Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 20:47:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524973.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_SRR10524973 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524973.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 20:47:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524973.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,696,170
Mapped reads	2,483,574 / 92.11%
Unmapped reads	212,596 / 7.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,765 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	151,473 / 5.62%
Duplication rate	4.6%
Clipped reads	2,481,918 / 92.05%

2.2. ACGT Content

Number/percentage of A's	36,976,660 / 25.75%
Number/percentage of C's	23,756,221 / 16.55%
Number/percentage of T's	46,474,782 / 32.37%
Number/percentage of G's	36,375,941 / 25.33%
Number/percentage of N's	1,769 / 0%
GC Percentage	41.88%

2.3. Coverage

Mean	0.0464

Standard Deviation	0.4053

2.4. Mapping Quality

Mean Mapping Quality	45.67

2.5. Mismatches and indels

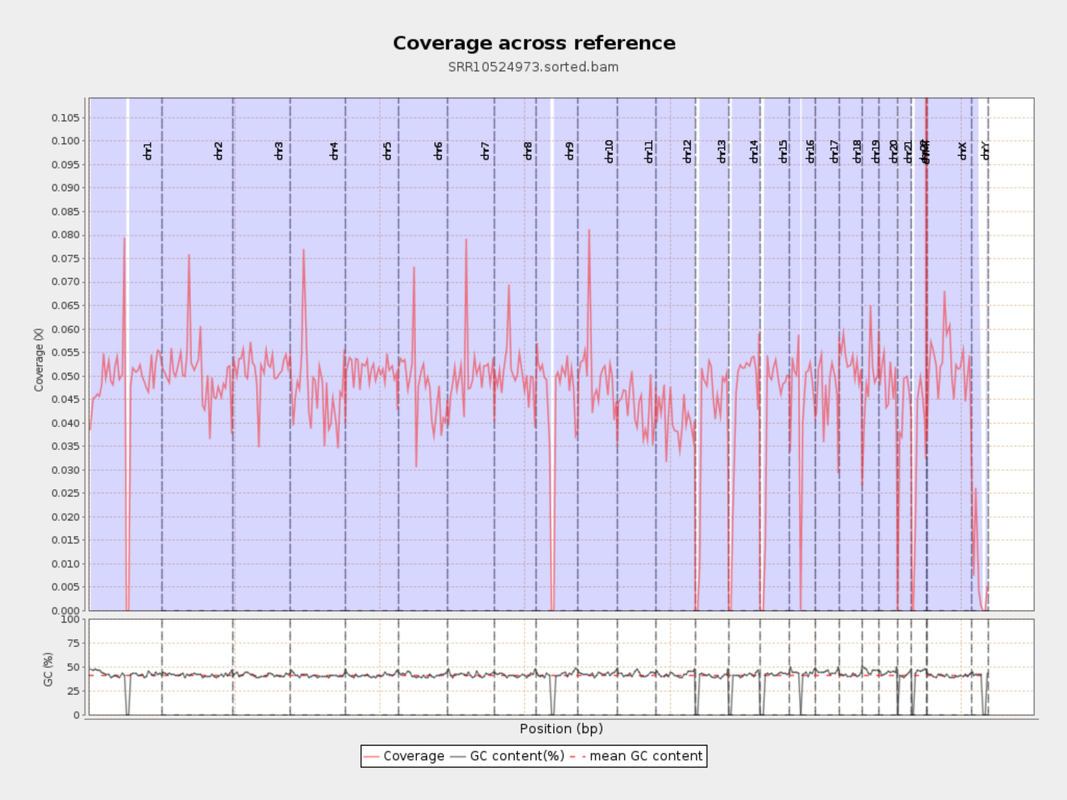
General error rate	0.49%
Mismatches	688,353
Insertions	9,794
Mapped reads with at least one insertion	0.39%
Deletions	25,338
Mapped reads with at least one deletion	1.01%
Homopolymer indels	43.72%

2.6. Chromosome stats

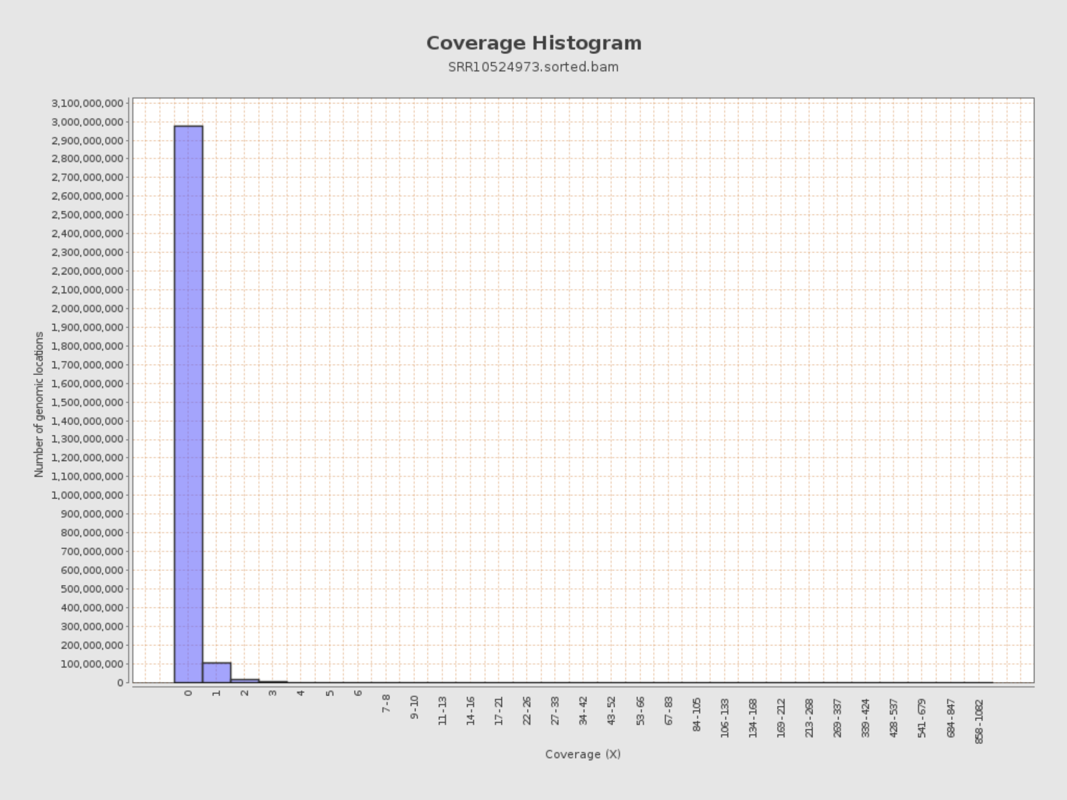
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11847135	0.0475	0.8074
chr2	243199373	12264647	0.0504	0.4417
chr3	198022430	10200683	0.0515	0.2663
chr4	191154276	8938386	0.0468	0.2908
chr5	180915260	9256534	0.0512	0.2661
chr6	171115067	8142999	0.0476	0.3528
chr7	159138663	8077738	0.0508	0.506

chr8	146364022	7380765	0.0504	0.4205
chr9	141213431	6128031	0.0434	0.3267
chr10	135534747	6870359	0.0507	0.3992
chr11	135006516	5787051	0.0429	0.3647
chr12	133851895	5433545	0.0406	0.24
chr13	115169878	4609282	0.04	0.2332
chr14	107349540	4561668	0.0425	0.2527
chr15	102531392	4126948	0.0403	0.2507
chr16	90354753	4066474	0.045	0.2699
chr17	81195210	3739625	0.0461	0.2946
chr18	78077248	4156842	0.0532	0.6173
chr19	59128983	2909556	0.0492	0.5145
chr20	63025520	3048290	0.0484	0.2652
chr21	48129895	1917296	0.0398	0.2615
chr22	51304566	1597444	0.0311	0.203
chrMT	16571	28386	1.713	1.8214
chrX	155270560	8108587	0.0522	0.3046
chrY	59373566	430249	0.0072	0.1991

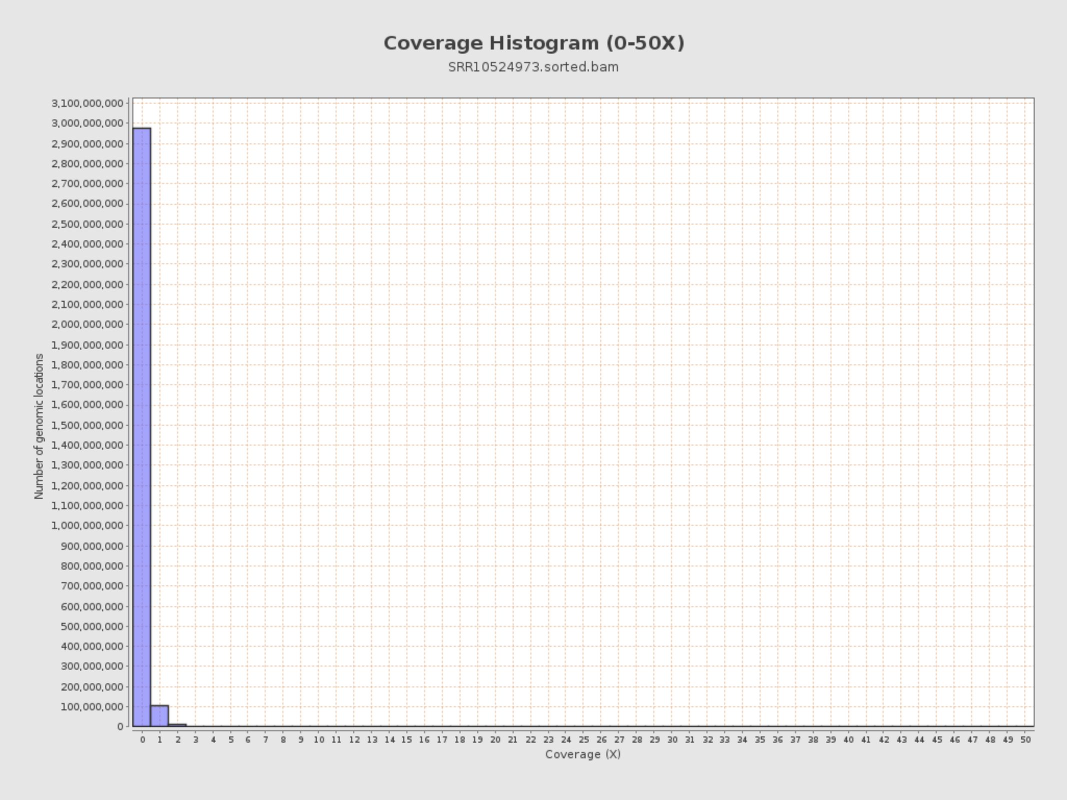
3. Results : Coverage across reference



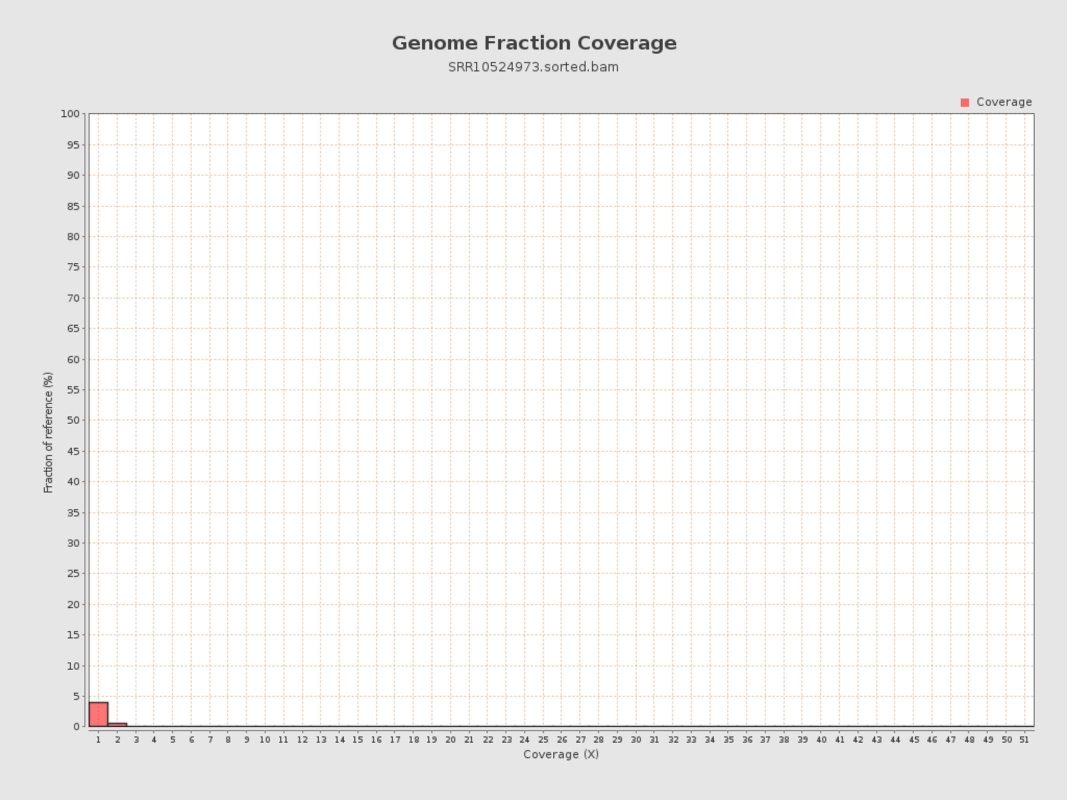
4. Results : Coverage Histogram



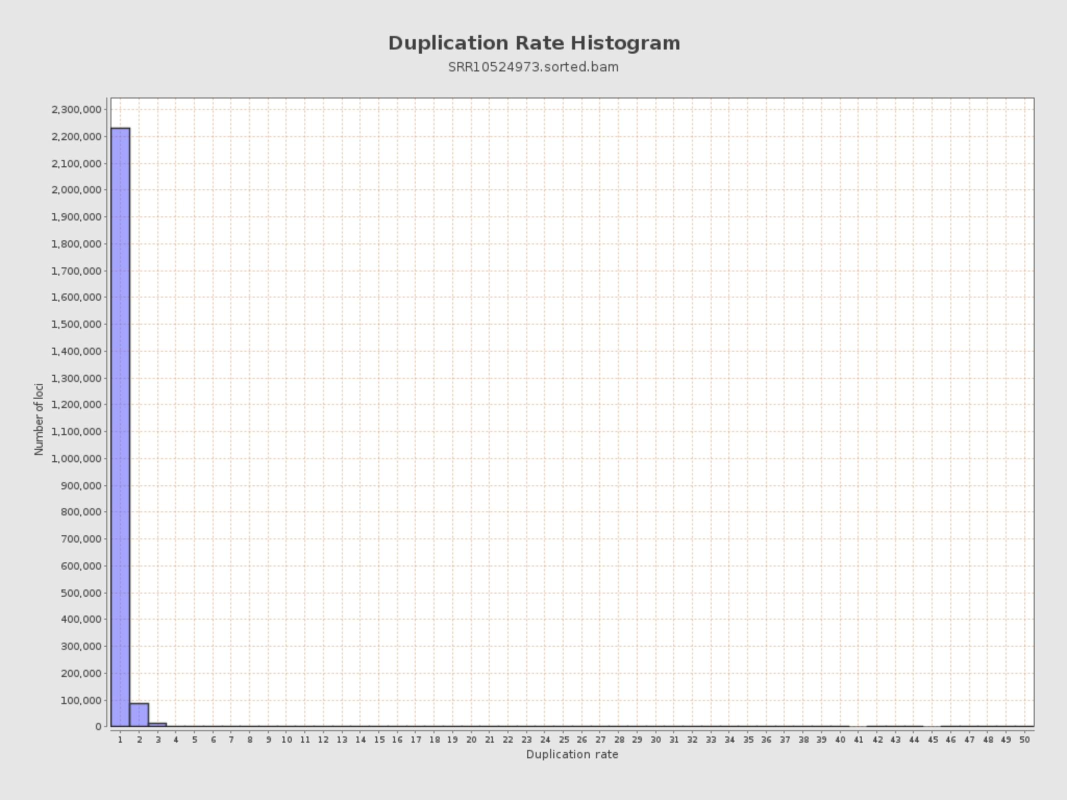
5. Results : Coverage Histogram (0-50X)



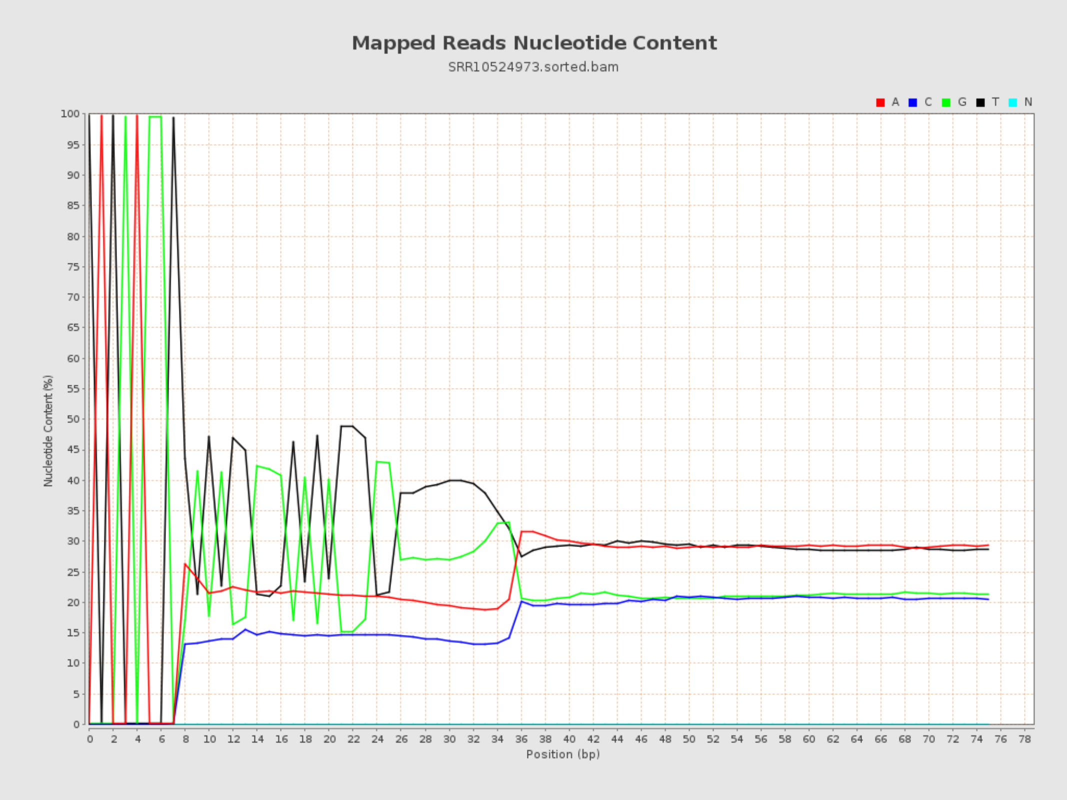
6. Results : Genome Fraction Coverage



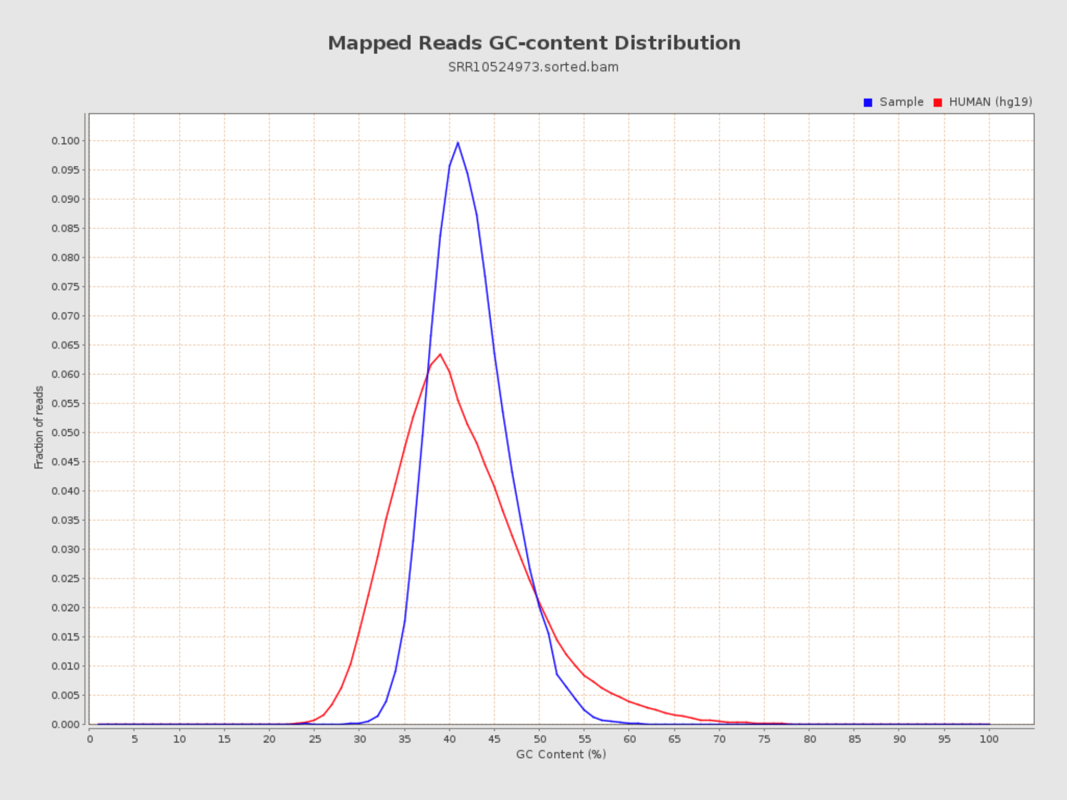
7. Results : Duplication Rate Histogram



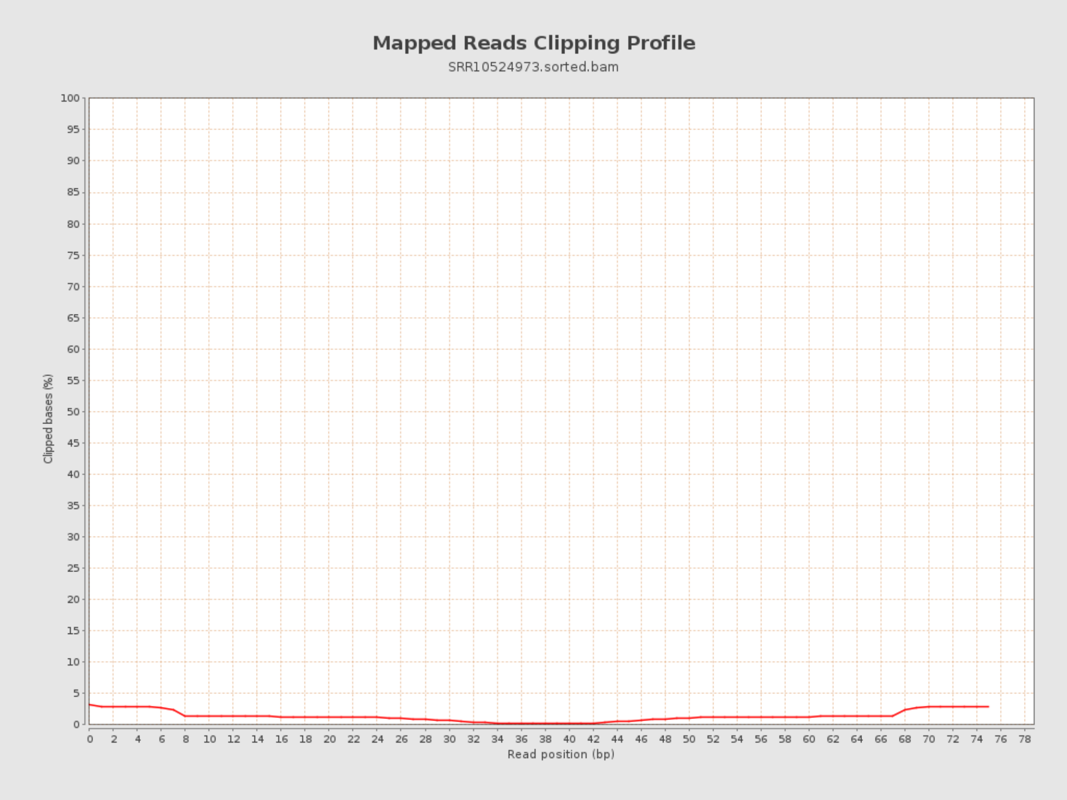
8. Results : Mapped Reads Nucleotide Content



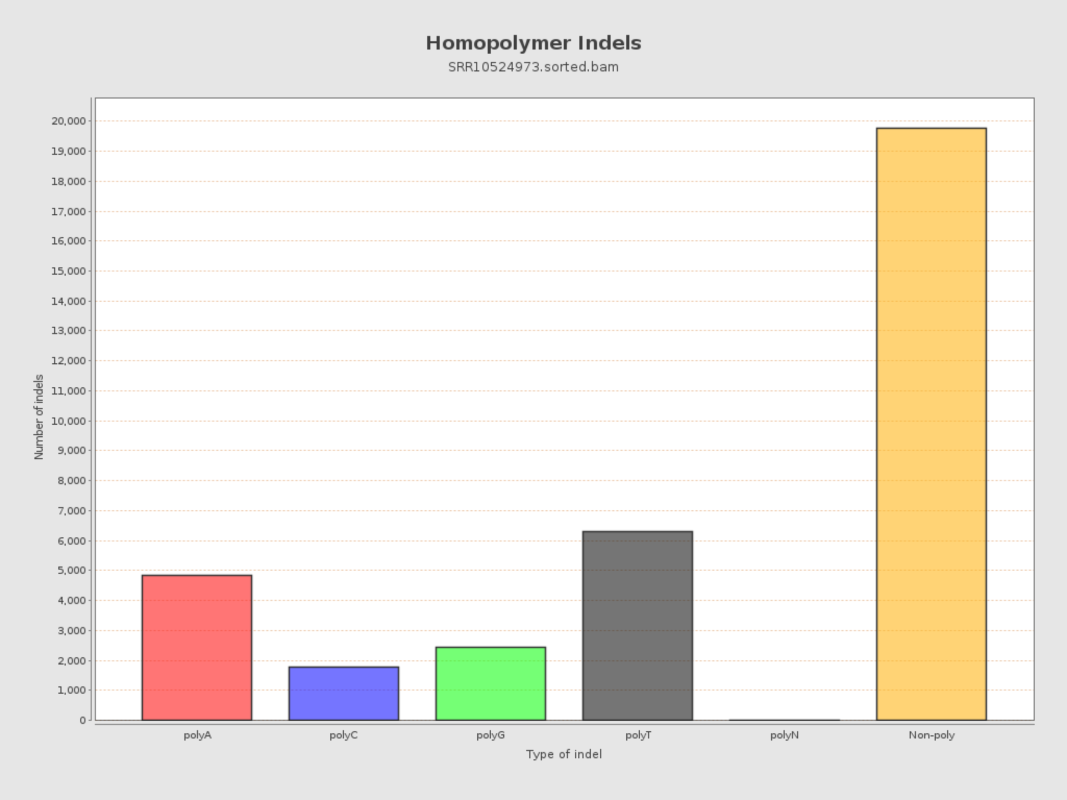
9. Results : Mapped Reads GC-content Distribution



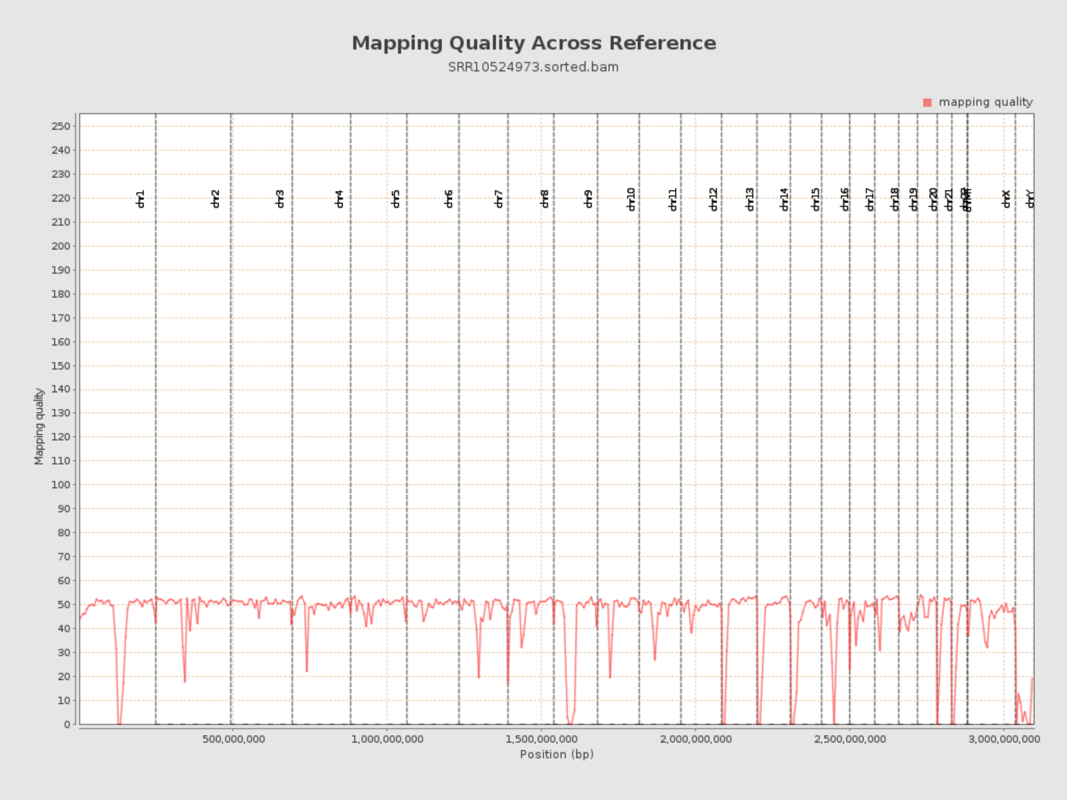
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram