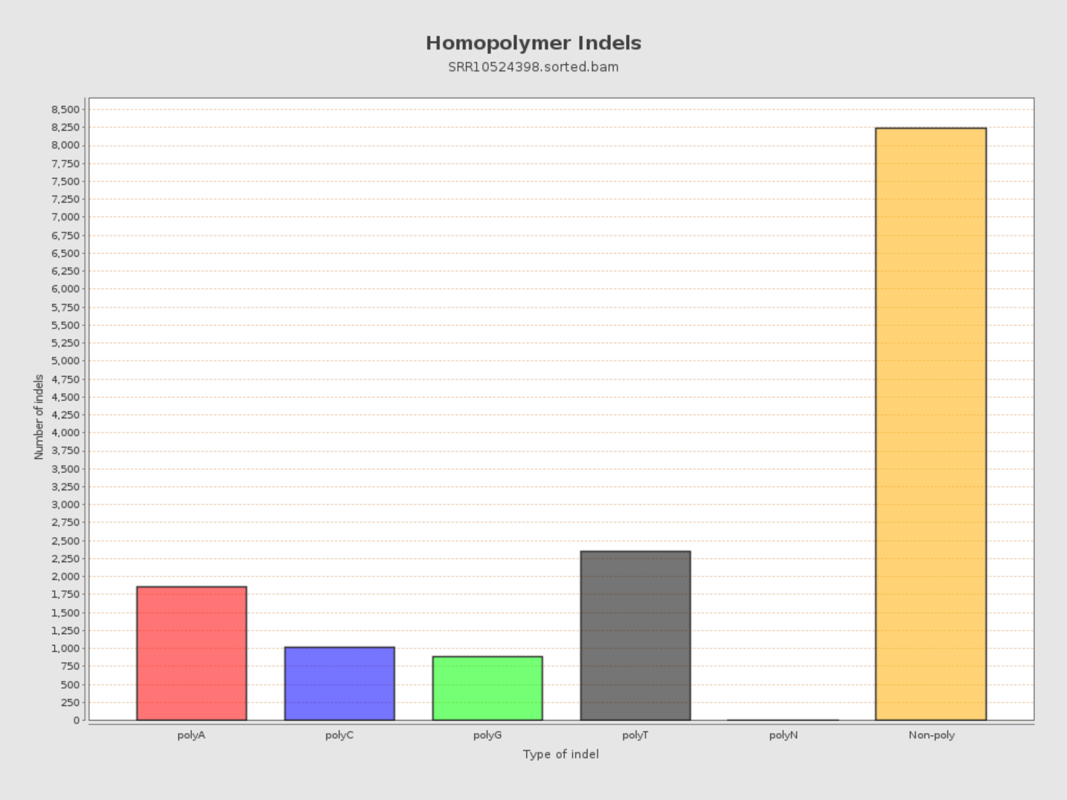
9. Results : Mapped Reads GC-content Distribution



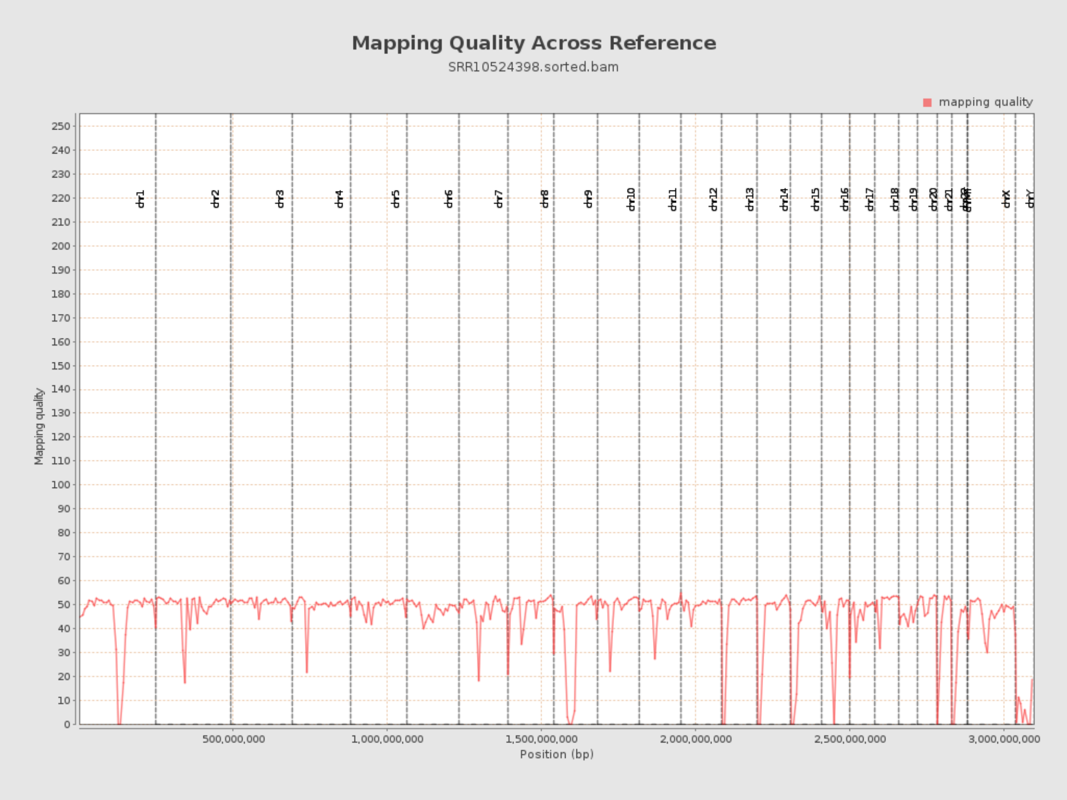
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram