Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 18:20:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716910.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_SRR9716910 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716910.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 18:20:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716910.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,427,915
Mapped reads	1,297,908 / 90.9%
Unmapped reads	130,007 / 9.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,048 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	34,835 / 2.44%
Duplication rate	2.04%
Clipped reads	1,299,816 / 91.03%

2.2. ACGT Content

Number/percentage of A's	19,504,322 / 25.84%
Number/percentage of C's	14,795,127 / 19.6%
Number/percentage of T's	22,442,021 / 29.73%
Number/percentage of G's	18,740,099 / 24.83%
Number/percentage of N's	570 / 0%
GC Percentage	44.43%

2.3. Coverage

Mean	0.0244

Standard Deviation	0.2084

2.4. Mapping Quality

Mean Mapping Quality	44.34

2.5. Mismatches and indels

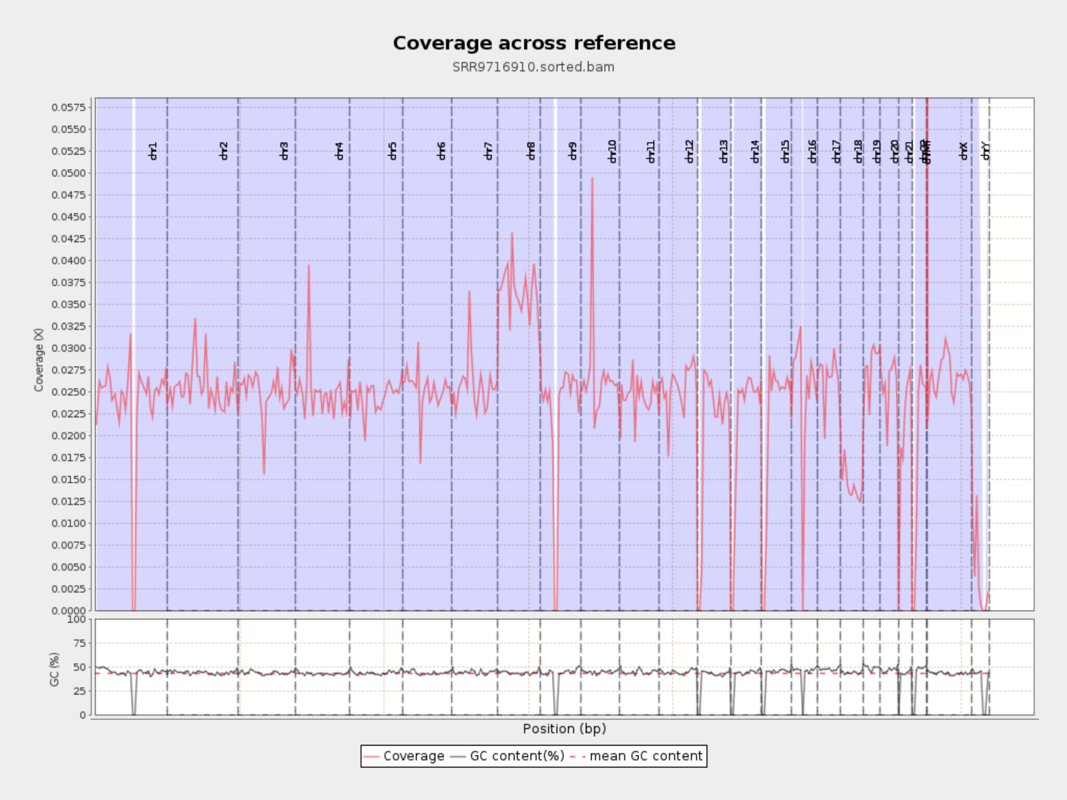
General error rate	0.53%
Mismatches	388,446
Insertions	5,847
Mapped reads with at least one insertion	0.45%
Deletions	14,265
Mapped reads with at least one deletion	1.09%
Homopolymer indels	40.32%

2.6. Chromosome stats

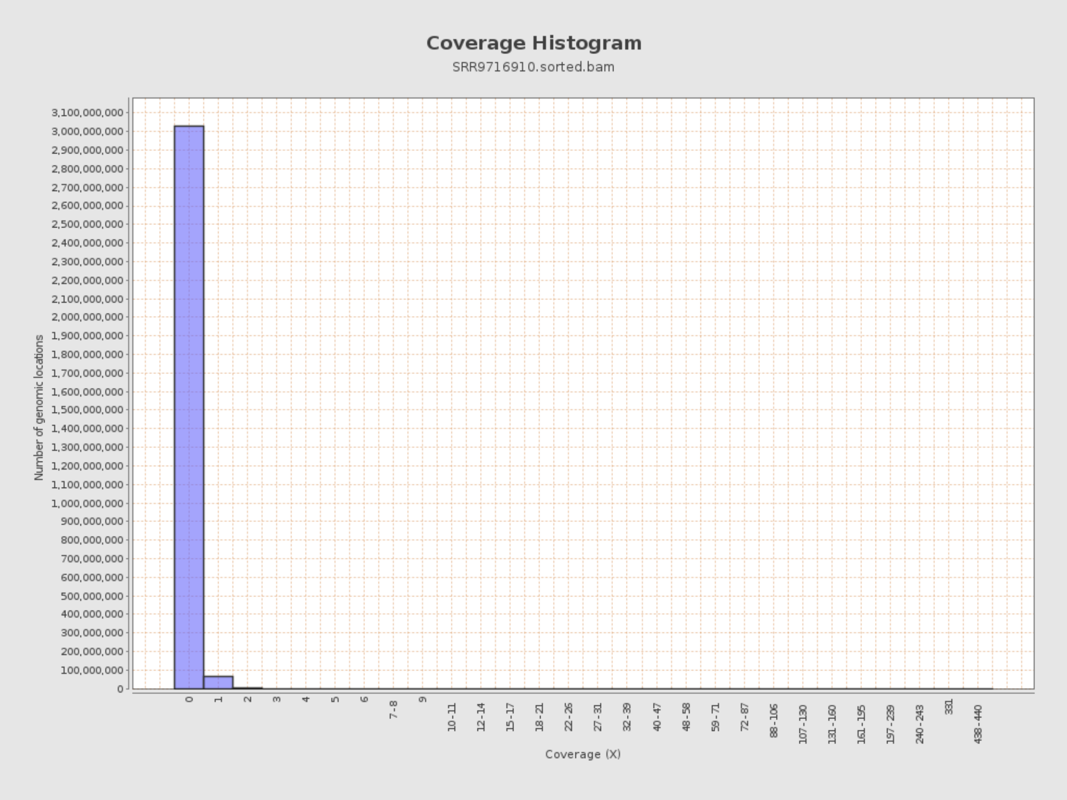
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5895289	0.0237	0.271
chr2	243199373	6238051	0.0256	0.2653
chr3	198022430	4985861	0.0252	0.1722
chr4	191154276	4803382	0.0251	0.186
chr5	180915260	4456330	0.0246	0.1692
chr6	171115067	4323082	0.0253	0.1915
chr7	159138663	4098718	0.0258	0.2577

chr8	146364022	5347146	0.0365	0.2395
chr9	141213431	3148961	0.0223	0.1822
chr10	135534747	3634168	0.0268	0.2659
chr11	135006516	3326039	0.0246	0.1899
chr12	133851895	3420850	0.0256	0.1736
chr13	115169878	2342124	0.0203	0.1546
chr14	107349540	2261302	0.0211	0.1638
chr15	102531392	2175220	0.0212	0.1589
chr16	90354753	2219770	0.0246	0.1826
chr17	81195210	2157569	0.0266	0.1841
chr18	78077248	1110821	0.0142	0.2455
chr19	59128983	1648398	0.0279	0.2468
chr20	63025520	1613668	0.0256	0.1777
chr21	48129895	988371	0.0205	0.1701
chr22	51304566	920949	0.018	0.1476
chrMT	16571	2848	0.1719	0.4448
chrX	155270560	4157978	0.0268	0.1846
chrY	59373566	228057	0.0038	0.1169

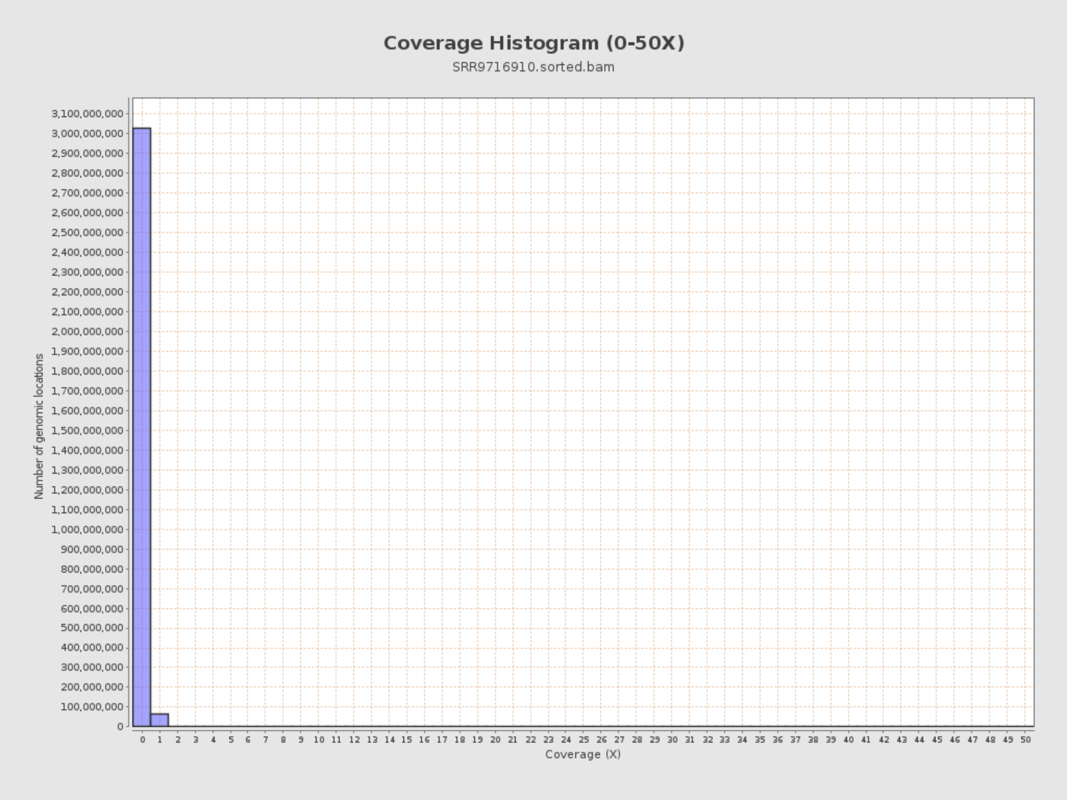
3. Results : Coverage across reference



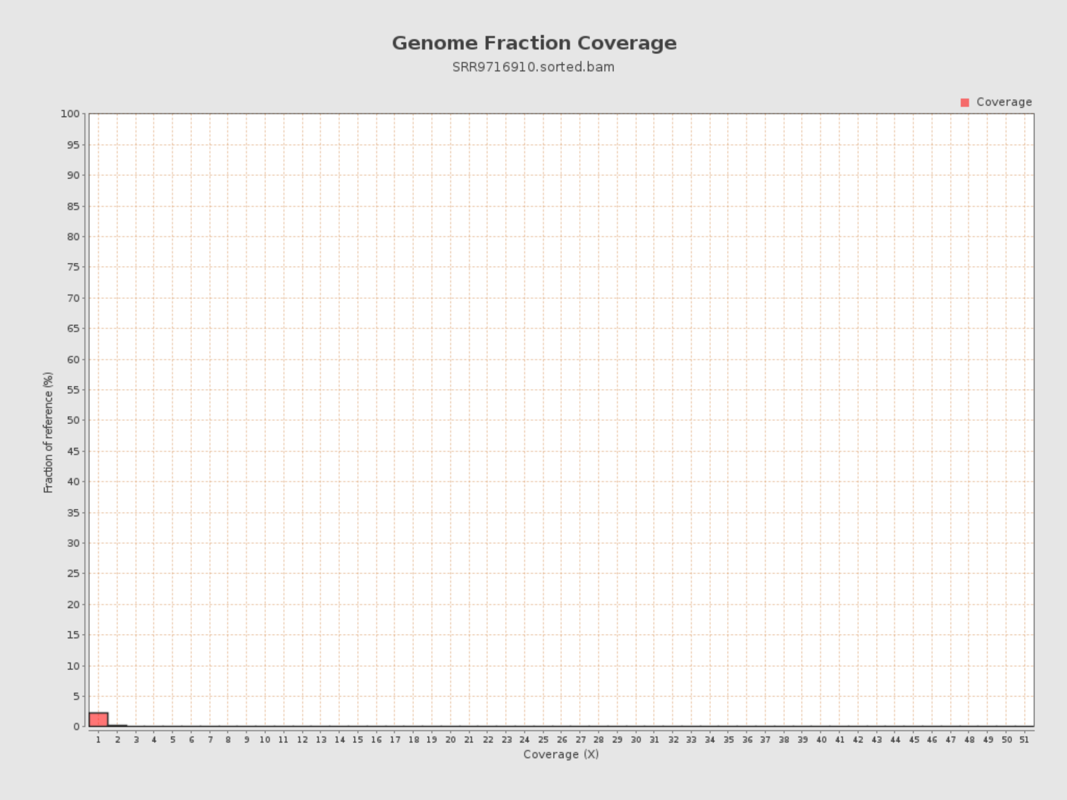
4. Results : Coverage Histogram



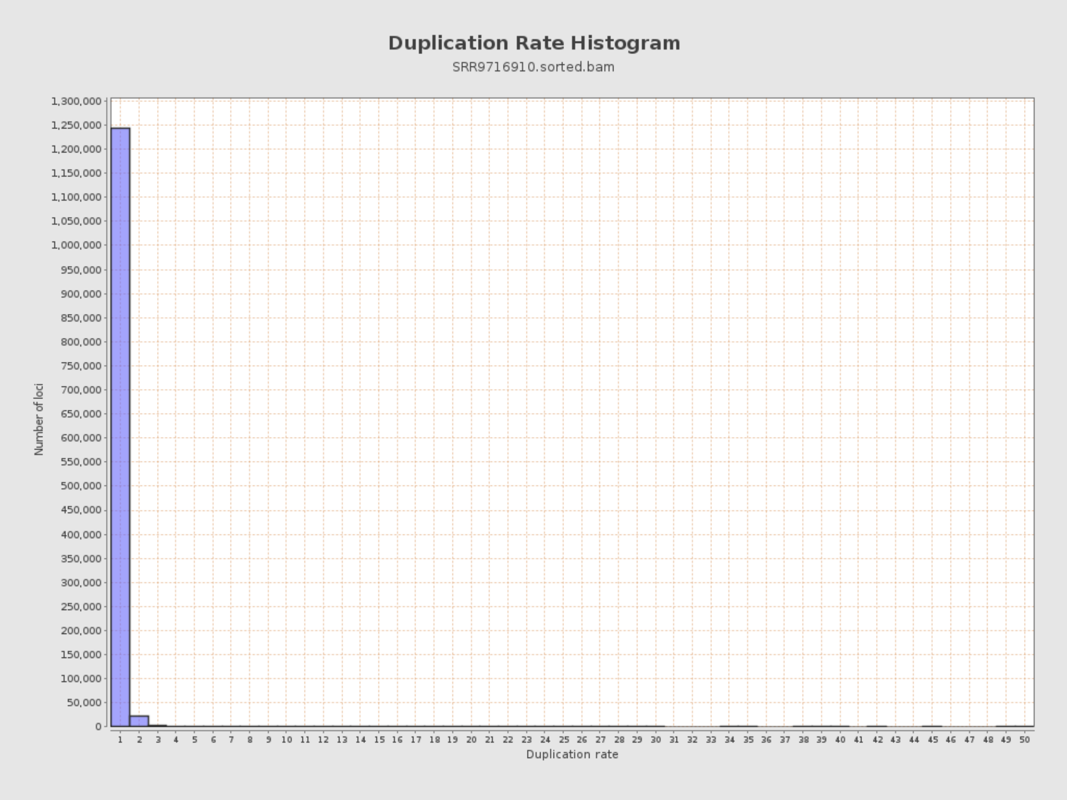
5. Results : Coverage Histogram (0-50X)



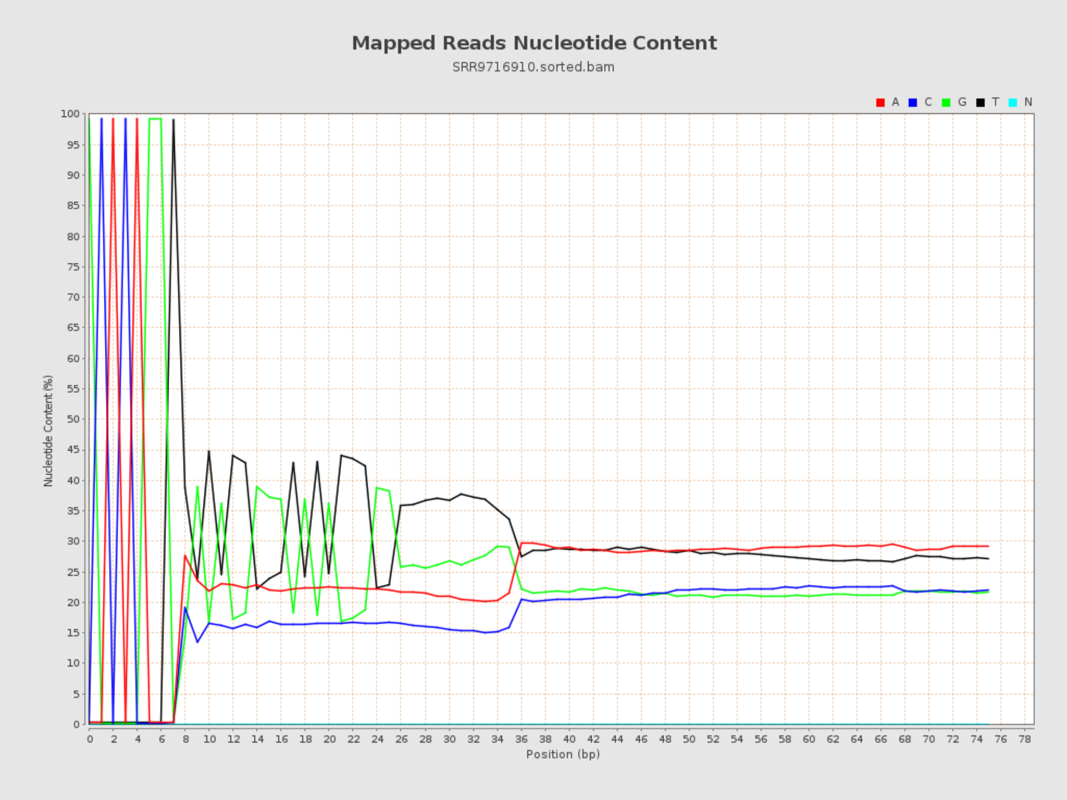
6. Results : Genome Fraction Coverage



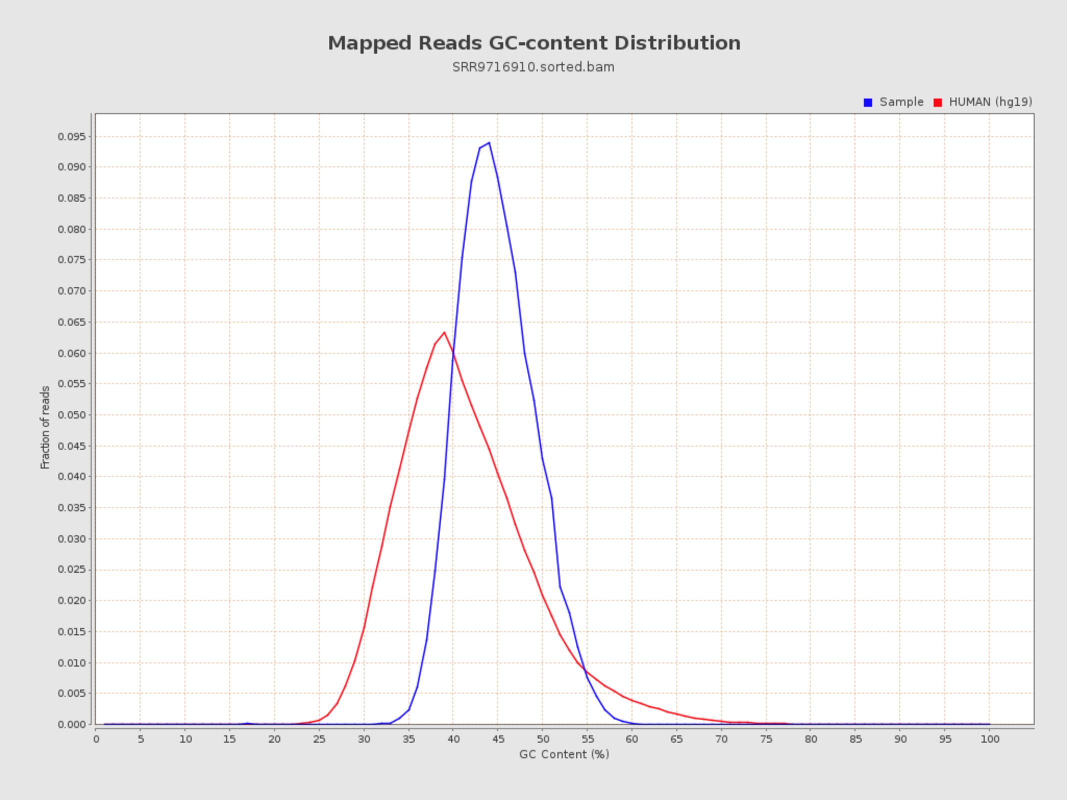
7. Results : Duplication Rate Histogram



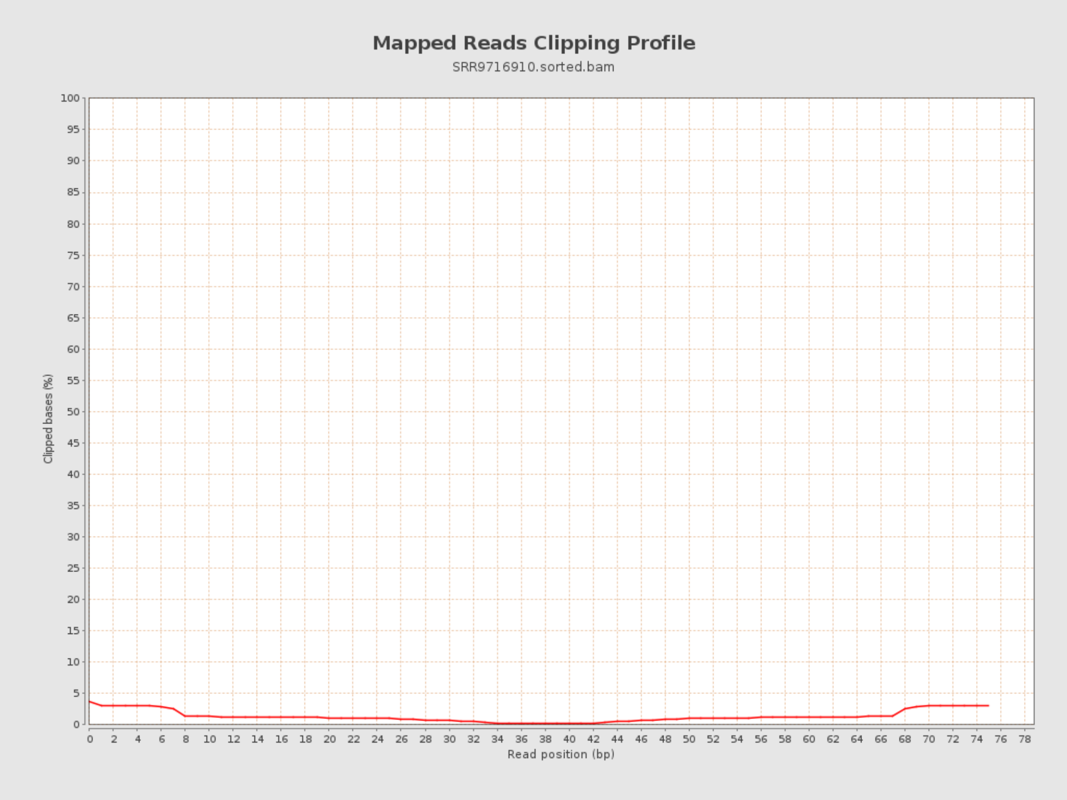
8. Results : Mapped Reads Nucleotide Content



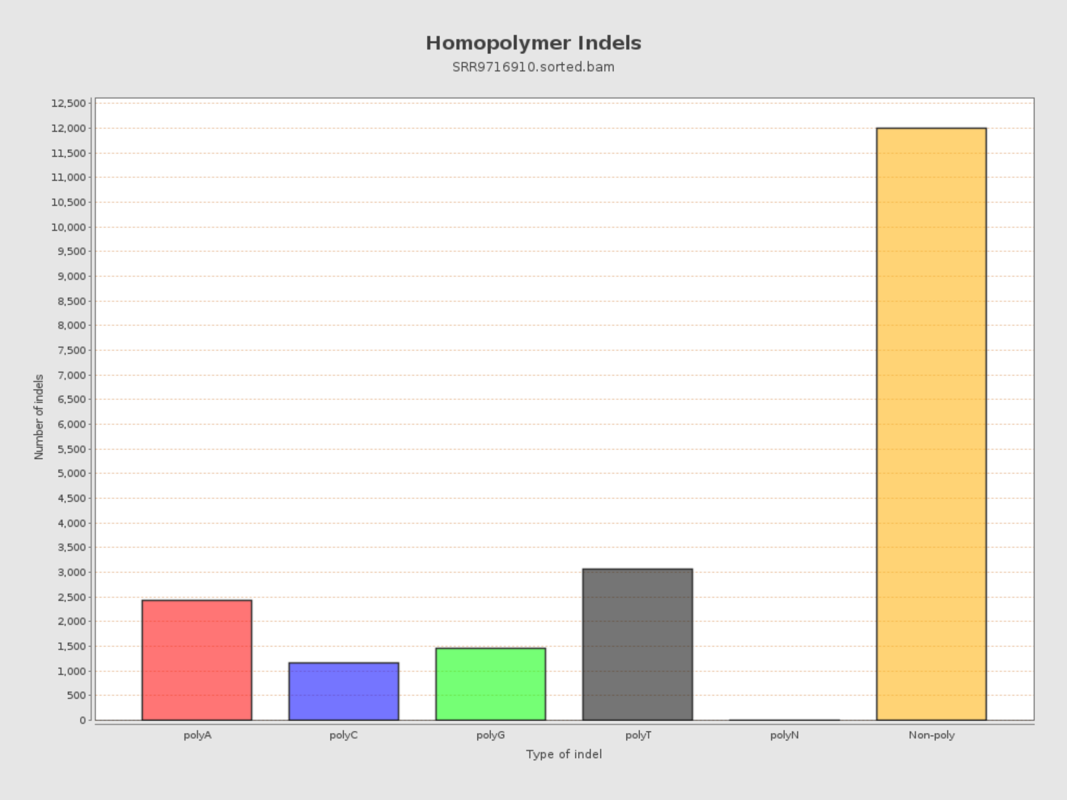
9. Results : Mapped Reads GC-content Distribution



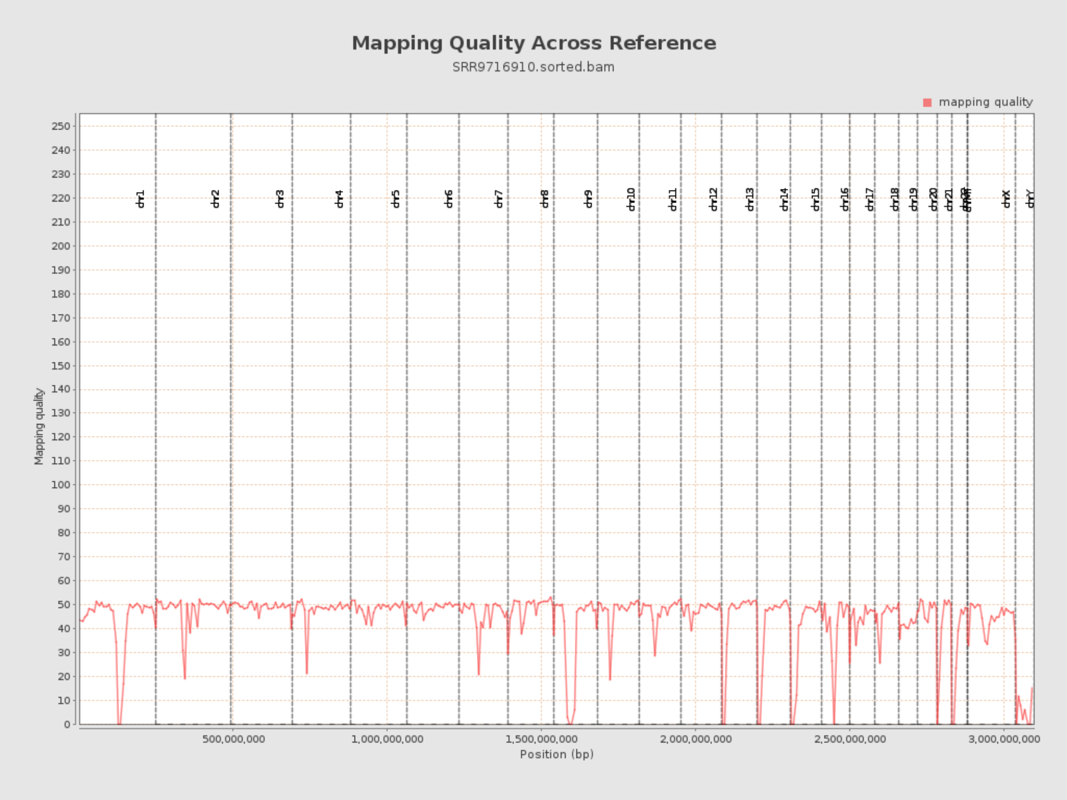
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram