Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 04:31:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524443.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_SRR10524443 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524443.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 04:31:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524443.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,363,883
Mapped reads	1,264,856 / 92.74%
Unmapped reads	99,027 / 7.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,086 / 0.23%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	42,602 / 3.12%
Duplication rate	2.56%
Clipped reads	1,264,362 / 92.7%

2.2. ACGT Content

Number/percentage of A's	17,862,301 / 24.18%
Number/percentage of C's	13,695,414 / 18.54%
Number/percentage of T's	23,603,735 / 31.96%
Number/percentage of G's	18,701,254 / 25.32%
Number/percentage of N's	1,502 / 0%
GC Percentage	43.86%

2.3. Coverage

Mean	0.0239

Standard Deviation	0.224

2.4. Mapping Quality

Mean Mapping Quality	45.95

2.5. Mismatches and indels

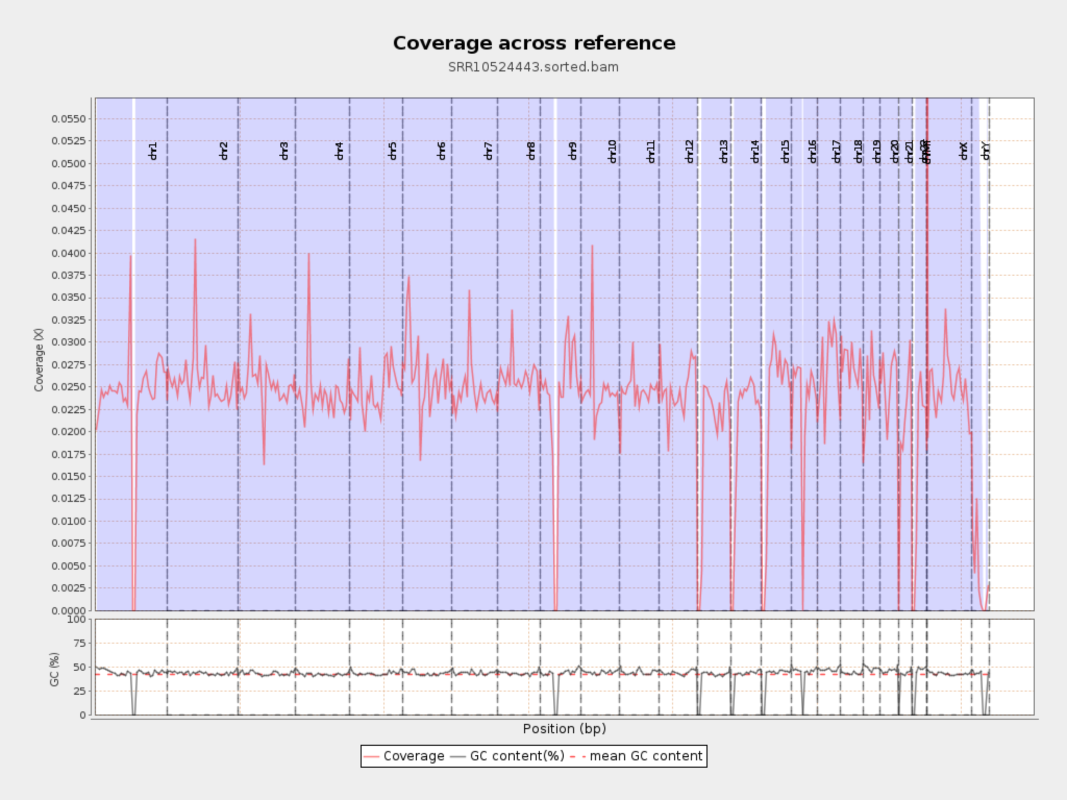
General error rate	0.47%
Mismatches	340,348
Insertions	4,436
Mapped reads with at least one insertion	0.35%
Deletions	13,808
Mapped reads with at least one deletion	1.08%
Homopolymer indels	43.57%

2.6. Chromosome stats

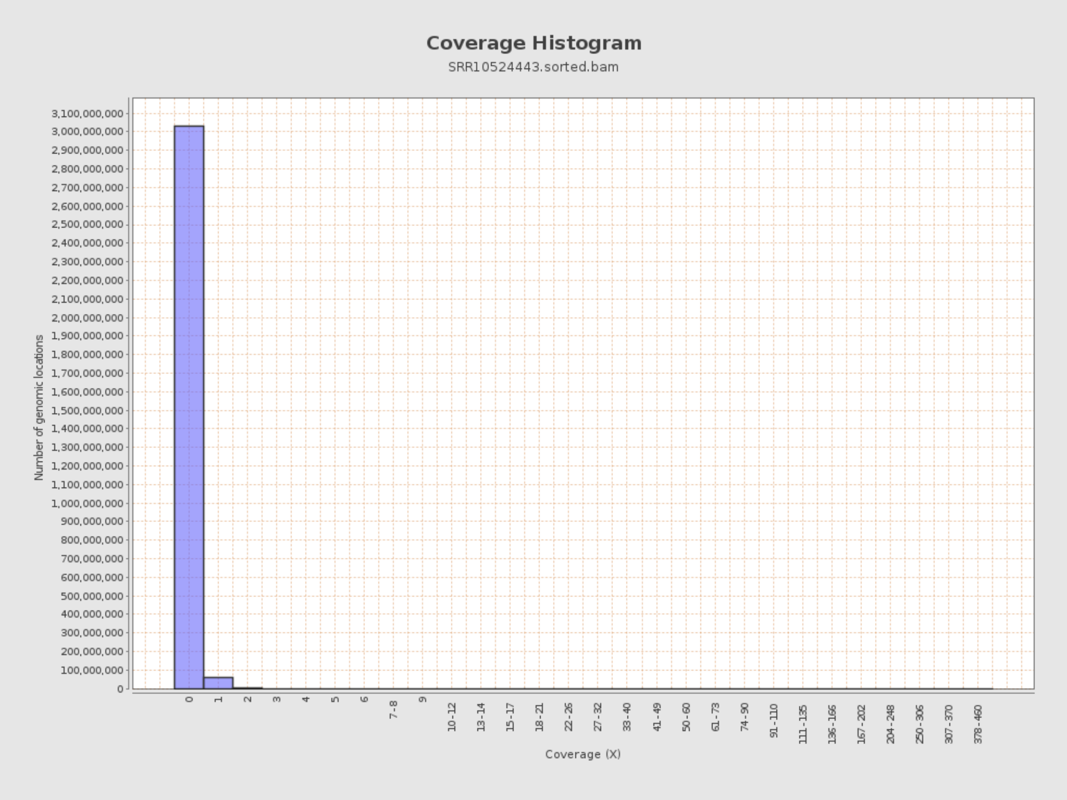
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5904503	0.0237	0.3754
chr2	243199373	6280990	0.0258	0.2573
chr3	198022430	4994799	0.0252	0.1724
chr4	191154276	4666051	0.0244	0.1837
chr5	180915260	4494808	0.0248	0.1703
chr6	171115067	4507112	0.0263	0.197
chr7	159138663	3933093	0.0247	0.2751

chr8	146364022	3828508	0.0262	0.2197
chr9	141213431	3257105	0.0231	0.2179
chr10	135534747	3334819	0.0246	0.2203
chr11	135006516	3332294	0.0247	0.2163
chr12	133851895	3304472	0.0247	0.172
chr13	115169878	2224985	0.0193	0.1508
chr14	107349540	2163621	0.0202	0.1566
chr15	102531392	2261123	0.0221	0.1648
chr16	90354753	2053725	0.0227	0.1716
chr17	81195210	2196169	0.027	0.1868
chr18	78077248	2144632	0.0275	0.3276
chr19	59128983	1467641	0.0248	0.2867
chr20	63025520	1597451	0.0253	0.1746
chr21	48129895	981448	0.0204	0.1627
chr22	51304566	847152	0.0165	0.1384
chrMT	16571	6419	0.3874	0.7038
chrX	155270560	3886033	0.025	0.1889
chrY	59373566	219269	0.0037	0.1017

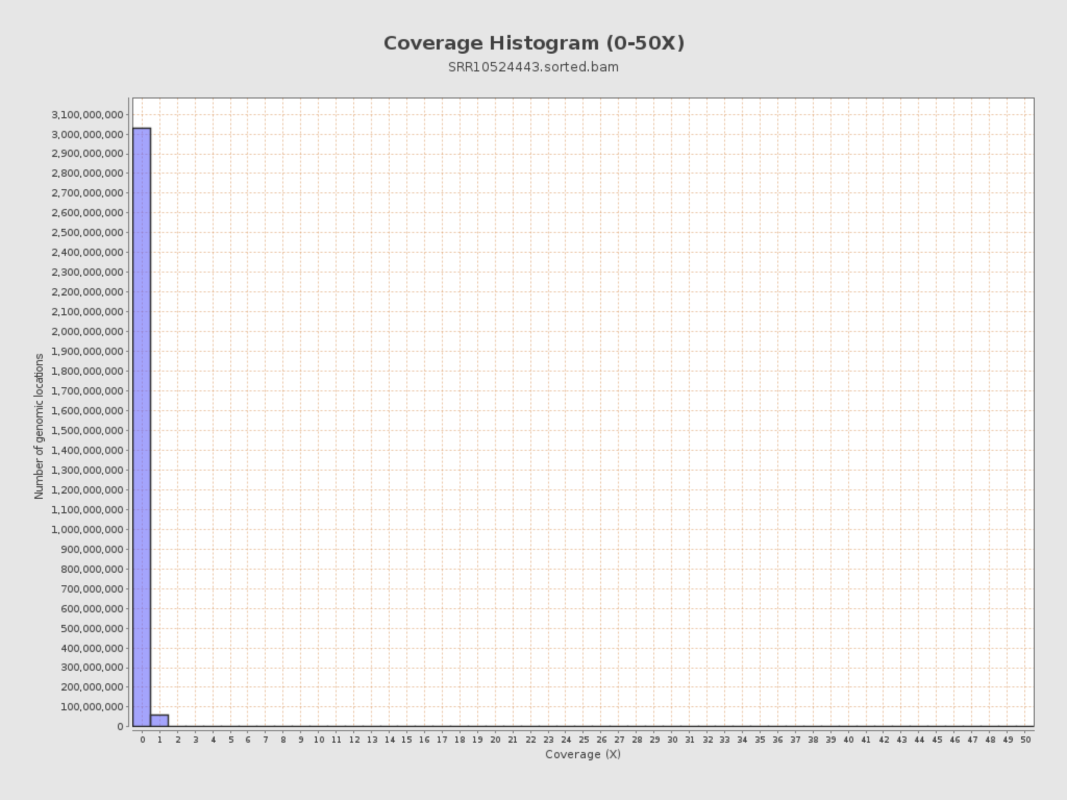
3. Results : Coverage across reference



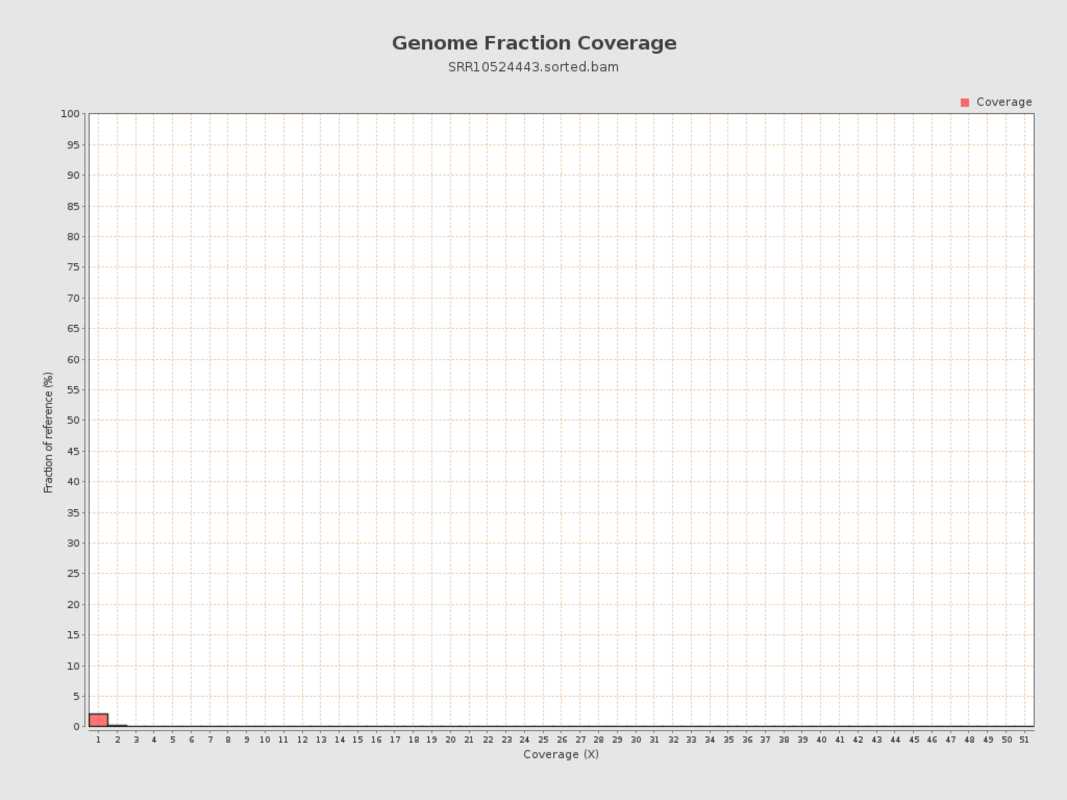
4. Results : Coverage Histogram



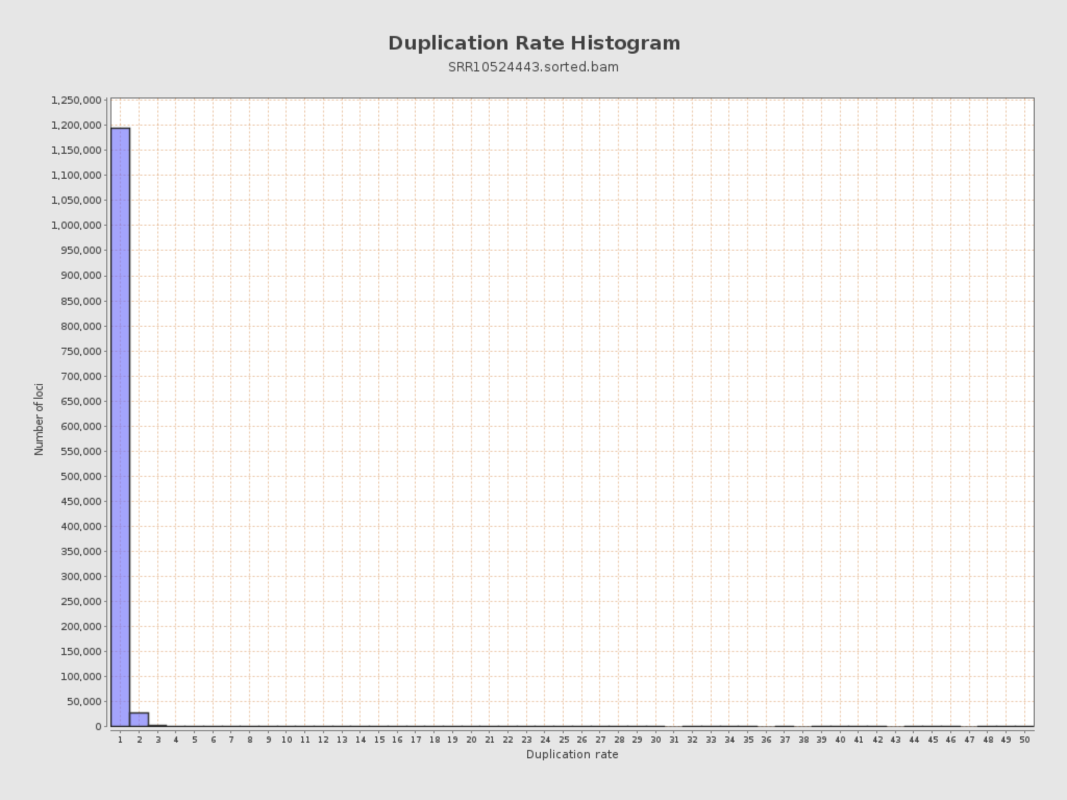
5. Results : Coverage Histogram (0-50X)



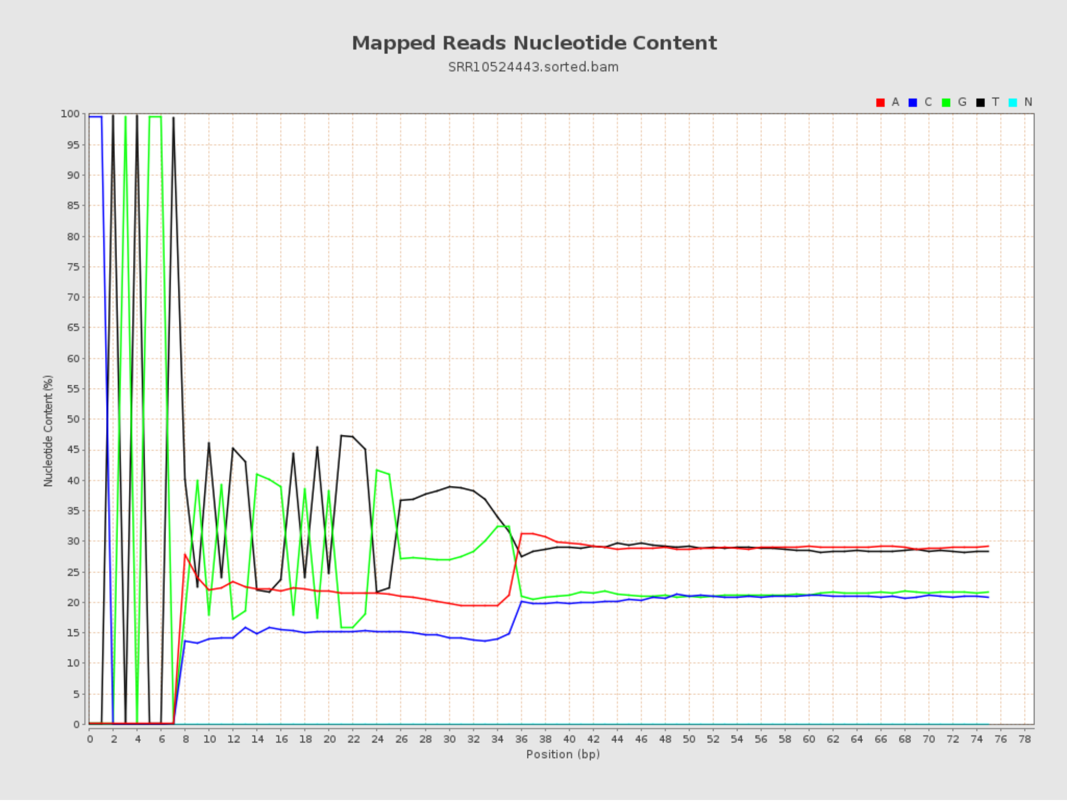
6. Results : Genome Fraction Coverage



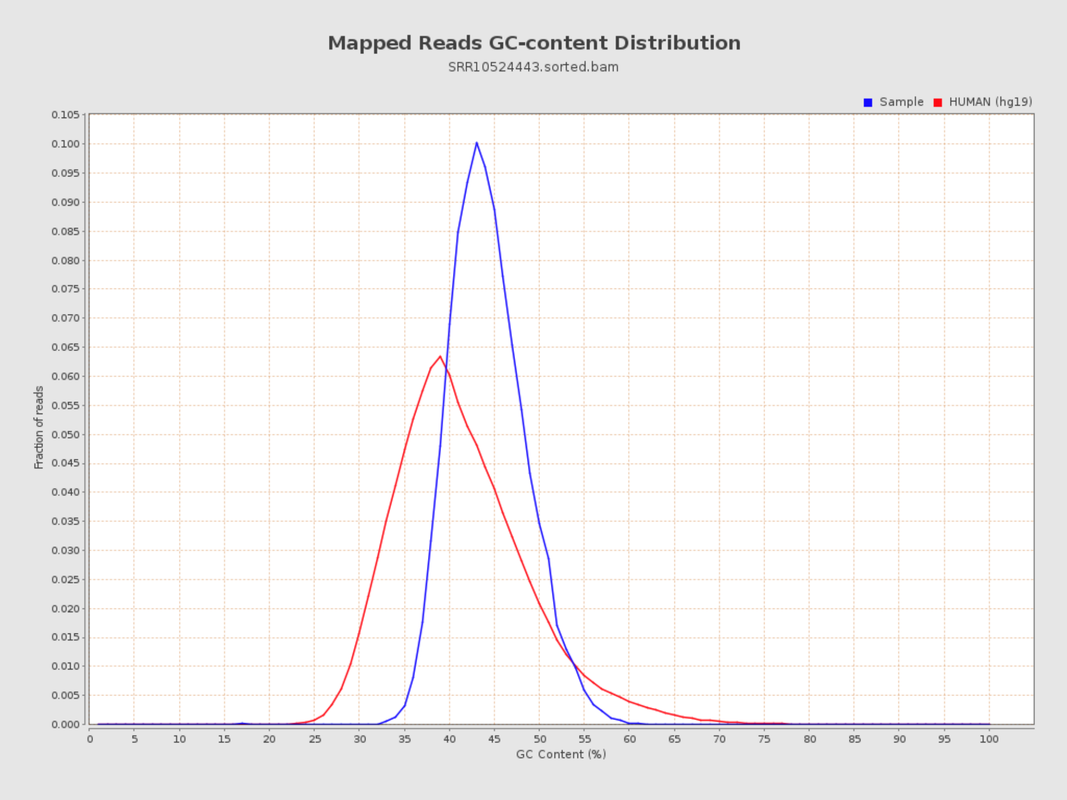
7. Results : Duplication Rate Histogram



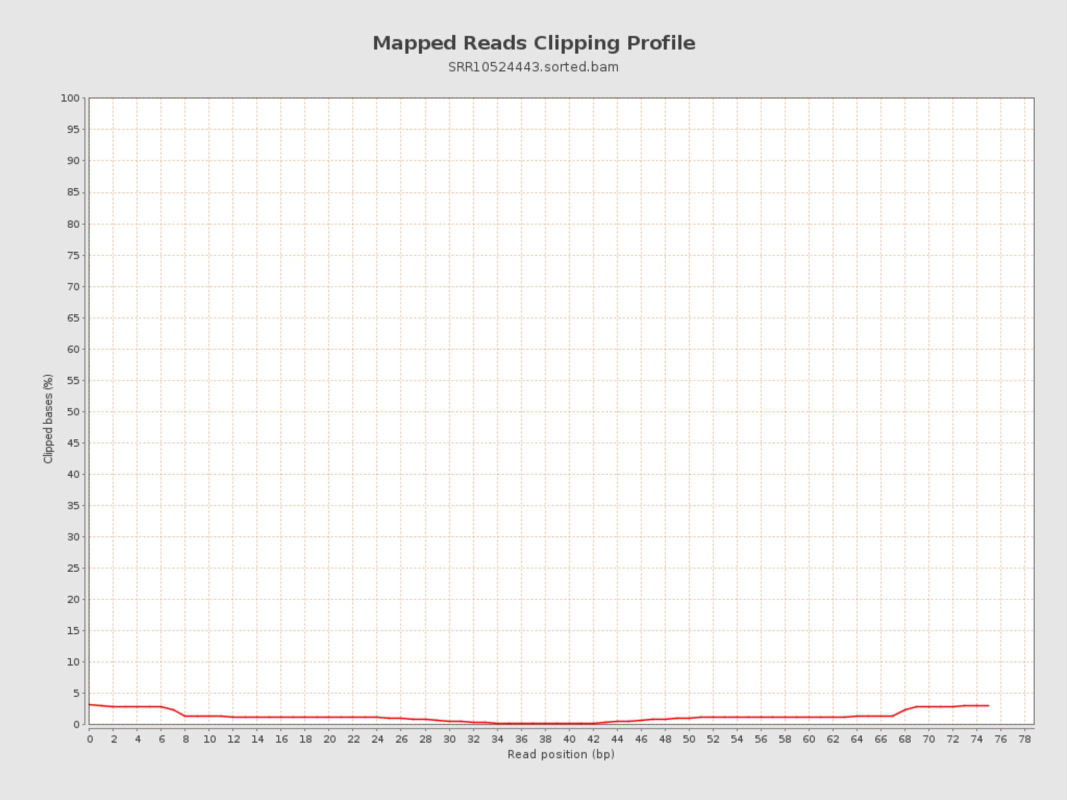
8. Results : Mapped Reads Nucleotide Content



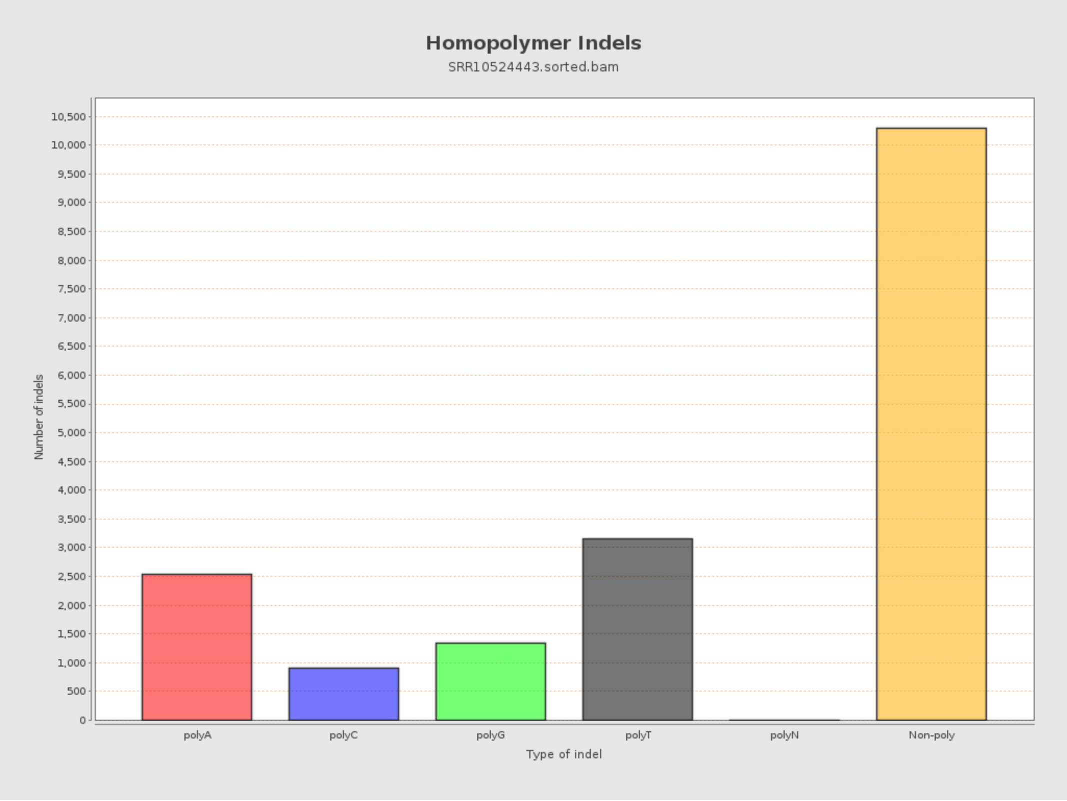
9. Results : Mapped Reads GC-content Distribution



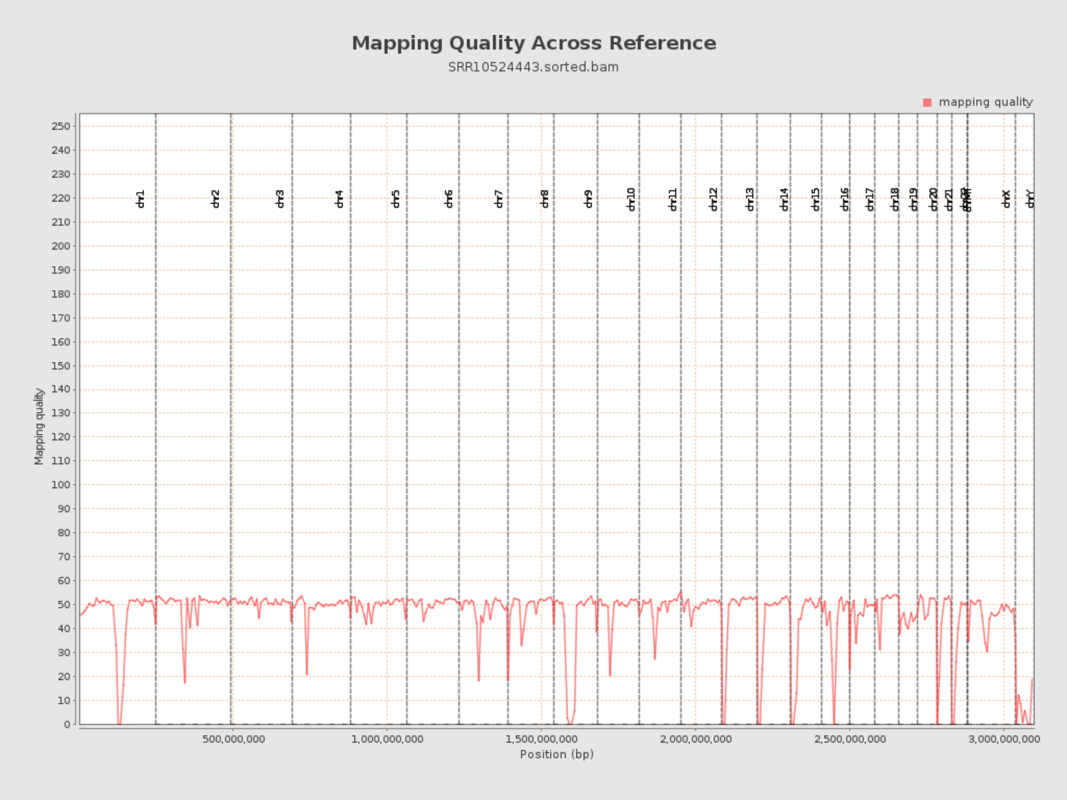
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram