Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 22:53:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082981.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_SRR3082981 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082981.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 22:53:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082981.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,358,457
Mapped reads	2,723,624 / 81.1%
Unmapped reads	634,833 / 18.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,925 / 0.56%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	122,964 / 3.66%
Duplication rate	3.11%
Clipped reads	1,163,268 / 34.64%

2.2. ACGT Content

Number/percentage of A's	51,624,807 / 28.11%
Number/percentage of C's	33,862,290 / 18.44%
Number/percentage of T's	58,205,944 / 31.69%
Number/percentage of G's	39,960,588 / 21.76%
Number/percentage of N's	18,128 / 0.01%
GC Percentage	40.19%

2.3. Coverage

Mean	0.0594

Standard Deviation	0.5667

2.4. Mapping Quality

Mean Mapping Quality	44.71

2.5. Mismatches and indels

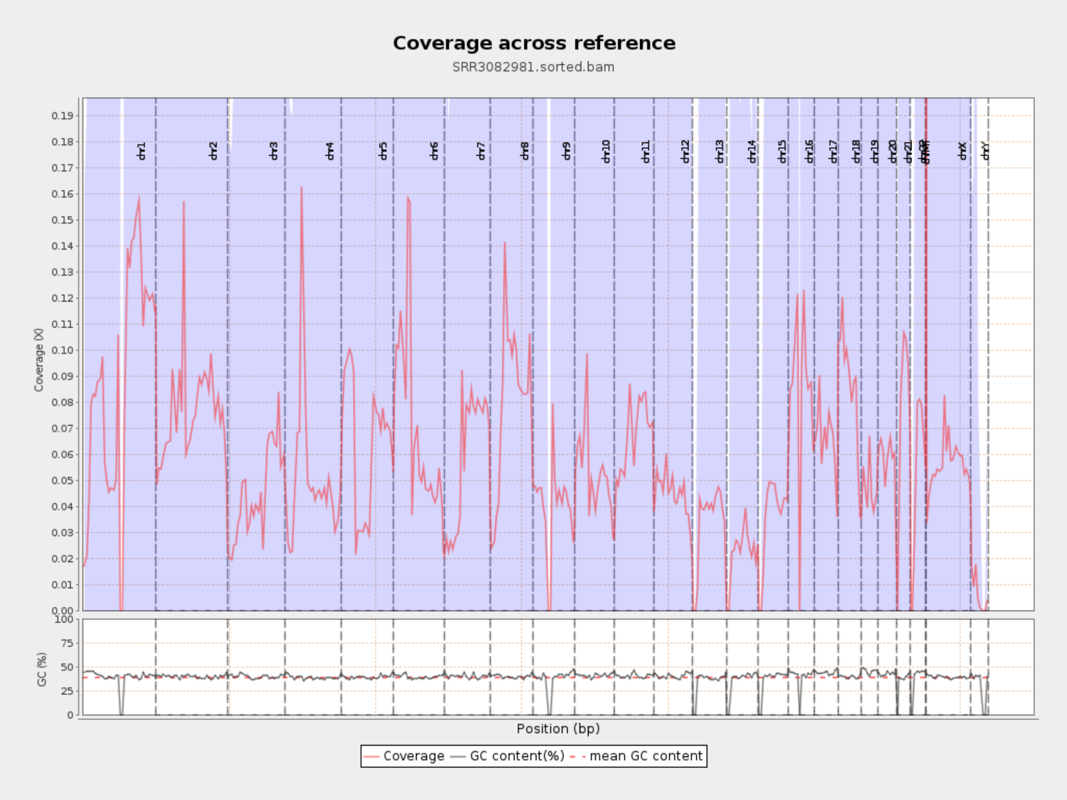
General error rate	0.98%
Mismatches	1,777,944
Insertions	16,961
Mapped reads with at least one insertion	0.62%
Deletions	44,221
Mapped reads with at least one deletion	1.61%
Homopolymer indels	47.52%

2.6. Chromosome stats

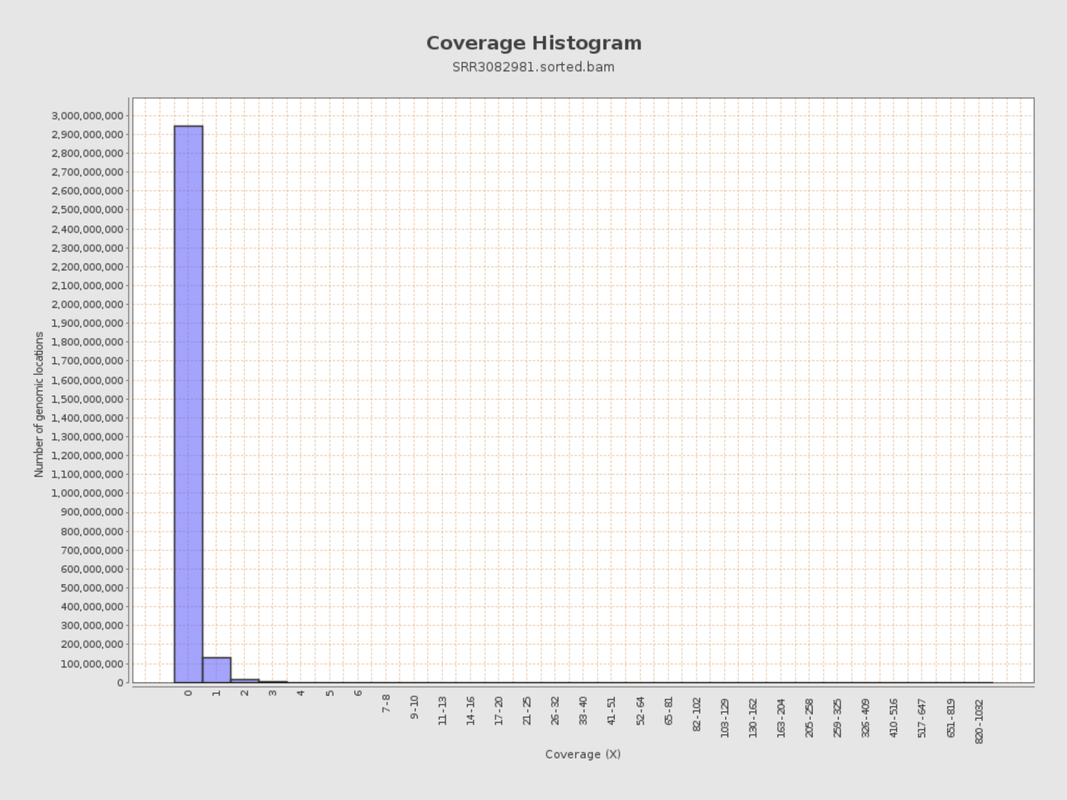
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21760257	0.0873	0.9461
chr2	243199373	18722080	0.077	0.8466
chr3	198022430	8815102	0.0445	0.2484
chr4	191154276	9988203	0.0523	0.278
chr5	180915260	11515020	0.0636	0.2948
chr6	171115067	12154604	0.071	0.4444
chr7	159138663	9377063	0.0589	0.6363

chr8	146364022	11784524	0.0805	0.6945
chr9	141213431	5637503	0.0399	0.6115
chr10	135534747	7219310	0.0533	0.4787
chr11	135006516	9043416	0.067	0.5593
chr12	133851895	6007608	0.0449	0.2617
chr13	115169878	3878024	0.0337	0.2082
chr14	107349540	2396699	0.0223	0.2788
chr15	102531392	3589851	0.035	0.2171
chr16	90354753	7579224	0.0839	0.413
chr17	81195210	5441514	0.067	0.4244
chr18	78077248	6935040	0.0888	1.3124
chr19	59128983	2815874	0.0476	0.7182
chr20	63025520	3710357	0.0589	0.301
chr21	48129895	3592865	0.0746	0.3416
chr22	51304566	2672121	0.0521	0.2632
chrMT	16571	17951	1.0833	1.391
chrX	155270560	8724838	0.0562	0.3579
chrY	59373566	369628	0.0062	0.1287

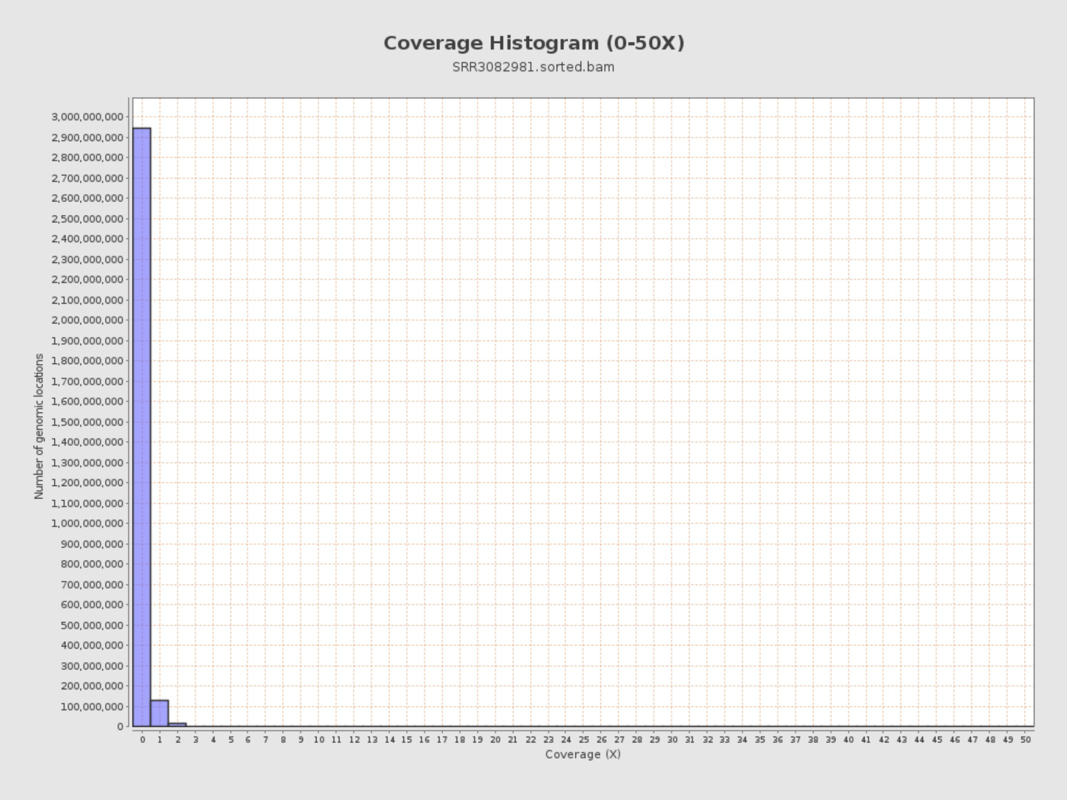
3. Results : Coverage across reference



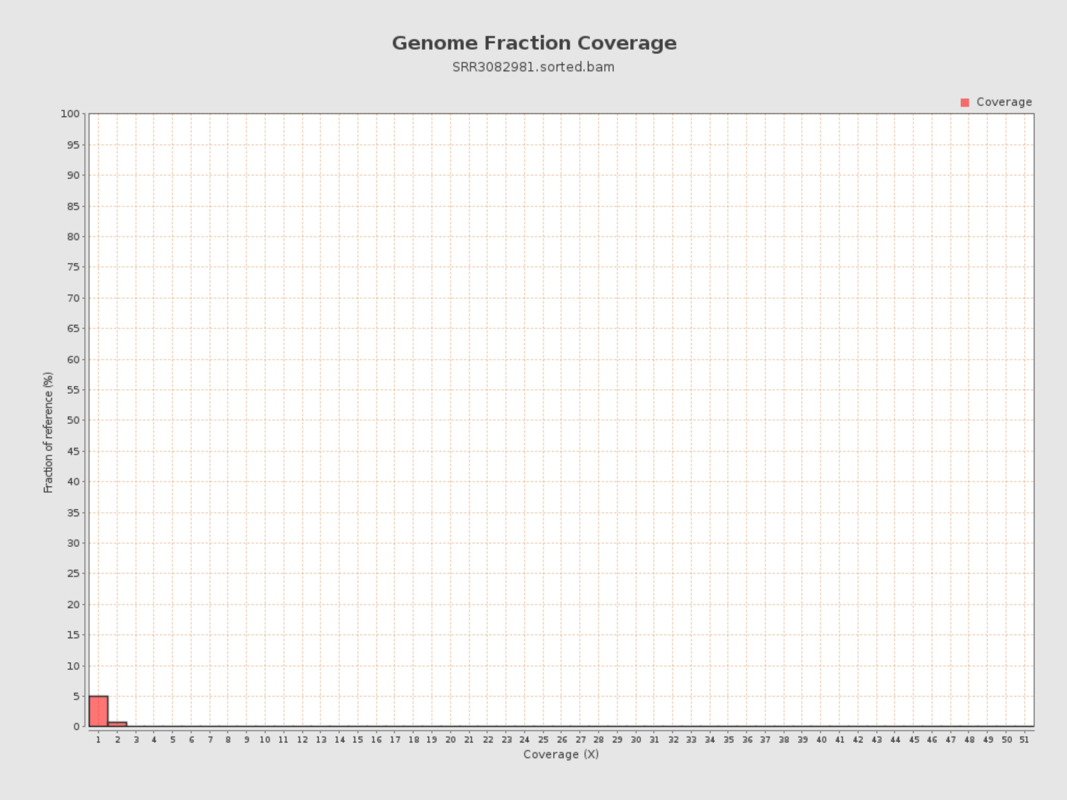
4. Results : Coverage Histogram



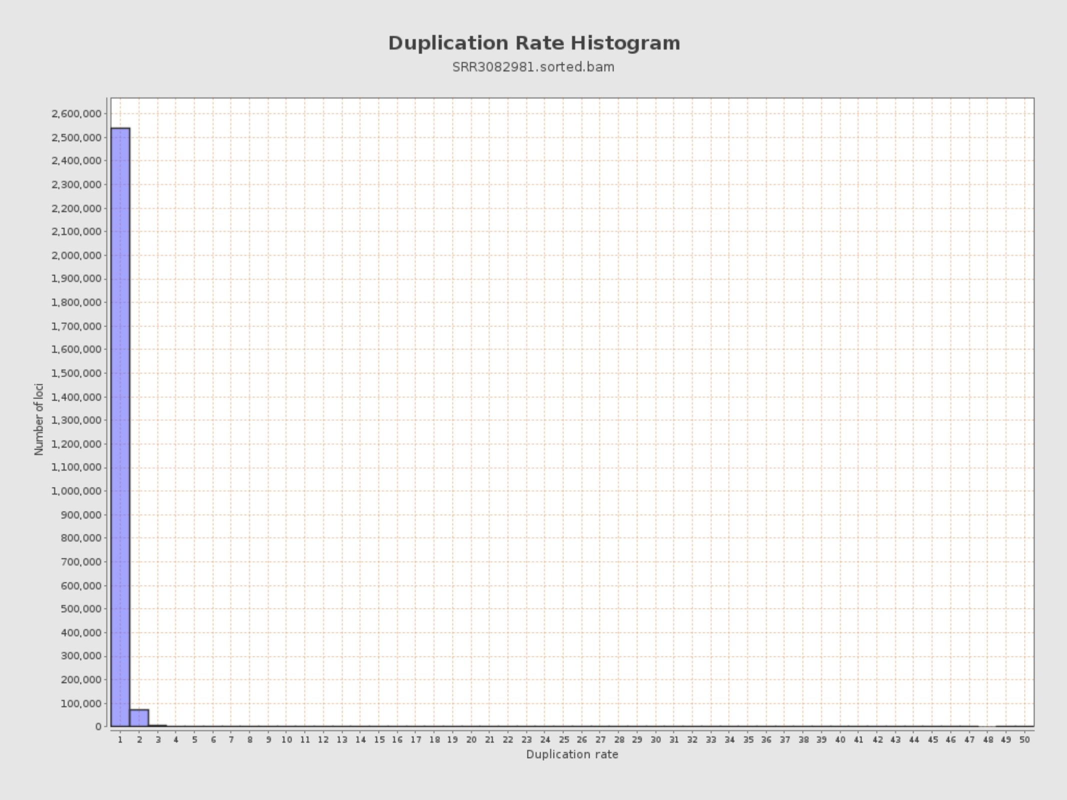
5. Results : Coverage Histogram (0-50X)



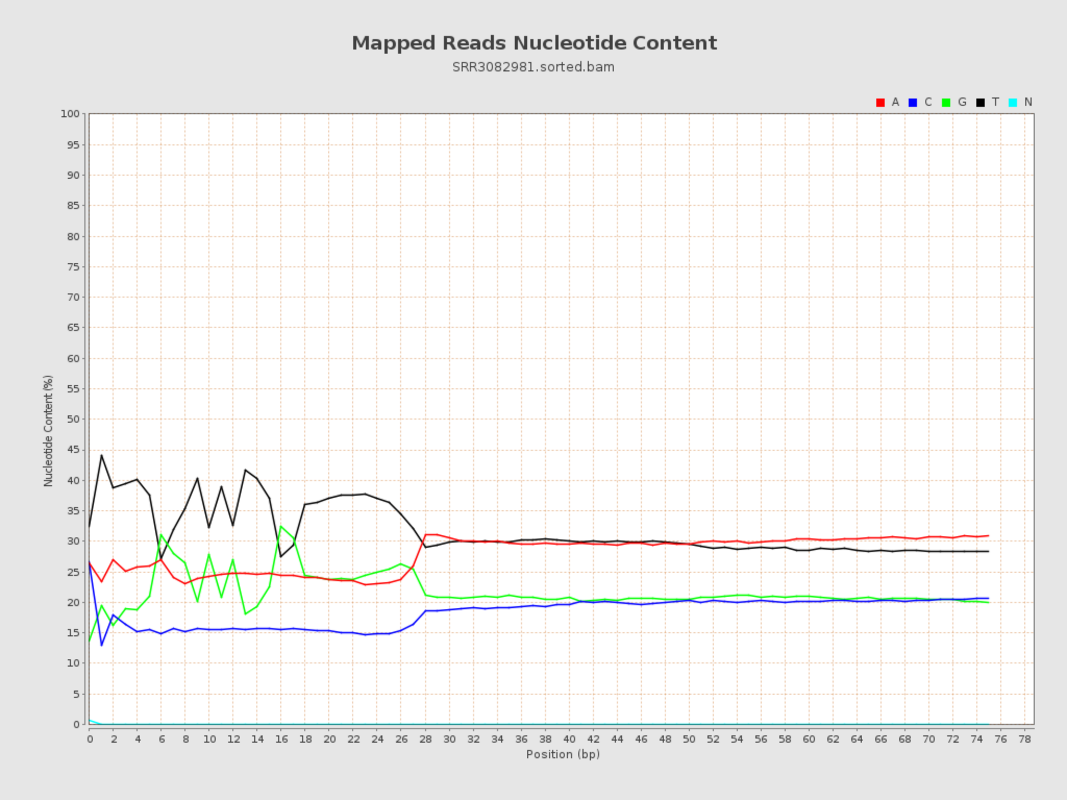
6. Results : Genome Fraction Coverage



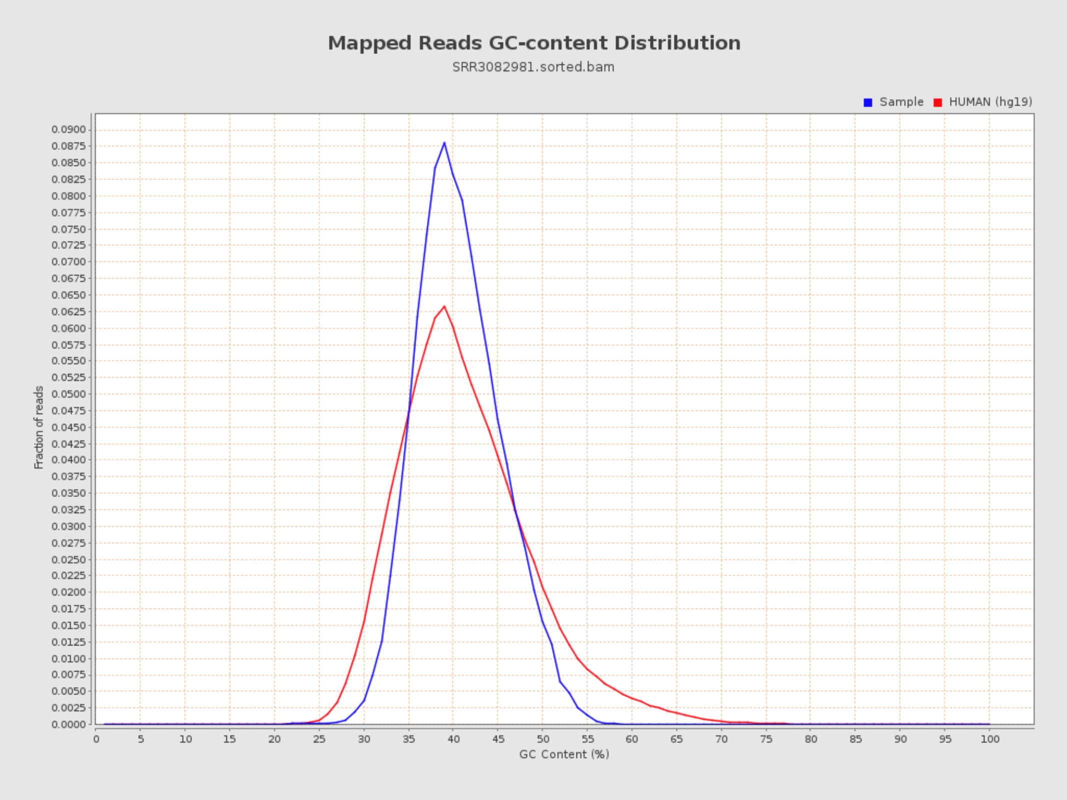
7. Results : Duplication Rate Histogram



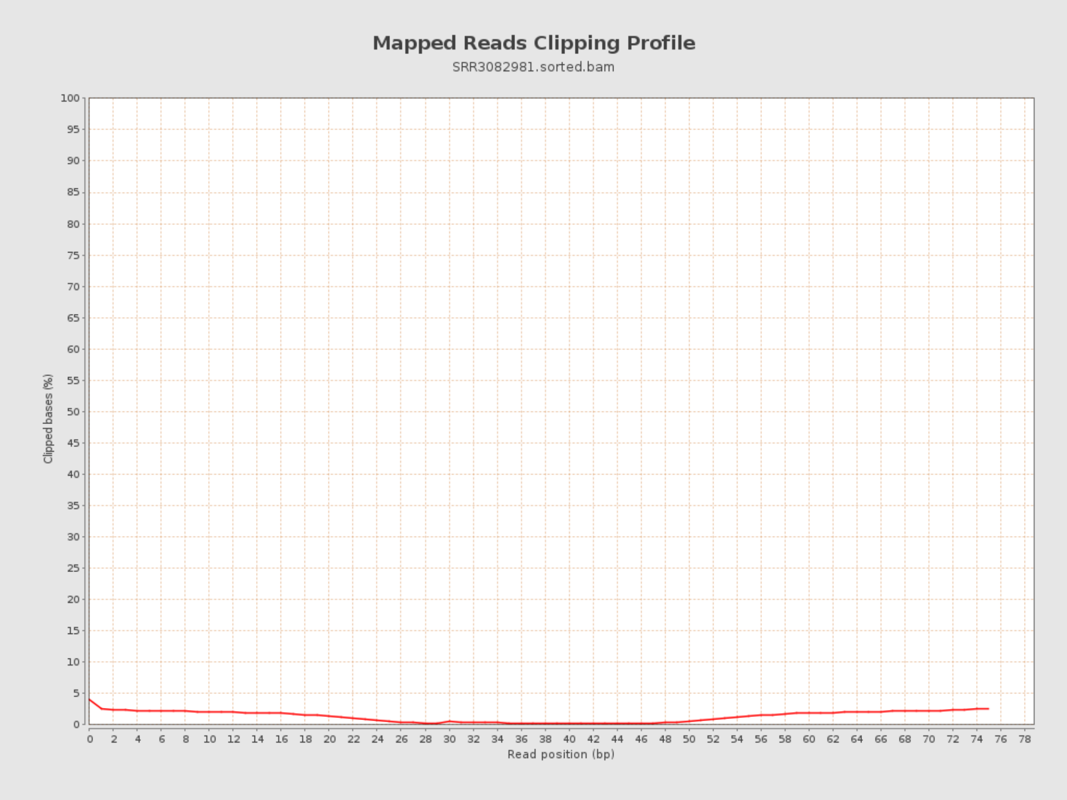
8. Results : Mapped Reads Nucleotide Content



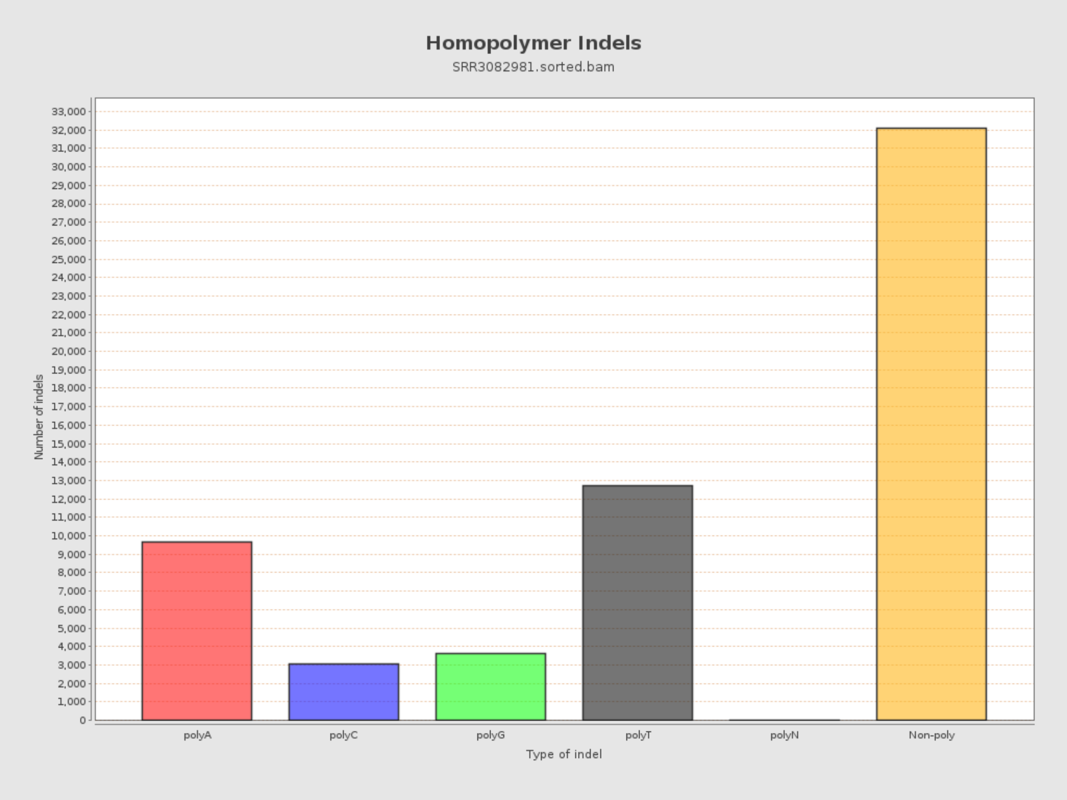
9. Results : Mapped Reads GC-content Distribution



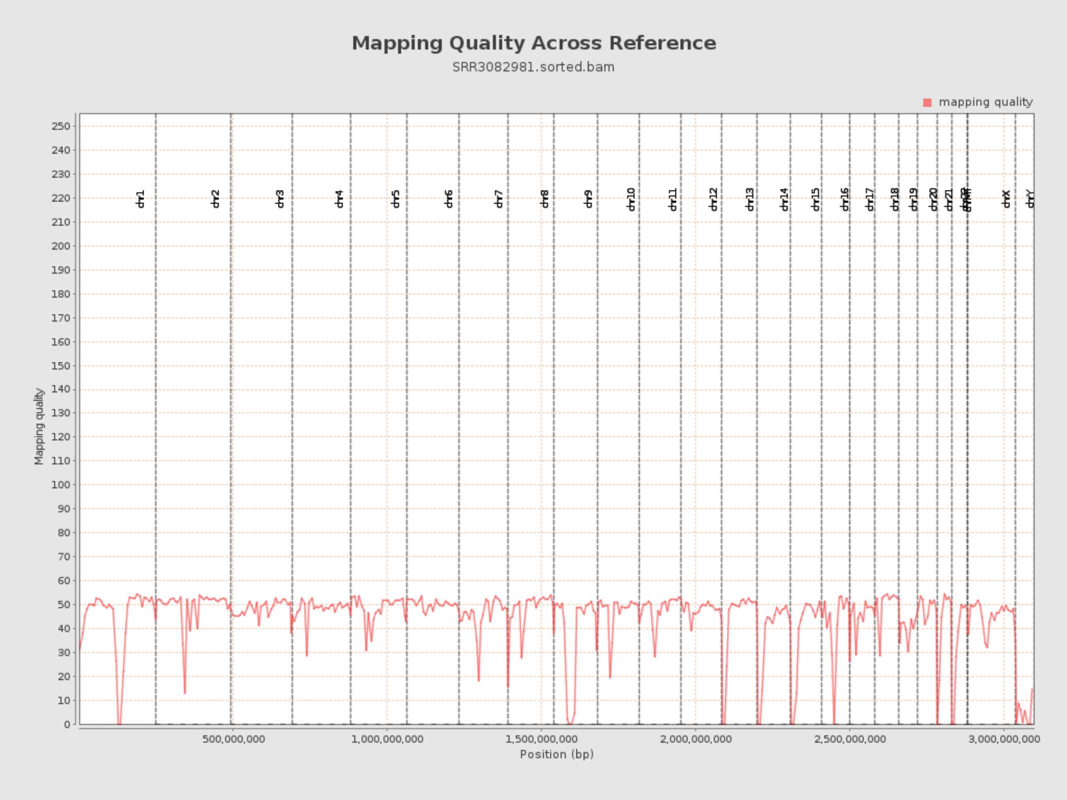
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram