Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 11:34:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716397.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_SRR9716397 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716397.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 11:34:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716397.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,428,139
Mapped reads	1,291,403 / 90.43%
Unmapped reads	136,736 / 9.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,803 / 1.46%
Read min/max/mean length	30 / 101 / 101.54
Duplicated reads (estimated)	51,869 / 3.63%
Duplication rate	2.16%
Clipped reads	1,308,933 / 91.65%

2.2. ACGT Content

Number/percentage of A's	25,179,725 / 24.95%
Number/percentage of C's	19,936,327 / 19.75%
Number/percentage of T's	31,042,919 / 30.76%
Number/percentage of G's	24,763,732 / 24.54%
Number/percentage of N's	5,730 / 0.01%
GC Percentage	44.29%

2.3. Coverage

Mean	0.0326

Standard Deviation	0.4649

2.4. Mapping Quality

Mean Mapping Quality	42.37

2.5. Mismatches and indels

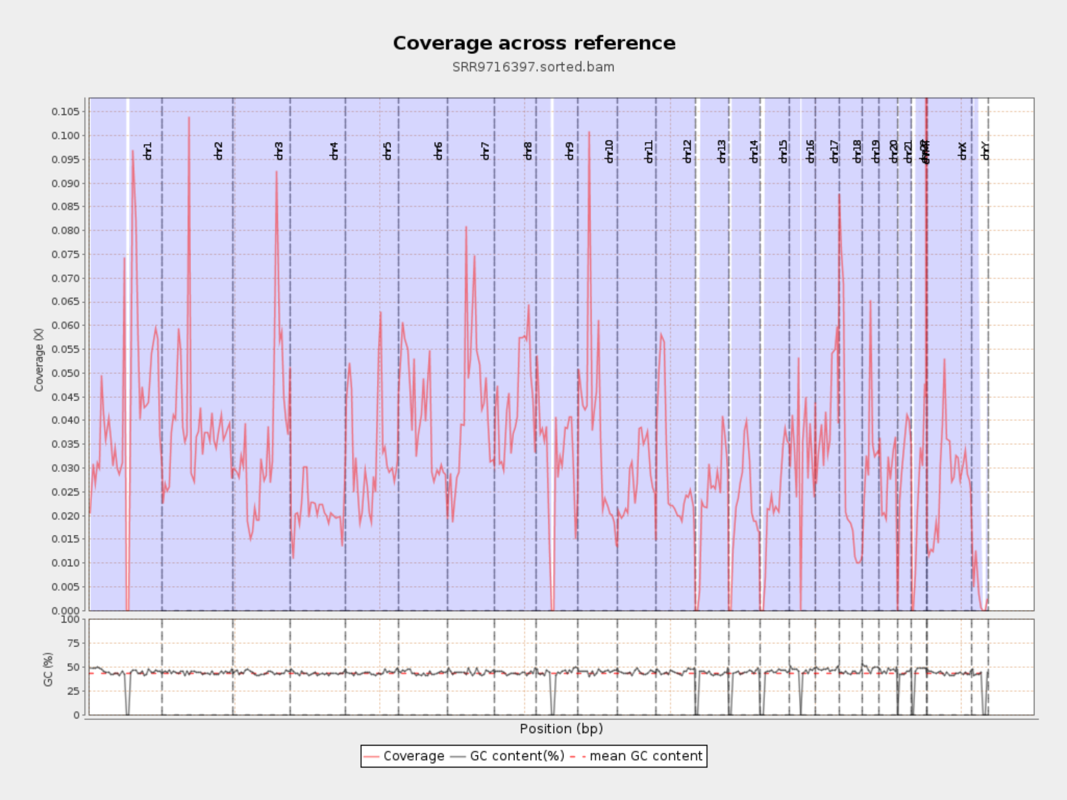
General error rate	0.89%
Mismatches	879,885
Insertions	10,350
Mapped reads with at least one insertion	0.79%
Deletions	25,480
Mapped reads with at least one deletion	1.94%
Homopolymer indels	43.28%

2.6. Chromosome stats

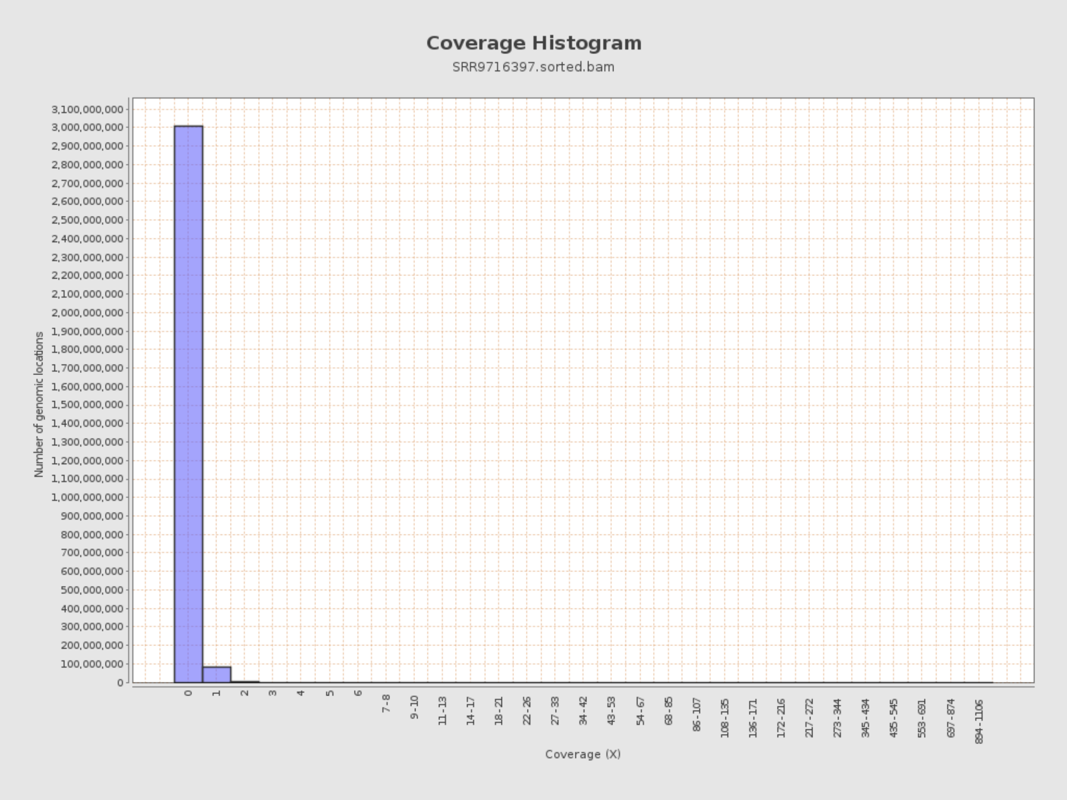
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10368406	0.0416	0.8274
chr2	243199373	9431763	0.0388	0.7841
chr3	198022430	6918819	0.0349	0.2299
chr4	191154276	3971045	0.0208	0.1677
chr5	180915260	5851927	0.0323	0.1998
chr6	171115067	7038885	0.0411	0.2873
chr7	159138663	6849556	0.043	0.6451

chr8	146364022	6485718	0.0443	0.5758
chr9	141213431	4304378	0.0305	0.4066
chr10	135534747	5254314	0.0388	0.6425
chr11	135006516	3747646	0.0278	0.299
chr12	133851895	3930937	0.0294	0.1939
chr13	115169878	2721874	0.0236	0.1667
chr14	107349540	2331818	0.0217	0.1925
chr15	102531392	2220668	0.0217	0.17
chr16	90354753	2910693	0.0322	0.2329
chr17	81195210	3322253	0.0409	0.2637
chr18	78077248	2309372	0.0296	0.6816
chr19	59128983	2049172	0.0347	0.6767
chr20	63025520	1731558	0.0275	0.1966
chr21	48129895	1474575	0.0306	0.1997
chr22	51304566	1185421	0.0231	0.1678
chrMT	16571	46880	2.829	2.5233
chrX	155270560	4270775	0.0275	0.2488
chrY	59373566	244502	0.0041	0.1148

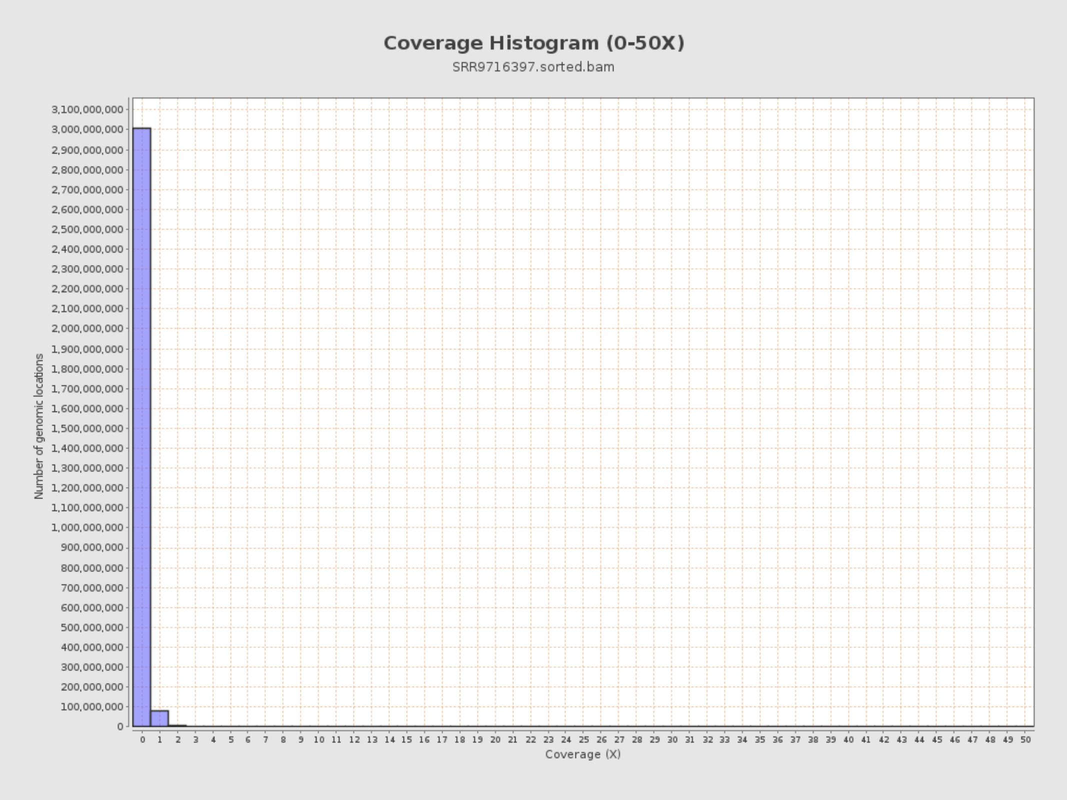
3. Results : Coverage across reference



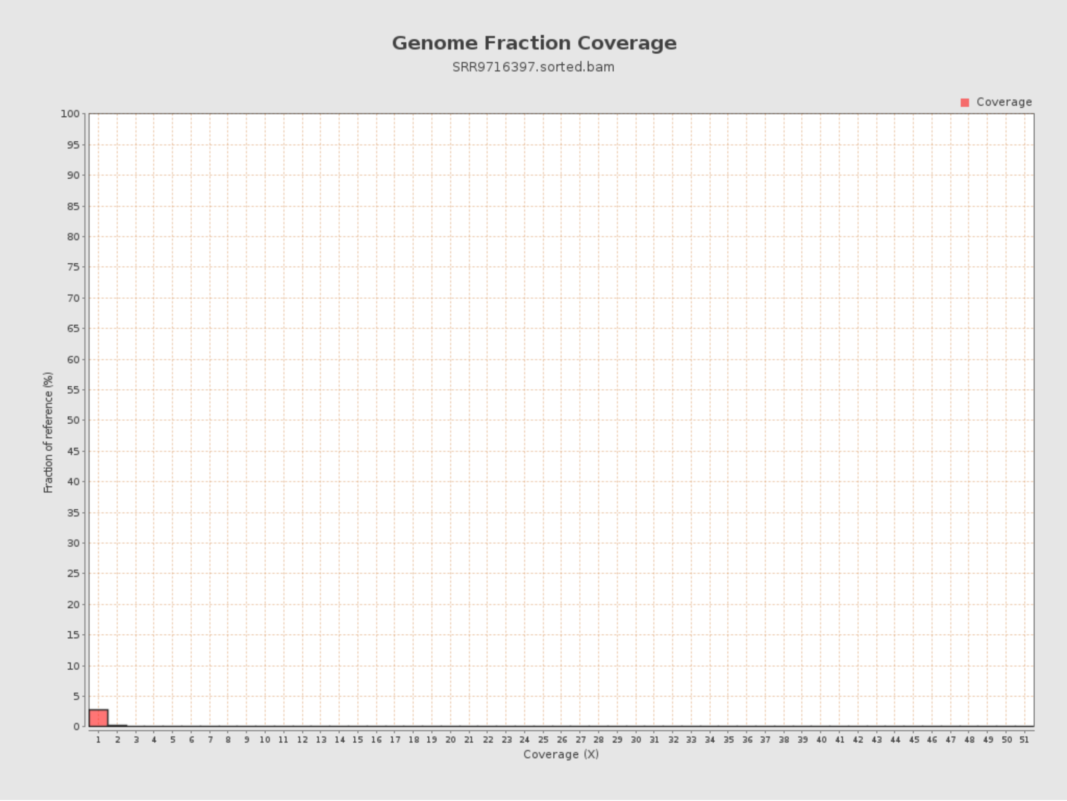
4. Results : Coverage Histogram



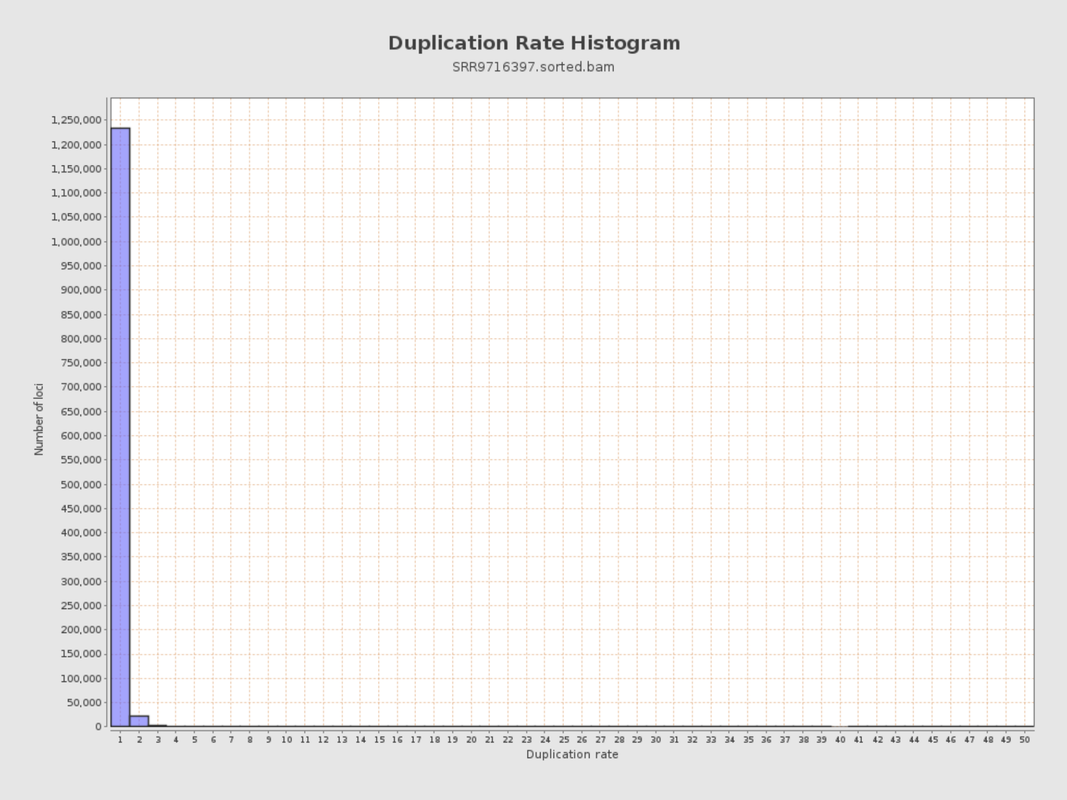
5. Results : Coverage Histogram (0-50X)



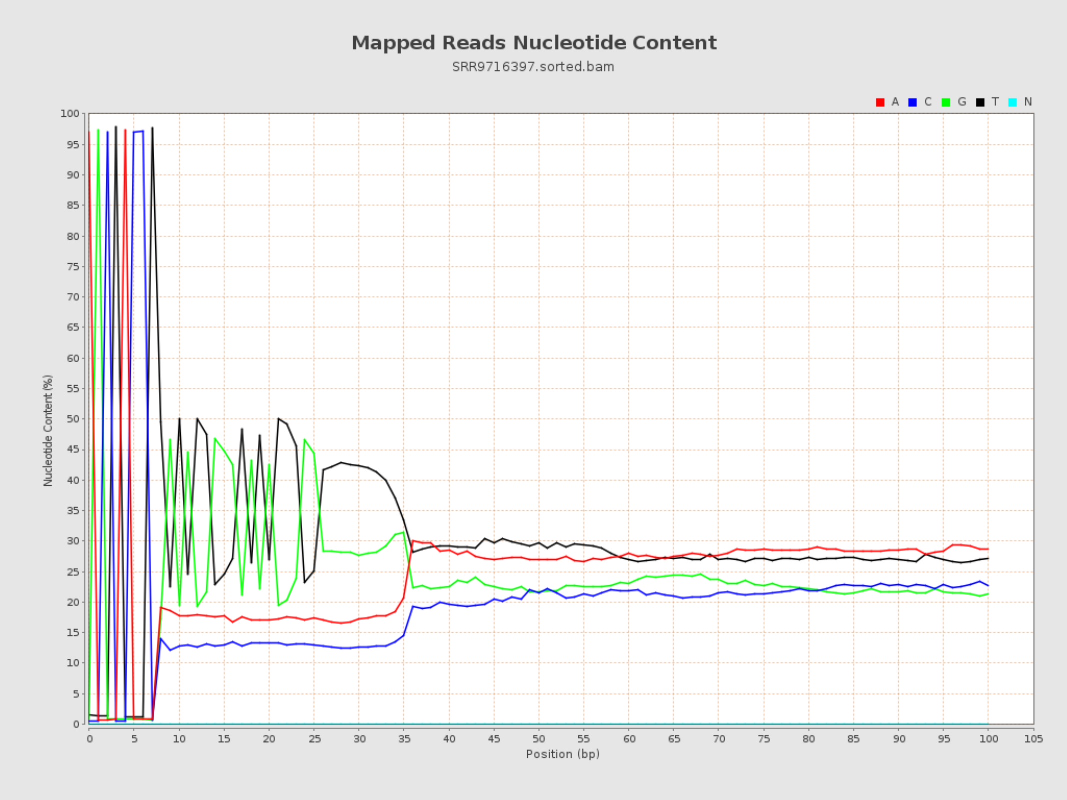
6. Results : Genome Fraction Coverage



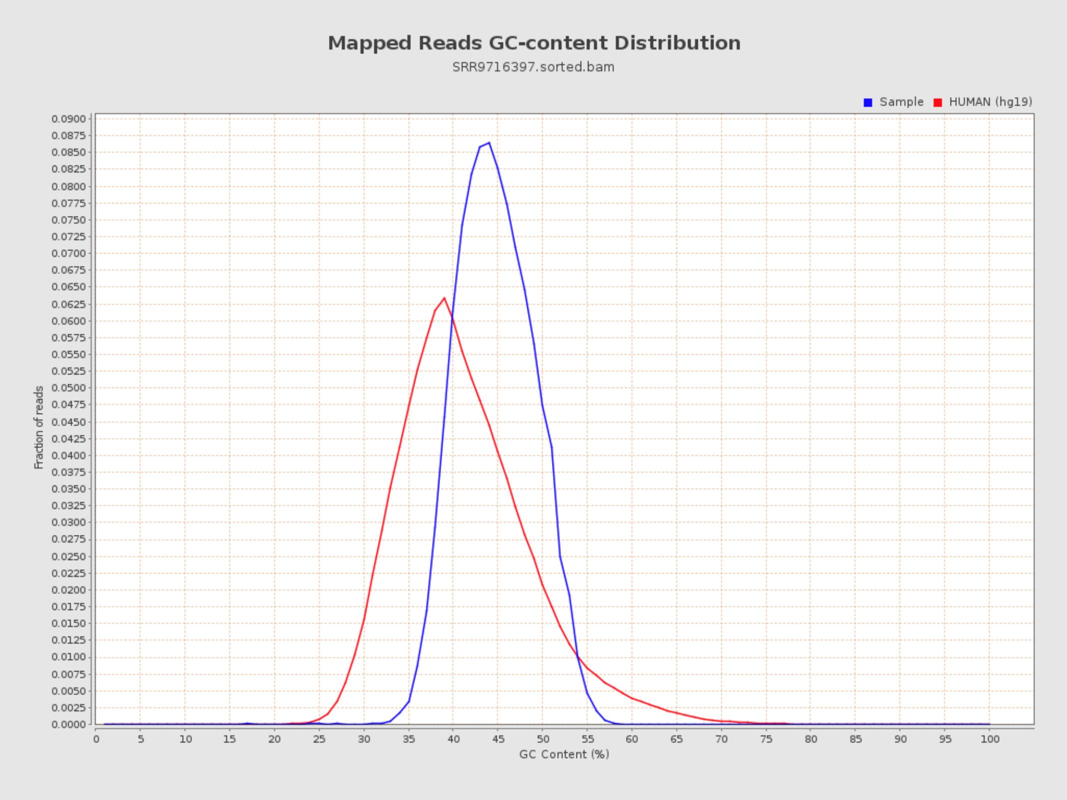
7. Results : Duplication Rate Histogram



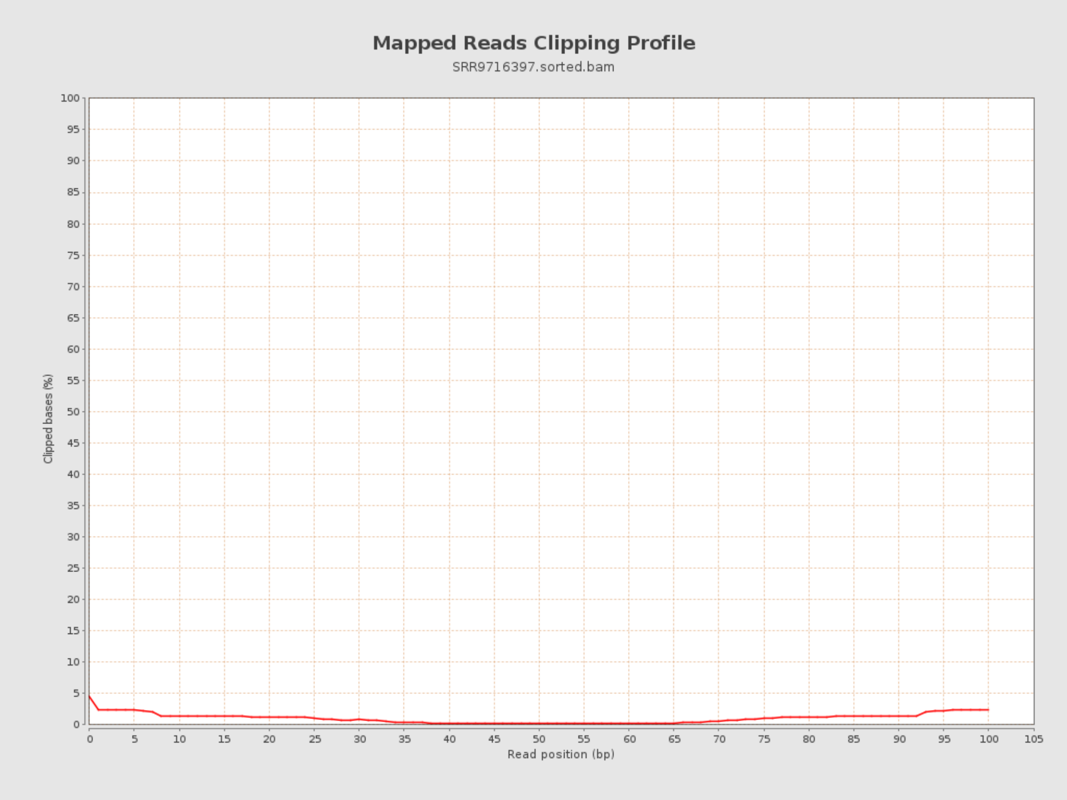
8. Results : Mapped Reads Nucleotide Content



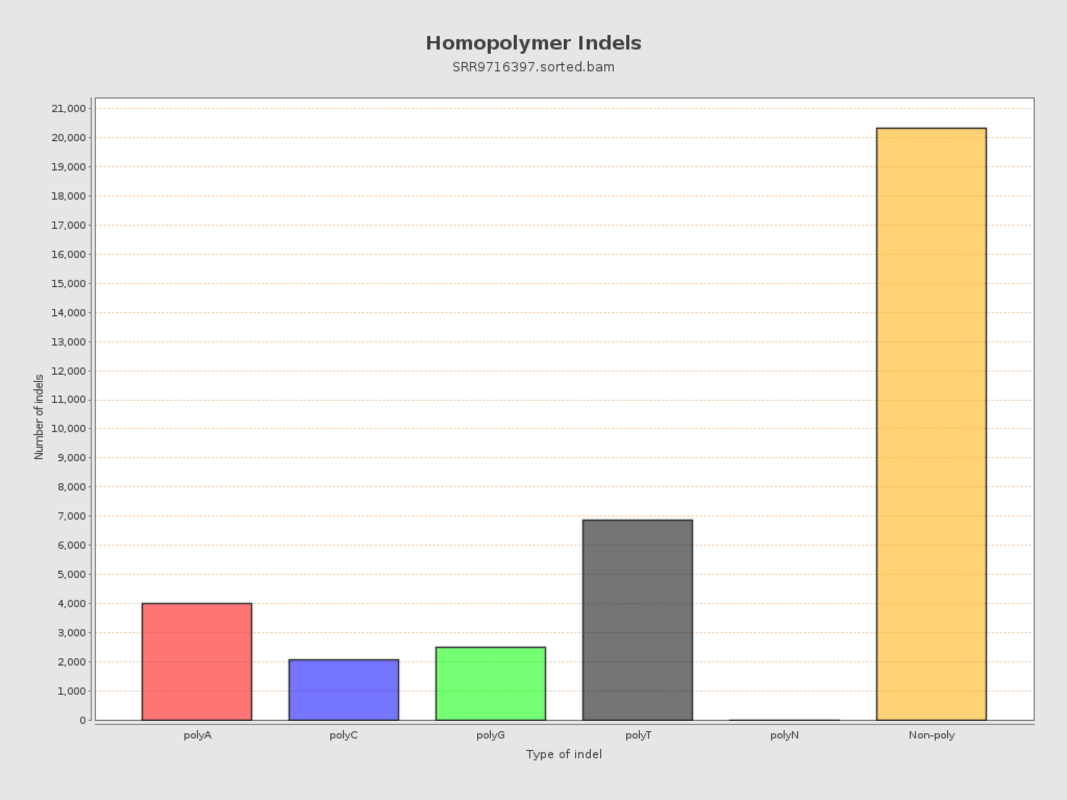
9. Results : Mapped Reads GC-content Distribution



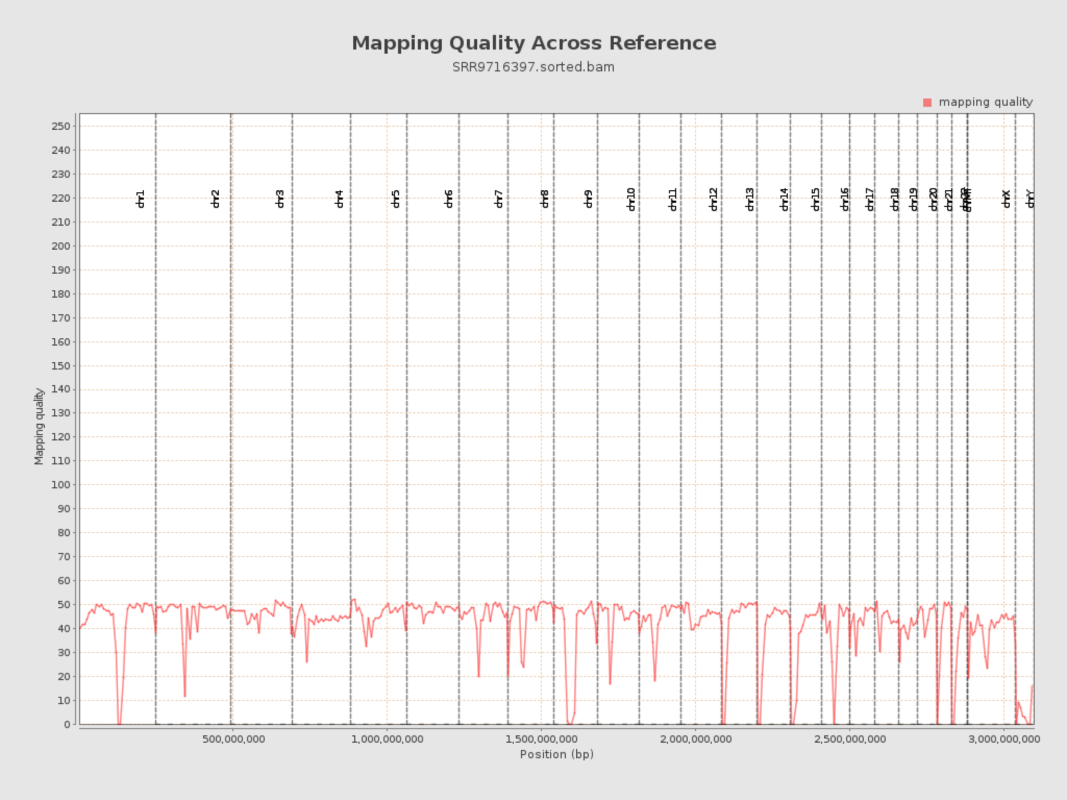
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram