Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 11:37:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716398.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_SRR9716398 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716398.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 11:37:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716398.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,273,620
Mapped reads	1,198,848 / 94.13%
Unmapped reads	74,772 / 5.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,327 / 1.52%
Read min/max/mean length	30 / 101 / 101.56
Duplicated reads (estimated)	46,572 / 3.66%
Duplication rate	2.11%
Clipped reads	1,217,690 / 95.61%

2.2. ACGT Content

Number/percentage of A's	22,909,025 / 24.07%
Number/percentage of C's	18,463,002 / 19.4%
Number/percentage of T's	29,569,402 / 31.07%
Number/percentage of G's	24,236,790 / 25.46%
Number/percentage of N's	5,526 / 0.01%
GC Percentage	44.86%

2.3. Coverage

Mean	0.0308

Standard Deviation	0.4265

2.4. Mapping Quality

Mean Mapping Quality	43.22

2.5. Mismatches and indels

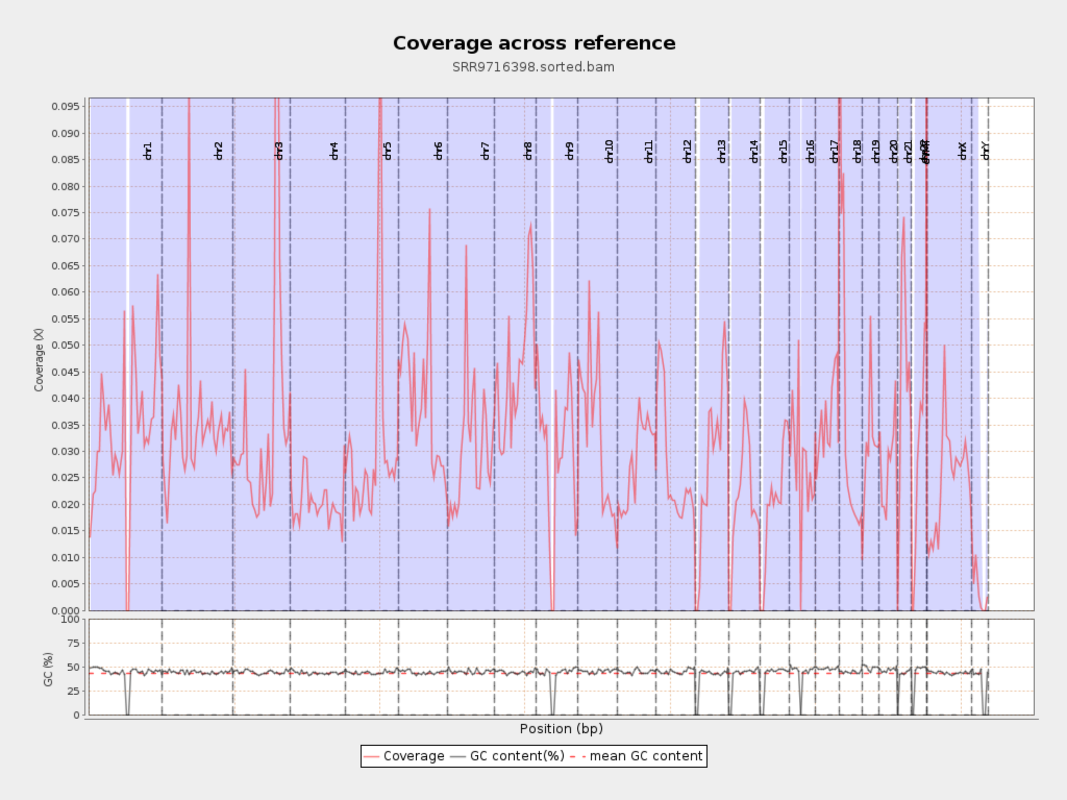
General error rate	0.83%
Mismatches	777,195
Insertions	8,345
Mapped reads with at least one insertion	0.69%
Deletions	23,439
Mapped reads with at least one deletion	1.93%
Homopolymer indels	44.85%

2.6. Chromosome stats

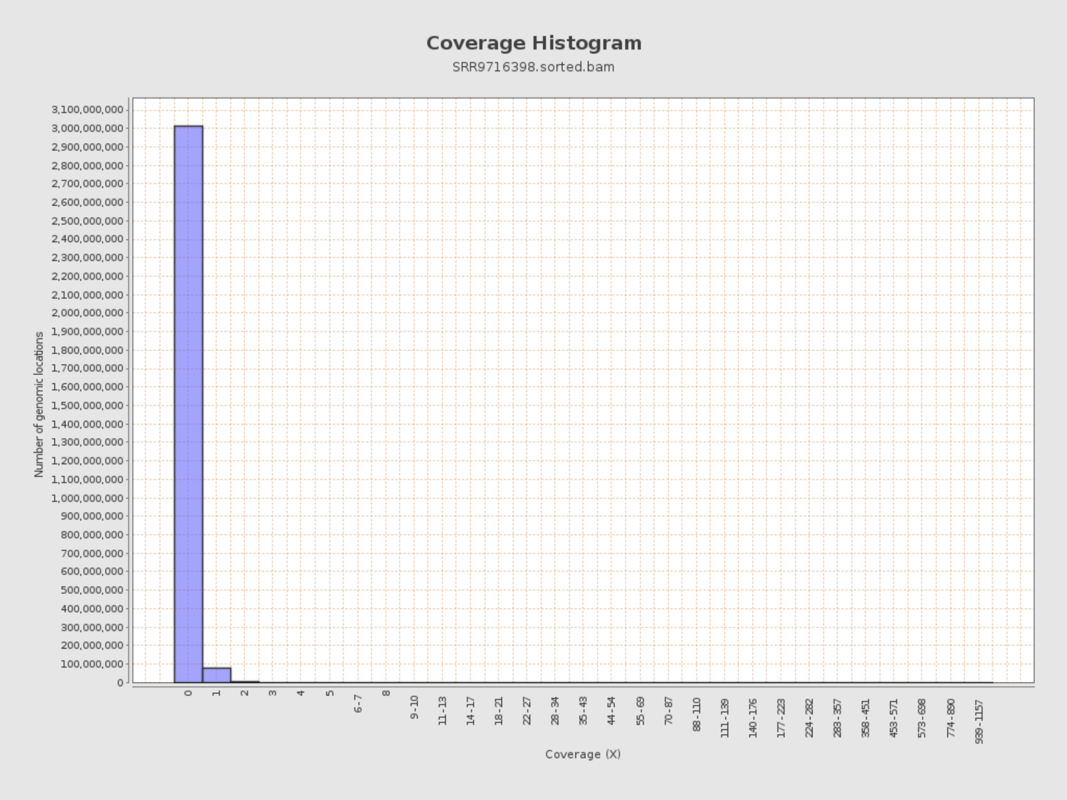
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8362383	0.0336	0.5942
chr2	243199373	8413905	0.0346	0.7887
chr3	198022430	7076203	0.0357	0.2126
chr4	191154276	3863360	0.0202	0.1675
chr5	180915260	5723438	0.0316	0.1991
chr6	171115067	6745949	0.0394	0.2772
chr7	159138663	4901138	0.0308	0.5908

chr8	146364022	6729618	0.046	0.5933
chr9	141213431	4180665	0.0296	0.4146
chr10	135534747	4606319	0.034	0.3521
chr11	135006516	3807749	0.0282	0.2828
chr12	133851895	3587743	0.0268	0.1856
chr13	115169878	3328071	0.0289	0.1855
chr14	107349540	2260502	0.0211	0.2053
chr15	102531392	2084268	0.0203	0.1614
chr16	90354753	2439271	0.027	0.2204
chr17	81195210	2922801	0.036	0.2504
chr18	78077248	2938560	0.0376	0.95
chr19	59128983	1892275	0.032	0.5174
chr20	63025520	1750906	0.0278	0.2311
chr21	48129895	2113365	0.0439	0.2406
chr22	51304566	1417935	0.0276	0.1851
chrMT	16571	2384	0.1439	0.5765
chrX	155270560	3857012	0.0248	0.2524
chrY	59373566	219171	0.0037	0.1064

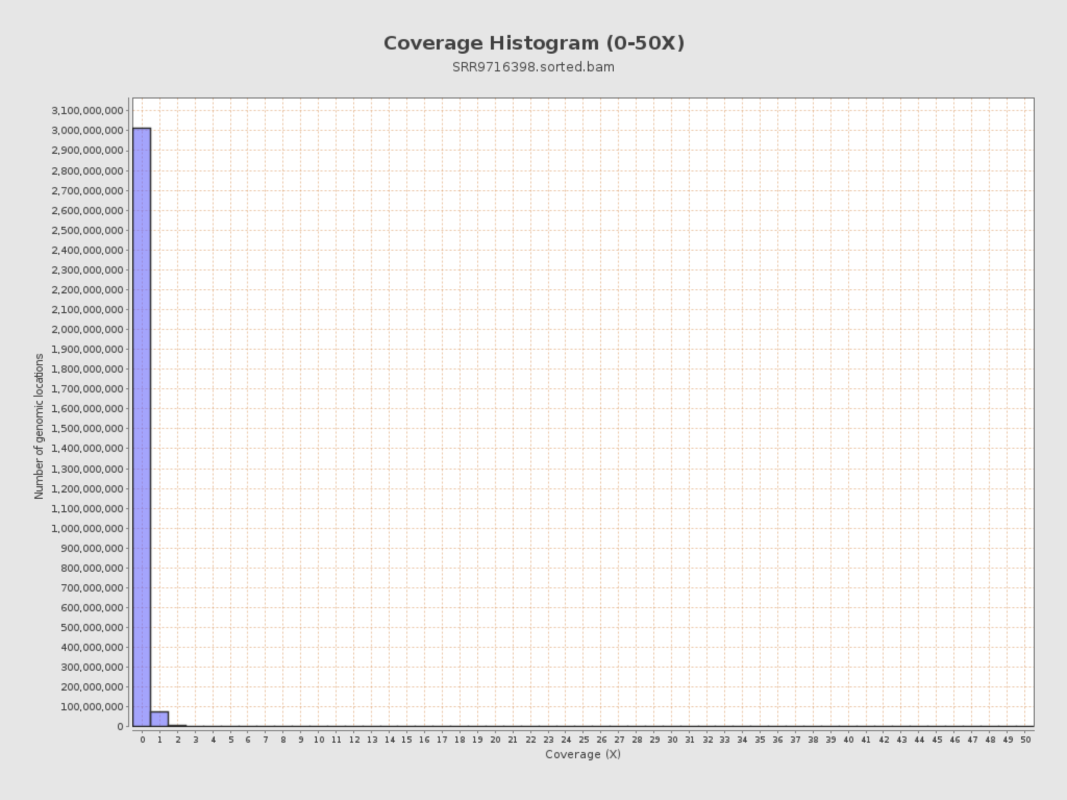
3. Results : Coverage across reference



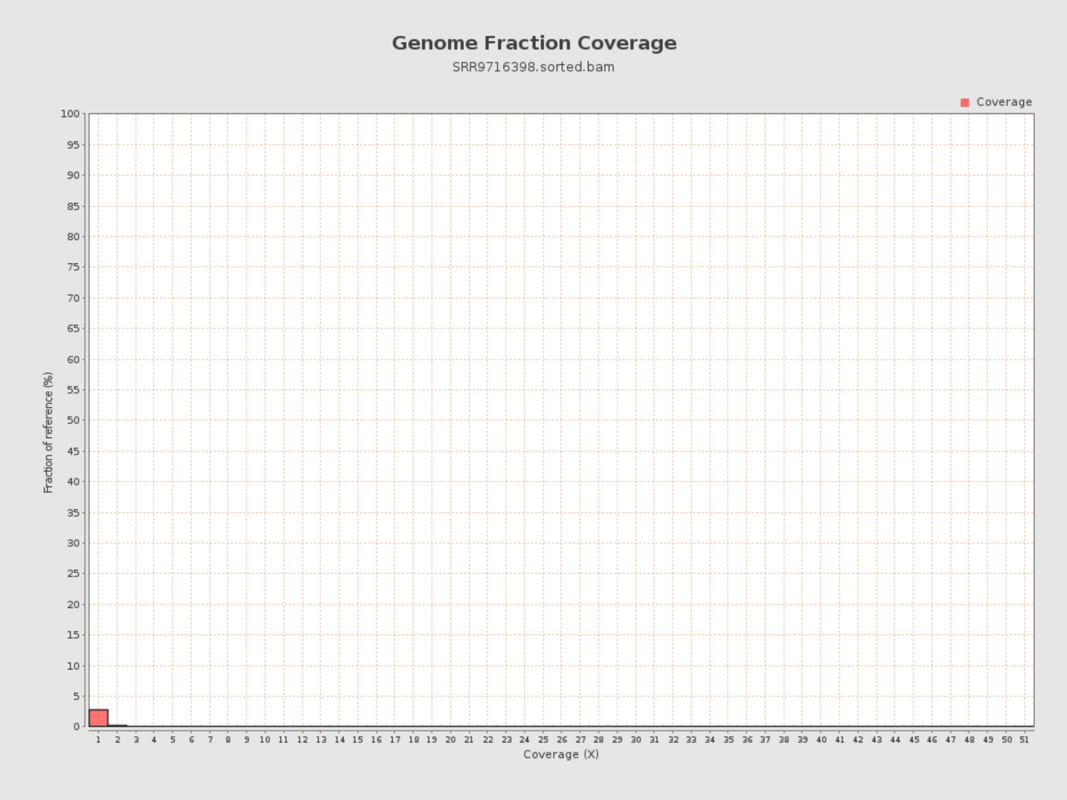
4. Results : Coverage Histogram



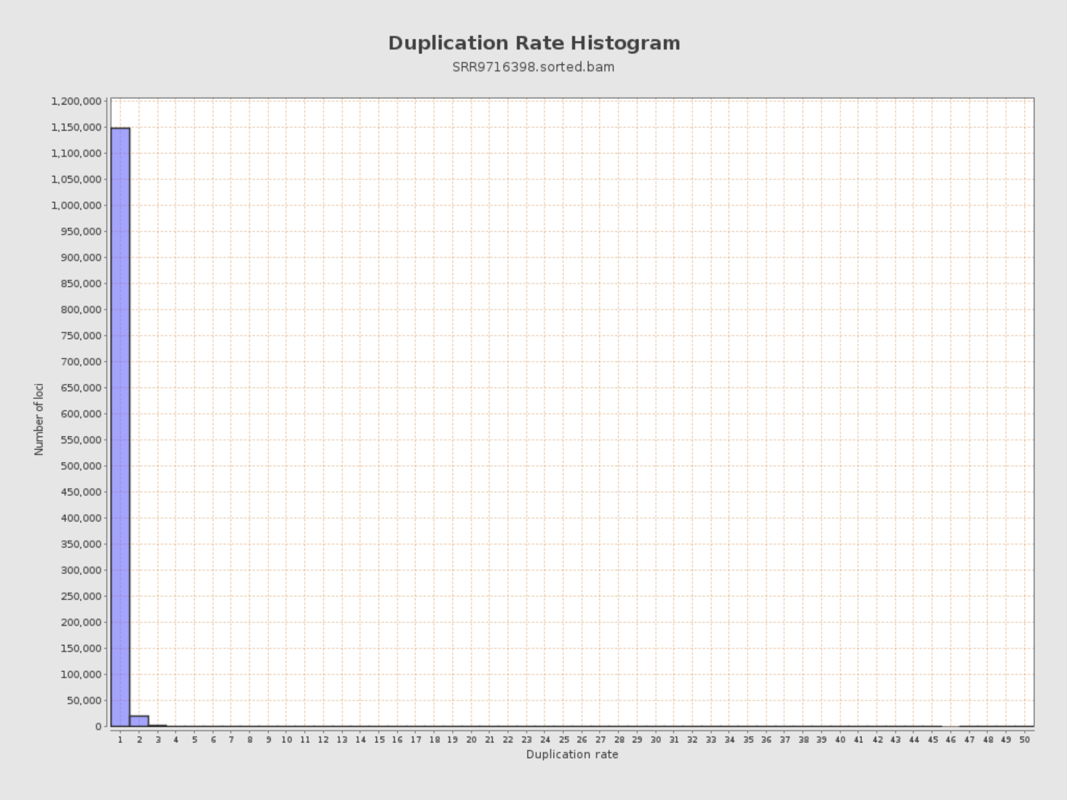
5. Results : Coverage Histogram (0-50X)



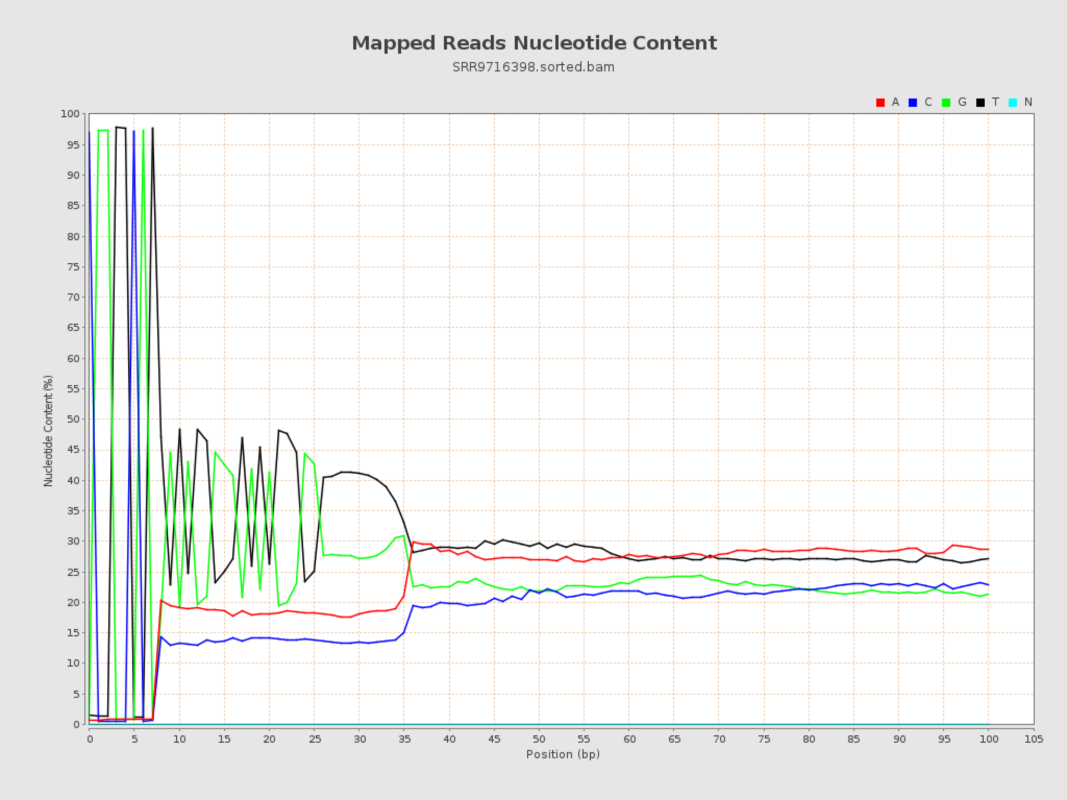
6. Results : Genome Fraction Coverage



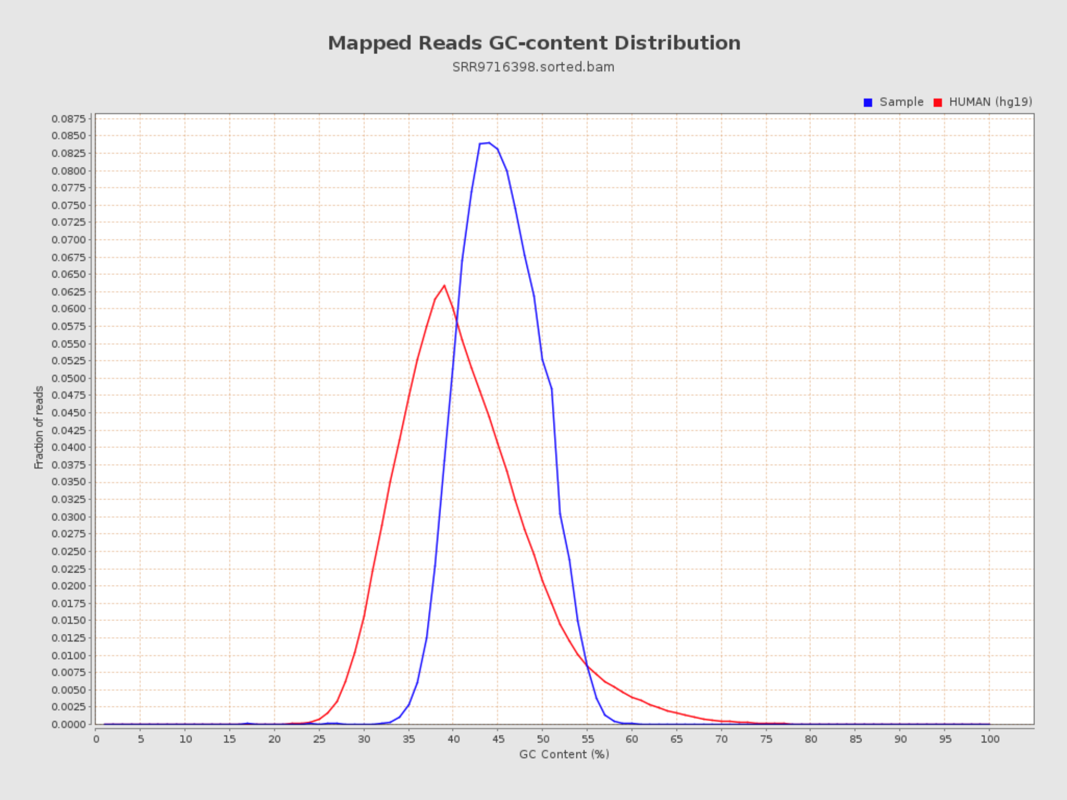
7. Results : Duplication Rate Histogram



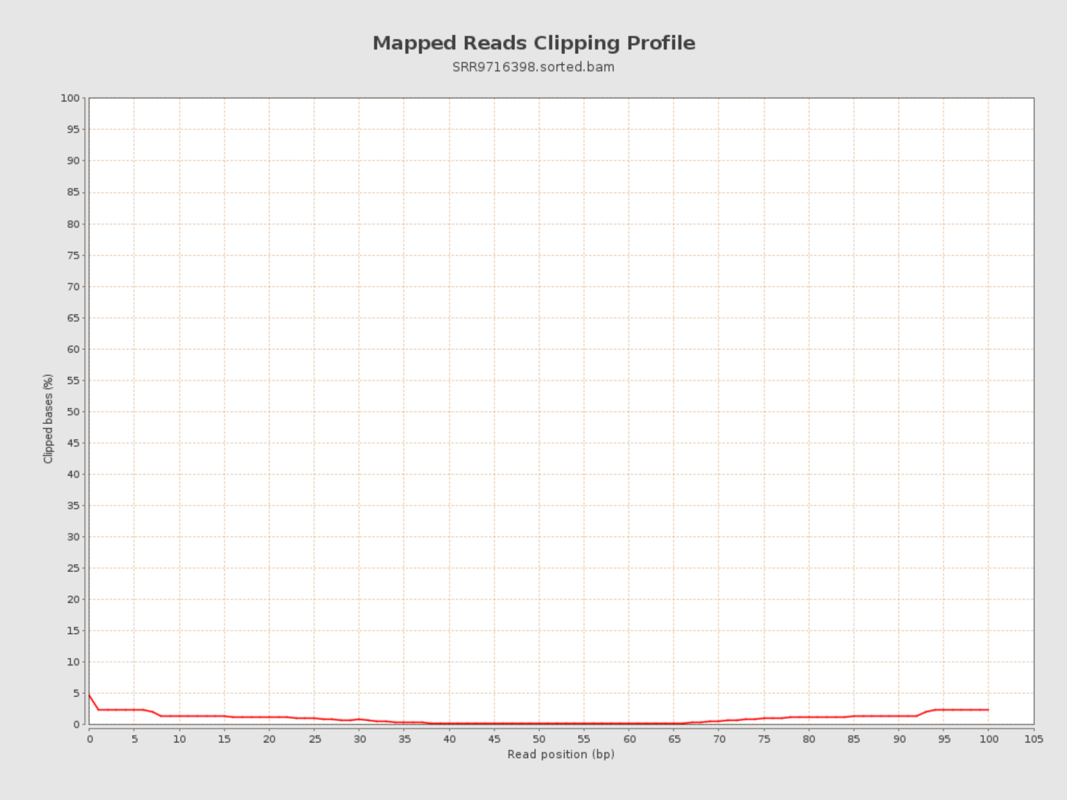
8. Results : Mapped Reads Nucleotide Content



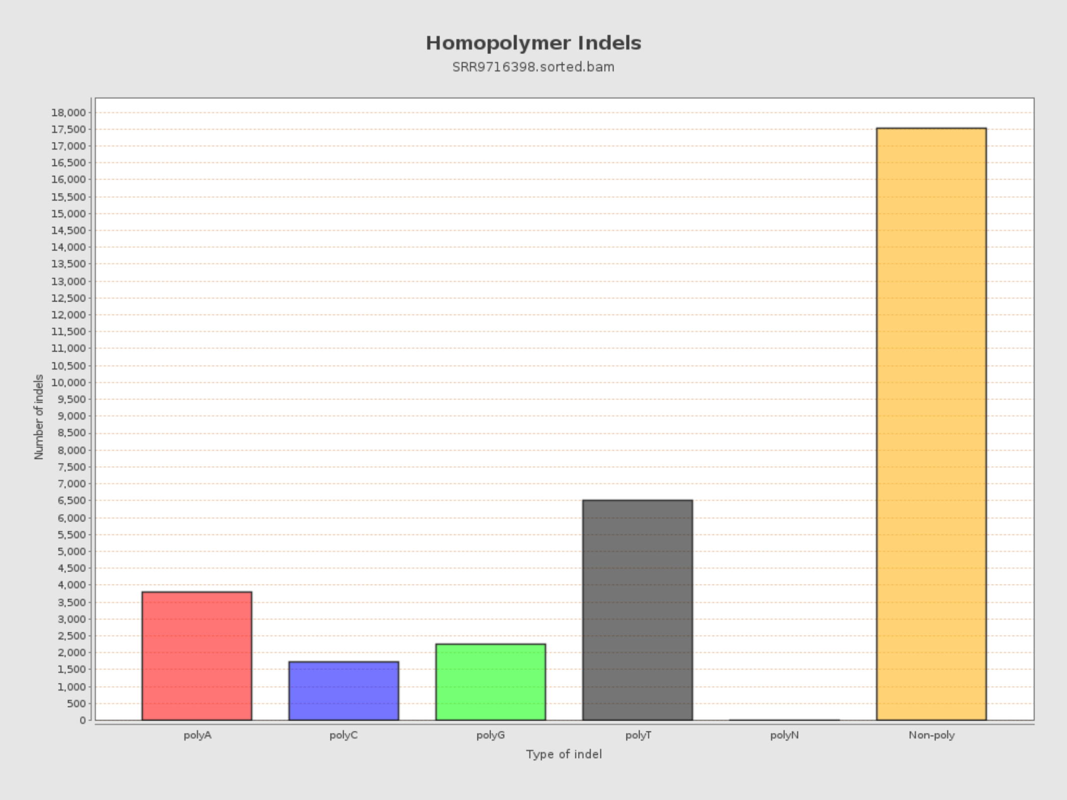
9. Results : Mapped Reads GC-content Distribution



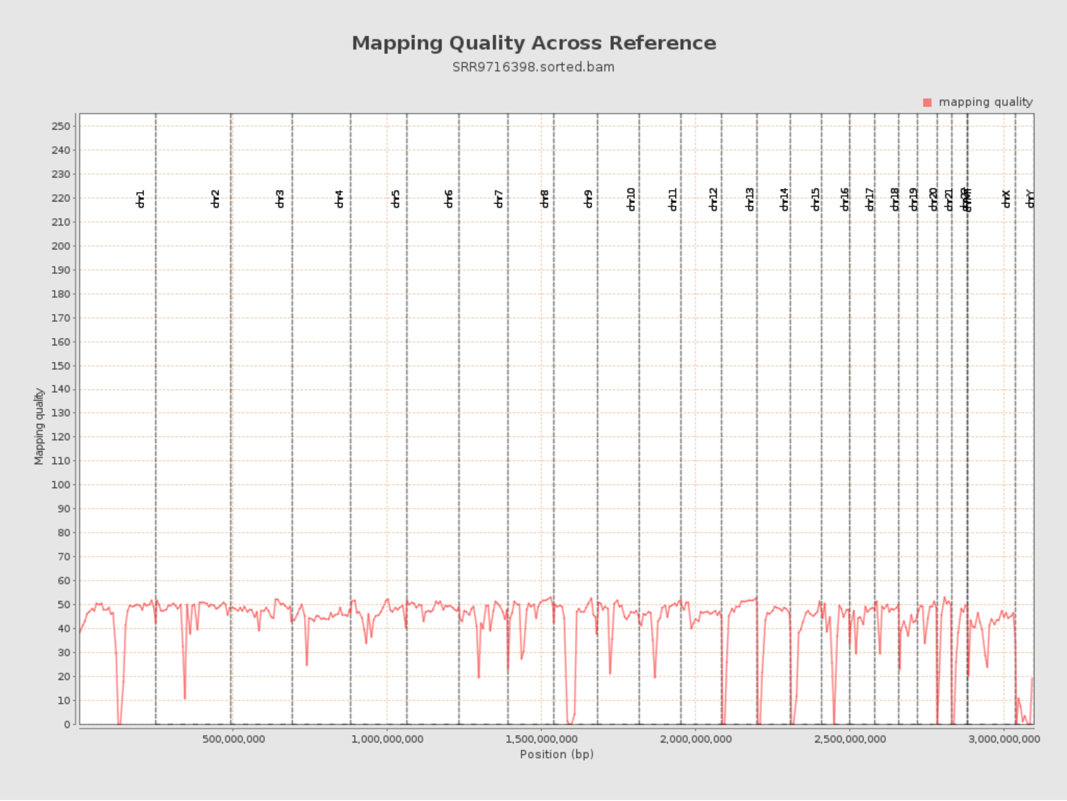
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram