Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 15:57:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524673.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_SRR10524673 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524673.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 15:57:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524673.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,027,963
Mapped reads	951,964 / 92.61%
Unmapped reads	75,999 / 7.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,351 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	27,720 / 2.7%
Duplication rate	2.12%
Clipped reads	953,084 / 92.72%

2.2. ACGT Content

Number/percentage of A's	13,893,129 / 24.61%
Number/percentage of C's	11,088,355 / 19.64%
Number/percentage of T's	18,450,404 / 32.68%
Number/percentage of G's	13,022,736 / 23.06%
Number/percentage of N's	7,772 / 0.01%
GC Percentage	42.7%

2.3. Coverage

Mean	0.0182

Standard Deviation	0.1956

2.4. Mapping Quality

Mean Mapping Quality	45.92

2.5. Mismatches and indels

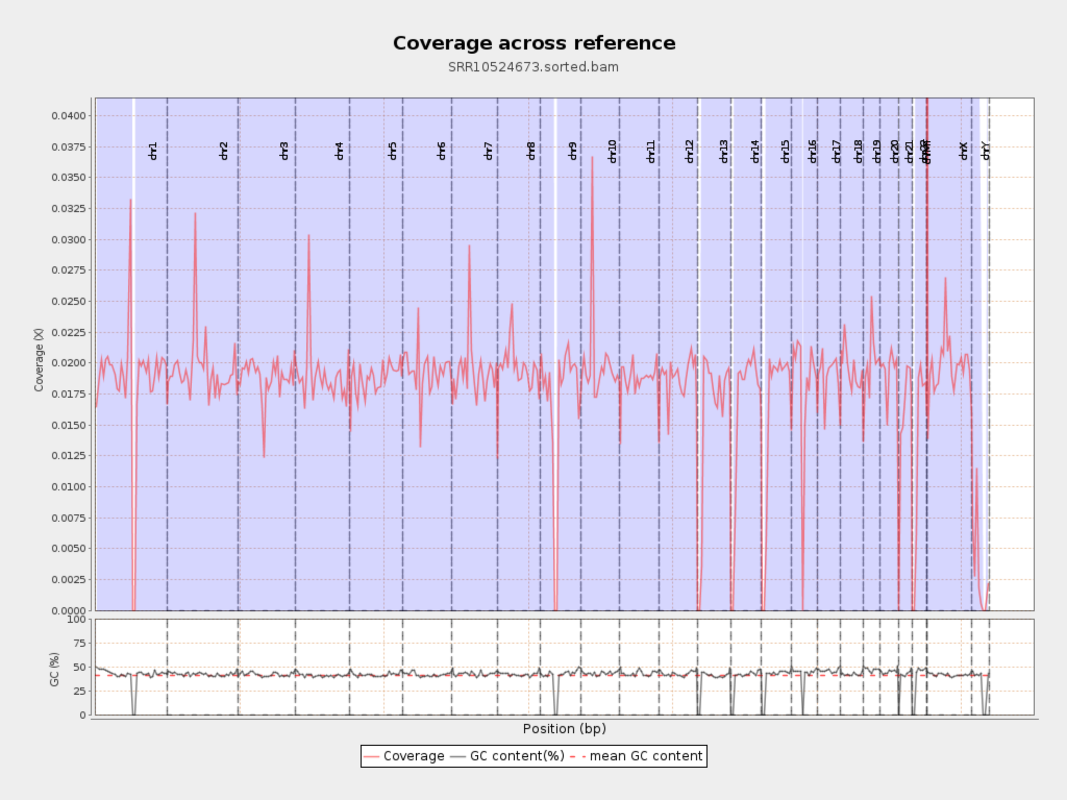
General error rate	0.51%
Mismatches	282,464
Insertions	4,202
Mapped reads with at least one insertion	0.44%
Deletions	10,777
Mapped reads with at least one deletion	1.12%
Homopolymer indels	44.29%

2.6. Chromosome stats

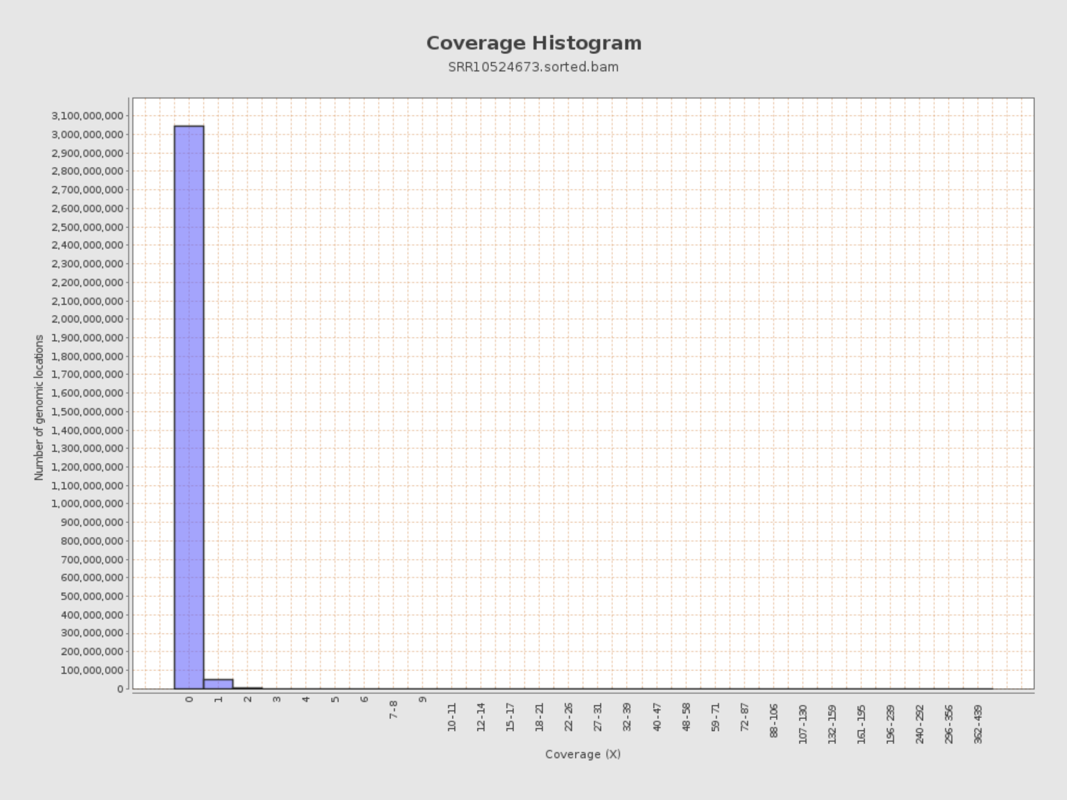
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4598207	0.0184	0.3359
chr2	243199373	4750568	0.0195	0.2484
chr3	198022430	3725627	0.0188	0.1444
chr4	191154276	3648077	0.0191	0.1567
chr5	180915260	3423329	0.0189	0.1453
chr6	171115067	3314816	0.0194	0.1618
chr7	159138663	3088695	0.0194	0.223

chr8	146364022	2894596	0.0198	0.2106
chr9	141213431	2368595	0.0168	0.1611
chr10	135534747	2726827	0.0201	0.2027
chr11	135006516	2547691	0.0189	0.1795
chr12	133851895	2530109	0.0189	0.1462
chr13	115169878	1782338	0.0155	0.1325
chr14	107349540	1715771	0.016	0.1353
chr15	102531392	1620443	0.0158	0.1325
chr16	90354753	1599836	0.0177	0.1478
chr17	81195210	1541791	0.019	0.1499
chr18	78077248	1519642	0.0195	0.281
chr19	59128983	1189683	0.0201	0.2532
chr20	63025520	1206314	0.0191	0.1479
chr21	48129895	748363	0.0155	0.1418
chr22	51304566	661964	0.0129	0.1199
chrMT	16571	11428	0.6896	0.915
chrX	155270560	3082386	0.0199	0.1581
chrY	59373566	182374	0.0031	0.1177

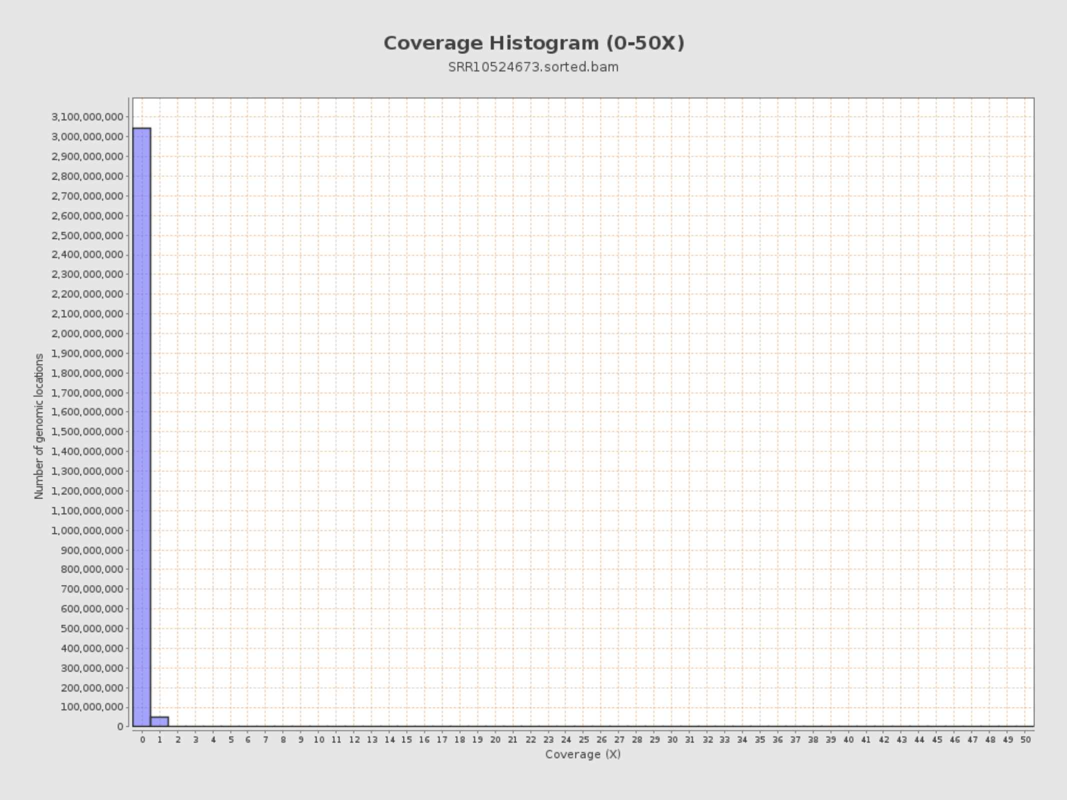
3. Results : Coverage across reference



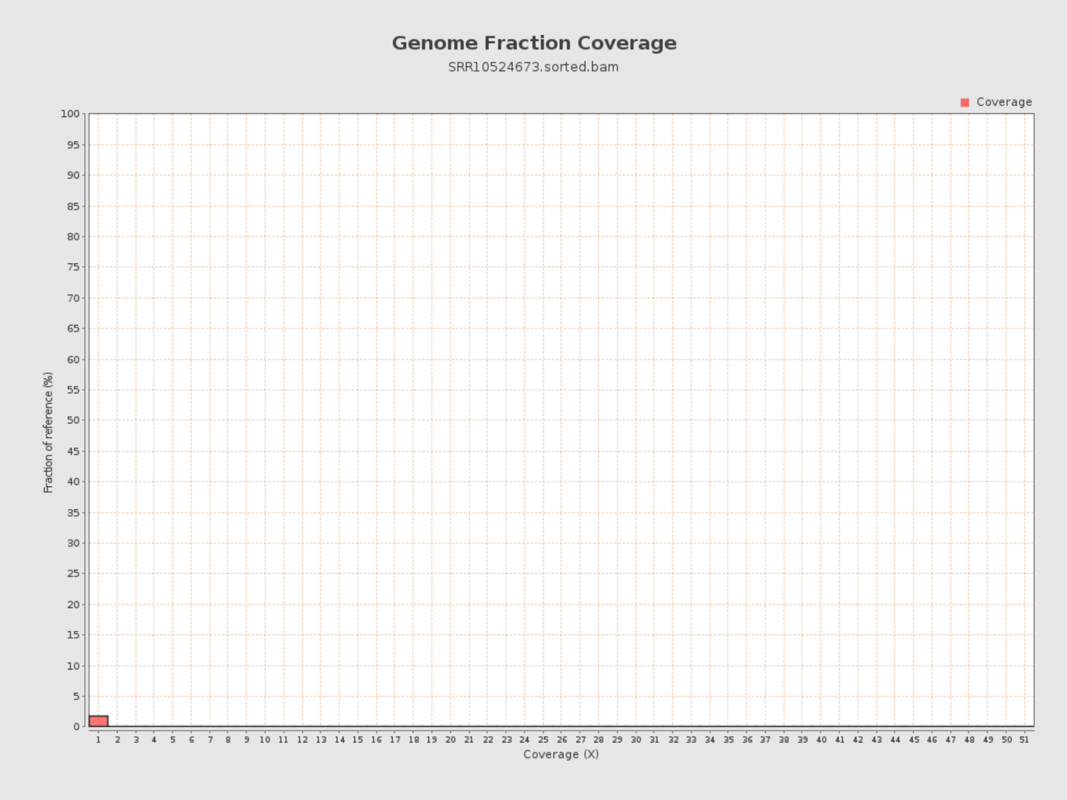
4. Results : Coverage Histogram



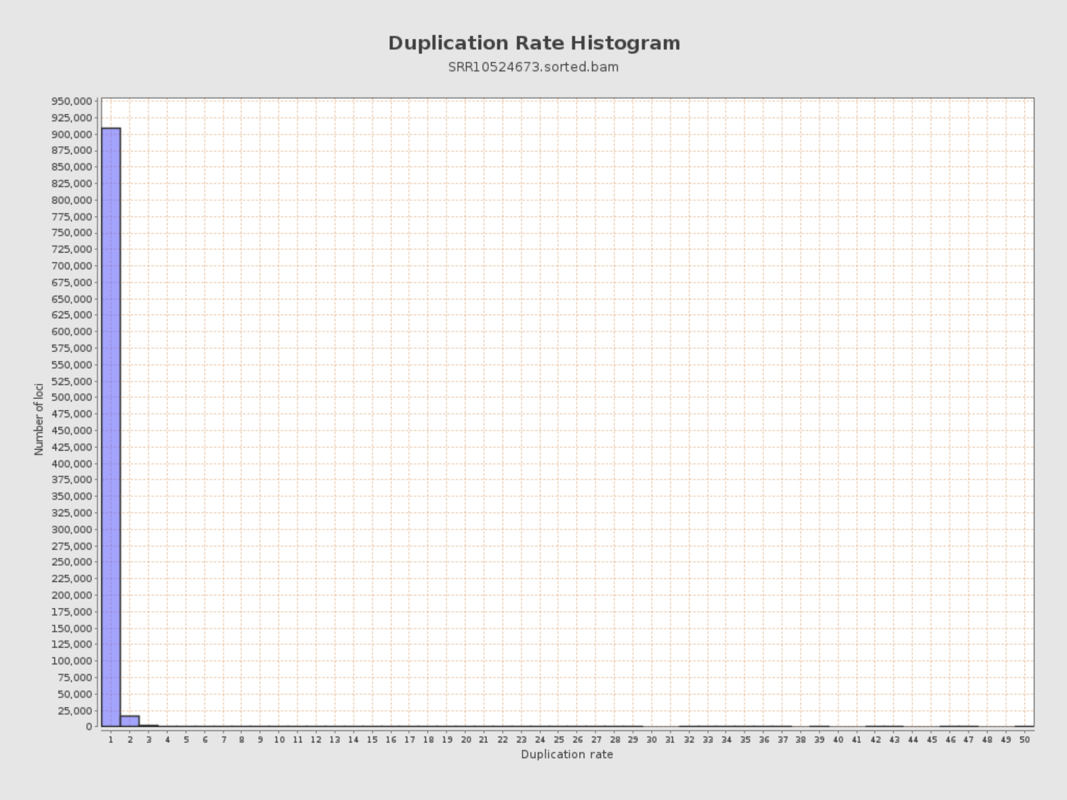
5. Results : Coverage Histogram (0-50X)



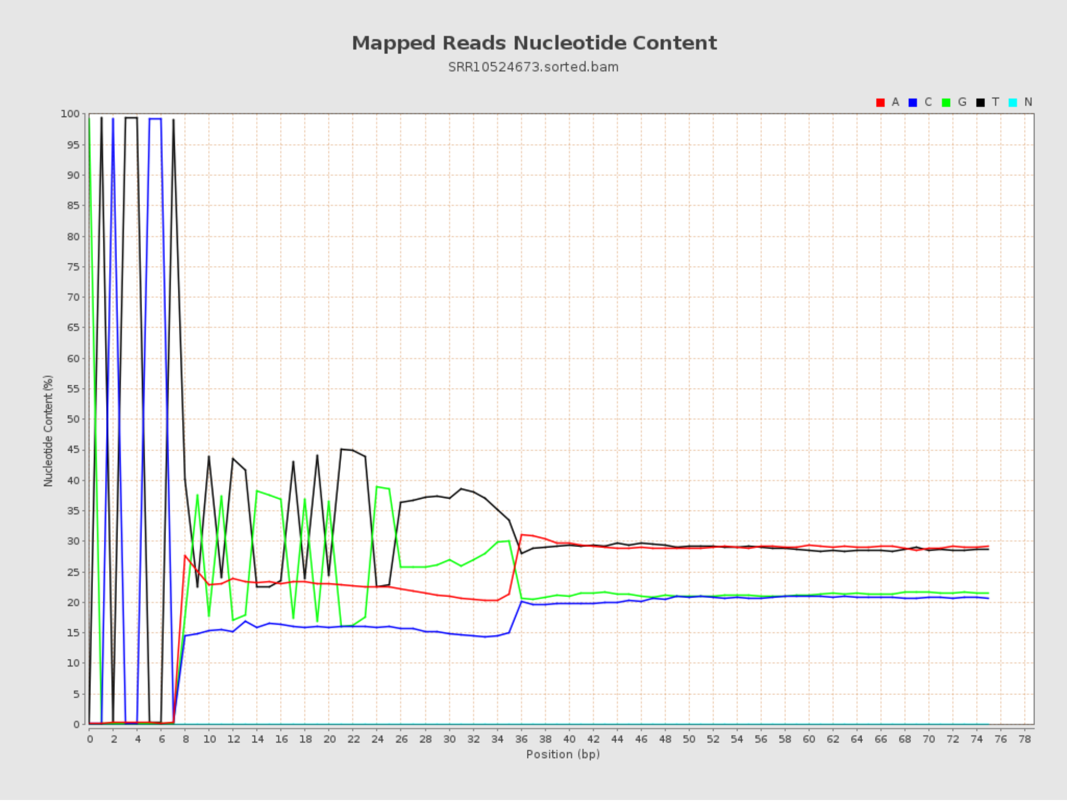
6. Results : Genome Fraction Coverage



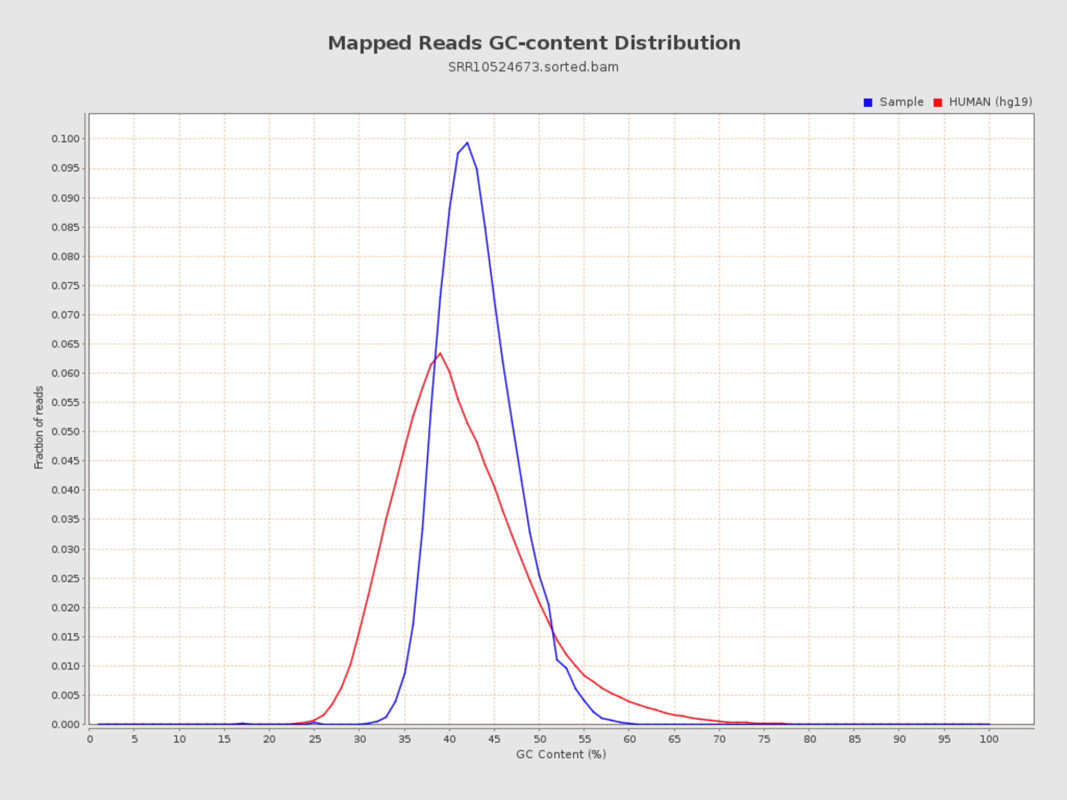
7. Results : Duplication Rate Histogram



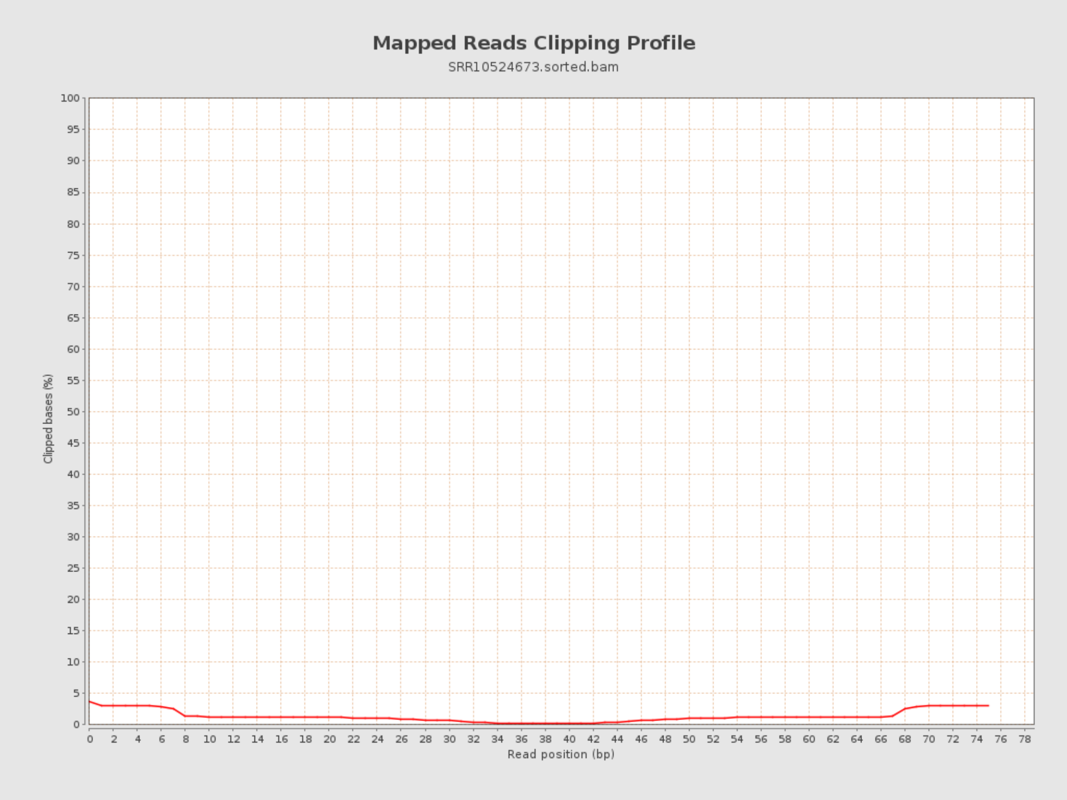
8. Results : Mapped Reads Nucleotide Content



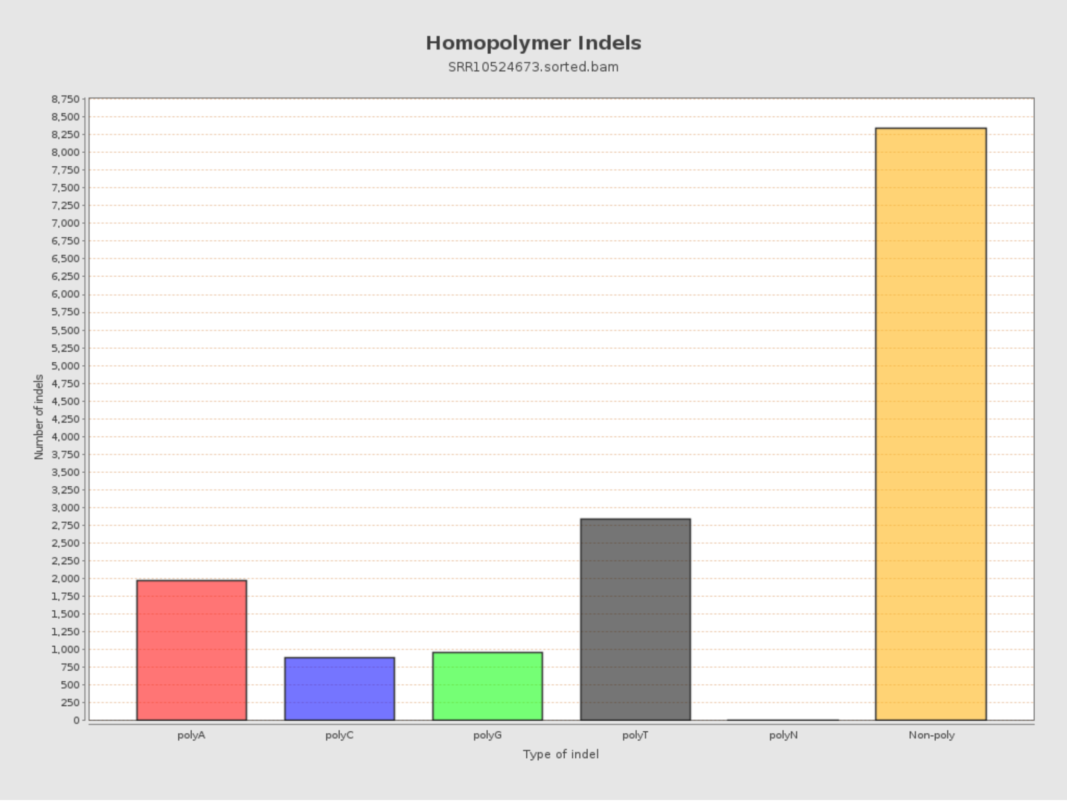
9. Results : Mapped Reads GC-content Distribution



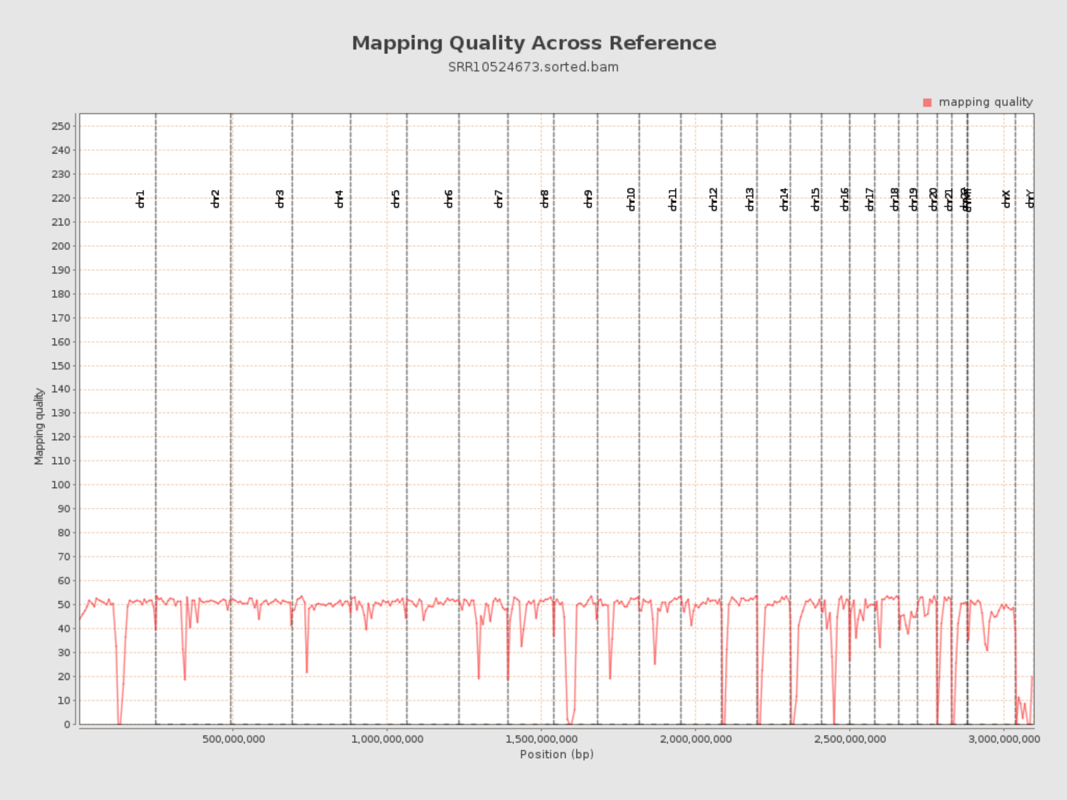
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram