Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 12:02:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524591.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_SRR10524591 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524591.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 12:02:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524591.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	886,752
Mapped reads	830,259 / 93.63%
Unmapped reads	56,493 / 6.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,944 / 0.22%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	23,499 / 2.65%
Duplication rate	2.19%
Clipped reads	828,839 / 93.47%

2.2. ACGT Content

Number/percentage of A's	12,329,511 / 25.19%
Number/percentage of C's	9,122,990 / 18.64%
Number/percentage of T's	15,699,114 / 32.07%
Number/percentage of G's	11,793,629 / 24.1%
Number/percentage of N's	314 / 0%
GC Percentage	42.73%

2.3. Coverage

Mean	0.0158

Standard Deviation	0.1671

2.4. Mapping Quality

Mean Mapping Quality	45.78

2.5. Mismatches and indels

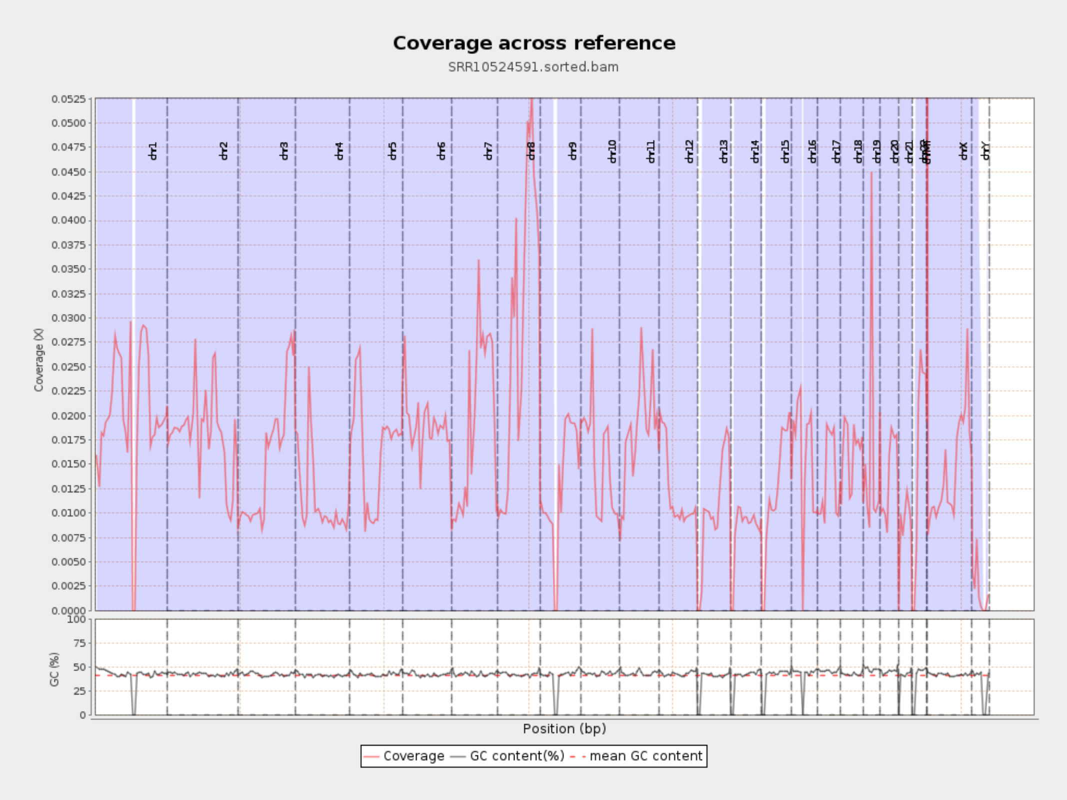
General error rate	0.48%
Mismatches	226,315
Insertions	3,779
Mapped reads with at least one insertion	0.45%
Deletions	8,972
Mapped reads with at least one deletion	1.07%
Homopolymer indels	42.04%

2.6. Chromosome stats

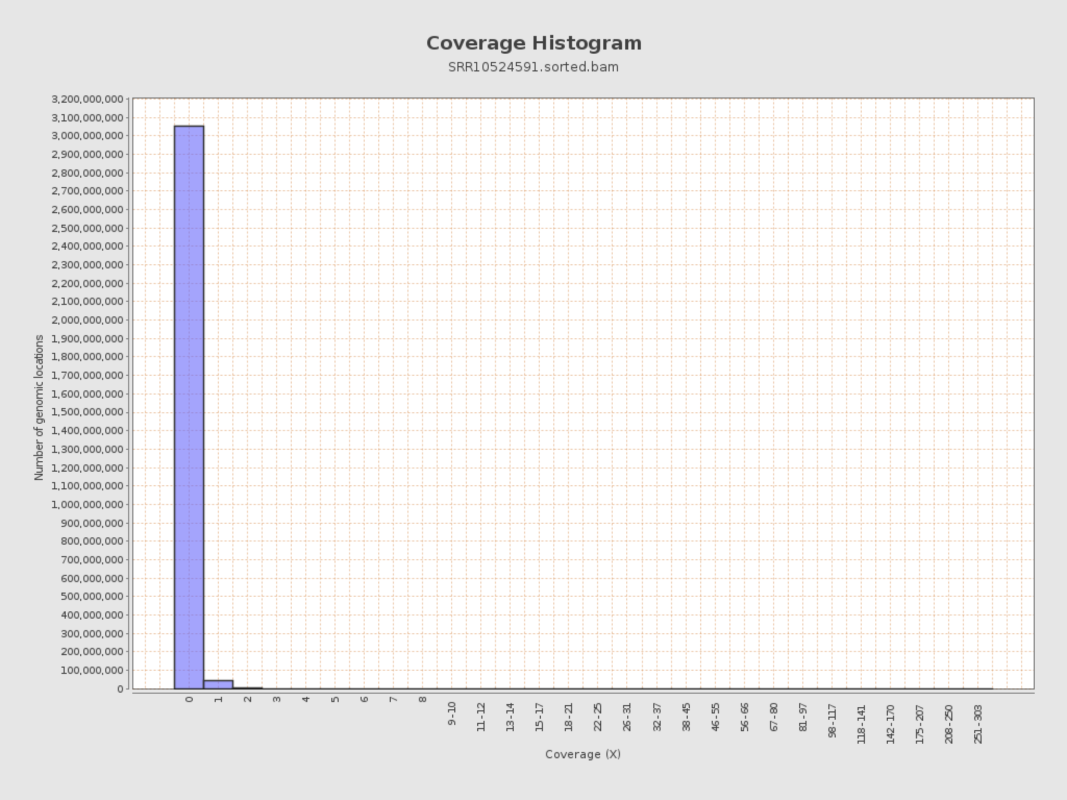
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5005700	0.0201	0.2783
chr2	243199373	4425195	0.0182	0.1832
chr3	198022430	3069248	0.0155	0.1322
chr4	191154276	2202903	0.0115	0.1254
chr5	180915260	3013559	0.0167	0.1374
chr6	171115067	3247250	0.019	0.1515
chr7	159138663	3070088	0.0193	0.21

chr8	146364022	4356011	0.0298	0.2254
chr9	141213431	1804782	0.0128	0.148
chr10	135534747	2087976	0.0154	0.1691
chr11	135006516	2521844	0.0187	0.1643
chr12	133851895	1632573	0.0122	0.1186
chr13	115169878	1197644	0.0104	0.1082
chr14	107349540	867840	0.0081	0.0988
chr15	102531392	1251009	0.0122	0.1204
chr16	90354753	1418866	0.0157	0.1386
chr17	81195210	1090513	0.0134	0.1248
chr18	78077248	1270512	0.0163	0.2125
chr19	59128983	932452	0.0158	0.1905
chr20	63025520	867030	0.0138	0.1262
chr21	48129895	424351	0.0088	0.1086
chr22	51304566	836424	0.0163	0.1356
chrMT	16571	6624	0.3997	0.6676
chrX	155270560	2240658	0.0144	0.135
chrY	59373566	119779	0.002	0.0637

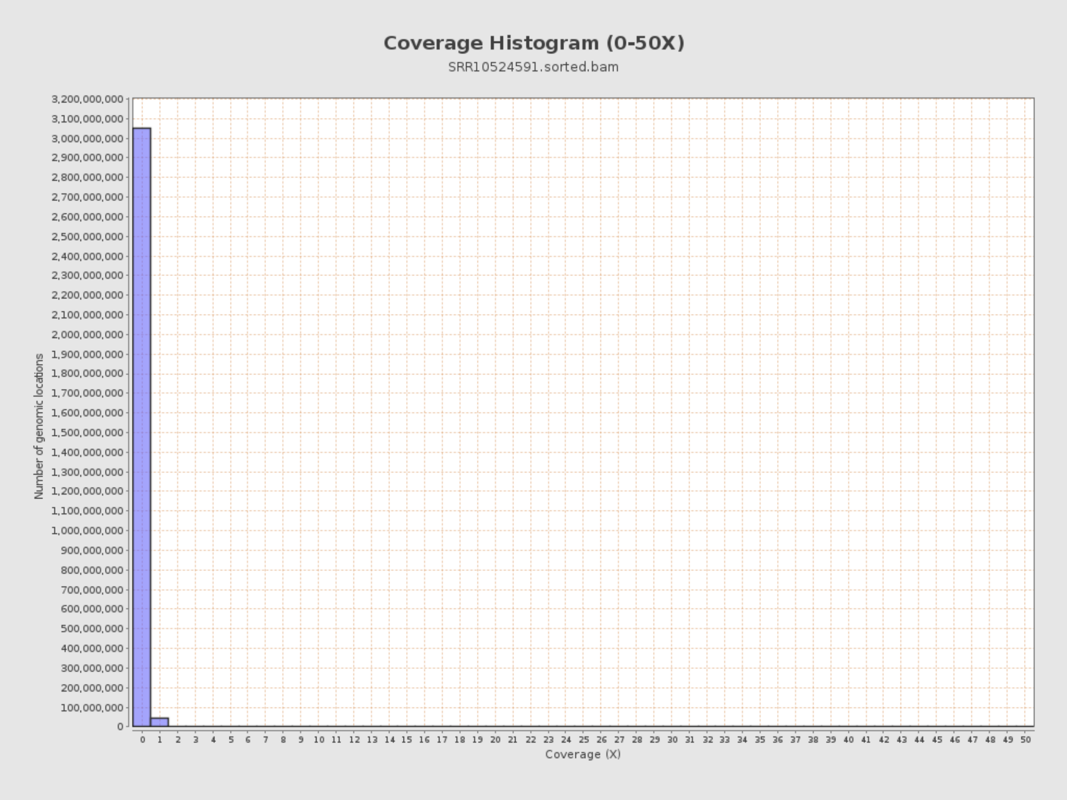
3. Results : Coverage across reference



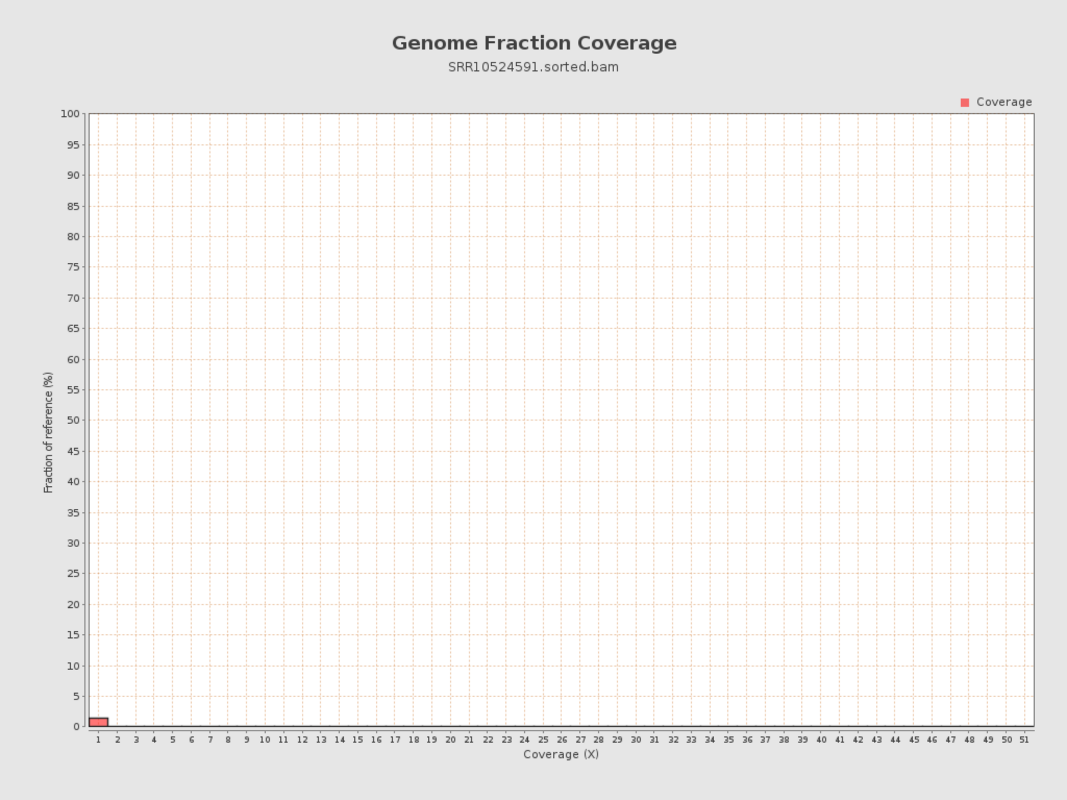
4. Results : Coverage Histogram



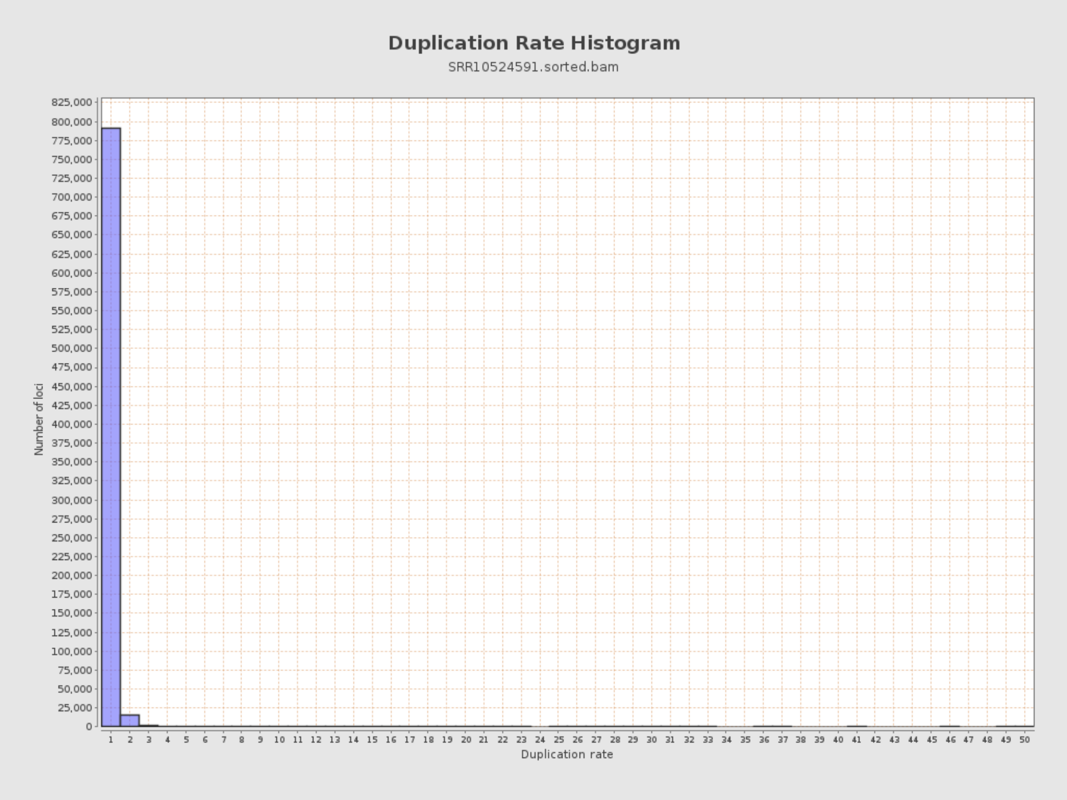
5. Results : Coverage Histogram (0-50X)



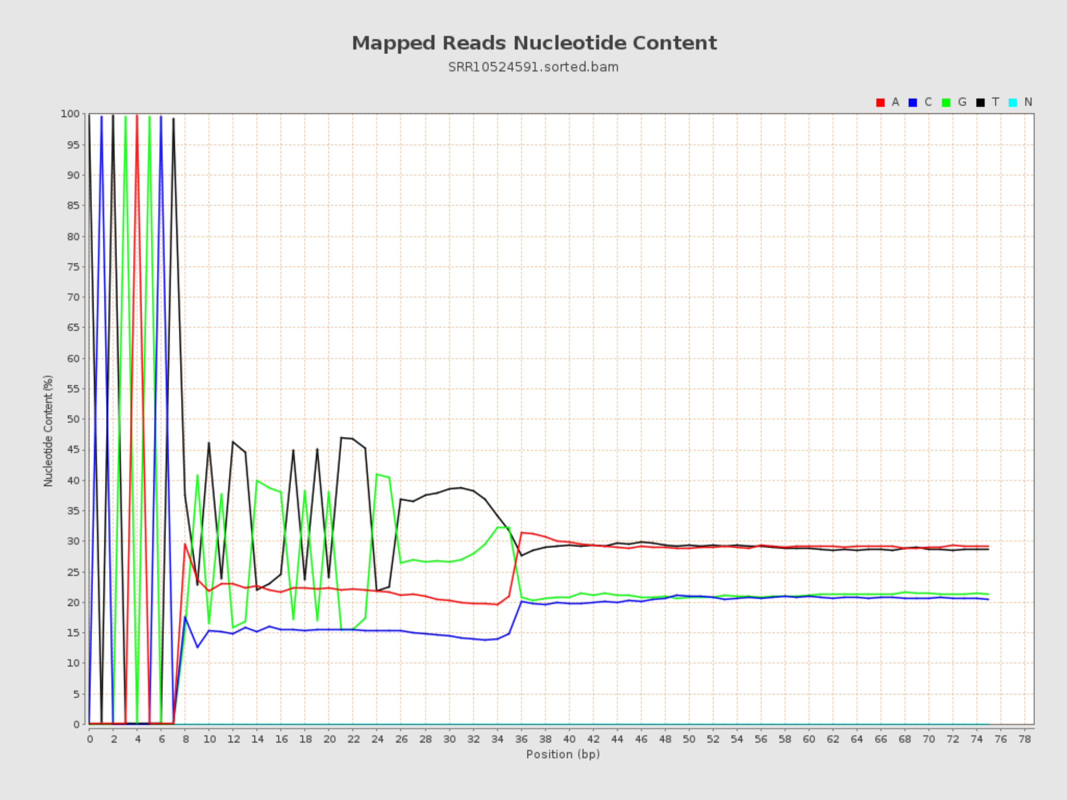
6. Results : Genome Fraction Coverage



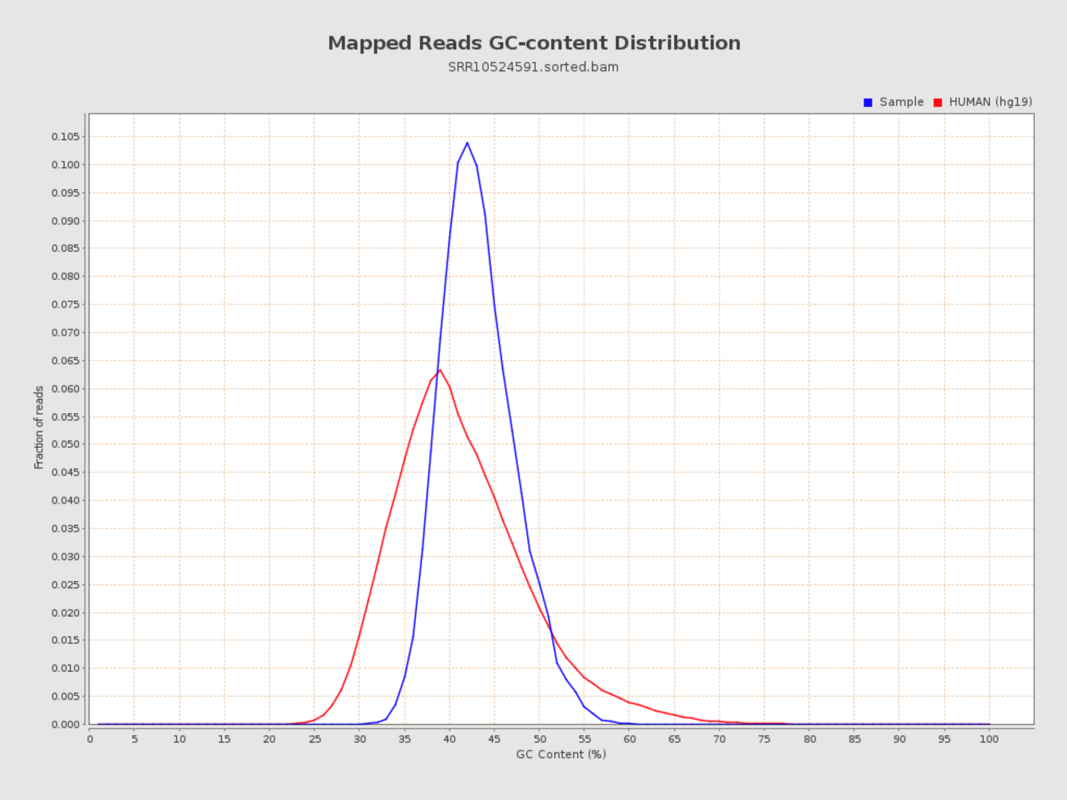
7. Results : Duplication Rate Histogram



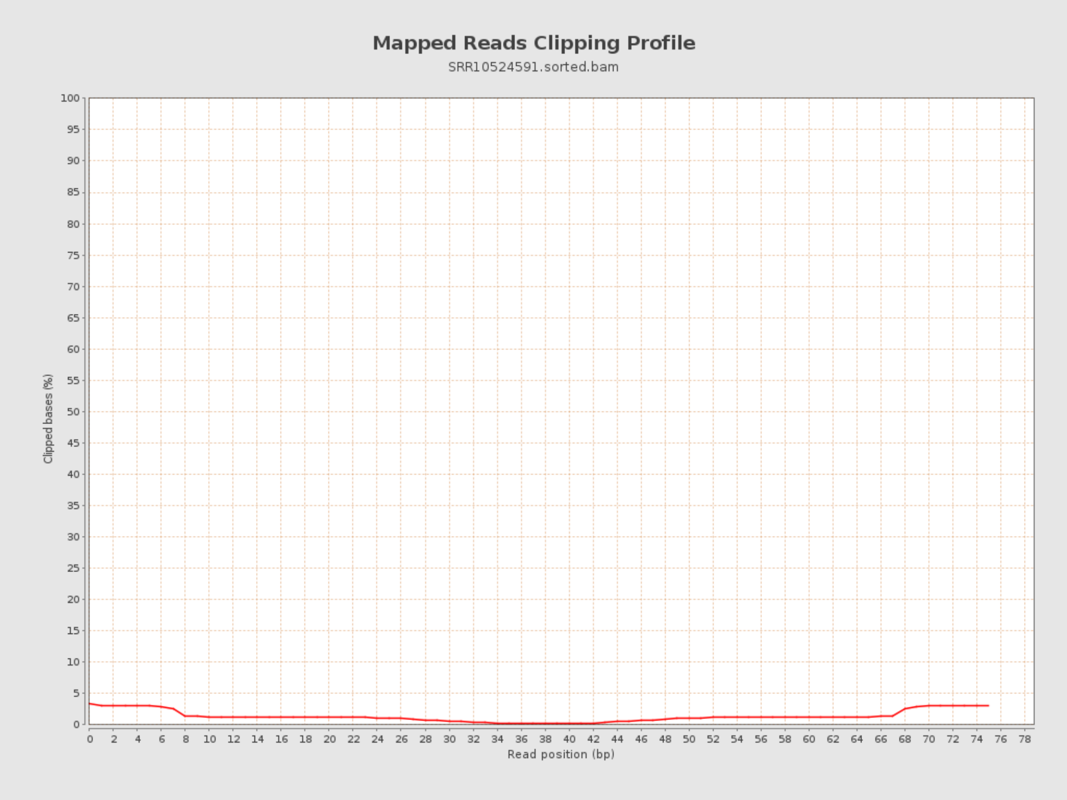
8. Results : Mapped Reads Nucleotide Content



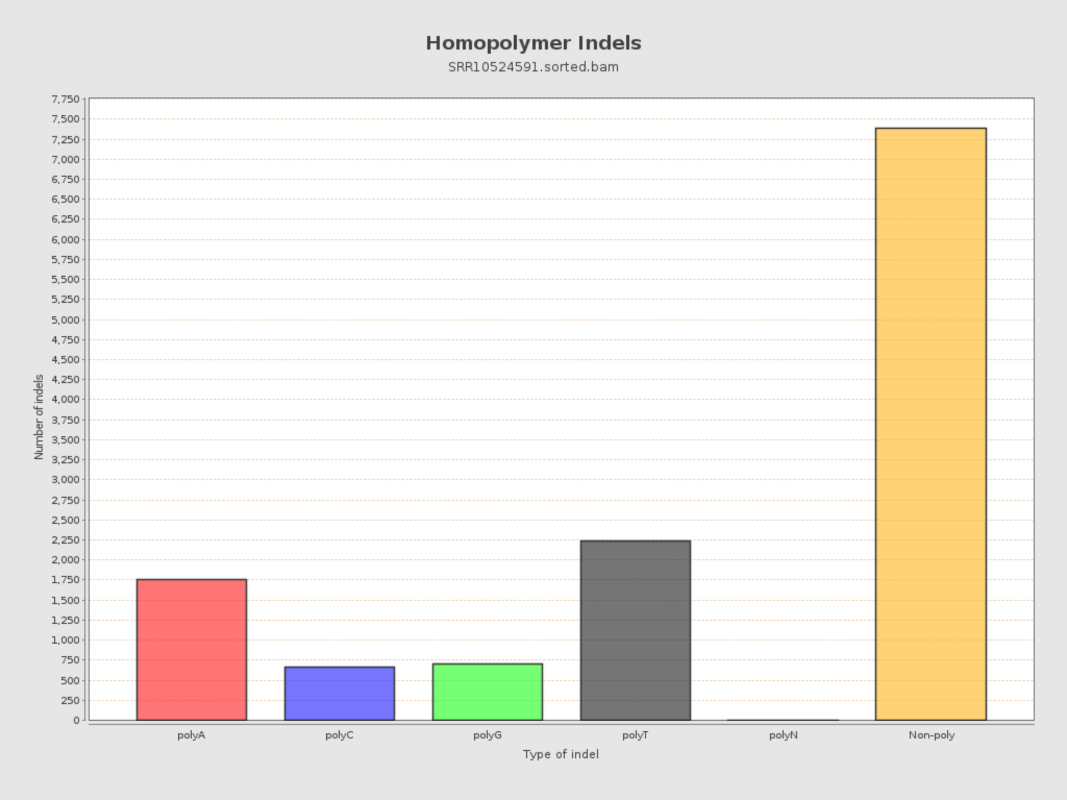
9. Results : Mapped Reads GC-content Distribution



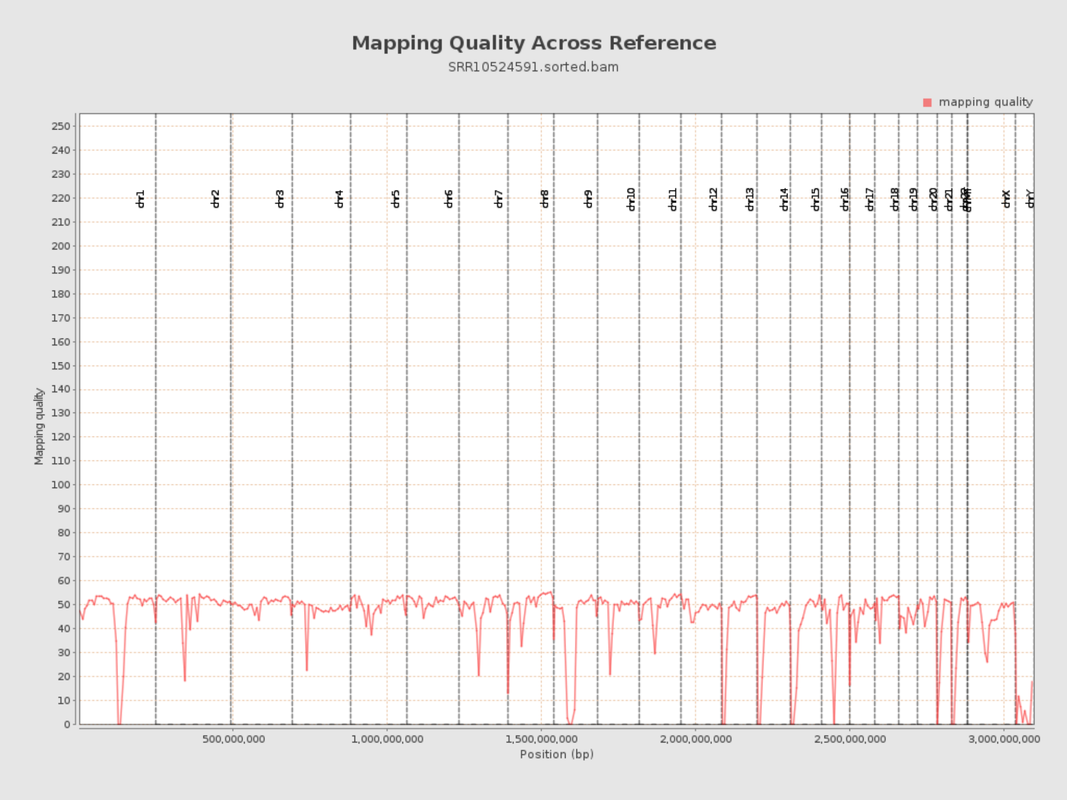
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram