Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 15:02:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716457.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_SRR9716457 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716457.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 15:02:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716457.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,008,422
Mapped reads	886,016 / 87.86%
Unmapped reads	122,406 / 12.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,516 / 0.25%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	27,710 / 2.75%
Duplication rate	2.46%
Clipped reads	885,120 / 87.77%

2.2. ACGT Content

Number/percentage of A's	12,890,900 / 25.36%
Number/percentage of C's	9,368,868 / 18.43%
Number/percentage of T's	16,580,858 / 32.61%
Number/percentage of G's	12,000,162 / 23.6%
Number/percentage of N's	576 / 0%
GC Percentage	42.03%

2.3. Coverage

Mean	0.0164

Standard Deviation	0.1698

2.4. Mapping Quality

Mean Mapping Quality	44.96

2.5. Mismatches and indels

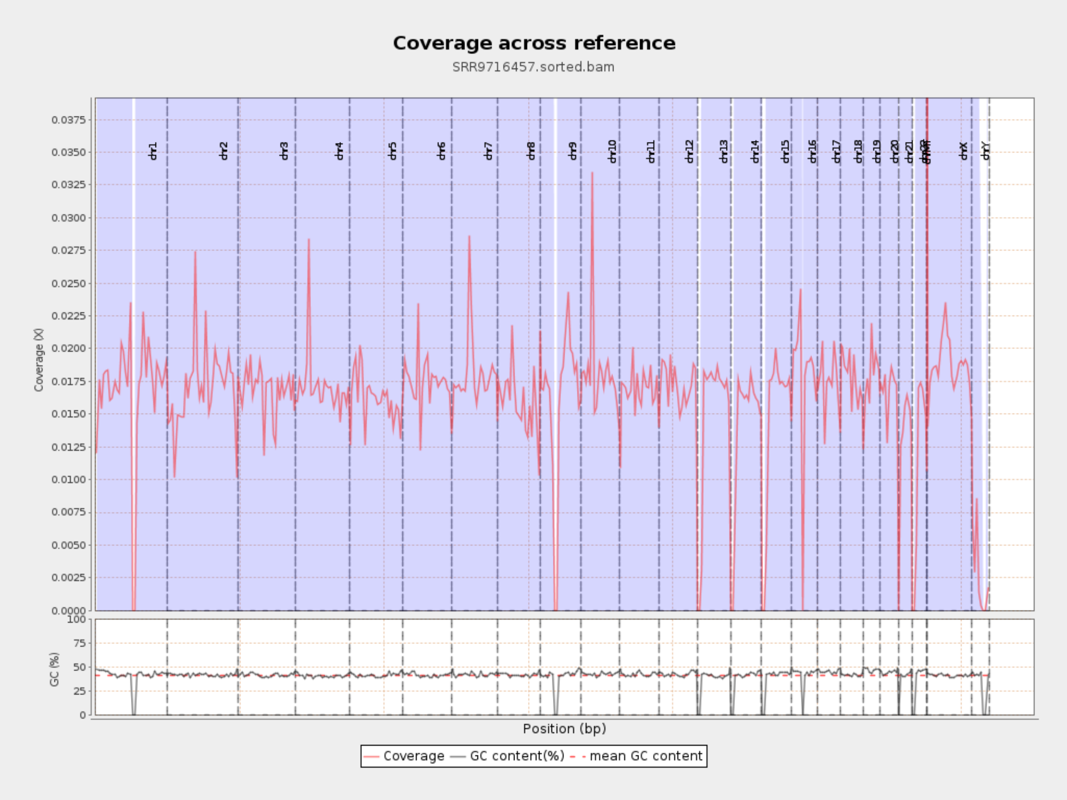
General error rate	0.51%
Mismatches	252,478
Insertions	4,213
Mapped reads with at least one insertion	0.47%
Deletions	10,366
Mapped reads with at least one deletion	1.16%
Homopolymer indels	42.66%

2.6. Chromosome stats

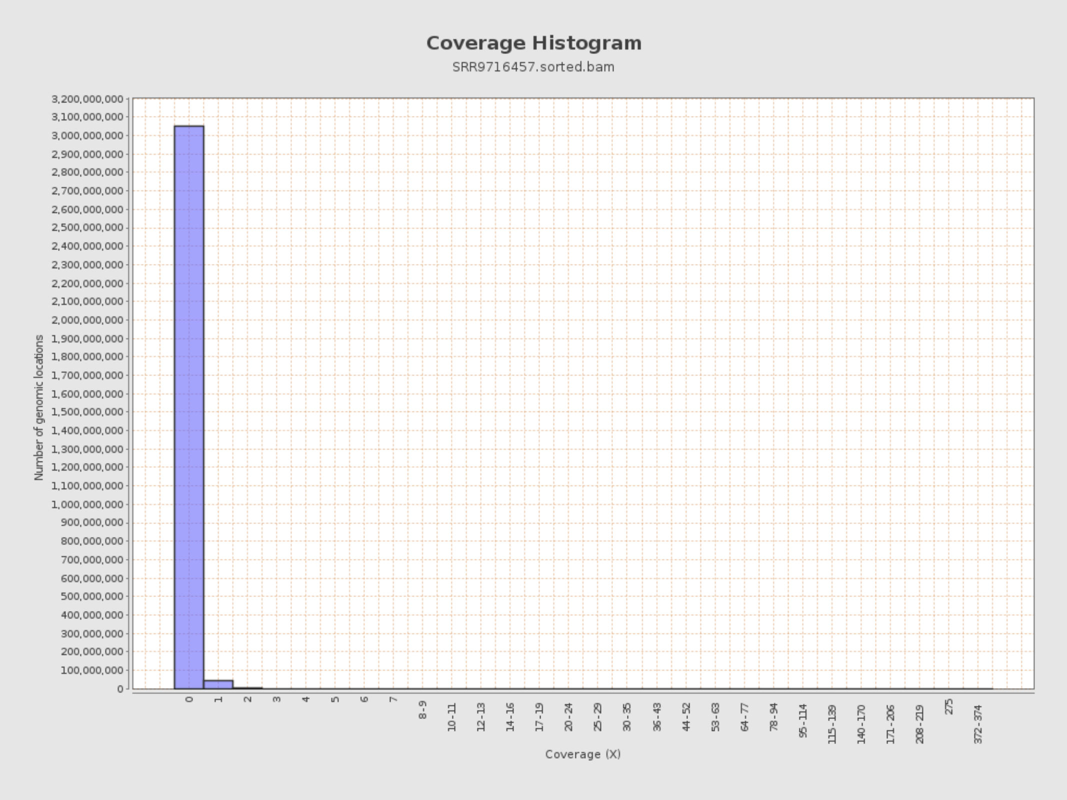
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4181682	0.0168	0.2142
chr2	243199373	4152813	0.0171	0.2307
chr3	198022430	3340405	0.0169	0.1405
chr4	191154276	3277084	0.0171	0.1486
chr5	180915260	2957467	0.0163	0.137
chr6	171115067	2985735	0.0174	0.1594
chr7	159138663	2892432	0.0182	0.2261

chr8	146364022	2323322	0.0159	0.1674
chr9	141213431	2256386	0.016	0.1522
chr10	135534747	2476192	0.0183	0.1927
chr11	135006516	2289921	0.017	0.1647
chr12	133851895	2299191	0.0172	0.1406
chr13	115169878	1679543	0.0146	0.1291
chr14	107349540	1478244	0.0138	0.1278
chr15	102531392	1464387	0.0143	0.1294
chr16	90354753	1585136	0.0175	0.1547
chr17	81195210	1417169	0.0175	0.1483
chr18	78077248	1397296	0.0179	0.2205
chr19	59128983	1059819	0.0179	0.1889
chr20	63025520	1050704	0.0167	0.1397
chr21	48129895	635577	0.0132	0.129
chr22	51304566	573260	0.0112	0.1134
chrMT	16571	2368	0.1429	0.4065
chrX	155270560	2931185	0.0189	0.1579
chrY	59373566	150393	0.0025	0.0766

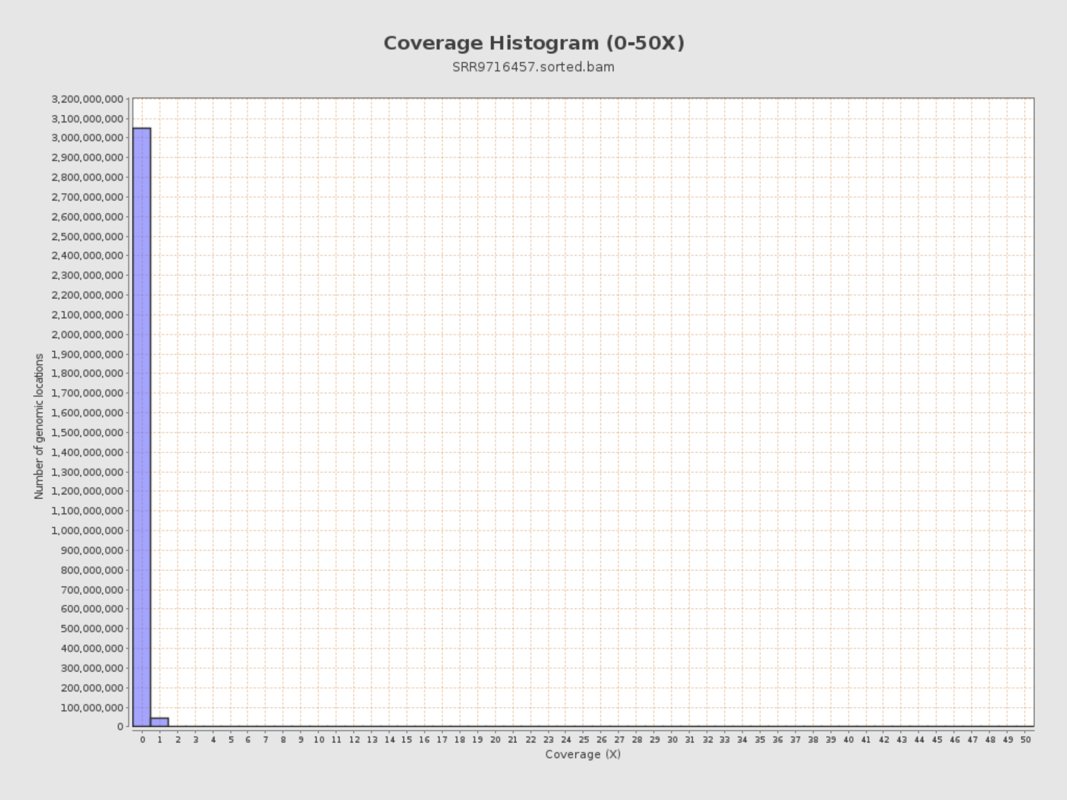
3. Results : Coverage across reference



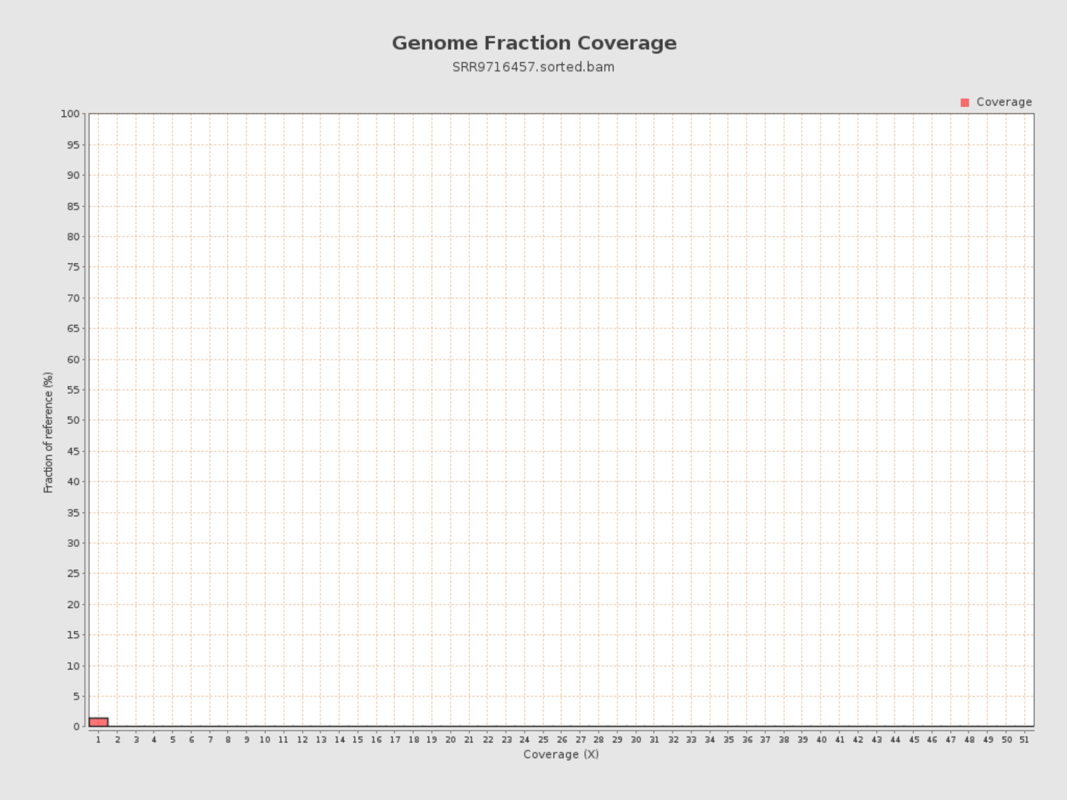
4. Results : Coverage Histogram



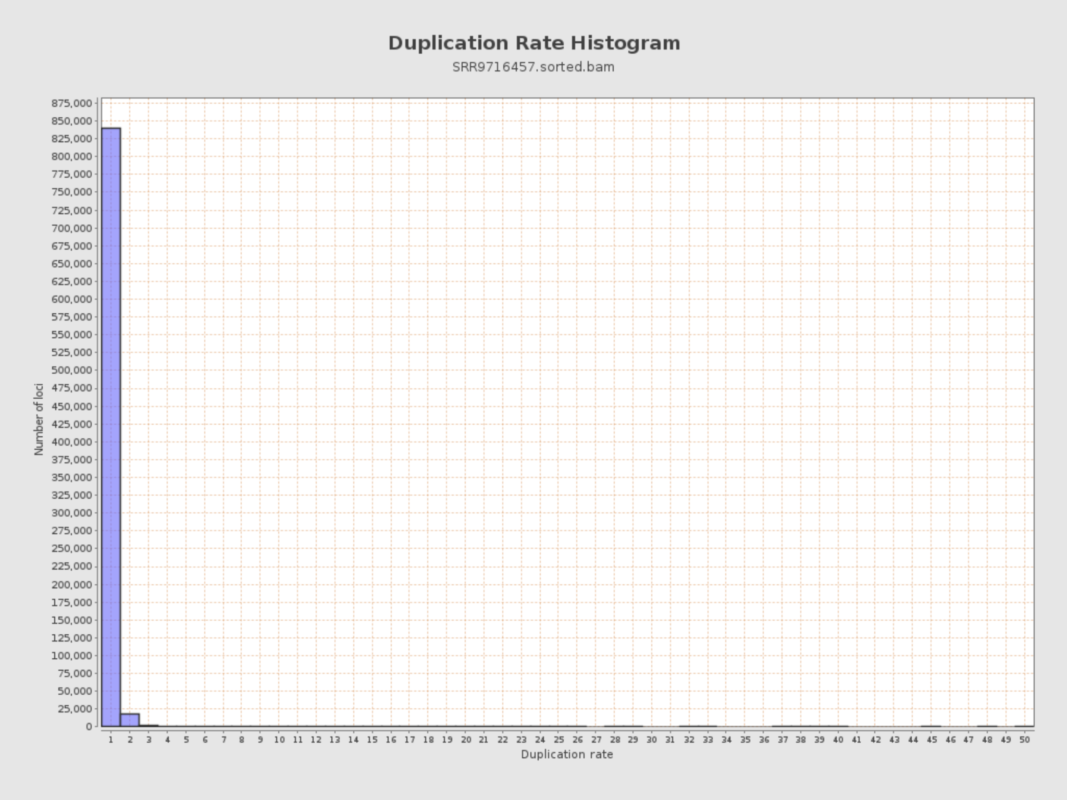
5. Results : Coverage Histogram (0-50X)



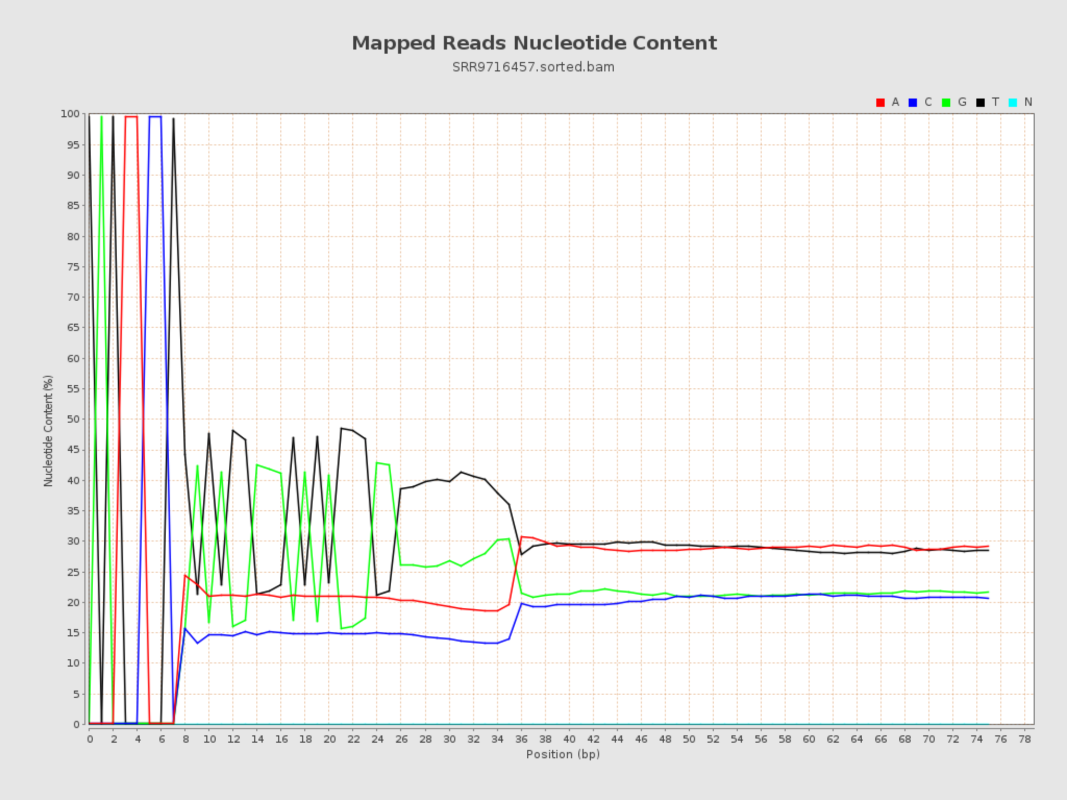
6. Results : Genome Fraction Coverage



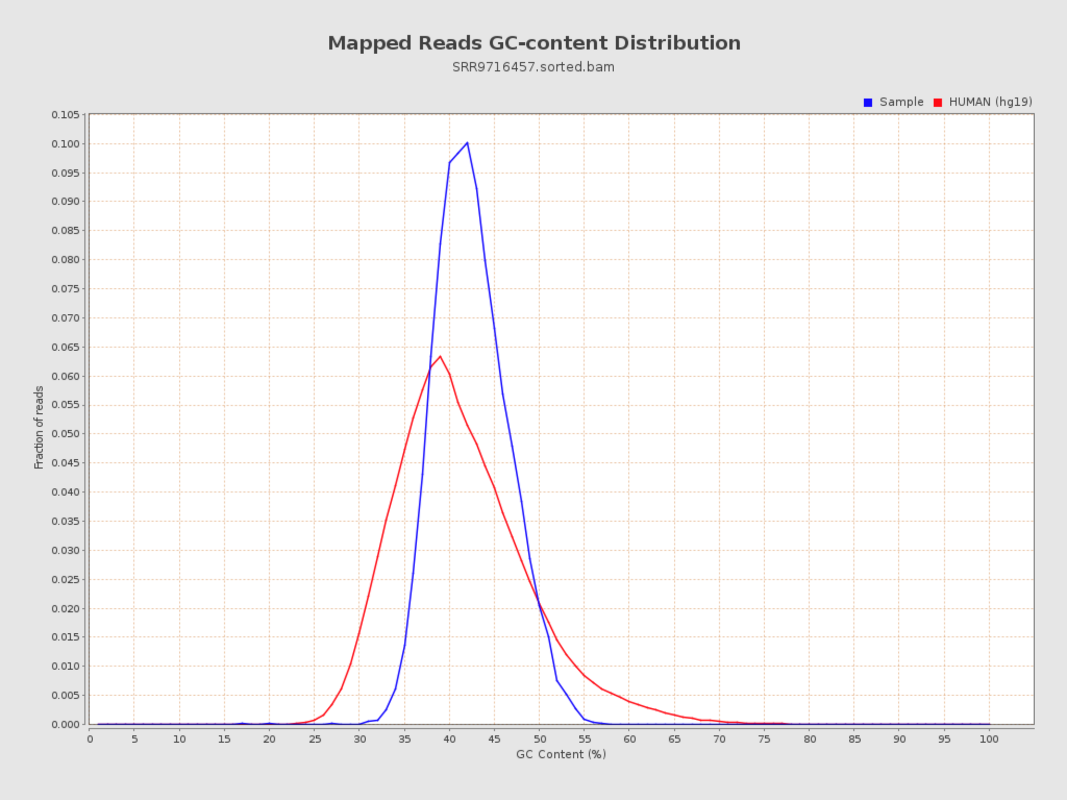
7. Results : Duplication Rate Histogram



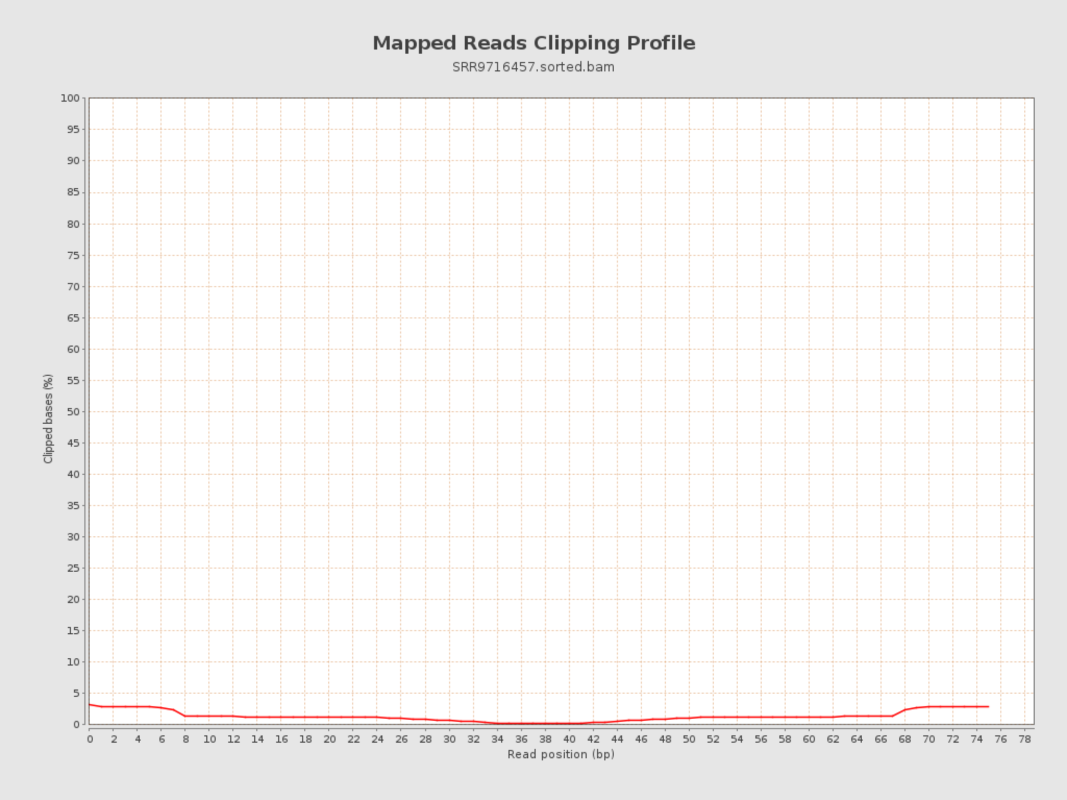
8. Results : Mapped Reads Nucleotide Content



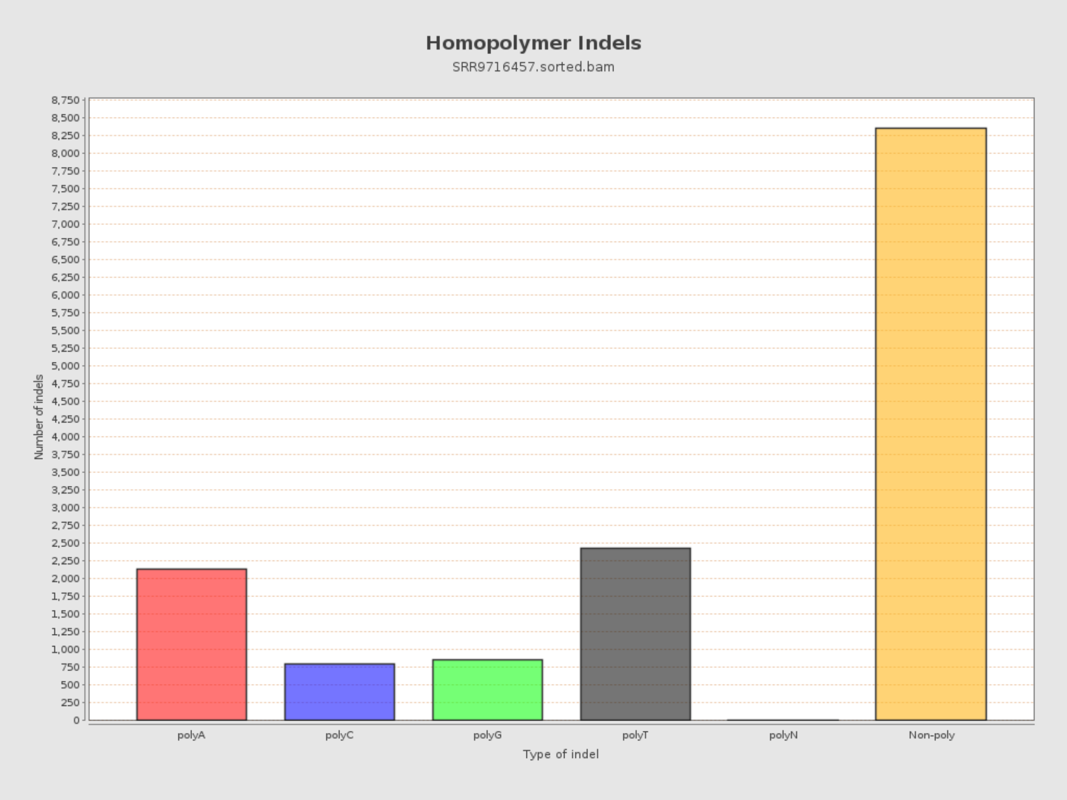
9. Results : Mapped Reads GC-content Distribution



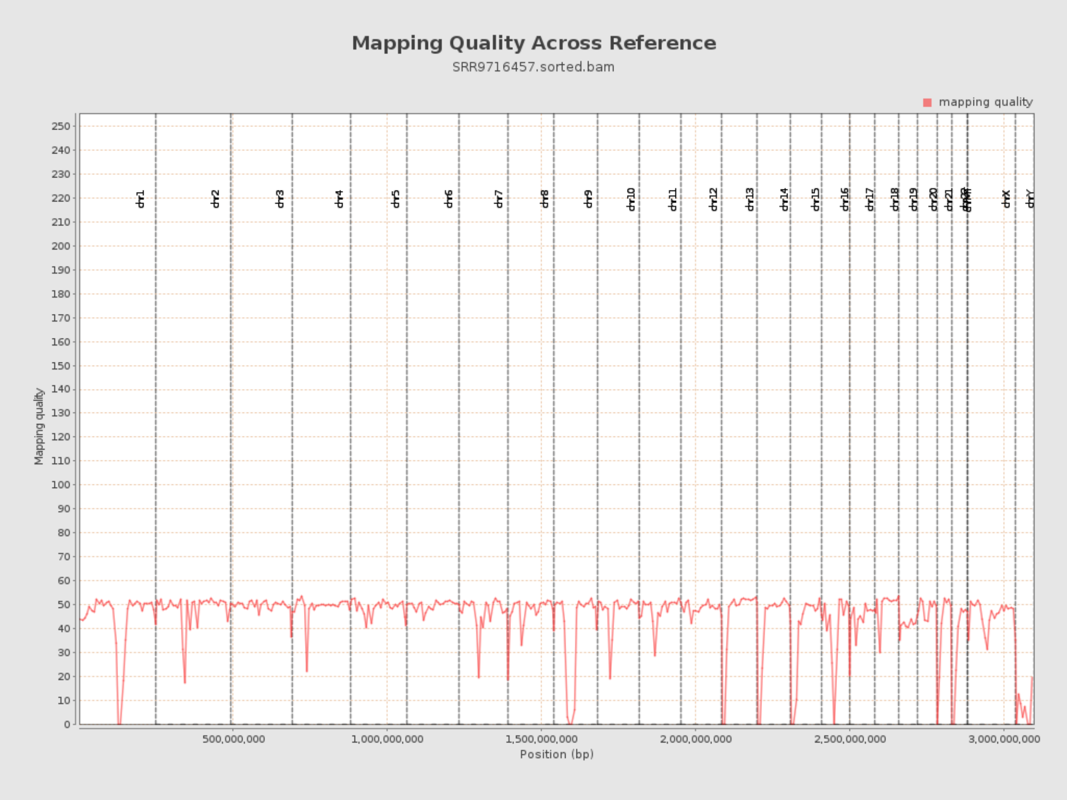
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram