Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 14:57:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716455.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_SRR9716455 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716455.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 14:57:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716455.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,311,632
Mapped reads	1,193,329 / 90.98%
Unmapped reads	118,303 / 9.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,218 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	45,989 / 3.51%
Duplication rate	2.85%
Clipped reads	1,194,996 / 91.11%

2.2. ACGT Content

Number/percentage of A's	17,488,699 / 25.25%
Number/percentage of C's	12,851,791 / 18.56%
Number/percentage of T's	22,463,746 / 32.44%
Number/percentage of G's	16,449,222 / 23.75%
Number/percentage of N's	1,289 / 0%
GC Percentage	42.31%

2.3. Coverage

Mean	0.0224

Standard Deviation	0.2291

2.4. Mapping Quality

Mean Mapping Quality	44.71

2.5. Mismatches and indels

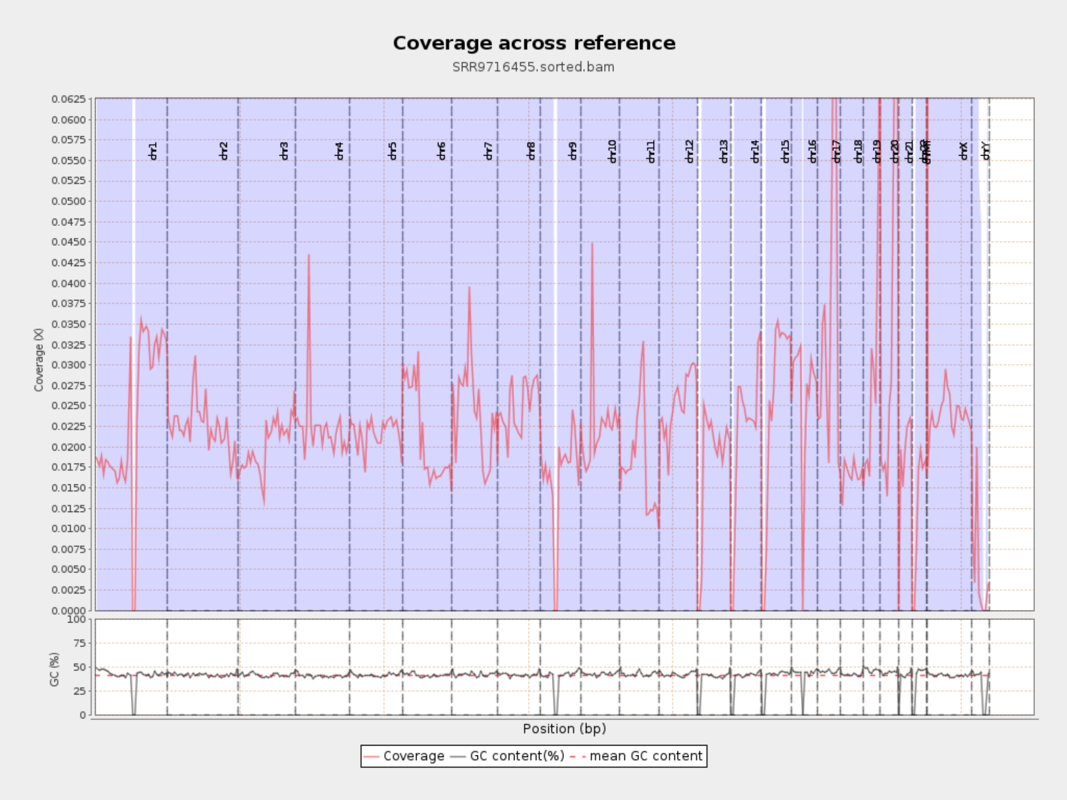
General error rate	0.52%
Mismatches	351,629
Insertions	4,939
Mapped reads with at least one insertion	0.41%
Deletions	14,097
Mapped reads with at least one deletion	1.17%
Homopolymer indels	42.81%

2.6. Chromosome stats

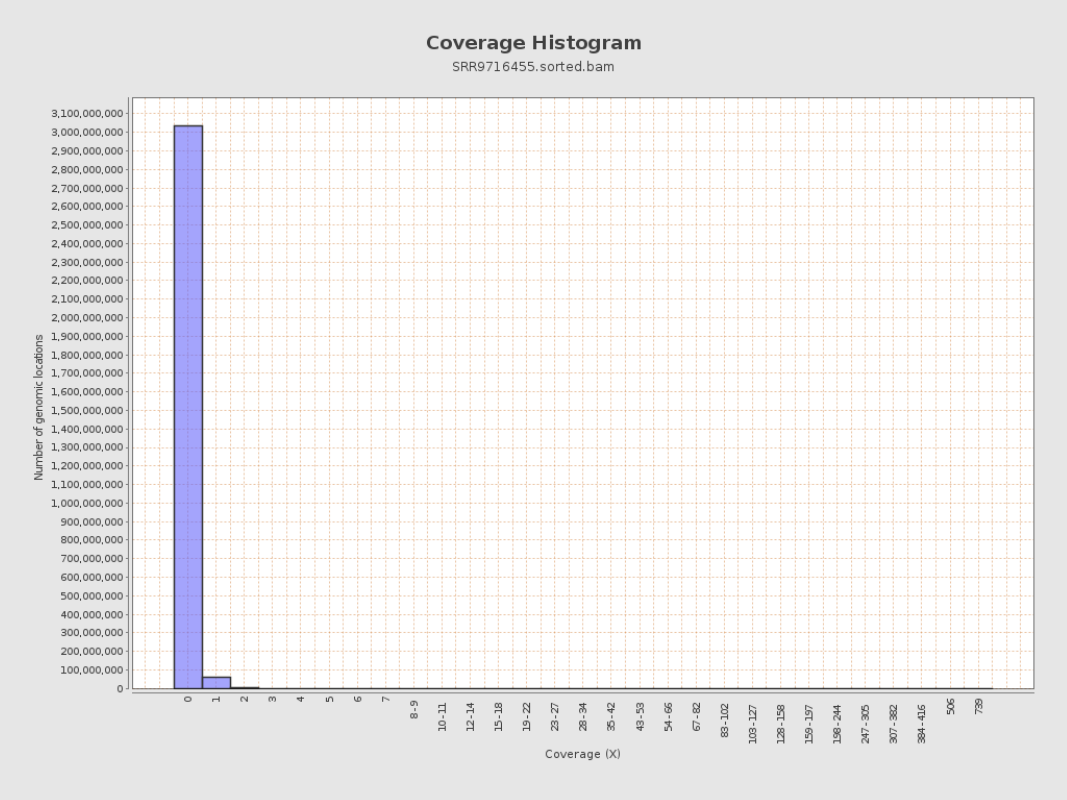
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5825866	0.0234	0.3357
chr2	243199373	5446237	0.0224	0.3423
chr3	198022430	3968169	0.02	0.1528
chr4	191154276	4295058	0.0225	0.1978
chr5	180915260	3938941	0.0218	0.1588
chr6	171115067	3654920	0.0214	0.1794
chr7	159138663	3909799	0.0246	0.2729

chr8	146364022	3656510	0.025	0.3007
chr9	141213431	2309126	0.0164	0.1655
chr10	135534747	3064692	0.0226	0.2445
chr11	135006516	2460386	0.0182	0.1797
chr12	133851895	3387829	0.0253	0.1739
chr13	115169878	2062142	0.0179	0.1452
chr14	107349540	2336901	0.0218	0.1619
chr15	102531392	2577746	0.0251	0.1721
chr16	90354753	2346461	0.026	0.1807
chr17	81195210	3027148	0.0373	0.2164
chr18	78077248	1284450	0.0165	0.2501
chr19	59128983	1778902	0.0301	0.2728
chr20	63025520	2294705	0.0364	0.2124
chr21	48129895	885605	0.0184	0.184
chr22	51304566	653208	0.0127	0.1214
chrMT	16571	117700	7.1028	5.1031
chrX	155270560	3716767	0.0239	0.1781
chrY	59373566	278342	0.0047	0.2032

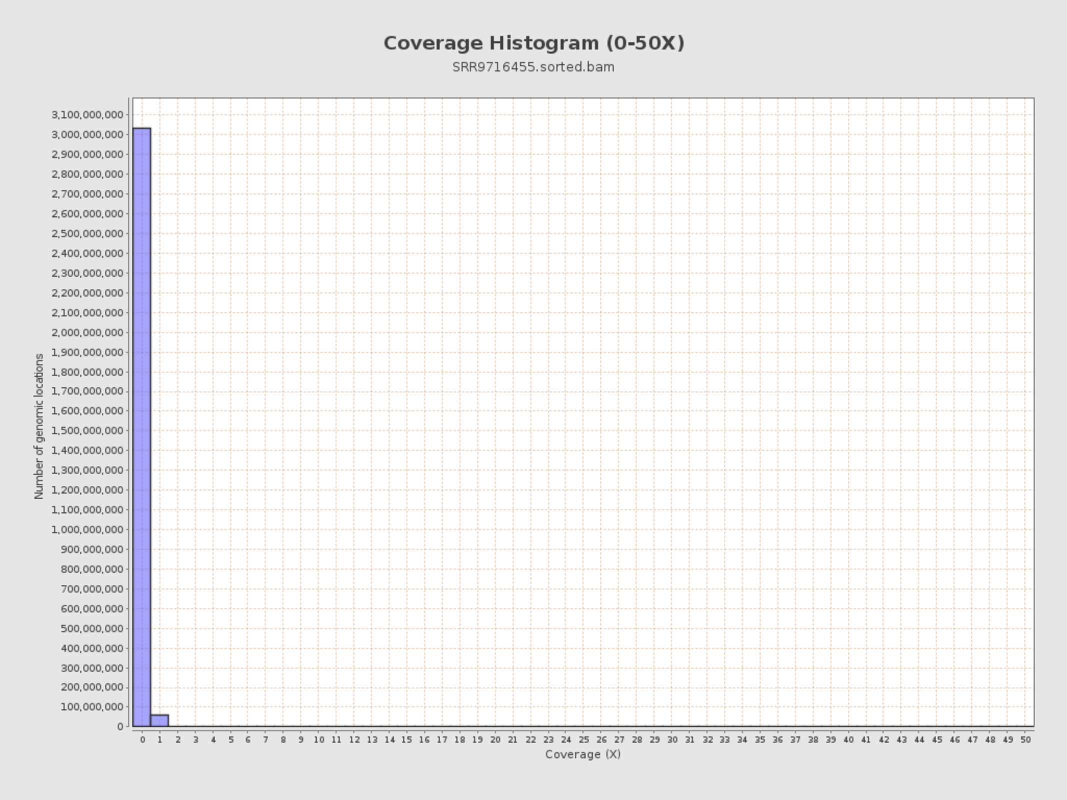
3. Results : Coverage across reference



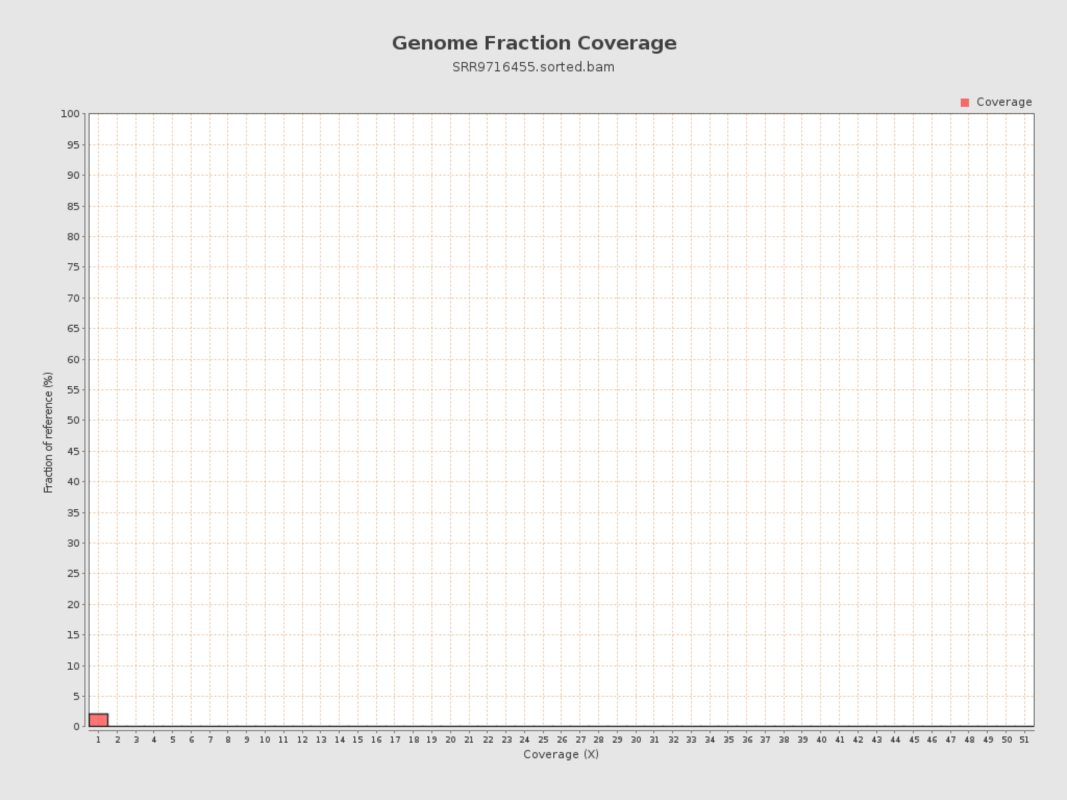
4. Results : Coverage Histogram



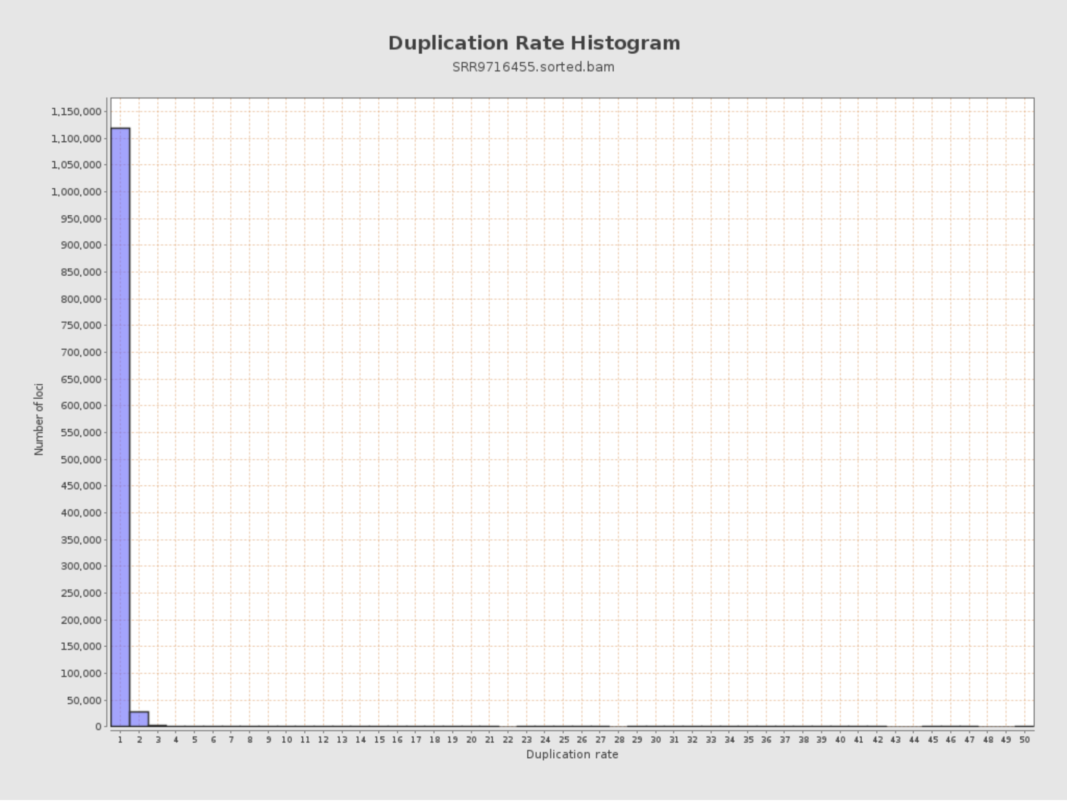
5. Results : Coverage Histogram (0-50X)



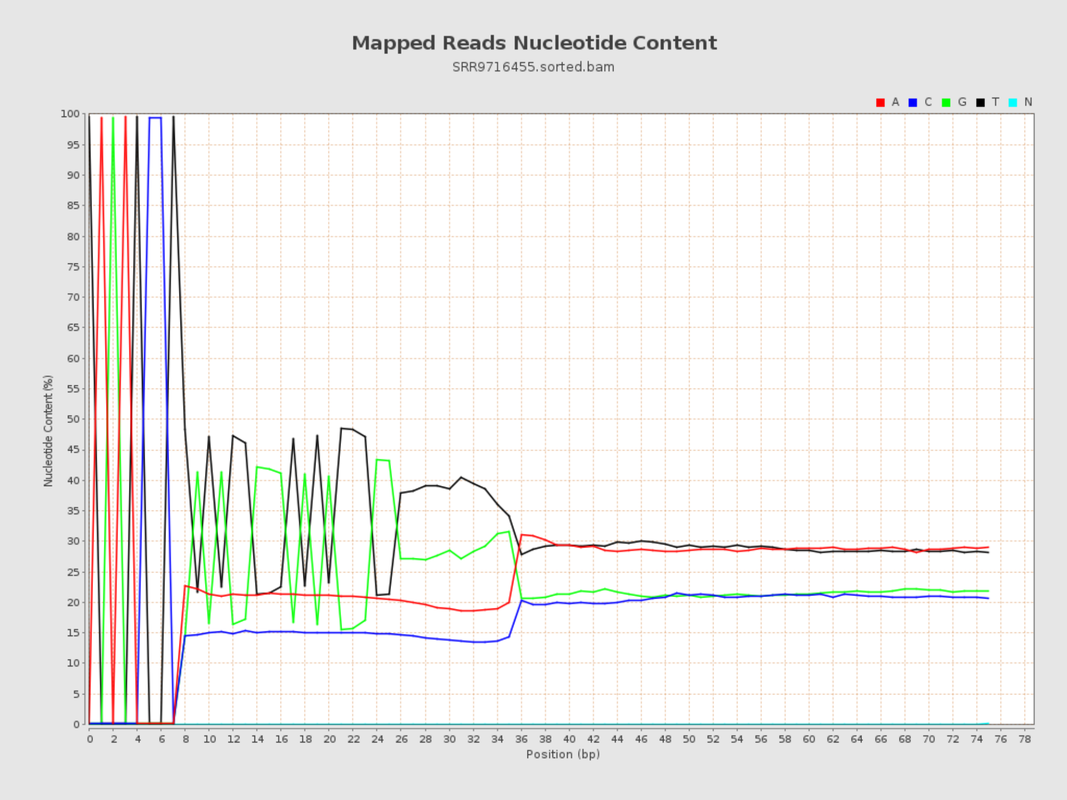
6. Results : Genome Fraction Coverage



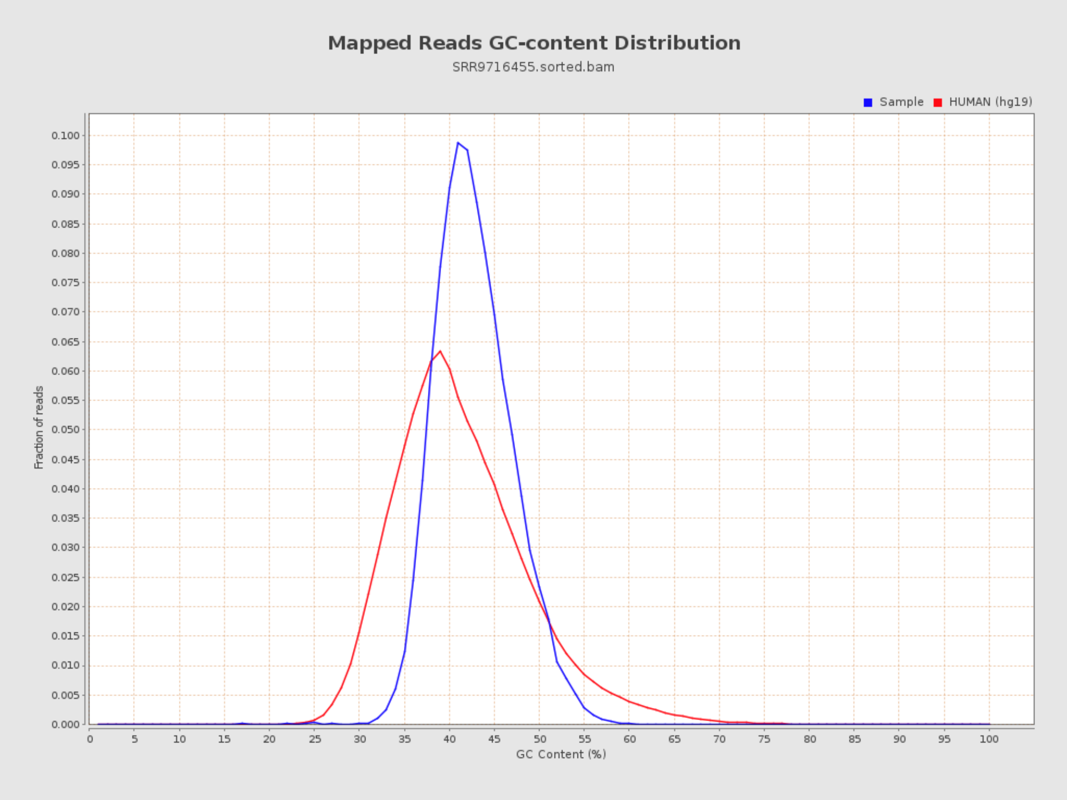
7. Results : Duplication Rate Histogram



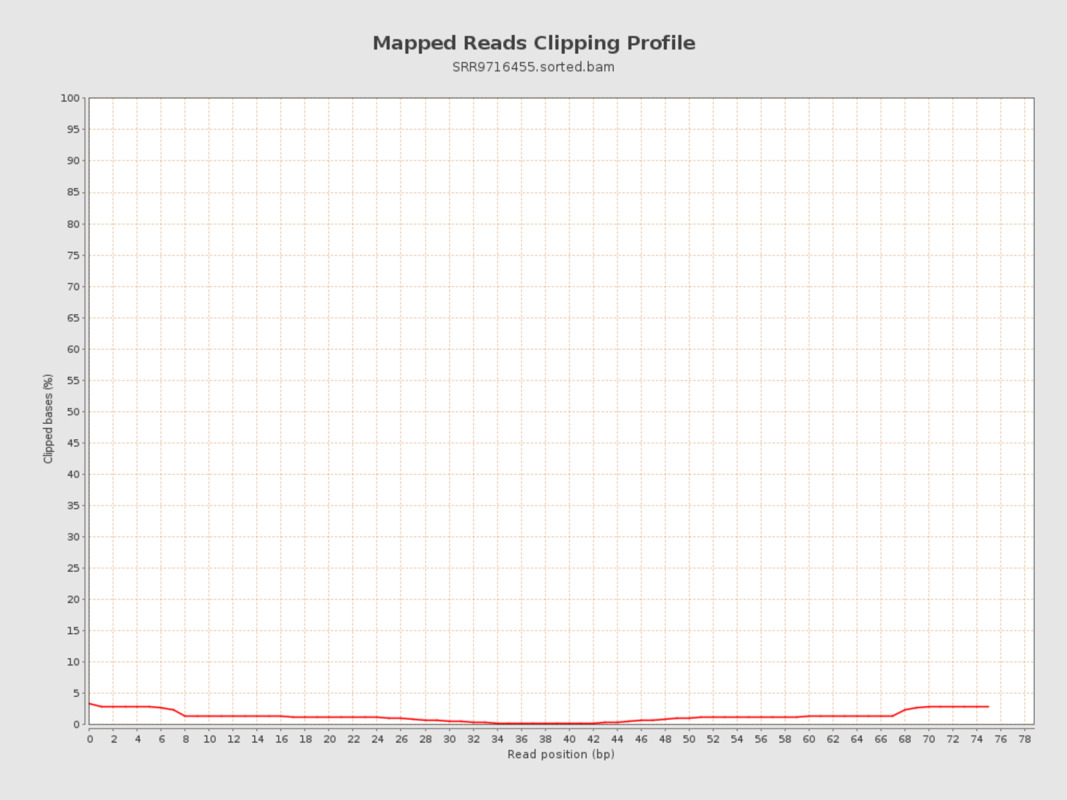
8. Results : Mapped Reads Nucleotide Content



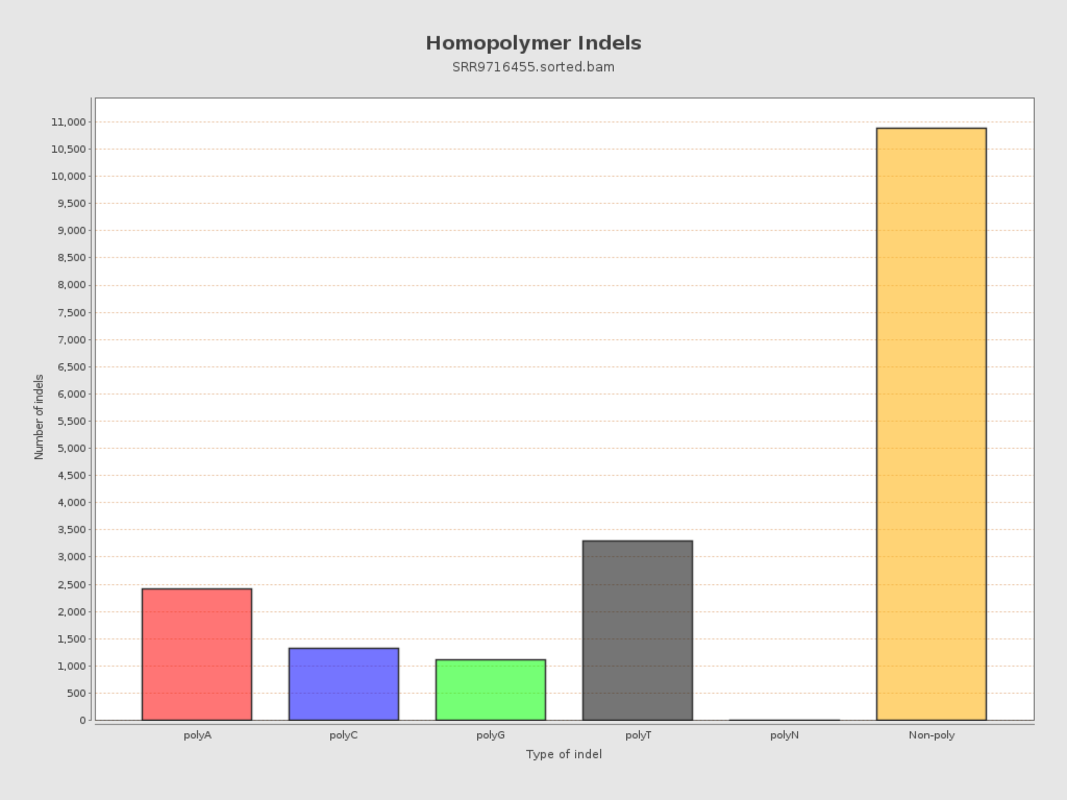
9. Results : Mapped Reads GC-content Distribution



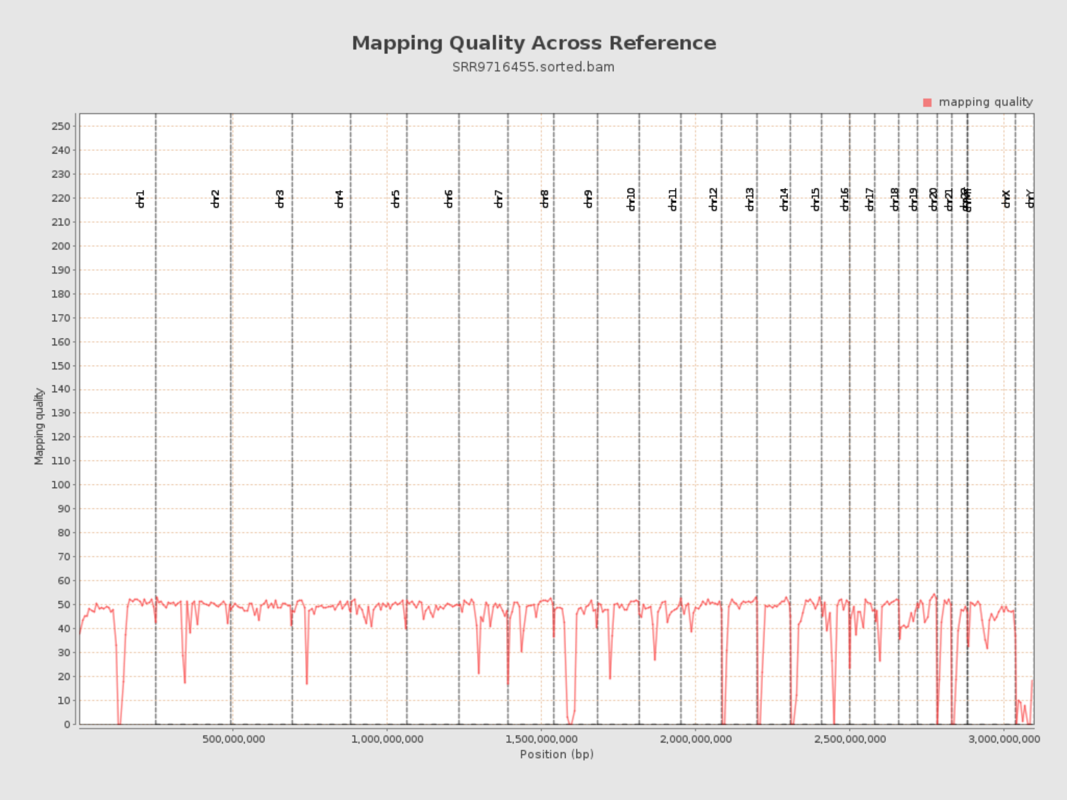
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram