Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 19:37:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084894.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_SRR3084894 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084894.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 19:37:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084894.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,797,730
Mapped reads	2,535,250 / 90.62%
Unmapped reads	262,480 / 9.38%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,046 / 0.61%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	112,652 / 4.03%
Duplication rate	3.72%
Clipped reads	971,424 / 34.72%

2.2. ACGT Content

Number/percentage of A's	49,355,357 / 28.53%
Number/percentage of C's	31,689,365 / 18.32%
Number/percentage of T's	54,938,350 / 31.76%
Number/percentage of G's	36,976,059 / 21.38%
Number/percentage of N's	27,106 / 0.02%
GC Percentage	39.69%

2.3. Coverage

Mean	0.0559

Standard Deviation	0.4002

2.4. Mapping Quality

Mean Mapping Quality	46.31

2.5. Mismatches and indels

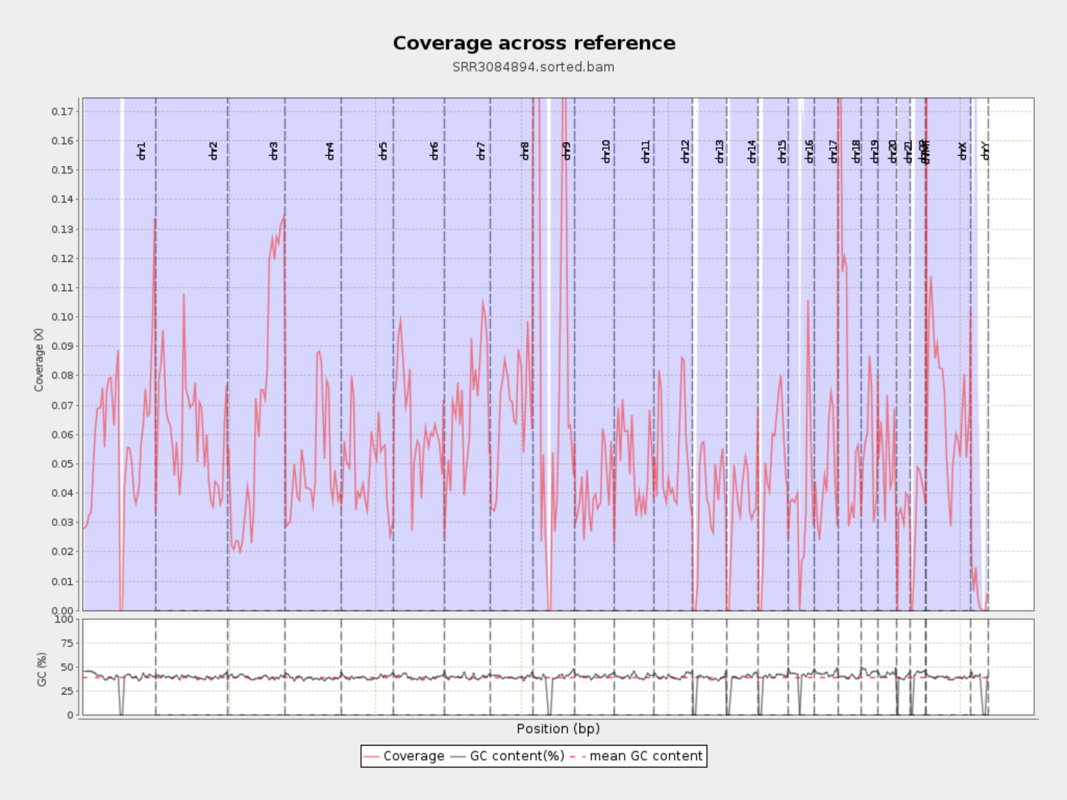
General error rate	0.84%
Mismatches	1,431,200
Insertions	13,352
Mapped reads with at least one insertion	0.52%
Deletions	37,047
Mapped reads with at least one deletion	1.45%
Homopolymer indels	48.97%

2.6. Chromosome stats

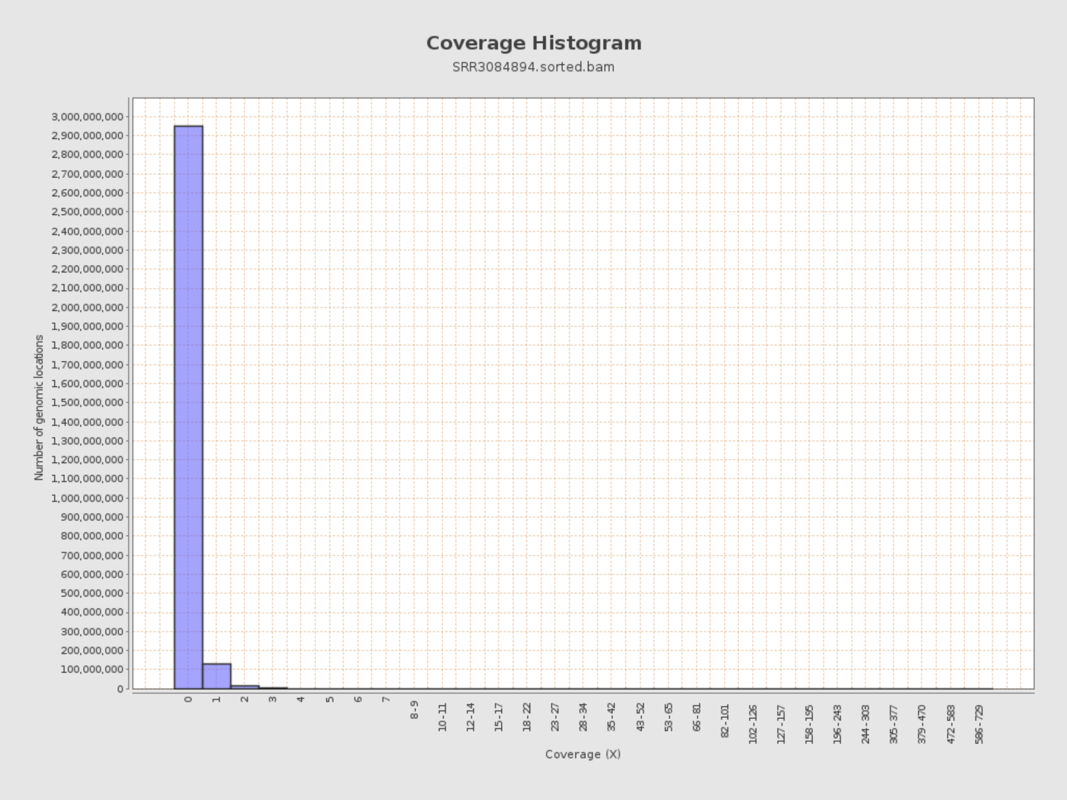
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14367190	0.0576	0.6812
chr2	243199373	14737318	0.0606	0.5243
chr3	198022430	13302085	0.0672	0.2927
chr4	191154276	9485546	0.0496	0.2526
chr5	180915260	8731842	0.0483	0.252
chr6	171115067	10907626	0.0637	0.2938
chr7	159138663	10874821	0.0683	0.465

chr8	146364022	9908411	0.0677	0.4932
chr9	141213431	13489204	0.0955	0.4976
chr10	135534747	5512099	0.0407	0.3268
chr11	135006516	6813894	0.0505	0.3263
chr12	133851895	7101742	0.0531	0.2669
chr13	115169878	4204308	0.0365	0.213
chr14	107349540	3670678	0.0342	0.2285
chr15	102531392	4745643	0.0463	0.2407
chr16	90354753	3312742	0.0367	0.2353
chr17	81195210	3747617	0.0462	0.2516
chr18	78077248	6728814	0.0862	0.6833
chr19	59128983	3360084	0.0568	0.4433
chr20	63025520	3316141	0.0526	0.2609
chr21	48129895	1499970	0.0312	0.2087
chr22	51304566	1599140	0.0312	0.1939
chrMT	16571	392865	23.708	11.7009
chrX	155270560	10897688	0.0702	0.3398
chrY	59373566	343924	0.0058	0.1179

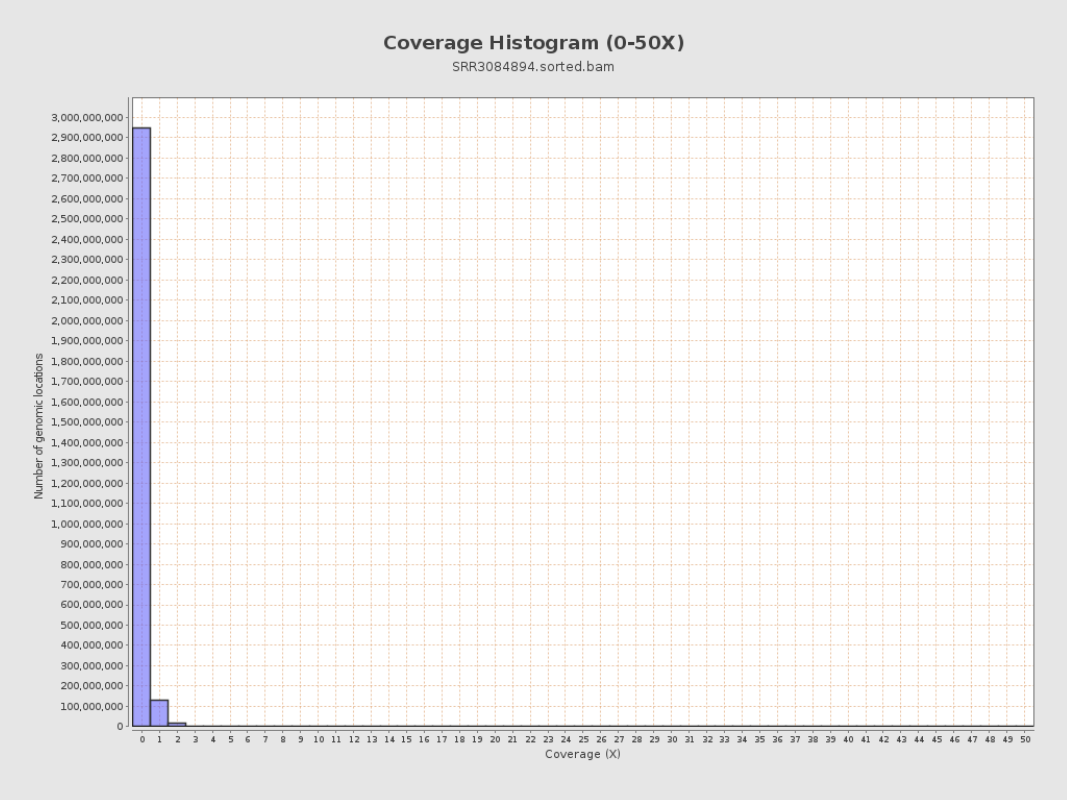
3. Results : Coverage across reference



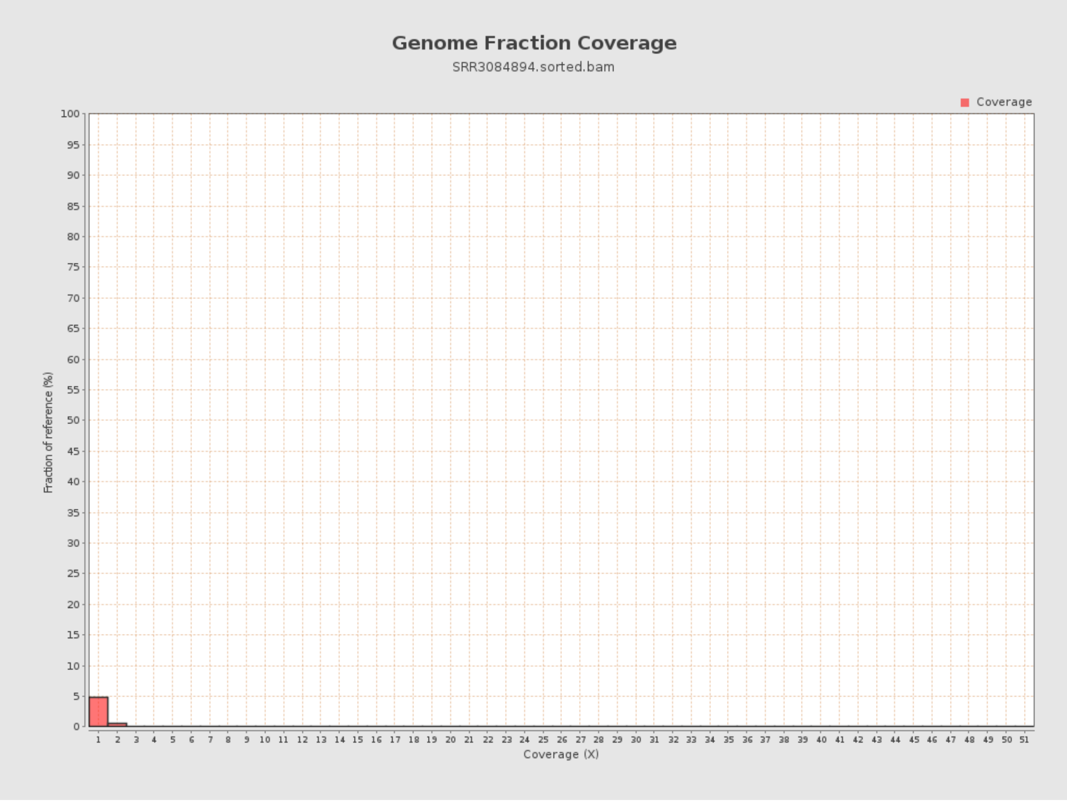
4. Results : Coverage Histogram



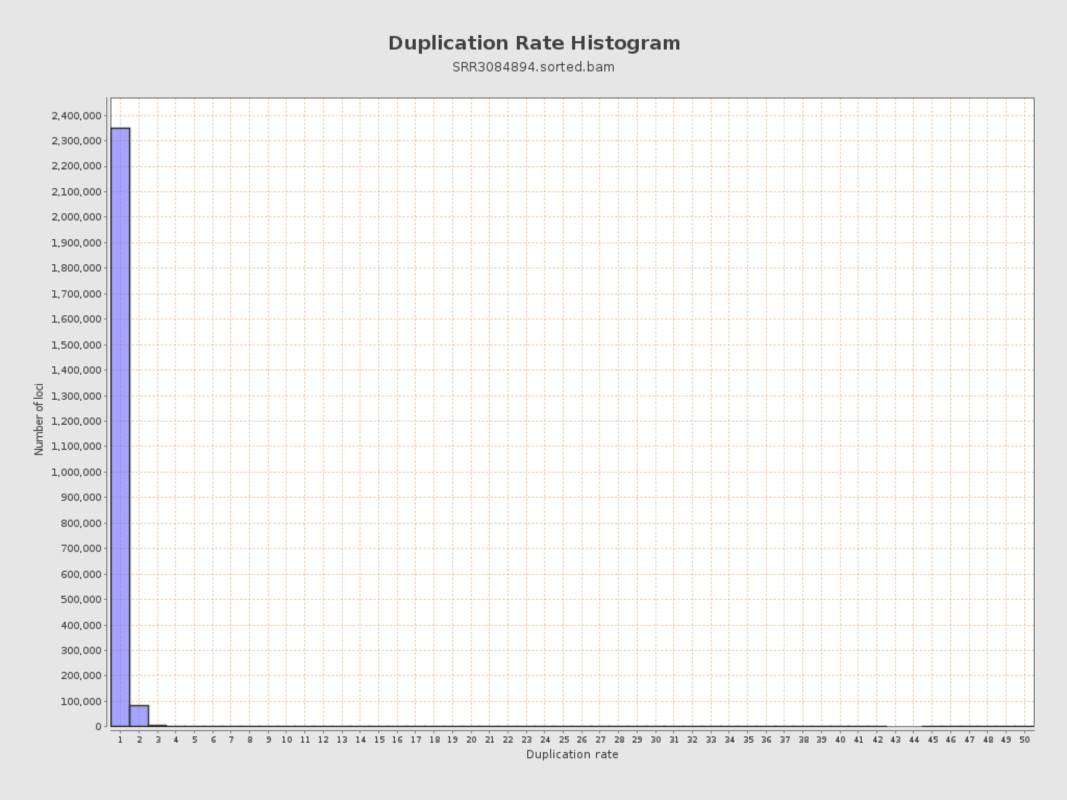
5. Results : Coverage Histogram (0-50X)



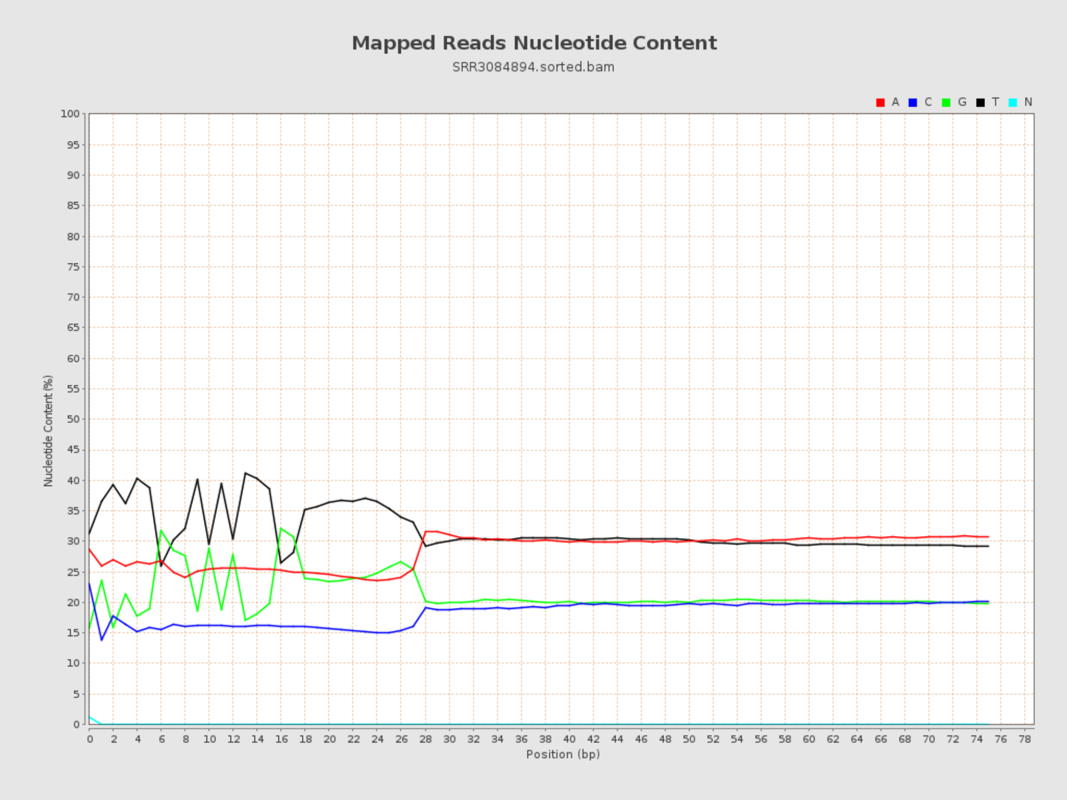
6. Results : Genome Fraction Coverage



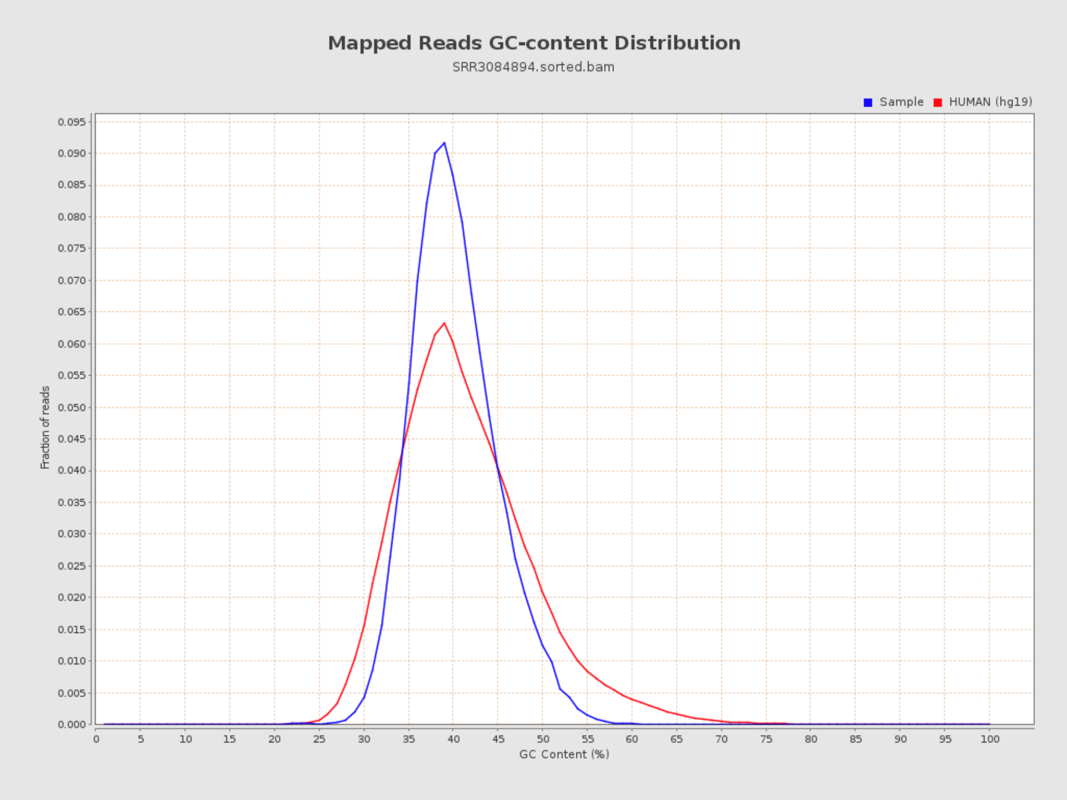
7. Results : Duplication Rate Histogram



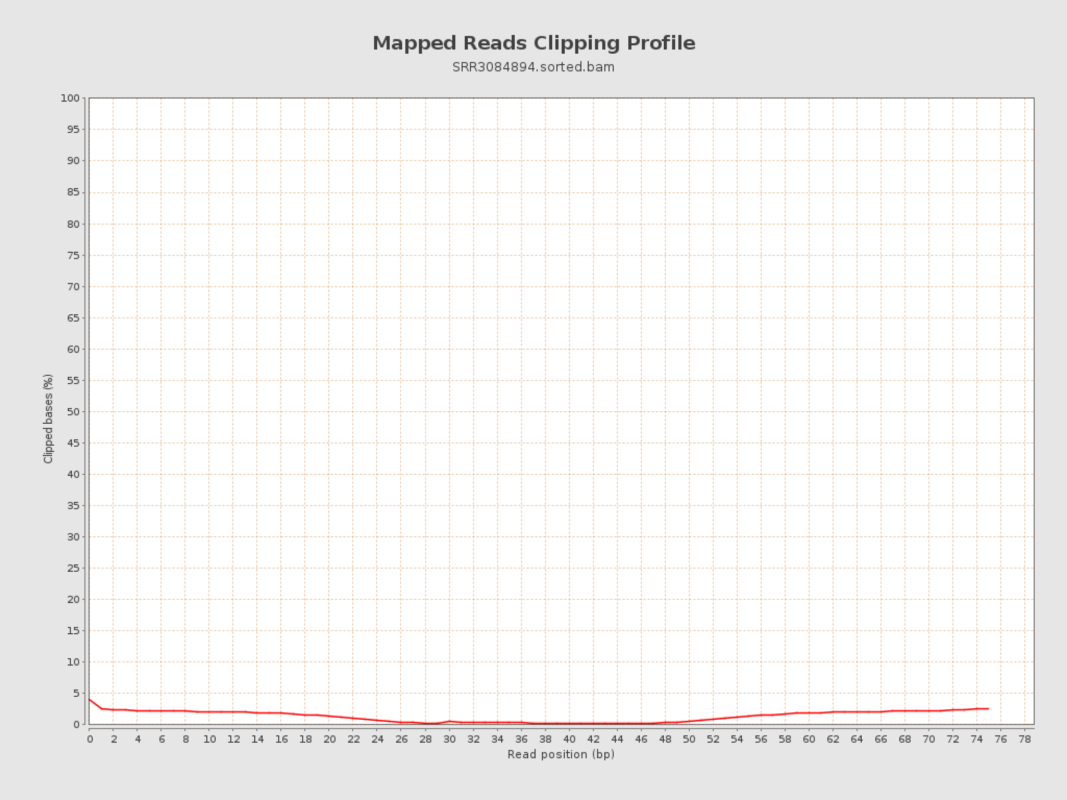
8. Results : Mapped Reads Nucleotide Content



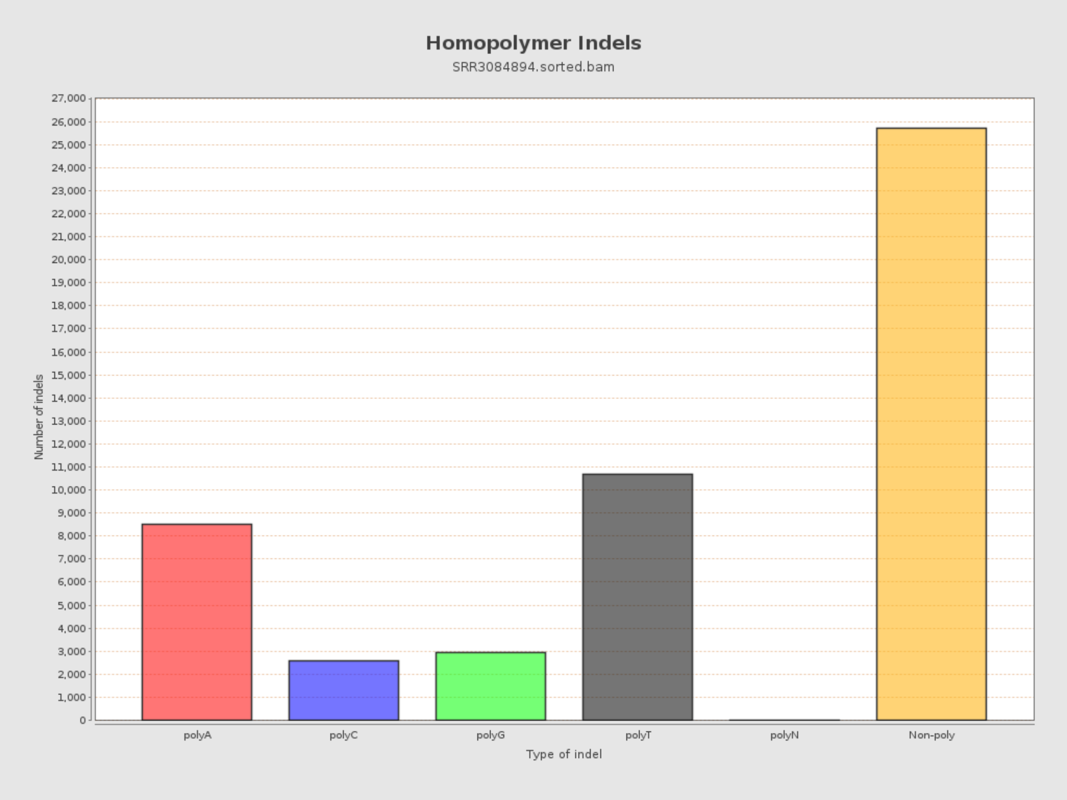
9. Results : Mapped Reads GC-content Distribution



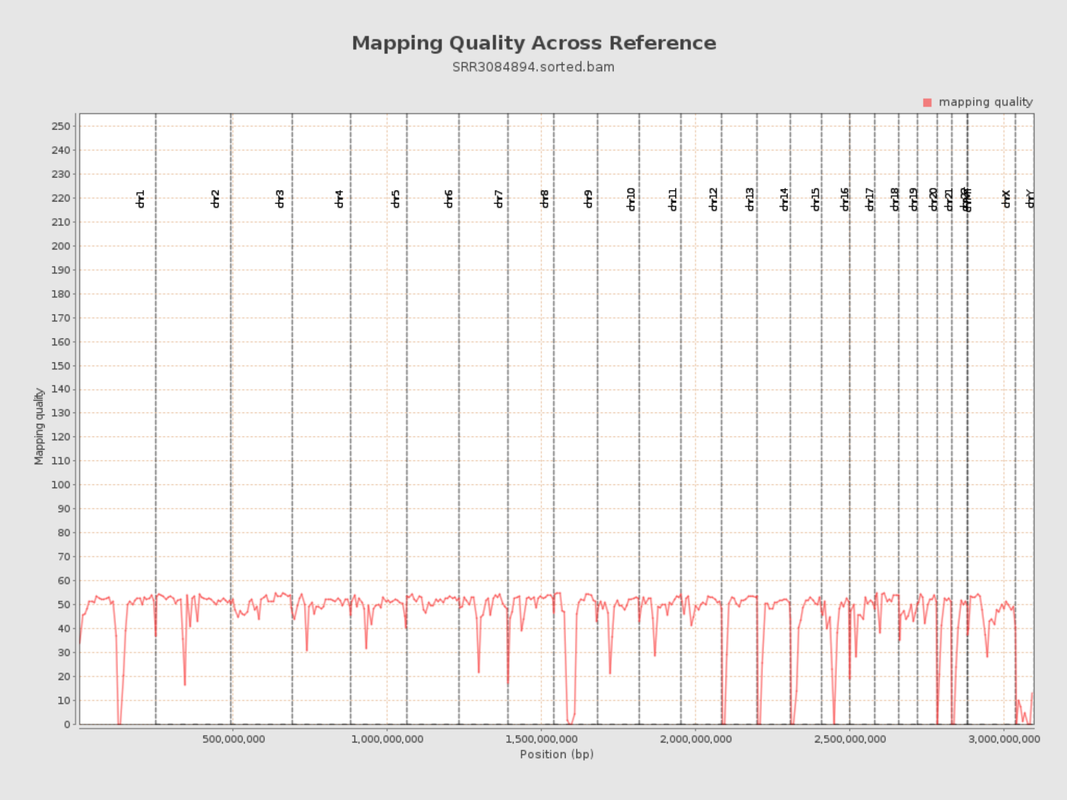
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram