Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 08:27:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716343.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_SRR9716343 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716343.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 08:27:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716343.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,656,415
Mapped reads	1,474,191 / 89%
Unmapped reads	182,224 / 11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,807 / 0.53%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	71,153 / 4.3%
Duplication rate	3.81%
Clipped reads	1,478,511 / 89.26%

2.2. ACGT Content

Number/percentage of A's	21,079,432 / 24.76%
Number/percentage of C's	17,069,645 / 20.05%
Number/percentage of T's	27,440,318 / 32.23%
Number/percentage of G's	19,543,976 / 22.96%
Number/percentage of N's	1,119 / 0%
GC Percentage	43.01%

2.3. Coverage

Mean	0.0275

Standard Deviation	0.2505

2.4. Mapping Quality

Mean Mapping Quality	44.65

2.5. Mismatches and indels

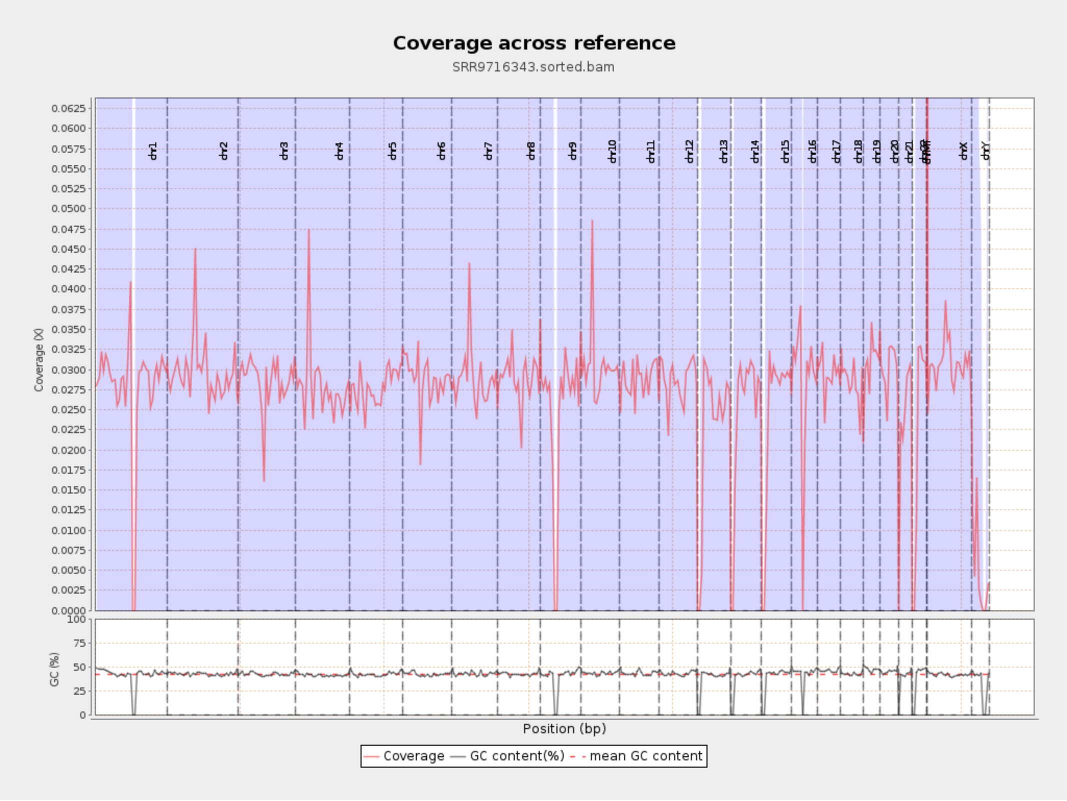
General error rate	0.52%
Mismatches	428,423
Insertions	5,761
Mapped reads with at least one insertion	0.39%
Deletions	15,235
Mapped reads with at least one deletion	1.02%
Homopolymer indels	41.55%

2.6. Chromosome stats

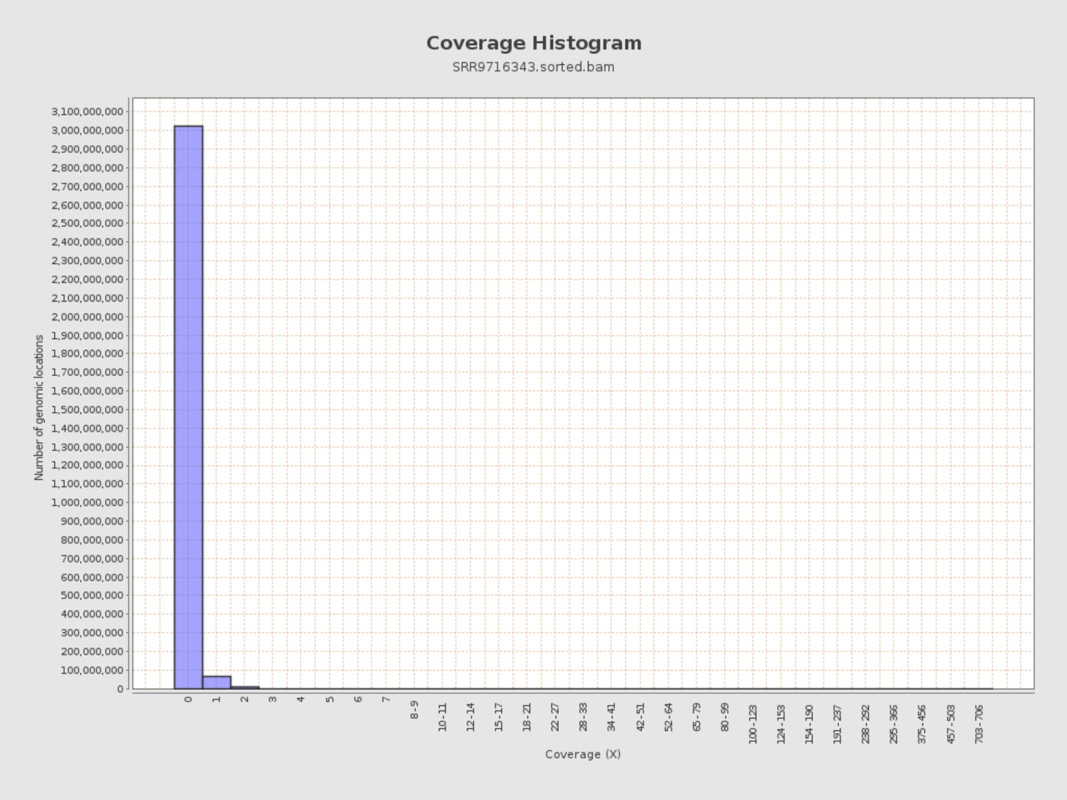
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6884282	0.0276	0.38
chr2	243199373	7225691	0.0297	0.3574
chr3	198022430	5647902	0.0285	0.19
chr4	191154276	5344961	0.028	0.2184
chr5	180915260	5048932	0.0279	0.1878
chr6	171115067	4918426	0.0287	0.2056
chr7	159138663	4632752	0.0291	0.3107

chr8	146364022	4235955	0.0289	0.2629
chr9	141213431	3486207	0.0247	0.2018
chr10	135534747	4139085	0.0305	0.2672
chr11	135006516	3910632	0.029	0.2294
chr12	133851895	3844004	0.0287	0.1941
chr13	115169878	2579039	0.0224	0.169
chr14	107349540	2600752	0.0242	0.1804
chr15	102531392	2464708	0.024	0.1765
chr16	90354753	2529181	0.028	0.199
chr17	81195210	2395675	0.0295	0.2035
chr18	78077248	2212829	0.0283	0.33
chr19	59128983	1838606	0.0311	0.2855
chr20	63025520	1887702	0.03	0.2007
chr21	48129895	1143619	0.0238	0.1935
chr22	51304566	1126331	0.022	0.1663
chrMT	16571	14026	0.8464	1.1095
chrX	155270560	4769052	0.0307	0.2121
chrY	59373566	278275	0.0047	0.1392

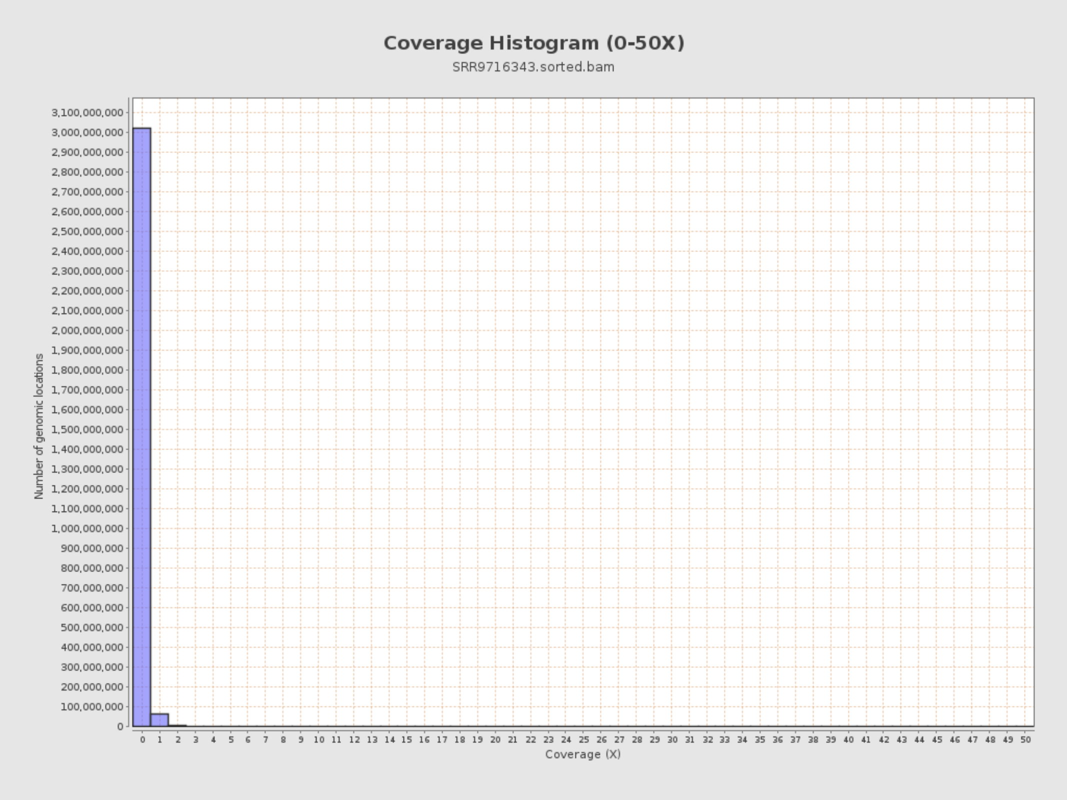
3. Results : Coverage across reference



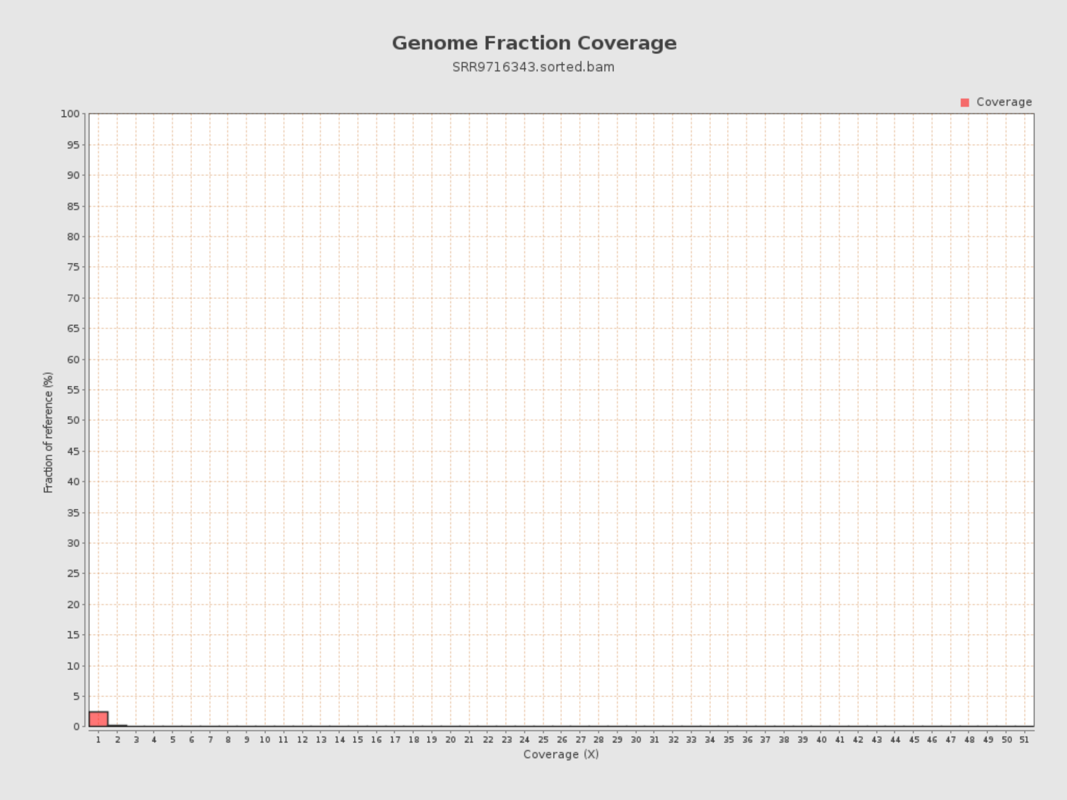
4. Results : Coverage Histogram



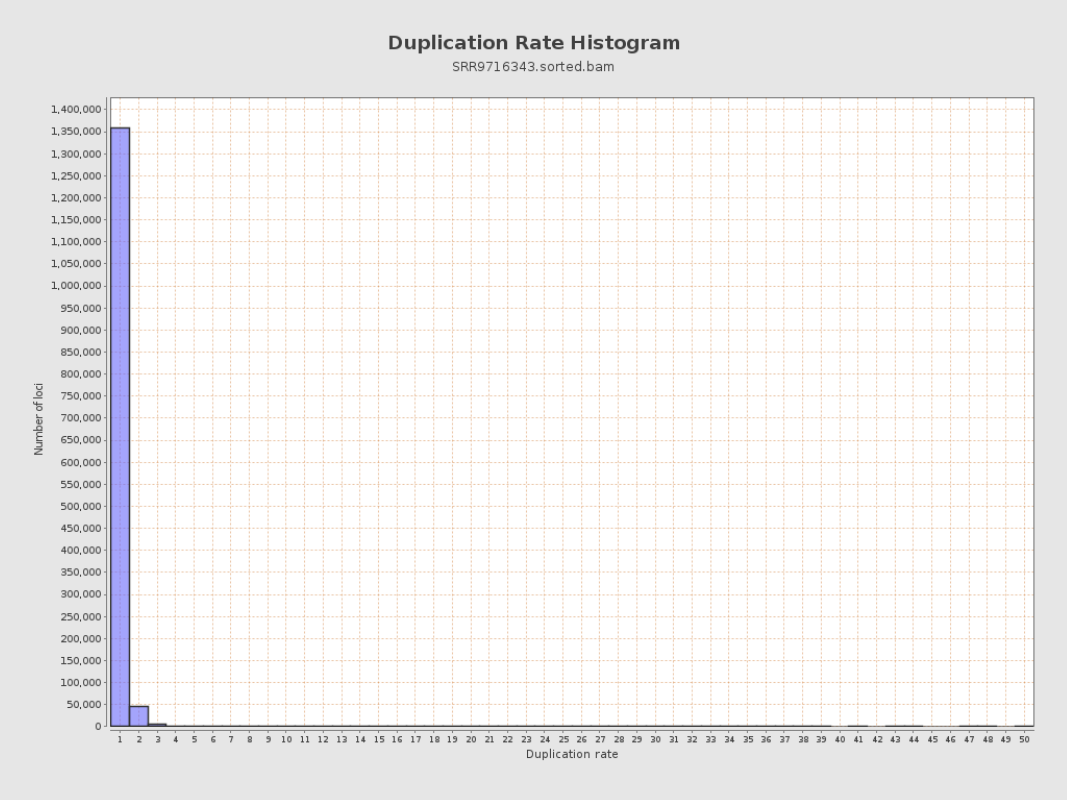
5. Results : Coverage Histogram (0-50X)



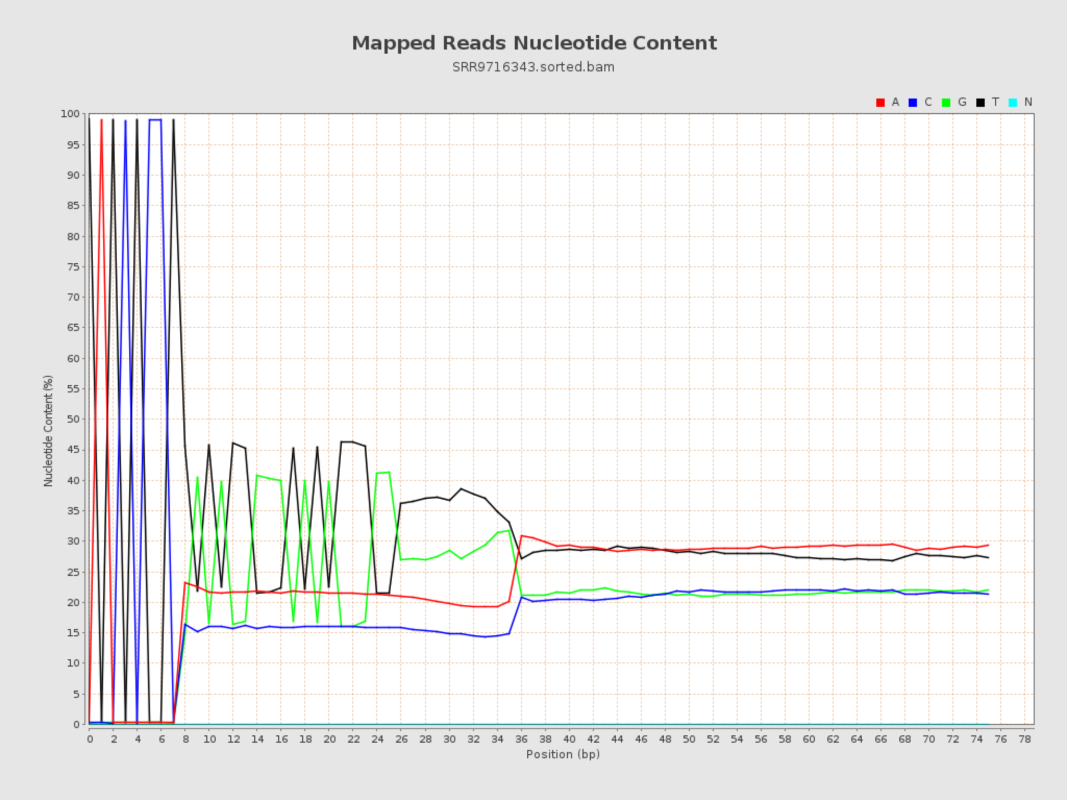
6. Results : Genome Fraction Coverage



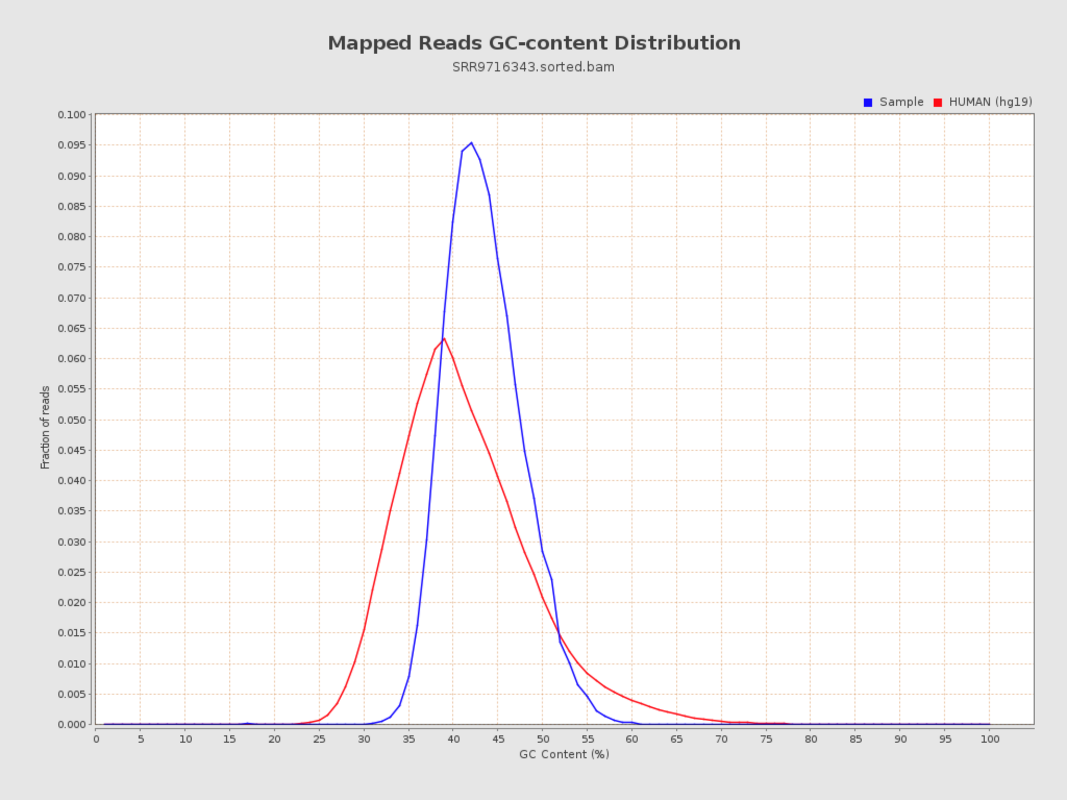
7. Results : Duplication Rate Histogram



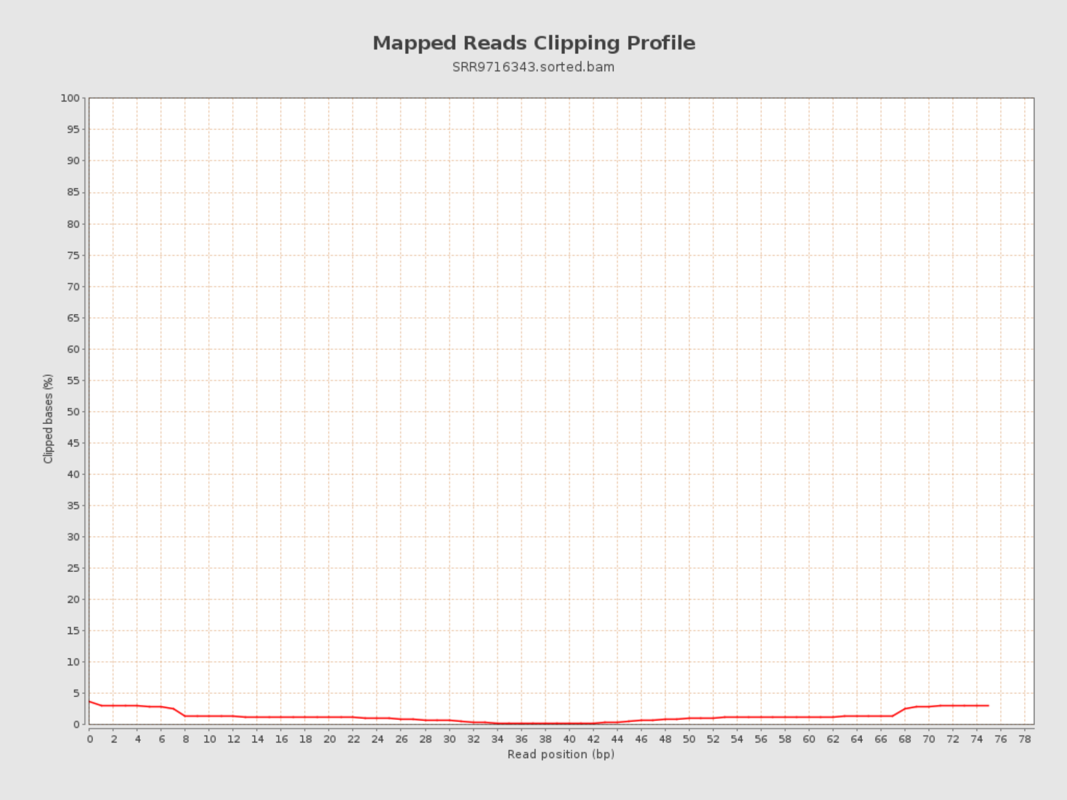
8. Results : Mapped Reads Nucleotide Content



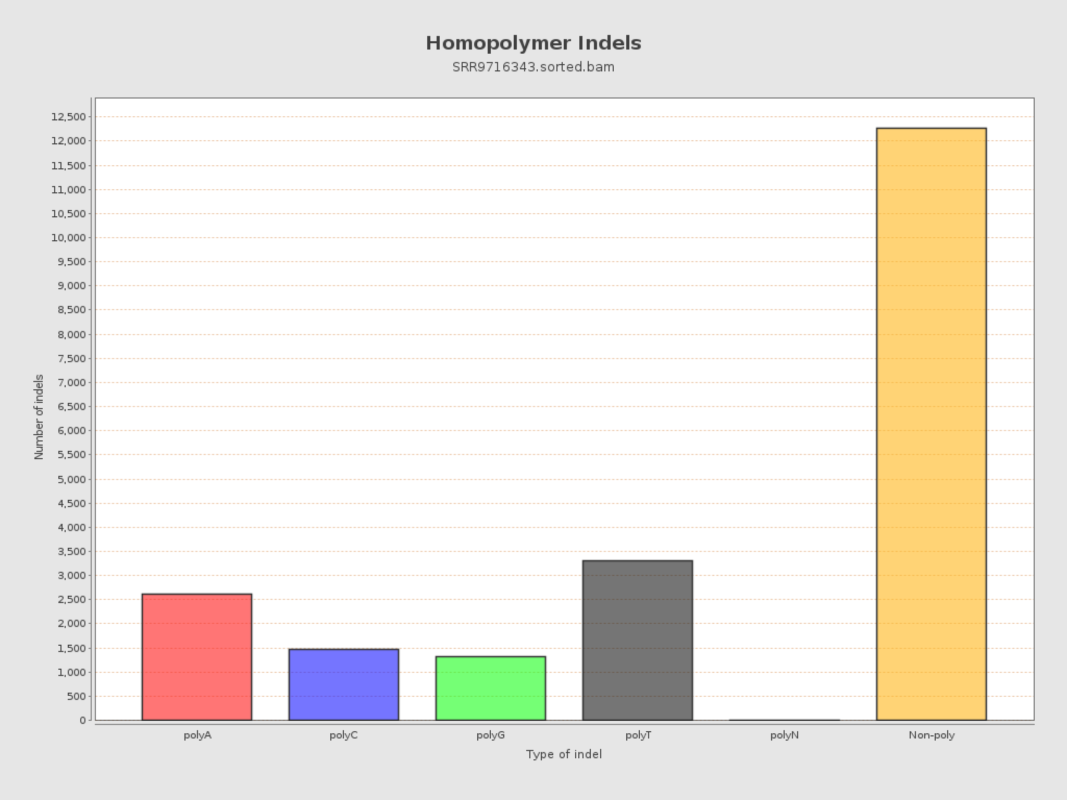
9. Results : Mapped Reads GC-content Distribution



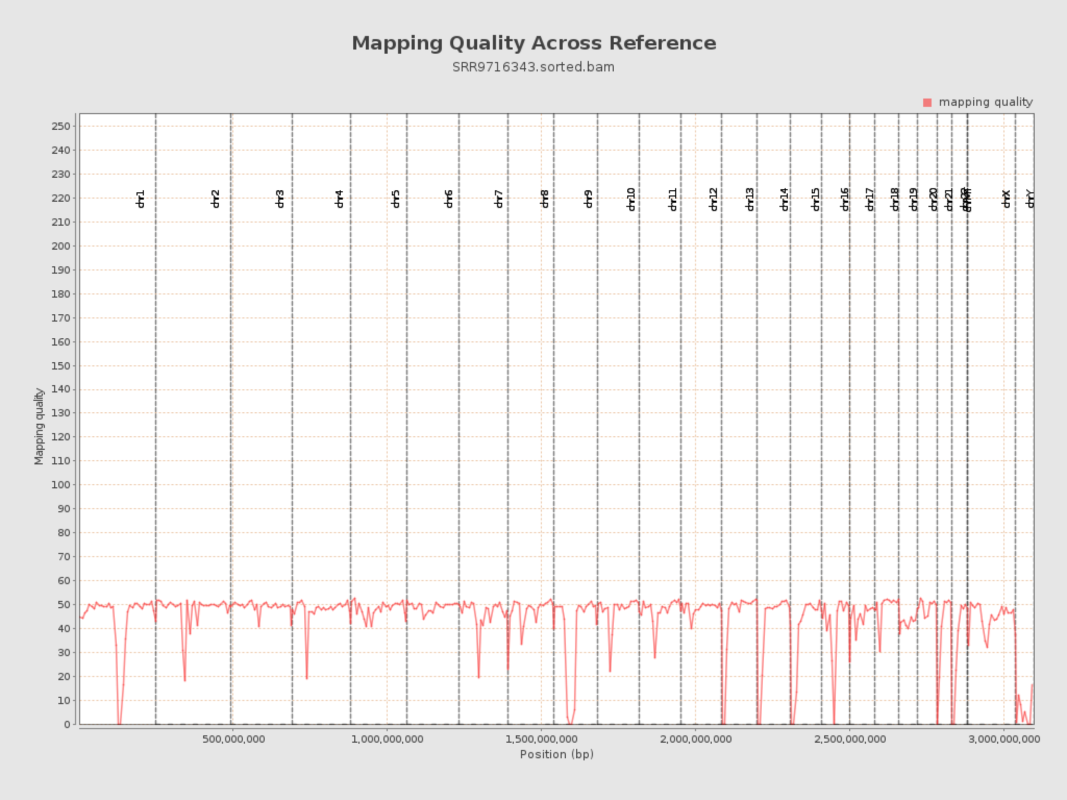
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram