Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 18:56:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084876.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_SRR3084876 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084876.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 18:56:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084876.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,630,326
Mapped reads	2,337,779 / 88.88%
Unmapped reads	292,547 / 11.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,685 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	104,574 / 3.98%
Duplication rate	3.87%
Clipped reads	793,289 / 30.16%

2.2. ACGT Content

Number/percentage of A's	47,104,368 / 29.12%
Number/percentage of C's	29,544,730 / 18.27%
Number/percentage of T's	51,917,077 / 32.1%
Number/percentage of G's	33,148,704 / 20.49%
Number/percentage of N's	25,780 / 0.02%
GC Percentage	38.76%

2.3. Coverage

Mean	0.0523

Standard Deviation	0.3626

2.4. Mapping Quality

Mean Mapping Quality	47.72

2.5. Mismatches and indels

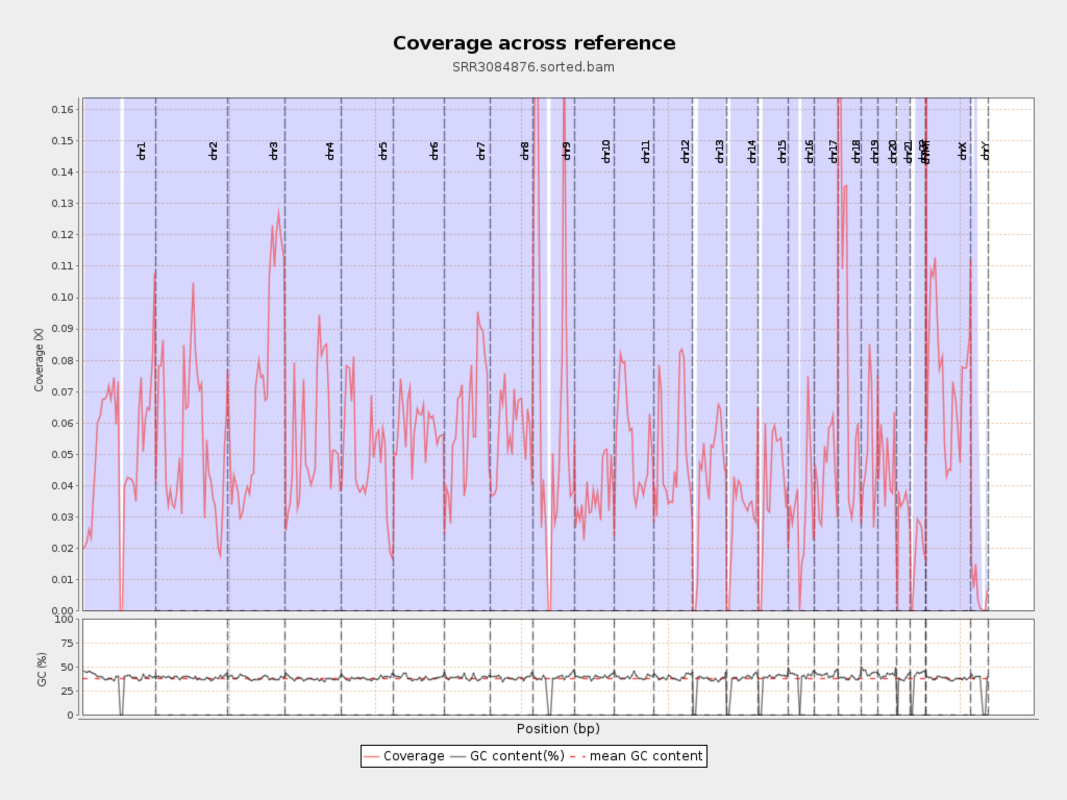
General error rate	0.81%
Mismatches	1,292,618
Insertions	12,678
Mapped reads with at least one insertion	0.54%
Deletions	34,371
Mapped reads with at least one deletion	1.45%
Homopolymer indels	49.13%

2.6. Chromosome stats

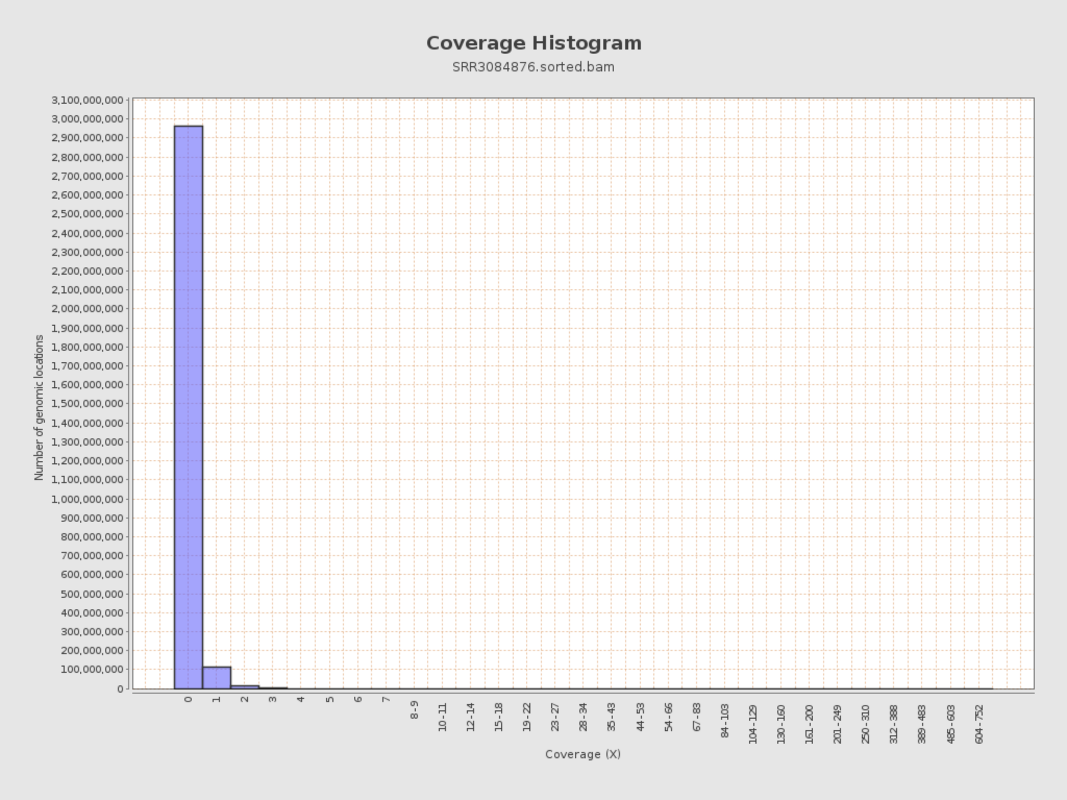
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12895804	0.0517	0.5901
chr2	243199373	12995987	0.0534	0.4051
chr3	198022430	13821408	0.0698	0.3057
chr4	191154276	10410323	0.0545	0.2707
chr5	180915260	8938439	0.0494	0.2622
chr6	171115067	10113316	0.0591	0.2853
chr7	159138663	9649033	0.0606	0.3929

chr8	146364022	8286427	0.0566	0.5861
chr9	141213431	9769192	0.0692	0.3979
chr10	135534747	4961759	0.0366	0.2688
chr11	135006516	7257015	0.0538	0.3275
chr12	133851895	6751555	0.0504	0.2605
chr13	115169878	4895267	0.0425	0.236
chr14	107349540	3251893	0.0303	0.2099
chr15	102531392	4033807	0.0393	0.2284
chr16	90354753	2776485	0.0307	0.2205
chr17	81195210	3720500	0.0458	0.2541
chr18	78077248	6860862	0.0879	0.6087
chr19	59128983	3067416	0.0519	0.3969
chr20	63025520	2962113	0.047	0.2559
chr21	48129895	1502222	0.0312	0.2129
chr22	51304566	923890	0.018	0.1513
chrMT	16571	58880	3.5532	2.6248
chrX	155270560	11560897	0.0745	0.3323
chrY	59373566	336871	0.0057	0.1193

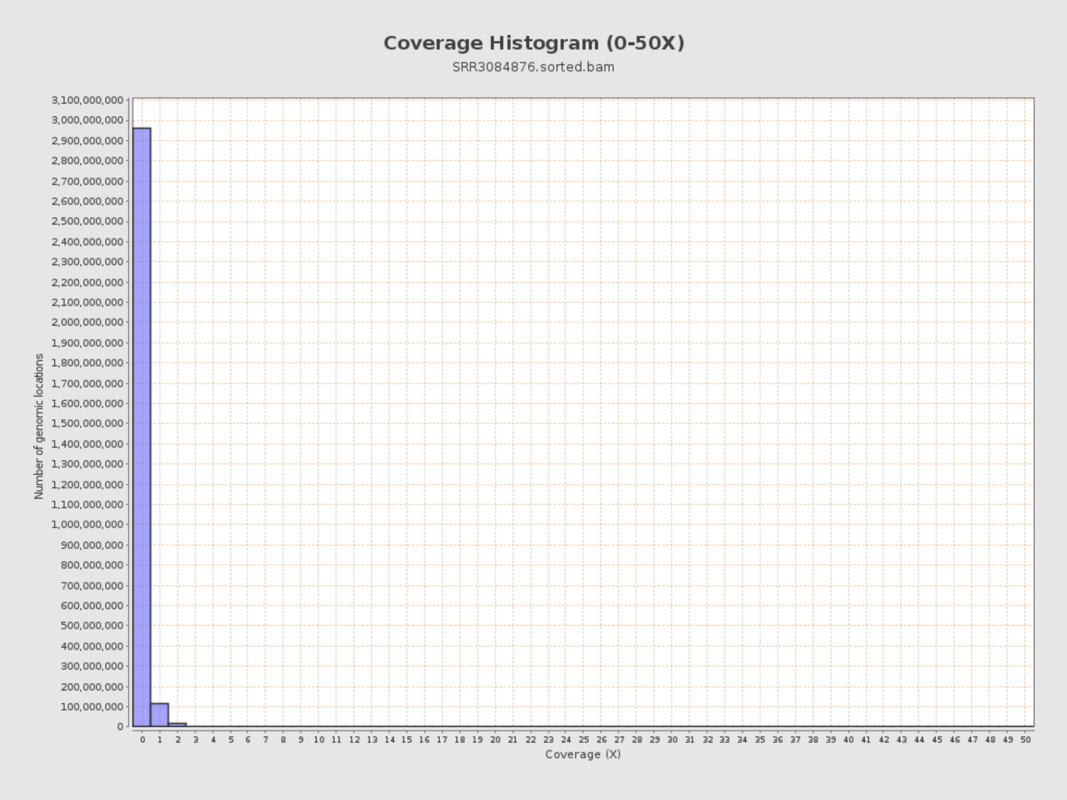
3. Results : Coverage across reference



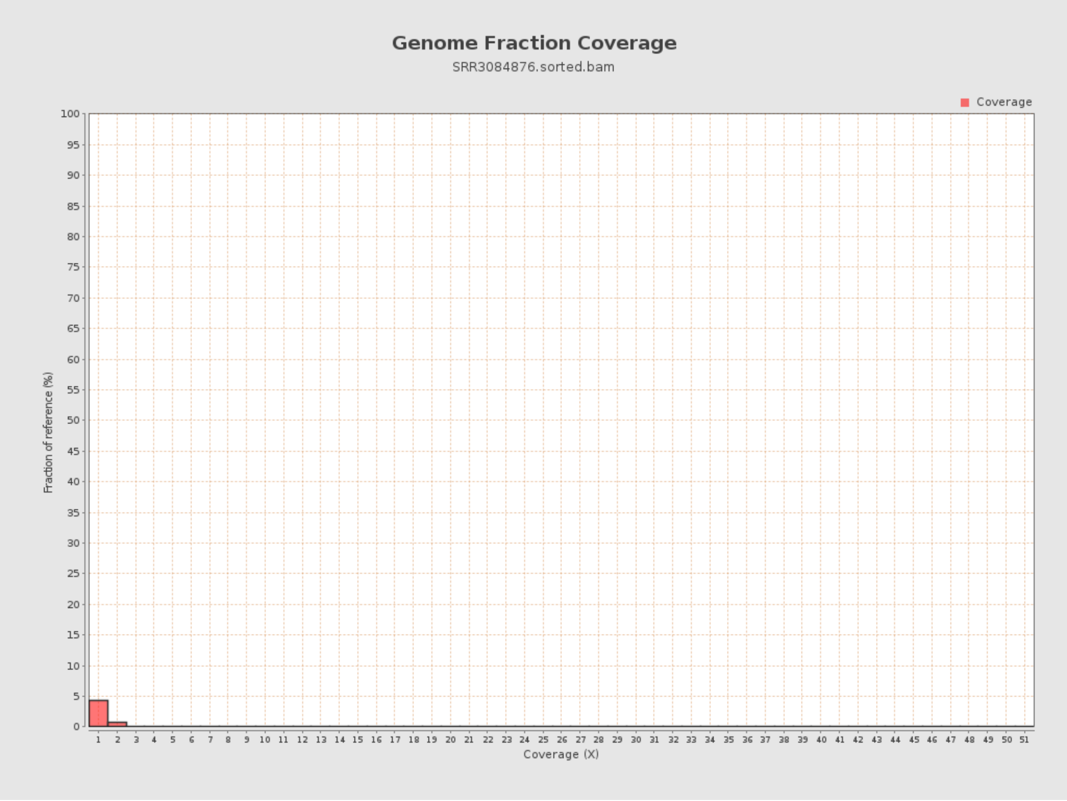
4. Results : Coverage Histogram



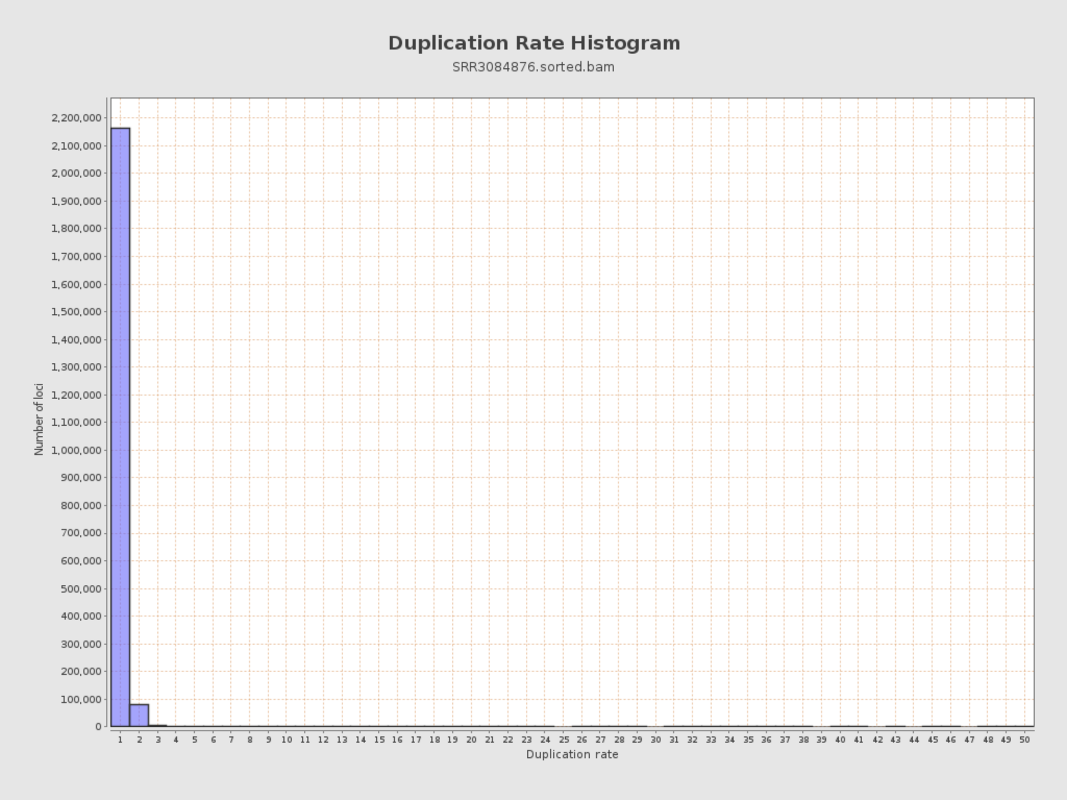
5. Results : Coverage Histogram (0-50X)



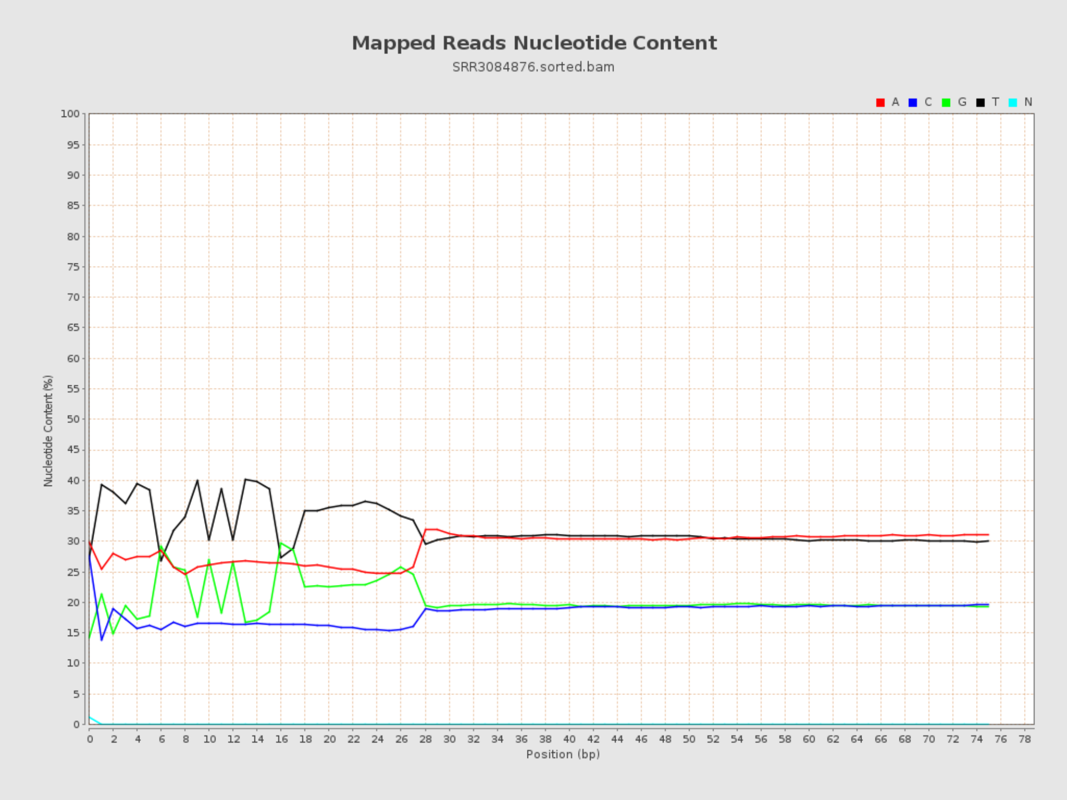
6. Results : Genome Fraction Coverage



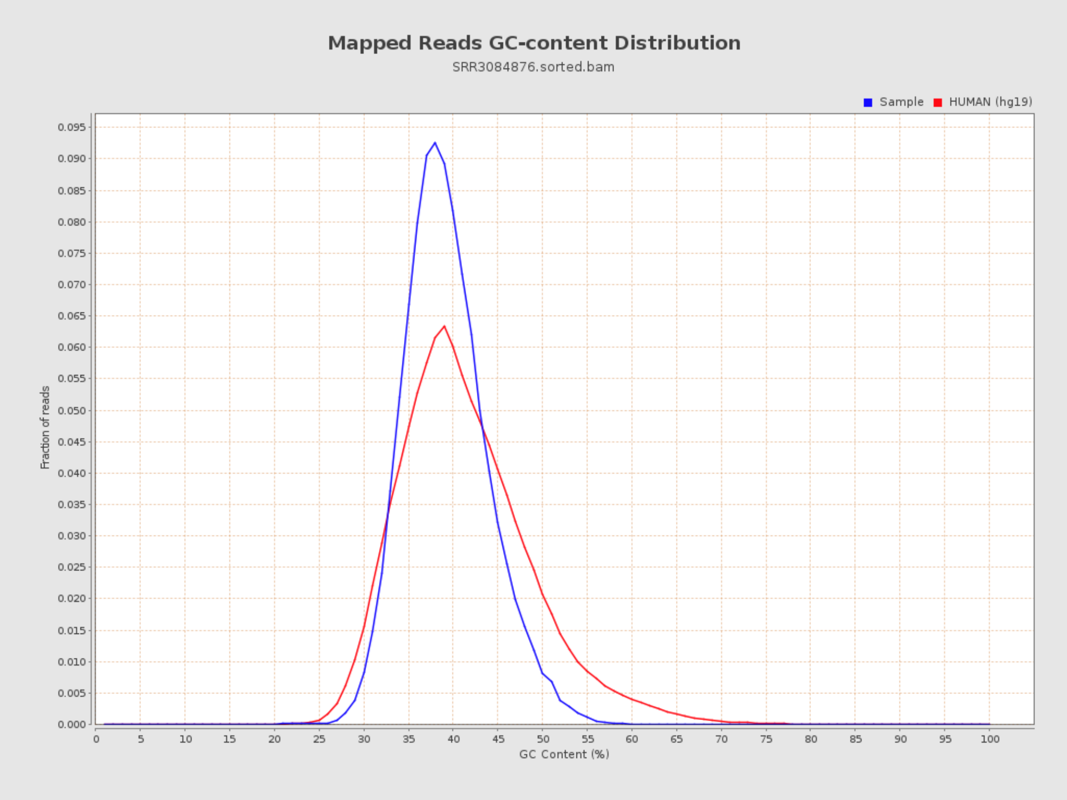
7. Results : Duplication Rate Histogram



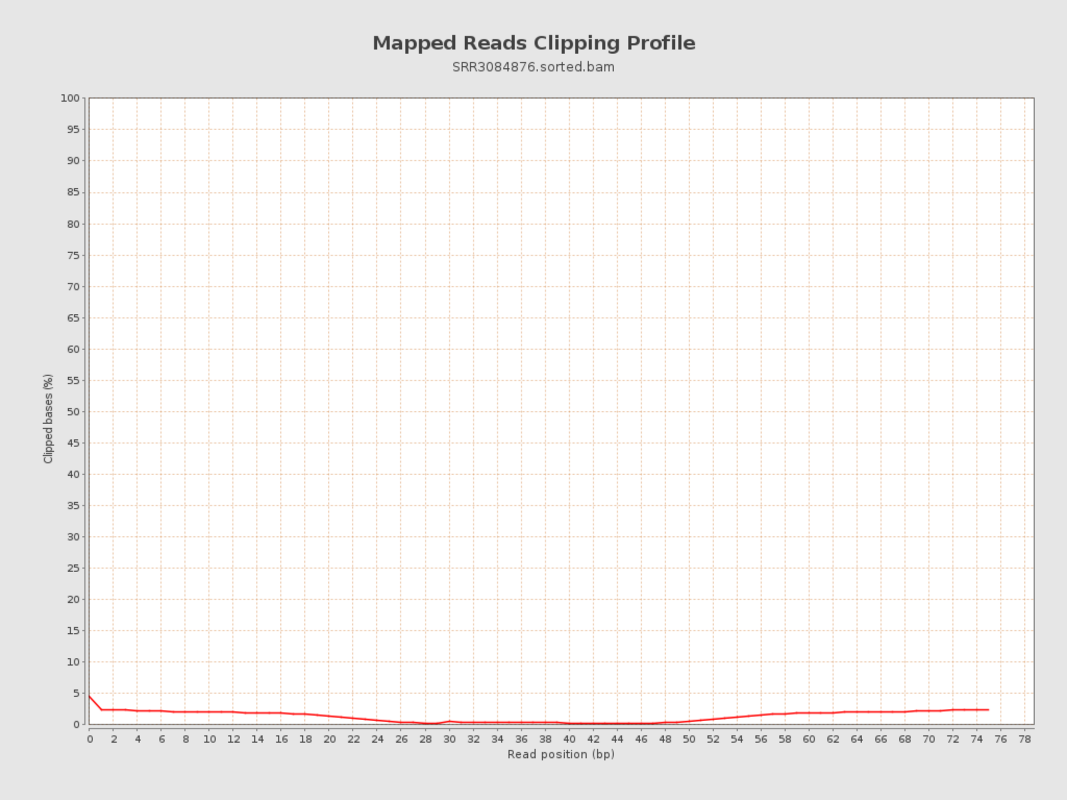
8. Results : Mapped Reads Nucleotide Content



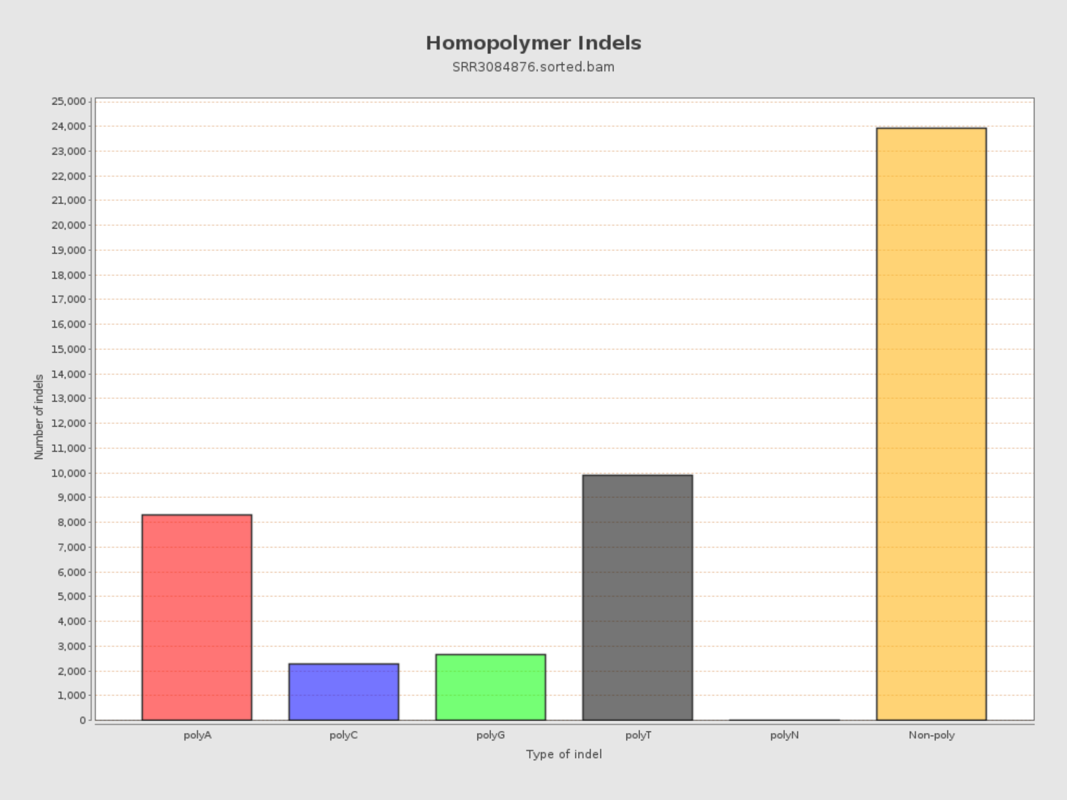
9. Results : Mapped Reads GC-content Distribution



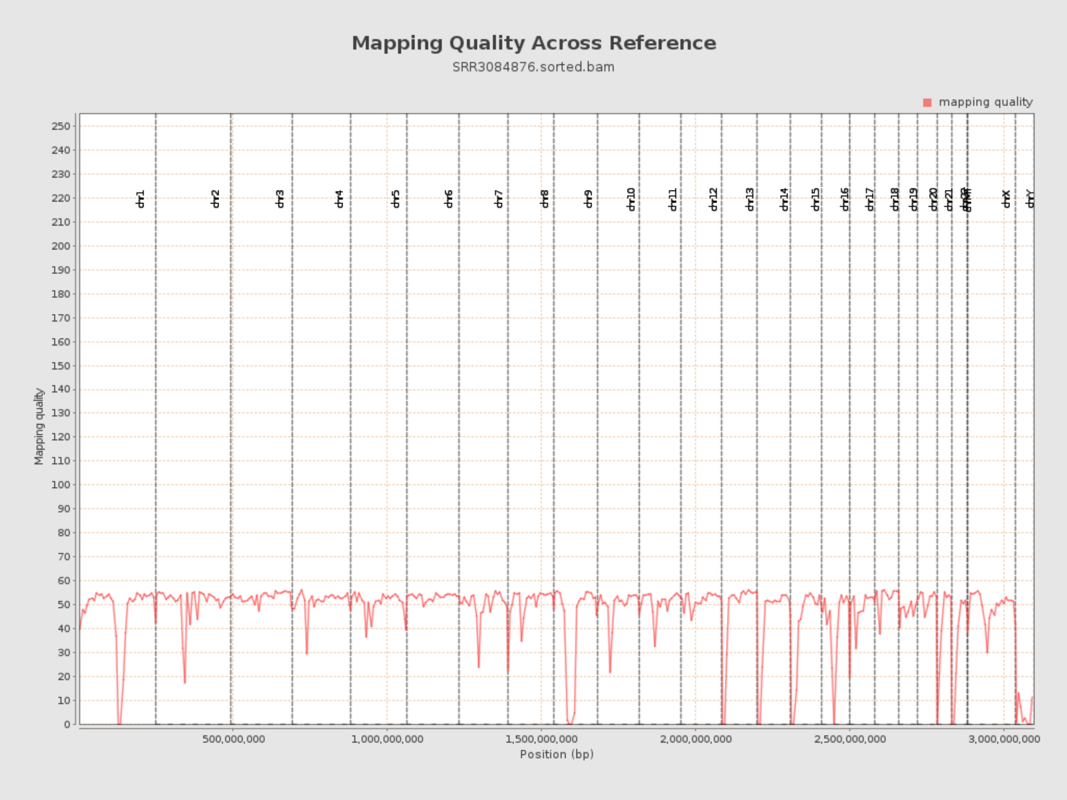
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram