Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 14:30:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716843.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_SRR9716843 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716843.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 14:30:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716843.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,407,856
Mapped reads	1,320,165 / 93.77%
Unmapped reads	87,691 / 6.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,900 / 1.77%
Read min/max/mean length	30 / 101 / 101.64
Duplicated reads (estimated)	46,119 / 3.28%
Duplication rate	2.41%
Clipped reads	1,343,835 / 95.45%

2.2. ACGT Content

Number/percentage of A's	27,387,034 / 26.28%
Number/percentage of C's	21,433,748 / 20.57%
Number/percentage of T's	31,095,237 / 29.84%
Number/percentage of G's	24,288,624 / 23.31%
Number/percentage of N's	7,797 / 0.01%
GC Percentage	43.87%

2.3. Coverage

Mean	0.0337

Standard Deviation	0.3485

2.4. Mapping Quality

Mean Mapping Quality	47.39

2.5. Mismatches and indels

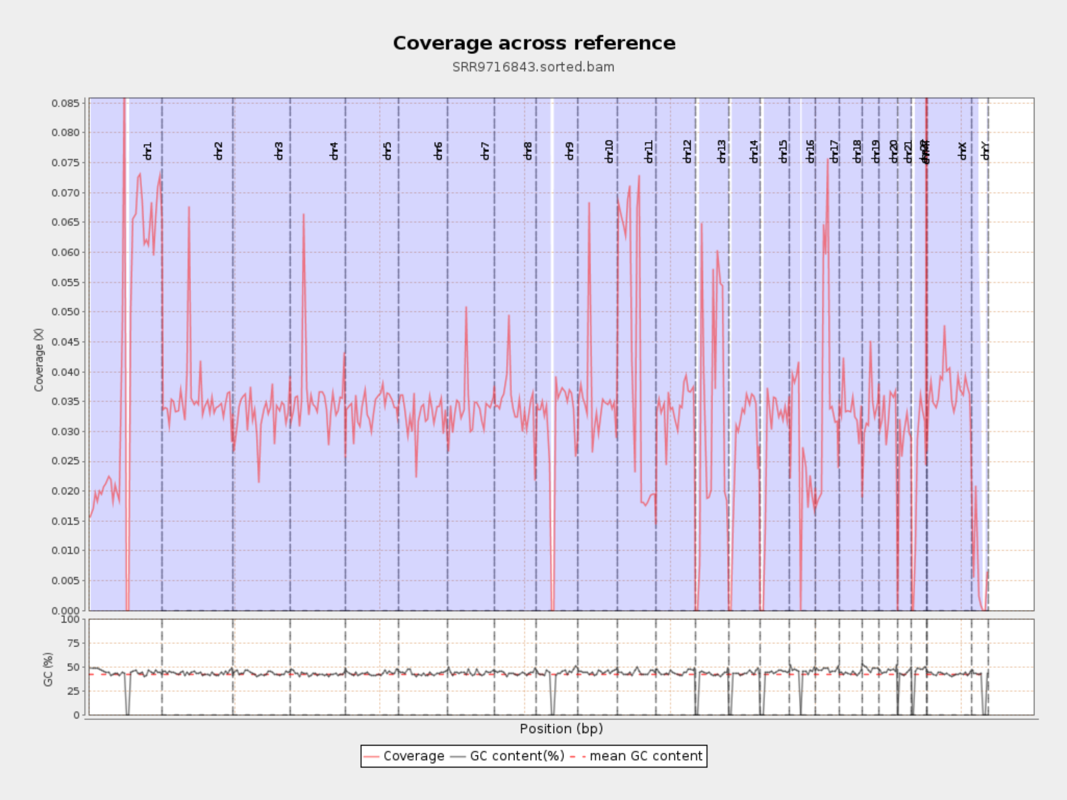
General error rate	0.67%
Mismatches	677,038
Insertions	8,235
Mapped reads with at least one insertion	0.61%
Deletions	24,379
Mapped reads with at least one deletion	1.82%
Homopolymer indels	42.61%

2.6. Chromosome stats

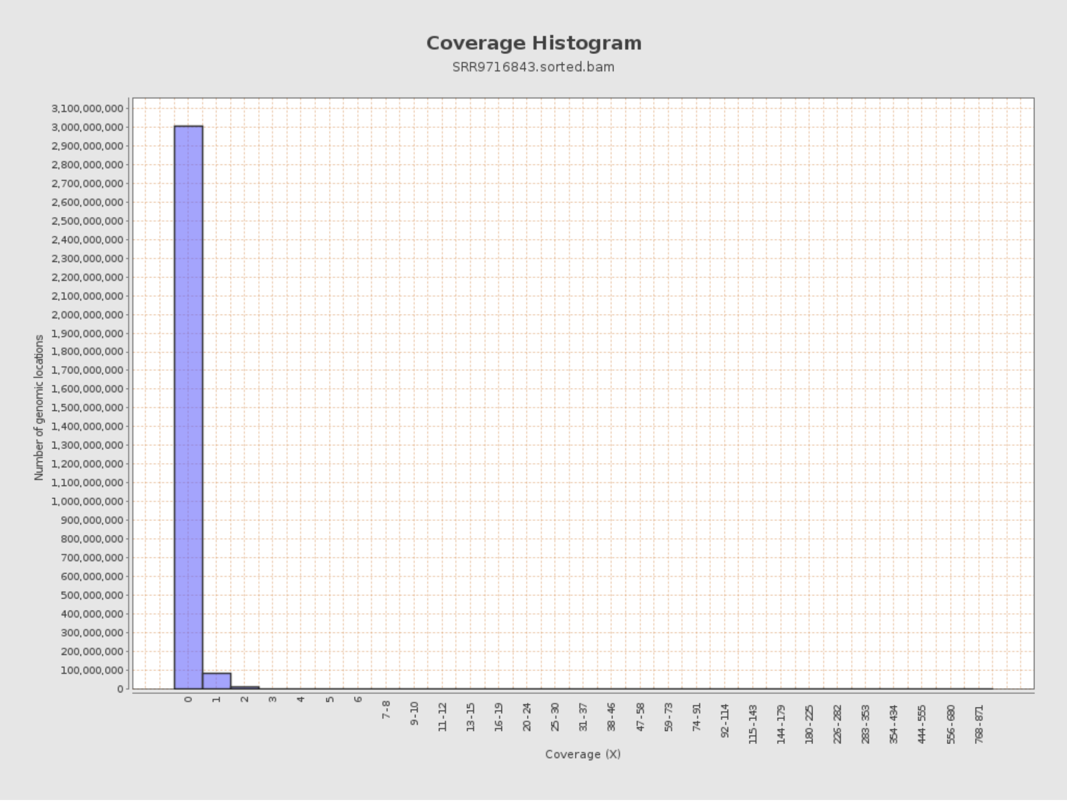
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10431621	0.0419	0.745
chr2	243199373	8666021	0.0356	0.365
chr3	198022430	6486712	0.0328	0.1994
chr4	191154276	6865786	0.0359	0.2486
chr5	180915260	6158704	0.034	0.2034
chr6	171115067	5611221	0.0328	0.2105
chr7	159138663	5412190	0.034	0.3833

chr8	146364022	5048388	0.0345	0.3997
chr9	141213431	4294428	0.0304	0.2854
chr10	135534747	4793327	0.0354	0.356
chr11	135006516	5835184	0.0432	0.3763
chr12	133851895	4588387	0.0343	0.2033
chr13	115169878	3679777	0.032	0.1971
chr14	107349540	2930362	0.0273	0.1965
chr15	102531392	2813494	0.0274	0.181
chr16	90354753	2330893	0.0258	0.191
chr17	81195210	3091846	0.0381	0.2529
chr18	78077248	2633505	0.0337	0.4482
chr19	59128983	1990718	0.0337	0.5269
chr20	63025520	2067880	0.0328	0.2068
chr21	48129895	1306770	0.0272	0.2052
chr22	51304566	1131475	0.0221	0.1624
chrMT	16571	5086	0.3069	0.5703
chrX	155270560	5746310	0.037	0.2496
chrY	59373566	338780	0.0057	0.1813

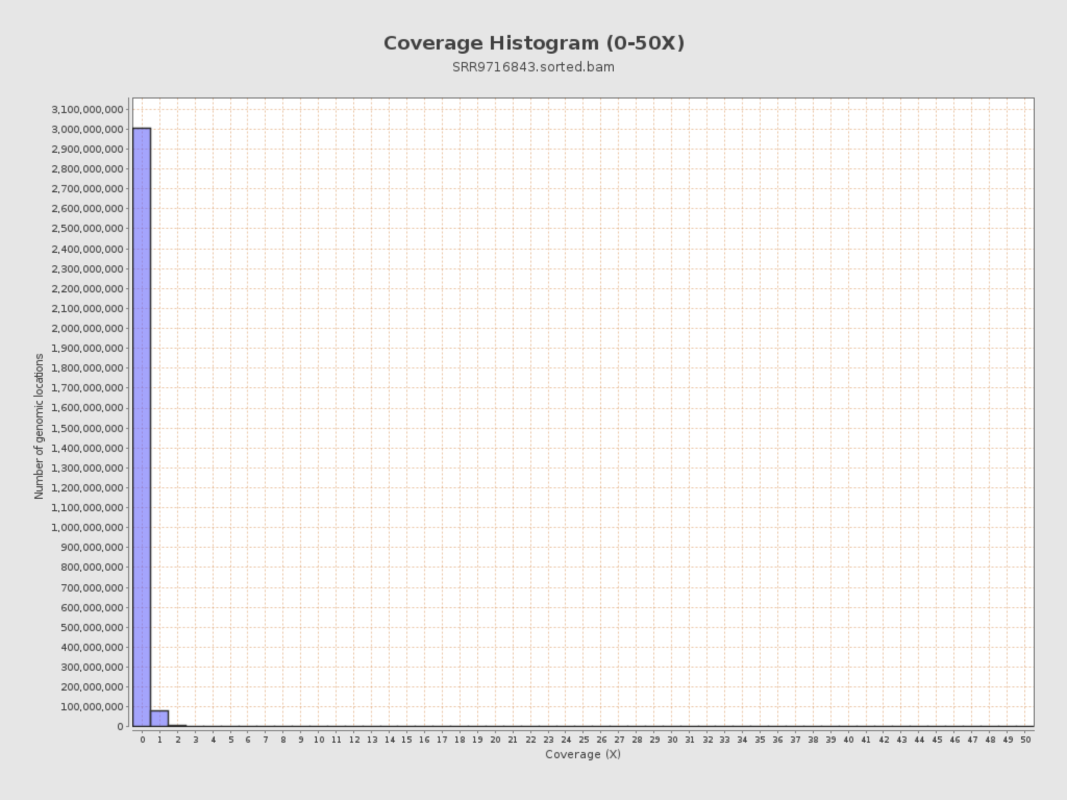
3. Results : Coverage across reference



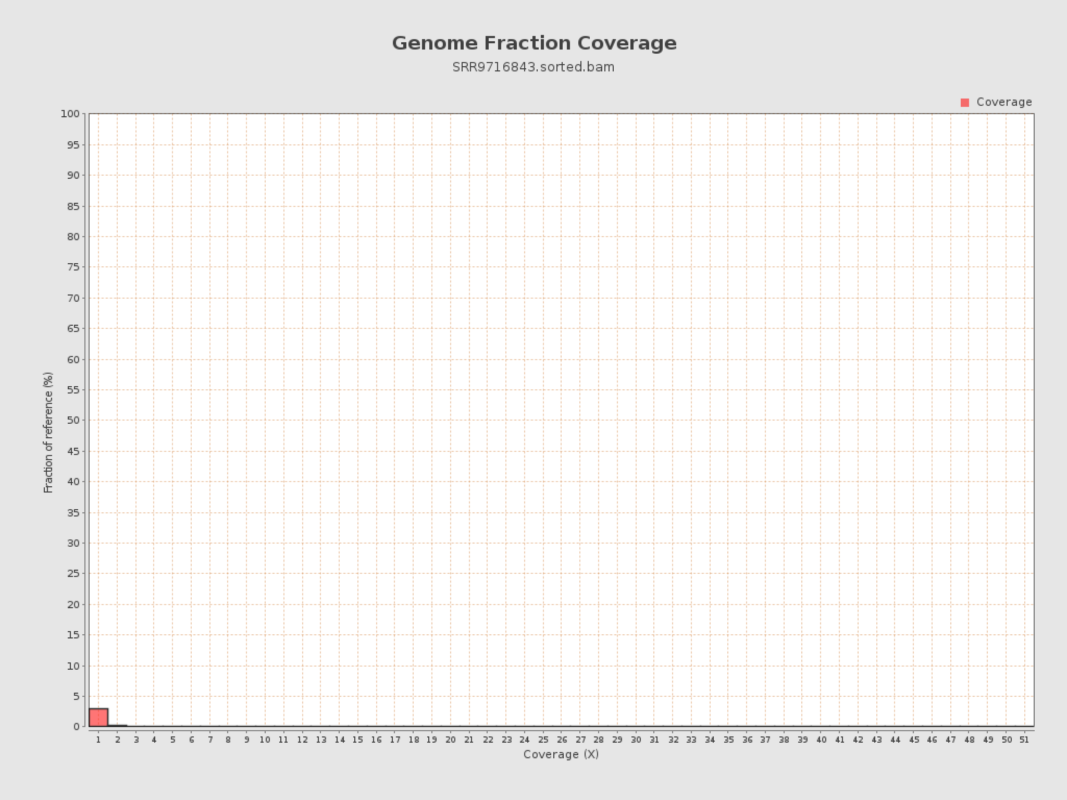
4. Results : Coverage Histogram



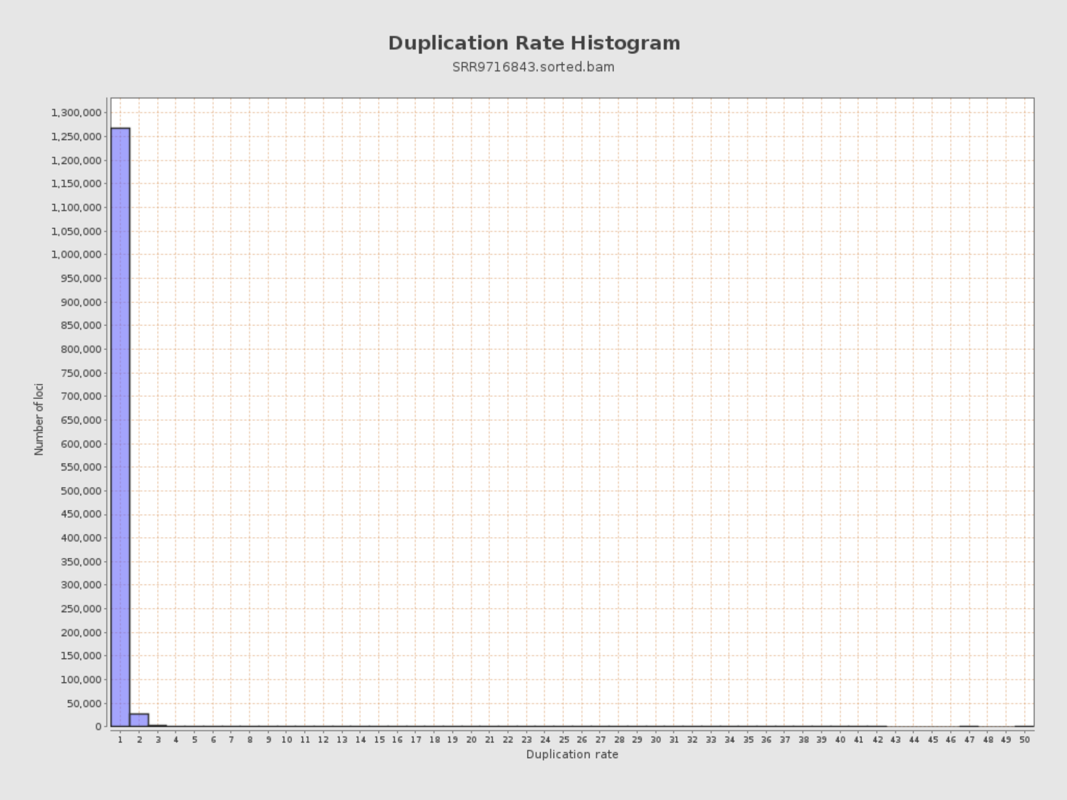
5. Results : Coverage Histogram (0-50X)



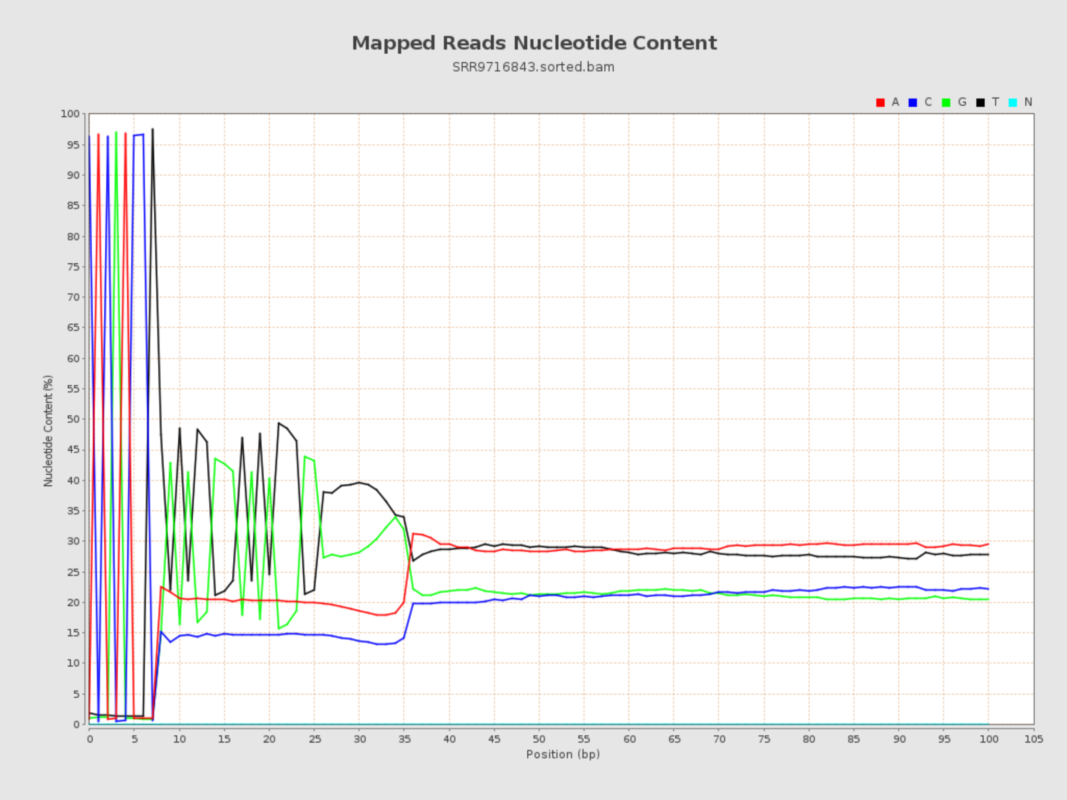
6. Results : Genome Fraction Coverage



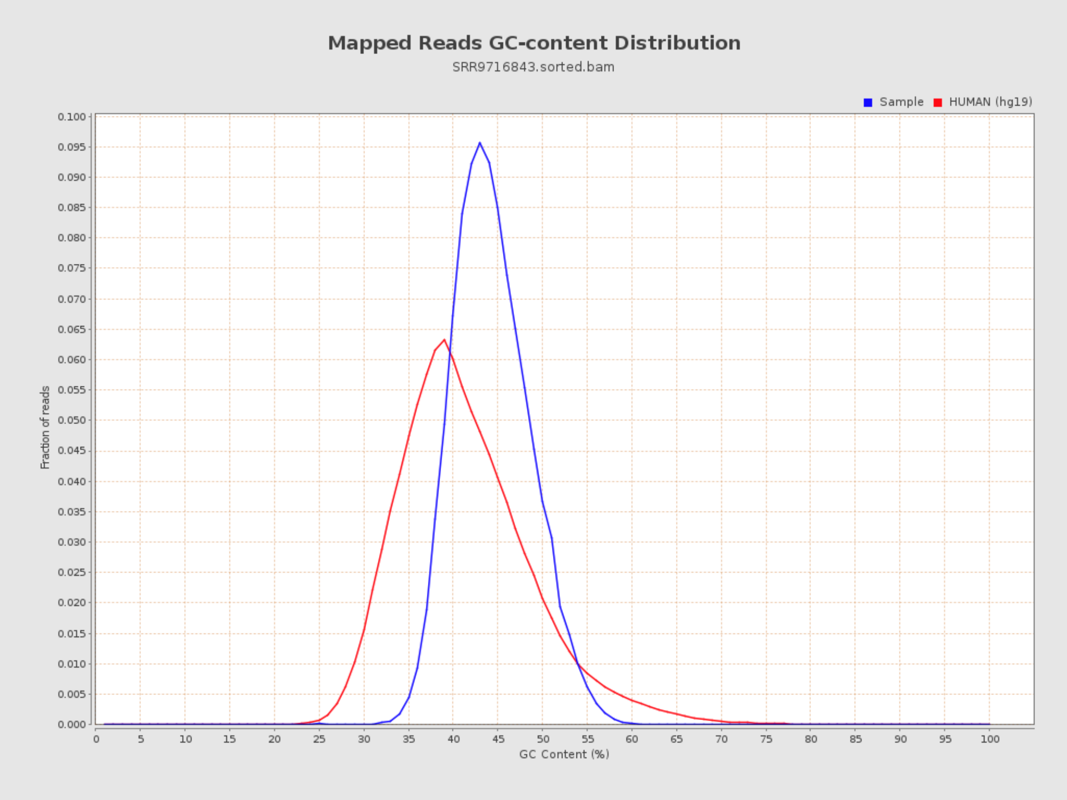
7. Results : Duplication Rate Histogram



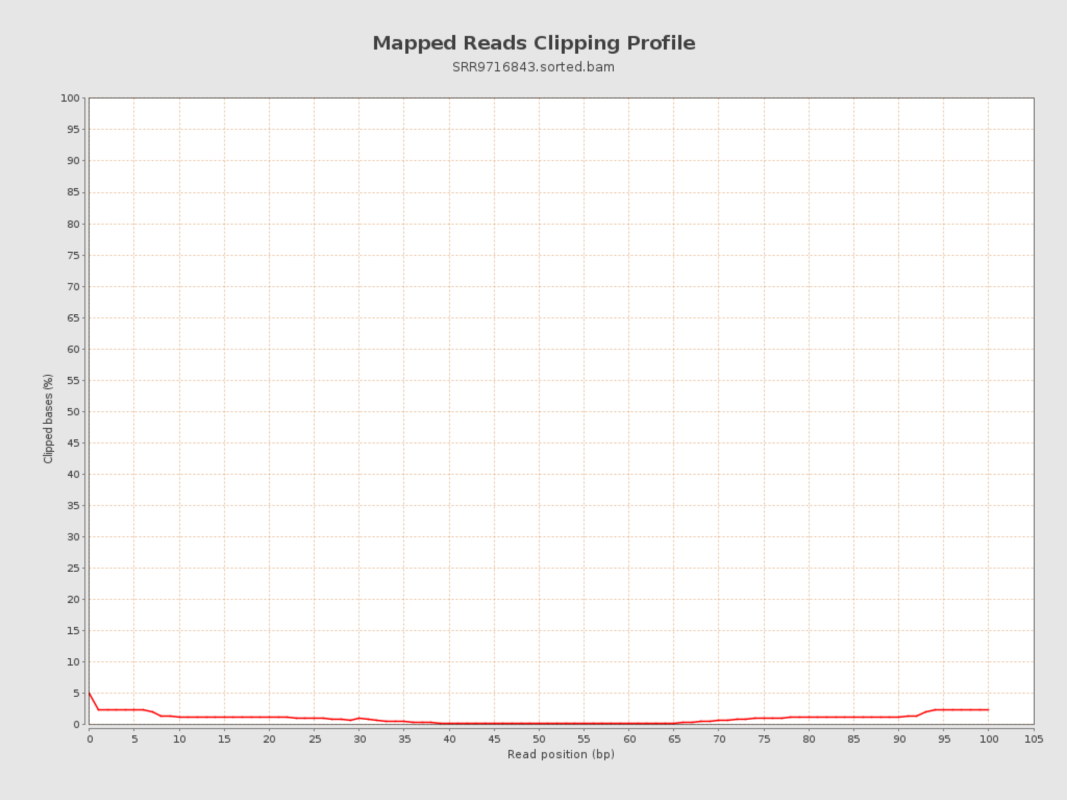
8. Results : Mapped Reads Nucleotide Content



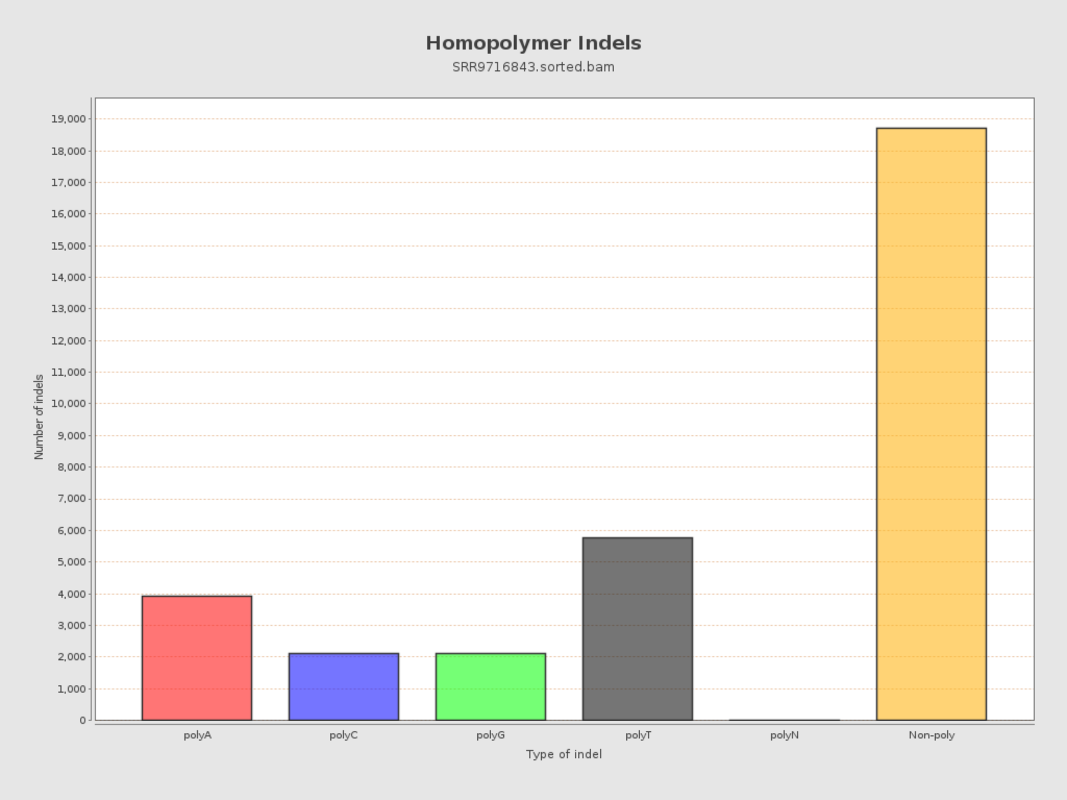
9. Results : Mapped Reads GC-content Distribution



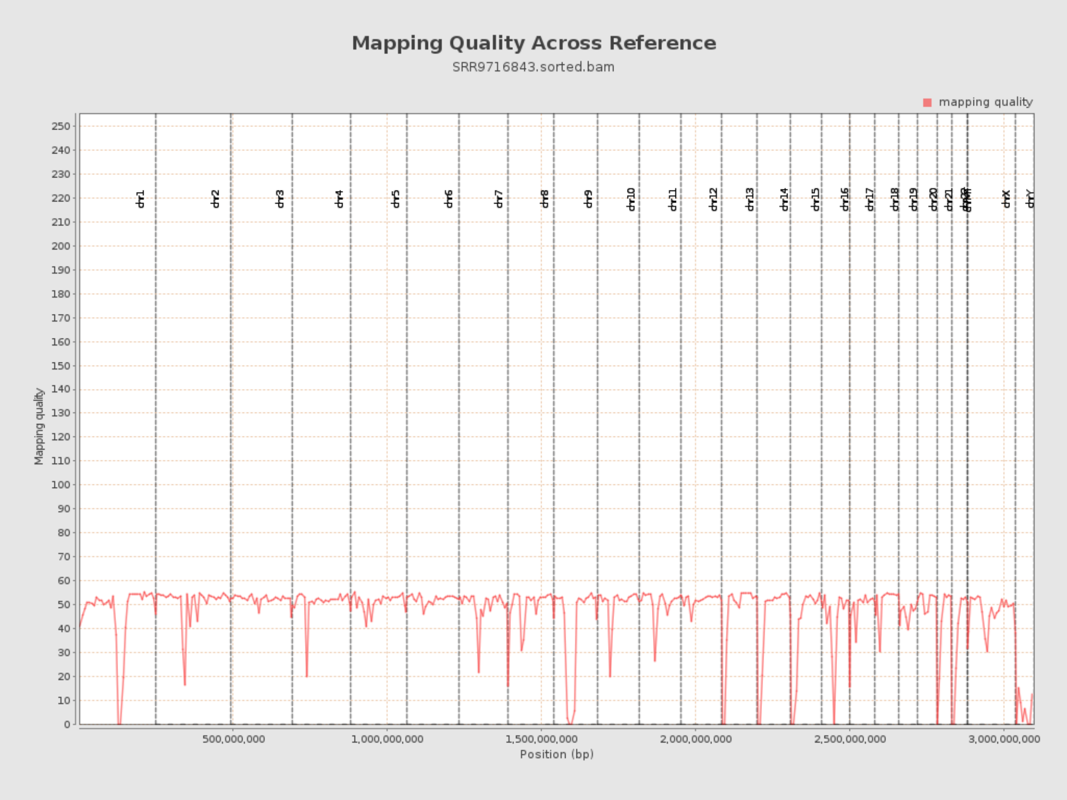
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram