Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 06:49:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716312.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_SRR9716312 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716312.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 06:49:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716312.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,322,786
Mapped reads	2,181,624 / 93.92%
Unmapped reads	141,162 / 6.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	40,956 / 1.76%
Read min/max/mean length	30 / 101 / 101.64
Duplicated reads (estimated)	103,908 / 4.47%
Duplication rate	3.46%
Clipped reads	2,216,638 / 95.43%

2.2. ACGT Content

Number/percentage of A's	45,264,774 / 26.19%
Number/percentage of C's	34,503,822 / 19.96%
Number/percentage of T's	52,509,721 / 30.38%
Number/percentage of G's	40,572,882 / 23.47%
Number/percentage of N's	11,993 / 0.01%
GC Percentage	43.43%

2.3. Coverage

Mean	0.0559

Standard Deviation	0.5024

2.4. Mapping Quality

Mean Mapping Quality	47.56

2.5. Mismatches and indels

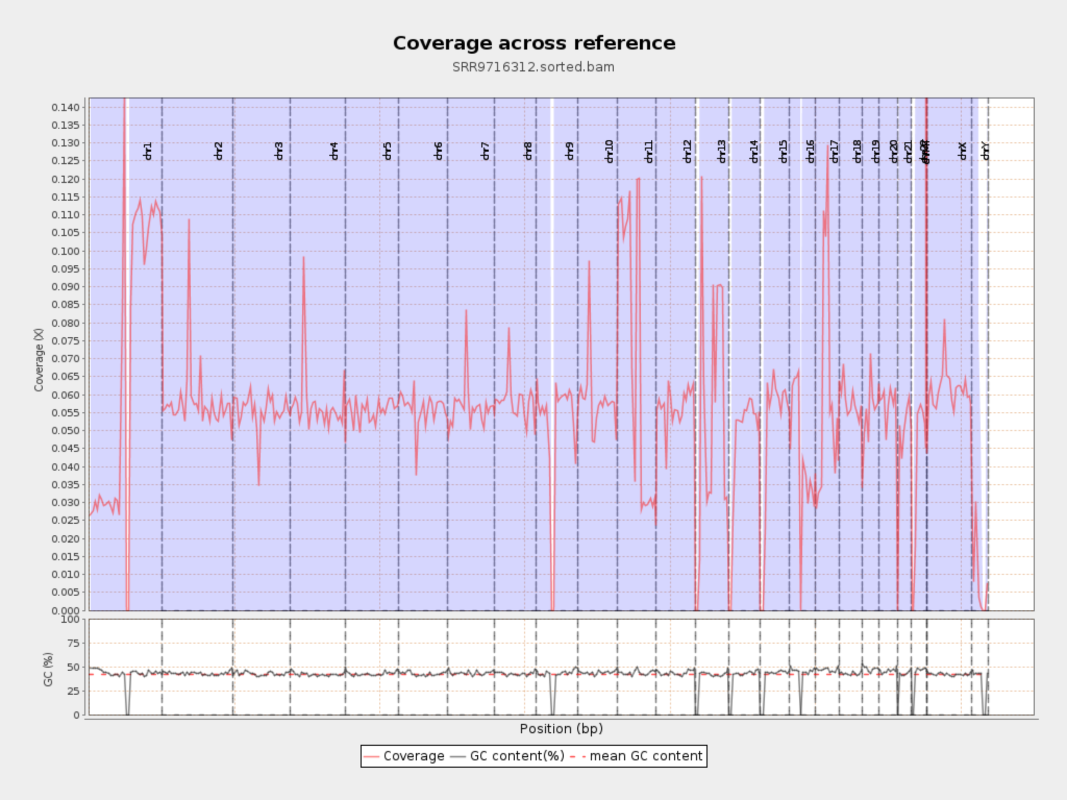
General error rate	0.66%
Mismatches	1,106,471
Insertions	15,600
Mapped reads with at least one insertion	0.71%
Deletions	41,193
Mapped reads with at least one deletion	1.86%
Homopolymer indels	41.91%

2.6. Chromosome stats

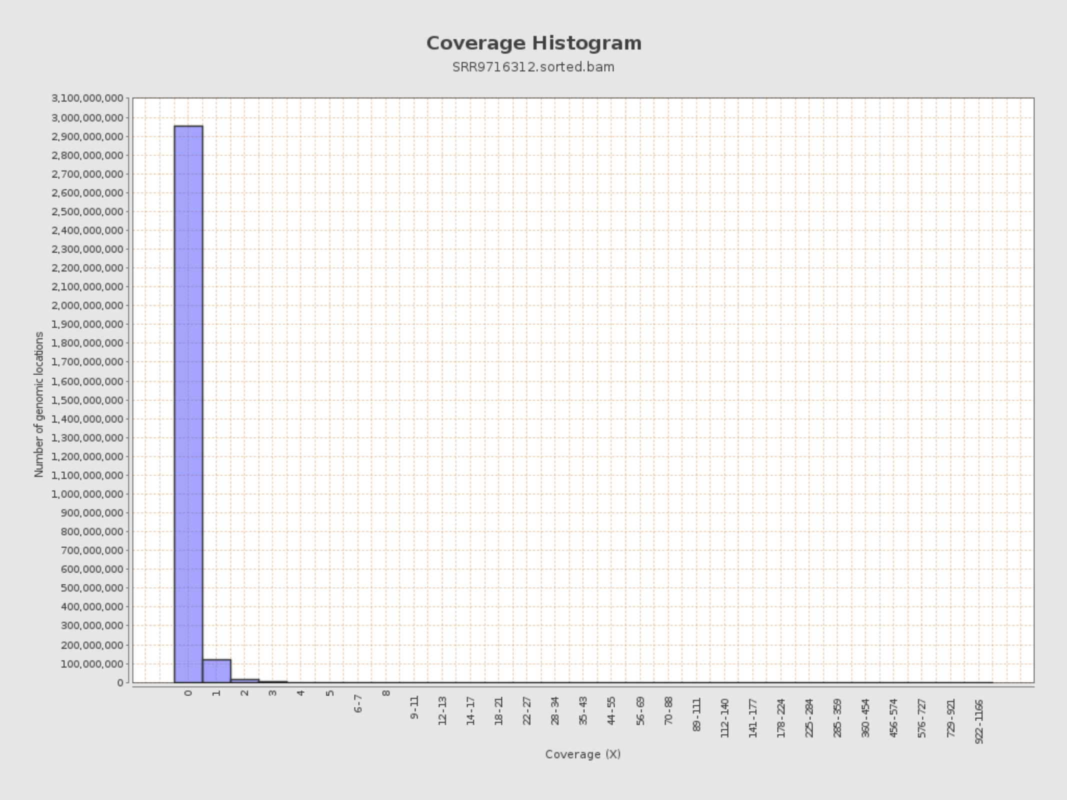
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16703704	0.067	1.0501
chr2	243199373	14189953	0.0583	0.5573
chr3	198022430	10972626	0.0554	0.2707
chr4	191154276	10954691	0.0573	0.3376
chr5	180915260	10061144	0.0556	0.2742
chr6	171115067	9616875	0.0562	0.3031
chr7	159138663	9059694	0.0569	0.6125

chr8	146364022	8527053	0.0583	0.5703
chr9	141213431	7051316	0.0499	0.4119
chr10	135534747	7981652	0.0589	0.4704
chr11	135006516	9613202	0.0712	0.5591
chr12	133851895	7589949	0.0567	0.2788
chr13	115169878	6037590	0.0524	0.2675
chr14	107349540	4889594	0.0455	0.2778
chr15	102531392	4996564	0.0487	0.255
chr16	90354753	3839904	0.0425	0.2712
chr17	81195210	5149612	0.0634	0.3628
chr18	78077248	4553027	0.0583	0.7322
chr19	59128983	3298496	0.0558	0.7537
chr20	63025520	3599140	0.0571	0.2907
chr21	48129895	2256604	0.0469	0.2873
chr22	51304566	1926503	0.0376	0.227
chrMT	16571	39790	2.4012	2.295
chrX	155270560	9534804	0.0614	0.3509
chrY	59373566	497511	0.0084	0.2594

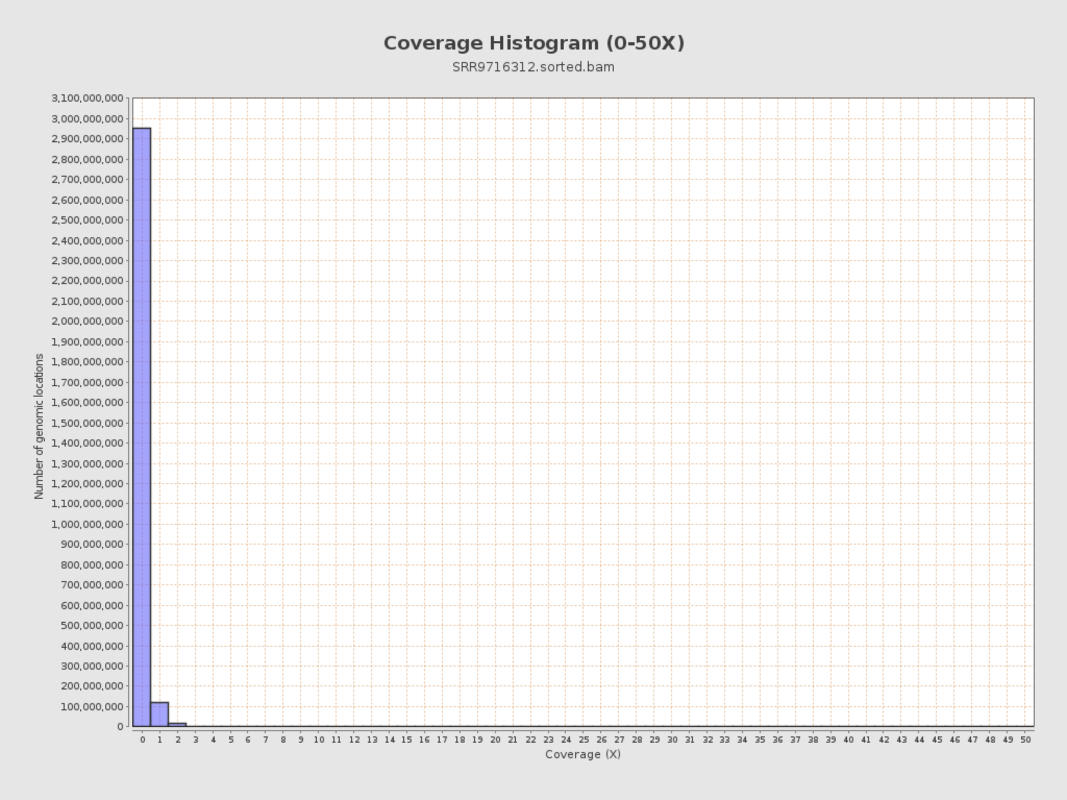
3. Results : Coverage across reference



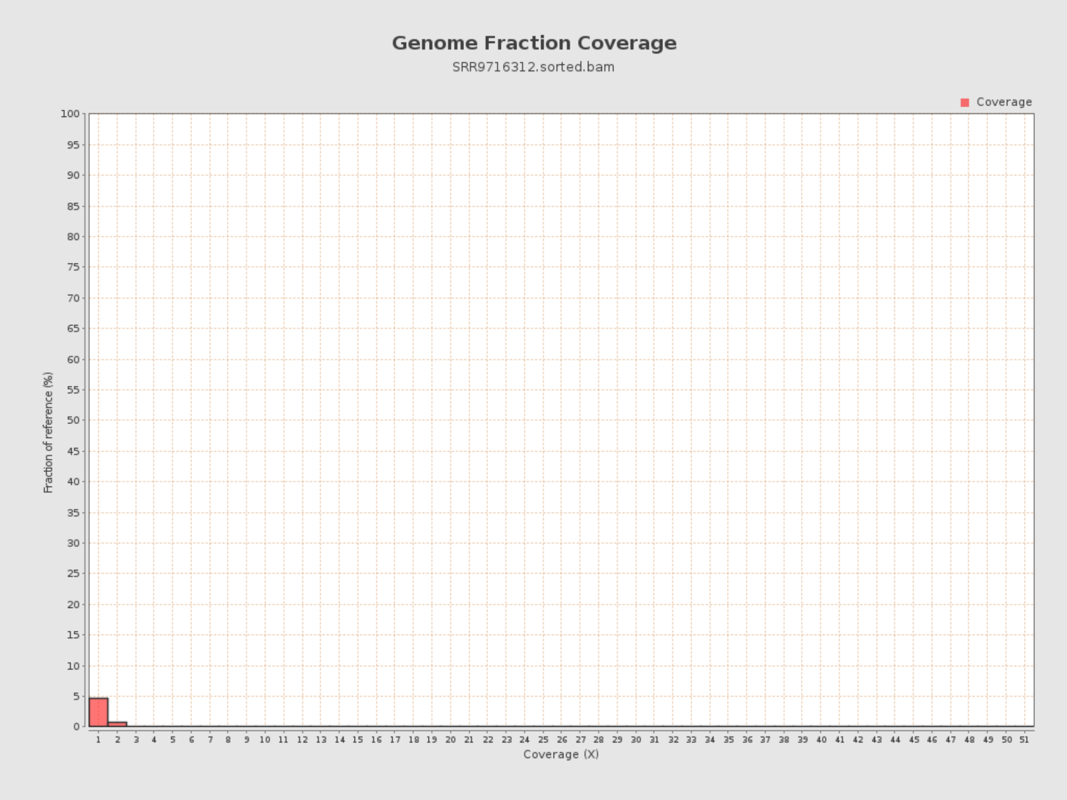
4. Results : Coverage Histogram



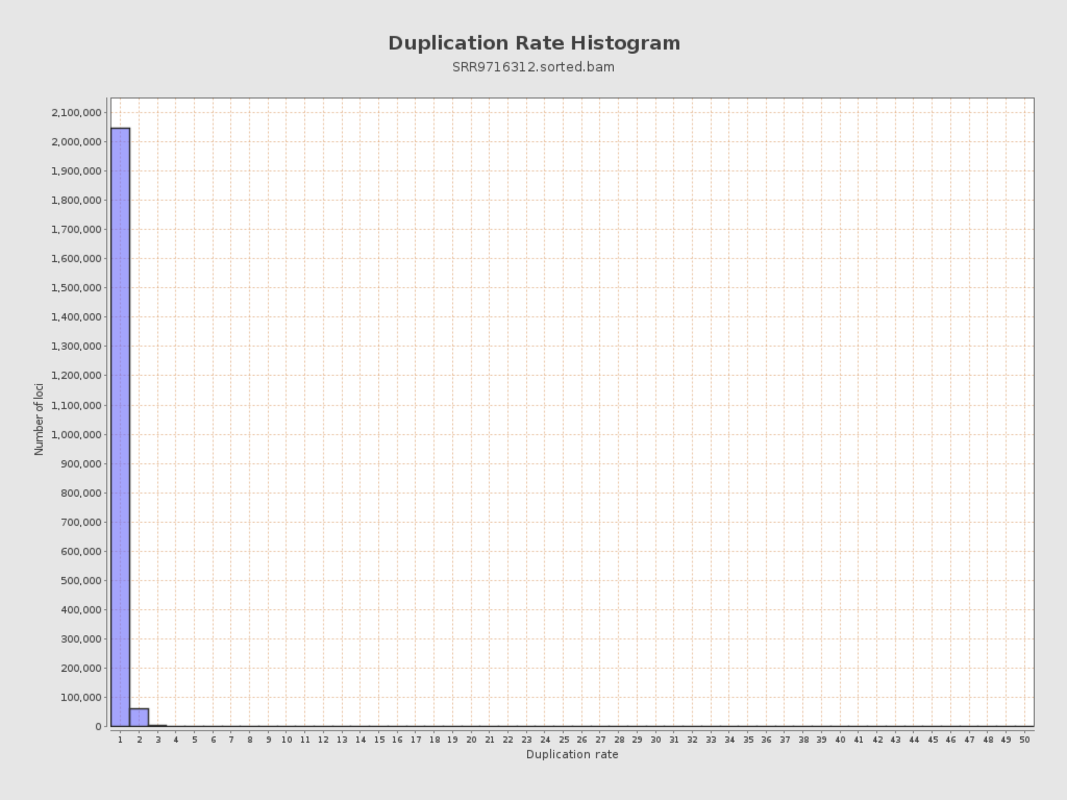
5. Results : Coverage Histogram (0-50X)



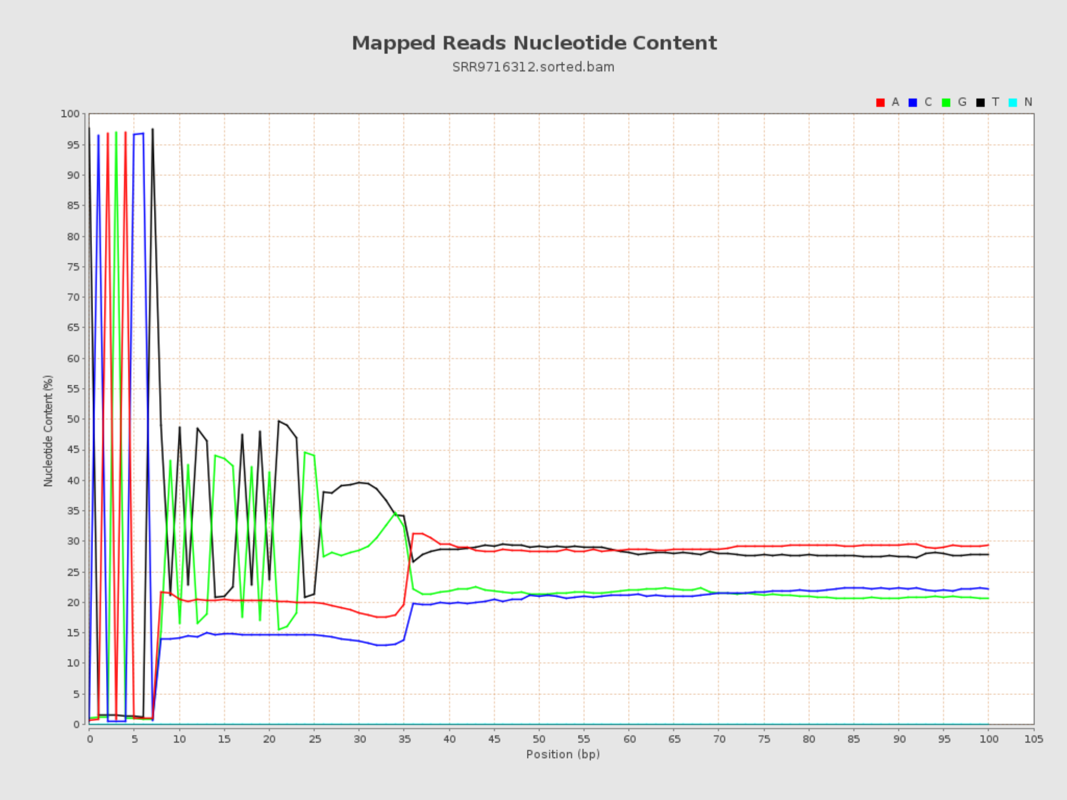
6. Results : Genome Fraction Coverage



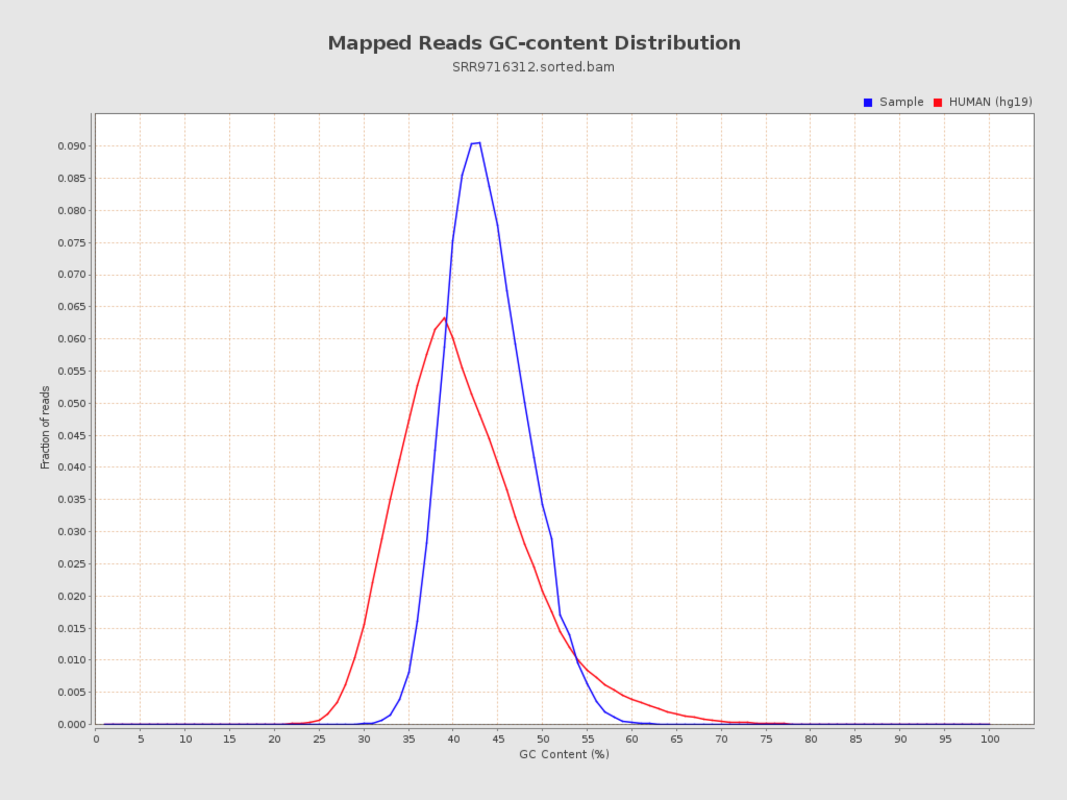
7. Results : Duplication Rate Histogram



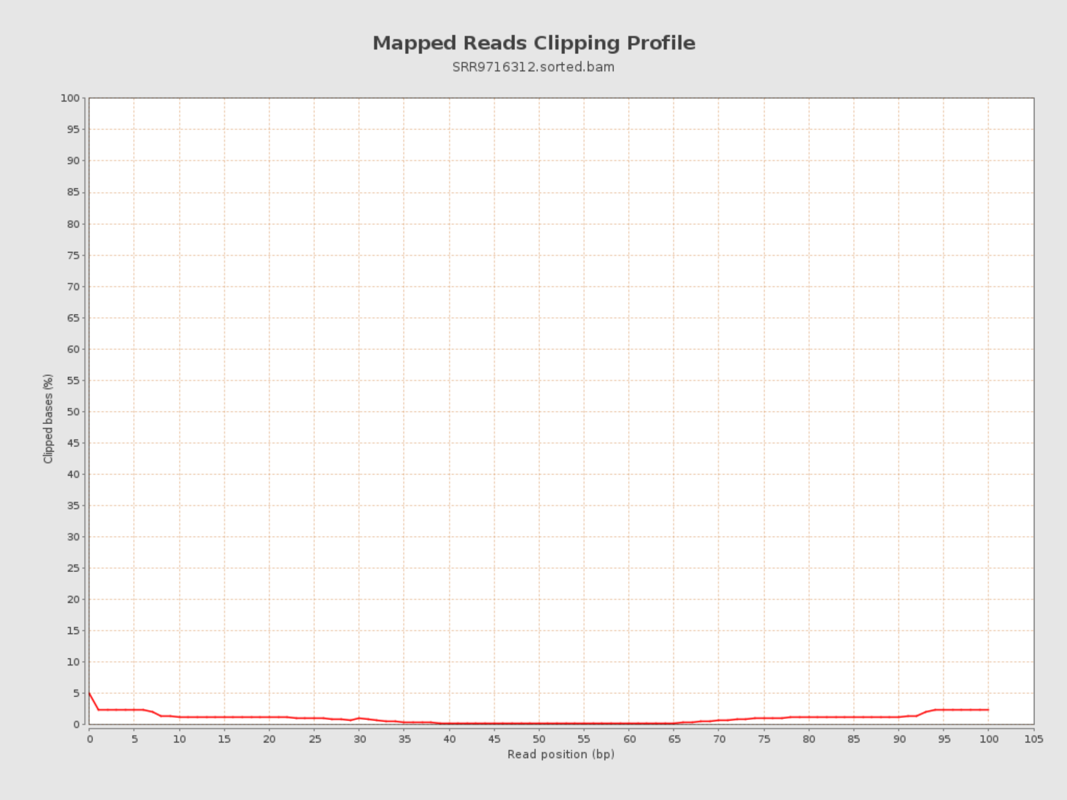
8. Results : Mapped Reads Nucleotide Content



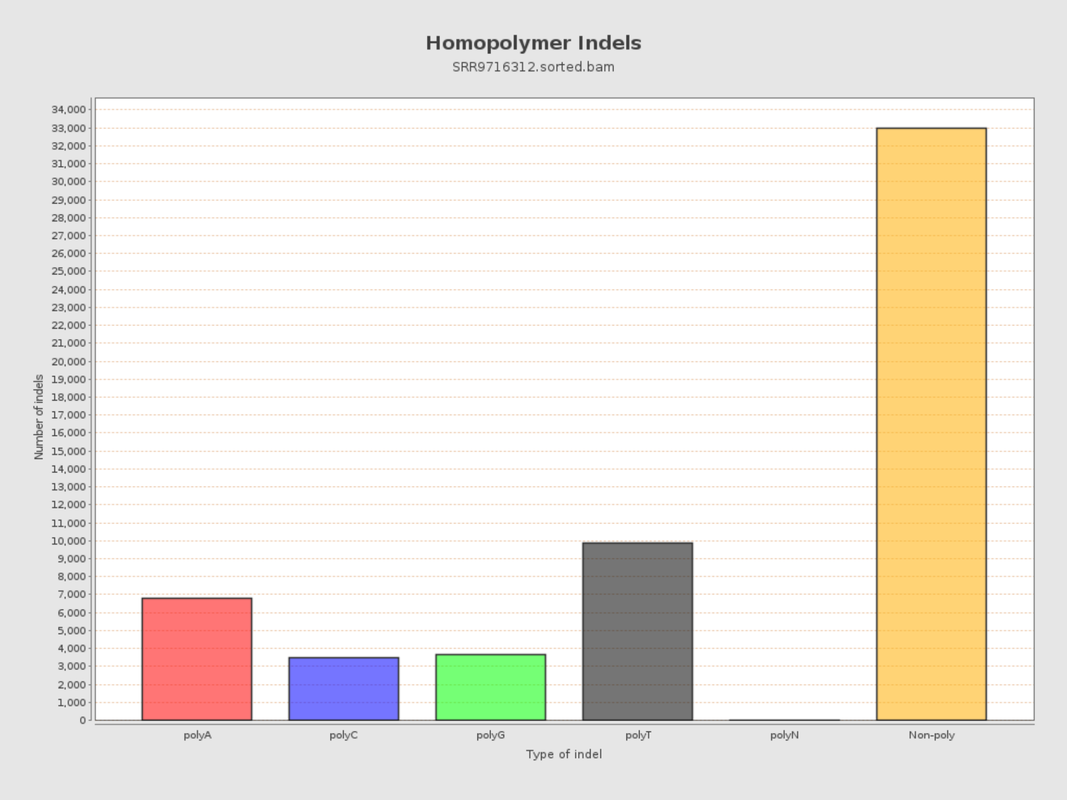
9. Results : Mapped Reads GC-content Distribution



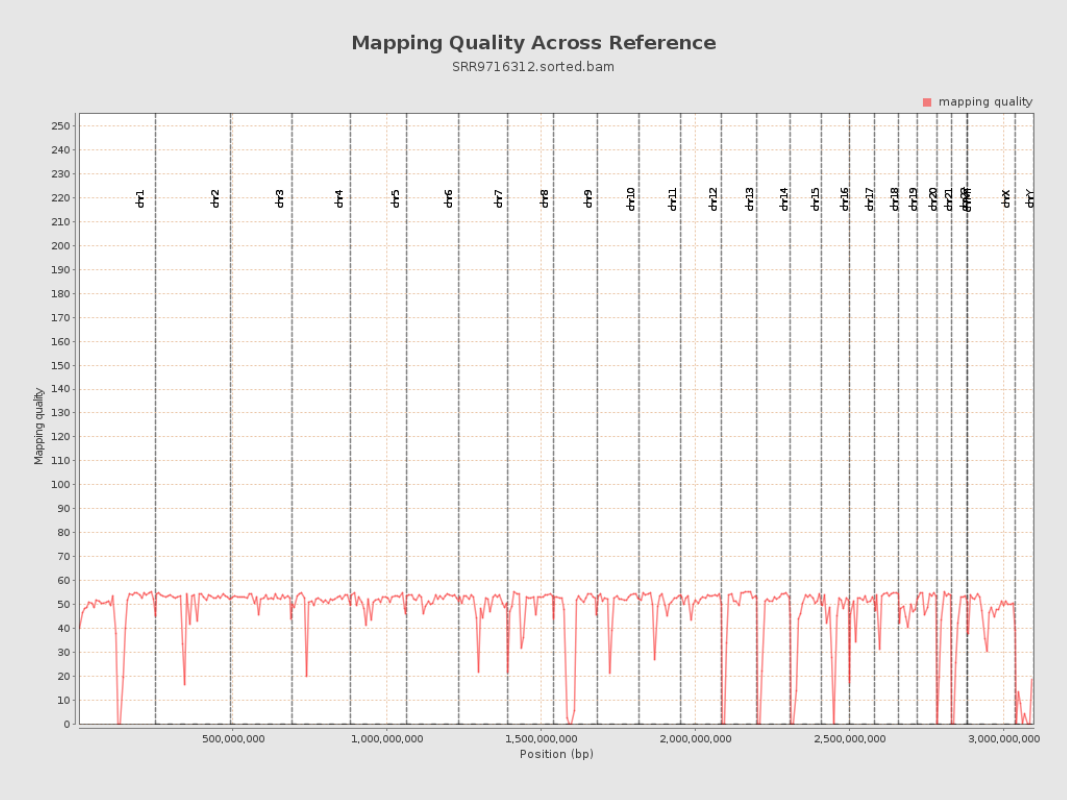
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram