Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 10:24:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524550.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_SRR10524550 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524550.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 10:24:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524550.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,884,115
Mapped reads	1,684,819 / 89.42%
Unmapped reads	199,296 / 10.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,910 / 0.37%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	69,780 / 3.7%
Duplication rate	3.05%
Clipped reads	1,688,751 / 89.63%

2.2. ACGT Content

Number/percentage of A's	24,890,865 / 25.46%
Number/percentage of C's	18,202,541 / 18.62%
Number/percentage of T's	31,524,711 / 32.24%
Number/percentage of G's	23,153,513 / 23.68%
Number/percentage of N's	1,409 / 0%
GC Percentage	42.3%

2.3. Coverage

Mean	0.0316

Standard Deviation	0.2991

2.4. Mapping Quality

Mean Mapping Quality	44.87

2.5. Mismatches and indels

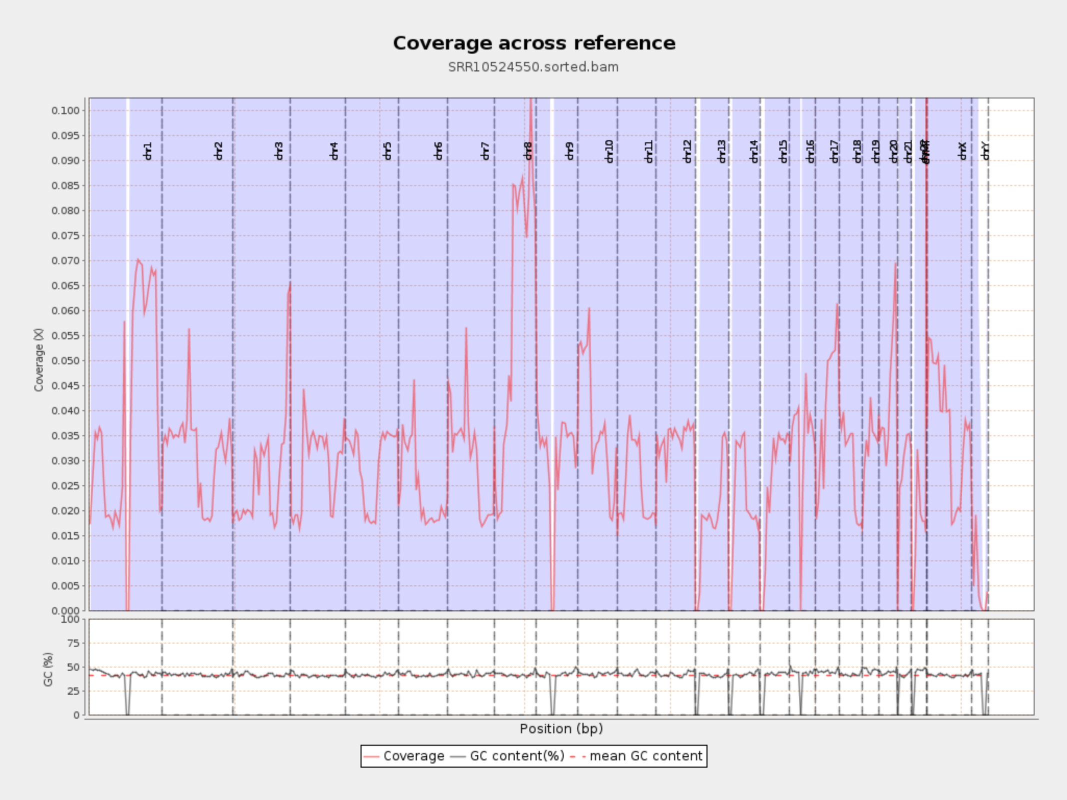
General error rate	0.53%
Mismatches	507,056
Insertions	5,761
Mapped reads with at least one insertion	0.34%
Deletions	18,264
Mapped reads with at least one deletion	1.08%
Homopolymer indels	42.93%

2.6. Chromosome stats

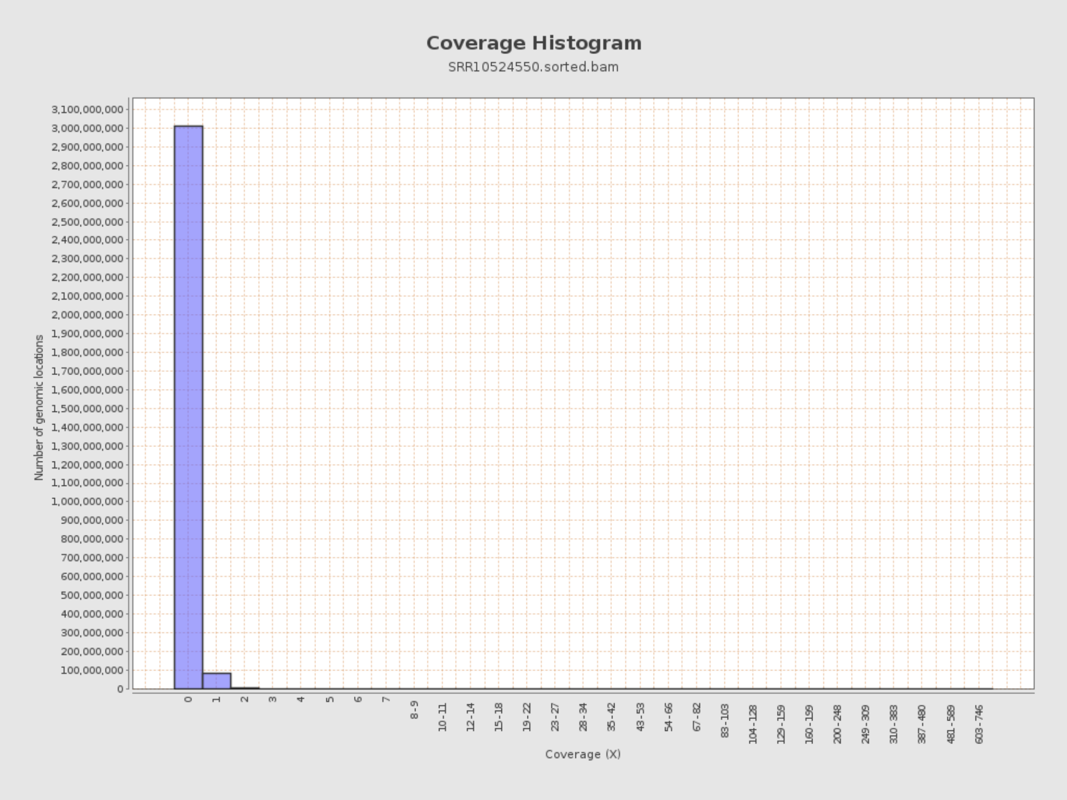
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9681001	0.0388	0.5727
chr2	243199373	7761980	0.0319	0.3498
chr3	198022430	5278119	0.0267	0.1822
chr4	191154276	5545766	0.029	0.2103
chr5	180915260	5337680	0.0295	0.1895
chr6	171115067	4194586	0.0245	0.2242
chr7	159138663	4896241	0.0308	0.3817

chr8	146364022	8998862	0.0615	0.3332
chr9	141213431	4193949	0.0297	0.2479
chr10	135534747	5106878	0.0377	0.3001
chr11	135006516	3391985	0.0251	0.2677
chr12	133851895	4627065	0.0346	0.2054
chr13	115169878	2189670	0.019	0.1508
chr14	107349540	2306024	0.0215	0.1639
chr15	102531392	2557217	0.0249	0.1822
chr16	90354753	3053596	0.0338	0.2163
chr17	81195210	3395816	0.0418	0.2381
chr18	78077248	2309584	0.0296	0.4497
chr19	59128983	1993377	0.0337	0.3877
chr20	63025520	2770385	0.044	0.2328
chr21	48129895	1335447	0.0277	0.2021
chr22	51304566	791841	0.0154	0.1355
chrMT	16571	4073	0.2458	0.5238
chrX	155270560	5765508	0.0371	0.2387
chrY	59373566	317138	0.0053	0.169

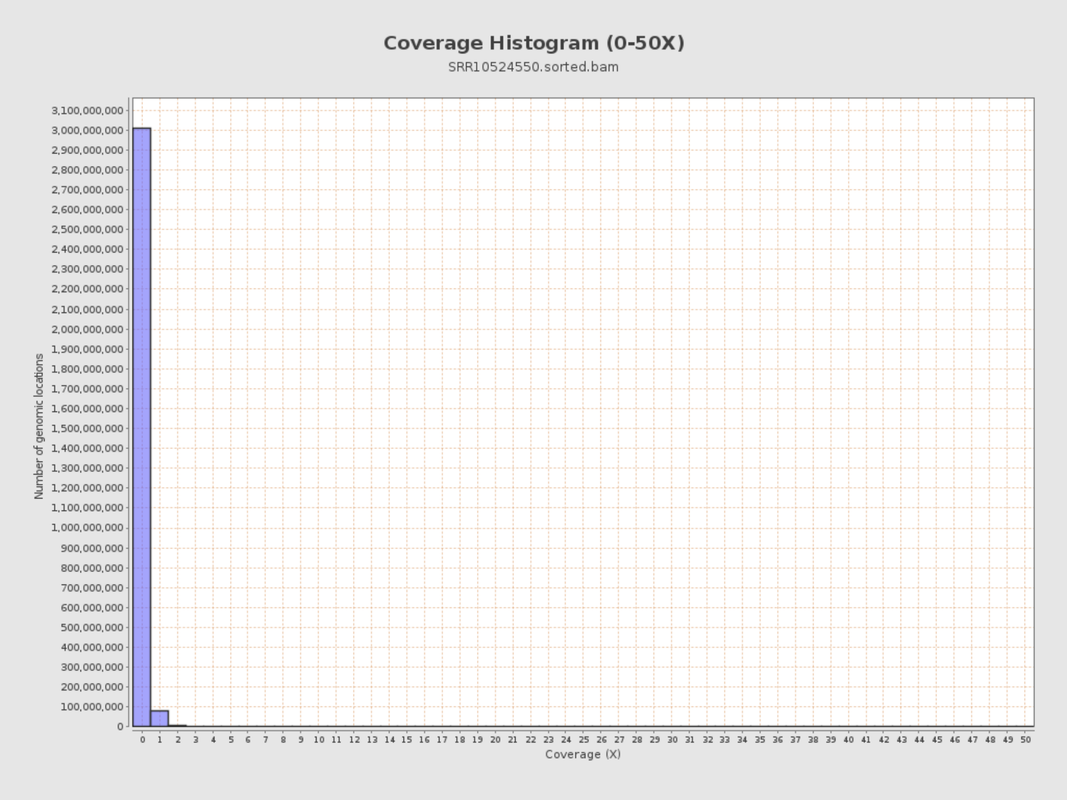
3. Results : Coverage across reference



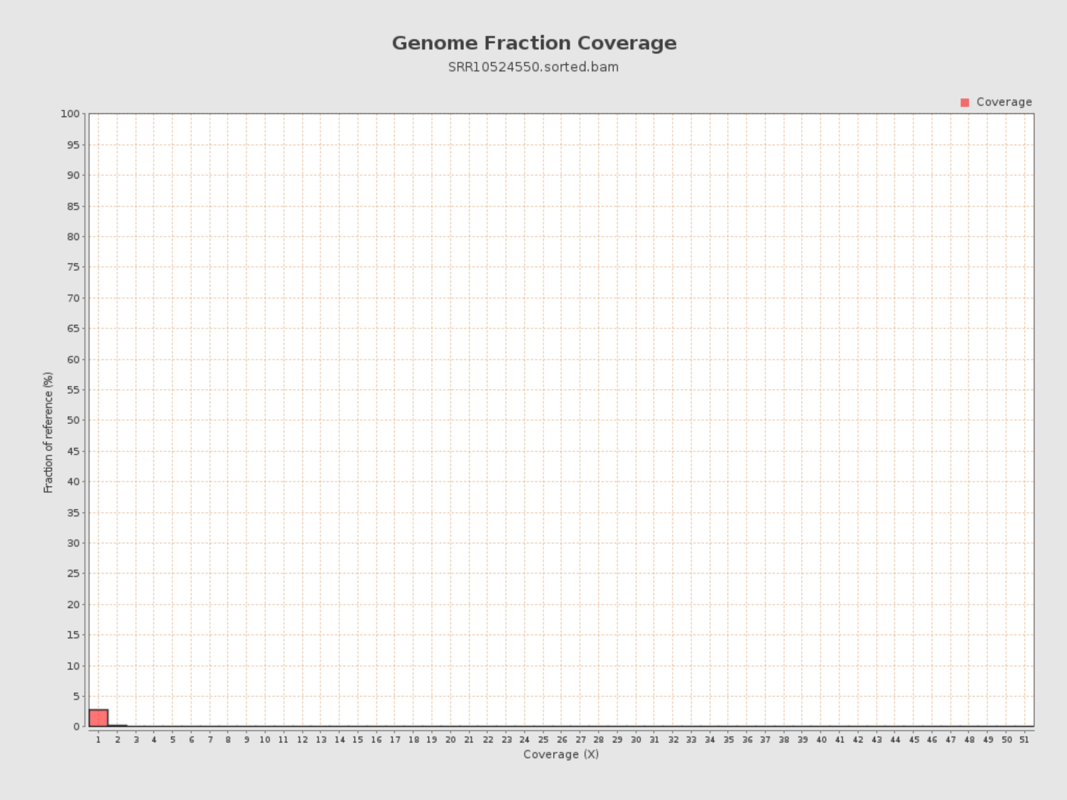
4. Results : Coverage Histogram



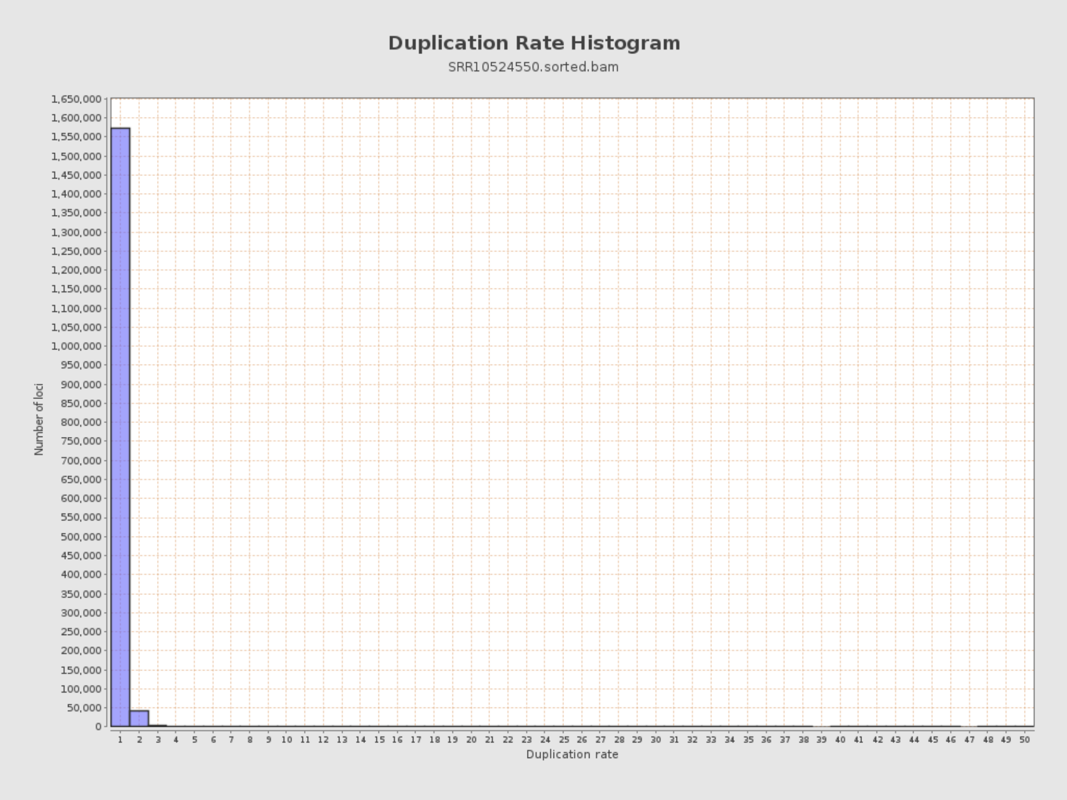
5. Results : Coverage Histogram (0-50X)



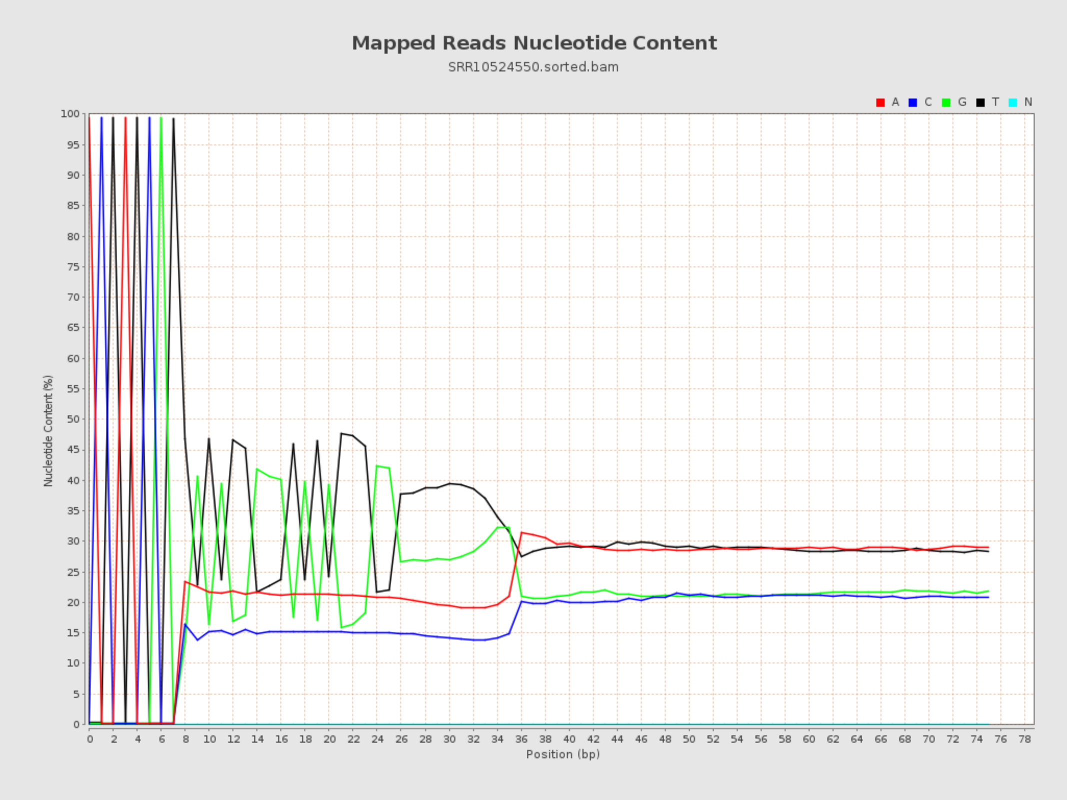
6. Results : Genome Fraction Coverage



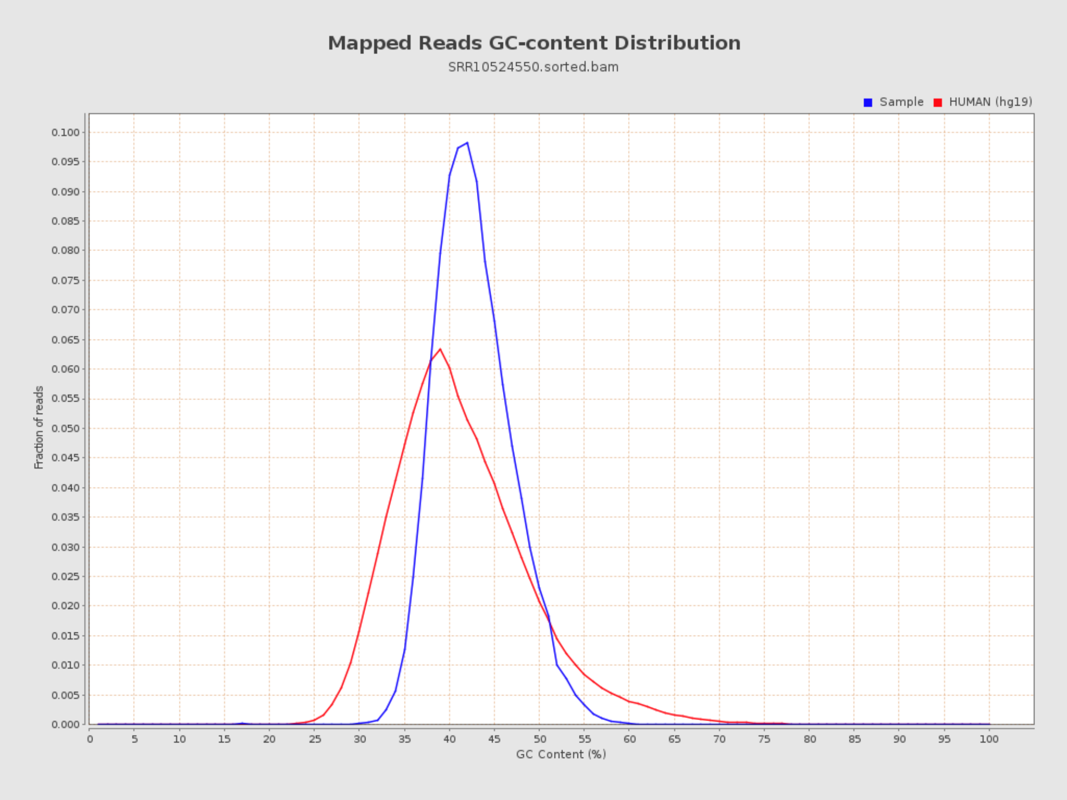
7. Results : Duplication Rate Histogram



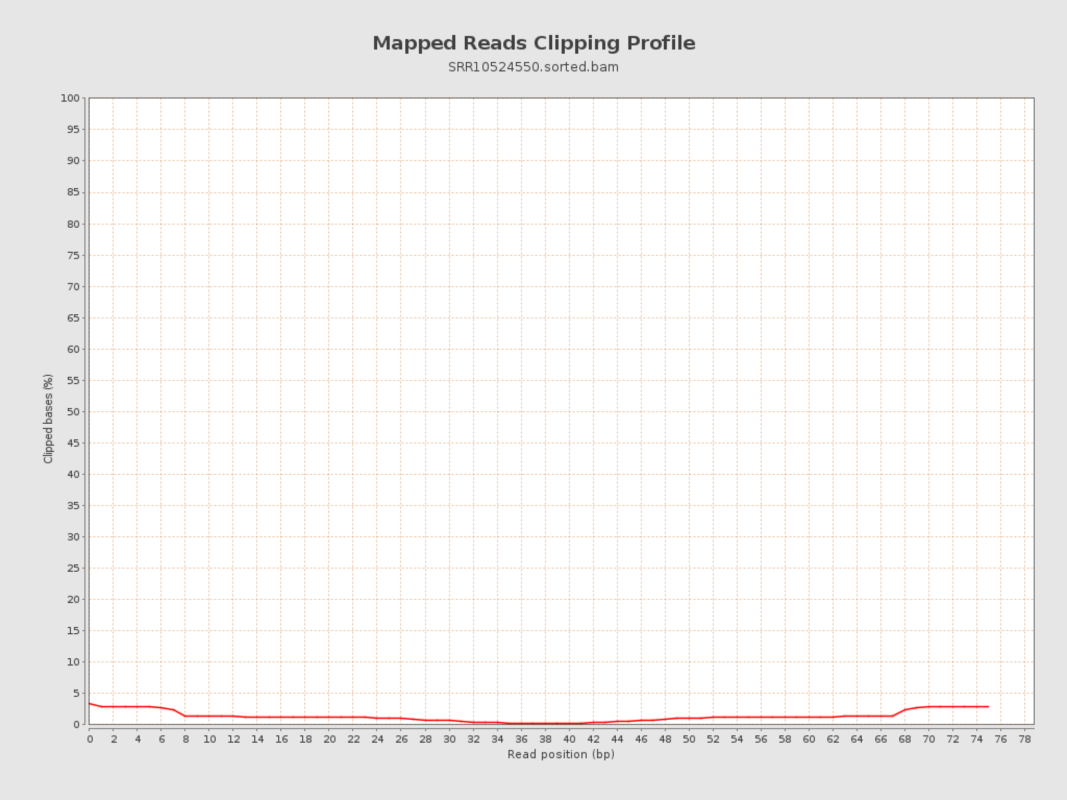
8. Results : Mapped Reads Nucleotide Content



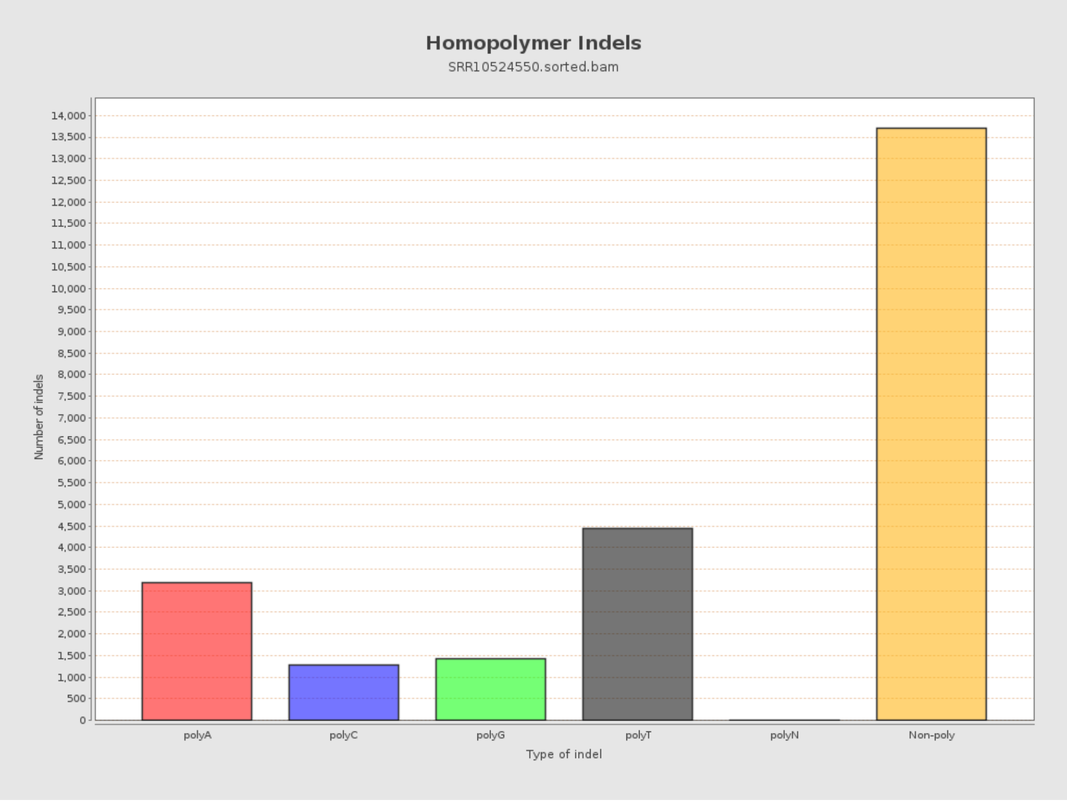
9. Results : Mapped Reads GC-content Distribution



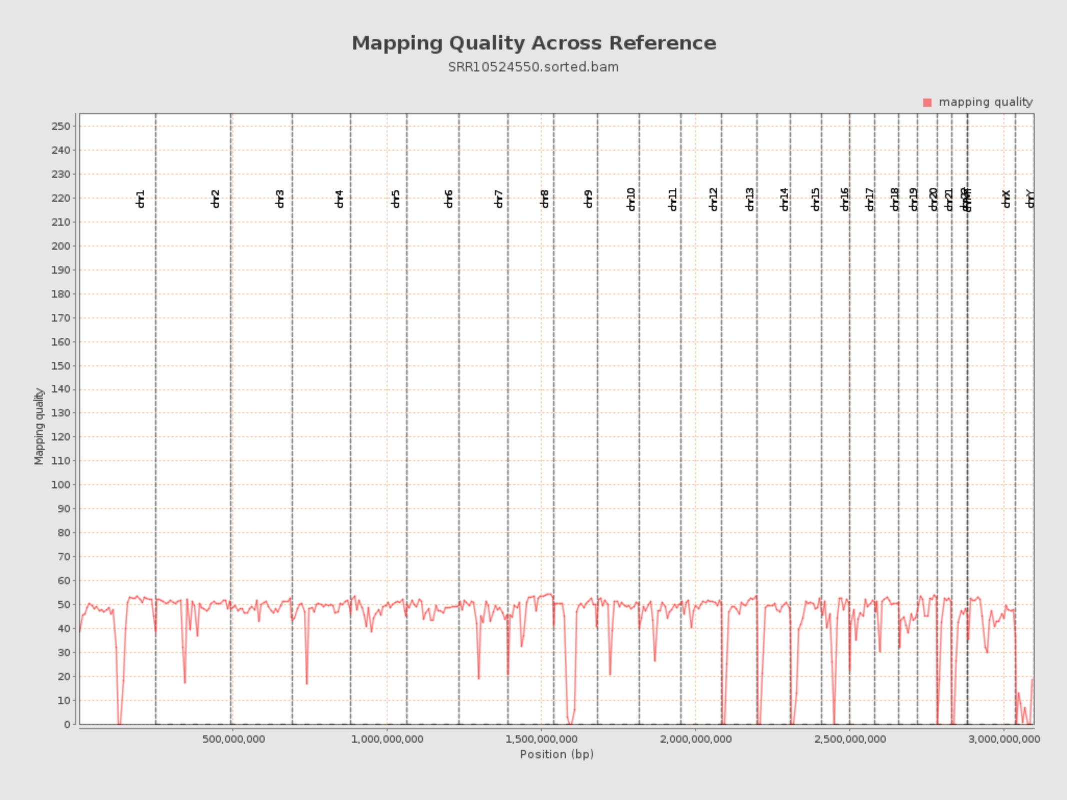
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram