Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 14:27:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716842.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_SRR9716842 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716842.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 14:27:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716842.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	601,681
Mapped reads	542,998 / 90.25%
Unmapped reads	58,683 / 9.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,192 / 1.36%
Read min/max/mean length	30 / 101 / 101.5
Duplicated reads (estimated)	14,517 / 2.41%
Duplication rate	1.57%
Clipped reads	549,939 / 91.4%

2.2. ACGT Content

Number/percentage of A's	11,000,669 / 25.49%
Number/percentage of C's	8,308,822 / 19.25%
Number/percentage of T's	13,007,714 / 30.14%
Number/percentage of G's	10,834,907 / 25.11%
Number/percentage of N's	2,160 / 0.01%
GC Percentage	44.36%

2.3. Coverage

Mean	0.0139

Standard Deviation	0.1881

2.4. Mapping Quality

Mean Mapping Quality	44.82

2.5. Mismatches and indels

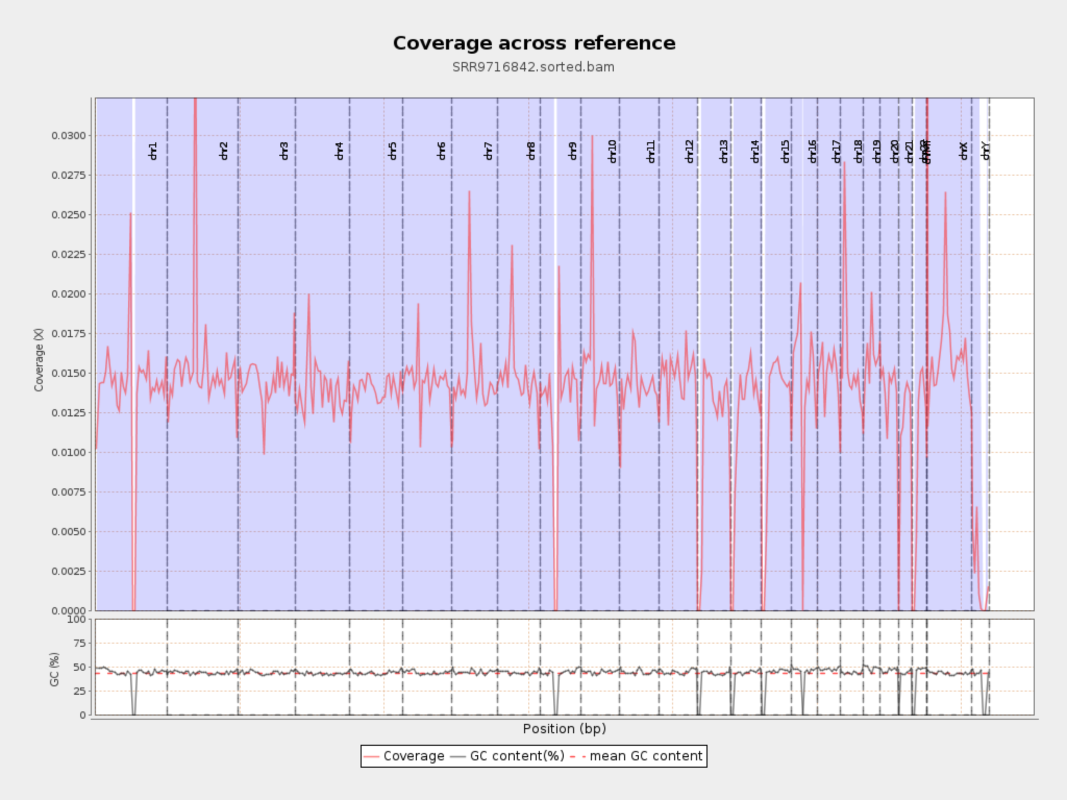
General error rate	0.85%
Mismatches	357,705
Insertions	4,345
Mapped reads with at least one insertion	0.78%
Deletions	11,004
Mapped reads with at least one deletion	1.99%
Homopolymer indels	43.03%

2.6. Chromosome stats

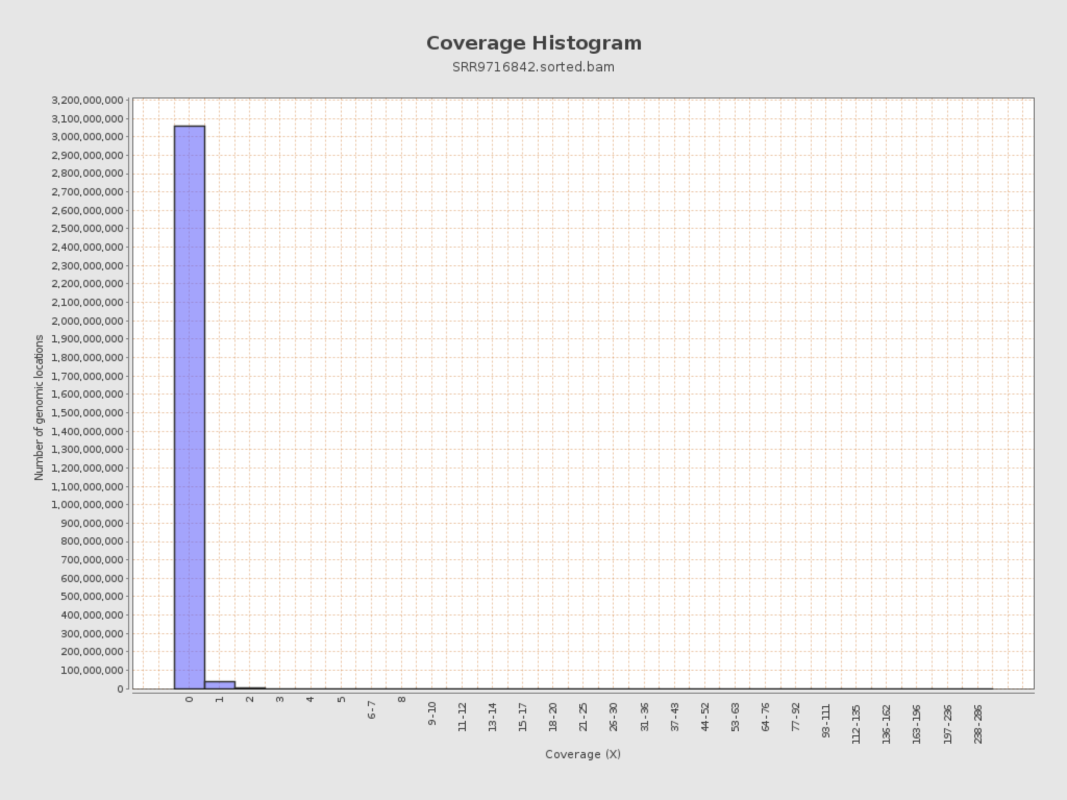
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3443547	0.0138	0.2611
chr2	243199373	3788828	0.0156	0.2604
chr3	198022430	2855418	0.0144	0.126
chr4	191154276	2683176	0.014	0.1312
chr5	180915260	2532865	0.014	0.1255
chr6	171115067	2483289	0.0145	0.1369
chr7	159138663	2356101	0.0148	0.216

chr8	146364022	2176695	0.0149	0.2447
chr9	141213431	1787042	0.0127	0.2108
chr10	135534747	2090627	0.0154	0.1916
chr11	135006516	1928931	0.0143	0.1831
chr12	133851895	1995325	0.0149	0.129
chr13	115169878	1320586	0.0115	0.1116
chr14	107349540	1268888	0.0118	0.1398
chr15	102531392	1236217	0.0121	0.1161
chr16	90354753	1280099	0.0142	0.1372
chr17	81195210	1214102	0.015	0.1385
chr18	78077248	1232170	0.0158	0.3784
chr19	59128983	950850	0.0161	0.2356
chr20	63025520	870658	0.0138	0.1264
chr21	48129895	547757	0.0114	0.1176
chr22	51304566	491425	0.0096	0.1021
chrMT	16571	7048	0.4253	0.7217
chrX	155270560	2514837	0.0162	0.1638
chrY	59373566	116696	0.002	0.0701

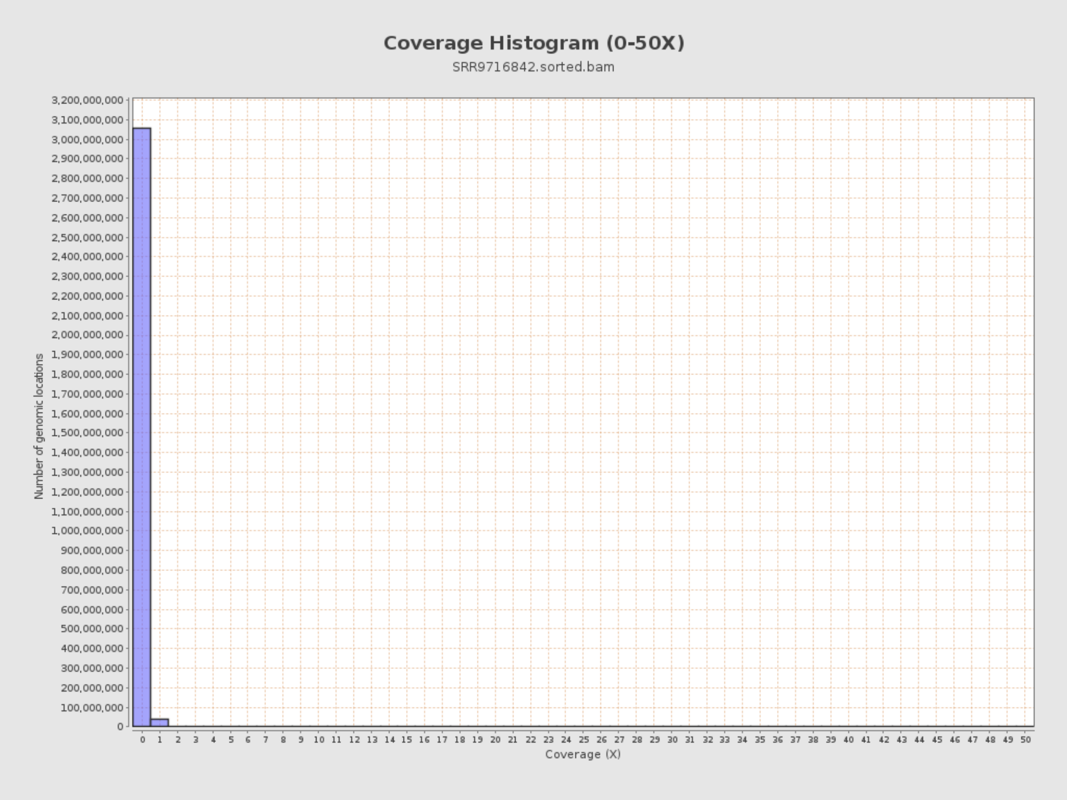
3. Results : Coverage across reference



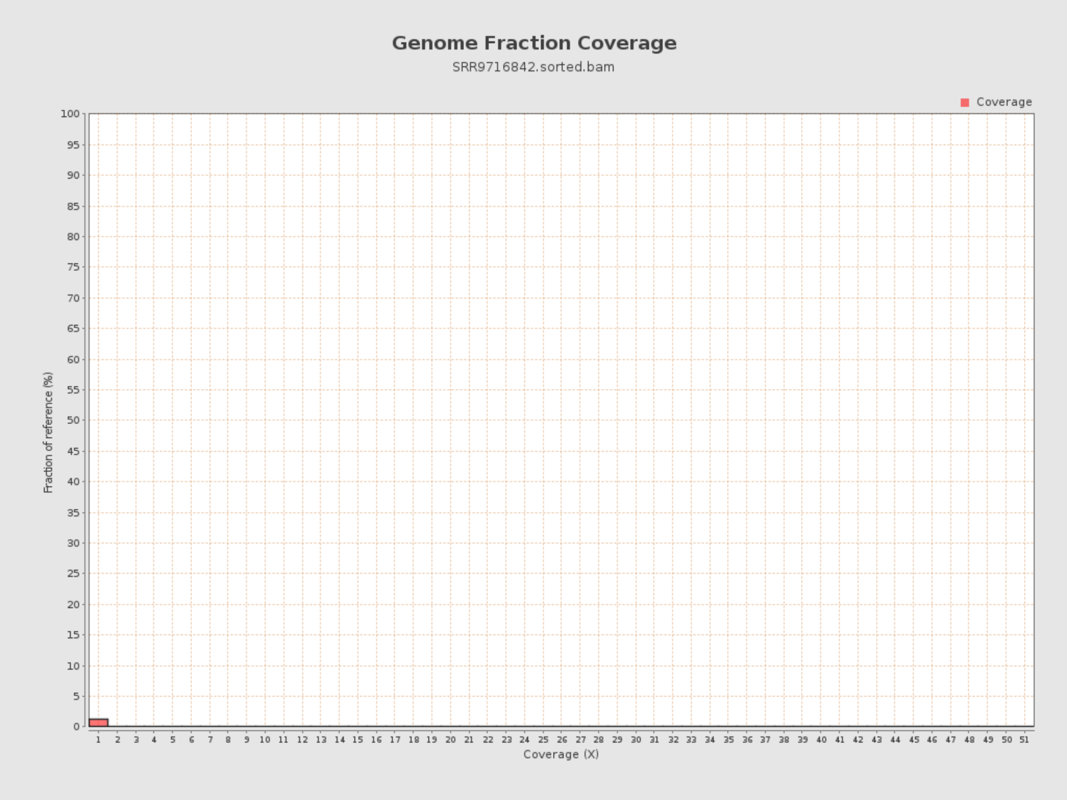
4. Results : Coverage Histogram



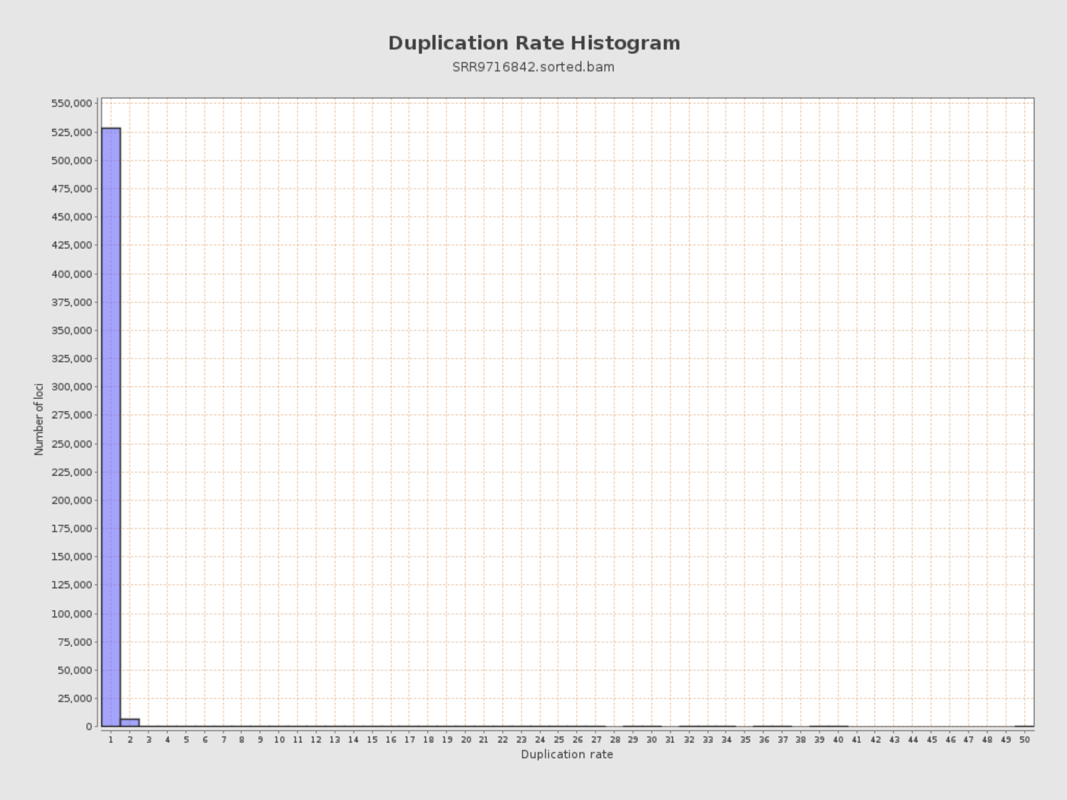
5. Results : Coverage Histogram (0-50X)



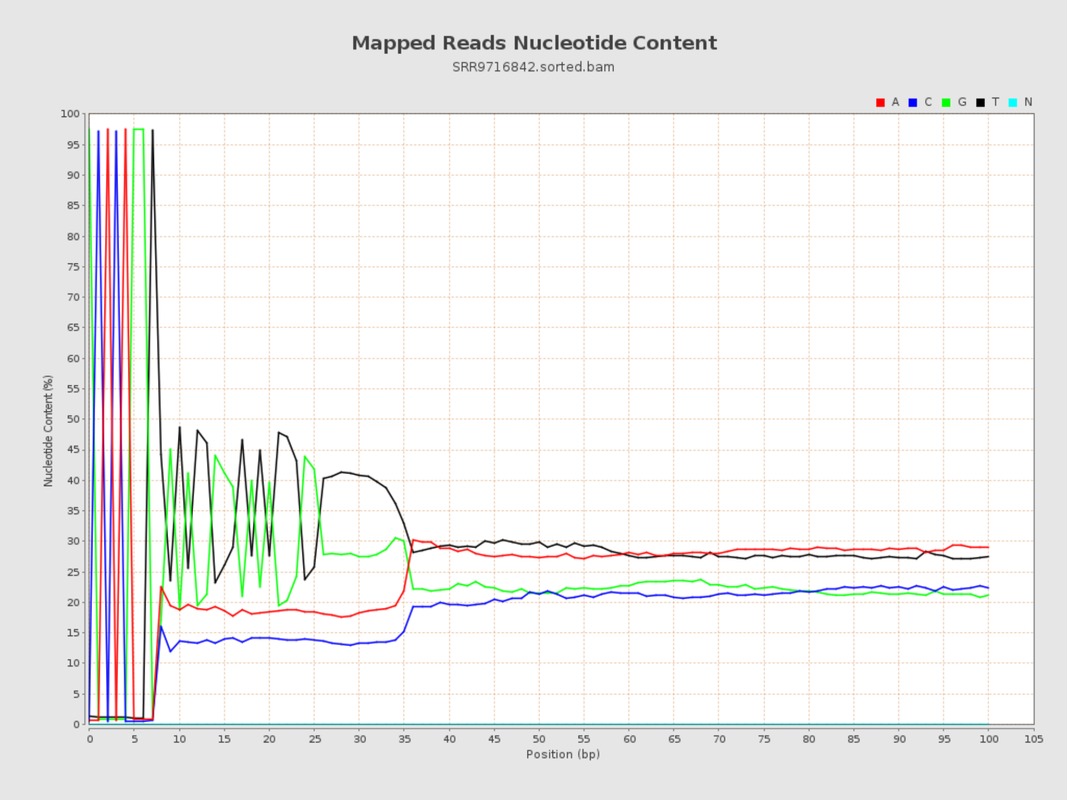
6. Results : Genome Fraction Coverage



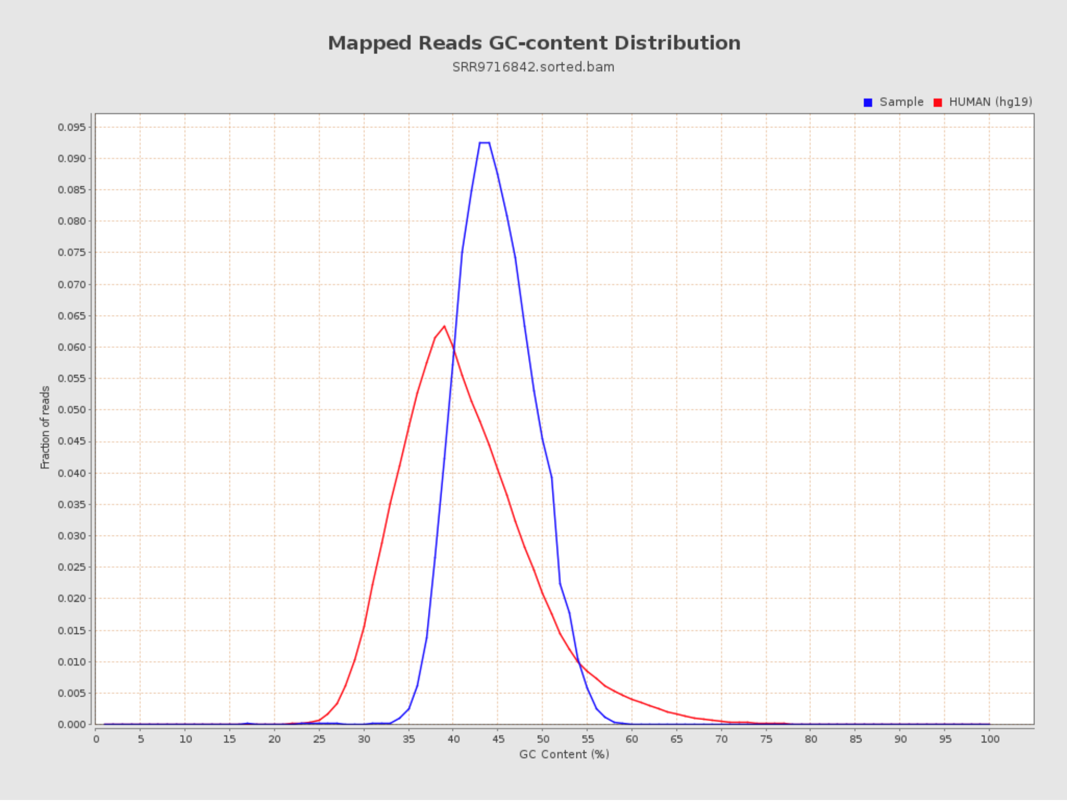
7. Results : Duplication Rate Histogram



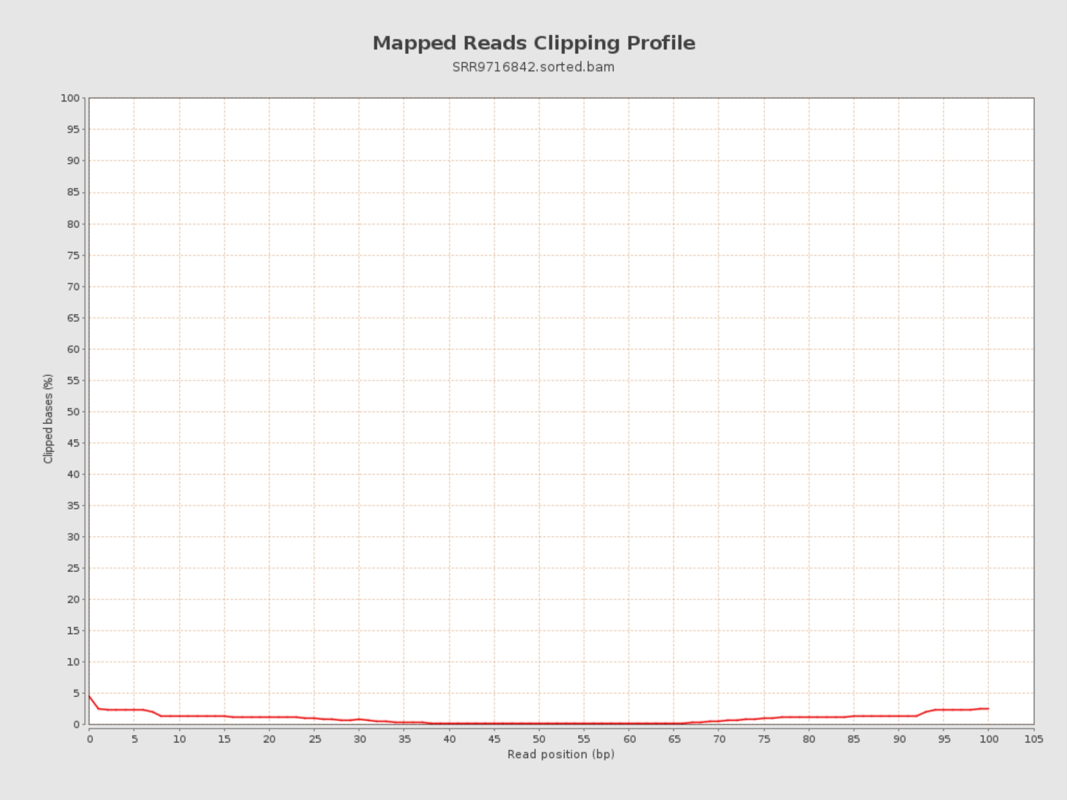
8. Results : Mapped Reads Nucleotide Content



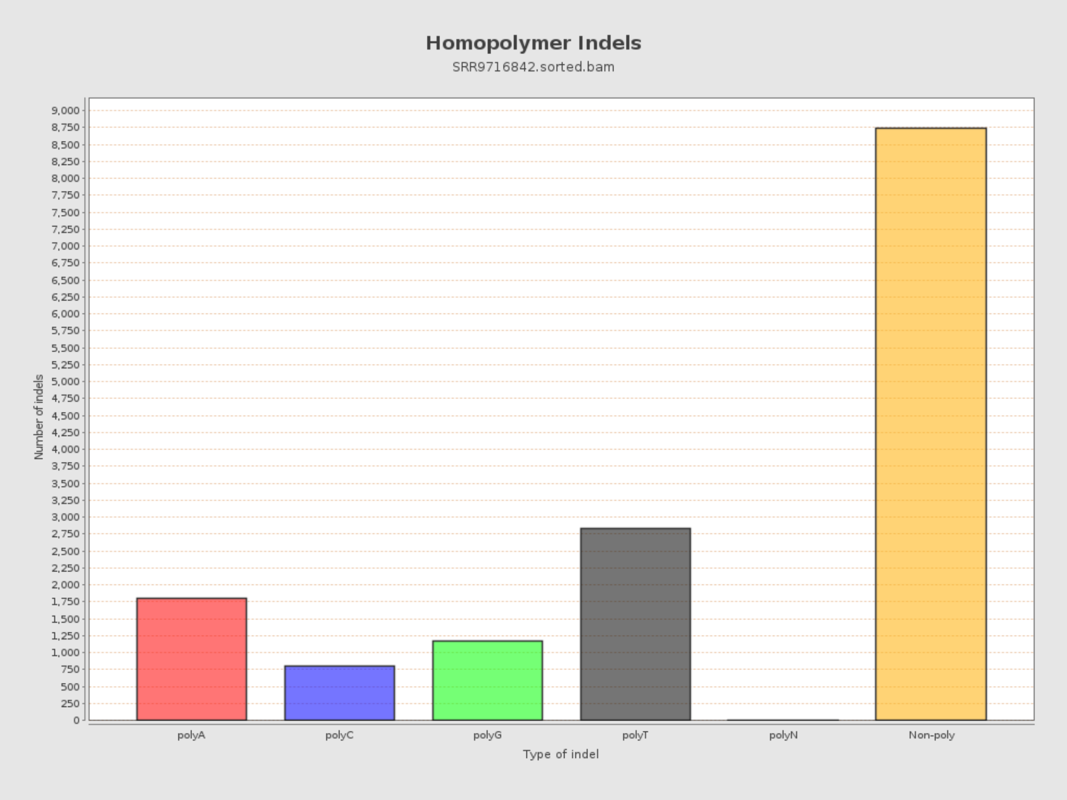
9. Results : Mapped Reads GC-content Distribution



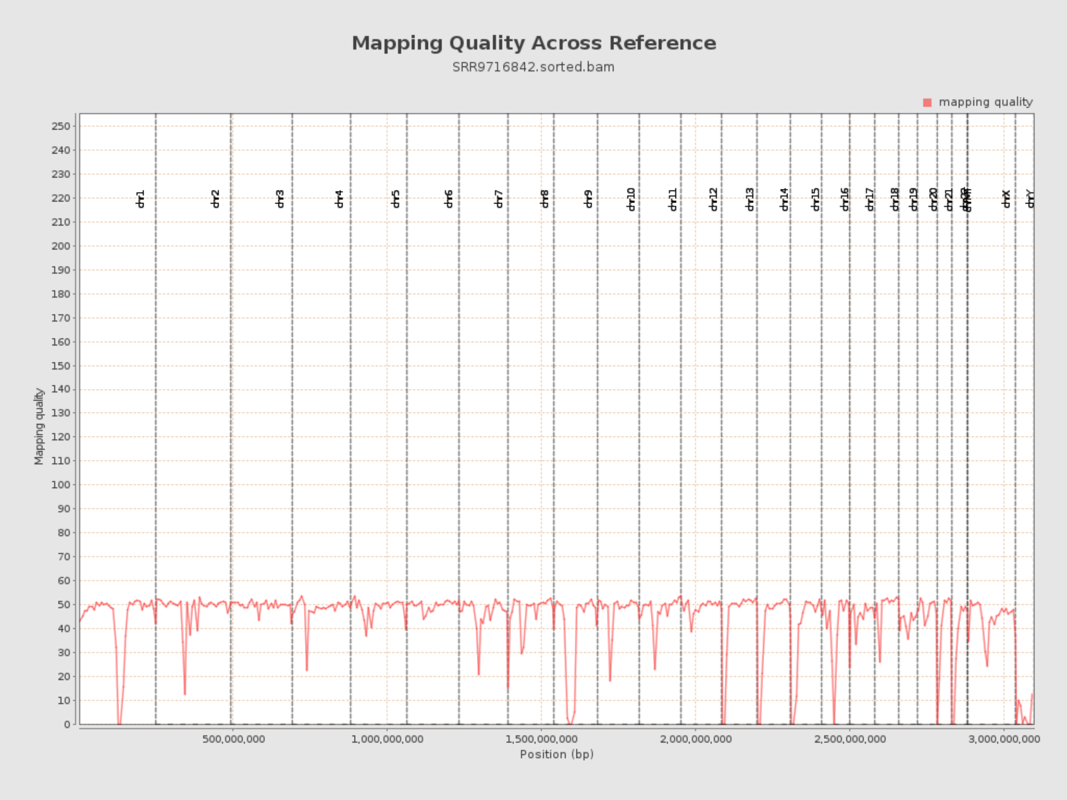
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram