Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 08:19:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716340.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_SRR9716340 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716340.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 08:19:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716340.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,717,597
Mapped reads	1,575,653 / 91.74%
Unmapped reads	141,944 / 8.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,084 / 0.59%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	60,860 / 3.54%
Duplication rate	2.97%
Clipped reads	1,581,794 / 92.09%

2.2. ACGT Content

Number/percentage of A's	22,899,613 / 24.98%
Number/percentage of C's	17,834,019 / 19.46%
Number/percentage of T's	28,634,351 / 31.24%
Number/percentage of G's	22,286,665 / 24.32%
Number/percentage of N's	1,128 / 0%
GC Percentage	43.77%

2.3. Coverage

Mean	0.0296

Standard Deviation	0.2579

2.4. Mapping Quality

Mean Mapping Quality	44.78

2.5. Mismatches and indels

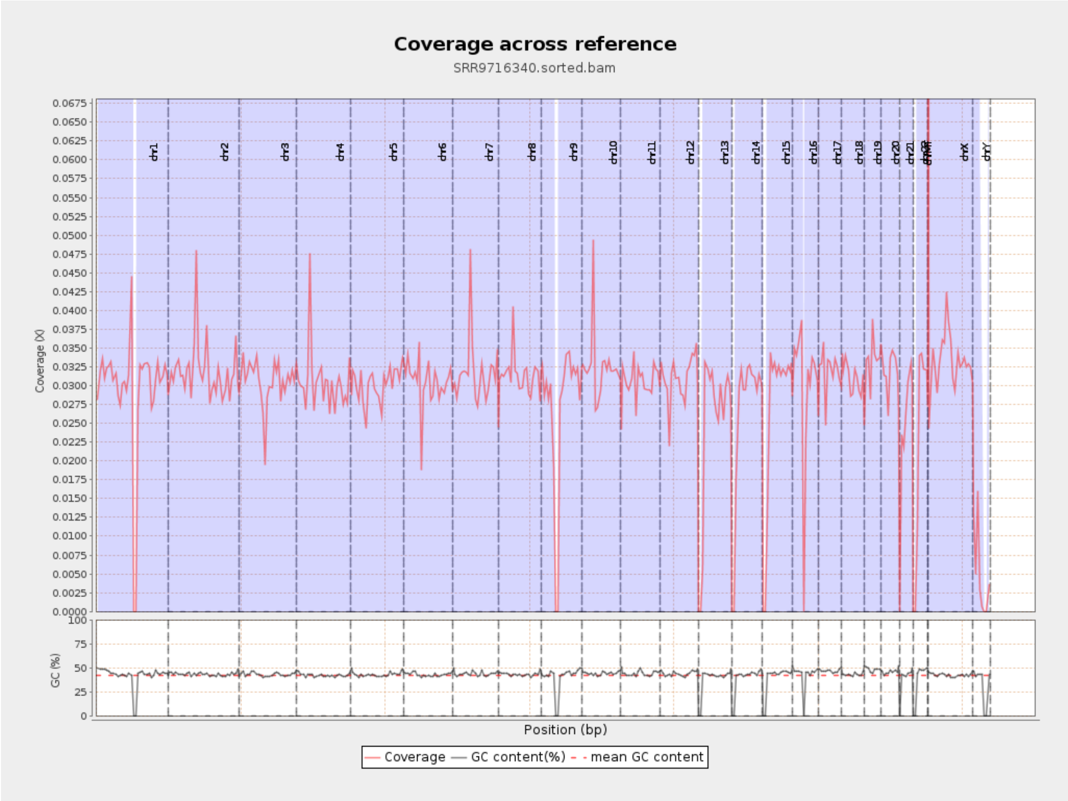
General error rate	0.51%
Mismatches	452,820
Insertions	6,836
Mapped reads with at least one insertion	0.43%
Deletions	16,462
Mapped reads with at least one deletion	1.04%
Homopolymer indels	41.79%

2.6. Chromosome stats

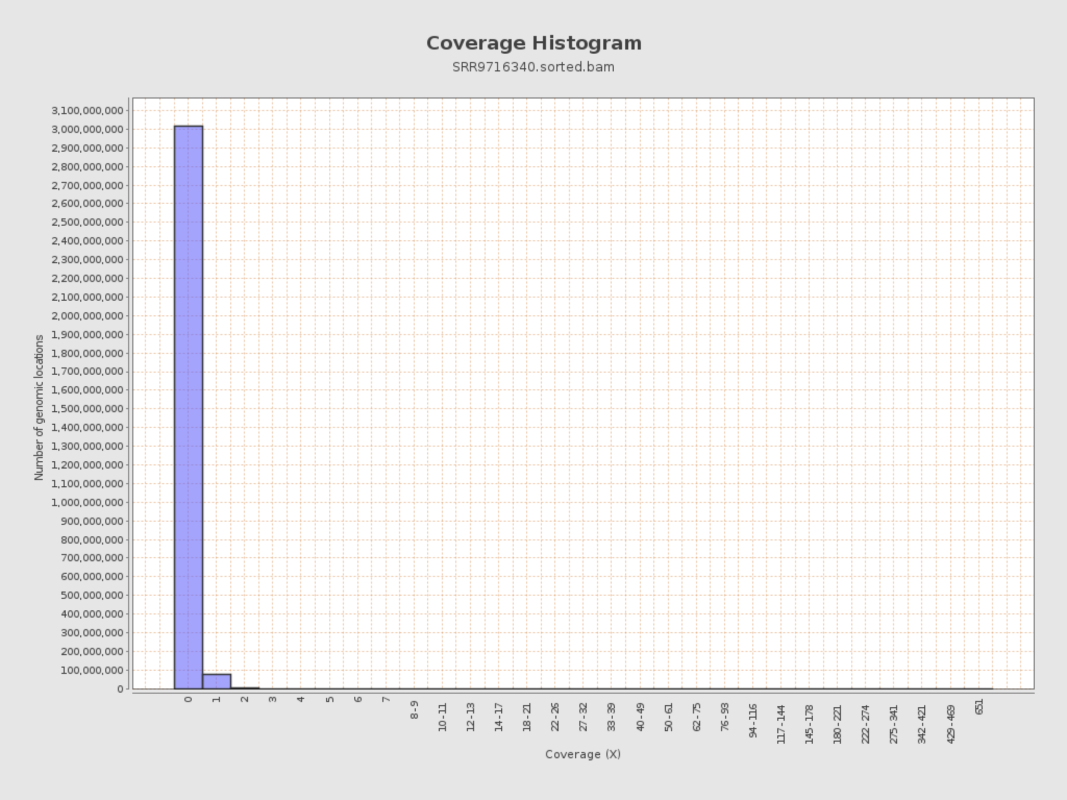
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7339966	0.0294	0.41
chr2	243199373	7764646	0.0319	0.3463
chr3	198022430	6056775	0.0306	0.1923
chr4	191154276	5832997	0.0305	0.213
chr5	180915260	5474411	0.0303	0.1921
chr6	171115067	5216303	0.0305	0.2105
chr7	159138663	5061452	0.0318	0.3322

chr8	146364022	4603188	0.0315	0.2593
chr9	141213431	3799977	0.0269	0.216
chr10	135534747	4408058	0.0325	0.2659
chr11	135006516	4152157	0.0308	0.2364
chr12	133851895	4144385	0.031	0.197
chr13	115169878	2849119	0.0247	0.1734
chr14	107349540	2796757	0.0261	0.1861
chr15	102531392	2694203	0.0263	0.182
chr16	90354753	2675431	0.0296	0.1958
chr17	81195210	2599512	0.032	0.2126
chr18	78077248	2419679	0.031	0.3624
chr19	59128983	1969647	0.0333	0.3254
chr20	63025520	2001328	0.0318	0.1995
chr21	48129895	1195763	0.0248	0.189
chr22	51304566	1165588	0.0227	0.1656
chrMT	16571	8366	0.5049	0.8147
chrX	155270560	5167168	0.0333	0.2165
chrY	59373566	285474	0.0048	0.1297

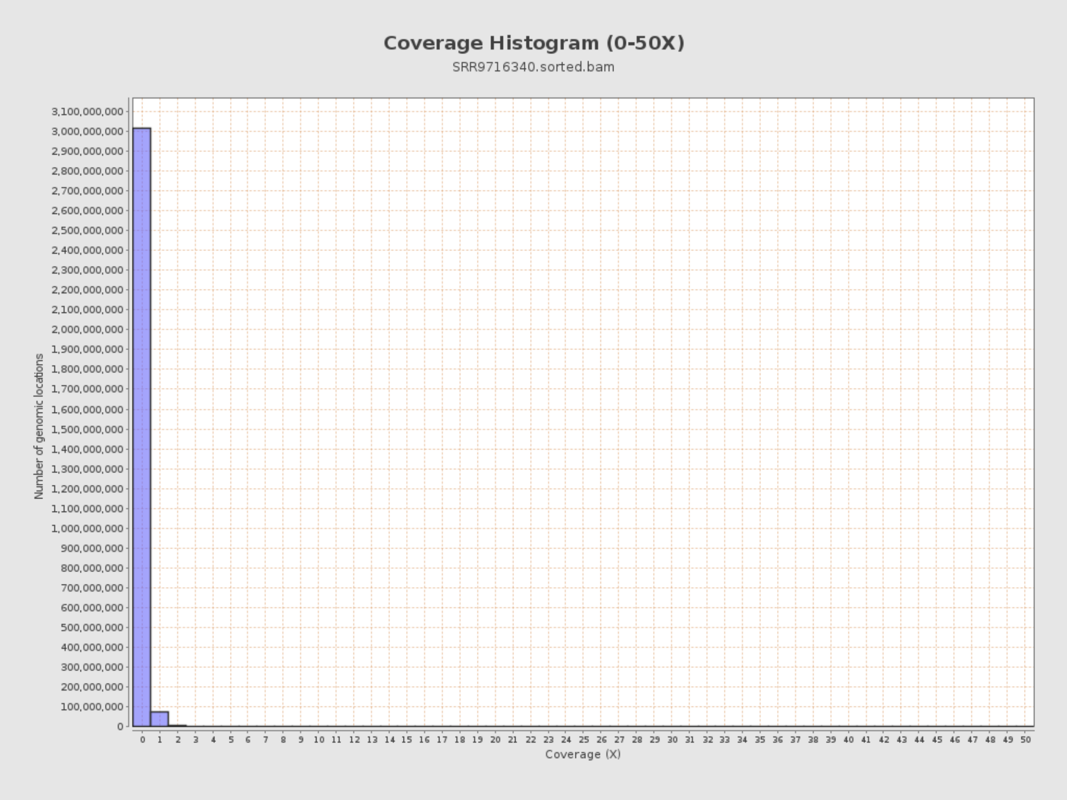
3. Results : Coverage across reference



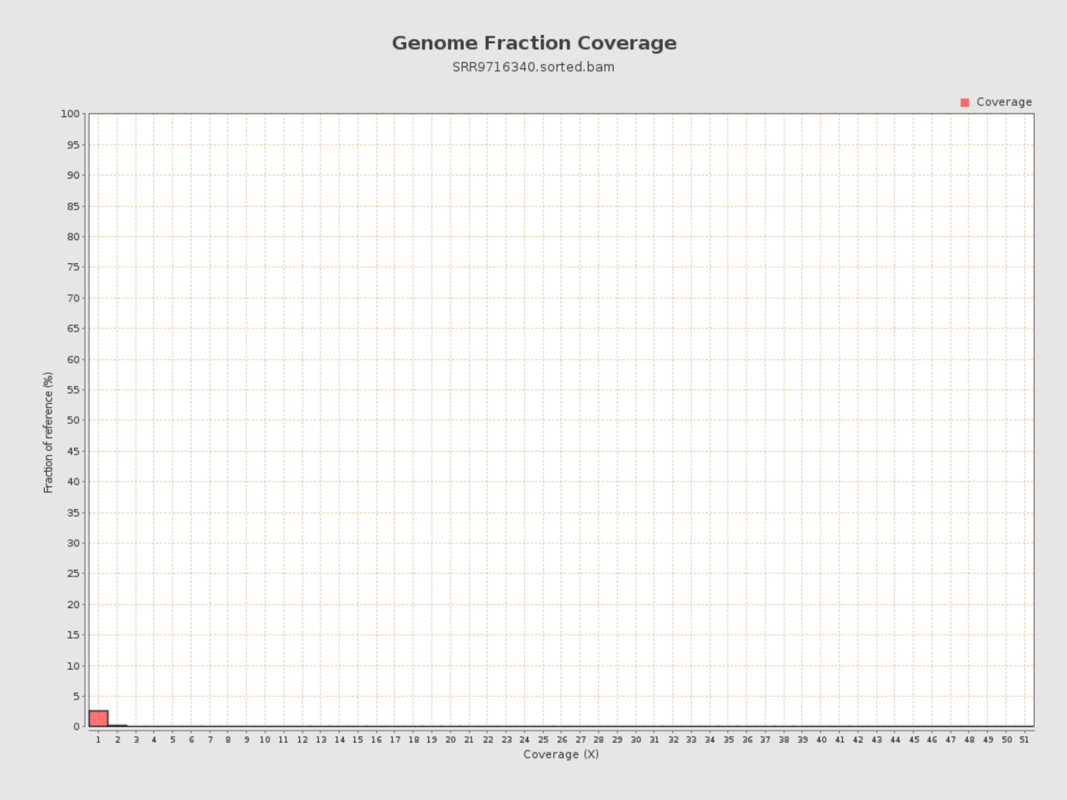
4. Results : Coverage Histogram



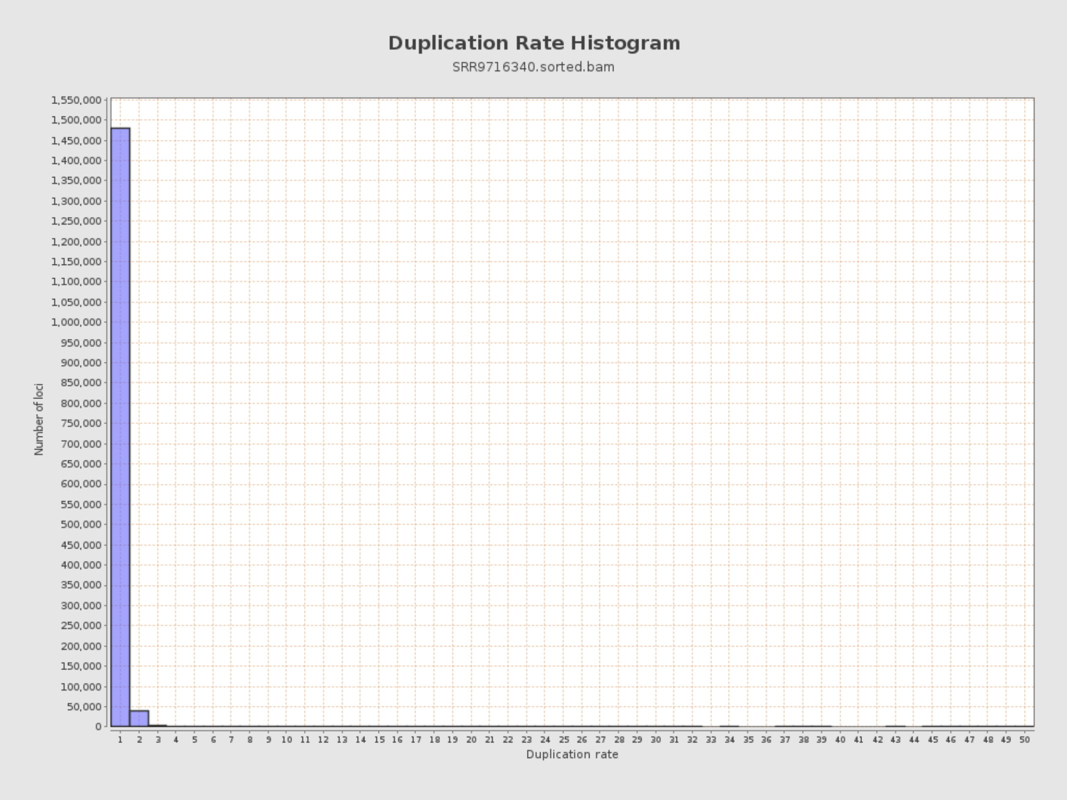
5. Results : Coverage Histogram (0-50X)



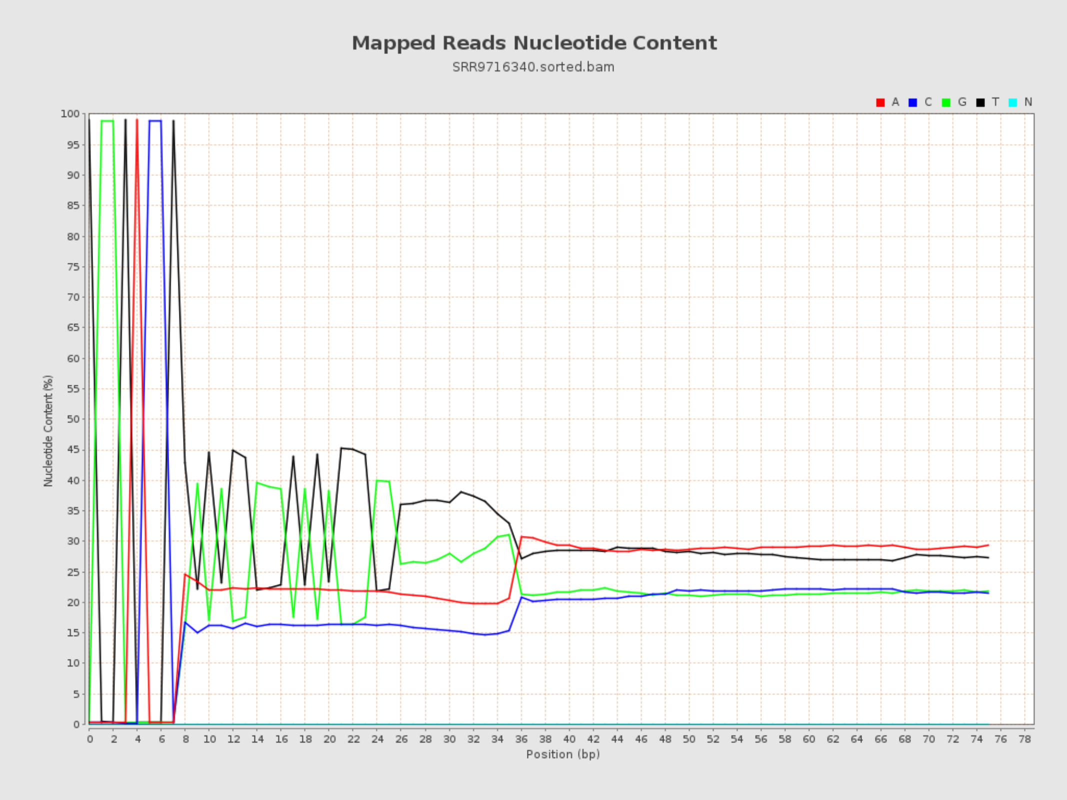
6. Results : Genome Fraction Coverage



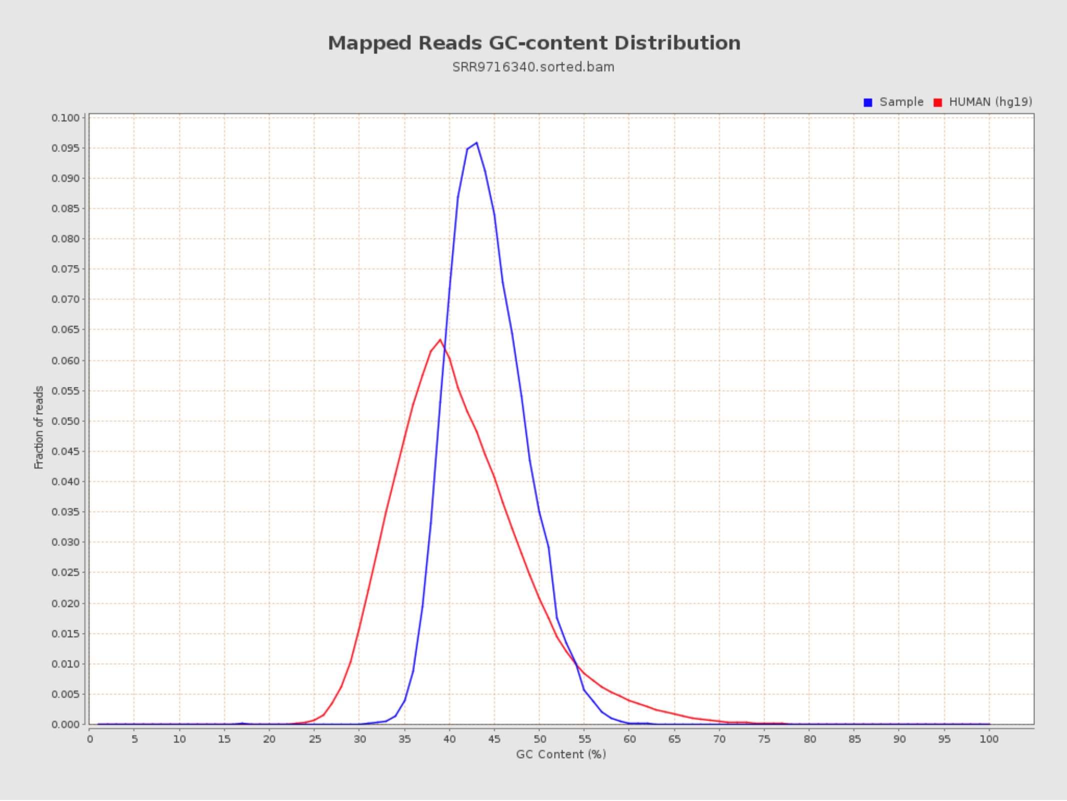
7. Results : Duplication Rate Histogram



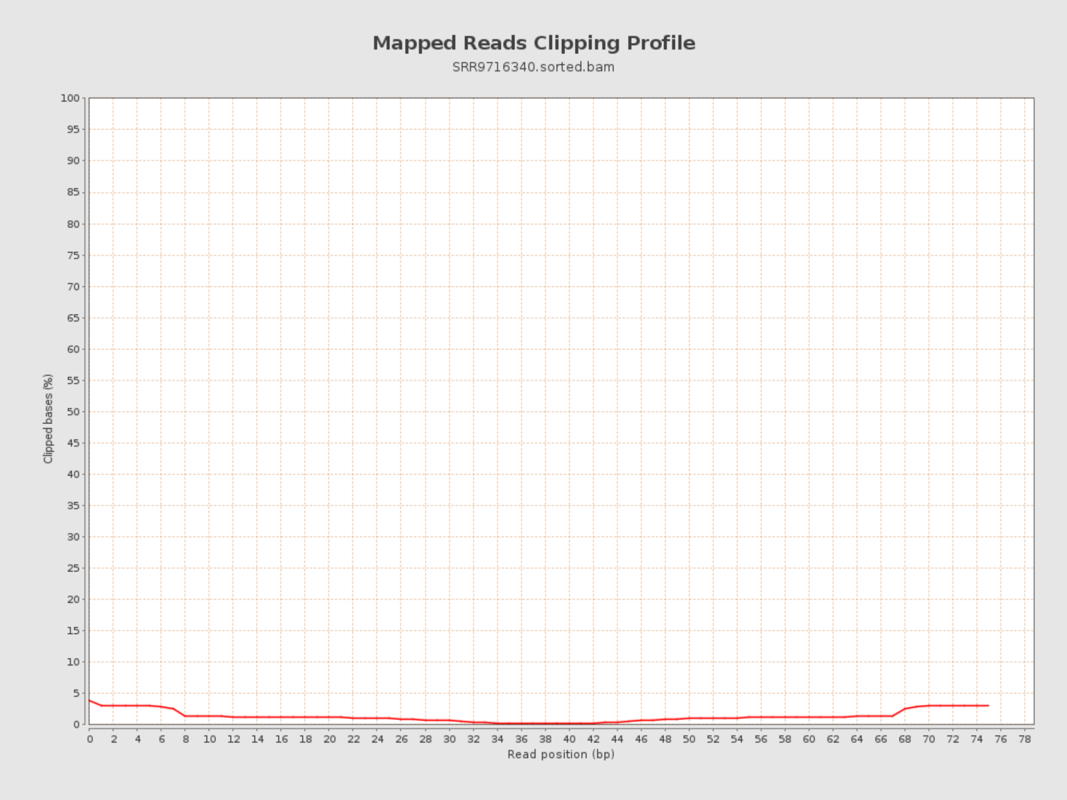
8. Results : Mapped Reads Nucleotide Content



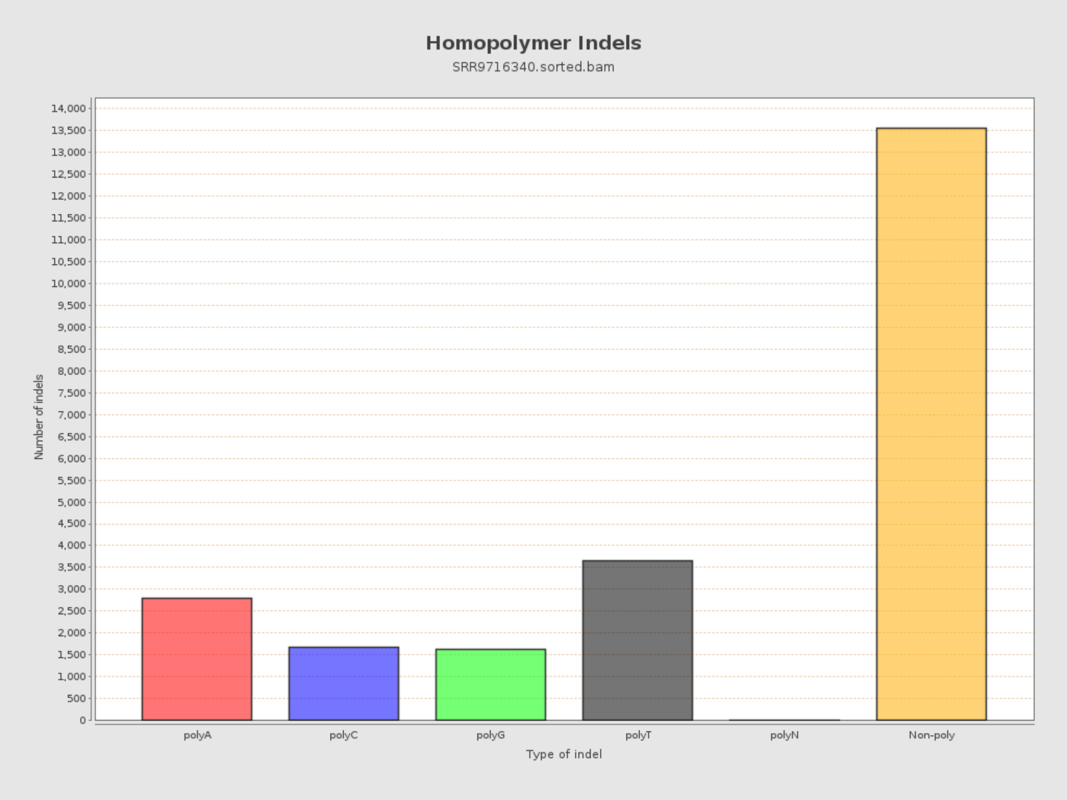
9. Results : Mapped Reads GC-content Distribution



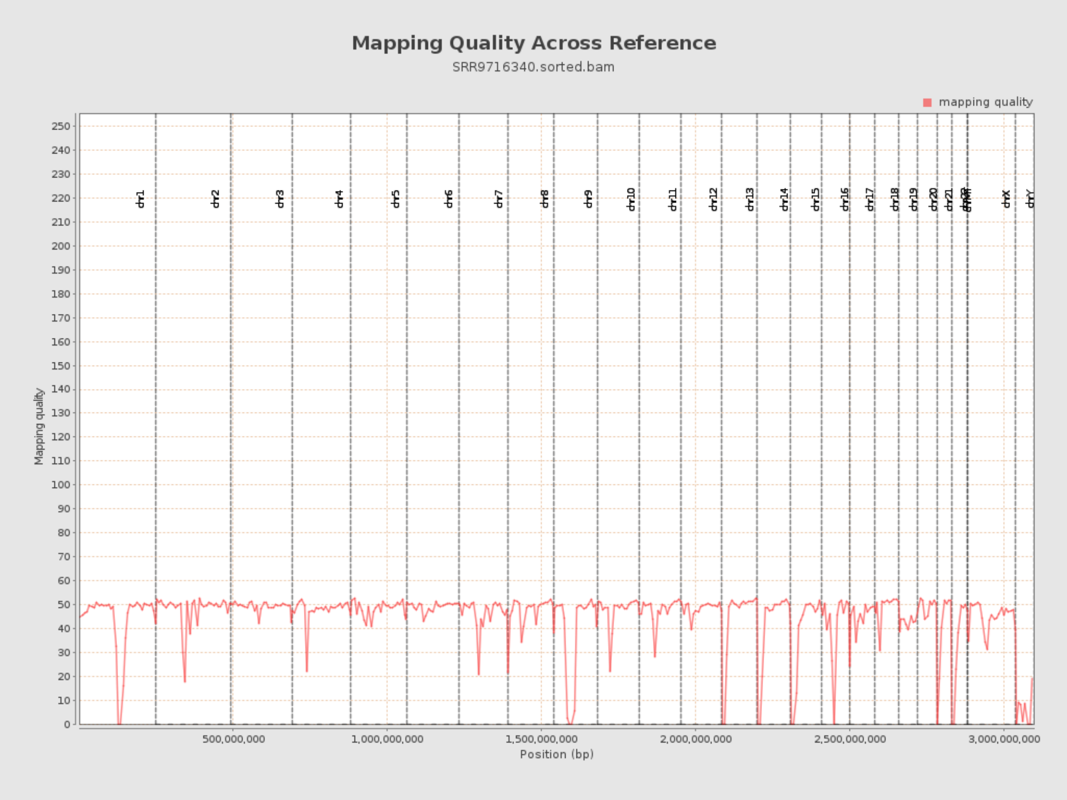
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram