

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 14:22:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716452.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_SRR9716452 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716452.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 14:22:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716452.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	603,874
Mapped reads	486,395 / 80.55%
Unmapped reads	117,479 / 19.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,989 / 1.16%
Read min/max/mean length	30 / 101 / 101.42
Duplicated reads (estimated)	12,600 / 2.09%
Duplication rate	1.66%
Clipped reads	492,611 / 81.58%

2.2. ACGT Content

Number/percentage of A's	9,724,248 / 25.58%
Number/percentage of C's	6,975,879 / 18.35%
Number/percentage of T's	11,765,039 / 30.95%
Number/percentage of G's	9,548,386 / 25.12%
Number/percentage of N's	2,328 / 0.01%
GC Percentage	43.47%

2.3. Coverage

Mean	0.0123

Standard Deviation	0.1629
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2.4. Mapping Quality

Mean Mapping Quality	44.62
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2.5. Mismatches and indels

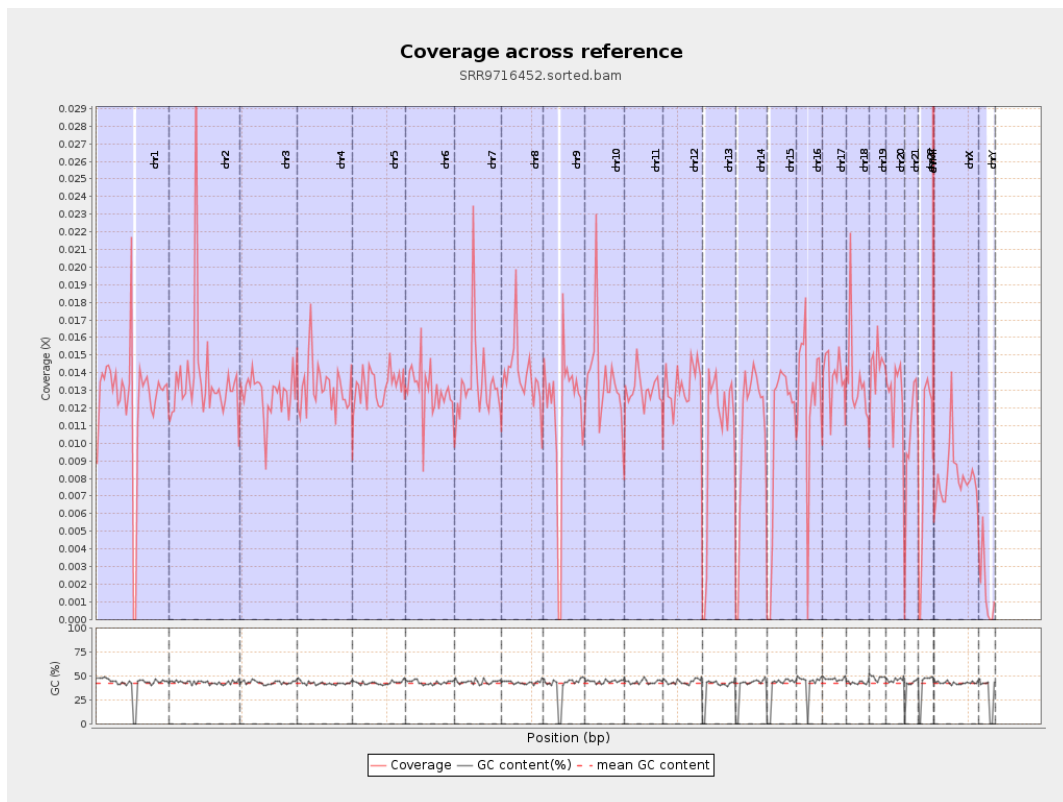
General error rate	0.86%
Mismatches	318,188
Insertions	3,471
Mapped reads with at least one insertion	0.7%
Deletions	9,347
Mapped reads with at least one deletion	1.89%
Homopolymer indels	42.99%

2.6. Chromosome stats

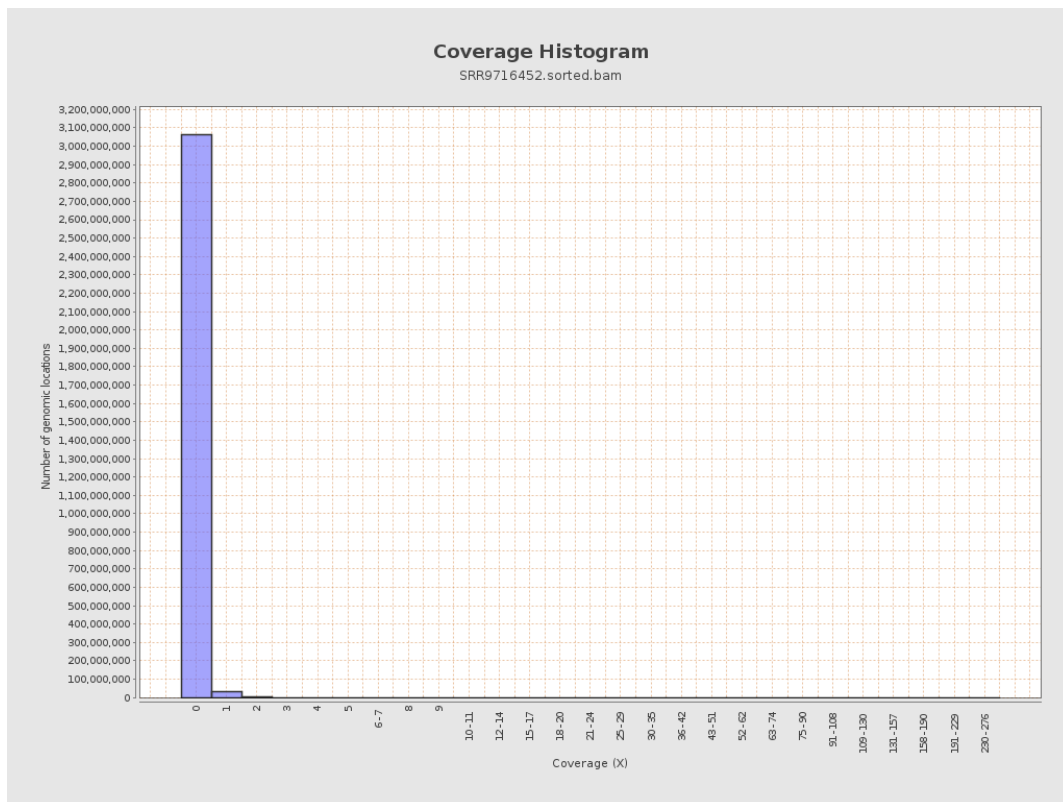
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	3103990	0.0125	0.2283
chr2	243199373	3316620	0.0136	0.2304
chr3	198022430	2532620	0.0128	0.118
chr4	191154276	2520537	0.0132	0.1257
chr5	180915260	2396044	0.0132	0.1215
chr6	171115067	2220022	0.013	0.1287
chr7	159138663	2146170	0.0135	0.2011

chr8	146364022	2019527	0.0138	0.1998
chr9	141213431	1652689	0.0117	0.171
chr10	135534747	1846000	0.0136	0.1535
chr11	135006516	1747843	0.0129	0.1625
chr12	133851895	1774857	0.0133	0.1213
chr13	115169878	1202885	0.0104	0.1065
chr14	107349540	1164414	0.0108	0.1268
chr15	102531392	1083145	0.0106	0.1086
chr16	90354753	1160434	0.0128	0.1263
chr17	81195210	1115163	0.0137	0.1273
chr18	78077248	1071155	0.0137	0.2936
chr19	59128983	852569	0.0144	0.1803
chr20	63025520	801223	0.0127	0.1213
chr21	48129895	490222	0.0102	0.1094
chr22	51304566	460079	0.009	0.0997
chrMT	16571	4803	0.2898	0.5708
chrX	155270560	1256642	0.0081	0.111
chrY	59373566	92577	0.0016	0.061

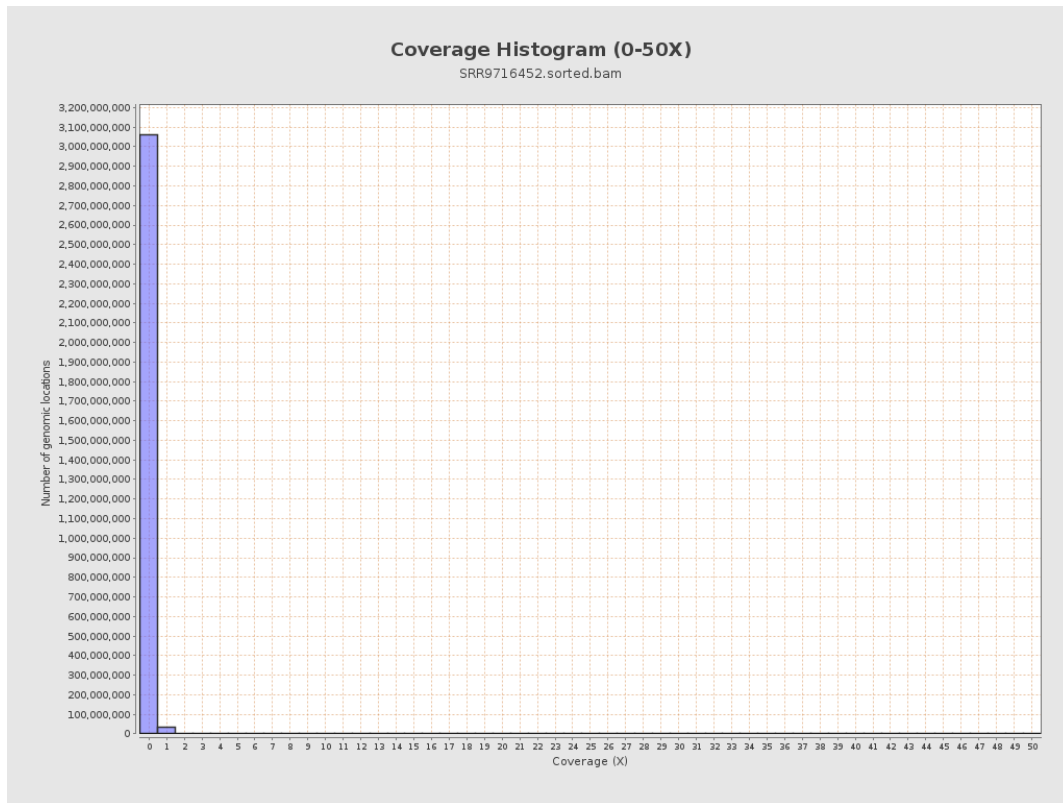
3. Results : Coverage across reference



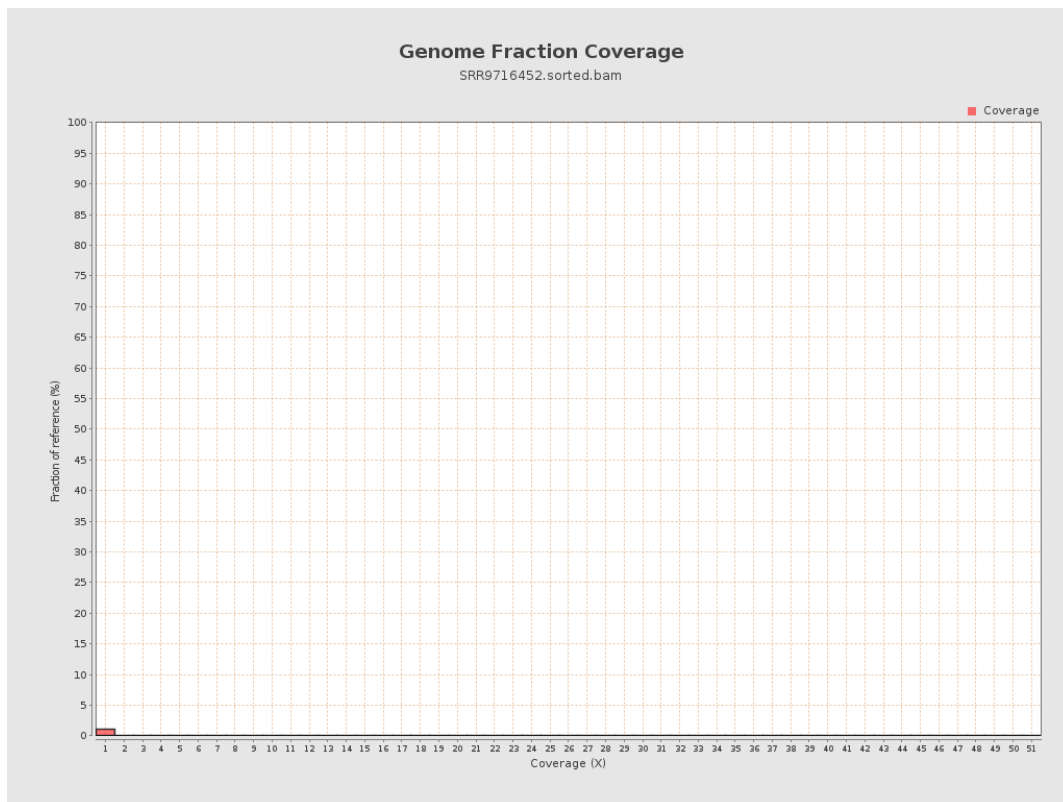
4. Results : Coverage Histogram



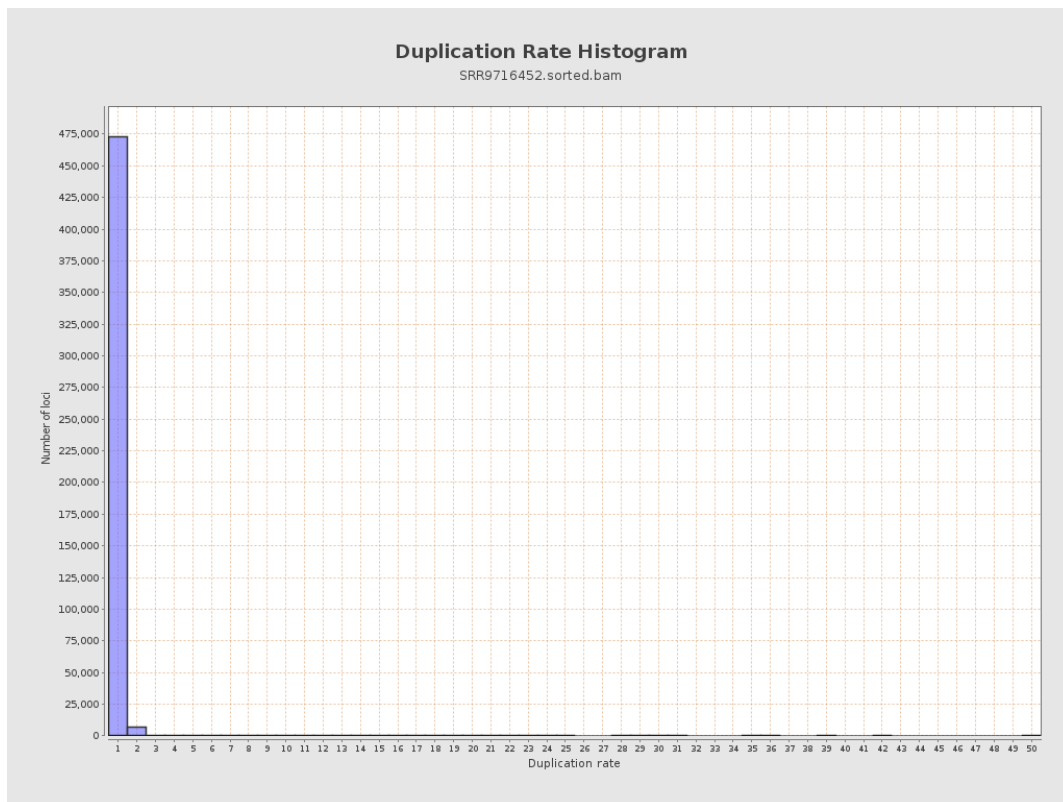
5. Results : Coverage Histogram (0-50X)



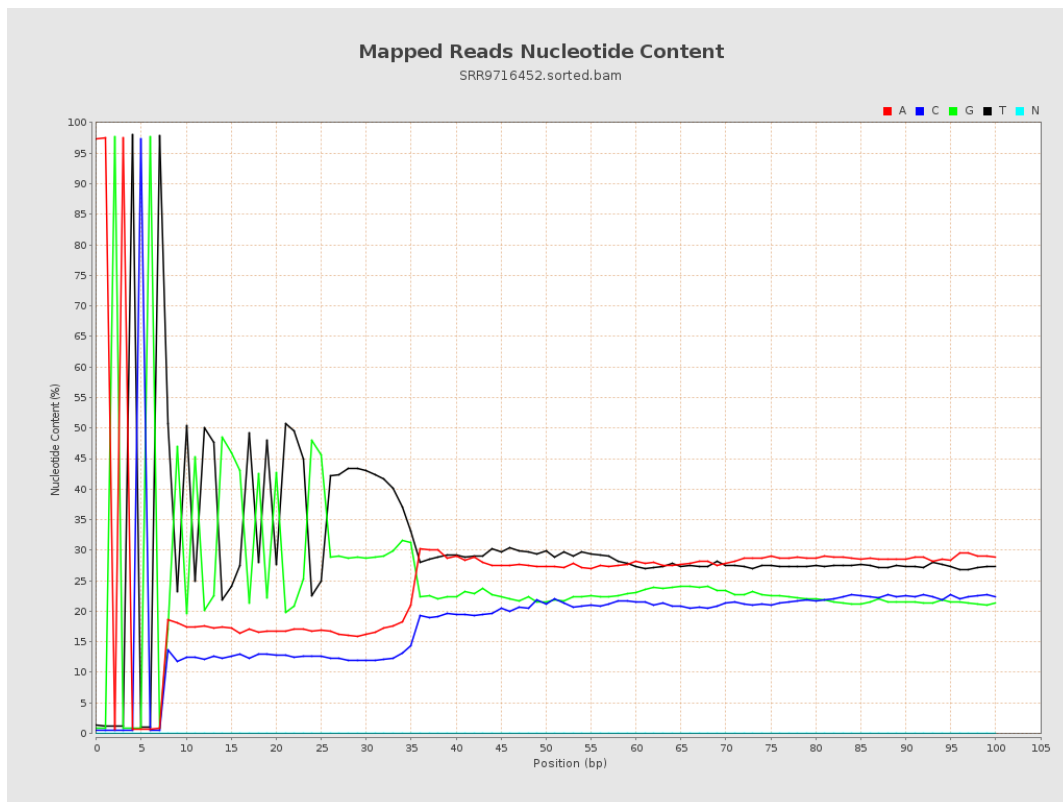
6. Results : Genome Fraction Coverage



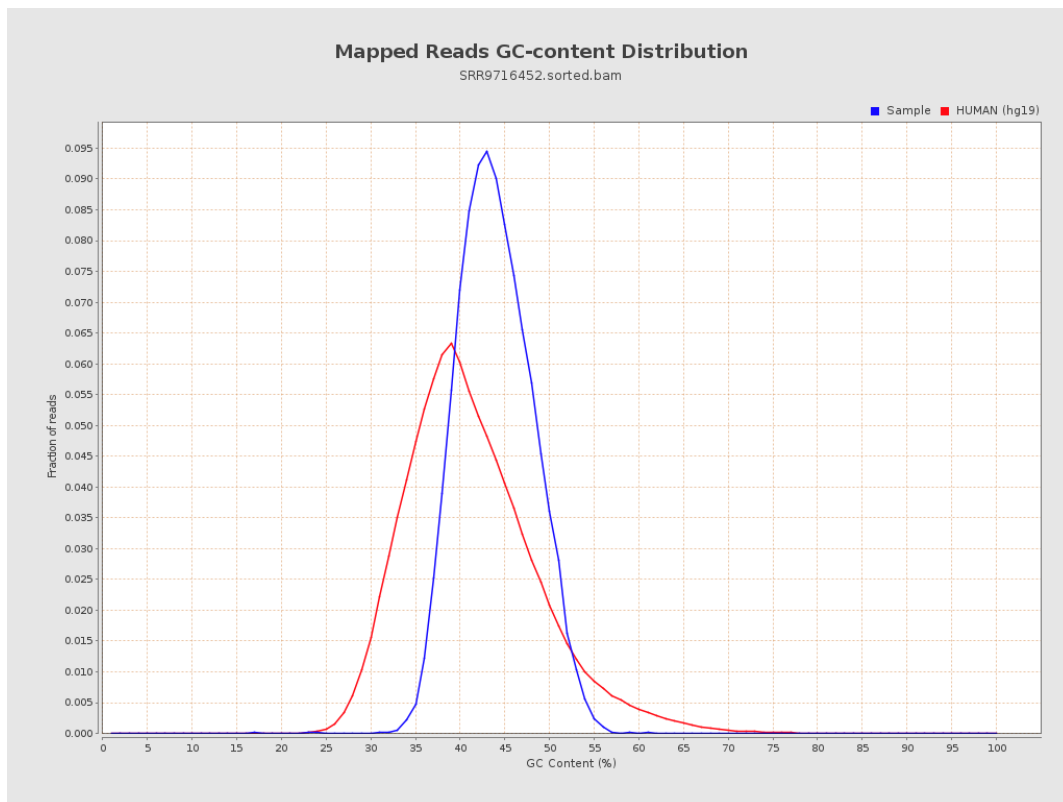
7. Results : Duplication Rate Histogram



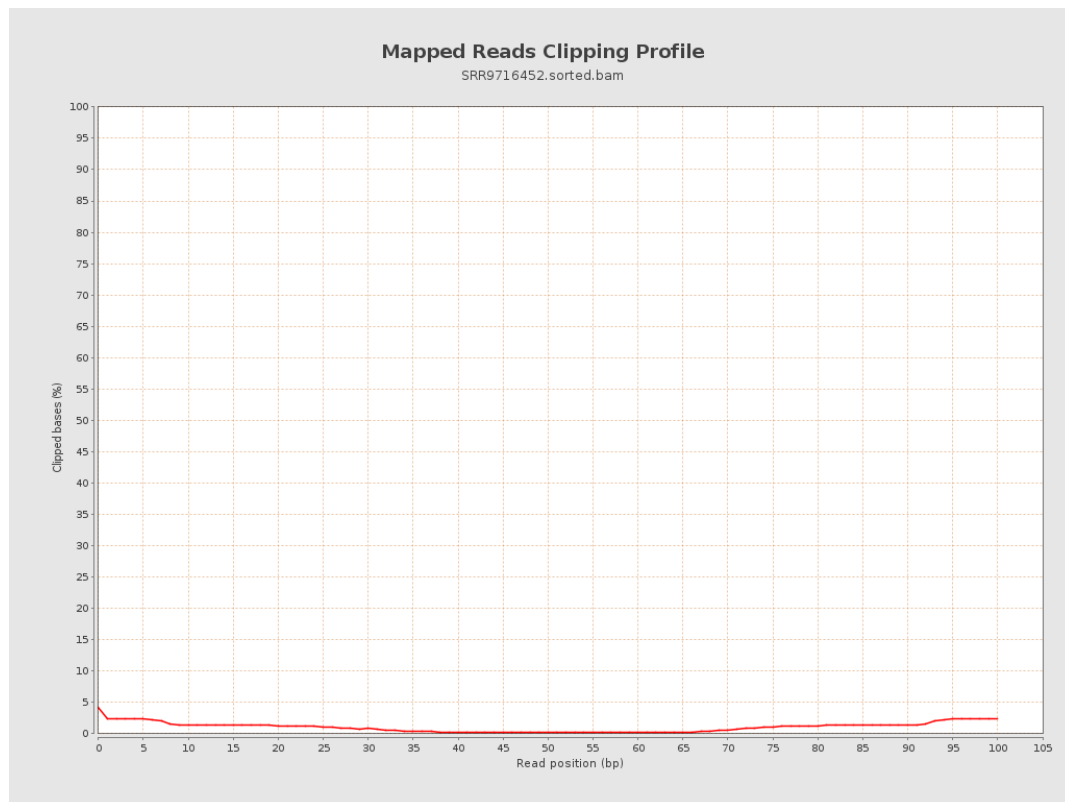
8. Results : Mapped Reads Nucleotide Content



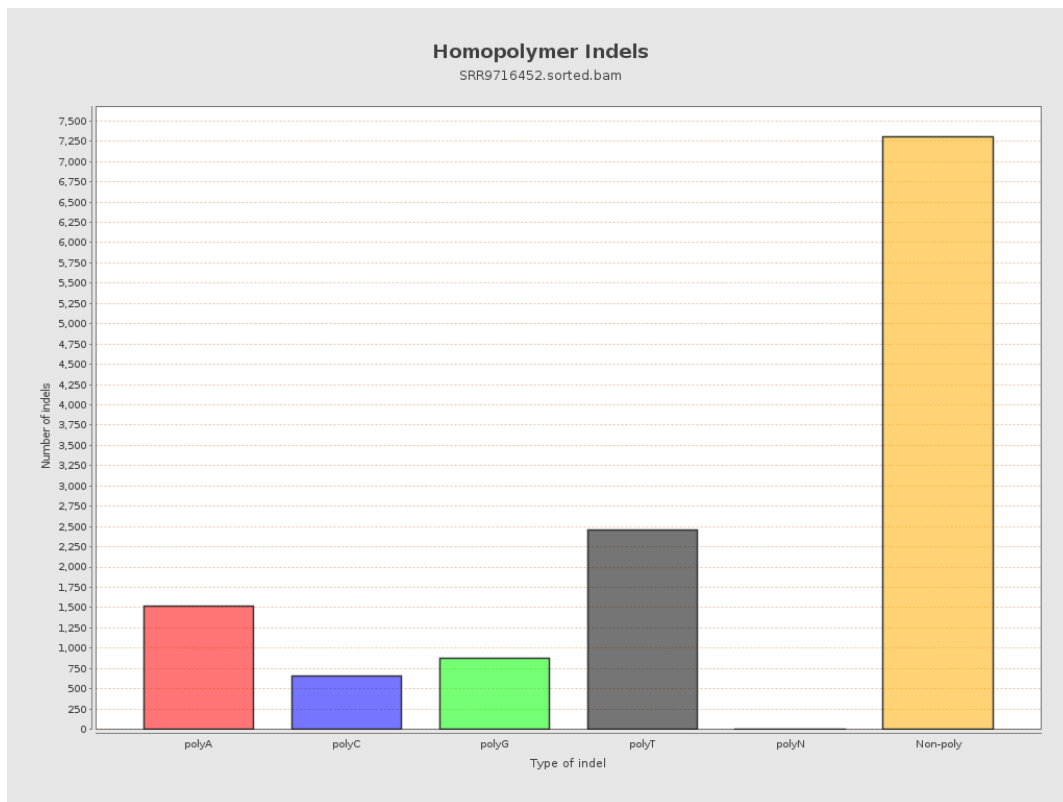
9. Results : Mapped Reads GC-content Distribution



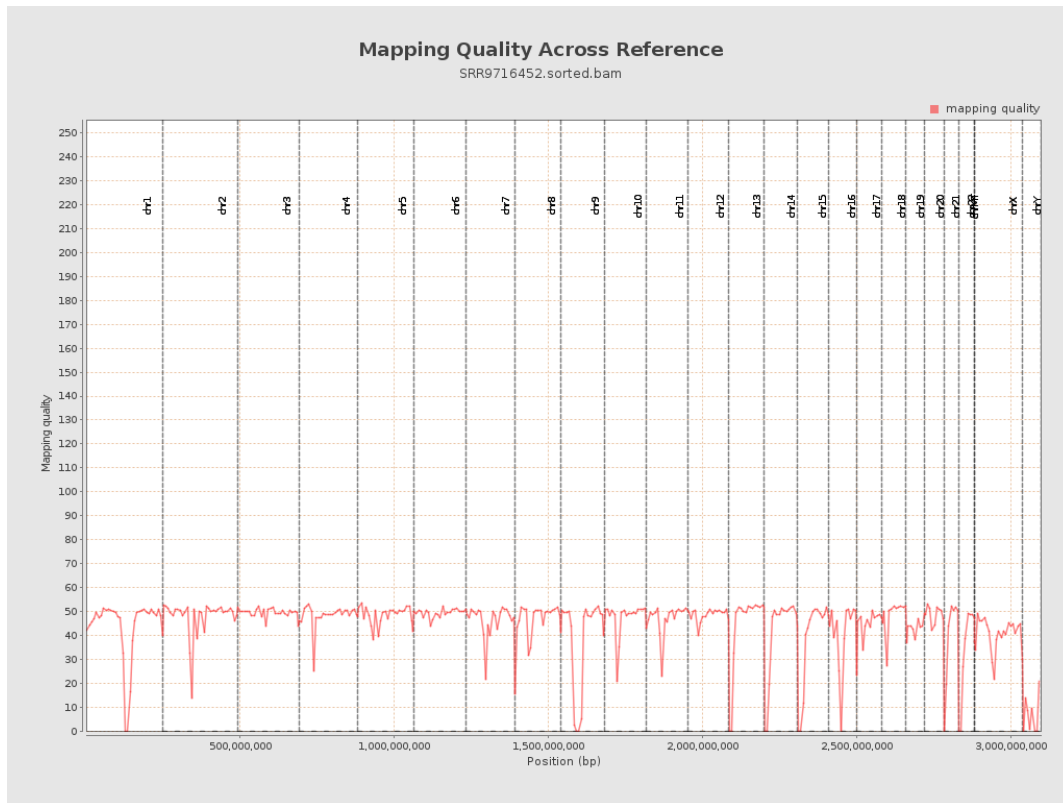
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

