Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 18:51:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716122.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_SRR9716122 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716122.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 18:51:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716122.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,051,760
Mapped reads	836,983 / 79.58%
Unmapped reads	214,777 / 20.42%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,385 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	17,791 / 1.69%
Duplication rate	1.47%
Clipped reads	838,681 / 79.74%

2.2. ACGT Content

Number/percentage of A's	12,009,507 / 25.69%
Number/percentage of C's	8,871,480 / 18.98%
Number/percentage of T's	14,955,022 / 32%
Number/percentage of G's	10,902,266 / 23.33%
Number/percentage of N's	688 / 0%
GC Percentage	42.31%

2.3. Coverage

Mean	0.0151

Standard Deviation	0.1702

2.4. Mapping Quality

Mean Mapping Quality	42.38

2.5. Mismatches and indels

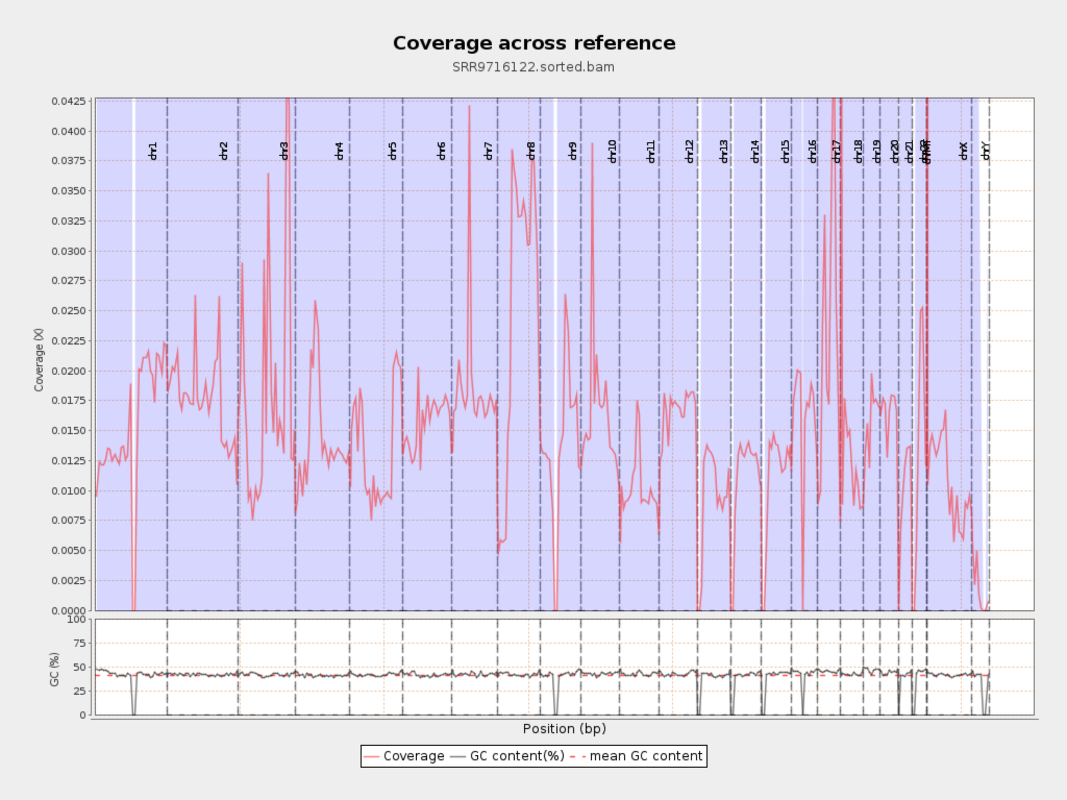
General error rate	0.53%
Mismatches	240,733
Insertions	3,535
Mapped reads with at least one insertion	0.42%
Deletions	8,896
Mapped reads with at least one deletion	1.05%
Homopolymer indels	41.07%

2.6. Chromosome stats

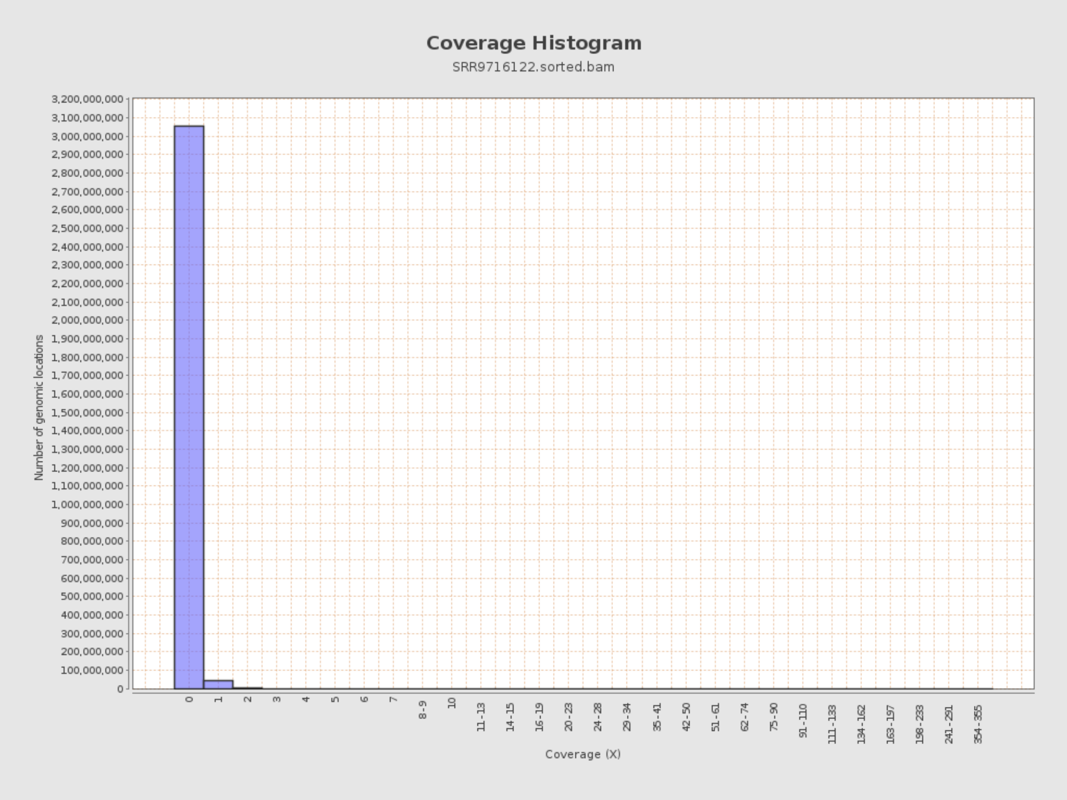
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3813125	0.0153	0.1936
chr2	243199373	4308622	0.0177	0.2088
chr3	198022430	3604996	0.0182	0.1473
chr4	191154276	2710326	0.0142	0.1273
chr5	180915260	2418861	0.0134	0.1213
chr6	171115067	2686465	0.0157	0.1396
chr7	159138663	2966076	0.0186	0.3647

chr8	146364022	3731057	0.0255	0.1817
chr9	141213431	1927860	0.0137	0.1359
chr10	135534747	2255358	0.0166	0.2119
chr11	135006516	1399866	0.0104	0.1224
chr12	133851895	2217363	0.0166	0.1381
chr13	115169878	1077023	0.0094	0.1005
chr14	107349540	1176889	0.011	0.1123
chr15	102531392	1108676	0.0108	0.1107
chr16	90354753	1433845	0.0159	0.1375
chr17	81195210	1907796	0.0235	0.1641
chr18	78077248	1105626	0.0142	0.1788
chr19	59128983	933135	0.0158	0.1881
chr20	63025520	1030381	0.0163	0.1347
chr21	48129895	481817	0.01	0.1053
chr22	51304566	663337	0.0129	0.1193
chrMT	16571	12580	0.7592	1.0357
chrX	155270560	1679609	0.0108	0.1185
chrY	59373566	101898	0.0017	0.0521

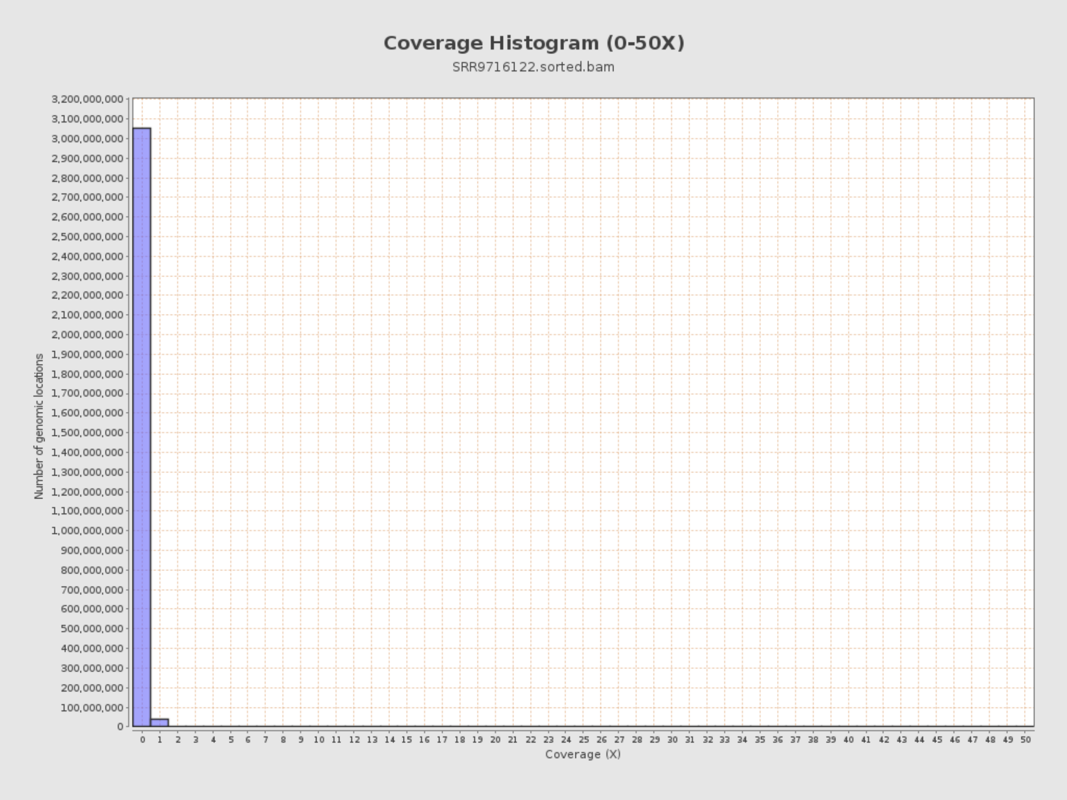
3. Results : Coverage across reference



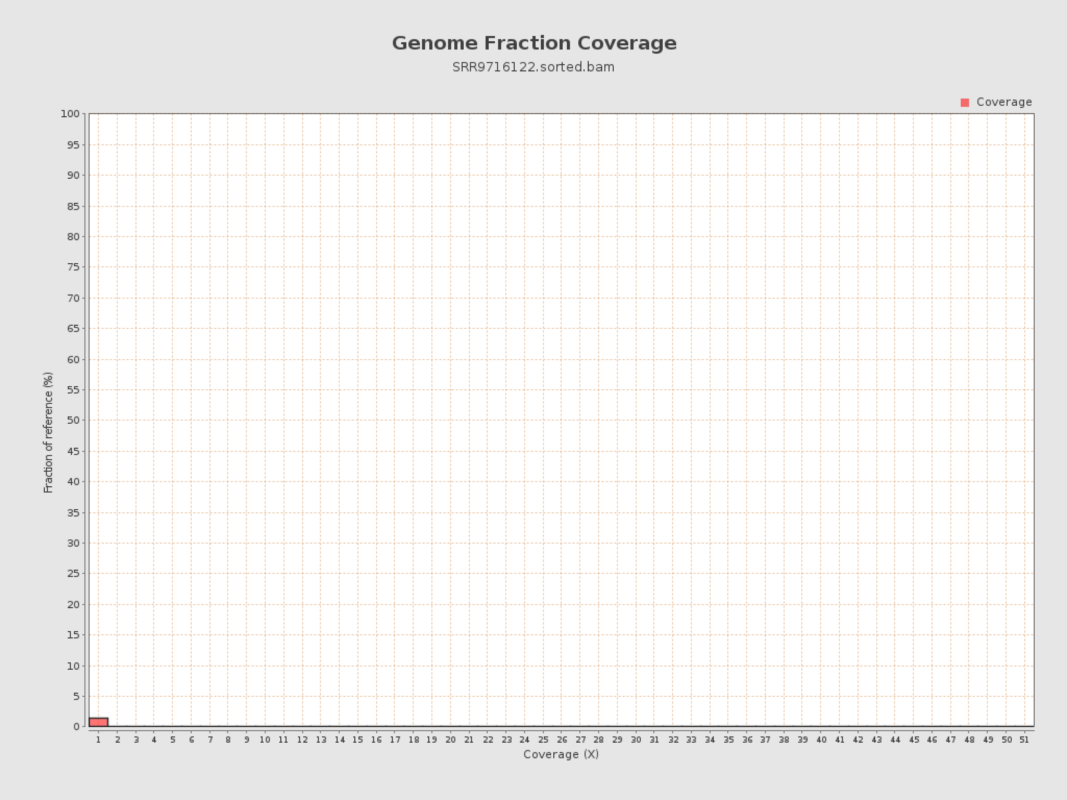
4. Results : Coverage Histogram



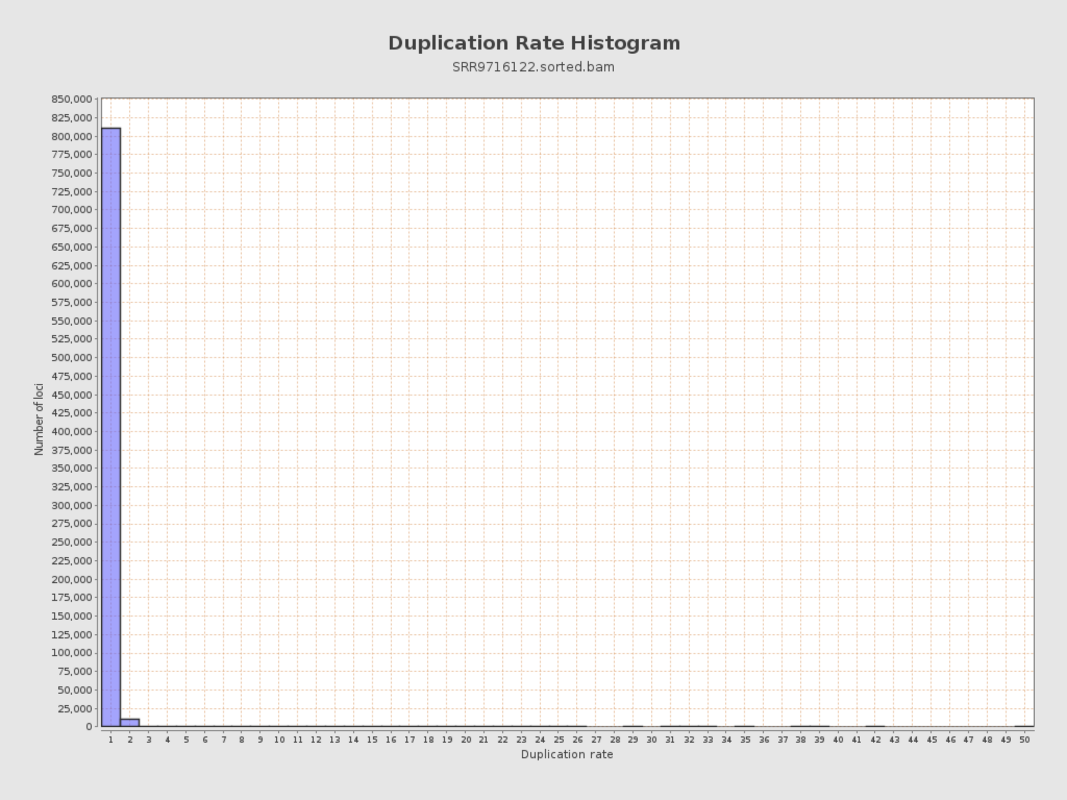
5. Results : Coverage Histogram (0-50X)



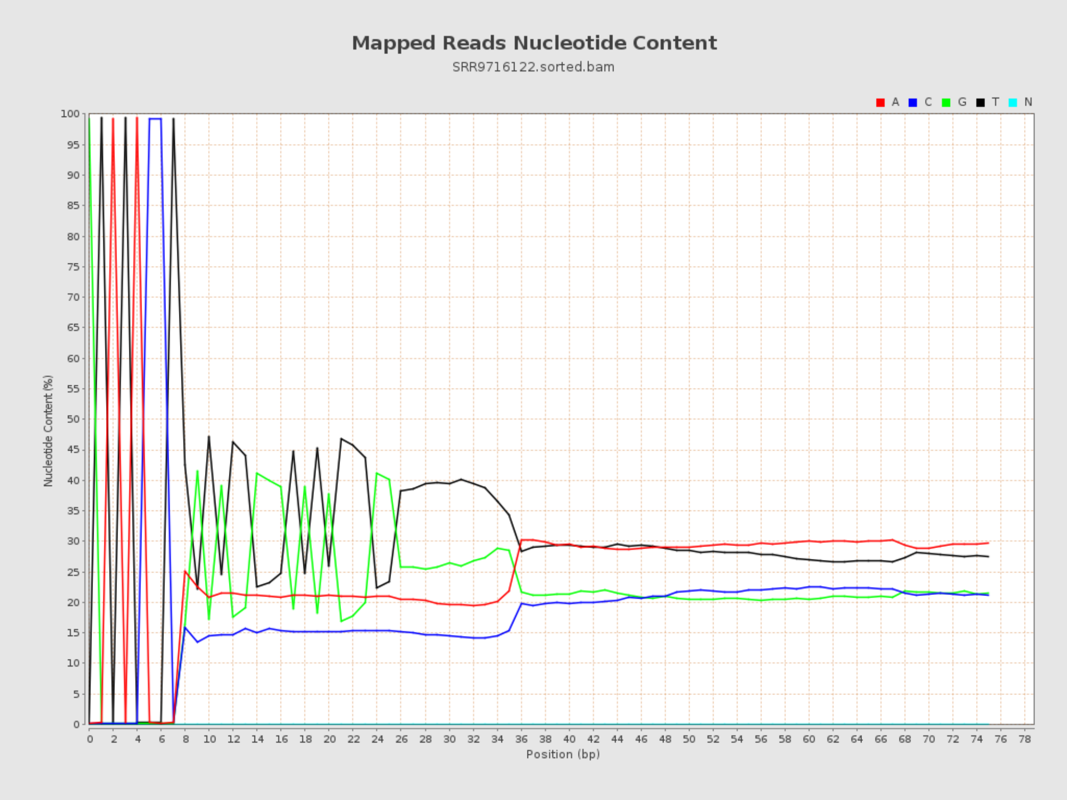
6. Results : Genome Fraction Coverage



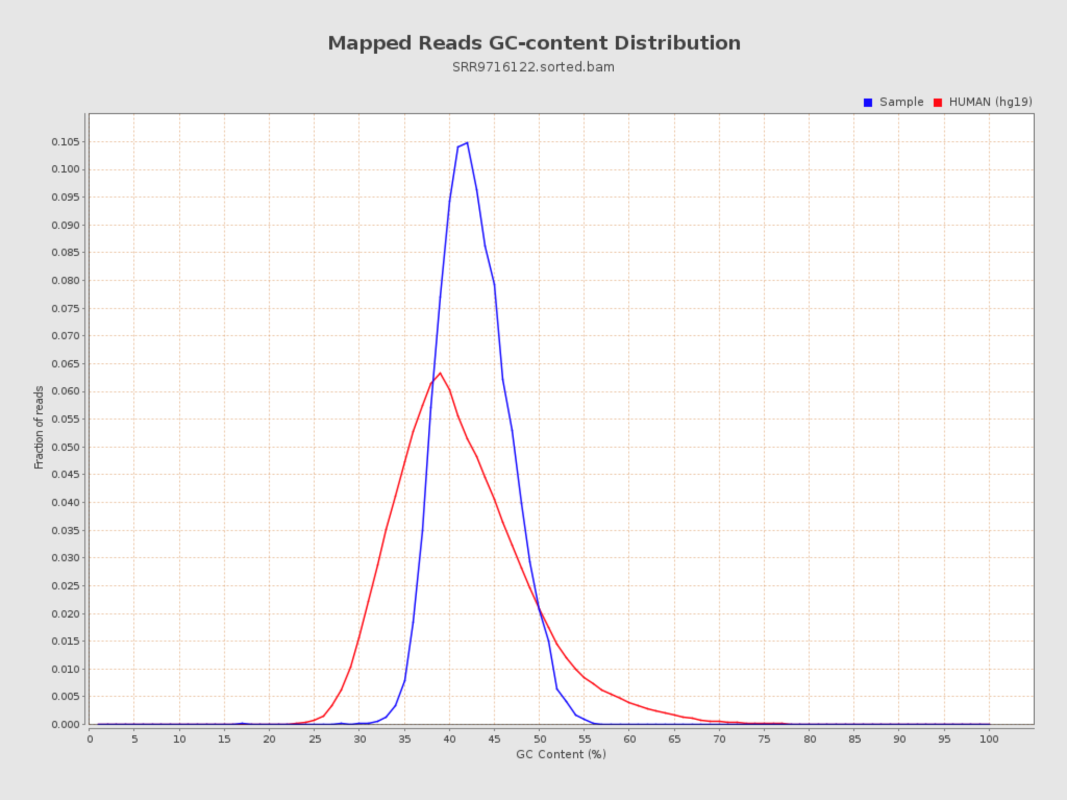
7. Results : Duplication Rate Histogram



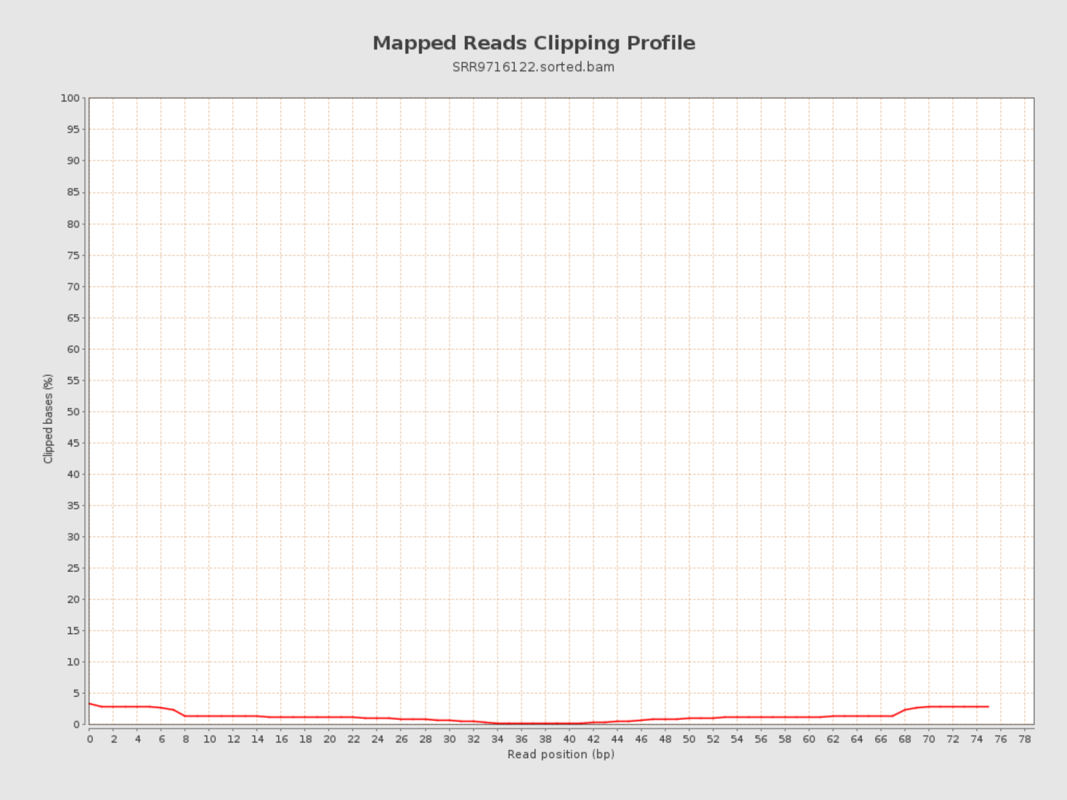
8. Results : Mapped Reads Nucleotide Content



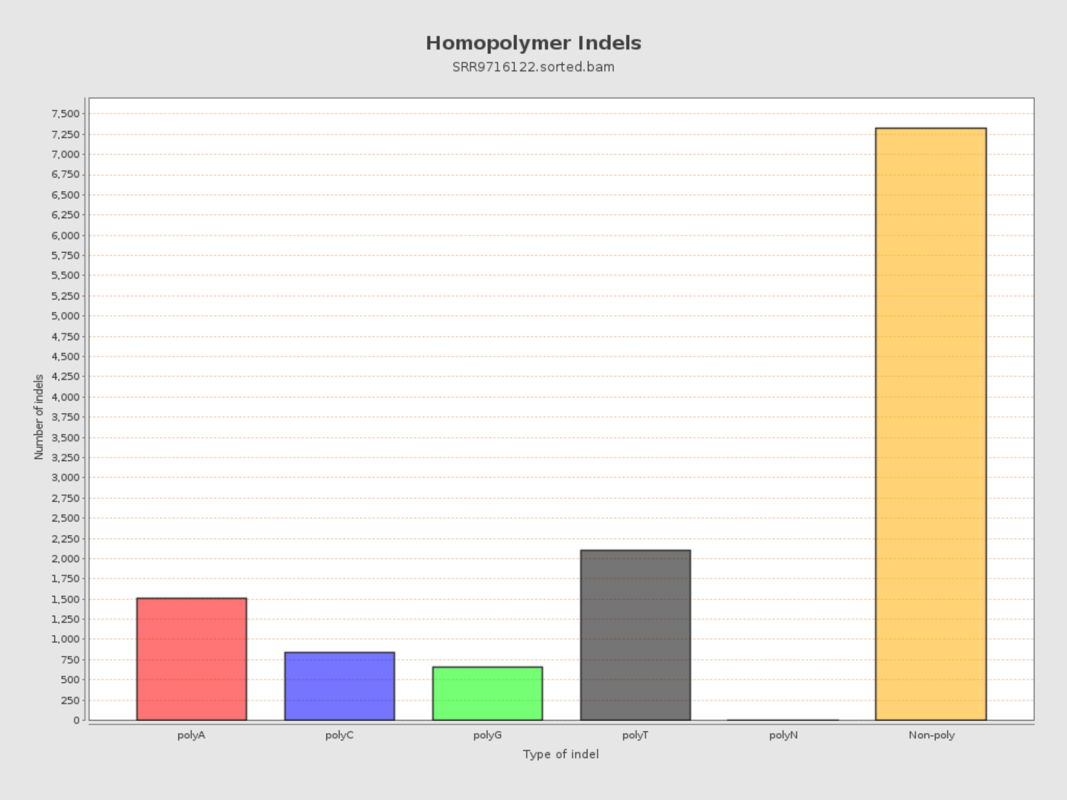
9. Results : Mapped Reads GC-content Distribution



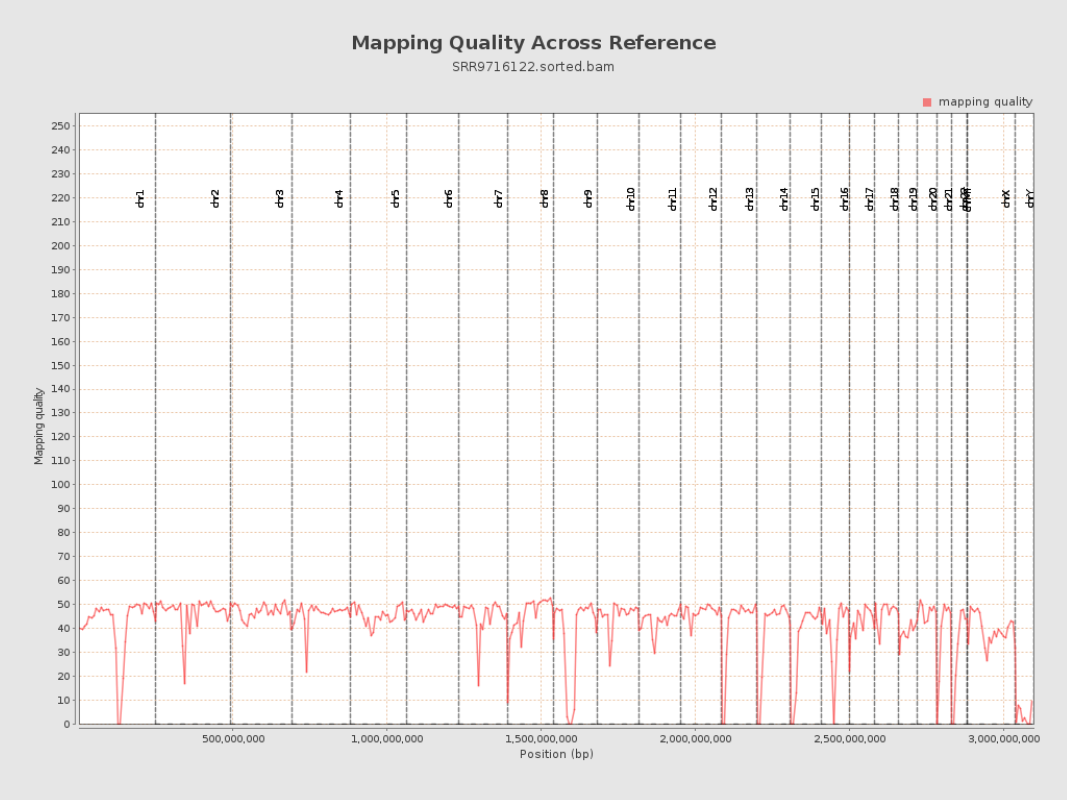
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram