Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 04:33:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524444.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_SRR10524444 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524444.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 04:33:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524444.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	719,502
Mapped reads	659,178 / 91.62%
Unmapped reads	60,324 / 8.38%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,347 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	16,911 / 2.35%
Duplication rate	1.94%
Clipped reads	659,674 / 91.68%

2.2. ACGT Content

Number/percentage of A's	9,645,468 / 25.13%
Number/percentage of C's	7,001,614 / 18.24%
Number/percentage of T's	12,510,323 / 32.59%
Number/percentage of G's	9,223,024 / 24.03%
Number/percentage of N's	858 / 0%
GC Percentage	42.27%

2.3. Coverage

Mean	0.0124

Standard Deviation	0.1483

2.4. Mapping Quality

Mean Mapping Quality	45.77

2.5. Mismatches and indels

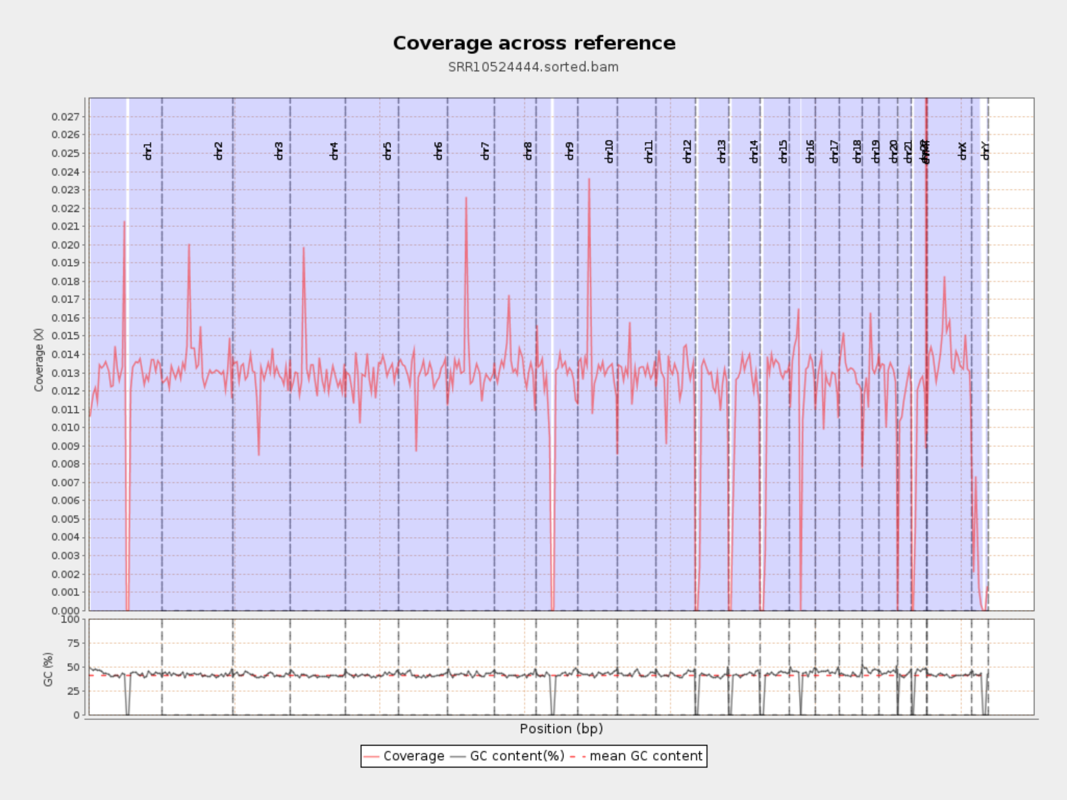
General error rate	0.52%
Mismatches	195,188
Insertions	2,645
Mapped reads with at least one insertion	0.4%
Deletions	7,948
Mapped reads with at least one deletion	1.2%
Homopolymer indels	44.35%

2.6. Chromosome stats

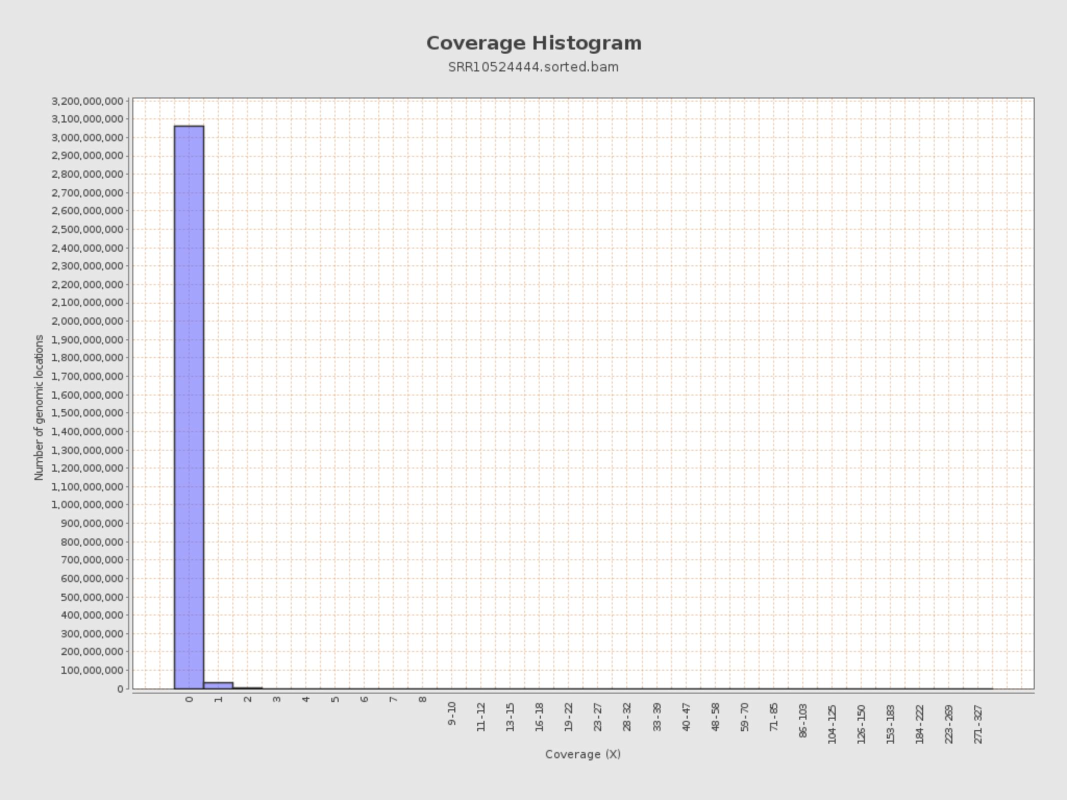
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3093166	0.0124	0.2303
chr2	243199373	3258648	0.0134	0.1852
chr3	198022430	2550490	0.0129	0.1186
chr4	191154276	2479311	0.013	0.1241
chr5	180915260	2325785	0.0129	0.1184
chr6	171115067	2218018	0.013	0.1259
chr7	159138663	2132845	0.0134	0.1946

chr8	146364022	1957608	0.0134	0.1631
chr9	141213431	1618078	0.0115	0.1282
chr10	135534747	1842596	0.0136	0.1486
chr11	135006516	1761353	0.013	0.1337
chr12	133851895	1730823	0.0129	0.1196
chr13	115169878	1216178	0.0106	0.1077
chr14	107349540	1161411	0.0108	0.1101
chr15	102531392	1094635	0.0107	0.1094
chr16	90354753	1117111	0.0124	0.1218
chr17	81195210	1000130	0.0123	0.1187
chr18	78077248	1038211	0.0133	0.1939
chr19	59128983	761669	0.0129	0.1777
chr20	63025520	796076	0.0126	0.1181
chr21	48129895	510686	0.0106	0.1118
chr22	51304566	435092	0.0085	0.0962
chrMT	16571	8000	0.4828	0.7124
chrX	155270560	2166076	0.014	0.1286
chrY	59373566	120104	0.002	0.0718

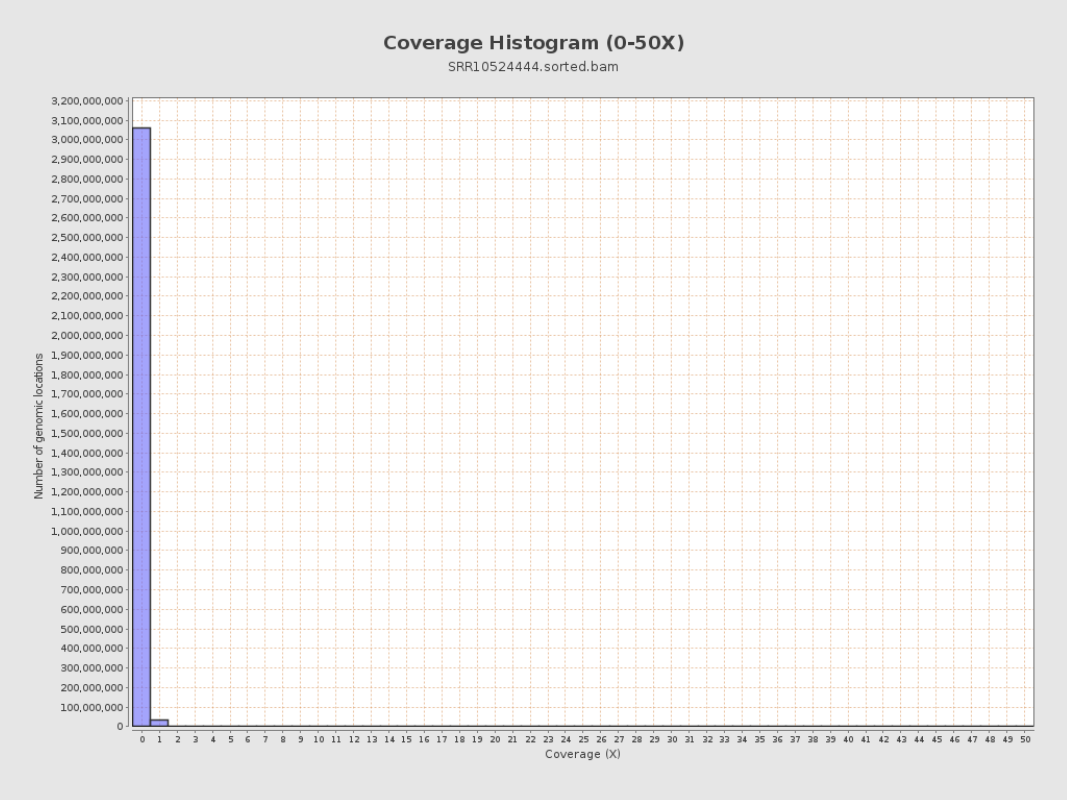
3. Results : Coverage across reference



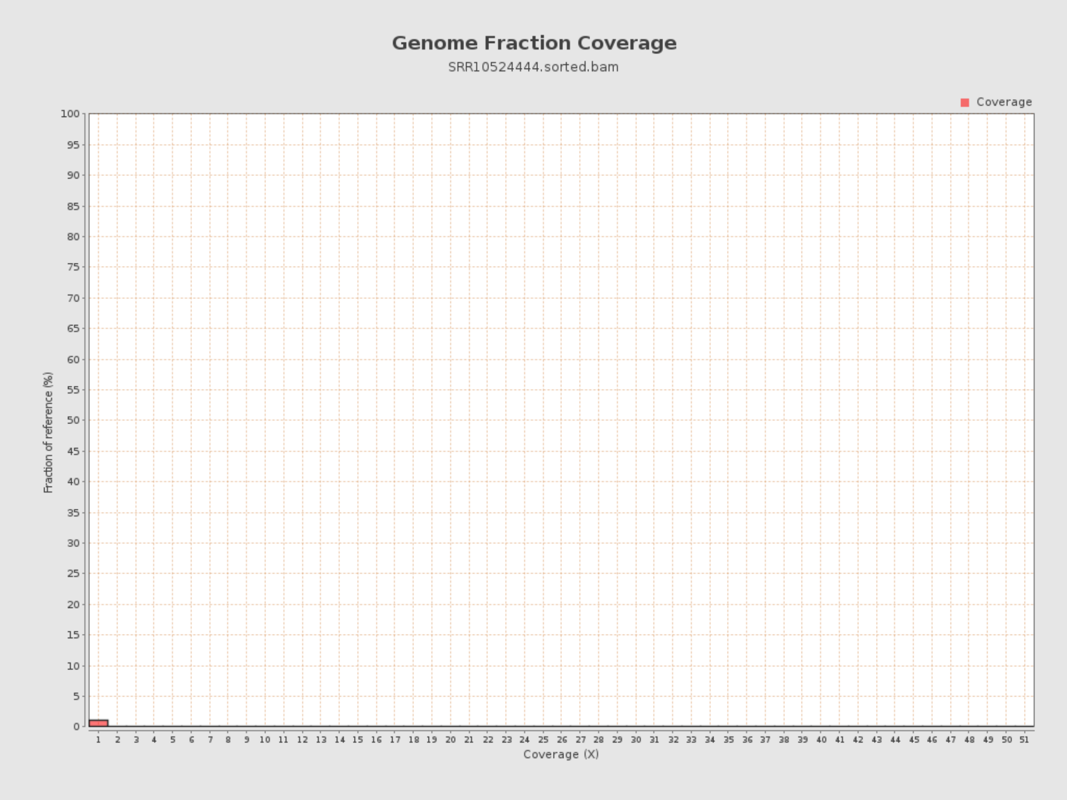
4. Results : Coverage Histogram



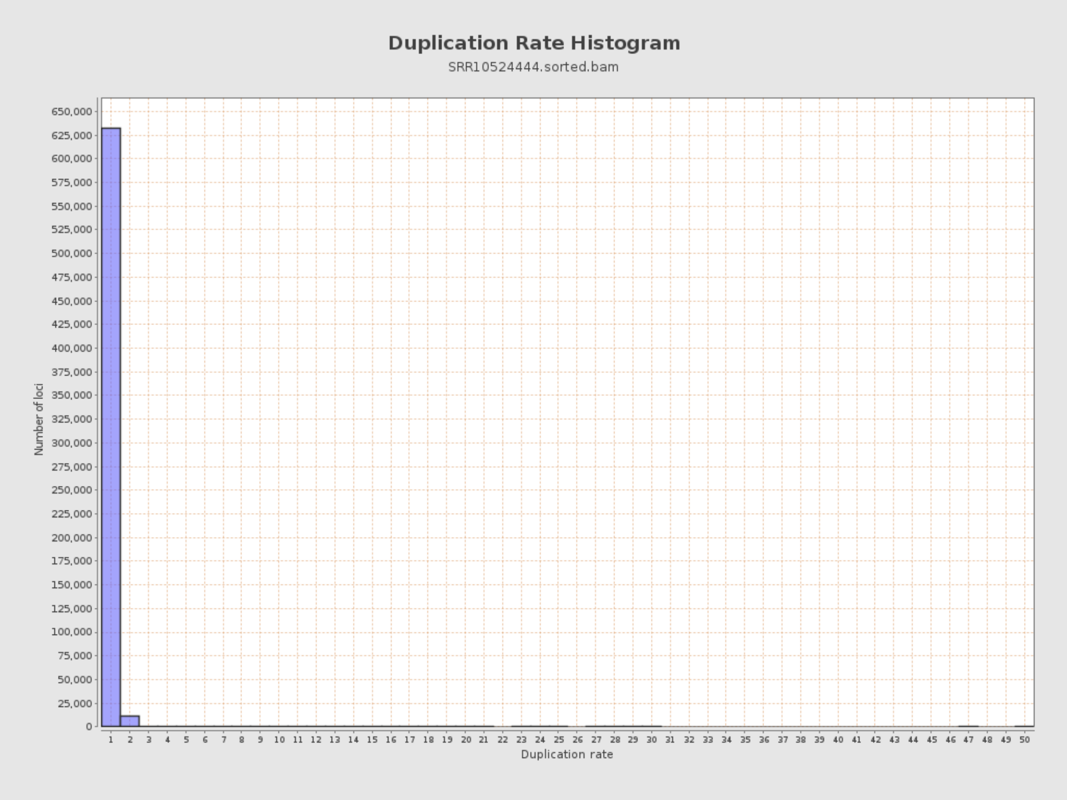
5. Results : Coverage Histogram (0-50X)



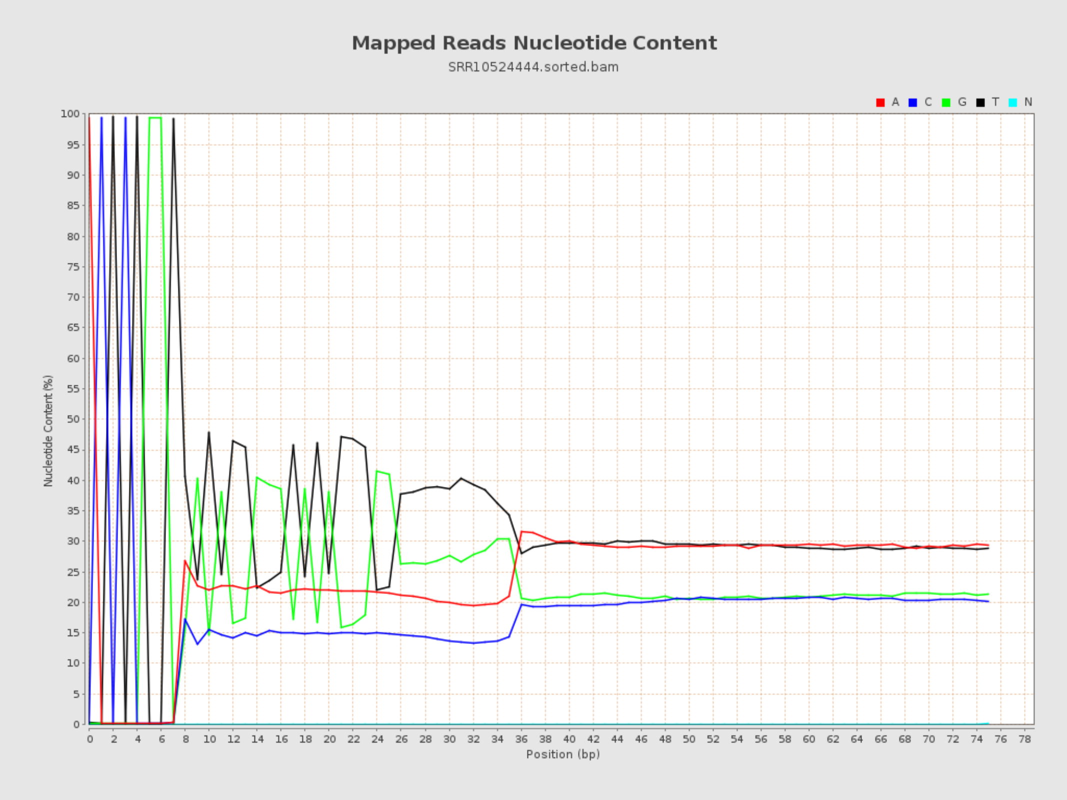
6. Results : Genome Fraction Coverage



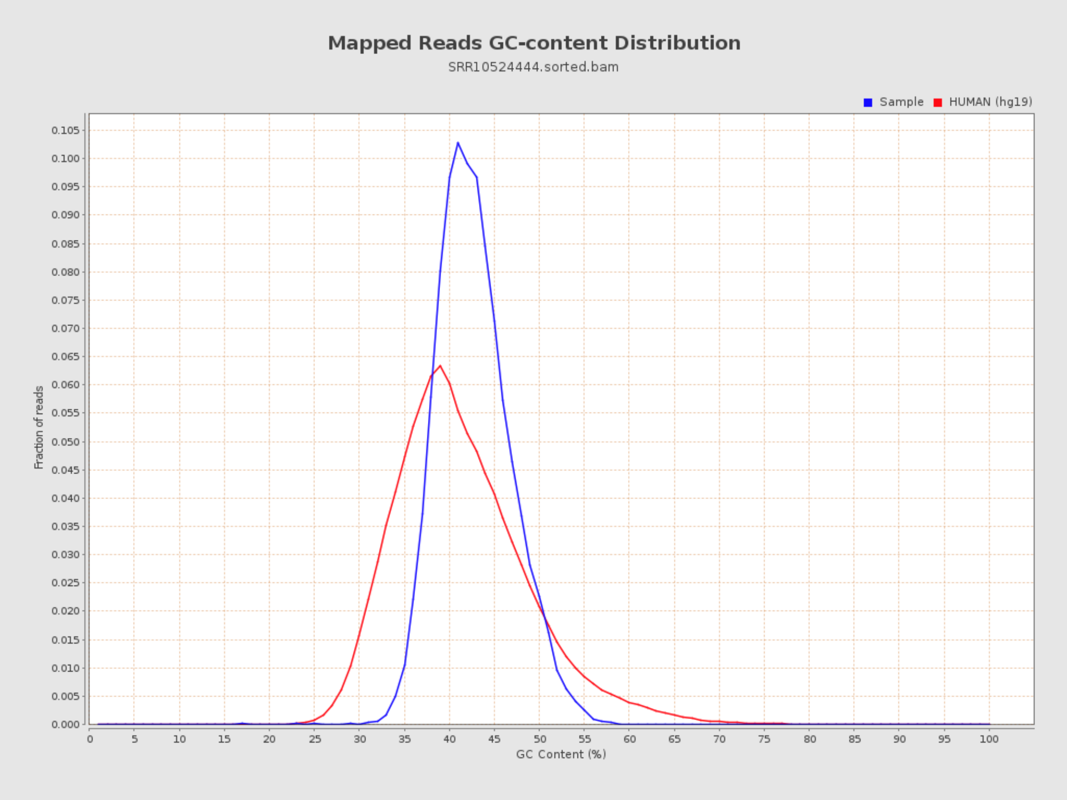
7. Results : Duplication Rate Histogram



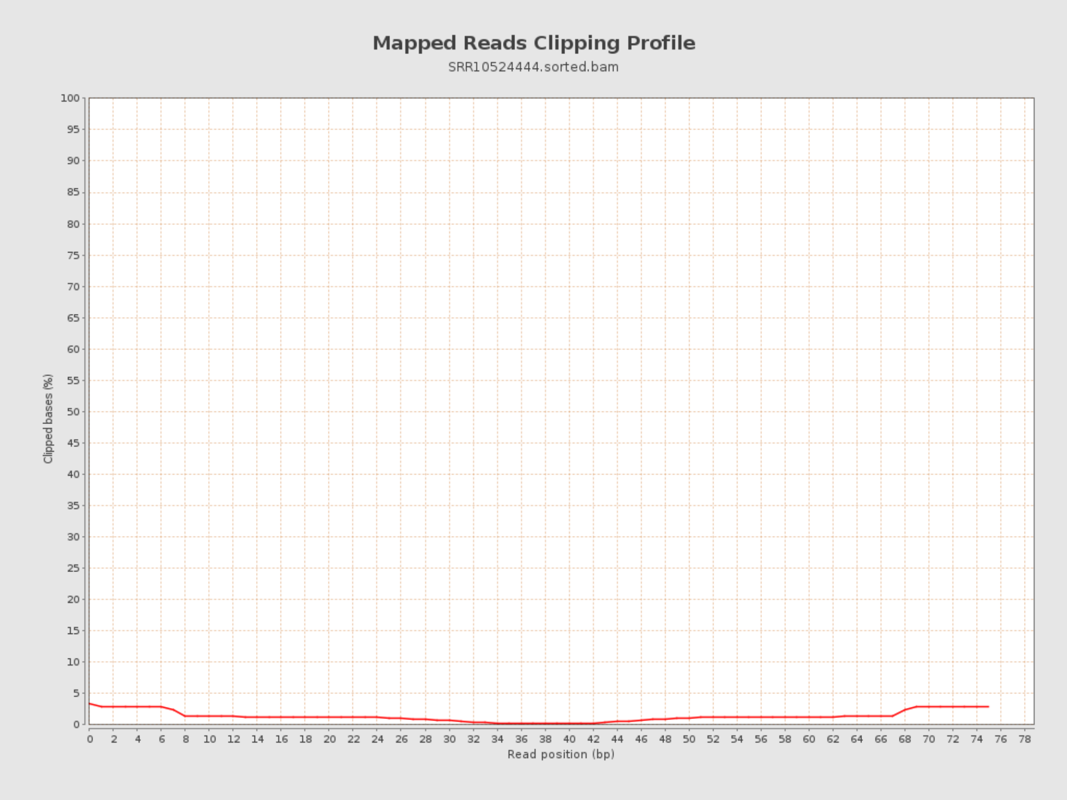
8. Results : Mapped Reads Nucleotide Content



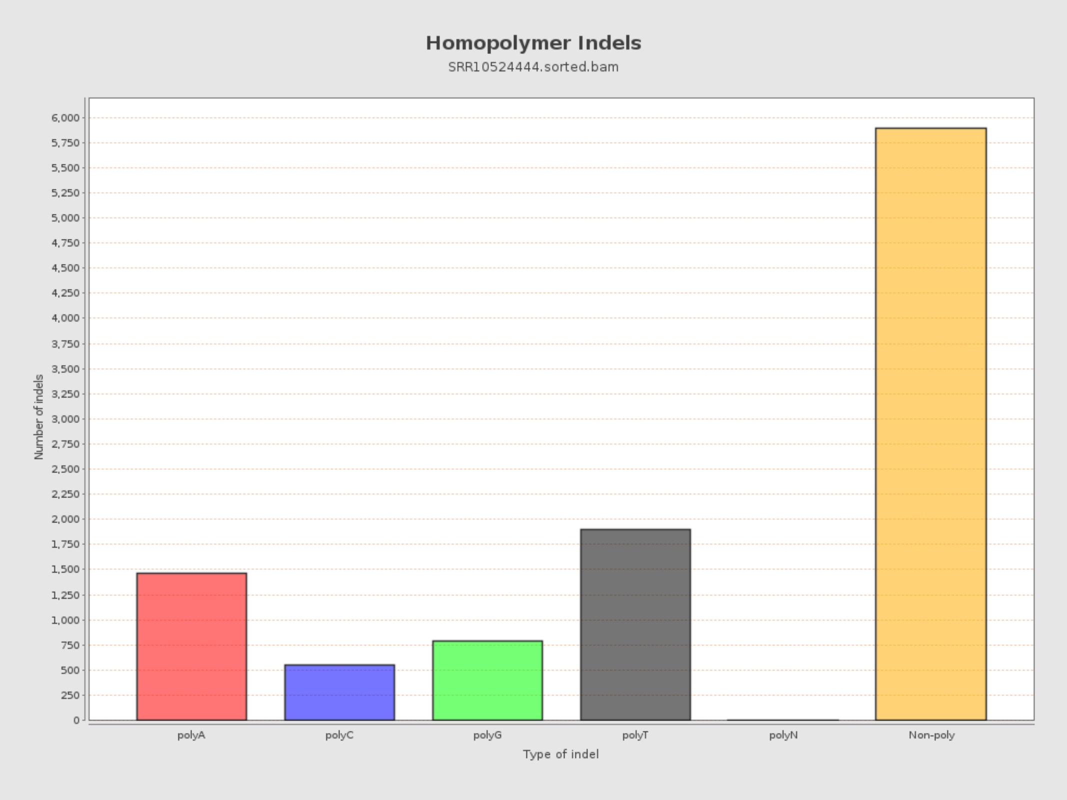
9. Results : Mapped Reads GC-content Distribution



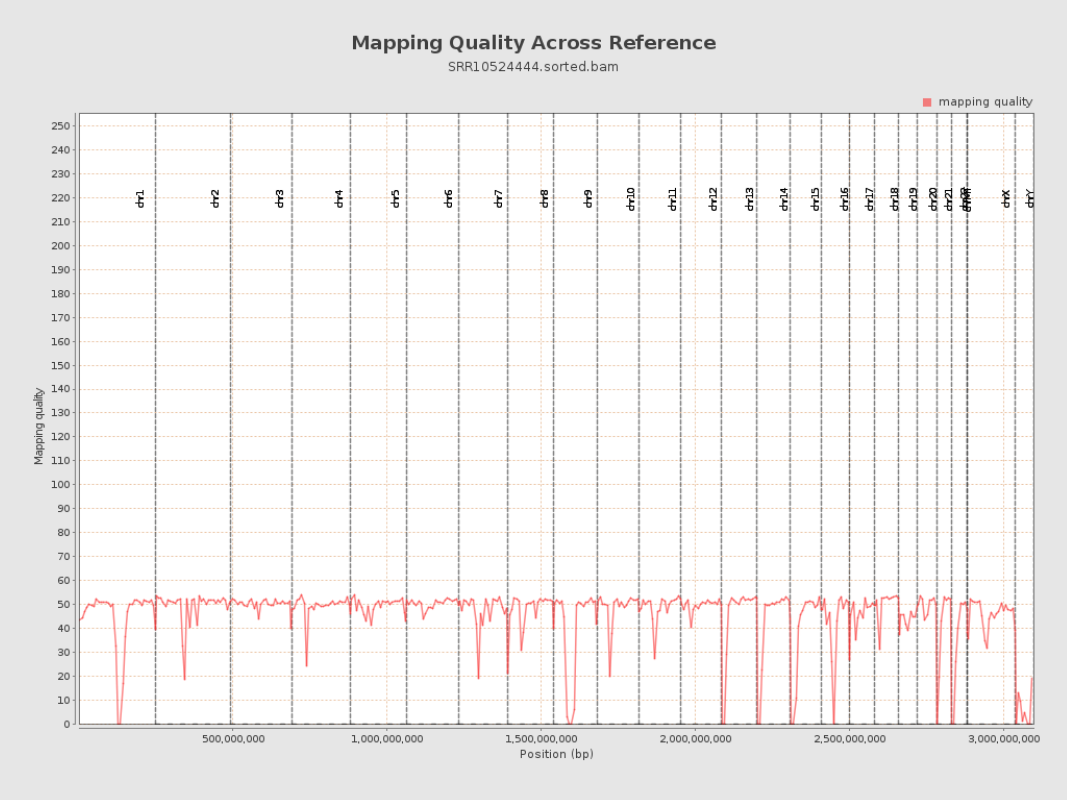
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram