Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 02:30:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524906.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_SRR10524906 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524906.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 02:30:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524906.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	375,114
Mapped reads	346,451 / 92.36%
Unmapped reads	28,663 / 7.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,154 / 0.31%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	6,860 / 1.83%
Duplication rate	1.56%
Clipped reads	347,317 / 92.59%

2.2. ACGT Content

Number/percentage of A's	4,748,685 / 23.66%
Number/percentage of C's	3,914,118 / 19.5%
Number/percentage of T's	6,312,199 / 31.45%
Number/percentage of G's	5,097,981 / 25.4%
Number/percentage of N's	190 / 0%
GC Percentage	44.9%

2.3. Coverage

Mean	0.0065

Standard Deviation	0.0946

2.4. Mapping Quality

Mean Mapping Quality	44.73

2.5. Mismatches and indels

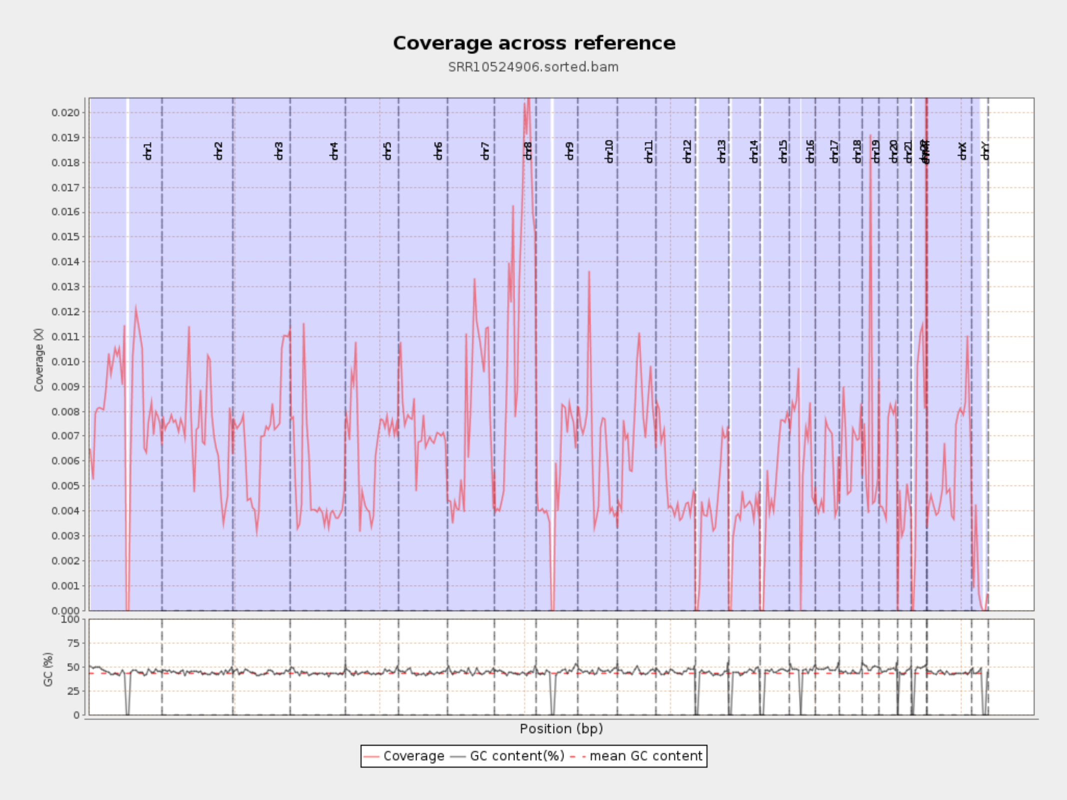
General error rate	0.51%
Mismatches	100,429
Insertions	1,144
Mapped reads with at least one insertion	0.33%
Deletions	3,720
Mapped reads with at least one deletion	1.06%
Homopolymer indels	43.87%

2.6. Chromosome stats

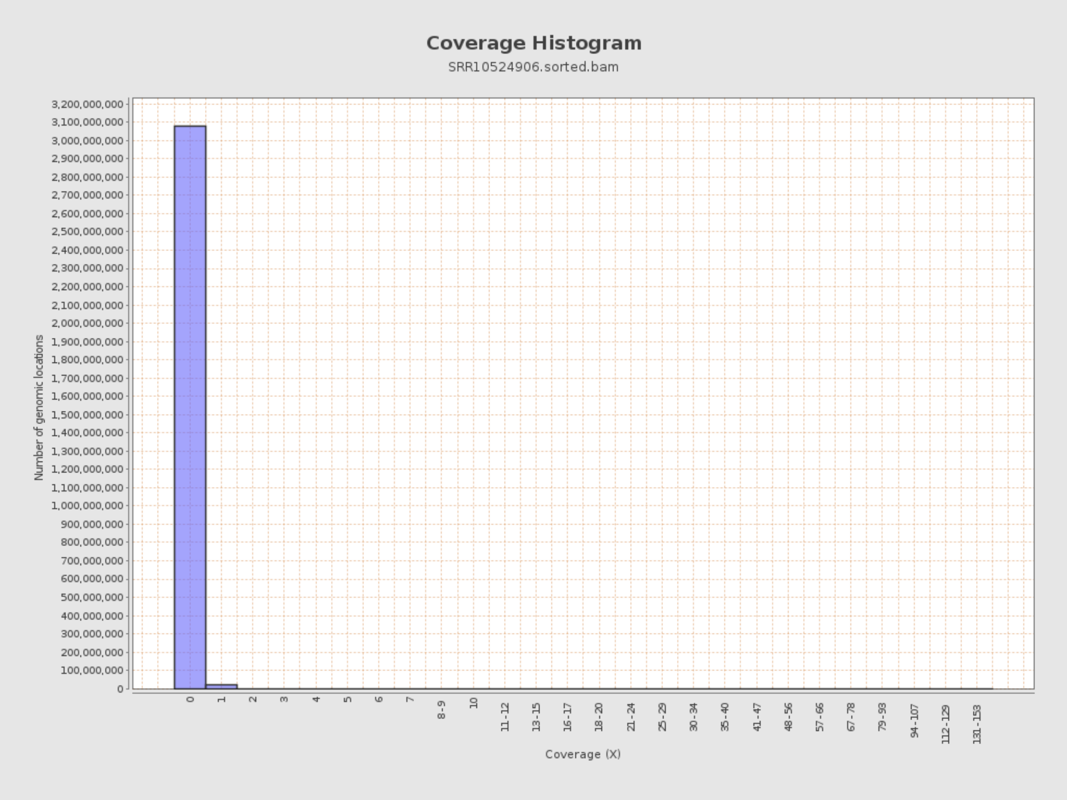
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2049762	0.0082	0.1376
chr2	243199373	1766085	0.0073	0.1082
chr3	198022430	1421643	0.0072	0.0876
chr4	191154276	912083	0.0048	0.0768
chr5	180915260	1197806	0.0066	0.084
chr6	171115067	1256217	0.0073	0.0898
chr7	159138663	1220820	0.0077	0.1081

chr8	146364022	1767634	0.0121	0.1304
chr9	141213431	730625	0.0052	0.0831
chr10	135534747	859257	0.0063	0.0981
chr11	135006516	1007455	0.0075	0.0933
chr12	133851895	666336	0.005	0.0738
chr13	115169878	472382	0.0041	0.066
chr14	107349540	378221	0.0035	0.0624
chr15	102531392	512166	0.005	0.0729
chr16	90354753	591021	0.0065	0.0847
chr17	81195210	439995	0.0054	0.0771
chr18	78077248	523709	0.0067	0.1083
chr19	59128983	418241	0.0071	0.1056
chr20	63025520	386634	0.0061	0.0809
chr21	48129895	178547	0.0037	0.0684
chr22	51304566	348410	0.0068	0.0853
chrMT	16571	4838	0.292	0.6005
chrX	155270560	908924	0.0059	0.0806
chrY	59373566	60814	0.001	0.046

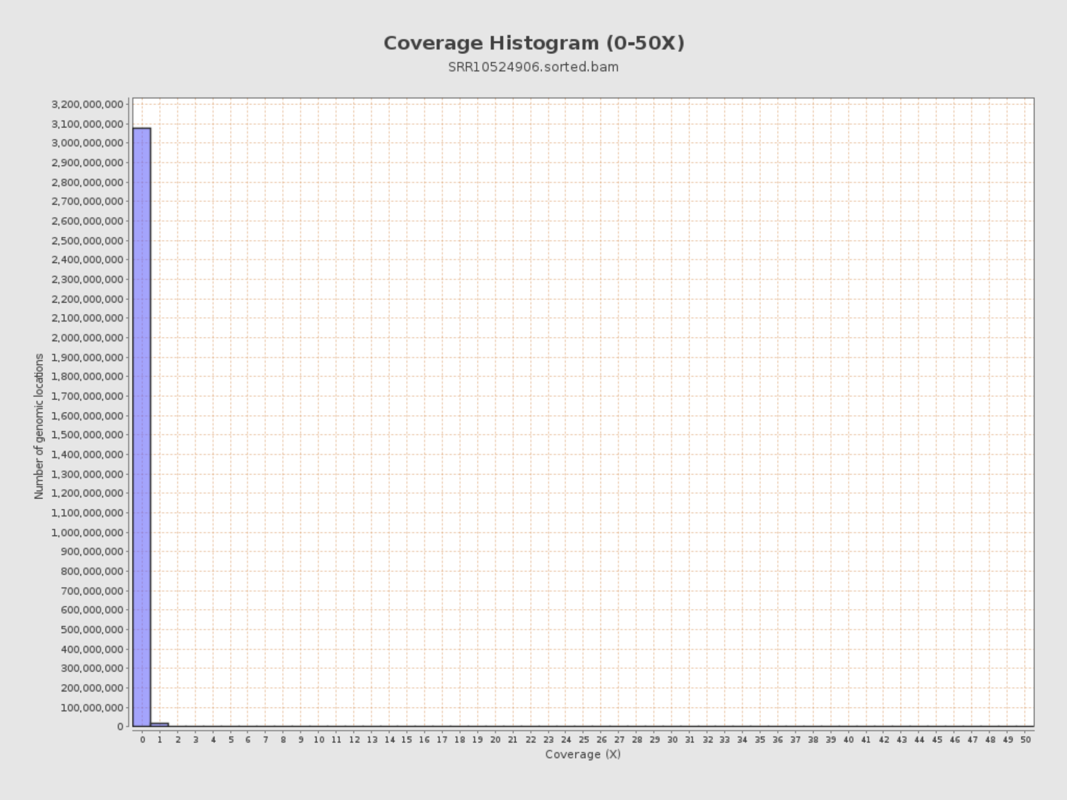
3. Results : Coverage across reference



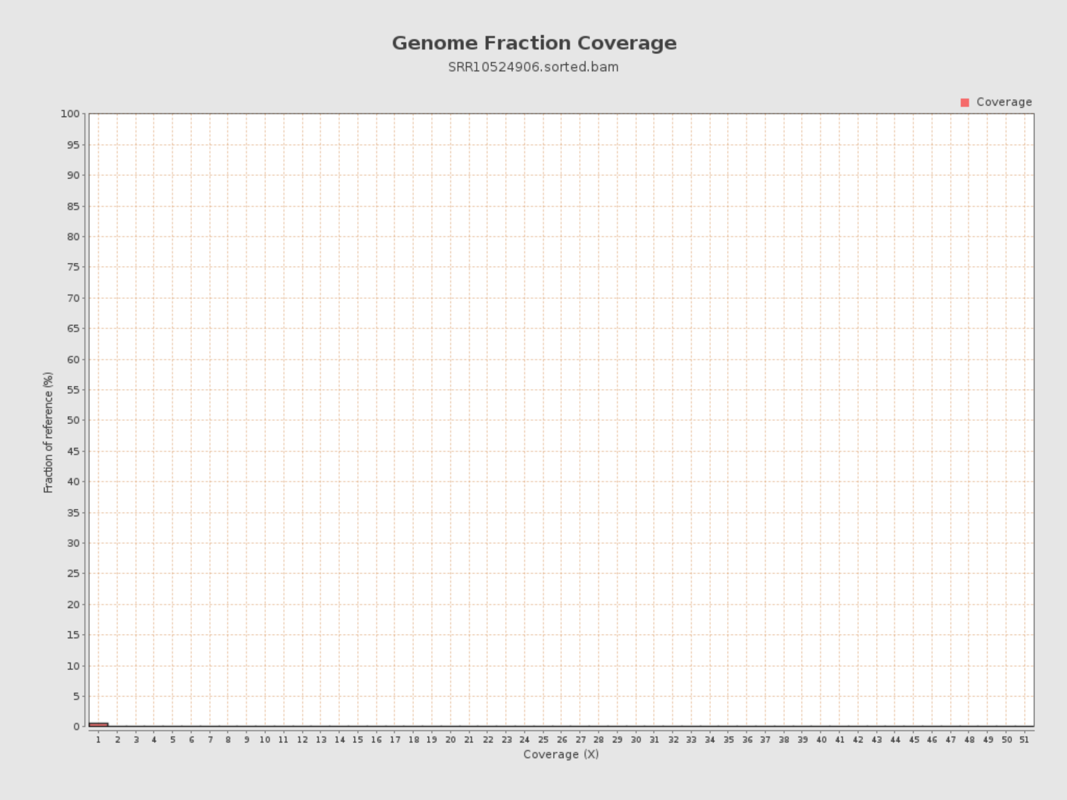
4. Results : Coverage Histogram



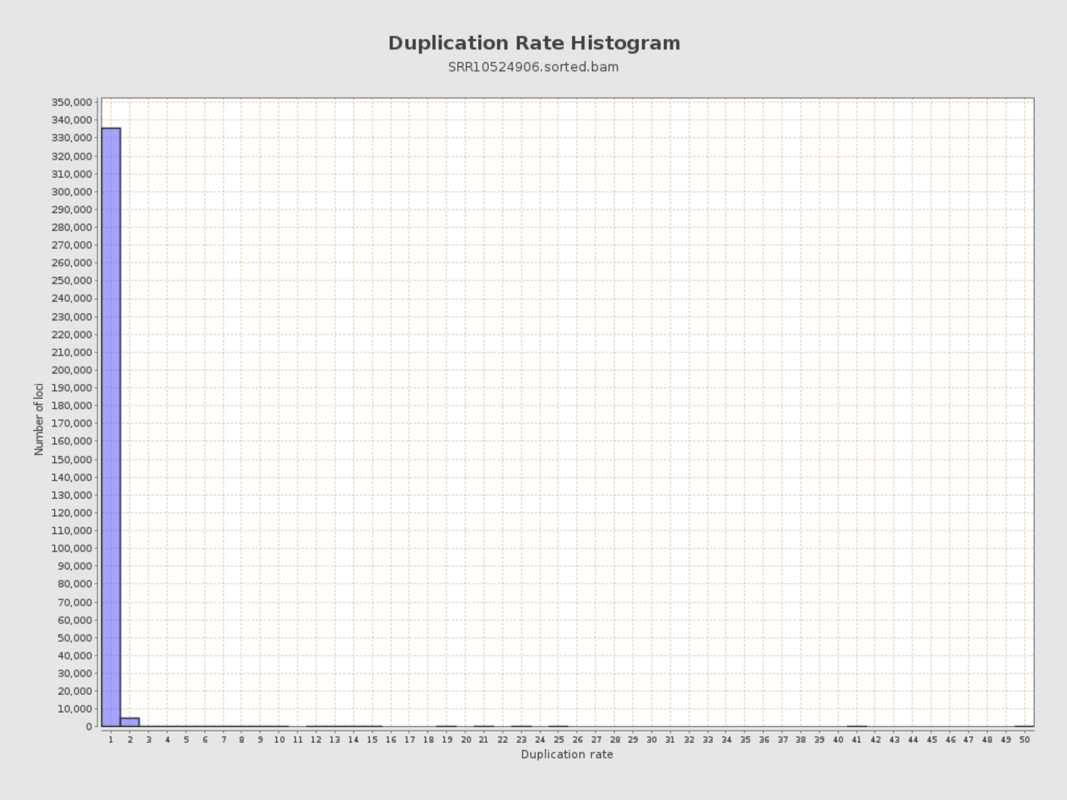
5. Results : Coverage Histogram (0-50X)



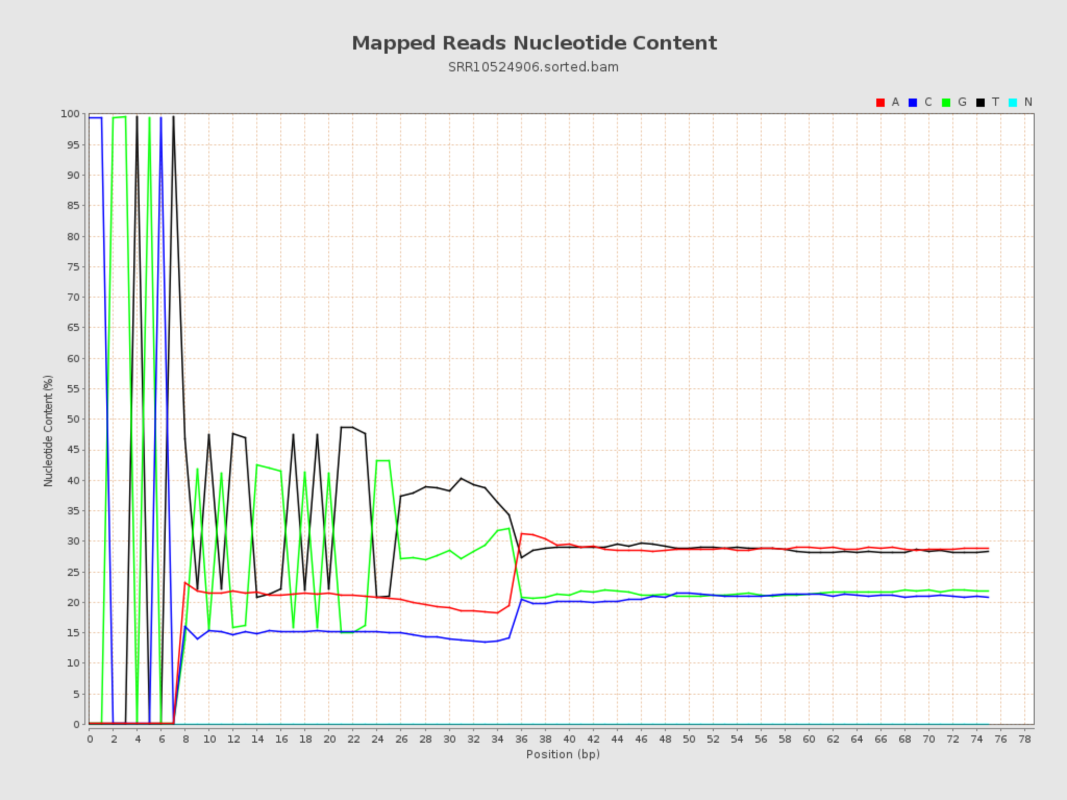
6. Results : Genome Fraction Coverage



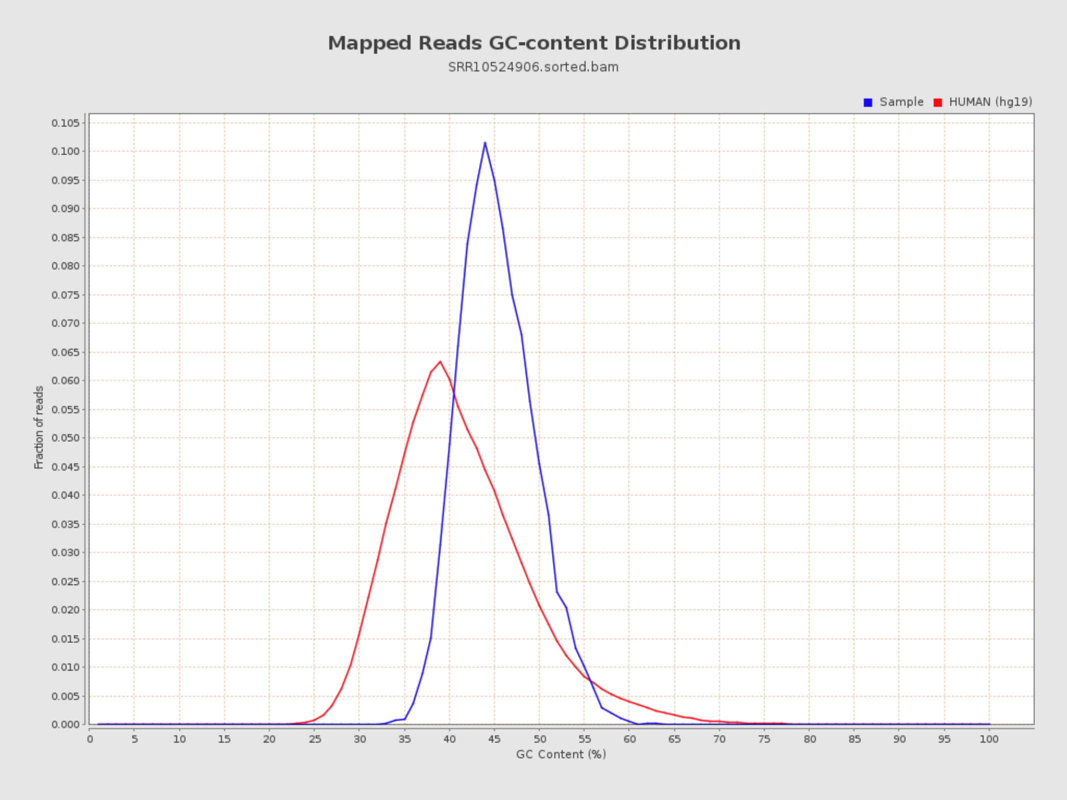
7. Results : Duplication Rate Histogram



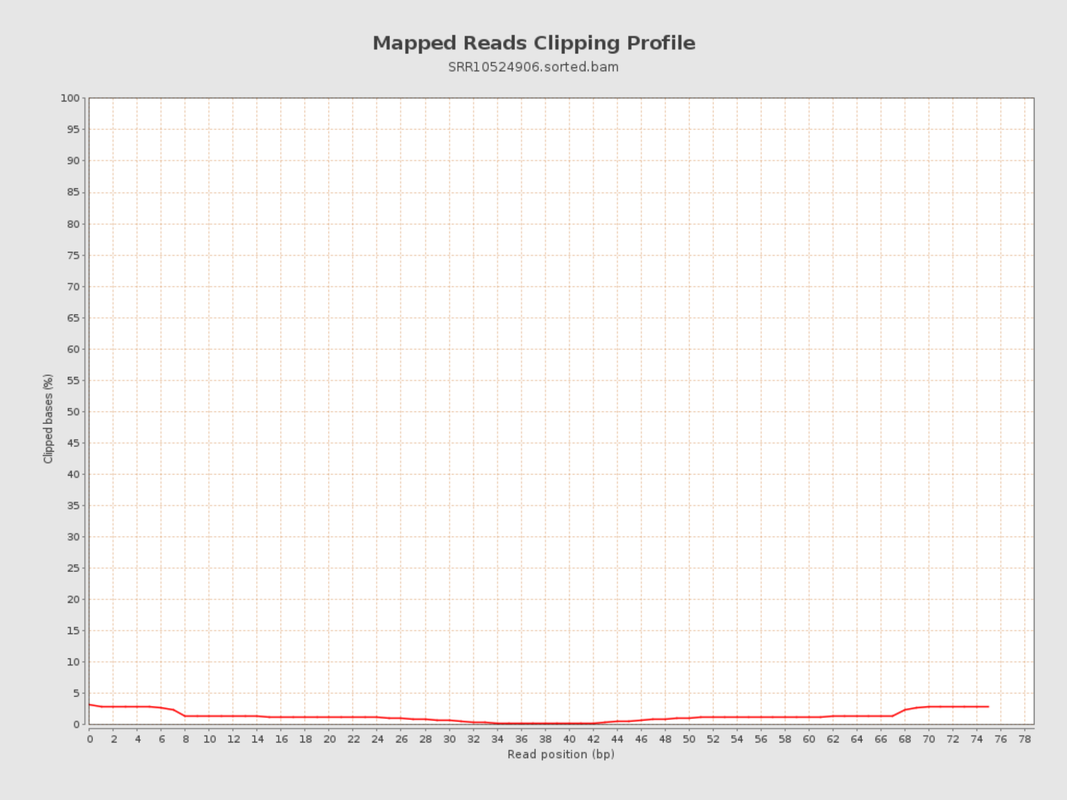
8. Results : Mapped Reads Nucleotide Content



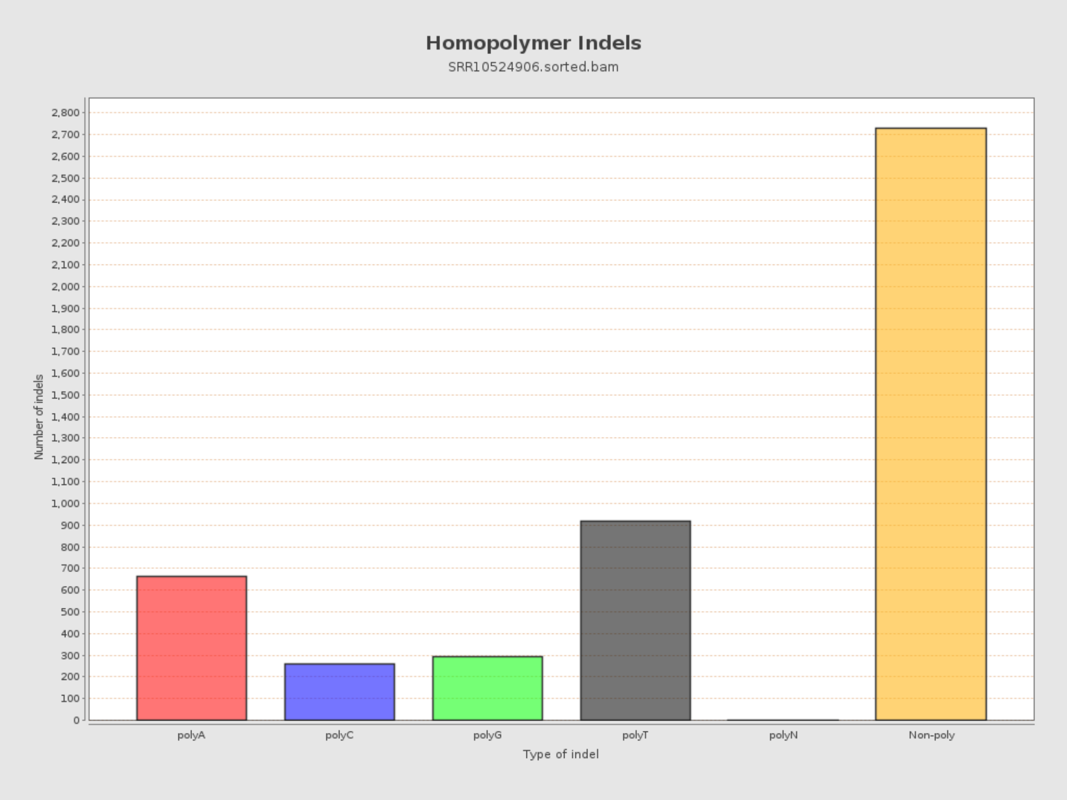
9. Results : Mapped Reads GC-content Distribution



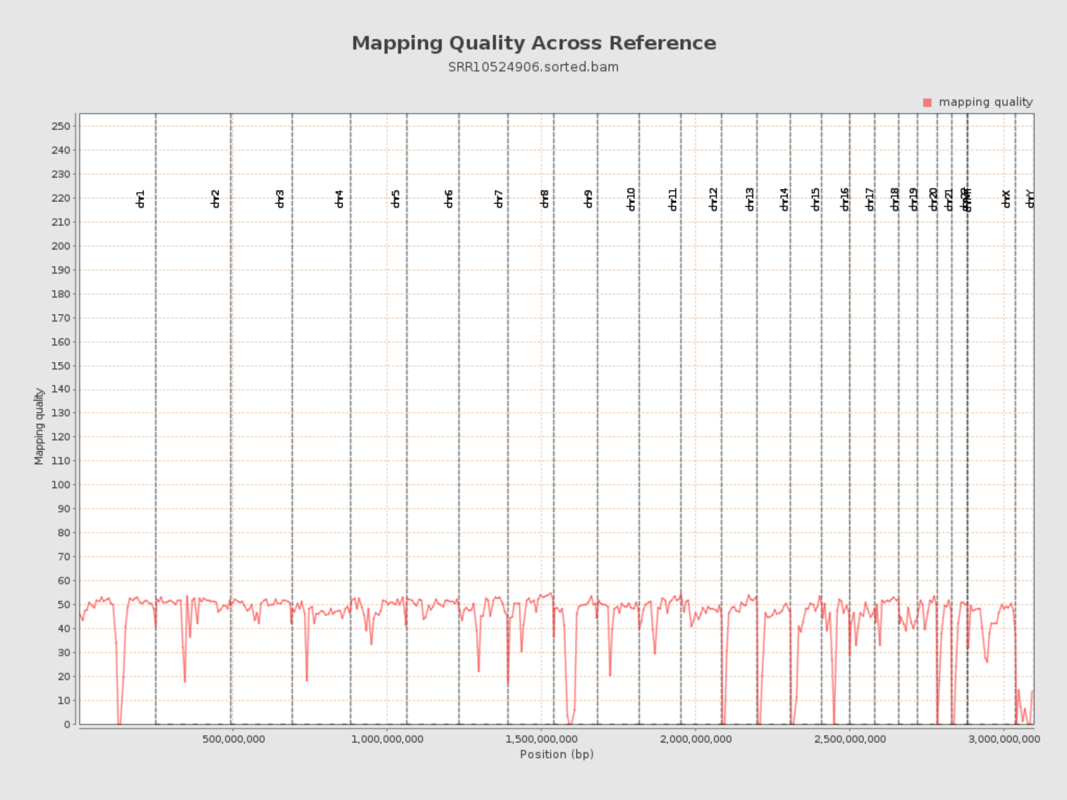
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram