Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 21:30:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524295.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_SRR10524295 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524295.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 21:30:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524295.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,940,775
Mapped reads	1,771,478 / 91.28%
Unmapped reads	169,297 / 8.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,647 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	59,801 / 3.08%
Duplication rate	2.36%
Clipped reads	1,773,721 / 91.39%

2.2. ACGT Content

Number/percentage of A's	24,161,879 / 23.56%
Number/percentage of C's	18,390,000 / 17.93%
Number/percentage of T's	33,788,946 / 32.94%
Number/percentage of G's	26,216,013 / 25.56%
Number/percentage of N's	13,466 / 0.01%
GC Percentage	43.49%

2.3. Coverage

Mean	0.0331

Standard Deviation	0.3068

2.4. Mapping Quality

Mean Mapping Quality	44.09

2.5. Mismatches and indels

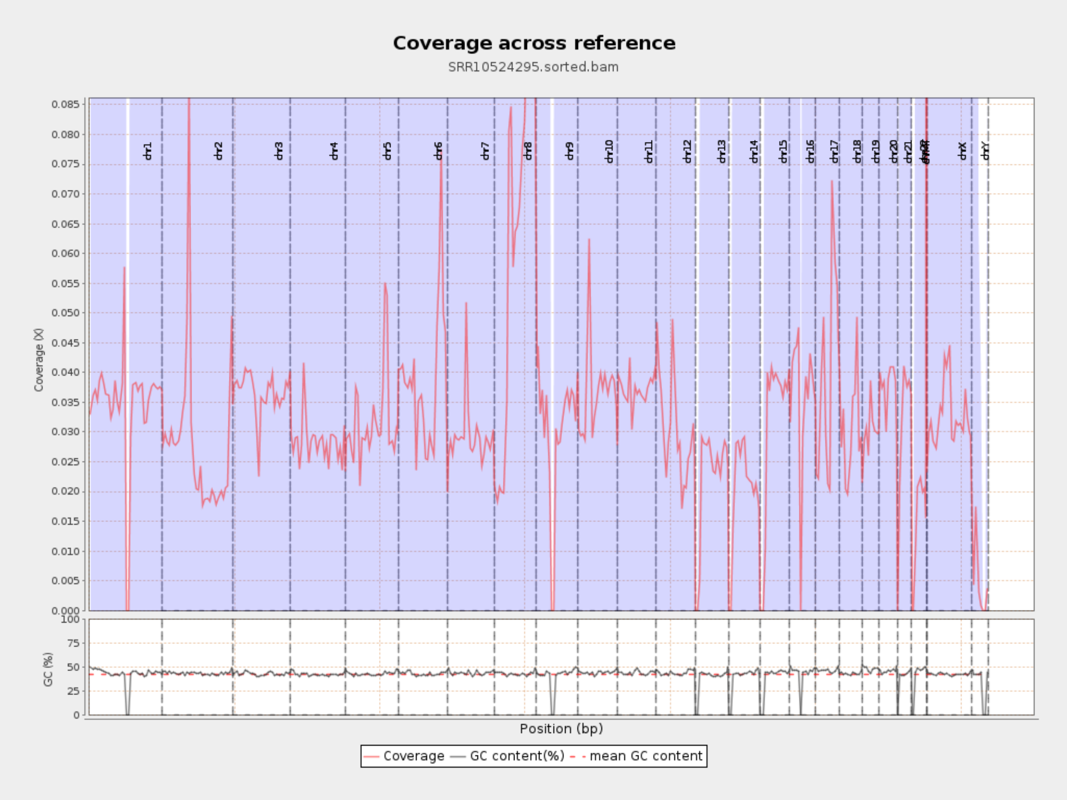
General error rate	0.52%
Mismatches	525,181
Insertions	6,962
Mapped reads with at least one insertion	0.39%
Deletions	17,769
Mapped reads with at least one deletion	1%
Homopolymer indels	42.24%

2.6. Chromosome stats

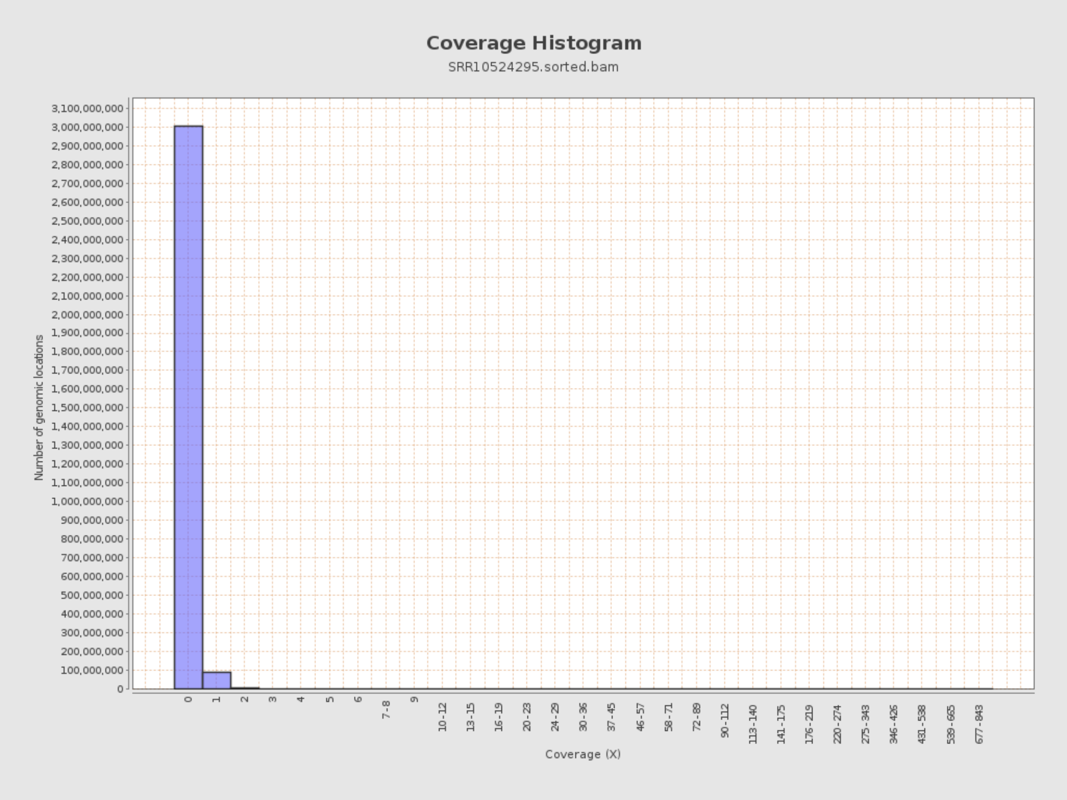
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8609134	0.0345	0.5875
chr2	243199373	6806987	0.028	0.3939
chr3	198022430	7224552	0.0365	0.2088
chr4	191154276	5403147	0.0283	0.2029
chr5	180915260	5769116	0.0319	0.1948
chr6	171115067	6607226	0.0386	0.2345
chr7	159138663	4701156	0.0295	0.3876

chr8	146364022	10605872	0.0725	0.3783
chr9	141213431	4206626	0.0298	0.2346
chr10	135534747	5007951	0.0369	0.2919
chr11	135006516	4987438	0.0369	0.2588
chr12	133851895	4086017	0.0305	0.1939
chr13	115169878	2542875	0.0221	0.1626
chr14	107349540	2186214	0.0204	0.164
chr15	102531392	3172131	0.0309	0.1999
chr16	90354753	3276060	0.0363	0.2199
chr17	81195210	3212373	0.0396	0.2349
chr18	78077248	2427686	0.0311	0.4089
chr19	59128983	1794716	0.0304	0.4091
chr20	63025520	2372942	0.0377	0.2142
chr21	48129895	1496003	0.0311	0.2062
chr22	51304566	753589	0.0147	0.1319
chrMT	16571	7112	0.4292	0.7704
chrX	155270560	5051305	0.0325	0.2179
chrY	59373566	290219	0.0049	0.14

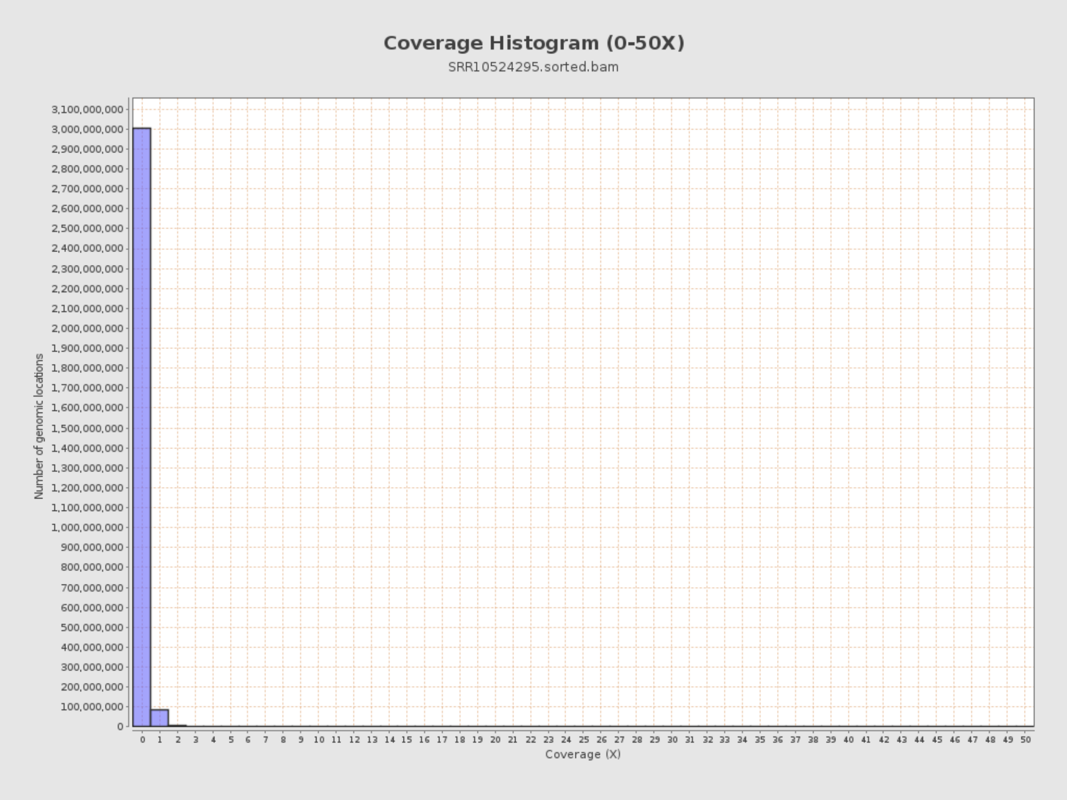
3. Results : Coverage across reference



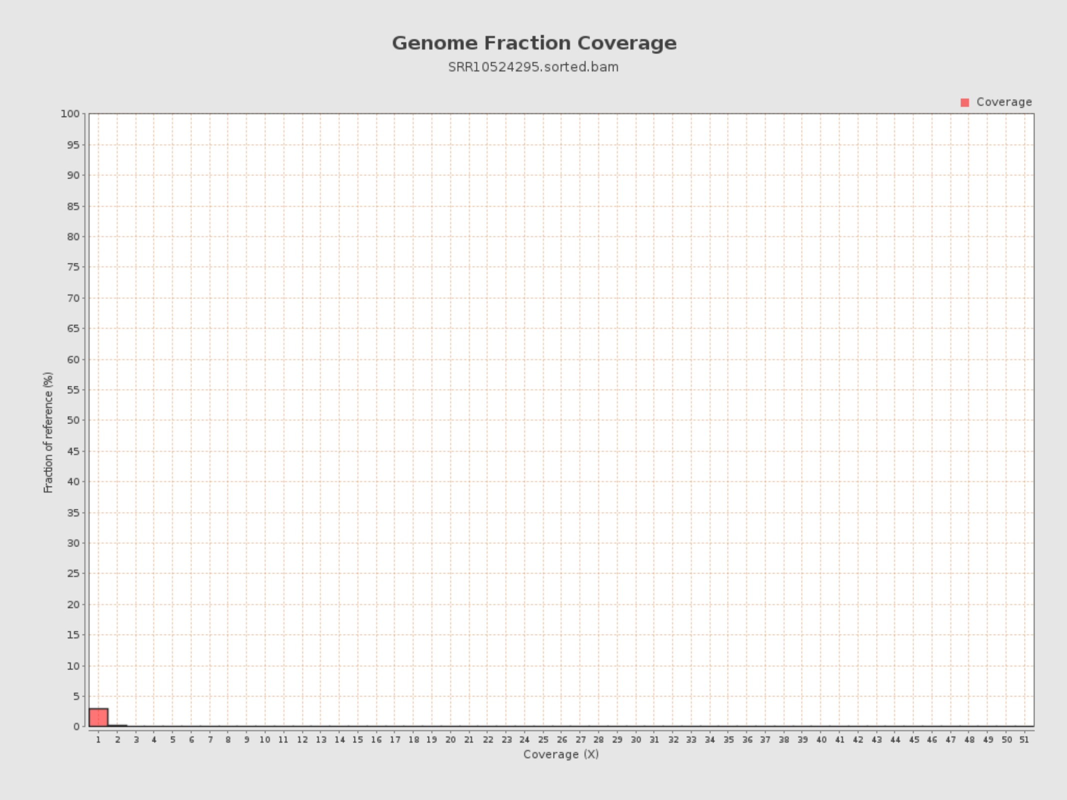
4. Results : Coverage Histogram



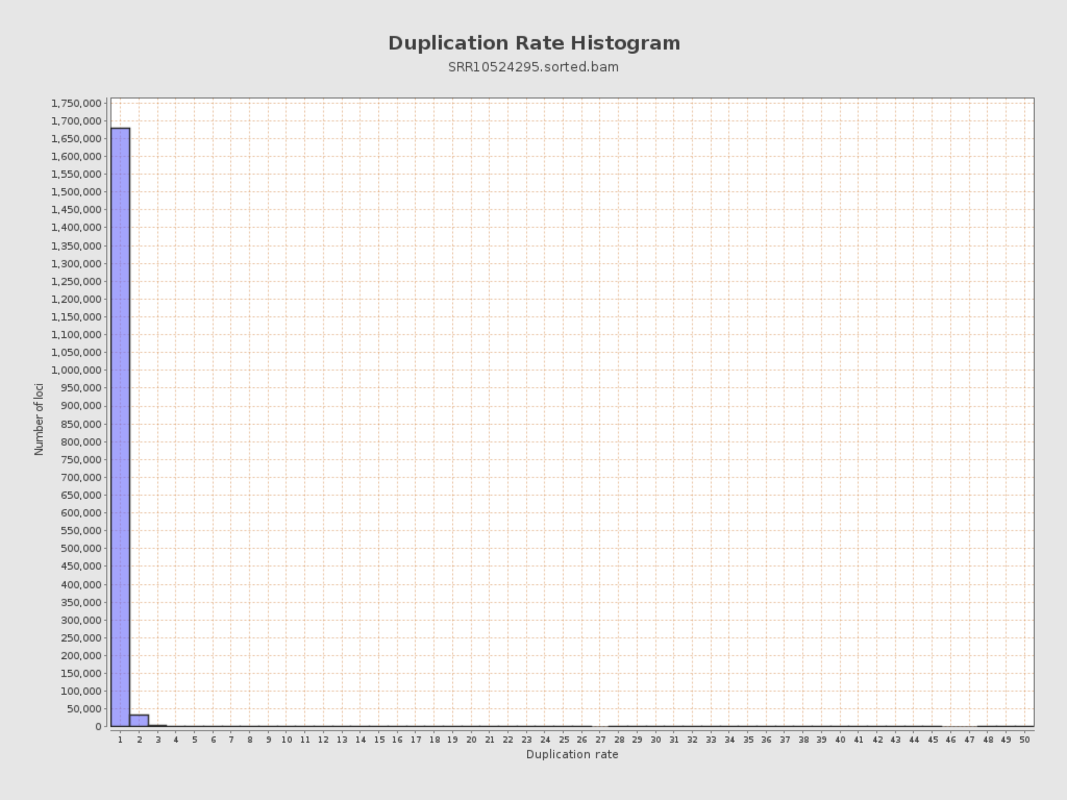
5. Results : Coverage Histogram (0-50X)



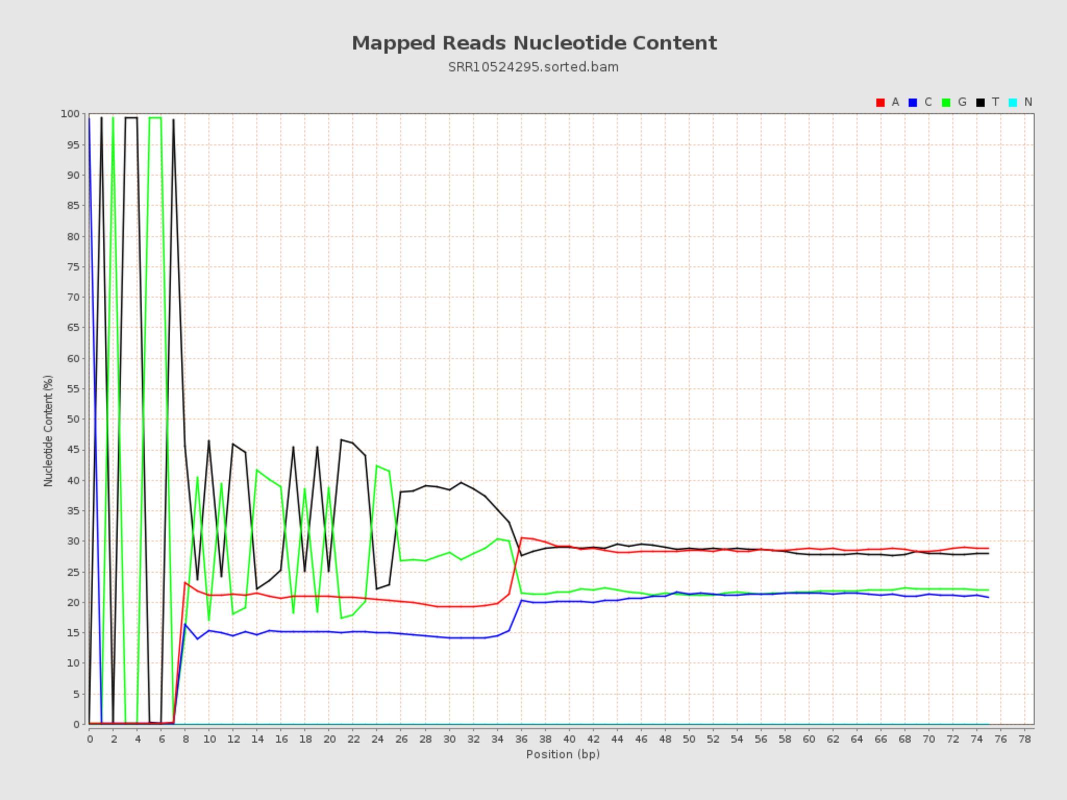
6. Results : Genome Fraction Coverage



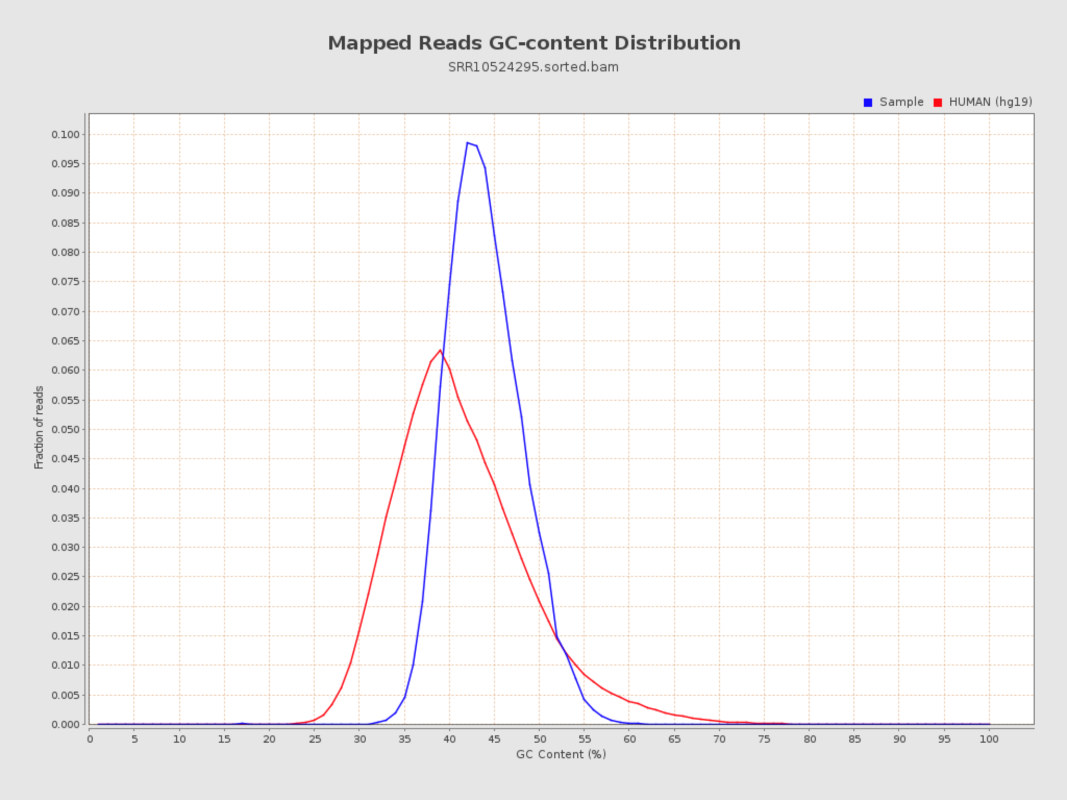
7. Results : Duplication Rate Histogram



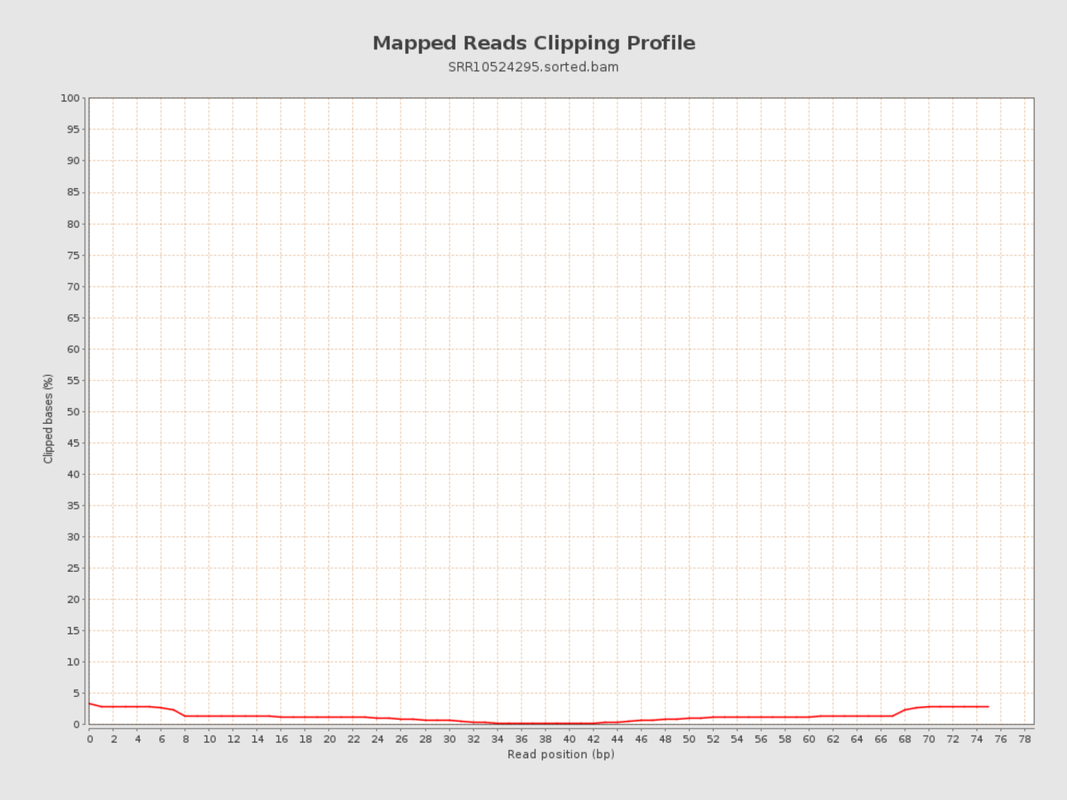
8. Results : Mapped Reads Nucleotide Content



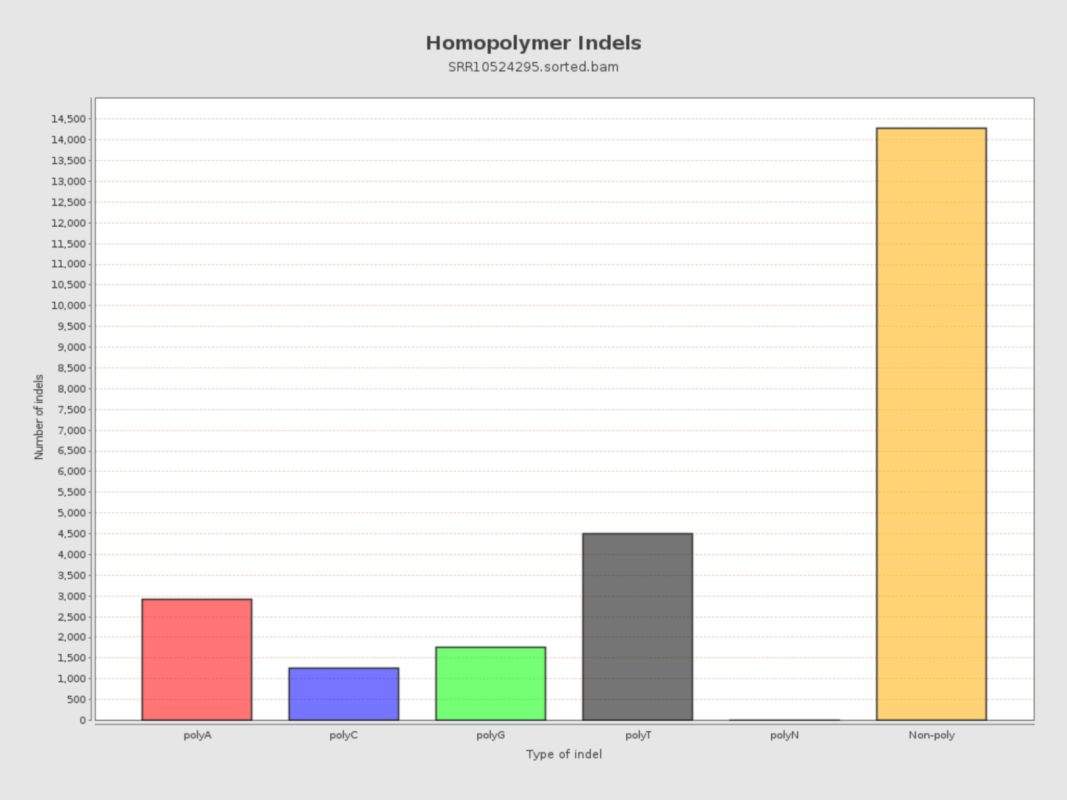
9. Results : Mapped Reads GC-content Distribution



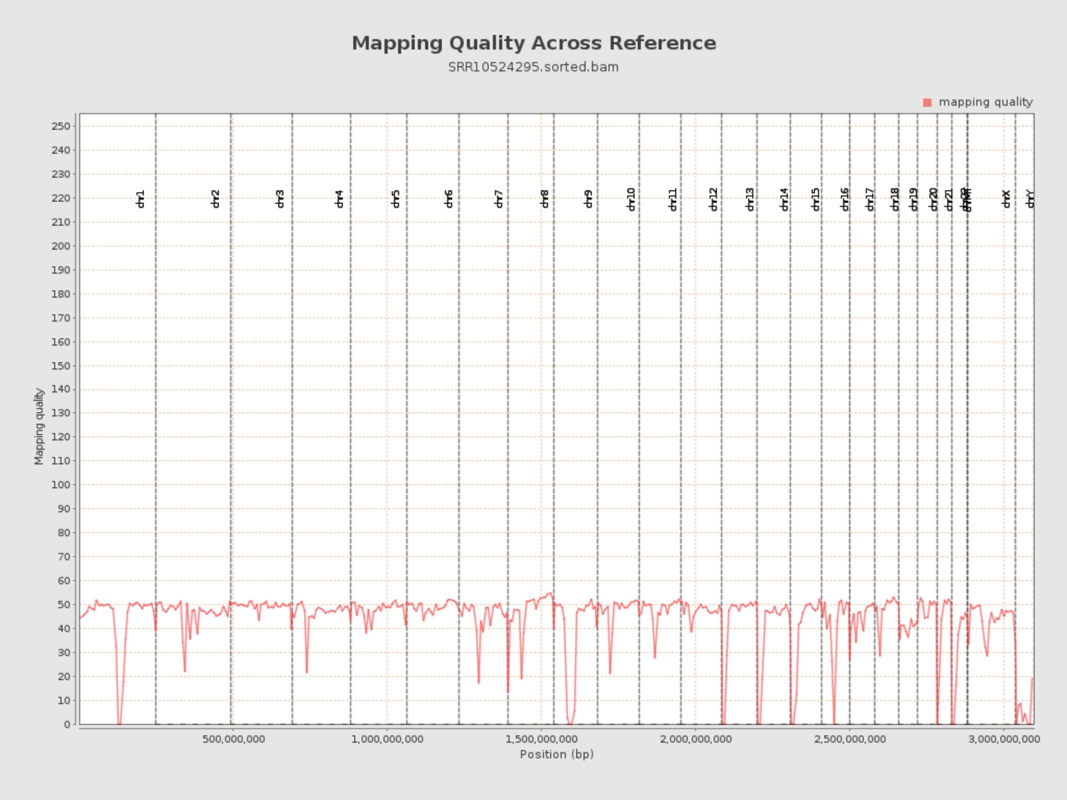
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram