Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 17:10:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524702.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_SRR10524702 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524702.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 17:10:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524702.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	717,477
Mapped reads	660,782 / 92.1%
Unmapped reads	56,695 / 7.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,543 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	15,209 / 2.12%
Duplication rate	1.68%
Clipped reads	660,598 / 92.07%

2.2. ACGT Content

Number/percentage of A's	10,745,395 / 27.31%
Number/percentage of C's	7,040,357 / 17.89%
Number/percentage of T's	12,272,993 / 31.19%
Number/percentage of G's	9,279,212 / 23.59%
Number/percentage of N's	5,395 / 0.01%
GC Percentage	41.48%

2.3. Coverage

Mean	0.0127

Standard Deviation	0.1498

2.4. Mapping Quality

Mean Mapping Quality	46.11

2.5. Mismatches and indels

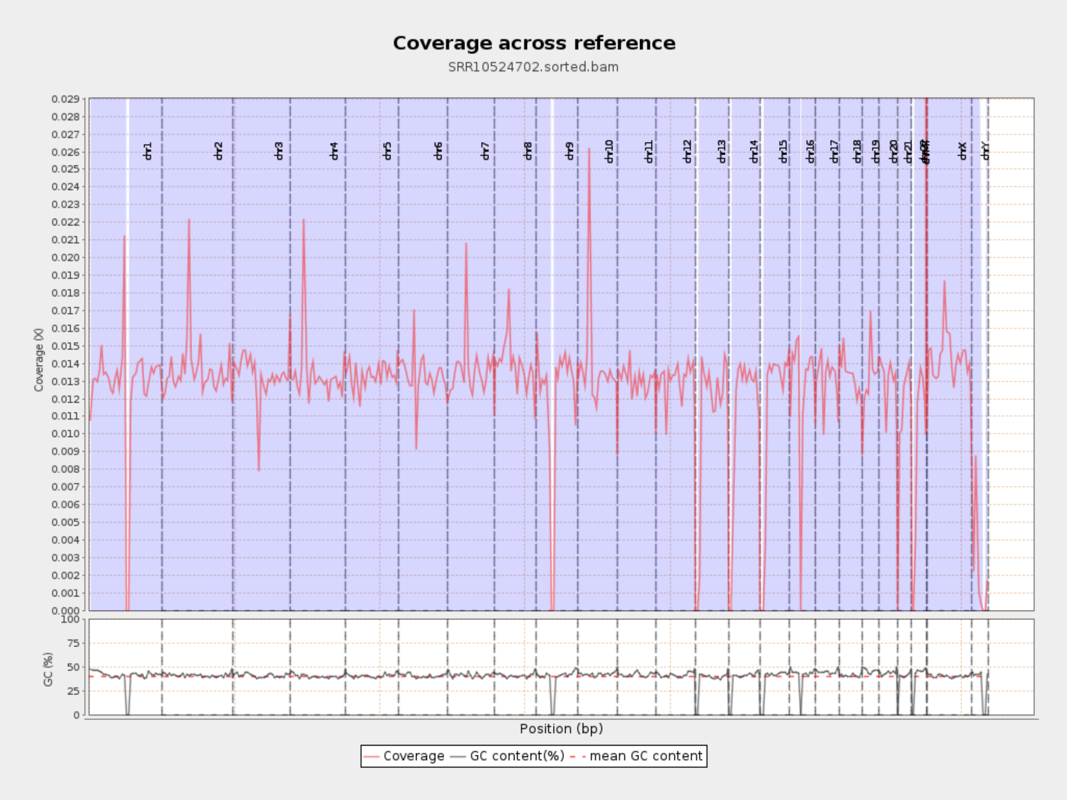
General error rate	0.52%
Mismatches	198,034
Insertions	3,402
Mapped reads with at least one insertion	0.51%
Deletions	7,509
Mapped reads with at least one deletion	1.13%
Homopolymer indels	41.02%

2.6. Chromosome stats

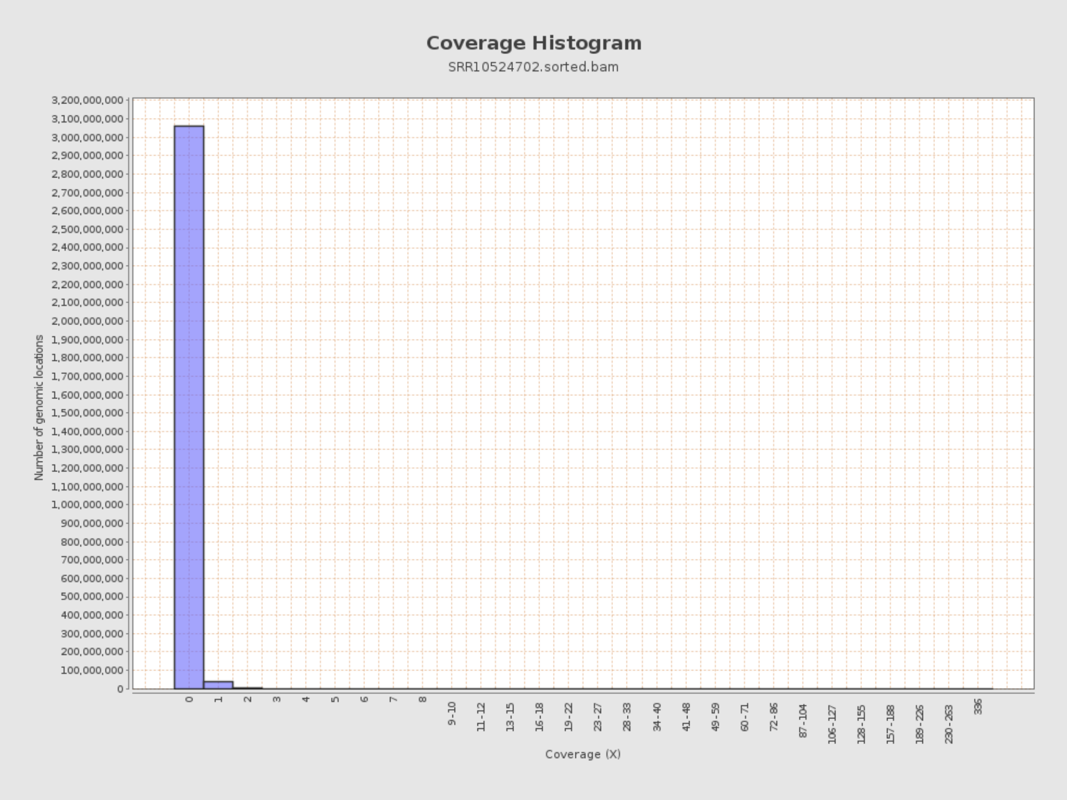
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3158605	0.0127	0.2346
chr2	243199373	3330269	0.0137	0.1918
chr3	198022430	2621993	0.0132	0.1199
chr4	191154276	2563962	0.0134	0.1283
chr5	180915260	2408823	0.0133	0.1205
chr6	171115067	2277126	0.0133	0.1286
chr7	159138663	2183438	0.0137	0.1686

chr8	146364022	2038335	0.0139	0.1641
chr9	141213431	1653804	0.0117	0.1317
chr10	135534747	1882447	0.0139	0.1576
chr11	135006516	1759313	0.013	0.1359
chr12	133851895	1750748	0.0131	0.1198
chr13	115169878	1233155	0.0107	0.1076
chr14	107349540	1173121	0.0109	0.1103
chr15	102531392	1124654	0.011	0.1091
chr16	90354753	1139518	0.0126	0.1225
chr17	81195210	1062463	0.0131	0.1206
chr18	78077248	1044570	0.0134	0.2057
chr19	59128983	786245	0.0133	0.1735
chr20	63025520	822441	0.013	0.1202
chr21	48129895	526660	0.0109	0.1153
chr22	51304566	440858	0.0086	0.0965
chrMT	16571	18140	1.0947	1.1434
chrX	155270560	2217102	0.0143	0.1292
chrY	59373566	137410	0.0023	0.0936

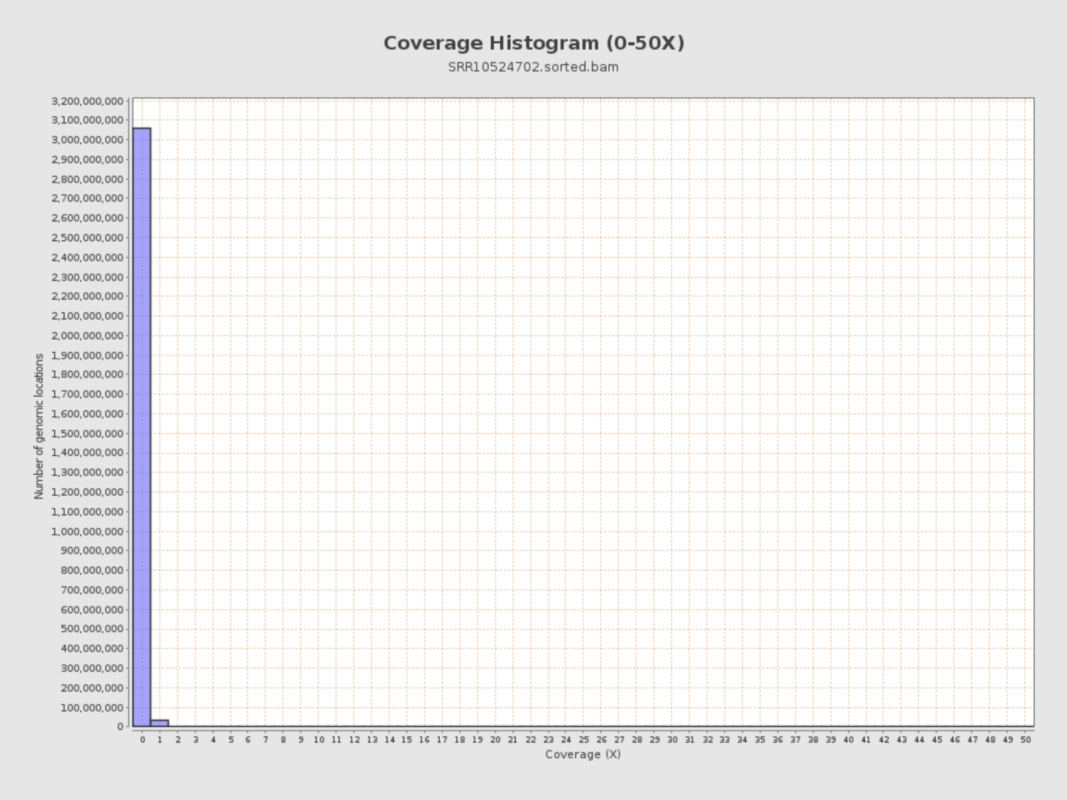
3. Results : Coverage across reference



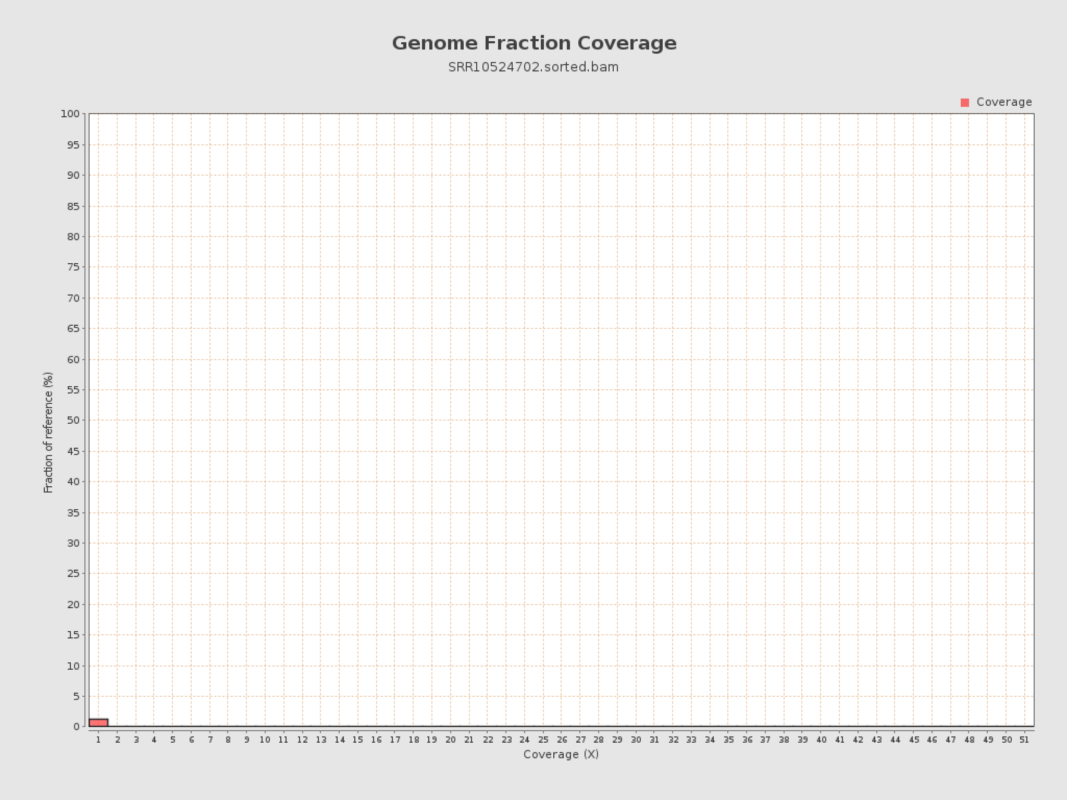
4. Results : Coverage Histogram



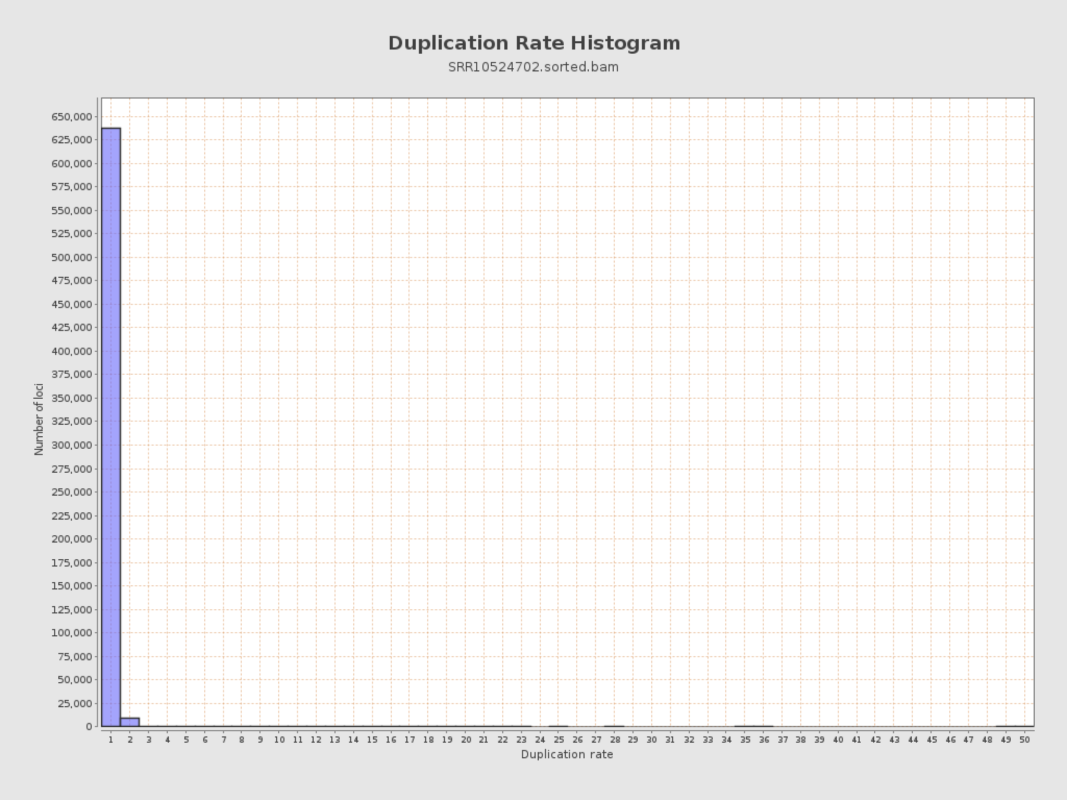
5. Results : Coverage Histogram (0-50X)



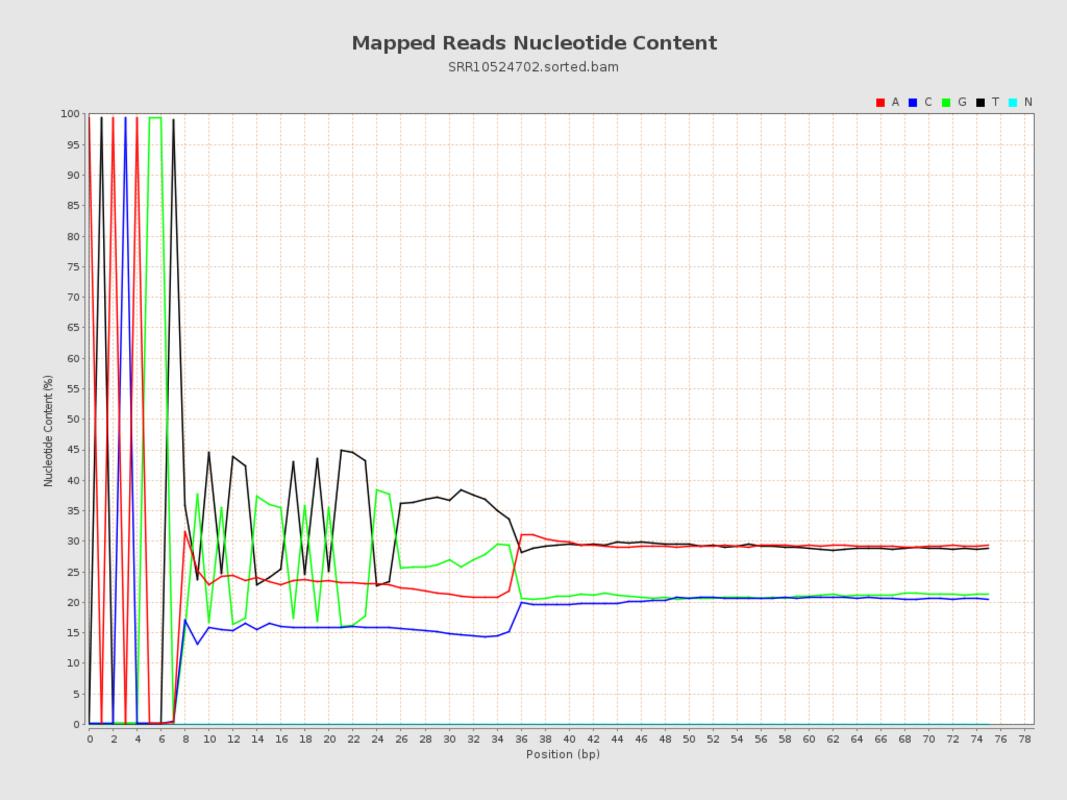
6. Results : Genome Fraction Coverage



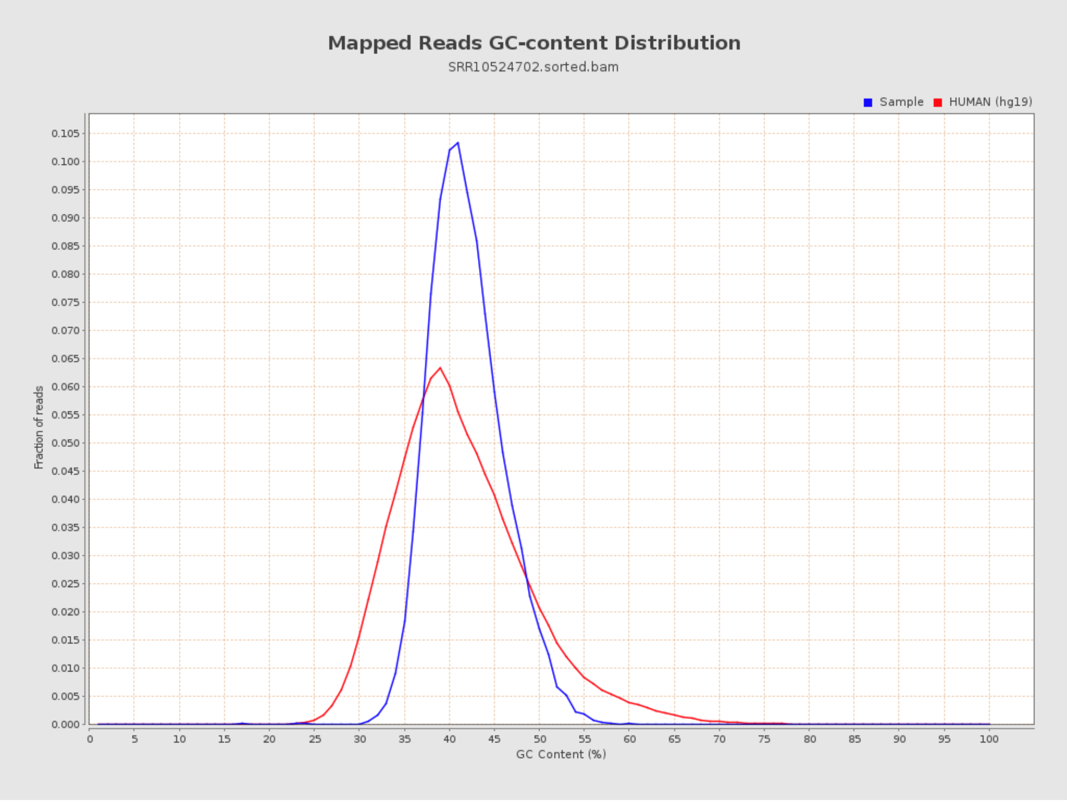
7. Results : Duplication Rate Histogram



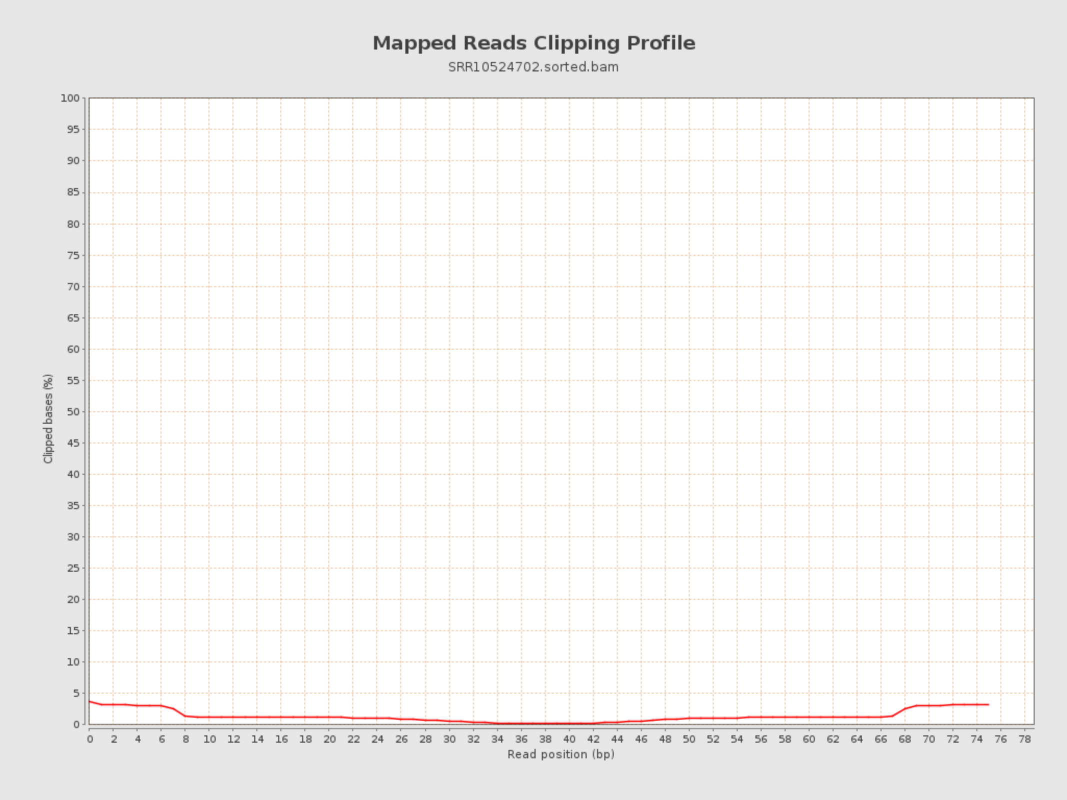
8. Results : Mapped Reads Nucleotide Content



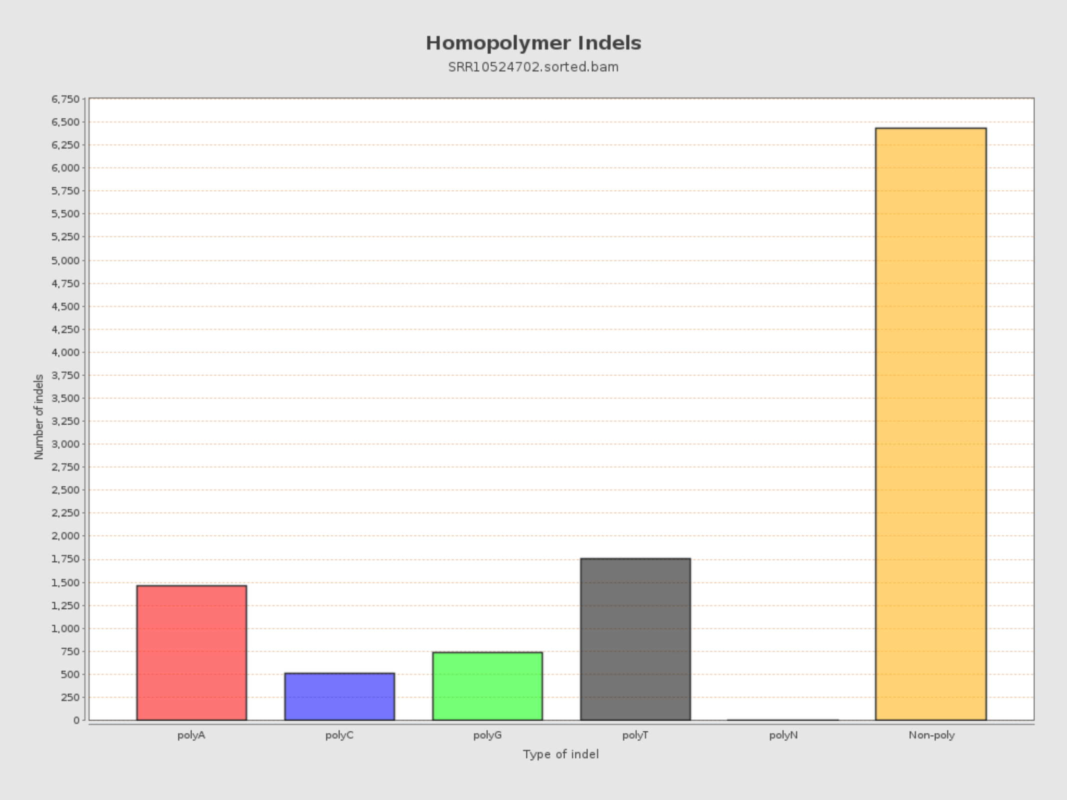
9. Results : Mapped Reads GC-content Distribution



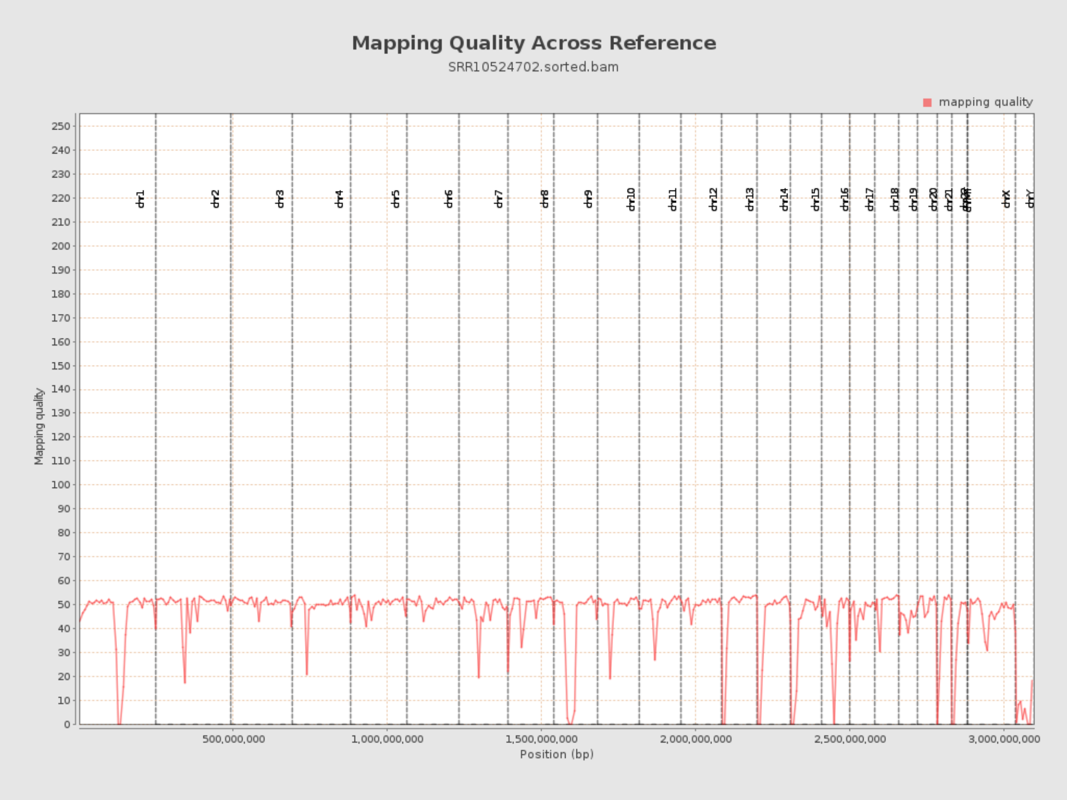
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram