Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 15:59:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524674.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_SRR10524674 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524674.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 15:59:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524674.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	867,994
Mapped reads	801,858 / 92.38%
Unmapped reads	66,136 / 7.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,494 / 0.4%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	20,871 / 2.4%
Duplication rate	1.87%
Clipped reads	802,888 / 92.5%

2.2. ACGT Content

Number/percentage of A's	12,420,174 / 26.21%
Number/percentage of C's	8,830,960 / 18.64%
Number/percentage of T's	15,188,794 / 32.06%
Number/percentage of G's	10,933,536 / 23.08%
Number/percentage of N's	6,256 / 0.01%
GC Percentage	41.72%

2.3. Coverage

Mean	0.0153

Standard Deviation	0.1729

2.4. Mapping Quality

Mean Mapping Quality	45.86

2.5. Mismatches and indels

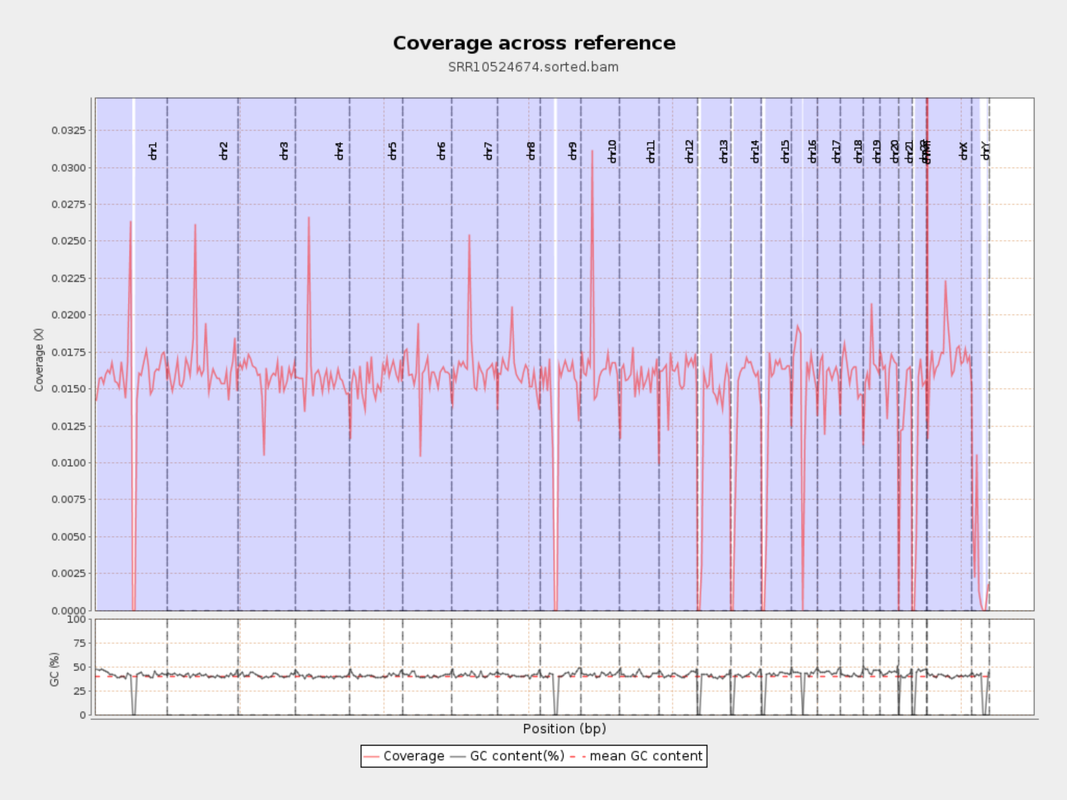
General error rate	0.52%
Mismatches	236,201
Insertions	3,960
Mapped reads with at least one insertion	0.49%
Deletions	8,783
Mapped reads with at least one deletion	1.09%
Homopolymer indels	42.45%

2.6. Chromosome stats

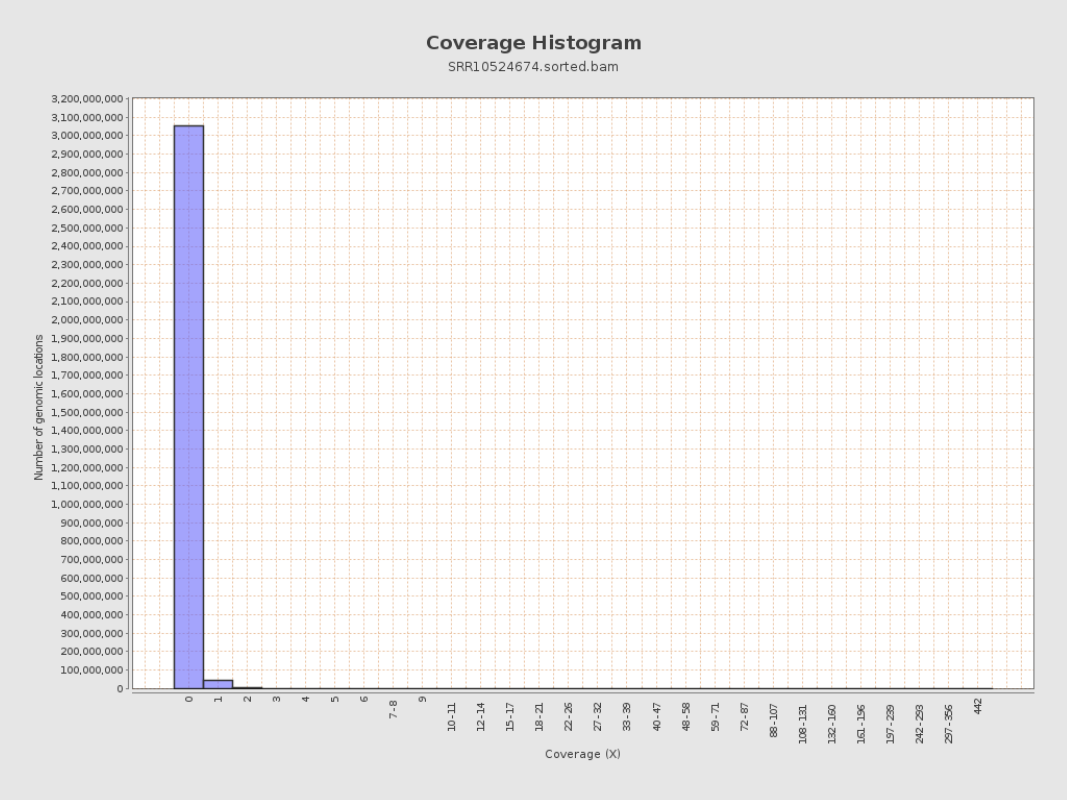
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3810329	0.0153	0.2865
chr2	243199373	4001900	0.0165	0.2283
chr3	198022430	3148513	0.0159	0.1315
chr4	191154276	3054138	0.016	0.1422
chr5	180915260	2849548	0.0158	0.1311
chr6	171115067	2741642	0.016	0.1444
chr7	159138663	2651764	0.0167	0.1971

chr8	146364022	2371480	0.0162	0.1784
chr9	141213431	1967426	0.0139	0.1502
chr10	135534747	2298188	0.017	0.1804
chr11	135006516	2136938	0.0158	0.155
chr12	133851895	2159849	0.0161	0.134
chr13	115169878	1474102	0.0128	0.1183
chr14	107349540	1441924	0.0134	0.1253
chr15	102531392	1364672	0.0133	0.1206
chr16	90354753	1352004	0.015	0.1337
chr17	81195210	1271986	0.0157	0.1344
chr18	78077248	1250524	0.016	0.2325
chr19	59128983	971570	0.0164	0.2035
chr20	63025520	1016462	0.0161	0.1341
chr21	48129895	627864	0.013	0.1329
chr22	51304566	558602	0.0109	0.1086
chrMT	16571	48586	2.932	2.3477
chrX	155270560	2664553	0.0172	0.1453
chrY	59373566	159111	0.0027	0.1076

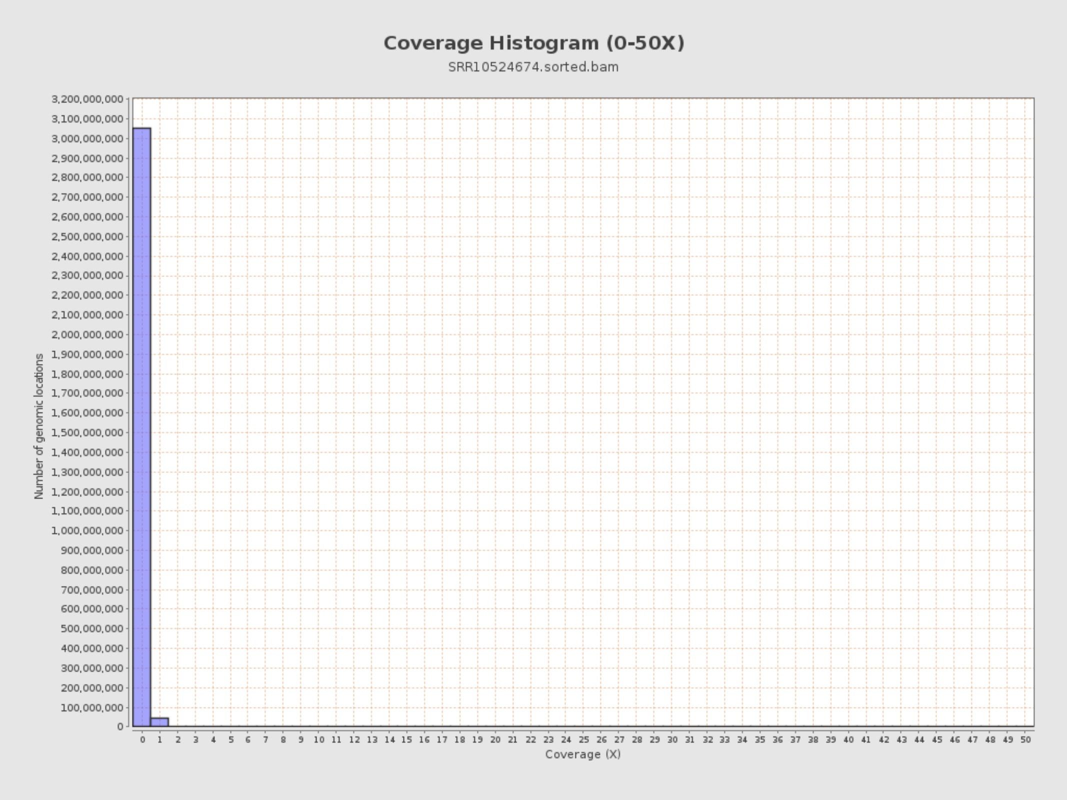
3. Results : Coverage across reference



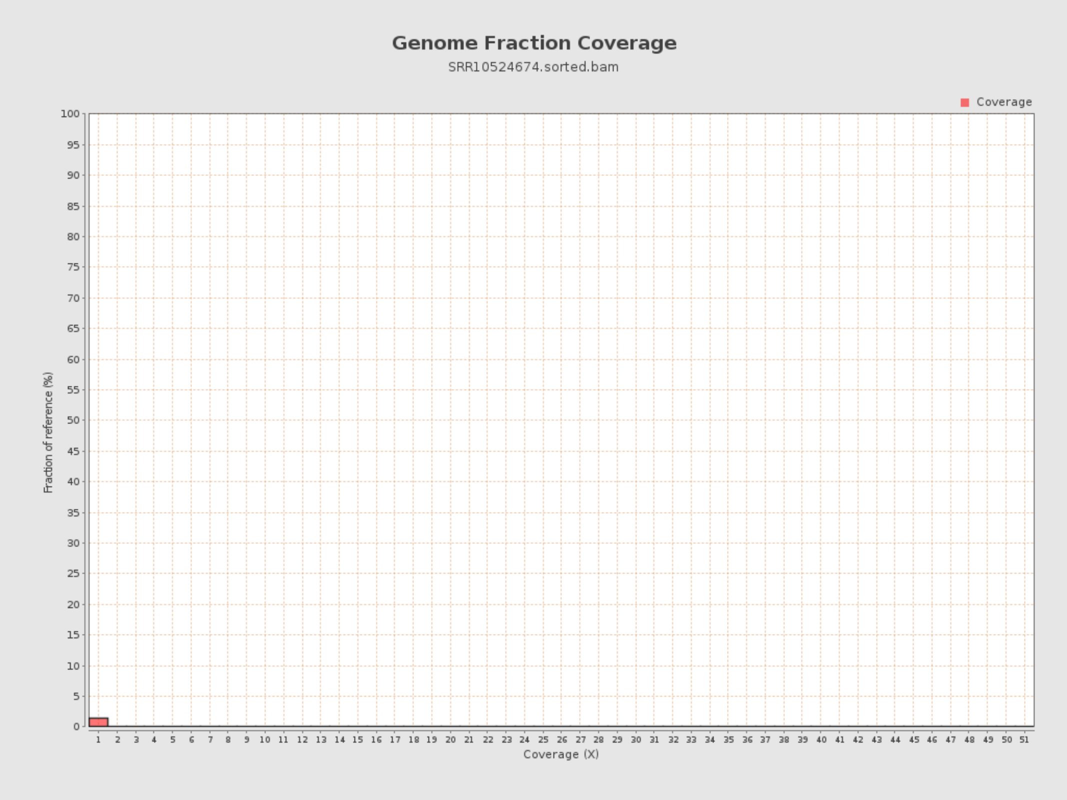
4. Results : Coverage Histogram



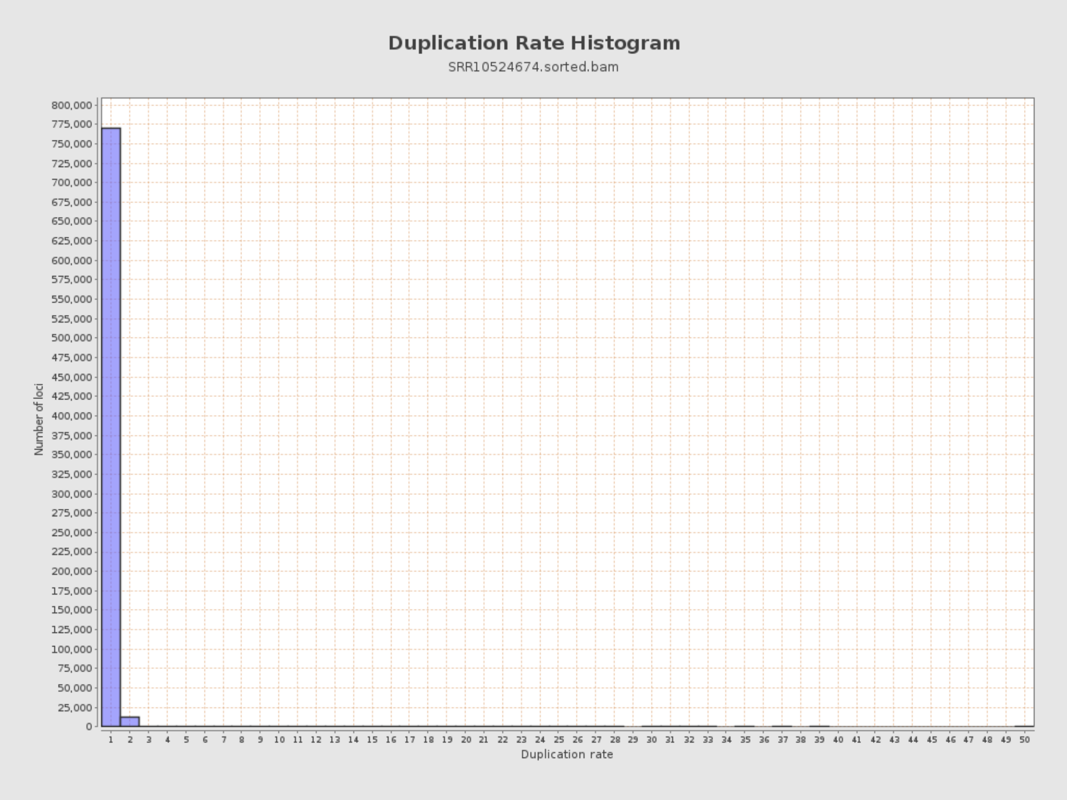
5. Results : Coverage Histogram (0-50X)



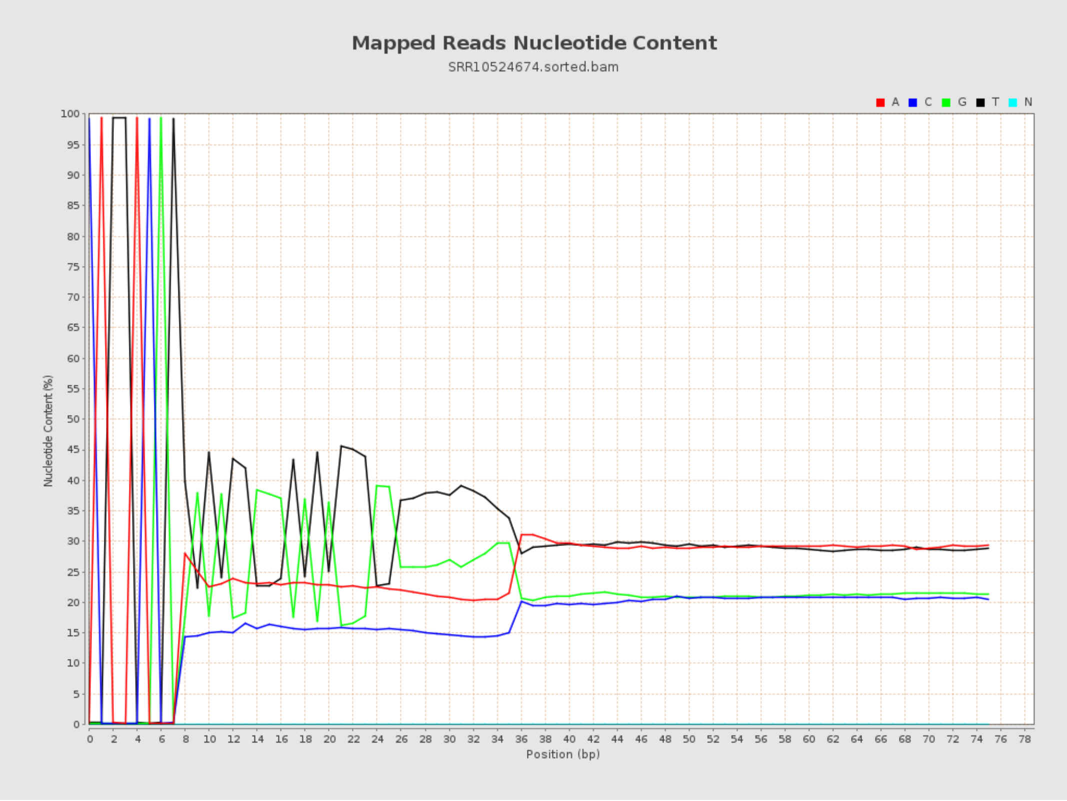
6. Results : Genome Fraction Coverage



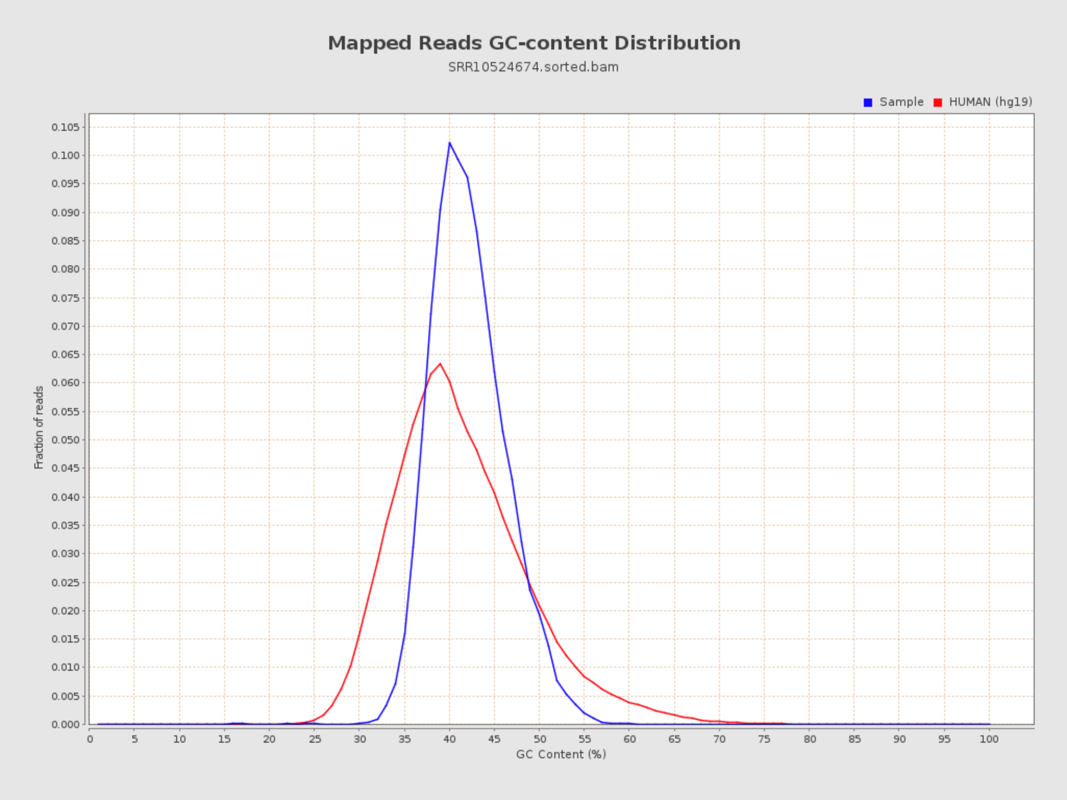
7. Results : Duplication Rate Histogram



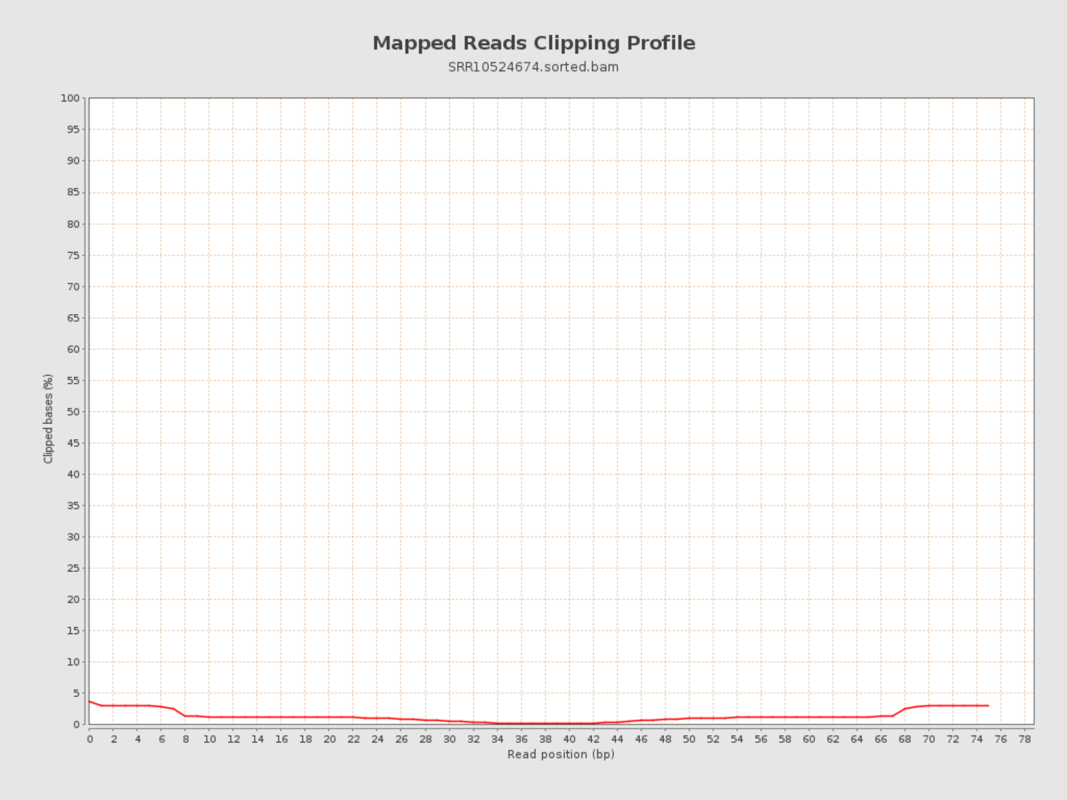
8. Results : Mapped Reads Nucleotide Content



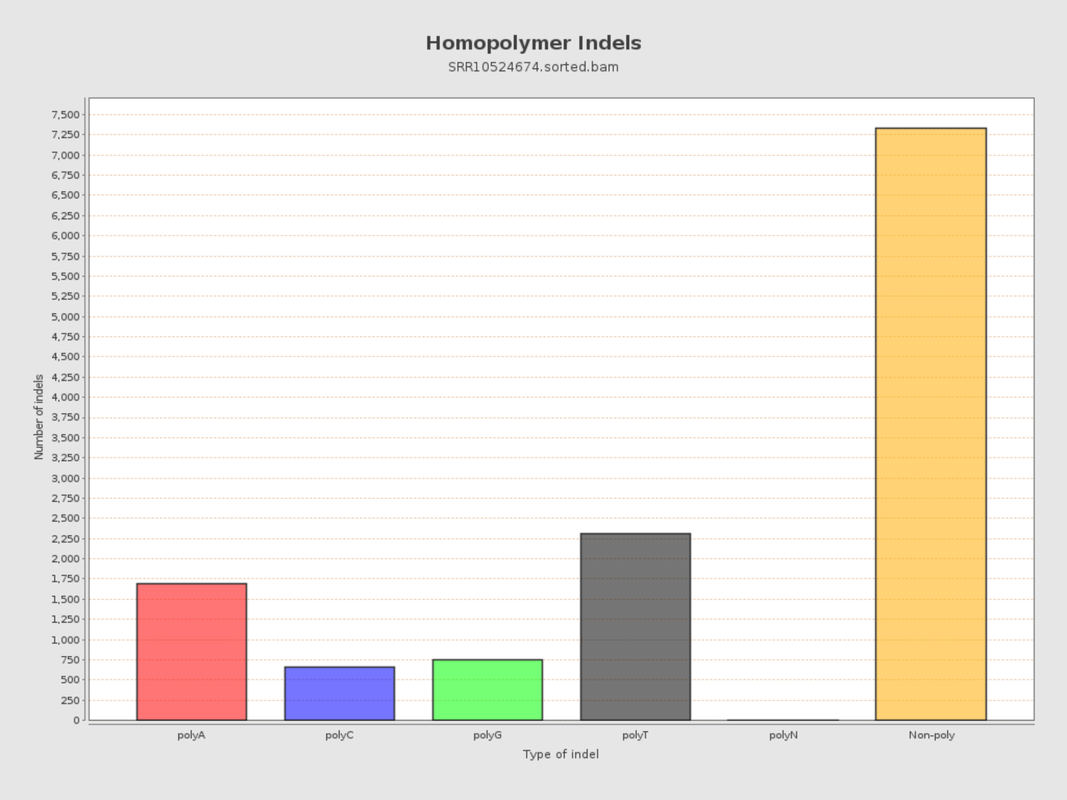
9. Results : Mapped Reads GC-content Distribution



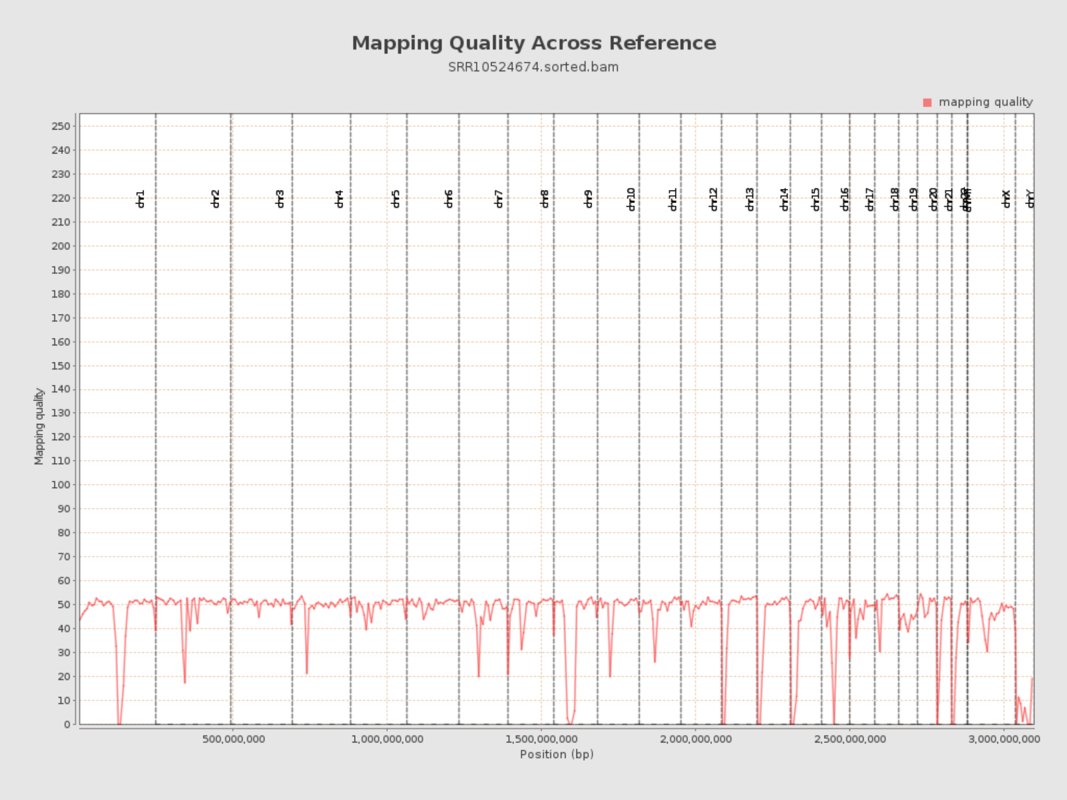
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram