Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 22:20:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716174.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_SRR9716174 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716174.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 22:20:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716174.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	869,662
Mapped reads	750,167 / 86.26%
Unmapped reads	119,495 / 13.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,086 / 2.42%
Read min/max/mean length	30 / 101 / 101.88
Duplicated reads (estimated)	12,879 / 1.48%
Duplication rate	1.08%
Clipped reads	769,684 / 88.5%

2.2. ACGT Content

Number/percentage of A's	14,229,632 / 25.57%
Number/percentage of C's	11,363,650 / 20.42%
Number/percentage of T's	16,700,418 / 30.01%
Number/percentage of G's	13,343,818 / 23.98%
Number/percentage of N's	6,683 / 0.01%
GC Percentage	44.4%

2.3. Coverage

Mean	0.018

Standard Deviation	0.1772

2.4. Mapping Quality

Mean Mapping Quality	44.21

2.5. Mismatches and indels

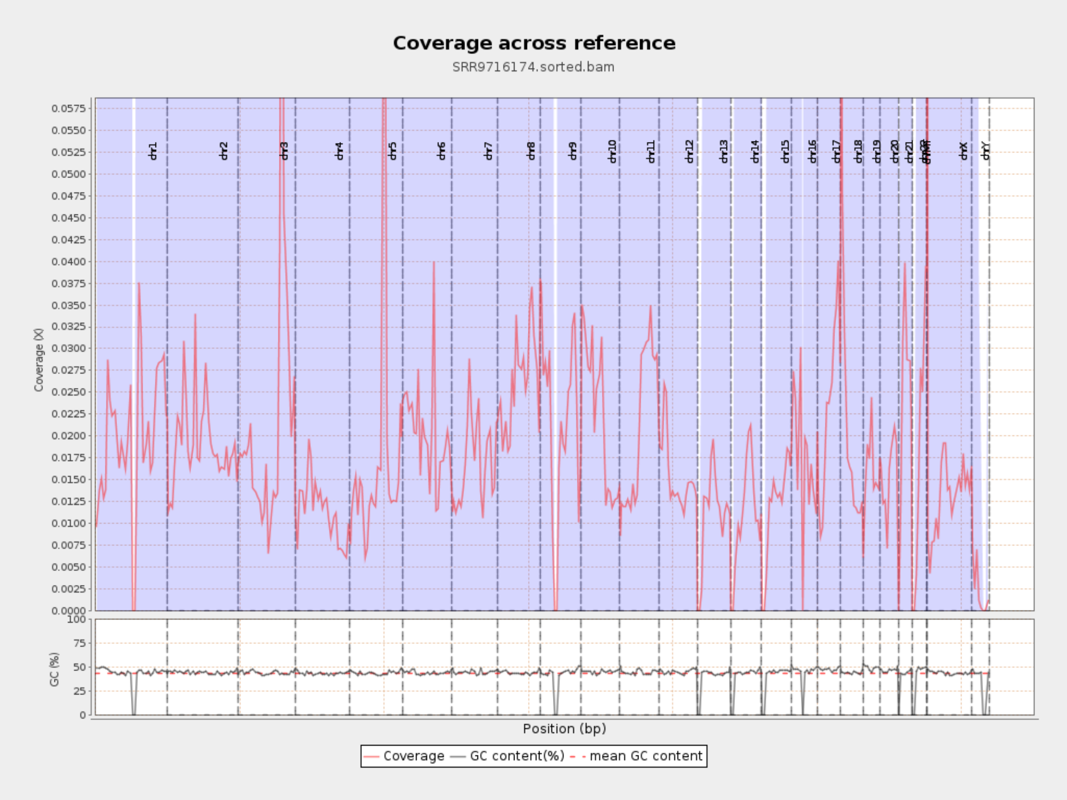
General error rate	0.77%
Mismatches	416,950
Insertions	5,093
Mapped reads with at least one insertion	0.67%
Deletions	11,307
Mapped reads with at least one deletion	1.49%
Homopolymer indels	38.39%

2.6. Chromosome stats

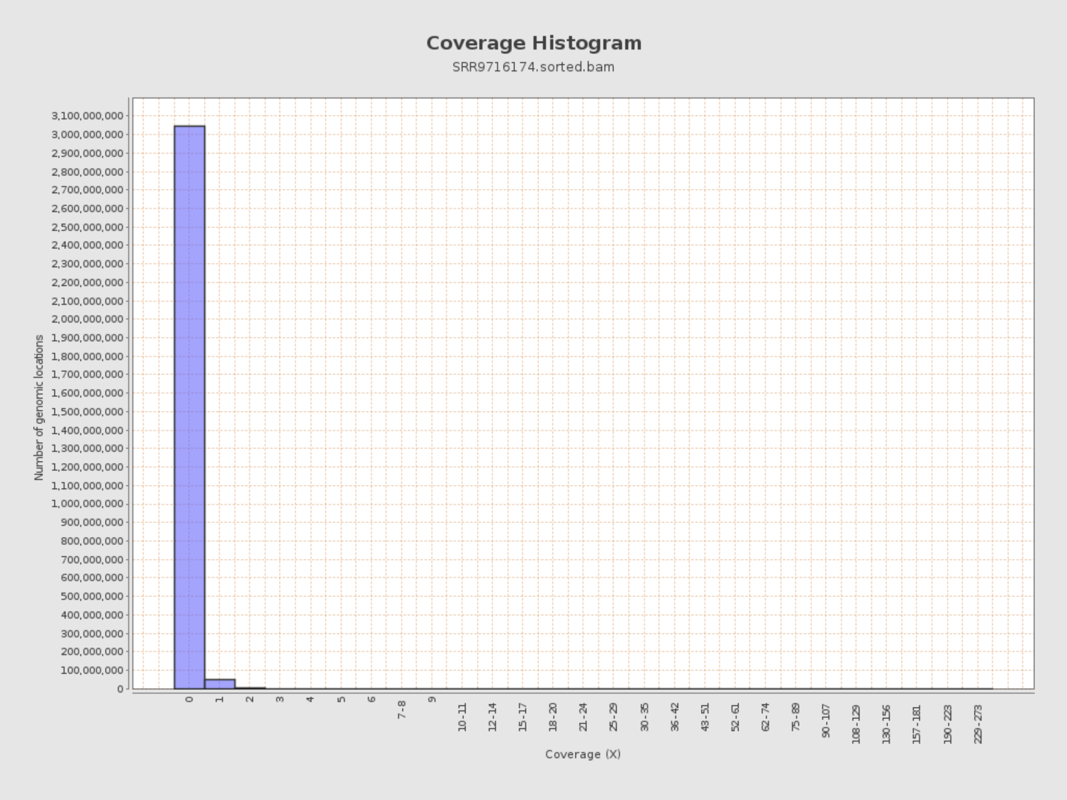
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4938986	0.0198	0.2161
chr2	243199373	4674857	0.0192	0.2504
chr3	198022430	4548348	0.023	0.1628
chr4	191154276	2155441	0.0113	0.1203
chr5	180915260	3324539	0.0184	0.1439
chr6	171115067	3508472	0.0205	0.1635
chr7	159138663	2705431	0.017	0.2148

chr8	146364022	3831581	0.0262	0.2206
chr9	141213431	3026728	0.0214	0.1828
chr10	135534747	3056255	0.0225	0.2017
chr11	135006516	2852758	0.0211	0.1716
chr12	133851895	2071108	0.0155	0.1306
chr13	115169878	1268467	0.011	0.1088
chr14	107349540	1165885	0.0109	0.1154
chr15	102531392	1202866	0.0117	0.1135
chr16	90354753	1554185	0.0172	0.1464
chr17	81195210	1877691	0.0231	0.1639
chr18	78077248	1694212	0.0217	0.2678
chr19	59128983	960781	0.0162	0.2053
chr20	63025520	953905	0.0151	0.1356
chr21	48129895	1193829	0.0248	0.1705
chr22	51304566	929822	0.0181	0.1438
chrMT	16571	8089	0.4881	0.8196
chrX	155270560	2028786	0.0131	0.132
chrY	59373566	131355	0.0022	0.0749

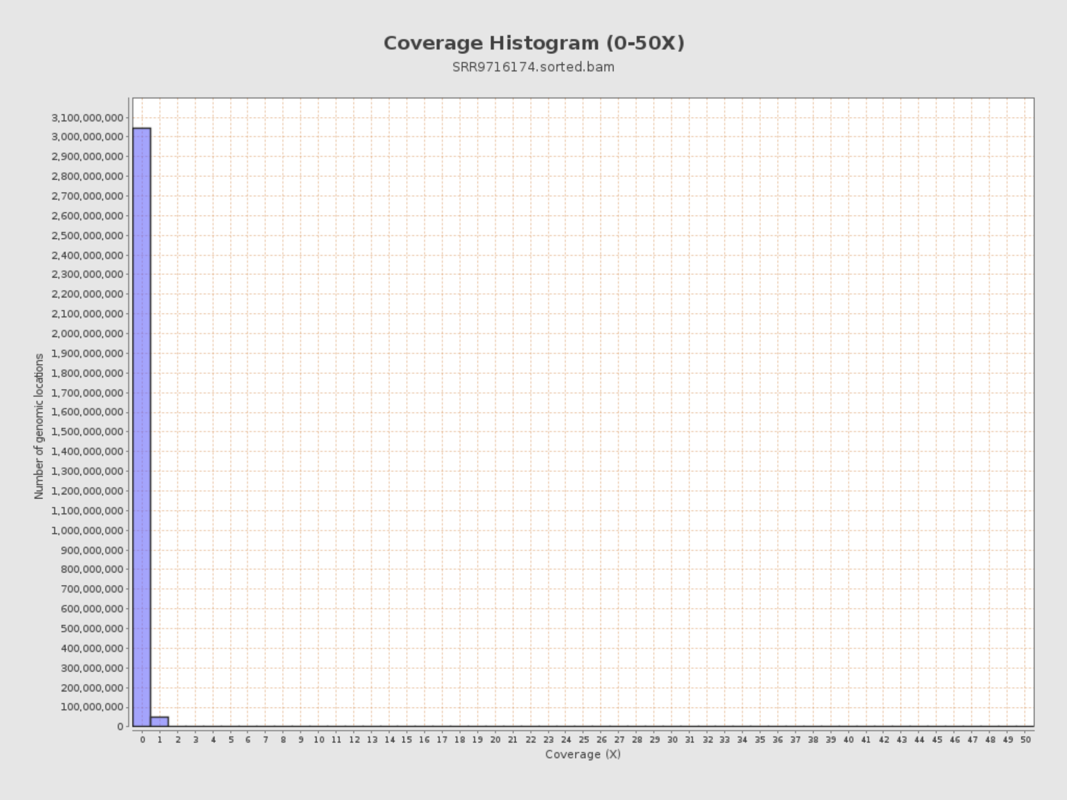
3. Results : Coverage across reference



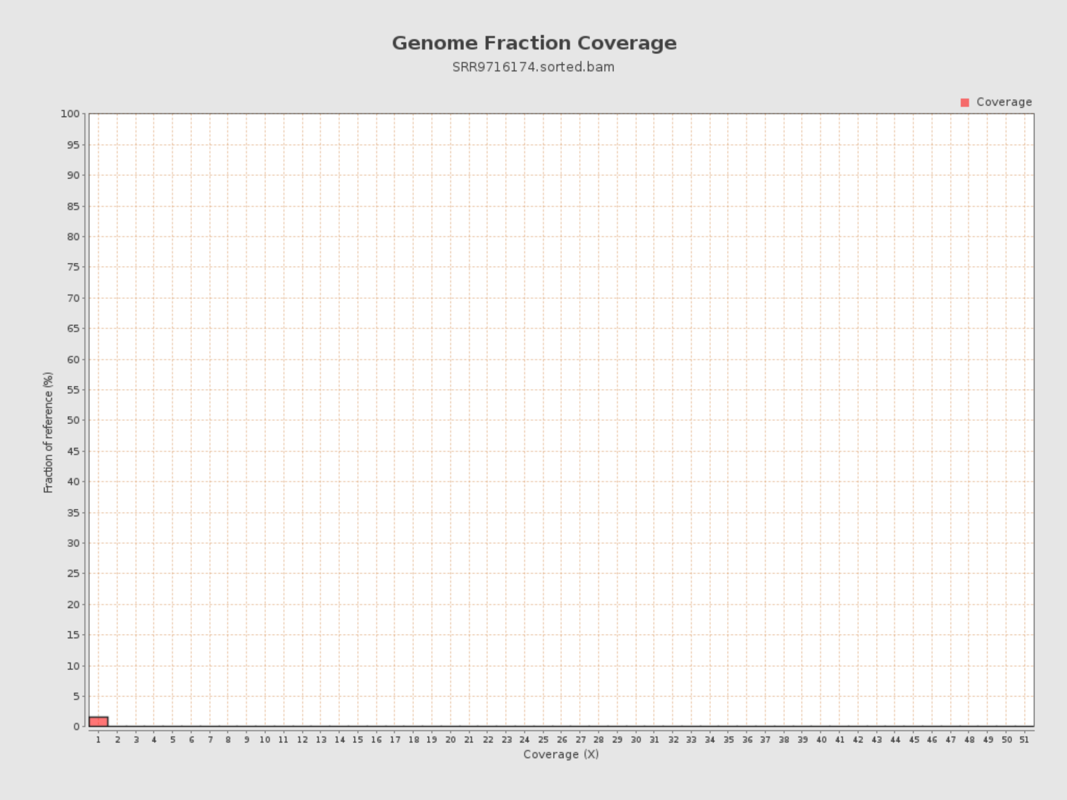
4. Results : Coverage Histogram



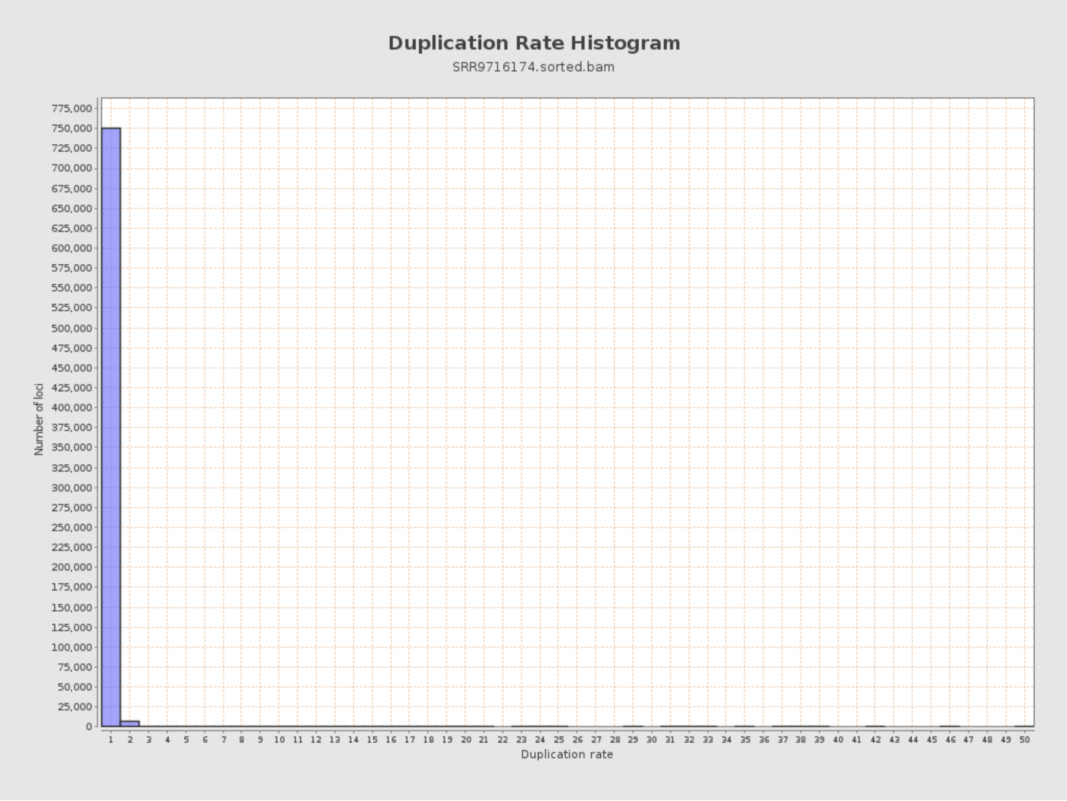
5. Results : Coverage Histogram (0-50X)



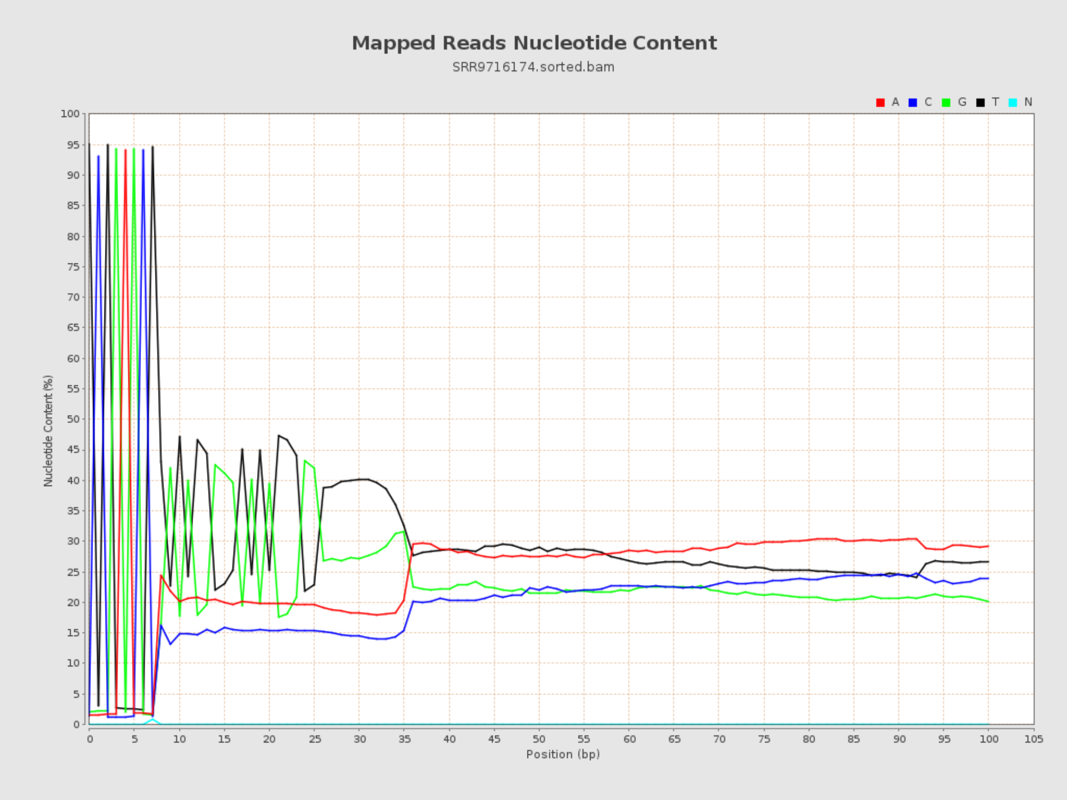
6. Results : Genome Fraction Coverage



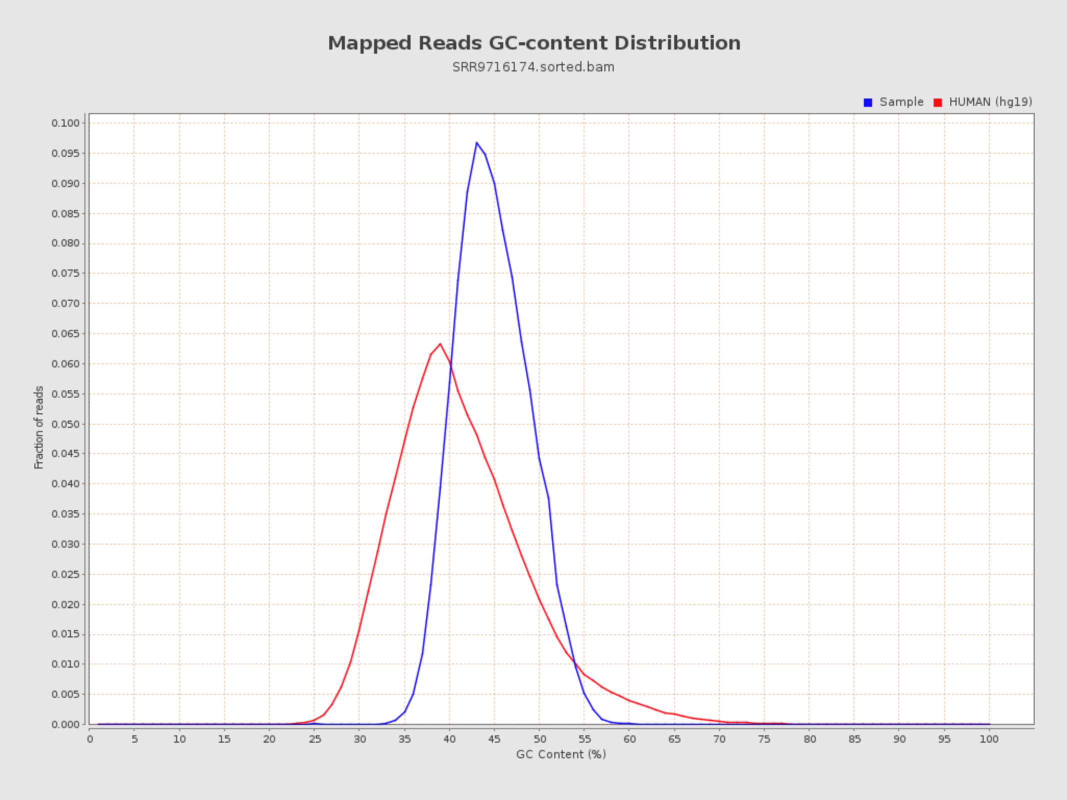
7. Results : Duplication Rate Histogram



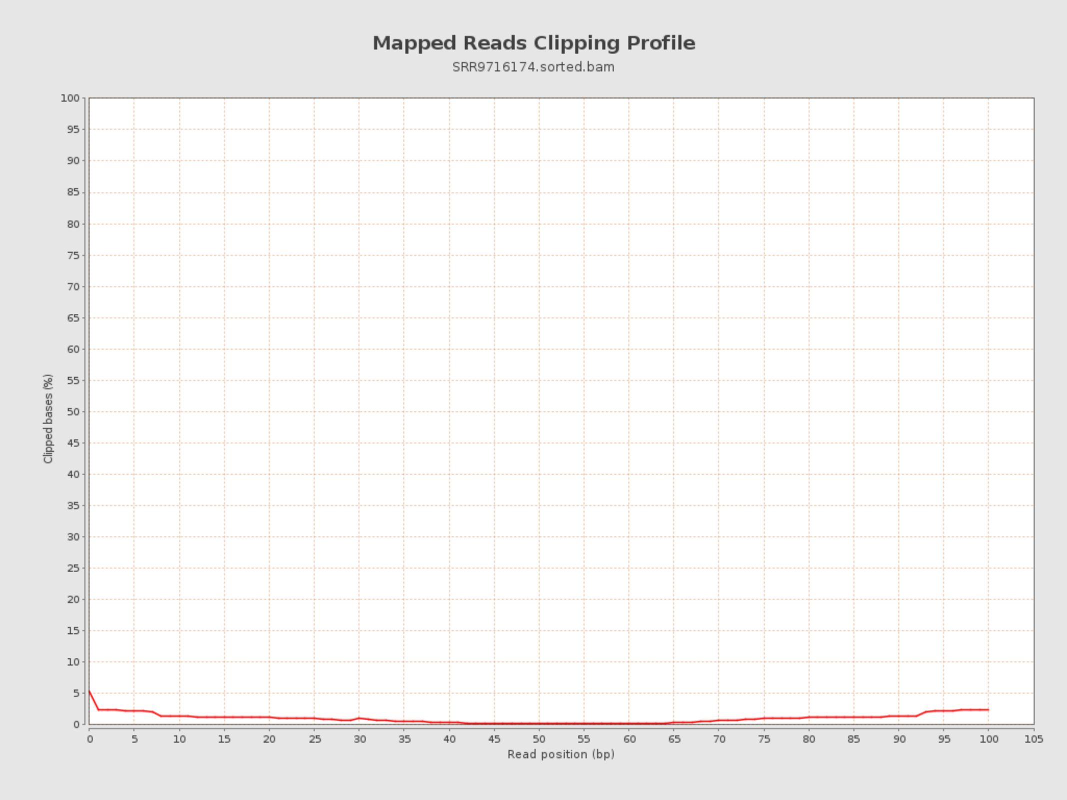
8. Results : Mapped Reads Nucleotide Content



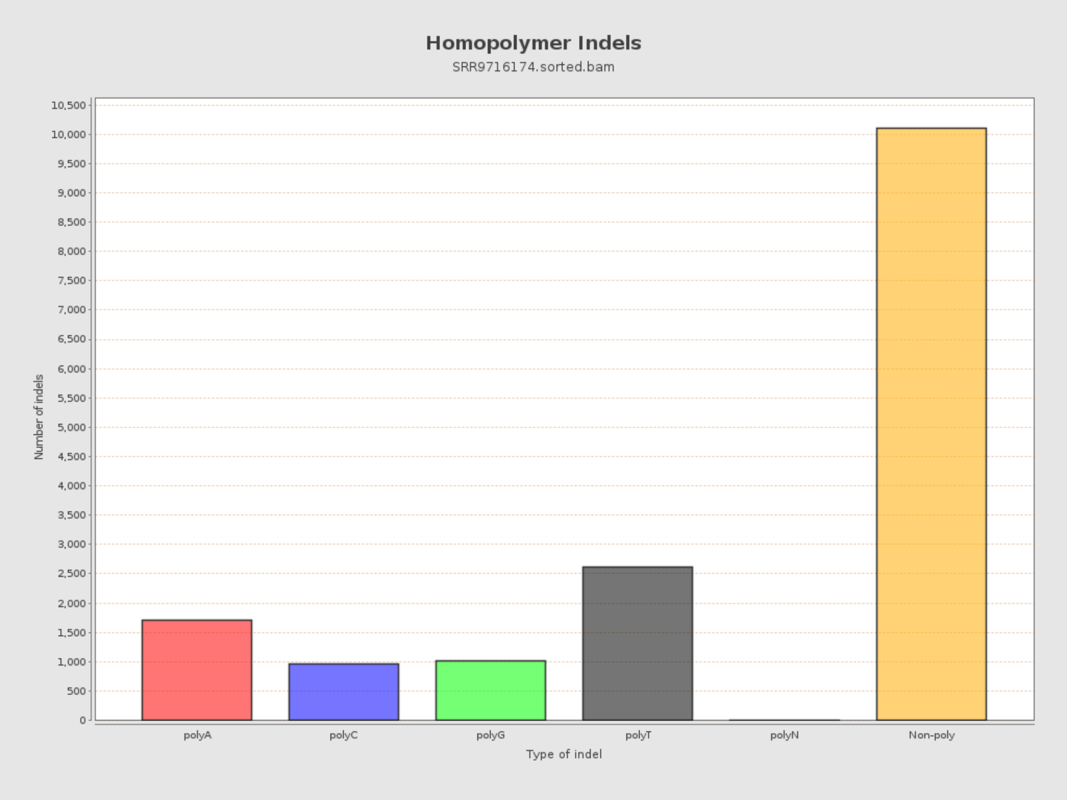
9. Results : Mapped Reads GC-content Distribution



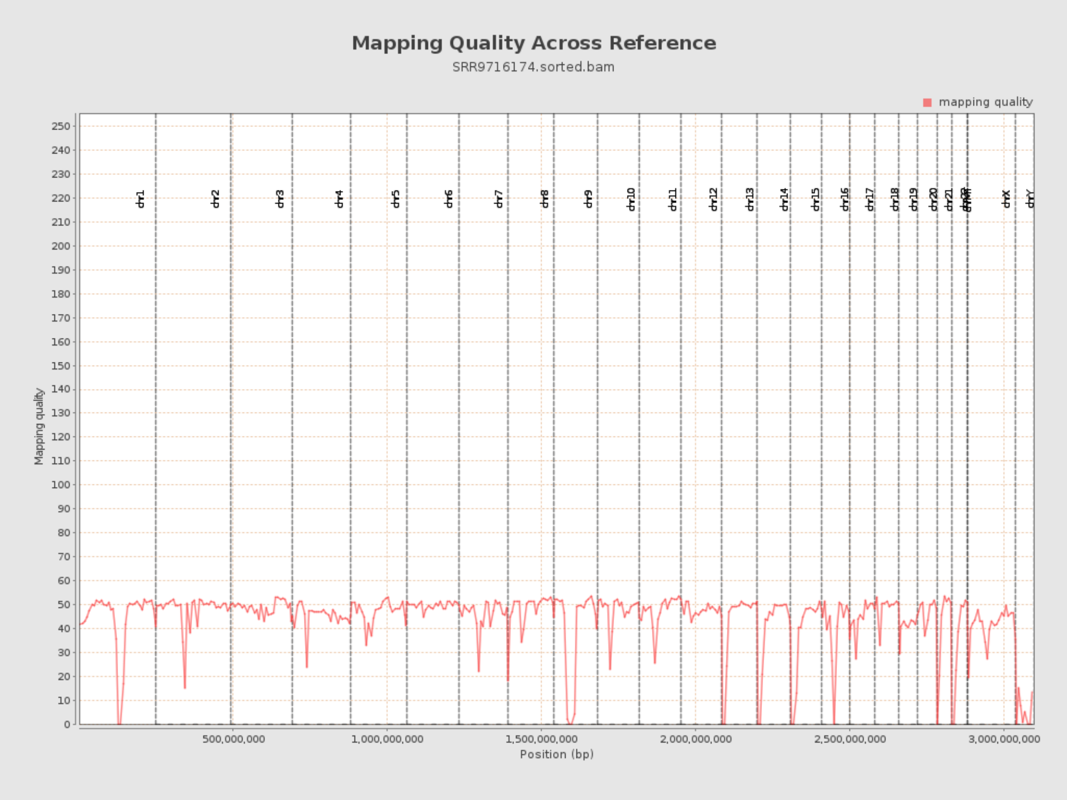
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram