Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 00:14:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004078.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_SRR6004078 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004078.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 00:14:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004078.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,839,821
Mapped reads	1,678,700 / 91.24%
Unmapped reads	161,121 / 8.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,142 / 0.77%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	77,139 / 4.19%
Duplication rate	3.79%
Clipped reads	731,665 / 39.77%

2.2. ACGT Content

Number/percentage of A's	31,700,384 / 28.15%
Number/percentage of C's	20,932,629 / 18.59%
Number/percentage of T's	35,575,232 / 31.6%
Number/percentage of G's	24,367,886 / 21.64%
Number/percentage of N's	21,206 / 0.02%
GC Percentage	40.23%

2.3. Coverage

Mean	0.0364

Standard Deviation	0.3189

2.4. Mapping Quality

Mean Mapping Quality	46.32

2.5. Mismatches and indels

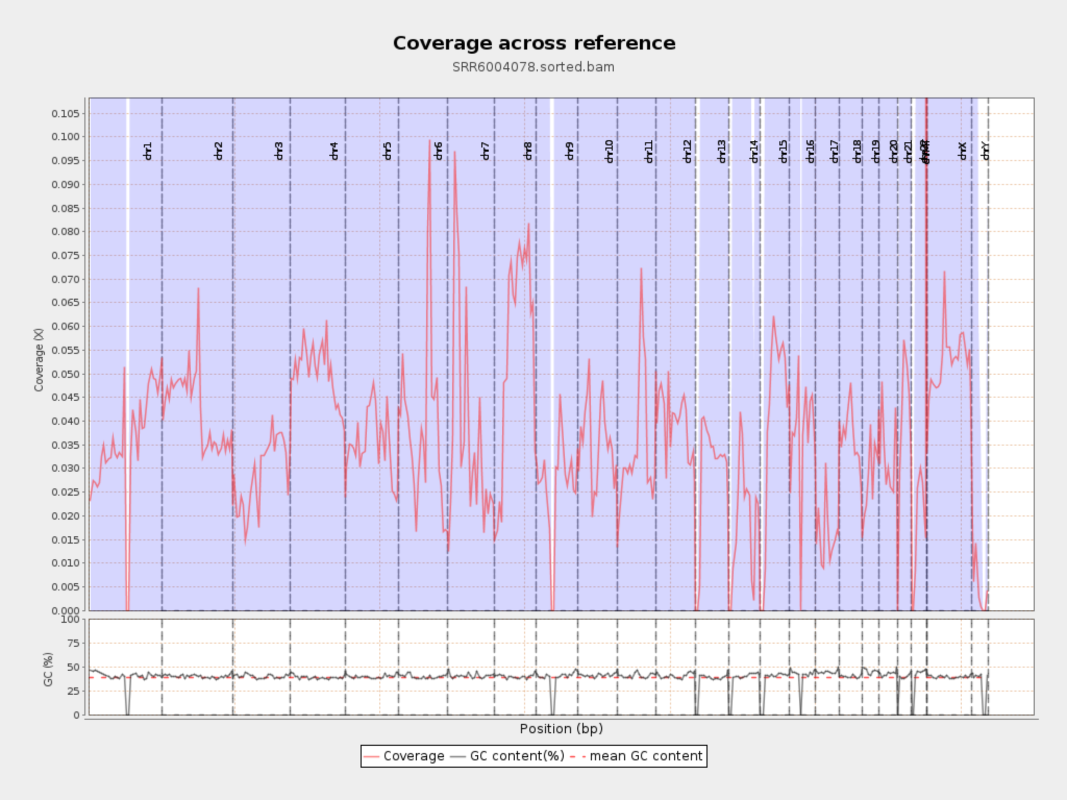
General error rate	0.85%
Mismatches	944,919
Insertions	7,856
Mapped reads with at least one insertion	0.46%
Deletions	29,355
Mapped reads with at least one deletion	1.73%
Homopolymer indels	46.03%

2.6. Chromosome stats

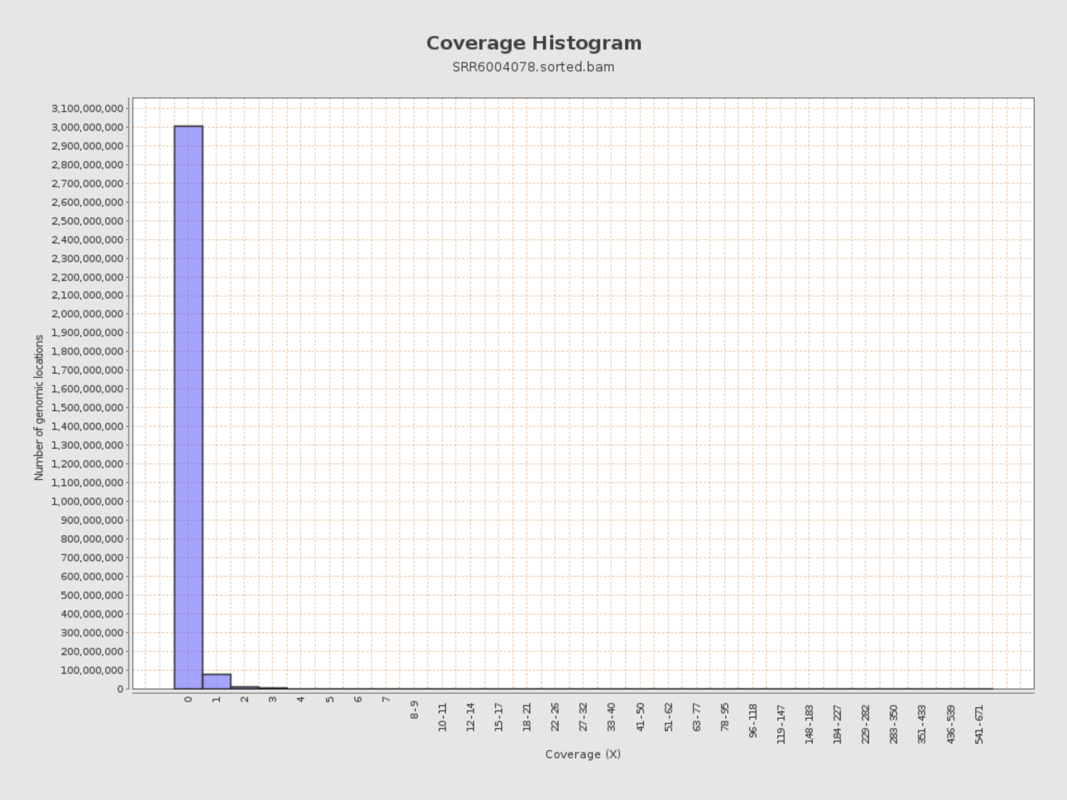
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8712116	0.035	0.5284
chr2	243199373	10357945	0.0426	0.3348
chr3	198022430	5713713	0.0289	0.1974
chr4	191154276	9634905	0.0504	0.2737
chr5	180915260	6448089	0.0356	0.2208
chr6	171115067	6713649	0.0392	0.239
chr7	159138663	6114573	0.0384	0.514

chr8	146364022	8223411	0.0562	0.4864
chr9	141213431	3681279	0.0261	0.2408
chr10	135534747	4851575	0.0358	0.2844
chr11	135006516	4709846	0.0349	0.2618
chr12	133851895	5335911	0.0399	0.2356
chr13	115169878	3334107	0.0289	0.2024
chr14	107349540	2007330	0.0187	0.1706
chr15	102531392	4213848	0.0411	0.2386
chr16	90354753	3353503	0.0371	0.2376
chr17	81195210	1293371	0.0159	0.161
chr18	78077248	2881638	0.0369	0.4243
chr19	59128983	1689656	0.0286	0.3778
chr20	63025520	2107175	0.0334	0.2187
chr21	48129895	1906608	0.0396	0.2439
chr22	51304566	882732	0.0172	0.1502
chrMT	16571	43812	2.6439	2.557
chrX	155270560	8138219	0.0524	0.2907
chrY	59373566	299131	0.005	0.108

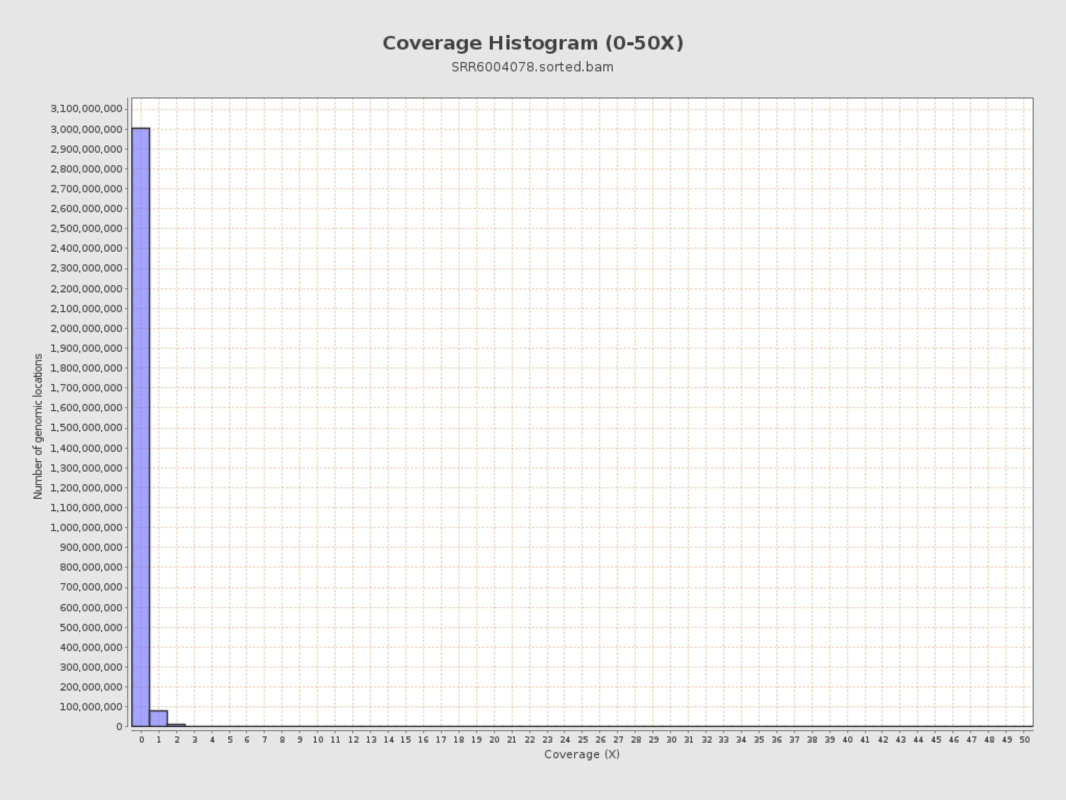
3. Results : Coverage across reference



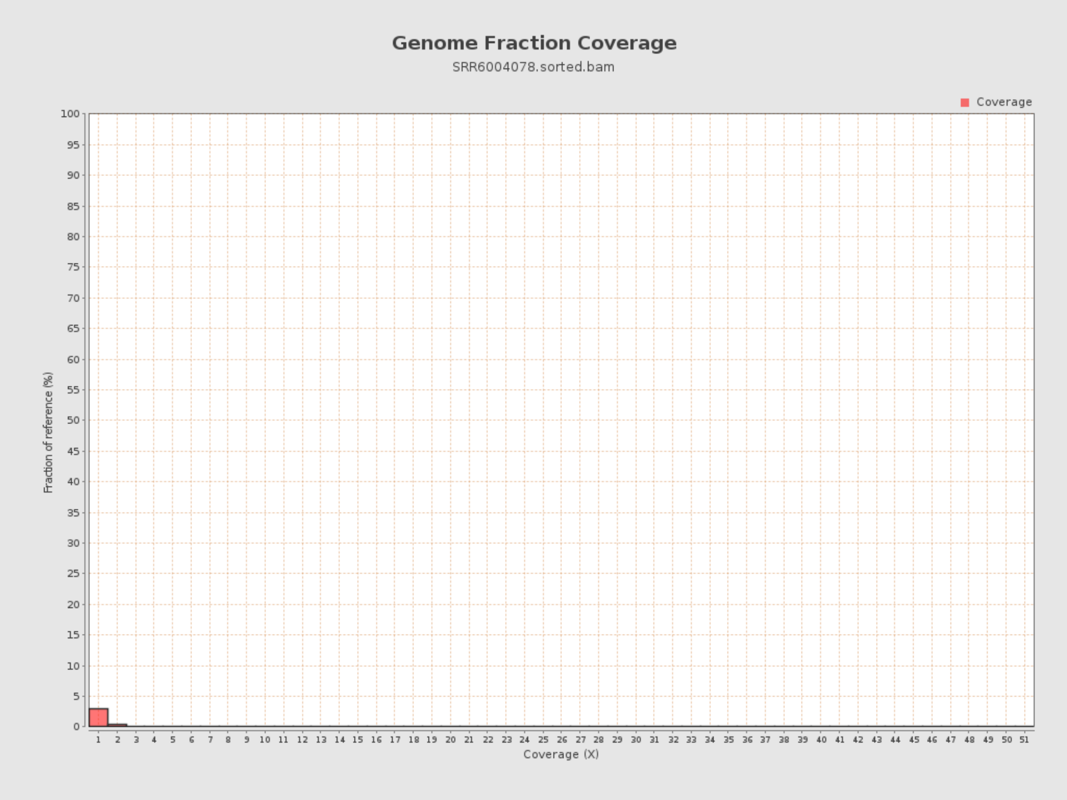
4. Results : Coverage Histogram



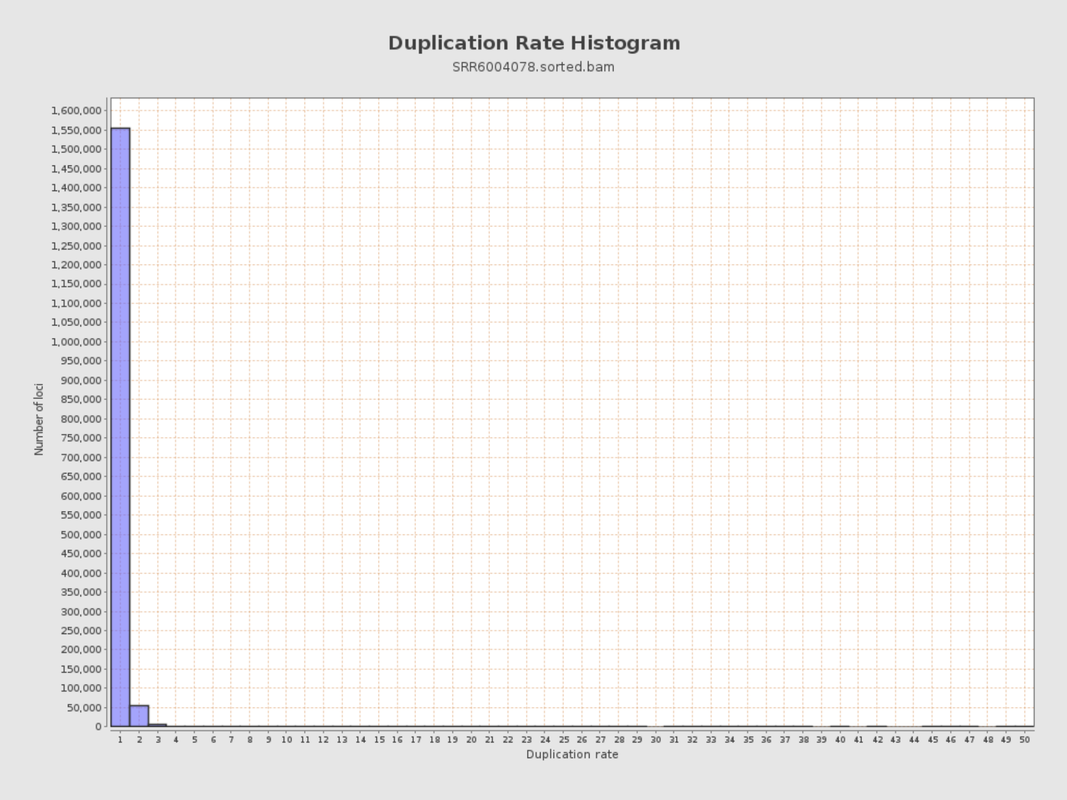
5. Results : Coverage Histogram (0-50X)



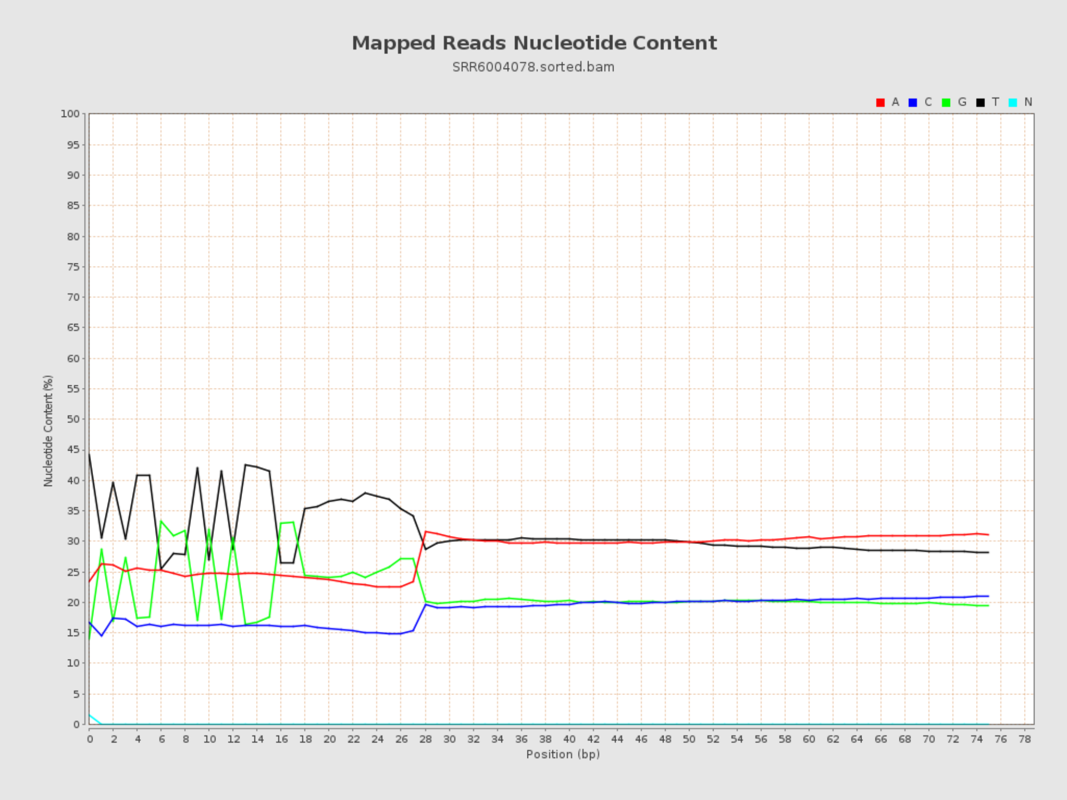
6. Results : Genome Fraction Coverage



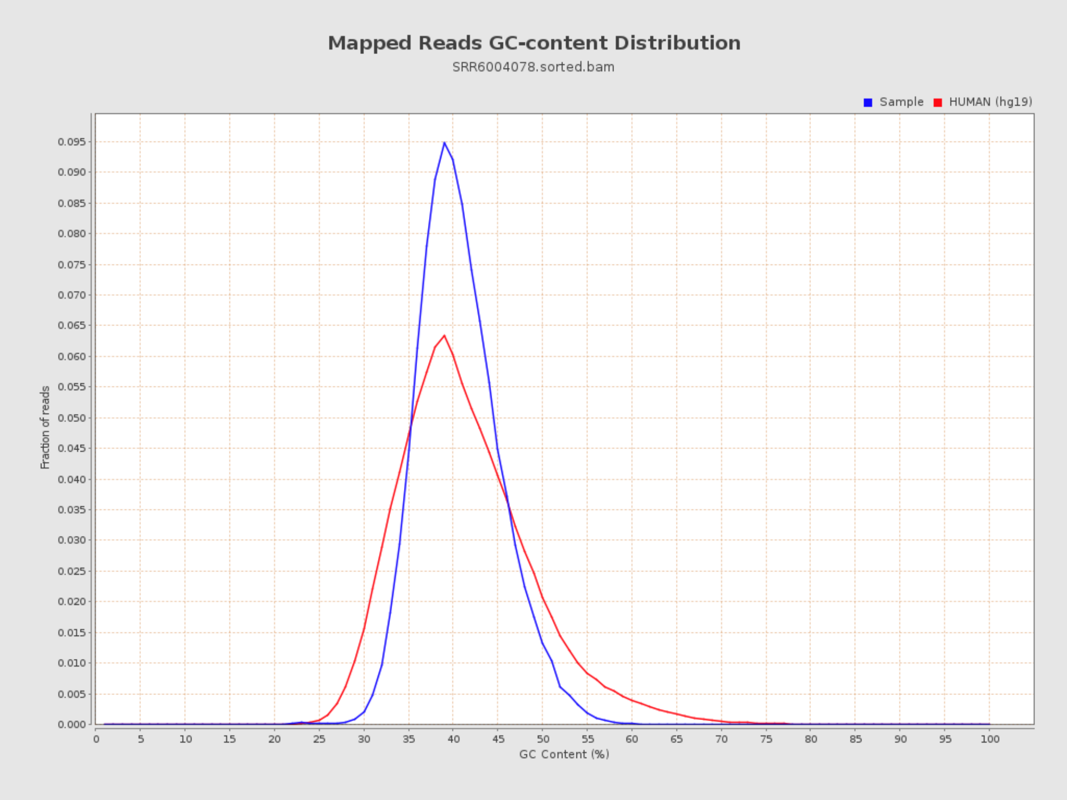
7. Results : Duplication Rate Histogram



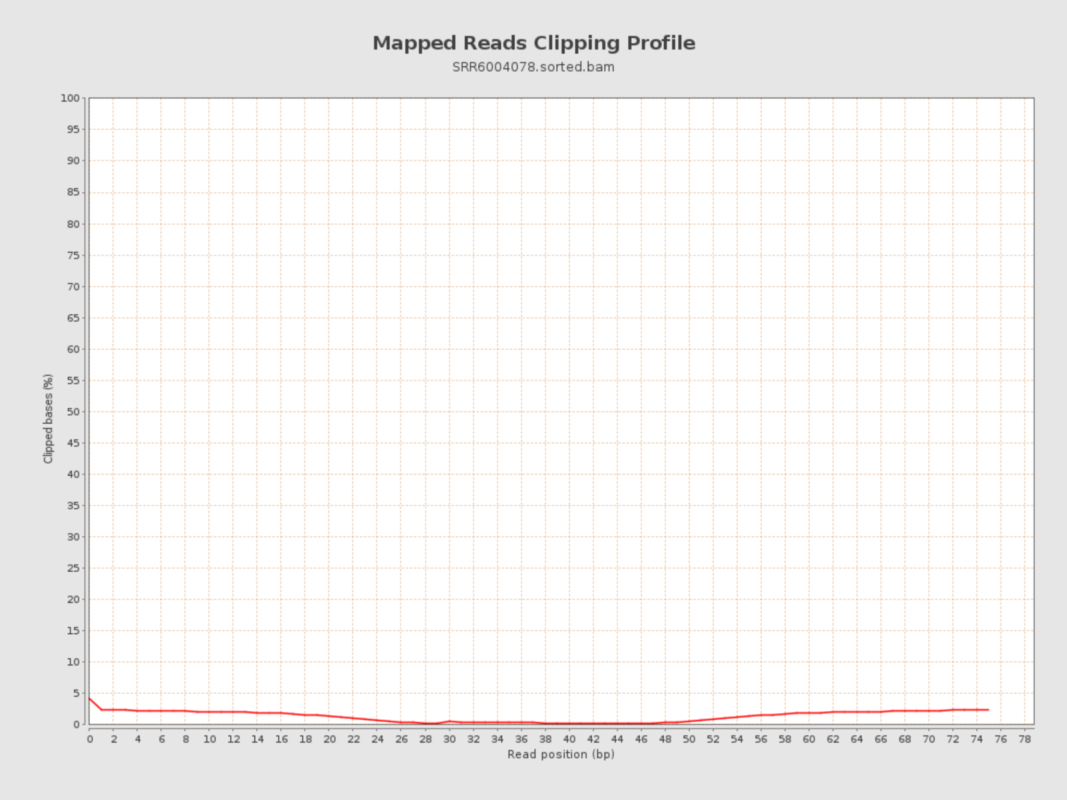
8. Results : Mapped Reads Nucleotide Content



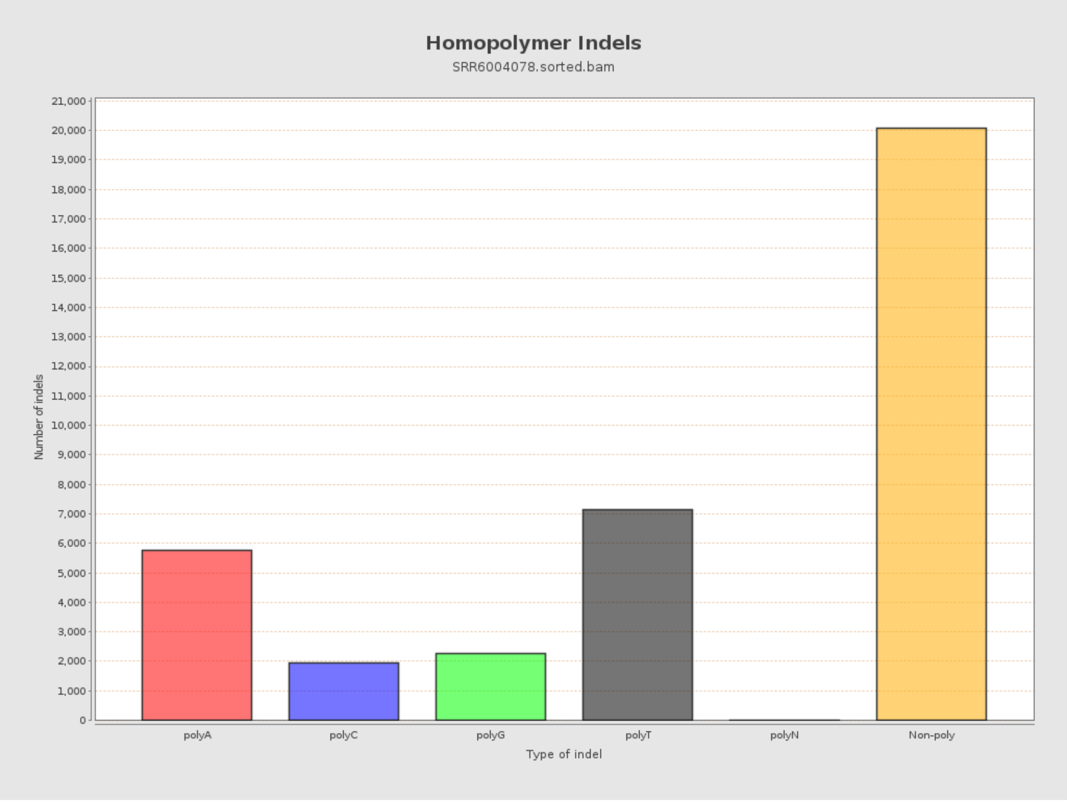
9. Results : Mapped Reads GC-content Distribution



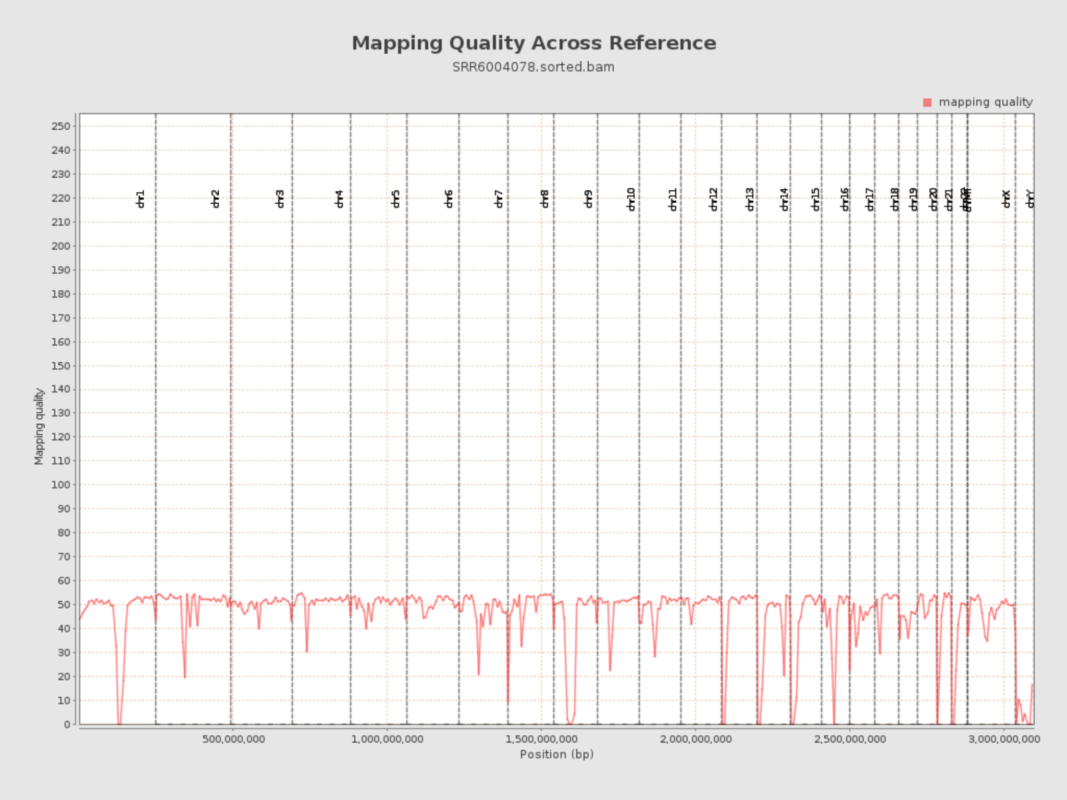
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram