

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 14:37:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716845.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_SRR9716845 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716845.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 14:37:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716845.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,056,013
Mapped reads	1,914,442 / 93.11%
Unmapped reads	141,571 / 6.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	35,699 / 1.74%
Read min/max/mean length	30 / 101 / 101.63
Duplicated reads (estimated)	84,211 / 4.1%
Duplication rate	3.13%
Clipped reads	1,945,465 / 94.62%

2.2. ACGT Content

Number/percentage of A's	38,032,109 / 25.06%
Number/percentage of C's	28,478,427 / 18.77%
Number/percentage of T's	47,810,726 / 31.51%
Number/percentage of G's	37,409,490 / 24.65%
Number/percentage of N's	10,261 / 0.01%
GC Percentage	43.42%

2.3. Coverage

Mean	0.049

Standard Deviation	0.4729
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	47.61
----------------------	-------

2.5. Mismatches and indels

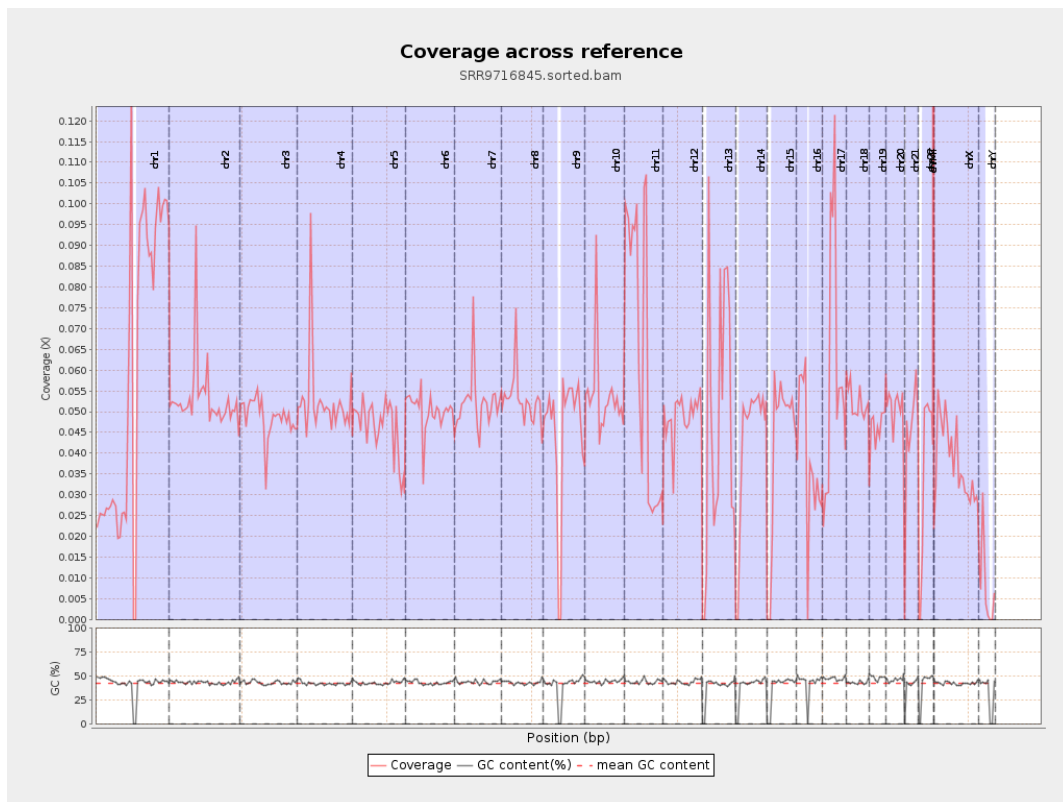
General error rate	0.68%
Mismatches	998,894
Insertions	13,091
Mapped reads with at least one insertion	0.67%
Deletions	36,537
Mapped reads with at least one deletion	1.88%
Homopolymer indels	43.48%

2.6. Chromosome stats

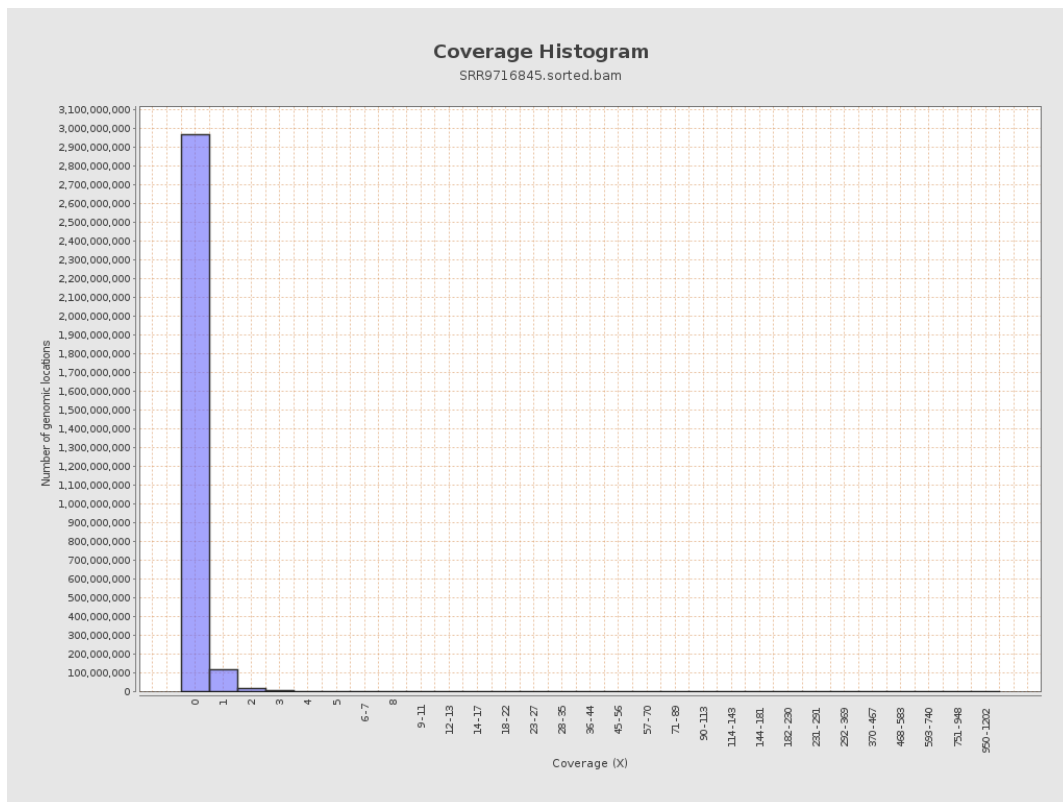
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	14622897	0.0587	1.0581
chr2	243199373	12923960	0.0531	0.4795
chr3	198022430	9632150	0.0486	0.2473
chr4	191154276	9998766	0.0523	0.3277
chr5	180915260	8347773	0.0461	0.2434
chr6	171115067	8584555	0.0502	0.2785
chr7	159138663	8308736	0.0522	0.5634

chr8	146364022	7735477	0.0529	0.5127
chr9	141213431	6387451	0.0452	0.3818
chr10	135534747	7262287	0.0536	0.4348
chr11	135006516	8504920	0.063	0.4979
chr12	133851895	6549059	0.0489	0.2516
chr13	115169878	5349302	0.0464	0.2448
chr14	107349540	4577500	0.0426	0.2533
chr15	102531392	4369245	0.0426	0.2321
chr16	90354753	3504197	0.0388	0.2478
chr17	81195210	4914820	0.0605	0.3379
chr18	78077248	4085536	0.0523	0.6393
chr19	59128983	2748962	0.0465	0.7351
chr20	63025520	3197229	0.0507	0.27
chr21	48129895	2132833	0.0443	0.2805
chr22	51304566	1780510	0.0347	0.2098
chrMT	16571	15192	0.9168	1.1675
chrX	155270560	5842593	0.0376	0.2604
chrY	59373566	434837	0.0073	0.2635

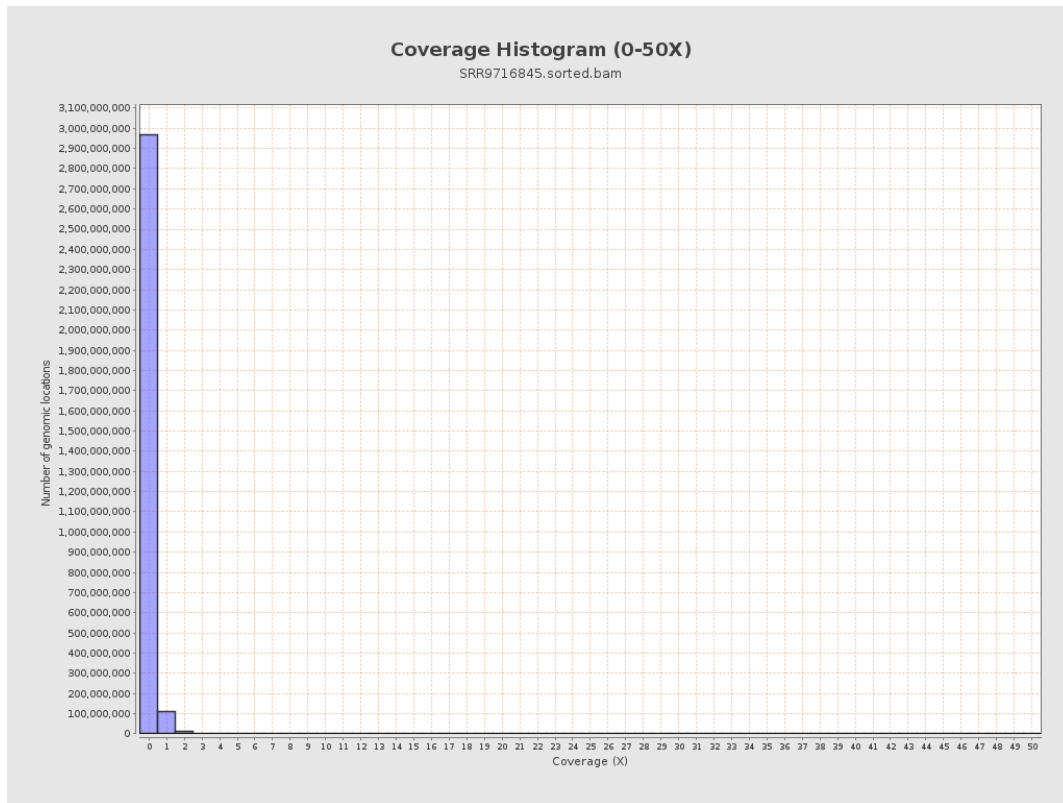
3. Results : Coverage across reference



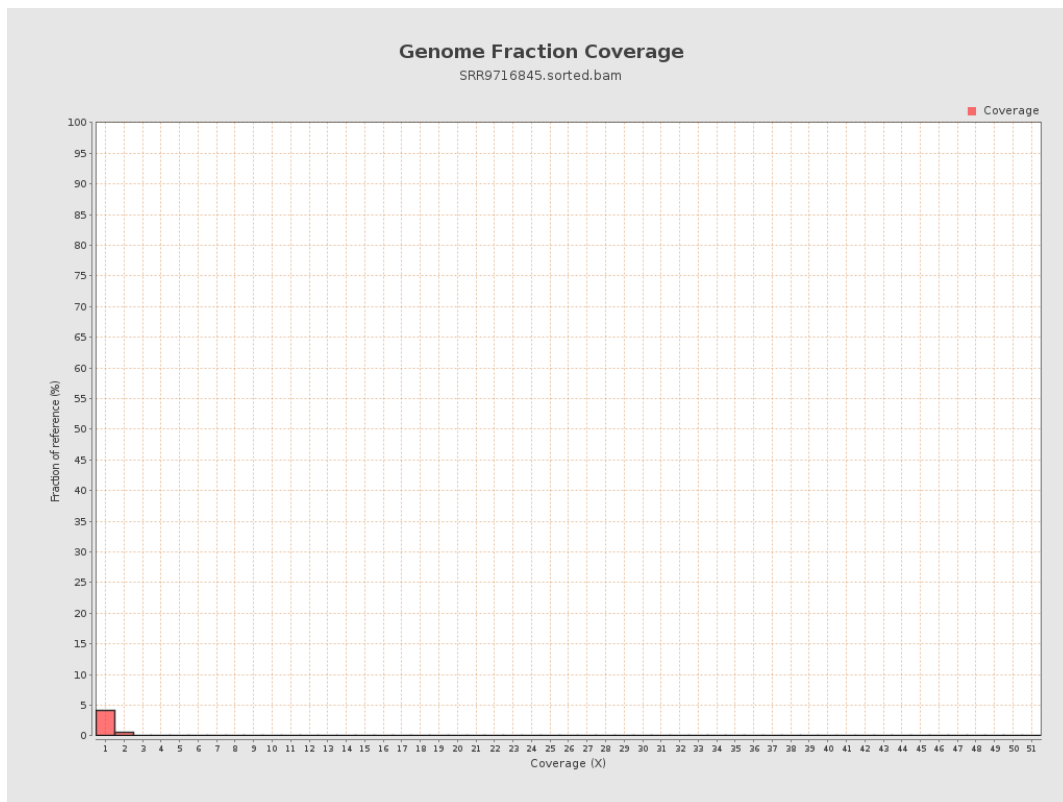
4. Results : Coverage Histogram



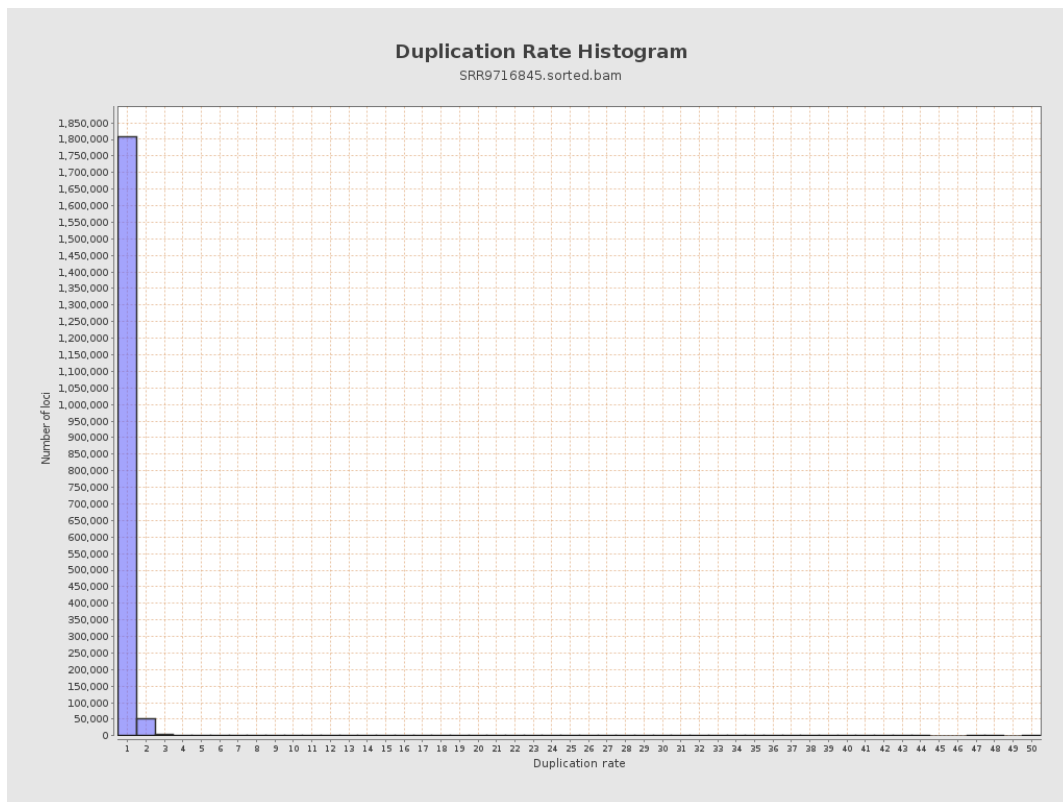
5. Results : Coverage Histogram (0-50X)



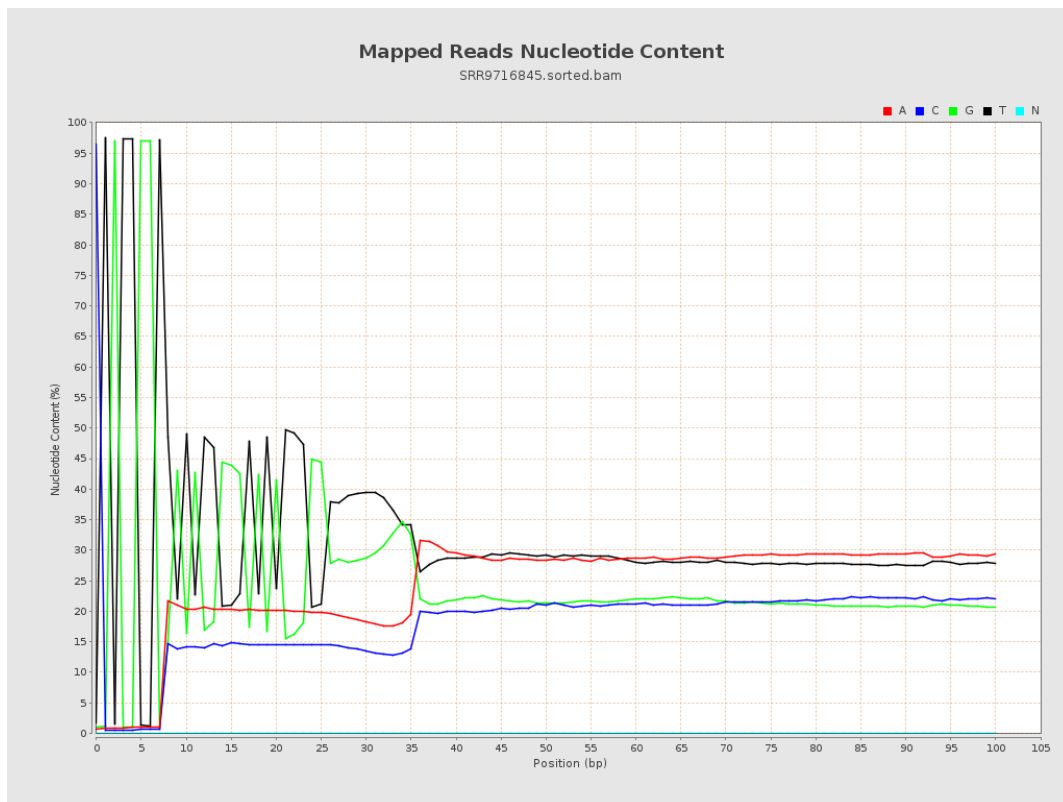
6. Results : Genome Fraction Coverage



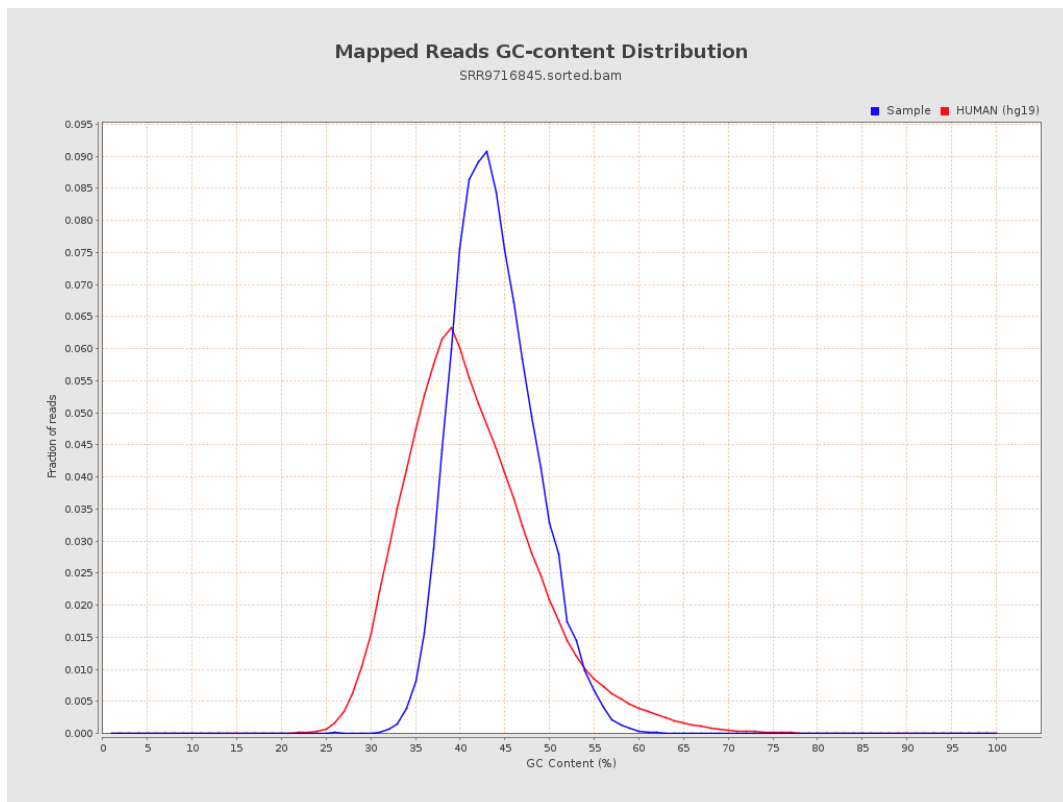
7. Results : Duplication Rate Histogram



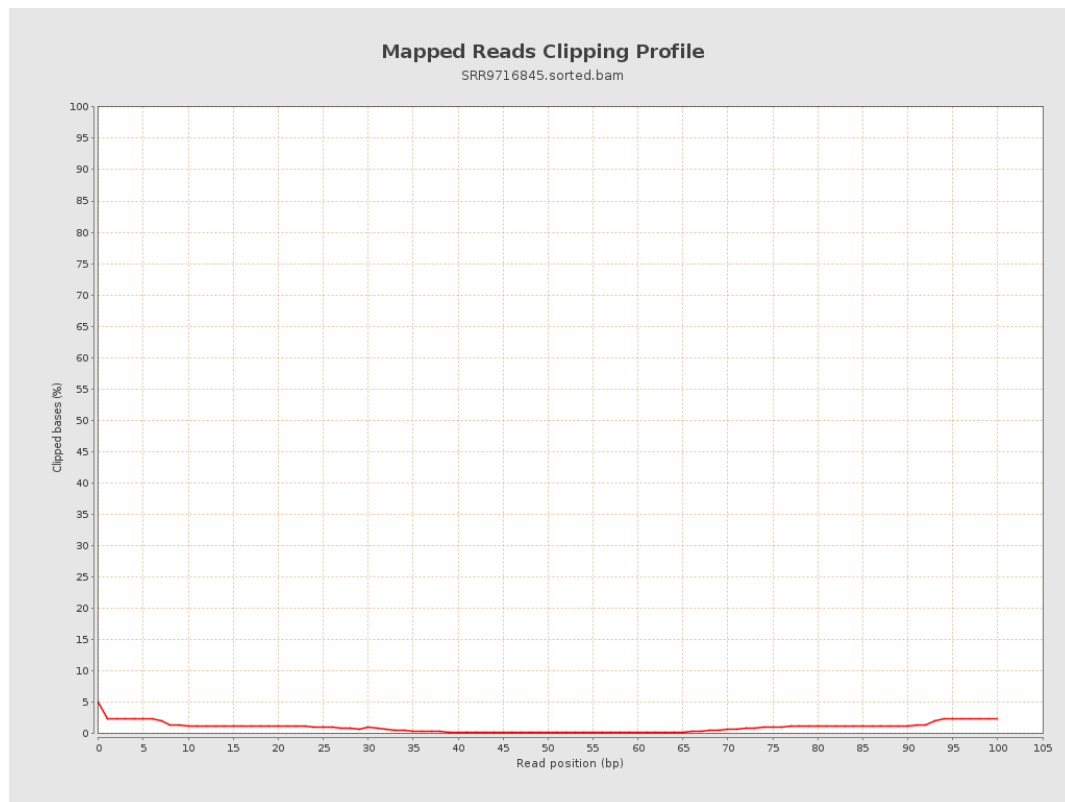
8. Results : Mapped Reads Nucleotide Content



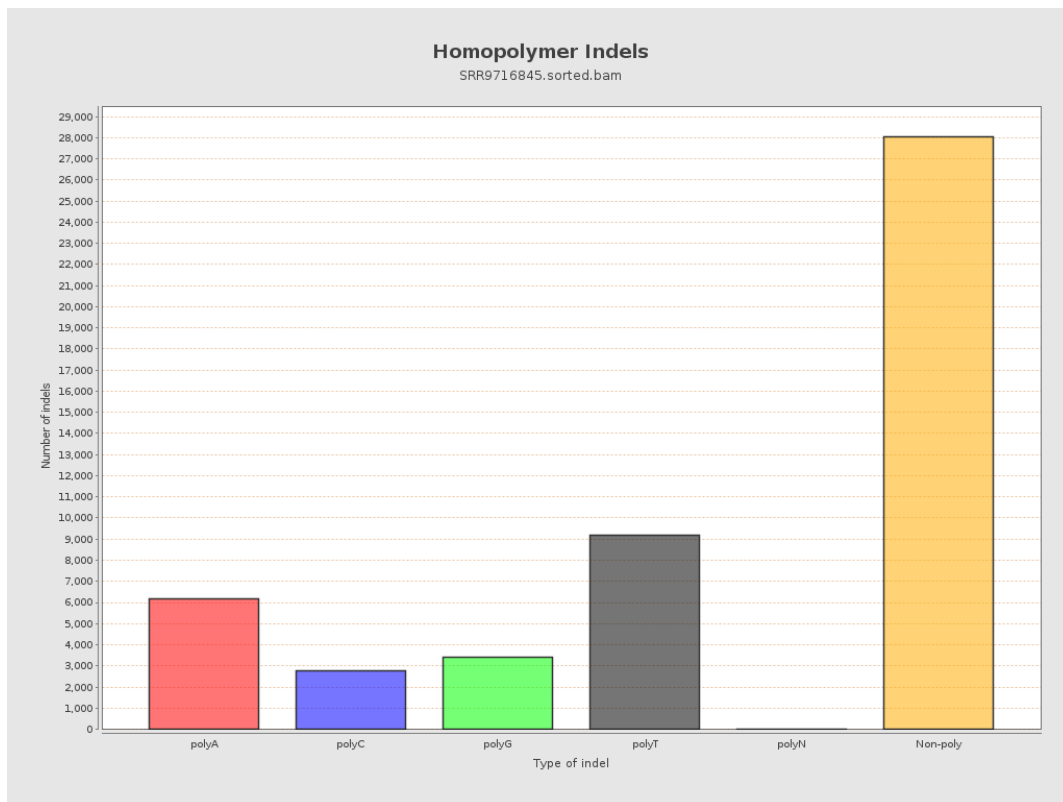
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

