Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 01:48:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524891.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_SRR10524891 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524891.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 01:48:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524891.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,614,270
Mapped reads	2,414,048 / 92.34%
Unmapped reads	200,222 / 7.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,428 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	121,414 / 4.64%
Duplication rate	3.68%
Clipped reads	2,415,576 / 92.4%

2.2. ACGT Content

Number/percentage of A's	34,416,718 / 24.39%
Number/percentage of C's	24,708,554 / 17.51%
Number/percentage of T's	46,822,313 / 33.19%
Number/percentage of G's	35,118,156 / 24.89%
Number/percentage of N's	18,287 / 0.01%
GC Percentage	42.41%

2.3. Coverage

Mean	0.0456

Standard Deviation	0.4282

2.4. Mapping Quality

Mean Mapping Quality	46.25

2.5. Mismatches and indels

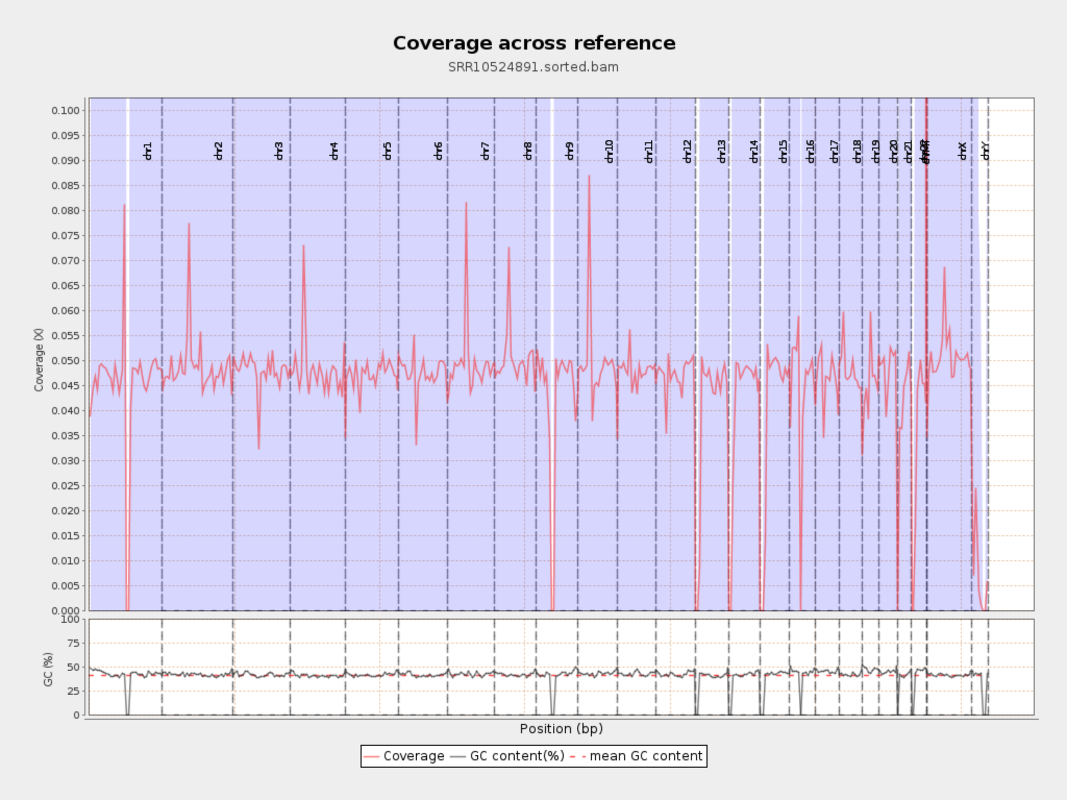
General error rate	0.5%
Mismatches	690,333
Insertions	9,843
Mapped reads with at least one insertion	0.41%
Deletions	27,177
Mapped reads with at least one deletion	1.12%
Homopolymer indels	44.35%

2.6. Chromosome stats

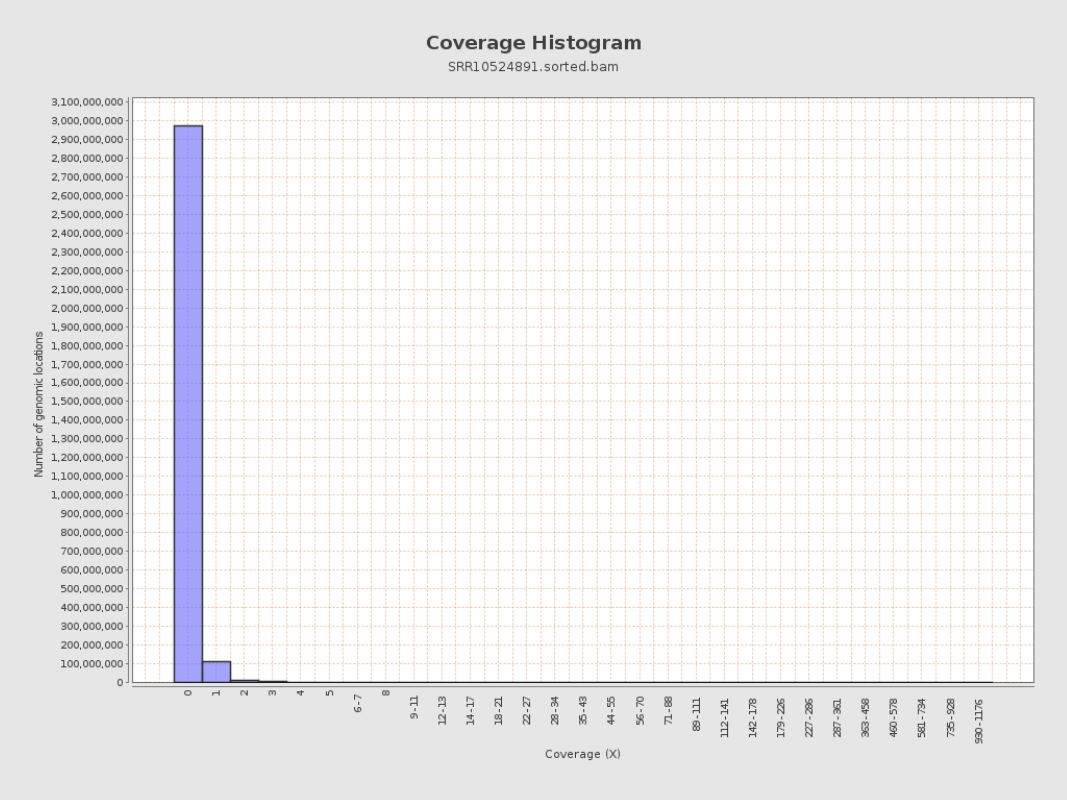
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11216916	0.045	0.8905
chr2	243199373	11890186	0.0489	0.4538
chr3	198022430	9505446	0.048	0.245
chr4	191154276	9184757	0.048	0.2855
chr5	180915260	8574751	0.0474	0.247
chr6	171115067	8141623	0.0476	0.281
chr7	159138663	7913010	0.0497	0.5756

chr8	146364022	7360659	0.0503	0.4142
chr9	141213431	5897881	0.0418	0.3734
chr10	135534747	6734035	0.0497	0.3948
chr11	135006516	6460085	0.0479	0.3698
chr12	133851895	6299664	0.0471	0.2528
chr13	115169878	4479722	0.0389	0.2205
chr14	107349540	4315129	0.0402	0.2442
chr15	102531392	4038116	0.0394	0.2216
chr16	90354753	4018997	0.0445	0.2631
chr17	81195210	3742278	0.0461	0.2671
chr18	78077248	3780688	0.0484	0.7624
chr19	59128983	2693102	0.0455	0.5972
chr20	63025520	3016037	0.0479	0.2575
chr21	48129895	1898928	0.0395	0.2604
chr22	51304566	1647404	0.0321	0.1999
chrMT	16571	26863	1.6211	1.6888
chrX	155270560	7870568	0.0507	0.3103
chrY	59373566	419909	0.0071	0.179

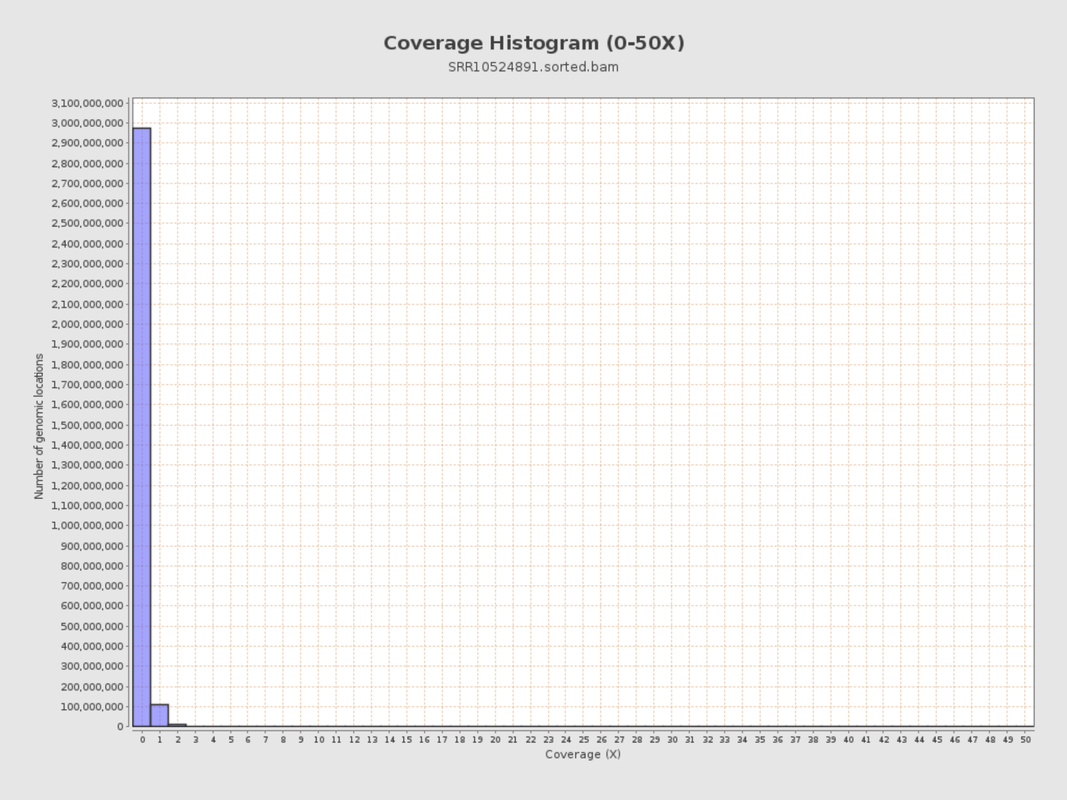
3. Results : Coverage across reference



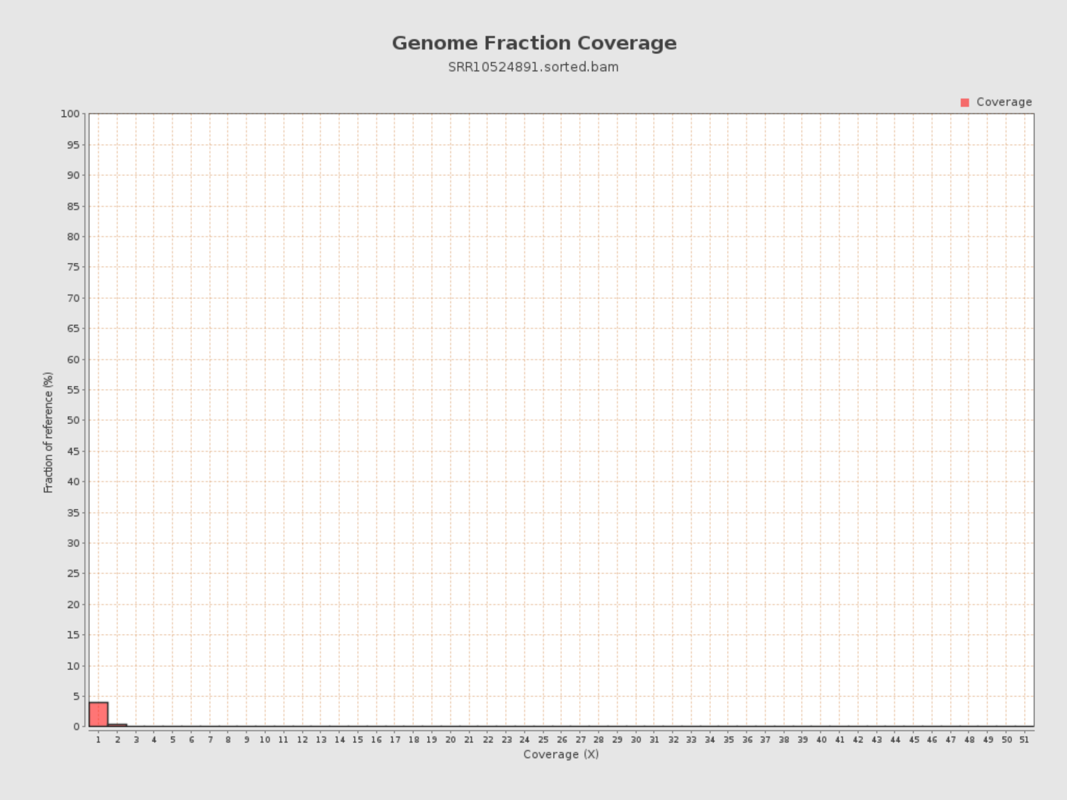
4. Results : Coverage Histogram



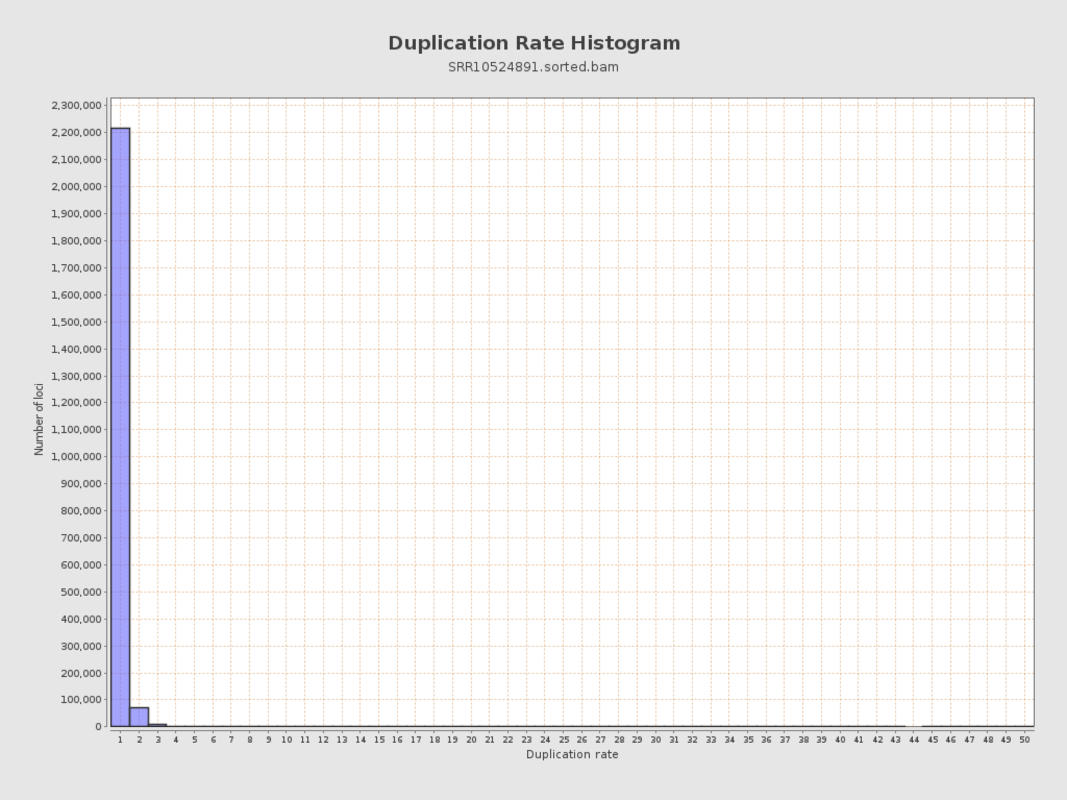
5. Results : Coverage Histogram (0-50X)



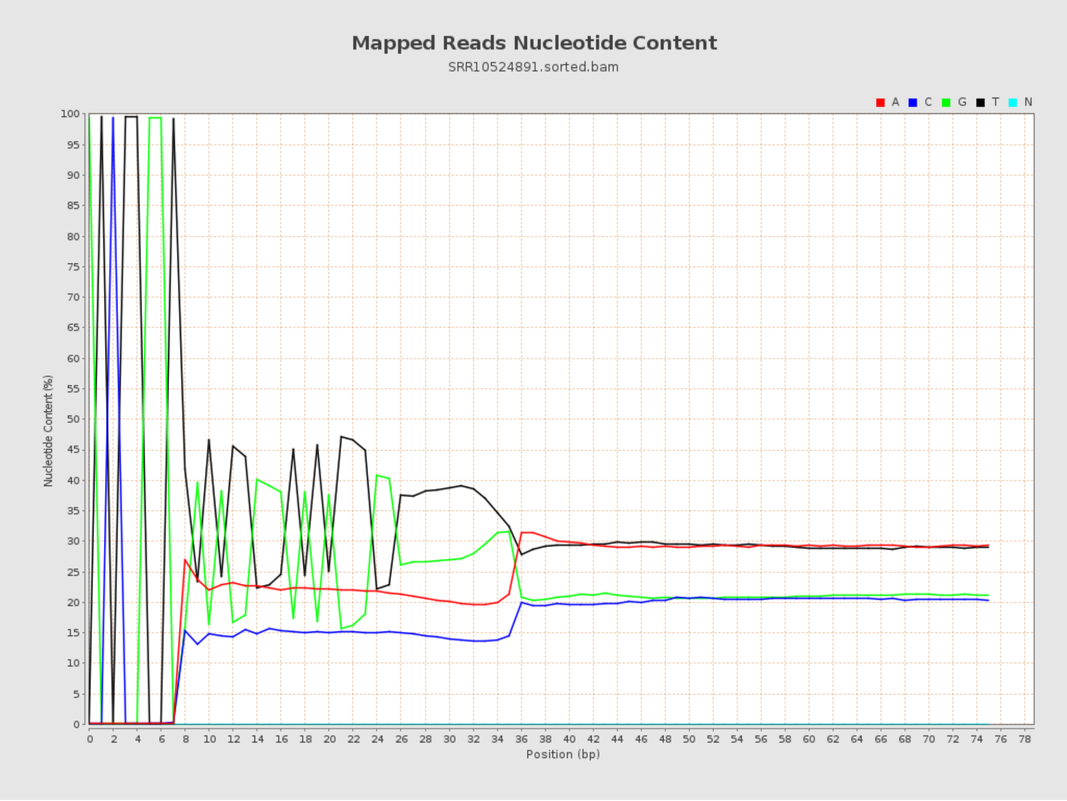
6. Results : Genome Fraction Coverage



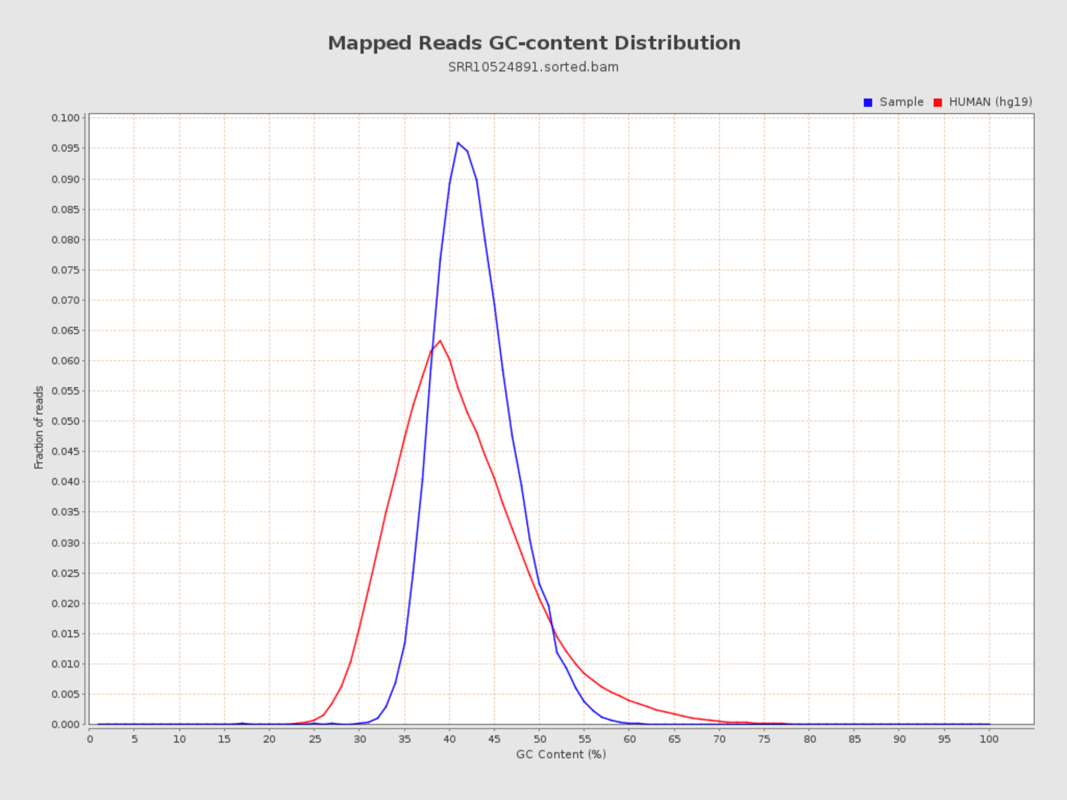
7. Results : Duplication Rate Histogram



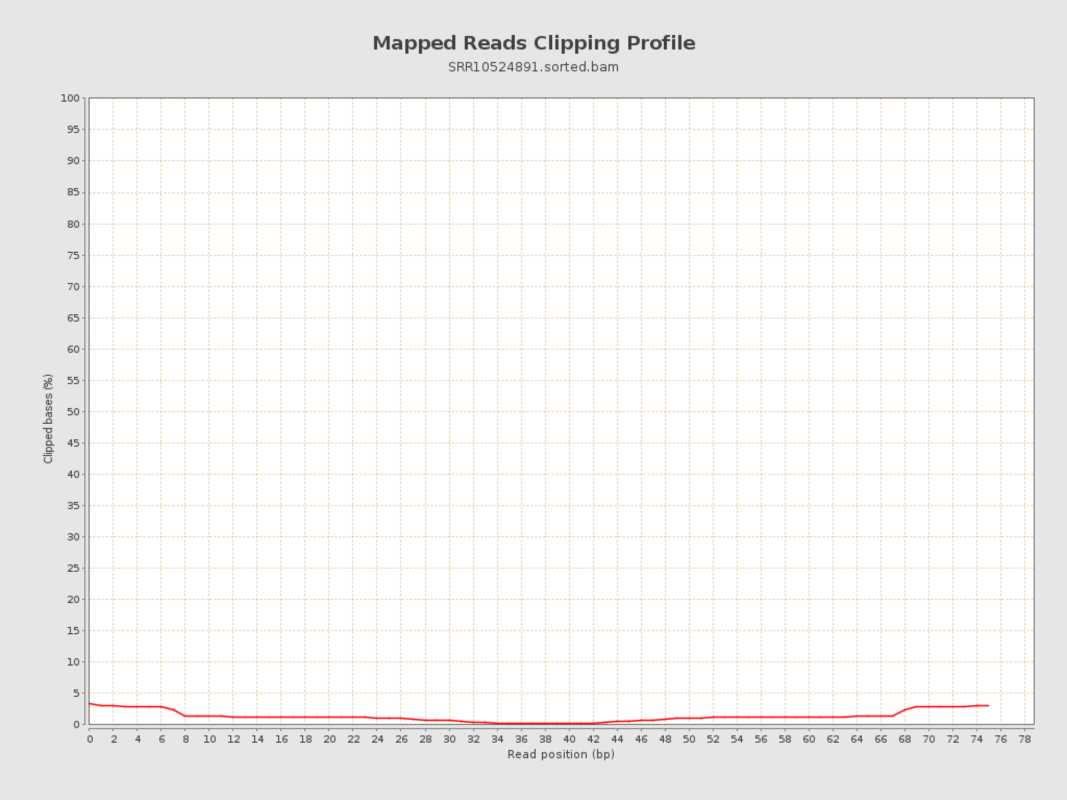
8. Results : Mapped Reads Nucleotide Content



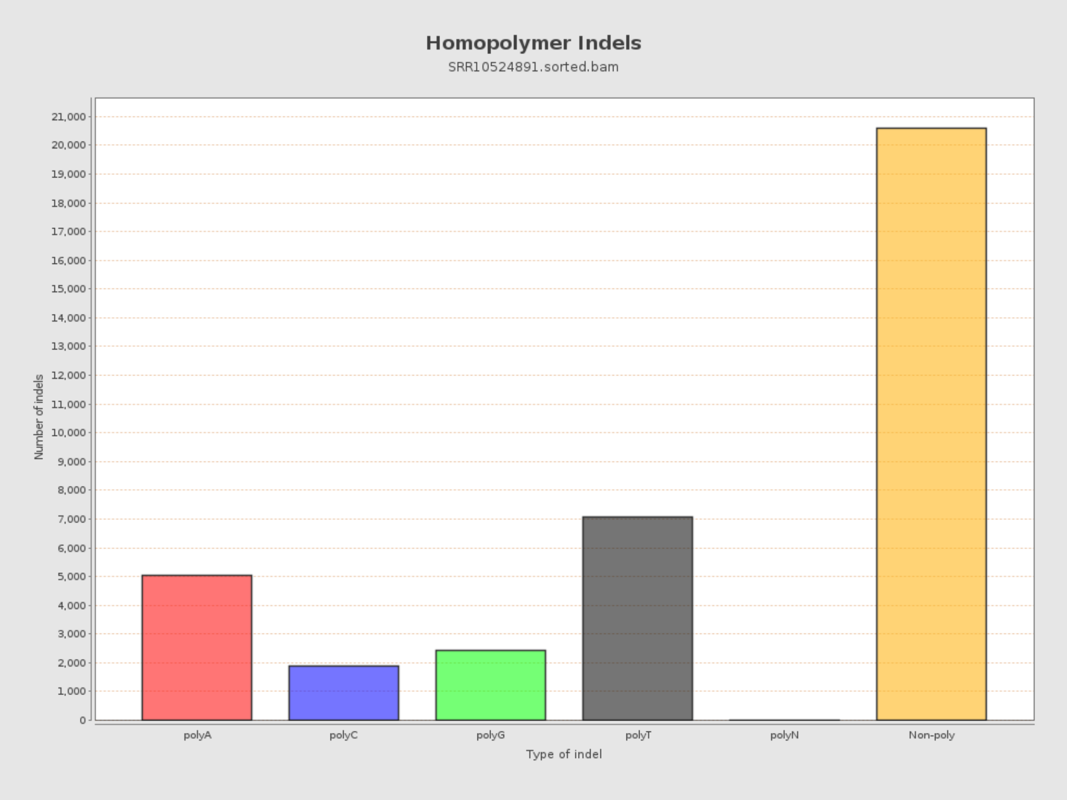
9. Results : Mapped Reads GC-content Distribution



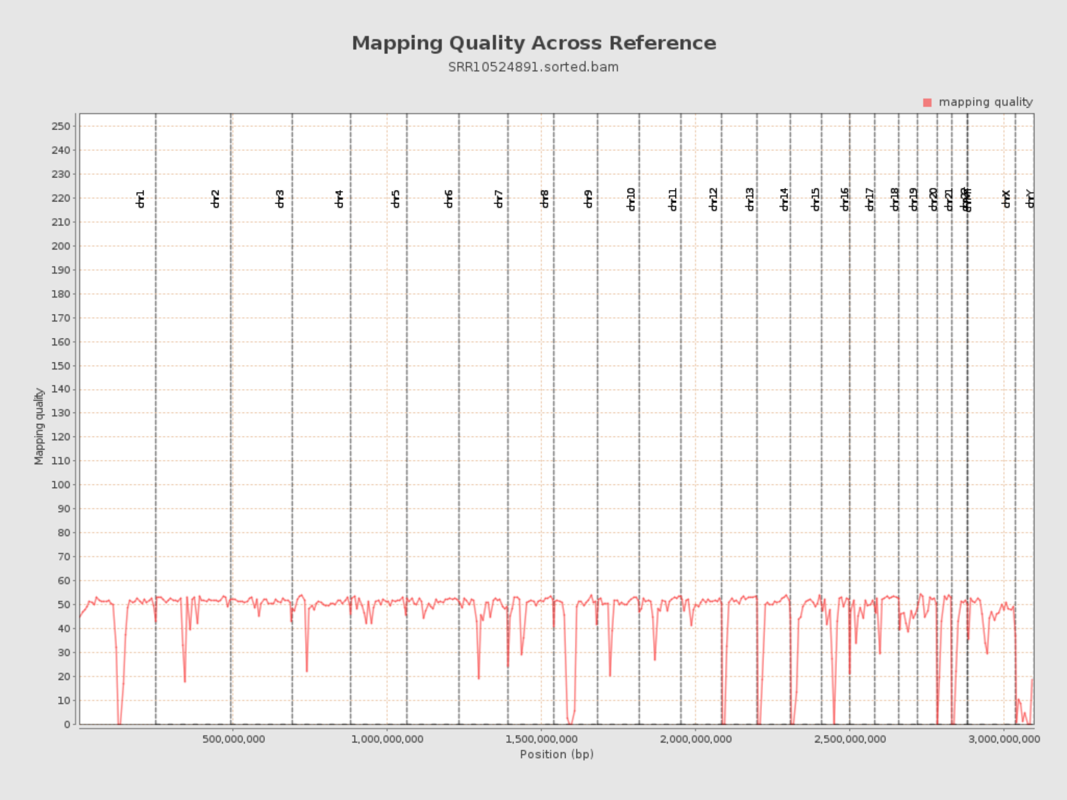
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram