Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 21:57:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082970.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_SRR3082970 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082970.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 21:57:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082970.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,910,291
Mapped reads	3,491,587 / 89.29%
Unmapped reads	418,704 / 10.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,357 / 0.34%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	212,748 / 5.44%
Duplication rate	4.77%
Clipped reads	1,835,473 / 46.94%

2.2. ACGT Content

Number/percentage of A's	61,112,551 / 26.81%
Number/percentage of C's	38,902,849 / 17.07%
Number/percentage of T's	75,949,442 / 33.32%
Number/percentage of G's	51,976,275 / 22.8%
Number/percentage of N's	21,931 / 0.01%
GC Percentage	39.87%

2.3. Coverage

Mean	0.0737

Standard Deviation	0.6031

2.4. Mapping Quality

Mean Mapping Quality	46.88

2.5. Mismatches and indels

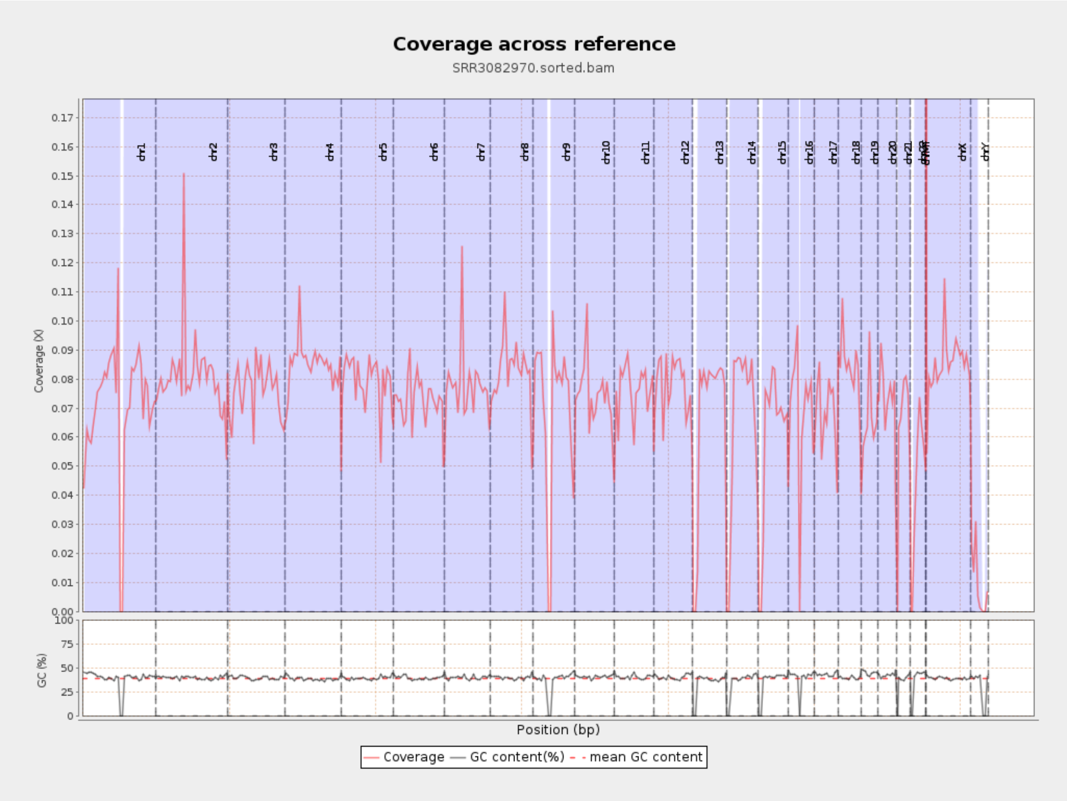
General error rate	0.88%
Mismatches	1,959,804
Insertions	21,241
Mapped reads with at least one insertion	0.6%
Deletions	54,909
Mapped reads with at least one deletion	1.56%
Homopolymer indels	48.53%

2.6. Chromosome stats

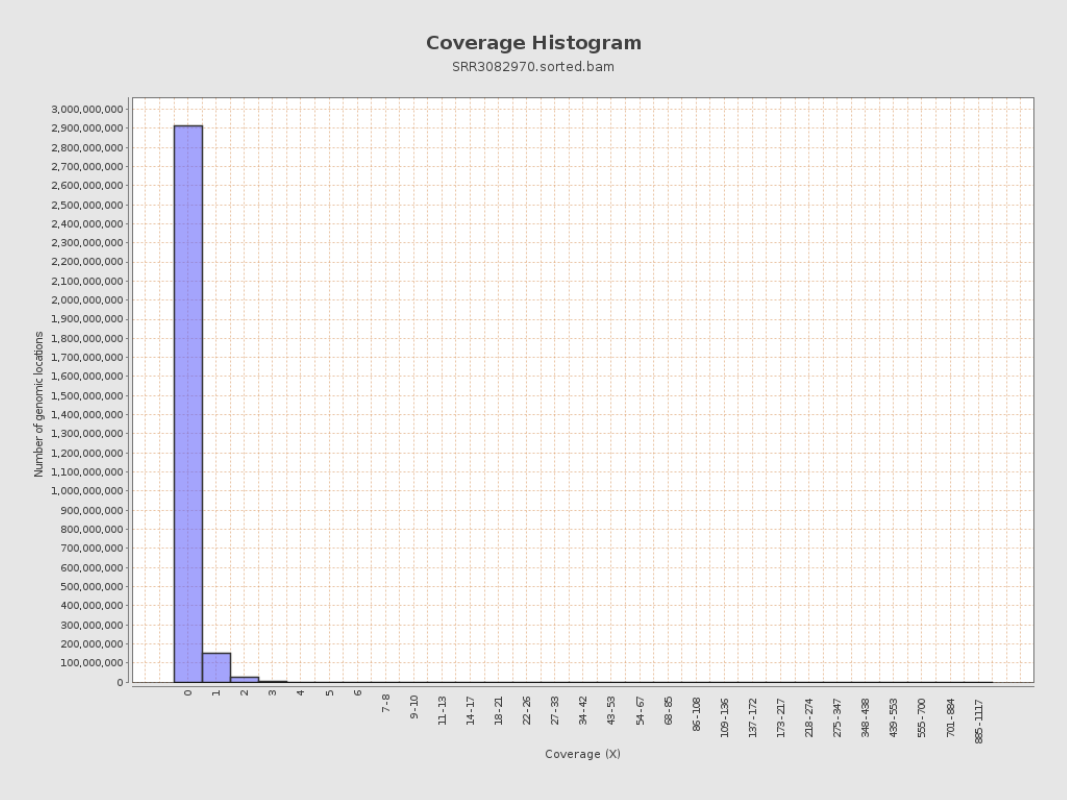
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17682887	0.0709	0.9718
chr2	243199373	19808341	0.0814	0.8074
chr3	198022430	15159001	0.0766	0.3289
chr4	191154276	16336432	0.0855	0.3831
chr5	180915260	14294330	0.079	0.3384
chr6	171115067	12528581	0.0732	0.464
chr7	159138663	12358239	0.0777	0.8757

chr8	146364022	12146333	0.083	0.6293
chr9	141213431	9893315	0.0701	0.7362
chr10	135534747	10127606	0.0747	0.4933
chr11	135006516	10227451	0.0758	0.5425
chr12	133851895	10428154	0.0779	0.348
chr13	115169878	7736951	0.0672	0.3066
chr14	107349540	7265417	0.0677	0.397
chr15	102531392	6018153	0.0587	0.2888
chr16	90354753	6016848	0.0666	0.3859
chr17	81195210	5621877	0.0692	0.407
chr18	78077248	6662194	0.0853	1.3102
chr19	59128983	3903758	0.066	0.7284
chr20	63025520	4693656	0.0745	0.3642
chr21	48129895	3068056	0.0637	0.3539
chr22	51304566	2272095	0.0443	0.2475
chrMT	16571	17080	1.0307	1.4074
chrX	155270560	13214629	0.0851	0.4374
chrY	59373566	570499	0.0096	0.2382

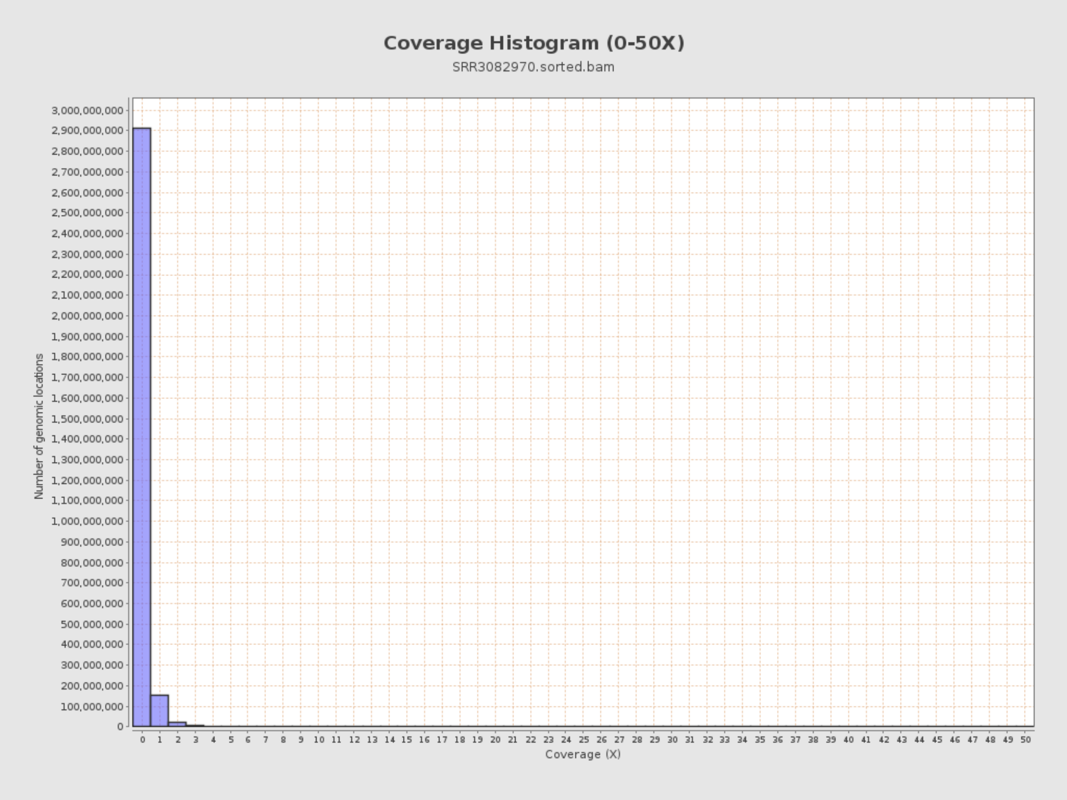
3. Results : Coverage across reference



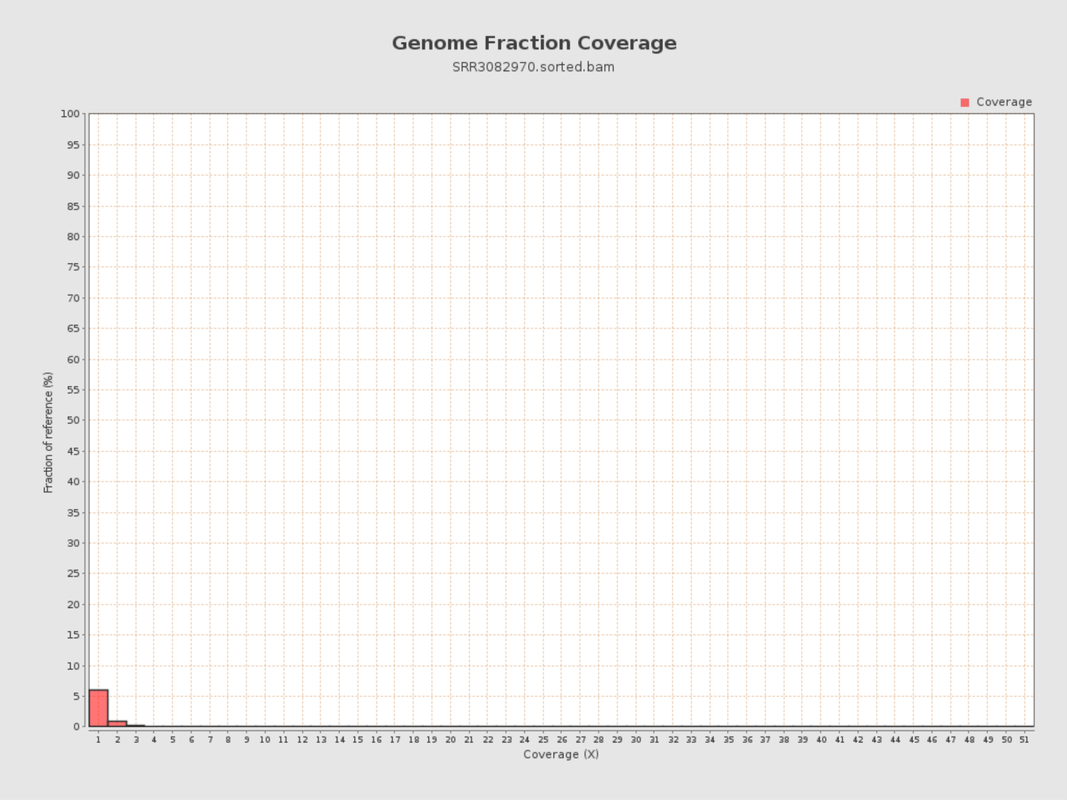
4. Results : Coverage Histogram



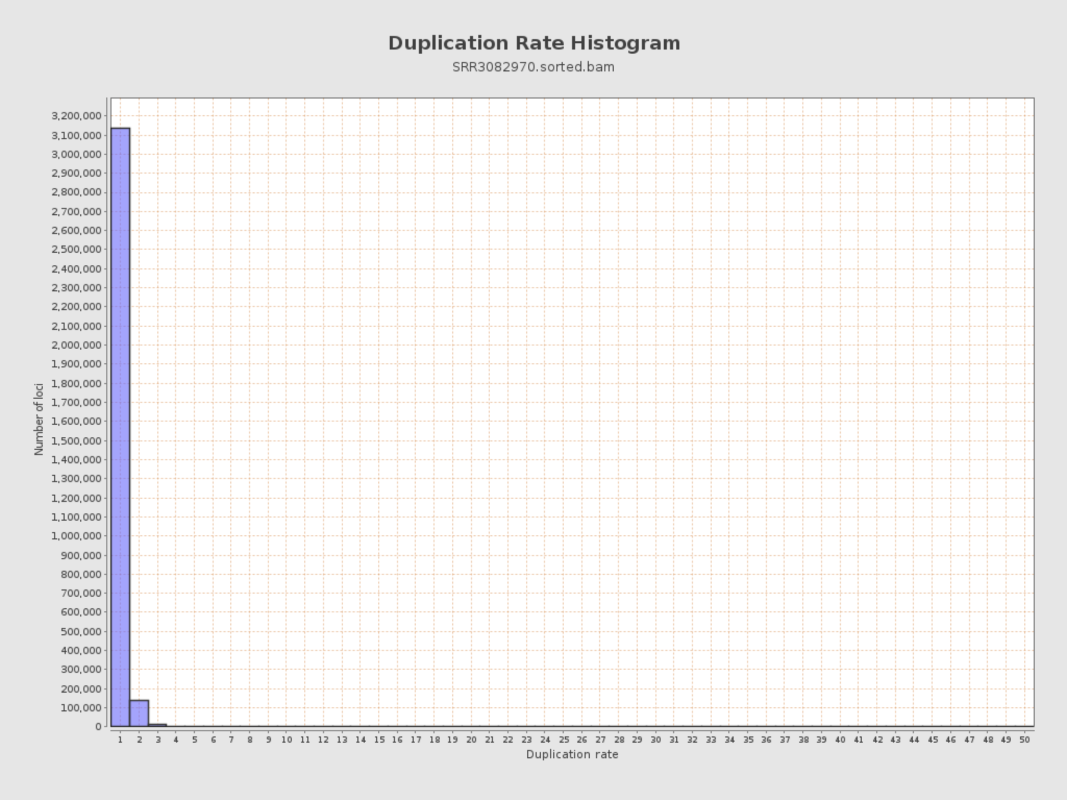
5. Results : Coverage Histogram (0-50X)



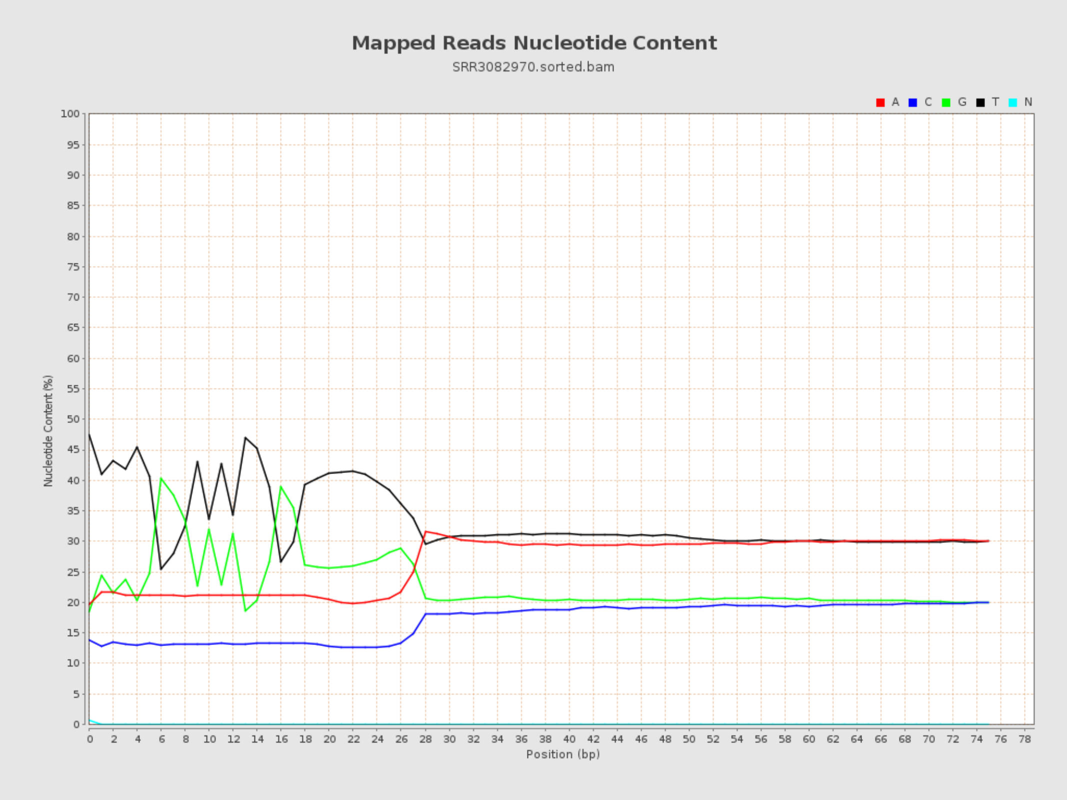
6. Results : Genome Fraction Coverage



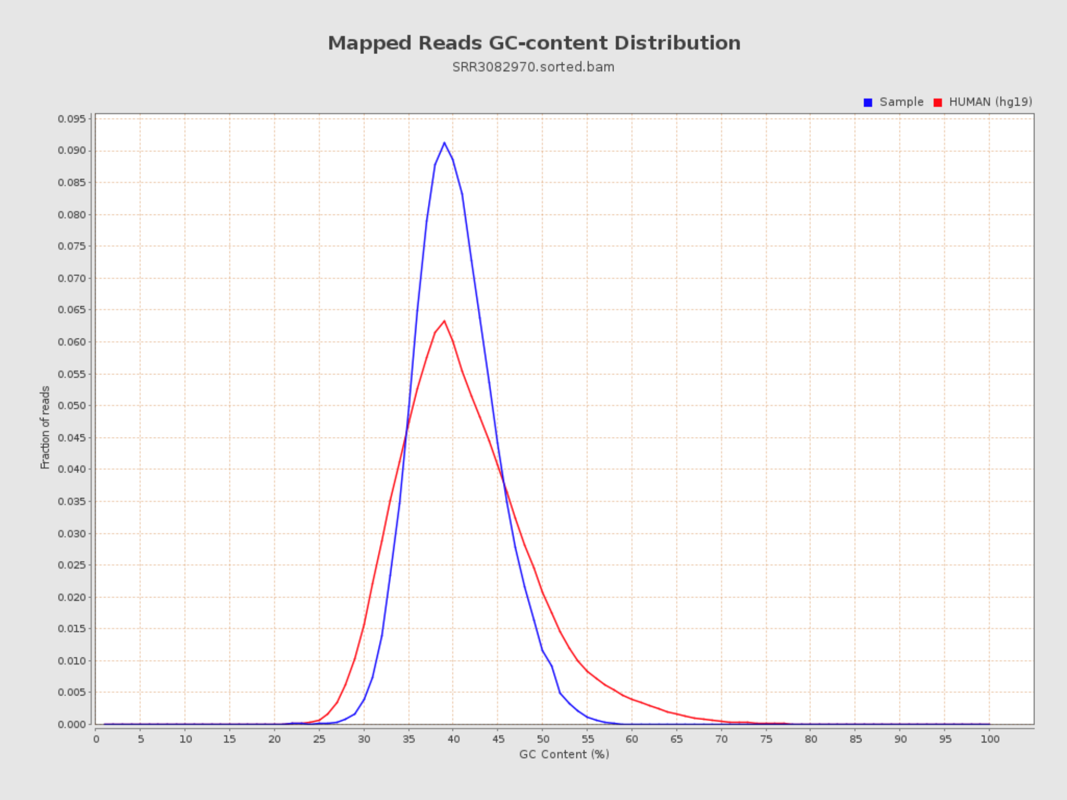
7. Results : Duplication Rate Histogram



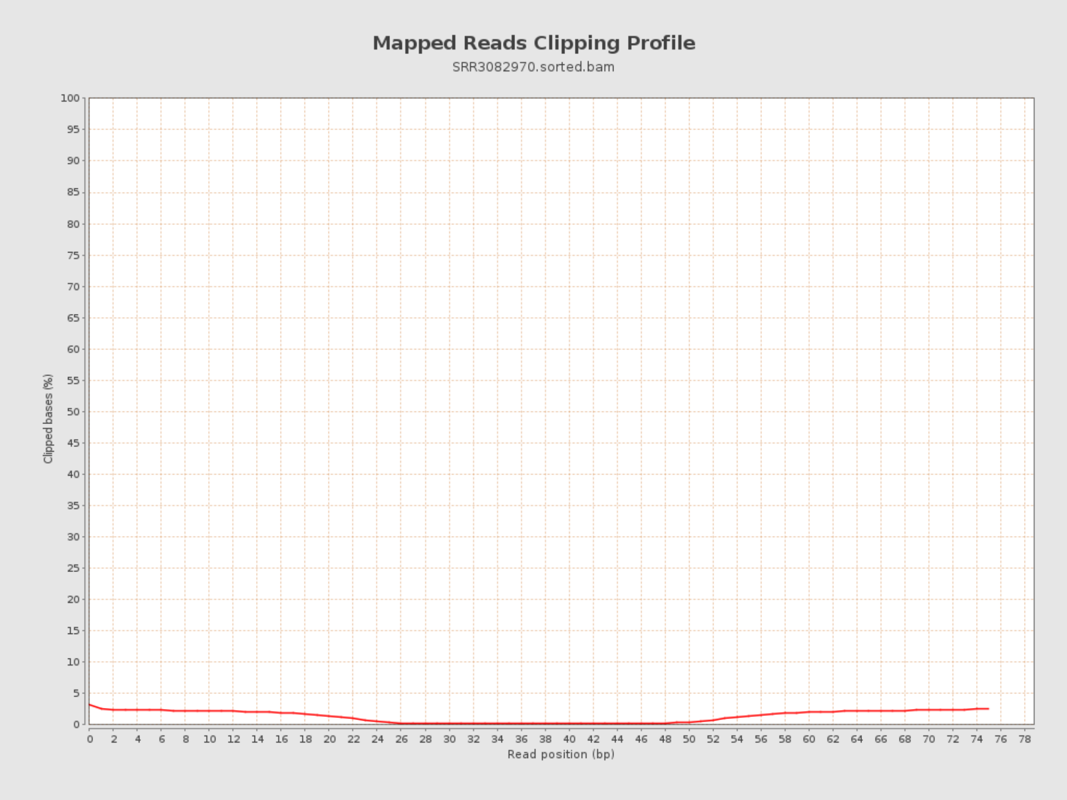
8. Results : Mapped Reads Nucleotide Content



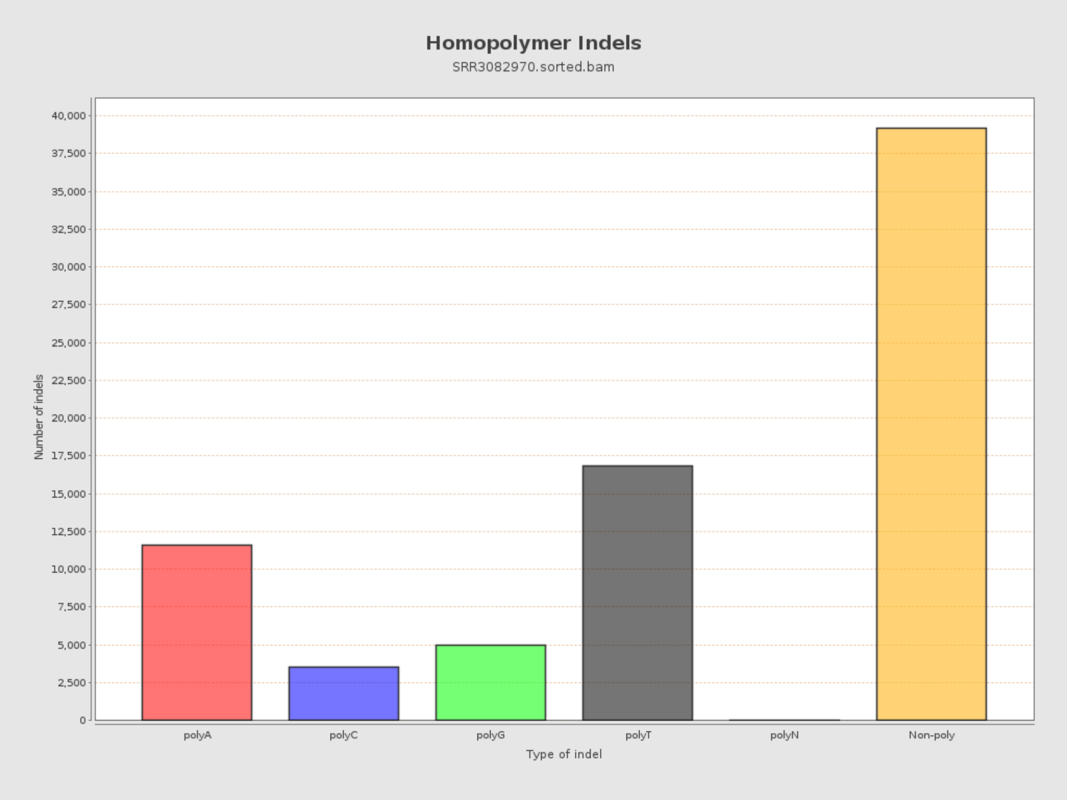
9. Results : Mapped Reads GC-content Distribution



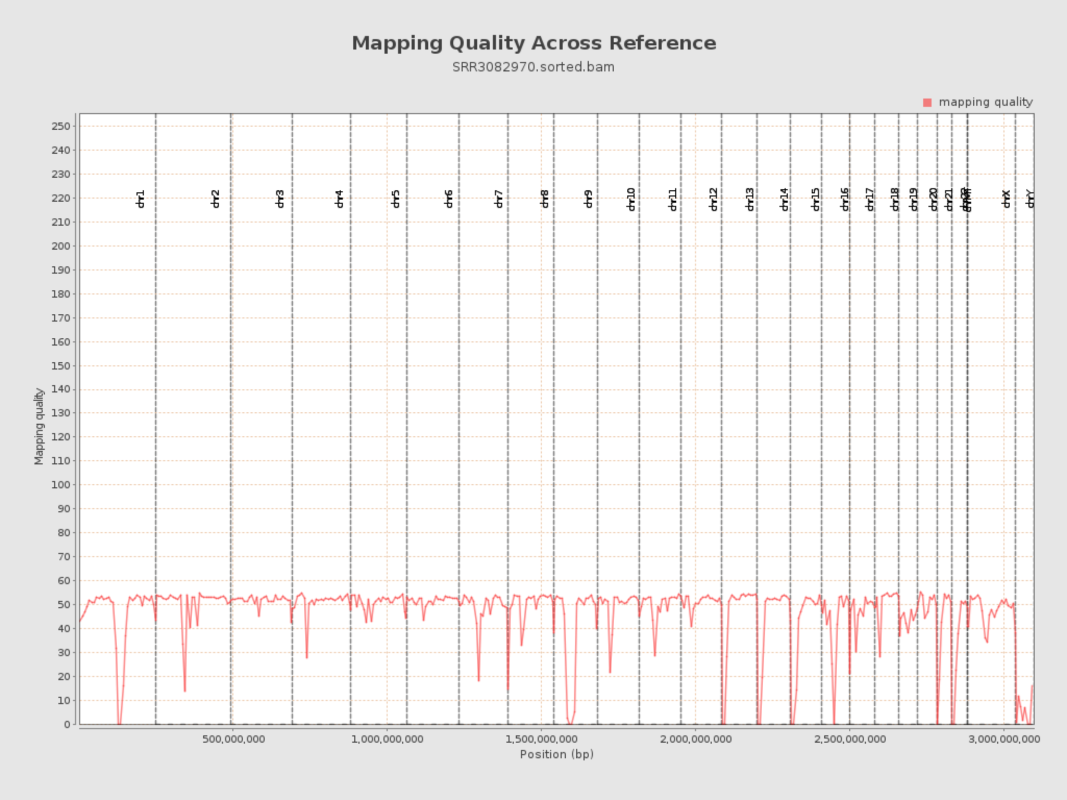
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram