Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 02:14:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524403.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_SRR10524403 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524403.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 02:14:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524403.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,058,464
Mapped reads	974,245 / 92.04%
Unmapped reads	84,219 / 7.96%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,655 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	24,167 / 2.28%
Duplication rate	1.73%
Clipped reads	974,140 / 92.03%

2.2. ACGT Content

Number/percentage of A's	15,374,612 / 26.87%
Number/percentage of C's	10,753,013 / 18.79%
Number/percentage of T's	17,245,605 / 30.13%
Number/percentage of G's	13,848,123 / 24.2%
Number/percentage of N's	7,536 / 0.01%
GC Percentage	42.99%

2.3. Coverage

Mean	0.0185

Standard Deviation	0.2033

2.4. Mapping Quality

Mean Mapping Quality	45.71

2.5. Mismatches and indels

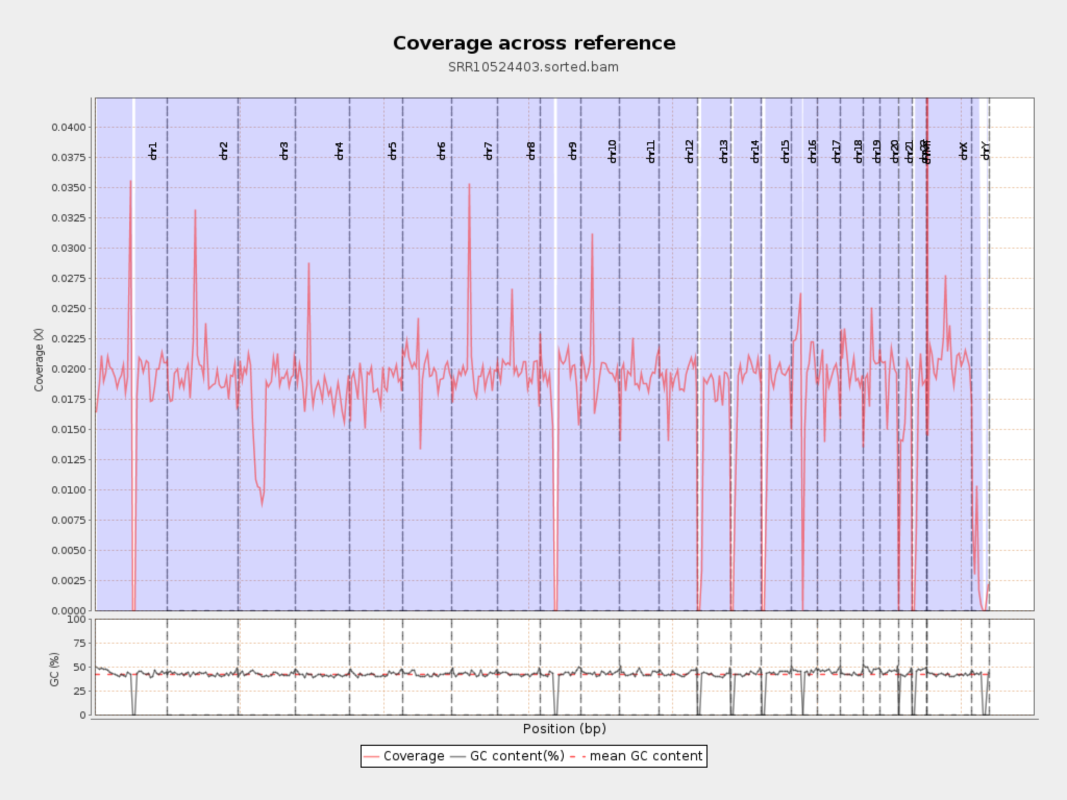
General error rate	0.5%
Mismatches	276,798
Insertions	4,888
Mapped reads with at least one insertion	0.5%
Deletions	10,394
Mapped reads with at least one deletion	1.06%
Homopolymer indels	41.81%

2.6. Chromosome stats

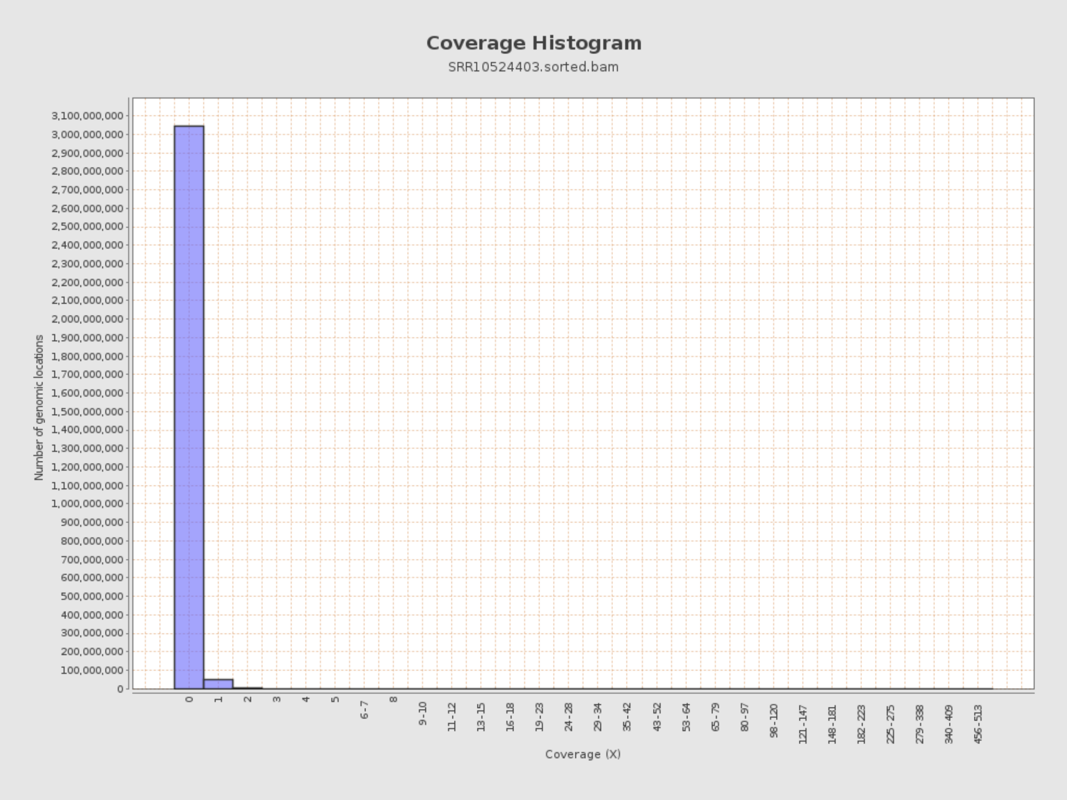
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4690781	0.0188	0.3861
chr2	243199373	4795302	0.0197	0.2189
chr3	198022430	3484636	0.0176	0.139
chr4	191154276	3555428	0.0186	0.1541
chr5	180915260	3423937	0.0189	0.1444
chr6	171115067	3423329	0.02	0.1628
chr7	159138663	3197125	0.0201	0.2801

chr8	146364022	2947881	0.0201	0.1901
chr9	141213431	2455998	0.0174	0.1732
chr10	135534747	2735358	0.0202	0.1861
chr11	135006516	2617232	0.0194	0.1857
chr12	133851895	2558894	0.0191	0.1472
chr13	115169878	1801305	0.0156	0.1316
chr14	107349540	1787845	0.0167	0.1424
chr15	102531392	1654997	0.0161	0.1334
chr16	90354753	1729119	0.0191	0.1512
chr17	81195210	1550853	0.0191	0.1542
chr18	78077248	1577879	0.0202	0.2797
chr19	59128983	1186564	0.0201	0.2689
chr20	63025520	1217893	0.0193	0.1493
chr21	48129895	737081	0.0153	0.1389
chr22	51304566	680004	0.0133	0.1203
chrMT	16571	10047	0.6063	0.8278
chrX	155270560	3252291	0.0209	0.1654
chrY	59373566	173577	0.0029	0.0915

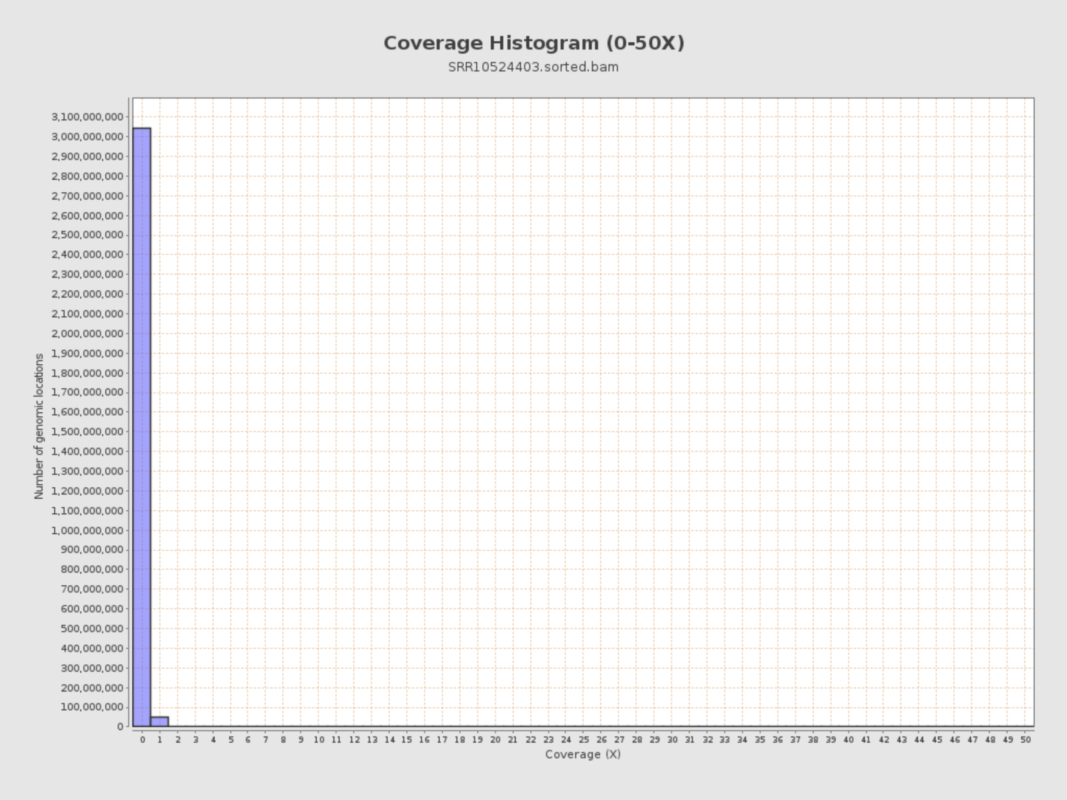
3. Results : Coverage across reference



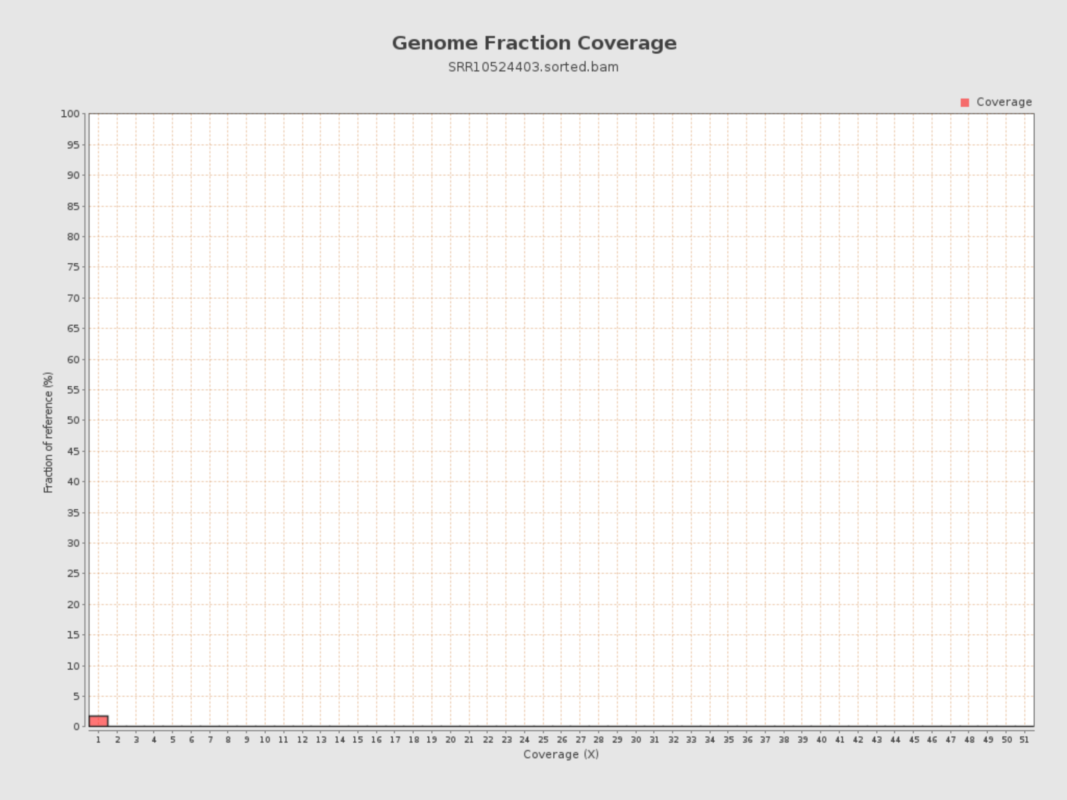
4. Results : Coverage Histogram



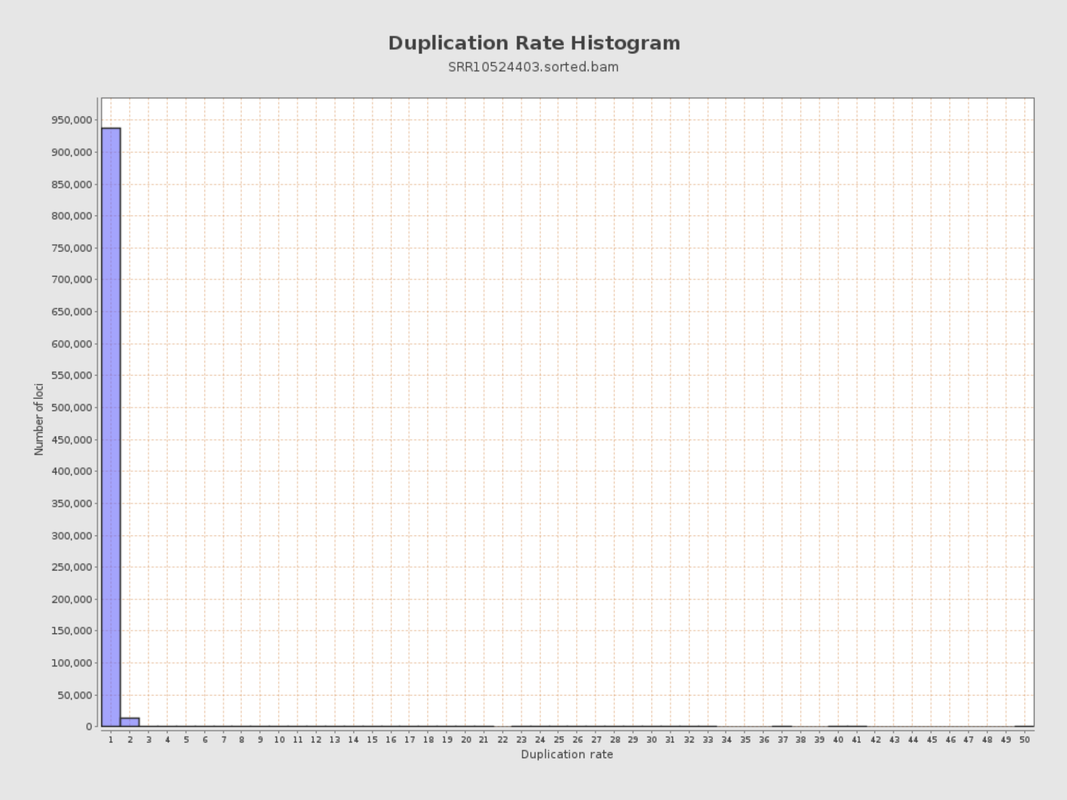
5. Results : Coverage Histogram (0-50X)



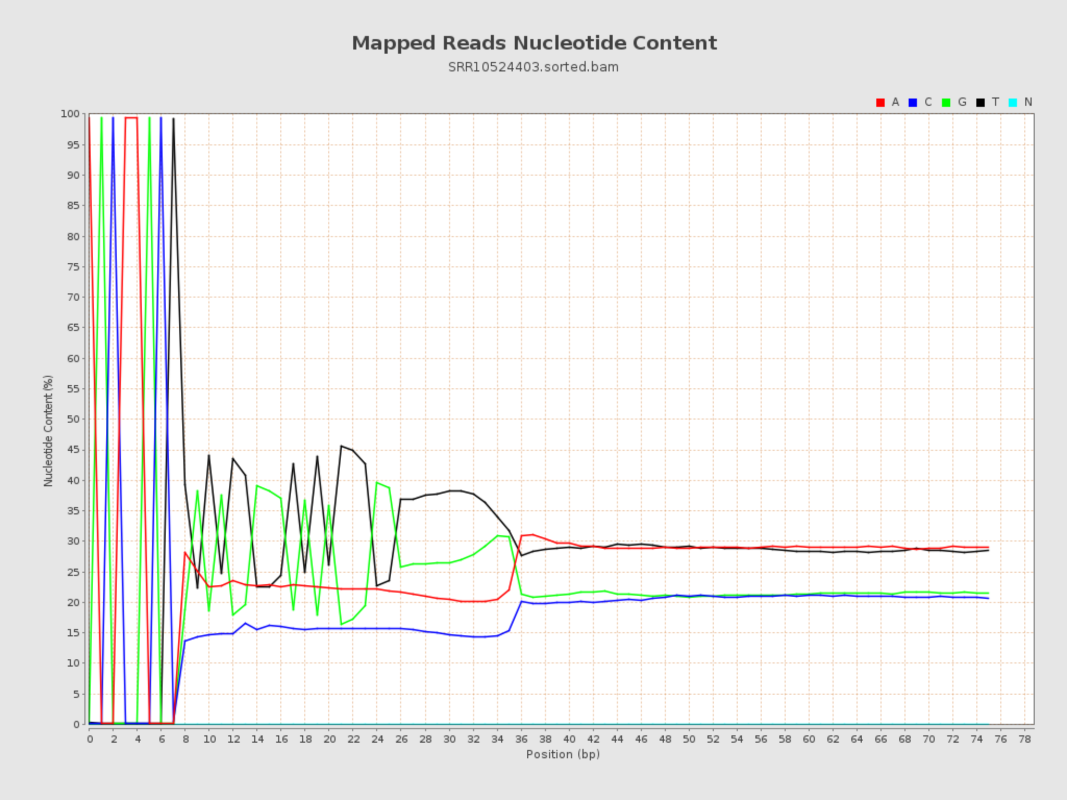
6. Results : Genome Fraction Coverage



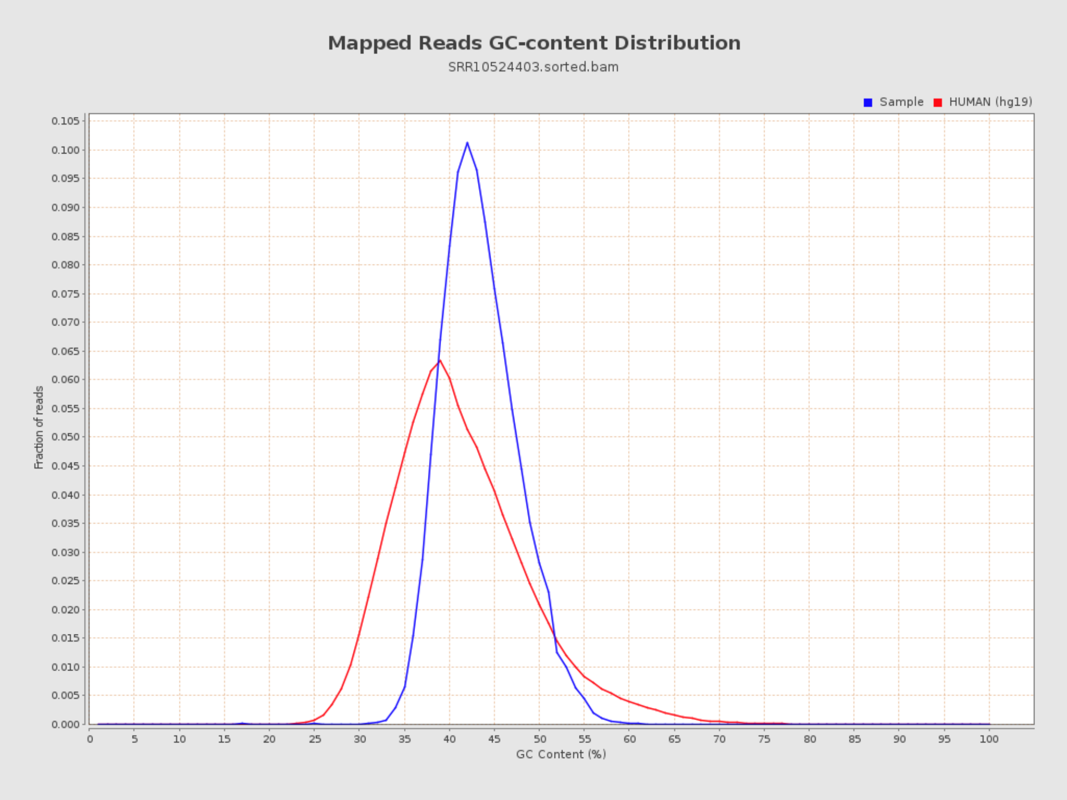
7. Results : Duplication Rate Histogram



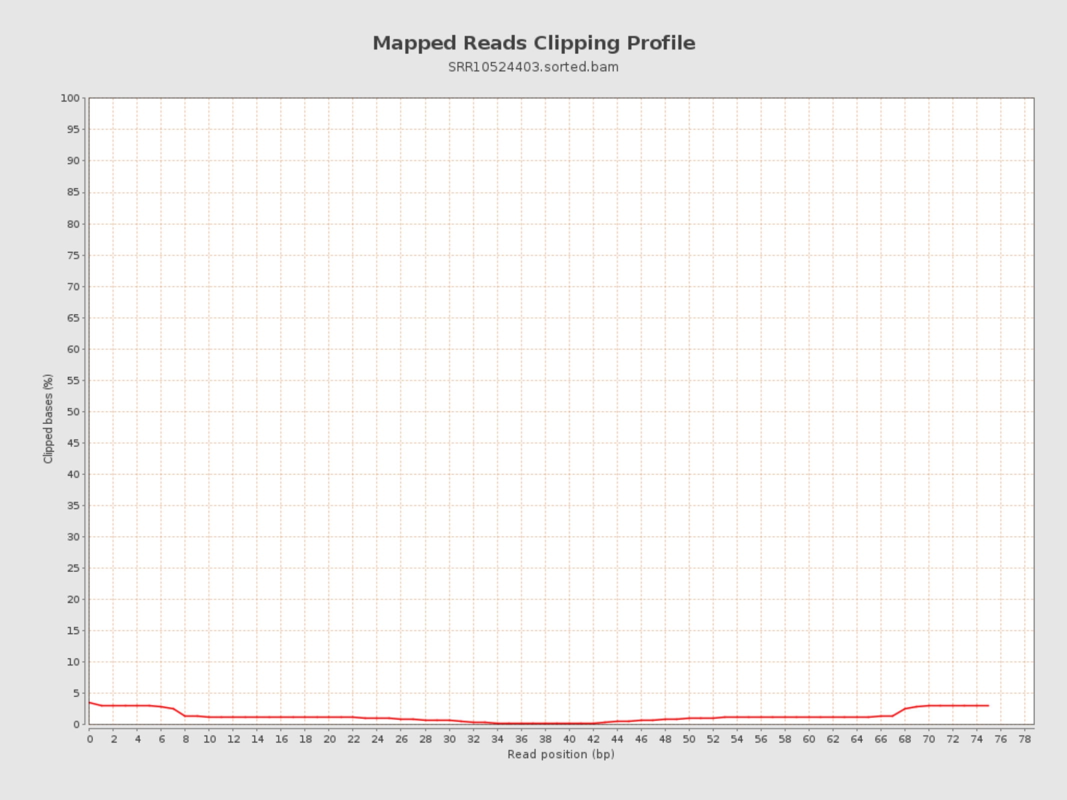
8. Results : Mapped Reads Nucleotide Content



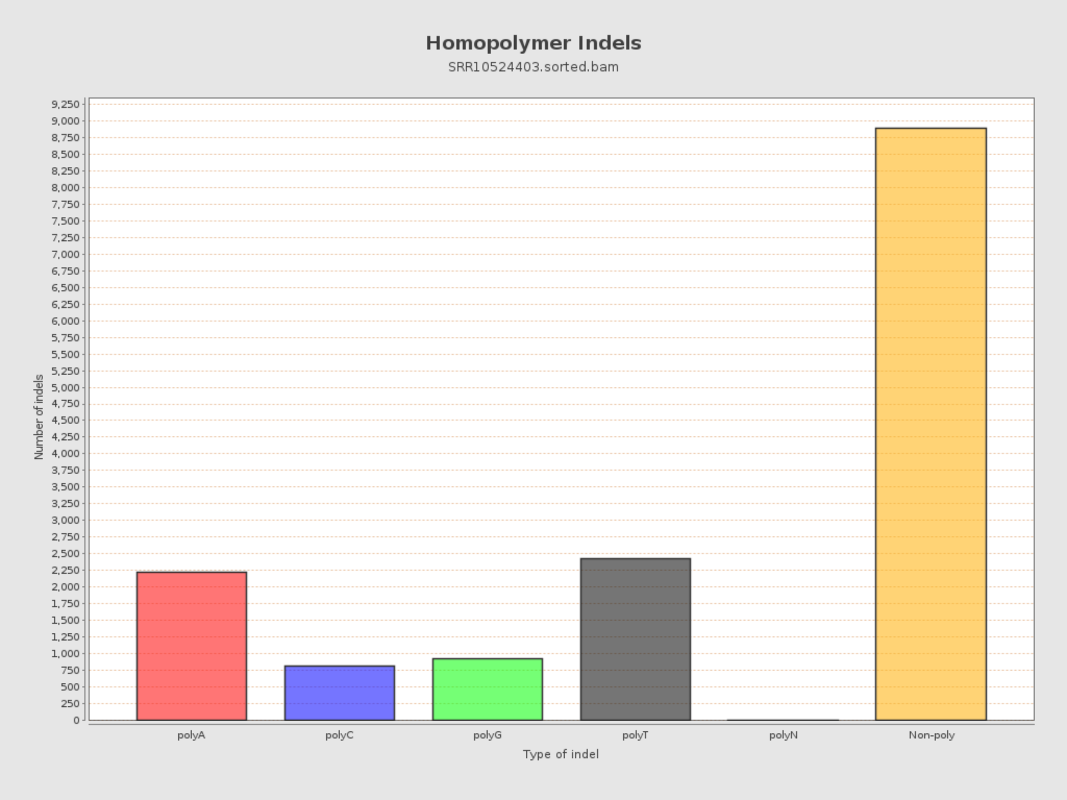
9. Results : Mapped Reads GC-content Distribution



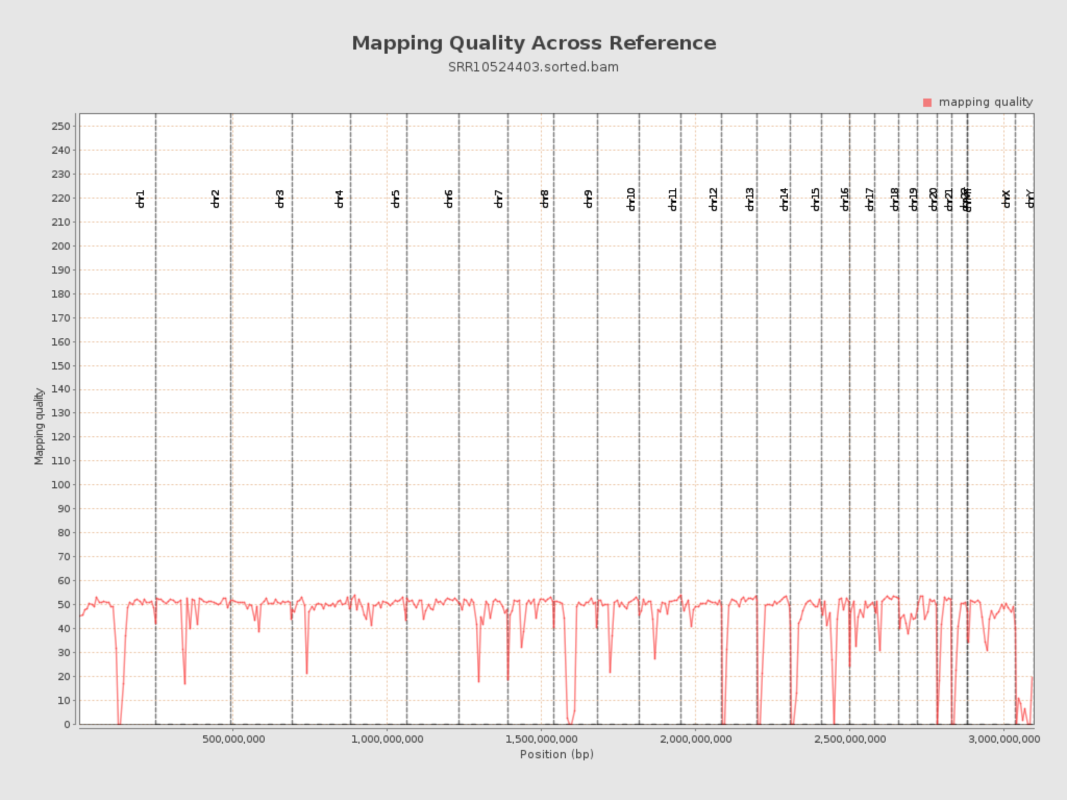
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram