Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 06:46:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716311.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_SRR9716311 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716311.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 06:46:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716311.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,028,678
Mapped reads	1,896,953 / 93.51%
Unmapped reads	131,725 / 6.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	39,546 / 1.95%
Read min/max/mean length	30 / 101 / 101.7
Duplicated reads (estimated)	80,548 / 3.97%
Duplication rate	3.01%
Clipped reads	1,930,654 / 95.17%

2.2. ACGT Content

Number/percentage of A's	39,614,910 / 26.36%
Number/percentage of C's	30,100,196 / 20.03%
Number/percentage of T's	45,528,151 / 30.29%
Number/percentage of G's	35,038,491 / 23.31%
Number/percentage of N's	10,671 / 0.01%
GC Percentage	43.34%

2.3. Coverage

Mean	0.0486

Standard Deviation	0.4674

2.4. Mapping Quality

Mean Mapping Quality	47.51

2.5. Mismatches and indels

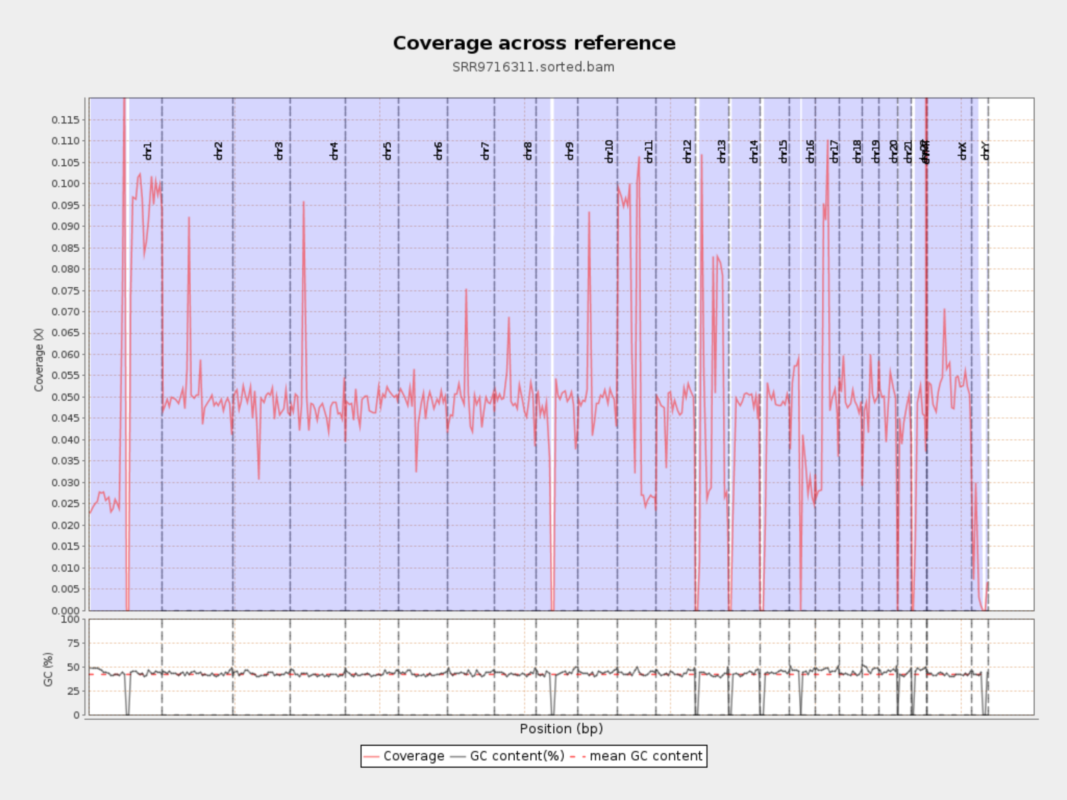
General error rate	0.66%
Mismatches	957,803
Insertions	13,942
Mapped reads with at least one insertion	0.72%
Deletions	36,657
Mapped reads with at least one deletion	1.9%
Homopolymer indels	42.31%

2.6. Chromosome stats

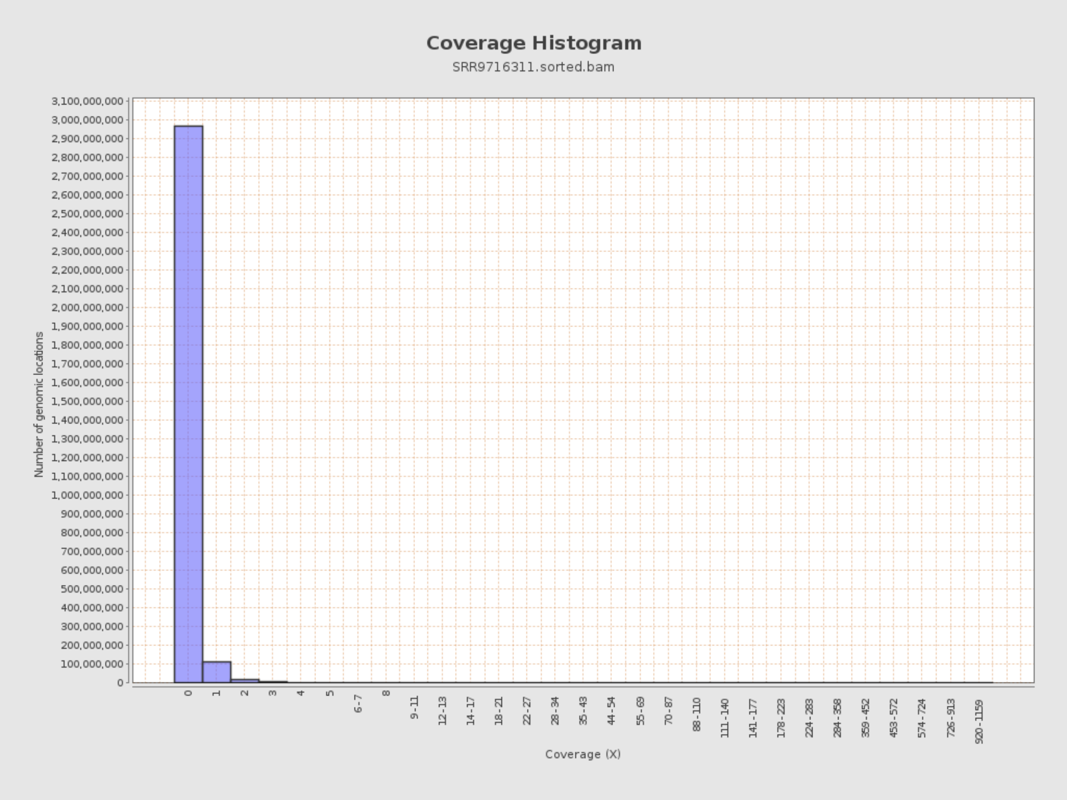
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14716293	0.059	1.0552
chr2	243199373	12323578	0.0507	0.4622
chr3	198022430	9569609	0.0483	0.247
chr4	191154276	9392040	0.0491	0.3286
chr5	180915260	8831235	0.0488	0.2512
chr6	171115067	8329730	0.0487	0.2748
chr7	159138663	7868550	0.0494	0.5272

chr8	146364022	7361152	0.0503	0.4956
chr9	141213431	6032420	0.0427	0.3536
chr10	135534747	6942082	0.0512	0.4502
chr11	135006516	8437559	0.0625	0.5178
chr12	133851895	6462125	0.0483	0.2503
chr13	115169878	5374408	0.0467	0.2462
chr14	107349540	4417685	0.0412	0.2517
chr15	102531392	4144032	0.0404	0.2266
chr16	90354753	3378970	0.0374	0.2459
chr17	81195210	4584762	0.0565	0.3246
chr18	78077248	3923804	0.0503	0.6236
chr19	59128983	2889488	0.0489	0.6845
chr20	63025520	3067698	0.0487	0.2634
chr21	48129895	1955876	0.0406	0.2641
chr22	51304566	1695991	0.0331	0.2044
chrMT	16571	13085	0.7896	1.0774
chrX	155270560	8192198	0.0528	0.3083
chrY	59373566	457967	0.0077	0.2572

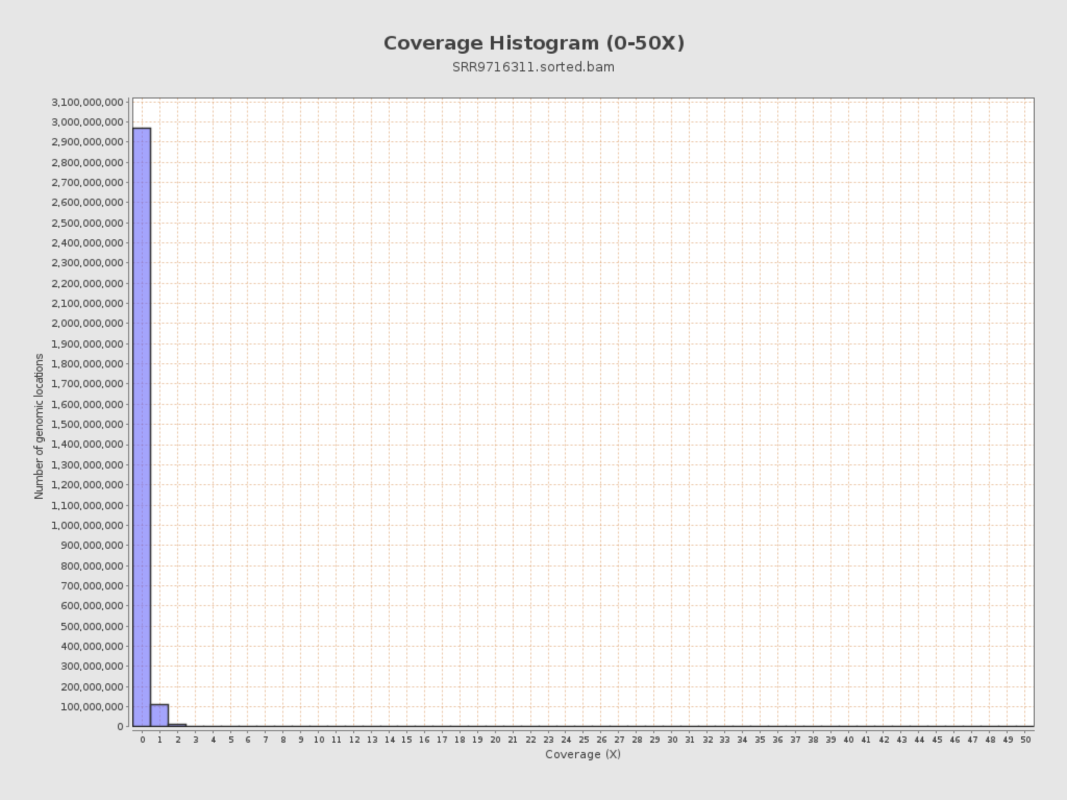
3. Results : Coverage across reference



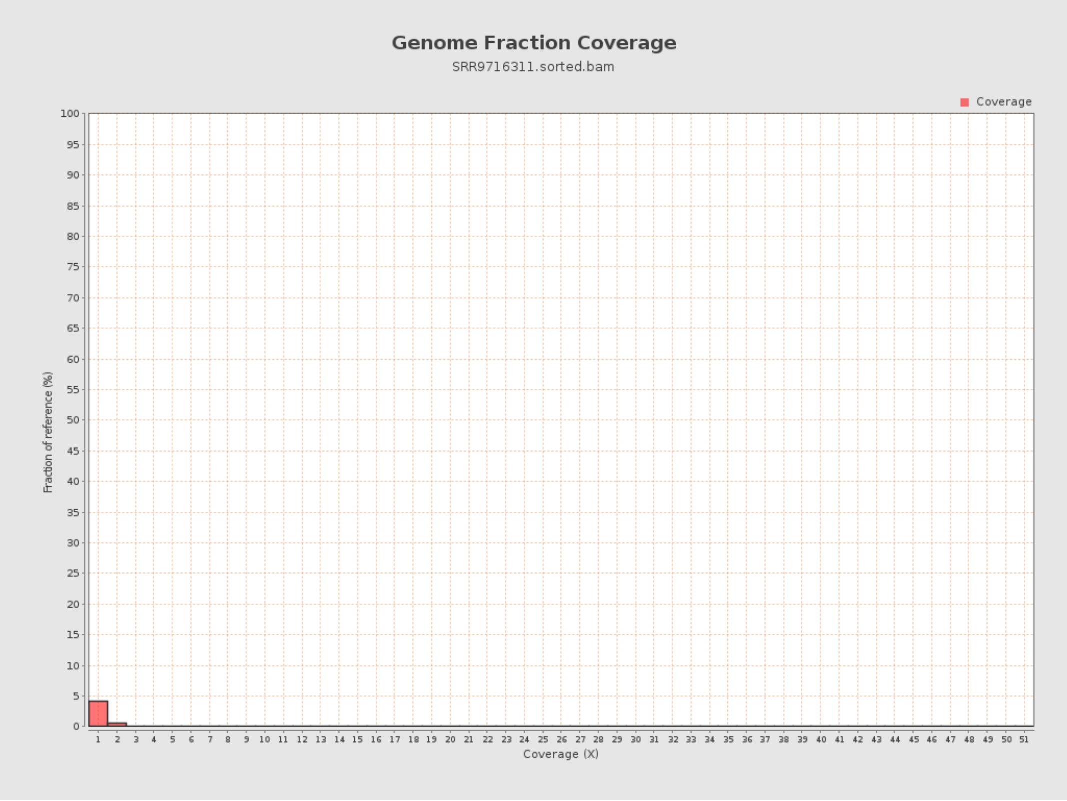
4. Results : Coverage Histogram



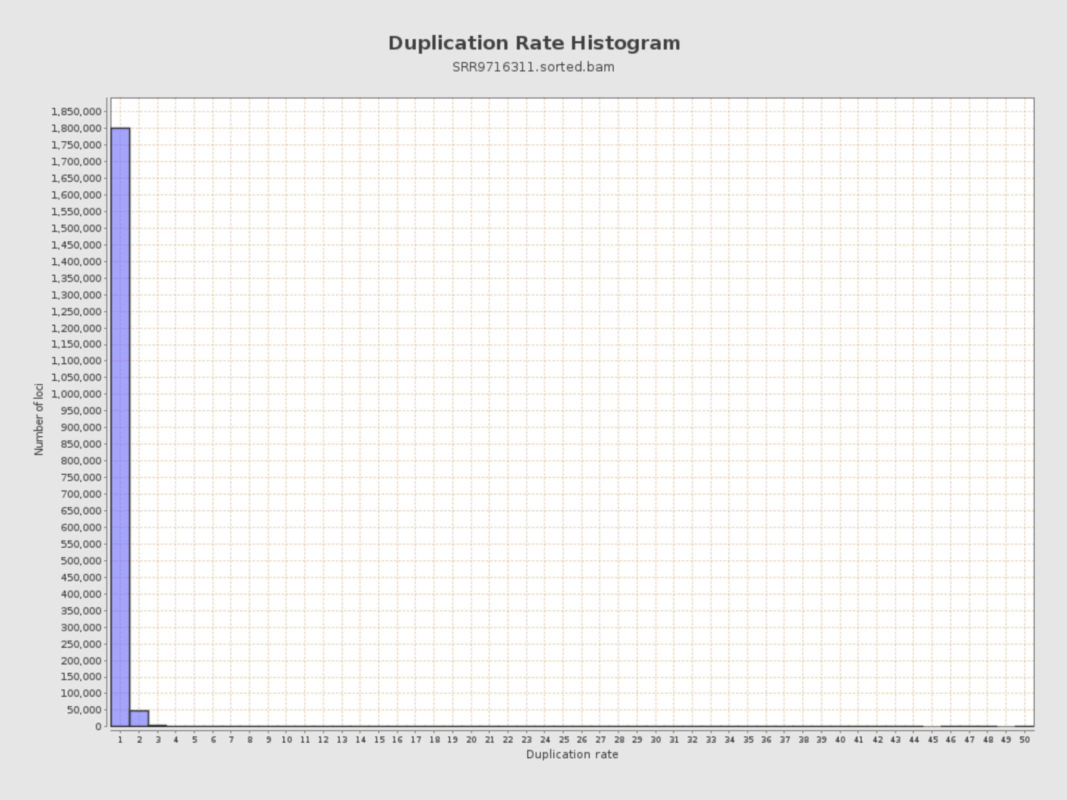
5. Results : Coverage Histogram (0-50X)



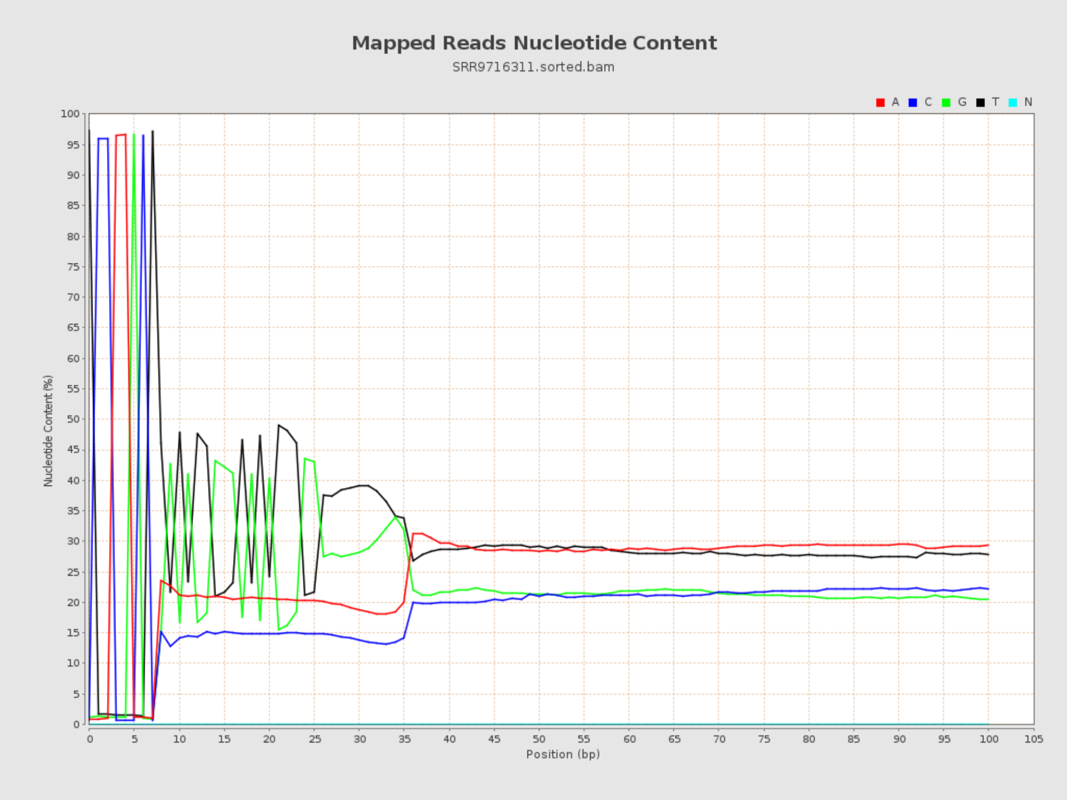
6. Results : Genome Fraction Coverage



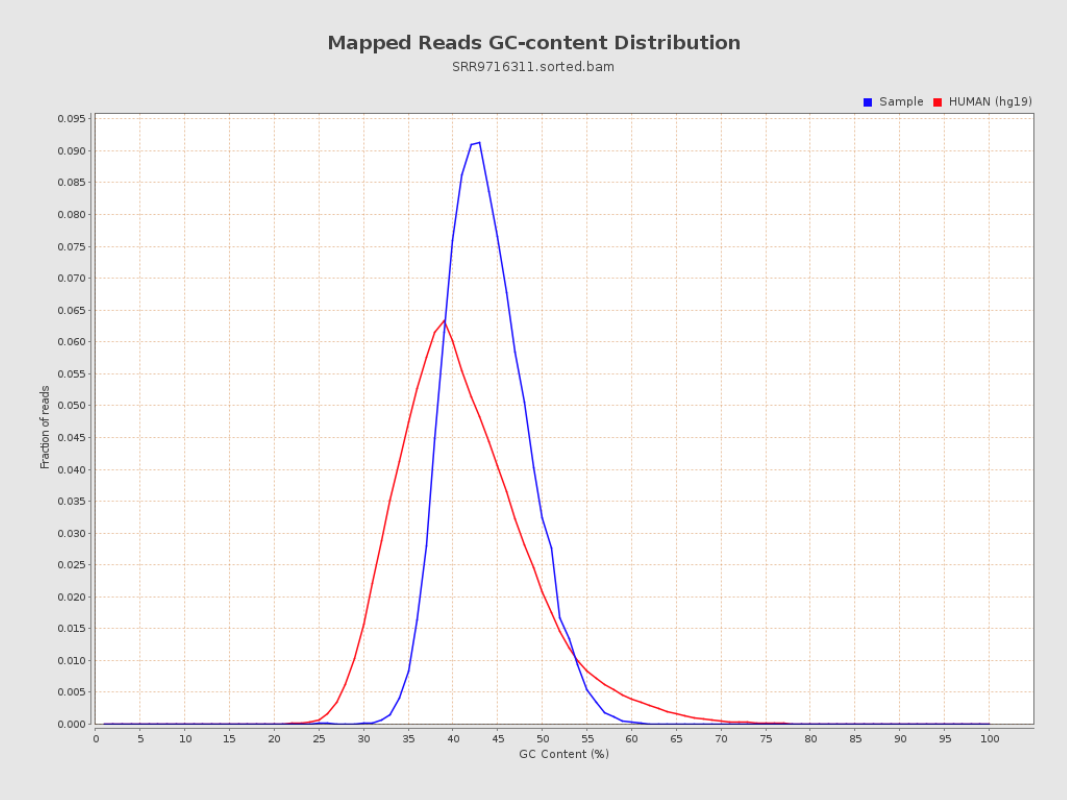
7. Results : Duplication Rate Histogram



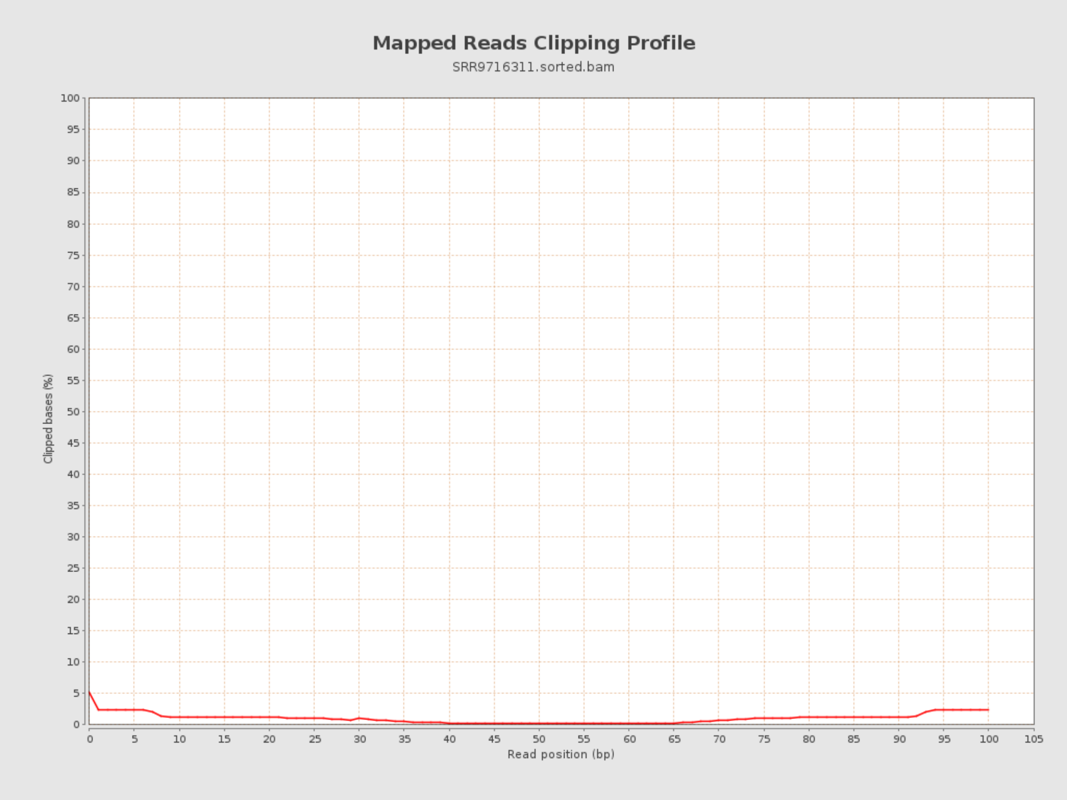
8. Results : Mapped Reads Nucleotide Content



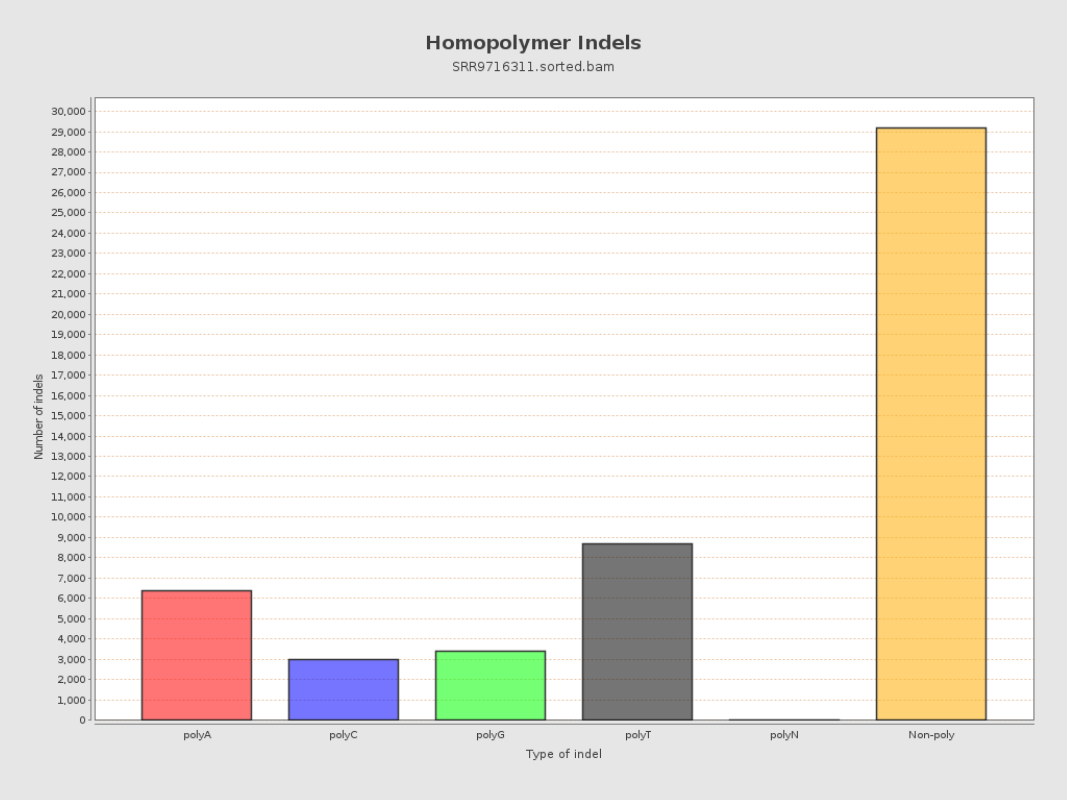
9. Results : Mapped Reads GC-content Distribution



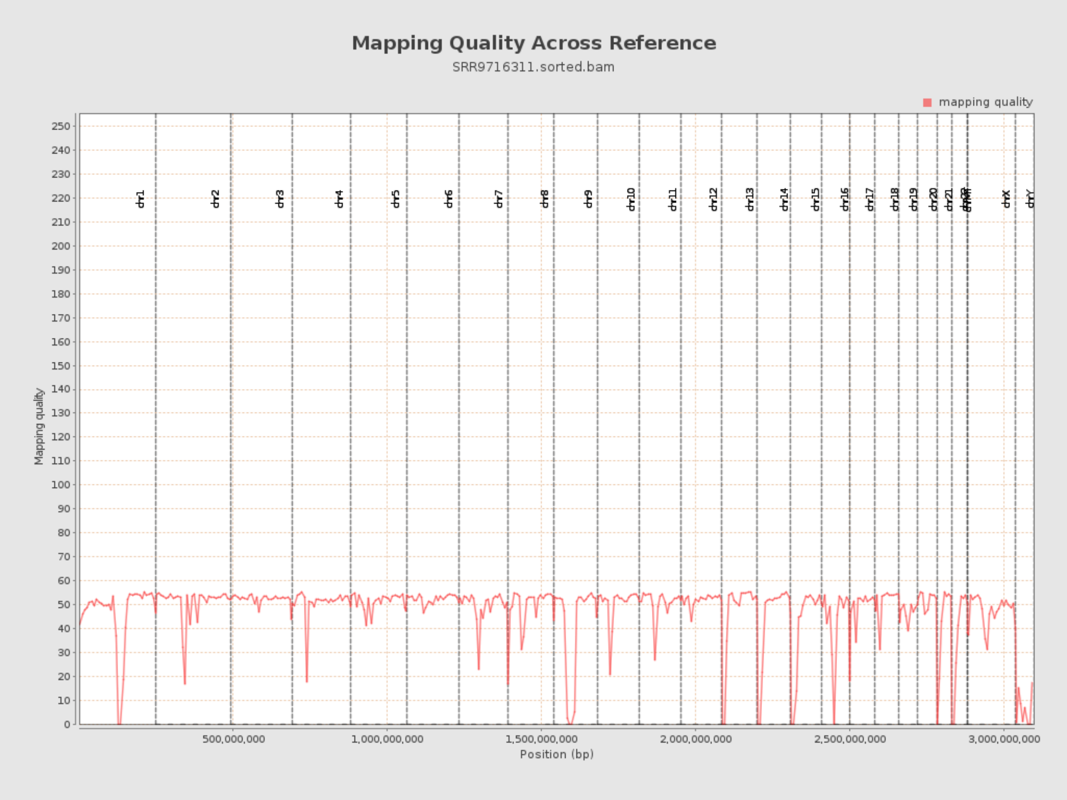
10. Results : Mapped Reads Clipping Profile



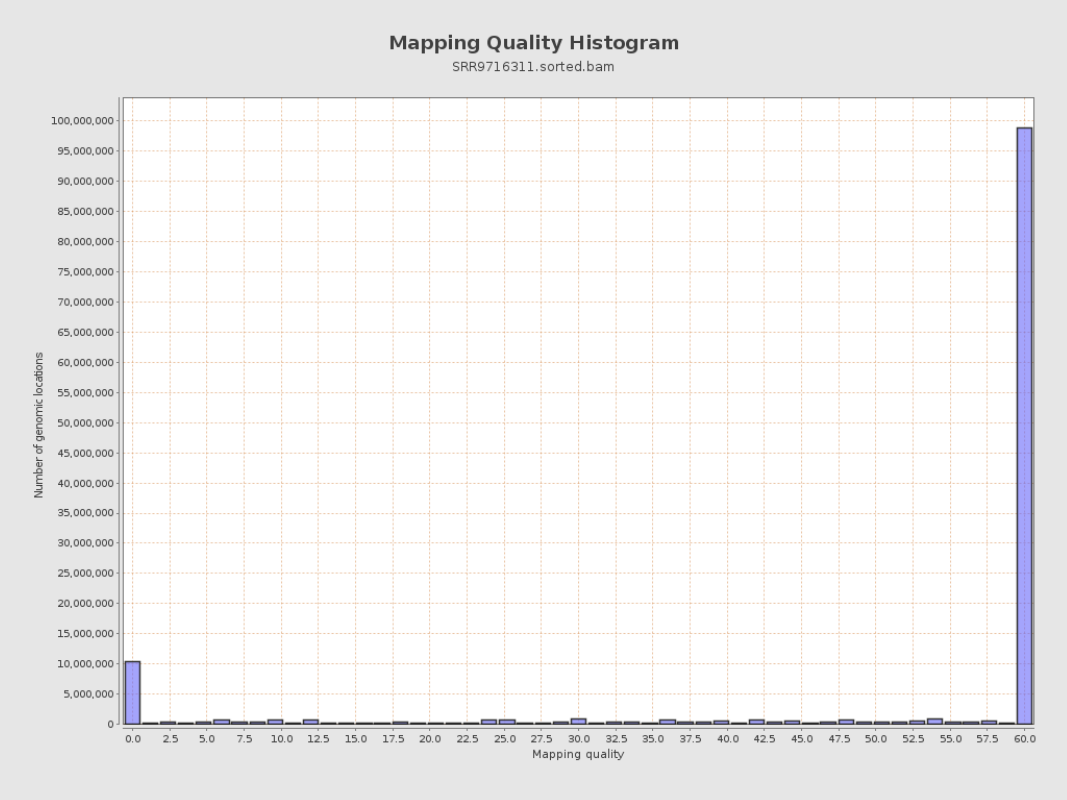
11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



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