Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 16:52:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524694.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_SRR10524694 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524694.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 16:52:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524694.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,714,963
Mapped reads	2,496,759 / 91.96%
Unmapped reads	218,204 / 8.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,270 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	125,123 / 4.61%
Duplication rate	3.64%
Clipped reads	2,496,795 / 91.96%

2.2. ACGT Content

Number/percentage of A's	36,968,875 / 25.11%
Number/percentage of C's	29,884,760 / 20.3%
Number/percentage of T's	47,301,924 / 32.13%
Number/percentage of G's	33,055,749 / 22.45%
Number/percentage of N's	19,275 / 0.01%
GC Percentage	42.75%

2.3. Coverage

Mean	0.0476

Standard Deviation	0.4226

2.4. Mapping Quality

Mean Mapping Quality	45.67

2.5. Mismatches and indels

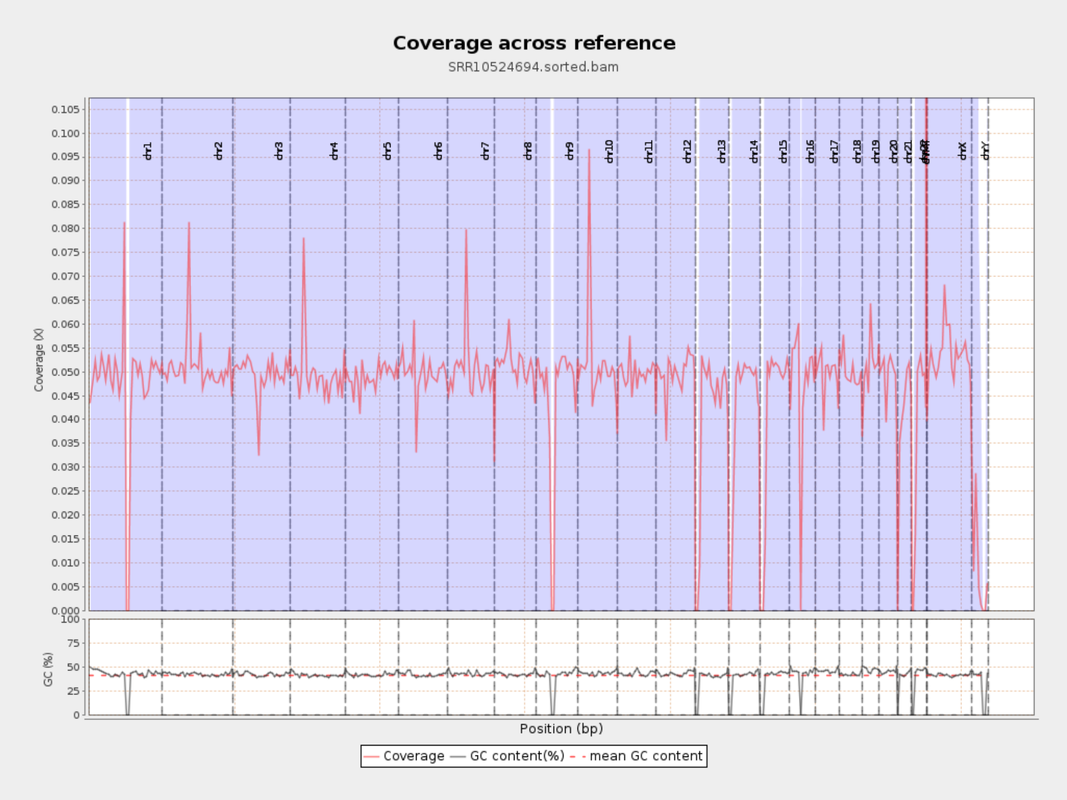
General error rate	0.52%
Mismatches	740,660
Insertions	13,067
Mapped reads with at least one insertion	0.52%
Deletions	28,164
Mapped reads with at least one deletion	1.12%
Homopolymer indels	42.06%

2.6. Chromosome stats

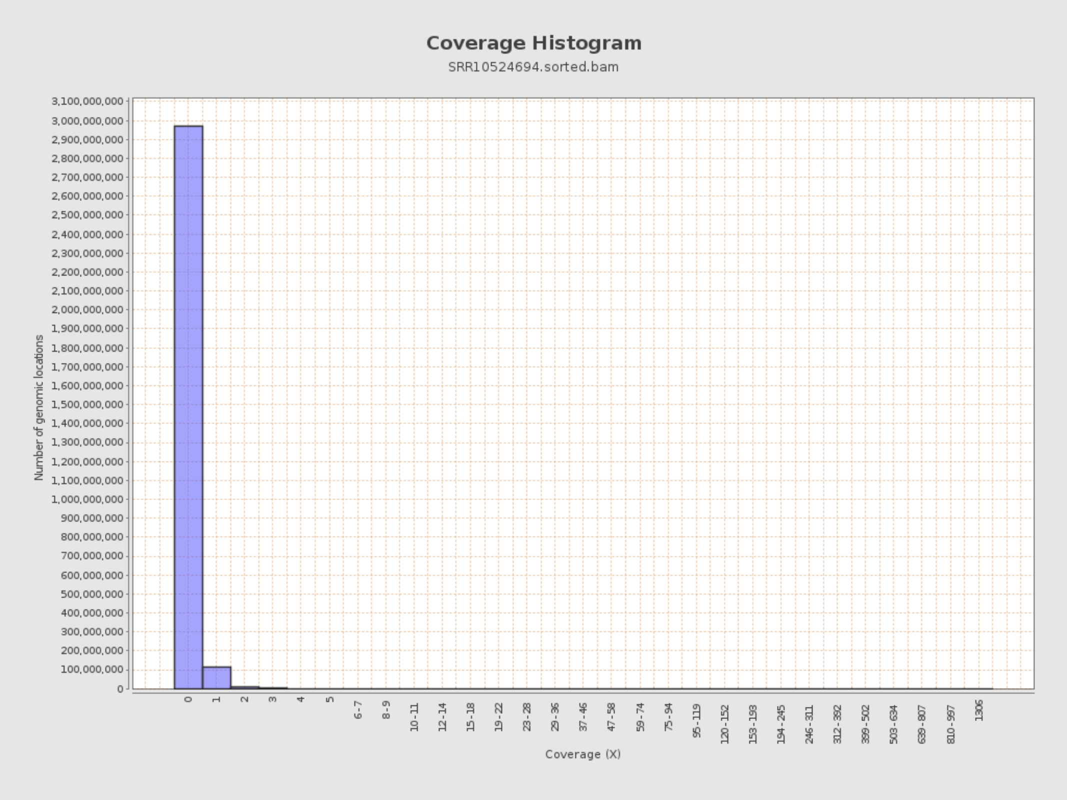
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11771202	0.0472	0.7794
chr2	243199373	12474525	0.0513	0.6216
chr3	198022430	9779891	0.0494	0.2529
chr4	191154276	9477533	0.0496	0.2934
chr5	180915260	8853839	0.0489	0.2537
chr6	171115067	8533370	0.0499	0.3054
chr7	159138663	8122578	0.051	0.5241

chr8	146364022	7531086	0.0515	0.4417
chr9	141213431	6196357	0.0439	0.341
chr10	135534747	7058196	0.0521	0.4397
chr11	135006516	6691466	0.0496	0.3481
chr12	133851895	6666743	0.0498	0.2565
chr13	115169878	4639151	0.0403	0.2291
chr14	107349540	4412232	0.0411	0.2409
chr15	102531392	4202030	0.041	0.2348
chr16	90354753	4265831	0.0472	0.2792
chr17	81195210	3998028	0.0492	0.2787
chr18	78077248	3916636	0.0502	0.6417
chr19	59128983	3055148	0.0517	0.5713
chr20	63025520	3102068	0.0492	0.2586
chr21	48129895	1927377	0.04	0.2663
chr22	51304566	1775181	0.0346	0.2121
chrMT	16571	40801	2.4622	2.1151
chrX	155270560	8308967	0.0535	0.2979
chrY	59373566	475241	0.008	0.2575

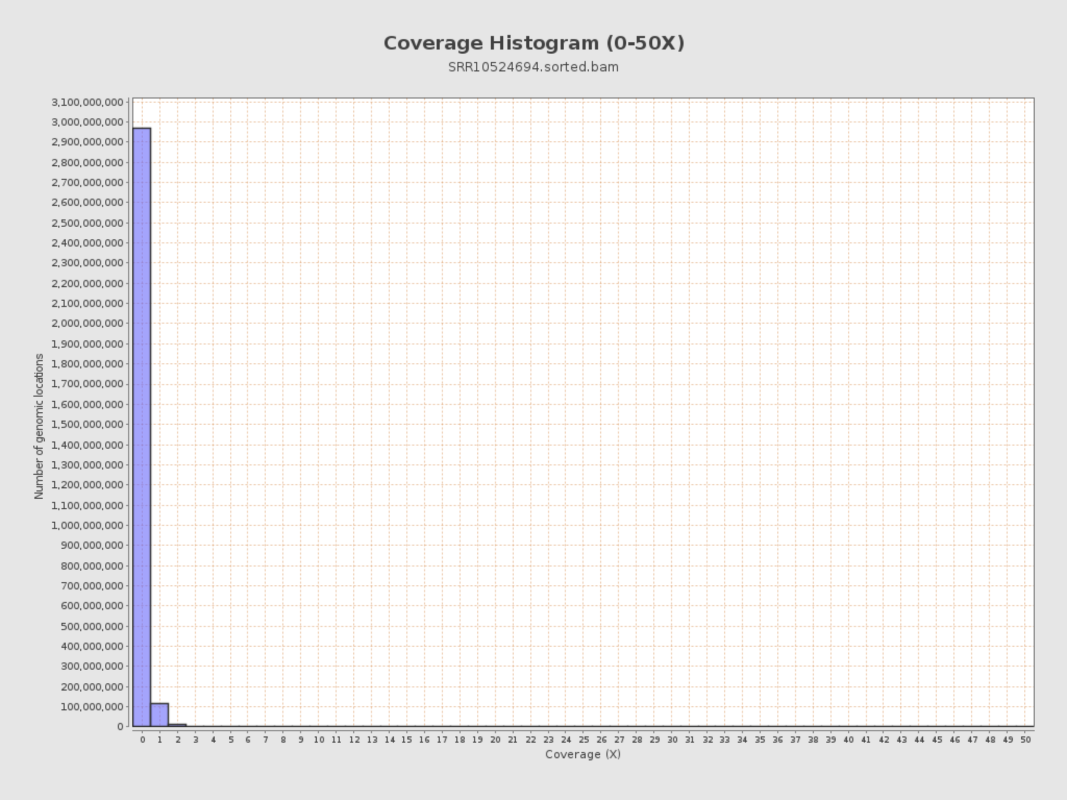
3. Results : Coverage across reference



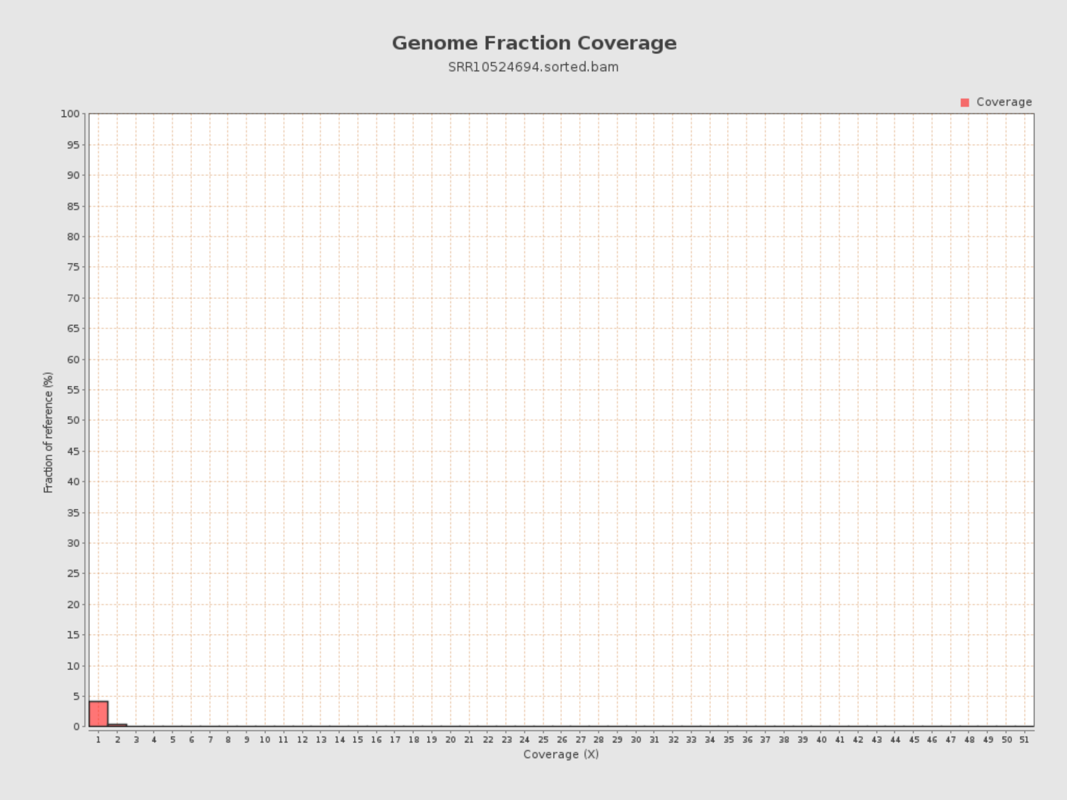
4. Results : Coverage Histogram



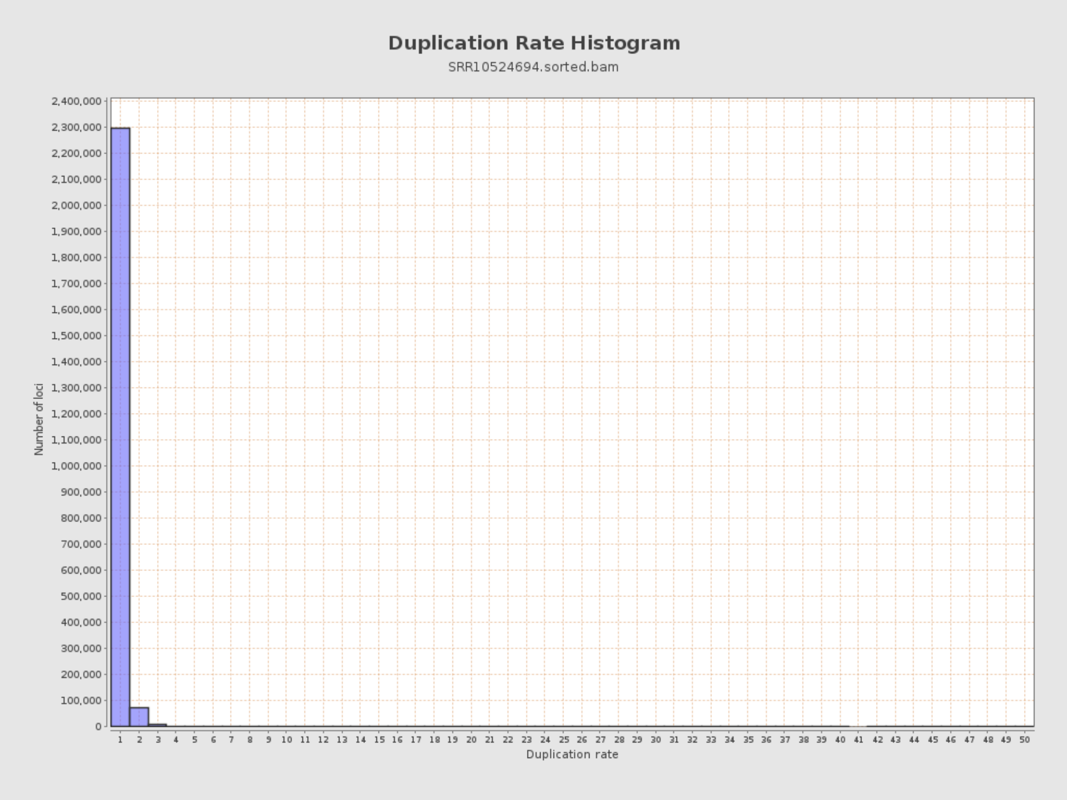
5. Results : Coverage Histogram (0-50X)



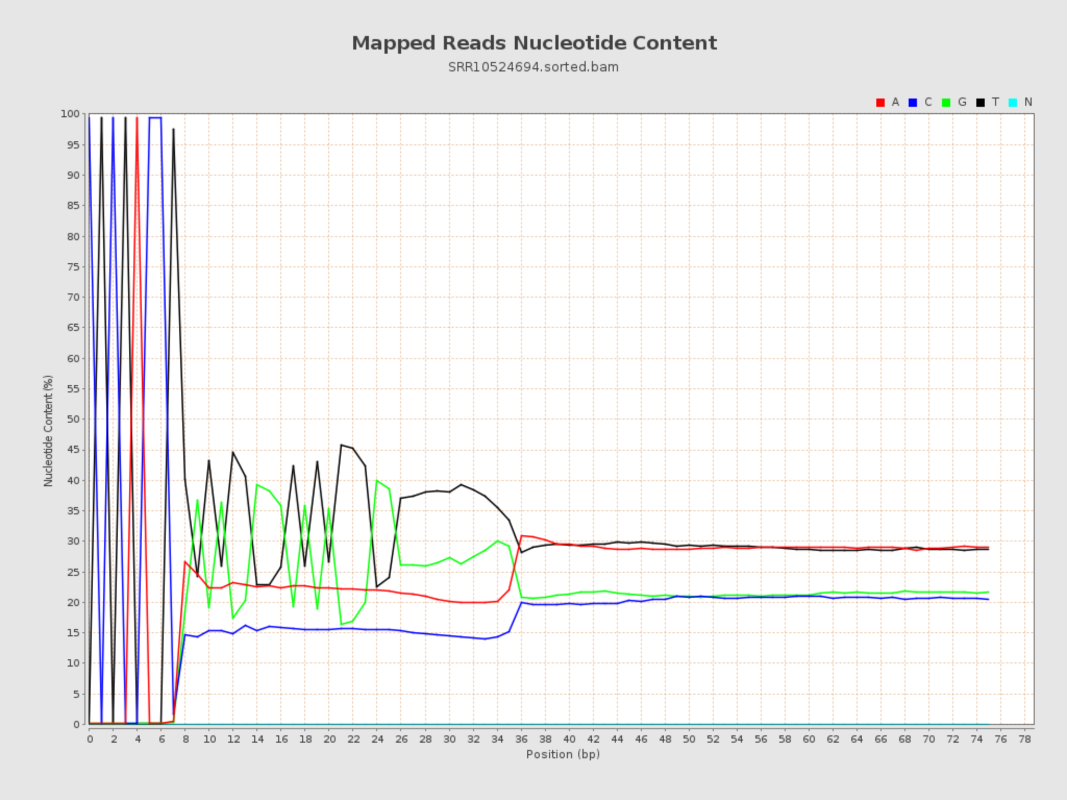
6. Results : Genome Fraction Coverage



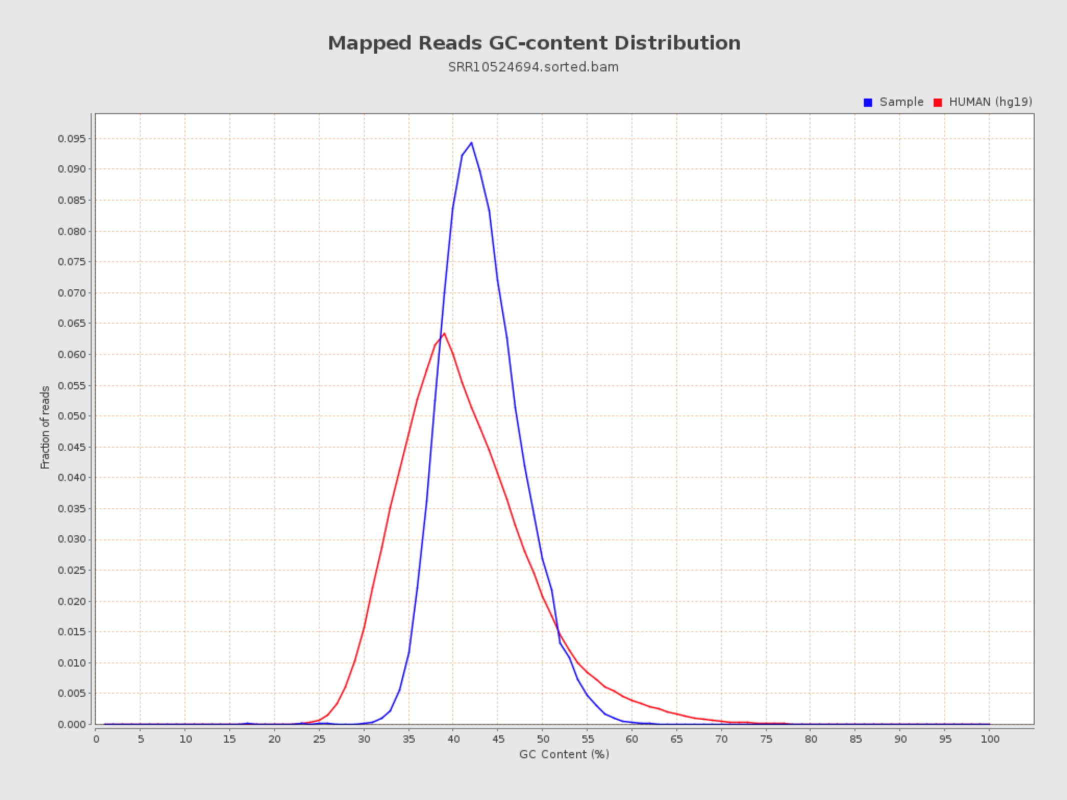
7. Results : Duplication Rate Histogram



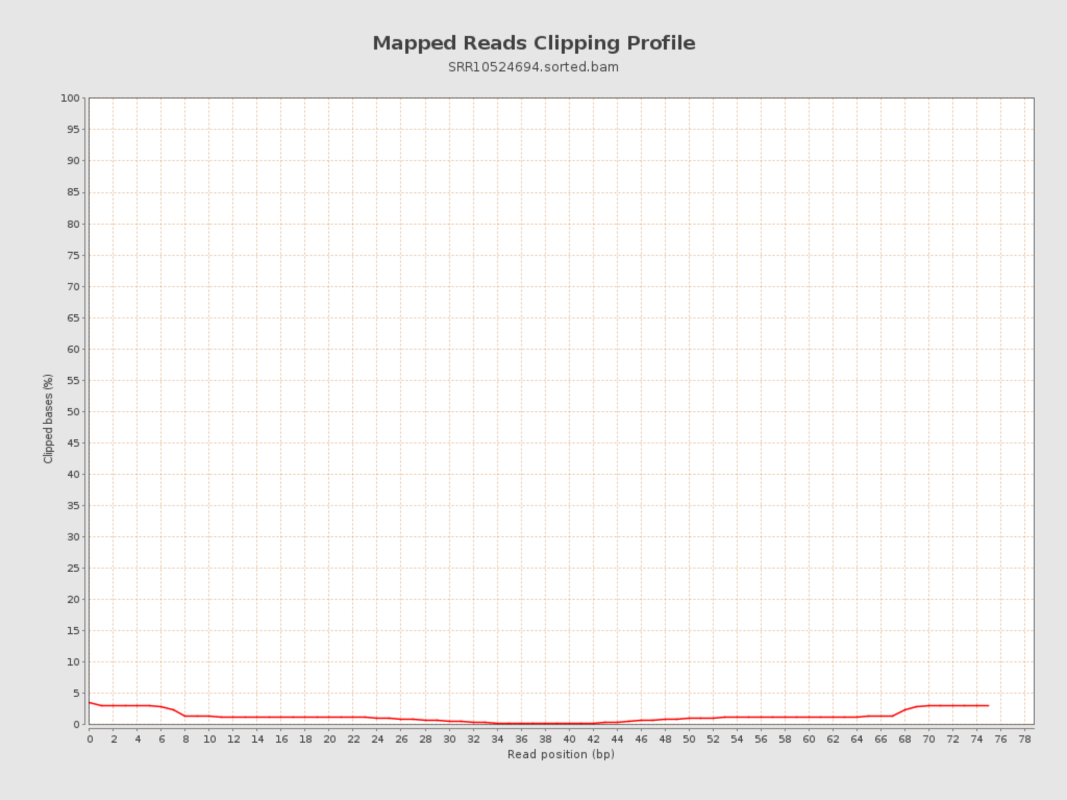
8. Results : Mapped Reads Nucleotide Content



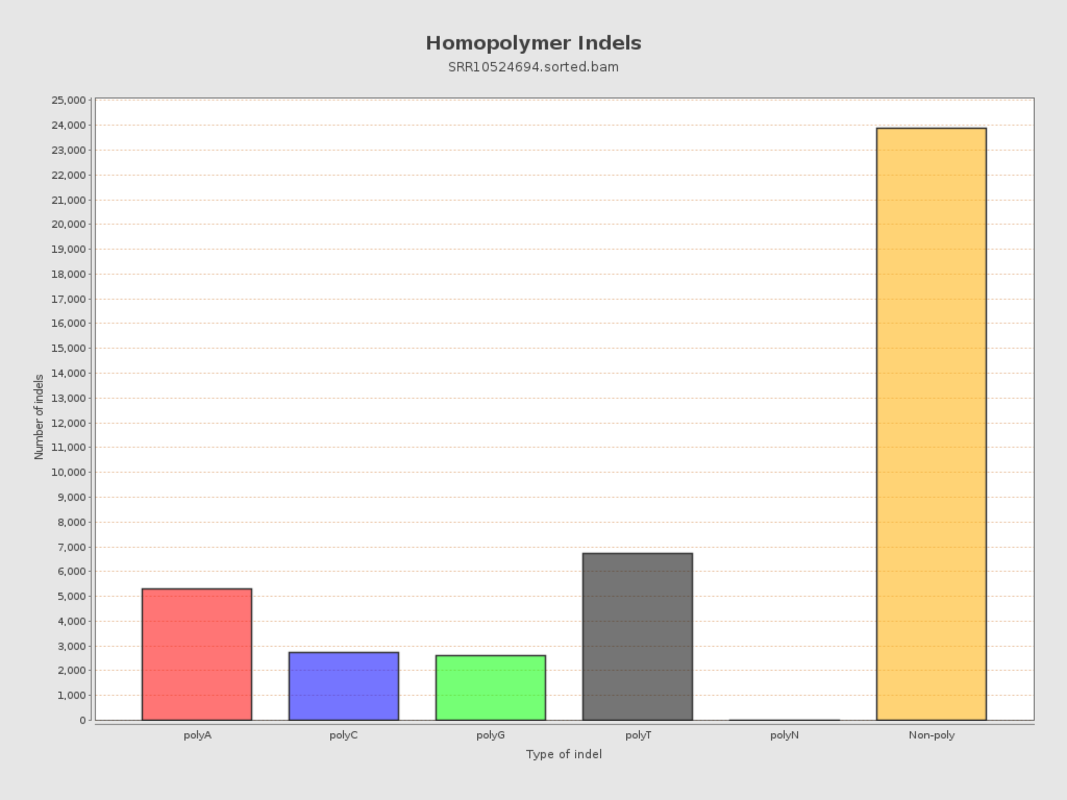
9. Results : Mapped Reads GC-content Distribution



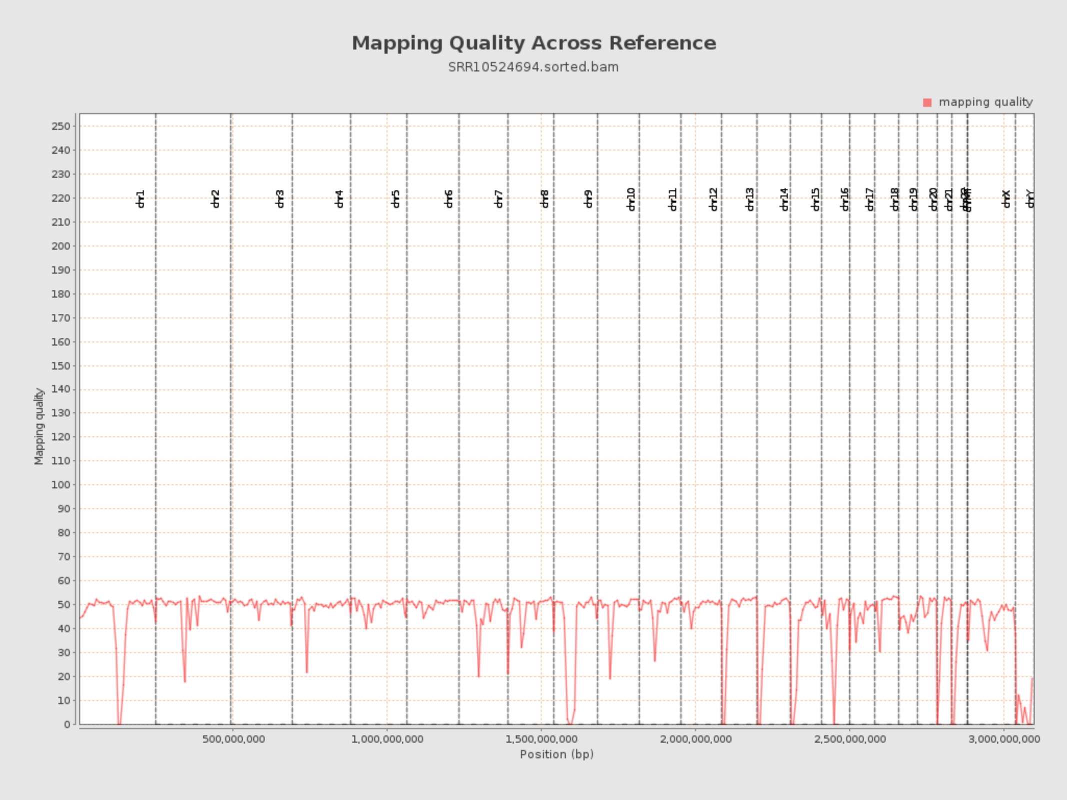
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram