Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 18:40:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082895.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_SRR3082895 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082895.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 18:40:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082895.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,042,096
Mapped reads	3,637,399 / 89.99%
Unmapped reads	404,697 / 10.01%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,616 / 0.66%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	165,092 / 4.08%
Duplication rate	3.56%
Clipped reads	1,219,530 / 30.17%

2.2. ACGT Content

Number/percentage of A's	74,112,131 / 29.25%
Number/percentage of C's	46,672,305 / 18.42%
Number/percentage of T's	81,732,973 / 32.26%
Number/percentage of G's	50,803,963 / 20.05%
Number/percentage of N's	14,588 / 0.01%
GC Percentage	38.48%

2.3. Coverage

Mean	0.0819

Standard Deviation	0.6281

2.4. Mapping Quality

Mean Mapping Quality	47.76

2.5. Mismatches and indels

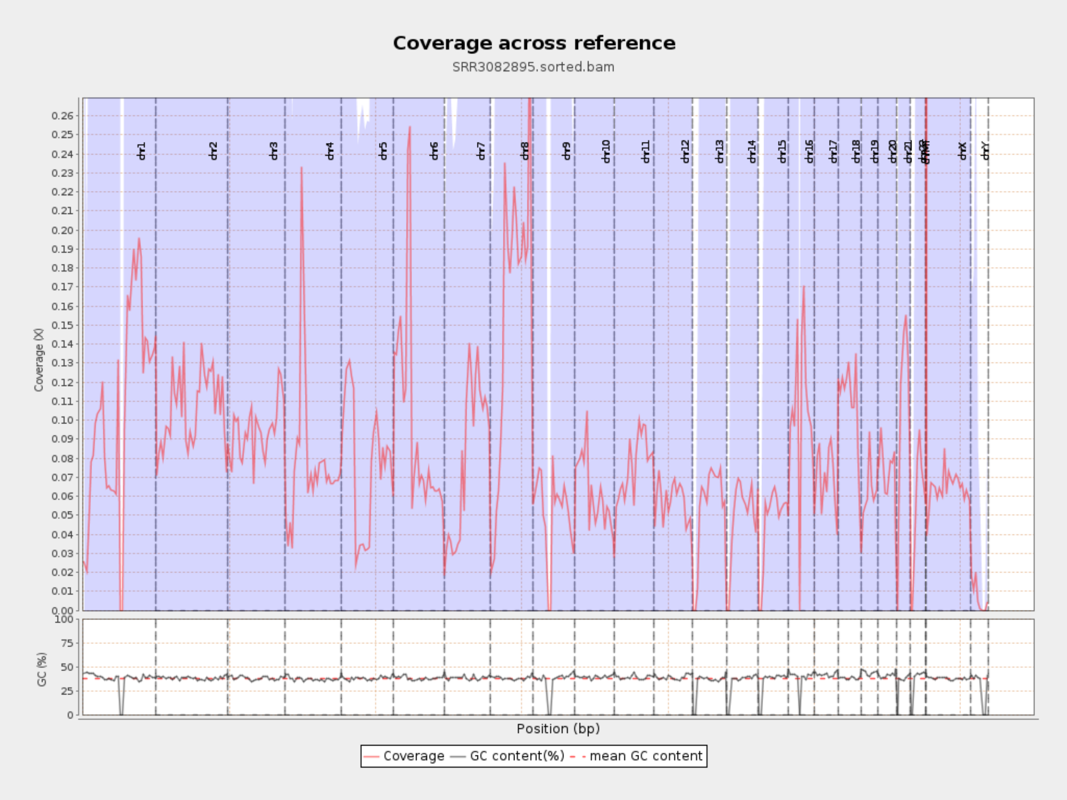
General error rate	0.89%
Mismatches	2,221,661
Insertions	20,425
Mapped reads with at least one insertion	0.56%
Deletions	55,834
Mapped reads with at least one deletion	1.52%
Homopolymer indels	47.83%

2.6. Chromosome stats

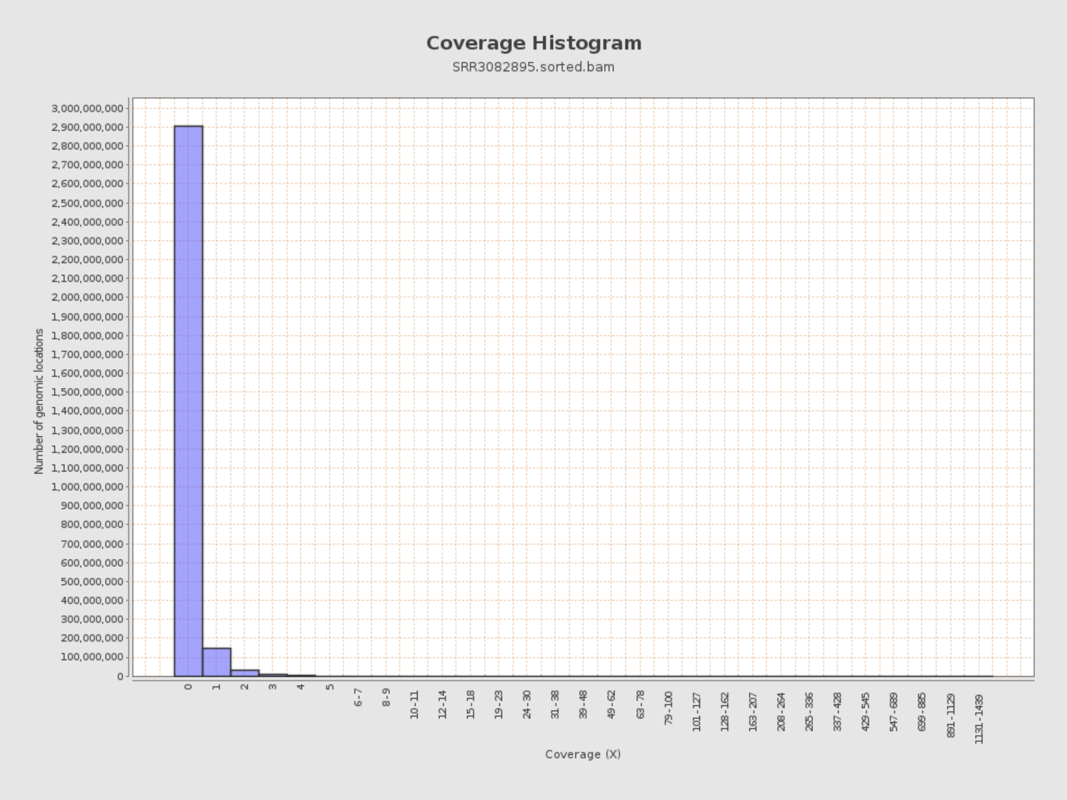
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	26257645	0.1053	1.3339
chr2	243199373	25948984	0.1067	0.6584
chr3	198022430	18718050	0.0945	0.3873
chr4	191154276	15321661	0.0802	0.369
chr5	180915260	13773806	0.0761	0.3497
chr6	171115067	17039231	0.0996	0.5583
chr7	159138663	12813837	0.0805	0.5469

chr8	146364022	23095326	0.1578	0.9088
chr9	141213431	7326770	0.0519	0.5027
chr10	135534747	8449962	0.0623	0.4822
chr11	135006516	10231752	0.0758	0.4838
chr12	133851895	7648538	0.0571	0.3107
chr13	115169878	6215676	0.054	0.2899
chr14	107349540	5268911	0.0491	0.3203
chr15	102531392	4680233	0.0456	0.2655
chr16	90354753	9249941	0.1024	0.464
chr17	81195210	5754479	0.0709	0.4239
chr18	78077248	8689252	0.1113	1.1446
chr19	59128983	3700779	0.0626	0.8128
chr20	63025520	4722528	0.0749	0.3571
chr21	48129895	5014306	0.1042	0.4256
chr22	51304566	2782282	0.0542	0.2856
chrMT	16571	387674	23.3947	15.0044
chrX	155270560	9928340	0.0639	0.3623
chrY	59373566	412521	0.0069	0.1342

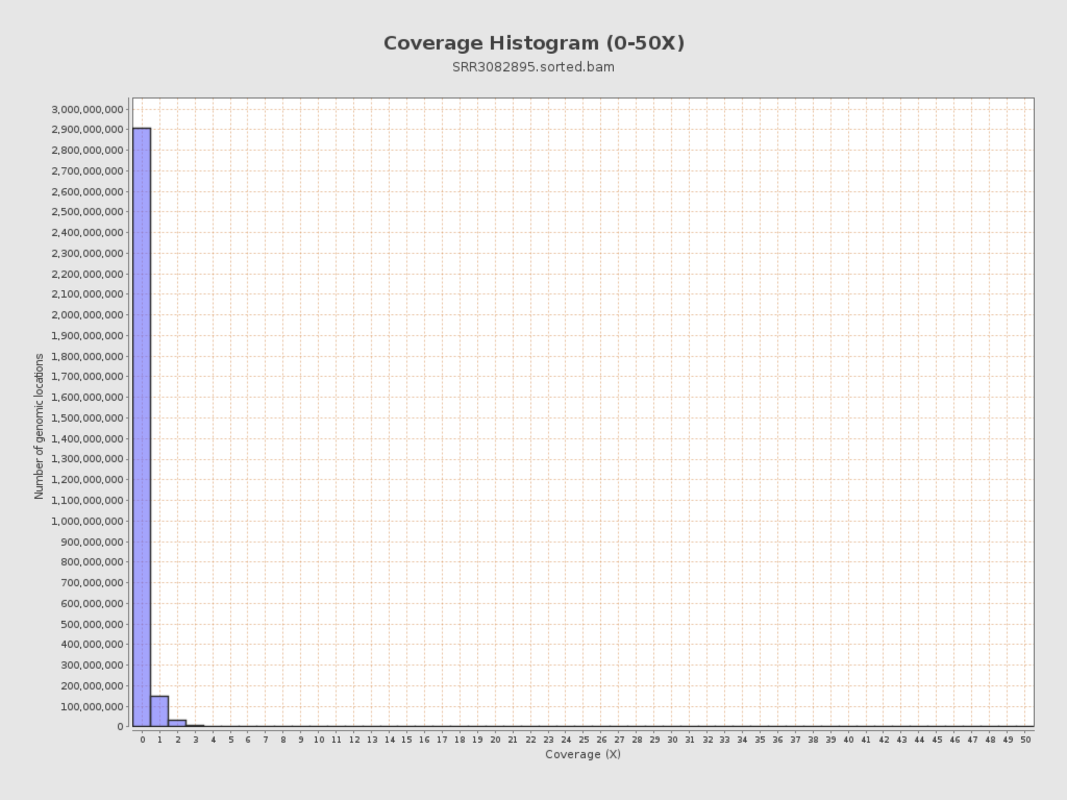
3. Results : Coverage across reference



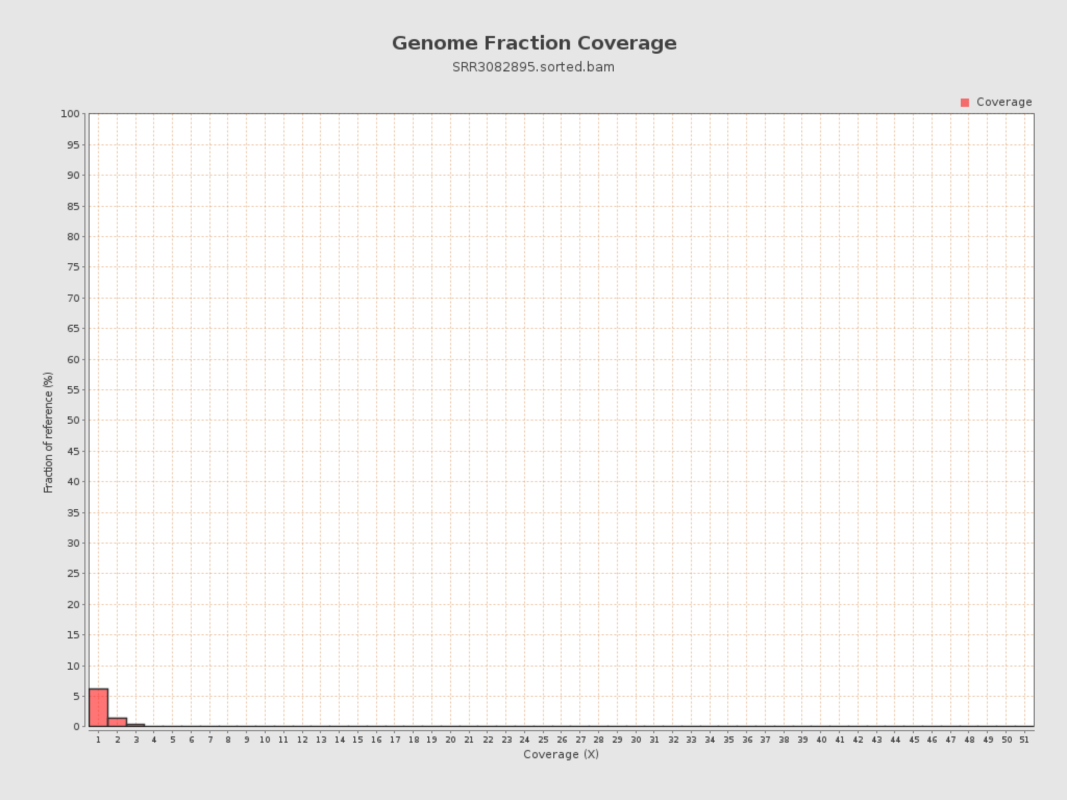
4. Results : Coverage Histogram



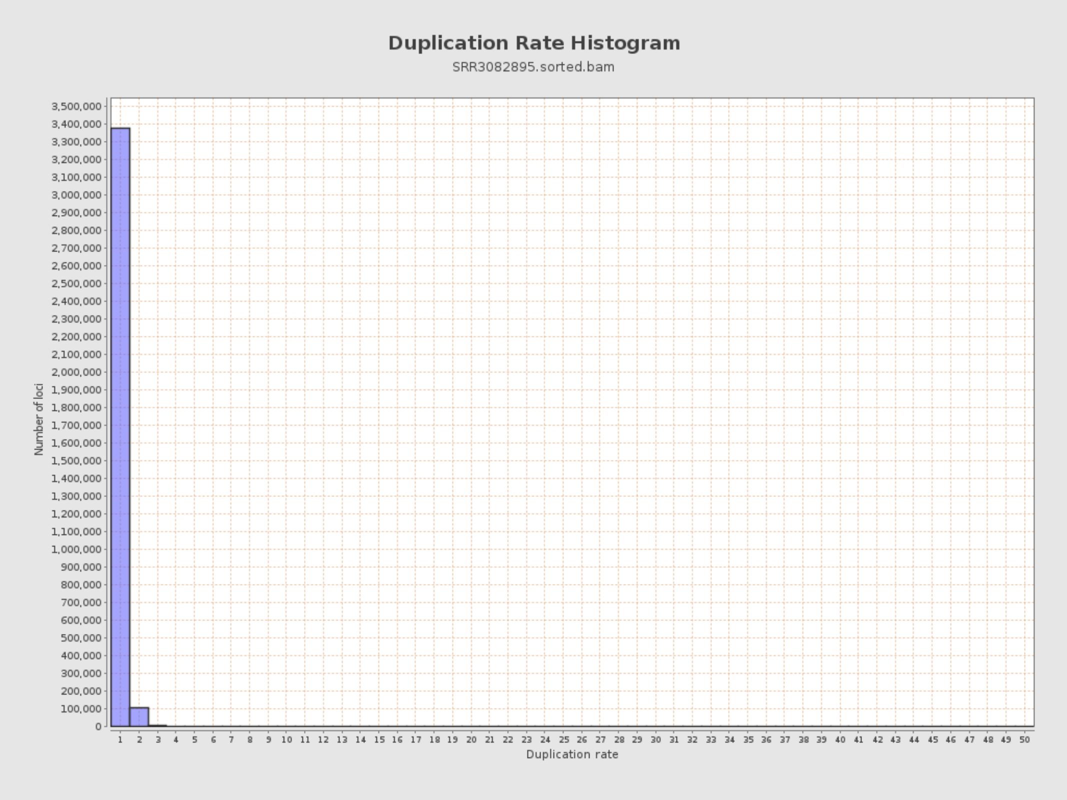
5. Results : Coverage Histogram (0-50X)



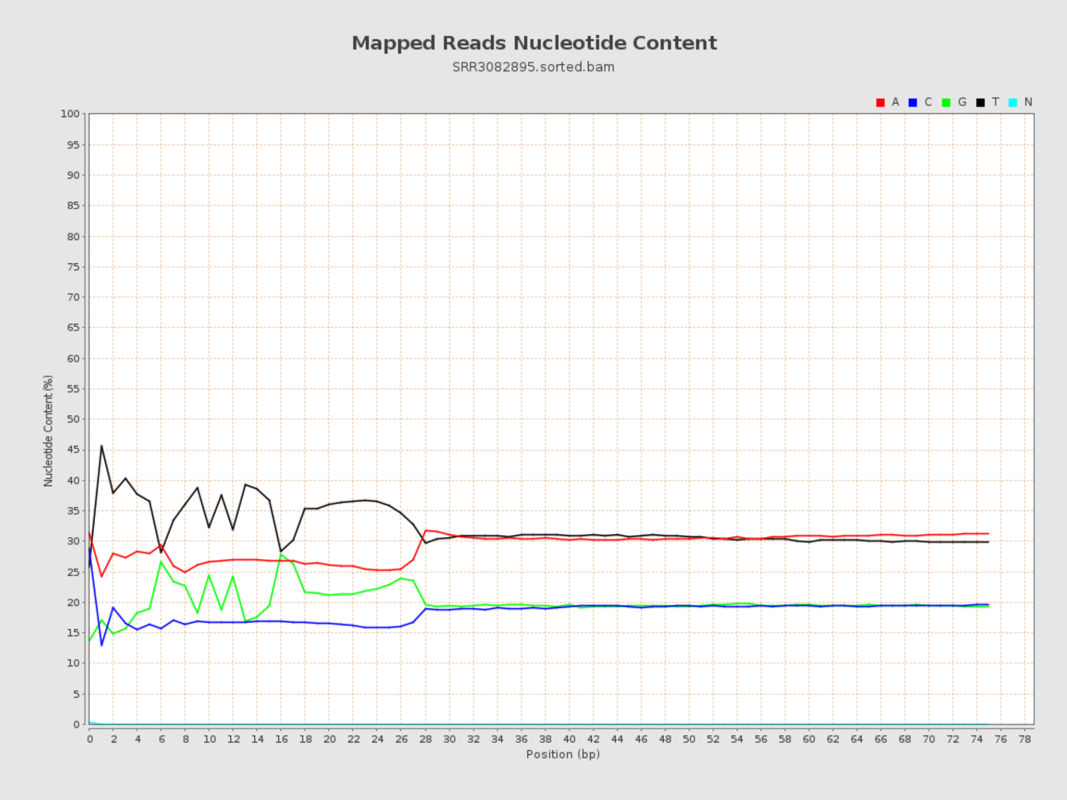
6. Results : Genome Fraction Coverage



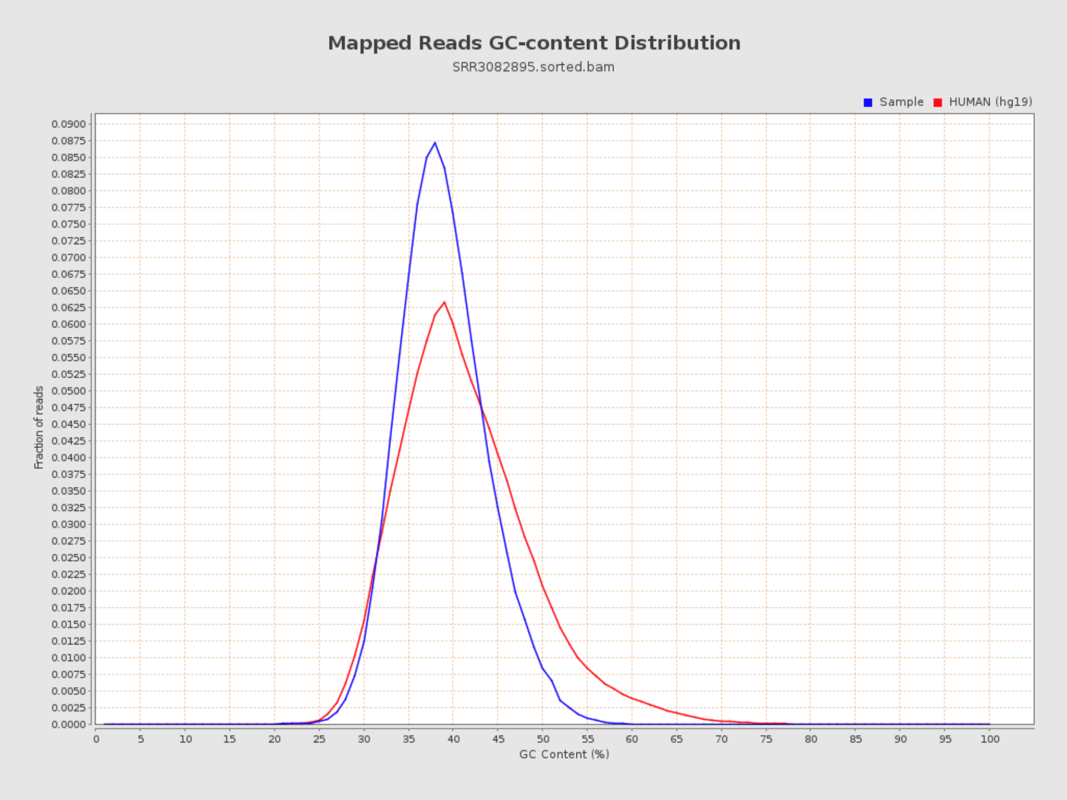
7. Results : Duplication Rate Histogram



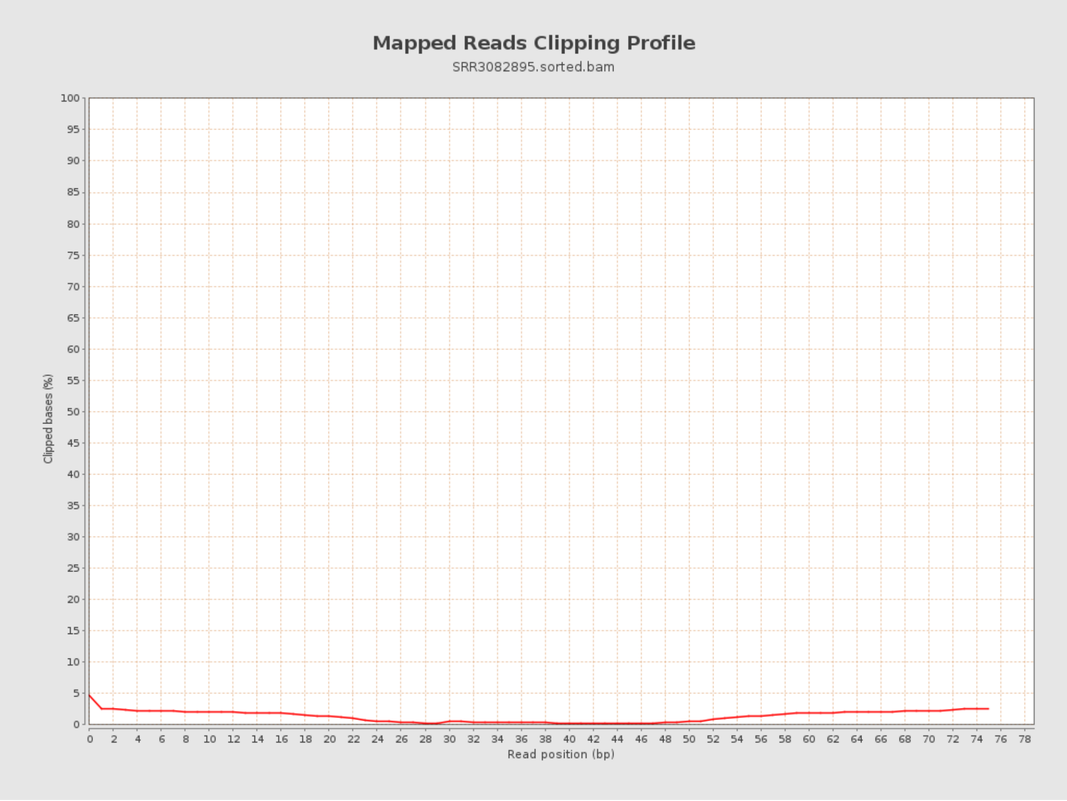
8. Results : Mapped Reads Nucleotide Content



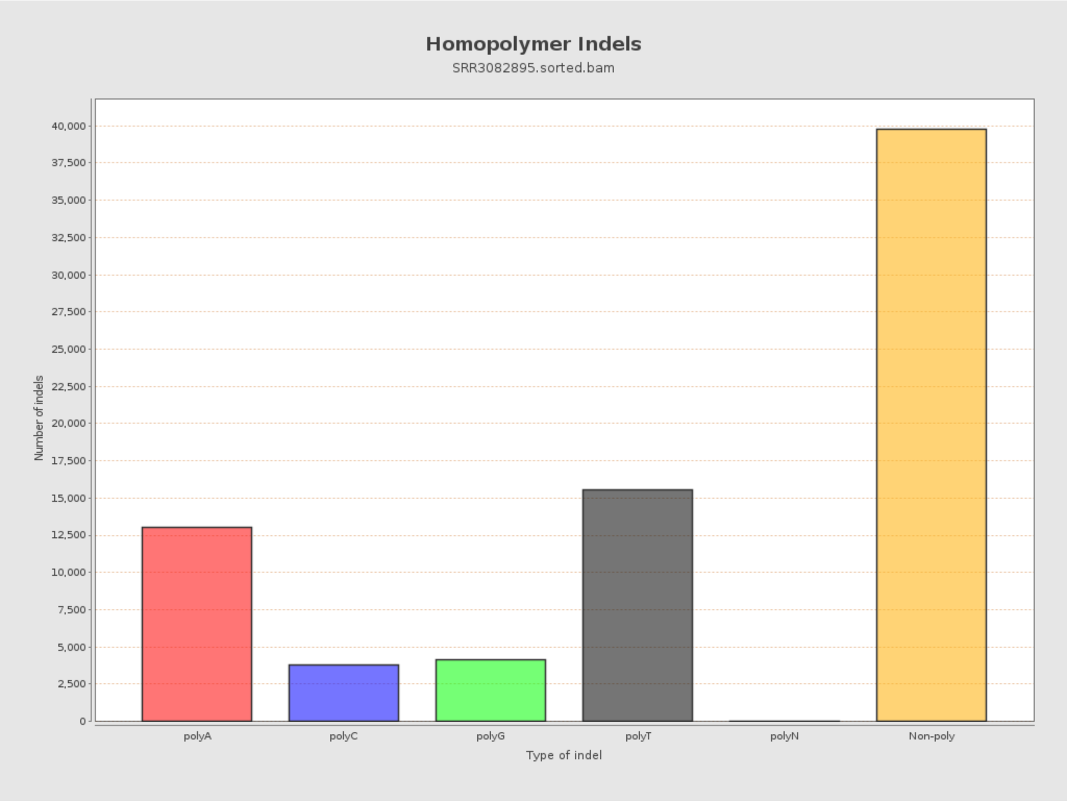
9. Results : Mapped Reads GC-content Distribution



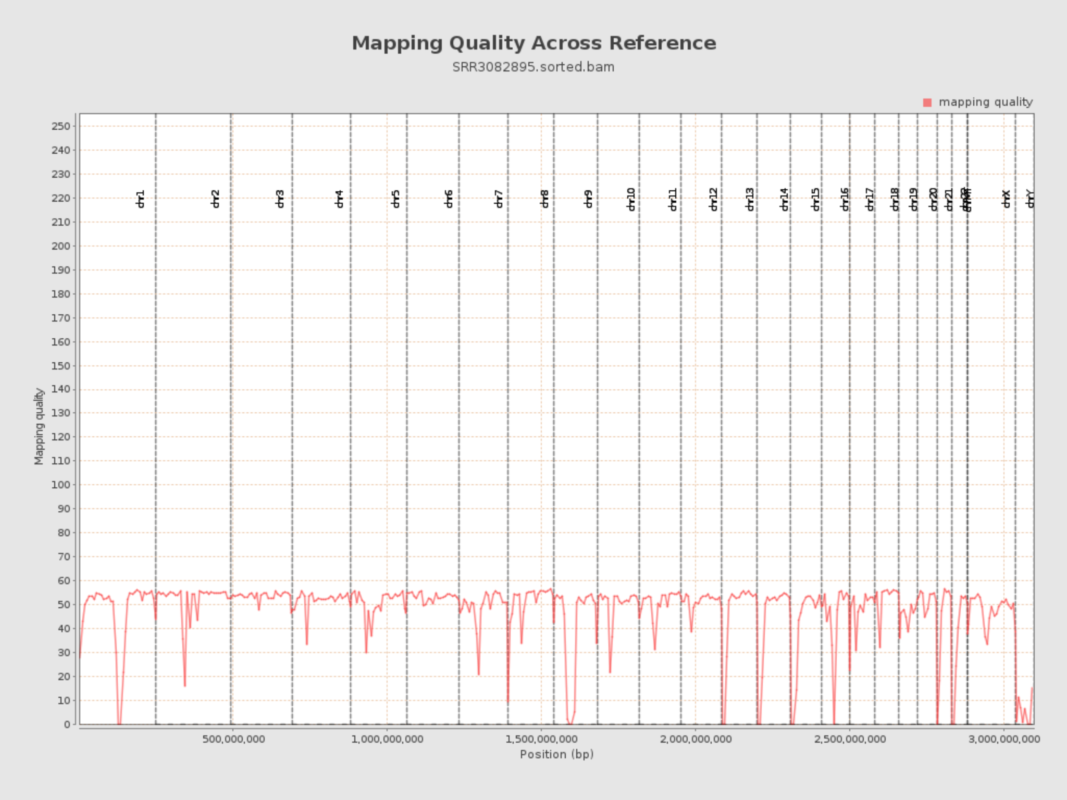
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram