Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 17:48:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524720.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_SRR10524720 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524720.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 17:48:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524720.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	234,783
Mapped reads	216,454 / 92.19%
Unmapped reads	18,329 / 7.81%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	748 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	2,654 / 1.13%
Duplication rate	0.93%
Clipped reads	216,560 / 92.24%

2.2. ACGT Content

Number/percentage of A's	3,287,998 / 25.58%
Number/percentage of C's	2,402,971 / 18.7%
Number/percentage of T's	4,126,334 / 32.11%
Number/percentage of G's	3,033,228 / 23.6%
Number/percentage of N's	2,008 / 0.02%
GC Percentage	42.3%

2.3. Coverage

Mean	0.0042

Standard Deviation	0.0721

2.4. Mapping Quality

Mean Mapping Quality	46.11

2.5. Mismatches and indels

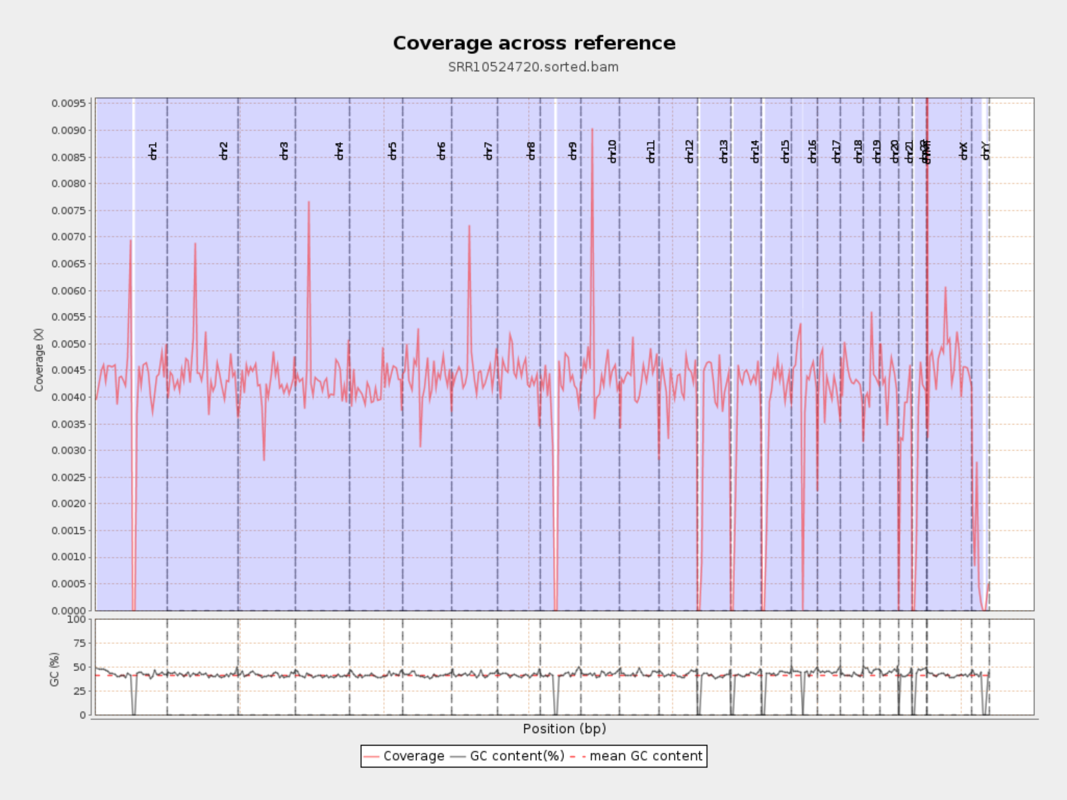
General error rate	0.52%
Mismatches	64,764
Insertions	931
Mapped reads with at least one insertion	0.43%
Deletions	2,484
Mapped reads with at least one deletion	1.14%
Homopolymer indels	44.54%

2.6. Chromosome stats

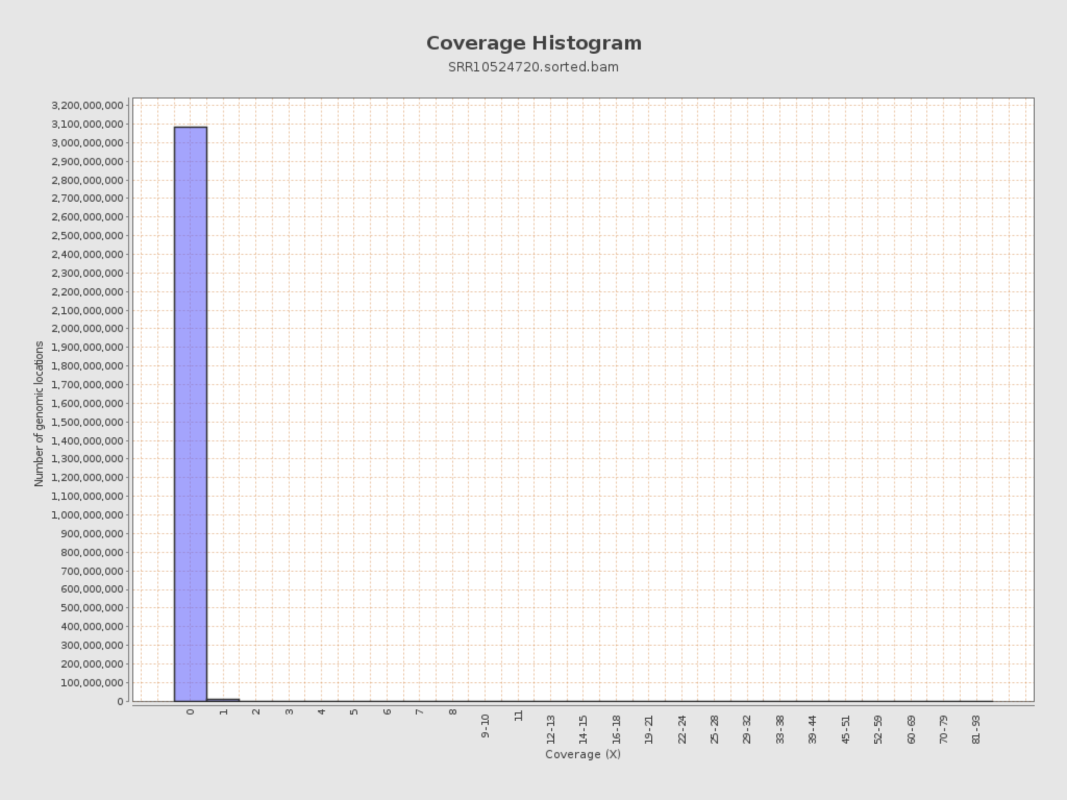
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1043158	0.0042	0.093
chr2	243199373	1087140	0.0045	0.081
chr3	198022430	840325	0.0042	0.0663
chr4	191154276	843765	0.0044	0.0691
chr5	180915260	763207	0.0042	0.0662
chr6	171115067	749067	0.0044	0.0688
chr7	159138663	723439	0.0045	0.0787

chr8	146364022	651462	0.0045	0.0766
chr9	141213431	535429	0.0038	0.0666
chr10	135534747	630865	0.0047	0.0776
chr11	135006516	594578	0.0044	0.0709
chr12	133851895	572306	0.0043	0.0663
chr13	115169878	413866	0.0036	0.061
chr14	107349540	390727	0.0036	0.0613
chr15	102531392	355273	0.0035	0.0596
chr16	90354753	371351	0.0041	0.0665
chr17	81195210	340293	0.0042	0.0663
chr18	78077248	340821	0.0044	0.0855
chr19	59128983	255796	0.0043	0.0818
chr20	63025520	270250	0.0043	0.0671
chr21	48129895	164259	0.0034	0.0612
chr22	51304566	146494	0.0029	0.0541
chrMT	16571	1713	0.1034	0.3341
chrX	155270560	724664	0.0047	0.0703
chrY	59373566	46289	0.0008	0.0384

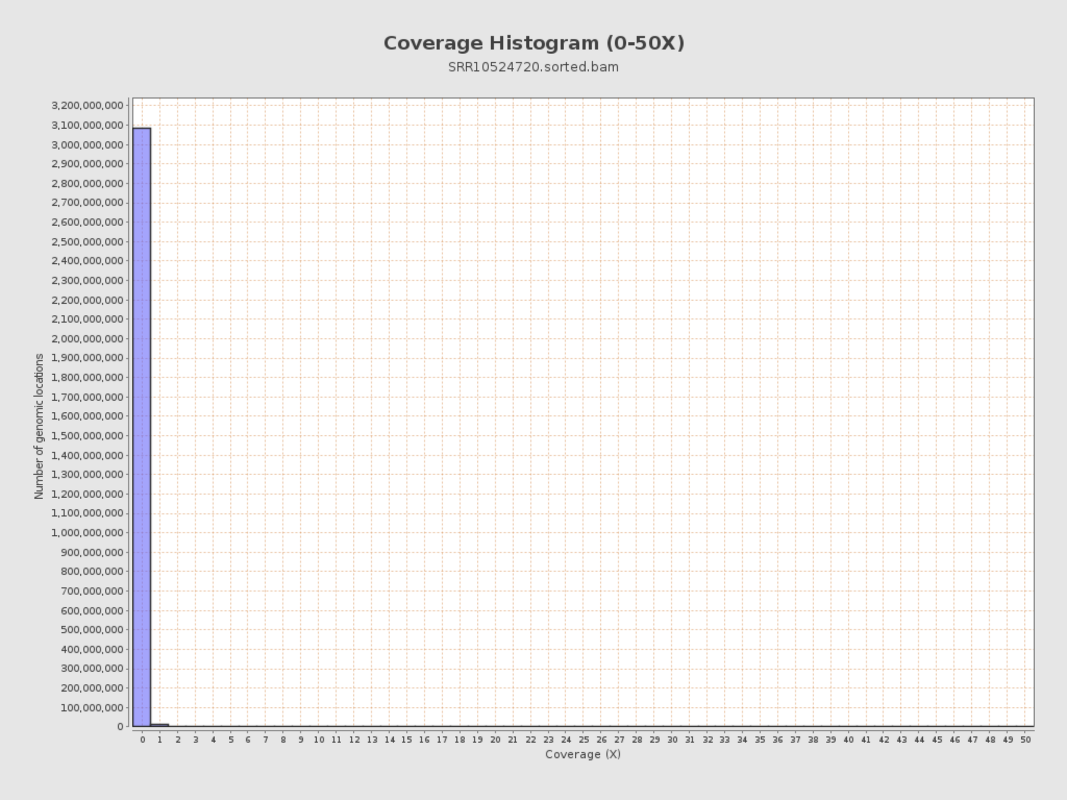
3. Results : Coverage across reference



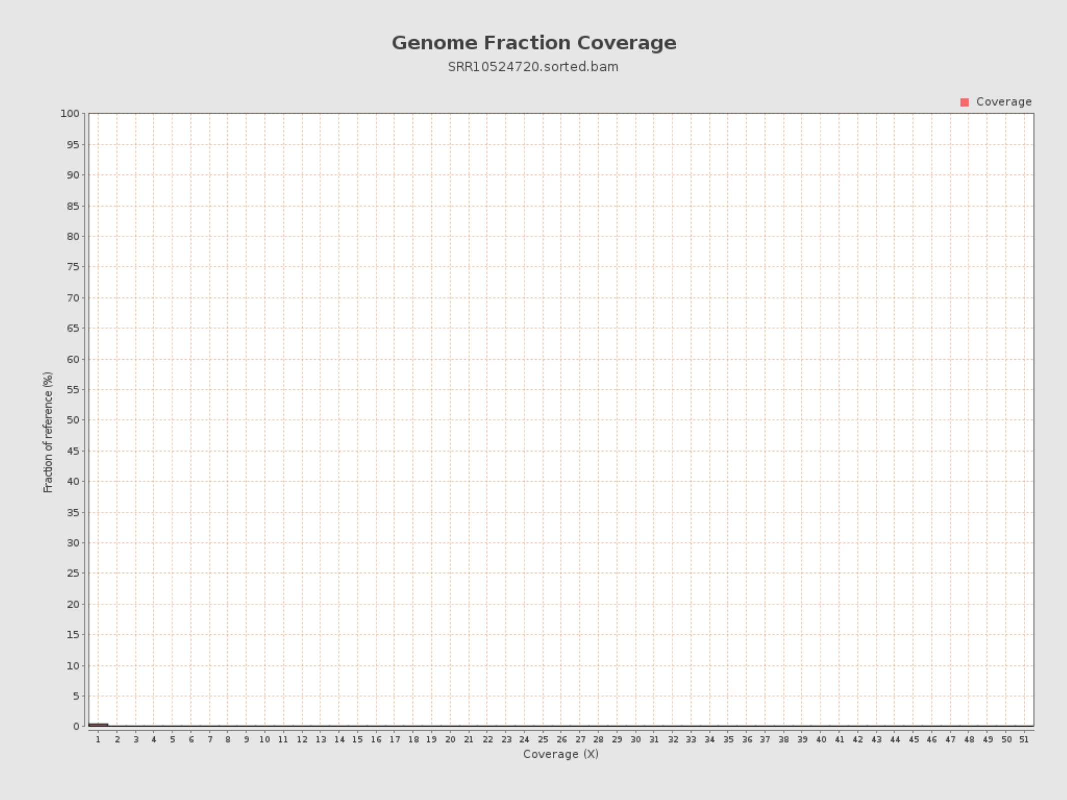
4. Results : Coverage Histogram



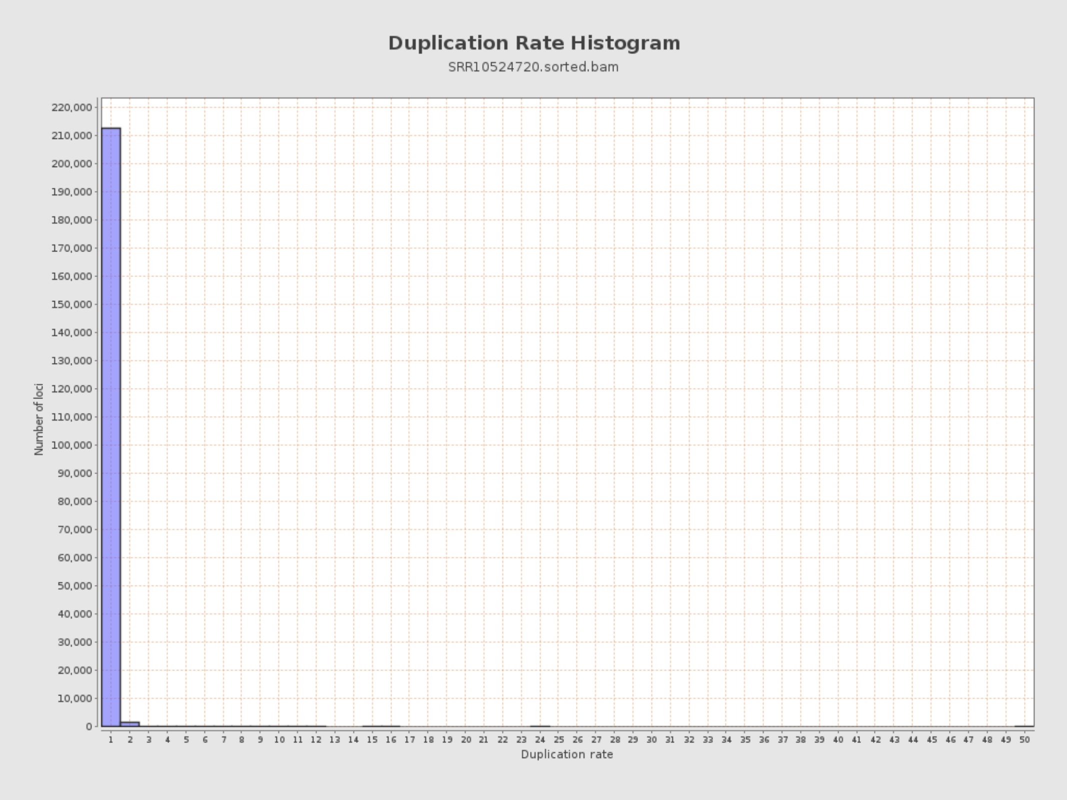
5. Results : Coverage Histogram (0-50X)



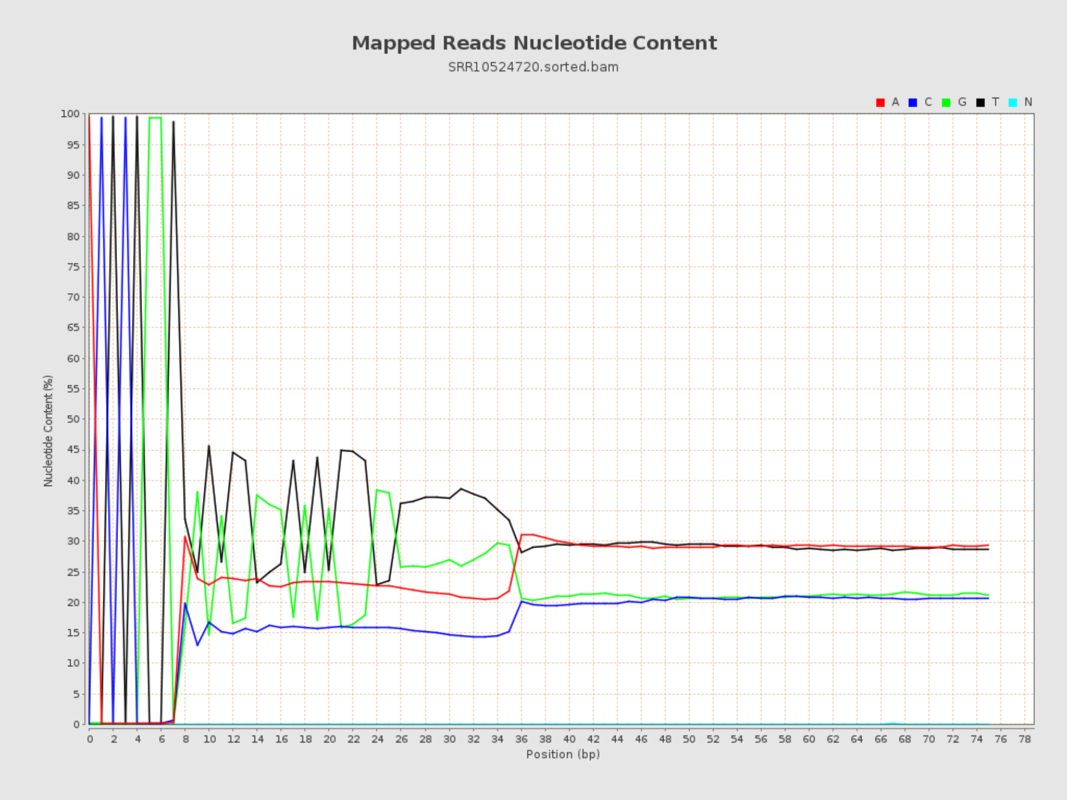
6. Results : Genome Fraction Coverage



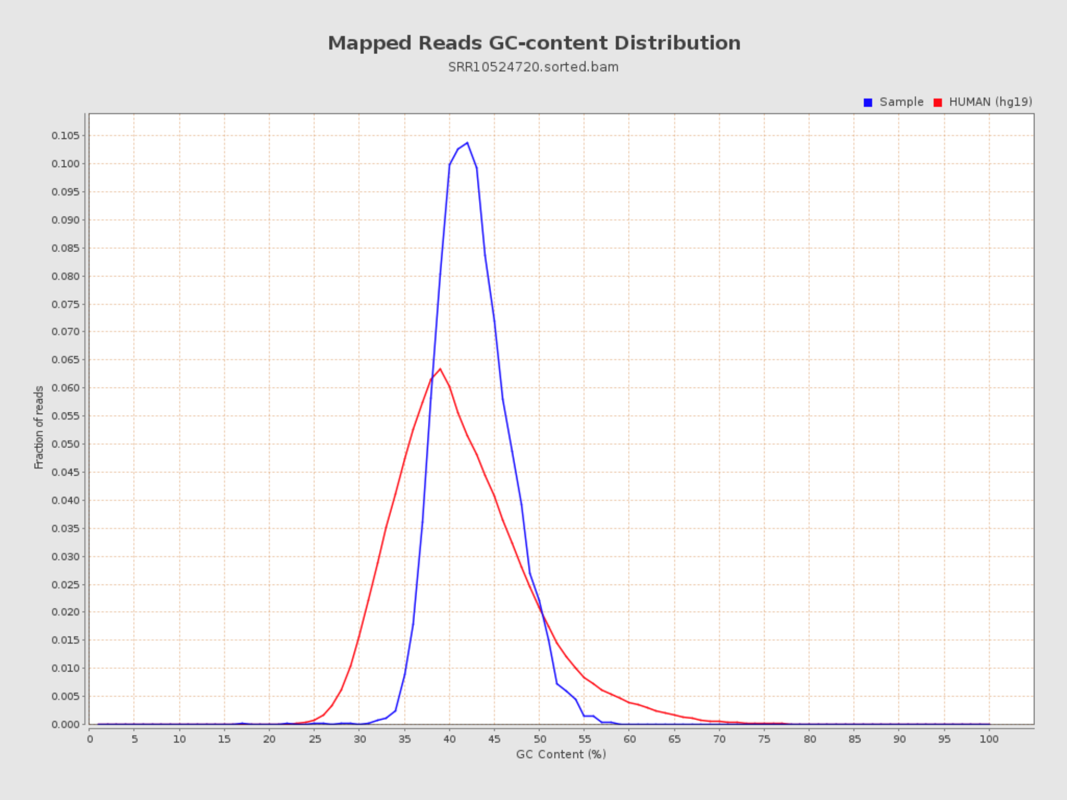
7. Results : Duplication Rate Histogram



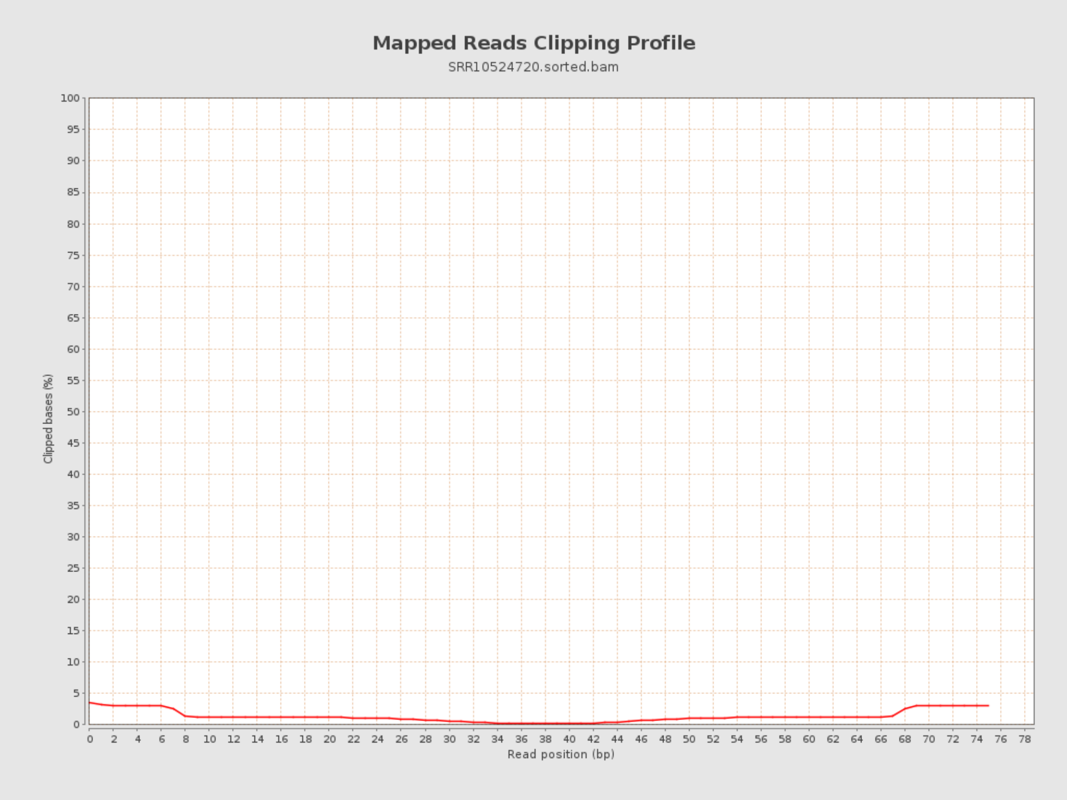
8. Results : Mapped Reads Nucleotide Content



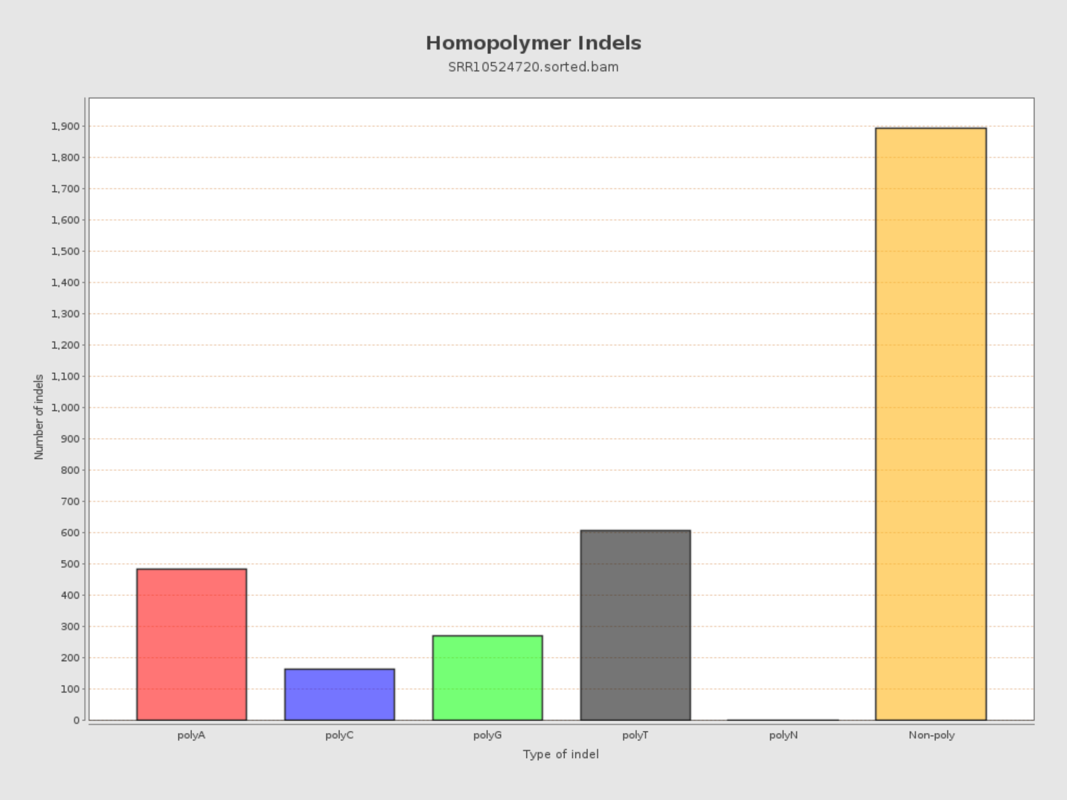
9. Results : Mapped Reads GC-content Distribution



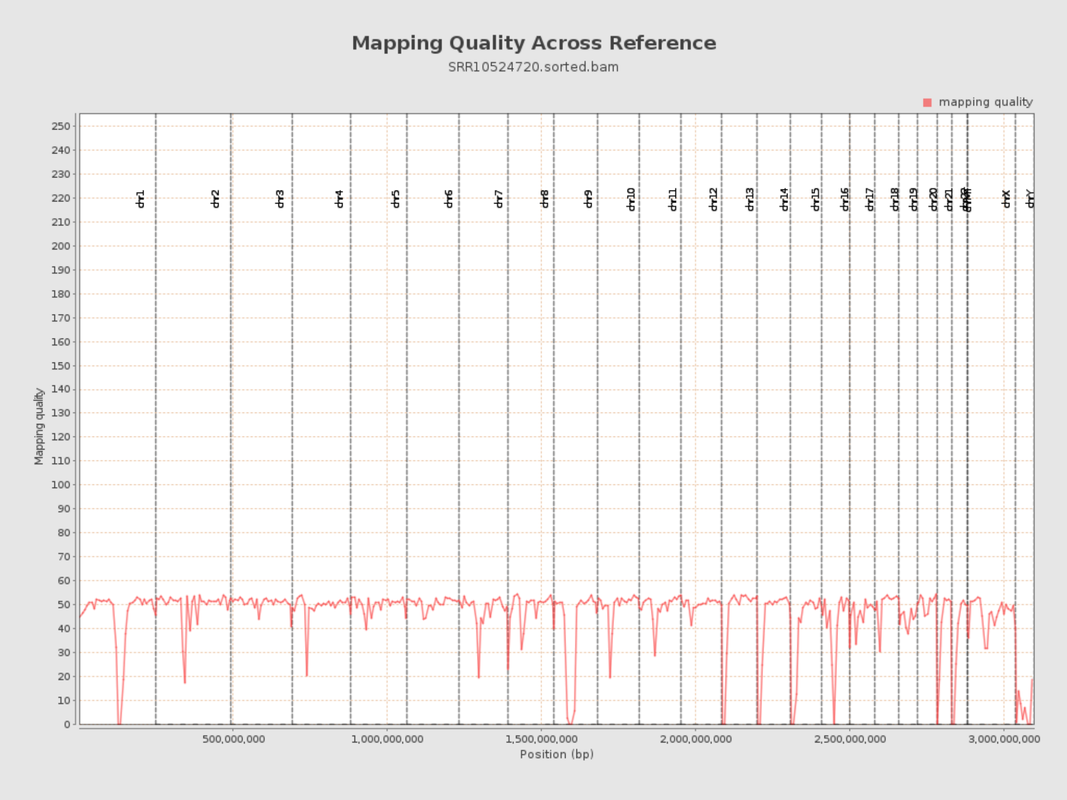
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram