Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.2-dev
2024/08/28 17:12:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524703.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_SRR10524703 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524703.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 17:12:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524703.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,179,127
Mapped reads	2,015,224 / 92.48%
Unmapped reads	163,903 / 7.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,322 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	91,475 / 4.2%
Duplication rate	3.3%
Clipped reads	2,016,568 / 92.54%

2.2. ACGT Content

Number/percentage of A's	29,252,700 / 24.54%
Number/percentage of C's	24,306,922 / 20.39%
Number/percentage of T's	38,037,826 / 31.91%
Number/percentage of G's	27,600,461 / 23.15%
Number/percentage of N's	16,901 / 0.01%
GC Percentage	43.54%

2.3. Coverage

Mean	0.0385

Standard Deviation	0.3583

2.4. Mapping Quality

Mean Mapping Quality	45.78

2.5. Mismatches and indels

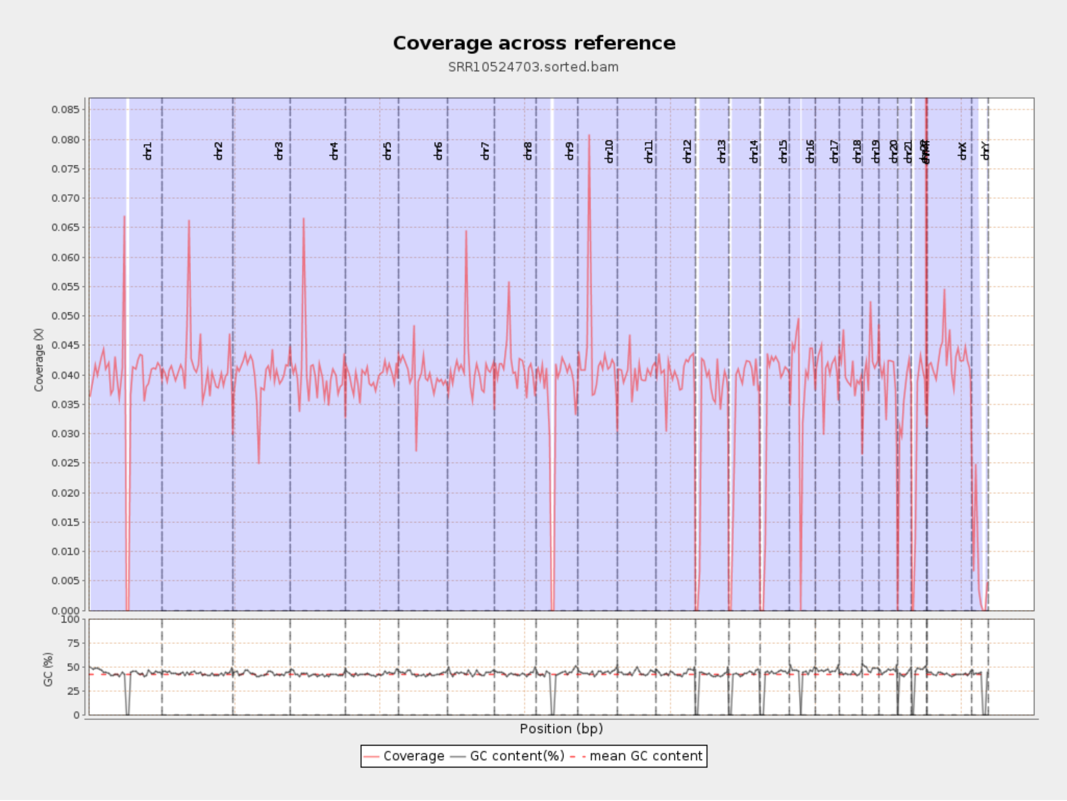
General error rate	0.52%
Mismatches	600,737
Insertions	8,785
Mapped reads with at least one insertion	0.43%
Deletions	23,283
Mapped reads with at least one deletion	1.15%
Homopolymer indels	42.65%

2.6. Chromosome stats

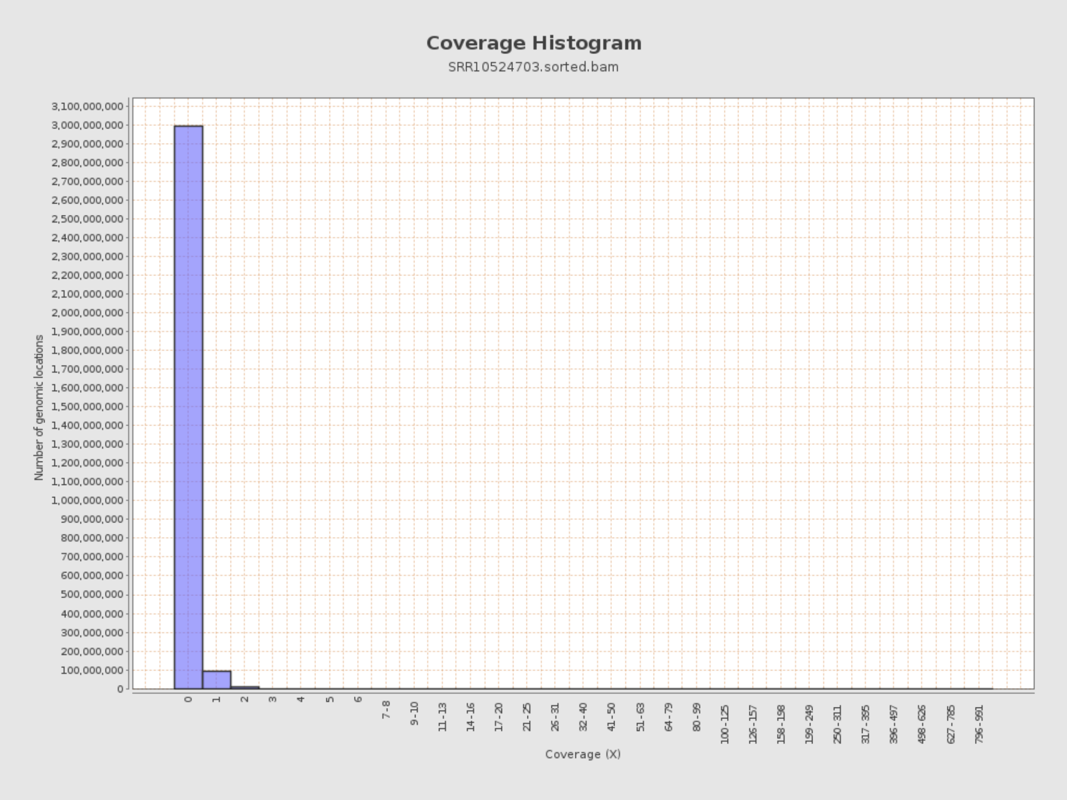
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9640199	0.0387	0.671
chr2	243199373	10028140	0.0412	0.494
chr3	198022430	7874923	0.0398	0.2221
chr4	191154276	7694884	0.0403	0.2584
chr5	180915260	7164835	0.0396	0.2222
chr6	171115067	6815112	0.0398	0.2532
chr7	159138663	6573696	0.0413	0.4275

chr8	146364022	6095297	0.0416	0.3868
chr9	141213431	4969199	0.0352	0.2937
chr10	135534747	5854632	0.0432	0.3815
chr11	135006516	5416810	0.0401	0.2888
chr12	133851895	5387051	0.0402	0.2258
chr13	115169878	3756195	0.0326	0.2009
chr14	107349540	3596800	0.0335	0.2136
chr15	102531392	3439743	0.0335	0.2029
chr16	90354753	3495236	0.0387	0.2382
chr17	81195210	3288137	0.0405	0.2396
chr18	78077248	3159802	0.0405	0.5473
chr19	59128983	2482455	0.042	0.486
chr20	63025520	2478484	0.0393	0.2265
chr21	48129895	1578194	0.0328	0.2385
chr22	51304566	1416858	0.0276	0.1836
chrMT	16571	35401	2.1363	1.8975
chrX	155270560	6612371	0.0426	0.2562
chrY	59373566	397359	0.0067	0.2359

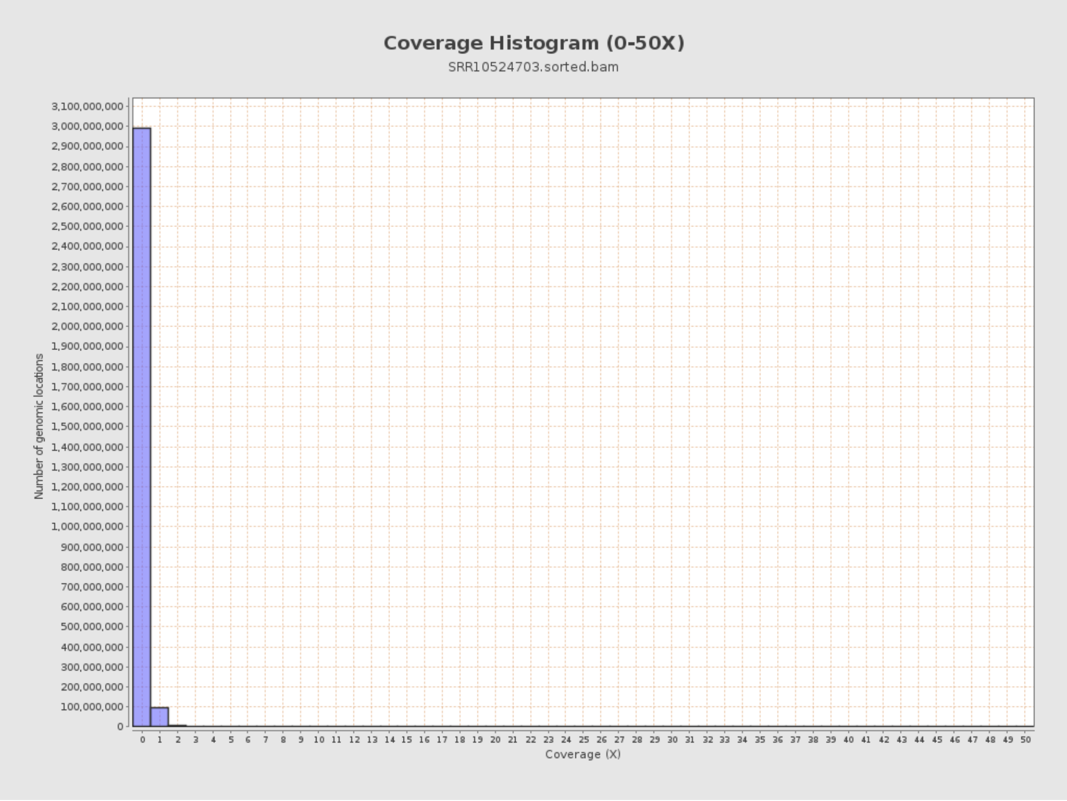
3. Results : Coverage across reference



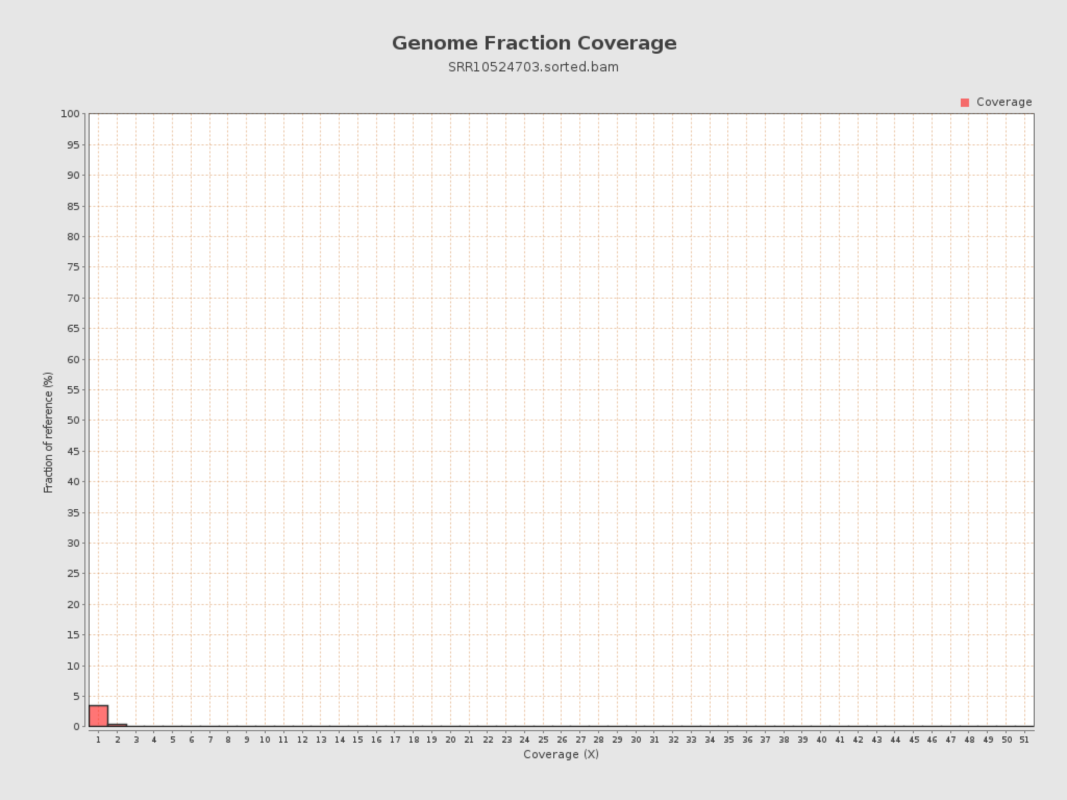
4. Results : Coverage Histogram



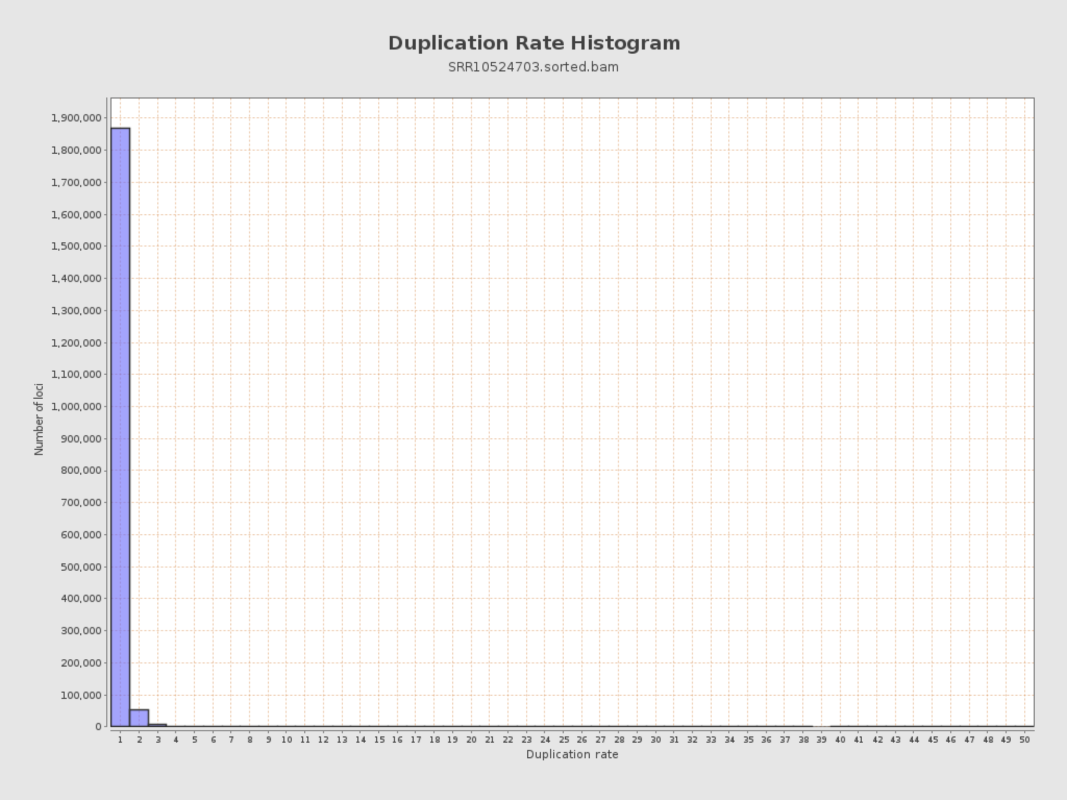
5. Results : Coverage Histogram (0-50X)



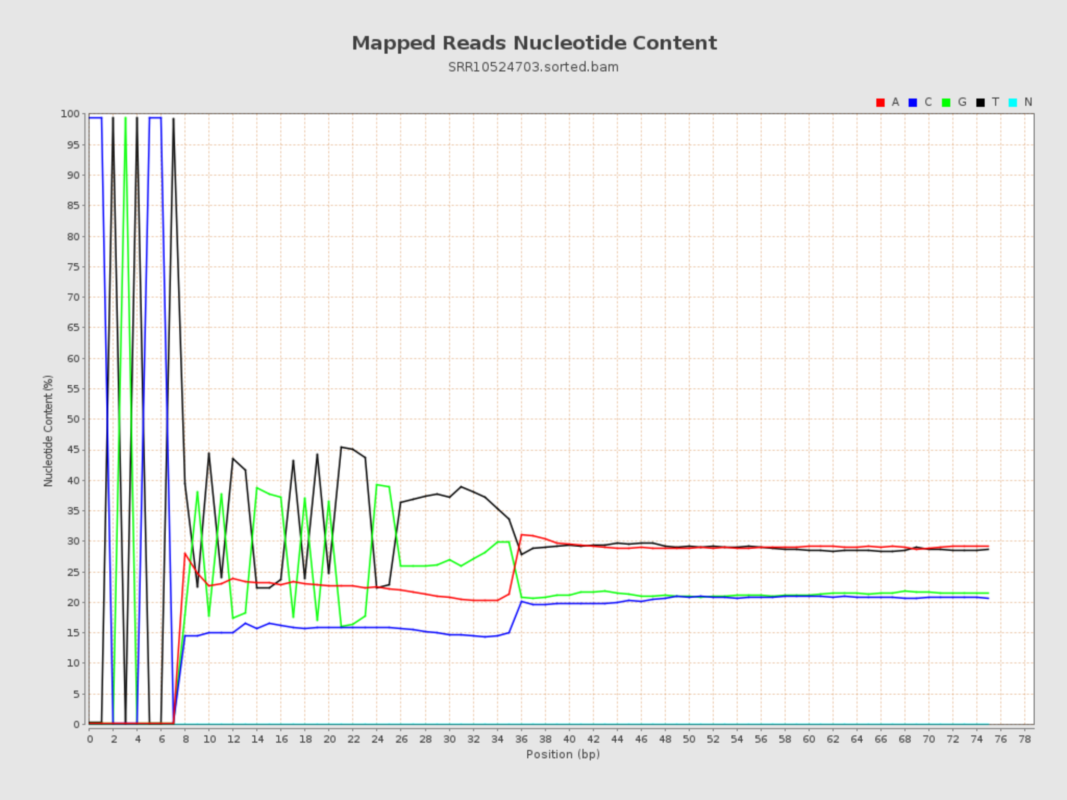
6. Results : Genome Fraction Coverage



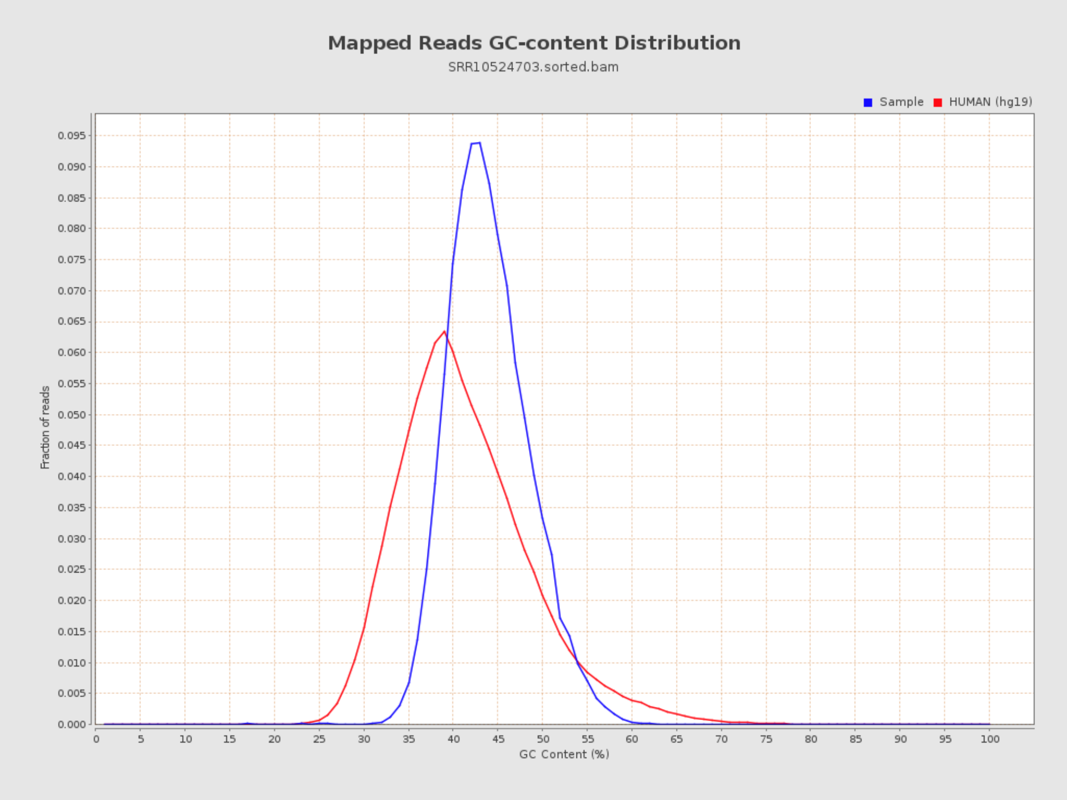
7. Results : Duplication Rate Histogram



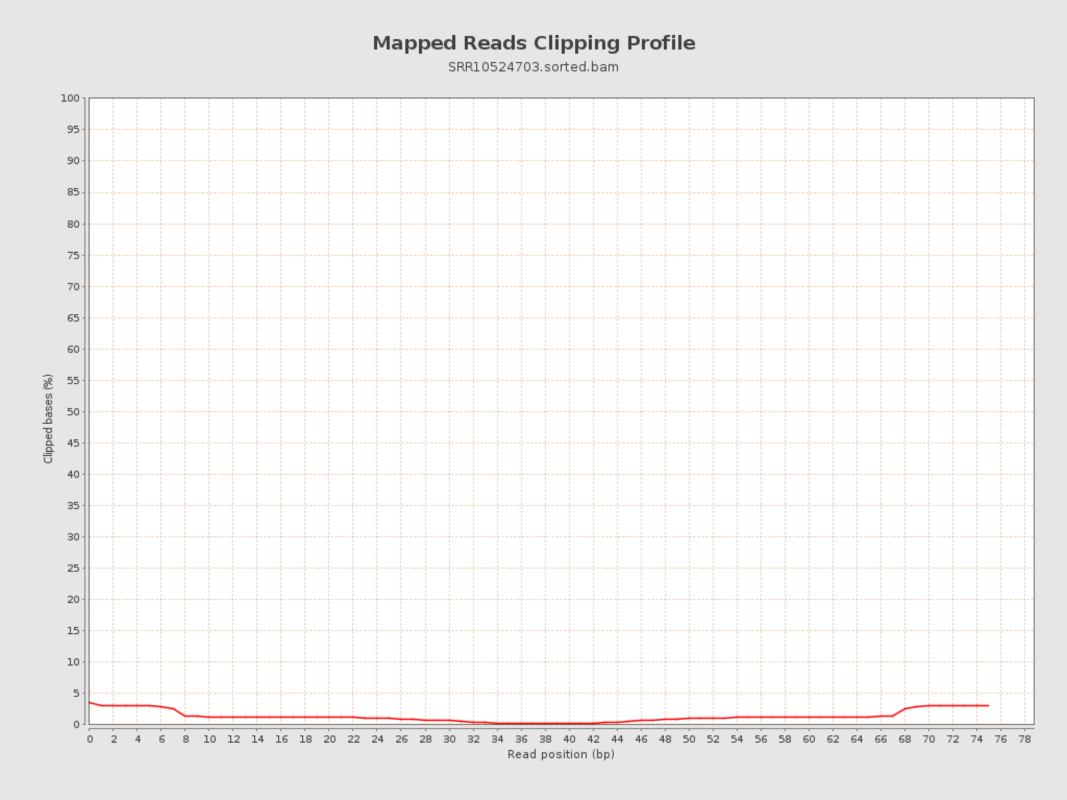
8. Results : Mapped Reads Nucleotide Content



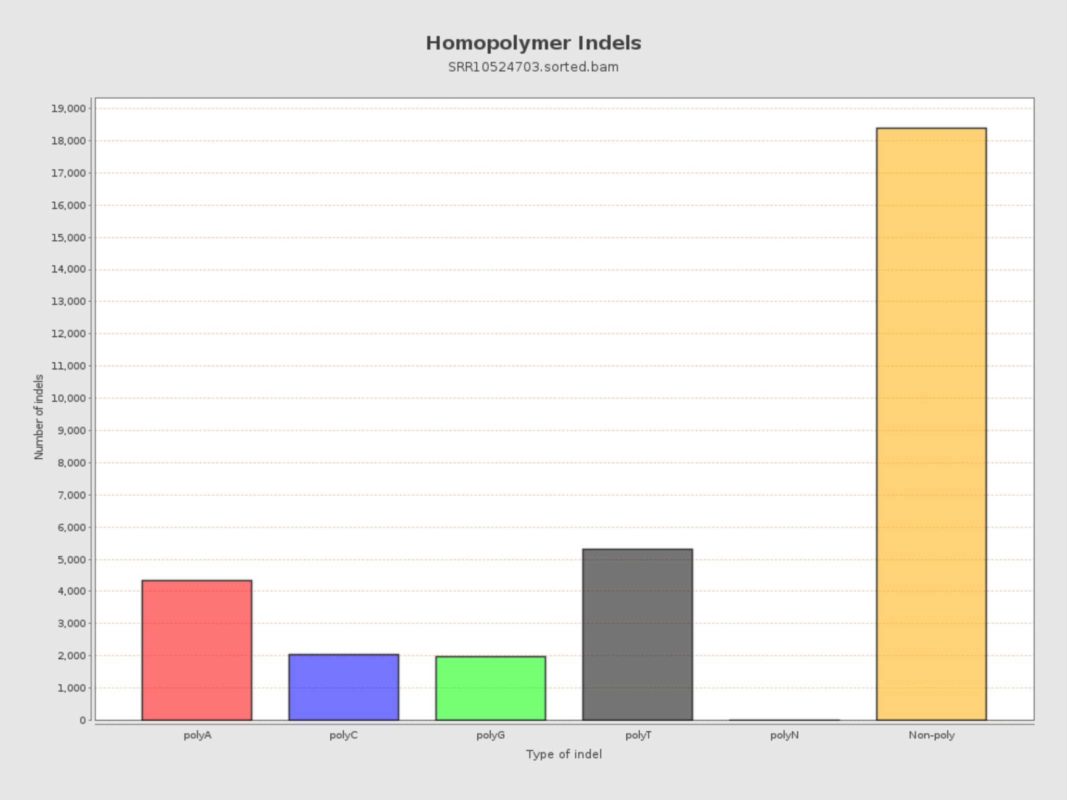
9. Results : Mapped Reads GC-content Distribution



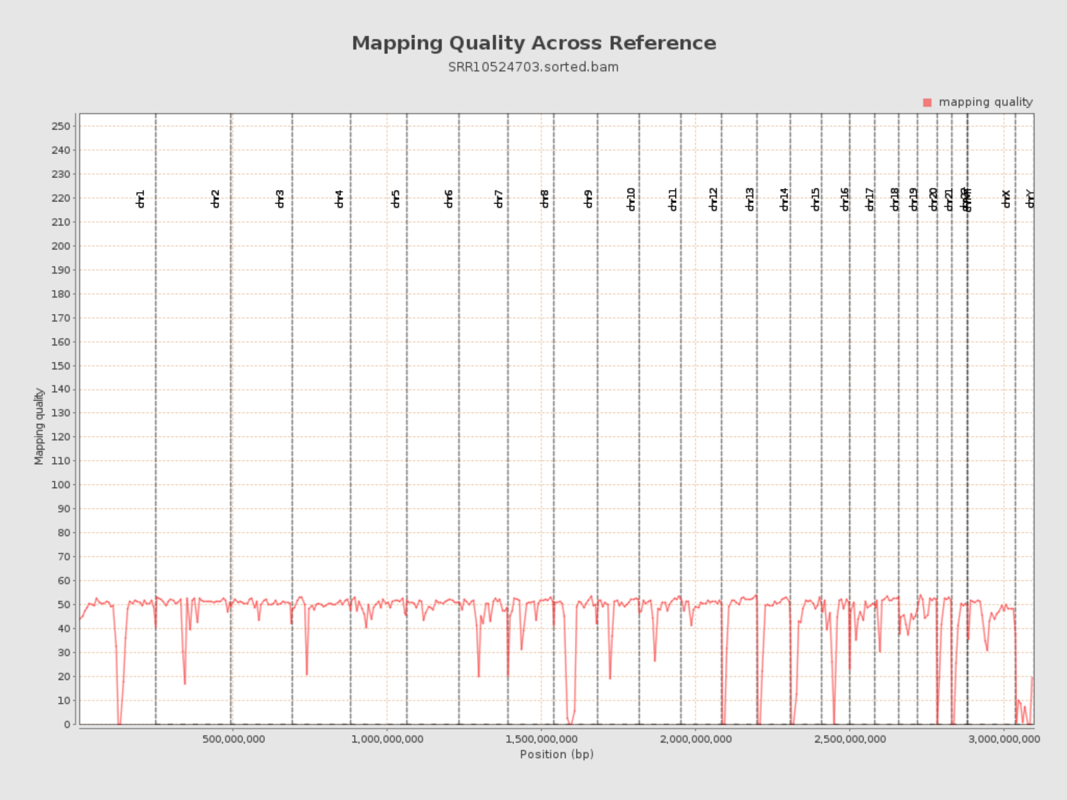
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram