Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 12:45:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716425.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_SRR9716425 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716425.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 12:45:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716425.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	945,399
Mapped reads	863,908 / 91.38%
Unmapped reads	81,491 / 8.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,874 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	24,029 / 2.54%
Duplication rate	1.96%
Clipped reads	864,571 / 91.45%

2.2. ACGT Content

Number/percentage of A's	12,579,579 / 25.19%
Number/percentage of C's	9,660,689 / 19.34%
Number/percentage of T's	15,815,373 / 31.67%
Number/percentage of G's	11,888,599 / 23.8%
Number/percentage of N's	886 / 0%
GC Percentage	43.15%

2.3. Coverage

Mean	0.0161

Standard Deviation	0.1796

2.4. Mapping Quality

Mean Mapping Quality	44.42

2.5. Mismatches and indels

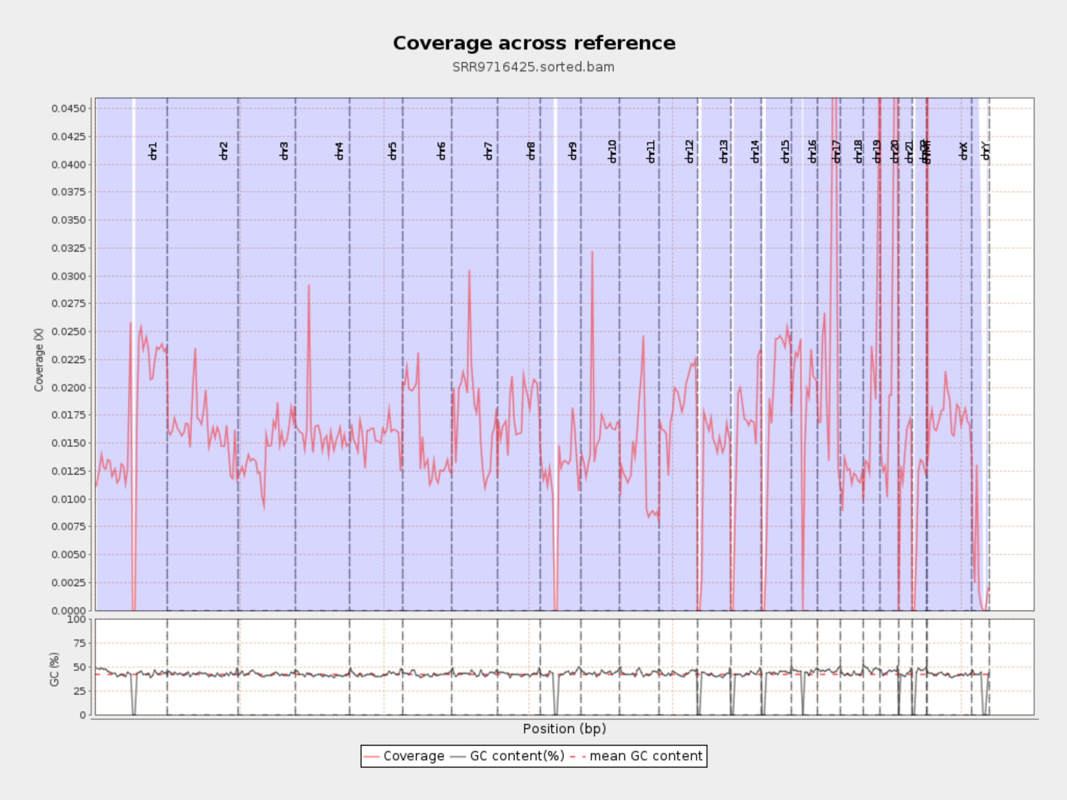
General error rate	0.53%
Mismatches	257,099
Insertions	3,462
Mapped reads with at least one insertion	0.4%
Deletions	9,975
Mapped reads with at least one deletion	1.15%
Homopolymer indels	43.34%

2.6. Chromosome stats

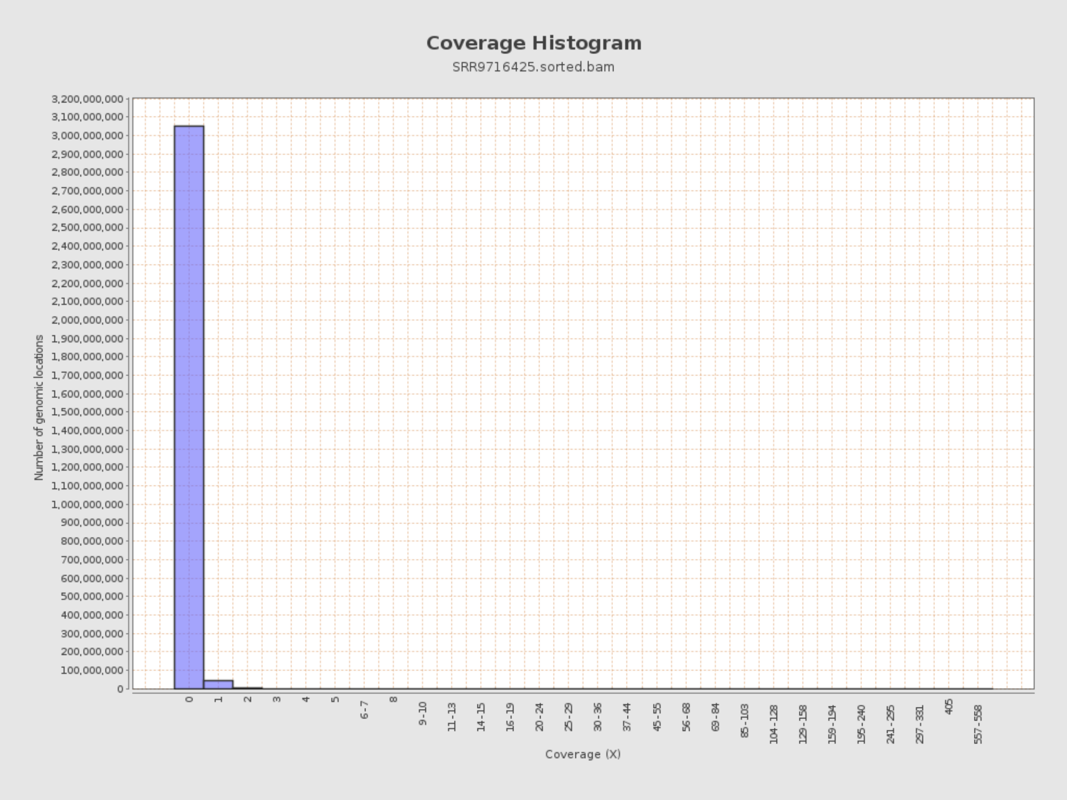
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4176132	0.0168	0.2681
chr2	243199373	3944053	0.0162	0.2602
chr3	198022430	2848557	0.0144	0.1266
chr4	191154276	3071171	0.0161	0.1498
chr5	180915260	2834548	0.0157	0.1316
chr6	171115067	2653876	0.0155	0.1467
chr7	159138663	2846962	0.0179	0.2188

chr8	146364022	2630527	0.018	0.2219
chr9	141213431	1669238	0.0118	0.1367
chr10	135534747	2201950	0.0162	0.1832
chr11	135006516	1759925	0.013	0.141
chr12	133851895	2476969	0.0185	0.1445
chr13	115169878	1517583	0.0132	0.1208
chr14	107349540	1666849	0.0155	0.1319
chr15	102531392	1869486	0.0182	0.1423
chr16	90354753	1721691	0.0191	0.1484
chr17	81195210	2184840	0.0269	0.1769
chr18	78077248	925862	0.0119	0.1883
chr19	59128983	1302864	0.022	0.2164
chr20	63025520	1638162	0.026	0.1747
chr21	48129895	637886	0.0133	0.1398
chr22	51304566	464649	0.0091	0.0994
chrMT	16571	30303	1.8287	1.7494
chrX	155270560	2699386	0.0174	0.1456
chrY	59373566	187816	0.0032	0.1422

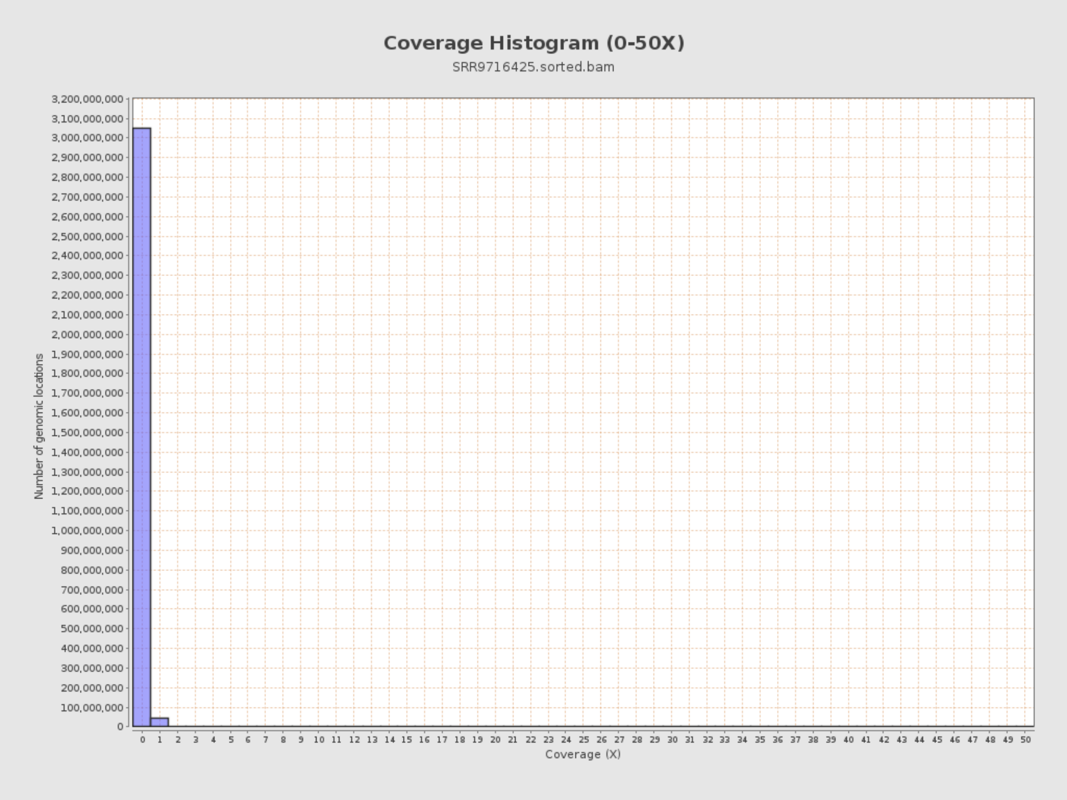
3. Results : Coverage across reference



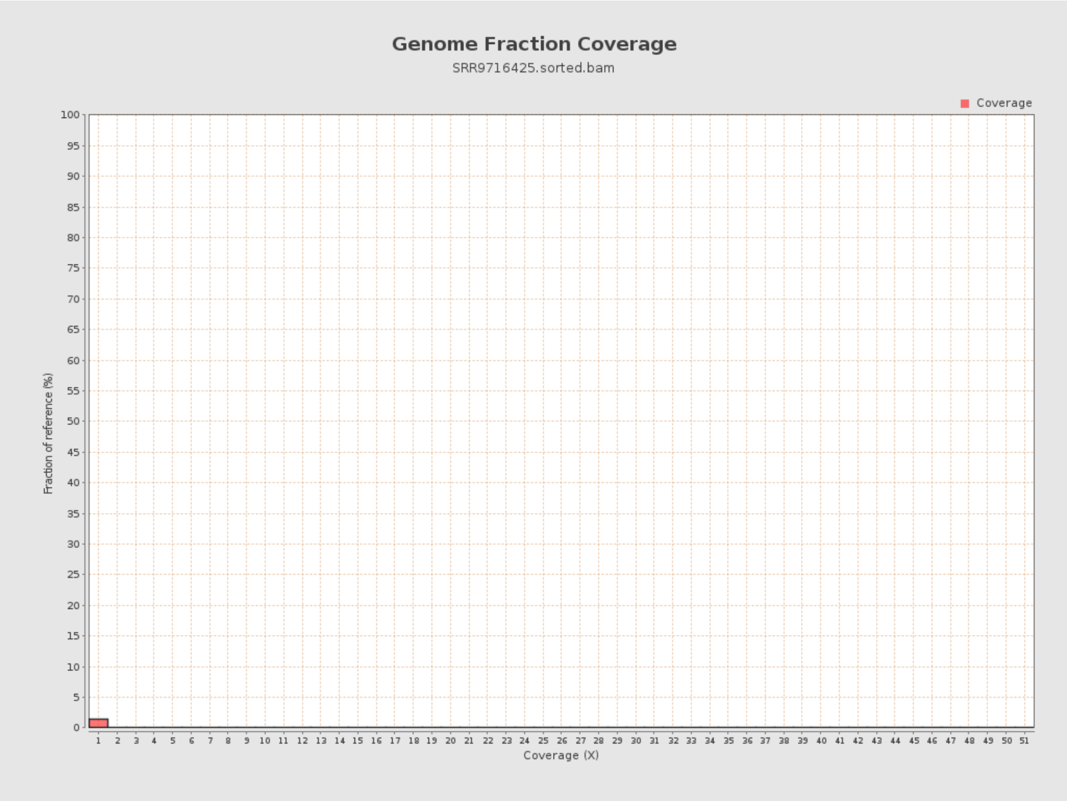
4. Results : Coverage Histogram



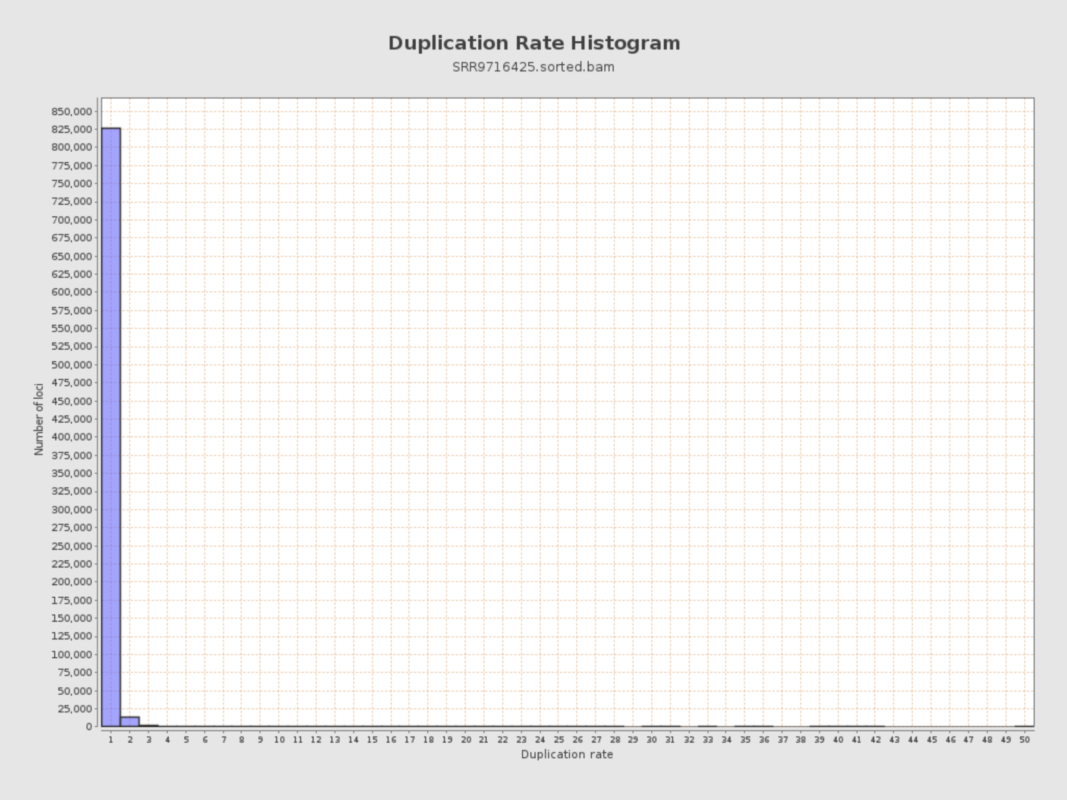
5. Results : Coverage Histogram (0-50X)



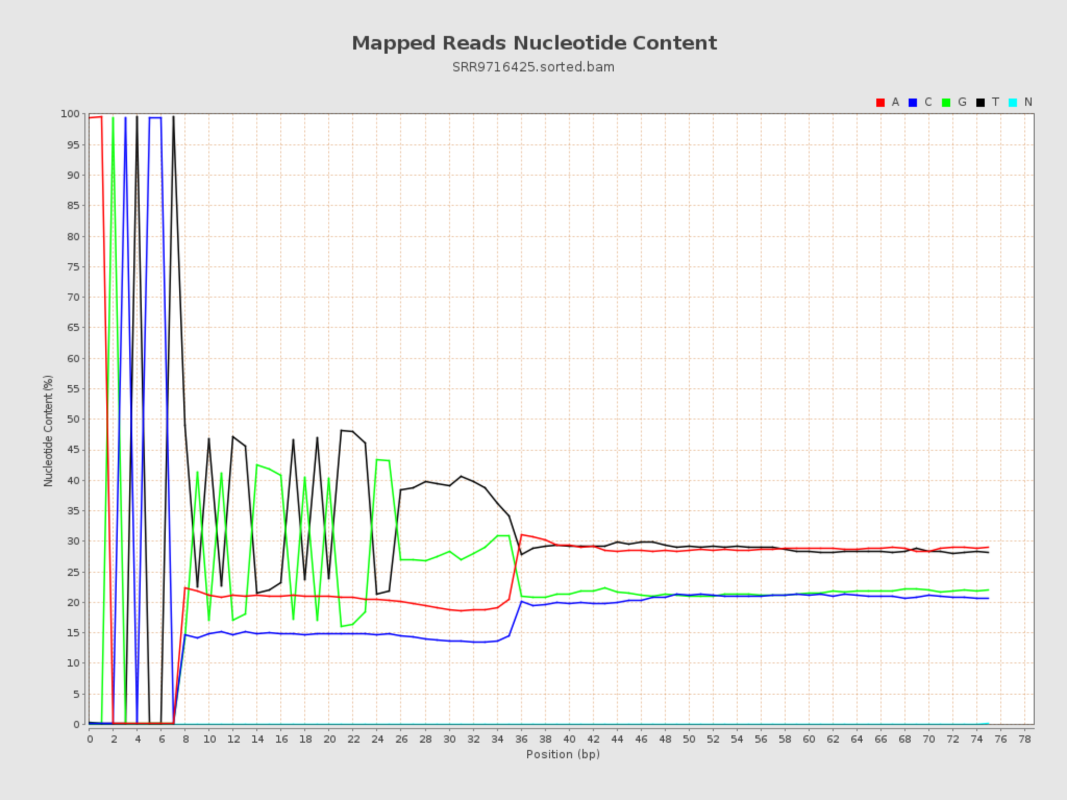
6. Results : Genome Fraction Coverage



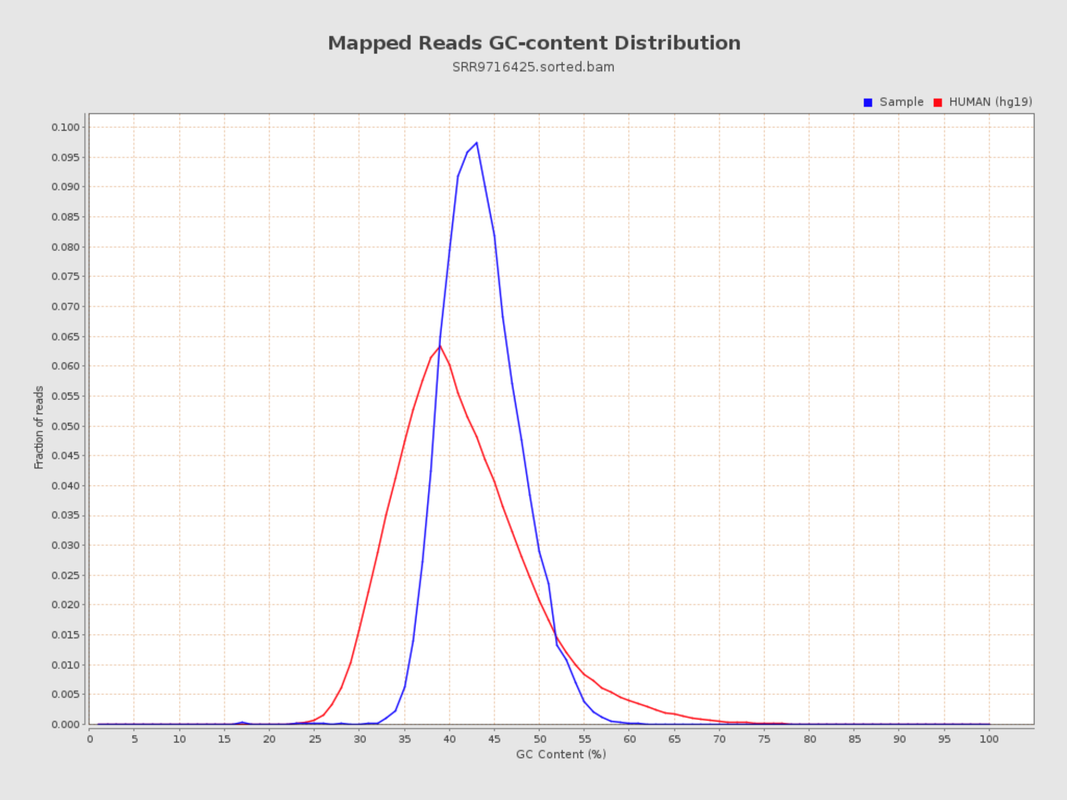
7. Results : Duplication Rate Histogram



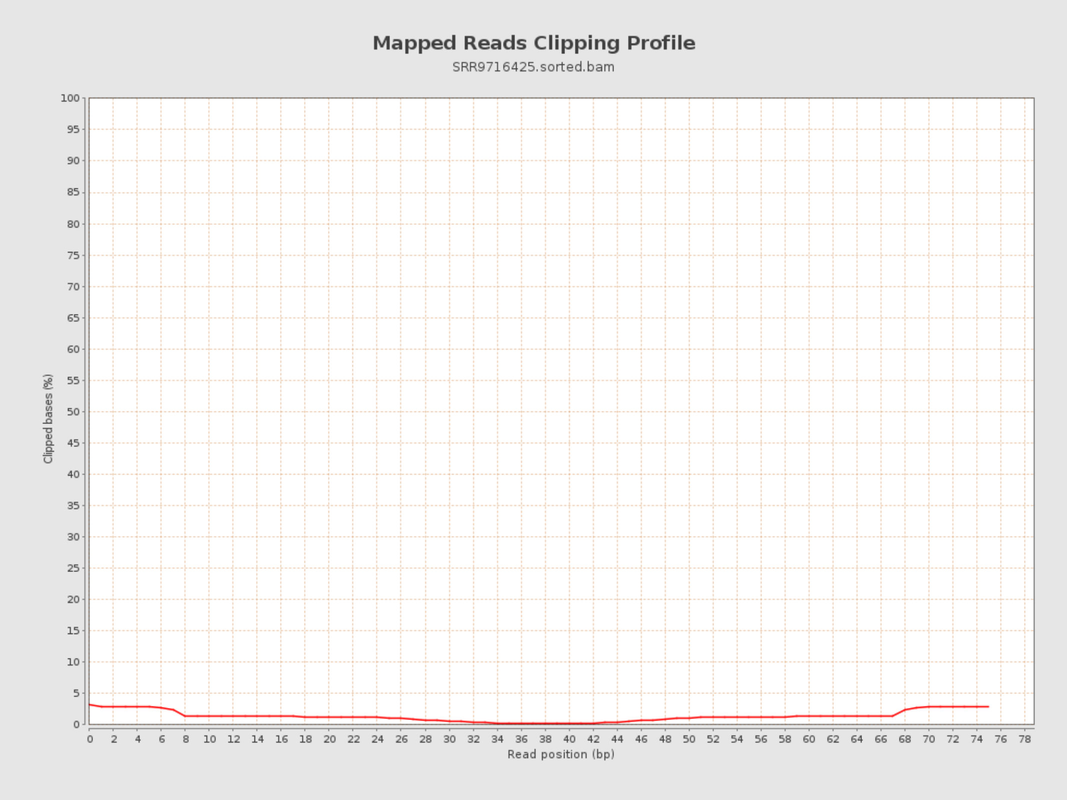
8. Results : Mapped Reads Nucleotide Content



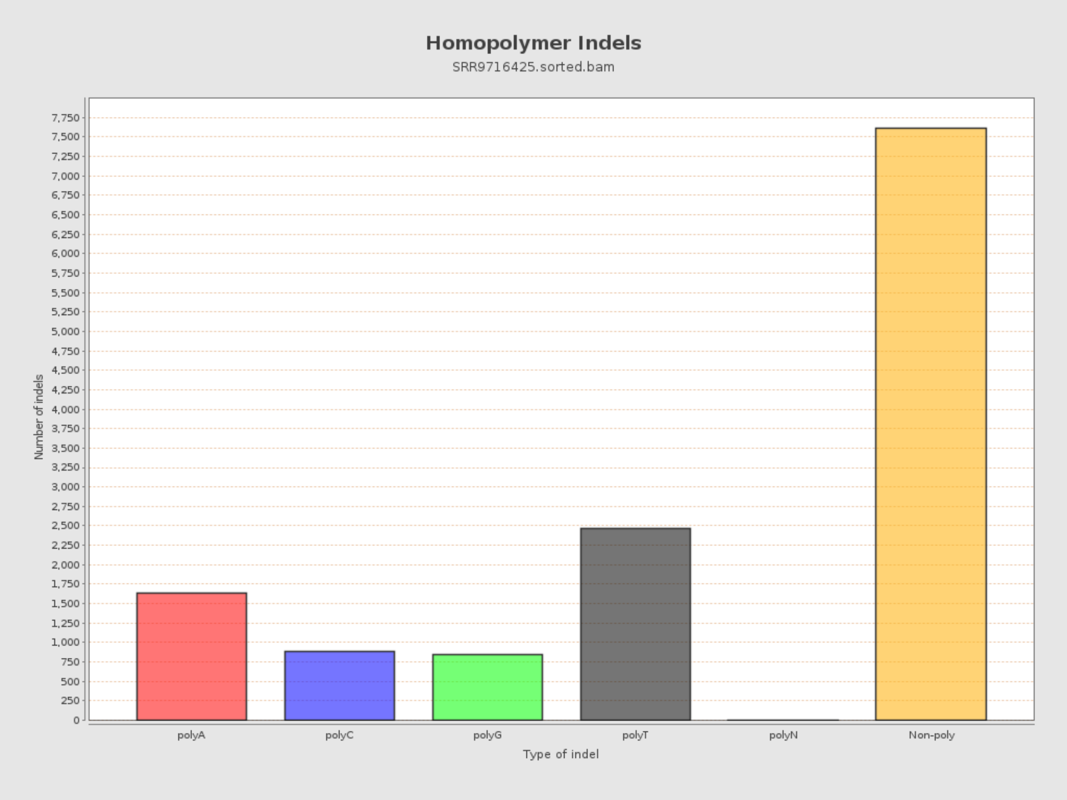
9. Results : Mapped Reads GC-content Distribution



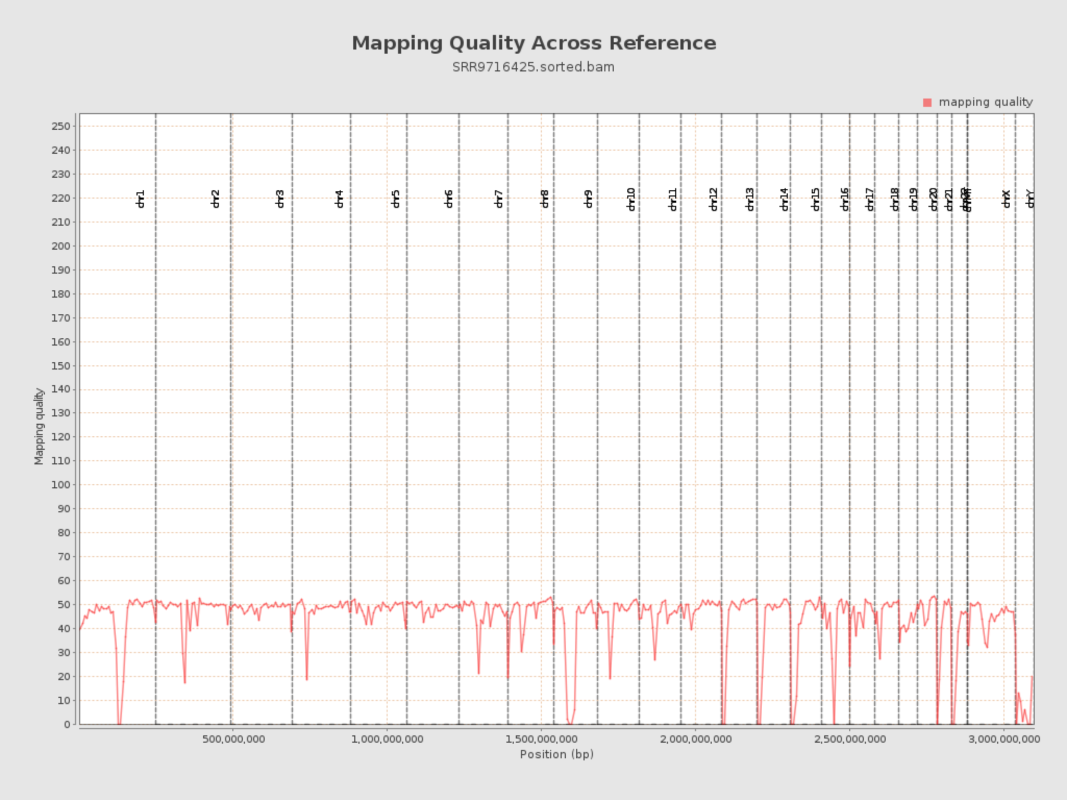
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram