Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 20:41:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524950.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_SRR10524950 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524950.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 20:41:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524950.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,414,478
Mapped reads	1,312,465 / 92.79%
Unmapped reads	102,013 / 7.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,270 / 0.23%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	34,899 / 2.47%
Duplication rate	1.9%
Clipped reads	1,311,674 / 92.73%

2.2. ACGT Content

Number/percentage of A's	19,678,165 / 25.62%
Number/percentage of C's	12,849,531 / 16.73%
Number/percentage of T's	24,585,841 / 32%
Number/percentage of G's	19,705,739 / 25.65%
Number/percentage of N's	933 / 0%
GC Percentage	42.38%

2.3. Coverage

Mean	0.0248

Standard Deviation	0.2309

2.4. Mapping Quality

Mean Mapping Quality	45.34

2.5. Mismatches and indels

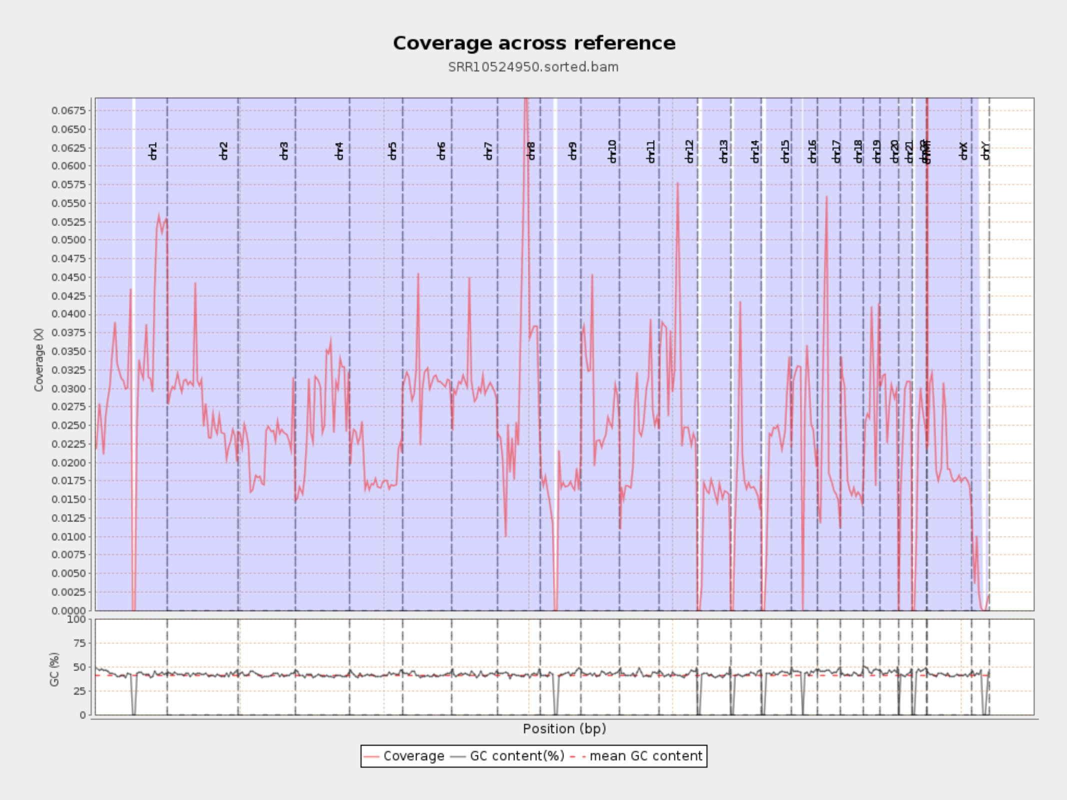
General error rate	0.49%
Mismatches	364,989
Insertions	5,004
Mapped reads with at least one insertion	0.38%
Deletions	14,390
Mapped reads with at least one deletion	1.09%
Homopolymer indels	44.18%

2.6. Chromosome stats

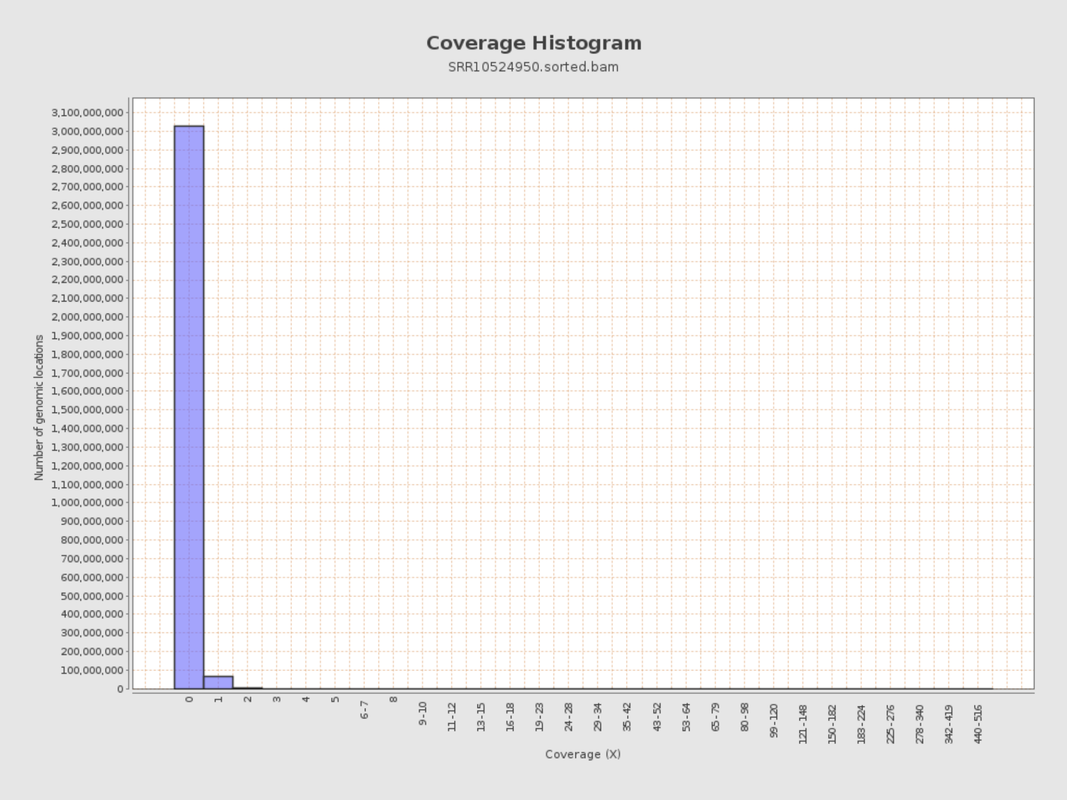
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8160225	0.0327	0.4133
chr2	243199373	6728537	0.0277	0.2557
chr3	198022430	4417006	0.0223	0.1607
chr4	191154276	5148988	0.0269	0.1847
chr5	180915260	3483679	0.0193	0.1502
chr6	171115067	5332741	0.0312	0.24
chr7	159138663	4875293	0.0306	0.3102

chr8	146364022	4827176	0.033	0.2584
chr9	141213431	2139208	0.0151	0.1807
chr10	135534747	3881870	0.0286	0.2271
chr11	135006516	3246759	0.024	0.2072
chr12	133851895	4234084	0.0316	0.1911
chr13	115169878	1548251	0.0134	0.1243
chr14	107349540	1776939	0.0166	0.14
chr15	102531392	2114454	0.0206	0.1635
chr16	90354753	2372228	0.0263	0.1829
chr17	81195210	1881769	0.0232	0.207
chr18	78077248	1546881	0.0198	0.278
chr19	59128983	1735520	0.0294	0.274
chr20	63025520	1797244	0.0285	0.1807
chr21	48129895	1134970	0.0236	0.1698
chr22	51304566	940704	0.0183	0.1431
chrMT	16571	67650	4.0824	3.2943
chrX	155270560	3261690	0.021	0.1729
chrY	59373566	190980	0.0032	0.0797

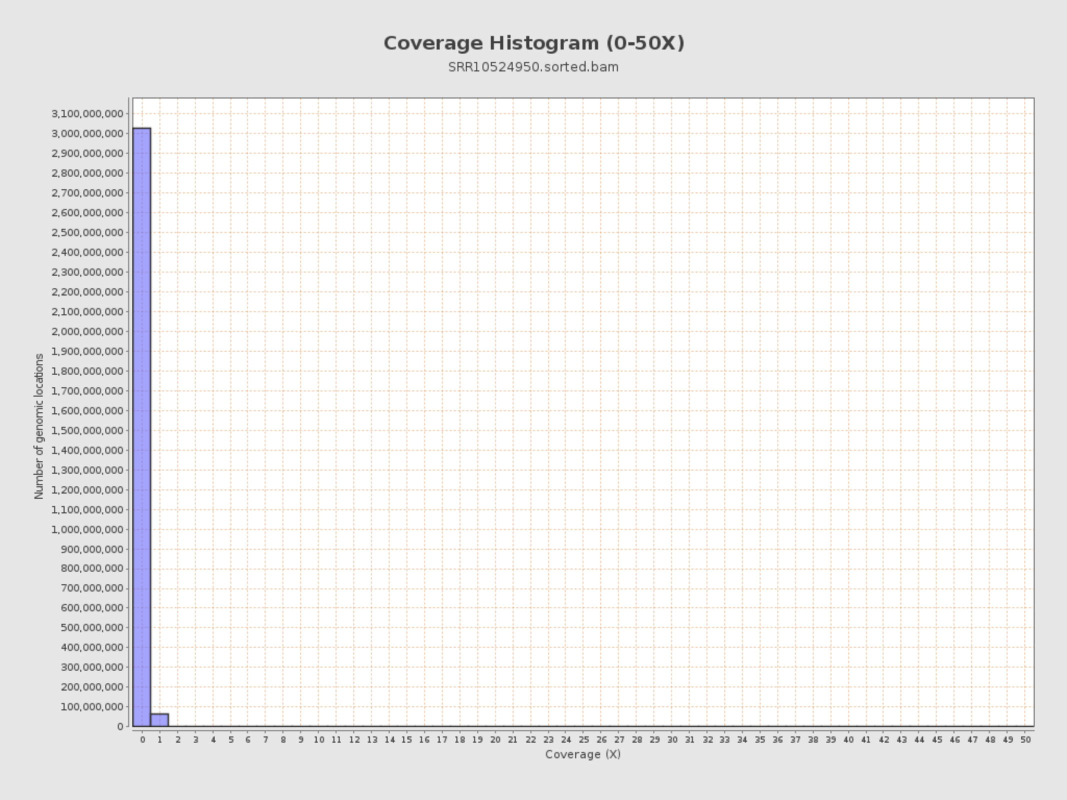
3. Results : Coverage across reference



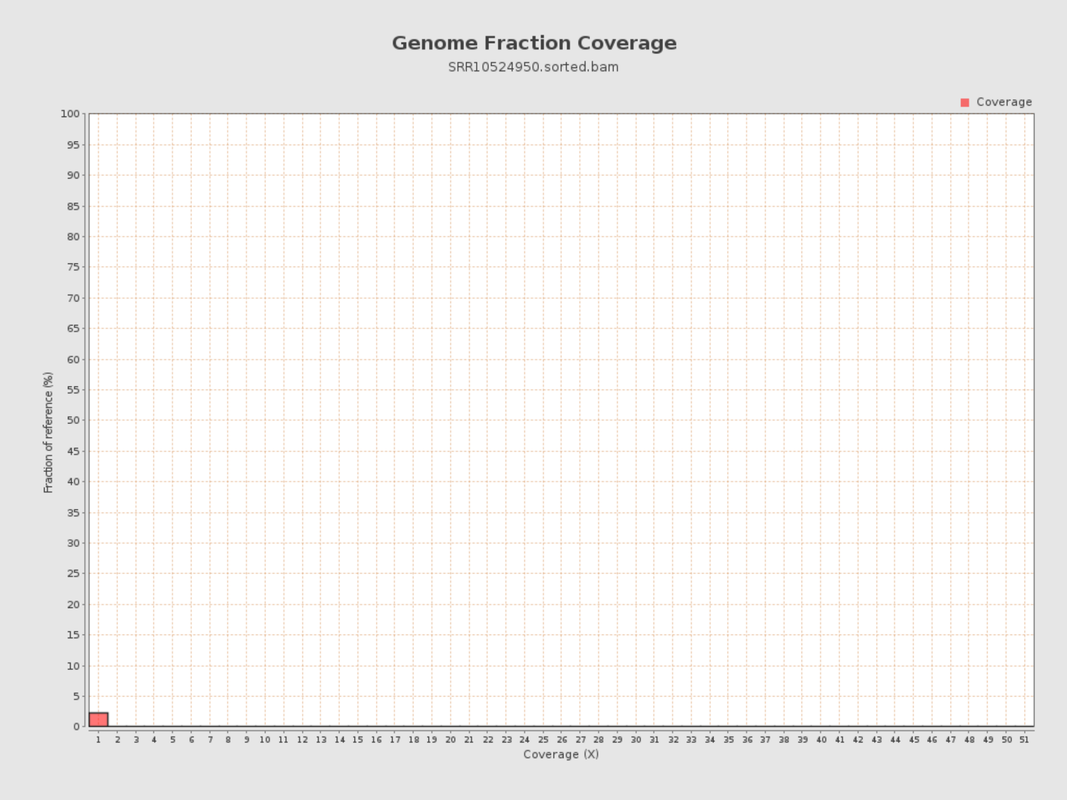
4. Results : Coverage Histogram



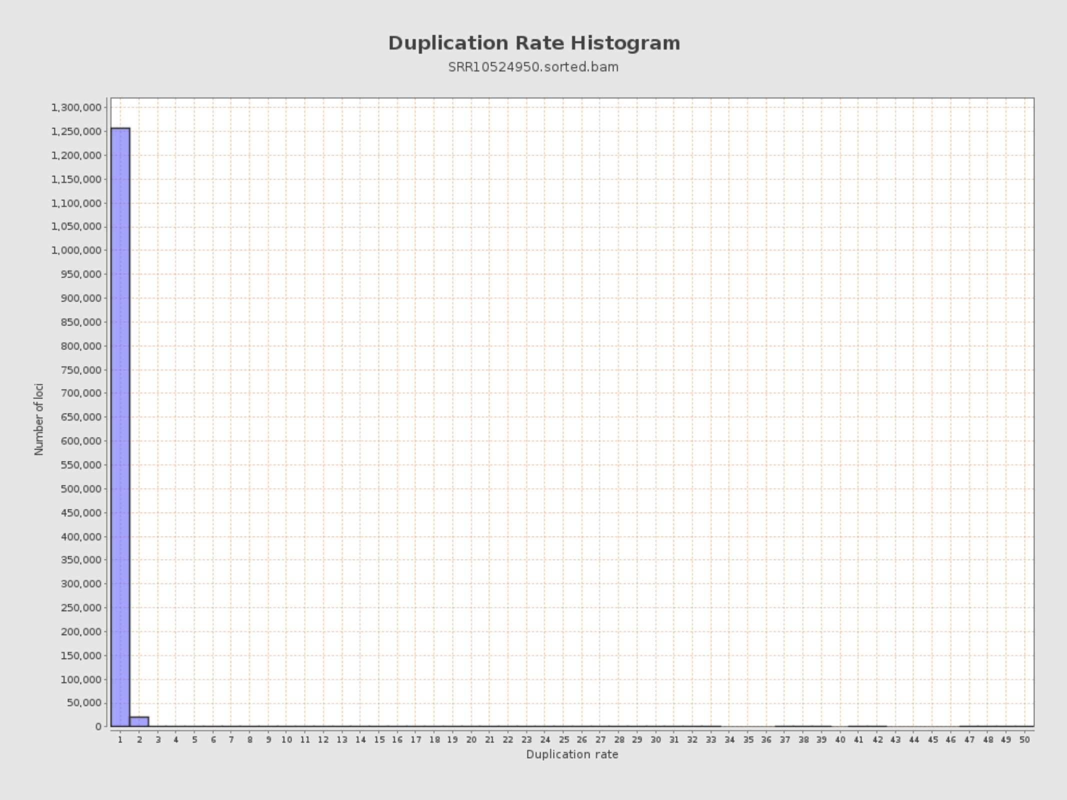
5. Results : Coverage Histogram (0-50X)



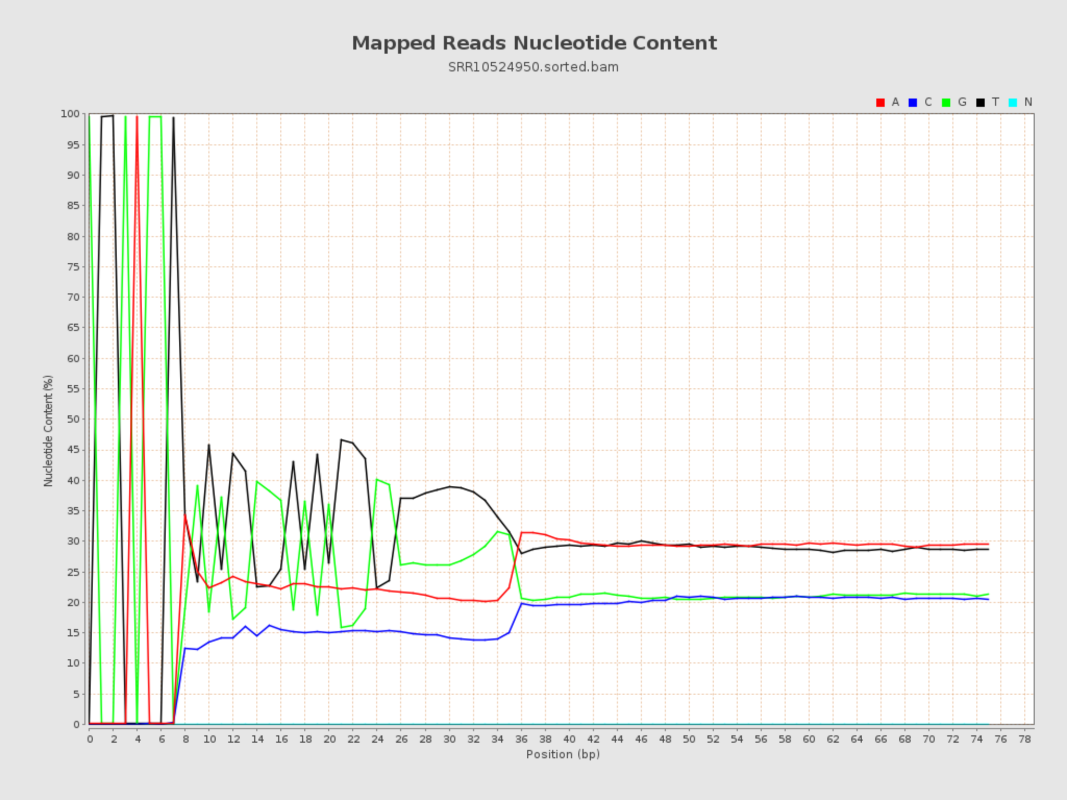
6. Results : Genome Fraction Coverage



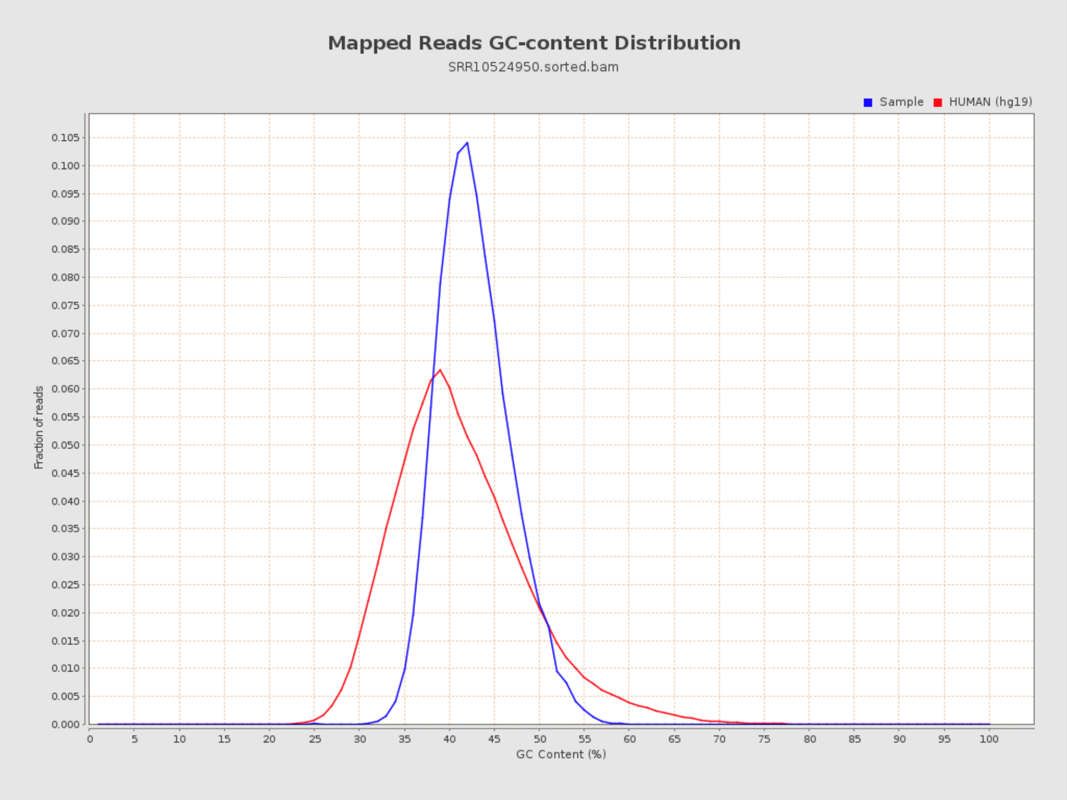
7. Results : Duplication Rate Histogram



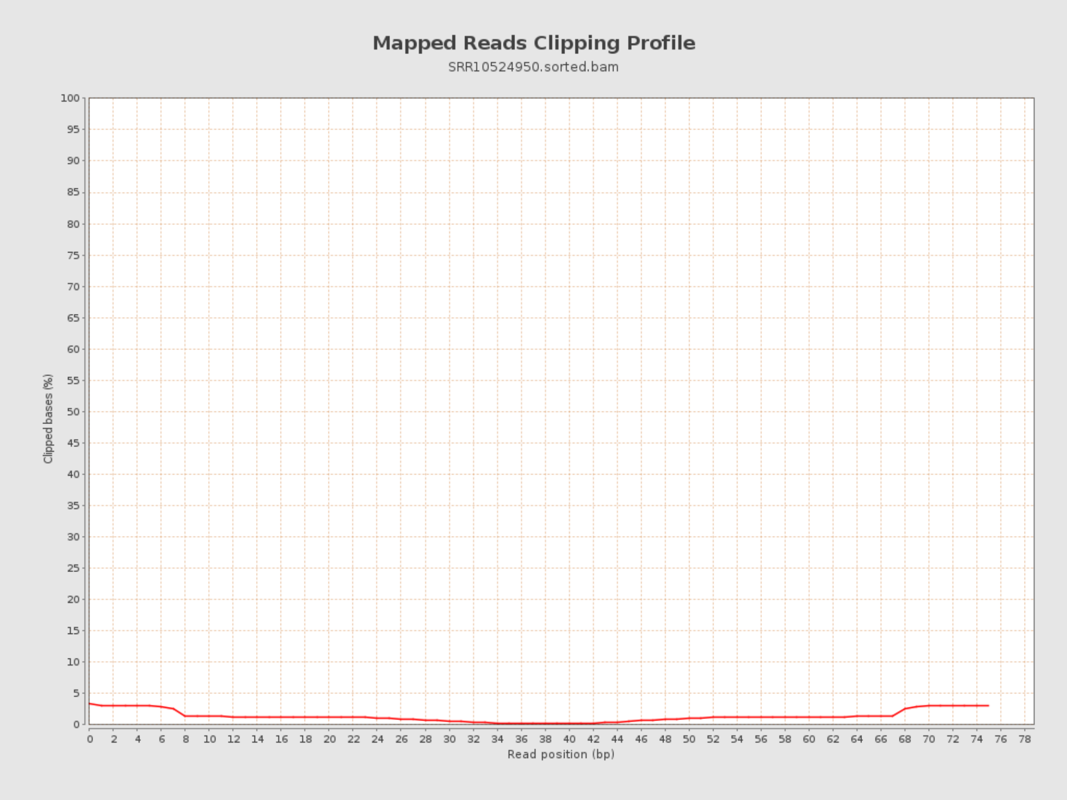
8. Results : Mapped Reads Nucleotide Content



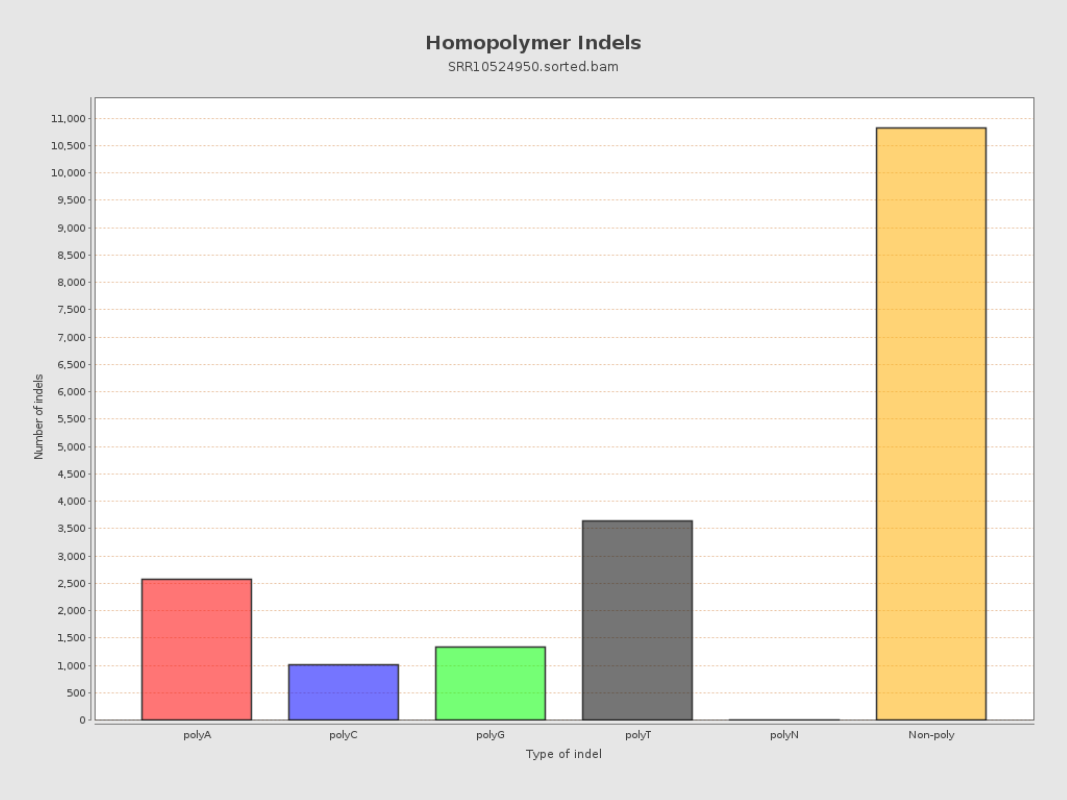
9. Results : Mapped Reads GC-content Distribution



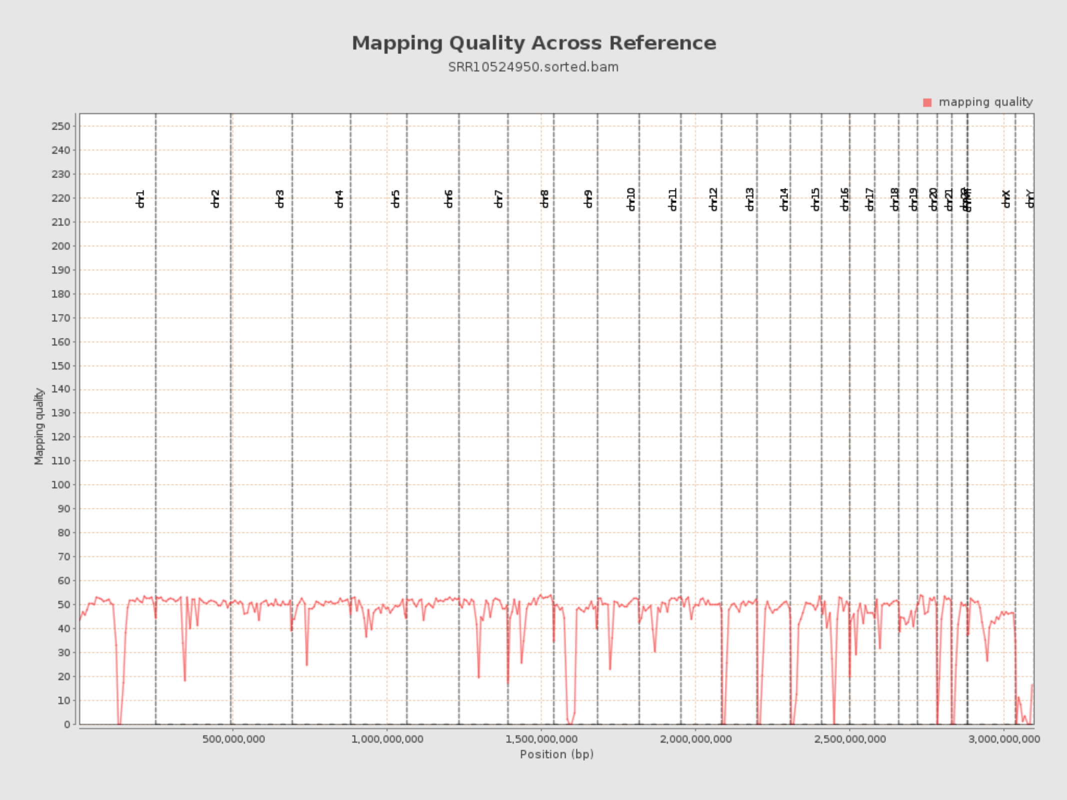
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram