Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 20:12:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524614.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_SRR10524614 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524614.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 20:12:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524614.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,769,165
Mapped reads	1,660,490 / 93.86%
Unmapped reads	108,675 / 6.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,575 / 0.2%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	67,441 / 3.81%
Duplication rate	3.18%
Clipped reads	1,662,683 / 93.98%

2.2. ACGT Content

Number/percentage of A's	23,171,203 / 23.82%
Number/percentage of C's	19,052,343 / 19.58%
Number/percentage of T's	30,229,468 / 31.07%
Number/percentage of G's	24,838,902 / 25.53%
Number/percentage of N's	602 / 0%
GC Percentage	45.11%

2.3. Coverage

Mean	0.0314

Standard Deviation	0.2589

2.4. Mapping Quality

Mean Mapping Quality	45.43

2.5. Mismatches and indels

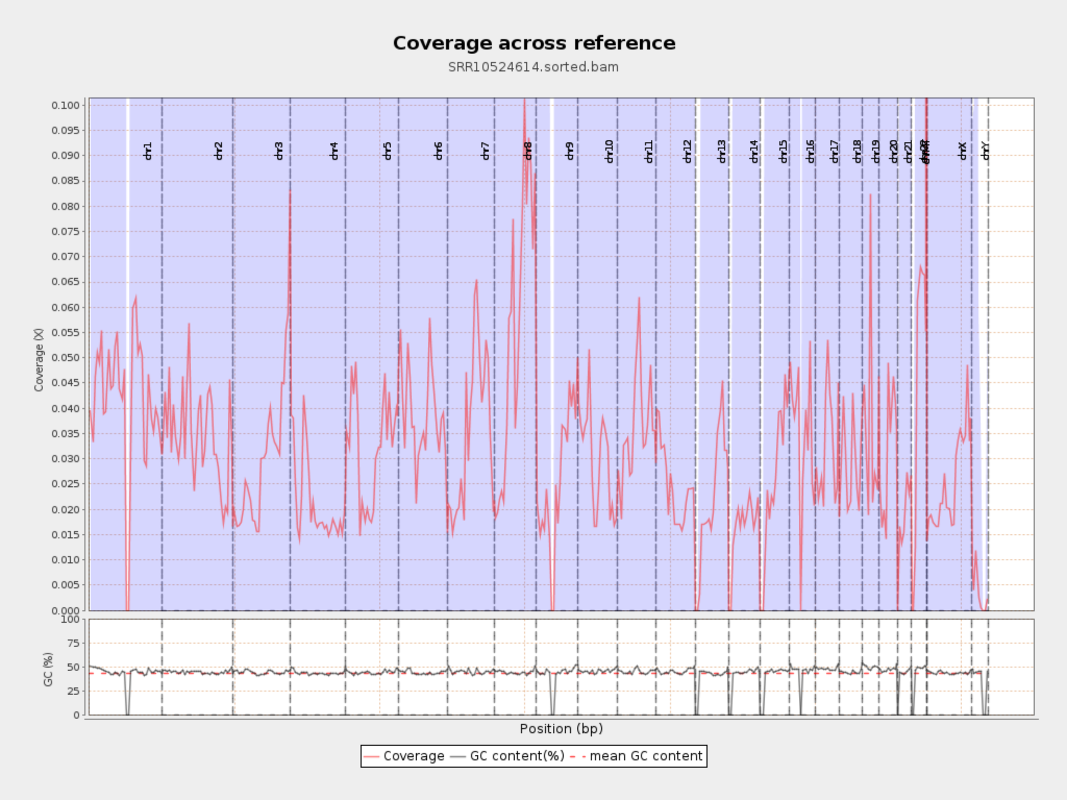
General error rate	0.46%
Mismatches	434,975
Insertions	5,049
Mapped reads with at least one insertion	0.3%
Deletions	18,151
Mapped reads with at least one deletion	1.08%
Homopolymer indels	44.74%

2.6. Chromosome stats

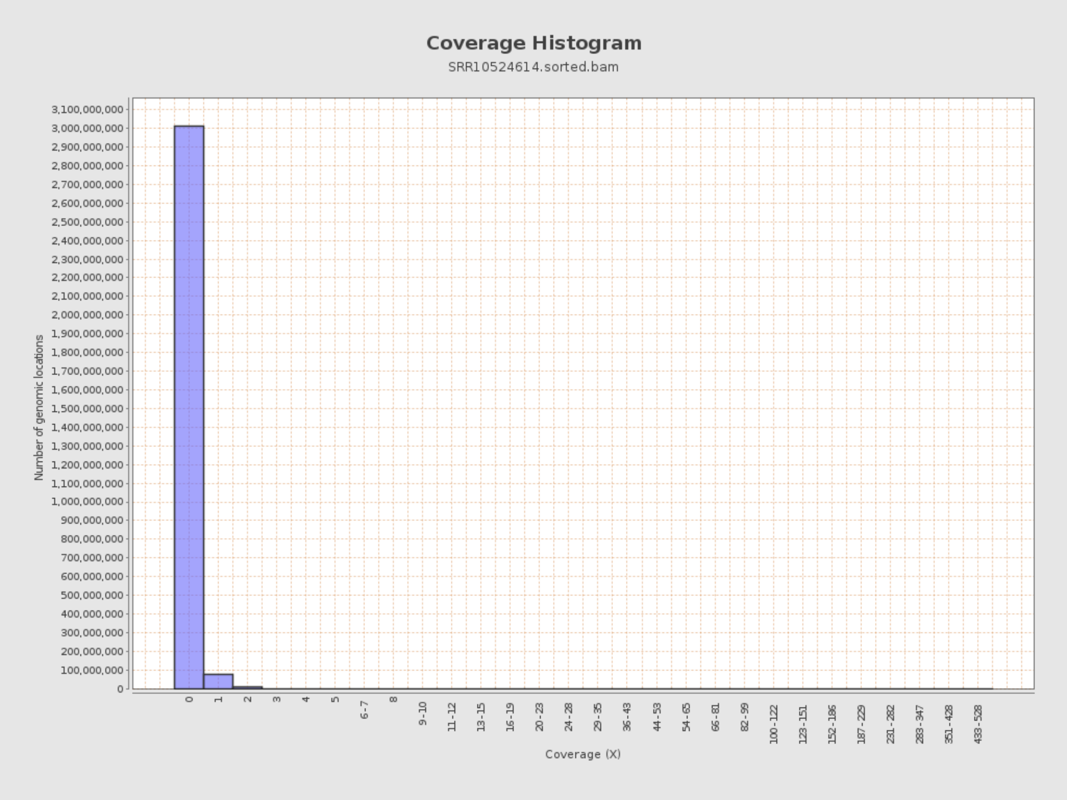
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10360361	0.0416	0.4314
chr2	243199373	8494533	0.0349	0.3012
chr3	198022430	5873614	0.0297	0.1915
chr4	191154276	4049534	0.0212	0.184
chr5	180915260	5864090	0.0324	0.2001
chr6	171115067	6670830	0.039	0.2344
chr7	159138663	5677308	0.0357	0.3335

chr8	146364022	8253981	0.0564	0.3336
chr9	141213431	3534259	0.025	0.2334
chr10	135534747	4051879	0.0299	0.2548
chr11	135006516	4935194	0.0366	0.2545
chr12	133851895	3273006	0.0245	0.1757
chr13	115169878	2526283	0.0219	0.1657
chr14	107349540	1748179	0.0163	0.1452
chr15	102531392	2628694	0.0256	0.1842
chr16	90354753	3086253	0.0342	0.2145
chr17	81195210	2660081	0.0328	0.2054
chr18	78077248	2287033	0.0293	0.3466
chr19	59128983	2140352	0.0362	0.3185
chr20	63025520	1973456	0.0313	0.1991
chr21	48129895	874315	0.0182	0.1631
chr22	51304566	2238620	0.0436	0.234
chrMT	16571	10129	0.6112	0.9673
chrX	155270560	3909389	0.0252	0.1953
chrY	59373566	202415	0.0034	0.1005

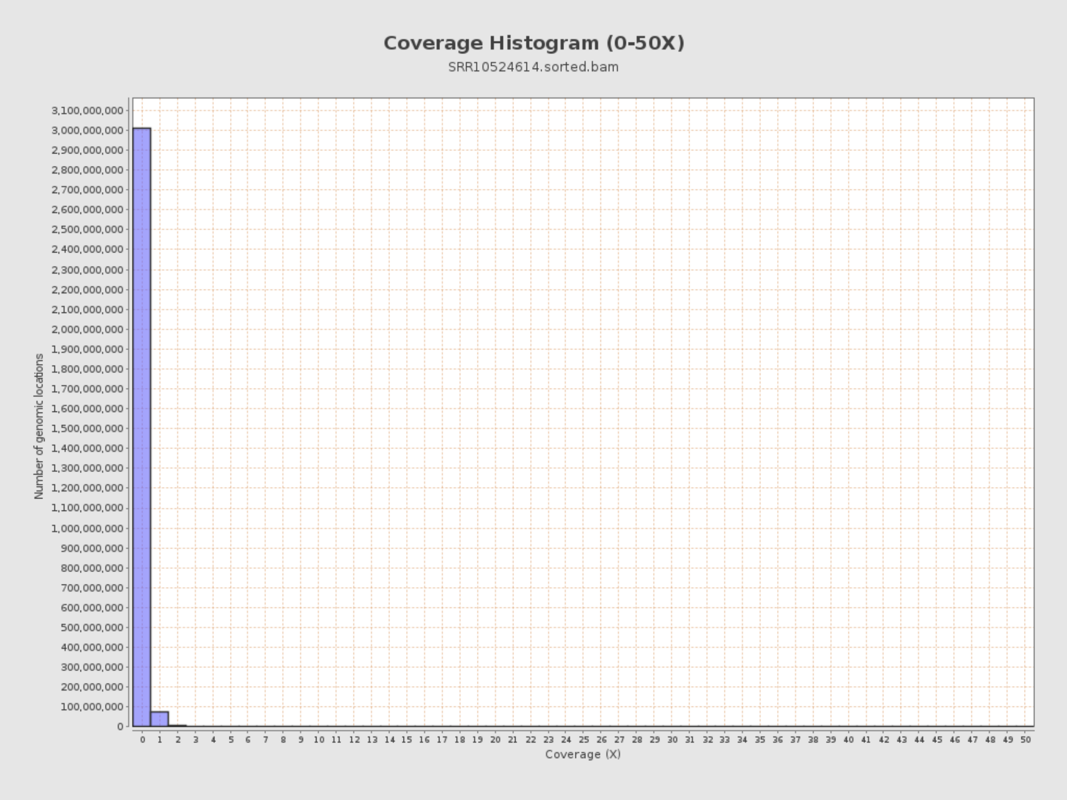
3. Results : Coverage across reference



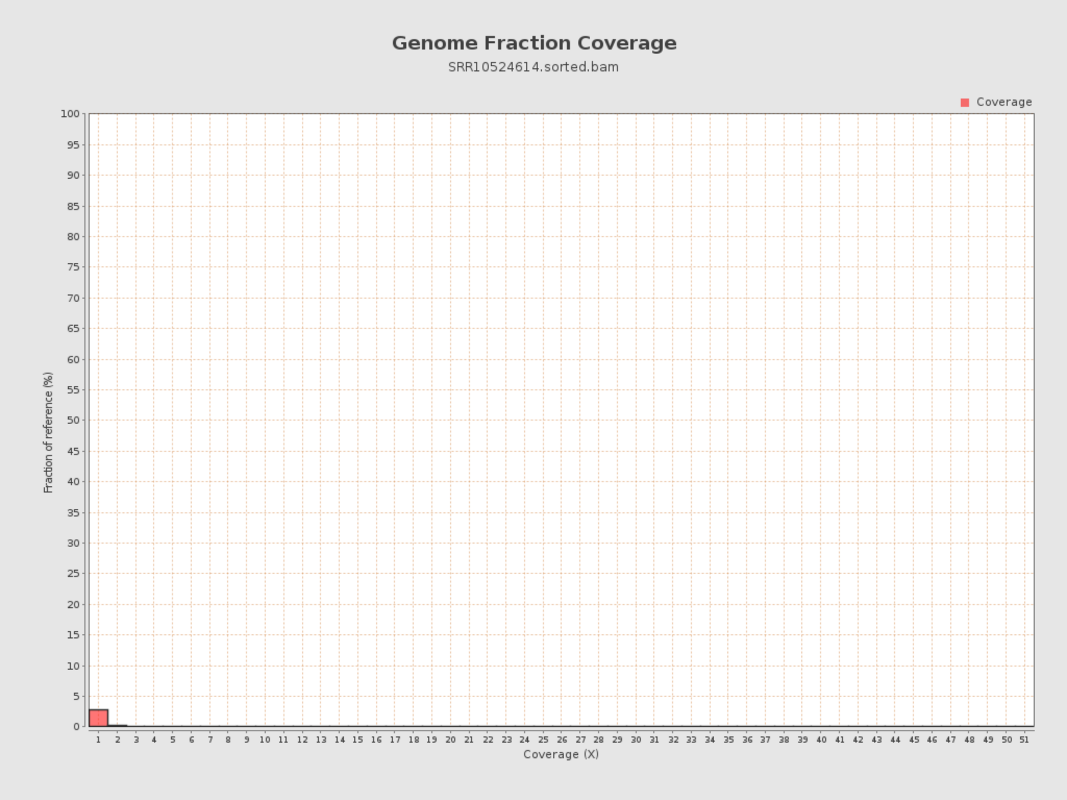
4. Results : Coverage Histogram



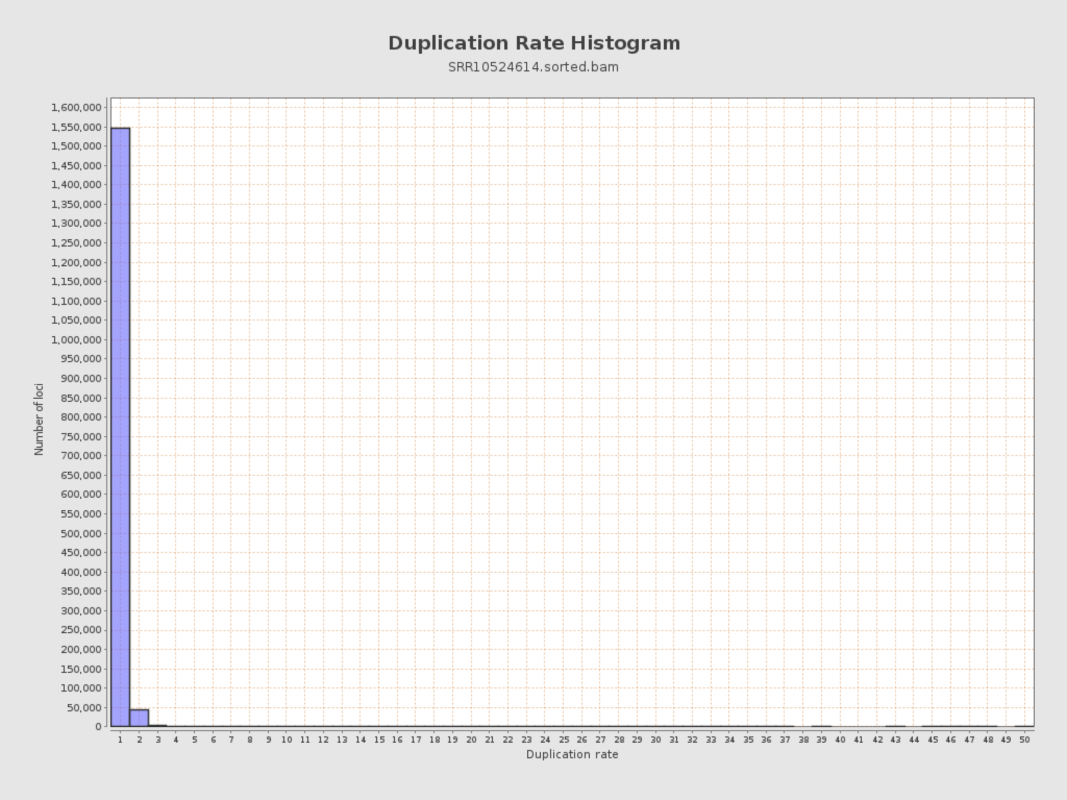
5. Results : Coverage Histogram (0-50X)



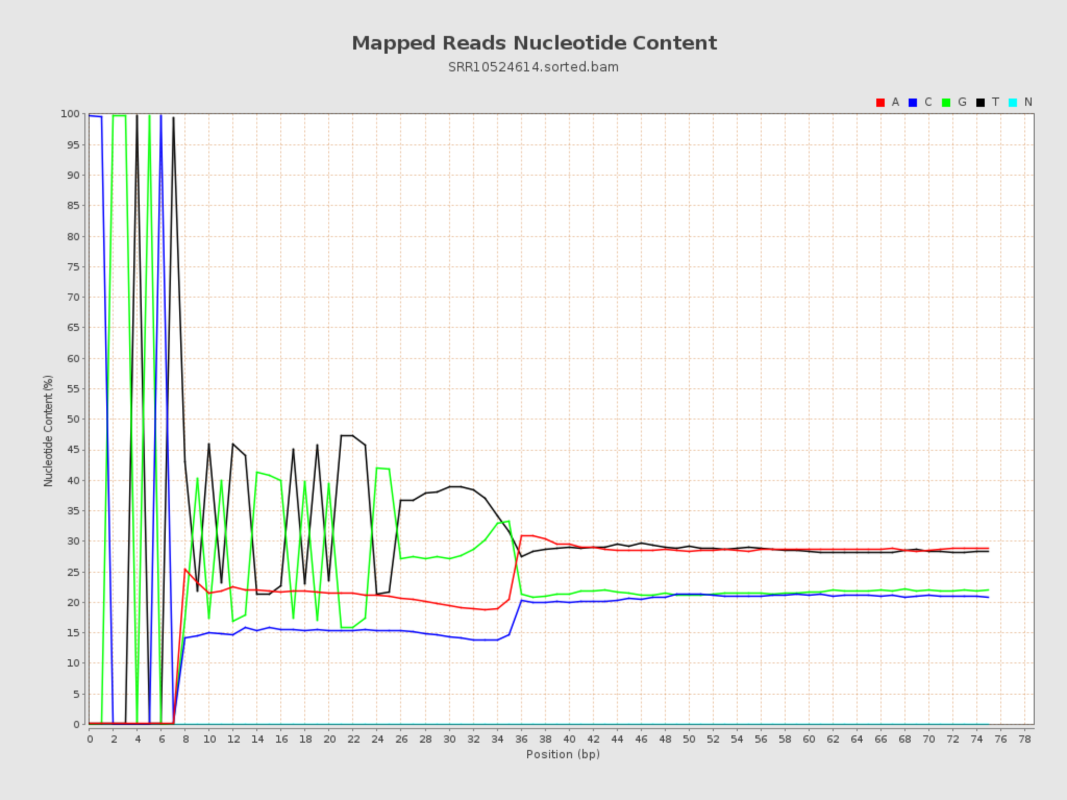
6. Results : Genome Fraction Coverage



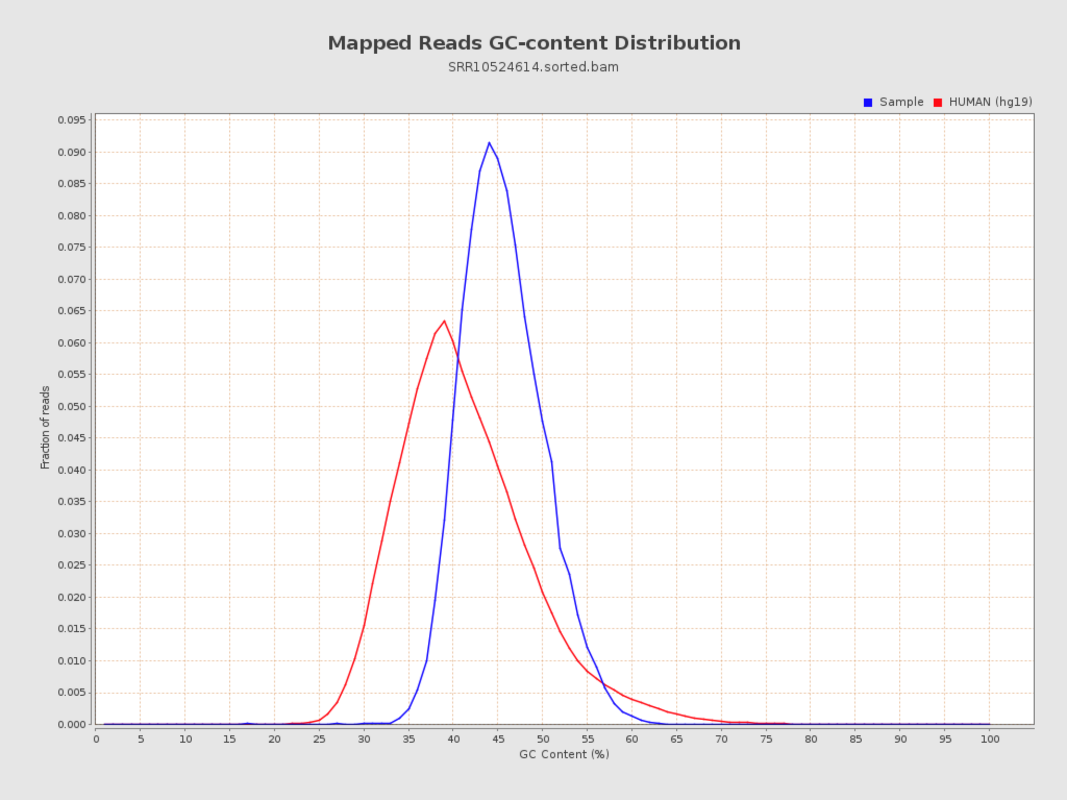
7. Results : Duplication Rate Histogram



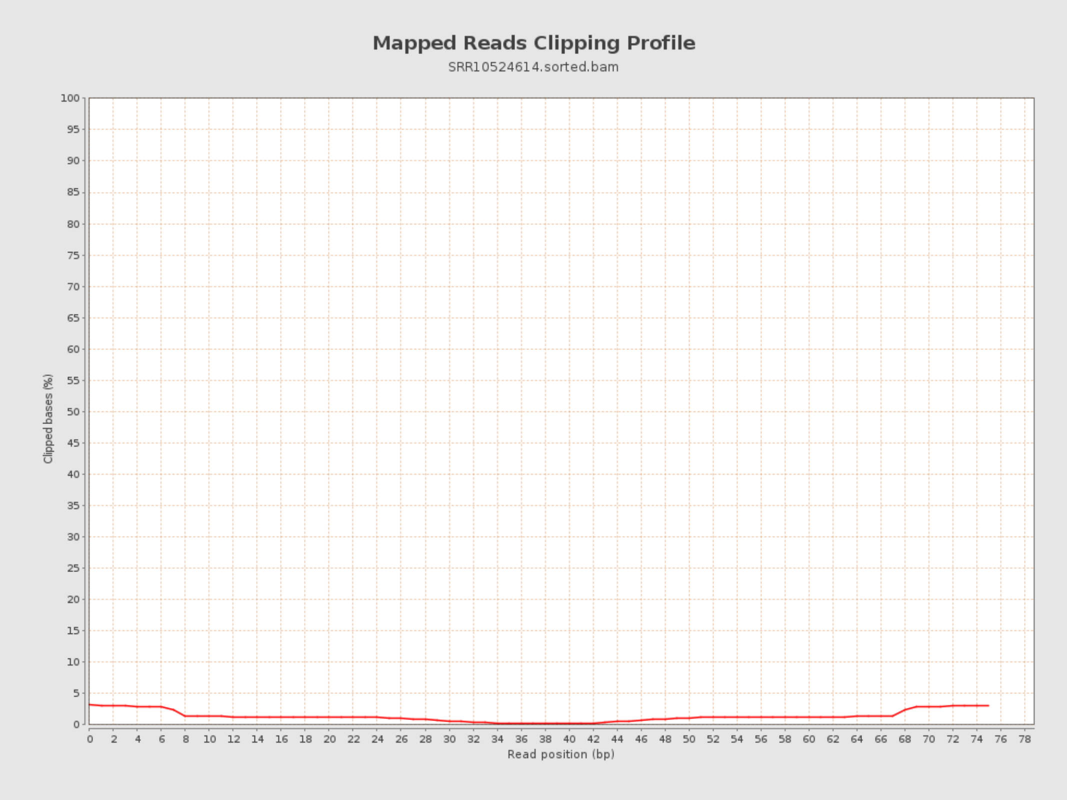
8. Results : Mapped Reads Nucleotide Content



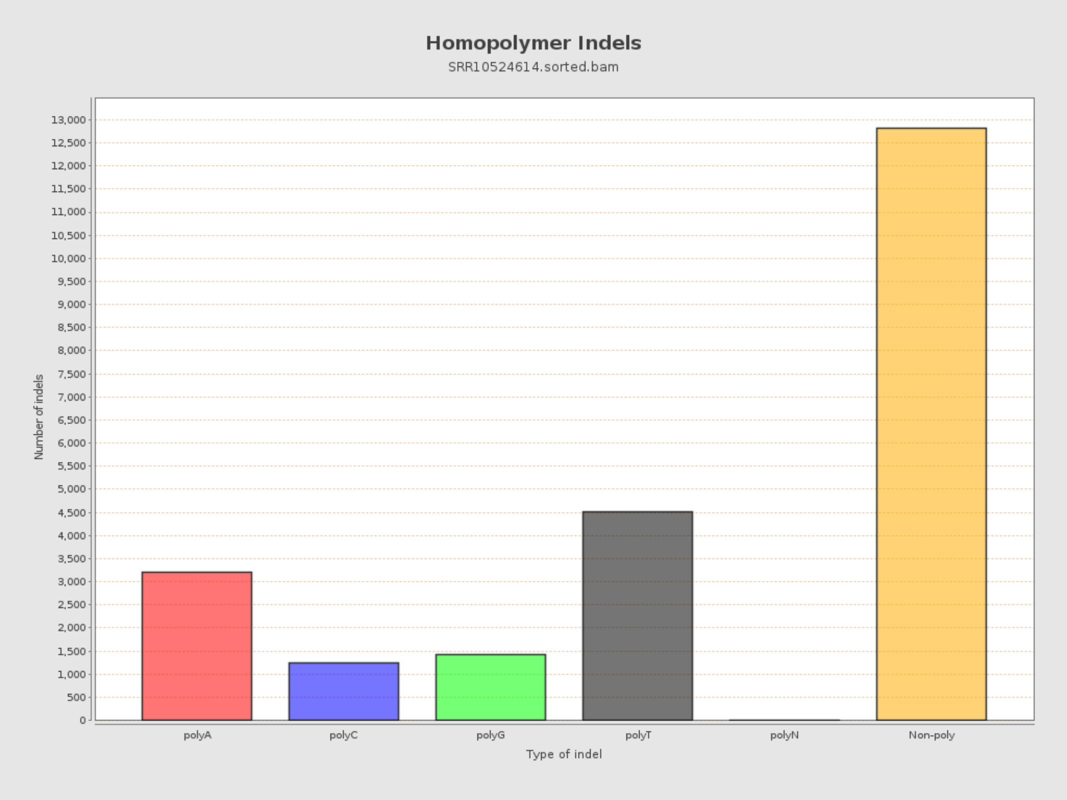
9. Results : Mapped Reads GC-content Distribution



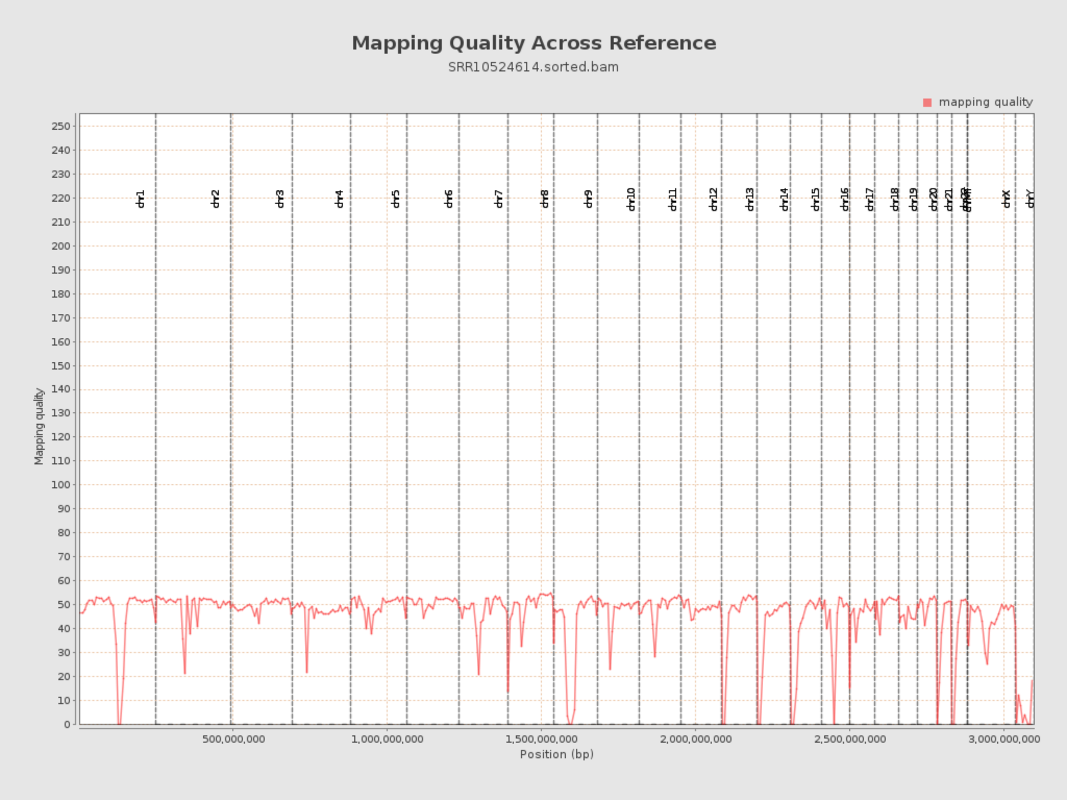
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram