Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 01:42:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524890.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_SRR10524890 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524890.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 01:42:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524890.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,085,159
Mapped reads	1,921,612 / 92.16%
Unmapped reads	163,547 / 7.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,646 / 0.37%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	80,288 / 3.85%
Duplication rate	3%
Clipped reads	1,923,513 / 92.25%

2.2. ACGT Content

Number/percentage of A's	28,182,088 / 25.13%
Number/percentage of C's	19,710,703 / 17.58%
Number/percentage of T's	37,125,312 / 33.11%
Number/percentage of G's	27,095,372 / 24.16%
Number/percentage of N's	14,594 / 0.01%
GC Percentage	41.74%

2.3. Coverage

Mean	0.0362

Standard Deviation	0.3504

2.4. Mapping Quality

Mean Mapping Quality	46.05

2.5. Mismatches and indels

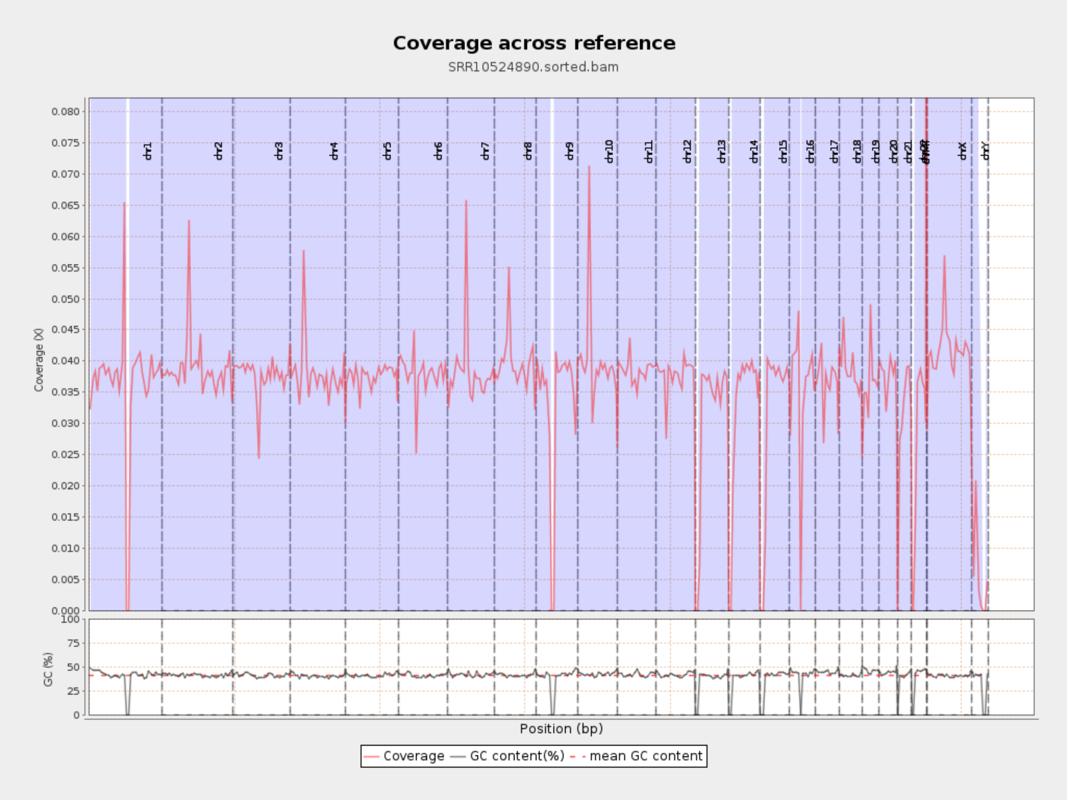
General error rate	0.51%
Mismatches	549,839
Insertions	9,005
Mapped reads with at least one insertion	0.47%
Deletions	21,093
Mapped reads with at least one deletion	1.09%
Homopolymer indels	42.5%

2.6. Chromosome stats

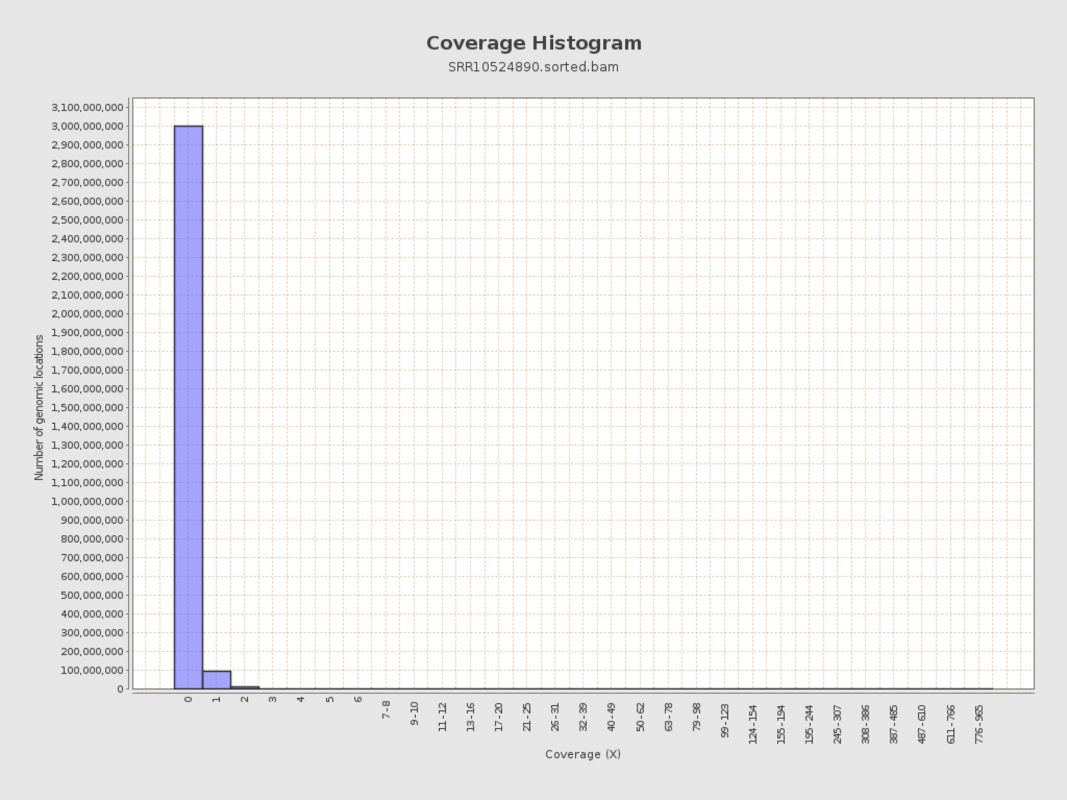
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9045011	0.0363	0.7068
chr2	243199373	9495186	0.039	0.3752
chr3	198022430	7430154	0.0375	0.2133
chr4	191154276	7245266	0.0379	0.2428
chr5	180915260	6803323	0.0376	0.2132
chr6	171115067	6506050	0.038	0.2405
chr7	159138663	6126187	0.0385	0.4786

chr8	146364022	5798854	0.0396	0.3277
chr9	141213431	4654019	0.033	0.3022
chr10	135534747	5419113	0.04	0.3396
chr11	135006516	5164616	0.0383	0.3141
chr12	133851895	5045526	0.0377	0.2206
chr13	115169878	3506813	0.0304	0.192
chr14	107349540	3416829	0.0318	0.2107
chr15	102531392	3172615	0.0309	0.1933
chr16	90354753	3204154	0.0355	0.2324
chr17	81195210	2956124	0.0364	0.2339
chr18	78077248	3033346	0.0389	0.6047
chr19	59128983	2162383	0.0366	0.4616
chr20	63025520	2369331	0.0376	0.217
chr21	48129895	1462587	0.0304	0.2187
chr22	51304566	1308824	0.0255	0.1741
chrMT	16571	10145	0.6122	0.9892
chrX	155270560	6479733	0.0417	0.263
chrY	59373566	345361	0.0058	0.1567

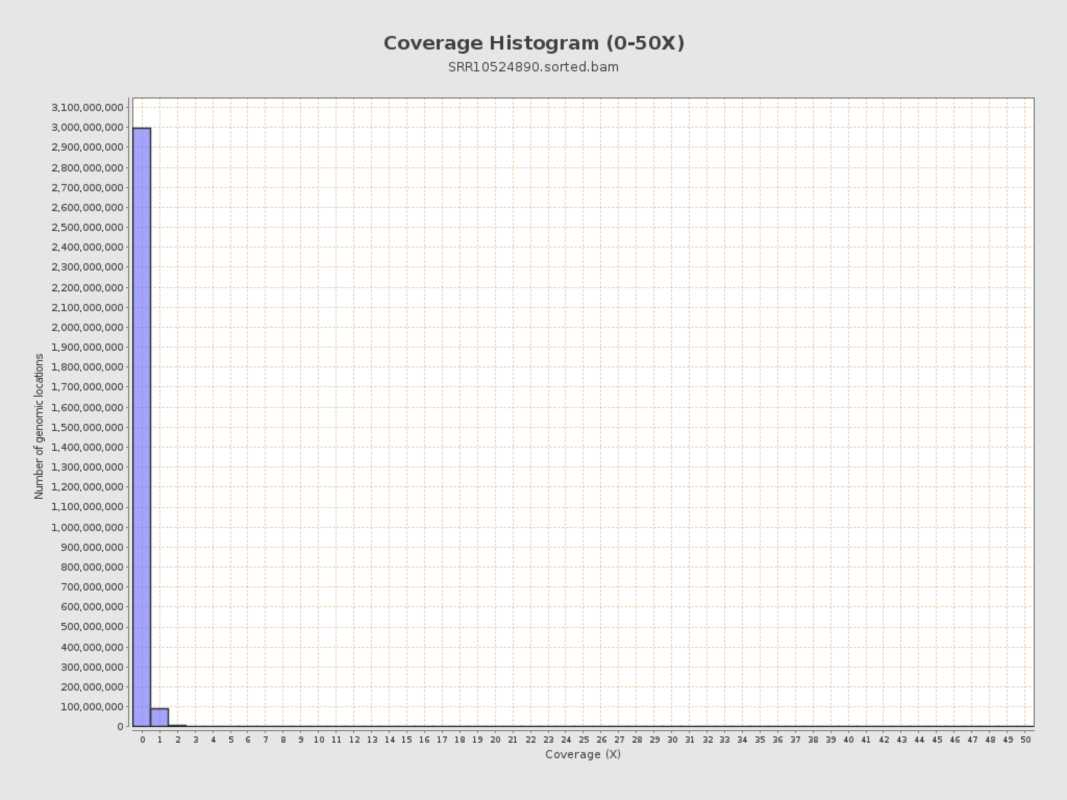
3. Results : Coverage across reference



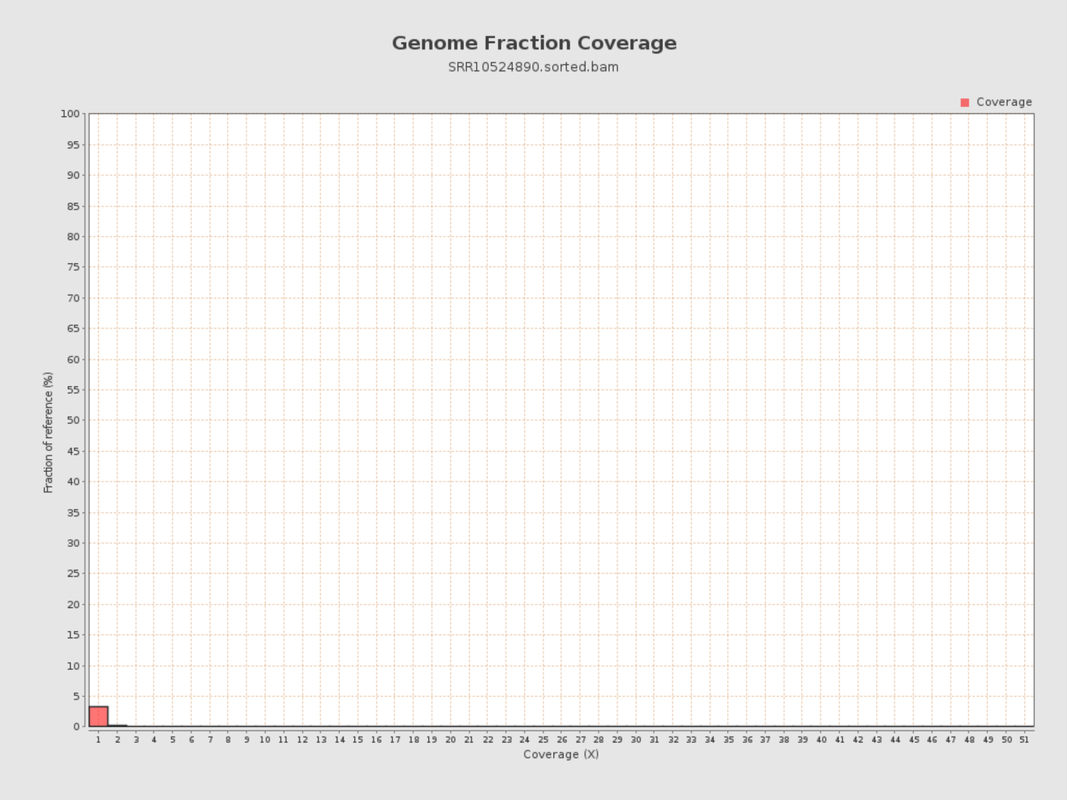
4. Results : Coverage Histogram



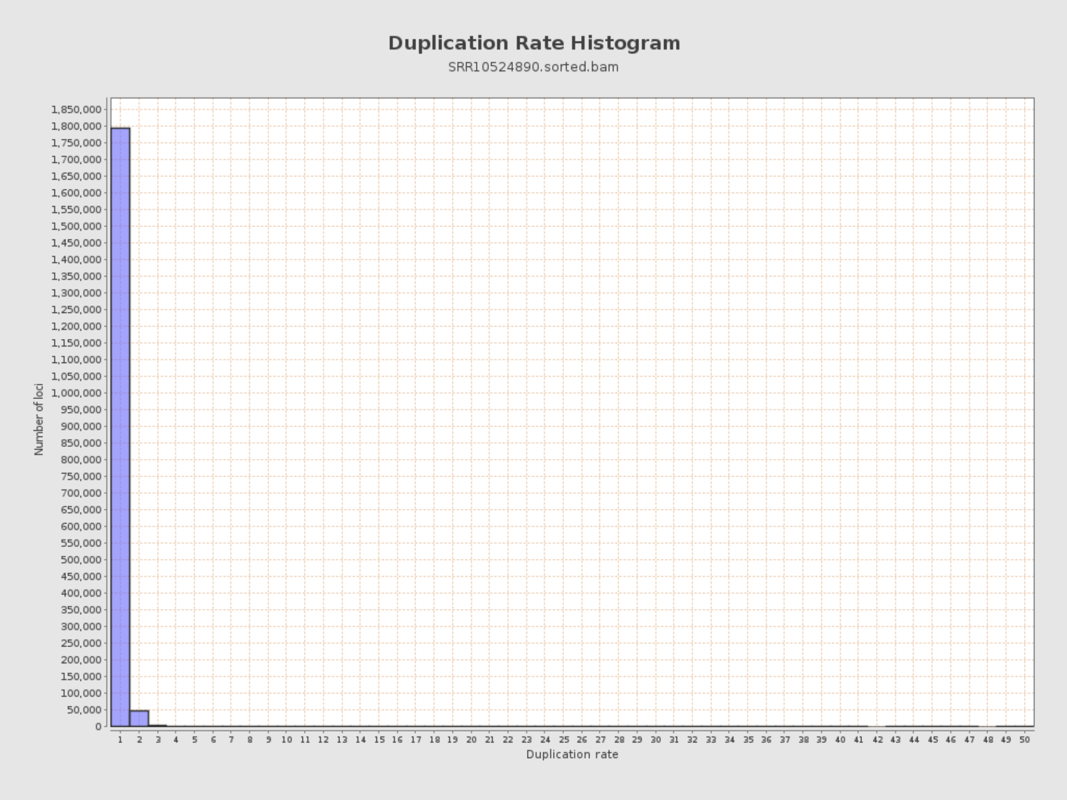
5. Results : Coverage Histogram (0-50X)



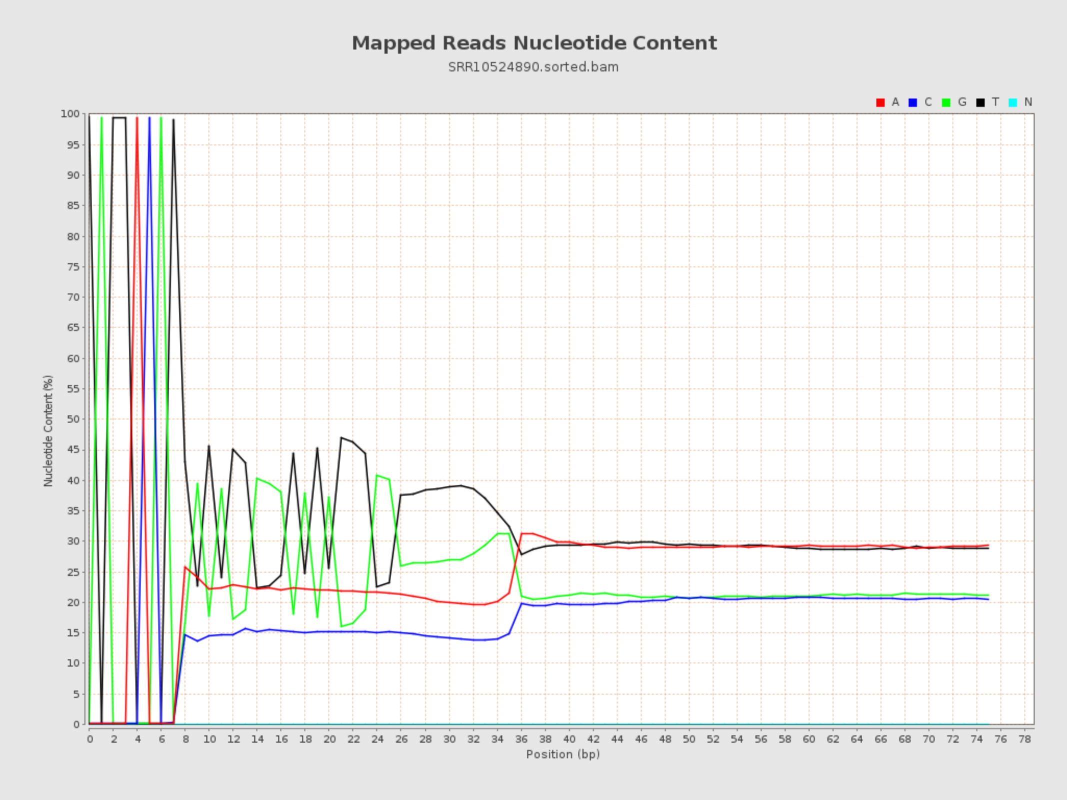
6. Results : Genome Fraction Coverage



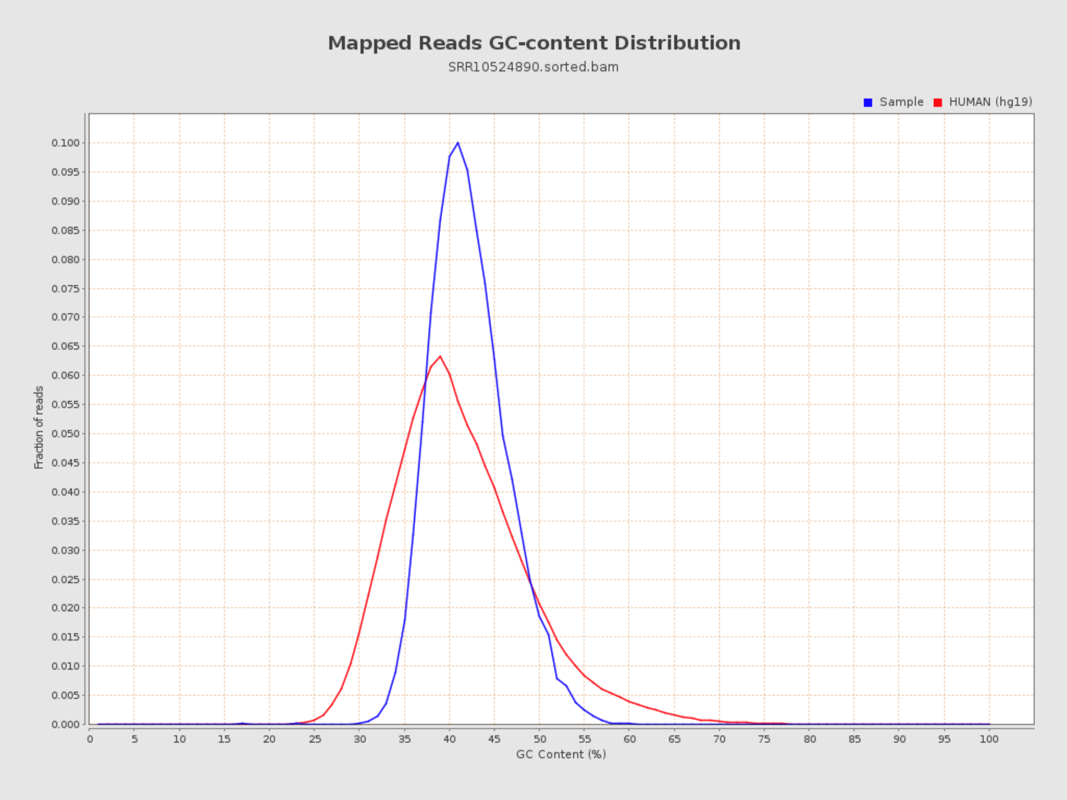
7. Results : Duplication Rate Histogram



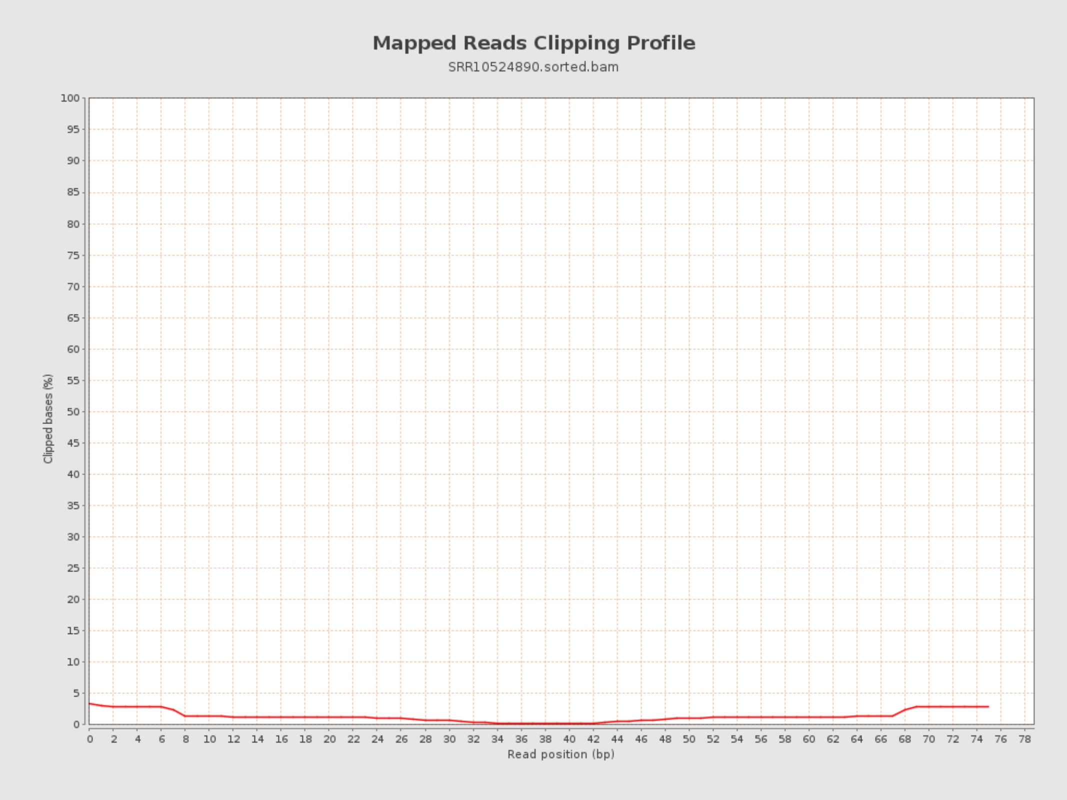
8. Results : Mapped Reads Nucleotide Content



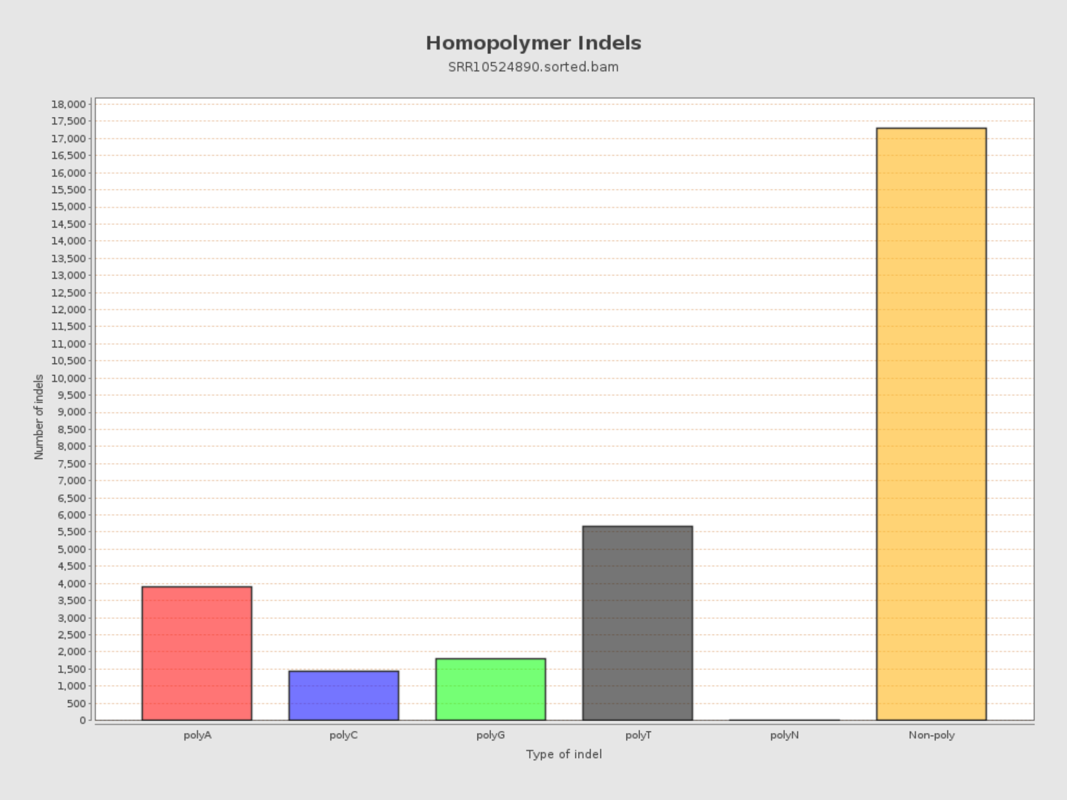
9. Results : Mapped Reads GC-content Distribution



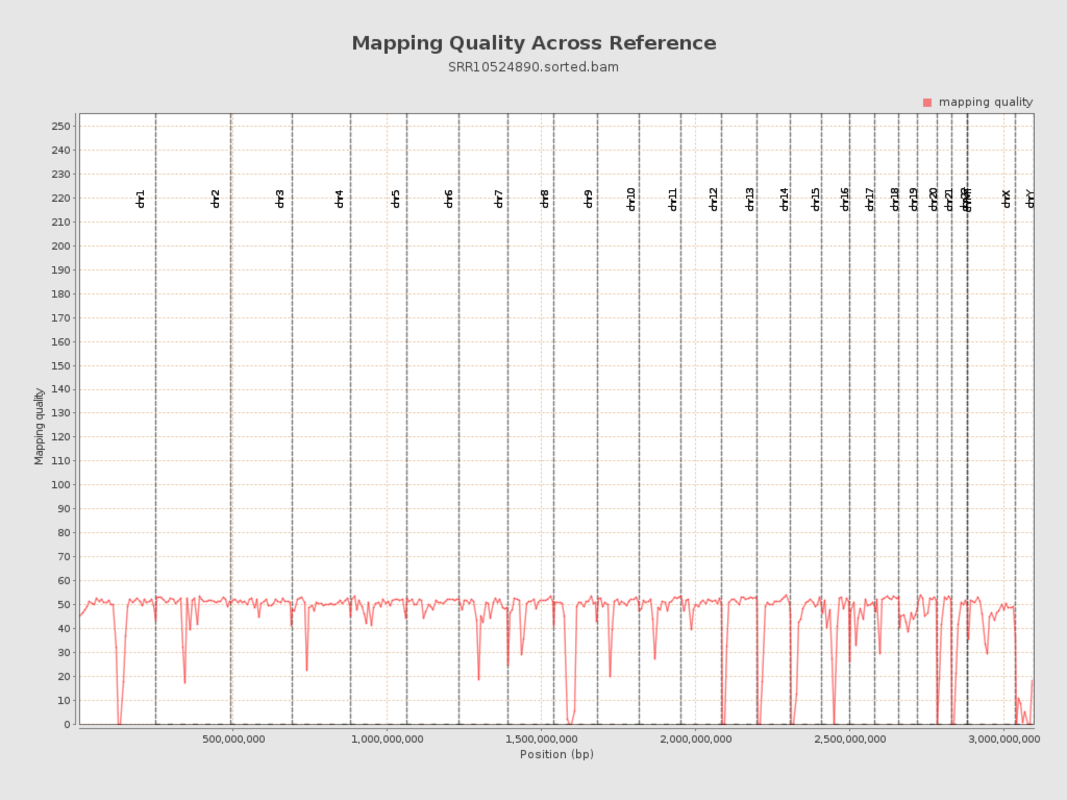
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram