Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 15:39:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524665.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_SRR10524665 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524665.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 15:39:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524665.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,839,890
Mapped reads	1,705,479 / 92.69%
Unmapped reads	134,411 / 7.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,574 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	69,954 / 3.8%
Duplication rate	3.02%
Clipped reads	1,711,629 / 93.03%

2.2. ACGT Content

Number/percentage of A's	24,673,076 / 24.43%
Number/percentage of C's	19,871,367 / 19.67%
Number/percentage of T's	31,273,085 / 30.96%
Number/percentage of G's	25,176,267 / 24.93%
Number/percentage of N's	12,849 / 0.01%
GC Percentage	44.6%

2.3. Coverage

Mean	0.0326

Standard Deviation	0.3032

2.4. Mapping Quality

Mean Mapping Quality	45.81

2.5. Mismatches and indels

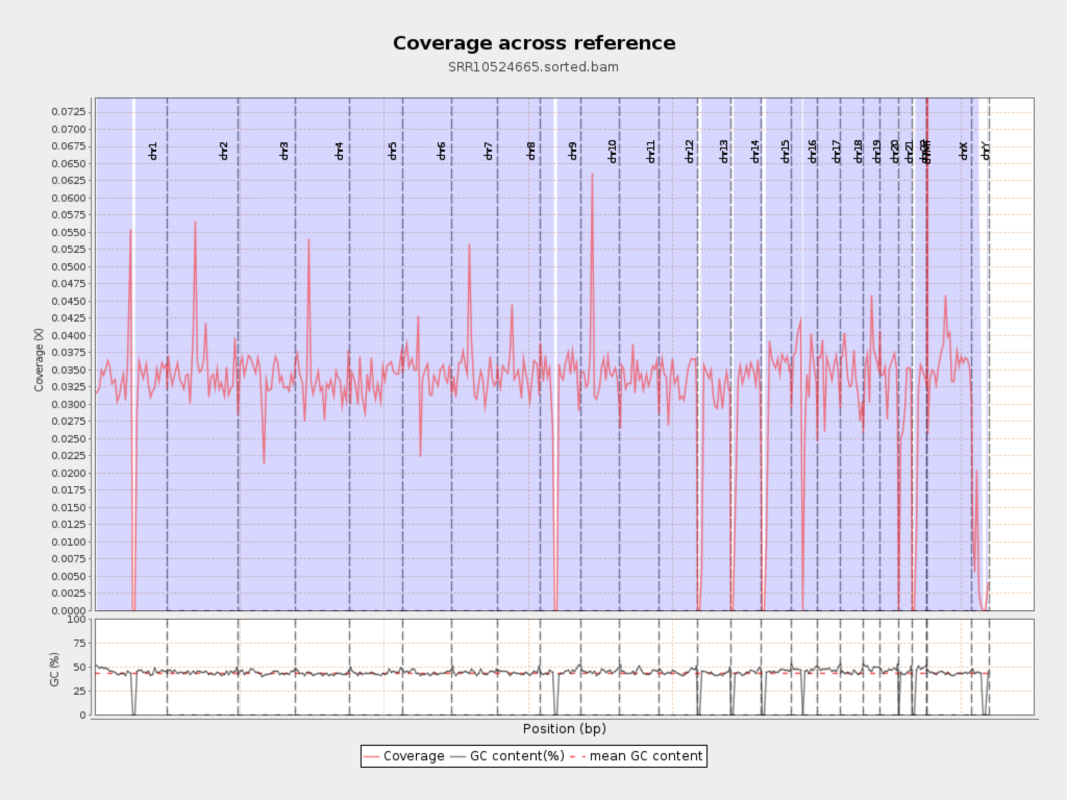
General error rate	0.51%
Mismatches	498,758
Insertions	6,039
Mapped reads with at least one insertion	0.35%
Deletions	18,633
Mapped reads with at least one deletion	1.08%
Homopolymer indels	44.59%

2.6. Chromosome stats

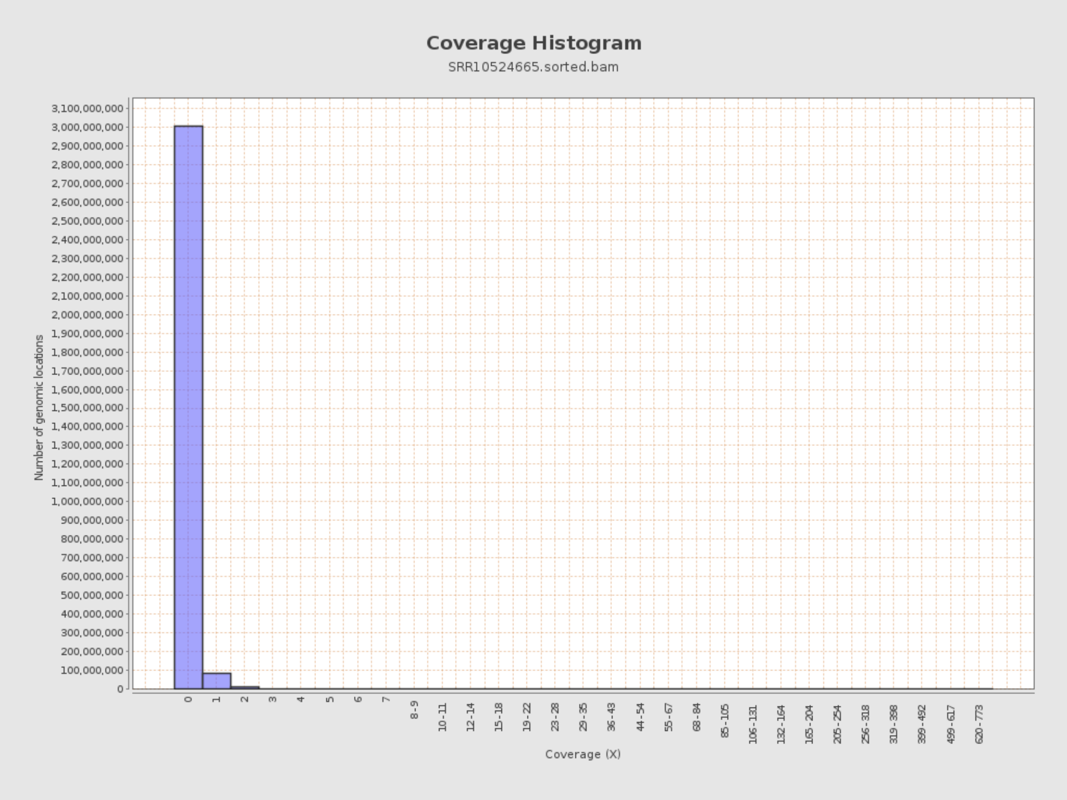
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8035605	0.0322	0.5394
chr2	243199373	8524509	0.0351	0.4039
chr3	198022430	6694329	0.0338	0.2015
chr4	191154276	6451154	0.0337	0.2276
chr5	180915260	6096358	0.0337	0.2017
chr6	171115067	5893813	0.0344	0.2287
chr7	159138663	5552668	0.0349	0.3528

chr8	146364022	5077776	0.0347	0.3399
chr9	141213431	4341060	0.0307	0.2531
chr10	135534747	4836468	0.0357	0.3102
chr11	135006516	4611473	0.0342	0.2651
chr12	133851895	4520989	0.0338	0.2043
chr13	115169878	3141065	0.0273	0.1827
chr14	107349540	3053990	0.0284	0.1929
chr15	102531392	2990625	0.0292	0.188
chr16	90354753	2924479	0.0324	0.2116
chr17	81195210	2839116	0.035	0.219
chr18	78077248	2658681	0.0341	0.4751
chr19	59128983	2165438	0.0366	0.4242
chr20	63025520	2146413	0.0341	0.2061
chr21	48129895	1324473	0.0275	0.2108
chr22	51304566	1205795	0.0235	0.1679
chrMT	16571	17379	1.0488	1.2176
chrX	155270560	5608031	0.0361	0.2289
chrY	59373566	324865	0.0055	0.1881

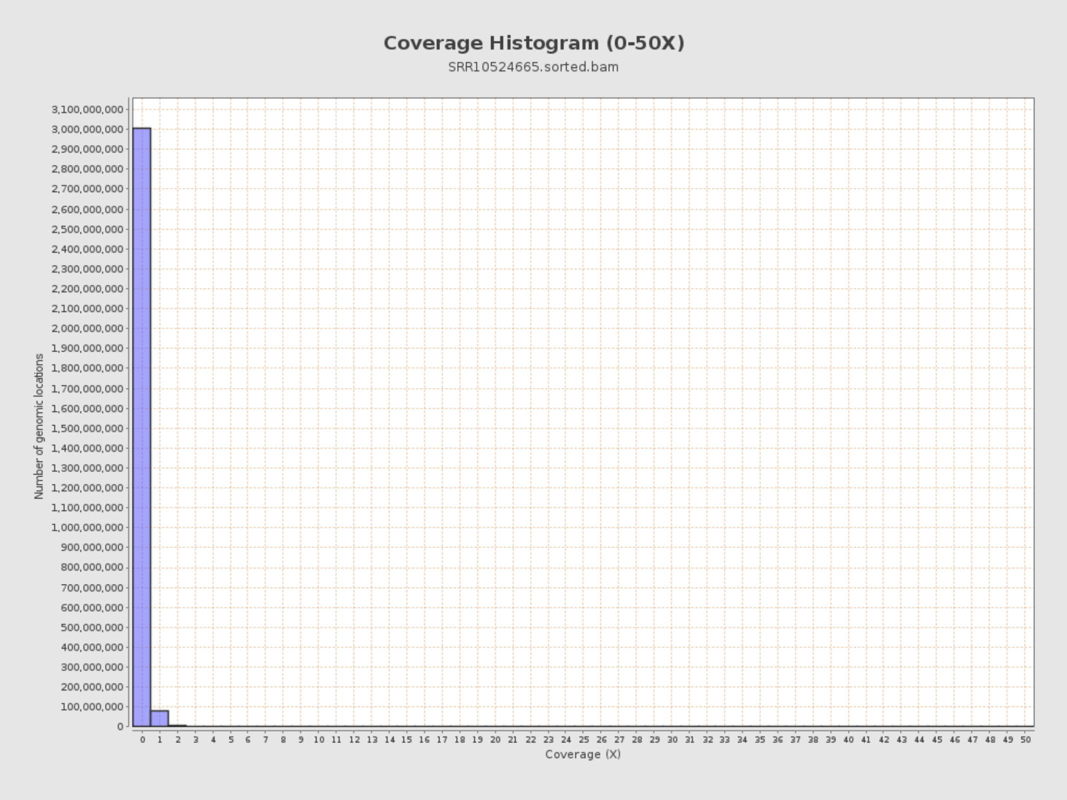
3. Results : Coverage across reference



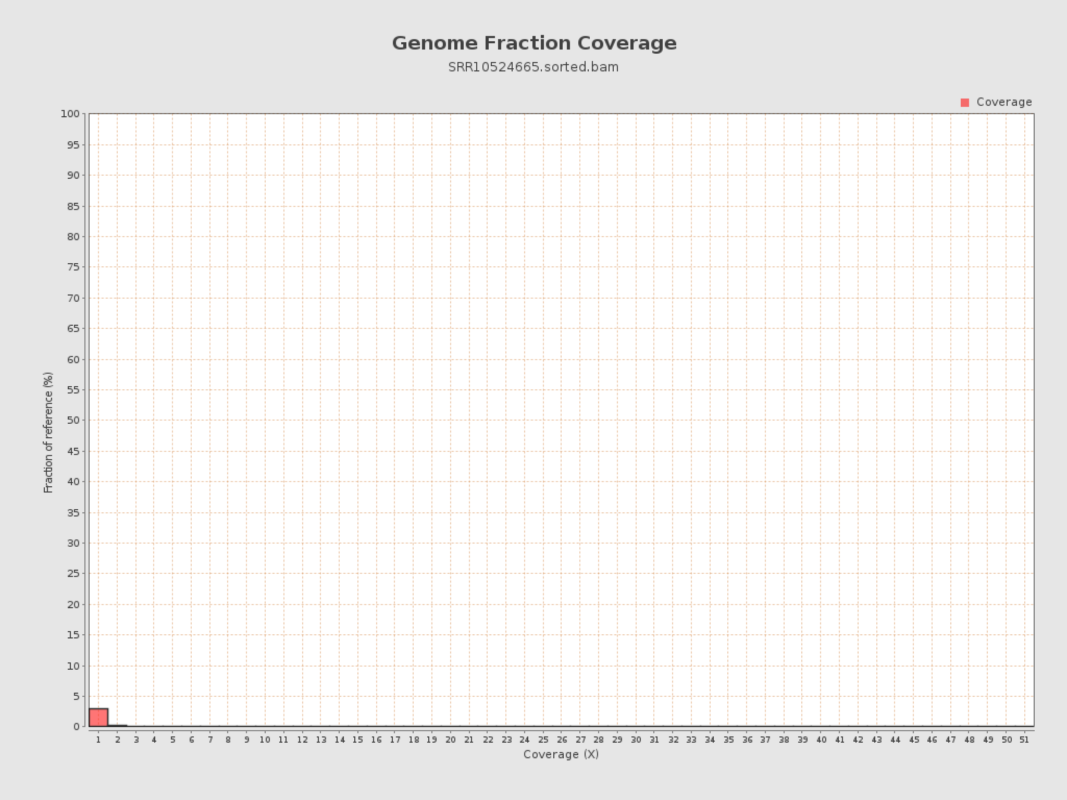
4. Results : Coverage Histogram



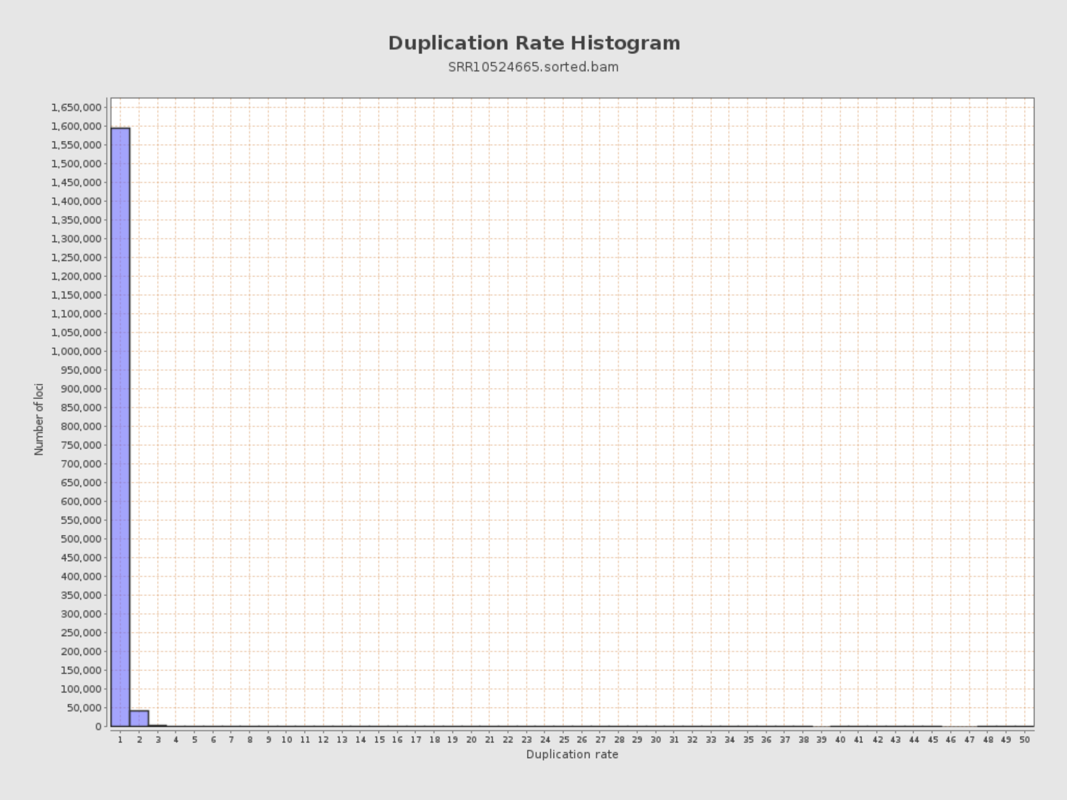
5. Results : Coverage Histogram (0-50X)



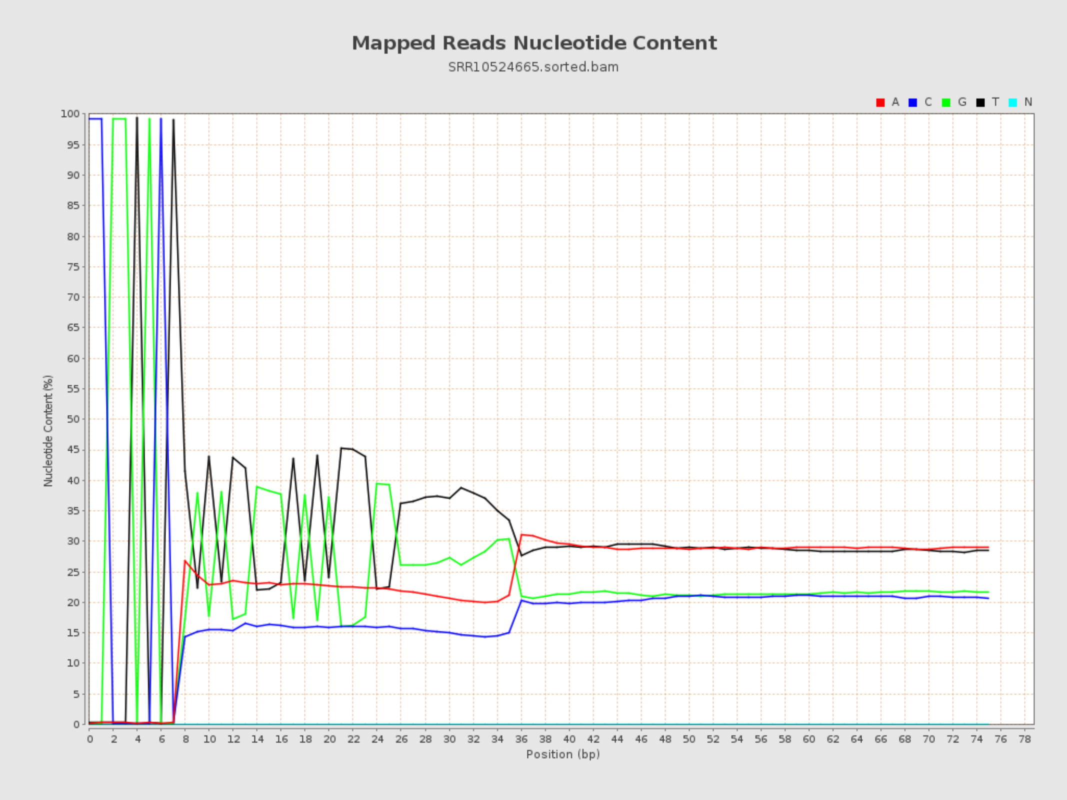
6. Results : Genome Fraction Coverage



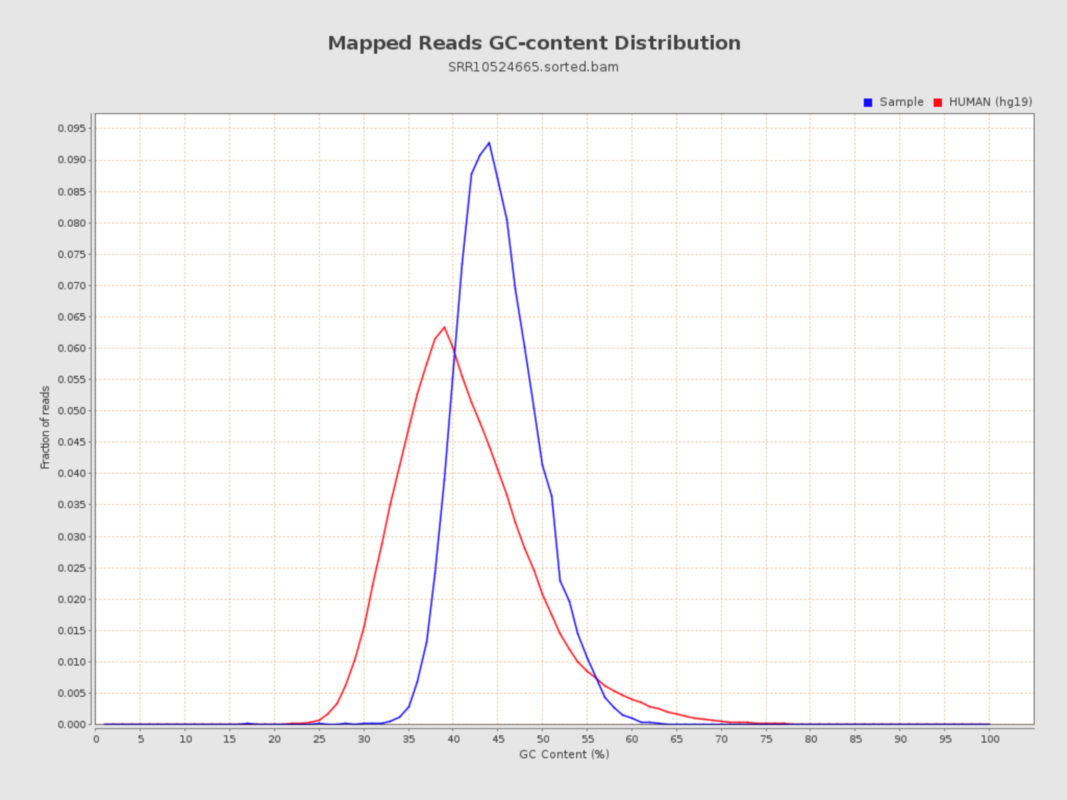
7. Results : Duplication Rate Histogram



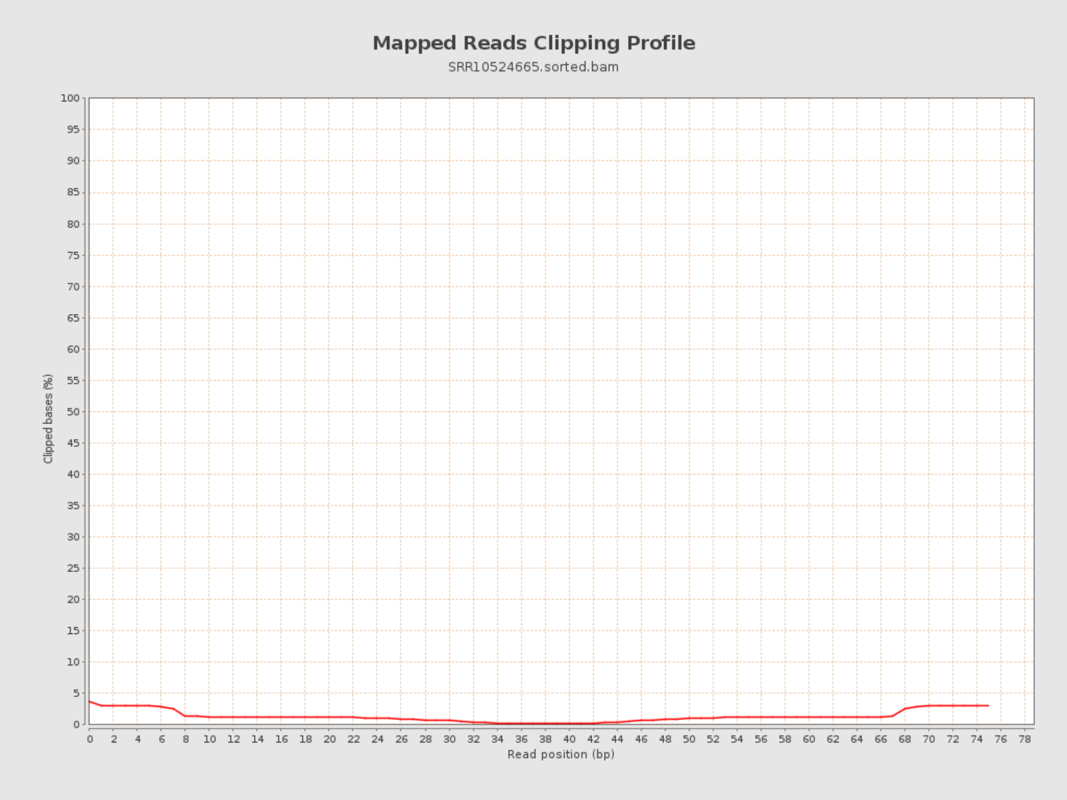
8. Results : Mapped Reads Nucleotide Content



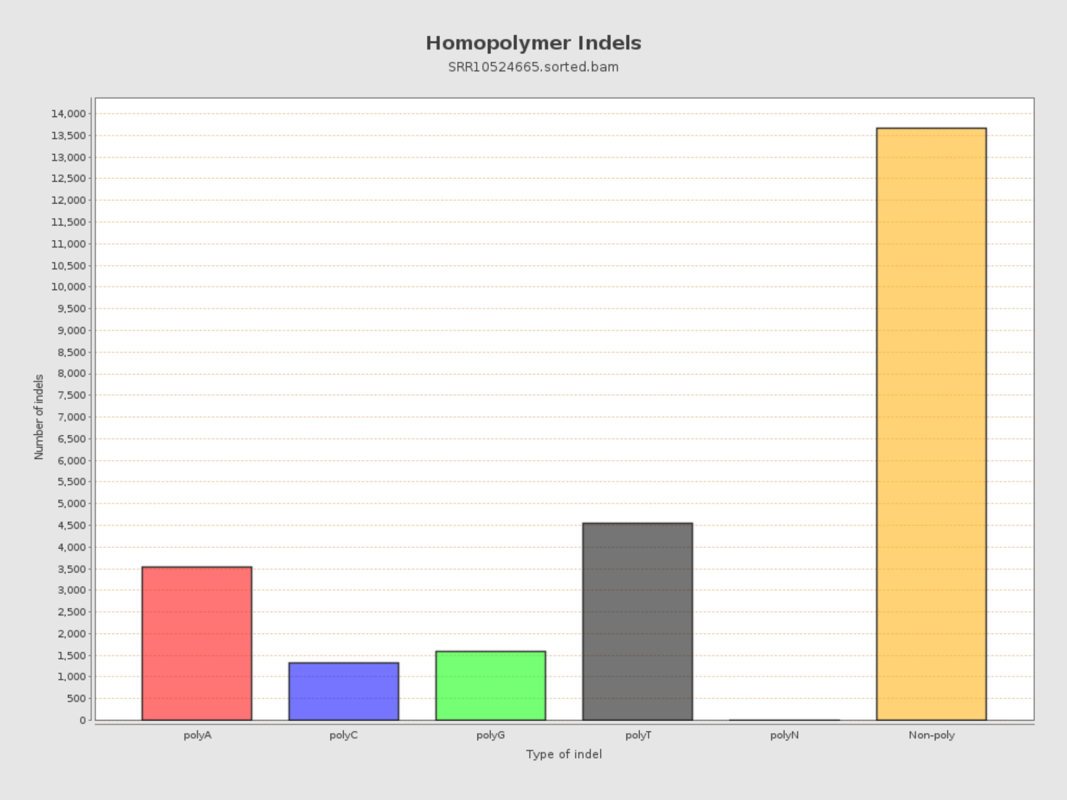
9. Results : Mapped Reads GC-content Distribution



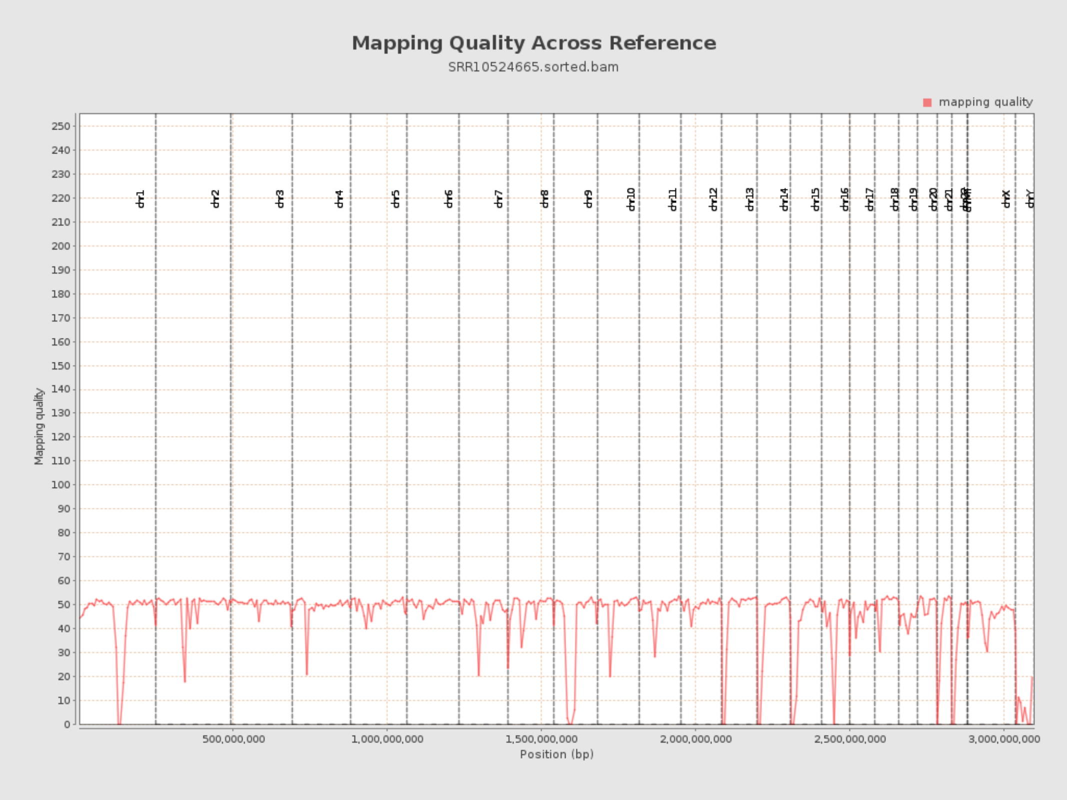
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram