Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 23:33:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716199.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_SRR9716199 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716199.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 23:33:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716199.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,208,137
Mapped reads	1,800,697 / 81.55%
Unmapped reads	407,440 / 18.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	39,743 / 1.8%
Read min/max/mean length	30 / 101 / 101.65
Duplicated reads (estimated)	60,094 / 2.72%
Duplication rate	2.29%
Clipped reads	1,838,571 / 83.26%

2.2. ACGT Content

Number/percentage of A's	34,712,371 / 25.77%
Number/percentage of C's	27,285,336 / 20.26%
Number/percentage of T's	40,699,326 / 30.21%
Number/percentage of G's	31,988,382 / 23.75%
Number/percentage of N's	16,743 / 0.01%
GC Percentage	44%

2.3. Coverage

Mean	0.0435

Standard Deviation	0.3572

2.4. Mapping Quality

Mean Mapping Quality	46.01

2.5. Mismatches and indels

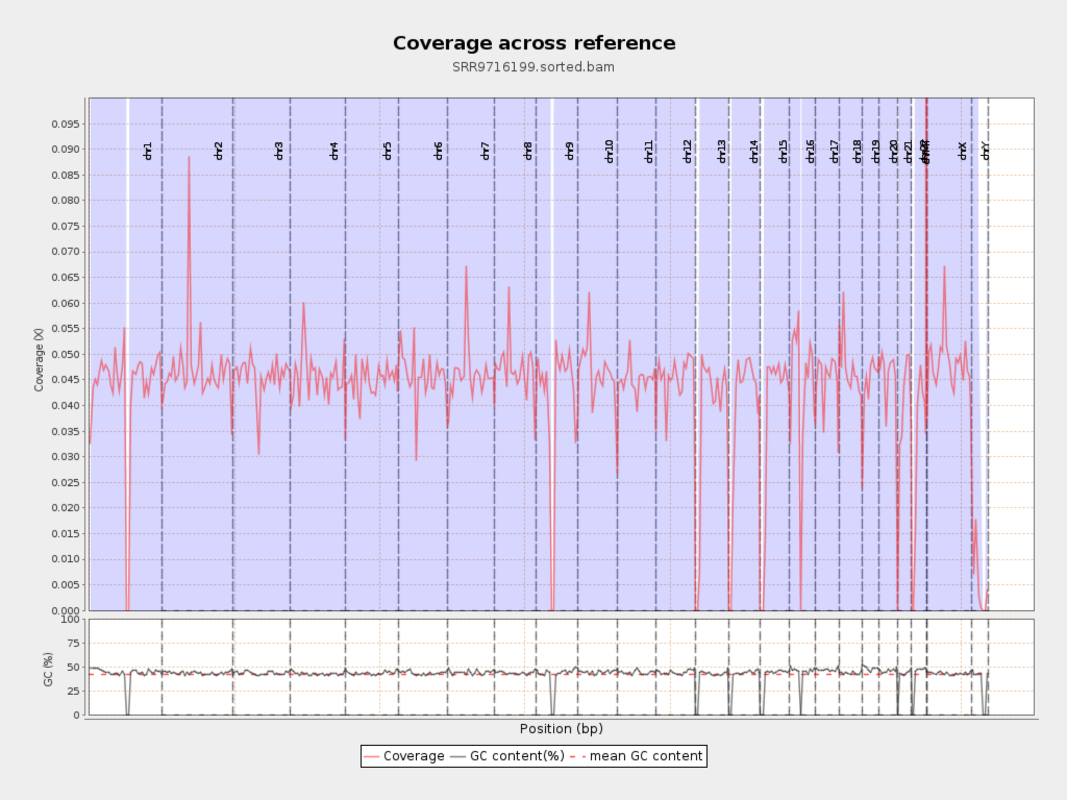
General error rate	0.76%
Mismatches	996,751
Insertions	11,075
Mapped reads with at least one insertion	0.61%
Deletions	28,157
Mapped reads with at least one deletion	1.54%
Homopolymer indels	40.6%

2.6. Chromosome stats

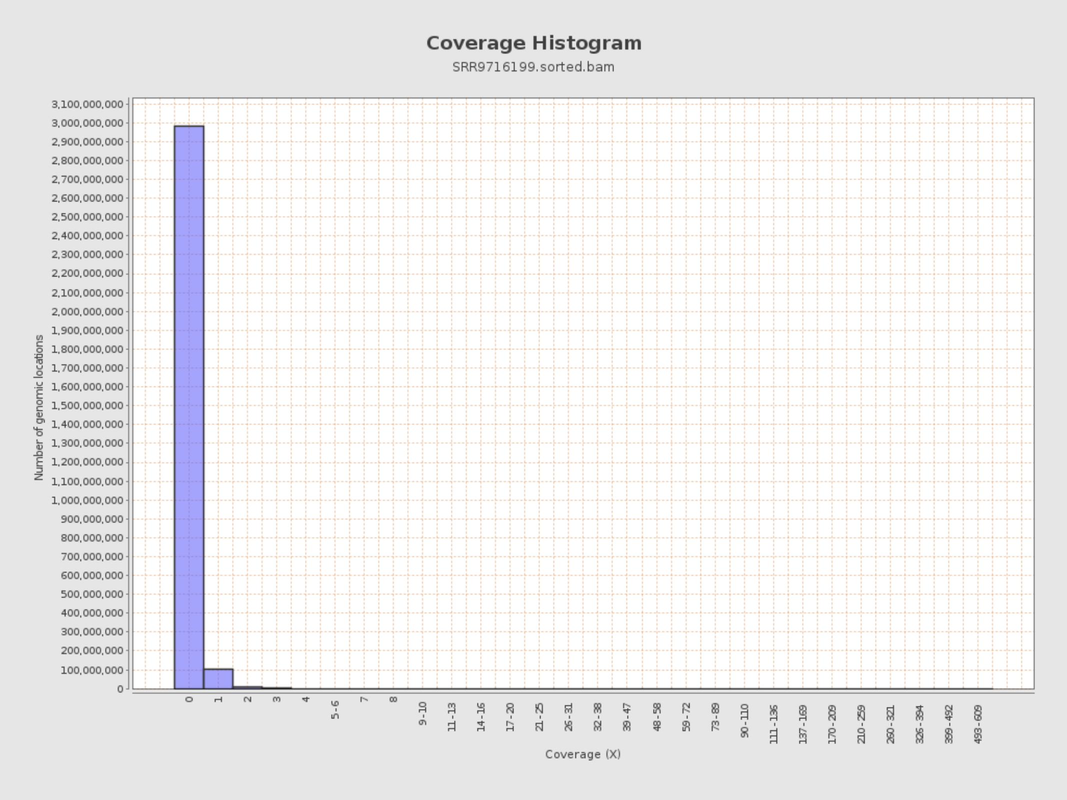
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10739998	0.0431	0.3912
chr2	243199373	11536809	0.0474	0.5312
chr3	198022430	9040623	0.0457	0.2396
chr4	191154276	8750650	0.0458	0.2609
chr5	180915260	8143035	0.045	0.2421
chr6	171115067	7866593	0.046	0.2837
chr7	159138663	7401776	0.0465	0.4674

chr8	146364022	6897858	0.0471	0.4722
chr9	141213431	5708686	0.0404	0.3894
chr10	135534747	6345909	0.0468	0.3284
chr11	135006516	6043161	0.0448	0.388
chr12	133851895	6092843	0.0455	0.244
chr13	115169878	4266502	0.037	0.2162
chr14	107349540	4094555	0.0381	0.2684
chr15	102531392	3839921	0.0375	0.2207
chr16	90354753	3944226	0.0437	0.2678
chr17	81195210	3644802	0.0449	0.2661
chr18	78077248	3713560	0.0476	0.7409
chr19	59128983	2648500	0.0448	0.3627
chr20	63025520	2849864	0.0452	0.2525
chr21	48129895	1802242	0.0374	0.2392
chr22	51304566	1508683	0.0294	0.1948
chrMT	16571	7929	0.4785	0.8795
chrX	155270560	7526284	0.0485	0.3256
chrY	59373566	335573	0.0057	0.1542

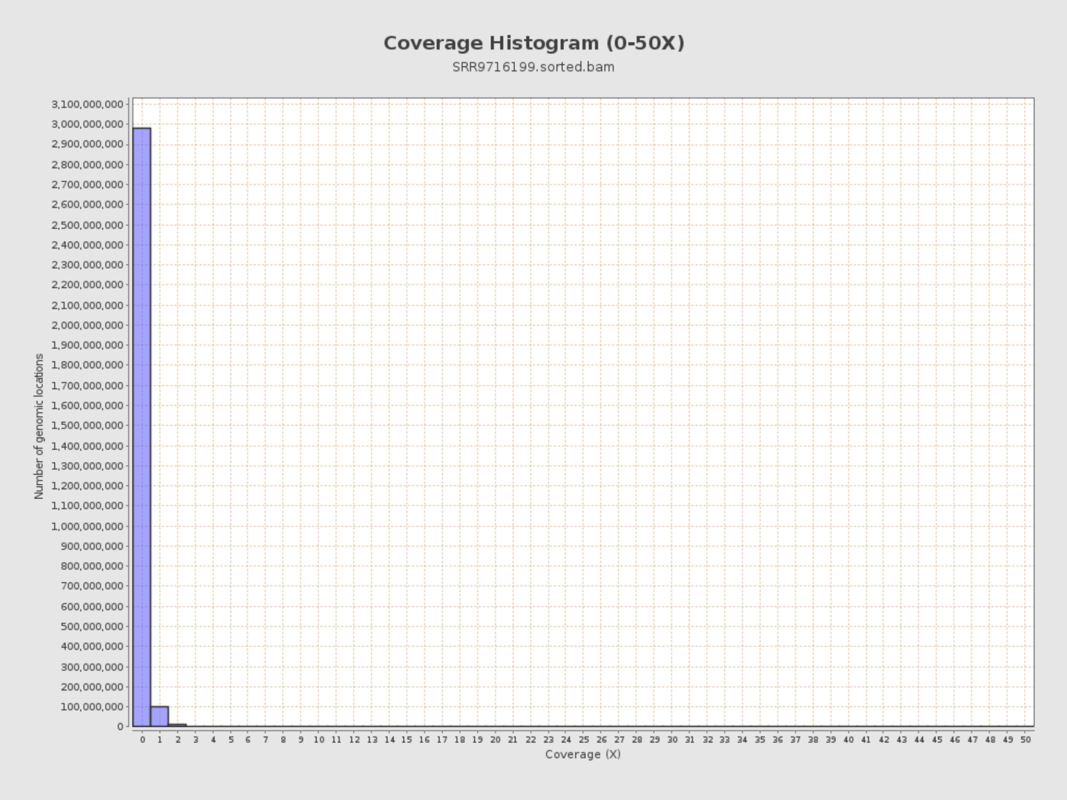
3. Results : Coverage across reference



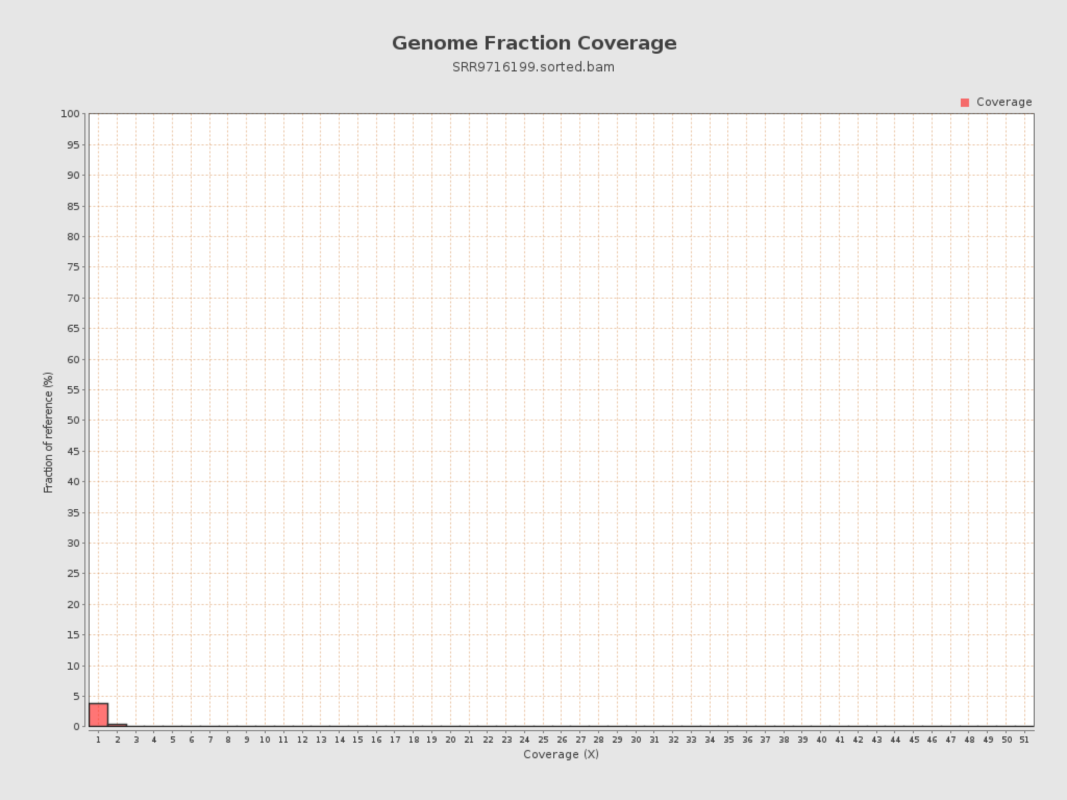
4. Results : Coverage Histogram



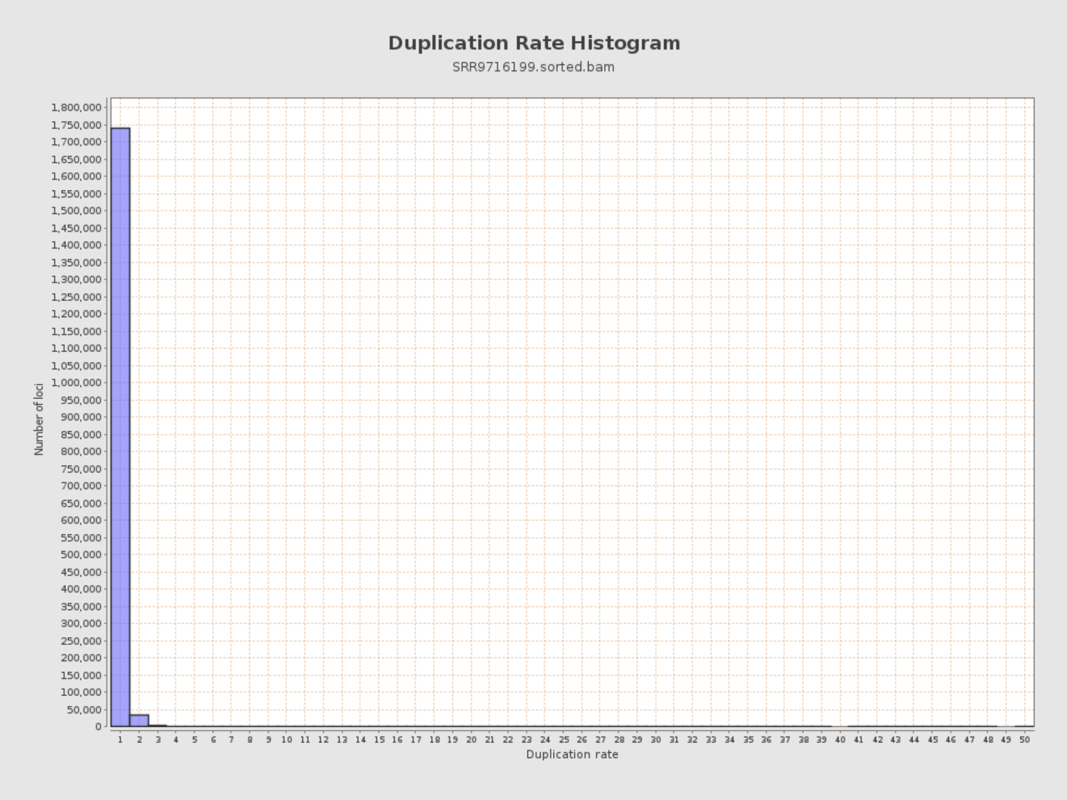
5. Results : Coverage Histogram (0-50X)



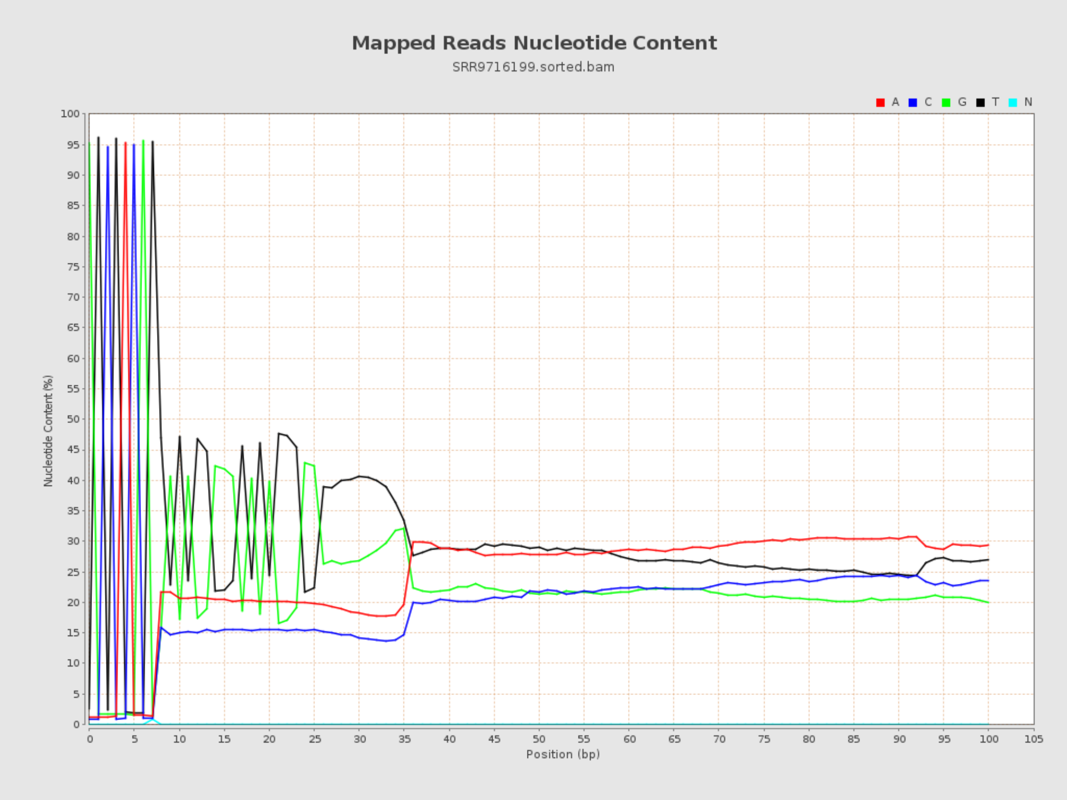
6. Results : Genome Fraction Coverage



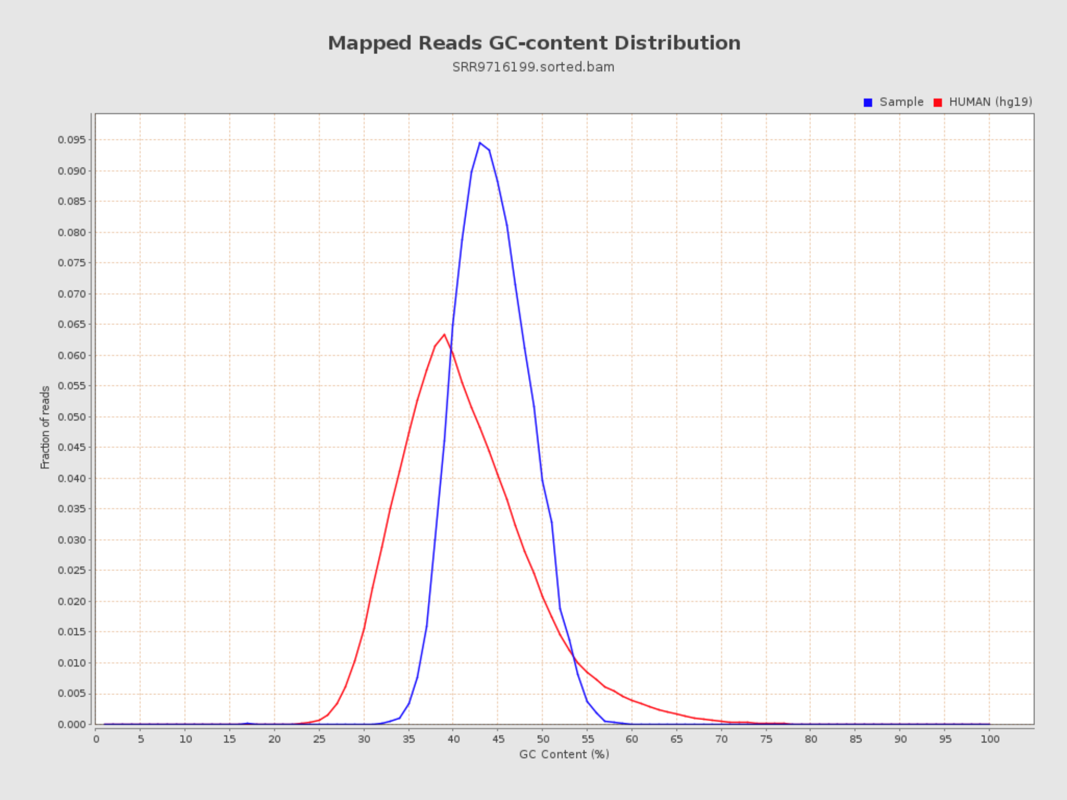
7. Results : Duplication Rate Histogram



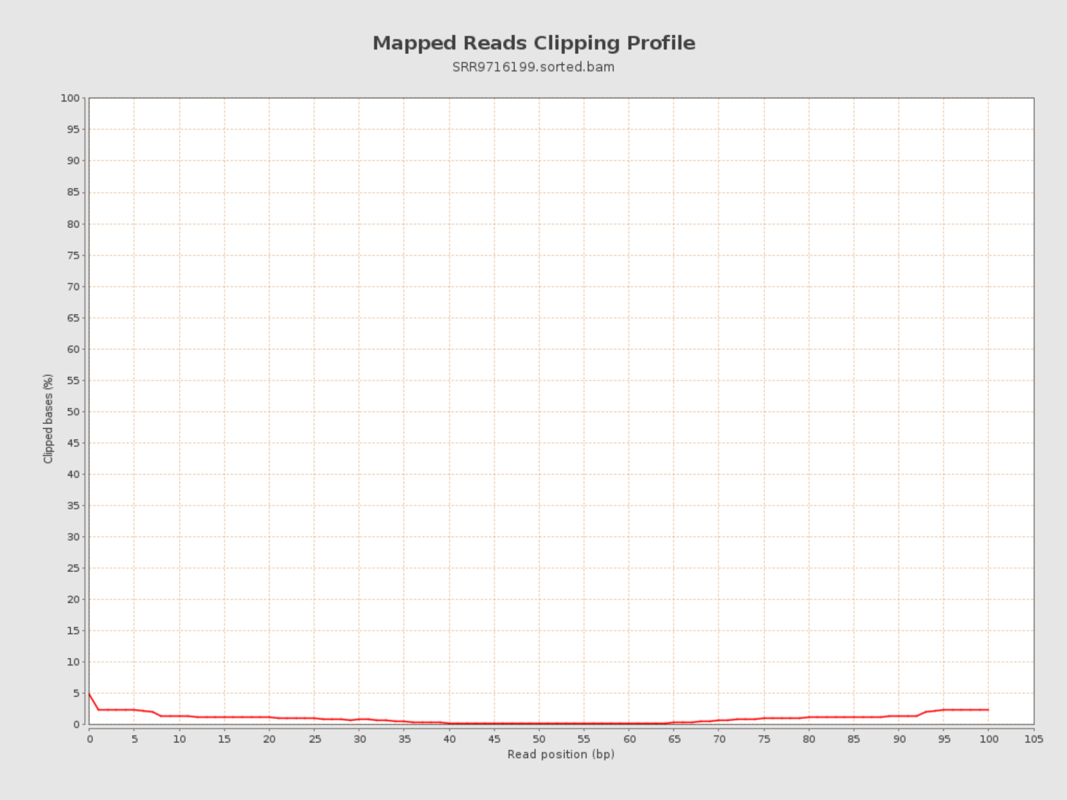
8. Results : Mapped Reads Nucleotide Content



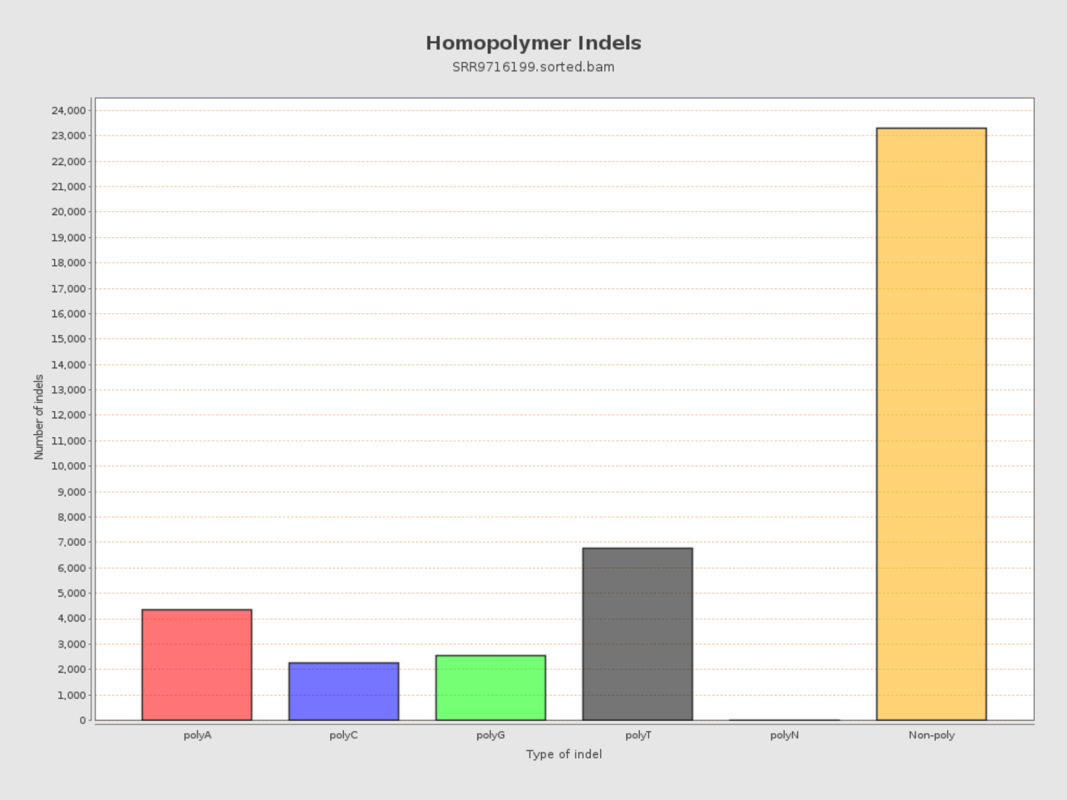
9. Results : Mapped Reads GC-content Distribution



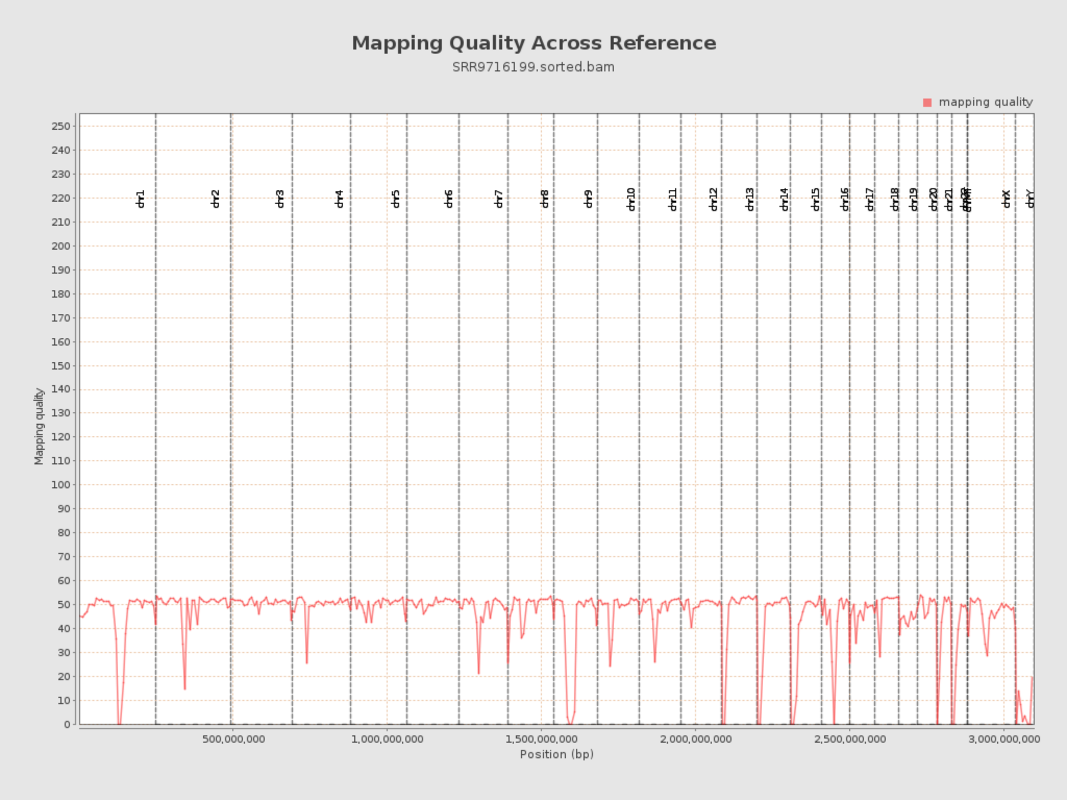
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram