Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 06:23:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716691.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_SRR9716691 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716691.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 06:23:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716691.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,523,714
Mapped reads	1,351,843 / 88.72%
Unmapped reads	171,871 / 11.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,646 / 1.49%
Read min/max/mean length	30 / 101 / 101.55
Duplicated reads (estimated)	54,655 / 3.59%
Duplication rate	2.23%
Clipped reads	1,373,820 / 90.16%

2.2. ACGT Content

Number/percentage of A's	27,108,900 / 25.35%
Number/percentage of C's	19,942,594 / 18.65%
Number/percentage of T's	32,824,594 / 30.69%
Number/percentage of G's	27,056,713 / 25.3%
Number/percentage of N's	6,410 / 0.01%
GC Percentage	43.95%

2.3. Coverage

Mean	0.0346

Standard Deviation	0.466

2.4. Mapping Quality

Mean Mapping Quality	43.29

2.5. Mismatches and indels

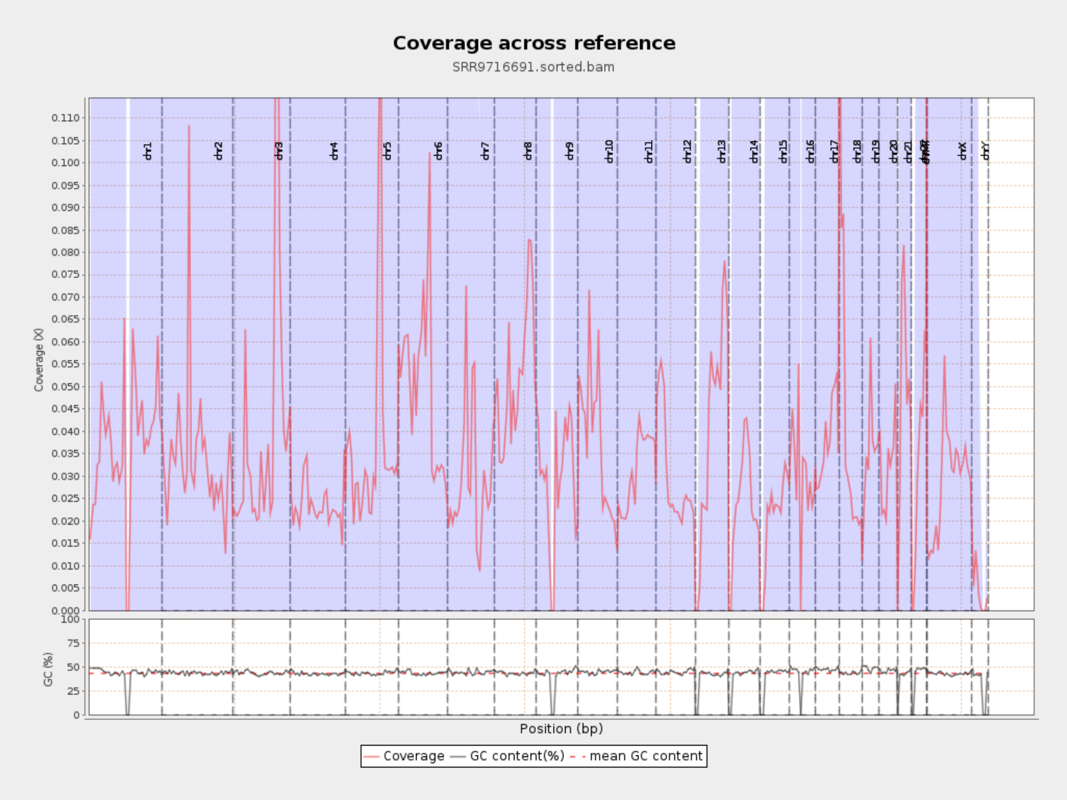
General error rate	0.81%
Mismatches	847,556
Insertions	9,235
Mapped reads with at least one insertion	0.67%
Deletions	26,544
Mapped reads with at least one deletion	1.94%
Homopolymer indels	44.88%

2.6. Chromosome stats

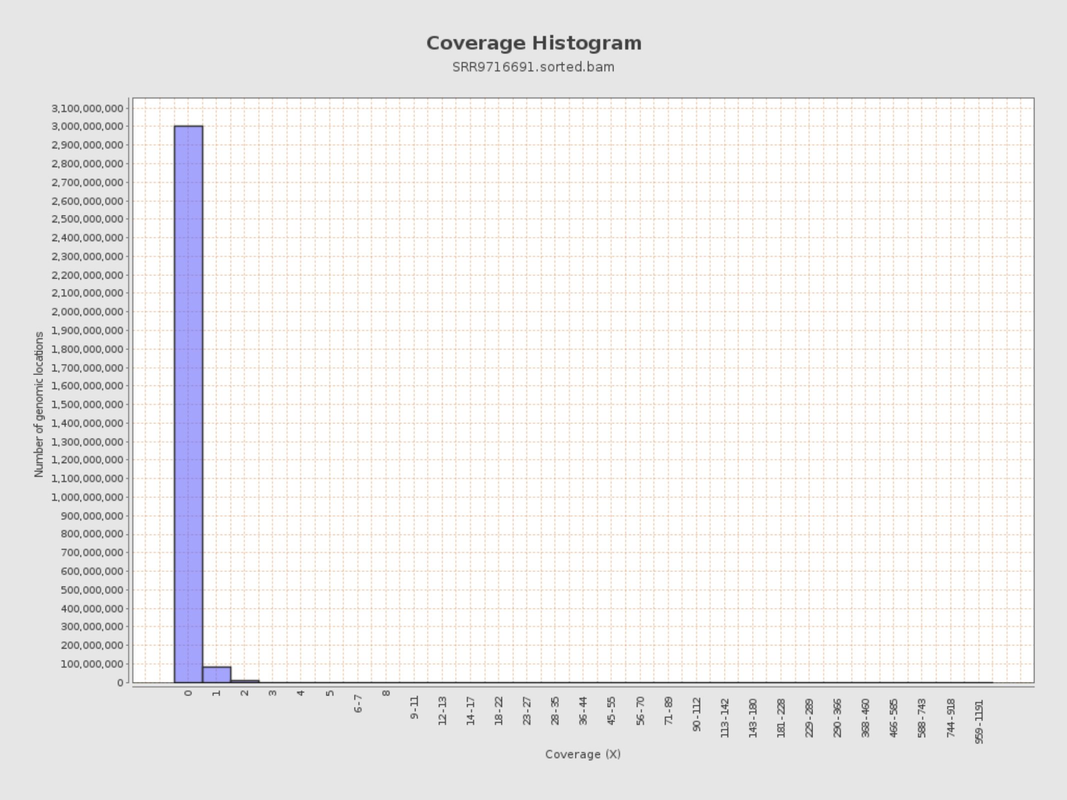
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9212900	0.037	0.7346
chr2	243199373	8263392	0.034	0.8217
chr3	198022430	7998441	0.0404	0.2301
chr4	191154276	4476051	0.0234	0.1803
chr5	180915260	6798159	0.0376	0.2185
chr6	171115067	8666521	0.0506	0.31
chr7	159138663	4739853	0.0298	0.6385

chr8	146364022	7734165	0.0528	0.643
chr9	141213431	4098469	0.029	0.4542
chr10	135534747	5180713	0.0382	0.384
chr11	135006516	4249818	0.0315	0.3209
chr12	133851895	4013554	0.03	0.199
chr13	115169878	4813669	0.0418	0.2259
chr14	107349540	2551679	0.0238	0.2227
chr15	102531392	2107828	0.0206	0.1599
chr16	90354753	2723702	0.0301	0.2352
chr17	81195210	3122564	0.0385	0.2517
chr18	78077248	3350369	0.0429	0.9429
chr19	59128983	2138334	0.0362	0.6161
chr20	63025520	2023140	0.0321	0.2528
chr21	48129895	2339490	0.0486	0.2523
chr22	51304566	1608570	0.0314	0.1965
chrMT	16571	2036	0.1229	0.5289
chrX	155270560	4509482	0.029	0.2767
chrY	59373566	262576	0.0044	0.1285

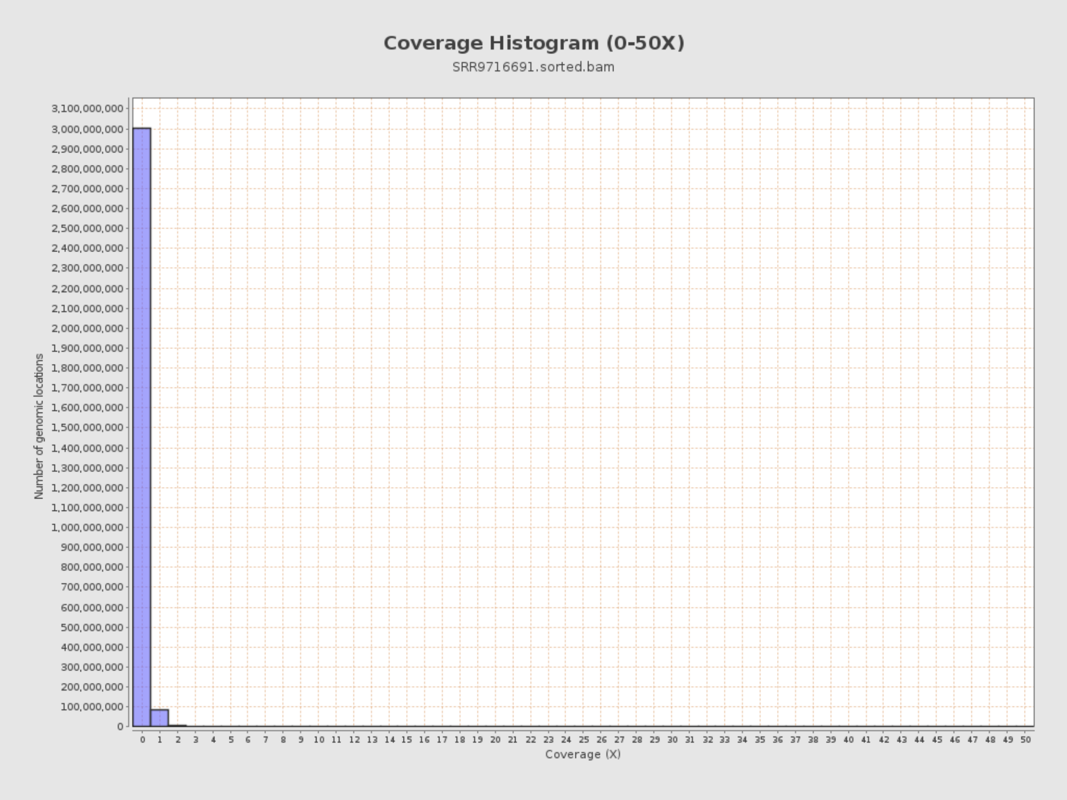
3. Results : Coverage across reference



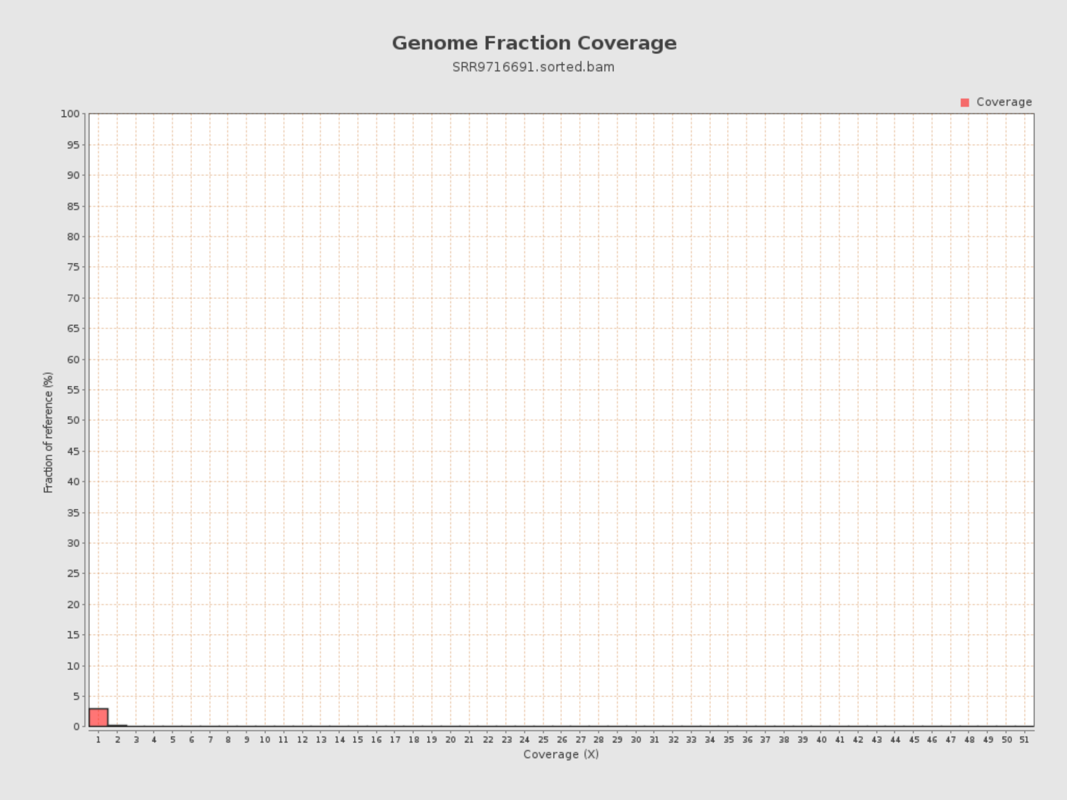
4. Results : Coverage Histogram



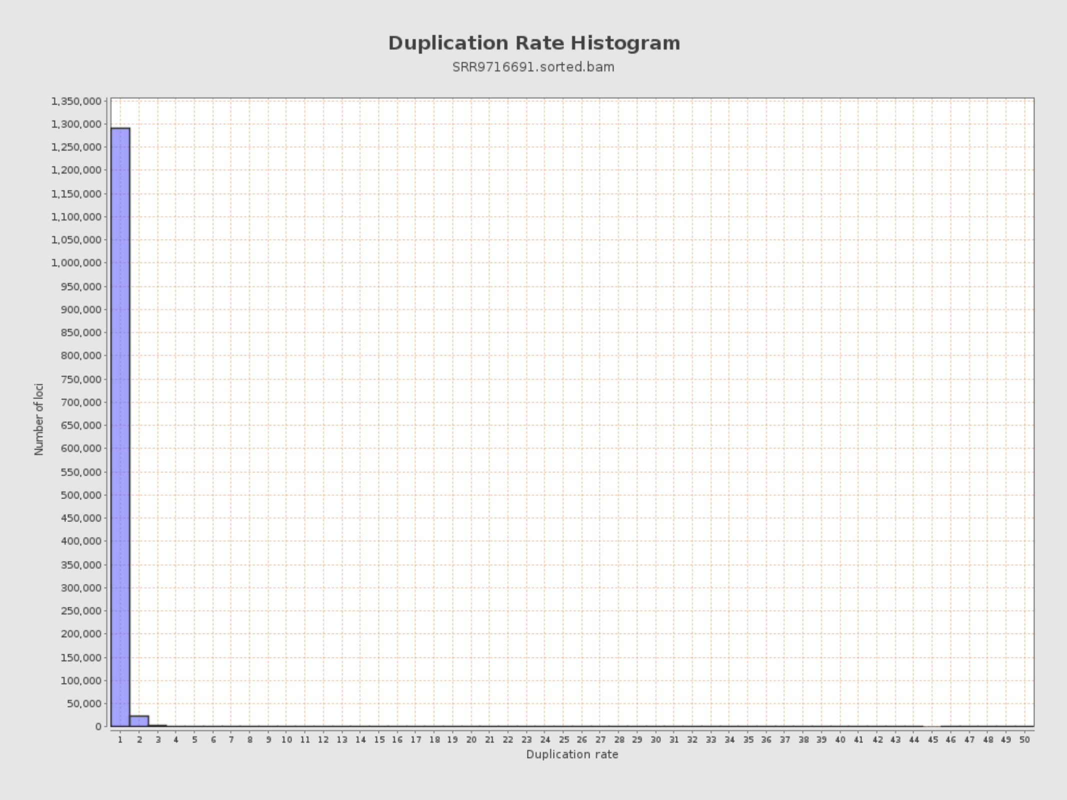
5. Results : Coverage Histogram (0-50X)



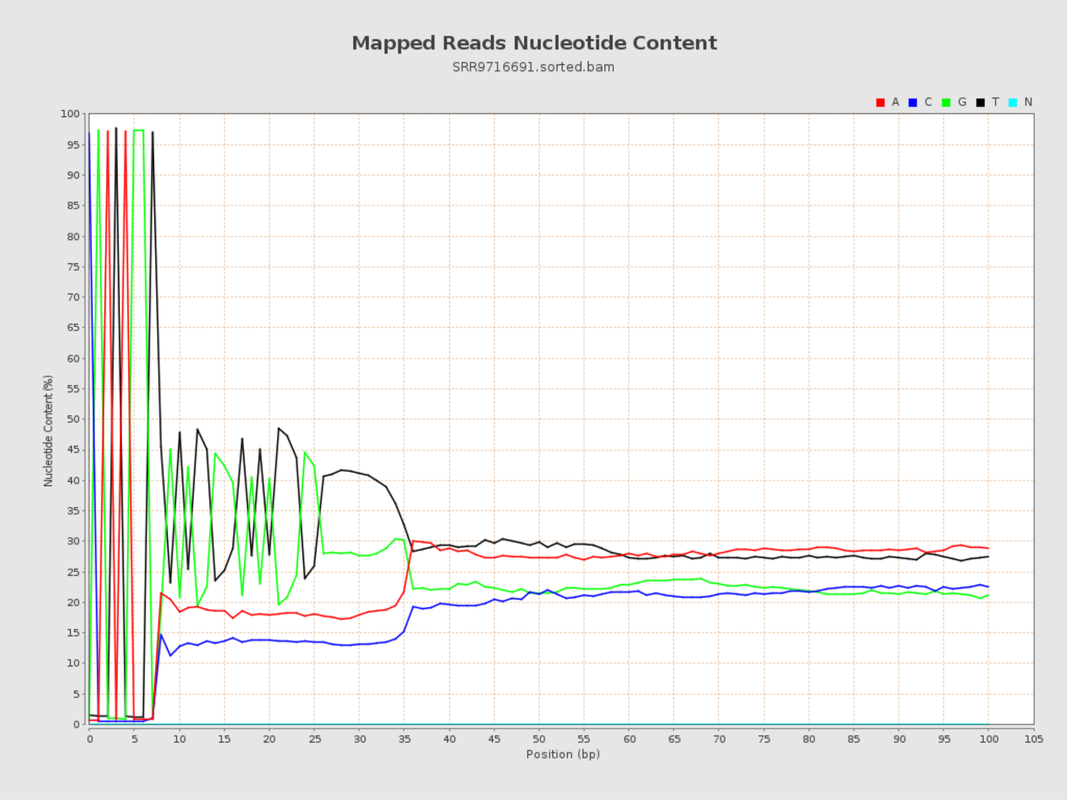
6. Results : Genome Fraction Coverage



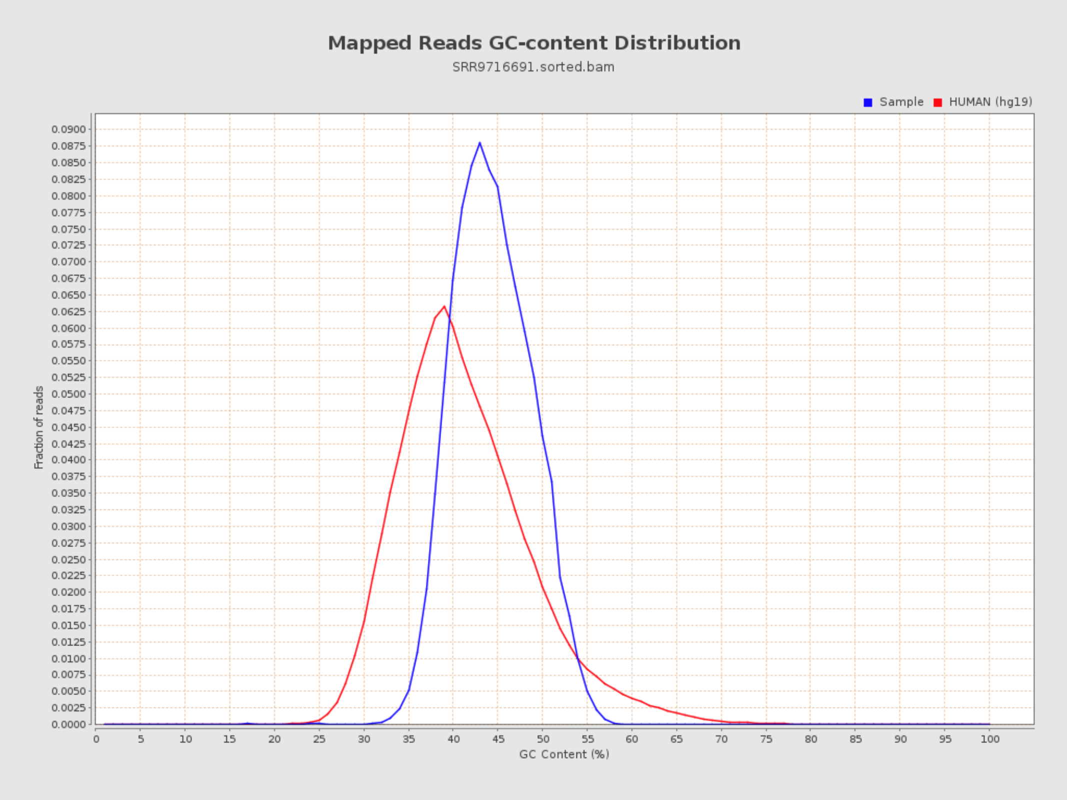
7. Results : Duplication Rate Histogram



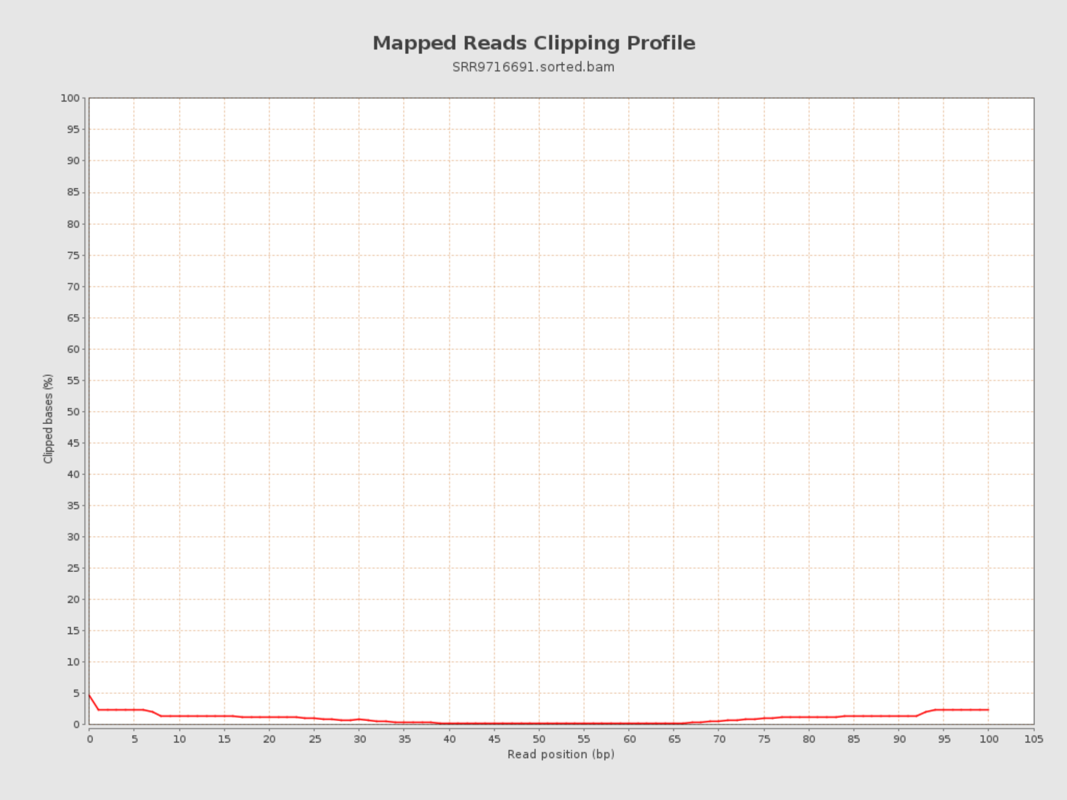
8. Results : Mapped Reads Nucleotide Content



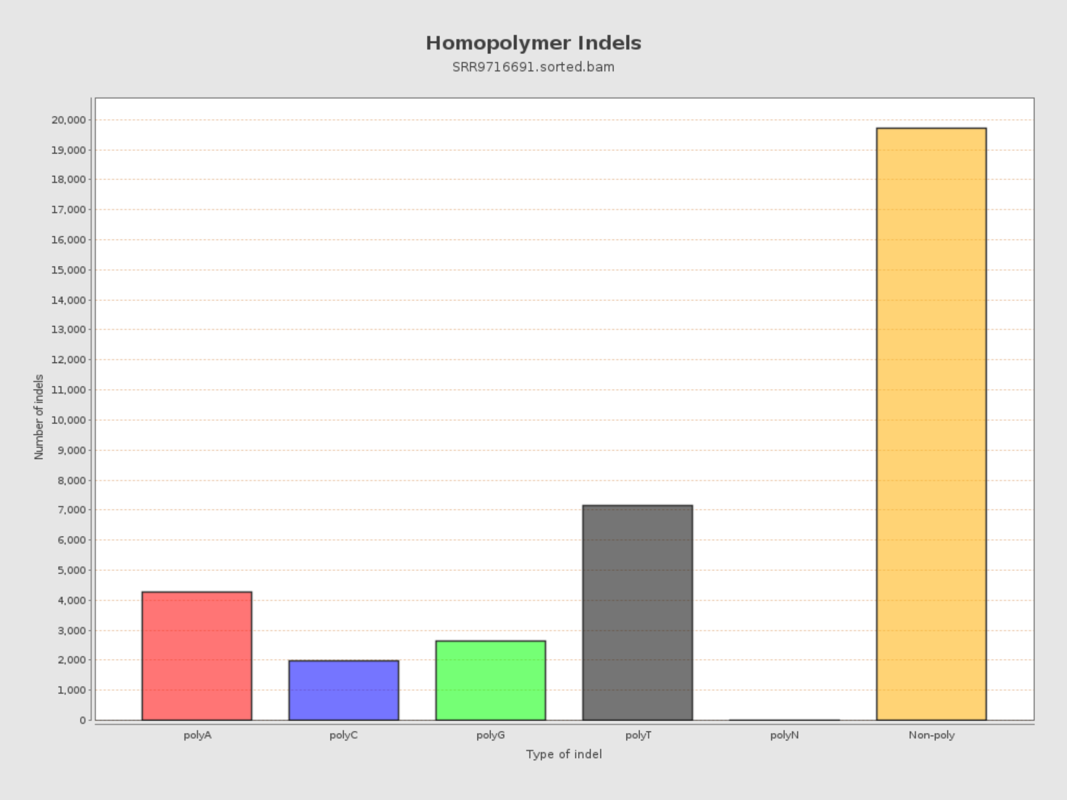
9. Results : Mapped Reads GC-content Distribution



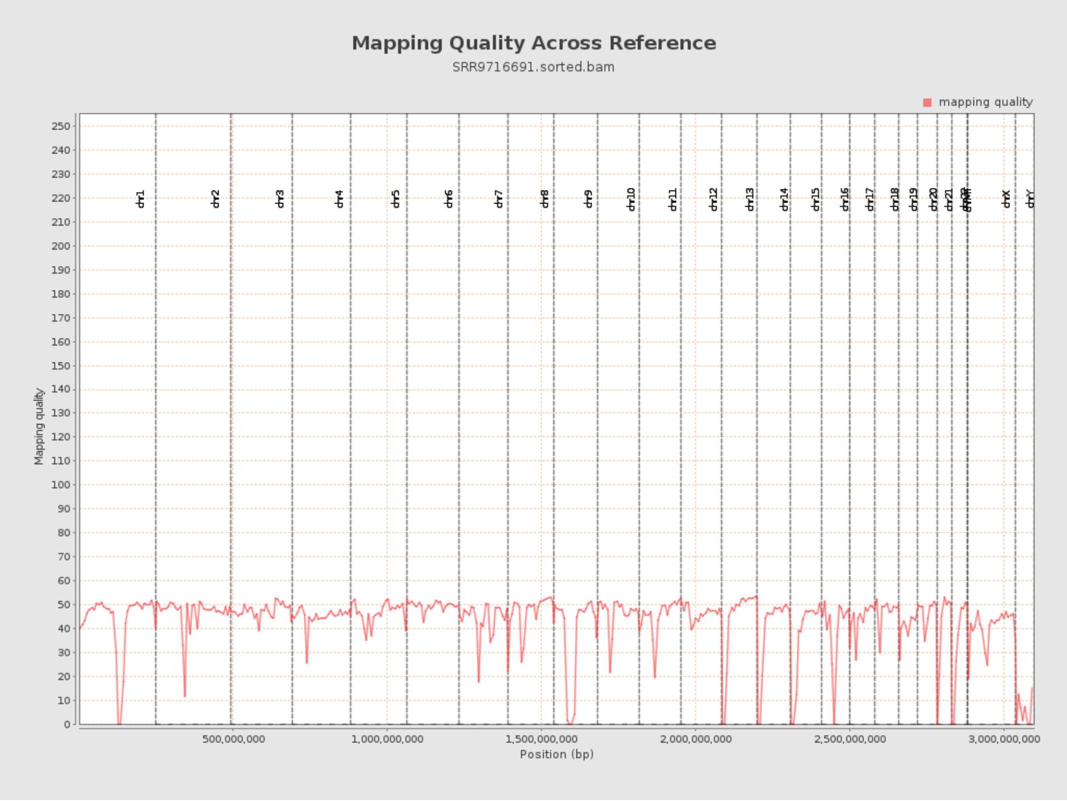
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram