Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 14:31:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524641.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_SRR10524641 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524641.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 14:31:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524641.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	608,548
Mapped reads	551,973 / 90.7%
Unmapped reads	56,575 / 9.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,114 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	14,106 / 2.32%
Duplication rate	2%
Clipped reads	551,927 / 90.7%

2.2. ACGT Content

Number/percentage of A's	7,964,346 / 24.75%
Number/percentage of C's	6,025,425 / 18.72%
Number/percentage of T's	10,382,465 / 32.26%
Number/percentage of G's	7,813,098 / 24.28%
Number/percentage of N's	266 / 0%
GC Percentage	43%

2.3. Coverage

Mean	0.0104

Standard Deviation	0.1293

2.4. Mapping Quality

Mean Mapping Quality	44.91

2.5. Mismatches and indels

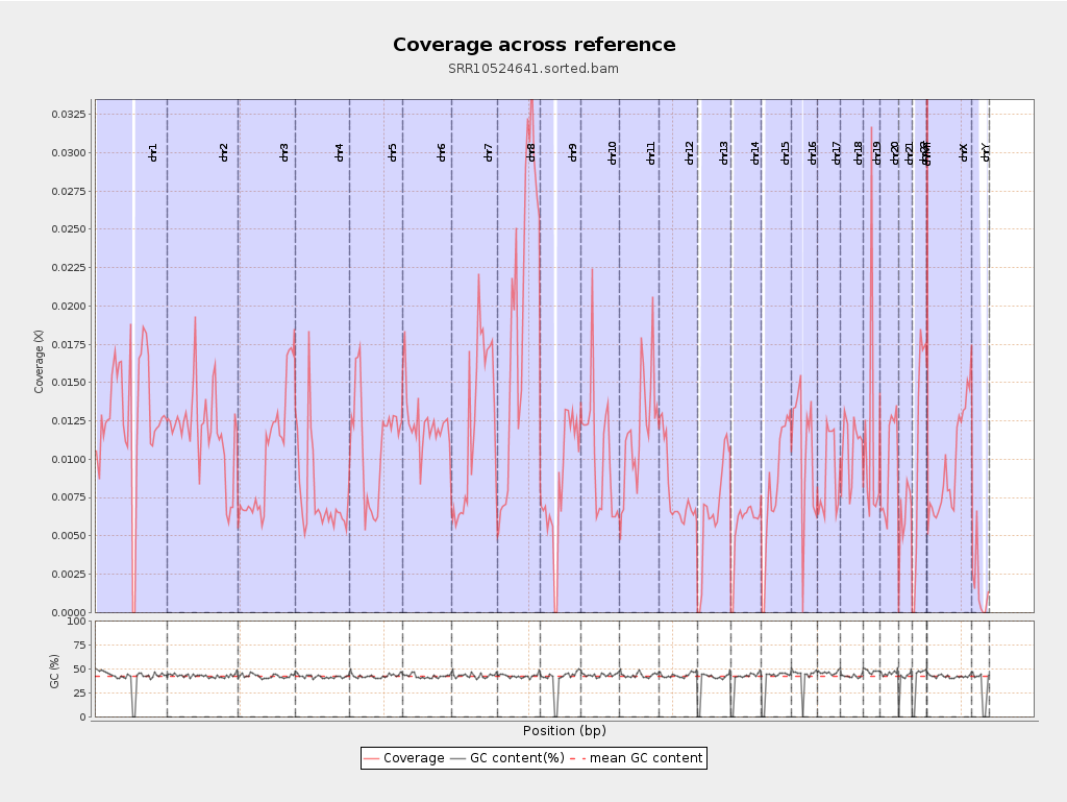
General error rate	0.53%
Mismatches	164,441
Insertions	2,571
Mapped reads with at least one insertion	0.46%
Deletions	6,403
Mapped reads with at least one deletion	1.15%
Homopolymer indels	41.13%

2.6. Chromosome stats

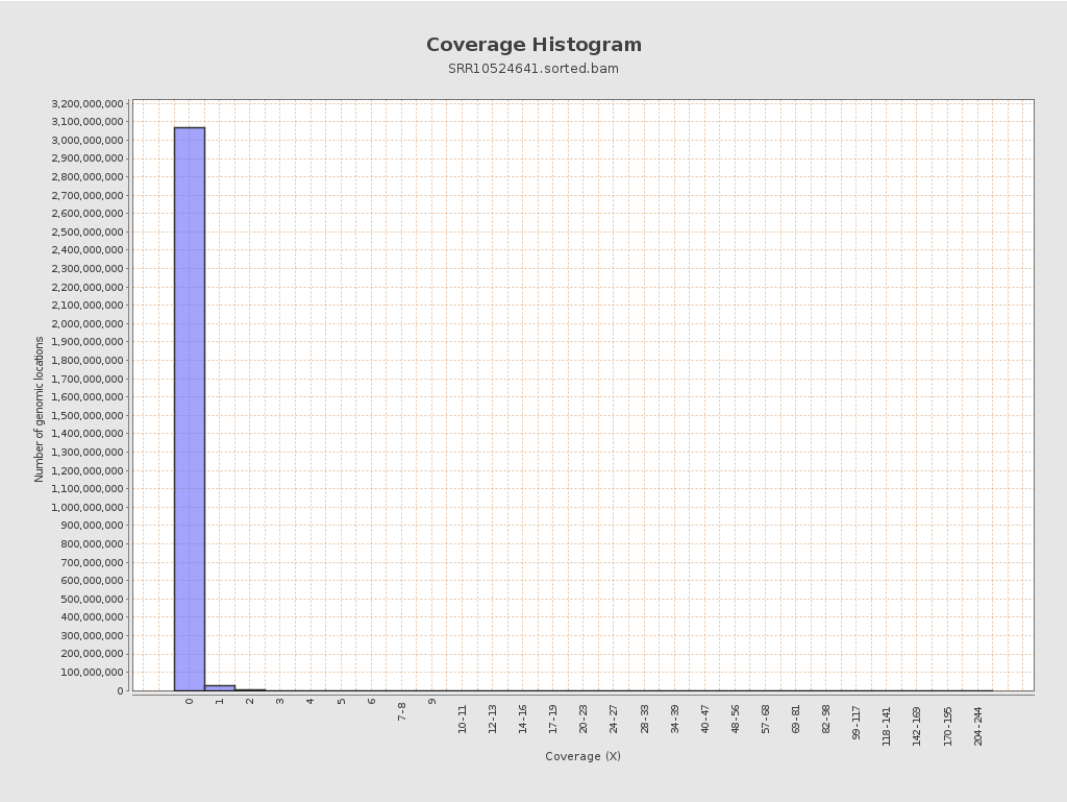
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	3186407	0.0128	0.2031
chr2	243199373	2871665	0.0118	0.1493
chr3	198022430	2019416	0.0102	0.1057
chr4	191154276	1467728	0.0077	0.1008
chr5	180915260	1995899	0.011	0.1097
chr6	171115067	2100978	0.0123	0.1192
chr7	159138663	1951776	0.0123	0.151

chr8	146364022	2867599	0.0196	0.1794
chr9	141213431	1177375	0.0083	0.1078
chr10	135534747	1425541	0.0105	0.1352
chr11	135006516	1607099	0.0119	0.125
chr12	133851895	1057666	0.0079	0.0953
chr13	115169878	764003	0.0066	0.0853
chr14	107349540	593625	0.0055	0.0795
chr15	102531392	841697	0.0082	0.0953
chr16	90354753	957057	0.0106	0.1107
chr17	81195210	722336	0.0089	0.0996
chr18	78077248	842765	0.0108	0.151
chr19	59128983	673509	0.0114	0.1622
chr20	63025520	608179	0.0096	0.1047
chr21	48129895	301940	0.0063	0.0917
chr22	51304566	584837	0.0114	0.1118
chrMT	16571	1510	0.0911	0.3168
chrX	155270560	1480793	0.0095	0.1066
chrY	59373566	94960	0.0016	0.0669

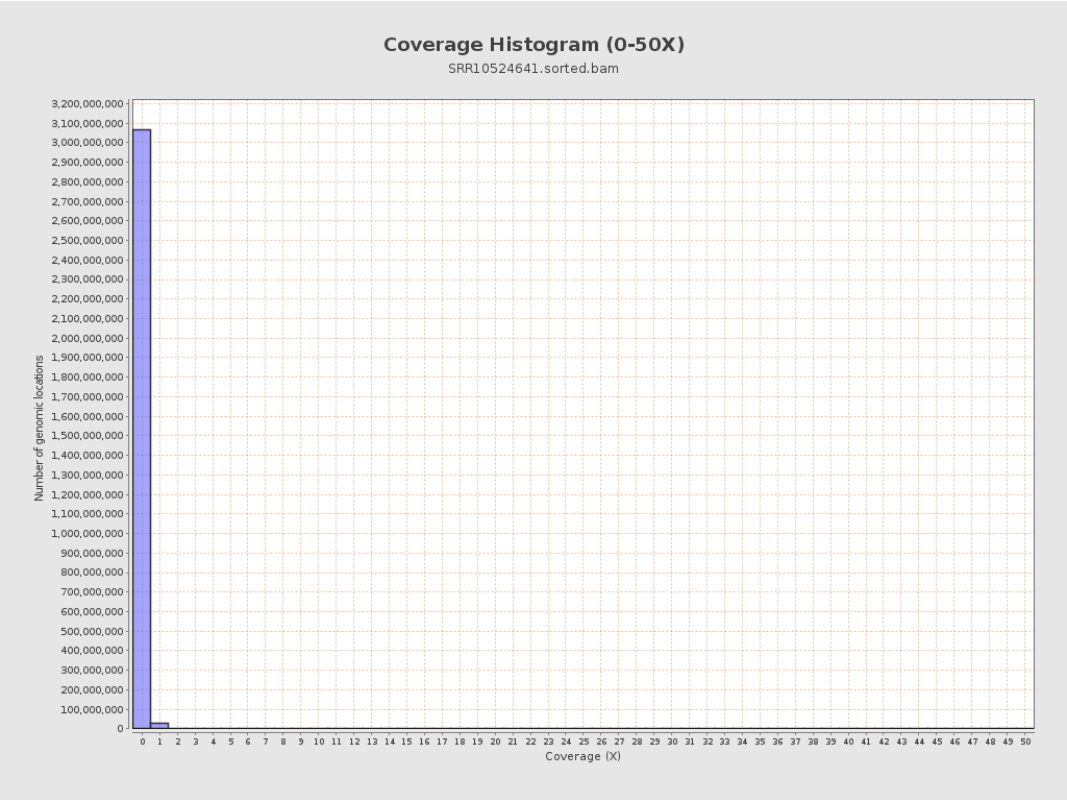
3. Results : Coverage across reference



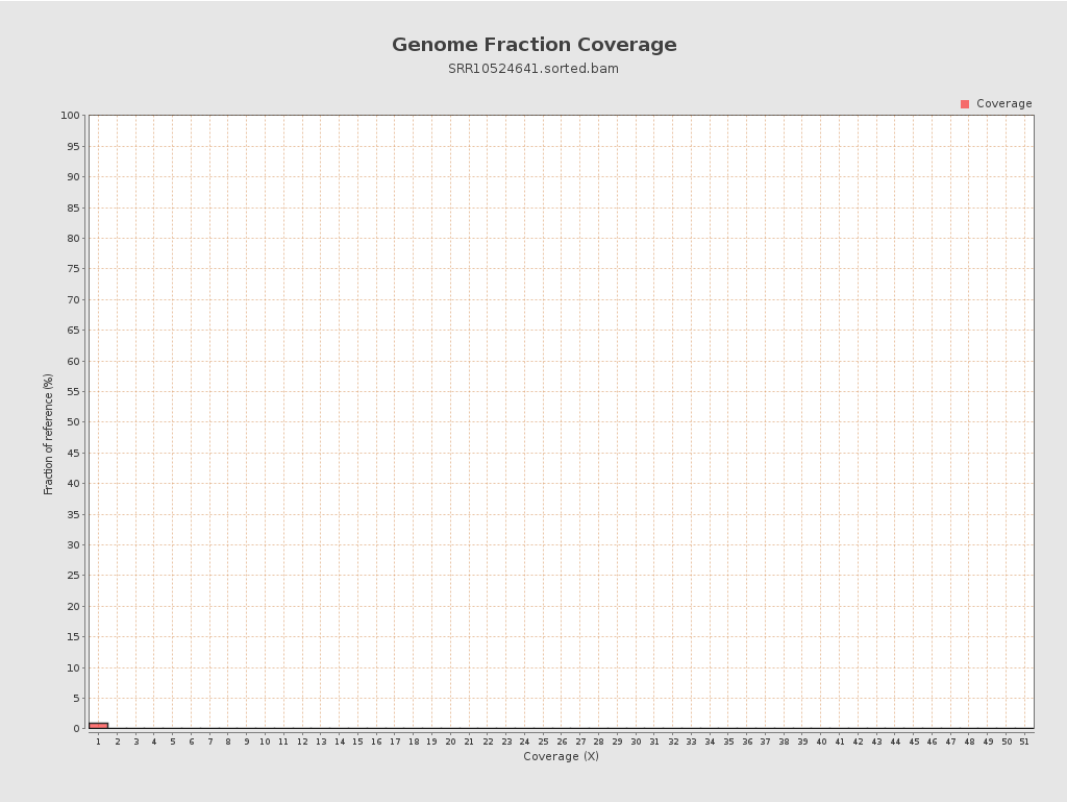
4. Results : Coverage Histogram



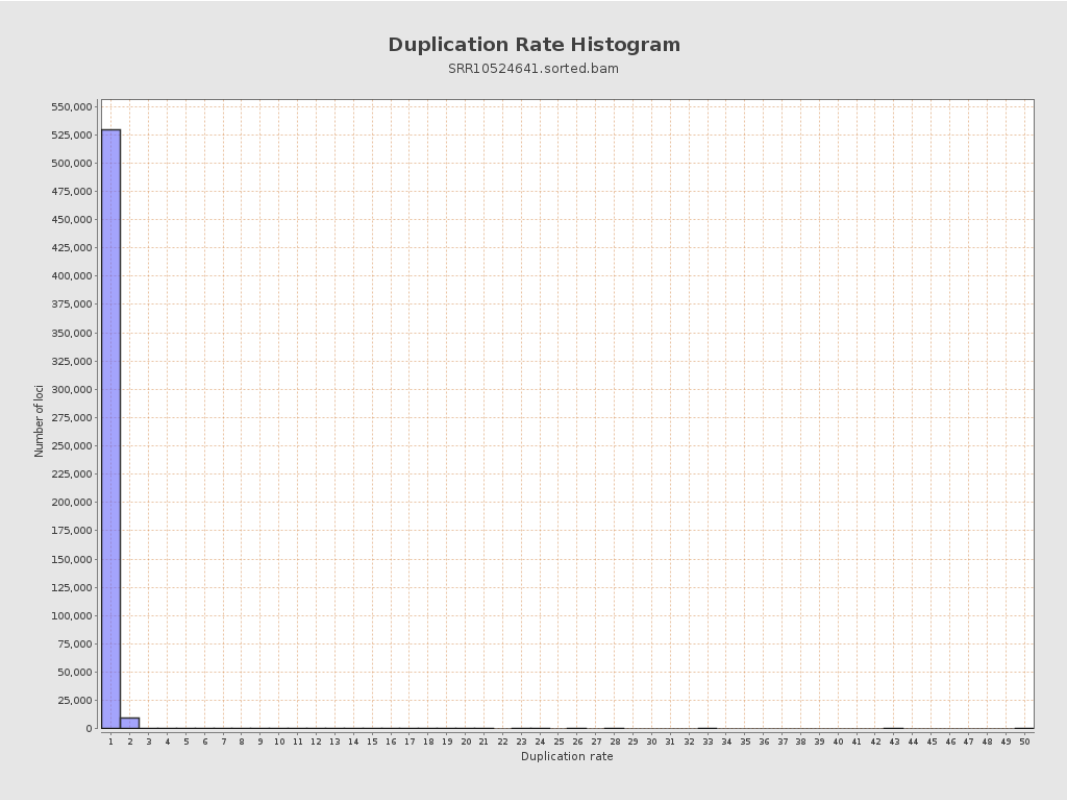
5. Results : Coverage Histogram (0-50X)



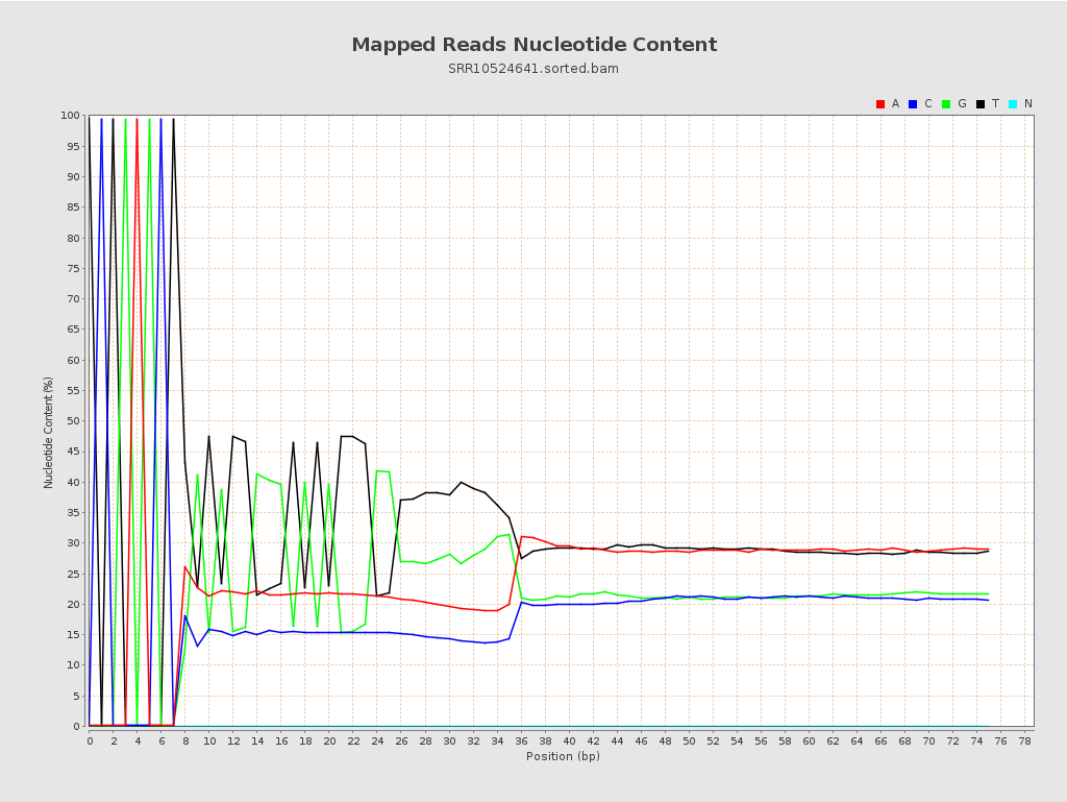
6. Results : Genome Fraction Coverage



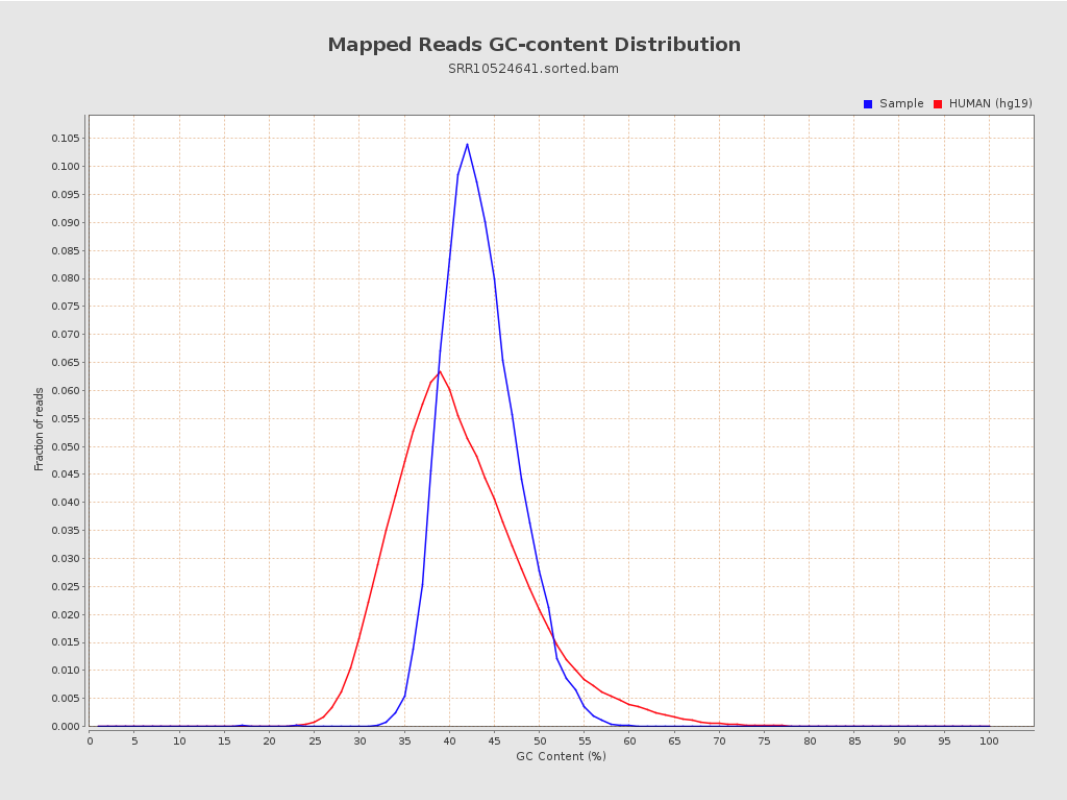
7. Results : Duplication Rate Histogram



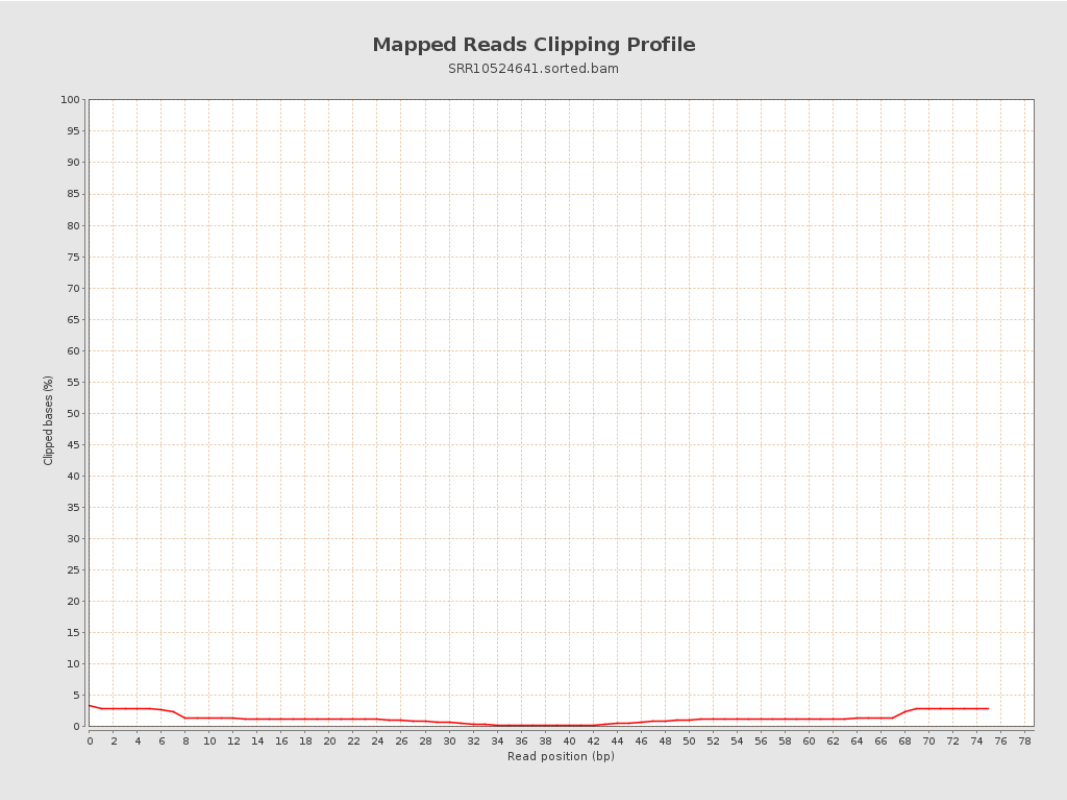
8. Results : Mapped Reads Nucleotide Content



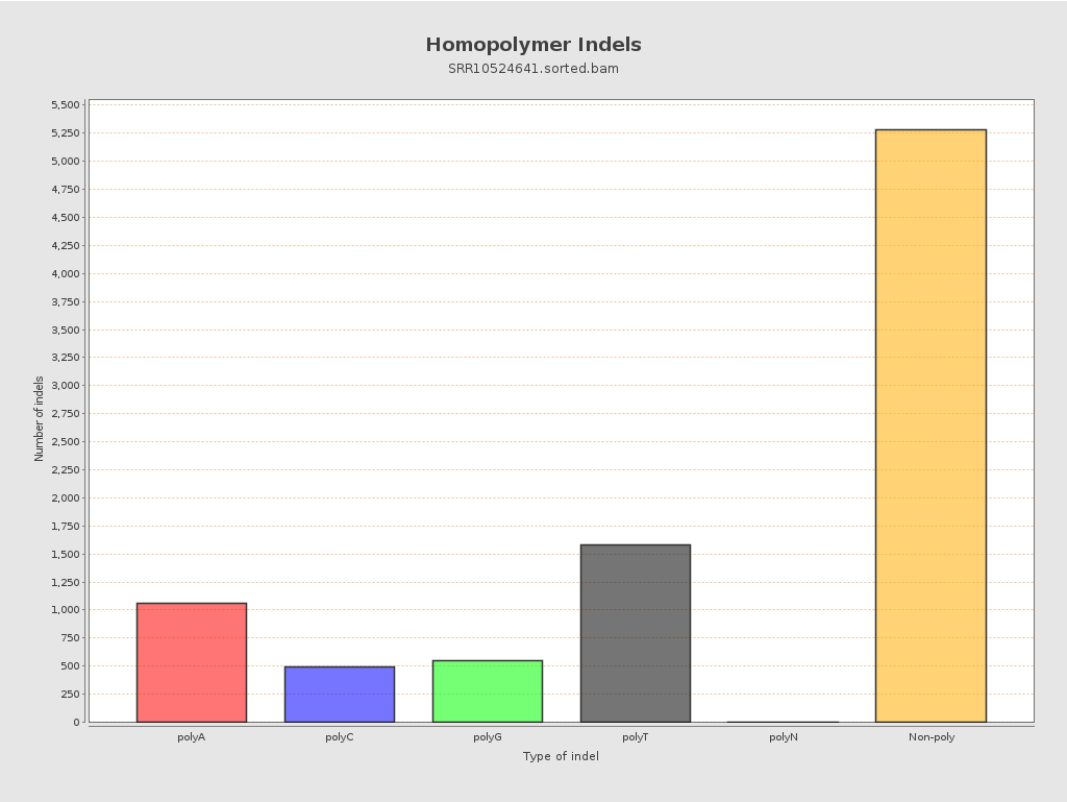
9. Results : Mapped Reads GC-content Distribution



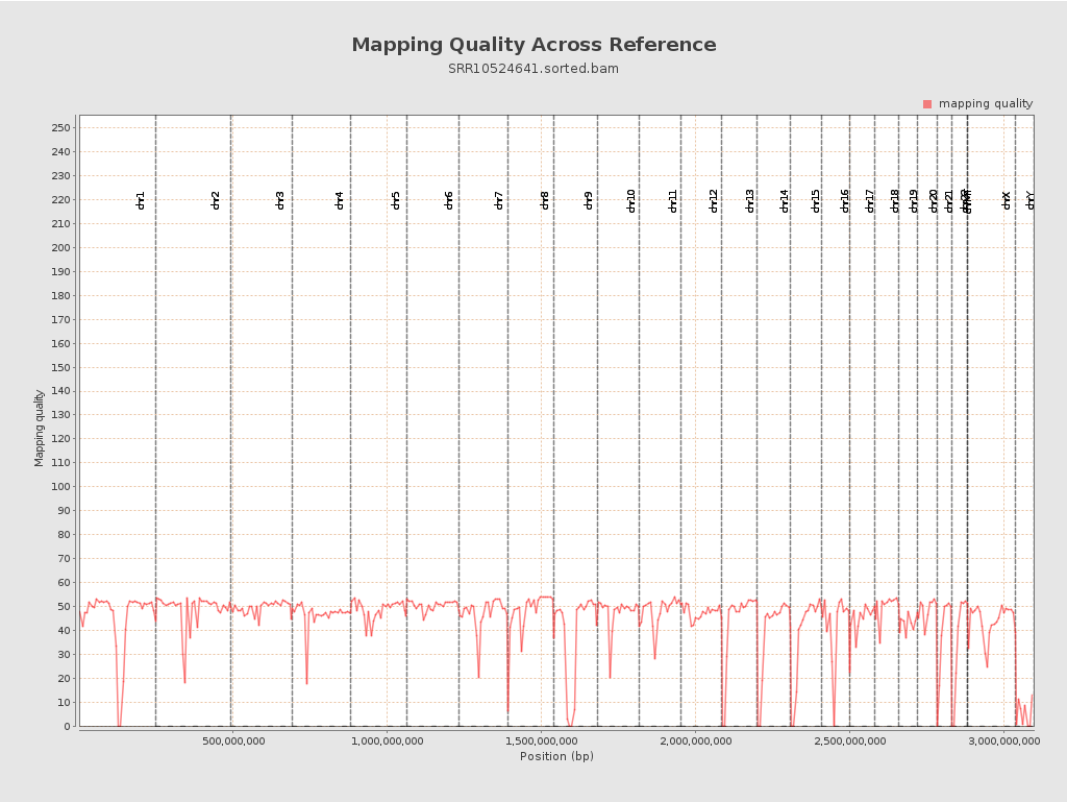
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram