Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 01:24:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716631.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_SRR9716631 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716631.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 01:24:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716631.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	950,240
Mapped reads	852,315 / 89.69%
Unmapped reads	97,925 / 10.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,720 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	16,671 / 1.75%
Duplication rate	1.49%
Clipped reads	853,576 / 89.83%

2.2. ACGT Content

Number/percentage of A's	11,670,890 / 24.22%
Number/percentage of C's	10,017,533 / 20.79%
Number/percentage of T's	15,177,704 / 31.49%
Number/percentage of G's	11,327,964 / 23.5%
Number/percentage of N's	998 / 0%
GC Percentage	44.29%

2.3. Coverage

Mean	0.0156

Standard Deviation	0.1504

2.4. Mapping Quality

Mean Mapping Quality	43.52

2.5. Mismatches and indels

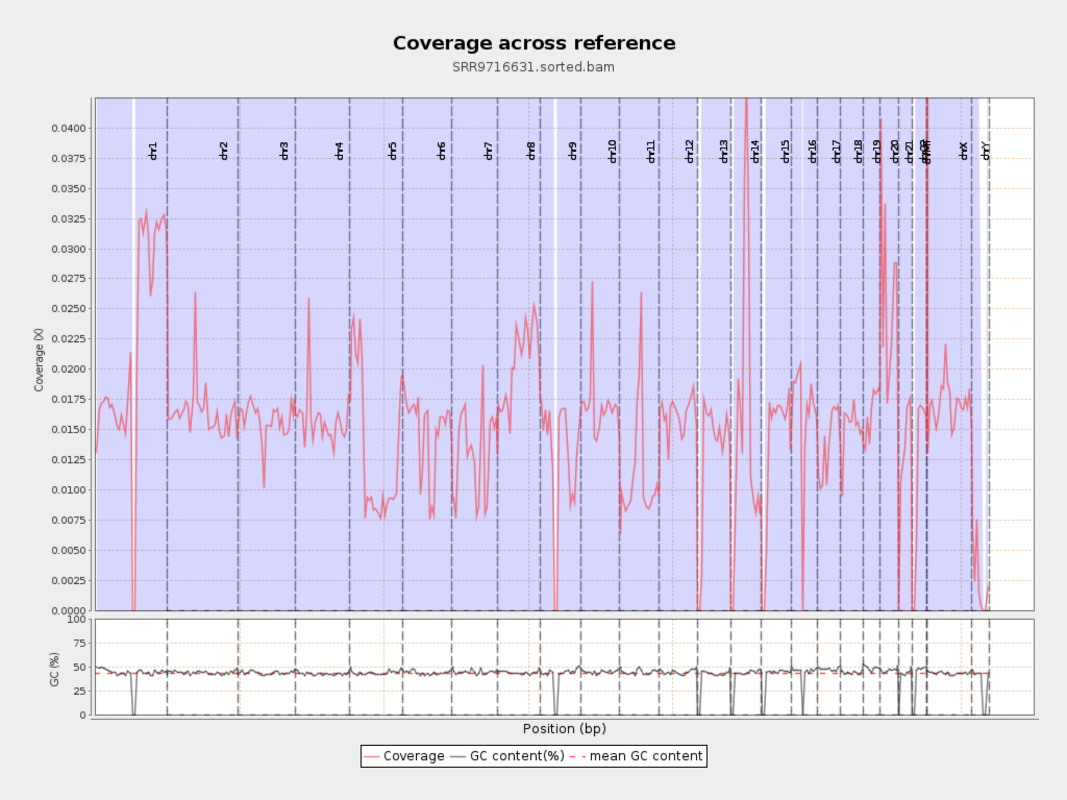
General error rate	0.51%
Mismatches	236,952
Insertions	3,460
Mapped reads with at least one insertion	0.4%
Deletions	7,873
Mapped reads with at least one deletion	0.92%
Homopolymer indels	41%

2.6. Chromosome stats

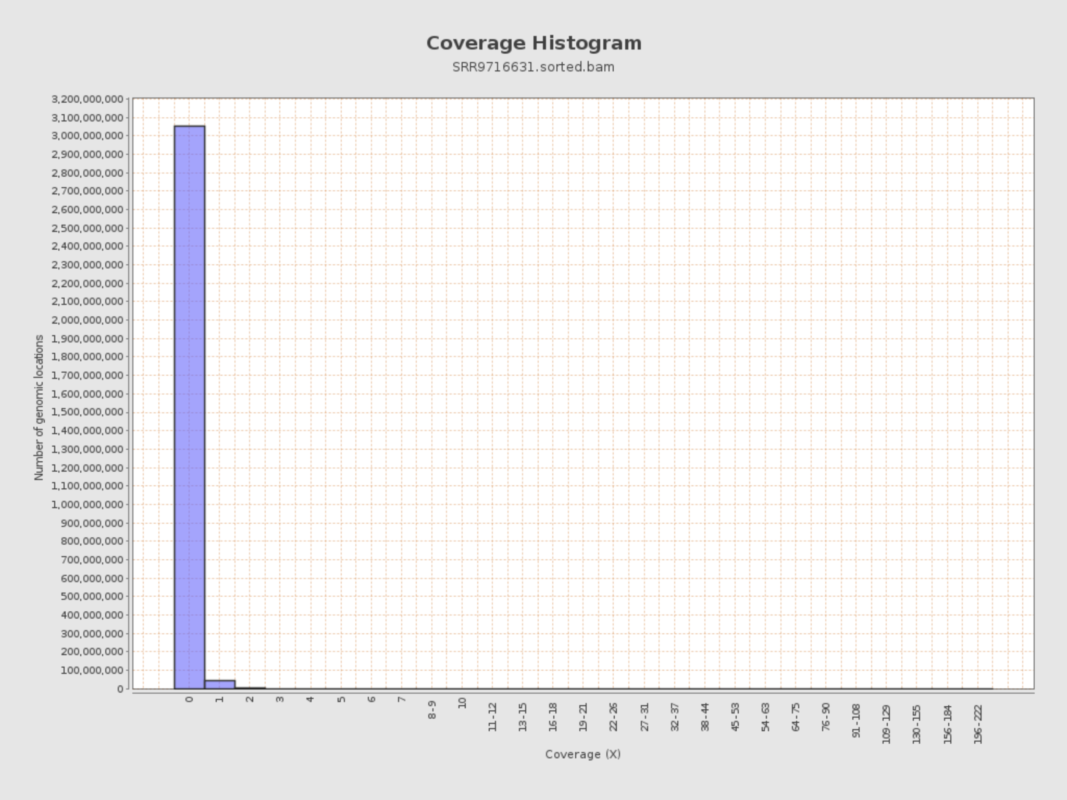
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5395993	0.0216	0.2126
chr2	243199373	4001848	0.0165	0.1662
chr3	198022430	3130574	0.0158	0.1332
chr4	191154276	3030021	0.0159	0.1395
chr5	180915260	2370436	0.0131	0.1206
chr6	171115067	2534568	0.0148	0.1326
chr7	159138663	2085819	0.0131	0.1342

chr8	146364022	3011218	0.0206	0.1605
chr9	141213431	1778561	0.0126	0.1474
chr10	135534747	2305617	0.017	0.1658
chr11	135006516	1539861	0.0114	0.1288
chr12	133851895	2175910	0.0163	0.1343
chr13	115169878	1472730	0.0128	0.1184
chr14	107349540	1664228	0.0155	0.1345
chr15	102531392	1376273	0.0134	0.121
chr16	90354753	1450038	0.016	0.1395
chr17	81195210	1116086	0.0137	0.1259
chr18	78077248	1166549	0.0149	0.2358
chr19	59128983	965553	0.0163	0.166
chr20	63025520	1624912	0.0258	0.1723
chr21	48129895	617405	0.0128	0.1254
chr22	51304566	585876	0.0114	0.1122
chrMT	16571	6408	0.3867	0.6729
chrX	155270560	2659508	0.0171	0.1482
chrY	59373566	142354	0.0024	0.0656

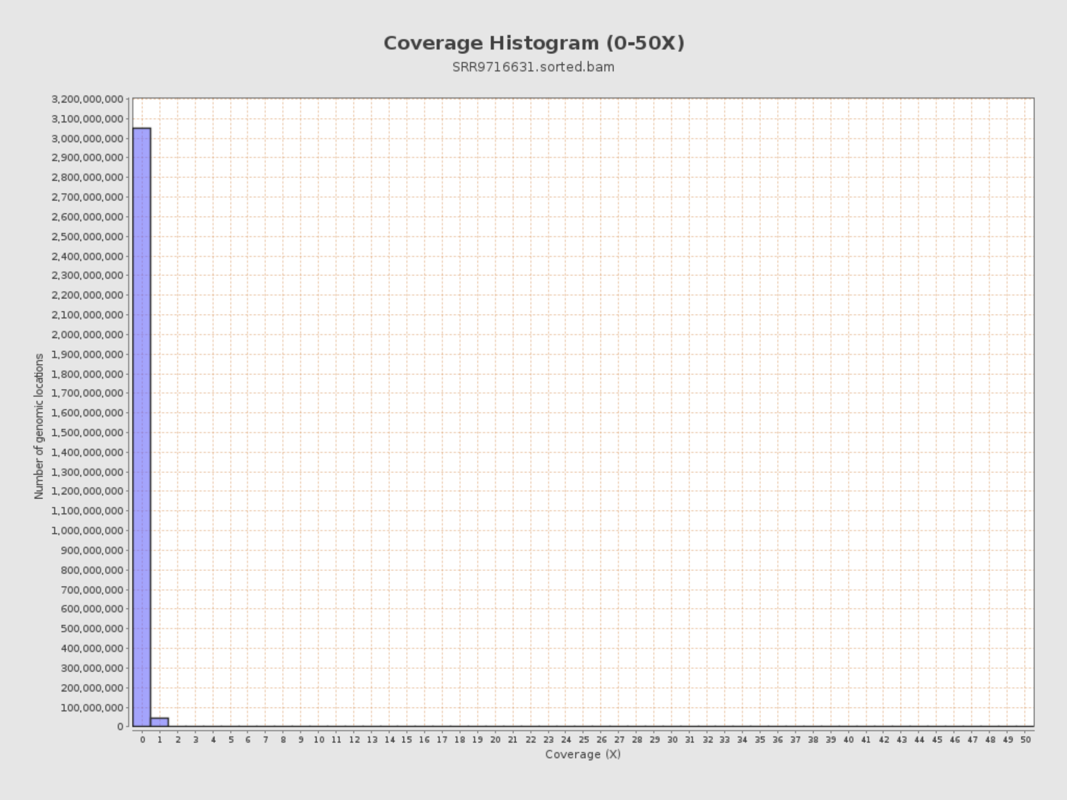
3. Results : Coverage across reference



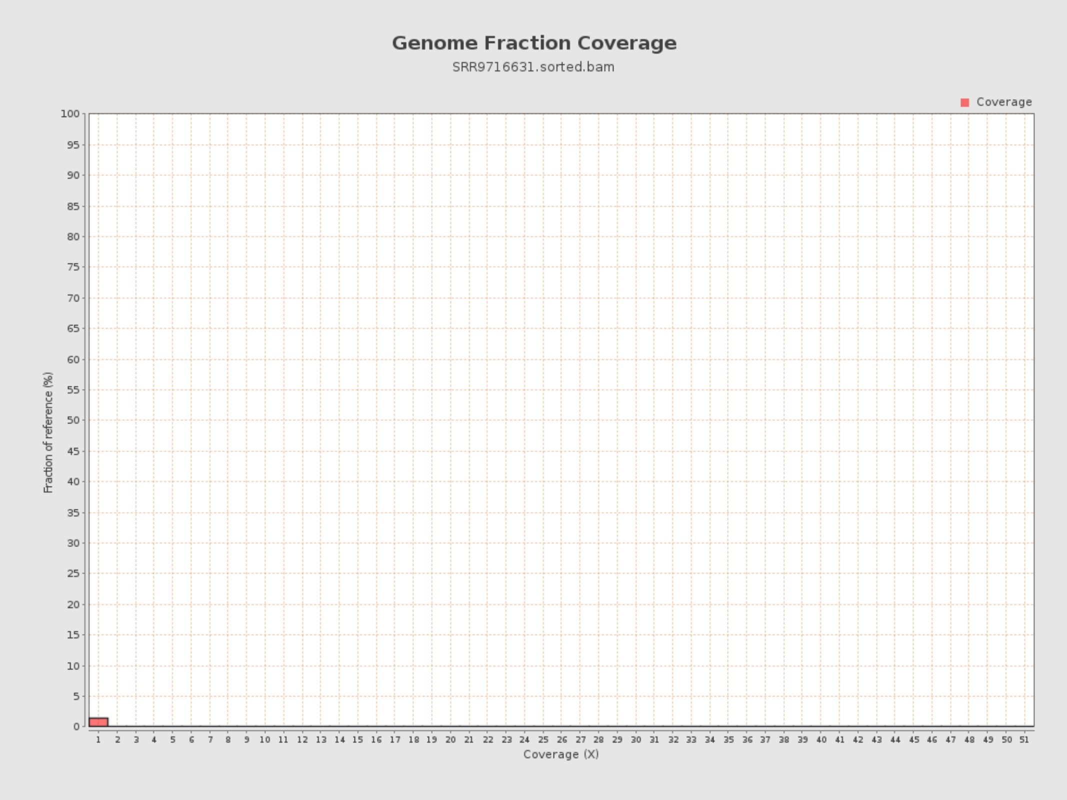
4. Results : Coverage Histogram



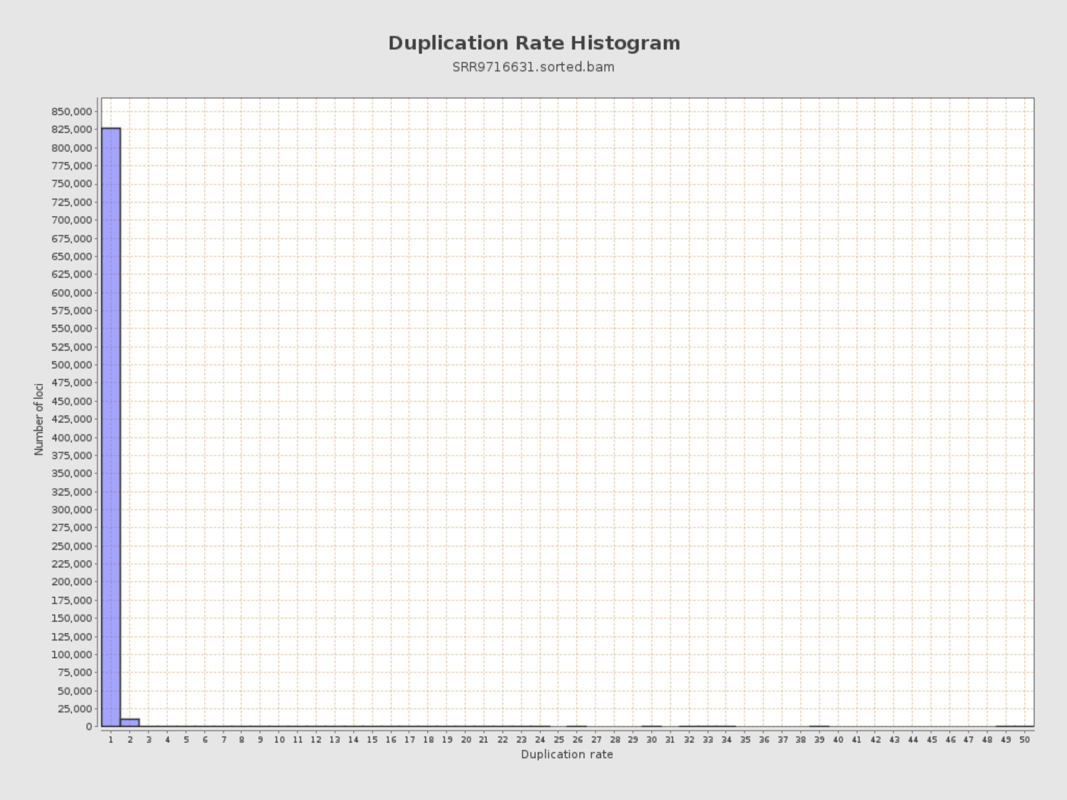
5. Results : Coverage Histogram (0-50X)



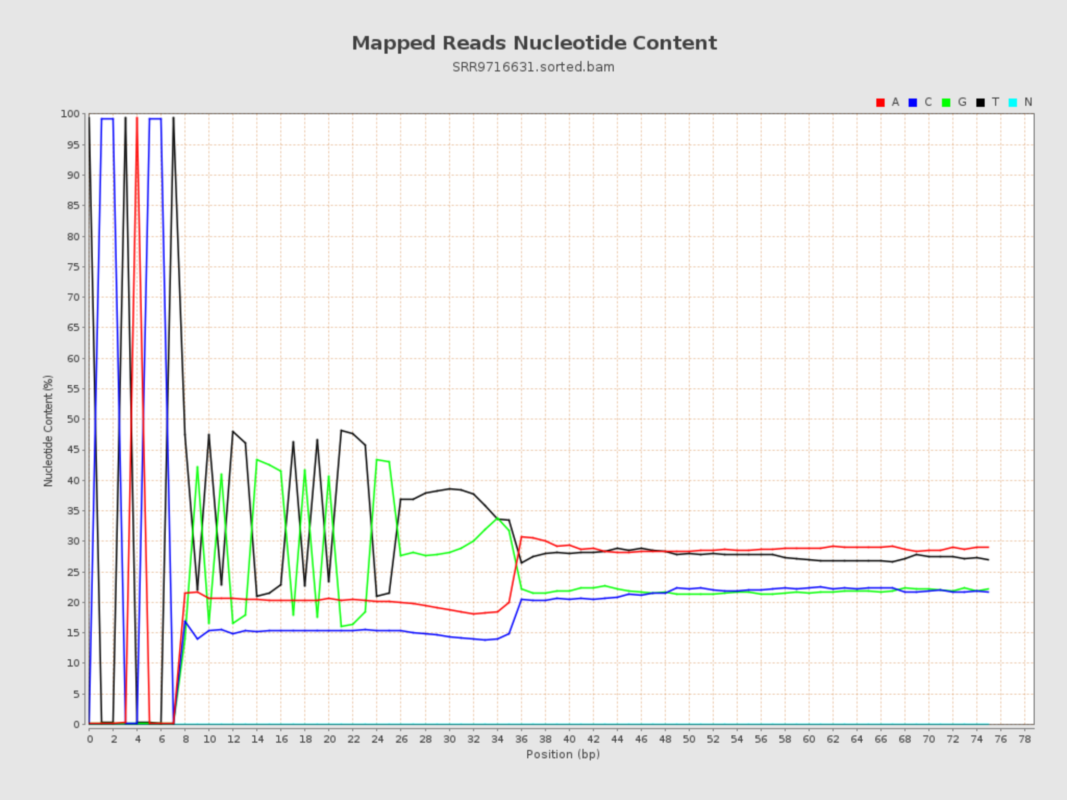
6. Results : Genome Fraction Coverage



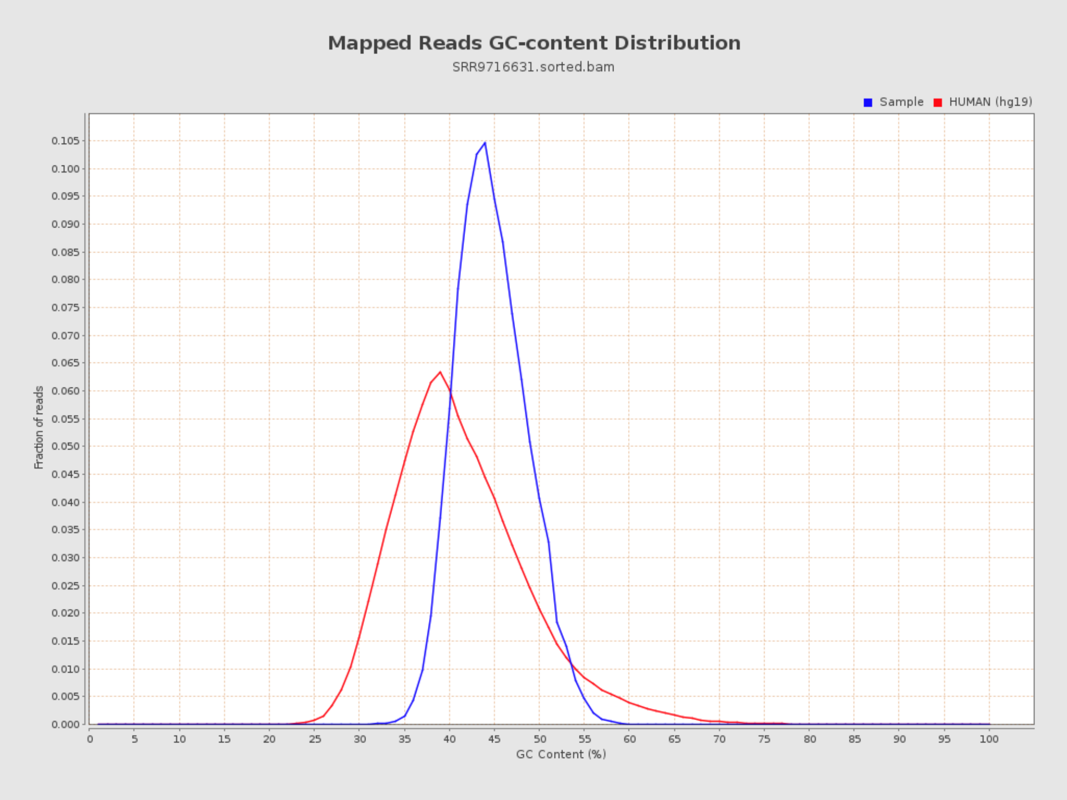
7. Results : Duplication Rate Histogram



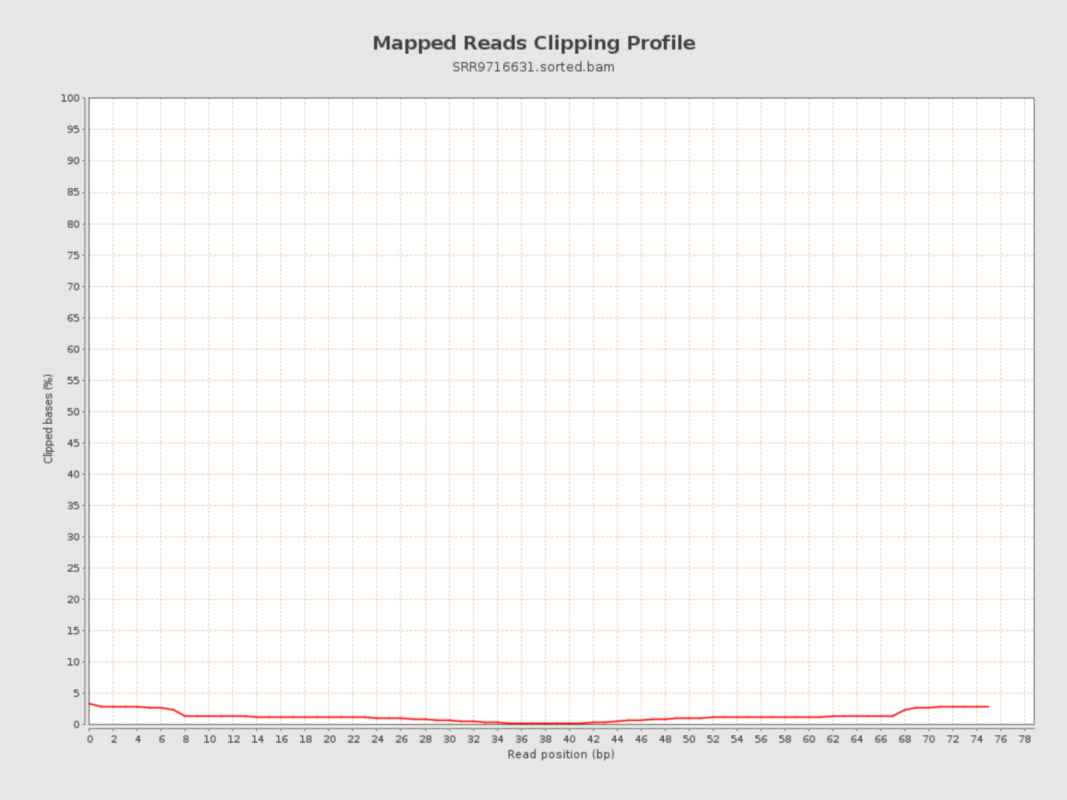
8. Results : Mapped Reads Nucleotide Content



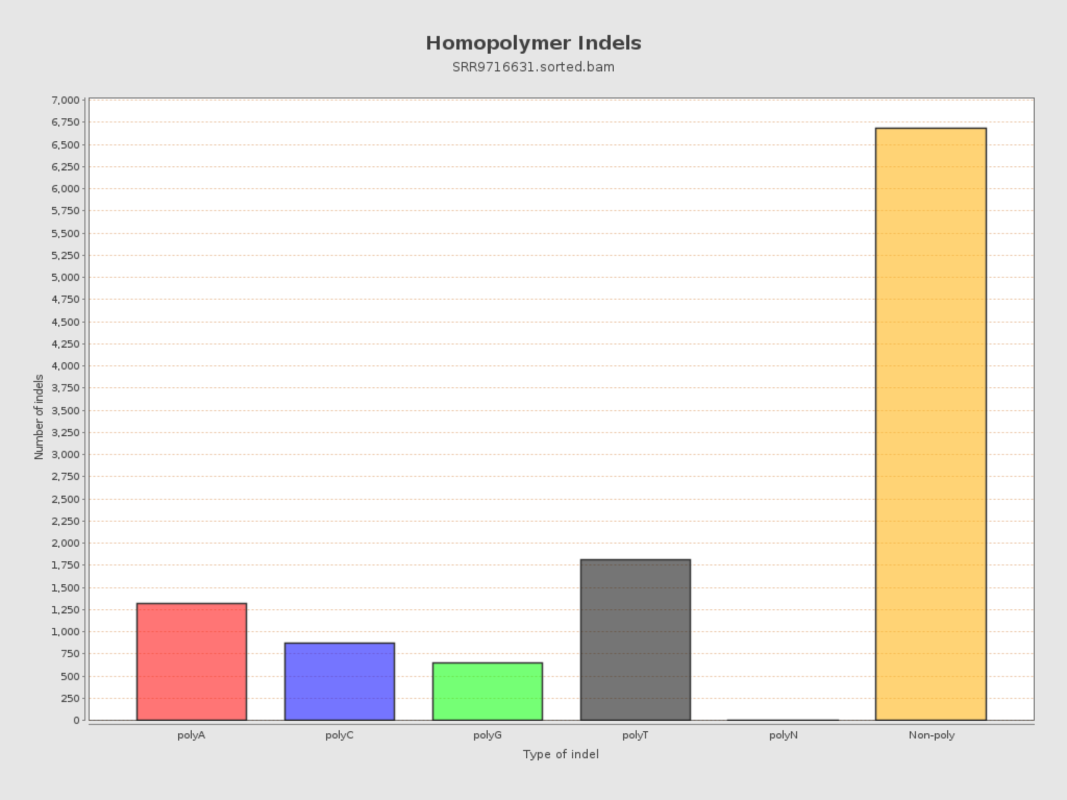
9. Results : Mapped Reads GC-content Distribution



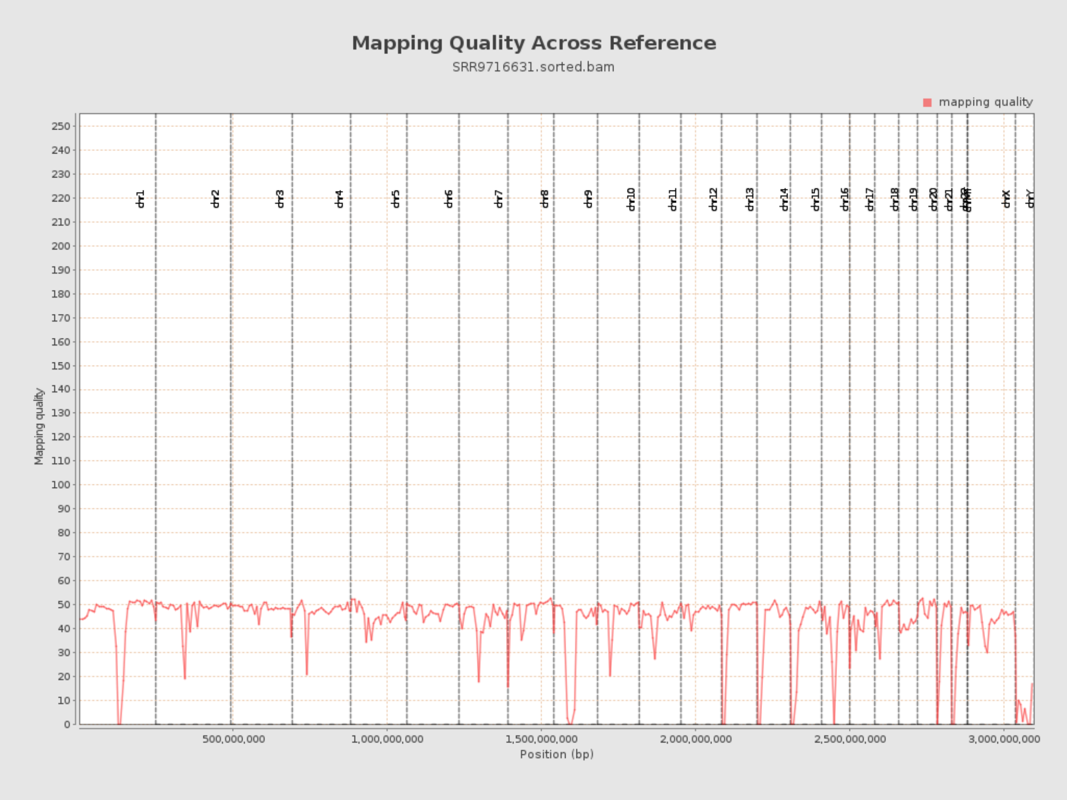
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram