Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 19:22:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716536.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_SRR9716536 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716536.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 19:22:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716536.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,635,347
Mapped reads	1,548,370 / 94.68%
Unmapped reads	86,977 / 5.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	31,387 / 1.92%
Read min/max/mean length	30 / 101 / 101.69
Duplicated reads (estimated)	53,413 / 3.27%
Duplication rate	2.35%
Clipped reads	1,578,892 / 96.55%

2.2. ACGT Content

Number/percentage of A's	31,156,414 / 25.27%
Number/percentage of C's	24,744,607 / 20.07%
Number/percentage of T's	37,315,927 / 30.26%
Number/percentage of G's	30,078,053 / 24.39%
Number/percentage of N's	8,900 / 0.01%
GC Percentage	44.46%

2.3. Coverage

Mean	0.0398

Standard Deviation	0.399

2.4. Mapping Quality

Mean Mapping Quality	47.51

2.5. Mismatches and indels

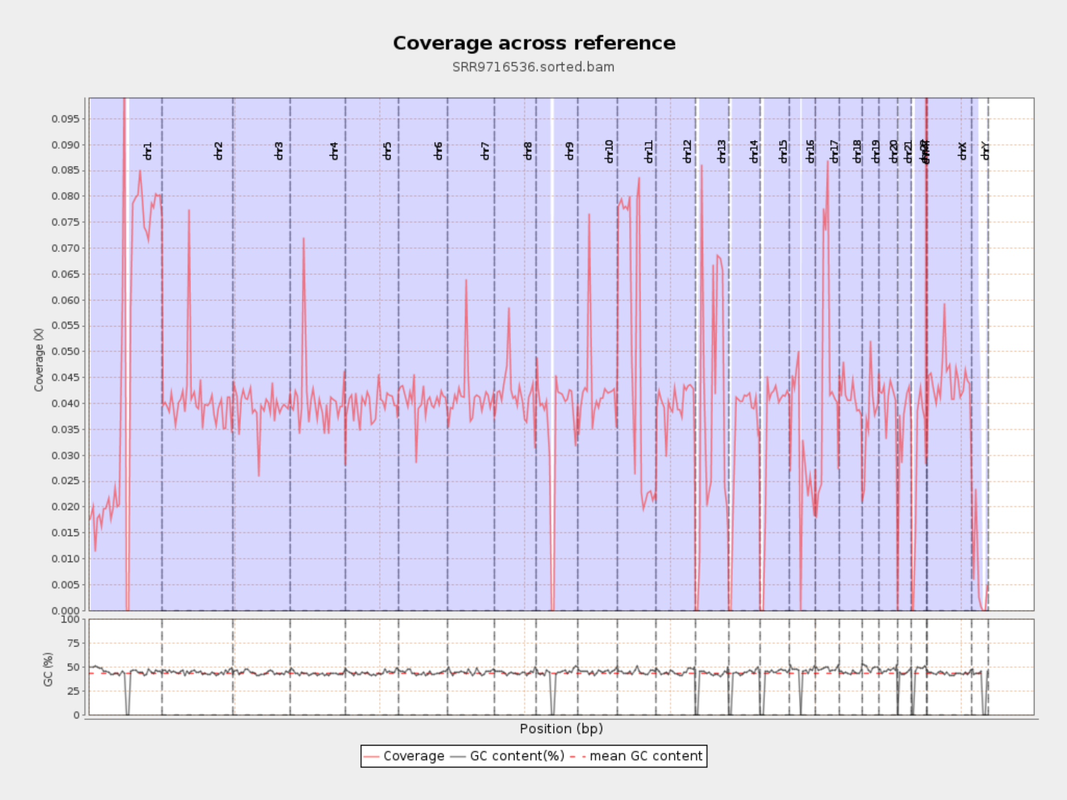
General error rate	0.64%
Mismatches	763,087
Insertions	8,980
Mapped reads with at least one insertion	0.57%
Deletions	28,457
Mapped reads with at least one deletion	1.81%
Homopolymer indels	43.43%

2.6. Chromosome stats

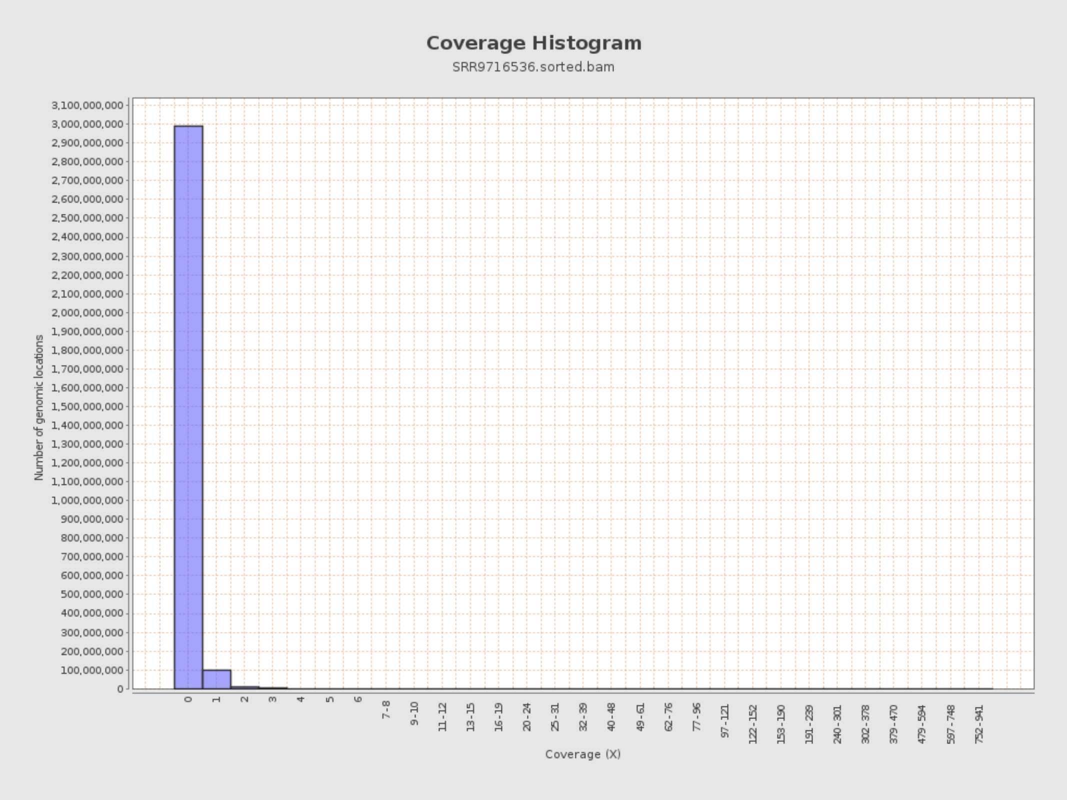
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11821429	0.0474	0.8849
chr2	243199373	9902267	0.0407	0.4029
chr3	198022430	7791174	0.0393	0.2184
chr4	191154276	7784466	0.0407	0.2648
chr5	180915260	7195029	0.0398	0.2205
chr6	171115067	6940787	0.0406	0.2451
chr7	159138663	6628357	0.0417	0.4762

chr8	146364022	6116402	0.0418	0.4331
chr9	141213431	5029524	0.0356	0.3103
chr10	135534747	5750577	0.0424	0.3827
chr11	135006516	6810750	0.0504	0.3984
chr12	133851895	5358420	0.04	0.2219
chr13	115169878	4404603	0.0382	0.2169
chr14	107349540	3594481	0.0335	0.2162
chr15	102531392	3506134	0.0342	0.2043
chr16	90354753	2722312	0.0301	0.21
chr17	81195210	3731052	0.046	0.2766
chr18	78077248	3246925	0.0416	0.541
chr19	59128983	2217087	0.0375	0.6096
chr20	63025520	2548666	0.0404	0.2303
chr21	48129895	1644888	0.0342	0.2347
chr22	51304566	1383218	0.027	0.1824
chrMT	16571	14038	0.8471	0.994
chrX	155270560	6852025	0.0441	0.2685
chrY	59373566	363668	0.0061	0.2046

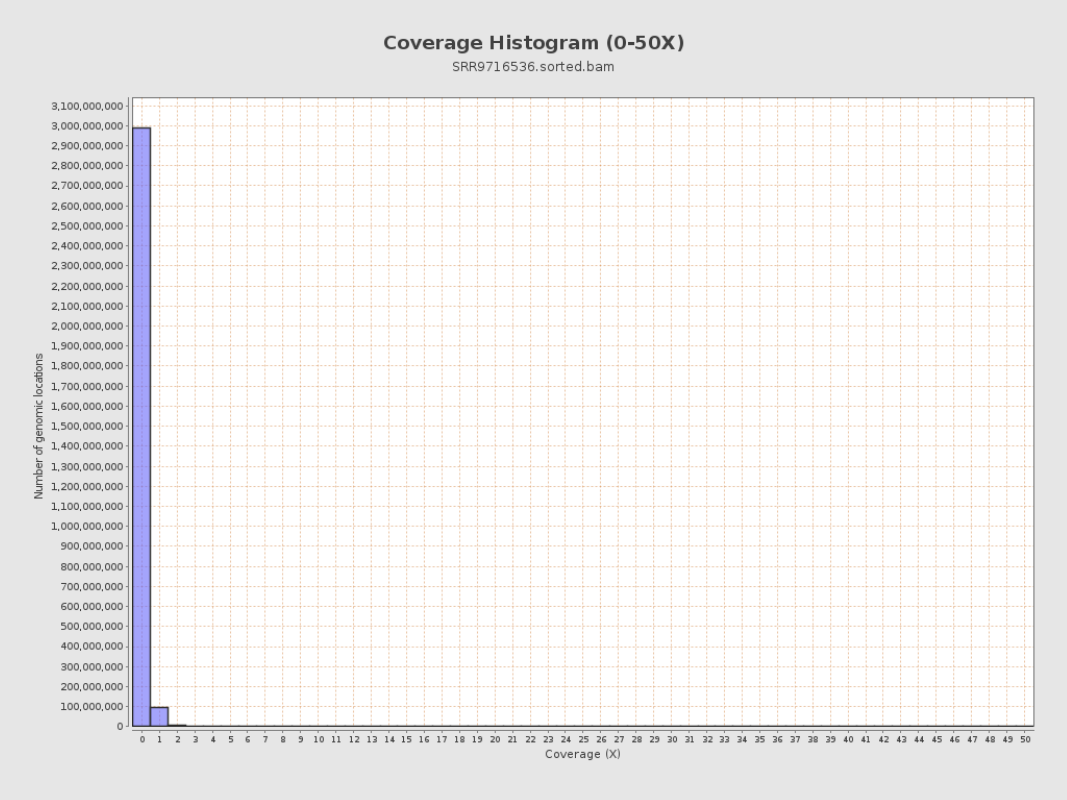
3. Results : Coverage across reference



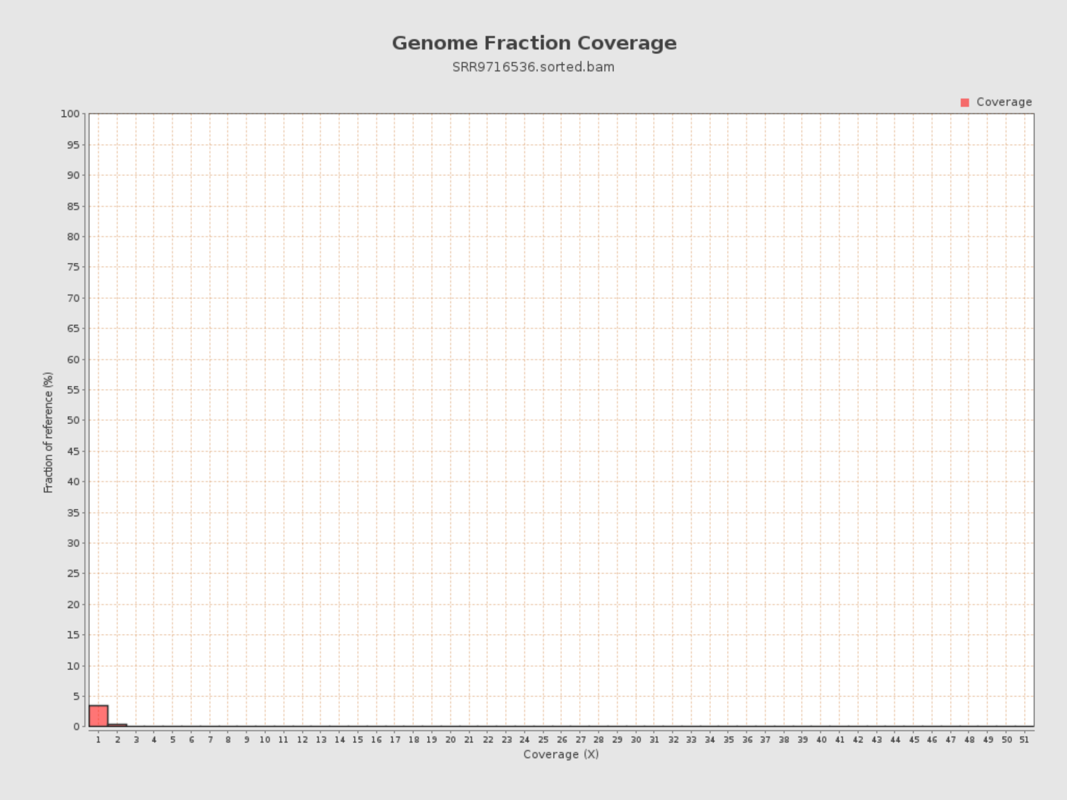
4. Results : Coverage Histogram



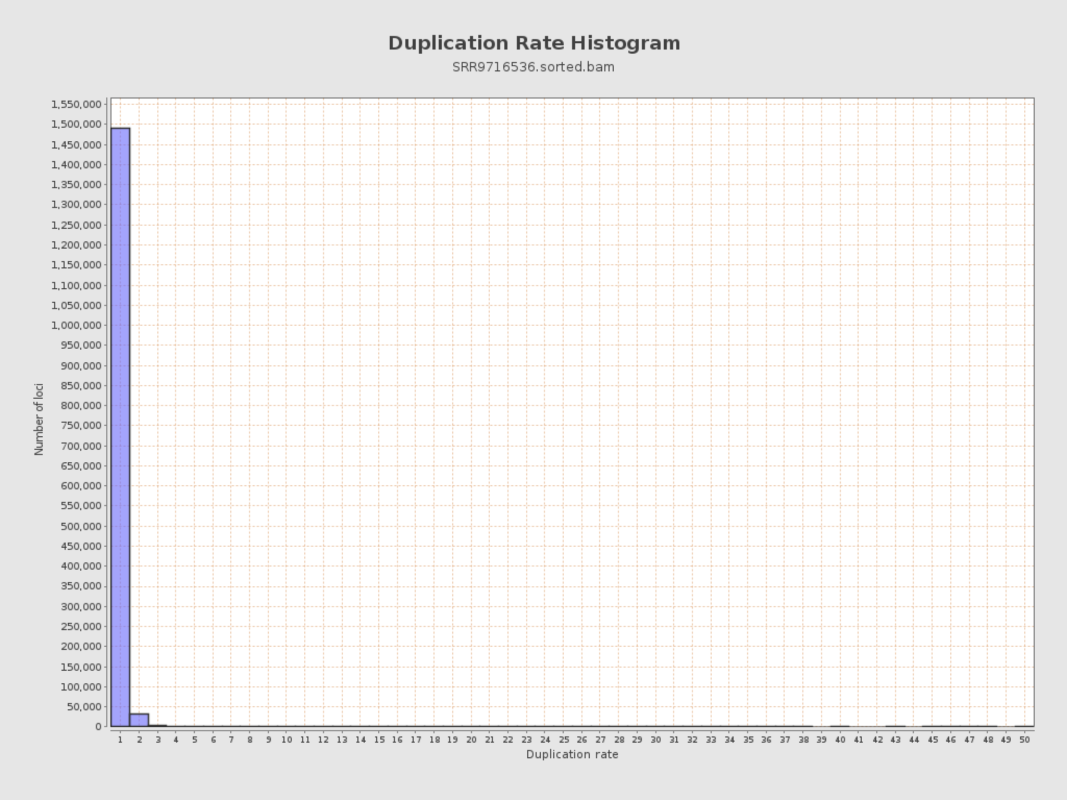
5. Results : Coverage Histogram (0-50X)



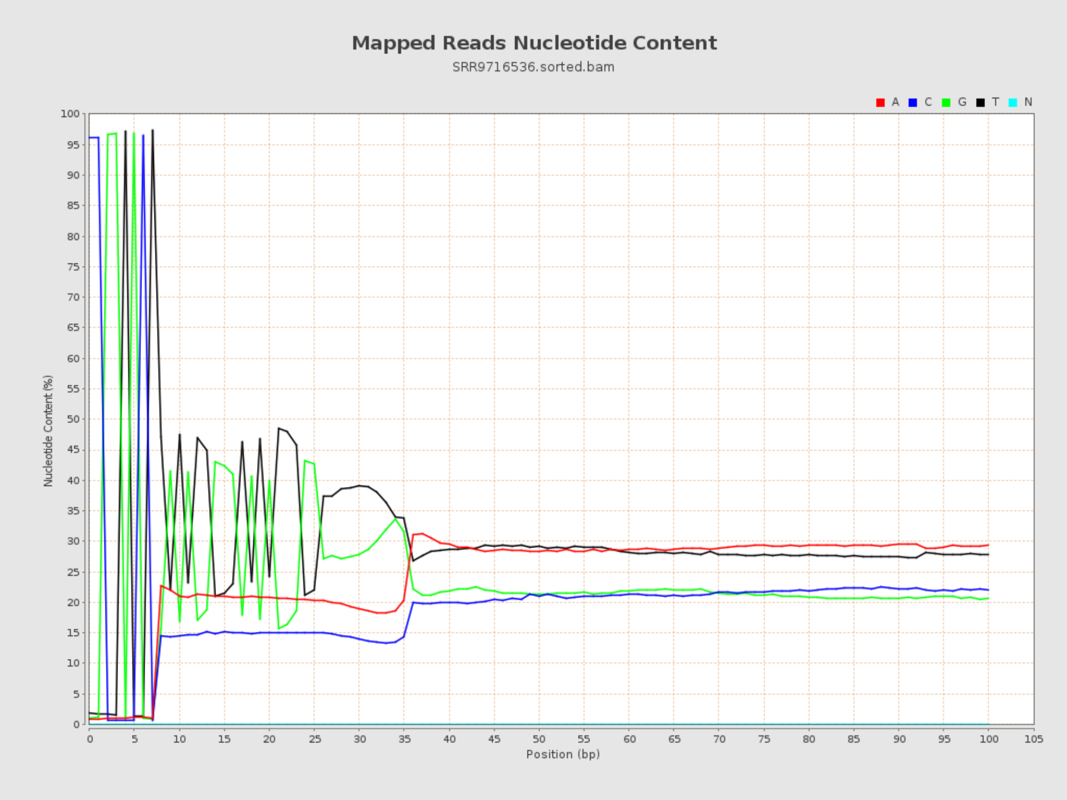
6. Results : Genome Fraction Coverage



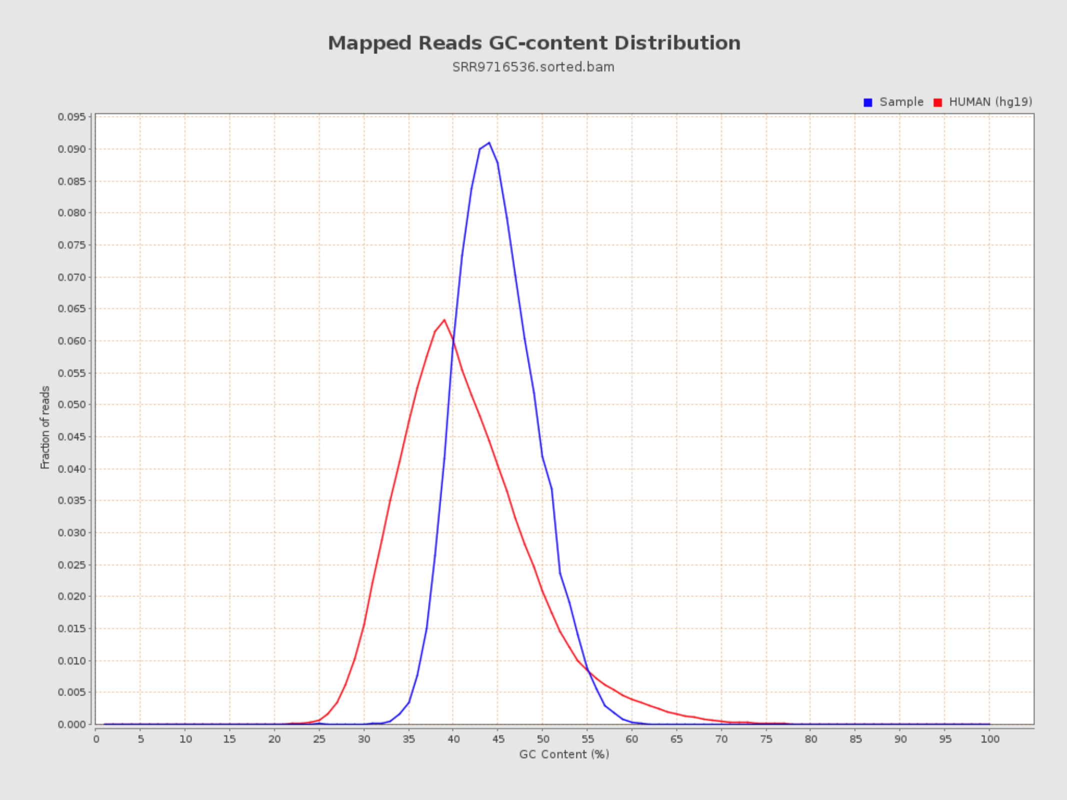
7. Results : Duplication Rate Histogram



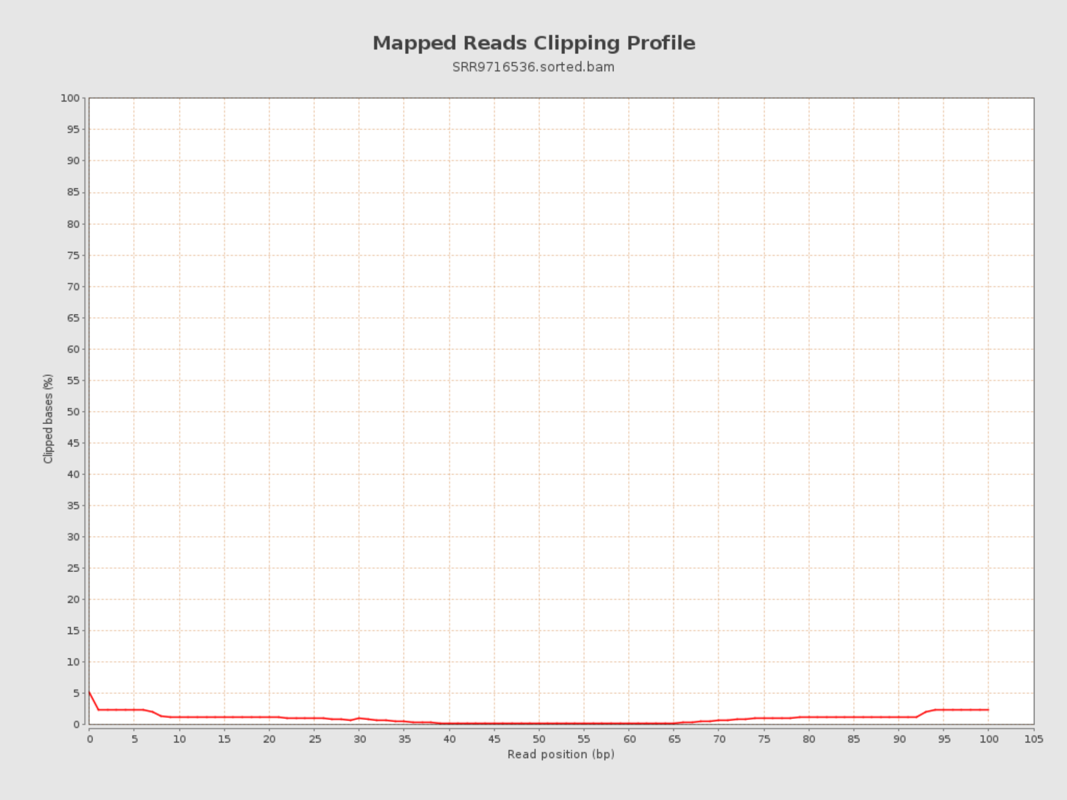
8. Results : Mapped Reads Nucleotide Content



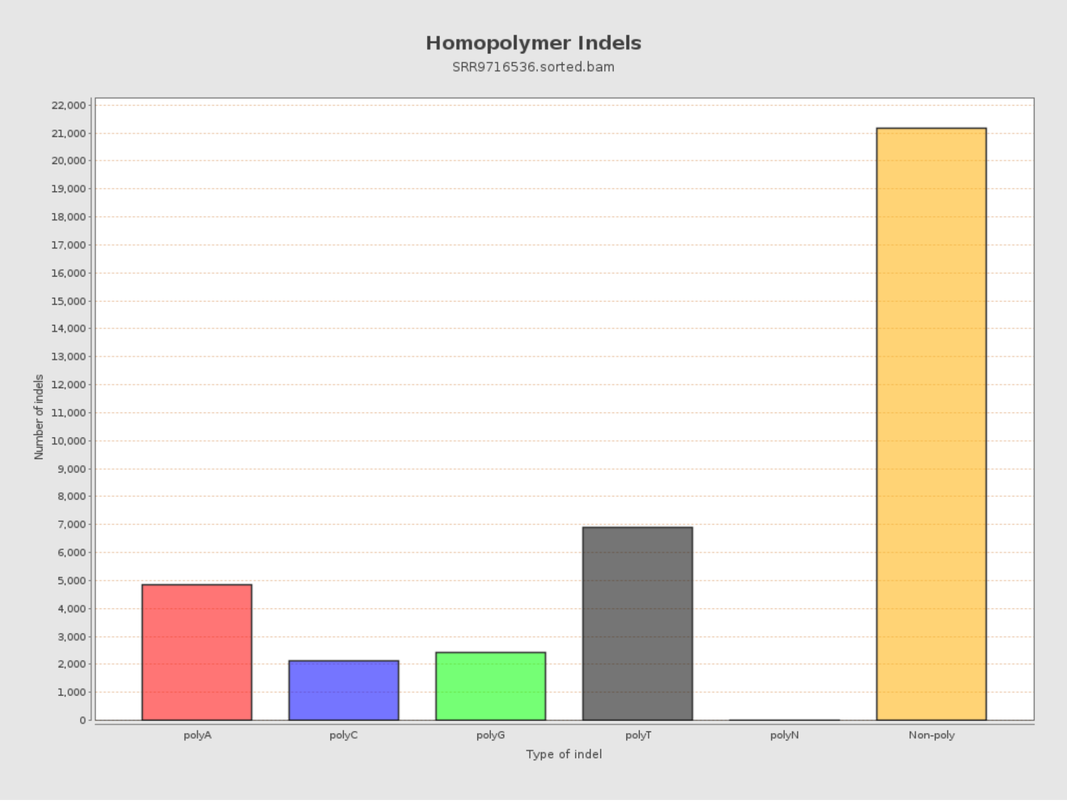
9. Results : Mapped Reads GC-content Distribution



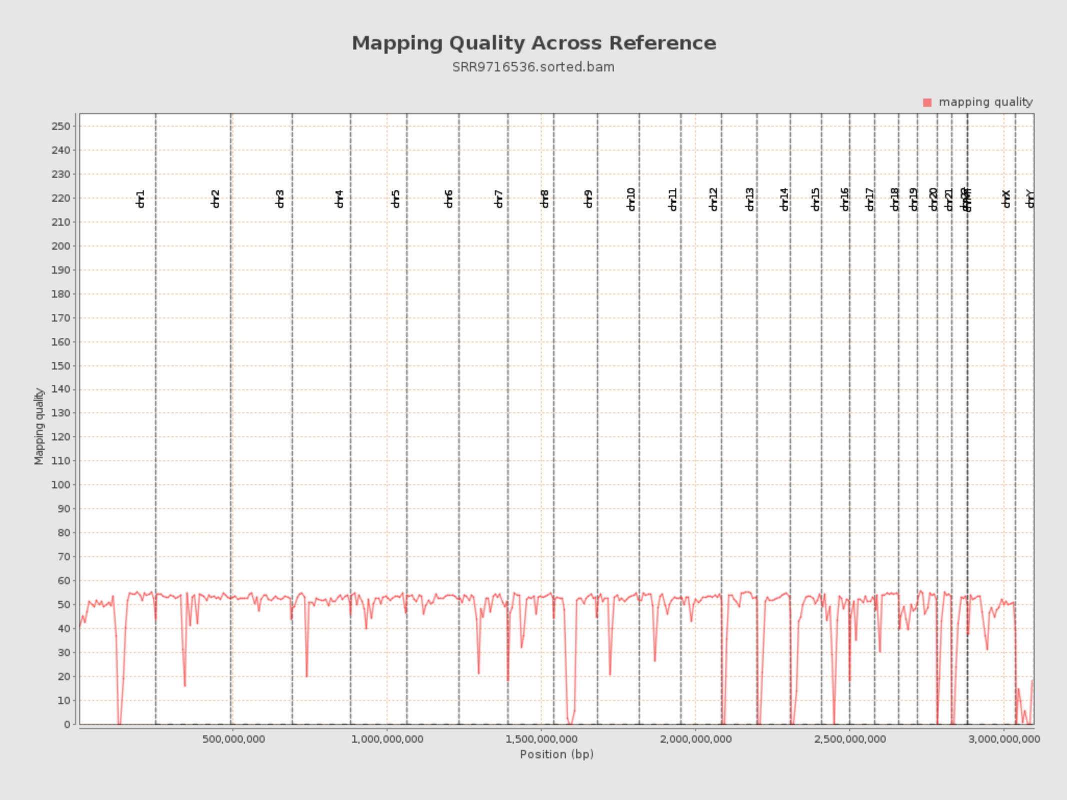
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram