

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 06:36:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716694.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_SRR9716694 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716694.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 06:36:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716694.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,523,799
Mapped reads	2,375,652 / 94.13%
Unmapped reads	148,147 / 5.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	39,796 / 1.58%
Read min/max/mean length	30 / 101 / 101.58
Duplicated reads (estimated)	119,101 / 4.72%
Duplication rate	2.74%
Clipped reads	2,414,042 / 95.65%

2.2. ACGT Content

Number/percentage of A's	45,807,612 / 24.22%
Number/percentage of C's	37,895,175 / 20.04%
Number/percentage of T's	57,613,046 / 30.46%
Number/percentage of G's	47,814,883 / 25.28%
Number/percentage of N's	11,075 / 0.01%
GC Percentage	45.32%

2.3. Coverage

Mean	0.0611

Standard Deviation	0.8066
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2.4. Mapping Quality

Mean Mapping Quality	43.47
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2.5. Mismatches and indels

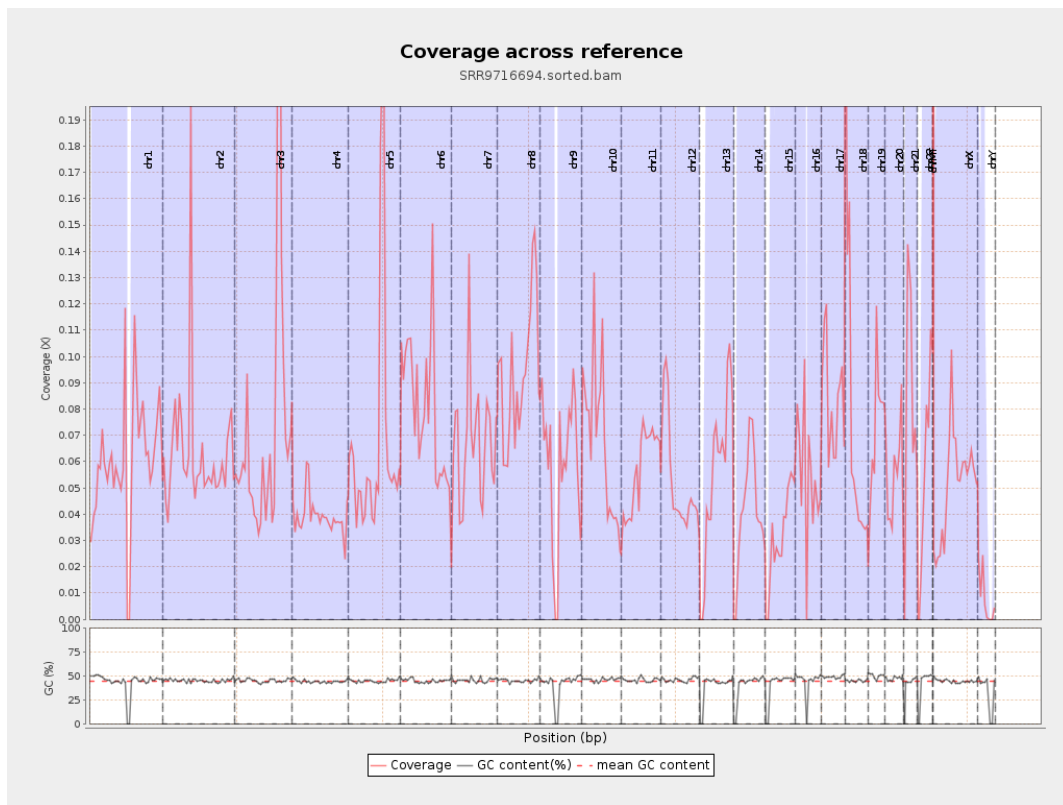
General error rate	0.83%
Mismatches	1,537,039
Insertions	16,109
Mapped reads with at least one insertion	0.67%
Deletions	47,591
Mapped reads with at least one deletion	1.97%
Homopolymer indels	44.23%

2.6. Chromosome stats

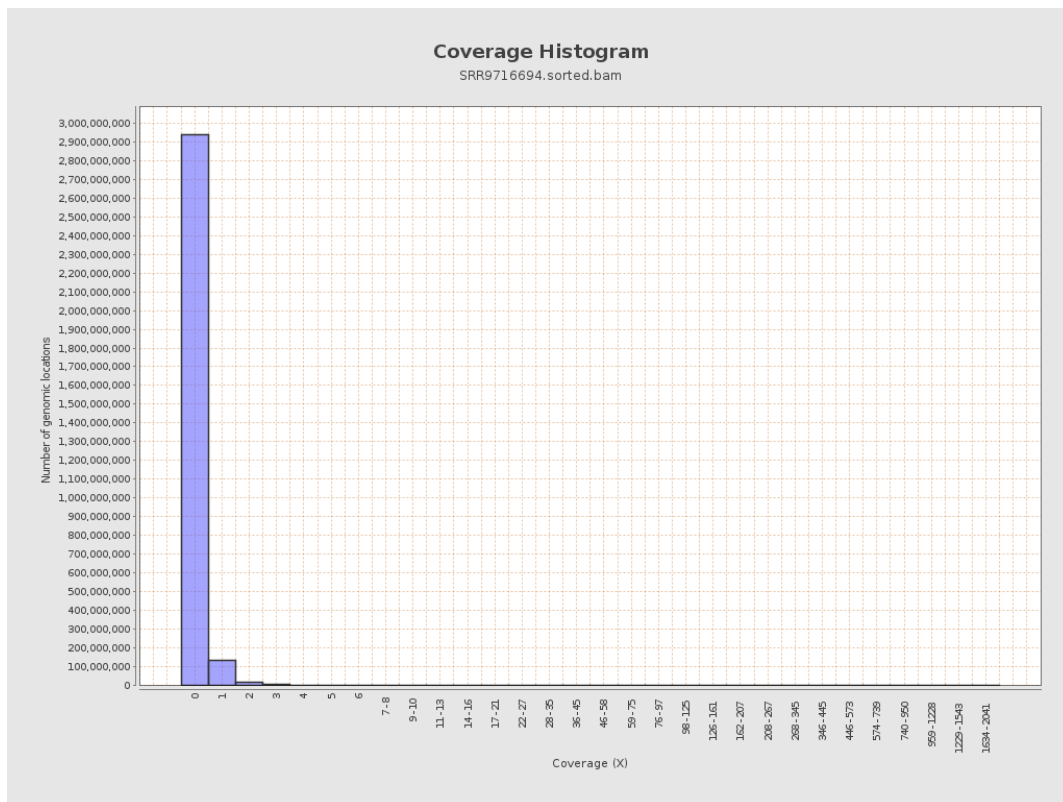
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	15062636	0.0604	1.2955
chr2	243199373	15514179	0.0638	1.4182
chr3	198022430	14262103	0.072	0.3346
chr4	191154276	7545744	0.0395	0.2649
chr5	180915260	11752984	0.065	0.3158
chr6	171115067	13633235	0.0797	0.4549
chr7	159138663	10588404	0.0665	1.124

chr8	146364022	13717312	0.0937	1.0839
chr9	141213431	8303183	0.0588	0.7607
chr10	135534747	9240031	0.0682	0.6811
chr11	135006516	7650364	0.0567	0.5439
chr12	133851895	7095349	0.053	0.2882
chr13	115169878	6516563	0.0566	0.2747
chr14	107349540	4487280	0.0418	0.3499
chr15	102531392	3165483	0.0309	0.216
chr16	90354753	4947047	0.0548	0.3676
chr17	81195210	6895503	0.0849	0.4216
chr18	78077248	5838120	0.0748	1.8905
chr19	59128983	4327812	0.0732	0.9919
chr20	63025520	3512537	0.0557	0.3973
chr21	48129895	3748173	0.0779	0.3546
chr22	51304566	2821997	0.055	0.2791
chrMT	16571	160978	9.7144	6.5856
chrX	155270560	7982132	0.0514	0.4569
chrY	59373566	456291	0.0077	0.2181

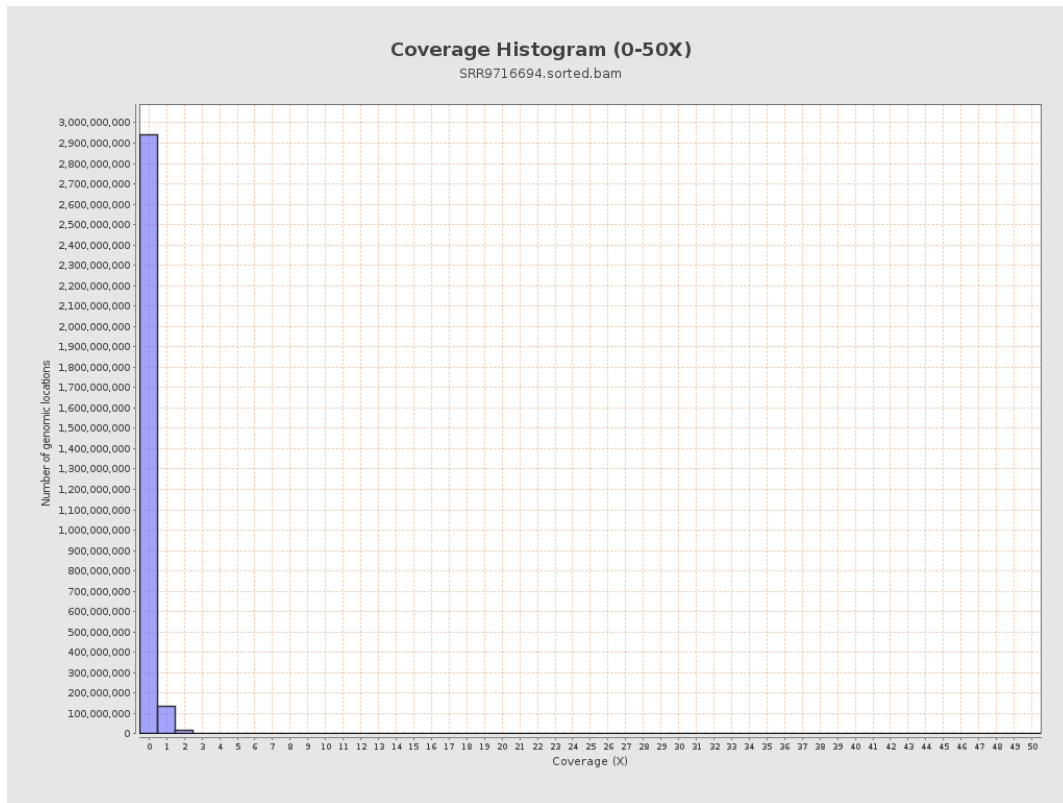
3. Results : Coverage across reference



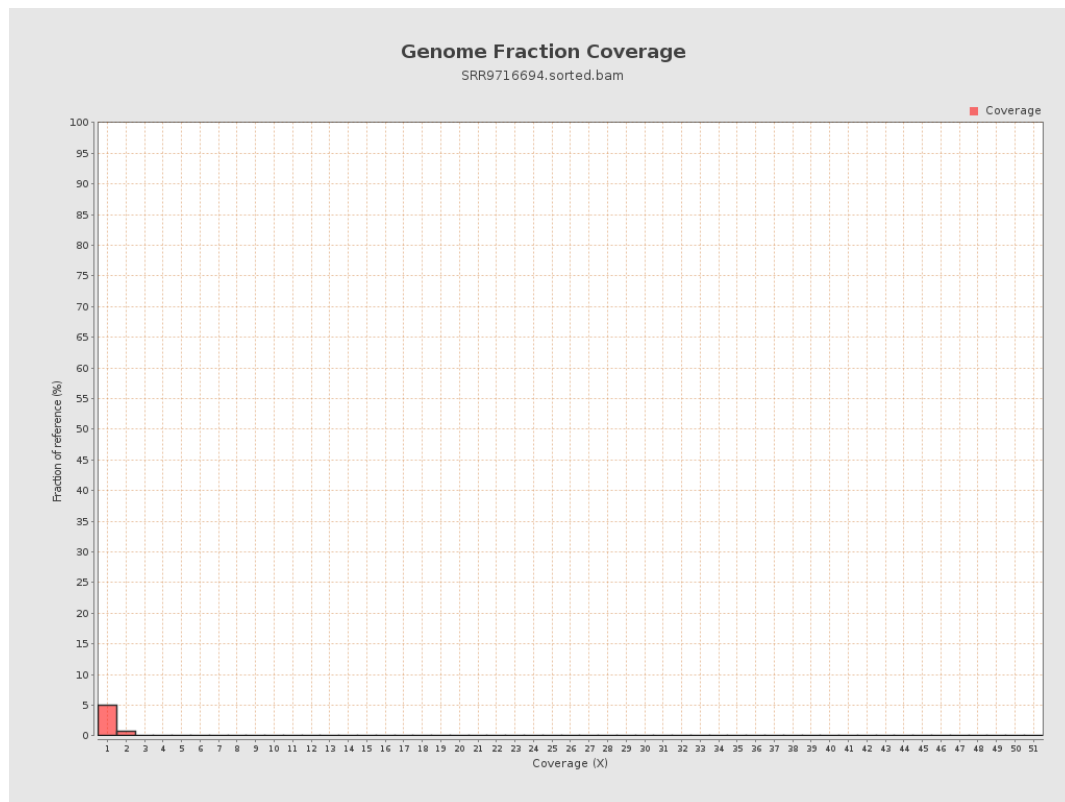
4. Results : Coverage Histogram



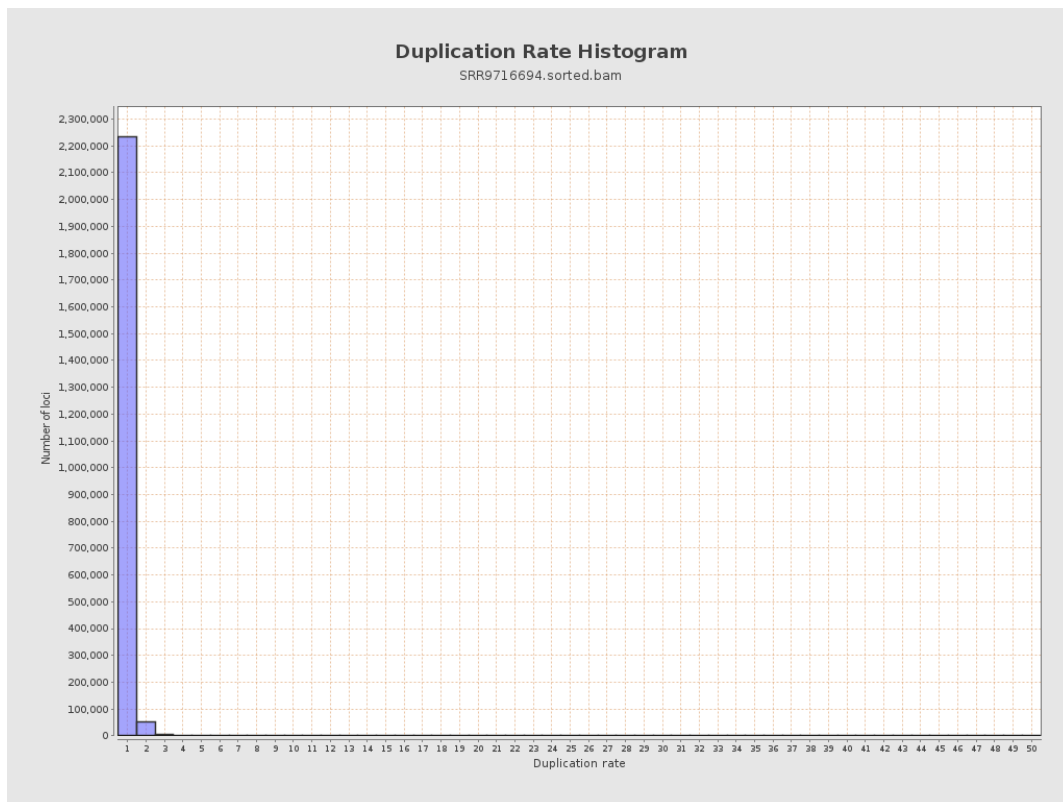
5. Results : Coverage Histogram (0-50X)



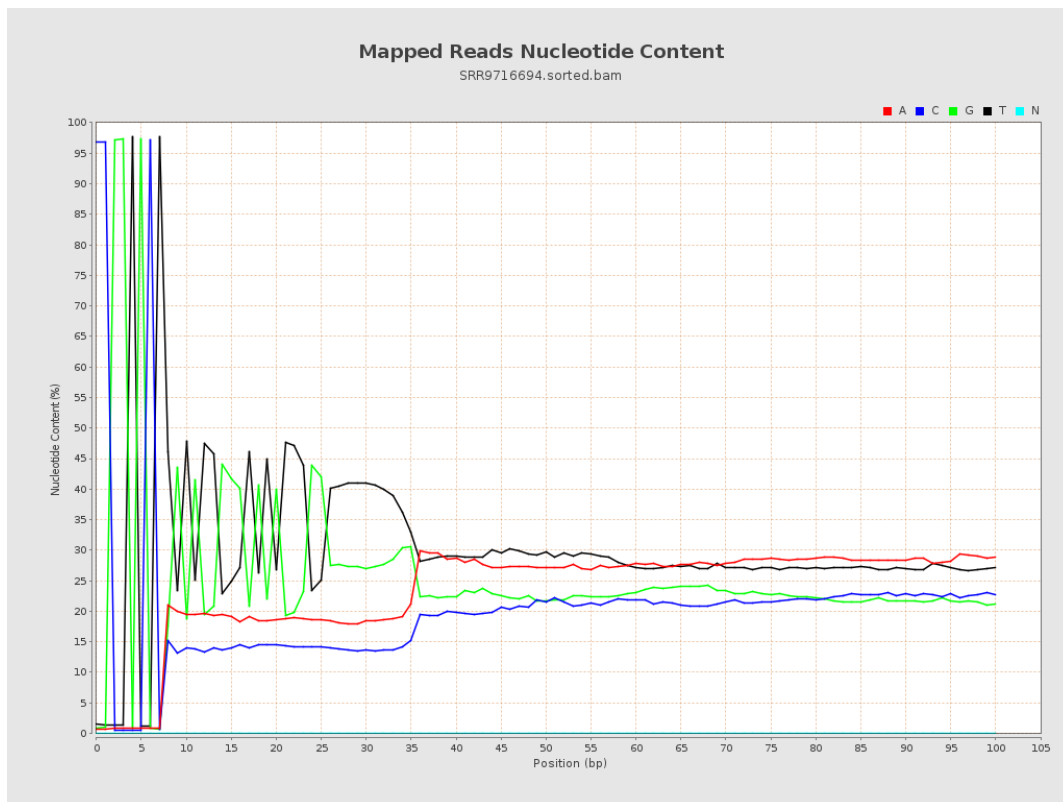
6. Results : Genome Fraction Coverage



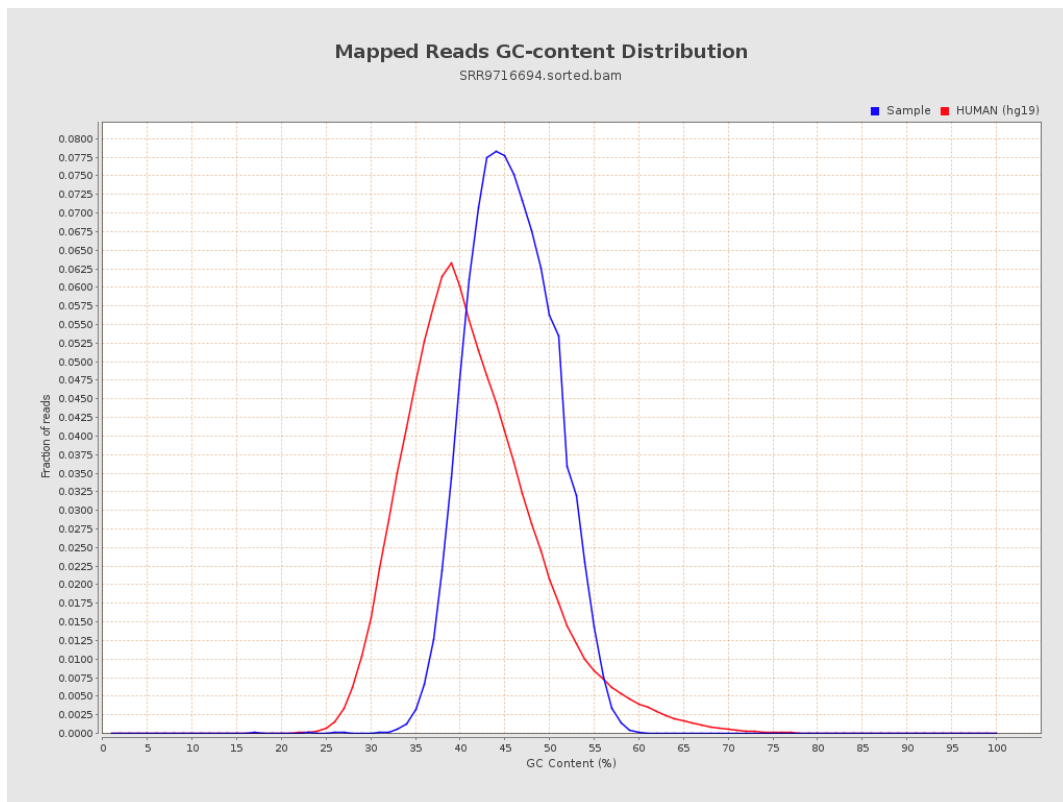
7. Results : Duplication Rate Histogram



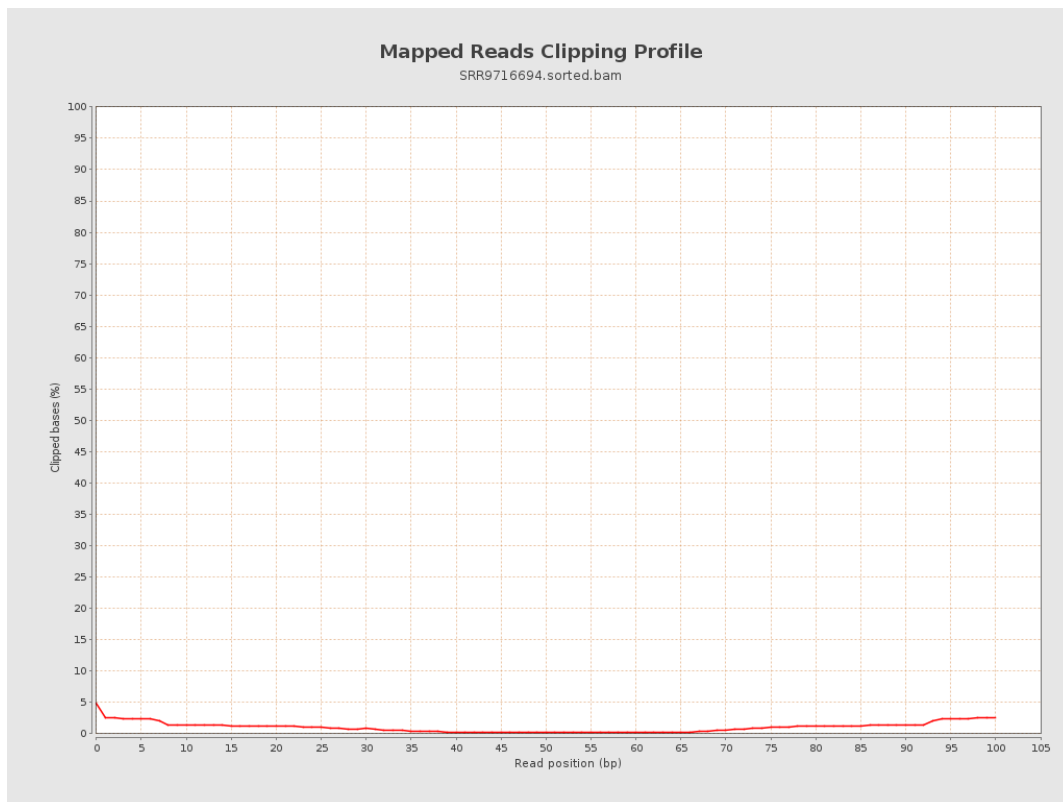
8. Results : Mapped Reads Nucleotide Content



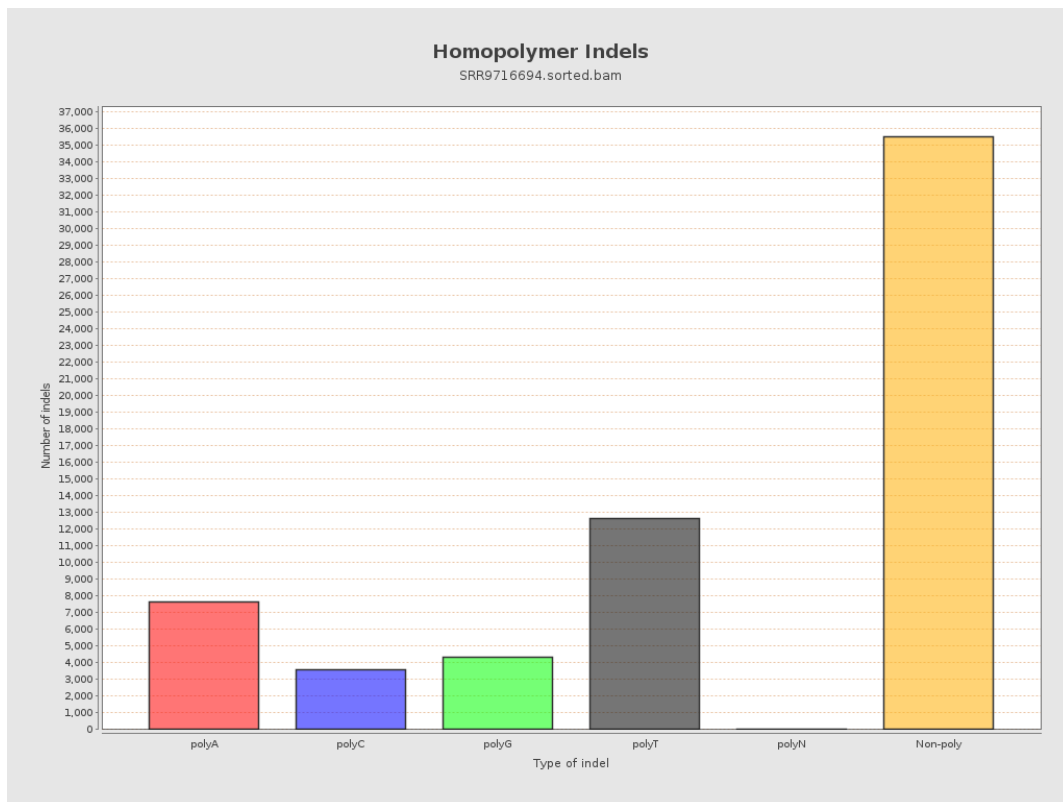
9. Results : Mapped Reads GC-content Distribution



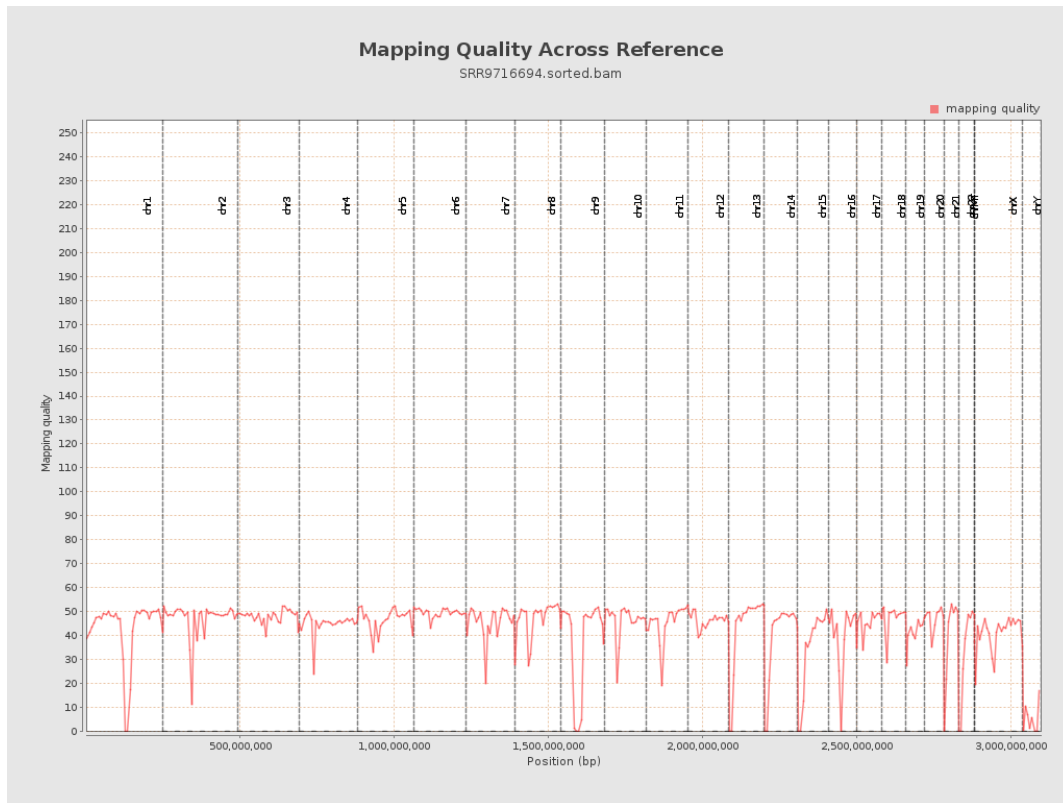
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

