Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 16:05:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084823.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_SRR3084823 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084823.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 16:05:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084823.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,001,890
Mapped reads	1,850,326 / 92.43%
Unmapped reads	151,564 / 7.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,688 / 0.93%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	80,667 / 4.03%
Duplication rate	3.74%
Clipped reads	739,148 / 36.92%

2.2. ACGT Content

Number/percentage of A's	35,173,151 / 28.07%
Number/percentage of C's	22,880,289 / 18.26%
Number/percentage of T's	40,153,092 / 32.04%
Number/percentage of G's	27,085,276 / 21.61%
Number/percentage of N's	17,877 / 0.01%
GC Percentage	39.87%

2.3. Coverage

Mean	0.0405

Standard Deviation	0.2916

2.4. Mapping Quality

Mean Mapping Quality	46.31

2.5. Mismatches and indels

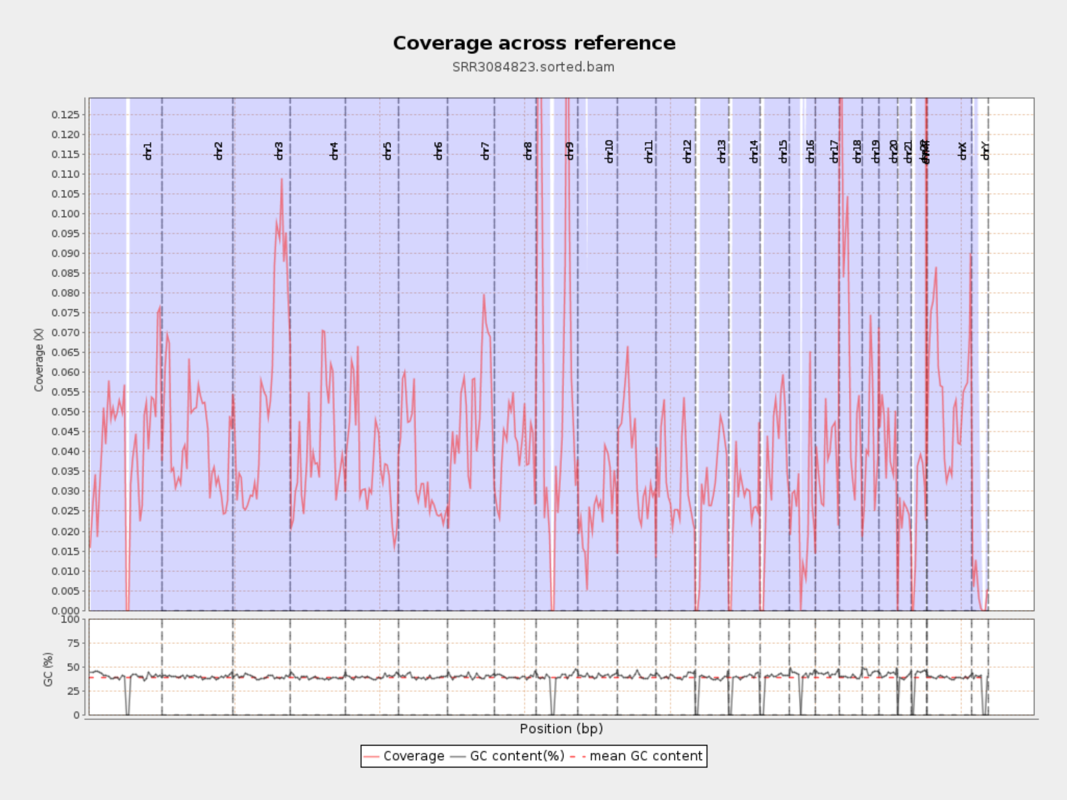
General error rate	0.8%
Mismatches	983,211
Insertions	10,139
Mapped reads with at least one insertion	0.54%
Deletions	29,884
Mapped reads with at least one deletion	1.6%
Homopolymer indels	49.09%

2.6. Chromosome stats

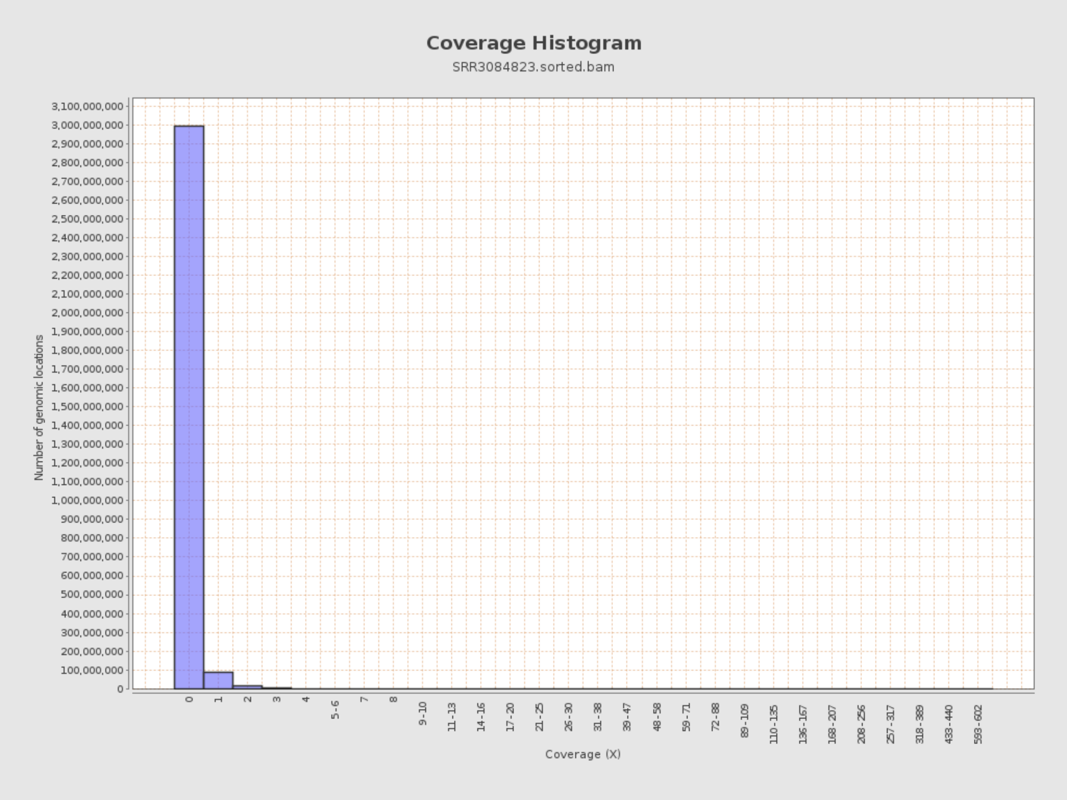
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10292677	0.0413	0.3579
chr2	243199373	10397044	0.0428	0.4123
chr3	198022430	10797102	0.0545	0.2718
chr4	191154276	7847231	0.0411	0.2374
chr5	180915260	6742589	0.0373	0.2258
chr6	171115067	6045864	0.0353	0.2323
chr7	159138663	8074530	0.0507	0.3225

chr8	146364022	5955589	0.0407	0.3339
chr9	141213431	8918708	0.0632	0.3606
chr10	135534747	3472940	0.0256	0.207
chr11	135006516	5146290	0.0381	0.2735
chr12	133851895	4430063	0.0331	0.2122
chr13	115169878	3378483	0.0293	0.1982
chr14	107349540	2727487	0.0254	0.1857
chr15	102531392	3725639	0.0363	0.2271
chr16	90354753	2198834	0.0243	0.1892
chr17	81195210	3064614	0.0377	0.2309
chr18	78077248	5514325	0.0706	0.5229
chr19	59128983	2543063	0.043	0.3097
chr20	63025520	2746762	0.0436	0.2431
chr21	48129895	1059658	0.022	0.179
chr22	51304566	1244773	0.0243	0.1763
chrMT	16571	236688	14.2833	7.812
chrX	155270560	8523309	0.0549	0.2825
chrY	59373566	275640	0.0046	0.1107

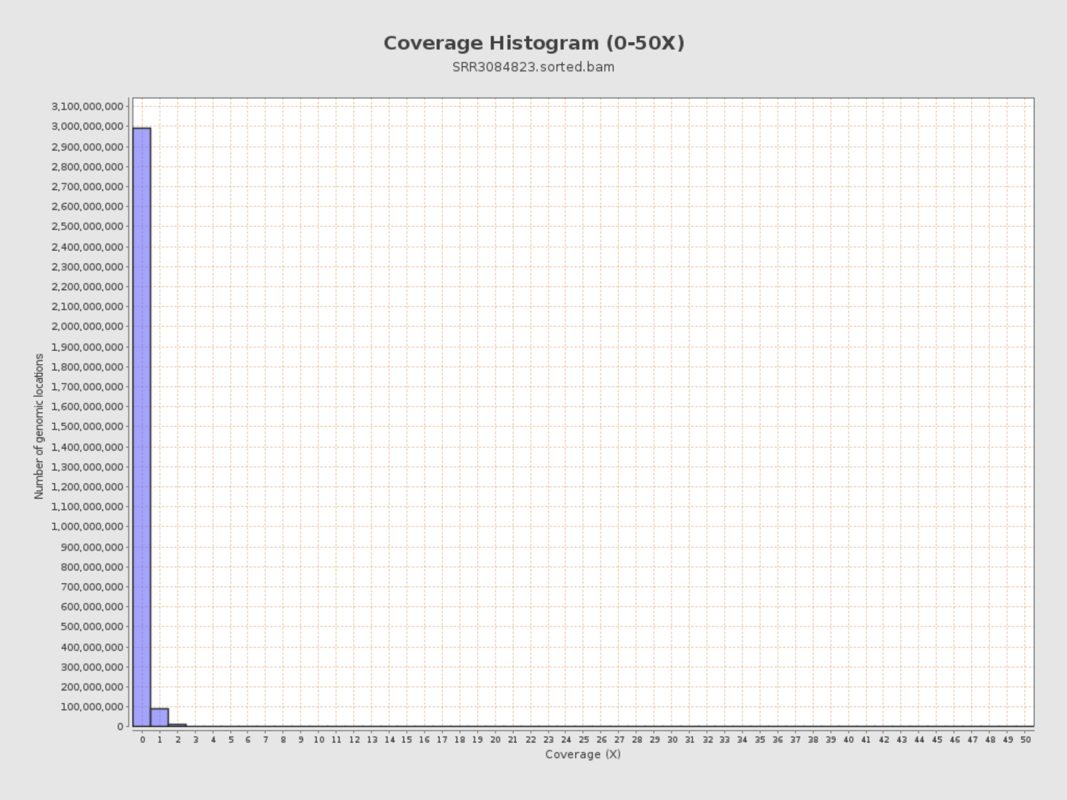
3. Results : Coverage across reference



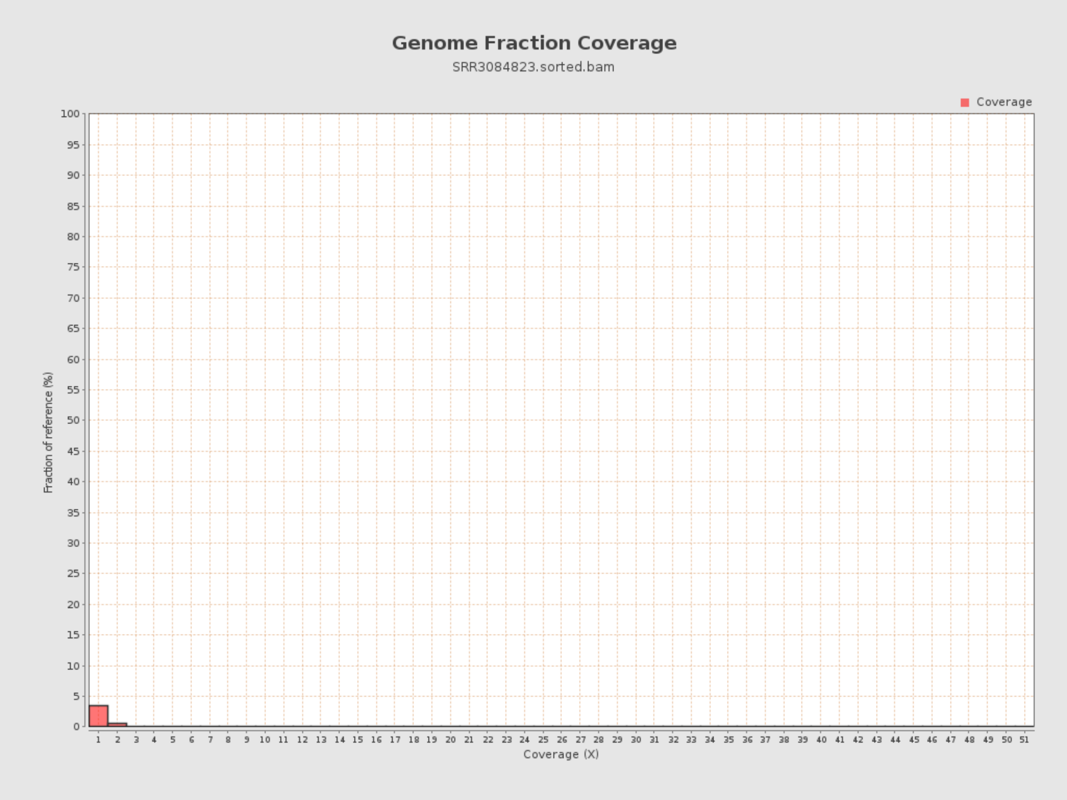
4. Results : Coverage Histogram



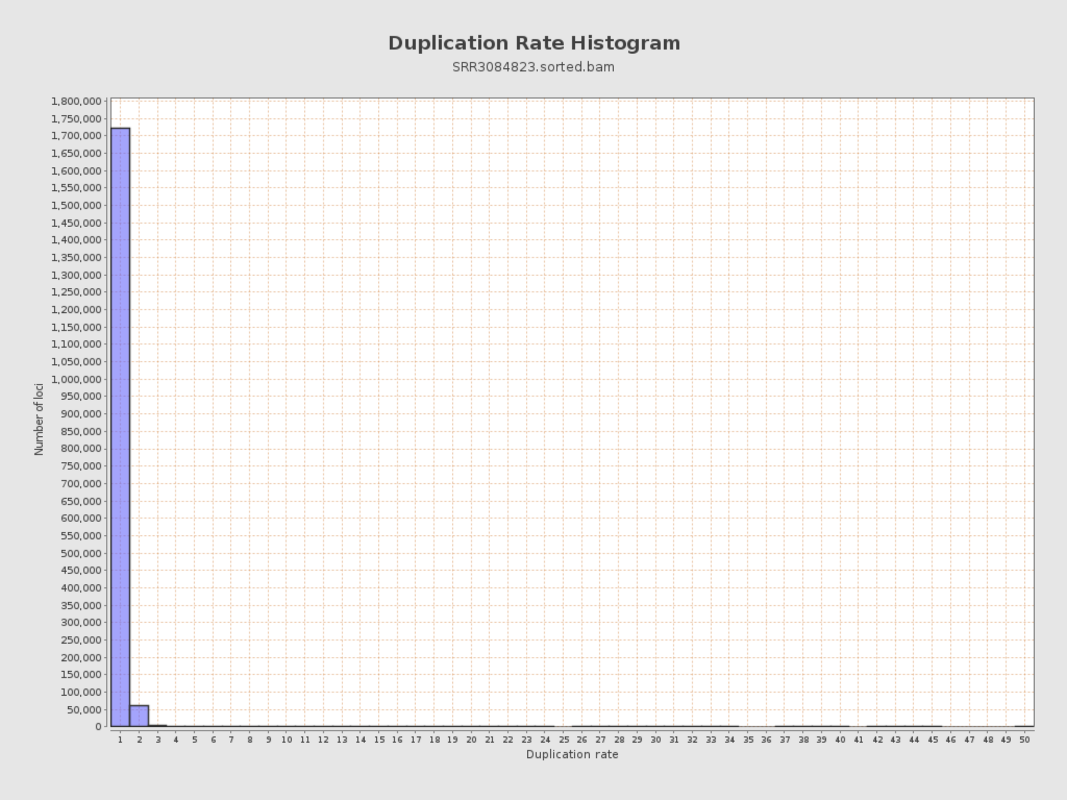
5. Results : Coverage Histogram (0-50X)



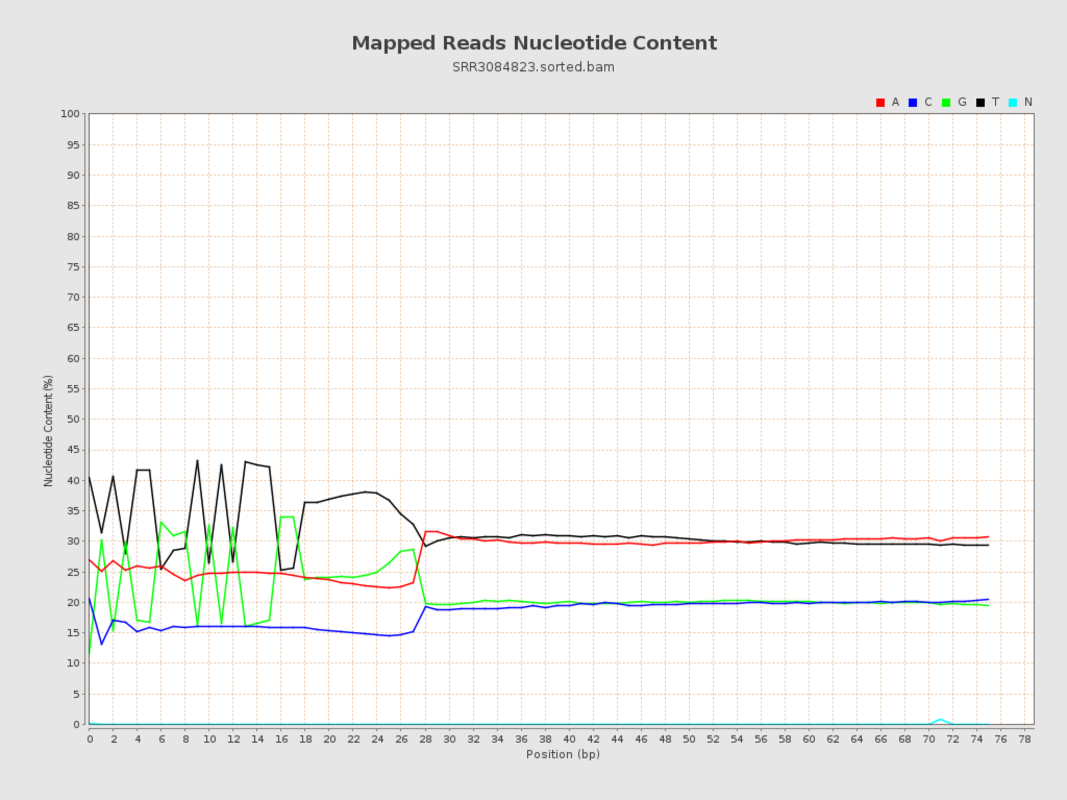
6. Results : Genome Fraction Coverage



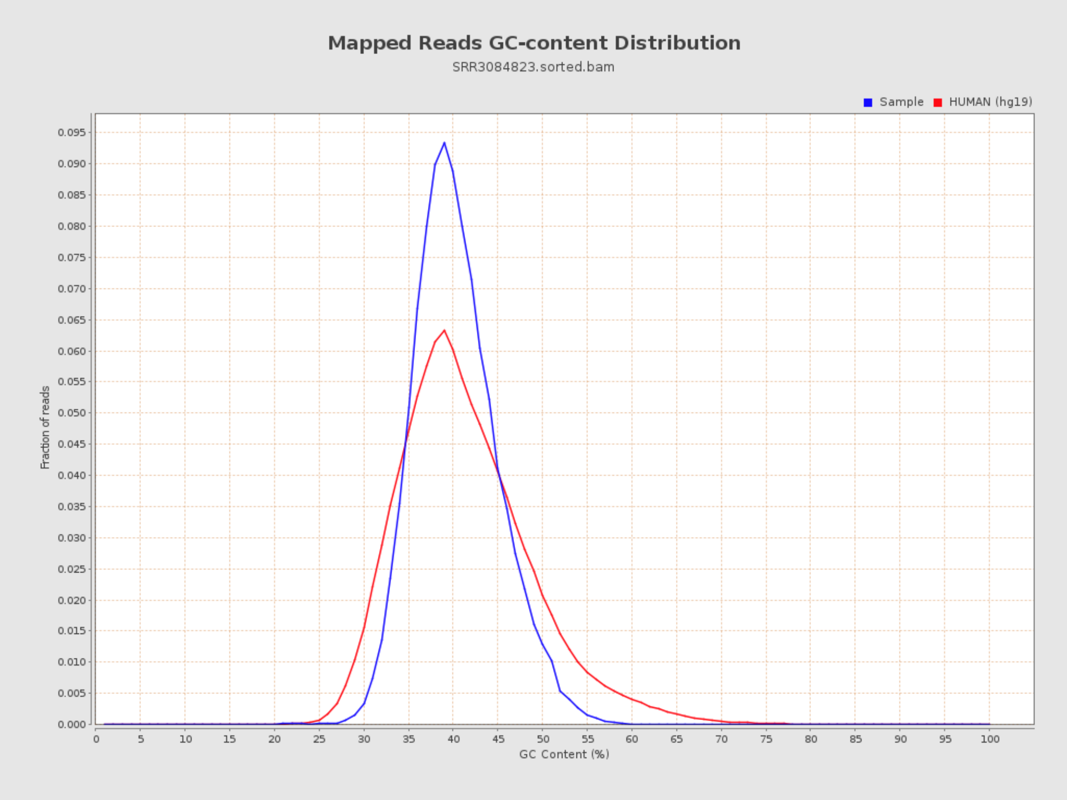
7. Results : Duplication Rate Histogram



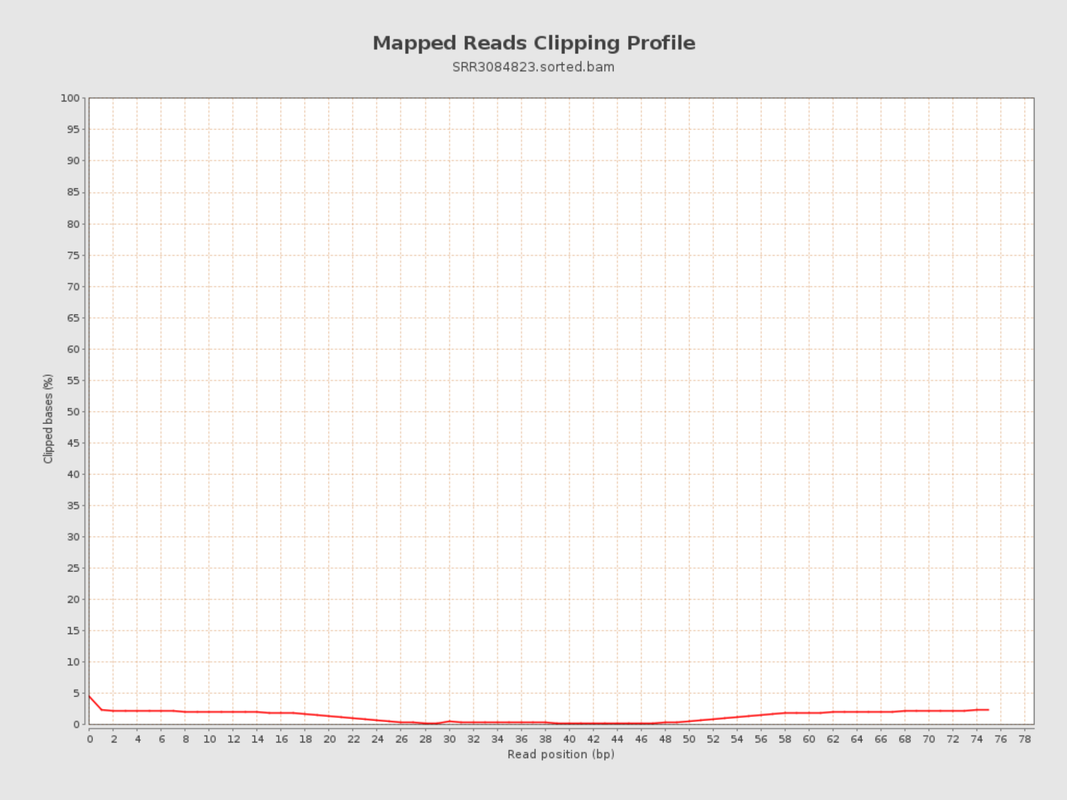
8. Results : Mapped Reads Nucleotide Content



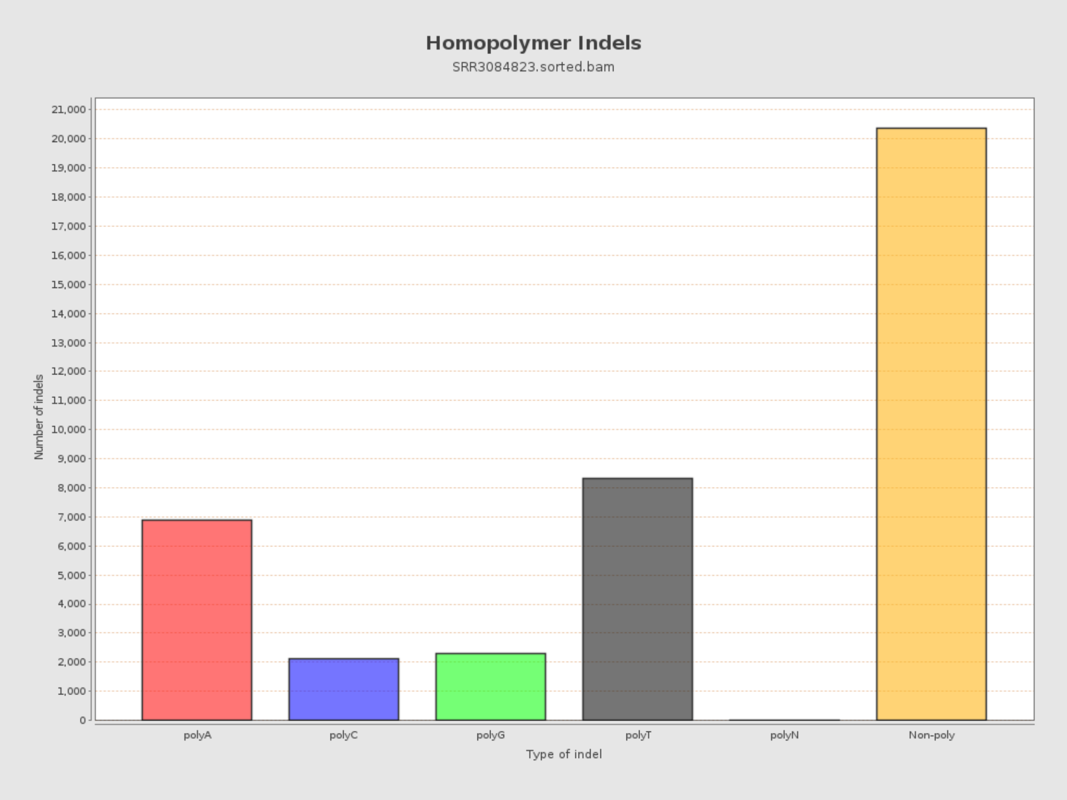
9. Results : Mapped Reads GC-content Distribution



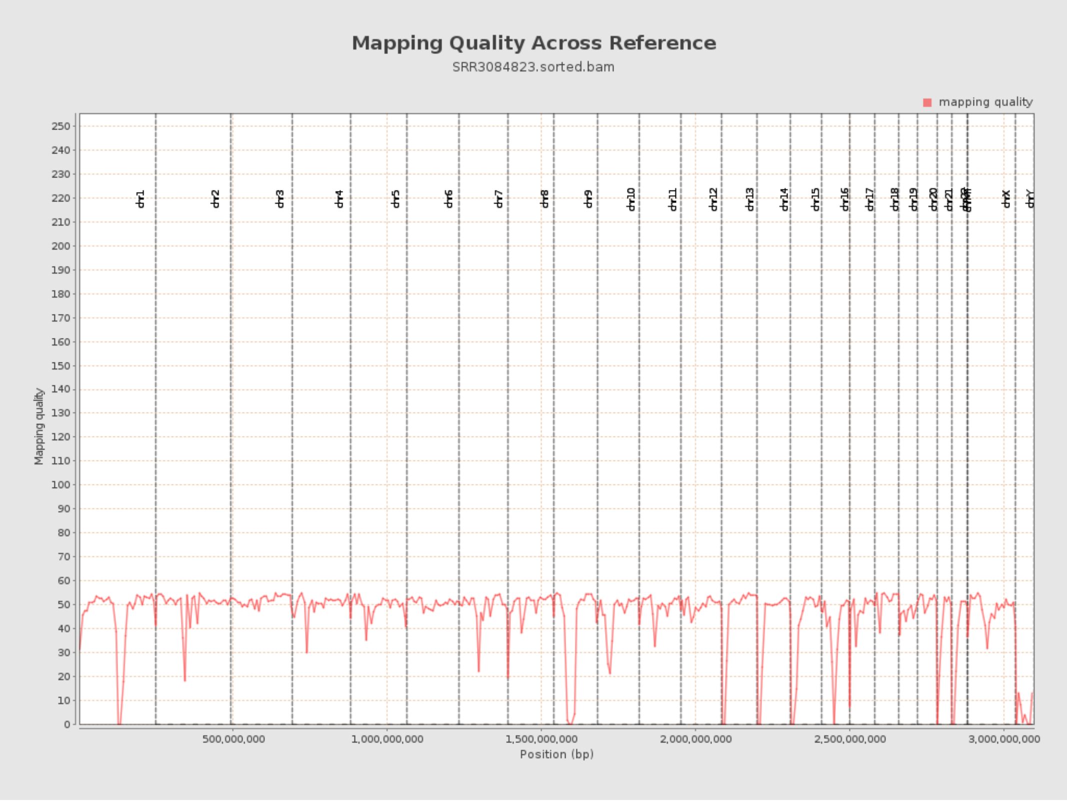
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram