Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 09:00:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524944.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_SRR10524944 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524944.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 09:00:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524944.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,583,157
Mapped reads	1,436,869 / 90.76%
Unmapped reads	146,288 / 9.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,955 / 0.31%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	38,249 / 2.42%
Duplication rate	1.8%
Clipped reads	1,438,738 / 90.88%

2.2. ACGT Content

Number/percentage of A's	21,276,259 / 25.9%
Number/percentage of C's	15,998,989 / 19.48%
Number/percentage of T's	25,676,330 / 31.26%
Number/percentage of G's	19,184,030 / 23.36%
Number/percentage of N's	2,343 / 0%
GC Percentage	42.83%

2.3. Coverage

Mean	0.0265

Standard Deviation	0.2491

2.4. Mapping Quality

Mean Mapping Quality	44.64

2.5. Mismatches and indels

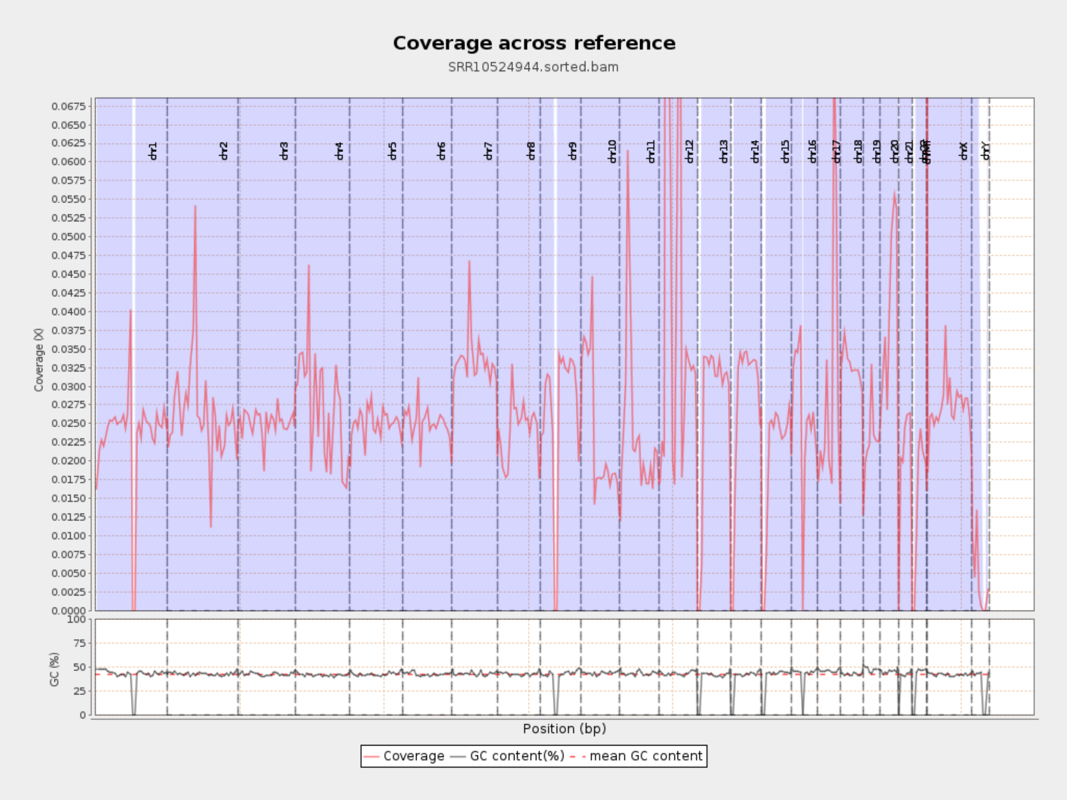
General error rate	0.5%
Mismatches	398,229
Insertions	5,506
Mapped reads with at least one insertion	0.38%
Deletions	12,762
Mapped reads with at least one deletion	0.88%
Homopolymer indels	41.62%

2.6. Chromosome stats

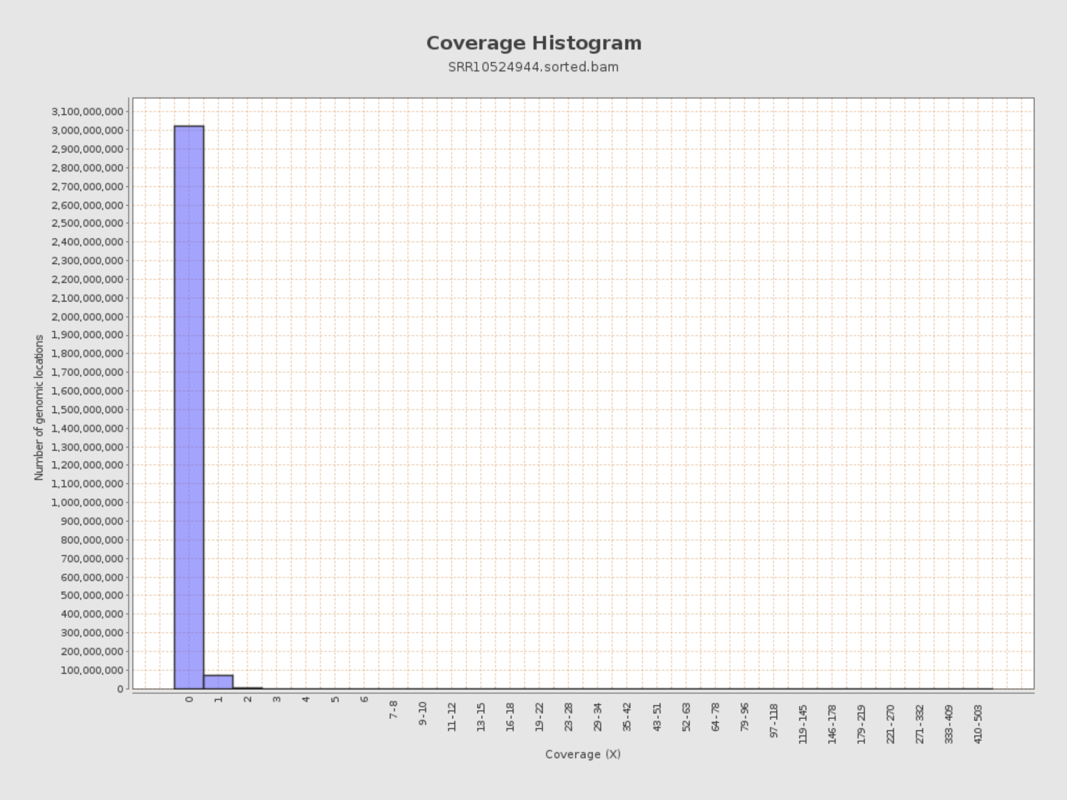
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5821021	0.0234	0.4062
chr2	243199373	6437255	0.0265	0.2775
chr3	198022430	4990069	0.0252	0.1694
chr4	191154276	5169226	0.027	0.1941
chr5	180915260	4565913	0.0252	0.1712
chr6	171115067	4289798	0.0251	0.1834
chr7	159138663	5323808	0.0335	0.3182

chr8	146364022	3558860	0.0243	0.2291
chr9	141213431	3744501	0.0265	0.2595
chr10	135534747	3242113	0.0239	0.2446
chr11	135006516	3225717	0.0239	0.2157
chr12	133851895	6201463	0.0463	0.2557
chr13	115169878	3099920	0.0269	0.1745
chr14	107349540	2924087	0.0272	0.1947
chr15	102531392	2072057	0.0202	0.1533
chr16	90354753	2310389	0.0256	0.1889
chr17	81195210	2451651	0.0302	0.1938
chr18	78077248	2568710	0.0329	0.4561
chr19	59128983	1368892	0.0232	0.3327
chr20	63025520	2534759	0.0402	0.2215
chr21	48129895	993373	0.0206	0.1749
chr22	51304566	776133	0.0151	0.1301
chrMT	16571	2549	0.1538	0.4049
chrX	155270560	4253273	0.0274	0.2071
chrY	59373566	233888	0.0039	0.1032

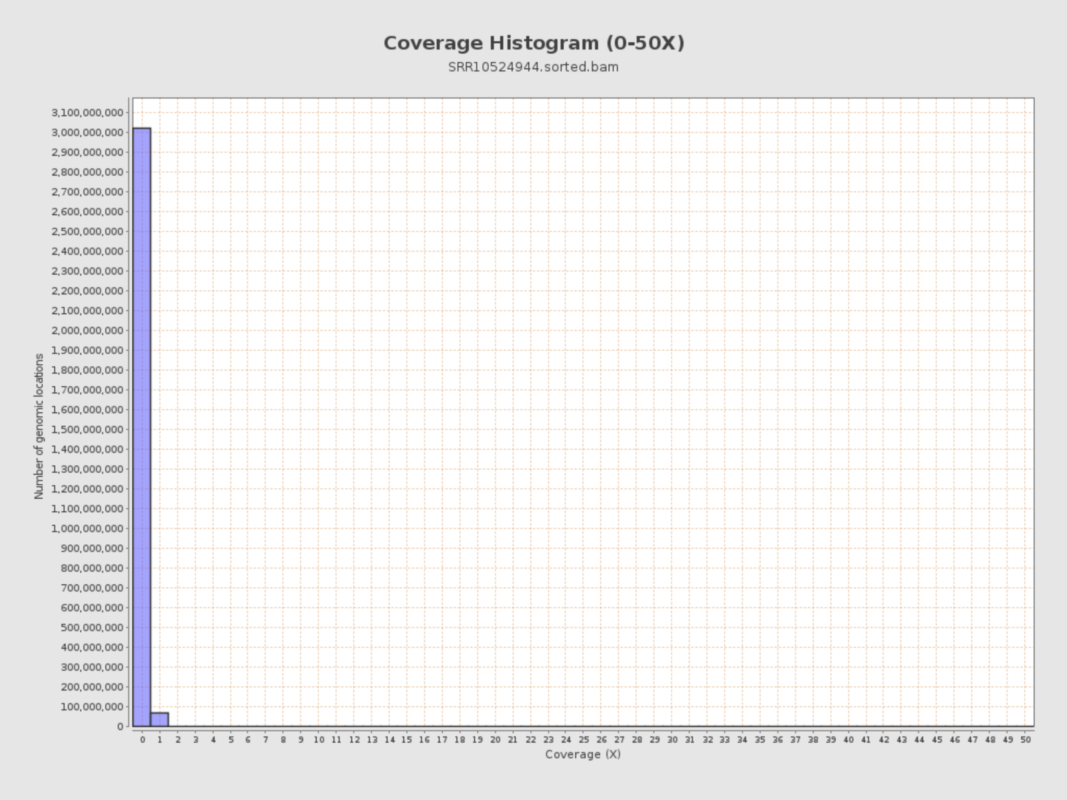
3. Results : Coverage across reference



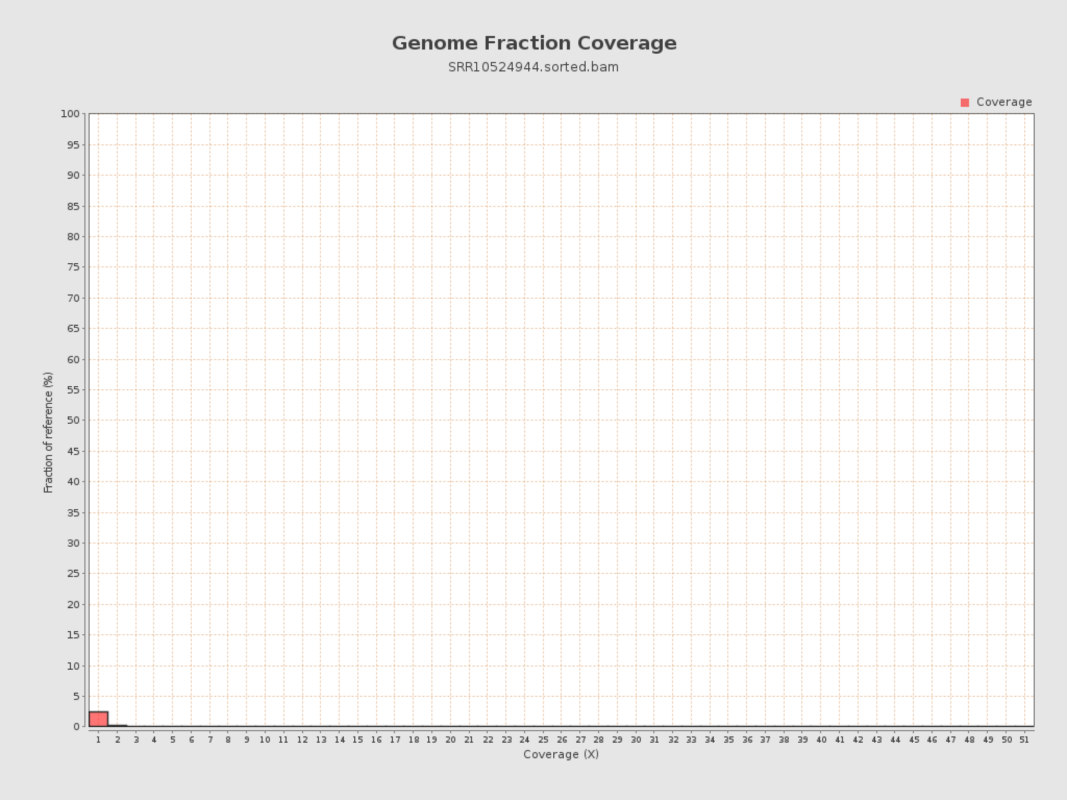
4. Results : Coverage Histogram



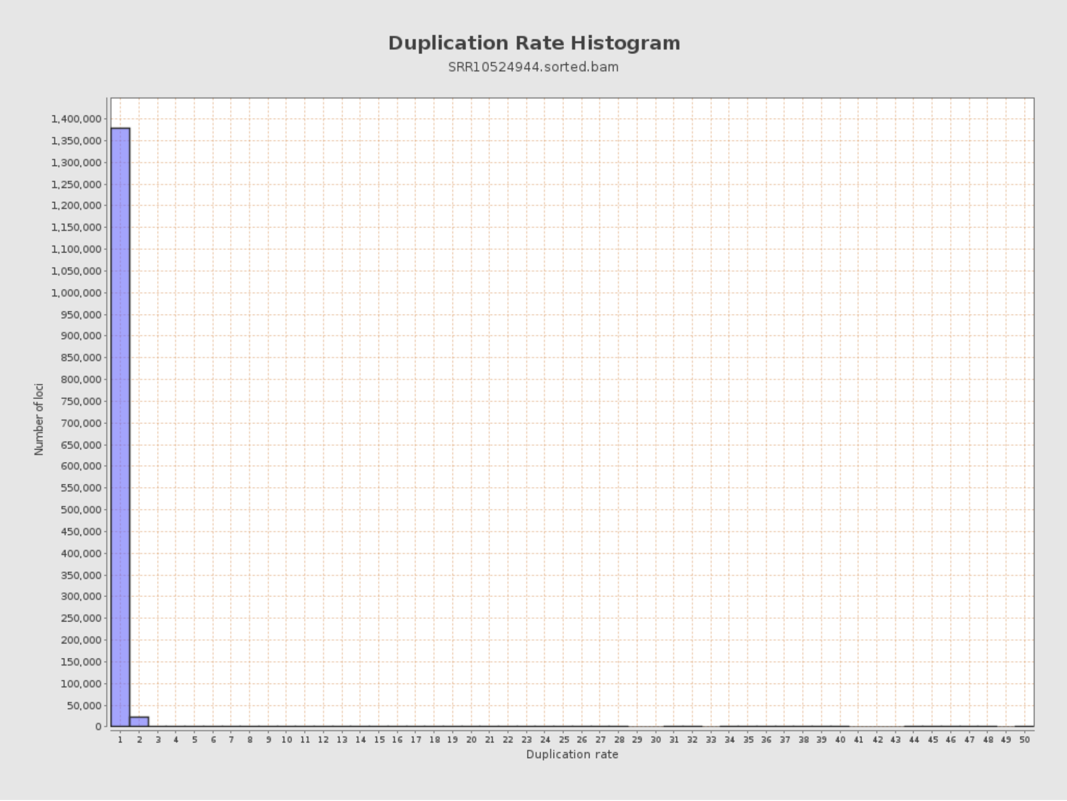
5. Results : Coverage Histogram (0-50X)



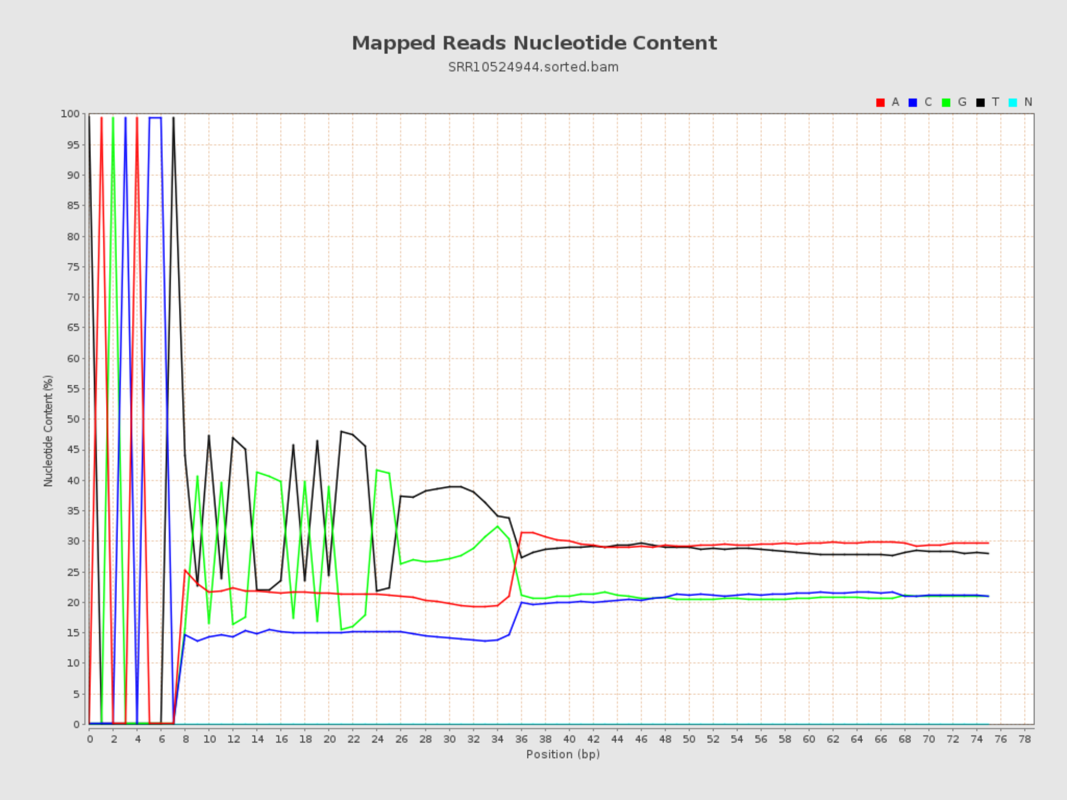
6. Results : Genome Fraction Coverage



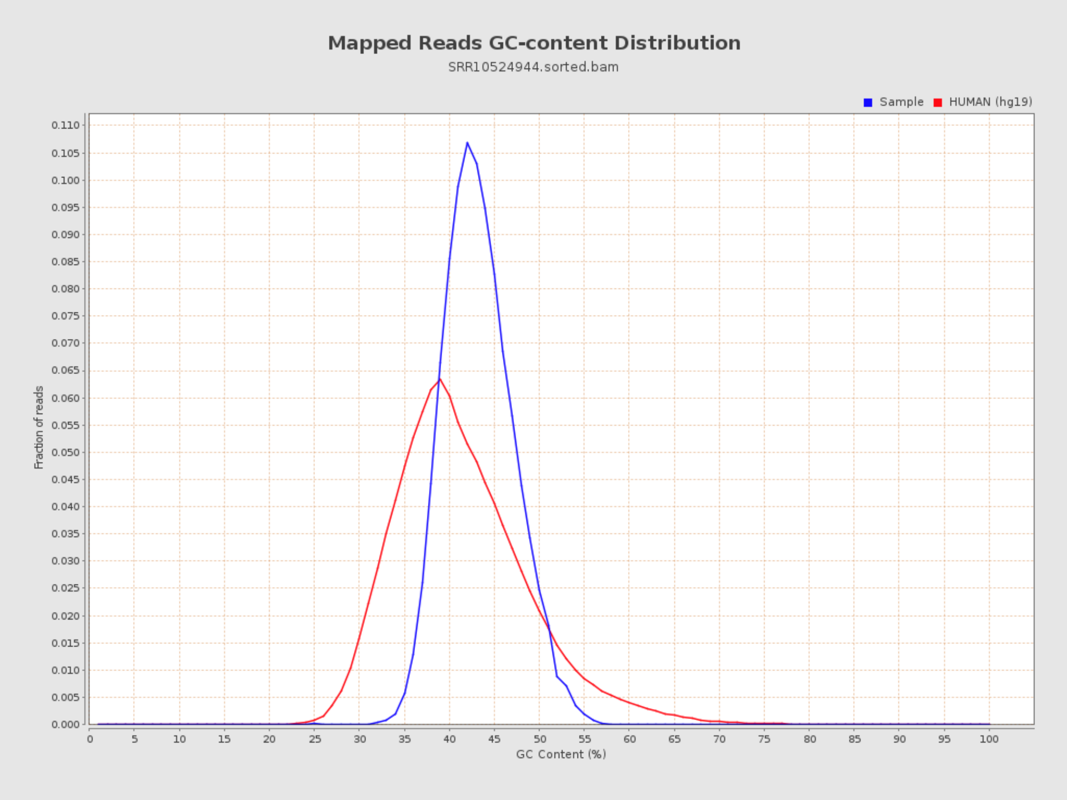
7. Results : Duplication Rate Histogram



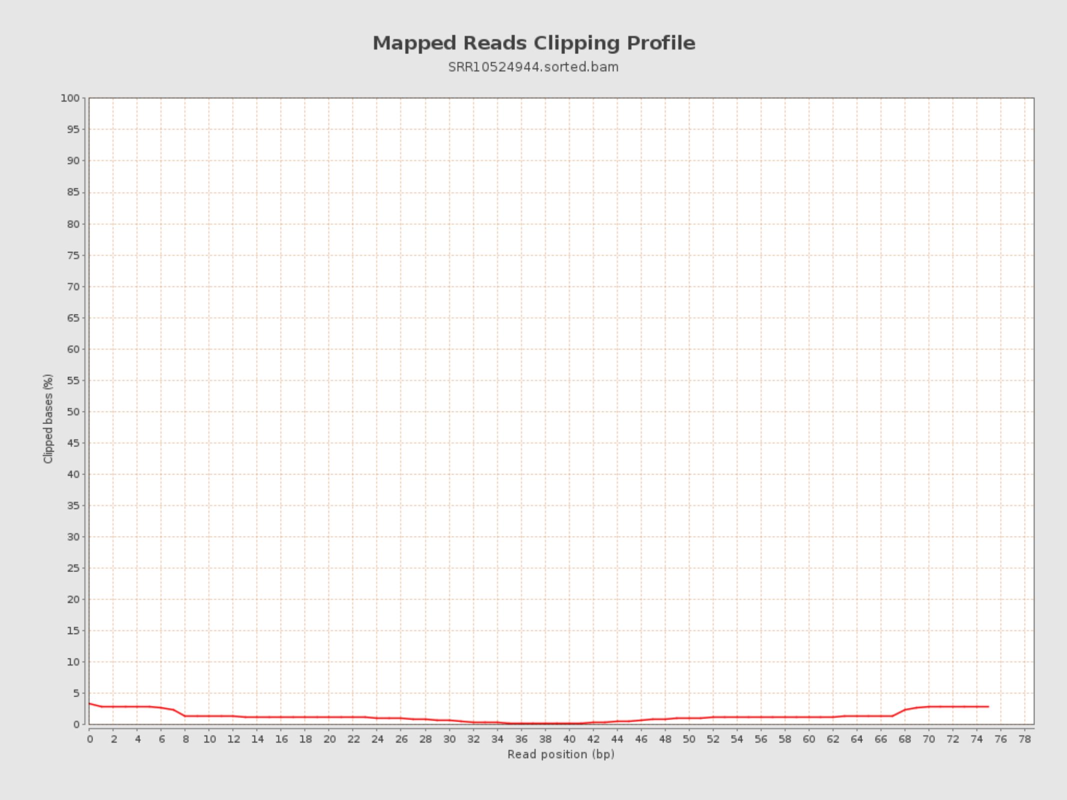
8. Results : Mapped Reads Nucleotide Content



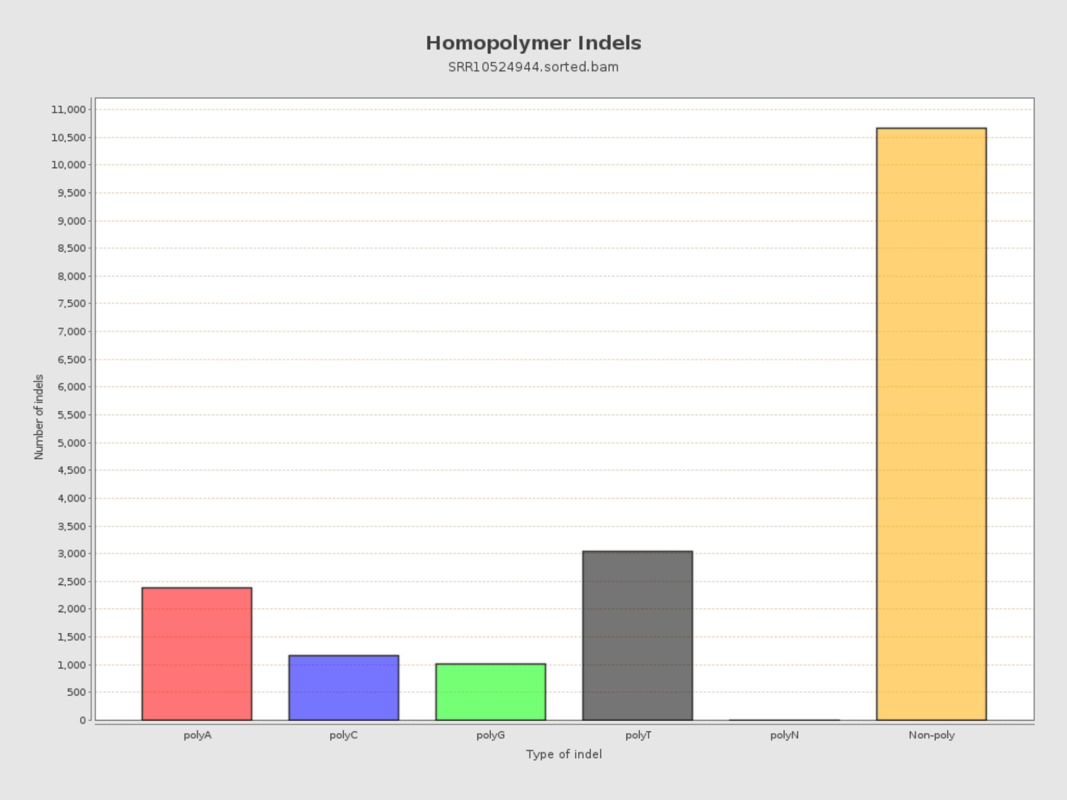
9. Results : Mapped Reads GC-content Distribution



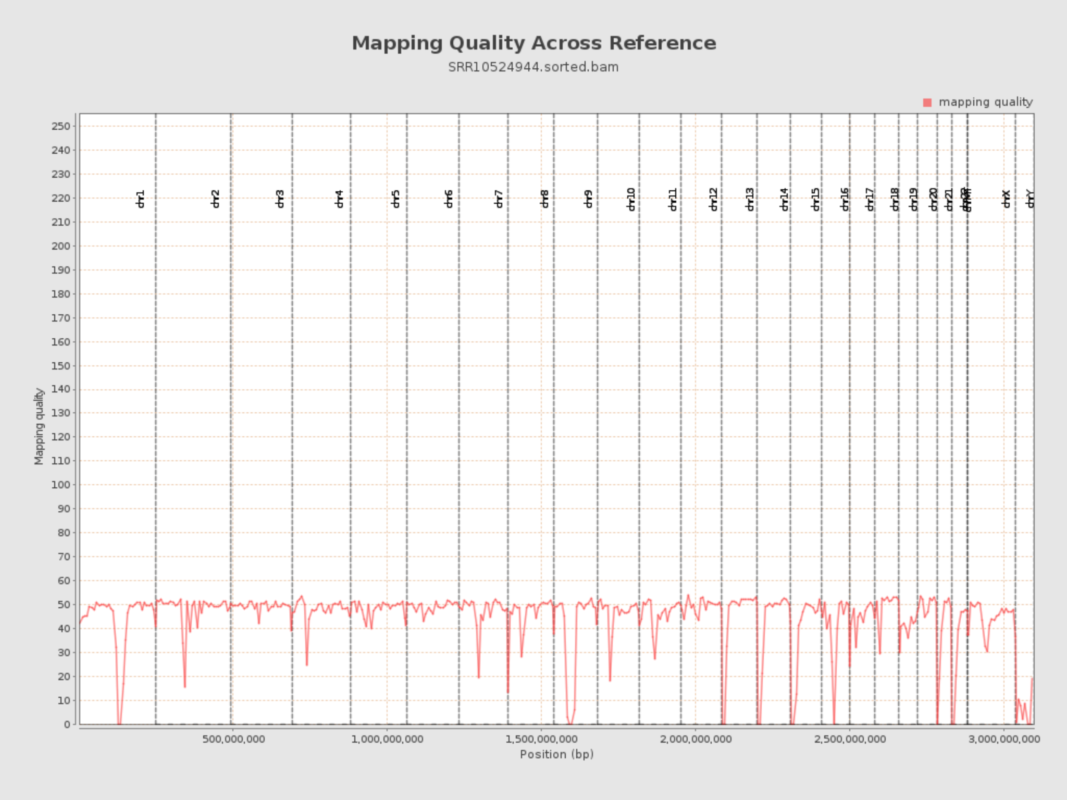
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram