Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 19:59:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524770.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_SRR10524770 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524770.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 19:59:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524770.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,056,132
Mapped reads	971,094 / 91.95%
Unmapped reads	85,038 / 8.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,799 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	27,028 / 2.56%
Duplication rate	2.11%
Clipped reads	974,136 / 92.24%

2.2. ACGT Content

Number/percentage of A's	13,149,591 / 23.47%
Number/percentage of C's	10,901,115 / 19.46%
Number/percentage of T's	17,595,594 / 31.41%
Number/percentage of G's	14,363,575 / 25.64%
Number/percentage of N's	6,800 / 0.01%
GC Percentage	45.1%

2.3. Coverage

Mean	0.0181

Standard Deviation	0.1773

2.4. Mapping Quality

Mean Mapping Quality	44.69

2.5. Mismatches and indels

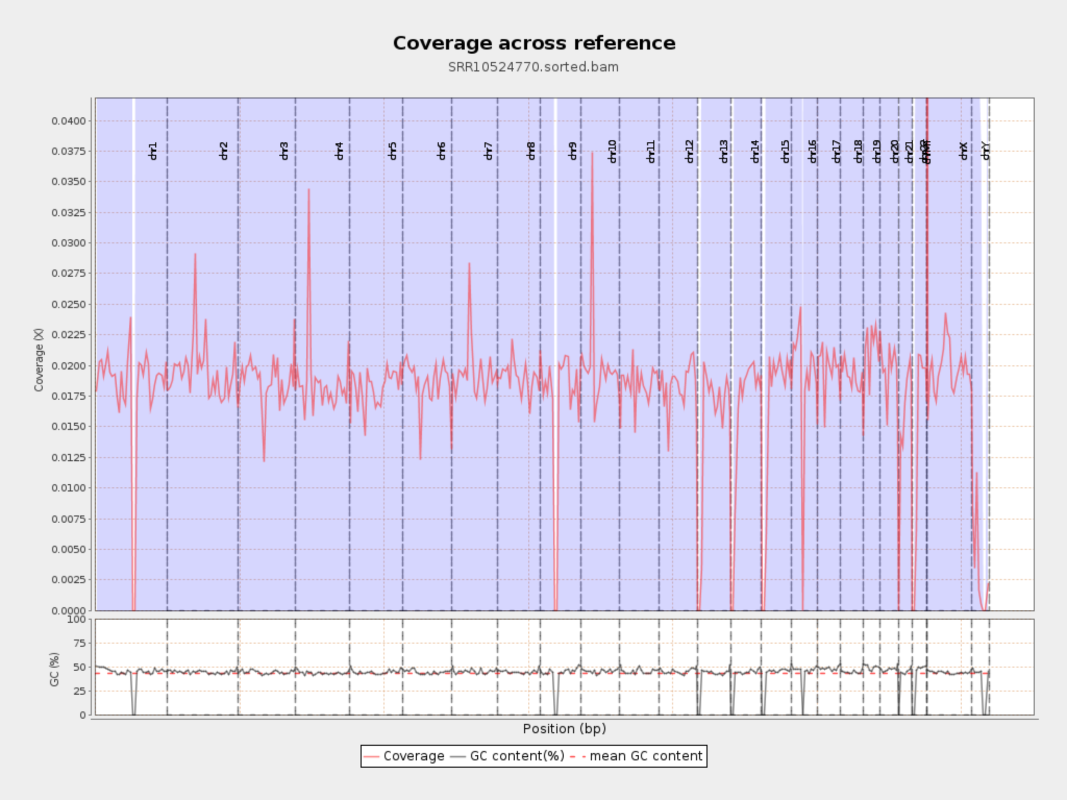
General error rate	0.51%
Mismatches	279,733
Insertions	3,251
Mapped reads with at least one insertion	0.33%
Deletions	11,260
Mapped reads with at least one deletion	1.15%
Homopolymer indels	43.46%

2.6. Chromosome stats

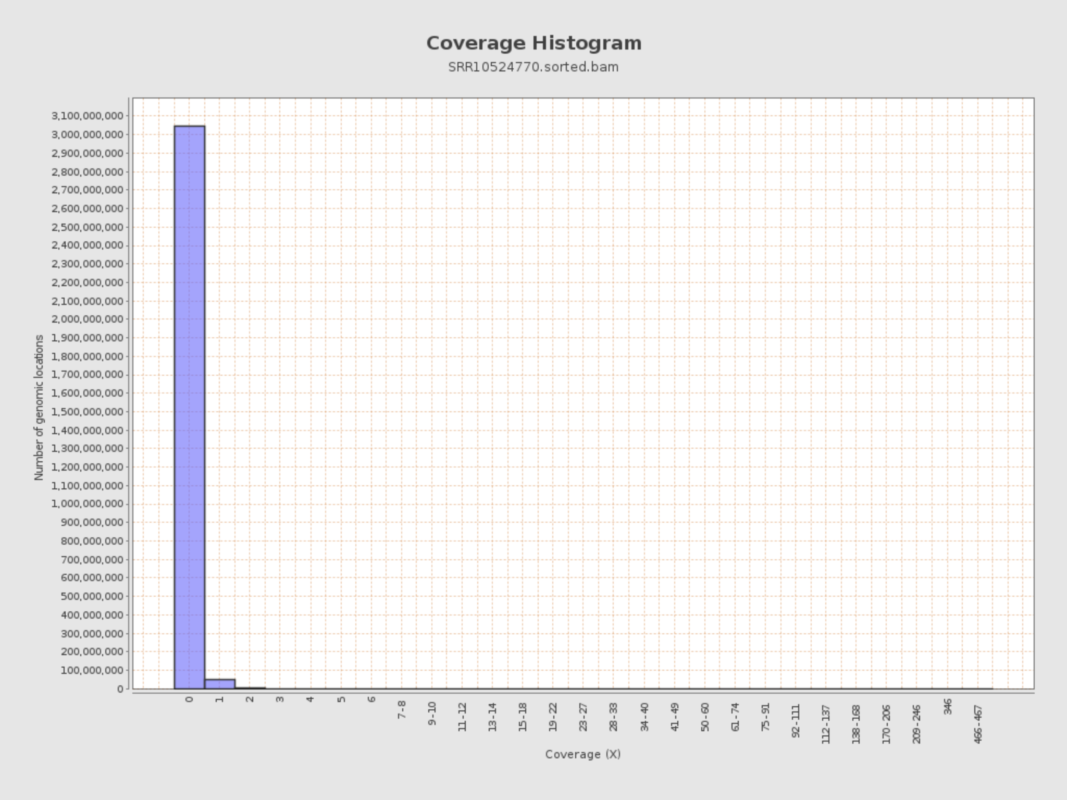
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4480404	0.018	0.2299
chr2	243199373	4763204	0.0196	0.2534
chr3	198022430	3692772	0.0186	0.1458
chr4	191154276	3584019	0.0187	0.161
chr5	180915260	3321009	0.0184	0.1442
chr6	171115067	3189162	0.0186	0.1547
chr7	159138663	3106428	0.0195	0.2142

chr8	146364022	2786291	0.019	0.1656
chr9	141213431	2360518	0.0167	0.1583
chr10	135534747	2731954	0.0202	0.2059
chr11	135006516	2501271	0.0185	0.1622
chr12	133851895	2456441	0.0184	0.1456
chr13	115169878	1715998	0.0149	0.1309
chr14	107349540	1680660	0.0157	0.137
chr15	102531392	1634381	0.0159	0.1355
chr16	90354753	1687979	0.0187	0.1557
chr17	81195210	1614844	0.0199	0.1558
chr18	78077248	1497436	0.0192	0.2329
chr19	59128983	1257393	0.0213	0.2057
chr20	63025520	1234360	0.0196	0.1559
chr21	48129895	743571	0.0154	0.1431
chr22	51304566	713659	0.0139	0.1263
chrMT	16571	20907	1.2617	1.3472
chrX	155270560	3068987	0.0198	0.1565
chrY	59373566	191260	0.0032	0.0978

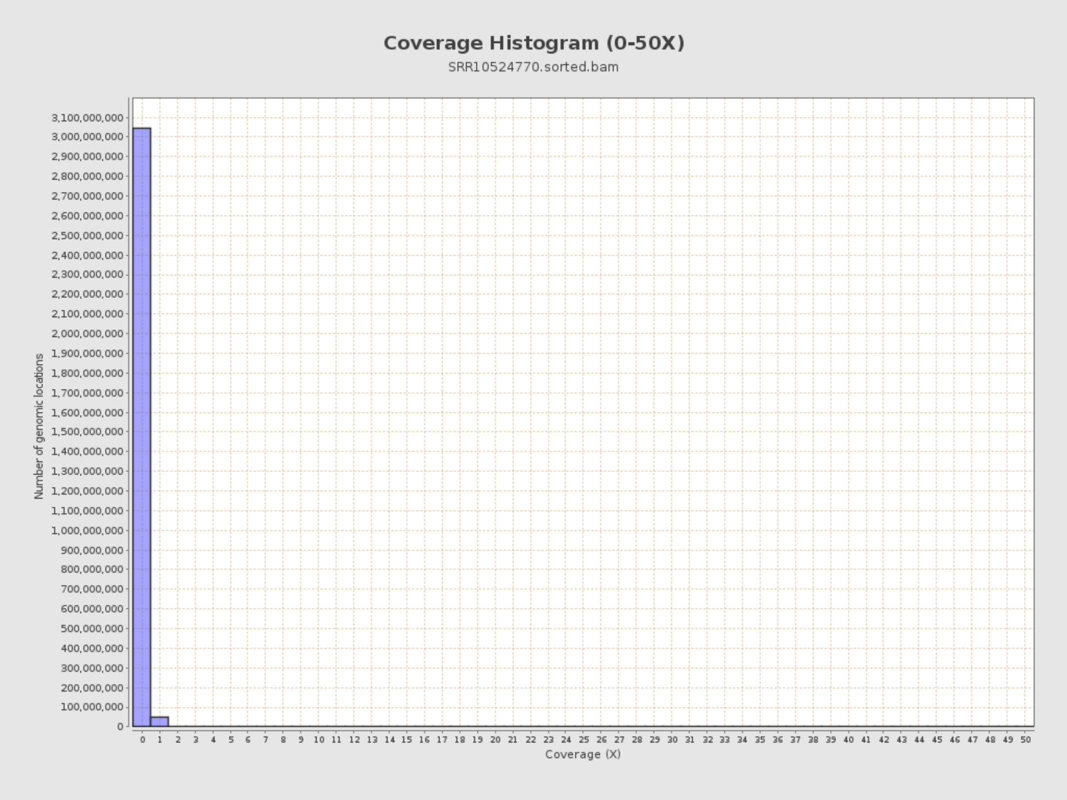
3. Results : Coverage across reference



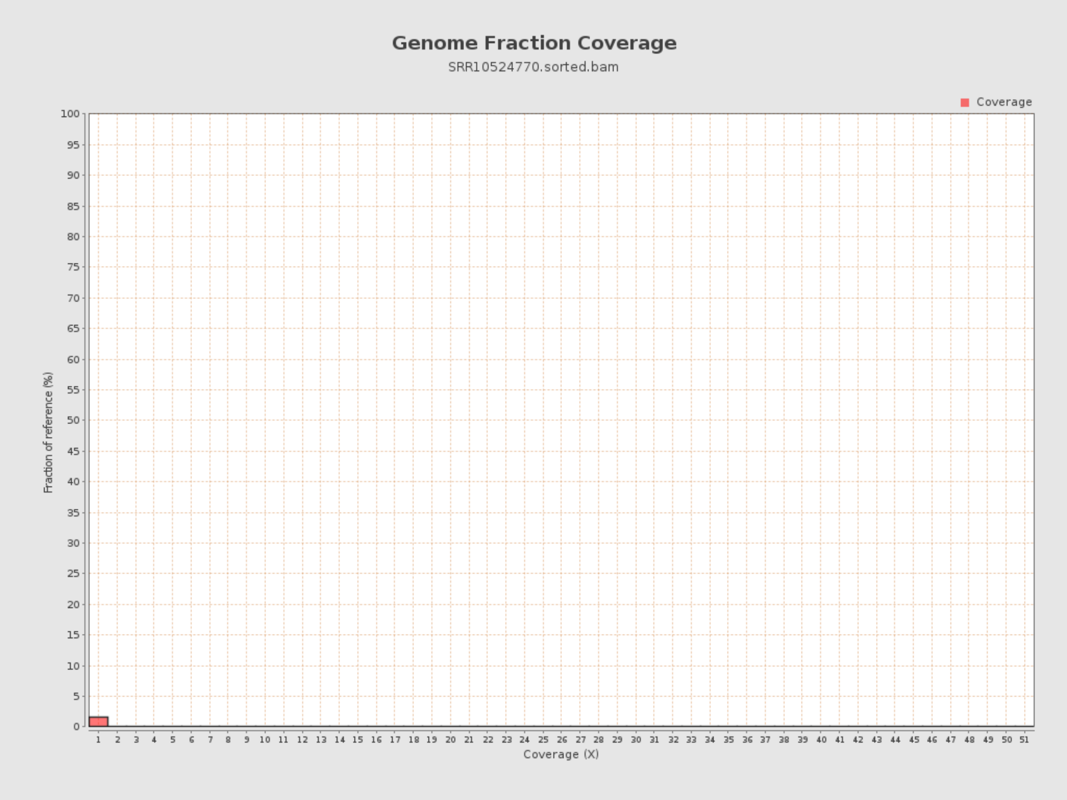
4. Results : Coverage Histogram



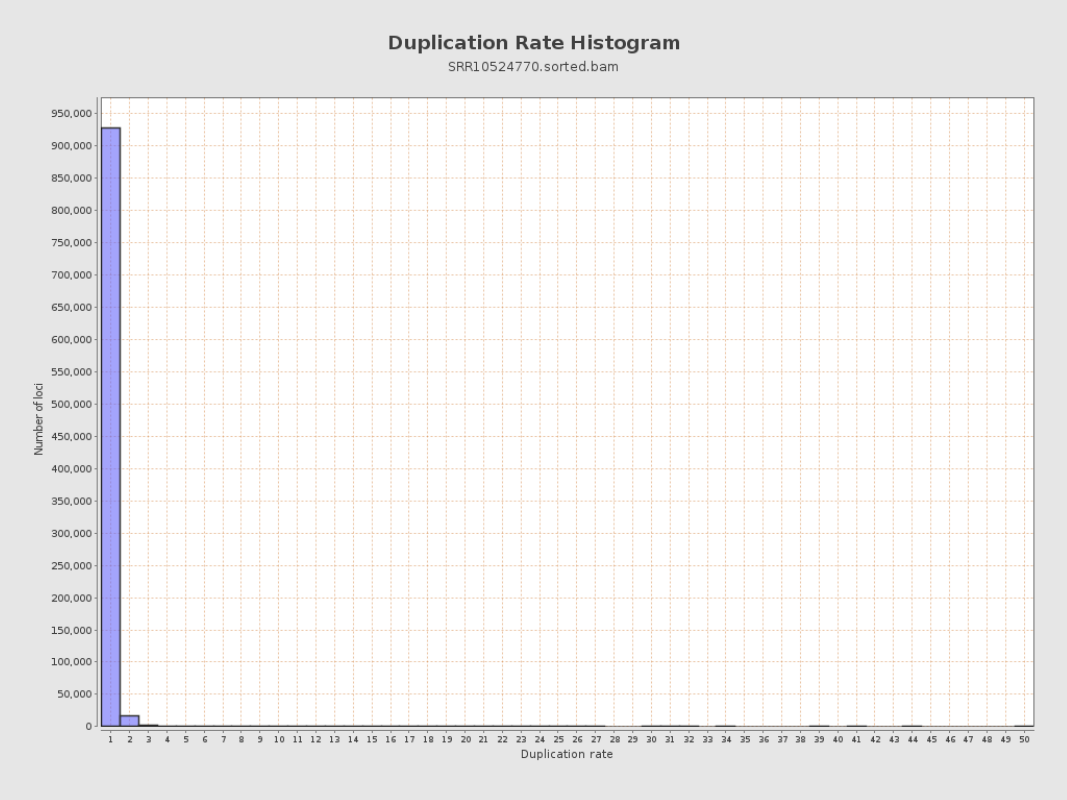
5. Results : Coverage Histogram (0-50X)



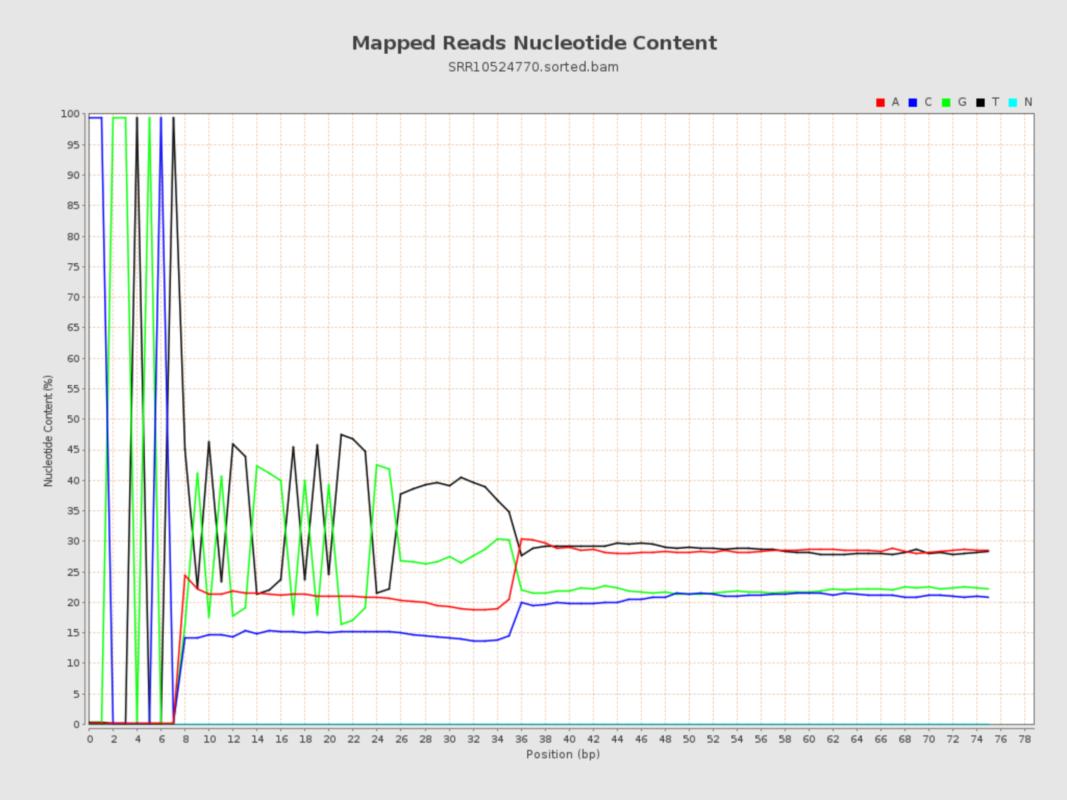
6. Results : Genome Fraction Coverage



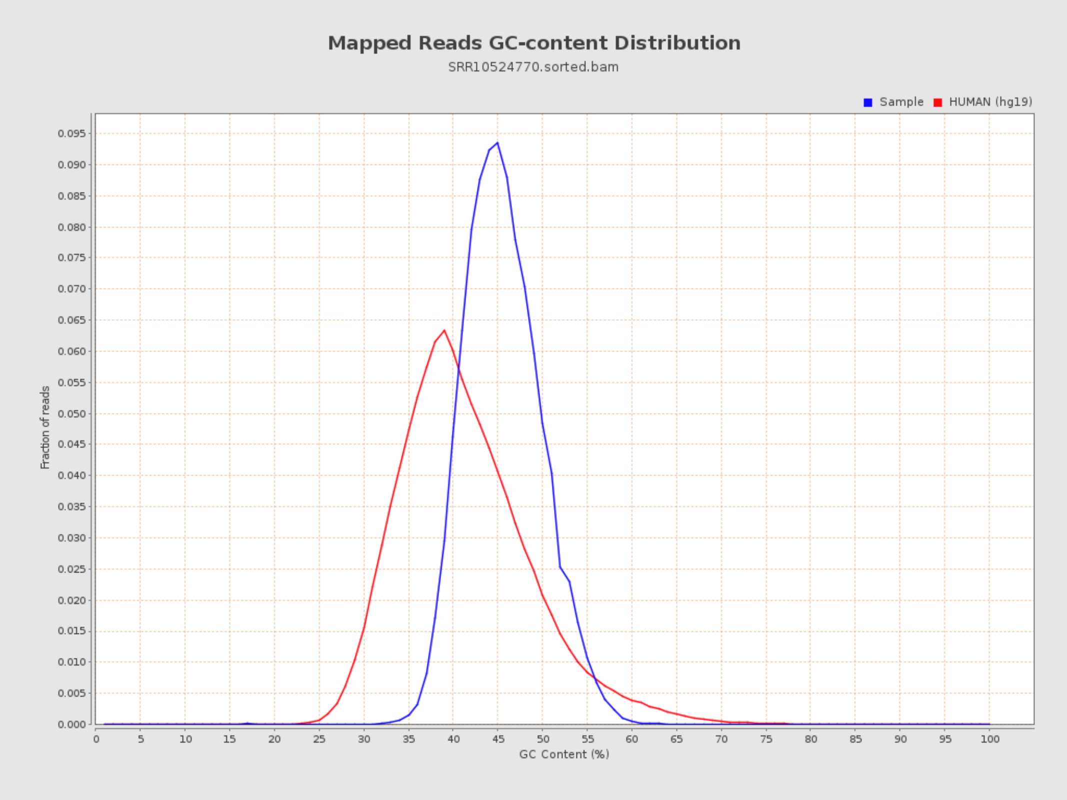
7. Results : Duplication Rate Histogram



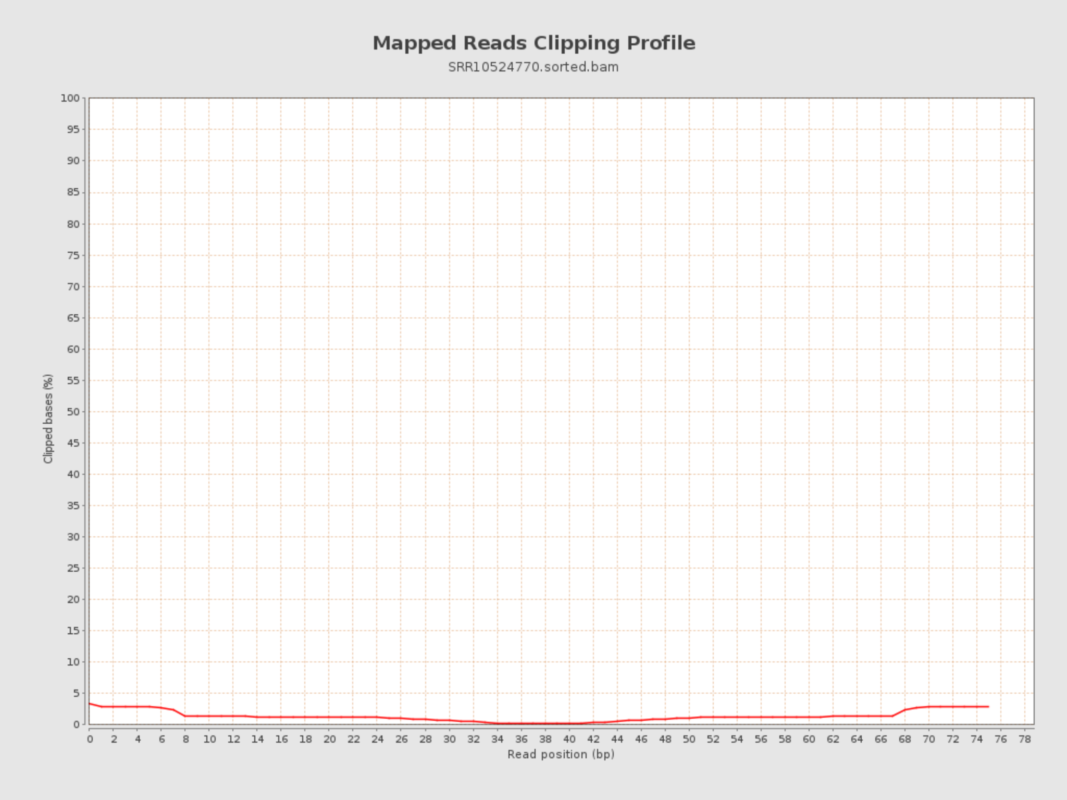
8. Results : Mapped Reads Nucleotide Content



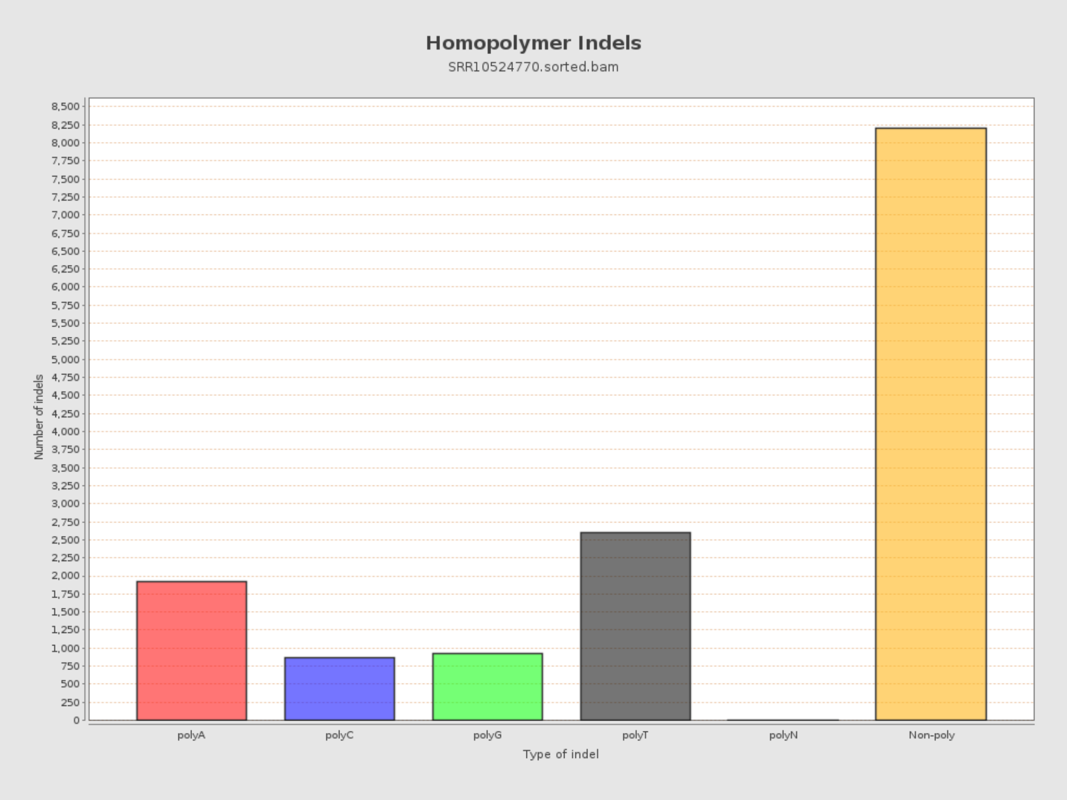
9. Results : Mapped Reads GC-content Distribution



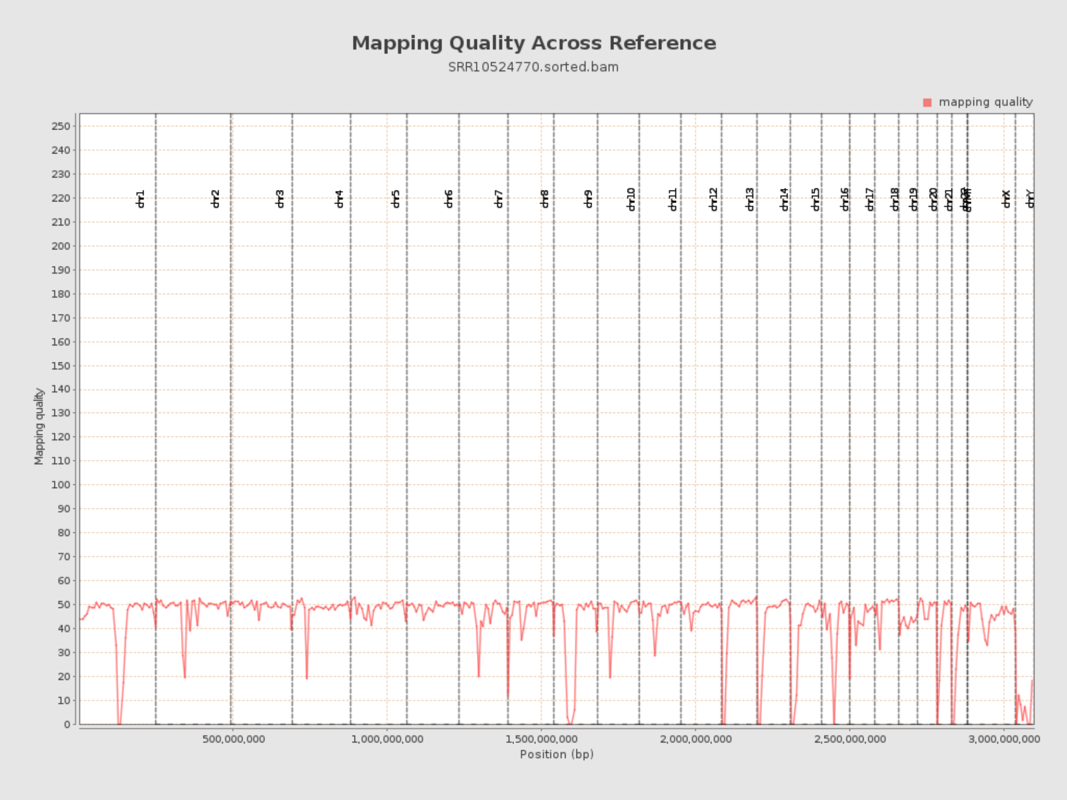
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram