Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 21:29:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524810.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_SRR10524810 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524810.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 21:29:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524810.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,785,950
Mapped reads	1,609,633 / 90.13%
Unmapped reads	176,317 / 9.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,625 / 0.31%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	62,740 / 3.51%
Duplication rate	2.97%
Clipped reads	1,611,281 / 90.22%

2.2. ACGT Content

Number/percentage of A's	22,588,903 / 24.72%
Number/percentage of C's	16,683,808 / 18.26%
Number/percentage of T's	29,812,622 / 32.63%
Number/percentage of G's	22,272,814 / 24.38%
Number/percentage of N's	10,902 / 0.01%
GC Percentage	42.64%

2.3. Coverage

Mean	0.0295

Standard Deviation	0.255

2.4. Mapping Quality

Mean Mapping Quality	44.46

2.5. Mismatches and indels

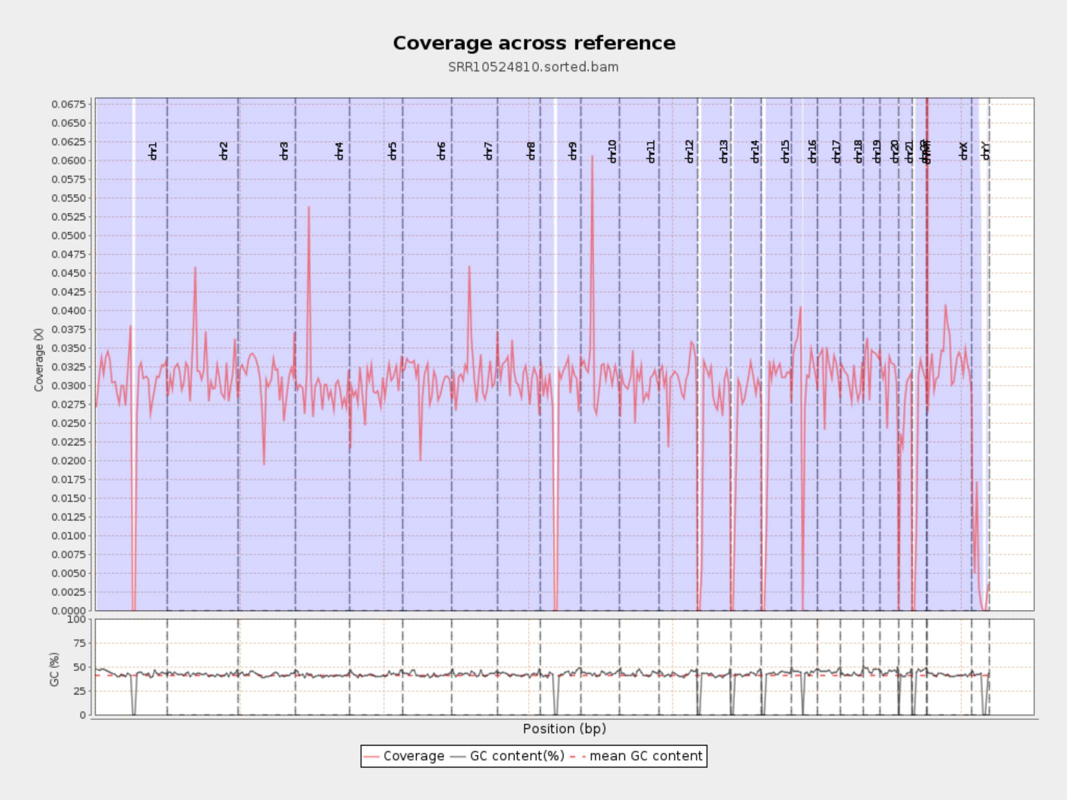
General error rate	0.53%
Mismatches	470,813
Insertions	5,983
Mapped reads with at least one insertion	0.37%
Deletions	17,896
Mapped reads with at least one deletion	1.1%
Homopolymer indels	41.8%

2.6. Chromosome stats

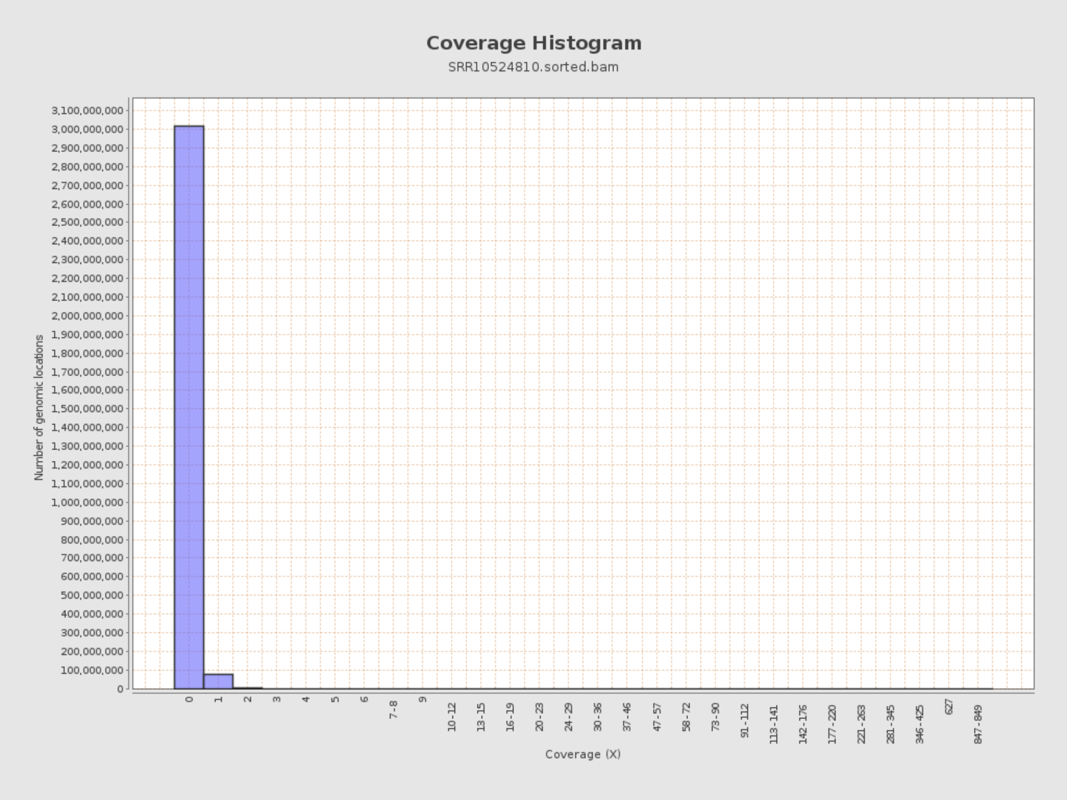
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7236318	0.029	0.323
chr2	243199373	7712136	0.0317	0.4152
chr3	198022430	6111304	0.0309	0.1973
chr4	191154276	5775032	0.0302	0.2182
chr5	180915260	5442112	0.0301	0.1912
chr6	171115067	5229968	0.0306	0.2136
chr7	159138663	5036147	0.0316	0.3168

chr8	146364022	4575980	0.0313	0.2307
chr9	141213431	3861838	0.0273	0.226
chr10	135534747	4473928	0.033	0.3045
chr11	135006516	4099117	0.0304	0.23
chr12	133851895	4153557	0.031	0.1965
chr13	115169878	2888296	0.0251	0.1757
chr14	107349540	2687966	0.025	0.1798
chr15	102531392	2642160	0.0258	0.1797
chr16	90354753	2740573	0.0303	0.2129
chr17	81195210	2613983	0.0322	0.2083
chr18	78077248	2392891	0.0306	0.3443
chr19	59128983	1980688	0.0335	0.2823
chr20	63025520	1947065	0.0309	0.2019
chr21	48129895	1203319	0.025	0.1889
chr22	51304566	1124248	0.0219	0.1645
chrMT	16571	21420	1.2926	1.3153
chrX	155270560	5145373	0.0331	0.2196
chrY	59373566	302464	0.0051	0.1334

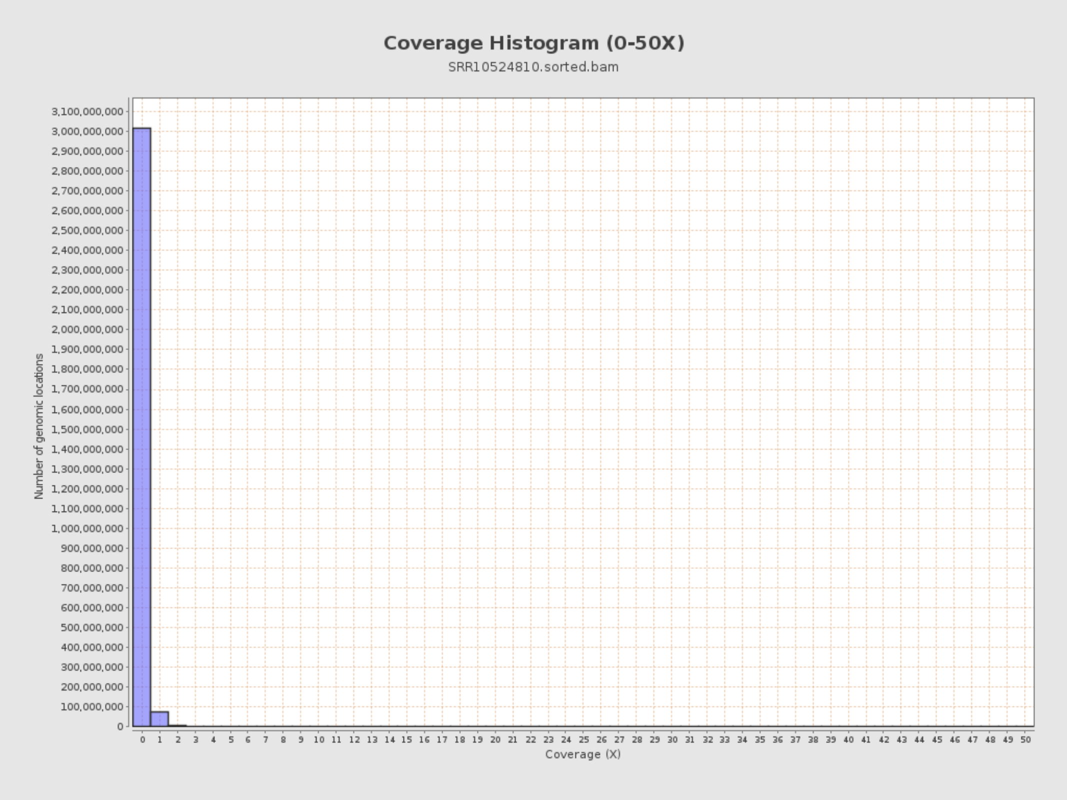
3. Results : Coverage across reference



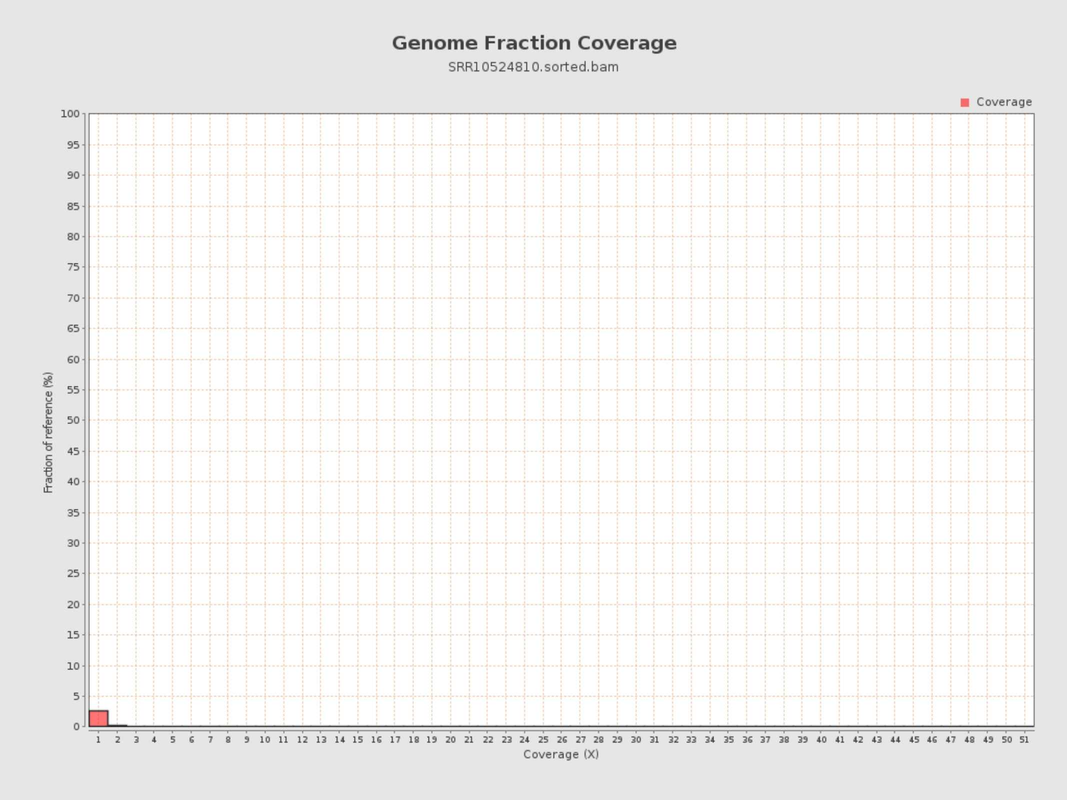
4. Results : Coverage Histogram



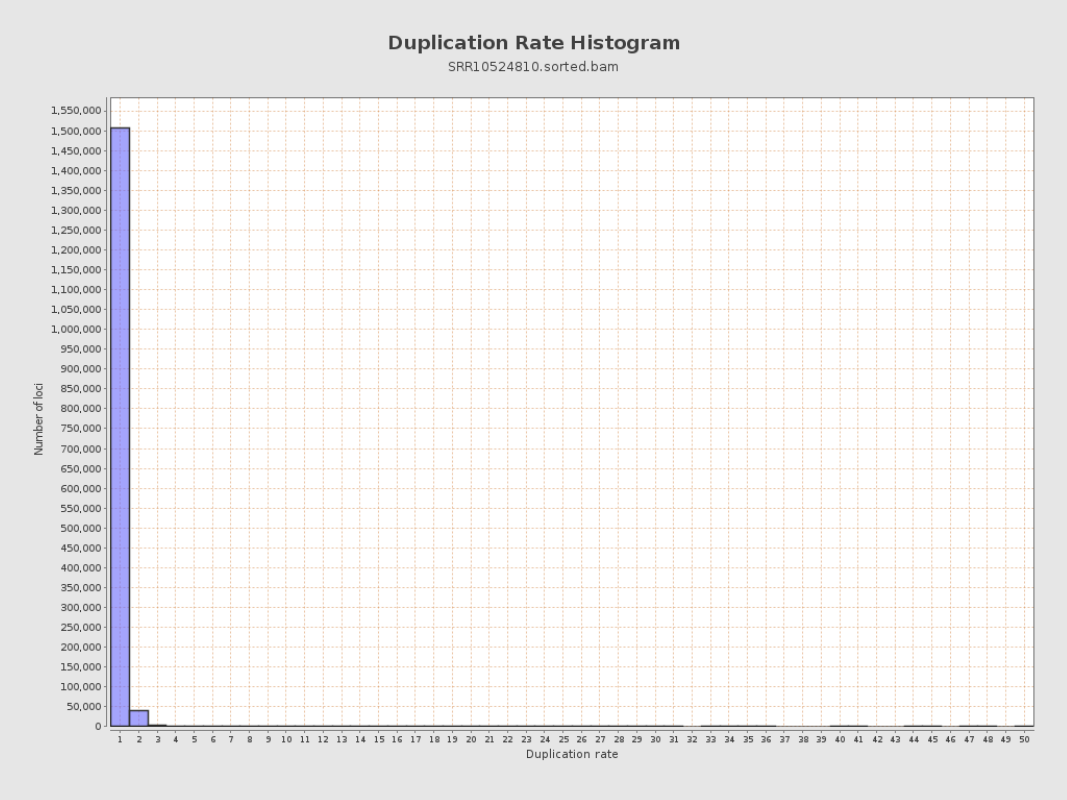
5. Results : Coverage Histogram (0-50X)



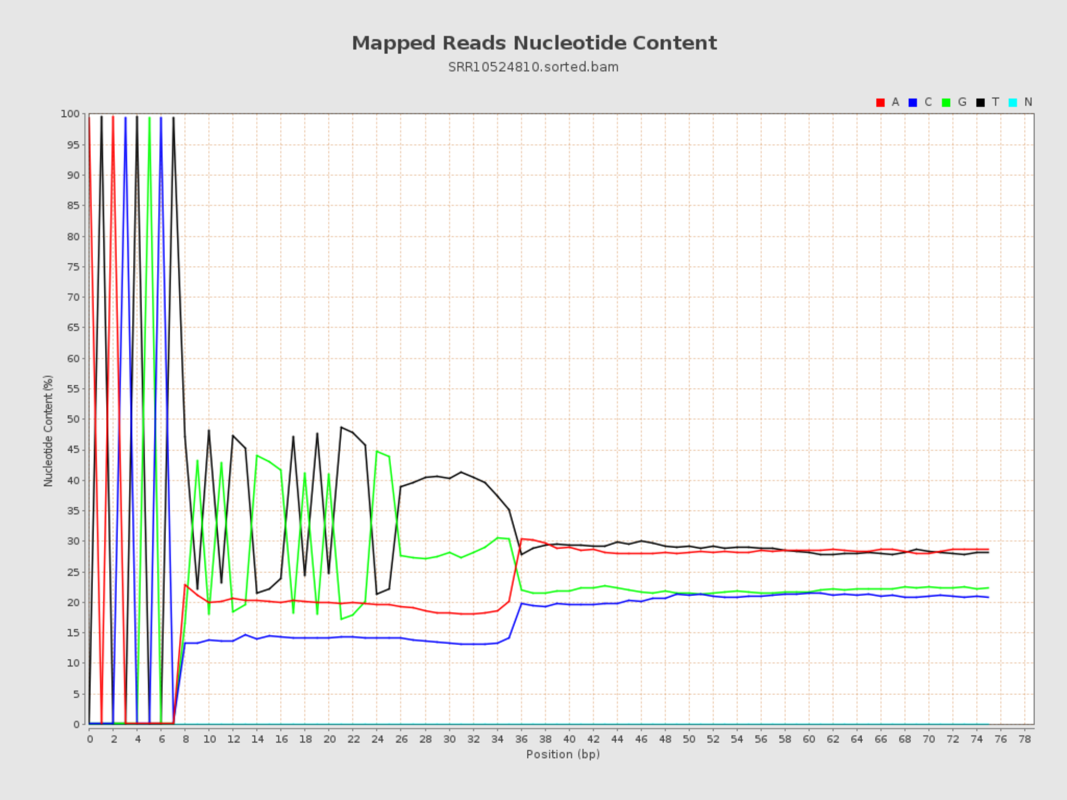
6. Results : Genome Fraction Coverage



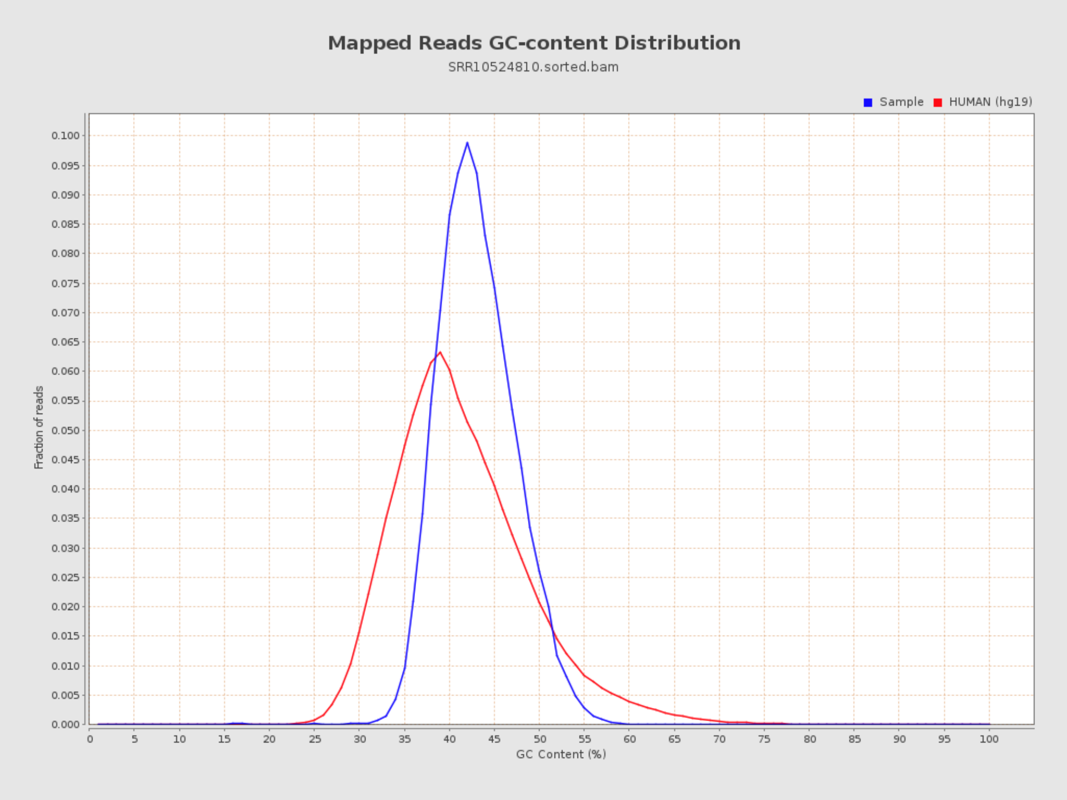
7. Results : Duplication Rate Histogram



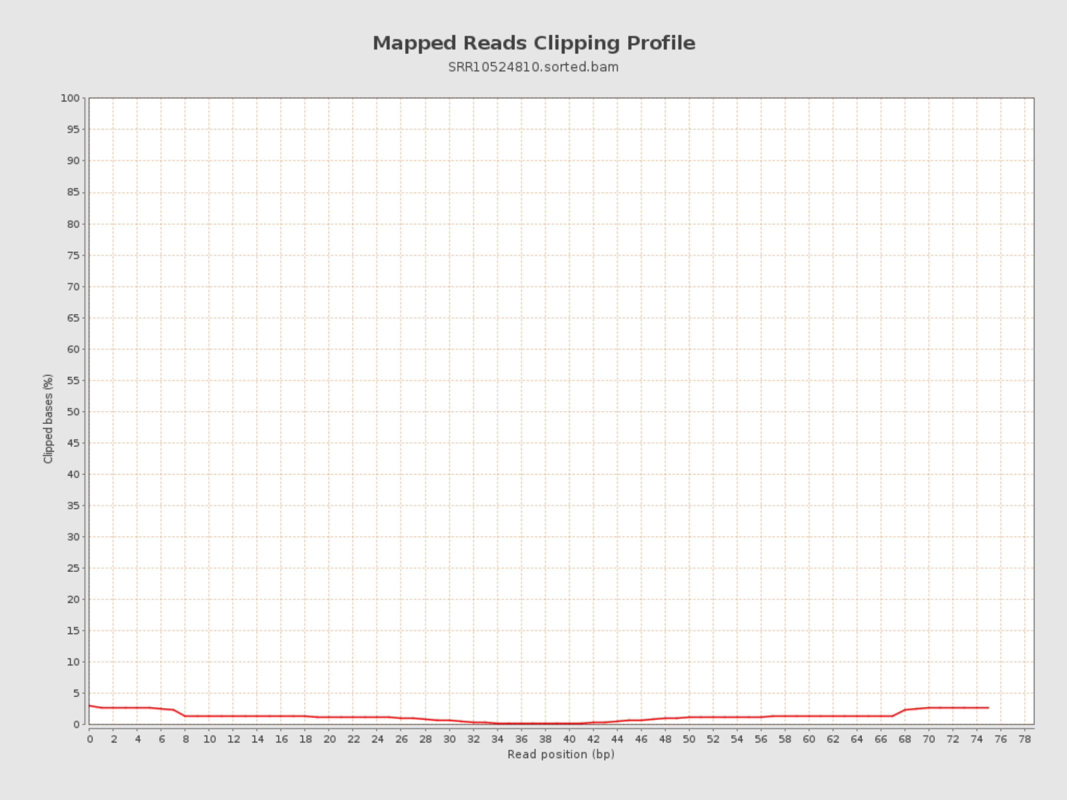
8. Results : Mapped Reads Nucleotide Content



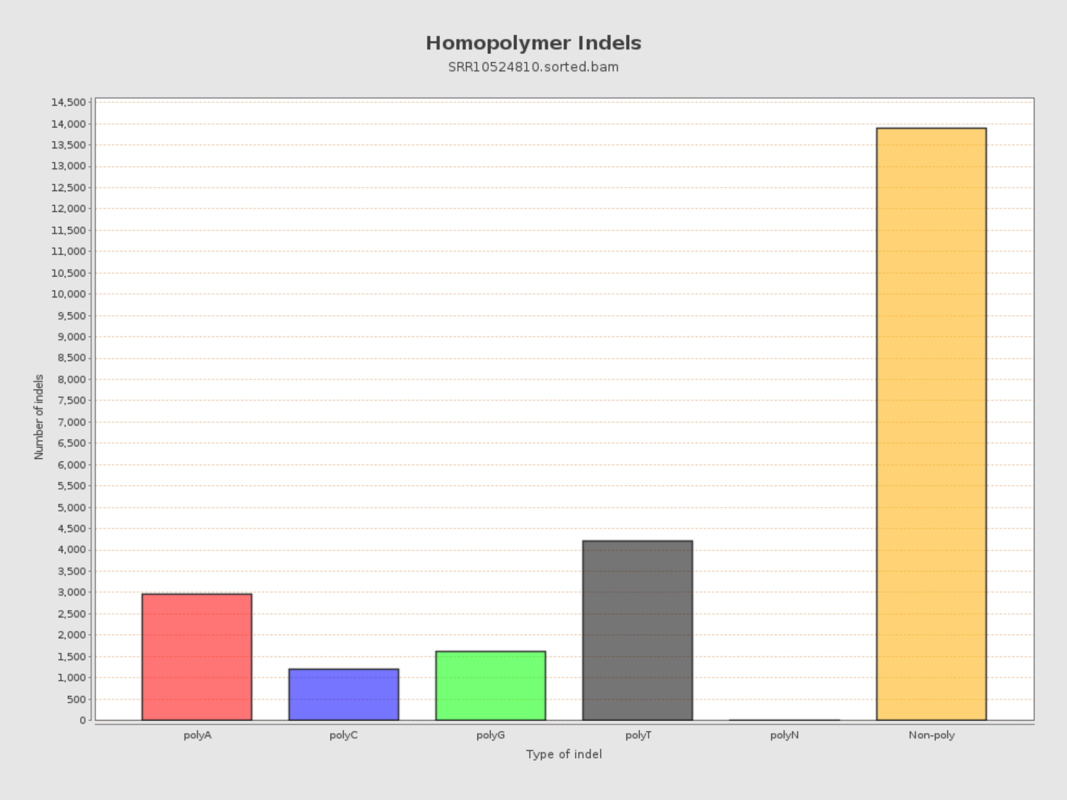
9. Results : Mapped Reads GC-content Distribution



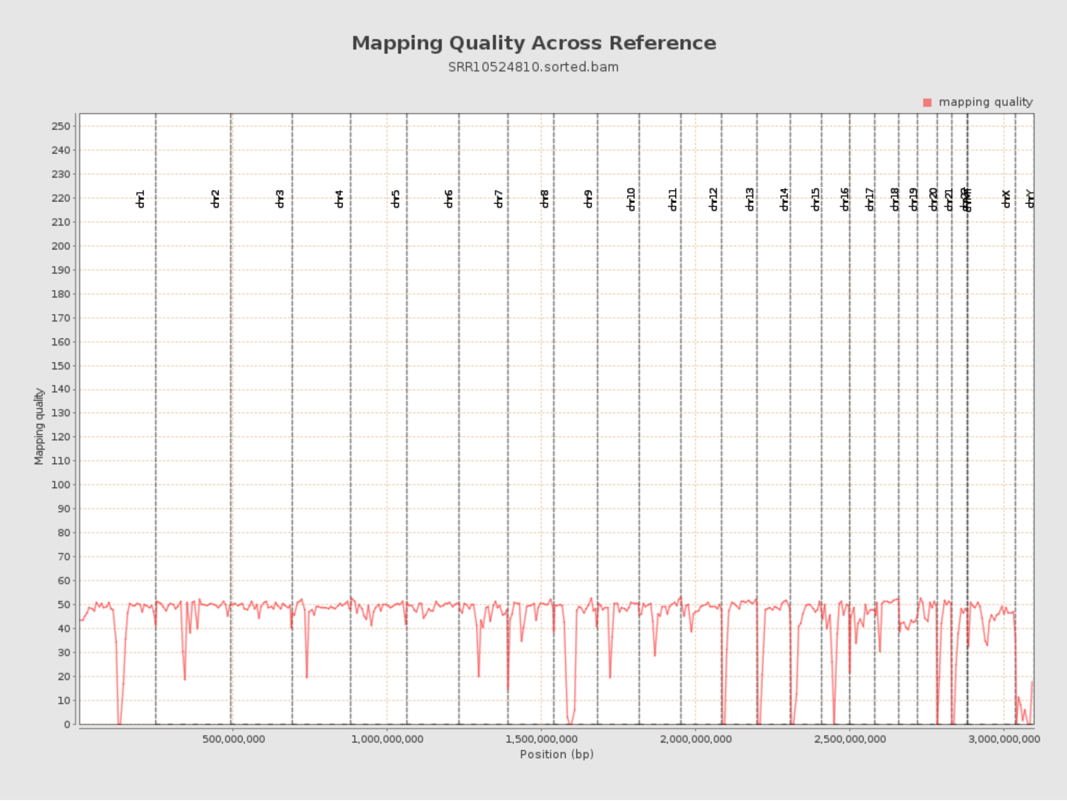
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram