

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 06:24:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708594.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_SRR1708594 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708594.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 06:24:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708594.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,651,782
Mapped reads	4,525,805 / 97.29%
Unmapped reads	125,977 / 2.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	141 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	43,101 / 0.93%
Duplication rate	0.95%
Clipped reads	59,742 / 1.28%

2.2. ACGT Content

Number/percentage of A's	69,833,140 / 30.94%
Number/percentage of C's	42,914,305 / 19.01%
Number/percentage of T's	69,552,352 / 30.81%
Number/percentage of G's	43,420,232 / 19.24%
Number/percentage of N's	6,018 / 0%
GC Percentage	38.25%

2.3. Coverage

Mean	0.0729

Standard Deviation	0.281
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2.4. Mapping Quality

Mean Mapping Quality	46.71
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2.5. Mismatches and indels

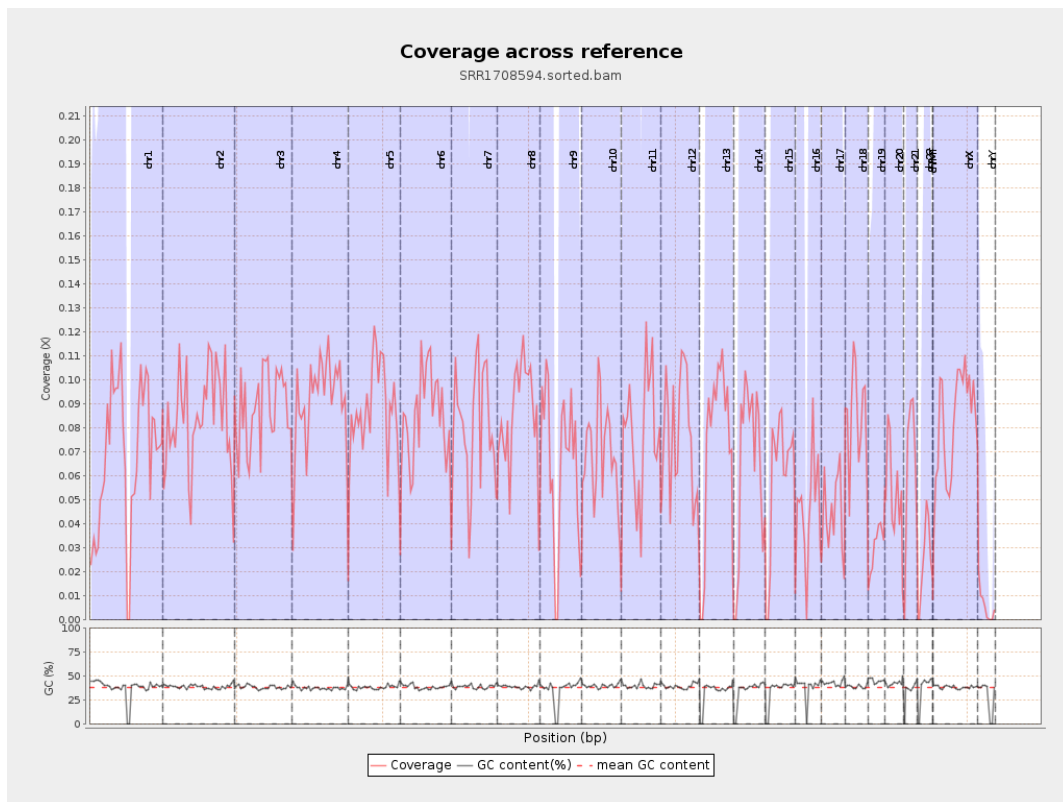
General error rate	0.15%
Mismatches	330,770
Insertions	14,206
Mapped reads with at least one insertion	0.31%
Deletions	11,505
Mapped reads with at least one deletion	0.25%
Homopolymer indels	48.96%

2.6. Chromosome stats

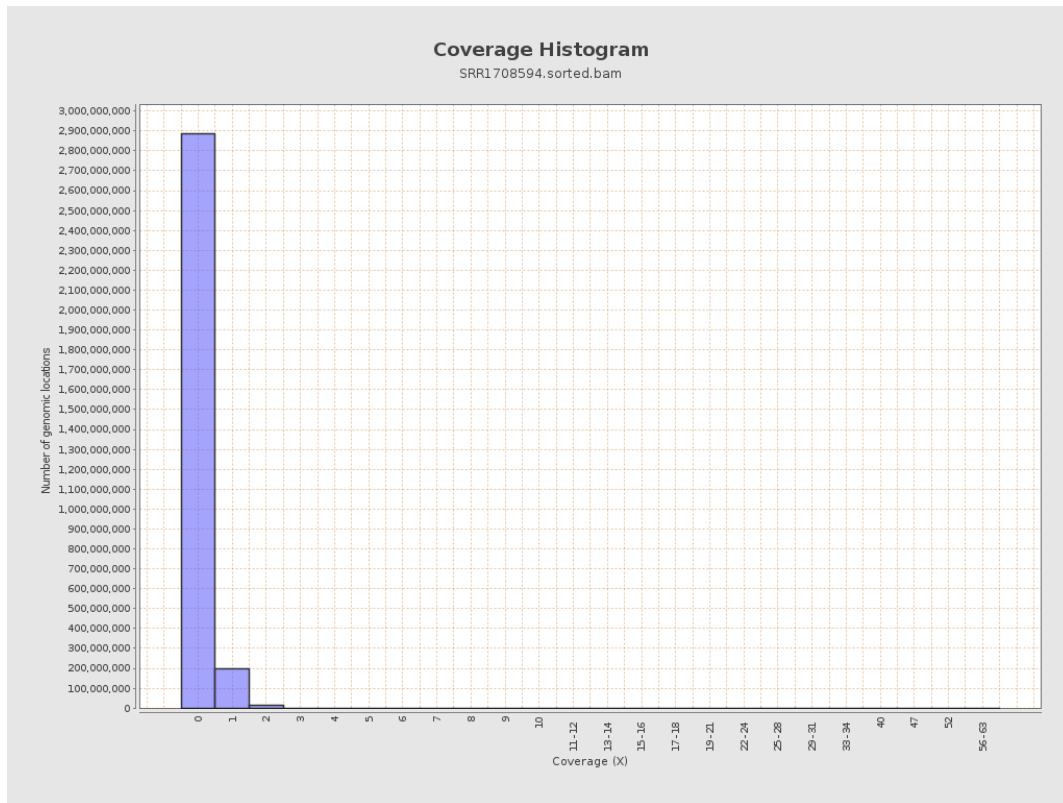
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	17077464	0.0685	0.2734
chr2	243199373	20376606	0.0838	0.3045
chr3	198022430	17449288	0.0881	0.3071
chr4	191154276	17527610	0.0917	0.313
chr5	180915260	15637288	0.0864	0.3043
chr6	171115067	14671902	0.0857	0.3026
chr7	159138663	12691631	0.0798	0.2932

chr8	146364022	12566451	0.0859	0.3032
chr9	141213431	9199676	0.0651	0.2652
chr10	135534747	9414967	0.0695	0.2726
chr11	135006516	10405599	0.0771	0.2892
chr12	133851895	10137605	0.0757	0.2853
chr13	115169878	8561862	0.0743	0.2835
chr14	107349540	6987759	0.0651	0.2655
chr15	102531392	6011506	0.0586	0.2524
chr16	90354753	4052154	0.0448	0.2195
chr17	81195210	3664999	0.0451	0.2205
chr18	78077248	6624067	0.0848	0.301
chr19	59128983	1847408	0.0312	0.1821
chr20	63025520	3408877	0.0541	0.2407
chr21	48129895	2937014	0.061	0.259
chr22	51304566	1296913	0.0253	0.1643
chrMT	16571	137	0.0083	0.0905
chrX	155270560	12864283	0.0829	0.2988
chrY	59373566	332688	0.0056	0.0785

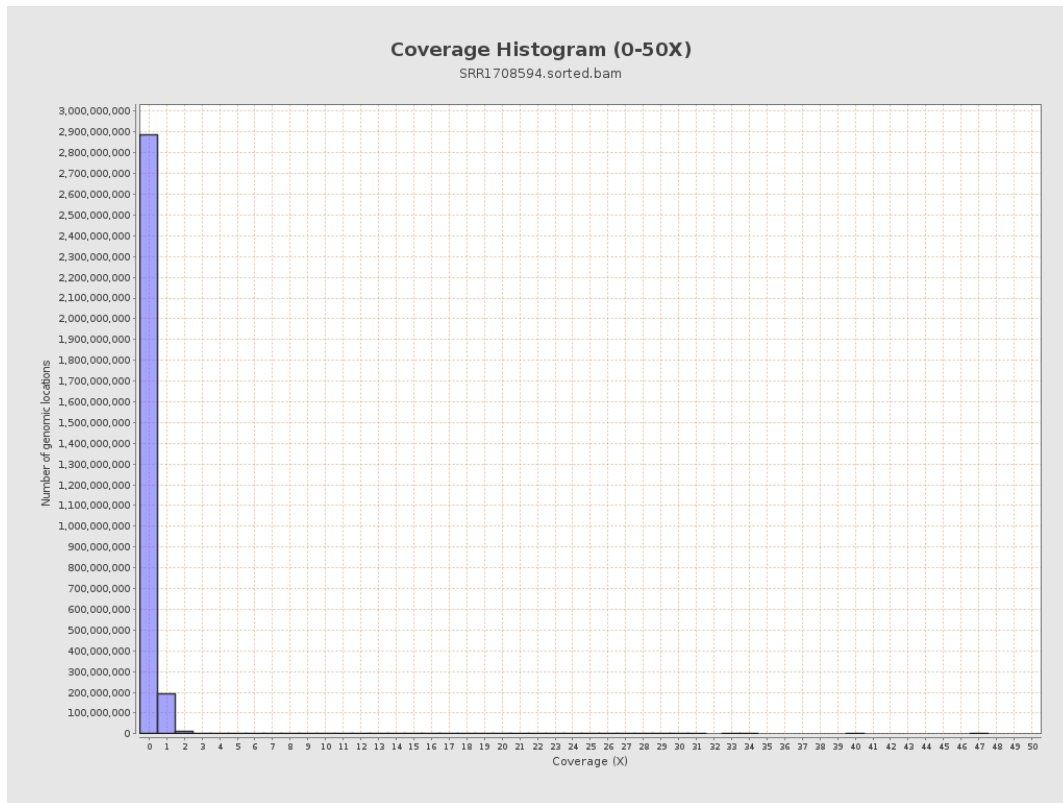
3. Results : Coverage across reference



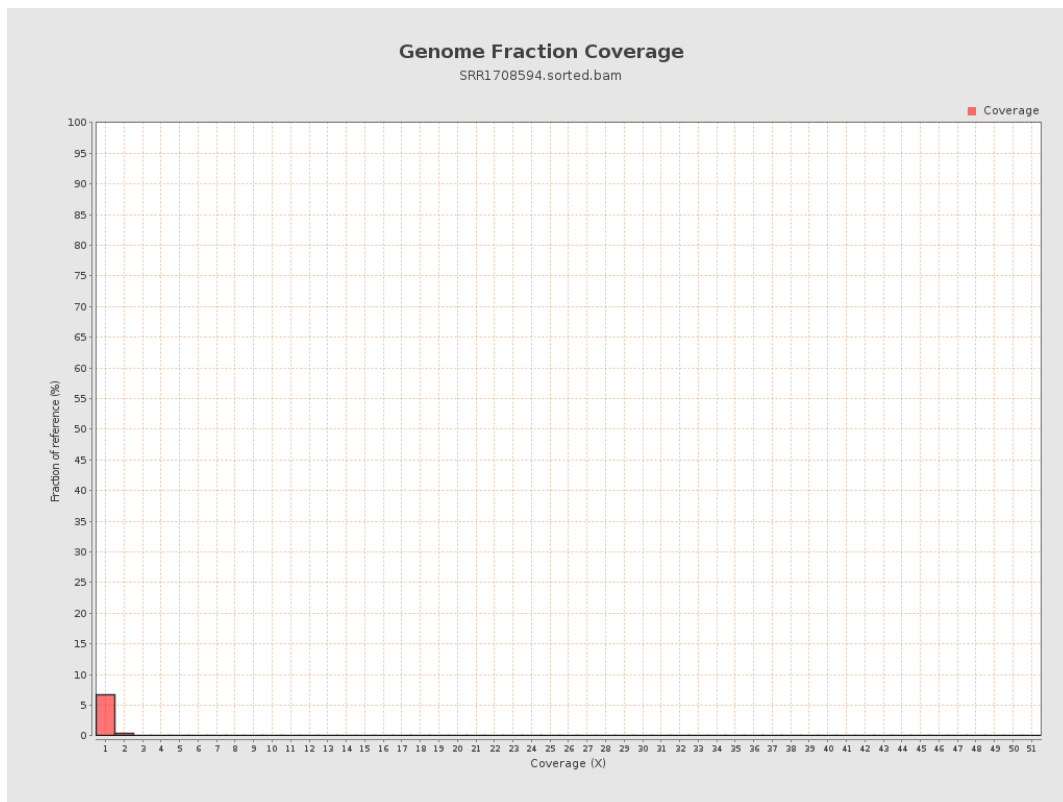
4. Results : Coverage Histogram



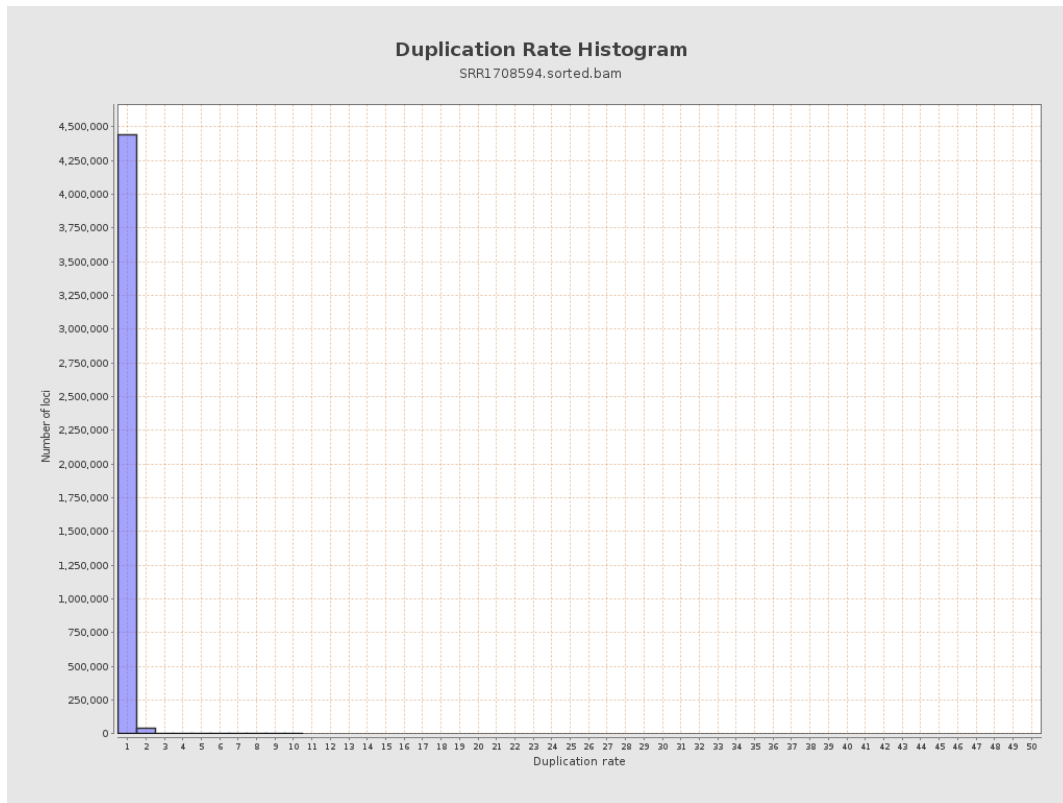
5. Results : Coverage Histogram (0-50X)



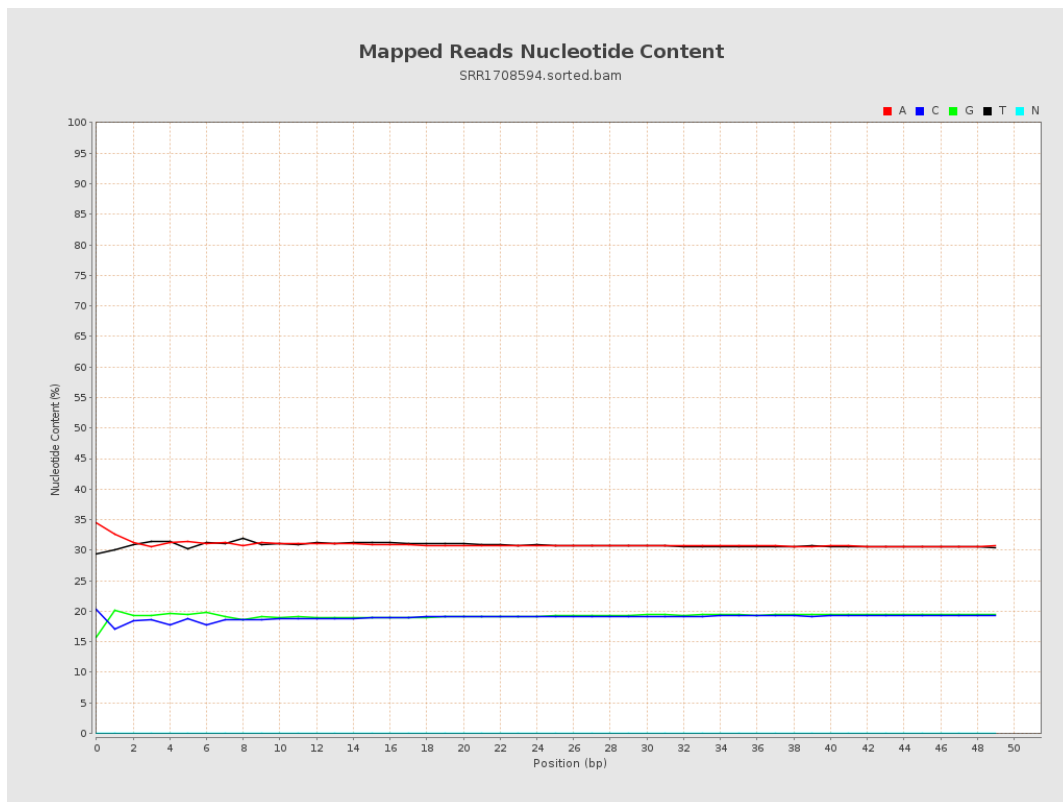
6. Results : Genome Fraction Coverage



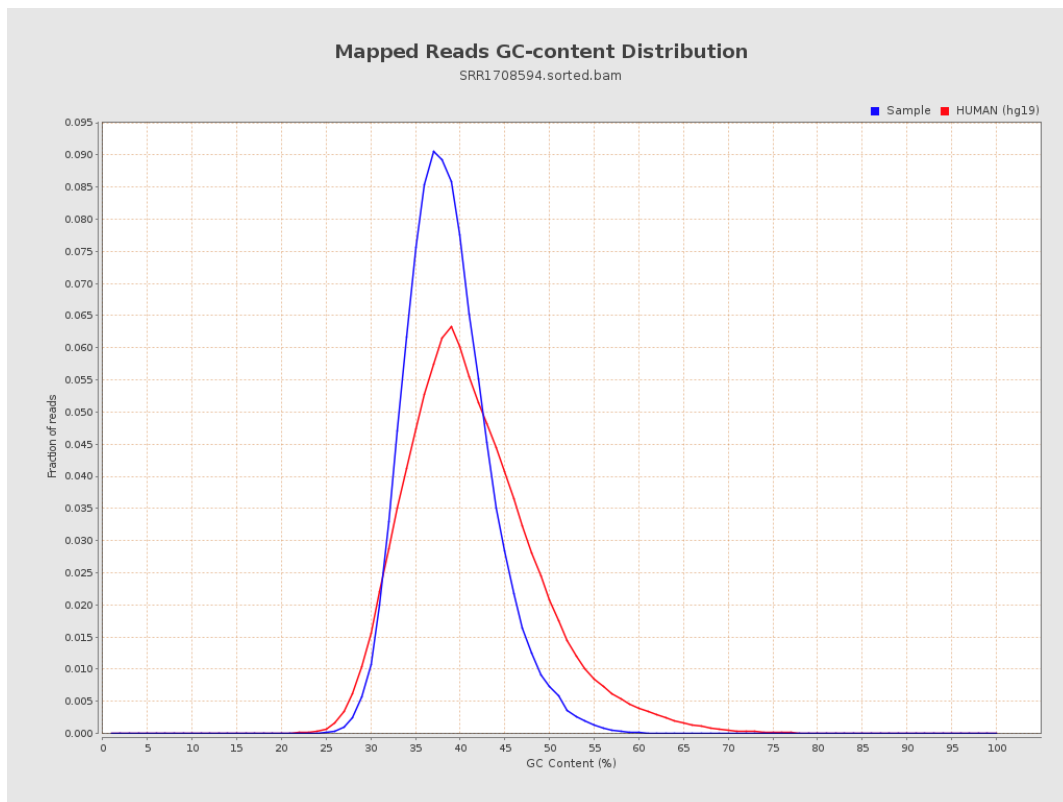
7. Results : Duplication Rate Histogram



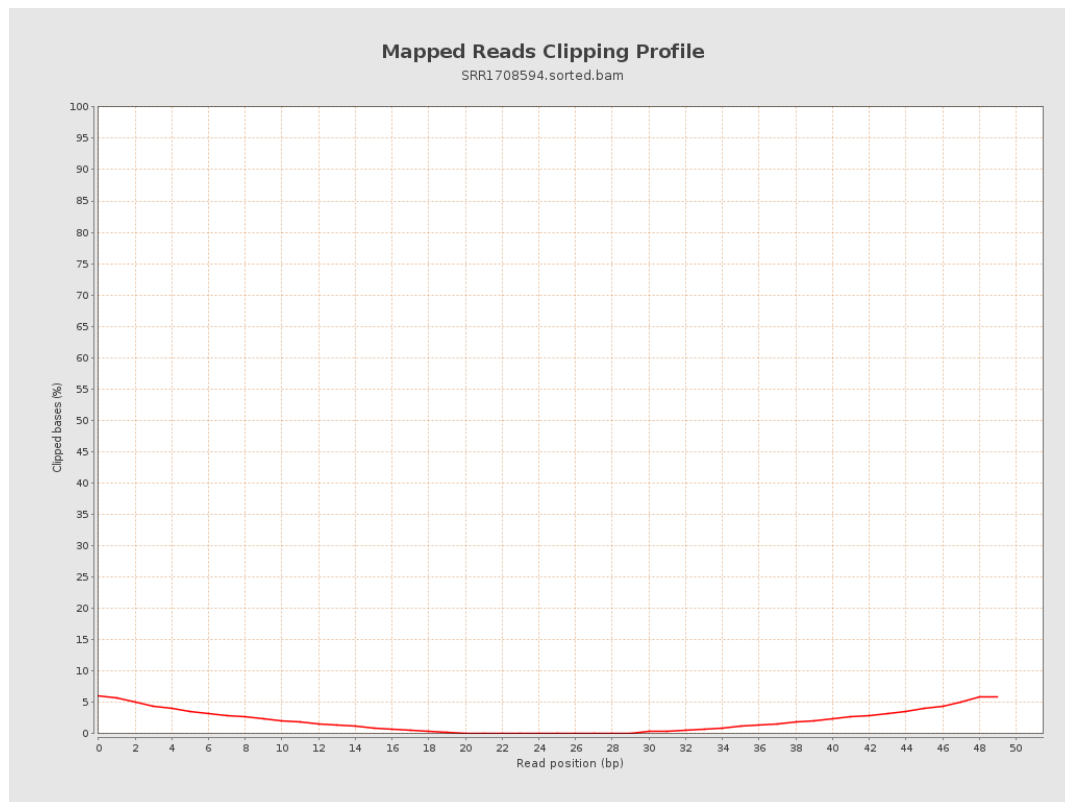
8. Results : Mapped Reads Nucleotide Content



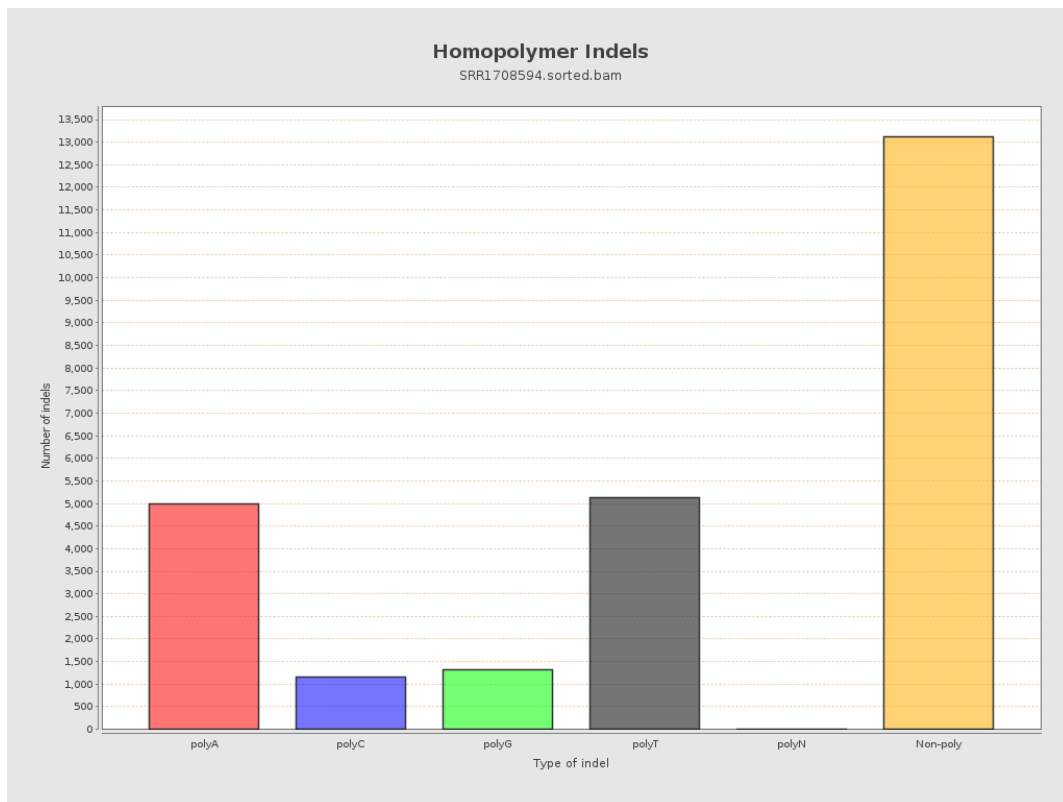
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

