Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 22:02:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524822.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_SRR10524822 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524822.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 22:02:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524822.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	745,061
Mapped reads	671,359 / 90.11%
Unmapped reads	73,702 / 9.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,736 / 0.37%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	14,567 / 1.96%
Duplication rate	1.57%
Clipped reads	672,328 / 90.24%

2.2. ACGT Content

Number/percentage of A's	9,896,252 / 25.72%
Number/percentage of C's	6,535,407 / 16.98%
Number/percentage of T's	12,399,762 / 32.22%
Number/percentage of G's	9,649,731 / 25.08%
Number/percentage of N's	713 / 0%
GC Percentage	42.06%

2.3. Coverage

Mean	0.0124

Standard Deviation	0.1501

2.4. Mapping Quality

Mean Mapping Quality	44.43

2.5. Mismatches and indels

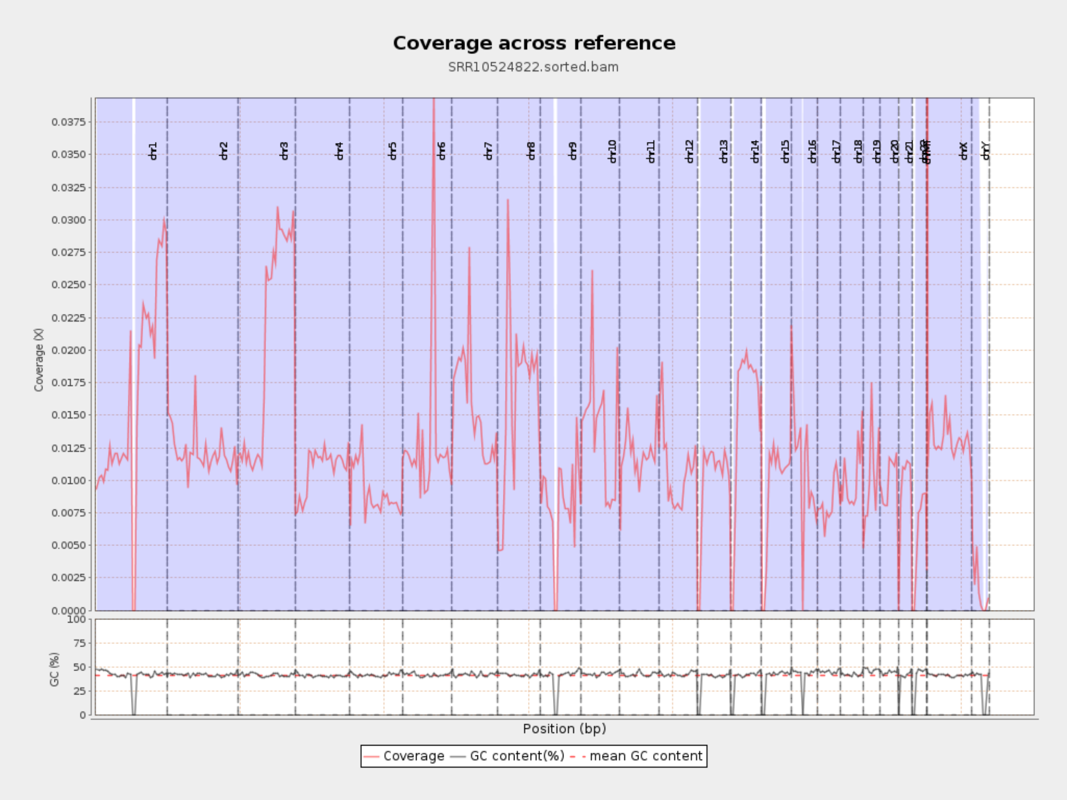
General error rate	0.53%
Mismatches	199,490
Insertions	2,532
Mapped reads with at least one insertion	0.38%
Deletions	7,954
Mapped reads with at least one deletion	1.18%
Homopolymer indels	43.49%

2.6. Chromosome stats

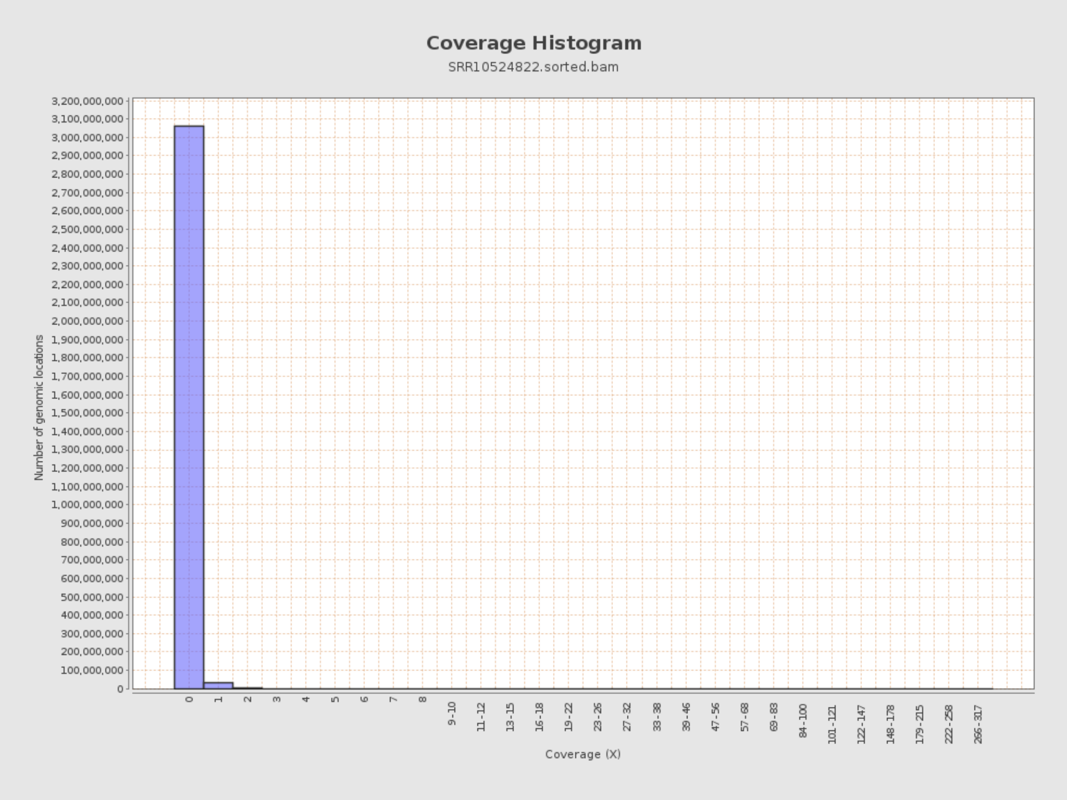
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4043888	0.0162	0.2444
chr2	243199373	2963570	0.0122	0.1744
chr3	198022430	4040870	0.0204	0.1488
chr4	191154276	2080667	0.0109	0.11
chr5	180915260	1661592	0.0092	0.1
chr6	171115067	2298616	0.0134	0.1267
chr7	159138663	2501711	0.0157	0.2359

chr8	146364022	2417596	0.0165	0.1606
chr9	141213431	1147040	0.0081	0.108
chr10	135534747	1899622	0.014	0.1616
chr11	135006516	1625895	0.012	0.1293
chr12	133851895	1456252	0.0109	0.1091
chr13	115169878	1141394	0.0099	0.1043
chr14	107349540	1622618	0.0151	0.1288
chr15	102531392	943776	0.0092	0.1009
chr16	90354753	1000101	0.0111	0.1154
chr17	81195210	678142	0.0084	0.0965
chr18	78077248	783431	0.01	0.177
chr19	59128983	609248	0.0103	0.1702
chr20	63025520	621157	0.0099	0.104
chr21	48129895	454701	0.0094	0.1031
chr22	51304566	291296	0.0057	0.078
chrMT	16571	52238	3.1524	2.4927
chrX	155270560	2057414	0.0133	0.1243
chrY	59373566	101749	0.0017	0.0526

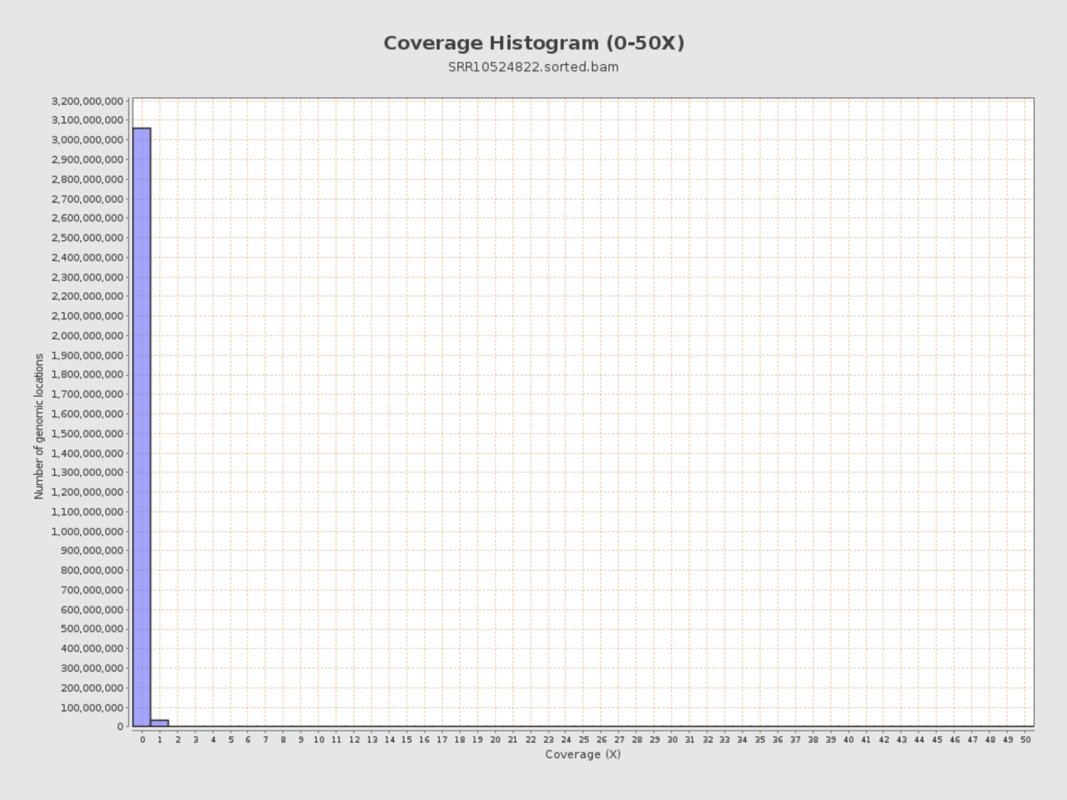
3. Results : Coverage across reference



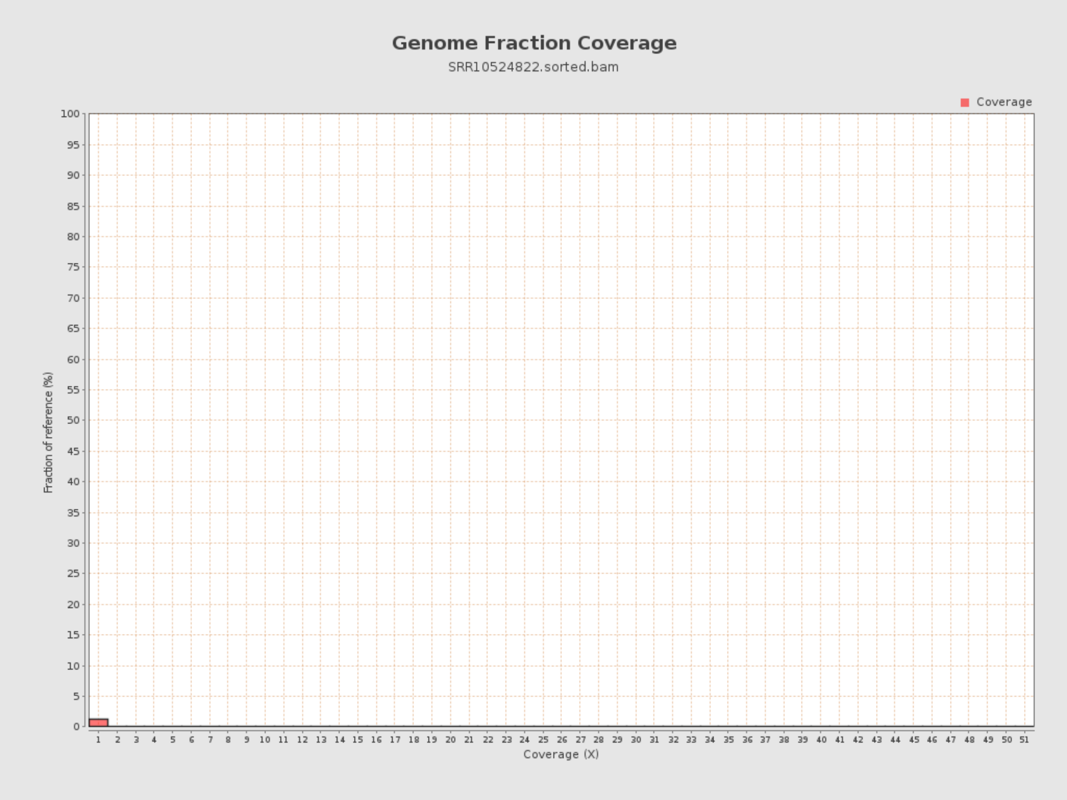
4. Results : Coverage Histogram



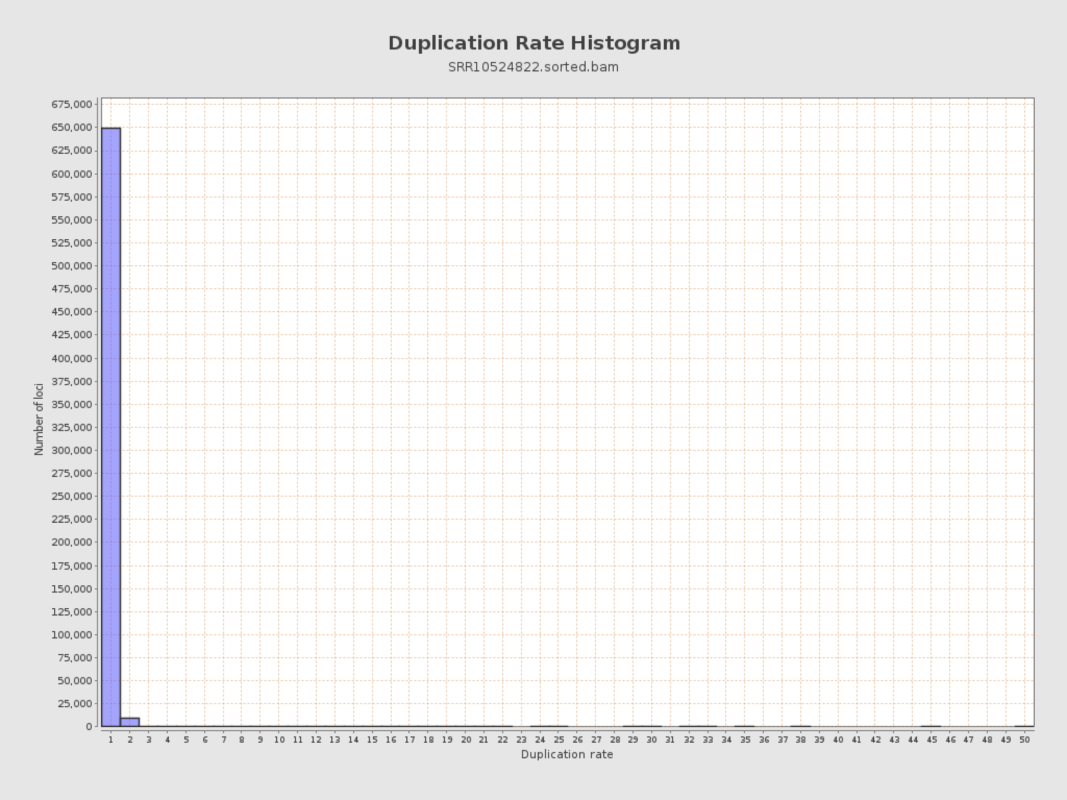
5. Results : Coverage Histogram (0-50X)



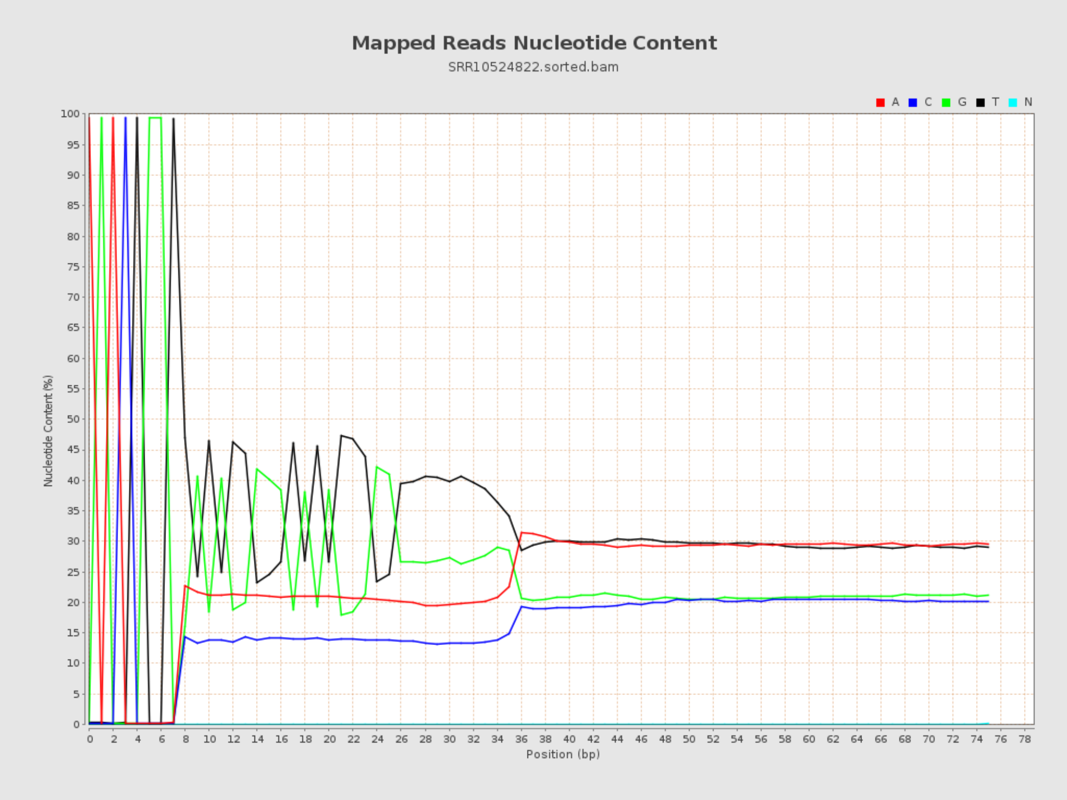
6. Results : Genome Fraction Coverage



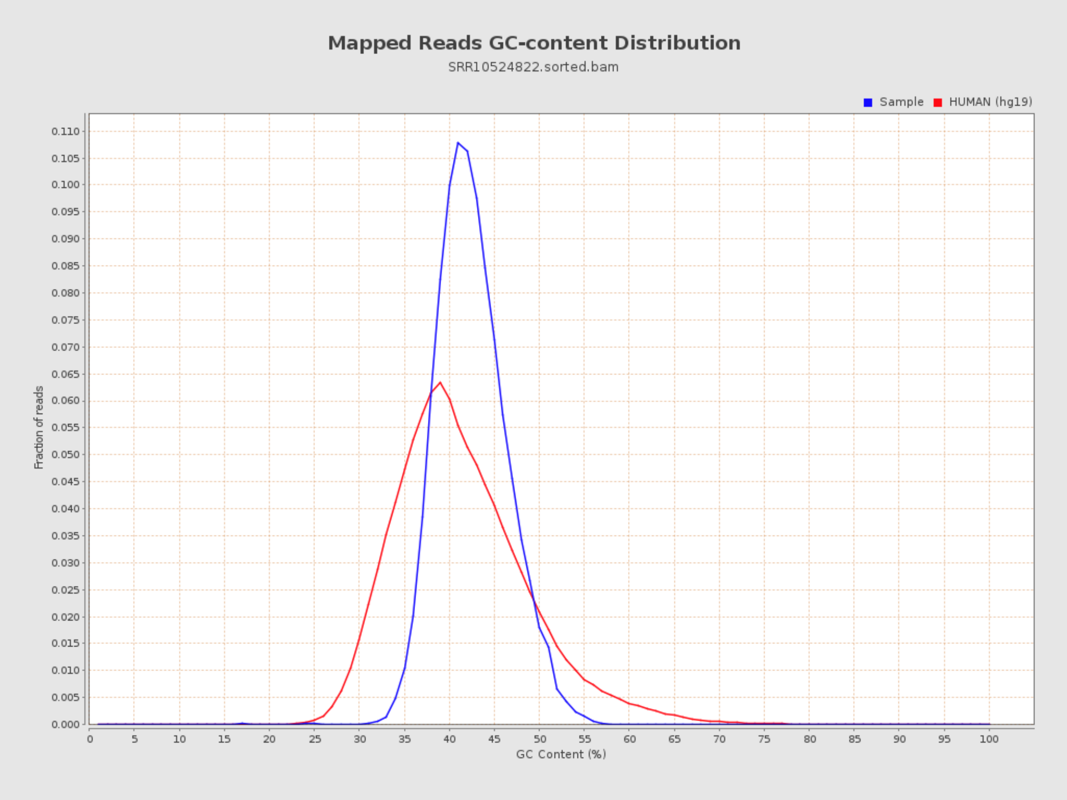
7. Results : Duplication Rate Histogram



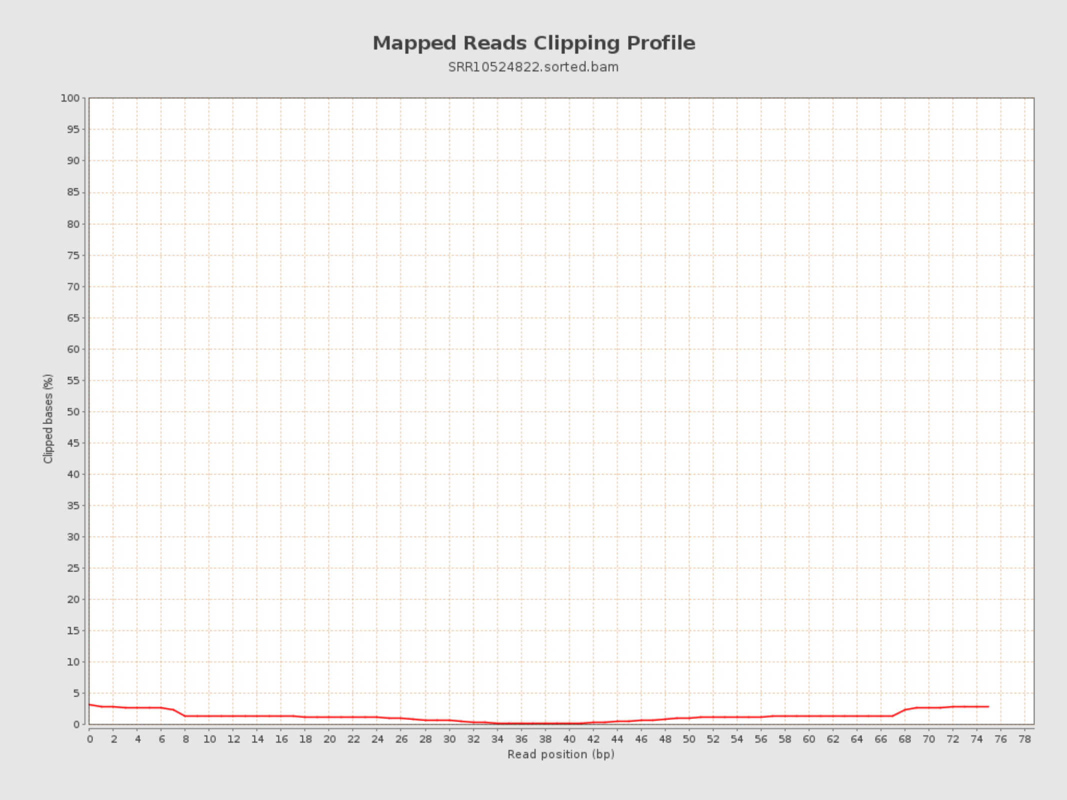
8. Results : Mapped Reads Nucleotide Content



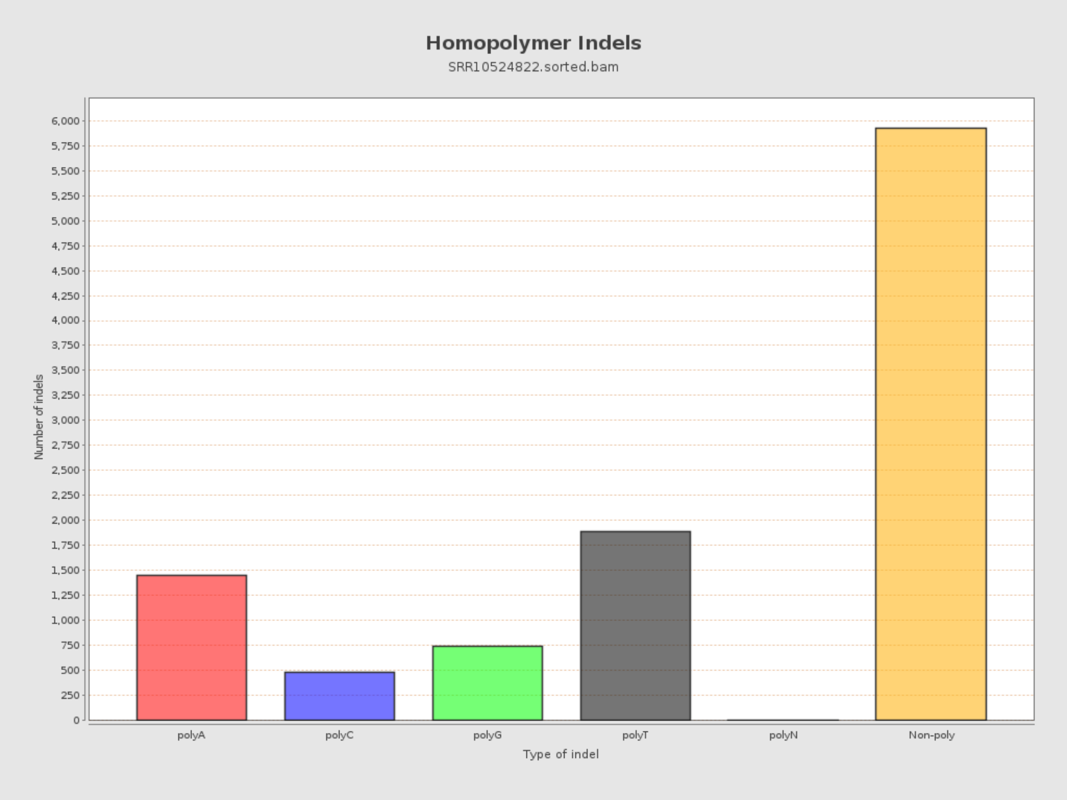
9. Results : Mapped Reads GC-content Distribution



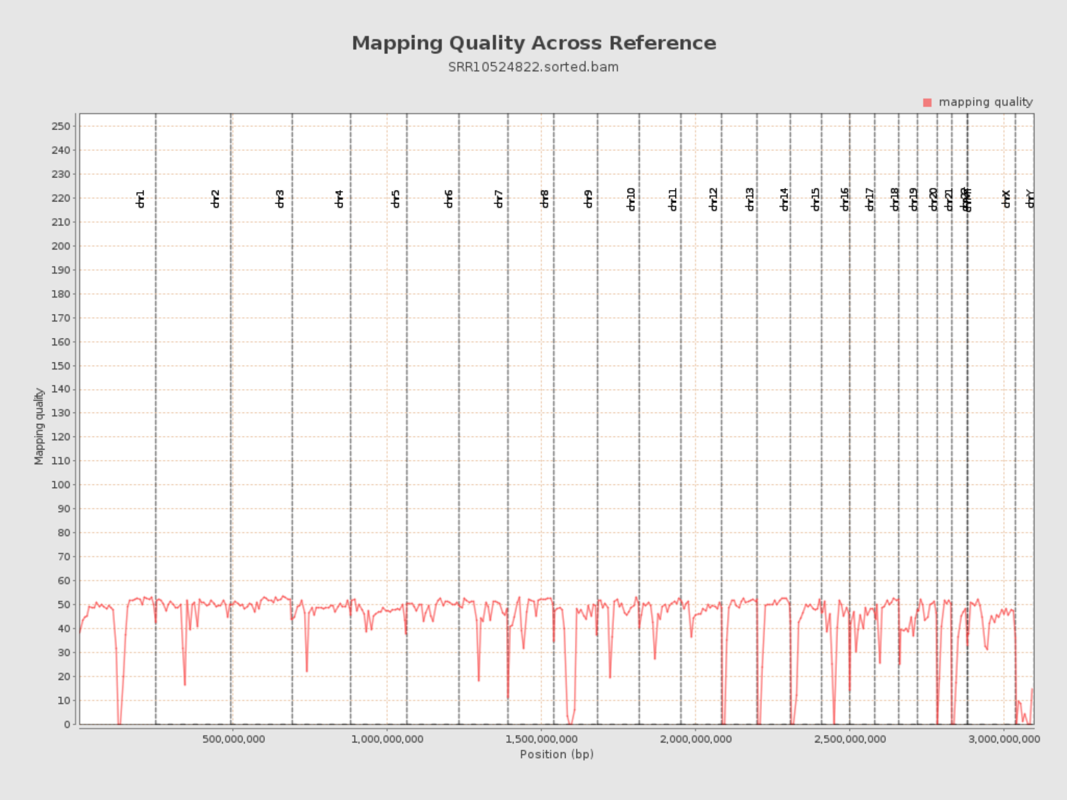
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram