Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 18:18:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716107.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_SRR9716107 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716107.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 18:18:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716107.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	910,679
Mapped reads	808,399 / 88.77%
Unmapped reads	102,280 / 11.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,530 / 0.28%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	14,298 / 1.57%
Duplication rate	1.24%
Clipped reads	809,576 / 88.9%

2.2. ACGT Content

Number/percentage of A's	10,922,758 / 23.66%
Number/percentage of C's	8,806,171 / 19.07%
Number/percentage of T's	14,738,895 / 31.93%
Number/percentage of G's	11,698,630 / 25.34%
Number/percentage of N's	351 / 0%
GC Percentage	44.41%

2.3. Coverage

Mean	0.0149

Standard Deviation	0.1538

2.4. Mapping Quality

Mean Mapping Quality	42.72

2.5. Mismatches and indels

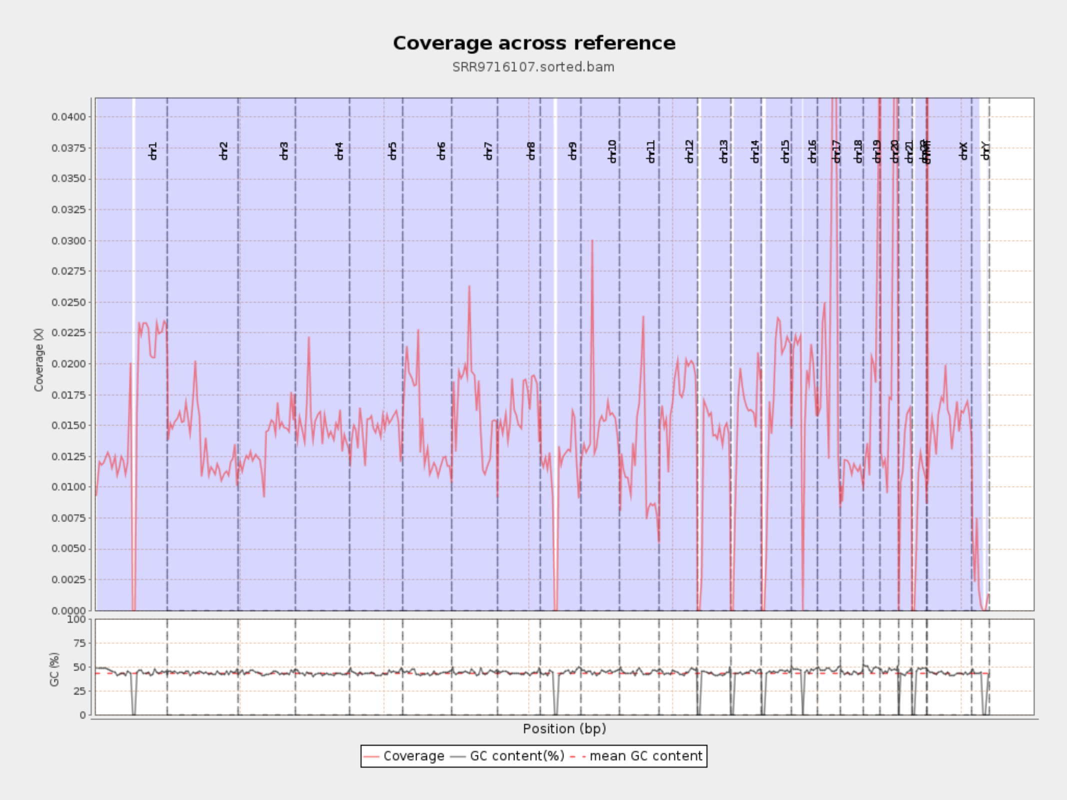
General error rate	0.54%
Mismatches	243,020
Insertions	3,016
Mapped reads with at least one insertion	0.37%
Deletions	8,886
Mapped reads with at least one deletion	1.09%
Homopolymer indels	42.15%

2.6. Chromosome stats

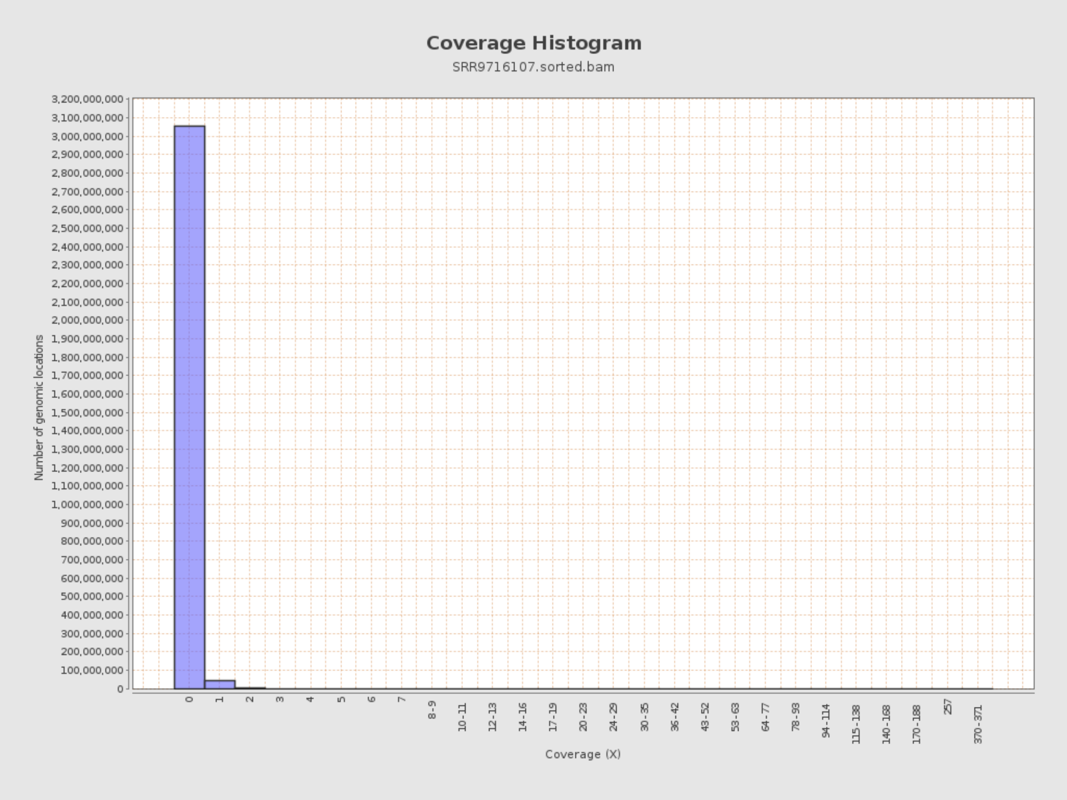
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3942177	0.0158	0.1941
chr2	243199373	3320803	0.0137	0.1969
chr3	198022430	2702416	0.0136	0.1237
chr4	191154276	2870605	0.015	0.1327
chr5	180915260	2681441	0.0148	0.1267
chr6	171115067	2499008	0.0146	0.142
chr7	159138663	2657519	0.0167	0.2043

chr8	146364022	2401147	0.0164	0.153
chr9	141213431	1568879	0.0111	0.1227
chr10	135534747	2076792	0.0153	0.185
chr11	135006516	1621832	0.012	0.1295
chr12	133851895	2337512	0.0175	0.1384
chr13	115169878	1437158	0.0125	0.1164
chr14	107349540	1566214	0.0146	0.1281
chr15	102531392	1675636	0.0163	0.1349
chr16	90354753	1610112	0.0178	0.1466
chr17	81195210	2079724	0.0256	0.1735
chr18	78077248	881055	0.0113	0.1703
chr19	59128983	1212259	0.0205	0.1897
chr20	63025520	1481693	0.0235	0.1644
chr21	48129895	592559	0.0123	0.1198
chr22	51304566	416612	0.0081	0.0948
chrMT	16571	4595	0.2773	0.5334
chrX	155270560	2408079	0.0155	0.1353
chrY	59373566	134858	0.0023	0.069

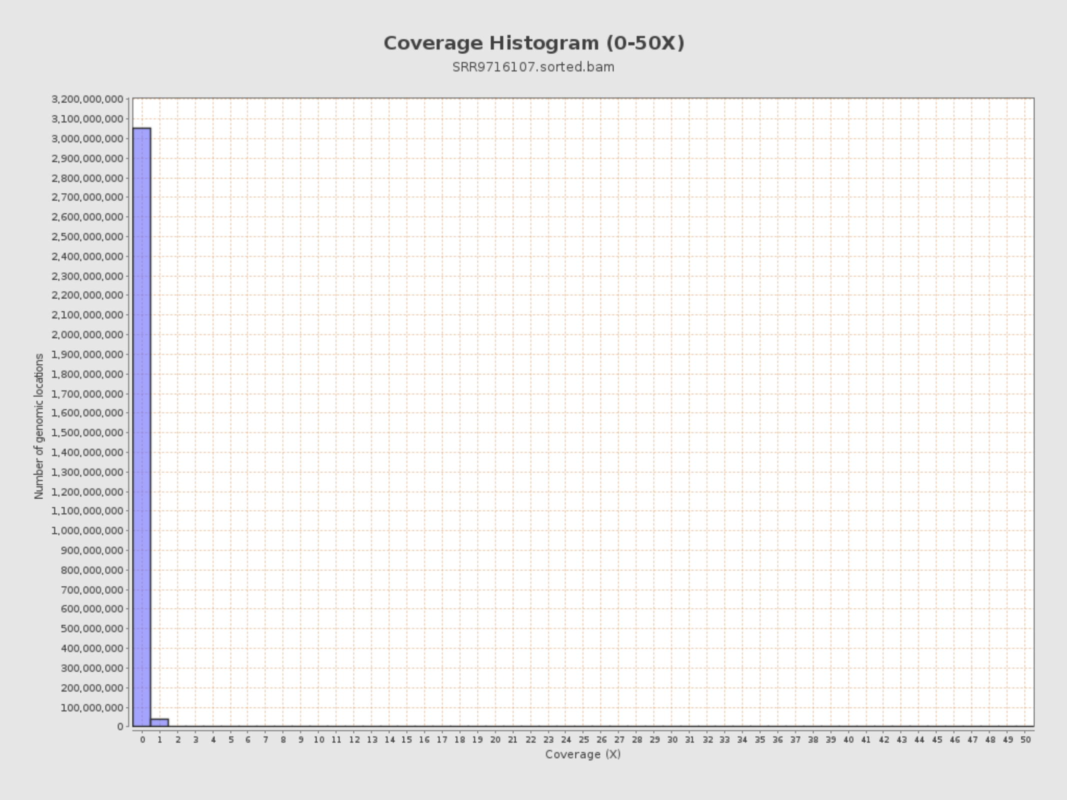
3. Results : Coverage across reference



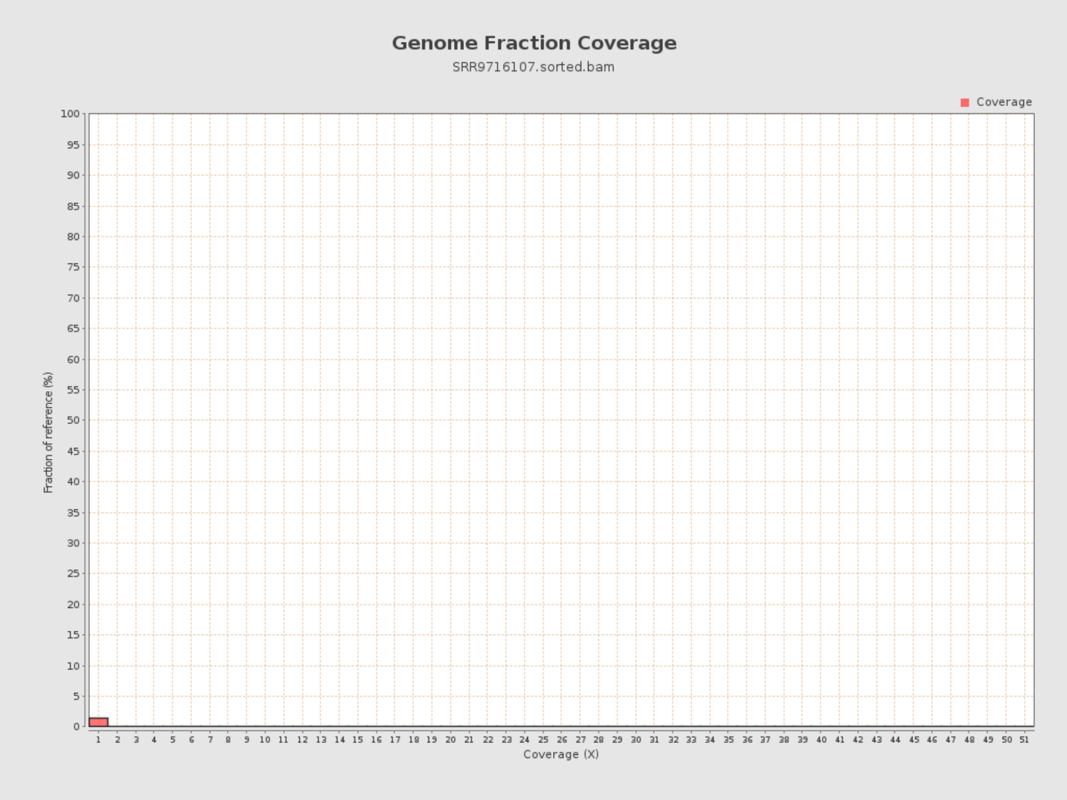
4. Results : Coverage Histogram



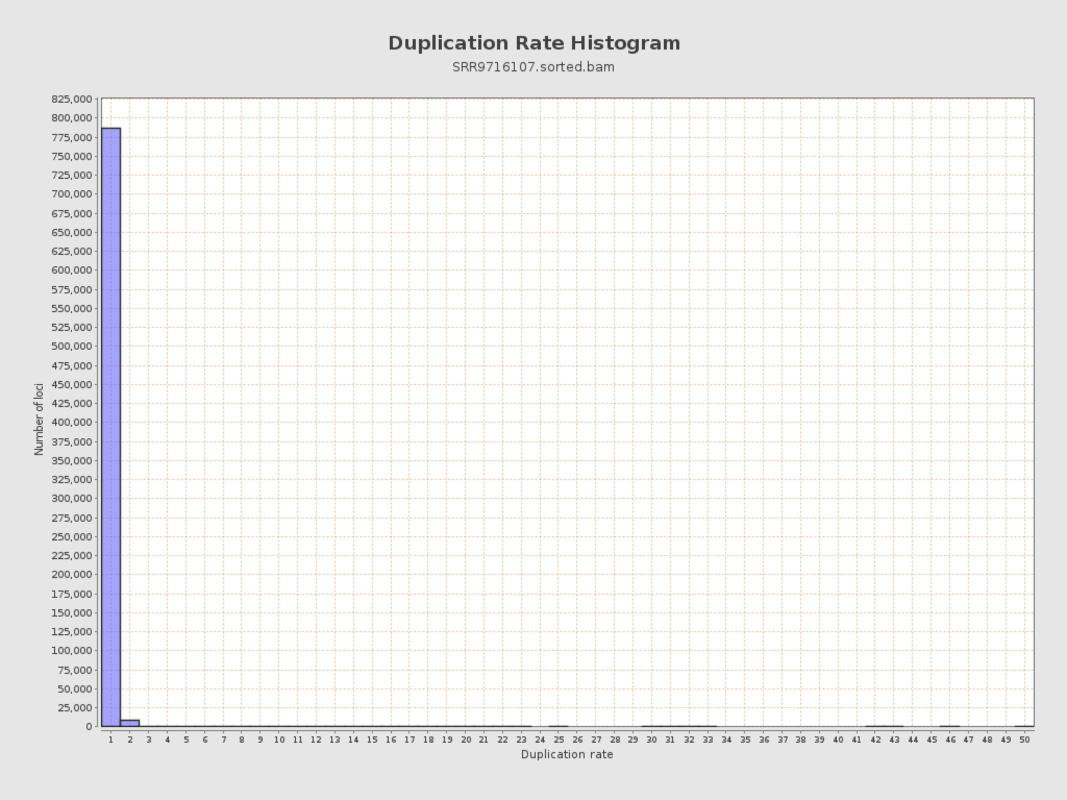
5. Results : Coverage Histogram (0-50X)



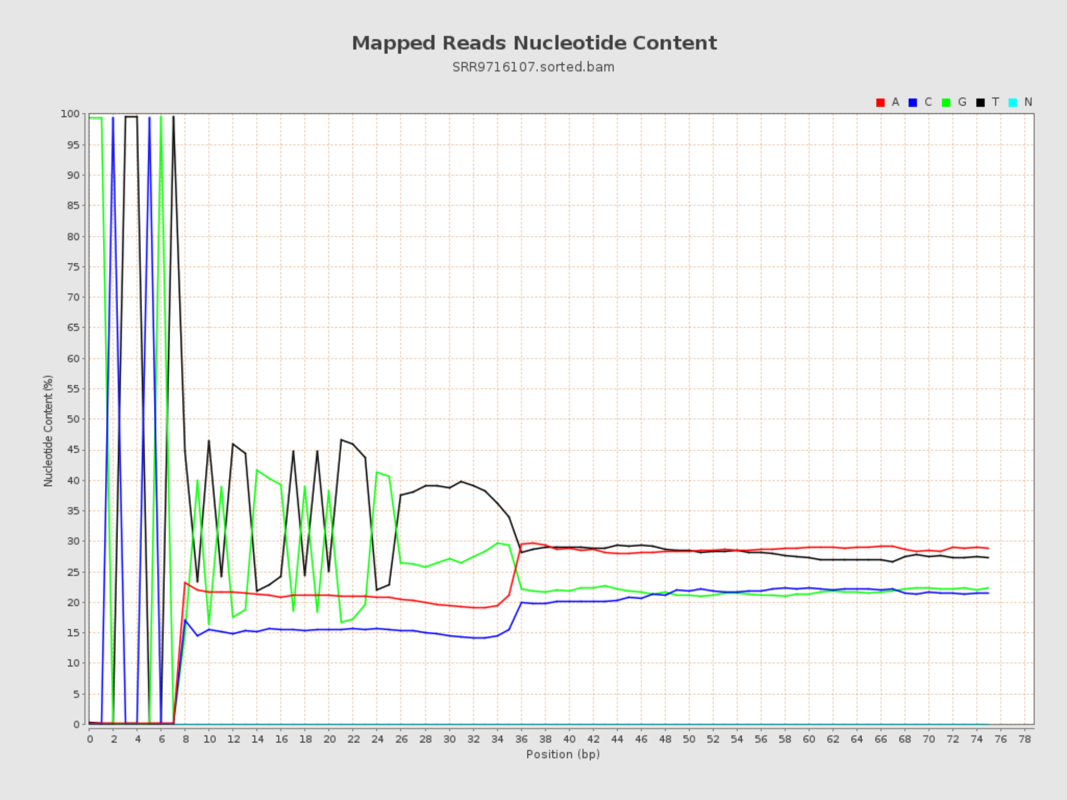
6. Results : Genome Fraction Coverage



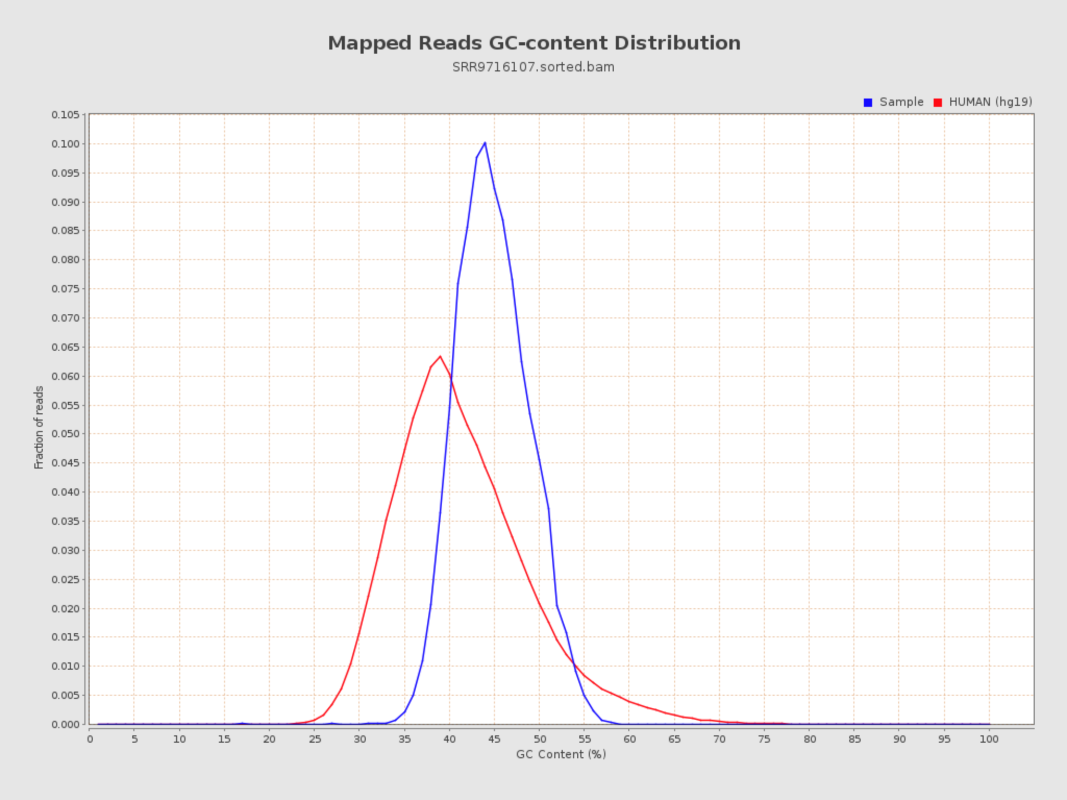
7. Results : Duplication Rate Histogram



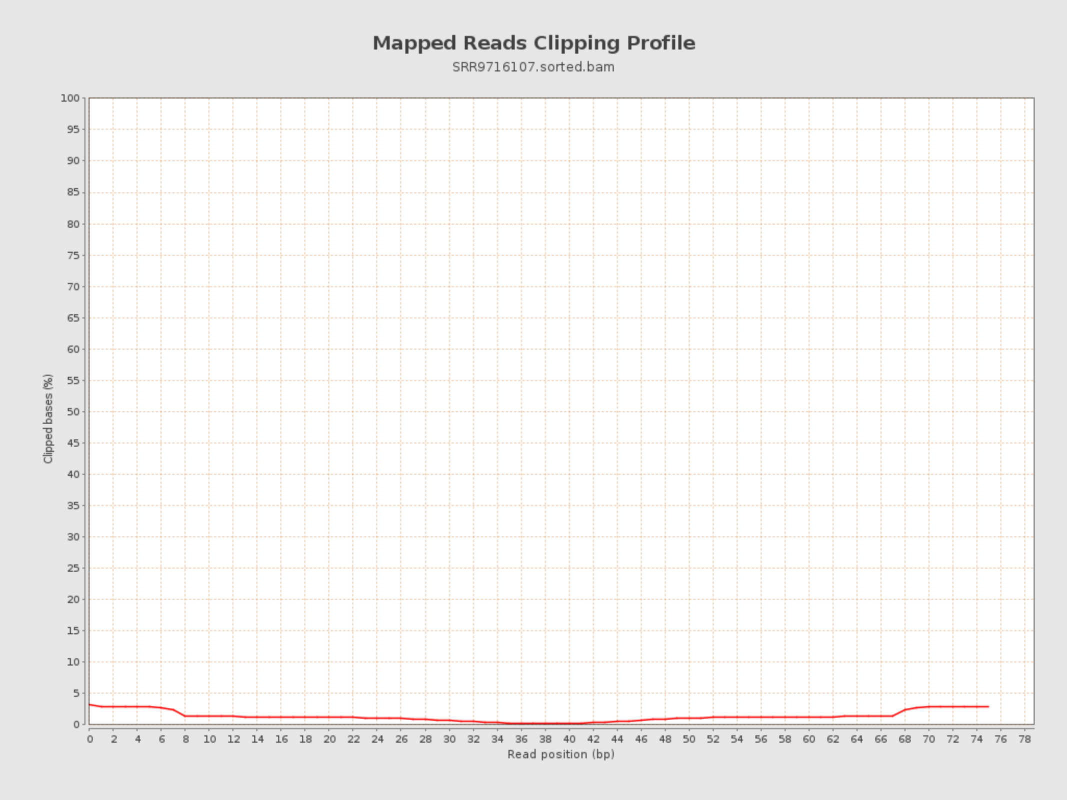
8. Results : Mapped Reads Nucleotide Content



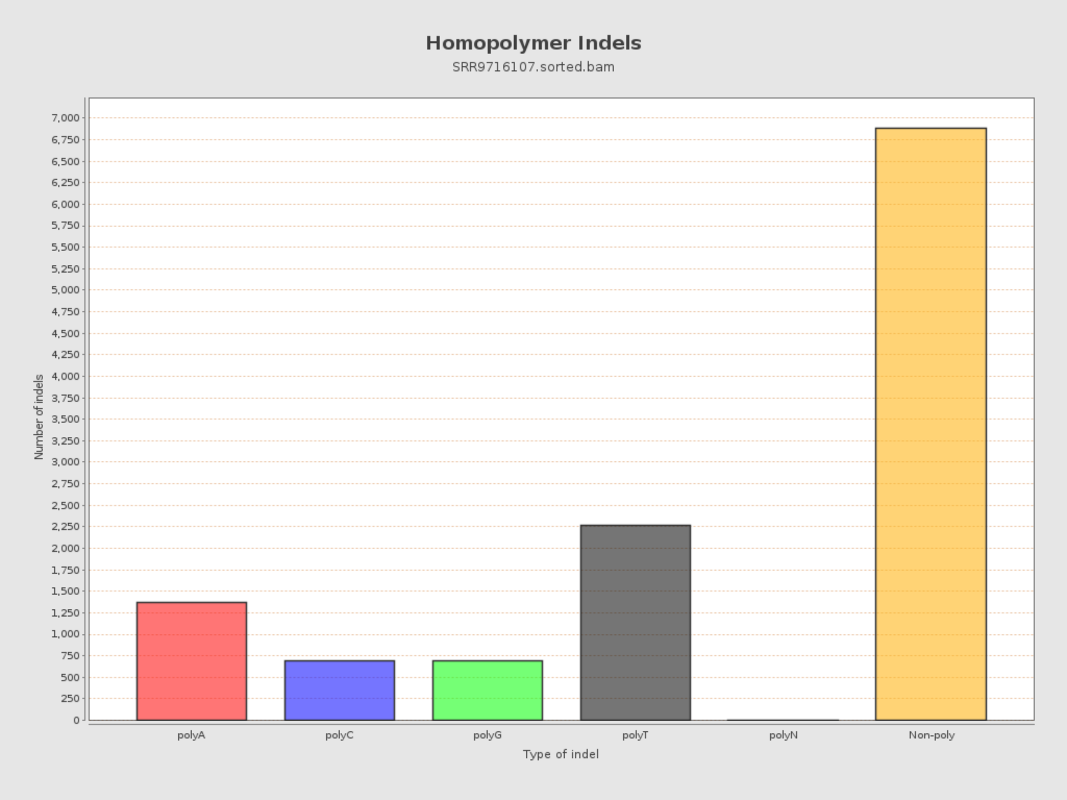
9. Results : Mapped Reads GC-content Distribution



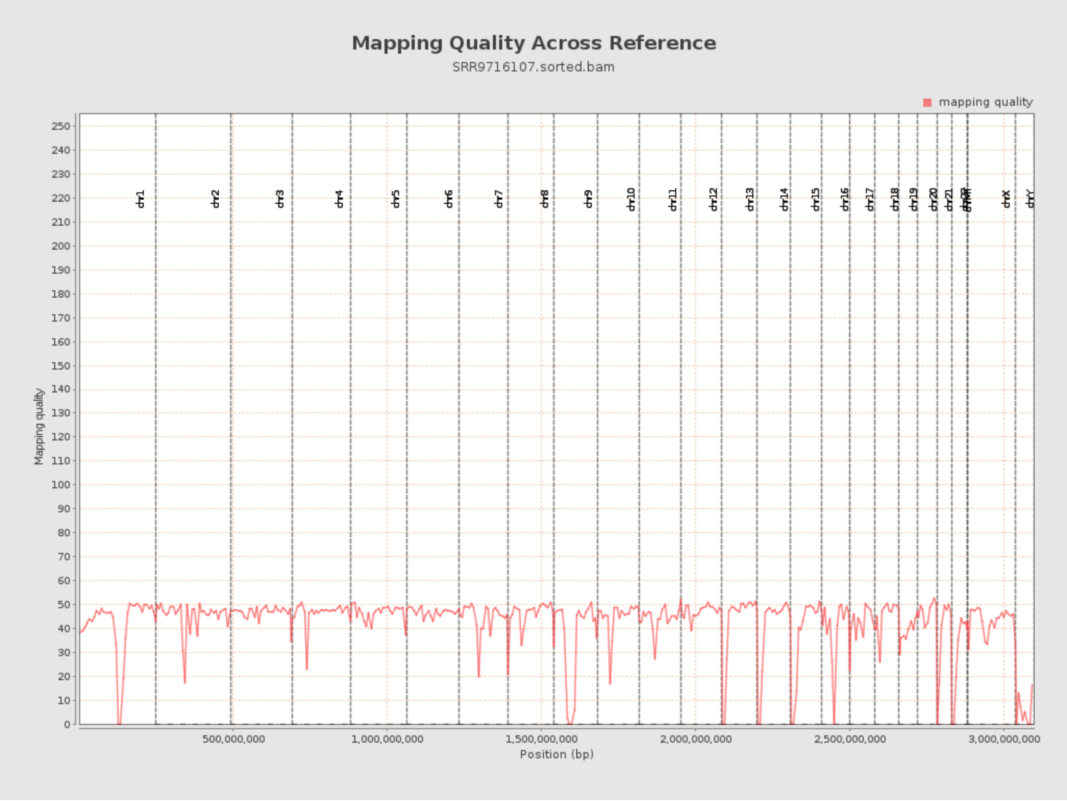
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram