Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 20:51:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716558.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_SRR9716558 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716558.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 20:51:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716558.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	24,088,948
Mapped reads	23,549,671 / 97.76%
Unmapped reads	539,277 / 2.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,231 / 0.05%
Read min/max/mean length	30 / 76 / 76.02
Duplicated reads (estimated)	1,357,088 / 5.63%
Duplication rate	1.87%
Clipped reads	23,450,938 / 97.35%

2.2. ACGT Content

Number/percentage of A's	454,525,386 / 28.45%
Number/percentage of C's	331,179,519 / 20.73%
Number/percentage of T's	475,377,381 / 29.75%
Number/percentage of G's	336,578,555 / 21.07%
Number/percentage of N's	79,811 / 0%
GC Percentage	41.79%

2.3. Coverage

Mean	0.5162

Standard Deviation	6.3968

2.4. Mapping Quality

Mean Mapping Quality	49.05

2.5. Mismatches and indels

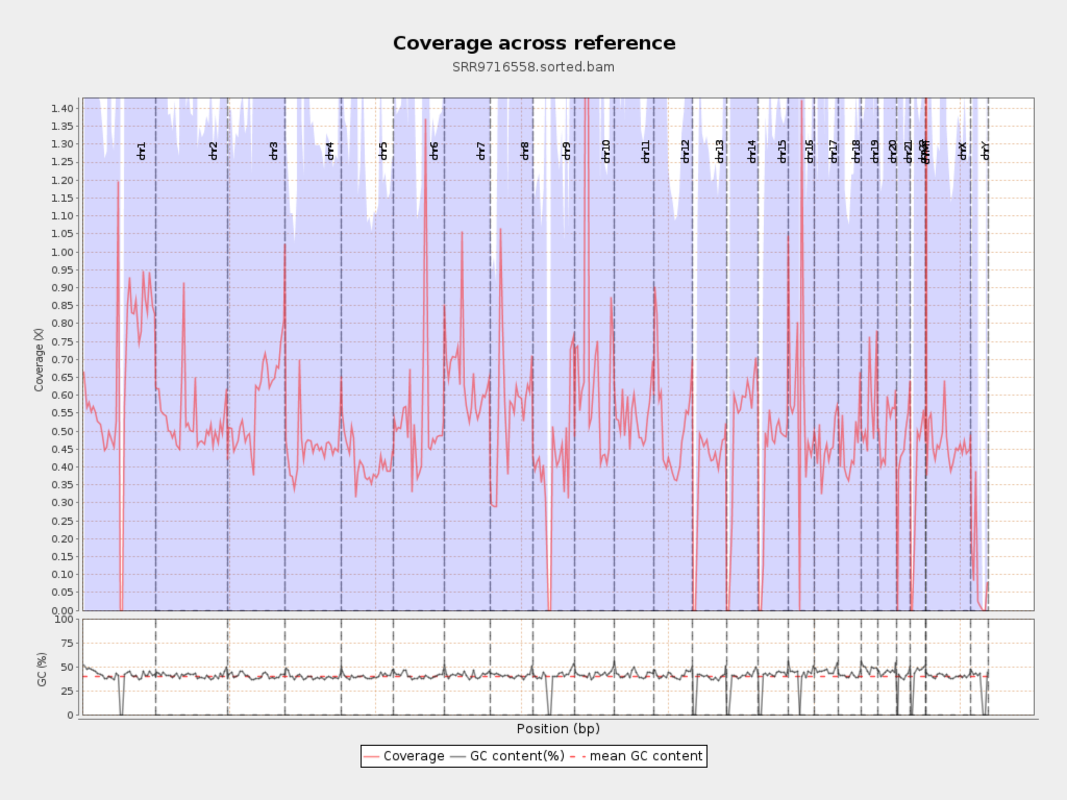
General error rate	0.32%
Mismatches	4,812,683
Insertions	126,843
Mapped reads with at least one insertion	0.54%
Deletions	140,473
Mapped reads with at least one deletion	0.59%
Homopolymer indels	39.22%

2.6. Chromosome stats

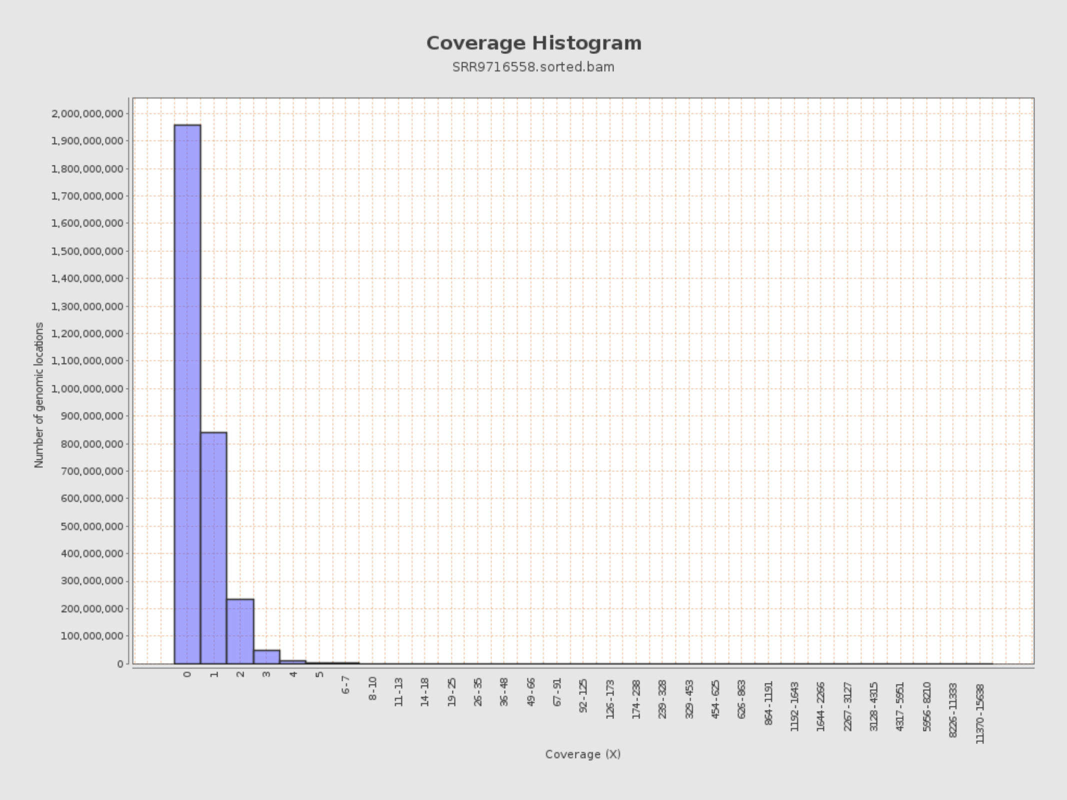
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	161507603	0.648	13.5849
chr2	243199373	128888234	0.53	3.2647
chr3	198022430	115018528	0.5808	3.247
chr4	191154276	86859554	0.4544	1.8636
chr5	180915260	75184931	0.4156	0.8701
chr6	171115067	91459346	0.5345	2.1151
chr7	159138663	103876160	0.6527	7.0683

chr8	146364022	83405528	0.5698	2.799
chr9	141213431	56645070	0.4011	2.5754
chr10	135534747	97778711	0.7214	18.6999
chr11	135006516	72888661	0.5399	2.2922
chr12	133851895	69436913	0.5188	1.0577
chr13	115169878	44801055	0.389	0.7275
chr14	107349540	53921253	0.5023	1.2574
chr15	102531392	40915996	0.3991	0.7105
chr16	90354753	53975267	0.5974	5.662
chr17	81195210	37023296	0.456	1.6313
chr18	78077248	35382385	0.4532	6.1287
chr19	59128983	33648005	0.5691	9.7991
chr20	63025520	31914906	0.5064	1.0904
chr21	48129895	21171203	0.4399	1.9262
chr22	51304566	18152042	0.3538	0.9614
chrMT	16571	6602490	398.4364	85.7494
chrX	155270560	72084854	0.4643	1.6143
chrY	59373566	5471853	0.0922	3.3061

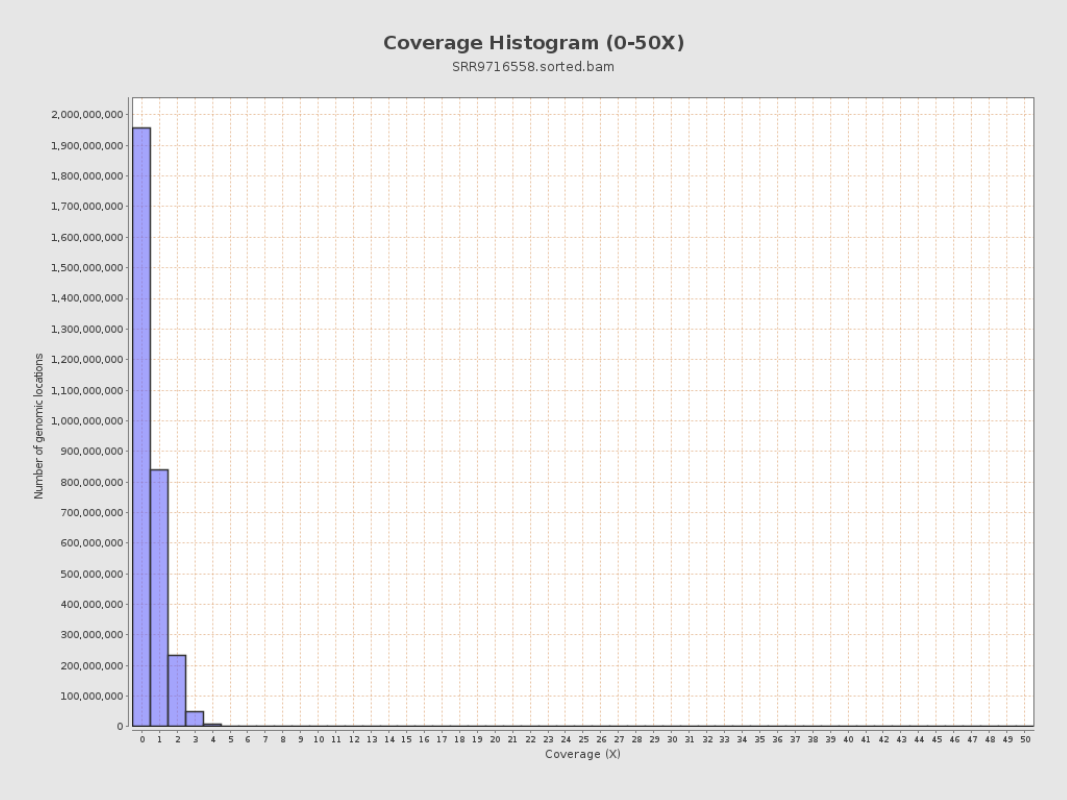
3. Results : Coverage across reference



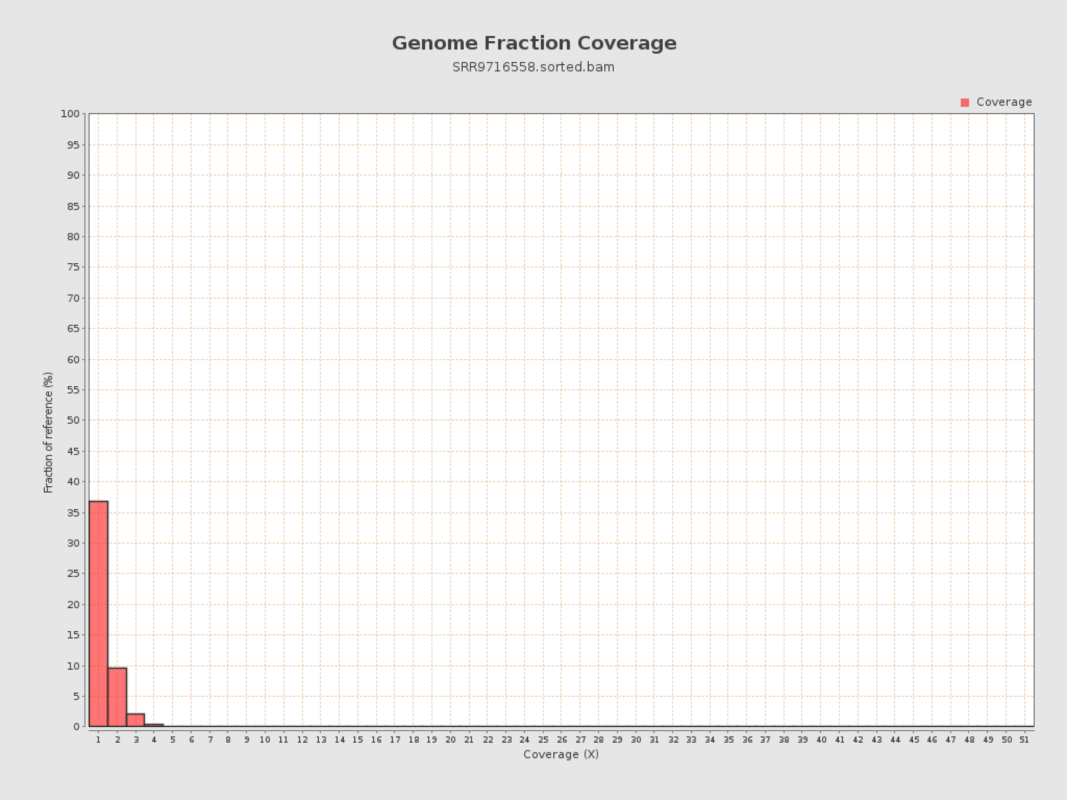
4. Results : Coverage Histogram



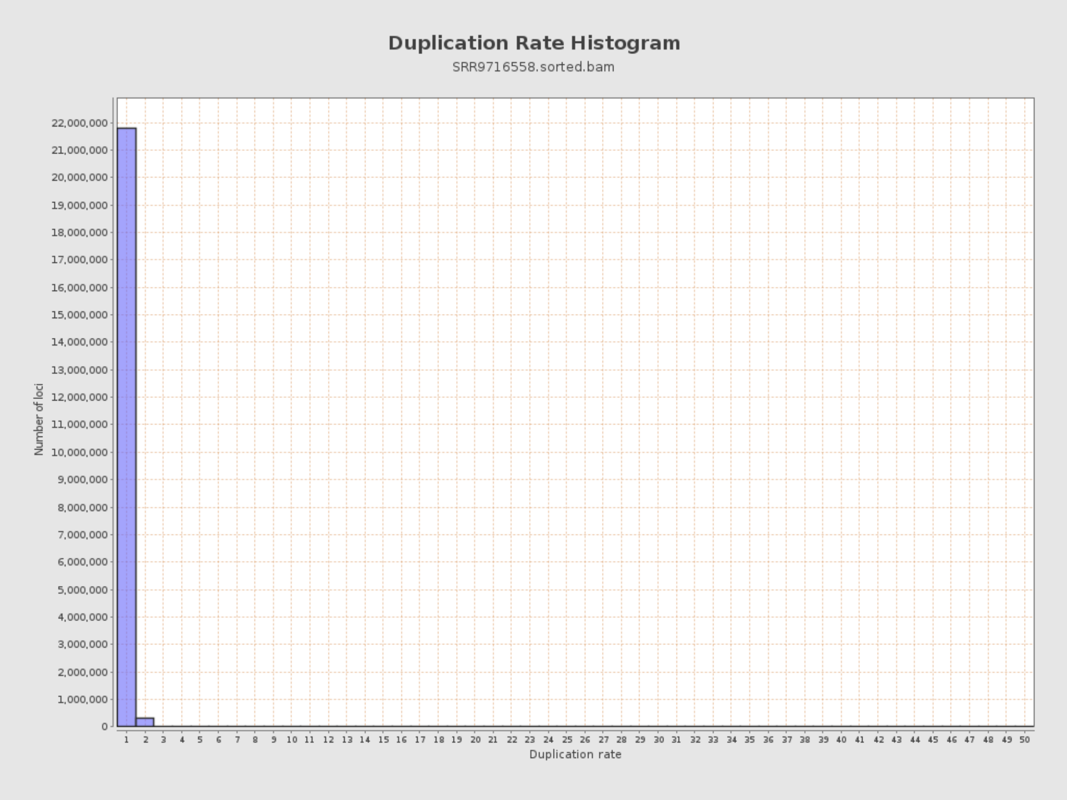
5. Results : Coverage Histogram (0-50X)



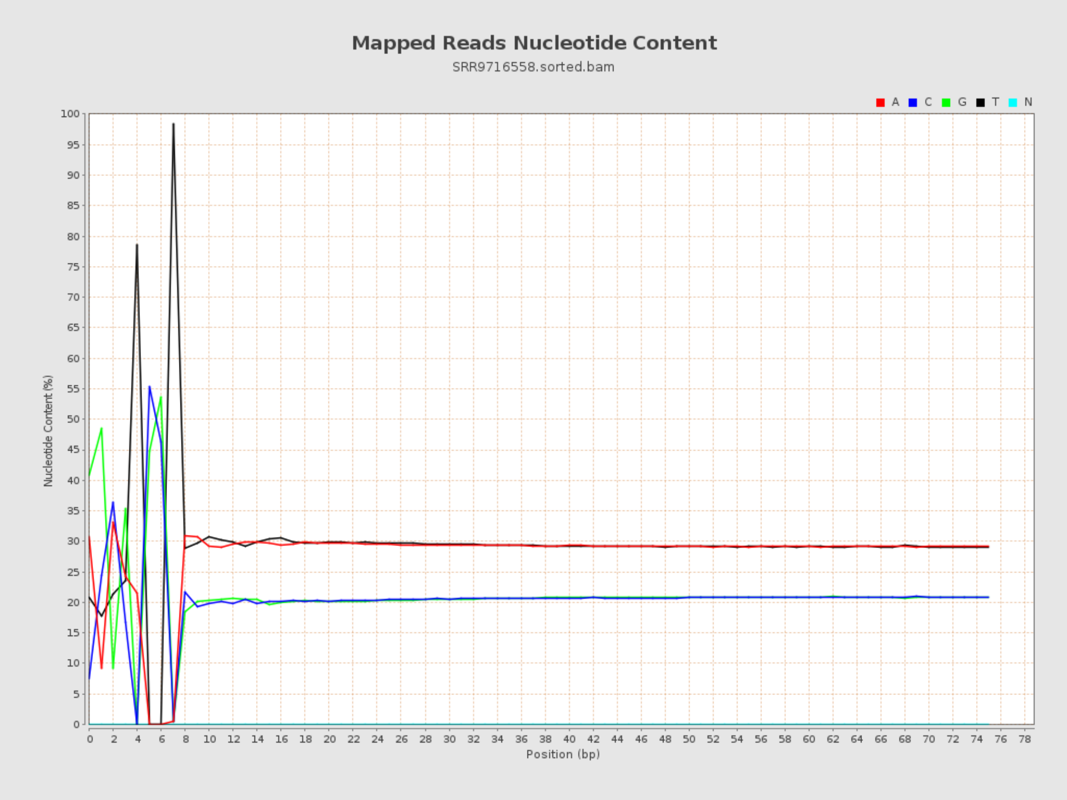
6. Results : Genome Fraction Coverage



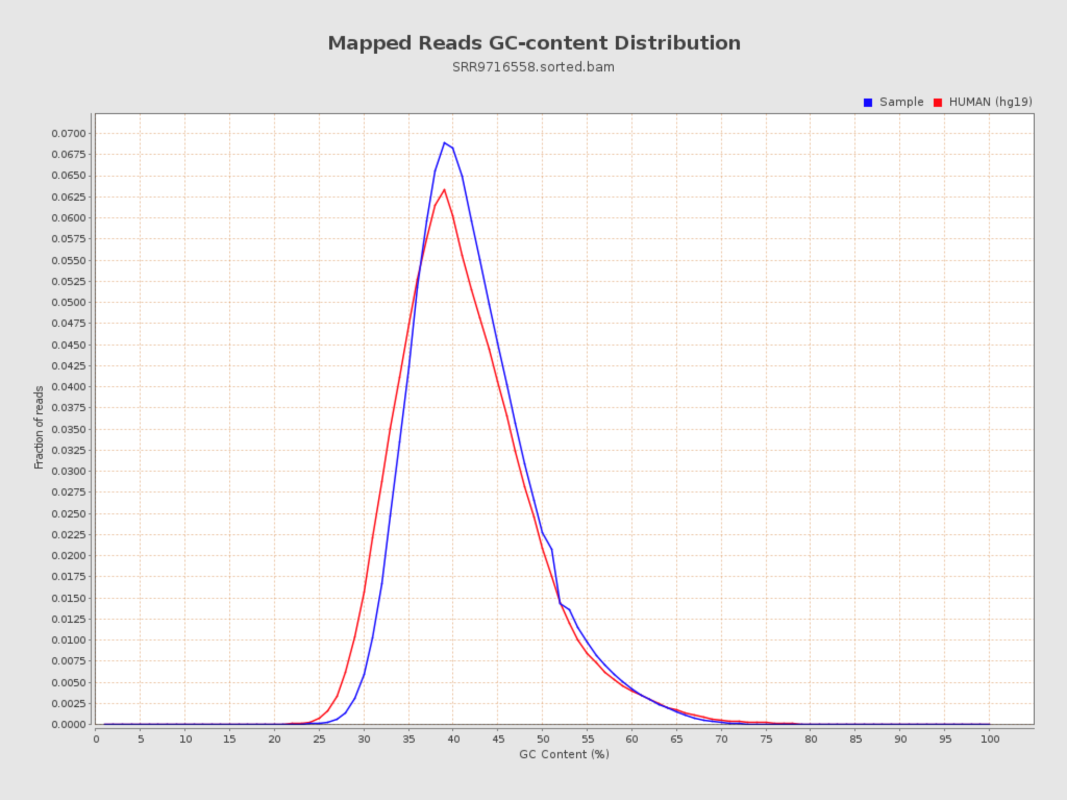
7. Results : Duplication Rate Histogram



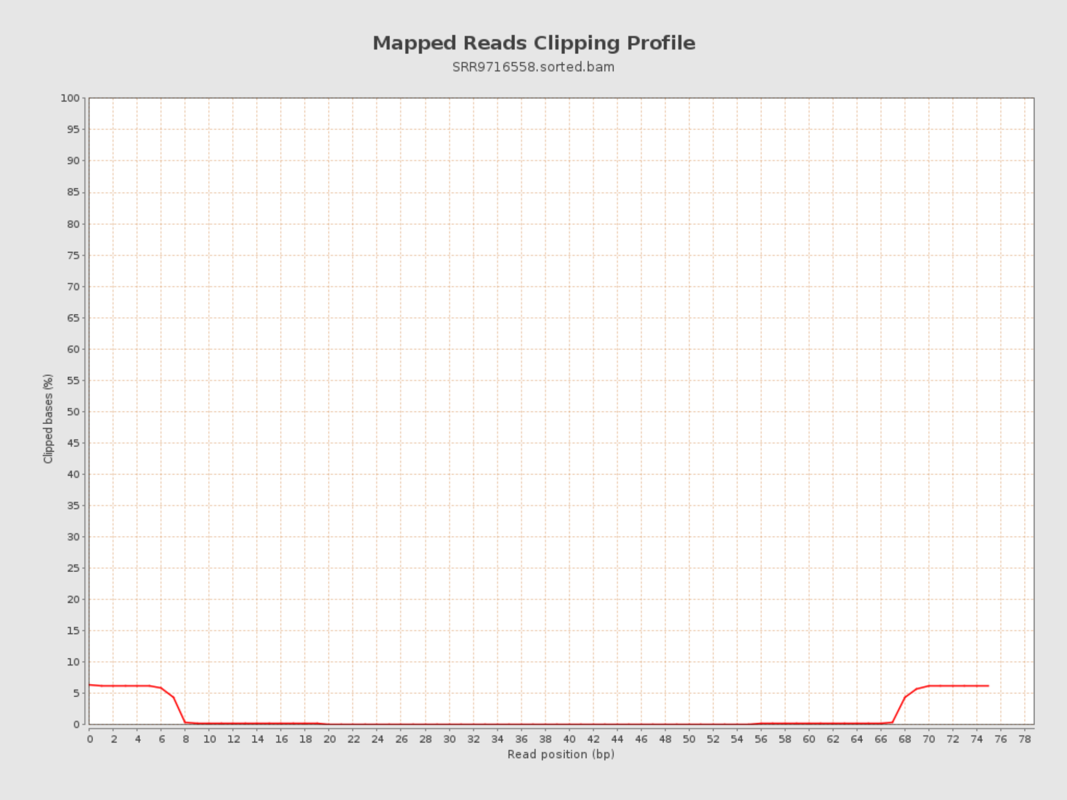
8. Results : Mapped Reads Nucleotide Content



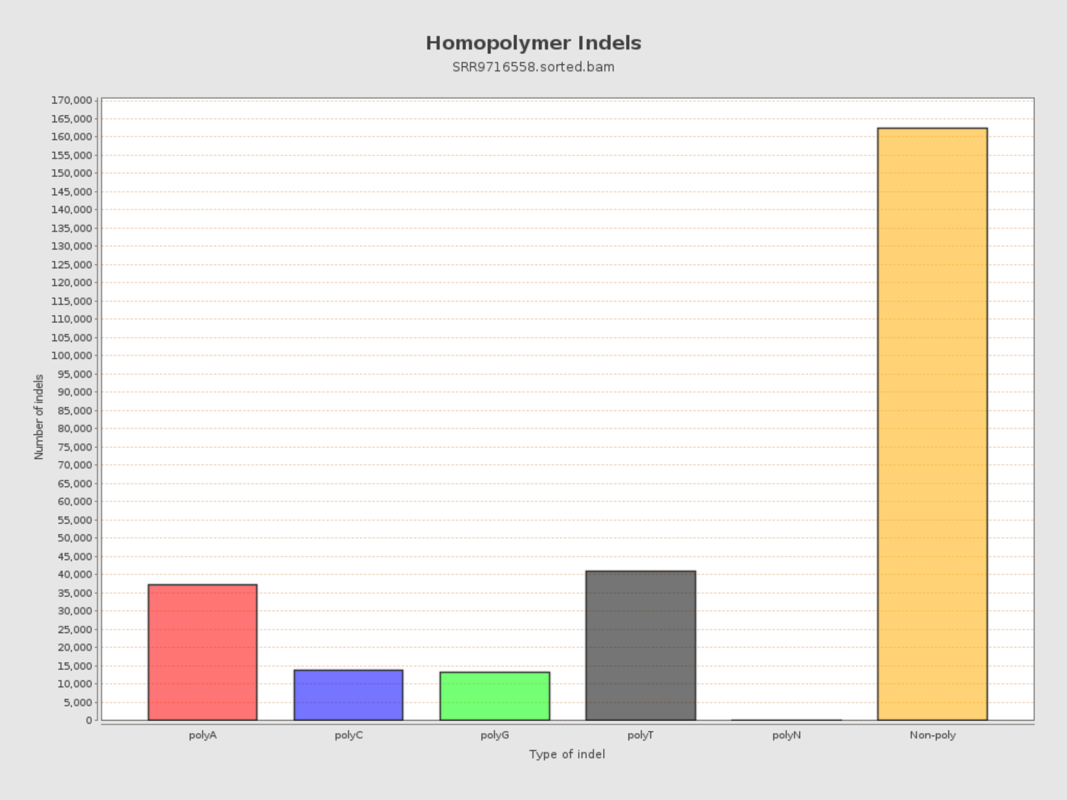
9. Results : Mapped Reads GC-content Distribution



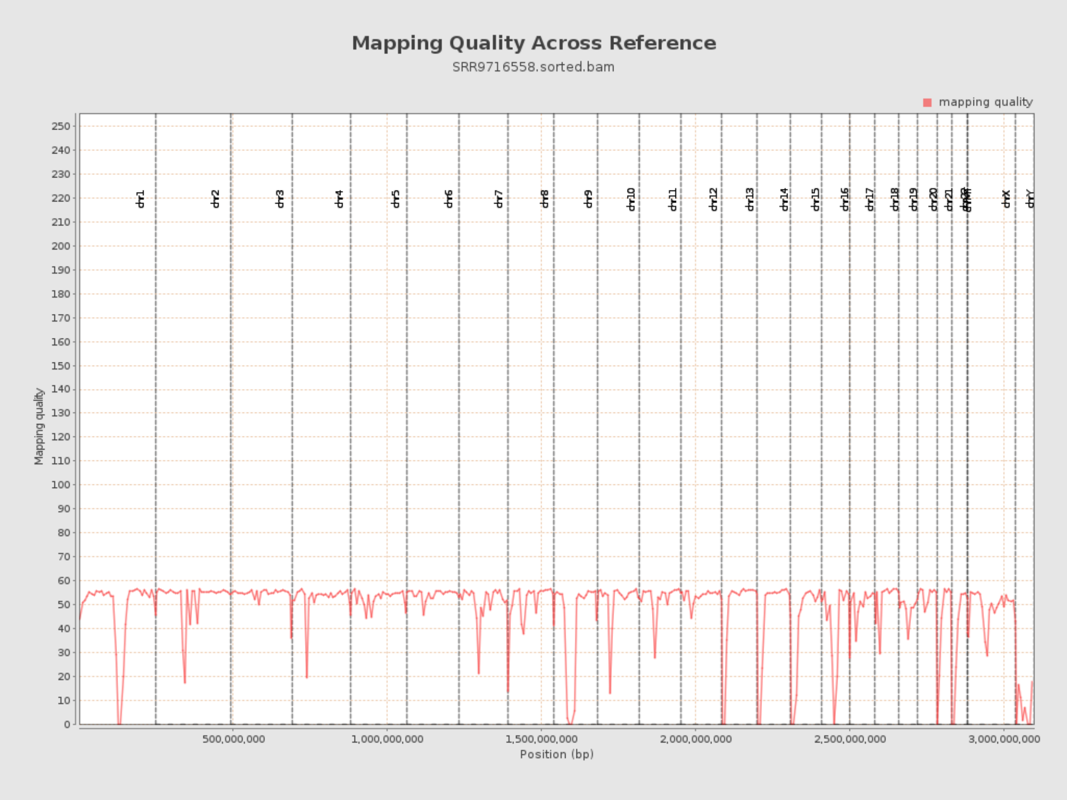
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram