Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 14:13:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084796.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_SRR3084796 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084796.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 14:13:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084796.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,150,178
Mapped reads	1,939,712 / 90.21%
Unmapped reads	210,466 / 9.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,037 / 0.93%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	89,223 / 4.15%
Duplication rate	3.99%
Clipped reads	888,464 / 41.32%

2.2. ACGT Content

Number/percentage of A's	34,947,528 / 27.1%
Number/percentage of C's	24,236,844 / 18.8%
Number/percentage of T's	40,419,227 / 31.35%
Number/percentage of G's	29,313,171 / 22.73%
Number/percentage of N's	17,629 / 0.01%
GC Percentage	41.53%

2.3. Coverage

Mean	0.0417

Standard Deviation	0.294

2.4. Mapping Quality

Mean Mapping Quality	45.41

2.5. Mismatches and indels

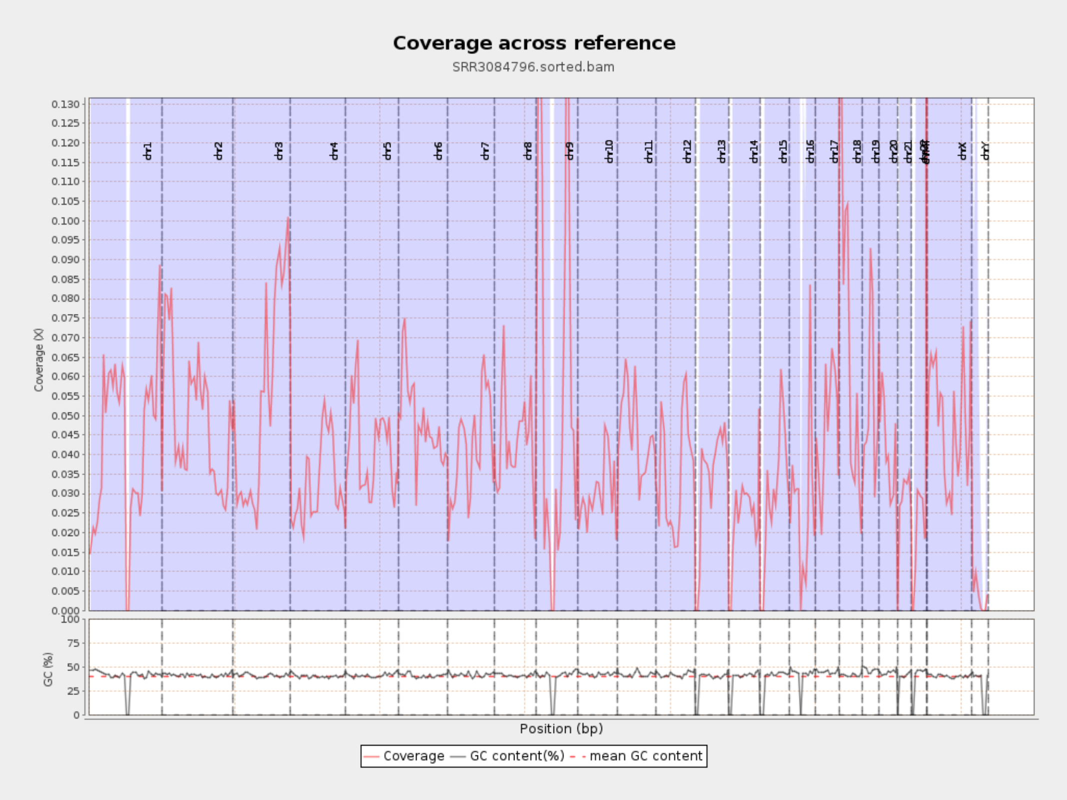
General error rate	0.77%
Mismatches	980,322
Insertions	9,923
Mapped reads with at least one insertion	0.51%
Deletions	29,401
Mapped reads with at least one deletion	1.5%
Homopolymer indels	47.58%

2.6. Chromosome stats

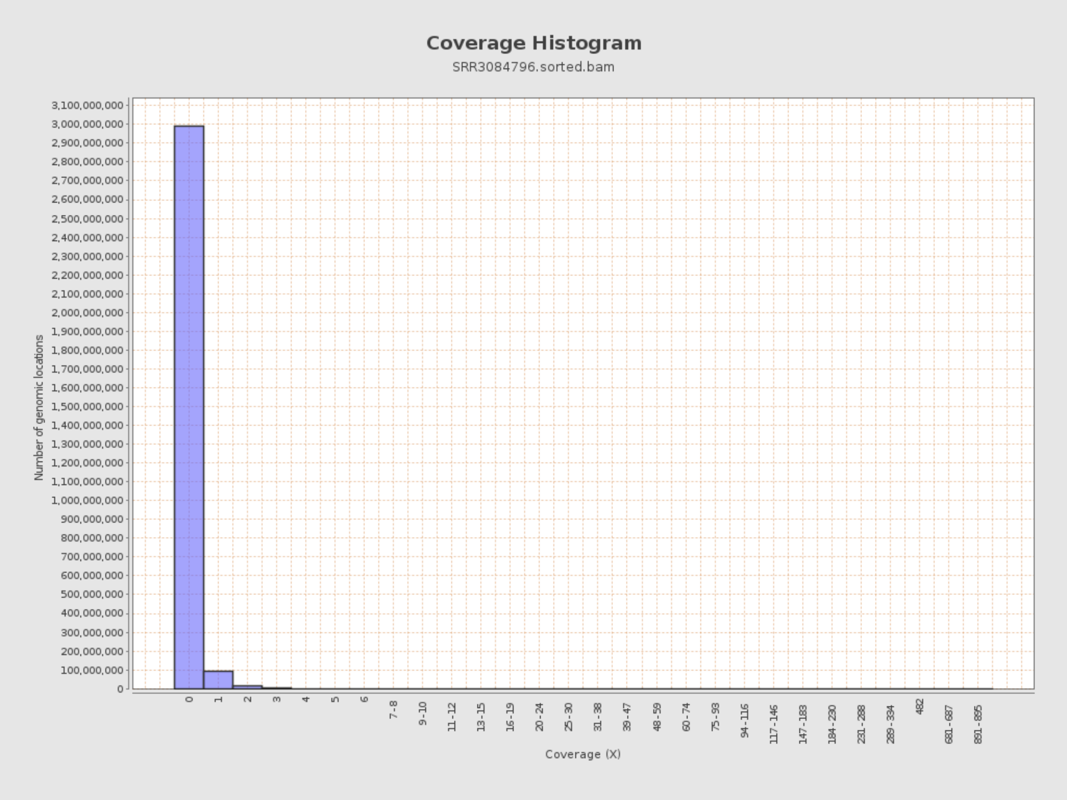
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10763603	0.0432	0.3721
chr2	243199373	11999580	0.0493	0.4842
chr3	198022430	10686003	0.054	0.2734
chr4	191154276	6253886	0.0327	0.2134
chr5	180915260	7598021	0.042	0.2401
chr6	171115067	8299591	0.0485	0.2764
chr7	159138663	6698188	0.0421	0.2986

chr8	146364022	6277159	0.0429	0.2895
chr9	141213431	8521293	0.0603	0.3378
chr10	135534747	4080654	0.0301	0.2141
chr11	135006516	6102908	0.0452	0.2998
chr12	133851895	4671714	0.0349	0.2198
chr13	115169878	3845552	0.0334	0.2139
chr14	107349540	2434737	0.0227	0.1797
chr15	102531392	3137322	0.0306	0.2129
chr16	90354753	2497620	0.0276	0.2015
chr17	81195210	3881152	0.0478	0.2628
chr18	78077248	5468406	0.07	0.4275
chr19	59128983	3195919	0.054	0.3222
chr20	63025520	2658282	0.0422	0.2441
chr21	48129895	1335352	0.0277	0.1979
chr22	51304566	950501	0.0185	0.1559
chrMT	16571	7430	0.4484	0.768
chrX	155270560	7382937	0.0475	0.2655
chrY	59373566	234364	0.0039	0.08

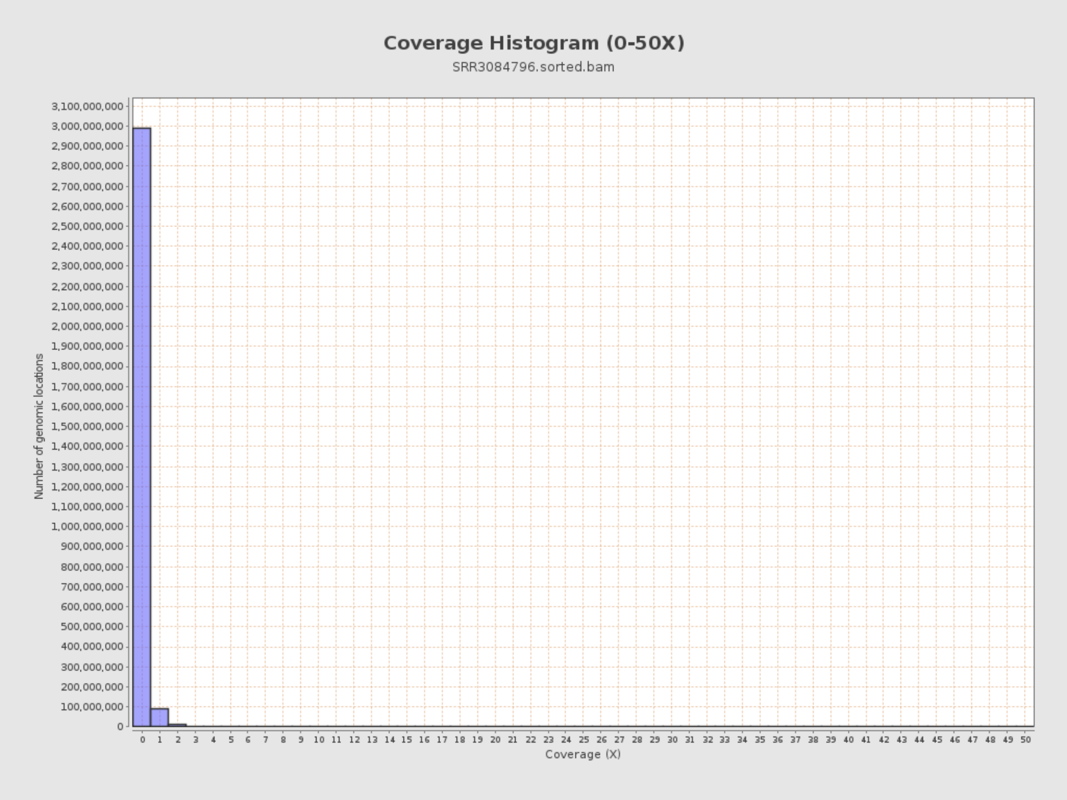
3. Results : Coverage across reference



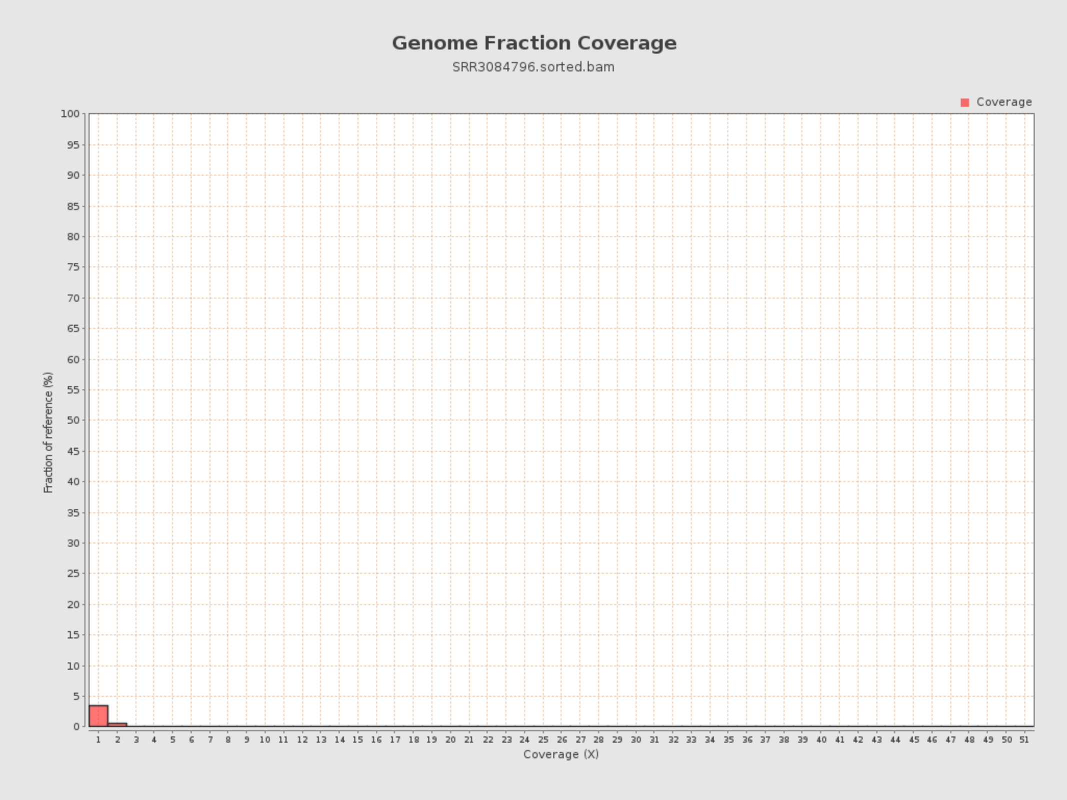
4. Results : Coverage Histogram



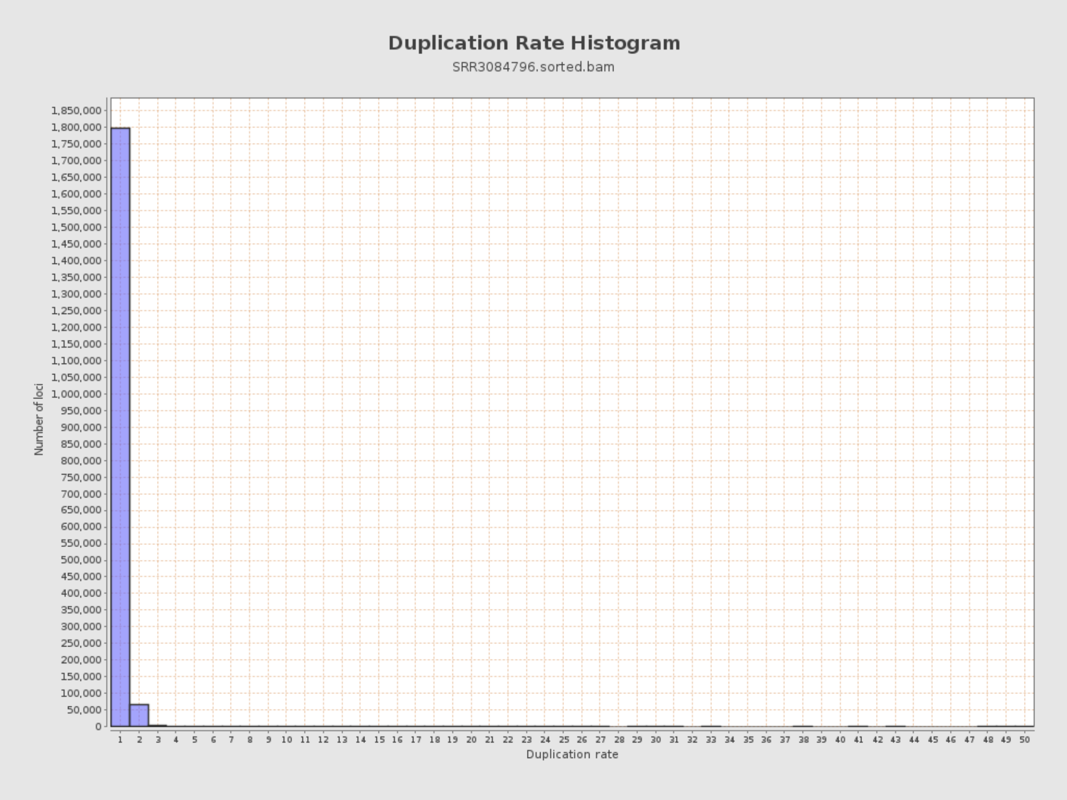
5. Results : Coverage Histogram (0-50X)



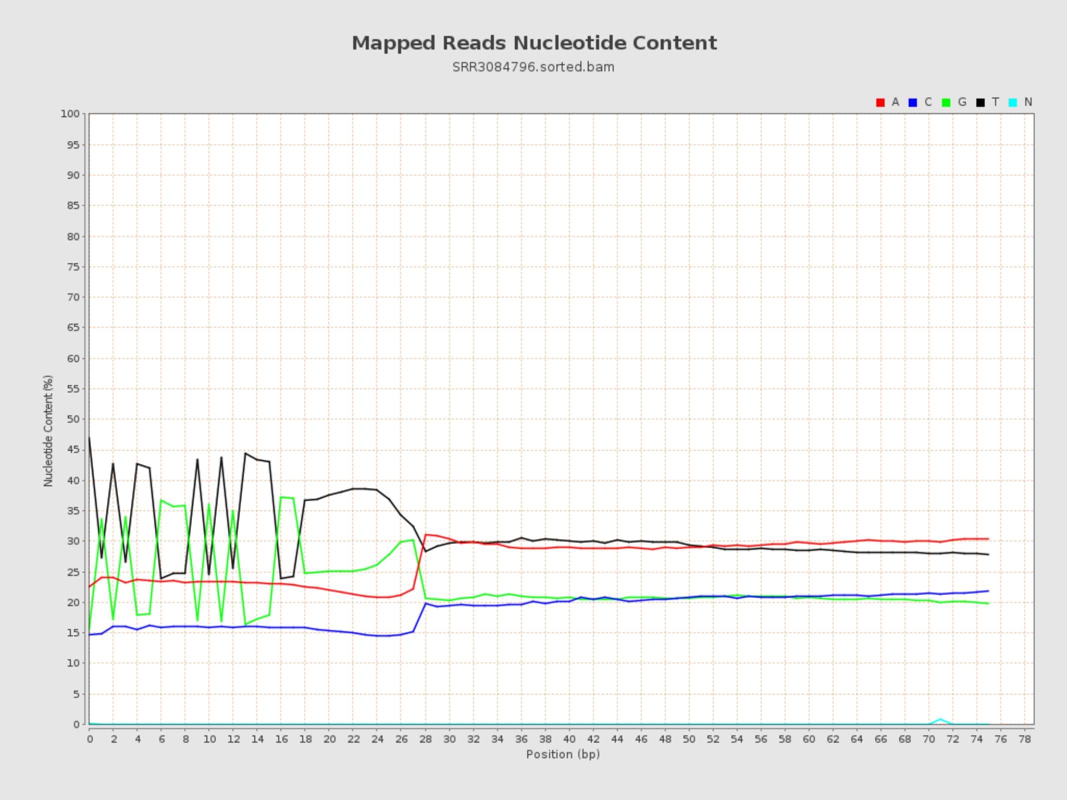
6. Results : Genome Fraction Coverage



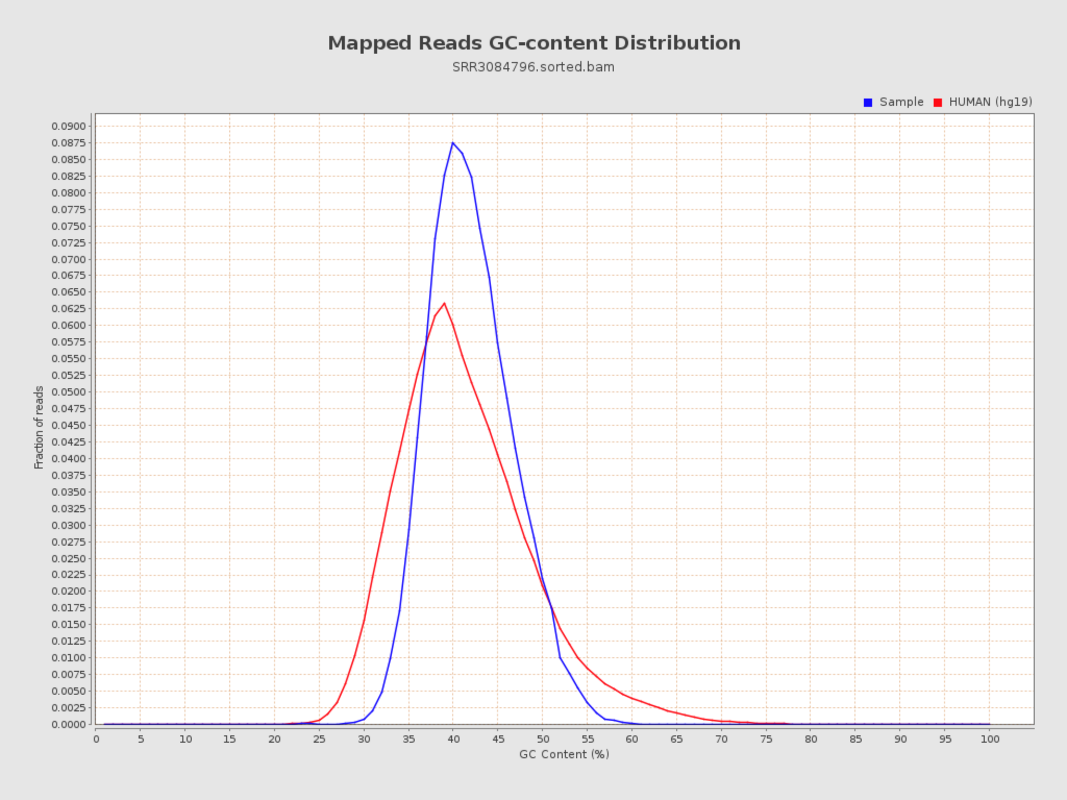
7. Results : Duplication Rate Histogram



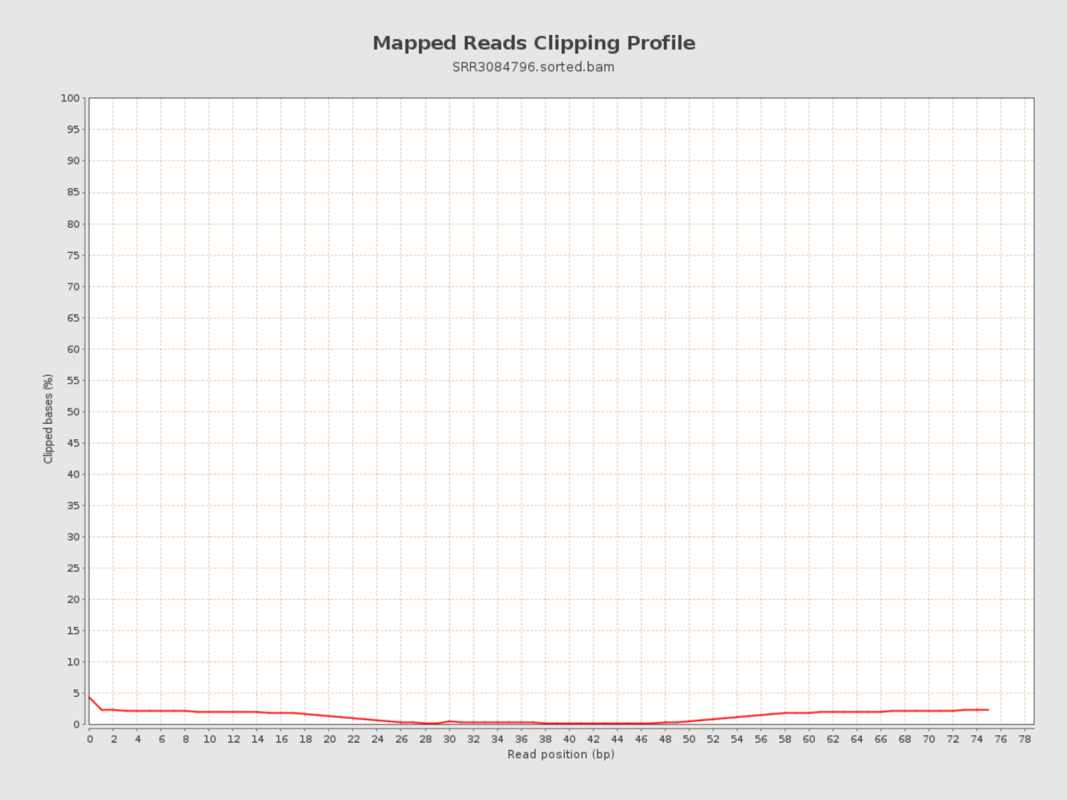
8. Results : Mapped Reads Nucleotide Content



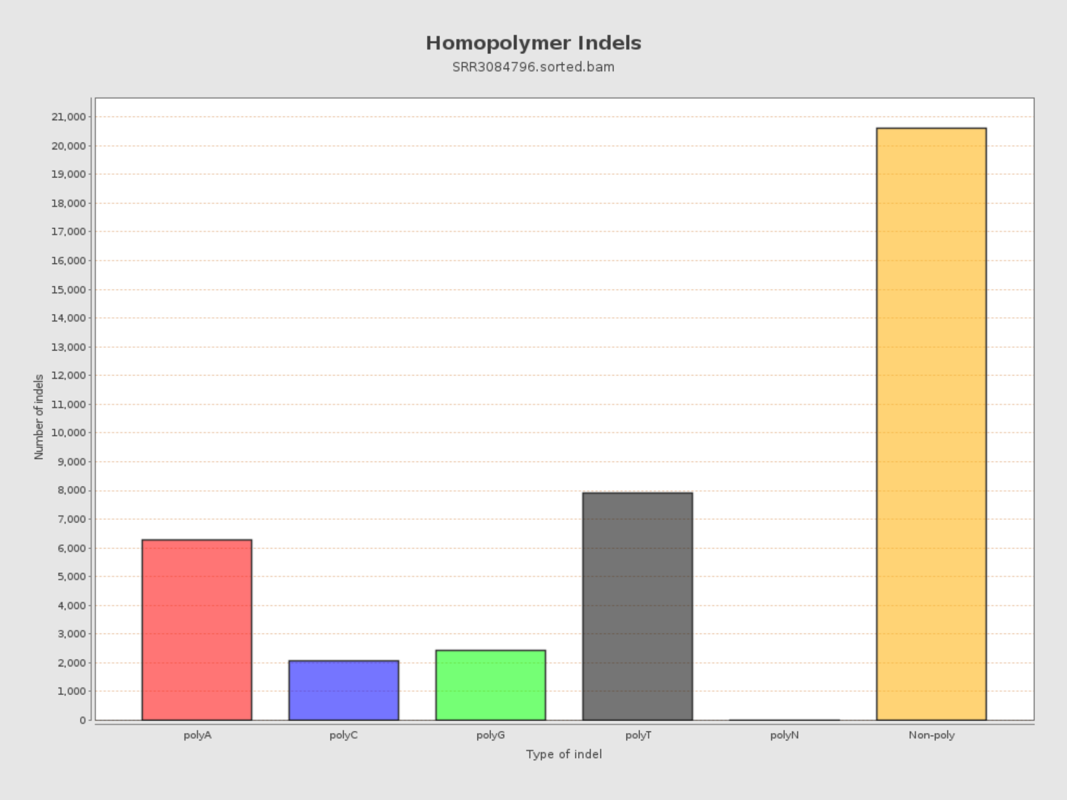
9. Results : Mapped Reads GC-content Distribution



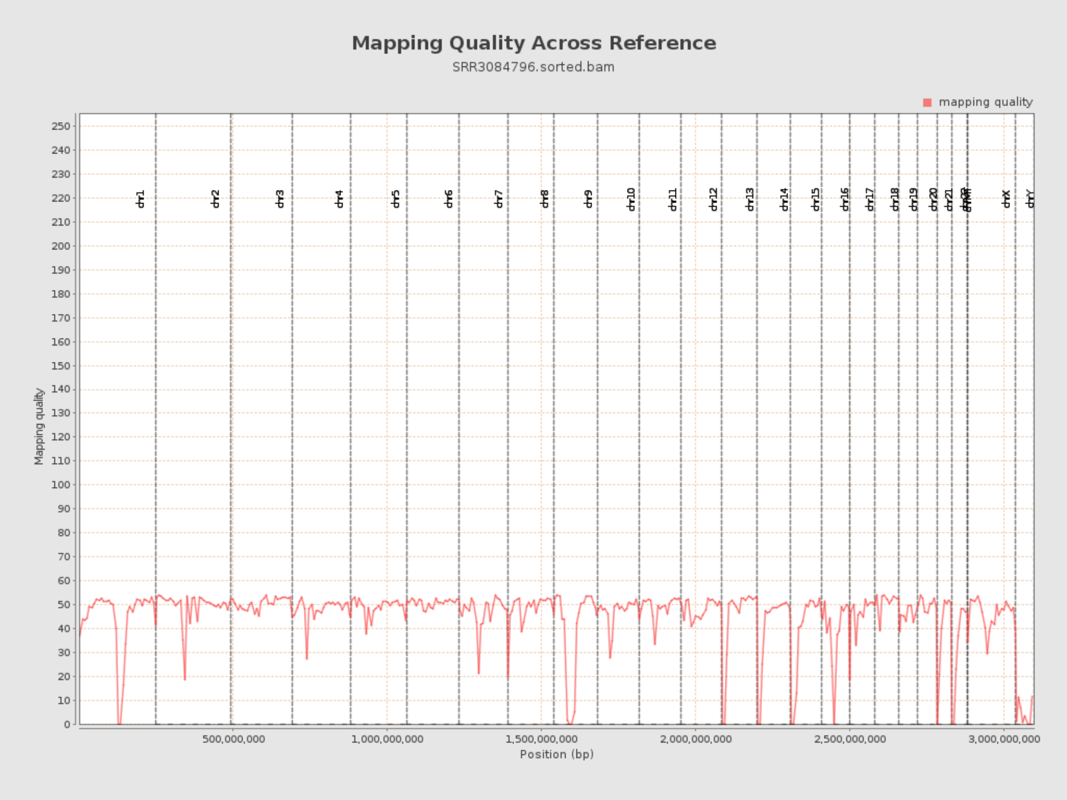
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram