Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 10:50:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716386.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_SRR9716386 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716386.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 10:50:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716386.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,380,451
Mapped reads	1,265,275 / 91.66%
Unmapped reads	115,176 / 8.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,974 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	28,214 / 2.04%
Duplication rate	1.72%
Clipped reads	1,266,603 / 91.75%

2.2. ACGT Content

Number/percentage of A's	17,355,691 / 23.85%
Number/percentage of C's	14,096,909 / 19.37%
Number/percentage of T's	22,775,682 / 31.3%
Number/percentage of G's	18,545,160 / 25.48%
Number/percentage of N's	1,605 / 0%
GC Percentage	44.85%

2.3. Coverage

Mean	0.0235

Standard Deviation	0.1935

2.4. Mapping Quality

Mean Mapping Quality	44.42

2.5. Mismatches and indels

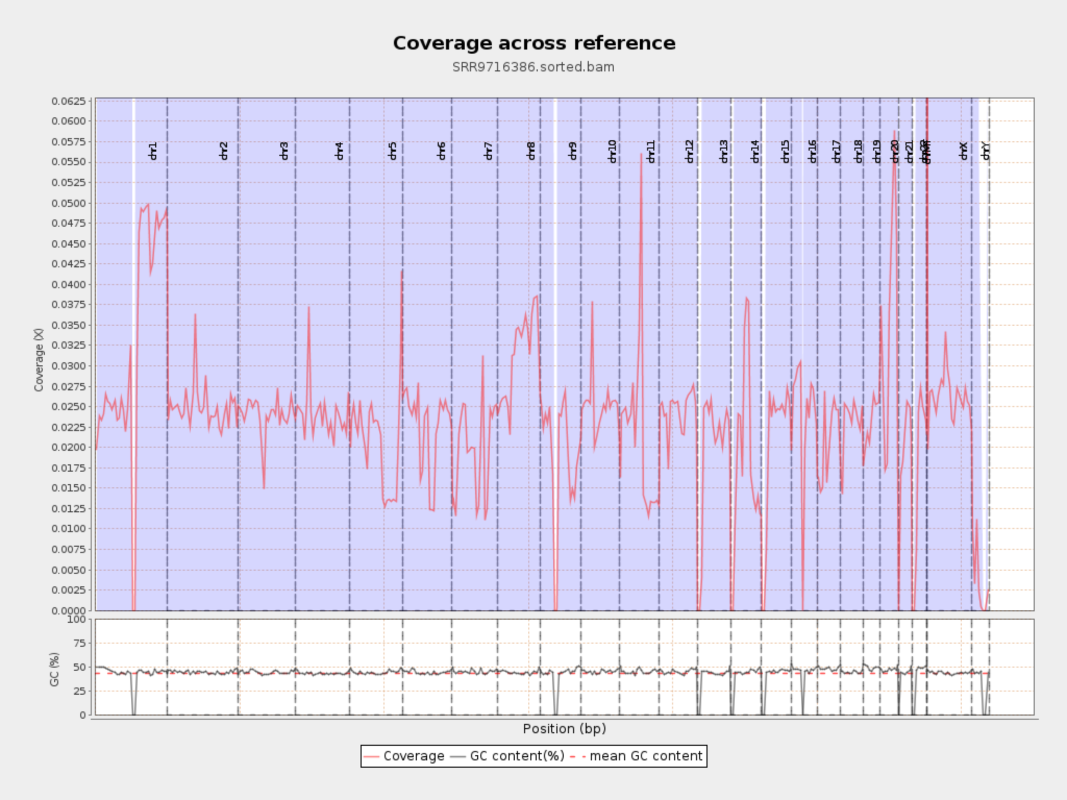
General error rate	0.51%
Mismatches	359,291
Insertions	4,673
Mapped reads with at least one insertion	0.37%
Deletions	11,537
Mapped reads with at least one deletion	0.91%
Homopolymer indels	41.55%

2.6. Chromosome stats

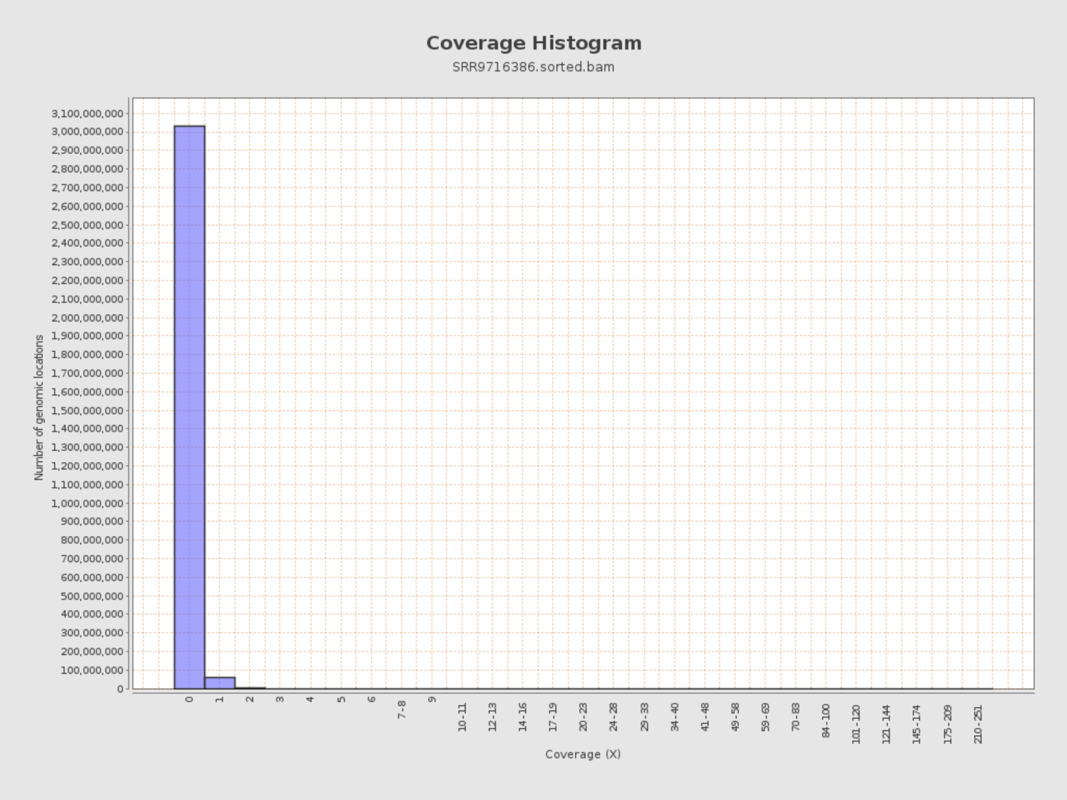
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8134821	0.0326	0.2753
chr2	243199373	6075367	0.025	0.2111
chr3	198022430	4745906	0.024	0.1654
chr4	191154276	4621290	0.0242	0.1759
chr5	180915260	3724530	0.0206	0.1548
chr6	171115067	3841252	0.0224	0.1674
chr7	159138663	3145952	0.0198	0.177

chr8	146364022	4585390	0.0313	0.2074
chr9	141213431	2638773	0.0187	0.1861
chr10	135534747	3423912	0.0253	0.2117
chr11	135006516	2978755	0.0221	0.2001
chr12	133851895	3284272	0.0245	0.1677
chr13	115169878	2229566	0.0194	0.1476
chr14	107349540	1981673	0.0185	0.1547
chr15	102531392	2083917	0.0203	0.1516
chr16	90354753	2144412	0.0237	0.1761
chr17	81195210	1680926	0.0207	0.1589
chr18	78077248	1783457	0.0228	0.3293
chr19	59128983	1376360	0.0233	0.2103
chr20	63025520	2206944	0.035	0.2056
chr21	48129895	935969	0.0194	0.1625
chr22	51304566	873942	0.017	0.1391
chrMT	16571	3437	0.2074	0.4453
chrX	155270560	4089543	0.0263	0.1881
chrY	59373566	204445	0.0034	0.0836

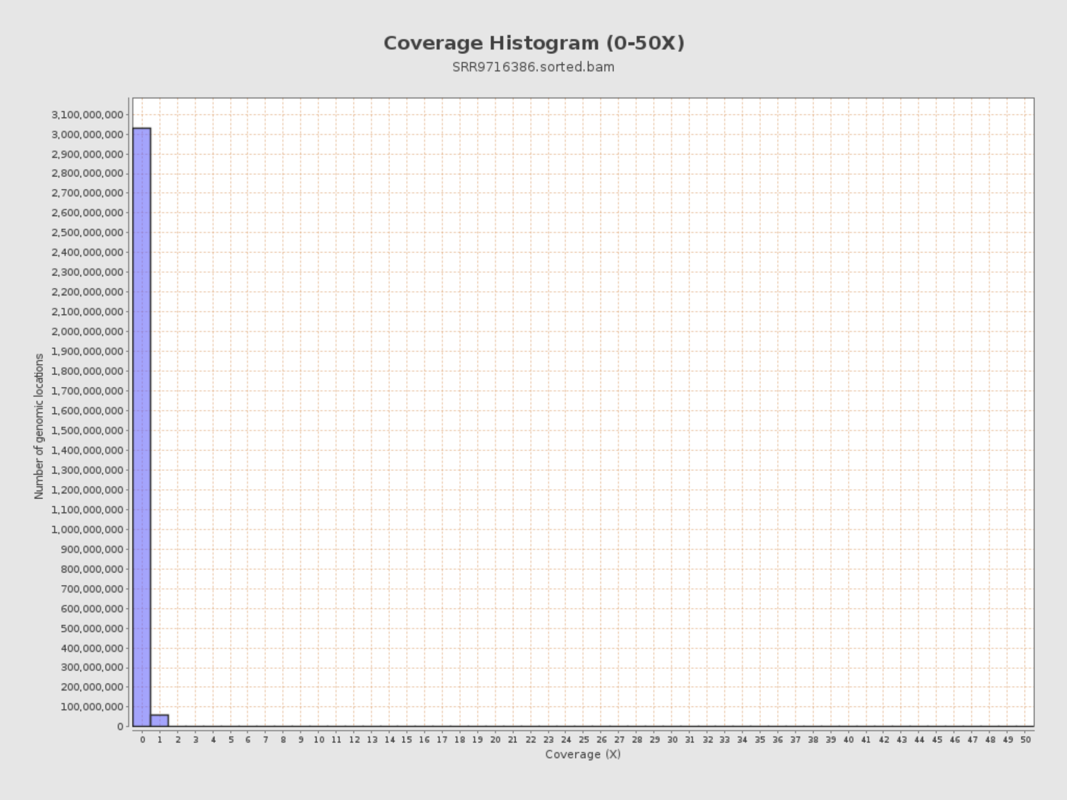
3. Results : Coverage across reference



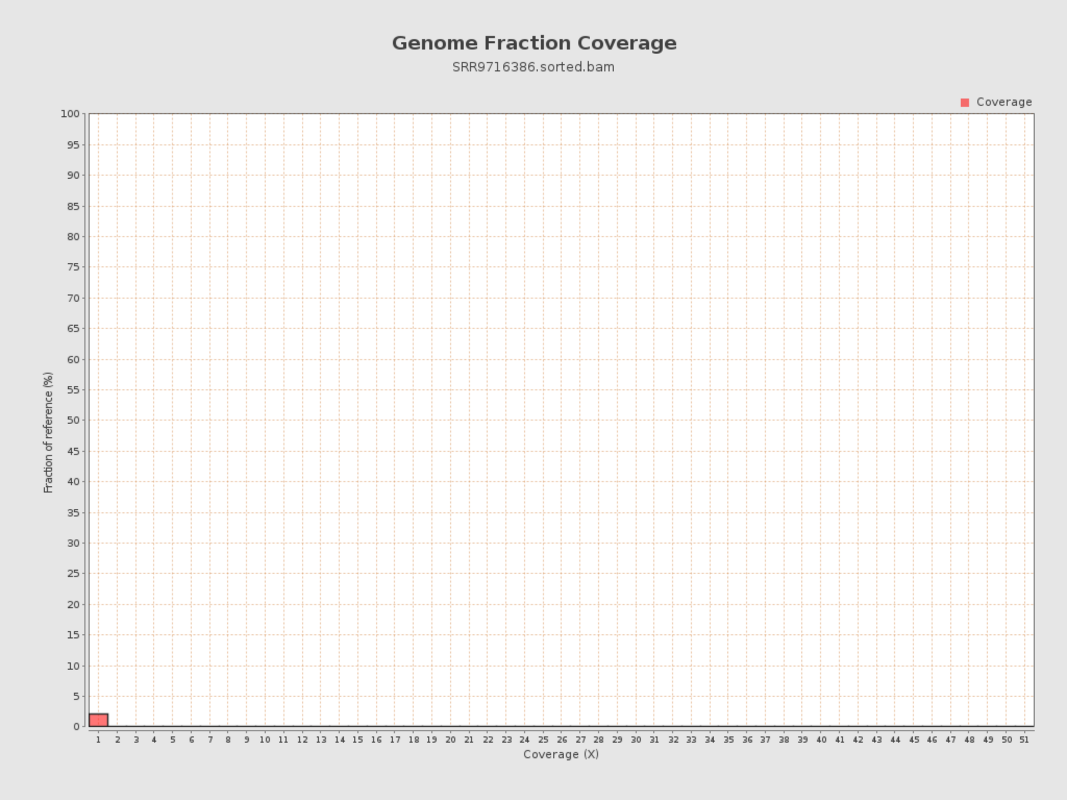
4. Results : Coverage Histogram



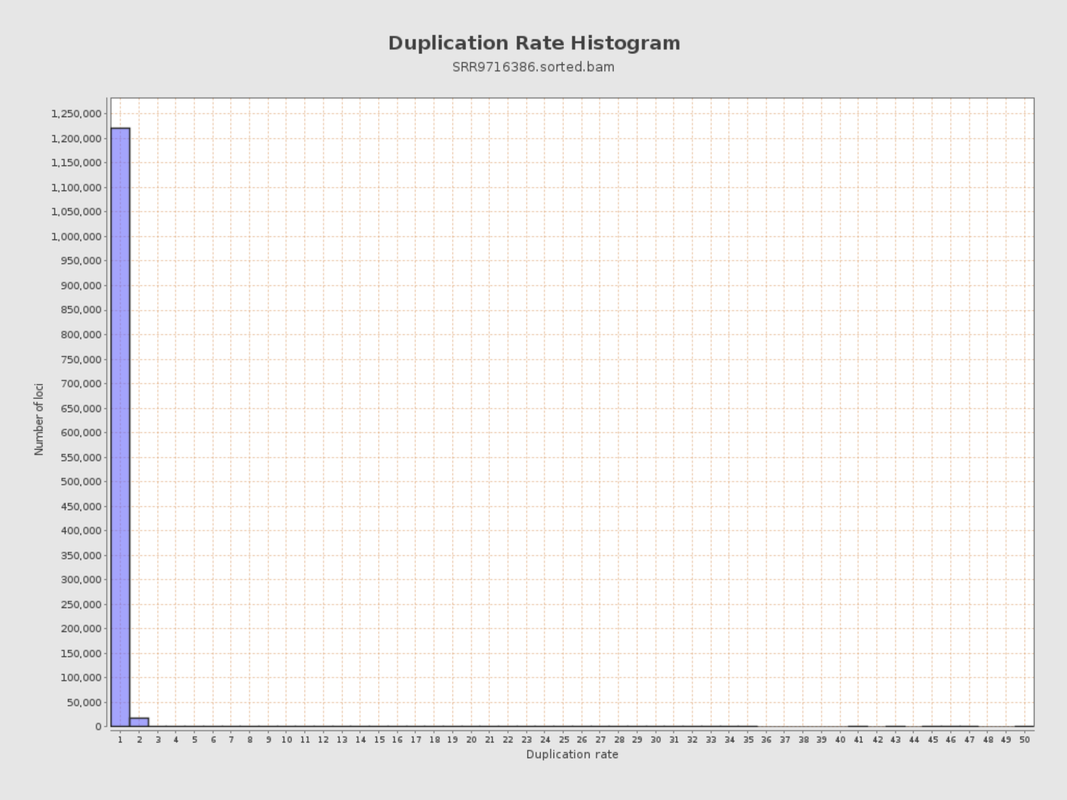
5. Results : Coverage Histogram (0-50X)



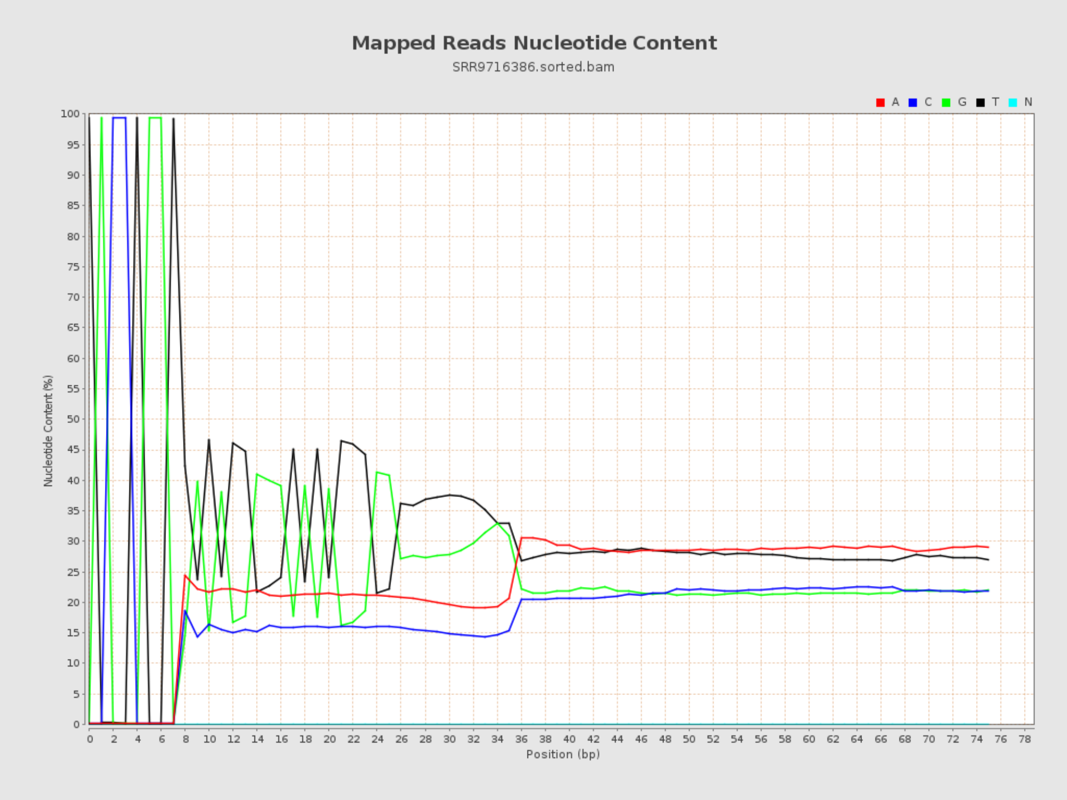
6. Results : Genome Fraction Coverage



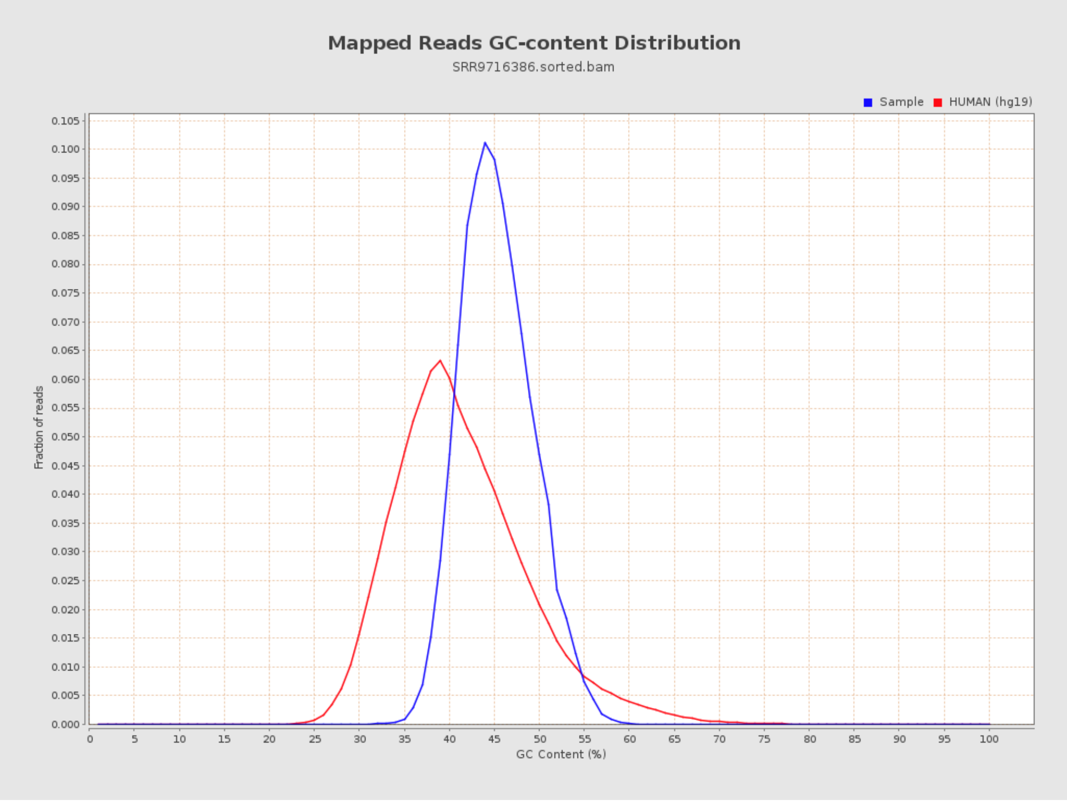
7. Results : Duplication Rate Histogram



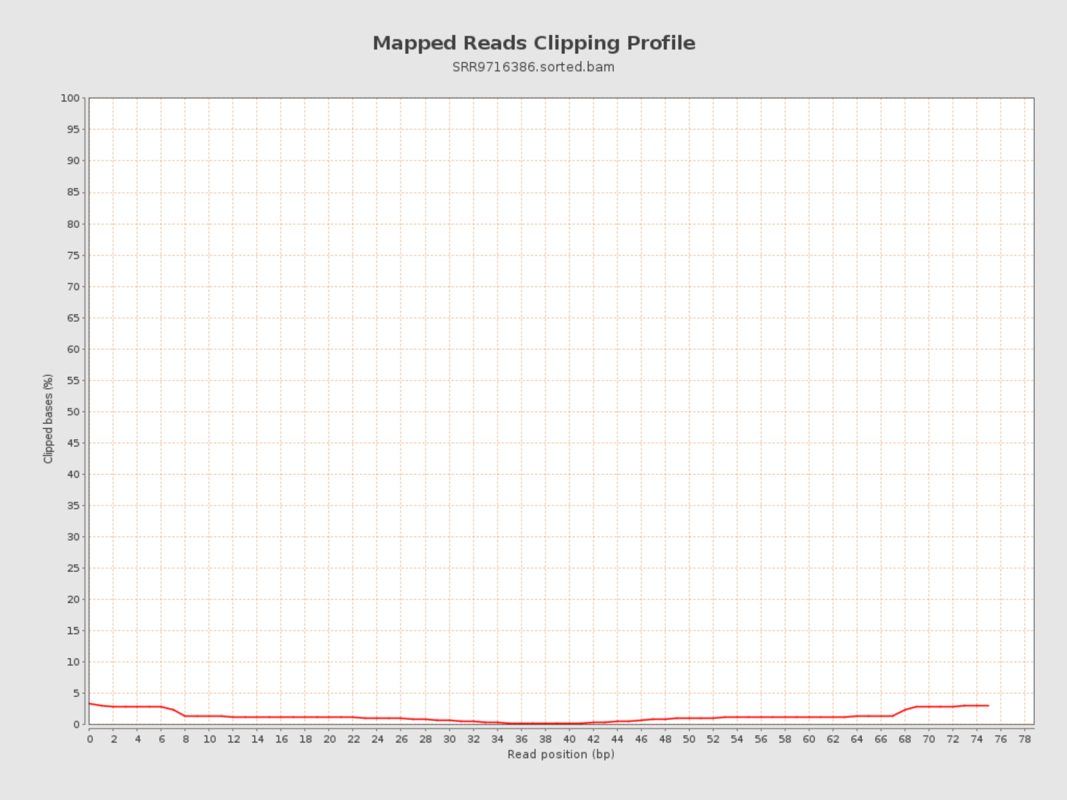
8. Results : Mapped Reads Nucleotide Content



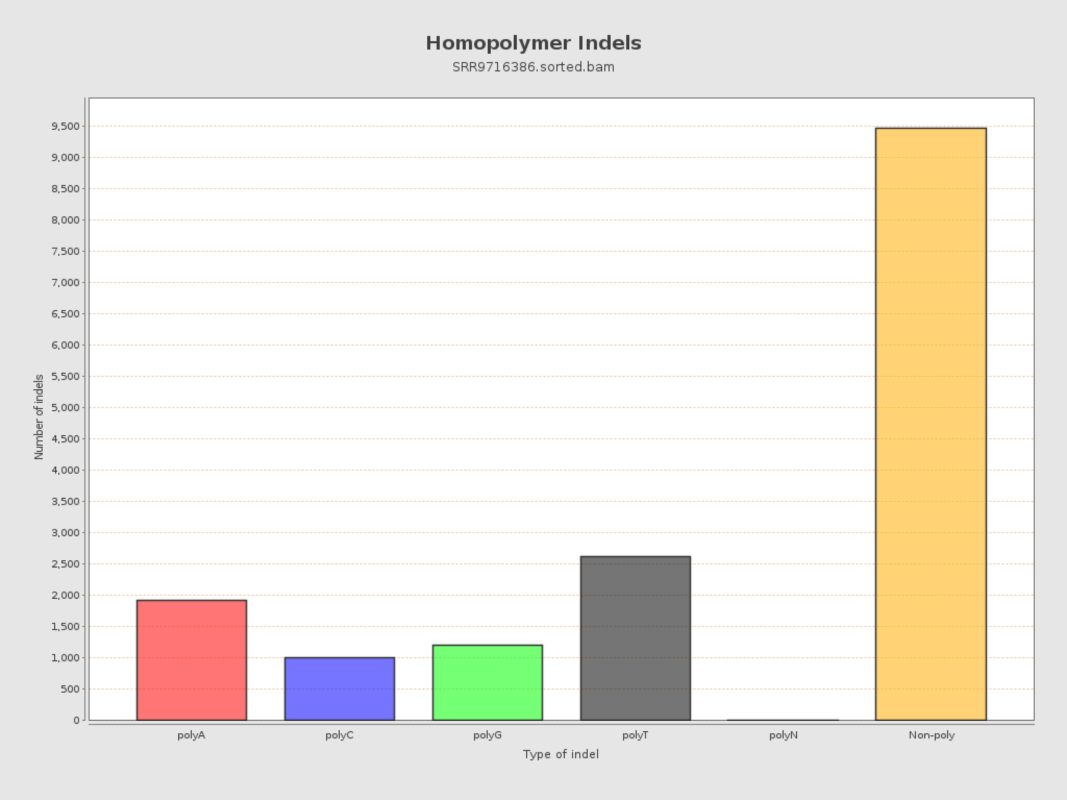
9. Results : Mapped Reads GC-content Distribution



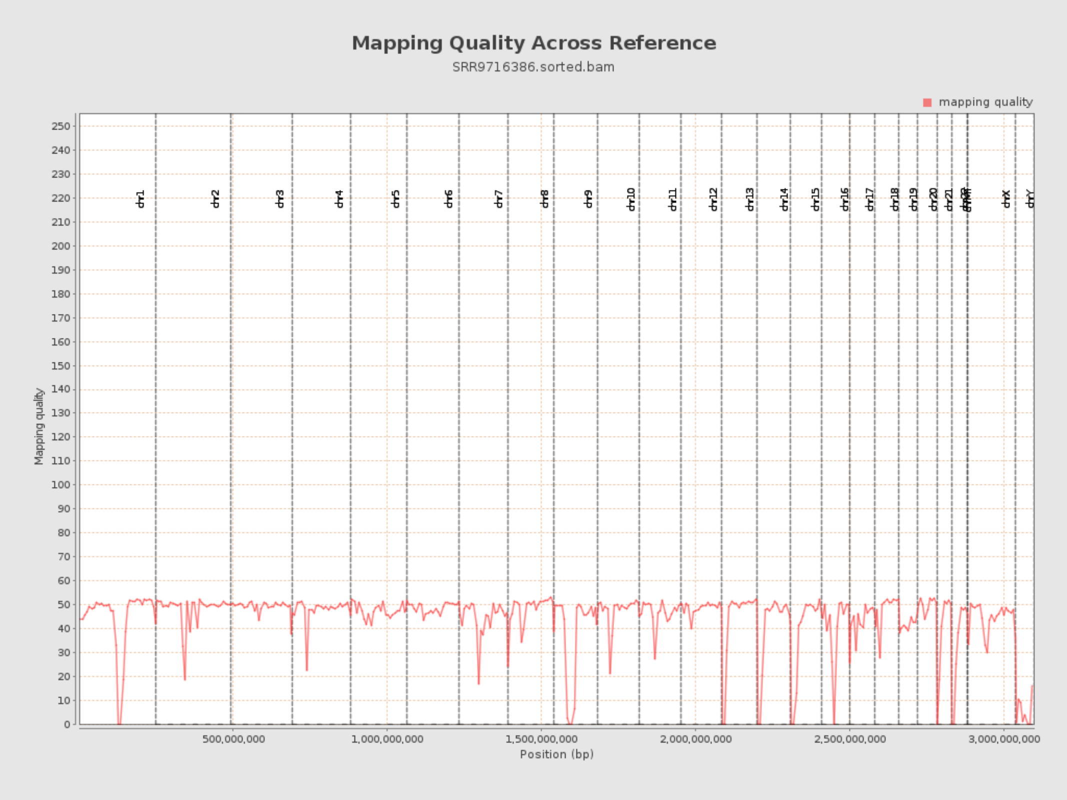
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram