Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 22:14:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716567.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_SRR9716567 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716567.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 22:14:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716567.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,025,467
Mapped reads	939,011 / 91.57%
Unmapped reads	86,456 / 8.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,995 / 2.05%
Read min/max/mean length	30 / 101 / 101.75
Duplicated reads (estimated)	29,978 / 2.92%
Duplication rate	2.5%
Clipped reads	958,390 / 93.46%

2.2. ACGT Content

Number/percentage of A's	18,127,368 / 25.04%
Number/percentage of C's	14,253,093 / 19.69%
Number/percentage of T's	22,171,760 / 30.62%
Number/percentage of G's	17,849,291 / 24.65%
Number/percentage of N's	2,958 / 0%
GC Percentage	44.34%

2.3. Coverage

Mean	0.0234

Standard Deviation	0.2056

2.4. Mapping Quality

Mean Mapping Quality	46.86

2.5. Mismatches and indels

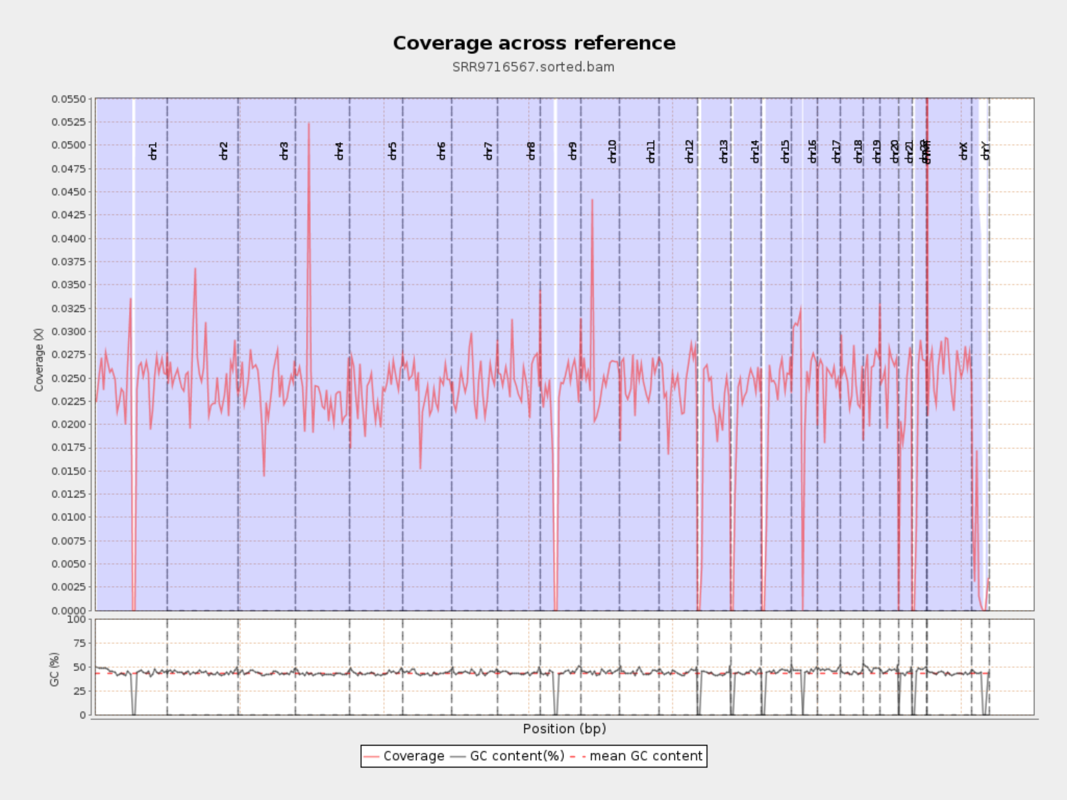
General error rate	0.69%
Mismatches	481,072
Insertions	6,194
Mapped reads with at least one insertion	0.65%
Deletions	13,803
Mapped reads with at least one deletion	1.45%
Homopolymer indels	39.13%

2.6. Chromosome stats

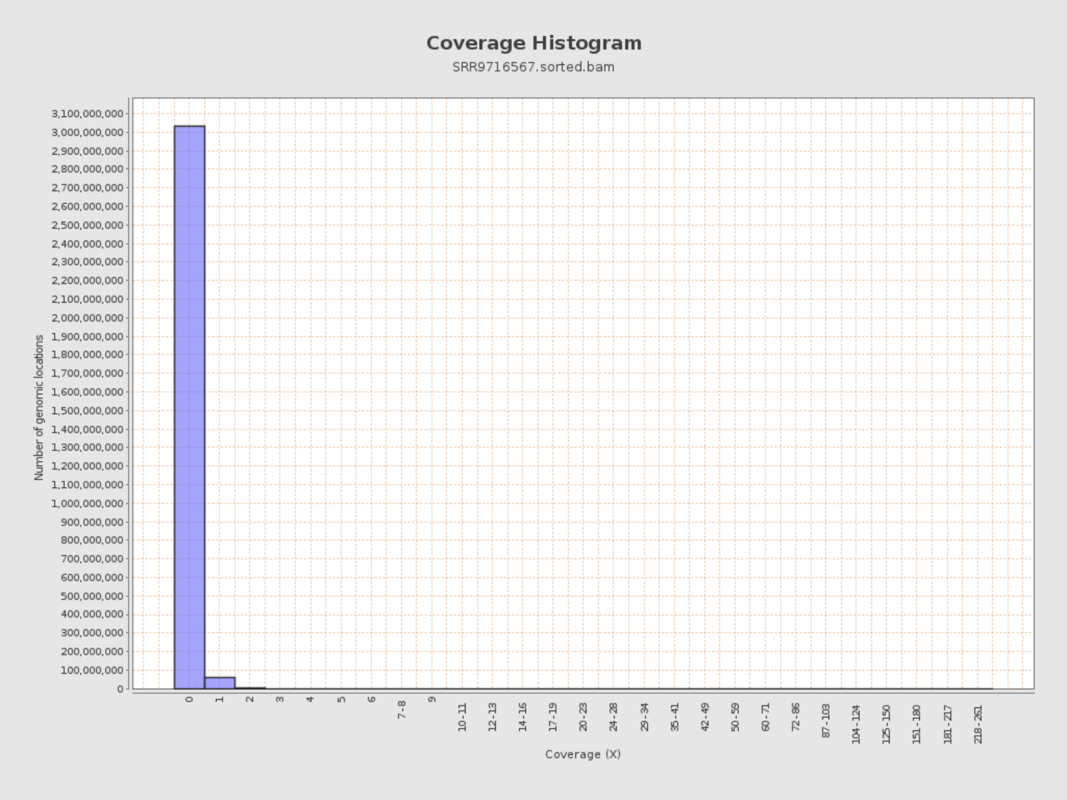
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5862913	0.0235	0.2904
chr2	243199373	6105445	0.0251	0.2224
chr3	198022430	4752627	0.024	0.168
chr4	191154276	4608399	0.0241	0.2205
chr5	180915260	4317708	0.0239	0.1681
chr6	171115067	4078379	0.0238	0.1727
chr7	159138663	3881569	0.0244	0.2155

chr8	146364022	3666664	0.0251	0.208
chr9	141213431	3036310	0.0215	0.1866
chr10	135534747	3499358	0.0258	0.2609
chr11	135006516	3345595	0.0248	0.2143
chr12	133851895	3260680	0.0244	0.1713
chr13	115169878	2202628	0.0191	0.1503
chr14	107349540	2188171	0.0204	0.1644
chr15	102531392	2082819	0.0203	0.155
chr16	90354753	2246372	0.0249	0.1814
chr17	81195210	2017174	0.0248	0.1855
chr18	78077248	1917879	0.0246	0.275
chr19	59128983	1519244	0.0257	0.2269
chr20	63025520	1595986	0.0253	0.183
chr21	48129895	998219	0.0207	0.1913
chr22	51304566	961540	0.0187	0.1535
chrMT	16571	4504	0.2718	0.5519
chrX	155270560	4033151	0.026	0.184
chrY	59373566	250244	0.0042	0.164

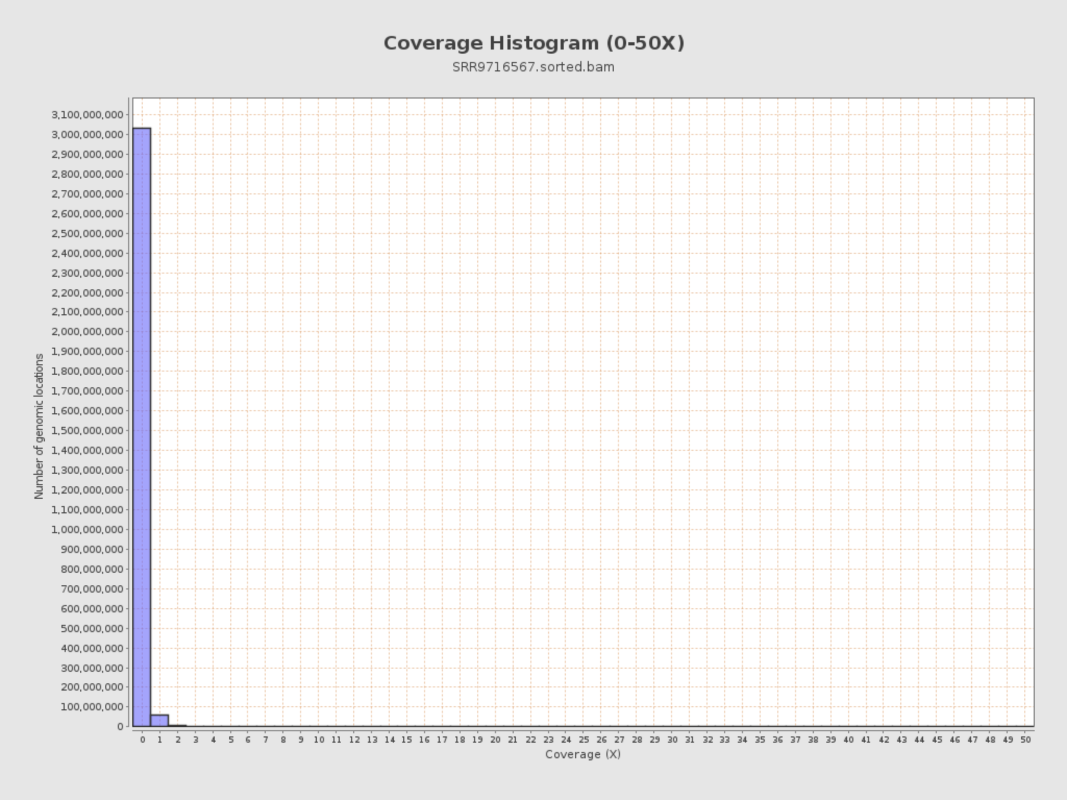
3. Results : Coverage across reference



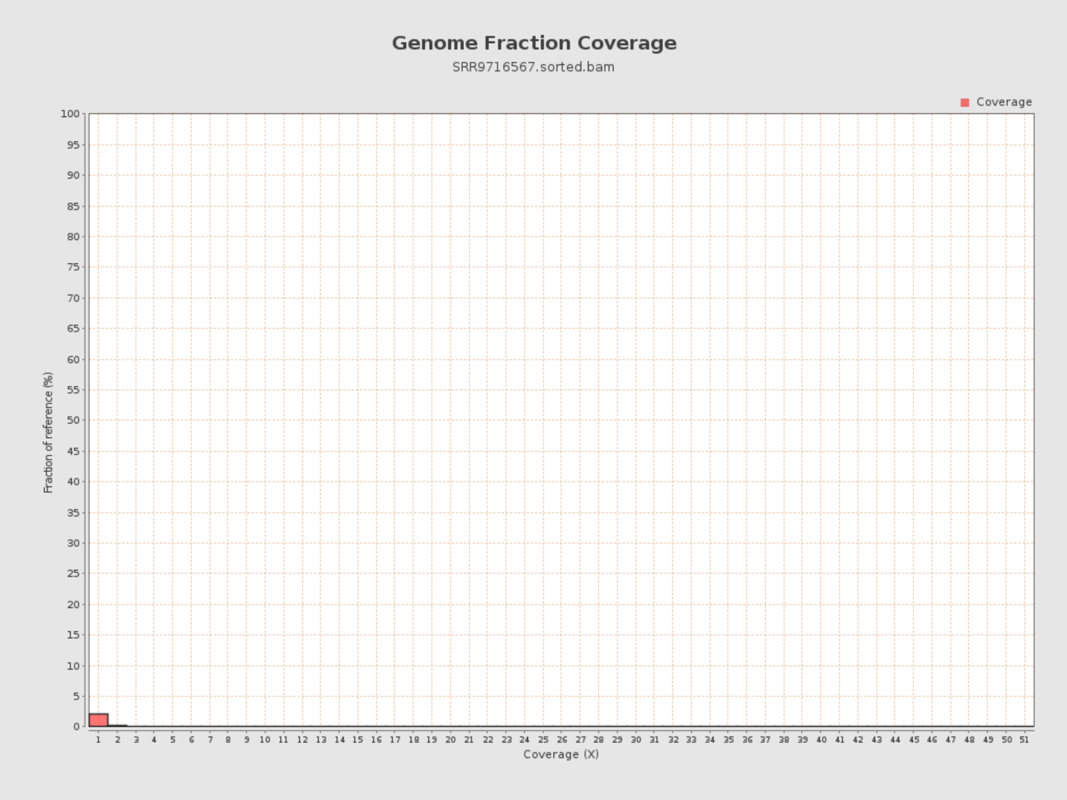
4. Results : Coverage Histogram



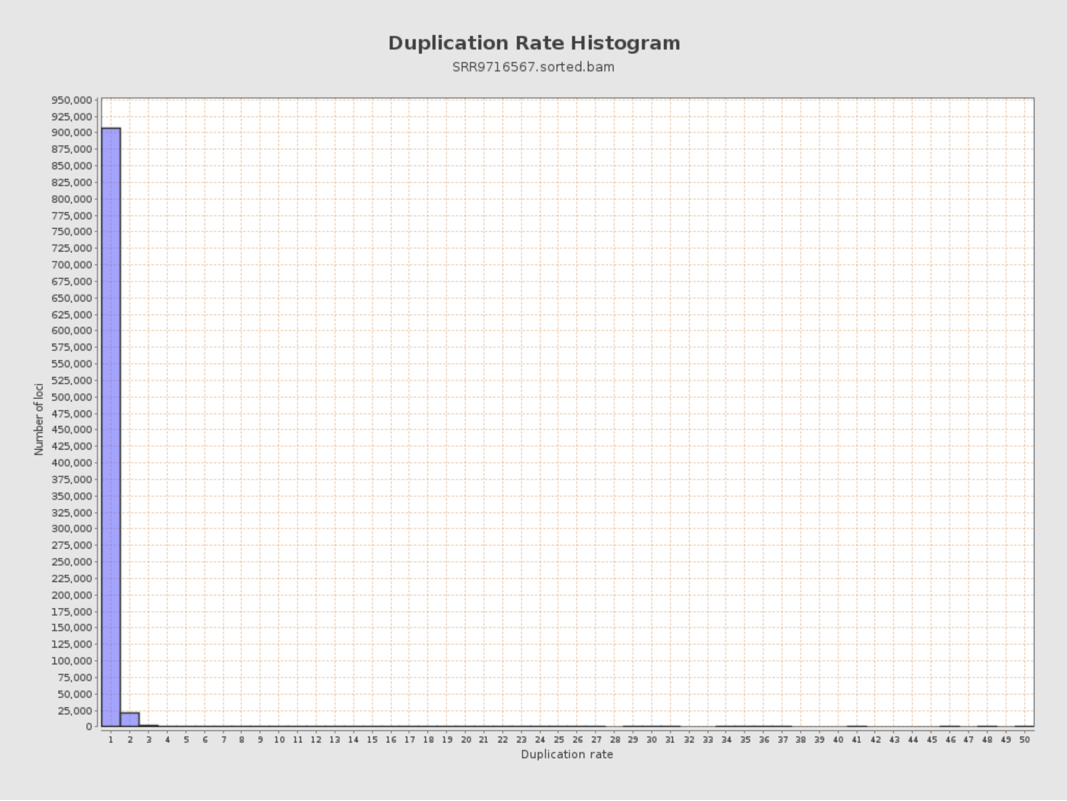
5. Results : Coverage Histogram (0-50X)



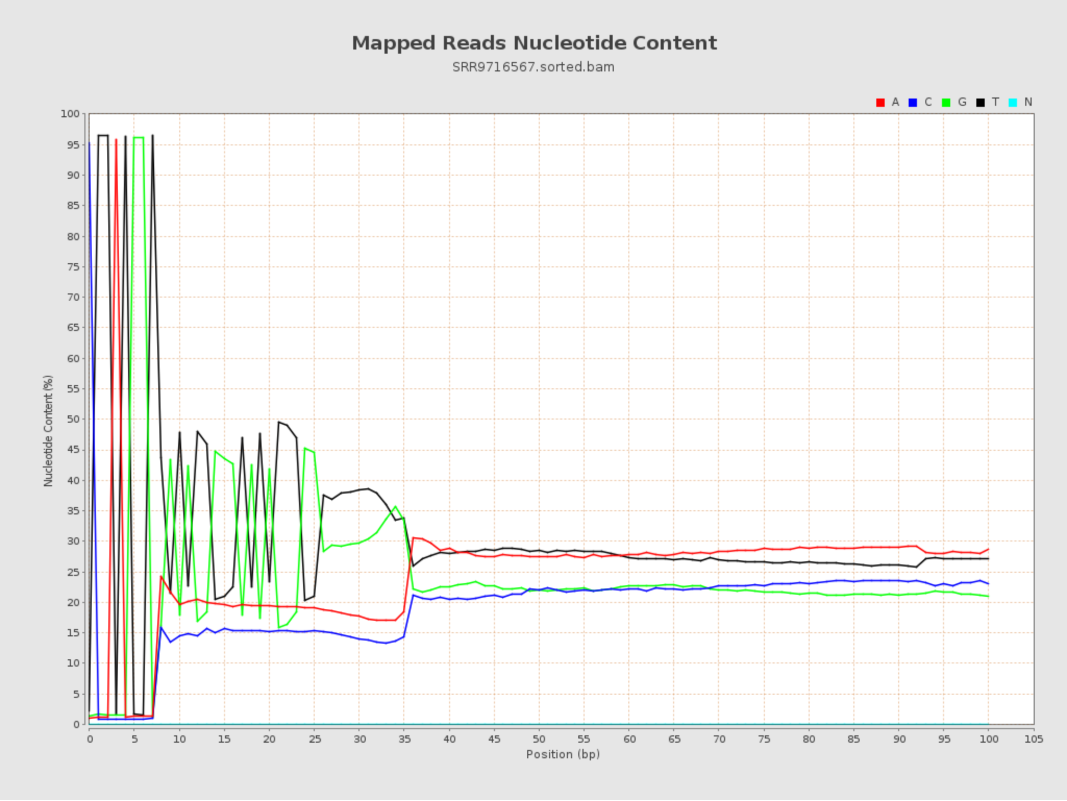
6. Results : Genome Fraction Coverage



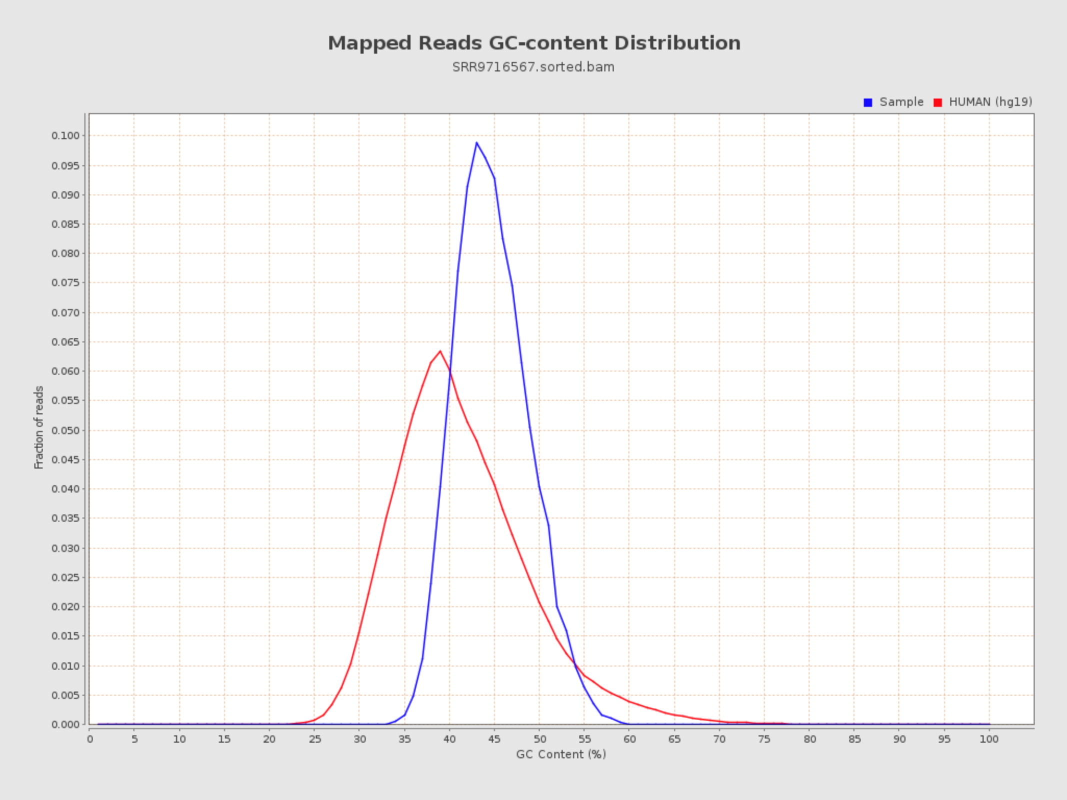
7. Results : Duplication Rate Histogram



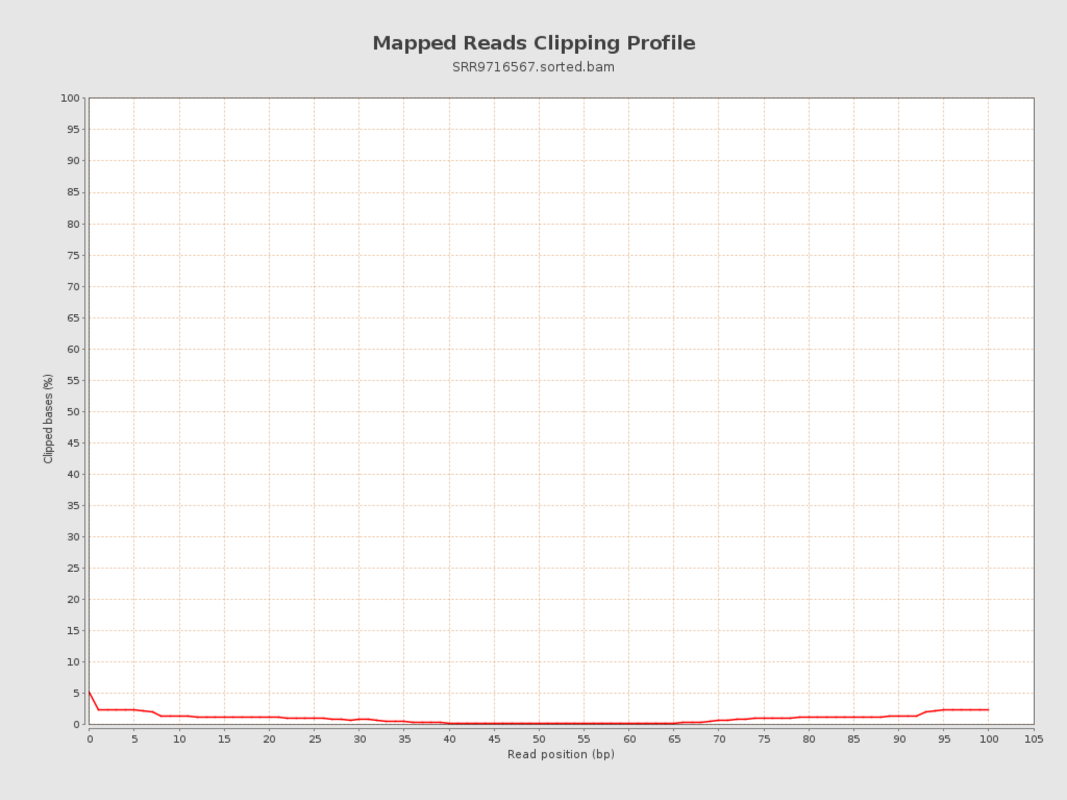
8. Results : Mapped Reads Nucleotide Content



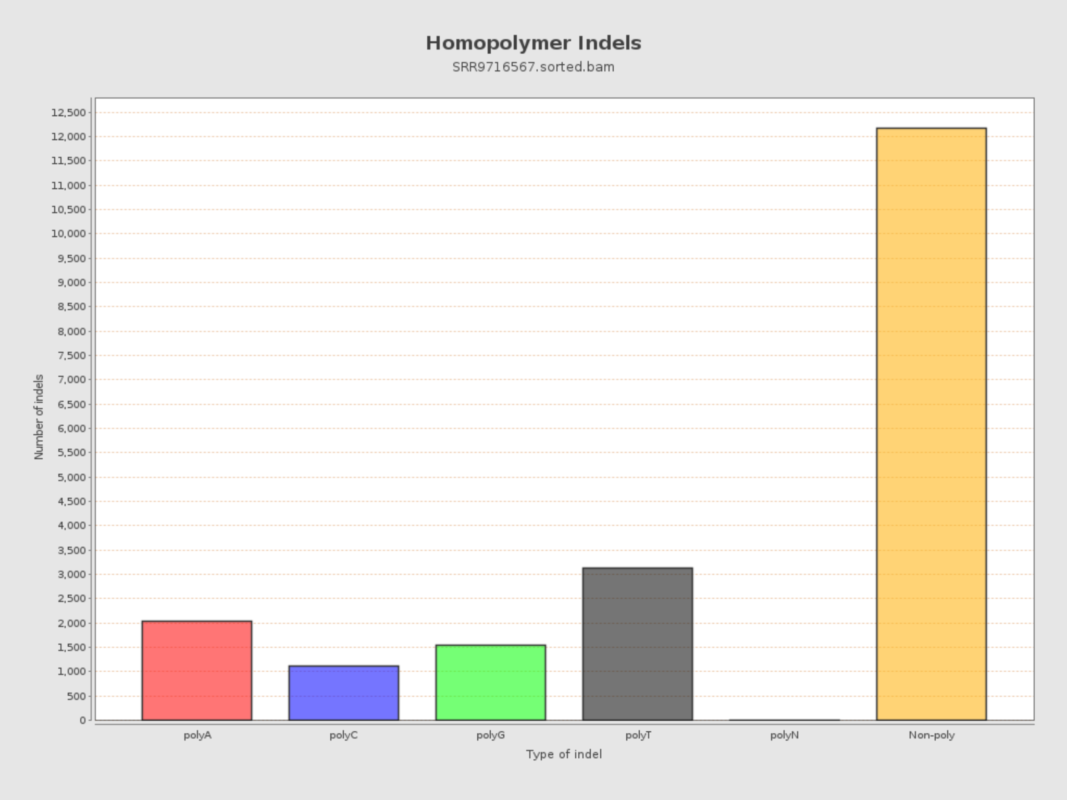
9. Results : Mapped Reads GC-content Distribution



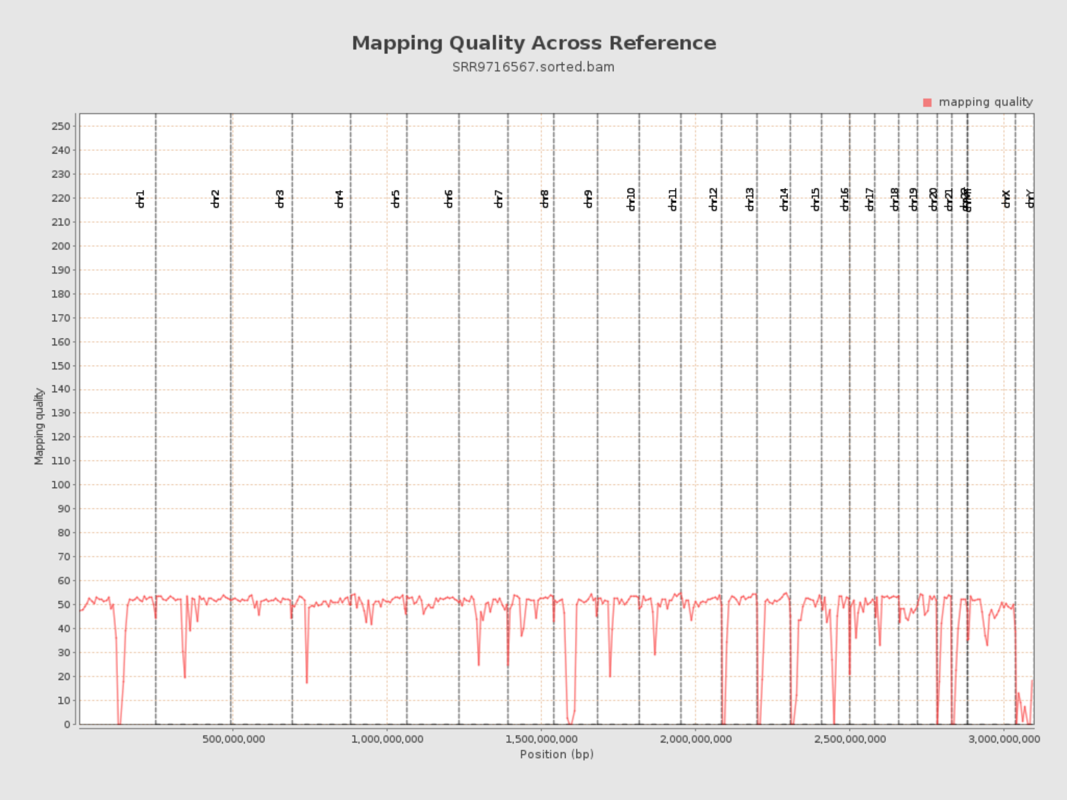
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram