Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 08:21:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716341.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_SRR9716341 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716341.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 08:21:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716341.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,361,140
Mapped reads	1,207,946 / 88.75%
Unmapped reads	153,194 / 11.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,967 / 0.51%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	34,244 / 2.52%
Duplication rate	2.14%
Clipped reads	1,211,881 / 89.03%

2.2. ACGT Content

Number/percentage of A's	18,127,550 / 25.72%
Number/percentage of C's	14,243,511 / 20.21%
Number/percentage of T's	21,511,347 / 30.53%
Number/percentage of G's	16,583,485 / 23.53%
Number/percentage of N's	842 / 0%
GC Percentage	43.75%

2.3. Coverage

Mean	0.0228

Standard Deviation	0.2074

2.4. Mapping Quality

Mean Mapping Quality	44.88

2.5. Mismatches and indels

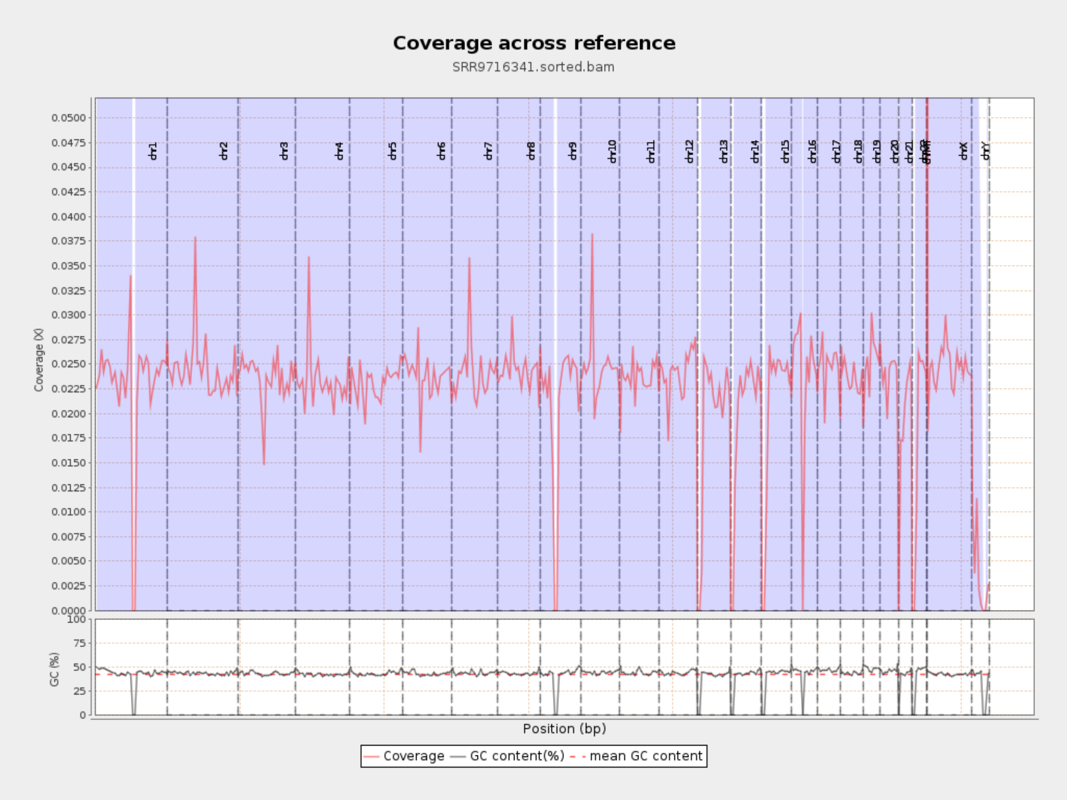
General error rate	0.51%
Mismatches	346,824
Insertions	5,051
Mapped reads with at least one insertion	0.42%
Deletions	12,821
Mapped reads with at least one deletion	1.05%
Homopolymer indels	42.14%

2.6. Chromosome stats

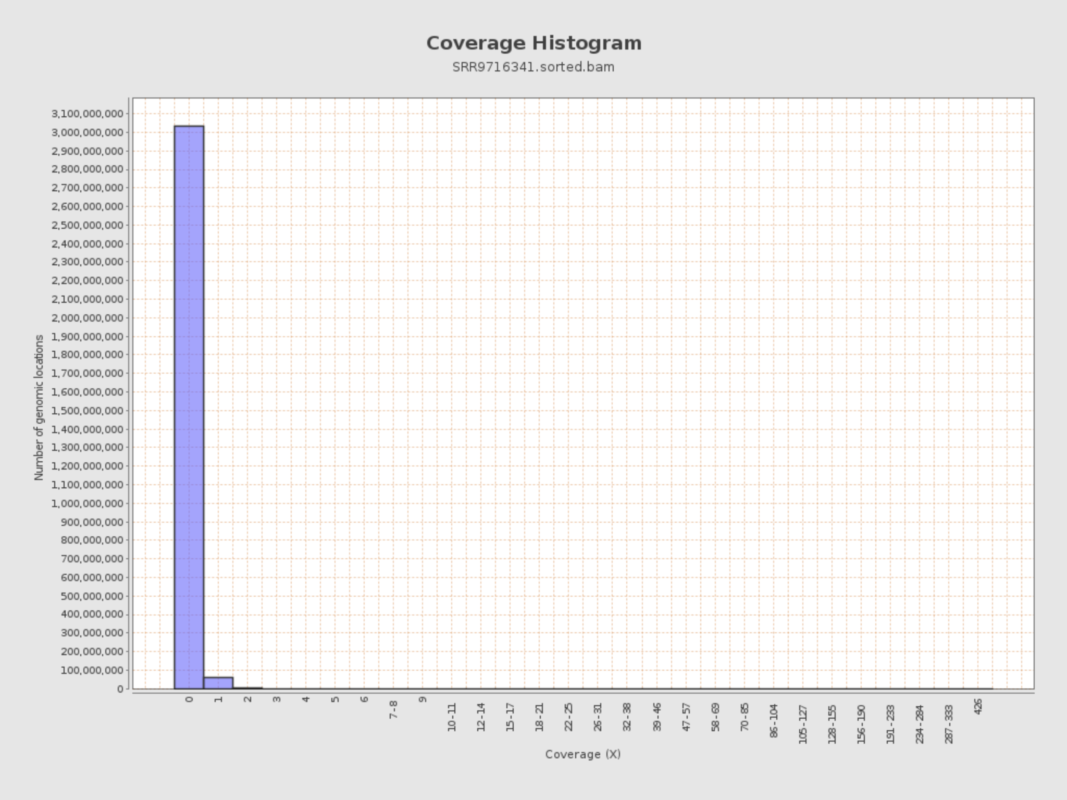
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5696310	0.0229	0.3091
chr2	243199373	5946392	0.0245	0.2633
chr3	198022430	4672521	0.0236	0.1644
chr4	191154276	4483841	0.0235	0.1778
chr5	180915260	4204485	0.0232	0.1638
chr6	171115067	4075360	0.0238	0.1785
chr7	159138663	3868777	0.0243	0.2693

chr8	146364022	3568322	0.0244	0.2018
chr9	141213431	2930712	0.0208	0.1786
chr10	135534747	3367527	0.0248	0.2154
chr11	135006516	3218683	0.0238	0.1988
chr12	133851895	3229632	0.0241	0.1677
chr13	115169878	2185476	0.019	0.1472
chr14	107349540	2106035	0.0196	0.1543
chr15	102531392	2069845	0.0202	0.1571
chr16	90354753	2117544	0.0234	0.1729
chr17	81195210	2007635	0.0247	0.1771
chr18	78077248	1850940	0.0237	0.2912
chr19	59128983	1511950	0.0256	0.2676
chr20	63025520	1499231	0.0238	0.1687
chr21	48129895	918116	0.0191	0.1623
chr22	51304566	896890	0.0175	0.1418
chrMT	16571	17784	1.0732	1.2899
chrX	155270560	3832196	0.0247	0.1786
chrY	59373566	211106	0.0036	0.094

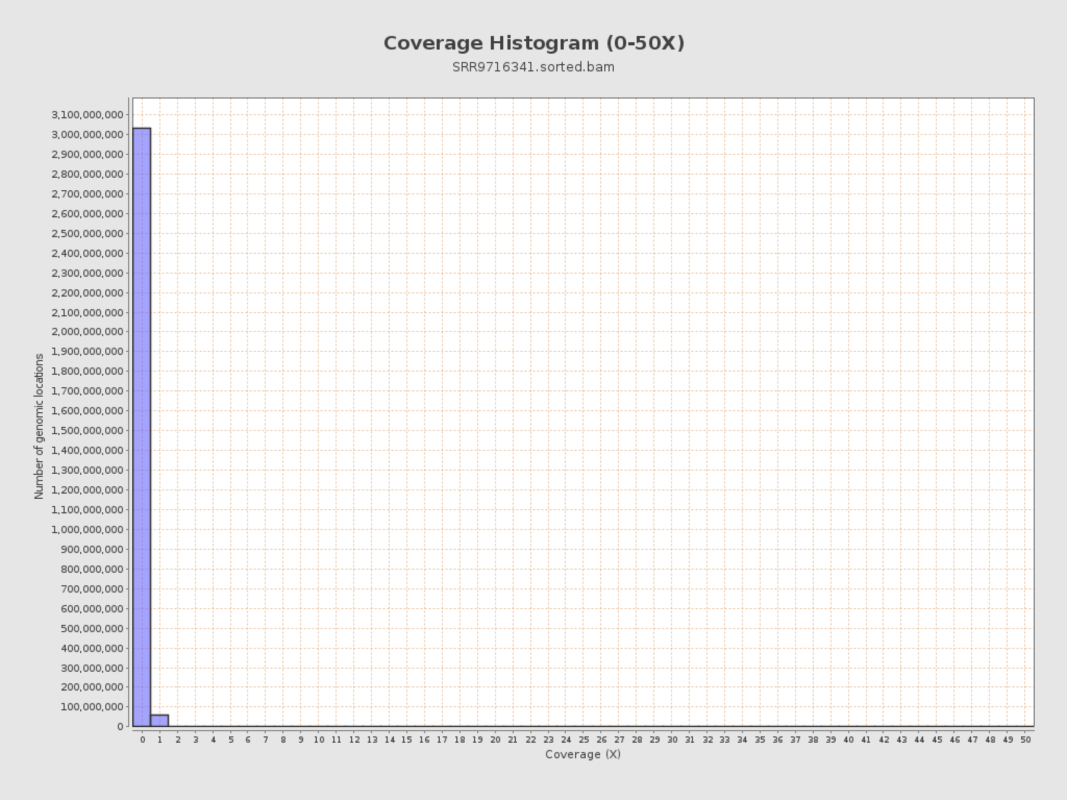
3. Results : Coverage across reference



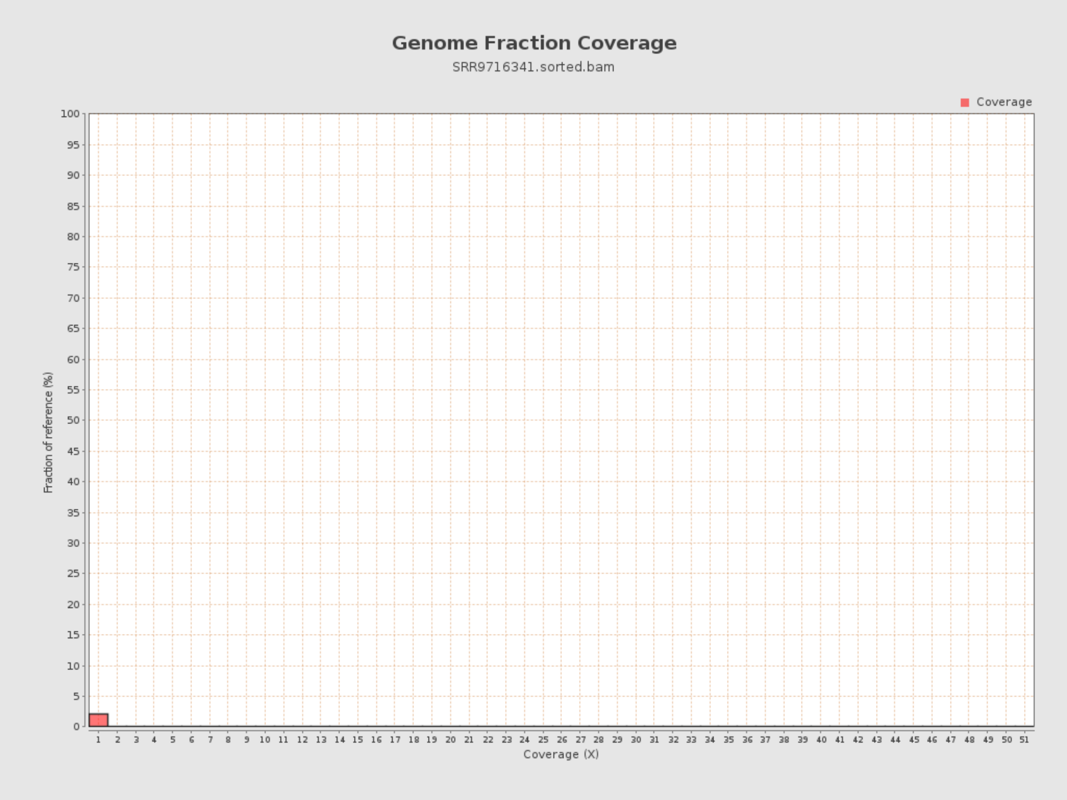
4. Results : Coverage Histogram



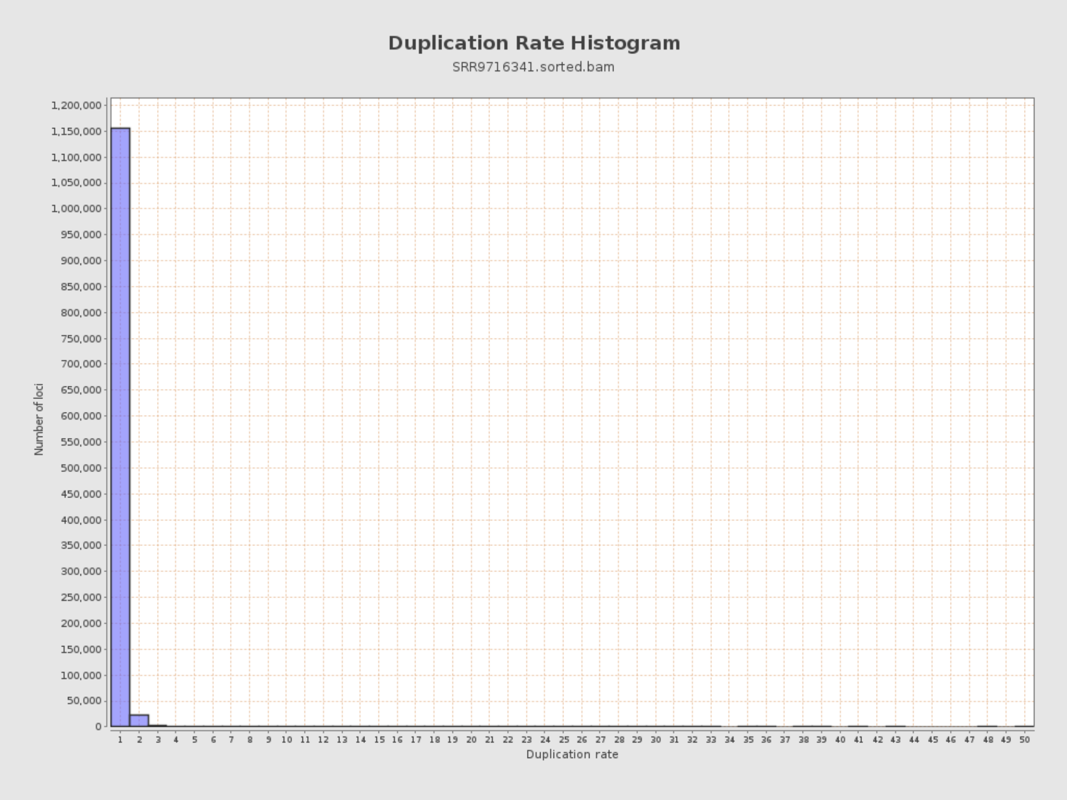
5. Results : Coverage Histogram (0-50X)



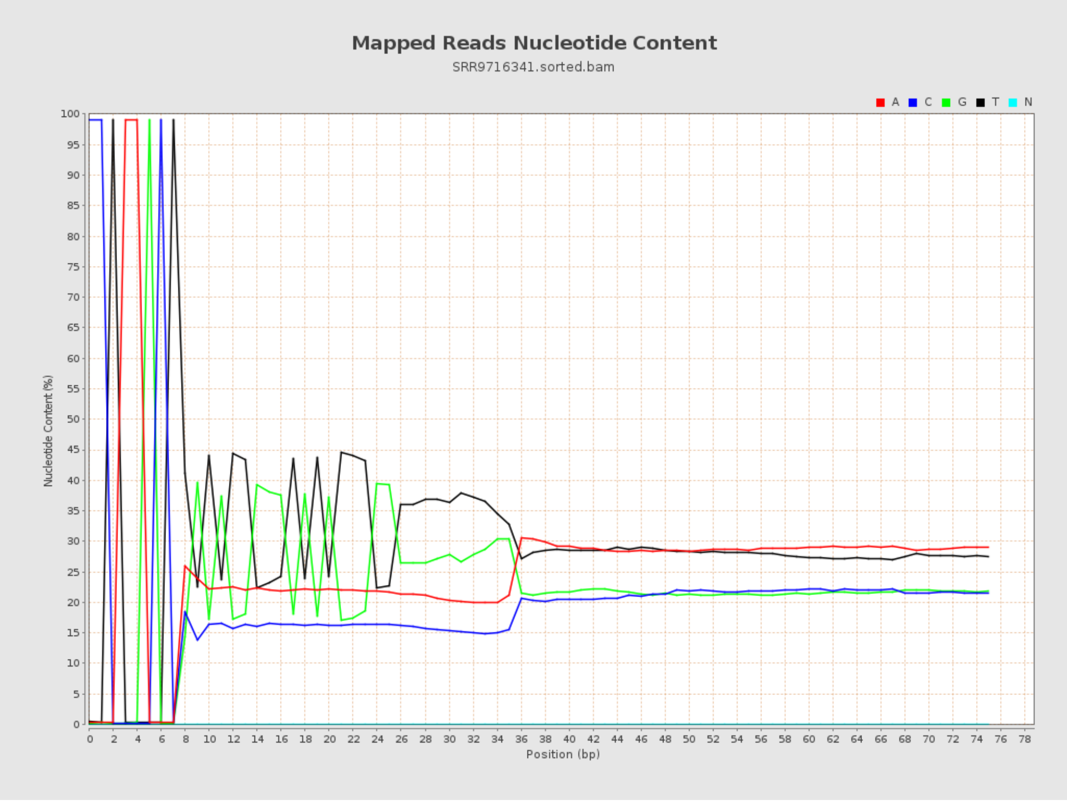
6. Results : Genome Fraction Coverage



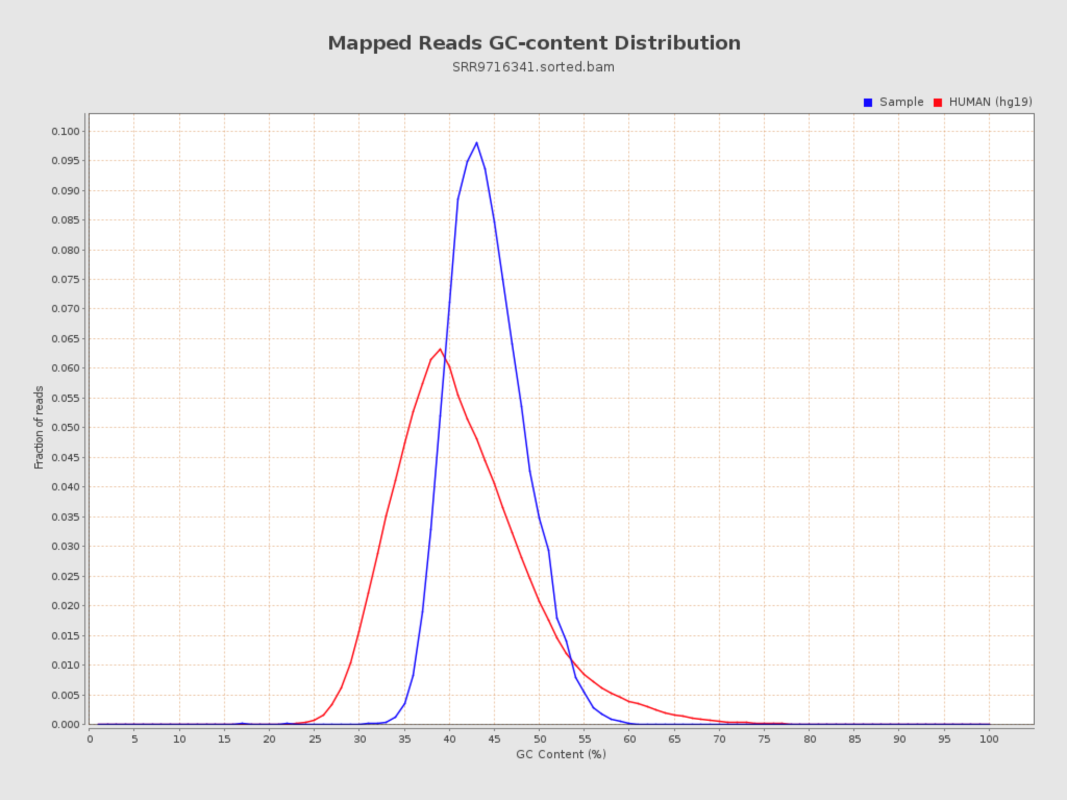
7. Results : Duplication Rate Histogram



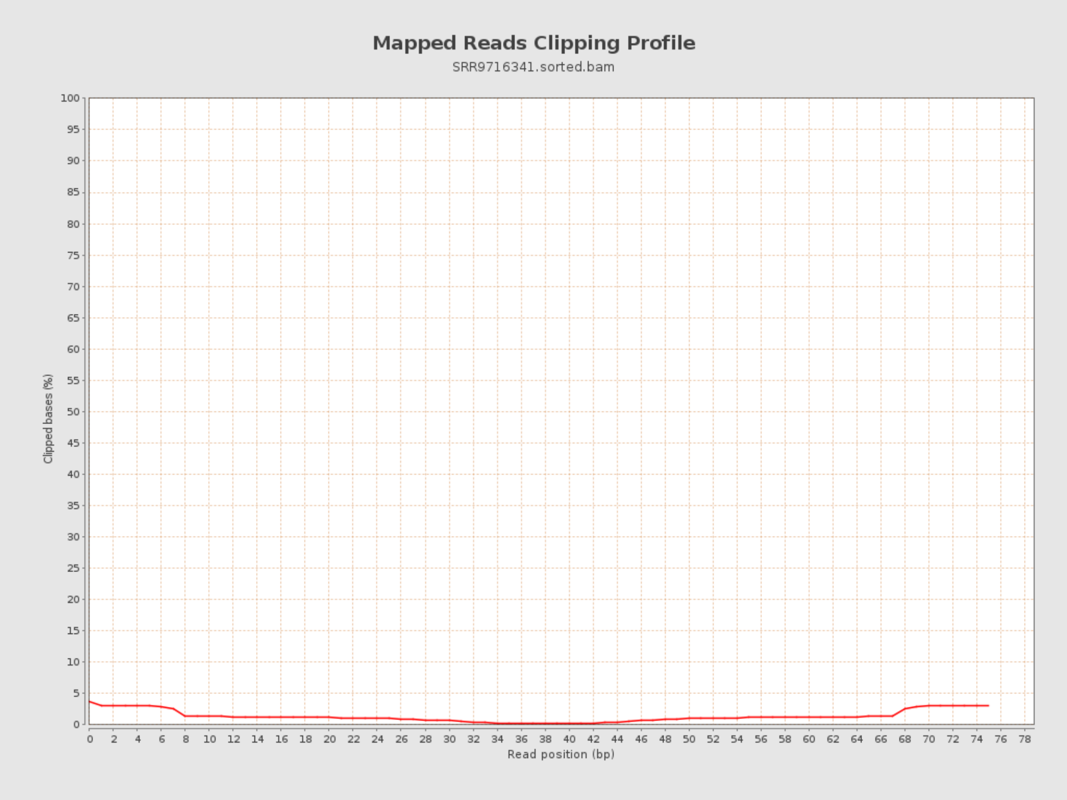
8. Results : Mapped Reads Nucleotide Content



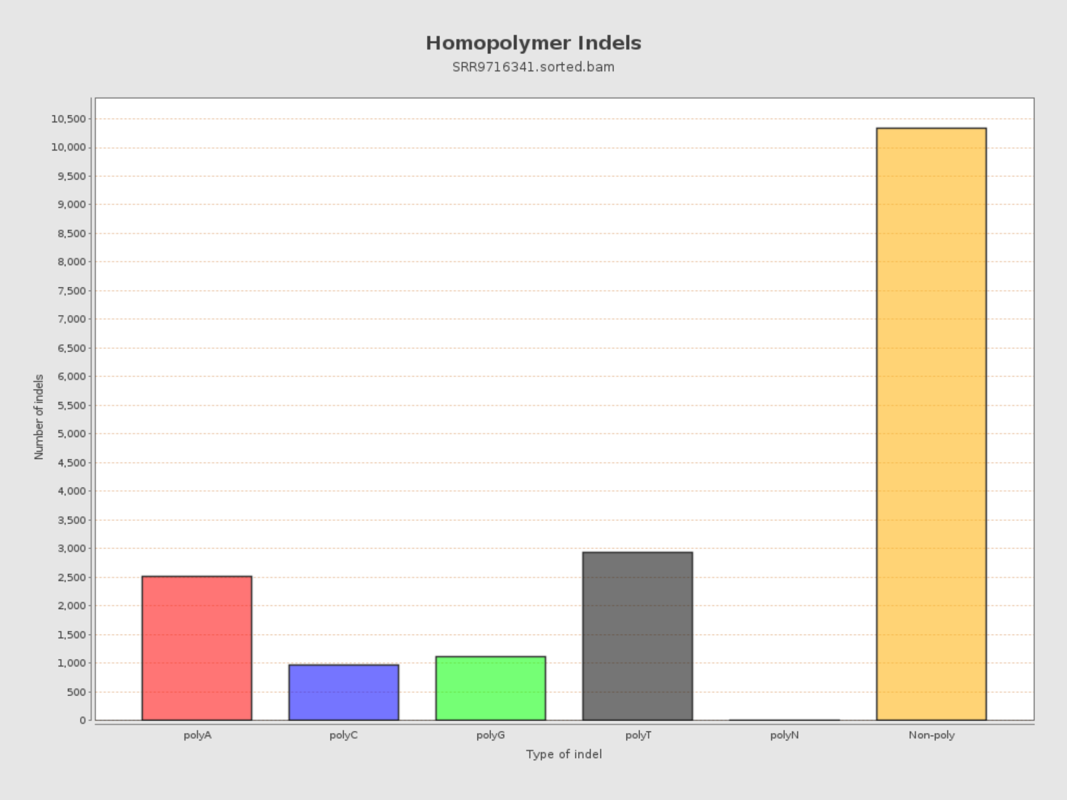
9. Results : Mapped Reads GC-content Distribution



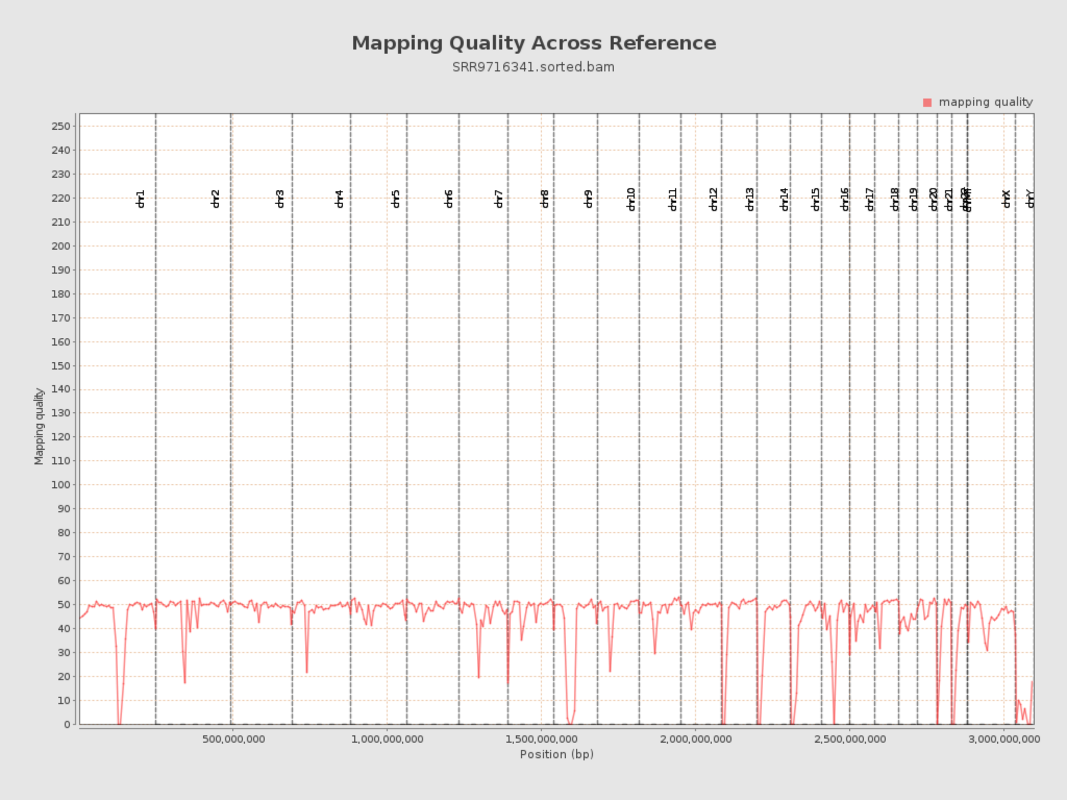
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram