Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 10:06:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084343.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_SRR3084343 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084343.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 10:06:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084343.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,590,479
Mapped reads	2,394,898 / 92.45%
Unmapped reads	195,581 / 7.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,095 / 0.43%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	87,080 / 3.36%
Duplication rate	3.08%
Clipped reads	850,321 / 32.82%

2.2. ACGT Content

Number/percentage of A's	46,582,562 / 28.35%
Number/percentage of C's	30,418,985 / 18.51%
Number/percentage of T's	52,193,104 / 31.76%
Number/percentage of G's	34,917,360 / 21.25%
Number/percentage of N's	227,276 / 0.14%
GC Percentage	39.76%

2.3. Coverage

Mean	0.0531

Standard Deviation	0.3517

2.4. Mapping Quality

Mean Mapping Quality	47.2

2.5. Mismatches and indels

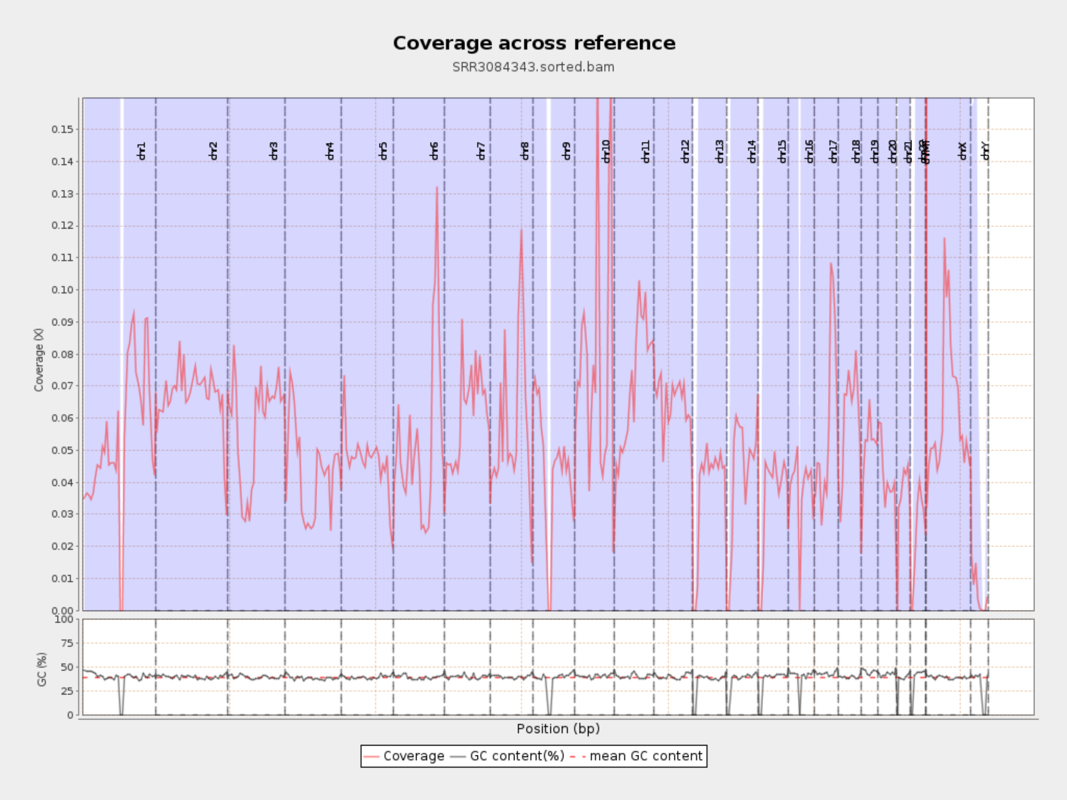
General error rate	0.94%
Mismatches	1,520,858
Insertions	11,234
Mapped reads with at least one insertion	0.47%
Deletions	34,095
Mapped reads with at least one deletion	1.41%
Homopolymer indels	48.92%

2.6. Chromosome stats

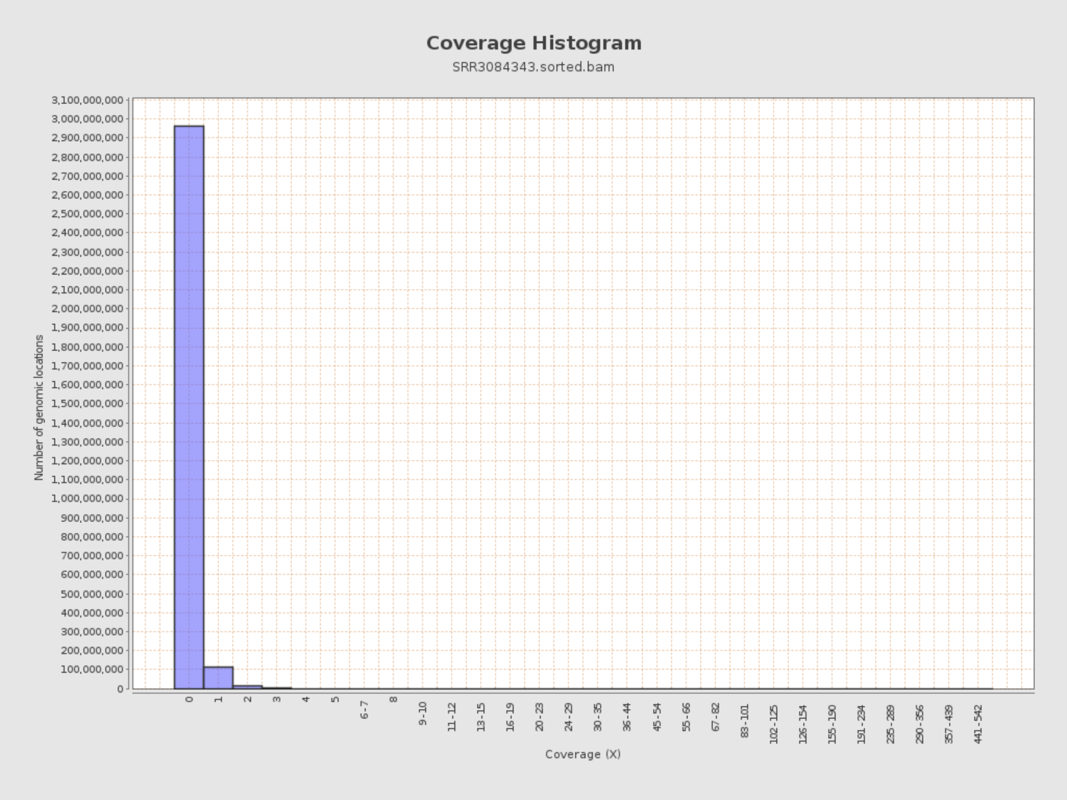
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13430168	0.0539	0.5416
chr2	243199373	16341805	0.0672	0.3764
chr3	198022430	11469837	0.0579	0.2842
chr4	191154276	8277864	0.0433	0.2496
chr5	180915260	8456172	0.0467	0.2518
chr6	171115067	9177230	0.0536	0.2962
chr7	159138663	9650301	0.0606	0.5257

chr8	146364022	8408946	0.0575	0.3976
chr9	141213431	6218153	0.044	0.3029
chr10	135534747	10659983	0.0787	0.4518
chr11	135006516	9515855	0.0705	0.3648
chr12	133851895	8703405	0.065	0.2983
chr13	115169878	4342496	0.0377	0.2259
chr14	107349540	4561146	0.0425	0.245
chr15	102531392	3573441	0.0349	0.2226
chr16	90354753	3302306	0.0365	0.2389
chr17	81195210	4823435	0.0594	0.3081
chr18	78077248	4717167	0.0604	0.4845
chr19	59128983	3047489	0.0515	0.3749
chr20	63025520	2637833	0.0419	0.2402
chr21	48129895	1692928	0.0352	0.2286
chr22	51304566	1220609	0.0238	0.1768
chrMT	16571	129793	7.8325	5.2439
chrX	155270560	9712881	0.0626	0.3194
chrY	59373566	327598	0.0055	0.1157

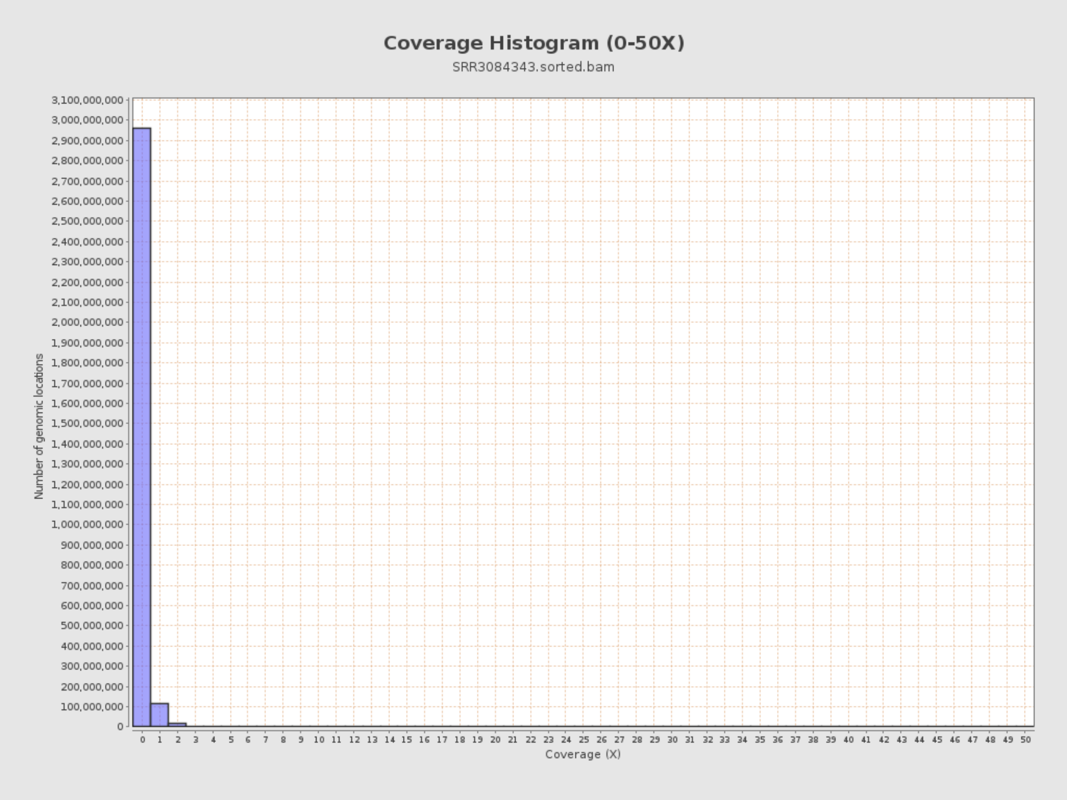
3. Results : Coverage across reference



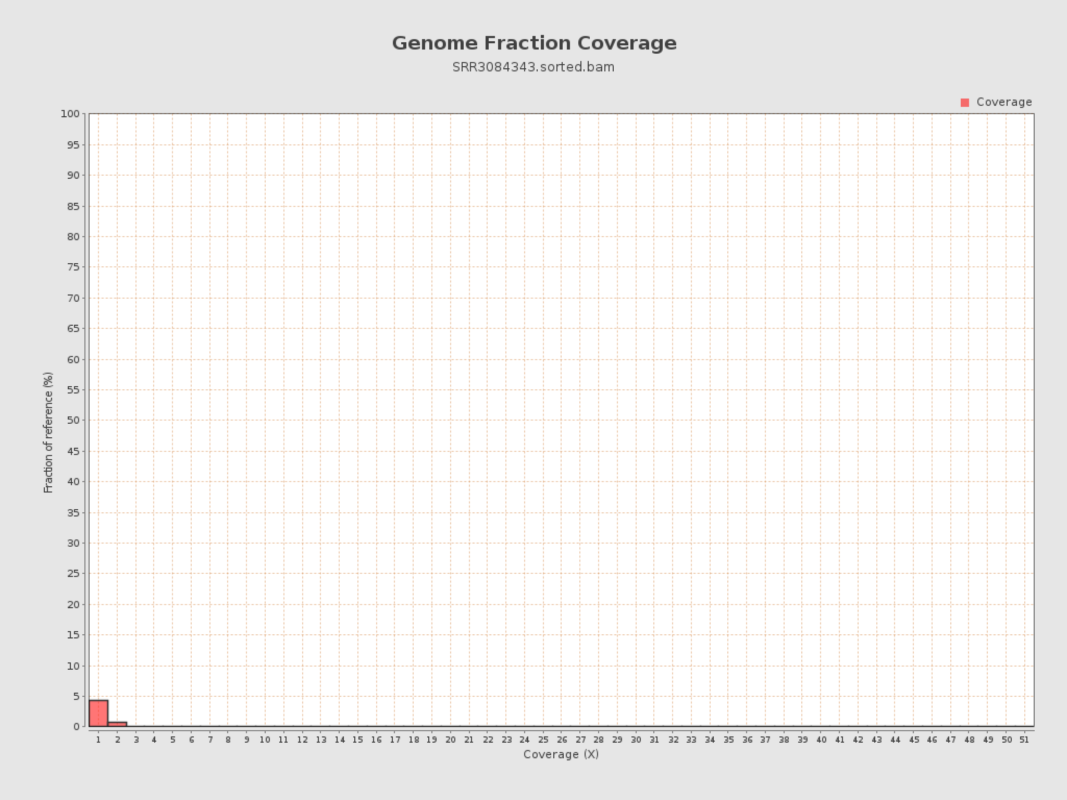
4. Results : Coverage Histogram



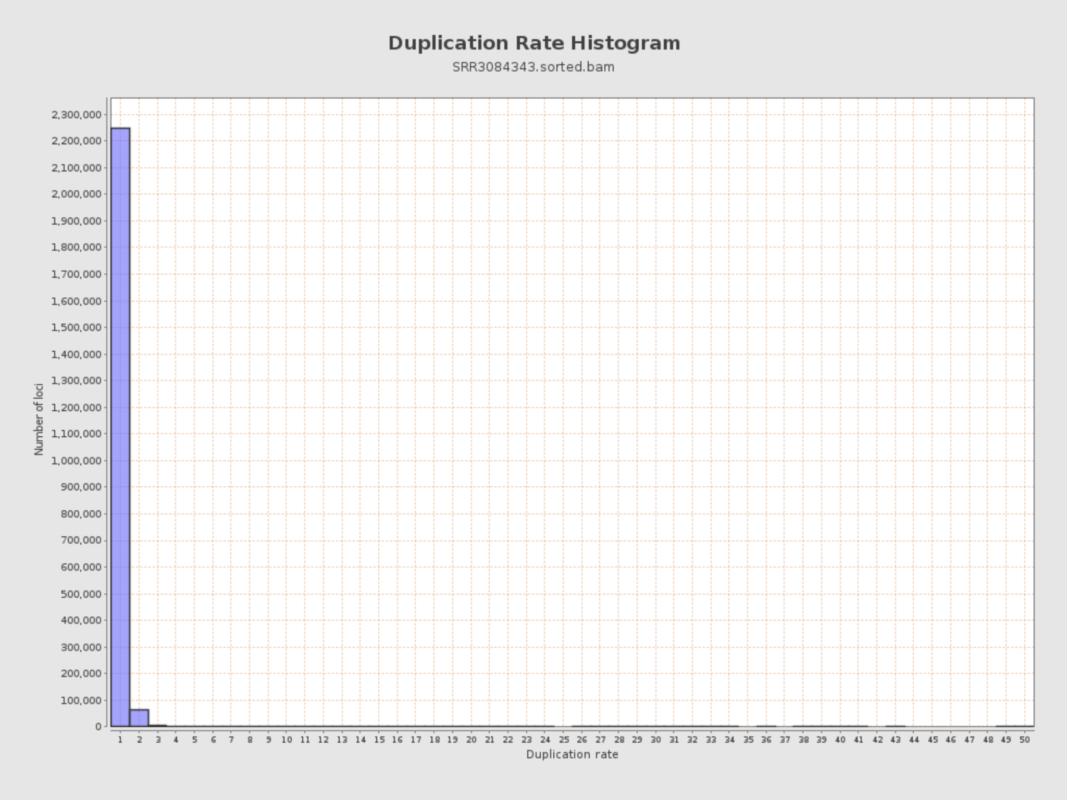
5. Results : Coverage Histogram (0-50X)



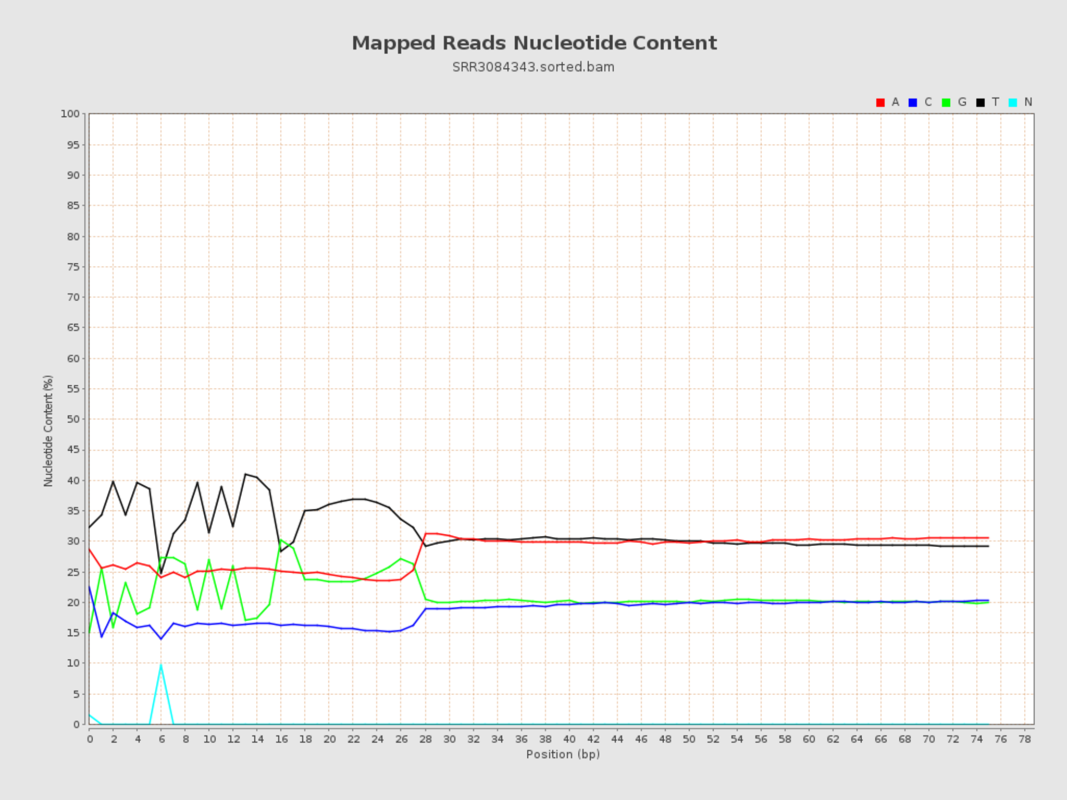
6. Results : Genome Fraction Coverage



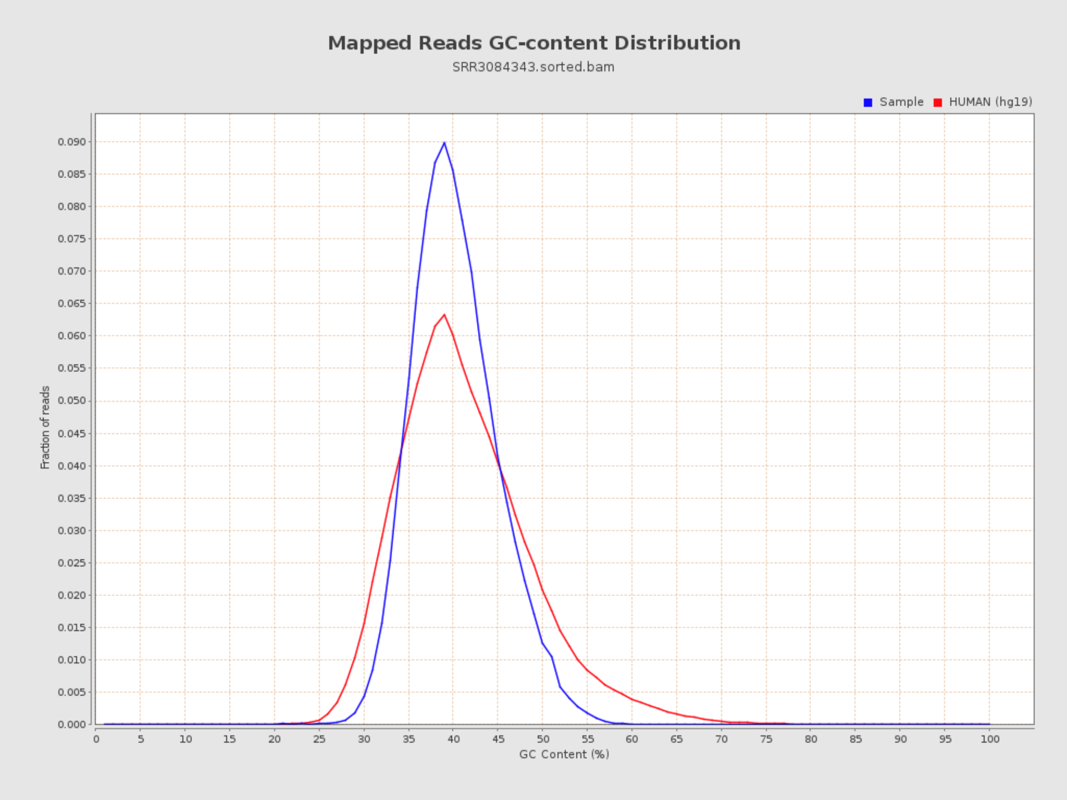
7. Results : Duplication Rate Histogram



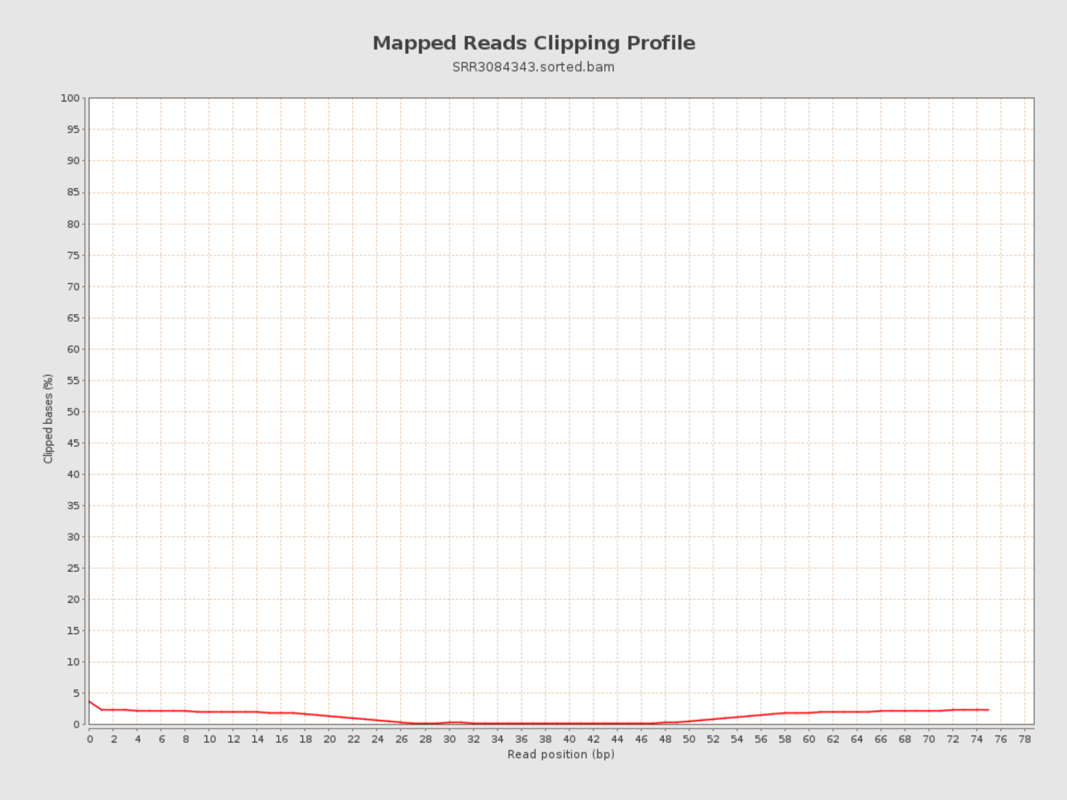
8. Results : Mapped Reads Nucleotide Content



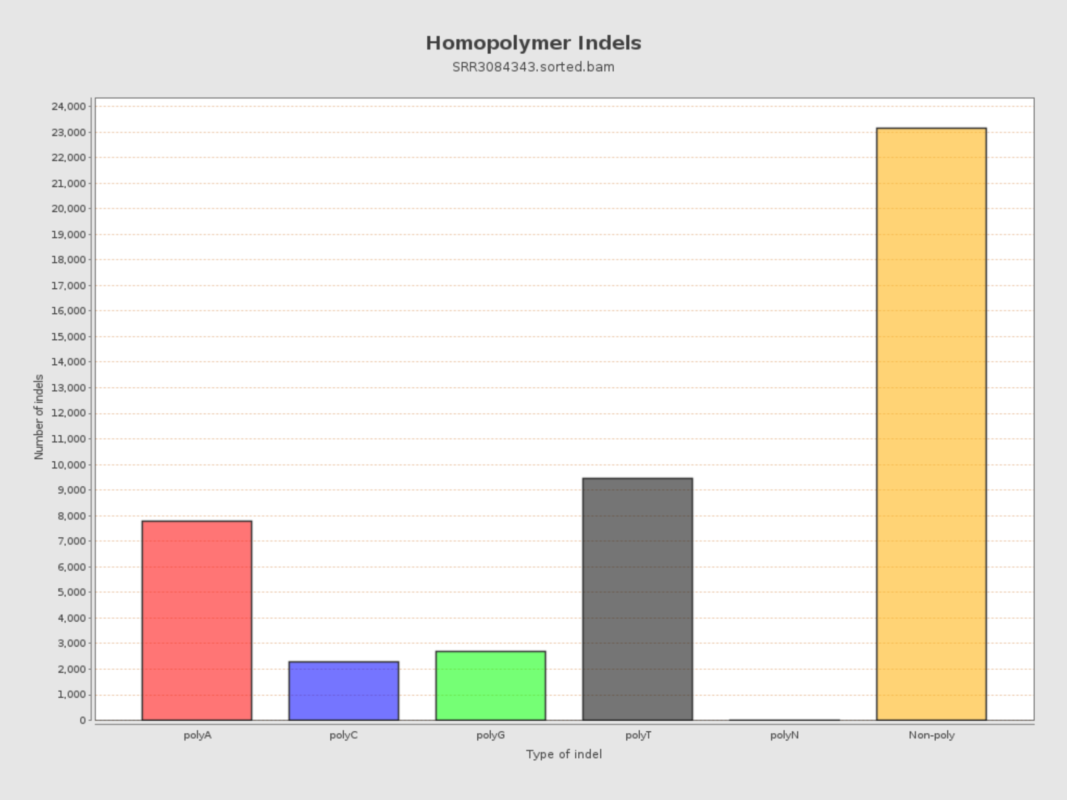
9. Results : Mapped Reads GC-content Distribution



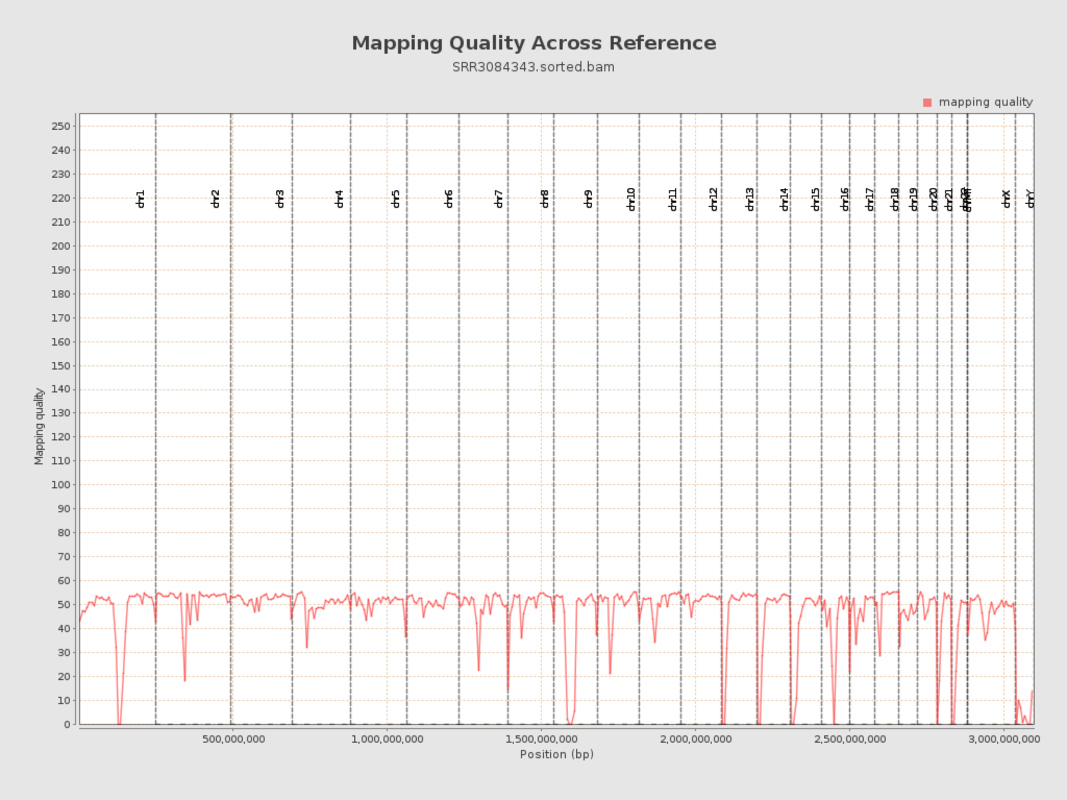
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram