Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 14:08:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716836.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_SRR9716836 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716836.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 14:08:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716836.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	630,135
Mapped reads	550,871 / 87.42%
Unmapped reads	79,264 / 12.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,334 / 0.53%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	19,434 / 3.08%
Duplication rate	2.92%
Clipped reads	553,245 / 87.8%

2.2. ACGT Content

Number/percentage of A's	8,188,698 / 25.18%
Number/percentage of C's	6,411,010 / 19.71%
Number/percentage of T's	10,065,716 / 30.95%
Number/percentage of G's	7,859,272 / 24.16%
Number/percentage of N's	197 / 0%
GC Percentage	43.87%

2.3. Coverage

Mean	0.0105

Standard Deviation	0.1276

2.4. Mapping Quality

Mean Mapping Quality	45.33

2.5. Mismatches and indels

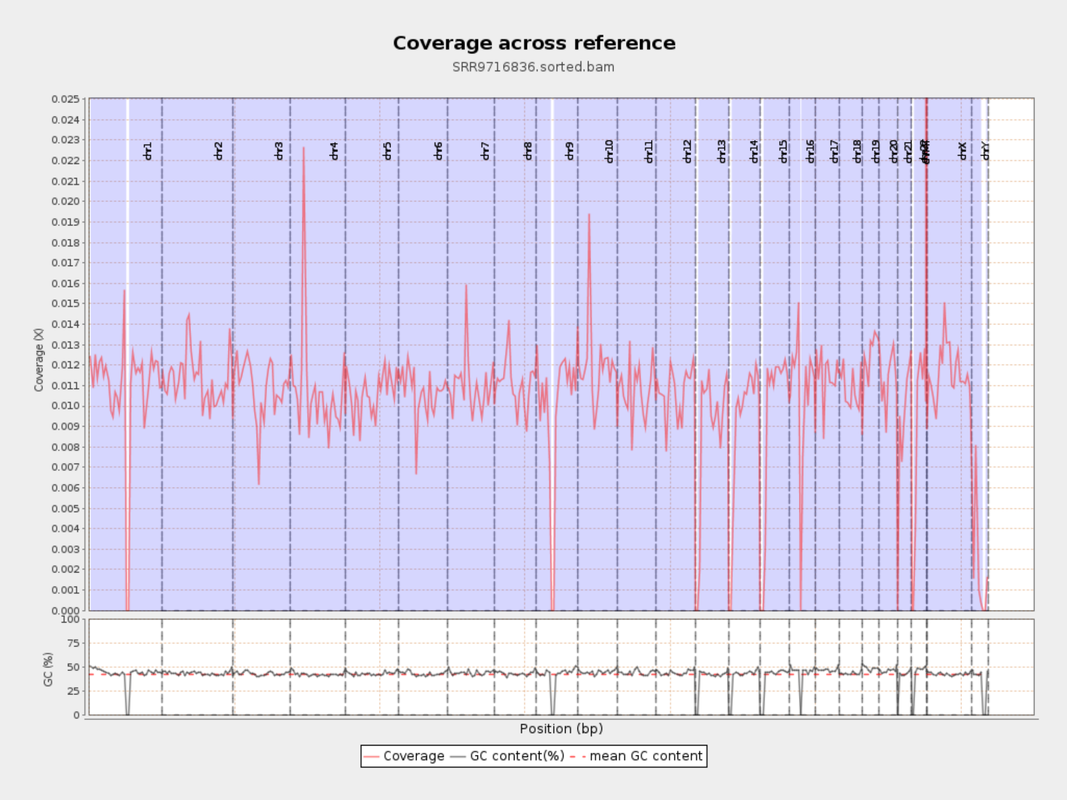
General error rate	0.51%
Mismatches	161,850
Insertions	2,471
Mapped reads with at least one insertion	0.45%
Deletions	5,592
Mapped reads with at least one deletion	1.01%
Homopolymer indels	40.05%

2.6. Chromosome stats

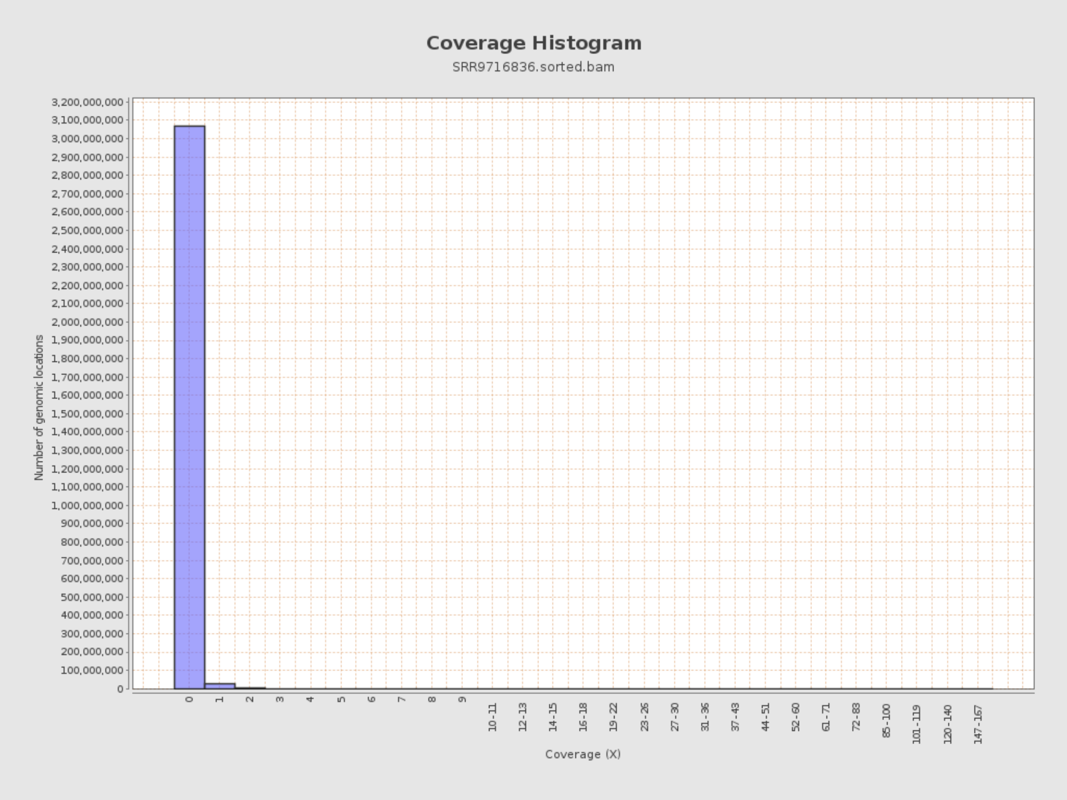
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2683167	0.0108	0.1607
chr2	243199373	2761937	0.0114	0.1481
chr3	198022430	2152463	0.0109	0.113
chr4	191154276	2051005	0.0107	0.1257
chr5	180915260	1920754	0.0106	0.1118
chr6	171115067	1828982	0.0107	0.115
chr7	159138663	1748913	0.011	0.1464

chr8	146364022	1620923	0.0111	0.1493
chr9	141213431	1365806	0.0097	0.115
chr10	135534747	1616769	0.0119	0.1451
chr11	135006516	1452584	0.0108	0.1203
chr12	133851895	1434274	0.0107	0.1123
chr13	115169878	986212	0.0086	0.1008
chr14	107349540	959348	0.0089	0.1033
chr15	102531392	956597	0.0093	0.1044
chr16	90354753	961670	0.0106	0.1136
chr17	81195210	936076	0.0115	0.1199
chr18	78077248	847279	0.0109	0.1552
chr19	59128983	737241	0.0125	0.1465
chr20	63025520	713567	0.0113	0.1176
chr21	48129895	444139	0.0092	0.1133
chr22	51304566	422004	0.0082	0.0984
chrMT	16571	11832	0.714	1.044
chrX	155270560	1798110	0.0116	0.1191
chrY	59373566	122381	0.0021	0.082

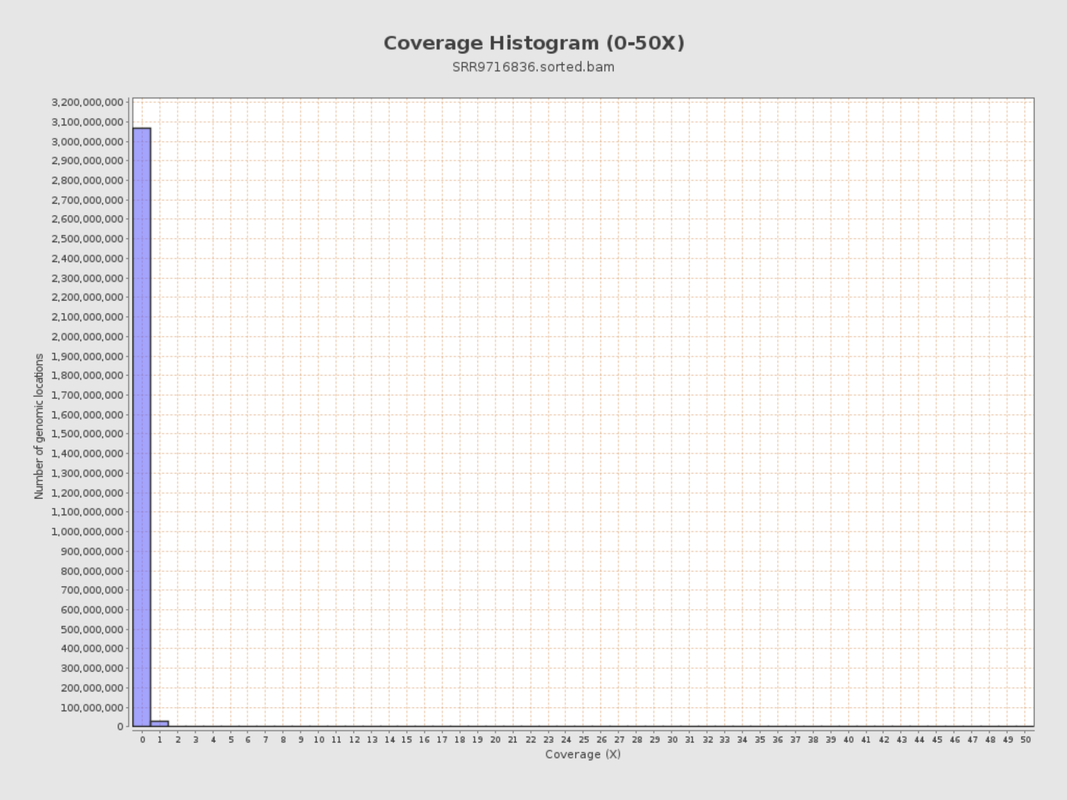
3. Results : Coverage across reference



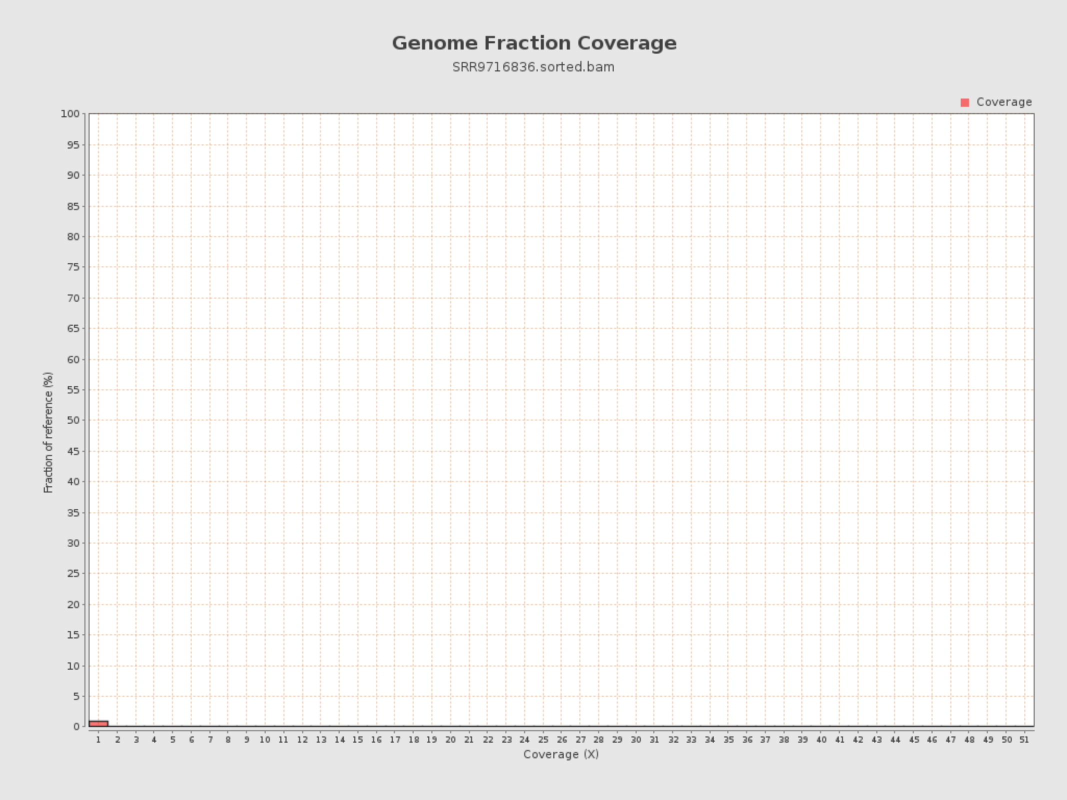
4. Results : Coverage Histogram



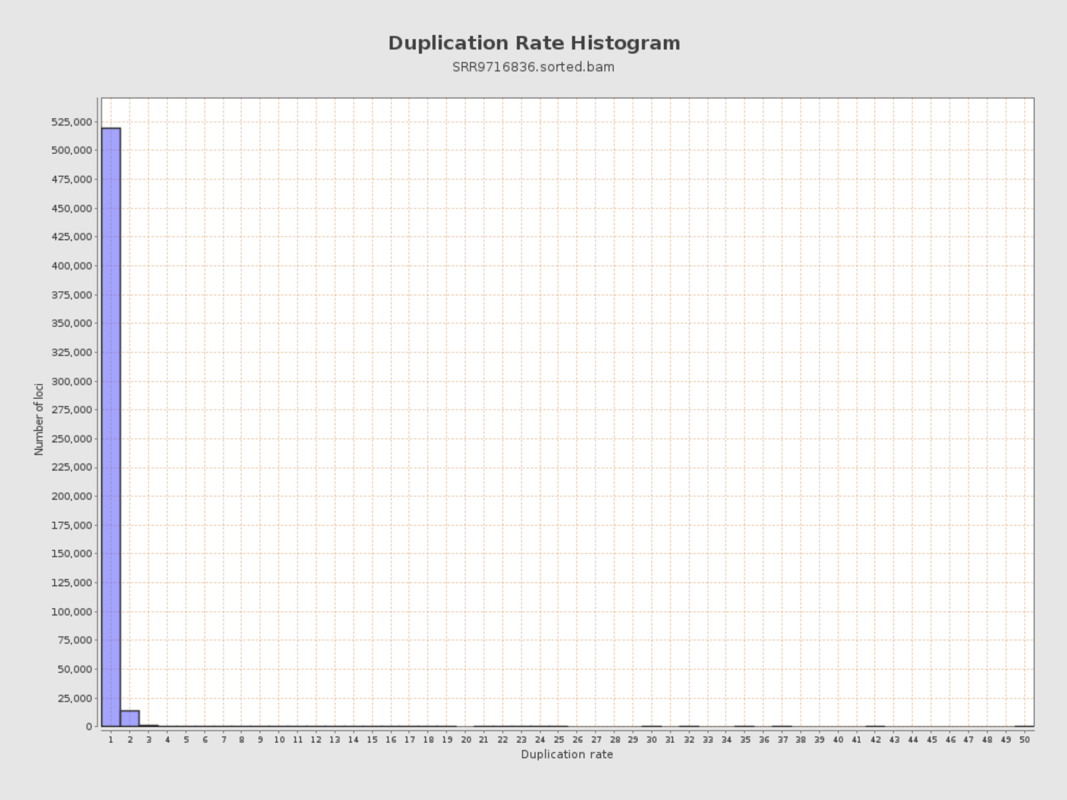
5. Results : Coverage Histogram (0-50X)



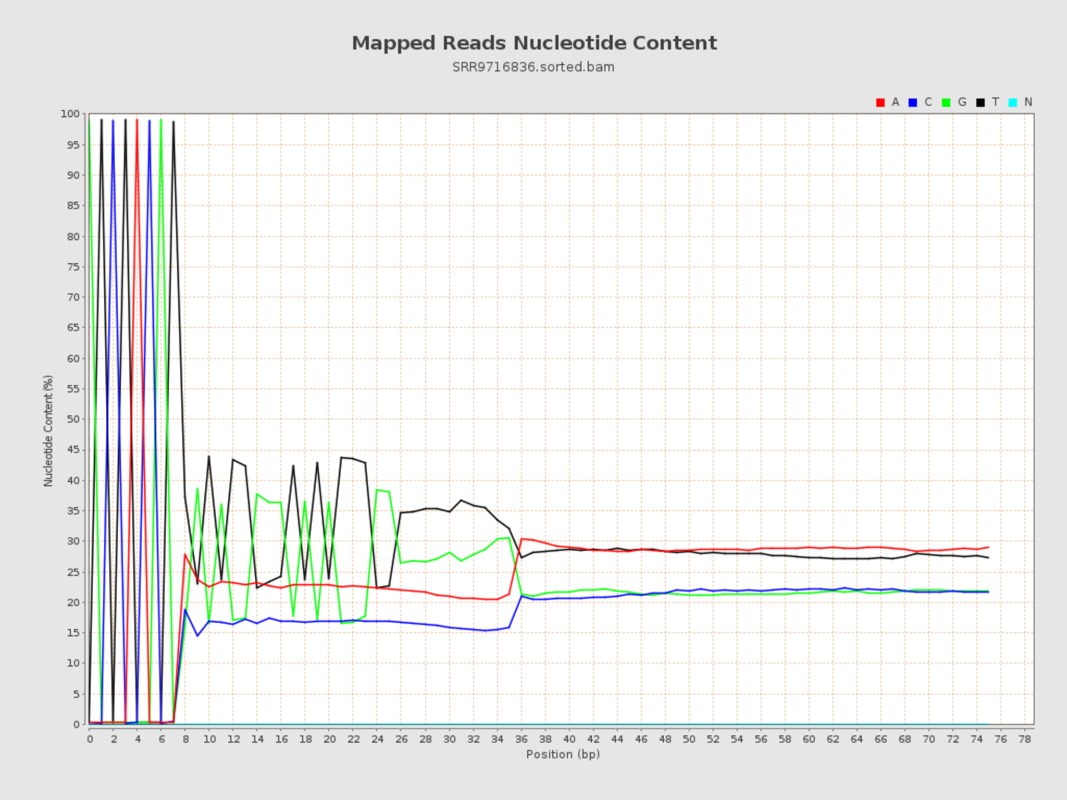
6. Results : Genome Fraction Coverage



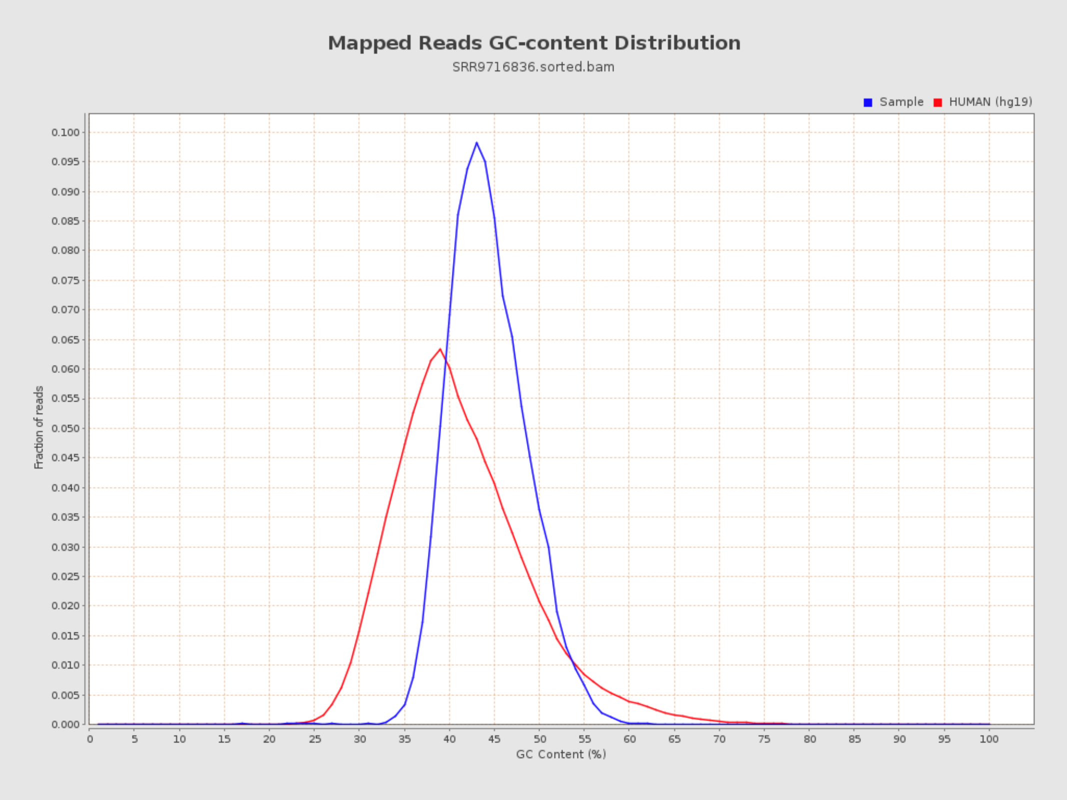
7. Results : Duplication Rate Histogram



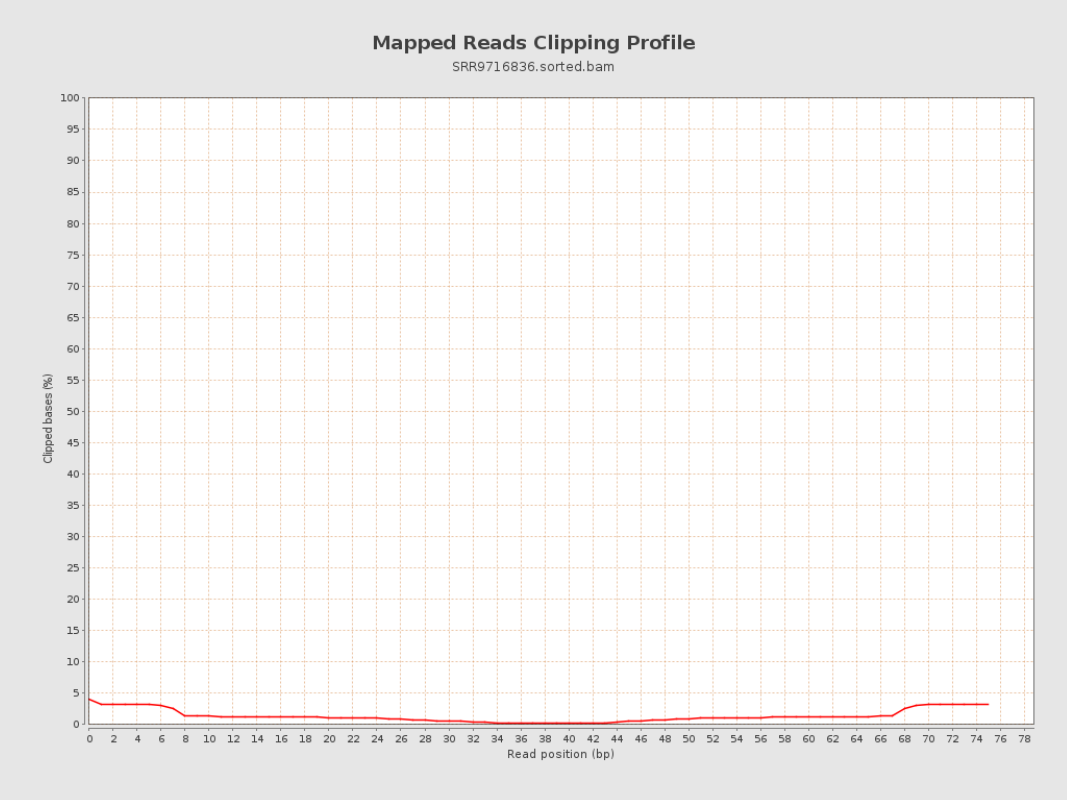
8. Results : Mapped Reads Nucleotide Content



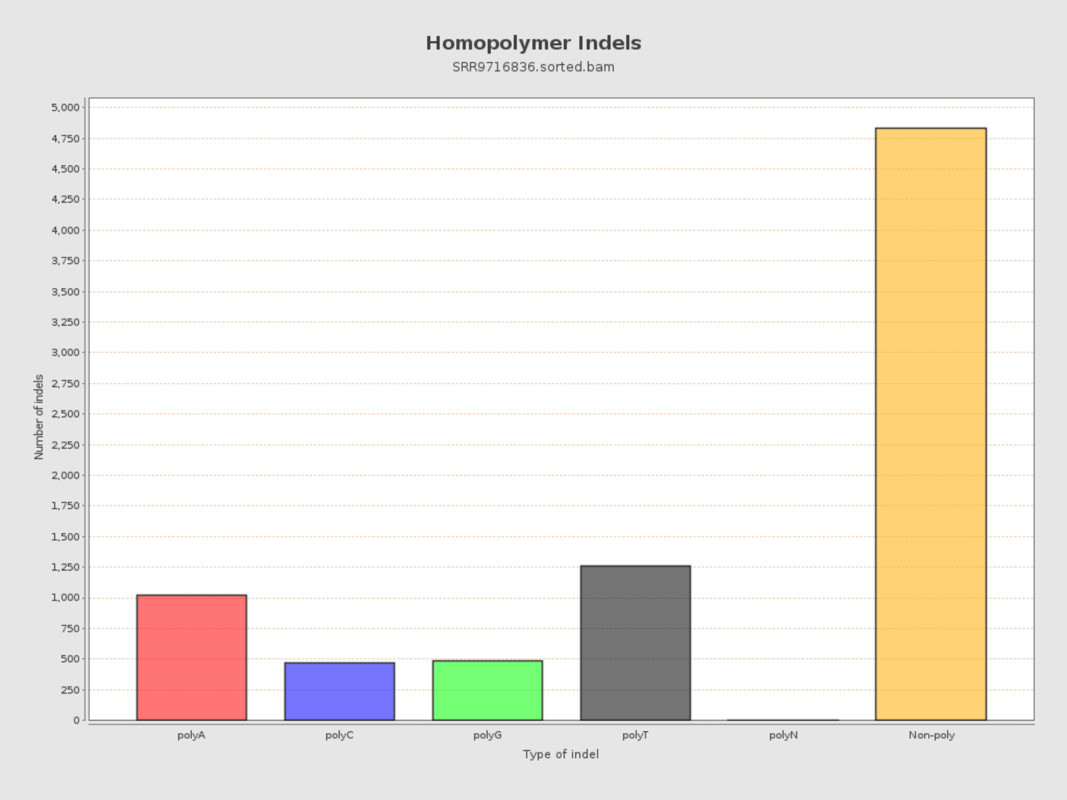
9. Results : Mapped Reads GC-content Distribution



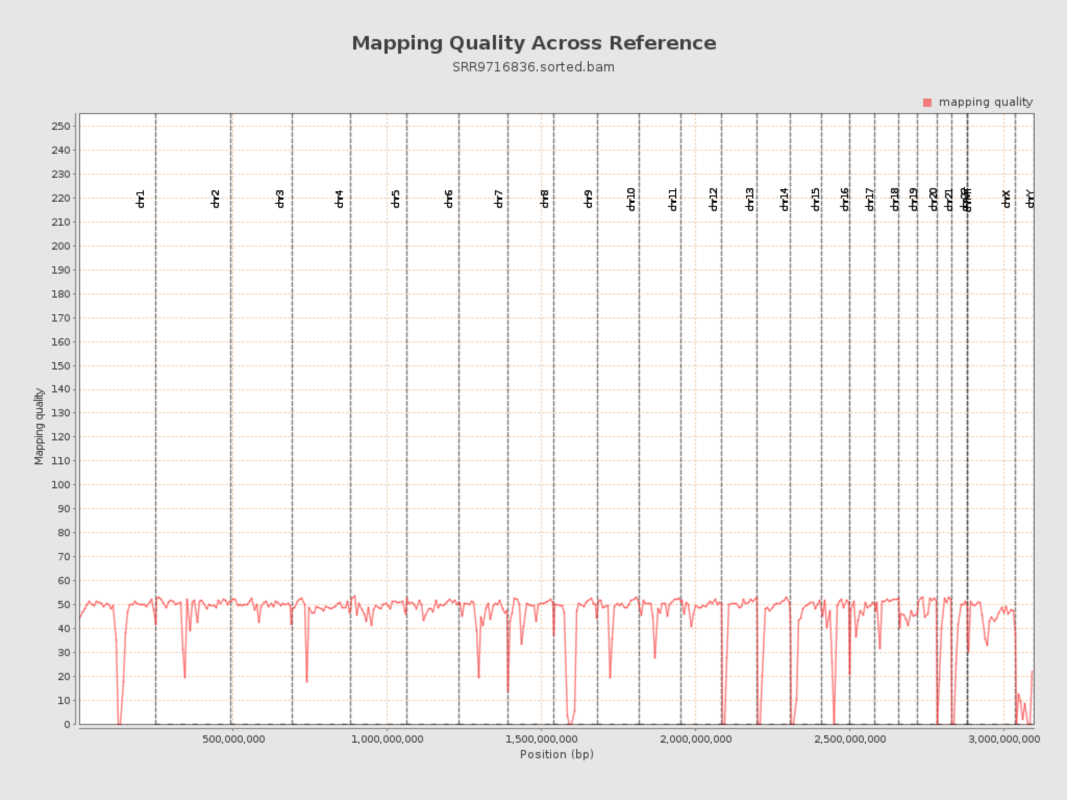
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram