Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 07:55:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084255.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_SRR3084255 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084255.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 07:55:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084255.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,476,137
Mapped reads	2,209,355 / 63.56%
Unmapped reads	1,266,782 / 36.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,259 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	90,213 / 2.6%
Duplication rate	3.46%
Clipped reads	1,233,274 / 35.48%

2.2. ACGT Content

Number/percentage of A's	39,157,348 / 27.85%
Number/percentage of C's	27,419,044 / 19.5%
Number/percentage of T's	42,302,057 / 30.08%
Number/percentage of G's	31,731,958 / 22.57%
Number/percentage of N's	1,524 / 0%
GC Percentage	42.07%

2.3. Coverage

Mean	0.0454

Standard Deviation	0.3085

2.4. Mapping Quality

Mean Mapping Quality	45.56

2.5. Mismatches and indels

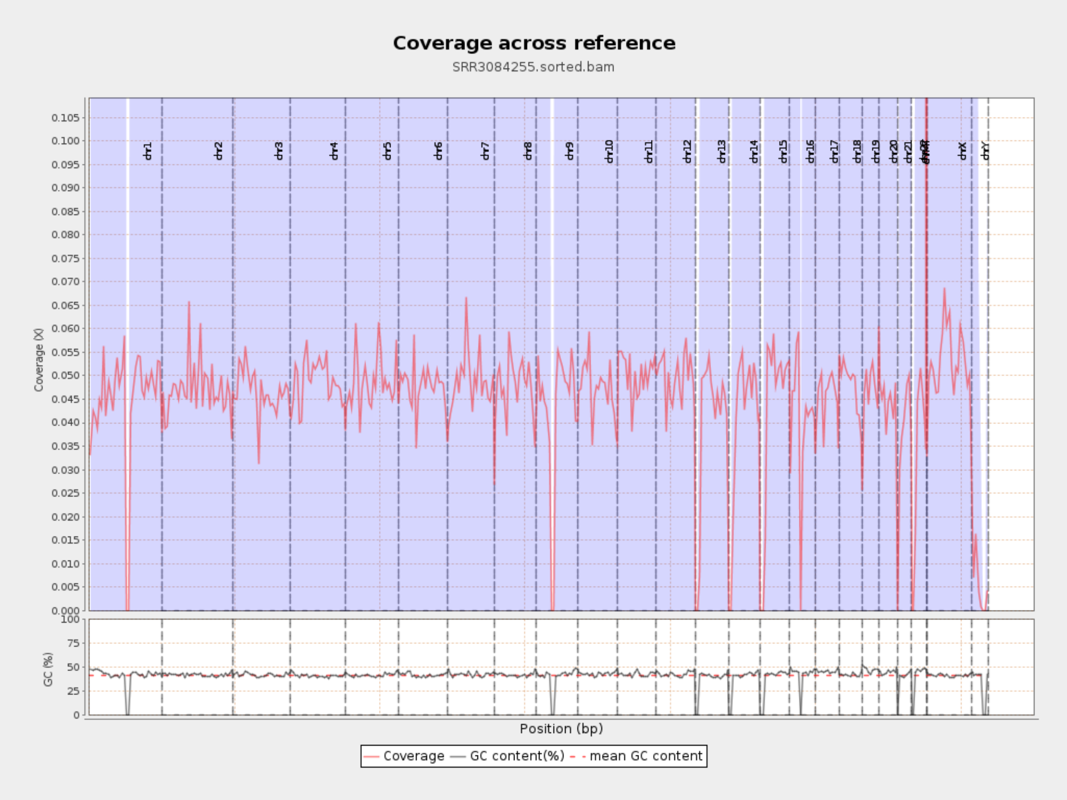
General error rate	0.82%
Mismatches	1,135,799
Insertions	10,202
Mapped reads with at least one insertion	0.46%
Deletions	28,748
Mapped reads with at least one deletion	1.29%
Homopolymer indels	46.43%

2.6. Chromosome stats

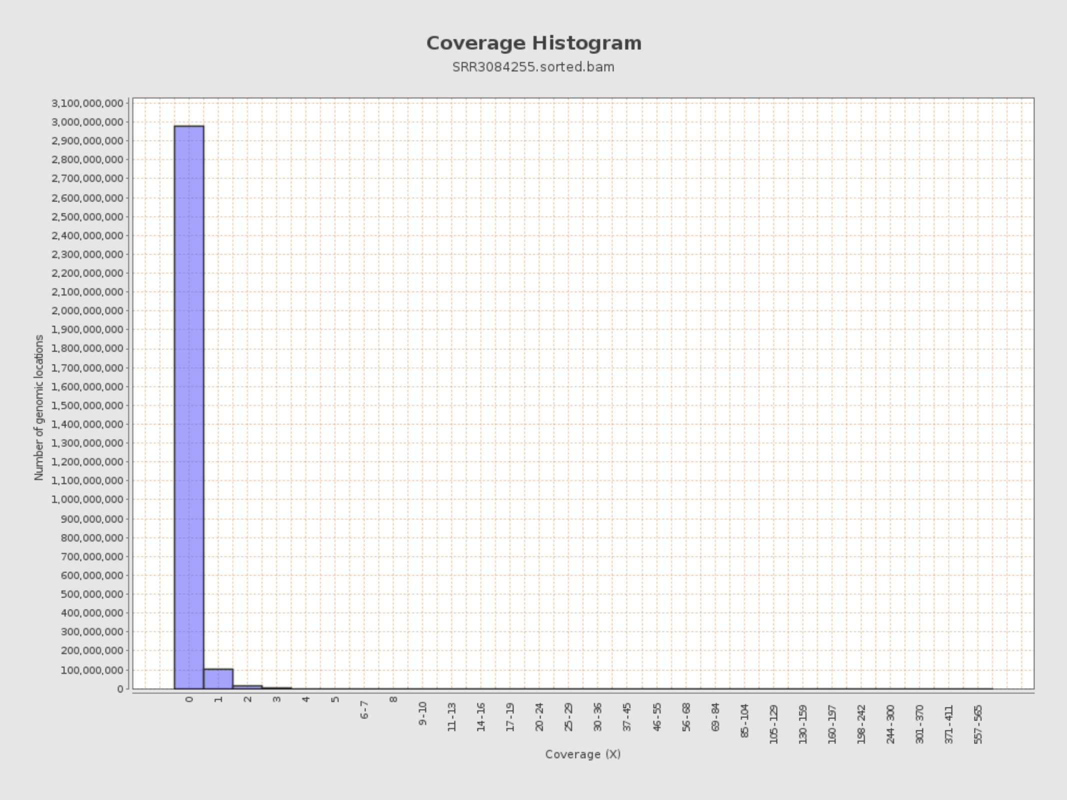
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11120258	0.0446	0.4283
chr2	243199373	11464036	0.0471	0.3968
chr3	198022430	9259683	0.0468	0.2464
chr4	191154276	9331501	0.0488	0.2599
chr5	180915260	8828274	0.0488	0.2527
chr6	171115067	8160982	0.0477	0.2829
chr7	159138663	7808683	0.0491	0.3746

chr8	146364022	7032422	0.048	0.3086
chr9	141213431	6032422	0.0427	0.2879
chr10	135534747	6453072	0.0476	0.308
chr11	135006516	6774683	0.0502	0.2864
chr12	133851895	6633958	0.0496	0.2573
chr13	115169878	4476408	0.0389	0.2283
chr14	107349540	4290029	0.04	0.2415
chr15	102531392	4346438	0.0424	0.2439
chr16	90354753	3680998	0.0407	0.2485
chr17	81195210	3674680	0.0453	0.2563
chr18	78077248	3771272	0.0483	0.5081
chr19	59128983	2807526	0.0475	0.3693
chr20	63025520	2760911	0.0438	0.2458
chr21	48129895	1777988	0.0369	0.2251
chr22	51304566	1604960	0.0313	0.2022
chrMT	16571	36036	2.1746	2.0104
chrX	155270560	8198606	0.0528	0.287
chrY	59373566	332008	0.0056	0.1141

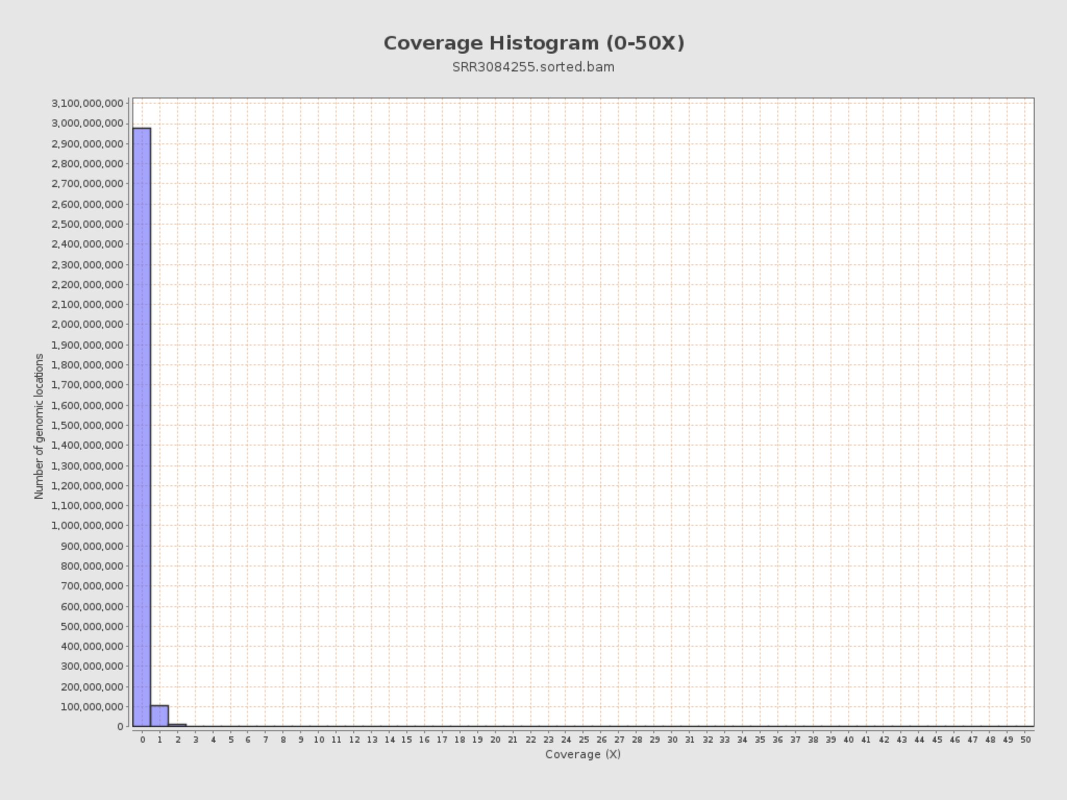
3. Results : Coverage across reference



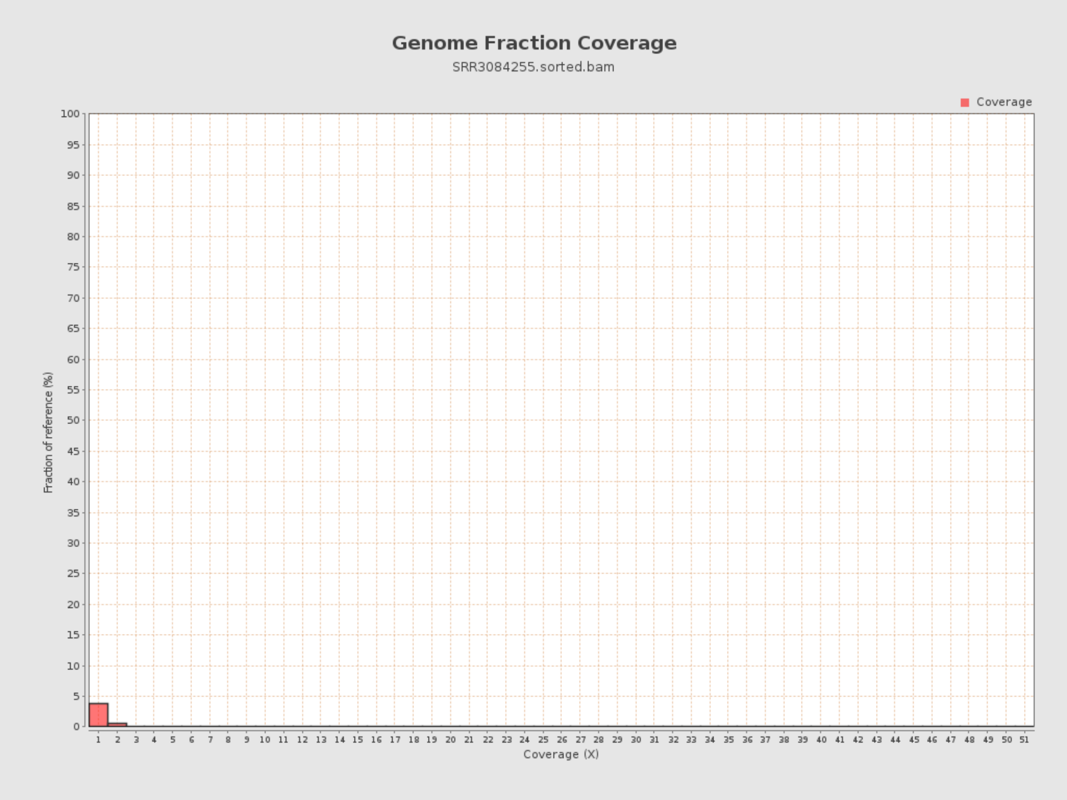
4. Results : Coverage Histogram



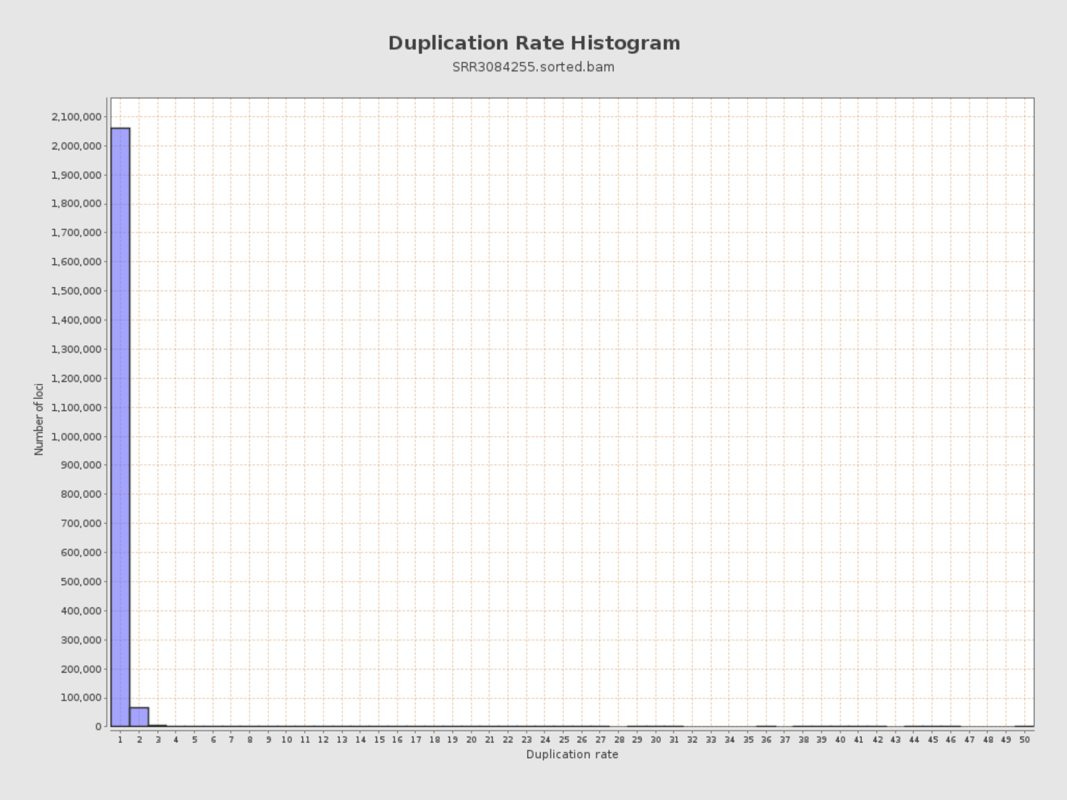
5. Results : Coverage Histogram (0-50X)



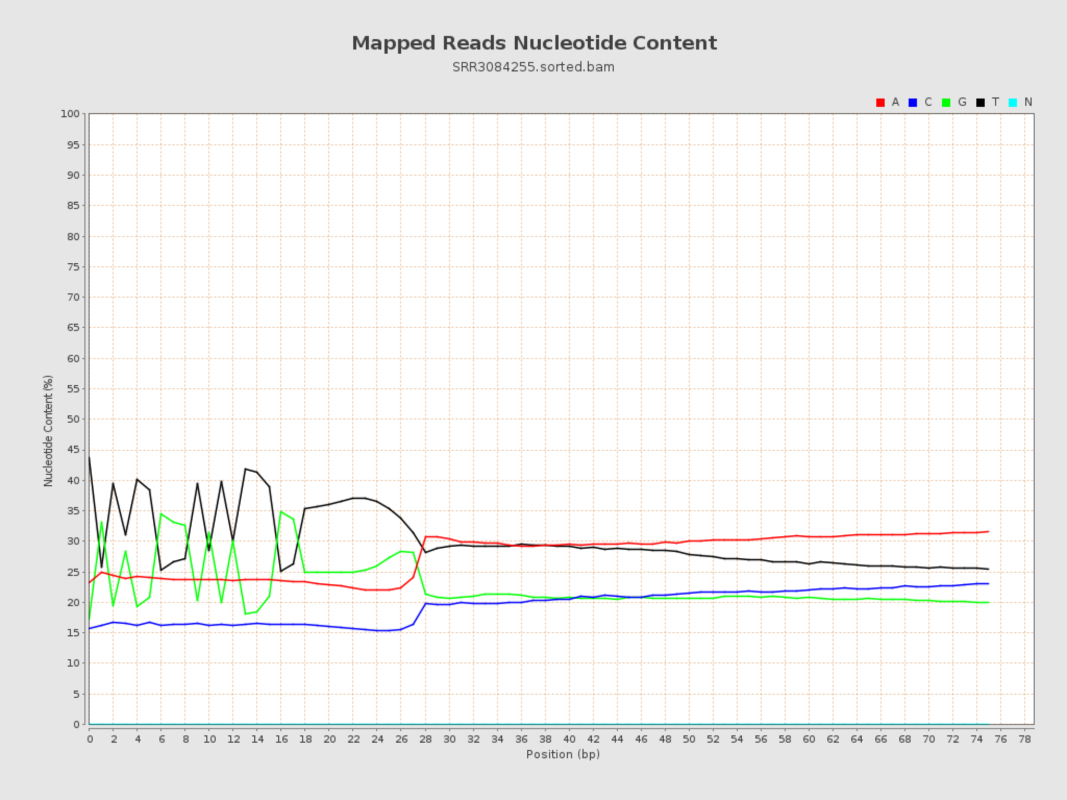
6. Results : Genome Fraction Coverage



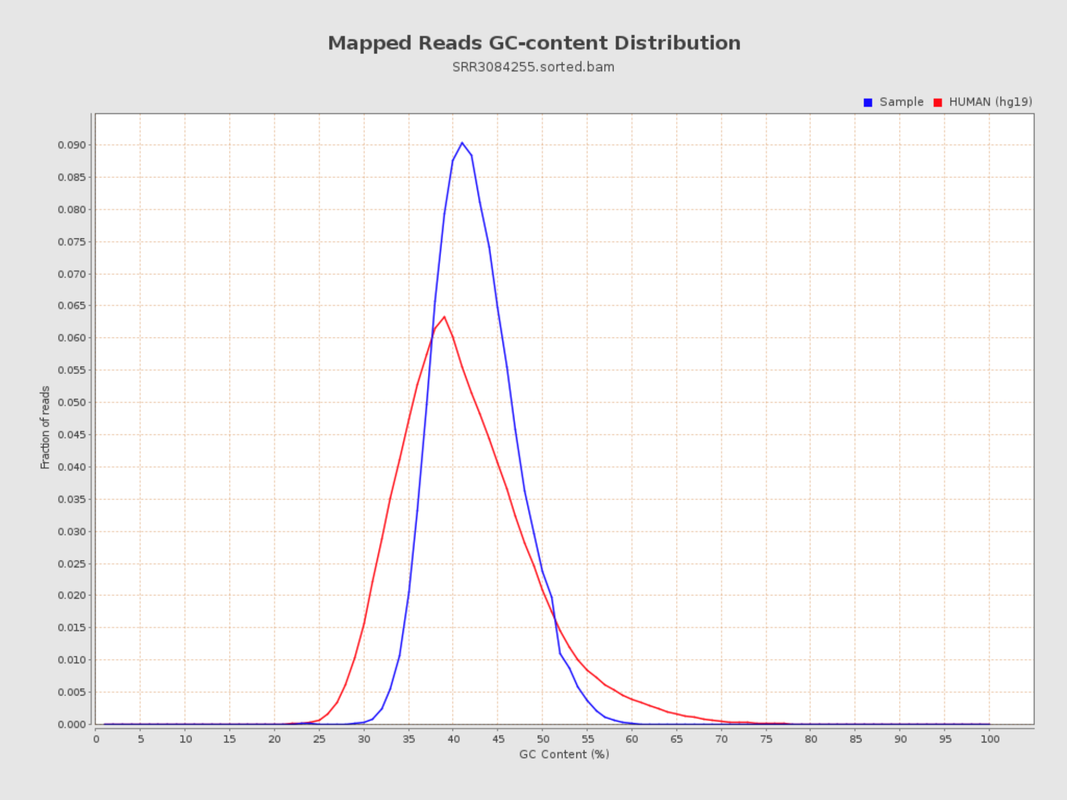
7. Results : Duplication Rate Histogram



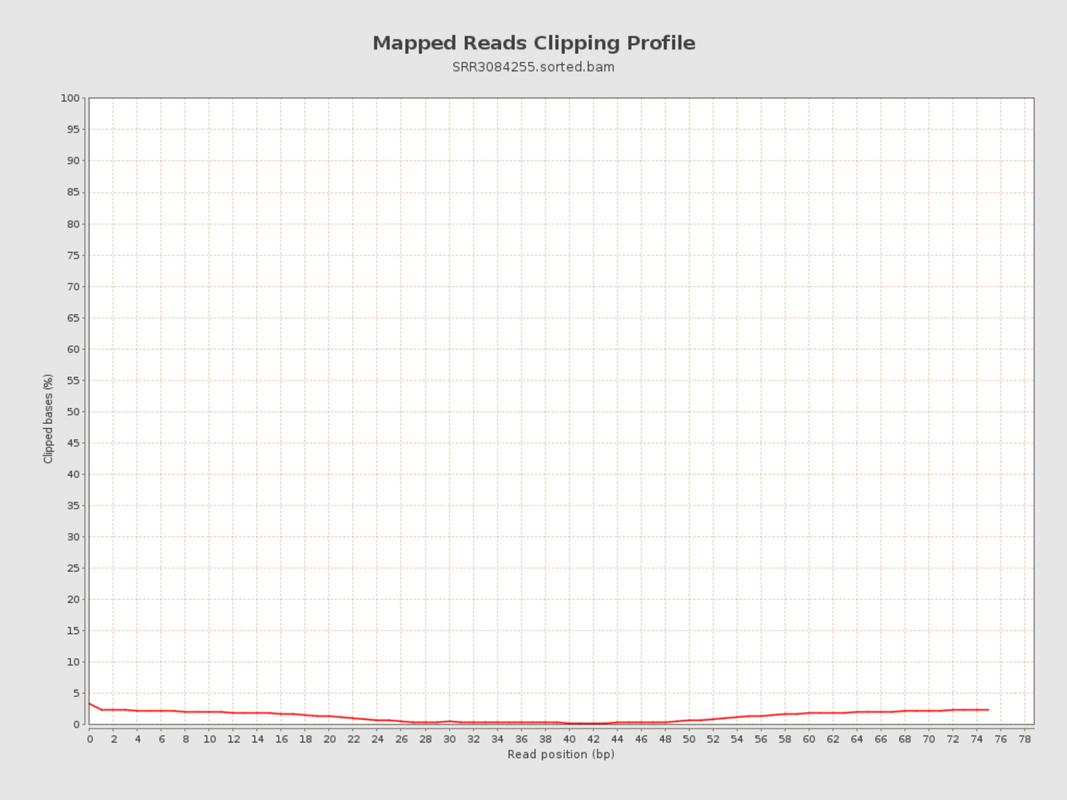
8. Results : Mapped Reads Nucleotide Content



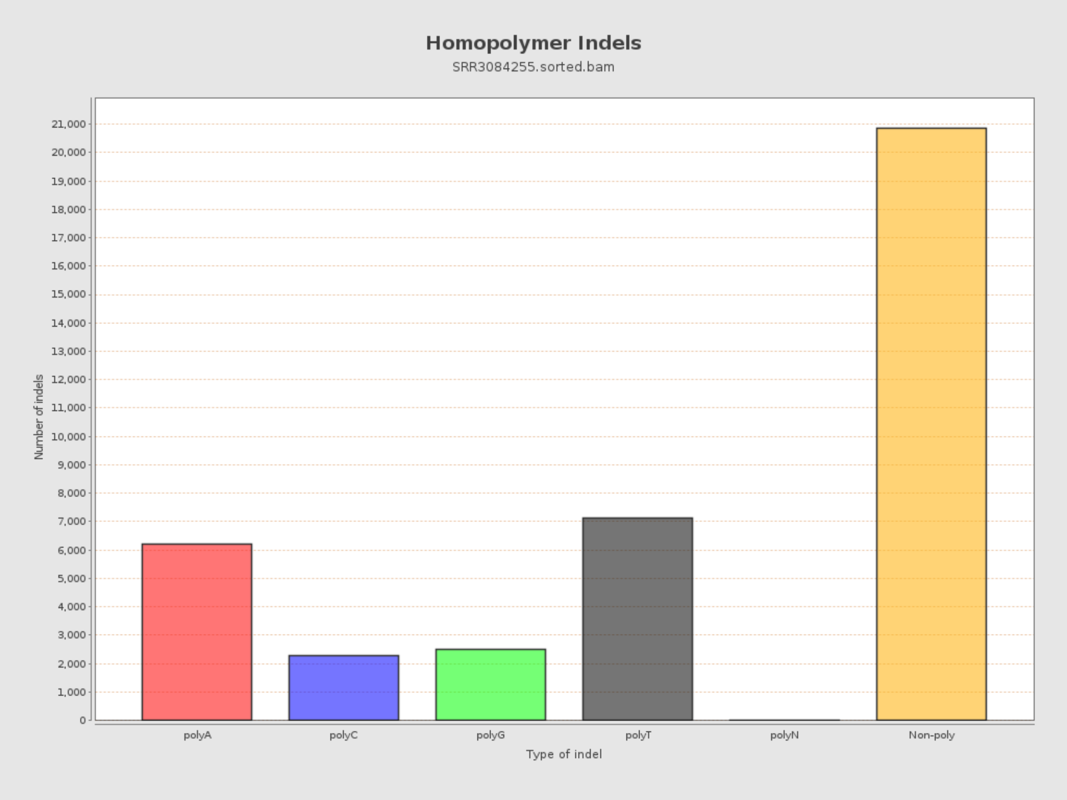
9. Results : Mapped Reads GC-content Distribution



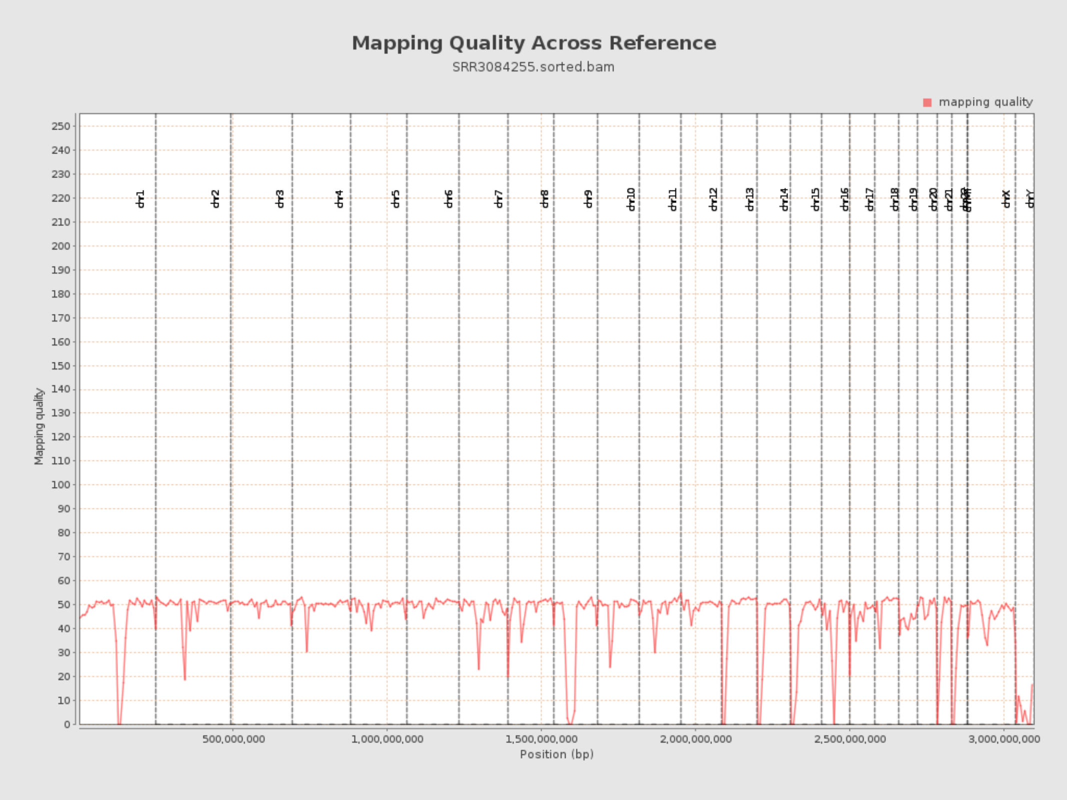
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram