Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 17:40:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084852.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_SRR3084852 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084852.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 17:40:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084852.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,245,565
Mapped reads	2,019,389 / 89.93%
Unmapped reads	226,176 / 10.07%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,834 / 1.11%
Read min/max/mean length	30 / 76 / 76.39
Duplicated reads (estimated)	102,366 / 4.56%
Duplication rate	4.22%
Clipped reads	902,441 / 40.19%

2.2. ACGT Content

Number/percentage of A's	36,667,775 / 27.2%
Number/percentage of C's	25,267,061 / 18.74%
Number/percentage of T's	42,385,183 / 31.44%
Number/percentage of G's	30,474,893 / 22.61%
Number/percentage of N's	18,524 / 0.01%
GC Percentage	41.35%

2.3. Coverage

Mean	0.0436

Standard Deviation	0.3422

2.4. Mapping Quality

Mean Mapping Quality	45.44

2.5. Mismatches and indels

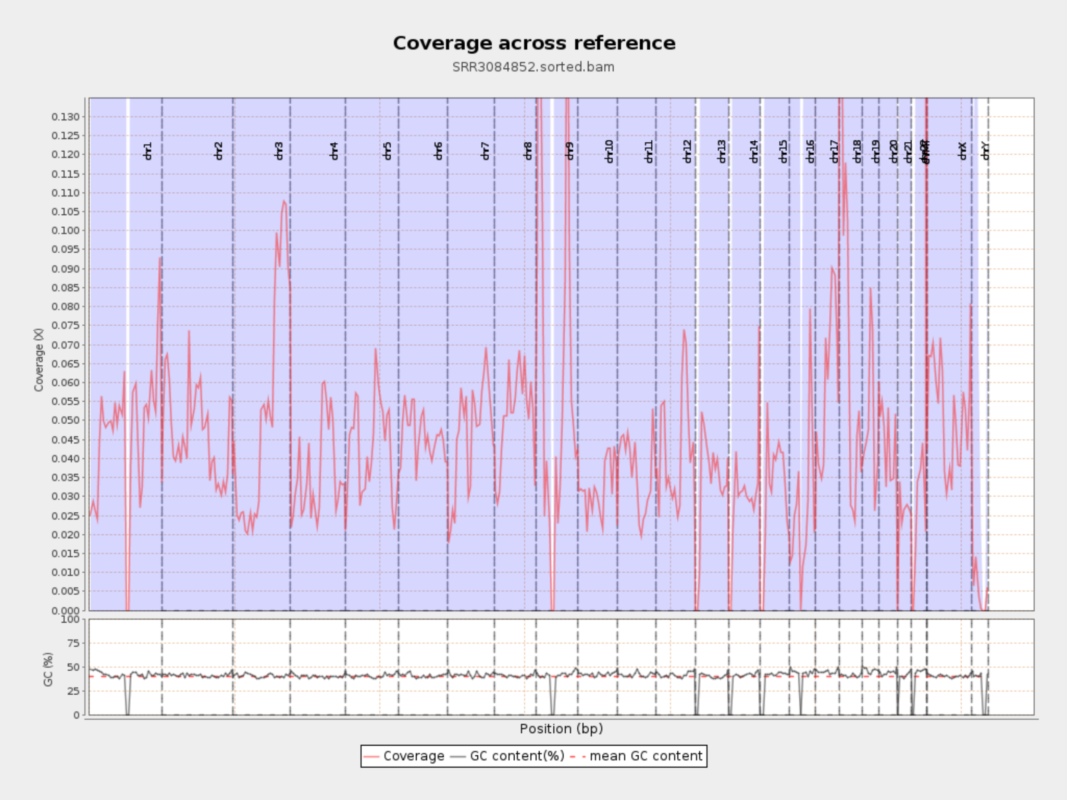
General error rate	0.8%
Mismatches	1,055,882
Insertions	10,895
Mapped reads with at least one insertion	0.54%
Deletions	32,247
Mapped reads with at least one deletion	1.58%
Homopolymer indels	47.44%

2.6. Chromosome stats

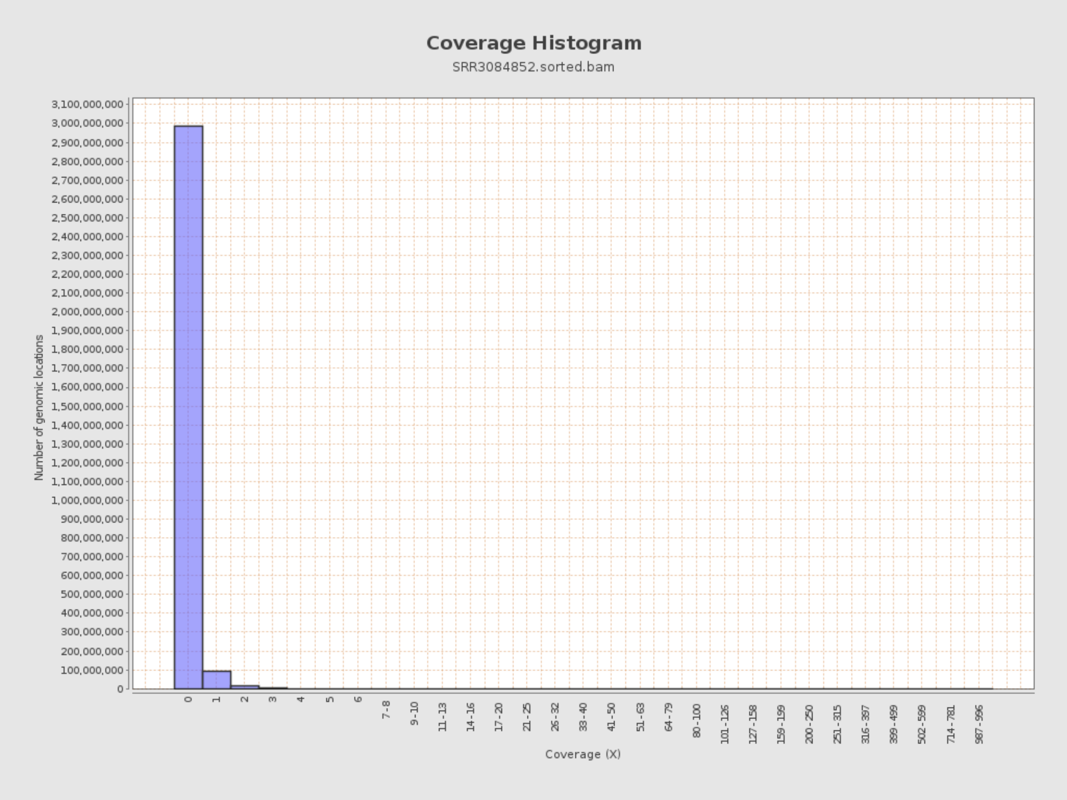
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11509830	0.0462	0.5558
chr2	243199373	11440246	0.047	0.5531
chr3	198022430	10353228	0.0523	0.2693
chr4	191154276	6927124	0.0362	0.2251
chr5	180915260	7768355	0.0429	0.2441
chr6	171115067	7831103	0.0458	0.272
chr7	159138663	7442530	0.0468	0.3221

chr8	146364022	7493915	0.0512	0.3761
chr9	141213431	9249432	0.0655	0.3903
chr10	135534747	4367986	0.0322	0.2282
chr11	135006516	4915883	0.0364	0.257
chr12	133851895	5678940	0.0424	0.2441
chr13	115169878	3745032	0.0325	0.2105
chr14	107349540	2924557	0.0272	0.2048
chr15	102531392	3186027	0.0311	0.2123
chr16	90354753	2501663	0.0277	0.206
chr17	81195210	4965031	0.0611	0.2941
chr18	78077248	5876635	0.0753	0.5758
chr19	59128983	3006941	0.0509	0.3739
chr20	63025520	2786163	0.0442	0.256
chr21	48129895	1194908	0.0248	0.195
chr22	51304566	1277829	0.0249	0.1808
chrMT	16571	61268	3.6973	2.8771
chrX	155270560	8049186	0.0518	0.2823
chrY	59373566	312730	0.0053	0.1195

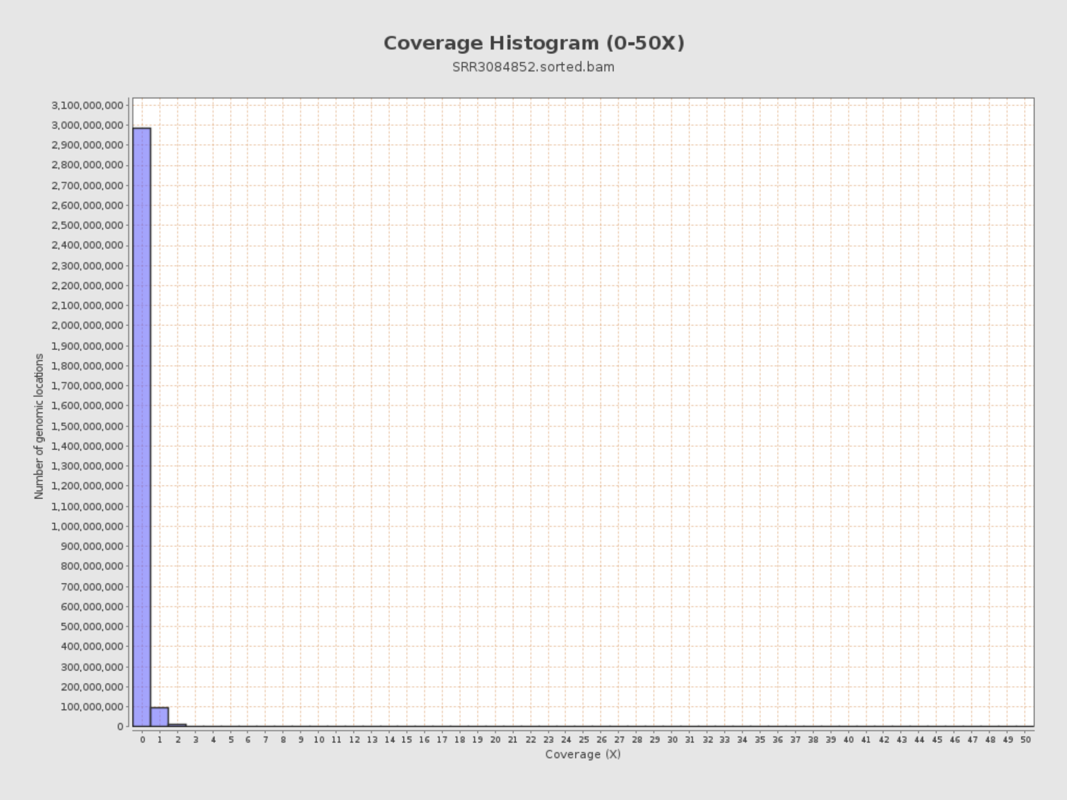
3. Results : Coverage across reference



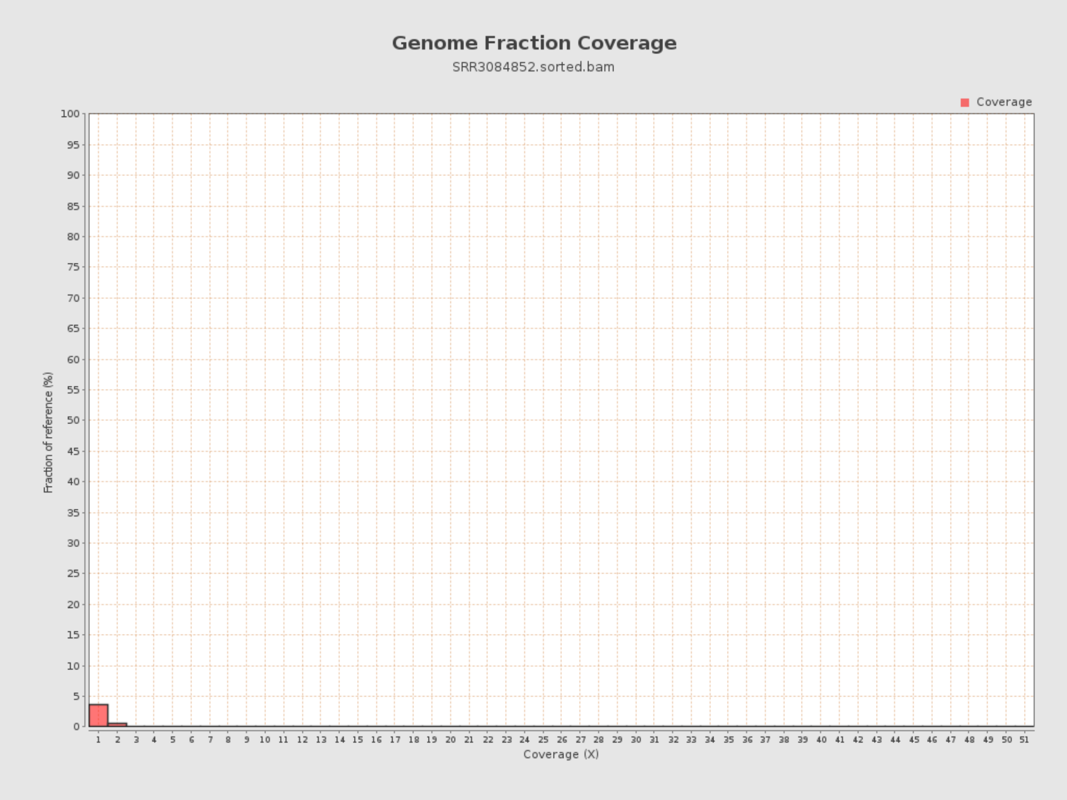
4. Results : Coverage Histogram



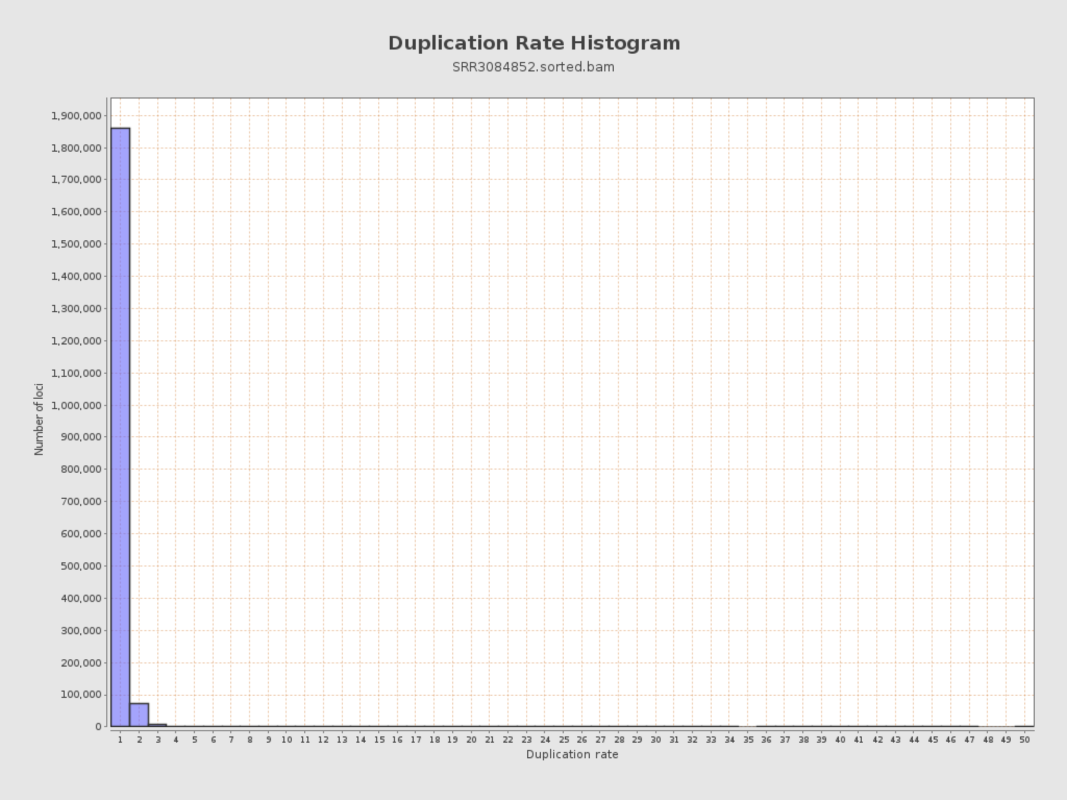
5. Results : Coverage Histogram (0-50X)



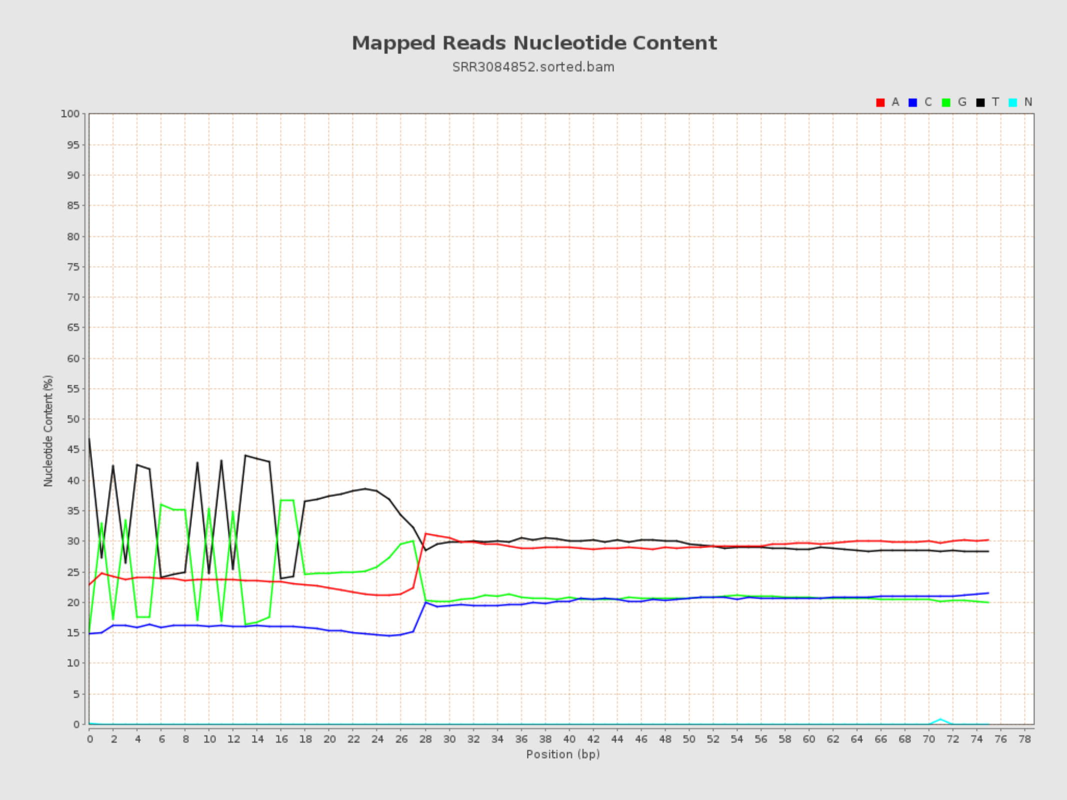
6. Results : Genome Fraction Coverage



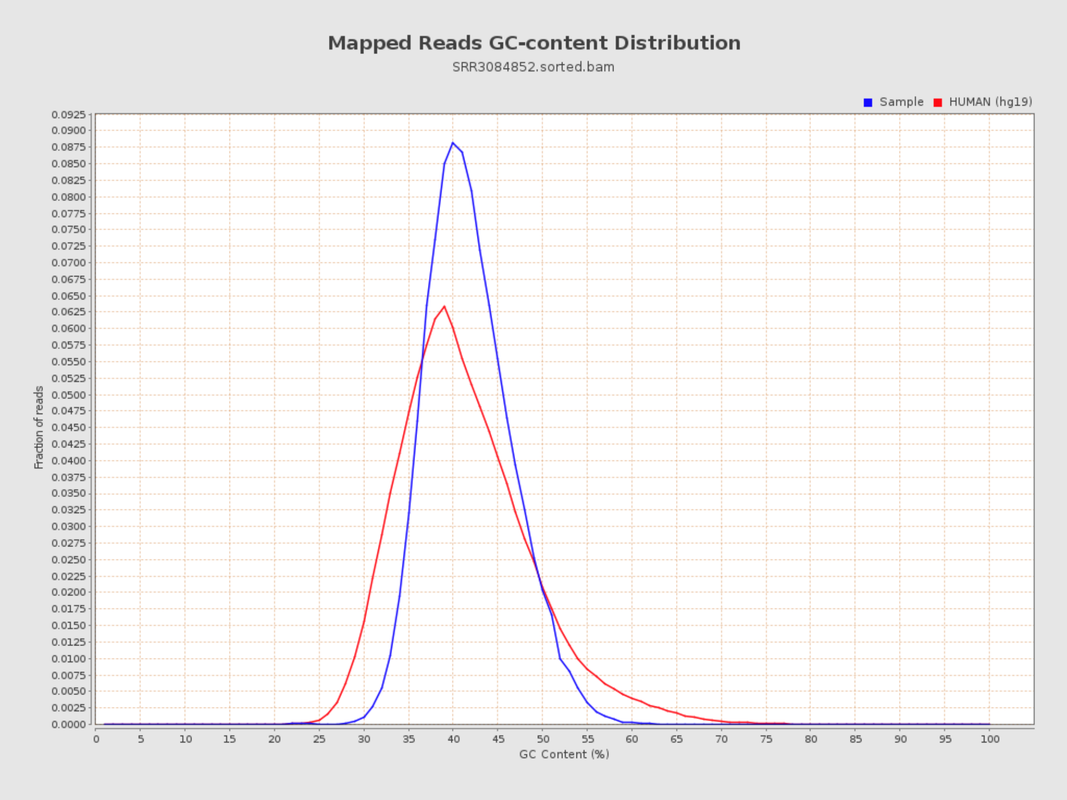
7. Results : Duplication Rate Histogram



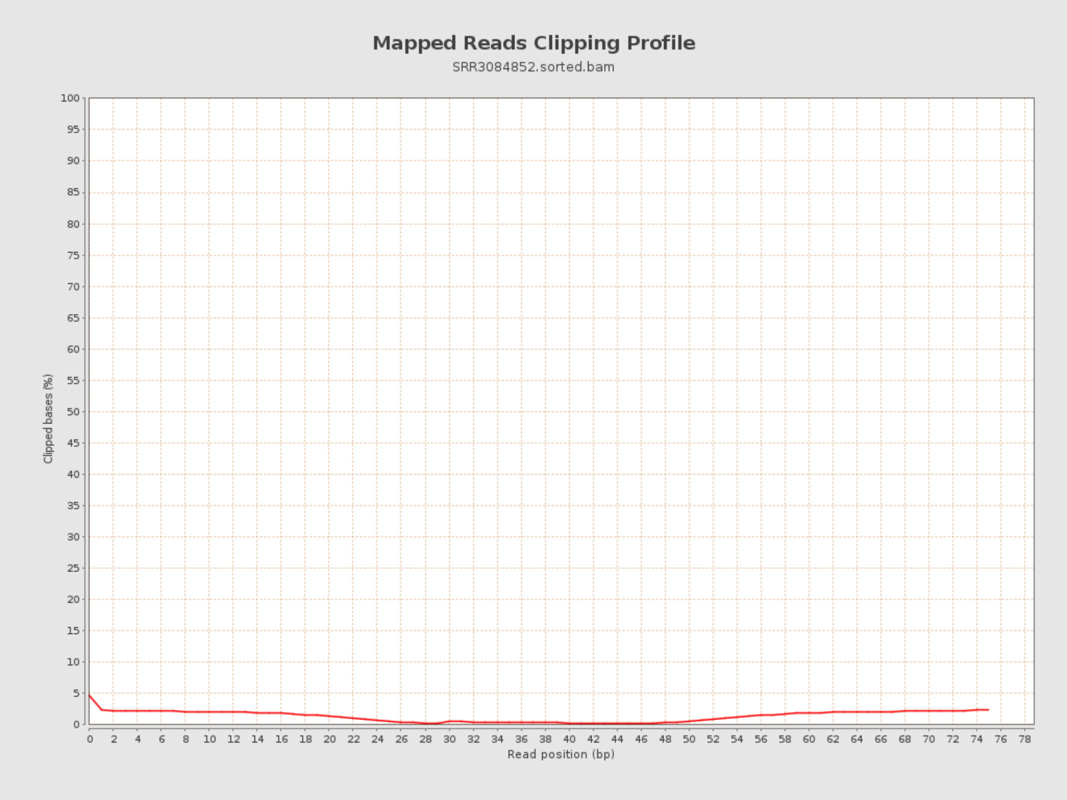
8. Results : Mapped Reads Nucleotide Content



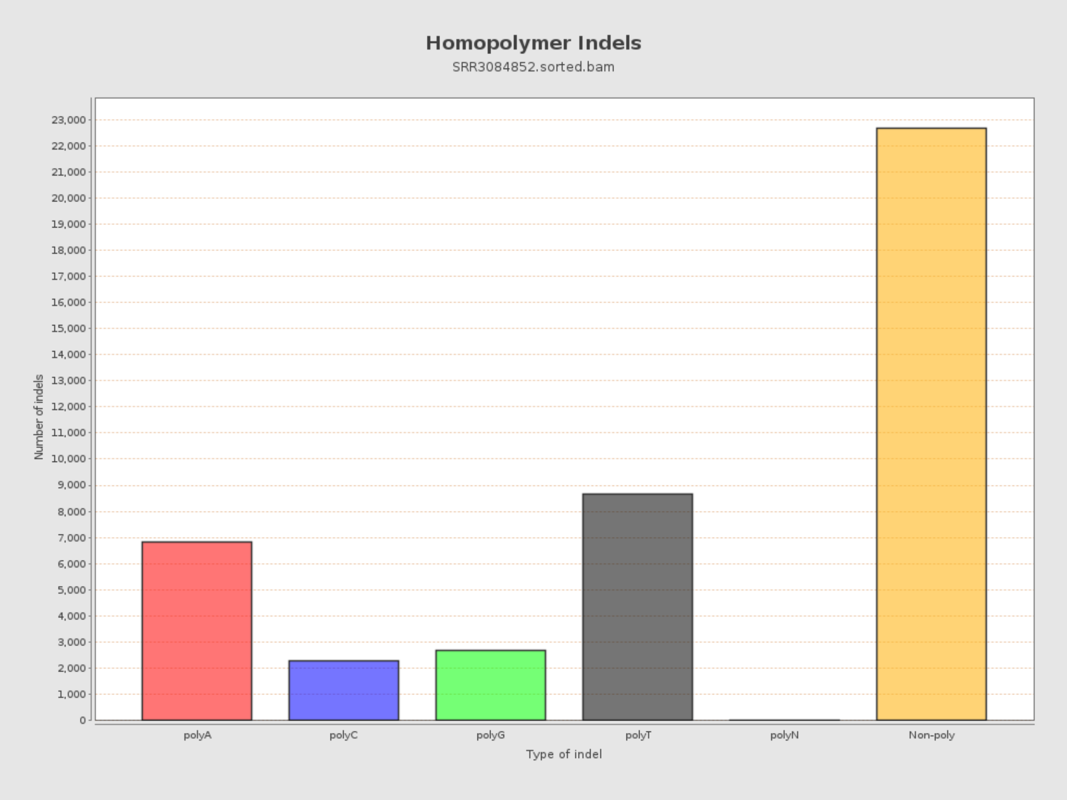
9. Results : Mapped Reads GC-content Distribution



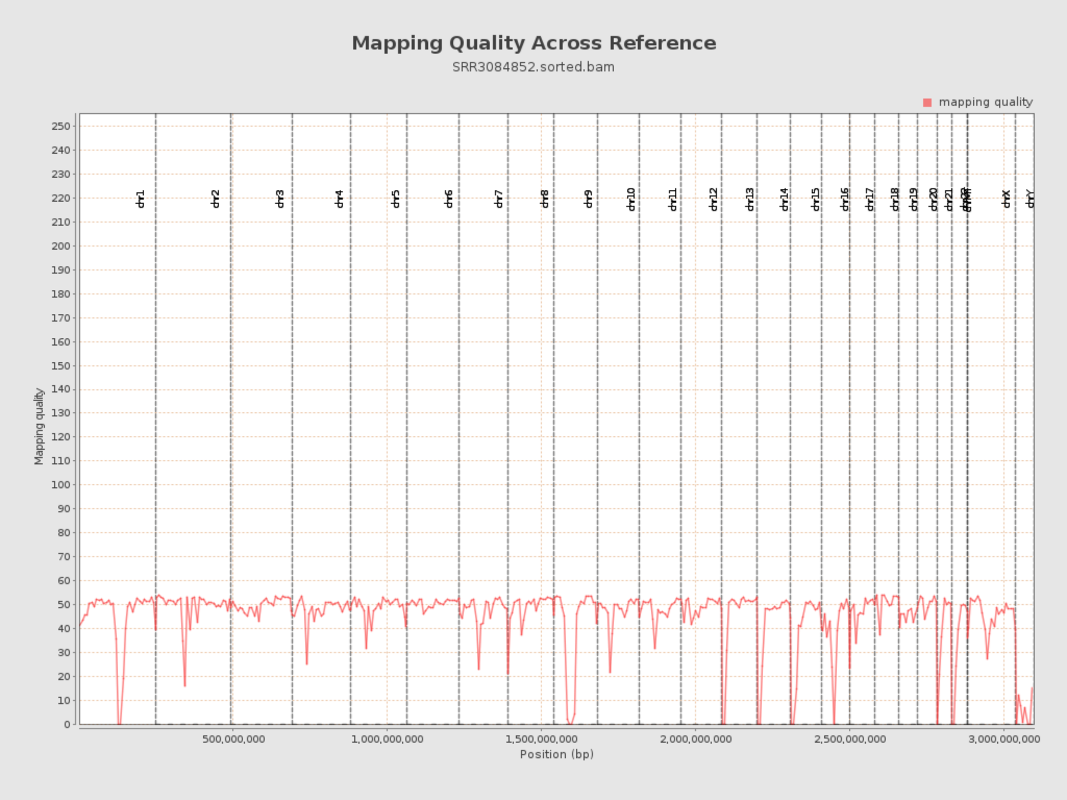
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram