Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 06:23:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081694.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_SRR3081694 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081694.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 06:23:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081694.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,742,175
Mapped reads	1,494,665 / 85.79%
Unmapped reads	247,510 / 14.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,005 / 0.86%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	84,391 / 4.84%
Duplication rate	4.94%
Clipped reads	660,906 / 37.94%

2.2. ACGT Content

Number/percentage of A's	28,219,839 / 28.29%
Number/percentage of C's	17,266,435 / 17.31%
Number/percentage of T's	32,981,805 / 33.07%
Number/percentage of G's	21,209,612 / 21.26%
Number/percentage of N's	67,861 / 0.07%
GC Percentage	38.57%

2.3. Coverage

Mean	0.0322

Standard Deviation	0.2572

2.4. Mapping Quality

Mean Mapping Quality	47.64

2.5. Mismatches and indels

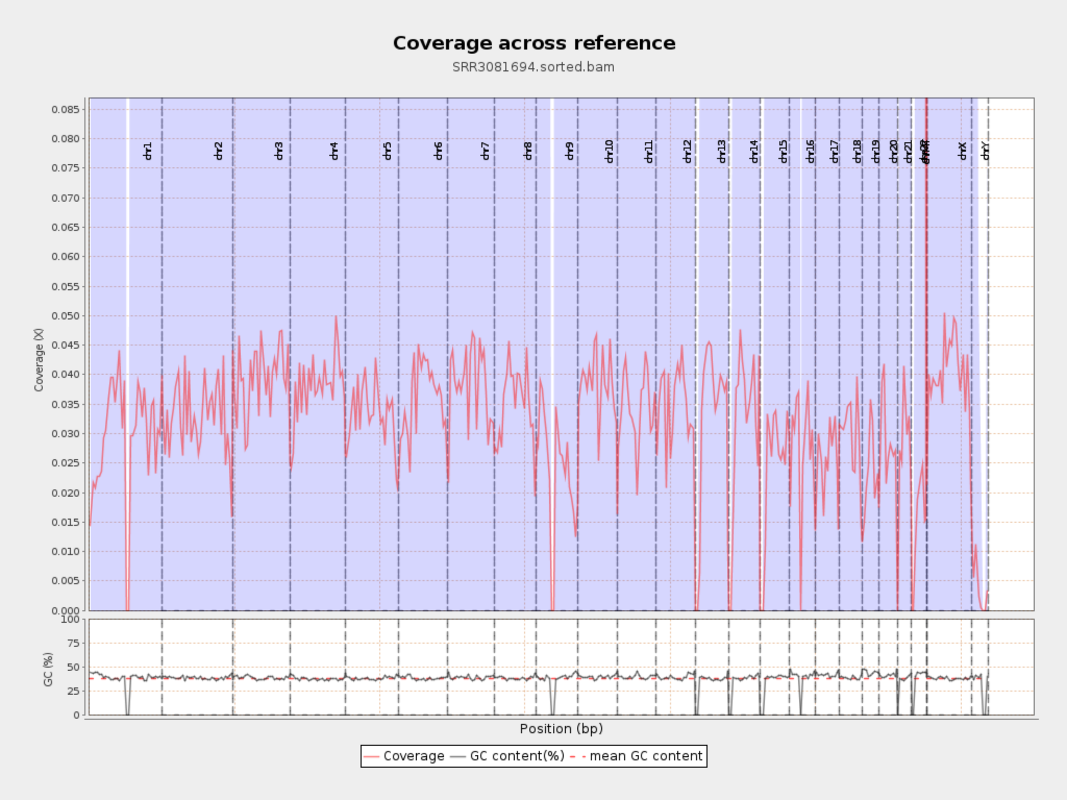
General error rate	0.86%
Mismatches	848,376
Insertions	8,131
Mapped reads with at least one insertion	0.54%
Deletions	22,426
Mapped reads with at least one deletion	1.49%
Homopolymer indels	49.23%

2.6. Chromosome stats

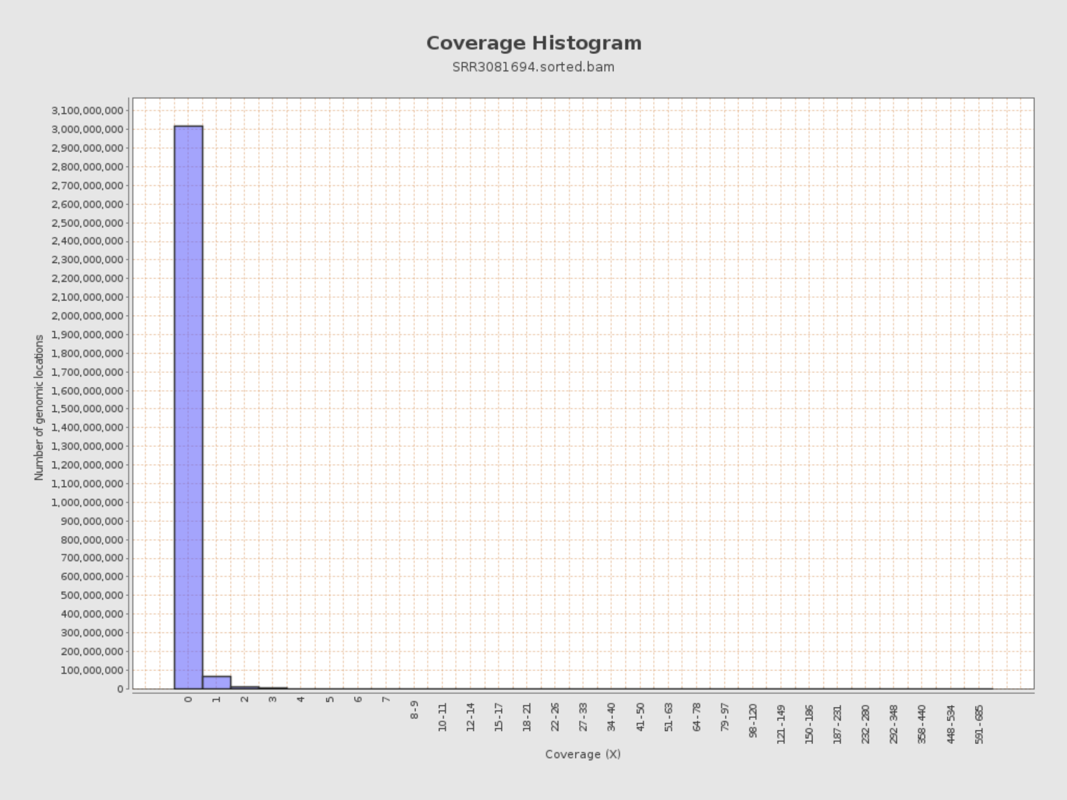
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7313159	0.0293	0.2976
chr2	243199373	7967192	0.0328	0.2638
chr3	198022430	7832243	0.0396	0.2399
chr4	191154276	7288174	0.0381	0.2396
chr5	180915260	6016755	0.0333	0.221
chr6	171115067	6128168	0.0358	0.2453
chr7	159138663	6153432	0.0387	0.3042

chr8	146364022	5118596	0.035	0.4596
chr9	141213431	3366837	0.0238	0.2189
chr10	135534747	5246903	0.0387	0.2604
chr11	135006516	4612499	0.0342	0.2365
chr12	133851895	4601506	0.0344	0.2249
chr13	115169878	3735331	0.0324	0.2174
chr14	107349540	3332290	0.031	0.2164
chr15	102531392	2451879	0.0239	0.1869
chr16	90354753	2484926	0.0275	0.2032
chr17	81195210	2044029	0.0252	0.1952
chr18	78077248	2356470	0.0302	0.3171
chr19	59128983	1390398	0.0235	0.246
chr20	63025520	1804565	0.0286	0.2058
chr21	48129895	1309125	0.0272	0.2024
chr22	51304566	744363	0.0145	0.143
chrMT	16571	22434	1.3538	1.5105
chrX	155270560	6238190	0.0402	0.2495
chrY	59373566	222148	0.0037	0.0847

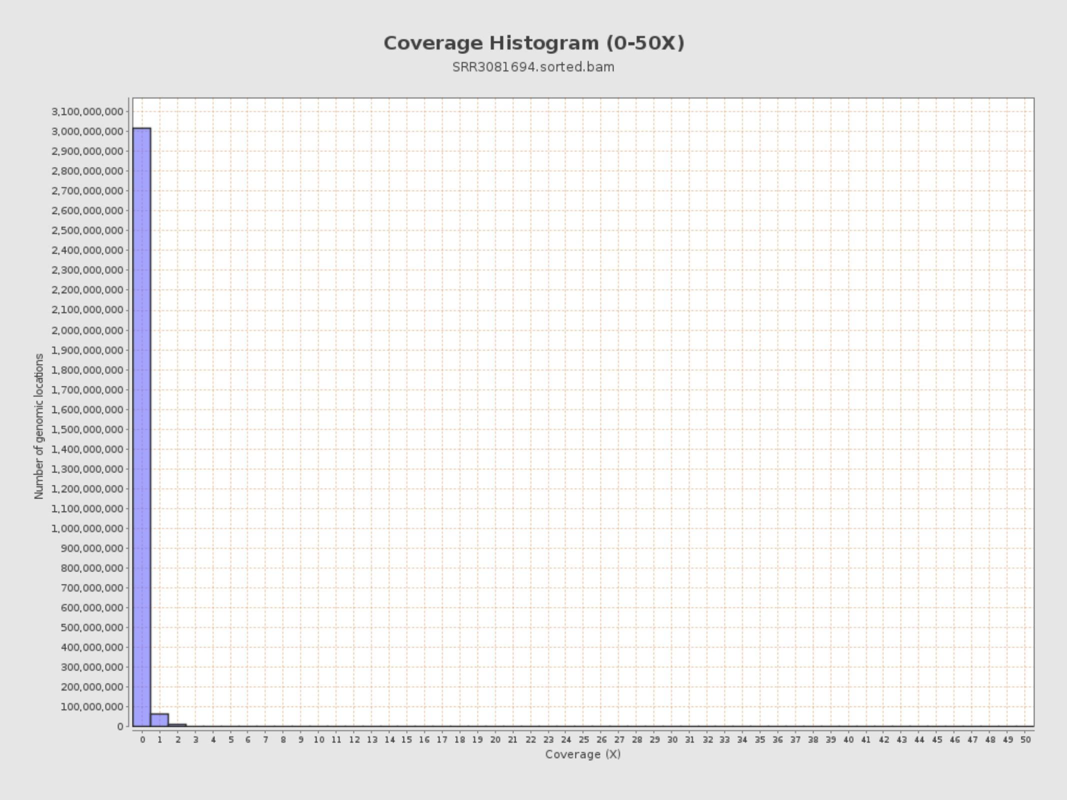
3. Results : Coverage across reference



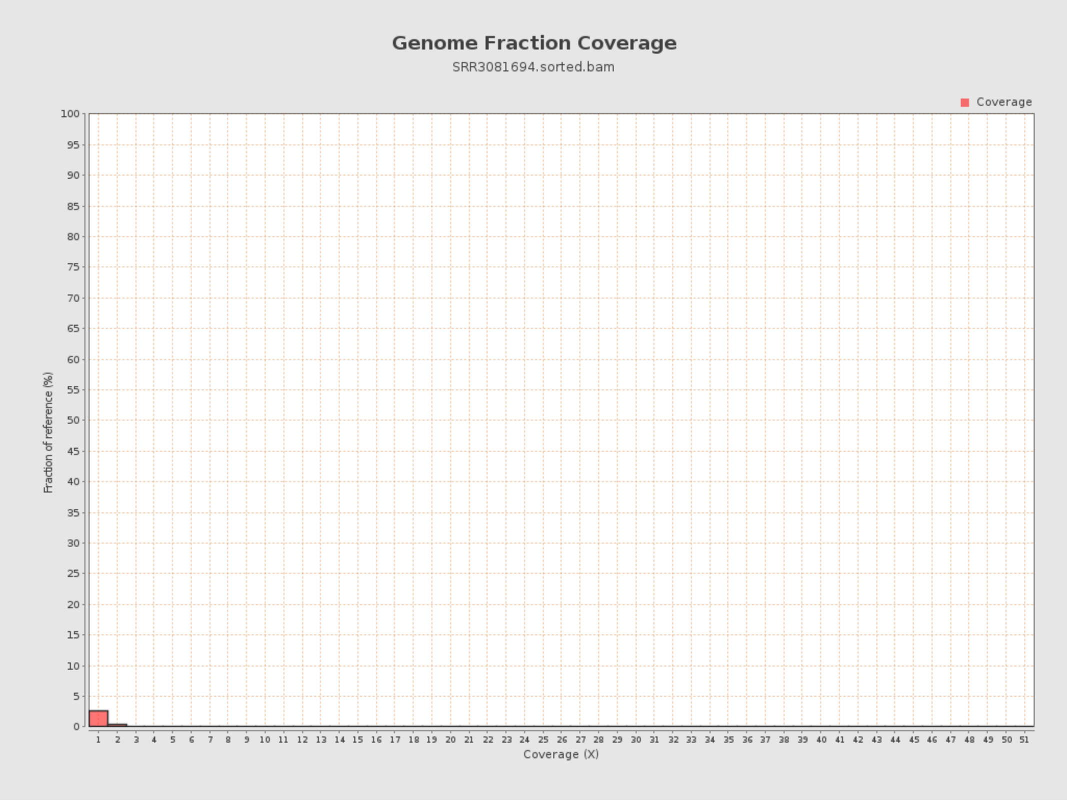
4. Results : Coverage Histogram



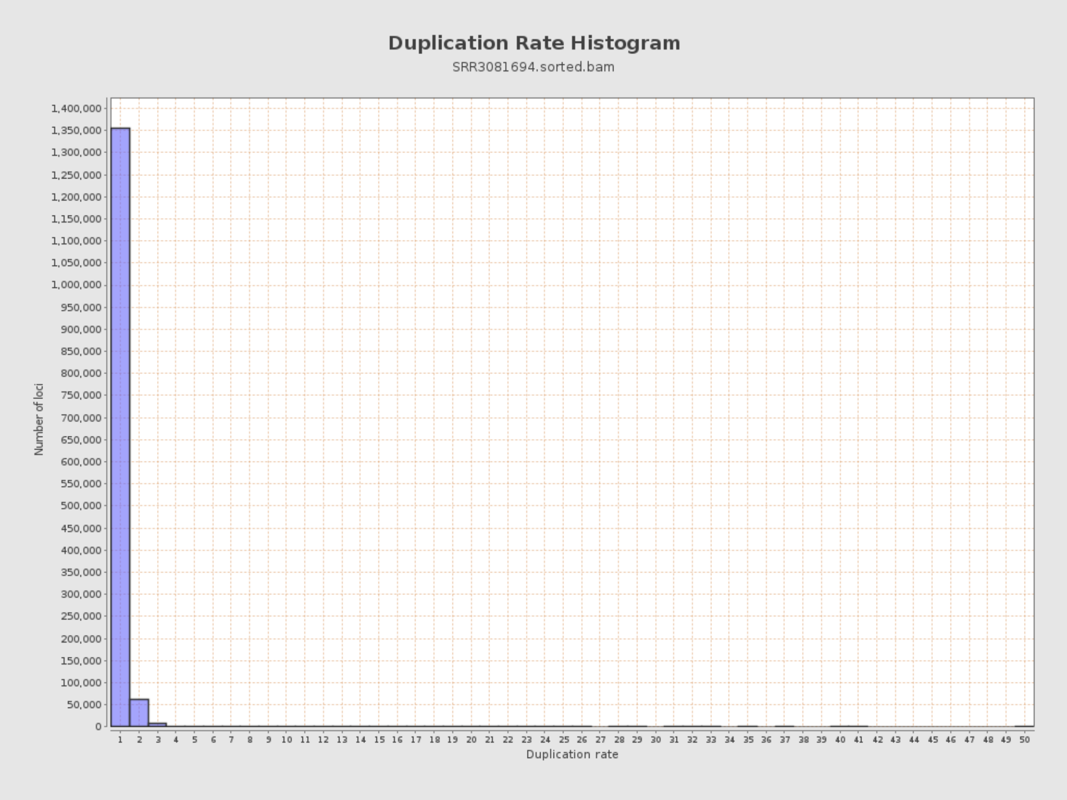
5. Results : Coverage Histogram (0-50X)



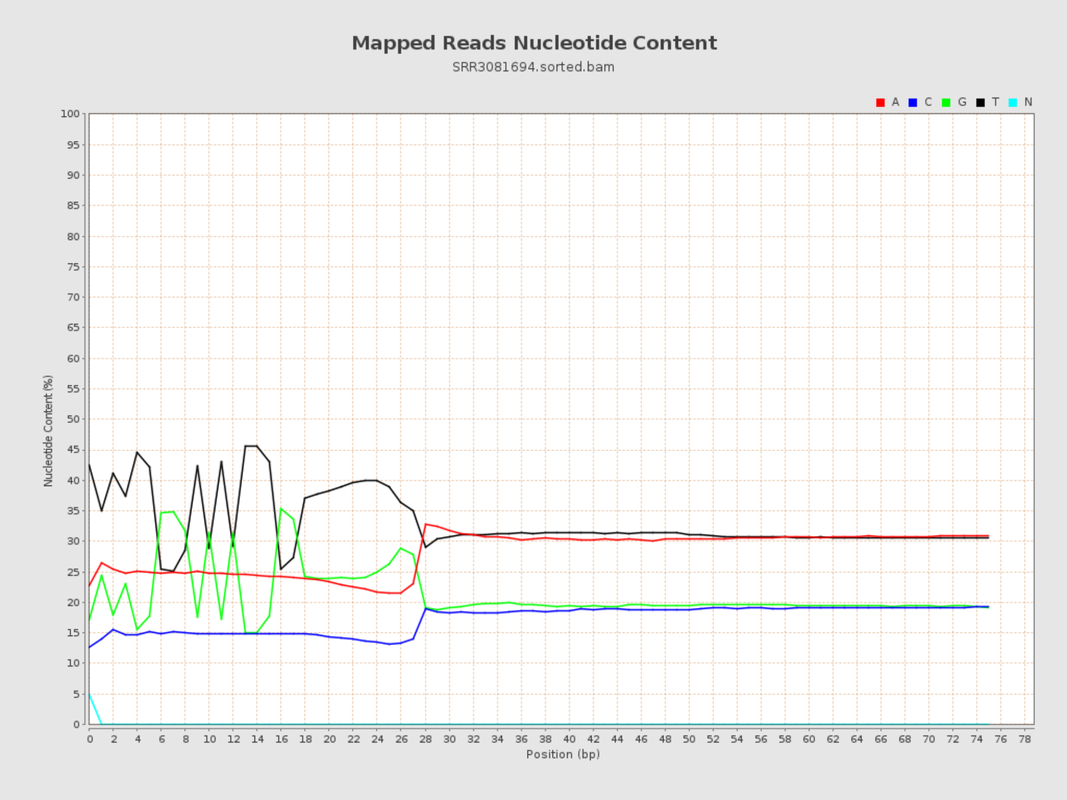
6. Results : Genome Fraction Coverage



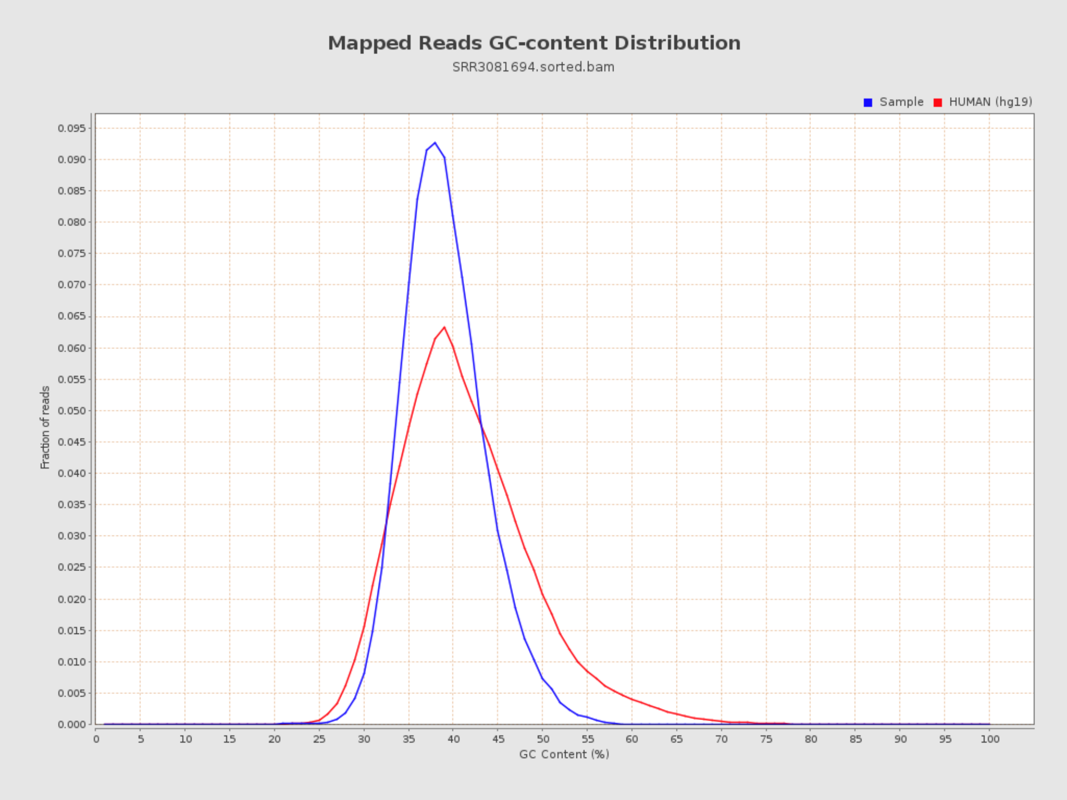
7. Results : Duplication Rate Histogram



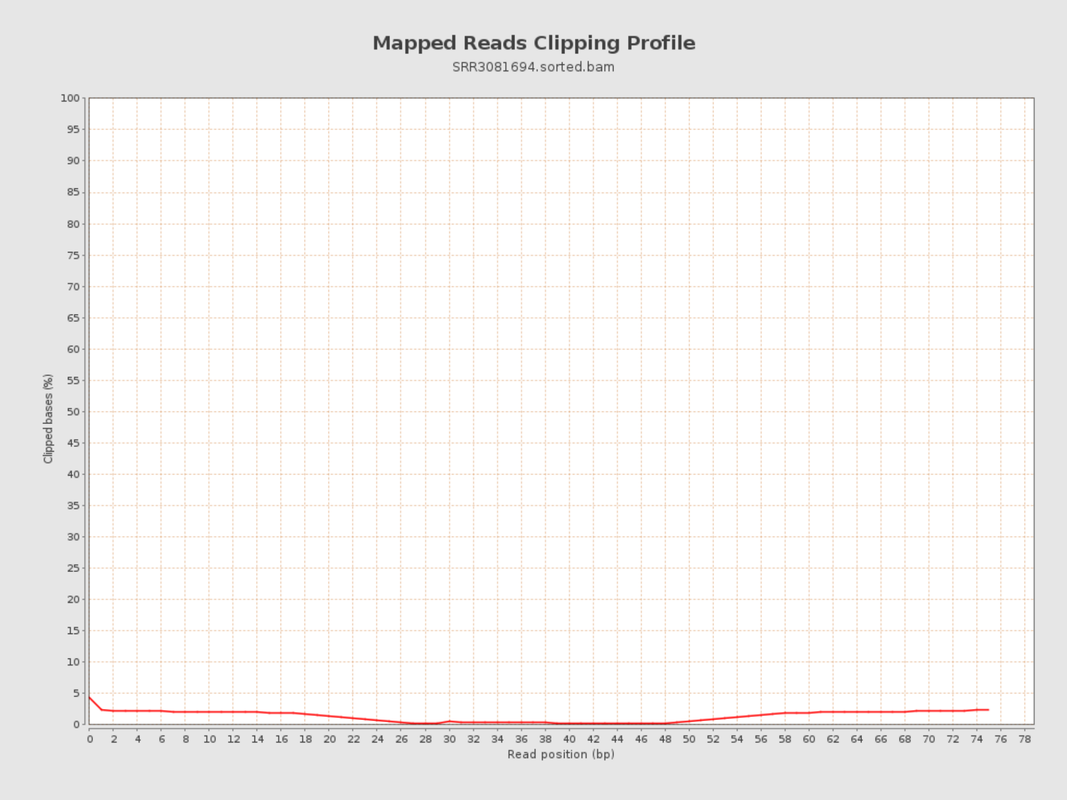
8. Results : Mapped Reads Nucleotide Content



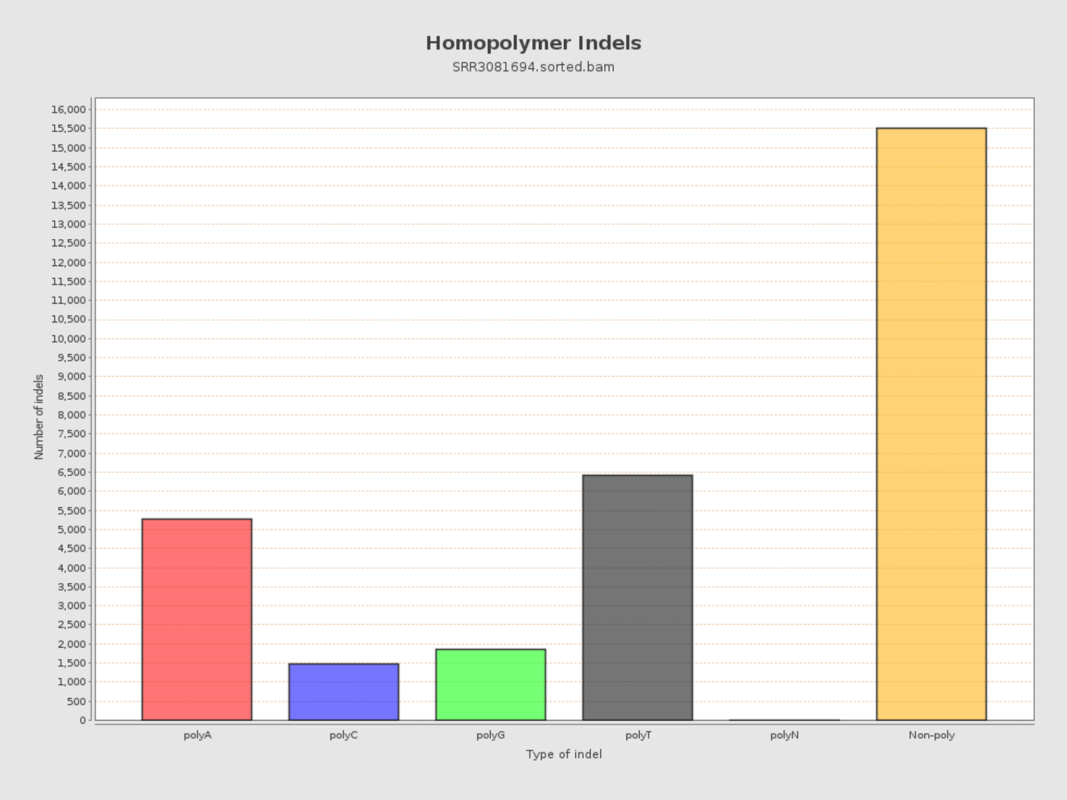
9. Results : Mapped Reads GC-content Distribution



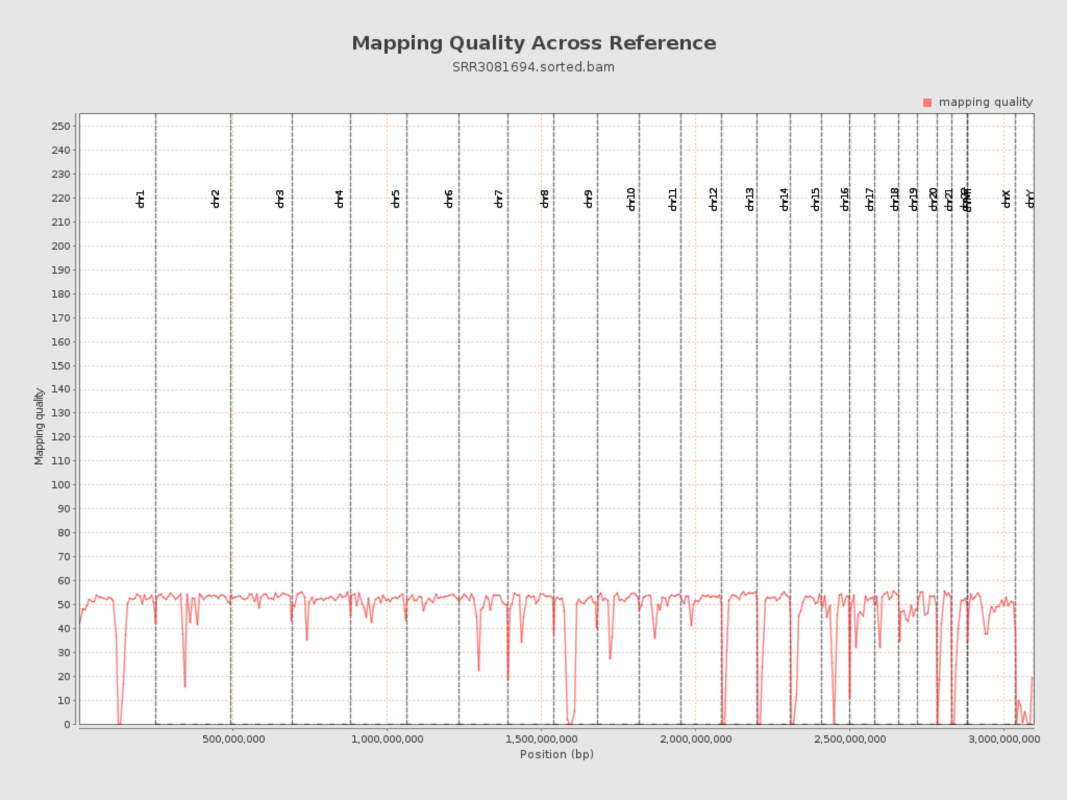
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram