Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 10:03:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524544.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_SRR10524544 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524544.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 10:03:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524544.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,344,288
Mapped reads	2,146,260 / 91.55%
Unmapped reads	198,028 / 8.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,984 / 0.51%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	71,360 / 3.04%
Duplication rate	2.35%
Clipped reads	2,151,872 / 91.79%

2.2. ACGT Content

Number/percentage of A's	32,573,089 / 26.26%
Number/percentage of C's	23,604,037 / 19.03%
Number/percentage of T's	39,286,159 / 31.68%
Number/percentage of G's	28,557,097 / 23.03%
Number/percentage of N's	3,784 / 0%
GC Percentage	42.06%

2.3. Coverage

Mean	0.0401

Standard Deviation	0.3307

2.4. Mapping Quality

Mean Mapping Quality	45.21

2.5. Mismatches and indels

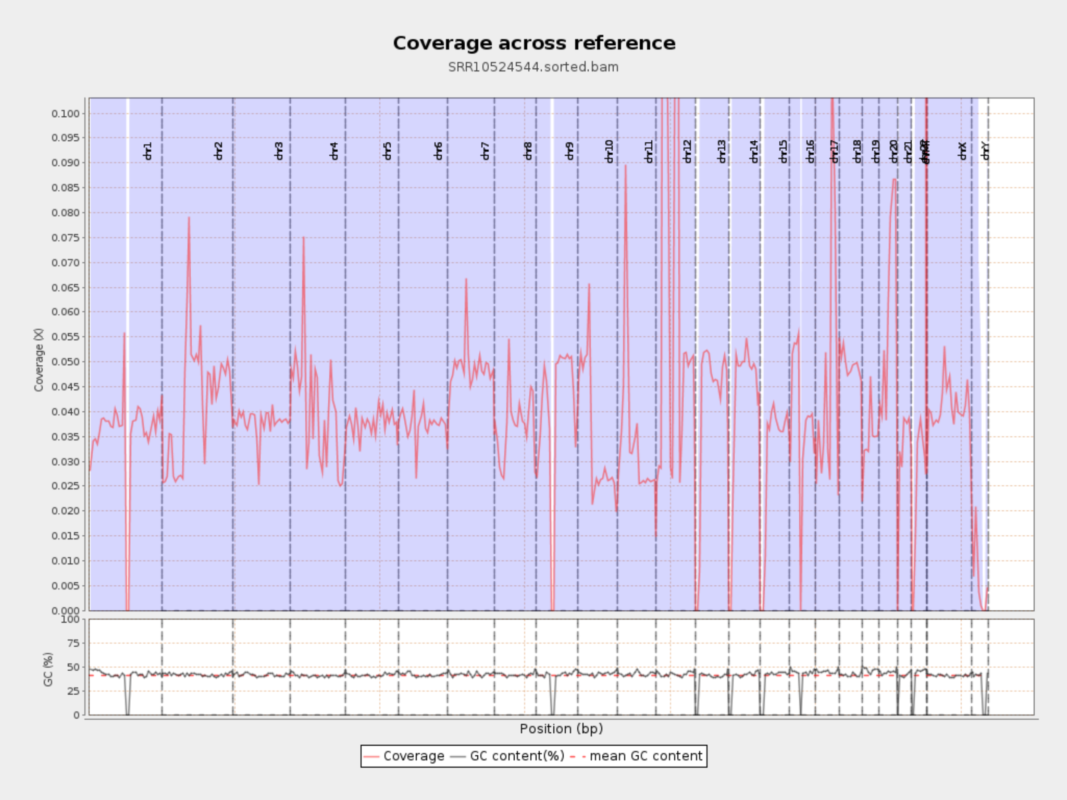
General error rate	0.49%
Mismatches	589,707
Insertions	9,605
Mapped reads with at least one insertion	0.45%
Deletions	19,813
Mapped reads with at least one deletion	0.92%
Homopolymer indels	39.74%

2.6. Chromosome stats

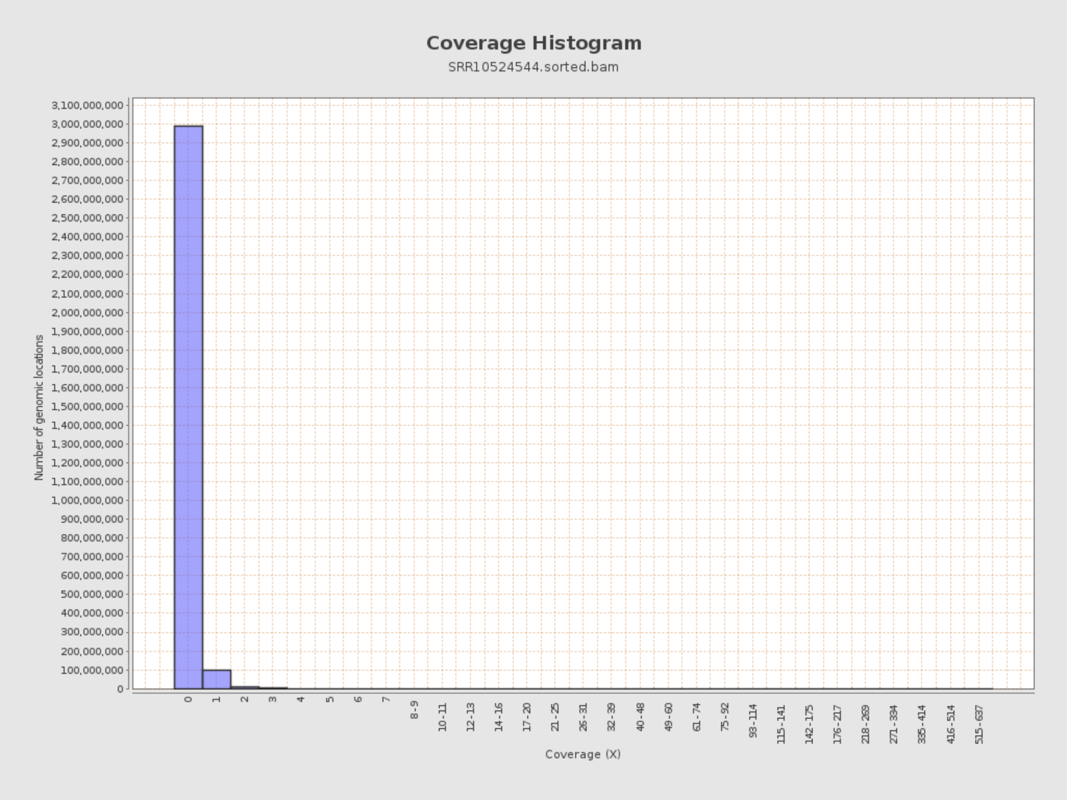
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8824864	0.0354	0.5342
chr2	243199373	10384165	0.0427	0.3858
chr3	198022430	7490898	0.0378	0.2133
chr4	191154276	7733721	0.0405	0.2622
chr5	180915260	6846289	0.0378	0.2169
chr6	171115067	6446067	0.0377	0.2373
chr7	159138663	7818884	0.0491	0.4365

chr8	146364022	5464182	0.0373	0.3165
chr9	141213431	5660216	0.0401	0.3405
chr10	135534747	4690949	0.0346	0.3403
chr11	135006516	4723899	0.035	0.2787
chr12	133851895	9290758	0.0694	0.3379
chr13	115169878	4649345	0.0404	0.2206
chr14	107349540	4421499	0.0412	0.2496
chr15	102531392	3131078	0.0305	0.1952
chr16	90354753	3507447	0.0388	0.2343
chr17	81195210	3704098	0.0456	0.2481
chr18	78077248	3880403	0.0497	0.627
chr19	59128983	2067775	0.035	0.4058
chr20	63025520	3846438	0.061	0.2825
chr21	48129895	1521082	0.0316	0.2306
chr22	51304566	1231422	0.024	0.1685
chrMT	16571	20092	1.2125	1.3622
chrX	155270560	6343809	0.0409	0.2629
chrY	59373566	358045	0.006	0.1524

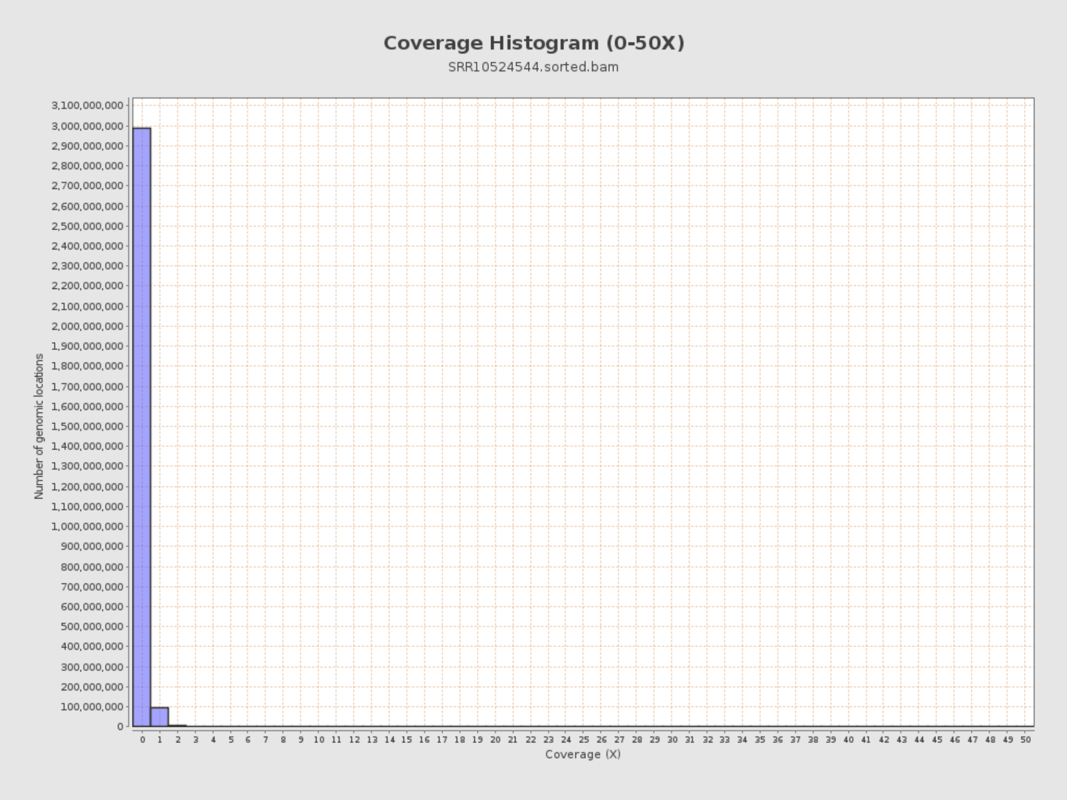
3. Results : Coverage across reference



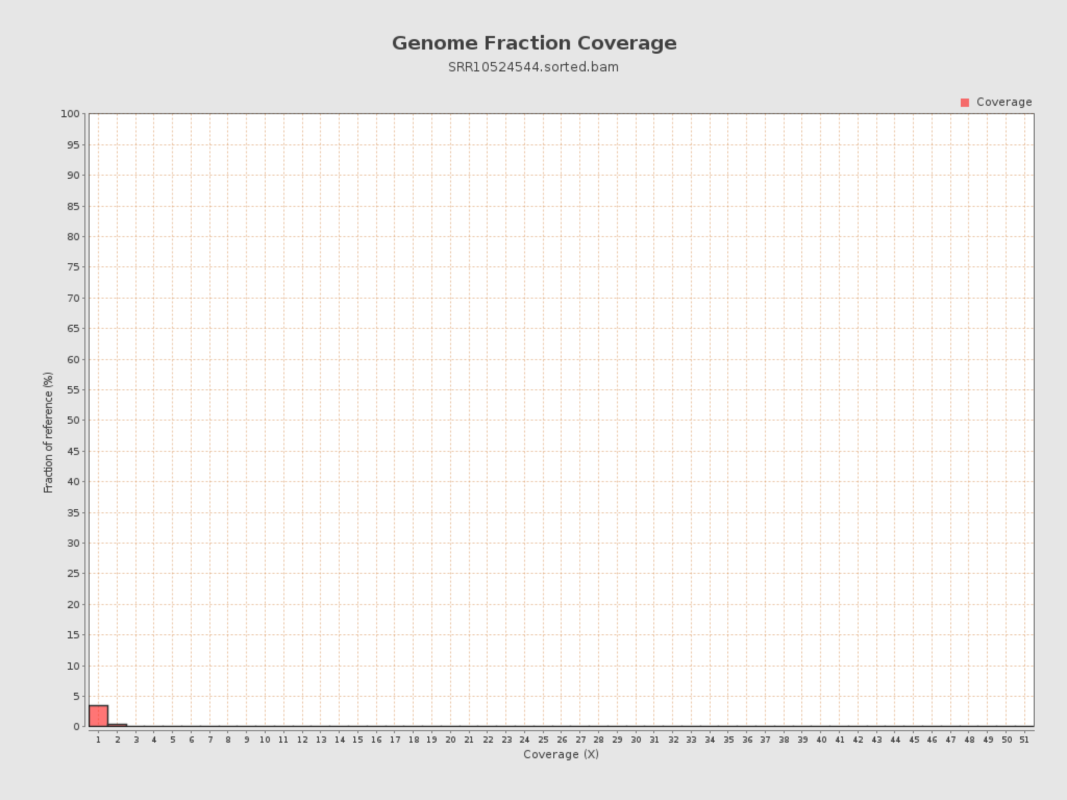
4. Results : Coverage Histogram



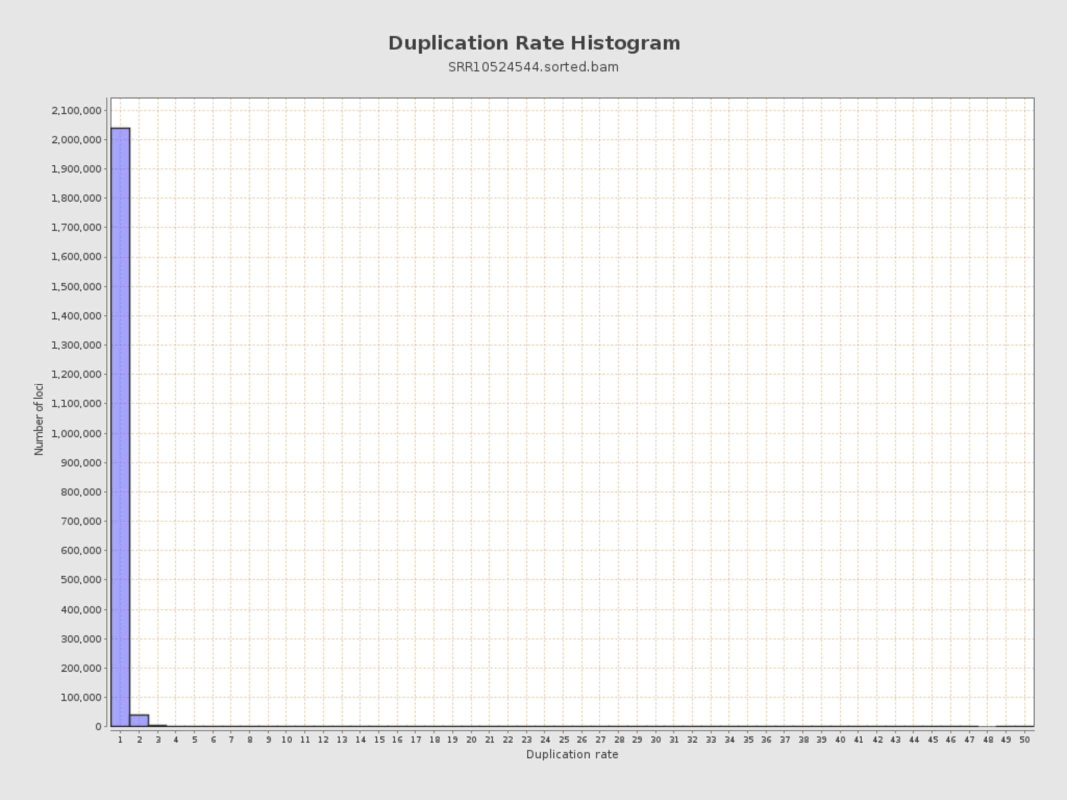
5. Results : Coverage Histogram (0-50X)



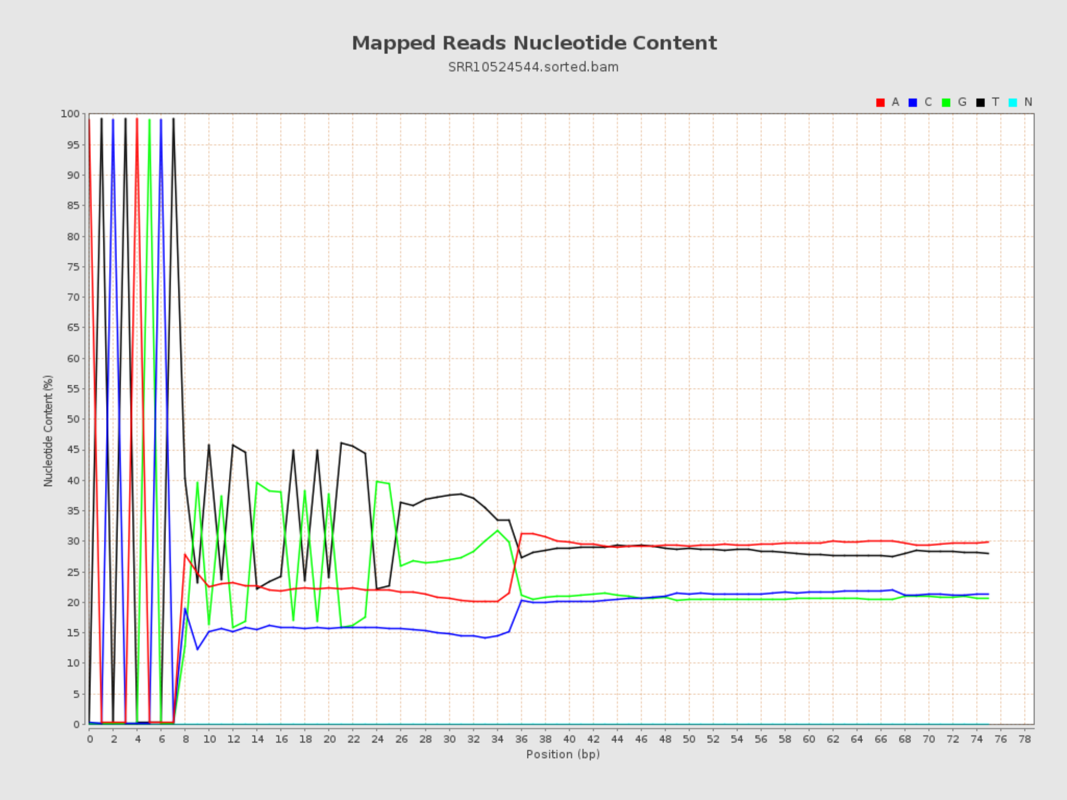
6. Results : Genome Fraction Coverage



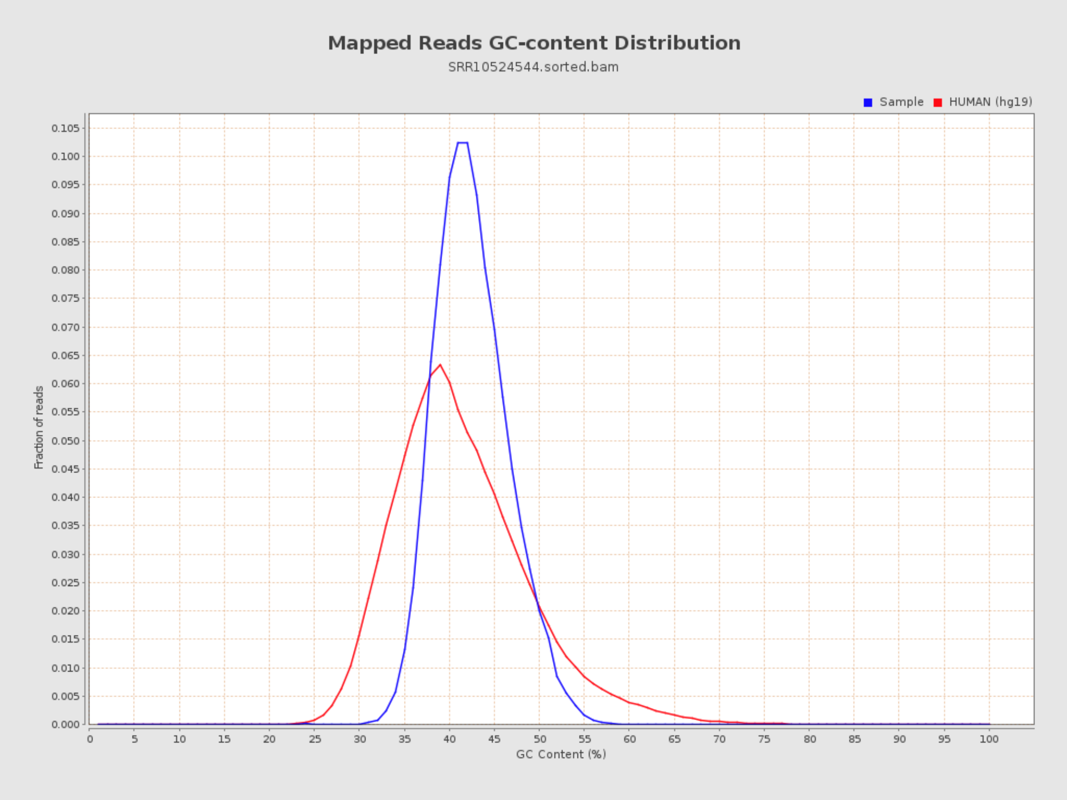
7. Results : Duplication Rate Histogram



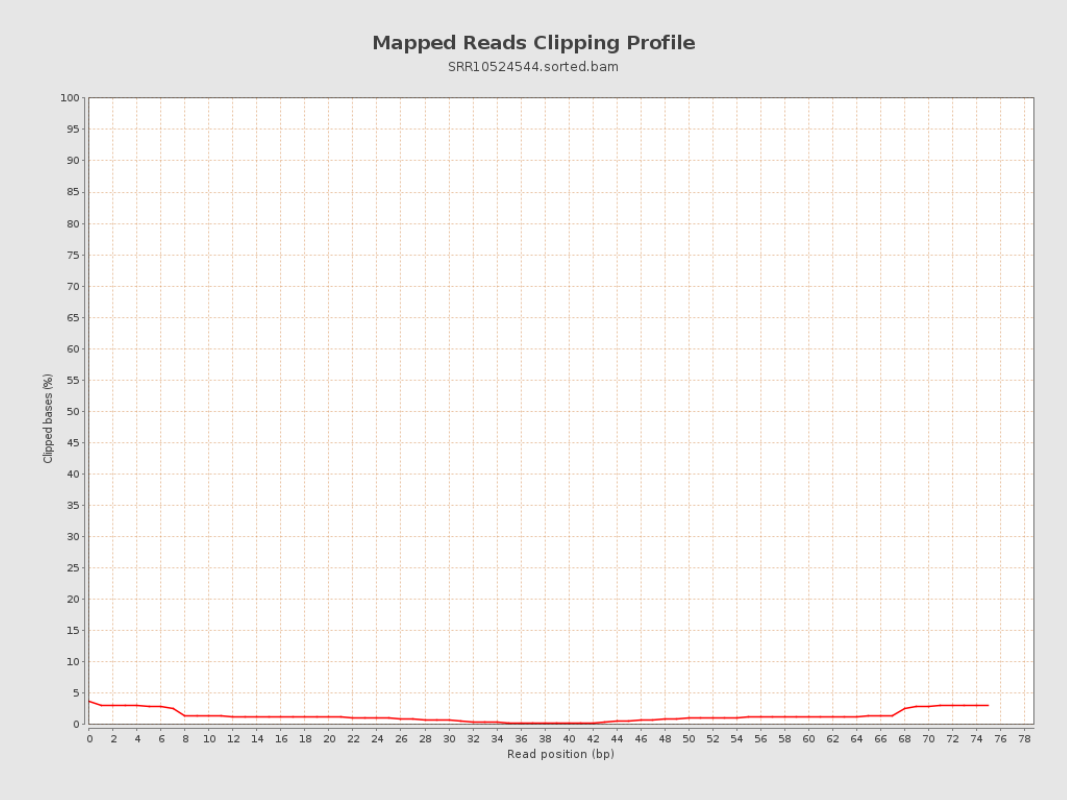
8. Results : Mapped Reads Nucleotide Content



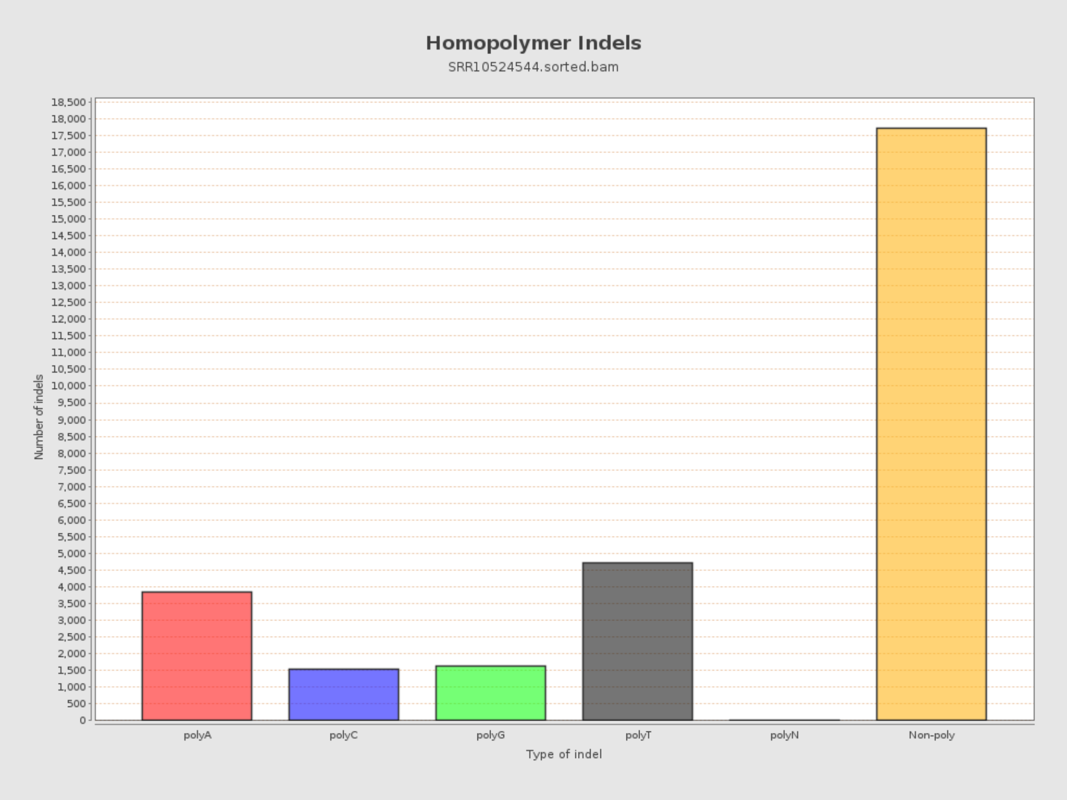
9. Results : Mapped Reads GC-content Distribution



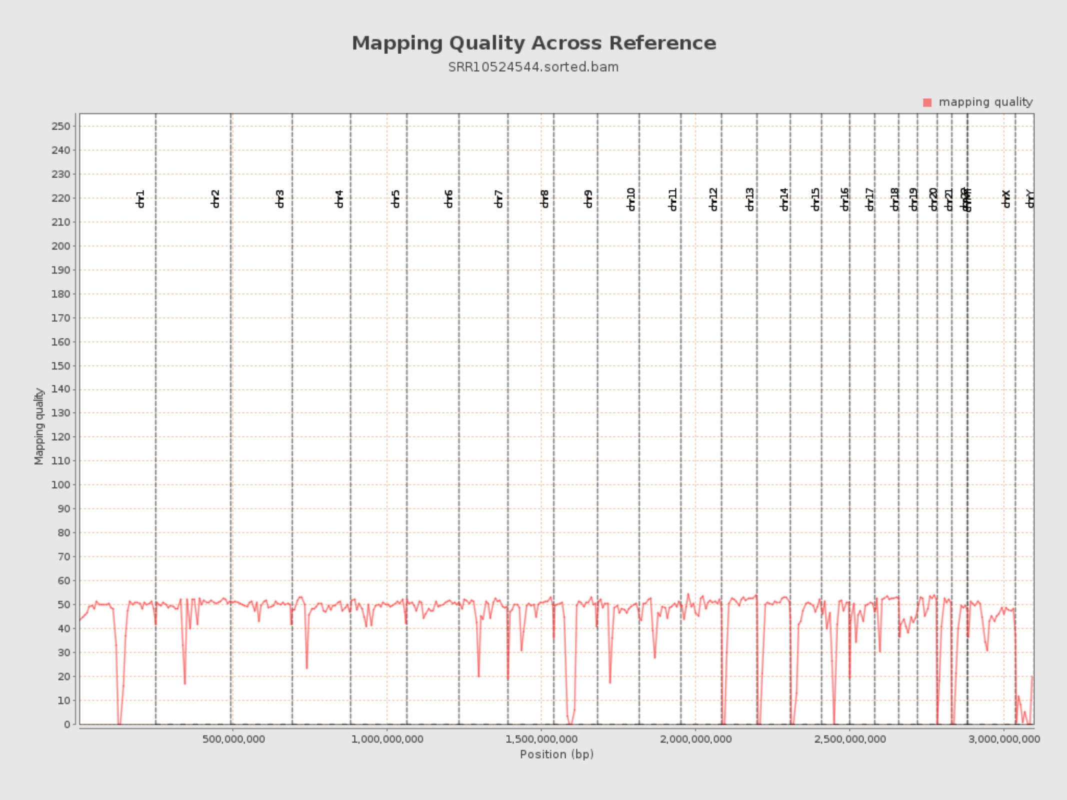
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram