Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 02:25:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716245.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_SRR9716245 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716245.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 02:25:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716245.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,484,886
Mapped reads	1,367,827 / 92.12%
Unmapped reads	117,059 / 7.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,478 / 1.38%
Read min/max/mean length	30 / 101 / 101.51
Duplicated reads (estimated)	56,775 / 3.82%
Duplication rate	2.47%
Clipped reads	1,385,758 / 93.32%

2.2. ACGT Content

Number/percentage of A's	27,456,579 / 25.41%
Number/percentage of C's	21,144,554 / 19.57%
Number/percentage of T's	33,520,236 / 31.02%
Number/percentage of G's	25,915,843 / 23.99%
Number/percentage of N's	6,617 / 0.01%
GC Percentage	43.56%

2.3. Coverage

Mean	0.0349

Standard Deviation	0.4192

2.4. Mapping Quality

Mean Mapping Quality	44.71

2.5. Mismatches and indels

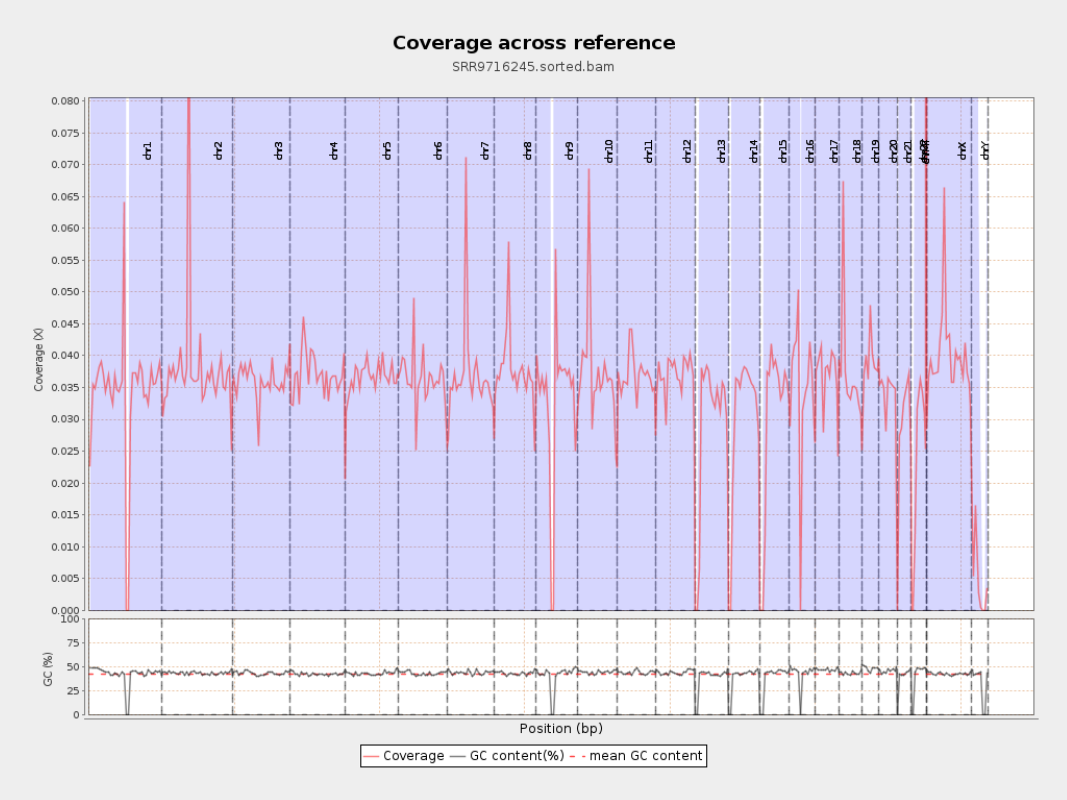
General error rate	0.86%
Mismatches	908,787
Insertions	9,977
Mapped reads with at least one insertion	0.72%
Deletions	27,816
Mapped reads with at least one deletion	2.01%
Homopolymer indels	44.43%

2.6. Chromosome stats

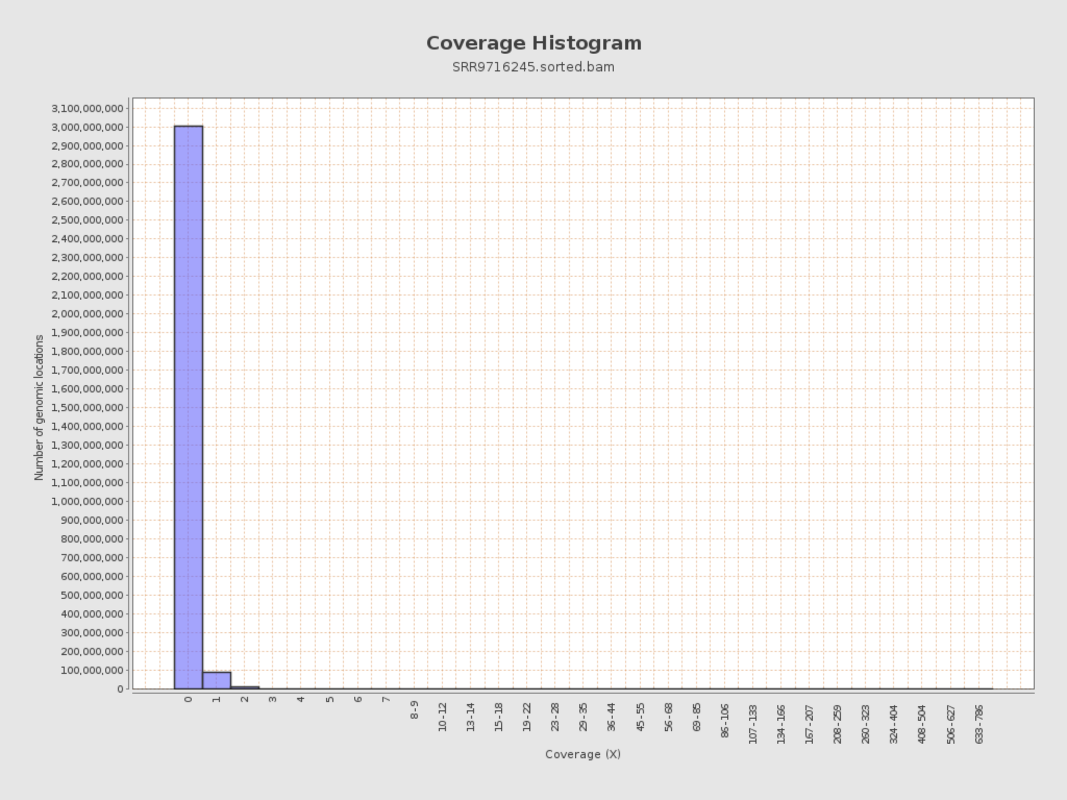
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8497844	0.0341	0.6576
chr2	243199373	9322367	0.0383	0.6204
chr3	198022430	7123284	0.036	0.2121
chr4	191154276	7084135	0.0371	0.2301
chr5	180915260	6631455	0.0367	0.2164
chr6	171115067	6221407	0.0364	0.2618
chr7	159138663	5930063	0.0373	0.5289

chr8	146364022	5518037	0.0377	0.568
chr9	141213431	4591754	0.0325	0.4843
chr10	135534747	5082636	0.0375	0.3927
chr11	135006516	4953911	0.0367	0.3958
chr12	133851895	4948365	0.037	0.2192
chr13	115169878	3321943	0.0288	0.1849
chr14	107349540	3216404	0.03	0.2674
chr15	102531392	3059125	0.0298	0.2015
chr16	90354753	3125462	0.0346	0.2444
chr17	81195210	2987756	0.0368	0.24
chr18	78077248	2968523	0.038	0.9047
chr19	59128983	2303580	0.039	0.5166
chr20	63025520	2131292	0.0338	0.2161
chr21	48129895	1371425	0.0285	0.2062
chr22	51304566	1174749	0.0229	0.1674
chrMT	16571	14806	0.8935	1.1685
chrX	155270560	6221235	0.0401	0.3299
chrY	59373566	290408	0.0049	0.1385

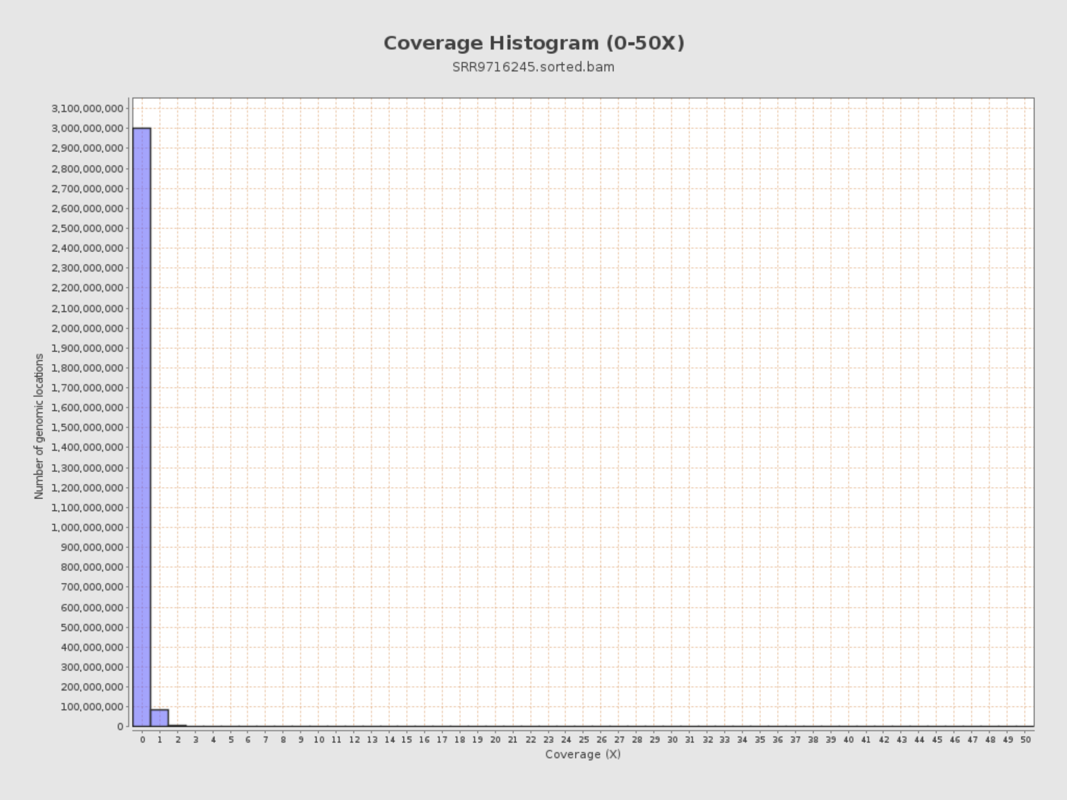
3. Results : Coverage across reference



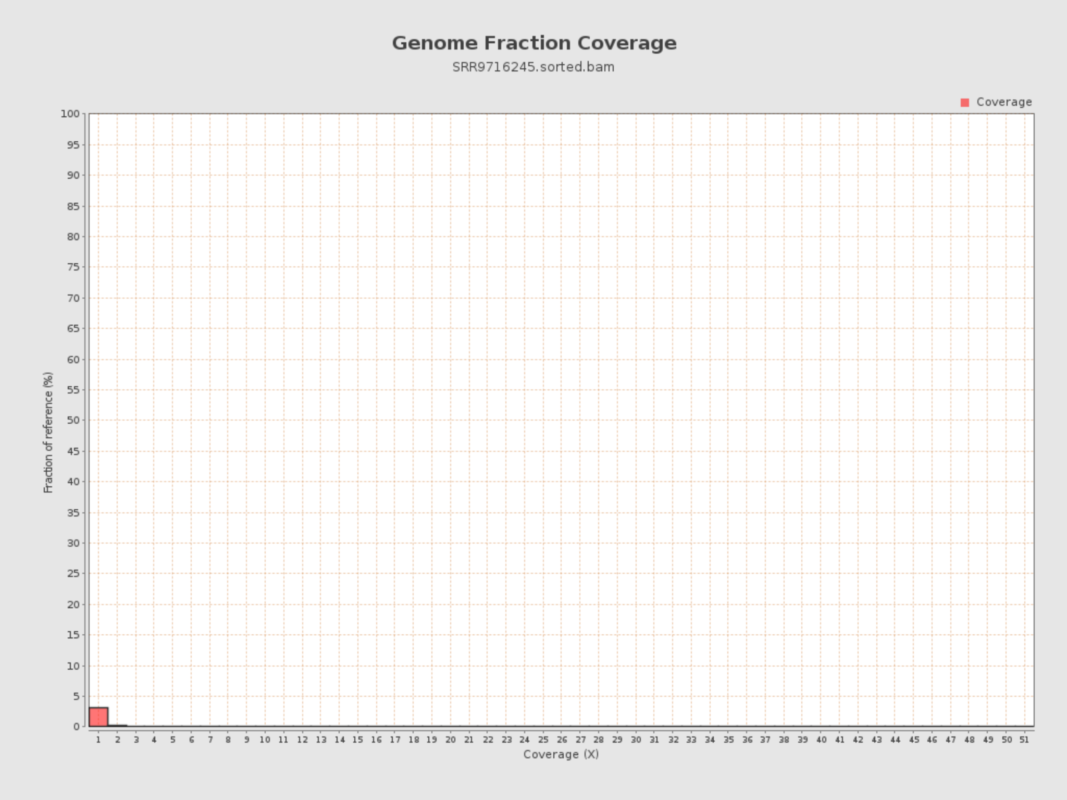
4. Results : Coverage Histogram



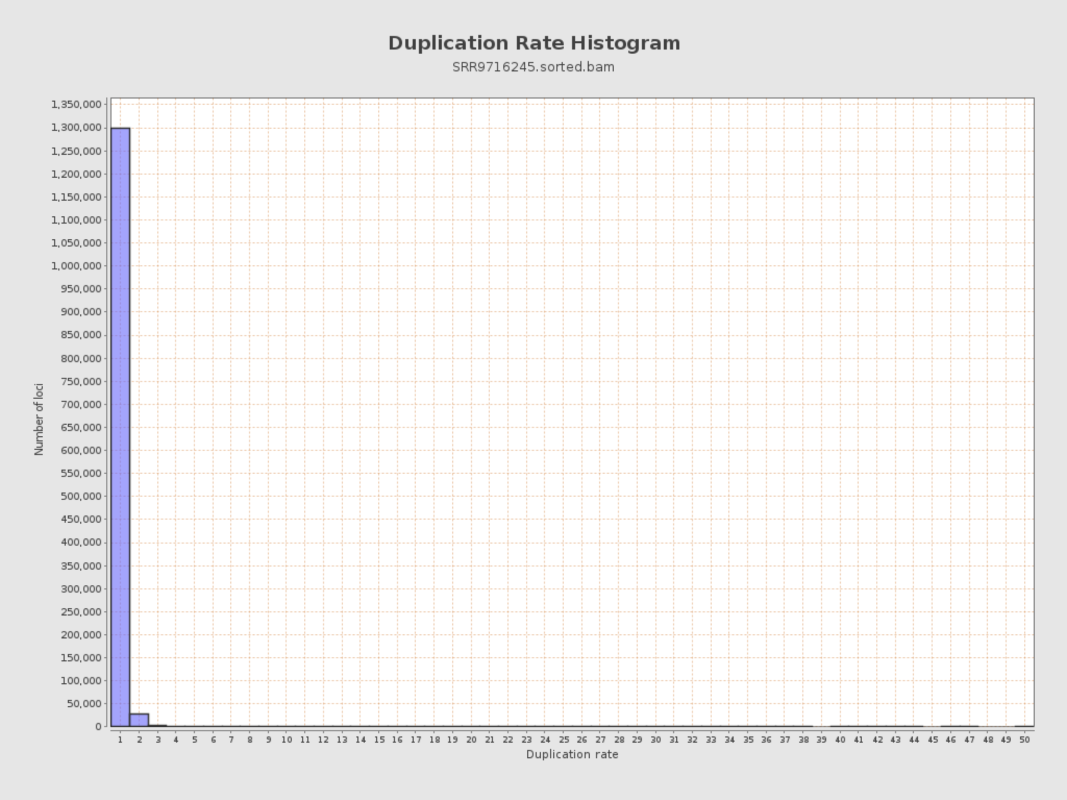
5. Results : Coverage Histogram (0-50X)



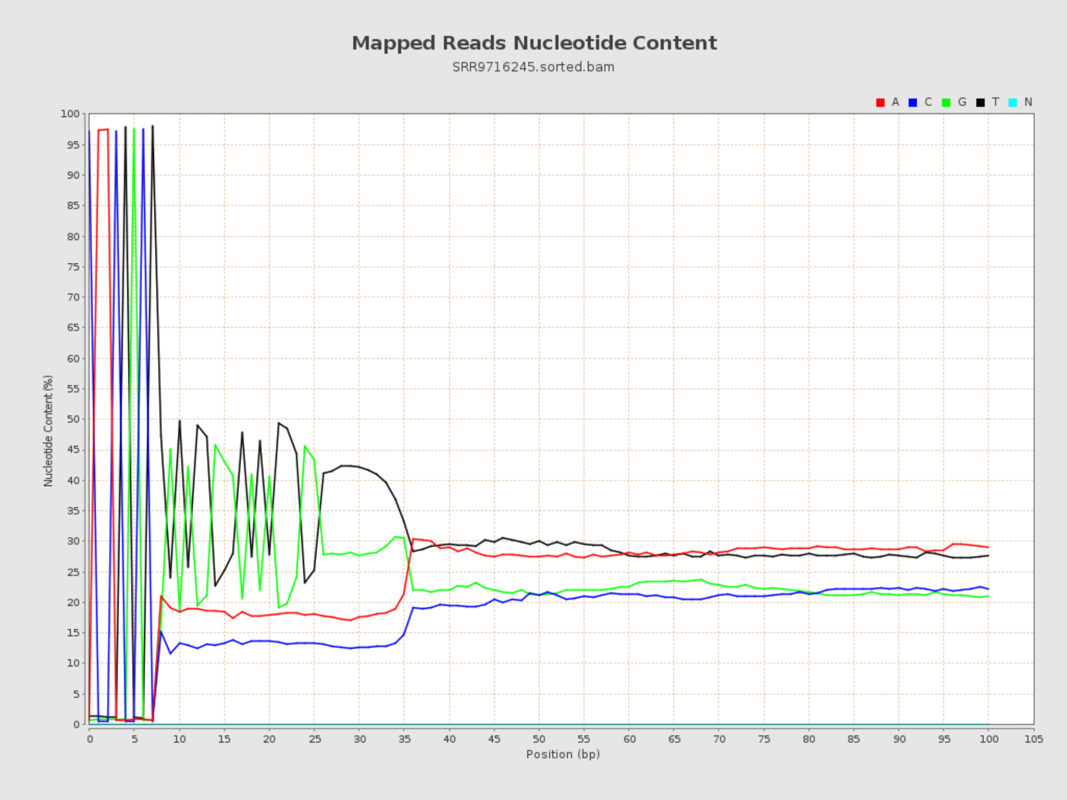
6. Results : Genome Fraction Coverage



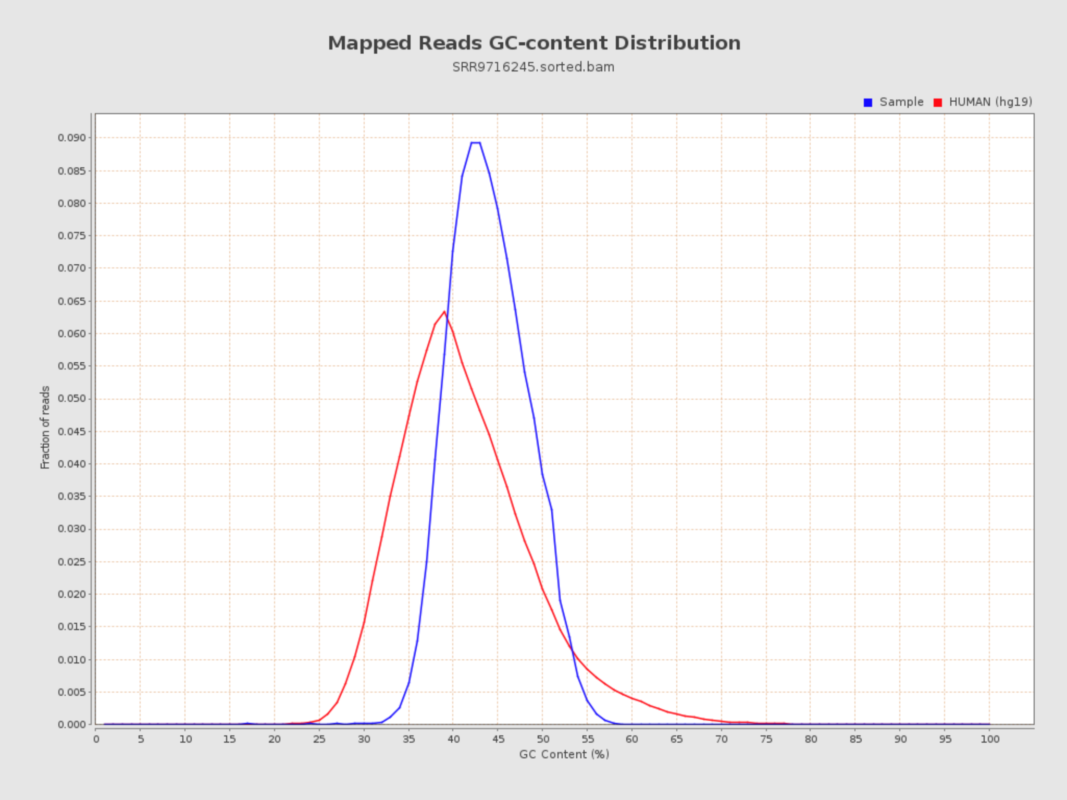
7. Results : Duplication Rate Histogram



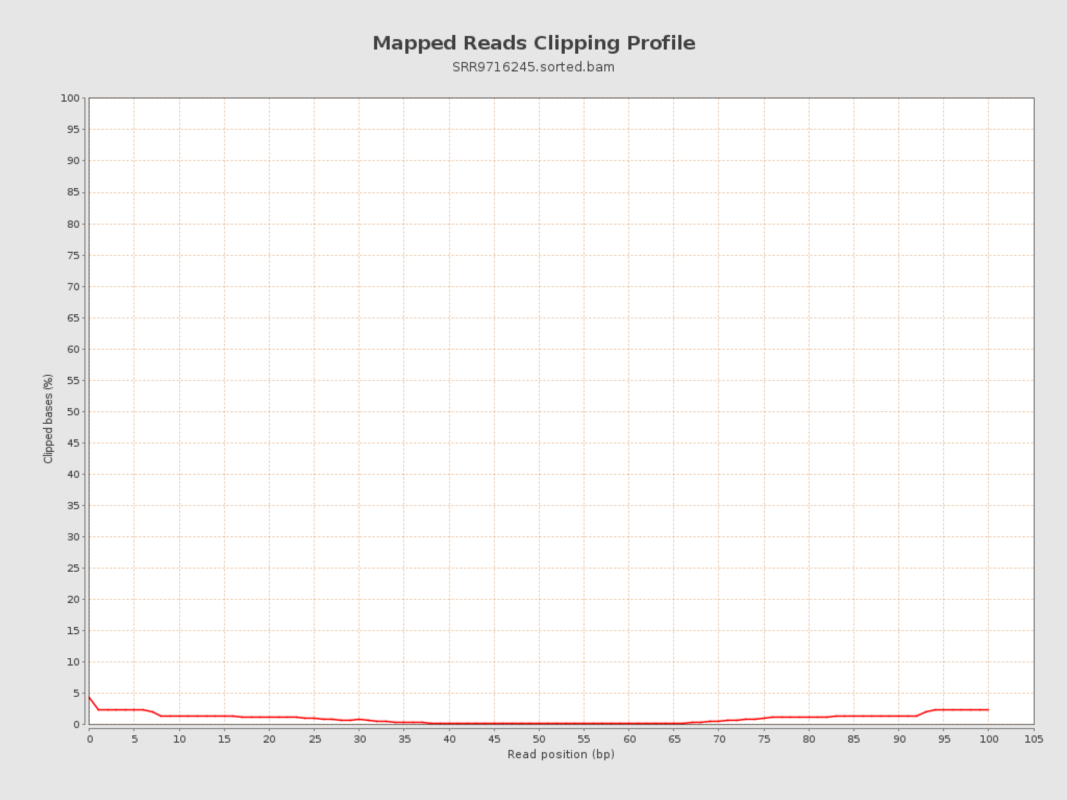
8. Results : Mapped Reads Nucleotide Content



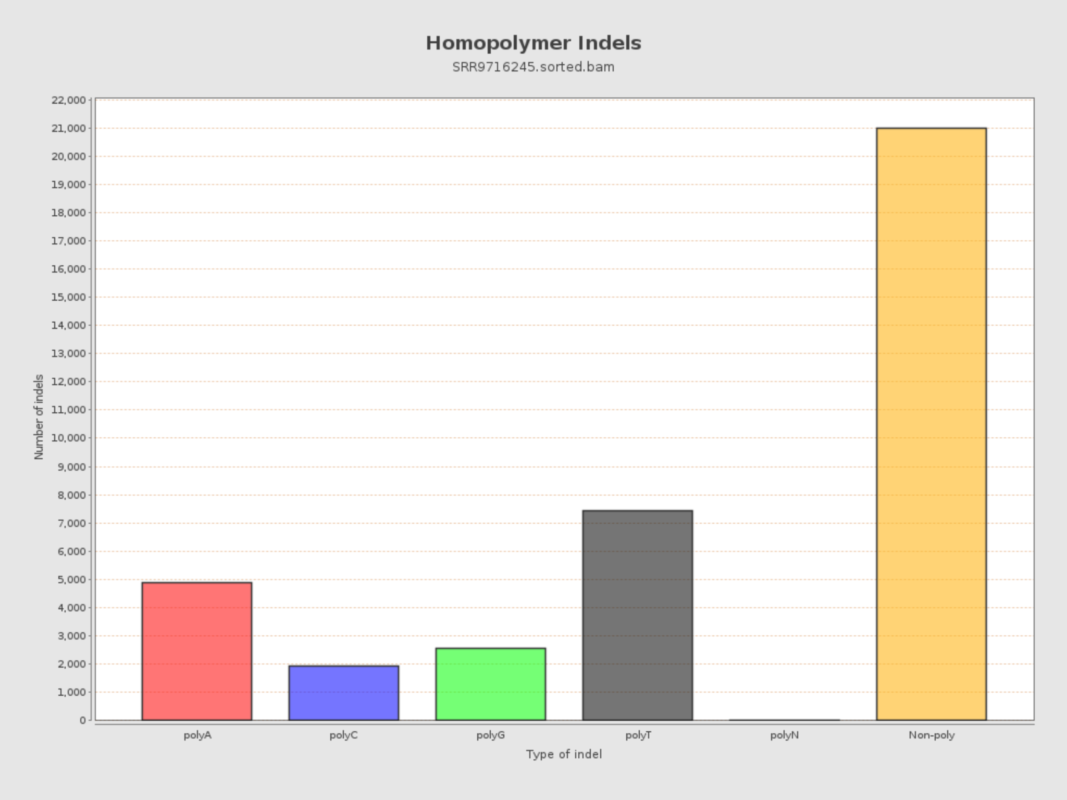
9. Results : Mapped Reads GC-content Distribution



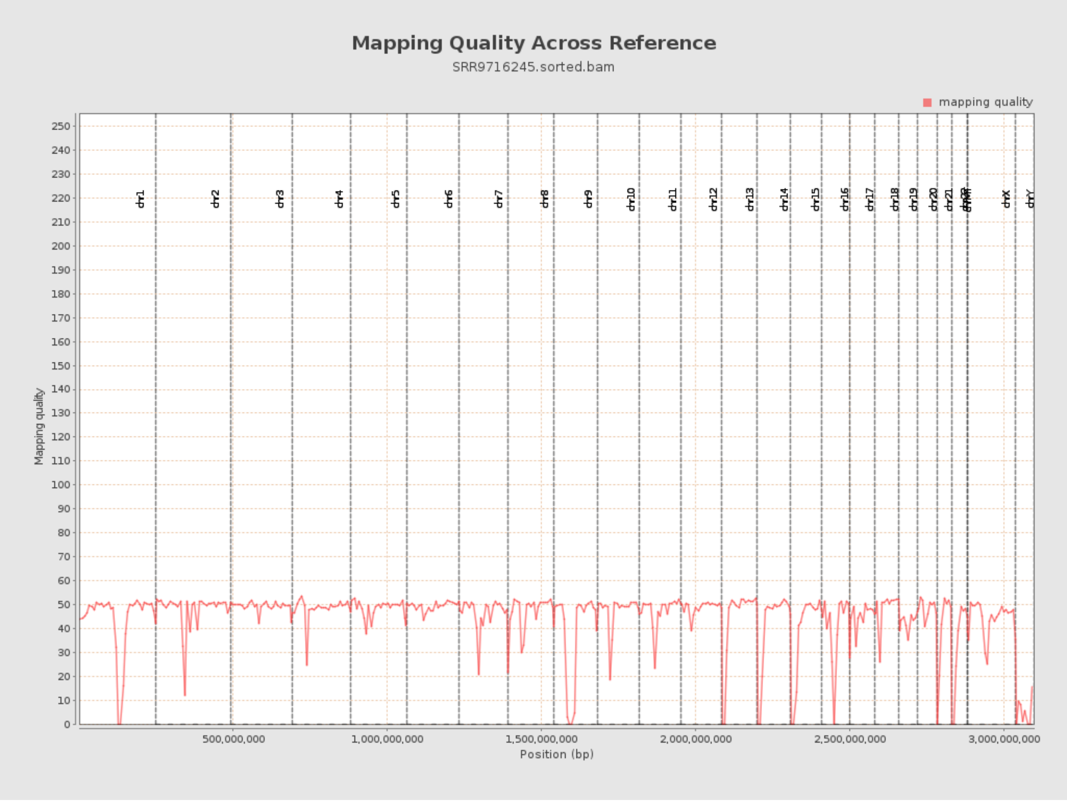
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram