Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 05:52:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524481.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_SRR10524481 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524481.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 05:52:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524481.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	824,920
Mapped reads	760,396 / 92.18%
Unmapped reads	64,524 / 7.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,575 / 0.19%
Read min/max/mean length	30 / 76 / 76.06
Duplicated reads (estimated)	23,167 / 2.81%
Duplication rate	2.41%
Clipped reads	759,508 / 92.07%

2.2. ACGT Content

Number/percentage of A's	10,826,621 / 24.57%
Number/percentage of C's	8,891,456 / 20.17%
Number/percentage of T's	14,166,404 / 32.14%
Number/percentage of G's	10,187,269 / 23.11%
Number/percentage of N's	1,004 / 0%
GC Percentage	43.29%

2.3. Coverage

Mean	0.0142

Standard Deviation	0.1558

2.4. Mapping Quality

Mean Mapping Quality	45.39

2.5. Mismatches and indels

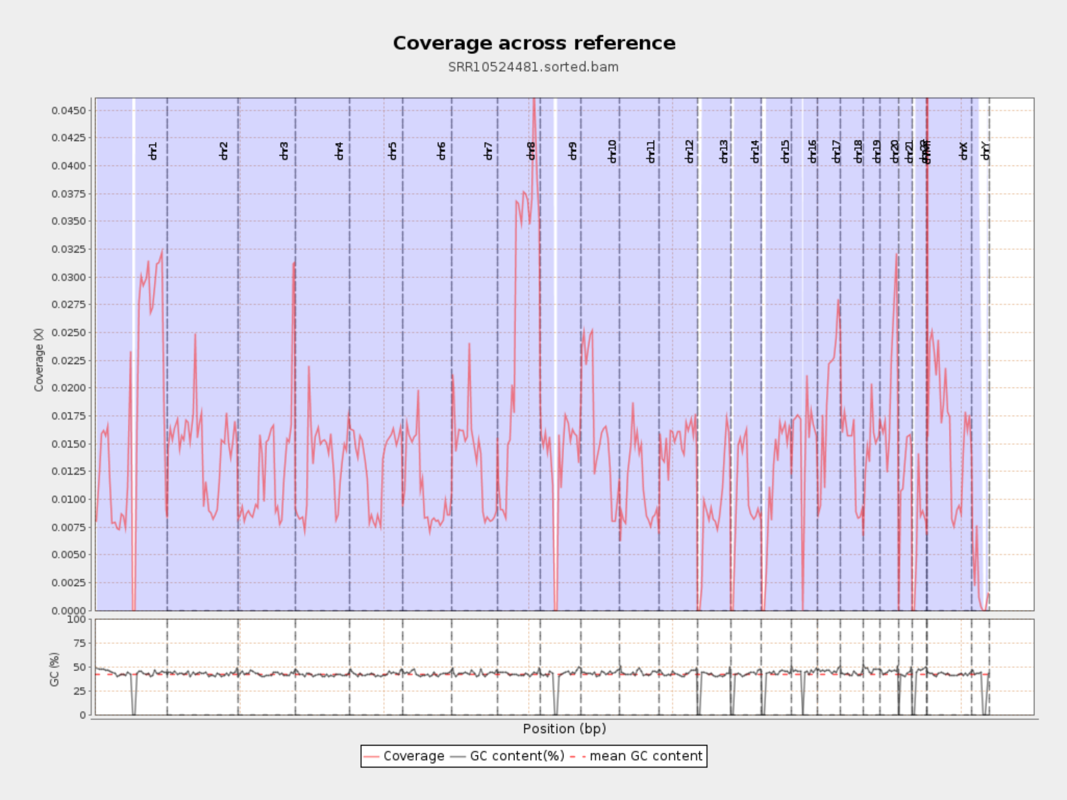
General error rate	0.48%
Mismatches	204,402
Insertions	3,125
Mapped reads with at least one insertion	0.41%
Deletions	8,120
Mapped reads with at least one deletion	1.06%
Homopolymer indels	42.3%

2.6. Chromosome stats

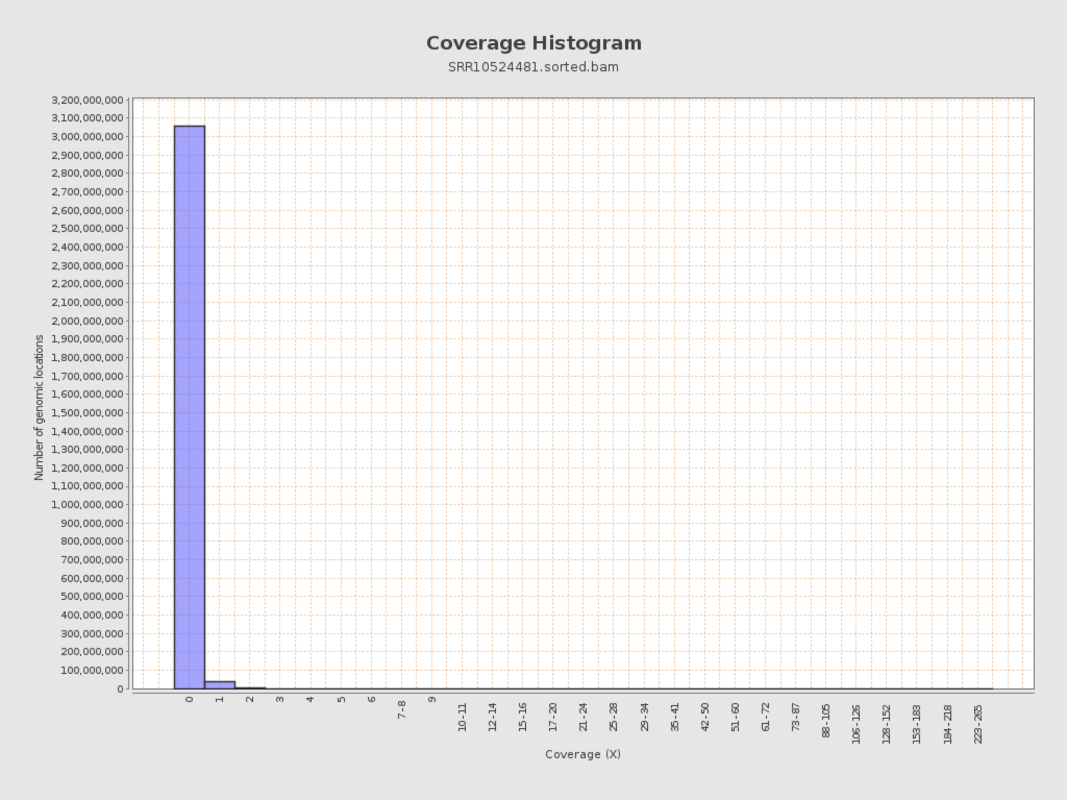
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4311089	0.0173	0.2406
chr2	243199373	3552199	0.0146	0.1707
chr3	198022430	2453544	0.0124	0.1187
chr4	191154276	2498911	0.0131	0.1331
chr5	180915260	2395015	0.0132	0.1227
chr6	171115067	1878093	0.011	0.126
chr7	159138663	2190444	0.0138	0.1918

chr8	146364022	3991596	0.0273	0.1886
chr9	141213431	1893321	0.0134	0.1476
chr10	135534747	2266134	0.0167	0.1614
chr11	135006516	1507968	0.0112	0.1462
chr12	133851895	2062507	0.0154	0.1324
chr13	115169878	1025523	0.0089	0.1011
chr14	107349540	1055556	0.0098	0.1069
chr15	102531392	1178536	0.0115	0.1166
chr16	90354753	1371030	0.0152	0.1358
chr17	81195210	1535824	0.0189	0.1497
chr18	78077248	1065382	0.0136	0.2128
chr19	59128983	889004	0.015	0.1863
chr20	63025520	1279098	0.0203	0.1529
chr21	48129895	586856	0.0122	0.1234
chr22	51304566	356749	0.007	0.0883
chrMT	16571	10800	0.6517	0.8749
chrX	155270560	2597534	0.0167	0.1451
chrY	59373566	133863	0.0023	0.0701

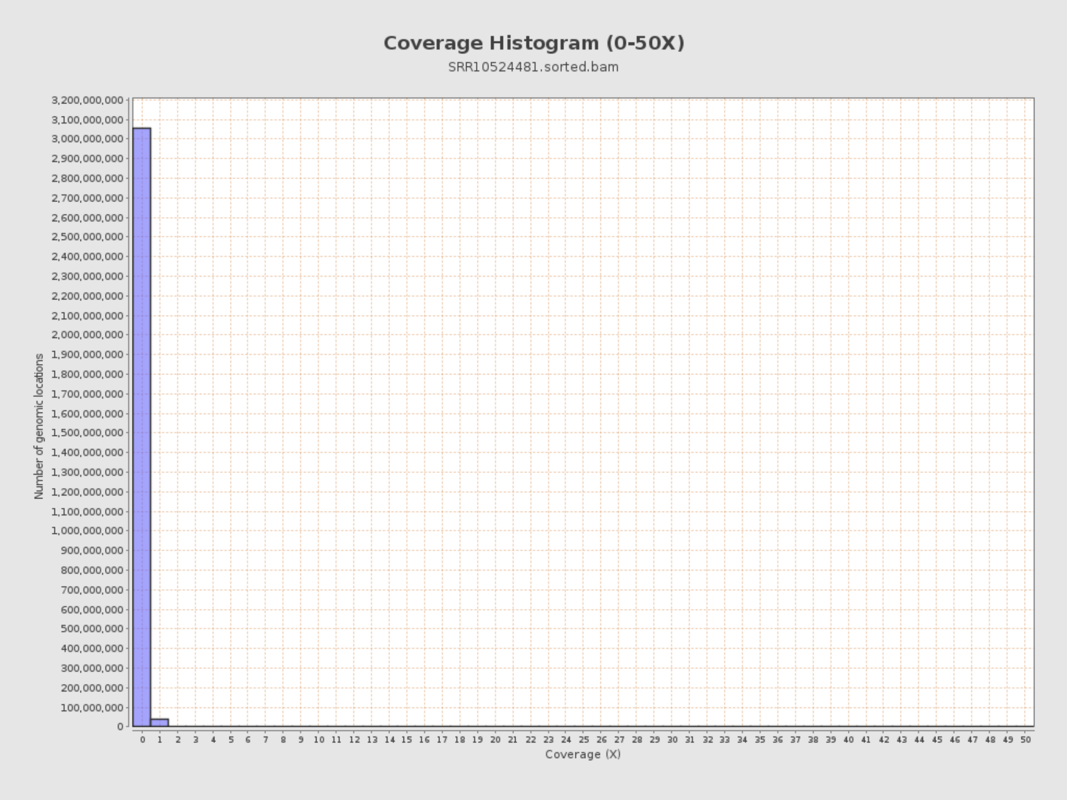
3. Results : Coverage across reference



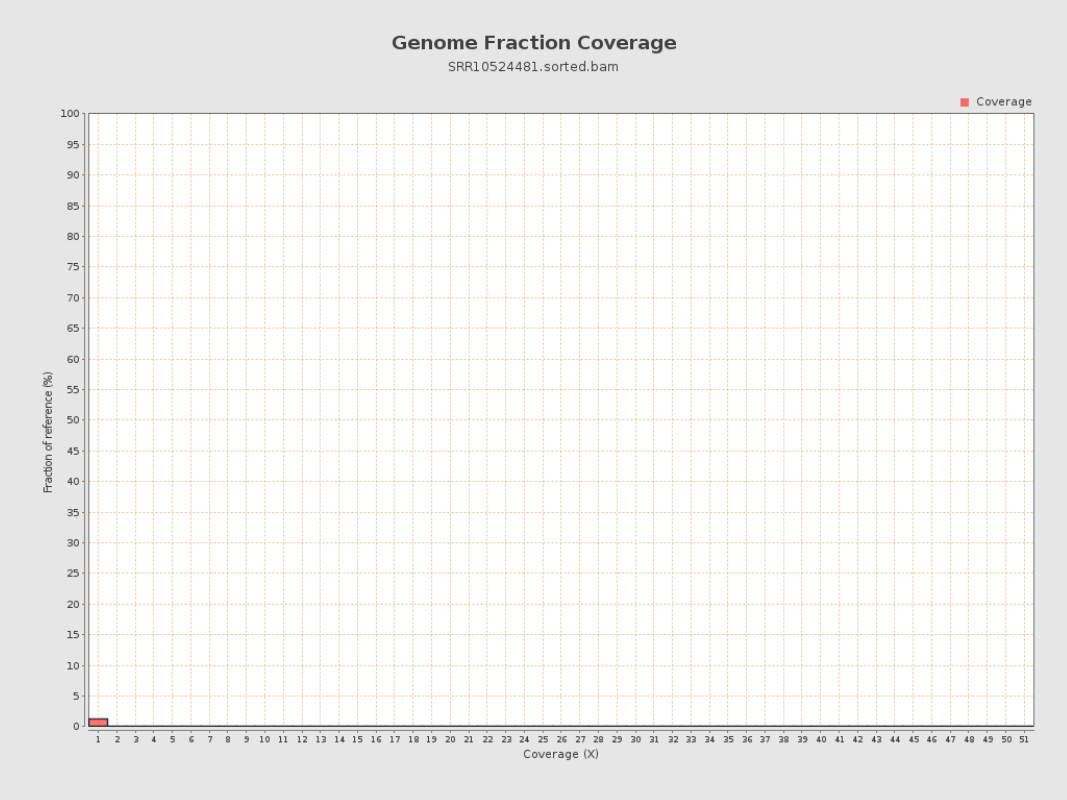
4. Results : Coverage Histogram



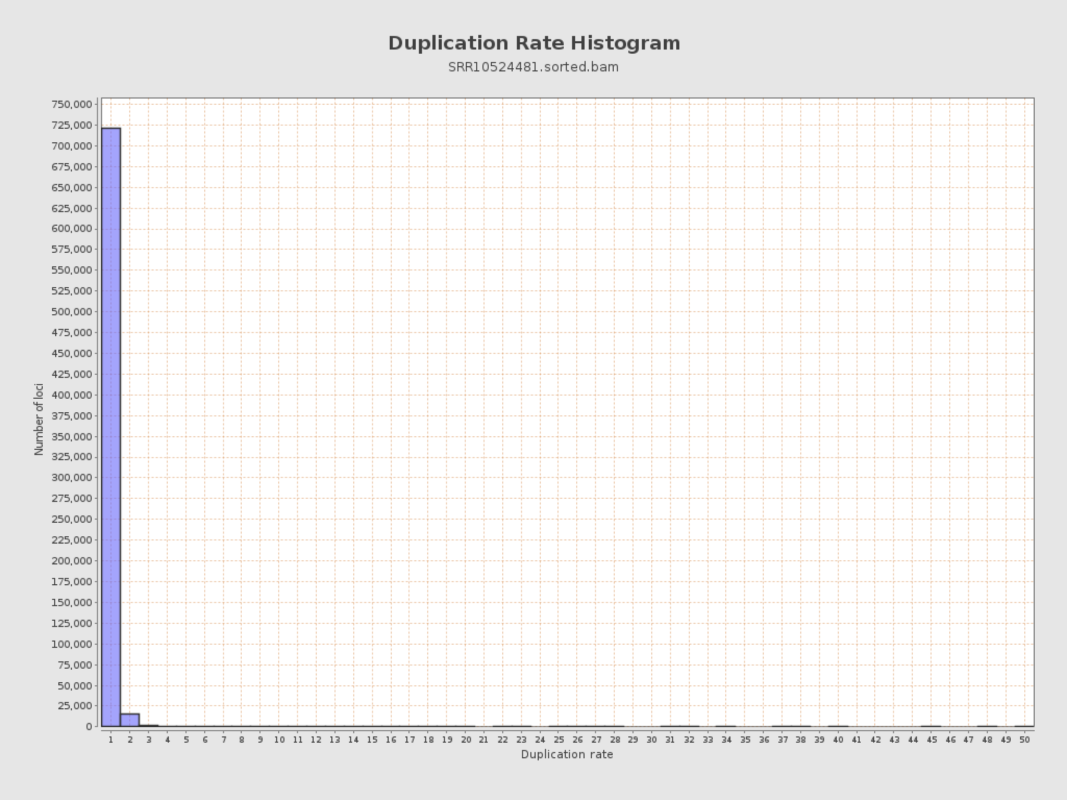
5. Results : Coverage Histogram (0-50X)



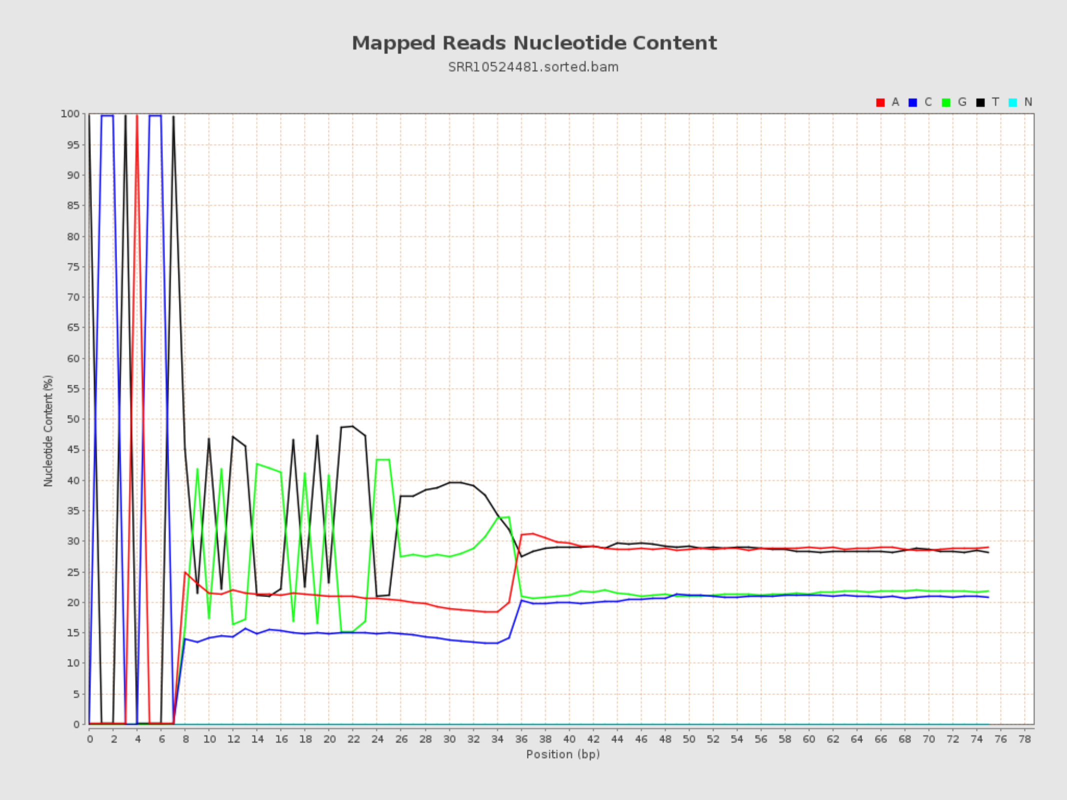
6. Results : Genome Fraction Coverage



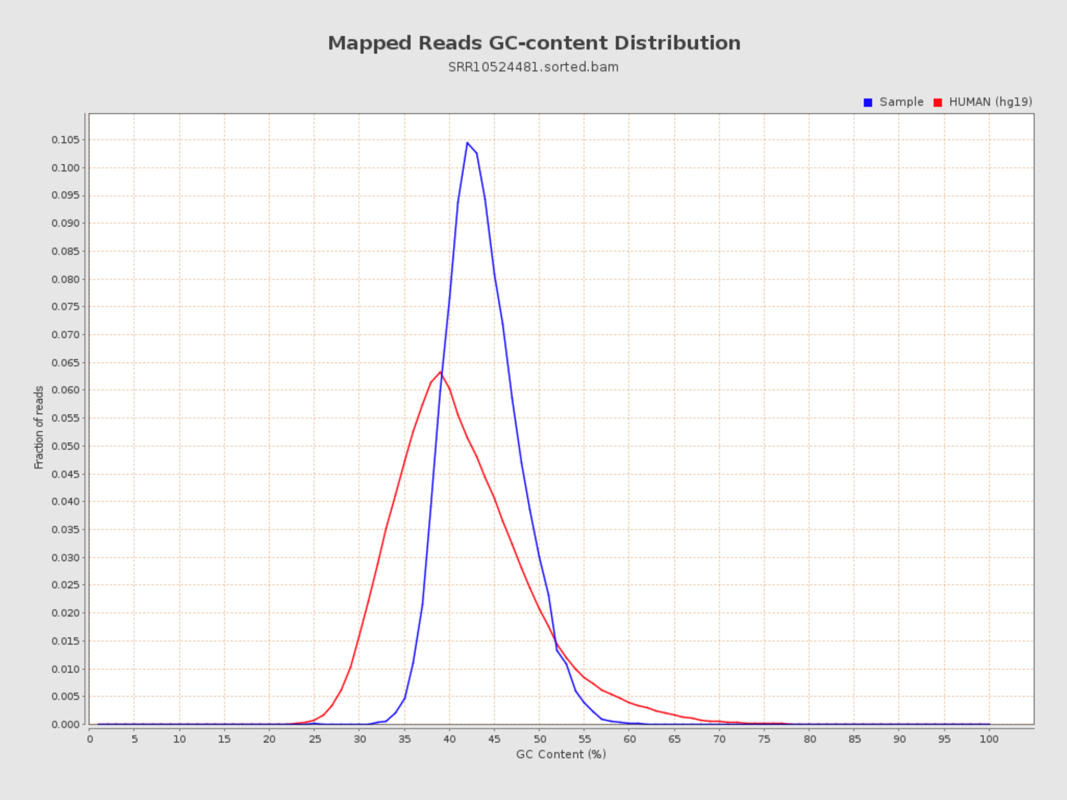
7. Results : Duplication Rate Histogram



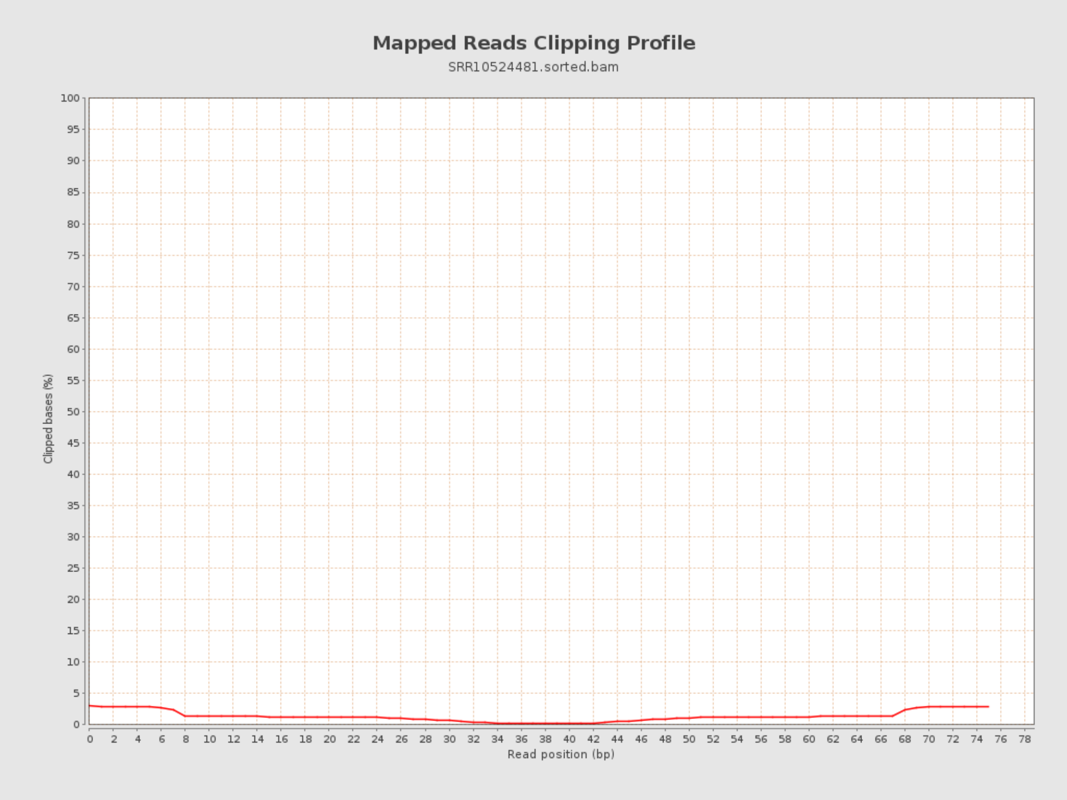
8. Results : Mapped Reads Nucleotide Content



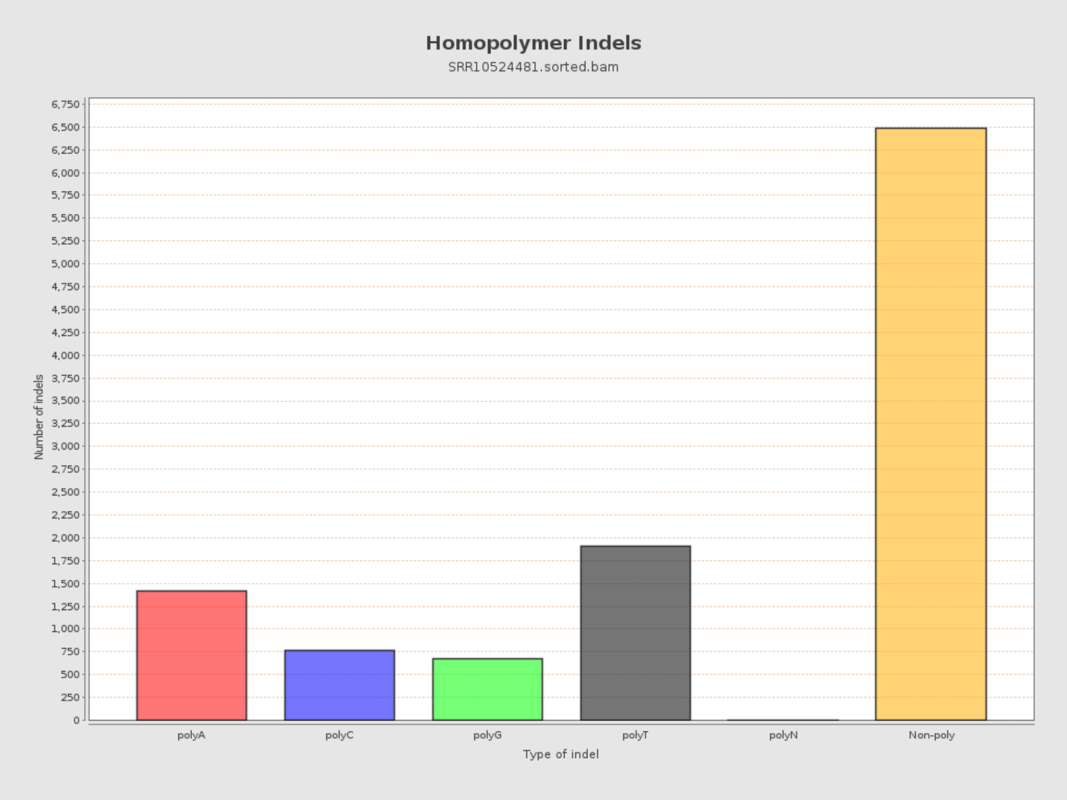
9. Results : Mapped Reads GC-content Distribution



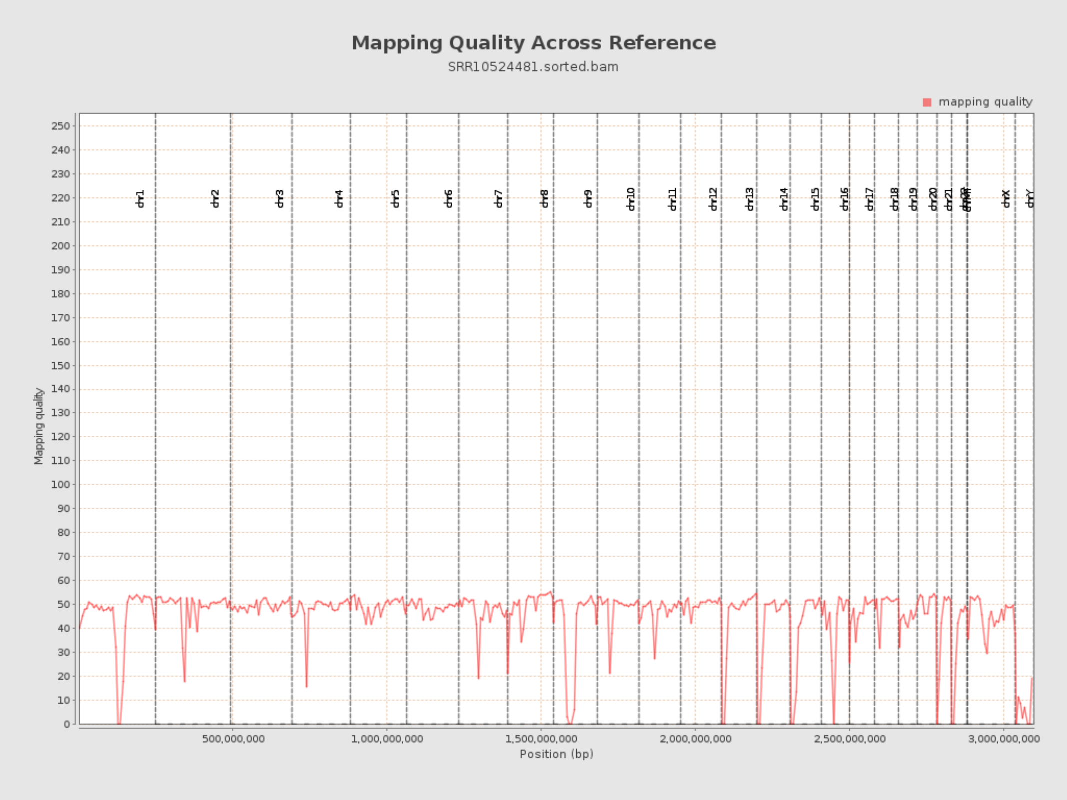
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram