Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 08:38:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524941.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_SRR10524941 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524941.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 08:38:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524941.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	604,299
Mapped reads	557,186 / 92.2%
Unmapped reads	47,113 / 7.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,340 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	12,305 / 2.04%
Duplication rate	1.71%
Clipped reads	558,125 / 92.36%

2.2. ACGT Content

Number/percentage of A's	8,470,417 / 25.95%
Number/percentage of C's	5,866,481 / 17.97%
Number/percentage of T's	10,192,658 / 31.22%
Number/percentage of G's	8,117,448 / 24.86%
Number/percentage of N's	262 / 0%
GC Percentage	42.83%

2.3. Coverage

Mean	0.0105

Standard Deviation	0.1275

2.4. Mapping Quality

Mean Mapping Quality	45.1

2.5. Mismatches and indels

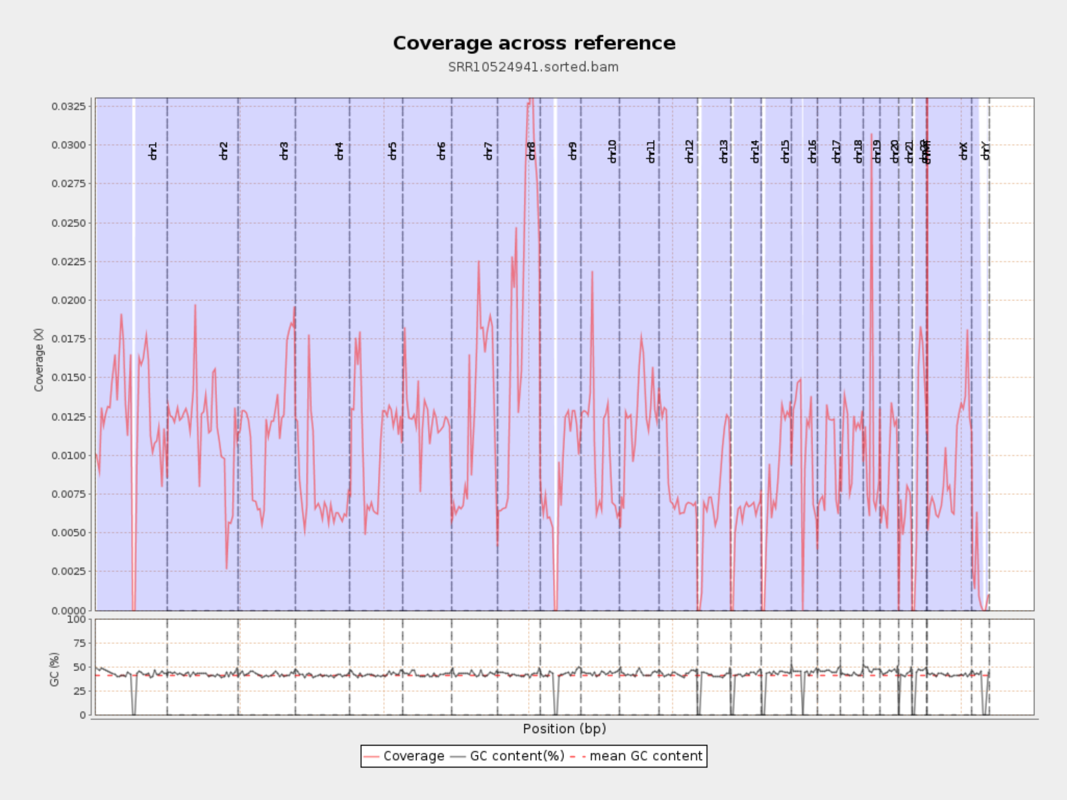
General error rate	0.51%
Mismatches	160,899
Insertions	2,282
Mapped reads with at least one insertion	0.41%
Deletions	6,334
Mapped reads with at least one deletion	1.13%
Homopolymer indels	42.54%

2.6. Chromosome stats

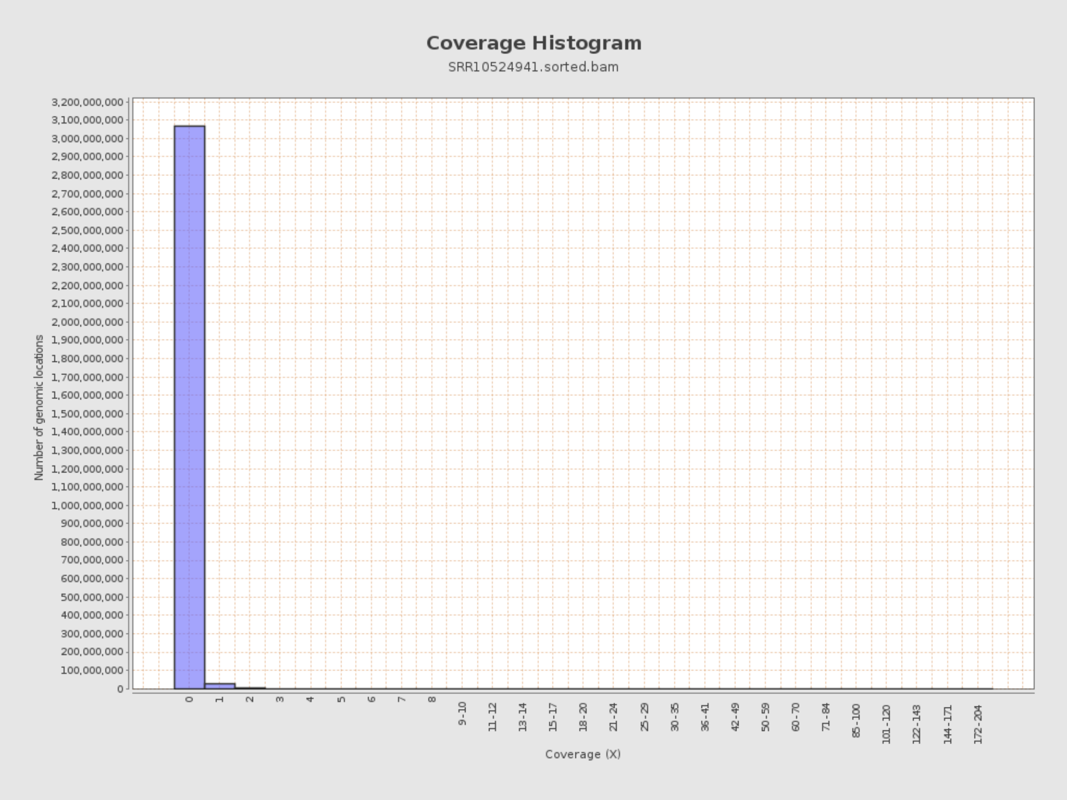
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3101352	0.0124	0.1956
chr2	243199373	2828336	0.0116	0.1431
chr3	198022430	2356855	0.0119	0.1135
chr4	191154276	1489948	0.0078	0.1002
chr5	180915260	2024412	0.0112	0.1101
chr6	171115067	2110357	0.0123	0.1182
chr7	159138663	1988951	0.0125	0.1444

chr8	146364022	2899369	0.0198	0.1715
chr9	141213431	1175619	0.0083	0.1078
chr10	135534747	1456569	0.0107	0.1352
chr11	135006516	1668660	0.0124	0.1263
chr12	133851895	1102113	0.0082	0.0956
chr13	115169878	812583	0.0071	0.0876
chr14	107349540	611635	0.0057	0.0793
chr15	102531392	836541	0.0082	0.0943
chr16	90354753	943669	0.0104	0.109
chr17	81195210	745589	0.0092	0.1014
chr18	78077248	872249	0.0112	0.164
chr19	59128983	658385	0.0111	0.1601
chr20	63025520	569546	0.009	0.1
chr21	48129895	288566	0.006	0.0876
chr22	51304566	555560	0.0108	0.108
chrMT	16571	1830	0.1104	0.3201
chrX	155270560	1468422	0.0095	0.1052
chrY	59373566	90748	0.0015	0.0681

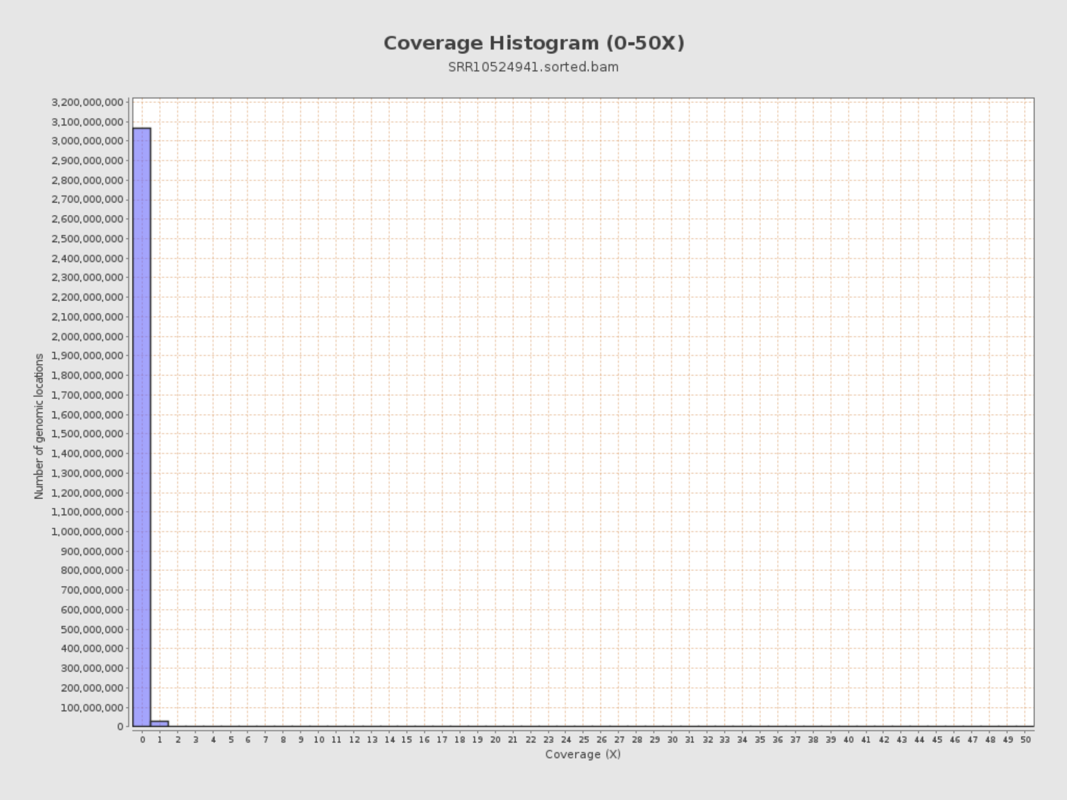
3. Results : Coverage across reference



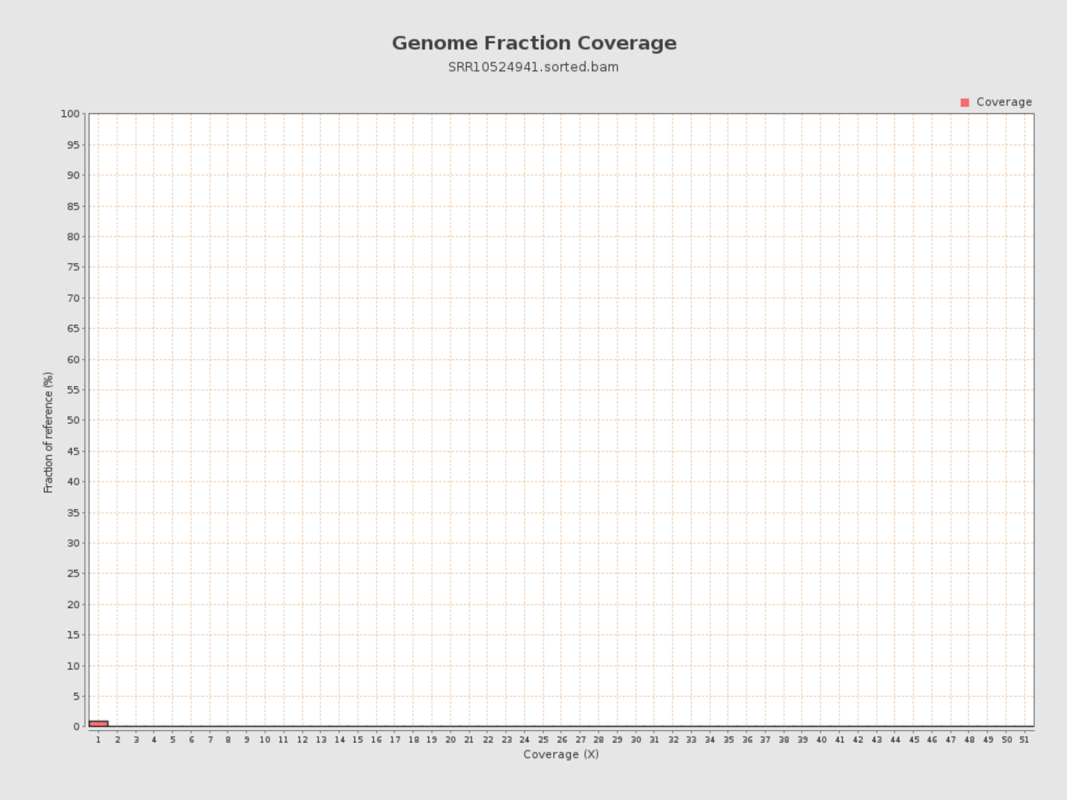
4. Results : Coverage Histogram



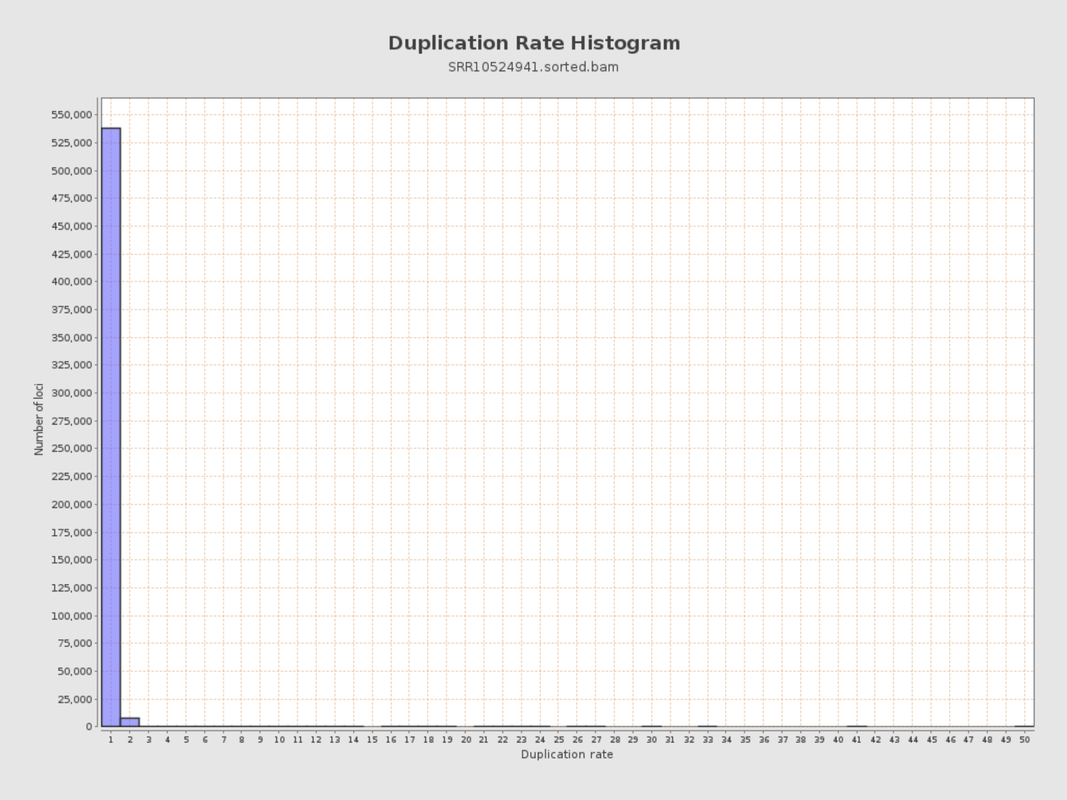
5. Results : Coverage Histogram (0-50X)



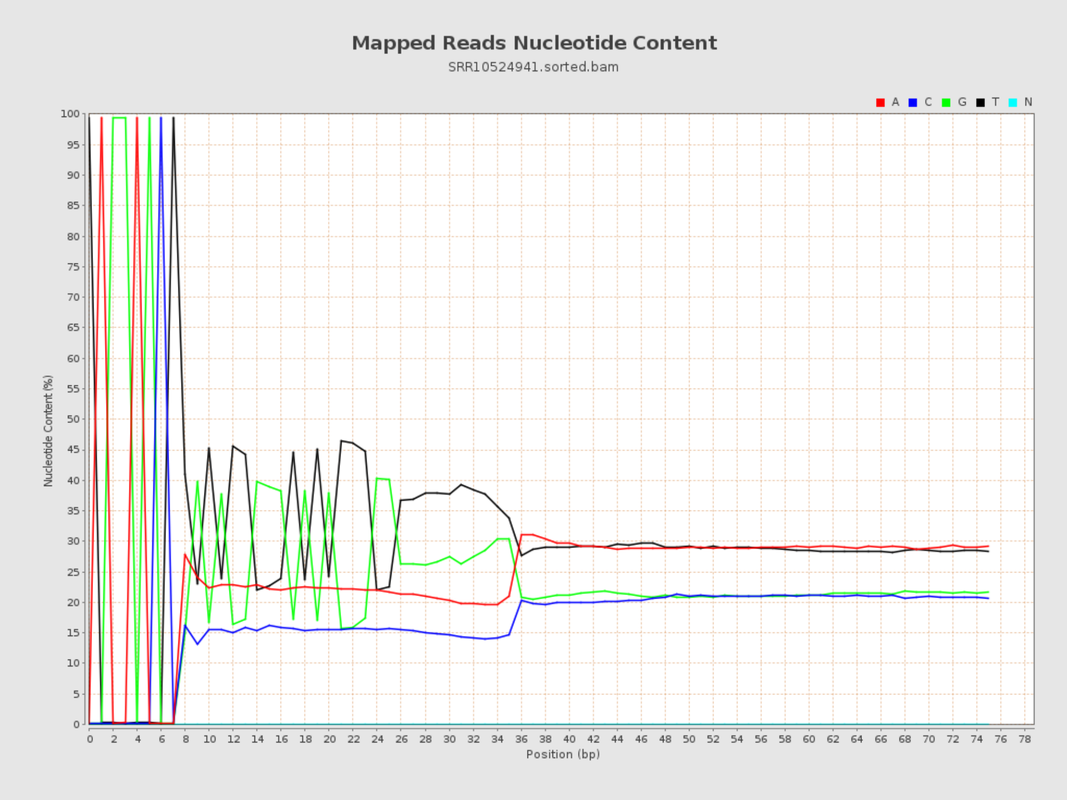
6. Results : Genome Fraction Coverage



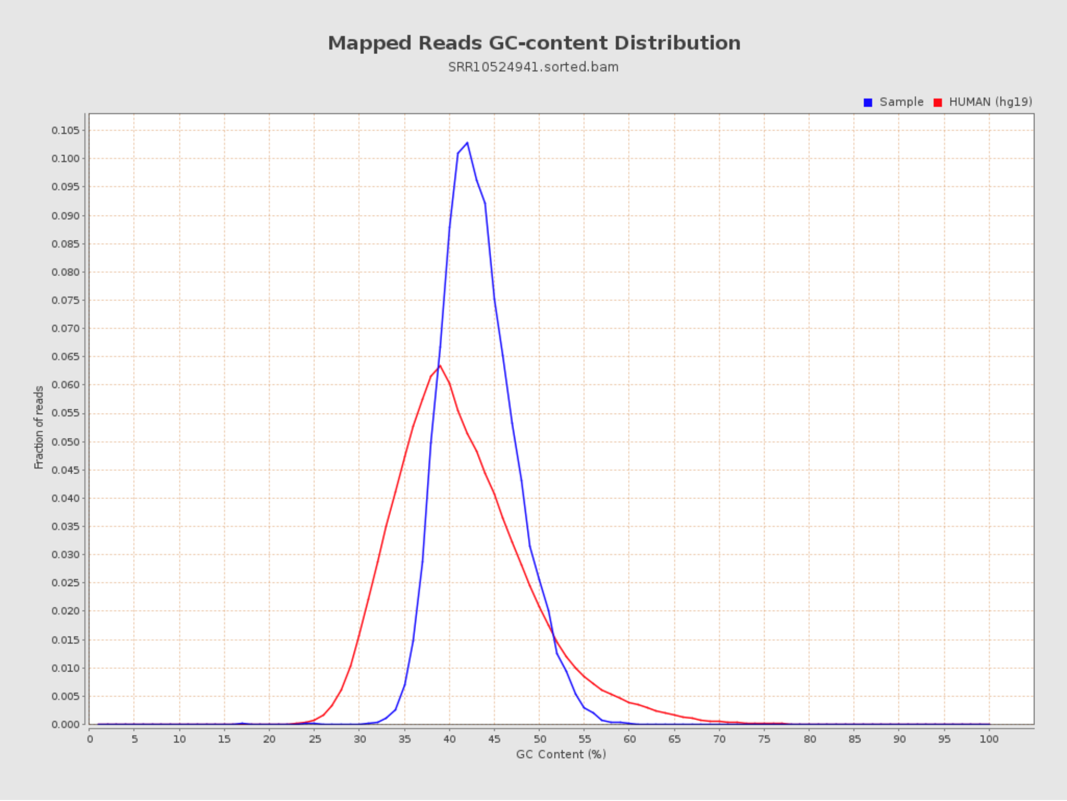
7. Results : Duplication Rate Histogram



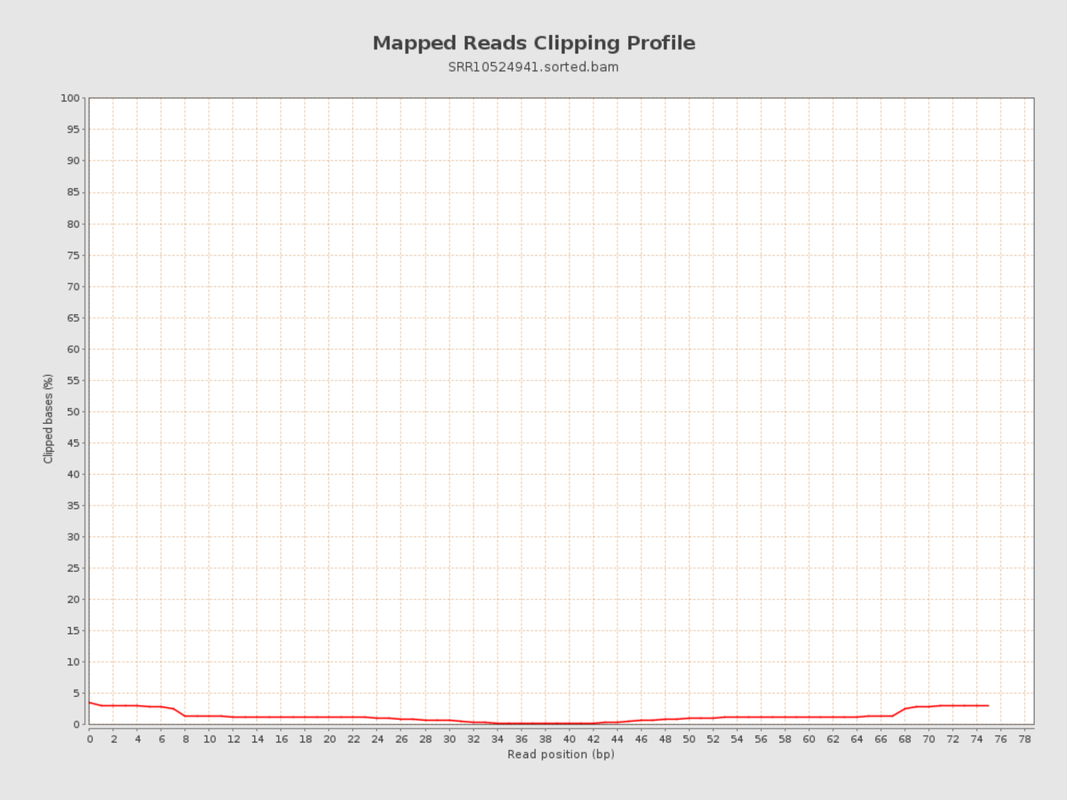
8. Results : Mapped Reads Nucleotide Content



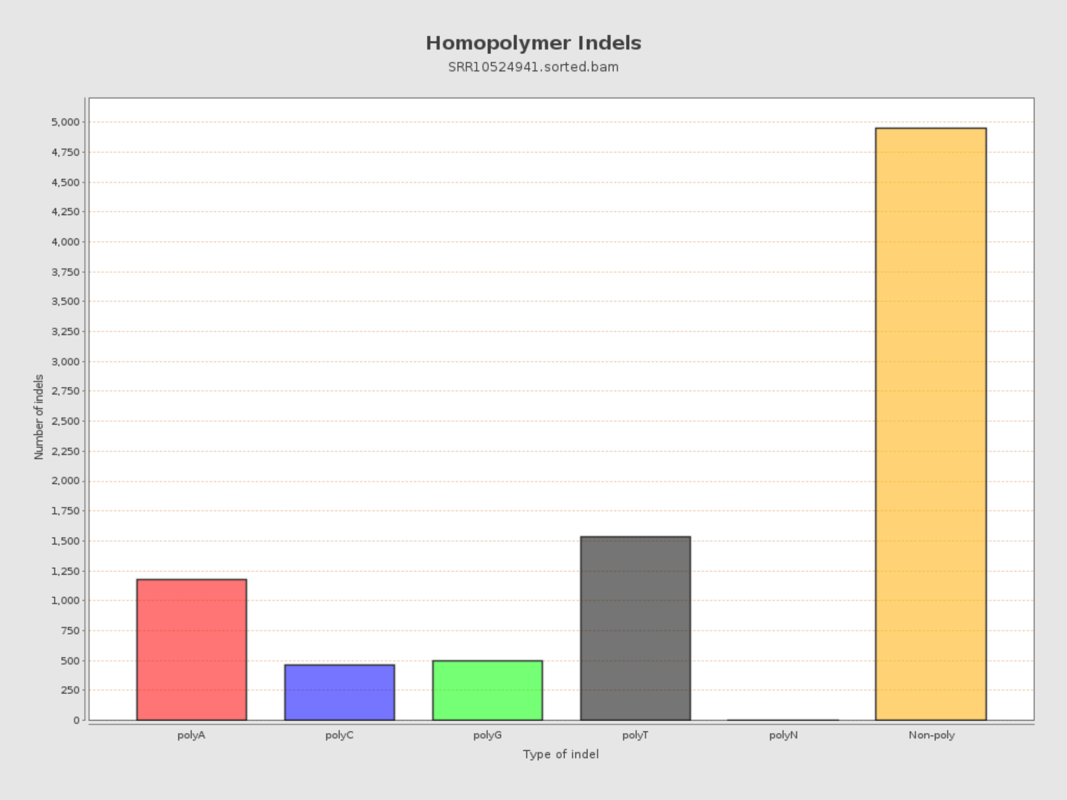
9. Results : Mapped Reads GC-content Distribution



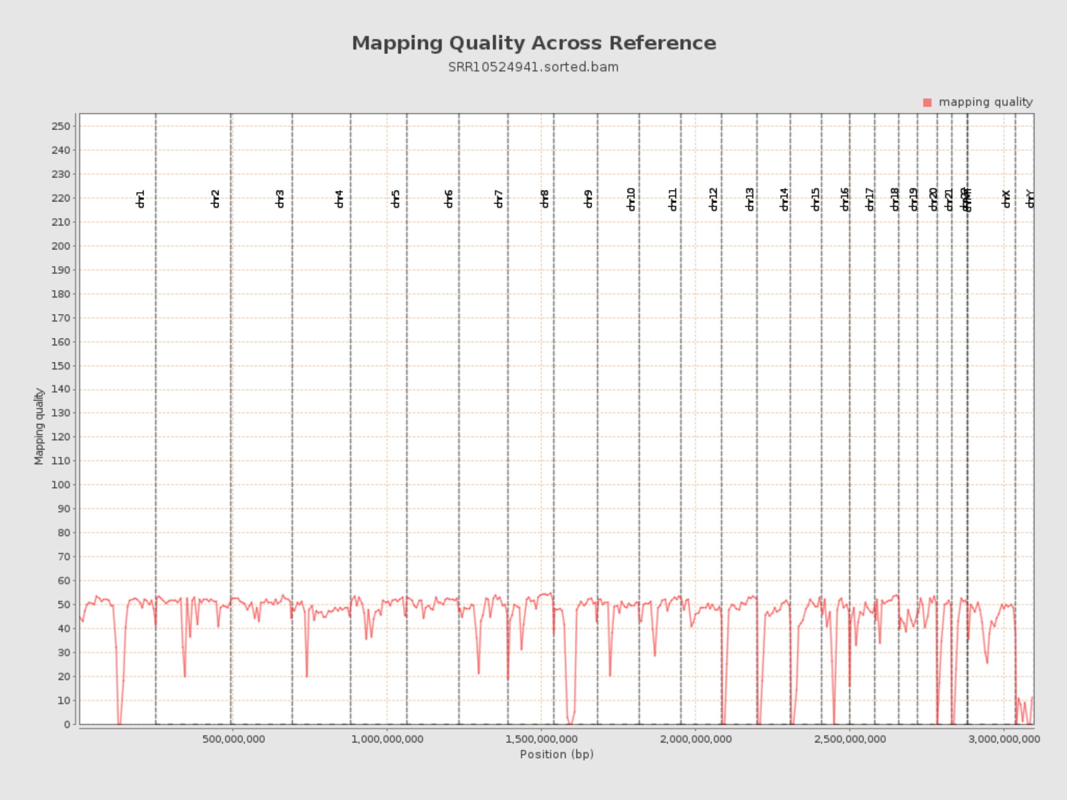
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram