Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 21:13:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084994.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_SRR3084994 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084994.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 21:13:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084994.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,269,883
Mapped reads	3,031,986 / 92.72%
Unmapped reads	237,897 / 7.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,134 / 0.92%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	134,066 / 4.1%
Duplication rate	3.33%
Clipped reads	1,124,900 / 34.4%

2.2. ACGT Content

Number/percentage of A's	60,707,723 / 29.1%
Number/percentage of C's	38,902,957 / 18.65%
Number/percentage of T's	65,562,218 / 31.43%
Number/percentage of G's	43,393,986 / 20.8%
Number/percentage of N's	29,423 / 0.01%
GC Percentage	39.45%

2.3. Coverage

Mean	0.0674

Standard Deviation	0.5834

2.4. Mapping Quality

Mean Mapping Quality	47.07

2.5. Mismatches and indels

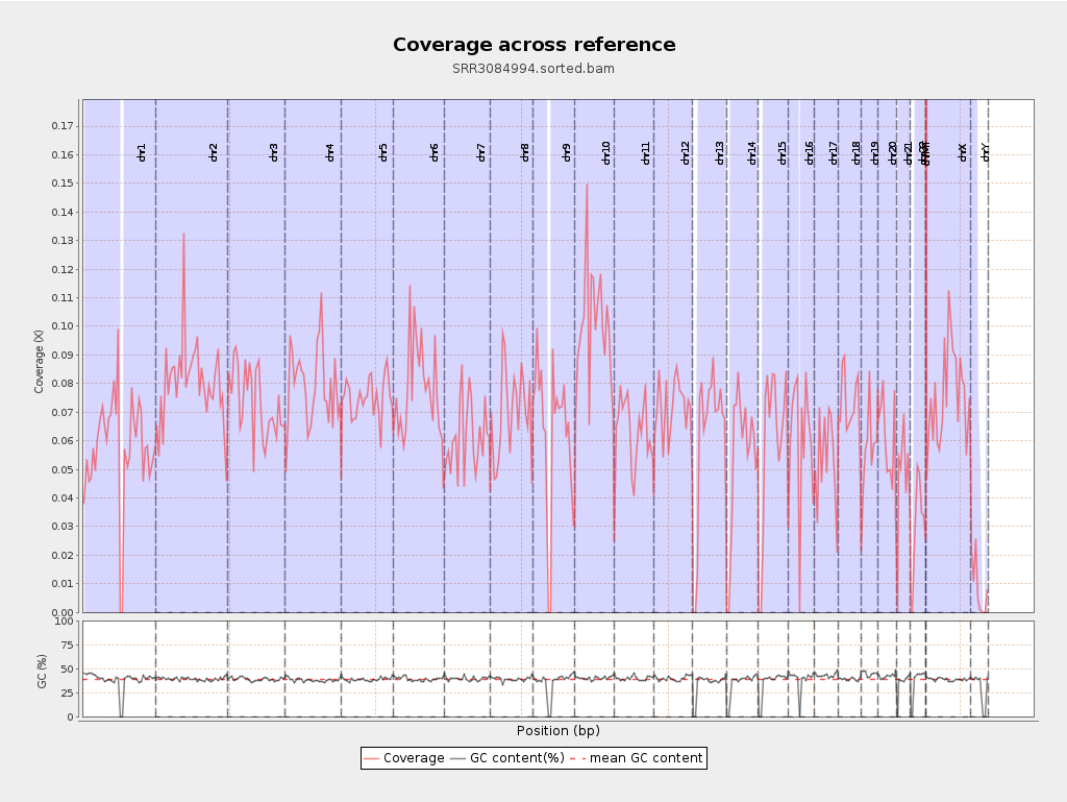
General error rate	0.84%
Mismatches	1,713,986
Insertions	17,153
Mapped reads with at least one insertion	0.56%
Deletions	49,266
Mapped reads with at least one deletion	1.61%
Homopolymer indels	47.86%

2.6. Chromosome stats

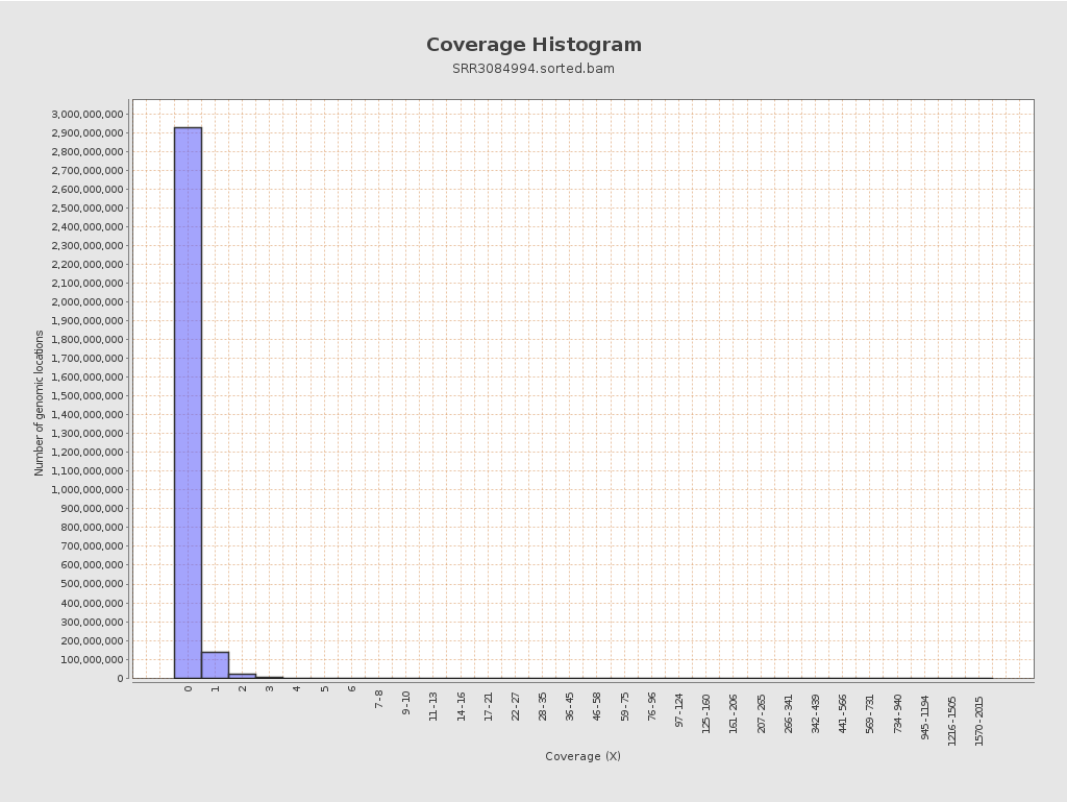
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	14324758	0.0575	1.0318
chr2	243199373	19494363	0.0802	0.6046
chr3	198022430	14502081	0.0732	0.3262
chr4	191154276	15156263	0.0793	0.3509
chr5	180915260	13530334	0.0748	0.3249
chr6	171115067	13357484	0.0781	0.466
chr7	159138663	9723823	0.0611	0.4354

chr8	146364022	10175215	0.0695	1.262
chr9	141213431	8895660	0.063	0.5338
chr10	135534747	13489935	0.0995	0.6663
chr11	135006516	8558911	0.0634	0.4531
chr12	133851895	9560910	0.0714	0.3245
chr13	115169878	7102274	0.0617	0.2916
chr14	107349540	5930099	0.0552	0.3155
chr15	102531392	6005949	0.0586	0.2853
chr16	90354753	5344678	0.0592	0.3648
chr17	81195210	4387646	0.054	0.3437
chr18	78077248	5718309	0.0732	0.9813
chr19	59128983	3433636	0.0581	0.7055
chr20	63025520	3849400	0.0611	0.3099
chr21	48129895	2267889	0.0471	0.2899
chr22	51304566	1524146	0.0297	0.2012
chrMT	16571	48049	2.8996	2.3429
chrX	155270560	11795512	0.076	0.3881
chrY	59373566	500034	0.0084	0.1637

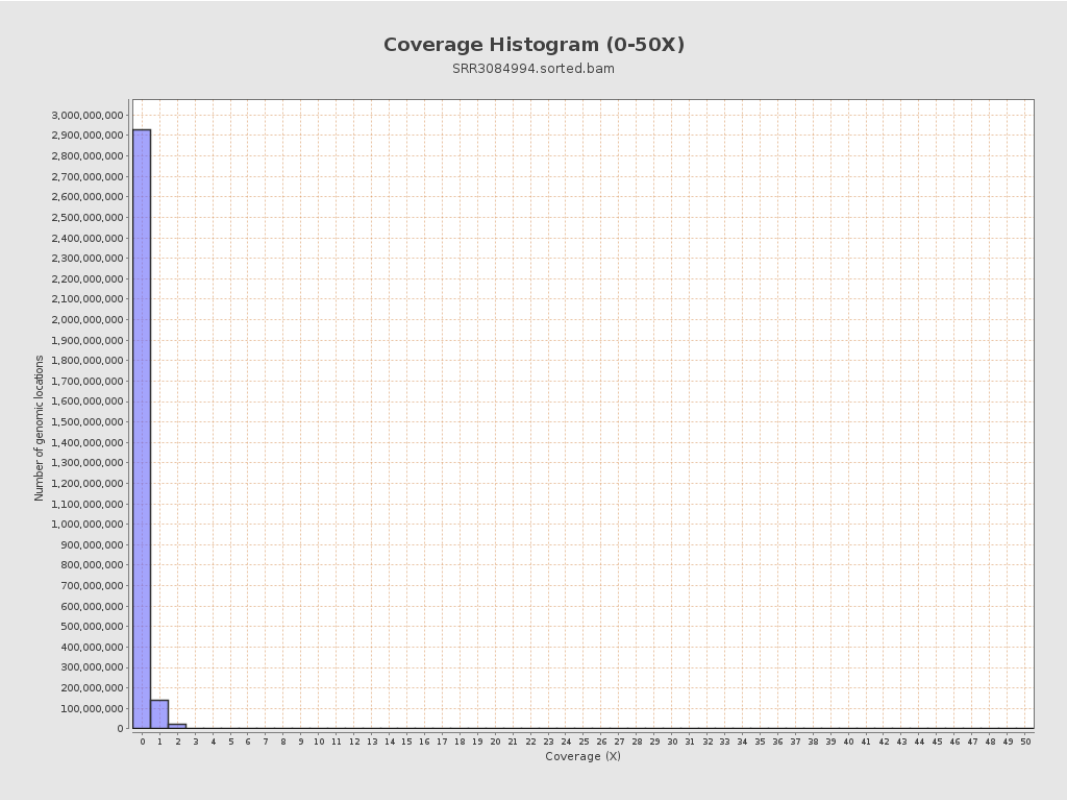
3. Results : Coverage across reference



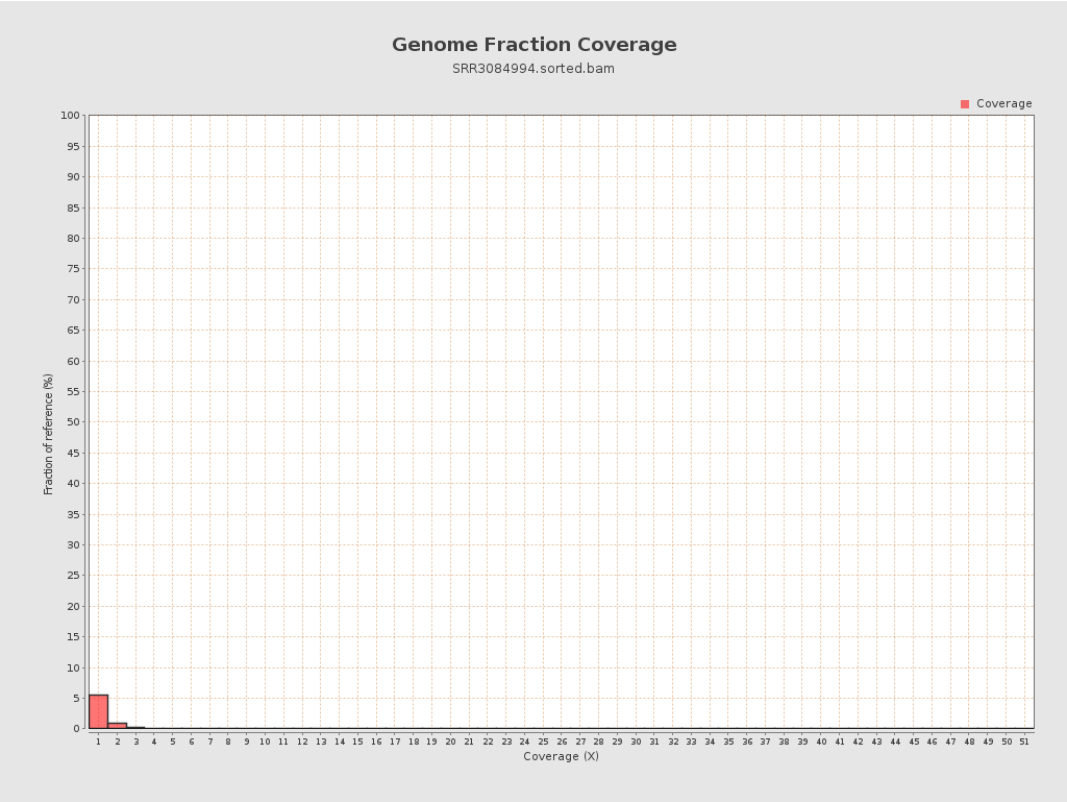
4. Results : Coverage Histogram



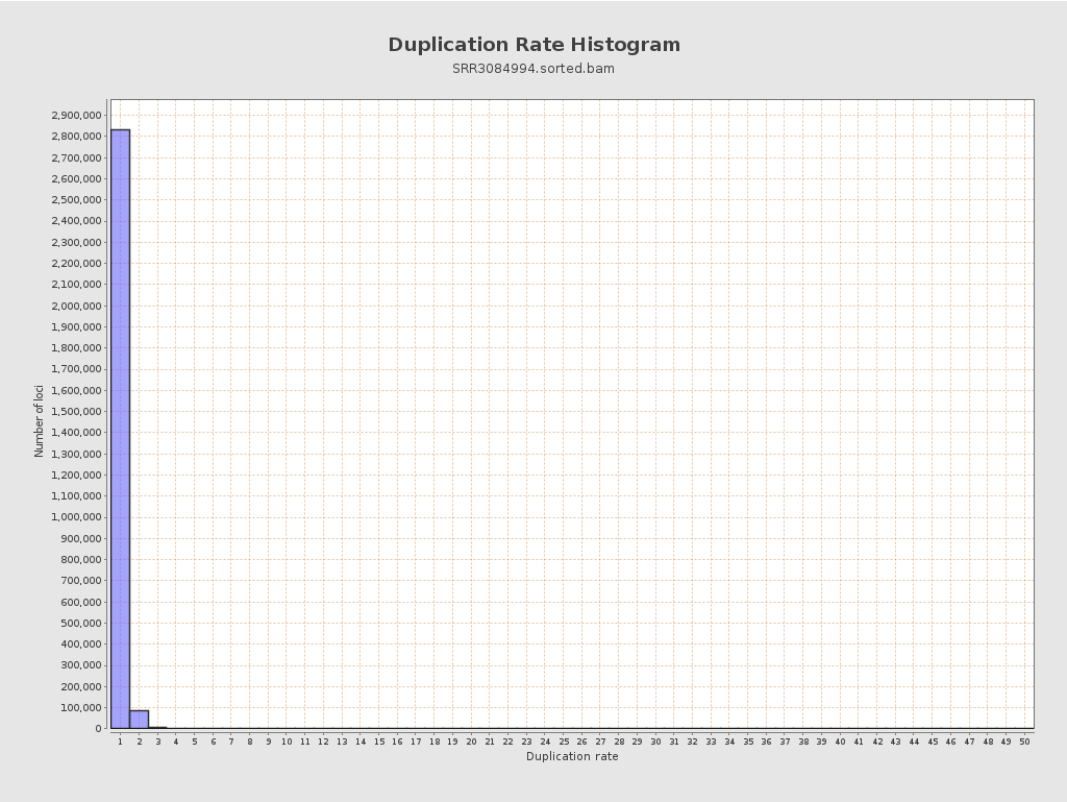
5. Results : Coverage Histogram (0-50X)



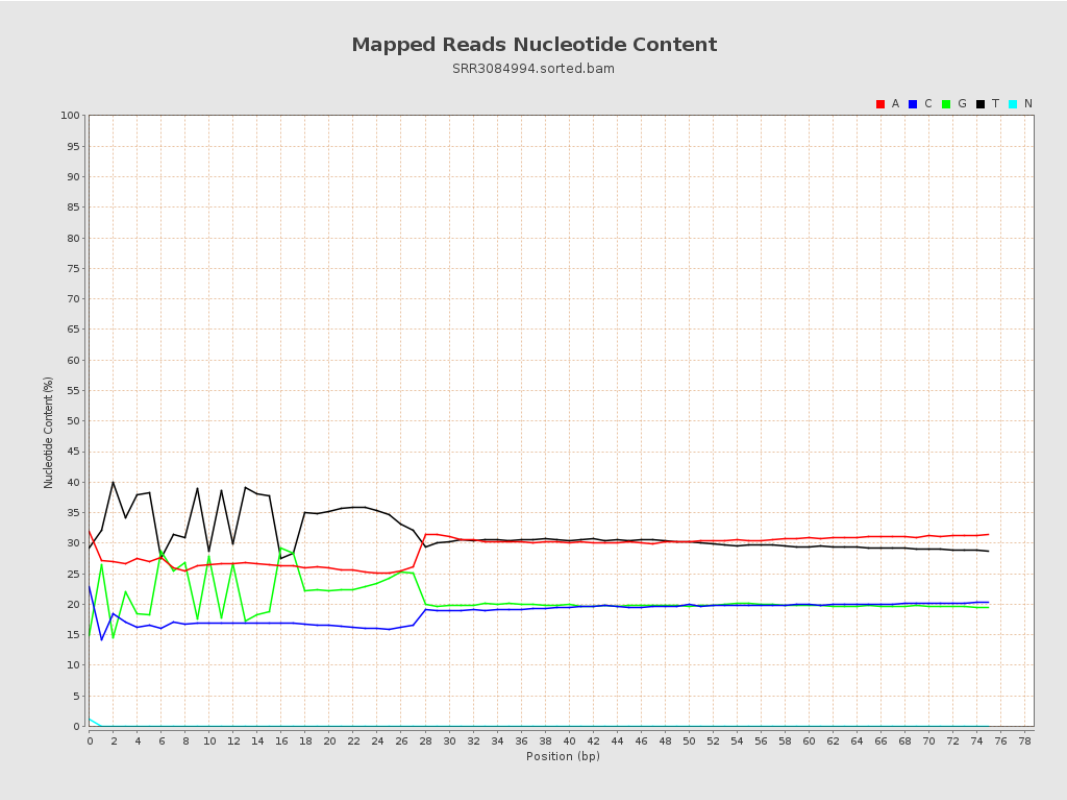
6. Results : Genome Fraction Coverage



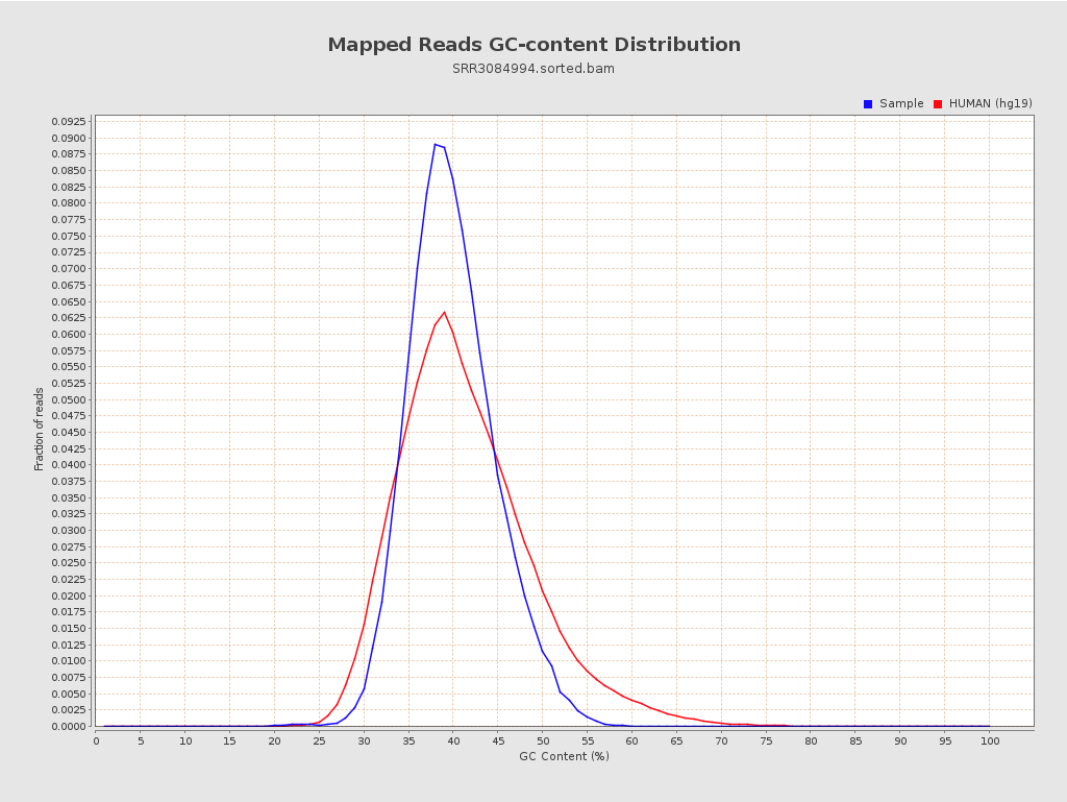
7. Results : Duplication Rate Histogram



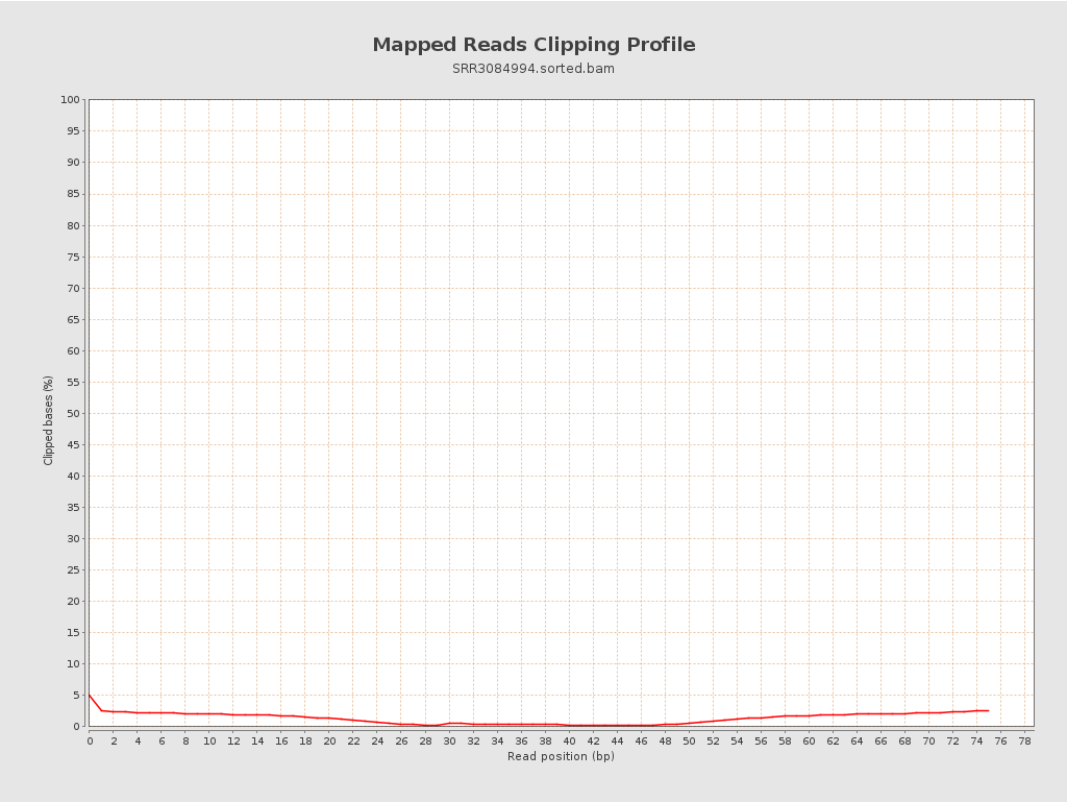
8. Results : Mapped Reads Nucleotide Content



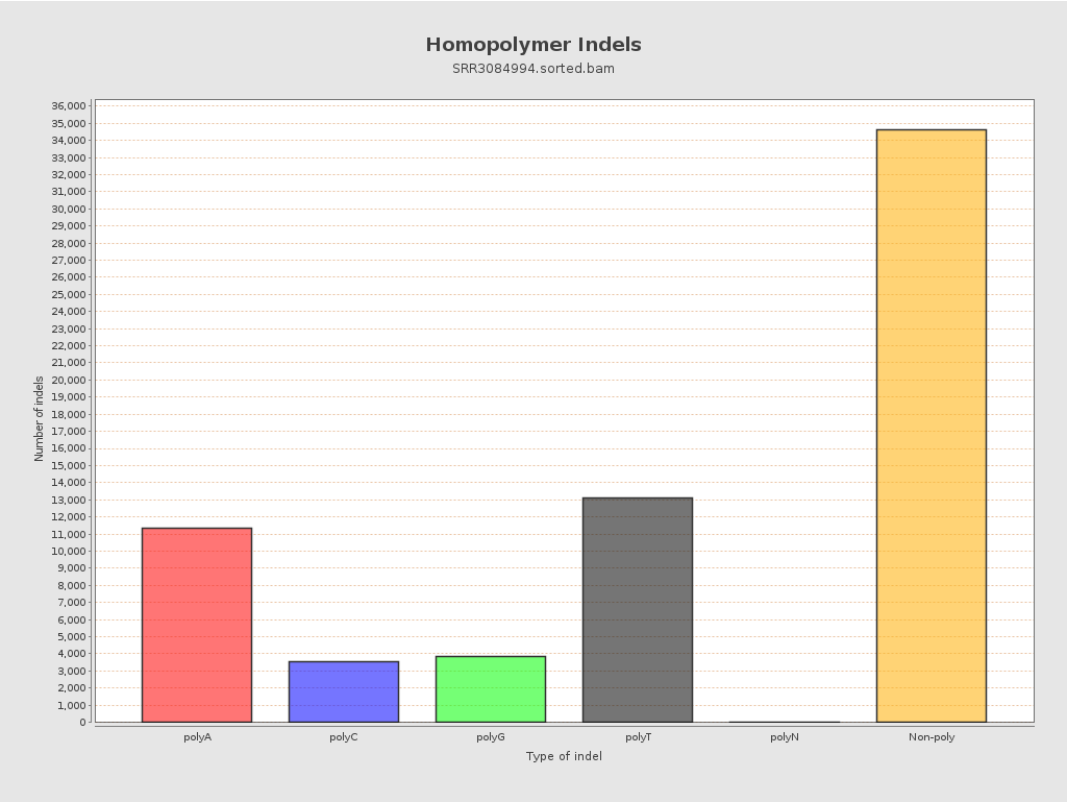
9. Results : Mapped Reads GC-content Distribution



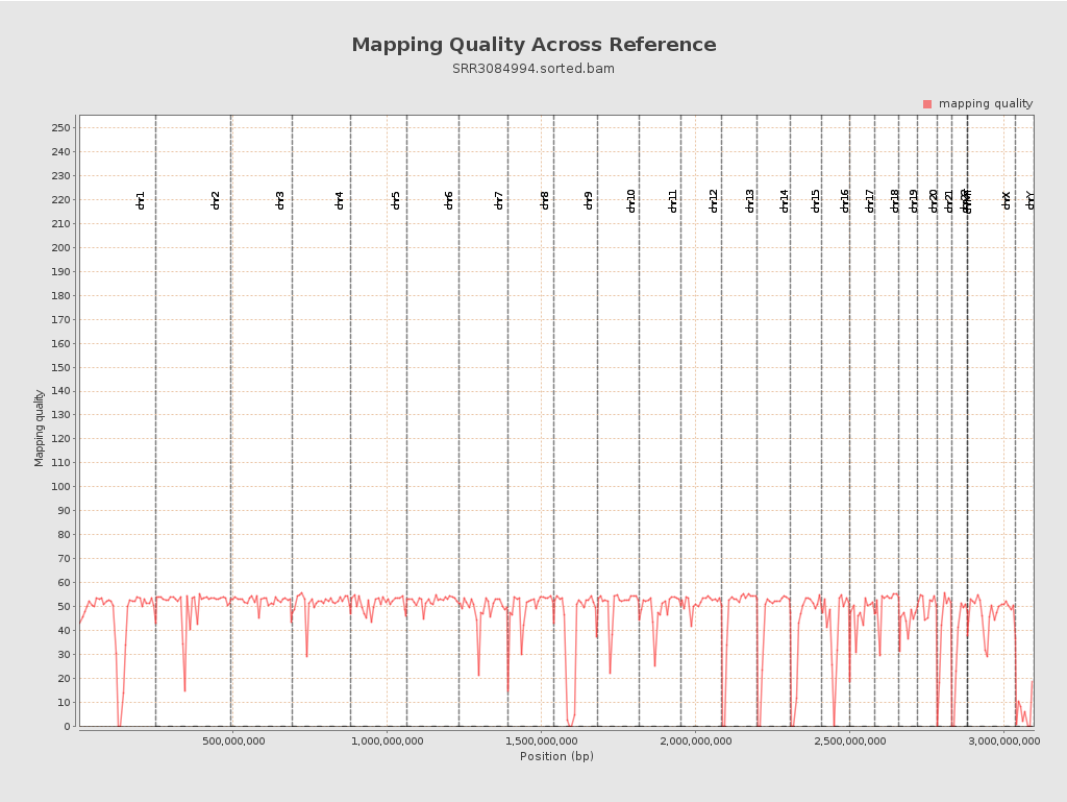
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram