Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 11:20:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080658.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_SRR3080658 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080658.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 11:20:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080658.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,218,225
Mapped reads	1,122,645 / 92.15%
Unmapped reads	95,580 / 7.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,764 / 0.88%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	34,988 / 2.87%
Duplication rate	2.71%
Clipped reads	462,263 / 37.95%

2.2. ACGT Content

Number/percentage of A's	21,173,564 / 28.01%
Number/percentage of C's	13,709,126 / 18.13%
Number/percentage of T's	24,249,188 / 32.08%
Number/percentage of G's	16,464,446 / 21.78%
Number/percentage of N's	3,325 / 0%
GC Percentage	39.91%

2.3. Coverage

Mean	0.0244

Standard Deviation	0.2058

2.4. Mapping Quality

Mean Mapping Quality	46.3

2.5. Mismatches and indels

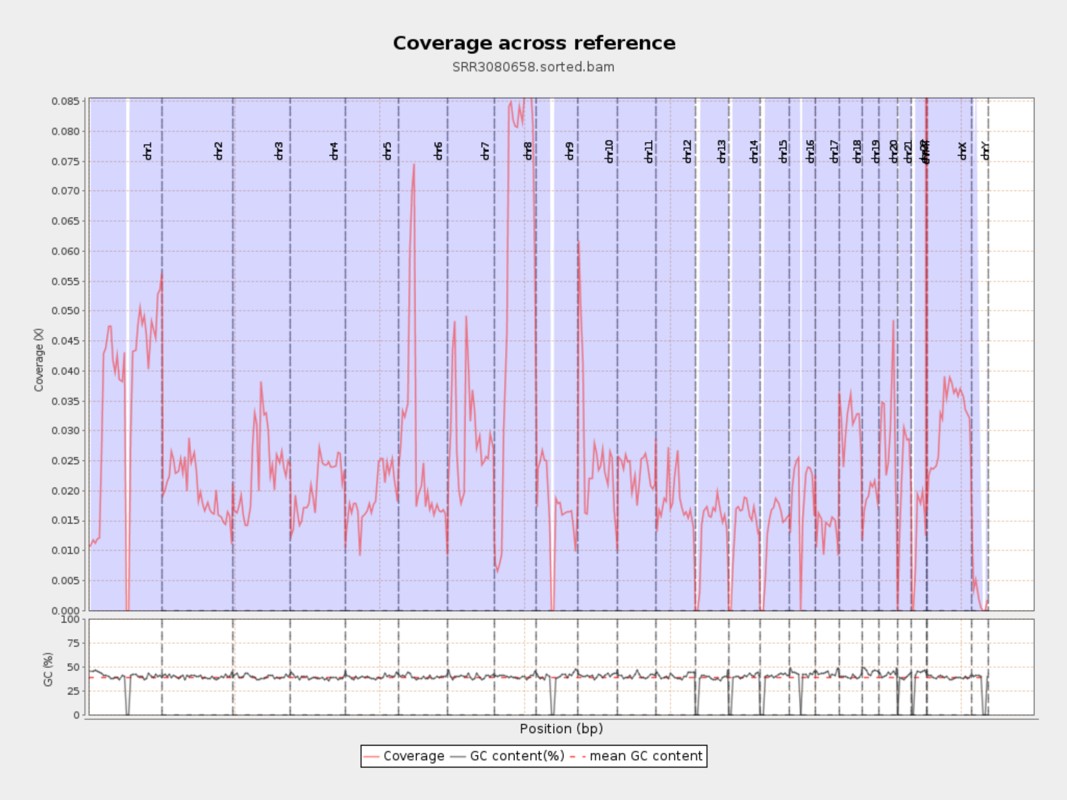
General error rate	0.69%
Mismatches	513,768
Insertions	5,941
Mapped reads with at least one insertion	0.53%
Deletions	17,763
Mapped reads with at least one deletion	1.57%
Homopolymer indels	48.76%

2.6. Chromosome stats

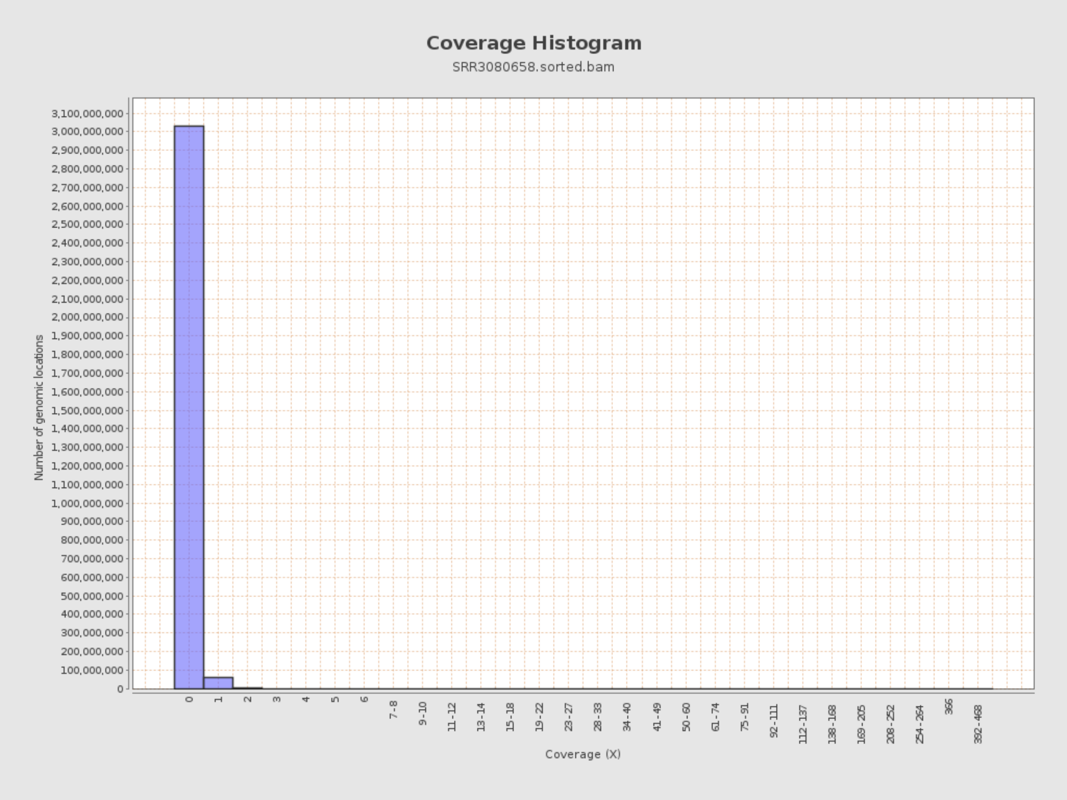
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9023409	0.0362	0.259
chr2	243199373	4907973	0.0202	0.2606
chr3	198022430	4688826	0.0237	0.169
chr4	191154276	3960765	0.0207	0.1587
chr5	180915260	3442470	0.019	0.1505
chr6	171115067	4697330	0.0275	0.2167
chr7	159138663	4824059	0.0303	0.3561

chr8	146364022	9086834	0.0621	0.308
chr9	141213431	2361312	0.0167	0.1572
chr10	135534747	3653602	0.027	0.1877
chr11	135006516	3102403	0.023	0.1726
chr12	133851895	2403840	0.018	0.1473
chr13	115169878	1543992	0.0134	0.1263
chr14	107349540	1483838	0.0138	0.1309
chr15	102531392	1332278	0.013	0.1307
chr16	90354753	1768765	0.0196	0.1546
chr17	81195210	1097887	0.0135	0.1297
chr18	78077248	2448701	0.0314	0.2286
chr19	59128983	1126873	0.0191	0.1734
chr20	63025520	1882043	0.0299	0.1898
chr21	48129895	1051307	0.0218	0.1634
chr22	51304566	643989	0.0126	0.122
chrMT	16571	12744	0.7691	1.0353
chrX	155270560	4935200	0.0318	0.2008
chrY	59373566	148012	0.0025	0.0562

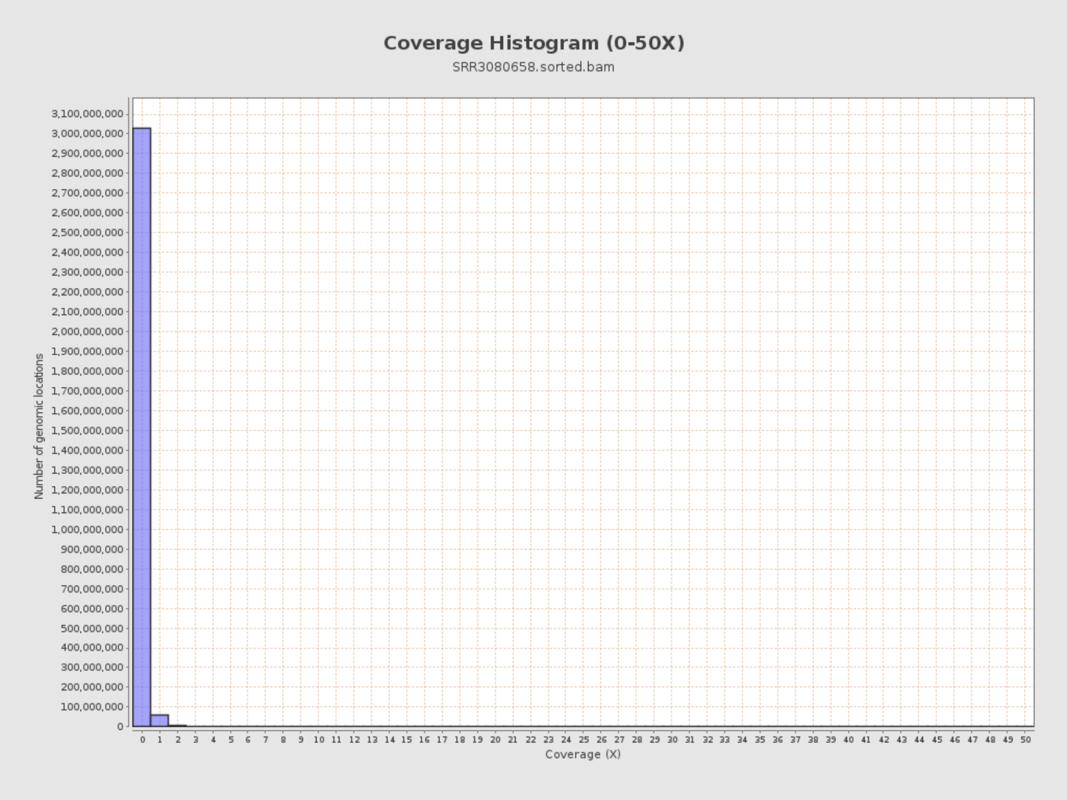
3. Results : Coverage across reference



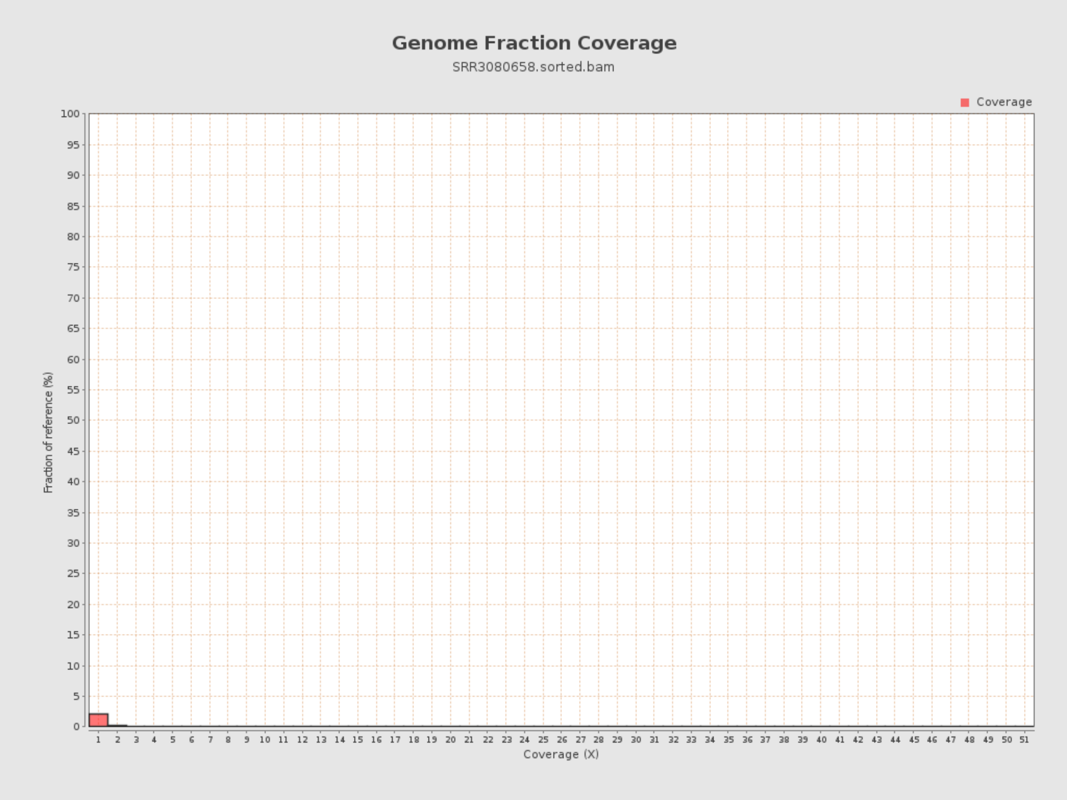
4. Results : Coverage Histogram



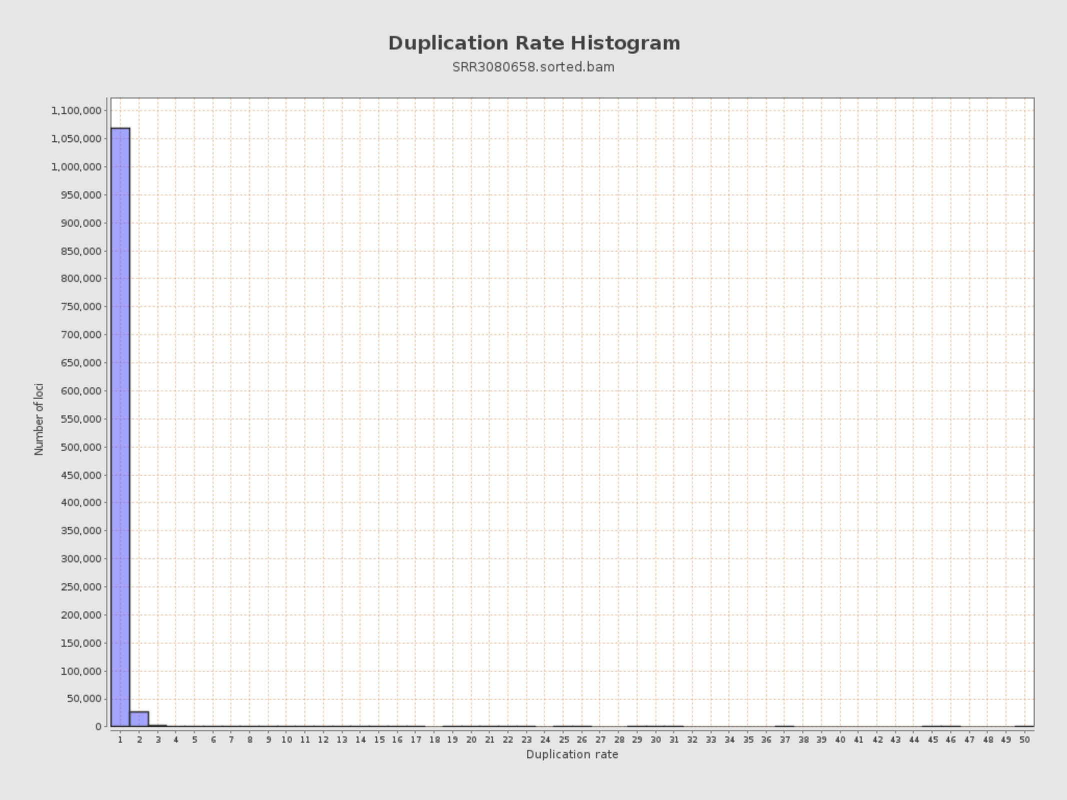
5. Results : Coverage Histogram (0-50X)



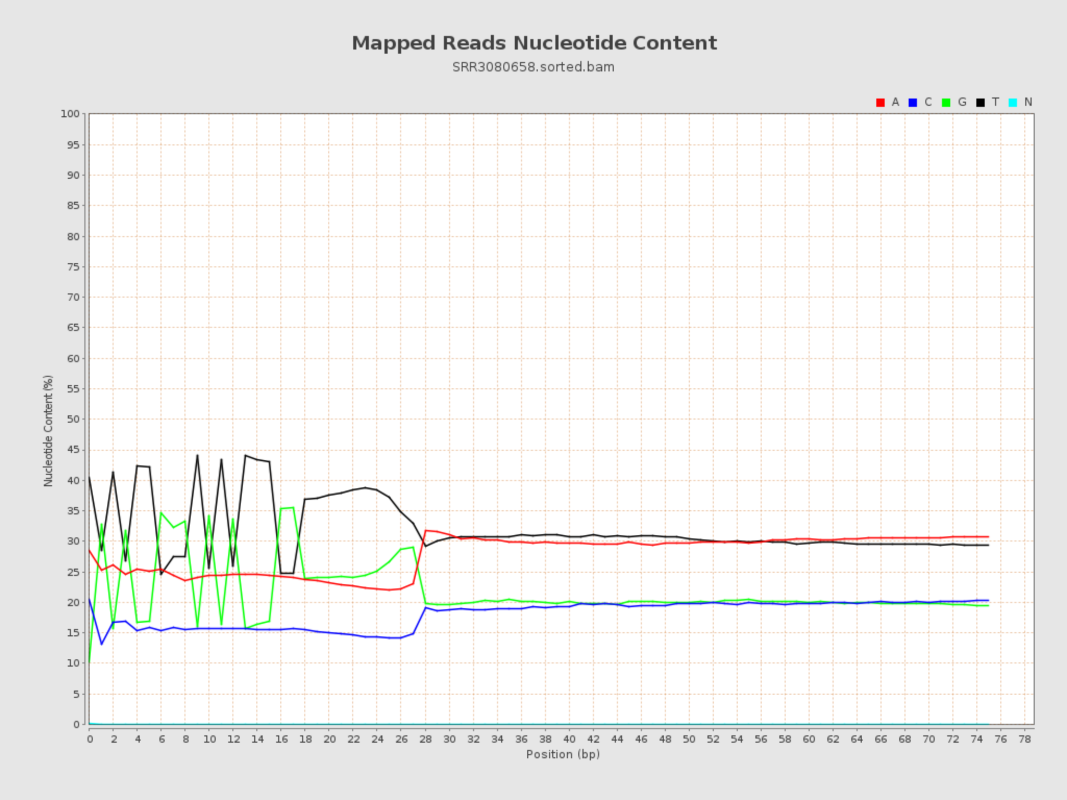
6. Results : Genome Fraction Coverage



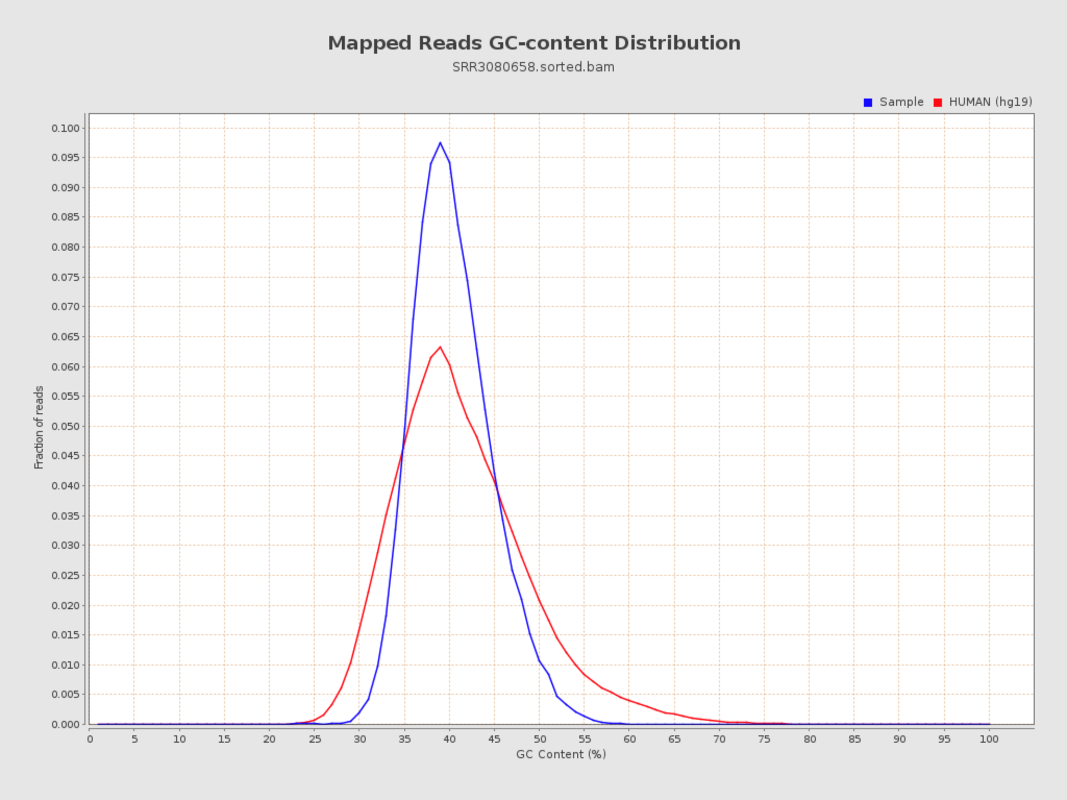
7. Results : Duplication Rate Histogram



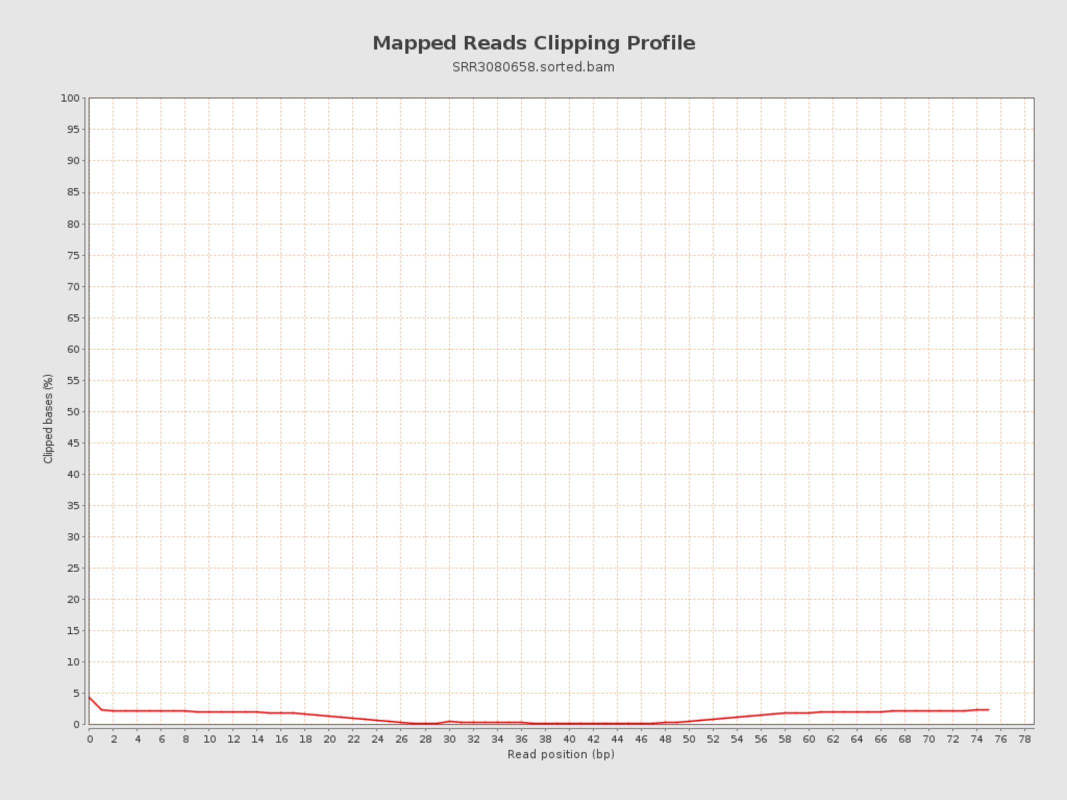
8. Results : Mapped Reads Nucleotide Content



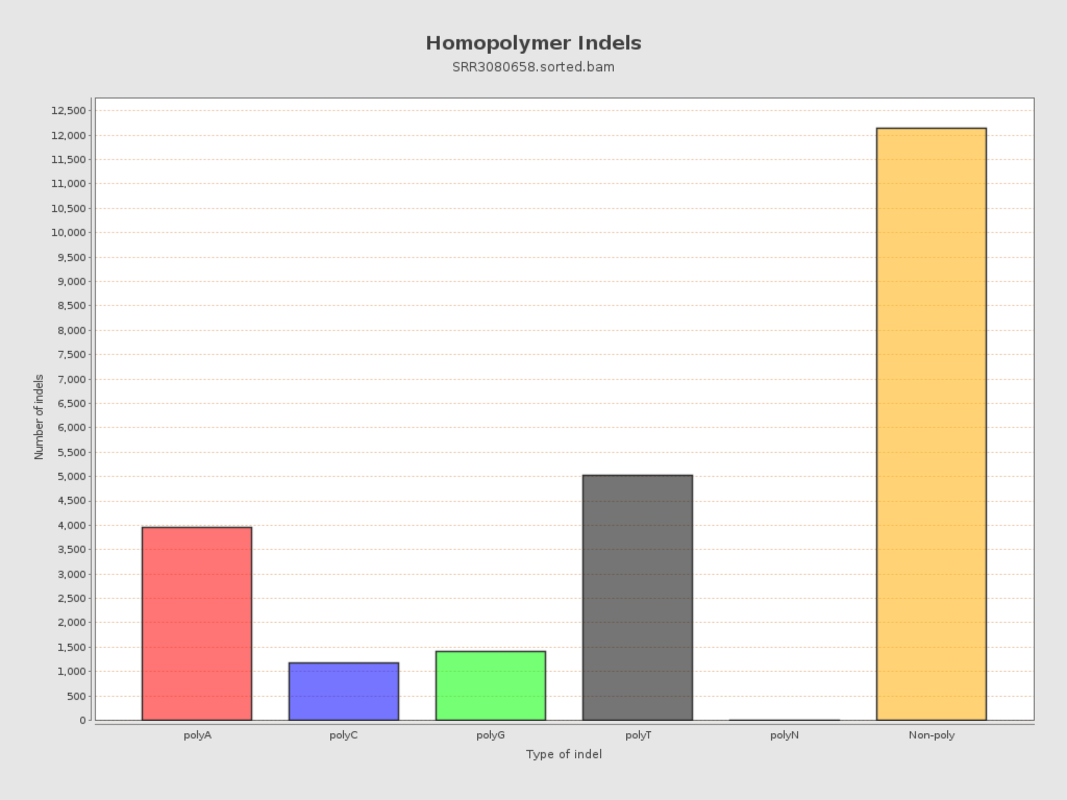
9. Results : Mapped Reads GC-content Distribution



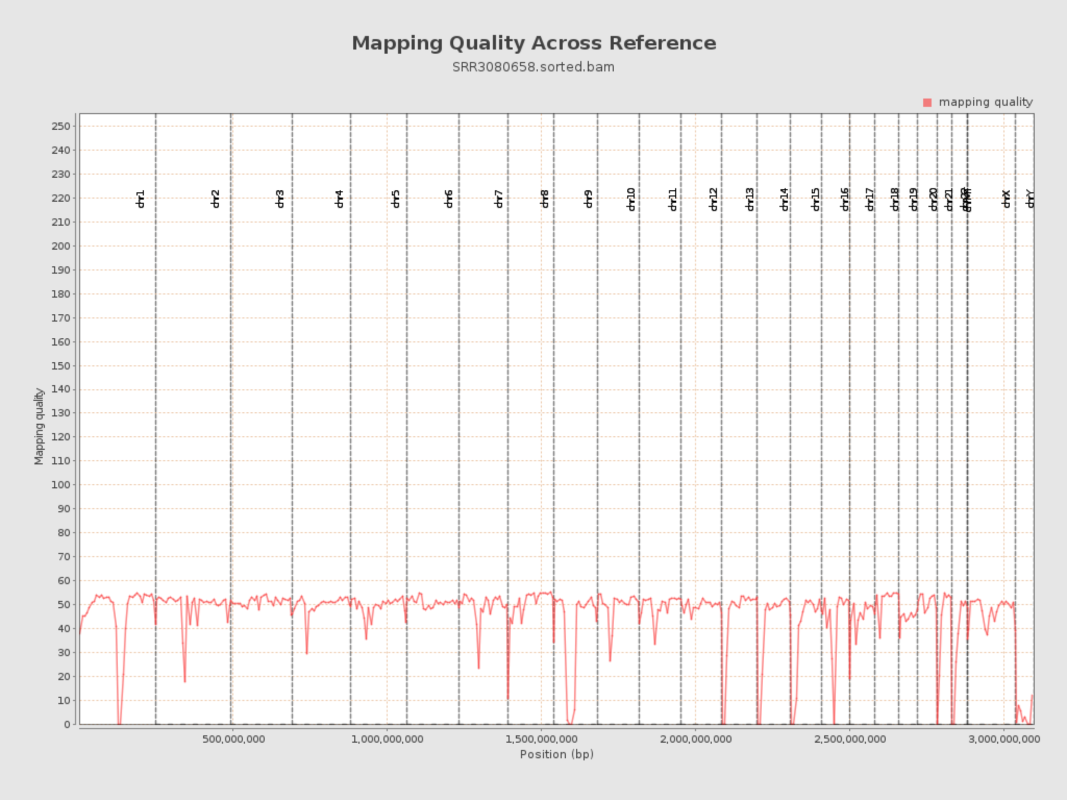
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram