

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 11:47:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716401.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_SRR9716401 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716401.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 11:47:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716401.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,176,438
Mapped reads	1,954,849 / 89.82%
Unmapped reads	221,589 / 10.18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,999 / 0.46%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	77,521 / 3.56%
Duplication rate	2.79%
Clipped reads	1,959,897 / 90.05%

2.2. ACGT Content

Number/percentage of A's	28,379,585 / 25.31%
Number/percentage of C's	22,508,557 / 20.07%
Number/percentage of T's	35,842,796 / 31.96%
Number/percentage of G's	25,406,557 / 22.66%
Number/percentage of N's	1,812 / 0%
GC Percentage	42.73%

2.3. Coverage

Mean	0.0362

Standard Deviation	0.3496
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2.4. Mapping Quality

Mean Mapping Quality	43.98
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2.5. Mismatches and indels

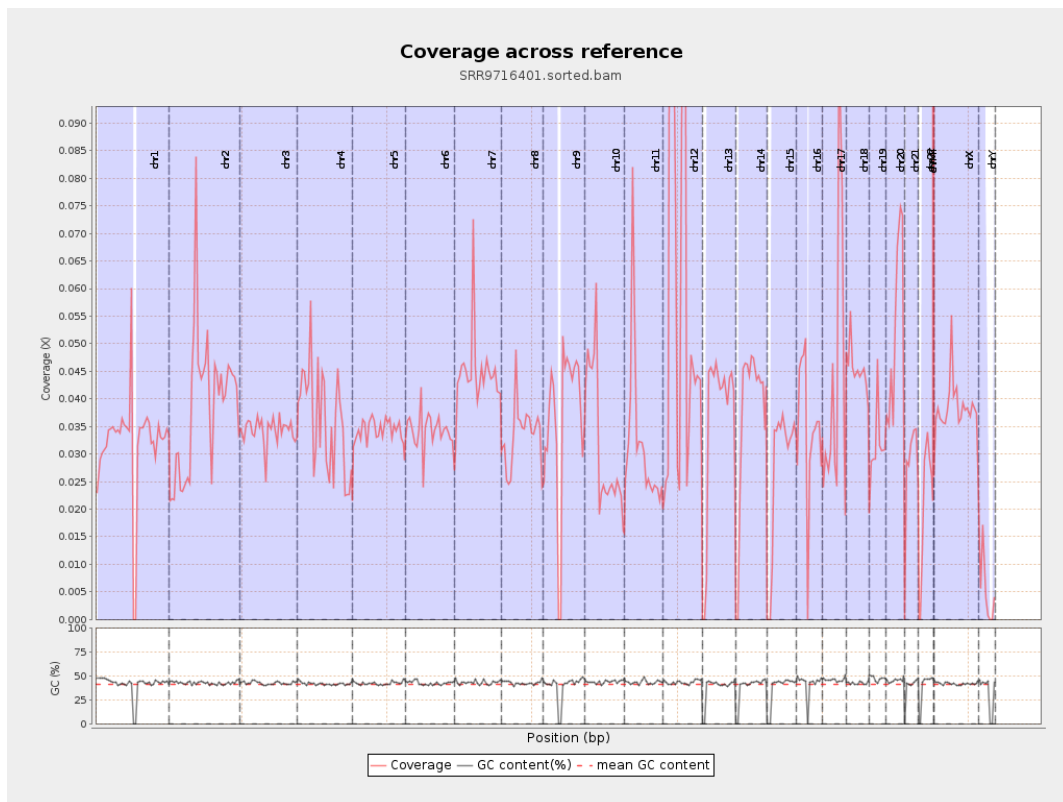
General error rate	0.55%
Mismatches	601,459
Insertions	7,178
Mapped reads with at least one insertion	0.37%
Deletions	18,535
Mapped reads with at least one deletion	0.94%
Homopolymer indels	43.39%

2.6. Chromosome stats

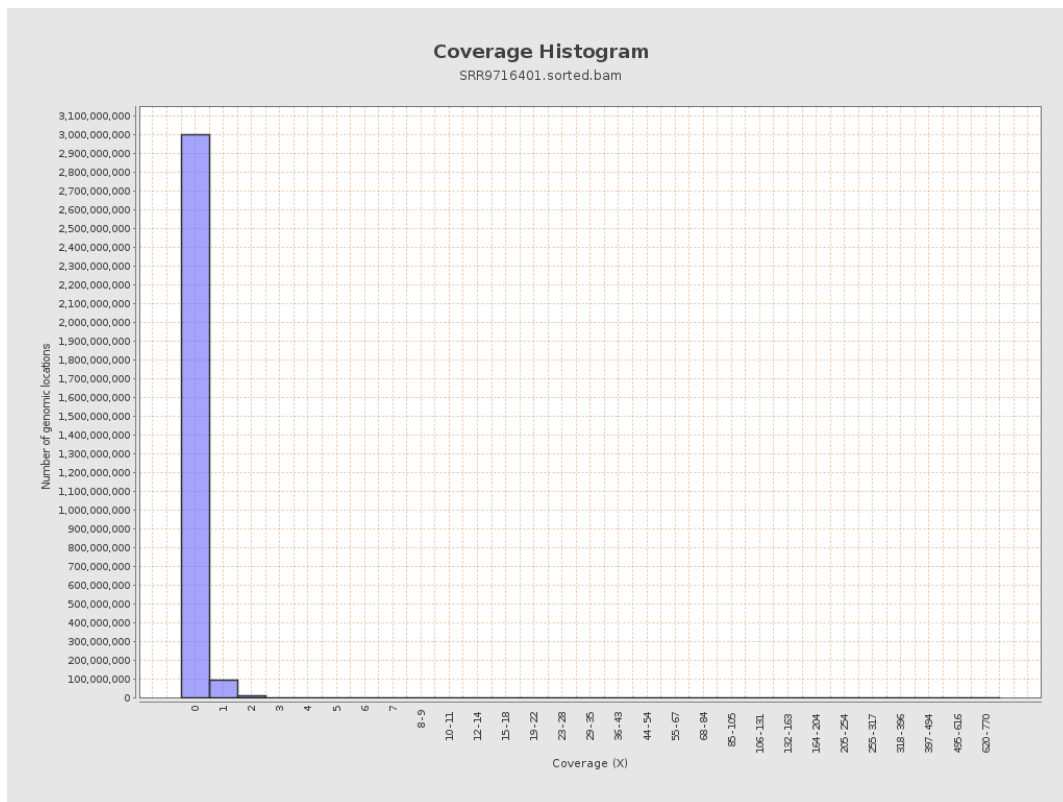
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7968860	0.032	0.6126
chr2	243199373	9449866	0.0389	0.4137
chr3	198022430	6783973	0.0343	0.2025
chr4	191154276	6887562	0.036	0.229
chr5	180915260	6197188	0.0343	0.2089
chr6	171115067	5840219	0.0341	0.2302
chr7	159138663	7155902	0.045	0.4815

chr8	146364022	4904156	0.0335	0.3287
chr9	141213431	5171758	0.0366	0.3896
chr10	135534747	4278041	0.0316	0.327
chr11	135006516	4314477	0.032	0.2877
chr12	133851895	8294200	0.062	0.3111
chr13	115169878	4155473	0.0361	0.2051
chr14	107349540	3977287	0.037	0.2426
chr15	102531392	2825564	0.0276	0.1827
chr16	90354753	3156220	0.0349	0.2306
chr17	81195210	3366114	0.0415	0.233
chr18	78077248	3563438	0.0456	0.6892
chr19	59128983	1885050	0.0319	0.4756
chr20	63025520	3326391	0.0528	0.261
chr21	48129895	1336917	0.0278	0.2193
chr22	51304566	1053399	0.0205	0.1547
chrMT	16571	26865	1.6212	1.7647
chrX	155270560	5941460	0.0383	0.2773
chrY	59373566	309708	0.0052	0.1207

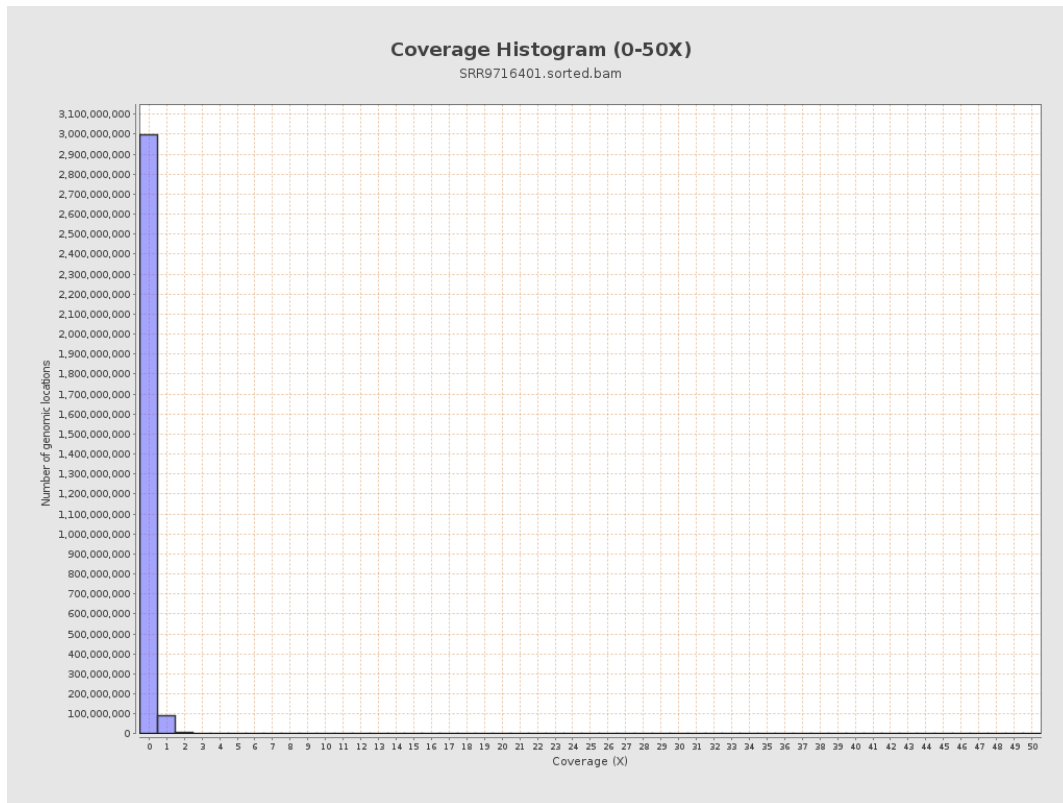
3. Results : Coverage across reference



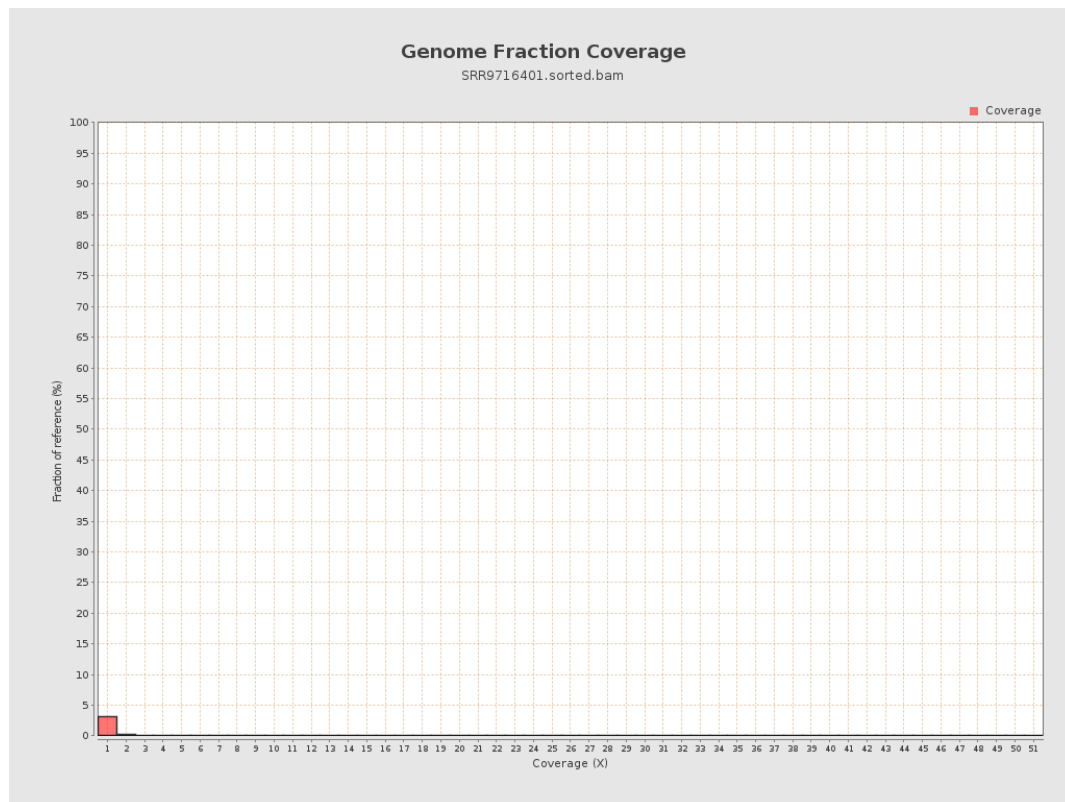
4. Results : Coverage Histogram



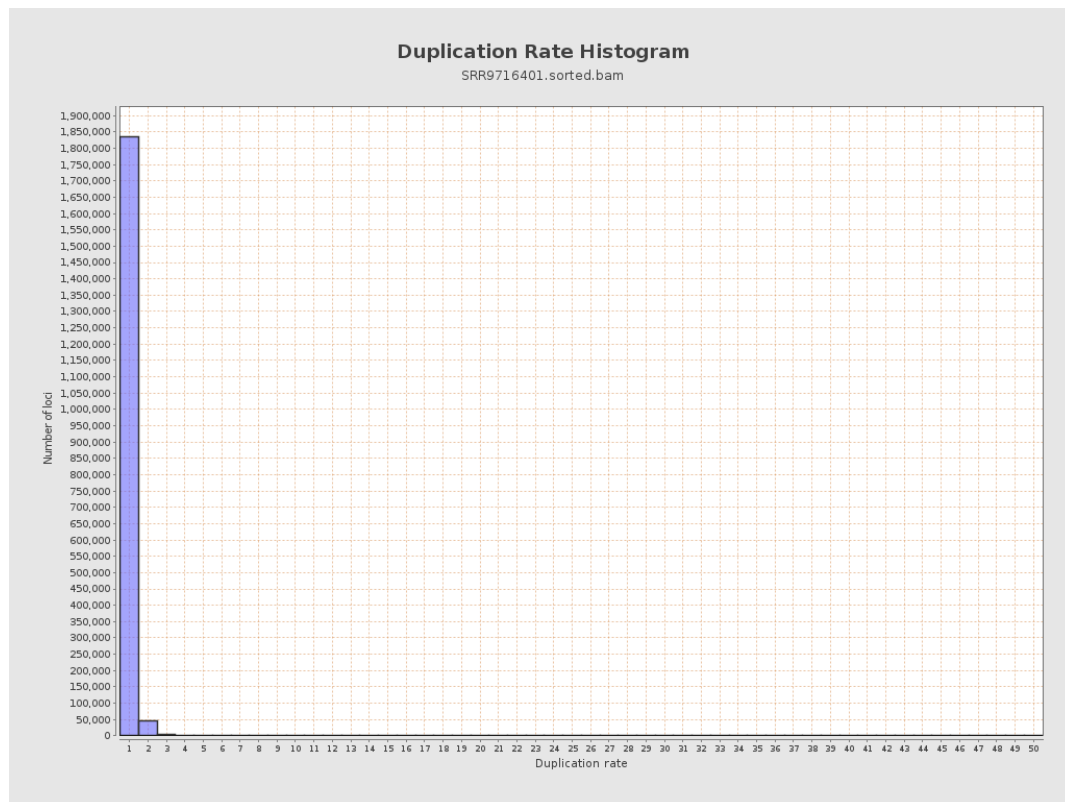
5. Results : Coverage Histogram (0-50X)



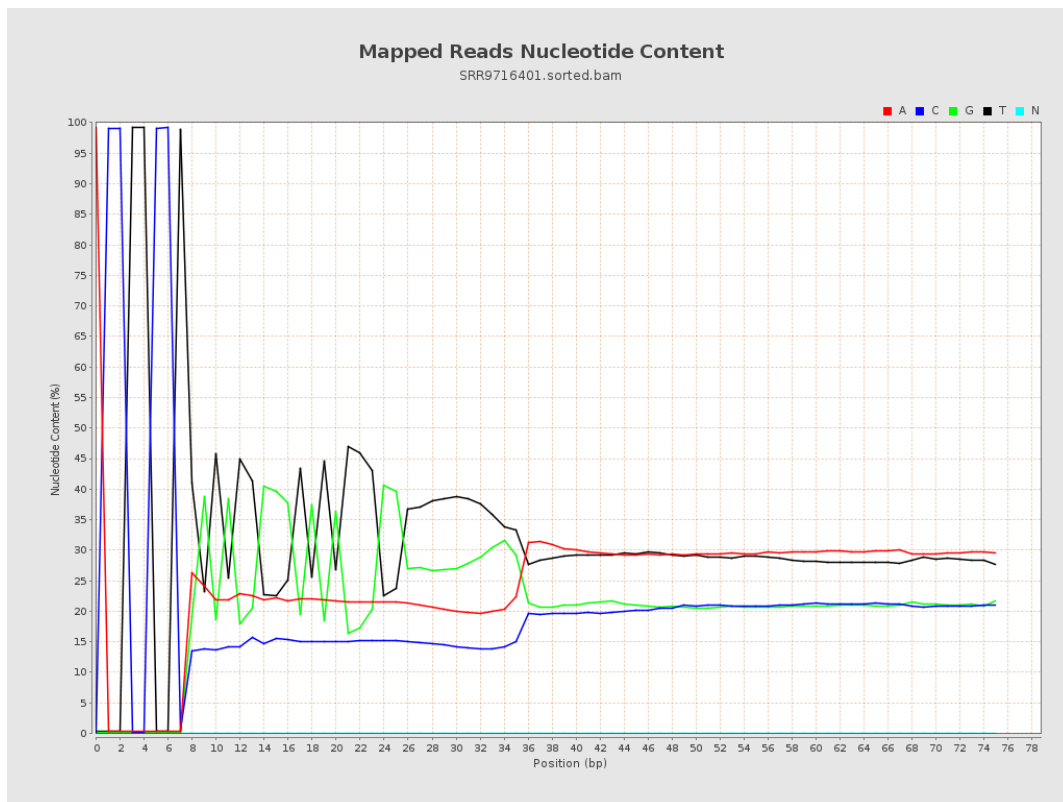
6. Results : Genome Fraction Coverage



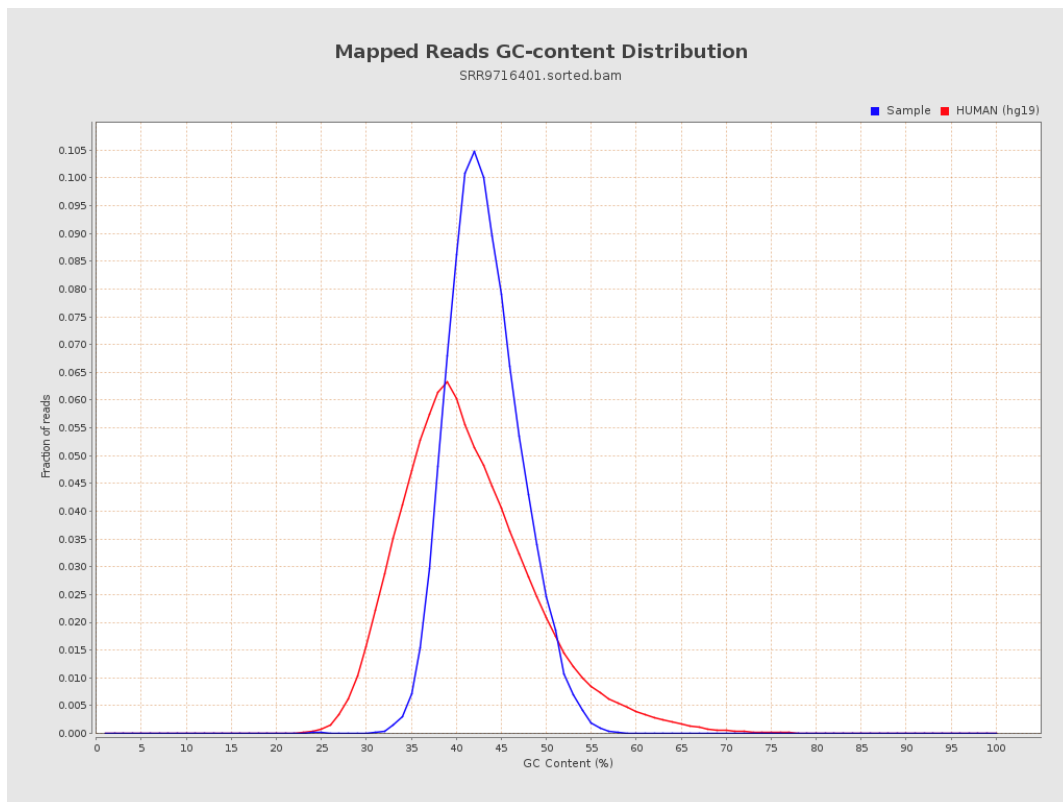
7. Results : Duplication Rate Histogram



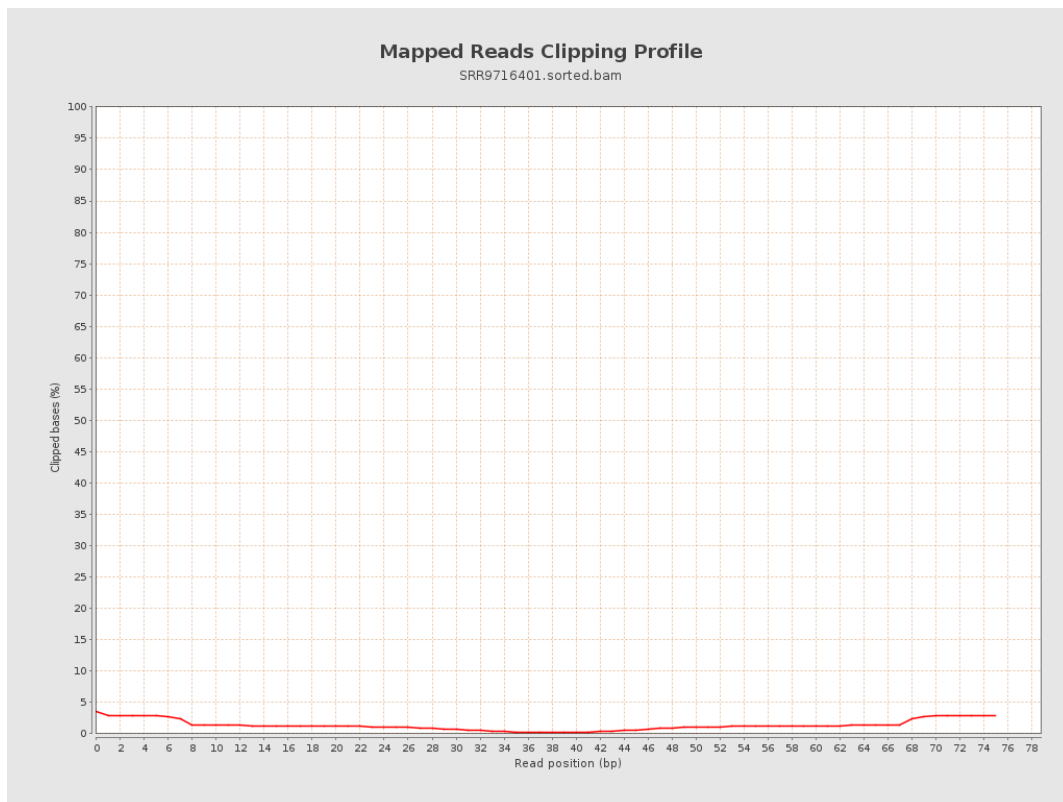
8. Results : Mapped Reads Nucleotide Content



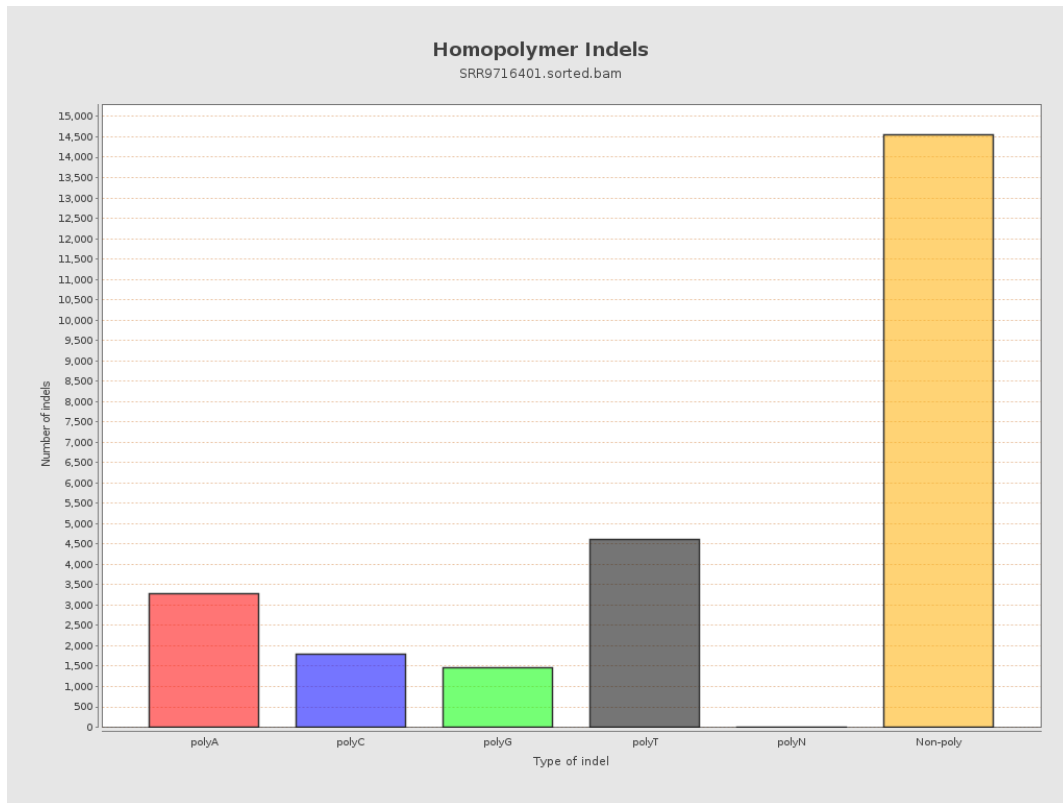
9. Results : Mapped Reads GC-content Distribution



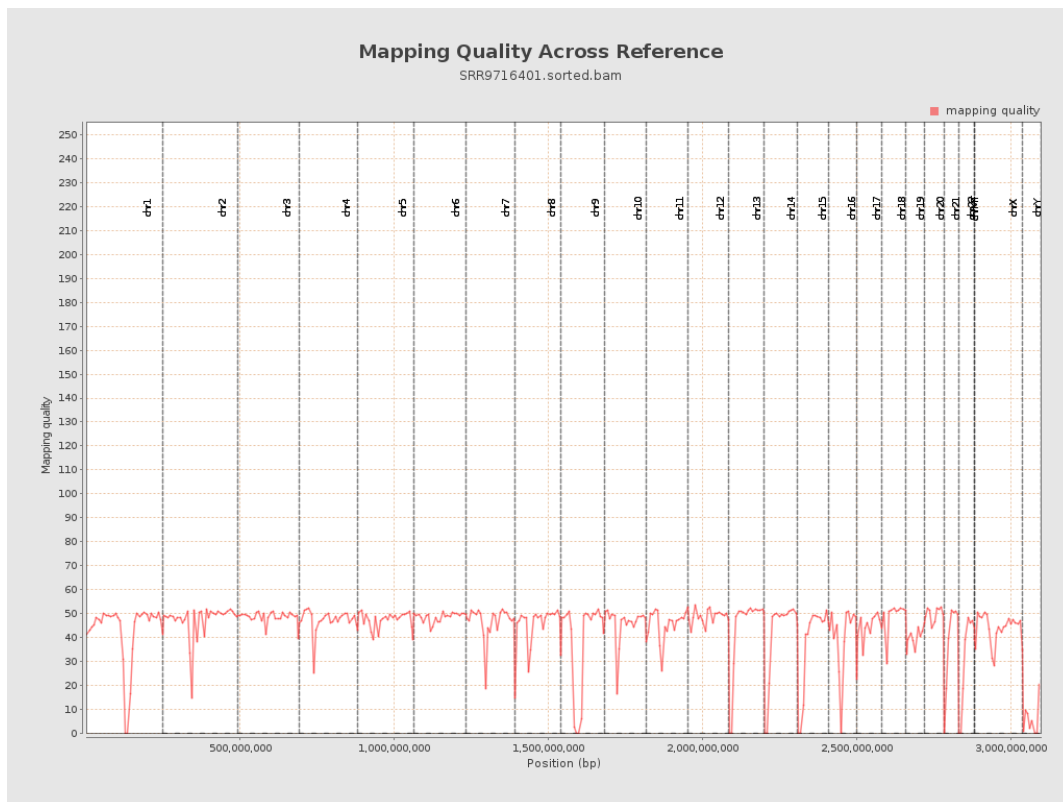
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

