Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 10:47:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084352.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_SRR3084352 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084352.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 10:47:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084352.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,140,716
Mapped reads	1,634,324 / 52.04%
Unmapped reads	1,506,392 / 47.96%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,290 / 0.26%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	54,190 / 1.73%
Duplication rate	2.75%
Clipped reads	873,846 / 27.82%

2.2. ACGT Content

Number/percentage of A's	29,268,523 / 28.09%
Number/percentage of C's	19,534,745 / 18.75%
Number/percentage of T's	31,826,224 / 30.55%
Number/percentage of G's	23,548,415 / 22.6%
Number/percentage of N's	1,165 / 0%
GC Percentage	41.35%

2.3. Coverage

Mean	0.0337

Standard Deviation	0.2577

2.4. Mapping Quality

Mean Mapping Quality	45.59

2.5. Mismatches and indels

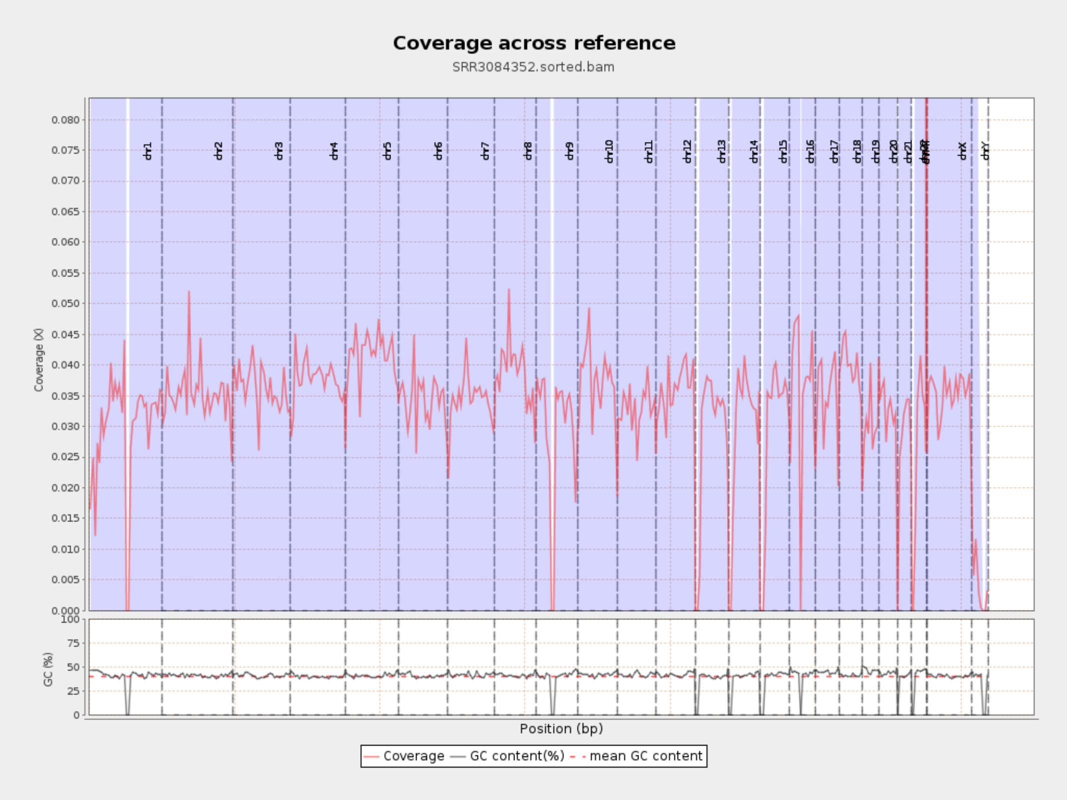
General error rate	0.84%
Mismatches	863,531
Insertions	7,482
Mapped reads with at least one insertion	0.45%
Deletions	21,310
Mapped reads with at least one deletion	1.29%
Homopolymer indels	46.36%

2.6. Chromosome stats

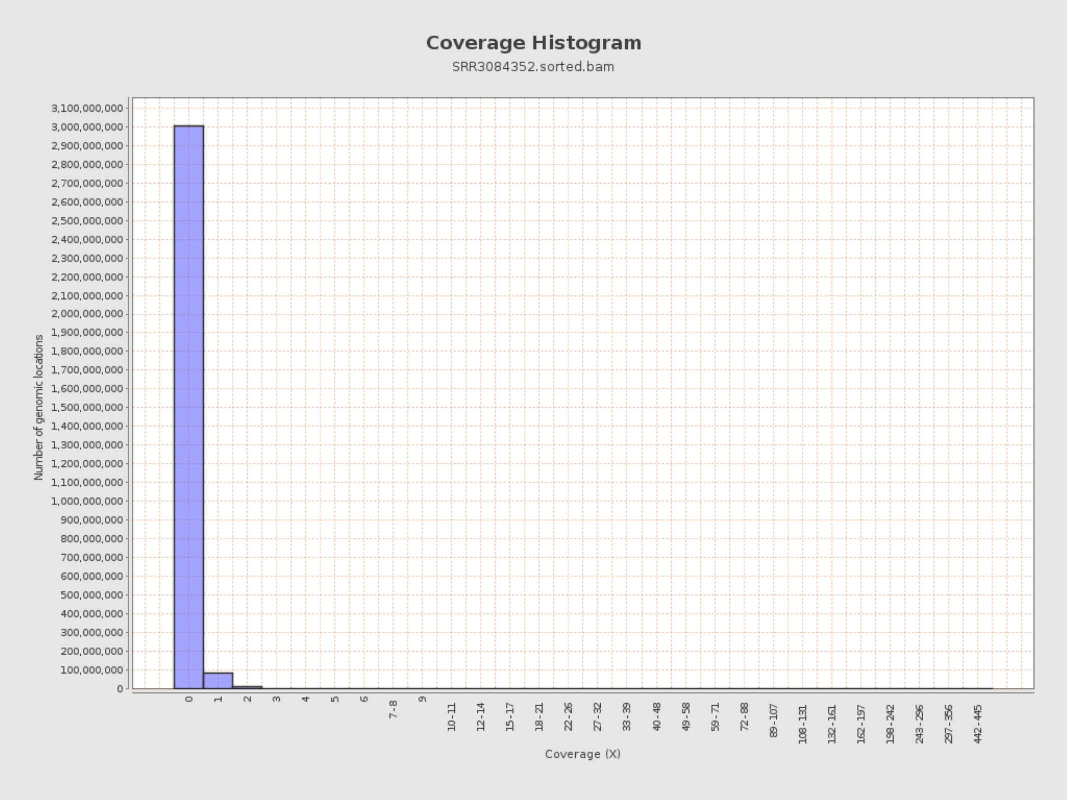
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7375289	0.0296	0.3405
chr2	243199373	8621896	0.0355	0.3321
chr3	198022430	7200105	0.0364	0.21
chr4	191154276	7199529	0.0377	0.2179
chr5	180915260	7557592	0.0418	0.224
chr6	171115067	5869635	0.0343	0.2267
chr7	159138663	5519006	0.0347	0.2719

chr8	146364022	5664339	0.0387	0.272
chr9	141213431	4082945	0.0289	0.2484
chr10	135534747	5126891	0.0378	0.2729
chr11	135006516	4421857	0.0328	0.2357
chr12	133851895	4830476	0.0361	0.21
chr13	115169878	3259065	0.0283	0.1852
chr14	107349540	3128423	0.0291	0.198
chr15	102531392	2989626	0.0292	0.1925
chr16	90354753	3278112	0.0363	0.2274
chr17	81195210	2791931	0.0344	0.2241
chr18	78077248	3131243	0.0401	0.4873
chr19	59128983	1794887	0.0304	0.31
chr20	63025520	2040200	0.0324	0.2033
chr21	48129895	1319264	0.0274	0.1884
chr22	51304566	1269967	0.0248	0.1727
chrMT	16571	40471	2.4423	2.0334
chrX	155270560	5462556	0.0352	0.2259
chrY	59373566	237772	0.004	0.0882

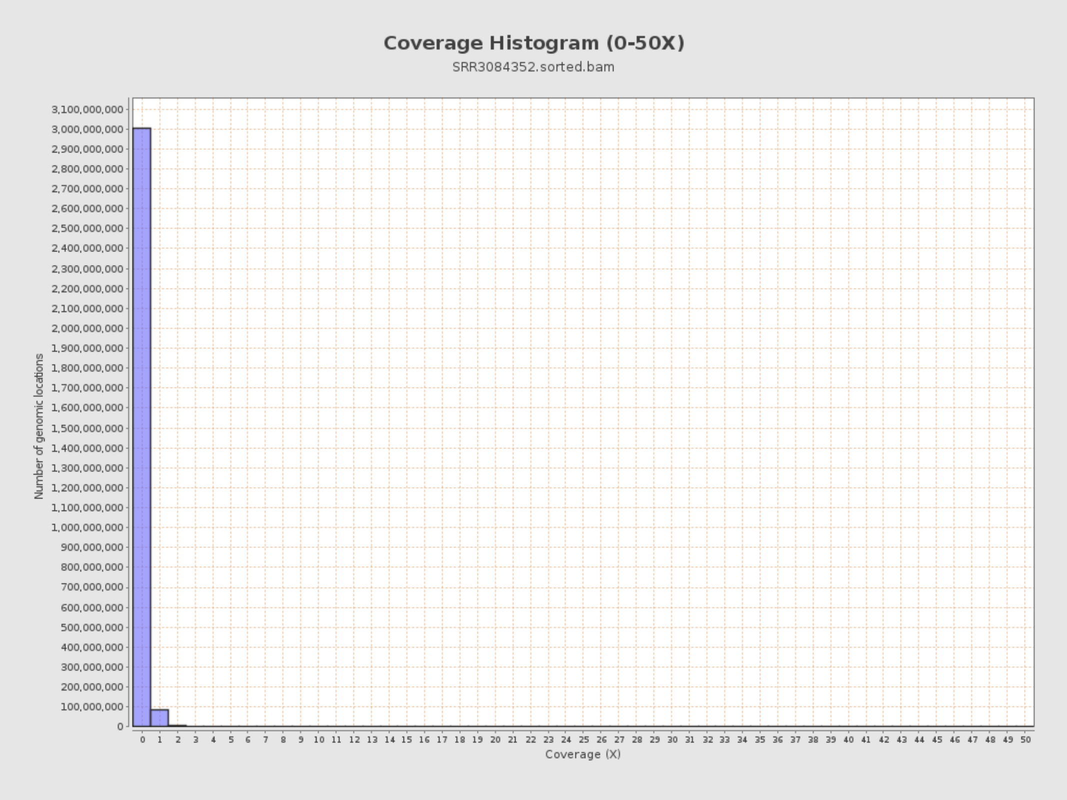
3. Results : Coverage across reference



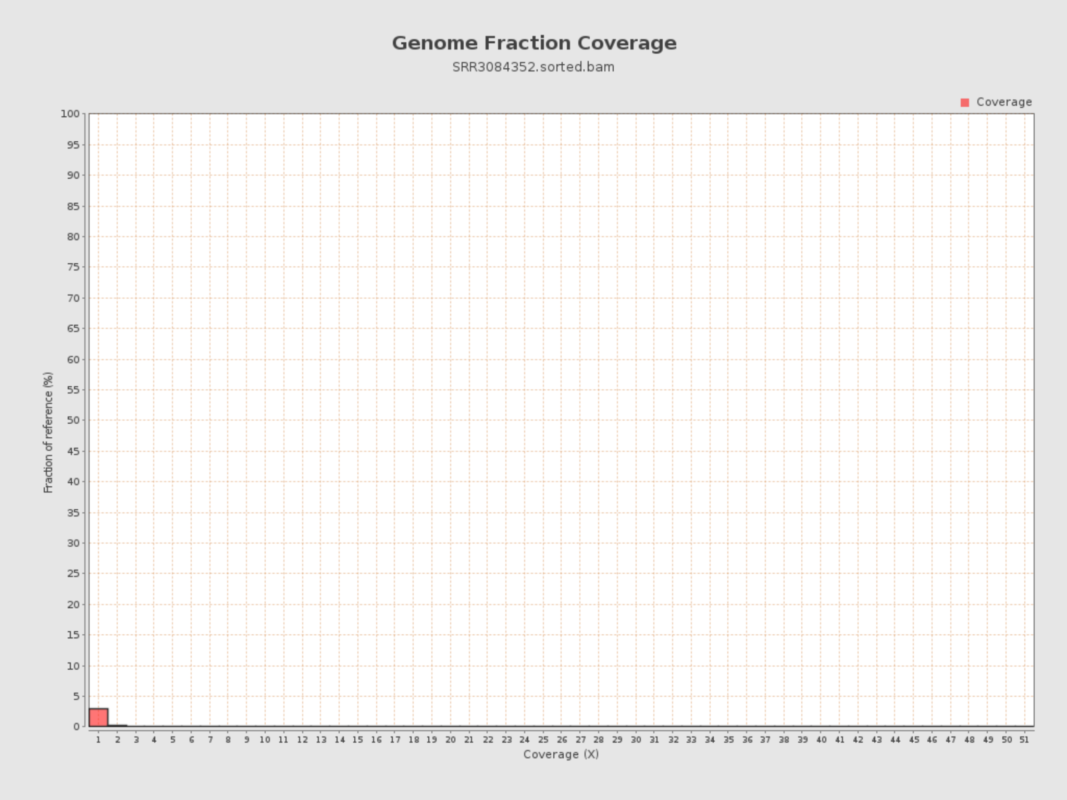
4. Results : Coverage Histogram



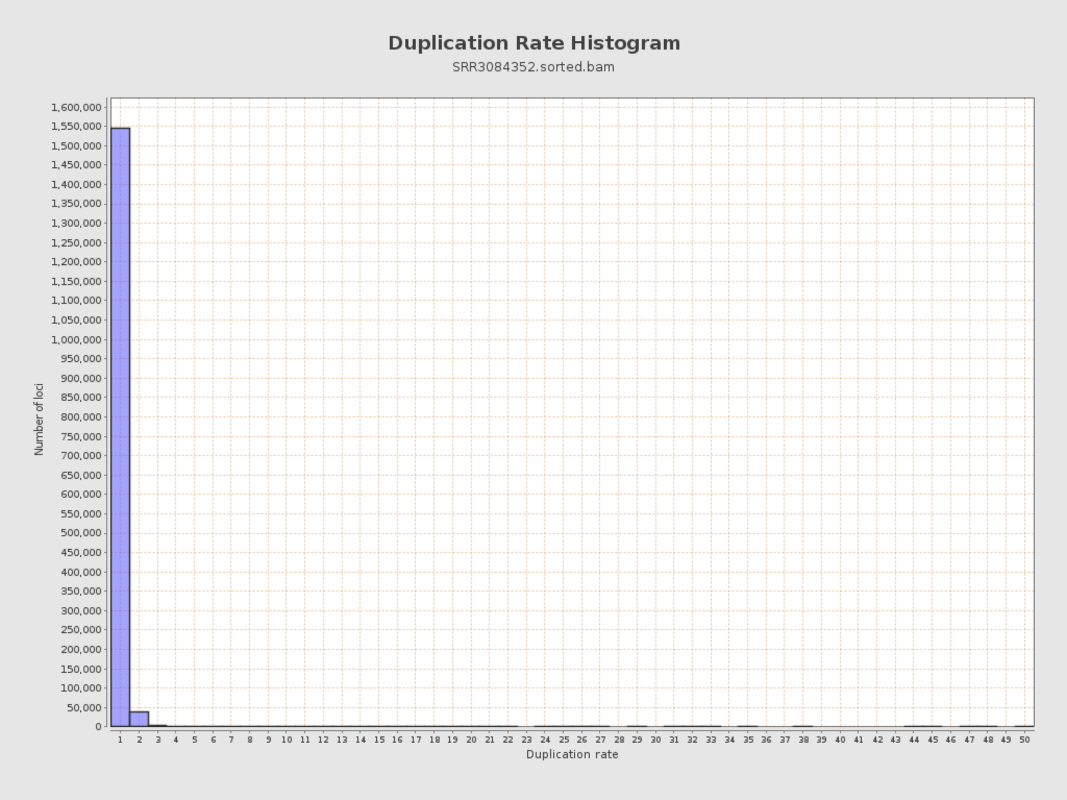
5. Results : Coverage Histogram (0-50X)



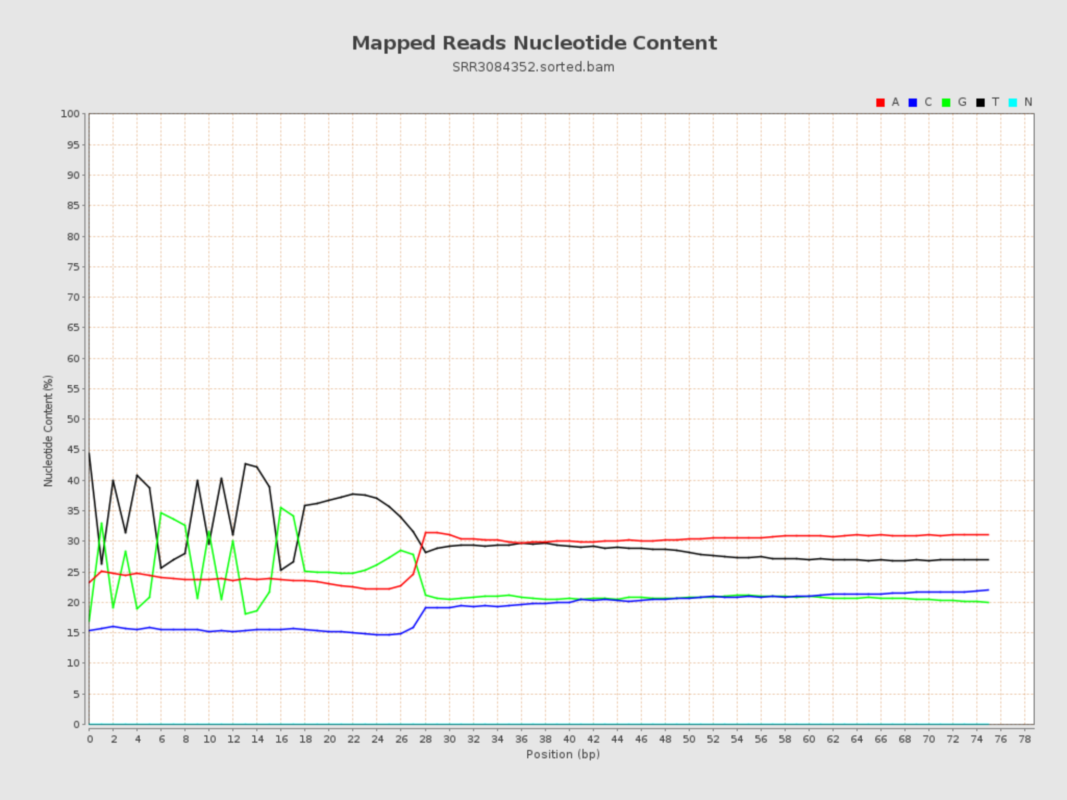
6. Results : Genome Fraction Coverage



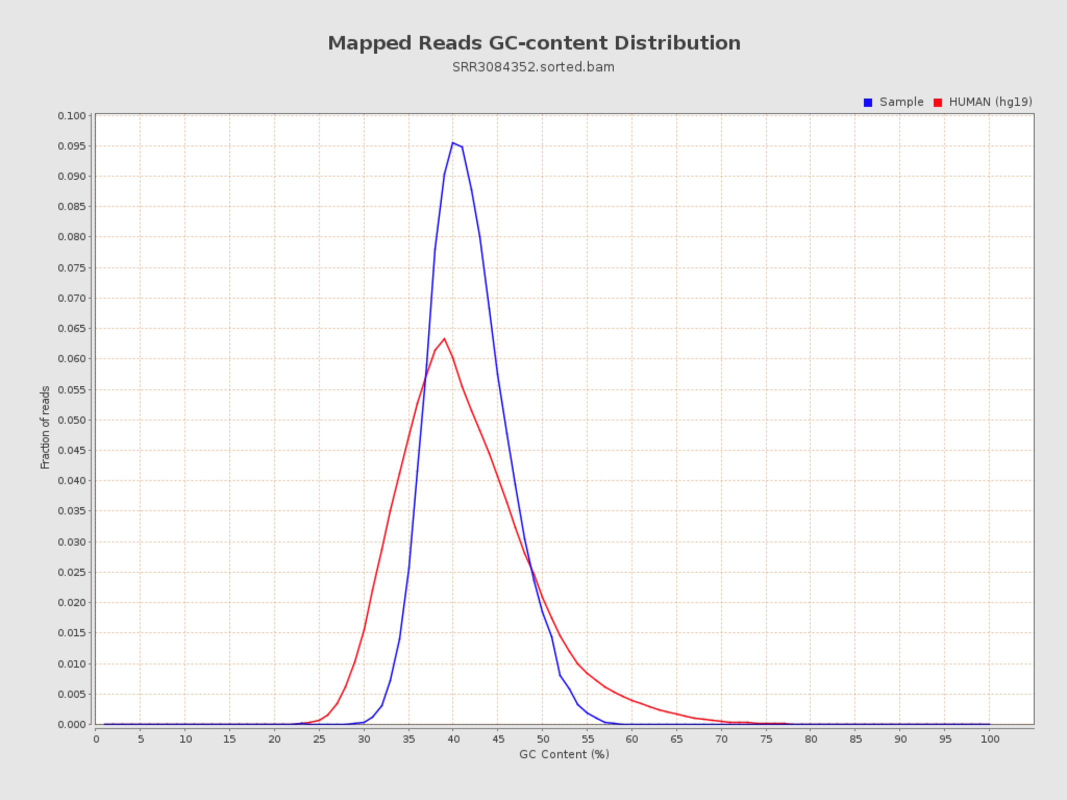
7. Results : Duplication Rate Histogram



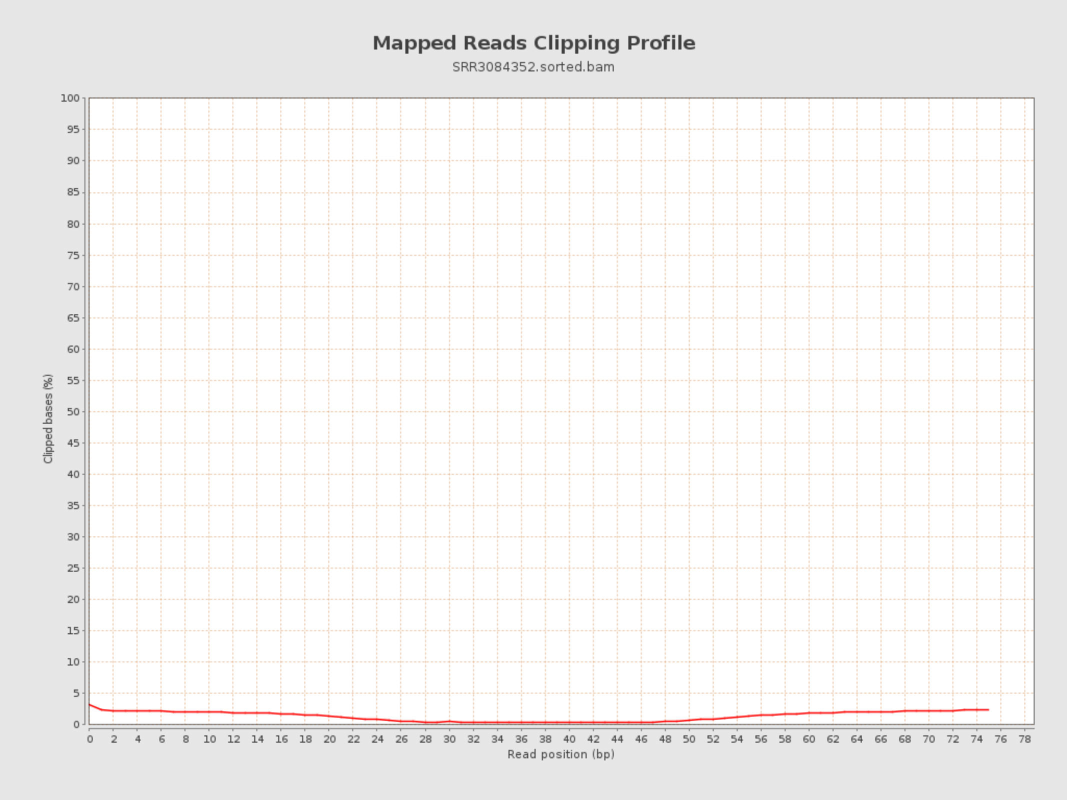
8. Results : Mapped Reads Nucleotide Content



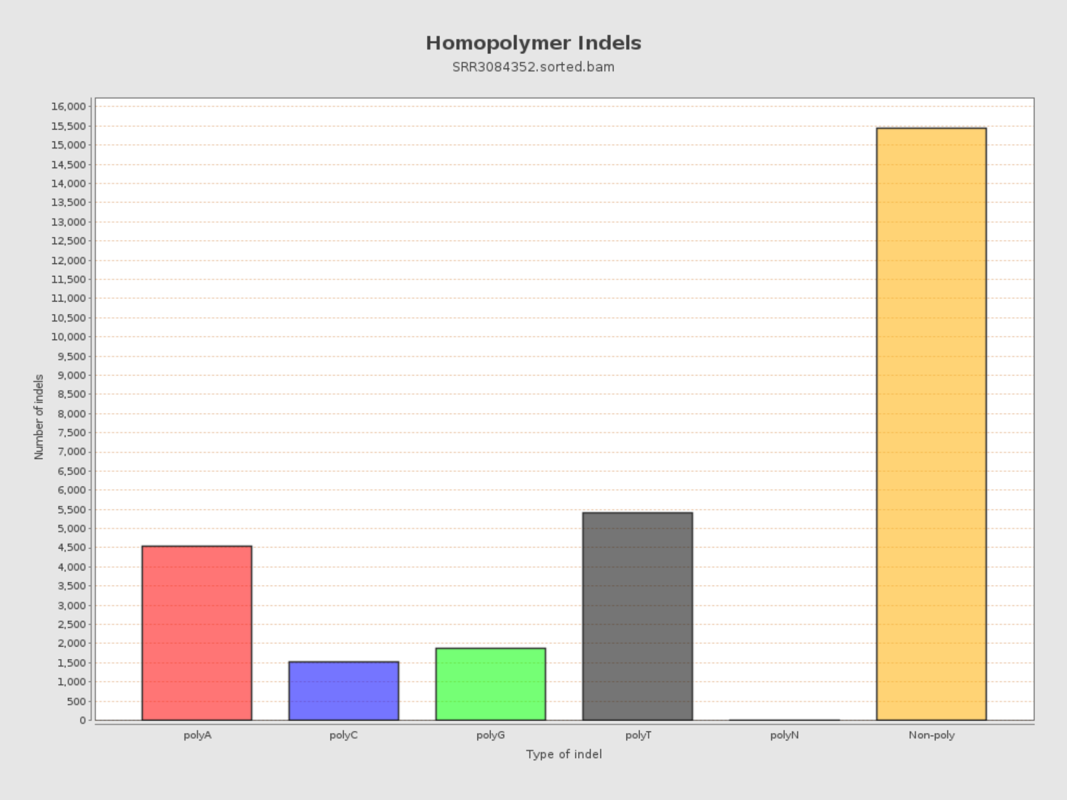
9. Results : Mapped Reads GC-content Distribution



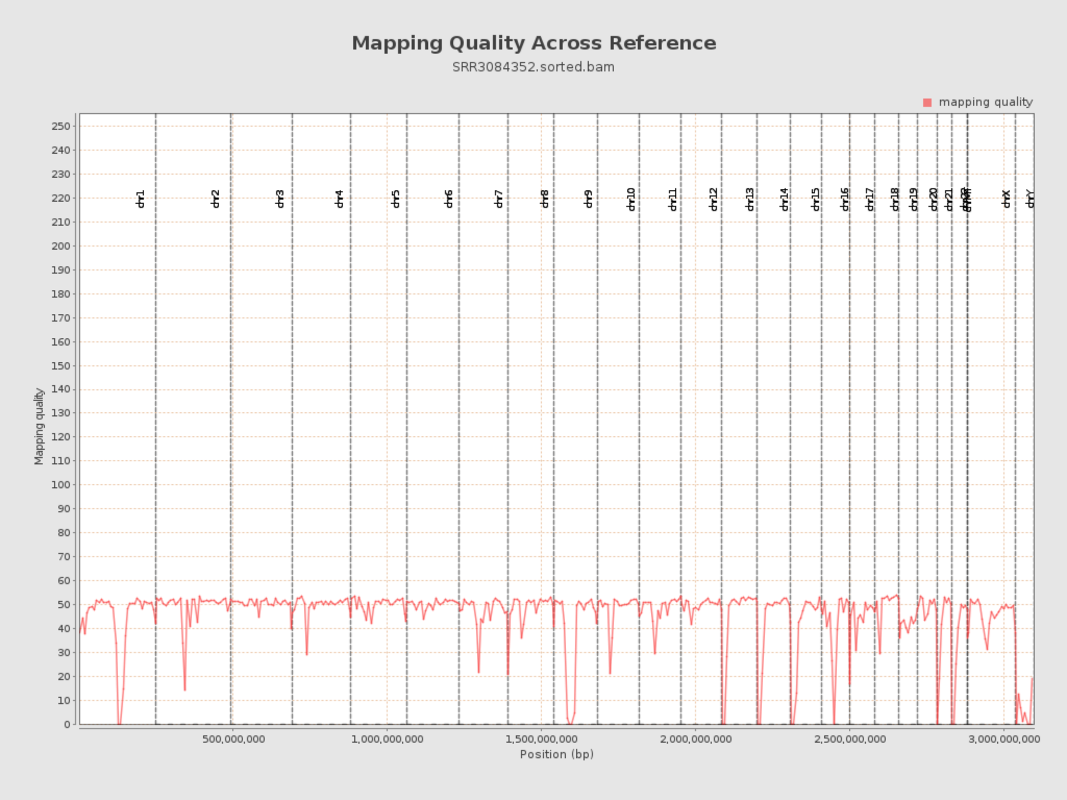
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram