Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 13:15:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716811.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_SRR9716811 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716811.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 13:15:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716811.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,454,739
Mapped reads	1,306,634 / 89.82%
Unmapped reads	148,105 / 10.18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,930 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	43,079 / 2.96%
Duplication rate	2.48%
Clipped reads	1,309,049 / 89.99%

2.2. ACGT Content

Number/percentage of A's	18,217,552 / 24.02%
Number/percentage of C's	14,123,556 / 18.62%
Number/percentage of T's	24,415,938 / 32.2%
Number/percentage of G's	19,074,801 / 25.15%
Number/percentage of N's	2,107 / 0%
GC Percentage	43.78%

2.3. Coverage

Mean	0.0245

Standard Deviation	0.2352

2.4. Mapping Quality

Mean Mapping Quality	44.97

2.5. Mismatches and indels

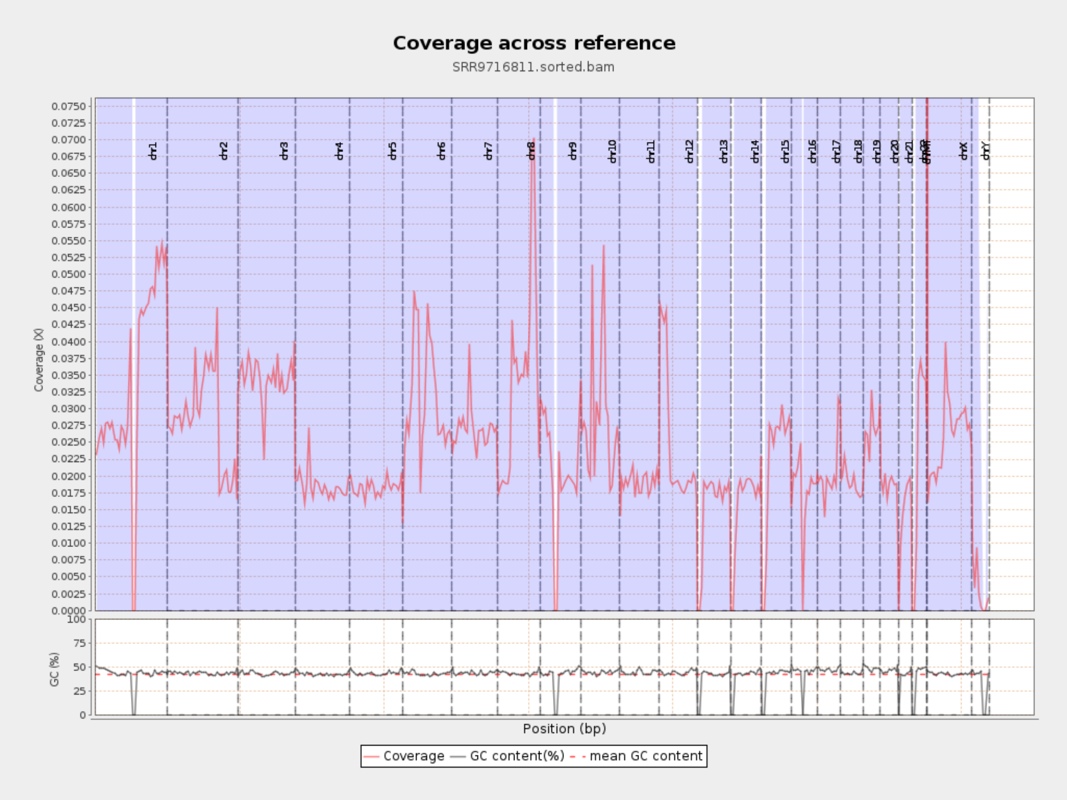
General error rate	0.5%
Mismatches	374,046
Insertions	4,926
Mapped reads with at least one insertion	0.38%
Deletions	13,878
Mapped reads with at least one deletion	1.06%
Homopolymer indels	42.96%

2.6. Chromosome stats

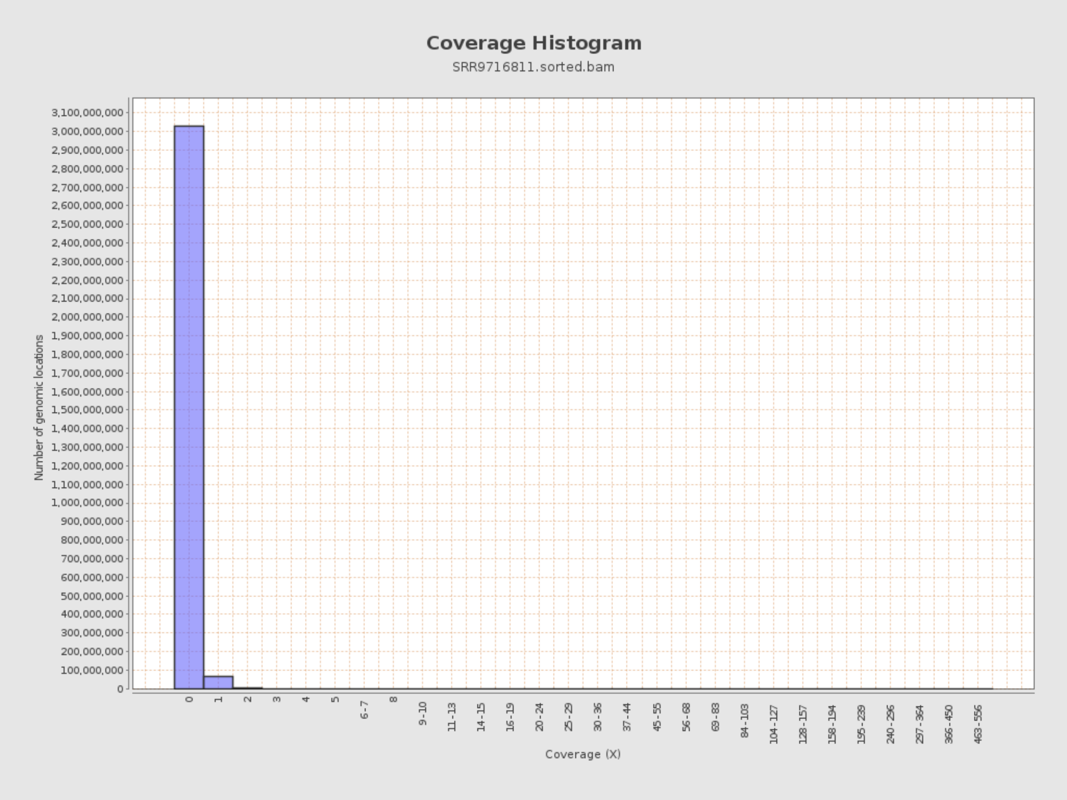
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8523839	0.0342	0.4237
chr2	243199373	6904140	0.0284	0.2985
chr3	198022430	6813283	0.0344	0.2014
chr4	191154276	3536940	0.0185	0.1545
chr5	180915260	3307711	0.0183	0.1473
chr6	171115067	5370457	0.0314	0.248
chr7	159138663	4319098	0.0271	0.2813

chr8	146364022	5022069	0.0343	0.223
chr9	141213431	2864386	0.0203	0.1938
chr10	135534747	3933502	0.029	0.2444
chr11	135006516	2566980	0.019	0.1813
chr12	133851895	3376998	0.0252	0.1748
chr13	115169878	1748110	0.0152	0.1362
chr14	107349540	1663617	0.0155	0.1428
chr15	102531392	2255043	0.022	0.1621
chr16	90354753	1573490	0.0174	0.1605
chr17	81195210	1660965	0.0205	0.1589
chr18	78077248	1478849	0.0189	0.3476
chr19	59128983	1580604	0.0267	0.2906
chr20	63025520	1167975	0.0185	0.1483
chr21	48129895	700687	0.0146	0.1387
chr22	51304566	1218232	0.0237	0.1664
chrMT	16571	31516	1.9019	1.7377
chrX	155270560	4055212	0.0261	0.1942
chrY	59373566	182104	0.0031	0.0776

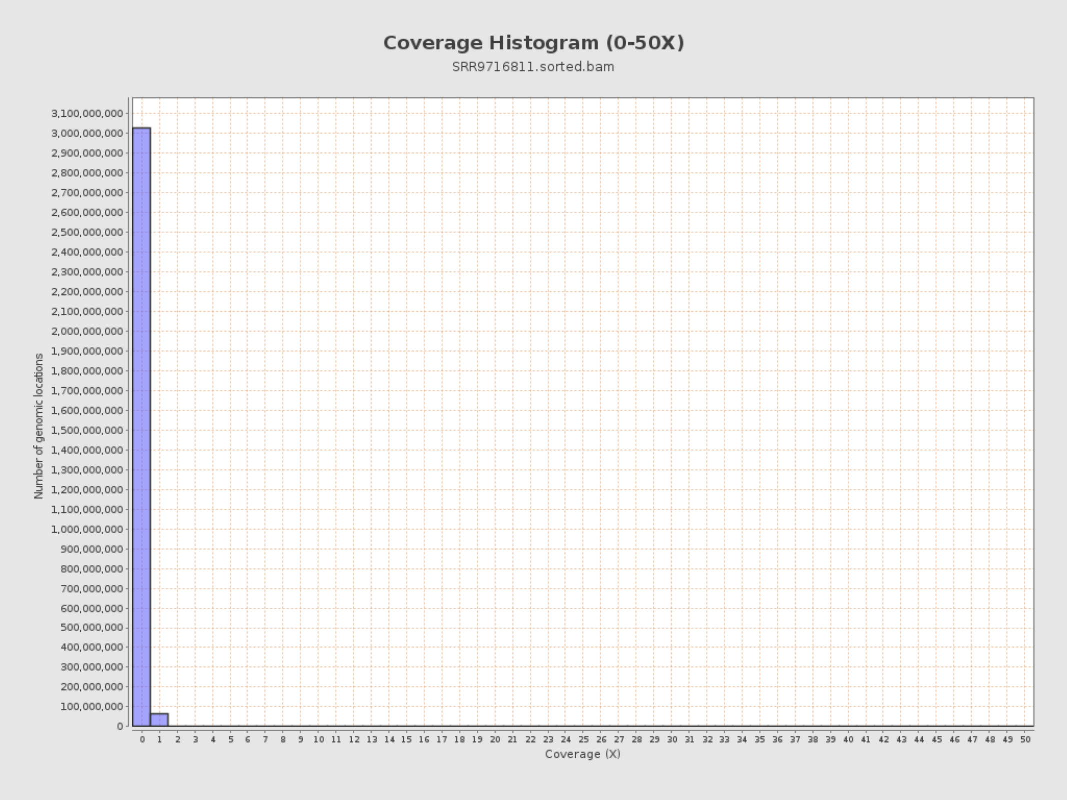
3. Results : Coverage across reference



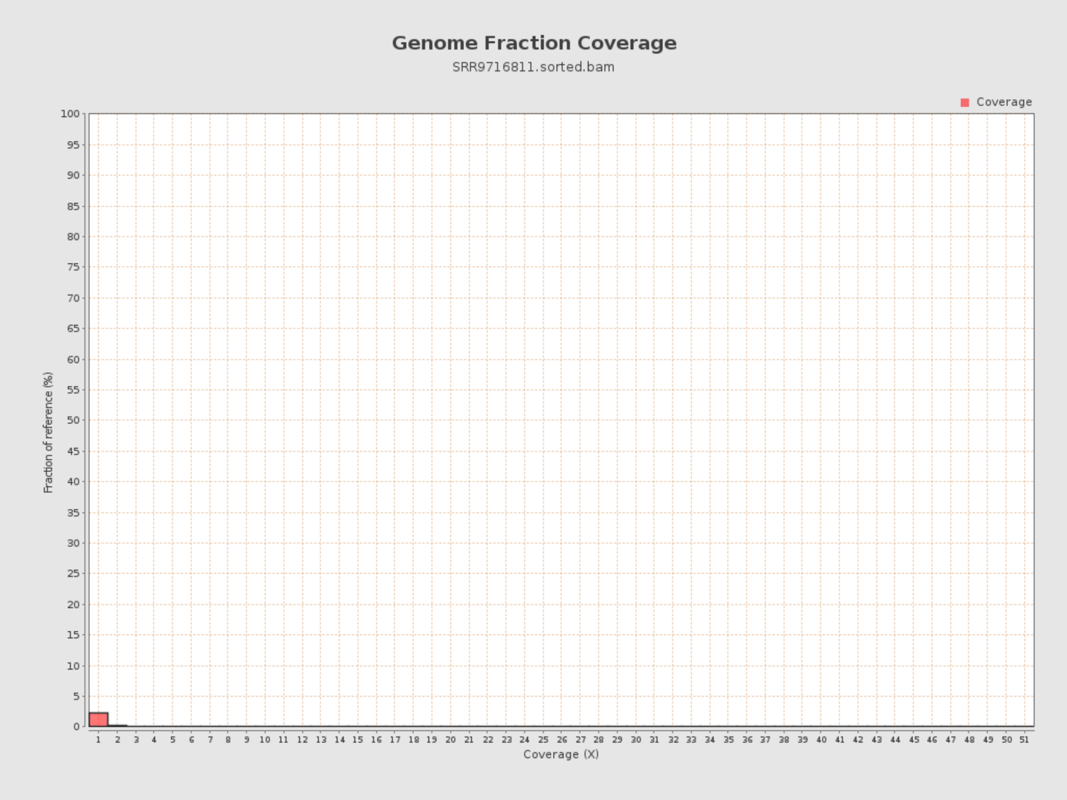
4. Results : Coverage Histogram



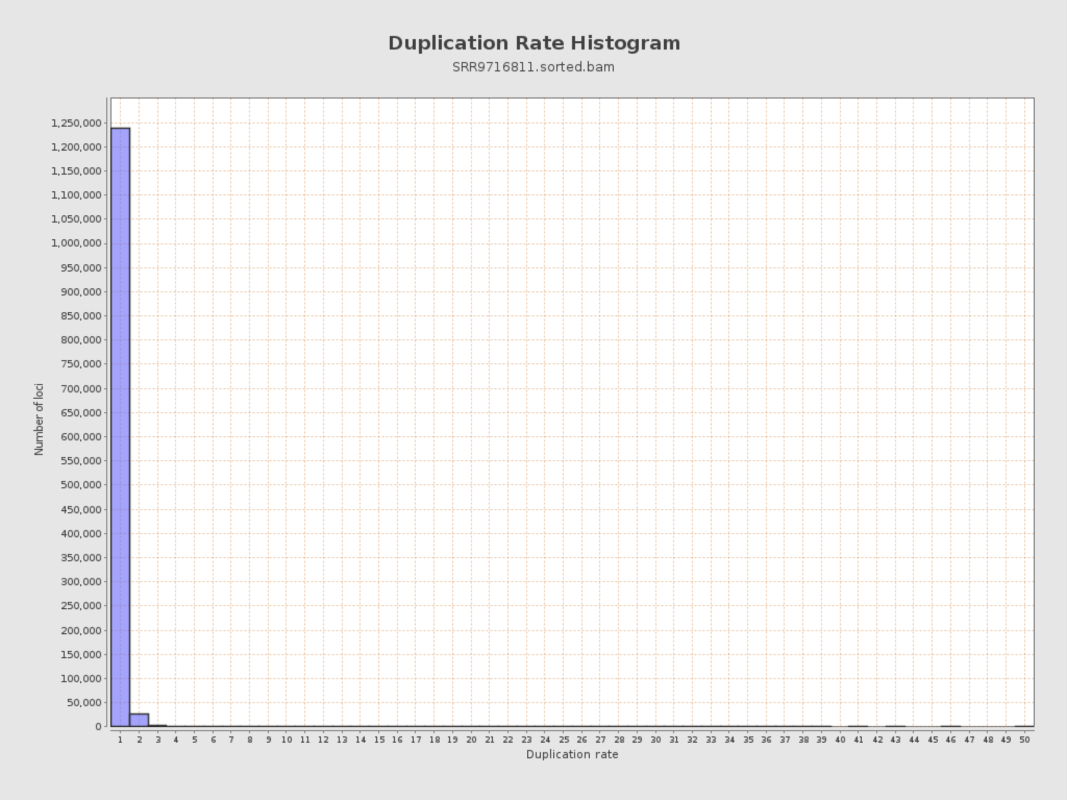
5. Results : Coverage Histogram (0-50X)



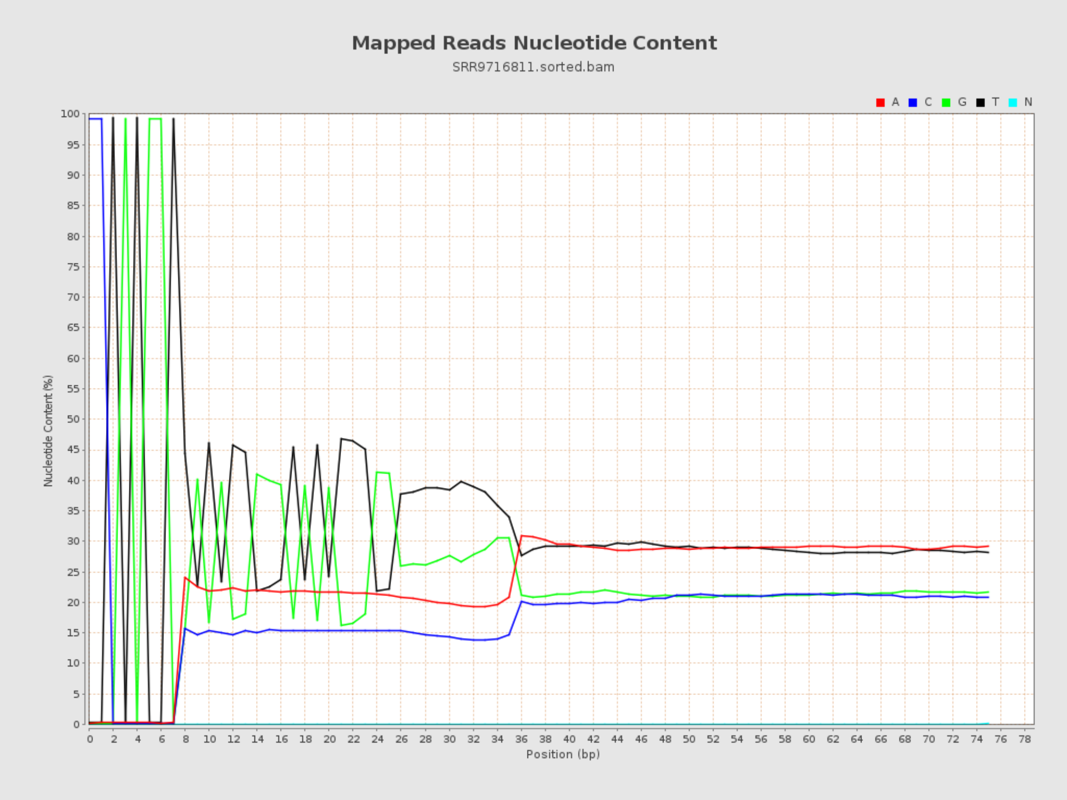
6. Results : Genome Fraction Coverage



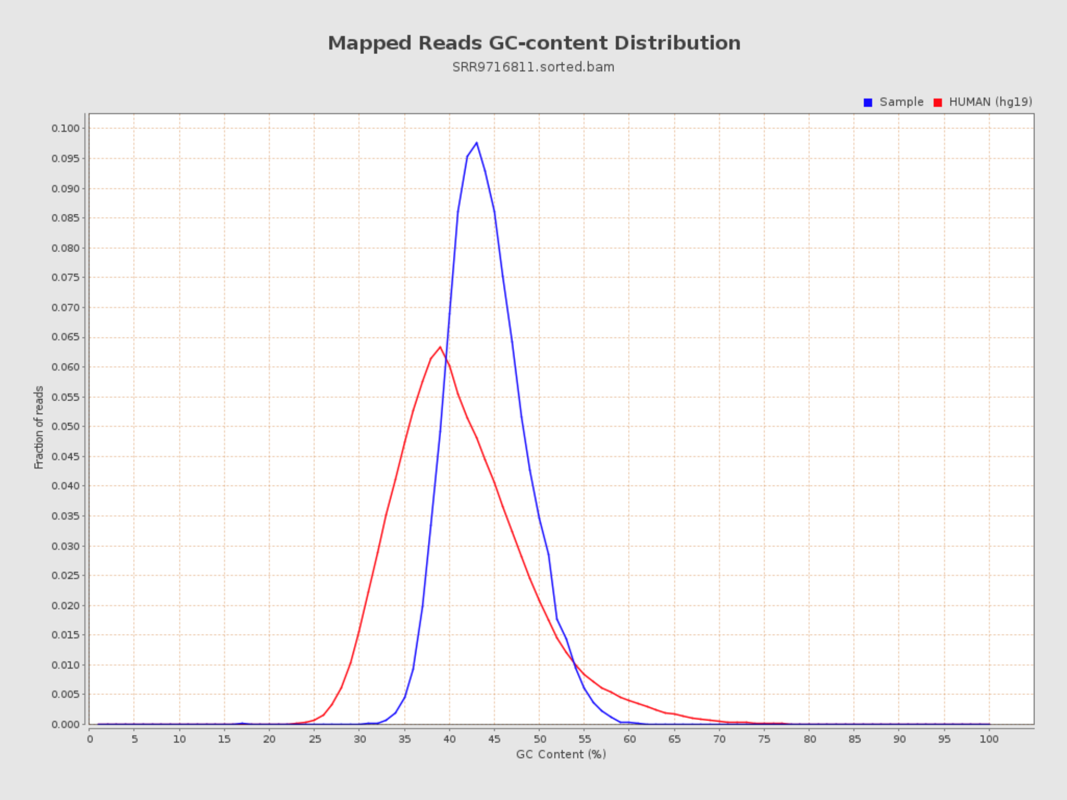
7. Results : Duplication Rate Histogram



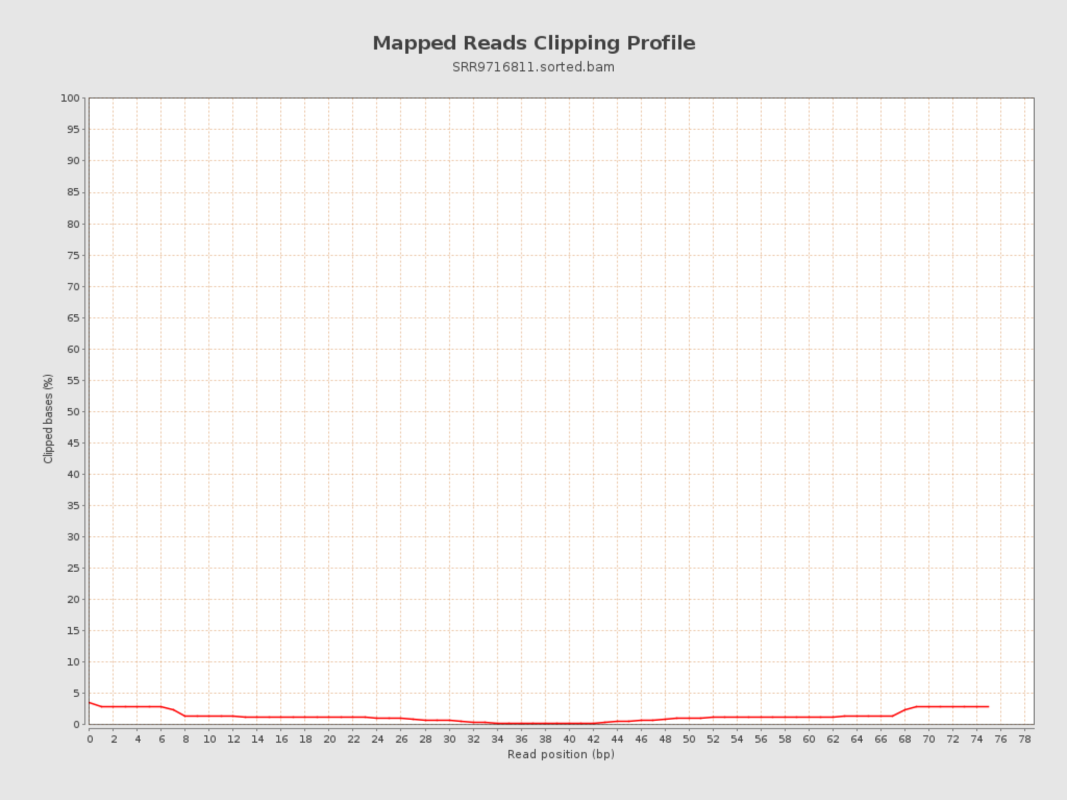
8. Results : Mapped Reads Nucleotide Content



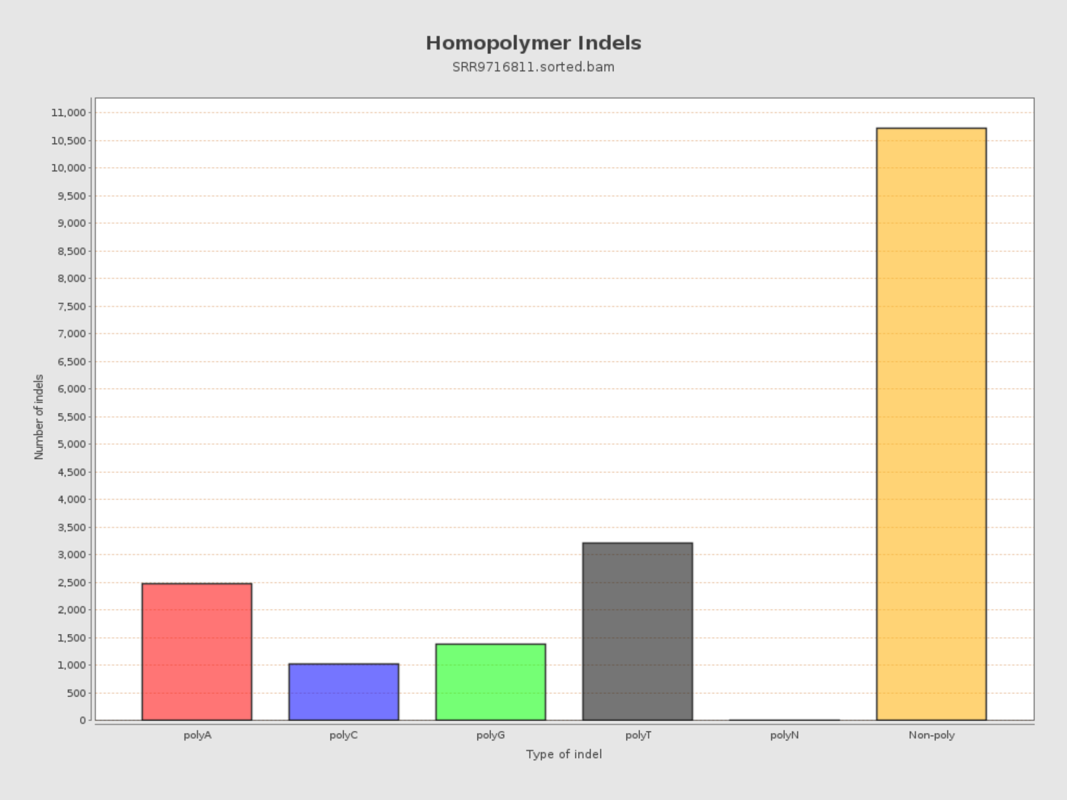
9. Results : Mapped Reads GC-content Distribution



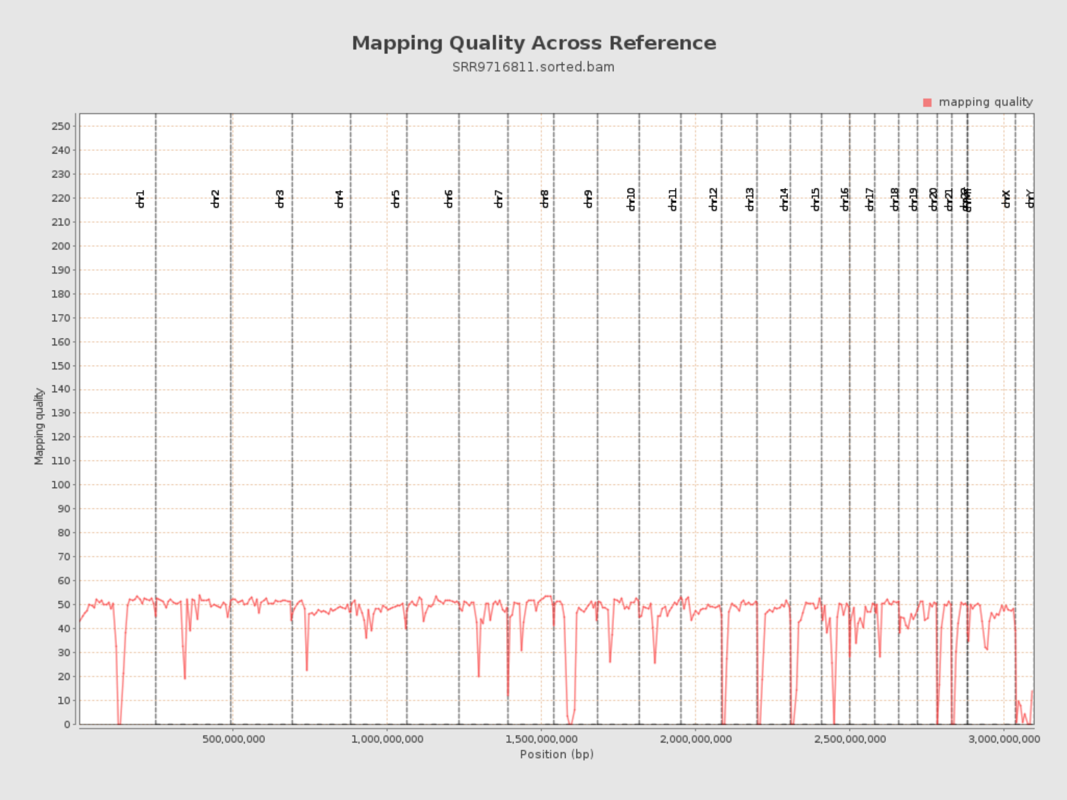
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram