Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 04:02:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524431.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_SRR10524431 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524431.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 04:02:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524431.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,213,690
Mapped reads	2,024,089 / 91.44%
Unmapped reads	189,601 / 8.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,943 / 0.4%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	117,882 / 5.33%
Duplication rate	4.22%
Clipped reads	2,031,873 / 91.79%

2.2. ACGT Content

Number/percentage of A's	28,612,814 / 24.16%
Number/percentage of C's	24,003,705 / 20.27%
Number/percentage of T's	36,344,341 / 30.69%
Number/percentage of G's	29,438,753 / 24.86%
Number/percentage of N's	12,482 / 0.01%
GC Percentage	45.13%

2.3. Coverage

Mean	0.0383

Standard Deviation	0.3865

2.4. Mapping Quality

Mean Mapping Quality	44.77

2.5. Mismatches and indels

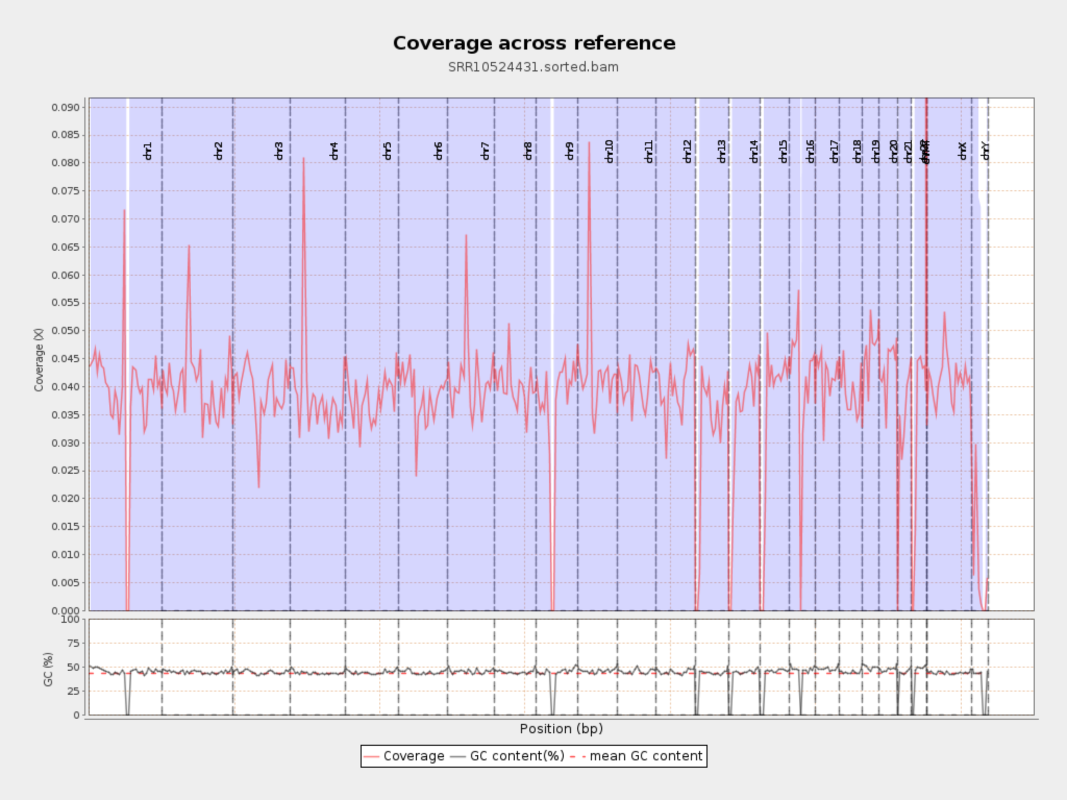
General error rate	0.53%
Mismatches	610,432
Insertions	7,411
Mapped reads with at least one insertion	0.36%
Deletions	21,115
Mapped reads with at least one deletion	1.04%
Homopolymer indels	41.95%

2.6. Chromosome stats

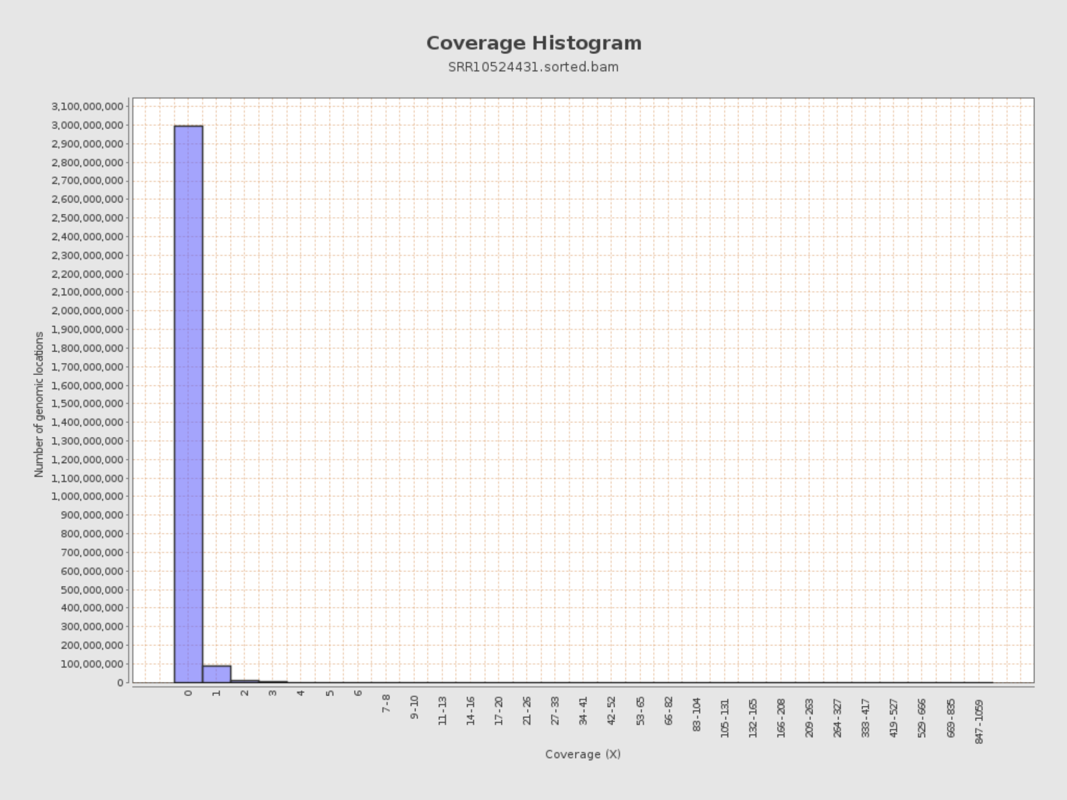
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9630761	0.0386	0.7989
chr2	243199373	9933044	0.0408	0.5176
chr3	198022430	7718092	0.039	0.2246
chr4	191154276	7386030	0.0386	0.3069
chr5	180915260	6864359	0.0379	0.2223
chr6	171115067	6589102	0.0385	0.2469
chr7	159138663	6549597	0.0412	0.4755

chr8	146364022	5863552	0.0401	0.2958
chr9	141213431	4971629	0.0352	0.2765
chr10	135534747	5806118	0.0428	0.4222
chr11	135006516	5446271	0.0403	0.3088
chr12	133851895	5378897	0.0402	0.2351
chr13	115169878	3559787	0.0309	0.2001
chr14	107349540	3547057	0.033	0.2117
chr15	102531392	3593882	0.0351	0.2129
chr16	90354753	3680041	0.0407	0.2534
chr17	81195210	3399935	0.0419	0.2561
chr18	78077248	3045574	0.039	0.5294
chr19	59128983	2734731	0.0463	0.5111
chr20	63025520	2725315	0.0432	0.2594
chr21	48129895	1580919	0.0328	0.2844
chr22	51304566	1561806	0.0304	0.2008
chrMT	16571	14288	0.8622	1.1437
chrX	155270560	6410204	0.0413	0.2561
chrY	59373566	455177	0.0077	0.2553

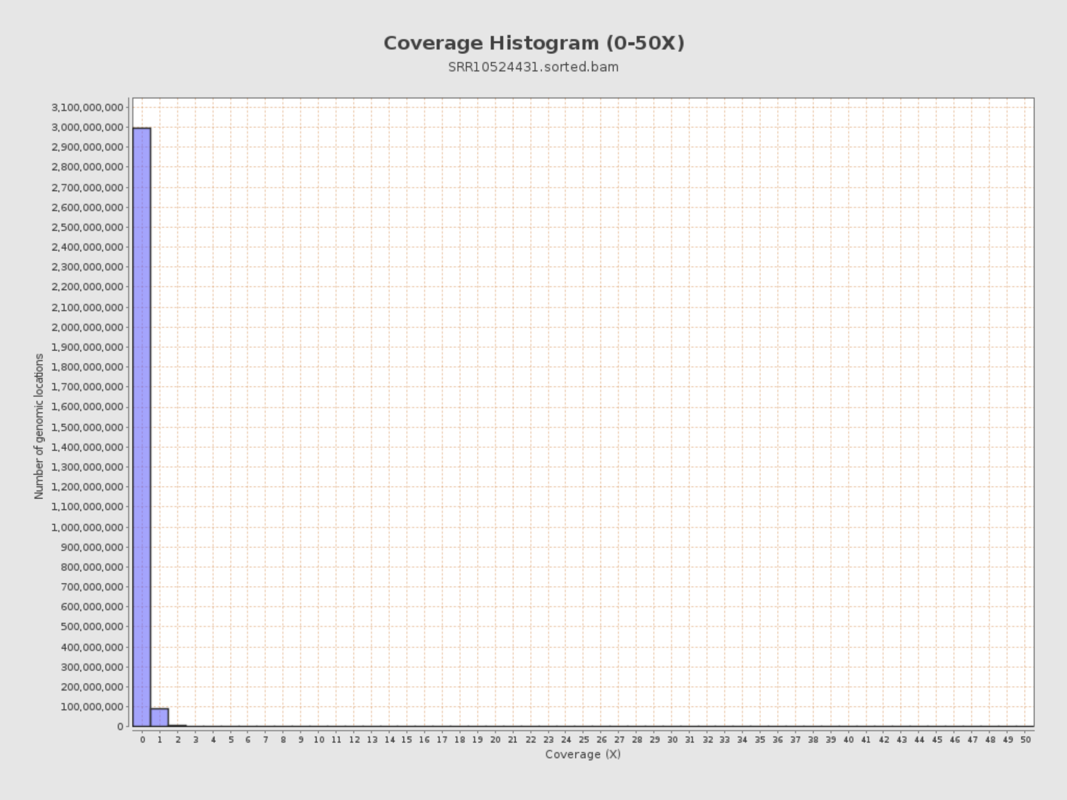
3. Results : Coverage across reference



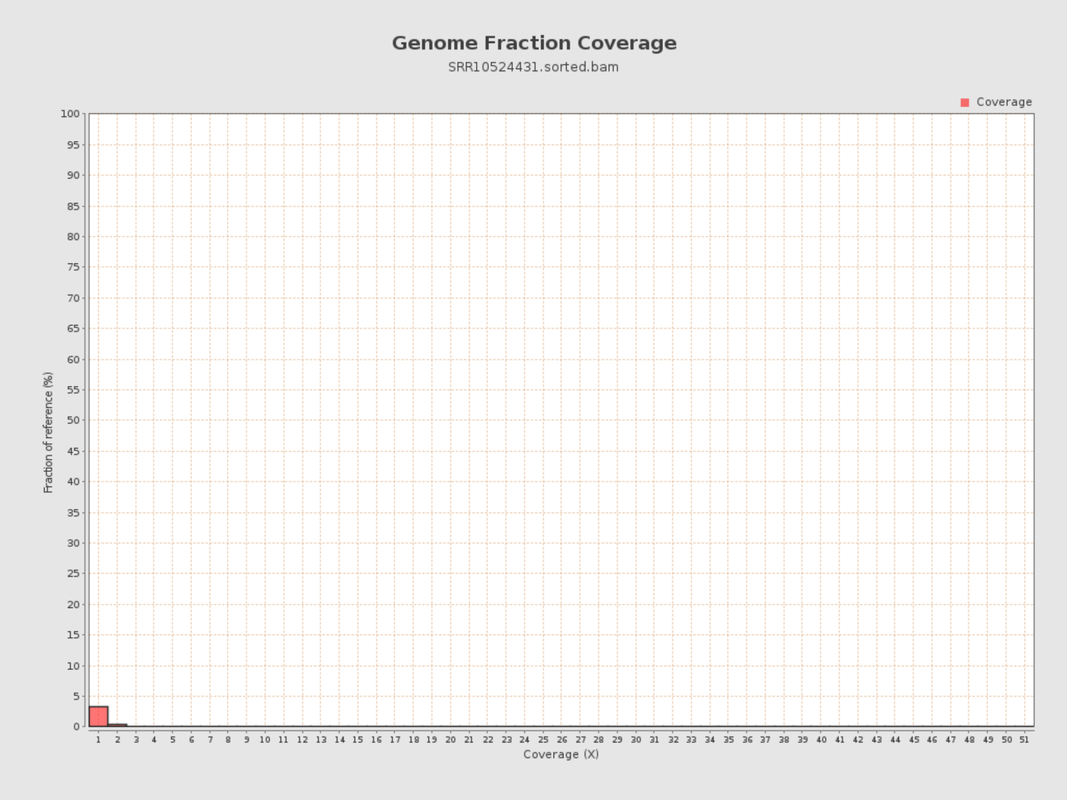
4. Results : Coverage Histogram



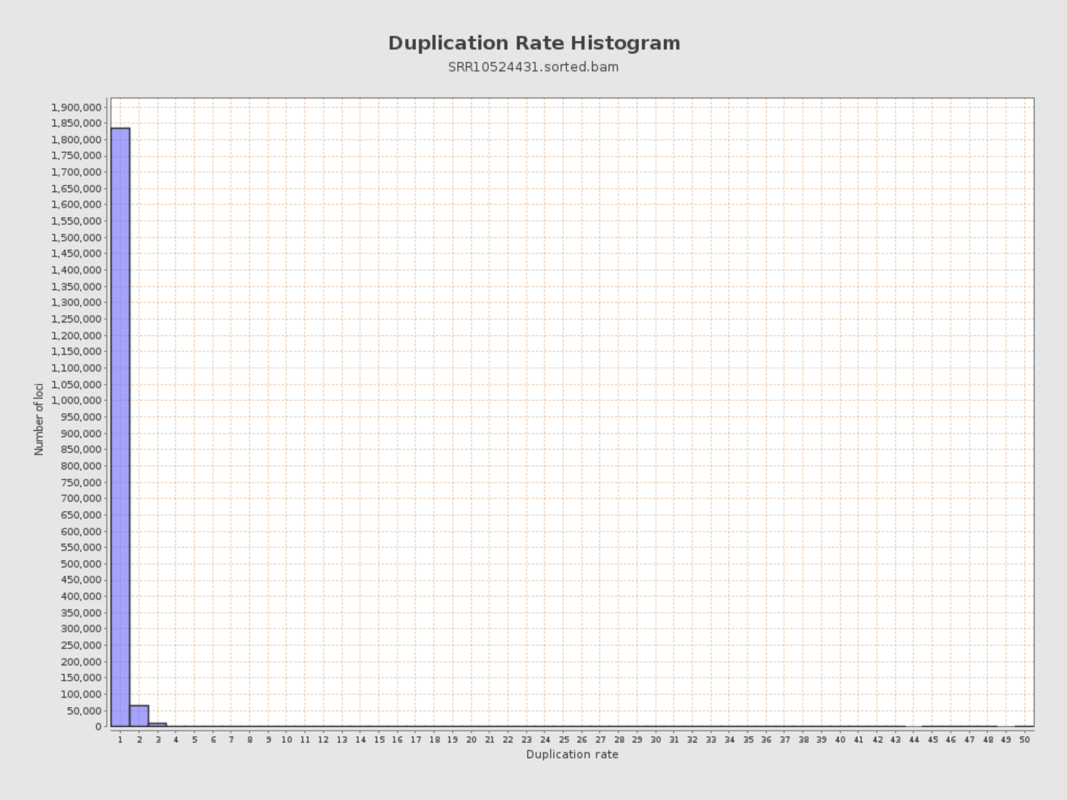
5. Results : Coverage Histogram (0-50X)



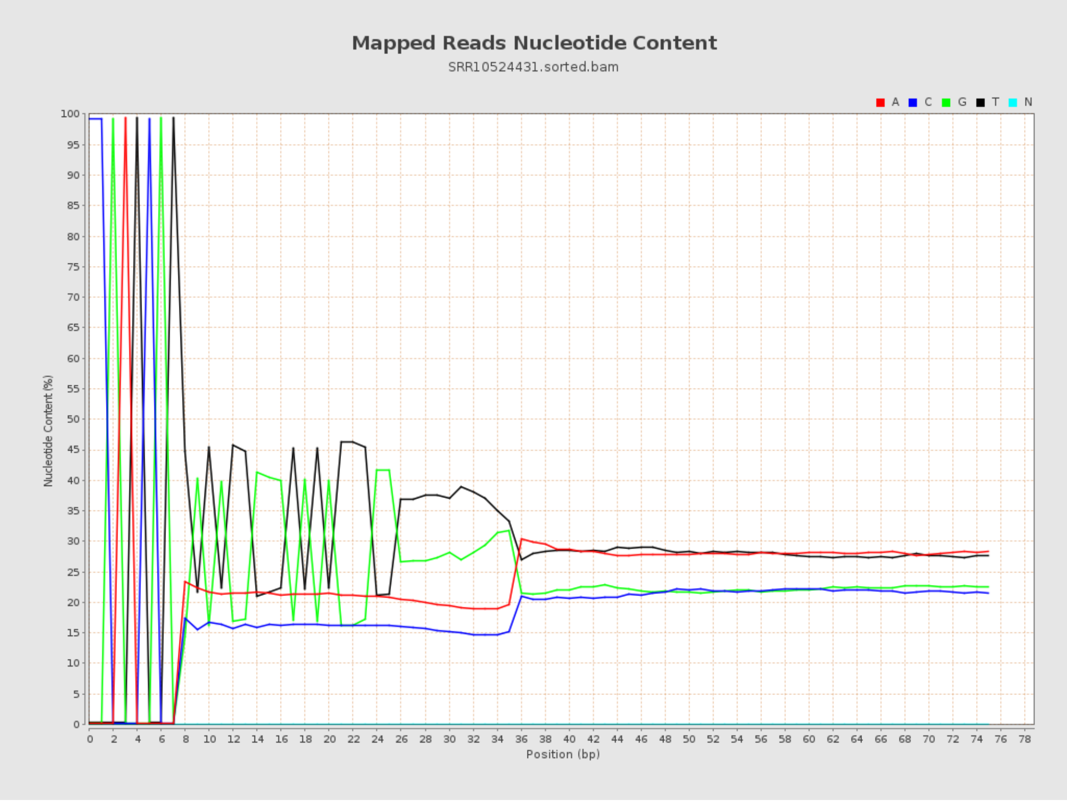
6. Results : Genome Fraction Coverage



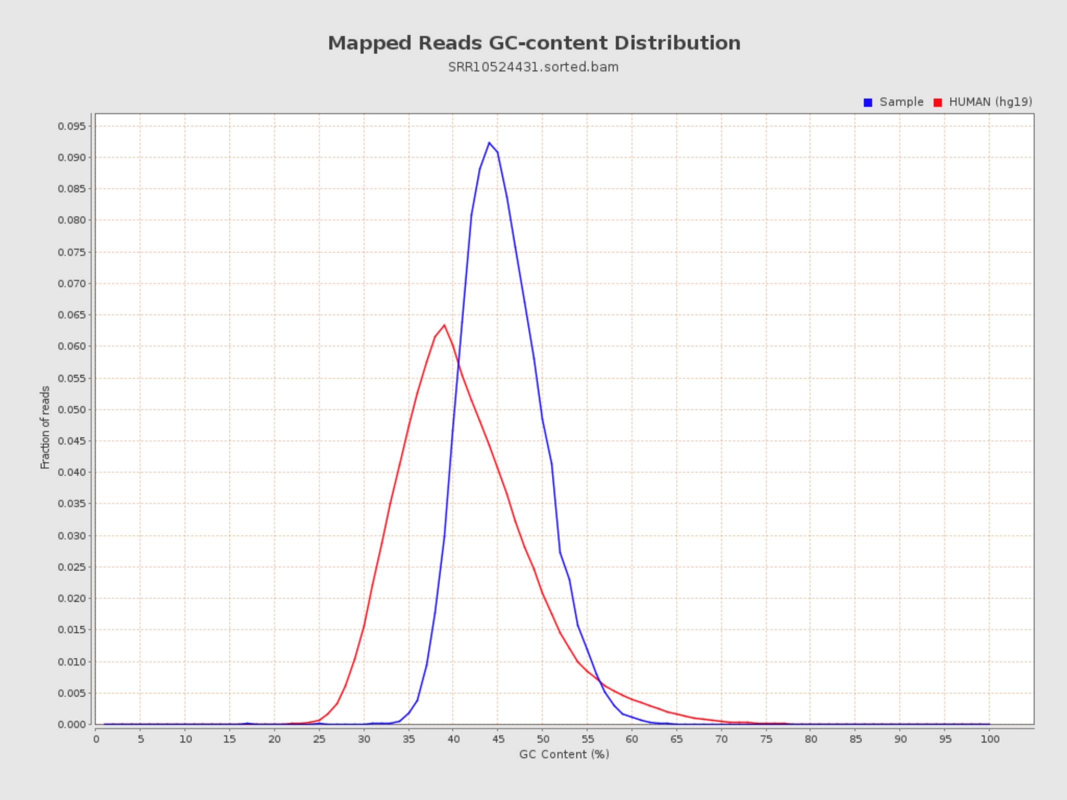
7. Results : Duplication Rate Histogram



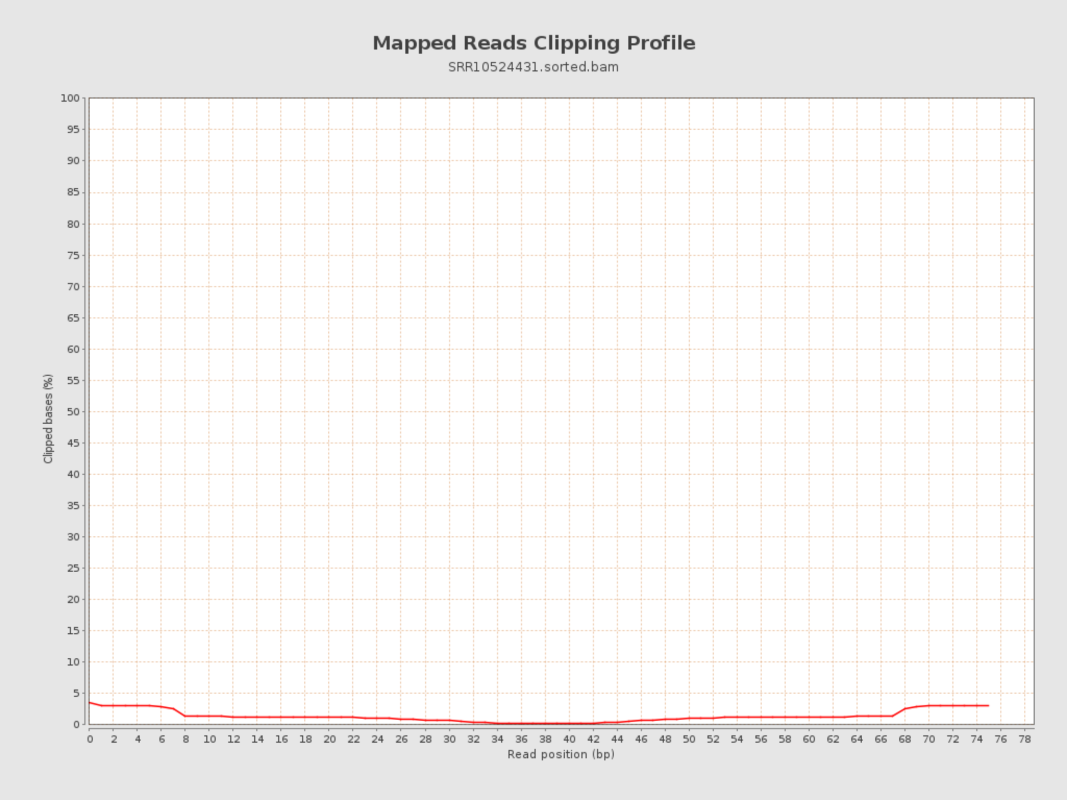
8. Results : Mapped Reads Nucleotide Content



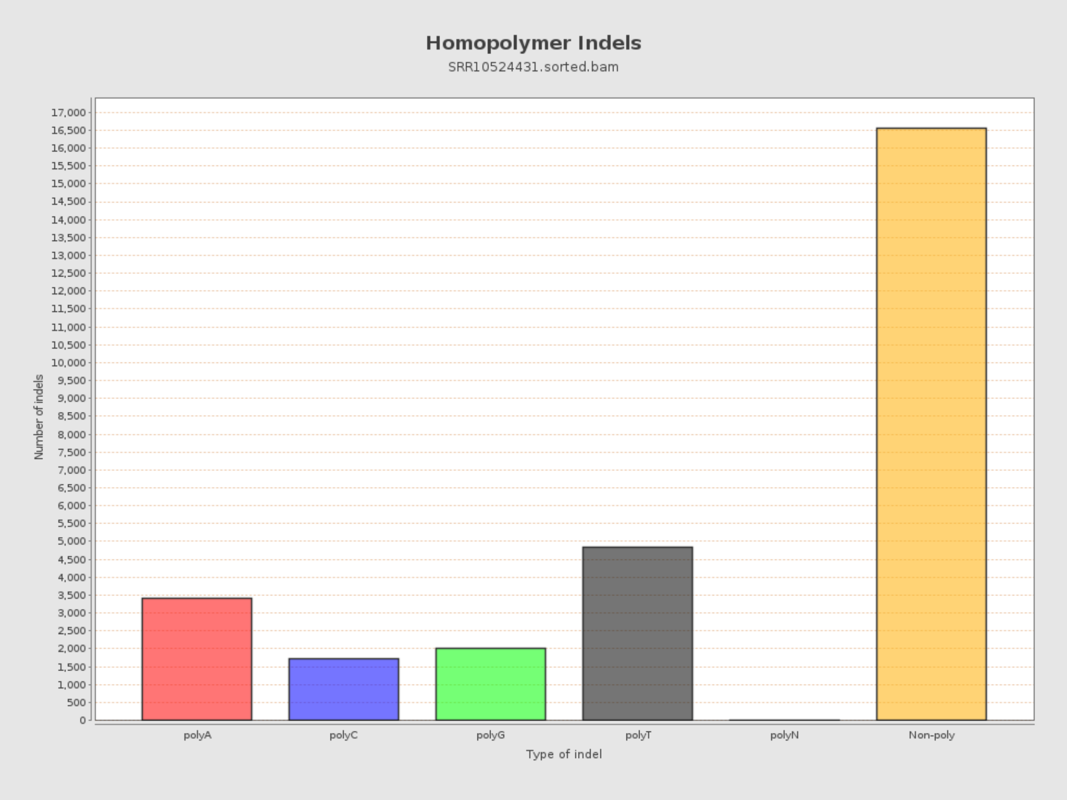
9. Results : Mapped Reads GC-content Distribution



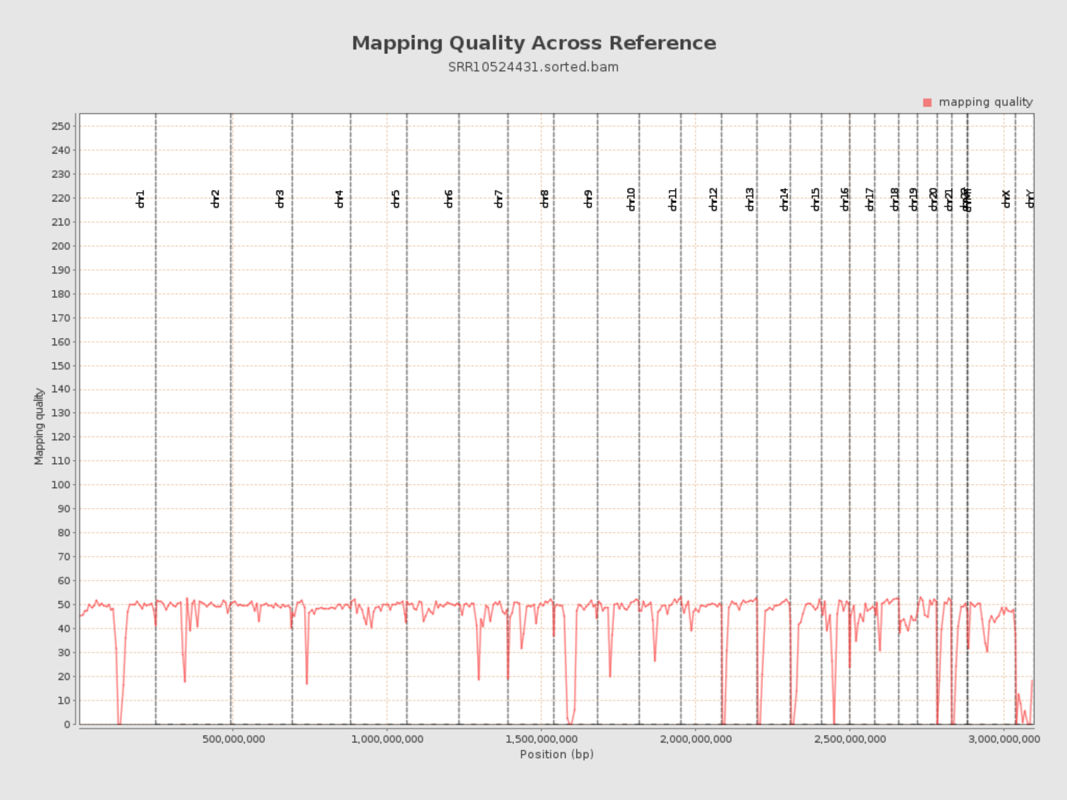
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram