Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 18:02:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084858.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_SRR3084858 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084858.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 18:02:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084858.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,308,651
Mapped reads	1,921,634 / 83.24%
Unmapped reads	387,017 / 16.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,718 / 0.77%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	116,561 / 5.05%
Duplication rate	5.31%
Clipped reads	895,905 / 38.81%

2.2. ACGT Content

Number/percentage of A's	35,121,078 / 27.56%
Number/percentage of C's	23,522,231 / 18.46%
Number/percentage of T's	40,453,571 / 31.75%
Number/percentage of G's	28,304,791 / 22.21%
Number/percentage of N's	18,280 / 0.01%
GC Percentage	40.67%

2.3. Coverage

Mean	0.0412

Standard Deviation	0.3181

2.4. Mapping Quality

Mean Mapping Quality	46.75

2.5. Mismatches and indels

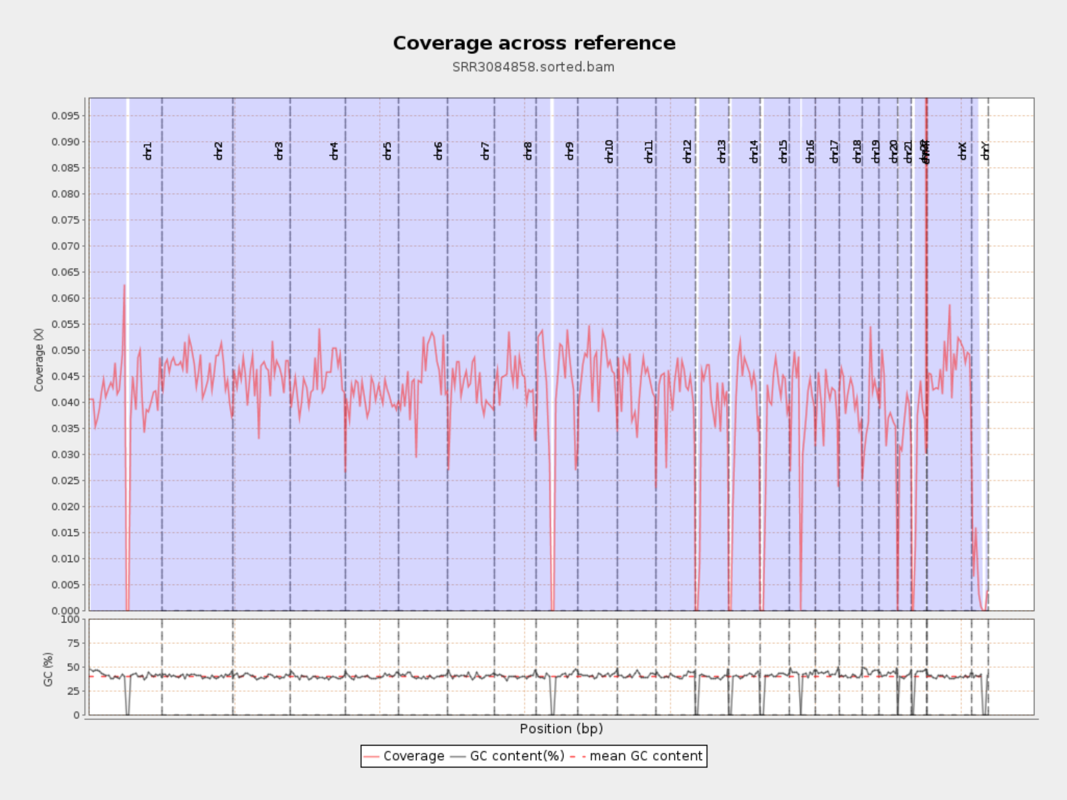
General error rate	0.87%
Mismatches	1,085,336
Insertions	9,605
Mapped reads with at least one insertion	0.5%
Deletions	26,285
Mapped reads with at least one deletion	1.35%
Homopolymer indels	47.68%

2.6. Chromosome stats

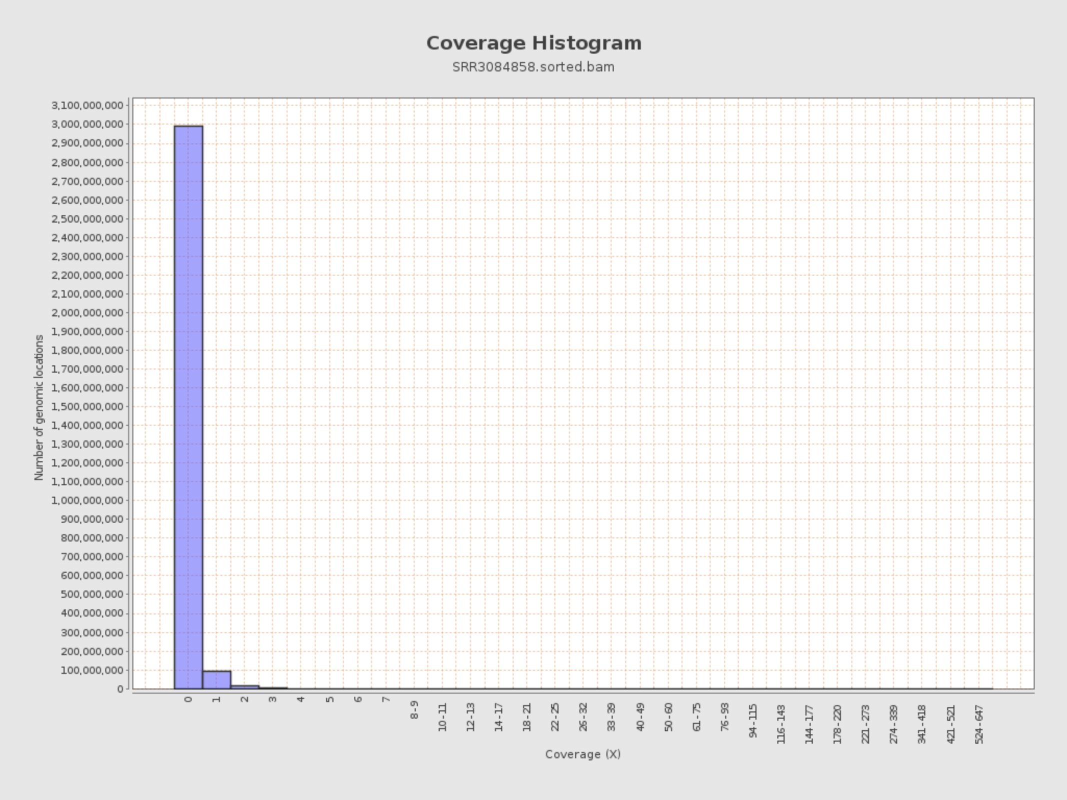
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9925982	0.0398	0.5631
chr2	243199373	11256253	0.0463	0.318
chr3	198022430	8947859	0.0452	0.2458
chr4	191154276	8448355	0.0442	0.2493
chr5	180915260	7447112	0.0412	0.2365
chr6	171115067	7687970	0.0449	0.2538
chr7	159138663	6770044	0.0425	0.2733

chr8	146364022	6467451	0.0442	0.4603
chr9	141213431	5717336	0.0405	0.2893
chr10	135534747	6339645	0.0468	0.3069
chr11	135006516	5822665	0.0431	0.2803
chr12	133851895	5665278	0.0423	0.2418
chr13	115169878	4022357	0.0349	0.2169
chr14	107349540	4021291	0.0375	0.2385
chr15	102531392	3591004	0.035	0.2182
chr16	90354753	3408105	0.0377	0.2359
chr17	81195210	3214224	0.0396	0.2407
chr18	78077248	3212139	0.0411	0.4904
chr19	59128983	2345830	0.0397	0.3964
chr20	63025520	2402277	0.0381	0.2344
chr21	48129895	1542487	0.032	0.2178
chr22	51304566	1373772	0.0268	0.19
chrMT	16571	270305	16.3119	8.294
chrX	155270560	7255742	0.0467	0.2606
chrY	59373566	310390	0.0052	0.114

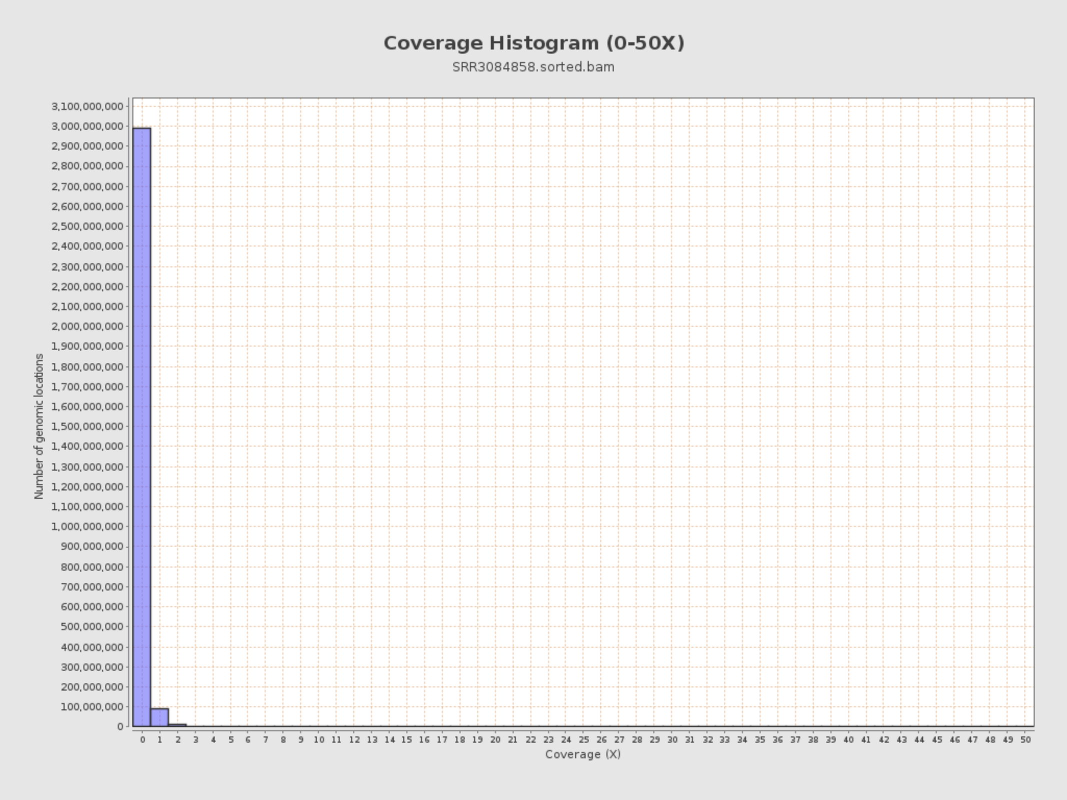
3. Results : Coverage across reference



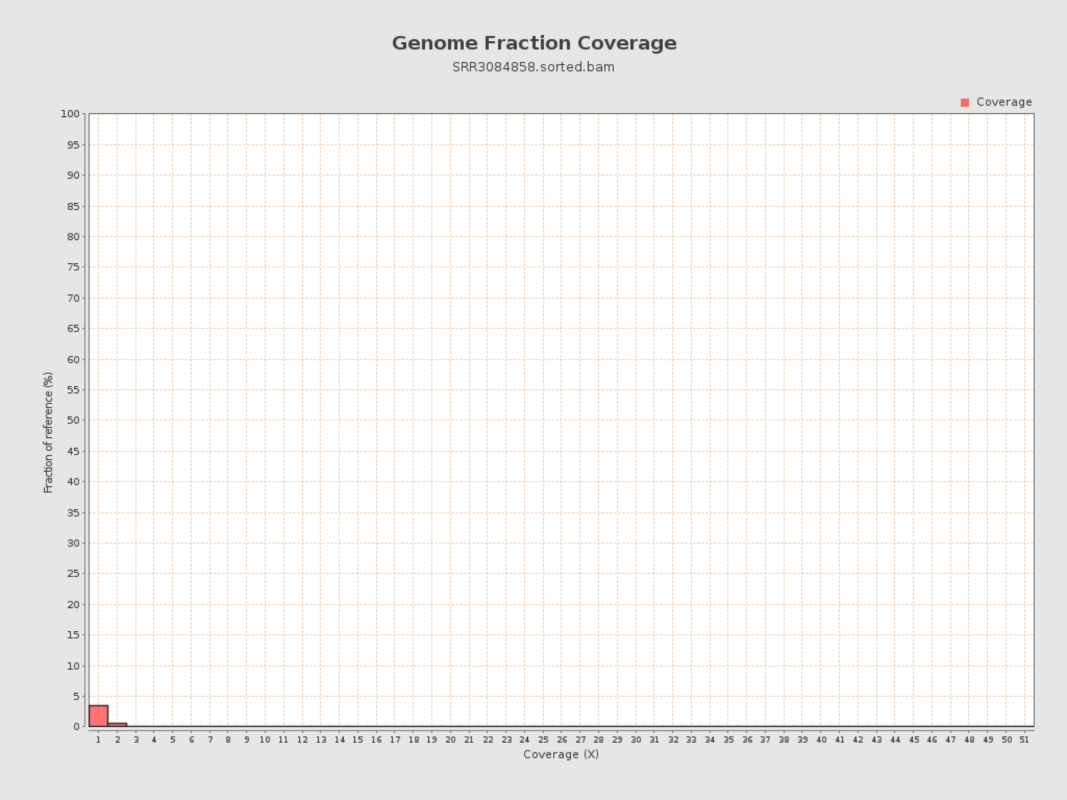
4. Results : Coverage Histogram



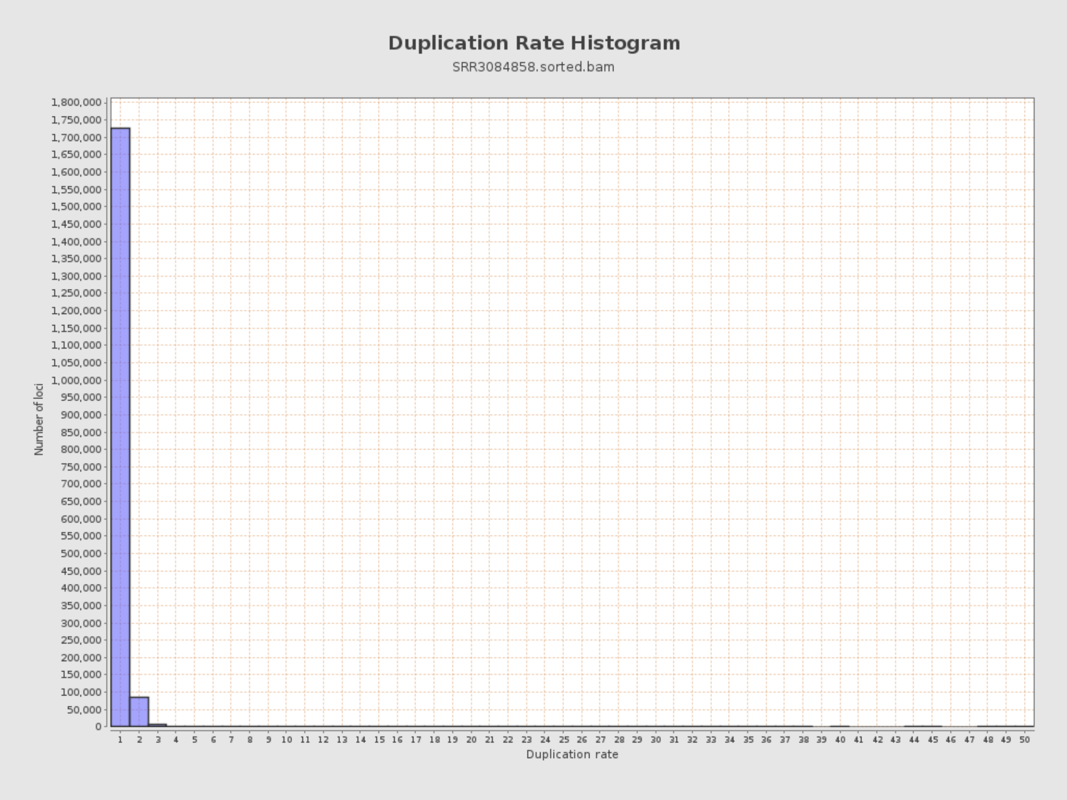
5. Results : Coverage Histogram (0-50X)



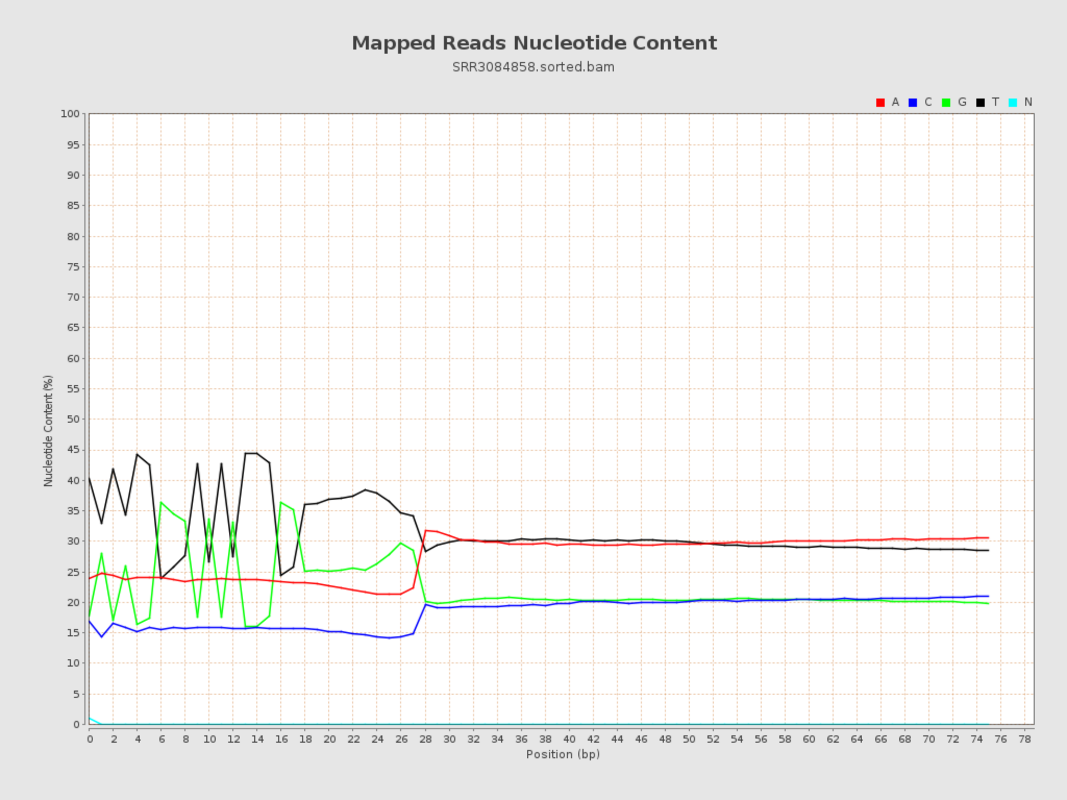
6. Results : Genome Fraction Coverage



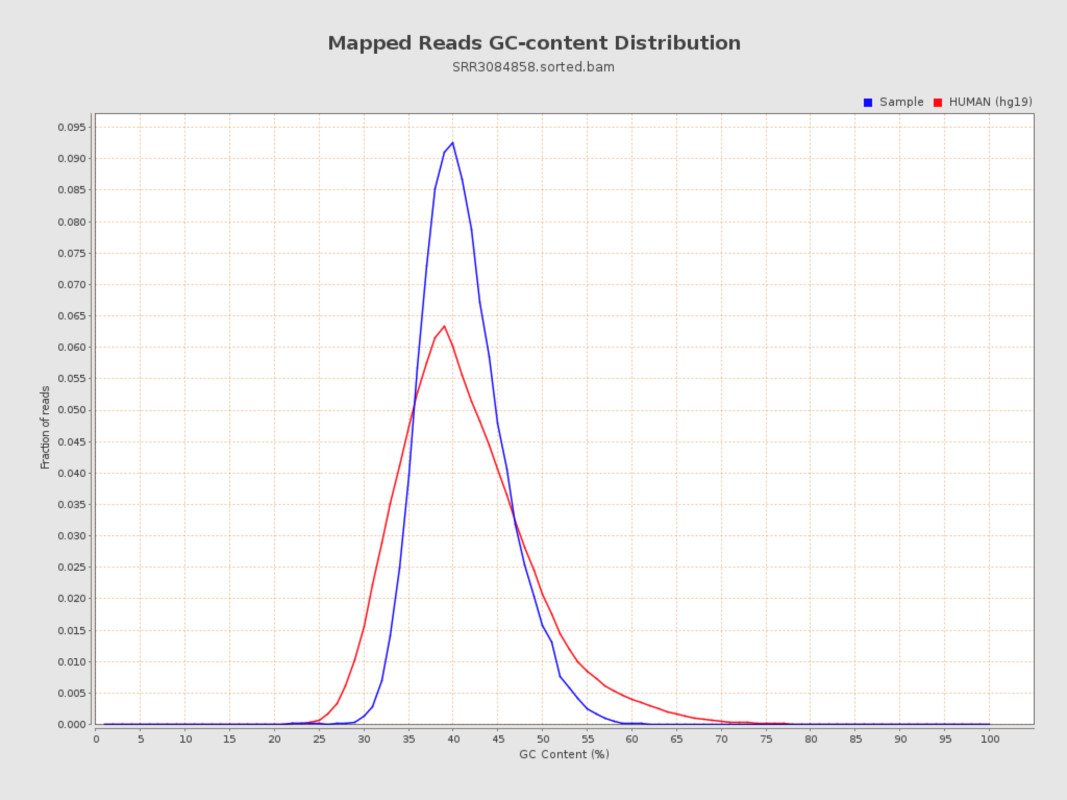
7. Results : Duplication Rate Histogram



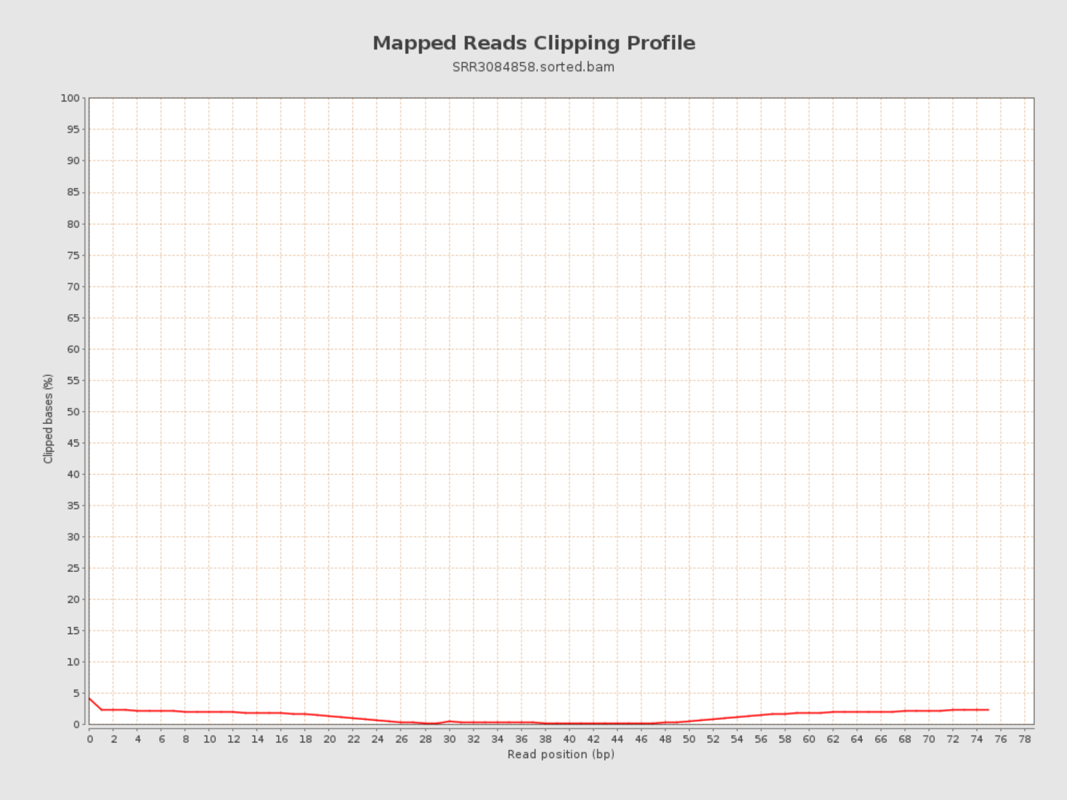
8. Results : Mapped Reads Nucleotide Content



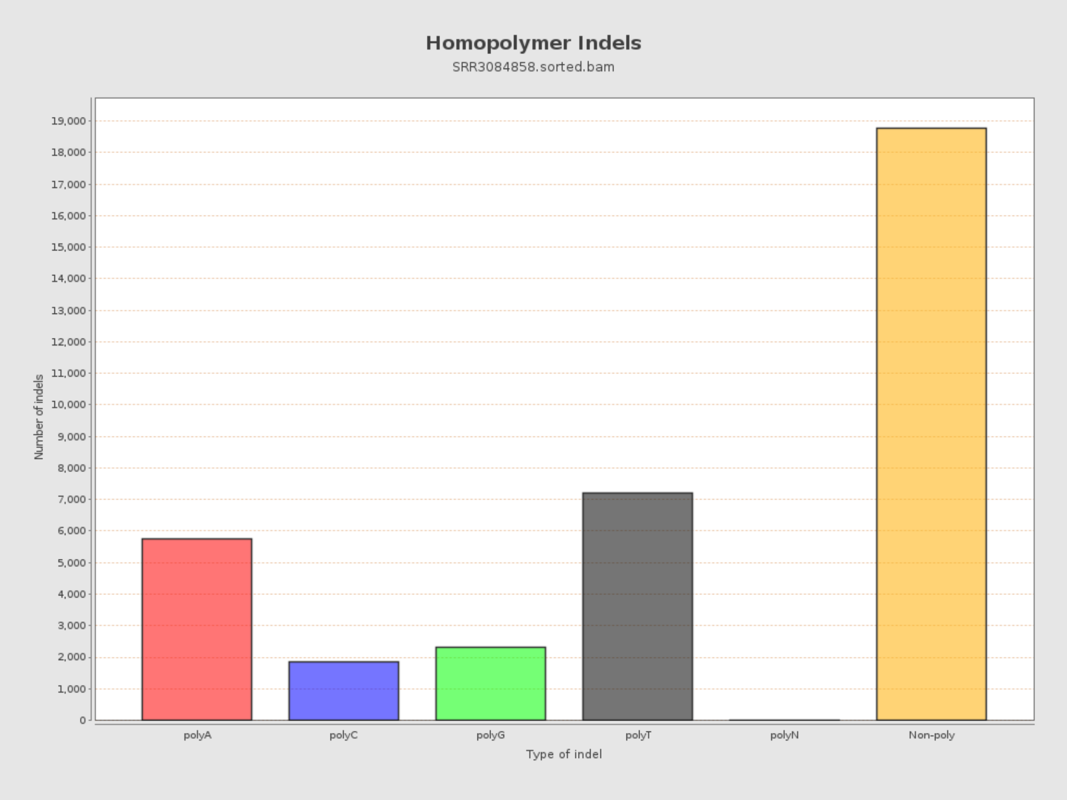
9. Results : Mapped Reads GC-content Distribution



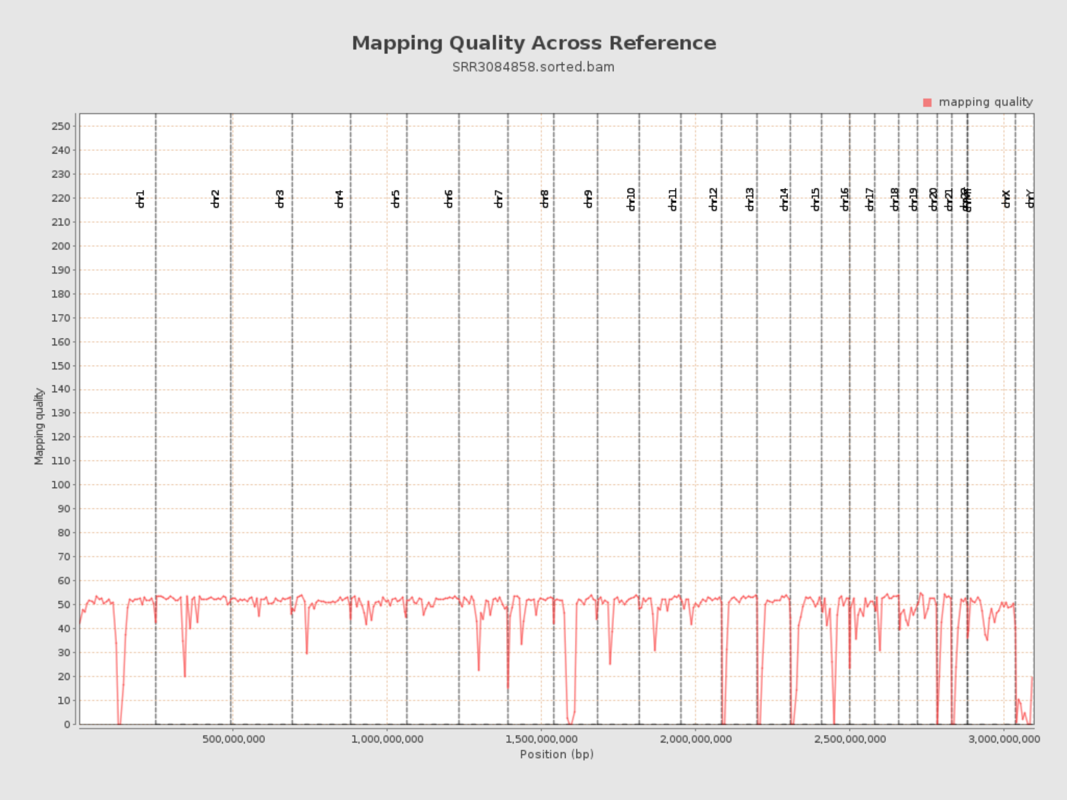
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram