Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 19:18:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525131.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_SRR10525131 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525131.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 19:18:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525131.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	920,715
Mapped reads	810,229 / 88%
Unmapped reads	110,486 / 12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,799 / 2.37%
Read min/max/mean length	30 / 101 / 101.87
Duplicated reads (estimated)	19,636 / 2.13%
Duplication rate	1.44%
Clipped reads	830,488 / 90.2%

2.2. ACGT Content

Number/percentage of A's	16,279,942 / 26.4%
Number/percentage of C's	12,340,829 / 20.01%
Number/percentage of T's	19,278,790 / 31.26%
Number/percentage of G's	13,762,940 / 22.32%
Number/percentage of N's	2,314 / 0%
GC Percentage	42.33%

2.3. Coverage

Mean	0.0199

Standard Deviation	0.2393

2.4. Mapping Quality

Mean Mapping Quality	45.92

2.5. Mismatches and indels

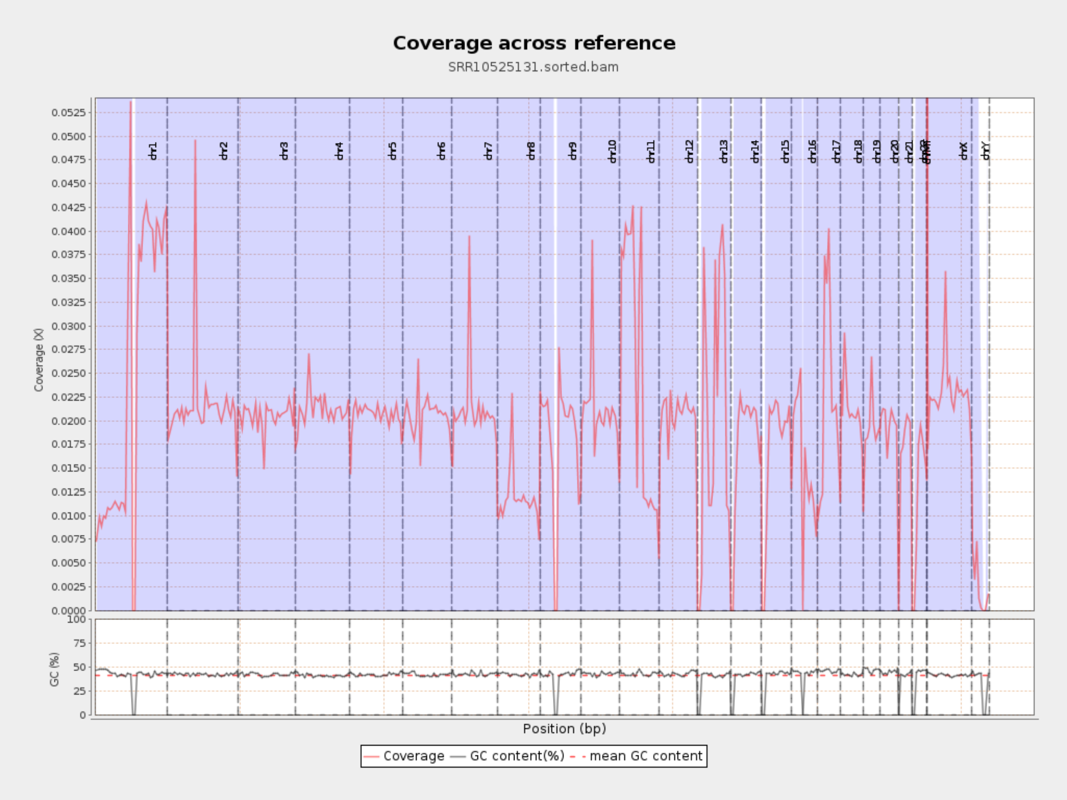
General error rate	0.8%
Mismatches	481,734
Insertions	5,316
Mapped reads with at least one insertion	0.65%
Deletions	14,759
Mapped reads with at least one deletion	1.8%
Homopolymer indels	42.7%

2.6. Chromosome stats

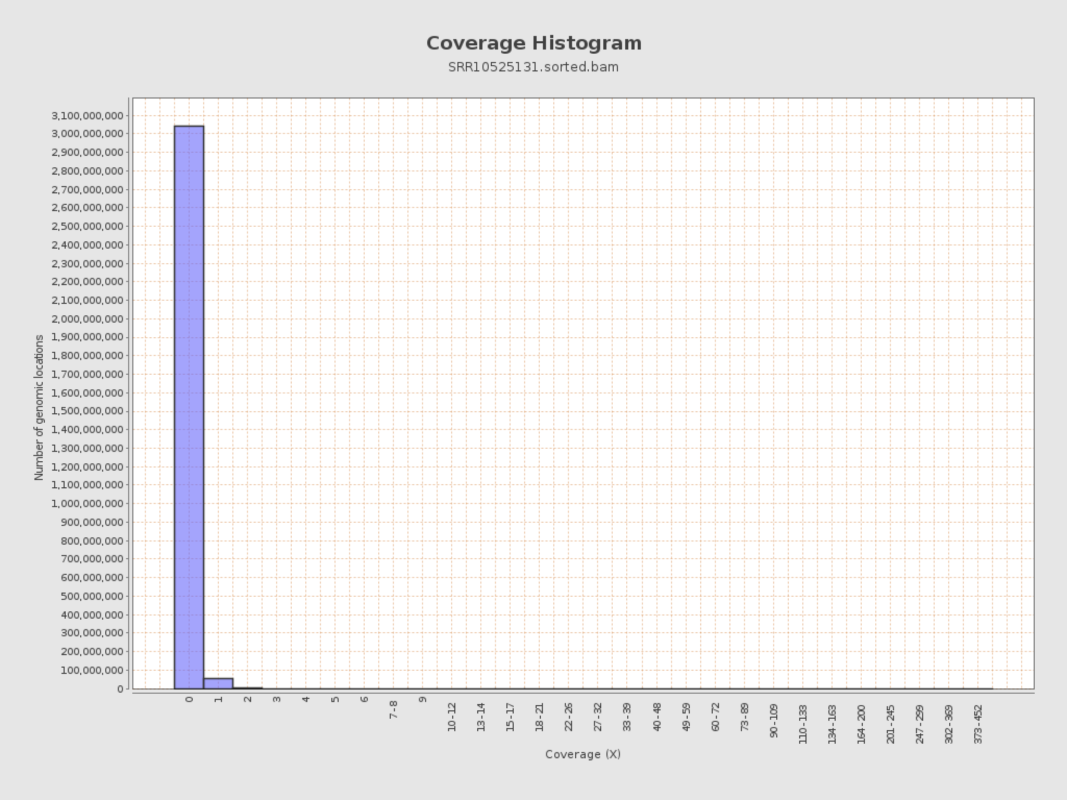
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6067664	0.0243	0.4127
chr2	243199373	5276947	0.0217	0.3146
chr3	198022430	4052200	0.0205	0.1515
chr4	191154276	4052456	0.0212	0.1589
chr5	180915260	3745663	0.0207	0.1535
chr6	171115067	3519875	0.0206	0.1656
chr7	159138663	3385522	0.0213	0.3195

chr8	146364022	1746247	0.0119	0.2503
chr9	141213431	2558972	0.0181	0.2128
chr10	135534747	2878588	0.0212	0.2509
chr11	135006516	3439976	0.0255	0.2952
chr12	133851895	2767613	0.0207	0.1516
chr13	115169878	2301960	0.02	0.15
chr14	107349540	1836185	0.0171	0.1503
chr15	102531392	1714992	0.0167	0.1358
chr16	90354753	1355178	0.015	0.1397
chr17	81195210	1798299	0.0221	0.1763
chr18	78077248	1669838	0.0214	0.3654
chr19	59128983	1144366	0.0194	0.3191
chr20	63025520	1219656	0.0194	0.1545
chr21	48129895	791343	0.0164	0.1406
chr22	51304566	623284	0.0121	0.1152
chrMT	16571	5034	0.3038	0.6804
chrX	155270560	3596154	0.0232	0.1992
chrY	59373566	142105	0.0024	0.0666

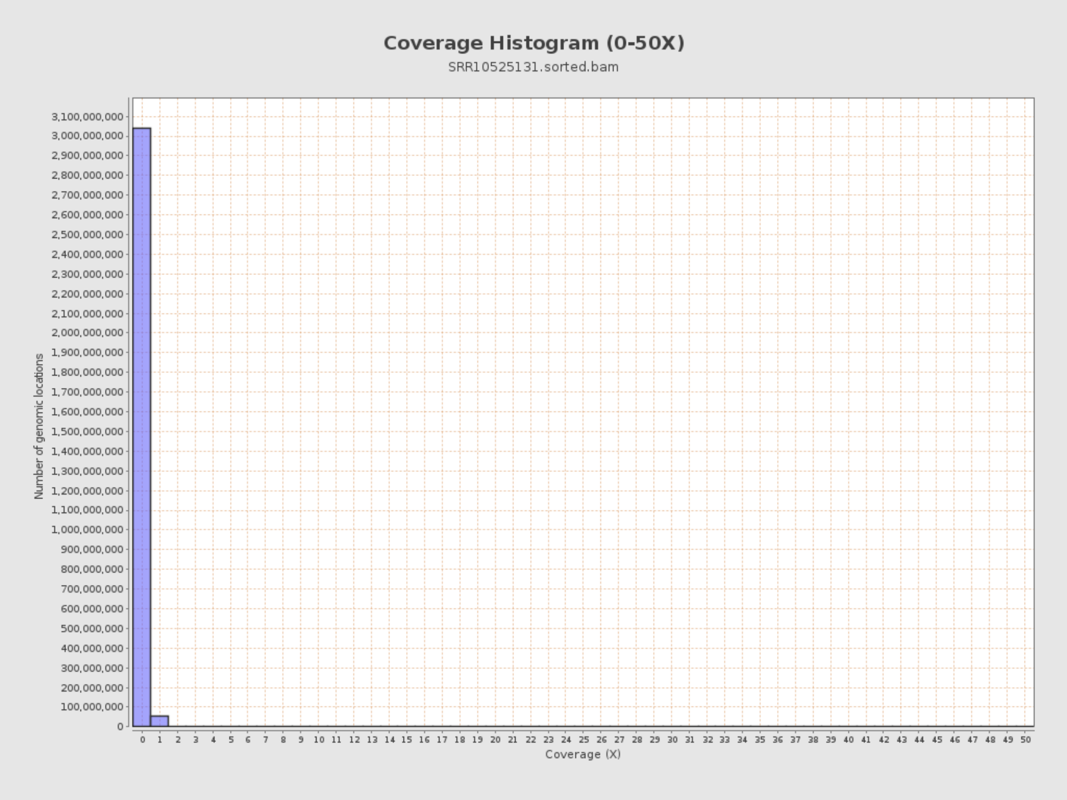
3. Results : Coverage across reference



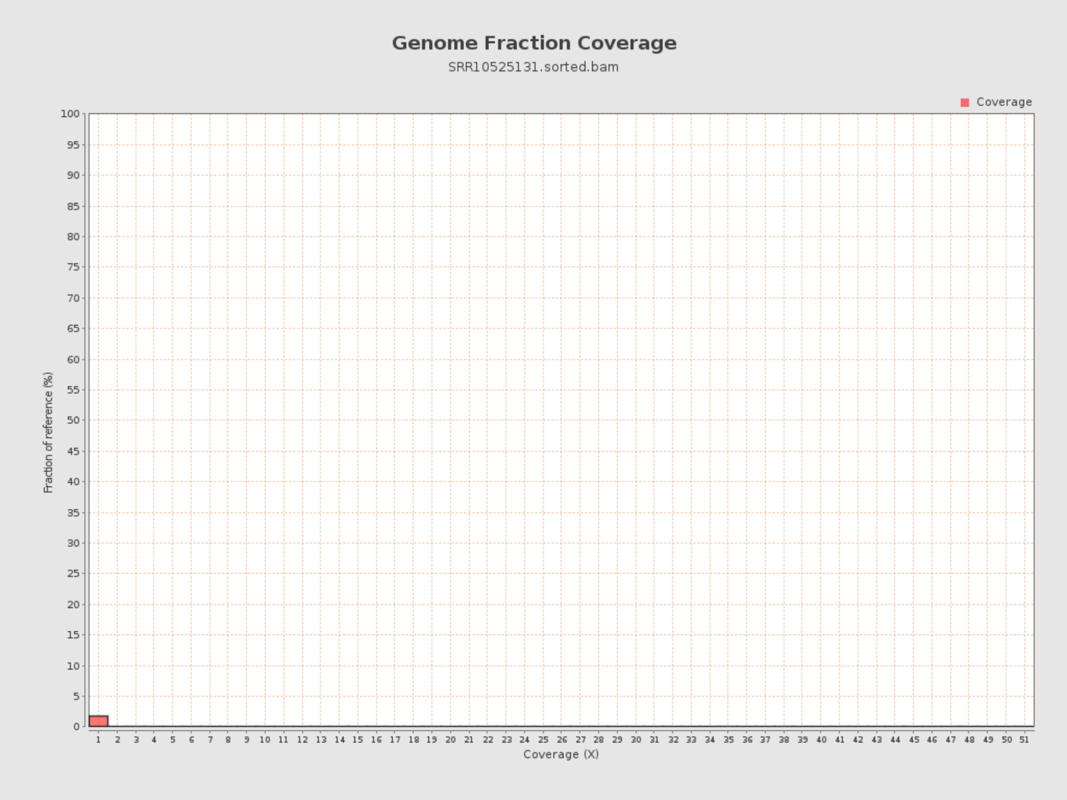
4. Results : Coverage Histogram



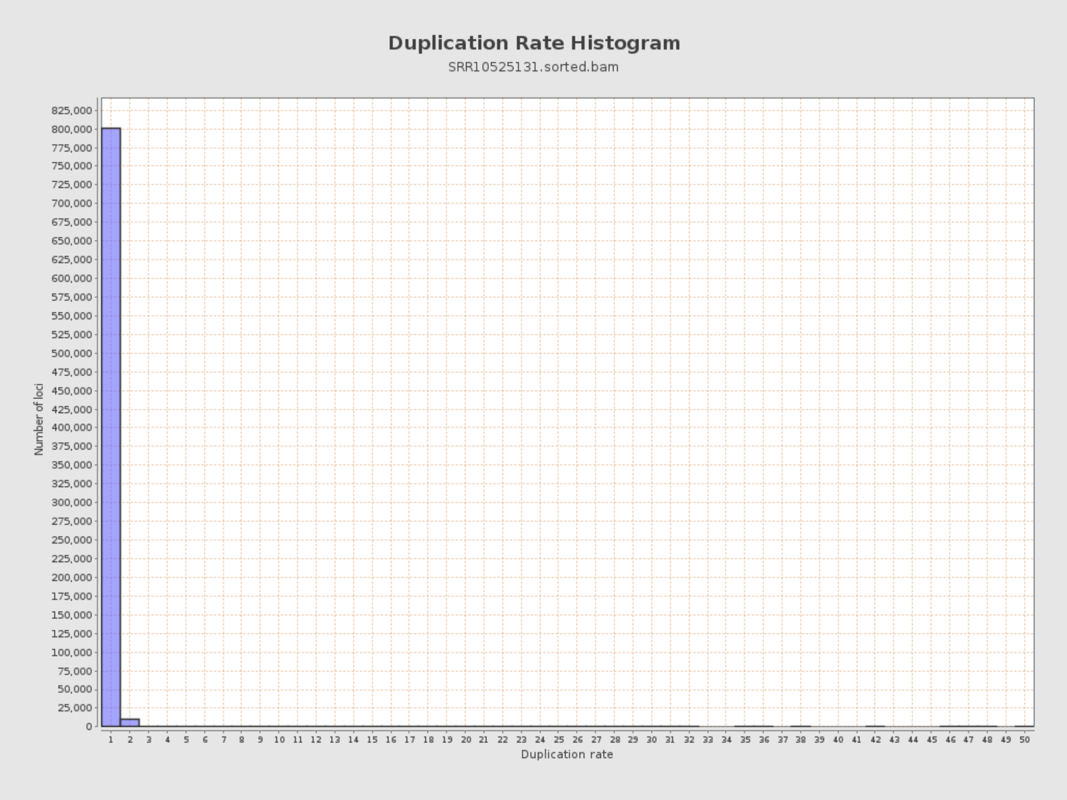
5. Results : Coverage Histogram (0-50X)



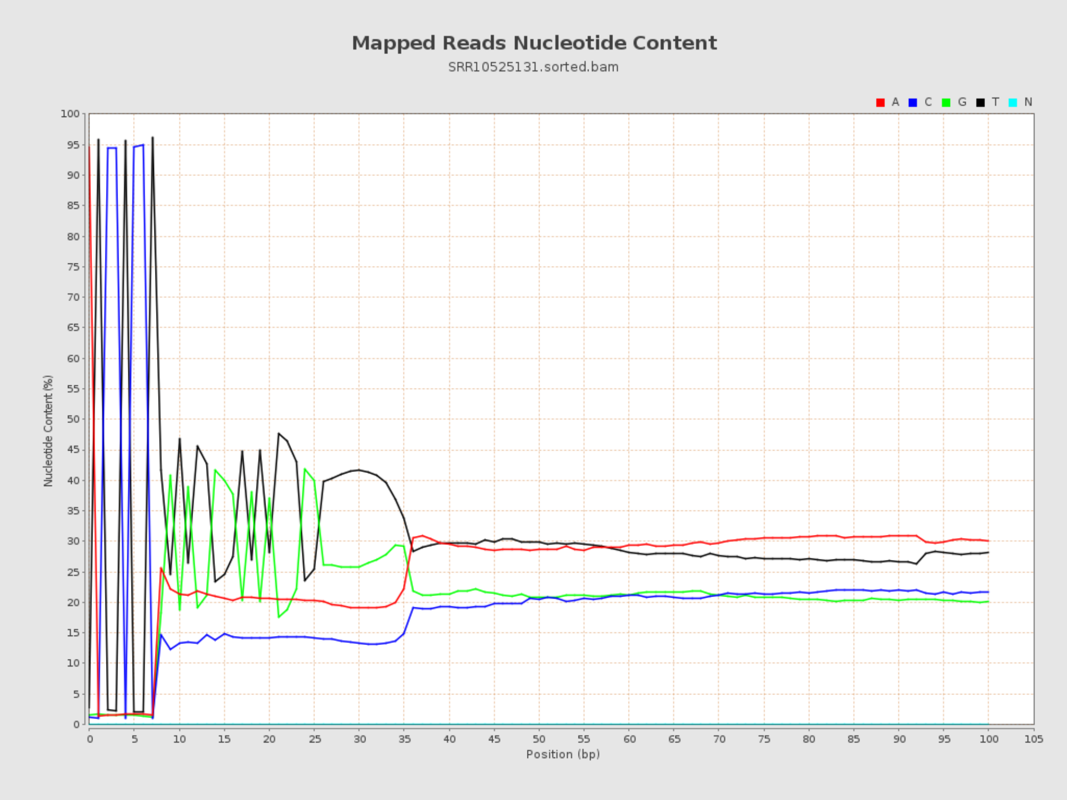
6. Results : Genome Fraction Coverage



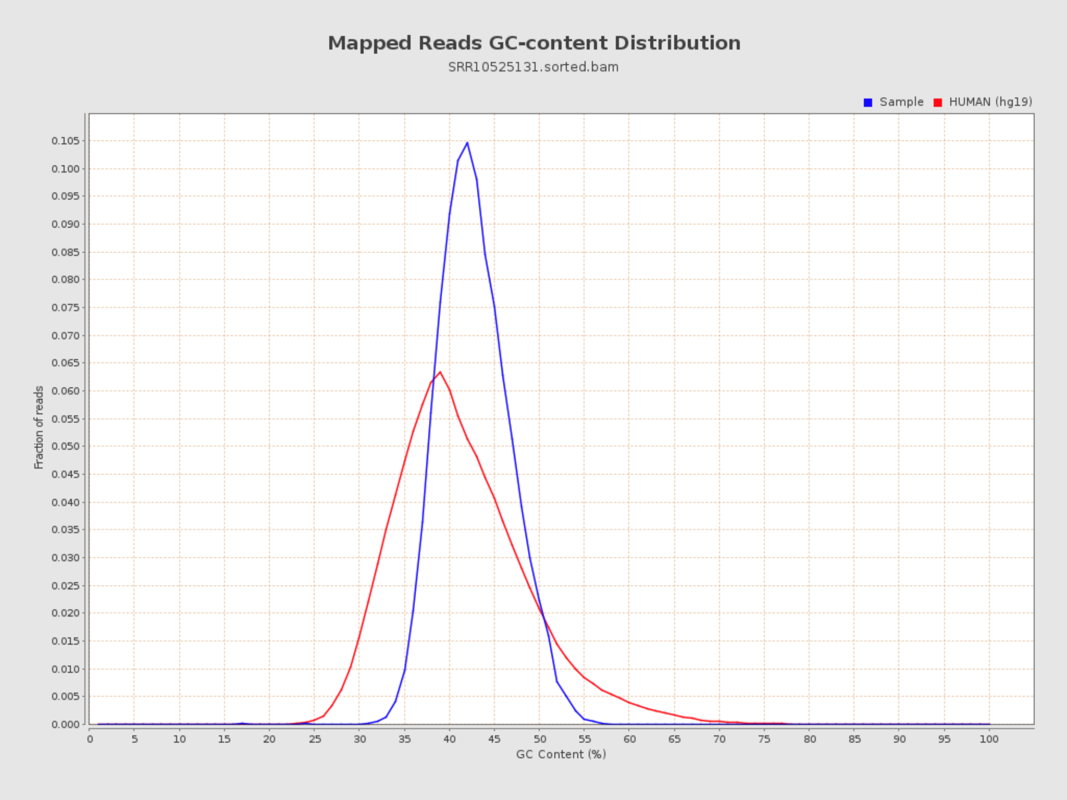
7. Results : Duplication Rate Histogram



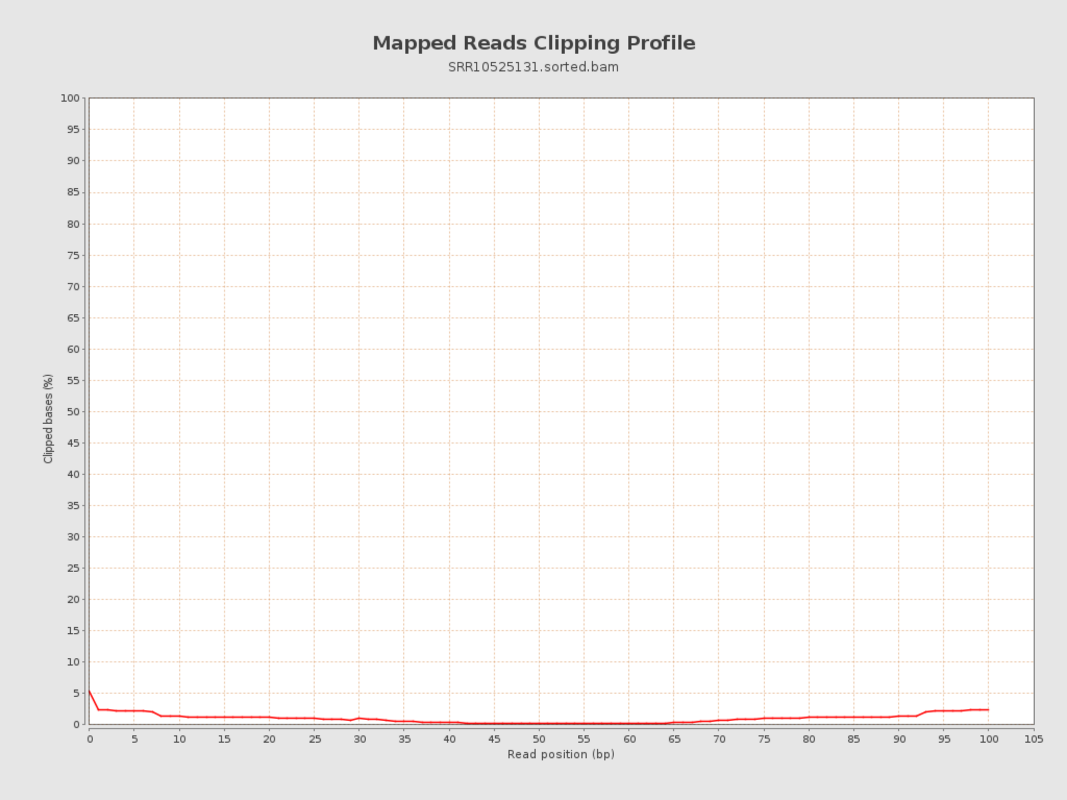
8. Results : Mapped Reads Nucleotide Content



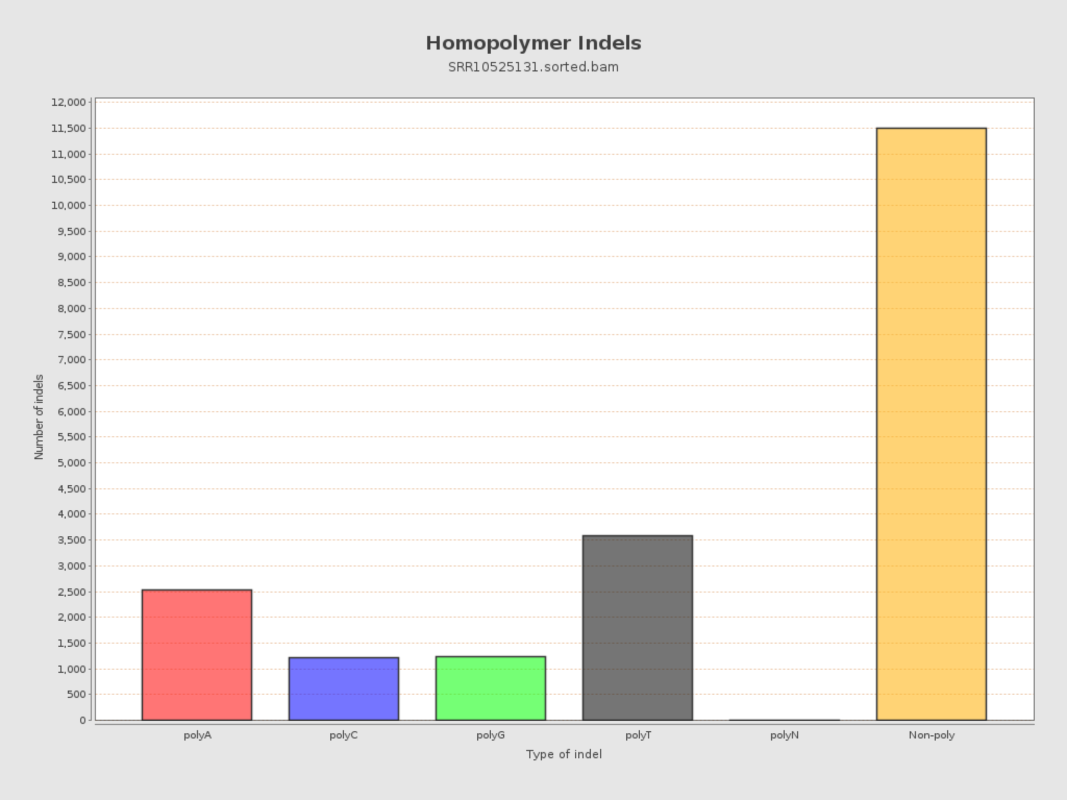
9. Results : Mapped Reads GC-content Distribution



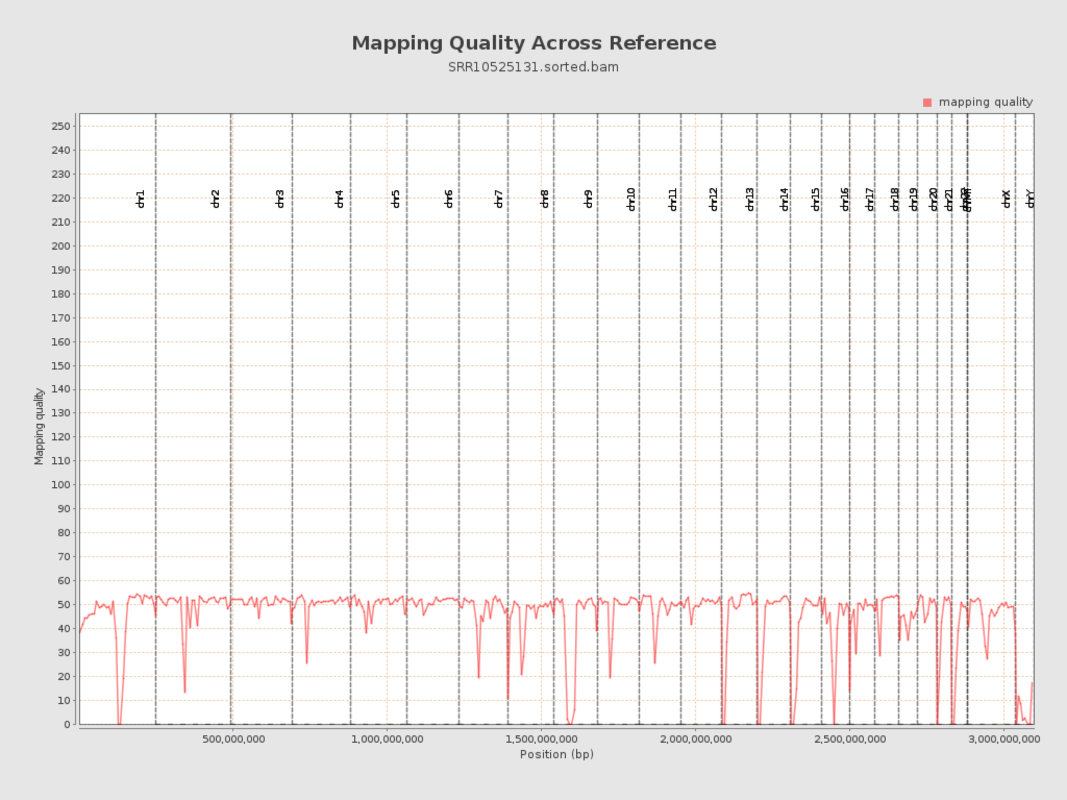
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram