Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 02:44:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716654.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_SRR9716654 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716654.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 02:44:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716654.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,015,601
Mapped reads	775,903 / 76.4%
Unmapped reads	239,698 / 23.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,126 / 2.18%
Read min/max/mean length	30 / 101 / 101.78
Duplicated reads (estimated)	12,646 / 1.25%
Duplication rate	0.99%
Clipped reads	797,273 / 78.5%

2.2. ACGT Content

Number/percentage of A's	15,140,029 / 26.27%
Number/percentage of C's	11,697,201 / 20.29%
Number/percentage of T's	17,410,191 / 30.2%
Number/percentage of G's	13,388,374 / 23.23%
Number/percentage of N's	7,328 / 0.01%
GC Percentage	43.52%

2.3. Coverage

Mean	0.0186

Standard Deviation	0.1868

2.4. Mapping Quality

Mean Mapping Quality	44.96

2.5. Mismatches and indels

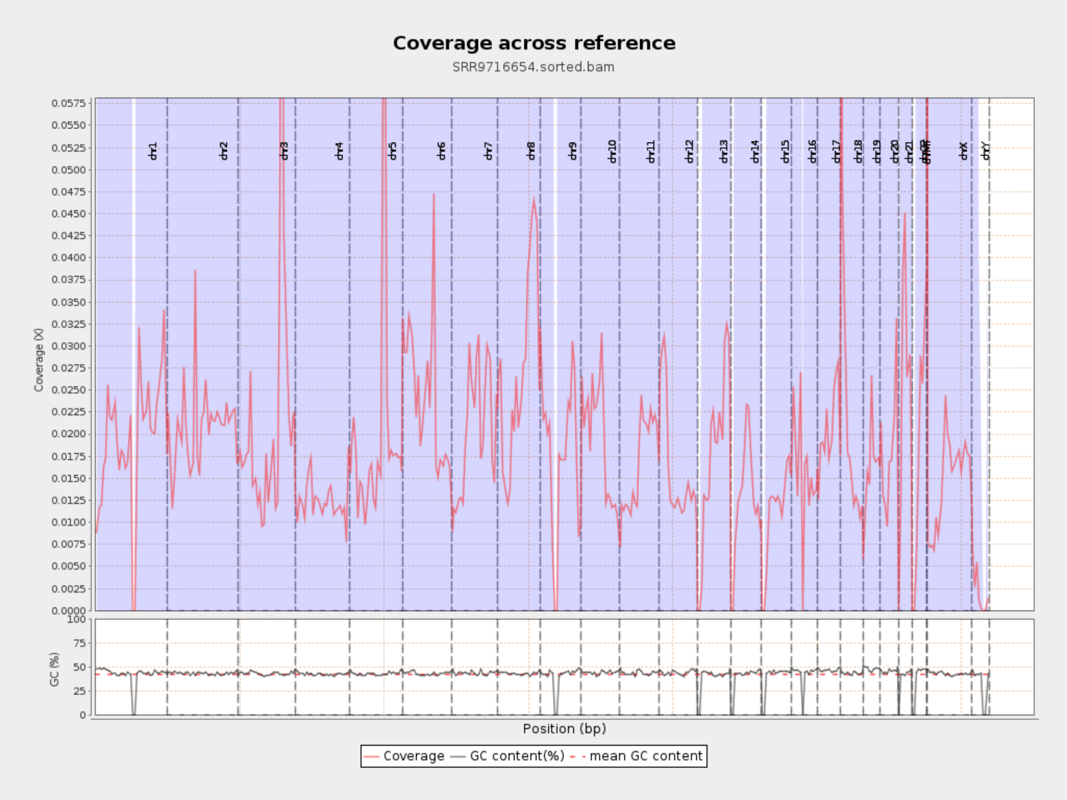
General error rate	0.77%
Mismatches	435,499
Insertions	4,464
Mapped reads with at least one insertion	0.57%
Deletions	11,457
Mapped reads with at least one deletion	1.46%
Homopolymer indels	40.07%

2.6. Chromosome stats

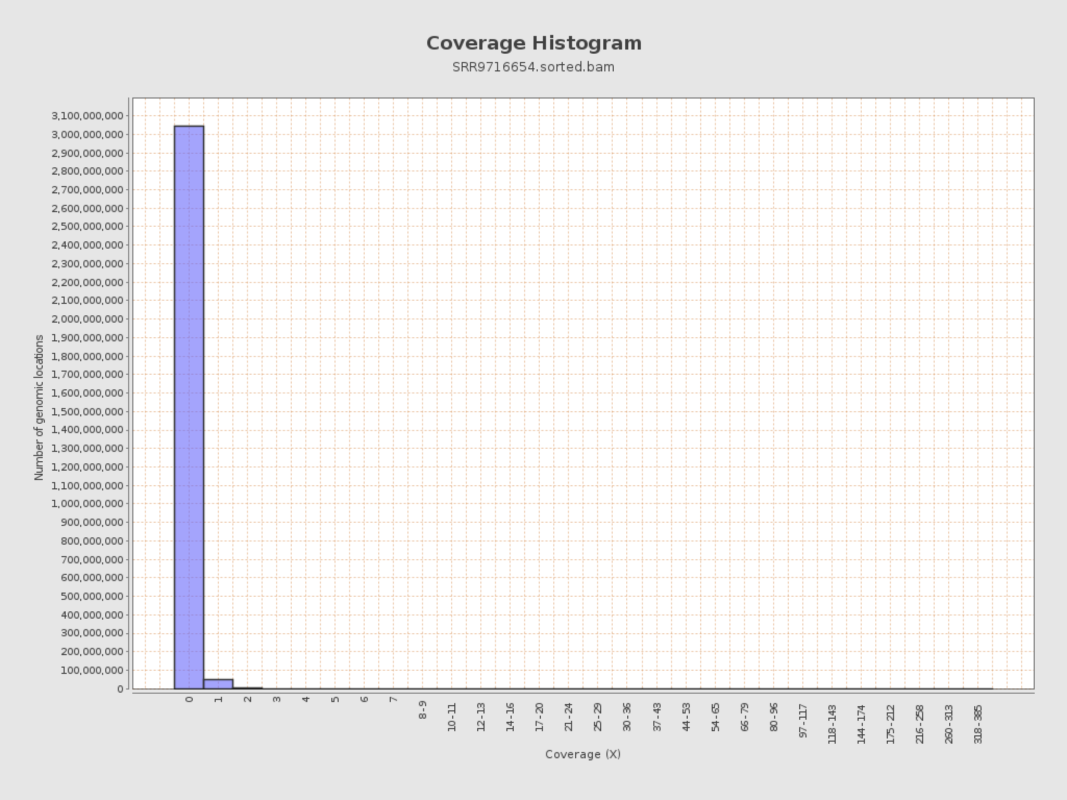
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4865060	0.0195	0.1963
chr2	243199373	5089016	0.0209	0.2961
chr3	198022430	4420906	0.0223	0.1598
chr4	191154276	2379622	0.0124	0.1193
chr5	180915260	3708866	0.0205	0.1523
chr6	171115067	4161639	0.0243	0.1739
chr7	159138663	3253213	0.0204	0.2311

chr8	146364022	4014765	0.0274	0.256
chr9	141213431	2504802	0.0177	0.1828
chr10	135534747	2626821	0.0194	0.1704
chr11	135006516	2272101	0.0168	0.16
chr12	133851895	2188447	0.0163	0.1354
chr13	115169878	2053852	0.0178	0.14
chr14	107349540	1362142	0.0127	0.1273
chr15	102531392	1125783	0.011	0.1107
chr16	90354753	1414391	0.0157	0.1398
chr17	81195210	1683407	0.0207	0.1649
chr18	78077248	1768433	0.0226	0.3223
chr19	59128983	976722	0.0165	0.196
chr20	63025520	1133959	0.018	0.1494
chr21	48129895	1266314	0.0263	0.1748
chr22	51304566	951863	0.0186	0.146
chrMT	16571	4585	0.2767	0.5979
chrX	155270560	2314237	0.0149	0.1491
chrY	59373566	121898	0.0021	0.0616

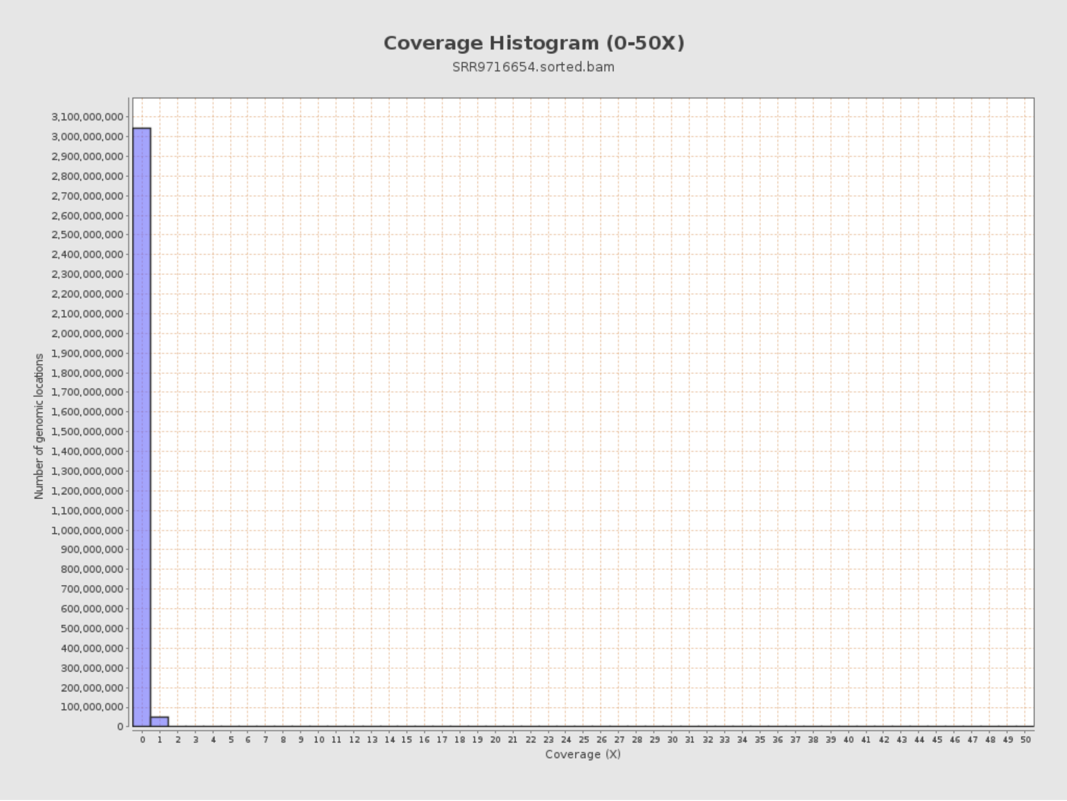
3. Results : Coverage across reference



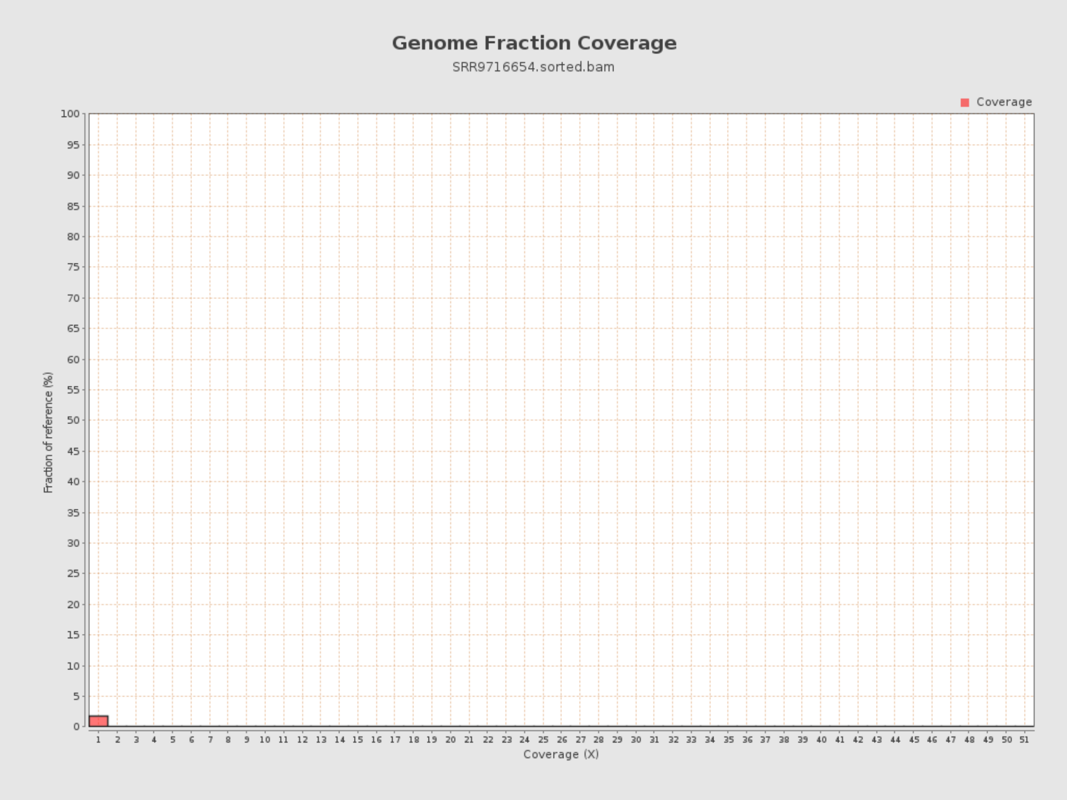
4. Results : Coverage Histogram



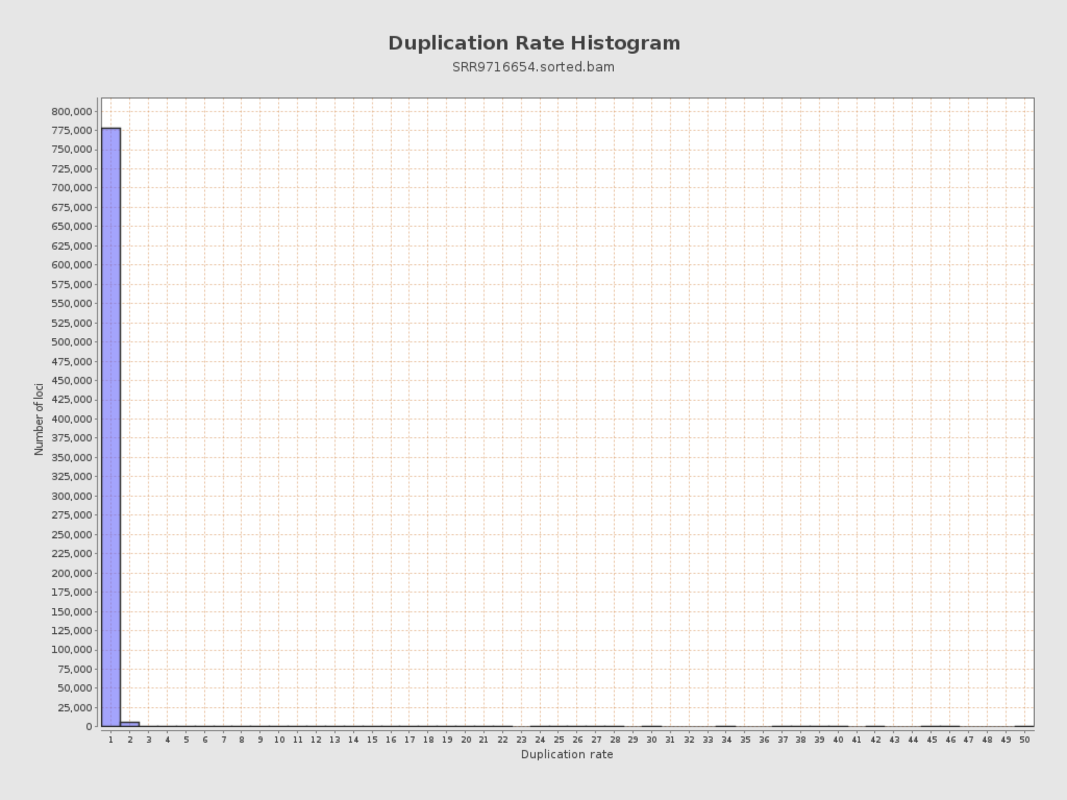
5. Results : Coverage Histogram (0-50X)



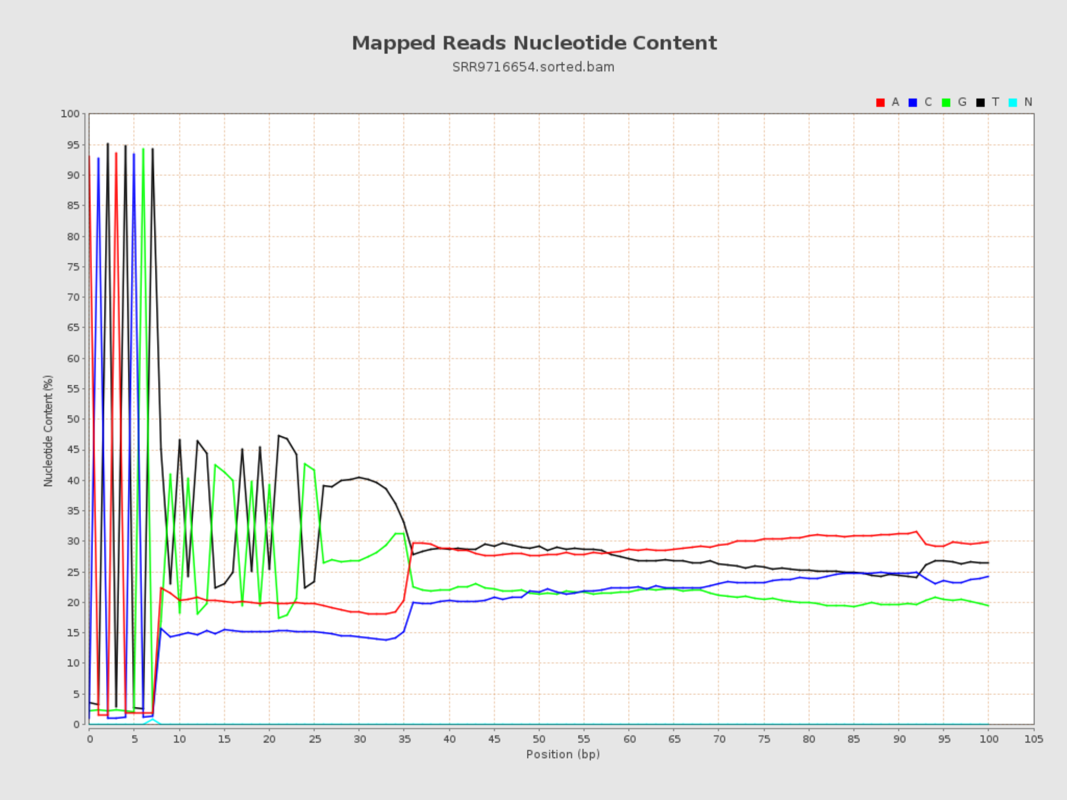
6. Results : Genome Fraction Coverage



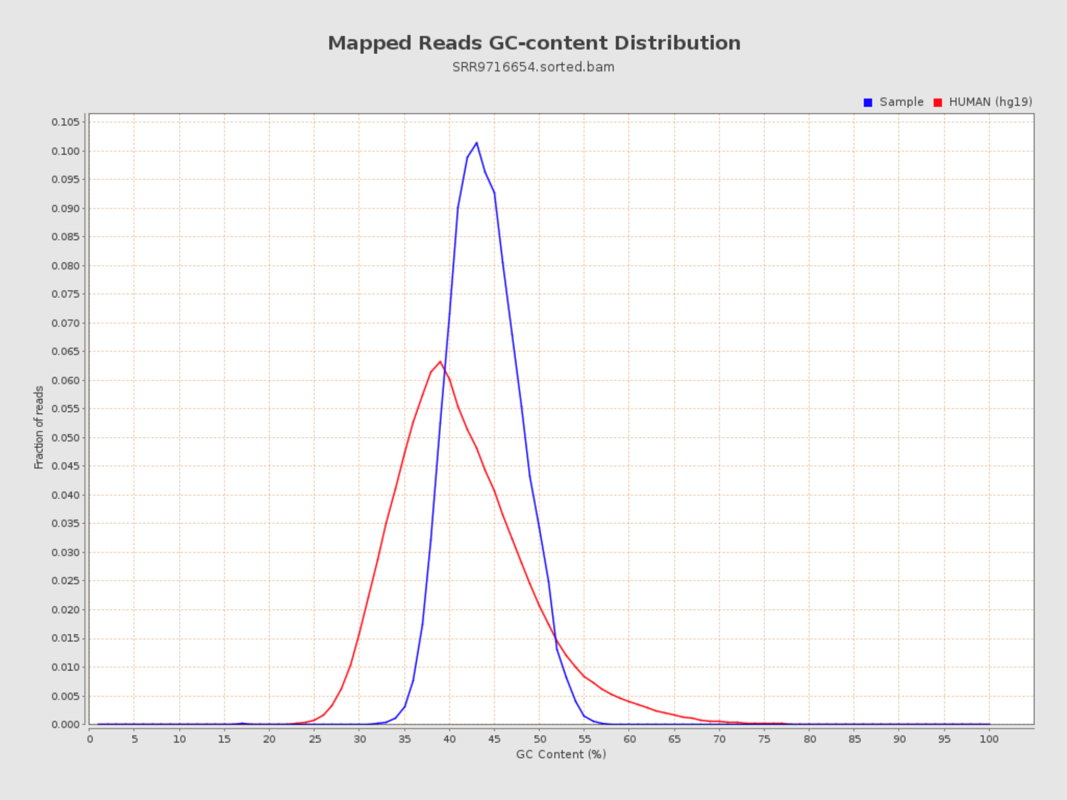
7. Results : Duplication Rate Histogram



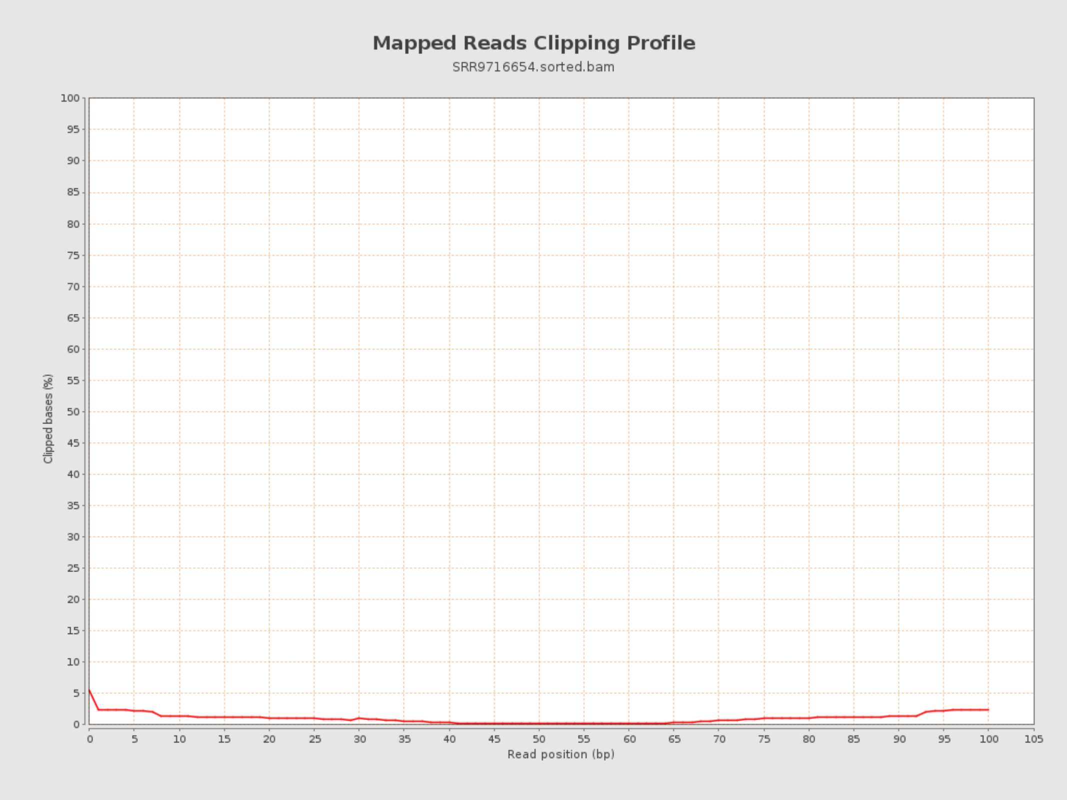
8. Results : Mapped Reads Nucleotide Content



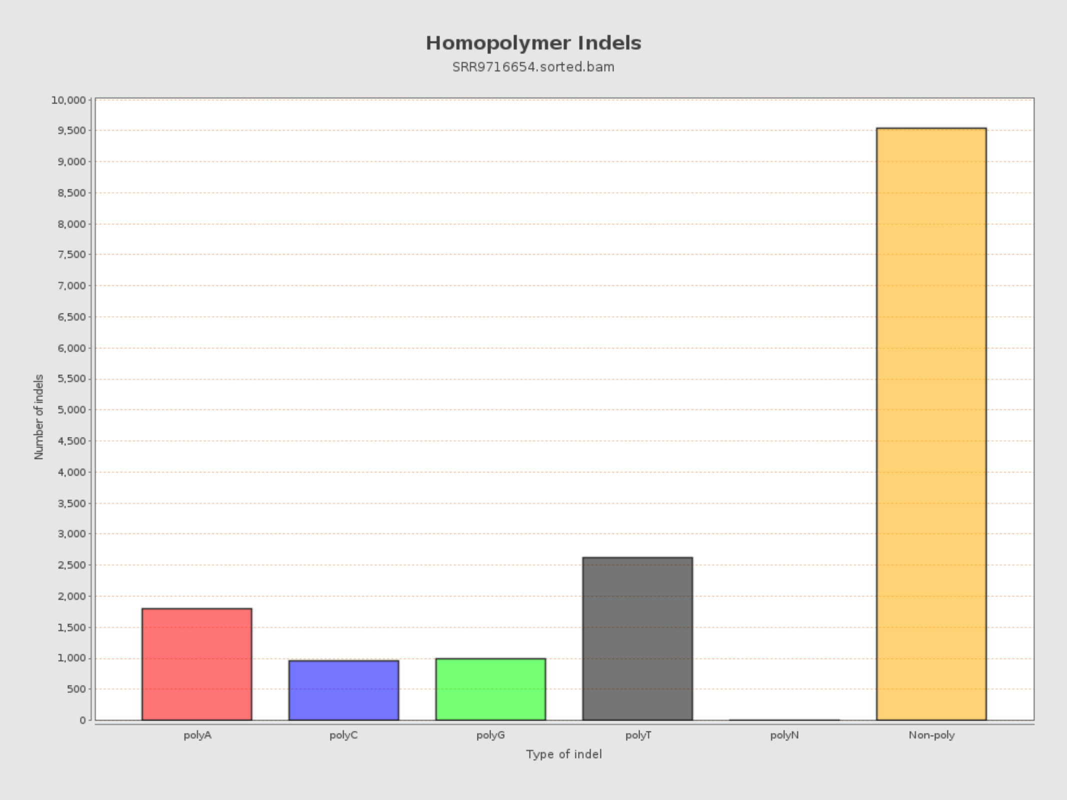
9. Results : Mapped Reads GC-content Distribution



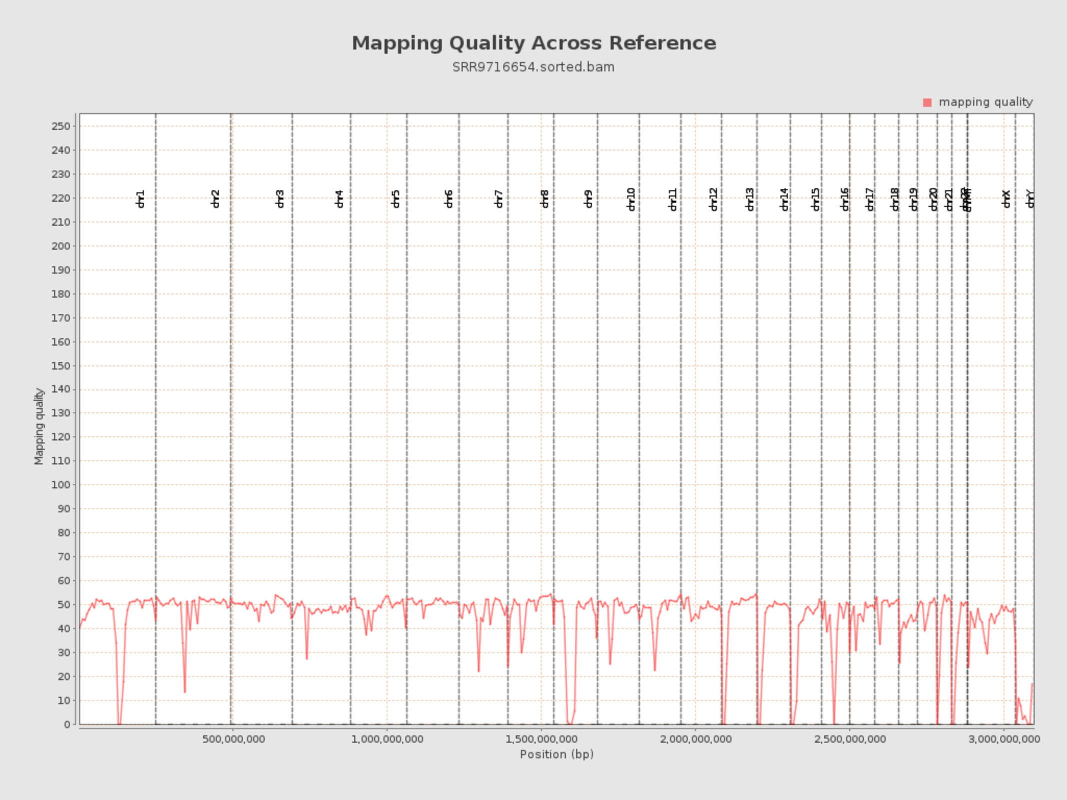
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram