Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 22:10:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082974.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_SRR3082974 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082974.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 22:10:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082974.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,852,943
Mapped reads	2,251,962 / 78.93%
Unmapped reads	600,981 / 21.07%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,217 / 0.6%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	84,215 / 2.95%
Duplication rate	3.09%
Clipped reads	1,088,670 / 38.16%

2.2. ACGT Content

Number/percentage of A's	42,837,247 / 28.8%
Number/percentage of C's	26,709,441 / 17.96%
Number/percentage of T's	46,926,445 / 31.55%
Number/percentage of G's	32,237,325 / 21.68%
Number/percentage of N's	14,219 / 0.01%
GC Percentage	39.63%

2.3. Coverage

Mean	0.0481

Standard Deviation	0.3462

2.4. Mapping Quality

Mean Mapping Quality	46.01

2.5. Mismatches and indels

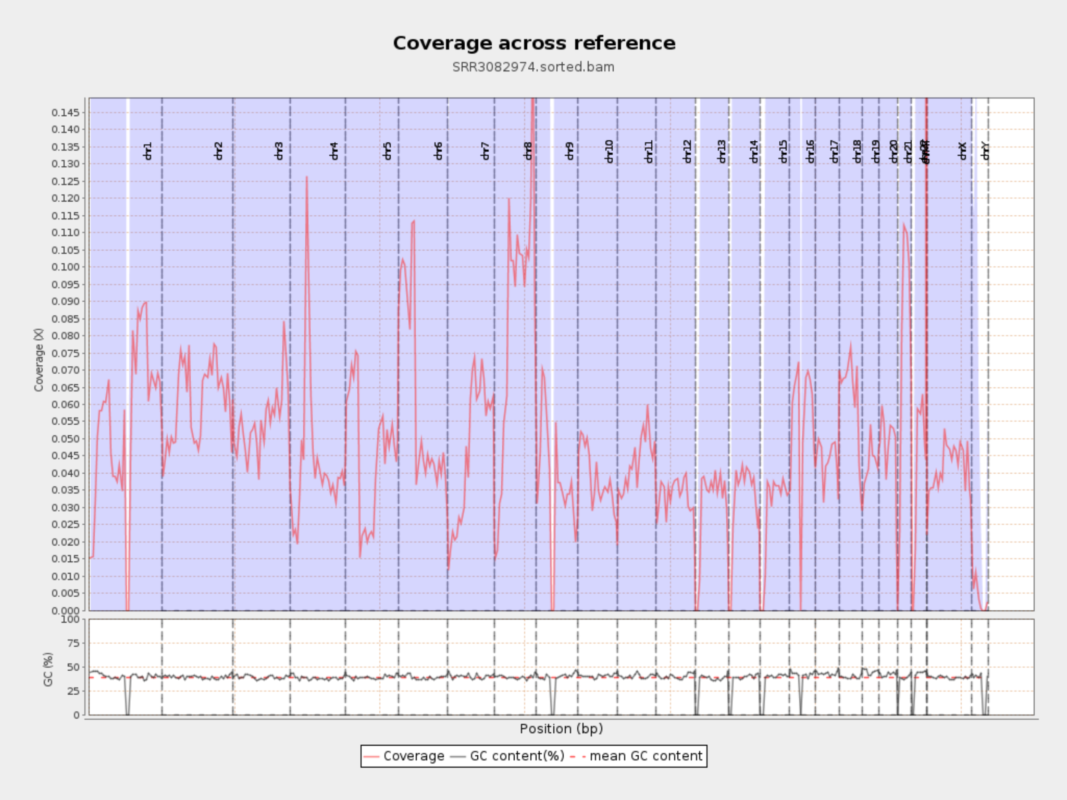
General error rate	0.96%
Mismatches	1,402,783
Insertions	12,326
Mapped reads with at least one insertion	0.54%
Deletions	33,284
Mapped reads with at least one deletion	1.46%
Homopolymer indels	46.85%

2.6. Chromosome stats

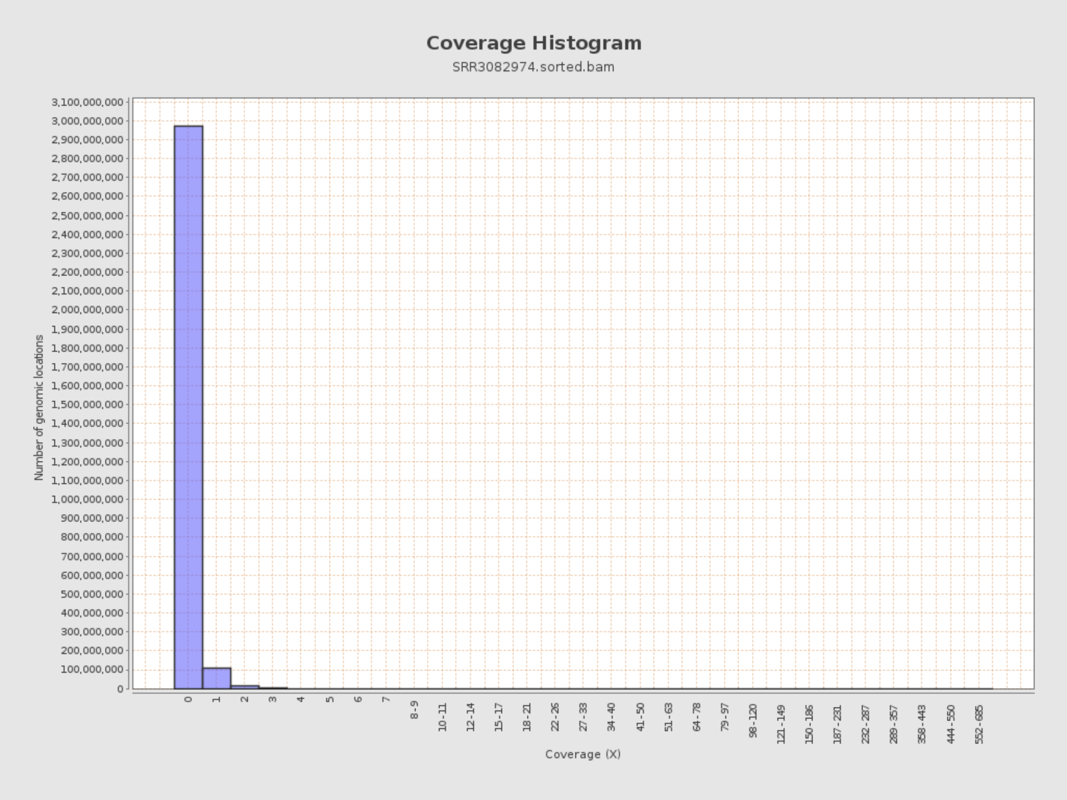
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13625901	0.0547	0.5537
chr2	243199373	14817804	0.0609	0.4613
chr3	198022430	11003579	0.0556	0.269
chr4	191154276	8330576	0.0436	0.2423
chr5	180915260	8285324	0.0458	0.2461
chr6	171115067	10556917	0.0617	0.3322
chr7	159138663	7488521	0.0471	0.3121

chr8	146364022	12524903	0.0856	0.483
chr9	141213431	5222291	0.037	0.3272
chr10	135534747	5277410	0.0389	0.2524
chr11	135006516	5813973	0.0431	0.2789
chr12	133851895	4470501	0.0334	0.2108
chr13	115169878	3468328	0.0301	0.1977
chr14	107349540	3375422	0.0314	0.2356
chr15	102531392	2933875	0.0286	0.194
chr16	90354753	5061677	0.056	0.2932
chr17	81195210	3540504	0.0436	0.2542
chr18	78077248	4954337	0.0635	0.6864
chr19	59128983	2524789	0.0427	0.3888
chr20	63025520	3098621	0.0492	0.2643
chr21	48129895	3642707	0.0757	0.3245
chr22	51304566	1982234	0.0386	0.2231
chrMT	16571	103804	6.2642	4.9465
chrX	155270560	6435928	0.0414	0.2581
chrY	59373566	242239	0.0041	0.0827

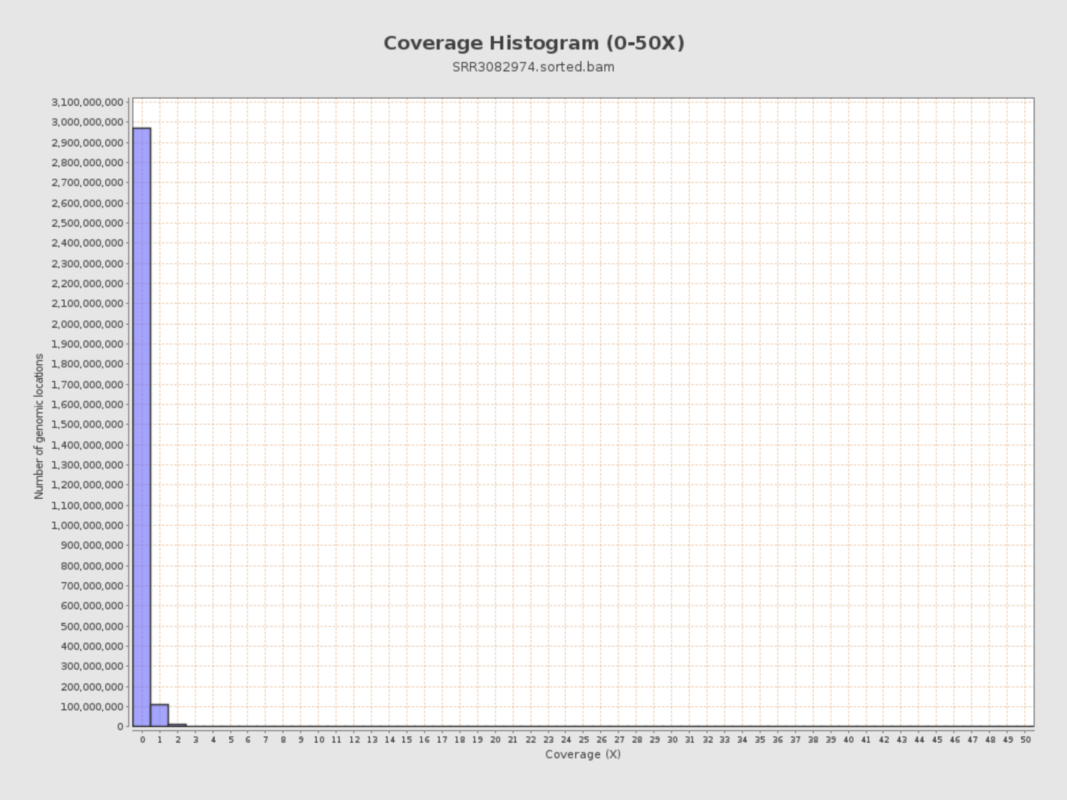
3. Results : Coverage across reference



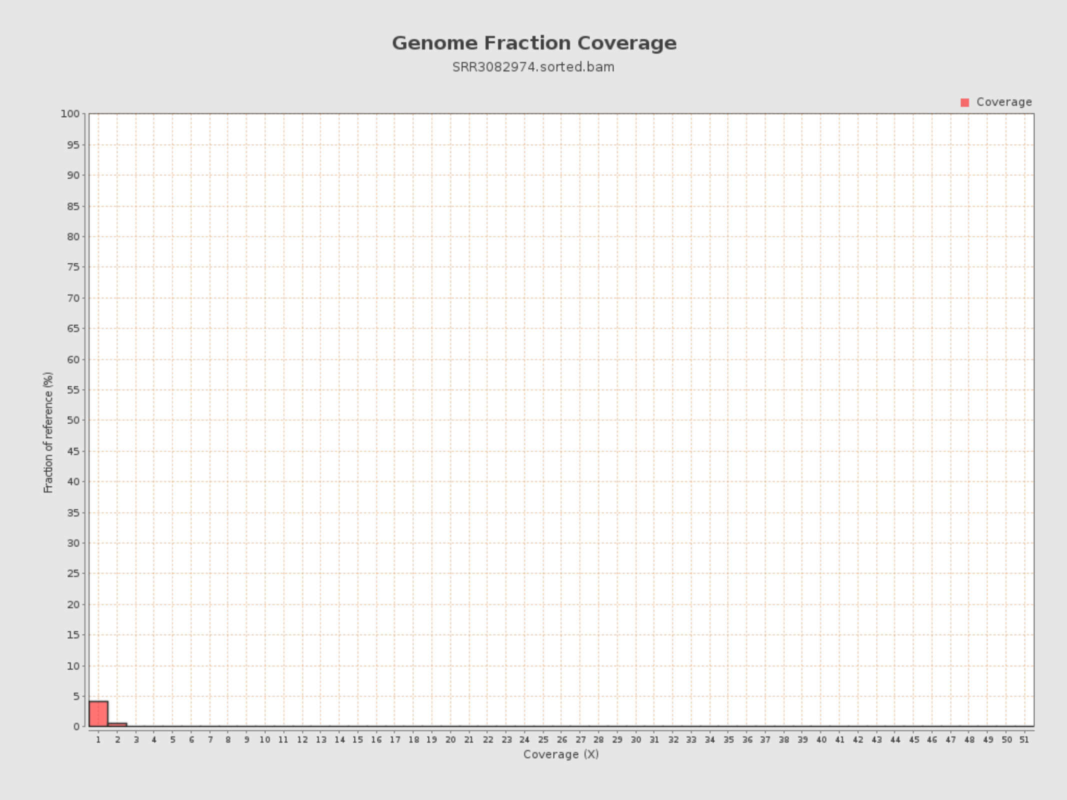
4. Results : Coverage Histogram



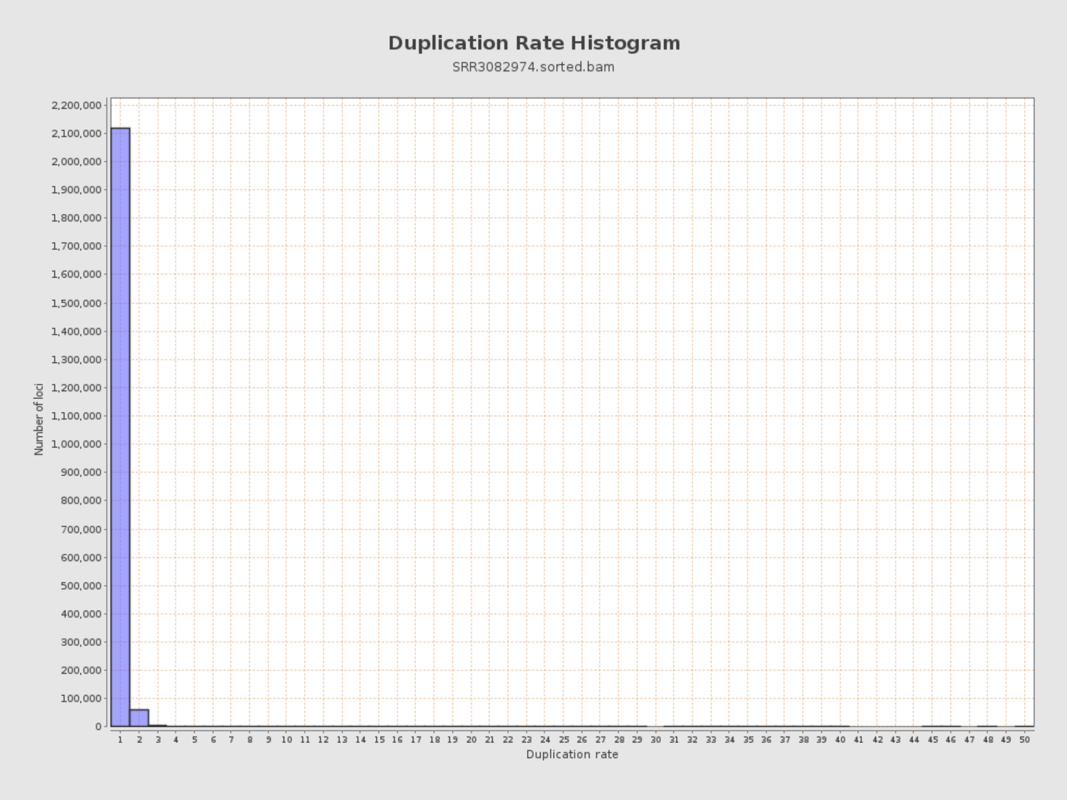
5. Results : Coverage Histogram (0-50X)



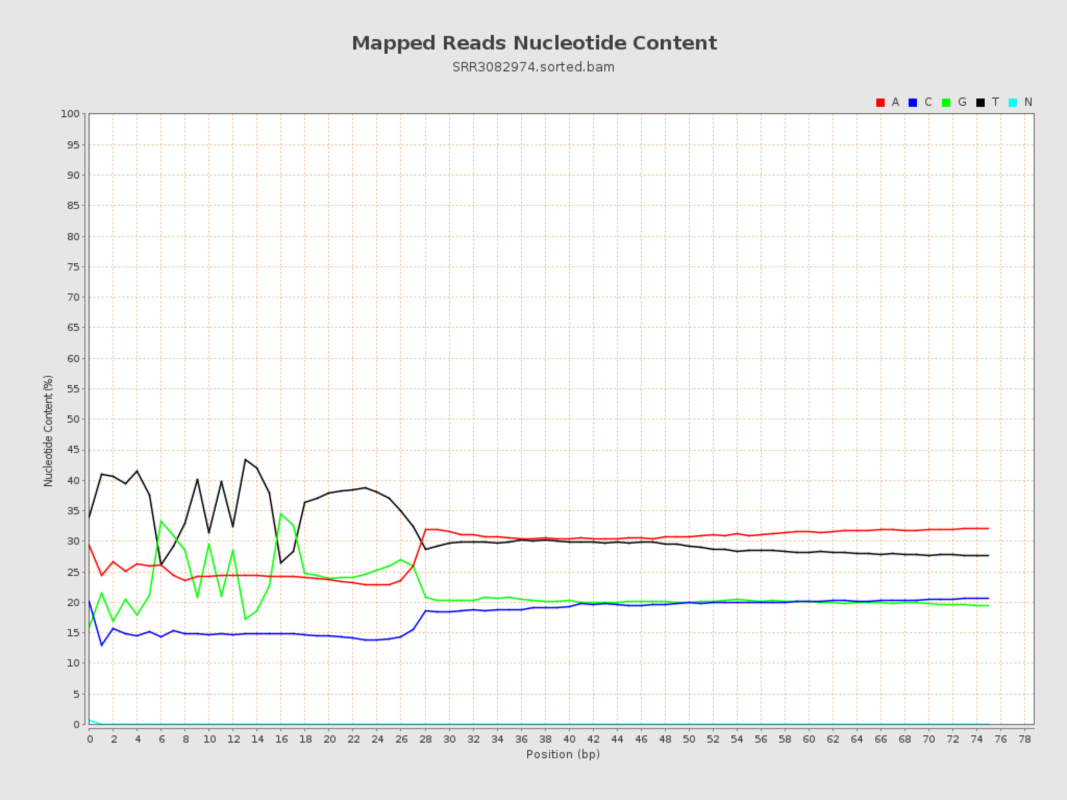
6. Results : Genome Fraction Coverage



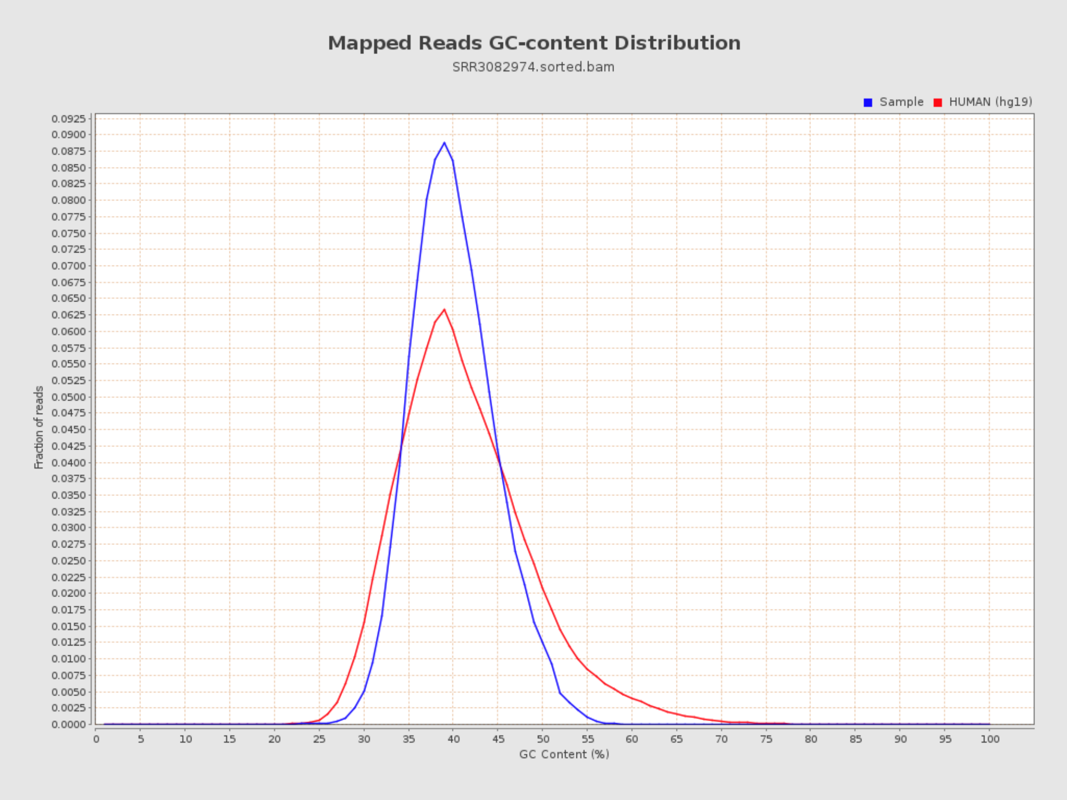
7. Results : Duplication Rate Histogram



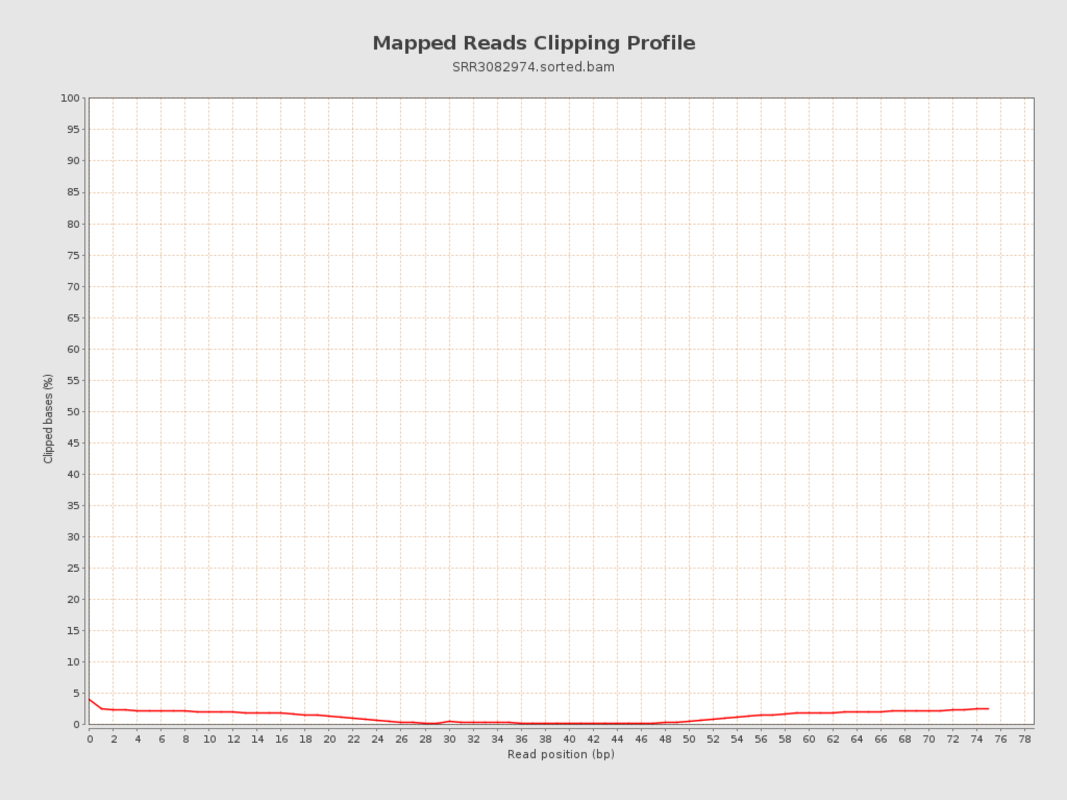
8. Results : Mapped Reads Nucleotide Content



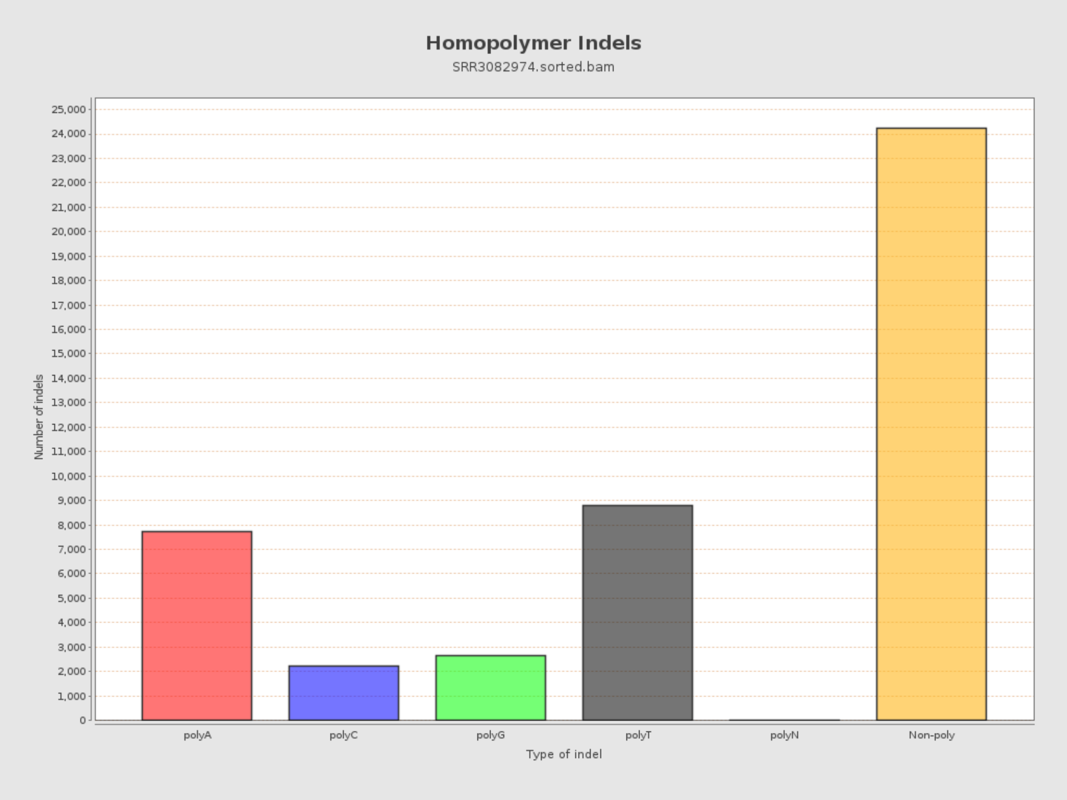
9. Results : Mapped Reads GC-content Distribution



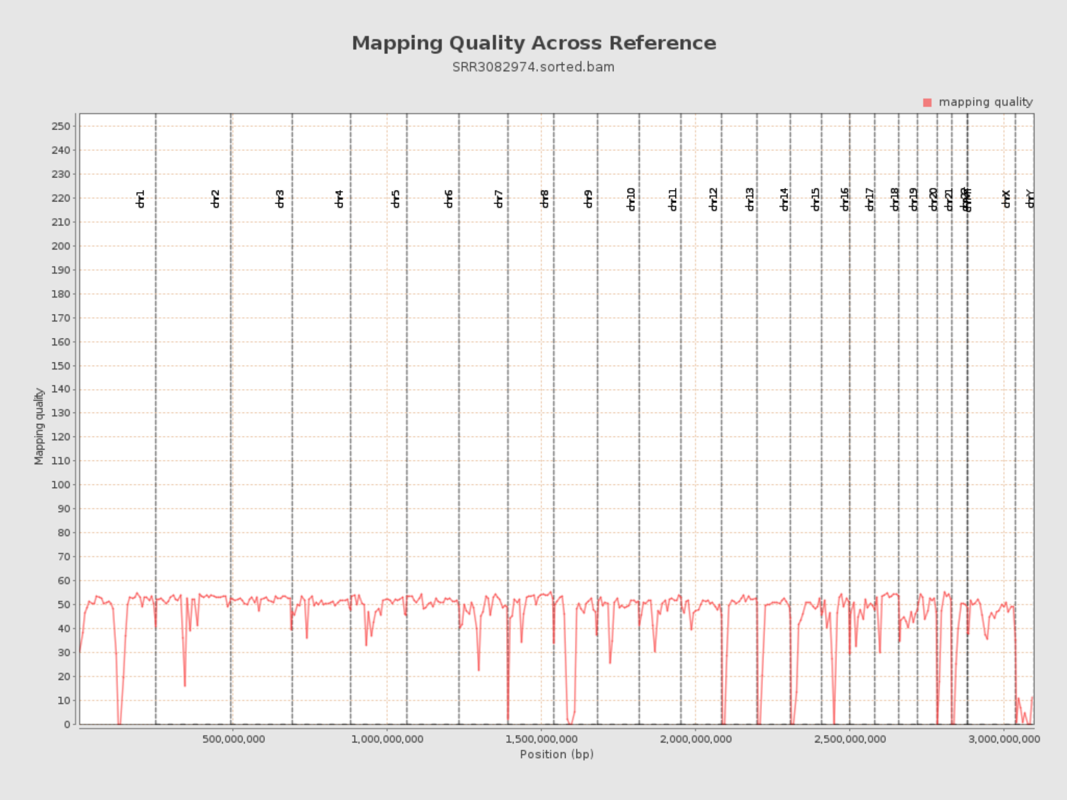
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram