Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 17:29:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524710.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_SRR10524710 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524710.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 17:29:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524710.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	924,597
Mapped reads	853,364 / 92.3%
Unmapped reads	71,233 / 7.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,125 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	23,492 / 2.54%
Duplication rate	1.98%
Clipped reads	856,272 / 92.61%

2.2. ACGT Content

Number/percentage of A's	12,518,590 / 24.72%
Number/percentage of C's	9,903,914 / 19.56%
Number/percentage of T's	15,773,476 / 31.15%
Number/percentage of G's	12,437,261 / 24.56%
Number/percentage of N's	6,494 / 0.01%
GC Percentage	44.12%

2.3. Coverage

Mean	0.0164

Standard Deviation	0.1851

2.4. Mapping Quality

Mean Mapping Quality	45.97

2.5. Mismatches and indels

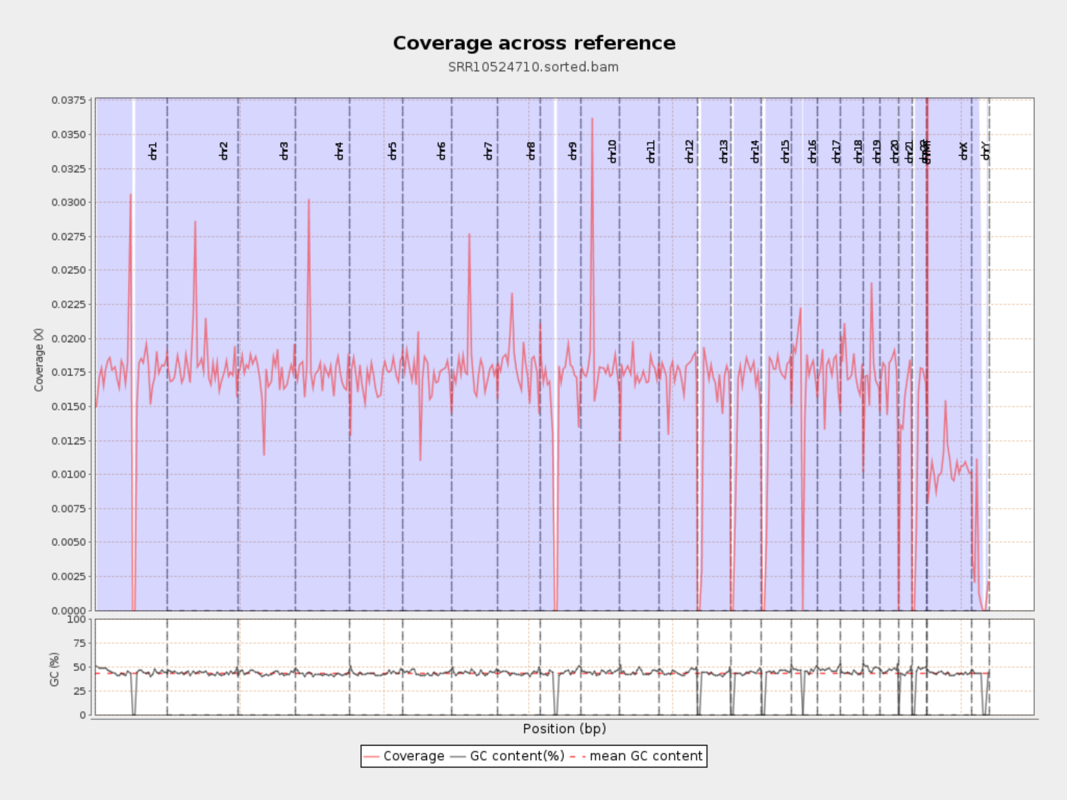
General error rate	0.51%
Mismatches	252,070
Insertions	3,138
Mapped reads with at least one insertion	0.37%
Deletions	9,498
Mapped reads with at least one deletion	1.1%
Homopolymer indels	44.3%

2.6. Chromosome stats

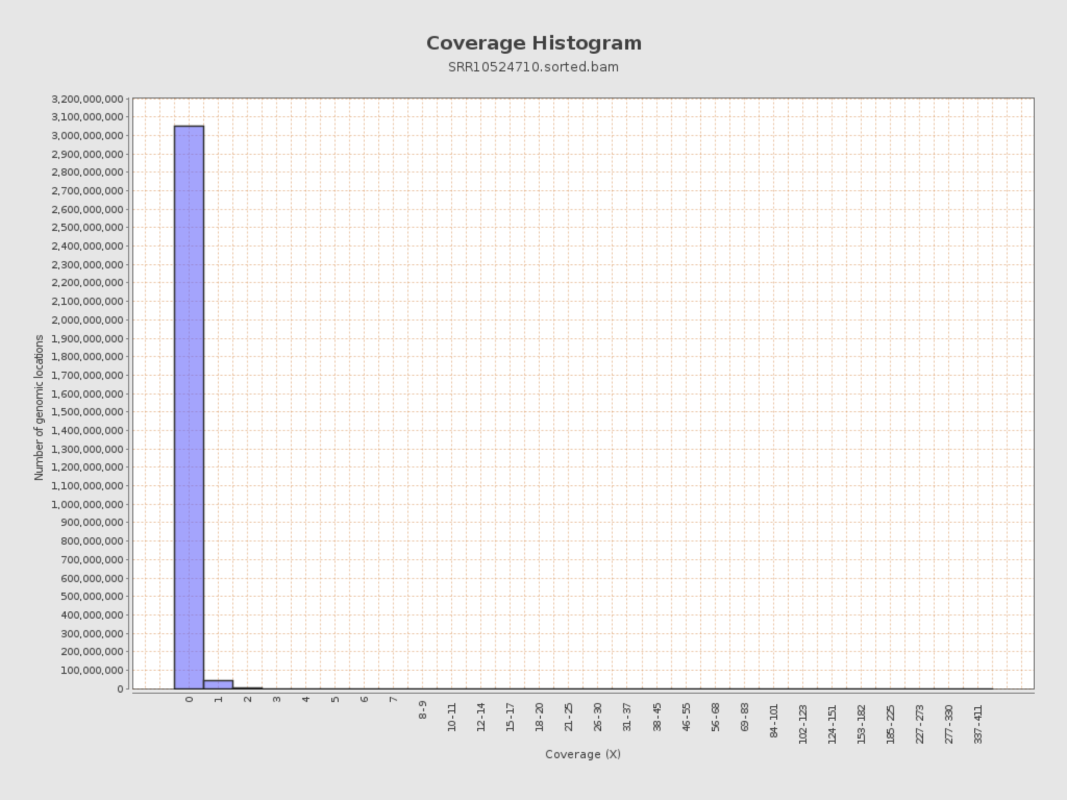
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4207481	0.0169	0.3202
chr2	243199373	4413419	0.0181	0.2331
chr3	198022430	3444960	0.0174	0.1386
chr4	191154276	3418540	0.0179	0.1538
chr5	180915260	3128984	0.0173	0.1382
chr6	171115067	2959545	0.0173	0.149
chr7	159138663	2854700	0.0179	0.2111

chr8	146364022	2654689	0.0181	0.2037
chr9	141213431	2151971	0.0152	0.1605
chr10	135534747	2516512	0.0186	0.1969
chr11	135006516	2360071	0.0175	0.1642
chr12	133851895	2333826	0.0174	0.1396
chr13	115169878	1647467	0.0143	0.126
chr14	107349540	1544728	0.0144	0.1283
chr15	102531392	1482995	0.0145	0.1267
chr16	90354753	1502693	0.0166	0.1444
chr17	81195210	1406995	0.0173	0.1431
chr18	78077248	1391667	0.0178	0.2635
chr19	59128983	1027782	0.0174	0.237
chr20	63025520	1099863	0.0175	0.1398
chr21	48129895	686935	0.0143	0.1393
chr22	51304566	604344	0.0118	0.114
chrMT	16571	23786	1.4354	1.6858
chrX	155270560	1639017	0.0106	0.1174
chrY	59373566	152235	0.0026	0.1154

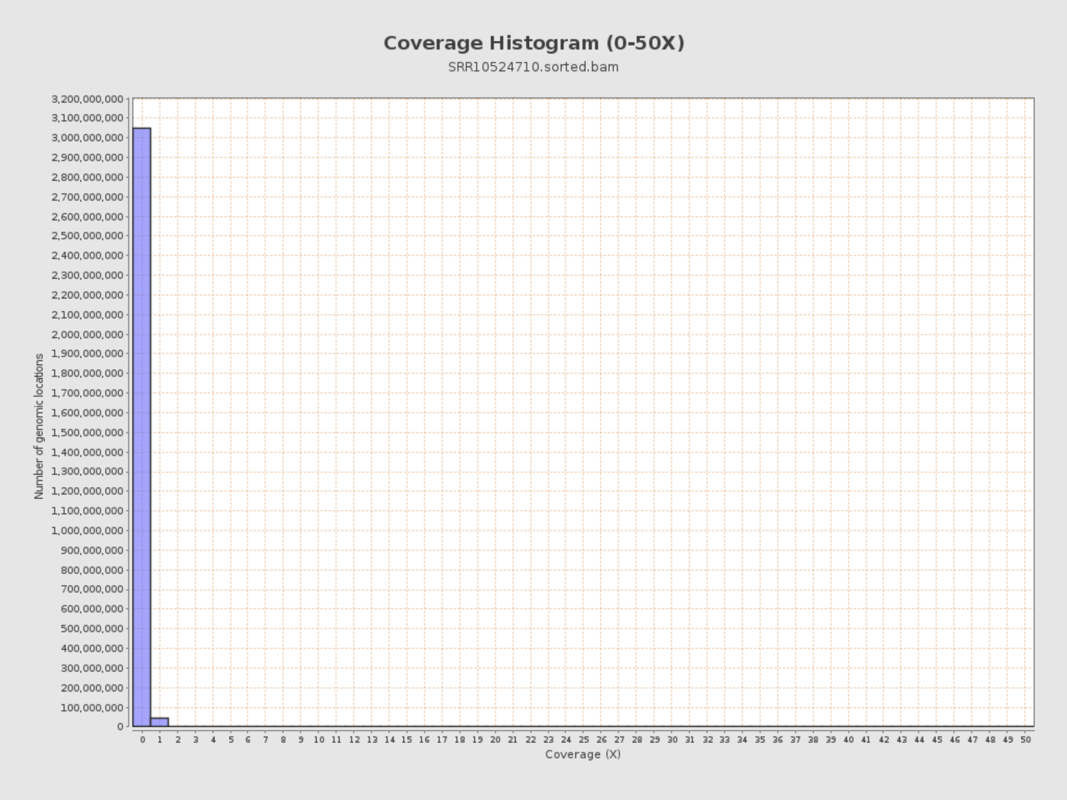
3. Results : Coverage across reference



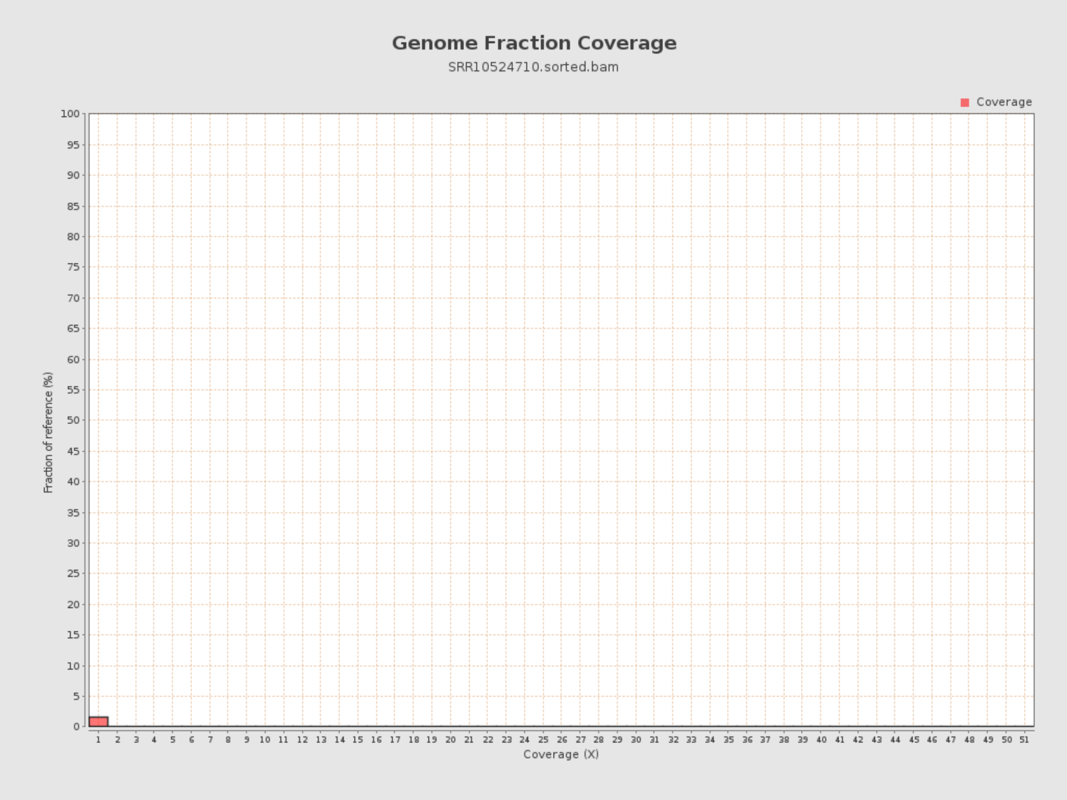
4. Results : Coverage Histogram



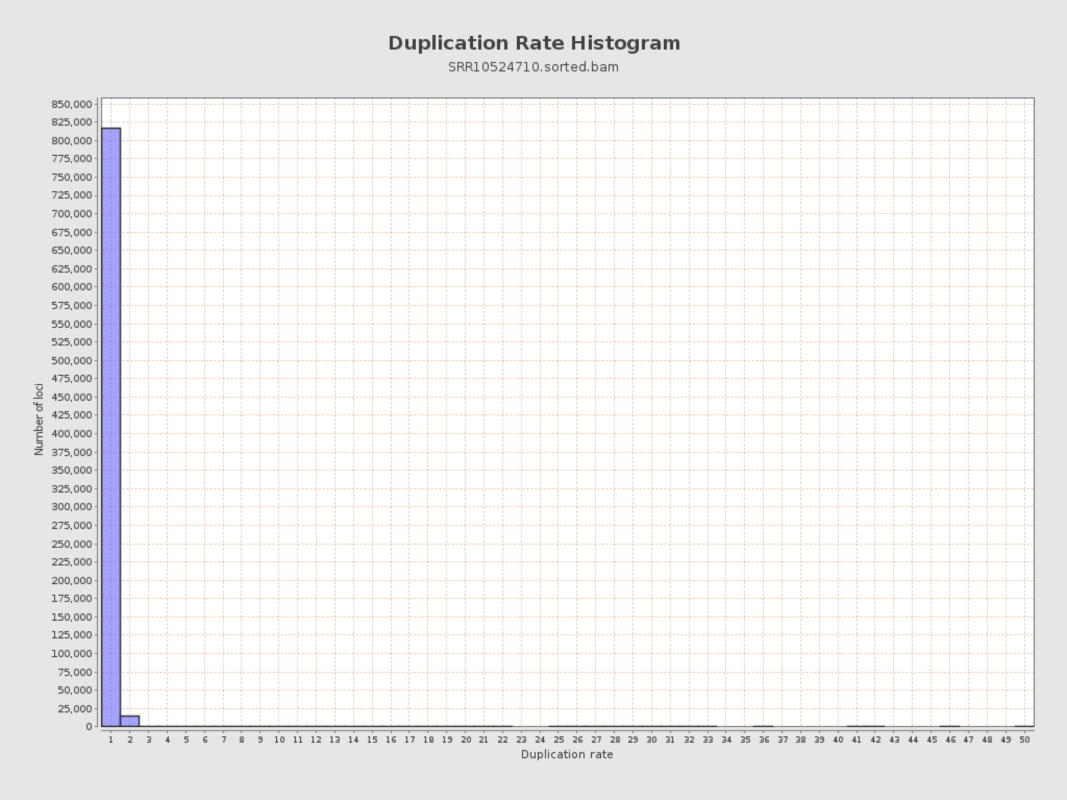
5. Results : Coverage Histogram (0-50X)



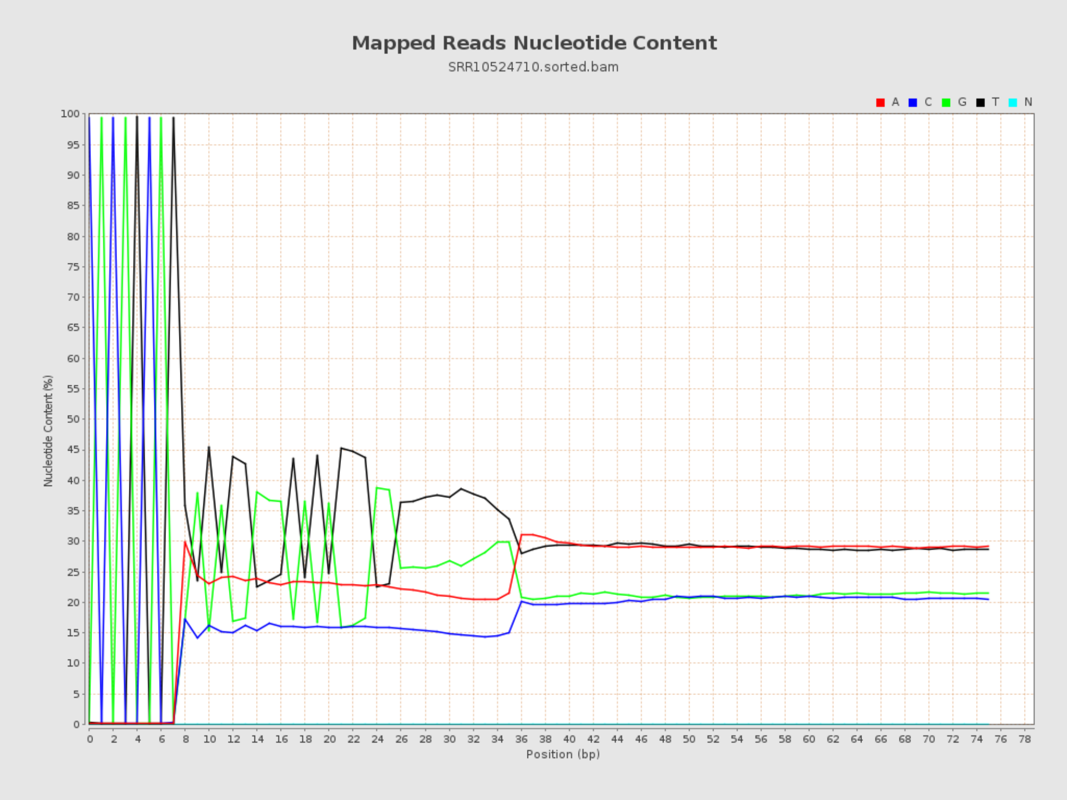
6. Results : Genome Fraction Coverage



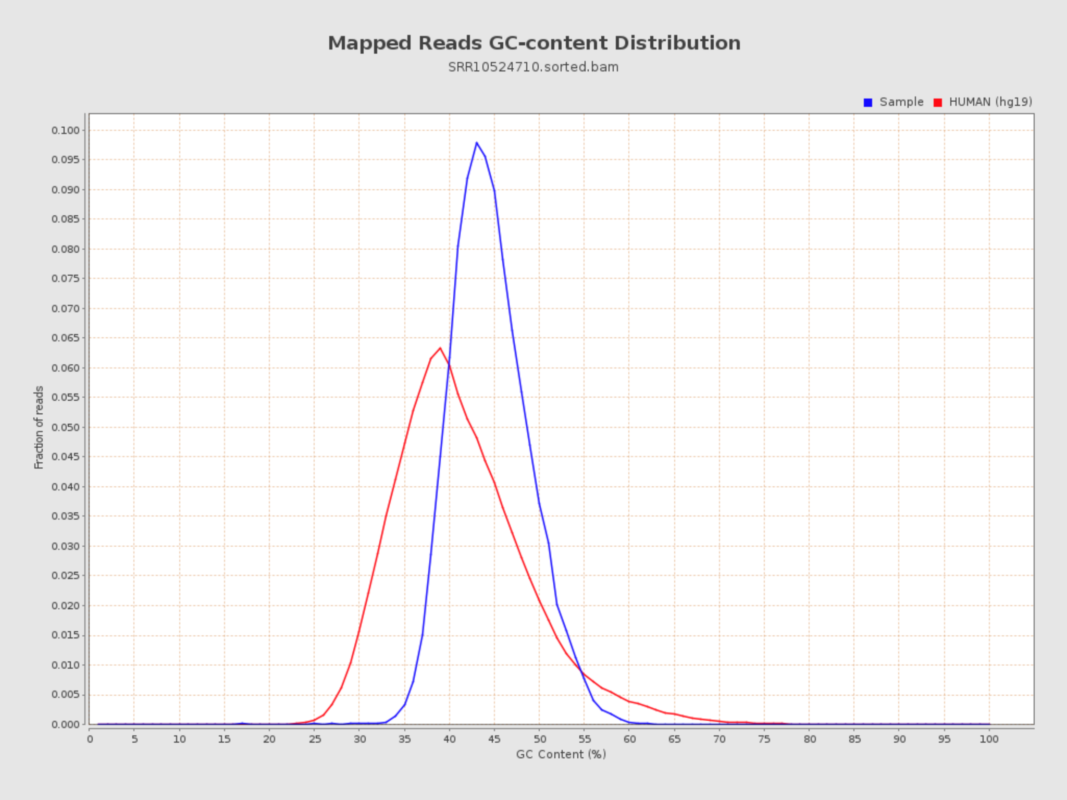
7. Results : Duplication Rate Histogram



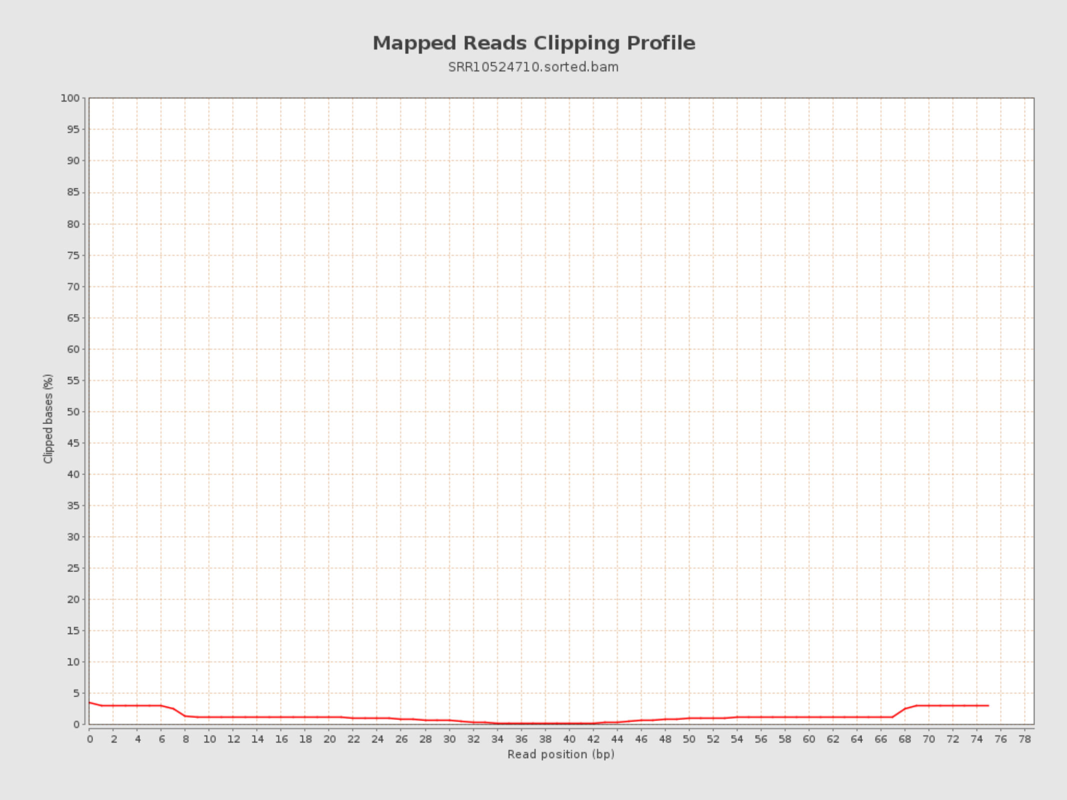
8. Results : Mapped Reads Nucleotide Content



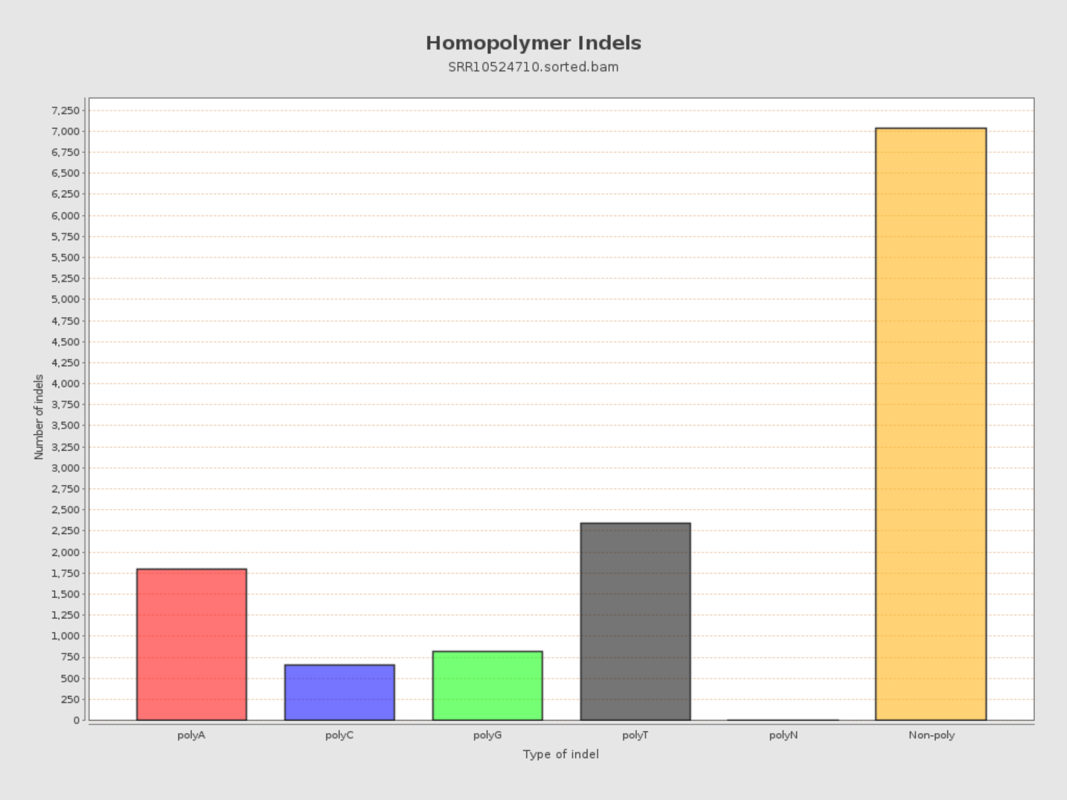
9. Results : Mapped Reads GC-content Distribution



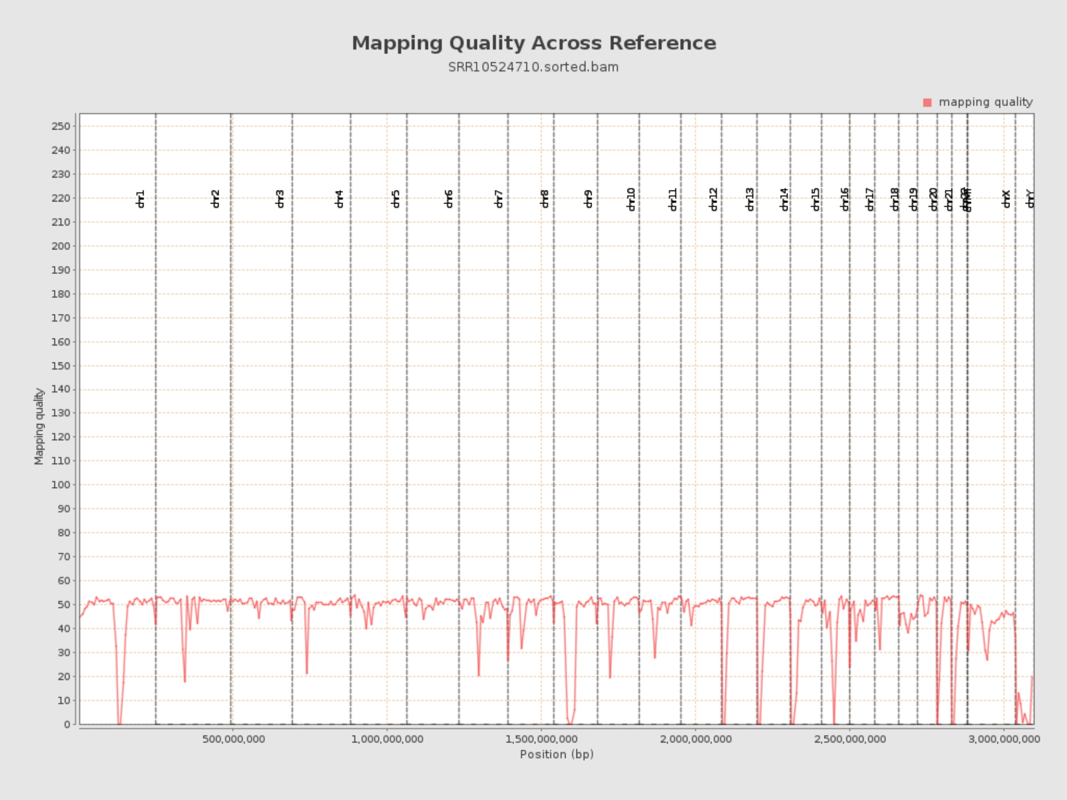
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram