Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 11:28:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524573.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_SRR10524573 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524573.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 11:28:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524573.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,495,412
Mapped reads	1,357,112 / 90.75%
Unmapped reads	138,300 / 9.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,688 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	46,511 / 3.11%
Duplication rate	2.5%
Clipped reads	1,359,024 / 90.88%

2.2. ACGT Content

Number/percentage of A's	19,249,672 / 24.55%
Number/percentage of C's	13,972,659 / 17.82%
Number/percentage of T's	25,913,570 / 33.05%
Number/percentage of G's	19,276,343 / 24.58%
Number/percentage of N's	1,084 / 0%
GC Percentage	42.4%

2.3. Coverage

Mean	0.0253

Standard Deviation	0.246

2.4. Mapping Quality

Mean Mapping Quality	44.61

2.5. Mismatches and indels

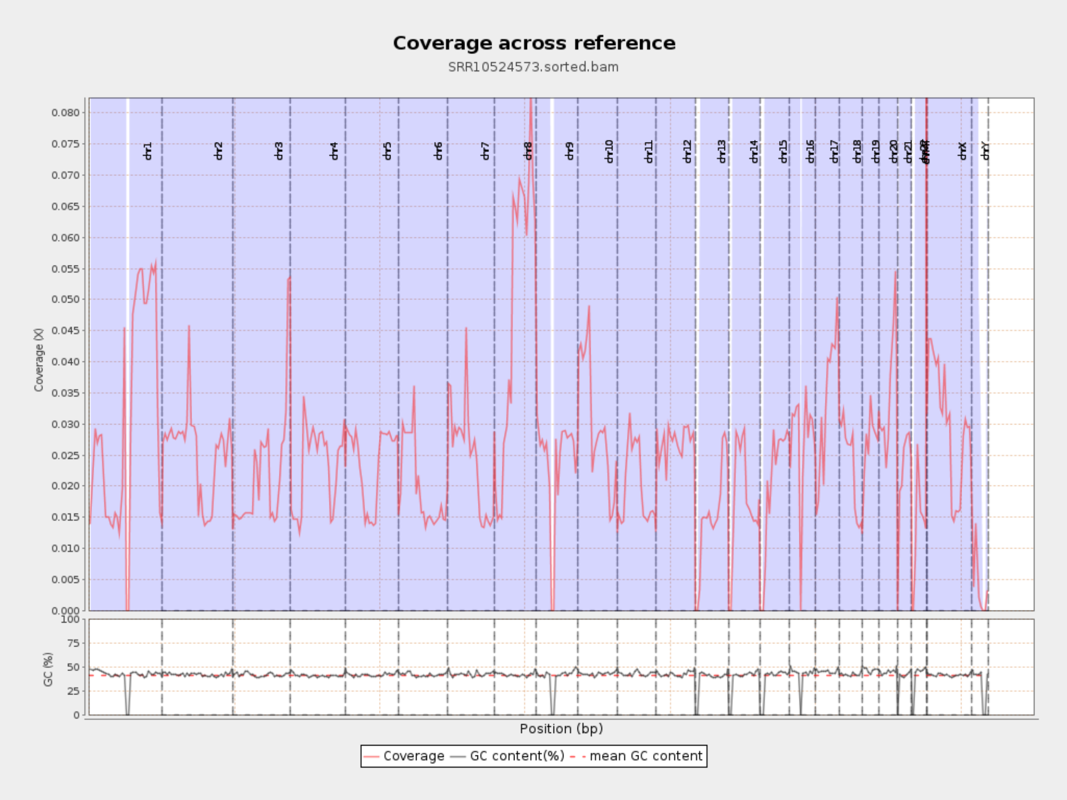
General error rate	0.53%
Mismatches	403,071
Insertions	5,798
Mapped reads with at least one insertion	0.43%
Deletions	15,118
Mapped reads with at least one deletion	1.11%
Homopolymer indels	42.22%

2.6. Chromosome stats

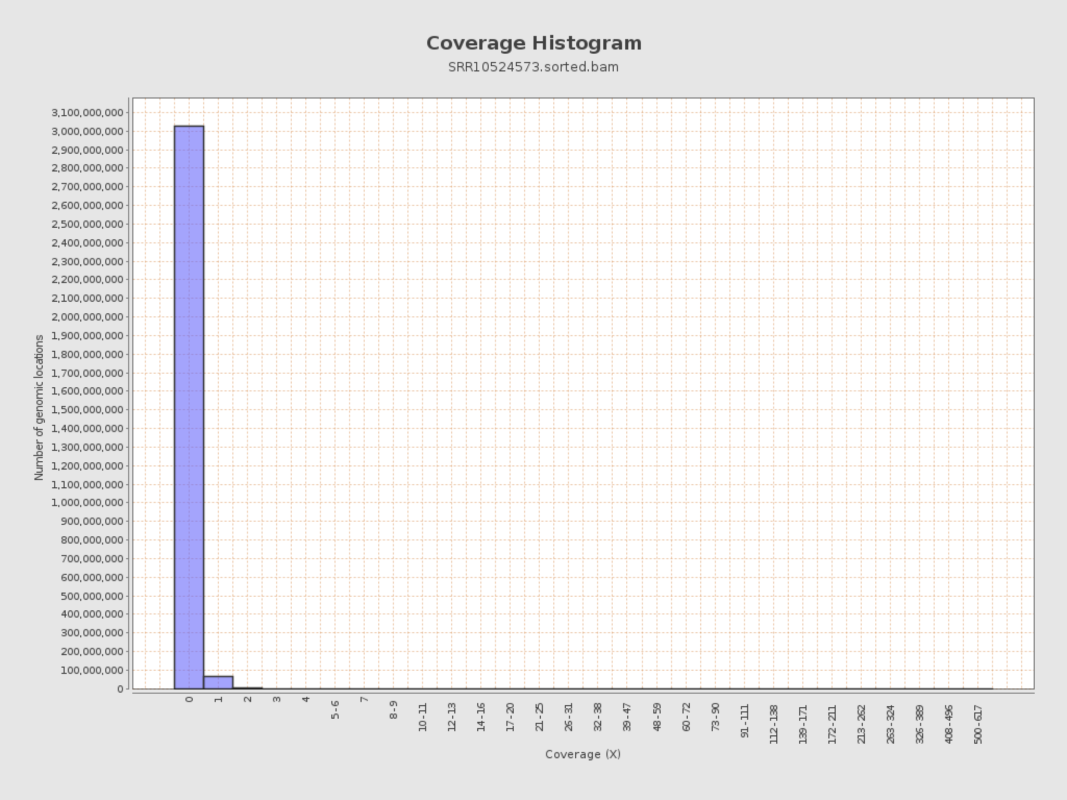
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7696049	0.0309	0.4481
chr2	243199373	6214697	0.0256	0.2784
chr3	198022430	4269511	0.0216	0.1611
chr4	191154276	4449098	0.0233	0.1823
chr5	180915260	4306501	0.0238	0.1673
chr6	171115067	3388880	0.0198	0.187
chr7	159138663	3918596	0.0246	0.3156

chr8	146364022	7175822	0.049	0.2765
chr9	141213431	3301500	0.0234	0.2066
chr10	135534747	4111393	0.0303	0.2545
chr11	135006516	2714236	0.0201	0.2209
chr12	133851895	3638705	0.0272	0.179
chr13	115169878	1763227	0.0153	0.1335
chr14	107349540	1889557	0.0176	0.1457
chr15	102531392	2065991	0.0201	0.1573
chr16	90354753	2471523	0.0274	0.1895
chr17	81195210	2754074	0.0339	0.2075
chr18	78077248	1842921	0.0236	0.3759
chr19	59128983	1621268	0.0274	0.3184
chr20	63025520	2213567	0.0351	0.2024
chr21	48129895	1067526	0.0222	0.1709
chr22	51304566	649081	0.0127	0.1209
chrMT	16571	4206	0.2538	0.5735
chrX	155270560	4664472	0.03	0.2083
chrY	59373566	245853	0.0041	0.1163

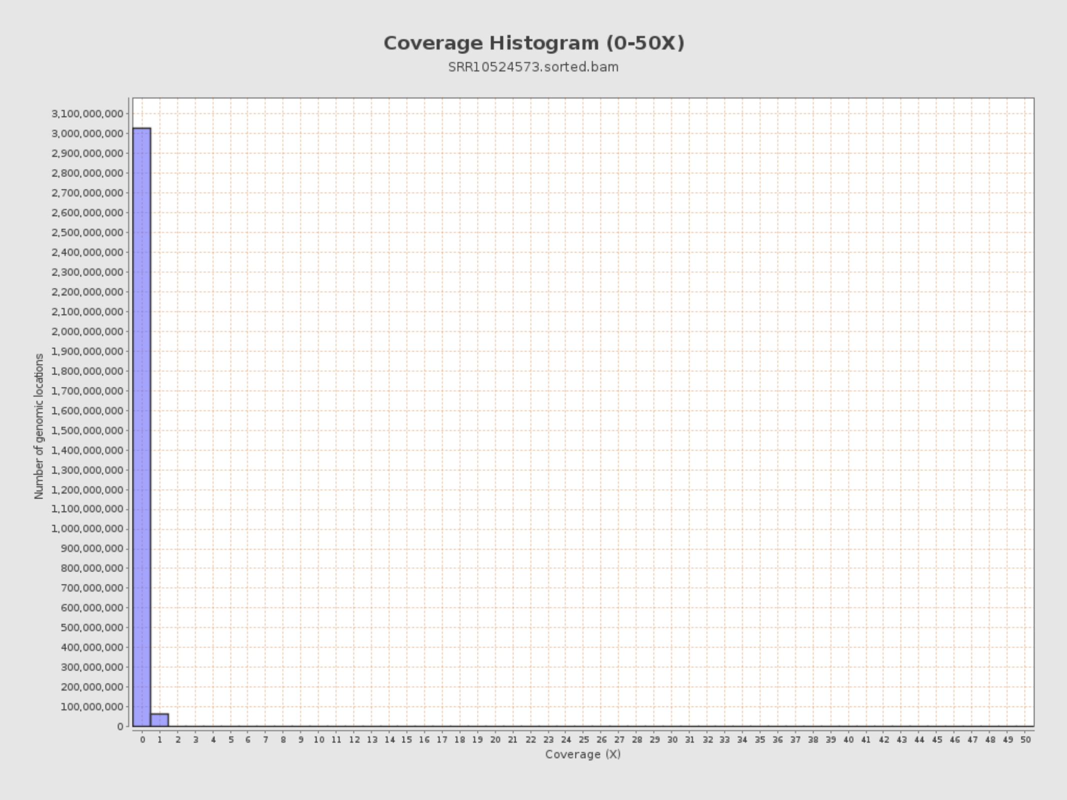
3. Results : Coverage across reference



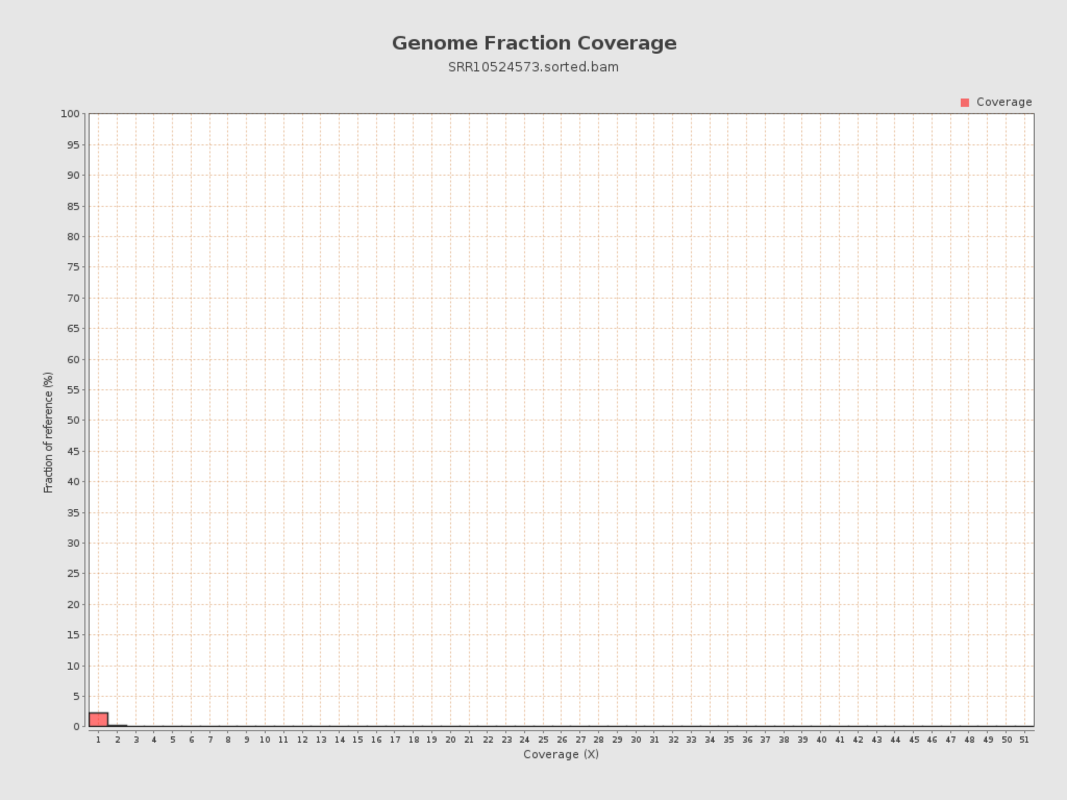
4. Results : Coverage Histogram



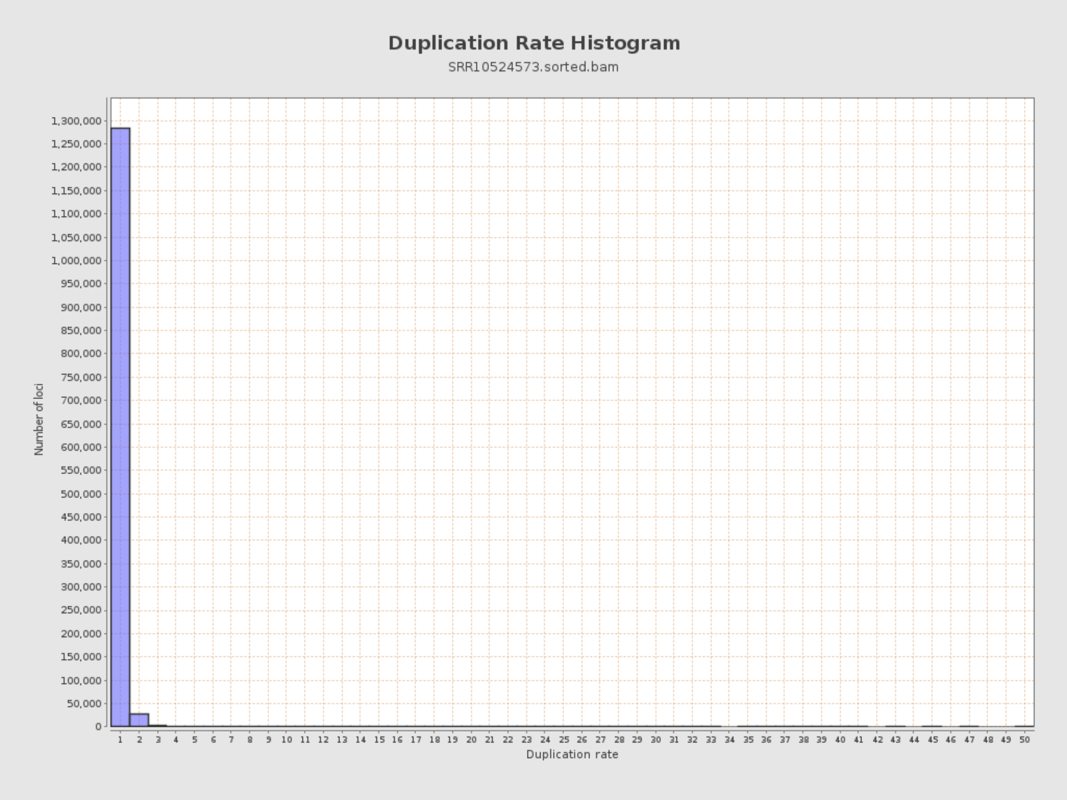
5. Results : Coverage Histogram (0-50X)



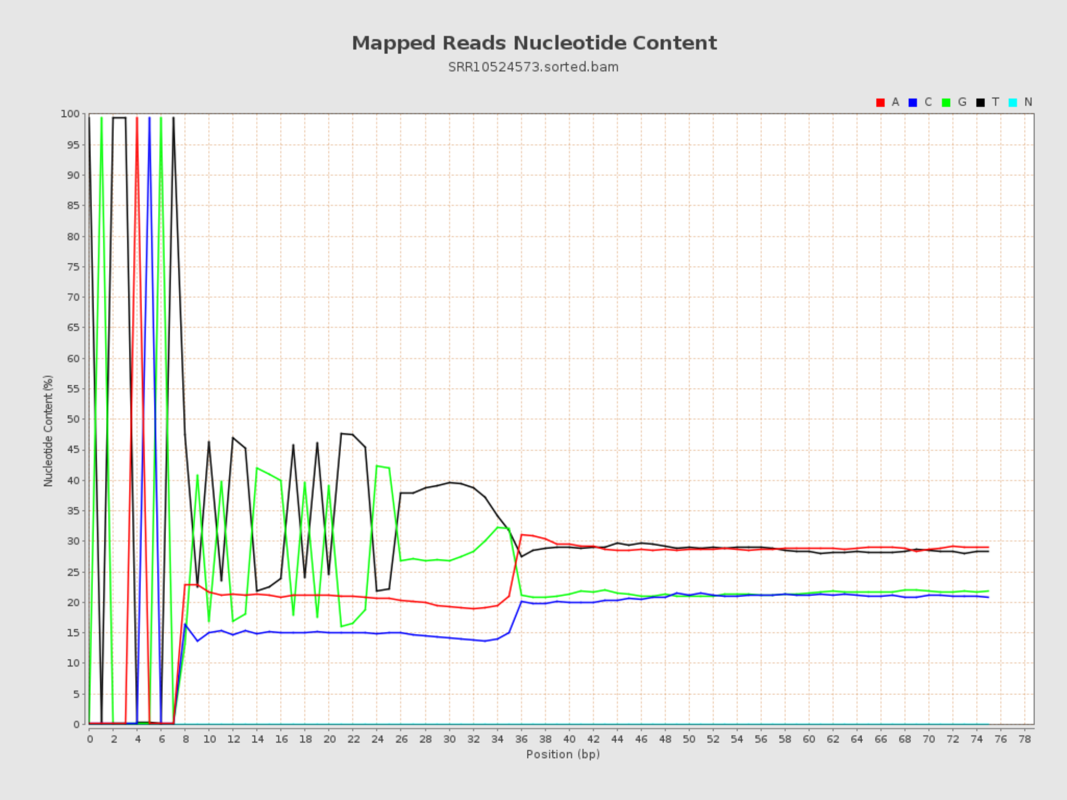
6. Results : Genome Fraction Coverage



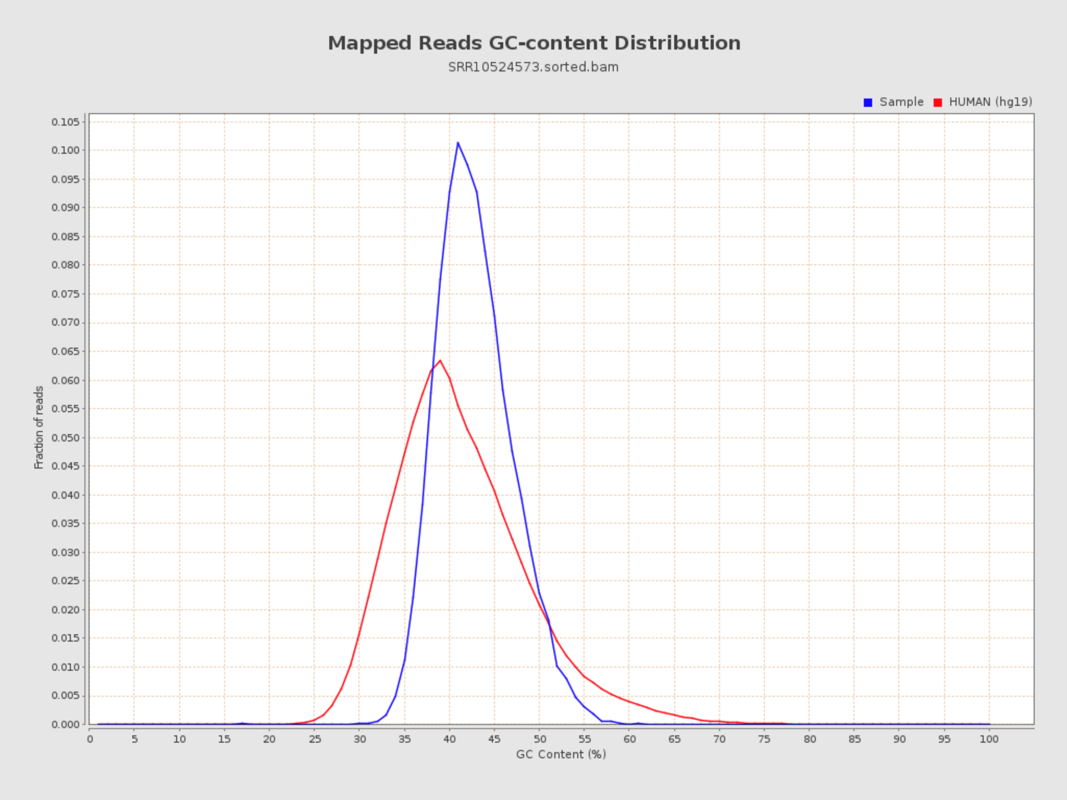
7. Results : Duplication Rate Histogram



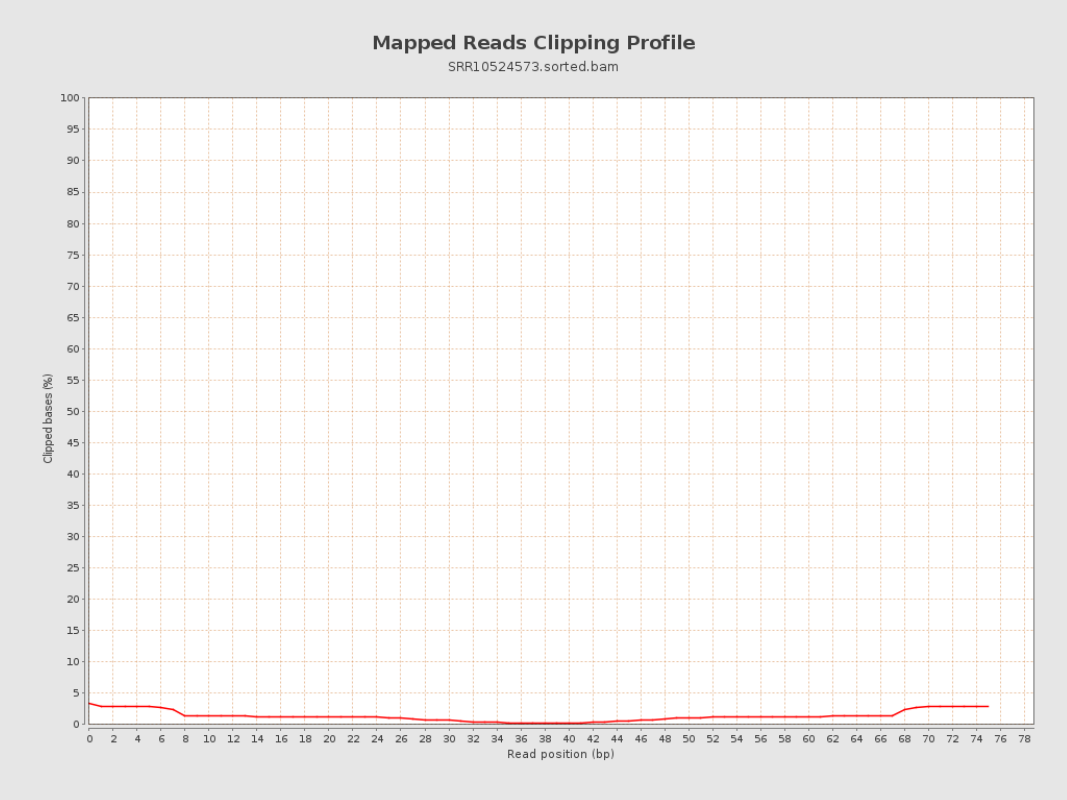
8. Results : Mapped Reads Nucleotide Content



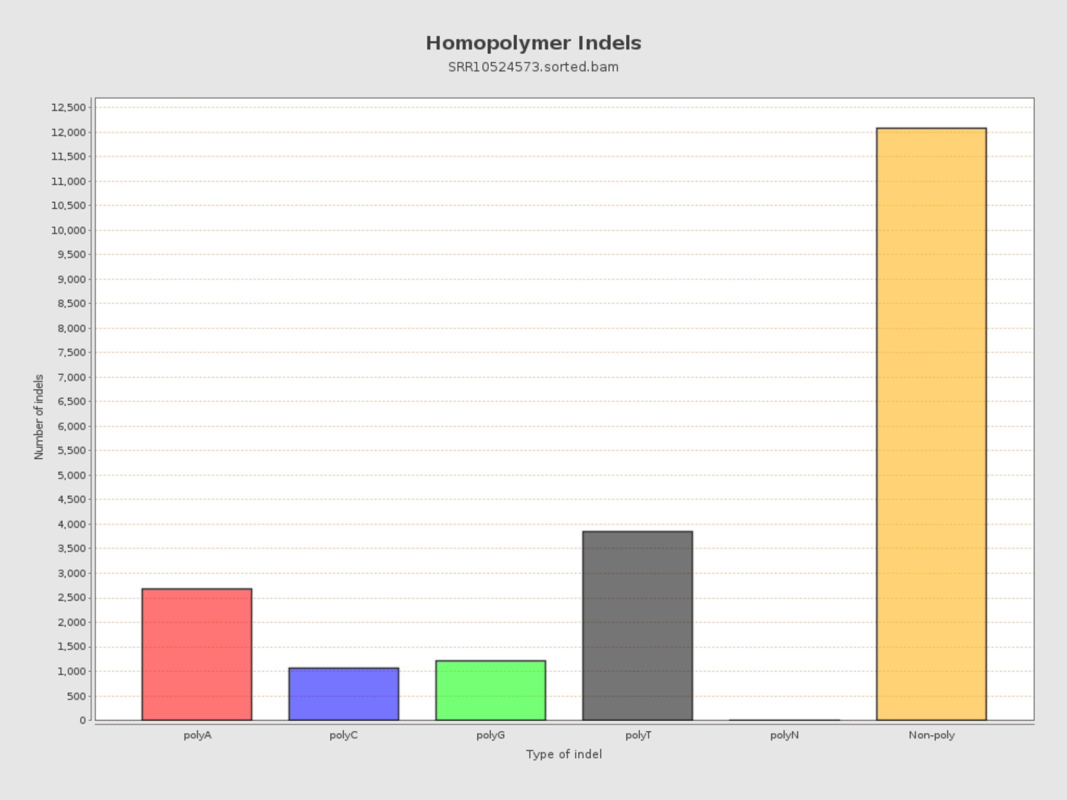
9. Results : Mapped Reads GC-content Distribution



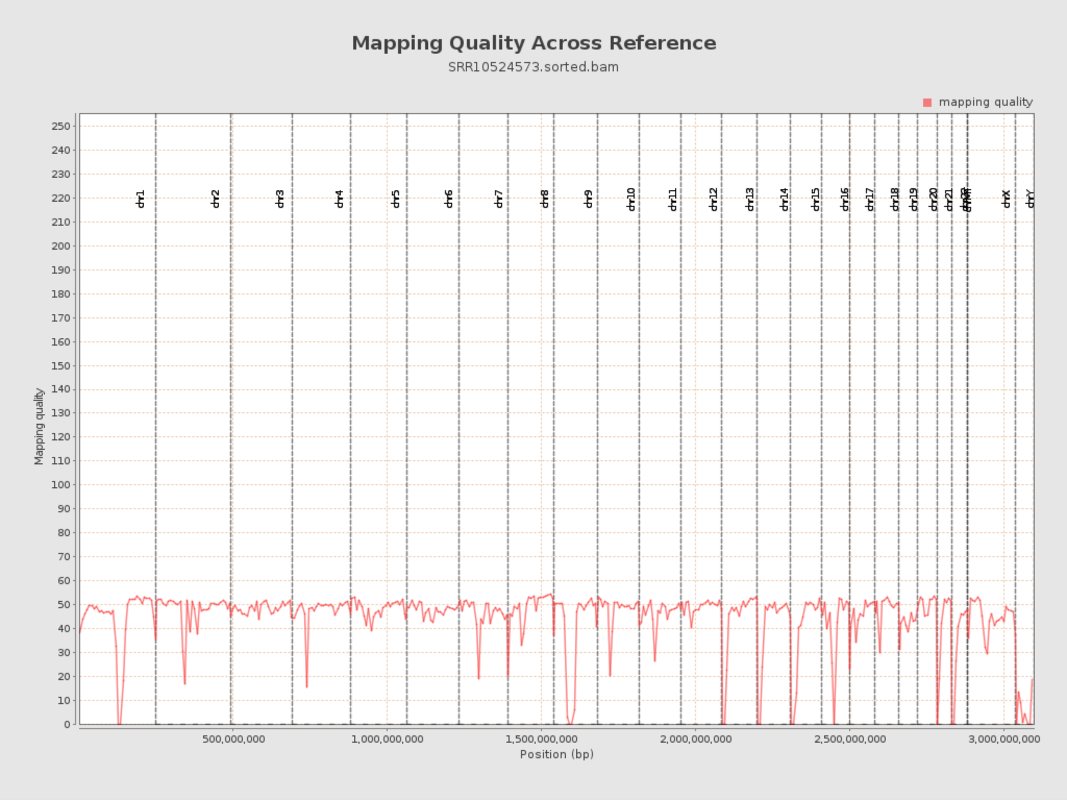
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram