Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 12:15:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524595.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_SRR10524595 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524595.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 12:15:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524595.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,891,799
Mapped reads	1,762,921 / 93.19%
Unmapped reads	128,878 / 6.81%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,850 / 0.2%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	87,735 / 4.64%
Duplication rate	3.91%
Clipped reads	1,762,514 / 93.17%

2.2. ACGT Content

Number/percentage of A's	26,409,888 / 25.67%
Number/percentage of C's	19,888,879 / 19.33%
Number/percentage of T's	32,271,814 / 31.36%
Number/percentage of G's	24,324,505 / 23.64%
Number/percentage of N's	729 / 0%
GC Percentage	42.97%

2.3. Coverage

Mean	0.0332

Standard Deviation	0.2847

2.4. Mapping Quality

Mean Mapping Quality	45.38

2.5. Mismatches and indels

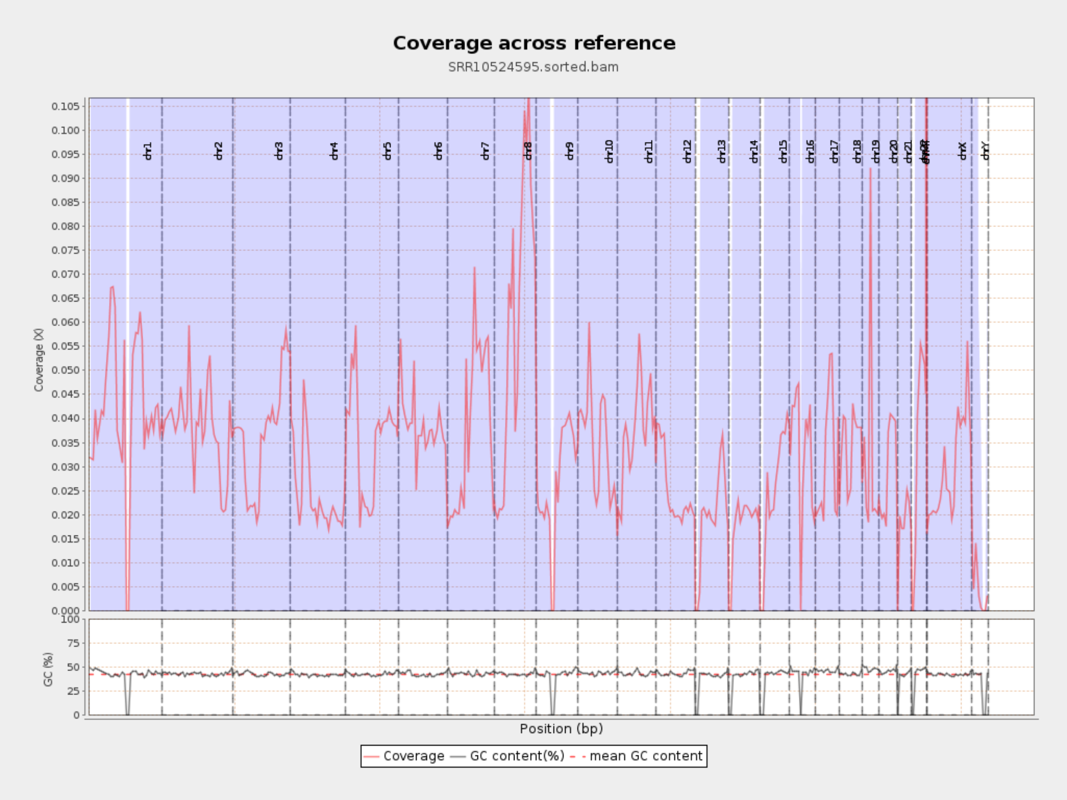
General error rate	0.48%
Mismatches	481,345
Insertions	6,289
Mapped reads with at least one insertion	0.36%
Deletions	19,033
Mapped reads with at least one deletion	1.07%
Homopolymer indels	45.79%

2.6. Chromosome stats

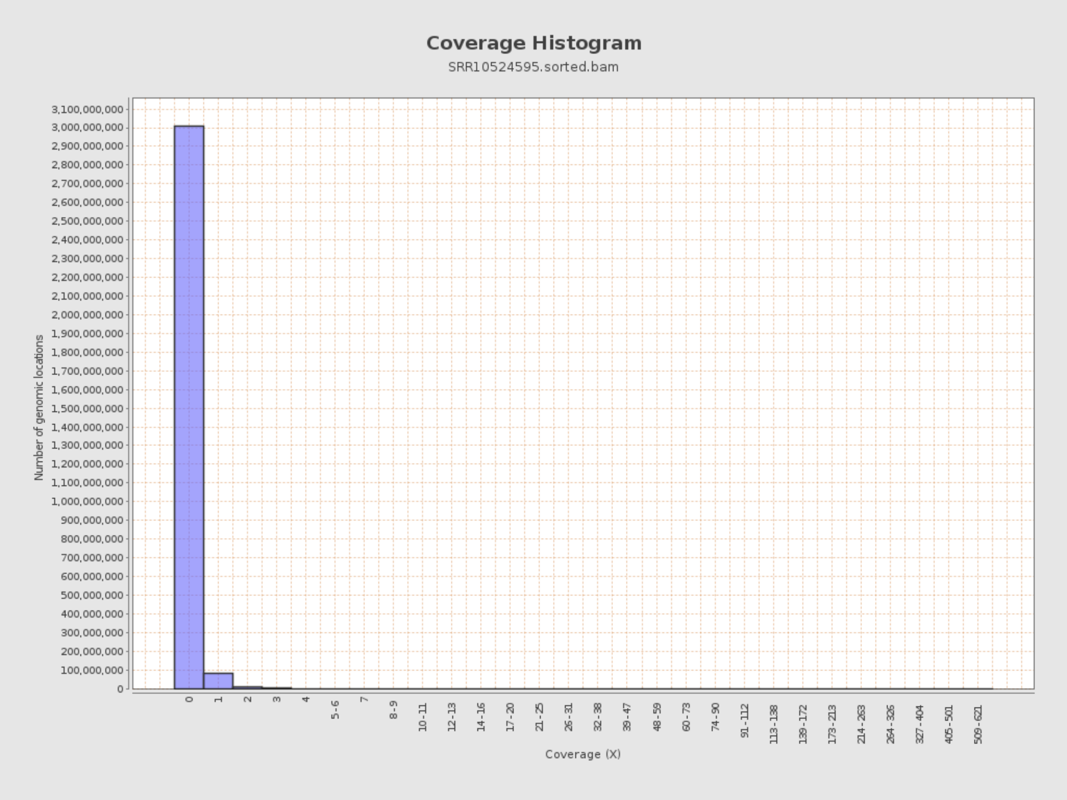
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10553170	0.0423	0.4896
chr2	243199373	9314284	0.0383	0.3293
chr3	198022430	7303340	0.0369	0.2164
chr4	191154276	4623006	0.0242	0.1995
chr5	180915260	6469905	0.0358	0.2128
chr6	171115067	6611066	0.0386	0.2423
chr7	159138663	6110151	0.0384	0.3701

chr8	146364022	8842070	0.0604	0.3862
chr9	141213431	3707308	0.0263	0.2489
chr10	135534747	4749948	0.035	0.2849
chr11	135006516	5078061	0.0376	0.2731
chr12	133851895	3318627	0.0248	0.1841
chr13	115169878	2247814	0.0195	0.1597
chr14	107349540	1887944	0.0176	0.1558
chr15	102531392	2549639	0.0249	0.1886
chr16	90354753	2982126	0.033	0.2157
chr17	81195210	2574793	0.0317	0.2071
chr18	78077248	2741246	0.0351	0.3994
chr19	59128983	1906792	0.0322	0.3577
chr20	63025520	1874779	0.0297	0.1983
chr21	48129895	871817	0.0181	0.1686
chr22	51304566	1736439	0.0338	0.2071
chrMT	16571	33389	2.0149	2.0342
chrX	155270560	4604449	0.0297	0.2205
chrY	59373566	235918	0.004	0.112

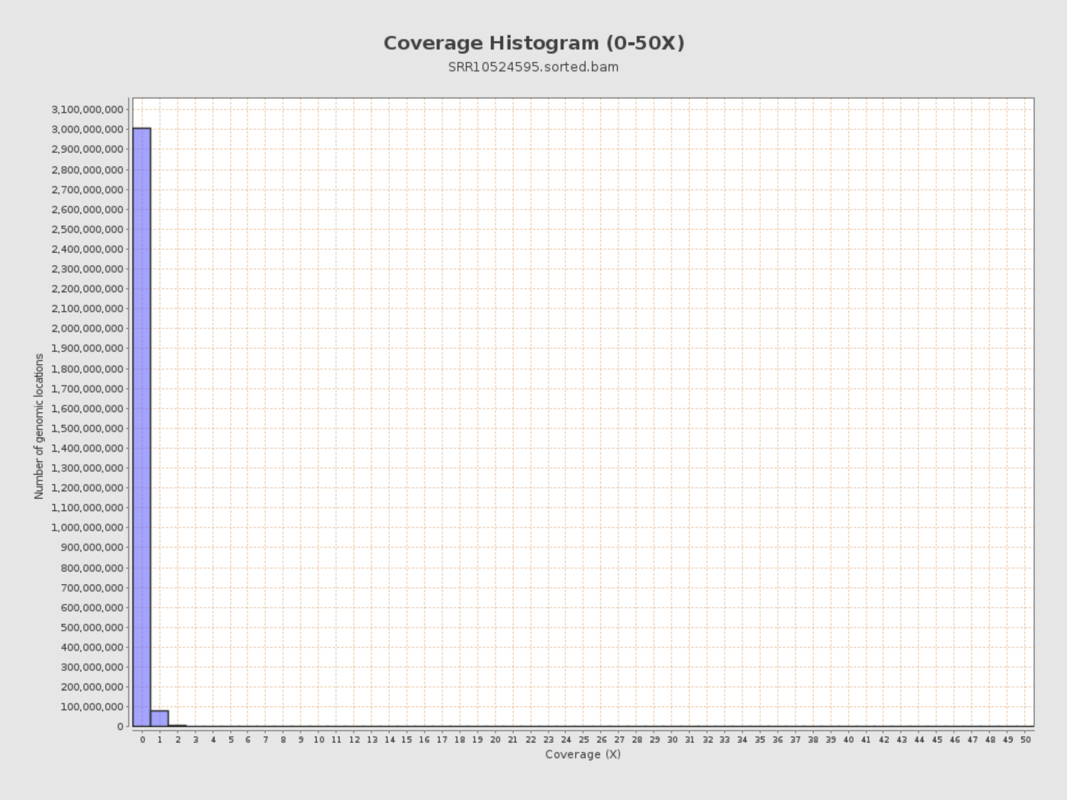
3. Results : Coverage across reference



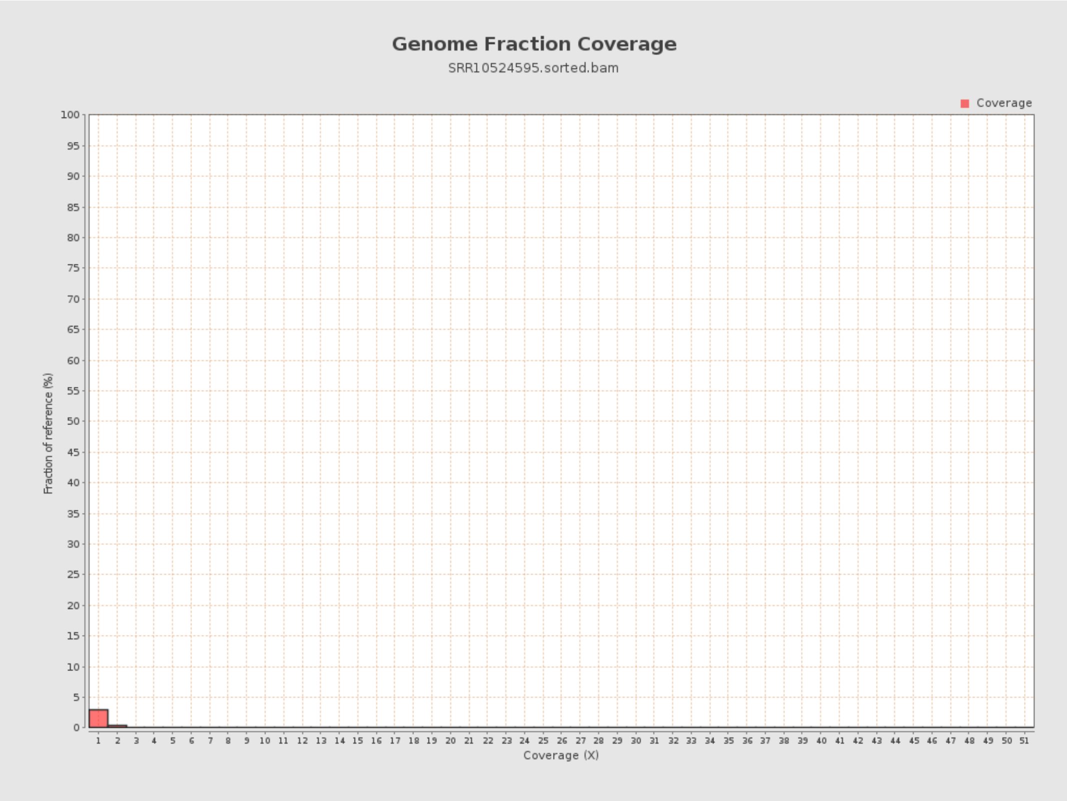
4. Results : Coverage Histogram



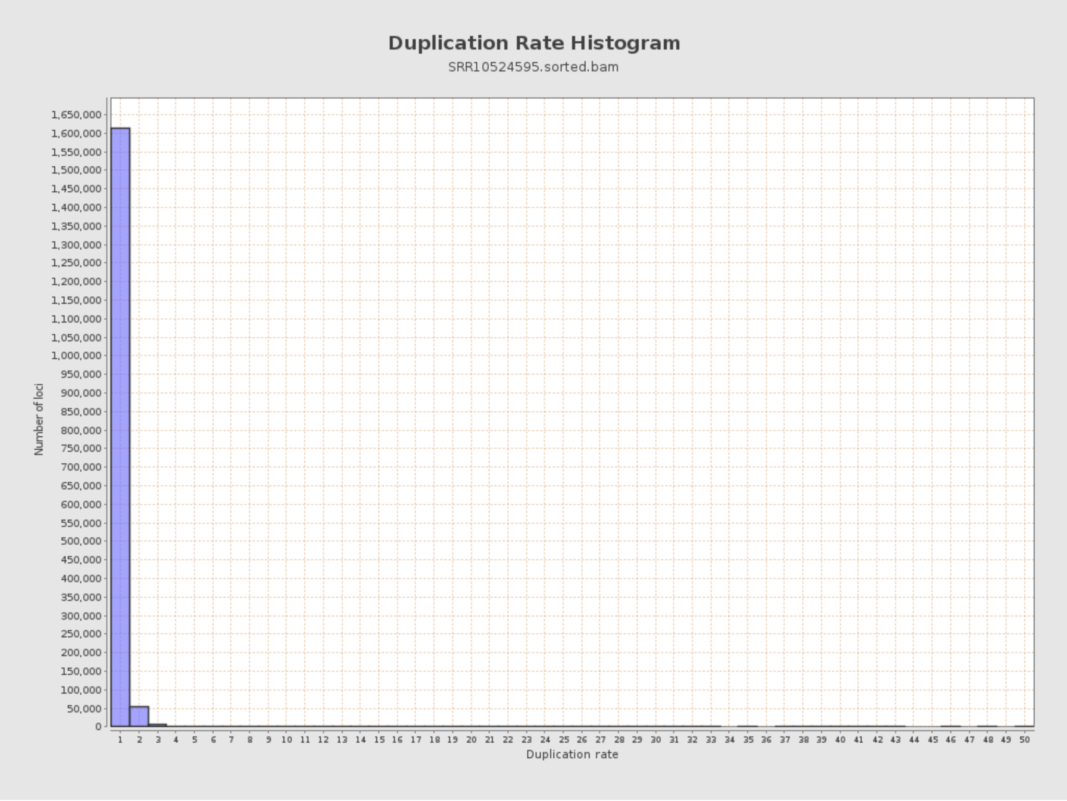
5. Results : Coverage Histogram (0-50X)



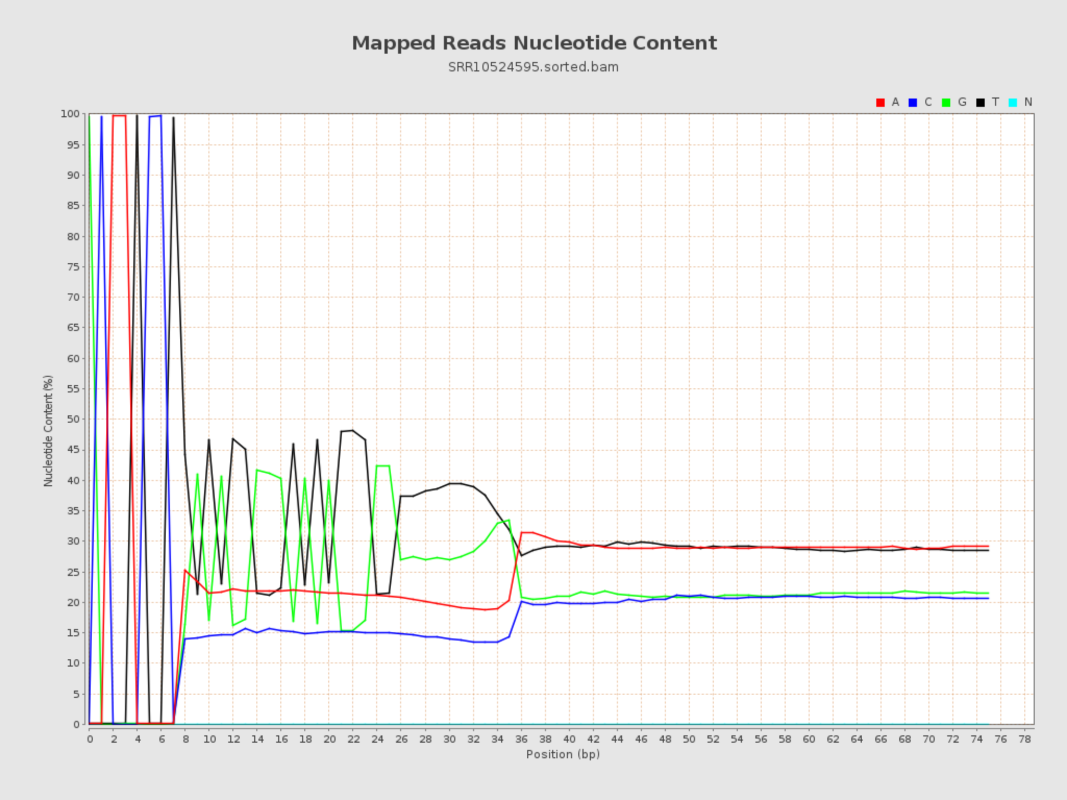
6. Results : Genome Fraction Coverage



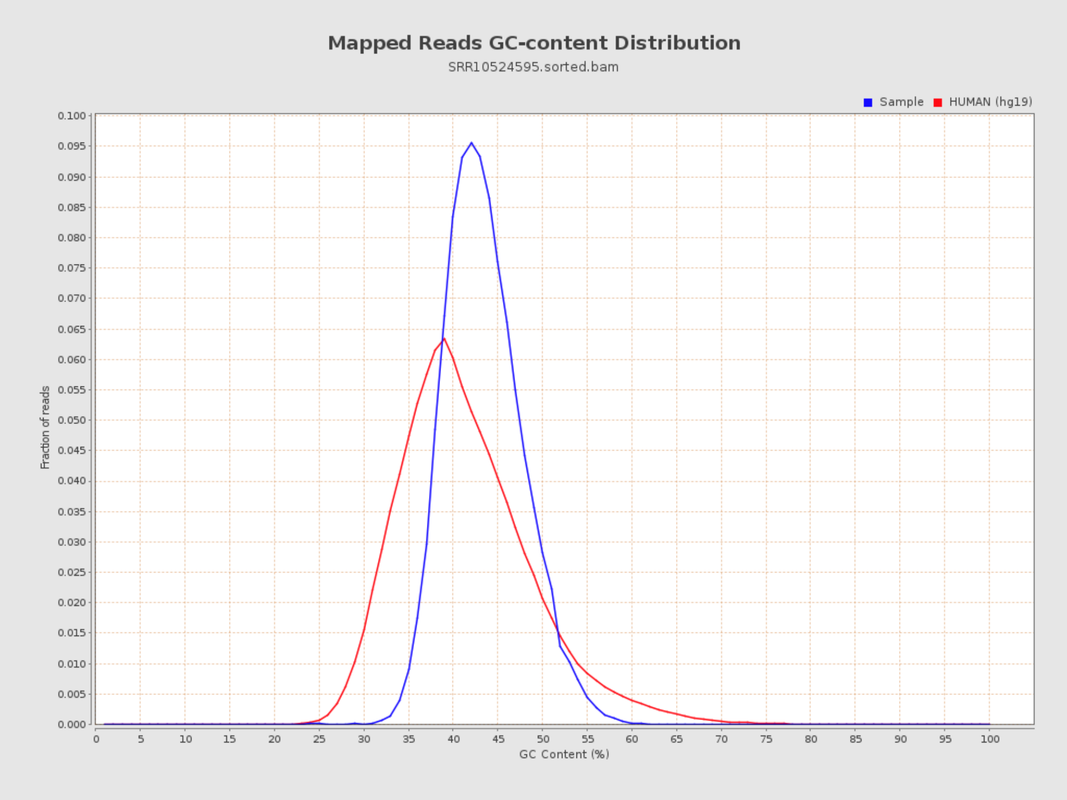
7. Results : Duplication Rate Histogram



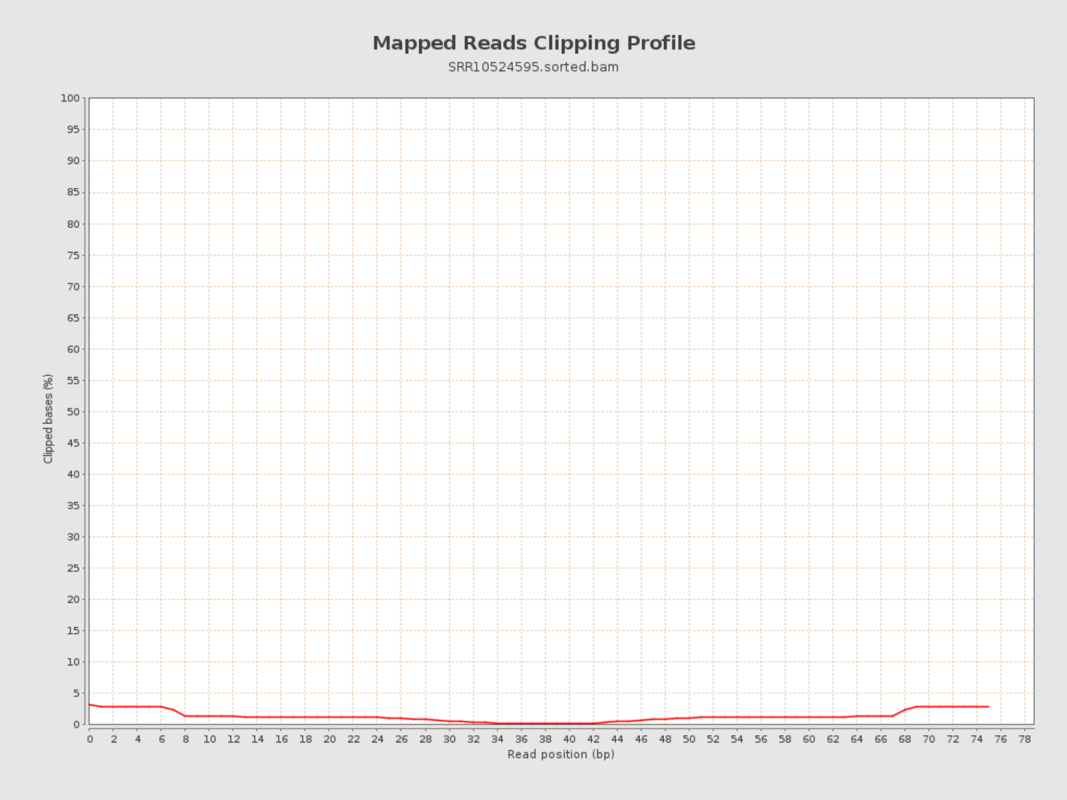
8. Results : Mapped Reads Nucleotide Content



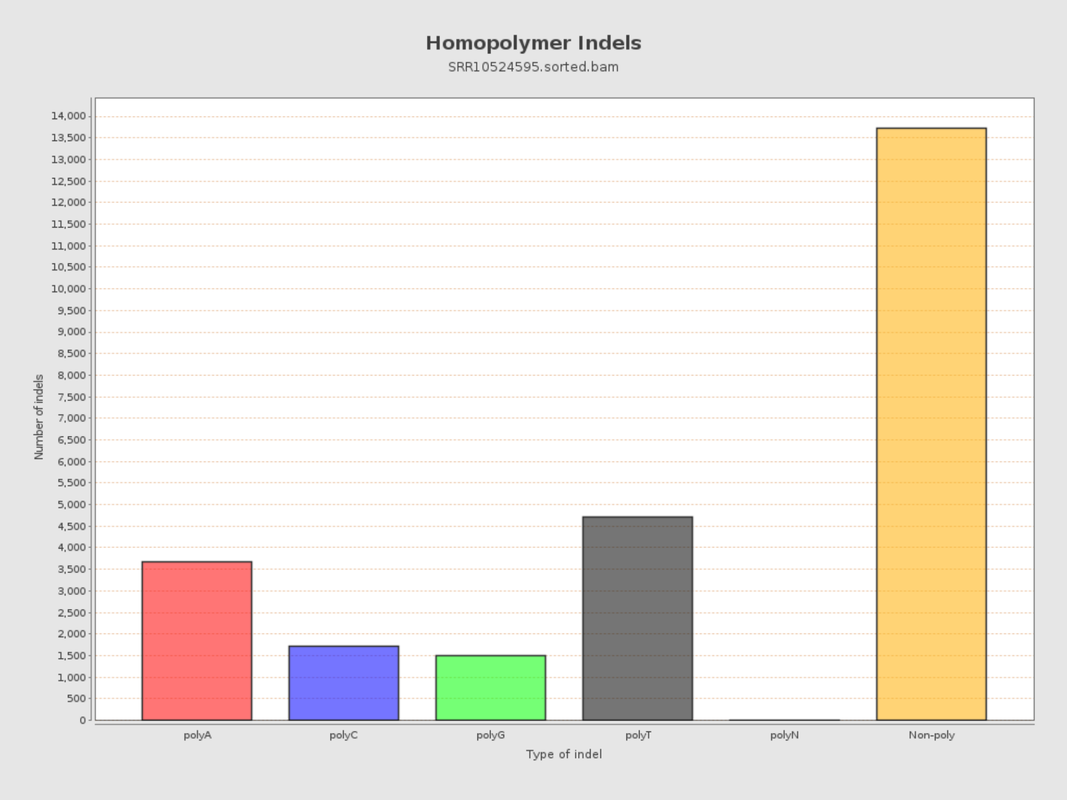
9. Results : Mapped Reads GC-content Distribution



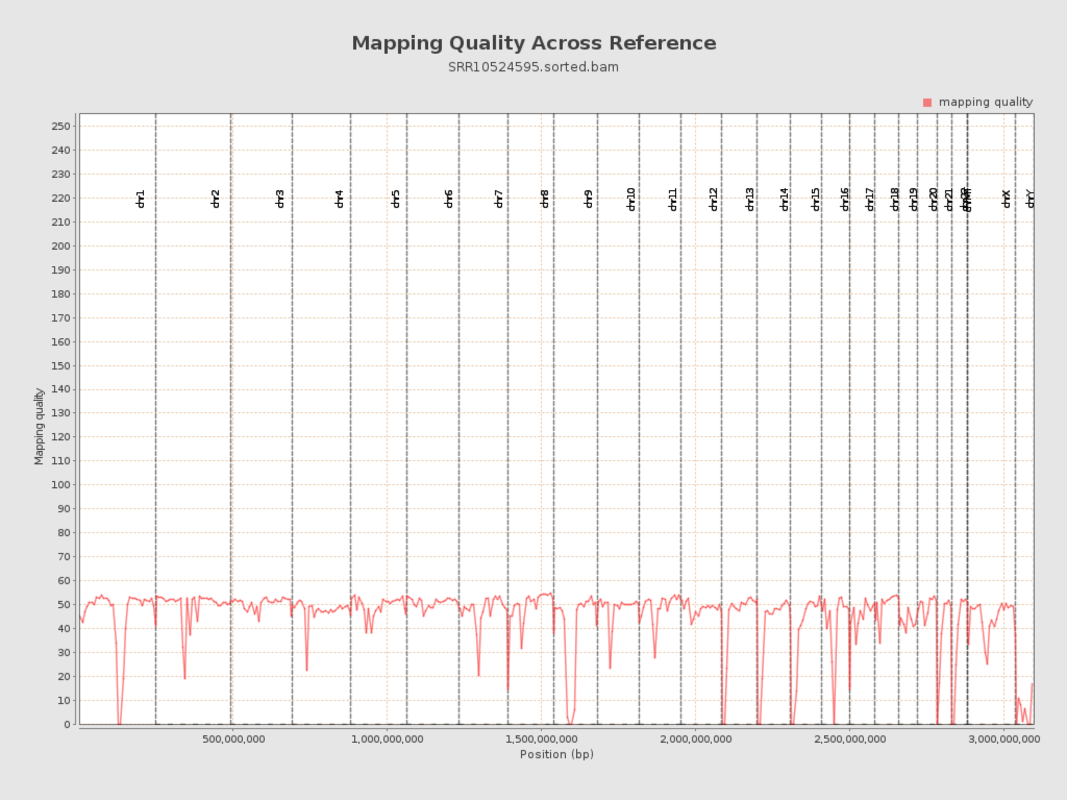
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram