Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 23:34:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524341.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_SRR10524341 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524341.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 23:34:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524341.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	574,585
Mapped reads	515,923 / 89.79%
Unmapped reads	58,662 / 10.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,194 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	8,840 / 1.54%
Duplication rate	1.17%
Clipped reads	516,913 / 89.96%

2.2. ACGT Content

Number/percentage of A's	7,296,375 / 24.85%
Number/percentage of C's	5,715,918 / 19.47%
Number/percentage of T's	9,246,556 / 31.5%
Number/percentage of G's	7,095,260 / 24.17%
Number/percentage of N's	3,822 / 0.01%
GC Percentage	43.64%

2.3. Coverage

Mean	0.0095

Standard Deviation	0.122

2.4. Mapping Quality

Mean Mapping Quality	42.3

2.5. Mismatches and indels

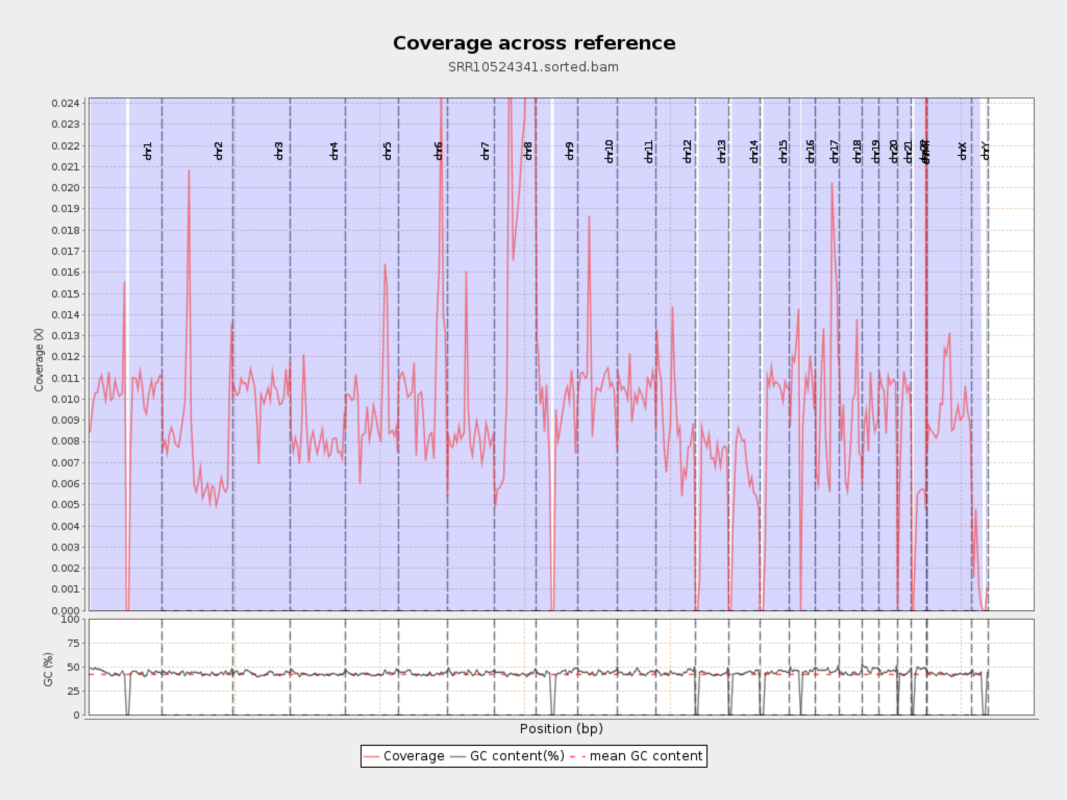
General error rate	0.54%
Mismatches	154,624
Insertions	1,881
Mapped reads with at least one insertion	0.36%
Deletions	4,850
Mapped reads with at least one deletion	0.93%
Homopolymer indels	42.15%

2.6. Chromosome stats

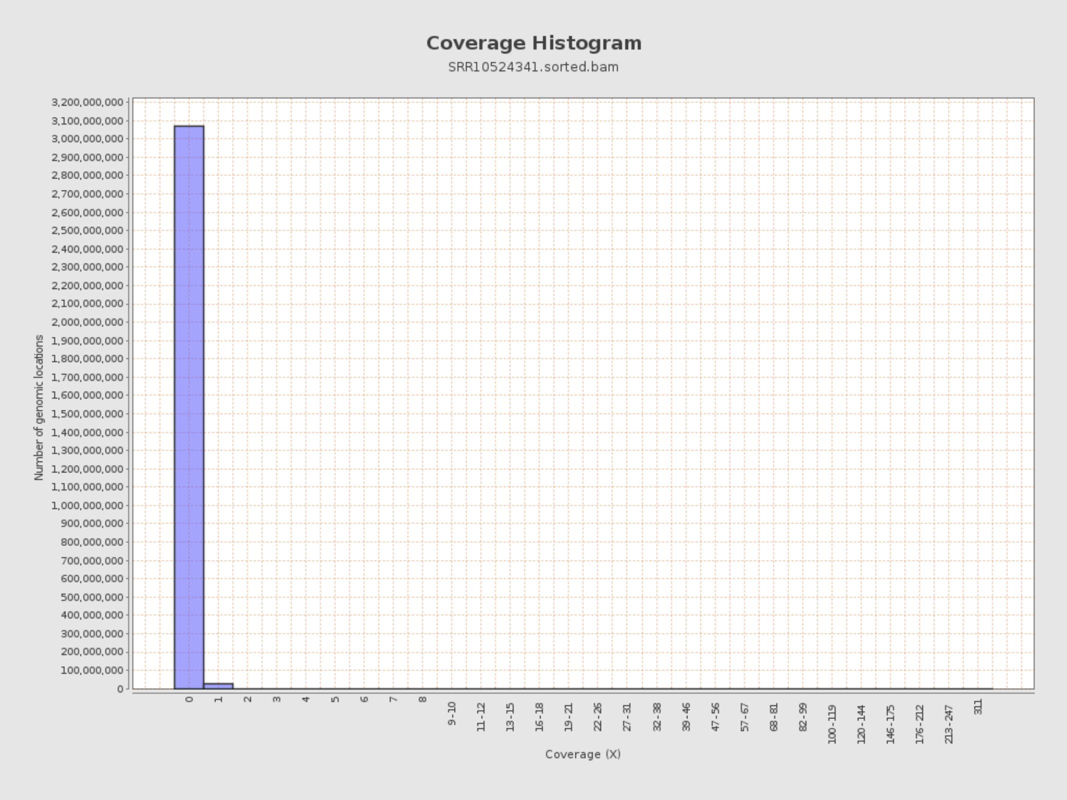
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2457524	0.0099	0.1756
chr2	243199373	1898725	0.0078	0.1534
chr3	198022430	2040605	0.0103	0.1049
chr4	191154276	1539118	0.0081	0.0968
chr5	180915260	1749787	0.0097	0.1017
chr6	171115067	1883510	0.011	0.1125
chr7	159138663	1361399	0.0086	0.1417

chr8	146364022	2997813	0.0205	0.1653
chr9	141213431	1213870	0.0086	0.1055
chr10	135534747	1489975	0.011	0.1261
chr11	135006516	1401710	0.0104	0.1132
chr12	133851895	1186114	0.0089	0.0981
chr13	115169878	732896	0.0064	0.0828
chr14	107349540	625674	0.0058	0.082
chr15	102531392	884318	0.0086	0.0965
chr16	90354753	926976	0.0103	0.108
chr17	81195210	895128	0.011	0.1131
chr18	78077248	686583	0.0088	0.1409
chr19	59128983	534603	0.009	0.1456
chr20	63025520	651730	0.0103	0.1057
chr21	48129895	414867	0.0086	0.0981
chr22	51304566	207430	0.004	0.0656
chrMT	16571	18606	1.1228	1.2507
chrX	155270560	1478556	0.0095	0.1066
chrY	59373566	88036	0.0015	0.0488

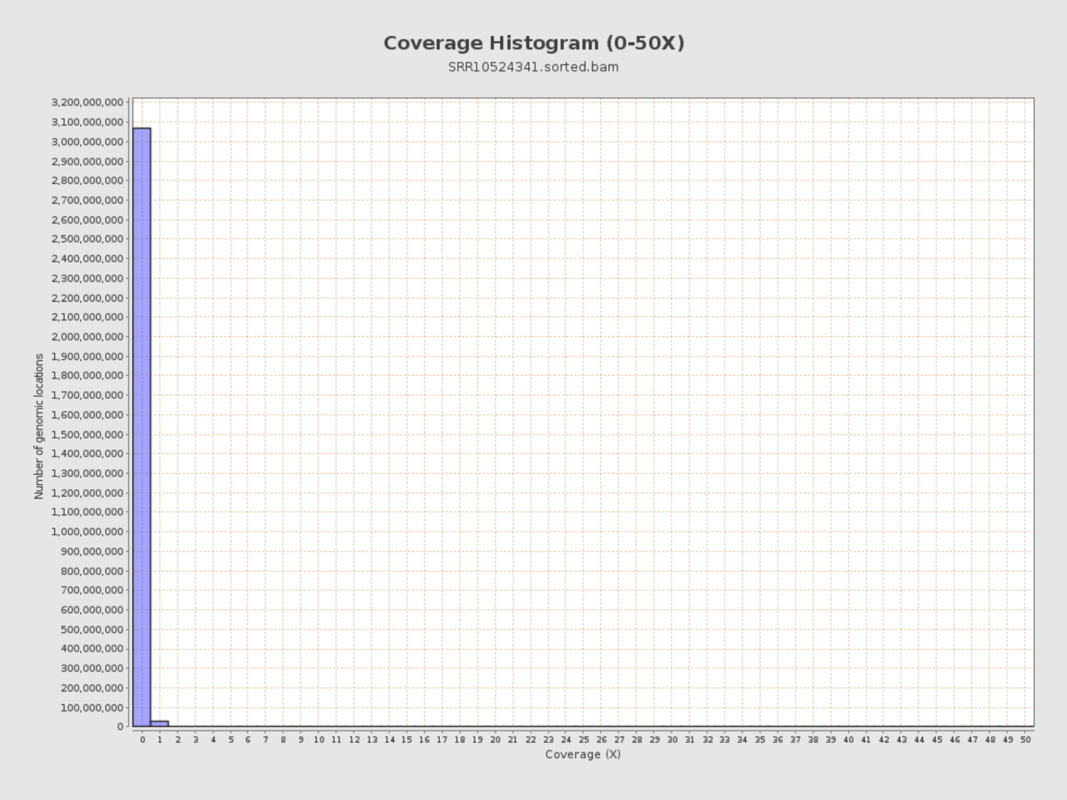
3. Results : Coverage across reference



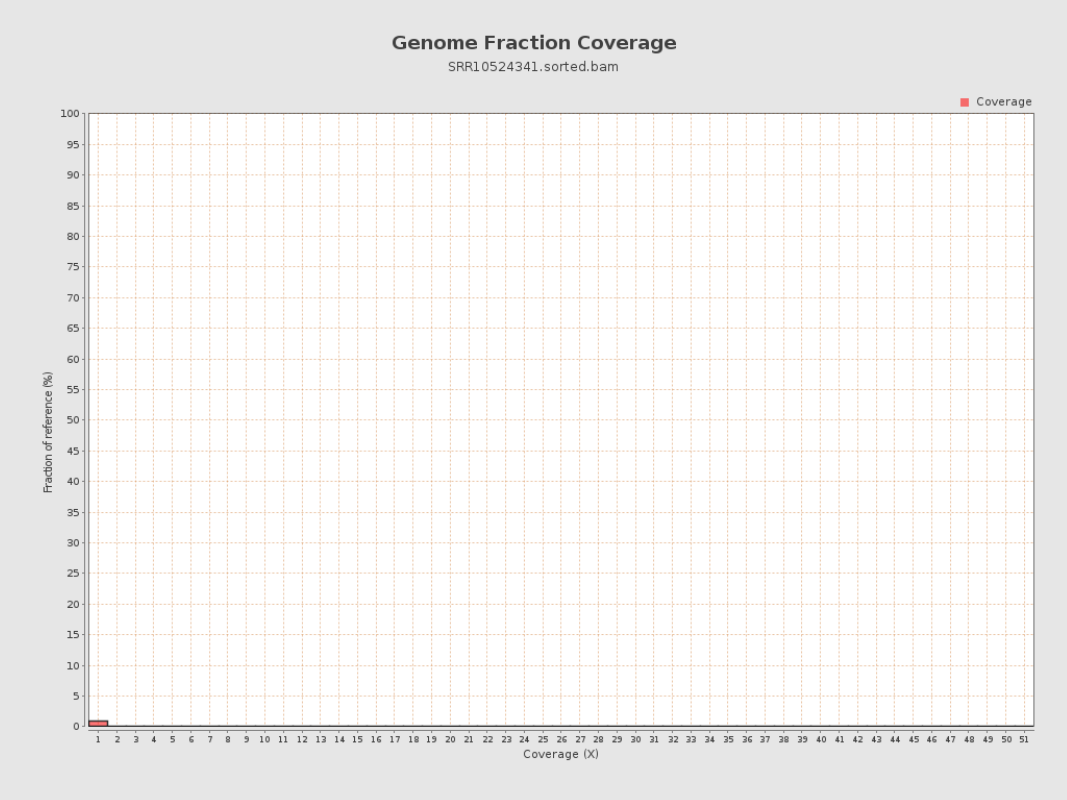
4. Results : Coverage Histogram



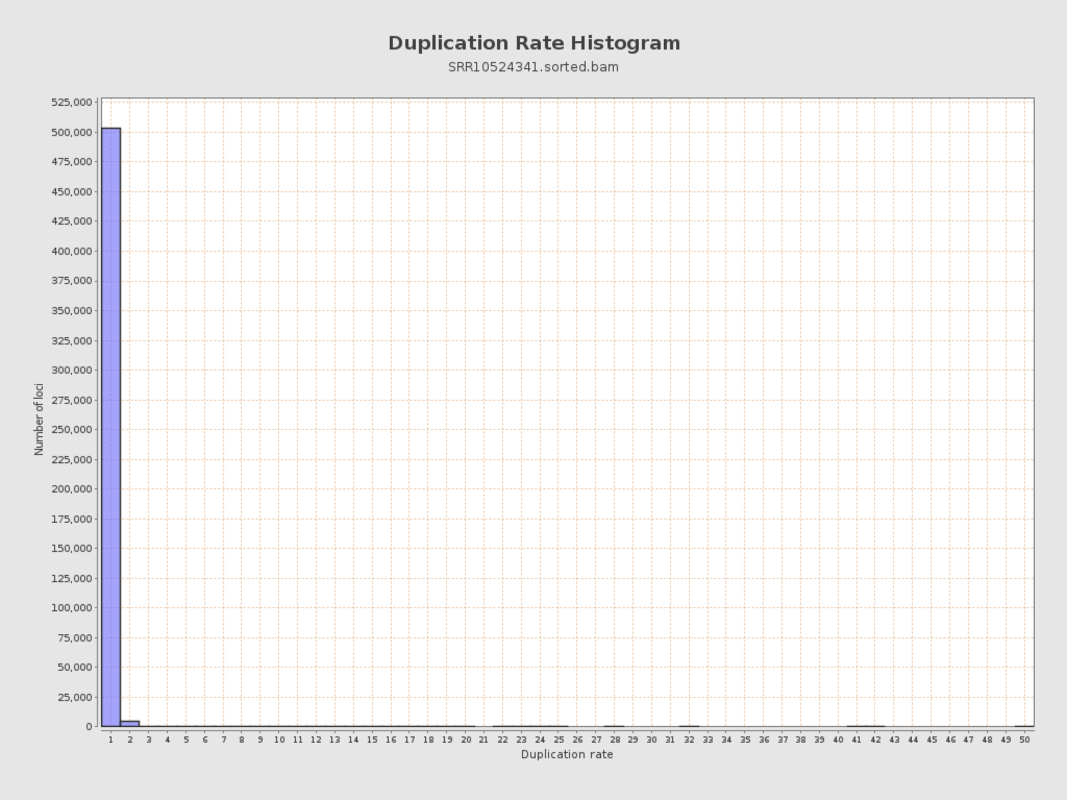
5. Results : Coverage Histogram (0-50X)



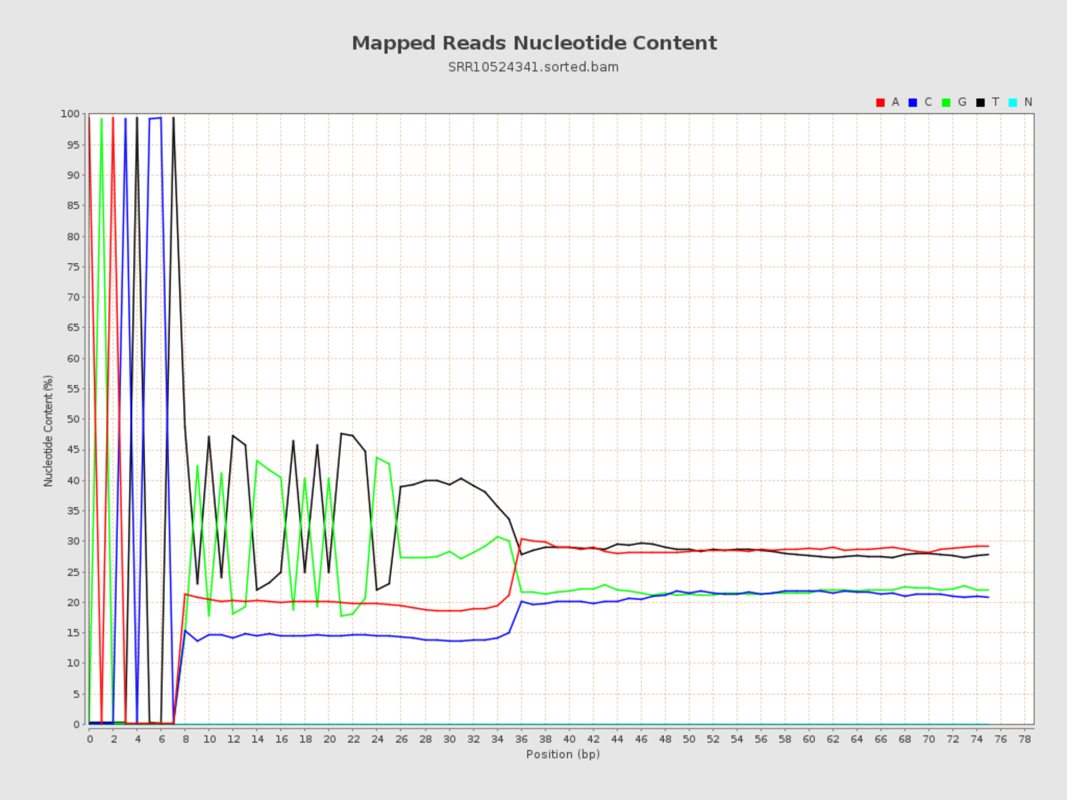
6. Results : Genome Fraction Coverage



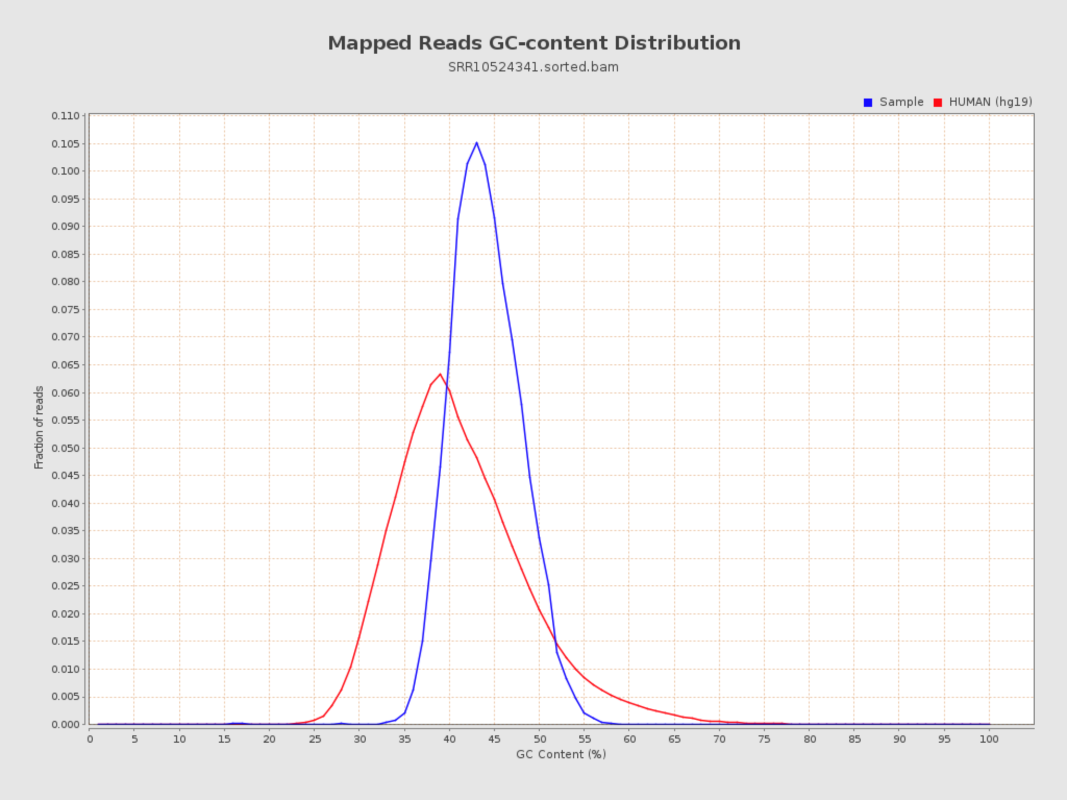
7. Results : Duplication Rate Histogram



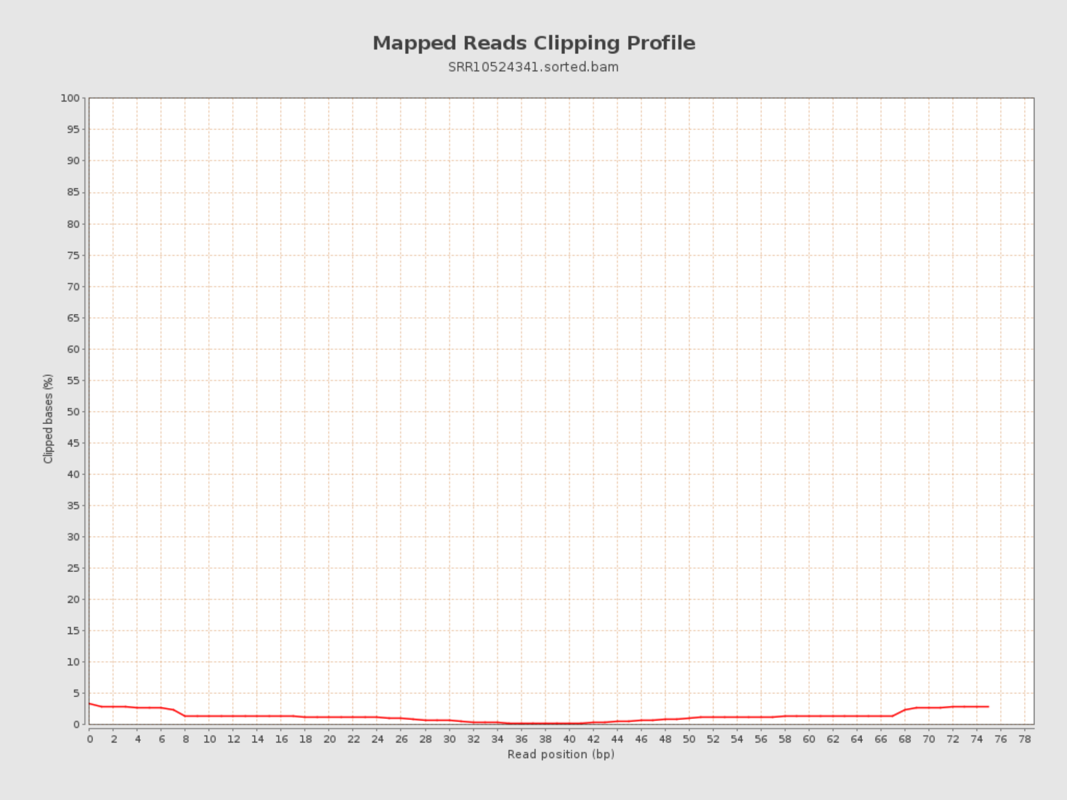
8. Results : Mapped Reads Nucleotide Content



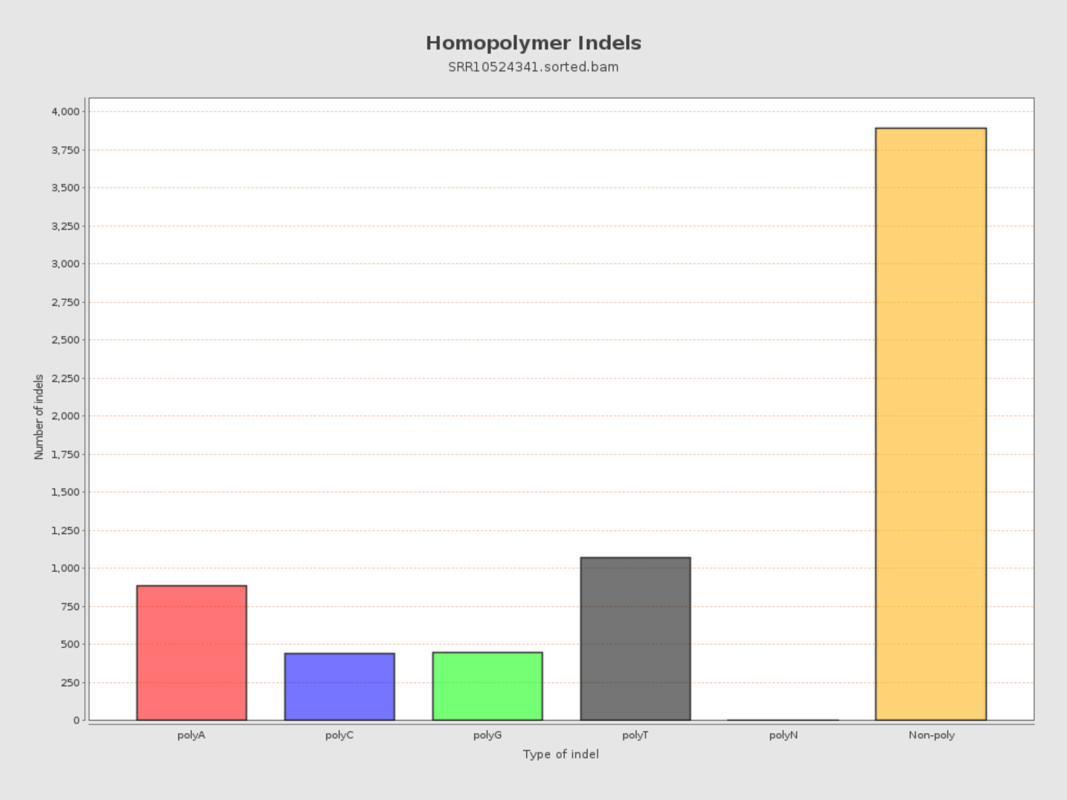
9. Results : Mapped Reads GC-content Distribution



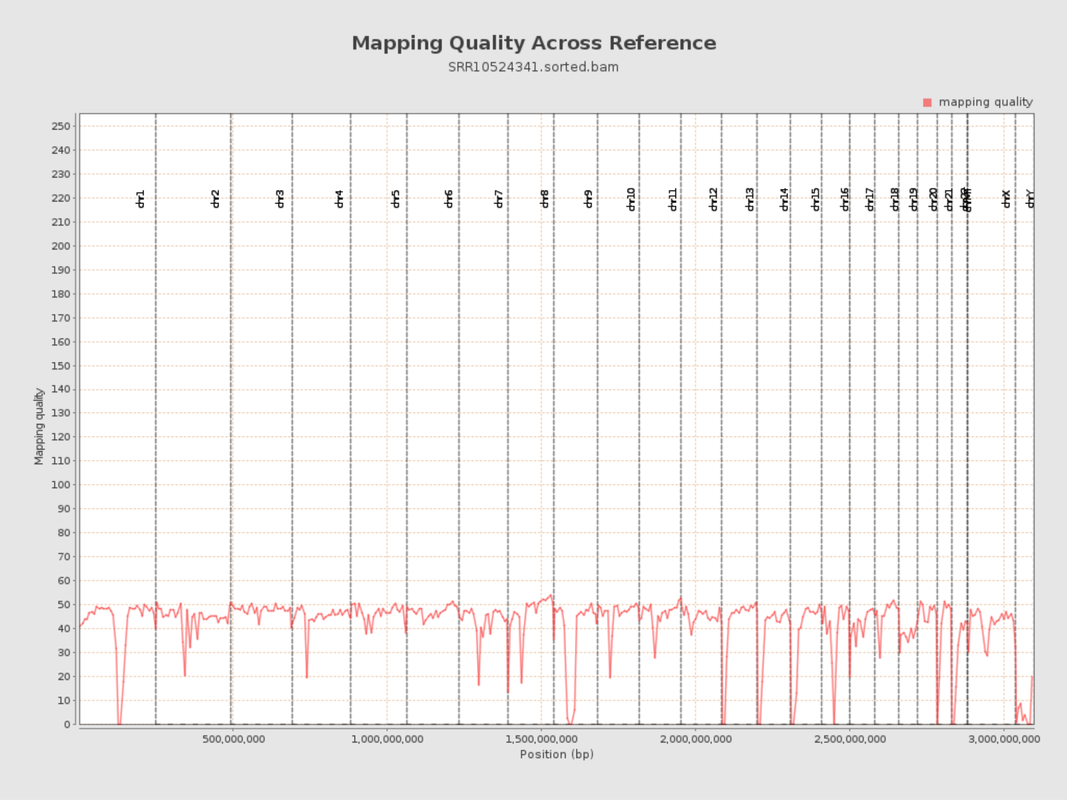
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram