

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 10:36:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716381.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_SRR9716381 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716381.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 10:36:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716381.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,017,064
Mapped reads	930,502 / 91.49%
Unmapped reads	86,562 / 8.51%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,883 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	19,037 / 1.87%
Duplication rate	1.59%
Clipped reads	931,955 / 91.63%

2.2. ACGT Content

Number/percentage of A's	12,730,798 / 23.81%
Number/percentage of C's	9,875,106 / 18.47%
Number/percentage of T's	17,193,407 / 32.16%
Number/percentage of G's	13,666,300 / 25.56%
Number/percentage of N's	1,154 / 0%
GC Percentage	44.03%

2.3. Coverage

Mean	0.0173

Standard Deviation	0.1614
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2.4. Mapping Quality

Mean Mapping Quality	44.5
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2.5. Mismatches and indels

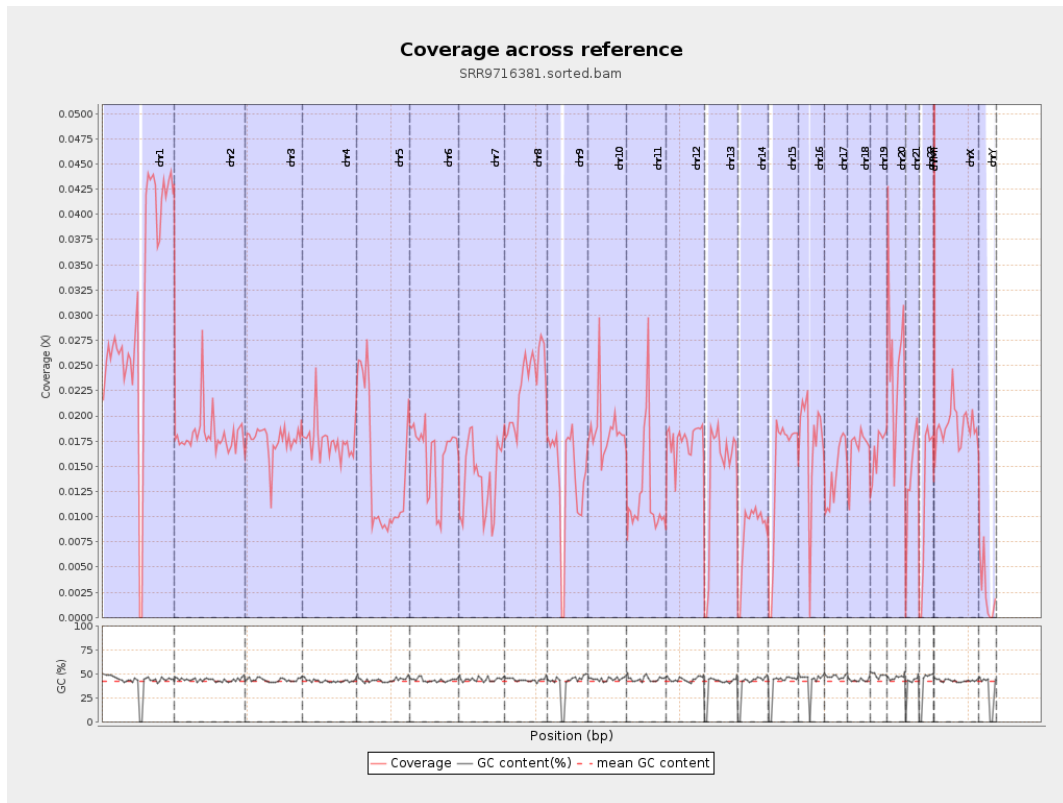
General error rate	0.5%
Mismatches	261,019
Insertions	3,323
Mapped reads with at least one insertion	0.35%
Deletions	8,224
Mapped reads with at least one deletion	0.88%
Homopolymer indels	39.36%

2.6. Chromosome stats

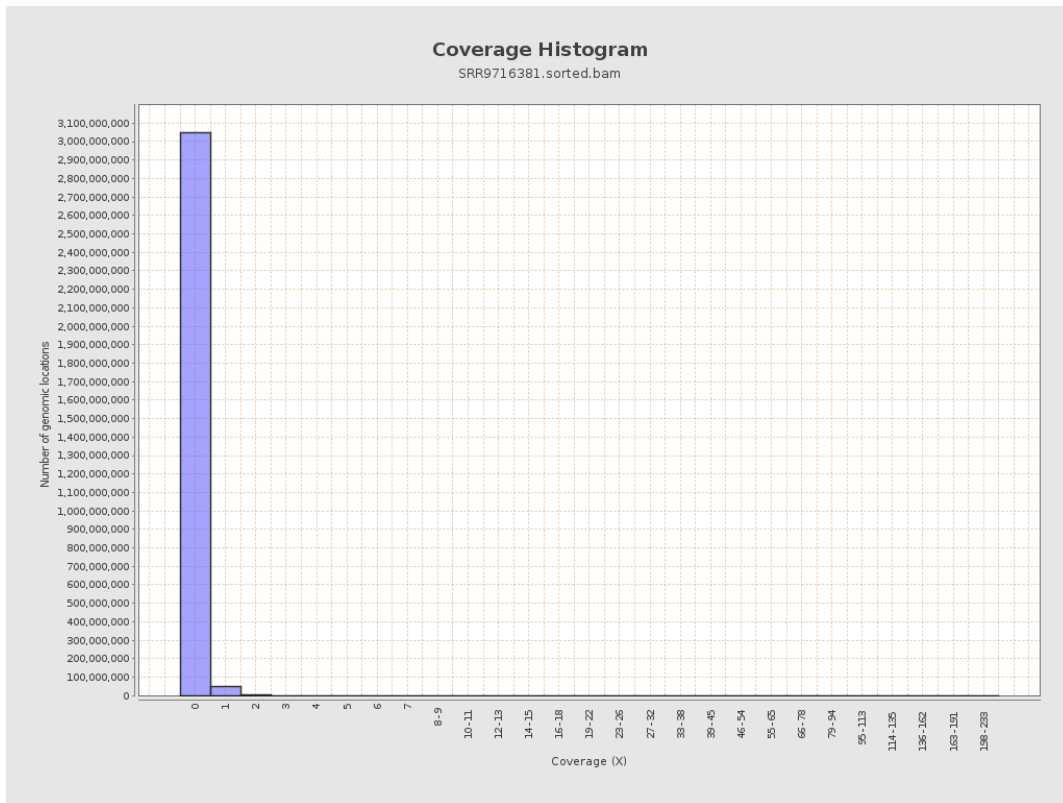
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7729707	0.031	0.259
chr2	243199373	4425362	0.0182	0.172
chr3	198022430	3473597	0.0175	0.1399
chr4	191154276	3350609	0.0175	0.1439
chr5	180915260	2603522	0.0144	0.1273
chr6	171115067	2759338	0.0161	0.1388
chr7	159138663	2204048	0.0138	0.1402

chr8	146364022	3354928	0.0229	0.1756
chr9	141213431	1927856	0.0137	0.1533
chr10	135534747	2518825	0.0186	0.177
chr11	135006516	1680415	0.0124	0.142
chr12	133851895	2358021	0.0176	0.1409
chr13	115169878	1633476	0.0142	0.125
chr14	107349540	899904	0.0084	0.1025
chr15	102531392	1514333	0.0148	0.1283
chr16	90354753	1561912	0.0173	0.1462
chr17	81195210	1161187	0.0143	0.1281
chr18	78077248	1298517	0.0166	0.2383
chr19	59128983	981747	0.0166	0.1962
chr20	63025520	1605411	0.0255	0.1707
chr21	48129895	687797	0.0143	0.1321
chr22	51304566	631294	0.0123	0.117
chrMT	16571	3714	0.2241	0.5221
chrX	155270560	2963072	0.0191	0.1557
chrY	59373566	152117	0.0026	0.0676

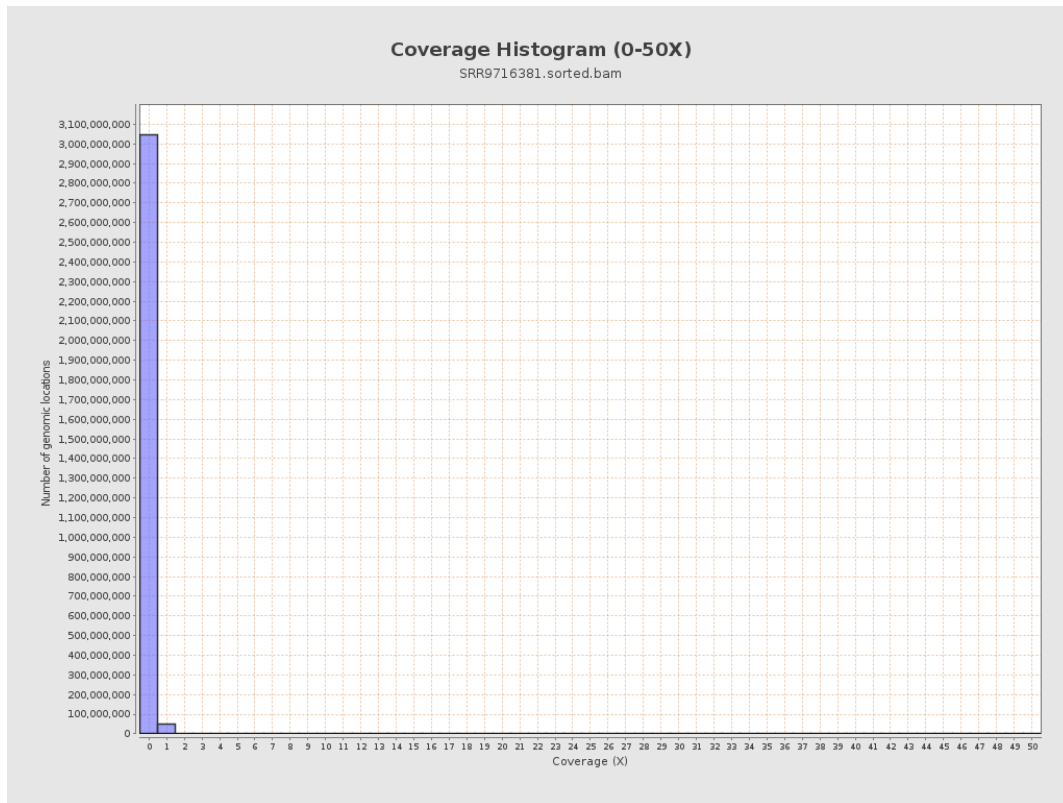
3. Results : Coverage across reference



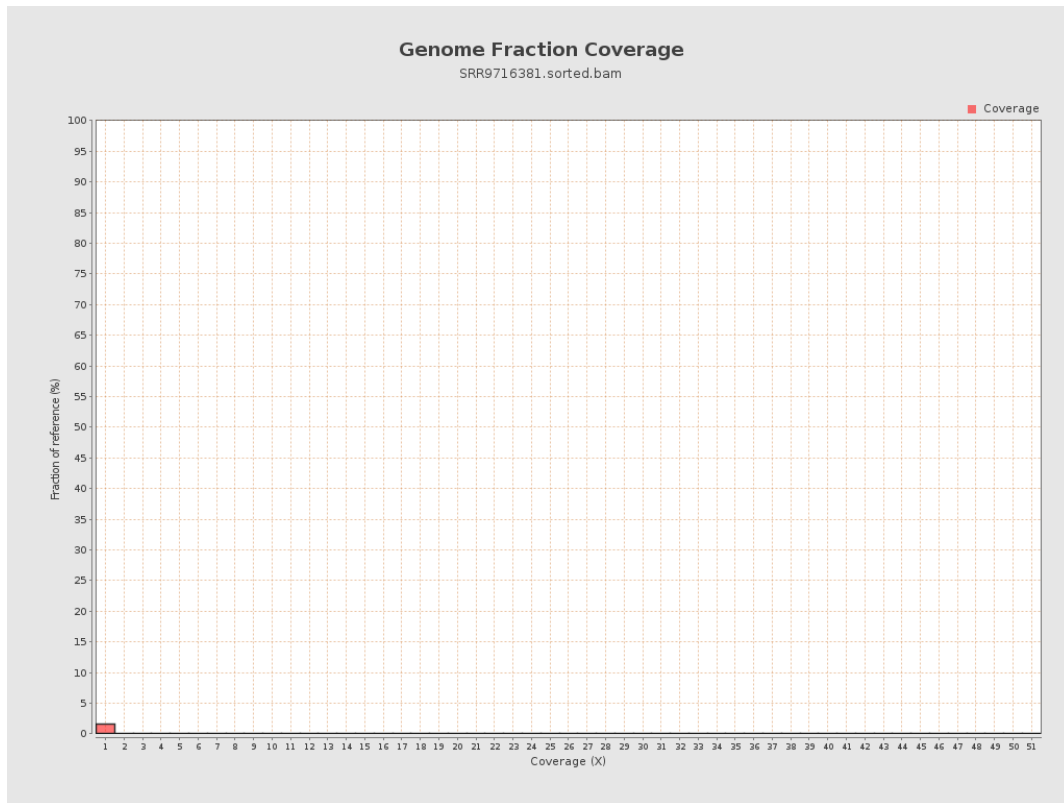
4. Results : Coverage Histogram



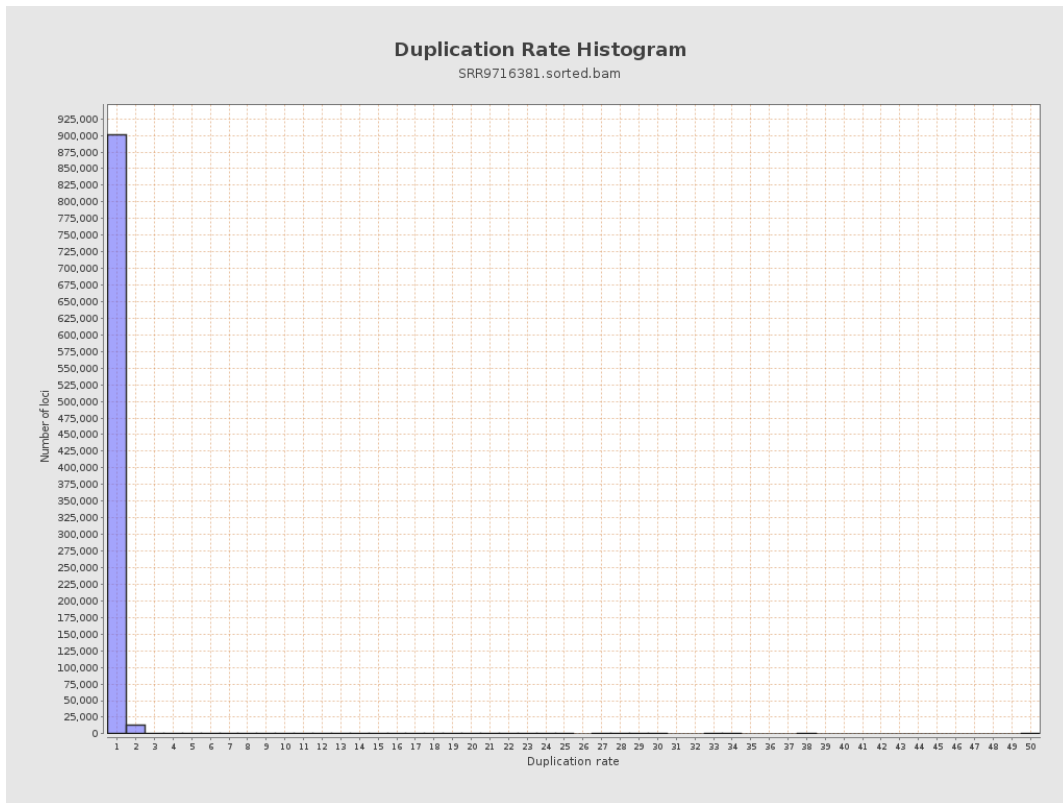
5. Results : Coverage Histogram (0-50X)



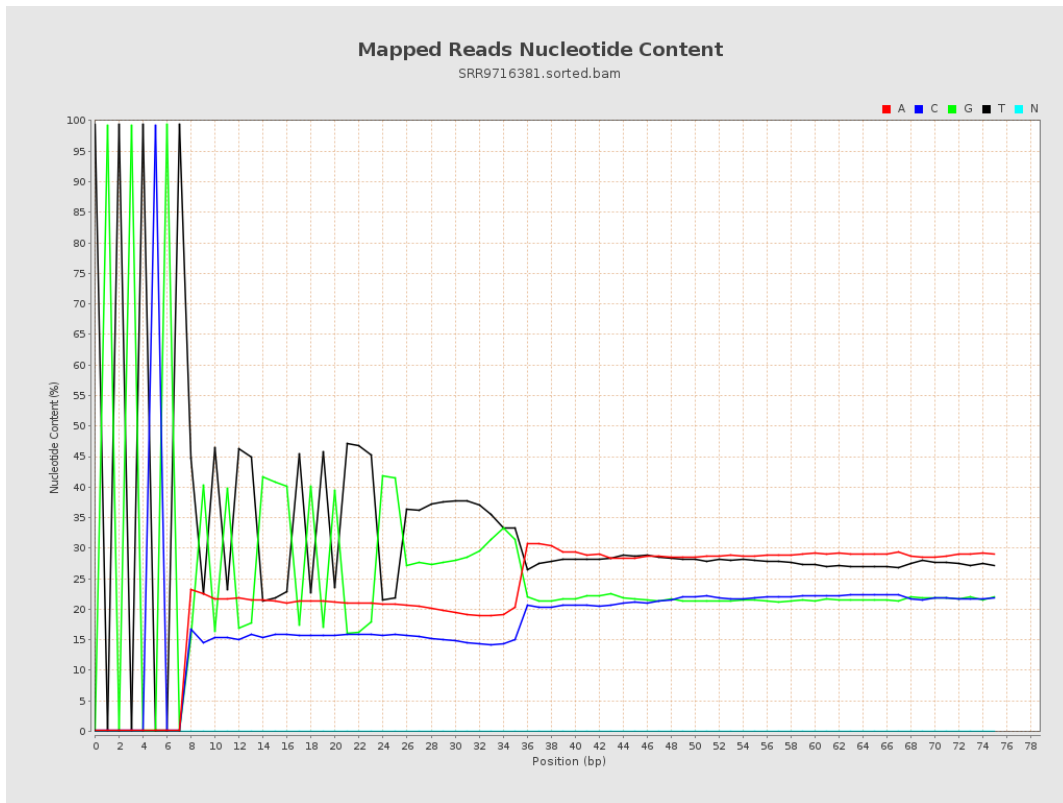
6. Results : Genome Fraction Coverage



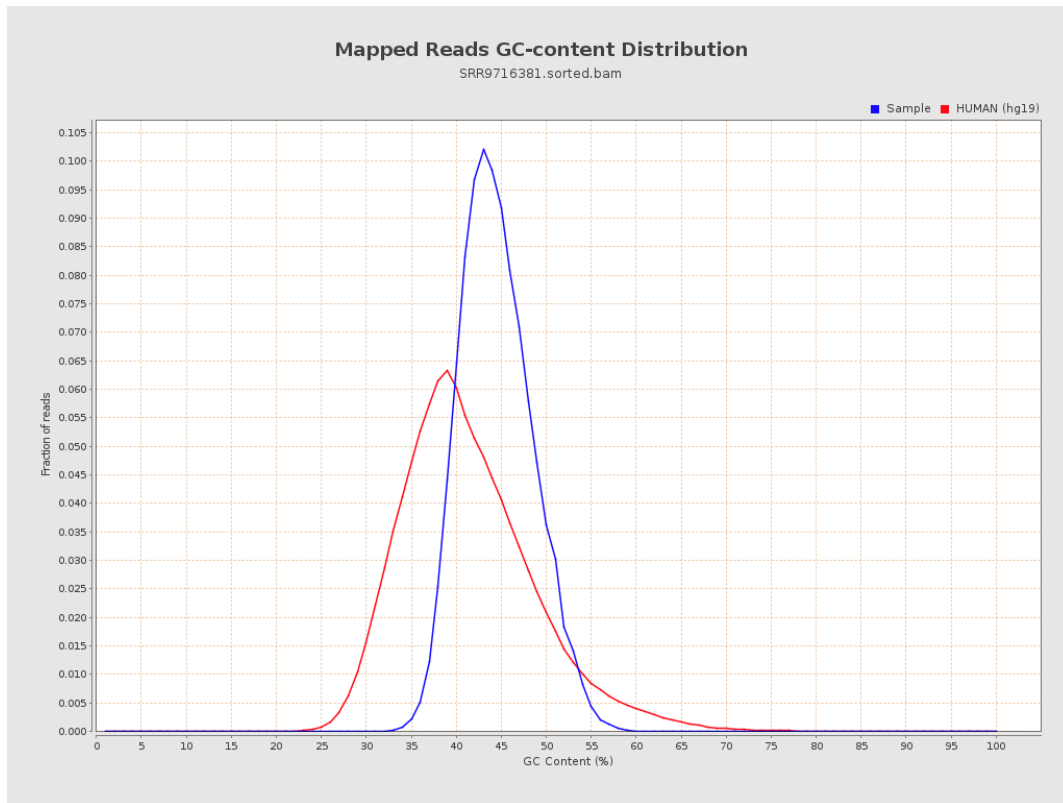
7. Results : Duplication Rate Histogram



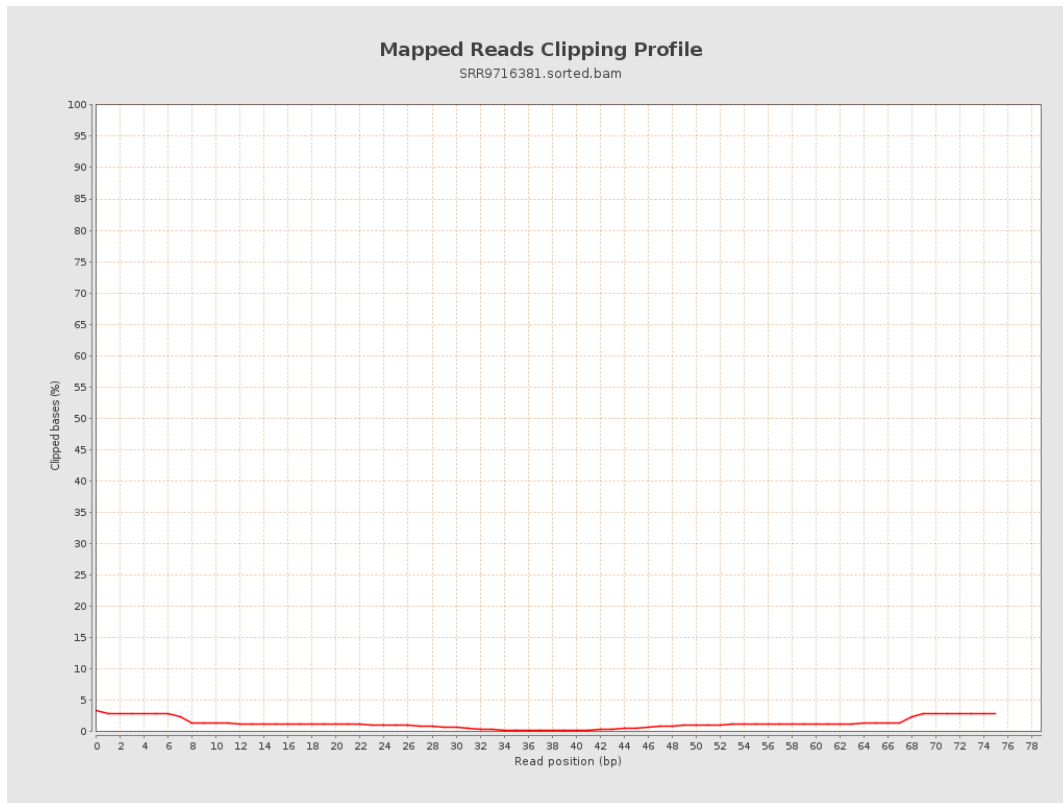
8. Results : Mapped Reads Nucleotide Content



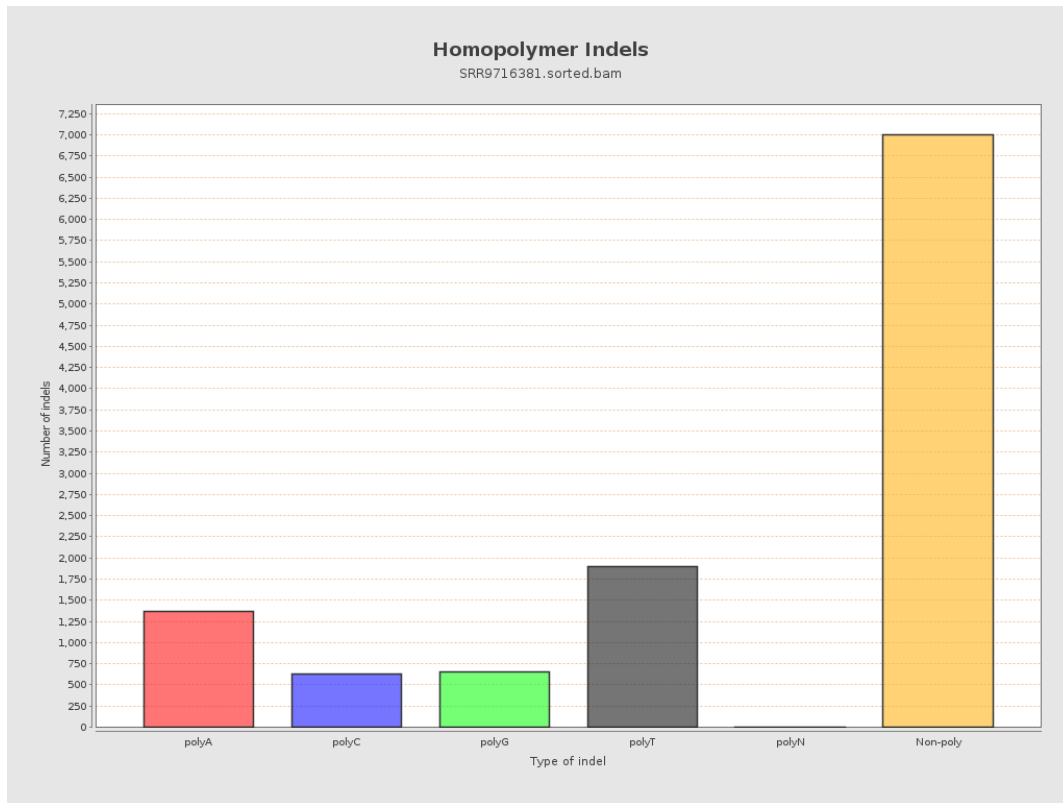
9. Results : Mapped Reads GC-content Distribution



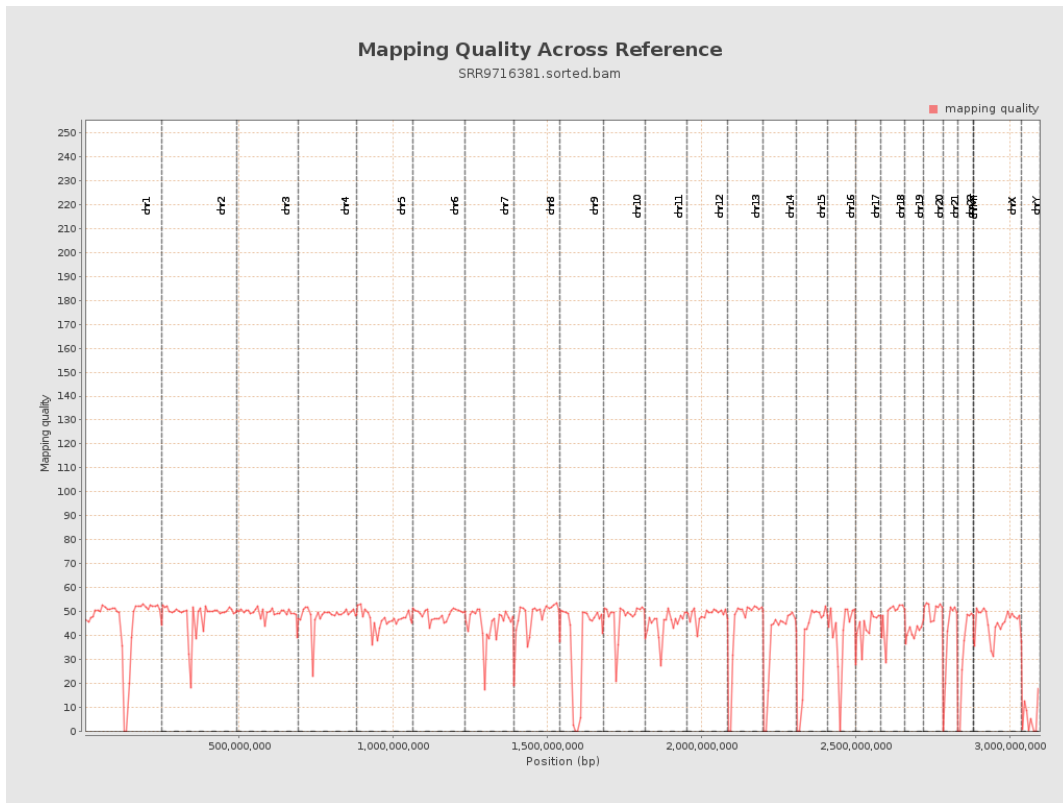
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

