Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 05:42:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524477.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_SRR10524477 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524477.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 05:42:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524477.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,171,420
Mapped reads	1,052,038 / 89.81%
Unmapped reads	119,382 / 10.19%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,051 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	24,616 / 2.1%
Duplication rate	1.65%
Clipped reads	1,052,880 / 89.88%

2.2. ACGT Content

Number/percentage of A's	14,746,915 / 24.34%
Number/percentage of C's	10,732,086 / 17.71%
Number/percentage of T's	19,935,169 / 32.9%
Number/percentage of G's	15,175,303 / 25.05%
Number/percentage of N's	1,814 / 0%
GC Percentage	42.76%

2.3. Coverage

Mean	0.0196

Standard Deviation	0.1927

2.4. Mapping Quality

Mean Mapping Quality	45.43

2.5. Mismatches and indels

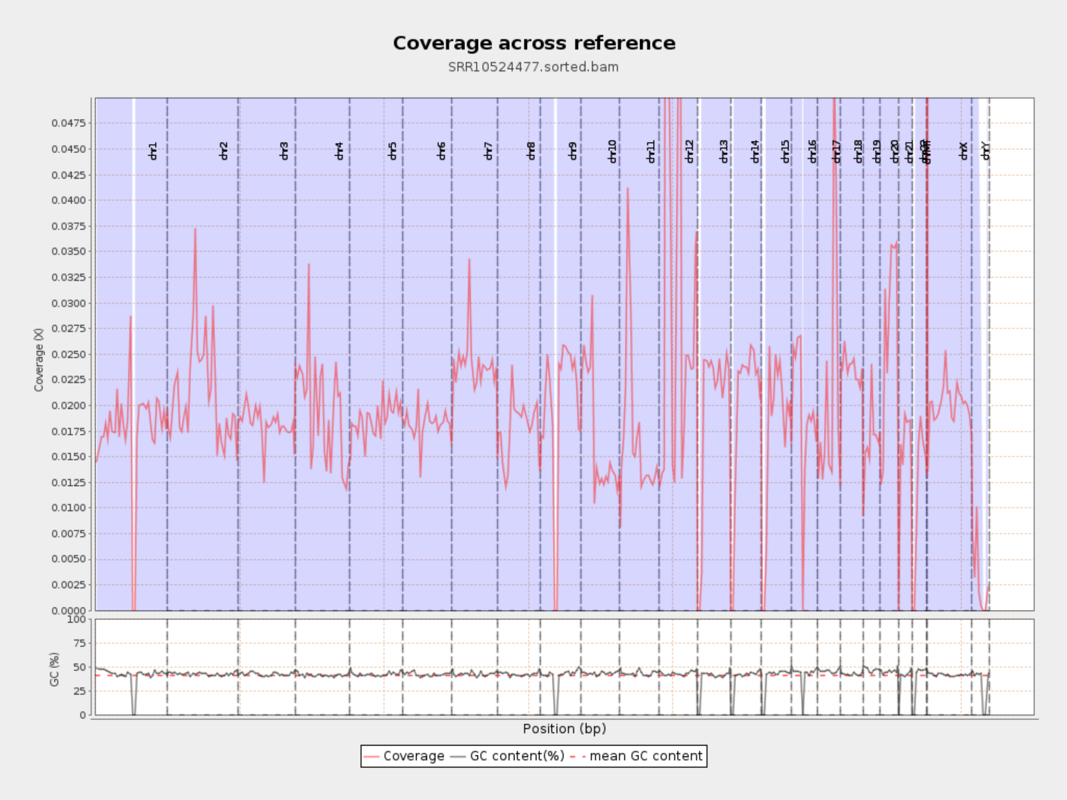
General error rate	0.49%
Mismatches	290,259
Insertions	4,198
Mapped reads with at least one insertion	0.4%
Deletions	9,909
Mapped reads with at least one deletion	0.94%
Homopolymer indels	43.38%

2.6. Chromosome stats

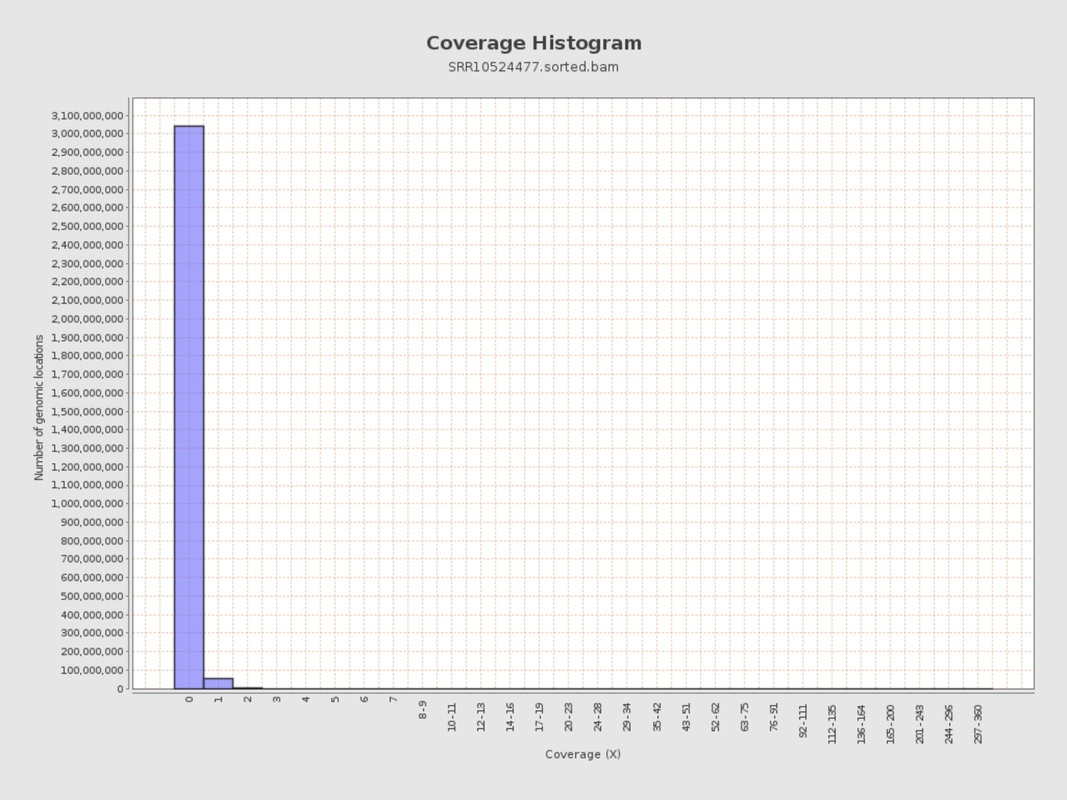
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4357151	0.0175	0.3019
chr2	243199373	5145256	0.0212	0.2059
chr3	198022430	3620376	0.0183	0.1416
chr4	191154276	3724310	0.0195	0.1628
chr5	180915260	3401241	0.0188	0.1459
chr6	171115067	3115192	0.0182	0.151
chr7	159138663	3838859	0.0241	0.2501

chr8	146364022	2622813	0.0179	0.1859
chr9	141213431	2805135	0.0199	0.193
chr10	135534747	2299459	0.017	0.1901
chr11	135006516	2289767	0.017	0.1641
chr12	133851895	4565260	0.0341	0.2088
chr13	115169878	2239994	0.0194	0.1465
chr14	107349540	2119120	0.0197	0.155
chr15	102531392	1765735	0.0172	0.1381
chr16	90354753	1704372	0.0189	0.1517
chr17	81195210	1768395	0.0218	0.1582
chr18	78077248	1842182	0.0236	0.3155
chr19	59128983	998256	0.0169	0.2288
chr20	63025520	1729918	0.0274	0.1788
chr21	48129895	740496	0.0154	0.1406
chr22	51304566	602584	0.0117	0.113
chrMT	16571	7476	0.4511	0.7586
chrX	155270560	3127870	0.0201	0.1669
chrY	59373566	176595	0.003	0.0837

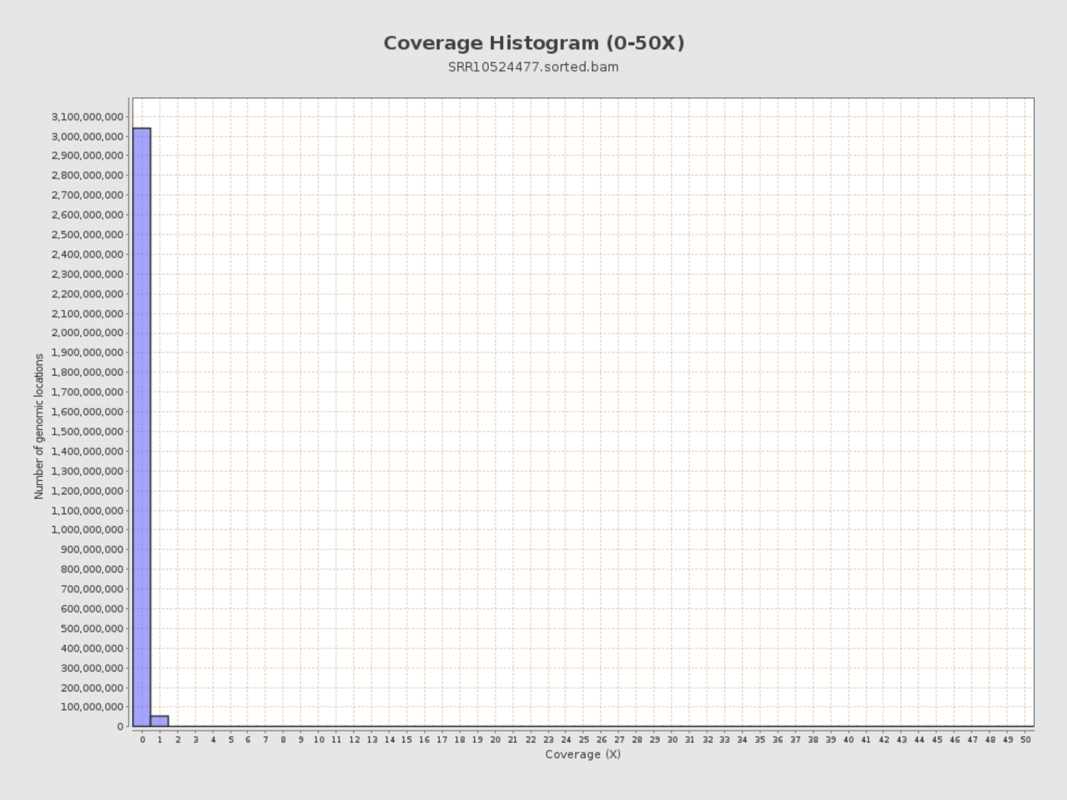
3. Results : Coverage across reference



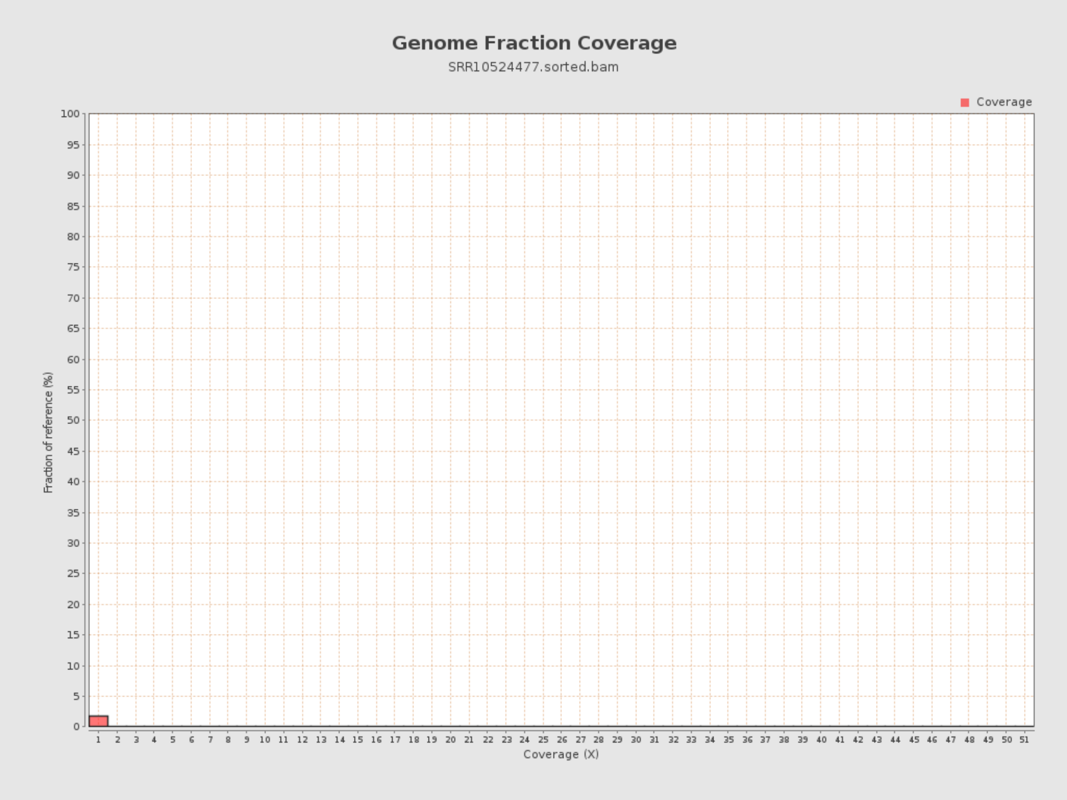
4. Results : Coverage Histogram



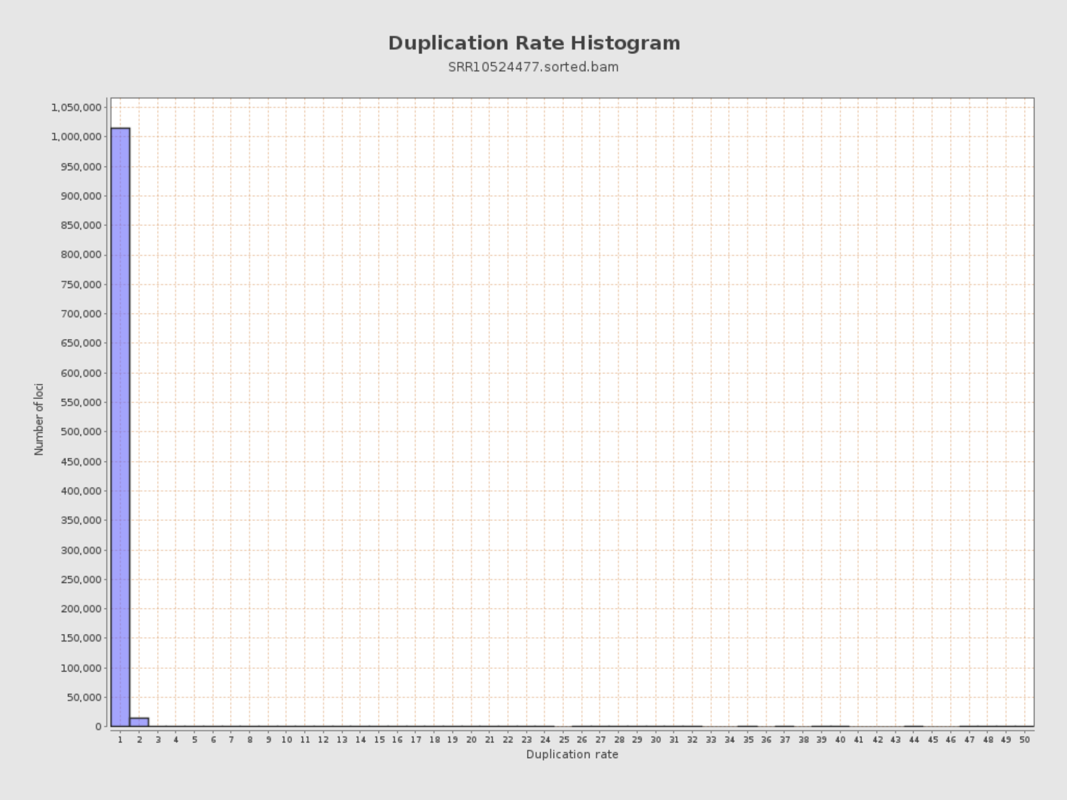
5. Results : Coverage Histogram (0-50X)



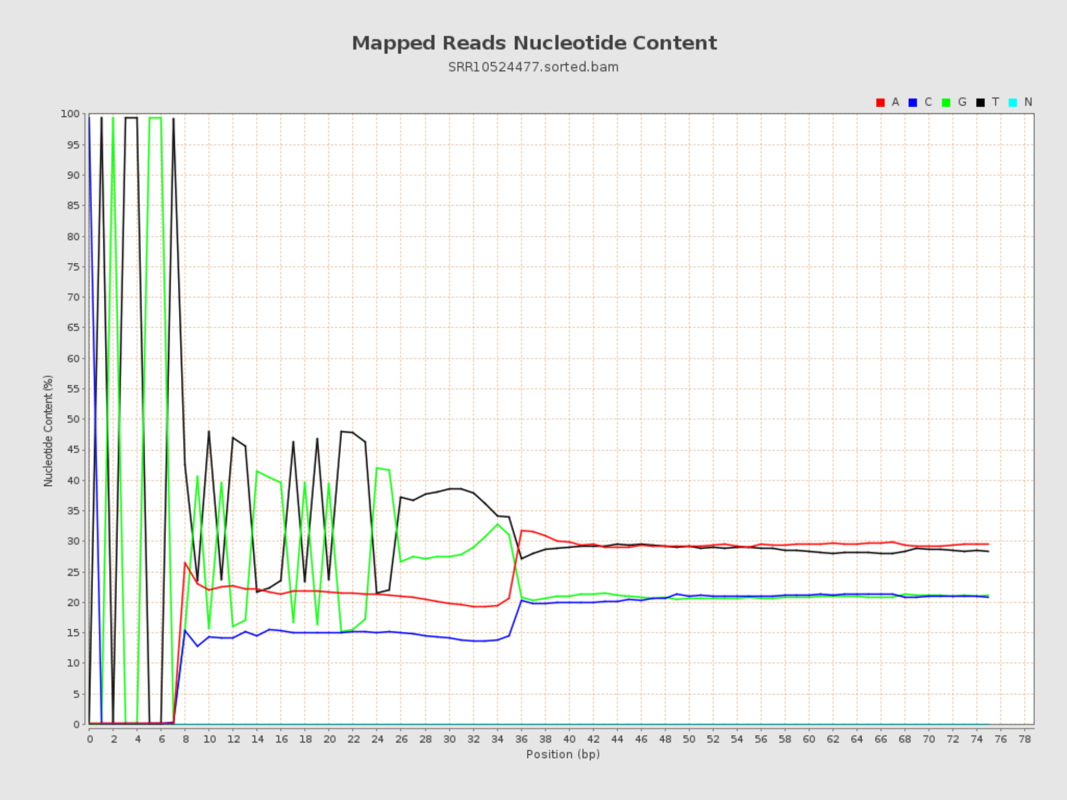
6. Results : Genome Fraction Coverage



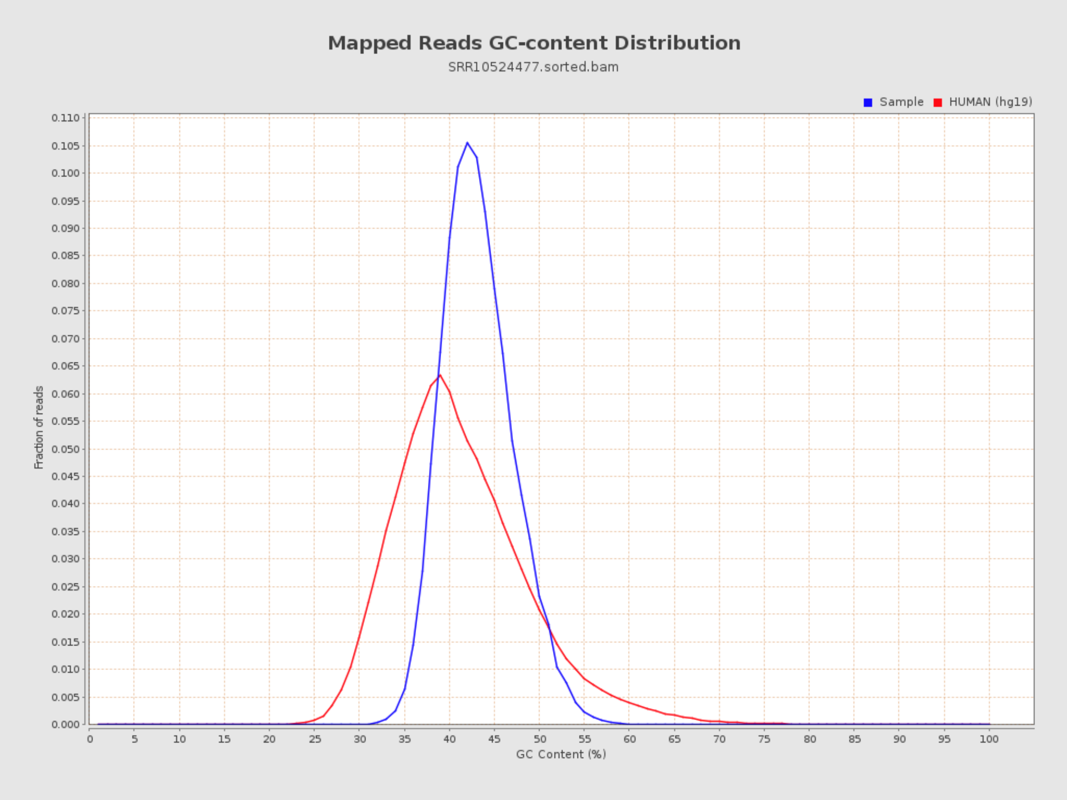
7. Results : Duplication Rate Histogram



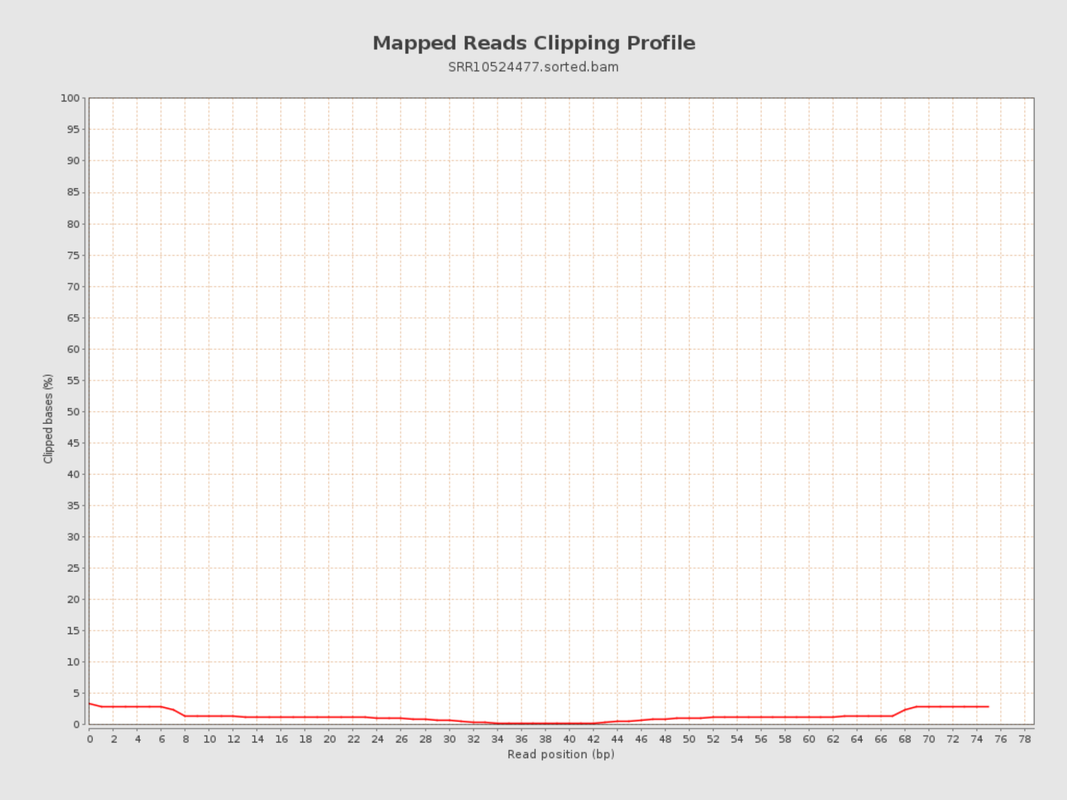
8. Results : Mapped Reads Nucleotide Content



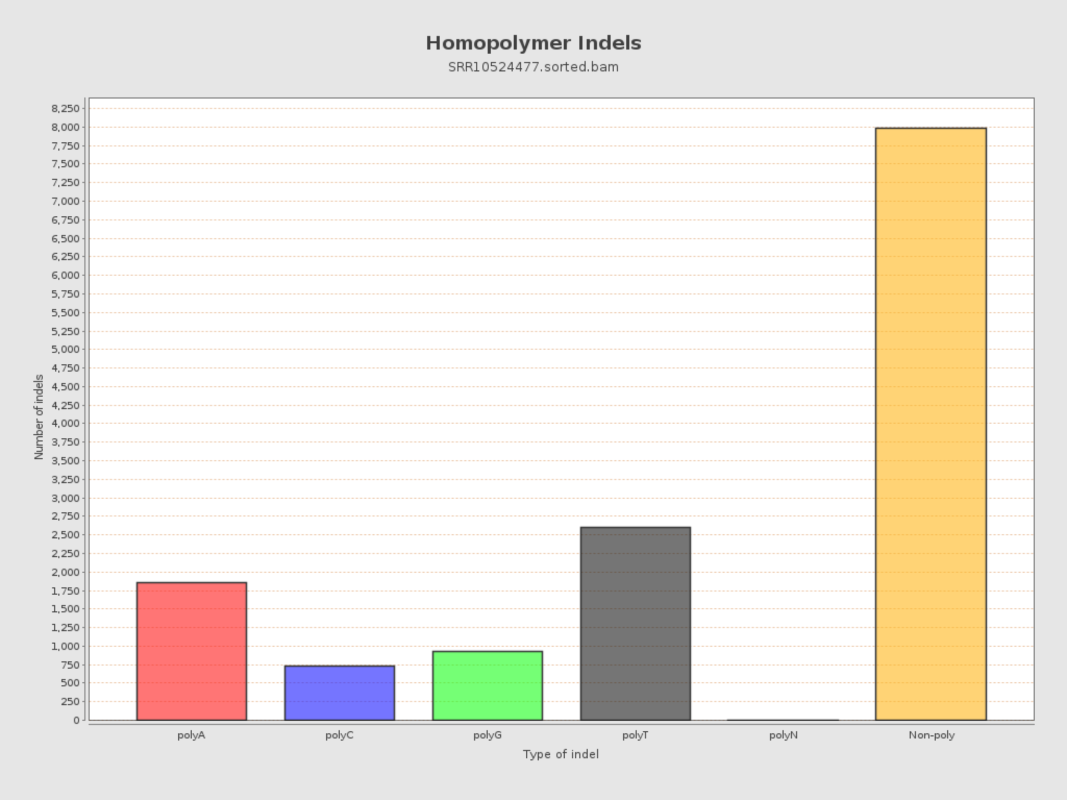
9. Results : Mapped Reads GC-content Distribution



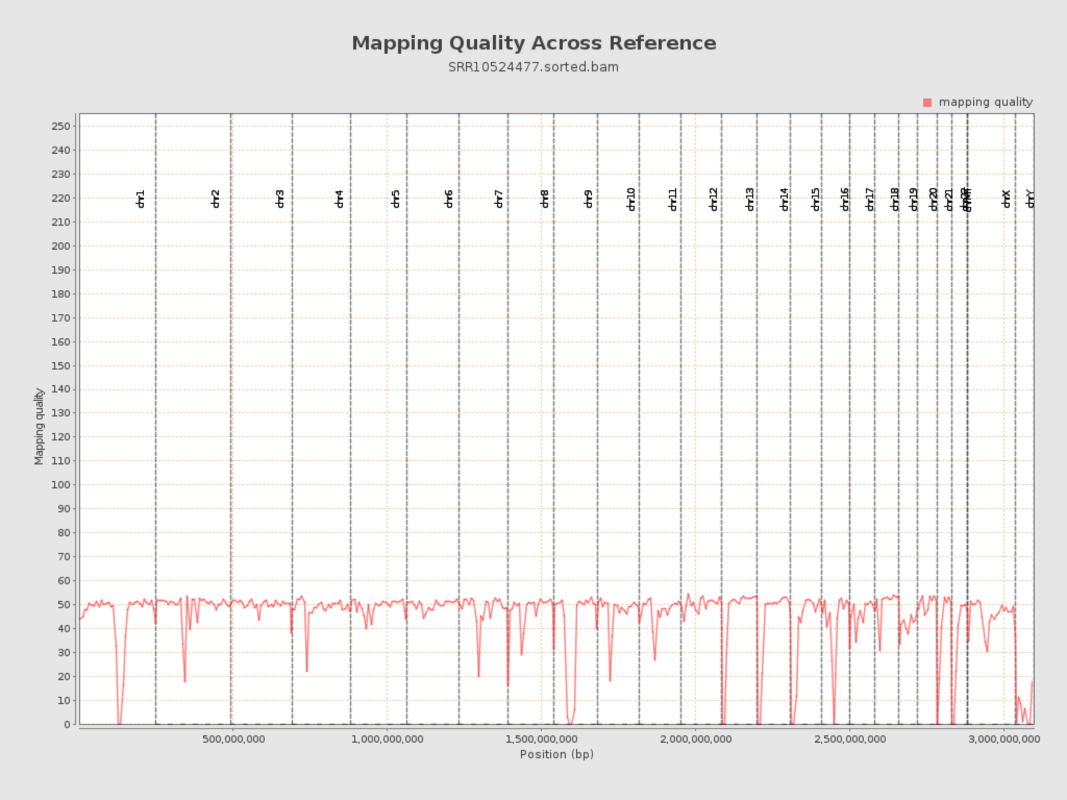
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram