Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 09:27:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524530.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_SRR10524530 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524530.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 09:27:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524530.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,085,077
Mapped reads	996,708 / 91.86%
Unmapped reads	88,369 / 8.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,403 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	42,445 / 3.91%
Duplication rate	3.34%
Clipped reads	998,056 / 91.98%

2.2. ACGT Content

Number/percentage of A's	14,015,089 / 24.07%
Number/percentage of C's	10,923,175 / 18.76%
Number/percentage of T's	18,734,409 / 32.18%
Number/percentage of G's	14,542,805 / 24.98%
Number/percentage of N's	837 / 0%
GC Percentage	43.74%

2.3. Coverage

Mean	0.0188

Standard Deviation	0.2011

2.4. Mapping Quality

Mean Mapping Quality	45.64

2.5. Mismatches and indels

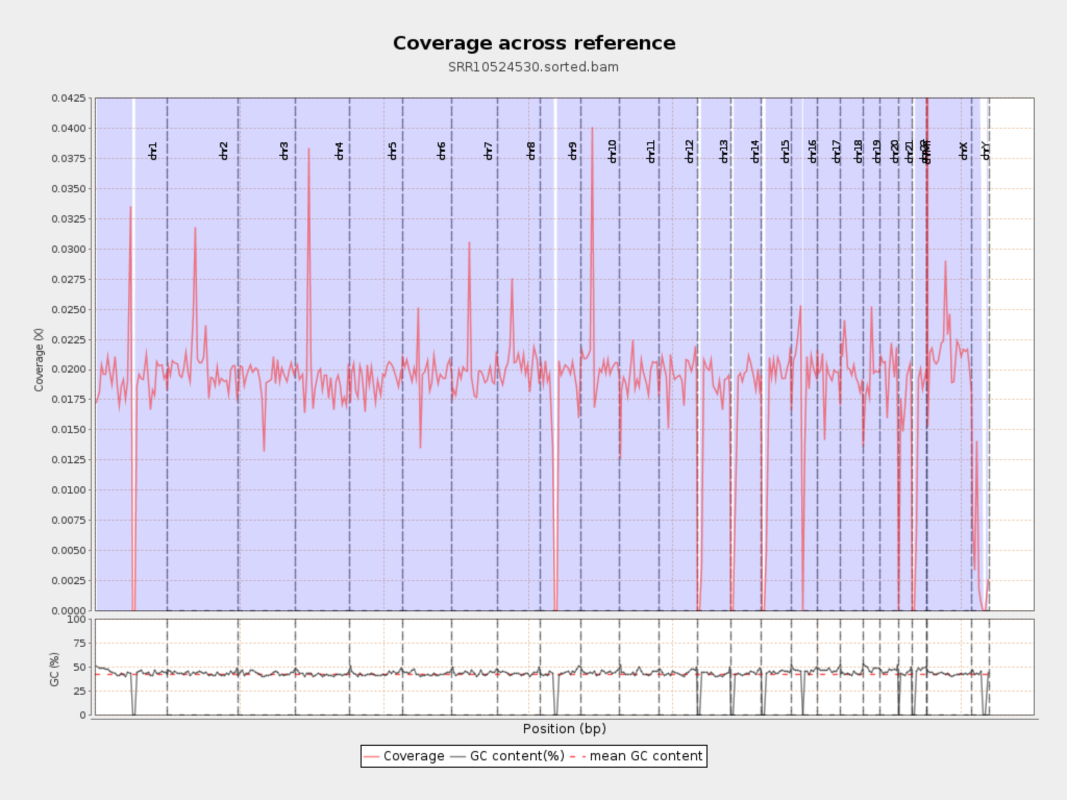
General error rate	0.53%
Mismatches	300,768
Insertions	3,829
Mapped reads with at least one insertion	0.38%
Deletions	10,921
Mapped reads with at least one deletion	1.09%
Homopolymer indels	44.09%

2.6. Chromosome stats

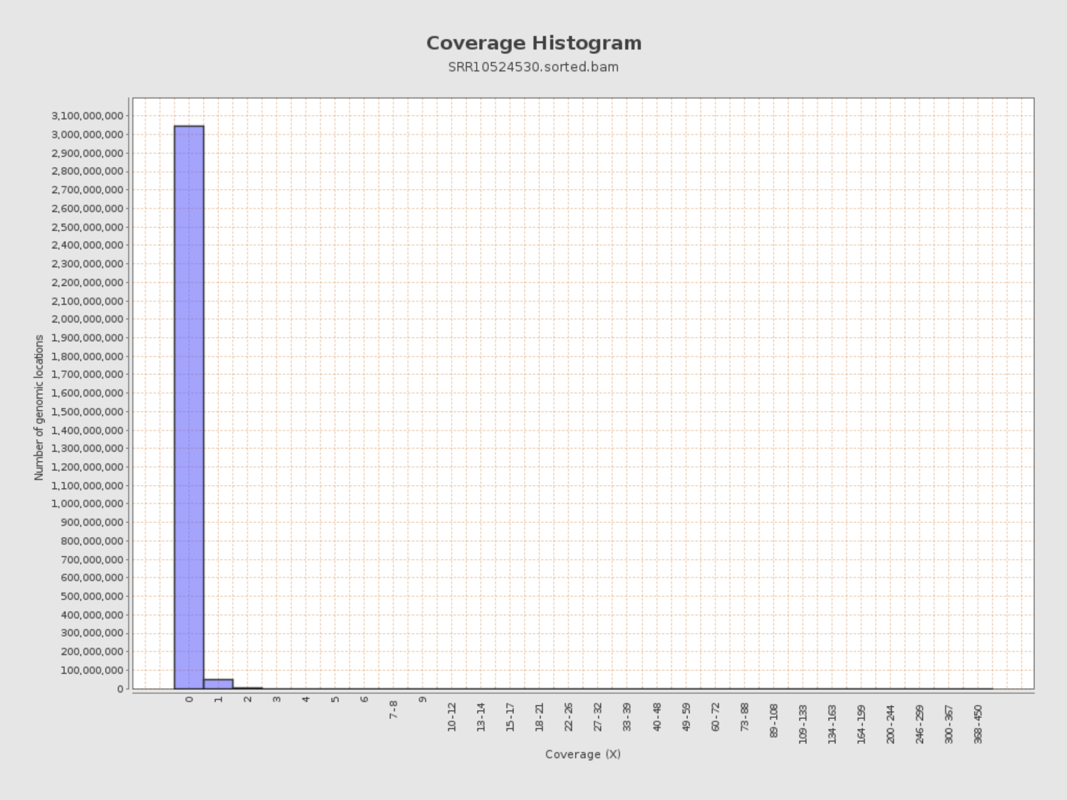
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4593357	0.0184	0.3488
chr2	243199373	4958107	0.0204	0.2292
chr3	198022430	3833284	0.0194	0.1513
chr4	191154276	3741983	0.0196	0.173
chr5	180915260	3483477	0.0193	0.1507
chr6	171115067	3385553	0.0198	0.168
chr7	159138663	3155359	0.0198	0.2334

chr8	146364022	3021083	0.0206	0.212
chr9	141213431	2416750	0.0171	0.1715
chr10	135534747	2886690	0.0213	0.2133
chr11	135006516	2621438	0.0194	0.1825
chr12	133851895	2635637	0.0197	0.1538
chr13	115169878	1846558	0.016	0.1373
chr14	107349540	1745349	0.0163	0.1411
chr15	102531392	1657958	0.0162	0.1379
chr16	90354753	1667164	0.0185	0.1564
chr17	81195210	1562173	0.0192	0.1563
chr18	78077248	1579640	0.0202	0.2931
chr19	59128983	1154135	0.0195	0.2441
chr20	63025520	1259471	0.02	0.1562
chr21	48129895	782017	0.0162	0.1606
chr22	51304566	686879	0.0134	0.1265
chrMT	16571	7373	0.4449	0.7538
chrX	155270560	3341301	0.0215	0.1681
chrY	59373566	211839	0.0036	0.1312

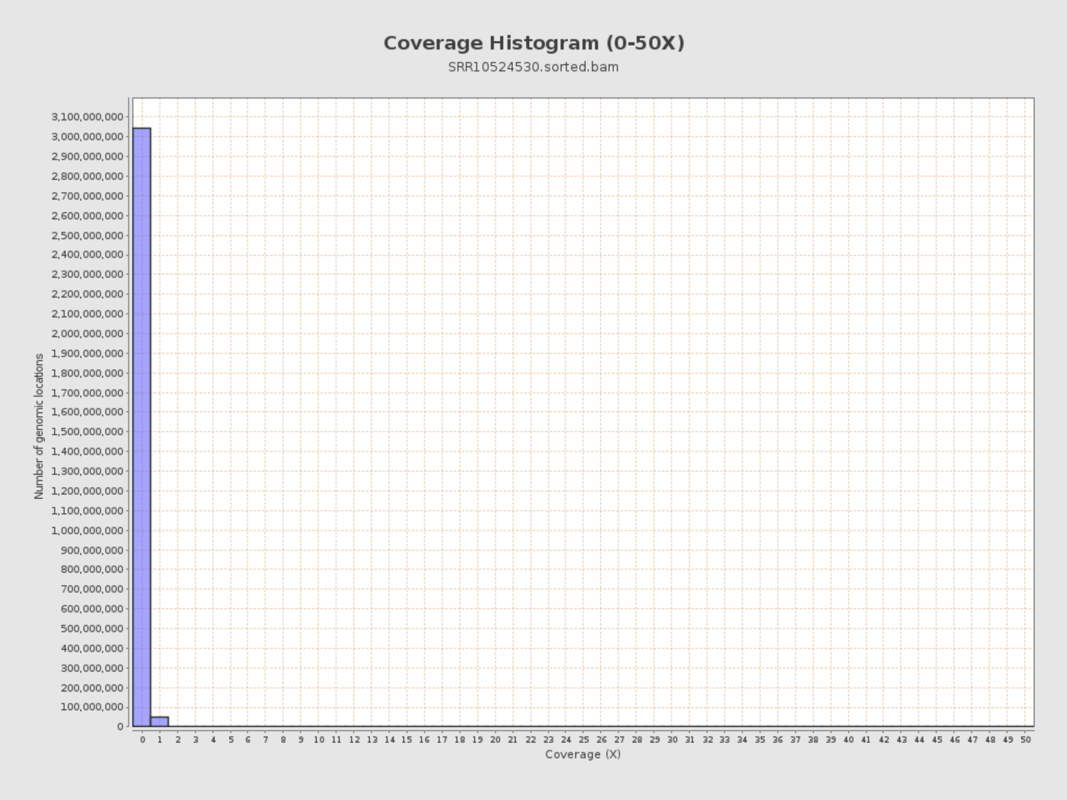
3. Results : Coverage across reference



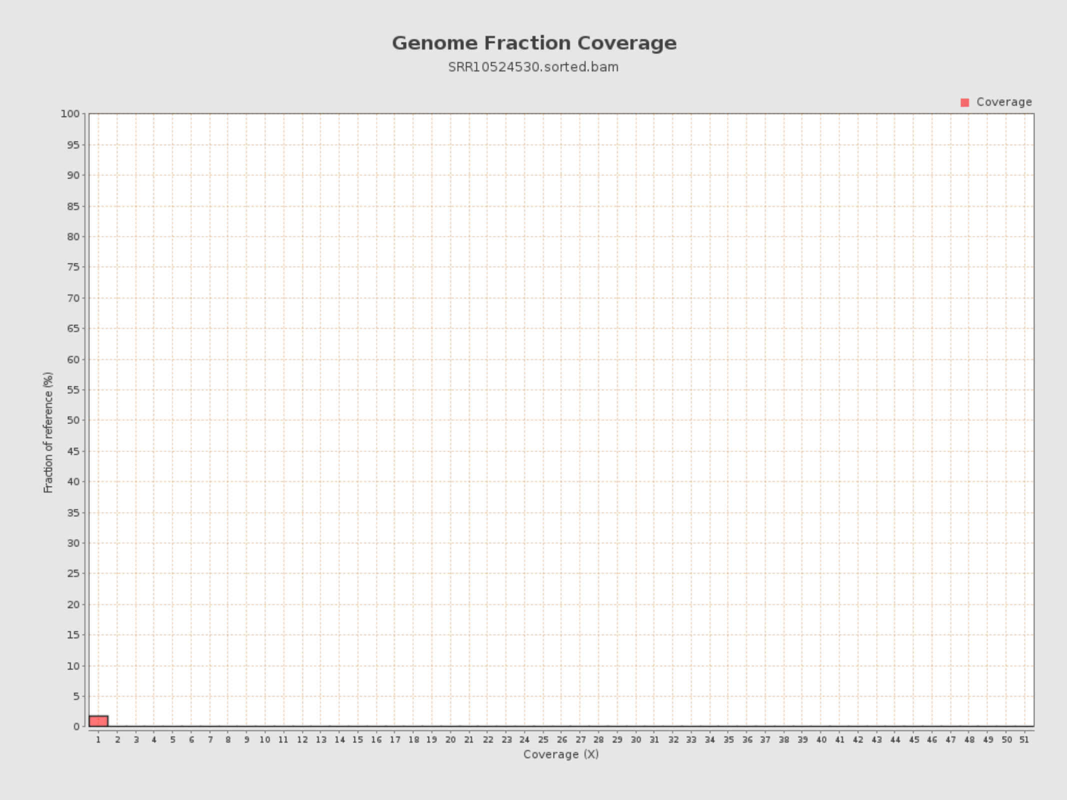
4. Results : Coverage Histogram



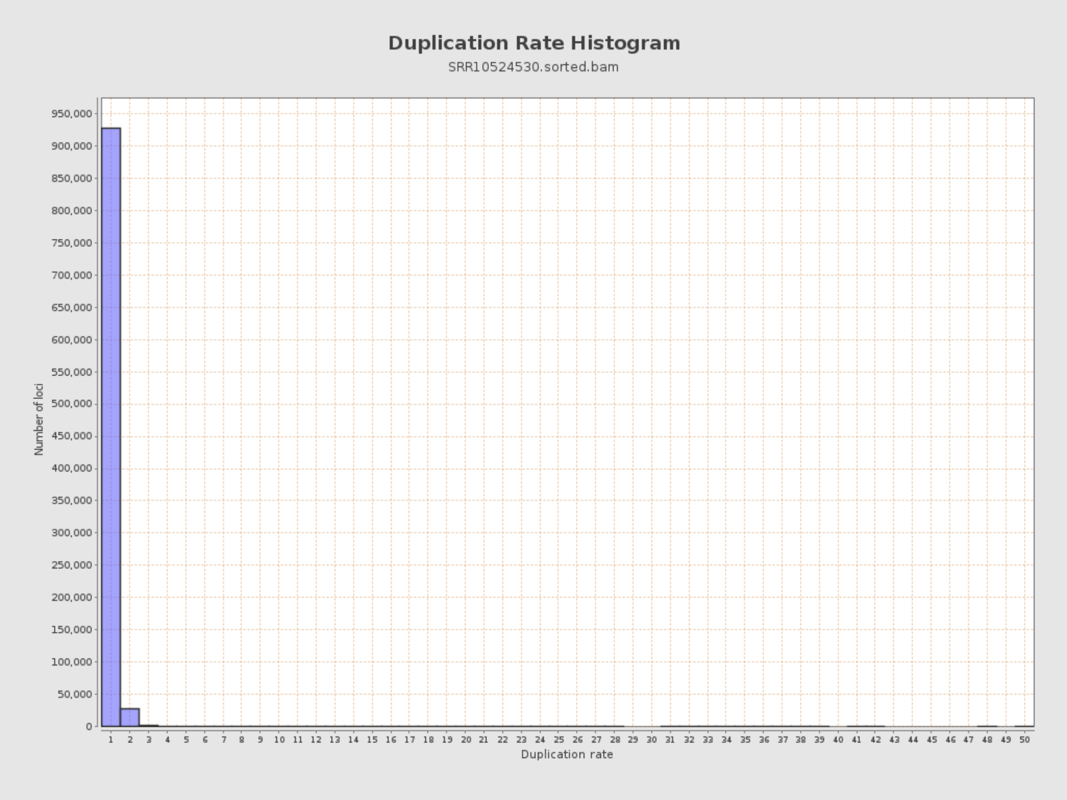
5. Results : Coverage Histogram (0-50X)



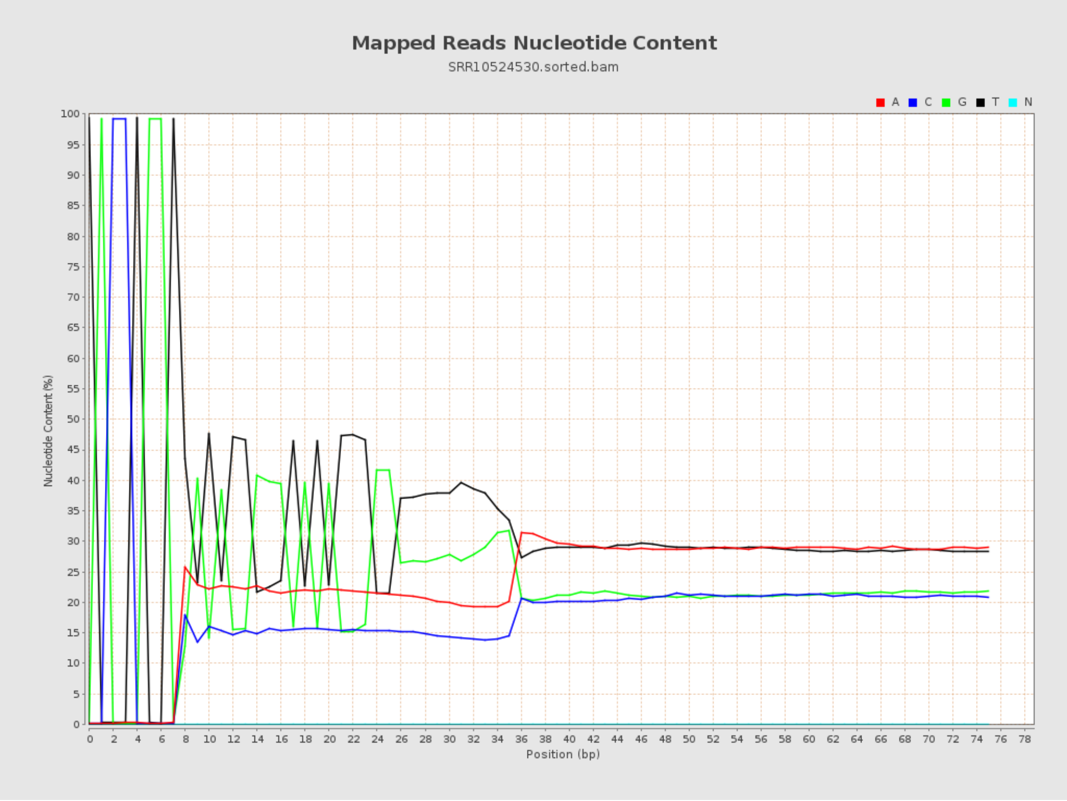
6. Results : Genome Fraction Coverage



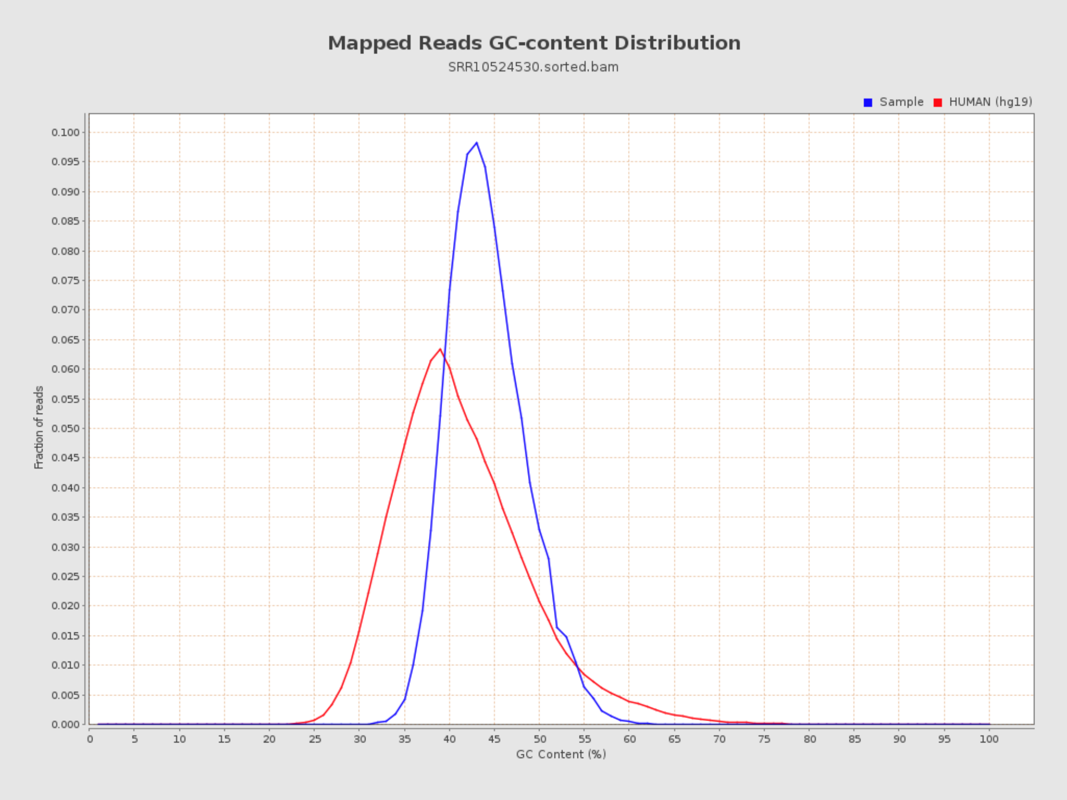
7. Results : Duplication Rate Histogram



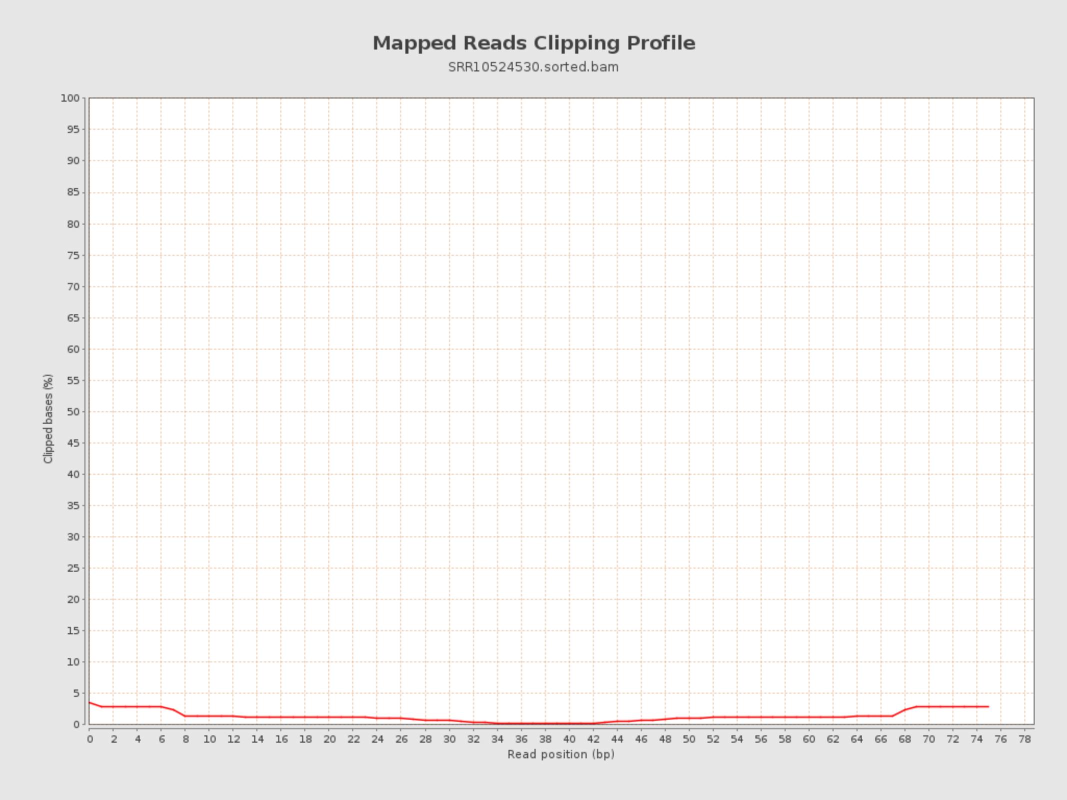
8. Results : Mapped Reads Nucleotide Content



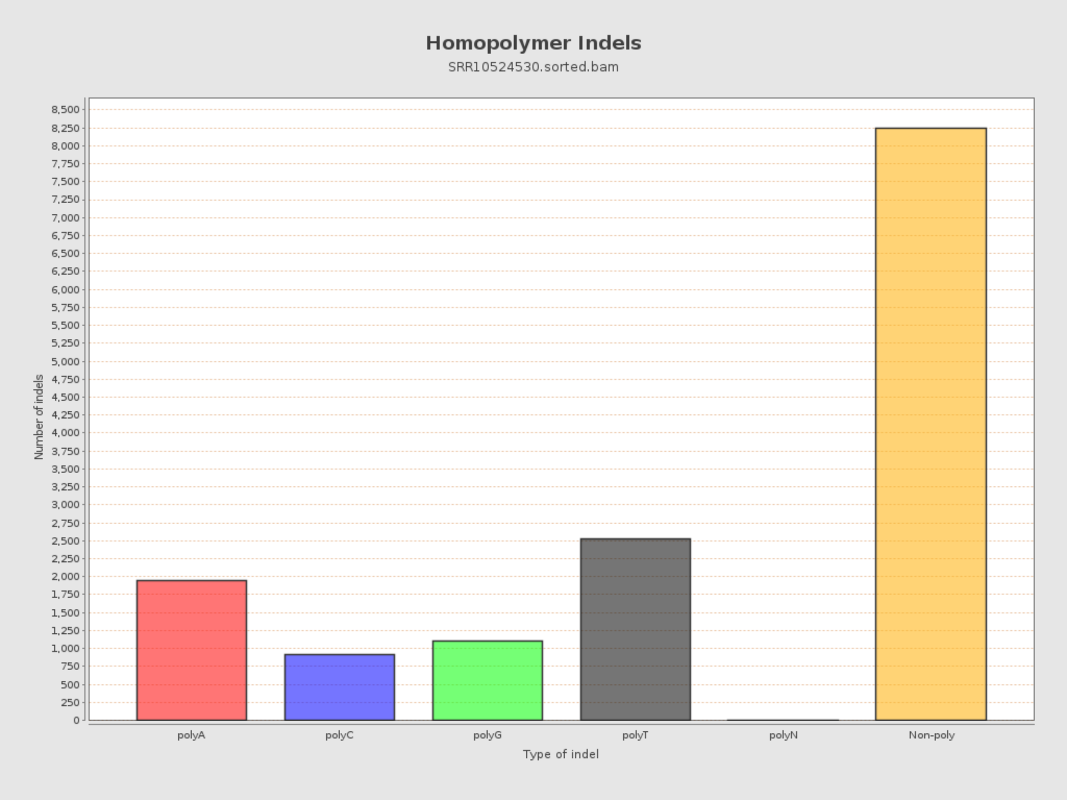
9. Results : Mapped Reads GC-content Distribution



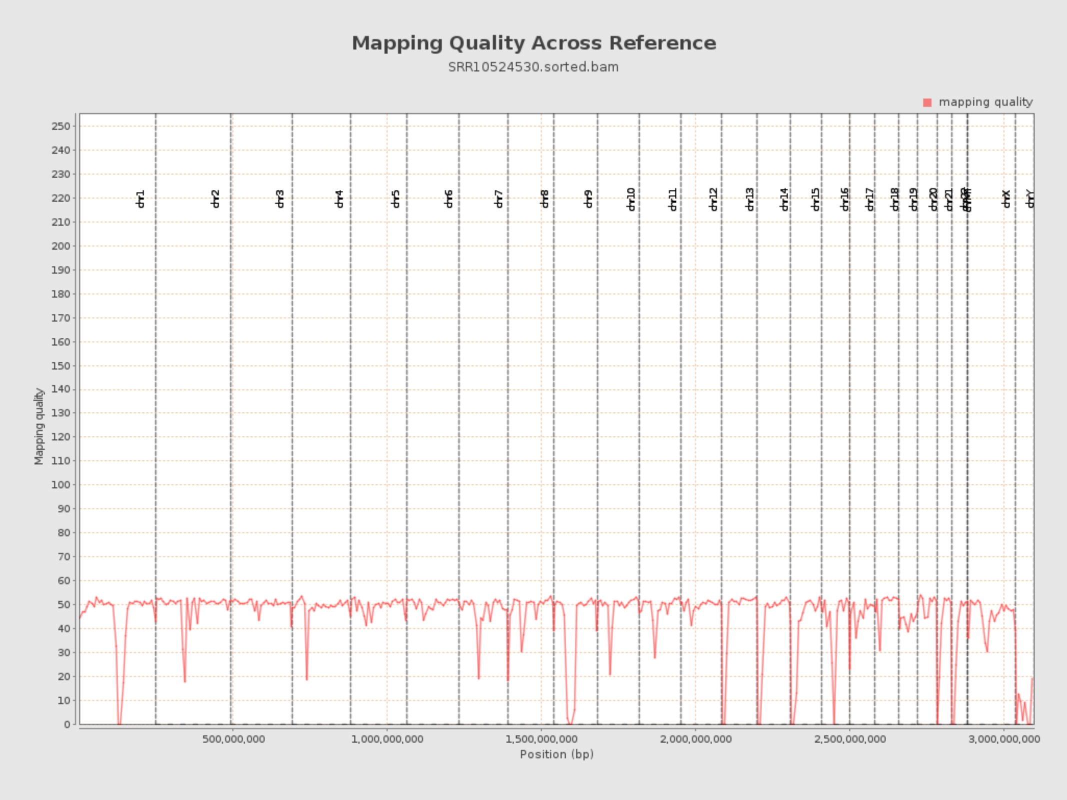
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram