Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 17:25:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524708.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_SRR10524708 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524708.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 17:25:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524708.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	612,026
Mapped reads	567,522 / 92.73%
Unmapped reads	44,504 / 7.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,318 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	11,447 / 1.87%
Duplication rate	1.46%
Clipped reads	567,421 / 92.71%

2.2. ACGT Content

Number/percentage of A's	9,411,874 / 27.58%
Number/percentage of C's	6,484,793 / 19%
Number/percentage of T's	10,253,566 / 30.05%
Number/percentage of G's	7,968,843 / 23.35%
Number/percentage of N's	4,950 / 0.01%
GC Percentage	42.36%

2.3. Coverage

Mean	0.011

Standard Deviation	0.1358

2.4. Mapping Quality

Mean Mapping Quality	46.24

2.5. Mismatches and indels

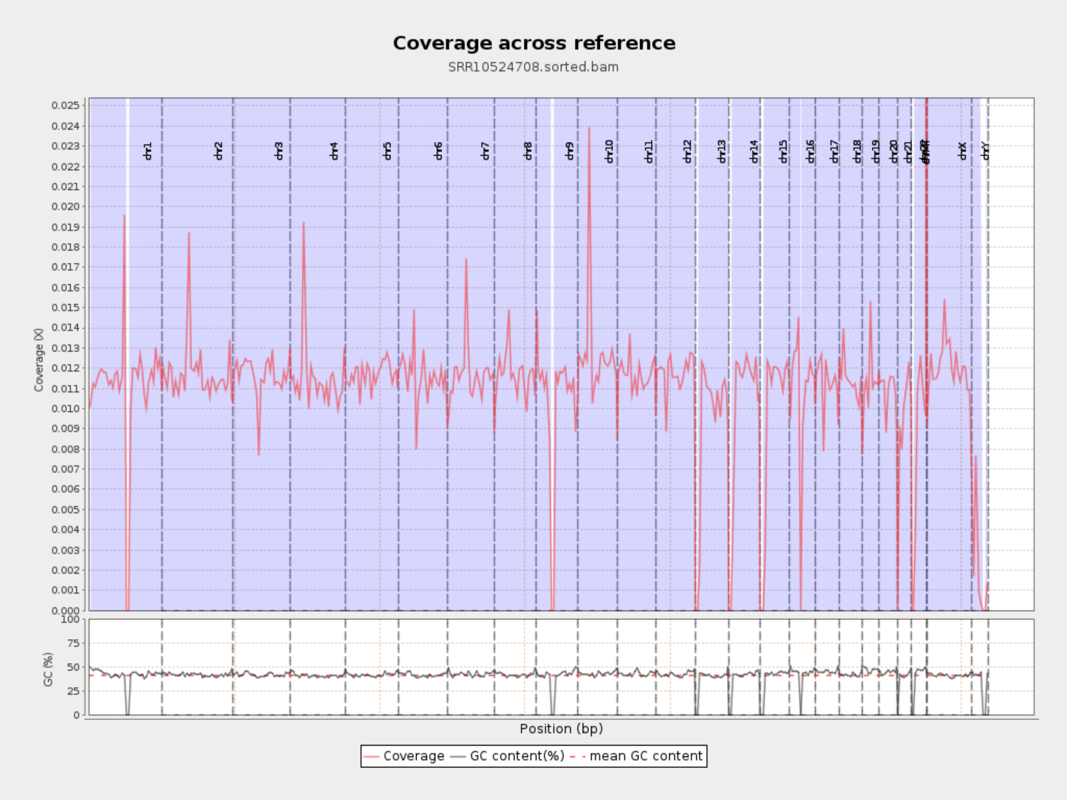
General error rate	0.52%
Mismatches	169,818
Insertions	3,073
Mapped reads with at least one insertion	0.54%
Deletions	6,775
Mapped reads with at least one deletion	1.18%
Homopolymer indels	42.8%

2.6. Chromosome stats

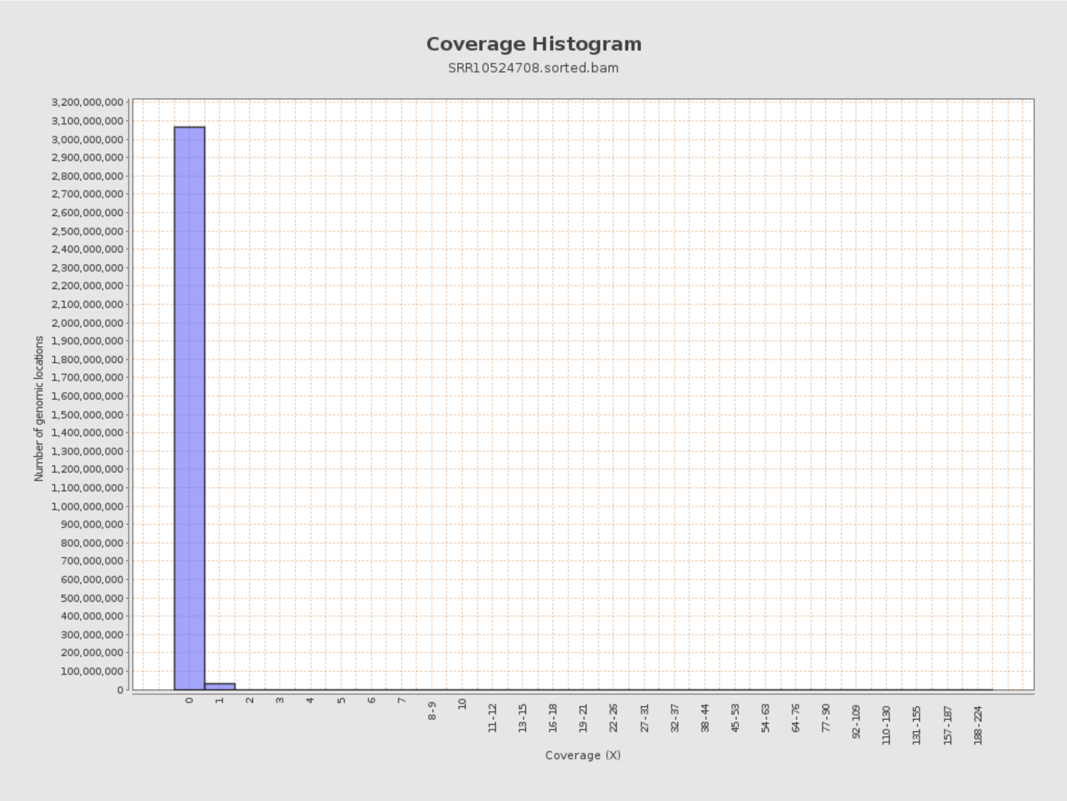
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2753310	0.011	0.2145
chr2	243199373	2870685	0.0118	0.1567
chr3	198022430	2302243	0.0116	0.1117
chr4	191154276	2191527	0.0115	0.1179
chr5	180915260	2120426	0.0117	0.1123
chr6	171115067	1978447	0.0116	0.1176
chr7	159138663	1871343	0.0118	0.15

chr8	146364022	1712228	0.0117	0.1484
chr9	141213431	1407489	0.01	0.1187
chr10	135534747	1732535	0.0128	0.1462
chr11	135006516	1572791	0.0116	0.1269
chr12	133851895	1576307	0.0118	0.1126
chr13	115169878	1046013	0.0091	0.0984
chr14	107349540	1052566	0.0098	0.1034
chr15	102531392	973497	0.0095	0.1007
chr16	90354753	978530	0.0108	0.1135
chr17	81195210	909596	0.0112	0.1125
chr18	78077248	895694	0.0115	0.1915
chr19	59128983	675971	0.0114	0.1677
chr20	63025520	685530	0.0109	0.1089
chr21	48129895	444548	0.0092	0.1055
chr22	51304566	393122	0.0077	0.0904
chrMT	16571	9309	0.5618	0.7969
chrX	155270560	1865357	0.012	0.1169
chrY	59373566	115907	0.002	0.083

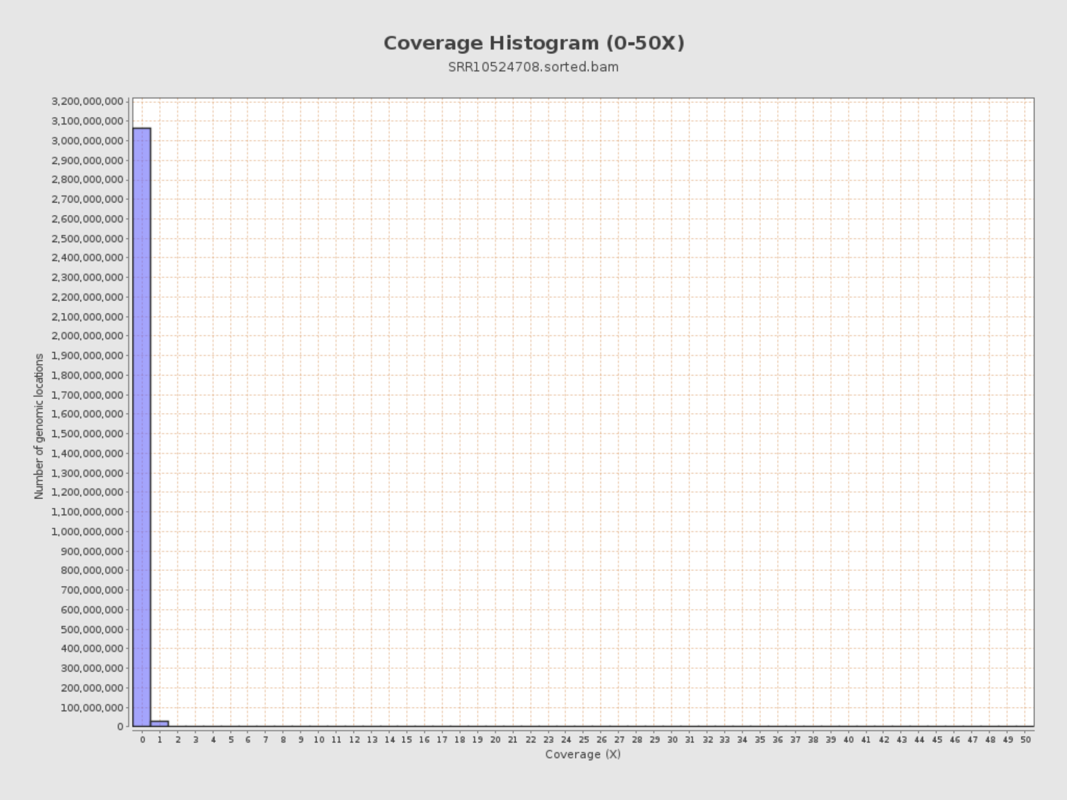
3. Results : Coverage across reference



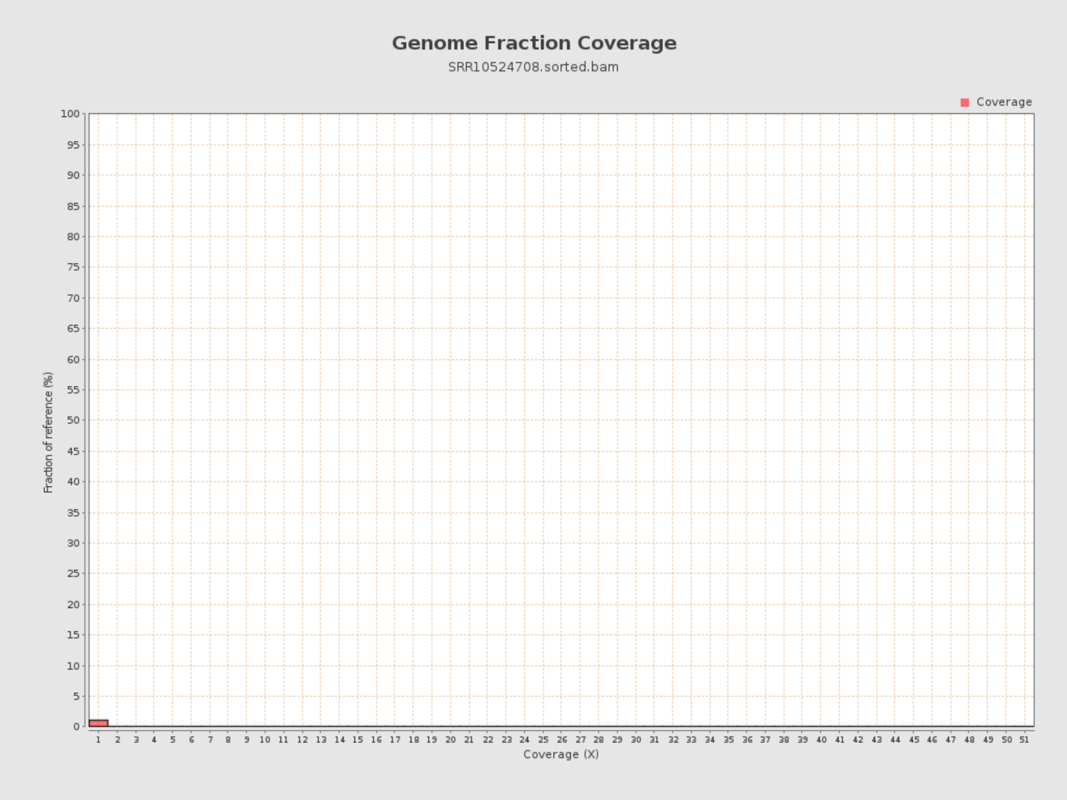
4. Results : Coverage Histogram



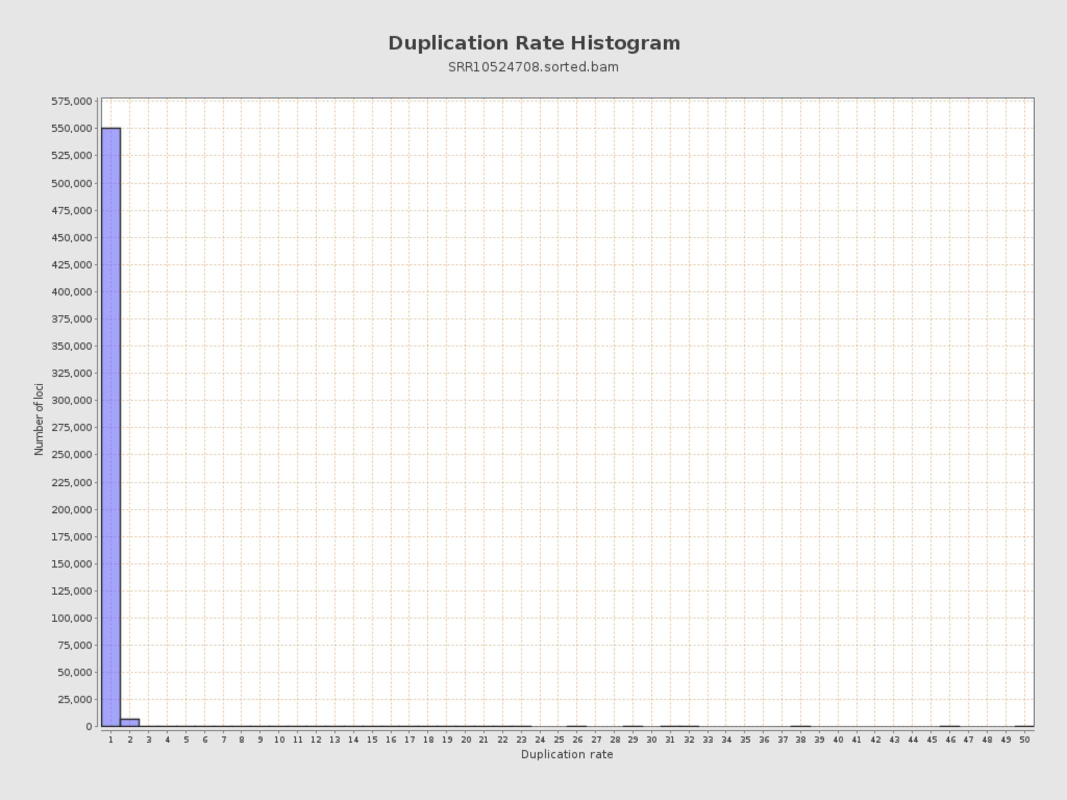
5. Results : Coverage Histogram (0-50X)



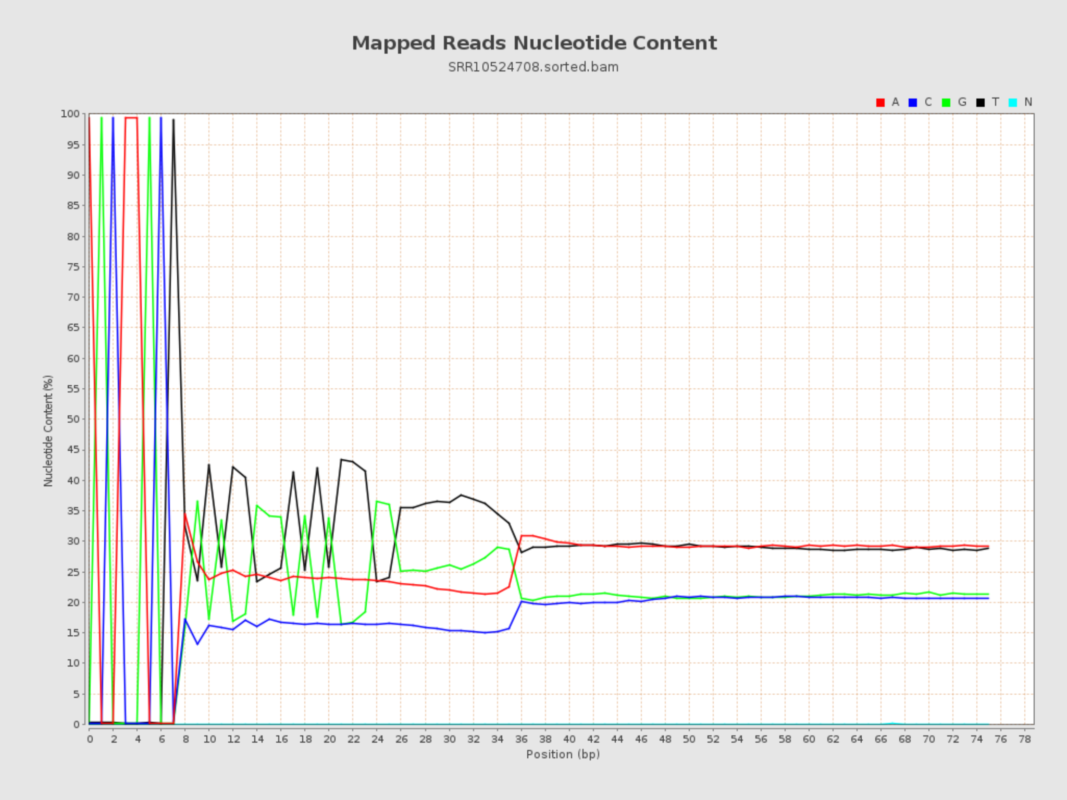
6. Results : Genome Fraction Coverage



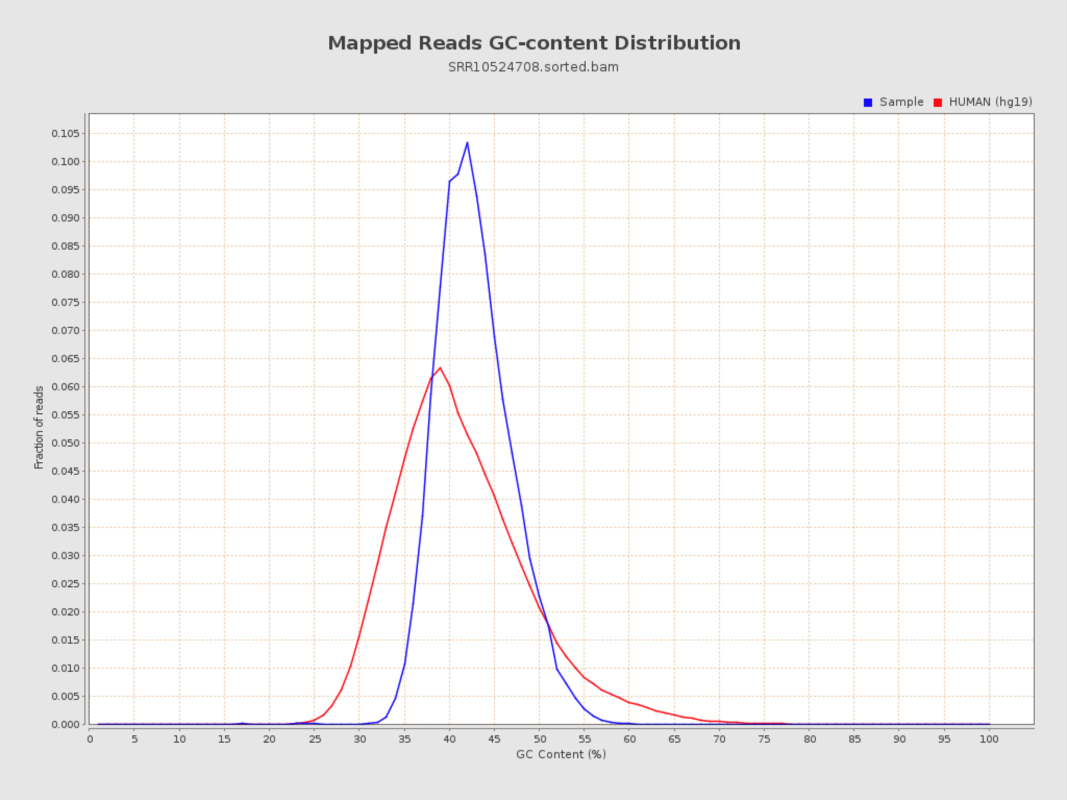
7. Results : Duplication Rate Histogram



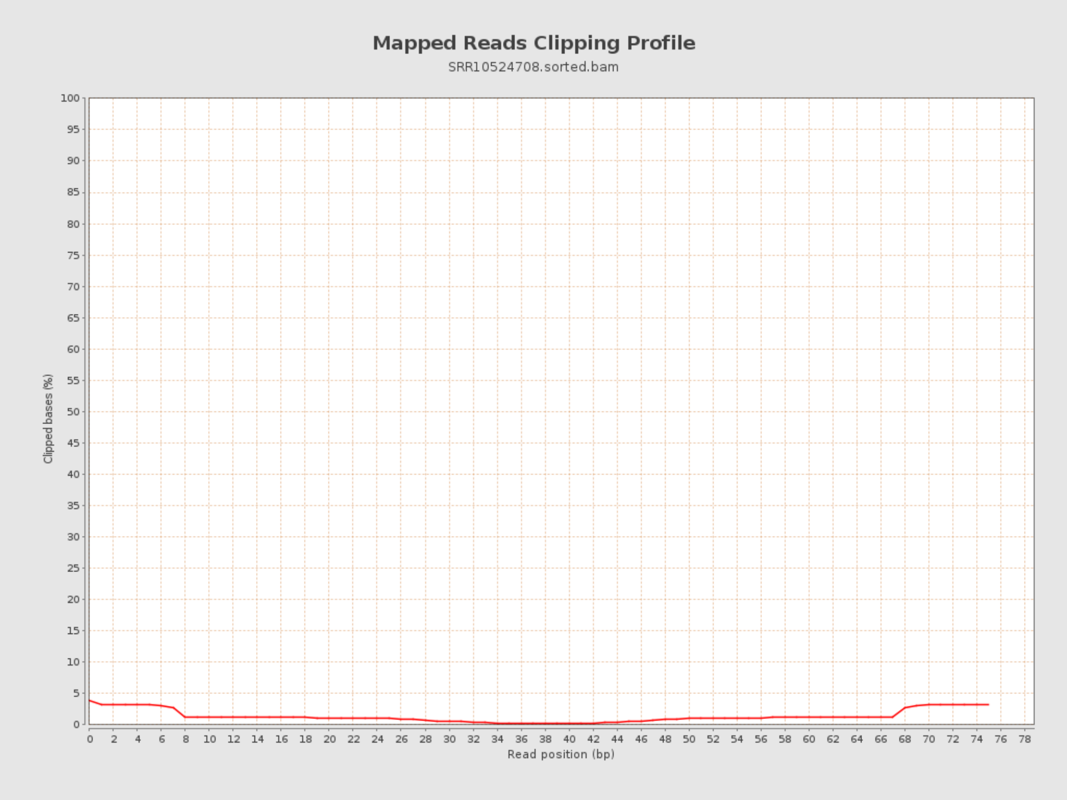
8. Results : Mapped Reads Nucleotide Content



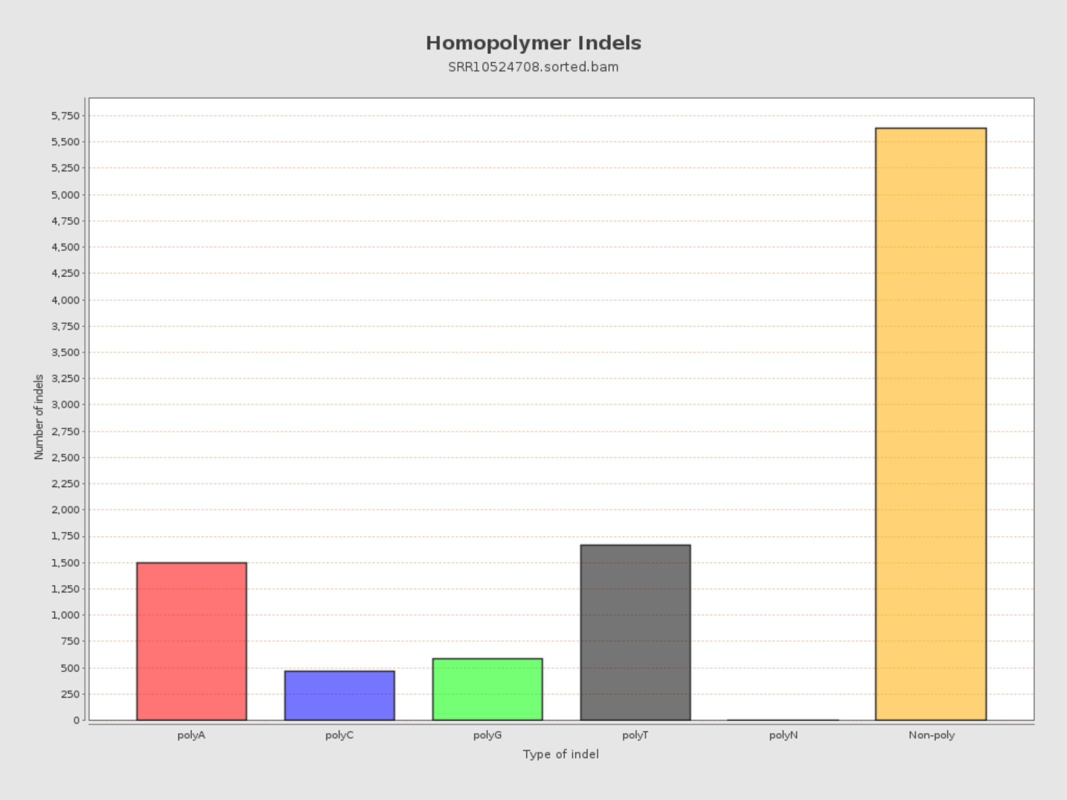
9. Results : Mapped Reads GC-content Distribution



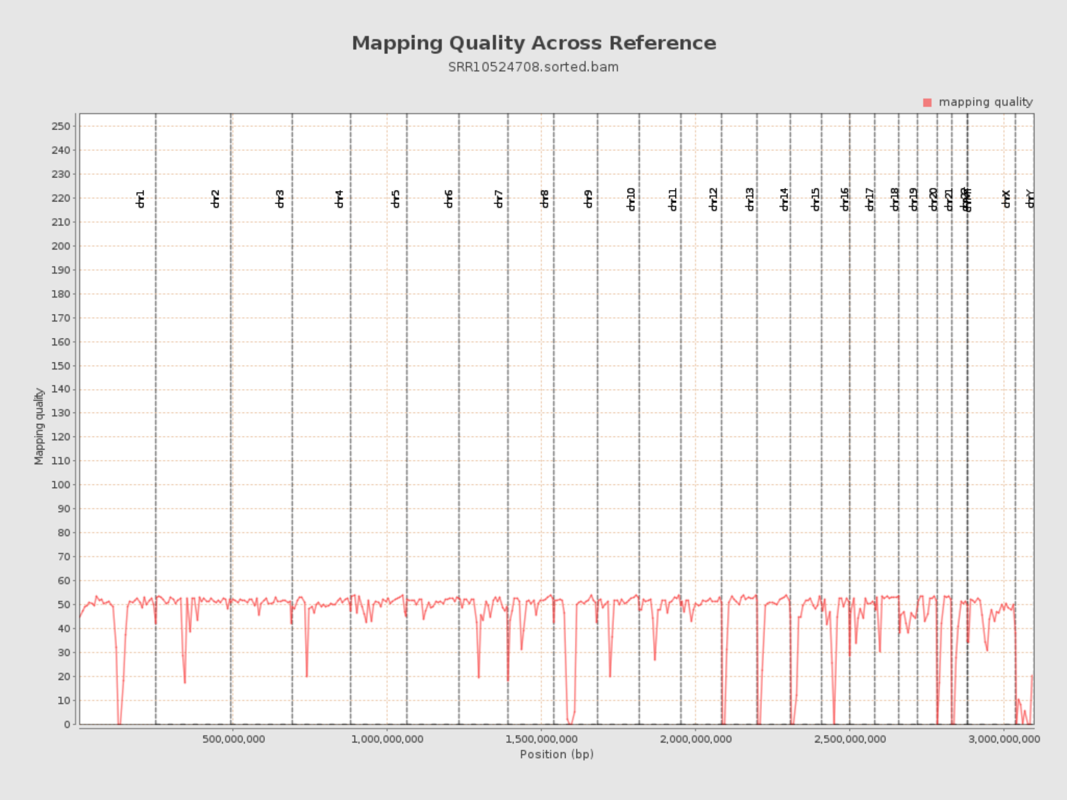
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram