Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 18:38:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524742.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_SRR10524742 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524742.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 18:38:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524742.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	936,386
Mapped reads	846,992 / 90.45%
Unmapped reads	89,394 / 9.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,310 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	22,835 / 2.44%
Duplication rate	2.03%
Clipped reads	847,857 / 90.55%

2.2. ACGT Content

Number/percentage of A's	12,100,491 / 25.06%
Number/percentage of C's	8,823,122 / 18.27%
Number/percentage of T's	15,763,344 / 32.64%
Number/percentage of G's	11,601,598 / 24.02%
Number/percentage of N's	6,130 / 0.01%
GC Percentage	42.29%

2.3. Coverage

Mean	0.0156

Standard Deviation	0.1633

2.4. Mapping Quality

Mean Mapping Quality	44.52

2.5. Mismatches and indels

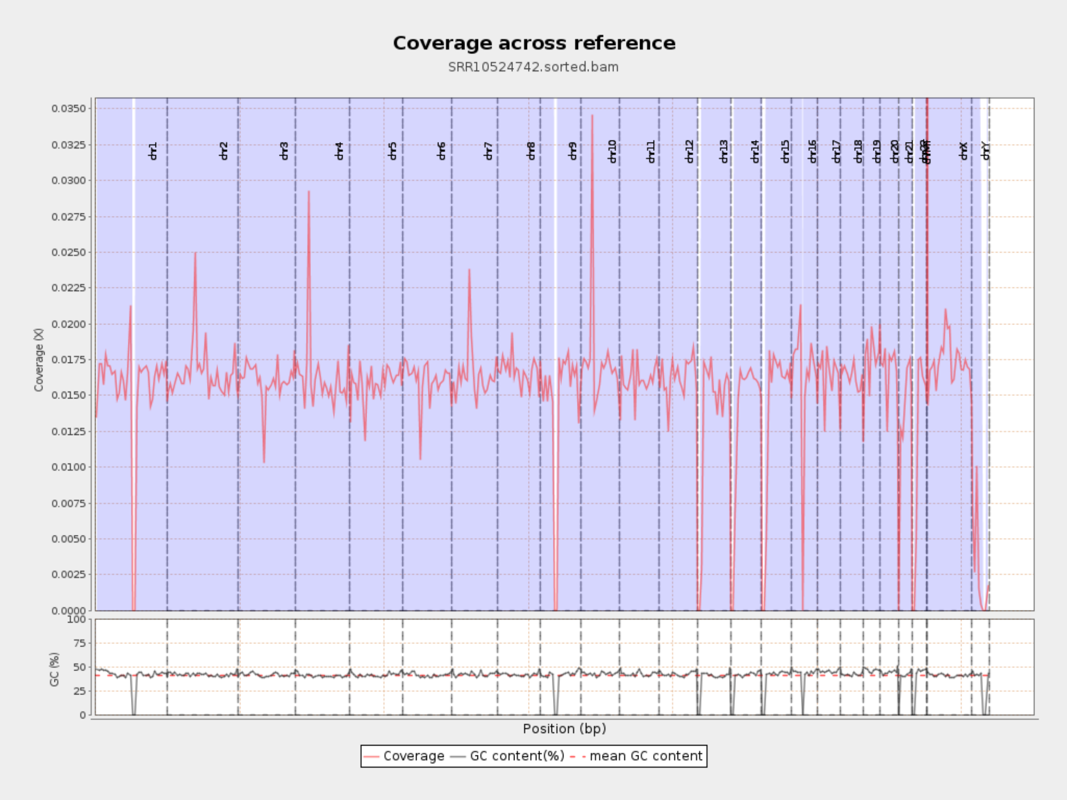
General error rate	0.53%
Mismatches	249,309
Insertions	3,866
Mapped reads with at least one insertion	0.45%
Deletions	9,826
Mapped reads with at least one deletion	1.15%
Homopolymer indels	41.64%

2.6. Chromosome stats

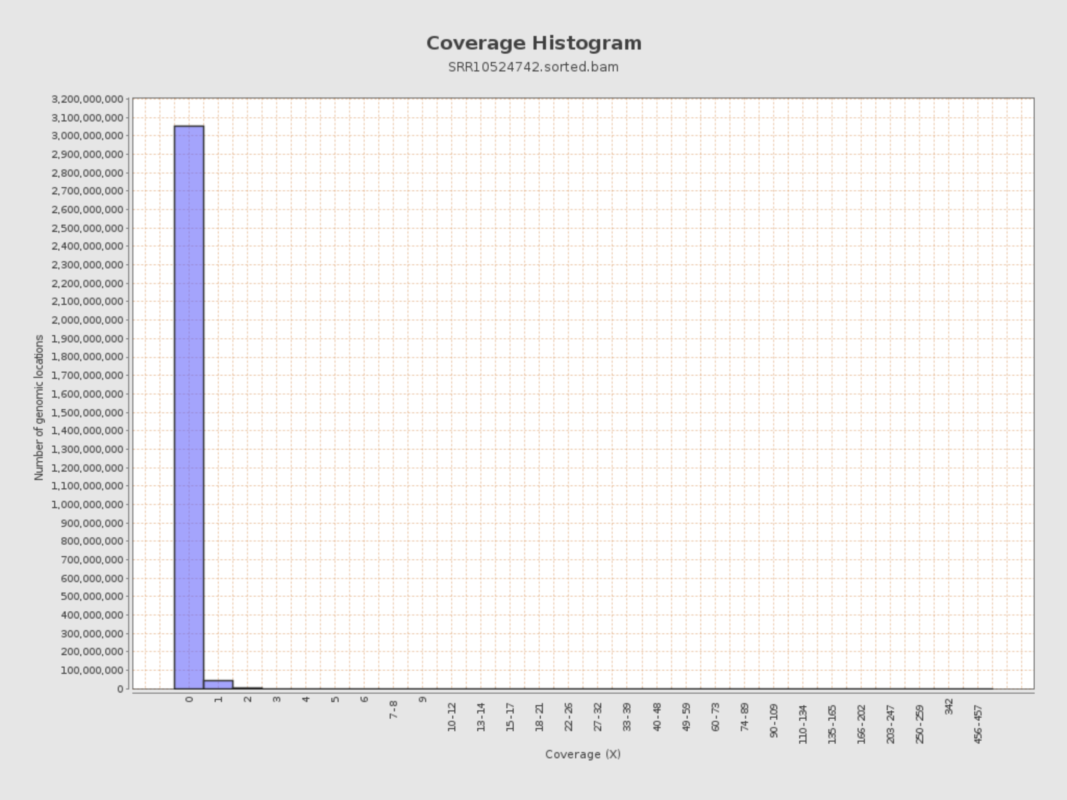
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3831809	0.0154	0.2149
chr2	243199373	4049704	0.0167	0.2395
chr3	198022430	3169700	0.016	0.136
chr4	191154276	3132821	0.0164	0.1474
chr5	180915260	2886858	0.016	0.1335
chr6	171115067	2748585	0.0161	0.1412
chr7	159138663	2628987	0.0165	0.1846

chr8	146364022	2439792	0.0167	0.1569
chr9	141213431	2035386	0.0144	0.145
chr10	135534747	2389135	0.0176	0.1946
chr11	135006516	2190151	0.0162	0.1496
chr12	133851895	2178038	0.0163	0.1359
chr13	115169878	1521759	0.0132	0.1218
chr14	107349540	1440506	0.0134	0.1246
chr15	102531392	1398374	0.0136	0.1252
chr16	90354753	1440501	0.0159	0.1426
chr17	81195210	1335714	0.0165	0.1392
chr18	78077248	1276295	0.0163	0.2026
chr19	59128983	1045378	0.0177	0.1786
chr20	63025520	1050972	0.0167	0.1402
chr21	48129895	646708	0.0134	0.1312
chr22	51304566	591545	0.0115	0.1141
chrMT	16571	16982	1.0248	1.1374
chrX	155270560	2701081	0.0174	0.146
chrY	59373566	163705	0.0028	0.0885

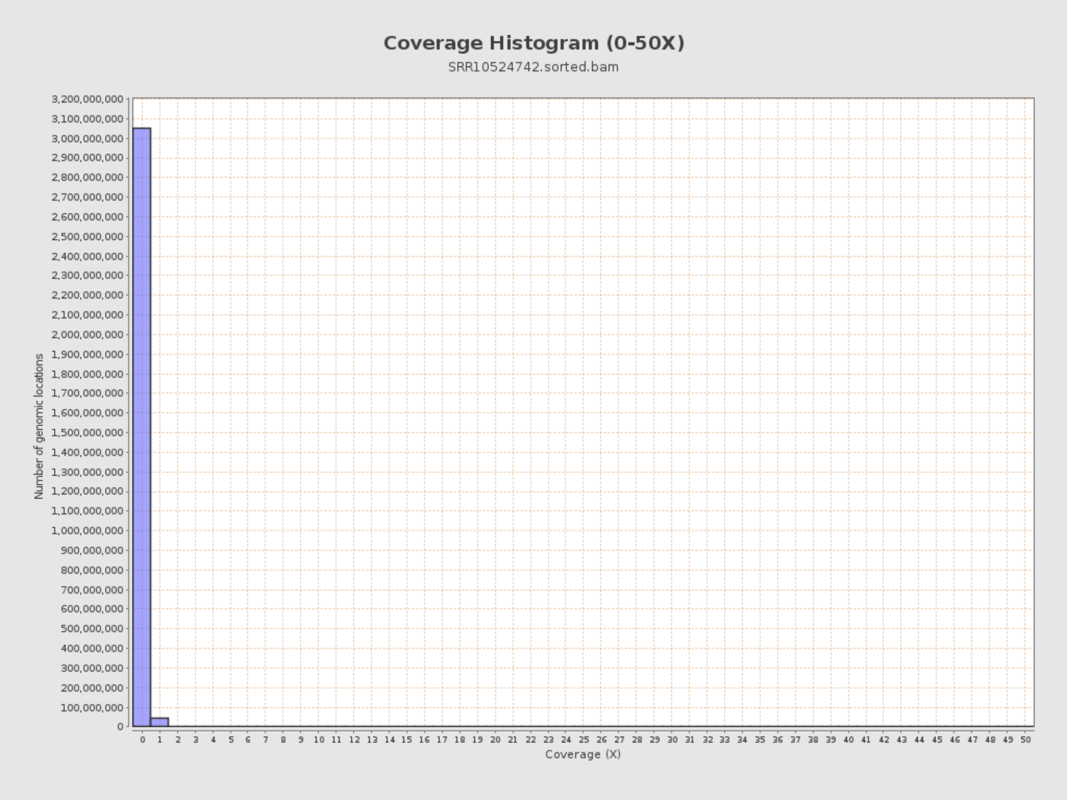
3. Results : Coverage across reference



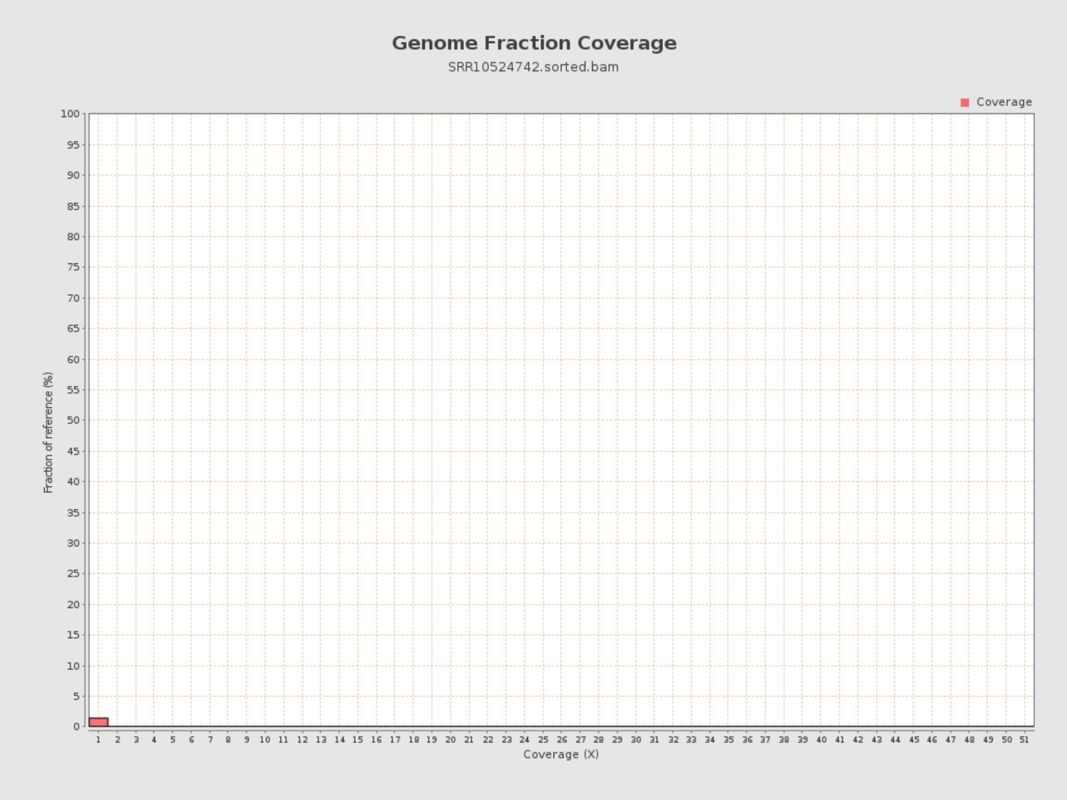
4. Results : Coverage Histogram



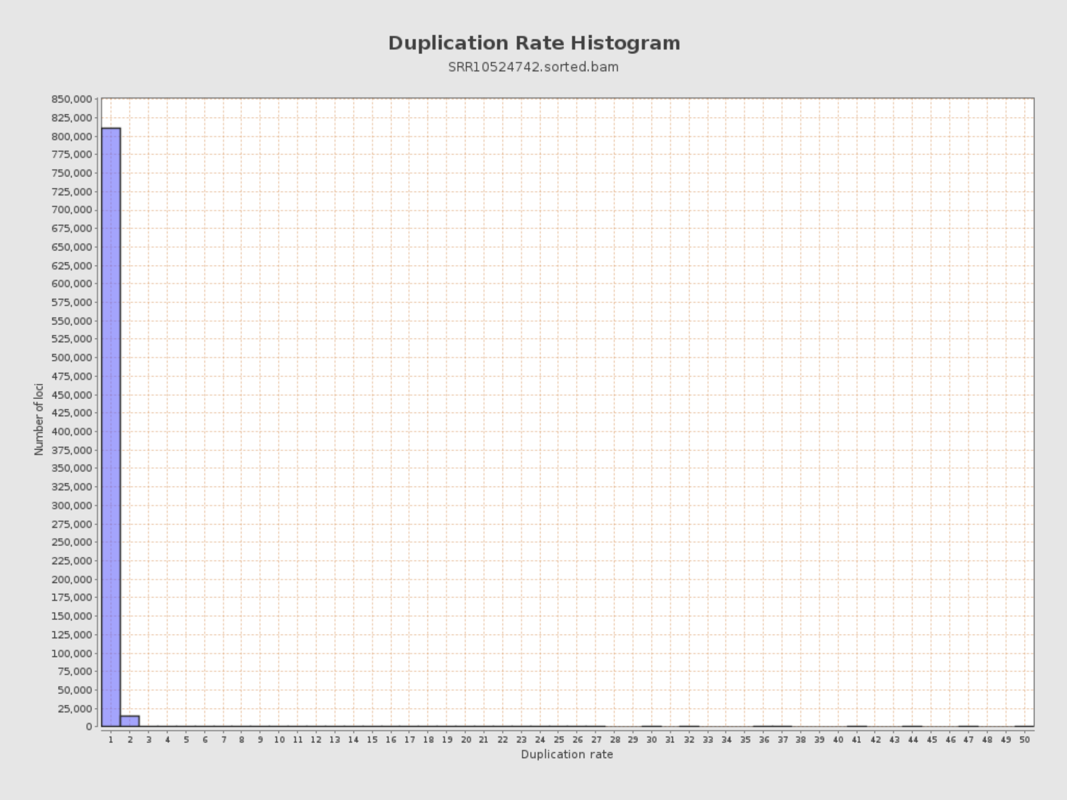
5. Results : Coverage Histogram (0-50X)



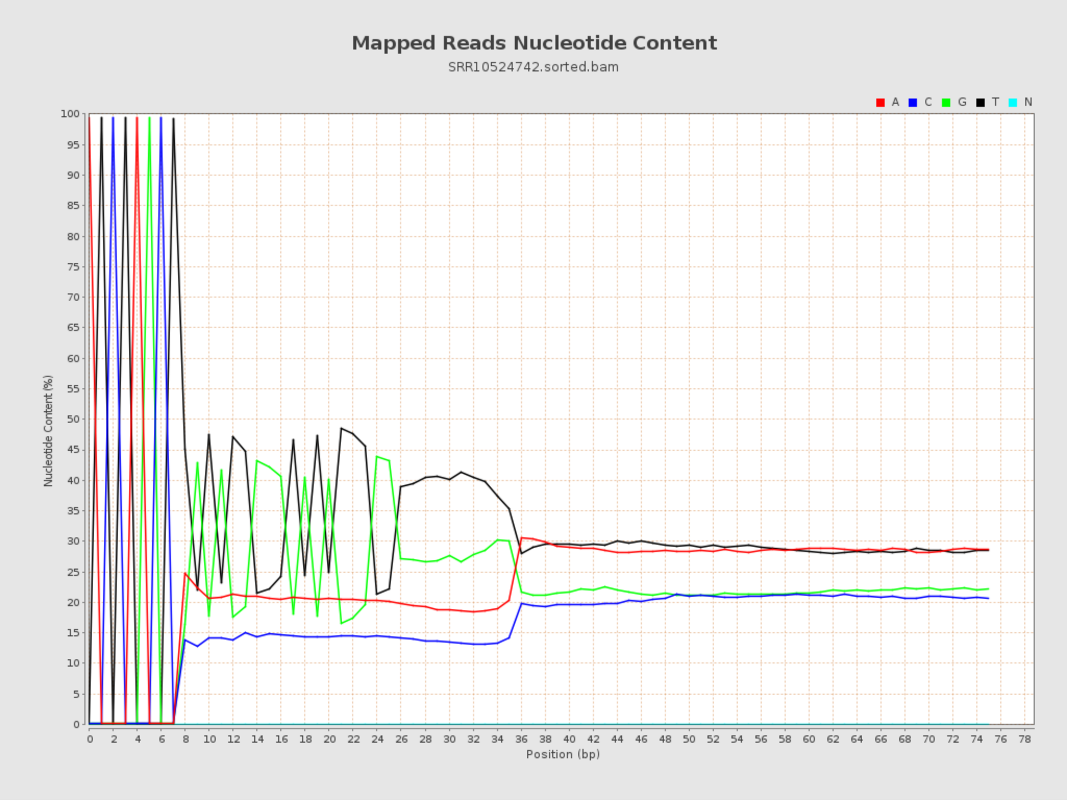
6. Results : Genome Fraction Coverage



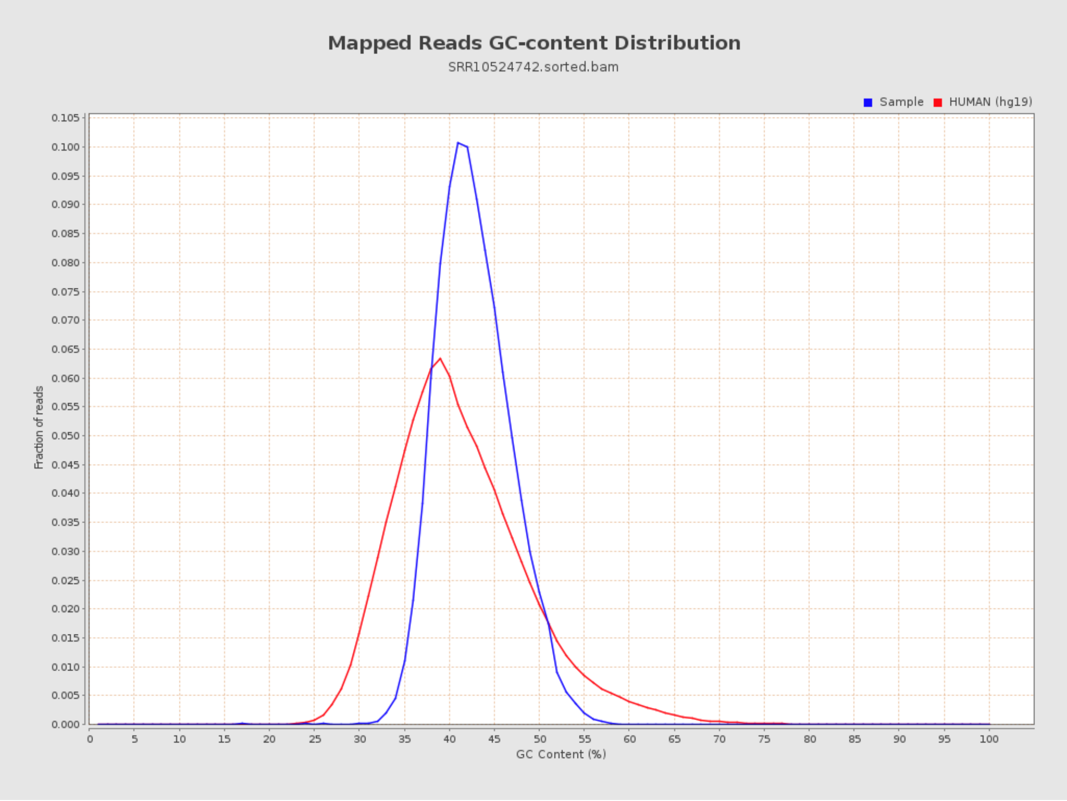
7. Results : Duplication Rate Histogram



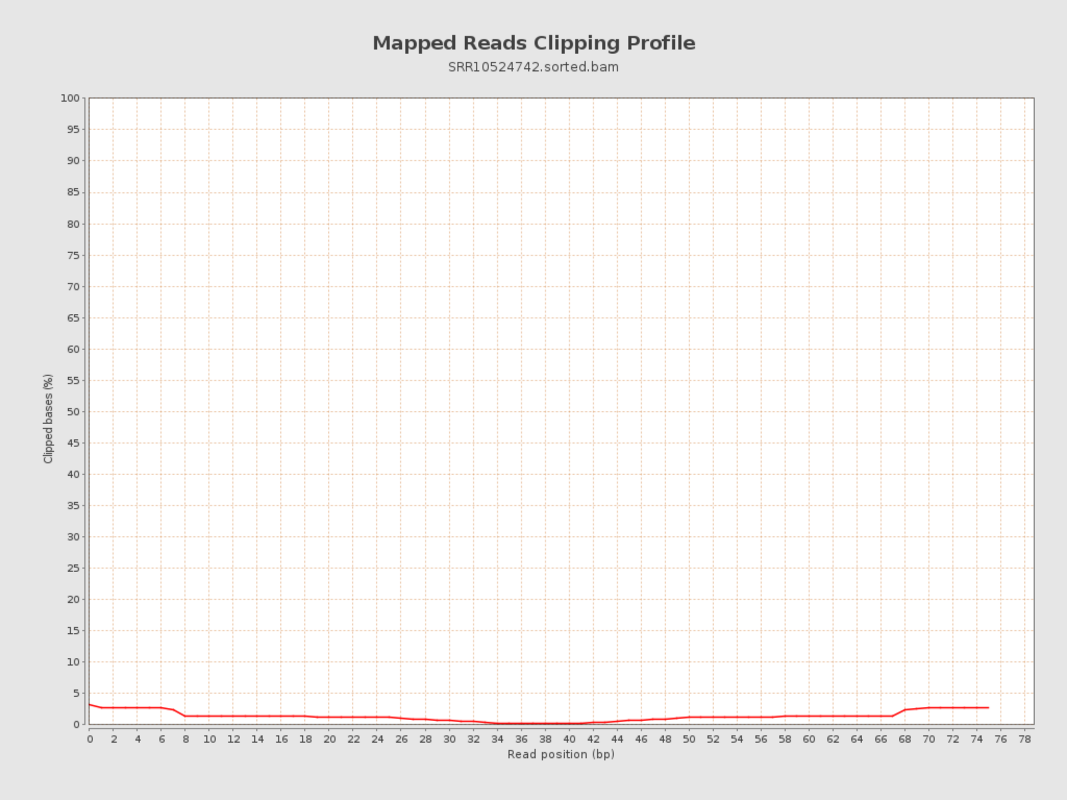
8. Results : Mapped Reads Nucleotide Content



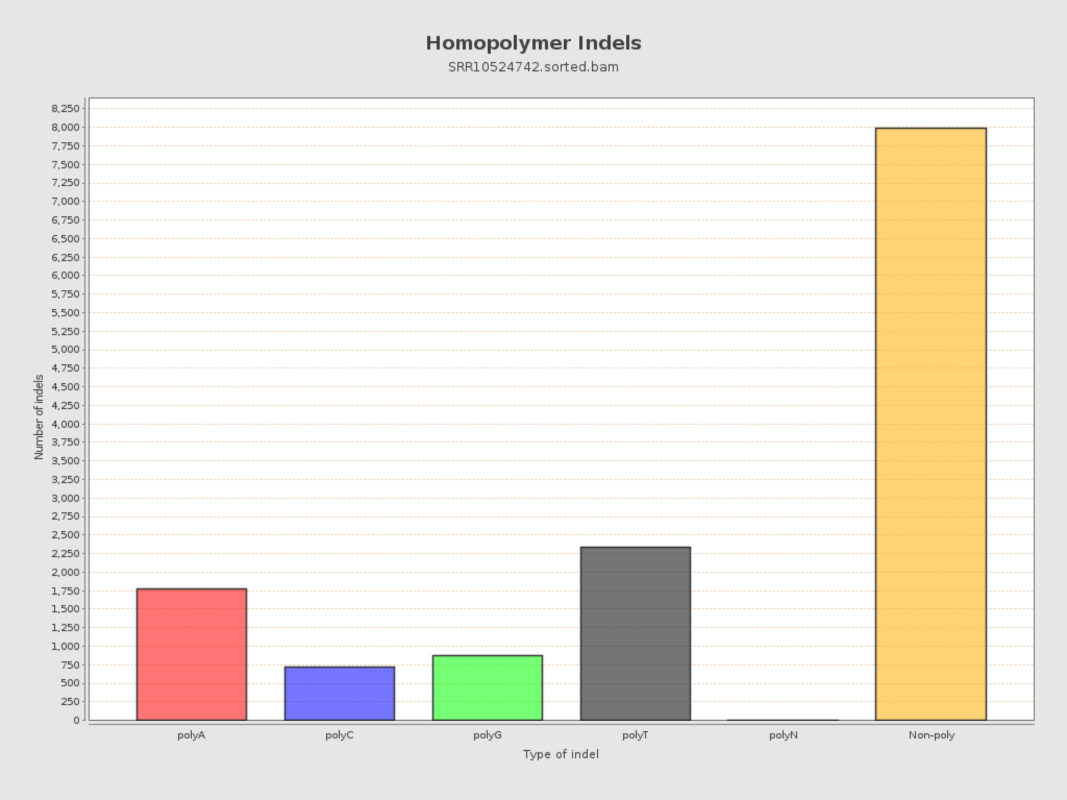
9. Results : Mapped Reads GC-content Distribution



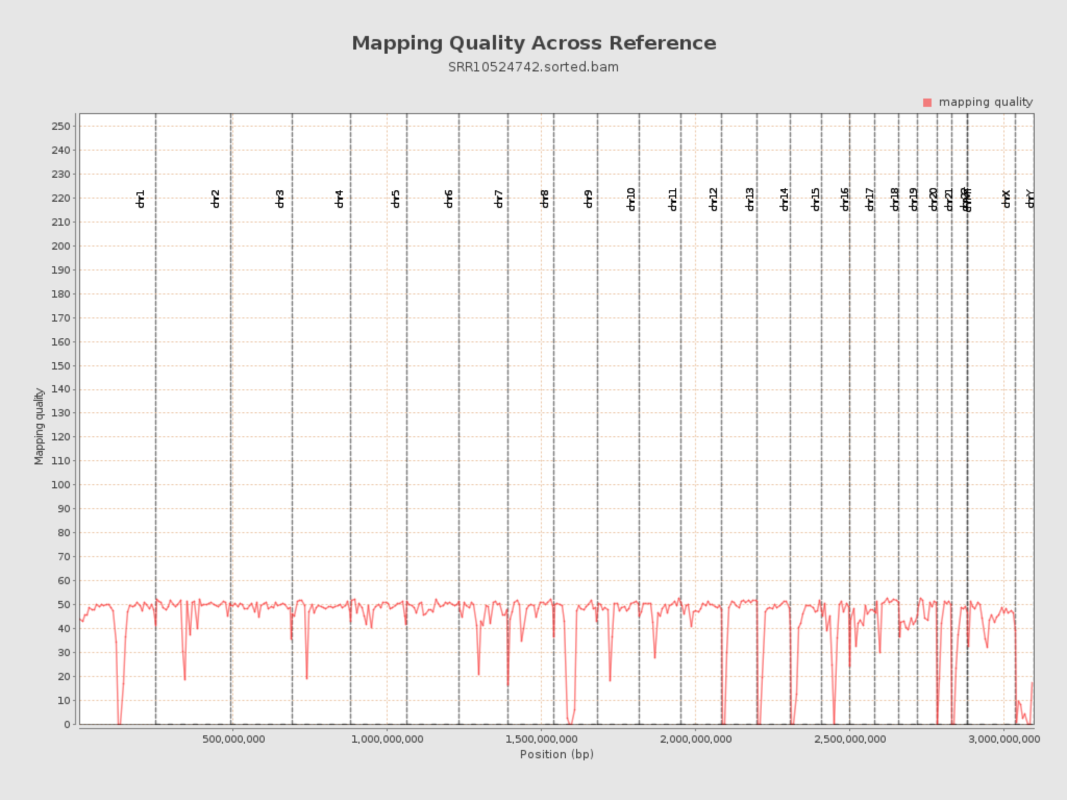
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram