Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 21:44:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082964.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_SRR3082964 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082964.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 21:44:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082964.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,004,701
Mapped reads	3,345,815 / 83.55%
Unmapped reads	658,886 / 16.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,076 / 0.48%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	166,719 / 4.16%
Duplication rate	4.12%
Clipped reads	1,210,509 / 30.23%

2.2. ACGT Content

Number/percentage of A's	65,658,826 / 28.52%
Number/percentage of C's	42,335,531 / 18.39%
Number/percentage of T's	74,525,112 / 32.38%
Number/percentage of G's	47,643,125 / 20.7%
Number/percentage of N's	24,313 / 0.01%
GC Percentage	39.09%

2.3. Coverage

Mean	0.0744

Standard Deviation	0.5053

2.4. Mapping Quality

Mean Mapping Quality	47.8

2.5. Mismatches and indels

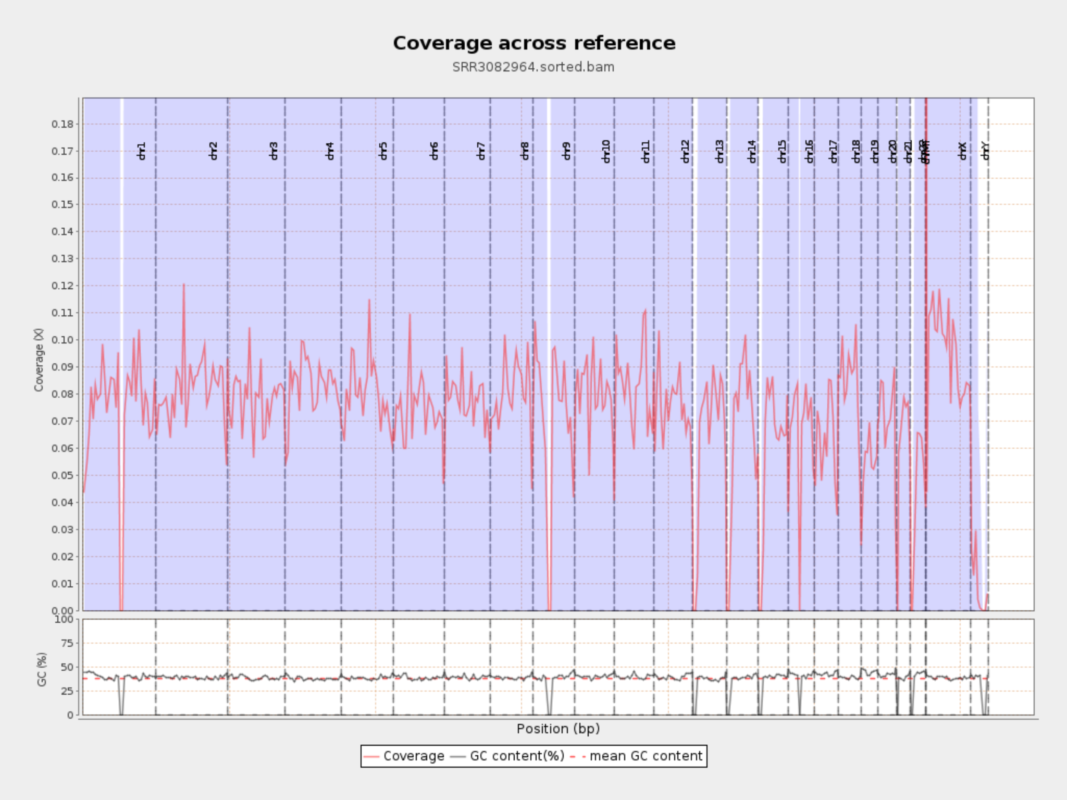
General error rate	0.89%
Mismatches	2,023,527
Insertions	19,117
Mapped reads with at least one insertion	0.57%
Deletions	51,298
Mapped reads with at least one deletion	1.52%
Homopolymer indels	47.9%

2.6. Chromosome stats

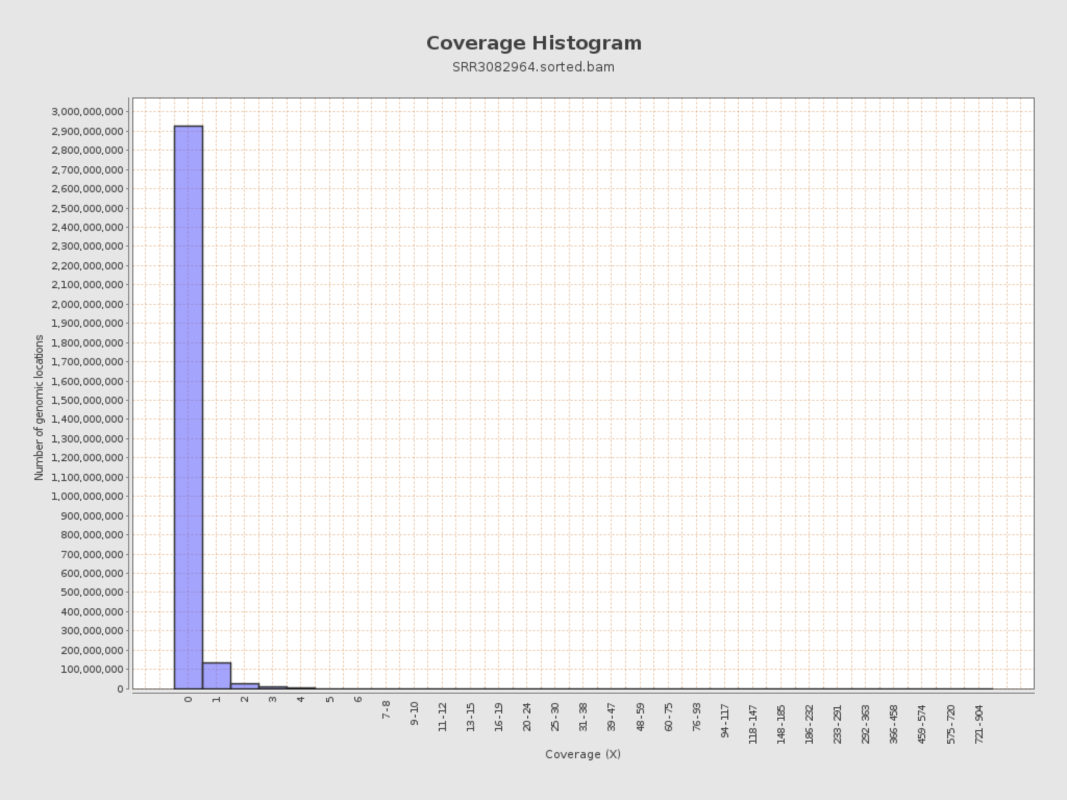
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18470435	0.0741	0.7623
chr2	243199373	19889086	0.0818	0.6505
chr3	198022430	15589499	0.0787	0.362
chr4	191154276	15921838	0.0833	0.387
chr5	180915260	14467209	0.08	0.365
chr6	171115067	12838450	0.075	0.3904
chr7	159138663	12367818	0.0777	0.584

chr8	146364022	11757156	0.0803	0.7148
chr9	141213431	10064372	0.0713	0.5239
chr10	135534747	10969457	0.0809	0.4499
chr11	135006516	11190791	0.0829	0.478
chr12	133851895	10104847	0.0755	0.359
chr13	115169878	7378730	0.0641	0.3259
chr14	107349540	7142843	0.0665	0.3502
chr15	102531392	5945806	0.058	0.3075
chr16	90354753	5849587	0.0647	0.3724
chr17	81195210	5149650	0.0634	0.3423
chr18	78077248	6702721	0.0858	0.9313
chr19	59128983	3282326	0.0555	0.5638
chr20	63025520	4664260	0.074	0.3562
chr21	48129895	3036639	0.0631	0.3561
chr22	51304566	2187719	0.0426	0.259
chrMT	16571	42085	2.5397	2.6967
chrX	155270560	14730279	0.0949	0.4373
chrY	59373566	532713	0.009	0.2184

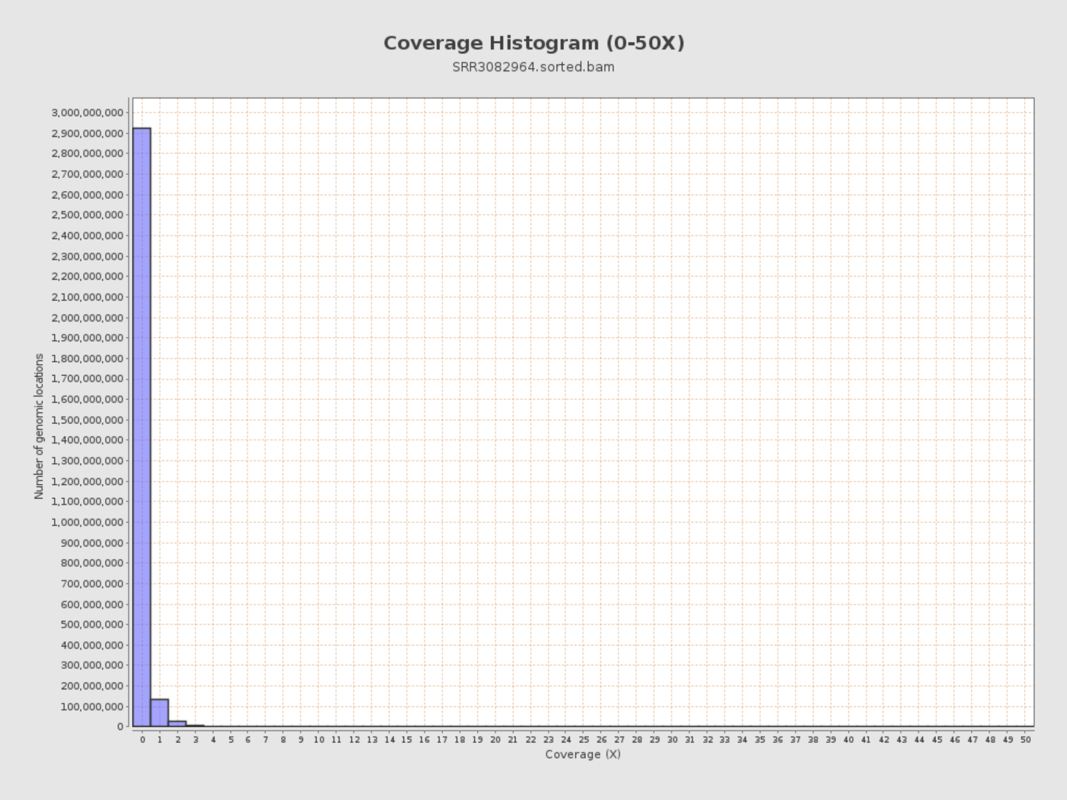
3. Results : Coverage across reference



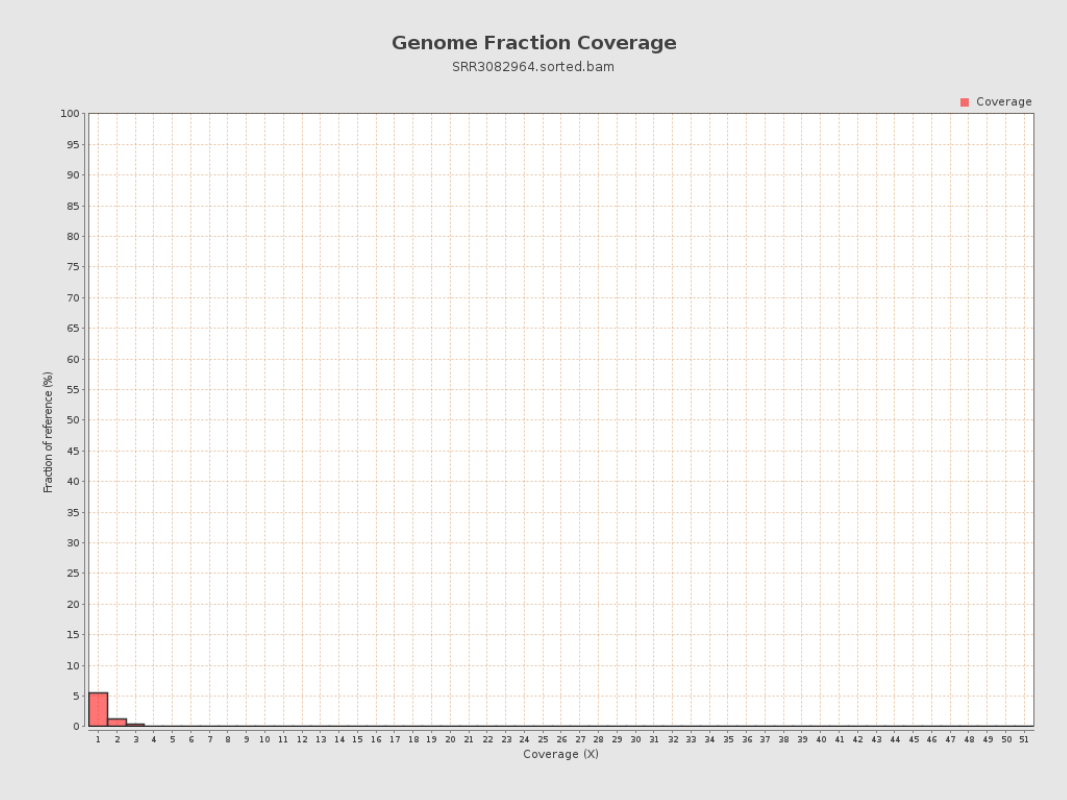
4. Results : Coverage Histogram



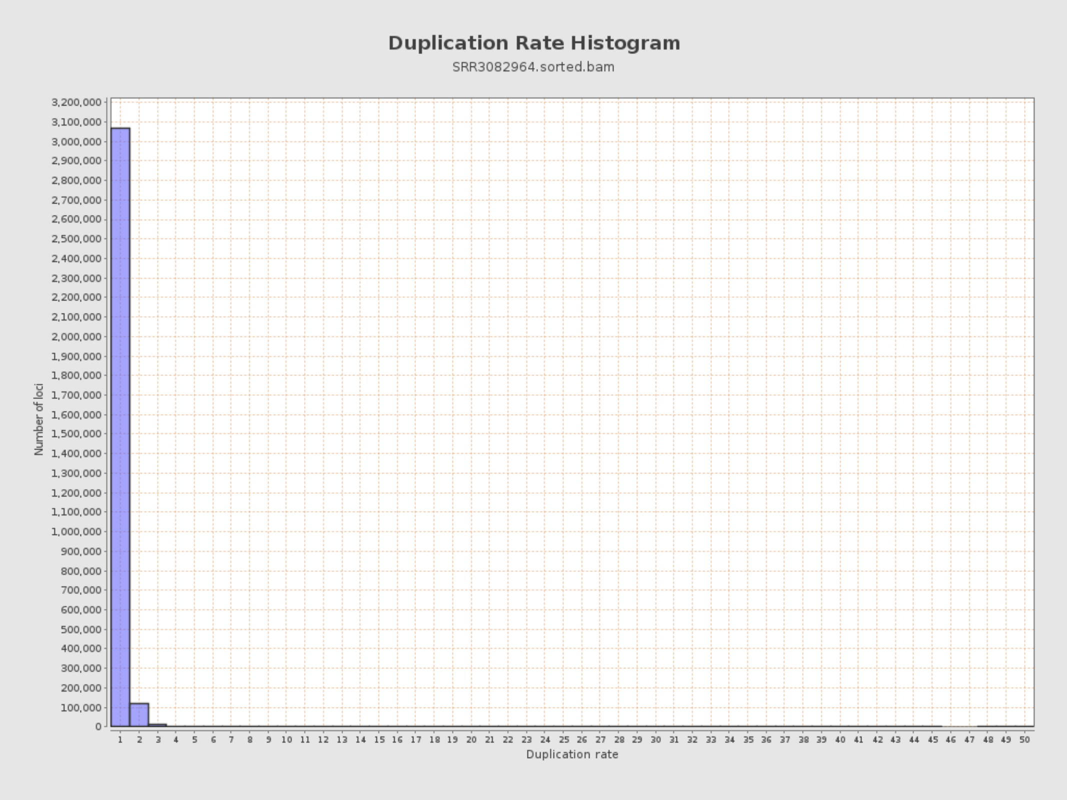
5. Results : Coverage Histogram (0-50X)



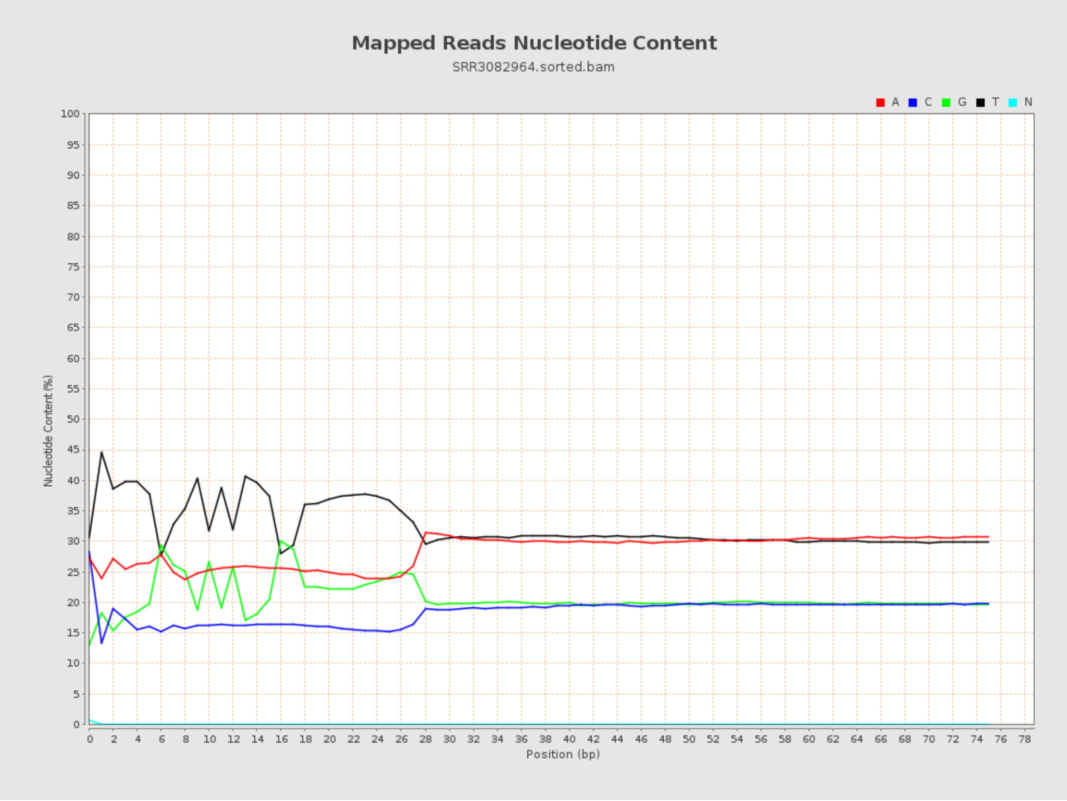
6. Results : Genome Fraction Coverage



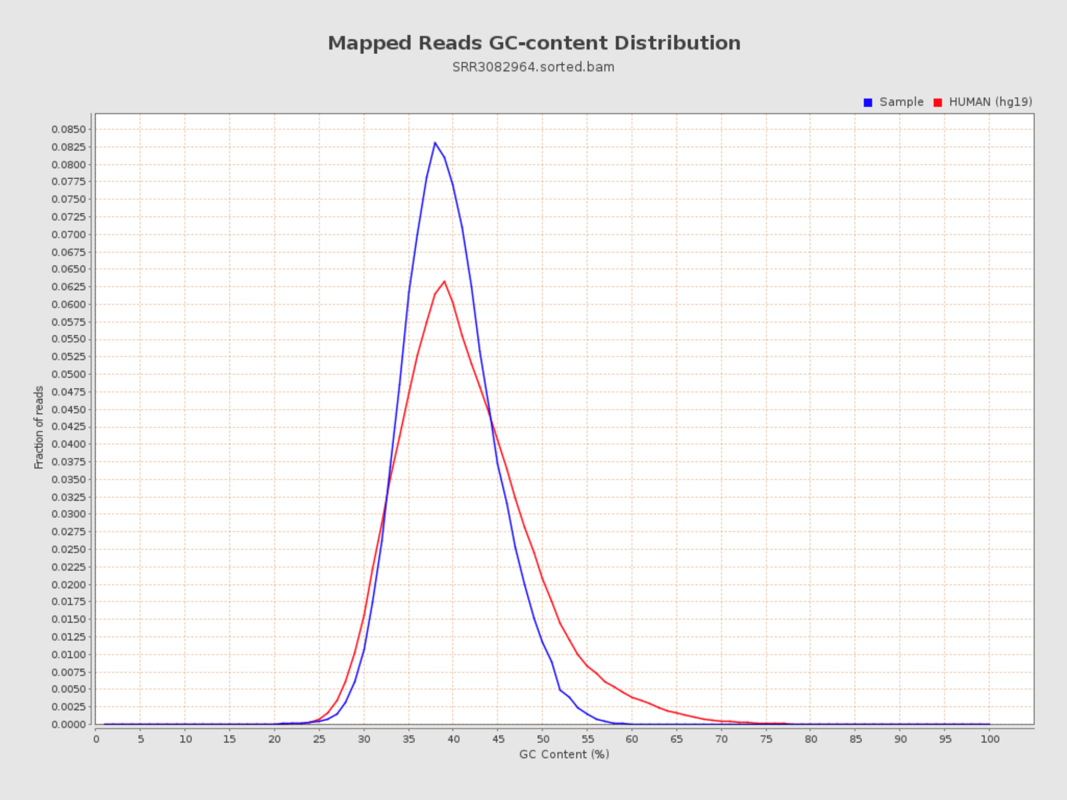
7. Results : Duplication Rate Histogram



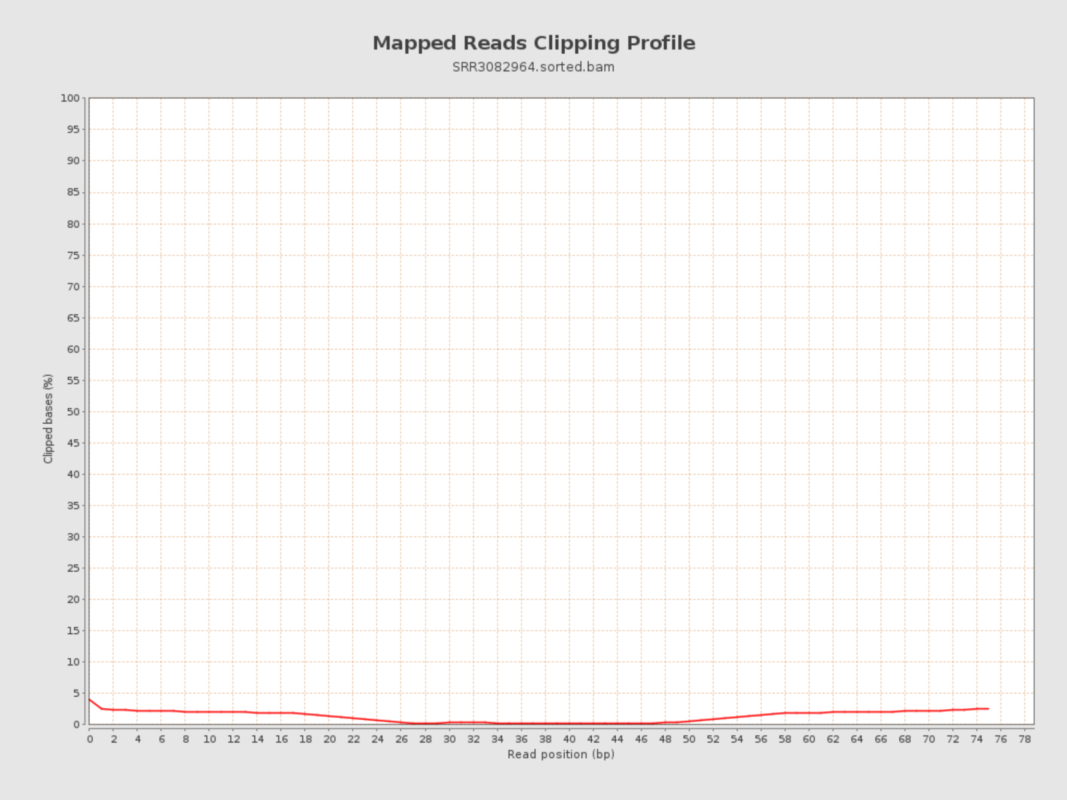
8. Results : Mapped Reads Nucleotide Content



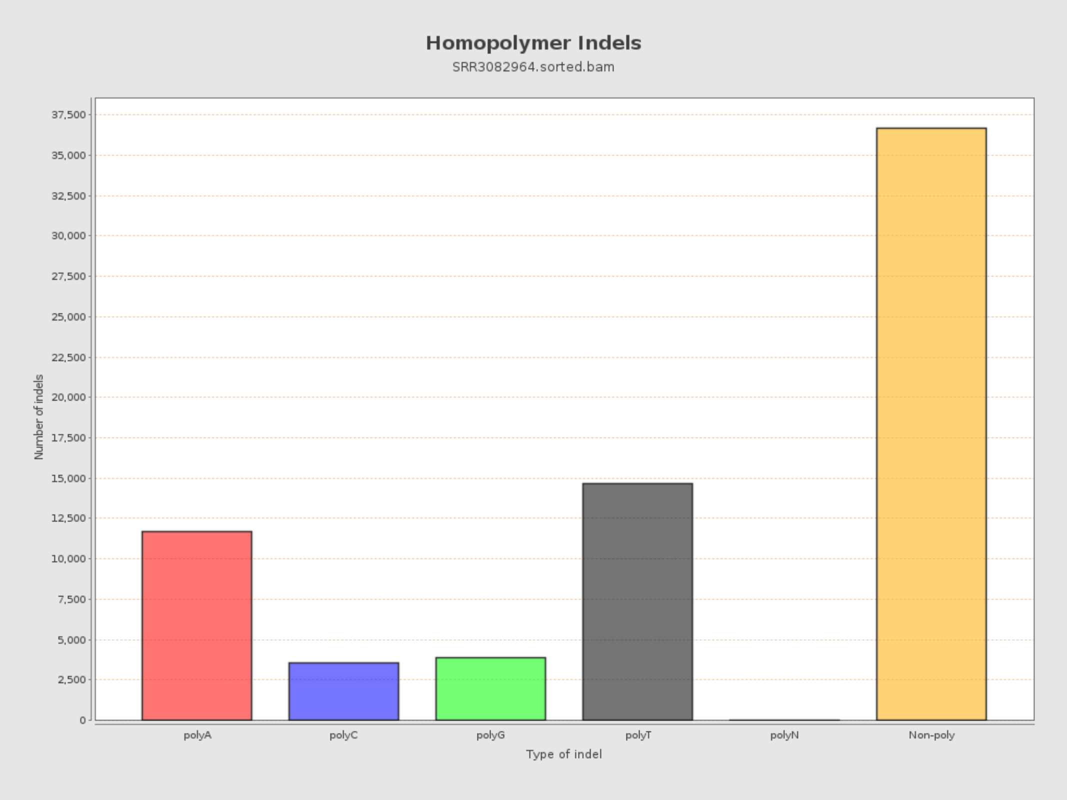
9. Results : Mapped Reads GC-content Distribution



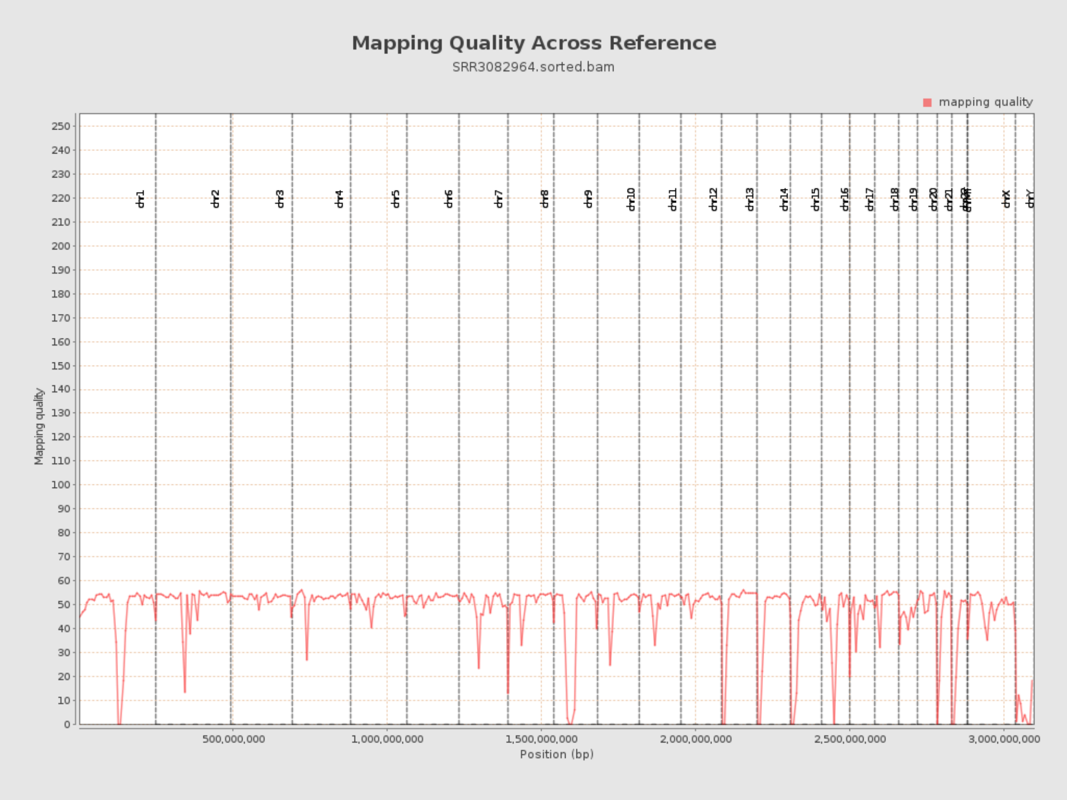
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram