

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 10:42:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716383.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_SRR9716383 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716383.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 10:42:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716383.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	944,689
Mapped reads	828,123 / 87.66%
Unmapped reads	116,566 / 12.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,117 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	14,590 / 1.54%
Duplication rate	1.26%
Clipped reads	829,378 / 87.79%

2.2. ACGT Content

Number/percentage of A's	12,057,905 / 25.45%
Number/percentage of C's	9,570,326 / 20.2%
Number/percentage of T's	14,566,886 / 30.75%
Number/percentage of G's	11,184,057 / 23.61%
Number/percentage of N's	347 / 0%
GC Percentage	43.8%

2.3. Coverage

Mean	0.0153

Standard Deviation	0.1559
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2.4. Mapping Quality

Mean Mapping Quality	42.47
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2.5. Mismatches and indels

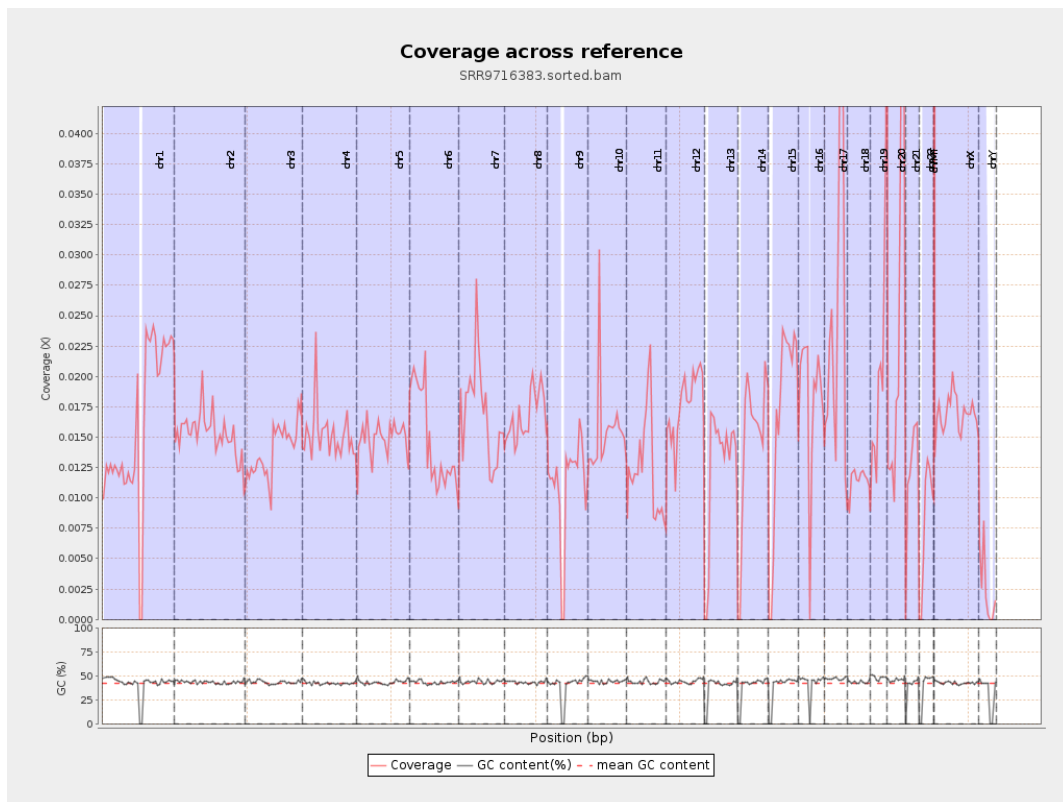
General error rate	0.54%
Mismatches	248,885
Insertions	3,633
Mapped reads with at least one insertion	0.44%
Deletions	9,096
Mapped reads with at least one deletion	1.09%
Homopolymer indels	39.35%

2.6. Chromosome stats

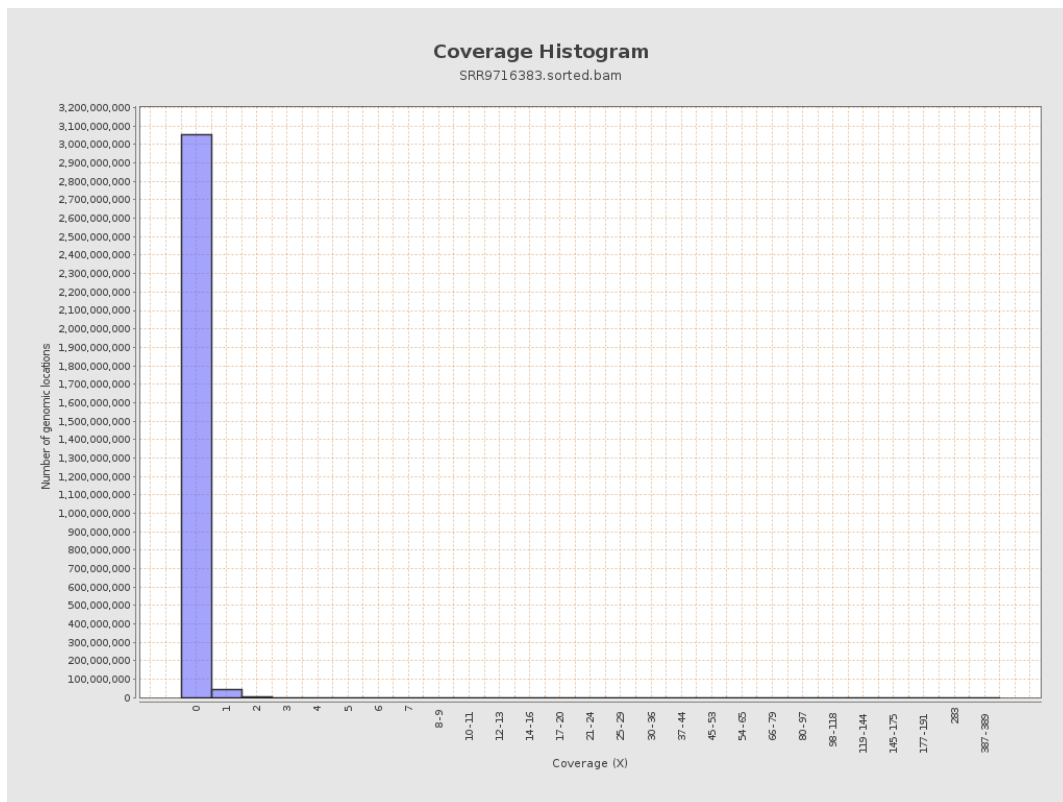
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	3972786	0.0159	0.1895
chr2	243199373	3716552	0.0153	0.2048
chr3	198022430	2747802	0.0139	0.1245
chr4	191154276	2902858	0.0152	0.1357
chr5	180915260	2715980	0.015	0.1279
chr6	171115067	2520055	0.0147	0.1387
chr7	159138663	2709909	0.017	0.2099

chr8	146364022	2454038	0.0168	0.1586
chr9	141213431	1568861	0.0111	0.1235
chr10	135534747	2102009	0.0155	0.1859
chr11	135006516	1687840	0.0125	0.1352
chr12	133851895	2363749	0.0177	0.1392
chr13	115169878	1439522	0.0125	0.1175
chr14	107349540	1580727	0.0147	0.1302
chr15	102531392	1734413	0.0169	0.1371
chr16	90354753	1615791	0.0179	0.1456
chr17	81195210	2086378	0.0257	0.1735
chr18	78077248	888982	0.0114	0.1761
chr19	59128983	1240193	0.021	0.1877
chr20	63025520	1541531	0.0245	0.1682
chr21	48129895	591884	0.0123	0.121
chr22	51304566	423688	0.0083	0.0952
chrMT	16571	12906	0.7788	0.9795
chrX	155270560	2632665	0.017	0.1417
chrY	59373566	142757	0.0024	0.0774

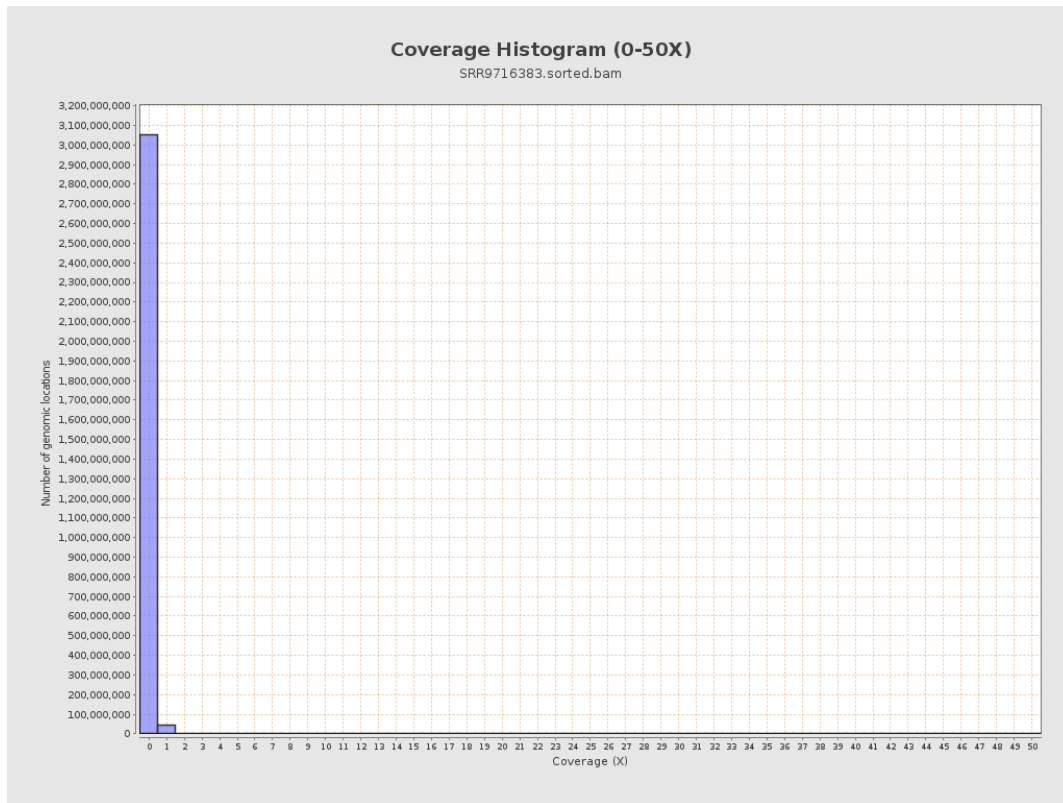
3. Results : Coverage across reference



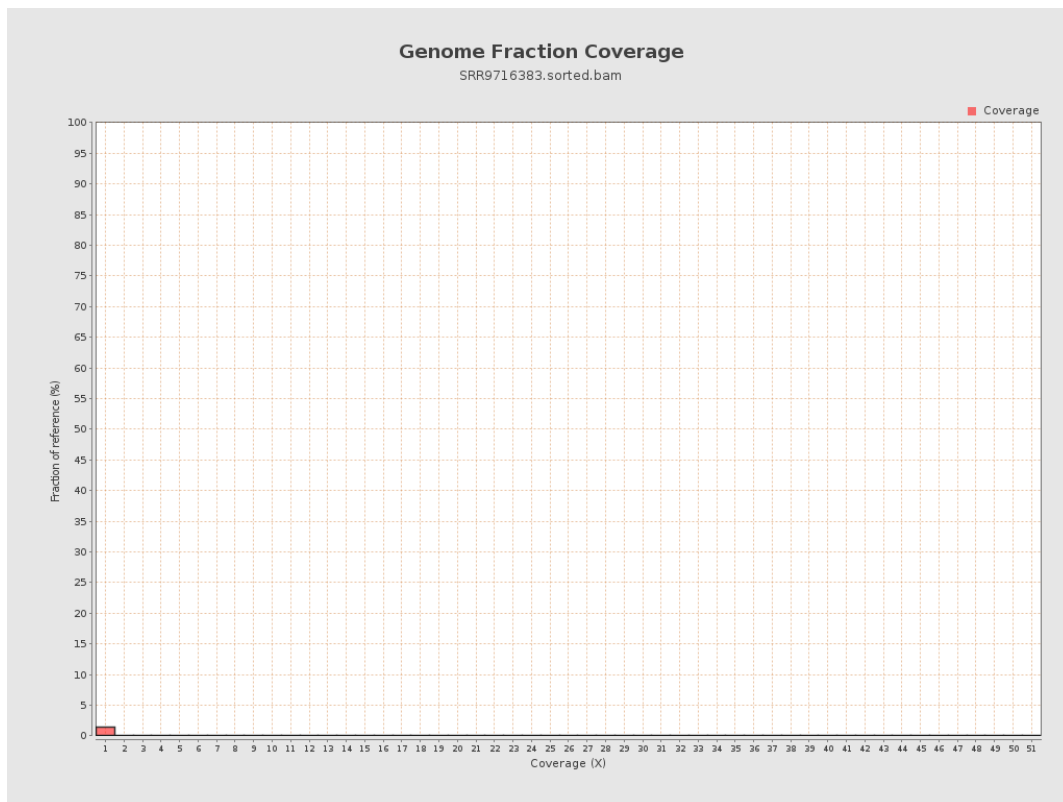
4. Results : Coverage Histogram



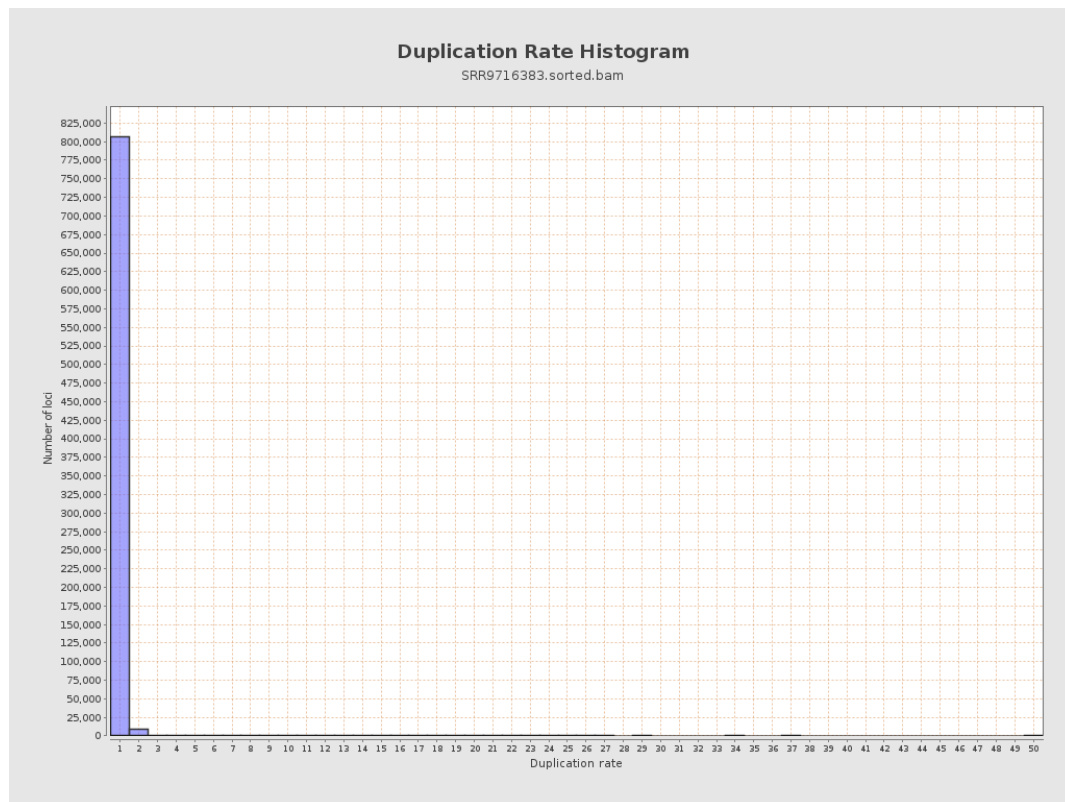
5. Results : Coverage Histogram (0-50X)



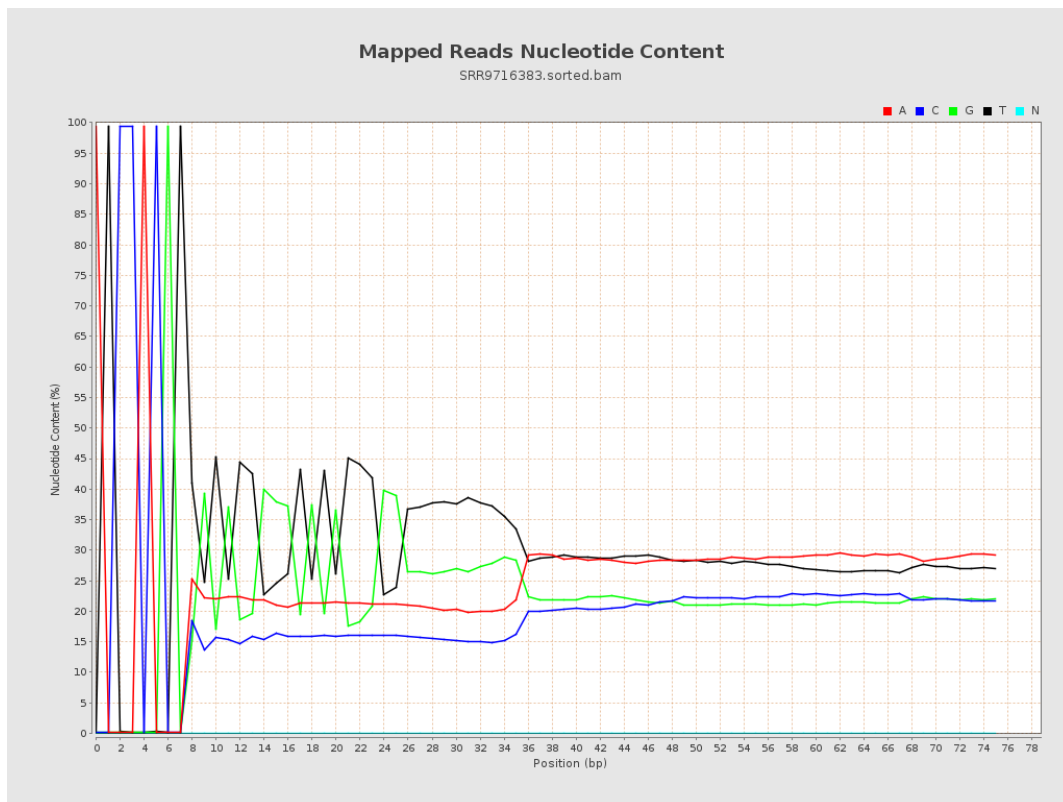
6. Results : Genome Fraction Coverage



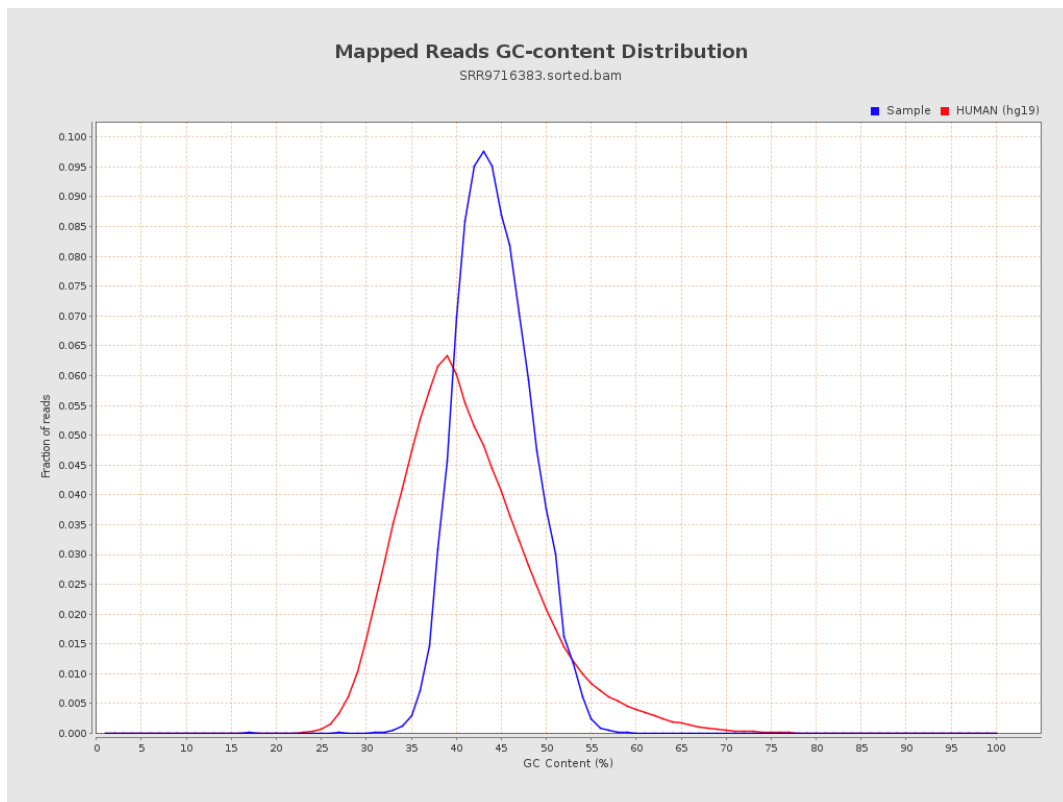
7. Results : Duplication Rate Histogram



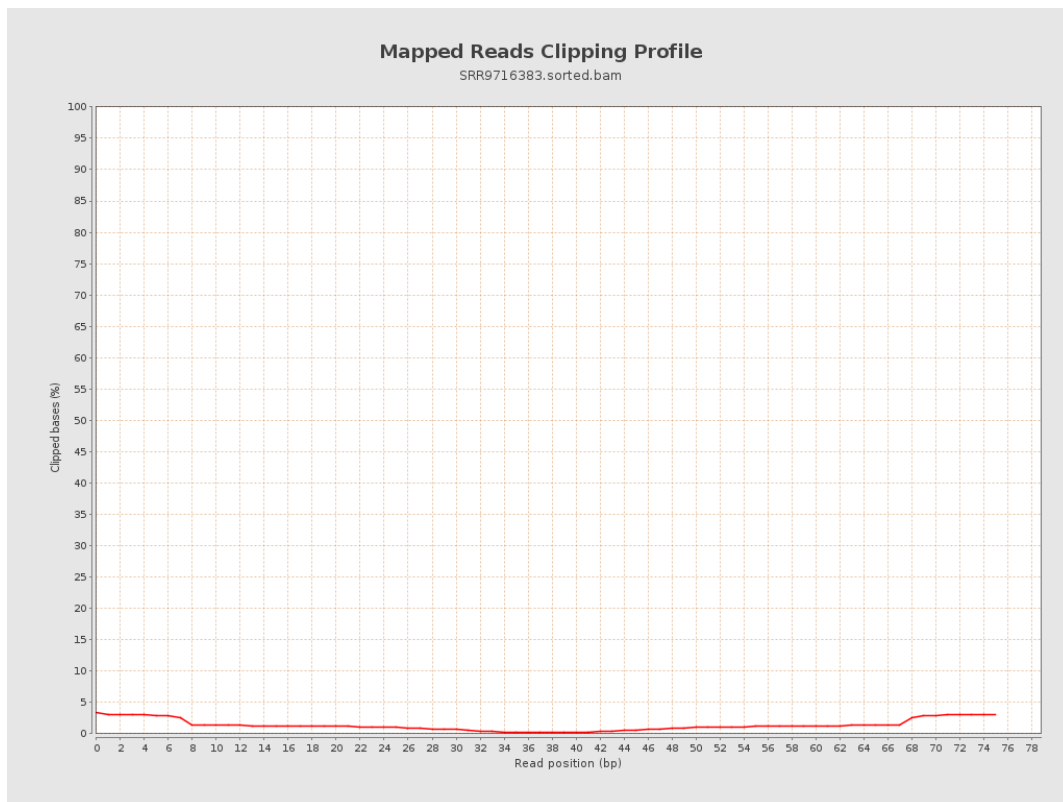
8. Results : Mapped Reads Nucleotide Content



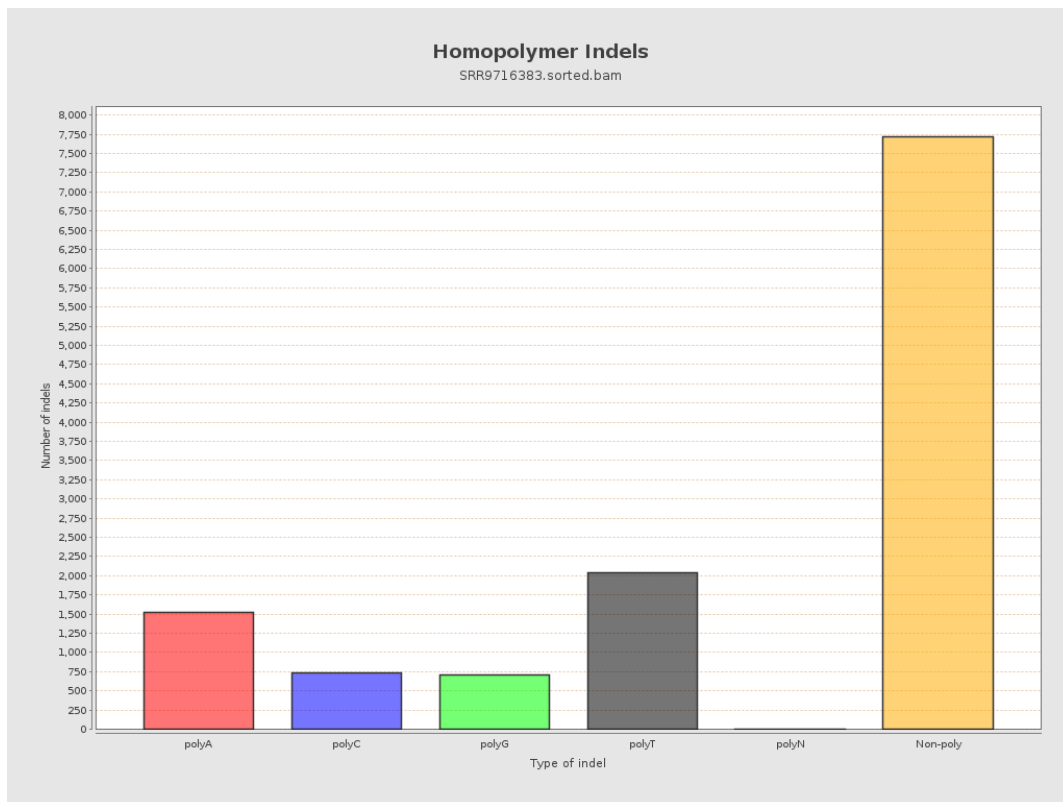
9. Results : Mapped Reads GC-content Distribution



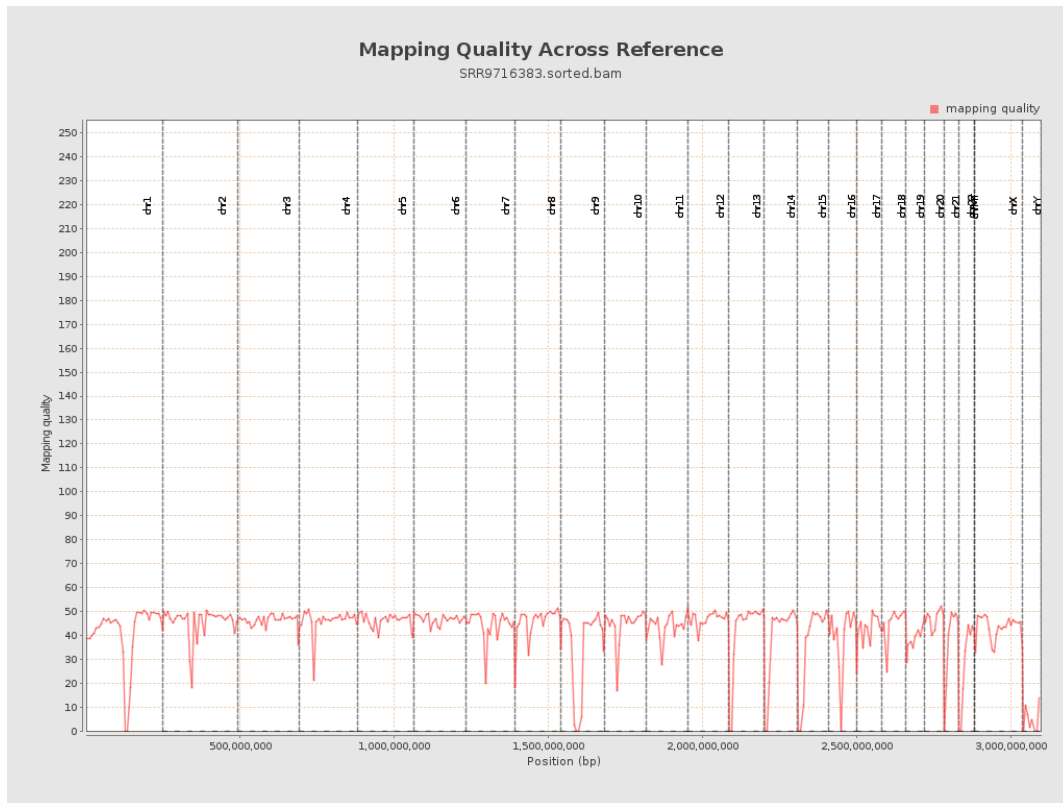
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

