Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 10:25:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716377.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_SRR9716377 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716377.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 10:25:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716377.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,504,116
Mapped reads	1,319,031 / 87.69%
Unmapped reads	185,085 / 12.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,086 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	29,843 / 1.98%
Duplication rate	1.57%
Clipped reads	1,320,743 / 87.81%

2.2. ACGT Content

Number/percentage of A's	18,894,943 / 25.27%
Number/percentage of C's	15,177,353 / 20.3%
Number/percentage of T's	22,823,858 / 30.52%
Number/percentage of G's	17,874,309 / 23.91%
Number/percentage of N's	646 / 0%
GC Percentage	44.2%

2.3. Coverage

Mean	0.0242

Standard Deviation	0.2133

2.4. Mapping Quality

Mean Mapping Quality	42.05

2.5. Mismatches and indels

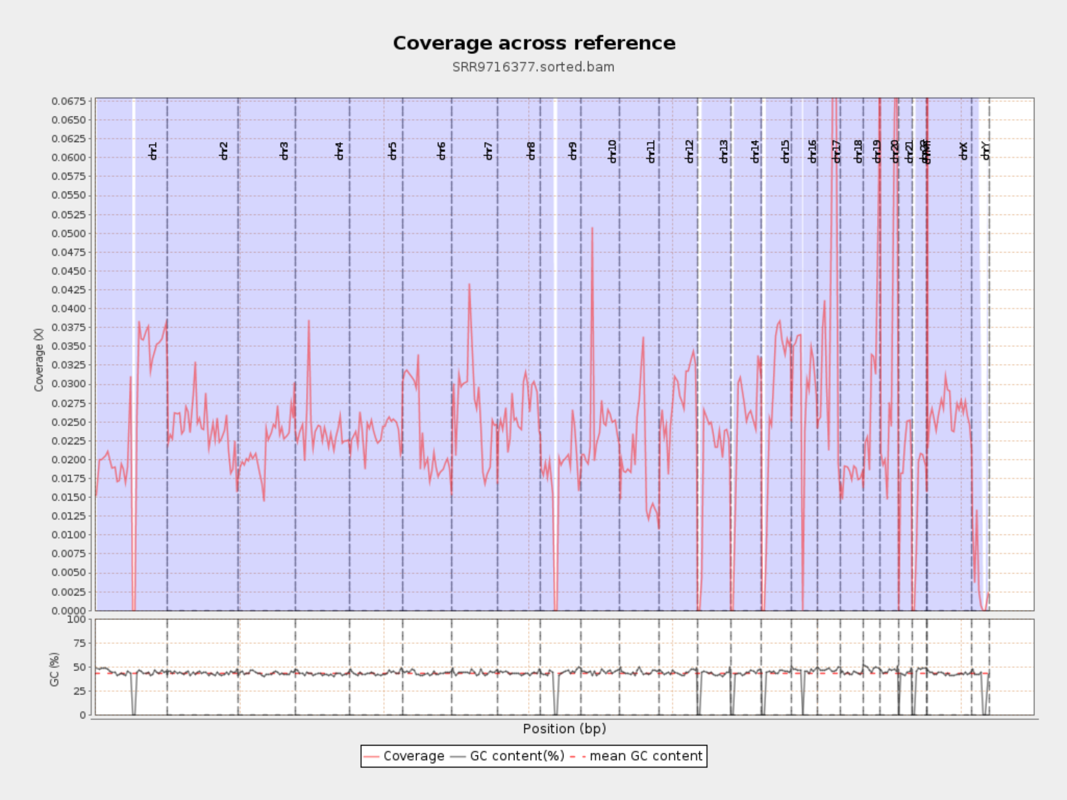
General error rate	0.53%
Mismatches	389,042
Insertions	5,337
Mapped reads with at least one insertion	0.4%
Deletions	14,272
Mapped reads with at least one deletion	1.08%
Homopolymer indels	41.15%

2.6. Chromosome stats

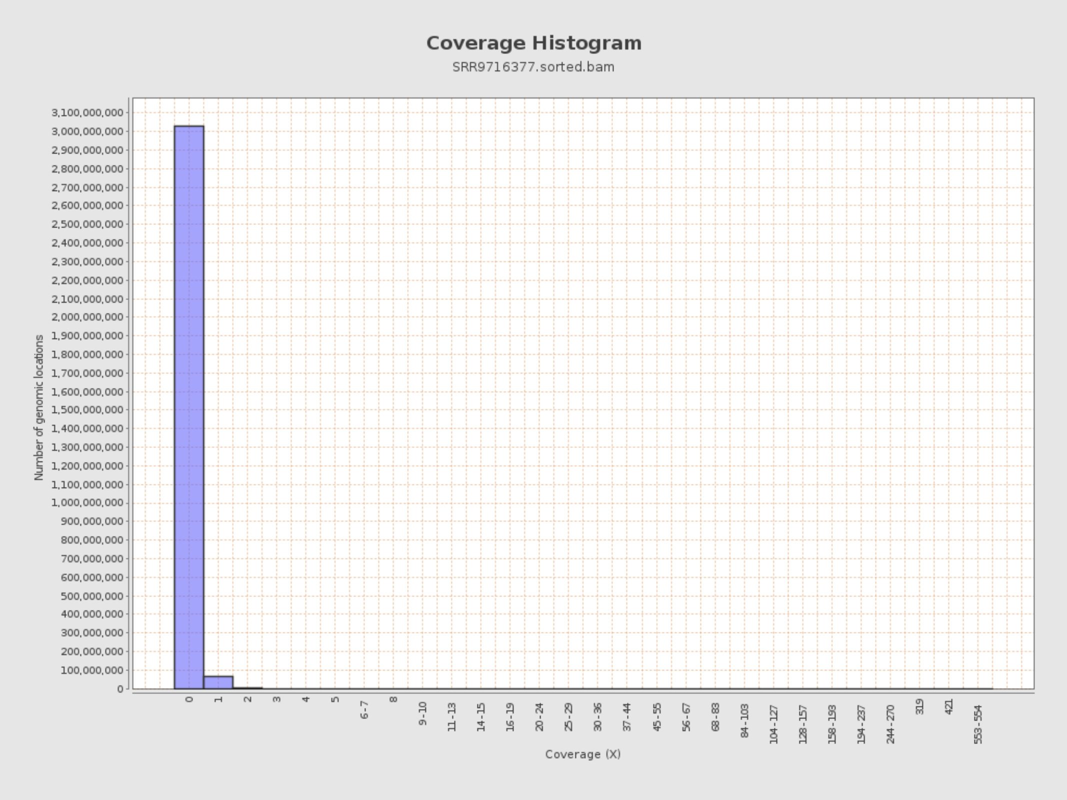
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6300117	0.0253	0.2653
chr2	243199373	5867290	0.0241	0.288
chr3	198022430	4318976	0.0218	0.1625
chr4	191154276	4566852	0.0239	0.1793
chr5	180915260	4287946	0.0237	0.1636
chr6	171115067	4008986	0.0234	0.1896
chr7	159138663	4289118	0.027	0.303

chr8	146364022	3870314	0.0264	0.2061
chr9	141213431	2484888	0.0176	0.162
chr10	135534747	3353452	0.0247	0.2808
chr11	135006516	2668149	0.0198	0.1829
chr12	133851895	3741404	0.028	0.18
chr13	115169878	2261883	0.0196	0.1506
chr14	107349540	2521504	0.0235	0.169
chr15	102531392	2751793	0.0268	0.1793
chr16	90354753	2639694	0.0292	0.1962
chr17	81195210	3328832	0.041	0.2273
chr18	78077248	1398715	0.0179	0.2467
chr19	59128983	1937778	0.0328	0.2711
chr20	63025520	2196323	0.0348	0.2083
chr21	48129895	945063	0.0196	0.1607
chr22	51304566	715114	0.0139	0.1272
chrMT	16571	17867	1.0782	1.1814
chrX	155270560	4086404	0.0263	0.1833
chrY	59373566	235177	0.004	0.1194

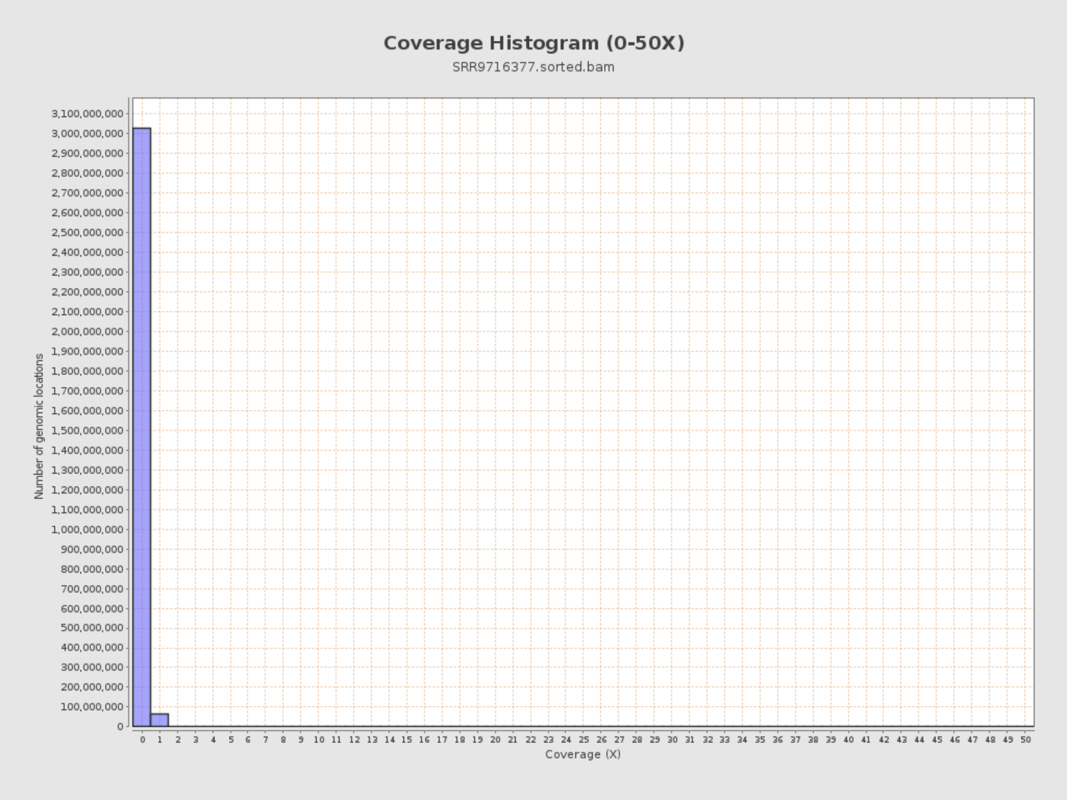
3. Results : Coverage across reference



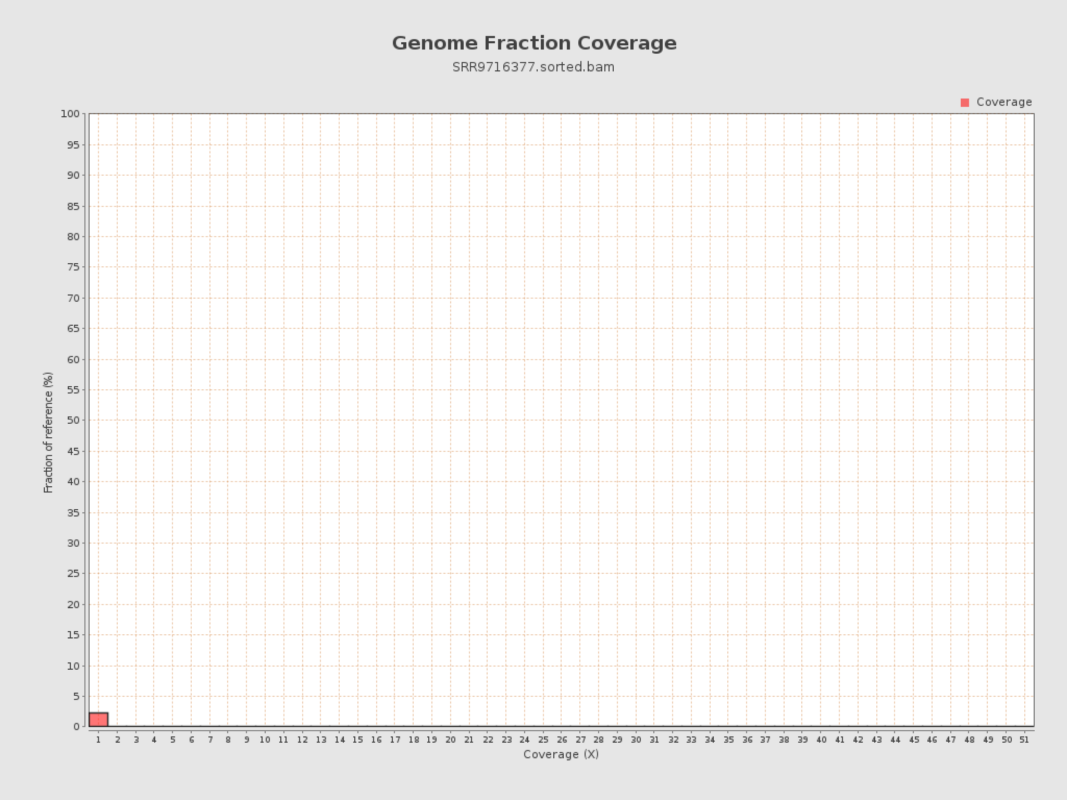
4. Results : Coverage Histogram



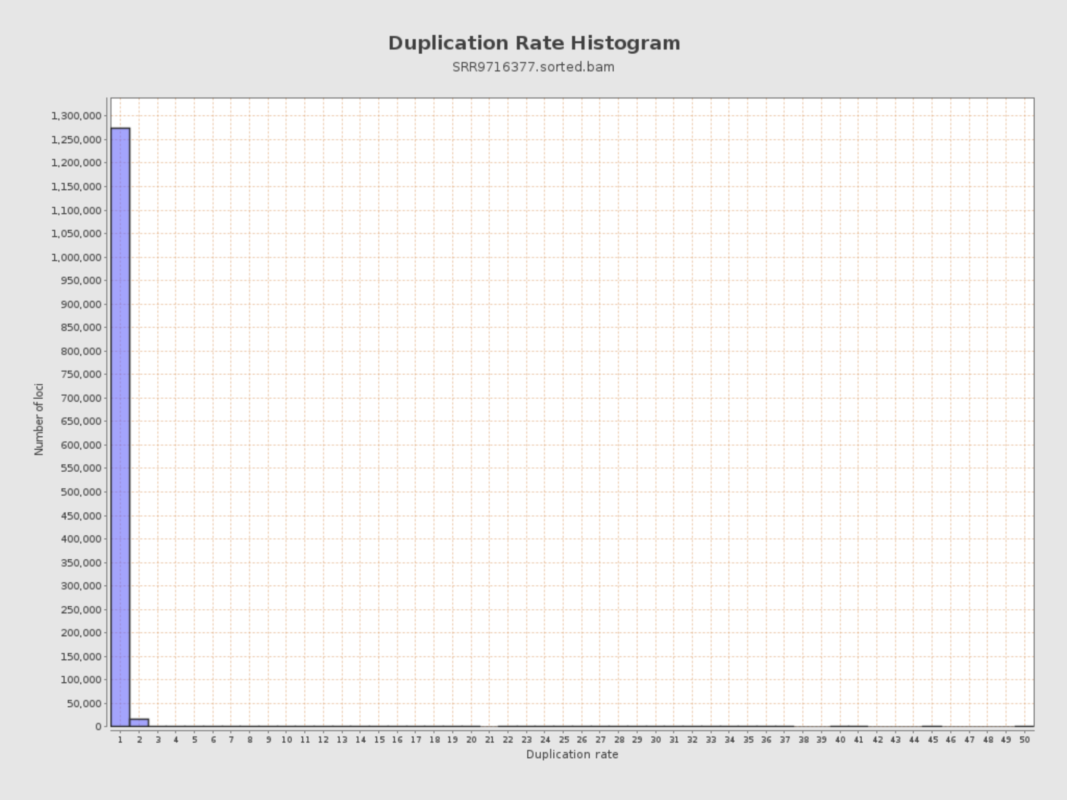
5. Results : Coverage Histogram (0-50X)



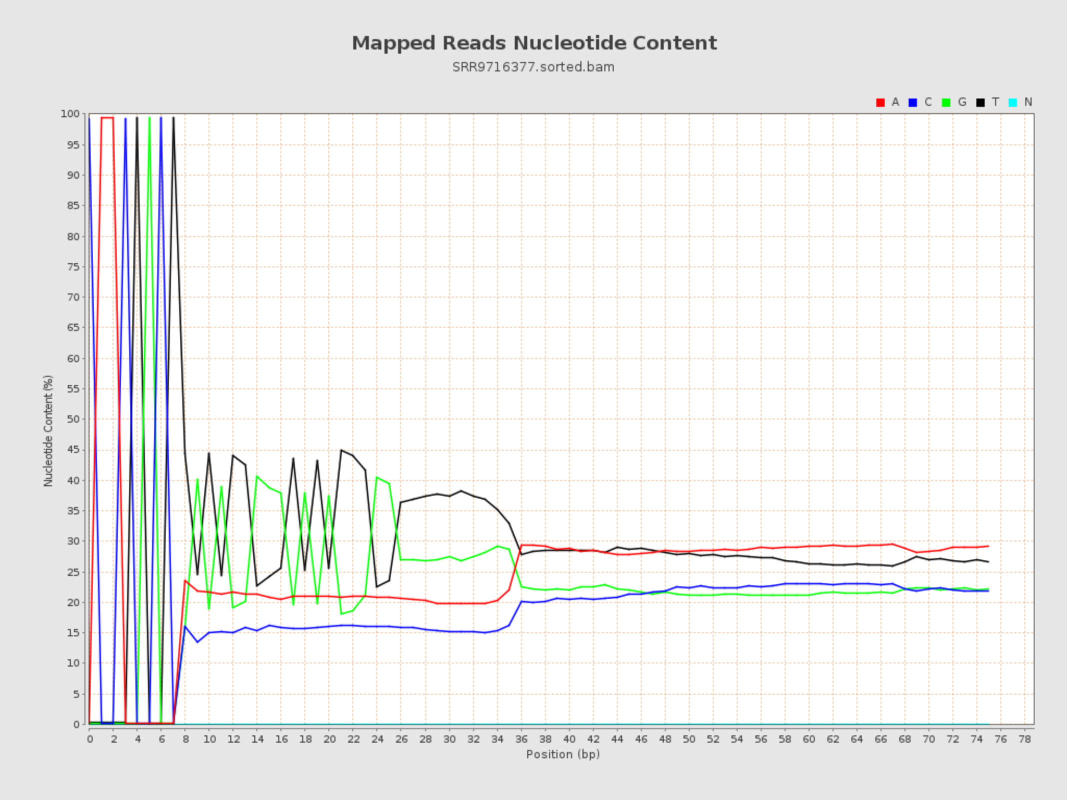
6. Results : Genome Fraction Coverage



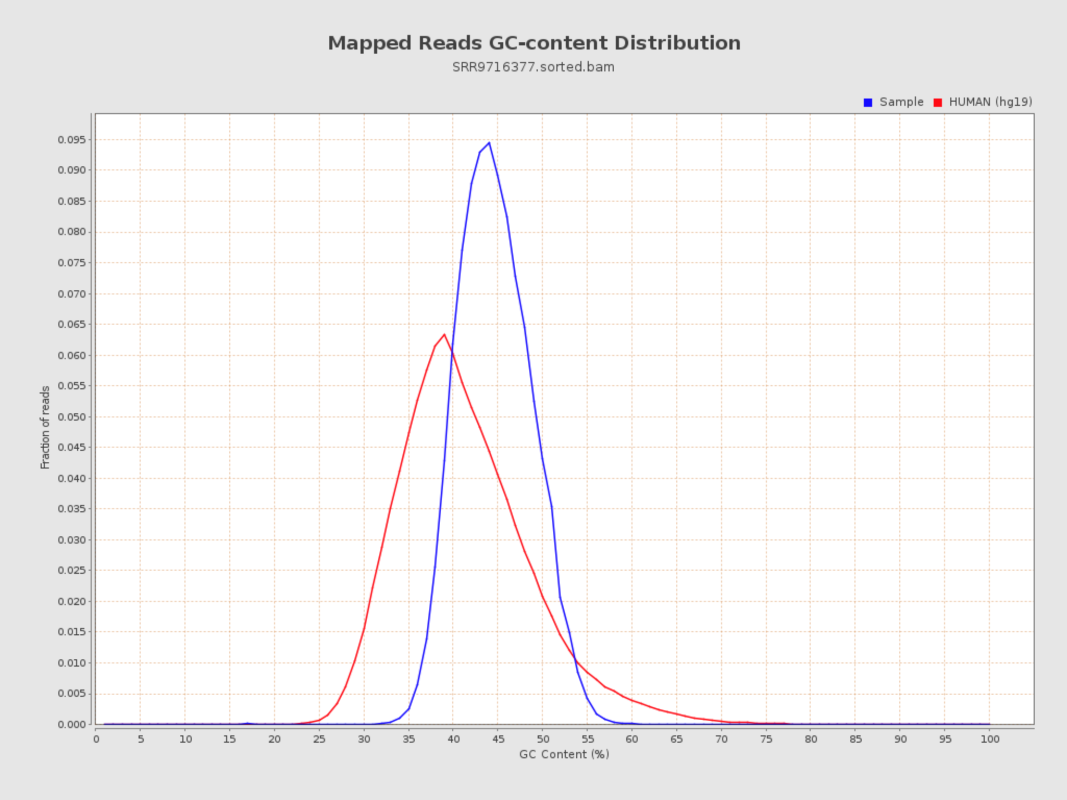
7. Results : Duplication Rate Histogram



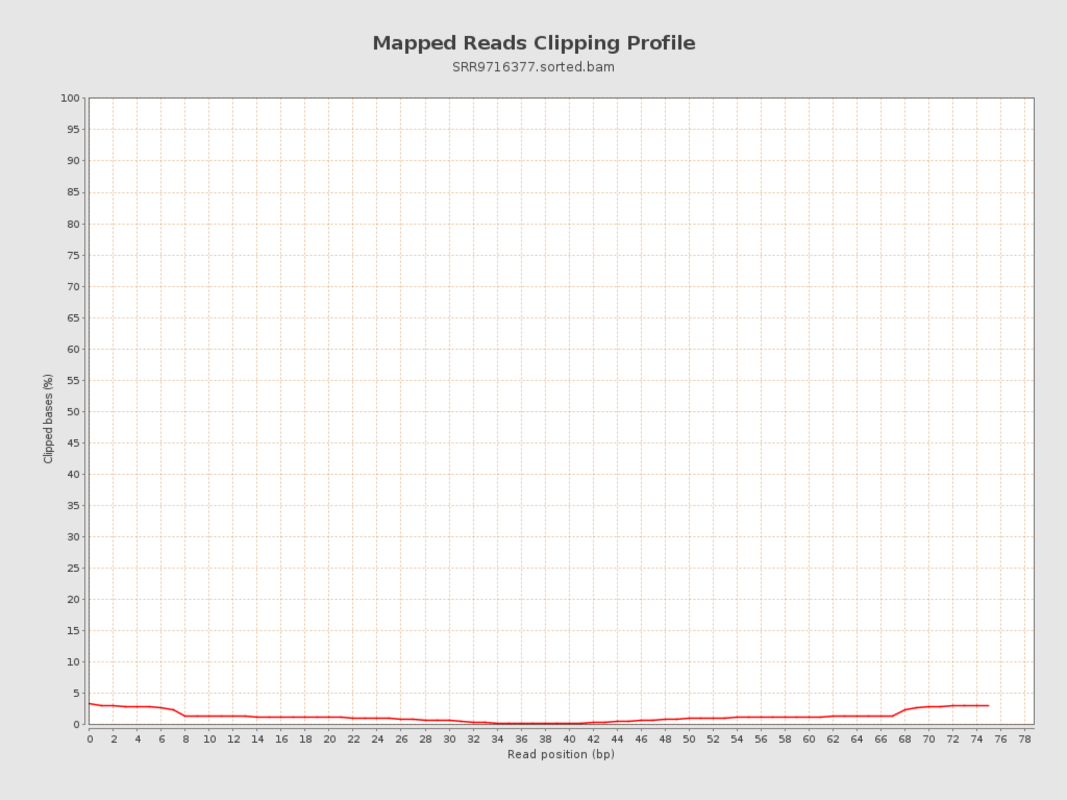
8. Results : Mapped Reads Nucleotide Content



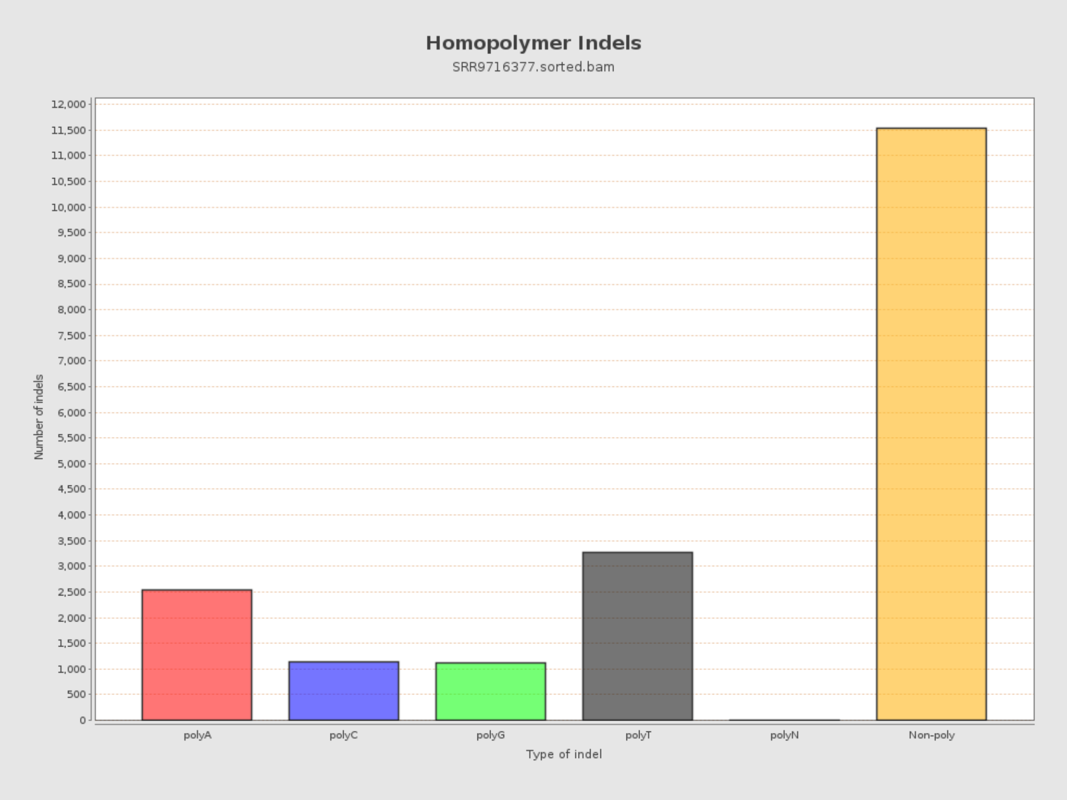
9. Results : Mapped Reads GC-content Distribution



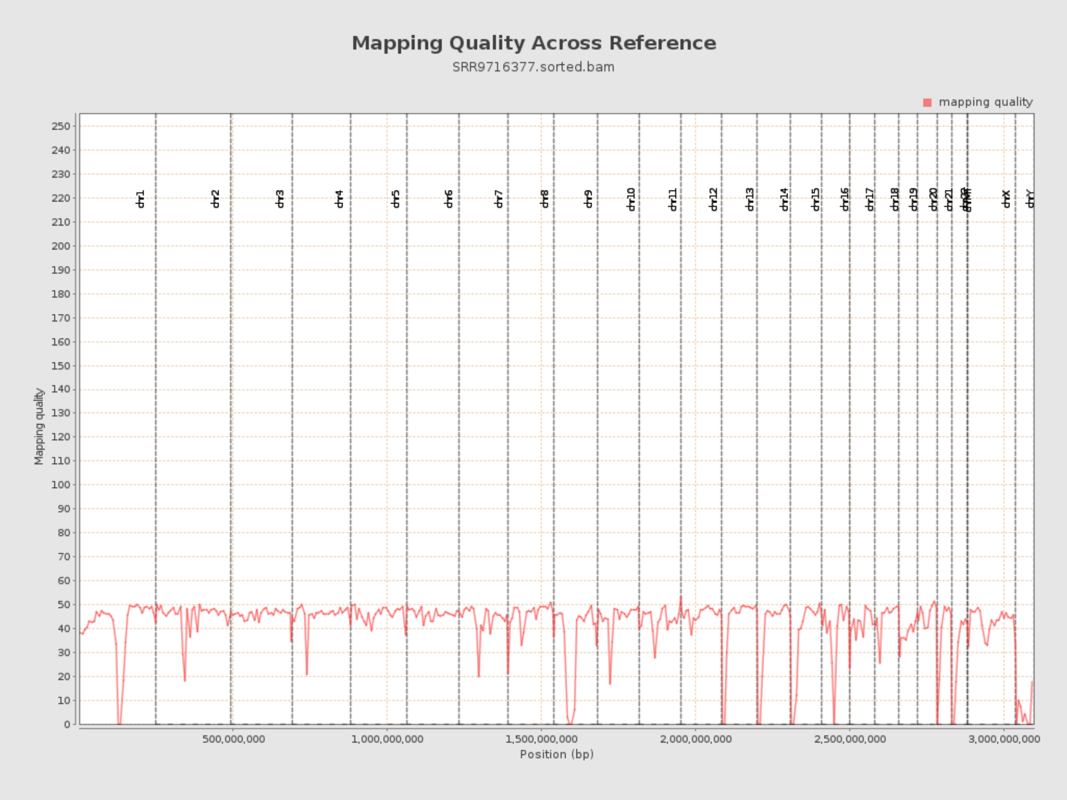
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram