Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 22:47:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082980.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_SRR3082980 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082980.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 22:47:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082980.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,626,410
Mapped reads	2,013,991 / 76.68%
Unmapped reads	612,419 / 23.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,718 / 0.52%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	69,566 / 2.65%
Duplication rate	2.42%
Clipped reads	884,505 / 33.68%

2.2. ACGT Content

Number/percentage of A's	38,481,925 / 28.39%
Number/percentage of C's	24,944,629 / 18.41%
Number/percentage of T's	42,747,034 / 31.54%
Number/percentage of G's	29,339,098 / 21.65%
Number/percentage of N's	13,162 / 0.01%
GC Percentage	40.05%

2.3. Coverage

Mean	0.0438

Standard Deviation	0.4166

2.4. Mapping Quality

Mean Mapping Quality	45.27

2.5. Mismatches and indels

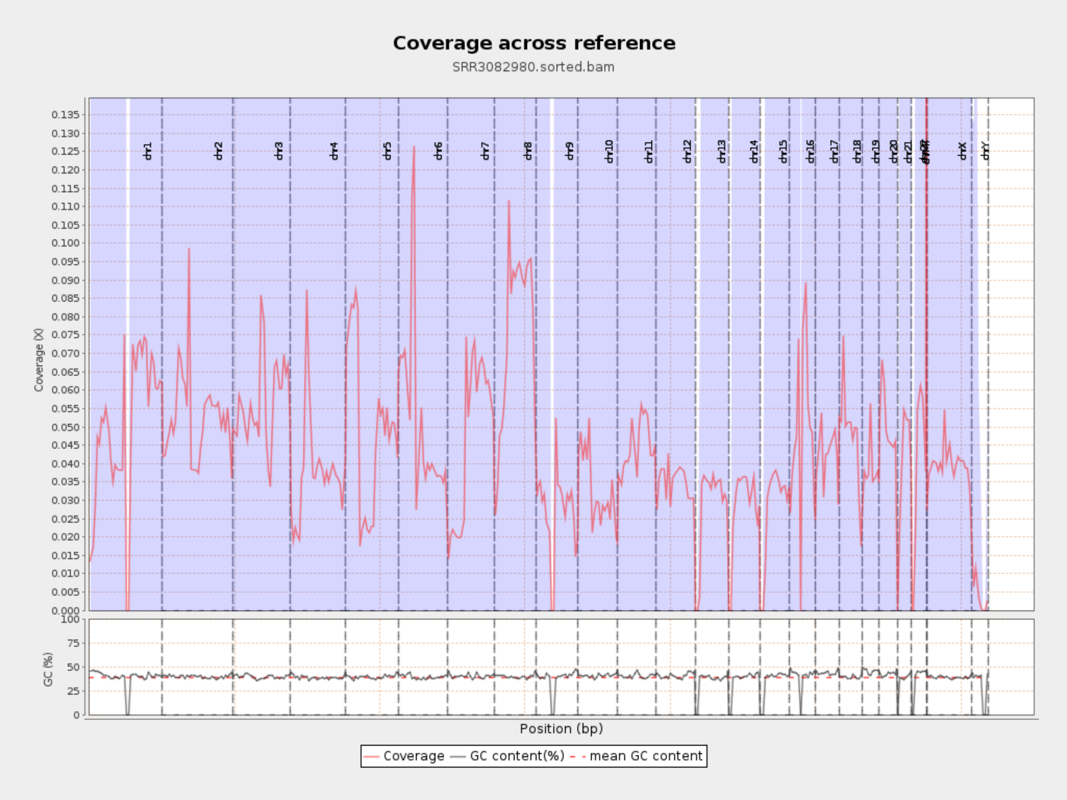
General error rate	1%
Mismatches	1,337,142
Insertions	12,410
Mapped reads with at least one insertion	0.61%
Deletions	33,171
Mapped reads with at least one deletion	1.63%
Homopolymer indels	46.87%

2.6. Chromosome stats

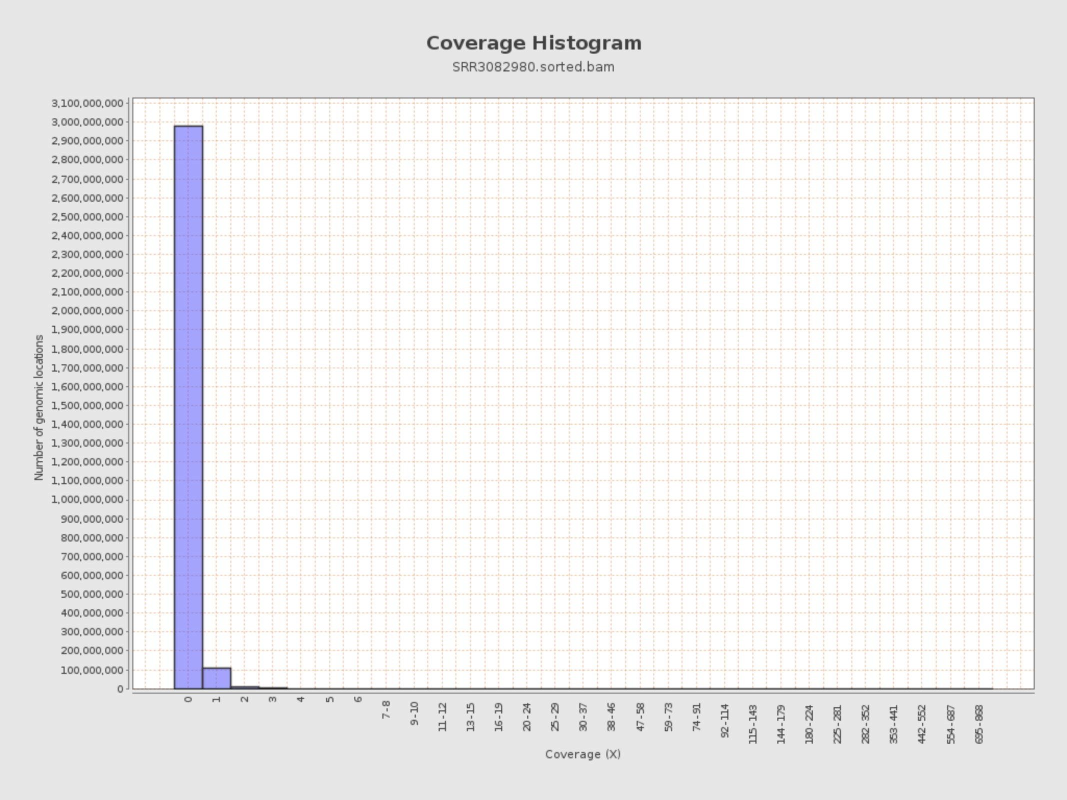
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12374445	0.0496	0.7898
chr2	243199373	12844412	0.0528	0.5168
chr3	198022430	11150934	0.0563	0.2627
chr4	191154276	7152948	0.0374	0.2161
chr5	180915260	8999604	0.0497	0.2491
chr6	171115067	8902248	0.052	0.3384
chr7	159138663	7623363	0.0479	0.4842

chr8	146364022	11151653	0.0762	0.4953
chr9	141213431	3831438	0.0271	0.3979
chr10	135534747	4513804	0.0333	0.2962
chr11	135006516	5976991	0.0443	0.3653
chr12	133851895	4654669	0.0348	0.2124
chr13	115169878	3223028	0.028	0.1816
chr14	107349540	3003387	0.028	0.2324
chr15	102531392	2832554	0.0276	0.1811
chr16	90354753	4415997	0.0489	0.3049
chr17	81195210	3448487	0.0425	0.2941
chr18	78077248	3794972	0.0486	0.9221
chr19	59128983	2287072	0.0387	0.5138
chr20	63025520	3182910	0.0505	0.2595
chr21	48129895	1891806	0.0393	0.2285
chr22	51304566	1931373	0.0376	0.2133
chrMT	16571	5753	0.3472	0.6472
chrX	155270560	6134781	0.0395	0.2715
chrY	59373566	253903	0.0043	0.0931

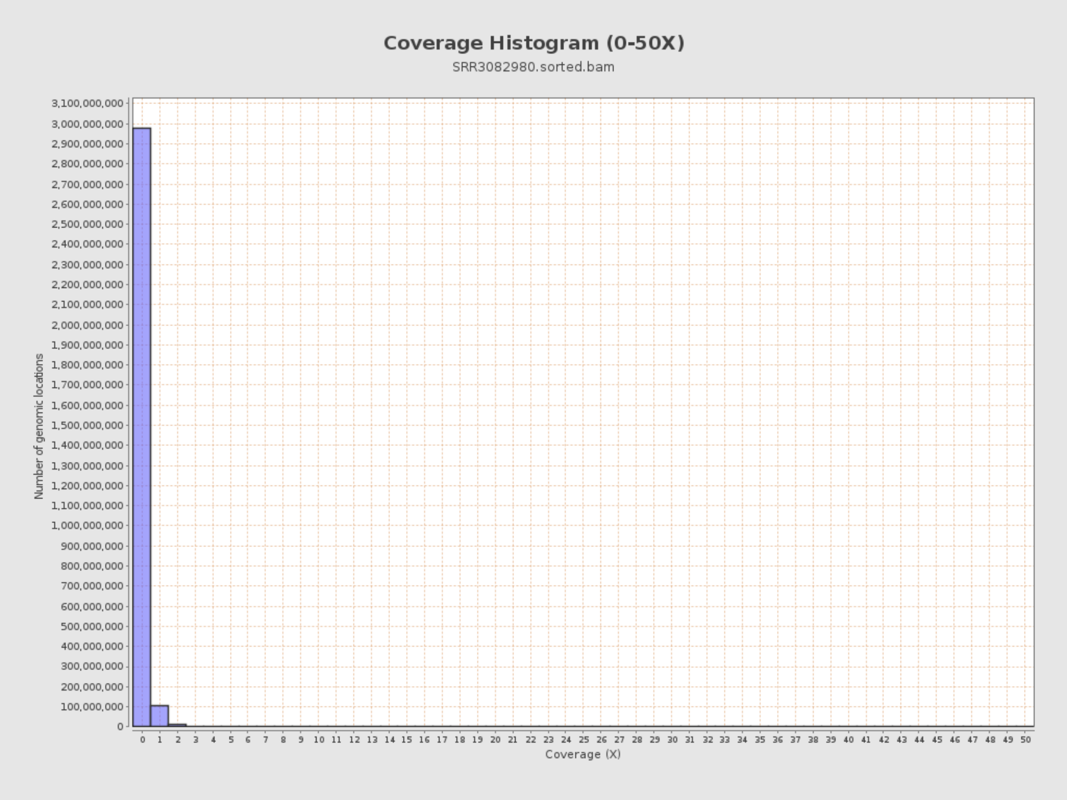
3. Results : Coverage across reference



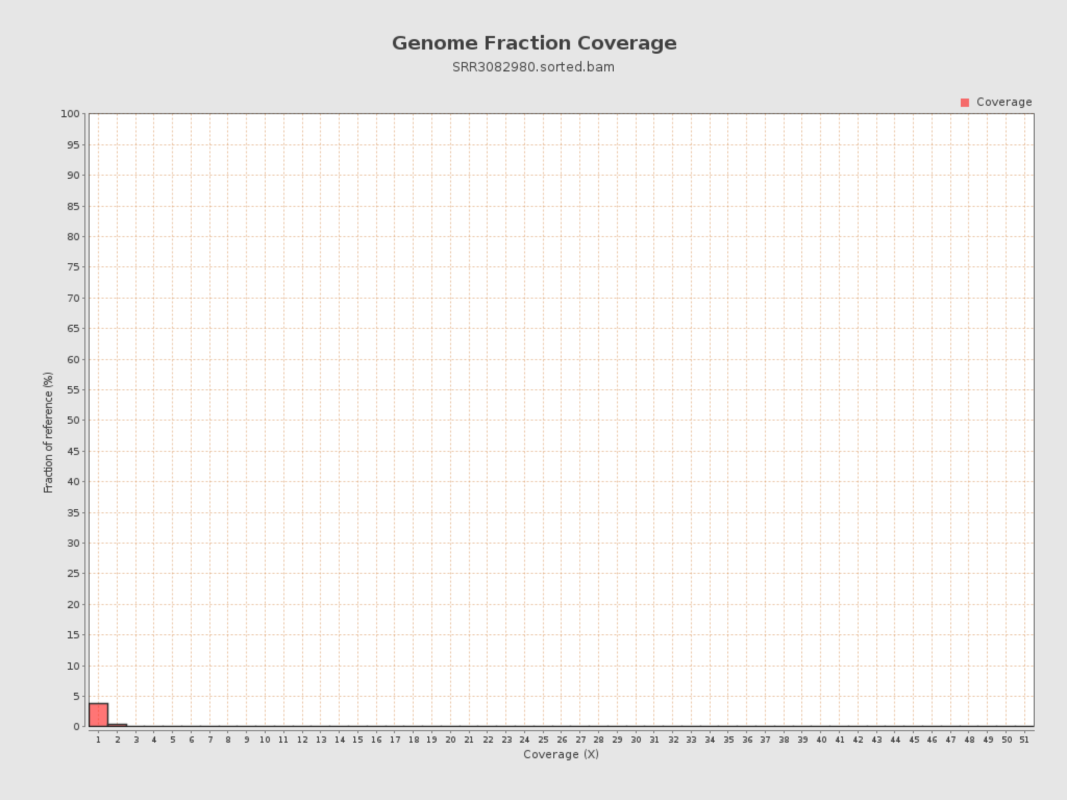
4. Results : Coverage Histogram



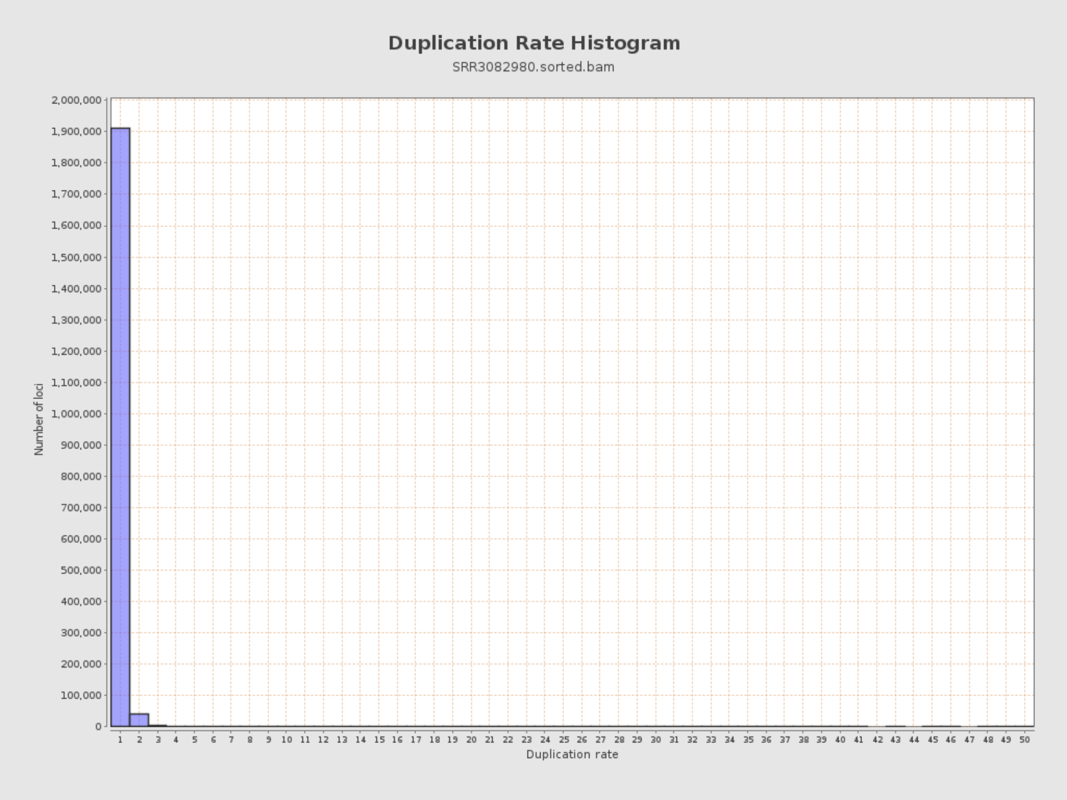
5. Results : Coverage Histogram (0-50X)



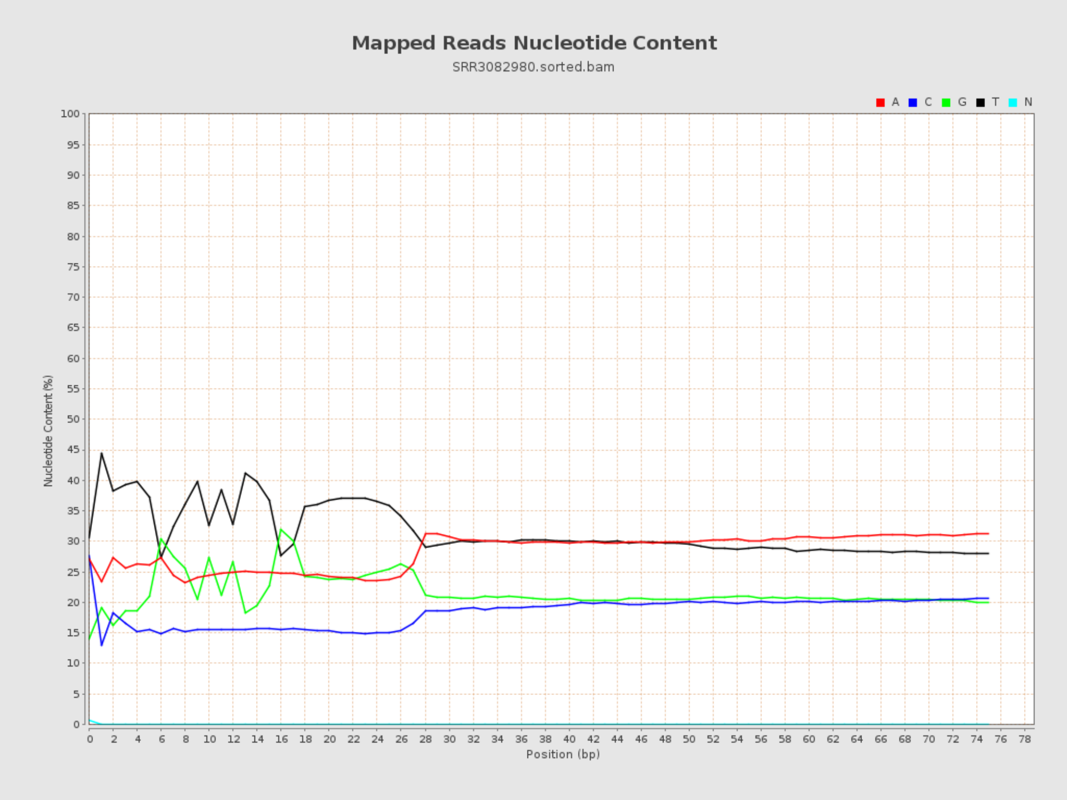
6. Results : Genome Fraction Coverage



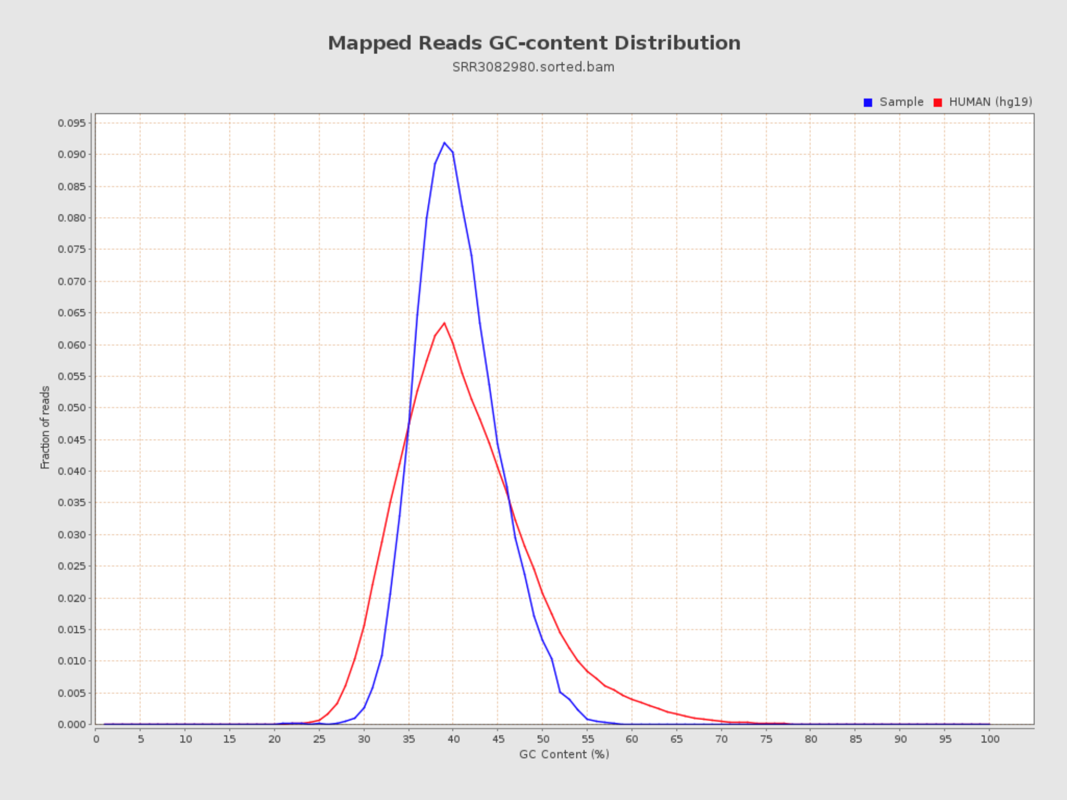
7. Results : Duplication Rate Histogram



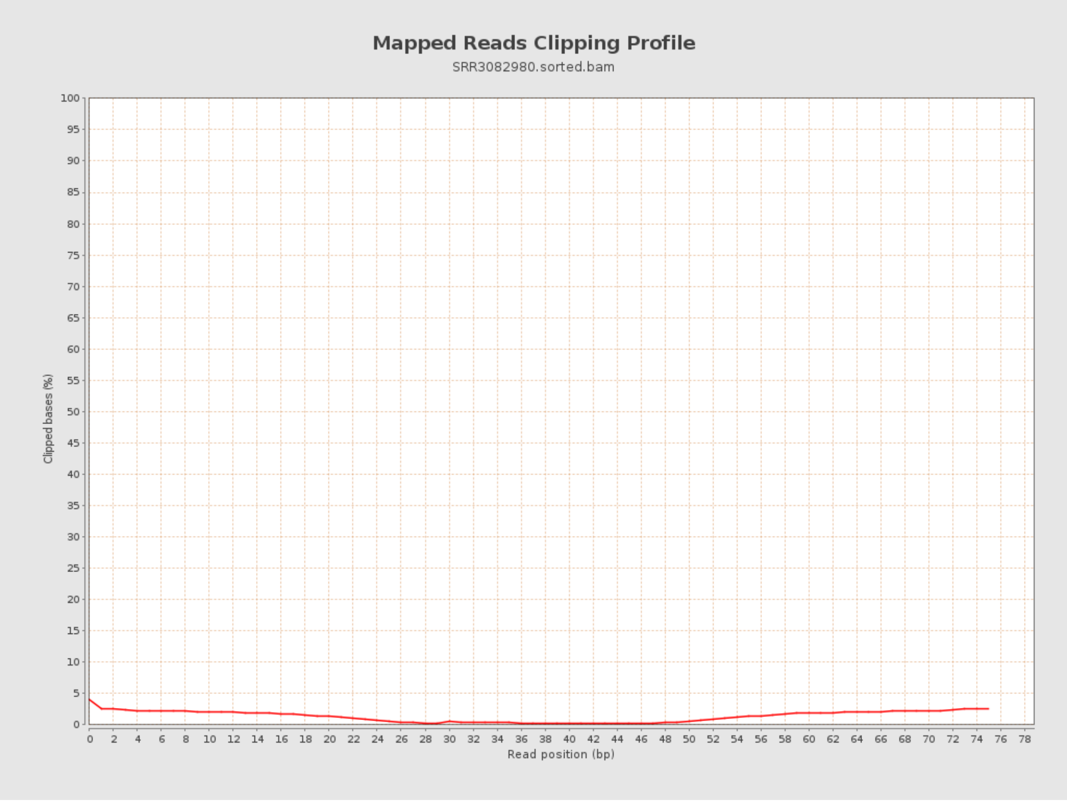
8. Results : Mapped Reads Nucleotide Content



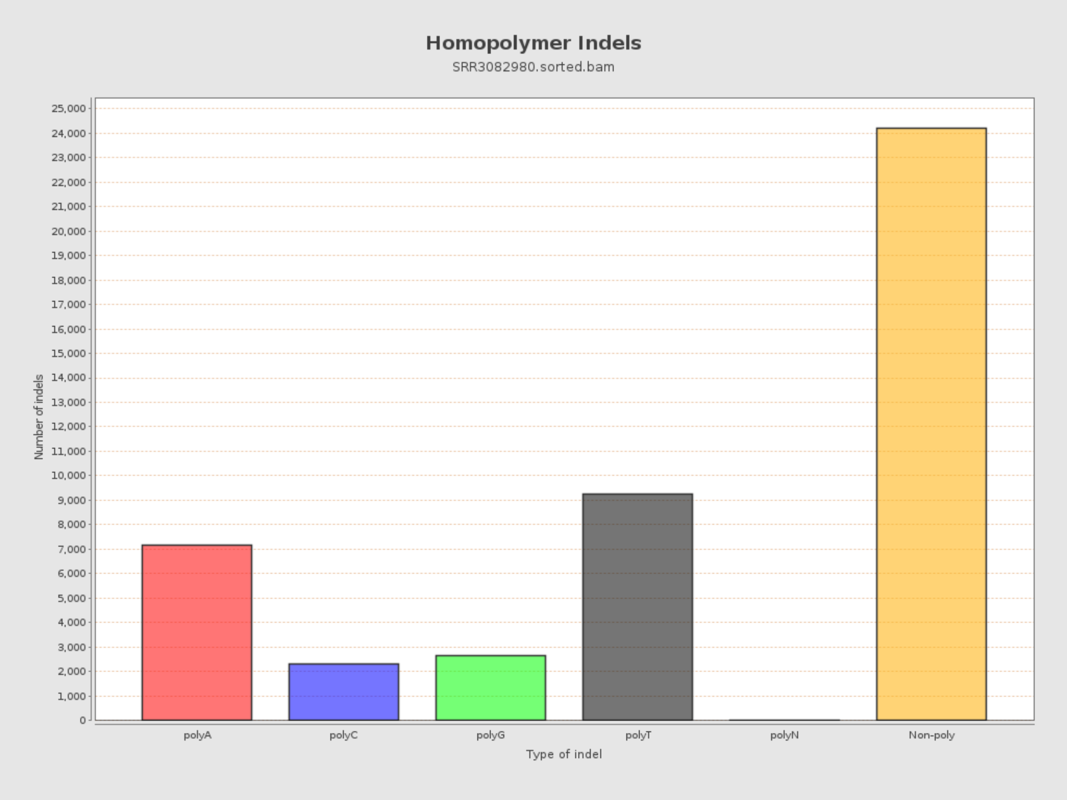
9. Results : Mapped Reads GC-content Distribution



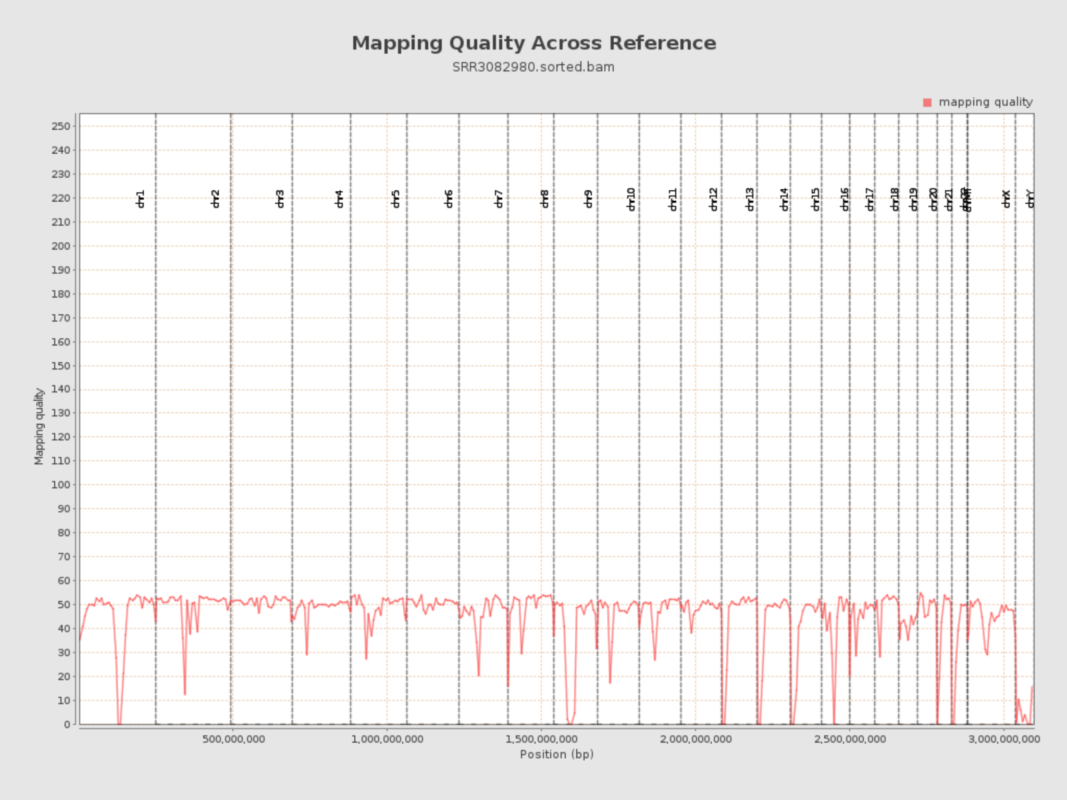
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram