Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 22:57:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524846.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_SRR10524846 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524846.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 22:57:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524846.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,959,264
Mapped reads	2,694,202 / 91.04%
Unmapped reads	265,062 / 8.96%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,081 / 0.44%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	119,458 / 4.04%
Duplication rate	3.03%
Clipped reads	2,702,603 / 91.33%

2.2. ACGT Content

Number/percentage of A's	37,361,790 / 24.18%
Number/percentage of C's	27,794,645 / 17.99%
Number/percentage of T's	50,743,712 / 32.84%
Number/percentage of G's	38,593,436 / 24.98%
Number/percentage of N's	19,480 / 0.01%
GC Percentage	42.97%

2.3. Coverage

Mean	0.0499

Standard Deviation	0.4639

2.4. Mapping Quality

Mean Mapping Quality	44.29

2.5. Mismatches and indels

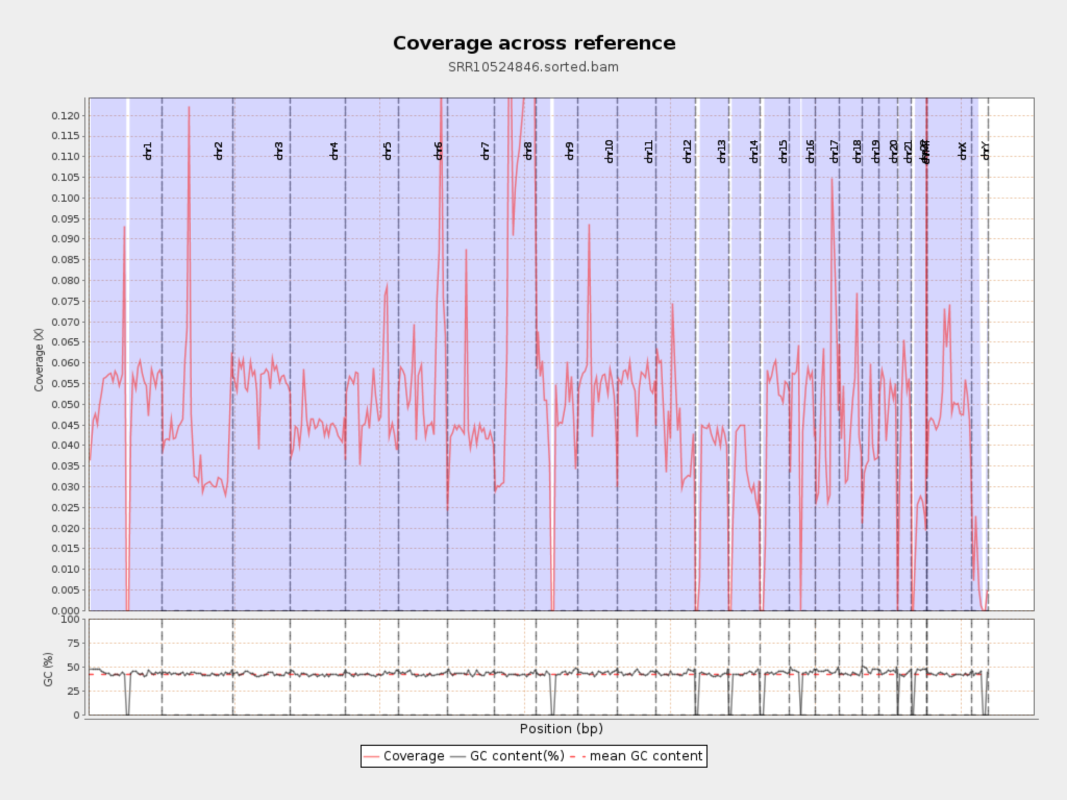
General error rate	0.5%
Mismatches	760,114
Insertions	9,986
Mapped reads with at least one insertion	0.37%
Deletions	28,199
Mapped reads with at least one deletion	1.04%
Homopolymer indels	45%

2.6. Chromosome stats

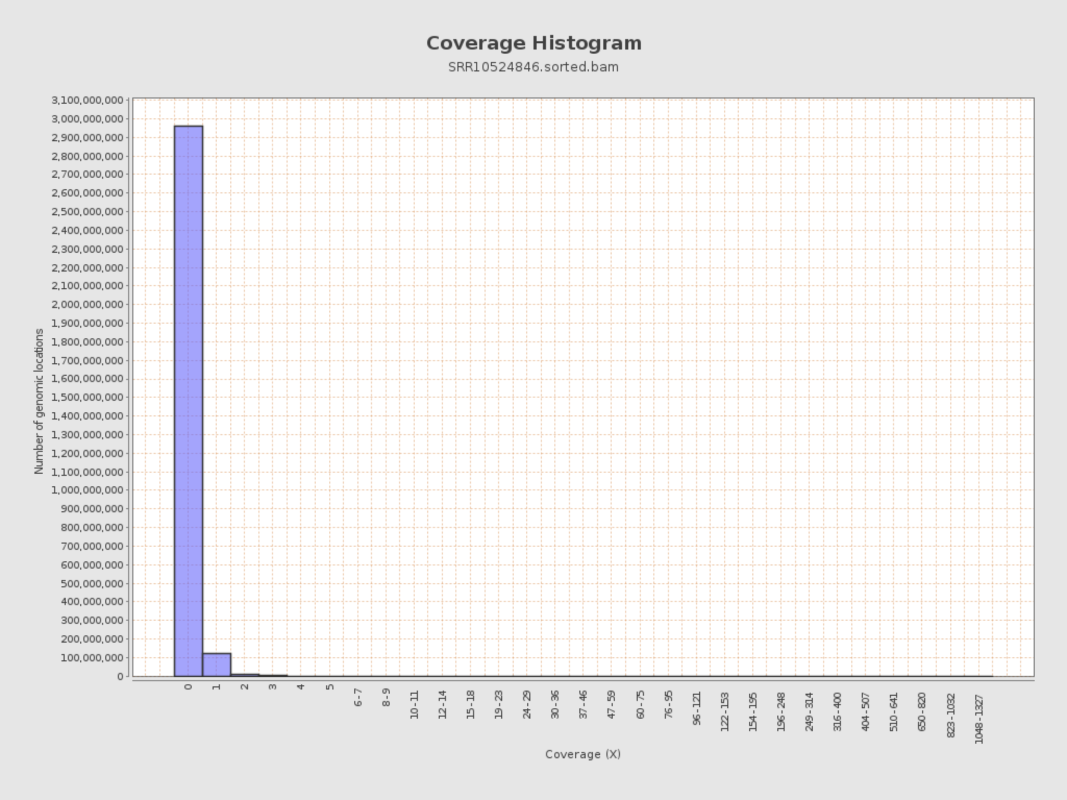
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12890334	0.0517	0.95
chr2	243199373	10094913	0.0415	0.4943
chr3	198022430	11142015	0.0563	0.2667
chr4	191154276	8475761	0.0443	0.2673
chr5	180915260	9345325	0.0517	0.2594
chr6	171115067	10132993	0.0592	0.3188
chr7	159138663	7123113	0.0448	0.6603

chr8	146364022	16496166	0.1127	0.6092
chr9	141213431	6386044	0.0452	0.3903
chr10	135534747	7662895	0.0565	0.4306
chr11	135006516	7409878	0.0549	0.4045
chr12	133851895	6109760	0.0456	0.254
chr13	115169878	4089912	0.0355	0.2197
chr14	107349540	3274646	0.0305	0.2236
chr15	102531392	4579153	0.0447	0.2426
chr16	90354753	4441441	0.0492	0.2858
chr17	81195210	4166530	0.0513	0.2979
chr18	78077248	3745841	0.048	0.7138
chr19	59128983	2306616	0.039	0.6493
chr20	63025520	3219292	0.0511	0.2587
chr21	48129895	2204090	0.0458	0.2659
chr22	51304566	940650	0.0183	0.1501
chrMT	16571	2489	0.1502	0.4413
chrX	155270560	7915974	0.051	0.3214
chrY	59373566	401546	0.0068	0.16

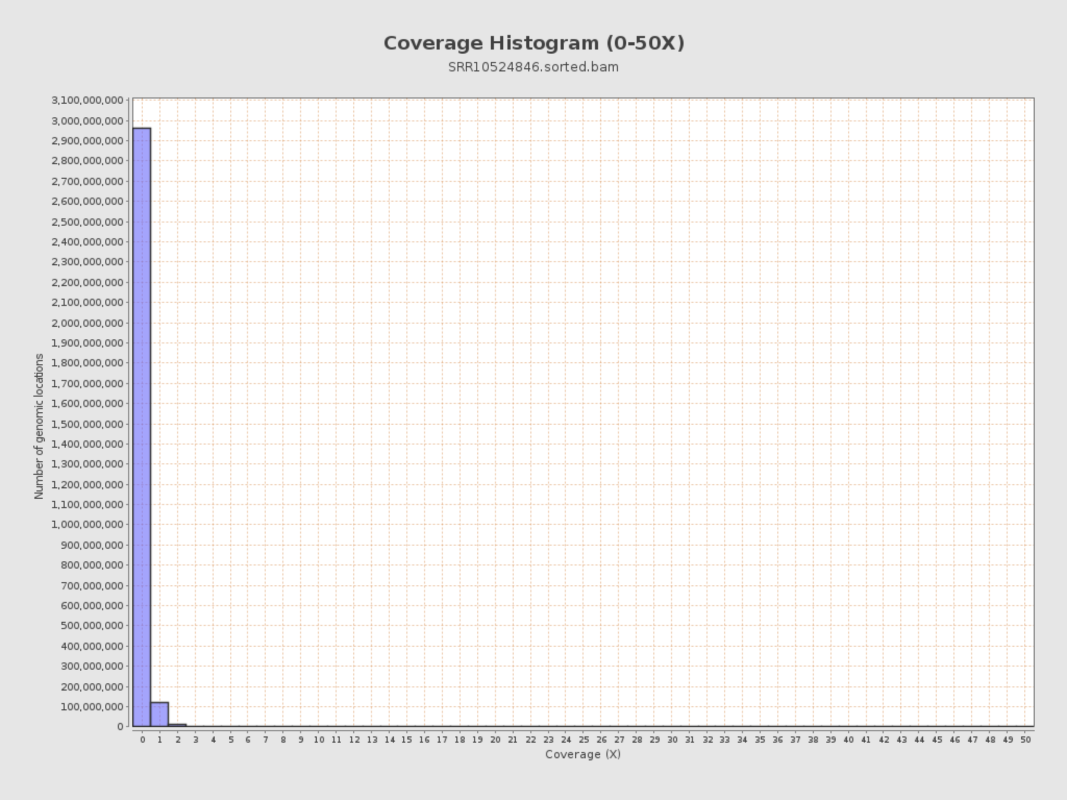
3. Results : Coverage across reference



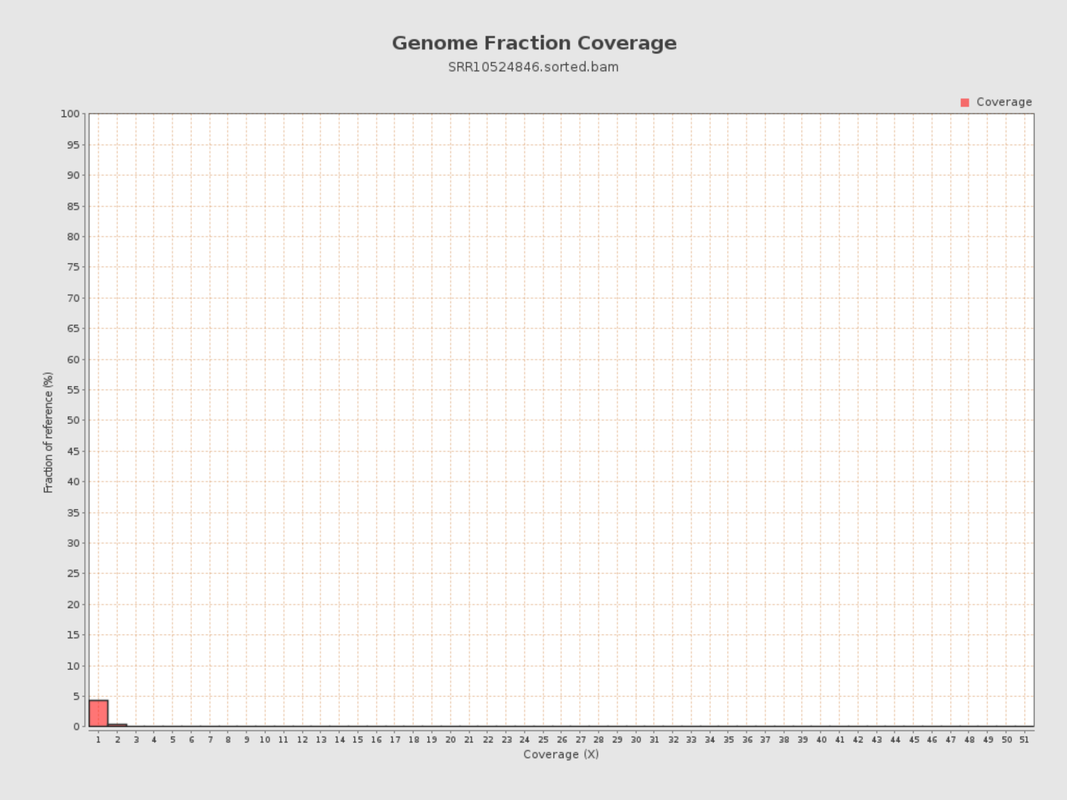
4. Results : Coverage Histogram



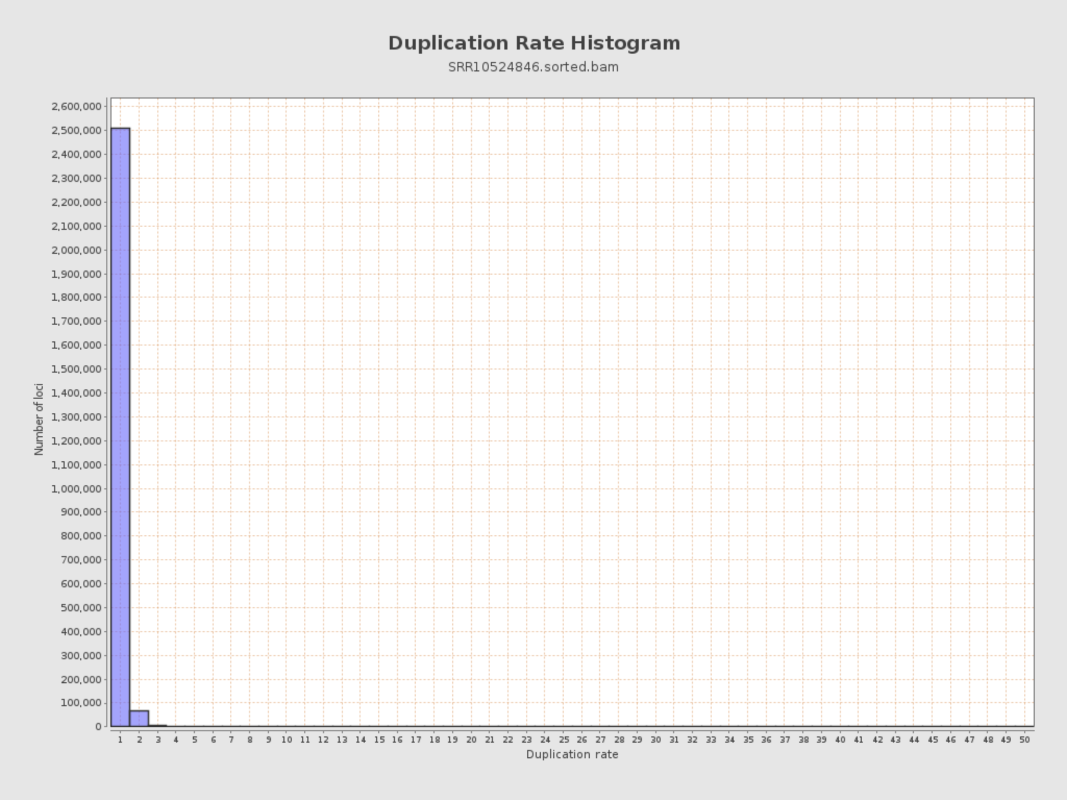
5. Results : Coverage Histogram (0-50X)



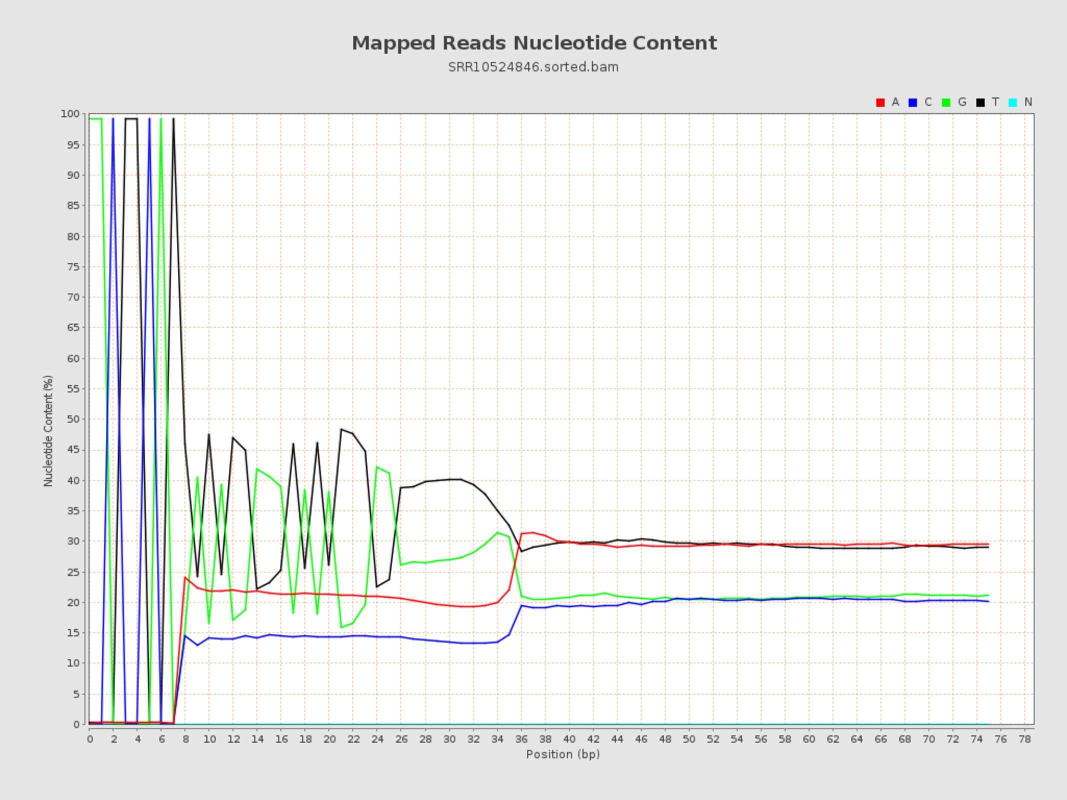
6. Results : Genome Fraction Coverage



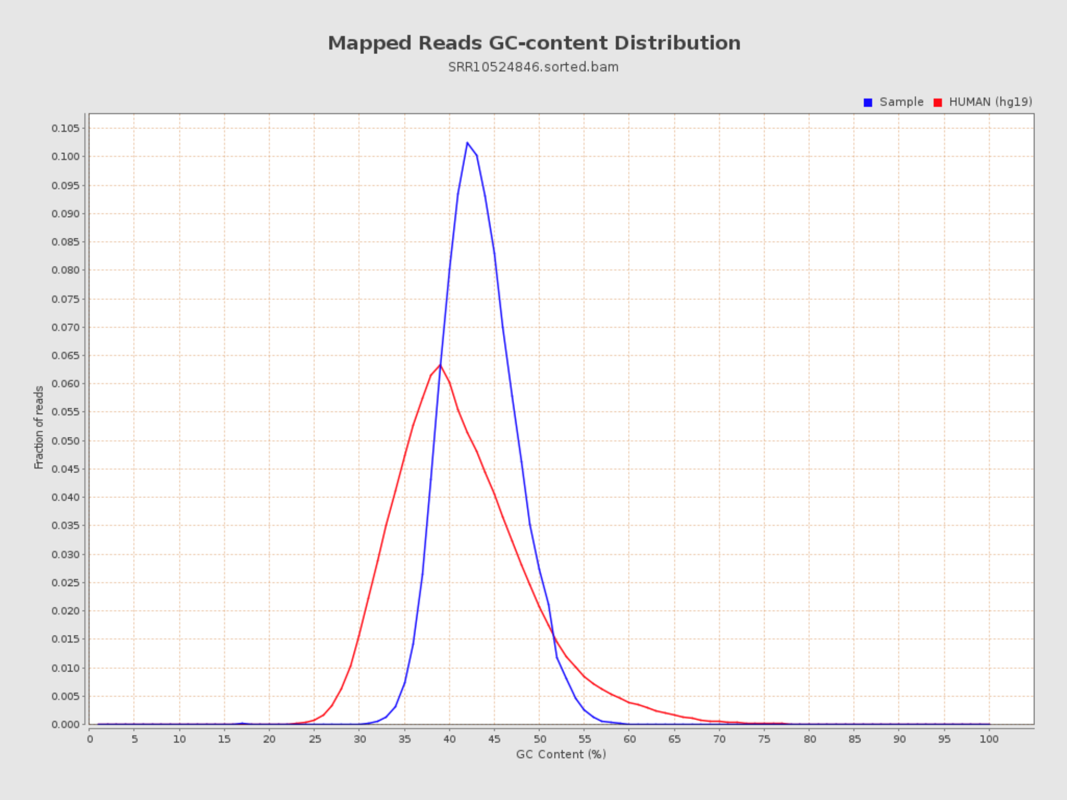
7. Results : Duplication Rate Histogram



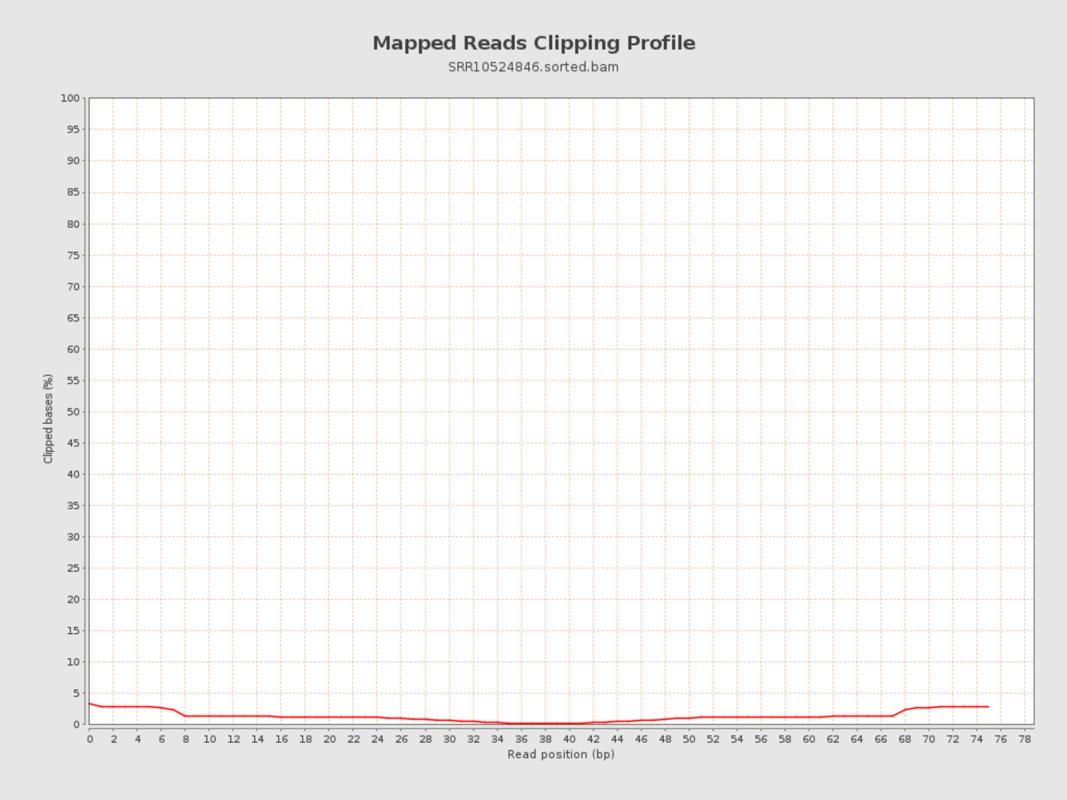
8. Results : Mapped Reads Nucleotide Content



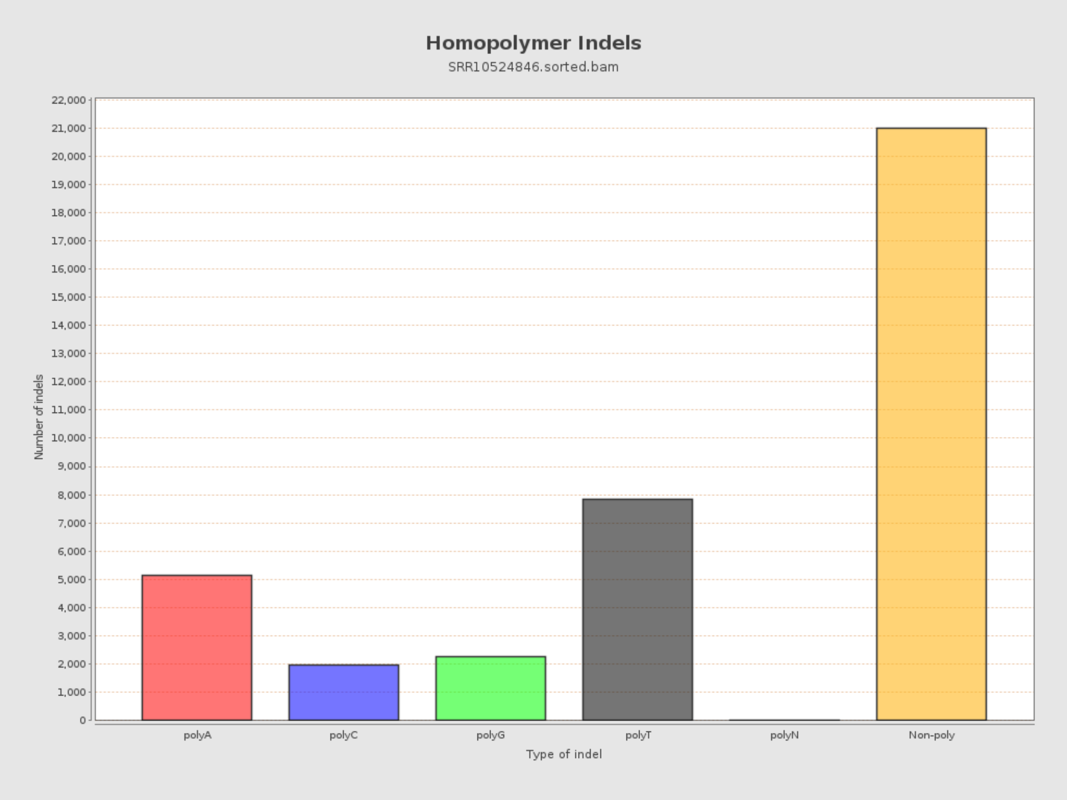
9. Results : Mapped Reads GC-content Distribution



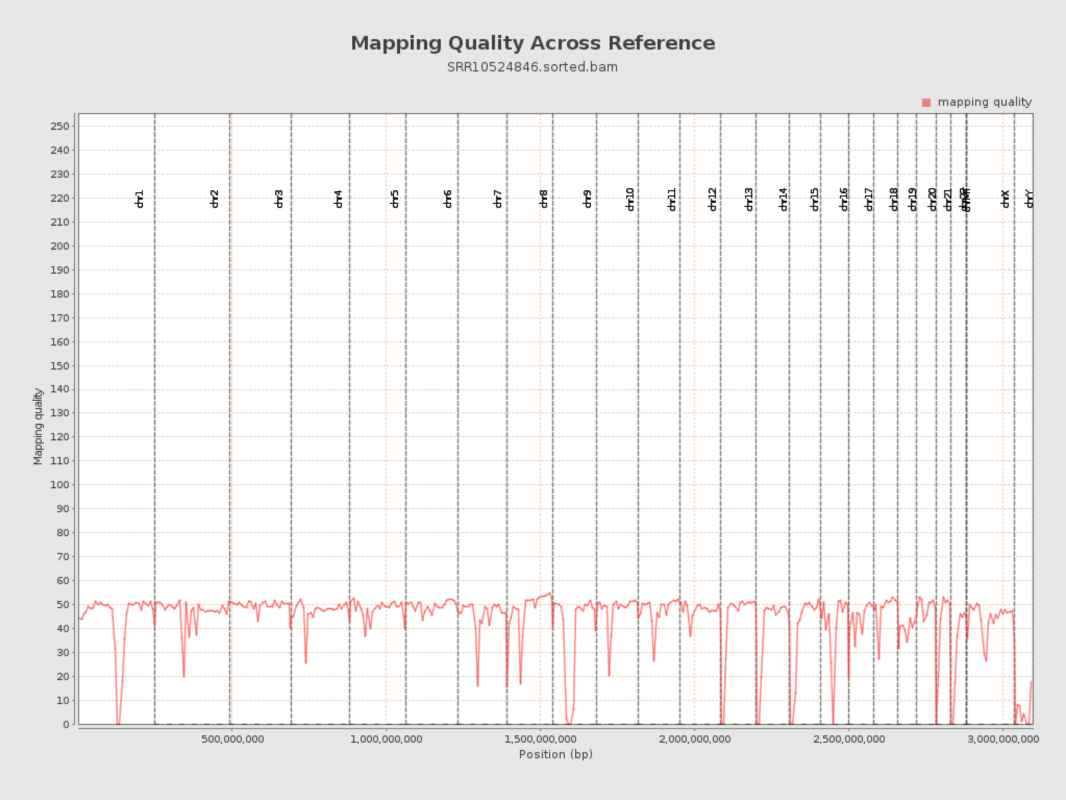
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram