Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 19:11:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716130.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_SRR9716130 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716130.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 19:11:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716130.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,082,959
Mapped reads	999,042 / 92.25%
Unmapped reads	83,917 / 7.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,054 / 1.85%
Read min/max/mean length	30 / 101 / 101.66
Duplicated reads (estimated)	21,992 / 2.03%
Duplication rate	1.45%
Clipped reads	1,016,212 / 93.84%

2.2. ACGT Content

Number/percentage of A's	20,059,645 / 25.58%
Number/percentage of C's	16,045,336 / 20.46%
Number/percentage of T's	24,257,479 / 30.93%
Number/percentage of G's	18,047,352 / 23.02%
Number/percentage of N's	5,773 / 0.01%
GC Percentage	43.48%

2.3. Coverage

Mean	0.0253

Standard Deviation	0.2367

2.4. Mapping Quality

Mean Mapping Quality	47.37

2.5. Mismatches and indels

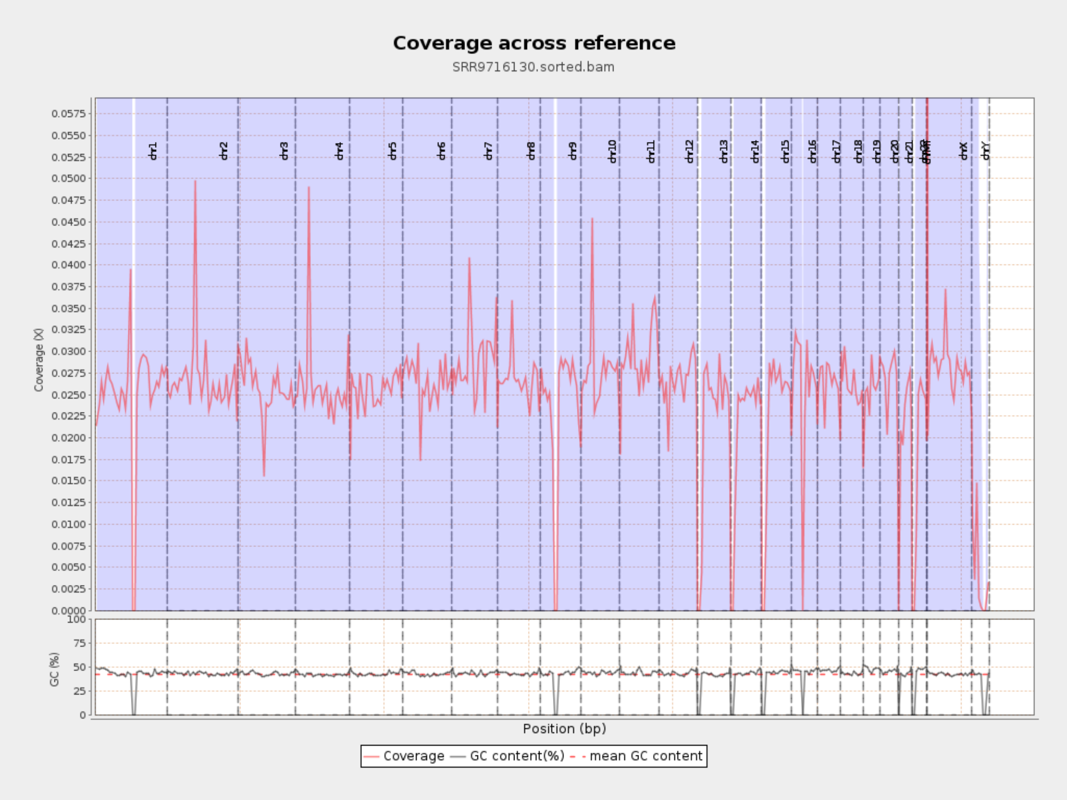
General error rate	0.69%
Mismatches	522,840
Insertions	7,266
Mapped reads with at least one insertion	0.72%
Deletions	18,902
Mapped reads with at least one deletion	1.86%
Homopolymer indels	42.42%

2.6. Chromosome stats

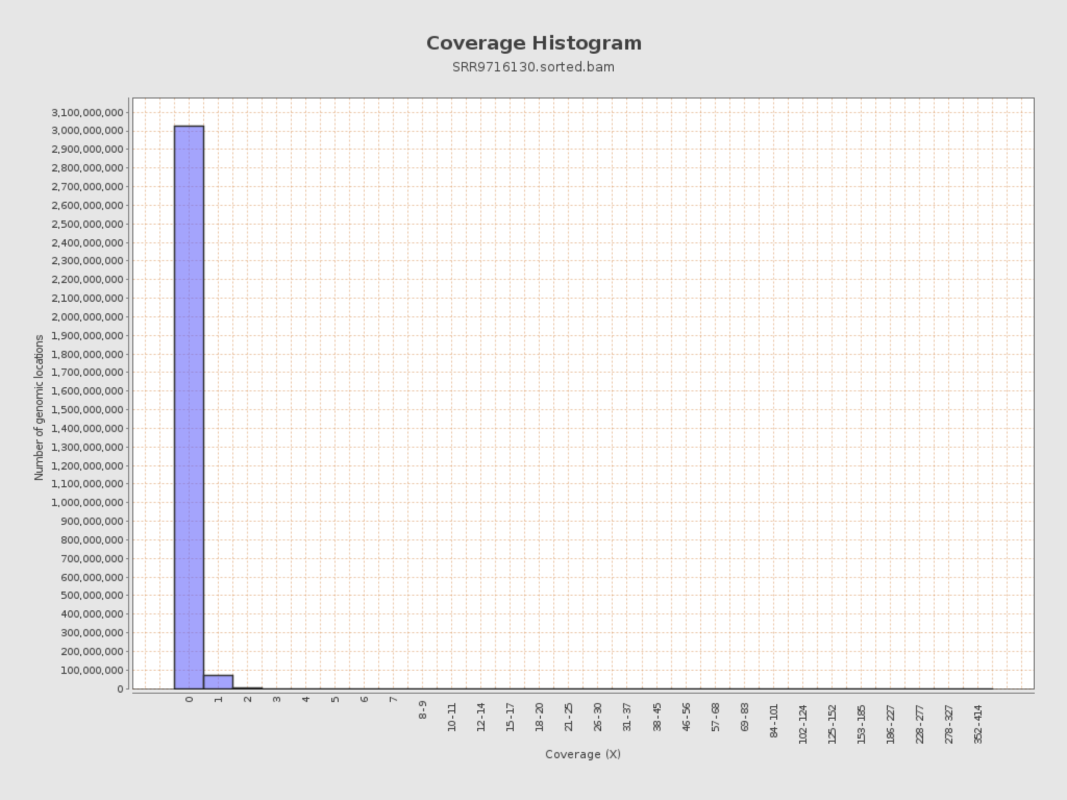
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6209276	0.0249	0.3693
chr2	243199373	6533959	0.0269	0.2864
chr3	198022430	5097129	0.0257	0.1681
chr4	191154276	5006182	0.0262	0.2012
chr5	180915260	4669314	0.0258	0.1696
chr6	171115067	4518794	0.0264	0.1816
chr7	159138663	4634412	0.0291	0.3297

chr8	146364022	3917210	0.0268	0.2817
chr9	141213431	3292615	0.0233	0.2173
chr10	135534747	3792034	0.028	0.2452
chr11	135006516	4004332	0.0297	0.256
chr12	133851895	3565919	0.0266	0.1717
chr13	115169878	2472730	0.0215	0.1531
chr14	107349540	2242189	0.0209	0.1611
chr15	102531392	2250152	0.0219	0.1562
chr16	90354753	2295943	0.0254	0.1762
chr17	81195210	2131521	0.0263	0.1847
chr18	78077248	2043585	0.0262	0.344
chr19	59128983	1515525	0.0256	0.269
chr20	63025520	1689036	0.0268	0.1794
chr21	48129895	1022050	0.0212	0.1686
chr22	51304566	898532	0.0175	0.1398
chrMT	16571	30437	1.8368	1.7707
chrX	155270560	4385849	0.0282	0.1974
chrY	59373566	232952	0.0039	0.1369

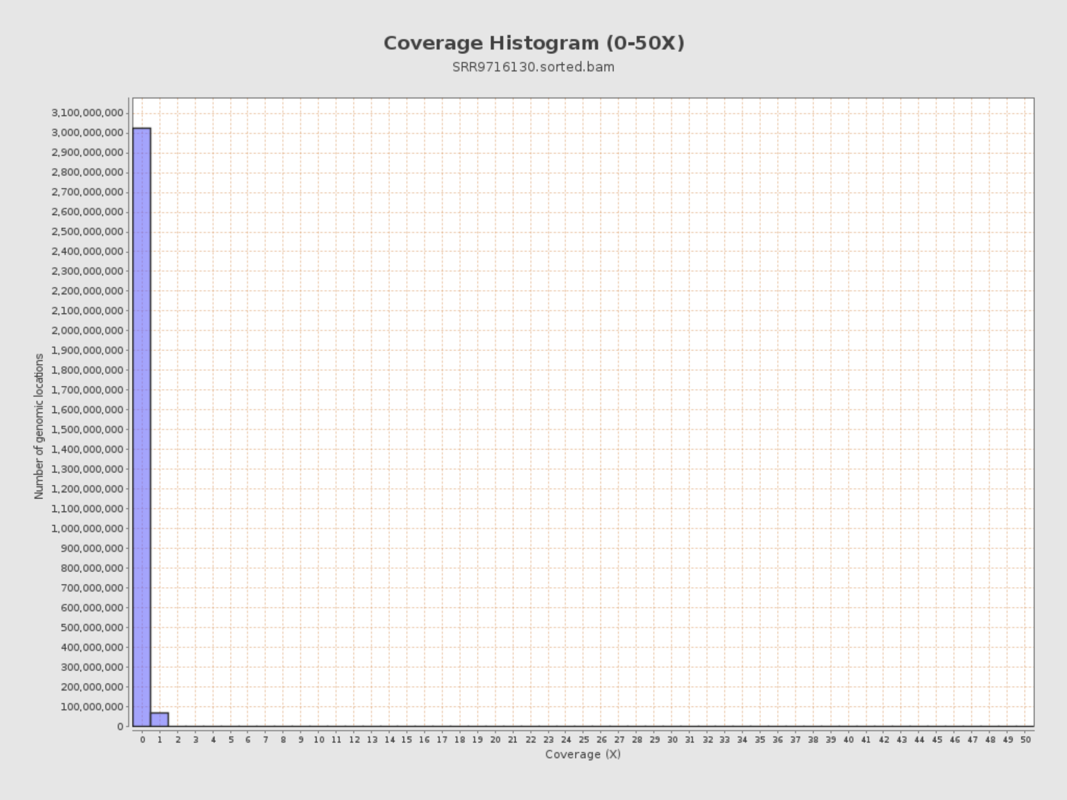
3. Results : Coverage across reference



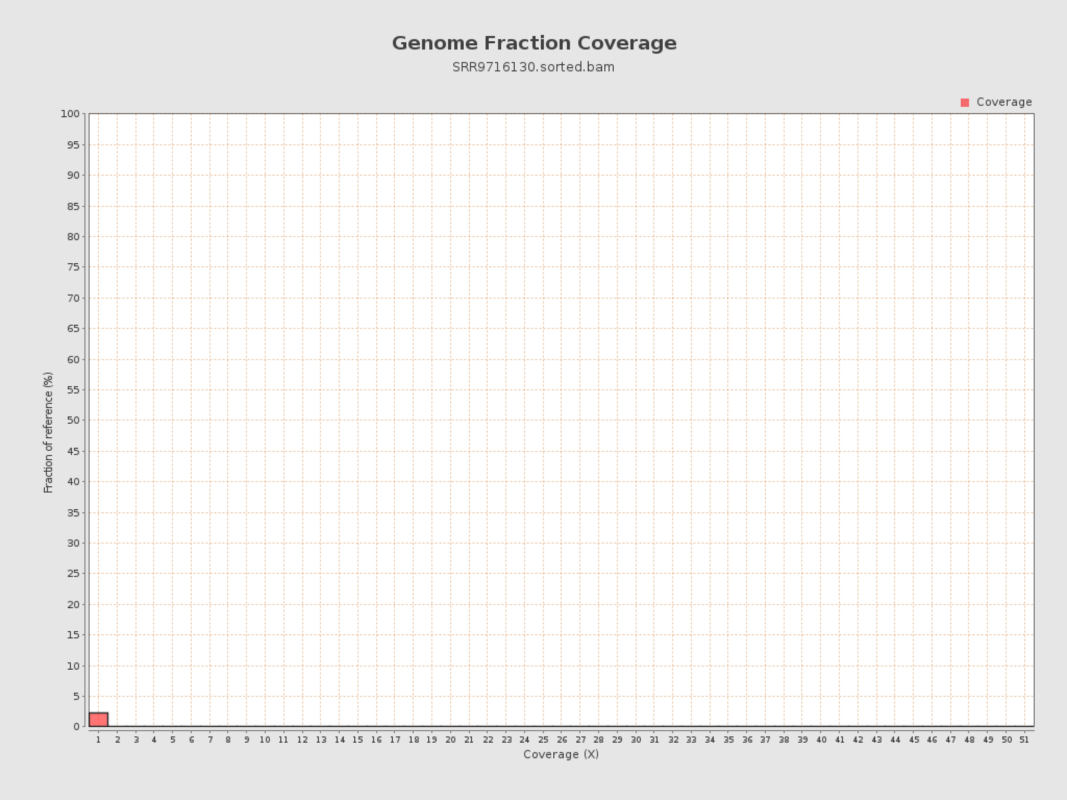
4. Results : Coverage Histogram



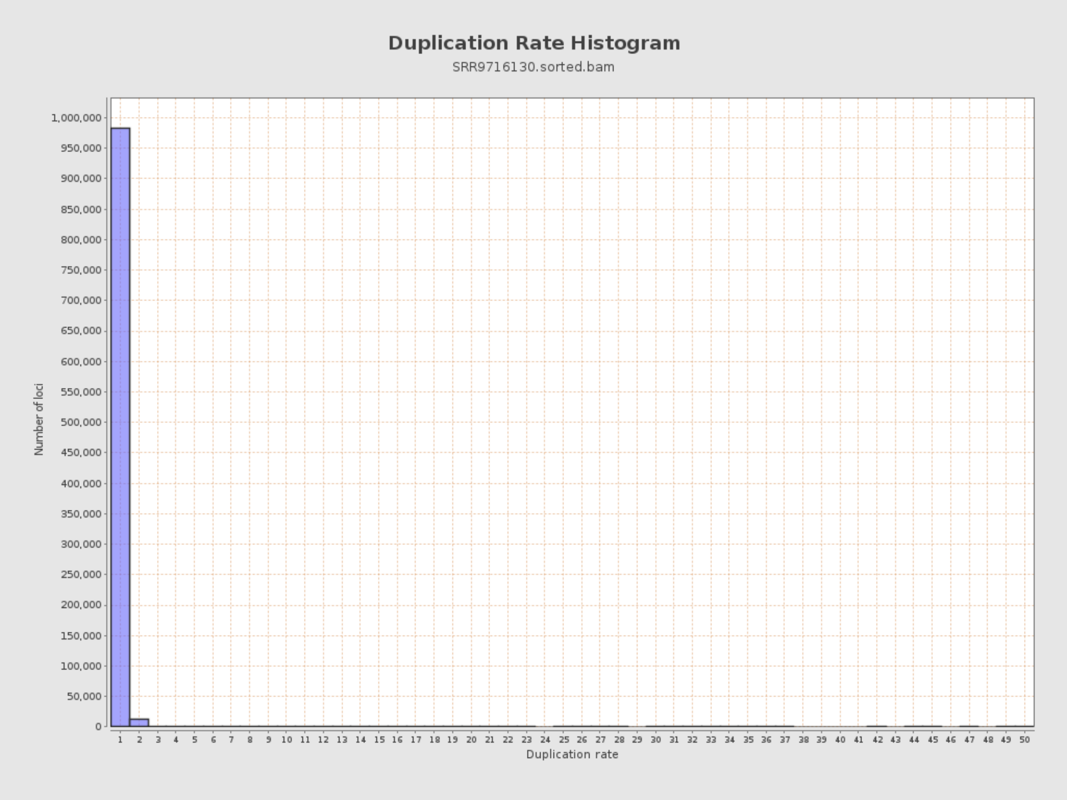
5. Results : Coverage Histogram (0-50X)



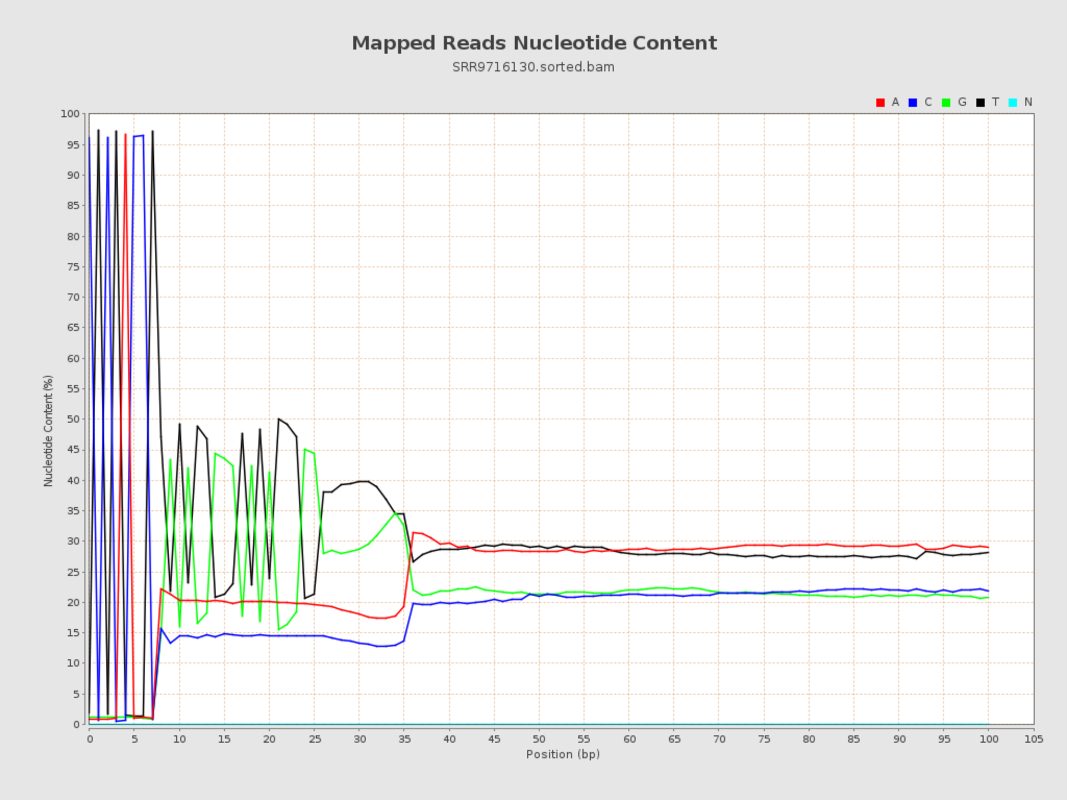
6. Results : Genome Fraction Coverage



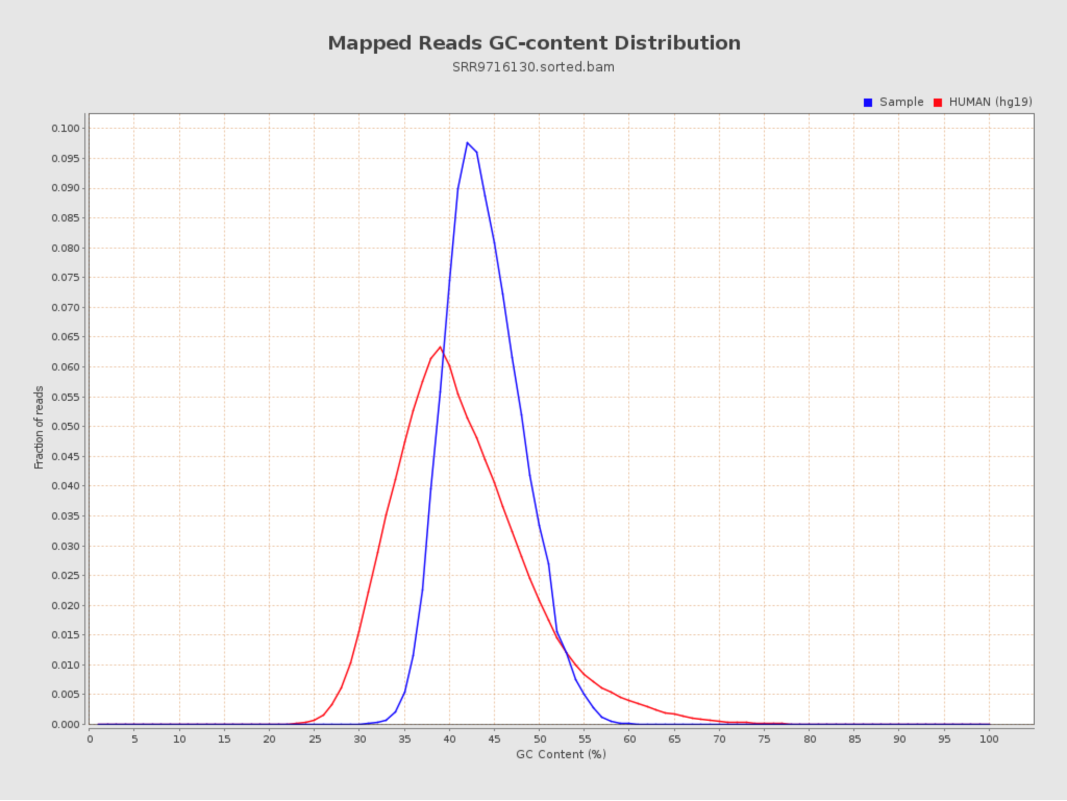
7. Results : Duplication Rate Histogram



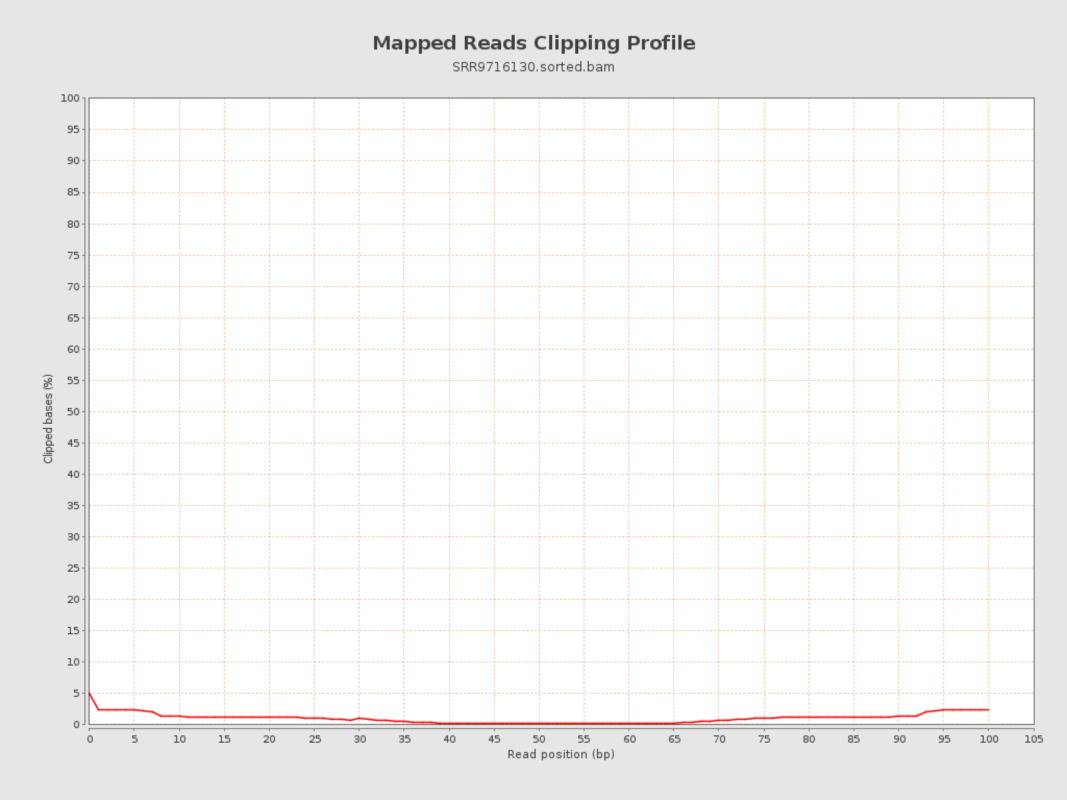
8. Results : Mapped Reads Nucleotide Content



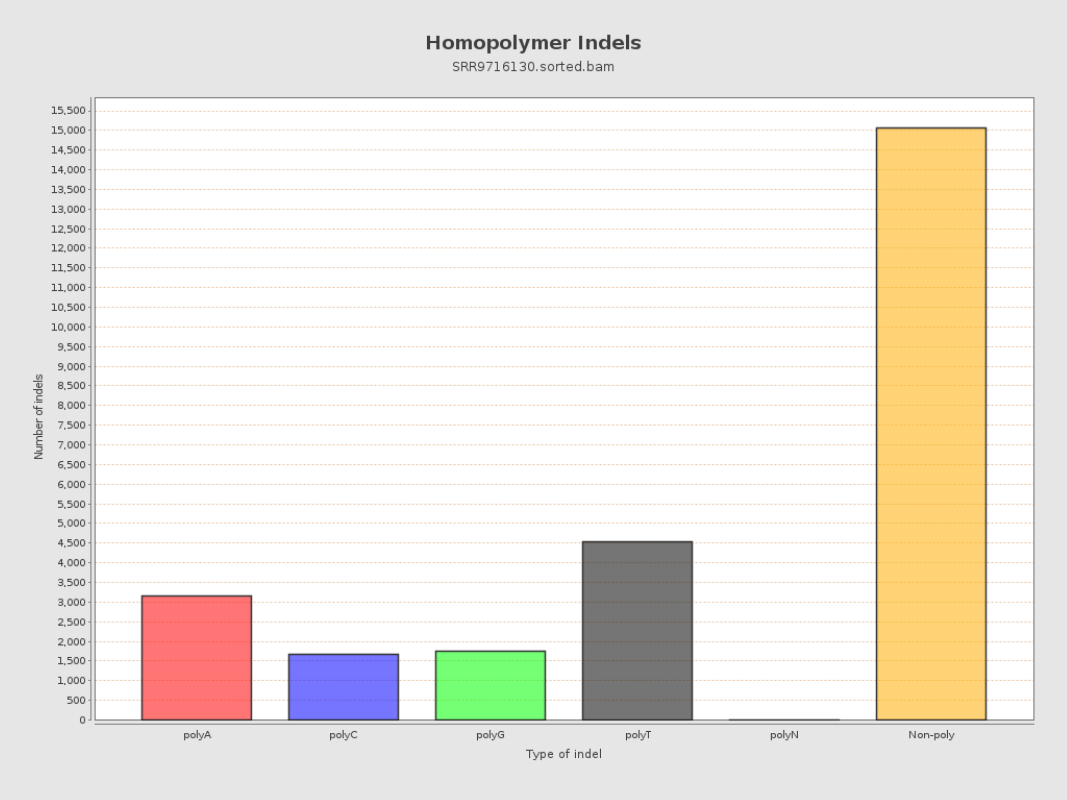
9. Results : Mapped Reads GC-content Distribution



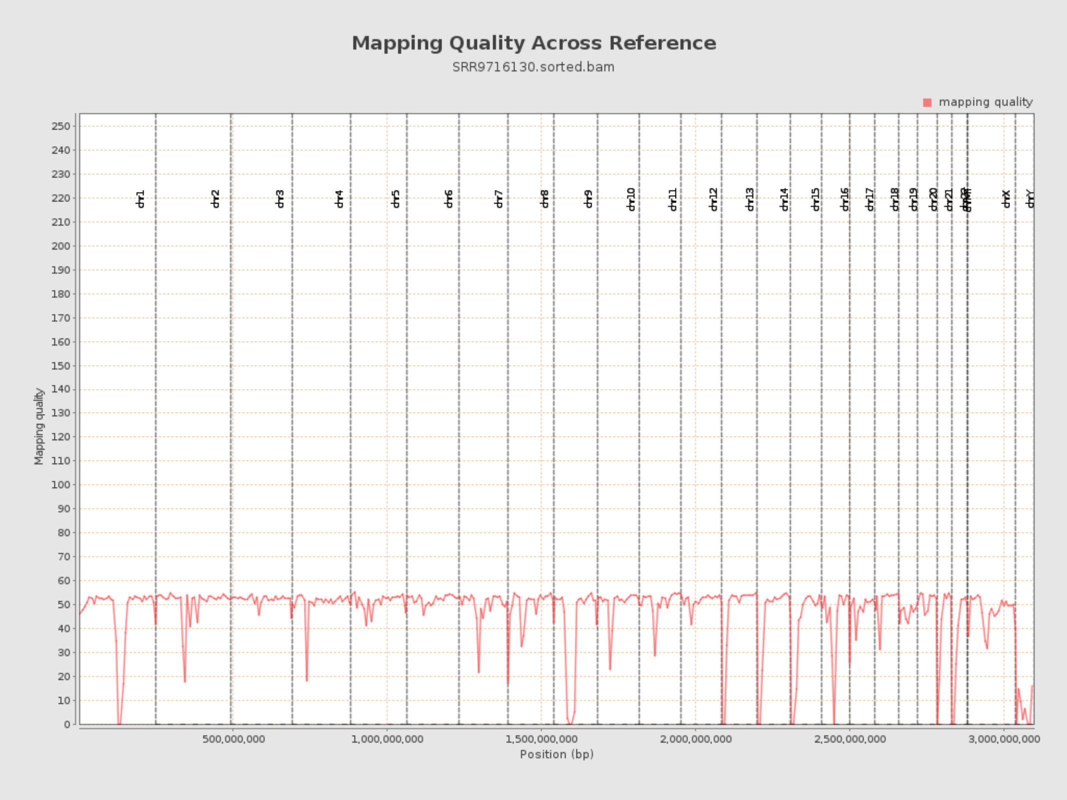
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram