Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 21:09:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716559.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_SRR9716559 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716559.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 21:09:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716559.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,461,283
Mapped reads	18,790,385 / 96.55%
Unmapped reads	670,898 / 3.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,195 / 0.05%
Read min/max/mean length	30 / 76 / 76.02
Duplicated reads (estimated)	932,197 / 4.79%
Duplication rate	1.71%
Clipped reads	18,682,889 / 96%

2.2. ACGT Content

Number/percentage of A's	365,999,099 / 28.65%
Number/percentage of C's	262,684,814 / 20.56%
Number/percentage of T's	384,737,702 / 30.12%
Number/percentage of G's	263,941,379 / 20.66%
Number/percentage of N's	63,922 / 0.01%
GC Percentage	41.23%

2.3. Coverage

Mean	0.4127

Standard Deviation	4.5528

2.4. Mapping Quality

Mean Mapping Quality	49.15

2.5. Mismatches and indels

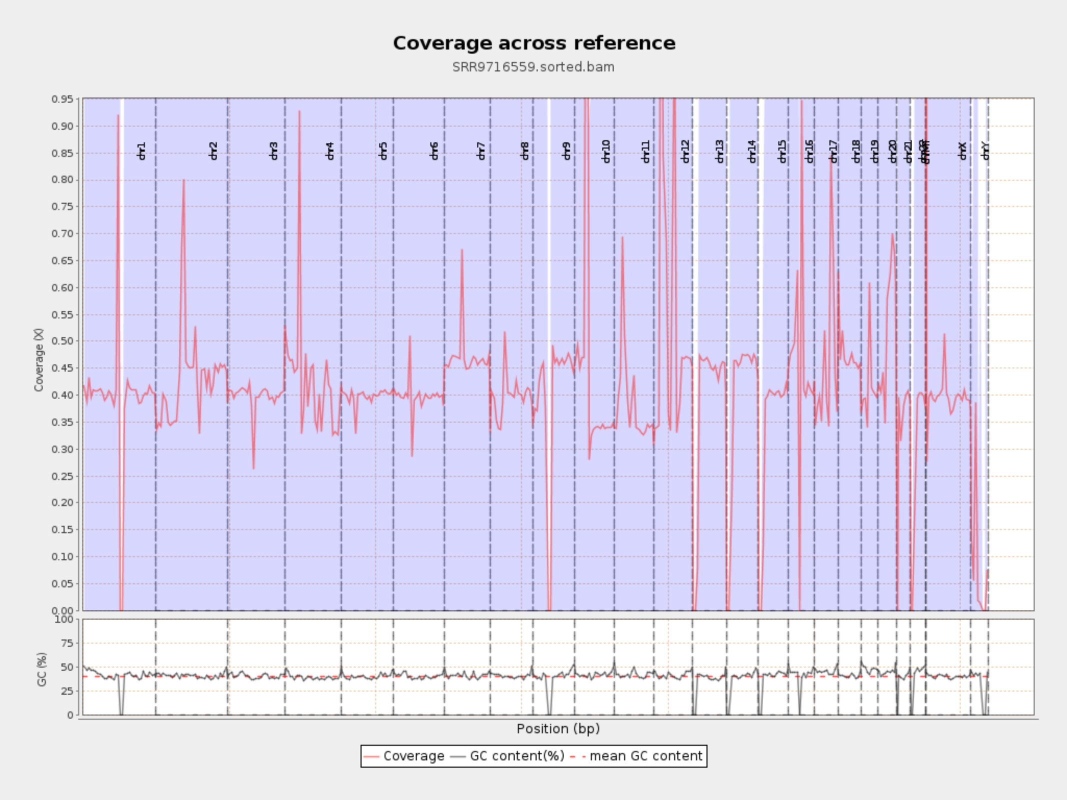
General error rate	0.32%
Mismatches	3,859,383
Insertions	112,872
Mapped reads with at least one insertion	0.6%
Deletions	111,218
Mapped reads with at least one deletion	0.59%
Homopolymer indels	38.59%

2.6. Chromosome stats

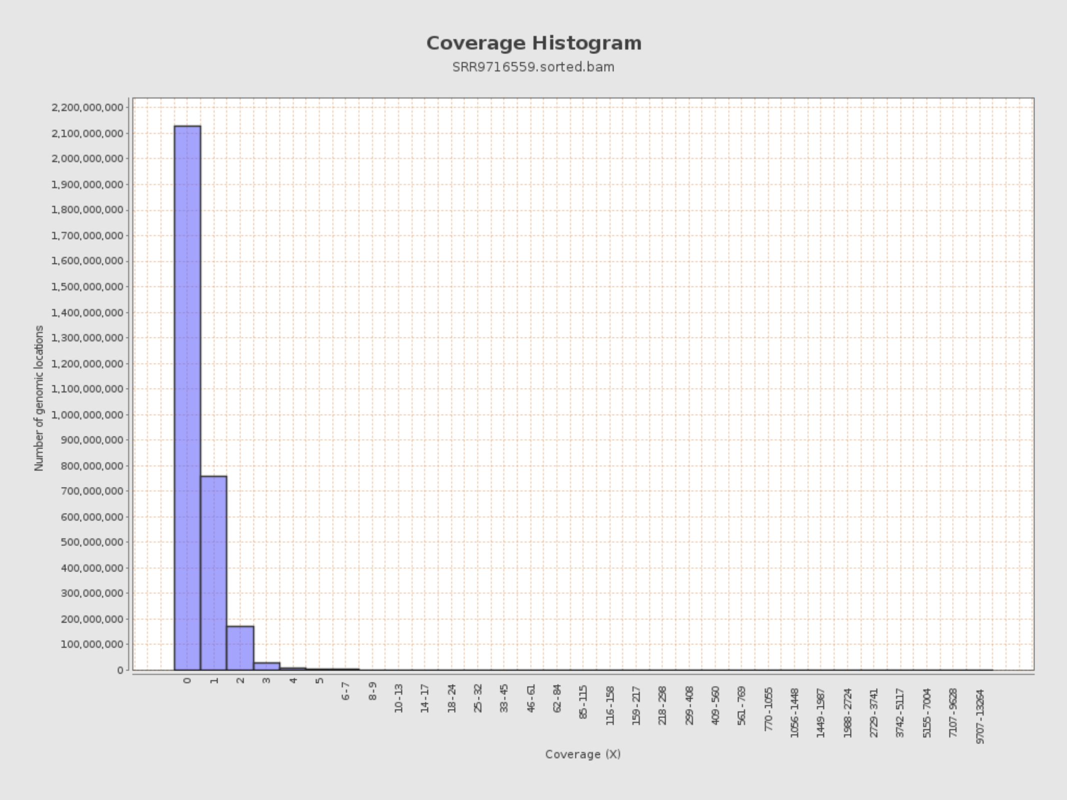
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	98399912	0.3948	11.4176
chr2	243199373	105475015	0.4337	3.1591
chr3	198022430	78870248	0.3983	1.6889
chr4	191154276	81803342	0.4279	2.431
chr5	180915260	72025741	0.3981	0.7789
chr6	171115067	68086025	0.3979	1.4893
chr7	159138663	75302714	0.4732	3.3455

chr8	146364022	58336611	0.3986	2.537
chr9	141213431	55858623	0.3956	2.4831
chr10	135534747	61612469	0.4546	10.0343
chr11	135006516	52511440	0.389	1.6538
chr12	133851895	76202099	0.5693	1.1746
chr13	115169878	43894043	0.3811	0.6553
chr14	107349540	41940495	0.3907	1.1541
chr15	102531392	33386996	0.3256	0.6138
chr16	90354753	41634118	0.4608	3.8995
chr17	81195210	37728763	0.4647	1.2359
chr18	78077248	37069837	0.4748	5.2328
chr19	59128983	24760726	0.4188	8.0274
chr20	63025520	33498918	0.5315	1.1842
chr21	48129895	16621591	0.3453	2.3153
chr22	51304566	14353488	0.2798	0.676
chrMT	16571	1834806	110.7239	26.7441
chrX	155270560	61504455	0.3961	1.3468
chrY	59373566	4933602	0.0831	3.4647

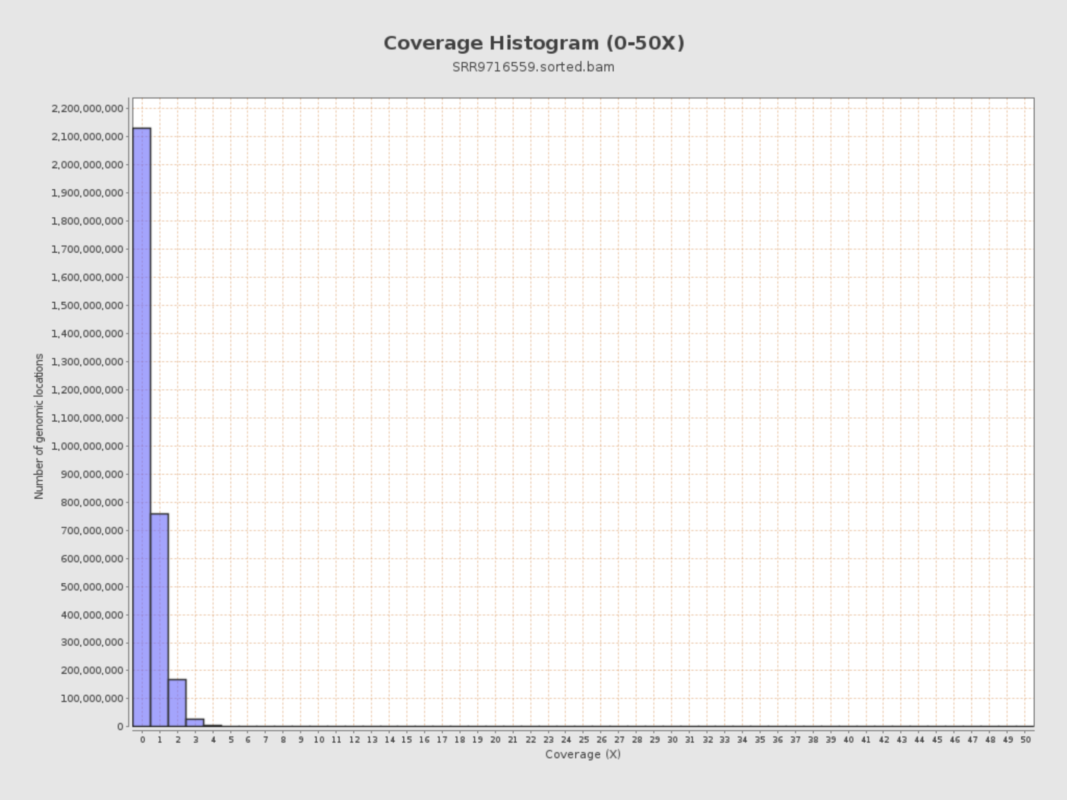
3. Results : Coverage across reference



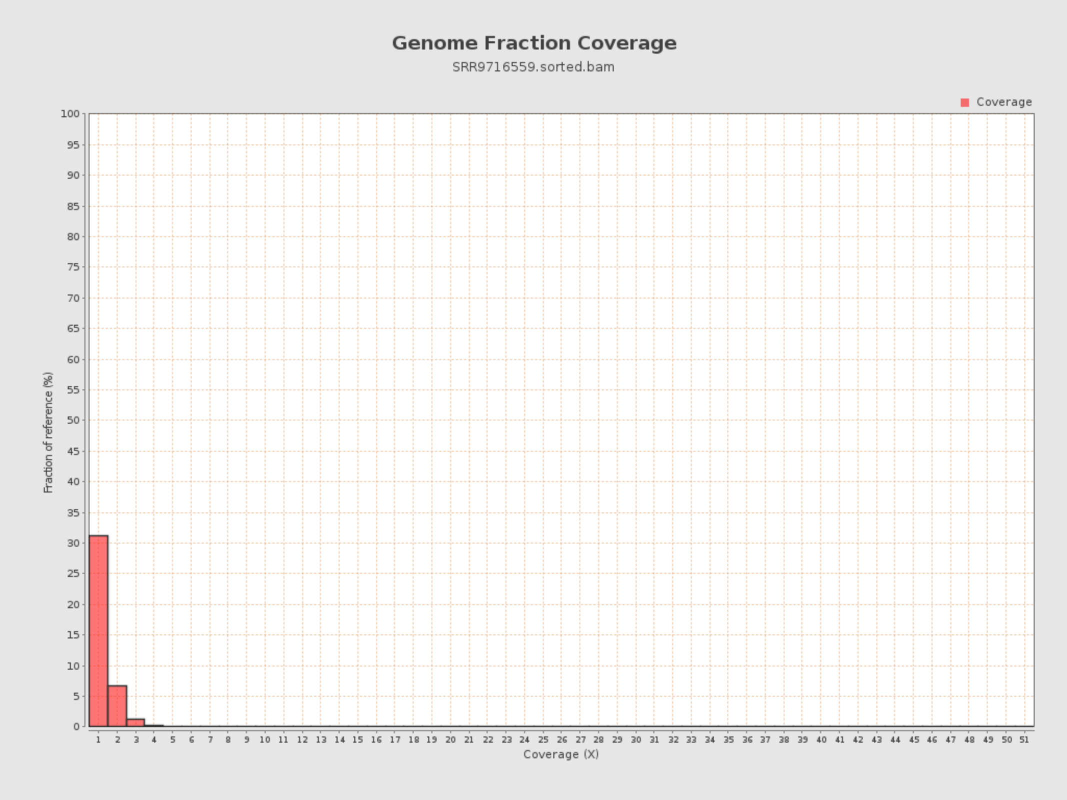
4. Results : Coverage Histogram



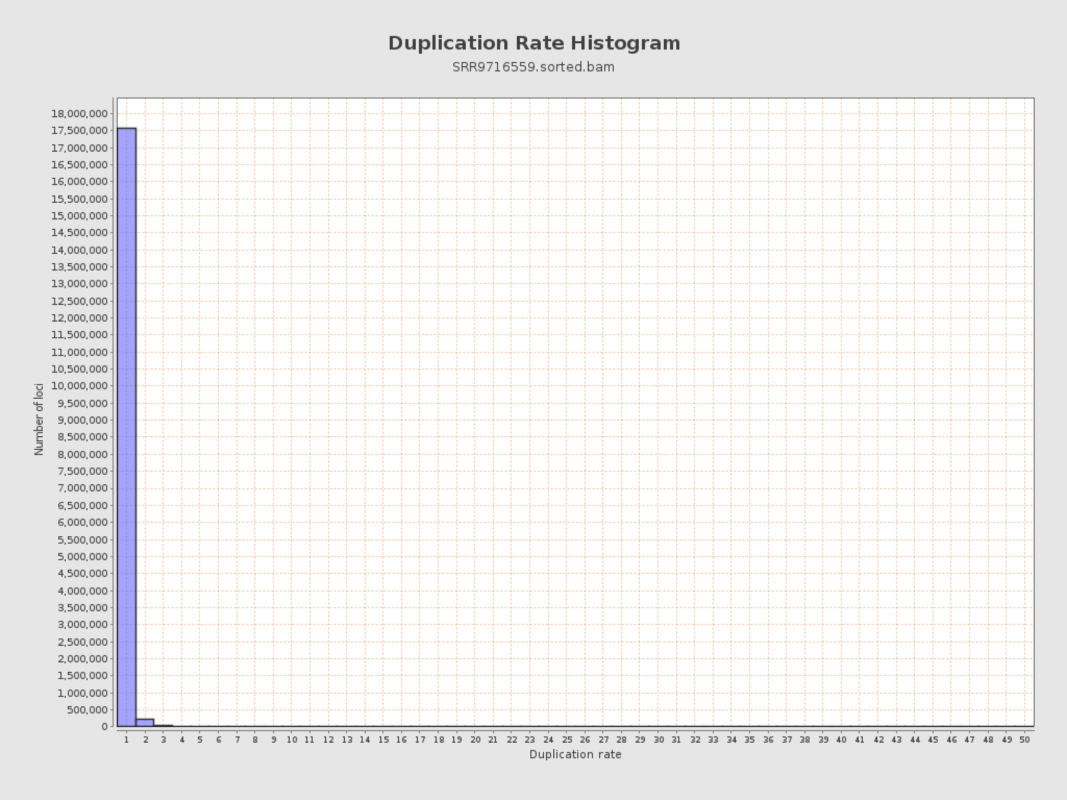
5. Results : Coverage Histogram (0-50X)



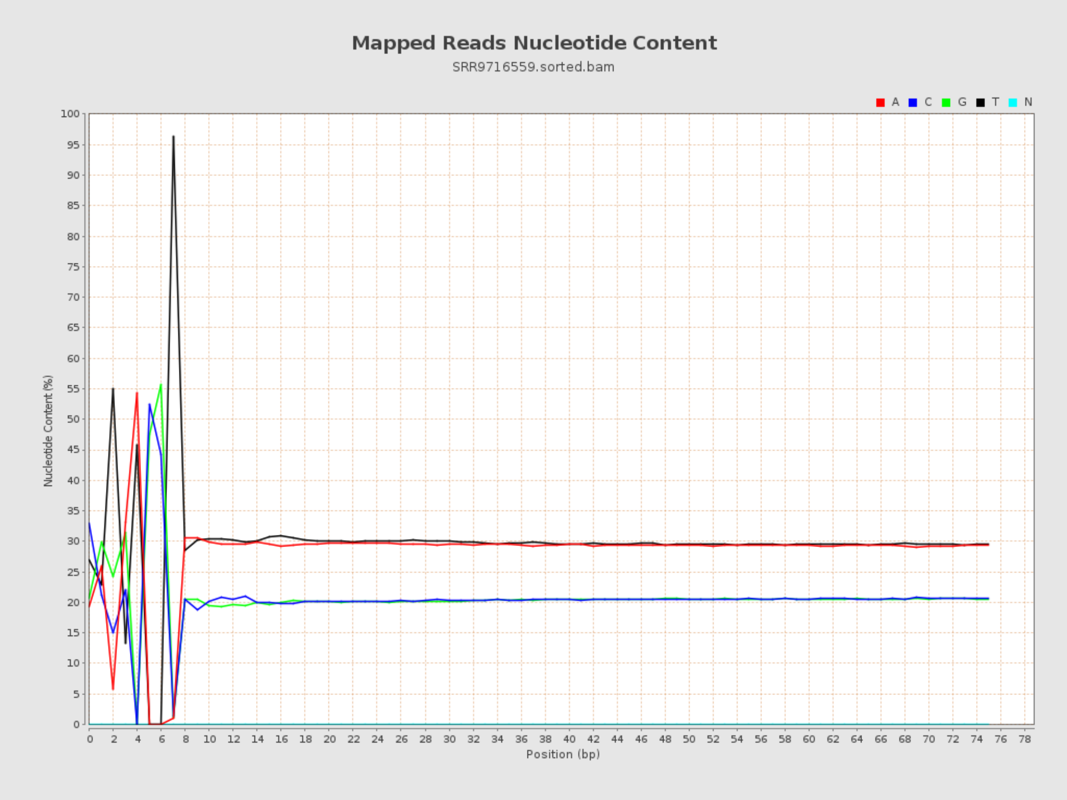
6. Results : Genome Fraction Coverage



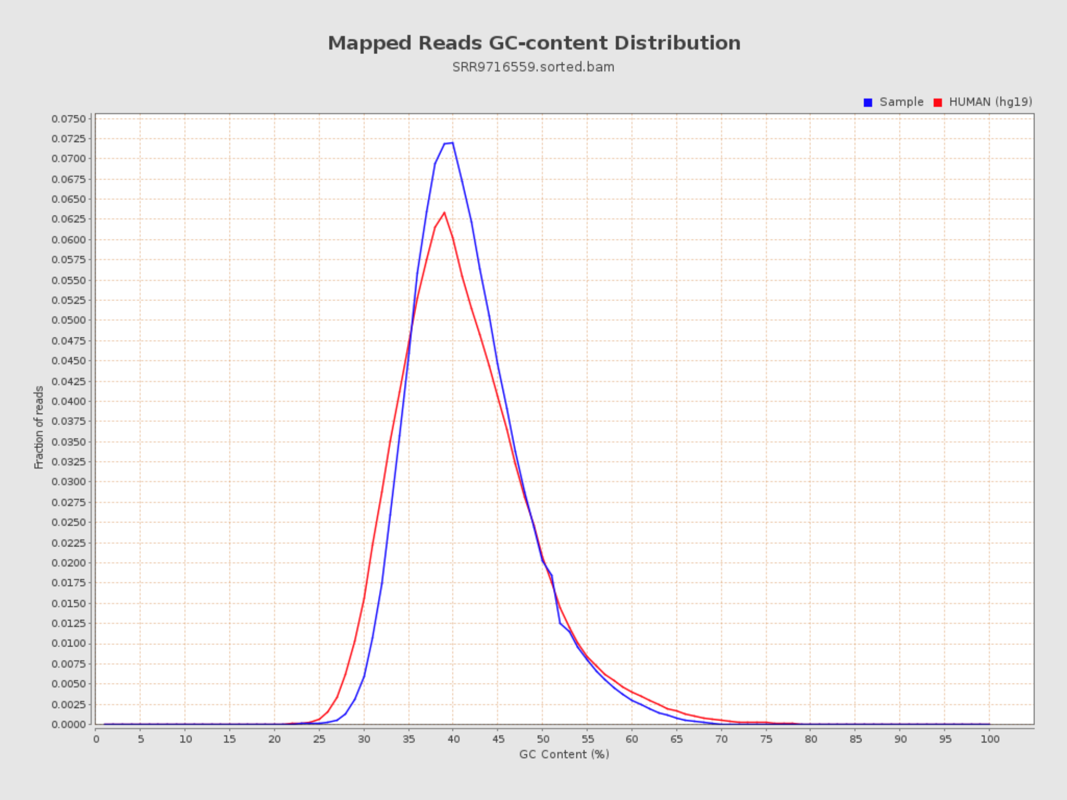
7. Results : Duplication Rate Histogram



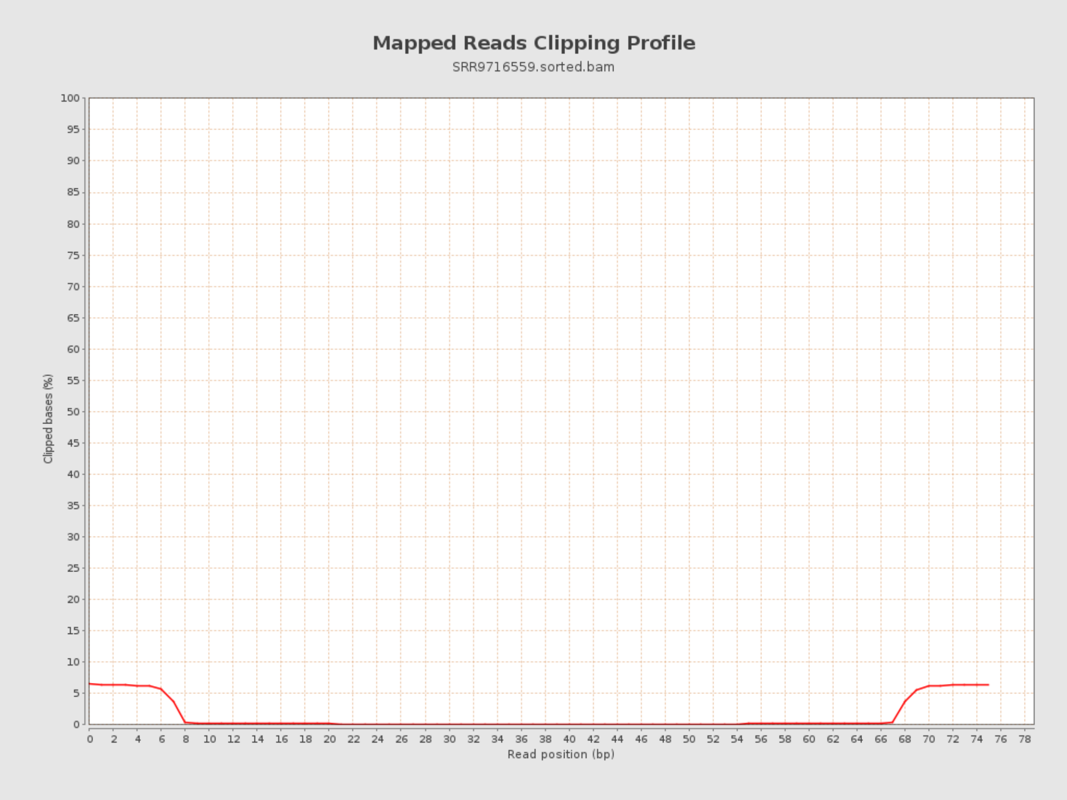
8. Results : Mapped Reads Nucleotide Content



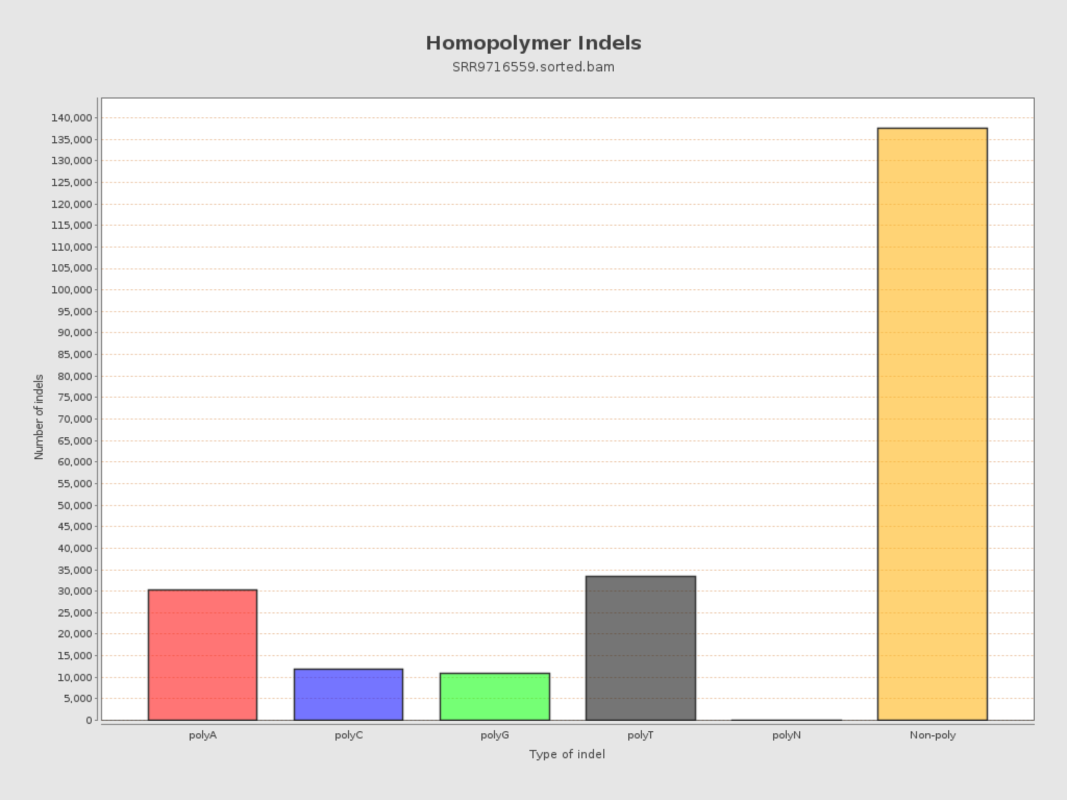
9. Results : Mapped Reads GC-content Distribution



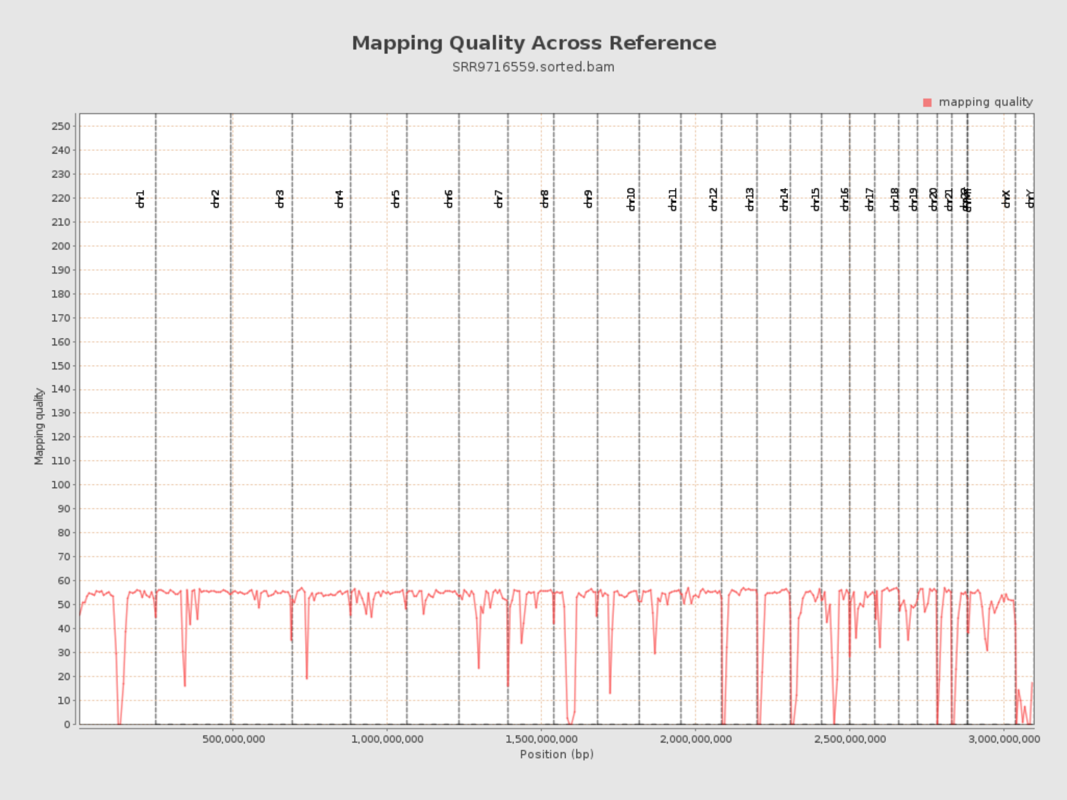
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram