Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 01:07:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524376.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_SRR10524376 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524376.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 01:07:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524376.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,091,096
Mapped reads	1,005,098 / 92.12%
Unmapped reads	85,998 / 7.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,854 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	27,286 / 2.5%
Duplication rate	1.94%
Clipped reads	1,006,241 / 92.22%

2.2. ACGT Content

Number/percentage of A's	15,210,197 / 25.85%
Number/percentage of C's	11,473,228 / 19.5%
Number/percentage of T's	18,332,396 / 31.15%
Number/percentage of G's	13,826,721 / 23.49%
Number/percentage of N's	7,567 / 0.01%
GC Percentage	42.99%

2.3. Coverage

Mean	0.019

Standard Deviation	0.2065

2.4. Mapping Quality

Mean Mapping Quality	45.76

2.5. Mismatches and indels

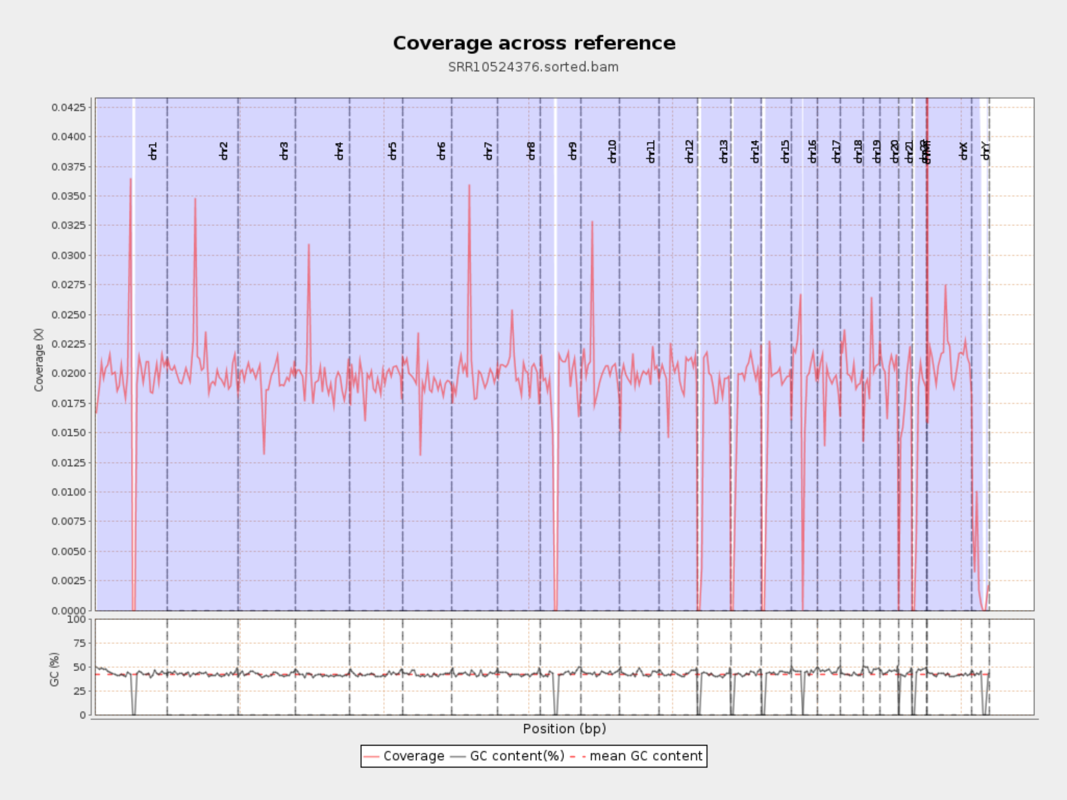
General error rate	0.5%
Mismatches	286,256
Insertions	3,990
Mapped reads with at least one insertion	0.39%
Deletions	10,507
Mapped reads with at least one deletion	1.04%
Homopolymer indels	42.92%

2.6. Chromosome stats

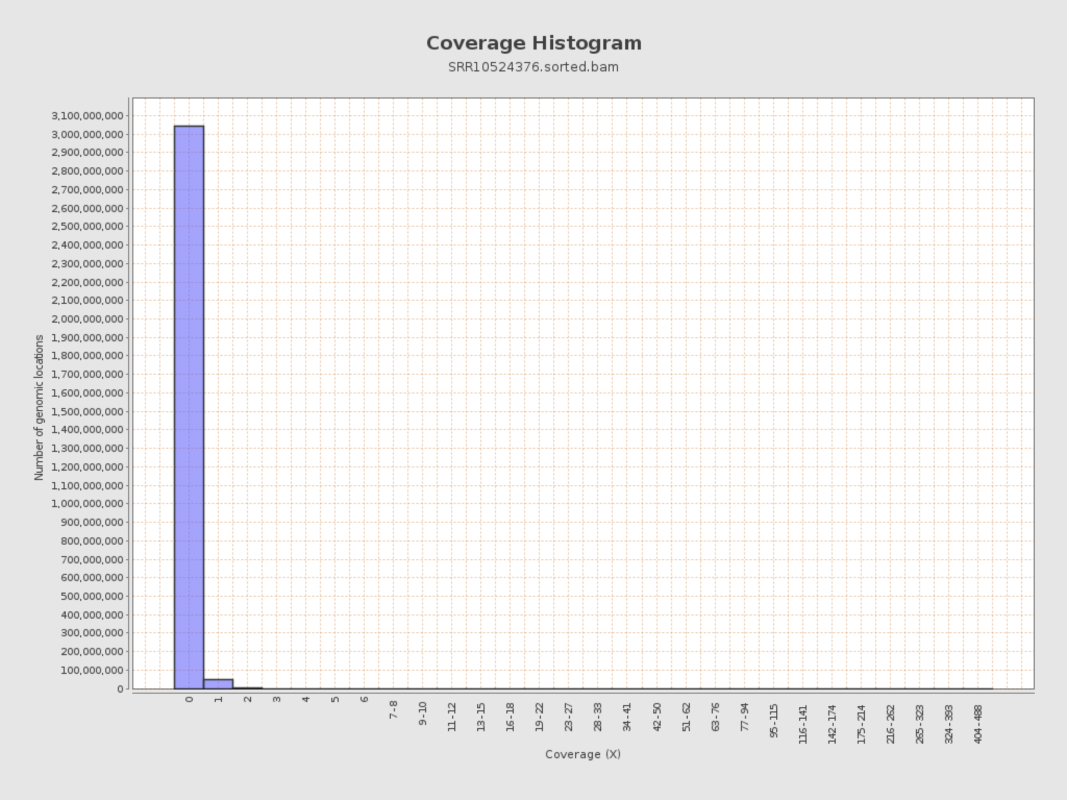
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4779248	0.0192	0.3944
chr2	243199373	5009609	0.0206	0.2283
chr3	198022430	3873957	0.0196	0.1468
chr4	191154276	3785779	0.0198	0.1593
chr5	180915260	3541018	0.0196	0.1475
chr6	171115067	3315573	0.0194	0.1586
chr7	159138663	3251278	0.0204	0.276

chr8	146364022	2979767	0.0204	0.19
chr9	141213431	2485996	0.0176	0.1717
chr10	135534747	2808161	0.0207	0.1872
chr11	135006516	2700126	0.02	0.1844
chr12	133851895	2689009	0.0201	0.153
chr13	115169878	1868685	0.0162	0.1339
chr14	107349540	1798040	0.0167	0.1408
chr15	102531392	1689253	0.0165	0.1348
chr16	90354753	1715222	0.019	0.1515
chr17	81195210	1557364	0.0192	0.1547
chr18	78077248	1592823	0.0204	0.2953
chr19	59128983	1207280	0.0204	0.2671
chr20	63025520	1264541	0.0201	0.1531
chr21	48129895	785832	0.0163	0.1441
chr22	51304566	687641	0.0134	0.1218
chrMT	16571	5239	0.3162	0.5713
chrX	155270560	3299720	0.0213	0.1673
chrY	59373566	175629	0.003	0.0876

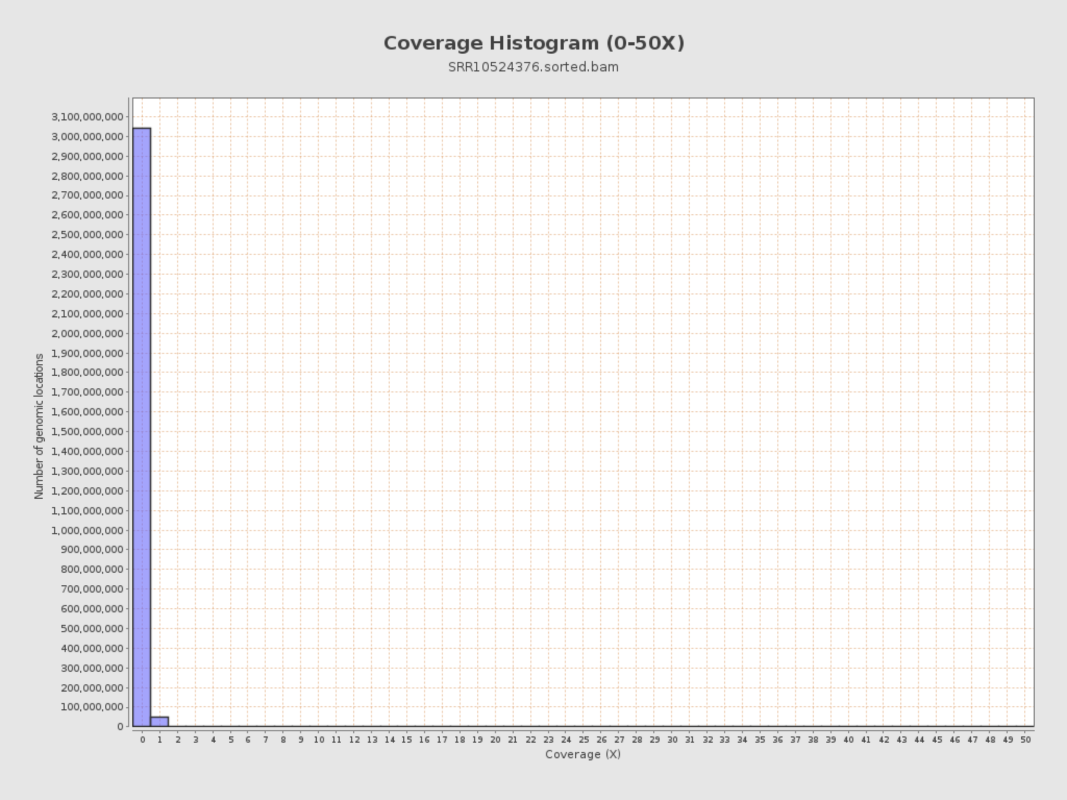
3. Results : Coverage across reference



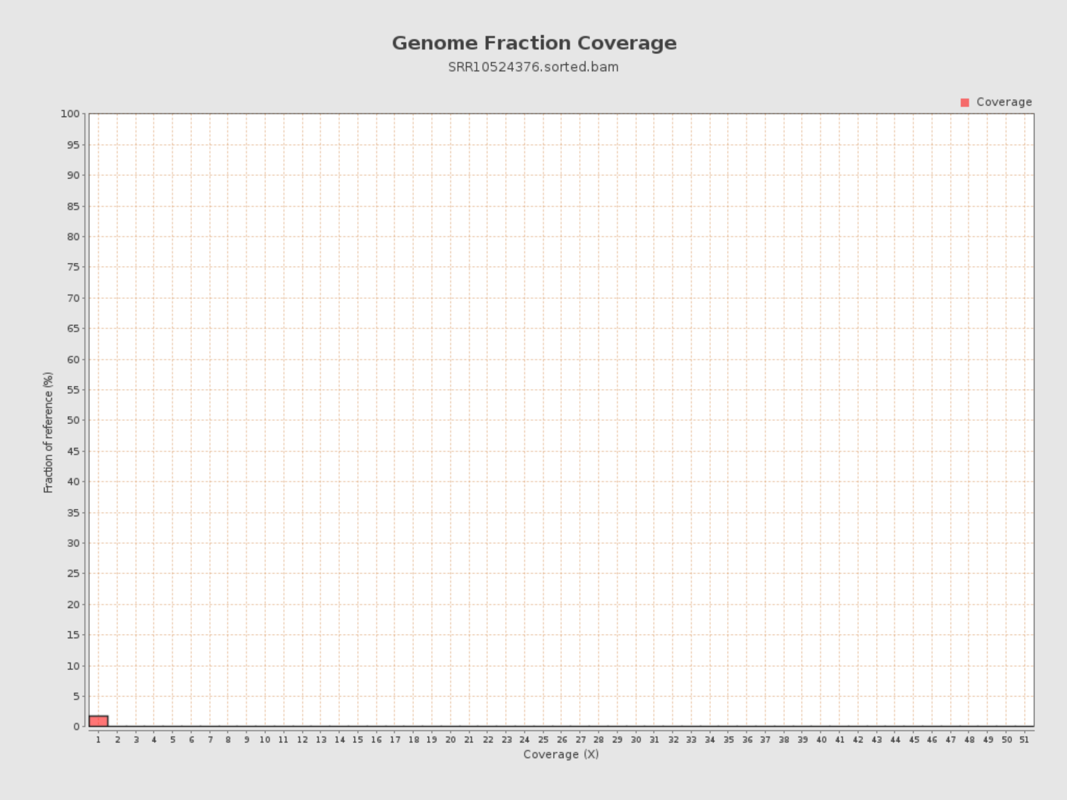
4. Results : Coverage Histogram



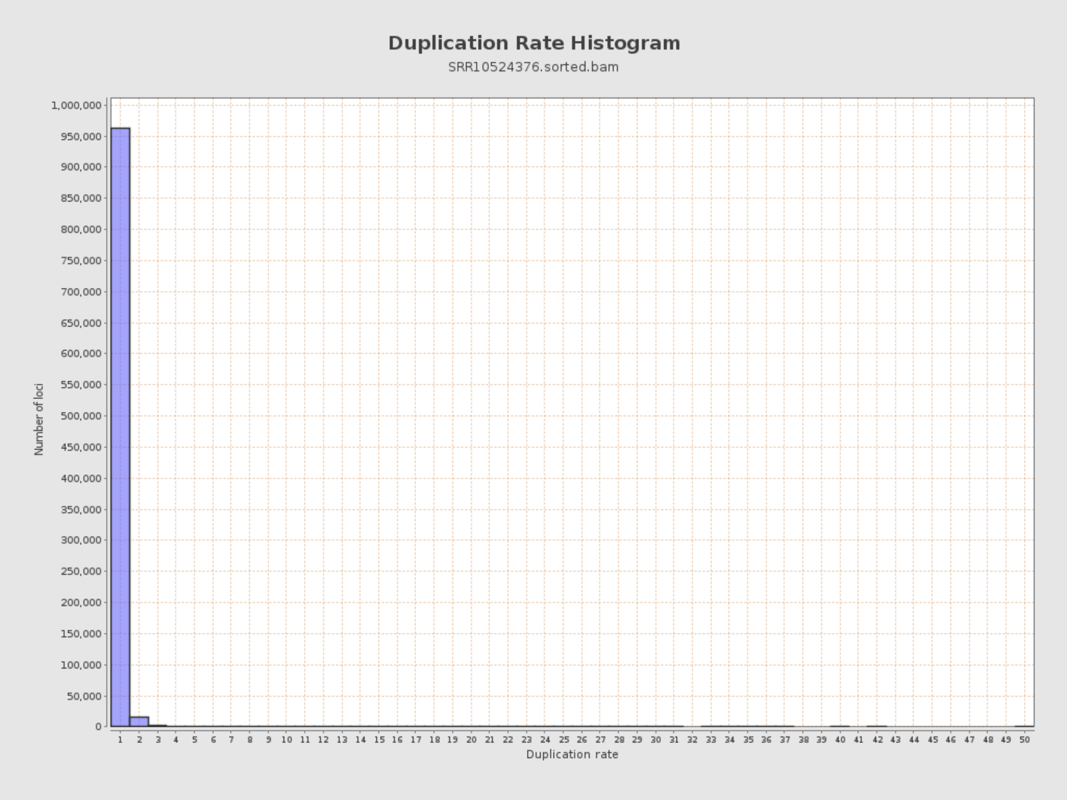
5. Results : Coverage Histogram (0-50X)



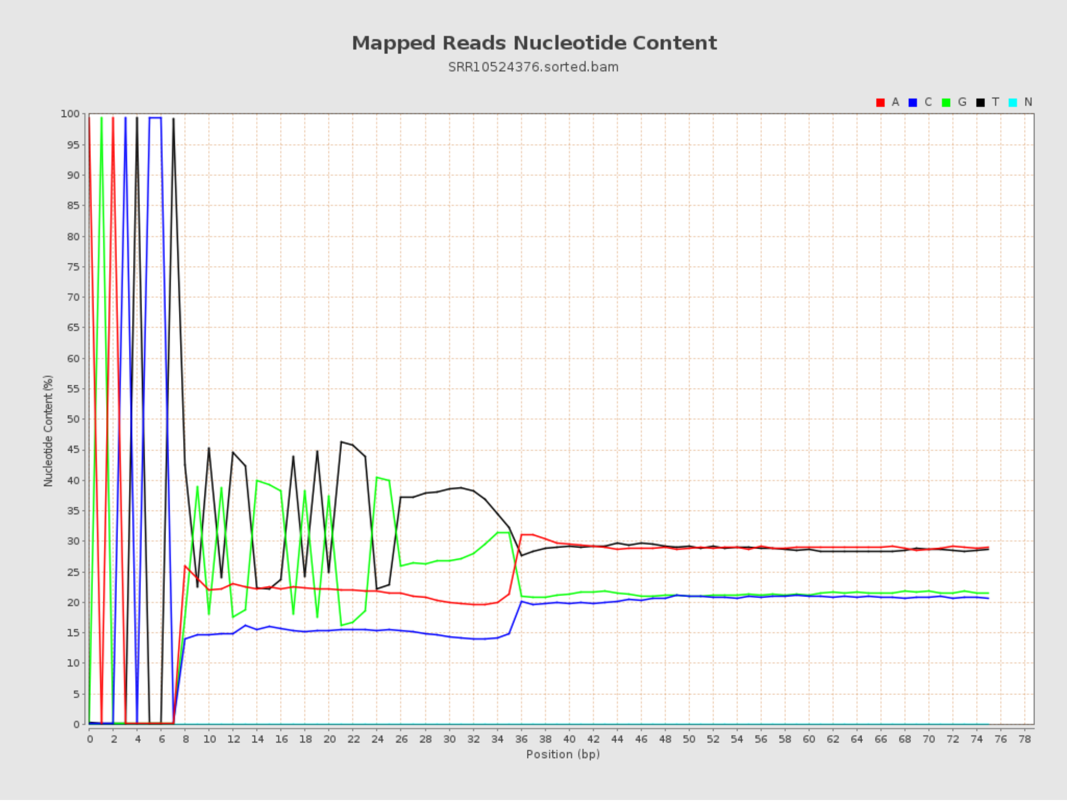
6. Results : Genome Fraction Coverage



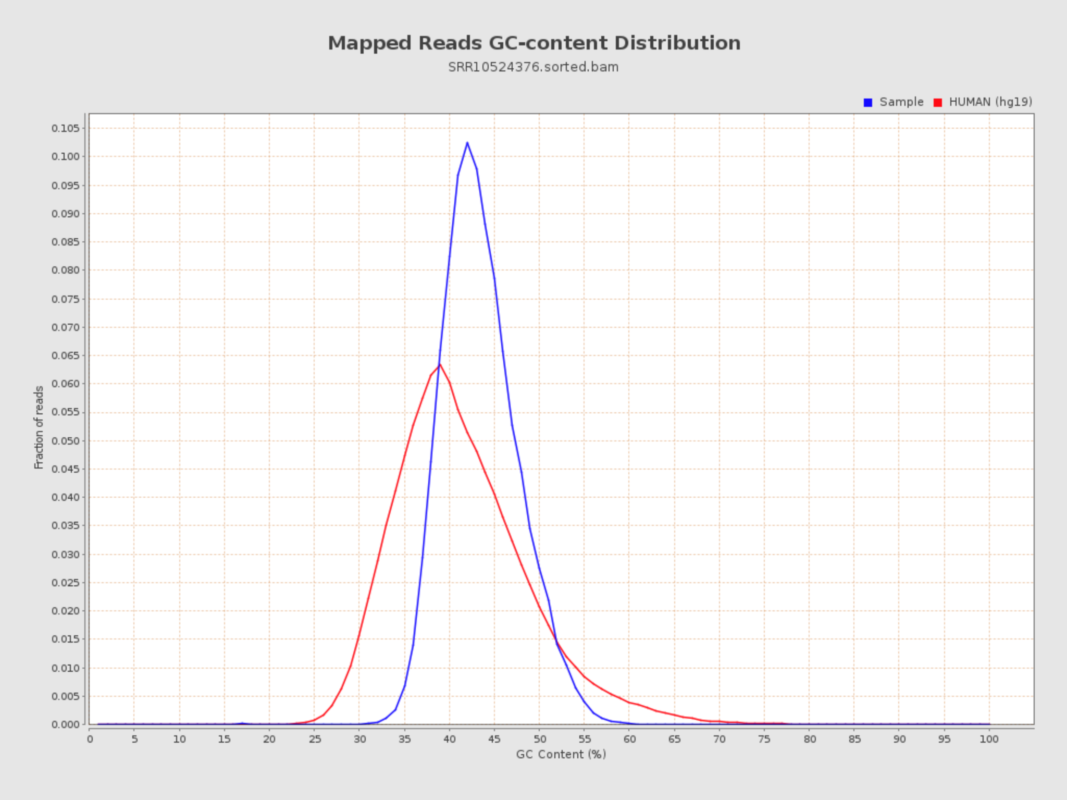
7. Results : Duplication Rate Histogram



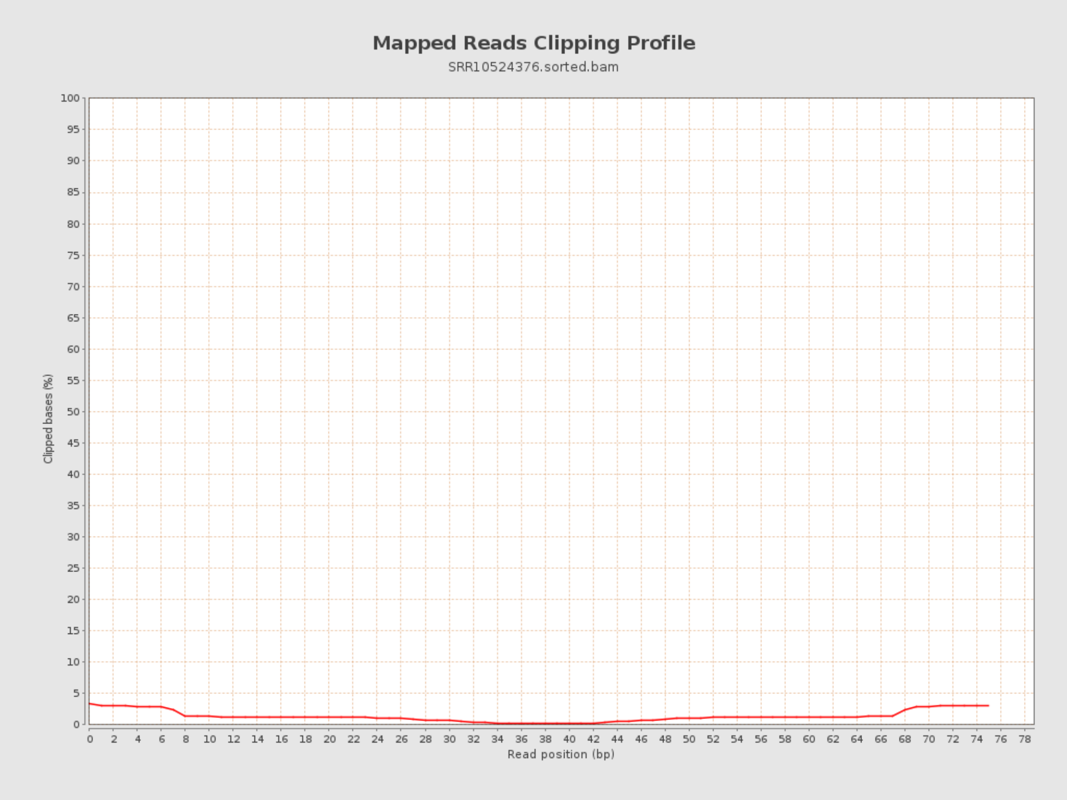
8. Results : Mapped Reads Nucleotide Content



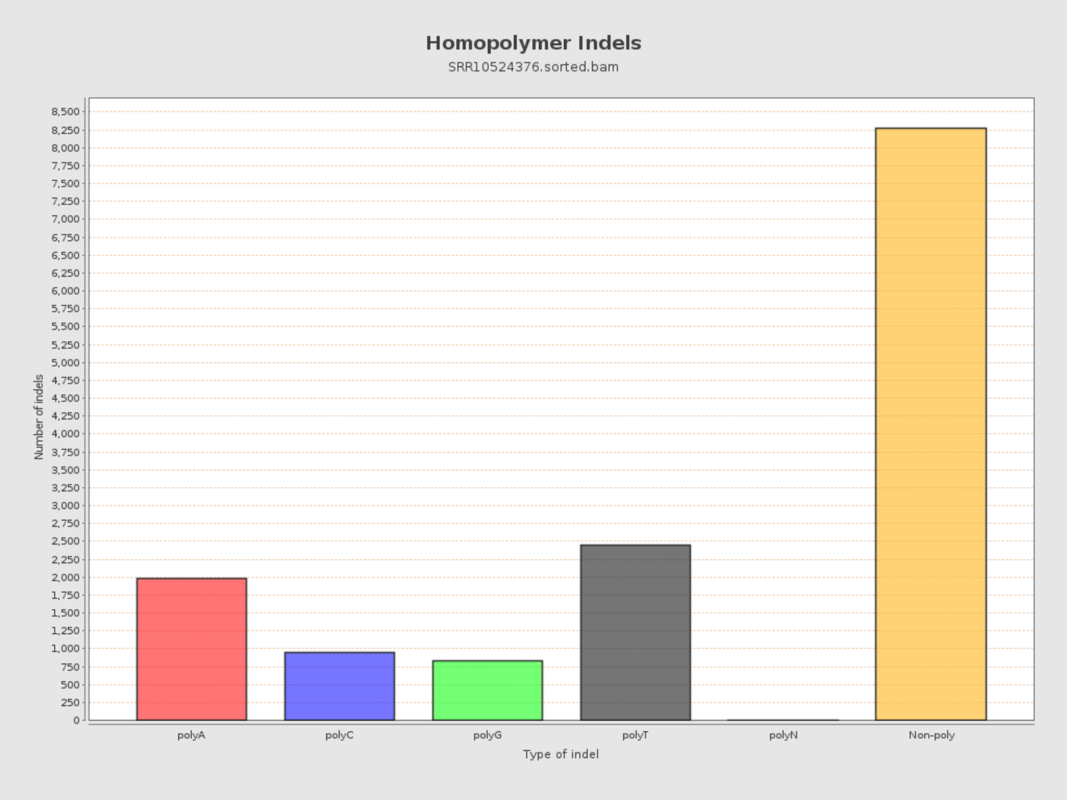
9. Results : Mapped Reads GC-content Distribution



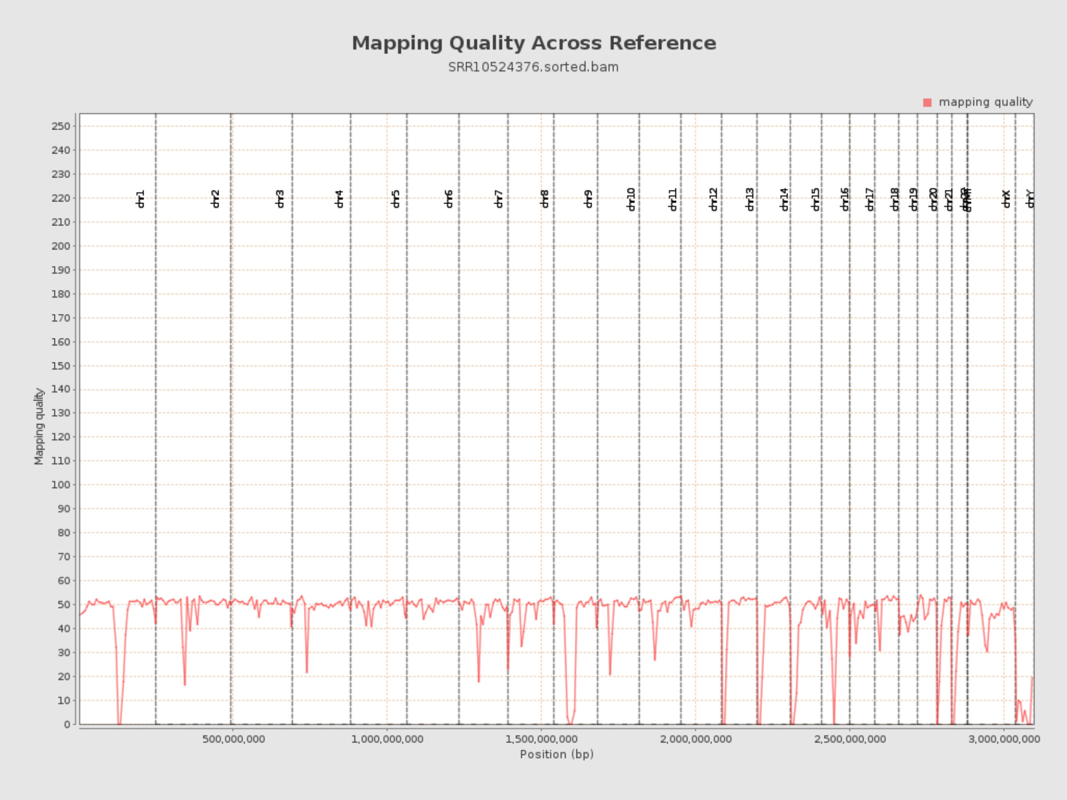
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram