Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 02:00:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716238.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_SRR9716238 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716238.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 02:00:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716238.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,399,838
Mapped reads	1,314,323 / 93.89%
Unmapped reads	85,515 / 6.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,765 / 1.77%
Read min/max/mean length	30 / 101 / 101.64
Duplicated reads (estimated)	43,631 / 3.12%
Duplication rate	2.41%
Clipped reads	1,338,437 / 95.61%

2.2. ACGT Content

Number/percentage of A's	27,364,914 / 26.29%
Number/percentage of C's	19,926,998 / 19.14%
Number/percentage of T's	31,372,571 / 30.14%
Number/percentage of G's	25,432,128 / 24.43%
Number/percentage of N's	8,079 / 0.01%
GC Percentage	43.57%

2.3. Coverage

Mean	0.0336

Standard Deviation	0.3164

2.4. Mapping Quality

Mean Mapping Quality	47.64

2.5. Mismatches and indels

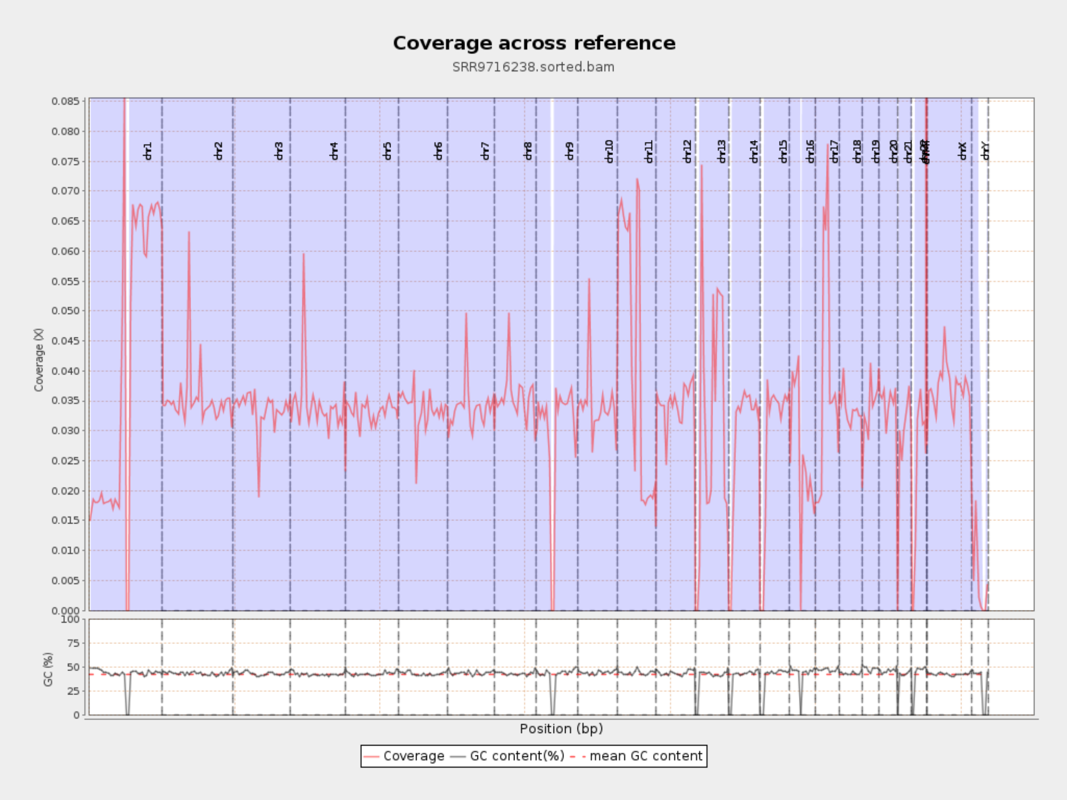
General error rate	0.63%
Mismatches	634,981
Insertions	7,670
Mapped reads with at least one insertion	0.57%
Deletions	23,767
Mapped reads with at least one deletion	1.78%
Homopolymer indels	42.94%

2.6. Chromosome stats

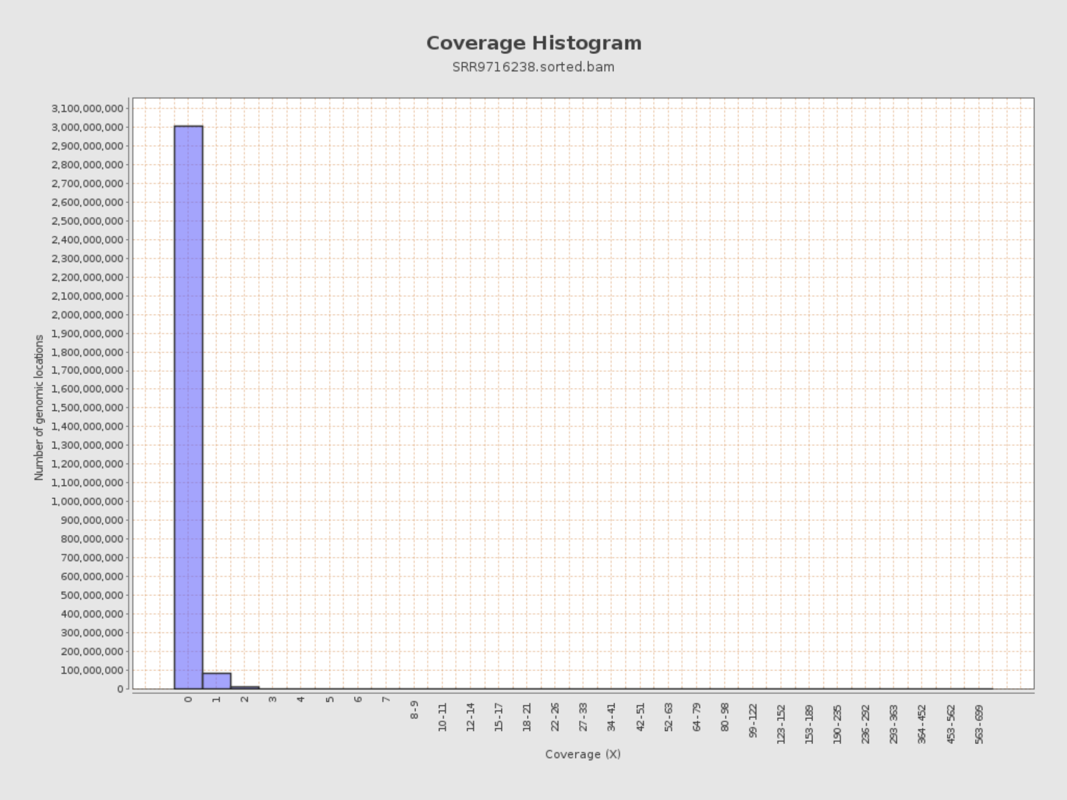
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10111035	0.0406	0.6316
chr2	243199373	8627536	0.0355	0.3311
chr3	198022430	6614551	0.0334	0.1991
chr4	191154276	6580974	0.0344	0.2351
chr5	180915260	6020917	0.0333	0.2007
chr6	171115067	5764189	0.0337	0.2175
chr7	159138663	5412312	0.034	0.3764

chr8	146364022	5228960	0.0357	0.3526
chr9	141213431	4192306	0.0297	0.2653
chr10	135534747	4654266	0.0343	0.2967
chr11	135006516	5786143	0.0429	0.3542
chr12	133851895	4616834	0.0345	0.2044
chr13	115169878	3602545	0.0313	0.1955
chr14	107349540	3077203	0.0287	0.1986
chr15	102531392	2925473	0.0285	0.1854
chr16	90354753	2329701	0.0258	0.191
chr17	81195210	3217626	0.0396	0.2562
chr18	78077248	2641815	0.0338	0.4417
chr19	59128983	1996892	0.0338	0.4521
chr20	63025520	2170974	0.0344	0.2123
chr21	48129895	1362003	0.0283	0.2086
chr22	51304566	1154516	0.0225	0.1644
chrMT	16571	9058	0.5466	0.8468
chrX	155270560	5753597	0.0371	0.2396
chrY	59373566	298953	0.005	0.156

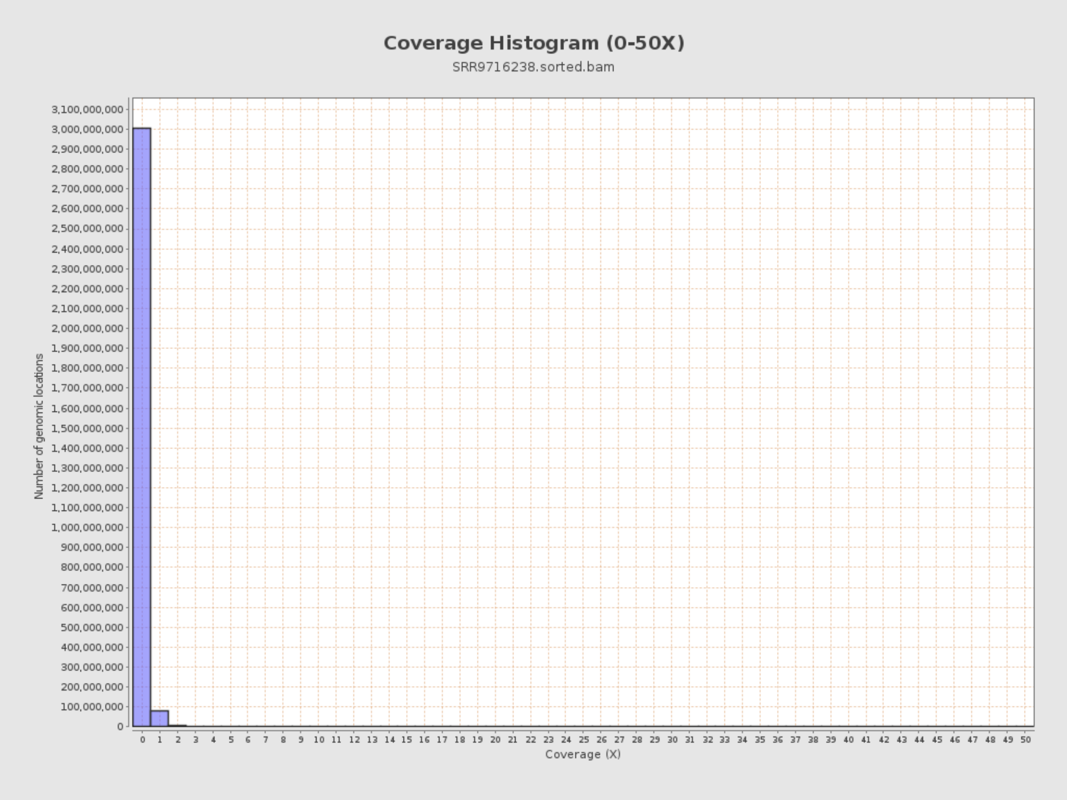
3. Results : Coverage across reference



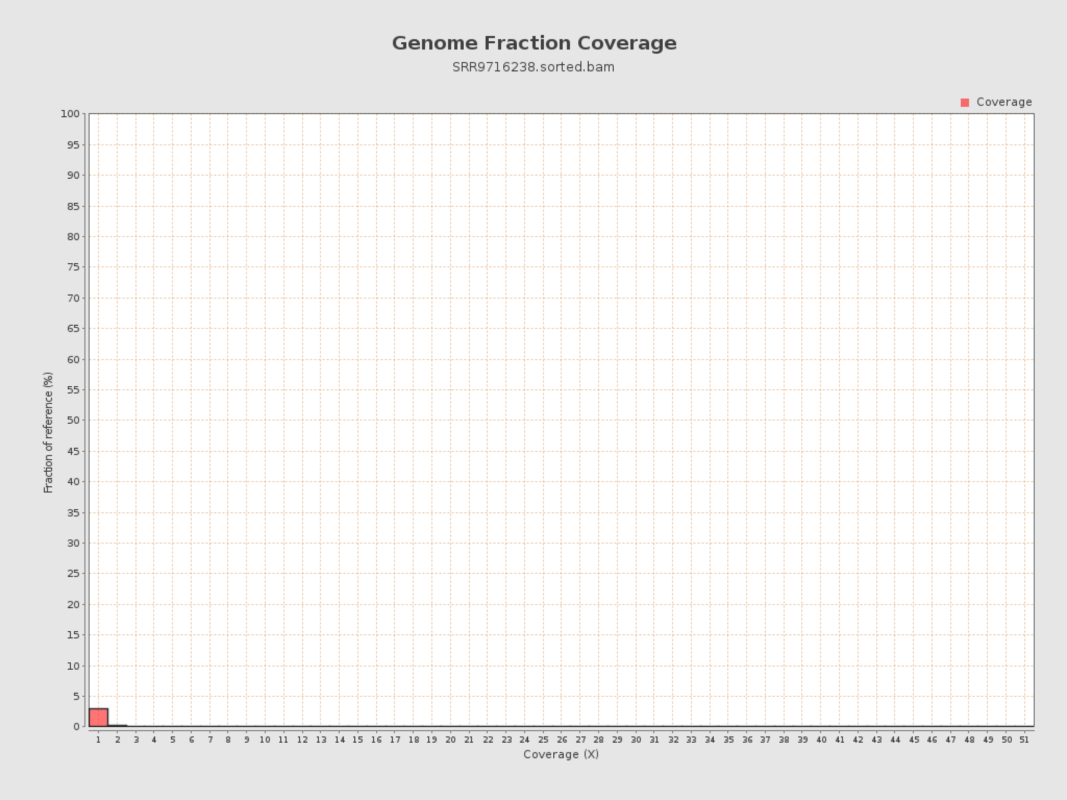
4. Results : Coverage Histogram



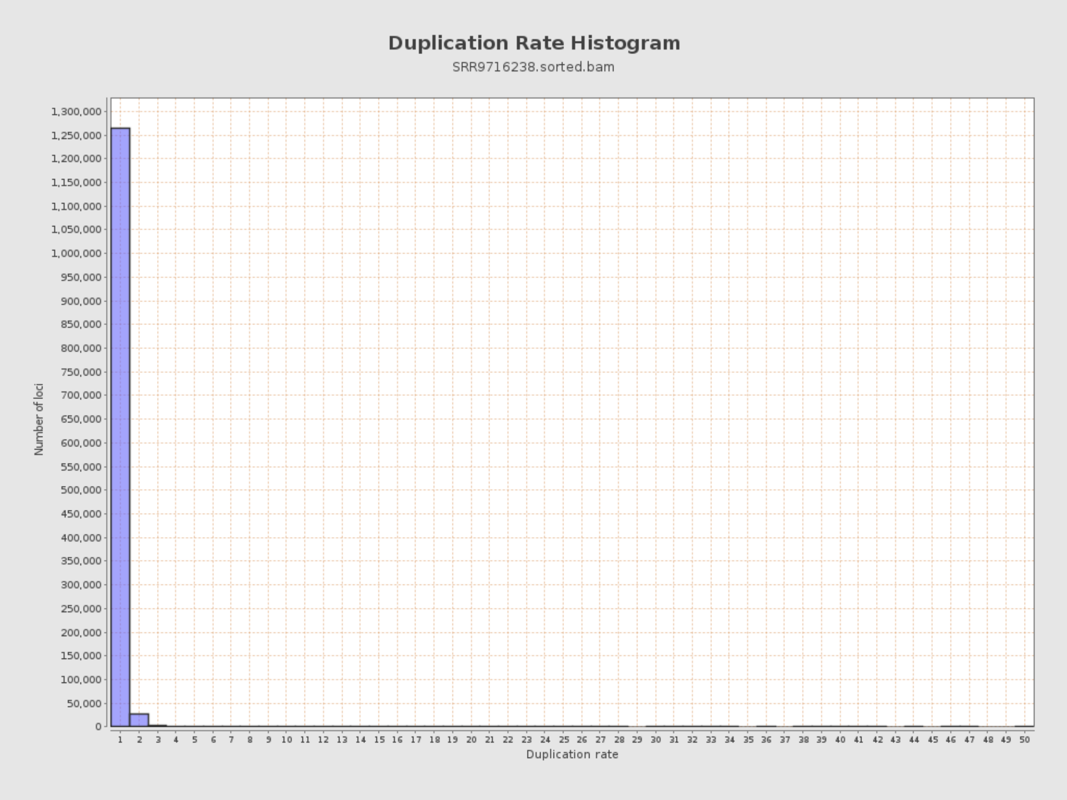
5. Results : Coverage Histogram (0-50X)



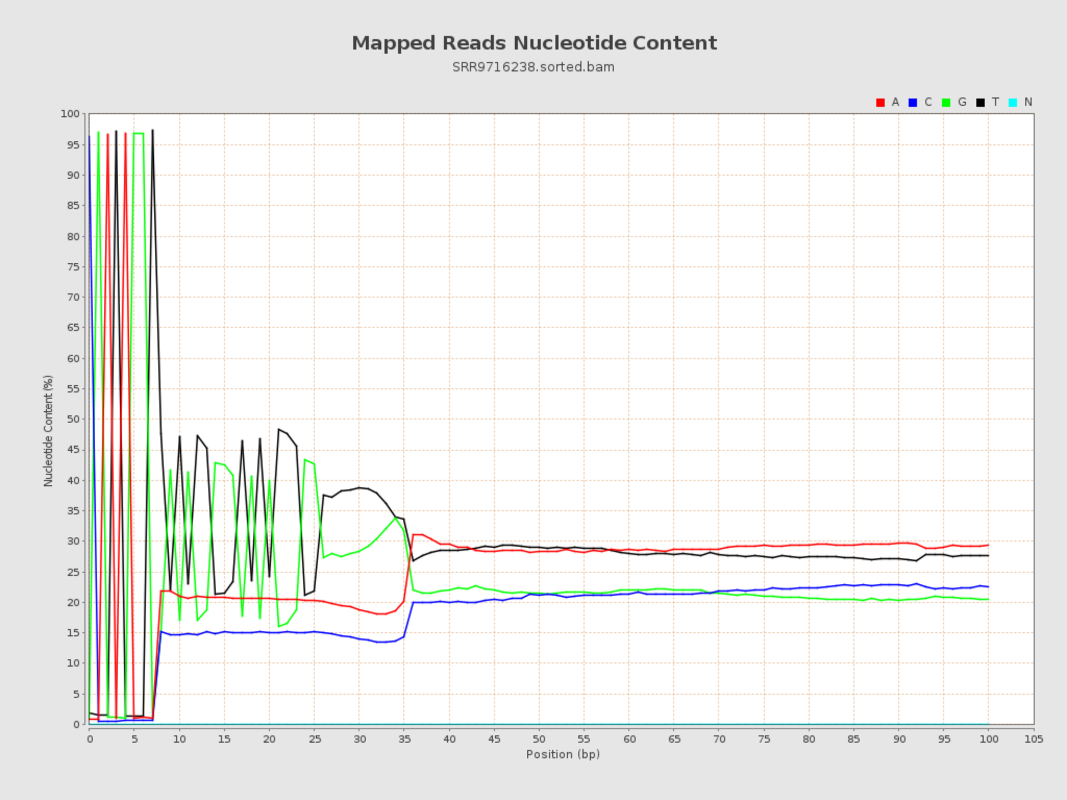
6. Results : Genome Fraction Coverage



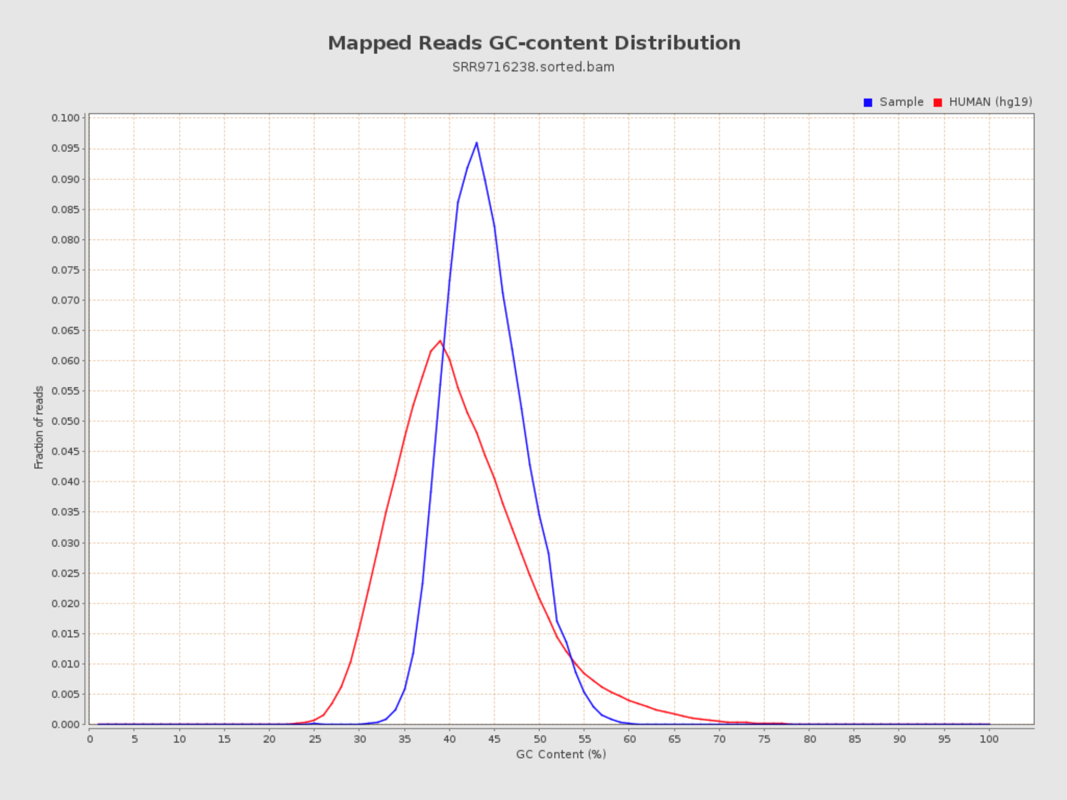
7. Results : Duplication Rate Histogram



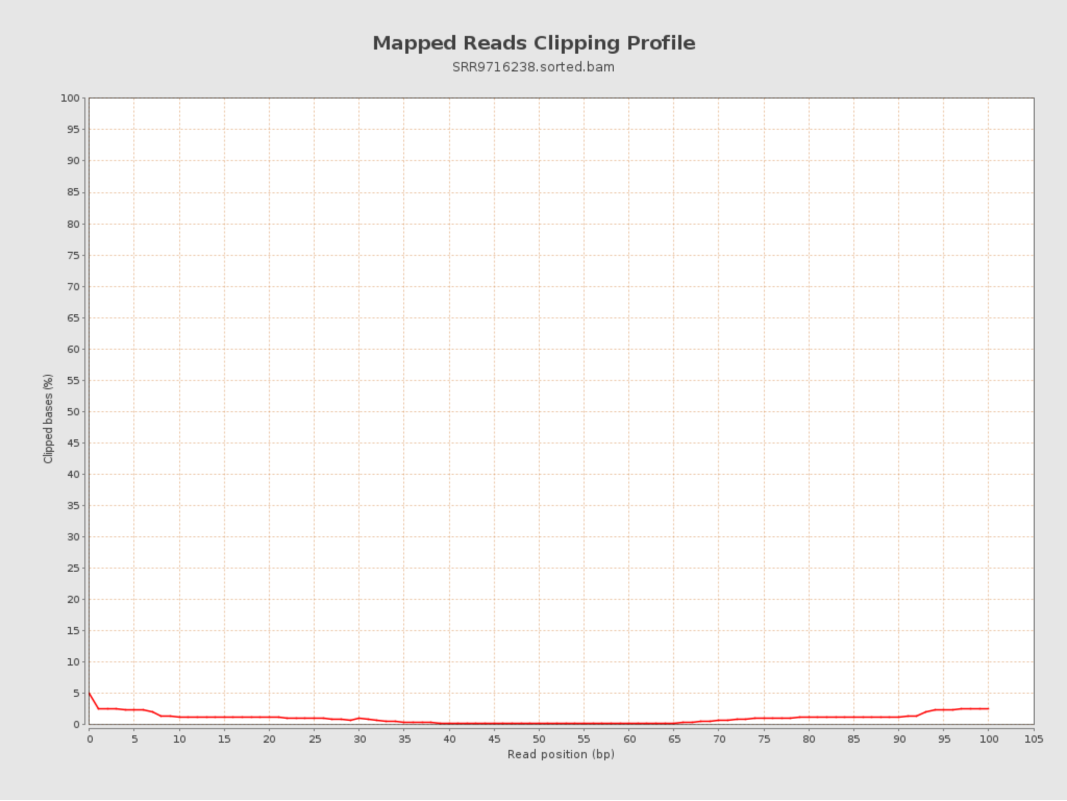
8. Results : Mapped Reads Nucleotide Content



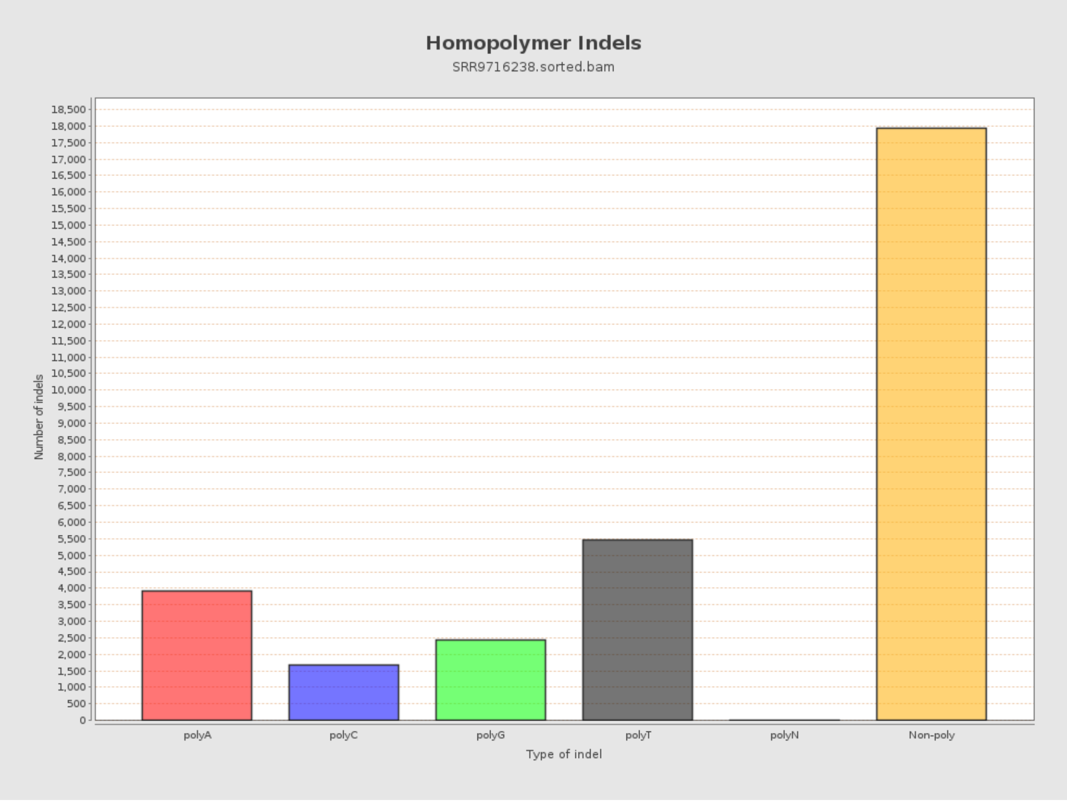
9. Results : Mapped Reads GC-content Distribution



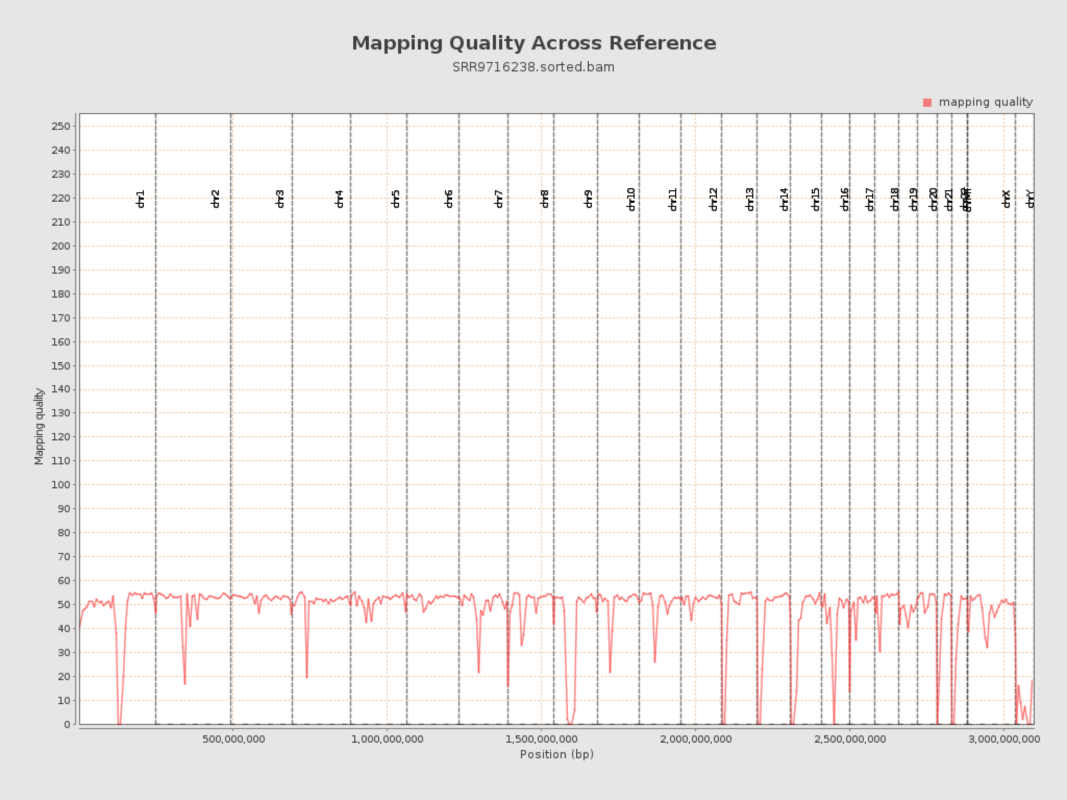
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram