Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 18:21:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716521.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_SRR9716521 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716521.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 18:21:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716521.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,638,997
Mapped reads	1,536,733 / 93.76%
Unmapped reads	102,264 / 6.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	36,445 / 2.22%
Read min/max/mean length	30 / 101 / 101.82
Duplicated reads (estimated)	70,648 / 4.31%
Duplication rate	3.55%
Clipped reads	1,569,482 / 95.76%

2.2. ACGT Content

Number/percentage of A's	29,200,407 / 24.61%
Number/percentage of C's	25,320,163 / 21.34%
Number/percentage of T's	35,713,743 / 30.1%
Number/percentage of G's	28,420,884 / 23.95%
Number/percentage of N's	5,030 / 0%
GC Percentage	45.29%

2.3. Coverage

Mean	0.0383

Standard Deviation	0.3277

2.4. Mapping Quality

Mean Mapping Quality	46.05

2.5. Mismatches and indels

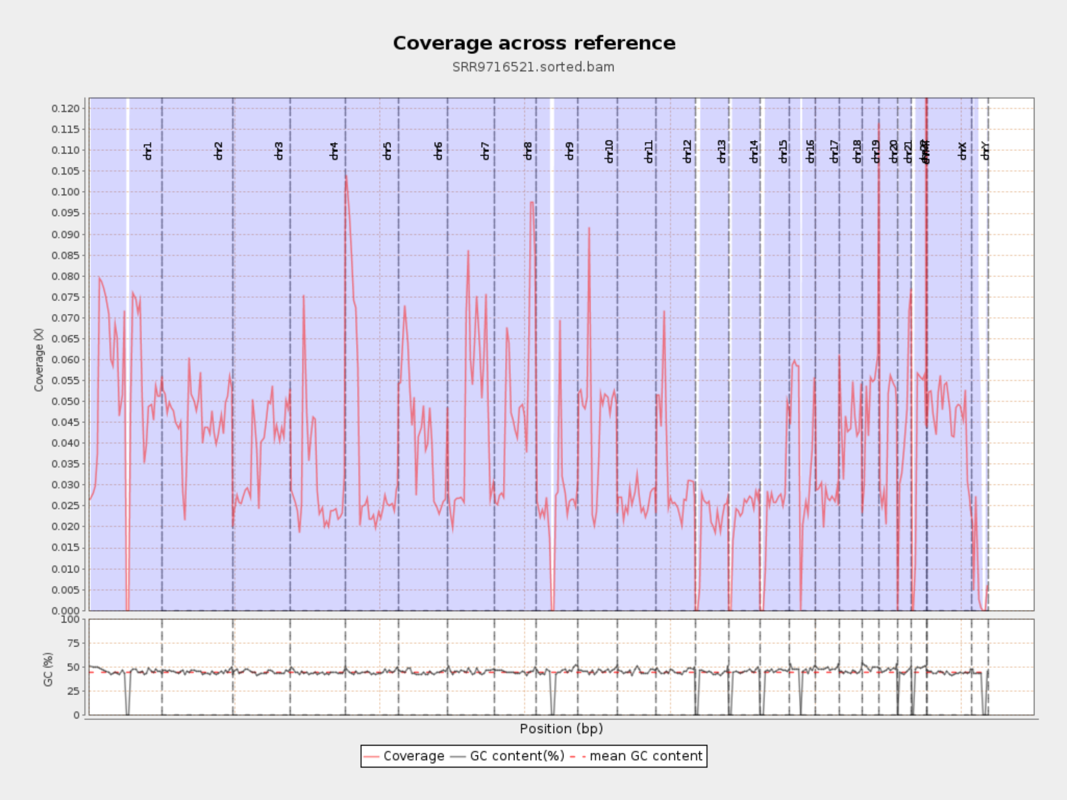
General error rate	0.7%
Mismatches	796,505
Insertions	11,288
Mapped reads with at least one insertion	0.72%
Deletions	24,020
Mapped reads with at least one deletion	1.53%
Homopolymer indels	38.93%

2.6. Chromosome stats

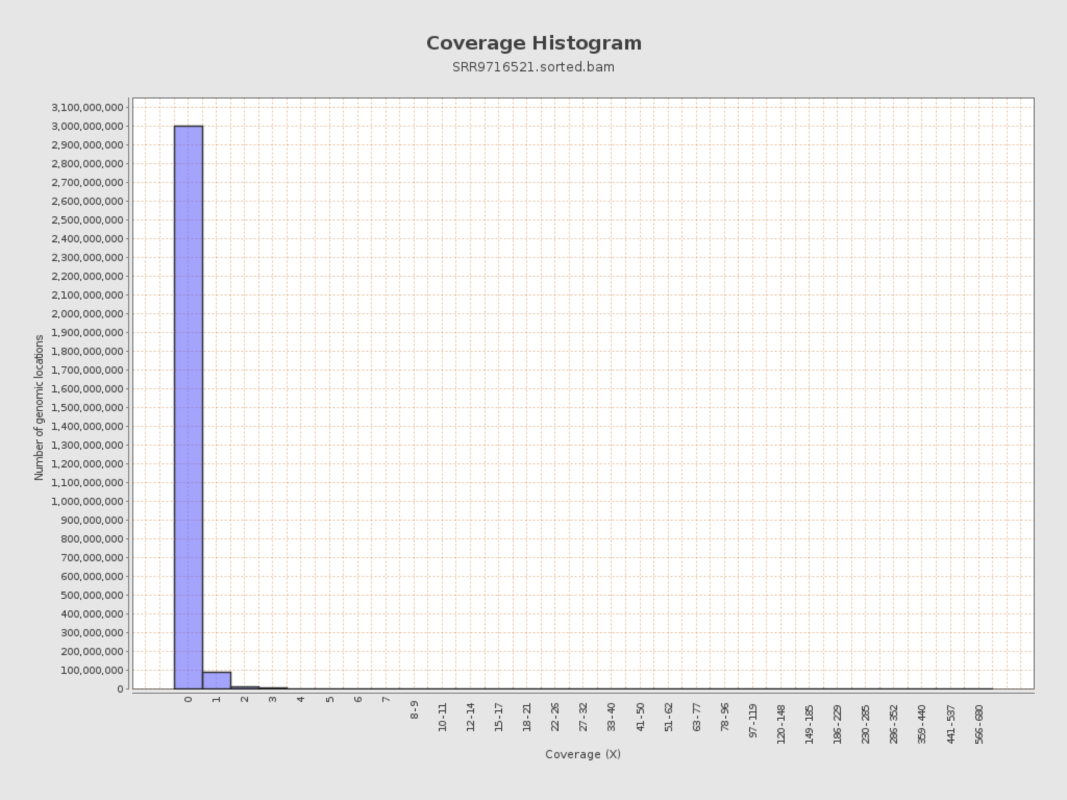
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13219998	0.053	0.616
chr2	243199373	11202863	0.0461	0.3277
chr3	198022430	7600764	0.0384	0.2257
chr4	191154276	5747967	0.0301	0.2954
chr5	180915260	7087244	0.0392	0.2325
chr6	171115067	7289044	0.0426	0.2521
chr7	159138663	7421337	0.0466	0.4261

chr8	146364022	7406866	0.0506	0.3538
chr9	141213431	3538844	0.0251	0.2181
chr10	135534747	6385946	0.0471	0.4592
chr11	135006516	3548213	0.0263	0.246
chr12	133851895	4531169	0.0339	0.2122
chr13	115169878	2277831	0.0198	0.1585
chr14	107349540	2333778	0.0217	0.1823
chr15	102531392	2463562	0.024	0.1764
chr16	90354753	3575198	0.0396	0.2439
chr17	81195210	2213412	0.0273	0.2123
chr18	78077248	3537534	0.0453	0.3564
chr19	59128983	3038412	0.0514	0.4634
chr20	63025520	2570388	0.0408	0.2462
chr21	48129895	2089007	0.0434	0.293
chr22	51304566	1911117	0.0373	0.2297
chrMT	16571	64380	3.8851	3.0826
chrX	155270560	7225690	0.0465	0.2618
chrY	59373566	428872	0.0072	0.2639

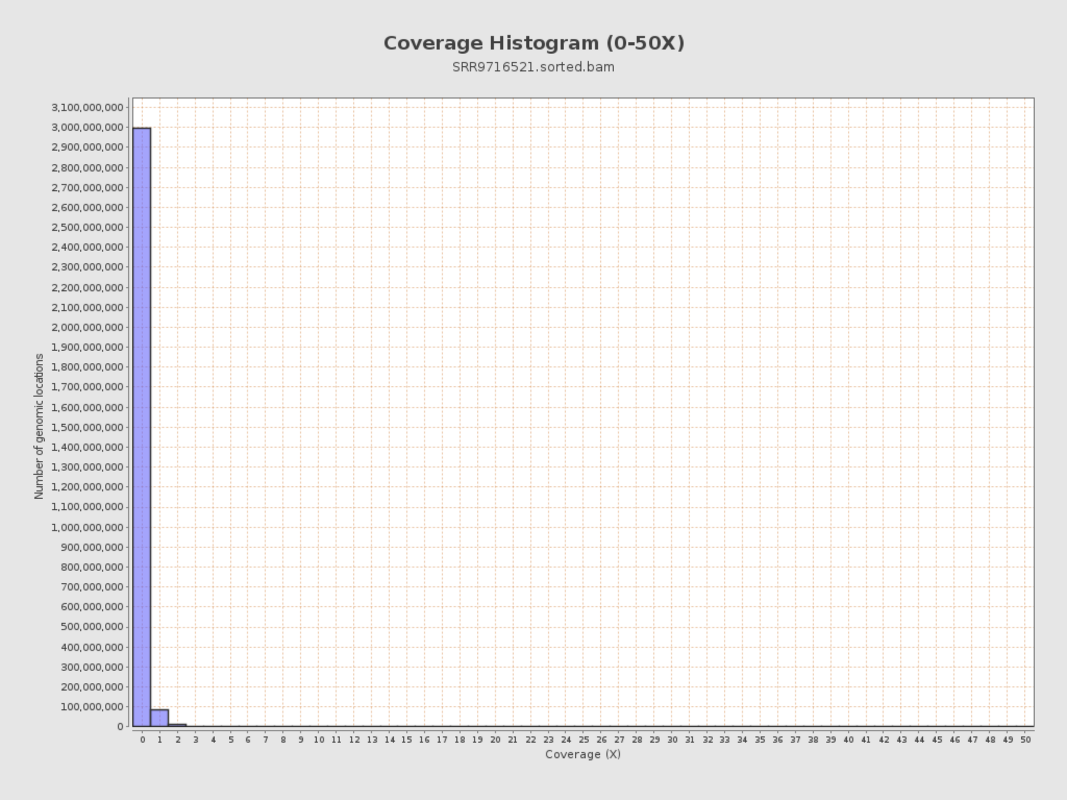
3. Results : Coverage across reference



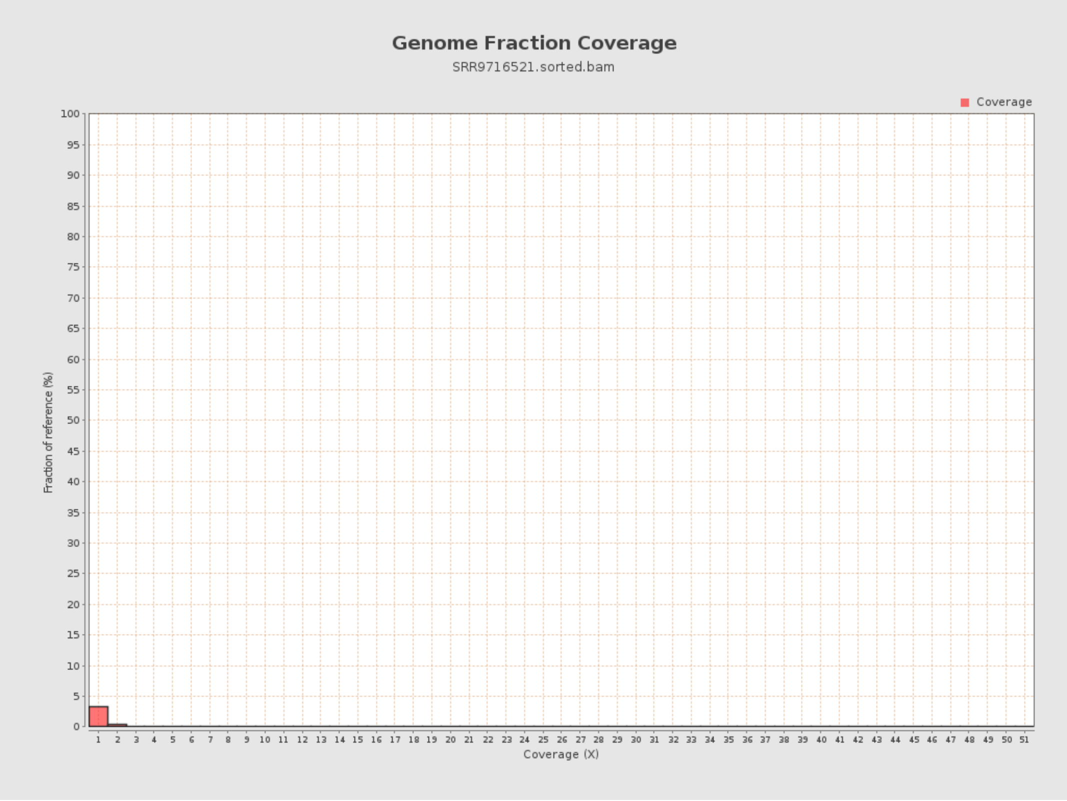
4. Results : Coverage Histogram



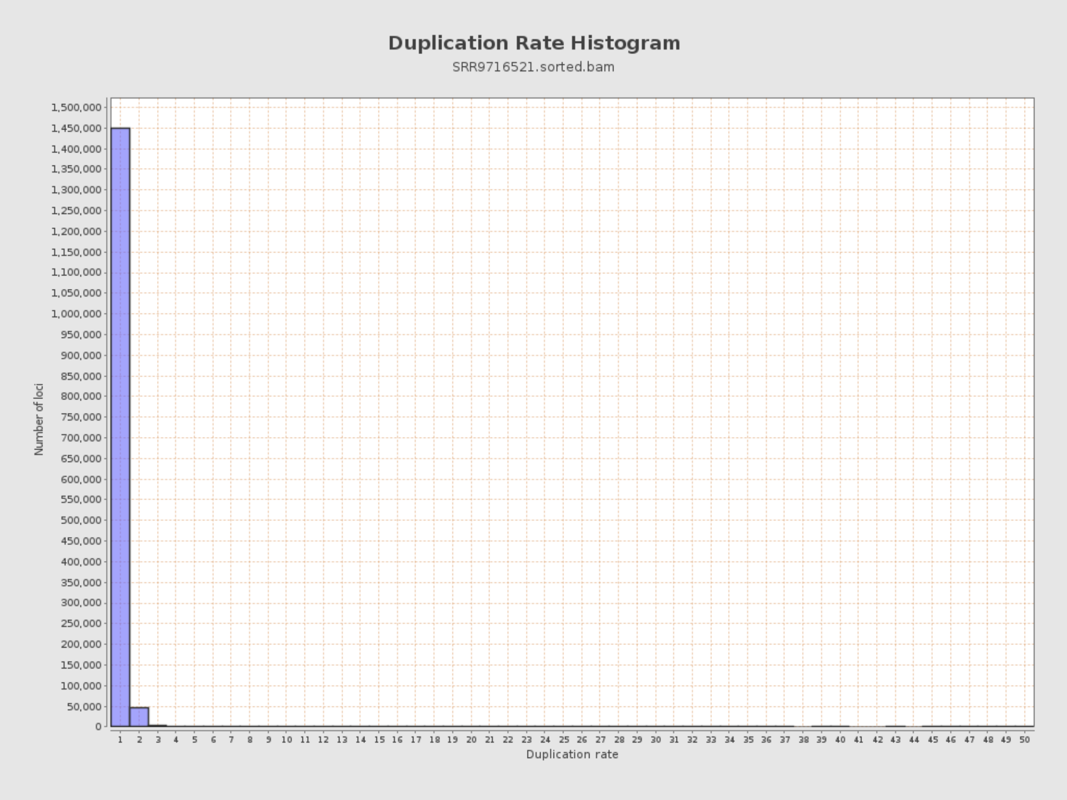
5. Results : Coverage Histogram (0-50X)



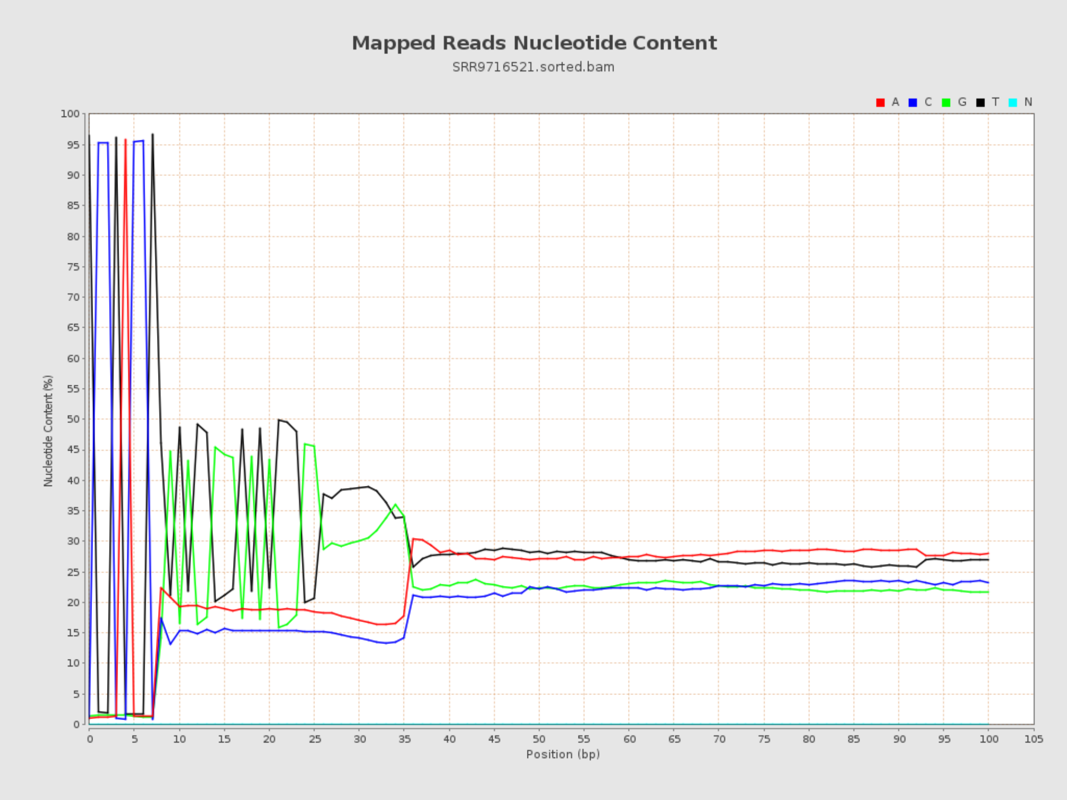
6. Results : Genome Fraction Coverage



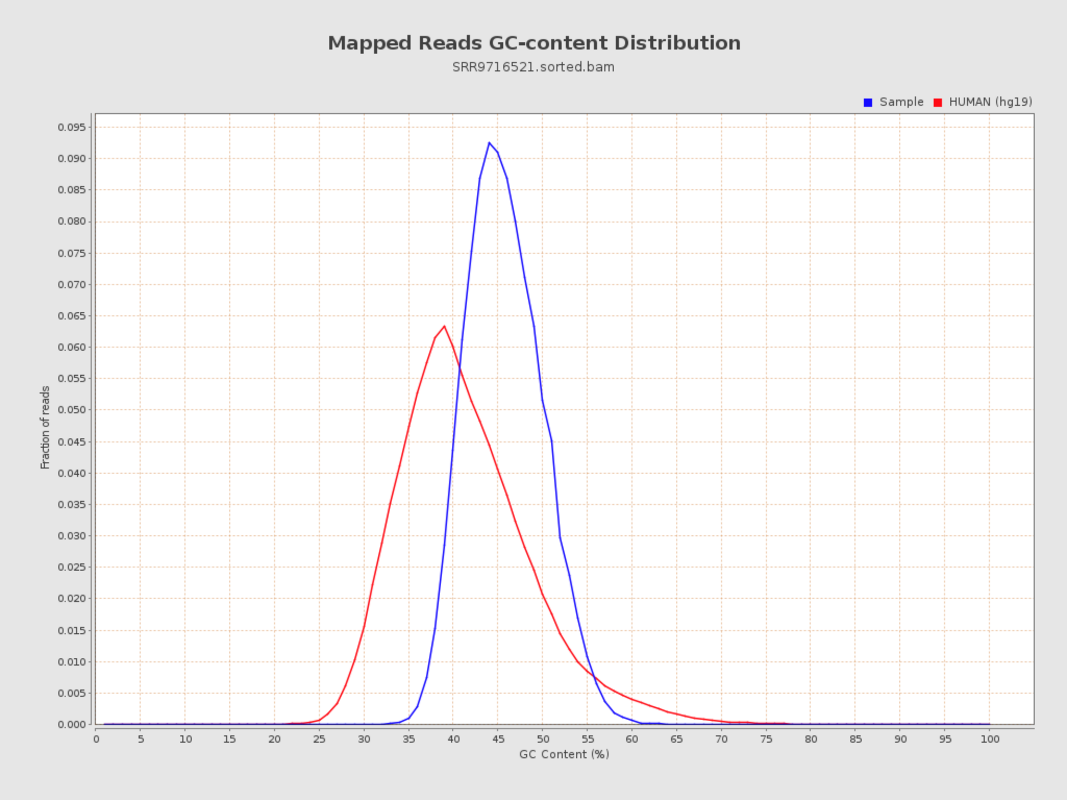
7. Results : Duplication Rate Histogram



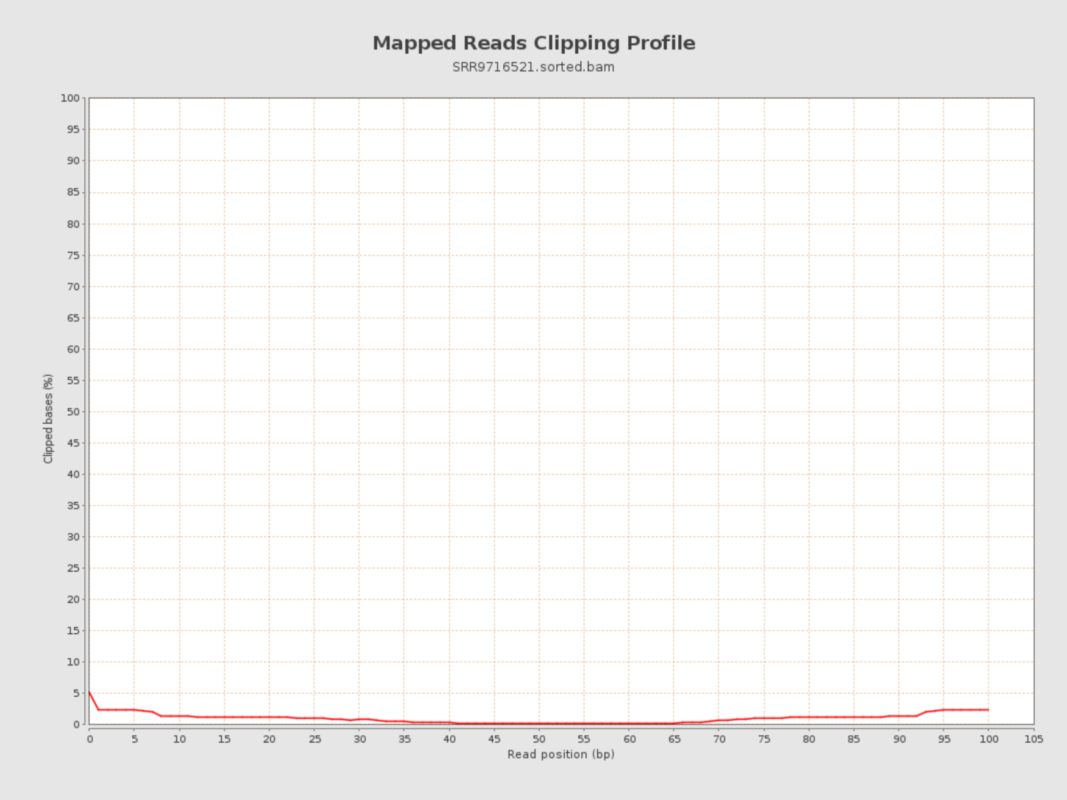
8. Results : Mapped Reads Nucleotide Content



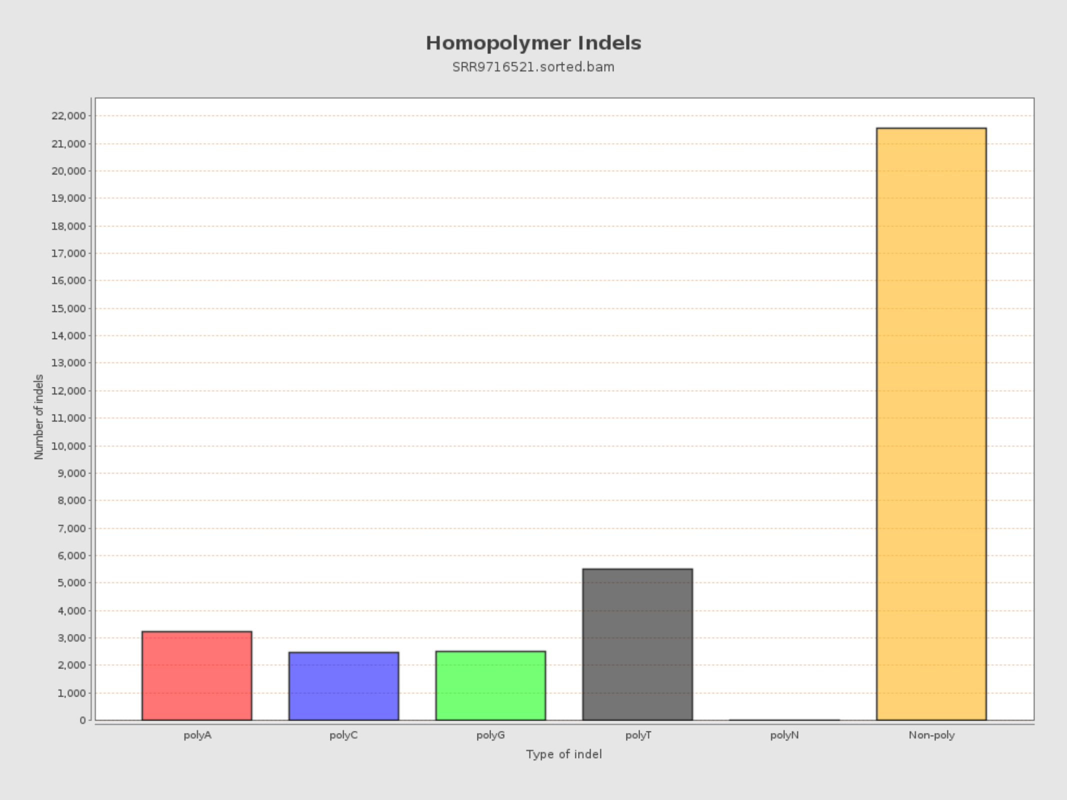
9. Results : Mapped Reads GC-content Distribution



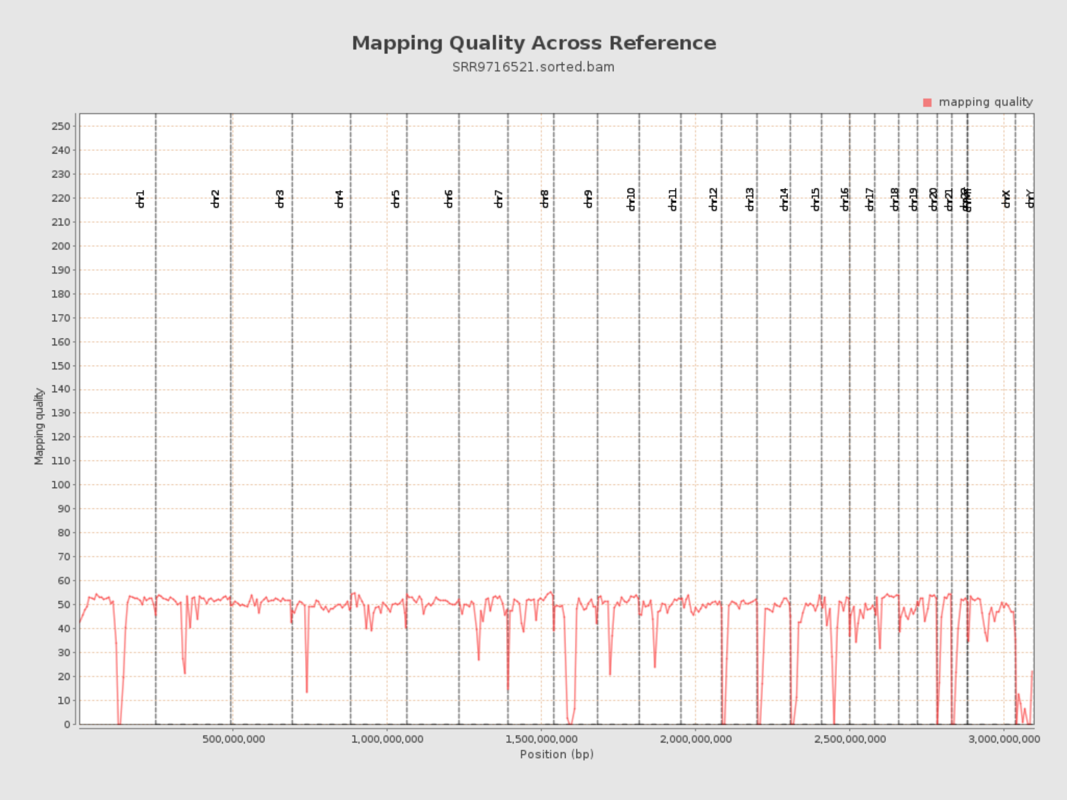
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram