Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 17:17:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524704.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_SRR10524704 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524704.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 17:17:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524704.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,581,502
Mapped reads	2,385,087 / 92.39%
Unmapped reads	196,415 / 7.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,172 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	141,688 / 5.49%
Duplication rate	4.47%
Clipped reads	2,389,158 / 92.55%

2.2. ACGT Content

Number/percentage of A's	35,131,207 / 25.03%
Number/percentage of C's	25,138,584 / 17.91%
Number/percentage of T's	43,767,396 / 31.18%
Number/percentage of G's	36,307,630 / 25.87%
Number/percentage of N's	19,099 / 0.01%
GC Percentage	43.78%

2.3. Coverage

Mean	0.0454

Standard Deviation	0.4039

2.4. Mapping Quality

Mean Mapping Quality	45.65

2.5. Mismatches and indels

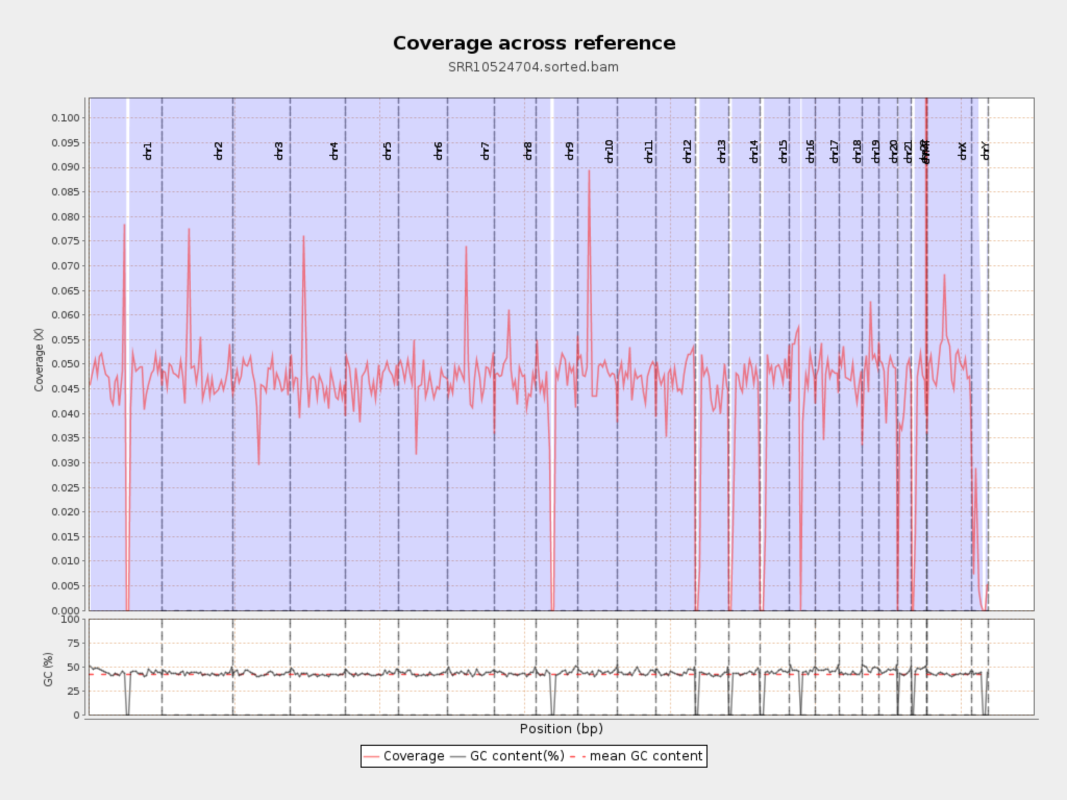
General error rate	0.51%
Mismatches	703,749
Insertions	9,836
Mapped reads with at least one insertion	0.41%
Deletions	27,008
Mapped reads with at least one deletion	1.12%
Homopolymer indels	43.27%

2.6. Chromosome stats

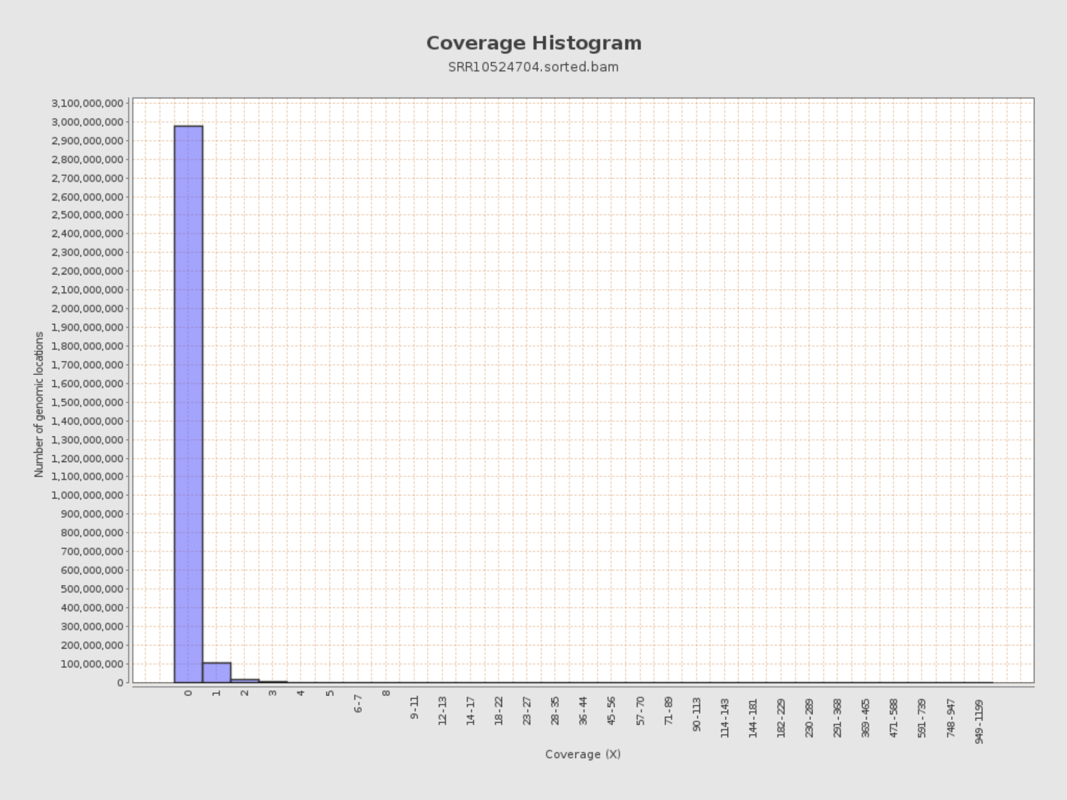
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11365637	0.0456	0.742
chr2	243199373	11838503	0.0487	0.5825
chr3	198022430	9206383	0.0465	0.2474
chr4	191154276	8928500	0.0467	0.2944
chr5	180915260	8492911	0.0469	0.2505
chr6	171115067	8001454	0.0468	0.2931
chr7	159138663	7706181	0.0484	0.4857

chr8	146364022	6965358	0.0476	0.4276
chr9	141213431	5900709	0.0418	0.3268
chr10	135534747	6829890	0.0504	0.4196
chr11	135006516	6407341	0.0475	0.3335
chr12	133851895	6361153	0.0475	0.2548
chr13	115169878	4393319	0.0381	0.2243
chr14	107349540	4219694	0.0393	0.2383
chr15	102531392	4055048	0.0395	0.2297
chr16	90354753	4121034	0.0456	0.2711
chr17	81195210	3862236	0.0476	0.2721
chr18	78077248	3733496	0.0478	0.5921
chr19	59128983	2997140	0.0507	0.5463
chr20	63025520	3011998	0.0478	0.2599
chr21	48129895	1896843	0.0394	0.267
chr22	51304566	1702501	0.0332	0.2096
chrMT	16571	116143	7.0088	4.8167
chrX	155270560	7834494	0.0505	0.2931
chrY	59373566	459307	0.0077	0.2585

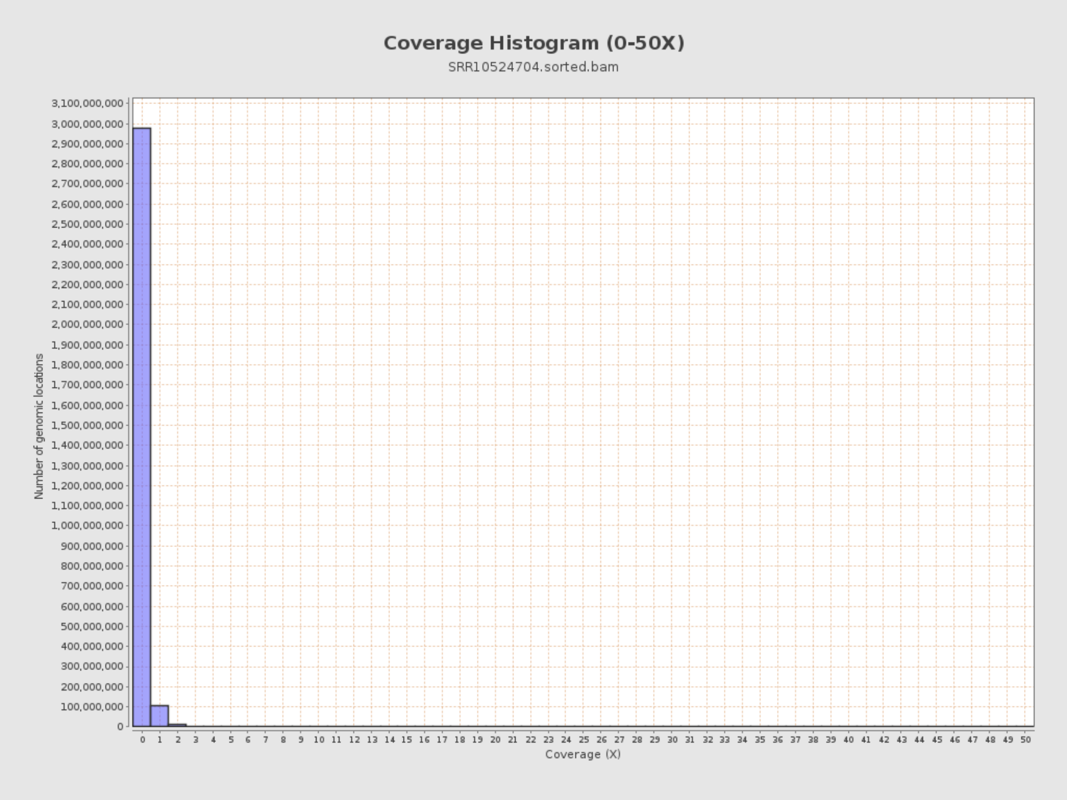
3. Results : Coverage across reference



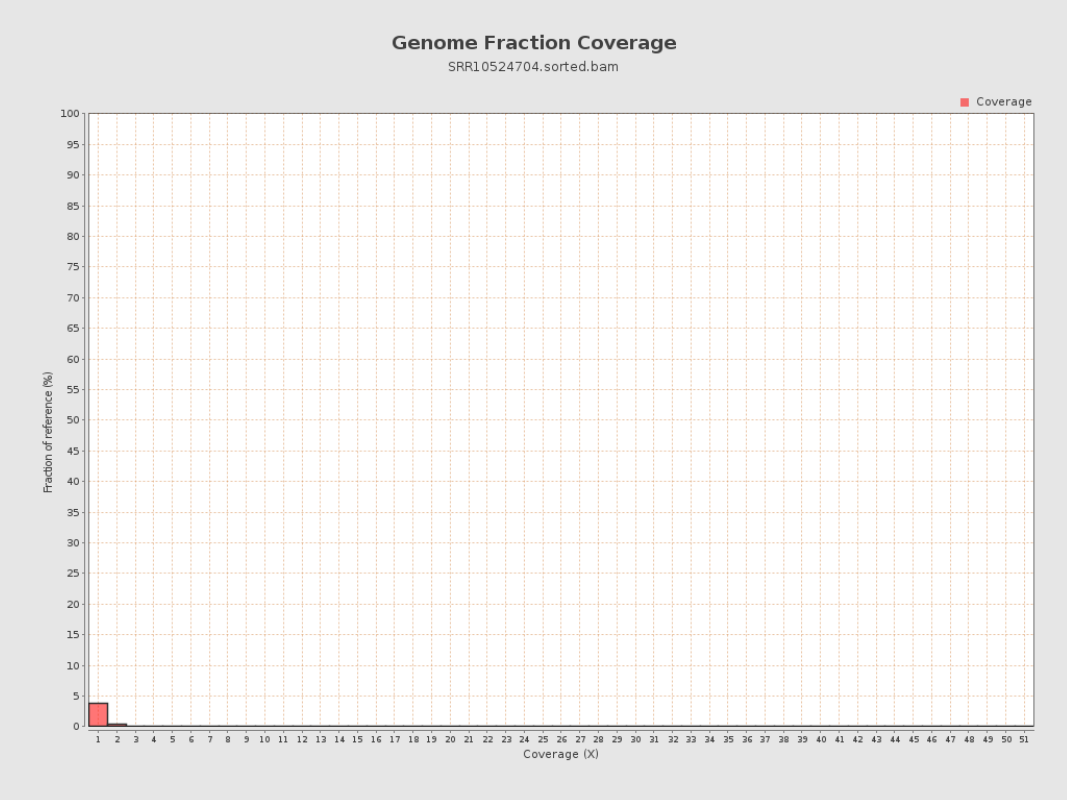
4. Results : Coverage Histogram



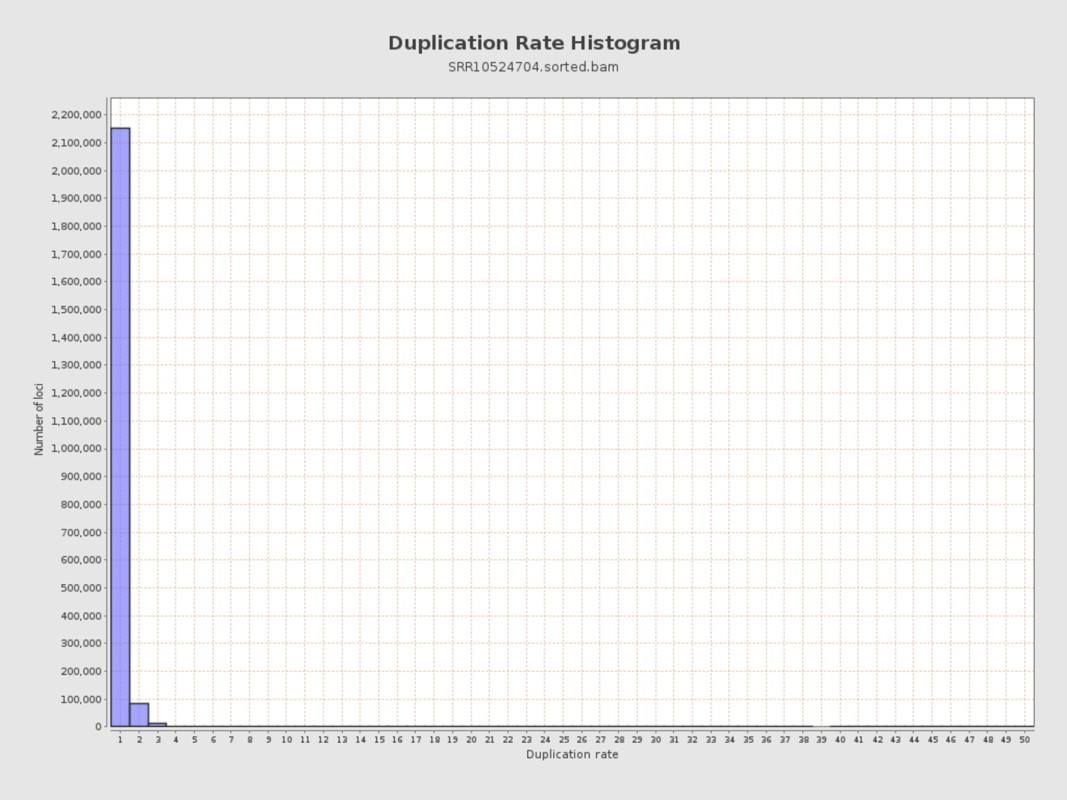
5. Results : Coverage Histogram (0-50X)



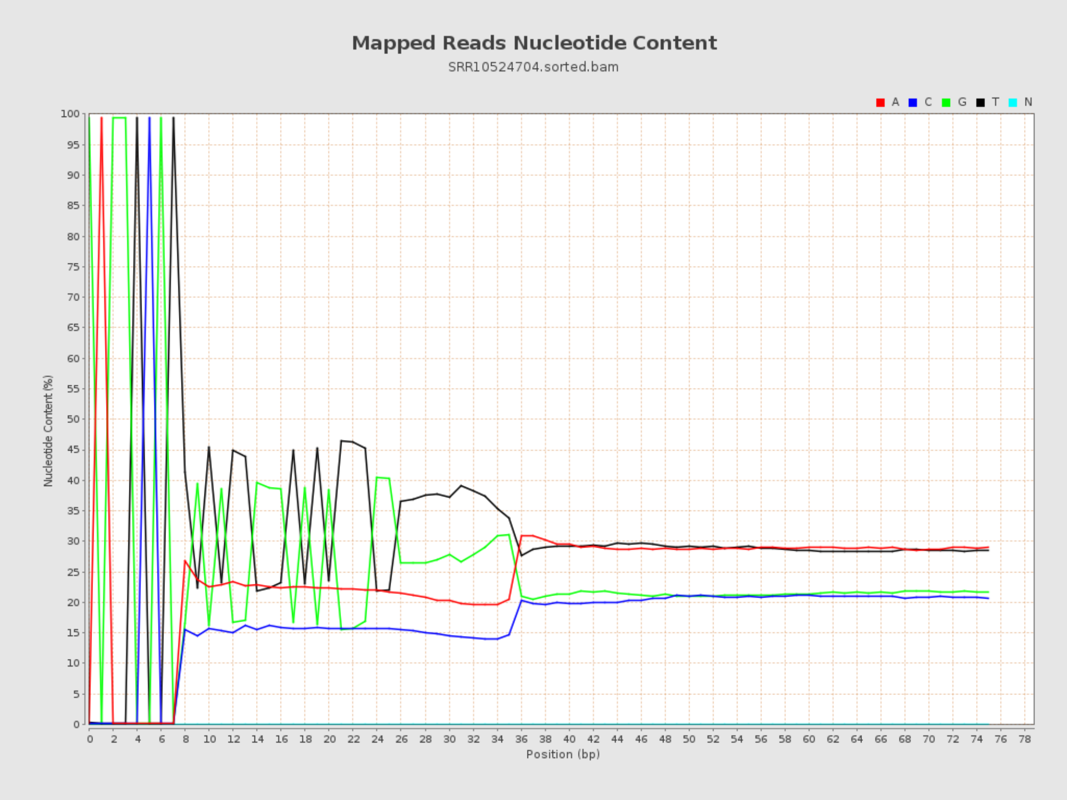
6. Results : Genome Fraction Coverage



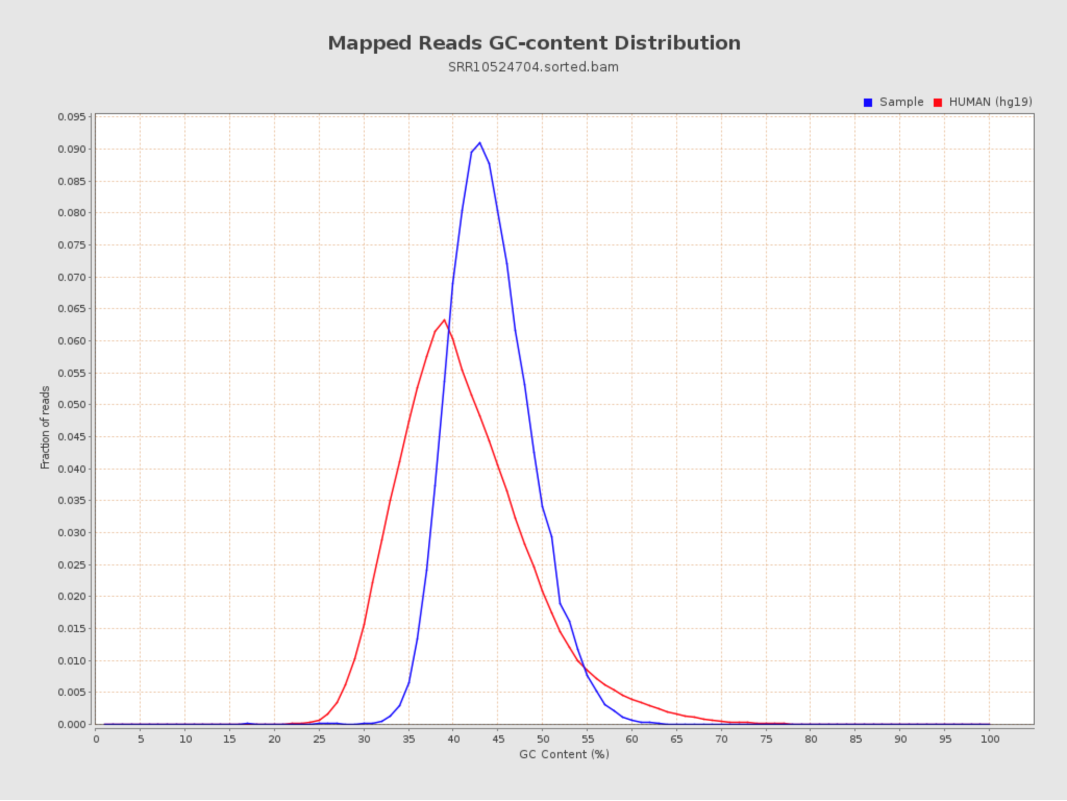
7. Results : Duplication Rate Histogram



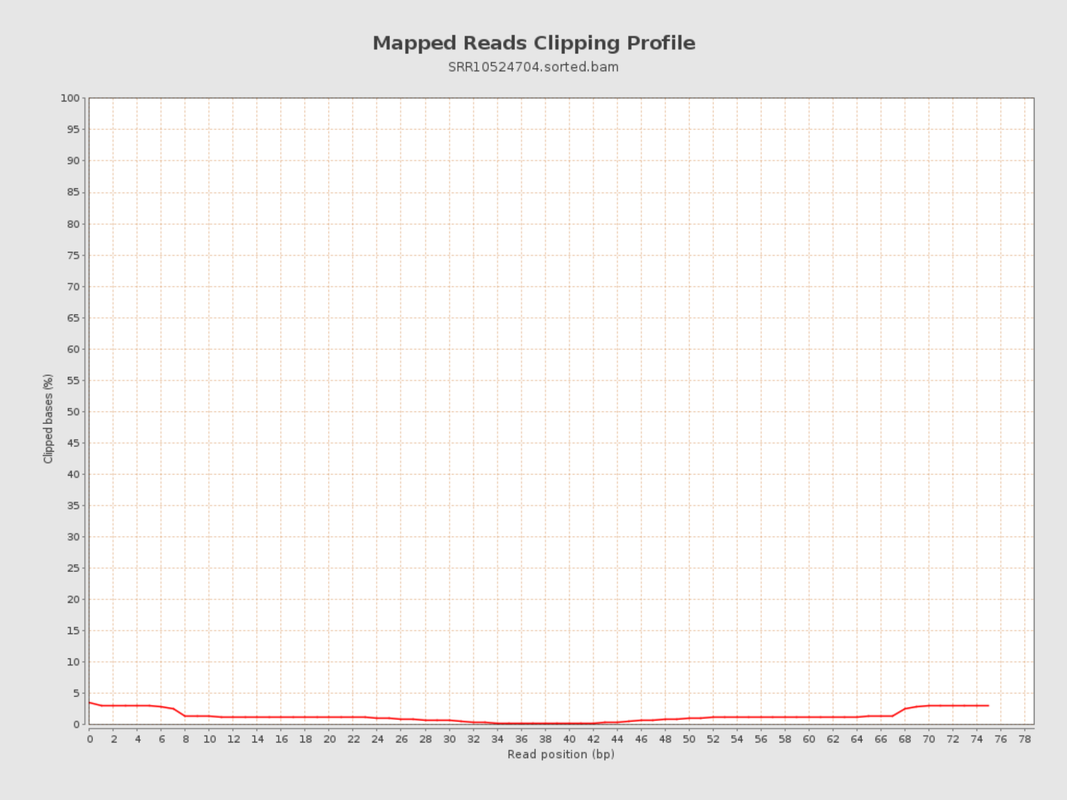
8. Results : Mapped Reads Nucleotide Content



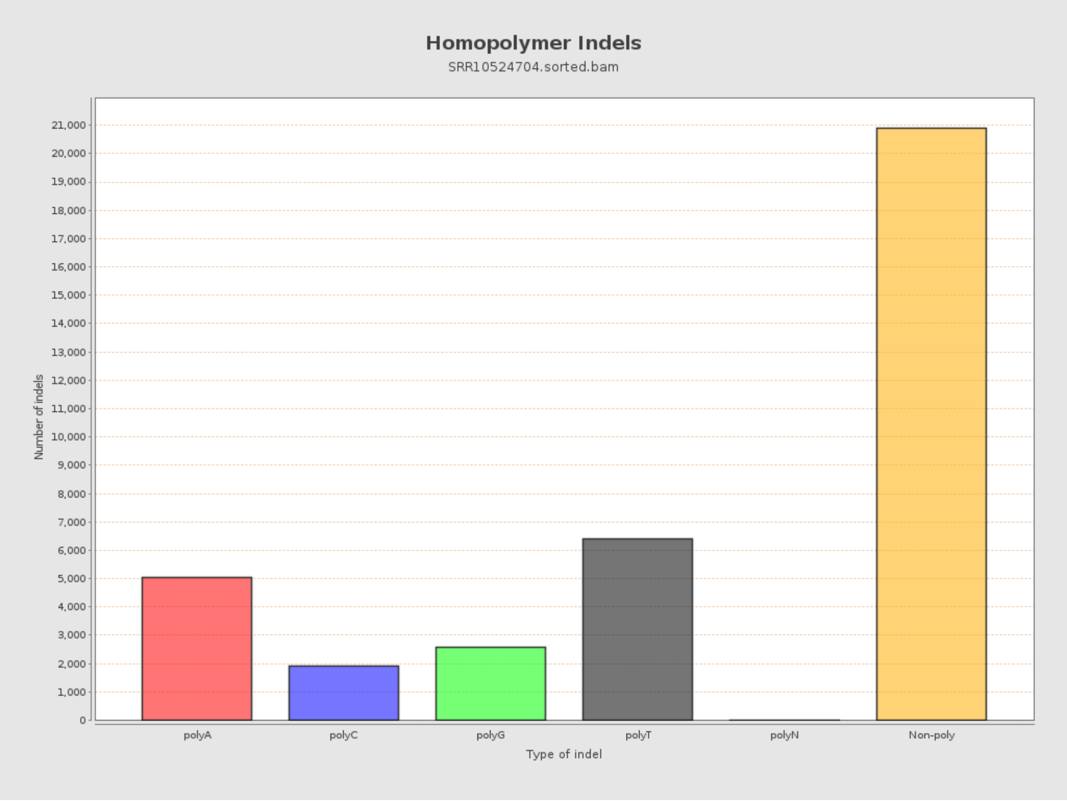
9. Results : Mapped Reads GC-content Distribution



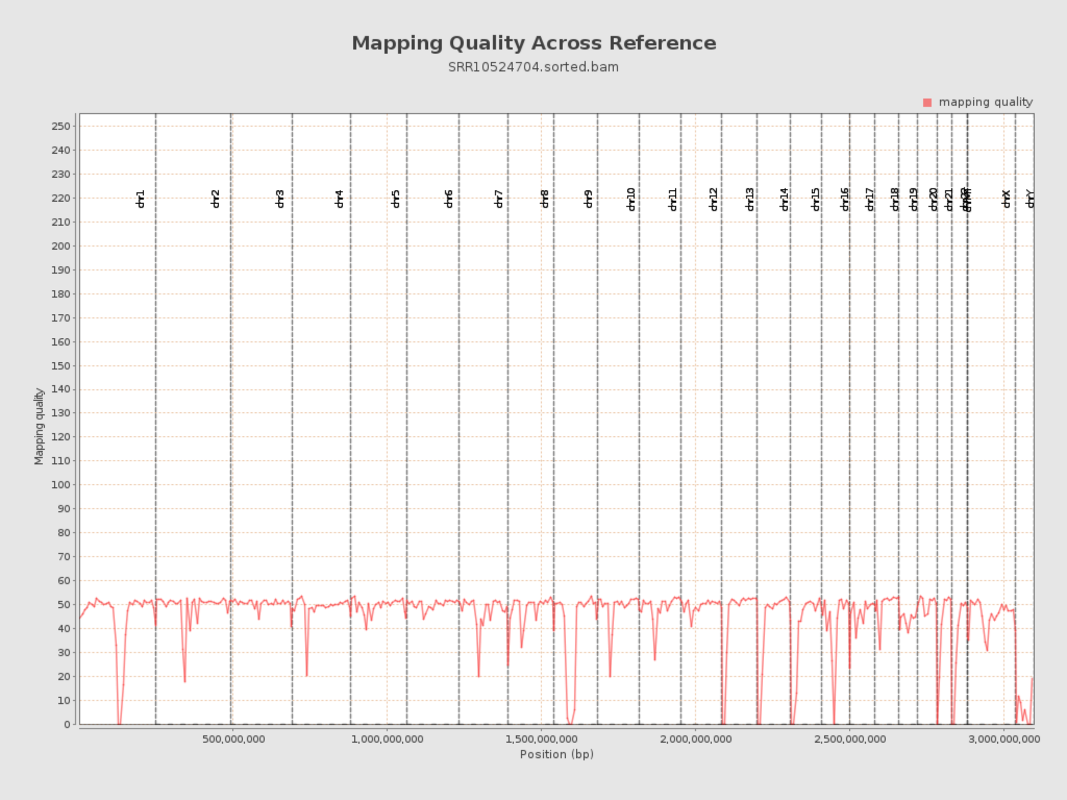
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram