Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 22:44:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524841.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_SRR10524841 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524841.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 22:44:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524841.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,079,218
Mapped reads	996,733 / 92.36%
Unmapped reads	82,485 / 7.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,264 / 0.4%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	23,841 / 2.21%
Duplication rate	1.62%
Clipped reads	998,255 / 92.5%

2.2. ACGT Content

Number/percentage of A's	14,988,310 / 25.7%
Number/percentage of C's	10,530,445 / 18.05%
Number/percentage of T's	19,047,270 / 32.66%
Number/percentage of G's	13,754,227 / 23.58%
Number/percentage of N's	7,696 / 0.01%
GC Percentage	41.63%

2.3. Coverage

Mean	0.0188

Standard Deviation	0.2106

2.4. Mapping Quality

Mean Mapping Quality	45.5

2.5. Mismatches and indels

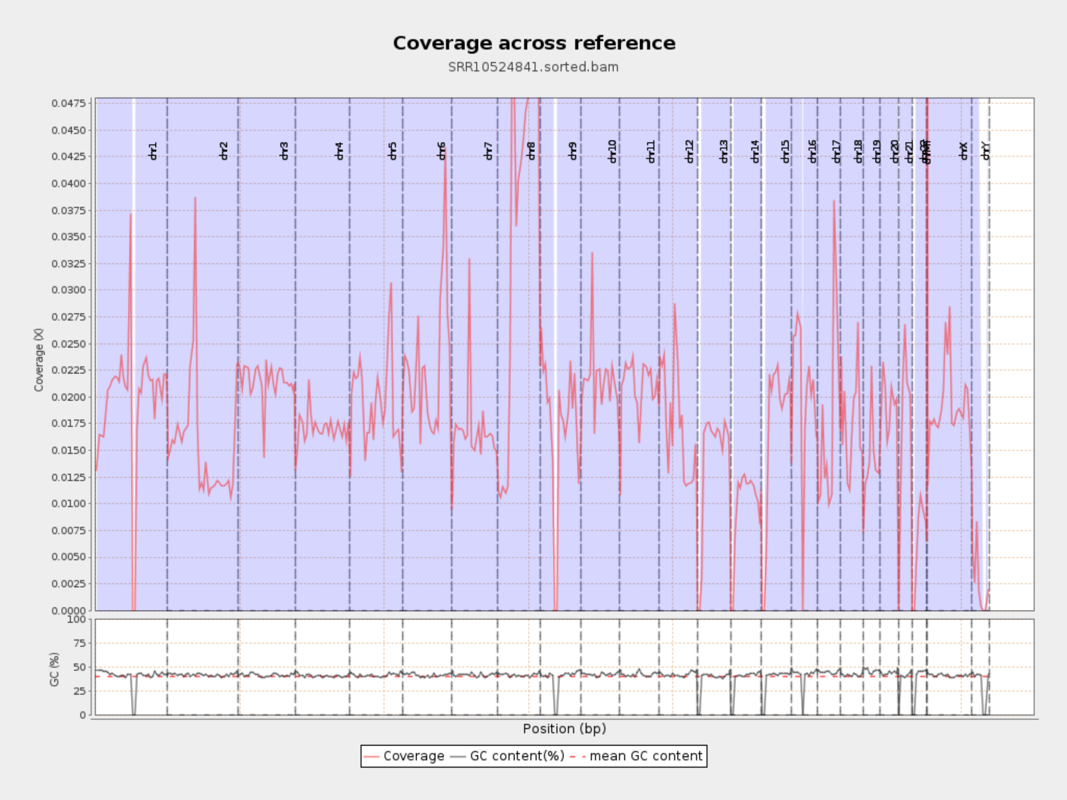
General error rate	0.49%
Mismatches	278,505
Insertions	4,163
Mapped reads with at least one insertion	0.42%
Deletions	10,809
Mapped reads with at least one deletion	1.08%
Homopolymer indels	43.73%

2.6. Chromosome stats

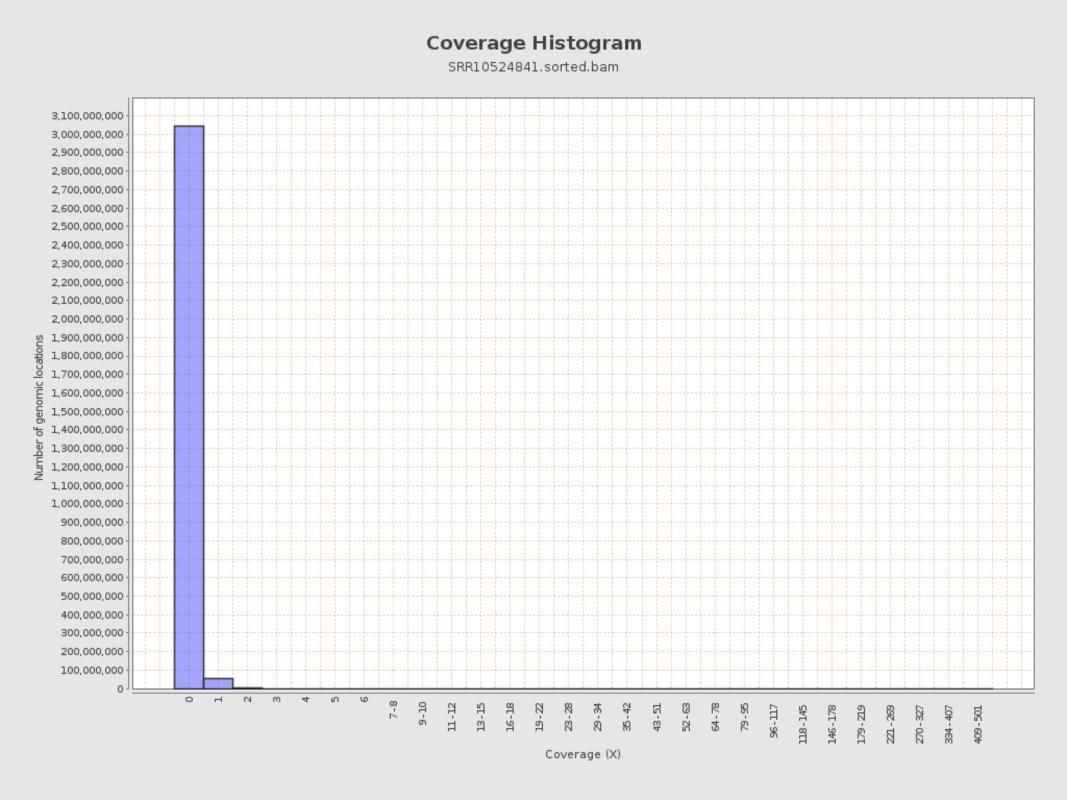
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4900069	0.0197	0.4156
chr2	243199373	3741946	0.0154	0.1992
chr3	198022430	4264501	0.0215	0.1532
chr4	191154276	3256715	0.017	0.1429
chr5	180915260	3582956	0.0198	0.1479
chr6	171115067	3875020	0.0226	0.1699
chr7	159138663	2696998	0.0169	0.2753

chr8	146364022	6030274	0.0412	0.2836
chr9	141213431	2441011	0.0173	0.1724
chr10	135534747	2930736	0.0216	0.1942
chr11	135006516	2846799	0.0211	0.1823
chr12	133851895	2333052	0.0174	0.1407
chr13	115169878	1606346	0.0139	0.1239
chr14	107349540	1037361	0.0097	0.1117
chr15	102531392	1736525	0.0169	0.1374
chr16	90354753	1813783	0.0201	0.1569
chr17	81195210	1469629	0.0181	0.1527
chr18	78077248	1383425	0.0177	0.2819
chr19	59128983	843961	0.0143	0.2727
chr20	63025520	1197293	0.019	0.1454
chr21	48129895	855555	0.0178	0.1449
chr22	51304566	338921	0.0066	0.0843
chrMT	16571	16827	1.0154	1.2374
chrX	155270560	3000224	0.0193	0.1589
chrY	59373566	145086	0.0024	0.0716

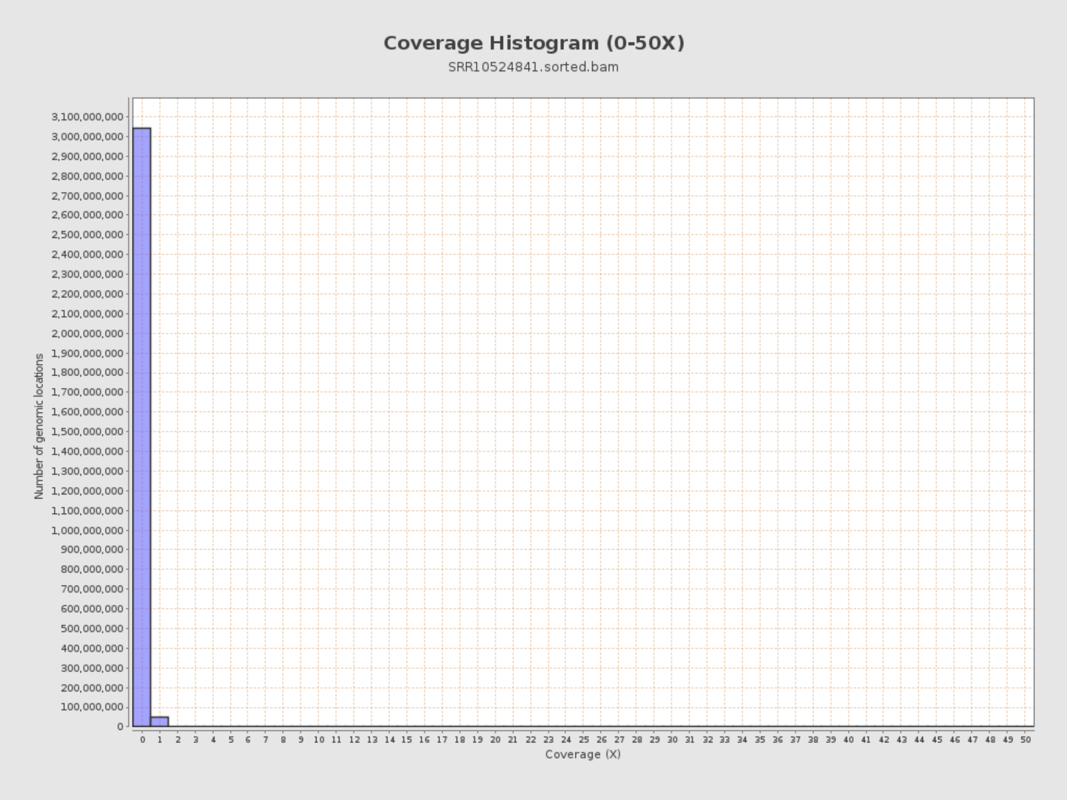
3. Results : Coverage across reference



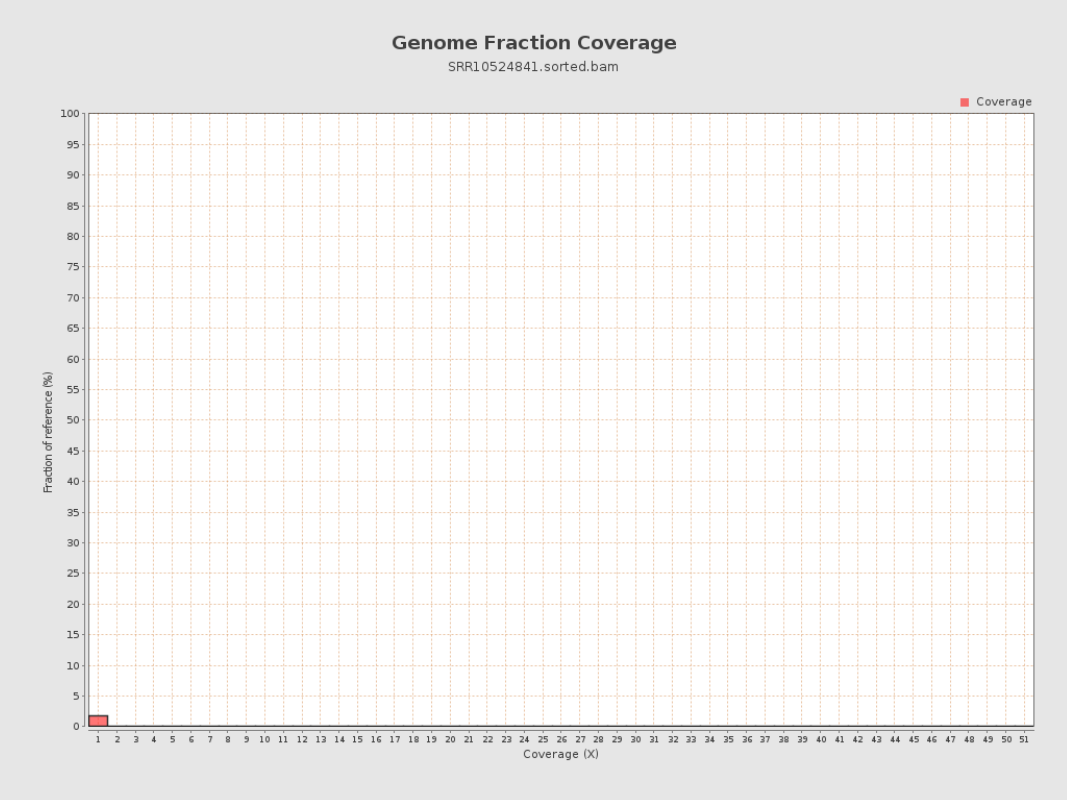
4. Results : Coverage Histogram



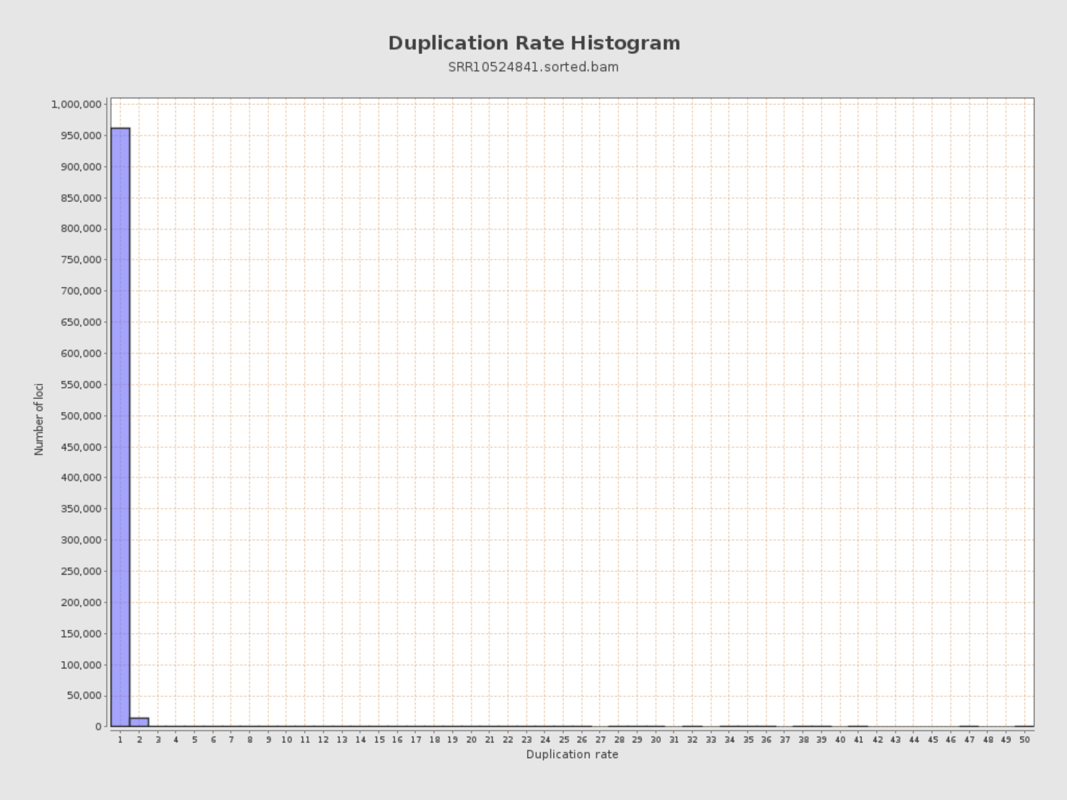
5. Results : Coverage Histogram (0-50X)



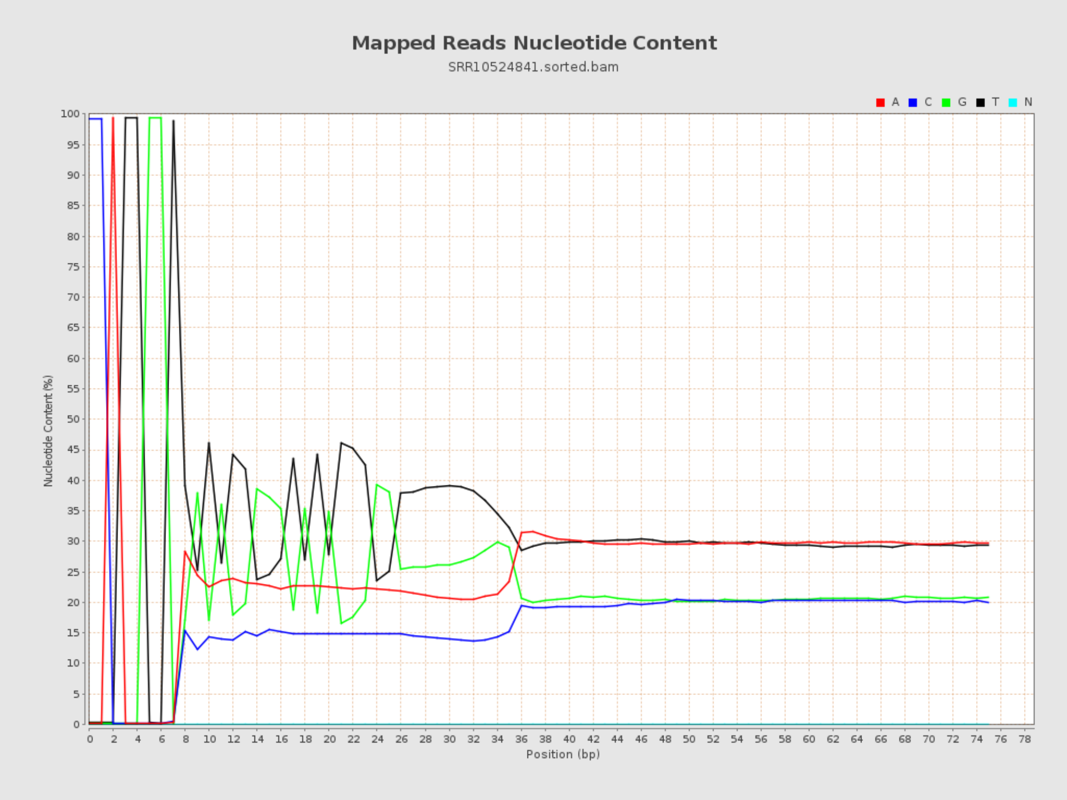
6. Results : Genome Fraction Coverage



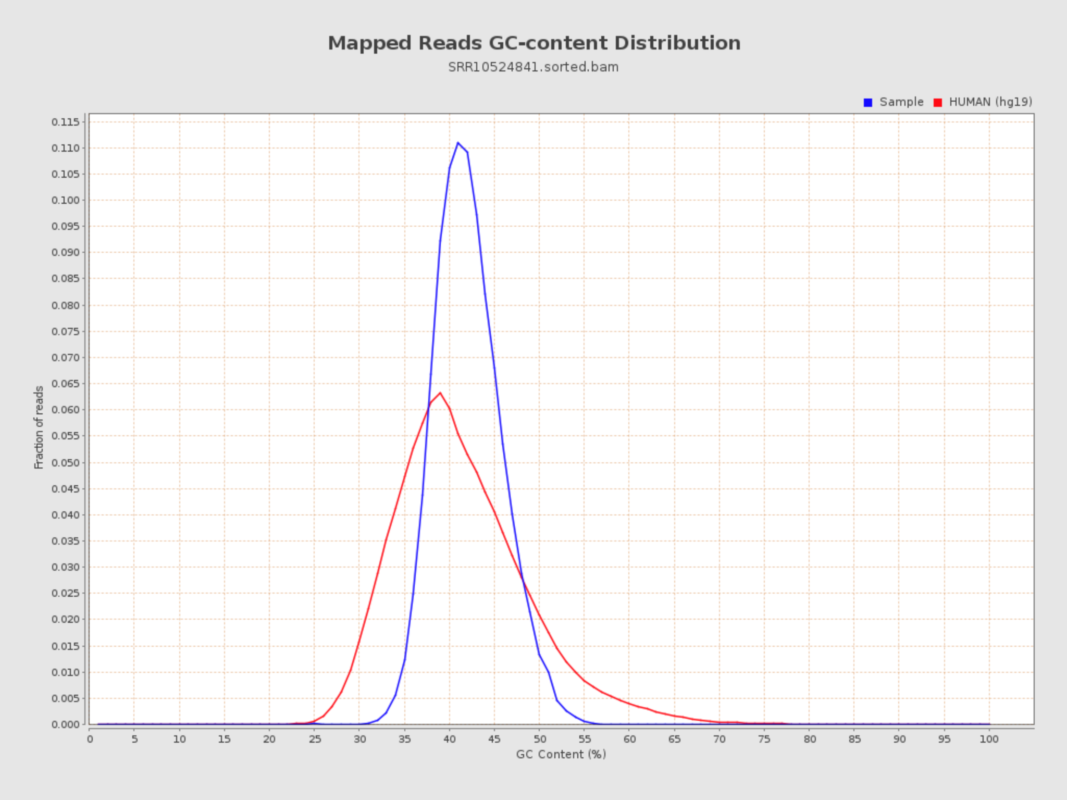
7. Results : Duplication Rate Histogram



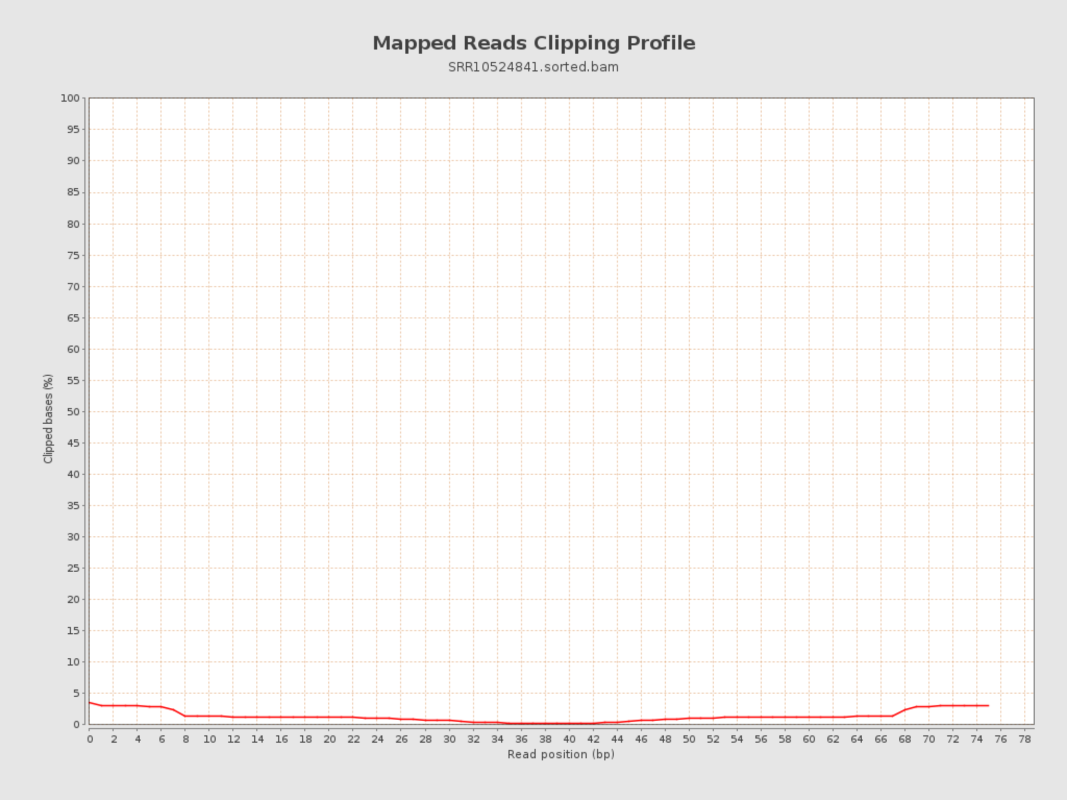
8. Results : Mapped Reads Nucleotide Content



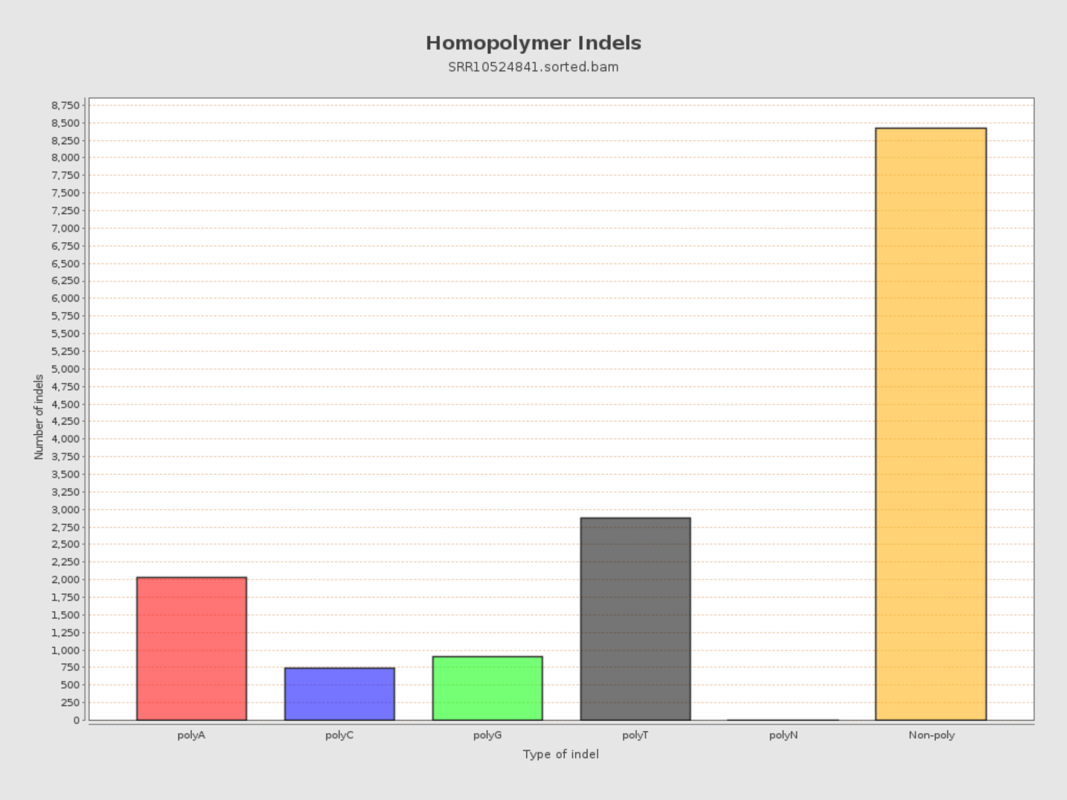
9. Results : Mapped Reads GC-content Distribution



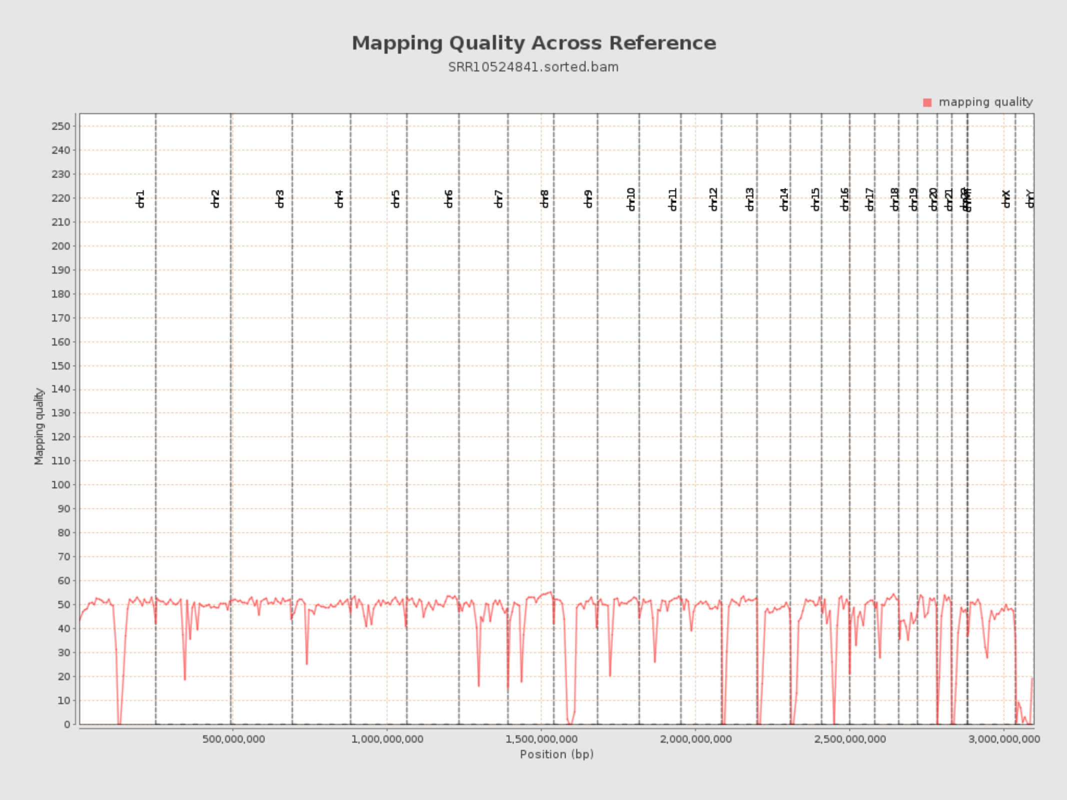
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram