Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 10:43:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084351.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_SRR3084351 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084351.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 10:43:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084351.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,322,856
Mapped reads	2,007,440 / 86.42%
Unmapped reads	315,416 / 13.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,533 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	63,994 / 2.75%
Duplication rate	2.71%
Clipped reads	891,716 / 38.39%

2.2. ACGT Content

Number/percentage of A's	37,143,517 / 27.63%
Number/percentage of C's	26,002,191 / 19.34%
Number/percentage of T's	41,168,155 / 30.63%
Number/percentage of G's	29,943,470 / 22.28%
Number/percentage of N's	164,460 / 0.12%
GC Percentage	41.62%

2.3. Coverage

Mean	0.0434

Standard Deviation	0.29

2.4. Mapping Quality

Mean Mapping Quality	45.65

2.5. Mismatches and indels

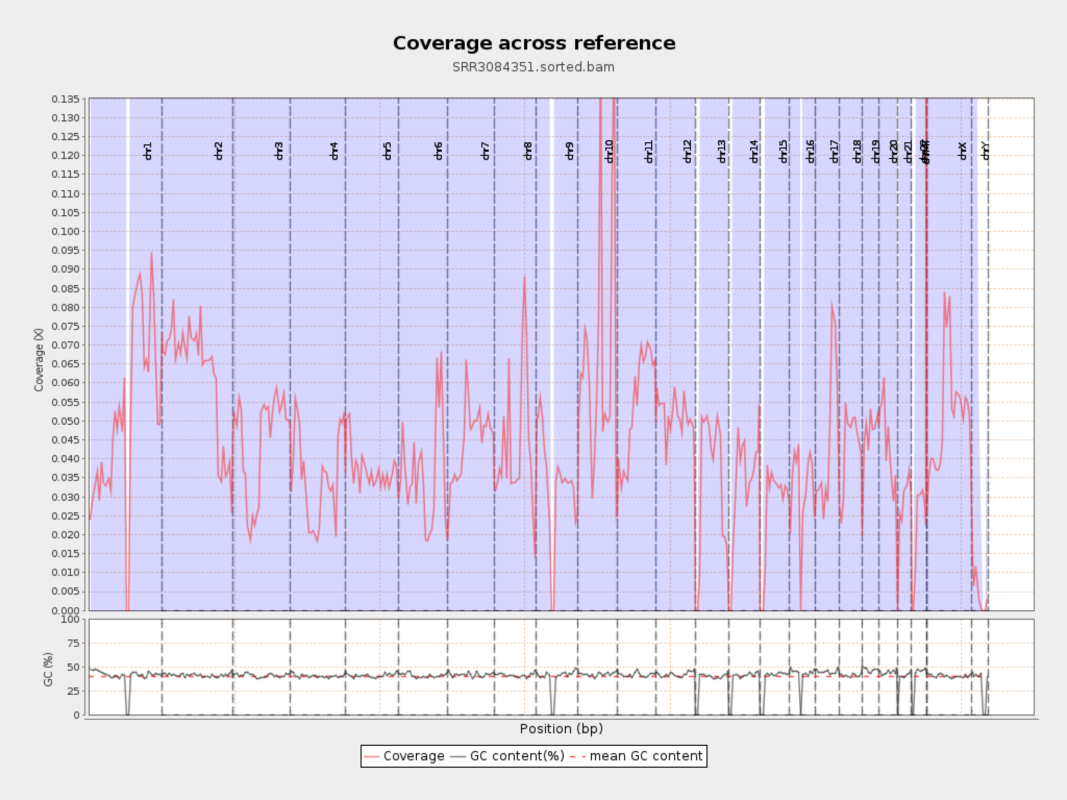
General error rate	0.97%
Mismatches	1,290,286
Insertions	9,160
Mapped reads with at least one insertion	0.45%
Deletions	26,206
Mapped reads with at least one deletion	1.29%
Homopolymer indels	46.15%

2.6. Chromosome stats

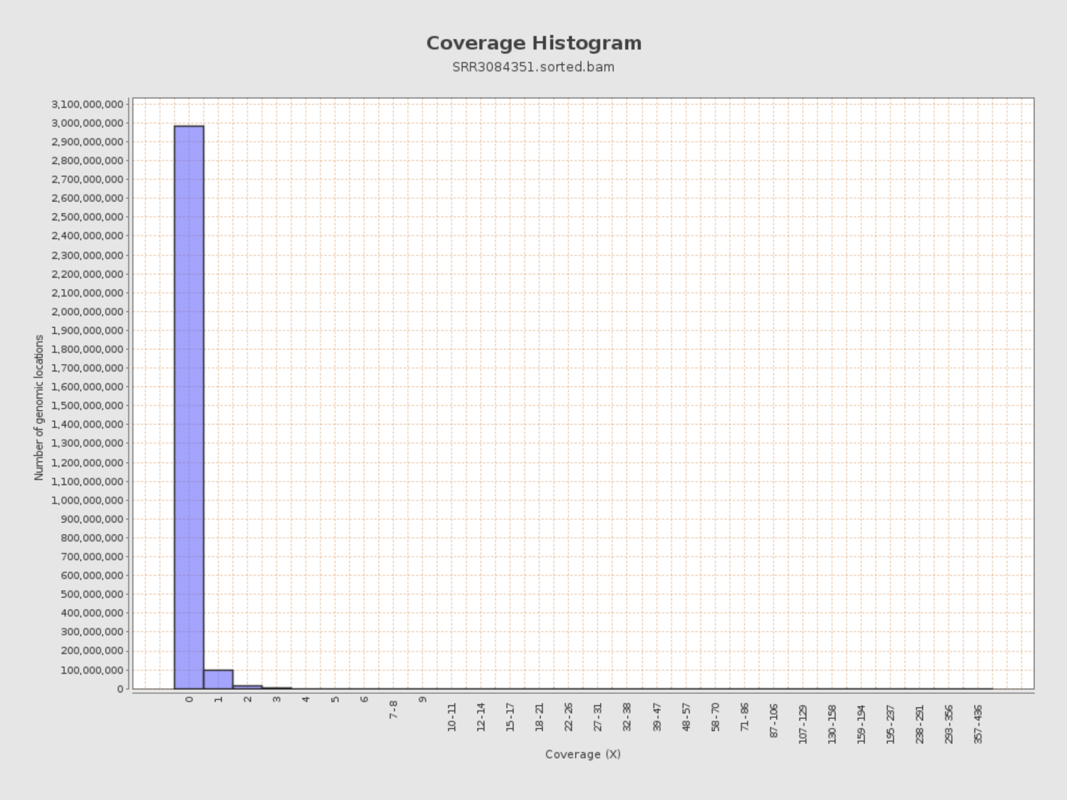
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12842731	0.0515	0.4224
chr2	243199373	15248791	0.0627	0.3714
chr3	198022430	8848342	0.0447	0.2405
chr4	191154276	6724728	0.0352	0.2168
chr5	180915260	6733287	0.0372	0.2181
chr6	171115067	6158160	0.036	0.2369
chr7	159138663	7194020	0.0452	0.3861

chr8	146364022	6347751	0.0434	0.2756
chr9	141213431	4693536	0.0332	0.2456
chr10	135534747	9313761	0.0687	0.3712
chr11	135006516	7297858	0.0541	0.3071
chr12	133851895	6871276	0.0513	0.2594
chr13	115169878	3823086	0.0332	0.2067
chr14	107349540	3485658	0.0325	0.2103
chr15	102531392	2764001	0.027	0.1901
chr16	90354753	2915133	0.0323	0.2167
chr17	81195210	3641673	0.0449	0.2502
chr18	78077248	3387524	0.0434	0.3828
chr19	59128983	2774822	0.0469	0.3269
chr20	63025520	2736324	0.0434	0.2408
chr21	48129895	1318142	0.0274	0.1934
chr22	51304566	1062284	0.0207	0.1615
chrMT	16571	9115	0.5501	0.805
chrX	155270560	8011729	0.0516	0.275
chrY	59373566	264109	0.0044	0.0924

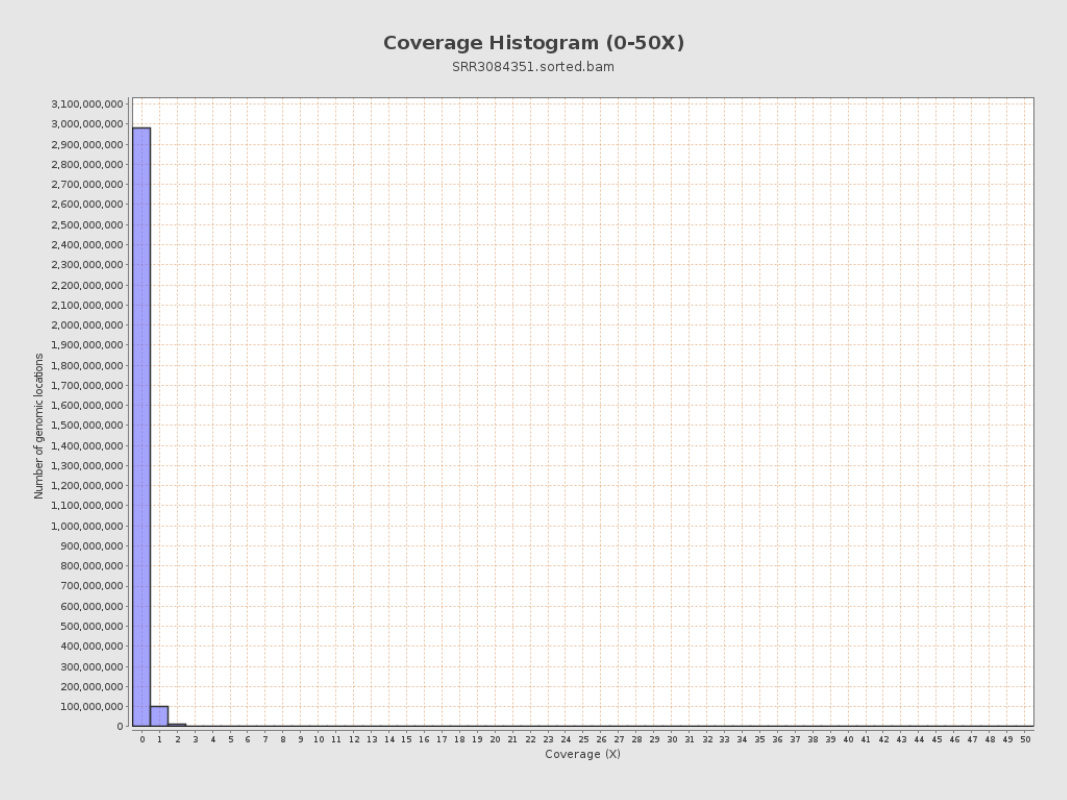
3. Results : Coverage across reference



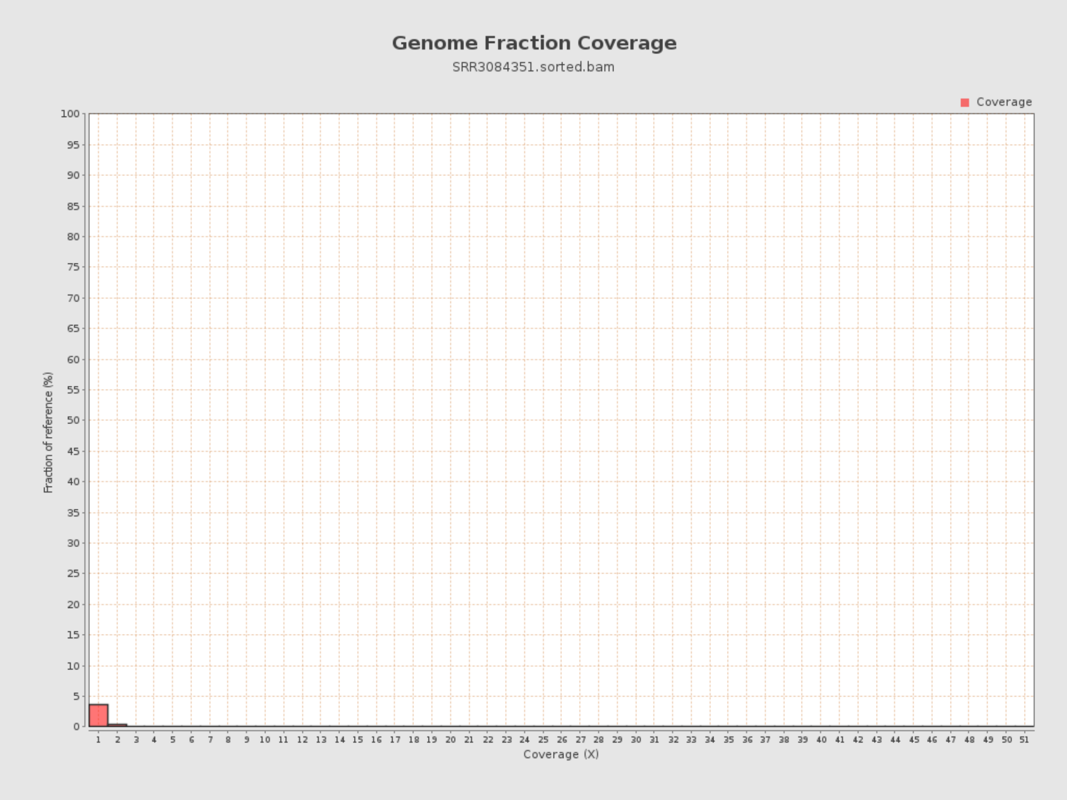
4. Results : Coverage Histogram



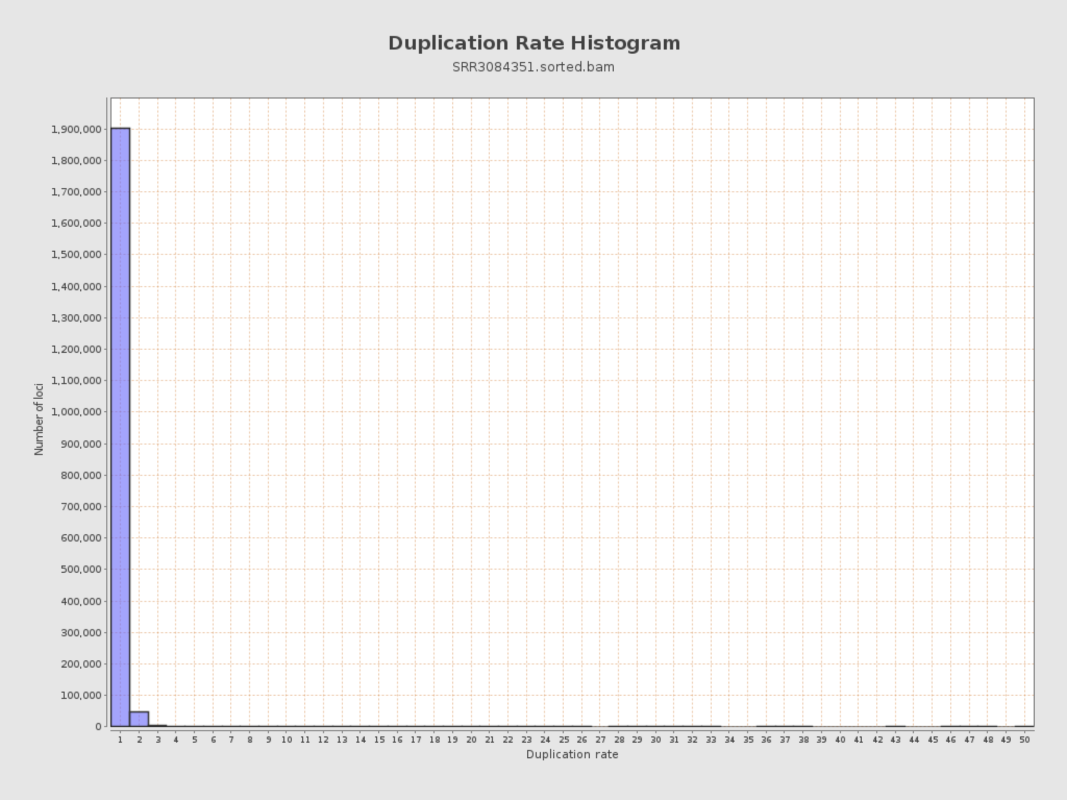
5. Results : Coverage Histogram (0-50X)



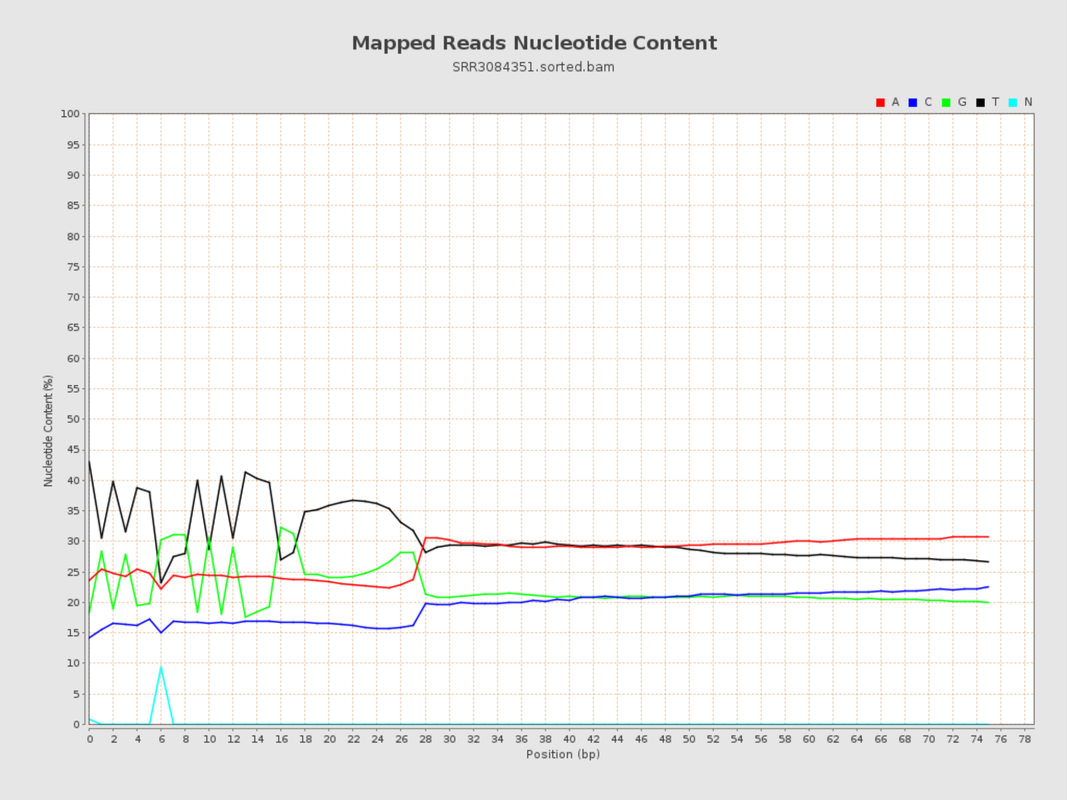
6. Results : Genome Fraction Coverage



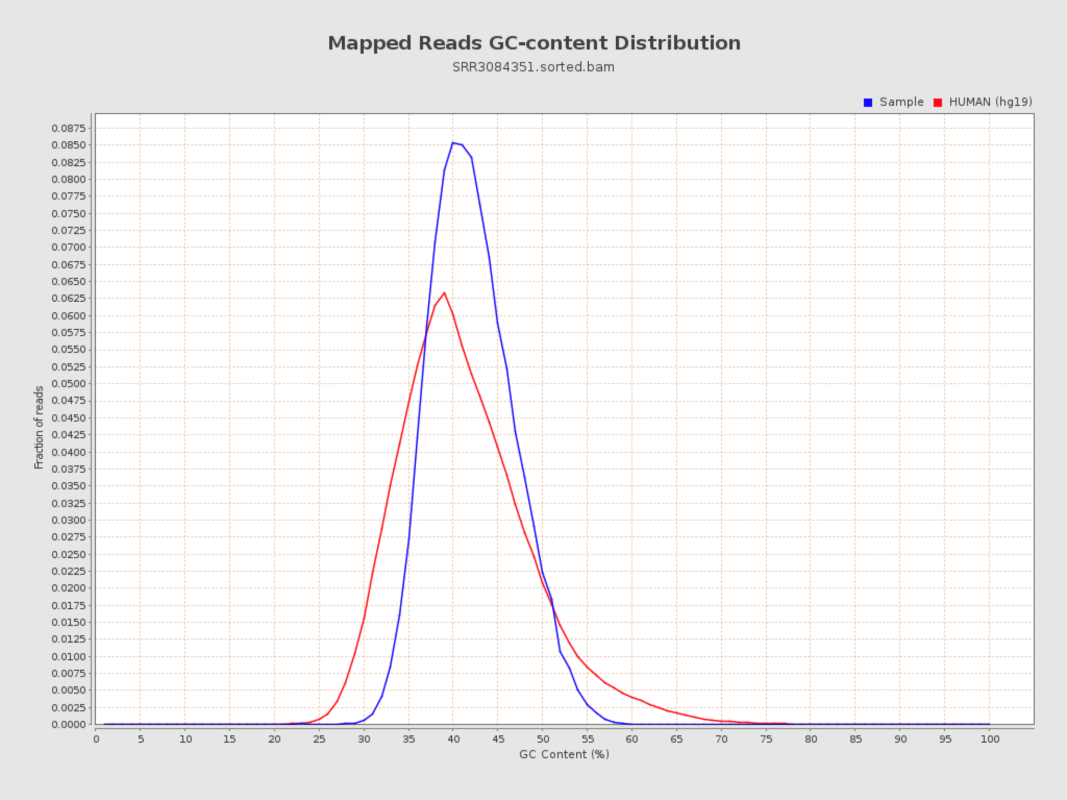
7. Results : Duplication Rate Histogram



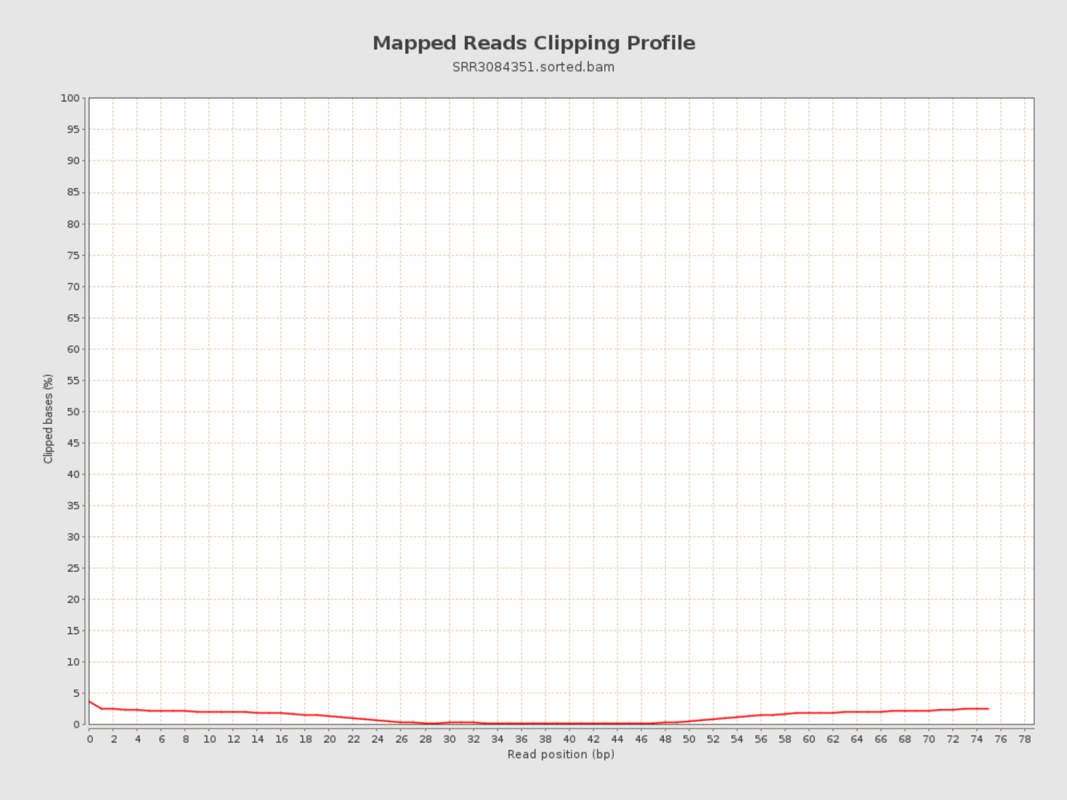
8. Results : Mapped Reads Nucleotide Content



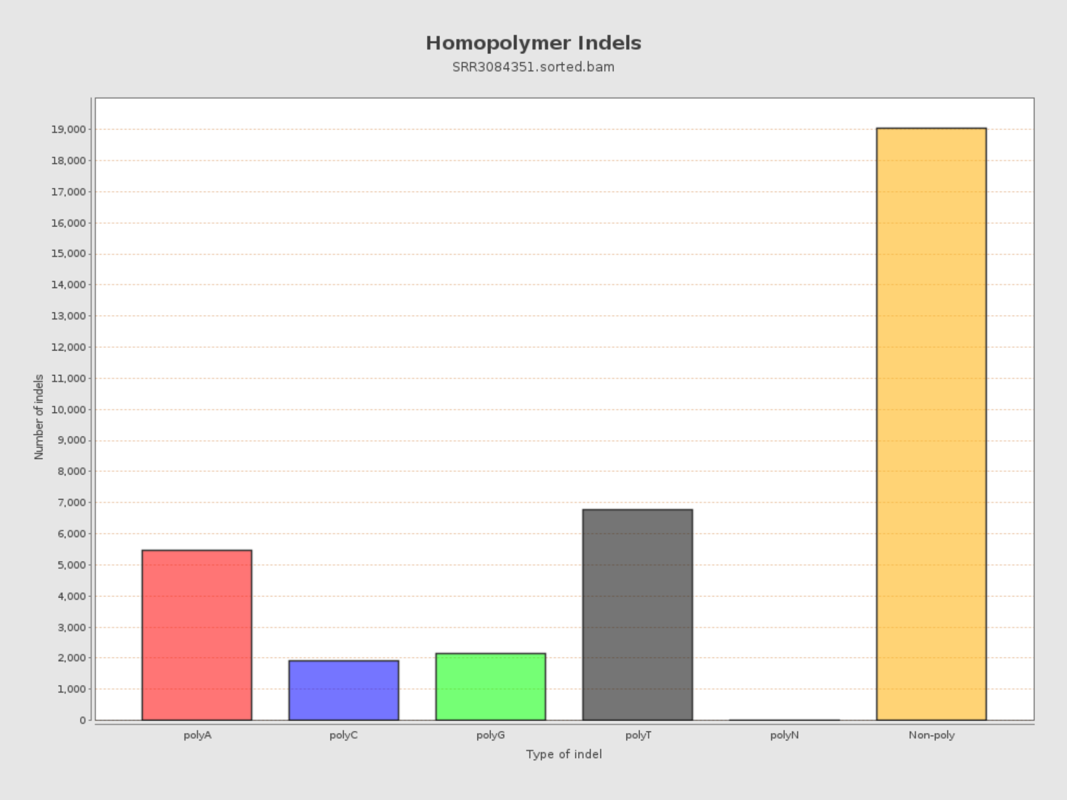
9. Results : Mapped Reads GC-content Distribution



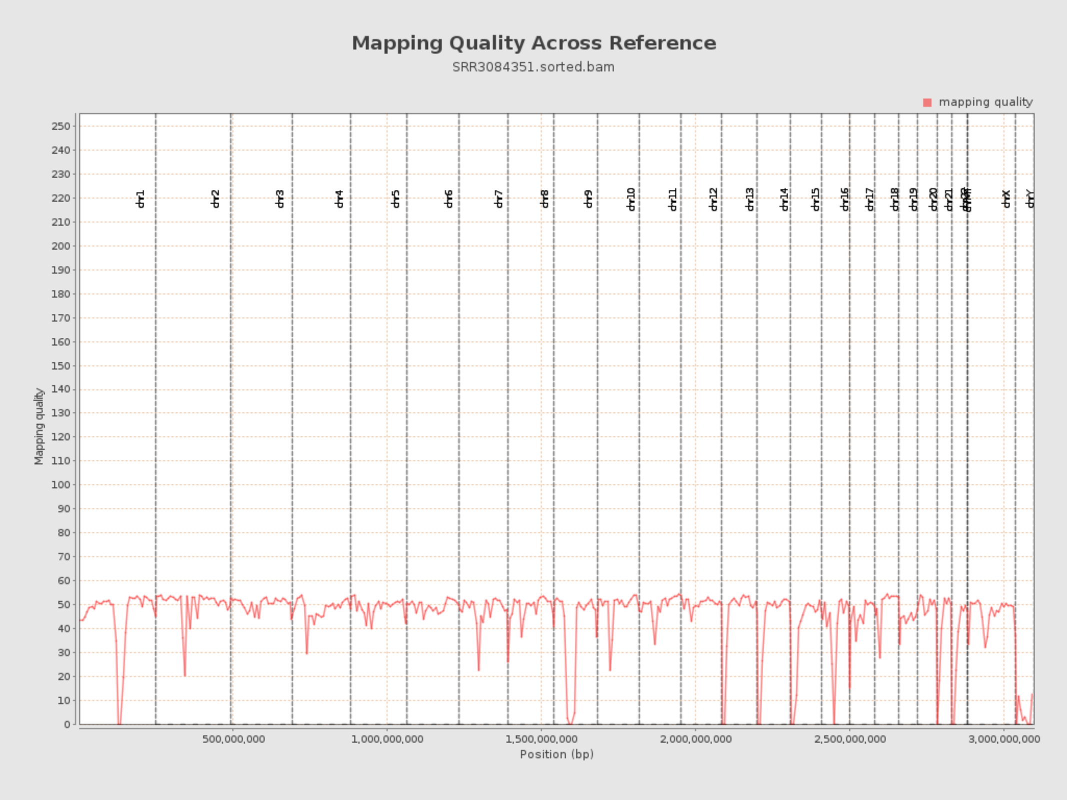
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram