Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 22:39:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524838.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_SRR10524838 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524838.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 22:39:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524838.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	830,576
Mapped reads	764,066 / 91.99%
Unmapped reads	66,510 / 8.01%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,357 / 0.77%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	15,369 / 1.85%
Duplication rate	1.36%
Clipped reads	767,912 / 92.46%

2.2. ACGT Content

Number/percentage of A's	12,249,119 / 27.39%
Number/percentage of C's	7,801,169 / 17.45%
Number/percentage of T's	14,059,962 / 31.44%
Number/percentage of G's	10,599,374 / 23.7%
Number/percentage of N's	6,044 / 0.01%
GC Percentage	41.15%

2.3. Coverage

Mean	0.0144

Standard Deviation	0.1681

2.4. Mapping Quality

Mean Mapping Quality	44.88

2.5. Mismatches and indels

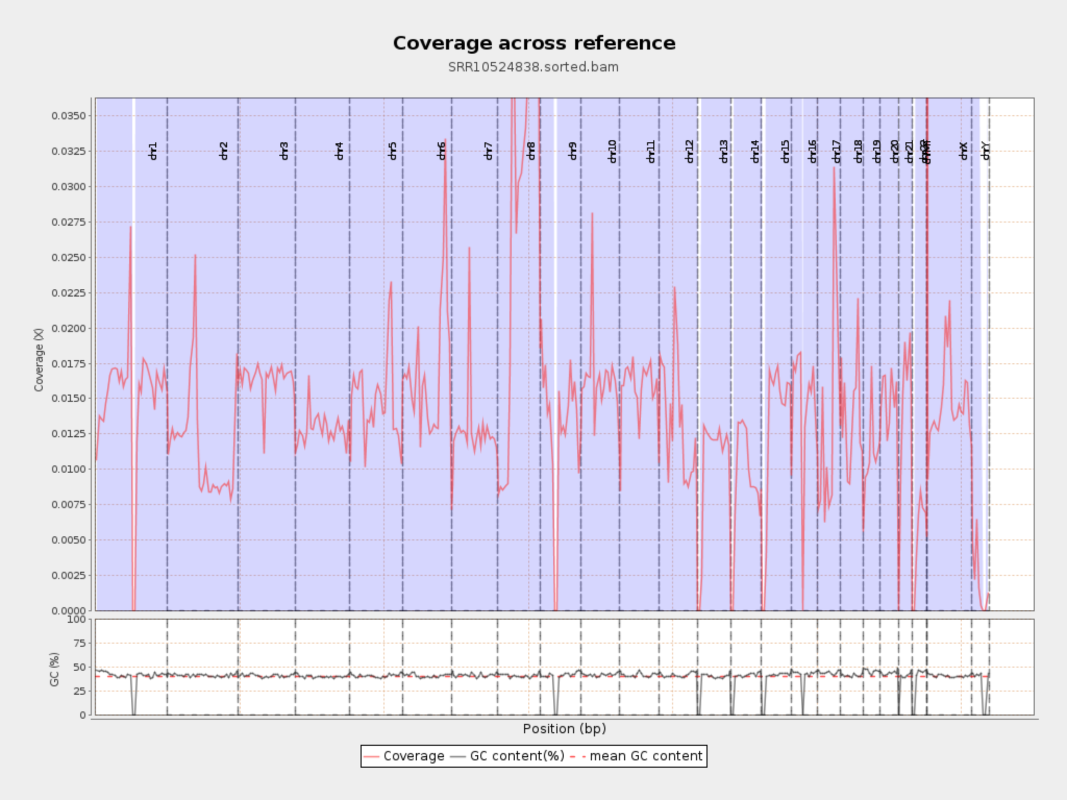
General error rate	0.5%
Mismatches	215,328
Insertions	3,571
Mapped reads with at least one insertion	0.47%
Deletions	8,631
Mapped reads with at least one deletion	1.12%
Homopolymer indels	44.04%

2.6. Chromosome stats

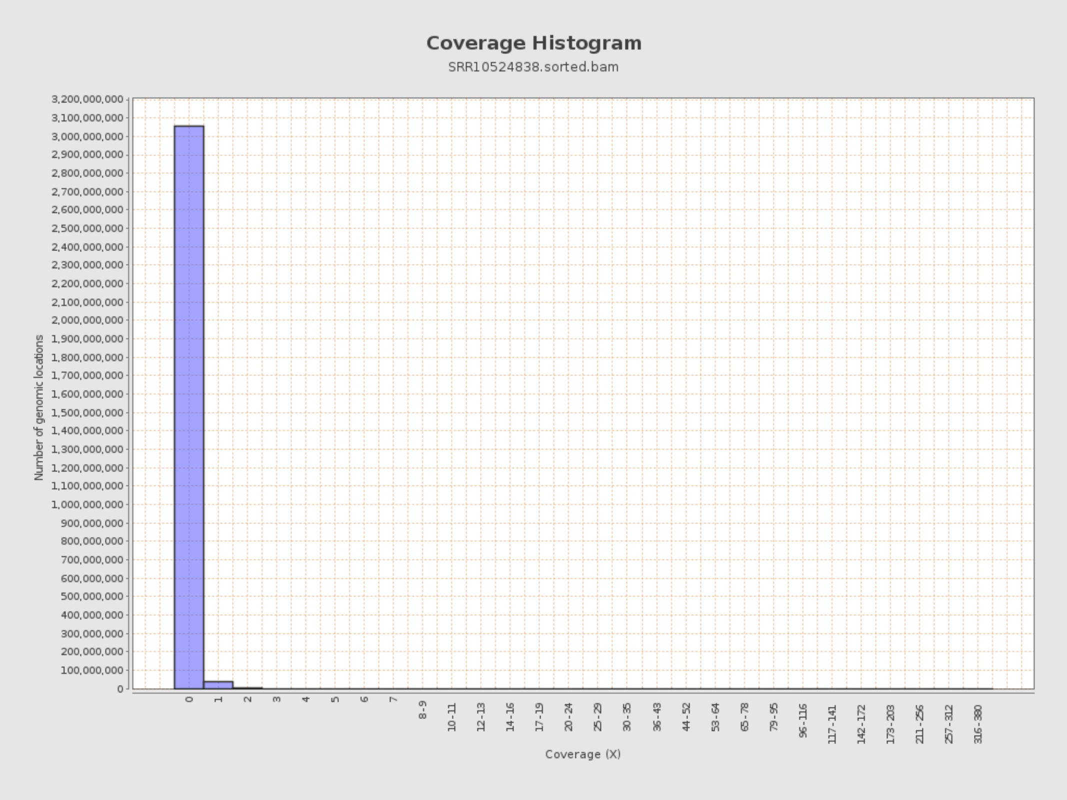
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3761560	0.0151	0.2965
chr2	243199373	2804981	0.0115	0.1614
chr3	198022430	3260119	0.0165	0.1335
chr4	191154276	2454871	0.0128	0.1226
chr5	180915260	2726327	0.0151	0.1279
chr6	171115067	2888679	0.0169	0.1427
chr7	159138663	2052261	0.0129	0.2153

chr8	146364022	4844758	0.0331	0.2281
chr9	141213431	1835970	0.013	0.1474
chr10	135534747	2229952	0.0165	0.1702
chr11	135006516	2155453	0.016	0.1559
chr12	133851895	1796411	0.0134	0.1215
chr13	115169878	1167493	0.0101	0.1045
chr14	107349540	969097	0.009	0.103
chr15	102531392	1318663	0.0129	0.1188
chr16	90354753	1285921	0.0142	0.1311
chr17	81195210	1123900	0.0138	0.1315
chr18	78077248	1079068	0.0138	0.2433
chr19	59128983	661964	0.0112	0.2048
chr20	63025520	931866	0.0148	0.1281
chr21	48129895	692919	0.0144	0.1277
chr22	51304566	267195	0.0052	0.074
chrMT	16571	6500	0.3923	0.6481
chrX	155270560	2297335	0.0148	0.1356
chrY	59373566	115923	0.002	0.0601

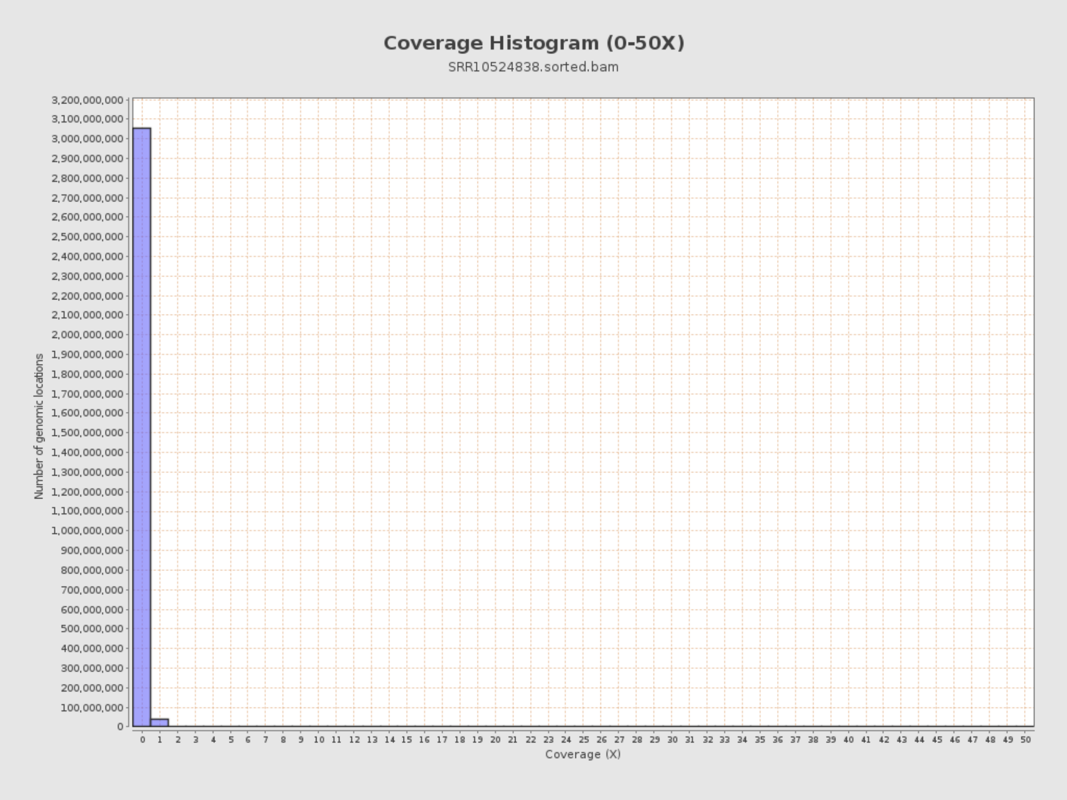
3. Results : Coverage across reference



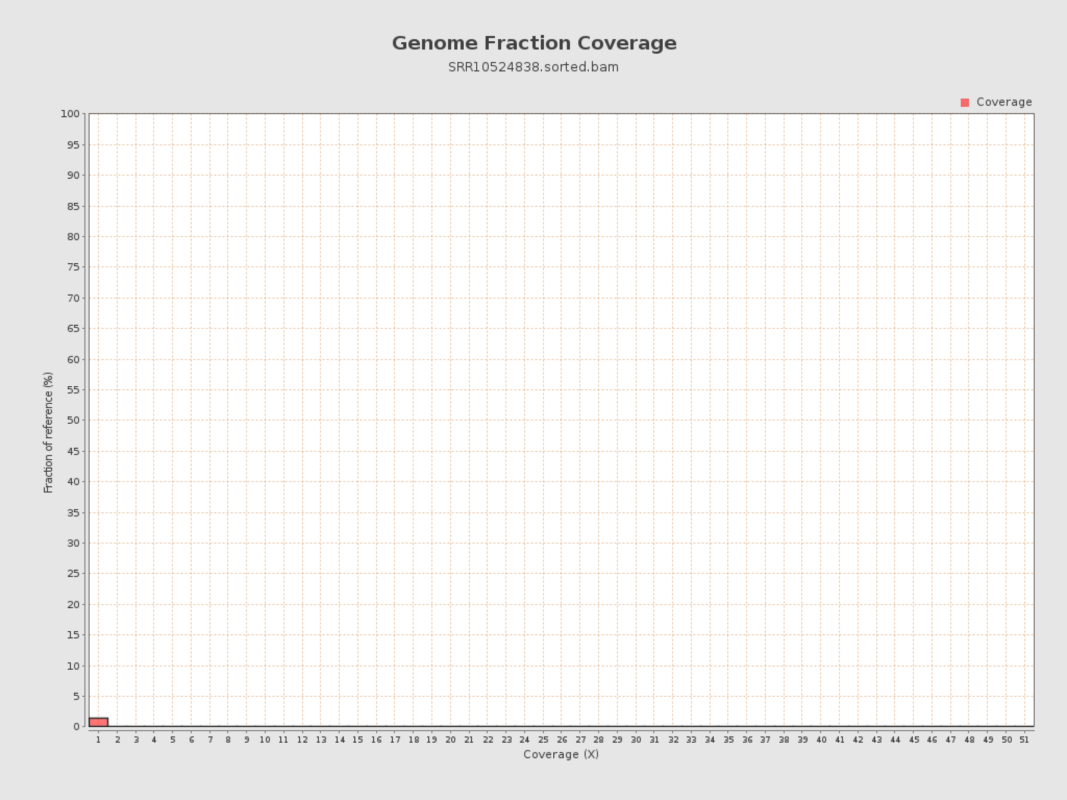
4. Results : Coverage Histogram



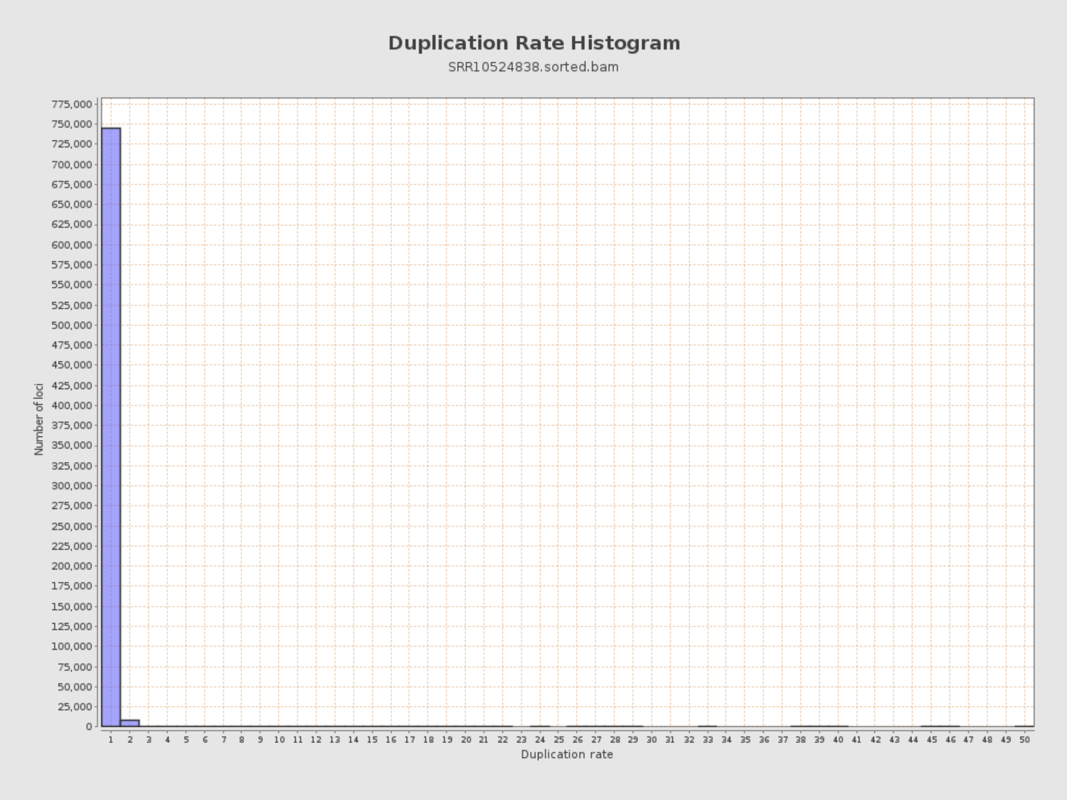
5. Results : Coverage Histogram (0-50X)



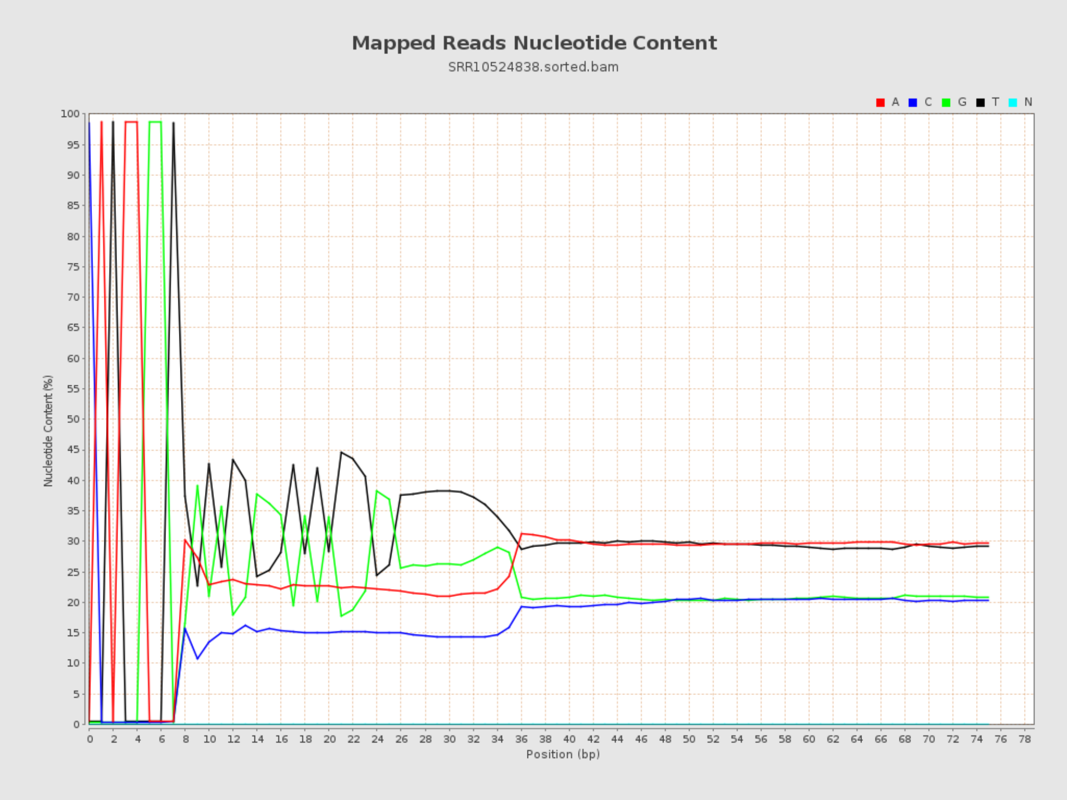
6. Results : Genome Fraction Coverage



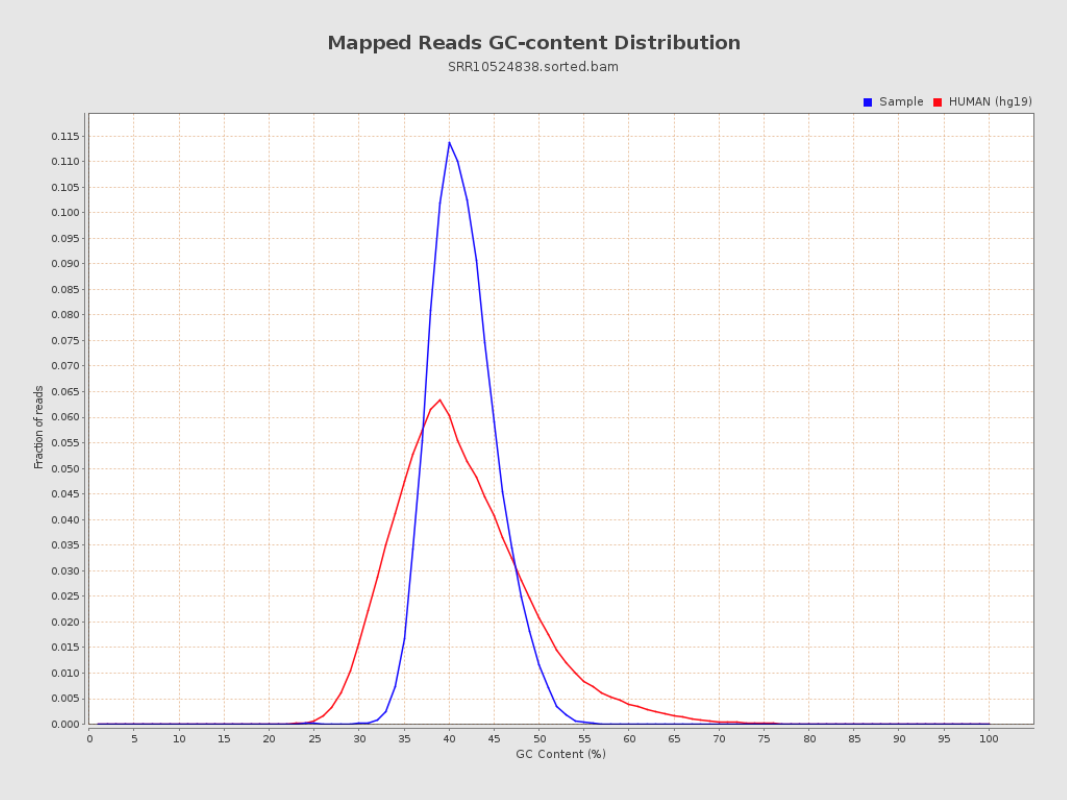
7. Results : Duplication Rate Histogram



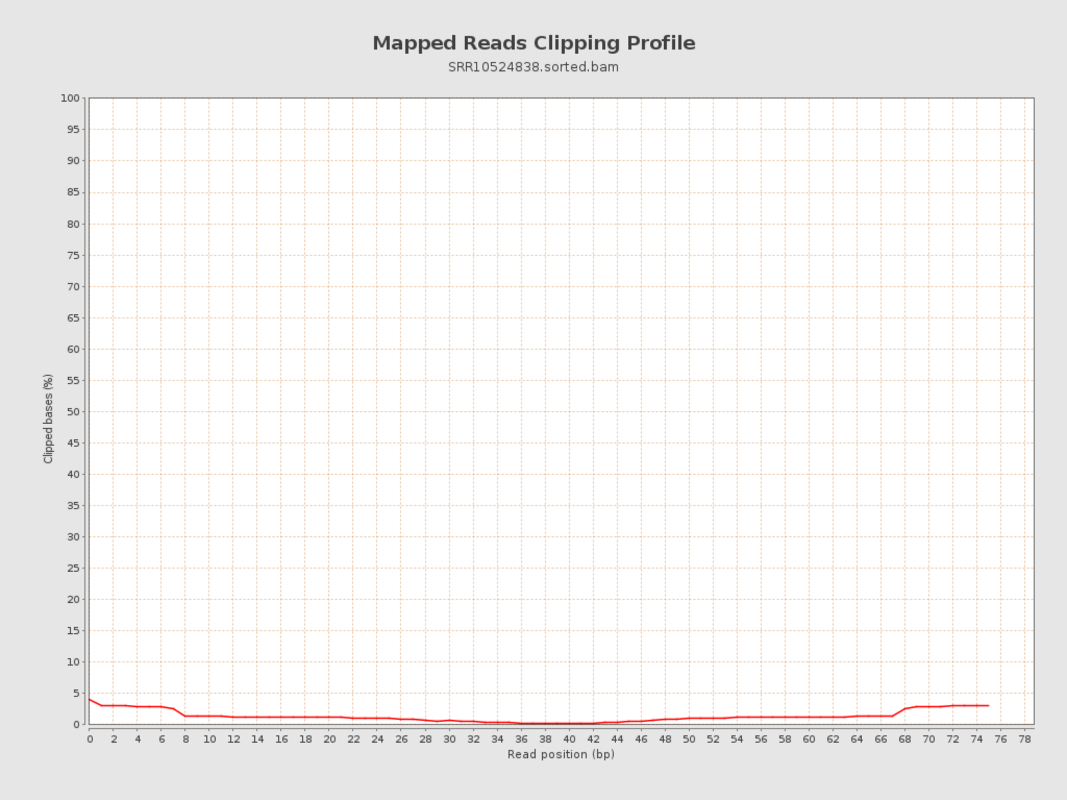
8. Results : Mapped Reads Nucleotide Content



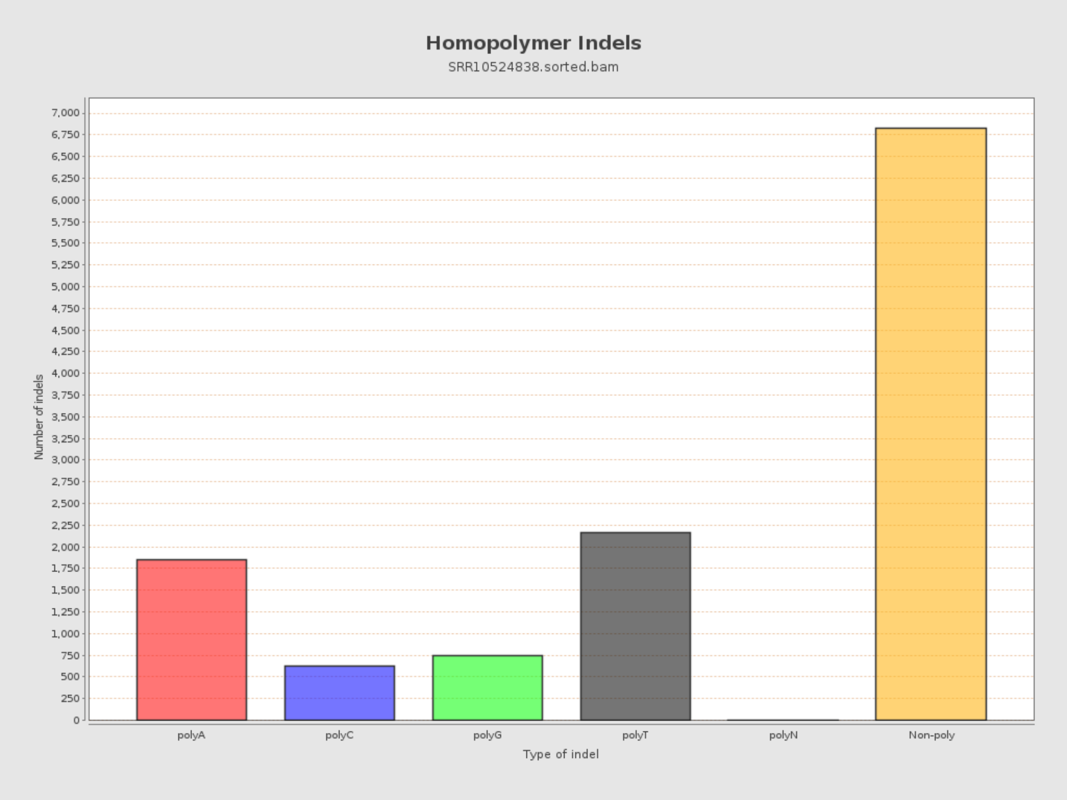
9. Results : Mapped Reads GC-content Distribution



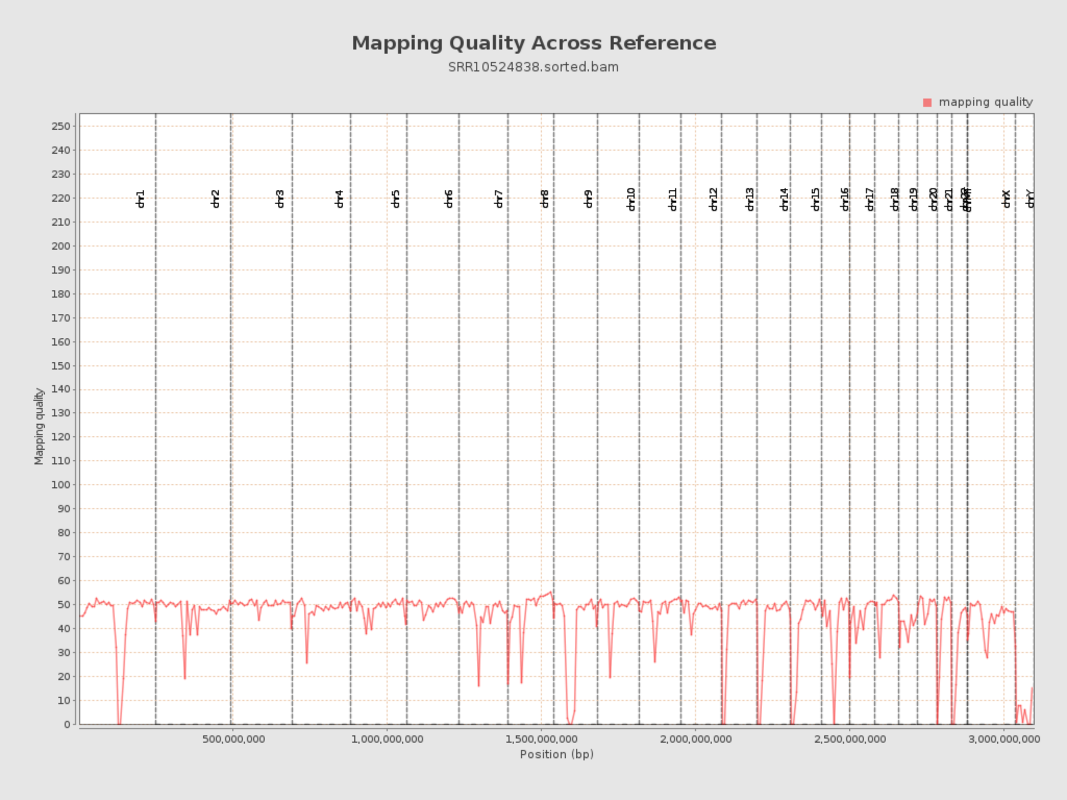
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram