Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 10:36:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524959.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_SRR10524959 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524959.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 10:36:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524959.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	805,508
Mapped reads	730,214 / 90.65%
Unmapped reads	75,294 / 9.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,217 / 0.28%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	15,369 / 1.91%
Duplication rate	1.52%
Clipped reads	731,758 / 90.84%

2.2. ACGT Content

Number/percentage of A's	10,844,968 / 25.68%
Number/percentage of C's	8,162,808 / 19.33%
Number/percentage of T's	13,156,534 / 31.15%
Number/percentage of G's	10,072,730 / 23.85%
Number/percentage of N's	545 / 0%
GC Percentage	43.17%

2.3. Coverage

Mean	0.0136

Standard Deviation	0.1519

2.4. Mapping Quality

Mean Mapping Quality	44.34

2.5. Mismatches and indels

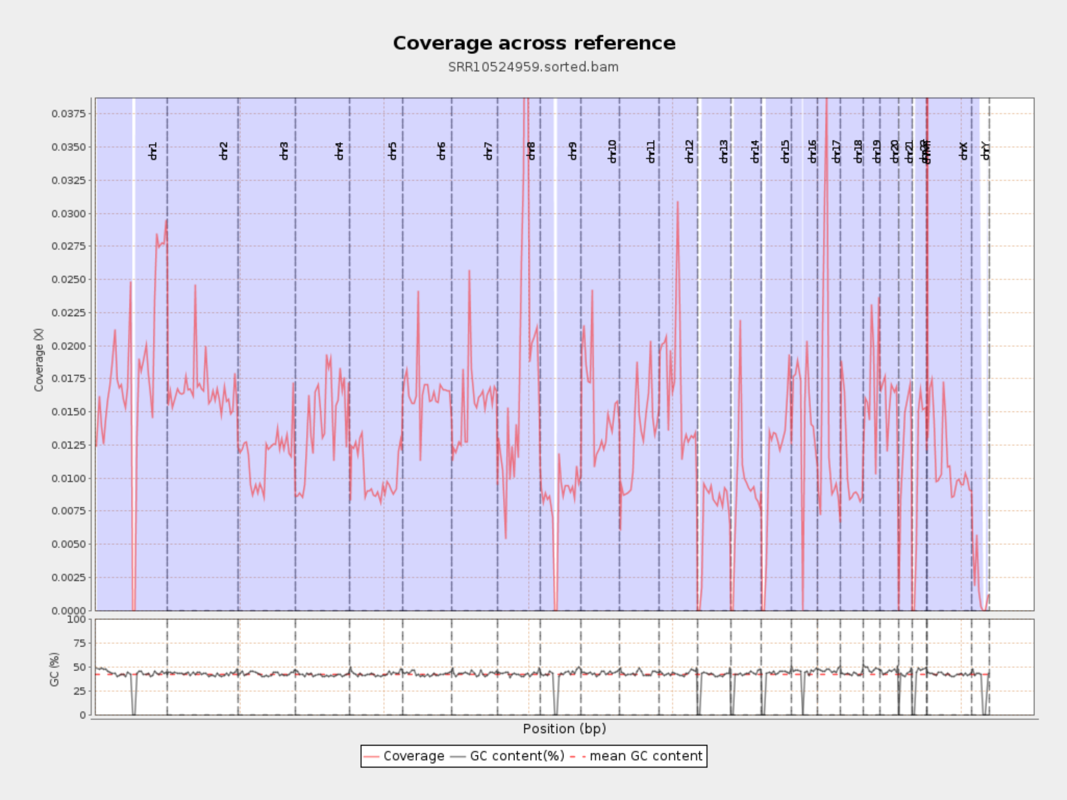
General error rate	0.5%
Mismatches	206,088
Insertions	2,311
Mapped reads with at least one insertion	0.31%
Deletions	8,177
Mapped reads with at least one deletion	1.11%
Homopolymer indels	44.77%

2.6. Chromosome stats

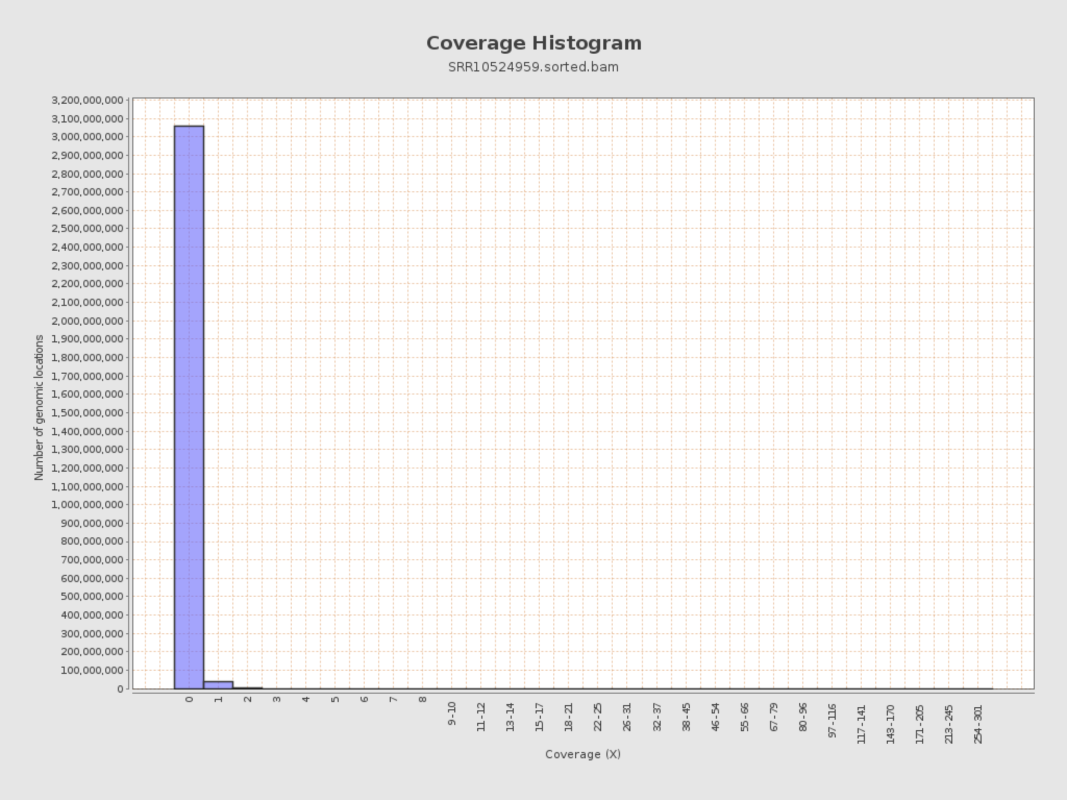
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4444825	0.0178	0.2499
chr2	243199373	4048707	0.0166	0.1728
chr3	198022430	2321157	0.0117	0.113
chr4	191154276	2720969	0.0142	0.1298
chr5	180915260	1855310	0.0103	0.1063
chr6	171115067	2831147	0.0165	0.1595
chr7	159138663	2480999	0.0156	0.2036

chr8	146364022	2836985	0.0194	0.1648
chr9	141213431	1156949	0.0082	0.1176
chr10	135534747	2102011	0.0155	0.1514
chr11	135006516	1763358	0.0131	0.1356
chr12	133851895	2268629	0.0169	0.1359
chr13	115169878	832120	0.0072	0.0884
chr14	107349540	961955	0.009	0.1002
chr15	102531392	1157408	0.0113	0.1147
chr16	90354753	1333547	0.0148	0.1297
chr17	81195210	1226827	0.0151	0.159
chr18	78077248	852969	0.0109	0.1697
chr19	59128983	1021678	0.0173	0.1798
chr20	63025520	999911	0.0159	0.1315
chr21	48129895	595743	0.0124	0.1183
chr22	51304566	543115	0.0106	0.1067
chrMT	16571	3768	0.2274	0.4646
chrX	155270560	1781407	0.0115	0.1195
chrY	59373566	109726	0.0018	0.0535

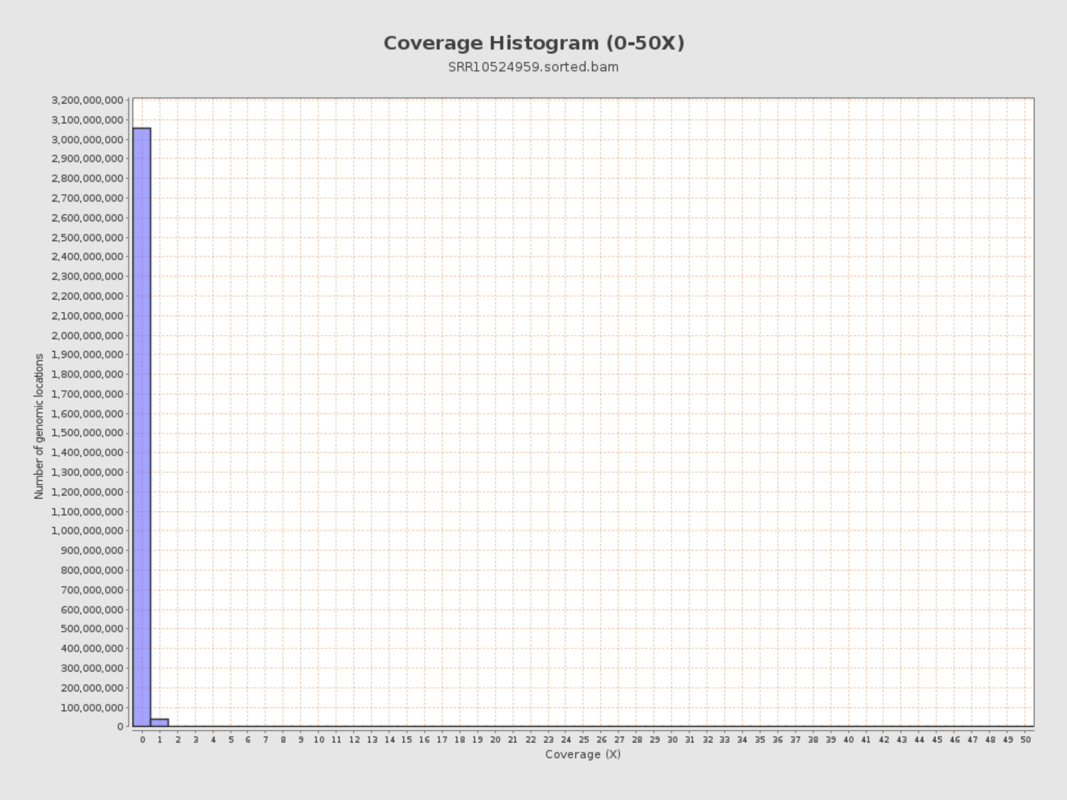
3. Results : Coverage across reference



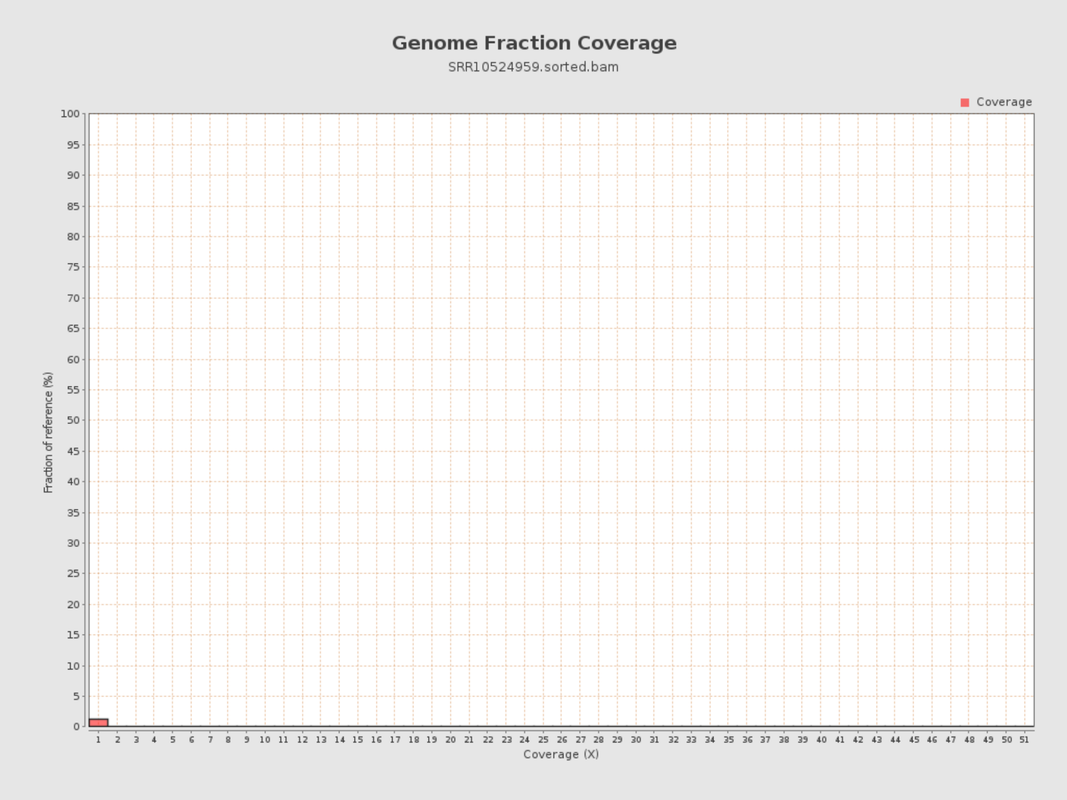
4. Results : Coverage Histogram



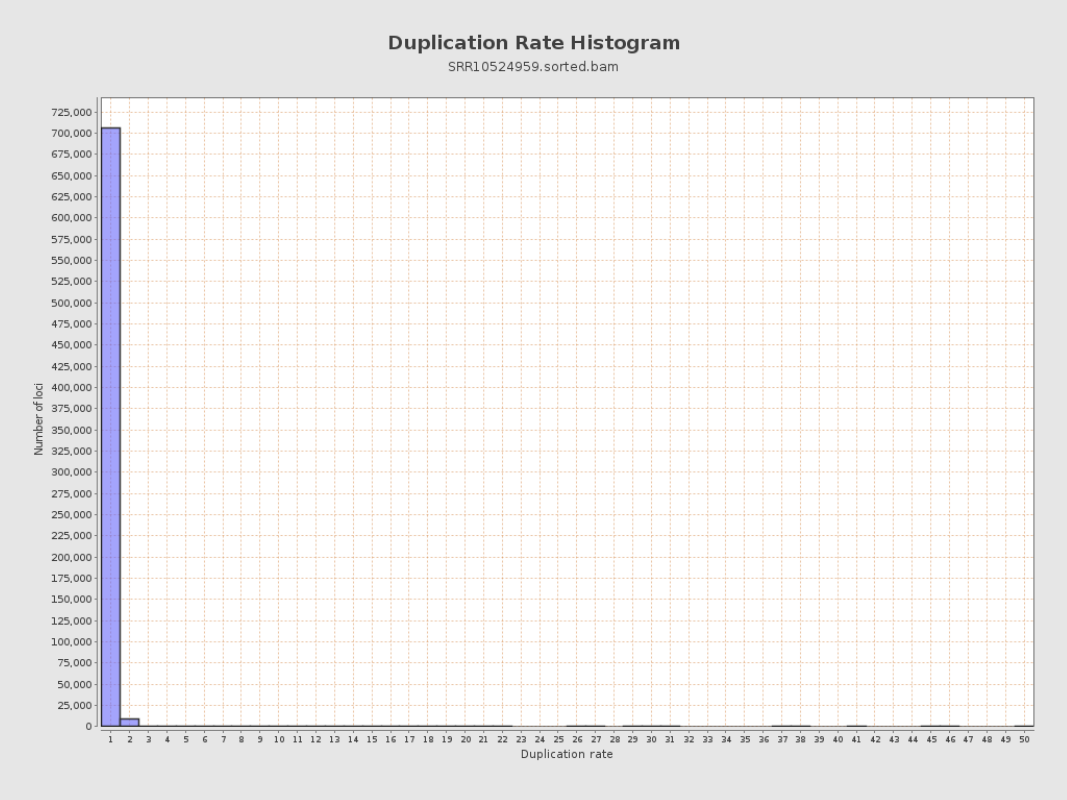
5. Results : Coverage Histogram (0-50X)



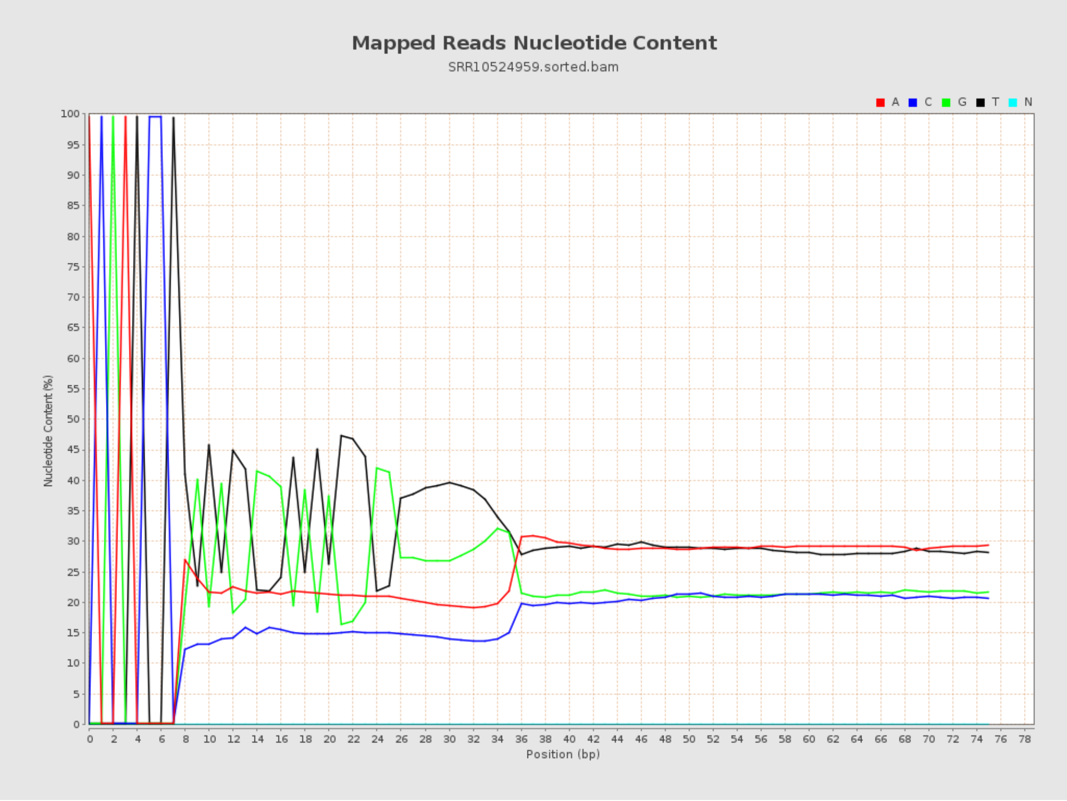
6. Results : Genome Fraction Coverage



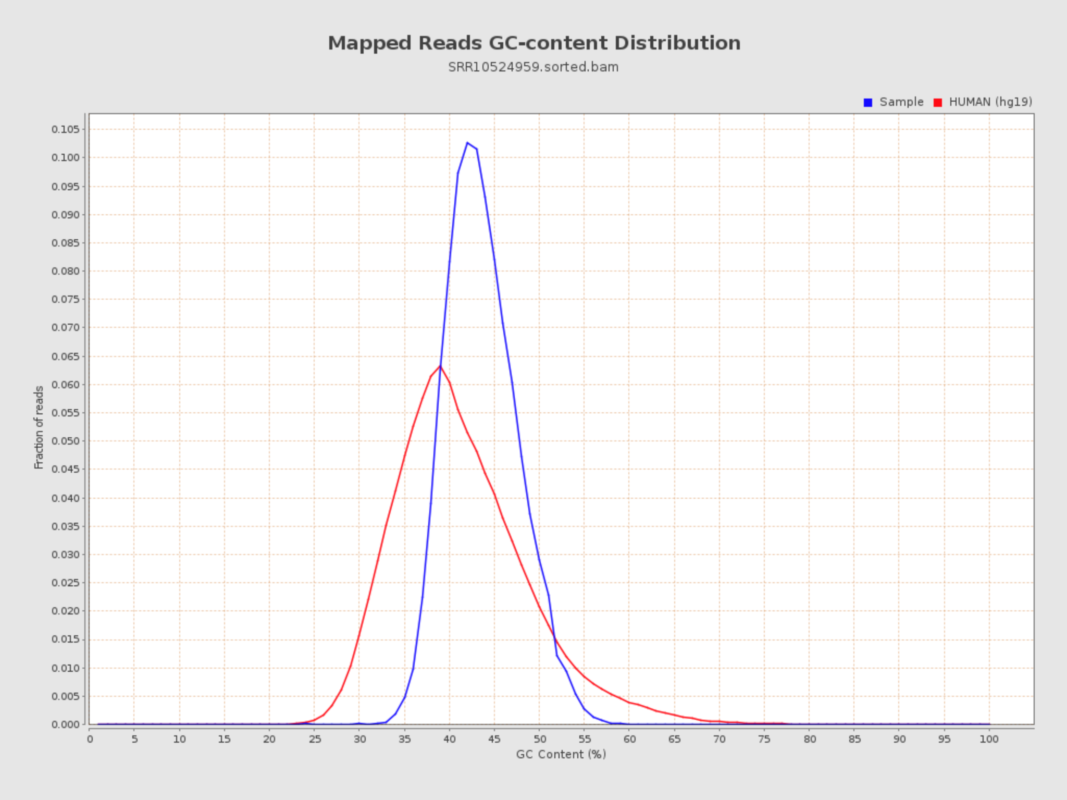
7. Results : Duplication Rate Histogram



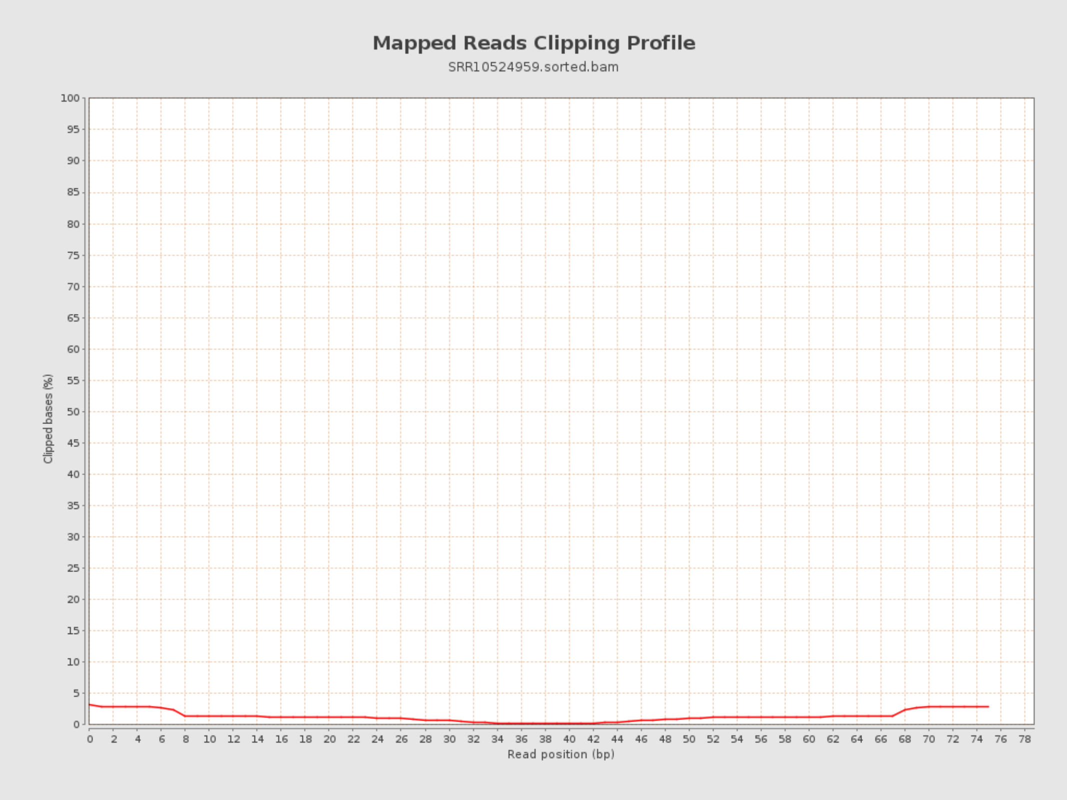
8. Results : Mapped Reads Nucleotide Content



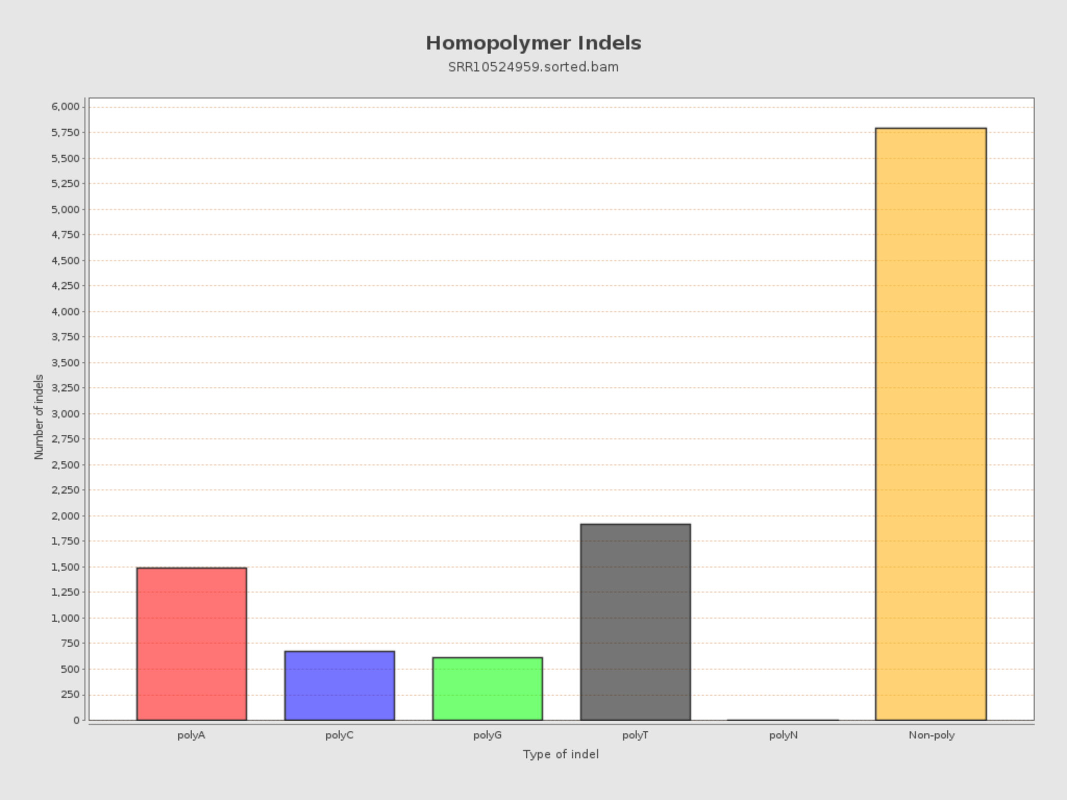
9. Results : Mapped Reads GC-content Distribution



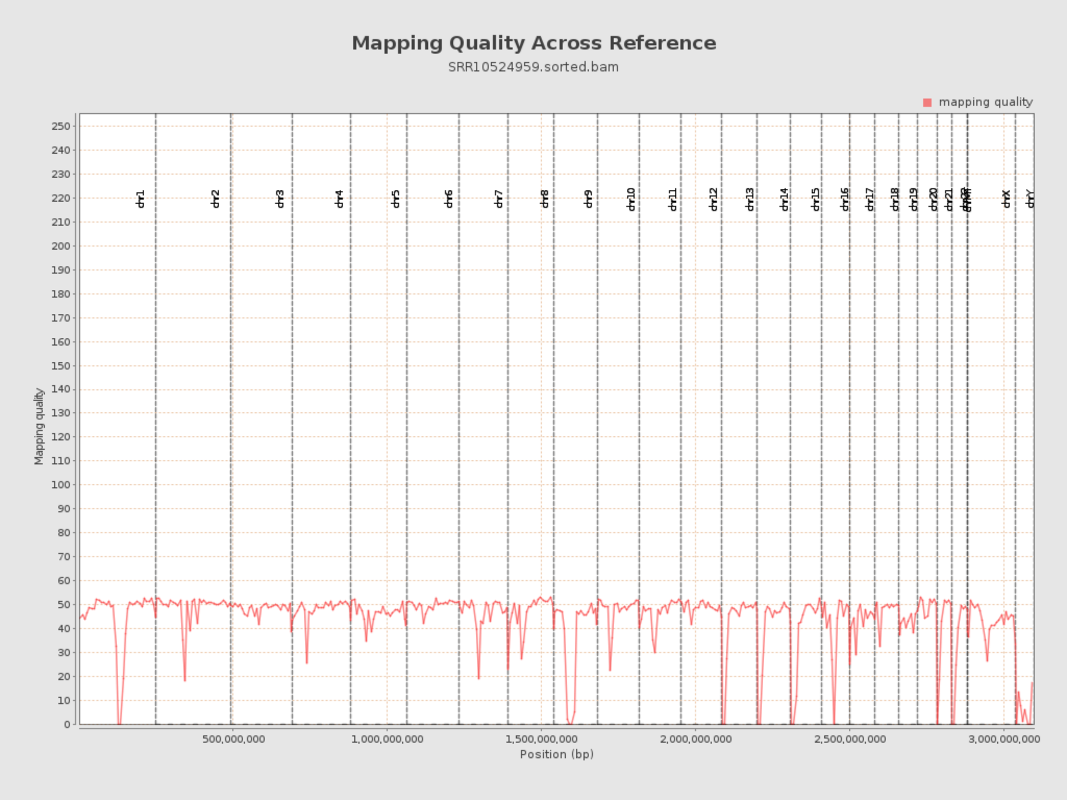
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram