Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 19:14:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716131.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_SRR9716131 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716131.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 19:14:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716131.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,244,770
Mapped reads	1,131,657 / 90.91%
Unmapped reads	113,113 / 9.09%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,366 / 1.88%
Read min/max/mean length	30 / 101 / 101.67
Duplicated reads (estimated)	35,082 / 2.82%
Duplication rate	2.16%
Clipped reads	1,152,289 / 92.57%

2.2. ACGT Content

Number/percentage of A's	23,378,868 / 26.29%
Number/percentage of C's	17,357,347 / 19.52%
Number/percentage of T's	27,394,096 / 30.81%
Number/percentage of G's	20,774,056 / 23.37%
Number/percentage of N's	6,019 / 0.01%
GC Percentage	42.89%

2.3. Coverage

Mean	0.0287

Standard Deviation	0.2863

2.4. Mapping Quality

Mean Mapping Quality	47.21

2.5. Mismatches and indels

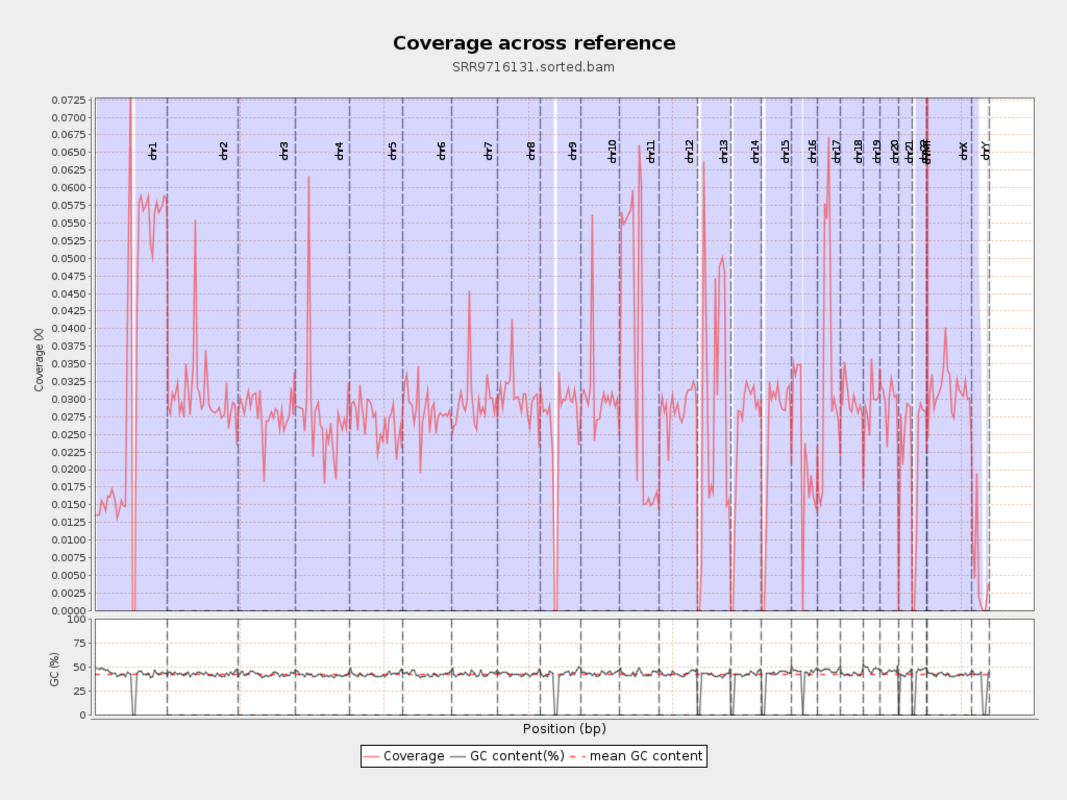
General error rate	0.69%
Mismatches	592,479
Insertions	7,785
Mapped reads with at least one insertion	0.68%
Deletions	20,107
Mapped reads with at least one deletion	1.75%
Homopolymer indels	42.47%

2.6. Chromosome stats

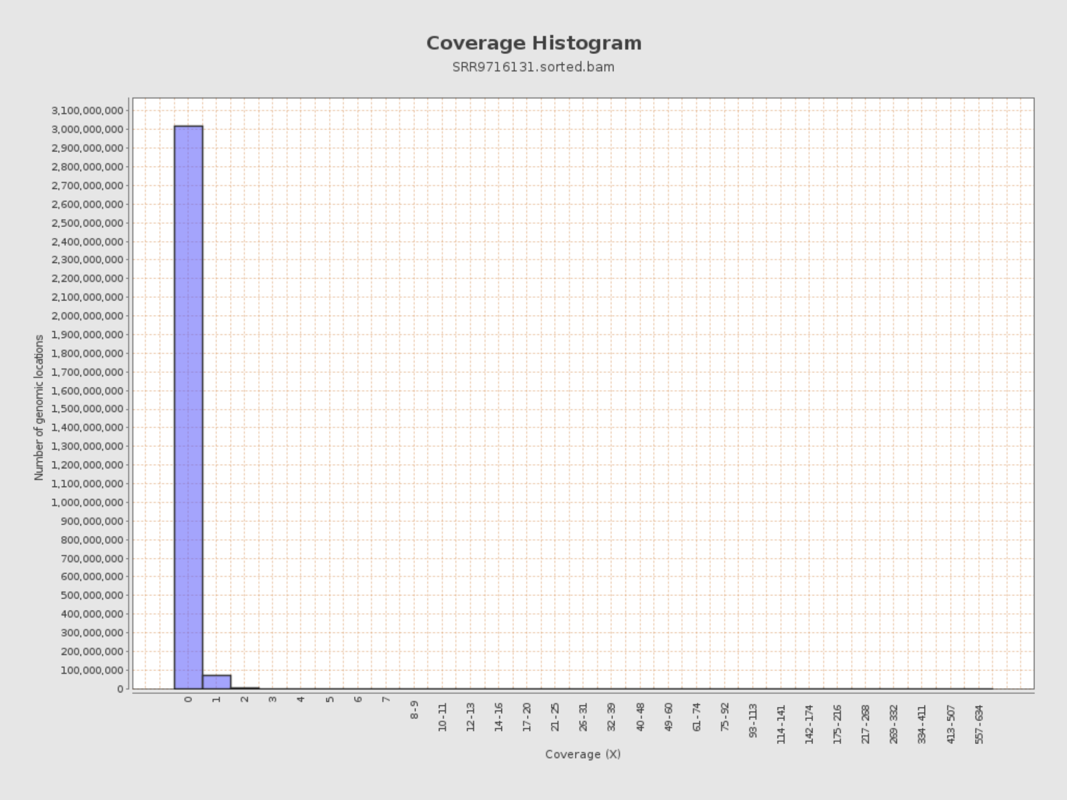
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8664578	0.0348	0.567
chr2	243199373	7412673	0.0305	0.3075
chr3	198022430	5565576	0.0281	0.181
chr4	191154276	5301605	0.0277	0.223
chr5	180915260	4889824	0.027	0.1786
chr6	171115067	4852026	0.0284	0.1926
chr7	159138663	4720309	0.0297	0.3261

chr8	146364022	4447714	0.0304	0.3237
chr9	141213431	3652776	0.0259	0.2468
chr10	135534747	4169566	0.0308	0.295
chr11	135006516	4969178	0.0368	0.3009
chr12	133851895	3877904	0.029	0.1844
chr13	115169878	3204146	0.0278	0.182
chr14	107349540	2667178	0.0248	0.1815
chr15	102531392	2543955	0.0248	0.1706
chr16	90354753	2036617	0.0225	0.1759
chr17	81195210	2745789	0.0338	0.2275
chr18	78077248	2345450	0.03	0.3956
chr19	59128983	1728481	0.0292	0.3864
chr20	63025520	1863961	0.0296	0.1948
chr21	48129895	1141208	0.0237	0.1945
chr22	51304566	1000174	0.0195	0.1519
chrMT	16571	7867	0.4747	0.7556
chrX	155270560	4857285	0.0313	0.2153
chrY	59373566	283670	0.0048	0.1828

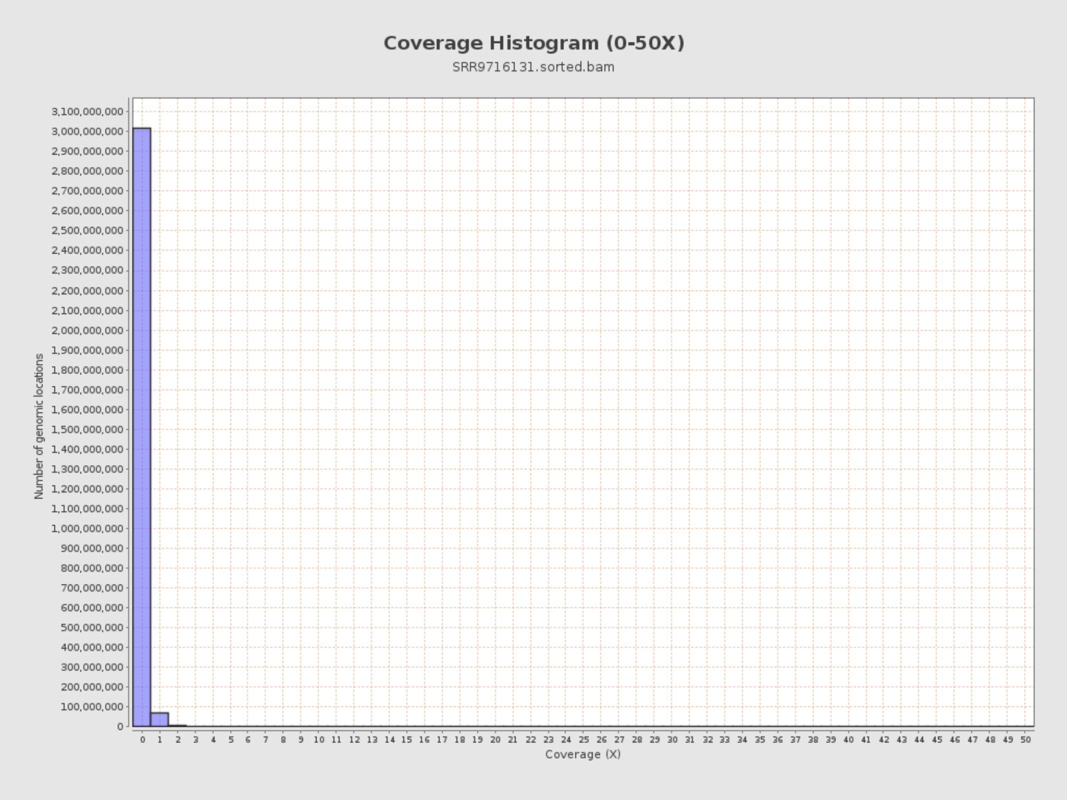
3. Results : Coverage across reference



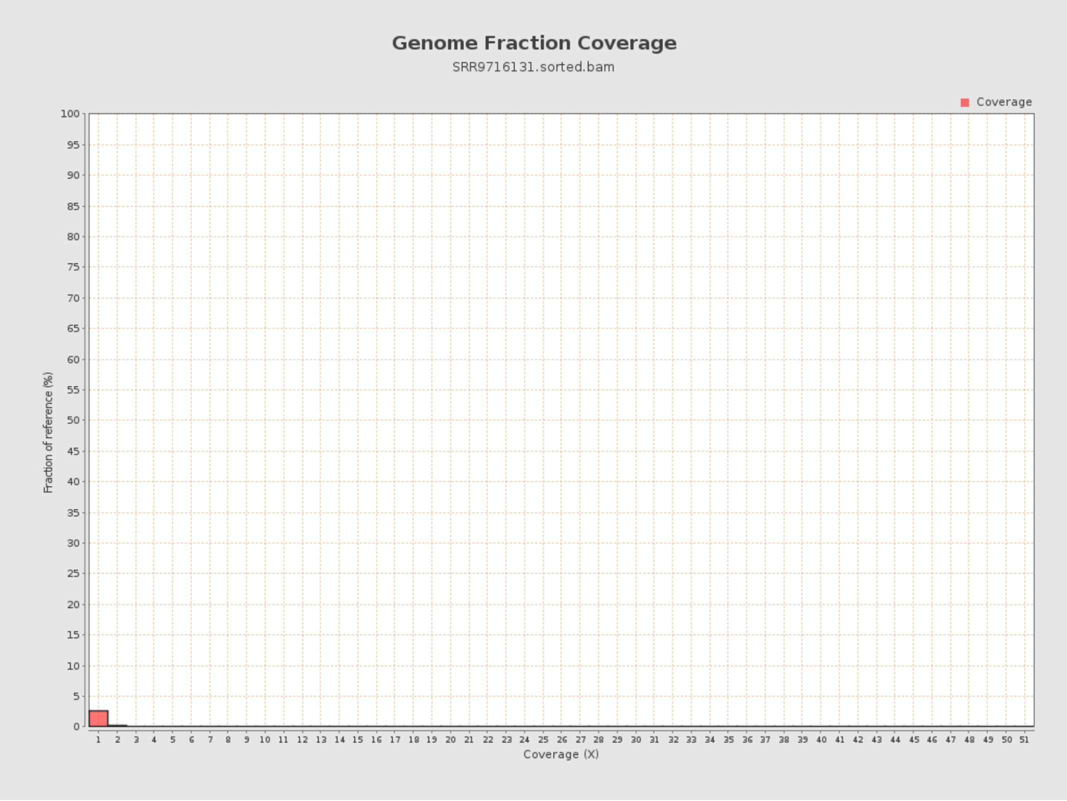
4. Results : Coverage Histogram



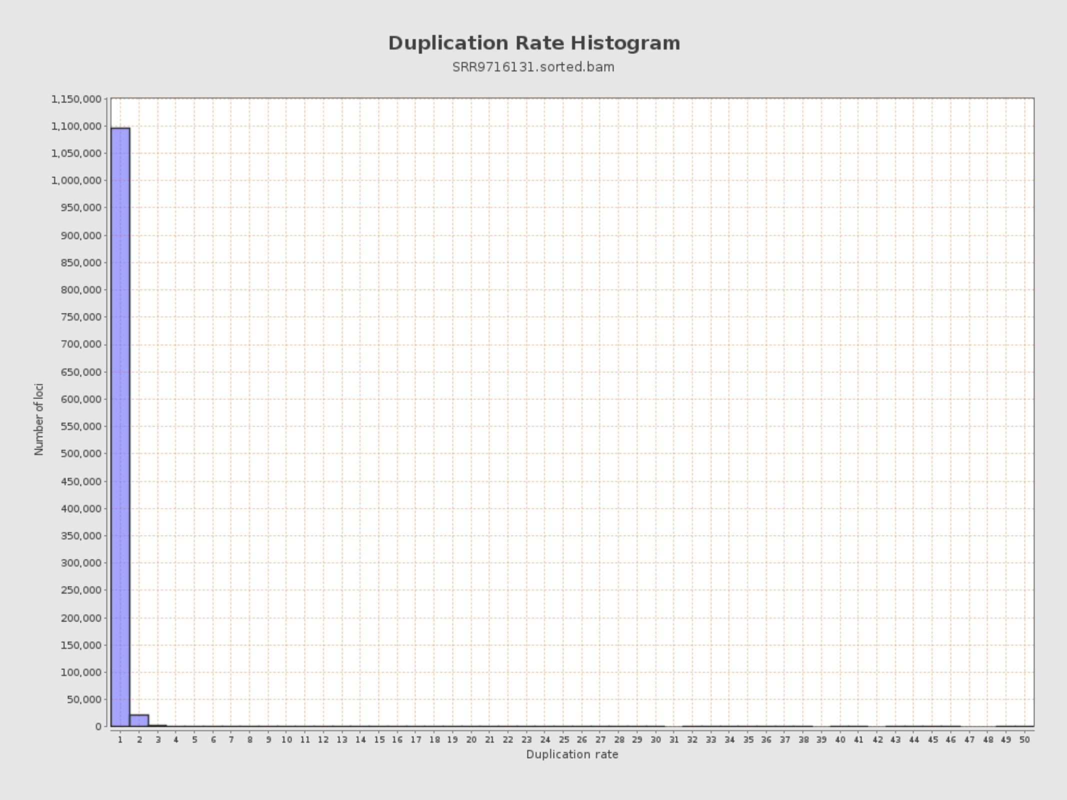
5. Results : Coverage Histogram (0-50X)



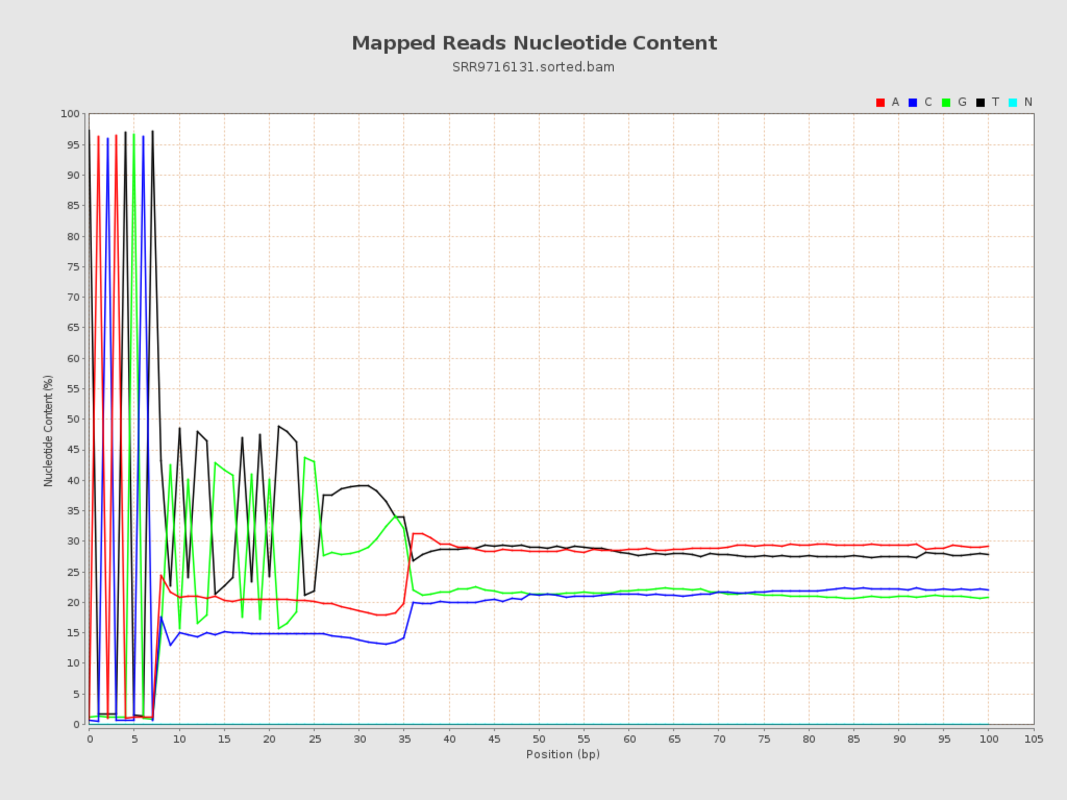
6. Results : Genome Fraction Coverage



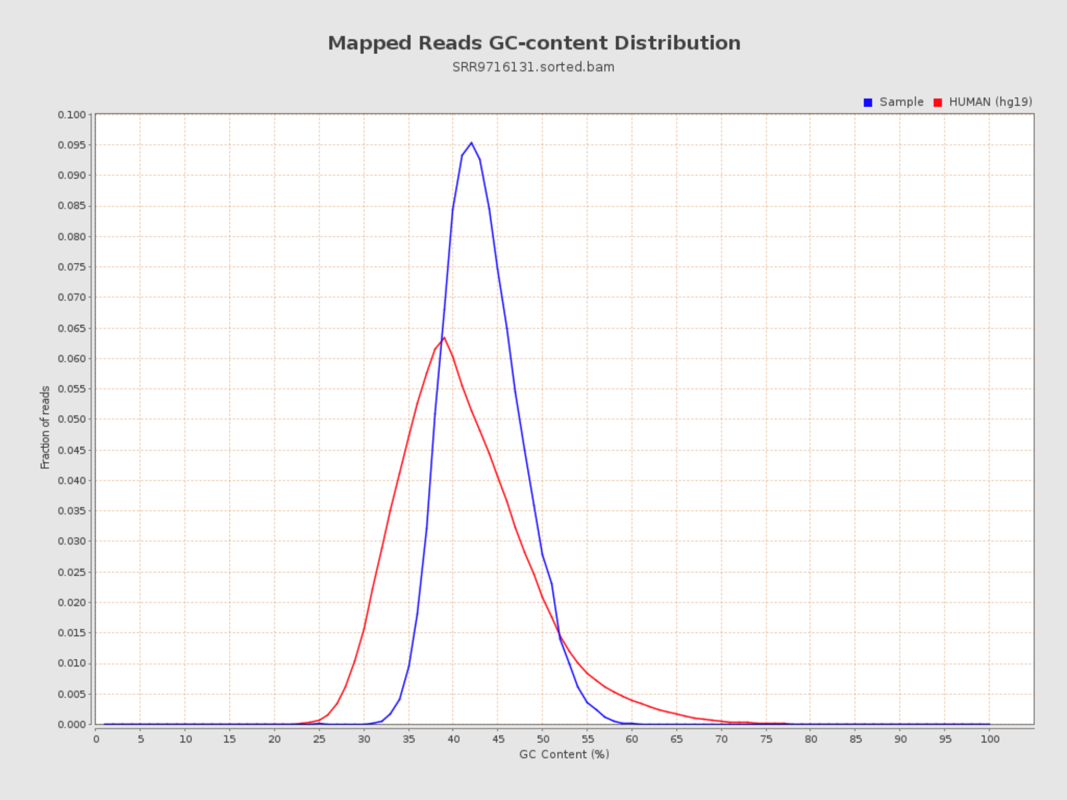
7. Results : Duplication Rate Histogram



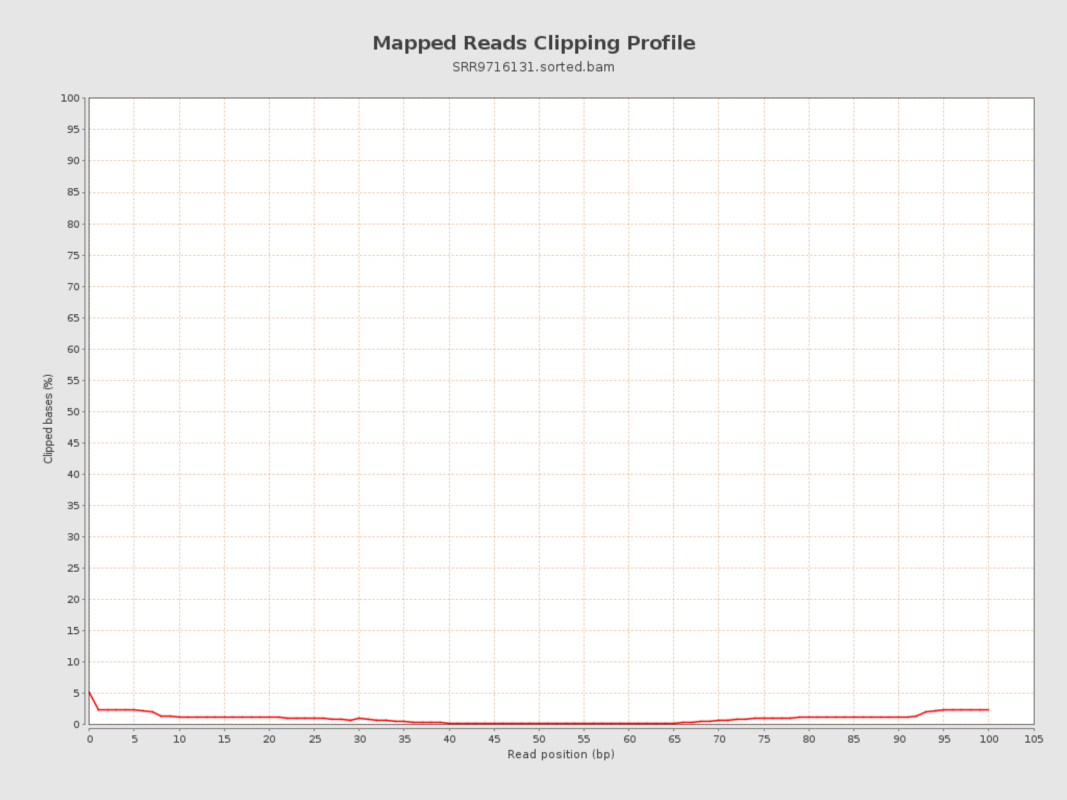
8. Results : Mapped Reads Nucleotide Content



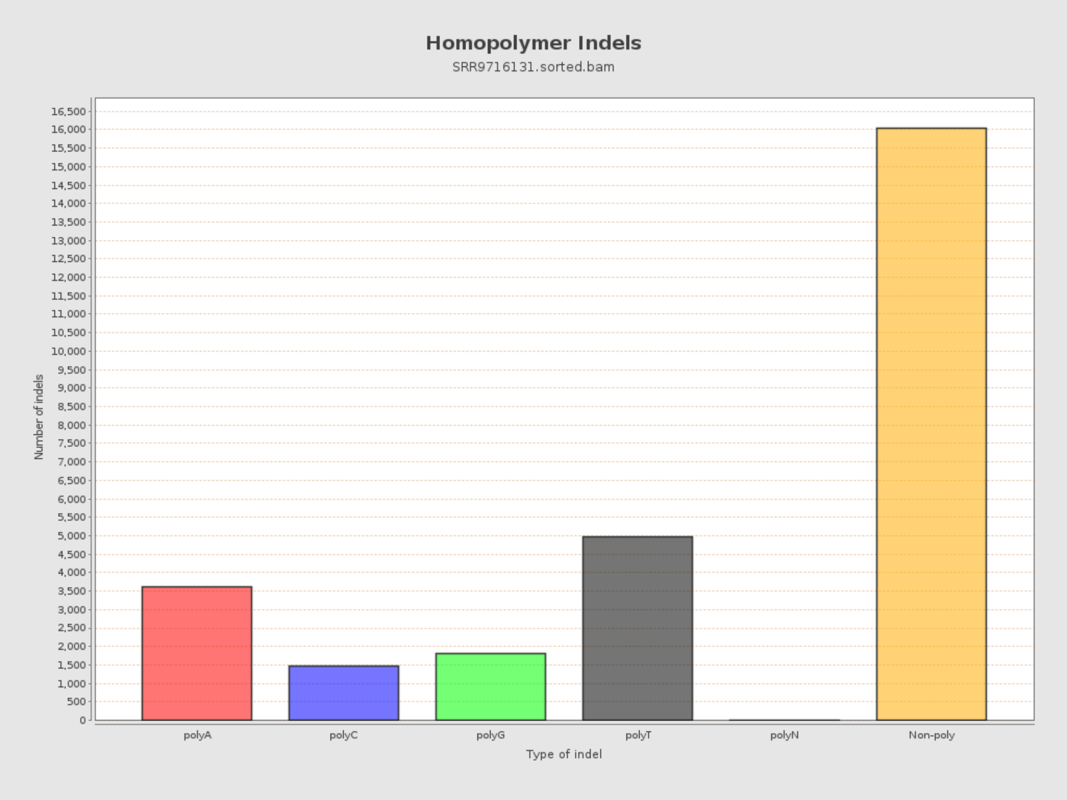
9. Results : Mapped Reads GC-content Distribution



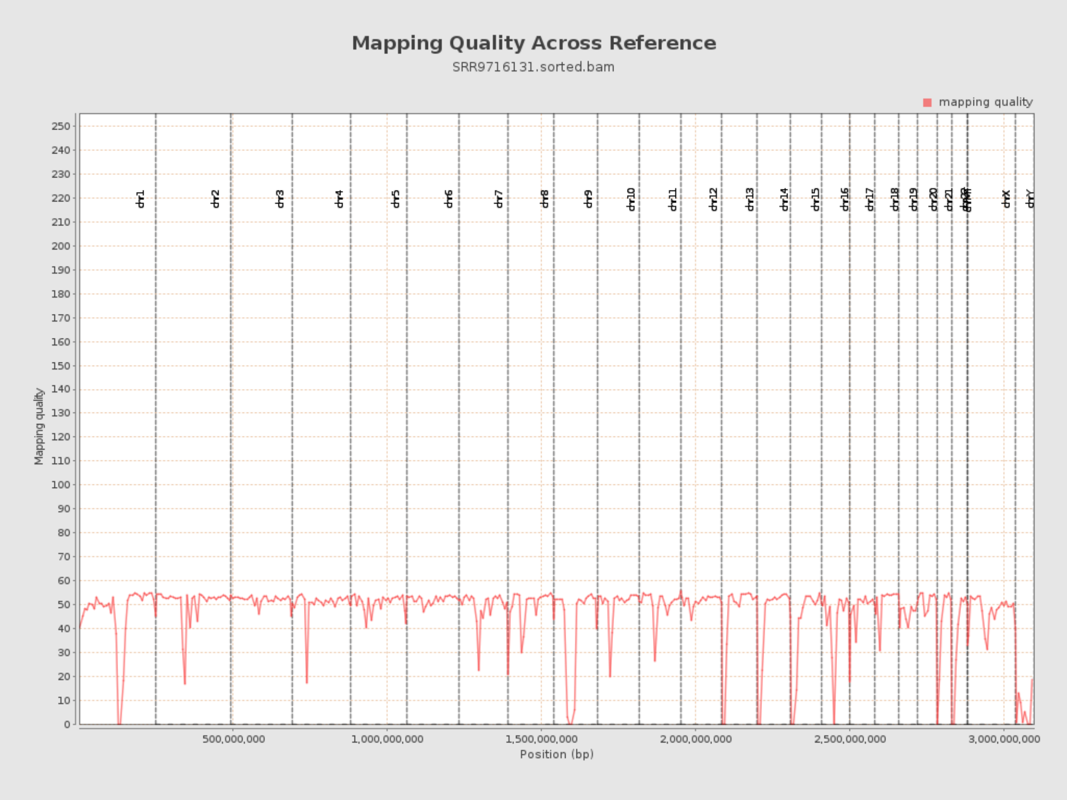
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram