Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 15:11:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716459.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_SRR9716459 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716459.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 15:11:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716459.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,484,022
Mapped reads	2,272,005 / 91.46%
Unmapped reads	212,017 / 8.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,577 / 0.59%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	136,325 / 5.49%
Duplication rate	4.71%
Clipped reads	2,279,930 / 91.78%

2.2. ACGT Content

Number/percentage of A's	35,025,342 / 26.36%
Number/percentage of C's	25,647,761 / 19.3%
Number/percentage of T's	39,722,974 / 29.9%
Number/percentage of G's	32,475,325 / 24.44%
Number/percentage of N's	946 / 0%
GC Percentage	43.74%

2.3. Coverage

Mean	0.0429

Standard Deviation	0.3576

2.4. Mapping Quality

Mean Mapping Quality	44.72

2.5. Mismatches and indels

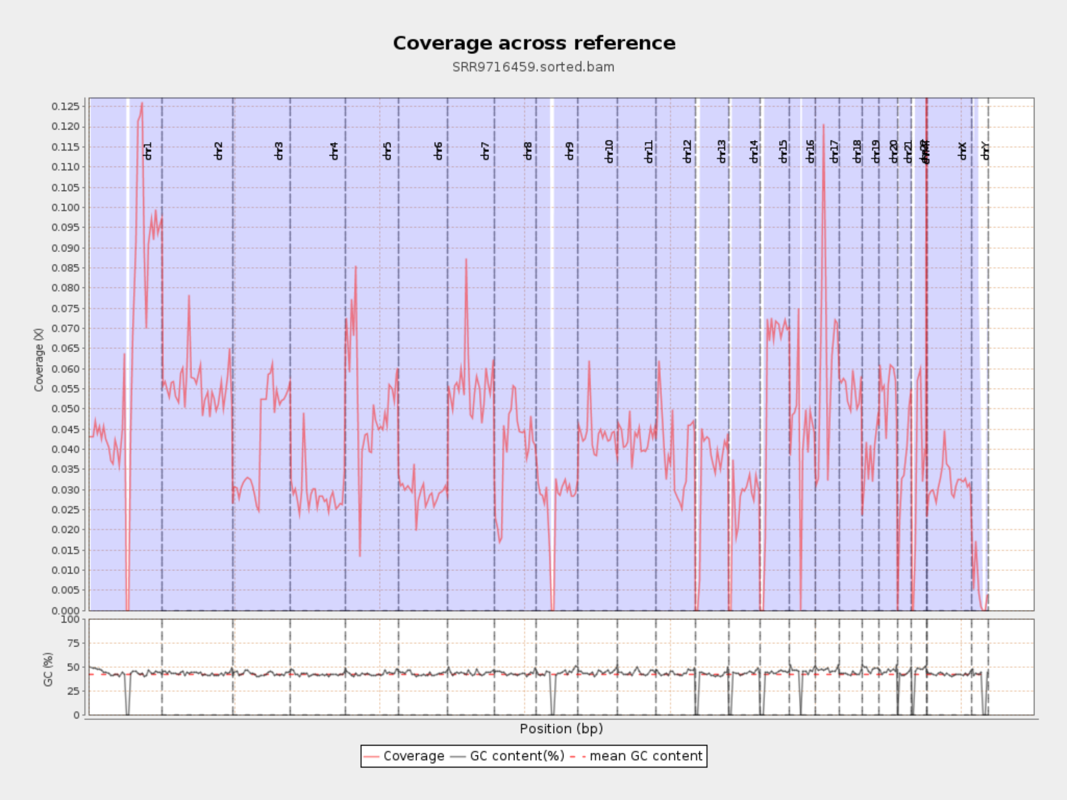
General error rate	0.51%
Mismatches	657,727
Insertions	10,117
Mapped reads with at least one insertion	0.44%
Deletions	23,128
Mapped reads with at least one deletion	1.01%
Homopolymer indels	40.86%

2.6. Chromosome stats

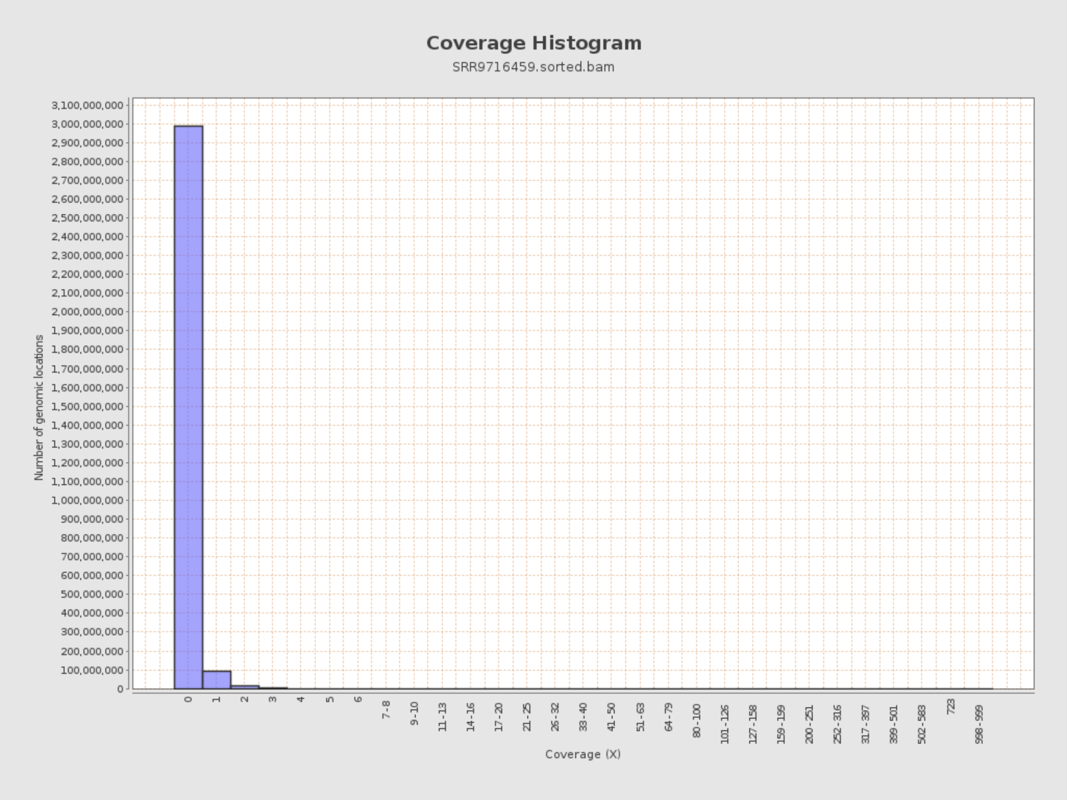
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15604208	0.0626	0.5715
chr2	243199373	13562565	0.0558	0.5286
chr3	198022430	8397391	0.0424	0.2395
chr4	191154276	5515110	0.0289	0.2338
chr5	180915260	9316409	0.0515	0.2652
chr6	171115067	5003018	0.0292	0.2291
chr7	159138663	8962575	0.0563	0.584

chr8	146364022	5870506	0.0401	0.3171
chr9	141213431	3640036	0.0258	0.2655
chr10	135534747	5944100	0.0439	0.3171
chr11	135006516	5743995	0.0425	0.317
chr12	133851895	5276481	0.0394	0.2356
chr13	115169878	3838905	0.0333	0.2135
chr14	107349540	2735069	0.0255	0.1996
chr15	102531392	5770251	0.0563	0.2797
chr16	90354753	4011079	0.0444	0.2628
chr17	81195210	5155731	0.0635	0.3274
chr18	78077248	4268498	0.0547	0.5725
chr19	59128983	2236847	0.0378	0.4287
chr20	63025520	3489653	0.0554	0.2807
chr21	48129895	1665365	0.0346	0.2314
chr22	51304566	1658406	0.0323	0.2098
chrMT	16571	4456	0.2689	0.5818
chrX	155270560	4928880	0.0317	0.2411
chrY	59373566	309505	0.0052	0.1374

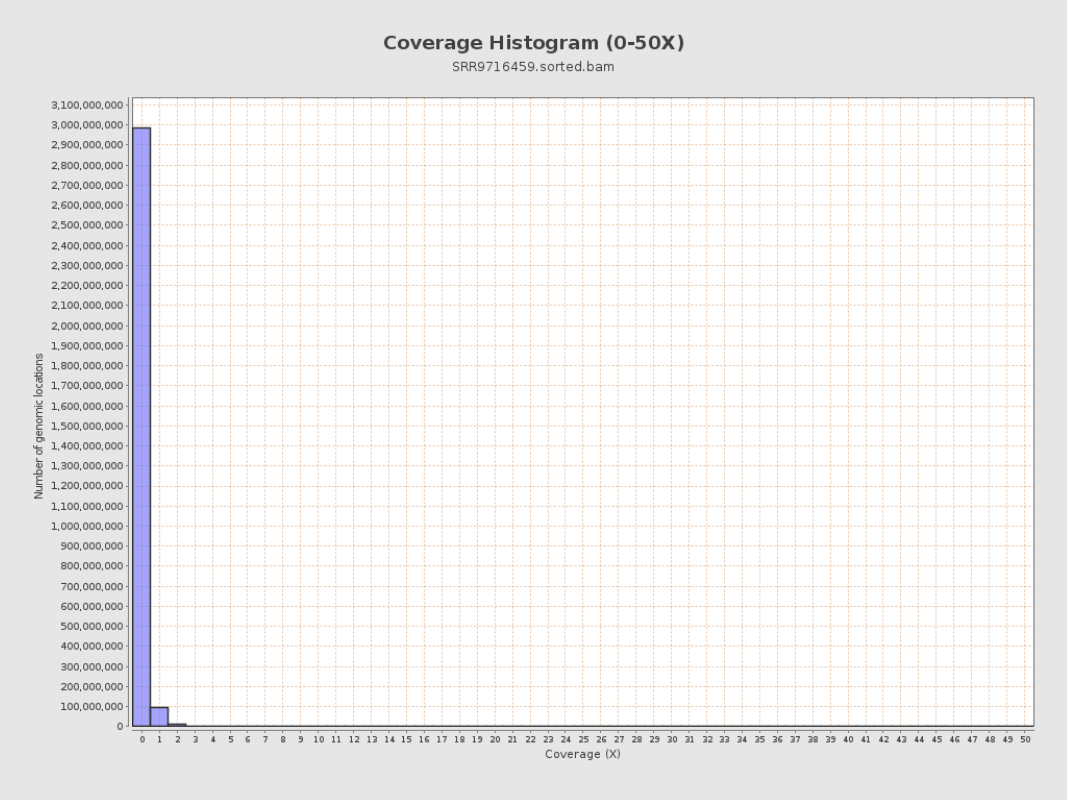
3. Results : Coverage across reference



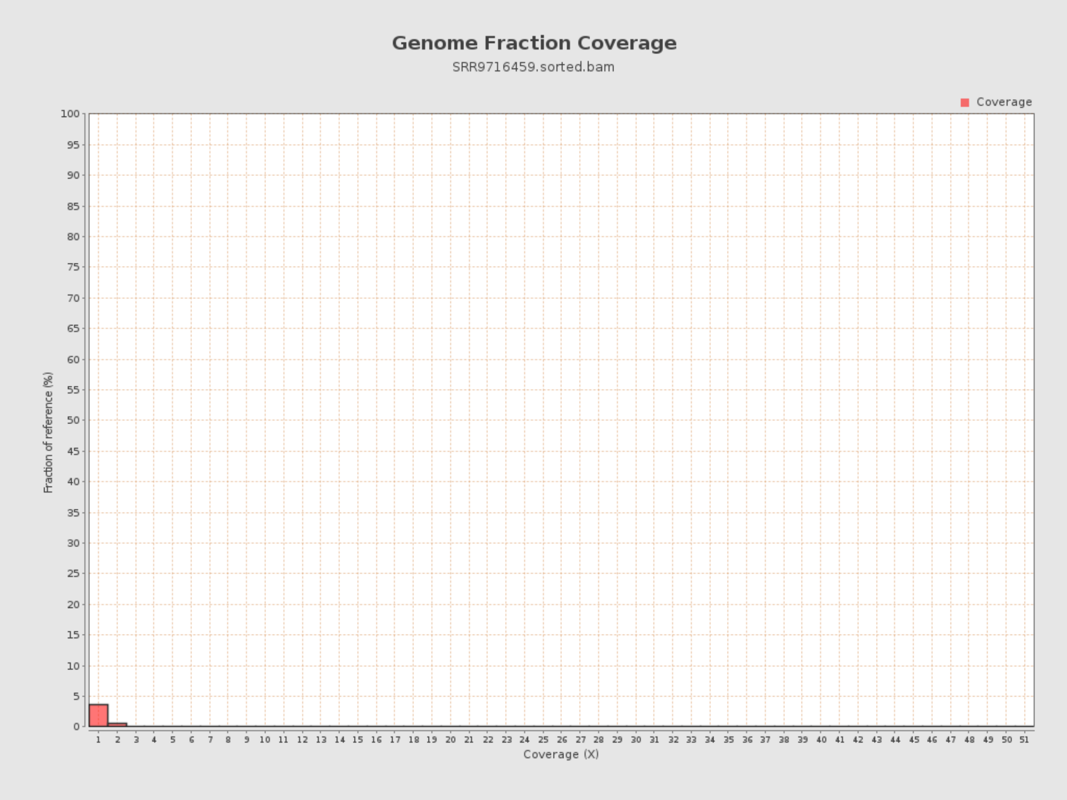
4. Results : Coverage Histogram



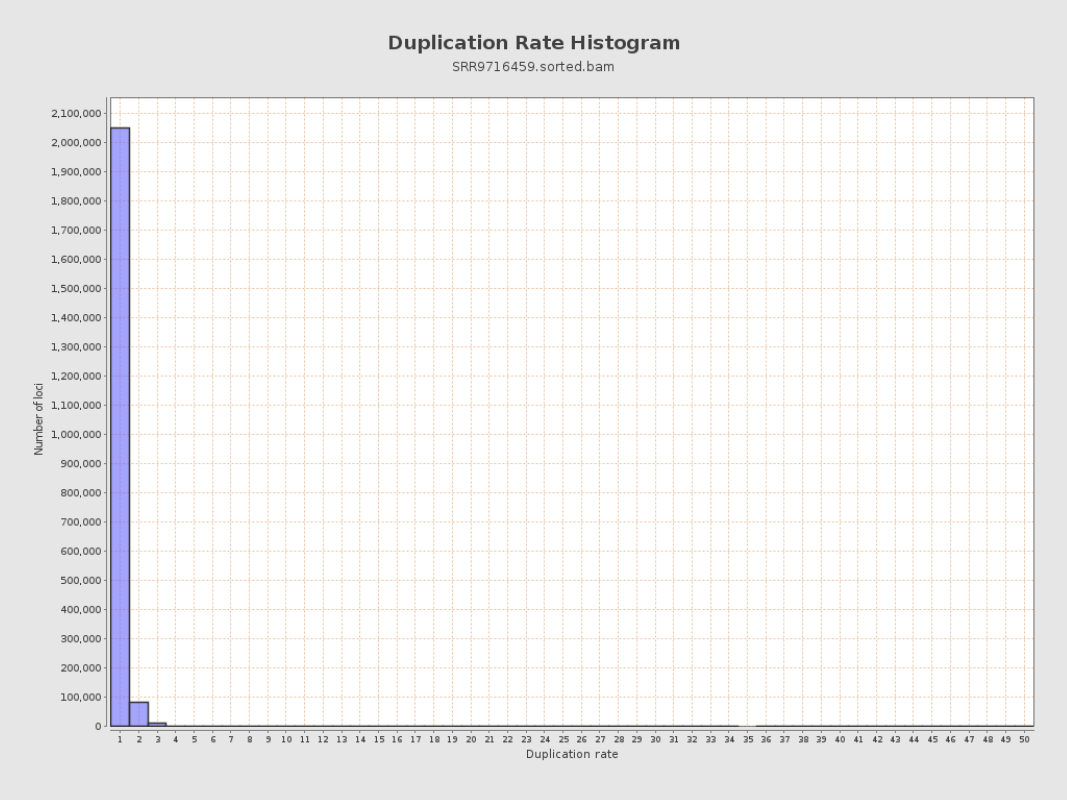
5. Results : Coverage Histogram (0-50X)



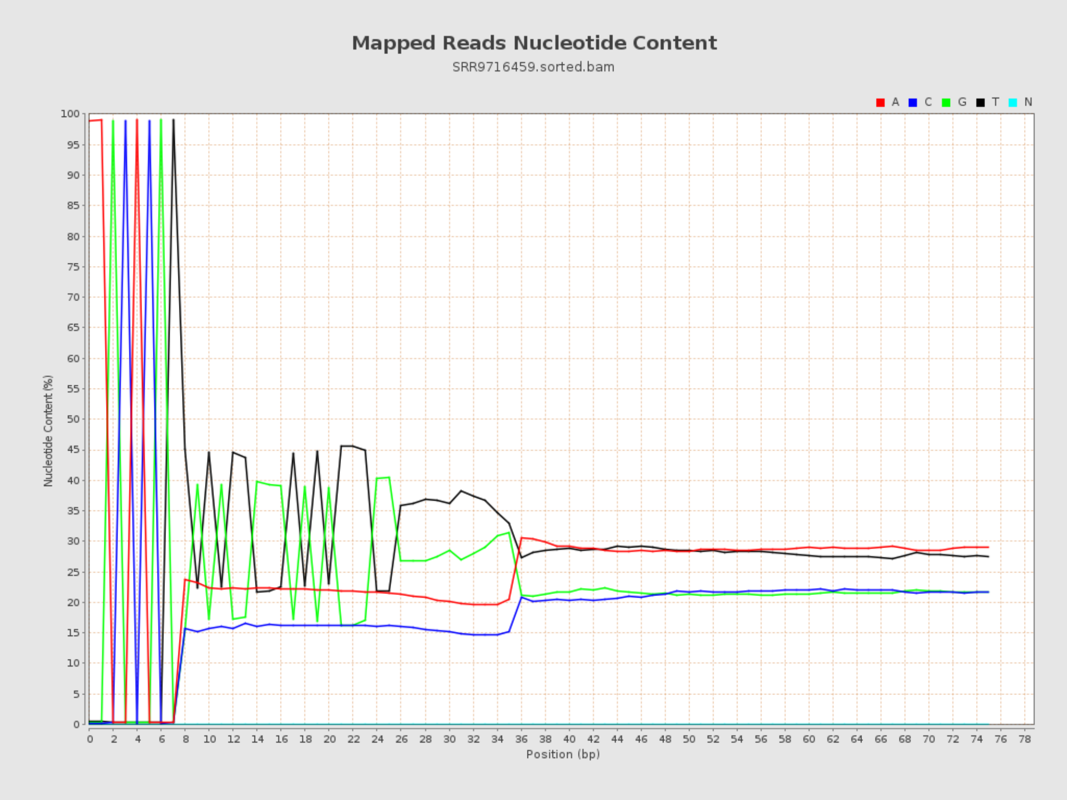
6. Results : Genome Fraction Coverage



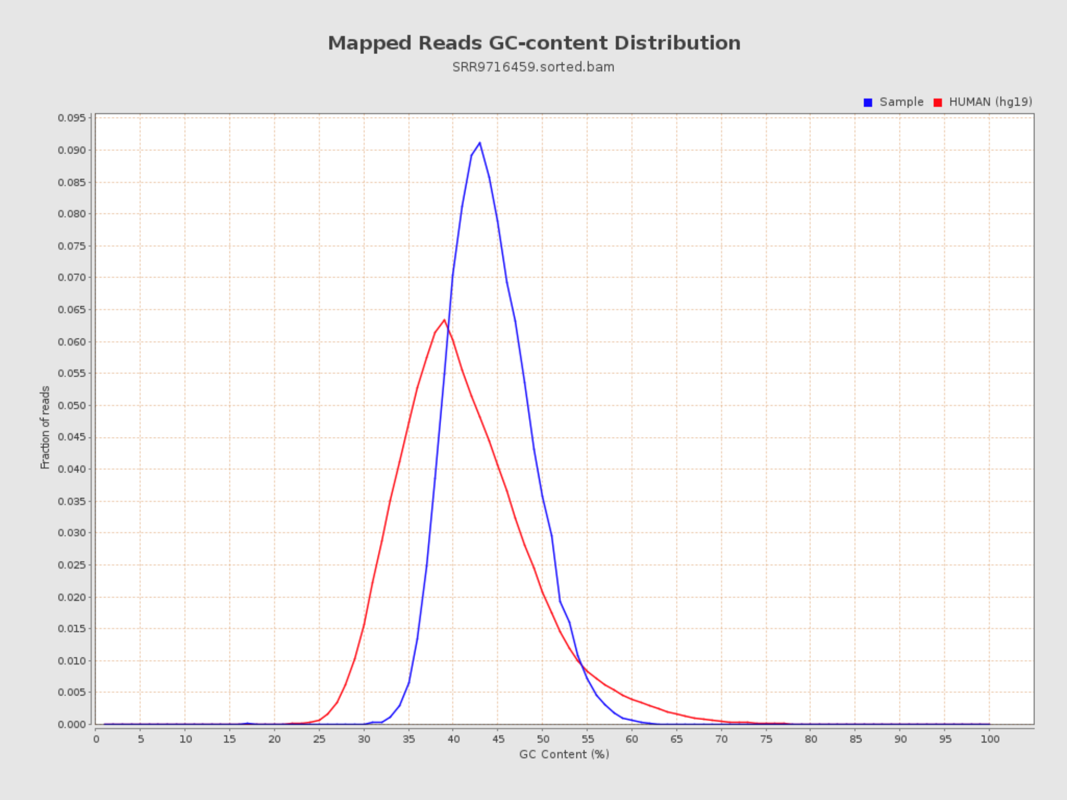
7. Results : Duplication Rate Histogram



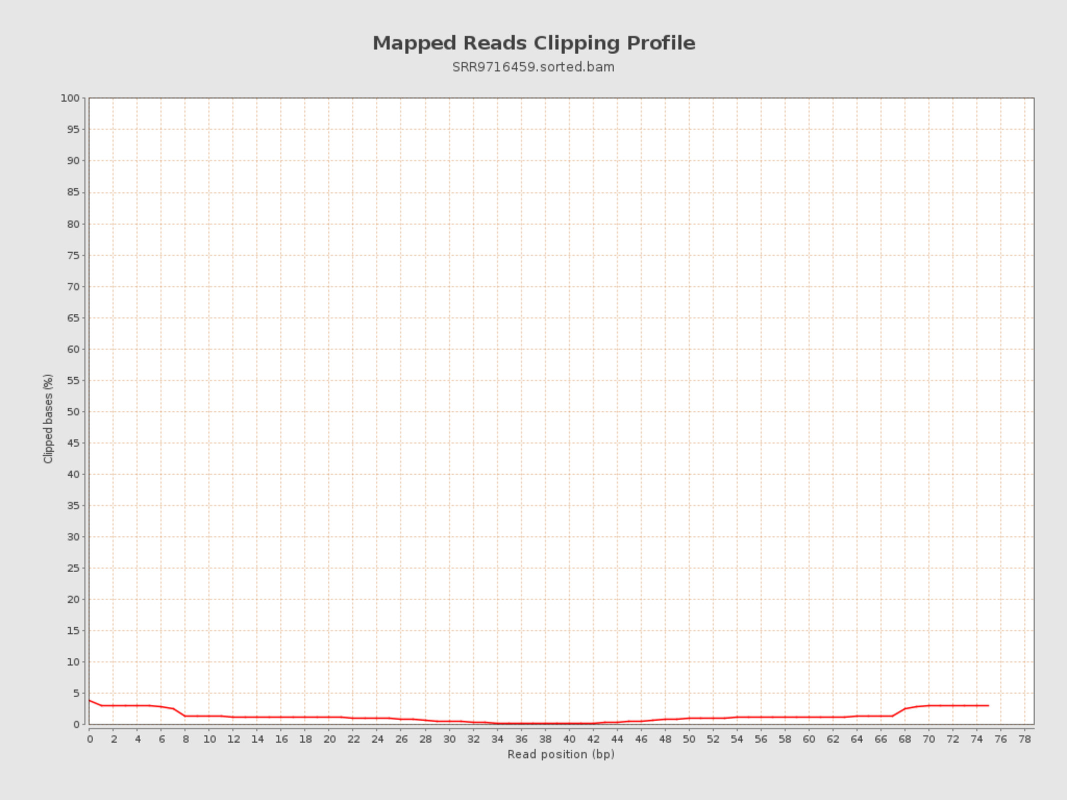
8. Results : Mapped Reads Nucleotide Content



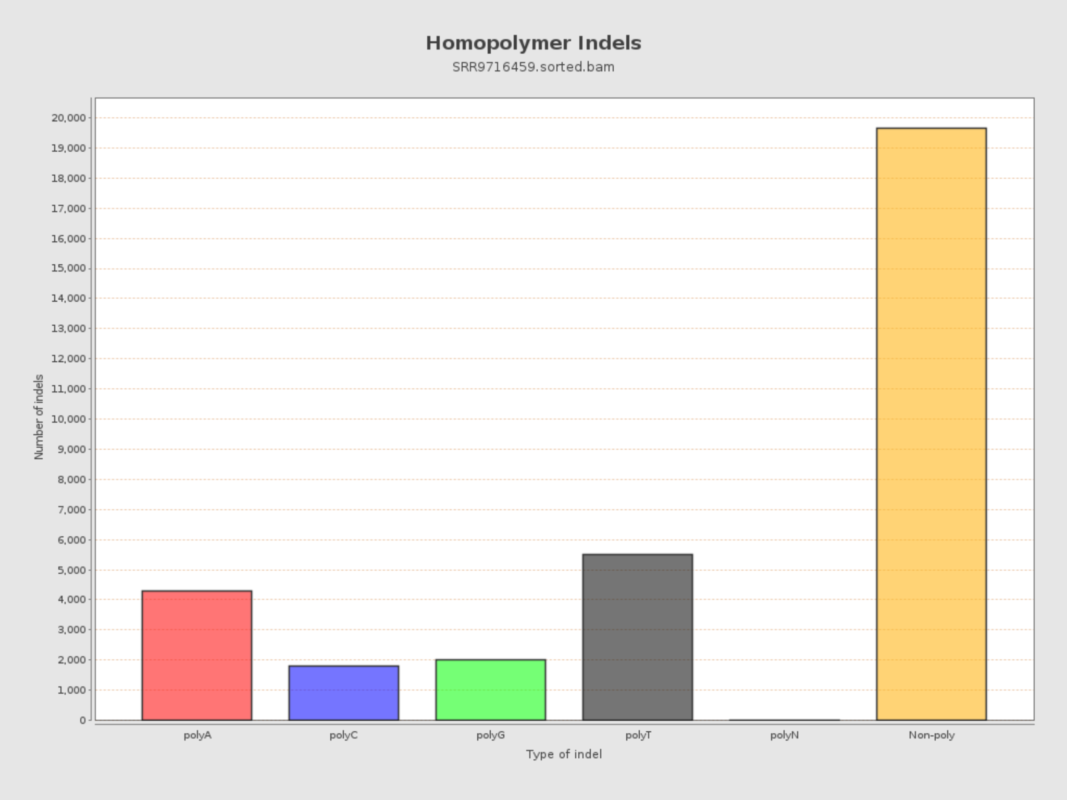
9. Results : Mapped Reads GC-content Distribution



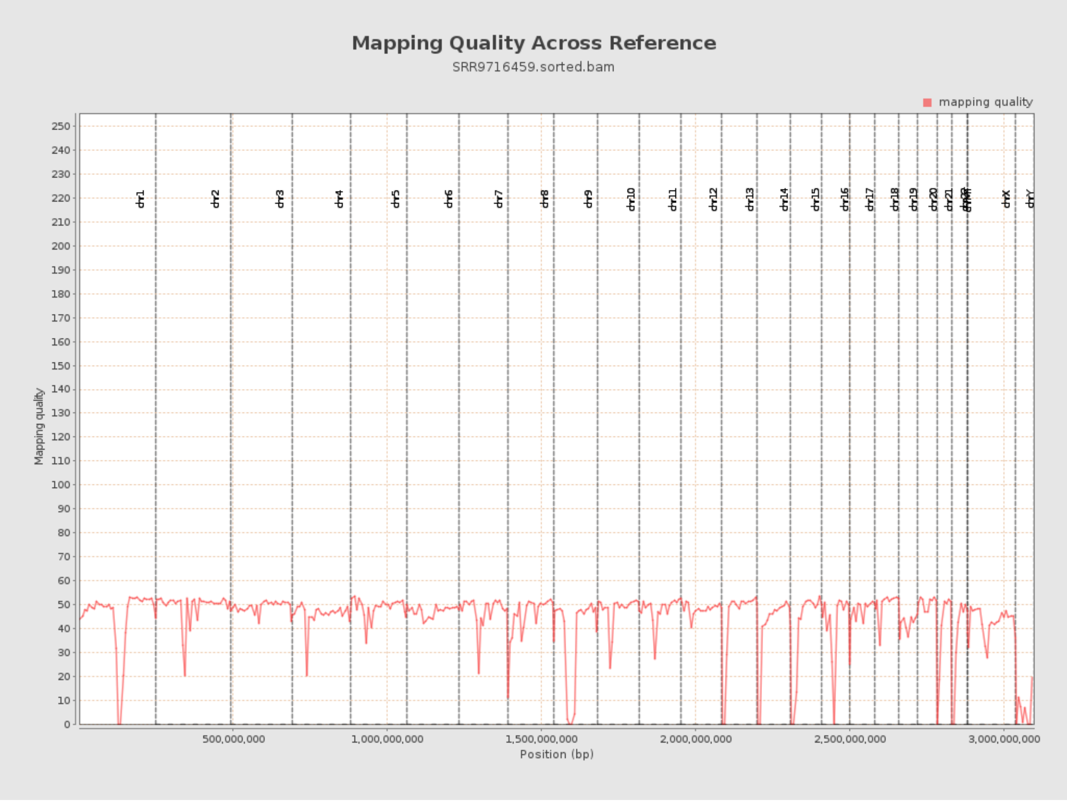
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram