Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 22:23:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524831.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_SRR10524831 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524831.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 22:23:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524831.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	658,382
Mapped reads	612,473 / 93.03%
Unmapped reads	45,909 / 6.97%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,827 / 0.58%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	11,496 / 1.75%
Duplication rate	1.3%
Clipped reads	614,113 / 93.28%

2.2. ACGT Content

Number/percentage of A's	9,766,803 / 26.86%
Number/percentage of C's	6,415,082 / 17.64%
Number/percentage of T's	11,466,530 / 31.53%
Number/percentage of G's	8,712,026 / 23.96%
Number/percentage of N's	5,249 / 0.01%
GC Percentage	41.6%

2.3. Coverage

Mean	0.0118

Standard Deviation	0.1483

2.4. Mapping Quality

Mean Mapping Quality	45.4

2.5. Mismatches and indels

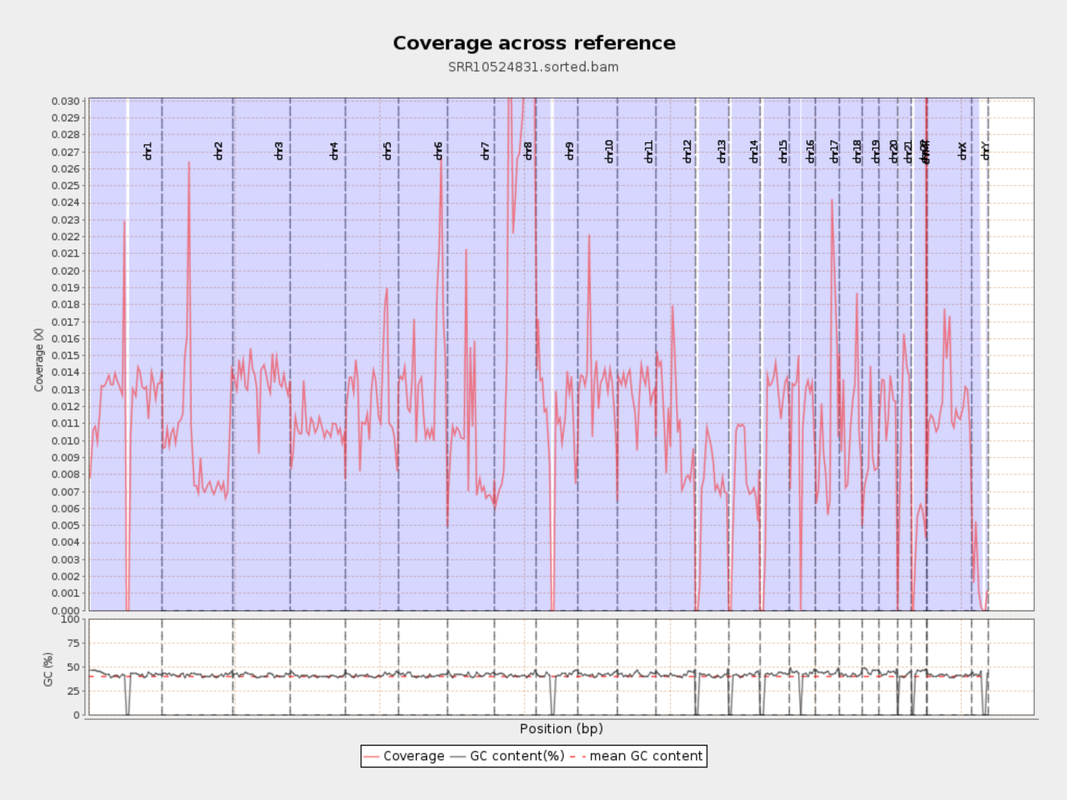
General error rate	0.48%
Mismatches	170,428
Insertions	2,991
Mapped reads with at least one insertion	0.49%
Deletions	6,823
Mapped reads with at least one deletion	1.1%
Homopolymer indels	40.82%

2.6. Chromosome stats

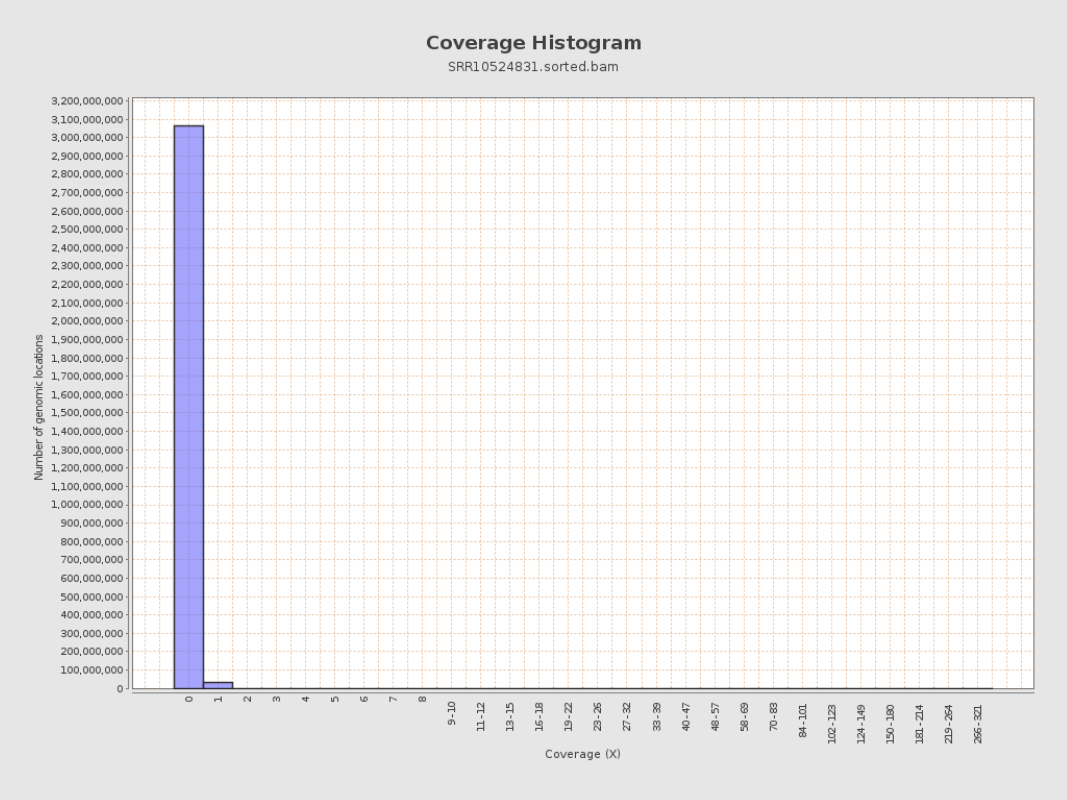
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3031768	0.0122	0.2628
chr2	243199373	2375749	0.0098	0.1324
chr3	198022430	2693755	0.0136	0.12
chr4	191154276	2034654	0.0106	0.1107
chr5	180915260	2255720	0.0125	0.1152
chr6	171115067	2372708	0.0139	0.1269
chr7	159138663	1564372	0.0098	0.1847

chr8	146364022	3992292	0.0273	0.2093
chr9	141213431	1509745	0.0107	0.1317
chr10	135534747	1844820	0.0136	0.1474
chr11	135006516	1746871	0.0129	0.1396
chr12	133851895	1460066	0.0109	0.1092
chr13	115169878	772637	0.0067	0.0848
chr14	107349540	777161	0.0072	0.0902
chr15	102531392	1084707	0.0106	0.1062
chr16	90354753	1036341	0.0115	0.1149
chr17	81195210	919563	0.0113	0.1181
chr18	78077248	897349	0.0115	0.2108
chr19	59128983	528345	0.0089	0.1823
chr20	63025520	760228	0.0121	0.1158
chr21	48129895	535209	0.0111	0.1118
chr22	51304566	207323	0.004	0.065
chrMT	16571	2017	0.1217	0.3864
chrX	155270560	1881680	0.0121	0.121
chrY	59373566	91485	0.0015	0.0525

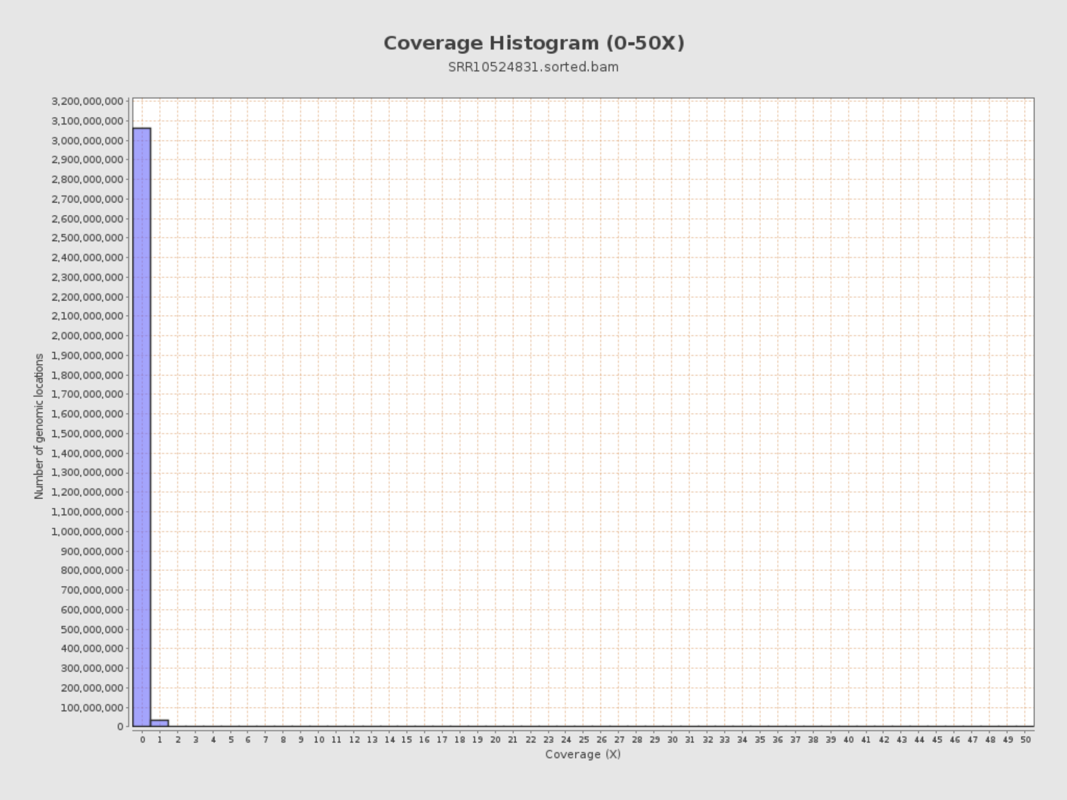
3. Results : Coverage across reference



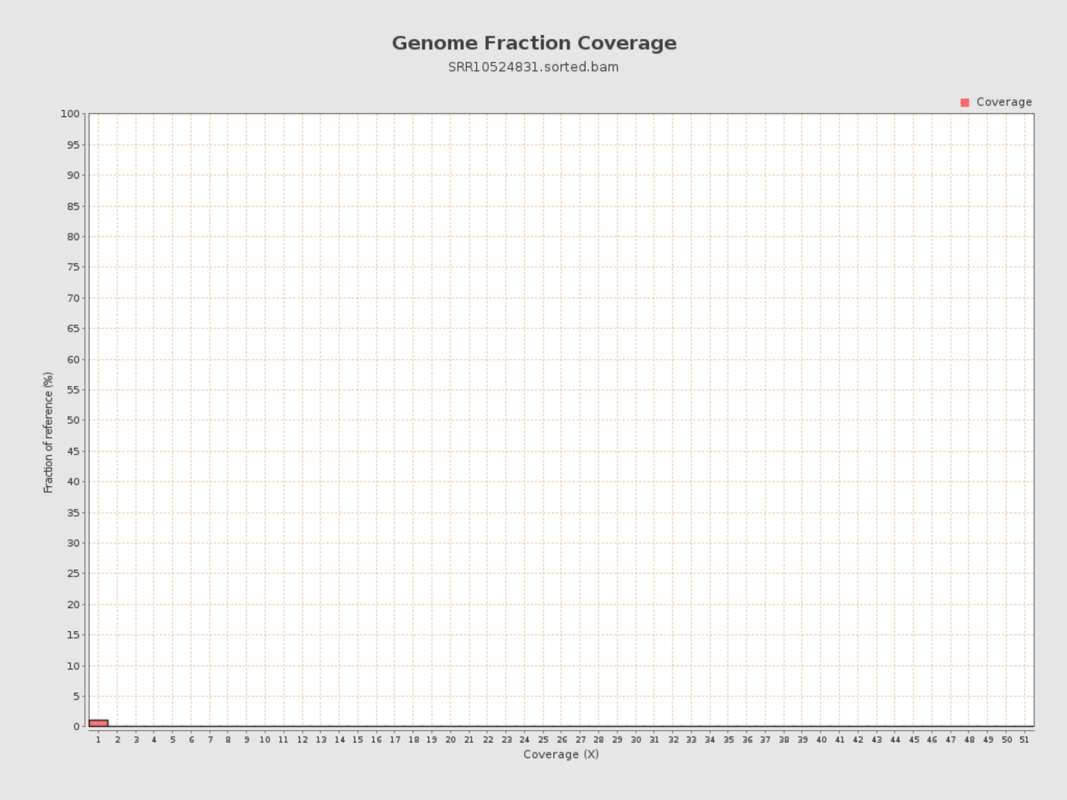
4. Results : Coverage Histogram



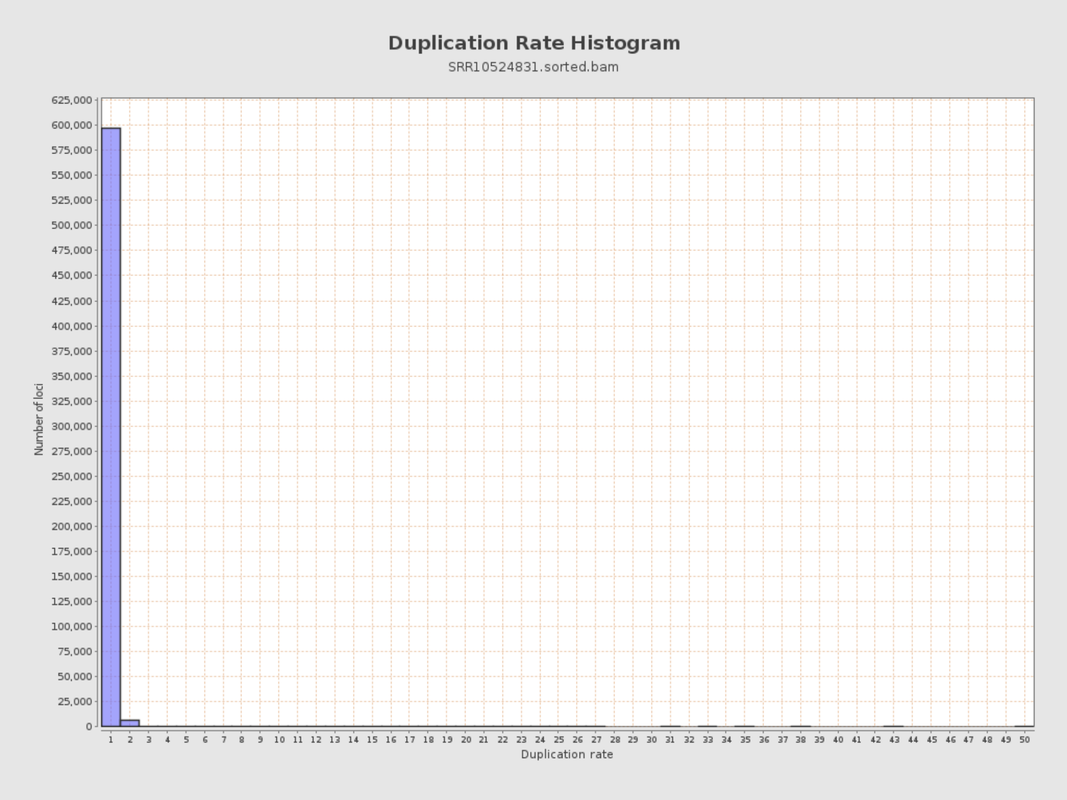
5. Results : Coverage Histogram (0-50X)



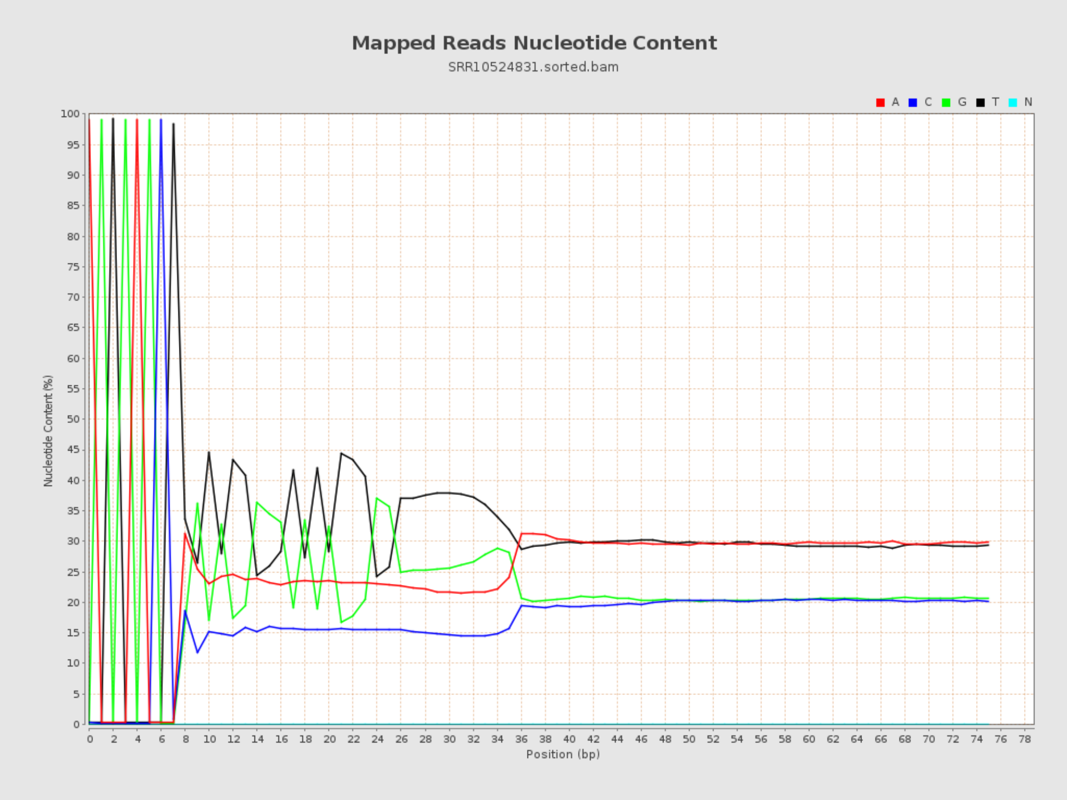
6. Results : Genome Fraction Coverage



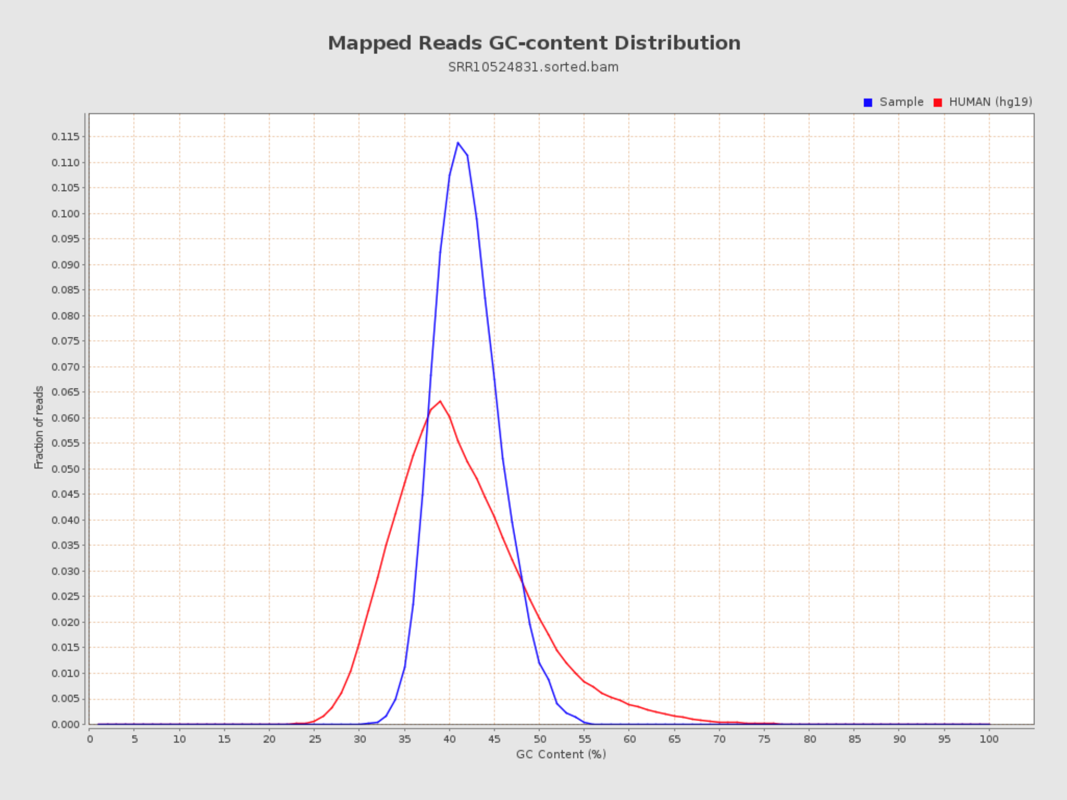
7. Results : Duplication Rate Histogram



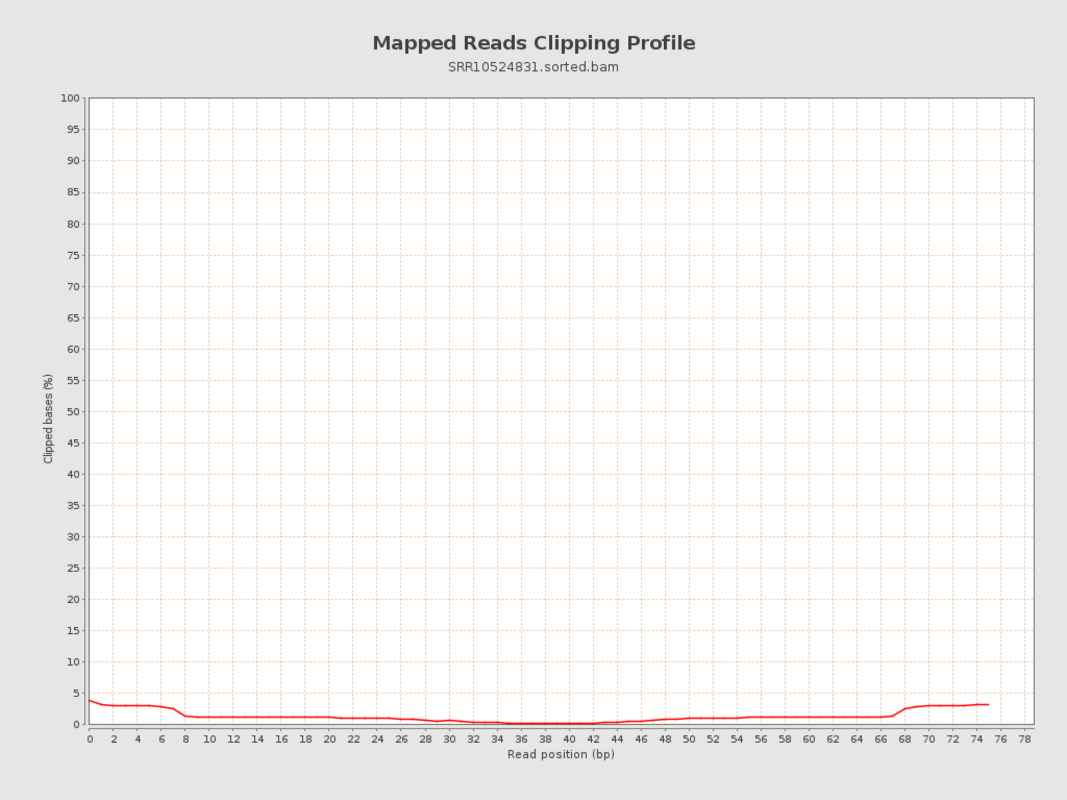
8. Results : Mapped Reads Nucleotide Content



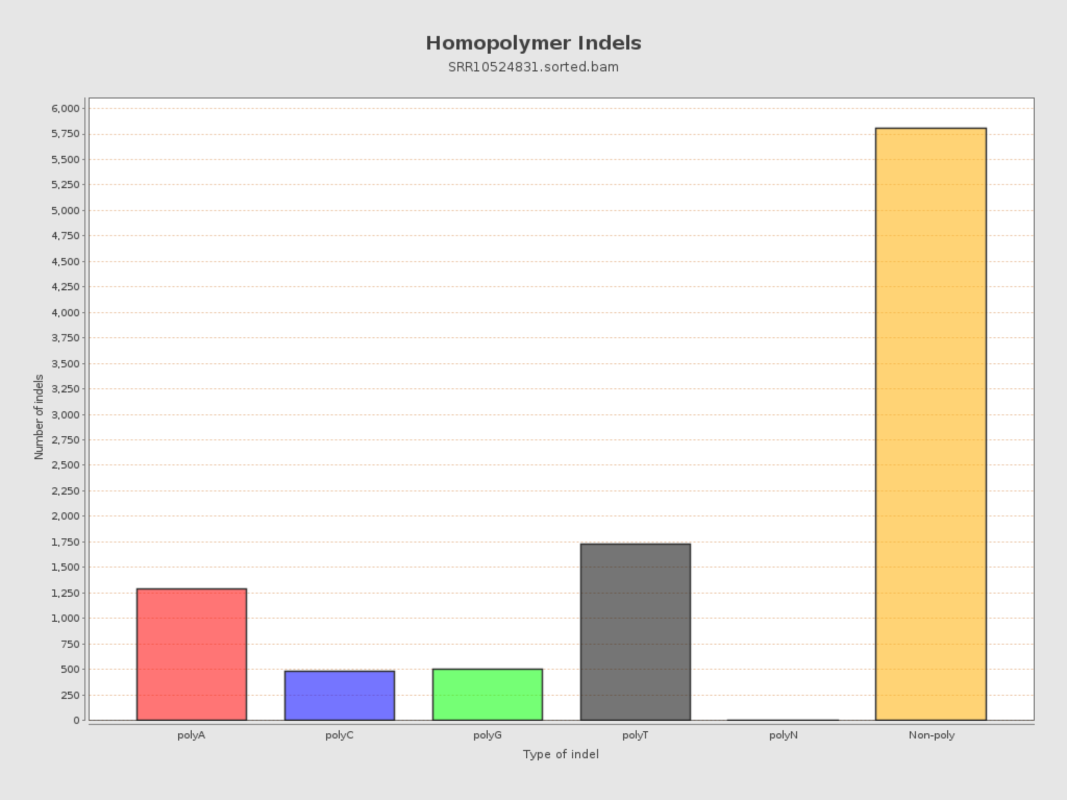
9. Results : Mapped Reads GC-content Distribution



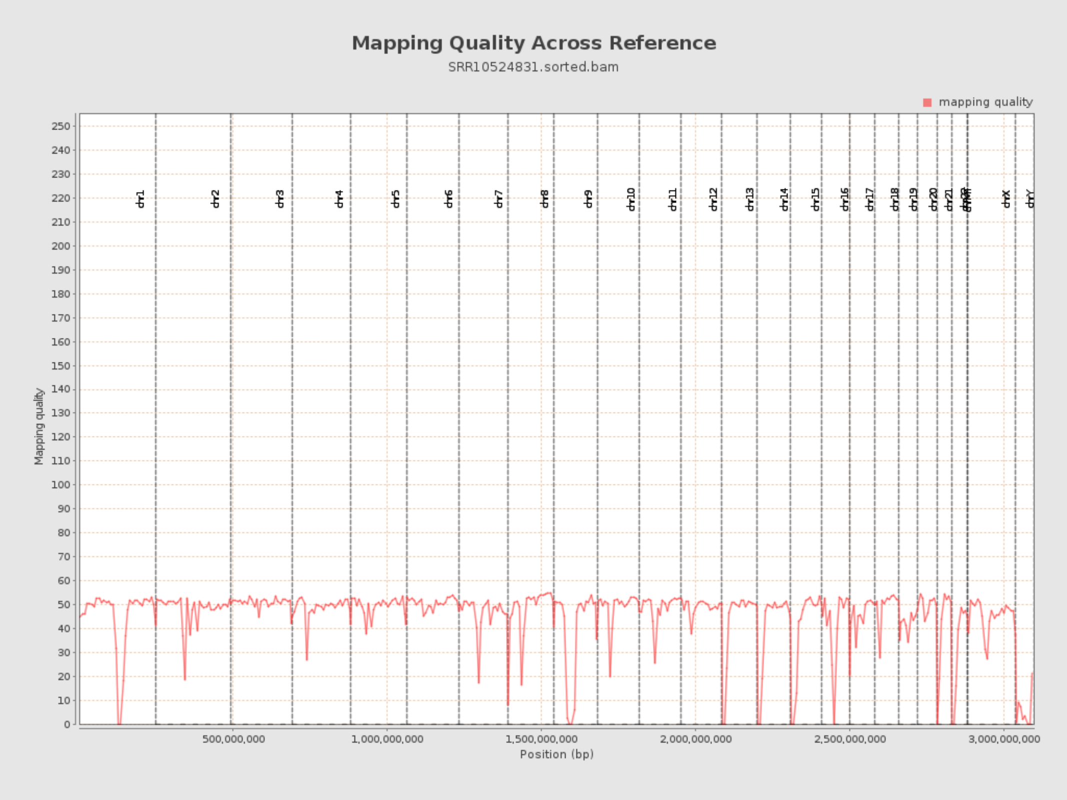
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram