Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 13:54:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080976.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_SRR3080976 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080976.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 13:54:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080976.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,244,403
Mapped reads	5,587,335 / 89.48%
Unmapped reads	657,068 / 10.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	51,371 / 0.82%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	406,397 / 6.51%
Duplication rate	5.74%
Clipped reads	2,311,428 / 37.02%

2.2. ACGT Content

Number/percentage of A's	106,080,281 / 28.03%
Number/percentage of C's	68,436,395 / 18.08%
Number/percentage of T's	121,121,174 / 32%
Number/percentage of G's	82,109,596 / 21.69%
Number/percentage of N's	758,456 / 0.2%
GC Percentage	39.77%

2.3. Coverage

Mean	0.1223

Standard Deviation	0.7896

2.4. Mapping Quality

Mean Mapping Quality	46.87

2.5. Mismatches and indels

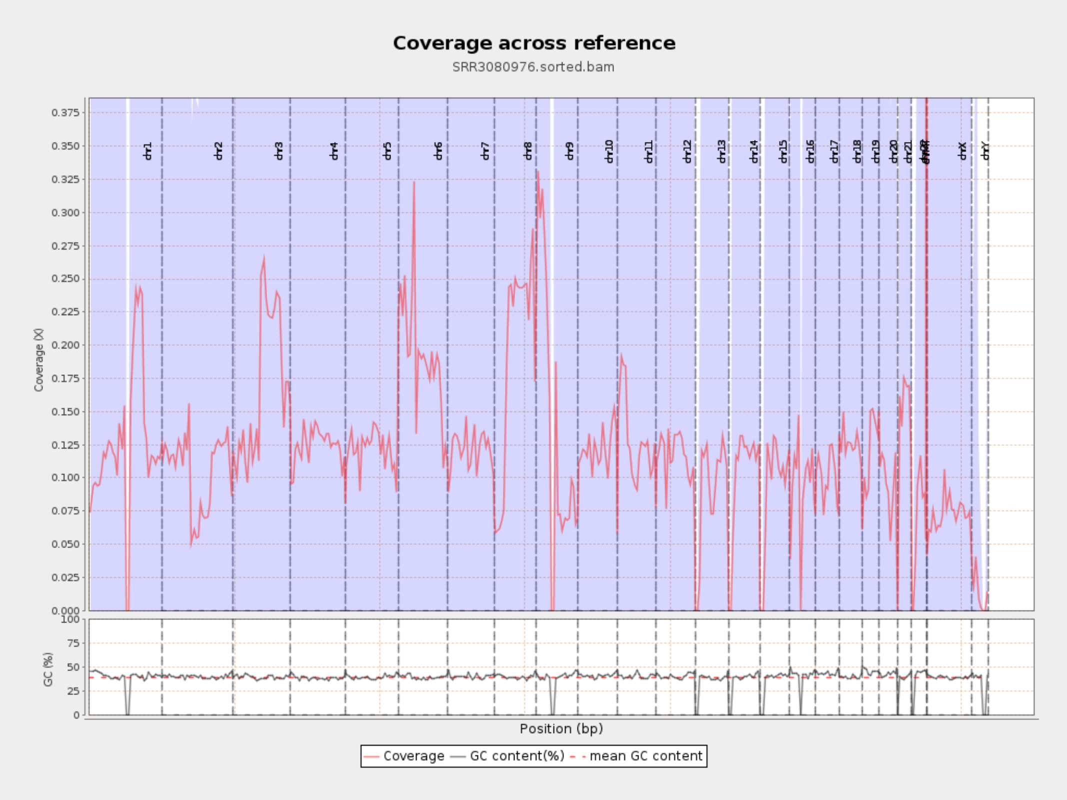
General error rate	1.01%
Mismatches	3,774,292
Insertions	29,422
Mapped reads with at least one insertion	0.52%
Deletions	83,273
Mapped reads with at least one deletion	1.47%
Homopolymer indels	49.09%

2.6. Chromosome stats

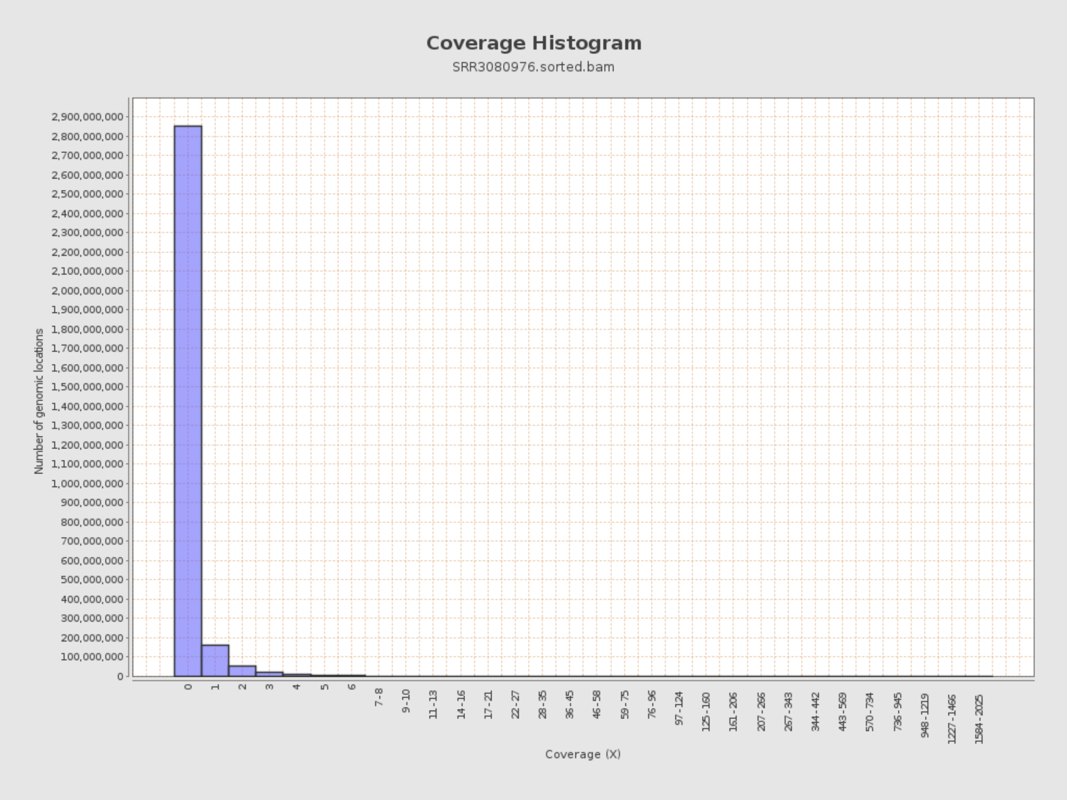
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	31589630	0.1267	1.0221
chr2	243199373	25792611	0.1061	0.7751
chr3	198022430	33253223	0.1679	0.5955
chr4	191154276	23803669	0.1245	0.5339
chr5	180915260	22012889	0.1217	0.5024
chr6	171115067	33034749	0.1931	0.956
chr7	159138663	19443420	0.1222	0.8833

chr8	146364022	28118644	0.1921	1.408
chr9	141213431	19663234	0.1392	1.0055
chr10	135534747	16638409	0.1228	0.643
chr11	135006516	17255610	0.1278	0.6767
chr12	133851895	15595207	0.1165	0.5366
chr13	115169878	10227210	0.0888	0.4265
chr14	107349540	10925504	0.1018	0.6582
chr15	102531392	9452198	0.0922	0.4377
chr16	90354753	8483992	0.0939	0.5816
chr17	81195210	8154805	0.1004	0.4806
chr18	78077248	9836033	0.126	1.6857
chr19	59128983	7124821	0.1205	0.8333
chr20	63025520	6019869	0.0955	0.5024
chr21	48129895	6860079	0.1425	0.6916
chr22	51304566	3369721	0.0657	0.3652
chrMT	16571	33788	2.039	2.3319
chrX	155270560	11193567	0.0721	0.4466
chrY	59373566	760236	0.0128	0.2429

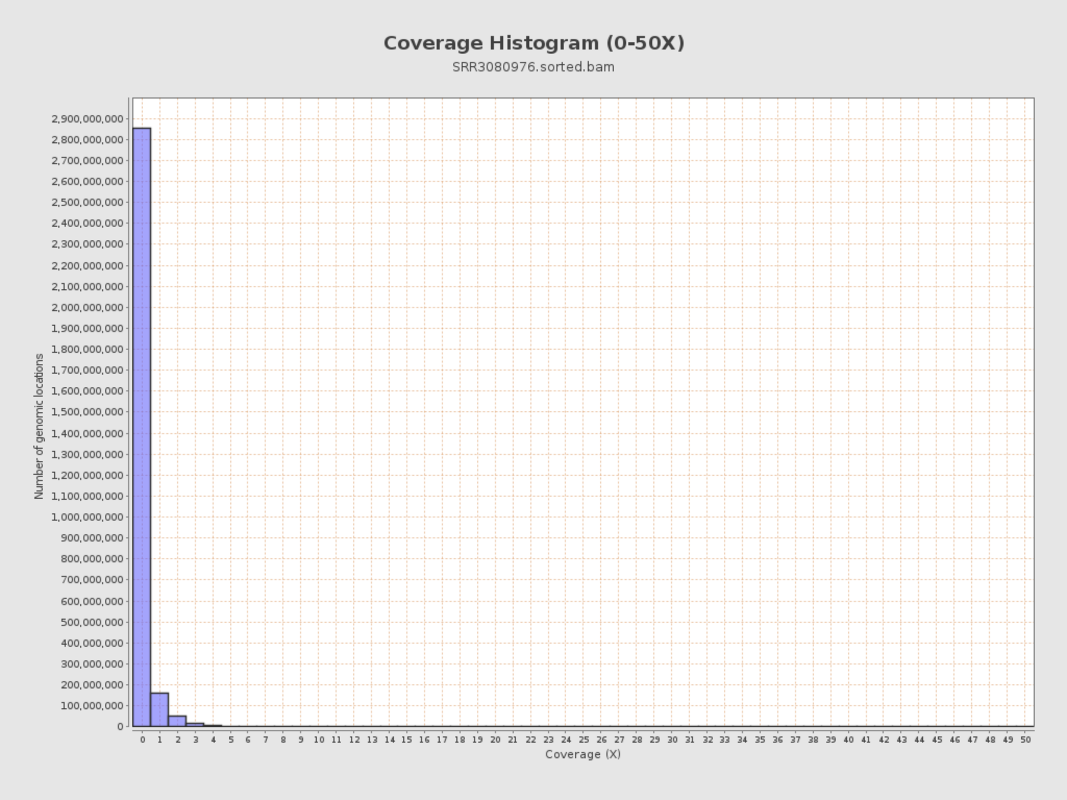
3. Results : Coverage across reference



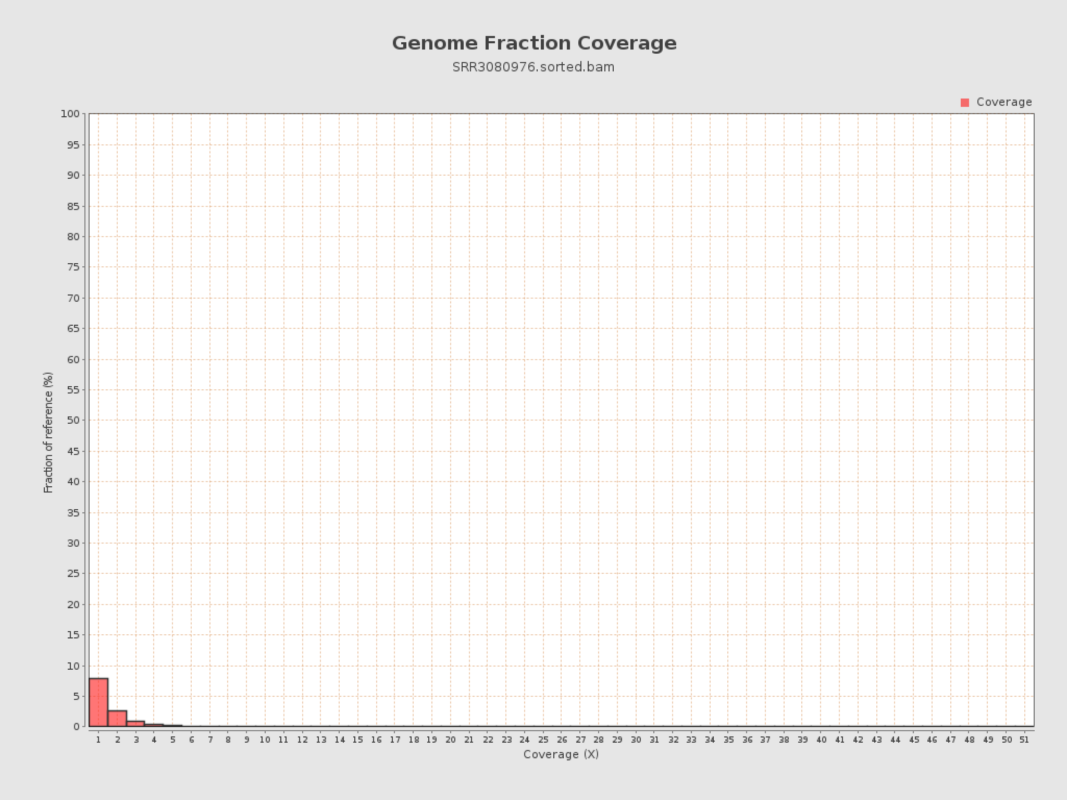
4. Results : Coverage Histogram



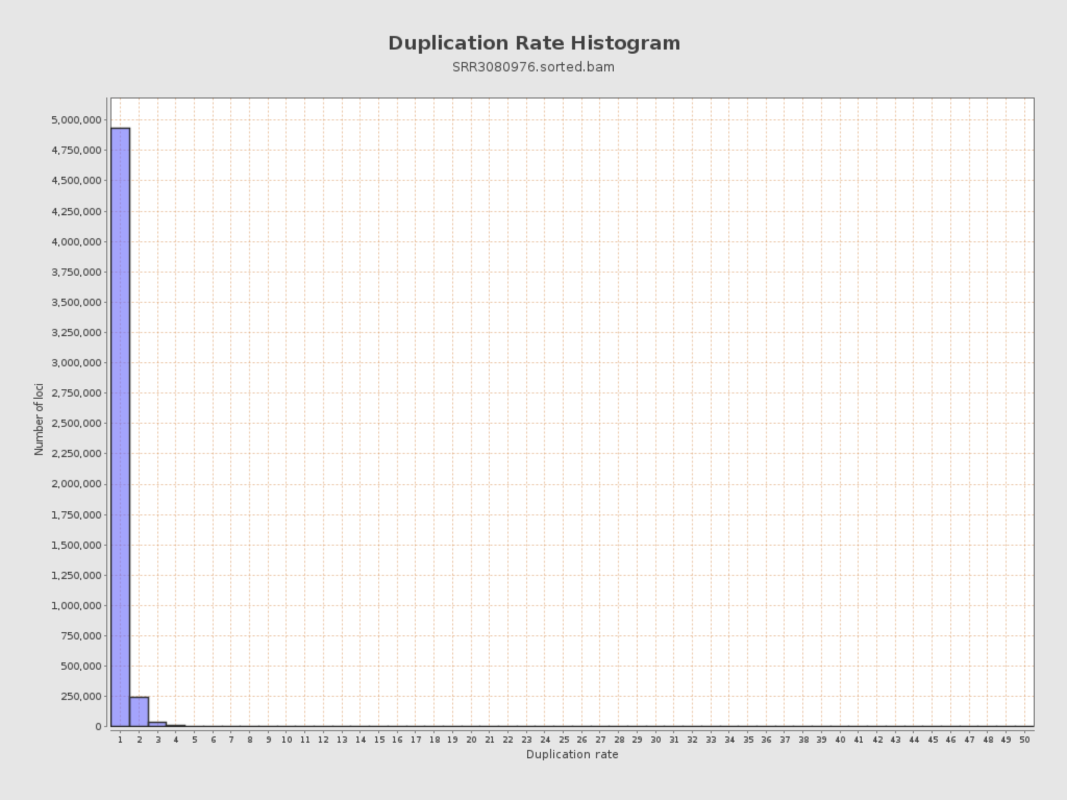
5. Results : Coverage Histogram (0-50X)



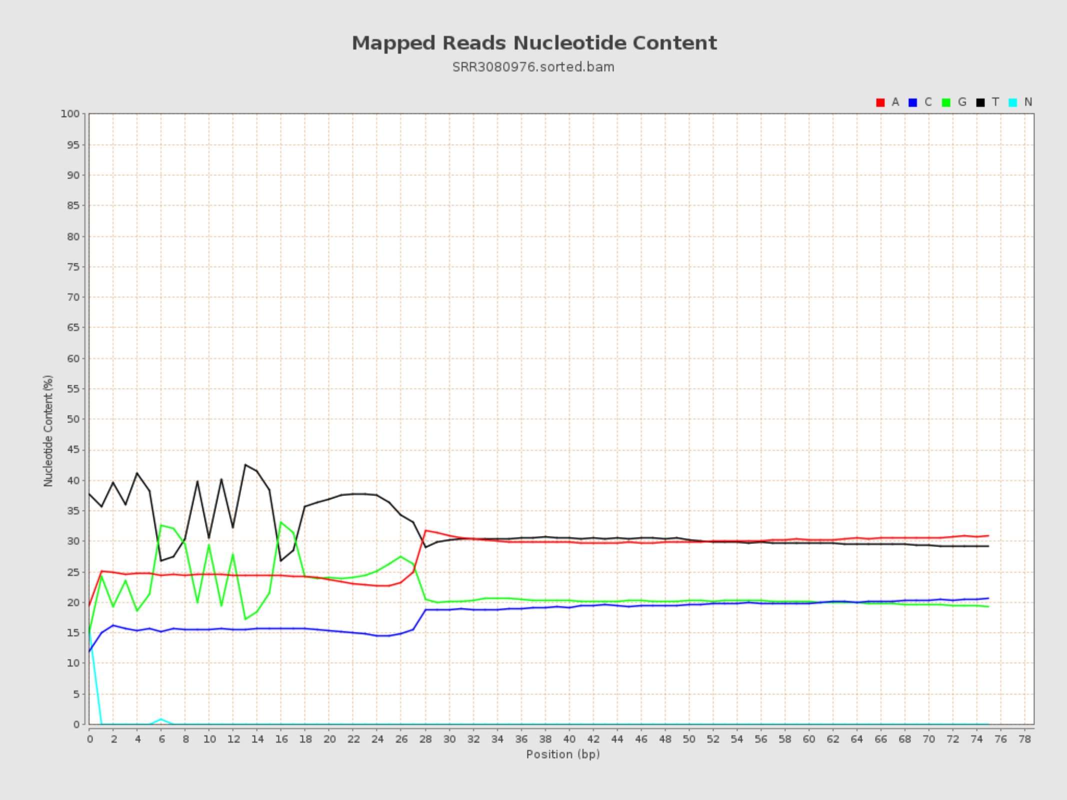
6. Results : Genome Fraction Coverage



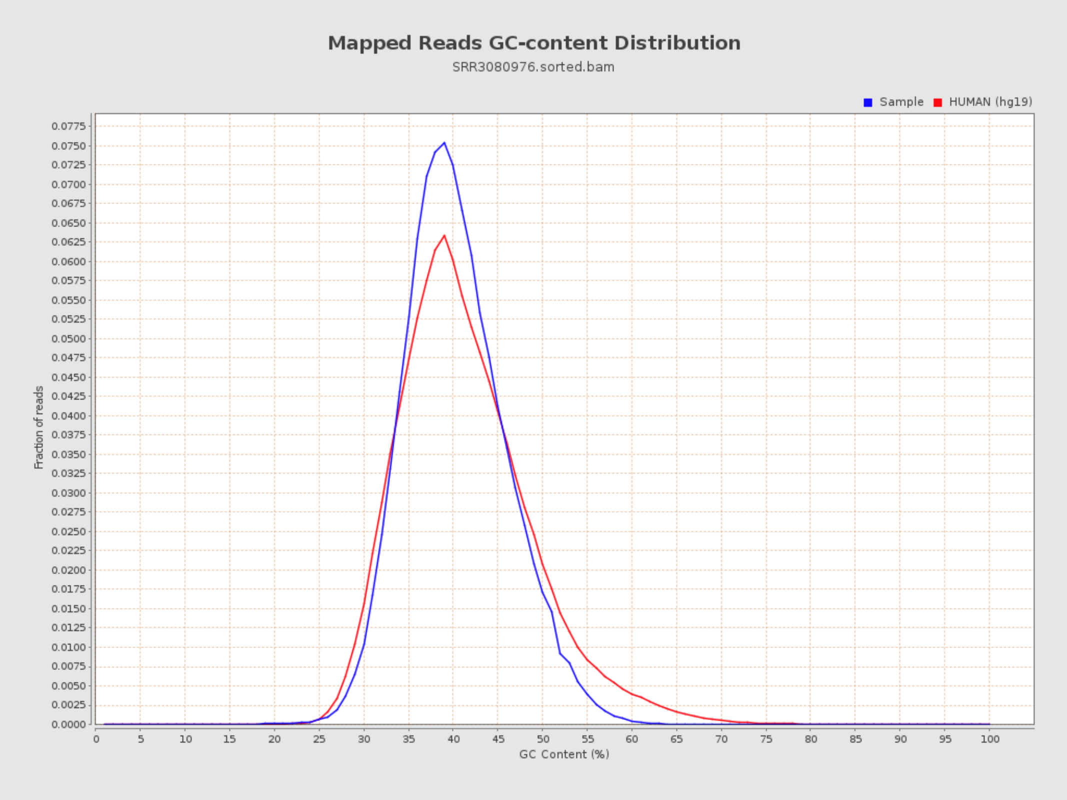
7. Results : Duplication Rate Histogram



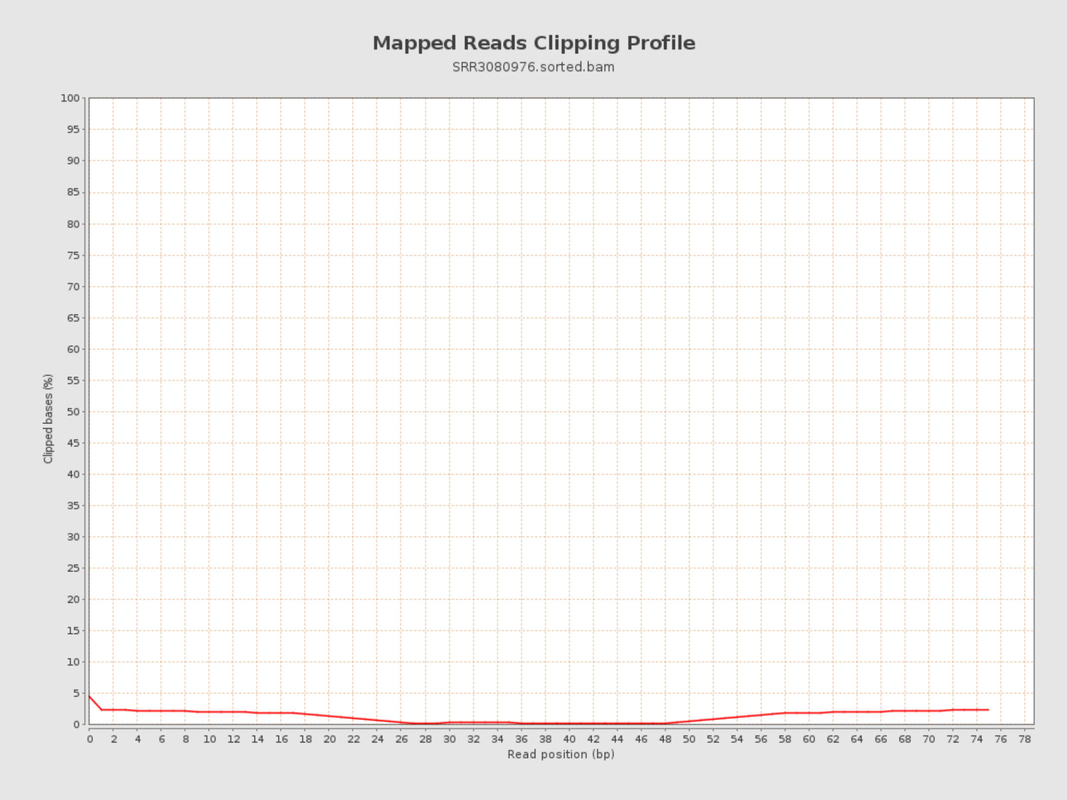
8. Results : Mapped Reads Nucleotide Content



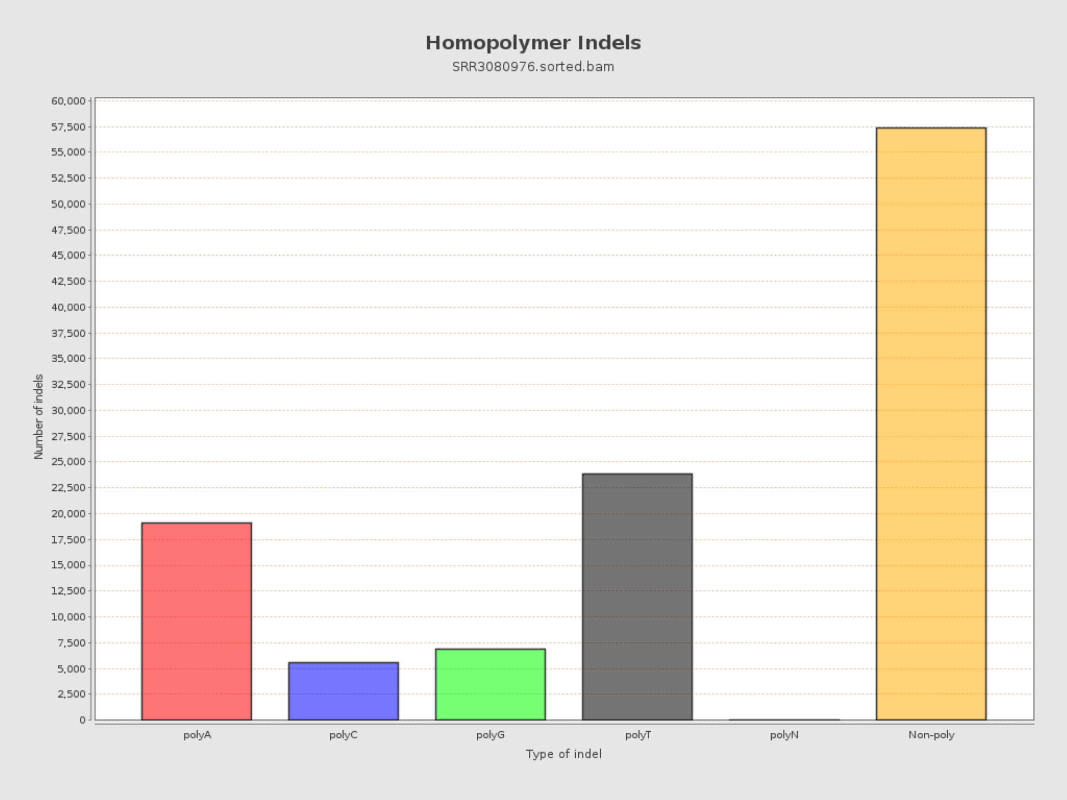
9. Results : Mapped Reads GC-content Distribution



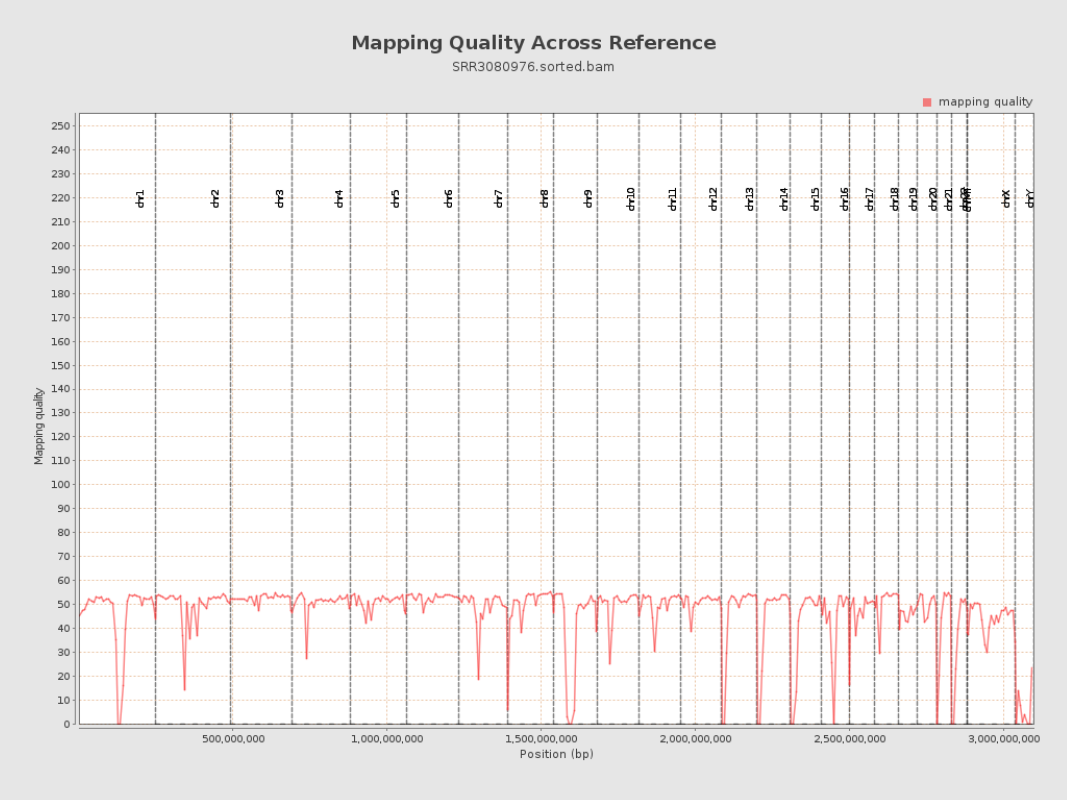
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram