Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 02:59:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549110.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_SRR1549110 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549110.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 02:59:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549110.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,377,591
Mapped reads	8,931,917 / 86.07%
Unmapped reads	1,445,674 / 13.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	432,616 / 4.17%
Duplication rate	3.62%
Clipped reads	404,380 / 3.9%

2.2. ACGT Content

Number/percentage of A's	104,955,468 / 29.58%
Number/percentage of C's	72,726,700 / 20.5%
Number/percentage of T's	105,266,879 / 29.67%
Number/percentage of G's	71,828,775 / 20.25%
Number/percentage of N's	1,424 / 0%
GC Percentage	40.75%

2.3. Coverage

Mean	0.1146
Standard Deviation	0.7973

2.4. Mapping Quality

Mean Mapping Quality	44.37

2.5. Mismatches and indels

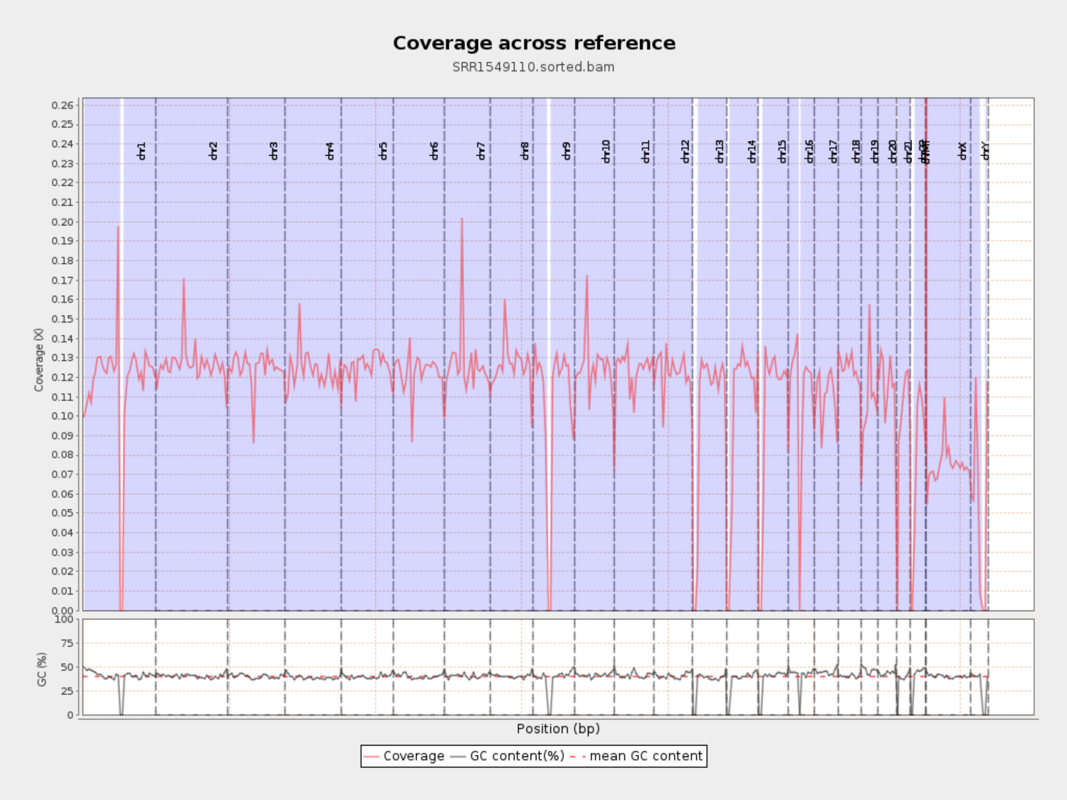
General error rate	0.3%
Mismatches	1,059,493
Insertions	8,611
Mapped reads with at least one insertion	0.1%
Deletions	26,715
Mapped reads with at least one deletion	0.3%
Homopolymer indels	45.45%

2.6. Chromosome stats

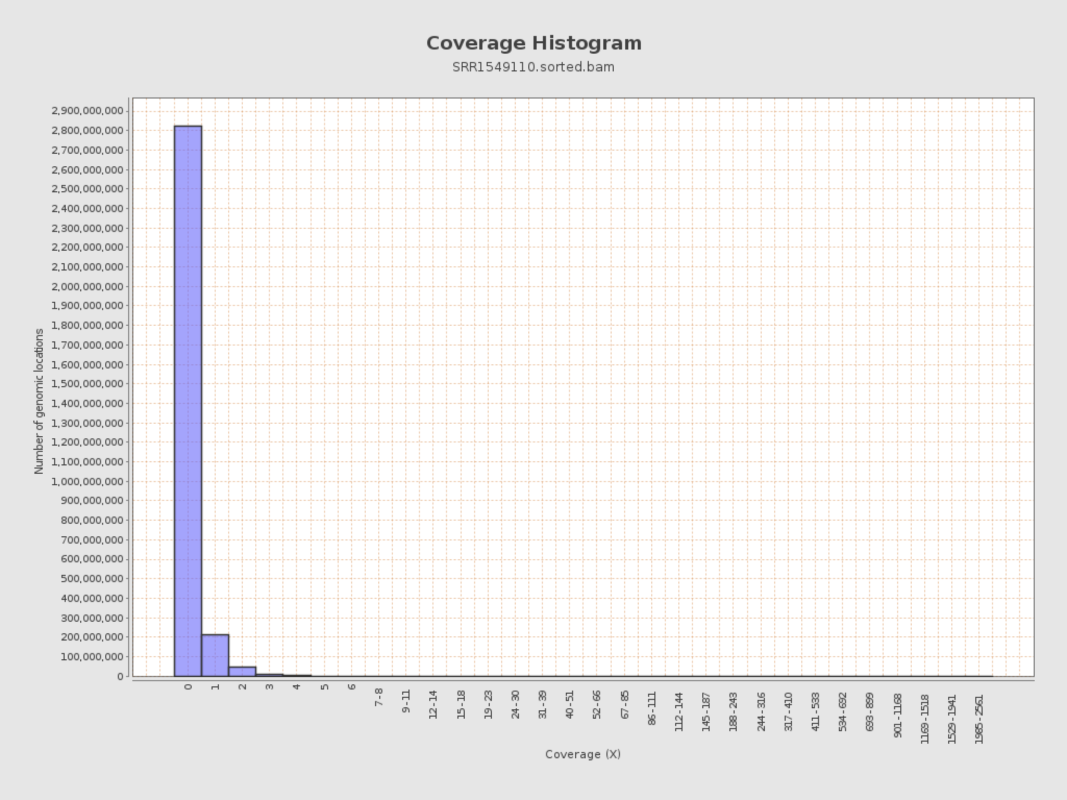
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	29078037	0.1167	1.7522
chr2	243199373	30908264	0.1271	0.6738
chr3	198022430	24704583	0.1248	0.4372
chr4	191154276	23714761	0.1241	0.4874
chr5	180915260	22677426	0.1253	0.4539
chr6	171115067	21036940	0.1229	0.4767
chr7	159138663	20186922	0.1269	1.1506
chr8	146364022	18450899	0.1261	0.712

chr9	141213431	15098003	0.1069	0.6286
chr10	135534747	16996687	0.1254	0.7167
chr11	135006516	16684063	0.1236	0.6424
chr12	133851895	16431805	0.1228	0.4625
chr13	115169878	11672178	0.1013	0.3876
chr14	107349540	11028301	0.1027	0.5347
chr15	102531392	10385380	0.1013	0.3882
chr16	90354753	9716908	0.1075	0.465
chr17	81195210	8986708	0.1107	0.4582
chr18	78077248	9786024	0.1253	1.3553
chr19	59128983	6441431	0.1089	1.3314
chr20	63025520	7344268	0.1165	0.4687
chr21	48129895	4668569	0.097	0.4907
chr22	51304566	3784461	0.0738	0.3548
chrMT	16571	134990	8.1462	10.7379
chrX	155270560	11652354	0.075	0.4588
chrY	59373566	3243009	0.0546	0.5998

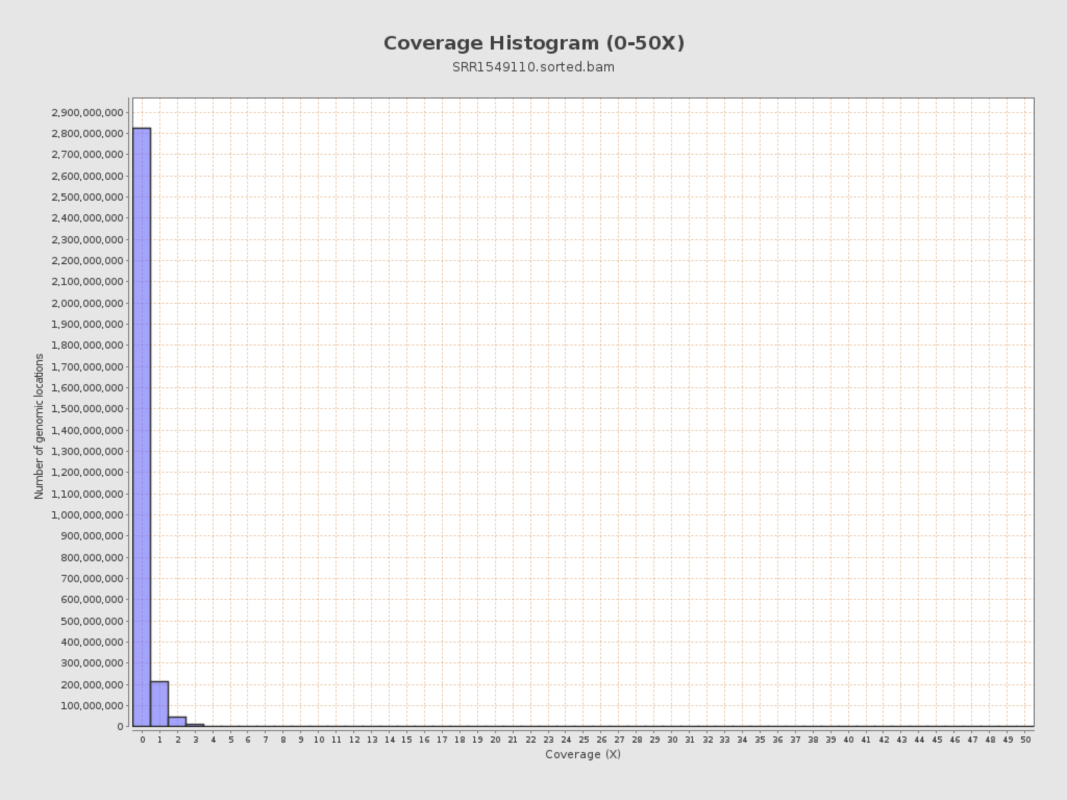
3. Results : Coverage across reference



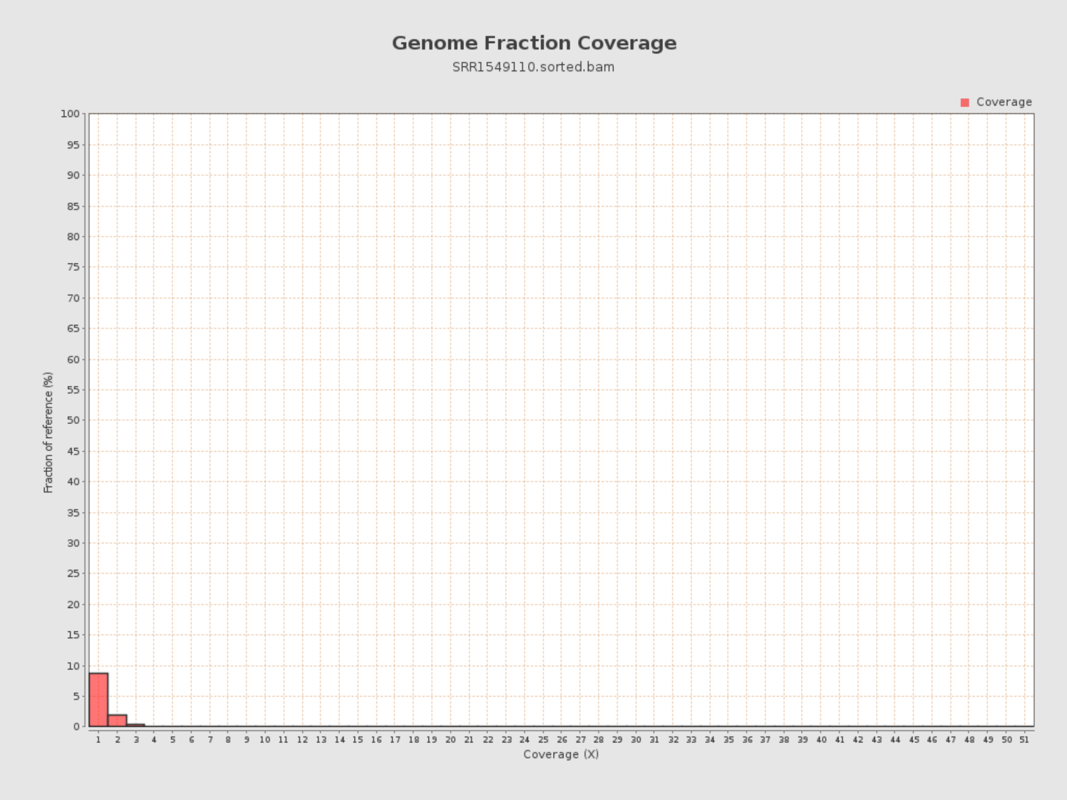
4. Results : Coverage Histogram



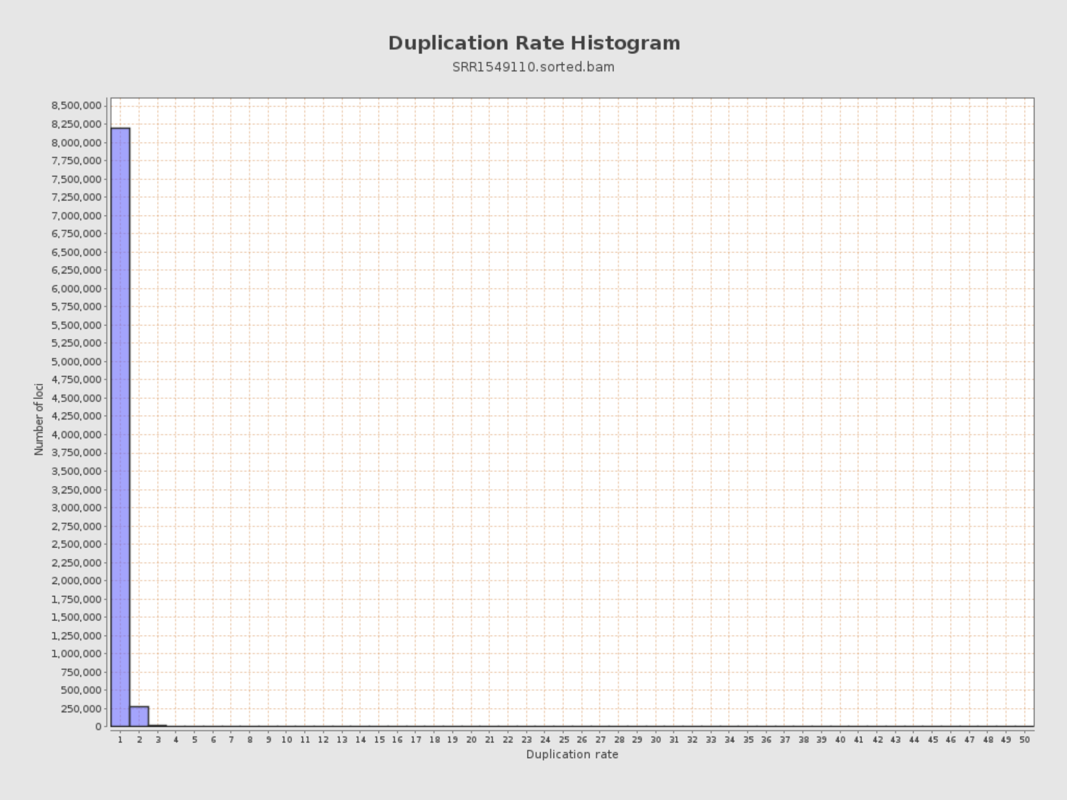
5. Results : Coverage Histogram (0-50X)



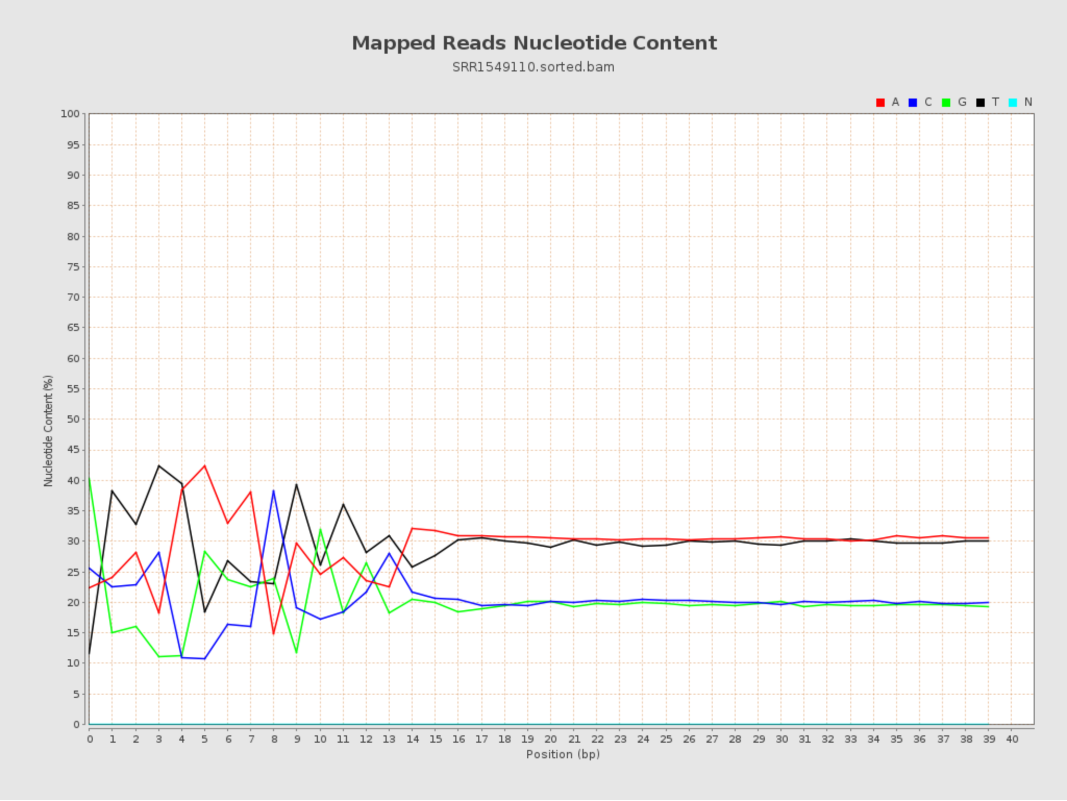
6. Results : Genome Fraction Coverage



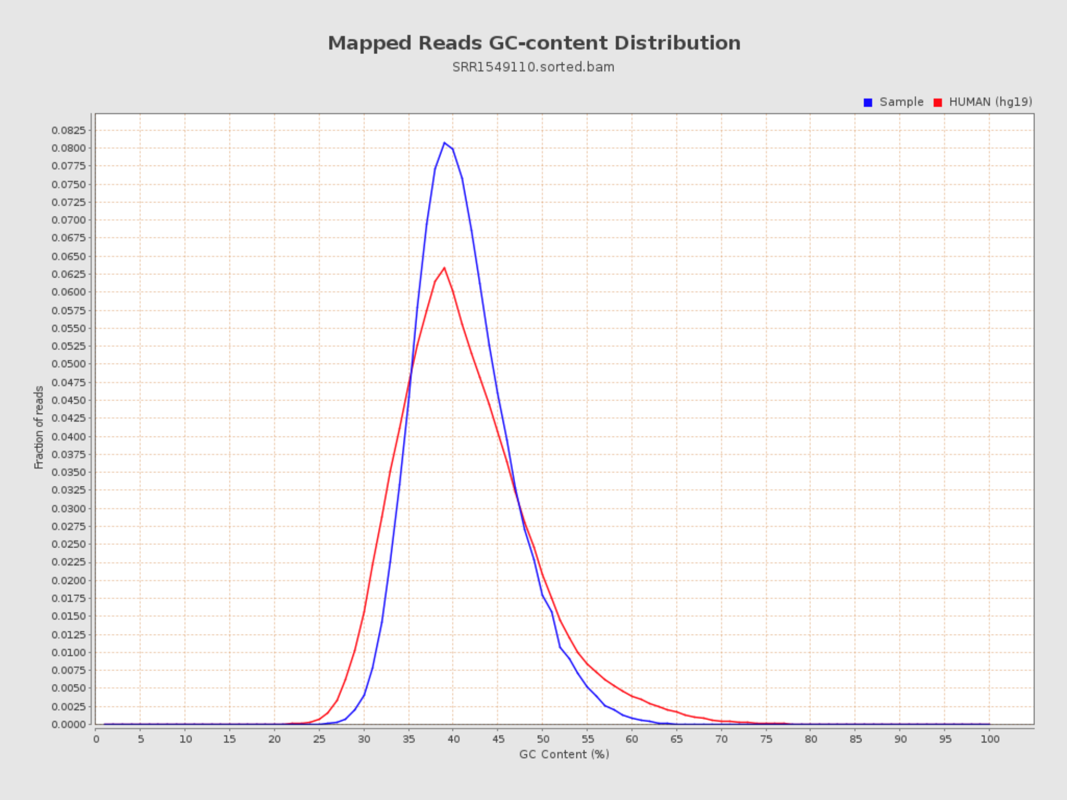
7. Results : Duplication Rate Histogram



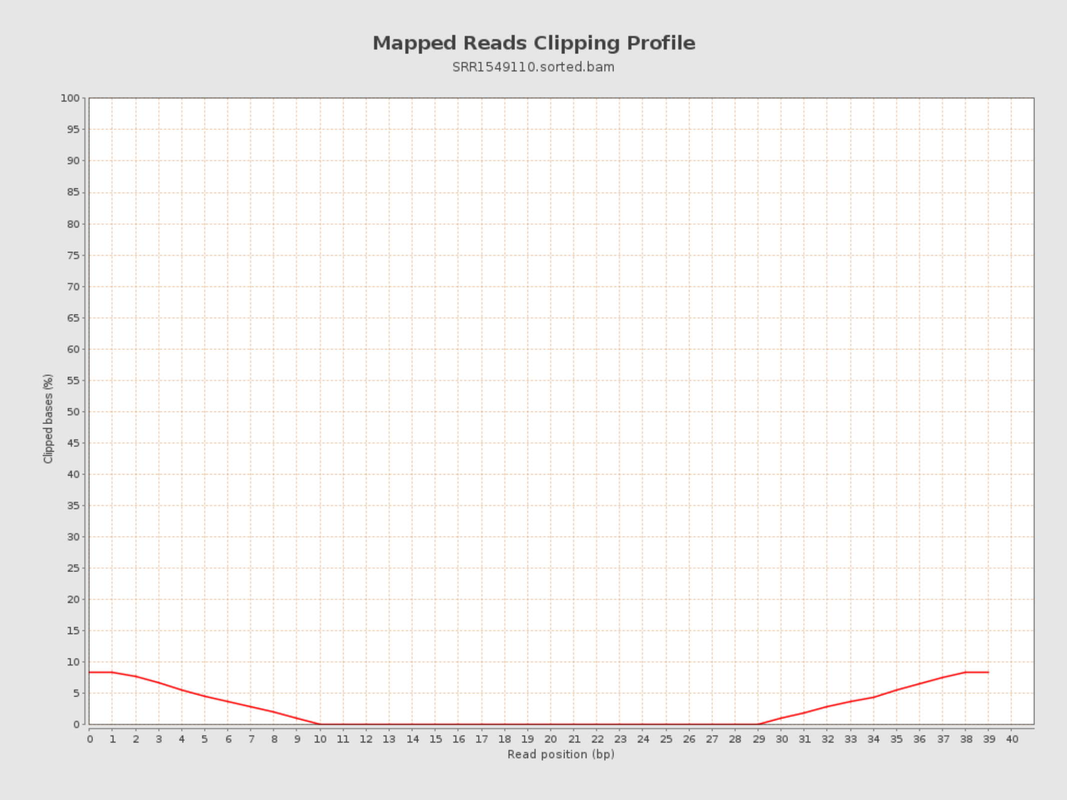
8. Results : Mapped Reads Nucleotide Content



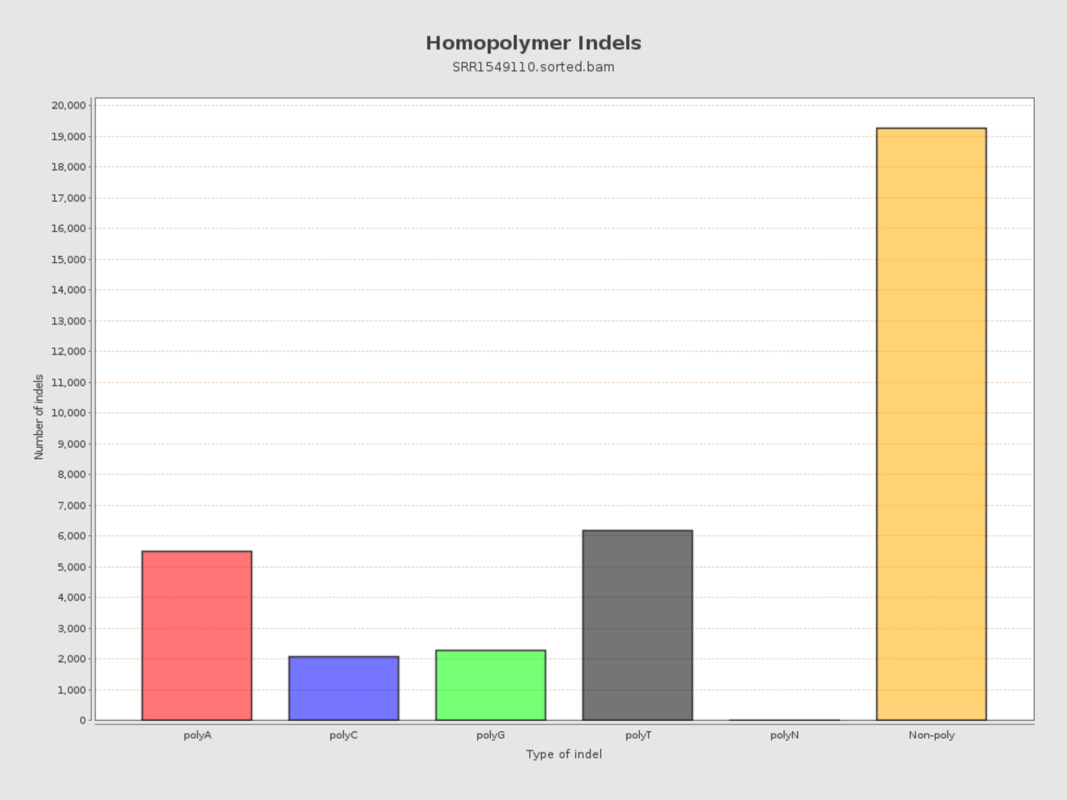
9. Results : Mapped Reads GC-content Distribution



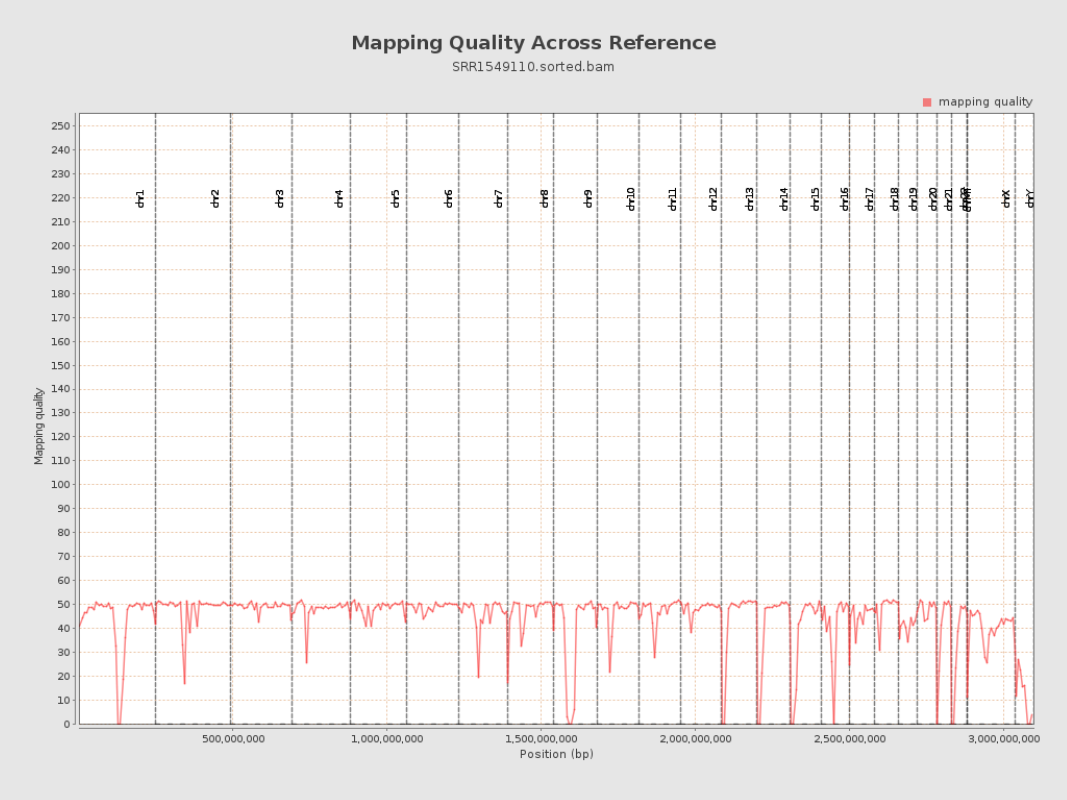
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram