Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 14:20:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084798.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_SRR3084798 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084798.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 14:20:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084798.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,030,303
Mapped reads	1,837,815 / 90.52%
Unmapped reads	192,488 / 9.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,083 / 0.89%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	82,179 / 4.05%
Duplication rate	3.76%
Clipped reads	823,792 / 40.57%

2.2. ACGT Content

Number/percentage of A's	32,957,805 / 26.91%
Number/percentage of C's	23,149,645 / 18.9%
Number/percentage of T's	38,196,641 / 31.18%
Number/percentage of G's	28,166,002 / 23%
Number/percentage of N's	17,296 / 0.01%
GC Percentage	41.89%

2.3. Coverage

Mean	0.0396

Standard Deviation	0.3023

2.4. Mapping Quality

Mean Mapping Quality	45.23

2.5. Mismatches and indels

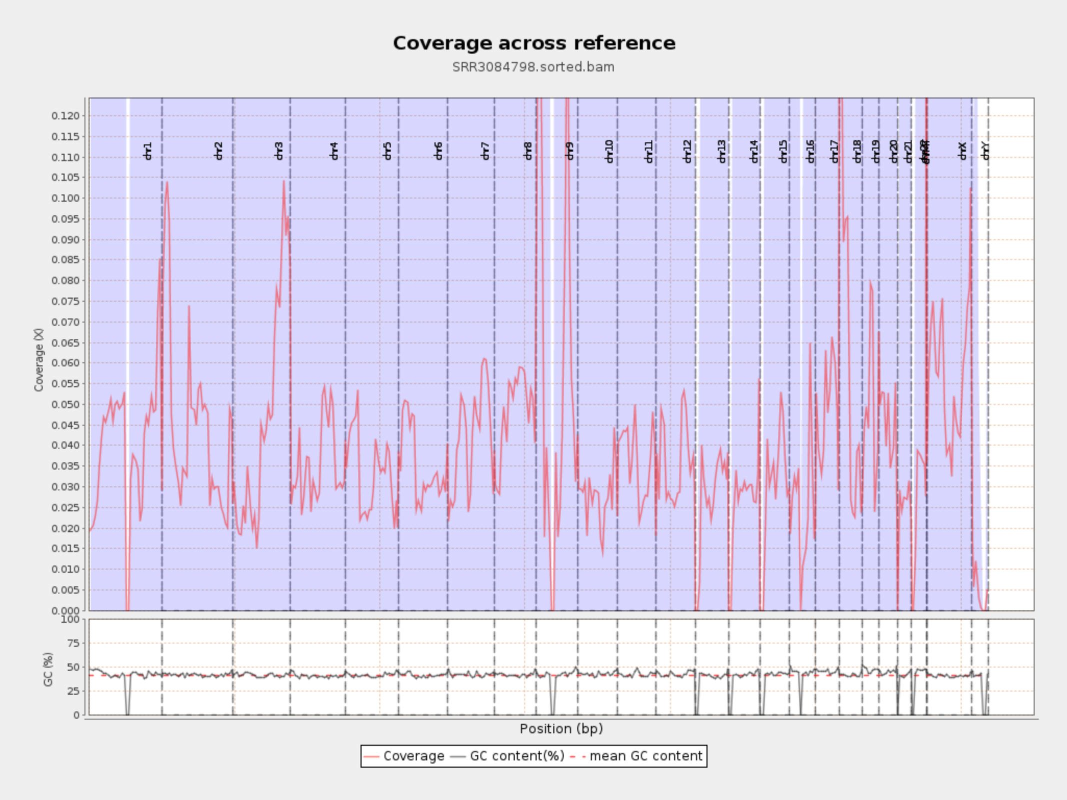
General error rate	0.79%
Mismatches	951,980
Insertions	9,679
Mapped reads with at least one insertion	0.52%
Deletions	28,422
Mapped reads with at least one deletion	1.53%
Homopolymer indels	48.17%

2.6. Chromosome stats

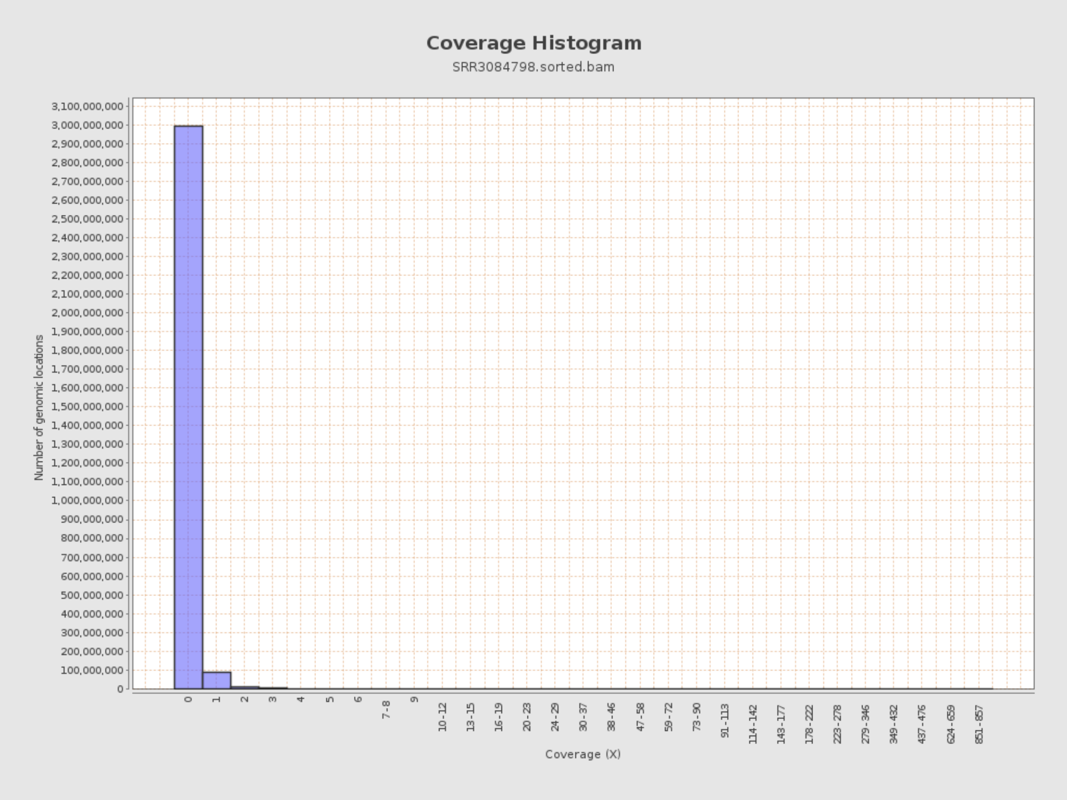
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10011373	0.0402	0.3906
chr2	243199373	11044045	0.0454	0.5195
chr3	198022430	9092632	0.0459	0.2485
chr4	191154276	6765905	0.0354	0.22
chr5	180915260	6040831	0.0334	0.2141
chr6	171115067	6012503	0.0351	0.2365
chr7	159138663	6709740	0.0422	0.2778

chr8	146364022	7029089	0.048	0.3051
chr9	141213431	8460935	0.0599	0.3725
chr10	135534747	3762799	0.0278	0.2122
chr11	135006516	4897527	0.0363	0.2672
chr12	133851895	4833084	0.0361	0.2205
chr13	115169878	3071797	0.0267	0.1881
chr14	107349540	2740980	0.0255	0.1918
chr15	102531392	3128894	0.0305	0.2108
chr16	90354753	2347308	0.026	0.1948
chr17	81195210	3998488	0.0492	0.2643
chr18	78077248	5062144	0.0648	0.5221
chr19	59128983	2982234	0.0504	0.3503
chr20	63025520	2915413	0.0463	0.2526
chr21	48129895	1188723	0.0247	0.1901
chr22	51304566	1300006	0.0253	0.1816
chrMT	16571	9105	0.5495	0.888
chrX	155270560	8845121	0.057	0.294
chrY	59373566	283644	0.0048	0.0991

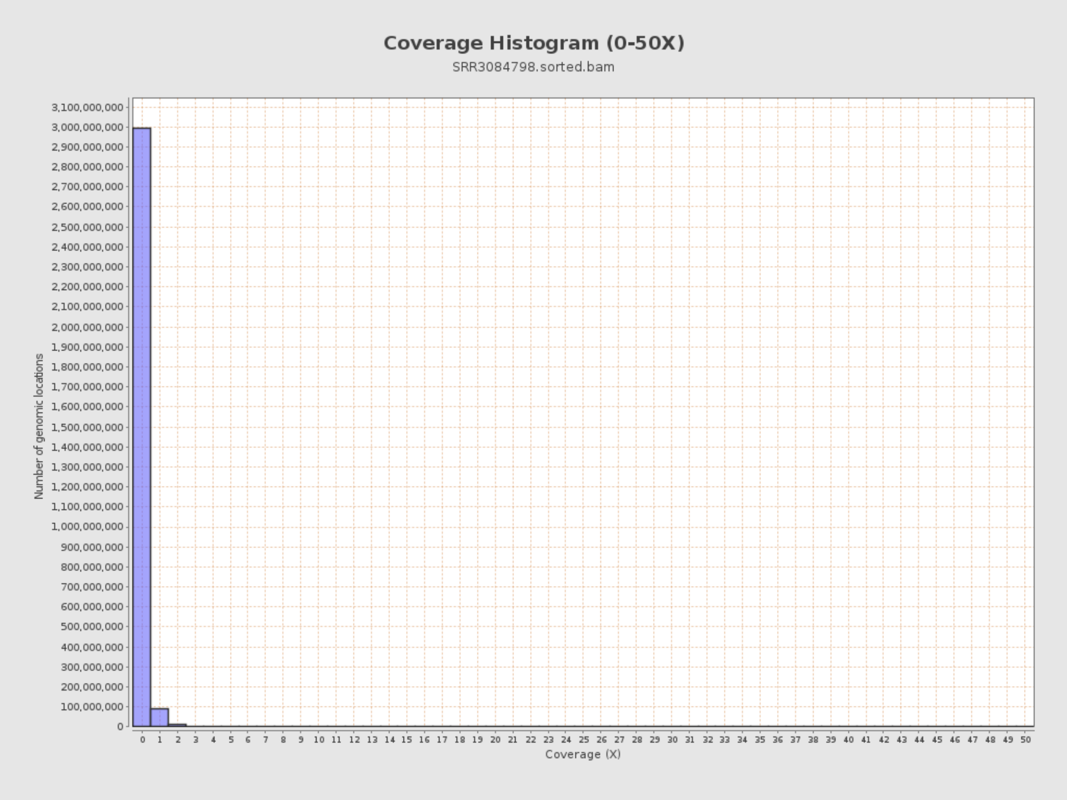
3. Results : Coverage across reference



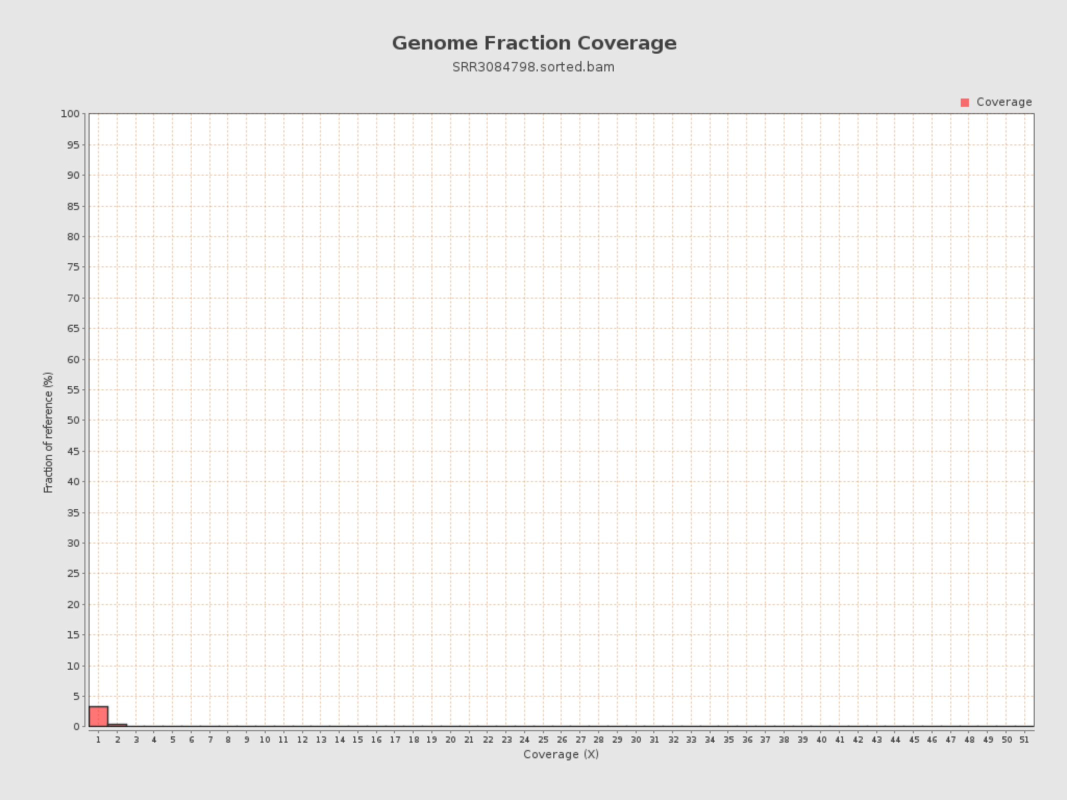
4. Results : Coverage Histogram



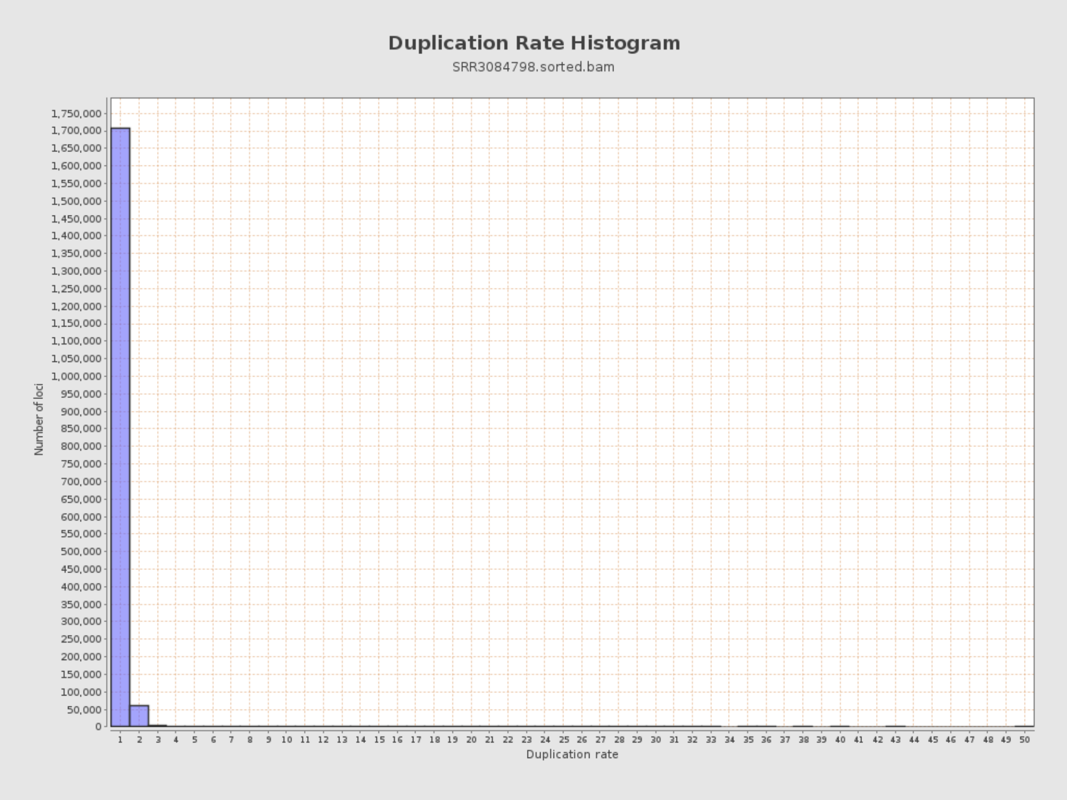
5. Results : Coverage Histogram (0-50X)



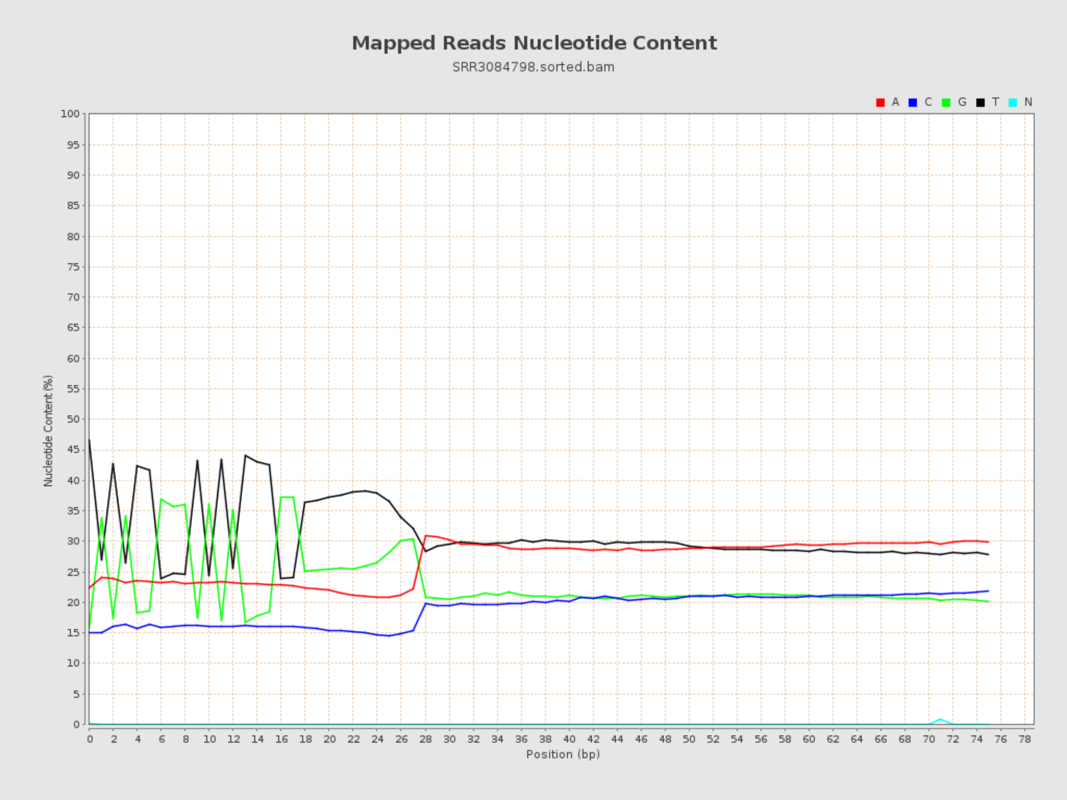
6. Results : Genome Fraction Coverage



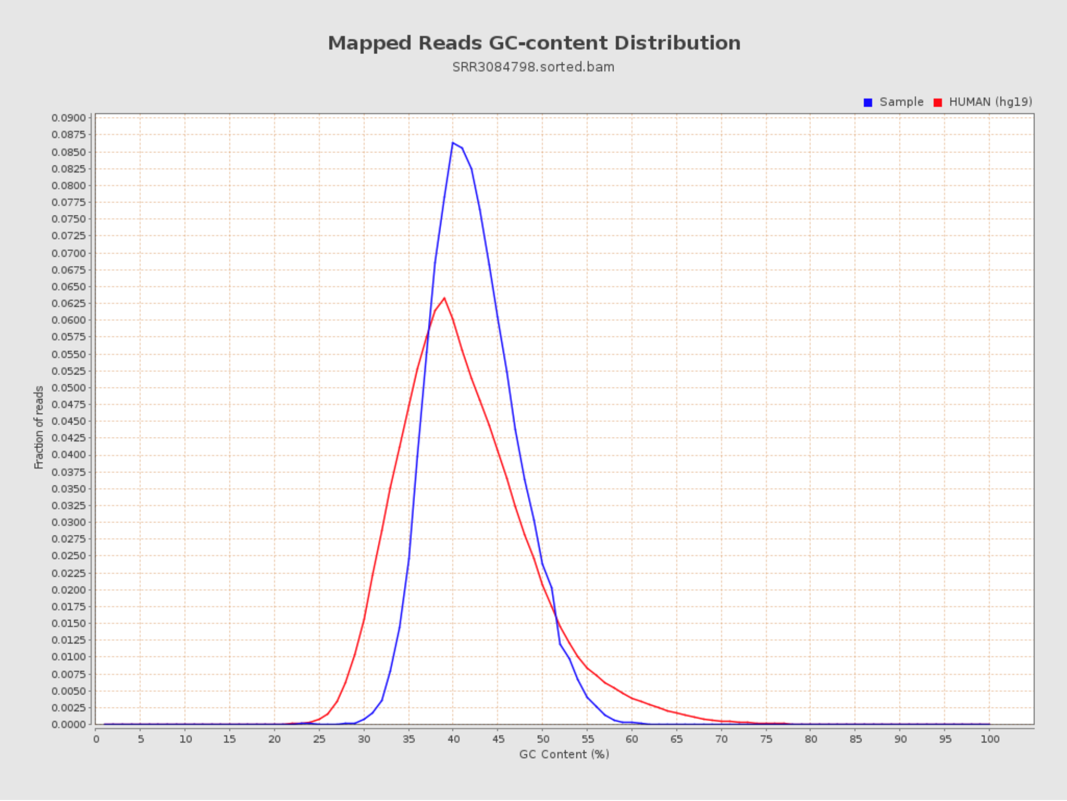
7. Results : Duplication Rate Histogram



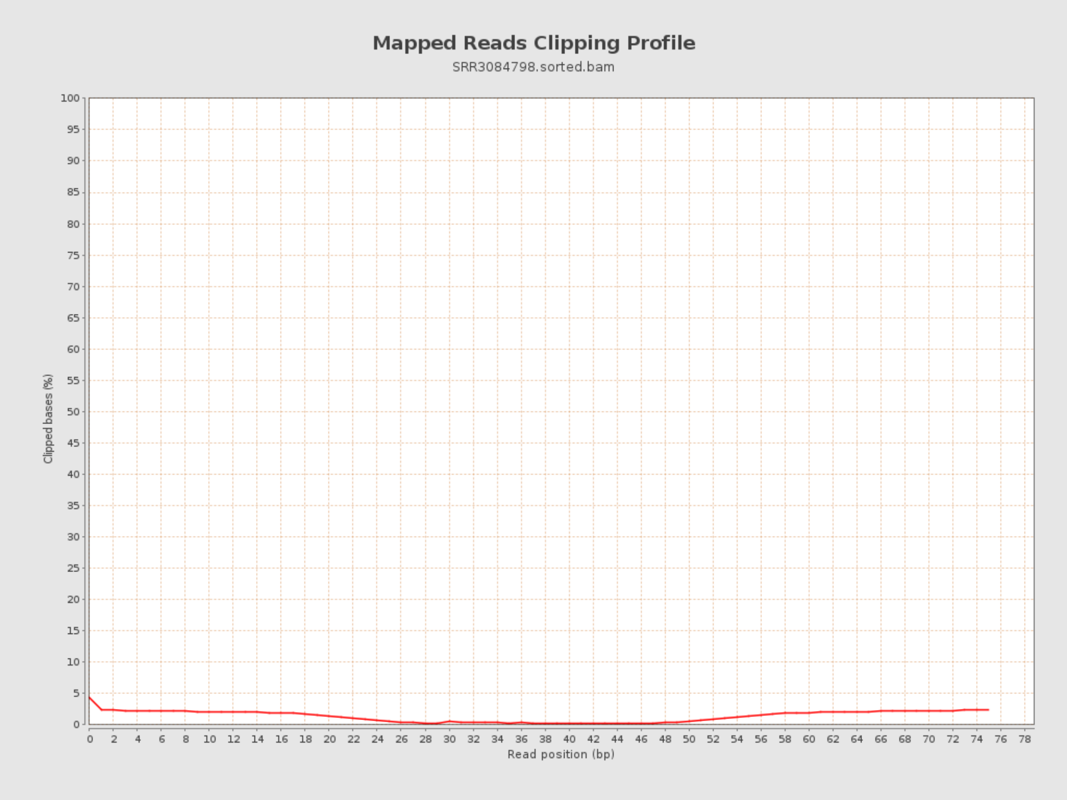
8. Results : Mapped Reads Nucleotide Content



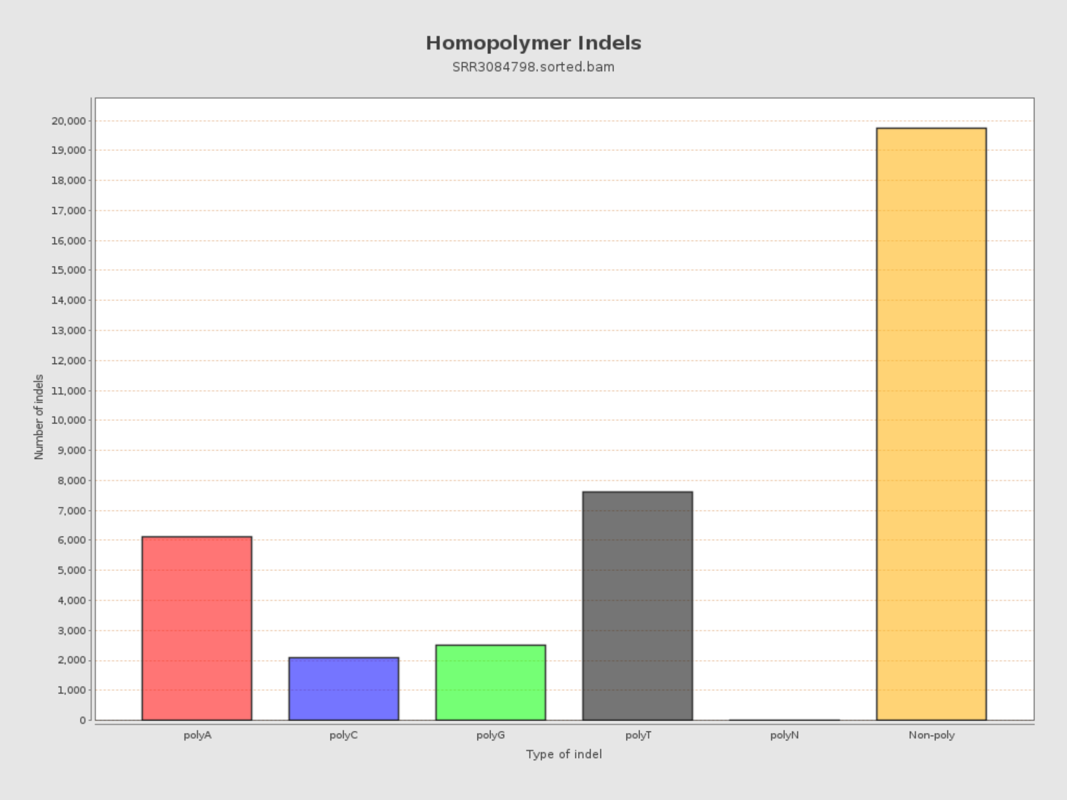
9. Results : Mapped Reads GC-content Distribution



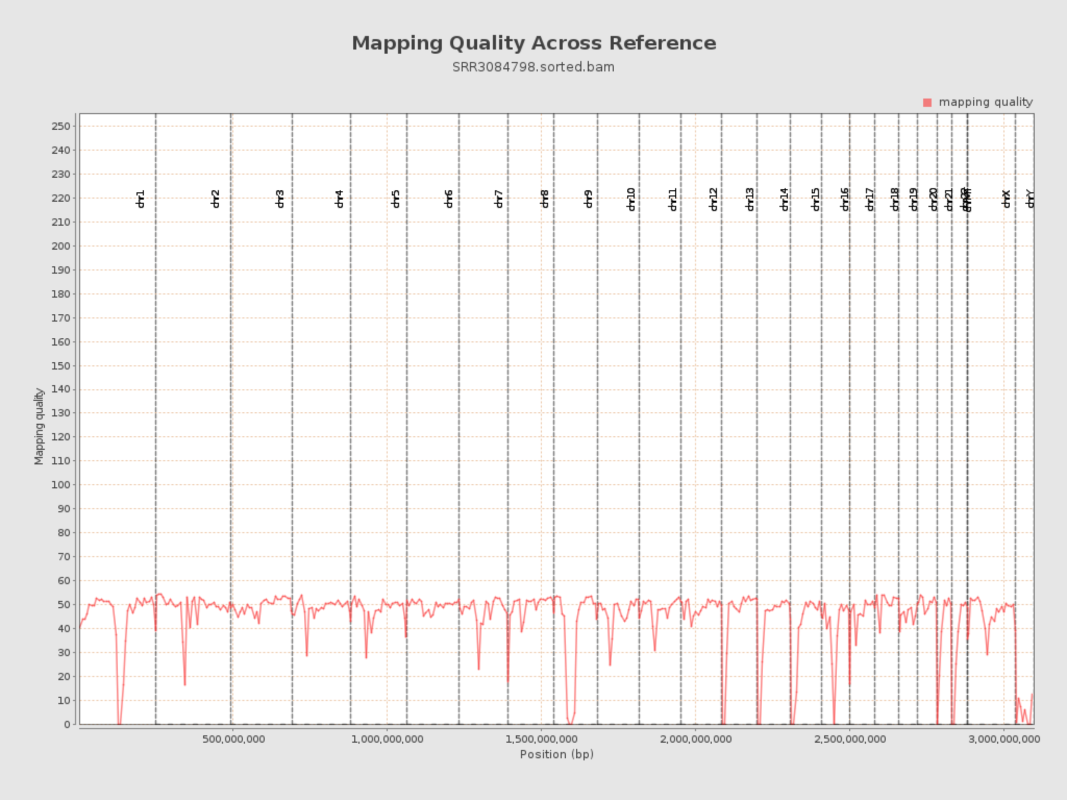
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram