Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 15:25:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084811.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_SRR3084811 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084811.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 15:25:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084811.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,380,320
Mapped reads	2,175,077 / 91.38%
Unmapped reads	205,243 / 8.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,917 / 0.92%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	97,175 / 4.08%
Duplication rate	3.81%
Clipped reads	926,713 / 38.93%

2.2. ACGT Content

Number/percentage of A's	39,904,122 / 27.3%
Number/percentage of C's	27,768,458 / 19%
Number/percentage of T's	45,444,795 / 31.09%
Number/percentage of G's	33,041,826 / 22.6%
Number/percentage of N's	20,174 / 0.01%
GC Percentage	41.6%

2.3. Coverage

Mean	0.0472

Standard Deviation	0.3226

2.4. Mapping Quality

Mean Mapping Quality	45.72

2.5. Mismatches and indels

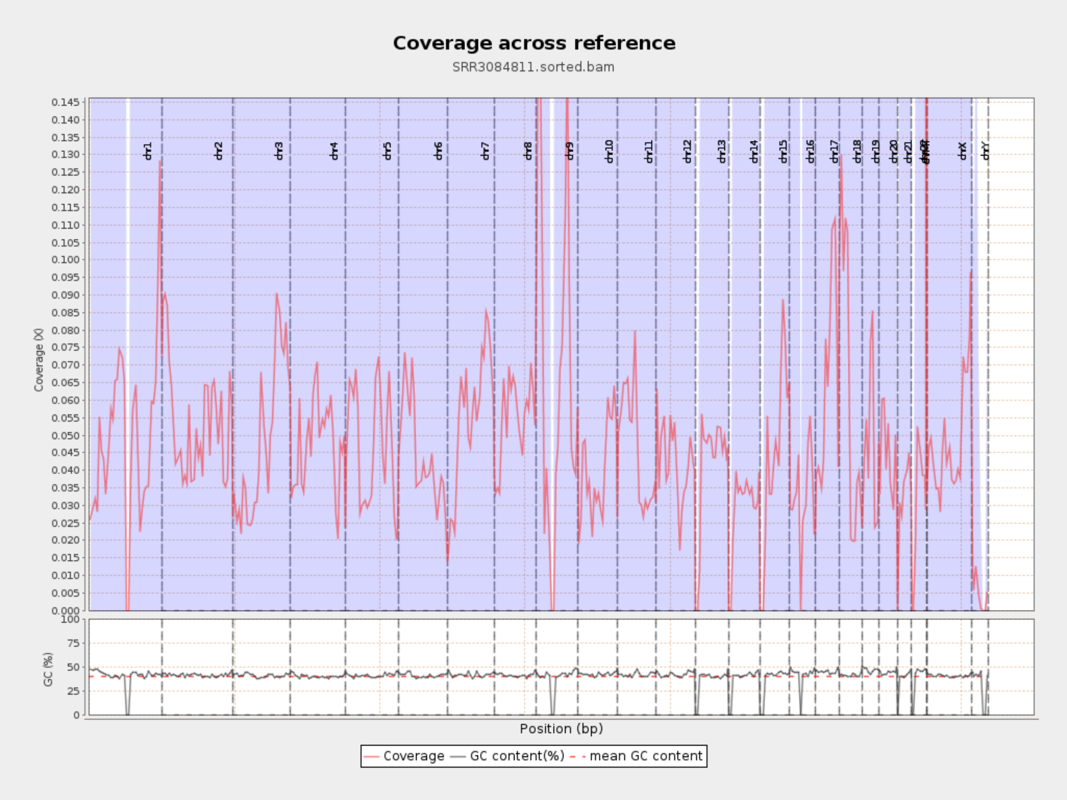
General error rate	0.78%
Mismatches	1,118,075
Insertions	11,532
Mapped reads with at least one insertion	0.53%
Deletions	34,065
Mapped reads with at least one deletion	1.55%
Homopolymer indels	48.21%

2.6. Chromosome stats

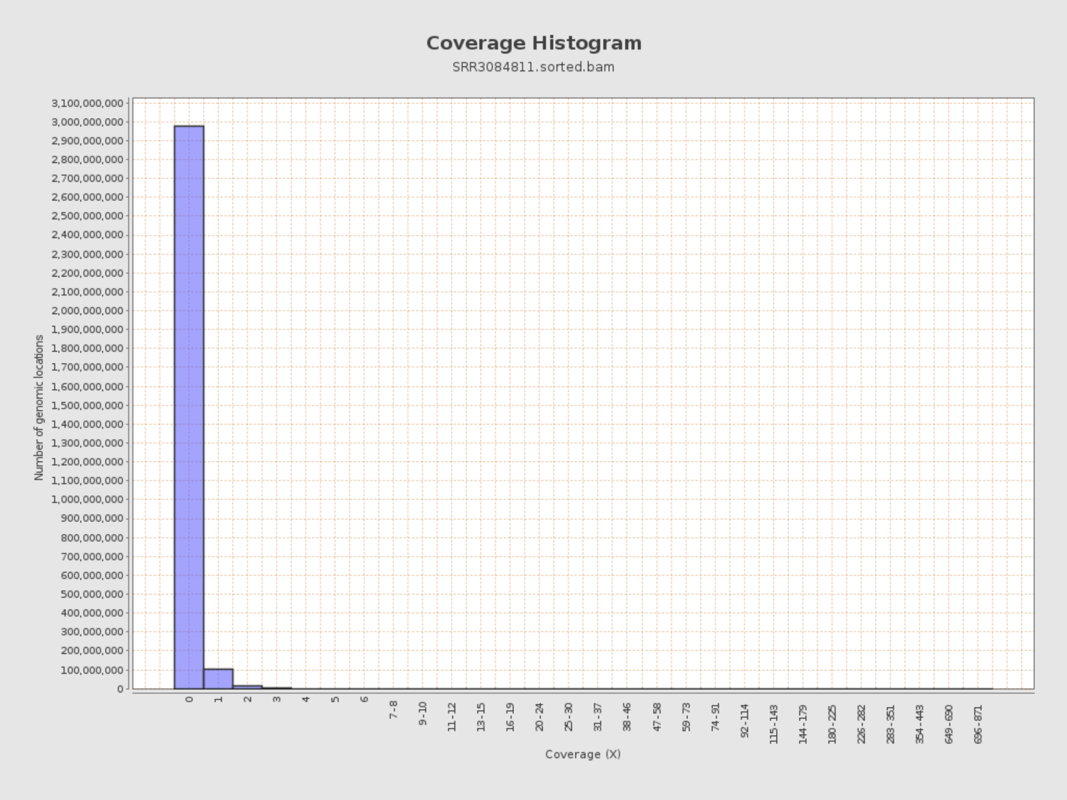
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12181179	0.0489	0.4178
chr2	243199373	12981725	0.0534	0.5113
chr3	198022430	9524313	0.0481	0.2555
chr4	191154276	9135577	0.0478	0.2604
chr5	180915260	8459680	0.0468	0.2538
chr6	171115067	7607482	0.0445	0.2671
chr7	159138663	8929169	0.0561	0.3422

chr8	146364022	8055662	0.055	0.3268
chr9	141213431	9729212	0.0689	0.3721
chr10	135534747	5376786	0.0397	0.2616
chr11	135006516	6242281	0.0462	0.3094
chr12	133851895	5631988	0.0421	0.2416
chr13	115169878	4687762	0.0407	0.2349
chr14	107349540	3071629	0.0286	0.2086
chr15	102531392	4601781	0.0449	0.2577
chr16	90354753	2949110	0.0326	0.2204
chr17	81195210	5375291	0.0662	0.312
chr18	78077248	5010347	0.0642	0.5139
chr19	59128983	2852487	0.0482	0.3552
chr20	63025520	2856064	0.0453	0.2551
chr21	48129895	1557255	0.0324	0.2161
chr22	51304566	1540176	0.03	0.2001
chrMT	16571	189026	11.407	6.1234
chrX	155270560	7404029	0.0477	0.27
chrY	59373566	285596	0.0048	0.0911

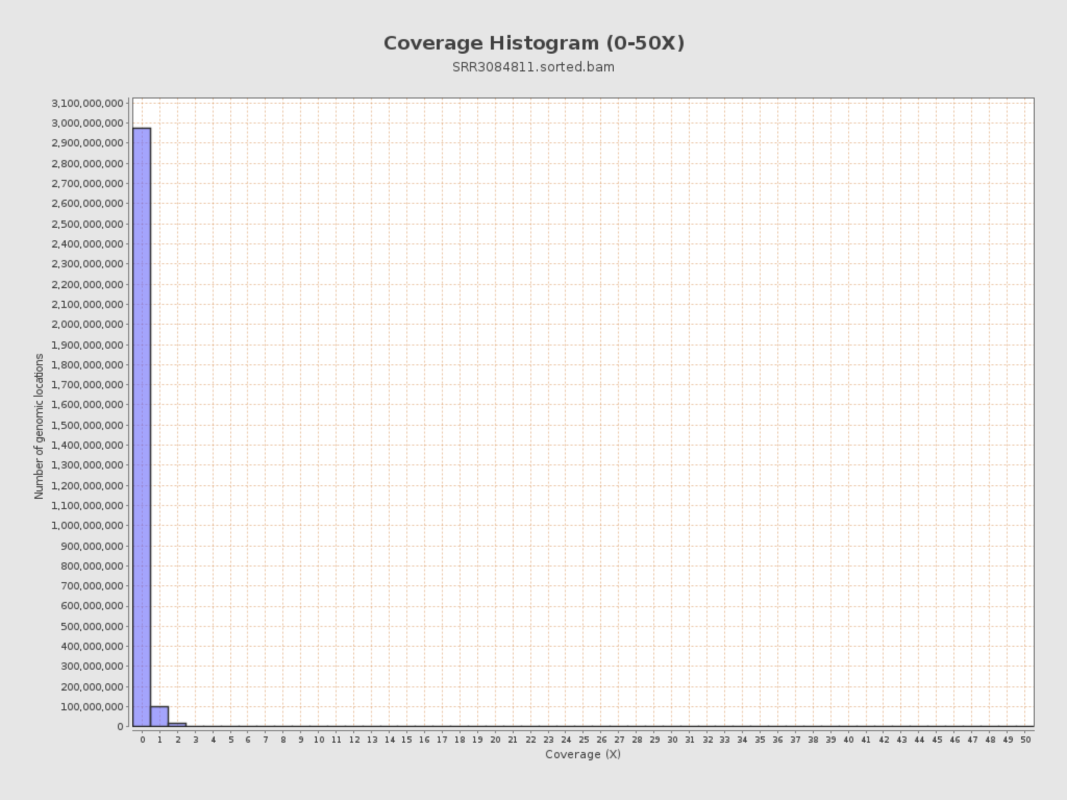
3. Results : Coverage across reference



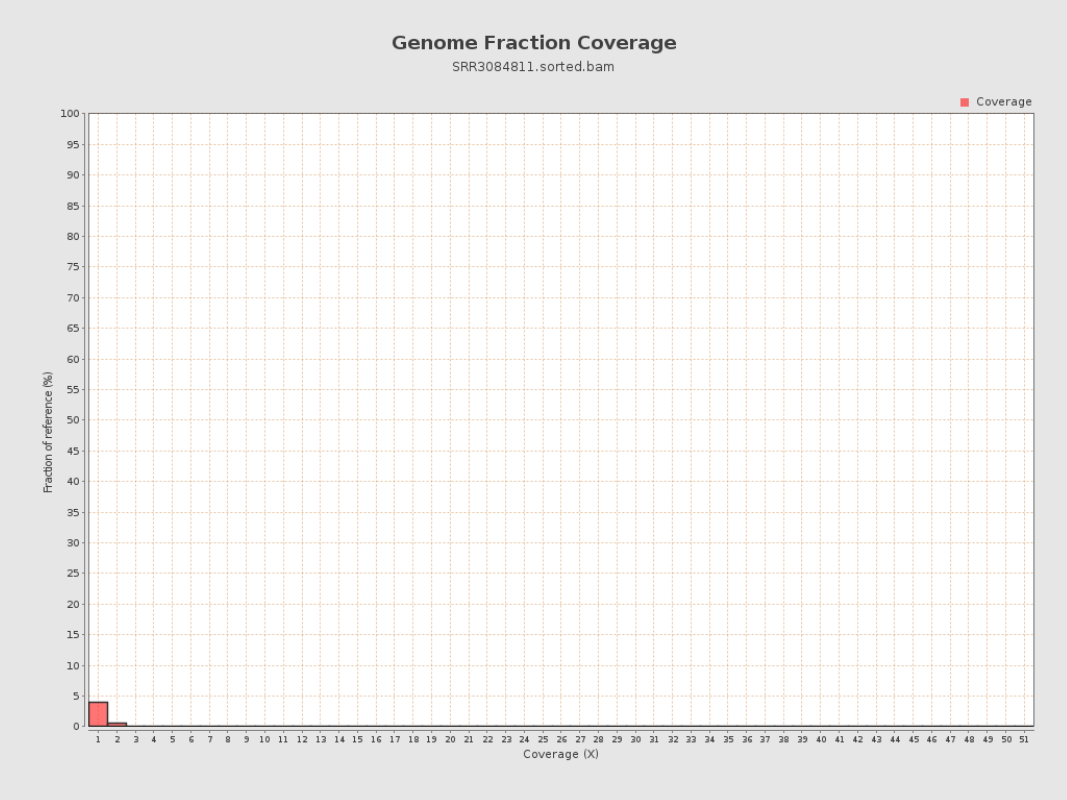
4. Results : Coverage Histogram



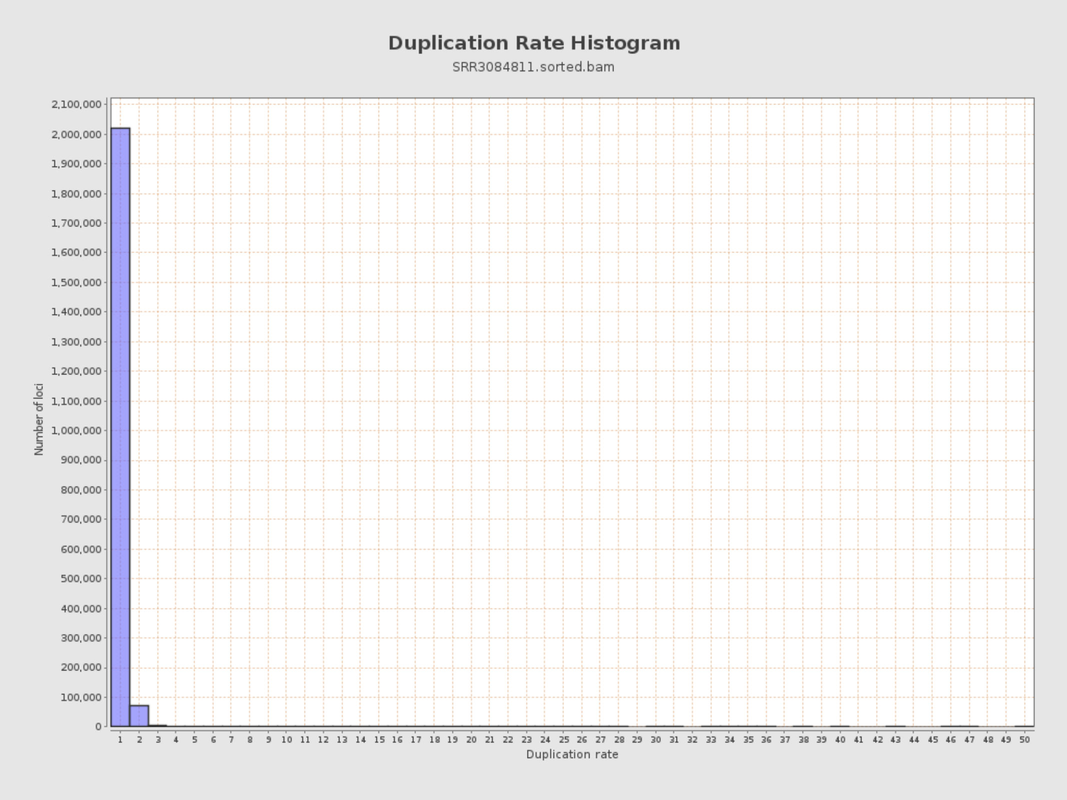
5. Results : Coverage Histogram (0-50X)



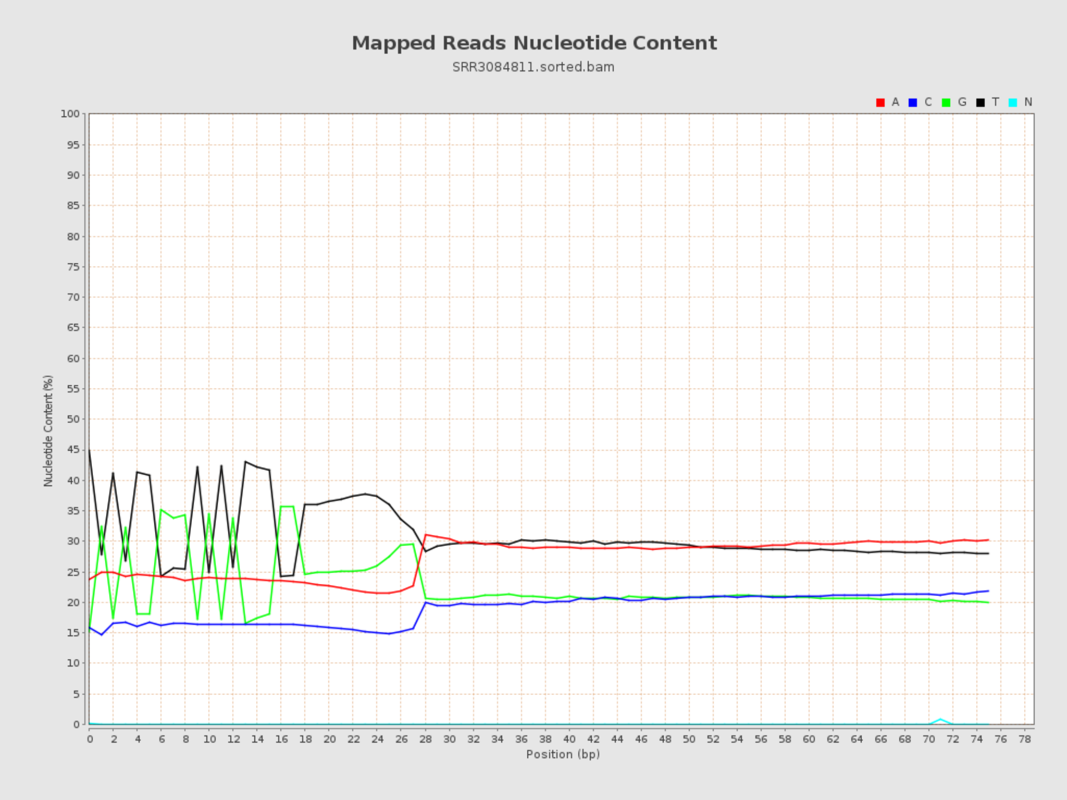
6. Results : Genome Fraction Coverage



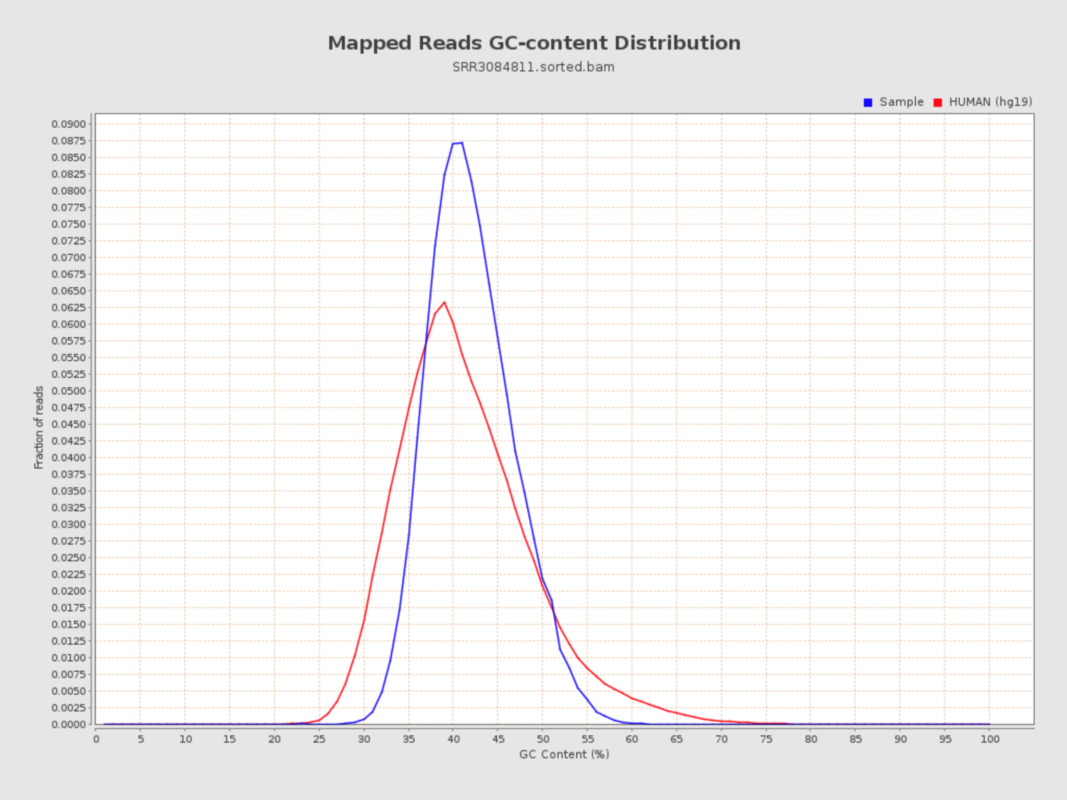
7. Results : Duplication Rate Histogram



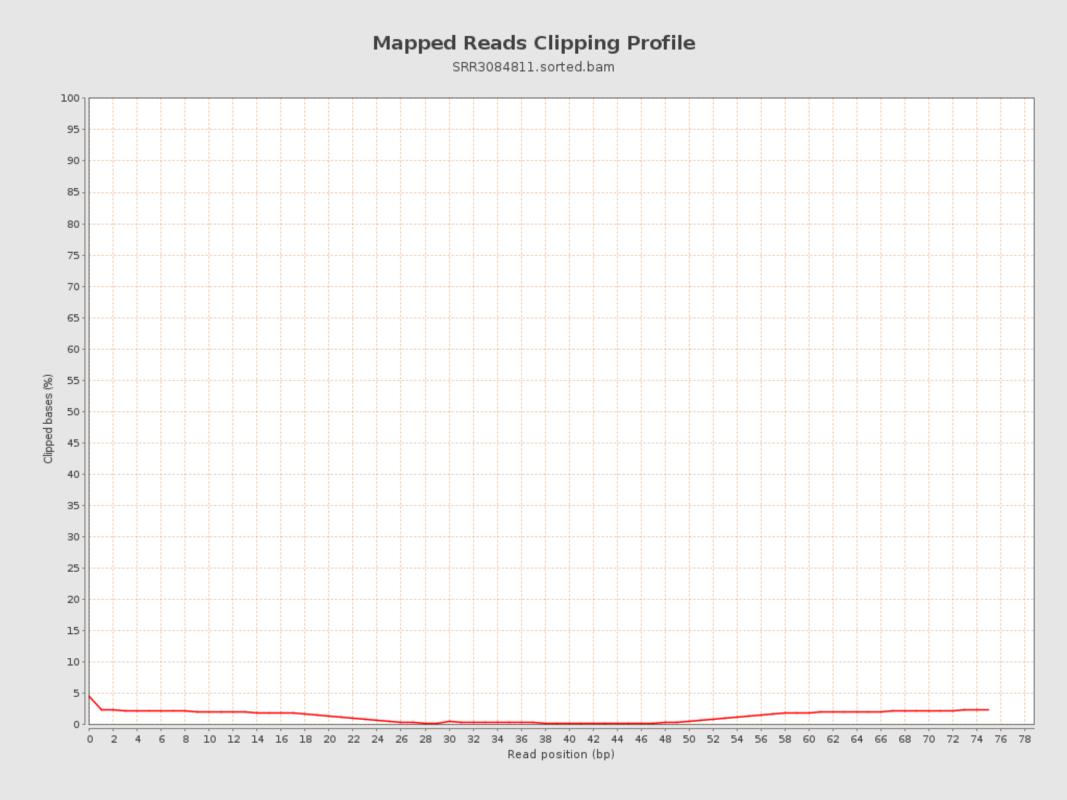
8. Results : Mapped Reads Nucleotide Content



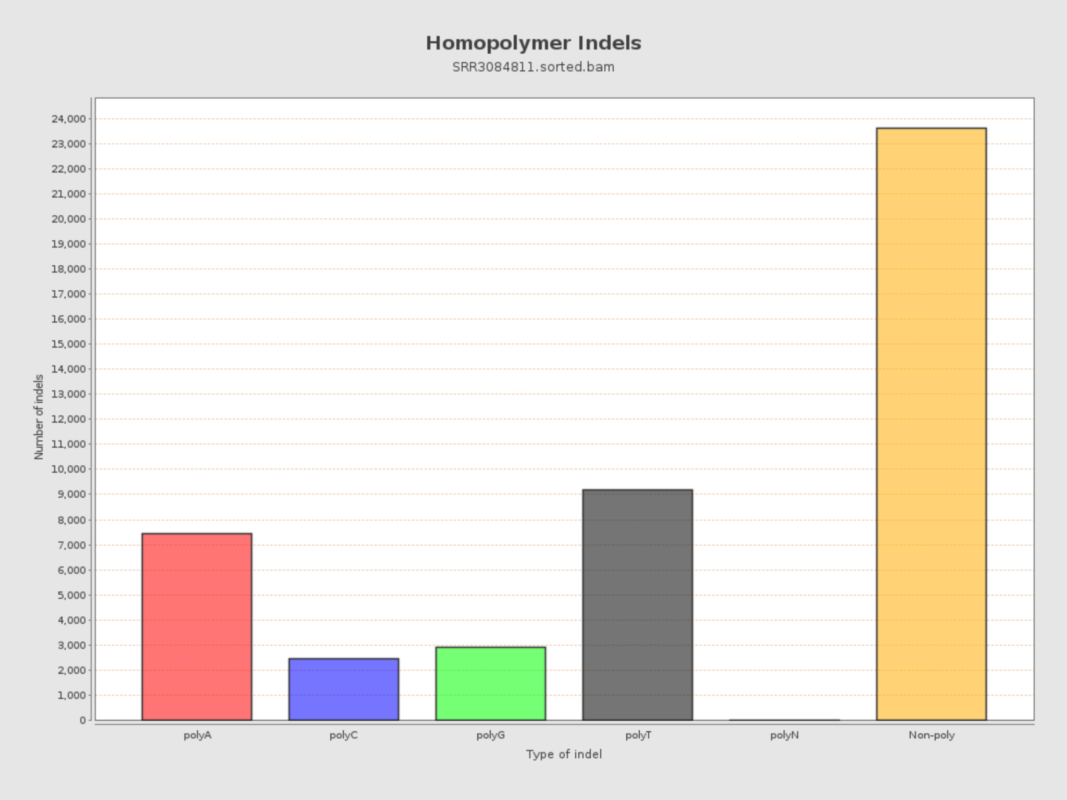
9. Results : Mapped Reads GC-content Distribution



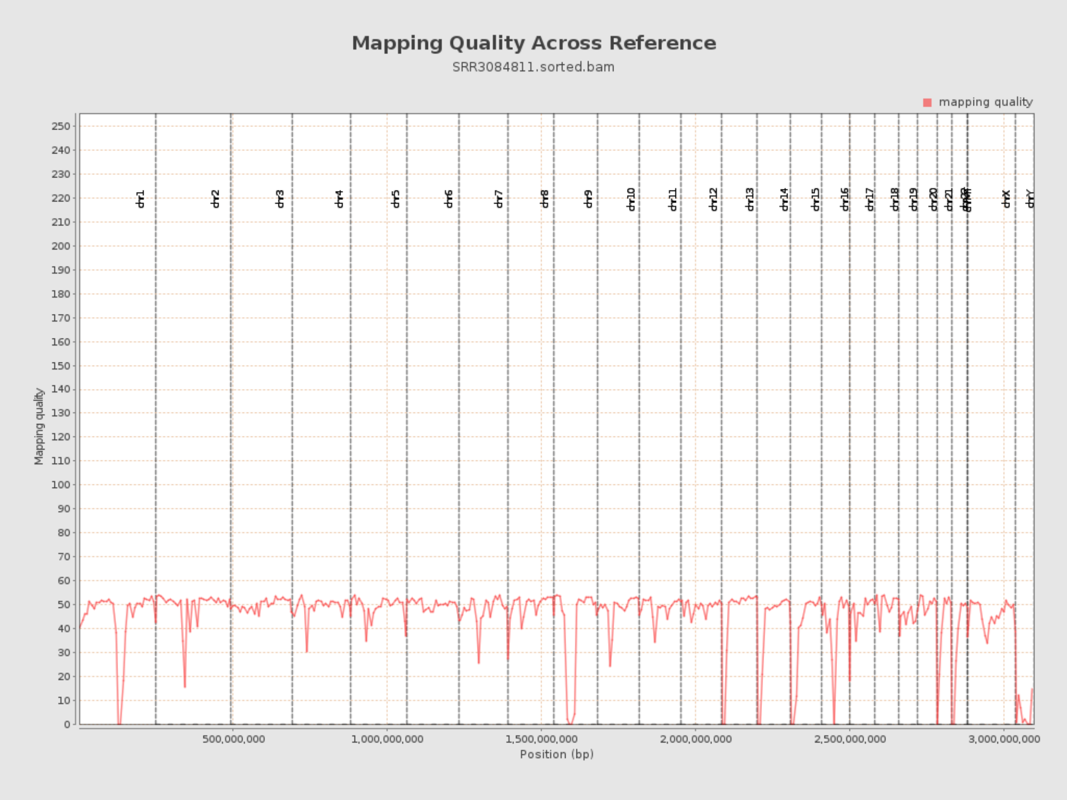
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram