Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 04:15:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085145.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_SRR3085145 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085145.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 04:15:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085145.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,329,337
Mapped reads	2,089,646 / 89.71%
Unmapped reads	239,691 / 10.29%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,067 / 0.9%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	78,506 / 3.37%
Duplication rate	2.88%
Clipped reads	925,508 / 39.73%

2.2. ACGT Content

Number/percentage of A's	39,325,037 / 28.04%
Number/percentage of C's	26,000,815 / 18.54%
Number/percentage of T's	43,966,072 / 31.35%
Number/percentage of G's	30,901,530 / 22.04%
Number/percentage of N's	30,975 / 0.02%
GC Percentage	40.58%

2.3. Coverage

Mean	0.0453

Standard Deviation	0.3822

2.4. Mapping Quality

Mean Mapping Quality	46.07

2.5. Mismatches and indels

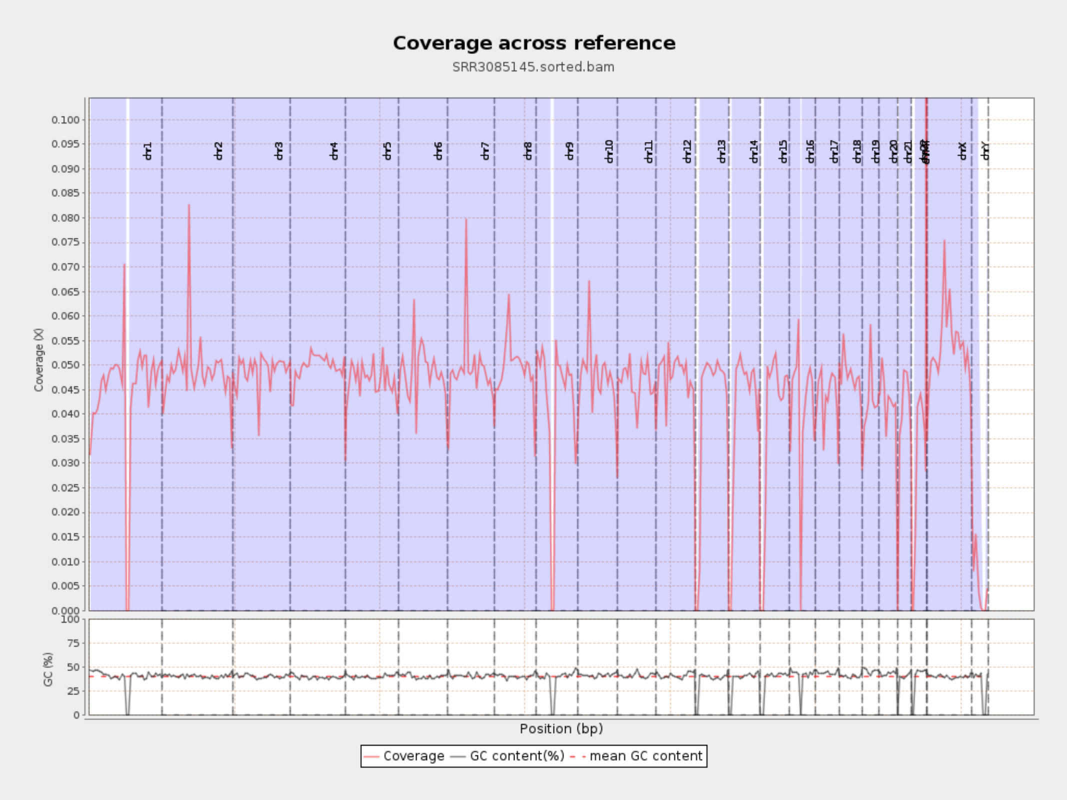
General error rate	0.89%
Mismatches	1,235,669
Insertions	10,943
Mapped reads with at least one insertion	0.52%
Deletions	30,730
Mapped reads with at least one deletion	1.46%
Homopolymer indels	47.37%

2.6. Chromosome stats

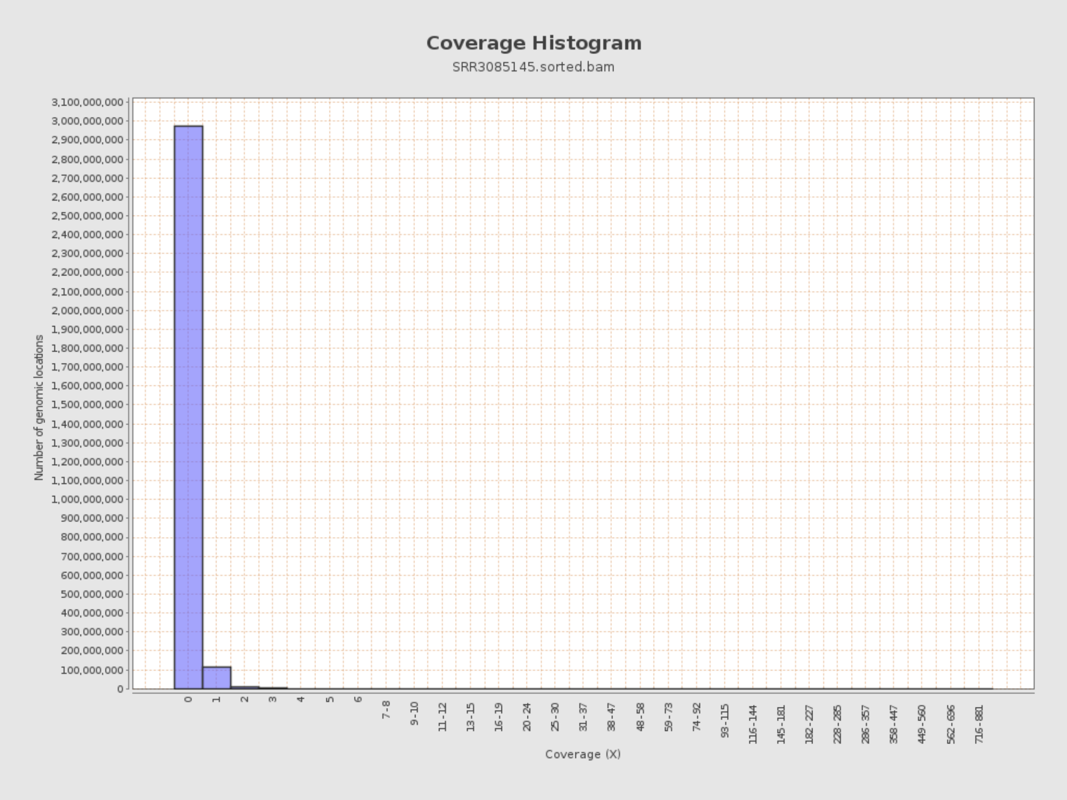
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11121691	0.0446	0.6392
chr2	243199373	11967306	0.0492	0.4724
chr3	198022430	9676134	0.0489	0.2425
chr4	191154276	9495745	0.0497	0.2525
chr5	180915260	8529859	0.0471	0.2394
chr6	171115067	8298453	0.0485	0.2941
chr7	159138663	7857689	0.0494	0.5273

chr8	146364022	7223089	0.0494	0.6006
chr9	141213431	5917045	0.0419	0.3504
chr10	135534747	6499978	0.048	0.3483
chr11	135006516	6263272	0.0464	0.3308
chr12	133851895	6391501	0.0478	0.244
chr13	115169878	4641913	0.0403	0.2214
chr14	107349540	4256003	0.0396	0.2384
chr15	102531392	3947907	0.0385	0.2257
chr16	90354753	3759948	0.0416	0.2483
chr17	81195210	3493066	0.043	0.2536
chr18	78077248	3759740	0.0482	0.6223
chr19	59128983	2524283	0.0427	0.4894
chr20	63025520	2680196	0.0425	0.233
chr21	48129895	1842269	0.0383	0.226
chr22	51304566	1436483	0.028	0.1821
chrMT	16571	11487	0.6932	0.9088
chrX	155270560	8347121	0.0538	0.288
chrY	59373566	331533	0.0056	0.1166

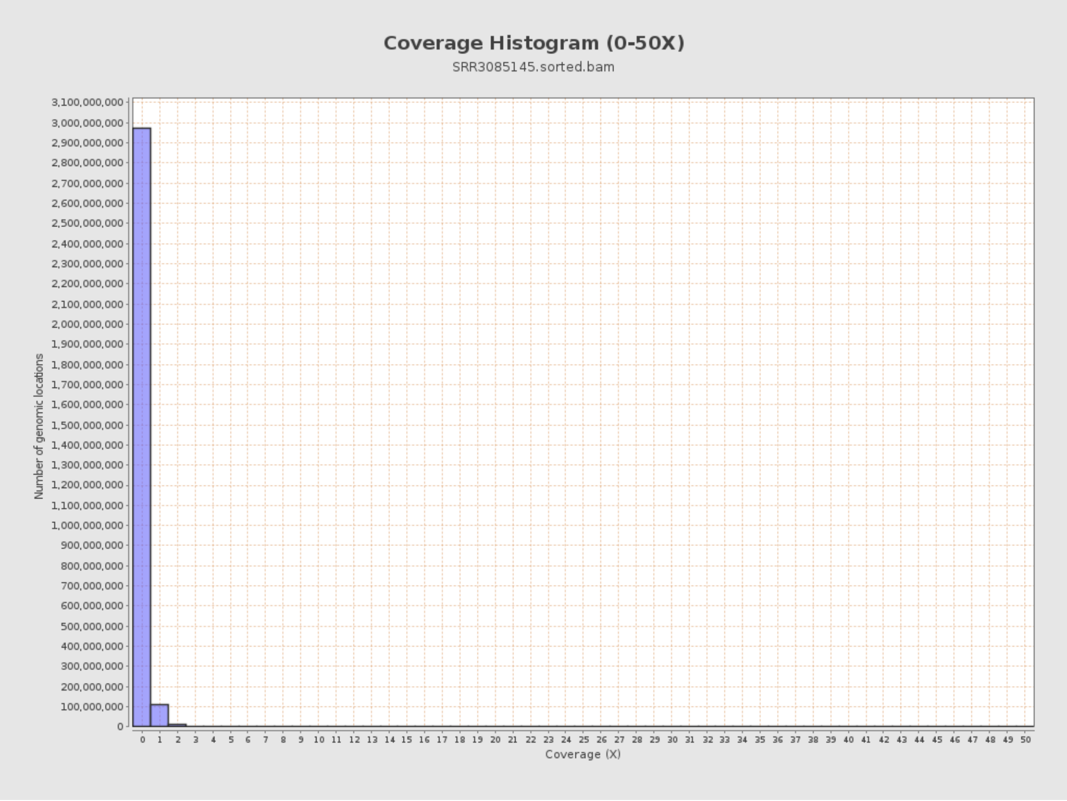
3. Results : Coverage across reference



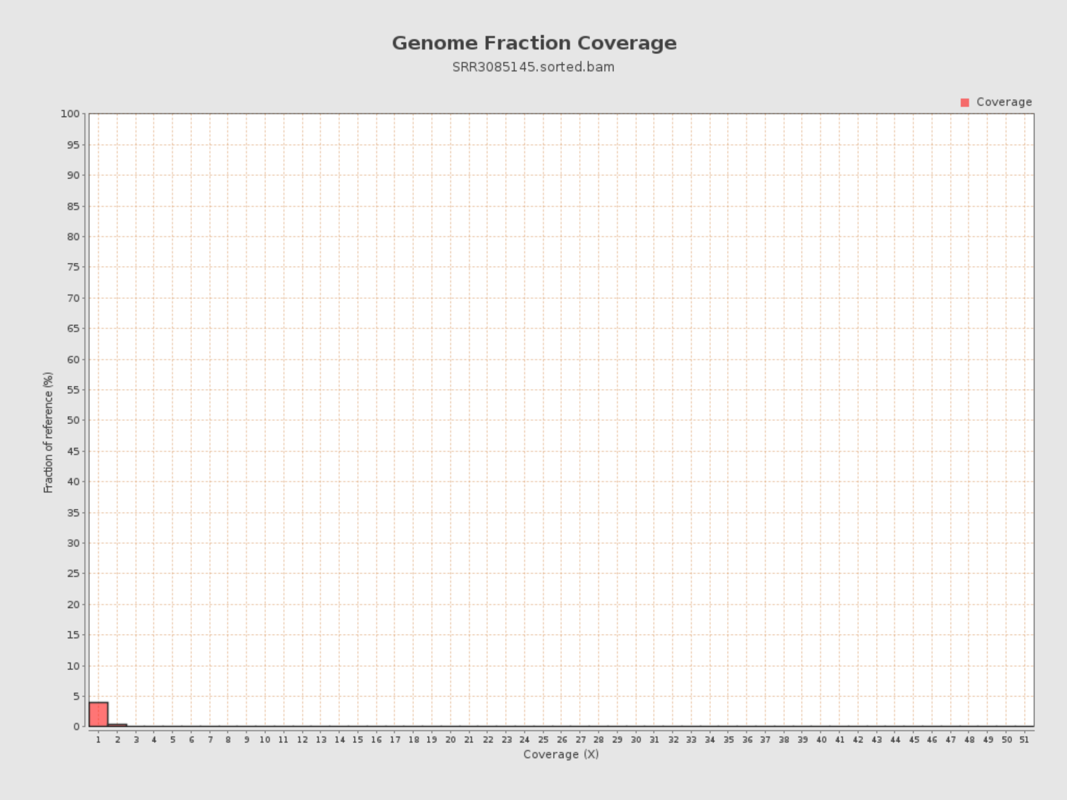
4. Results : Coverage Histogram



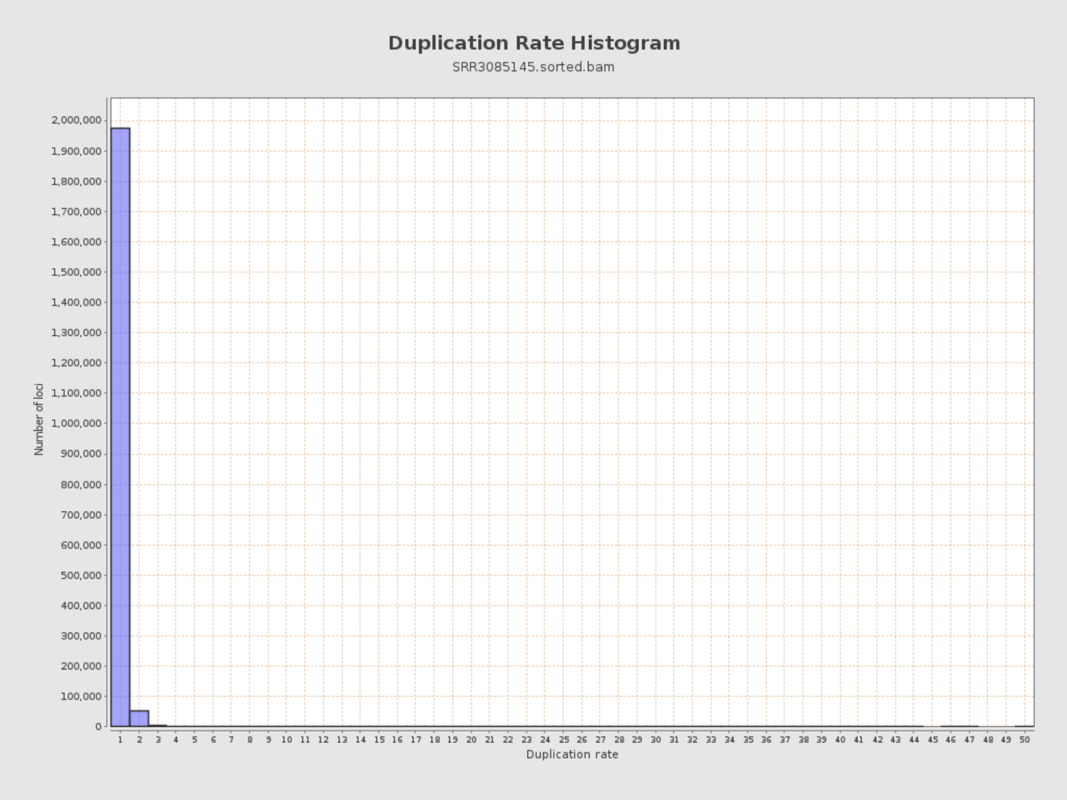
5. Results : Coverage Histogram (0-50X)



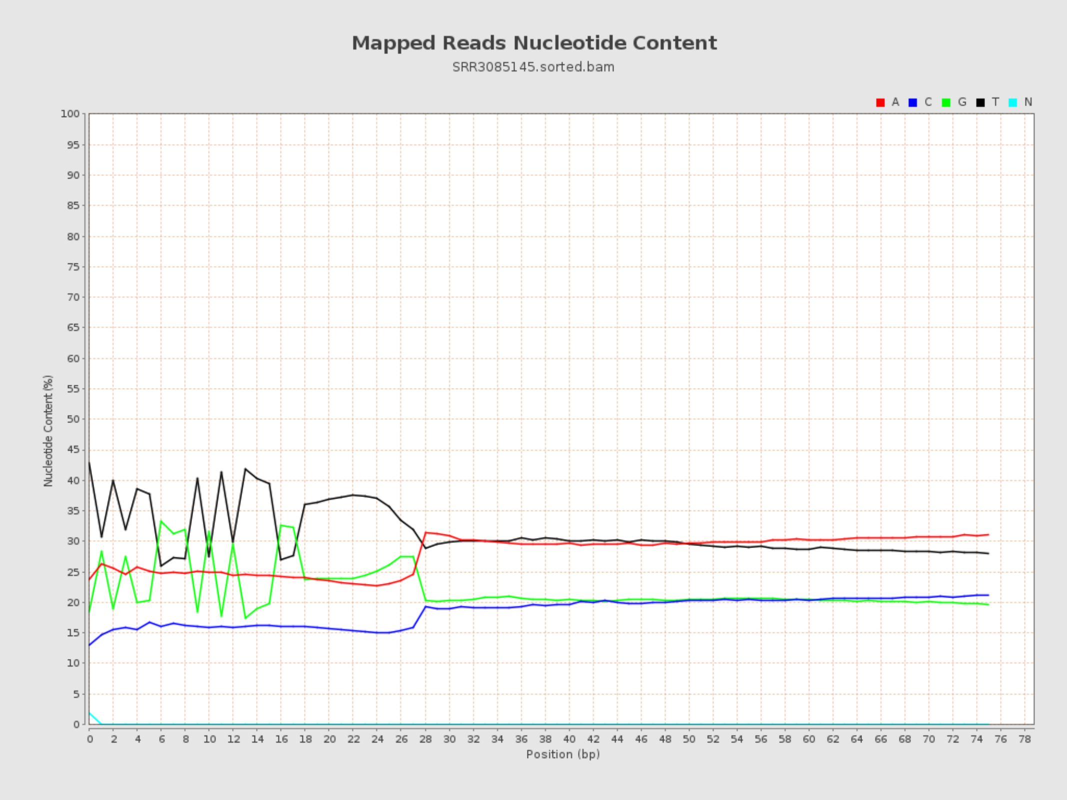
6. Results : Genome Fraction Coverage



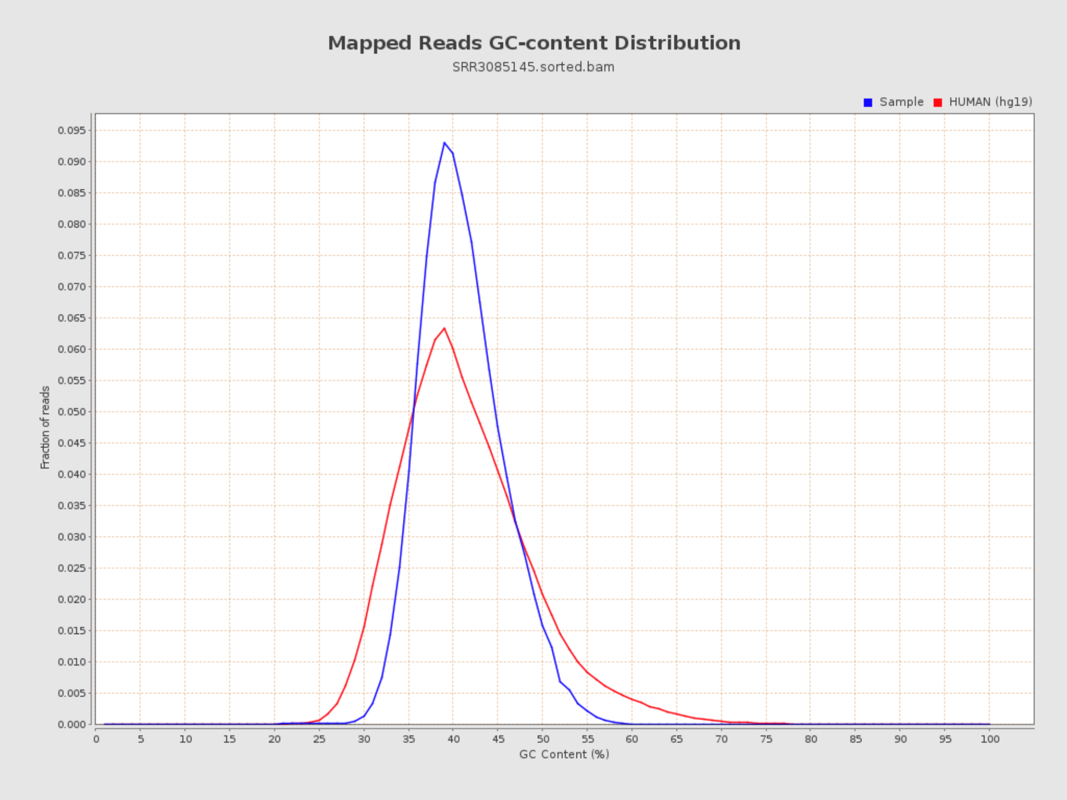
7. Results : Duplication Rate Histogram



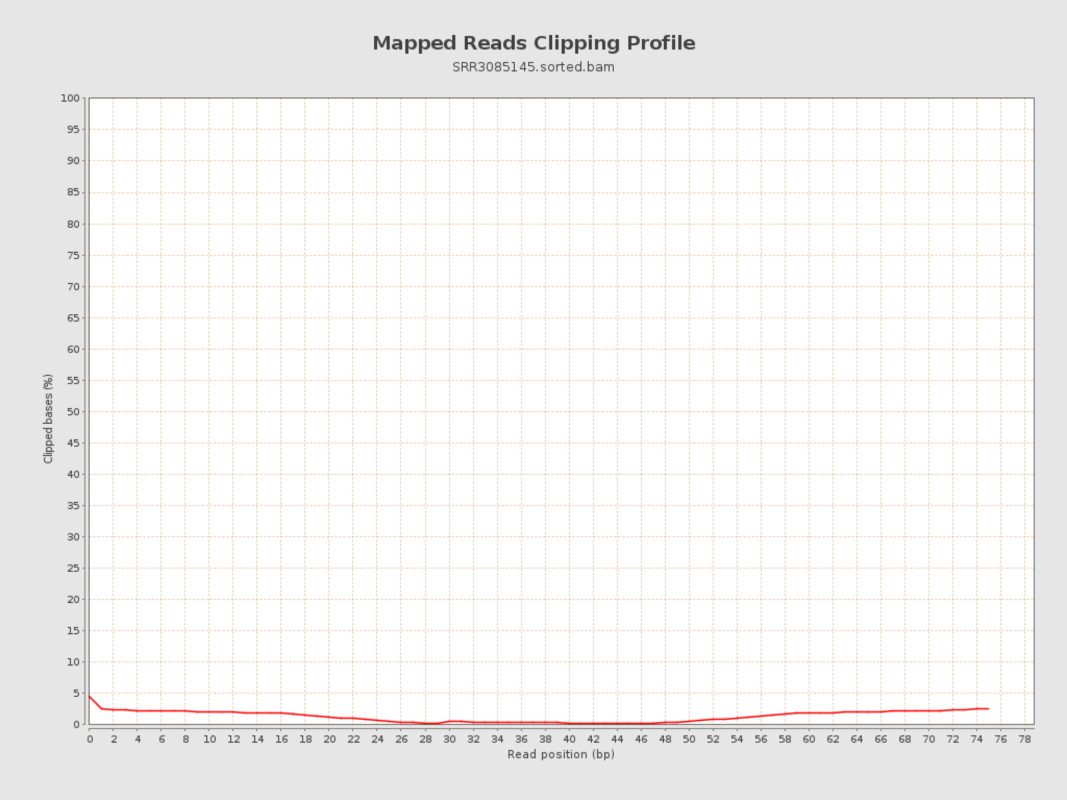
8. Results : Mapped Reads Nucleotide Content



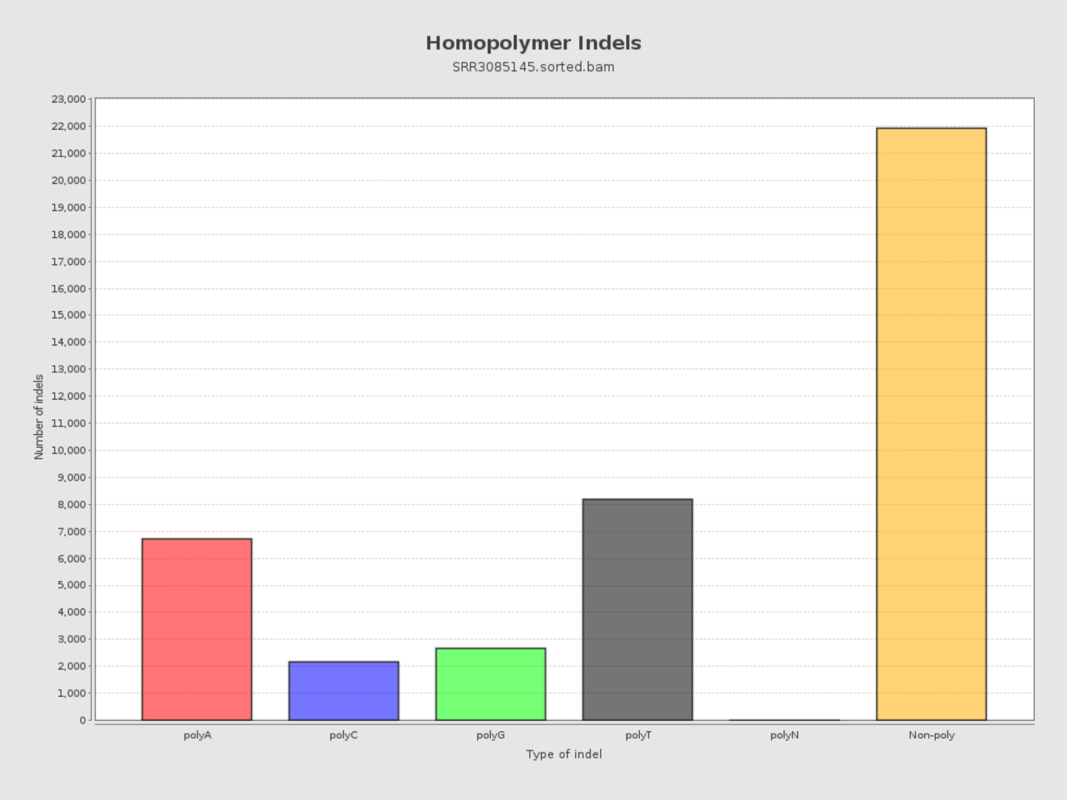
9. Results : Mapped Reads GC-content Distribution



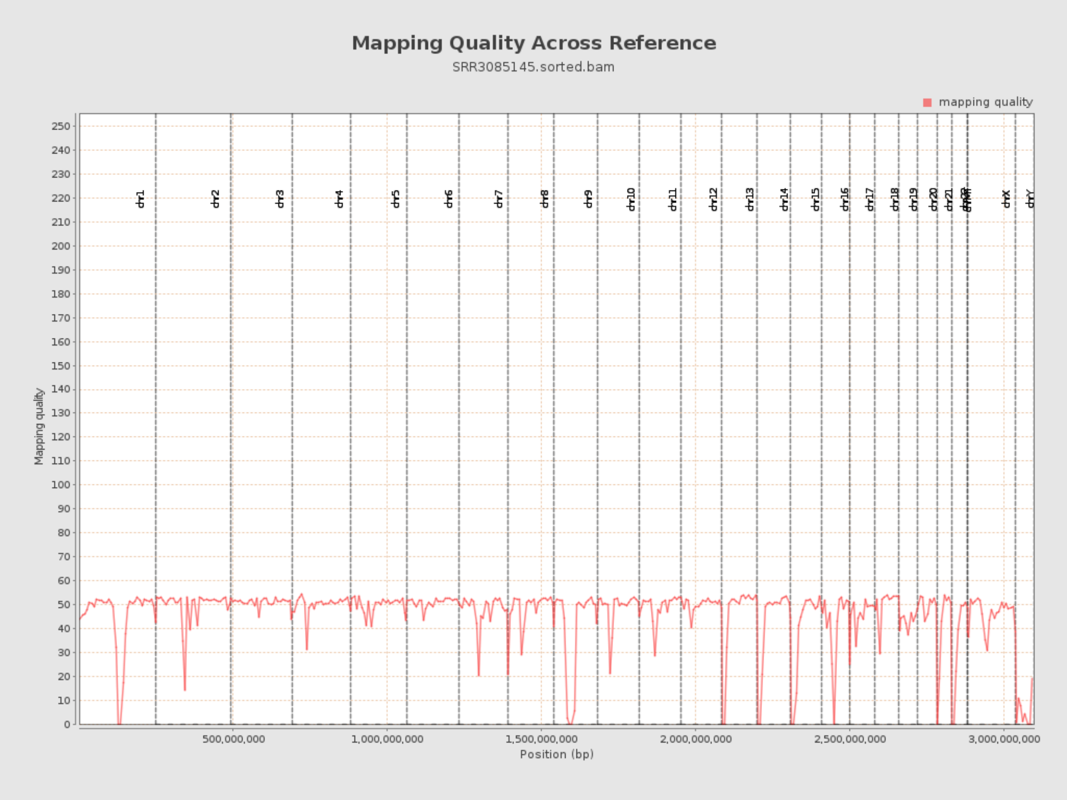
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram