Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 18:45:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082896.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_SRR3082896 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082896.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 18:45:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082896.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,813,574
Mapped reads	3,296,138 / 86.43%
Unmapped reads	517,436 / 13.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,186 / 0.61%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	165,383 / 4.34%
Duplication rate	4%
Clipped reads	1,169,017 / 30.65%

2.2. ACGT Content

Number/percentage of A's	65,595,872 / 28.84%
Number/percentage of C's	41,377,244 / 18.19%
Number/percentage of T's	73,918,400 / 32.5%
Number/percentage of G's	46,543,752 / 20.46%
Number/percentage of N's	12,486 / 0.01%
GC Percentage	38.66%

2.3. Coverage

Mean	0.0735

Standard Deviation	0.5603

2.4. Mapping Quality

Mean Mapping Quality	47.85

2.5. Mismatches and indels

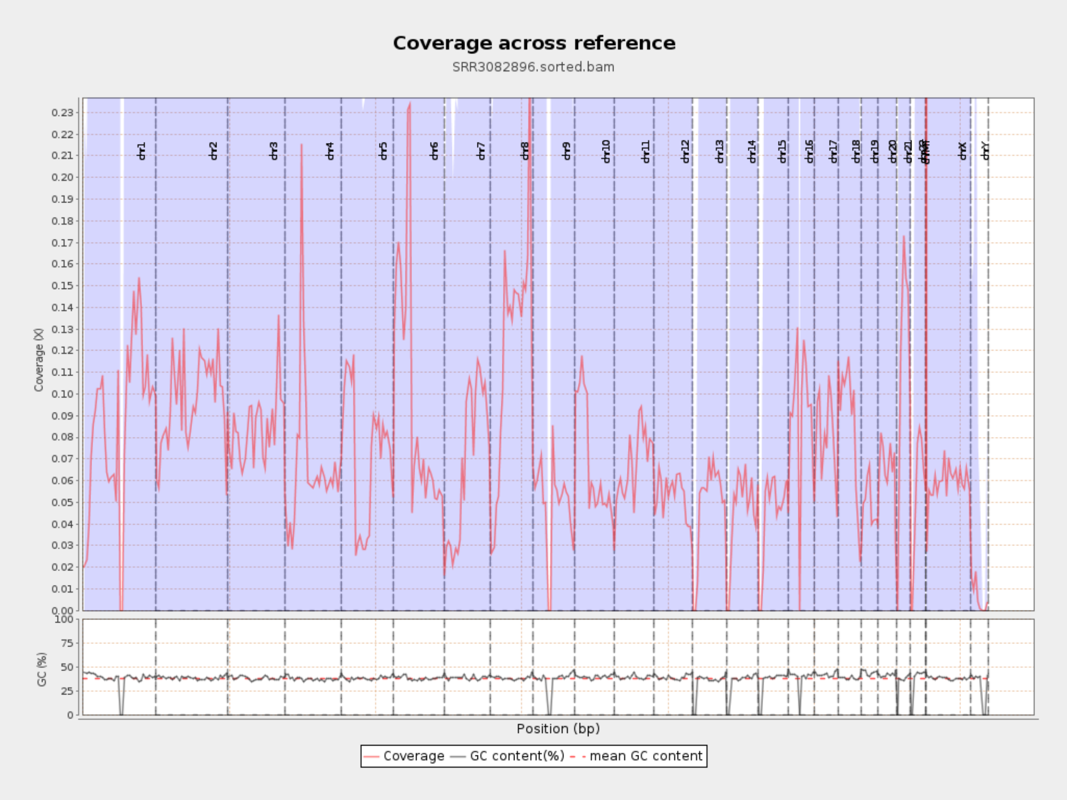
General error rate	0.89%
Mismatches	1,987,784
Insertions	18,491
Mapped reads with at least one insertion	0.56%
Deletions	49,601
Mapped reads with at least one deletion	1.49%
Homopolymer indels	47.63%

2.6. Chromosome stats

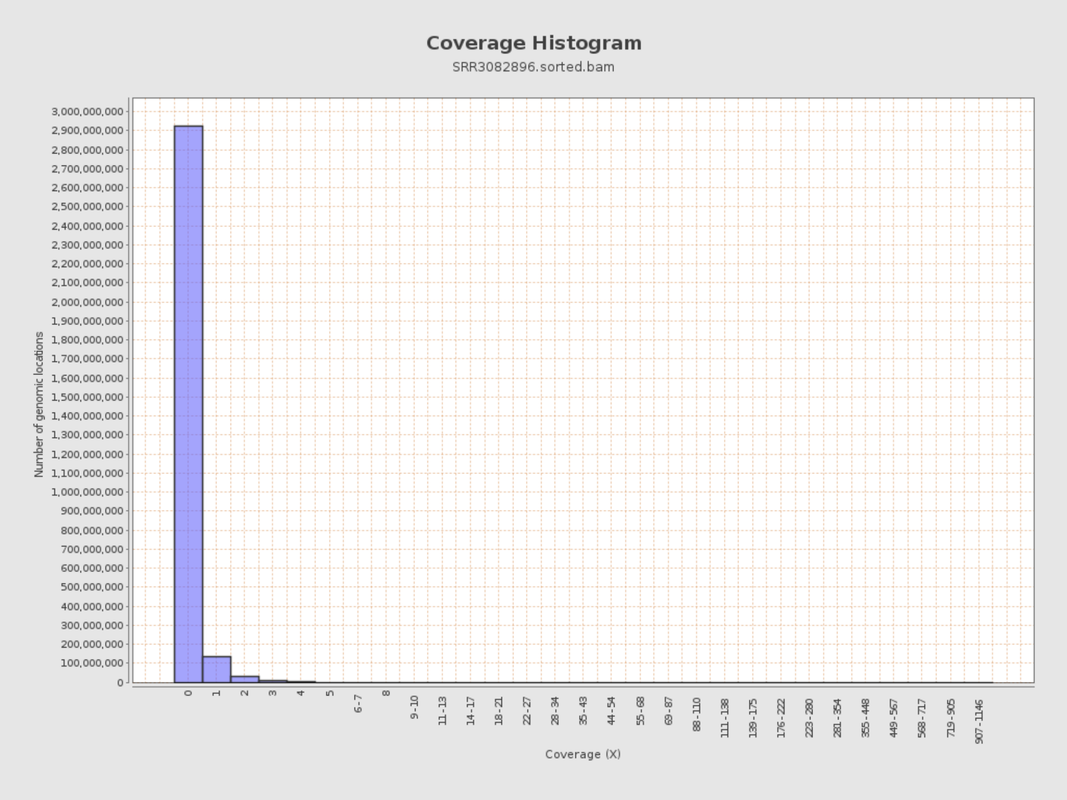
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21510371	0.0863	1.0769
chr2	243199373	23686192	0.0974	0.646
chr3	198022430	16752687	0.0846	0.3629
chr4	191154276	13021094	0.0681	0.3383
chr5	180915260	12880862	0.0712	0.3373
chr6	171115067	16781962	0.0981	0.5681
chr7	159138663	10904875	0.0685	0.45

chr8	146364022	17936551	0.1225	0.8386
chr9	141213431	6990243	0.0495	0.5151
chr10	135534747	9353036	0.069	0.4509
chr11	135006516	9175827	0.068	0.4371
chr12	133851895	7034193	0.0526	0.3016
chr13	115169878	5658780	0.0491	0.2744
chr14	107349540	4908383	0.0457	0.3069
chr15	102531392	4515972	0.044	0.2588
chr16	90354753	8019109	0.0888	0.4213
chr17	81195210	6642691	0.0818	0.4512
chr18	78077248	6872221	0.088	1.0603
chr19	59128983	2897978	0.049	0.6914
chr20	63025520	4256037	0.0675	0.3456
chr21	48129895	5390478	0.112	0.4355
chr22	51304566	2706644	0.0528	0.2815
chrMT	16571	177797	10.7294	6.9412
chrX	155270560	9094865	0.0586	0.3514
chrY	59373566	364190	0.0061	0.1295

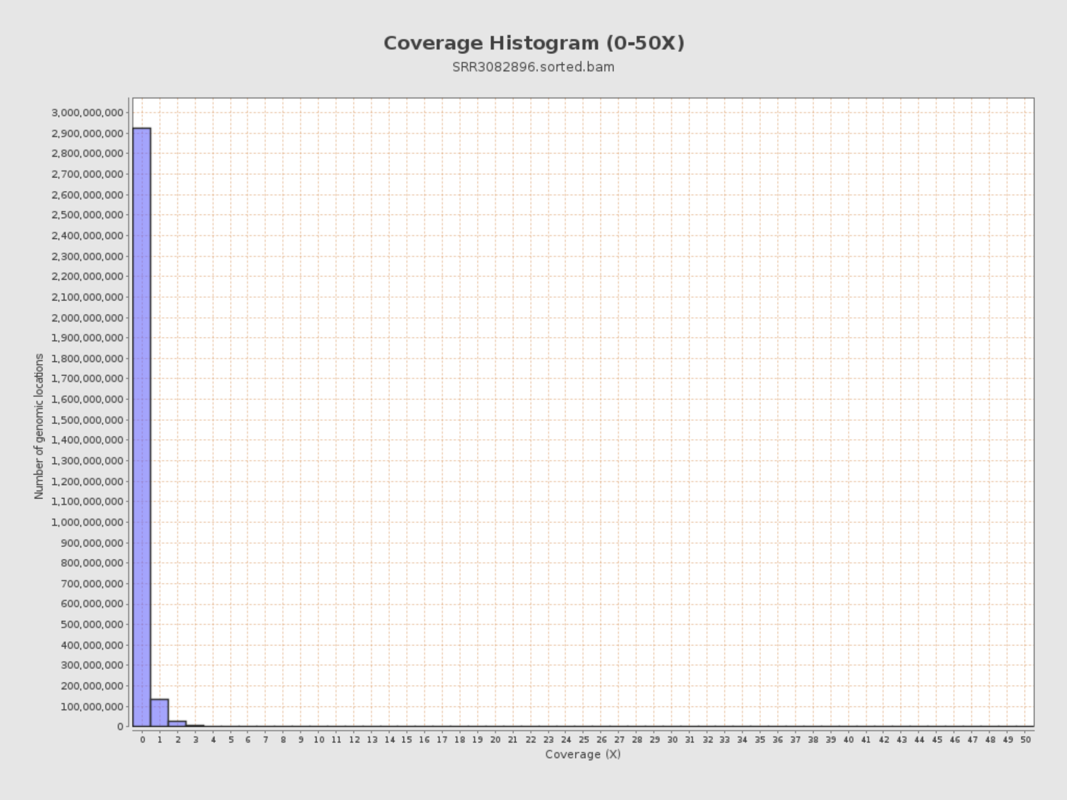
3. Results : Coverage across reference



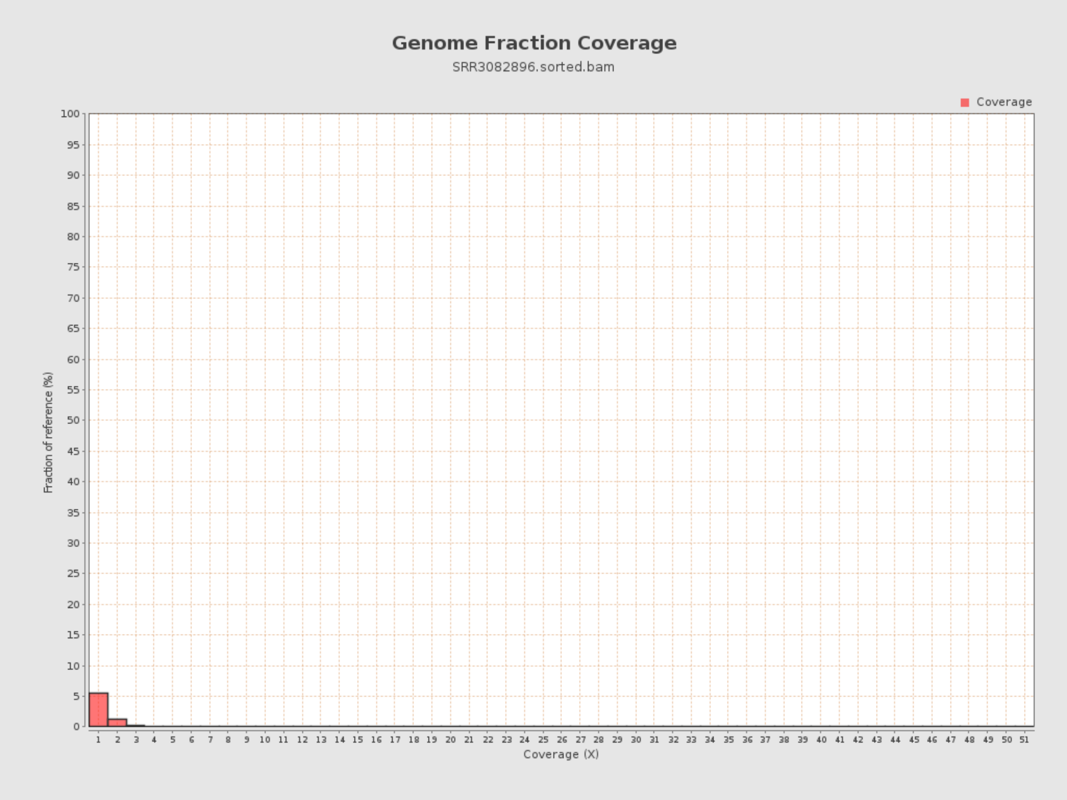
4. Results : Coverage Histogram



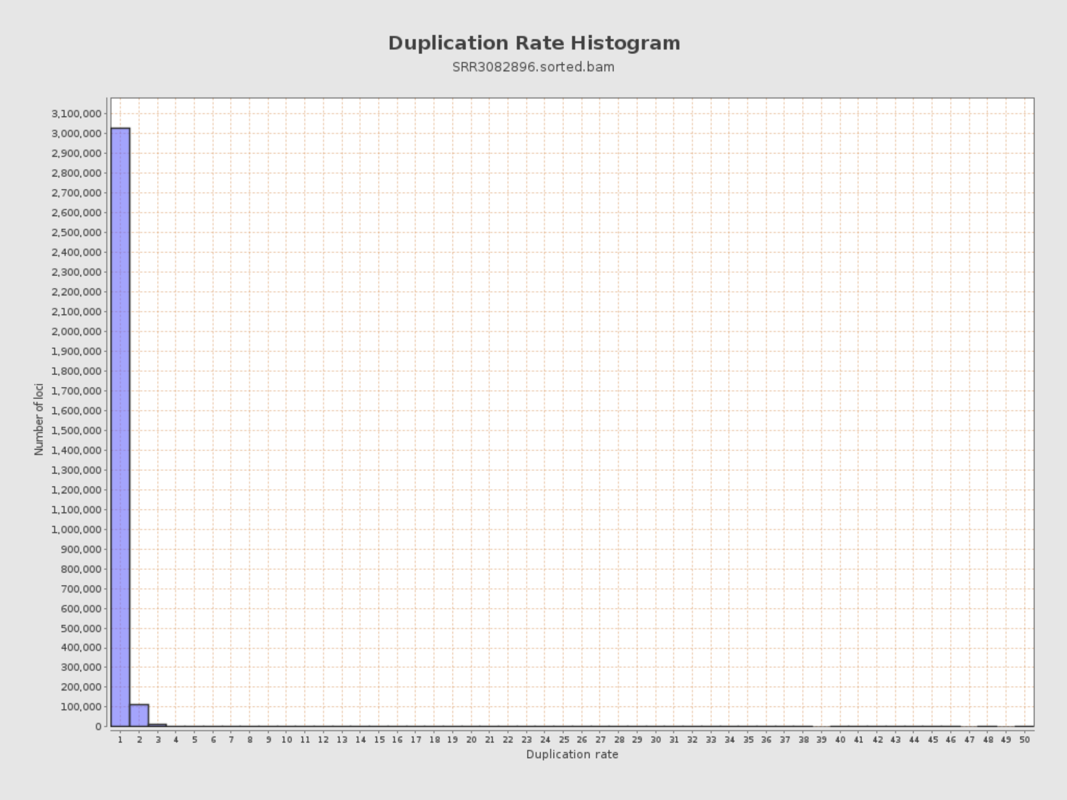
5. Results : Coverage Histogram (0-50X)



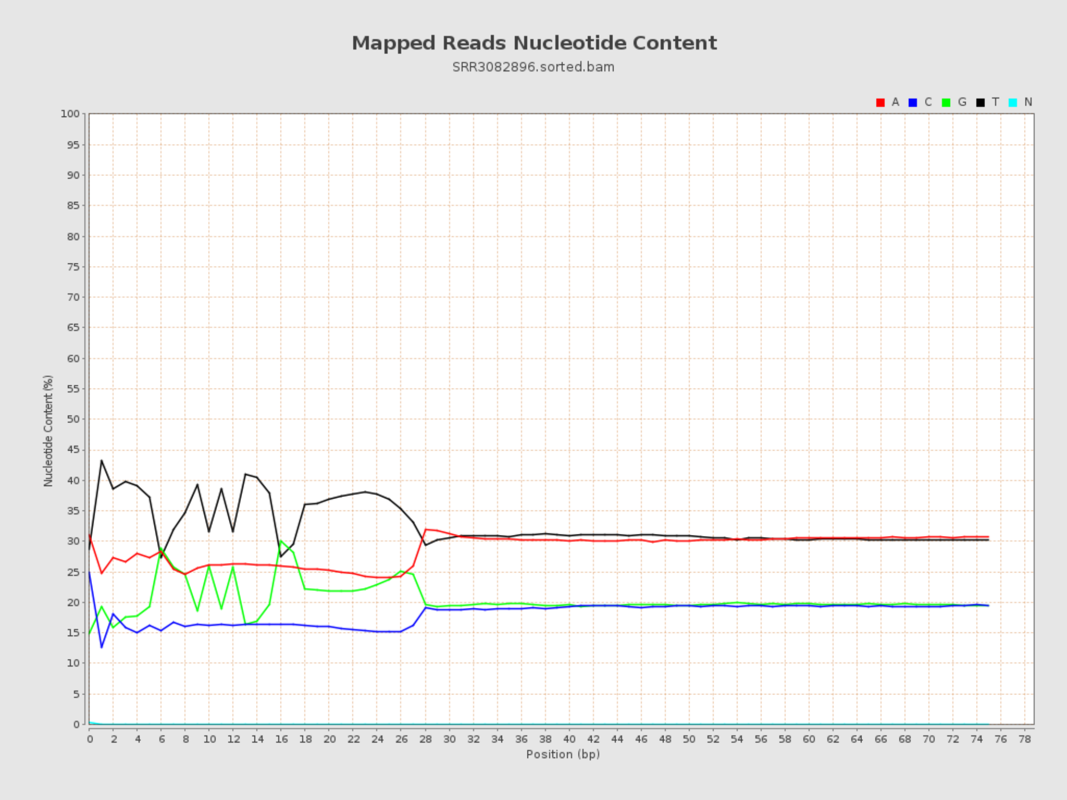
6. Results : Genome Fraction Coverage



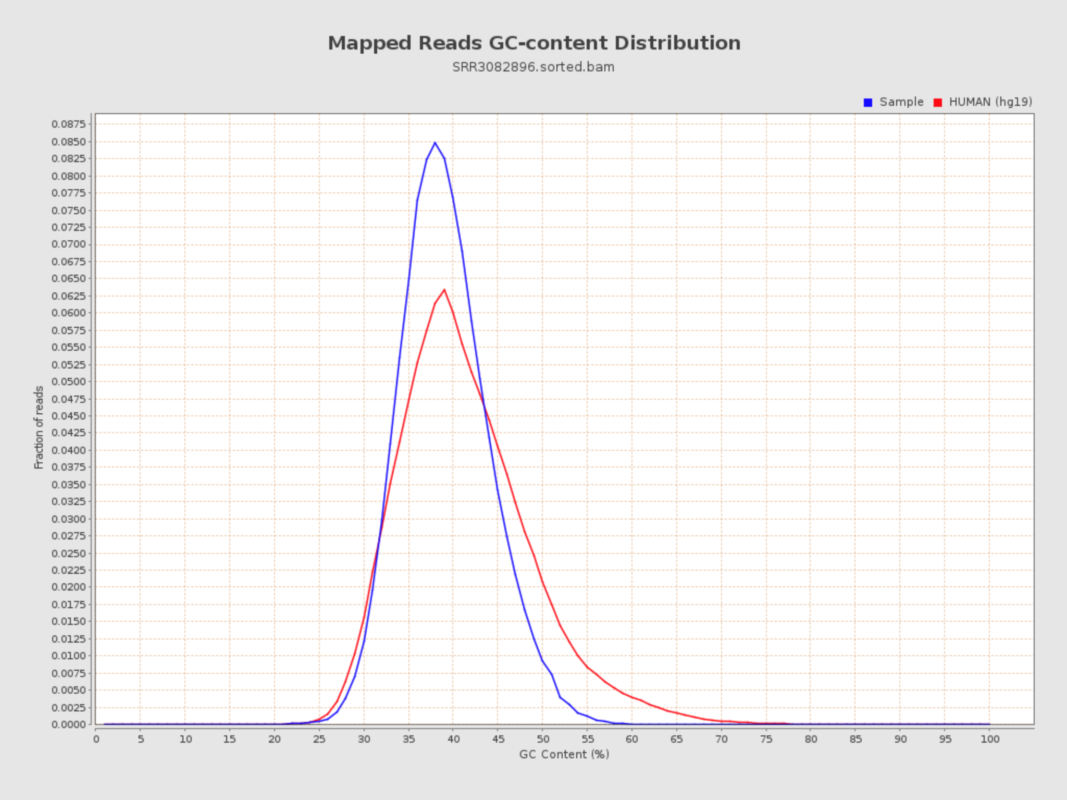
7. Results : Duplication Rate Histogram



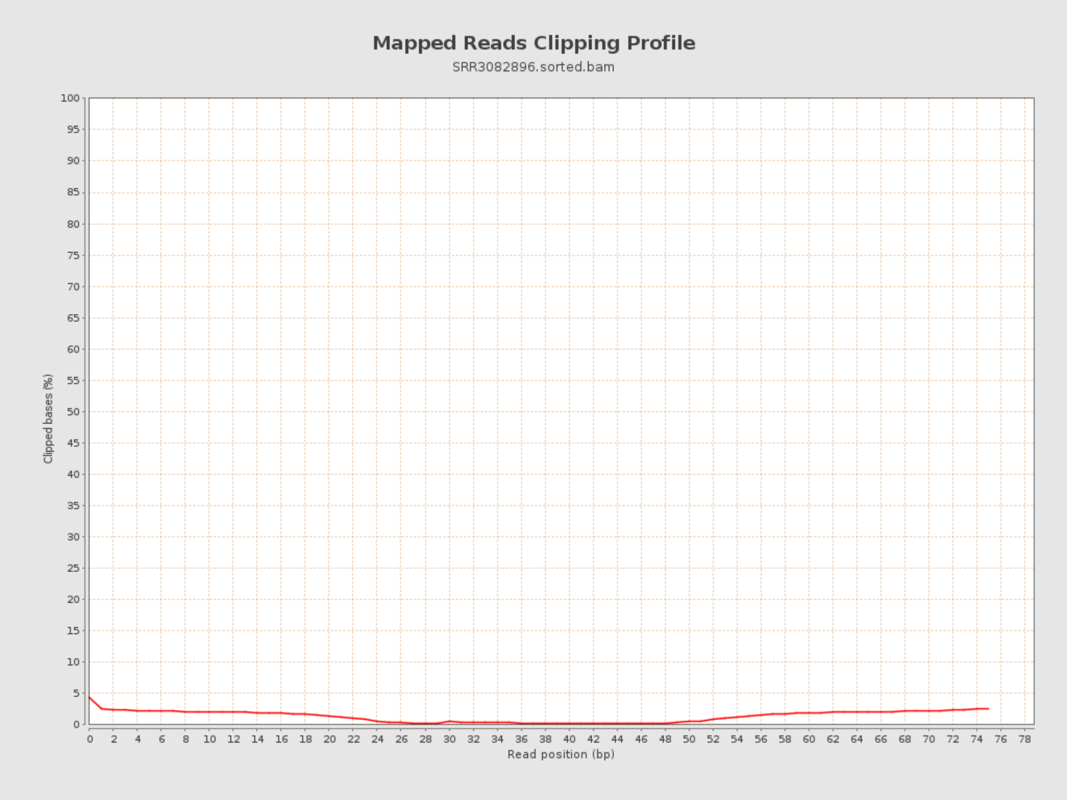
8. Results : Mapped Reads Nucleotide Content



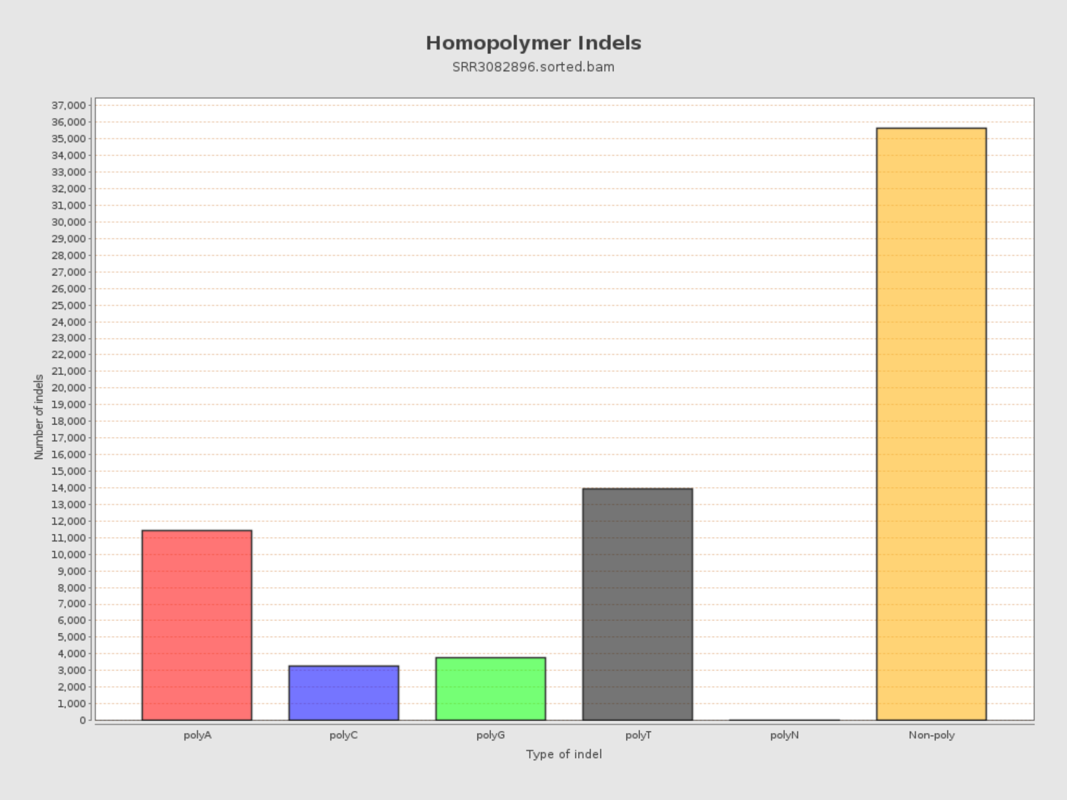
9. Results : Mapped Reads GC-content Distribution



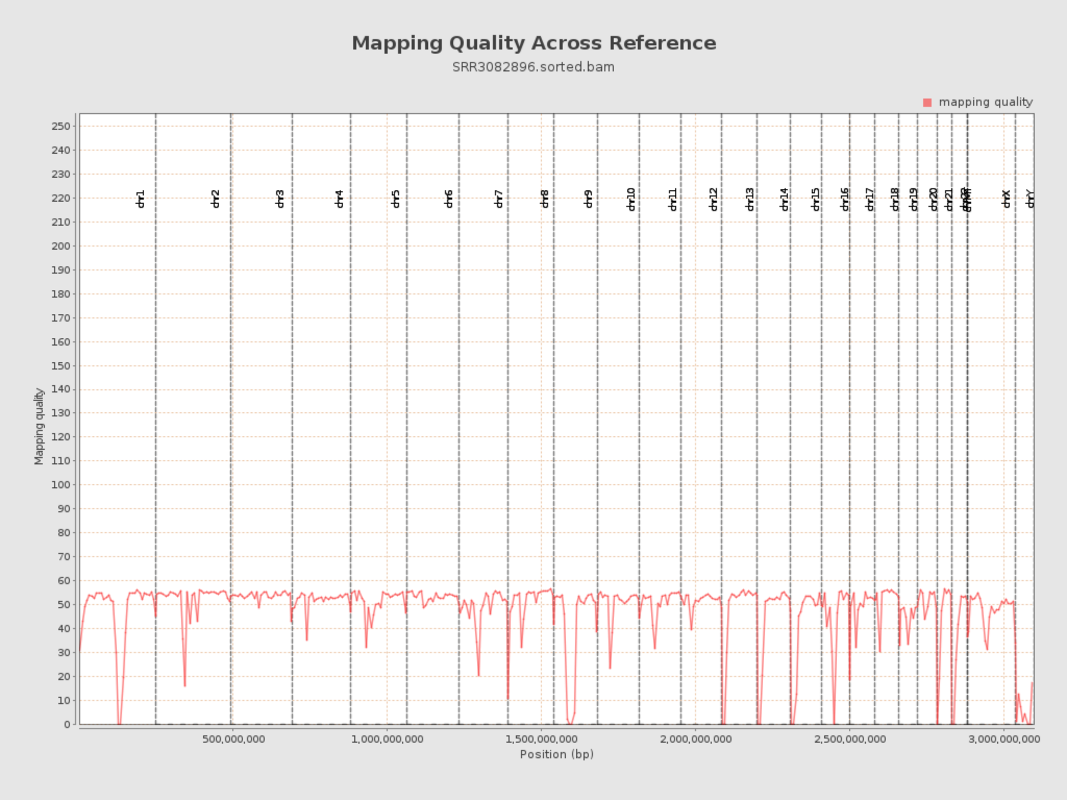
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram