Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 09:29:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524531.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_SRR10524531 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524531.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 09:29:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524531.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,457,145
Mapped reads	1,330,374 / 91.3%
Unmapped reads	126,771 / 8.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,779 / 0.4%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	67,292 / 4.62%
Duplication rate	3.94%
Clipped reads	1,334,787 / 91.6%

2.2. ACGT Content

Number/percentage of A's	18,949,877 / 24.57%
Number/percentage of C's	14,438,041 / 18.72%
Number/percentage of T's	24,894,857 / 32.28%
Number/percentage of G's	18,835,774 / 24.42%
Number/percentage of N's	1,135 / 0%
GC Percentage	43.15%

2.3. Coverage

Mean	0.0249

Standard Deviation	0.2512

2.4. Mapping Quality

Mean Mapping Quality	45.24

2.5. Mismatches and indels

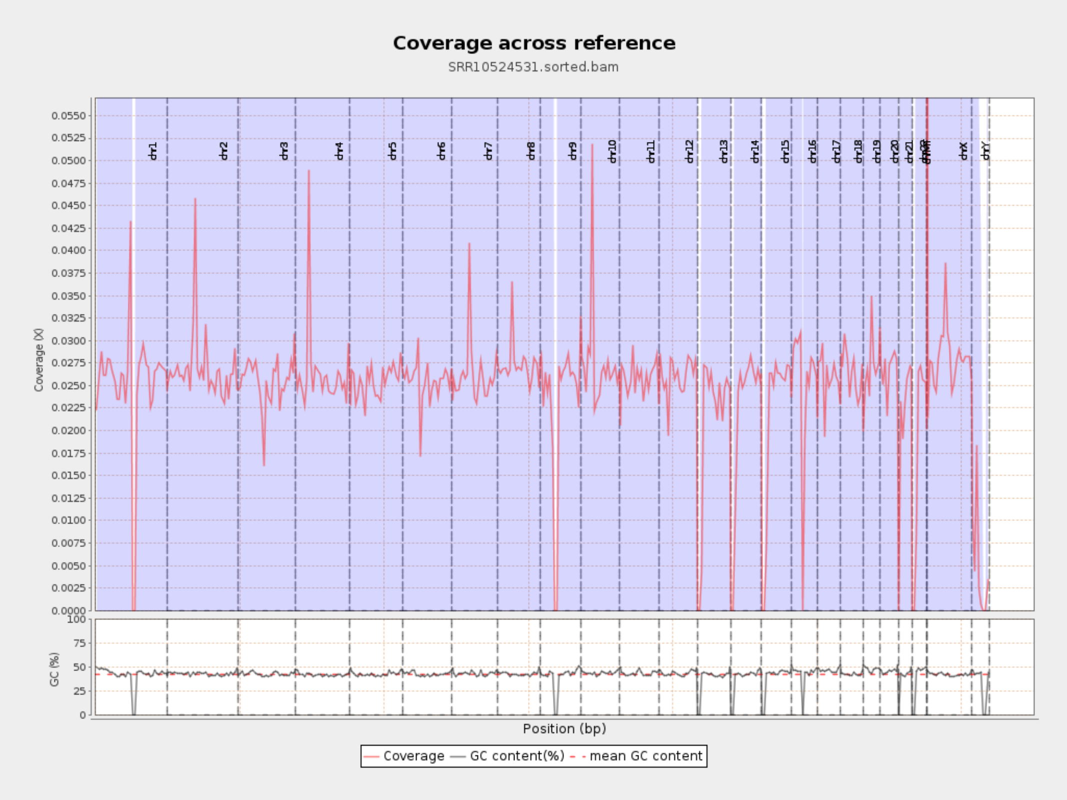
General error rate	0.53%
Mismatches	397,983
Insertions	4,371
Mapped reads with at least one insertion	0.33%
Deletions	14,009
Mapped reads with at least one deletion	1.04%
Homopolymer indels	42.73%

2.6. Chromosome stats

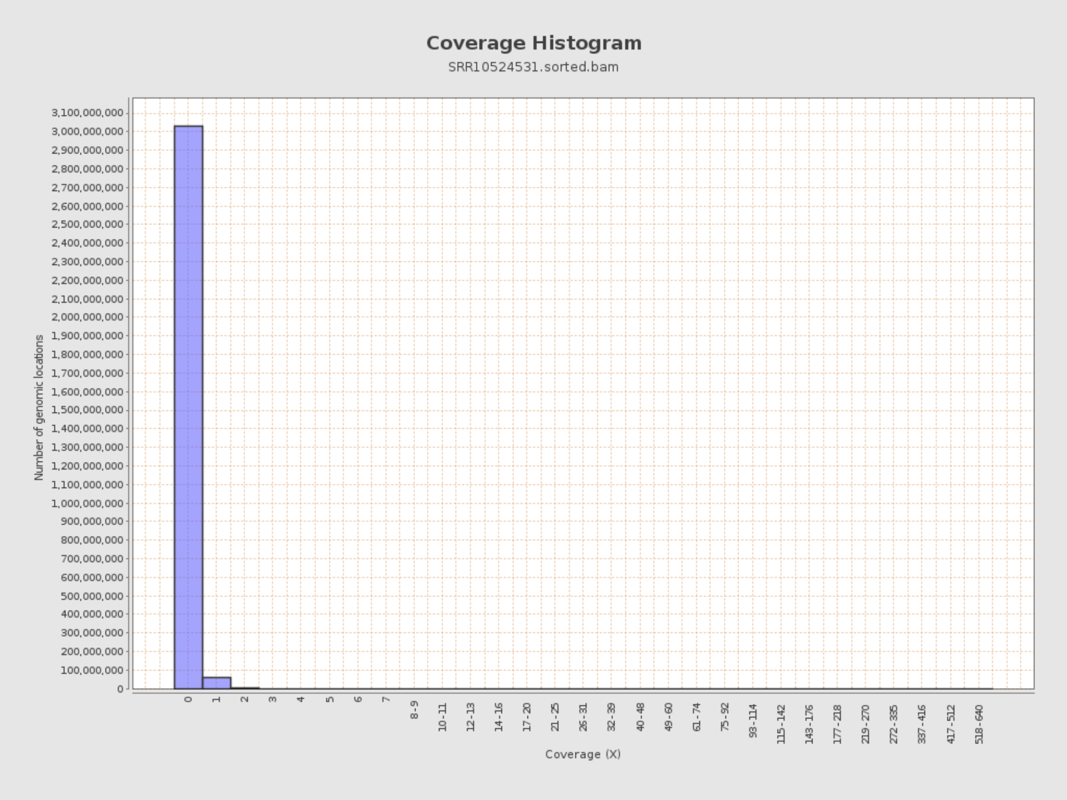
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6239533	0.025	0.4597
chr2	243199373	6534398	0.0269	0.3132
chr3	198022430	5027975	0.0254	0.1762
chr4	191154276	5049839	0.0264	0.2087
chr5	180915260	4630357	0.0256	0.1777
chr6	171115067	4351767	0.0254	0.1932
chr7	159138663	4184454	0.0263	0.2922

chr8	146364022	3992491	0.0273	0.2454
chr9	141213431	3214297	0.0228	0.2083
chr10	135534747	3744181	0.0276	0.259
chr11	135006516	3517002	0.0261	0.2208
chr12	133851895	3488302	0.0261	0.1821
chr13	115169878	2376543	0.0206	0.1589
chr14	107349540	2322127	0.0216	0.1651
chr15	102531392	2174231	0.0212	0.1625
chr16	90354753	2232960	0.0247	0.1875
chr17	81195210	2108779	0.026	0.1867
chr18	78077248	2057242	0.0263	0.3594
chr19	59128983	1610870	0.0272	0.3225
chr20	63025520	1672651	0.0265	0.185
chr21	48129895	1048286	0.0218	0.1819
chr22	51304566	917083	0.0179	0.1504
chrMT	16571	5790	0.3494	0.6622
chrX	155270560	4360501	0.0281	0.2021
chrY	59373566	281361	0.0047	0.1599

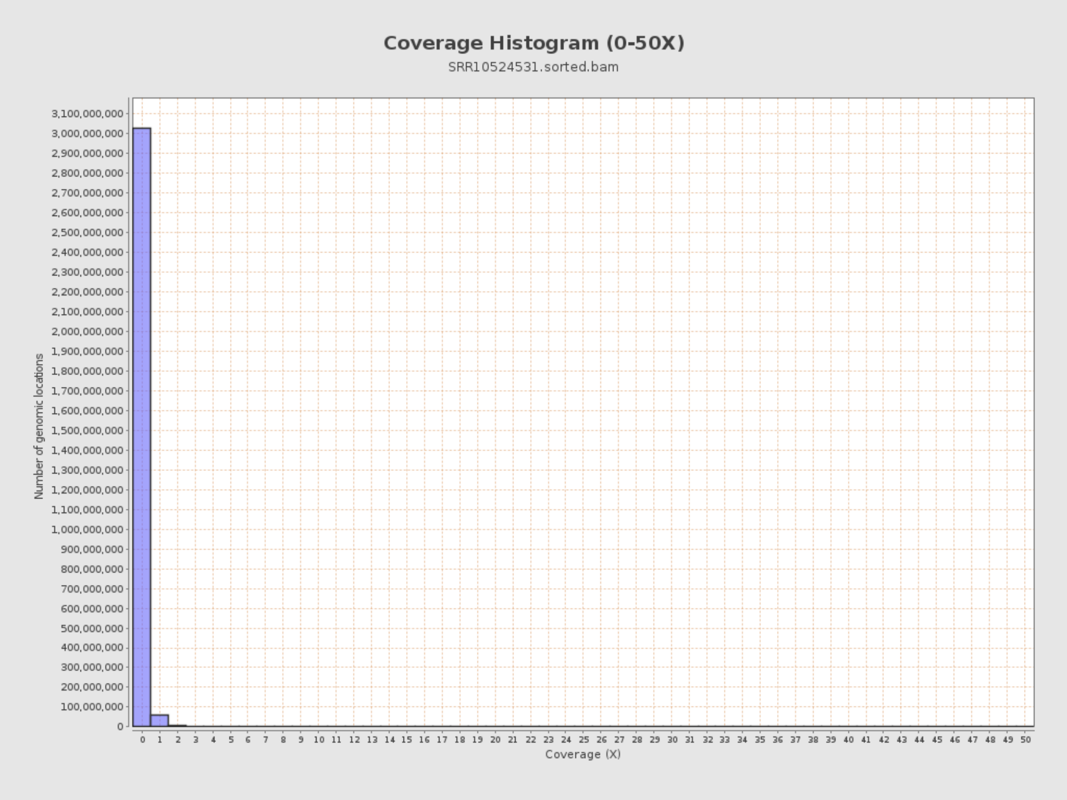
3. Results : Coverage across reference



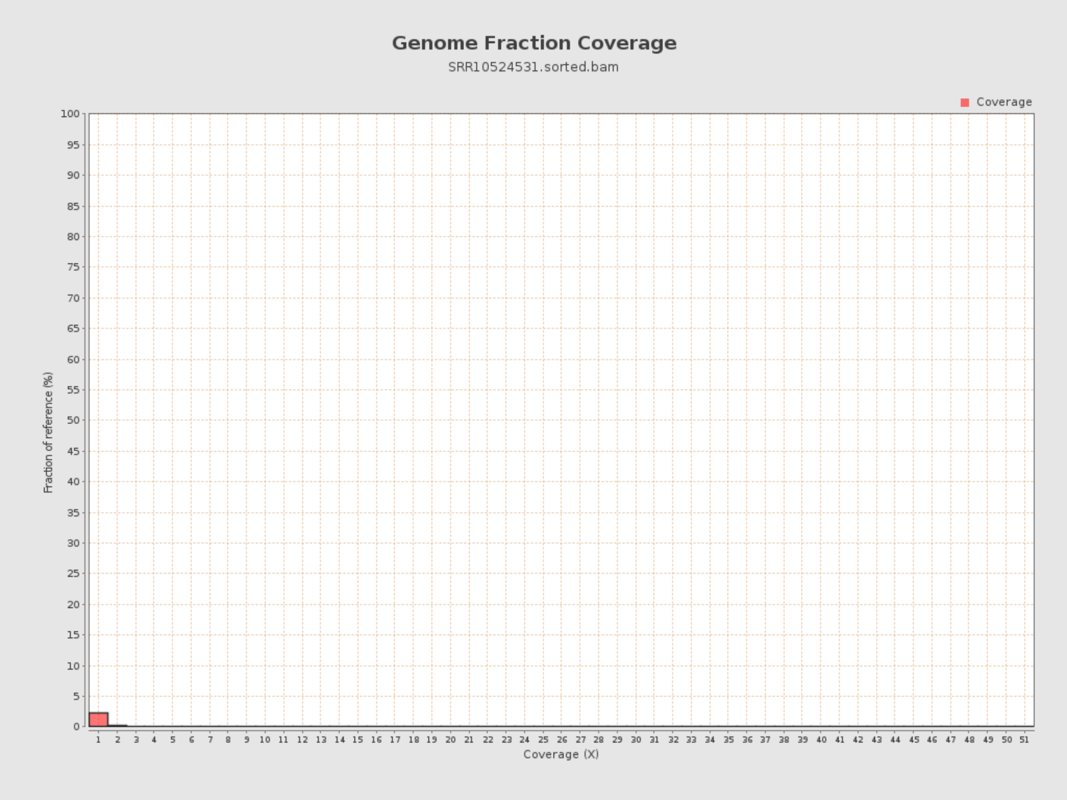
4. Results : Coverage Histogram



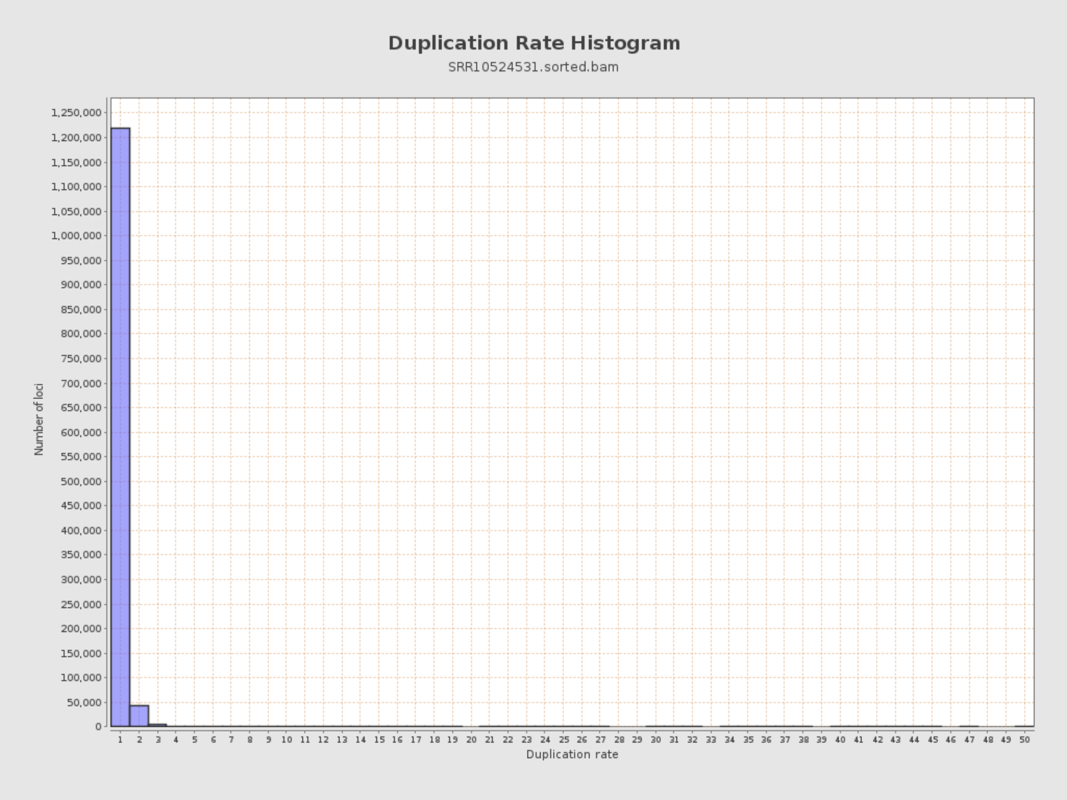
5. Results : Coverage Histogram (0-50X)



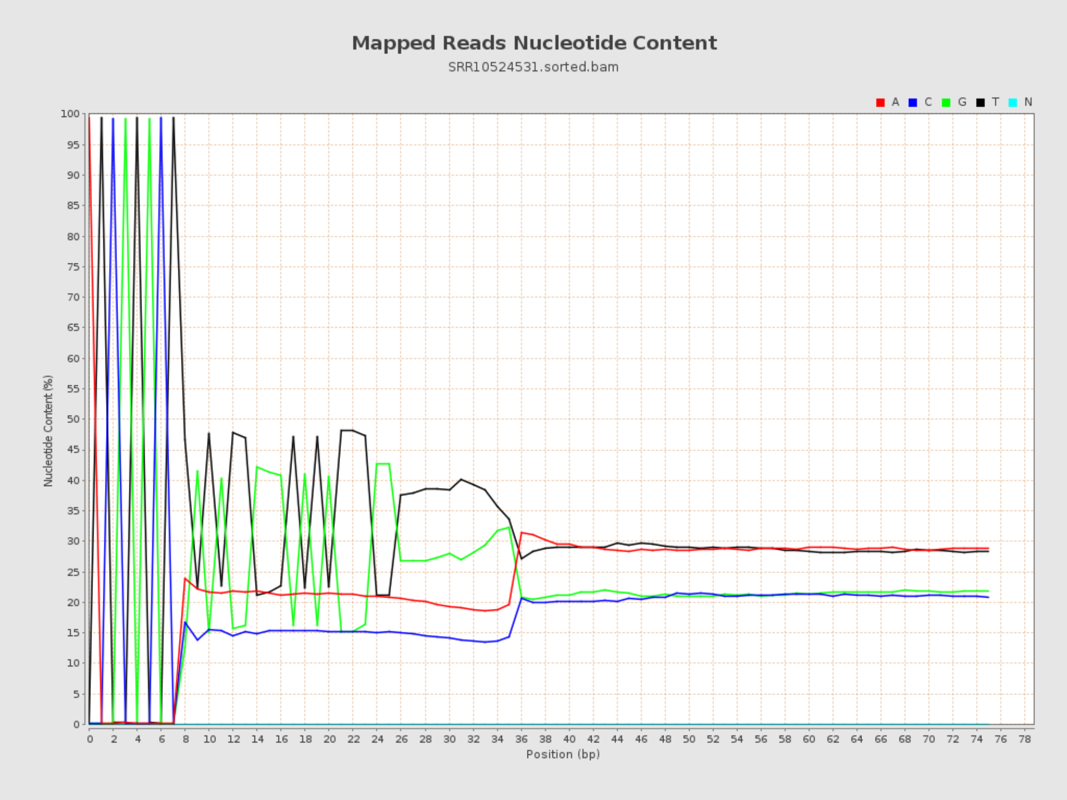
6. Results : Genome Fraction Coverage



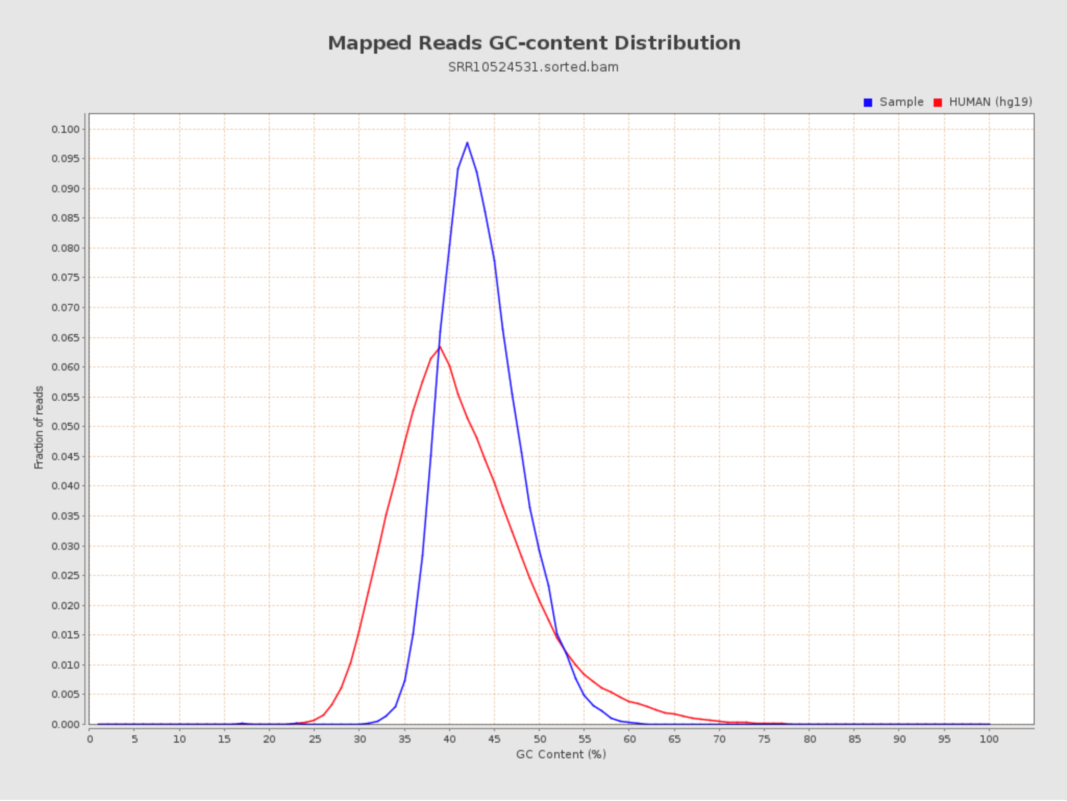
7. Results : Duplication Rate Histogram



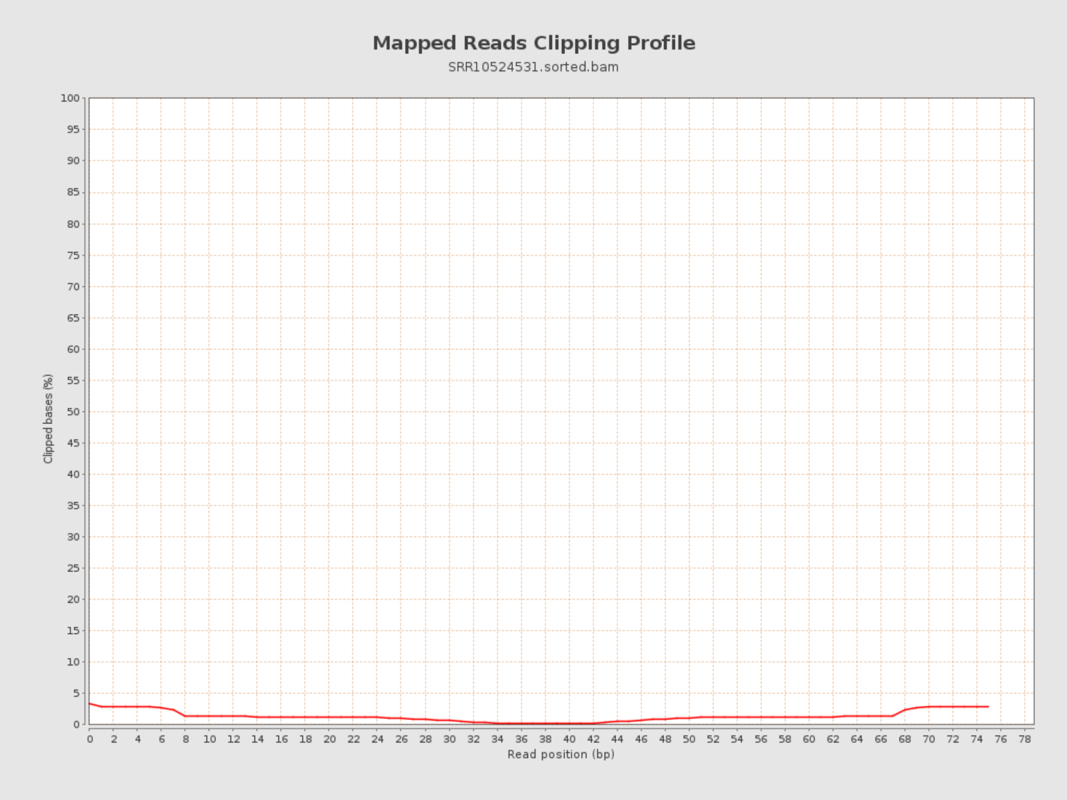
8. Results : Mapped Reads Nucleotide Content



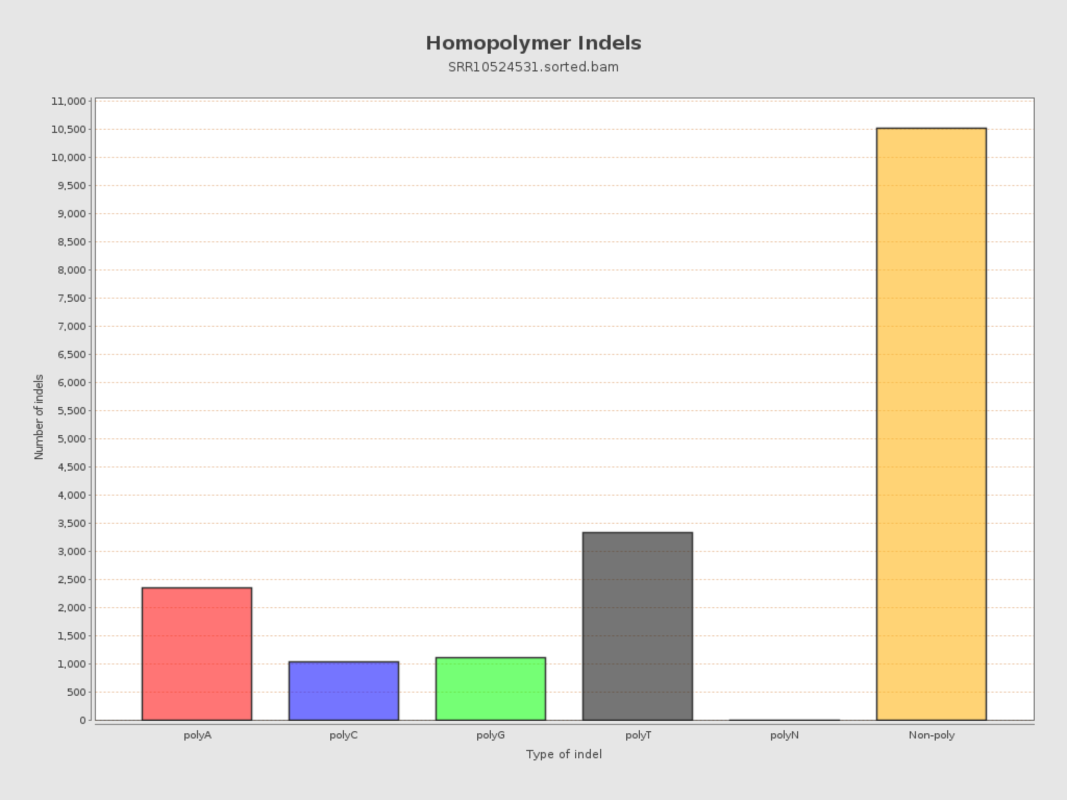
9. Results : Mapped Reads GC-content Distribution



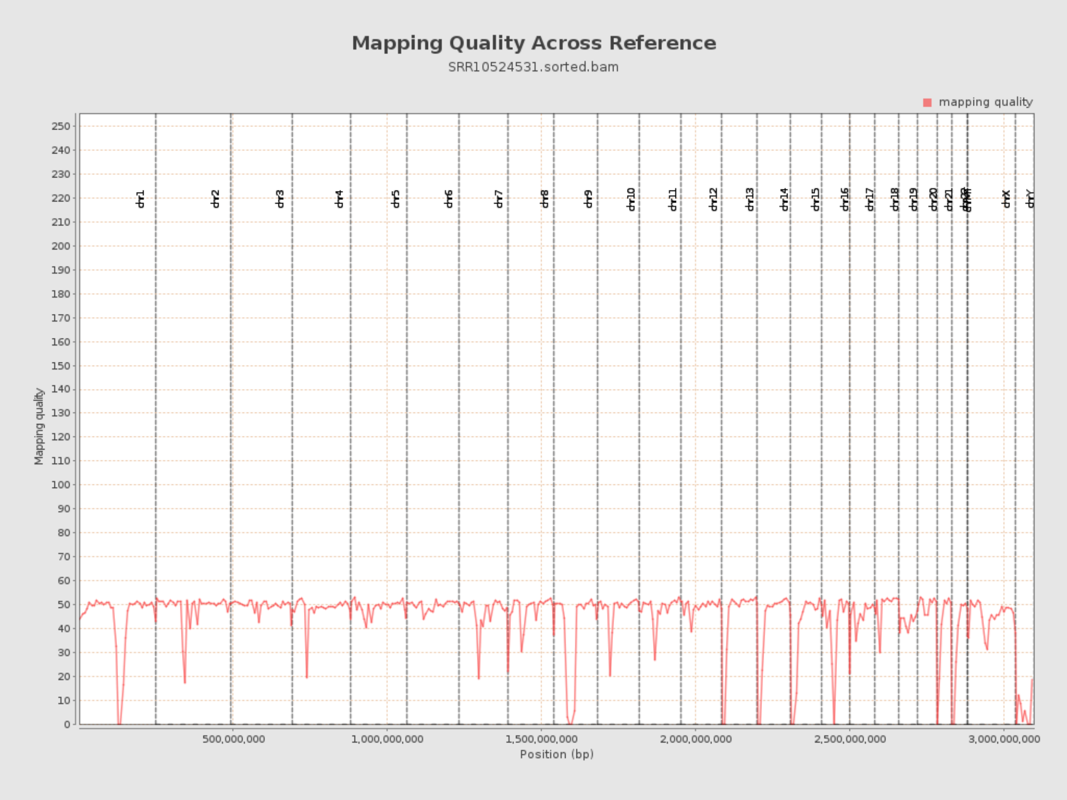
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram