Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 14:02:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716445.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_SRR9716445 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716445.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 14:02:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716445.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	980,146
Mapped reads	903,213 / 92.15%
Unmapped reads	76,933 / 7.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,711 / 1.4%
Read min/max/mean length	30 / 101 / 101.52
Duplicated reads (estimated)	28,722 / 2.93%
Duplication rate	1.89%
Clipped reads	914,835 / 93.34%

2.2. ACGT Content

Number/percentage of A's	17,639,381 / 24.59%
Number/percentage of C's	13,946,581 / 19.44%
Number/percentage of T's	22,243,418 / 31.01%
Number/percentage of G's	17,904,868 / 24.96%
Number/percentage of N's	4,520 / 0.01%
GC Percentage	44.4%

2.3. Coverage

Mean	0.0232

Standard Deviation	0.277

2.4. Mapping Quality

Mean Mapping Quality	44.6

2.5. Mismatches and indels

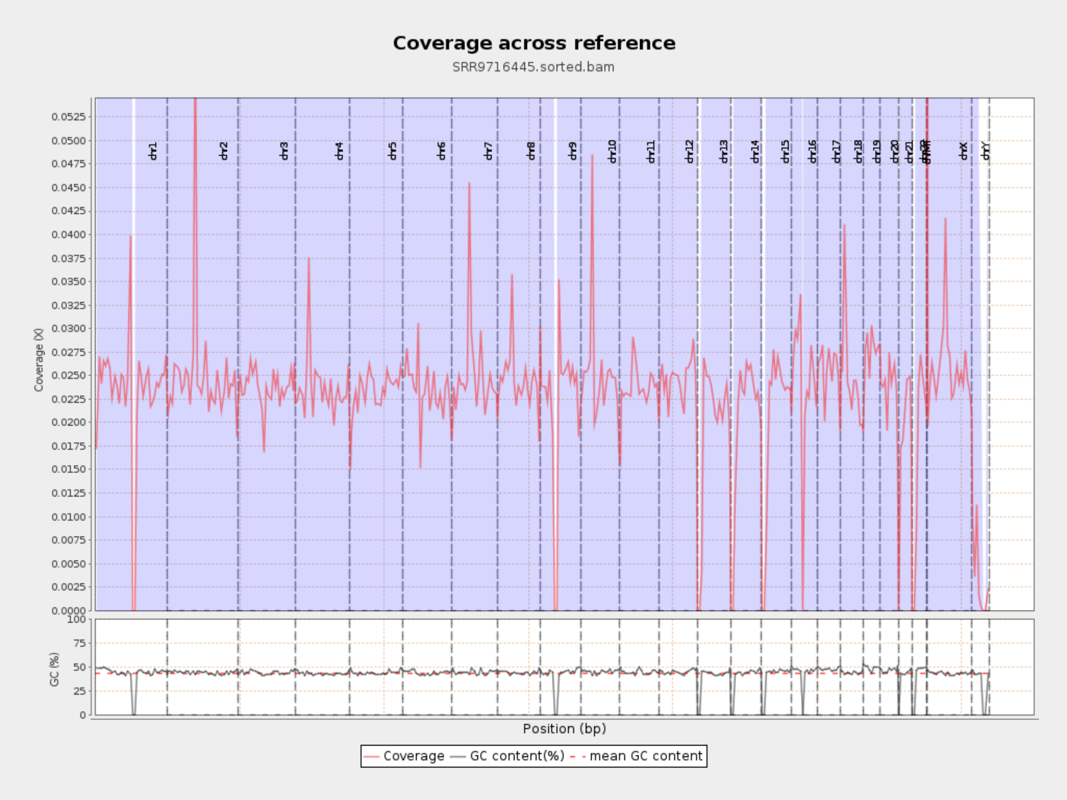
General error rate	0.83%
Mismatches	581,986
Insertions	6,917
Mapped reads with at least one insertion	0.75%
Deletions	18,442
Mapped reads with at least one deletion	2.01%
Homopolymer indels	43.62%

2.6. Chromosome stats

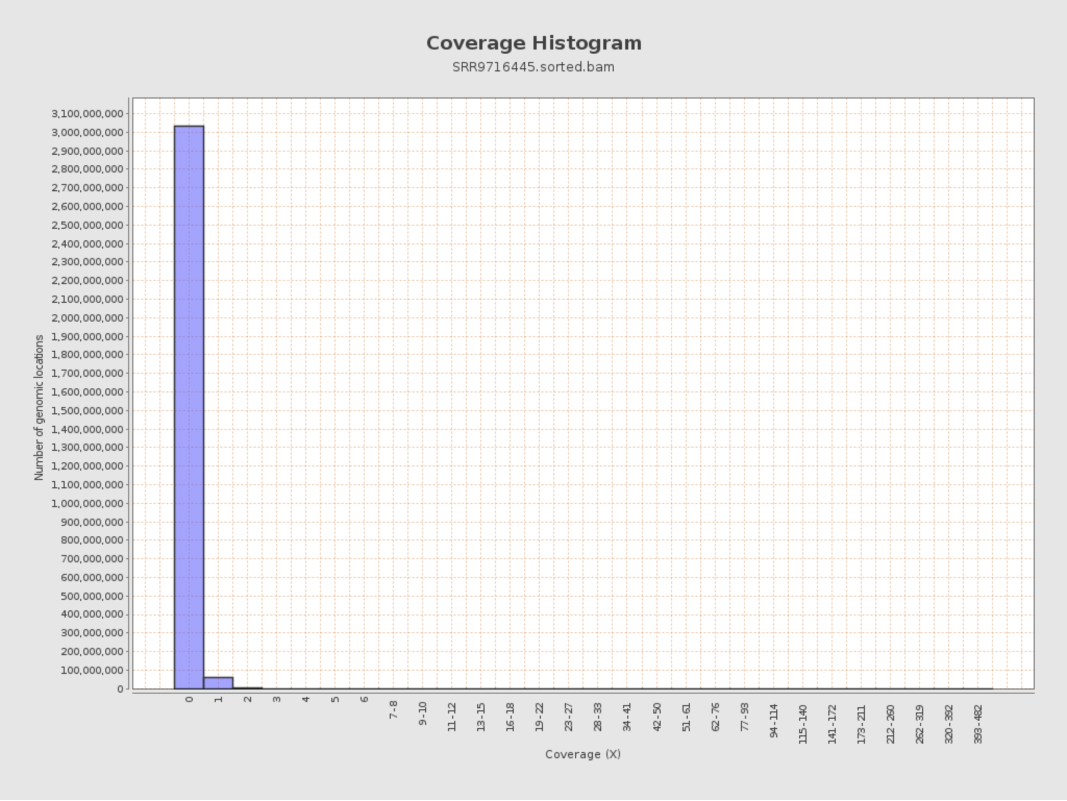
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5774005	0.0232	0.4157
chr2	243199373	6134003	0.0252	0.3987
chr3	198022430	4692732	0.0237	0.1659
chr4	191154276	4539254	0.0237	0.1821
chr5	180915260	4268758	0.0236	0.1679
chr6	171115067	4026104	0.0235	0.1905
chr7	159138663	3999740	0.0251	0.3433

chr8	146364022	3599480	0.0246	0.3653
chr9	141213431	3098011	0.0219	0.3061
chr10	135534747	3420888	0.0252	0.2799
chr11	135006516	3234138	0.024	0.2626
chr12	133851895	3291634	0.0246	0.1723
chr13	115169878	2188276	0.019	0.1469
chr14	107349540	2146997	0.02	0.1926
chr15	102531392	2053542	0.02	0.1537
chr16	90354753	2139301	0.0237	0.1857
chr17	81195210	2074691	0.0256	0.1829
chr18	78077248	1951345	0.025	0.5621
chr19	59128983	1637066	0.0277	0.3105
chr20	63025520	1493294	0.0237	0.1759
chr21	48129895	913695	0.019	0.1595
chr22	51304566	865129	0.0169	0.1396
chrMT	16571	6331	0.3821	0.6958
chrX	155270560	4024556	0.0259	0.2163
chrY	59373566	198835	0.0033	0.109

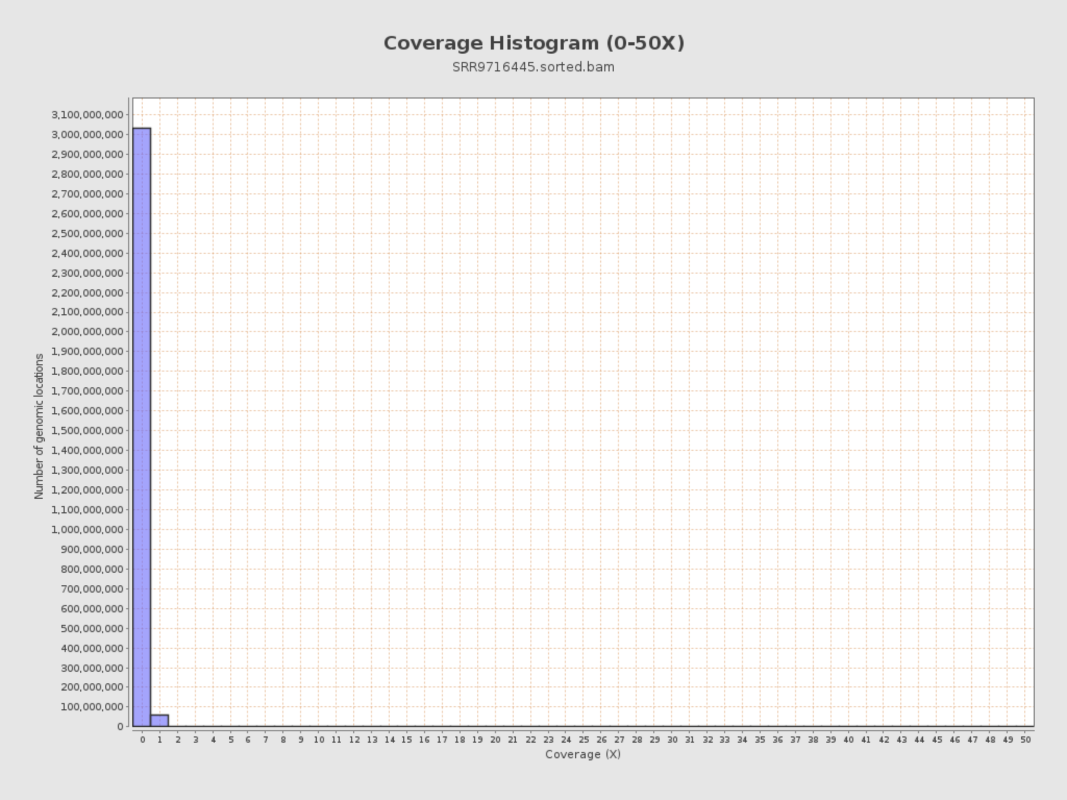
3. Results : Coverage across reference



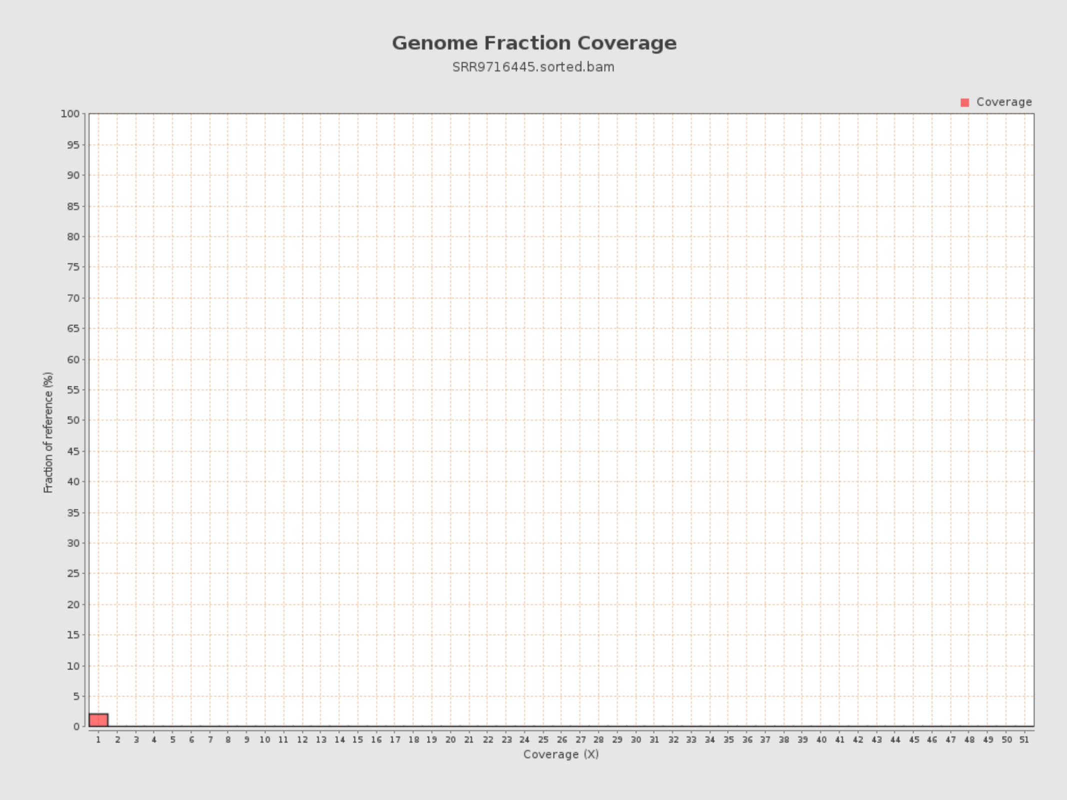
4. Results : Coverage Histogram



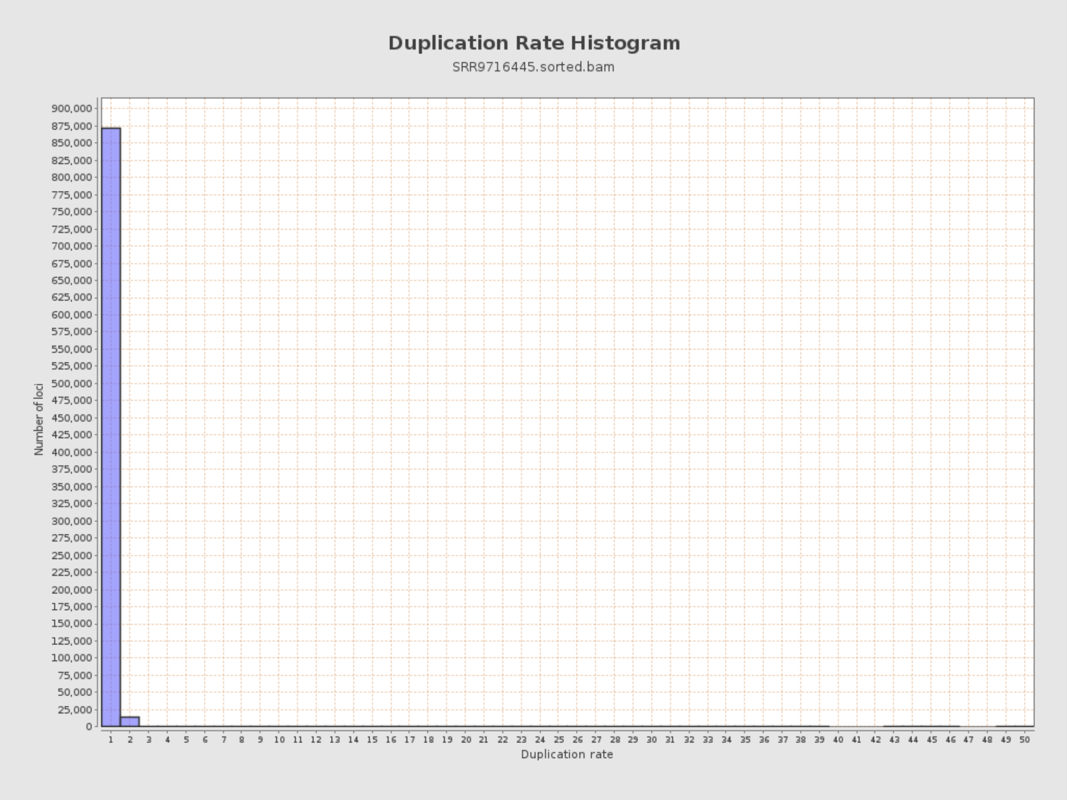
5. Results : Coverage Histogram (0-50X)



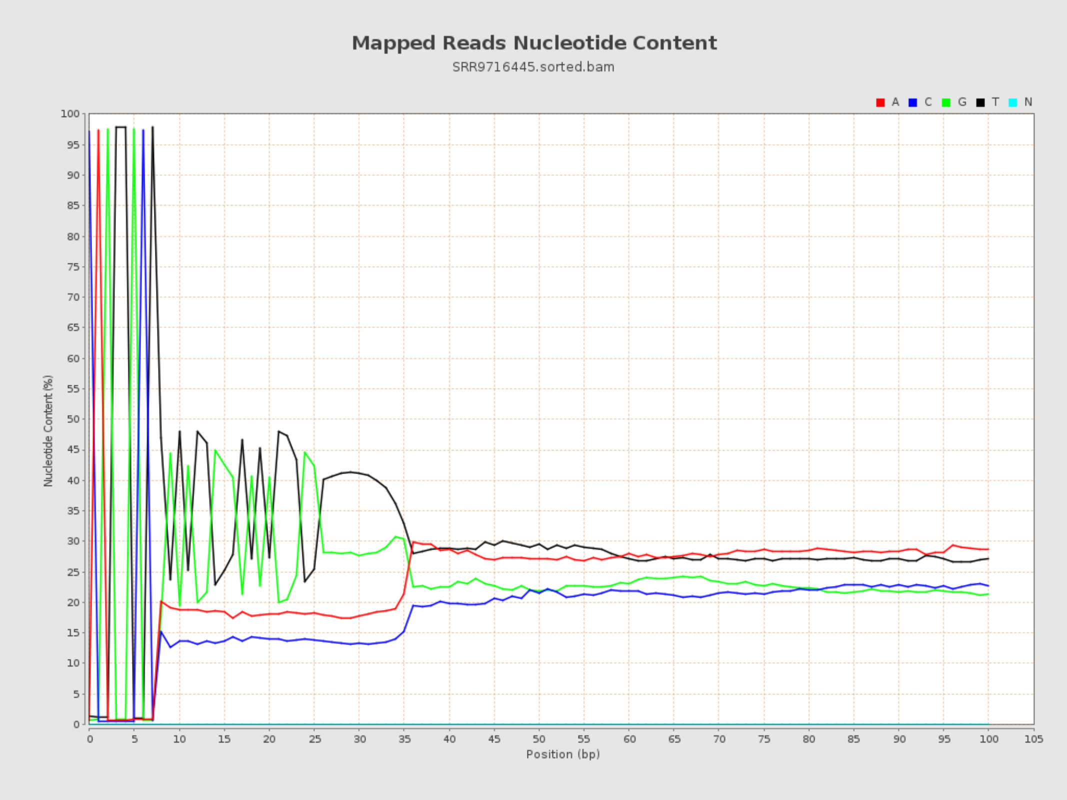
6. Results : Genome Fraction Coverage



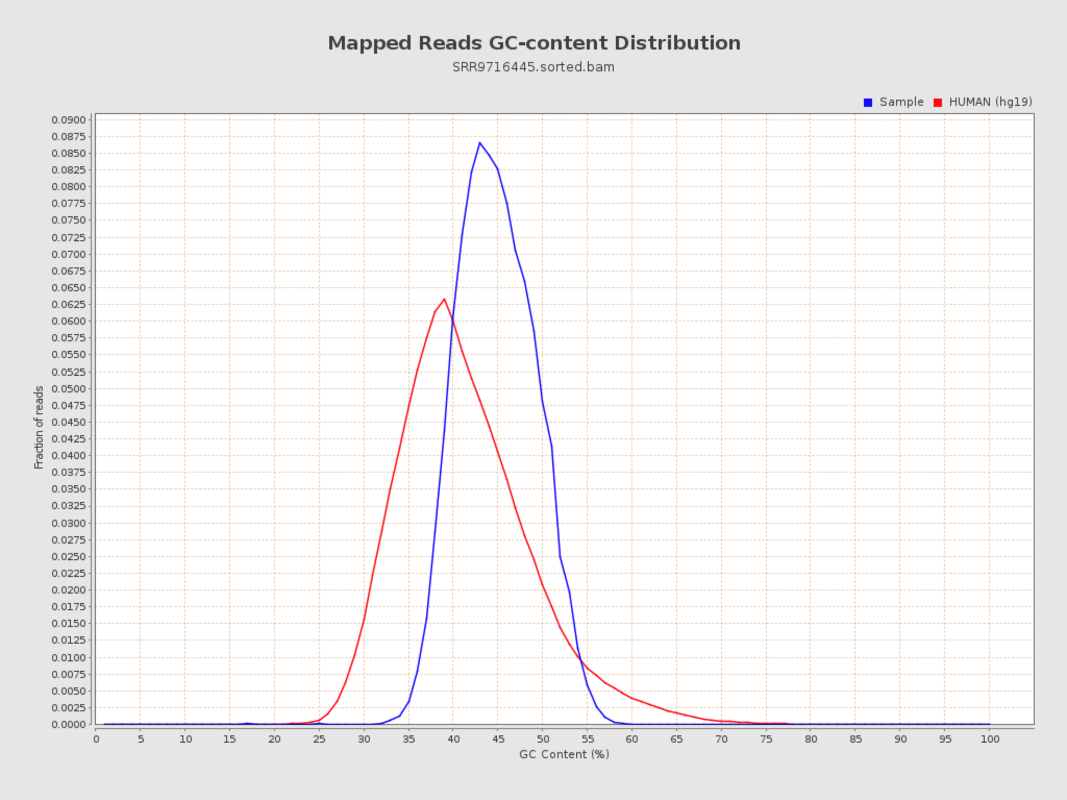
7. Results : Duplication Rate Histogram



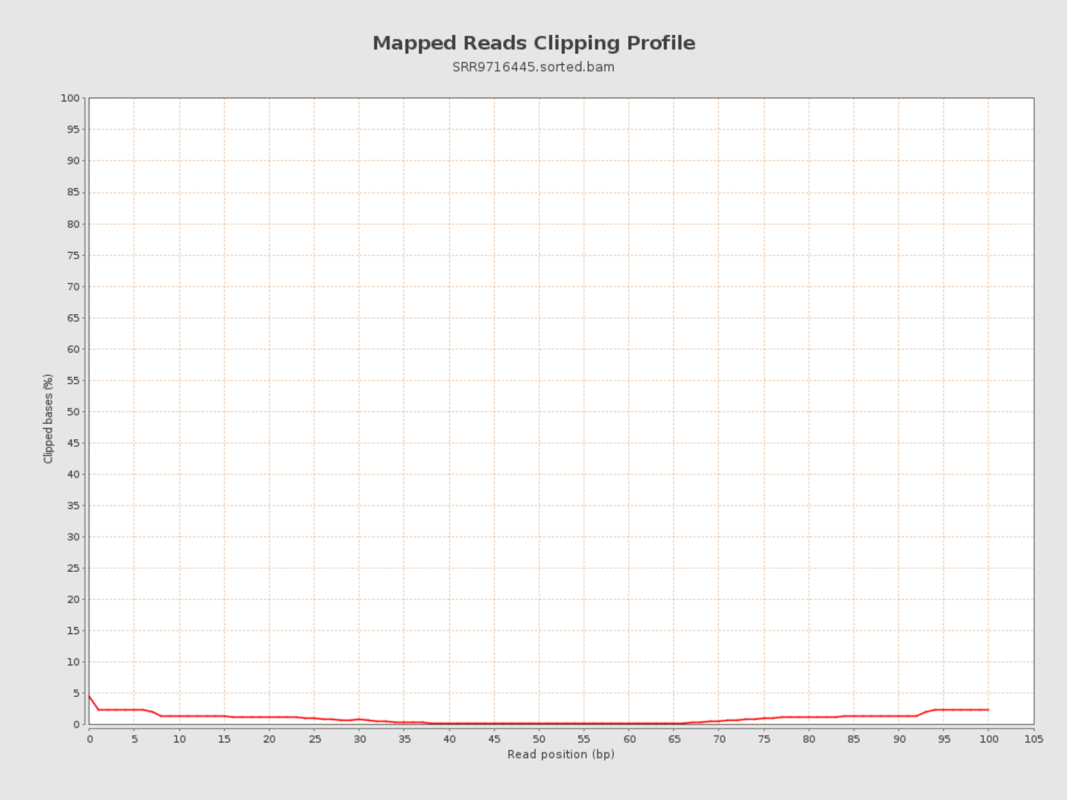
8. Results : Mapped Reads Nucleotide Content



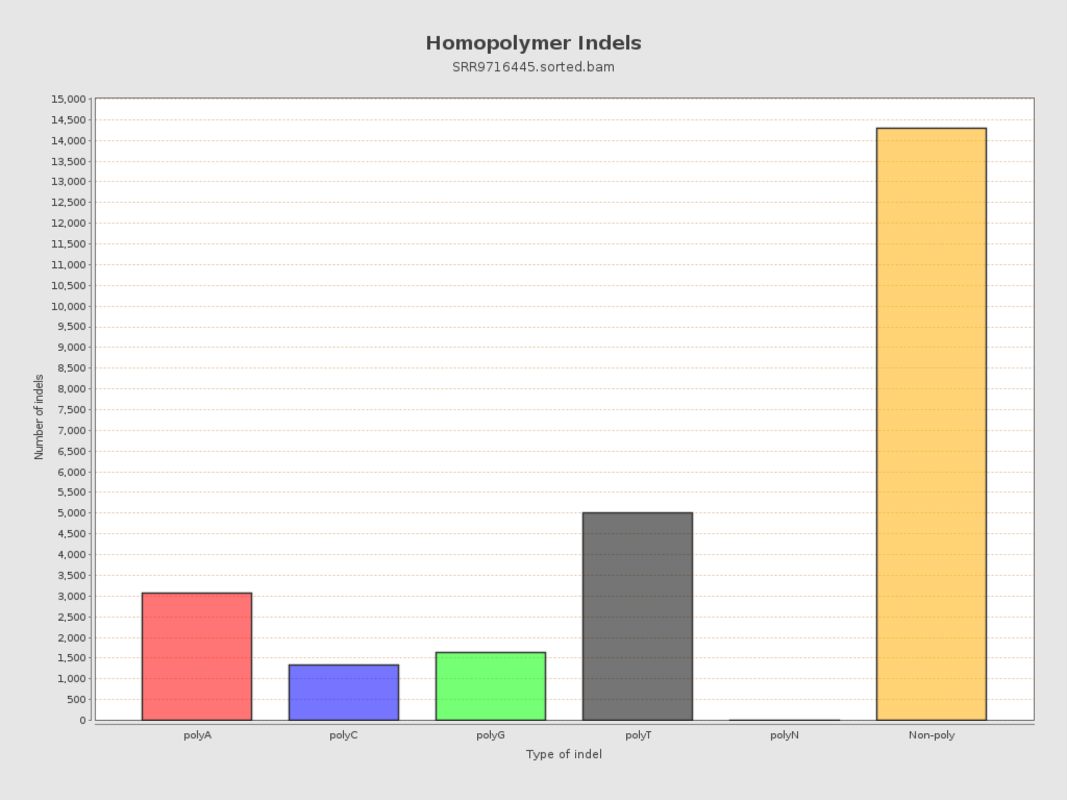
9. Results : Mapped Reads GC-content Distribution



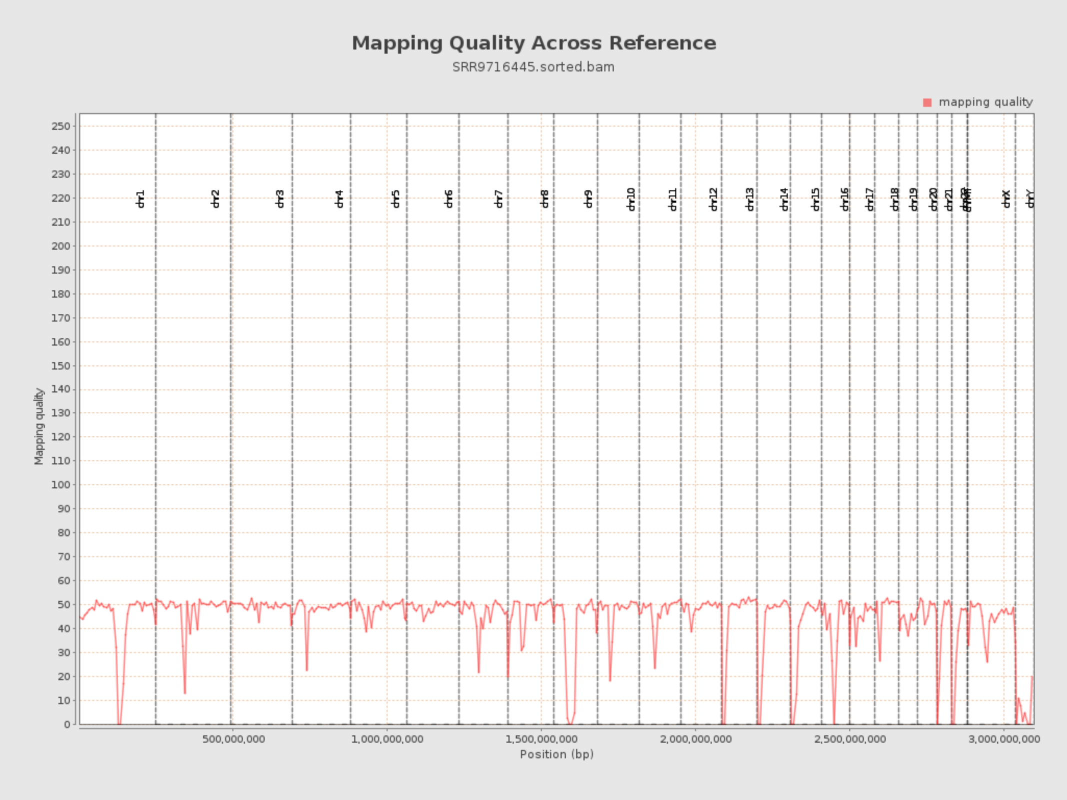
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram