Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 11:04:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524564.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_SRR10524564 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524564.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 11:04:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524564.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,414,113
Mapped reads	1,287,245 / 91.03%
Unmapped reads	126,868 / 8.97%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,014 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	50,243 / 3.55%
Duplication rate	2.97%
Clipped reads	1,288,598 / 91.12%

2.2. ACGT Content

Number/percentage of A's	19,074,966 / 25.51%
Number/percentage of C's	13,339,681 / 17.84%
Number/percentage of T's	23,424,772 / 31.32%
Number/percentage of G's	18,939,402 / 25.33%
Number/percentage of N's	1,142 / 0%
GC Percentage	43.17%

2.3. Coverage

Mean	0.0242

Standard Deviation	0.2363

2.4. Mapping Quality

Mean Mapping Quality	45.05

2.5. Mismatches and indels

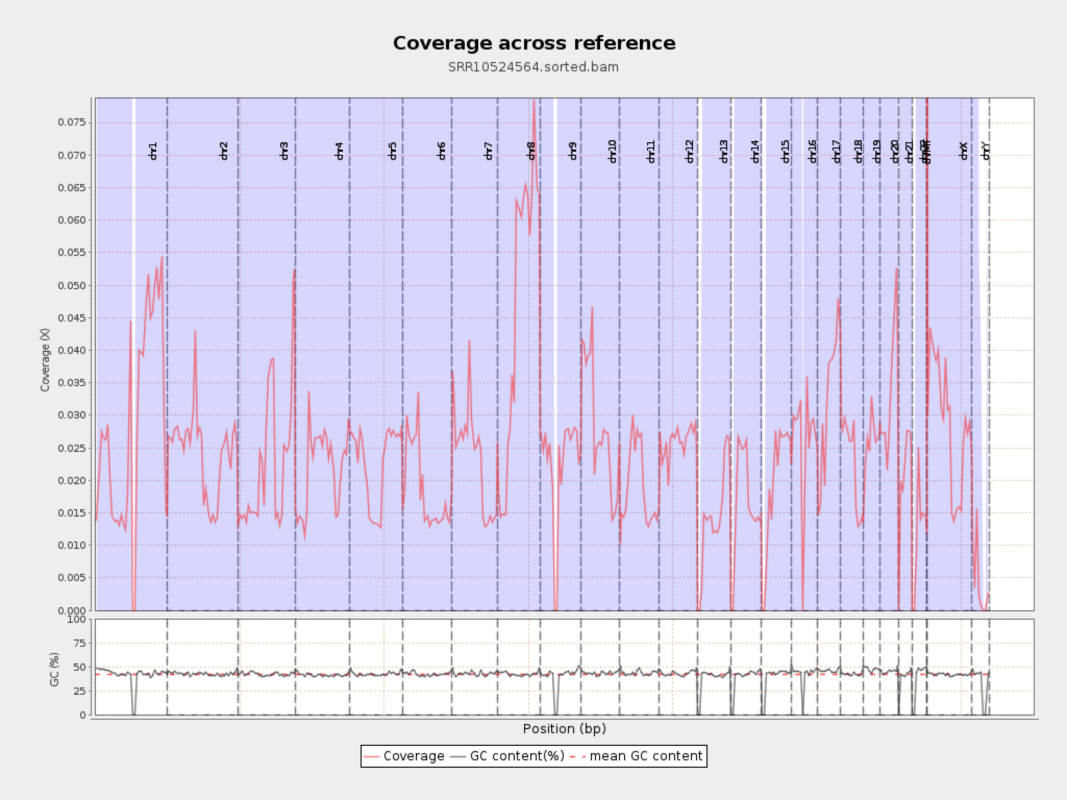
General error rate	0.53%
Mismatches	386,683
Insertions	4,680
Mapped reads with at least one insertion	0.36%
Deletions	14,695
Mapped reads with at least one deletion	1.13%
Homopolymer indels	42.75%

2.6. Chromosome stats

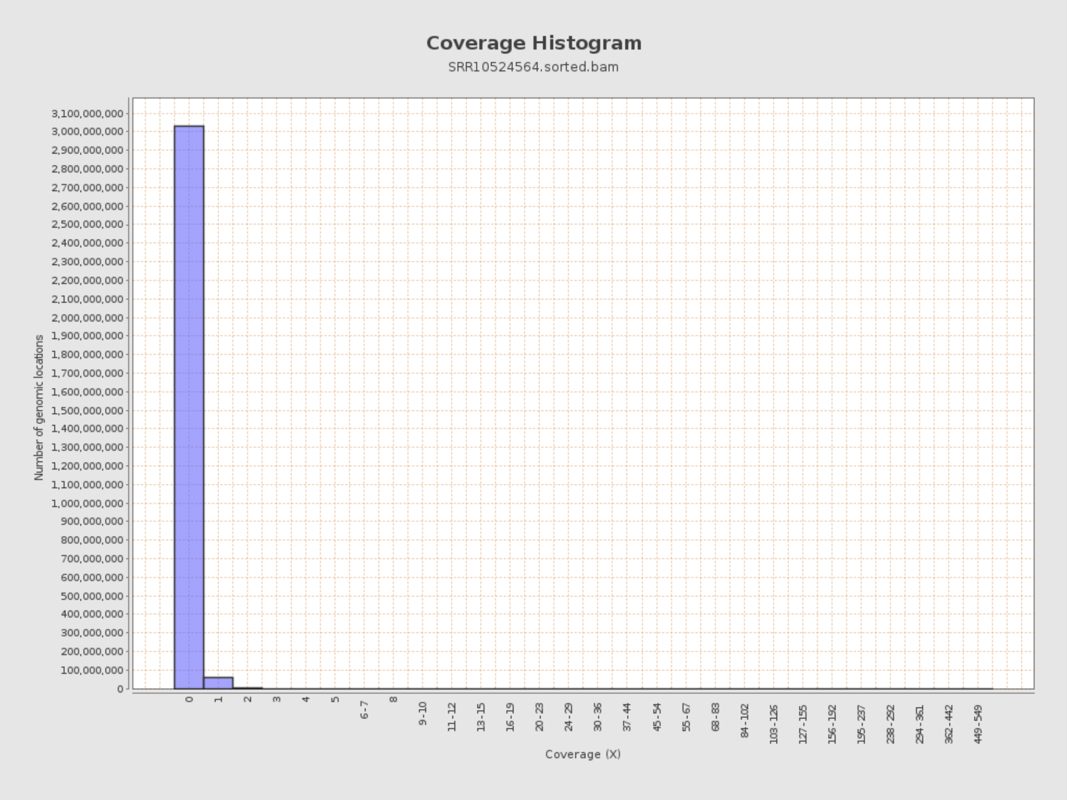
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7057471	0.0283	0.4307
chr2	243199373	5917369	0.0243	0.2625
chr3	198022430	4398951	0.0222	0.1645
chr4	191154276	4189389	0.0219	0.1802
chr5	180915260	4091843	0.0226	0.1643
chr6	171115067	3198298	0.0187	0.1818
chr7	159138663	3770366	0.0237	0.2846

chr8	146364022	6846171	0.0468	0.2738
chr9	141213431	3168346	0.0224	0.2
chr10	135534747	3904403	0.0288	0.2476
chr11	135006516	2580297	0.0191	0.2052
chr12	133851895	3475933	0.026	0.176
chr13	115169878	1636161	0.0142	0.131
chr14	107349540	1760237	0.0164	0.1421
chr15	102531392	1976371	0.0193	0.1538
chr16	90354753	2329340	0.0258	0.1846
chr17	81195210	2623296	0.0323	0.2061
chr18	78077248	1784145	0.0229	0.346
chr19	59128983	1555022	0.0263	0.295
chr20	63025520	2138478	0.0339	0.2021
chr21	48129895	1022040	0.0212	0.1761
chr22	51304566	619195	0.0121	0.1188
chrMT	16571	4052	0.2445	0.5101
chrX	155270560	4505323	0.029	0.2044
chrY	59373566	252126	0.0042	0.1326

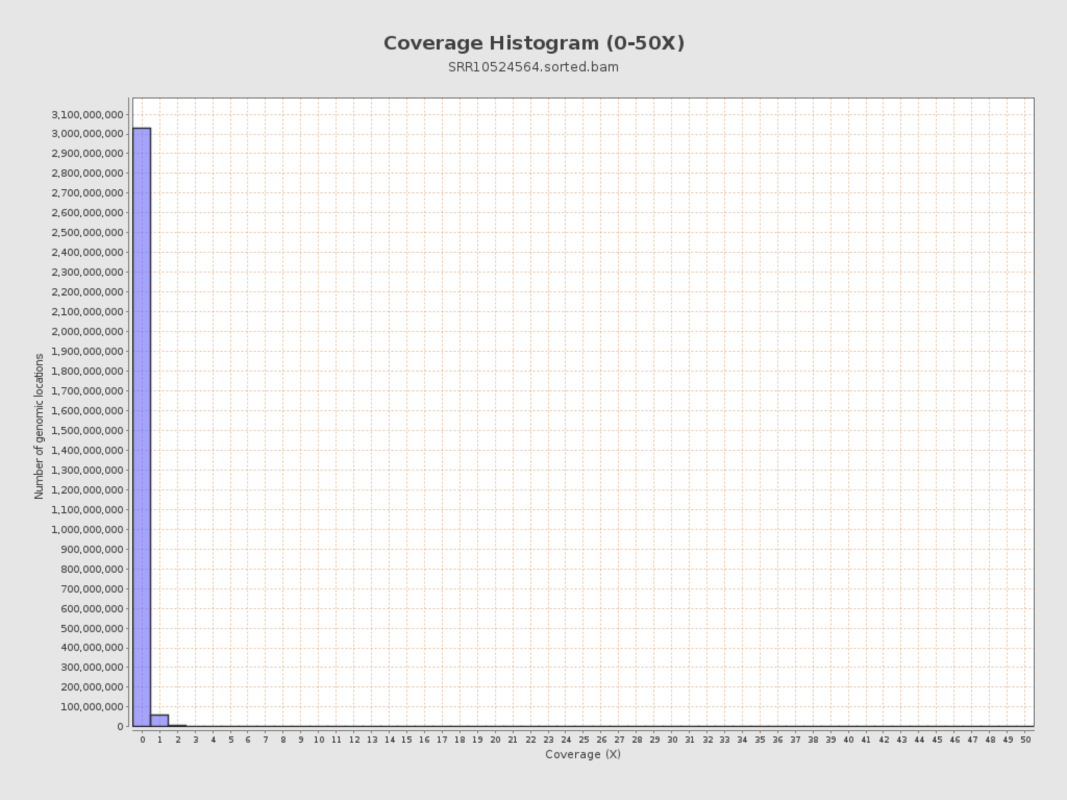
3. Results : Coverage across reference



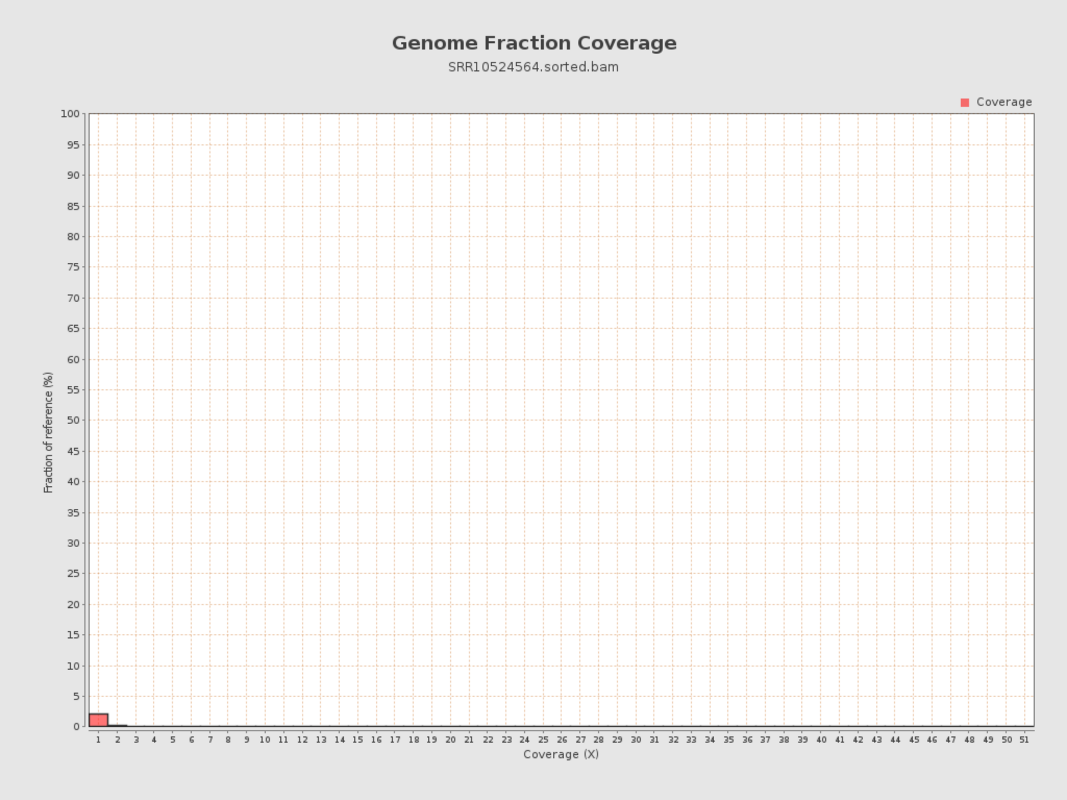
4. Results : Coverage Histogram



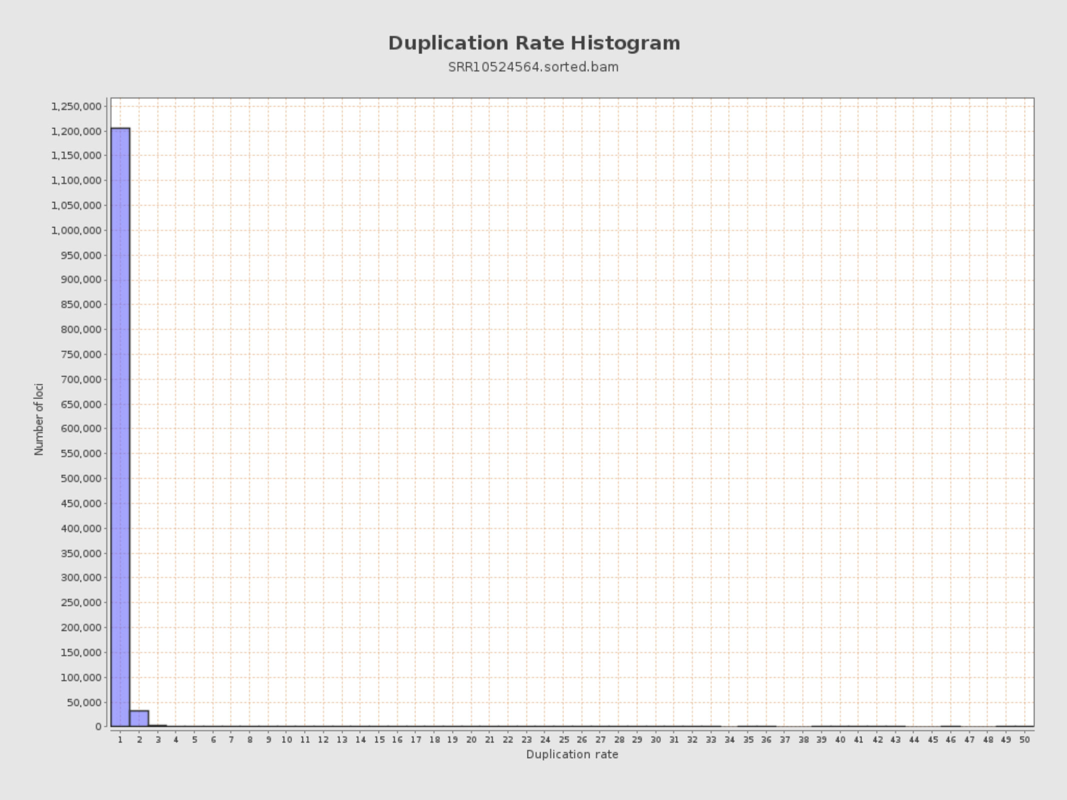
5. Results : Coverage Histogram (0-50X)



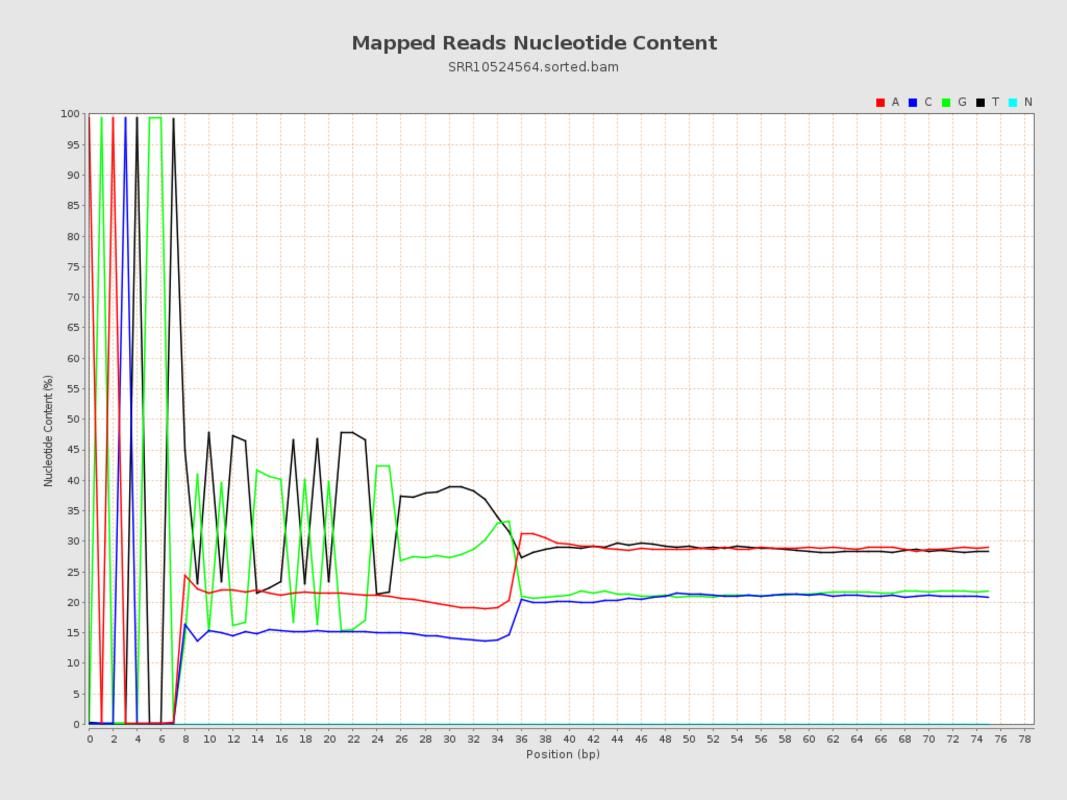
6. Results : Genome Fraction Coverage



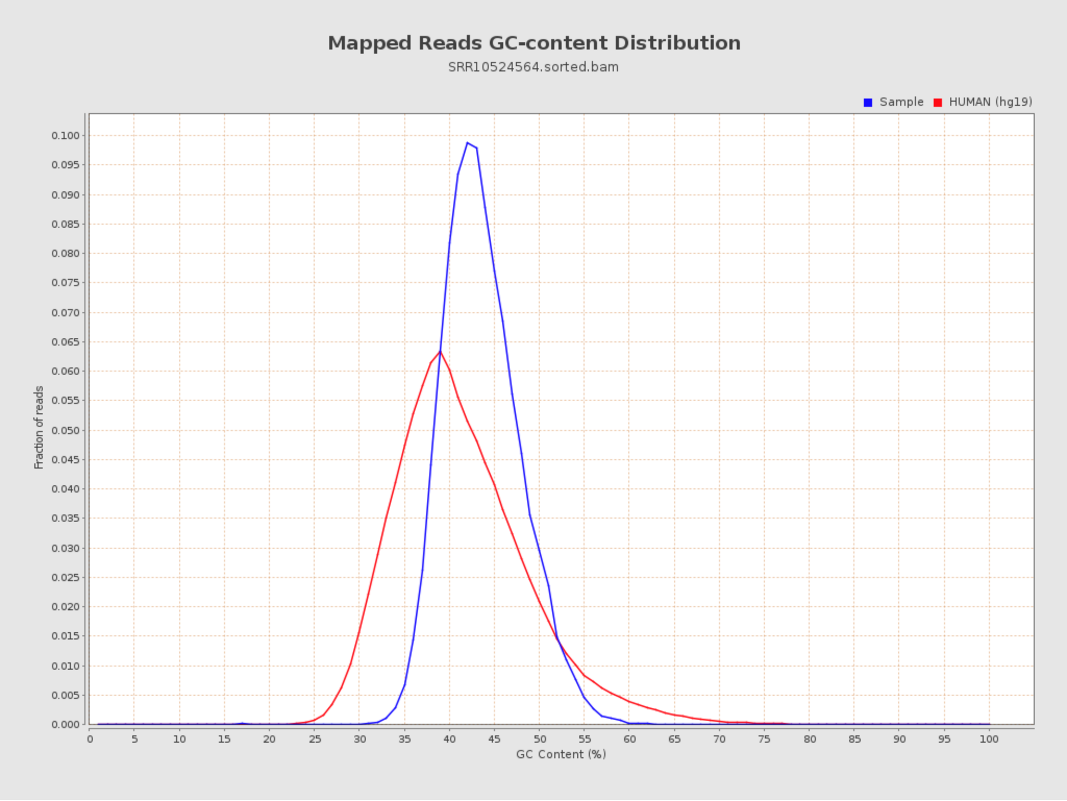
7. Results : Duplication Rate Histogram



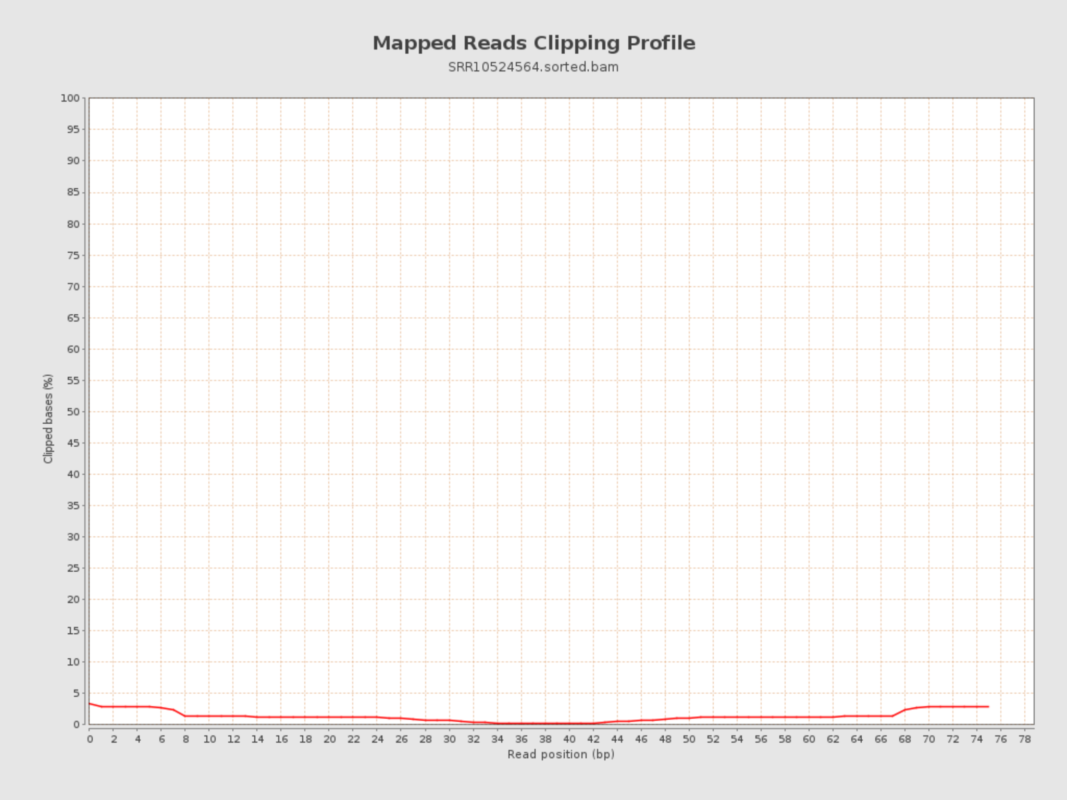
8. Results : Mapped Reads Nucleotide Content



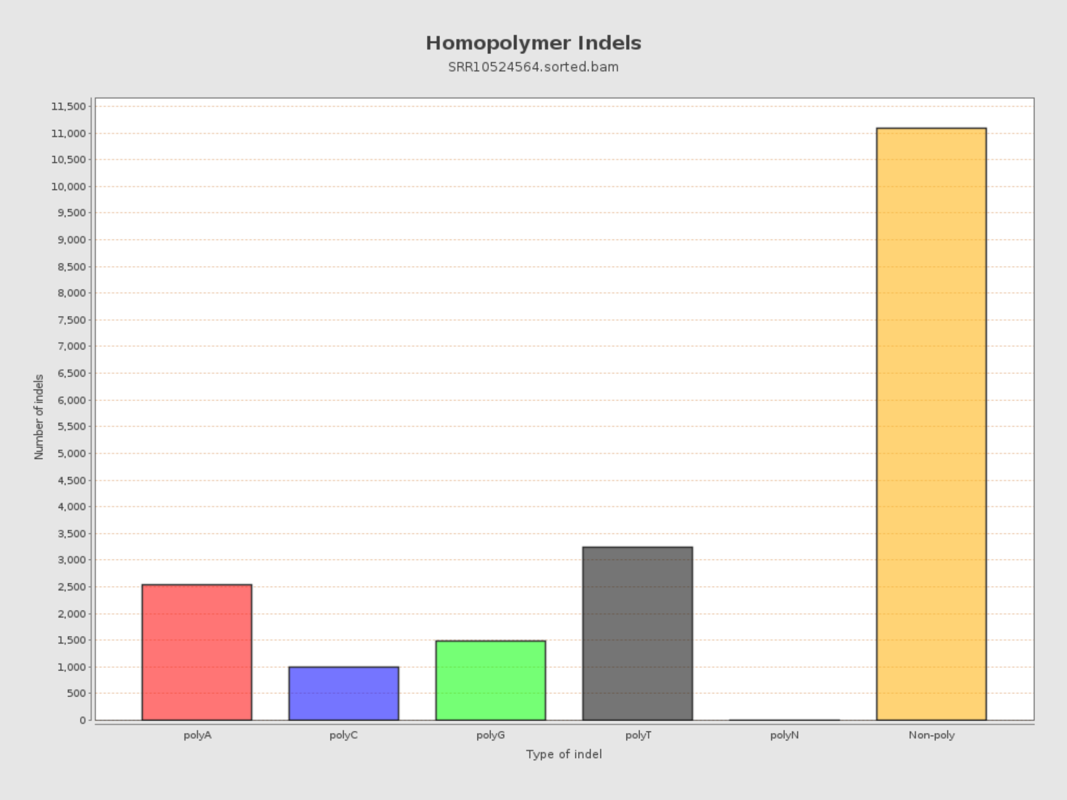
9. Results : Mapped Reads GC-content Distribution



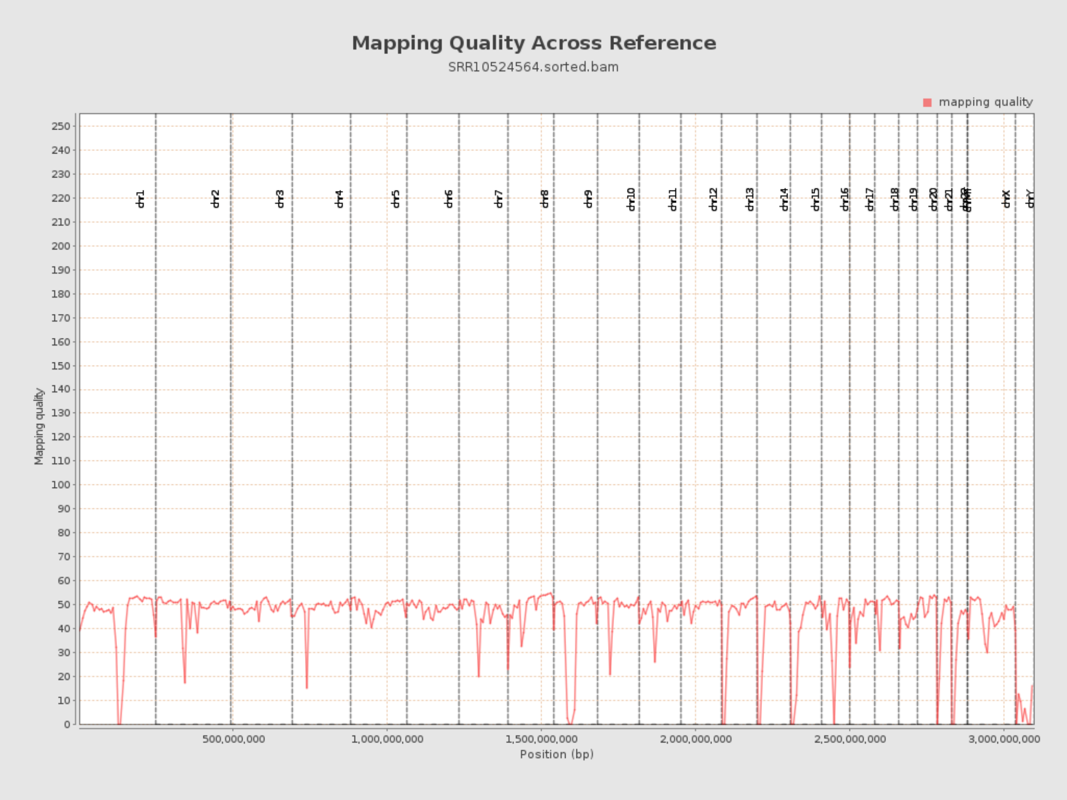
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram