Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 03:18:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716257.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_SRR9716257 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716257.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 03:18:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716257.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,049,643
Mapped reads	994,954 / 94.79%
Unmapped reads	54,689 / 5.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,569 / 1.96%
Read min/max/mean length	30 / 101 / 101.71
Duplicated reads (estimated)	32,826 / 3.13%
Duplication rate	2.64%
Clipped reads	1,015,010 / 96.7%

2.2. ACGT Content

Number/percentage of A's	19,797,847 / 25.63%
Number/percentage of C's	15,471,797 / 20.03%
Number/percentage of T's	22,691,470 / 29.38%
Number/percentage of G's	19,265,877 / 24.95%
Number/percentage of N's	2,877 / 0%
GC Percentage	44.98%

2.3. Coverage

Mean	0.025

Standard Deviation	0.229

2.4. Mapping Quality

Mean Mapping Quality	46.89

2.5. Mismatches and indels

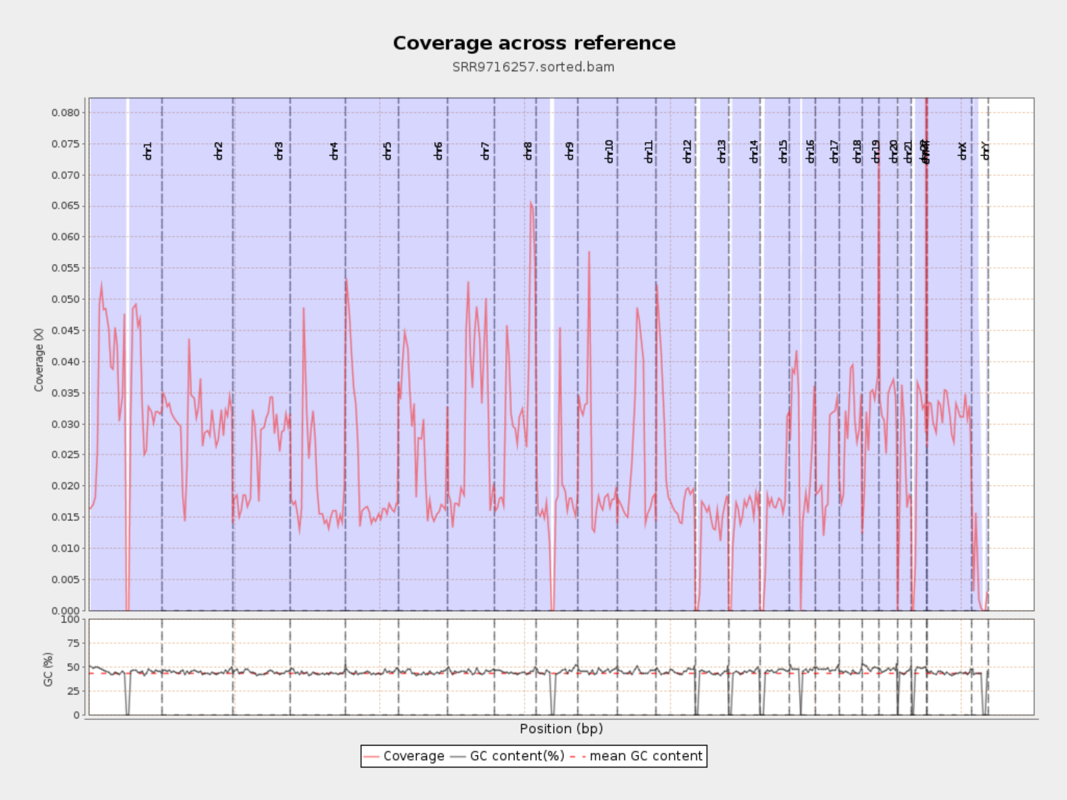
General error rate	0.63%
Mismatches	473,112
Insertions	5,901
Mapped reads with at least one insertion	0.58%
Deletions	14,918
Mapped reads with at least one deletion	1.48%
Homopolymer indels	38.99%

2.6. Chromosome stats

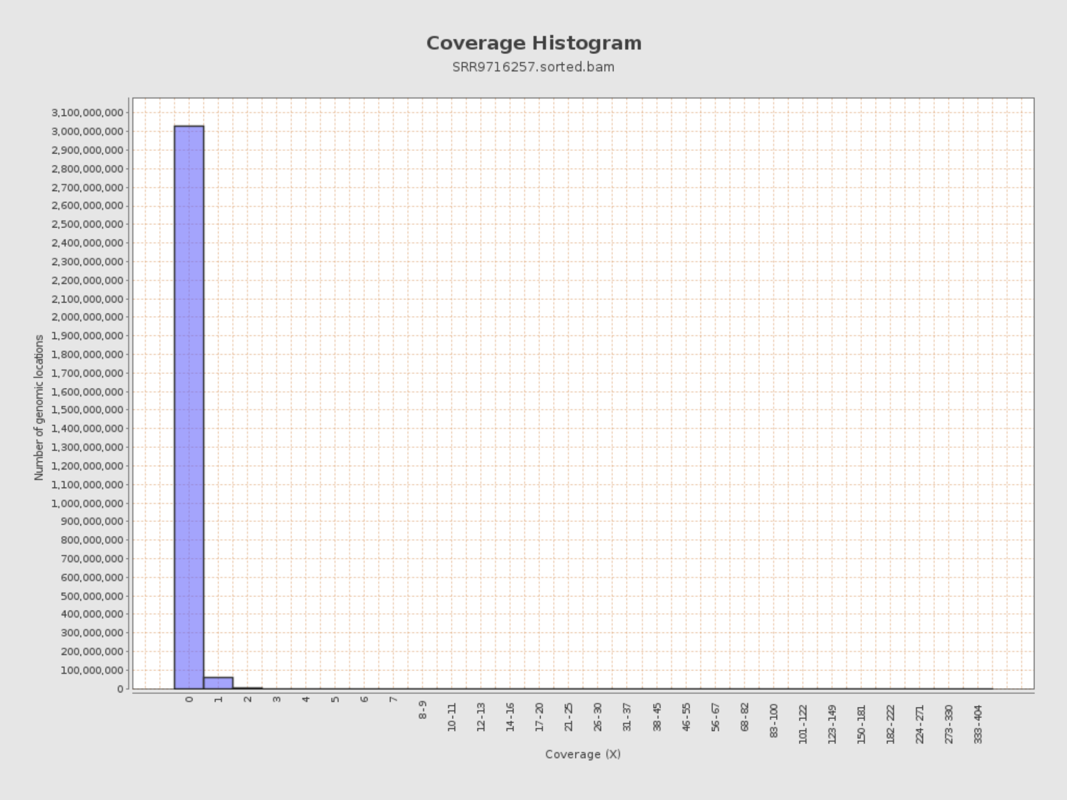
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8523546	0.0342	0.4107
chr2	243199373	7395491	0.0304	0.2476
chr3	198022430	5038591	0.0254	0.1772
chr4	191154276	3776366	0.0198	0.1969
chr5	180915260	3970271	0.0219	0.1635
chr6	171115067	4379321	0.0256	0.1824
chr7	159138663	4942335	0.0311	0.2858

chr8	146364022	4859315	0.0332	0.2501
chr9	141213431	2320791	0.0164	0.1663
chr10	135534747	3199980	0.0236	0.2843
chr11	135006516	3306074	0.0245	0.2078
chr12	133851895	3104057	0.0232	0.1685
chr13	115169878	1495568	0.013	0.1246
chr14	107349540	1524117	0.0142	0.1353
chr15	102531392	1587274	0.0155	0.1368
chr16	90354753	2355395	0.0261	0.1827
chr17	81195210	1926399	0.0237	0.1801
chr18	78077248	2257133	0.0289	0.2404
chr19	59128983	1885649	0.0319	0.2983
chr20	63025520	2060201	0.0327	0.204
chr21	48129895	1011646	0.021	0.1853
chr22	51304566	1176651	0.0229	0.1688
chrMT	16571	9577	0.5779	0.9154
chrX	155270560	4910736	0.0316	0.2021
chrY	59373566	244340	0.0041	0.1465

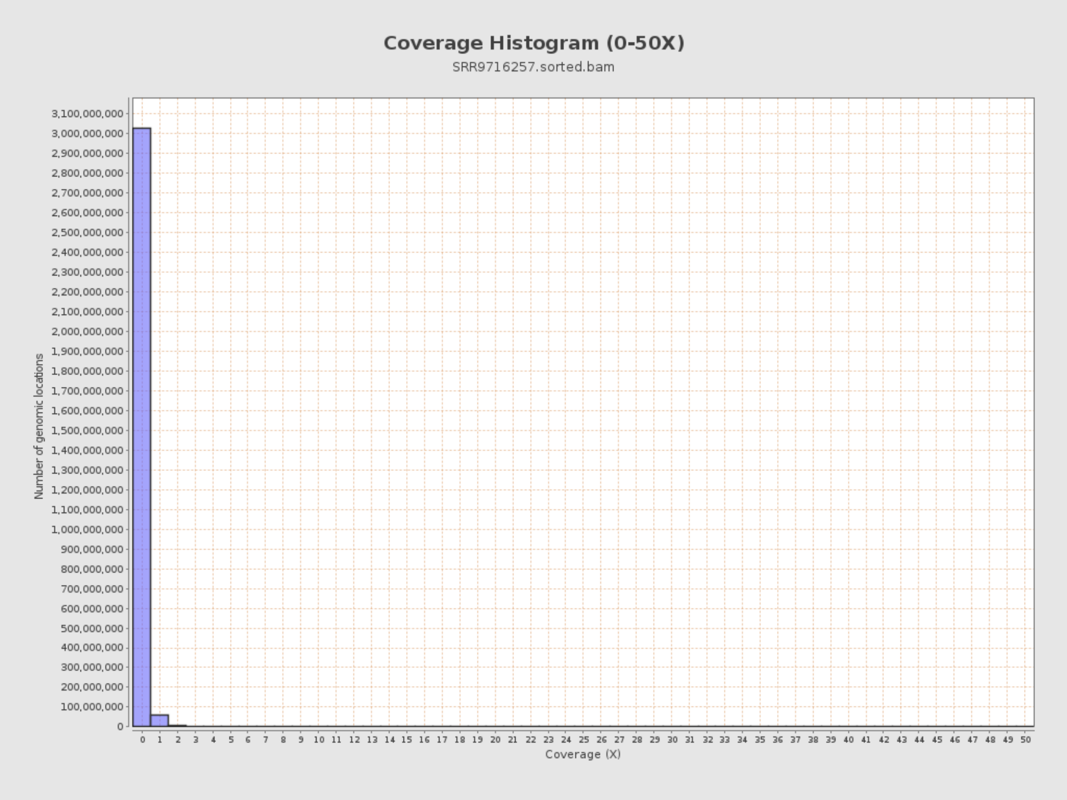
3. Results : Coverage across reference



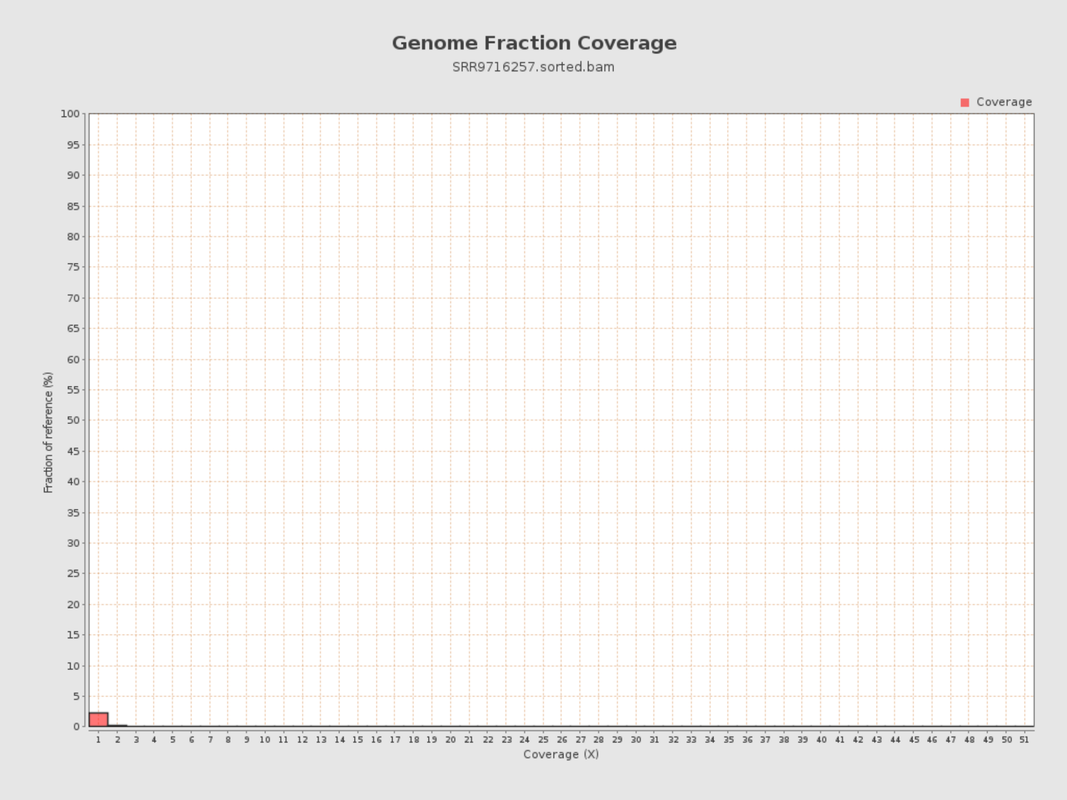
4. Results : Coverage Histogram



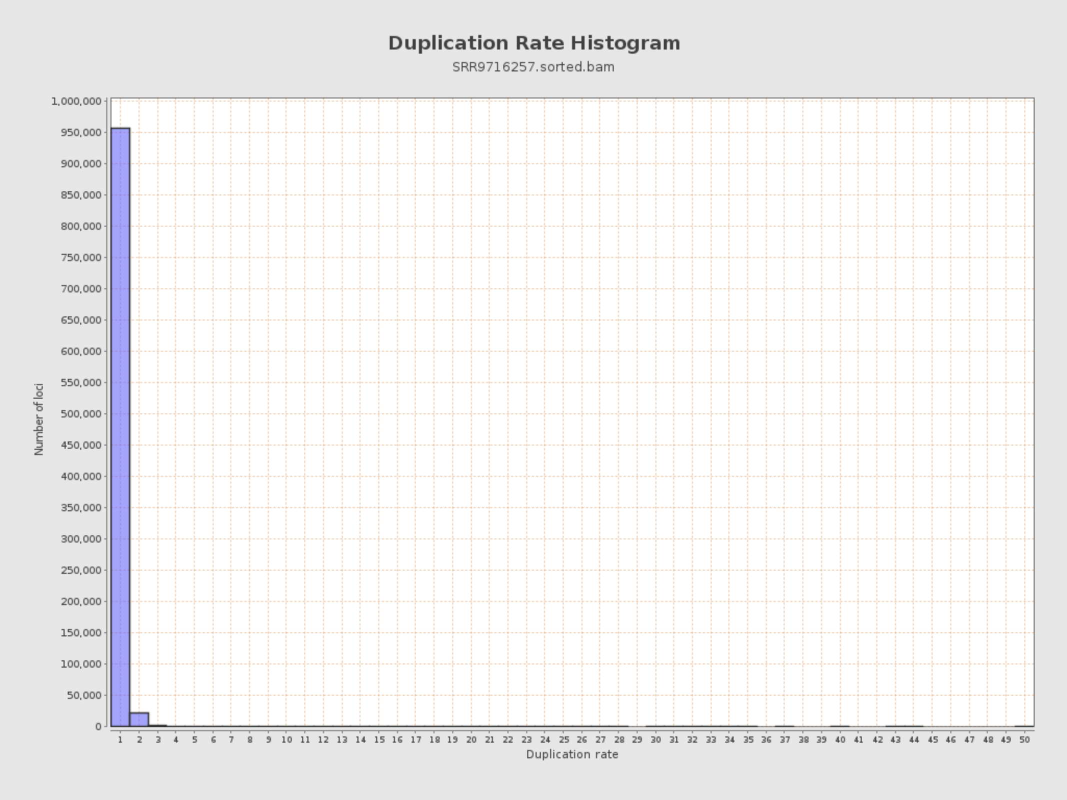
5. Results : Coverage Histogram (0-50X)



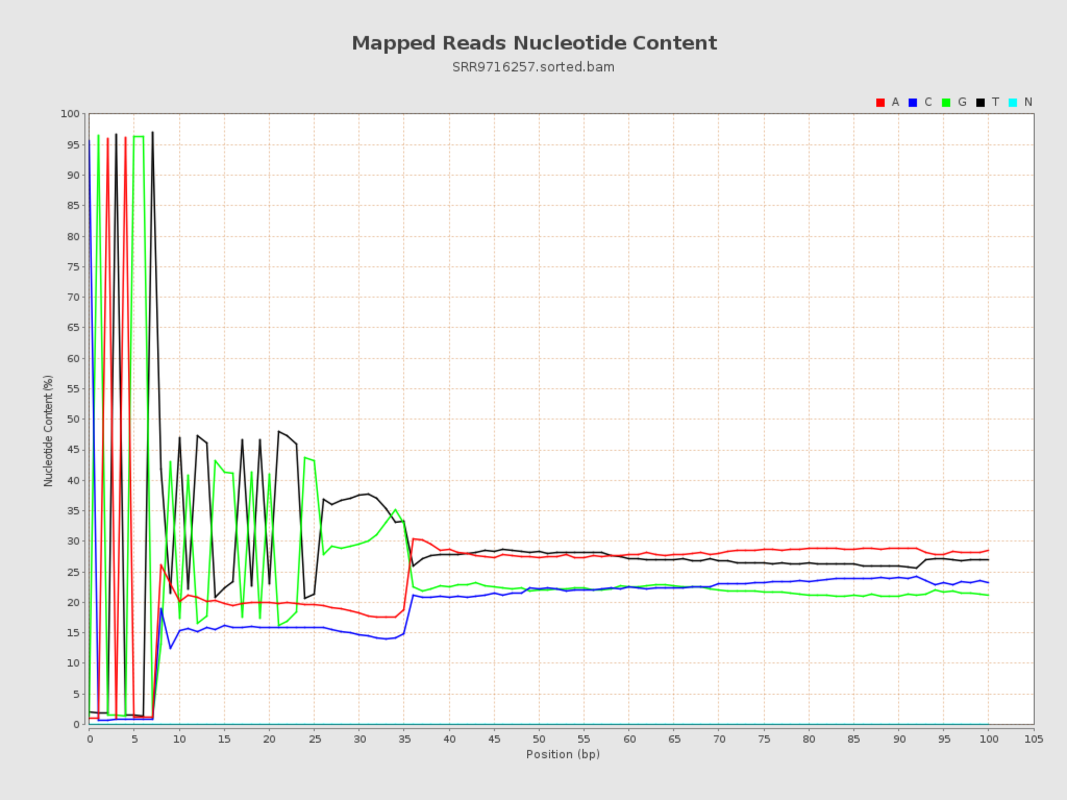
6. Results : Genome Fraction Coverage



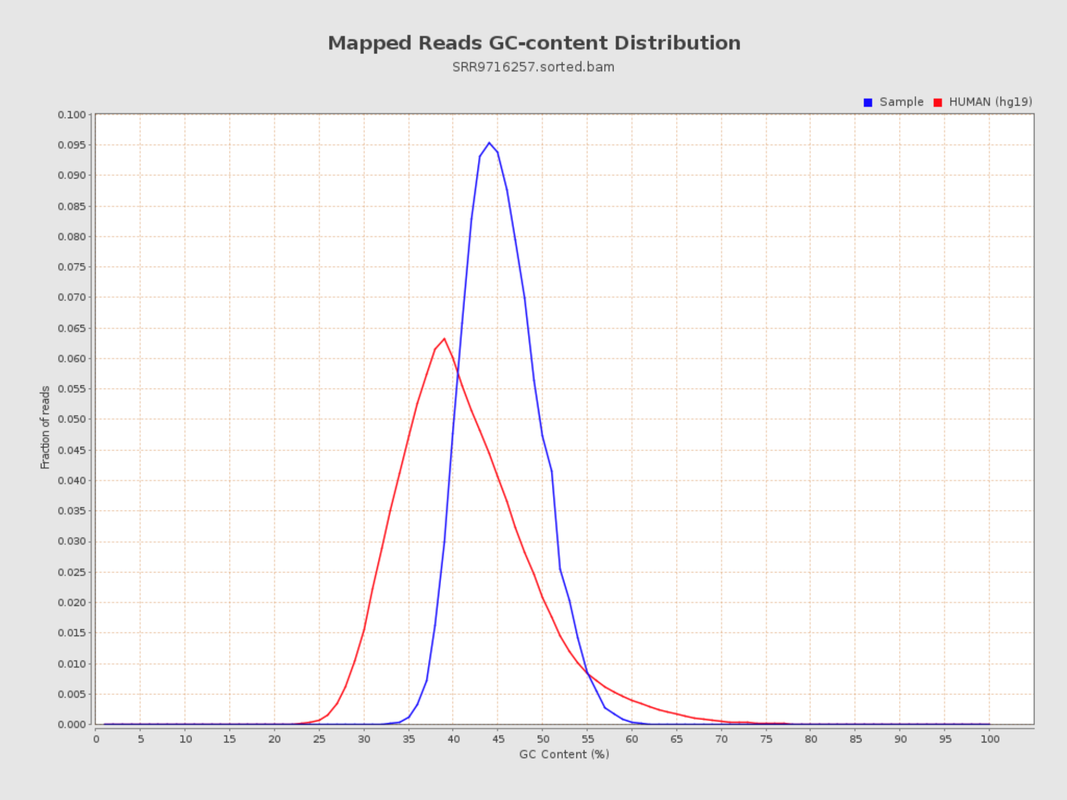
7. Results : Duplication Rate Histogram



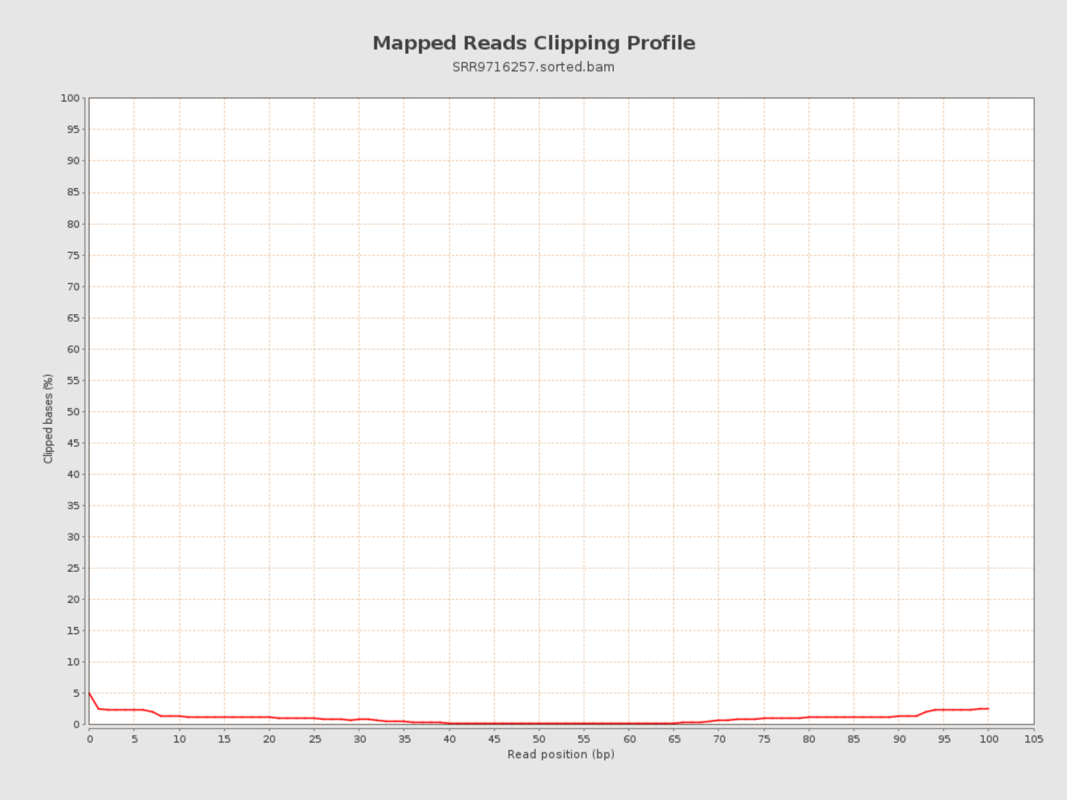
8. Results : Mapped Reads Nucleotide Content



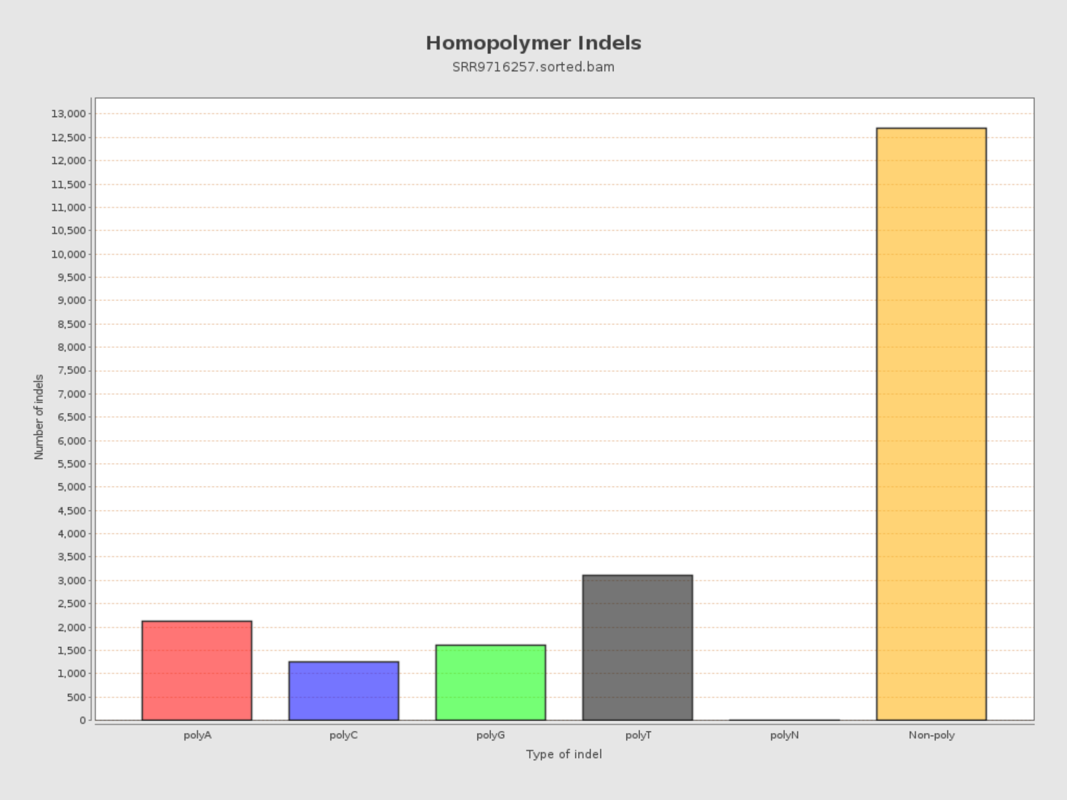
9. Results : Mapped Reads GC-content Distribution



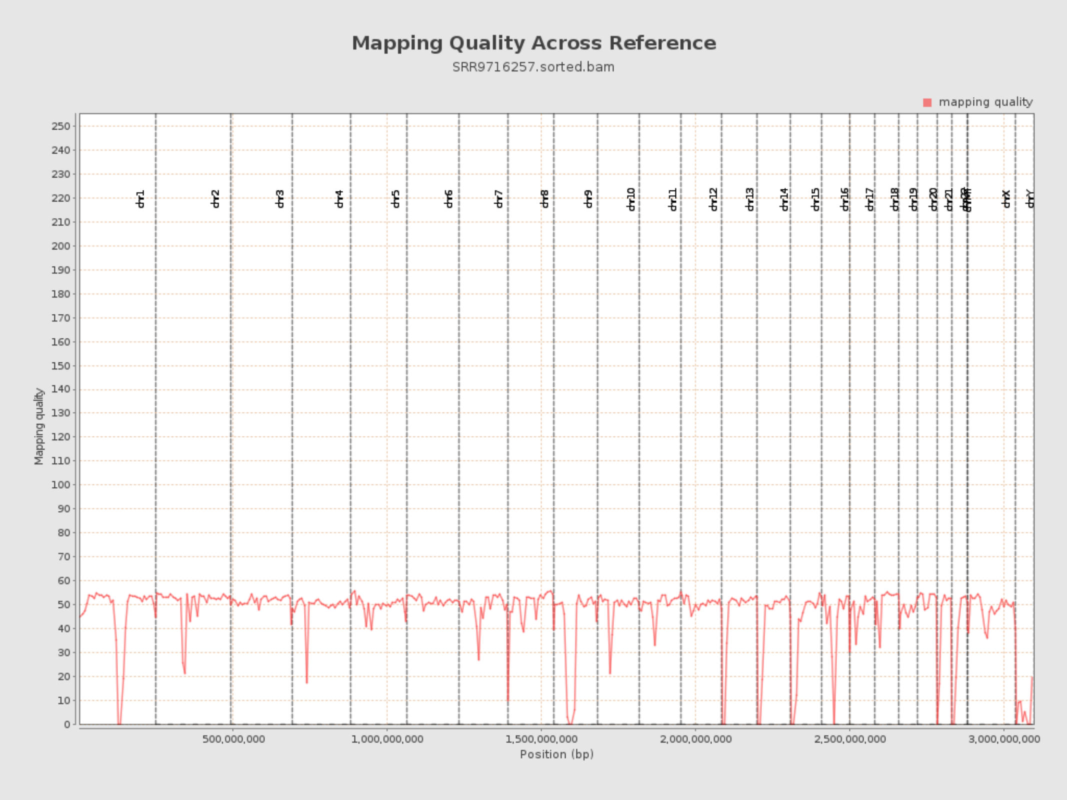
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram