Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 05:30:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716280.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_SRR9716280 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716280.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 05:30:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716280.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	607,860
Mapped reads	506,425 / 83.31%
Unmapped reads	101,435 / 16.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,195 / 0.2%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	8,343 / 1.37%
Duplication rate	1.14%
Clipped reads	506,001 / 83.24%

2.2. ACGT Content

Number/percentage of A's	6,524,645 / 23.27%
Number/percentage of C's	5,611,505 / 20.01%
Number/percentage of T's	8,728,515 / 31.12%
Number/percentage of G's	7,178,567 / 25.6%
Number/percentage of N's	723 / 0%
GC Percentage	45.61%

2.3. Coverage

Mean	0.0091

Standard Deviation	0.1107

2.4. Mapping Quality

Mean Mapping Quality	40.03

2.5. Mismatches and indels

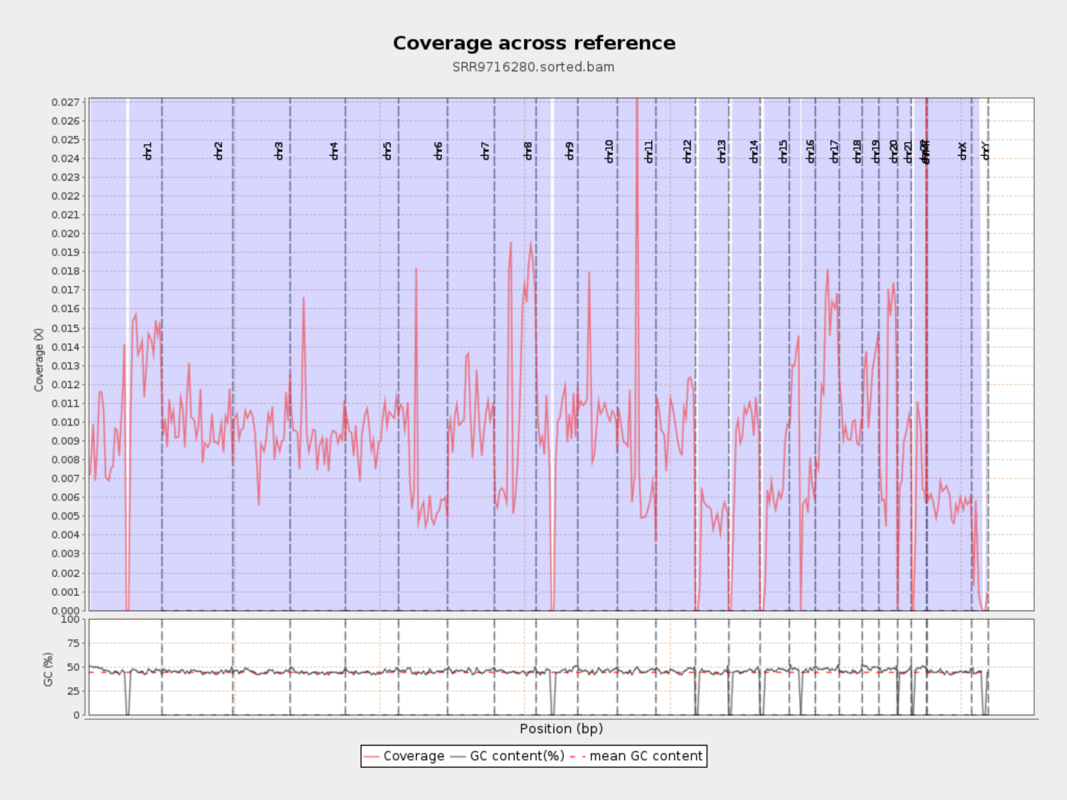
General error rate	0.54%
Mismatches	148,232
Insertions	2,253
Mapped reads with at least one insertion	0.44%
Deletions	5,058
Mapped reads with at least one deletion	0.99%
Homopolymer indels	39.53%

2.6. Chromosome stats

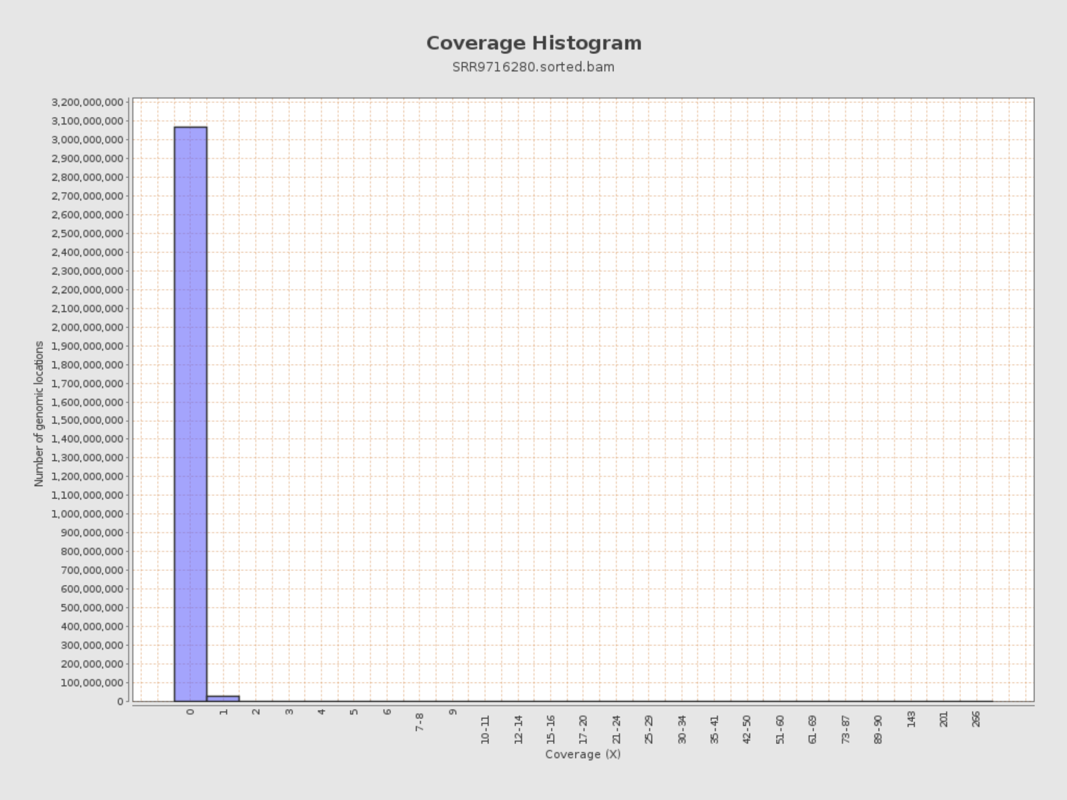
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2680848	0.0108	0.128
chr2	243199373	2402586	0.0099	0.1506
chr3	198022430	1875154	0.0095	0.1045
chr4	191154276	1804308	0.0094	0.1052
chr5	180915260	1728933	0.0096	0.102
chr6	171115067	1218924	0.0071	0.0931
chr7	159138663	1651335	0.0104	0.1221

chr8	146364022	1734850	0.0119	0.119
chr9	141213431	1229349	0.0087	0.102
chr10	135534747	1458488	0.0108	0.1284
chr11	135006516	1166749	0.0086	0.1102
chr12	133851895	1359187	0.0102	0.1059
chr13	115169878	509368	0.0044	0.0696
chr14	107349540	896025	0.0083	0.0976
chr15	102531392	564333	0.0055	0.0786
chr16	90354753	765175	0.0085	0.0999
chr17	81195210	1119003	0.0138	0.1255
chr18	78077248	757301	0.0097	0.1189
chr19	59128983	740696	0.0125	0.1279
chr20	63025520	722242	0.0115	0.1133
chr21	48129895	376013	0.0078	0.0963
chr22	51304566	299370	0.0058	0.0805
chrMT	16571	900	0.0543	0.2266
chrX	155270560	901188	0.0058	0.0857
chrY	59373566	89670	0.0015	0.0556

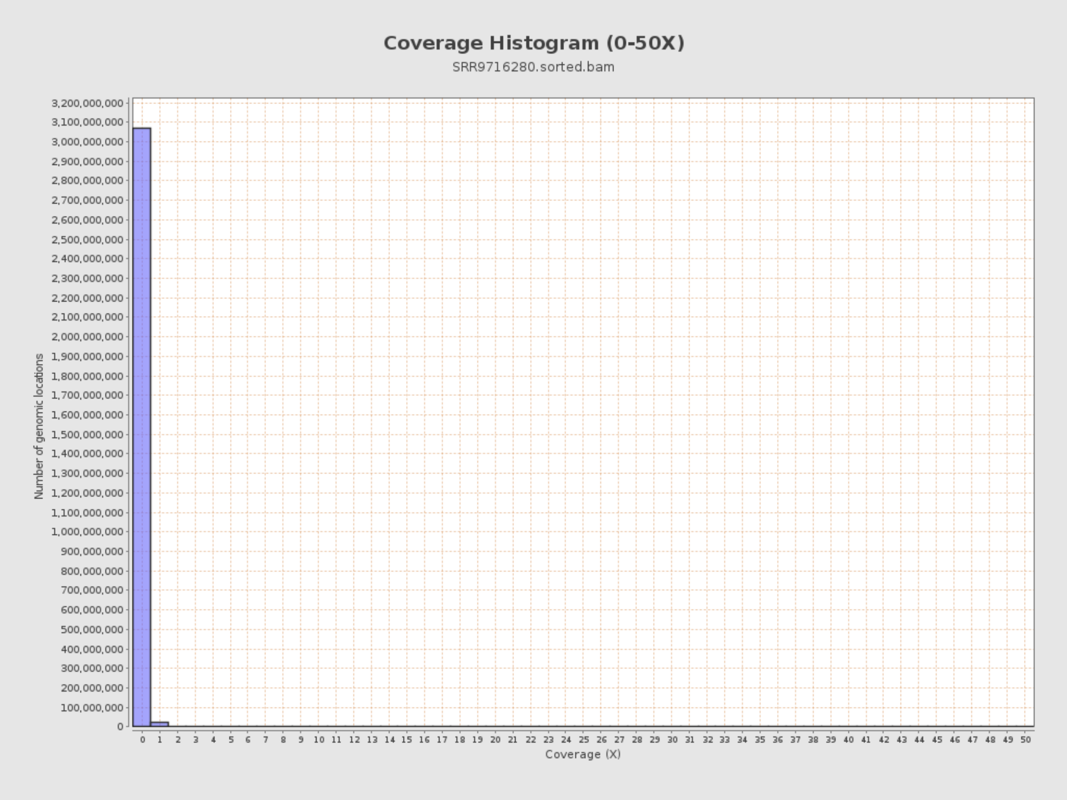
3. Results : Coverage across reference



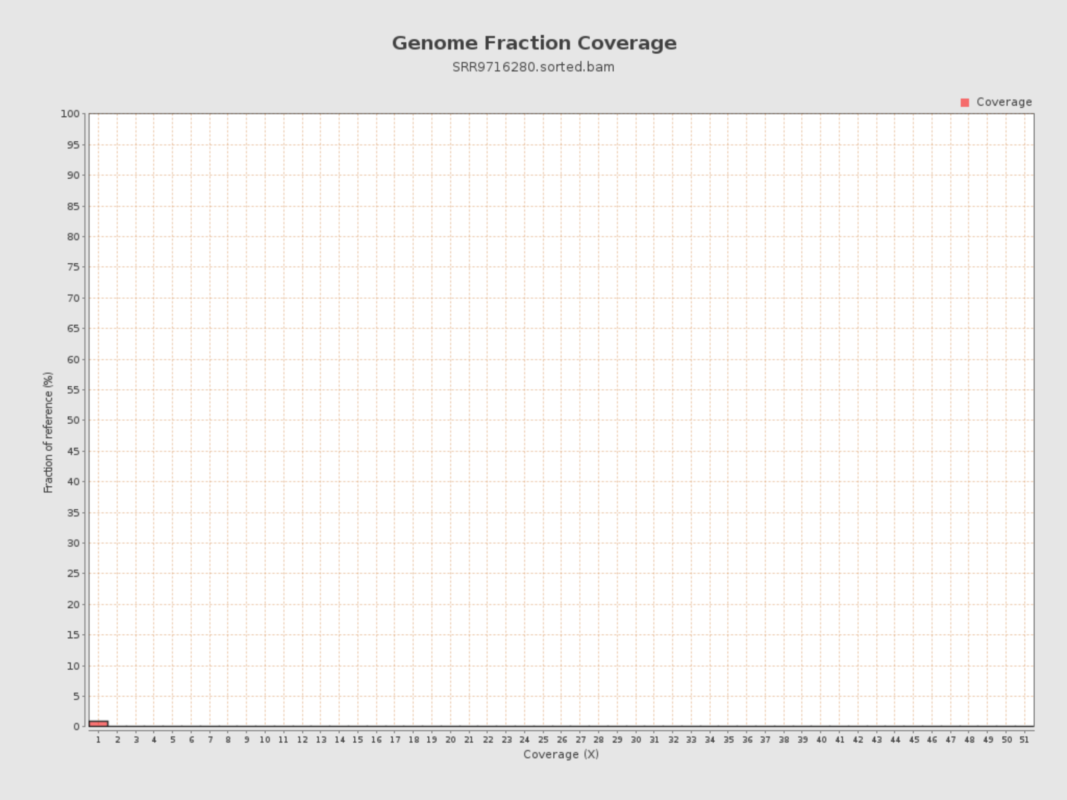
4. Results : Coverage Histogram



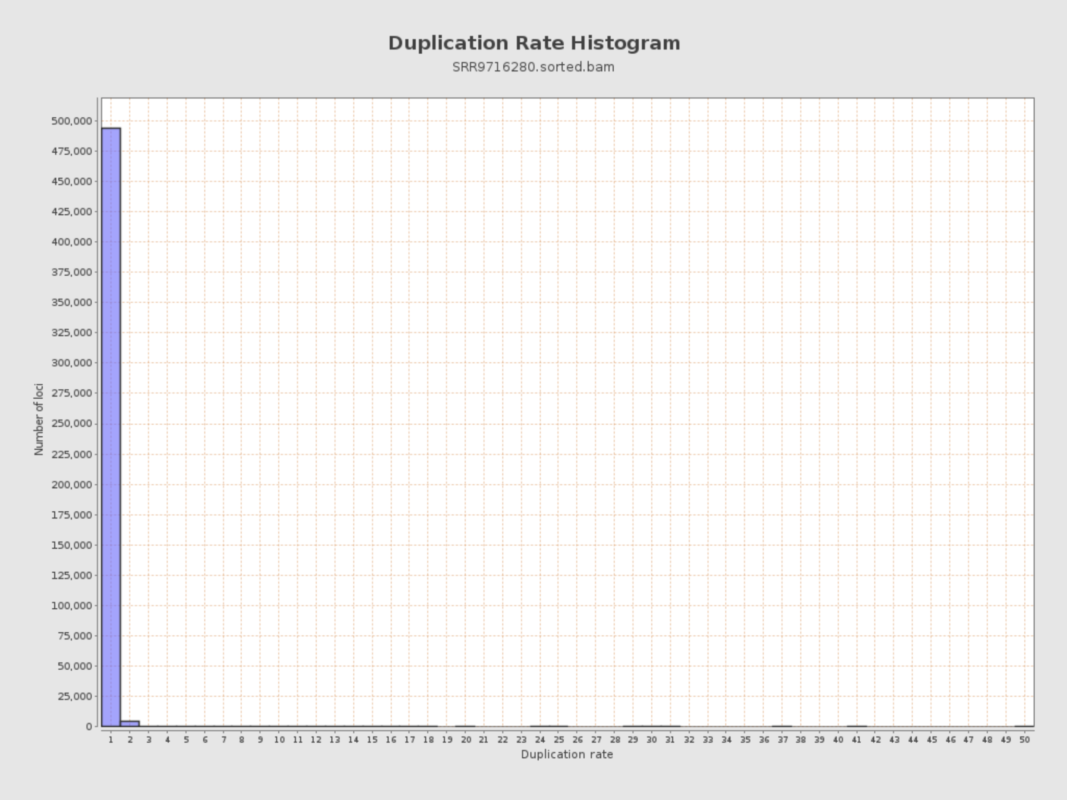
5. Results : Coverage Histogram (0-50X)



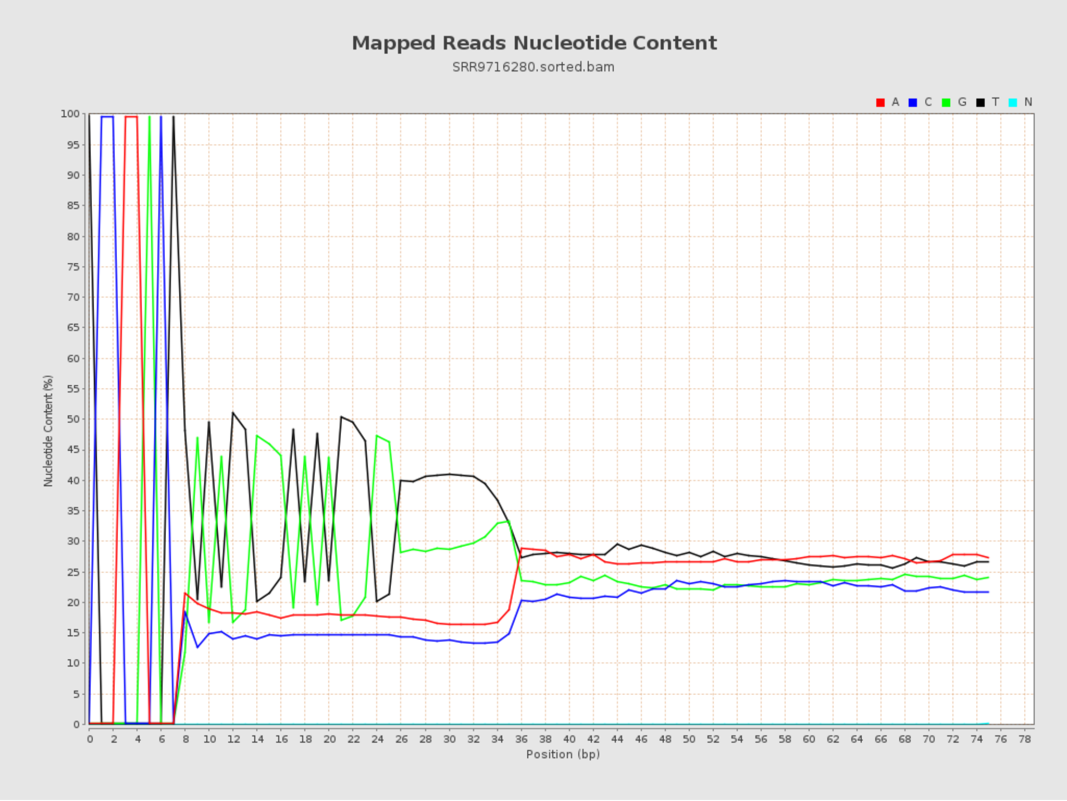
6. Results : Genome Fraction Coverage



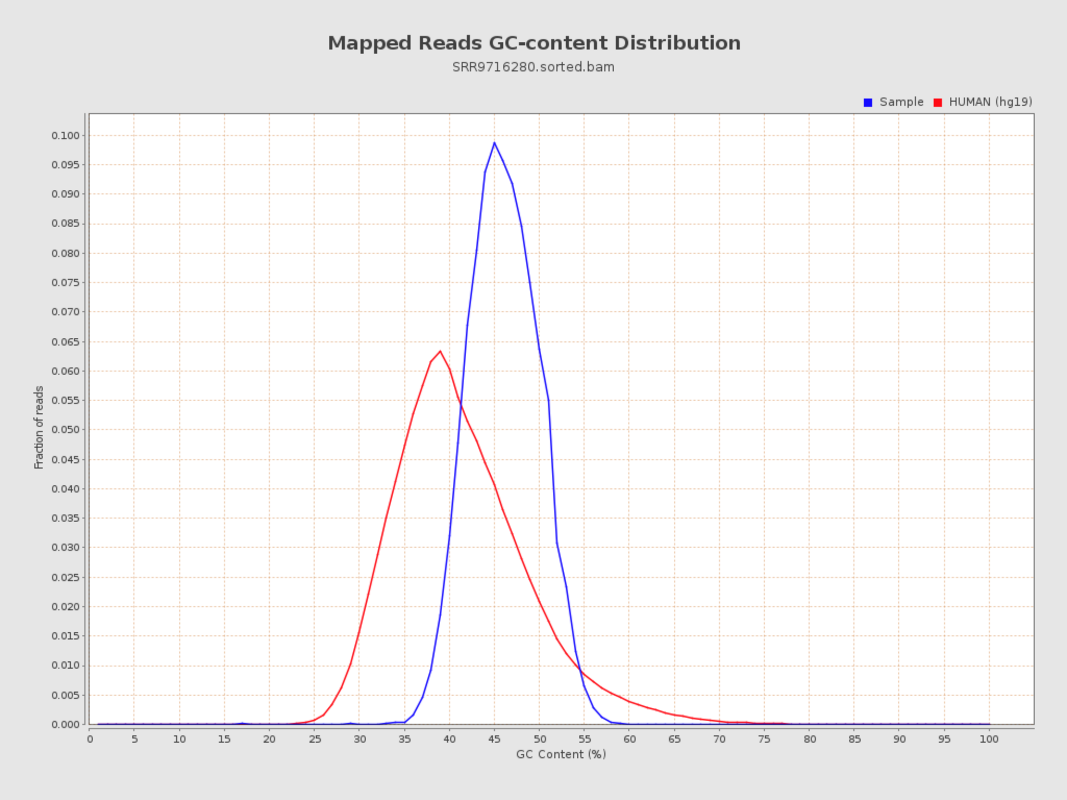
7. Results : Duplication Rate Histogram



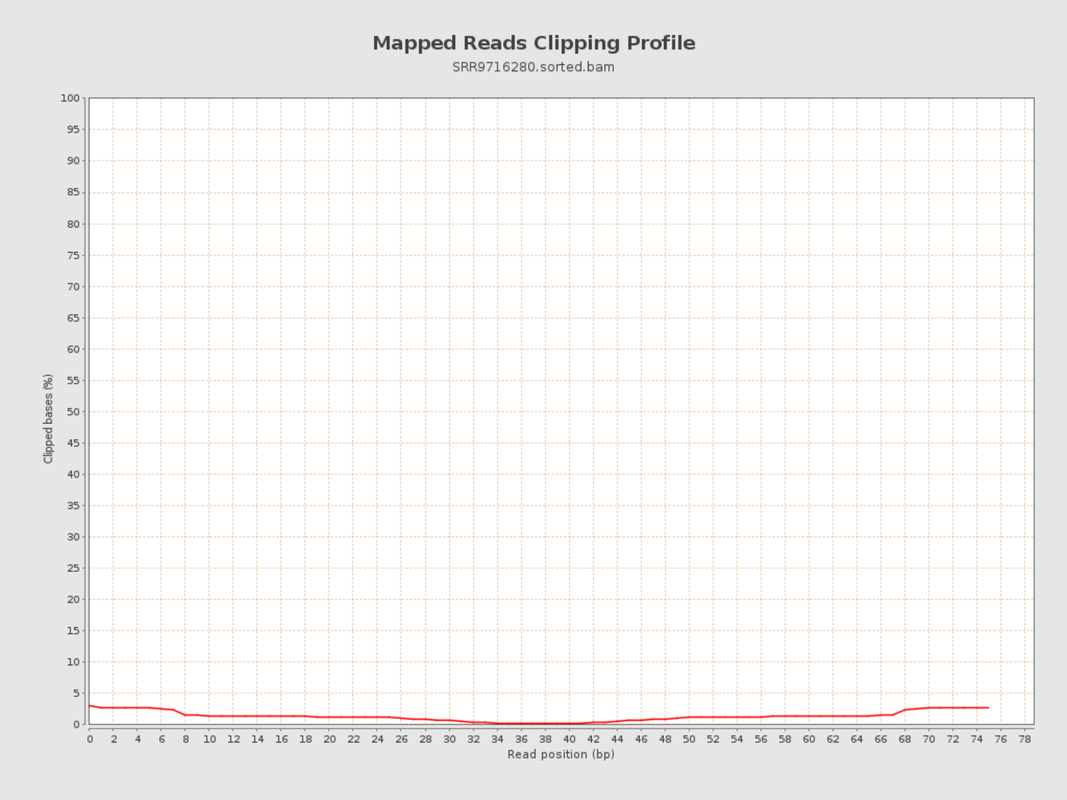
8. Results : Mapped Reads Nucleotide Content



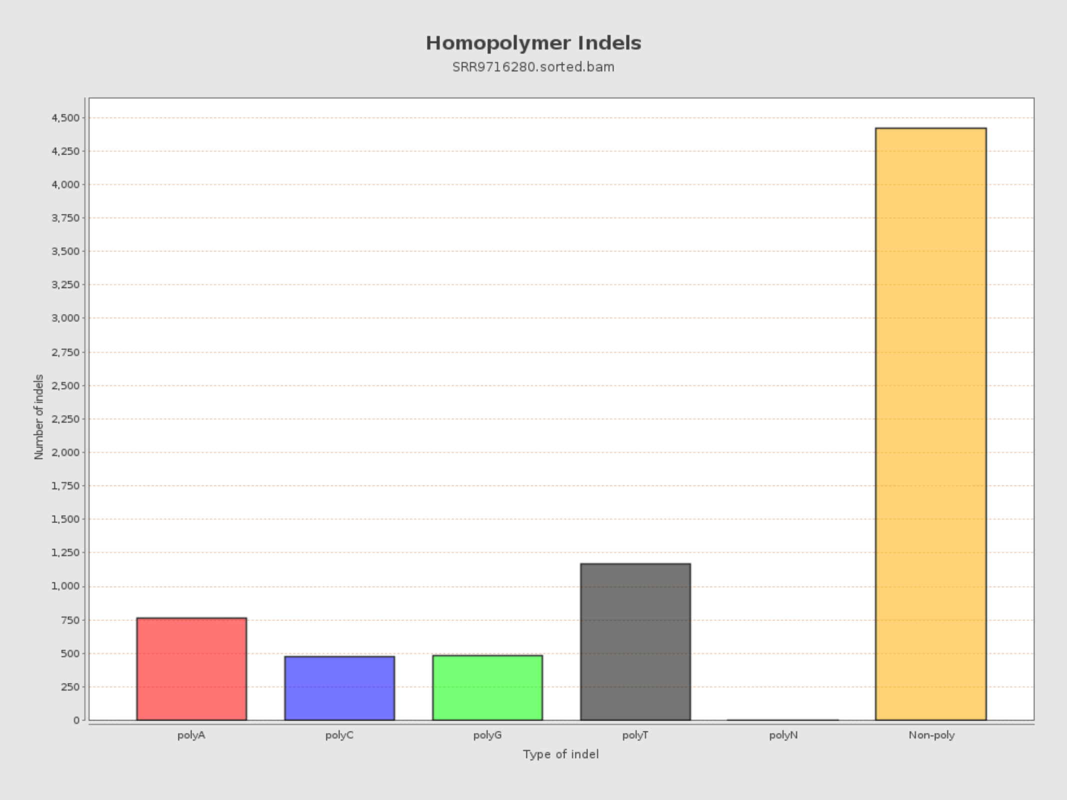
9. Results : Mapped Reads GC-content Distribution



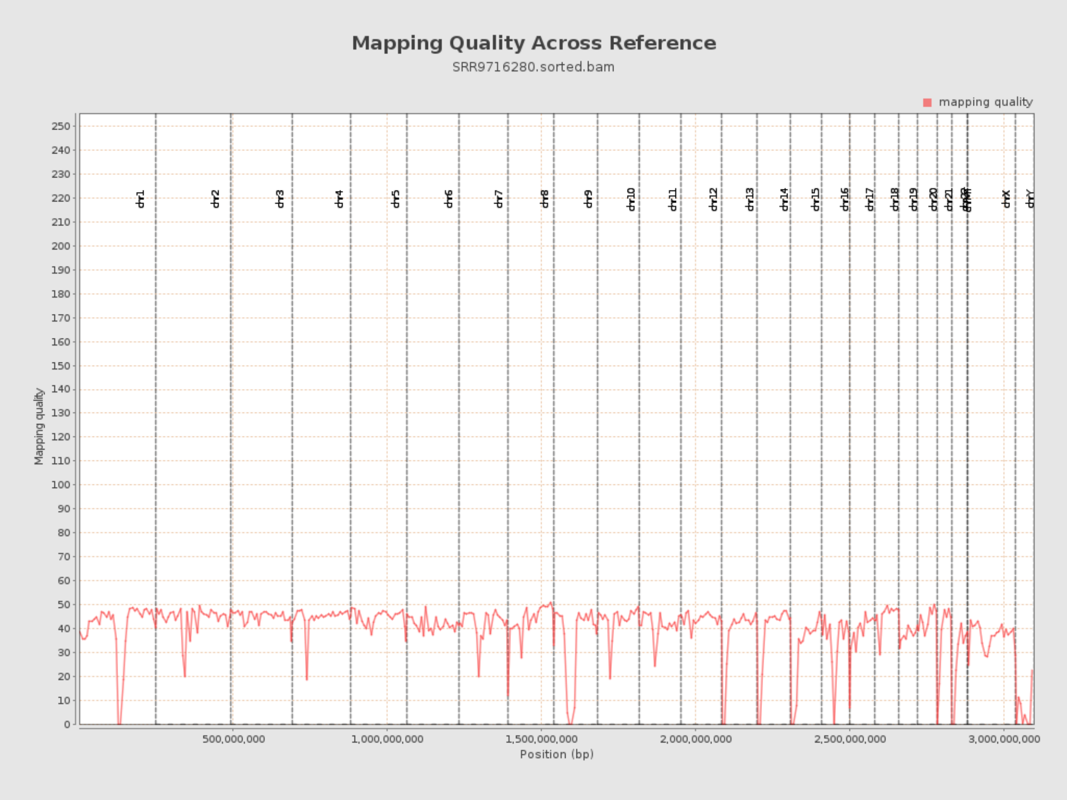
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram