Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 20:29:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716961.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_SRR9716961 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716961.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 20:29:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716961.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,833,011
Mapped reads	1,734,319 / 94.62%
Unmapped reads	98,692 / 5.38%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	38,135 / 2.08%
Read min/max/mean length	30 / 101 / 101.76
Duplicated reads (estimated)	86,252 / 4.71%
Duplication rate	3.82%
Clipped reads	1,770,939 / 96.61%

2.2. ACGT Content

Number/percentage of A's	33,730,485 / 24.88%
Number/percentage of C's	27,183,104 / 20.05%
Number/percentage of T's	39,701,138 / 29.29%
Number/percentage of G's	34,938,780 / 25.77%
Number/percentage of N's	5,760 / 0%
GC Percentage	45.83%

2.3. Coverage

Mean	0.0438

Standard Deviation	0.3407

2.4. Mapping Quality

Mean Mapping Quality	47.07

2.5. Mismatches and indels

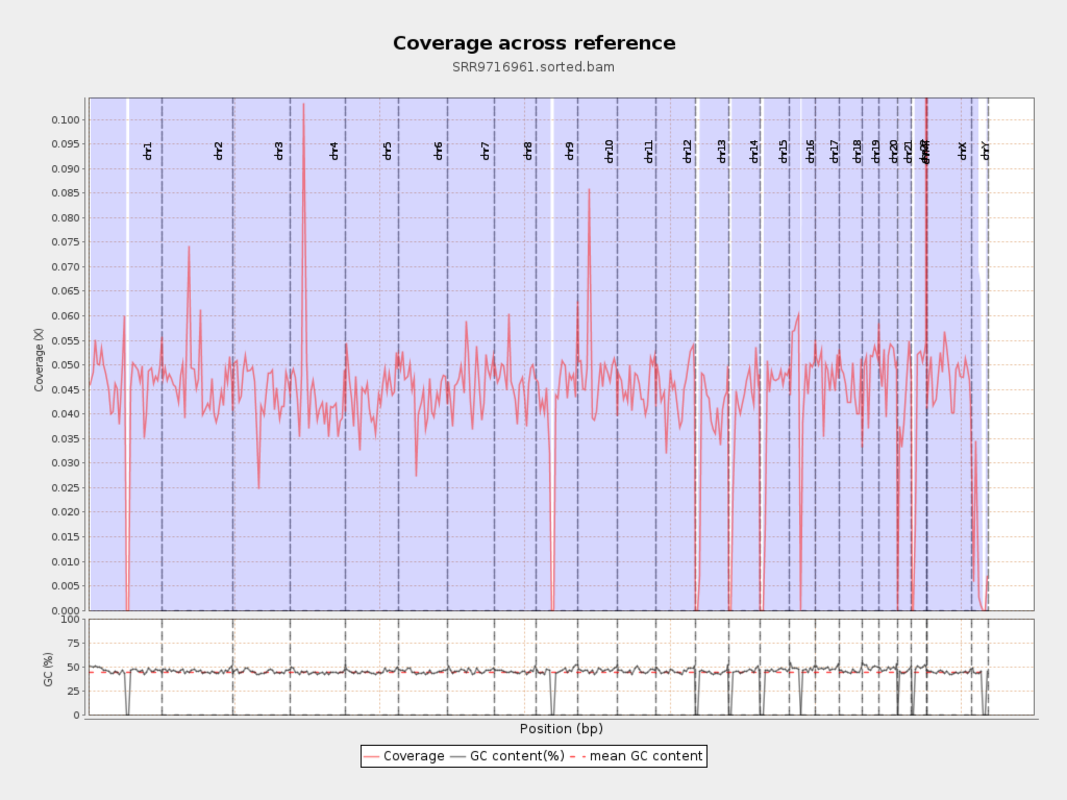
General error rate	0.66%
Mismatches	868,049
Insertions	10,889
Mapped reads with at least one insertion	0.62%
Deletions	24,569
Mapped reads with at least one deletion	1.39%
Homopolymer indels	39.06%

2.6. Chromosome stats

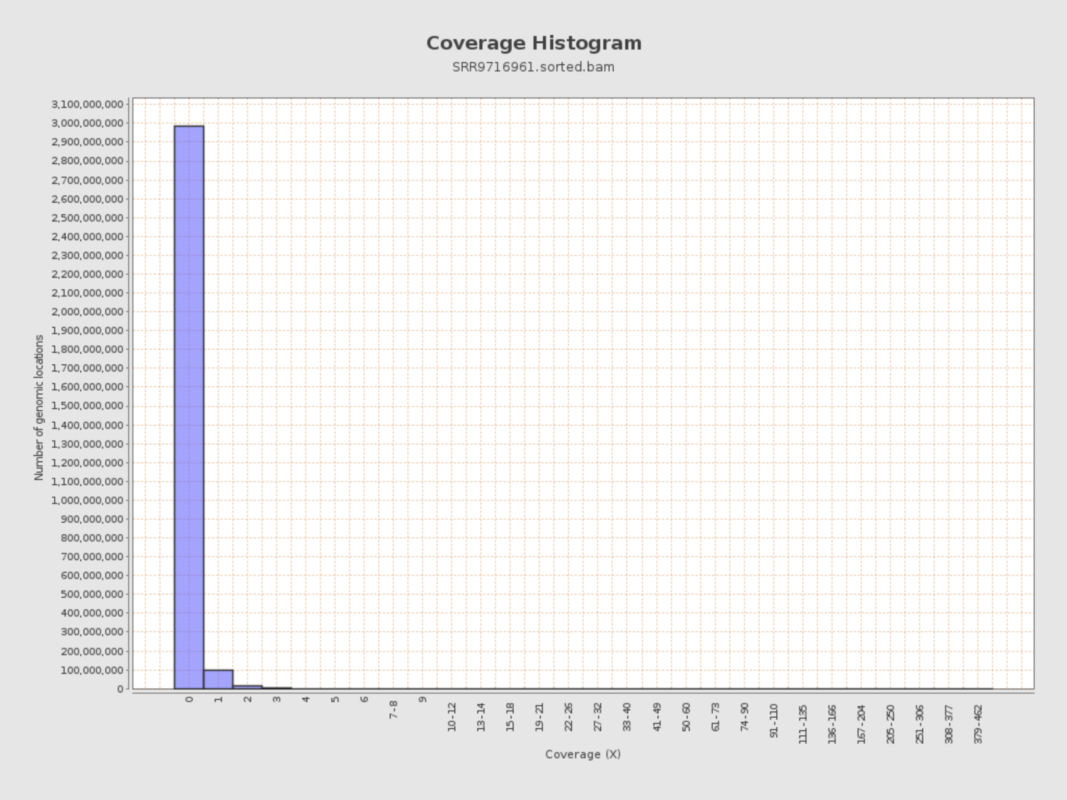
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11083160	0.0445	0.4721
chr2	243199373	11430067	0.047	0.4002
chr3	198022430	8848456	0.0447	0.2454
chr4	191154276	8568829	0.0448	0.3672
chr5	180915260	7942435	0.0439	0.2453
chr6	171115067	7577044	0.0443	0.2559
chr7	159138663	7388758	0.0464	0.4106

chr8	146364022	6849761	0.0468	0.3617
chr9	141213431	5627048	0.0398	0.3094
chr10	135534747	6642917	0.049	0.4672
chr11	135006516	6171148	0.0457	0.3752
chr12	133851895	6032013	0.0451	0.2506
chr13	115169878	4011359	0.0348	0.2168
chr14	107349540	4073650	0.0379	0.2515
chr15	102531392	3964464	0.0387	0.2309
chr16	90354753	4228479	0.0468	0.2798
chr17	81195210	3894922	0.048	0.2953
chr18	78077248	3555417	0.0455	0.4643
chr19	59128983	2908086	0.0492	0.3782
chr20	63025520	3134353	0.0497	0.2871
chr21	48129895	1872893	0.0389	0.3059
chr22	51304566	1857931	0.0362	0.2298
chrMT	16571	43145	2.6036	2.4877
chrX	155270560	7411926	0.0477	0.2785
chrY	59373566	493340	0.0083	0.3359

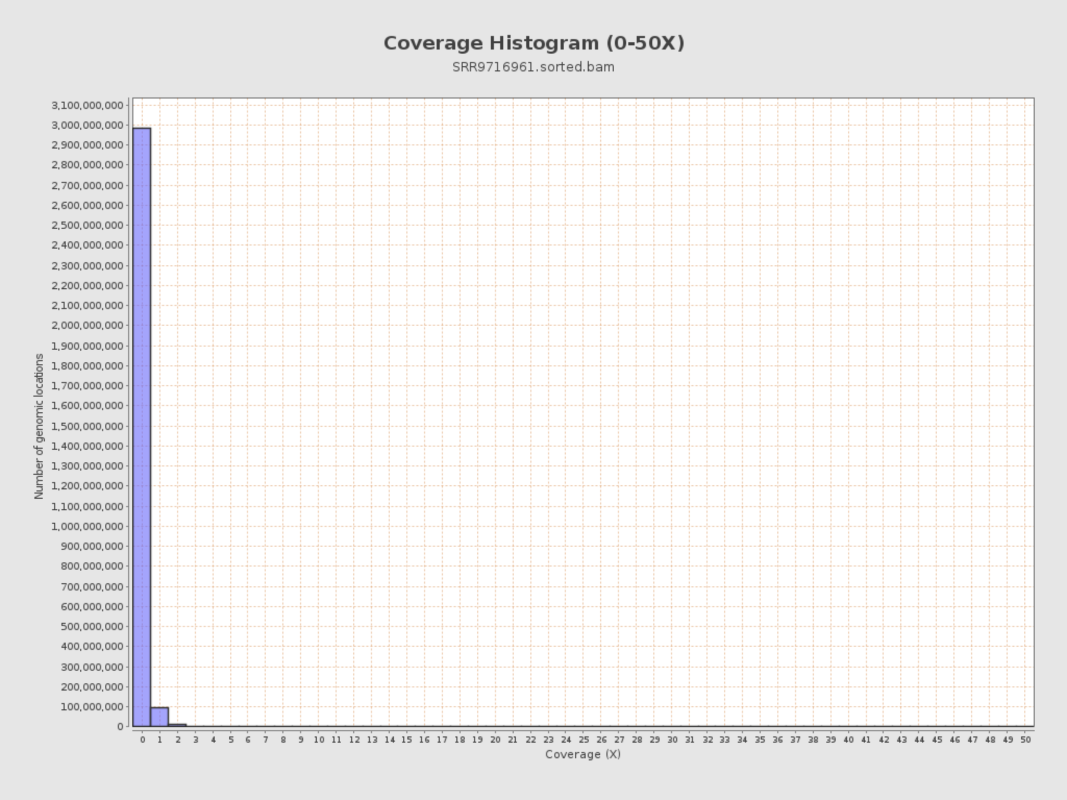
3. Results : Coverage across reference



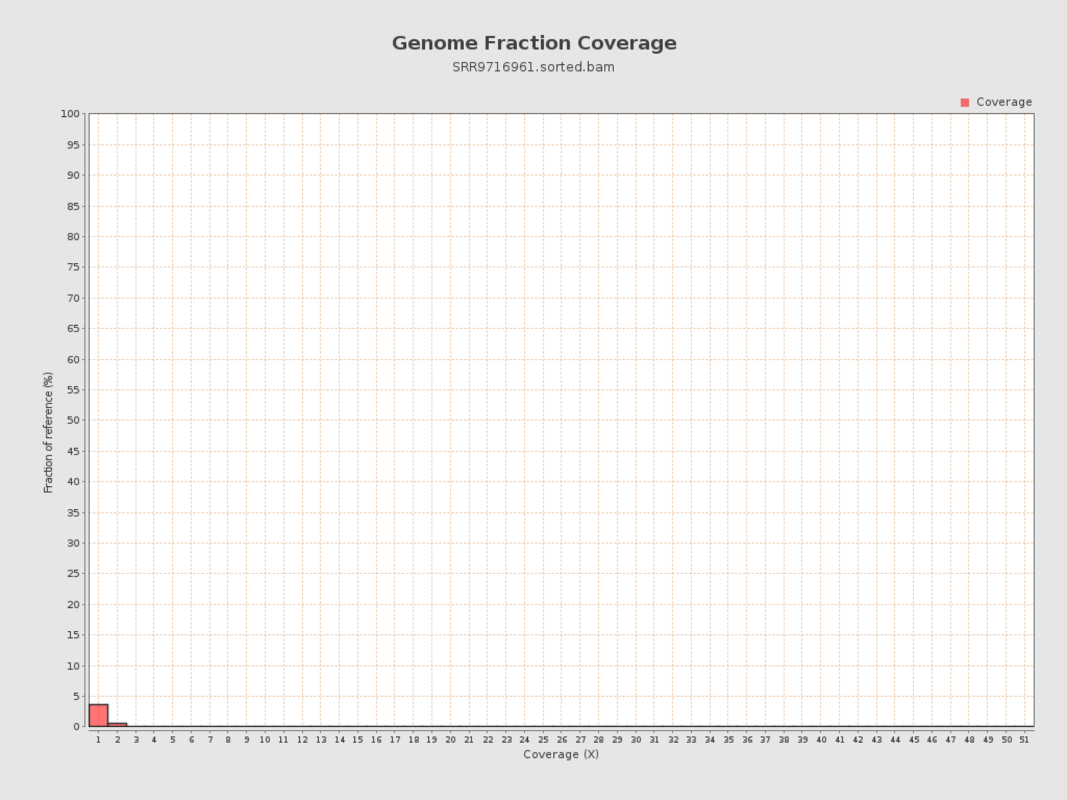
4. Results : Coverage Histogram



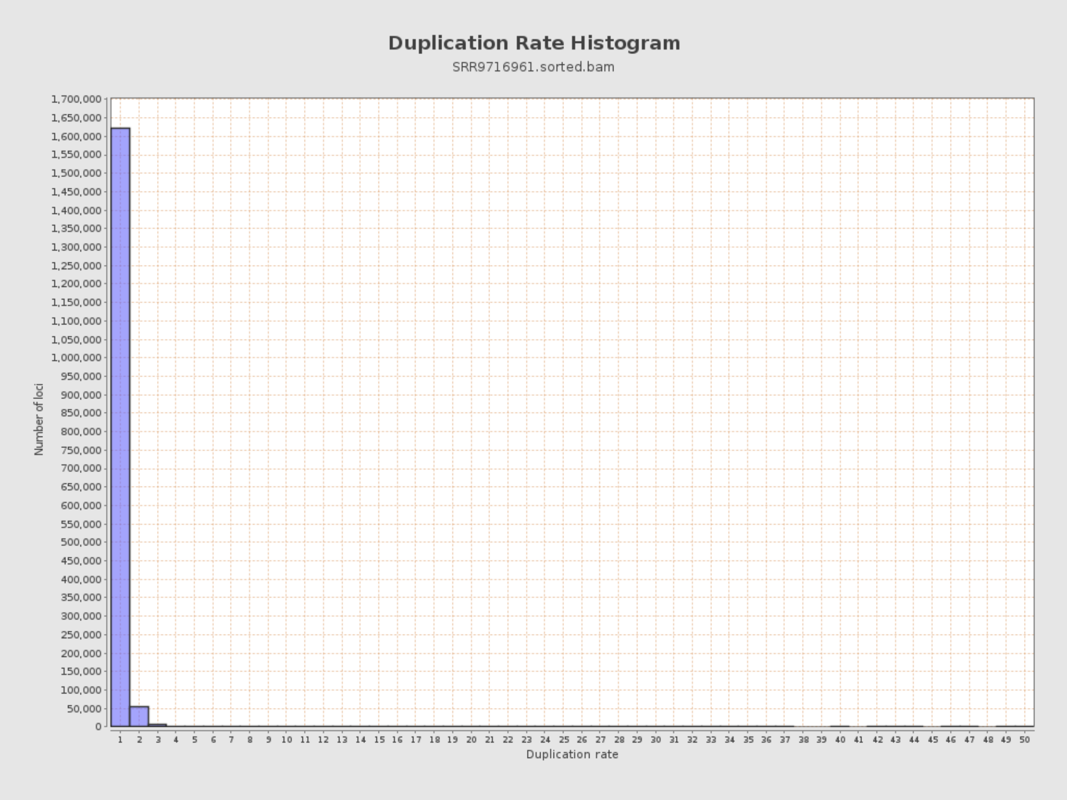
5. Results : Coverage Histogram (0-50X)



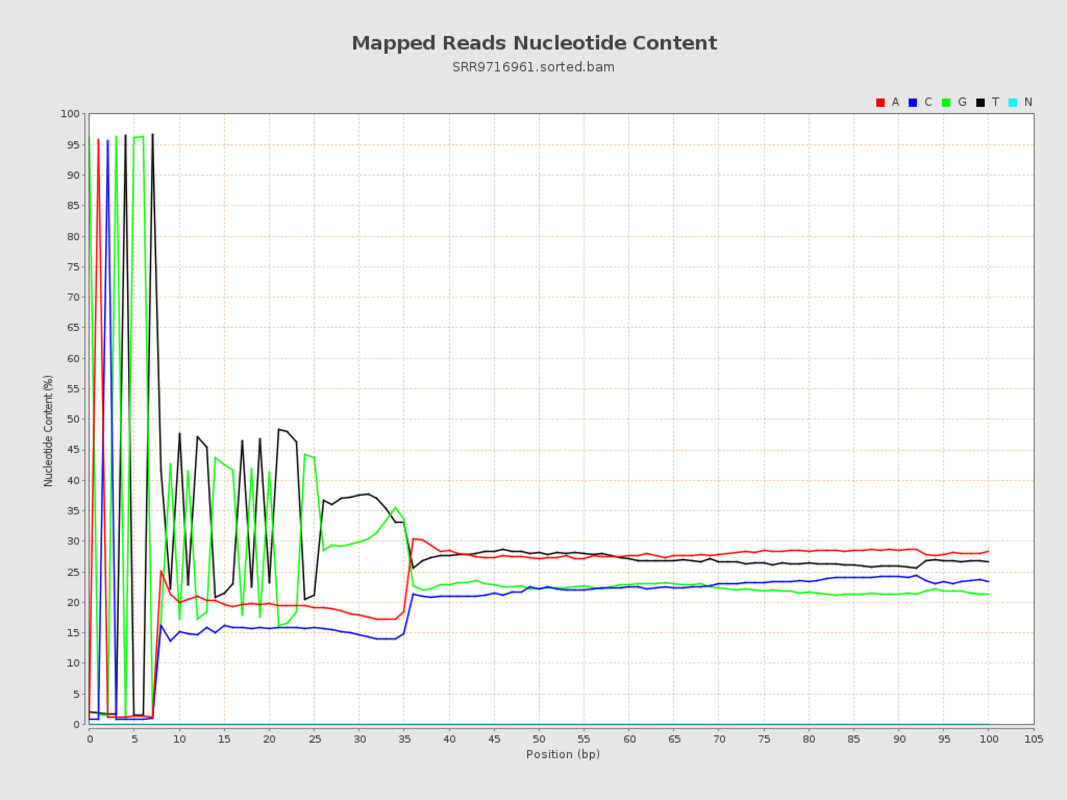
6. Results : Genome Fraction Coverage



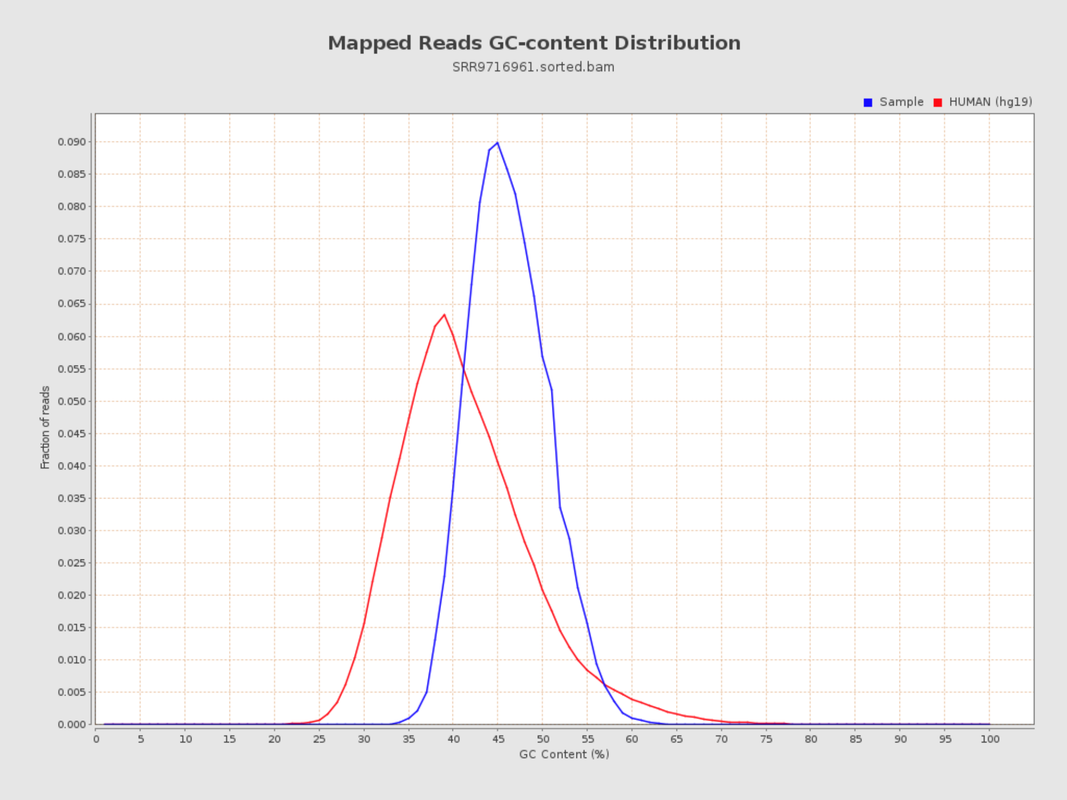
7. Results : Duplication Rate Histogram



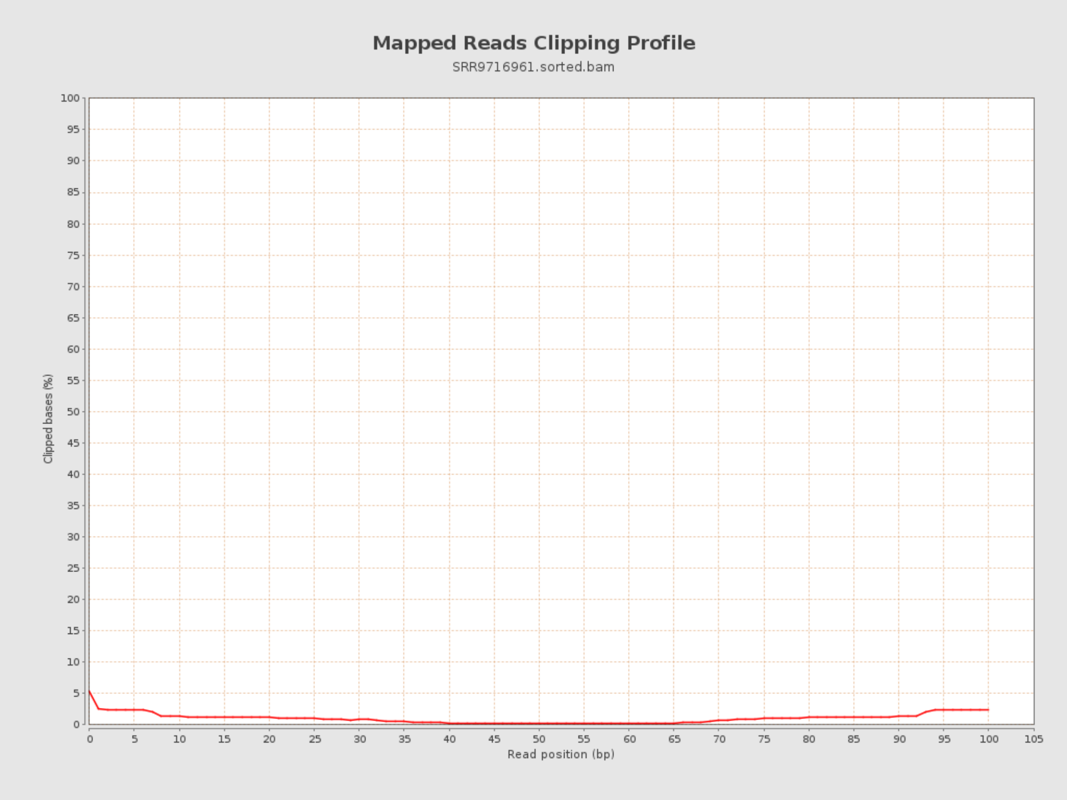
8. Results : Mapped Reads Nucleotide Content



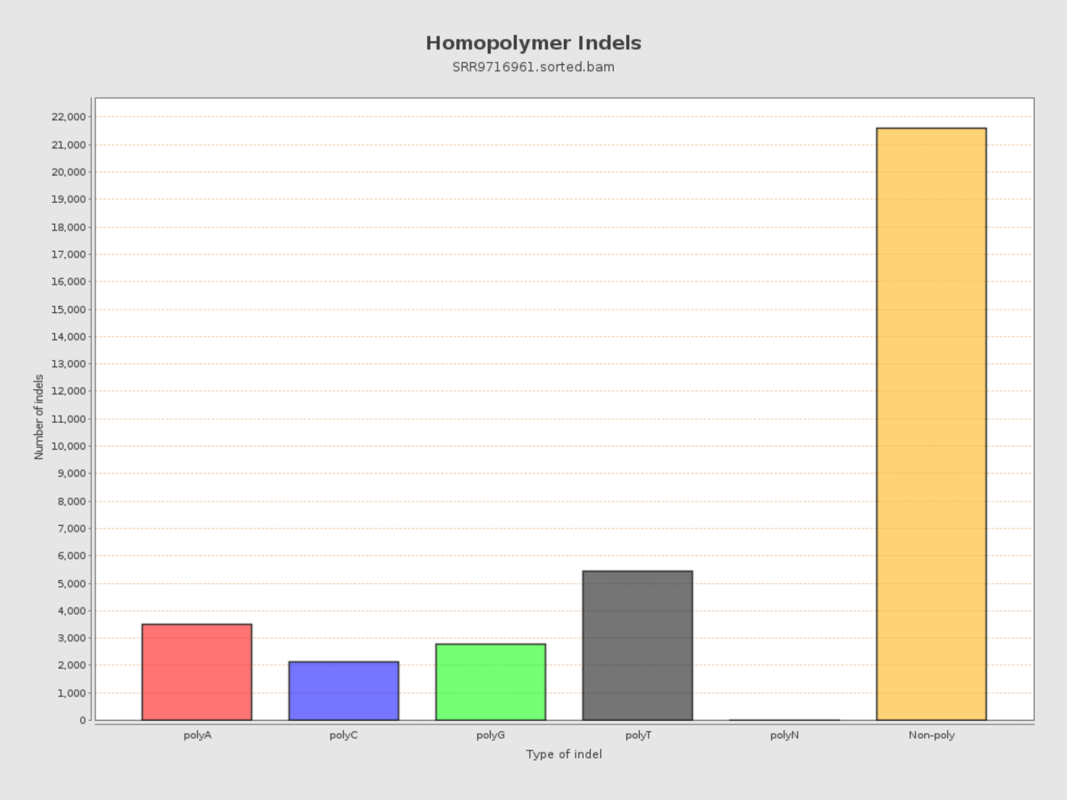
9. Results : Mapped Reads GC-content Distribution



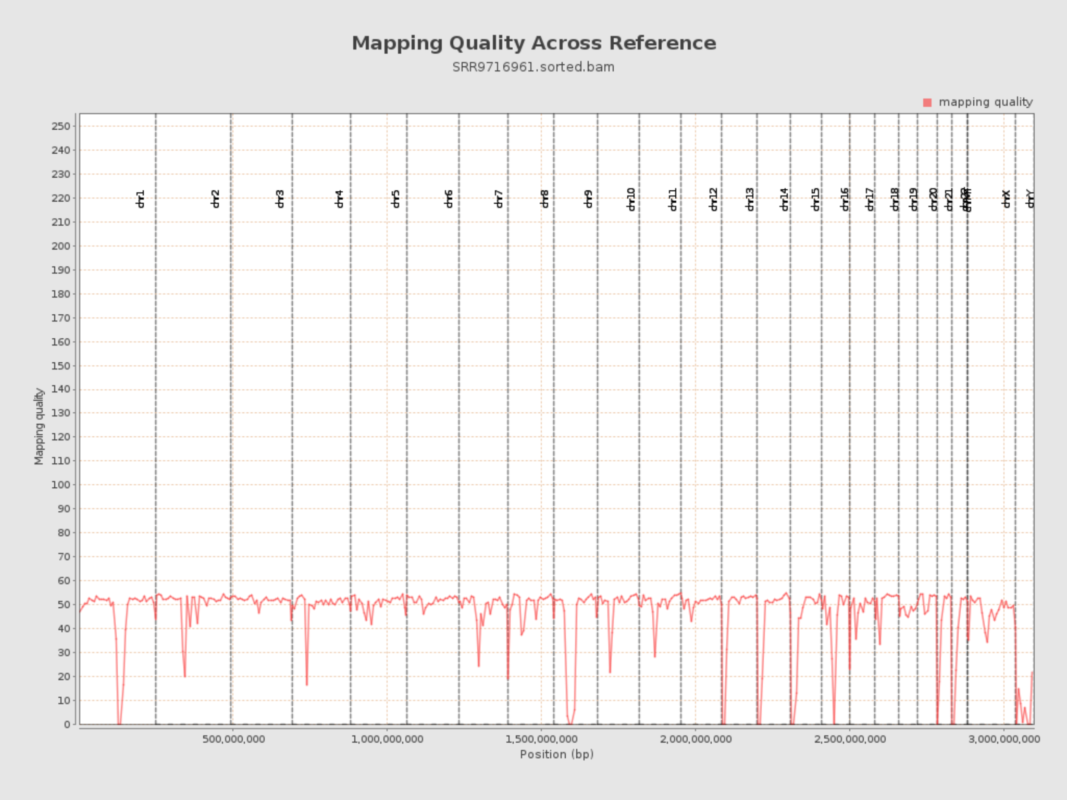
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram