Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 00:11:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525231.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_SRR10525231 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525231.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 00:11:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525231.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	451,742
Mapped reads	415,793 / 92.04%
Unmapped reads	35,949 / 7.96%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,467 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	6,091 / 1.35%
Duplication rate	1.12%
Clipped reads	415,821 / 92.05%

2.2. ACGT Content

Number/percentage of A's	6,998,660 / 27.22%
Number/percentage of C's	5,352,415 / 20.82%
Number/percentage of T's	7,599,872 / 29.56%
Number/percentage of G's	5,762,533 / 22.41%
Number/percentage of N's	695 / 0%
GC Percentage	43.22%

2.3. Coverage

Mean	0.0083

Standard Deviation	0.109

2.4. Mapping Quality

Mean Mapping Quality	46.48

2.5. Mismatches and indels

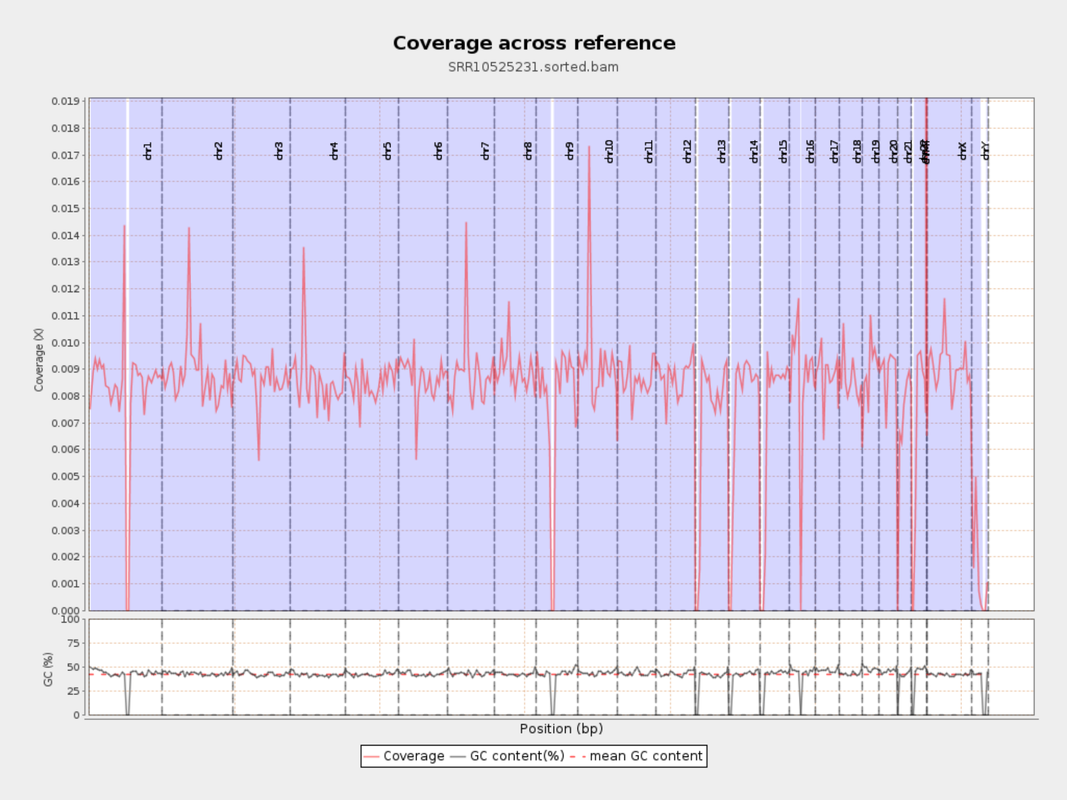
General error rate	0.5%
Mismatches	123,298
Insertions	2,050
Mapped reads with at least one insertion	0.49%
Deletions	5,219
Mapped reads with at least one deletion	1.24%
Homopolymer indels	43.22%

2.6. Chromosome stats

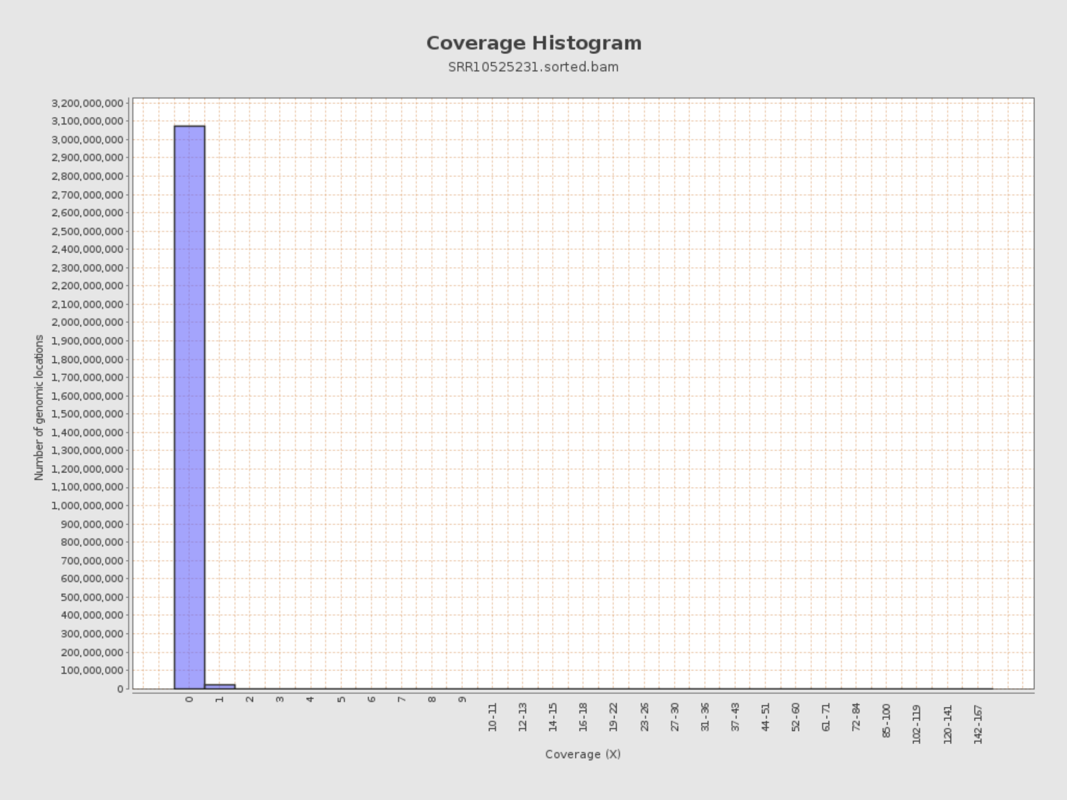
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2046065	0.0082	0.1606
chr2	243199373	2160104	0.0089	0.119
chr3	198022430	1713609	0.0087	0.0952
chr4	191154276	1643303	0.0086	0.0981
chr5	180915260	1537237	0.0085	0.0945
chr6	171115067	1483211	0.0087	0.0986
chr7	159138663	1410350	0.0089	0.1307

chr8	146364022	1314385	0.009	0.1064
chr9	141213431	1077478	0.0076	0.0967
chr10	135534747	1266577	0.0093	0.1189
chr11	135006516	1168232	0.0087	0.1009
chr12	133851895	1168611	0.0087	0.096
chr13	115169878	806890	0.007	0.086
chr14	107349540	790417	0.0074	0.0894
chr15	102531392	725289	0.0071	0.0862
chr16	90354753	778520	0.0086	0.0992
chr17	81195210	711302	0.0088	0.0975
chr18	78077248	677100	0.0087	0.1465
chr19	59128983	532308	0.009	0.1265
chr20	63025520	559489	0.0089	0.0976
chr21	48129895	336552	0.007	0.0894
chr22	51304566	324890	0.0063	0.0817
chrMT	16571	3329	0.2009	0.4456
chrX	155270560	1406022	0.0091	0.0997
chrY	59373566	81699	0.0014	0.0546

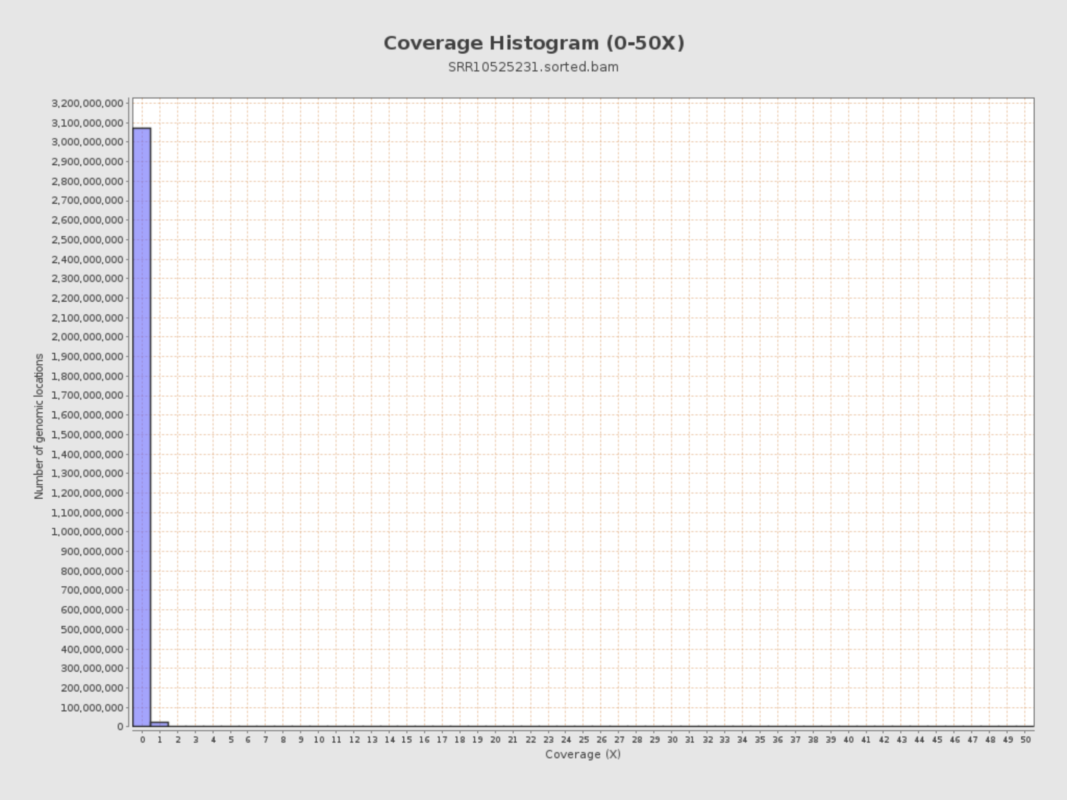
3. Results : Coverage across reference



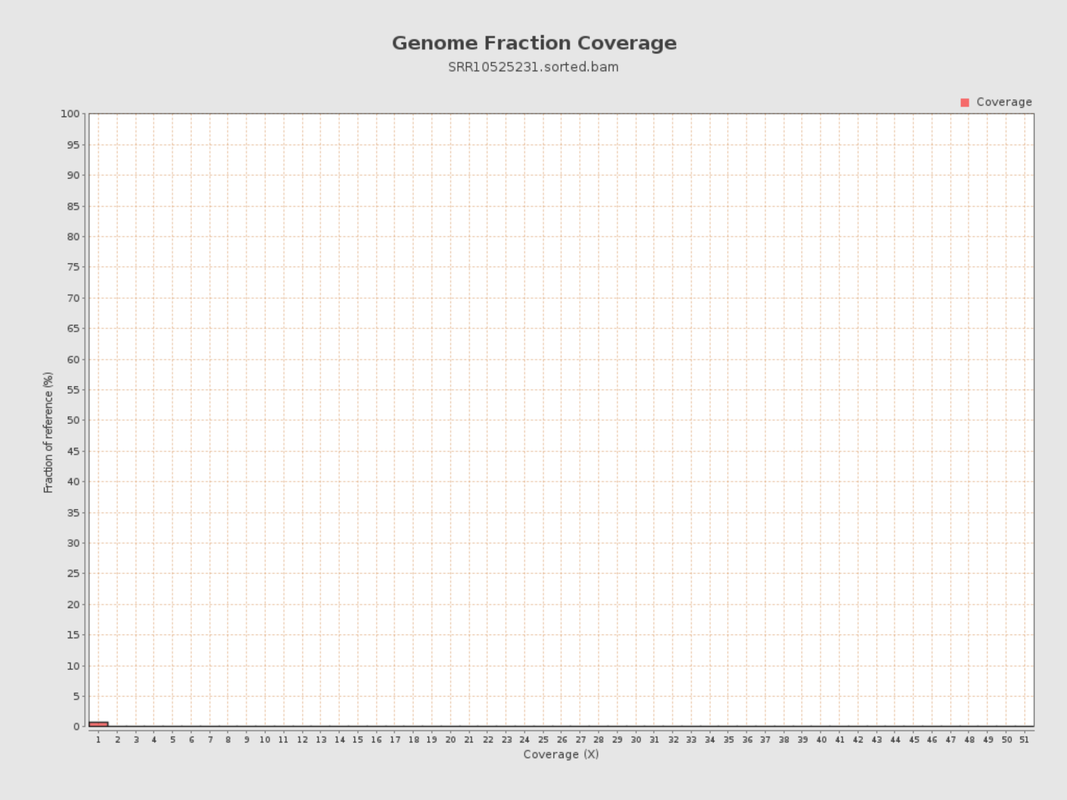
4. Results : Coverage Histogram



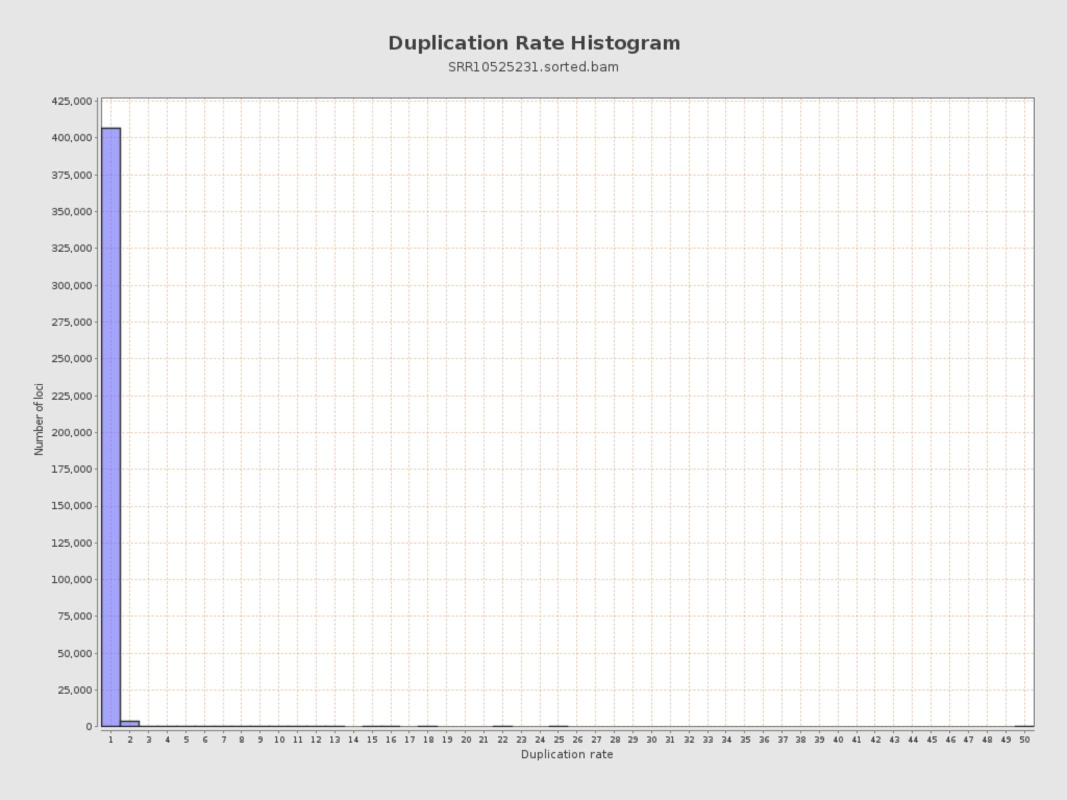
5. Results : Coverage Histogram (0-50X)



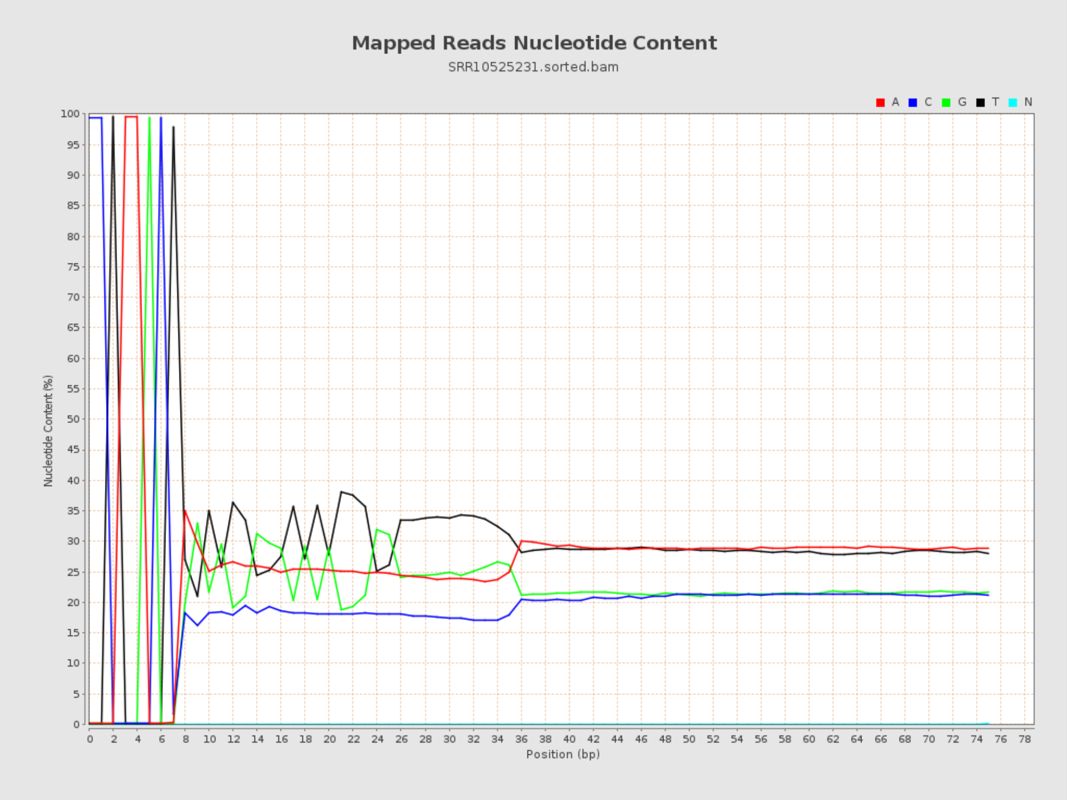
6. Results : Genome Fraction Coverage



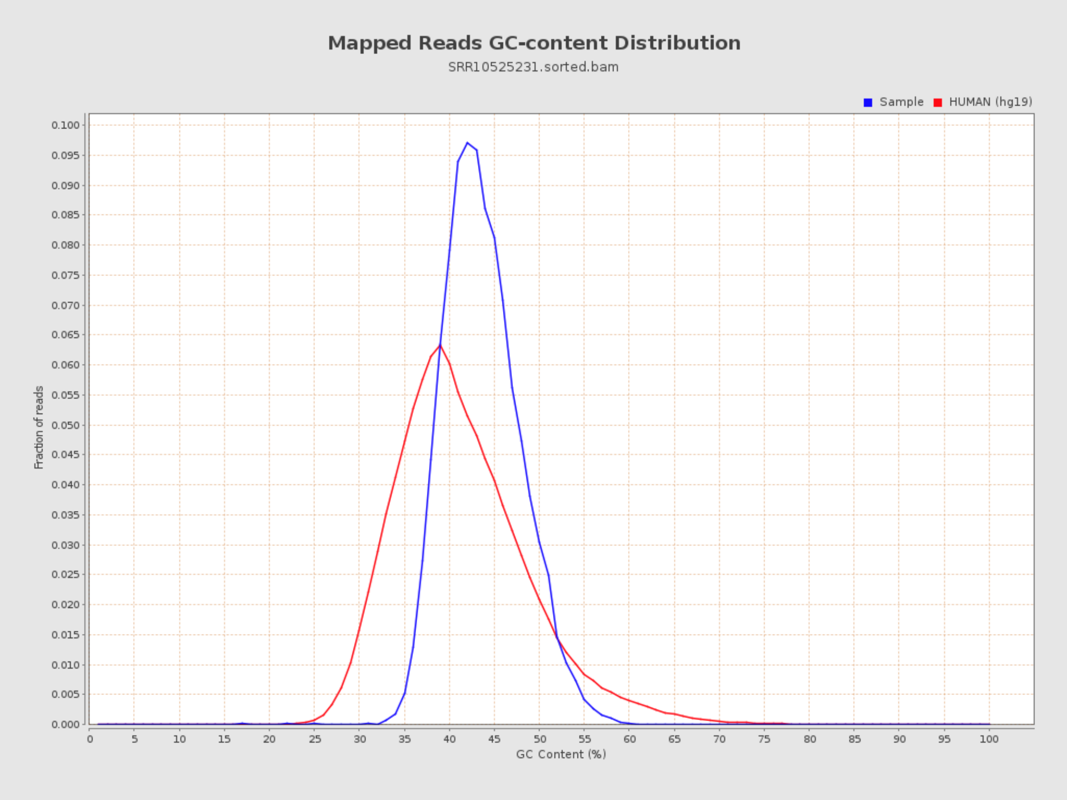
7. Results : Duplication Rate Histogram



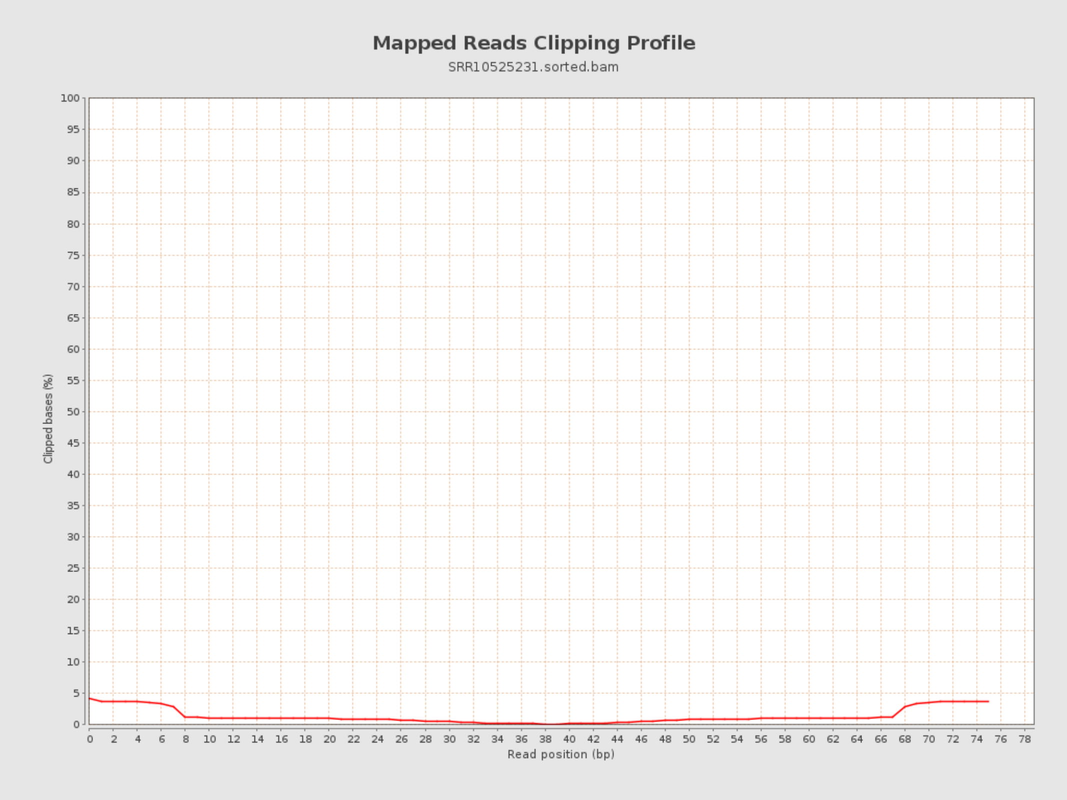
8. Results : Mapped Reads Nucleotide Content



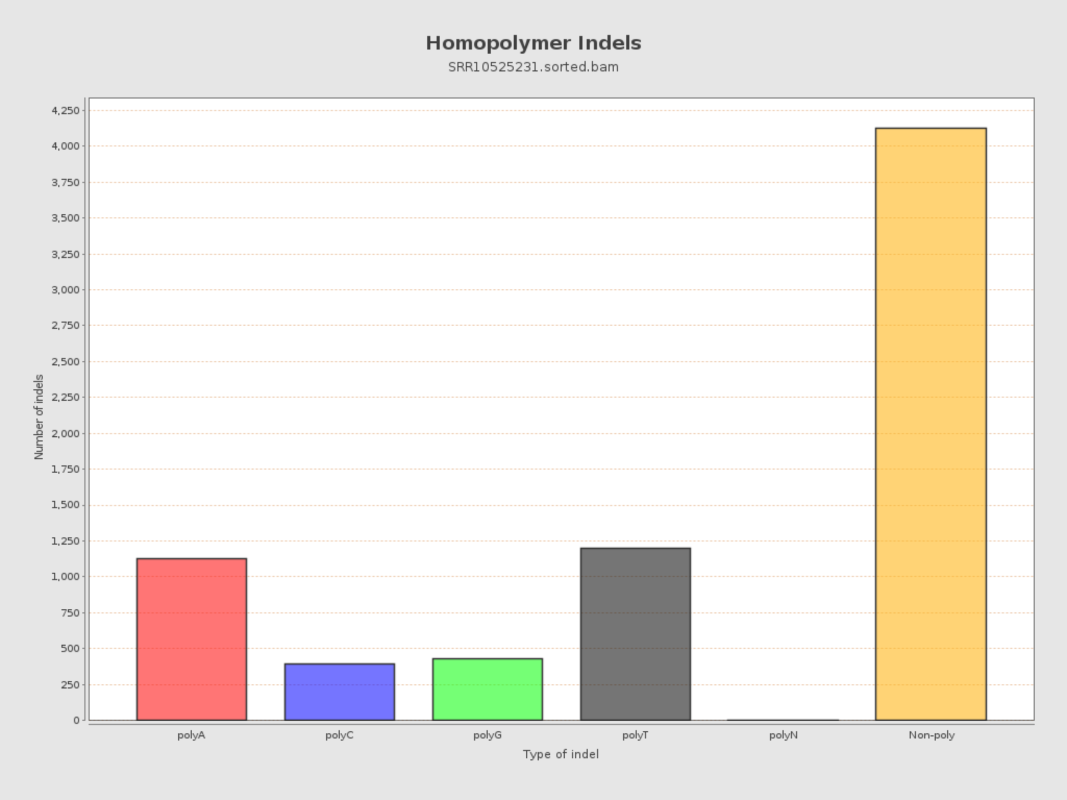
9. Results : Mapped Reads GC-content Distribution



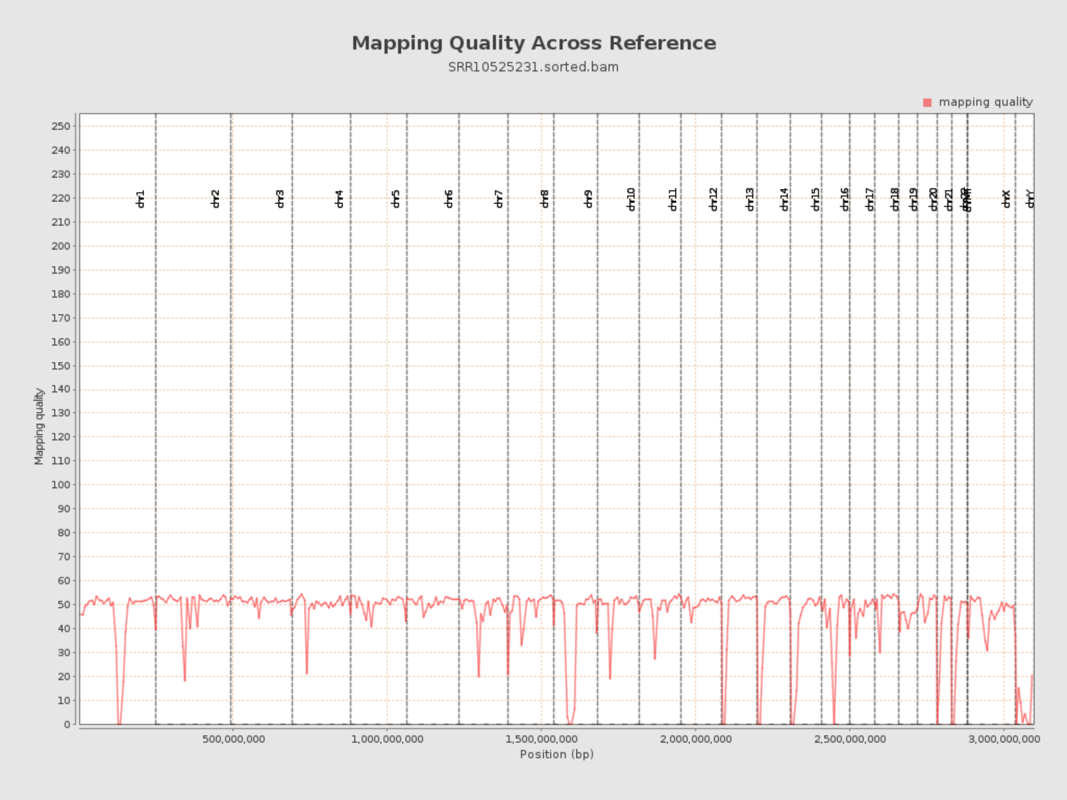
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram