Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 21:57:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524820.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_SRR10524820 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524820.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 21:57:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524820.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,839,000
Mapped reads	1,687,818 / 91.78%
Unmapped reads	151,182 / 8.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,015 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	65,068 / 3.54%
Duplication rate	2.9%
Clipped reads	1,691,578 / 91.98%

2.2. ACGT Content

Number/percentage of A's	23,431,385 / 24.1%
Number/percentage of C's	19,114,006 / 19.66%
Number/percentage of T's	30,230,596 / 31.09%
Number/percentage of G's	24,435,935 / 25.13%
Number/percentage of N's	11,228 / 0.01%
GC Percentage	44.79%

2.3. Coverage

Mean	0.0314

Standard Deviation	0.2582

2.4. Mapping Quality

Mean Mapping Quality	44.59

2.5. Mismatches and indels

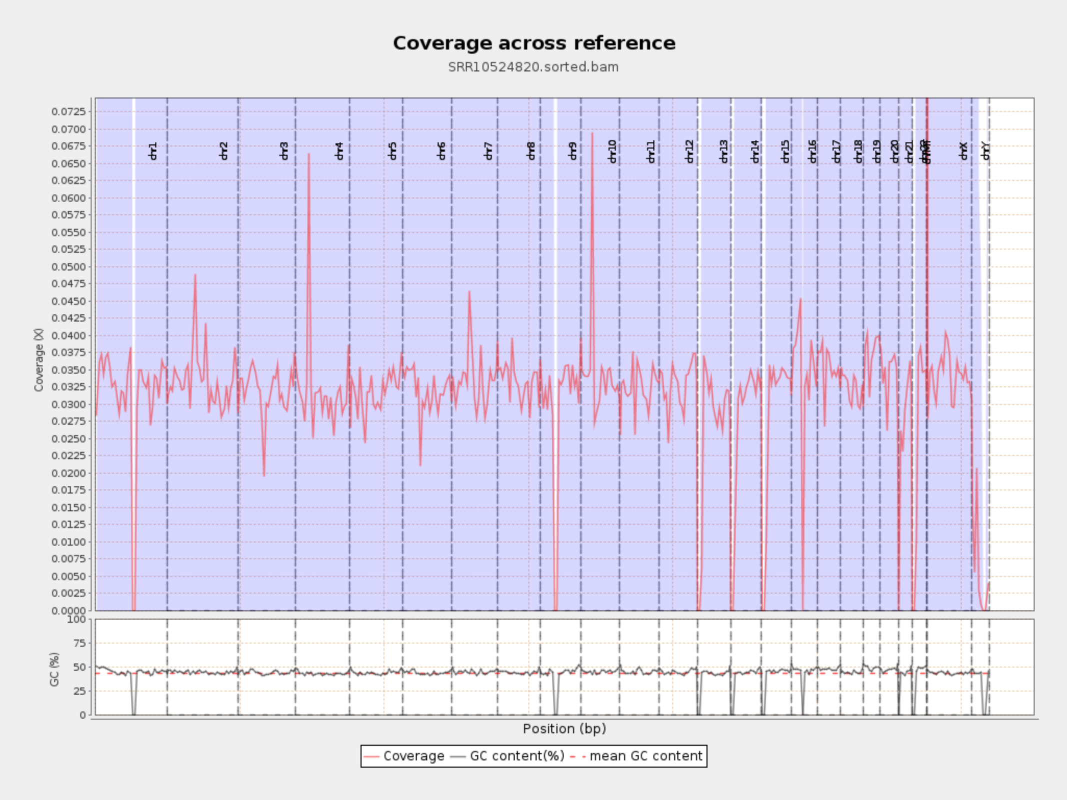
General error rate	0.51%
Mismatches	480,946
Insertions	6,195
Mapped reads with at least one insertion	0.36%
Deletions	18,632
Mapped reads with at least one deletion	1.1%
Homopolymer indels	43.34%

2.6. Chromosome stats

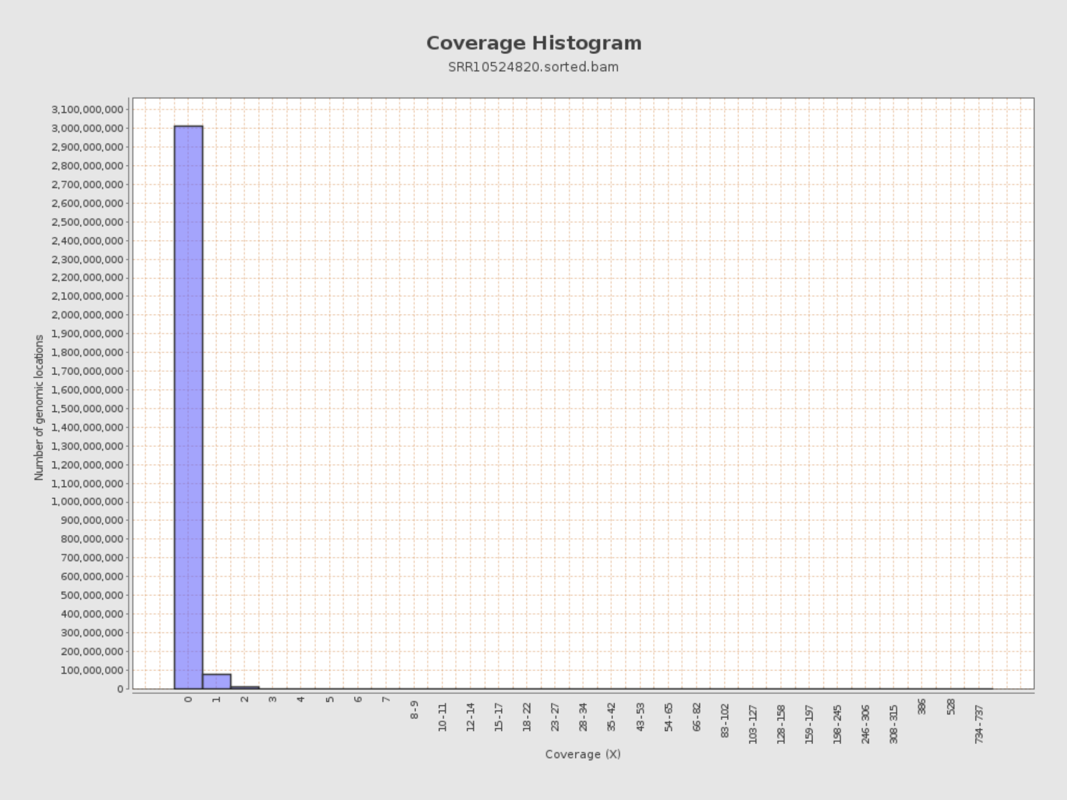
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7770169	0.0312	0.3078
chr2	243199373	8172528	0.0336	0.3986
chr3	198022430	6311533	0.0319	0.2018
chr4	191154276	6176367	0.0323	0.2479
chr5	180915260	5780463	0.032	0.1992
chr6	171115067	5466908	0.0319	0.2179
chr7	159138663	5353909	0.0336	0.3038

chr8	146364022	4875302	0.0333	0.2361
chr9	141213431	4112072	0.0291	0.2295
chr10	135534747	4739604	0.035	0.3414
chr11	135006516	4390018	0.0325	0.237
chr12	133851895	4398393	0.0329	0.2032
chr13	115169878	2979149	0.0259	0.1789
chr14	107349540	2901318	0.027	0.1854
chr15	102531392	2820770	0.0275	0.1853
chr16	90354753	3022086	0.0334	0.2353
chr17	81195210	2864778	0.0353	0.2198
chr18	78077248	2518044	0.0323	0.3385
chr19	59128983	2206967	0.0373	0.2758
chr20	63025520	2156846	0.0342	0.2239
chr21	48129895	1295468	0.0269	0.216
chr22	51304566	1263420	0.0246	0.1773
chrMT	16571	27299	1.6474	1.7633
chrX	155270560	5313944	0.0342	0.2201
chrY	59373566	336004	0.0057	0.1763

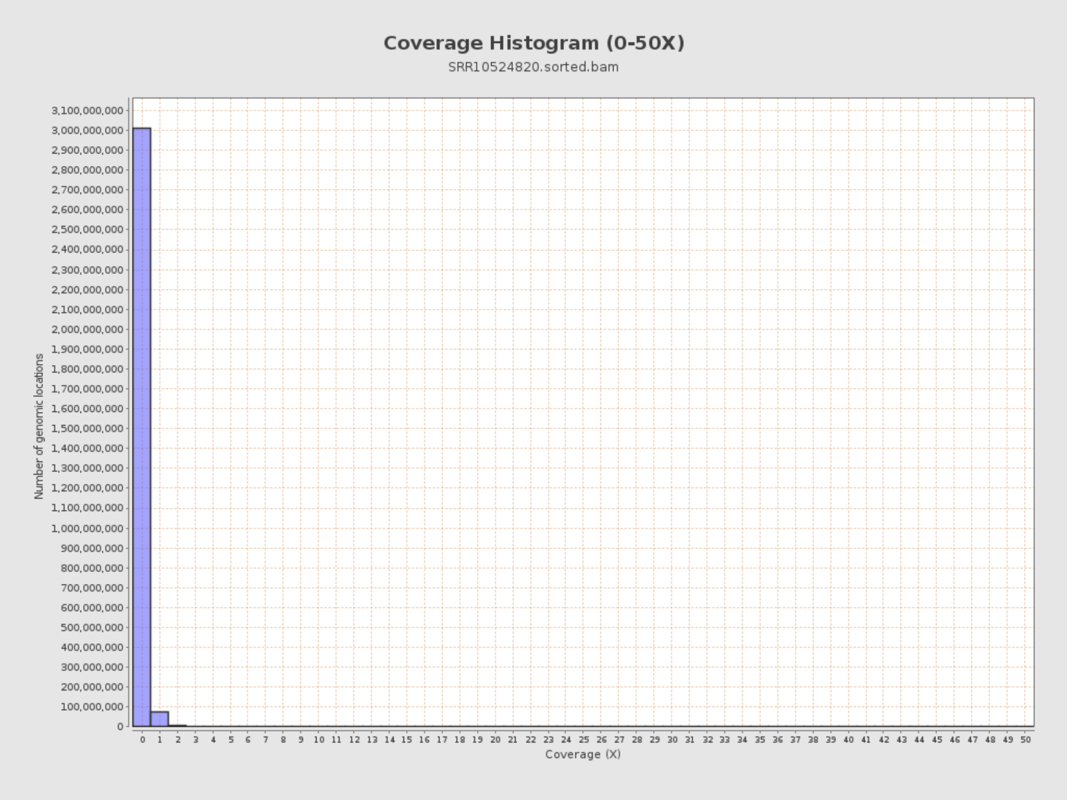
3. Results : Coverage across reference



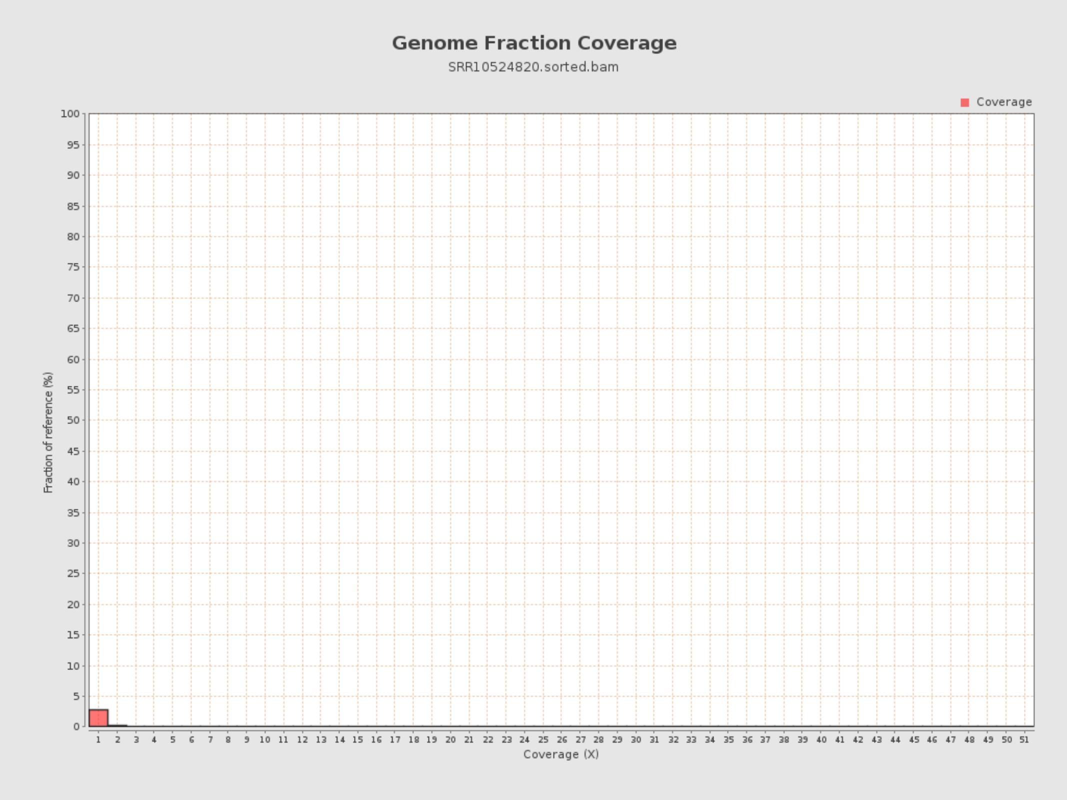
4. Results : Coverage Histogram



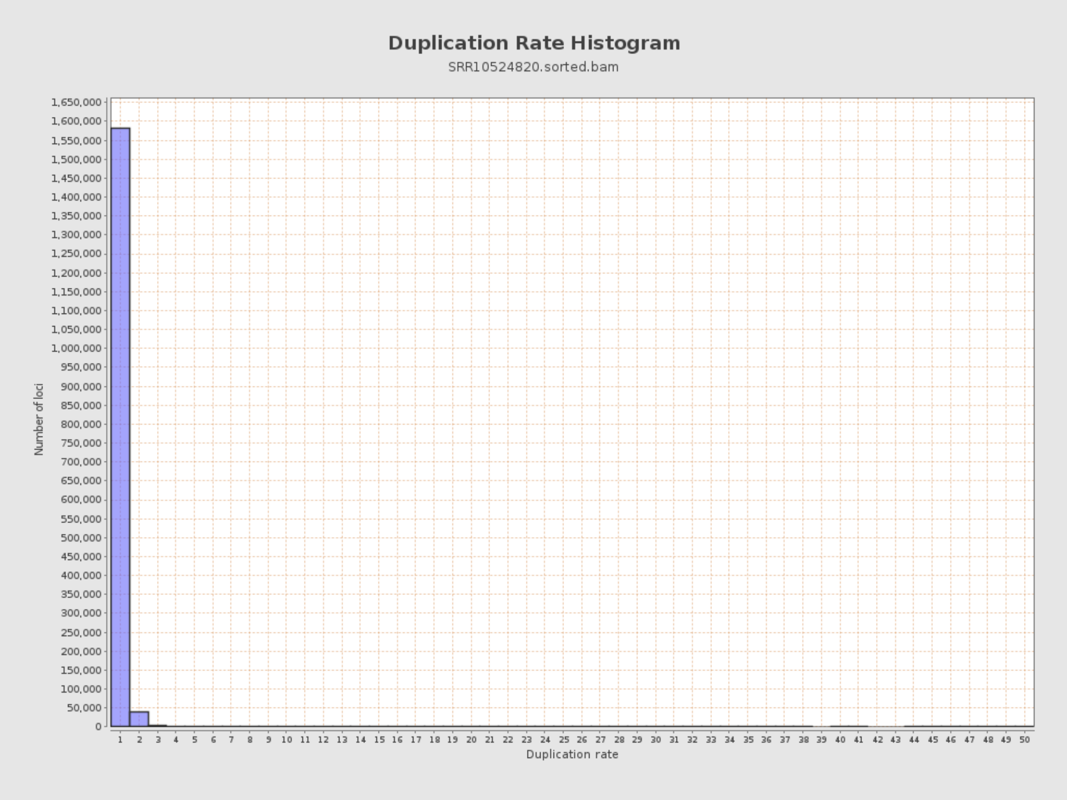
5. Results : Coverage Histogram (0-50X)



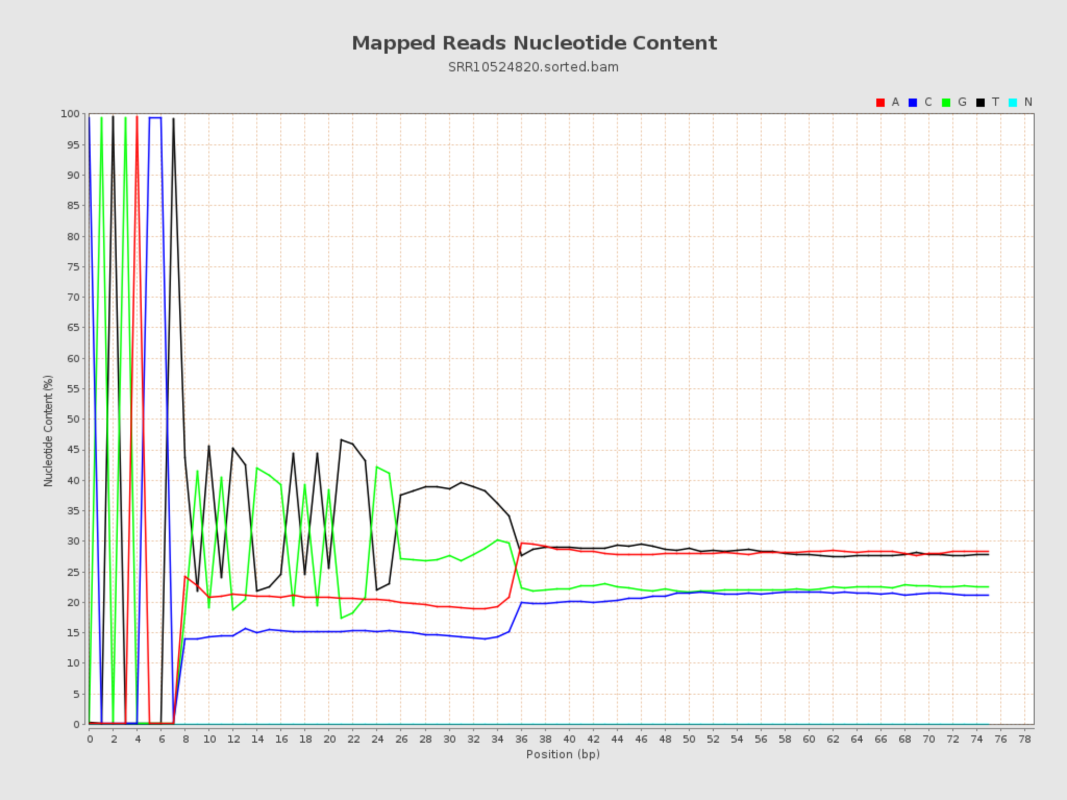
6. Results : Genome Fraction Coverage



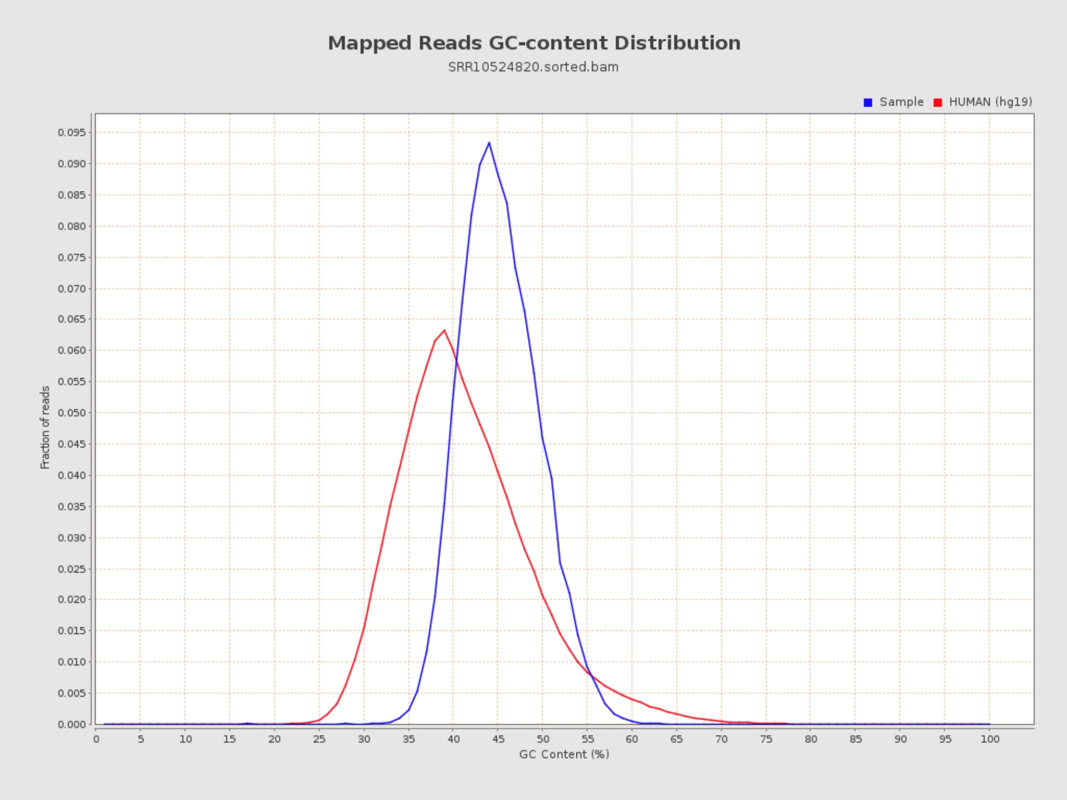
7. Results : Duplication Rate Histogram



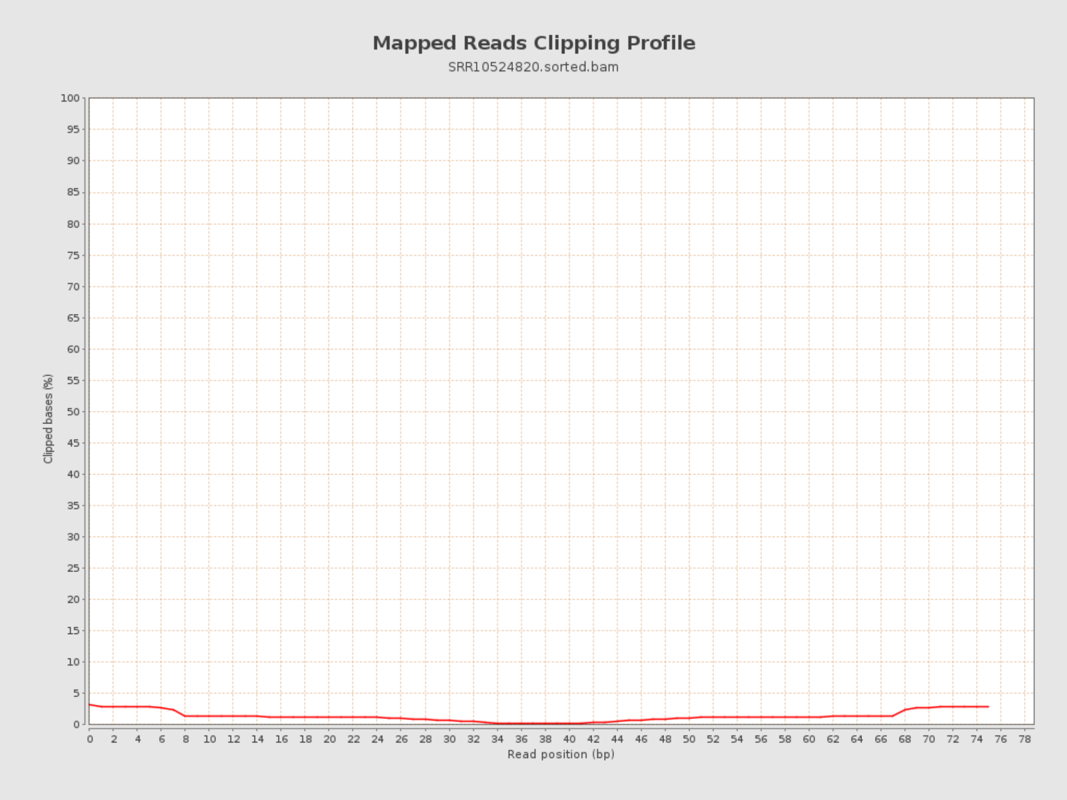
8. Results : Mapped Reads Nucleotide Content



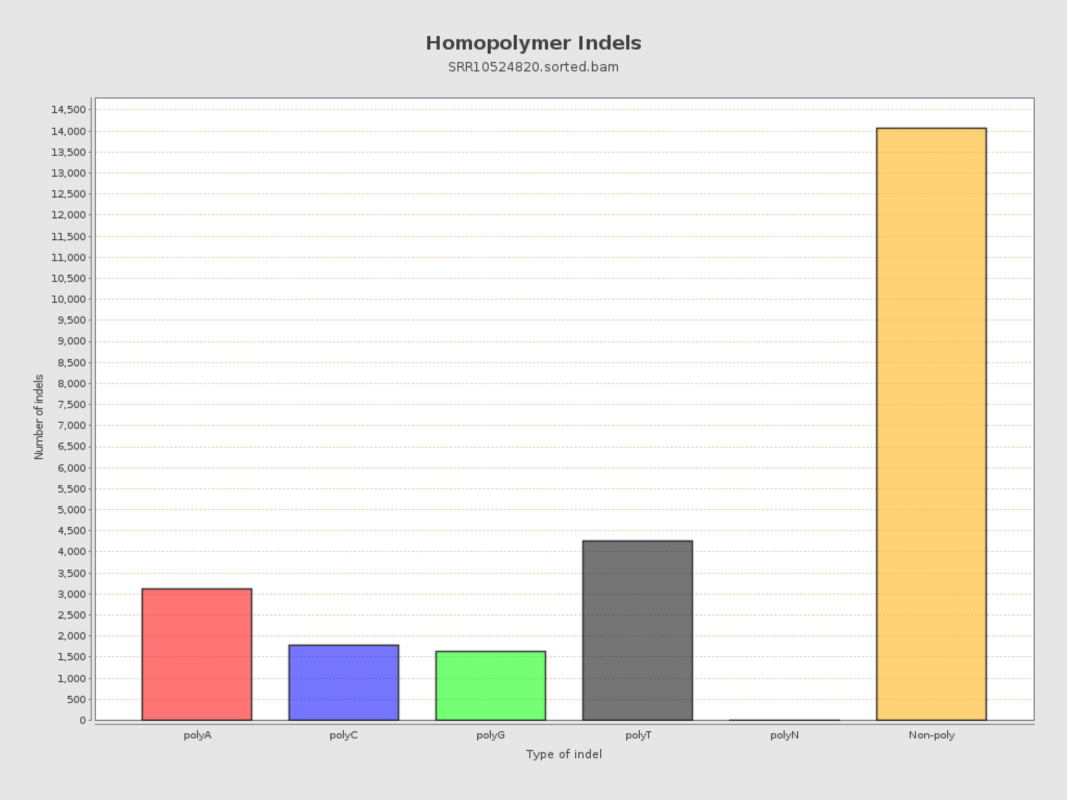
9. Results : Mapped Reads GC-content Distribution



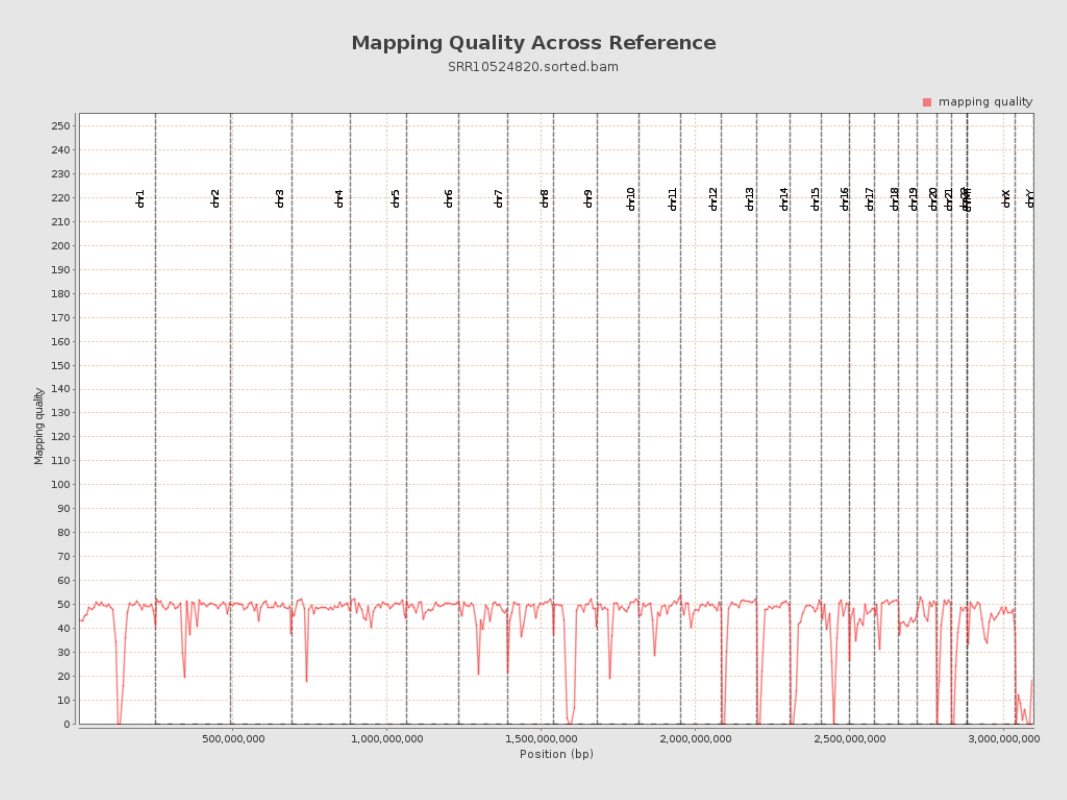
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram