Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 02:18:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716649.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_SRR9716649 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716649.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 02:18:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716649.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,213,545
Mapped reads	2,010,684 / 90.84%
Unmapped reads	202,861 / 9.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	59,358 / 2.68%
Read min/max/mean length	30 / 101 / 101.97
Duplicated reads (estimated)	55,328 / 2.5%
Duplication rate	1.89%
Clipped reads	2,067,270 / 93.39%

2.2. ACGT Content

Number/percentage of A's	39,058,278 / 25.67%
Number/percentage of C's	31,897,450 / 20.97%
Number/percentage of T's	44,983,415 / 29.57%
Number/percentage of G's	36,172,620 / 23.78%
Number/percentage of N's	18,349 / 0.01%
GC Percentage	44.74%

2.3. Coverage

Mean	0.0492

Standard Deviation	0.3635

2.4. Mapping Quality

Mean Mapping Quality	45.07

2.5. Mismatches and indels

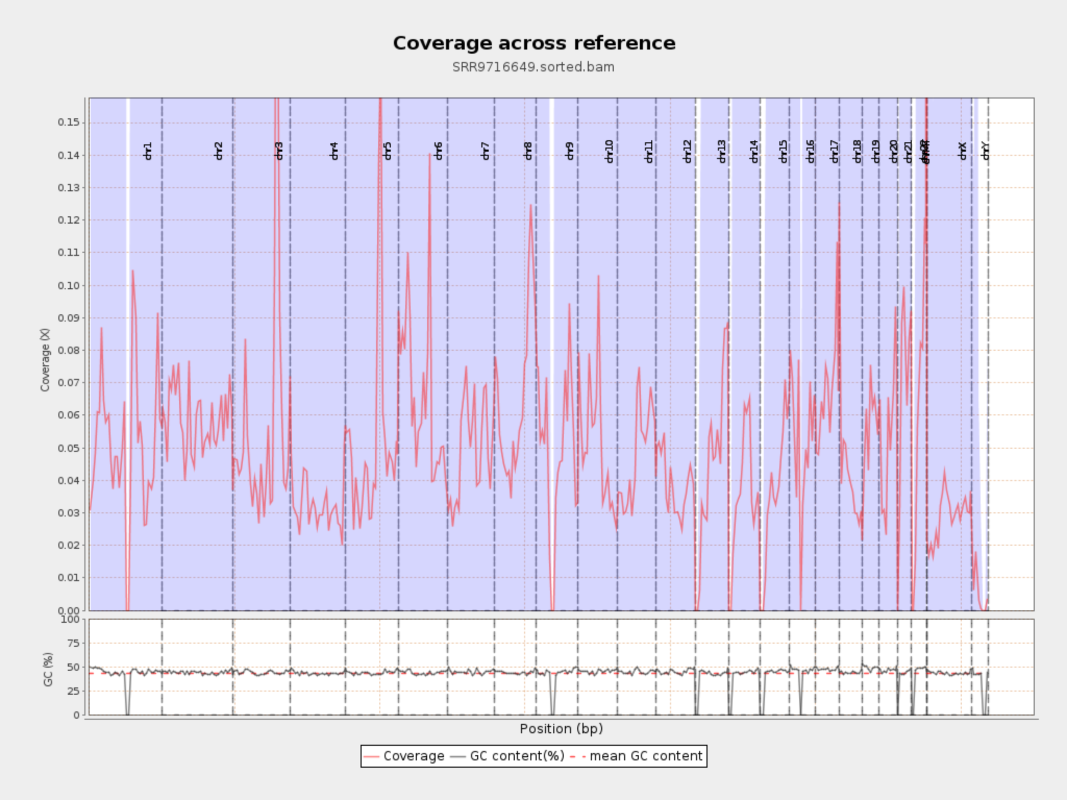
General error rate	0.79%
Mismatches	1,181,732
Insertions	12,977
Mapped reads with at least one insertion	0.64%
Deletions	33,008
Mapped reads with at least one deletion	1.62%
Homopolymer indels	40.09%

2.6. Chromosome stats

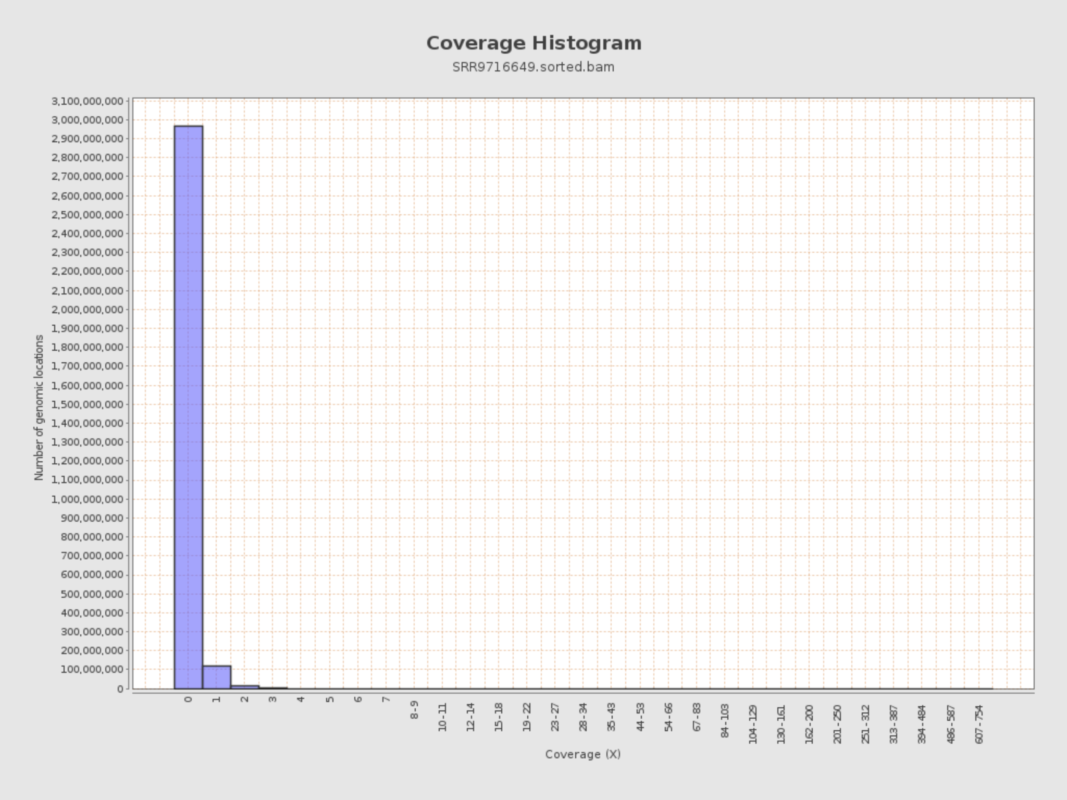
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12641602	0.0507	0.5747
chr2	243199373	14308073	0.0588	0.4854
chr3	198022430	11077896	0.0559	0.2725
chr4	191154276	6095687	0.0319	0.2166
chr5	180915260	9340736	0.0516	0.2572
chr6	171115067	11364287	0.0664	0.3271
chr7	159138663	7940327	0.0499	0.5091

chr8	146364022	9722024	0.0664	0.3949
chr9	141213431	6898385	0.0489	0.3085
chr10	135534747	7074989	0.0522	0.3645
chr11	135006516	6507202	0.0482	0.3074
chr12	133851895	5149389	0.0385	0.2192
chr13	115169878	5198569	0.0451	0.2374
chr14	107349540	3765366	0.0351	0.2289
chr15	102531392	3695317	0.036	0.2128
chr16	90354753	4672394	0.0517	0.2827
chr17	81195210	5541939	0.0683	0.32
chr18	78077248	3286118	0.0421	0.6289
chr19	59128983	3347712	0.0566	0.4701
chr20	63025520	3395552	0.0539	0.286
chr21	48129895	3287336	0.0683	0.3067
chr22	51304566	2976122	0.058	0.2809
chrMT	16571	85519	5.1608	4.1364
chrX	155270560	4486247	0.0289	0.2228
chrY	59373566	329312	0.0055	0.1778

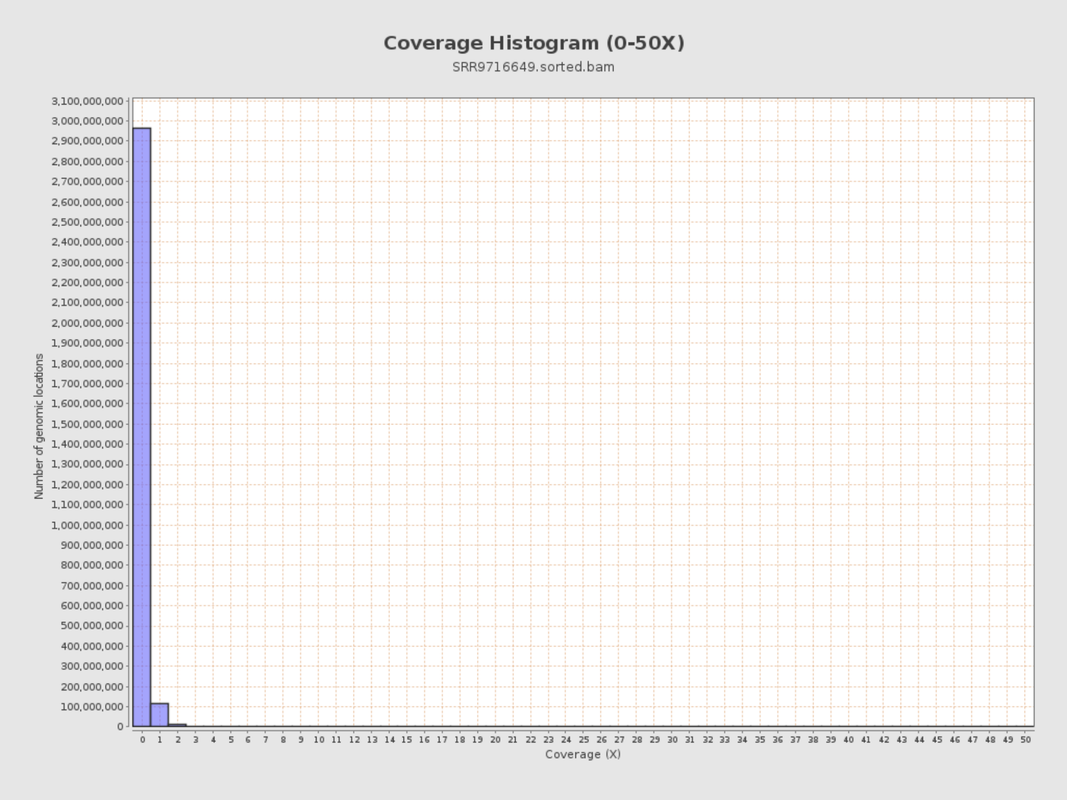
3. Results : Coverage across reference



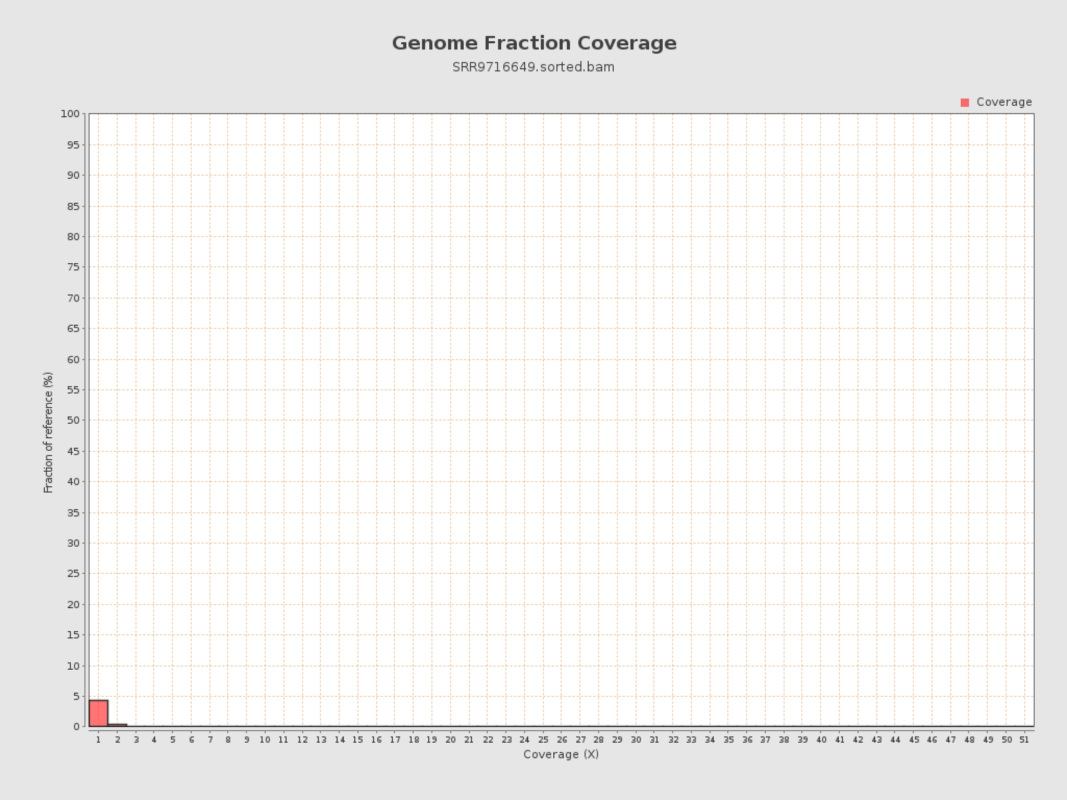
4. Results : Coverage Histogram



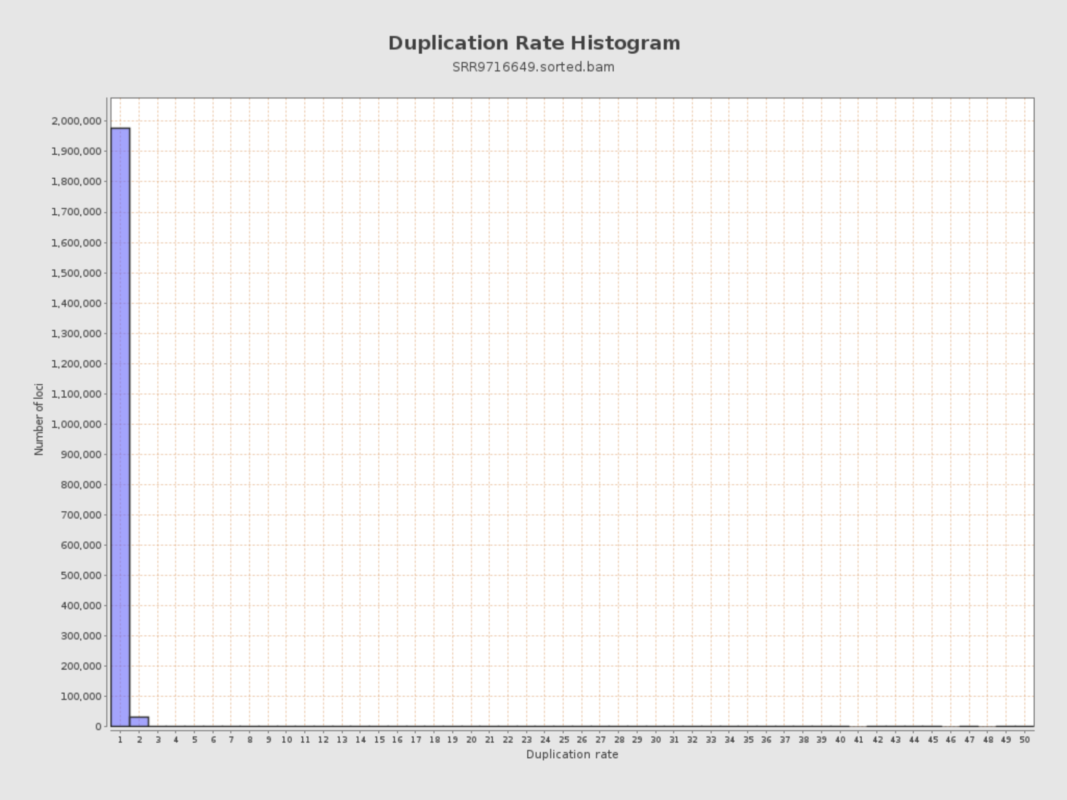
5. Results : Coverage Histogram (0-50X)



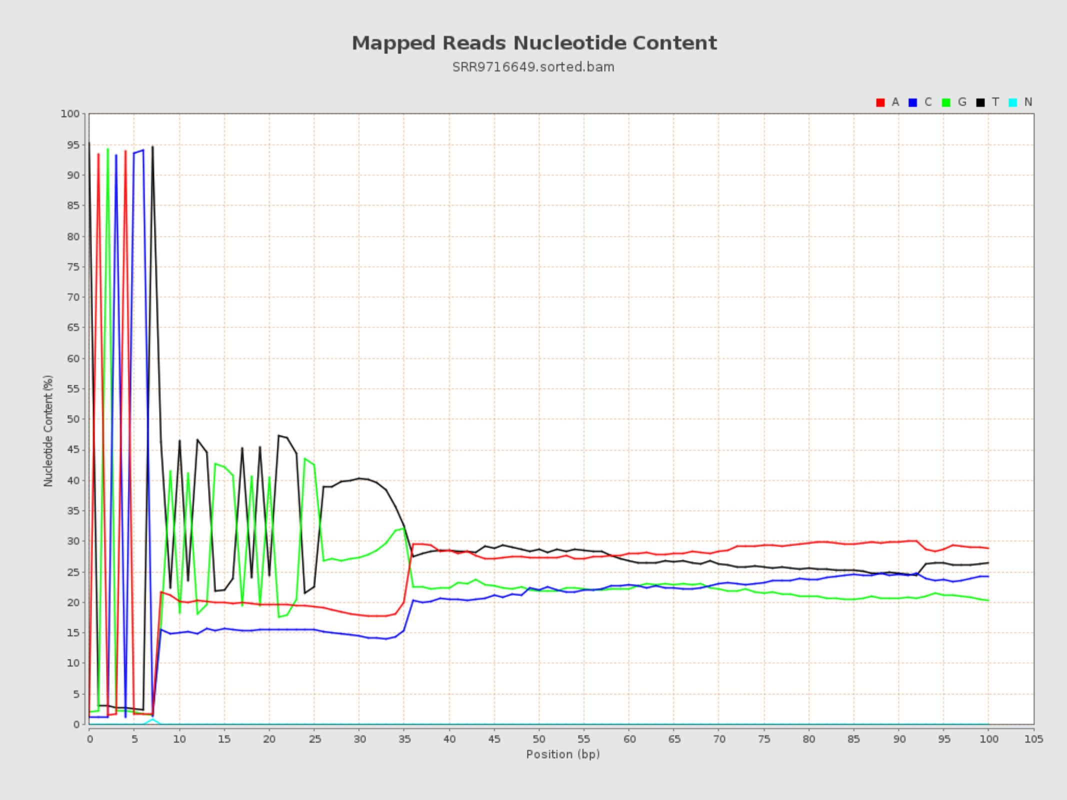
6. Results : Genome Fraction Coverage



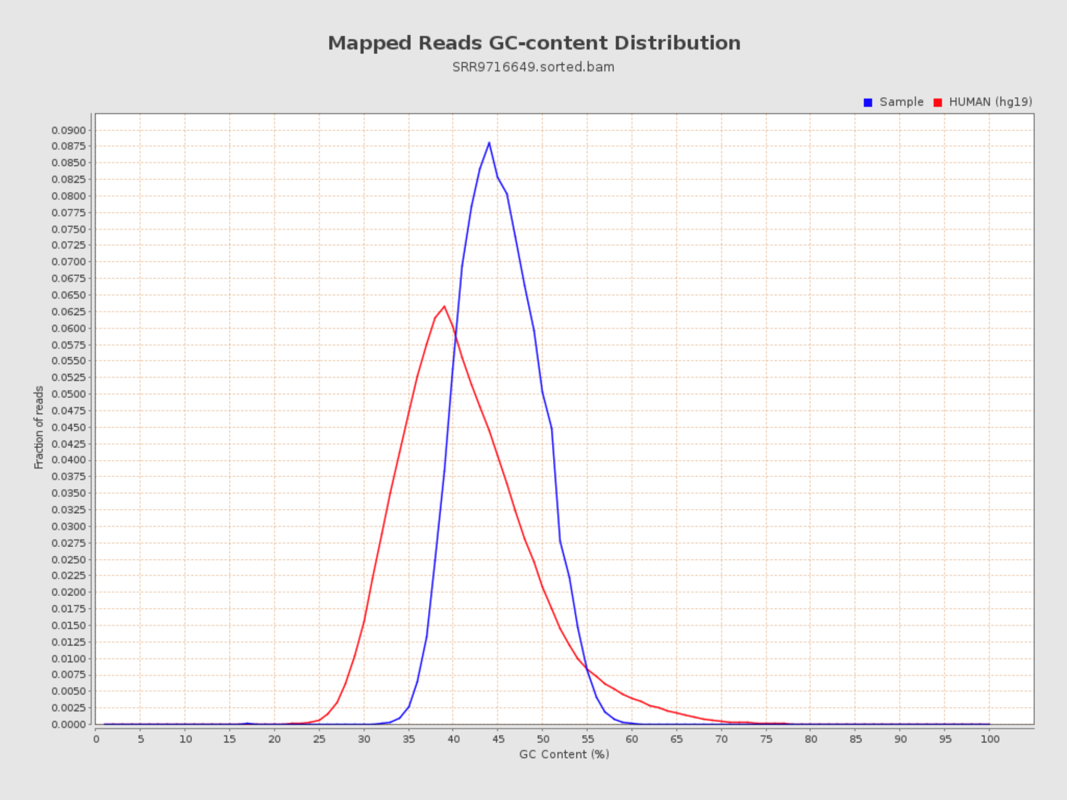
7. Results : Duplication Rate Histogram



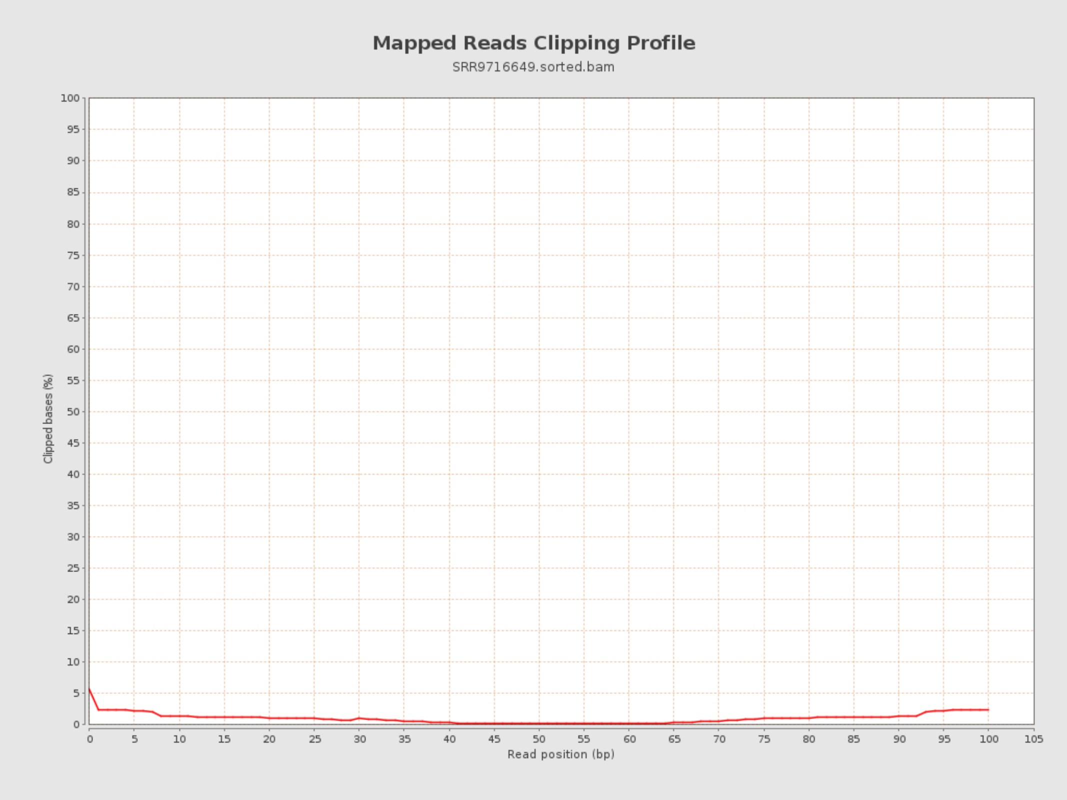
8. Results : Mapped Reads Nucleotide Content



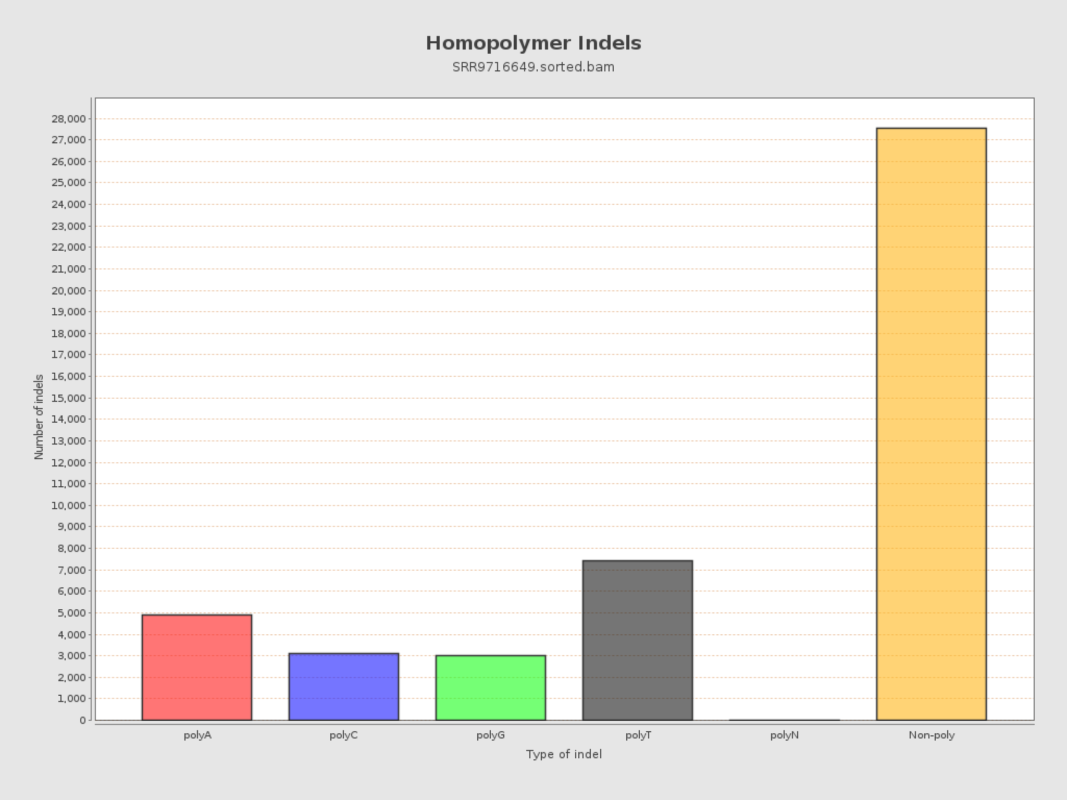
9. Results : Mapped Reads GC-content Distribution



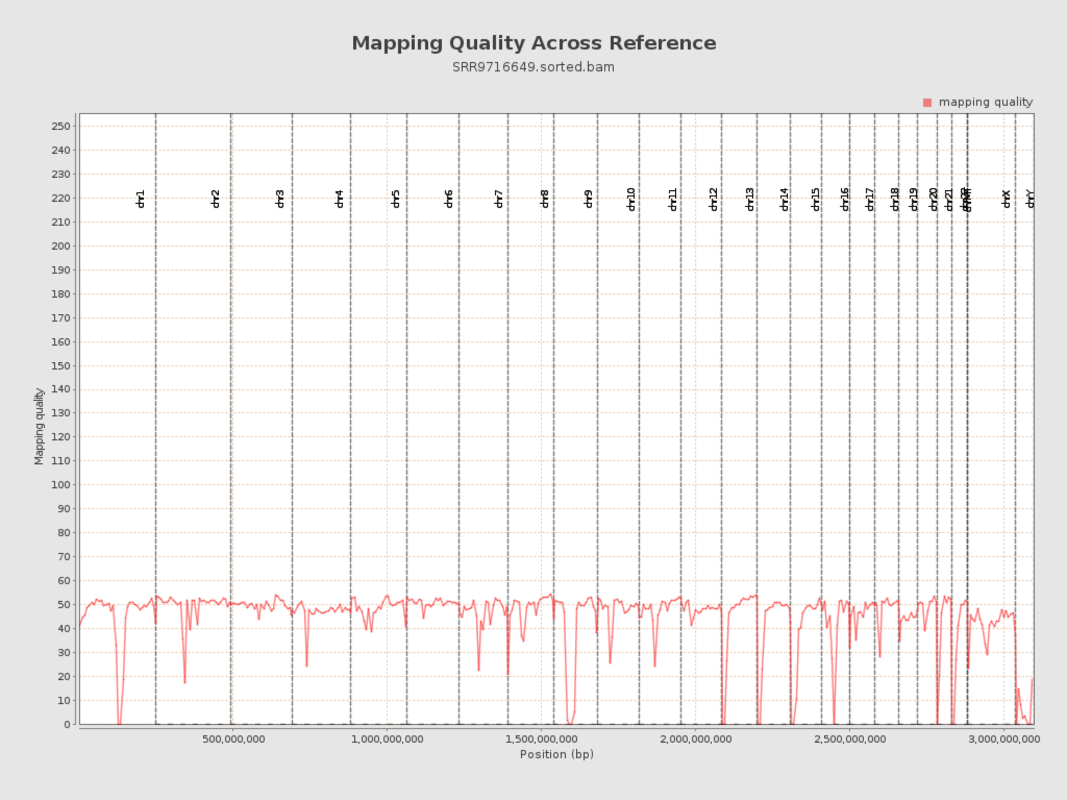
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram