Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 18:15:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524732.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_SRR10524732 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524732.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 18:15:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524732.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,383,056
Mapped reads	1,244,865 / 90.01%
Unmapped reads	138,191 / 9.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,799 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	46,122 / 3.33%
Duplication rate	2.85%
Clipped reads	1,246,447 / 90.12%

2.2. ACGT Content

Number/percentage of A's	16,882,990 / 23.86%
Number/percentage of C's	14,189,983 / 20.05%
Number/percentage of T's	23,068,227 / 32.6%
Number/percentage of G's	16,621,122 / 23.49%
Number/percentage of N's	8,026 / 0.01%
GC Percentage	43.54%

2.3. Coverage

Mean	0.0229

Standard Deviation	0.2161

2.4. Mapping Quality

Mean Mapping Quality	44.38

2.5. Mismatches and indels

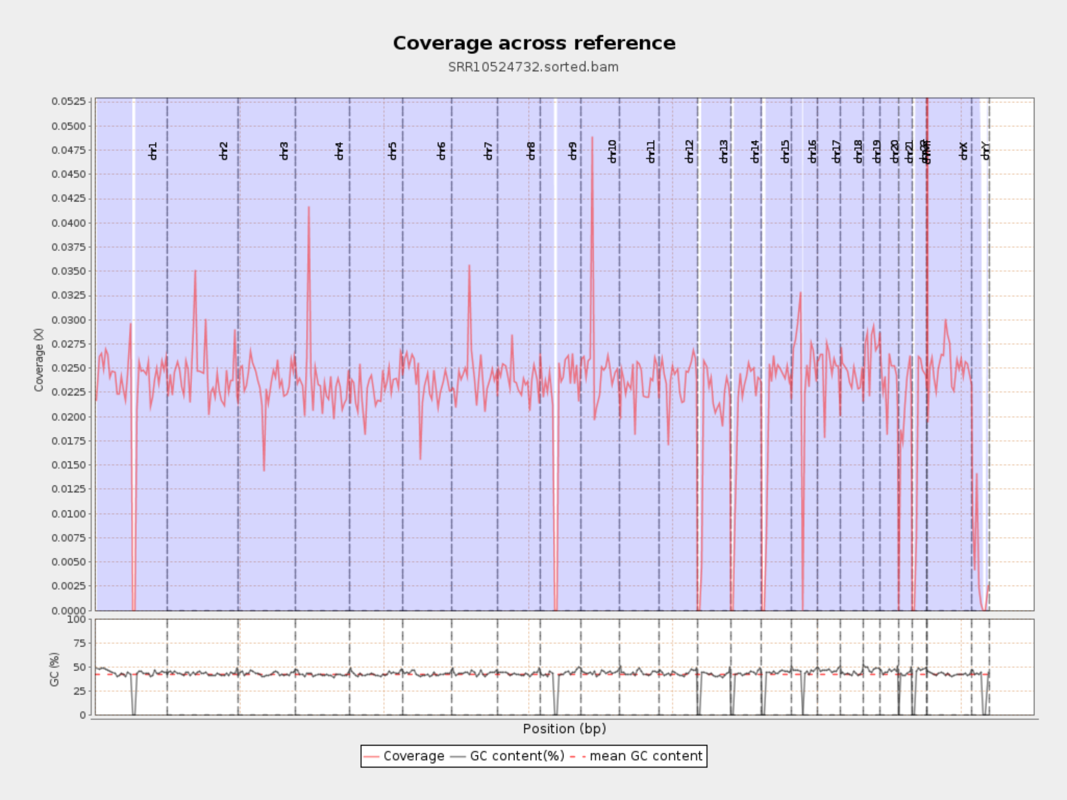
General error rate	0.53%
Mismatches	368,199
Insertions	4,866
Mapped reads with at least one insertion	0.39%
Deletions	13,986
Mapped reads with at least one deletion	1.12%
Homopolymer indels	43.79%

2.6. Chromosome stats

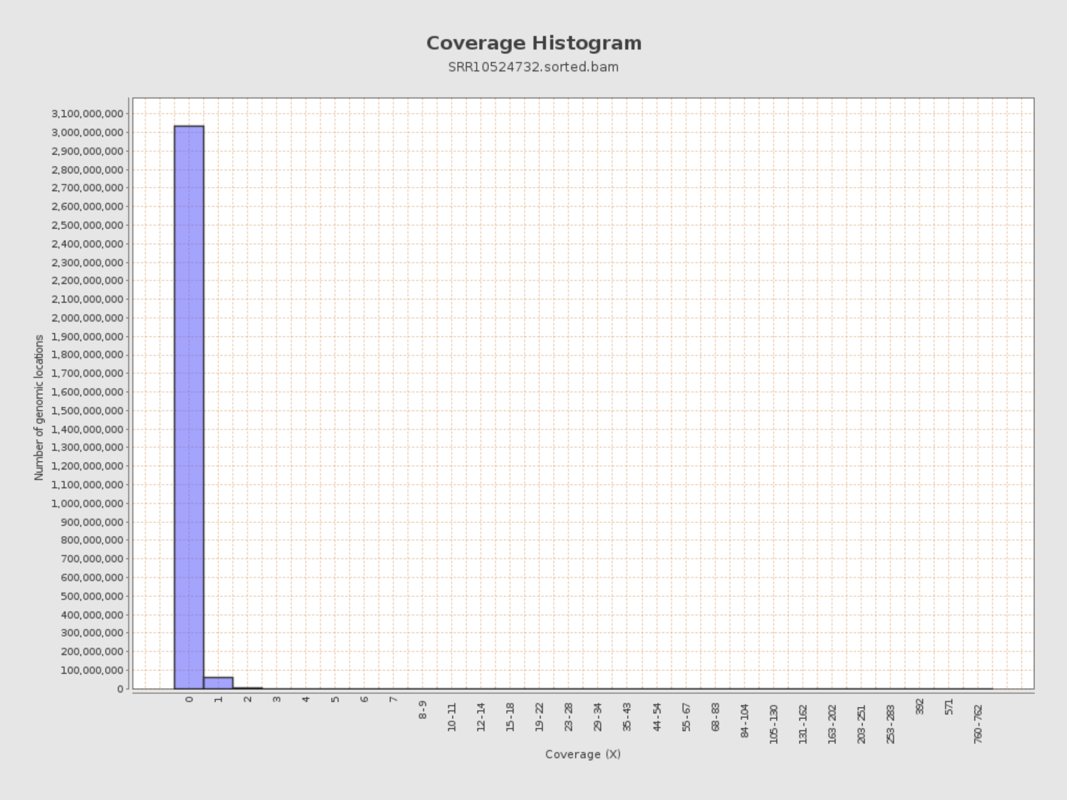
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5700694	0.0229	0.2699
chr2	243199373	5917564	0.0243	0.3587
chr3	198022430	4652941	0.0235	0.1682
chr4	191154276	4514117	0.0236	0.1875
chr5	180915260	4167938	0.023	0.165
chr6	171115067	4026656	0.0235	0.1838
chr7	159138663	3873884	0.0243	0.2512

chr8	146364022	3495335	0.0239	0.1998
chr9	141213431	3029165	0.0215	0.1888
chr10	135534747	3479895	0.0257	0.2613
chr11	135006516	3183261	0.0236	0.1909
chr12	133851895	3203404	0.0239	0.1705
chr13	115169878	2177107	0.0189	0.1502
chr14	107349540	2122948	0.0198	0.1559
chr15	102531392	2040858	0.0199	0.155
chr16	90354753	2177657	0.0241	0.1838
chr17	81195210	2020626	0.0249	0.177
chr18	78077248	1898915	0.0243	0.2733
chr19	59128983	1597808	0.027	0.2402
chr20	63025520	1496824	0.0237	0.1764
chr21	48129895	942721	0.0196	0.1659
chr22	51304566	887250	0.0173	0.1444
chrMT	16571	34879	2.1048	1.8049
chrX	155270560	3914146	0.0252	0.1834
chrY	59373566	236103	0.004	0.1187

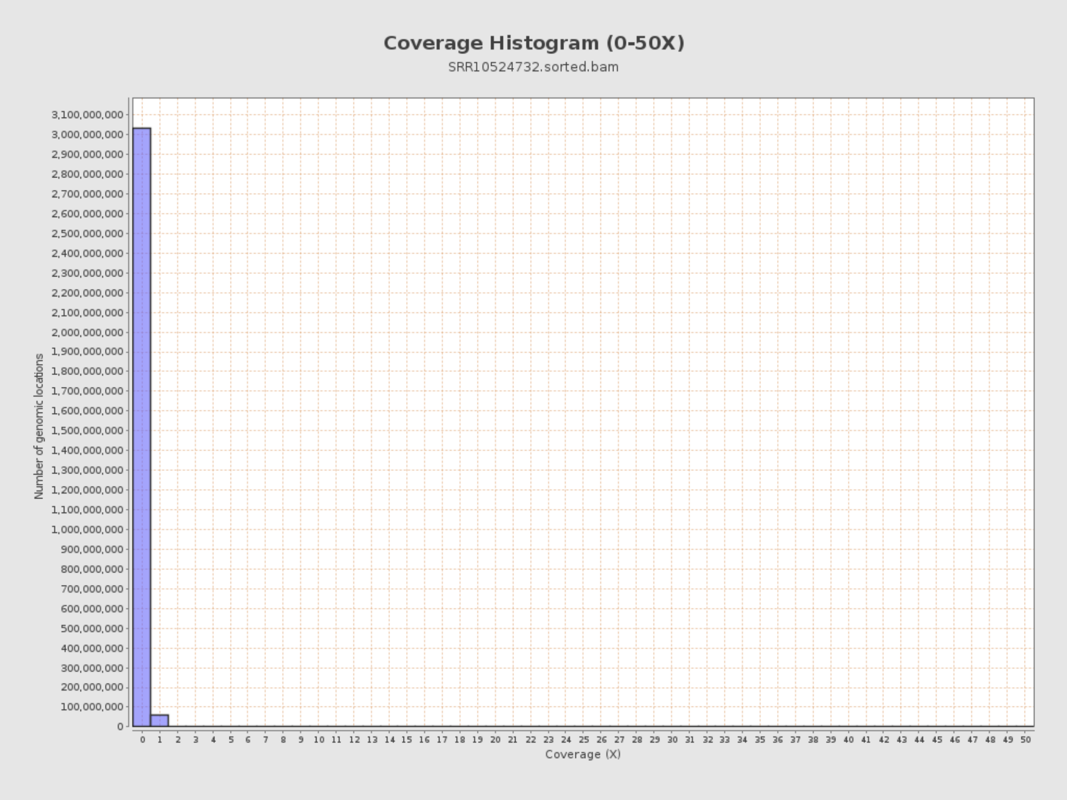
3. Results : Coverage across reference



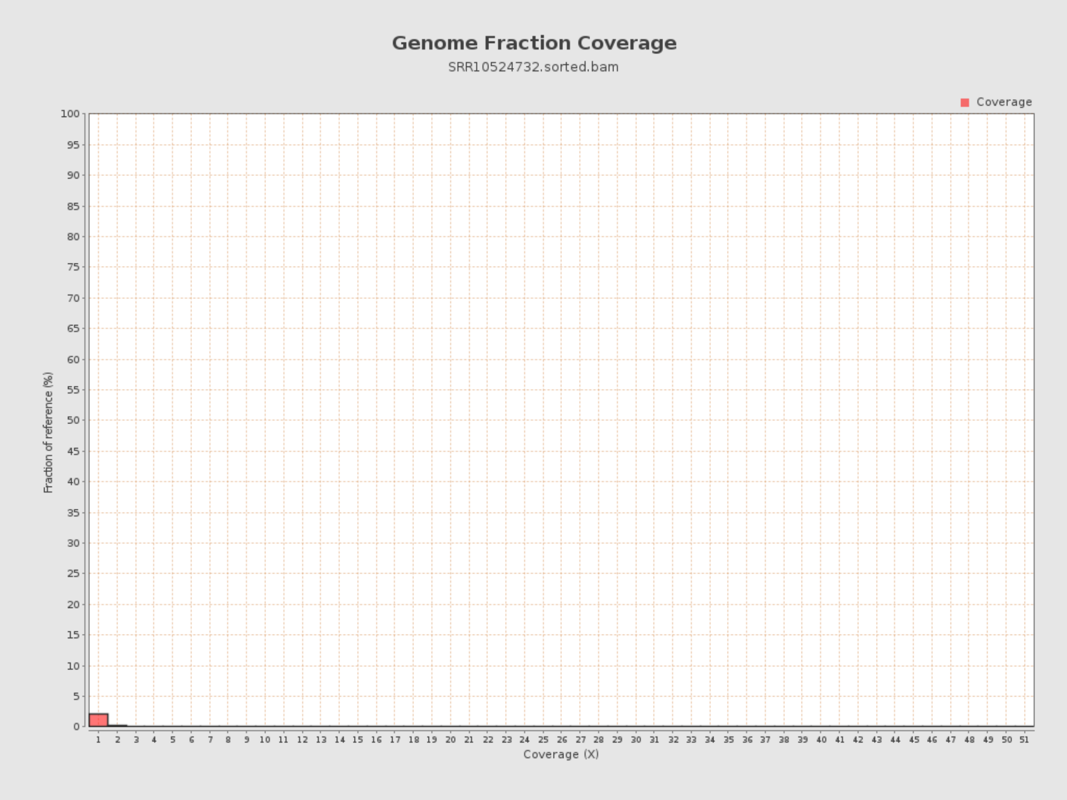
4. Results : Coverage Histogram



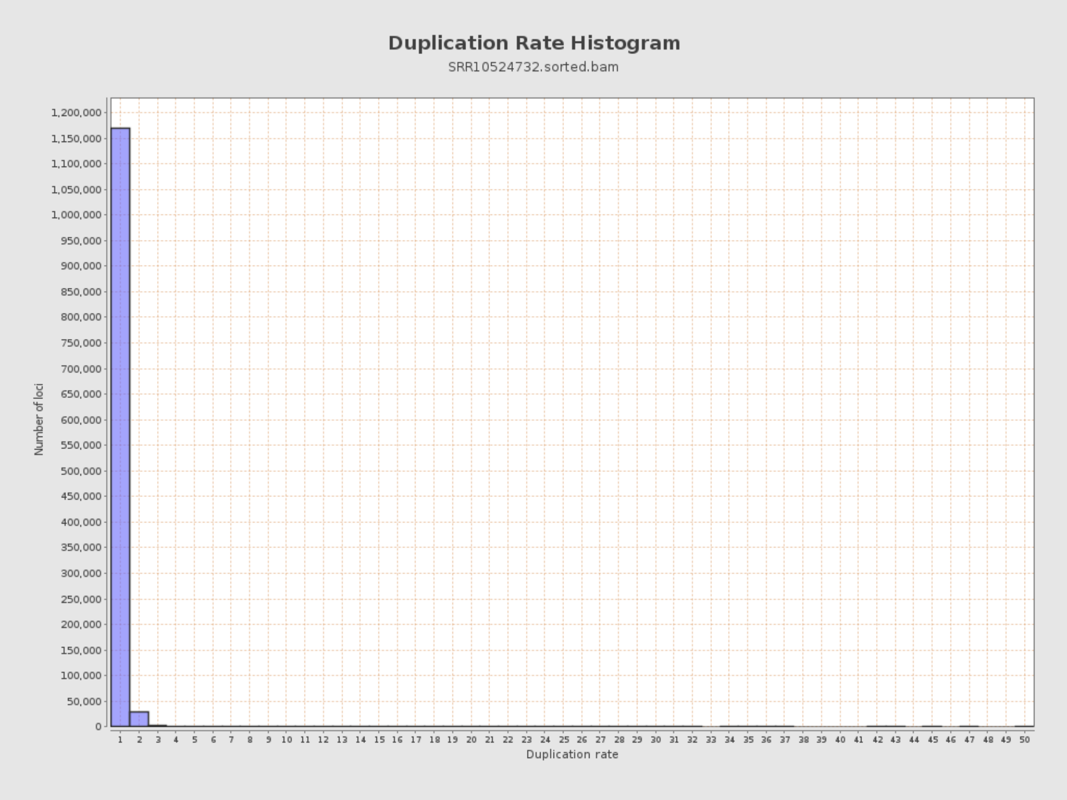
5. Results : Coverage Histogram (0-50X)



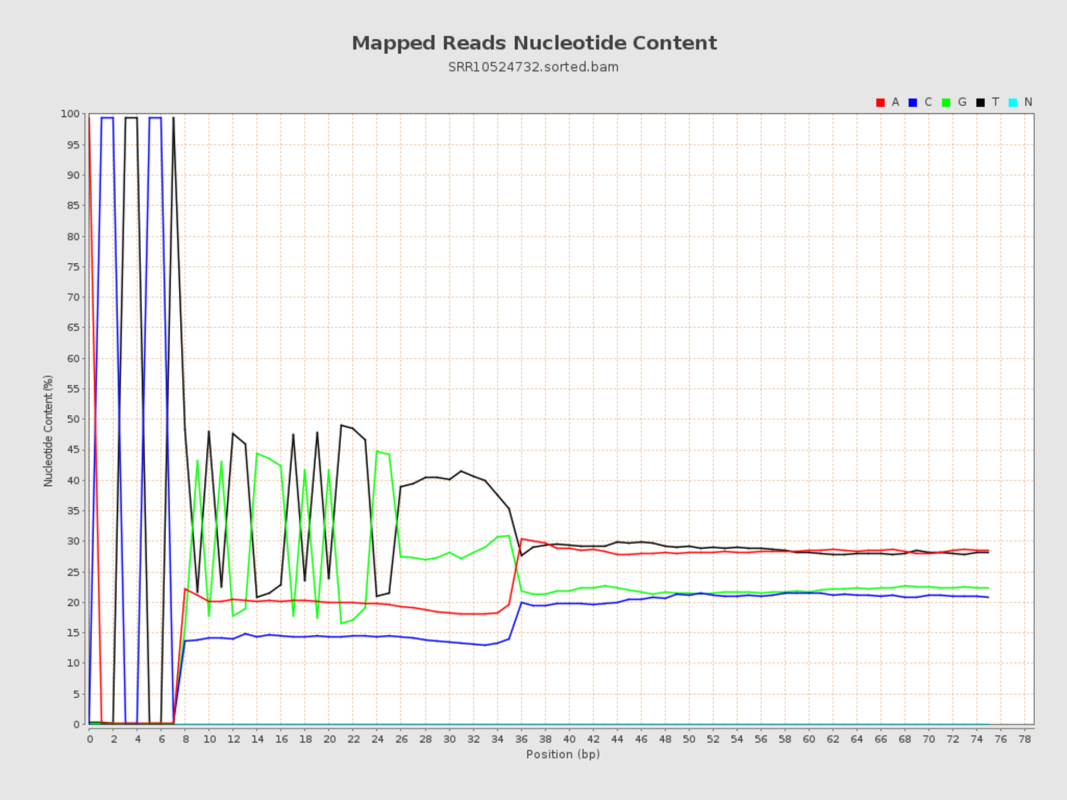
6. Results : Genome Fraction Coverage



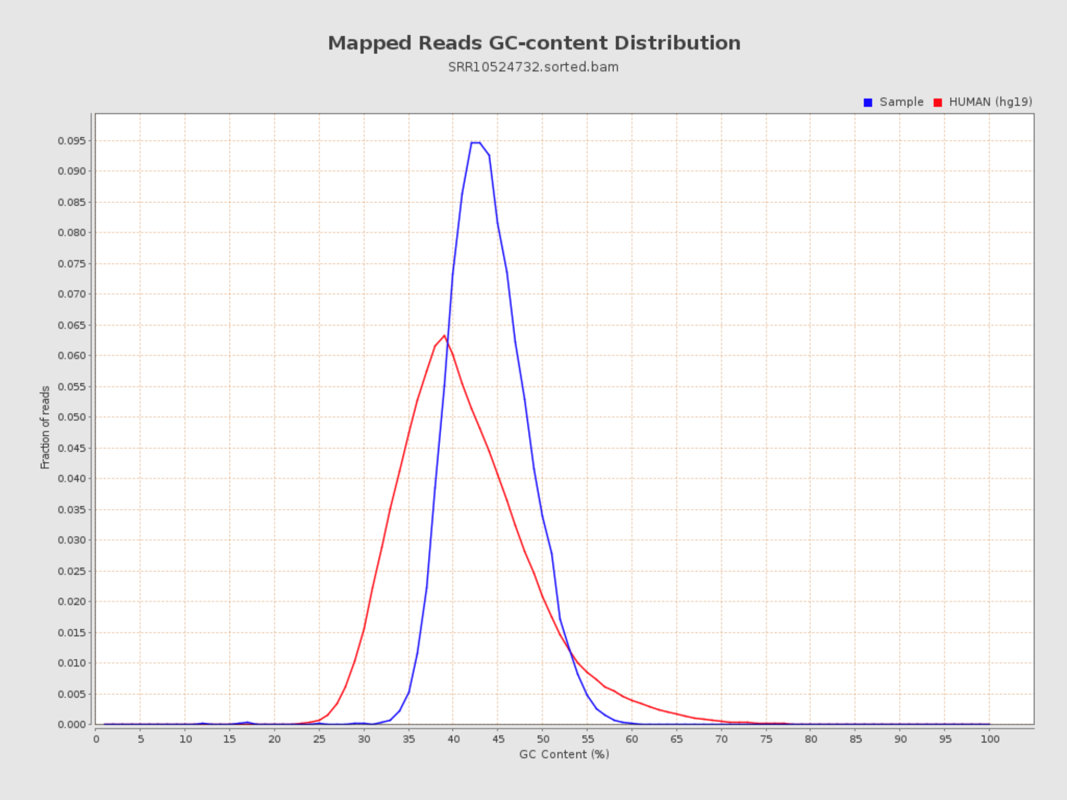
7. Results : Duplication Rate Histogram



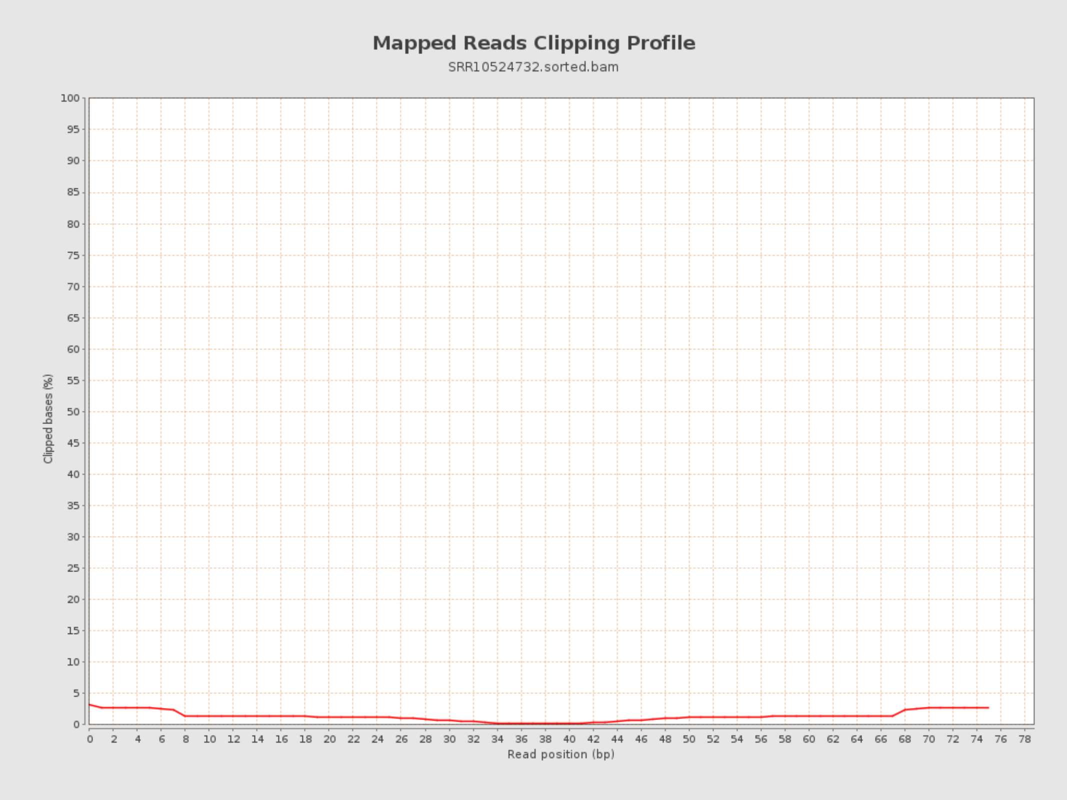
8. Results : Mapped Reads Nucleotide Content



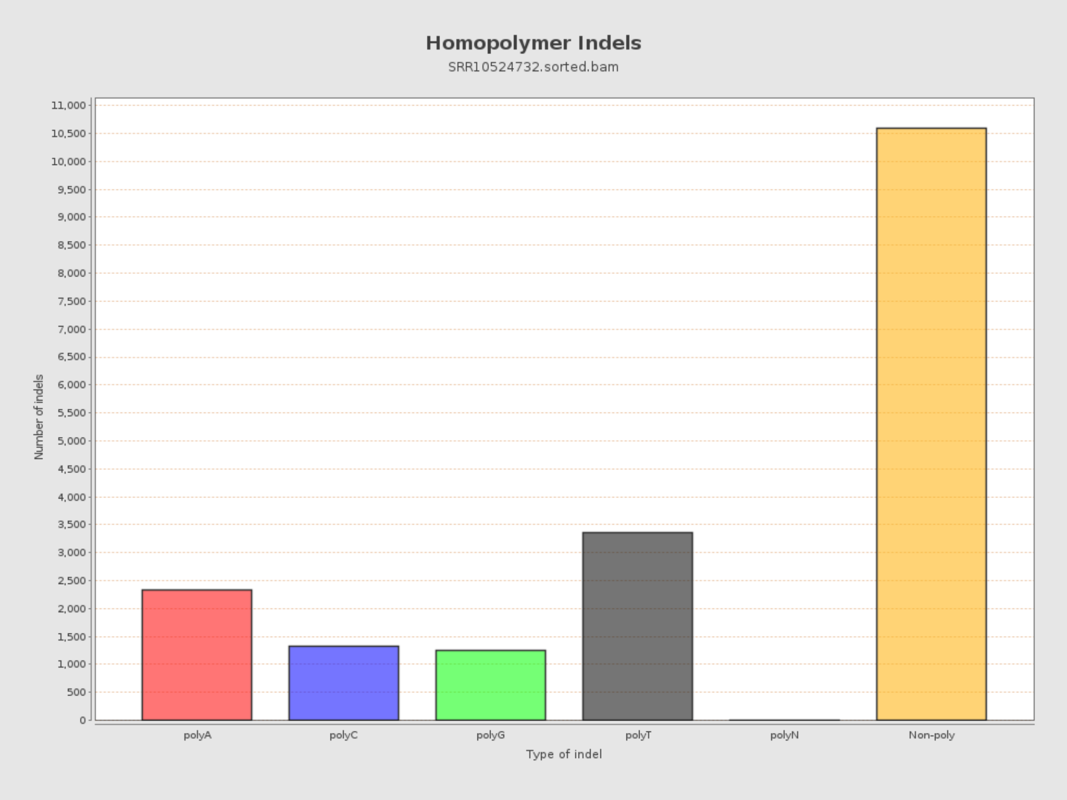
9. Results : Mapped Reads GC-content Distribution



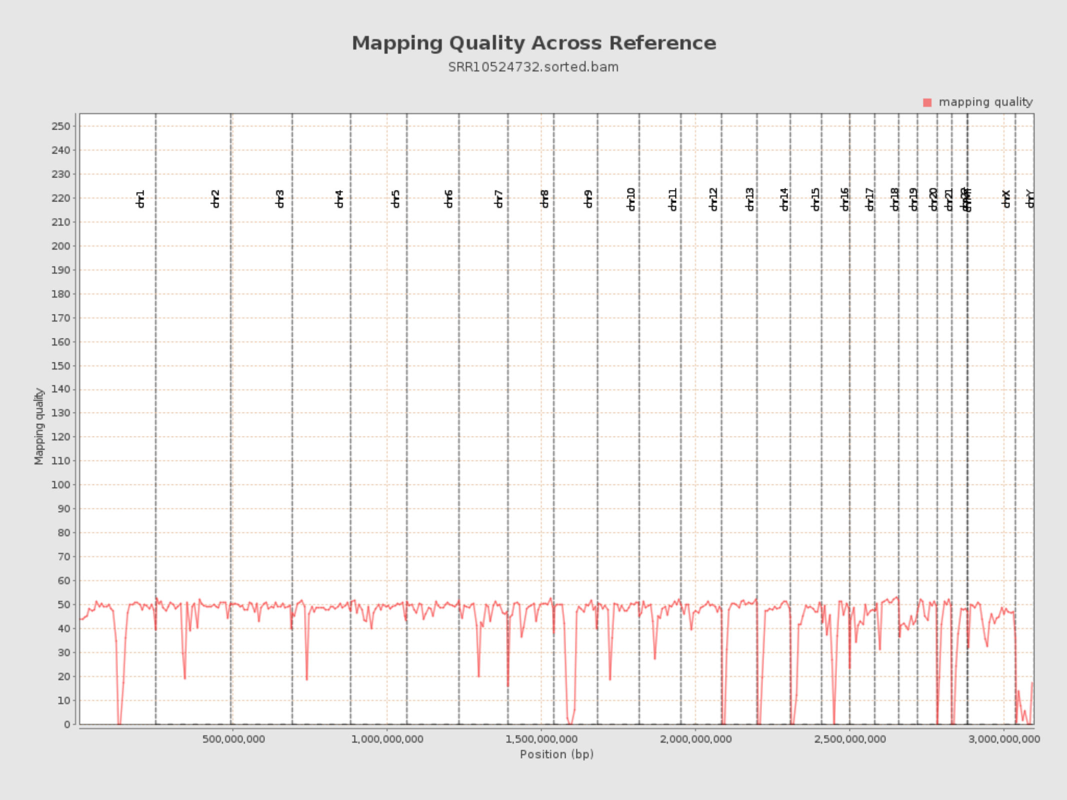
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram