

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 08:45:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716352.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_SRR9716352 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716352.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 08:45:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716352.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	477,225
Mapped reads	444,364 / 93.11%
Unmapped reads	32,861 / 6.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,272 / 1.73%
Read min/max/mean length	30 / 101 / 101.63
Duplicated reads (estimated)	7,761 / 1.63%
Duplication rate	1.24%
Clipped reads	451,327 / 94.57%

2.2. ACGT Content

Number/percentage of A's	9,613,336 / 27.09%
Number/percentage of C's	6,988,389 / 19.69%
Number/percentage of T's	10,470,906 / 29.5%
Number/percentage of G's	8,416,388 / 23.71%
Number/percentage of N's	2,407 / 0.01%
GC Percentage	43.4%

2.3. Coverage

Mean	0.0115

Standard Deviation	0.1414
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2.4. Mapping Quality

Mean Mapping Quality	47.77
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2.5. Mismatches and indels

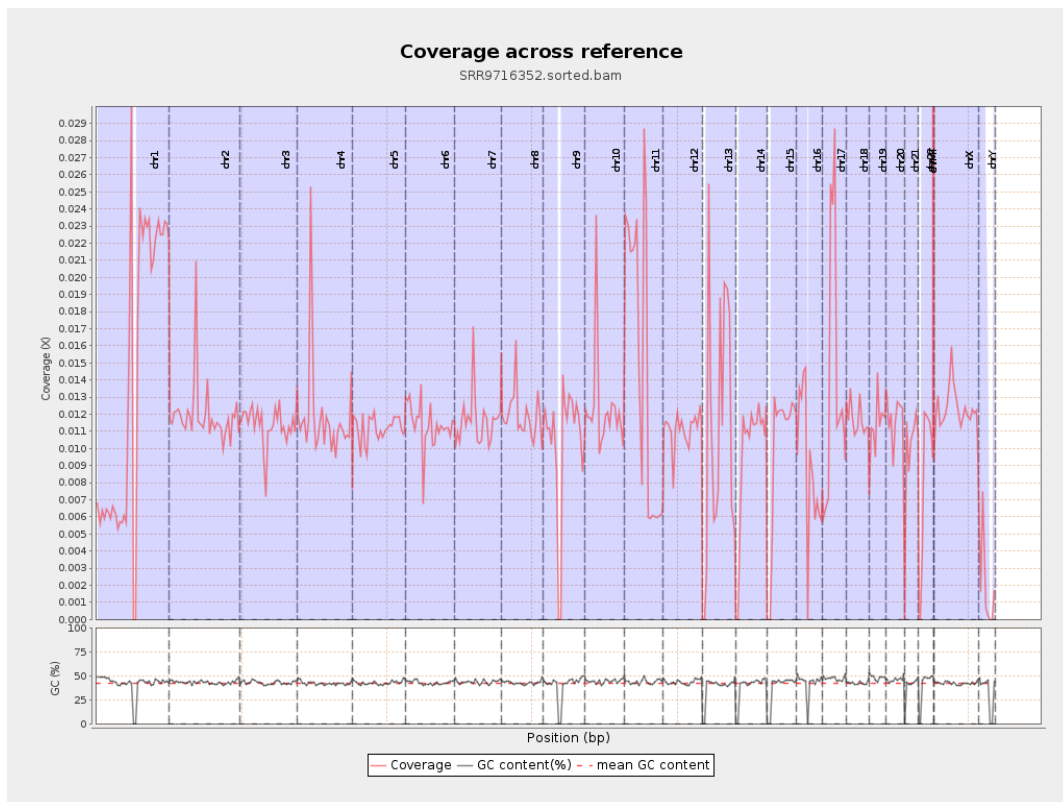
General error rate	0.67%
Mismatches	228,152
Insertions	3,425
Mapped reads with at least one insertion	0.76%
Deletions	9,049
Mapped reads with at least one deletion	2%
Homopolymer indels	42.18%

2.6. Chromosome stats

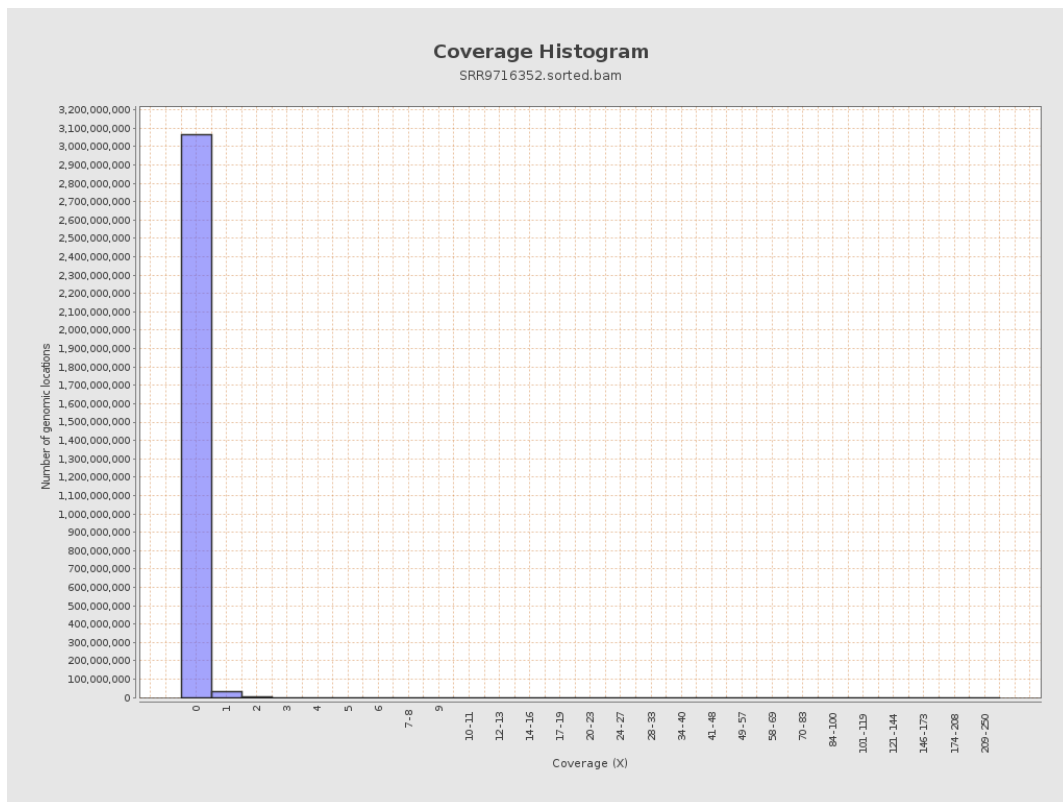
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	3467018	0.0139	0.2528
chr2	243199373	2908265	0.012	0.1432
chr3	198022430	2248007	0.0114	0.1104
chr4	191154276	2241236	0.0117	0.1253
chr5	180915260	2016845	0.0111	0.1093
chr6	171115067	1945635	0.0114	0.1129
chr7	159138663	1846031	0.0116	0.1523

chr8	146364022	1738541	0.0119	0.1494
chr9	141213431	1457145	0.0103	0.1284
chr10	135534747	1659792	0.0122	0.1451
chr11	135006516	2005052	0.0149	0.1496
chr12	133851895	1486991	0.0111	0.1091
chr13	115169878	1244682	0.0108	0.1076
chr14	107349540	1028238	0.0096	0.1042
chr15	102531392	1018278	0.0099	0.1029
chr16	90354753	812335	0.009	0.1023
chr17	81195210	1149941	0.0142	0.131
chr18	78077248	917192	0.0117	0.1712
chr19	59128983	678408	0.0115	0.1735
chr20	63025520	727231	0.0115	0.1138
chr21	48129895	471204	0.0098	0.1096
chr22	51304566	406526	0.0079	0.0922
chrMT	16571	11681	0.7049	0.9562
chrX	155270560	1909769	0.0123	0.1215
chrY	59373566	112545	0.0019	0.0737

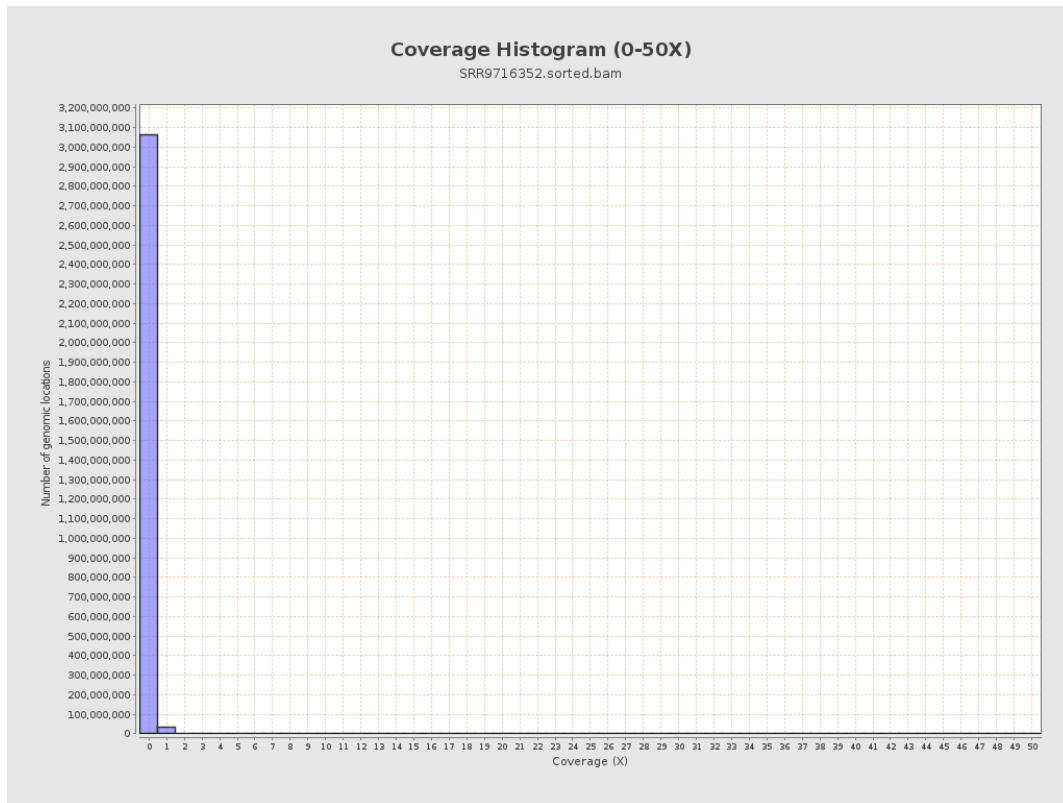
3. Results : Coverage across reference



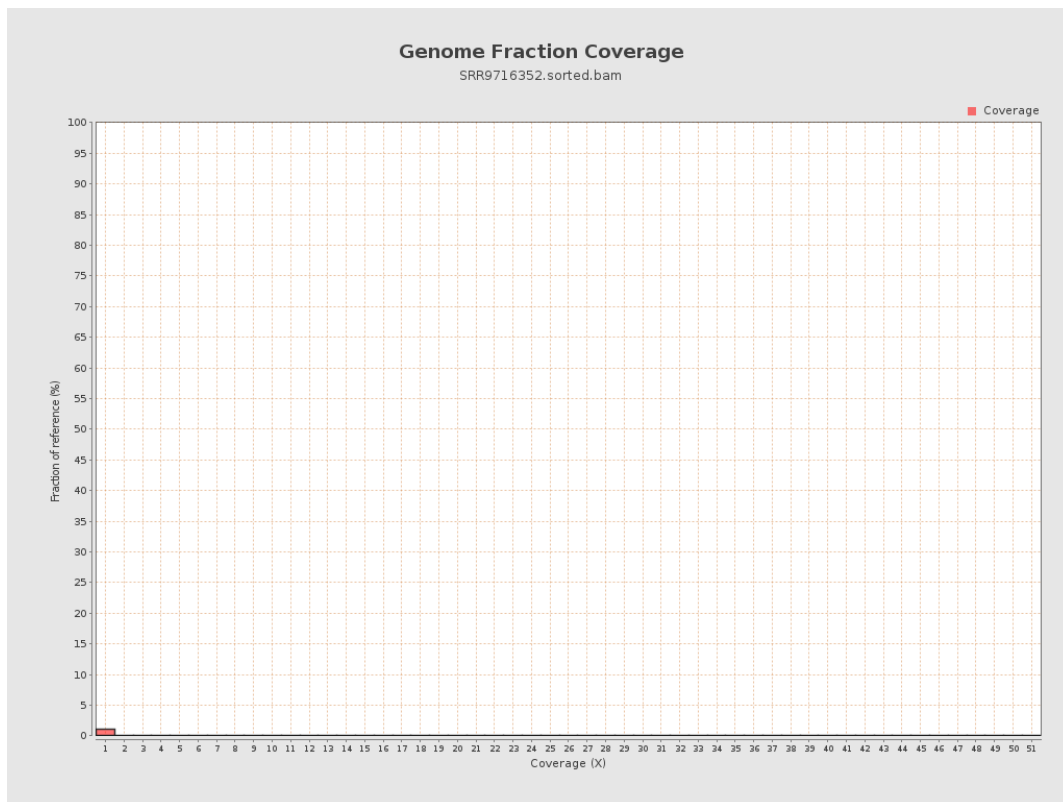
4. Results : Coverage Histogram



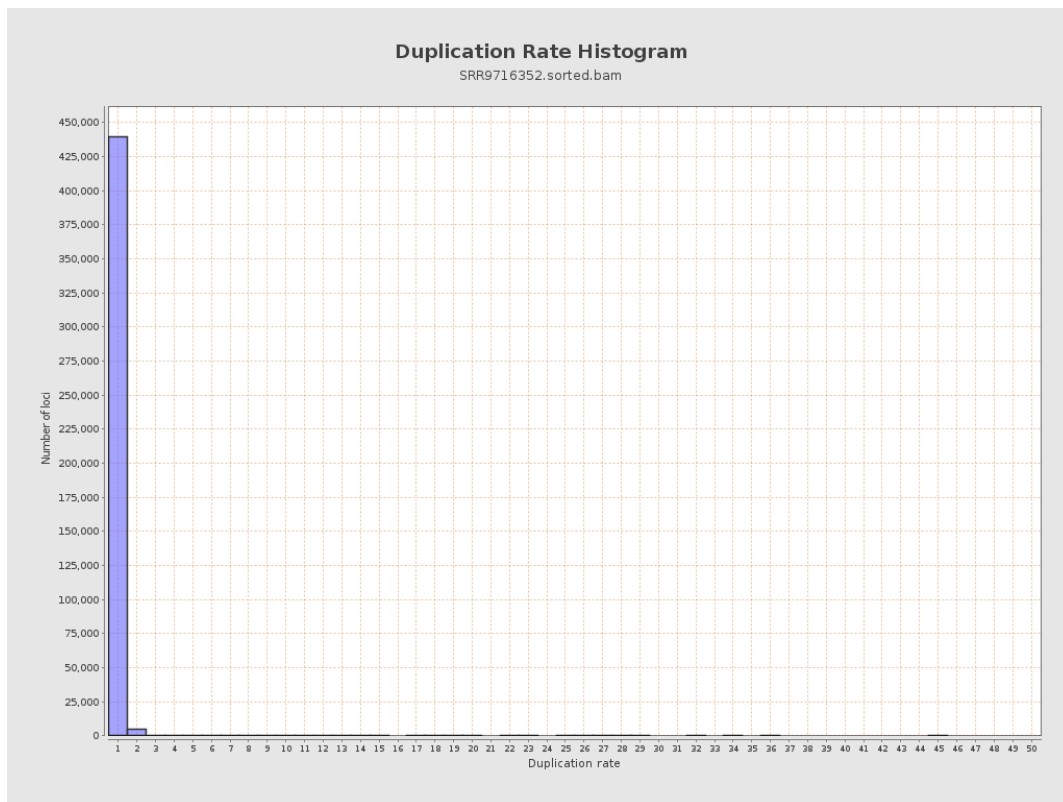
5. Results : Coverage Histogram (0-50X)



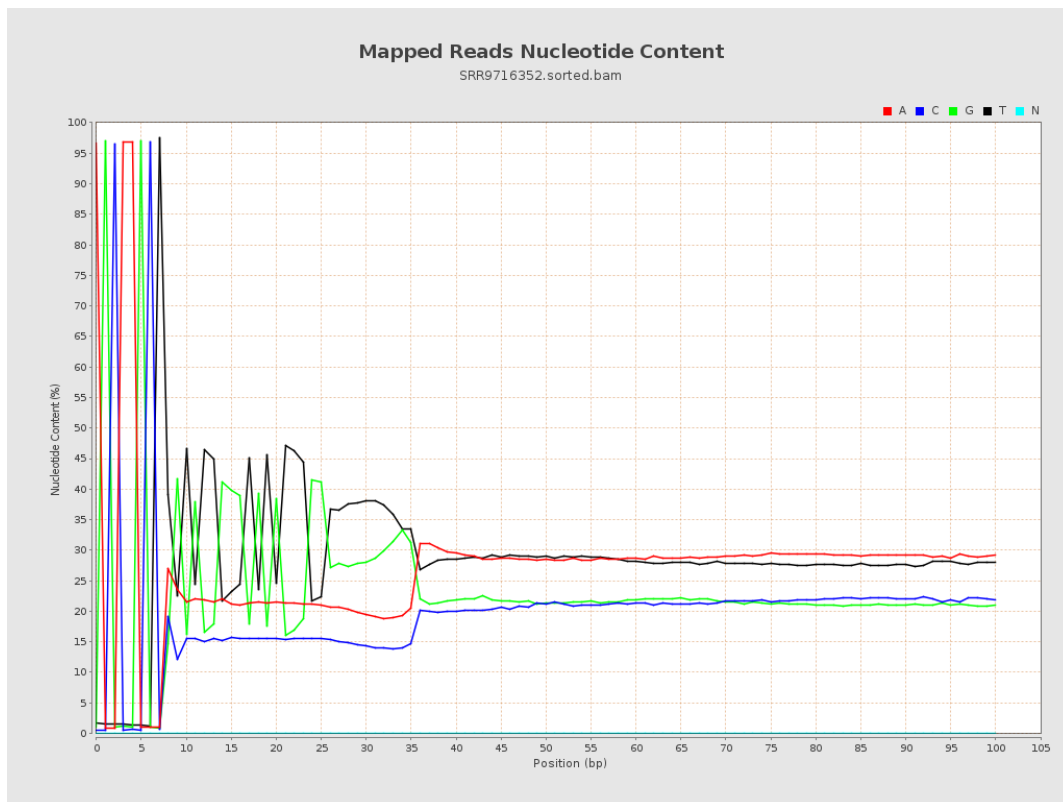
6. Results : Genome Fraction Coverage



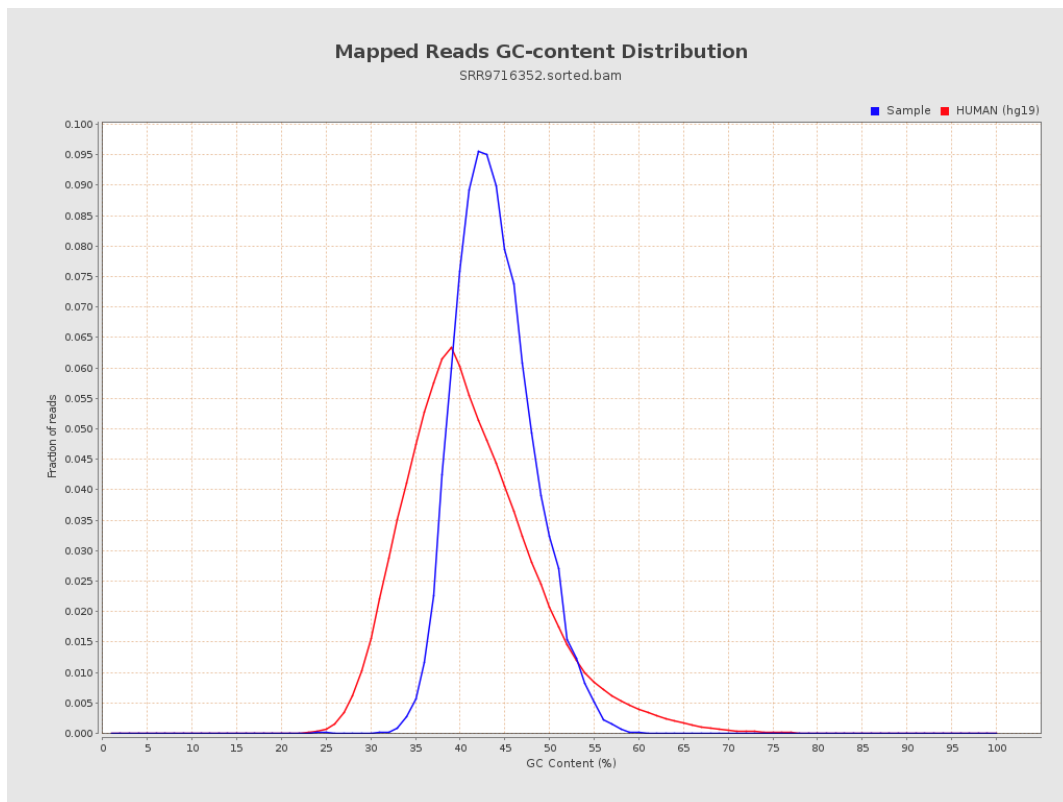
7. Results : Duplication Rate Histogram



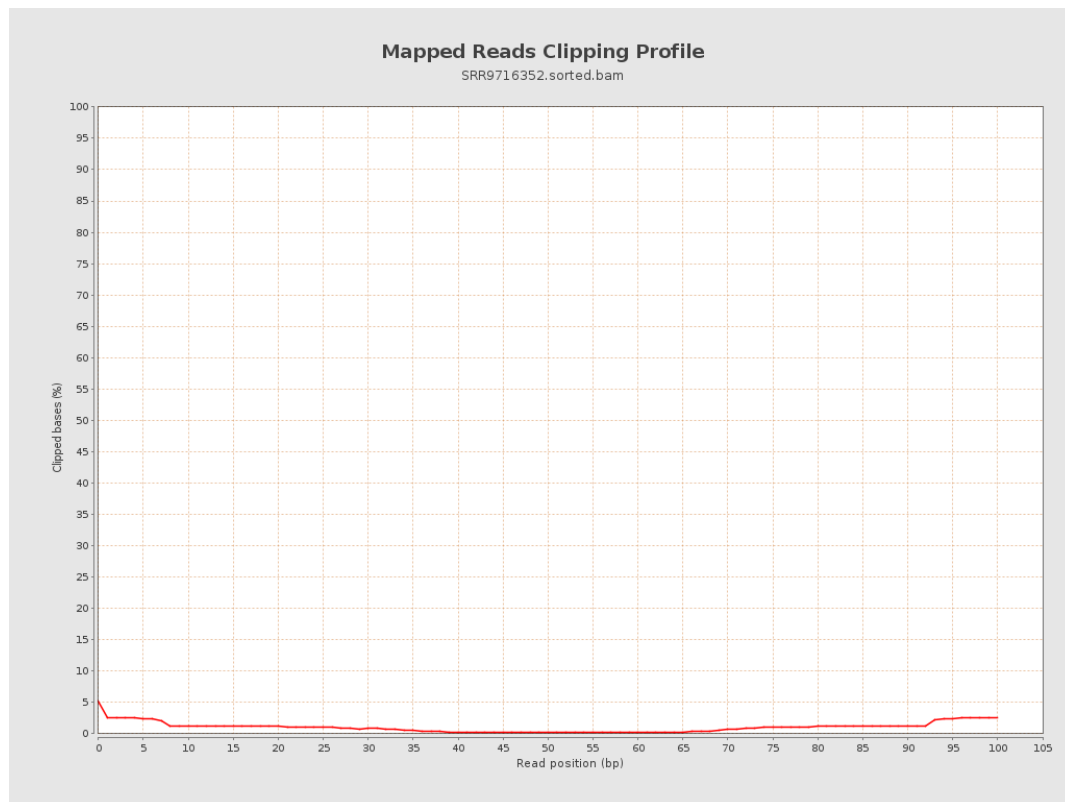
8. Results : Mapped Reads Nucleotide Content



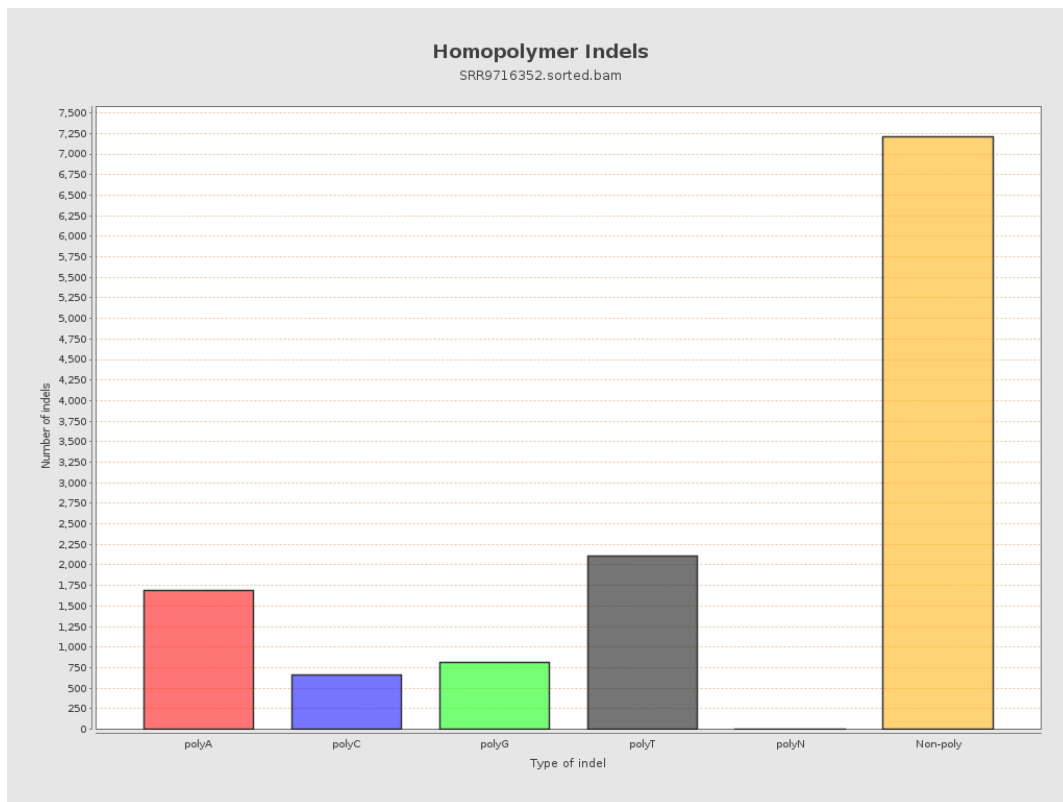
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

