Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 08:32:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524940.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_SRR10524940 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524940.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 08:32:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524940.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	418,744
Mapped reads	385,572 / 92.08%
Unmapped reads	33,172 / 7.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,598 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	8,210 / 1.96%
Duplication rate	1.7%
Clipped reads	386,125 / 92.21%

2.2. ACGT Content

Number/percentage of A's	5,496,188 / 24.62%
Number/percentage of C's	4,147,311 / 18.57%
Number/percentage of T's	7,228,050 / 32.37%
Number/percentage of G's	5,456,333 / 24.44%
Number/percentage of N's	188 / 0%
GC Percentage	43.01%

2.3. Coverage

Mean	0.0072

Standard Deviation	0.1005

2.4. Mapping Quality

Mean Mapping Quality	44.38

2.5. Mismatches and indels

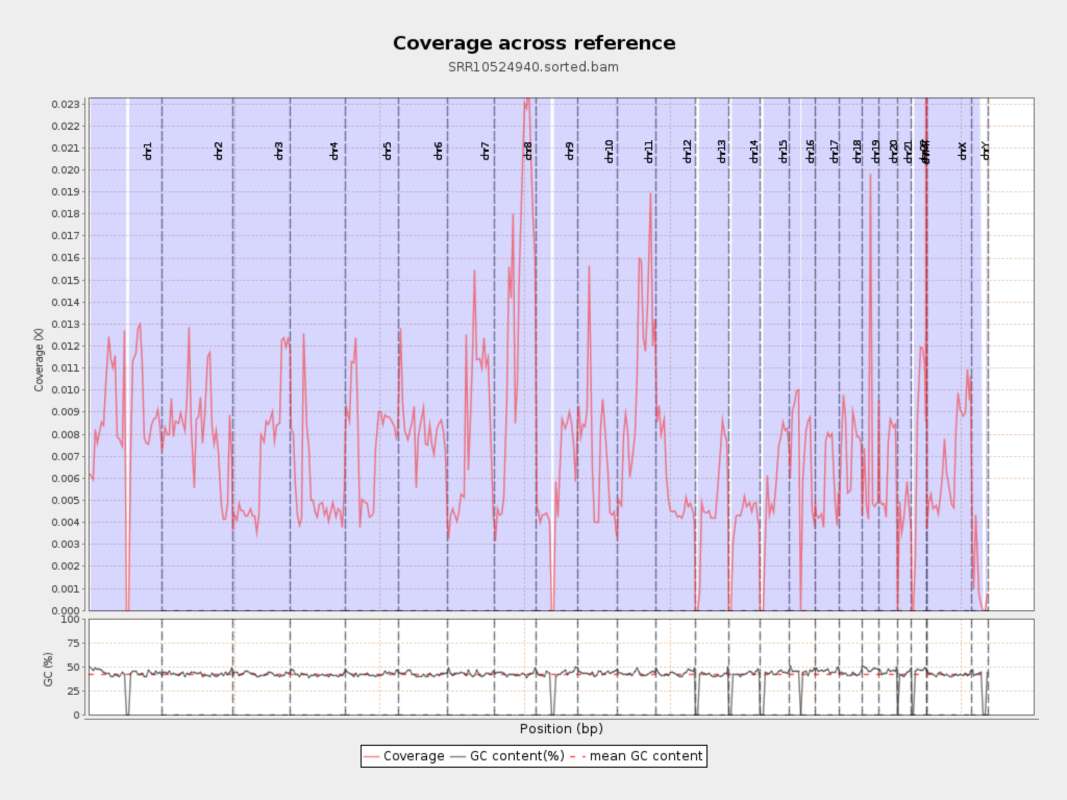
General error rate	0.52%
Mismatches	113,821
Insertions	1,504
Mapped reads with at least one insertion	0.39%
Deletions	4,504
Mapped reads with at least one deletion	1.16%
Homopolymer indels	43.86%

2.6. Chromosome stats

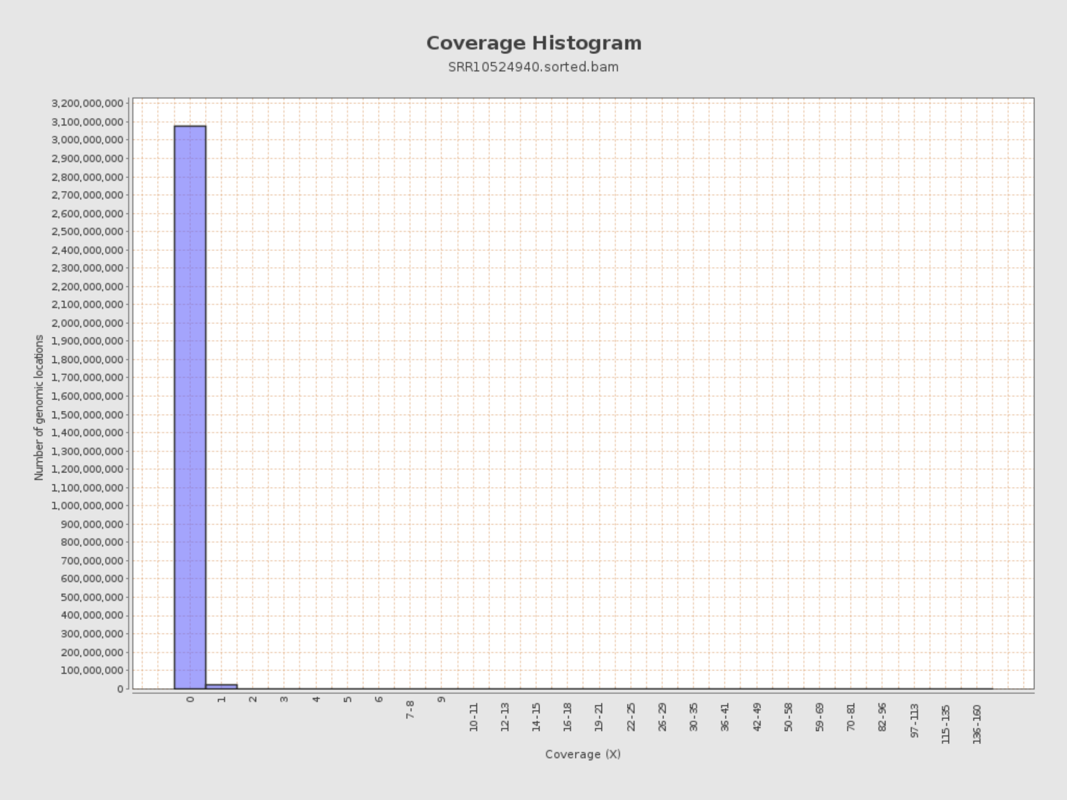
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2170685	0.0087	0.1465
chr2	243199373	1985274	0.0082	0.1139
chr3	198022430	1392927	0.007	0.0871
chr4	191154276	1036945	0.0054	0.0802
chr5	180915260	1401540	0.0077	0.0912
chr6	171115067	1414353	0.0083	0.096
chr7	159138663	1316992	0.0083	0.1187

chr8	146364022	1980313	0.0135	0.136
chr9	141213431	777564	0.0055	0.0823
chr10	135534747	961214	0.0071	0.1055
chr11	135006516	1412452	0.0105	0.1095
chr12	133851895	745400	0.0056	0.0779
chr13	115169878	543179	0.0047	0.0716
chr14	107349540	419859	0.0039	0.066
chr15	102531392	554300	0.0054	0.0765
chr16	90354753	636188	0.007	0.0891
chr17	81195210	463753	0.0057	0.0794
chr18	78077248	596137	0.0076	0.1169
chr19	59128983	424382	0.0072	0.1096
chr20	63025520	409221	0.0065	0.0845
chr21	48129895	198074	0.0041	0.0696
chr22	51304566	374770	0.0073	0.089
chrMT	16571	2337	0.141	0.4087
chrX	155270560	1051810	0.0068	0.0878
chrY	59373566	65799	0.0011	0.0524

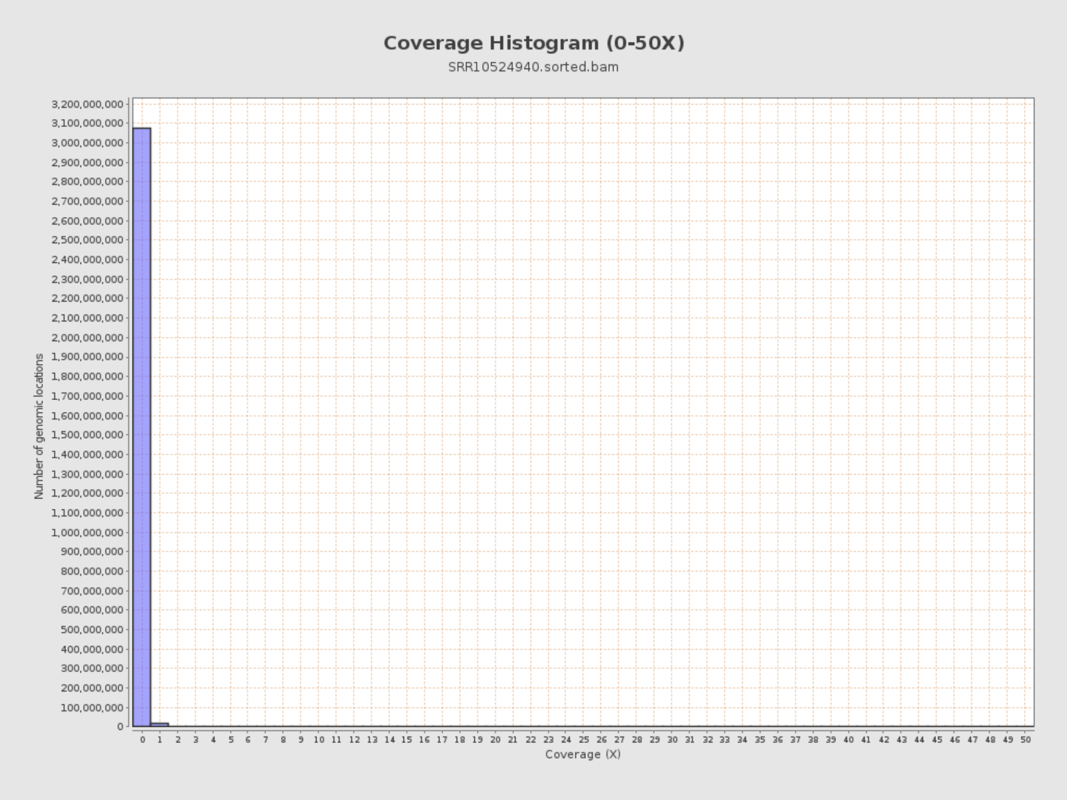
3. Results : Coverage across reference



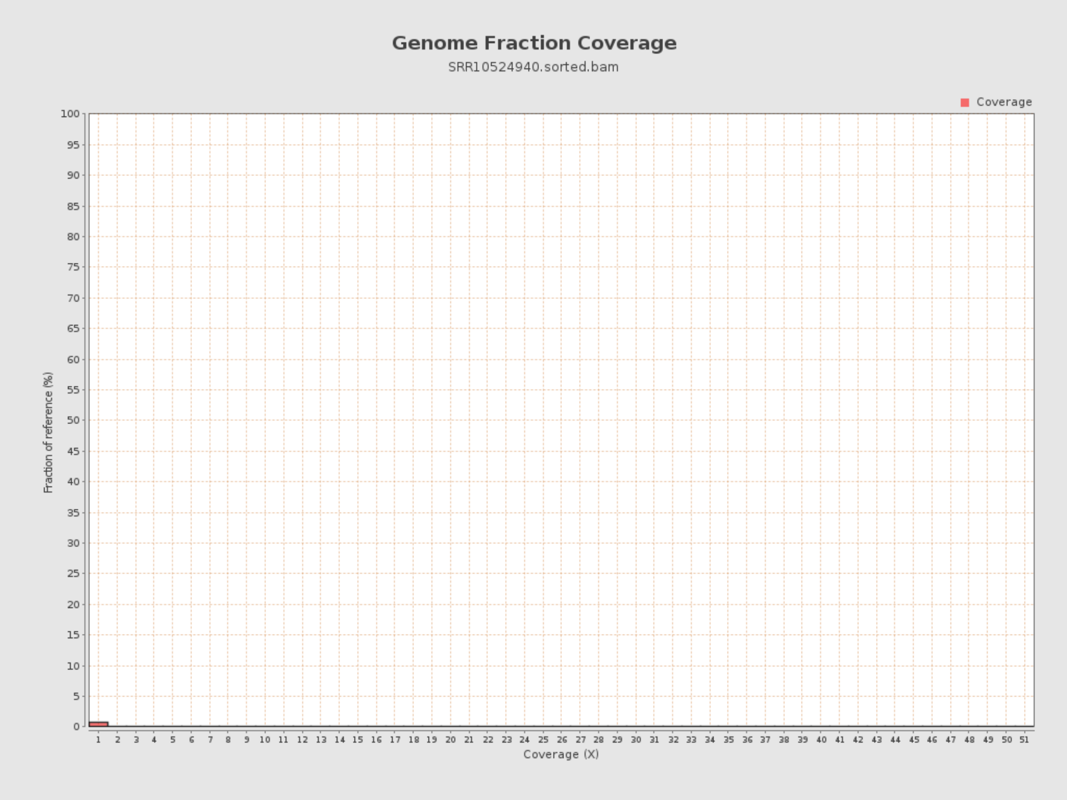
4. Results : Coverage Histogram



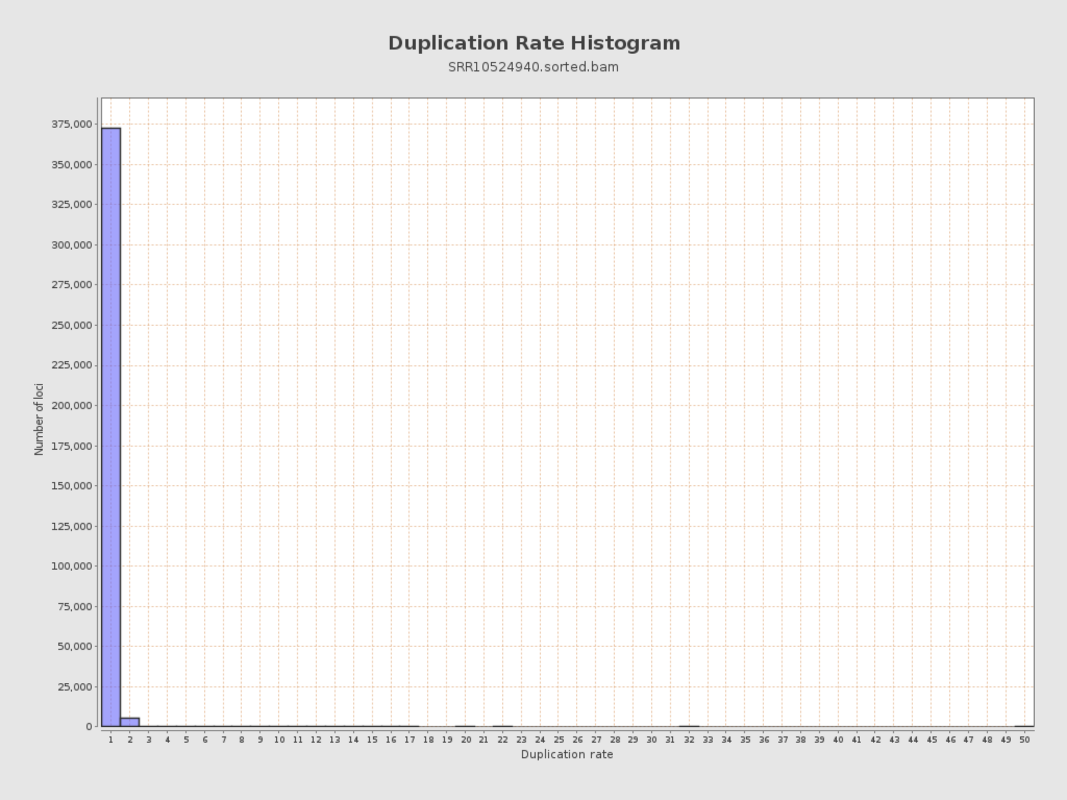
5. Results : Coverage Histogram (0-50X)



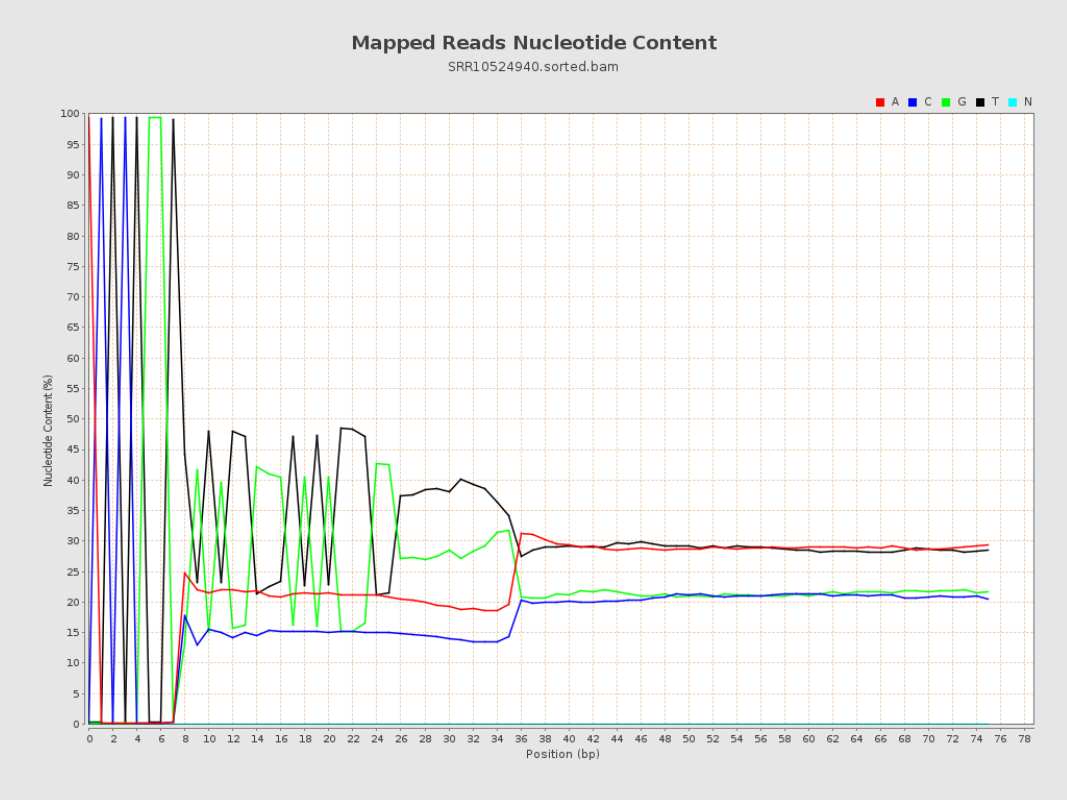
6. Results : Genome Fraction Coverage



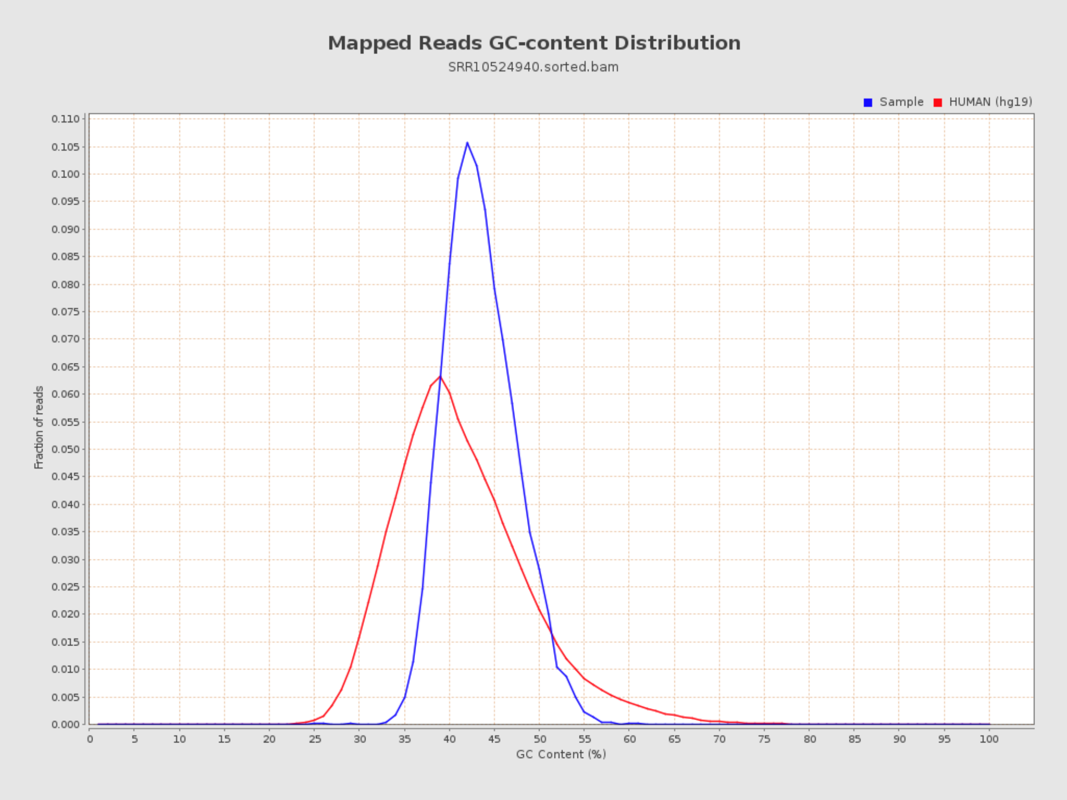
7. Results : Duplication Rate Histogram



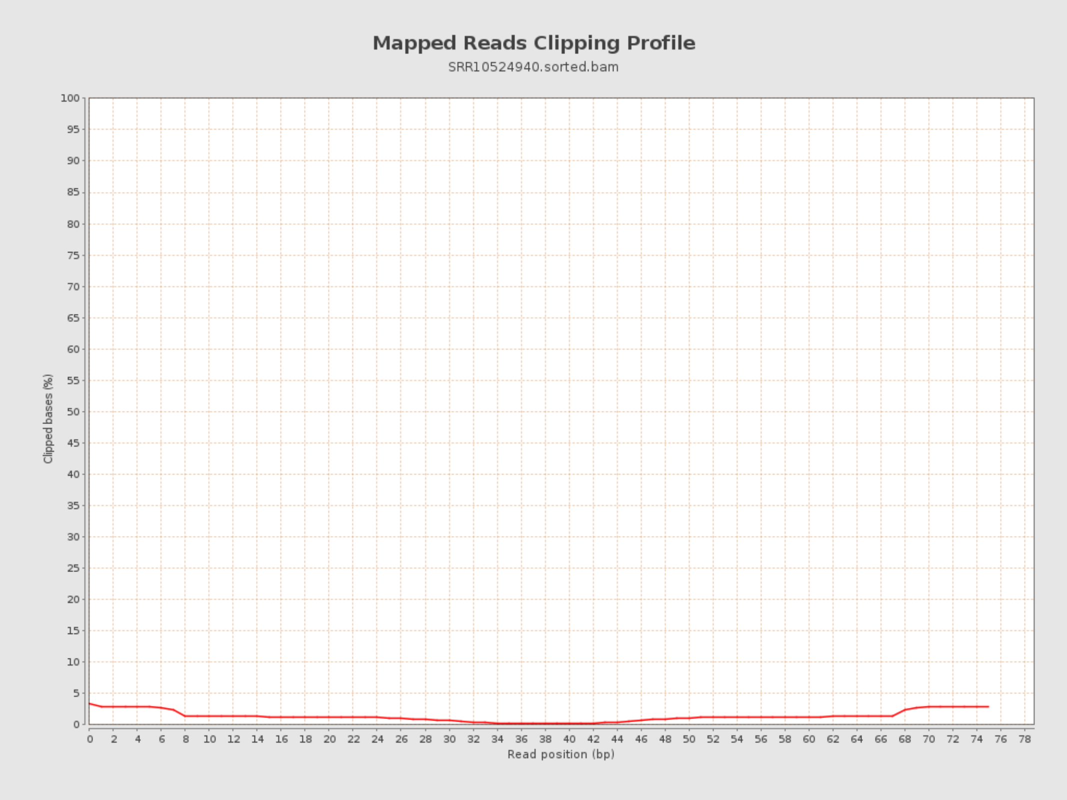
8. Results : Mapped Reads Nucleotide Content



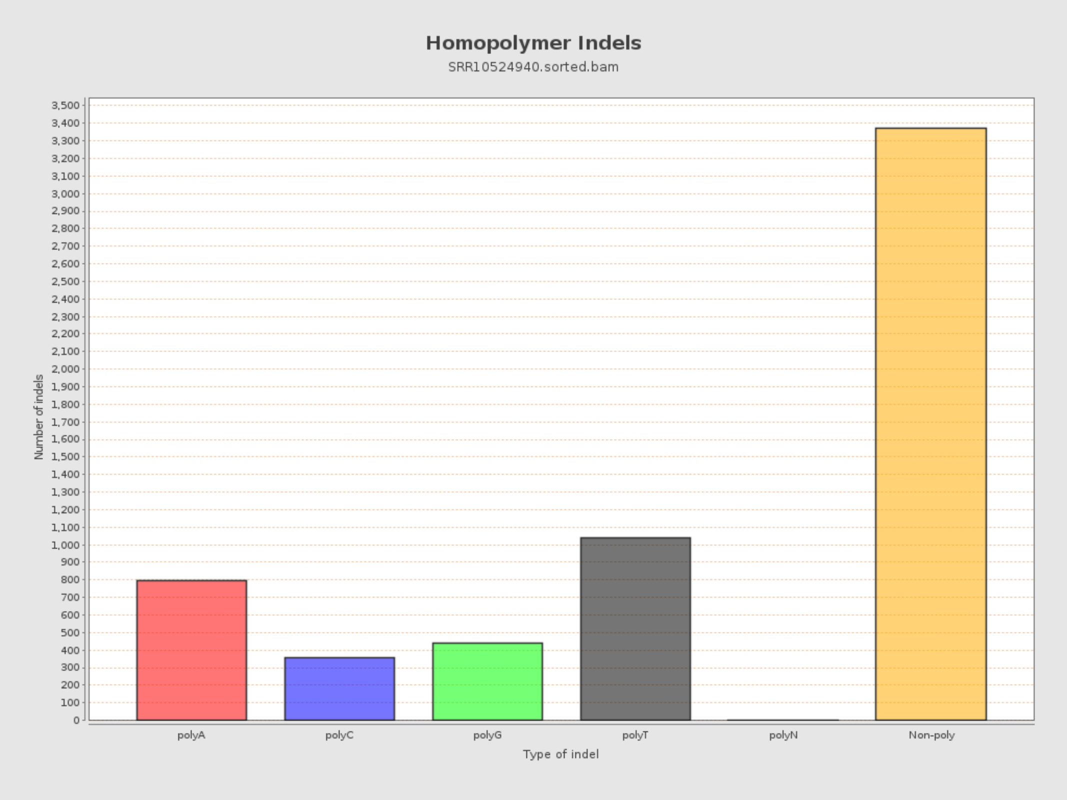
9. Results : Mapped Reads GC-content Distribution



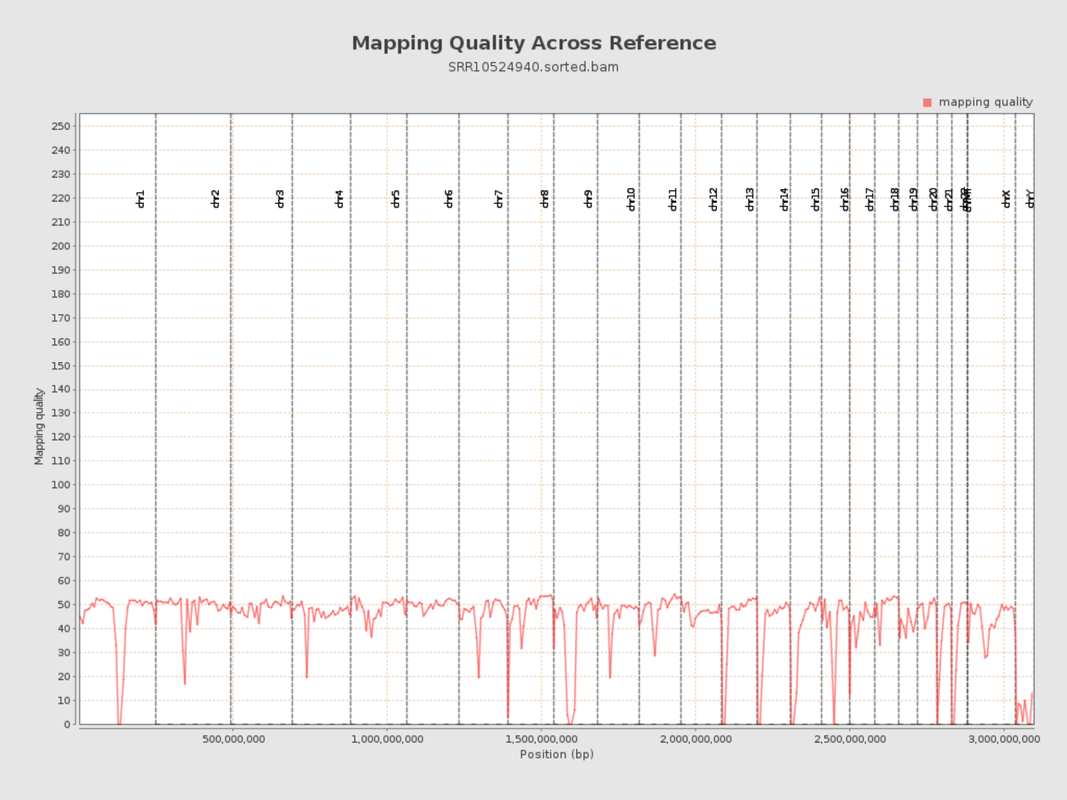
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram