Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 01:11:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524378.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_SRR10524378 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524378.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 01:11:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524378.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	973,817
Mapped reads	897,377 / 92.15%
Unmapped reads	76,440 / 7.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,987 / 0.31%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	28,805 / 2.96%
Duplication rate	2.45%
Clipped reads	900,161 / 92.44%

2.2. ACGT Content

Number/percentage of A's	12,682,407 / 24.28%
Number/percentage of C's	9,982,231 / 19.11%
Number/percentage of T's	16,584,142 / 31.74%
Number/percentage of G's	12,994,422 / 24.87%
Number/percentage of N's	1,109 / 0%
GC Percentage	43.98%

2.3. Coverage

Mean	0.0169

Standard Deviation	0.1864

2.4. Mapping Quality

Mean Mapping Quality	45.7

2.5. Mismatches and indels

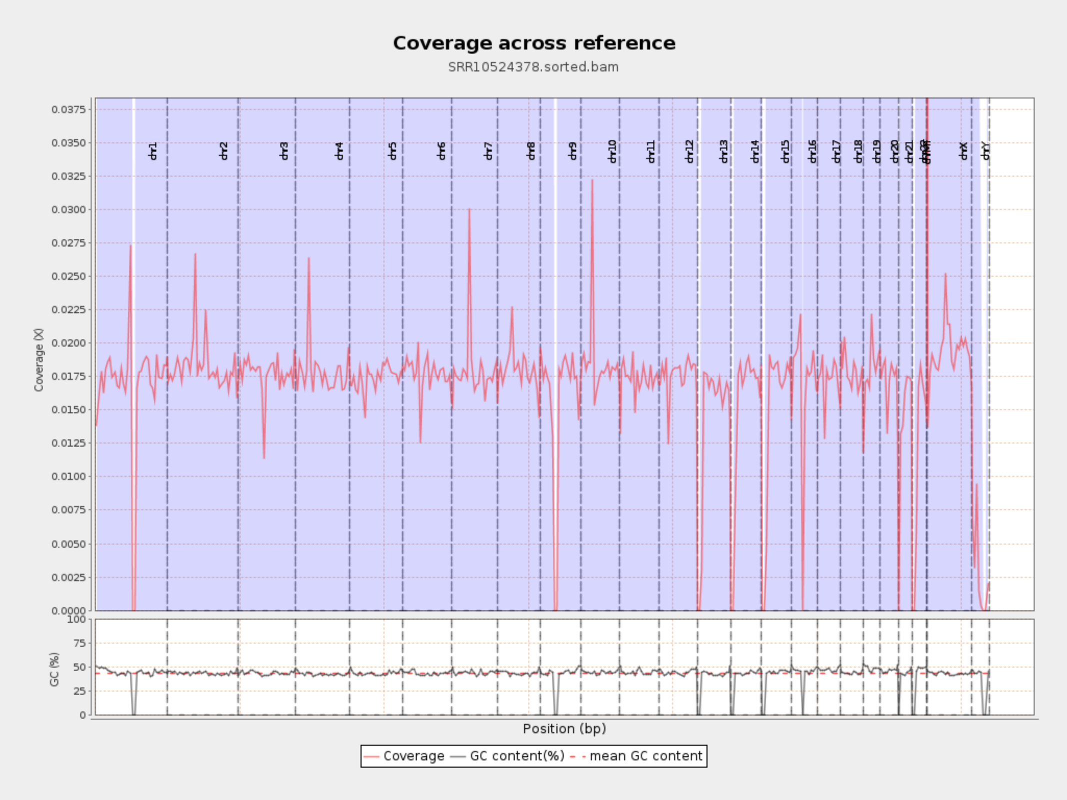
General error rate	0.51%
Mismatches	259,743
Insertions	3,166
Mapped reads with at least one insertion	0.35%
Deletions	10,580
Mapped reads with at least one deletion	1.17%
Homopolymer indels	43.93%

2.6. Chromosome stats

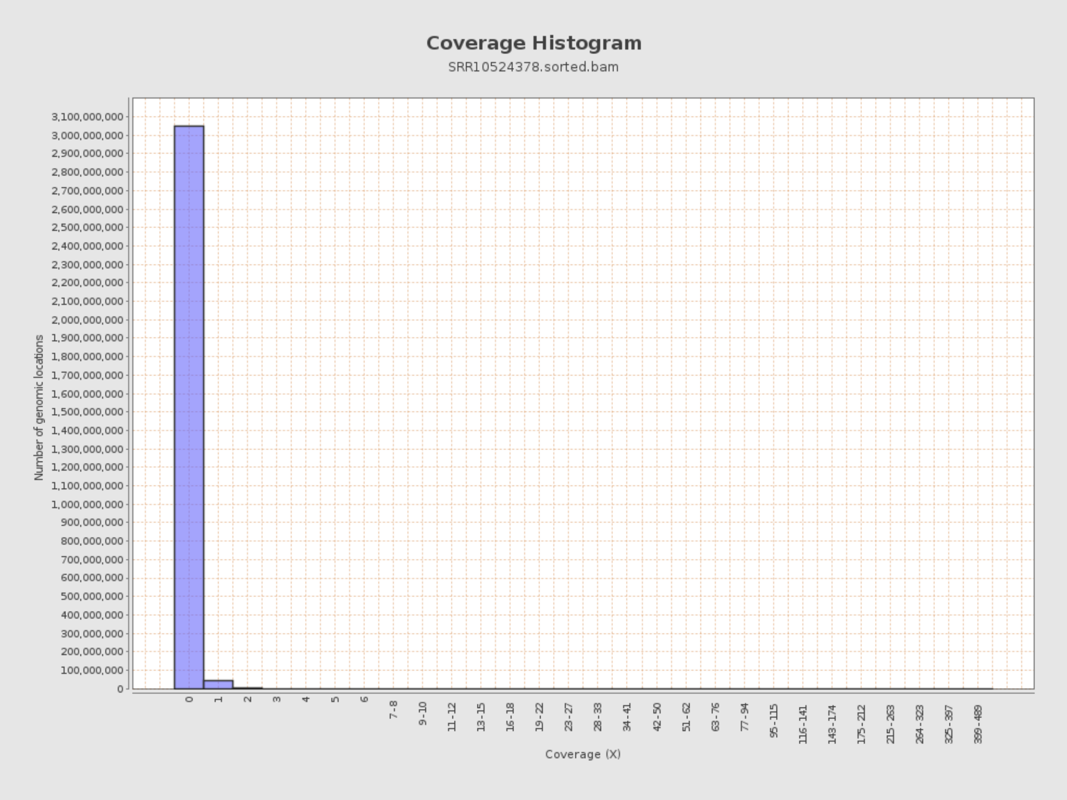
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4164606	0.0167	0.3056
chr2	243199373	4446617	0.0183	0.2509
chr3	198022430	3488789	0.0176	0.1417
chr4	191154276	3418195	0.0179	0.1489
chr5	180915260	3156136	0.0174	0.1406
chr6	171115067	3022990	0.0177	0.149
chr7	159138663	2878052	0.0181	0.2435

chr8	146364022	2643882	0.0181	0.1981
chr9	141213431	2195231	0.0155	0.159
chr10	135534747	2532877	0.0187	0.1828
chr11	135006516	2346168	0.0174	0.1608
chr12	133851895	2360698	0.0176	0.142
chr13	115169878	1609621	0.014	0.1259
chr14	107349540	1583961	0.0148	0.1312
chr15	102531392	1481908	0.0145	0.1273
chr16	90354753	1504141	0.0166	0.1466
chr17	81195210	1398104	0.0172	0.1418
chr18	78077248	1397057	0.0179	0.2503
chr19	59128983	1073725	0.0182	0.2286
chr20	63025520	1081439	0.0172	0.1403
chr21	48129895	689902	0.0143	0.1345
chr22	51304566	596808	0.0116	0.1143
chrMT	16571	6070	0.3663	0.619
chrX	155270560	3021717	0.0195	0.1563
chrY	59373566	162464	0.0027	0.0889

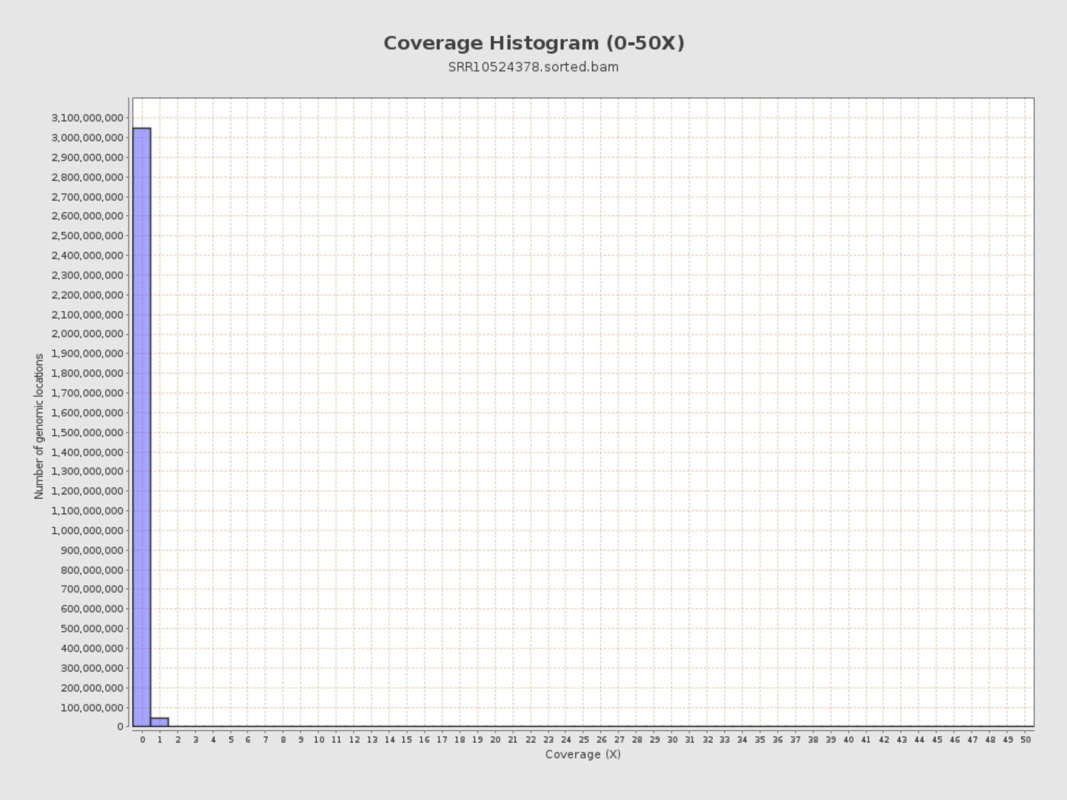
3. Results : Coverage across reference



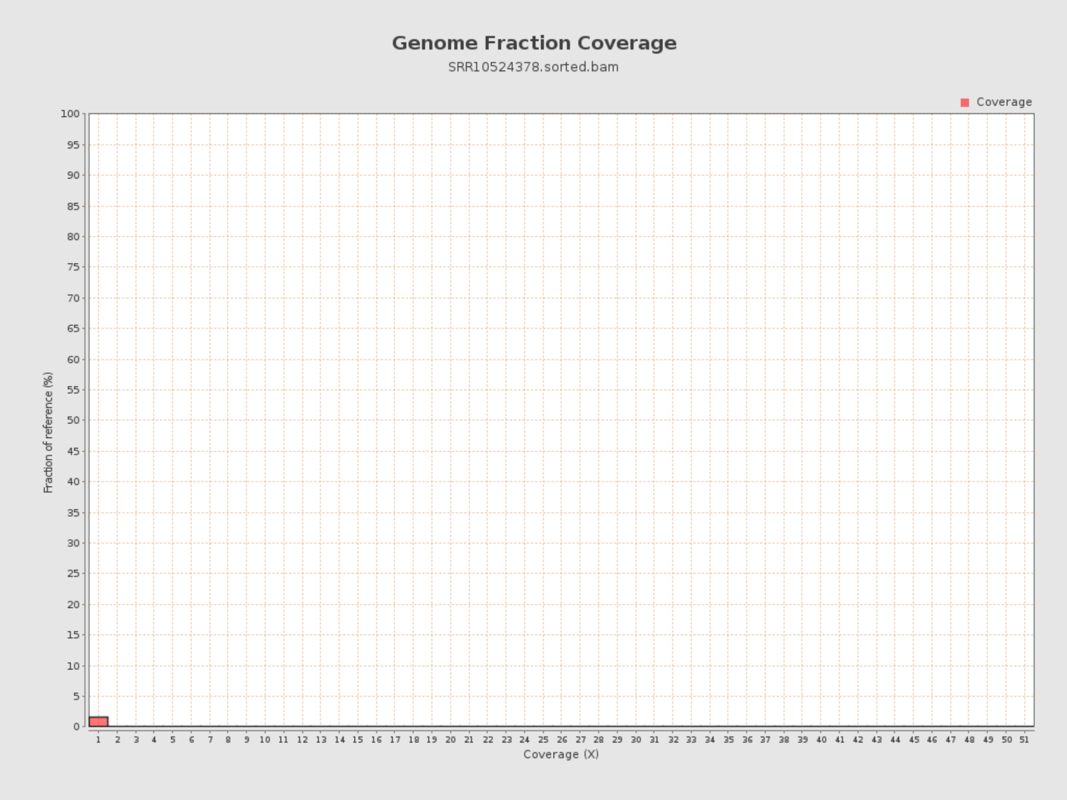
4. Results : Coverage Histogram



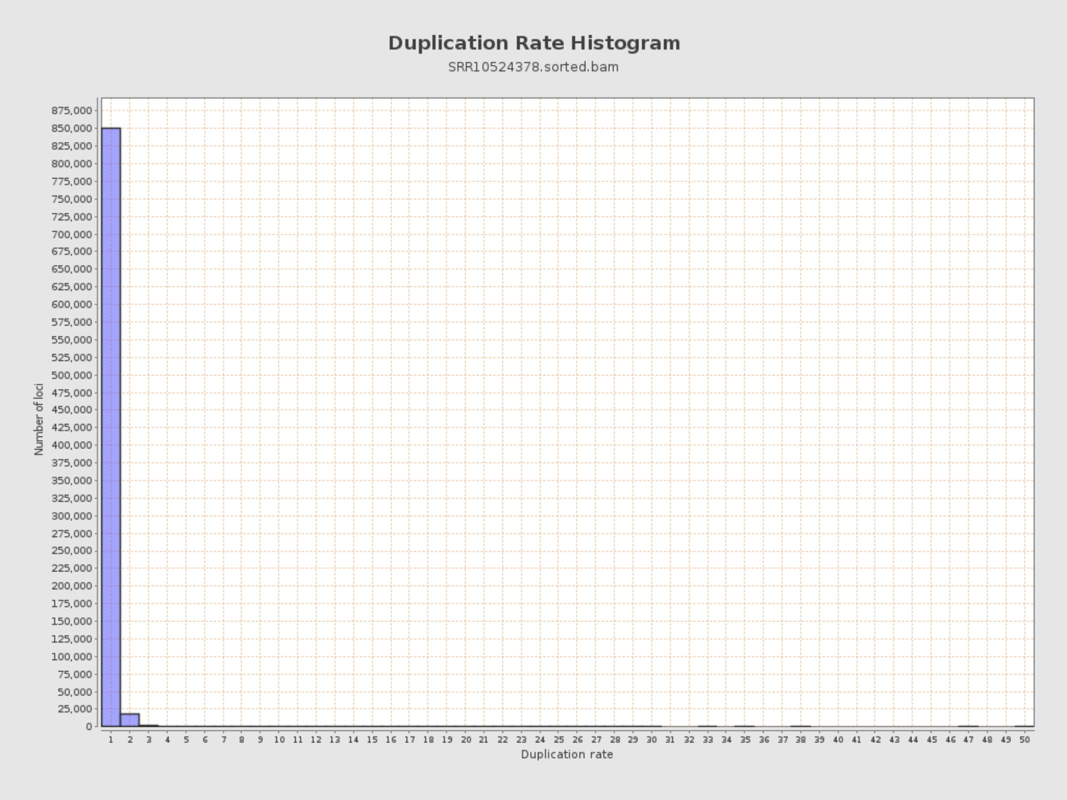
5. Results : Coverage Histogram (0-50X)



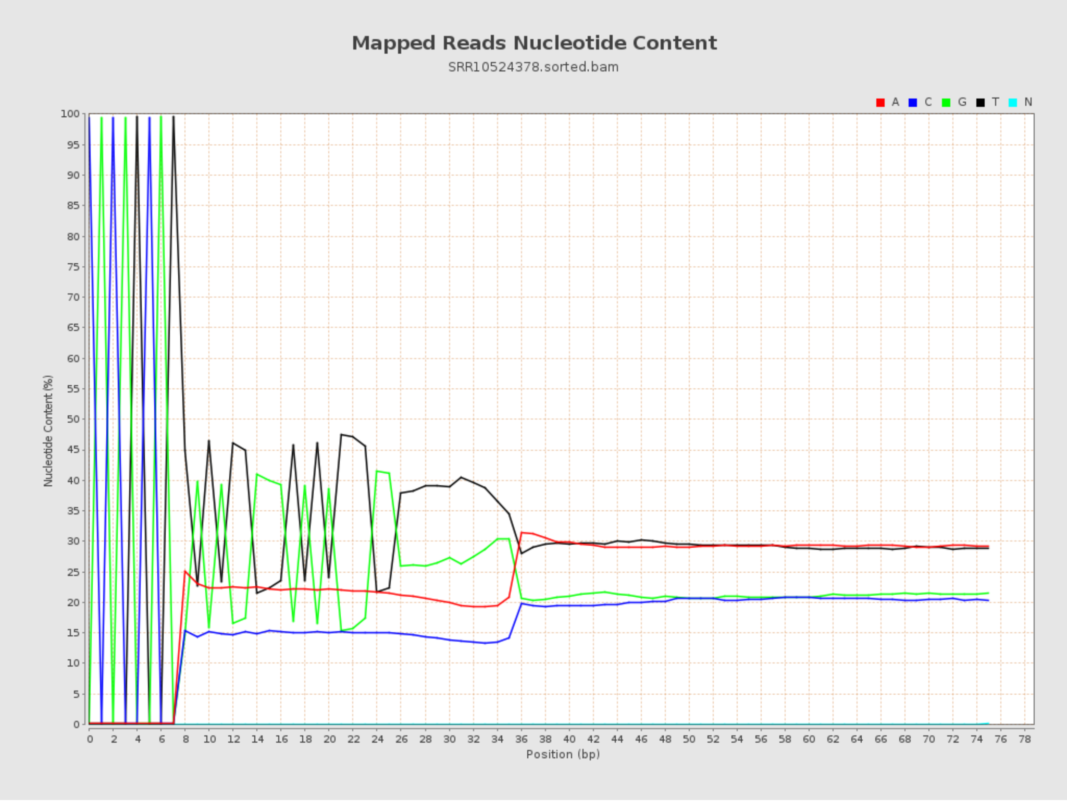
6. Results : Genome Fraction Coverage



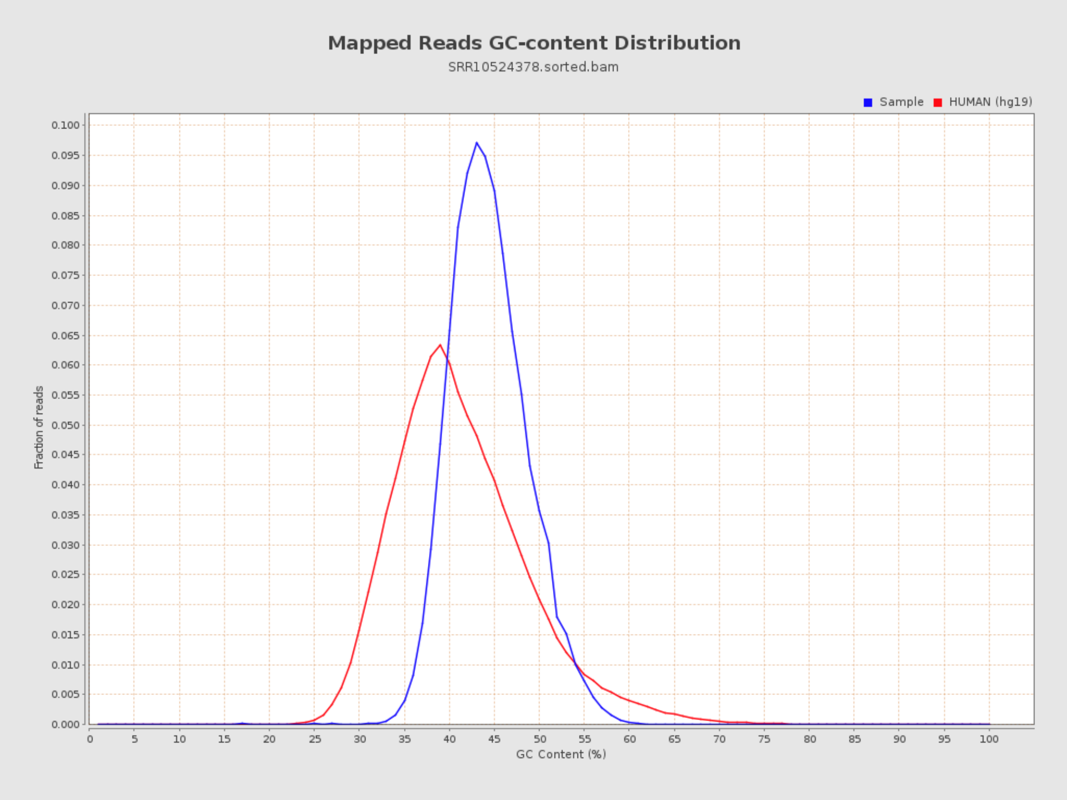
7. Results : Duplication Rate Histogram



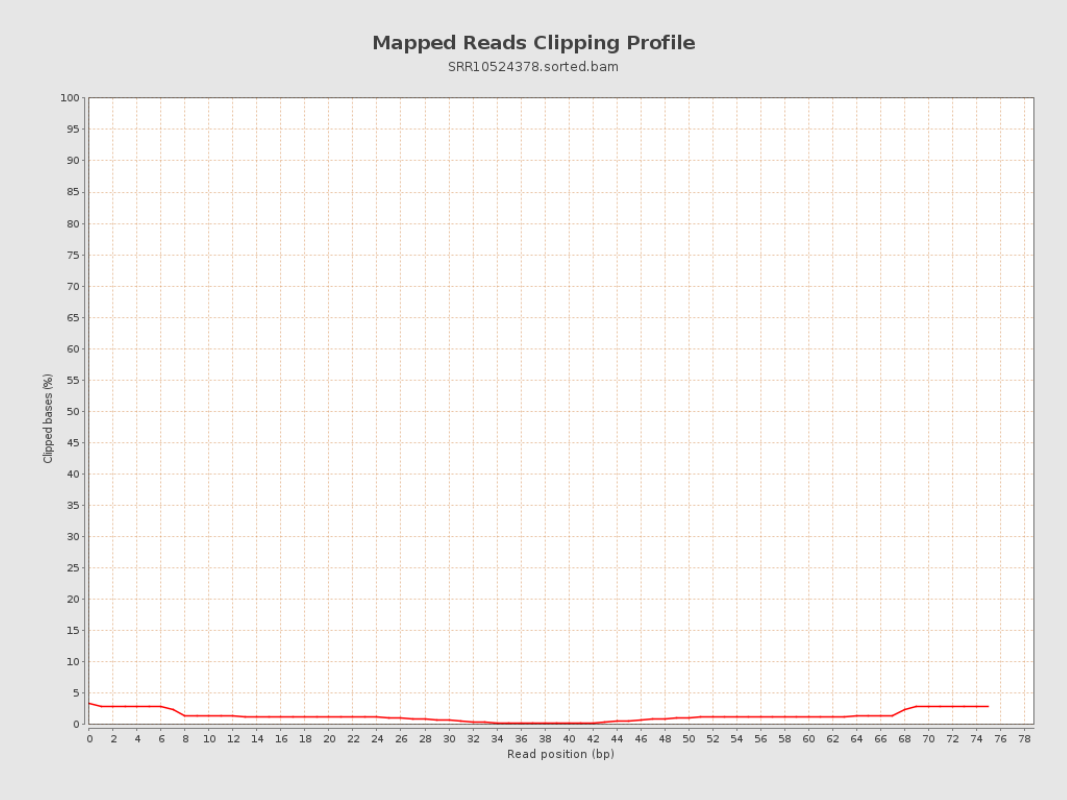
8. Results : Mapped Reads Nucleotide Content



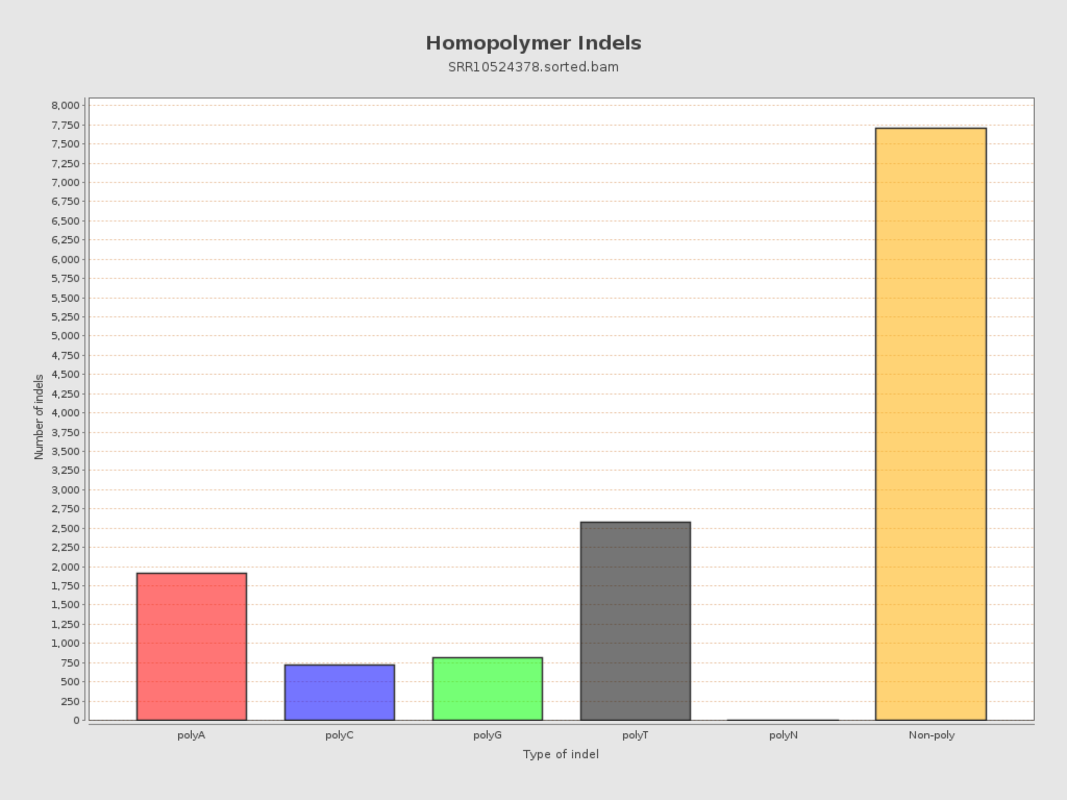
9. Results : Mapped Reads GC-content Distribution



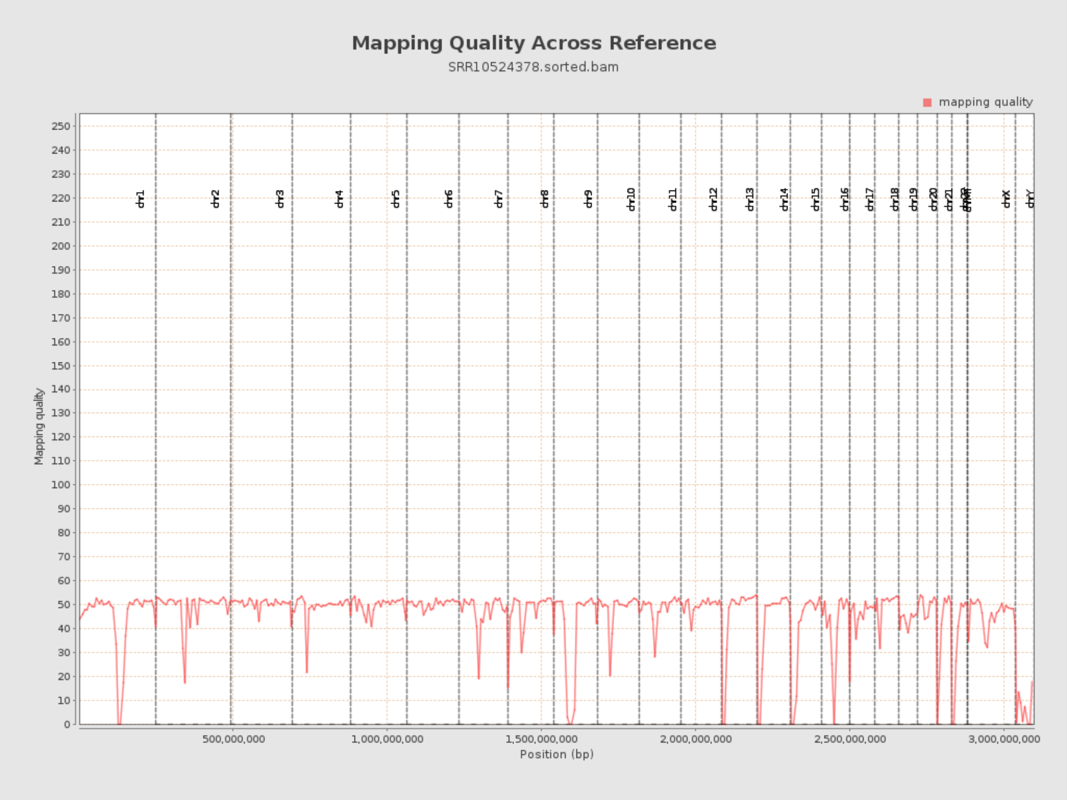
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram