Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 08:16:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716339.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_SRR9716339 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716339.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 08:16:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716339.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,685,295
Mapped reads	1,946,424 / 72.48%
Unmapped reads	738,871 / 27.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,883 / 0.48%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	92,916 / 3.46%
Duplication rate	3.7%
Clipped reads	1,954,725 / 72.79%

2.2. ACGT Content

Number/percentage of A's	28,410,414 / 24.96%
Number/percentage of C's	21,180,513 / 18.61%
Number/percentage of T's	36,490,136 / 32.06%
Number/percentage of G's	27,724,767 / 24.36%
Number/percentage of N's	1,407 / 0%
GC Percentage	42.97%

2.3. Coverage

Mean	0.0368

Standard Deviation	0.3069

2.4. Mapping Quality

Mean Mapping Quality	44.88

2.5. Mismatches and indels

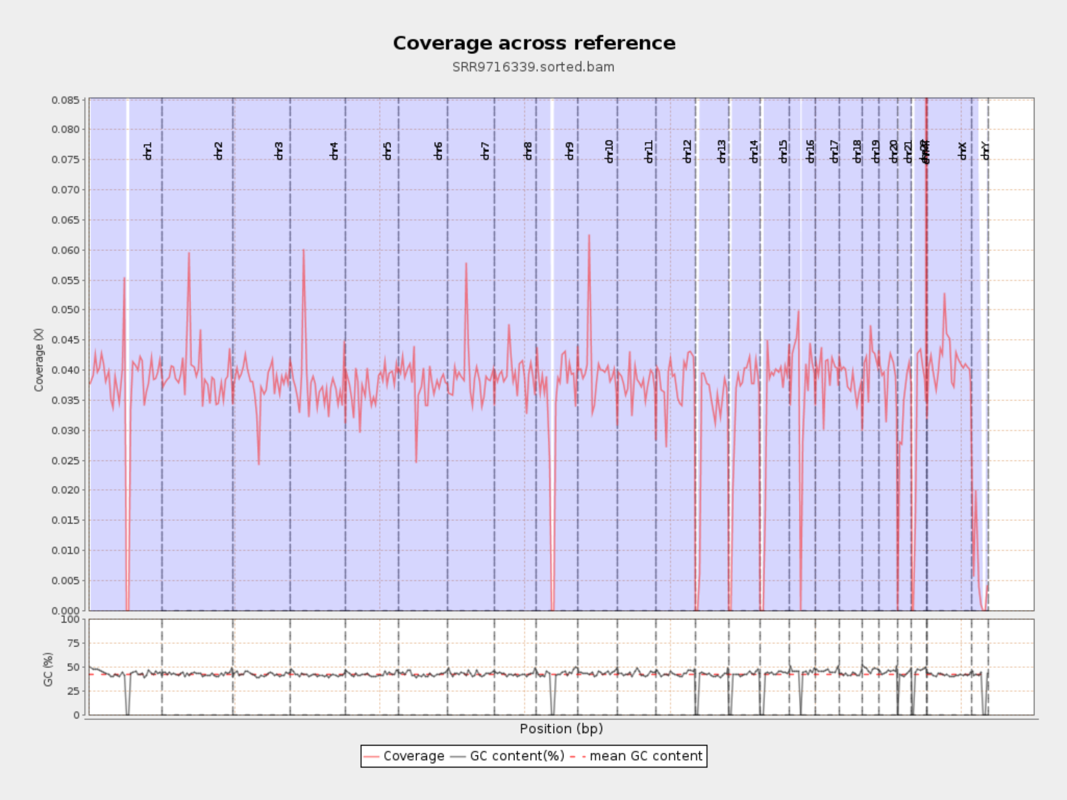
General error rate	0.51%
Mismatches	565,630
Insertions	7,540
Mapped reads with at least one insertion	0.39%
Deletions	20,296
Mapped reads with at least one deletion	1.03%
Homopolymer indels	42.02%

2.6. Chromosome stats

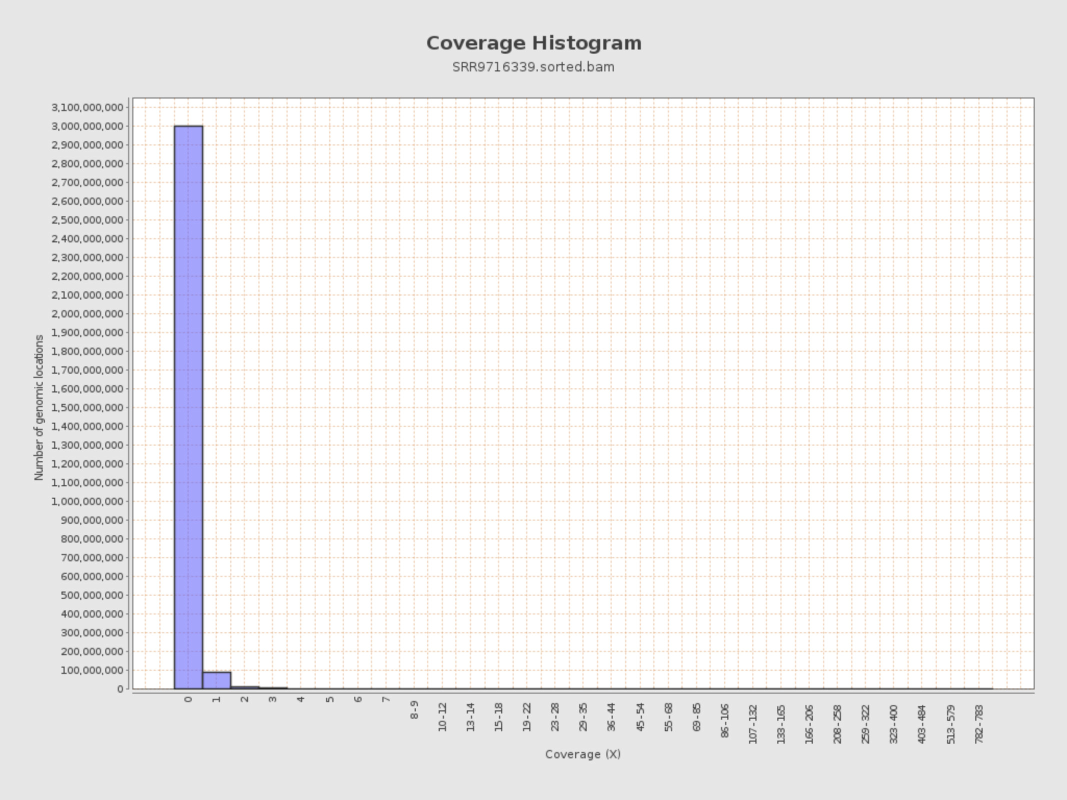
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9230498	0.037	0.4942
chr2	243199373	9611616	0.0395	0.4186
chr3	198022430	7483139	0.0378	0.2202
chr4	191154276	7202784	0.0377	0.2542
chr5	180915260	6778164	0.0375	0.2197
chr6	171115067	6501099	0.038	0.2406
chr7	159138663	6217304	0.0391	0.4005

chr8	146364022	5756396	0.0393	0.3235
chr9	141213431	4761058	0.0337	0.2523
chr10	135534747	5442446	0.0402	0.3155
chr11	135006516	5100352	0.0378	0.2798
chr12	133851895	5152883	0.0385	0.226
chr13	115169878	3466183	0.0301	0.1987
chr14	107349540	3532778	0.0329	0.2137
chr15	102531392	3350352	0.0327	0.2098
chr16	90354753	3376374	0.0374	0.2329
chr17	81195210	3220432	0.0397	0.2477
chr18	78077248	2974025	0.0381	0.4327
chr19	59128983	2437172	0.0412	0.3863
chr20	63025520	2453042	0.0389	0.2281
chr21	48129895	1513599	0.0314	0.228
chr22	51304566	1463101	0.0285	0.192
chrMT	16571	54412	3.2836	2.9719
chrX	155270560	6414450	0.0413	0.2505
chrY	59373566	345829	0.0058	0.1679

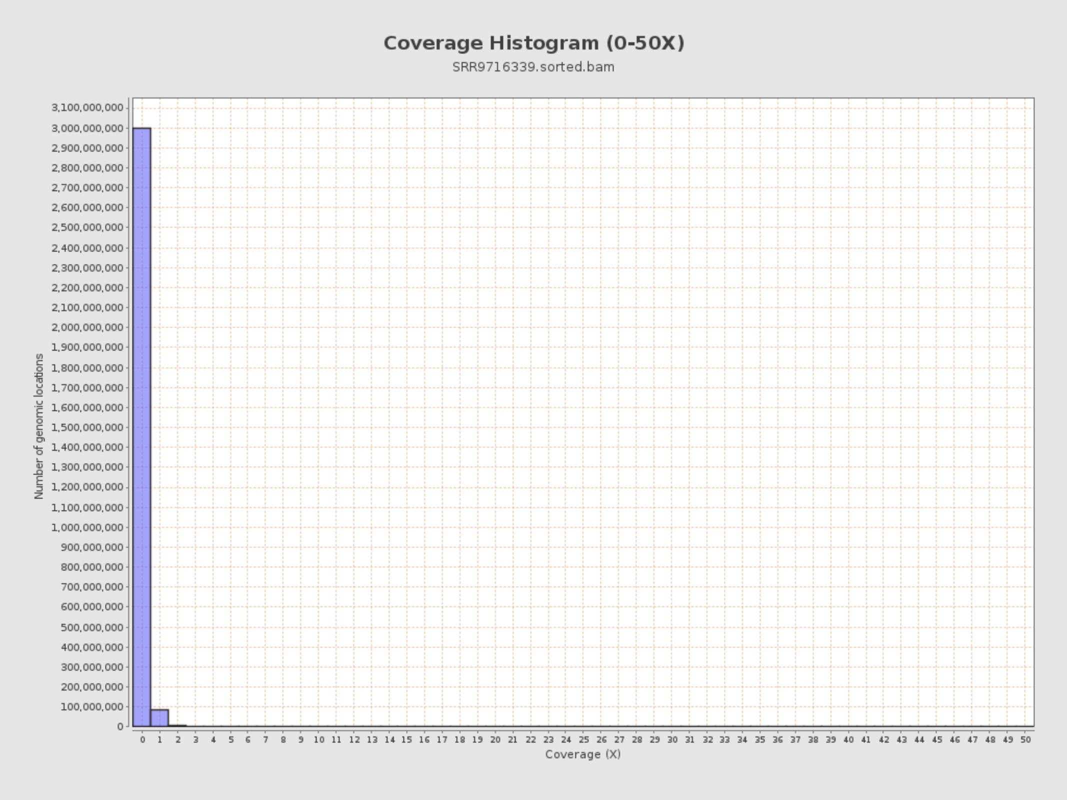
3. Results : Coverage across reference



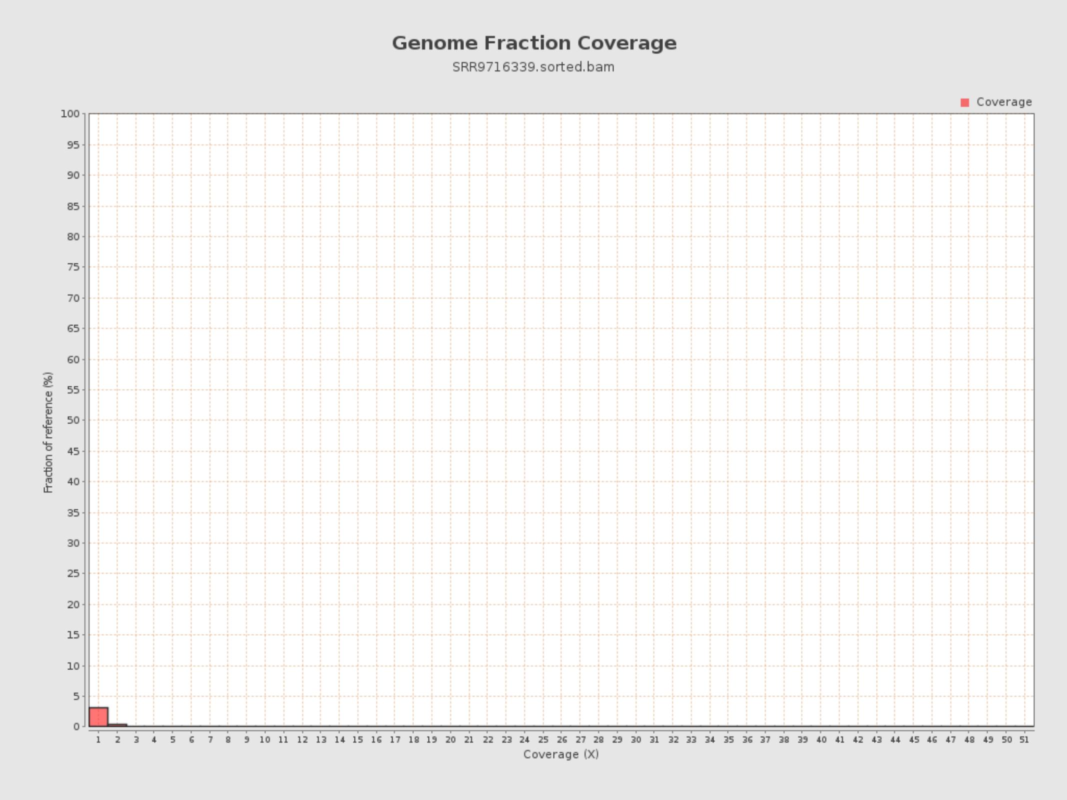
4. Results : Coverage Histogram



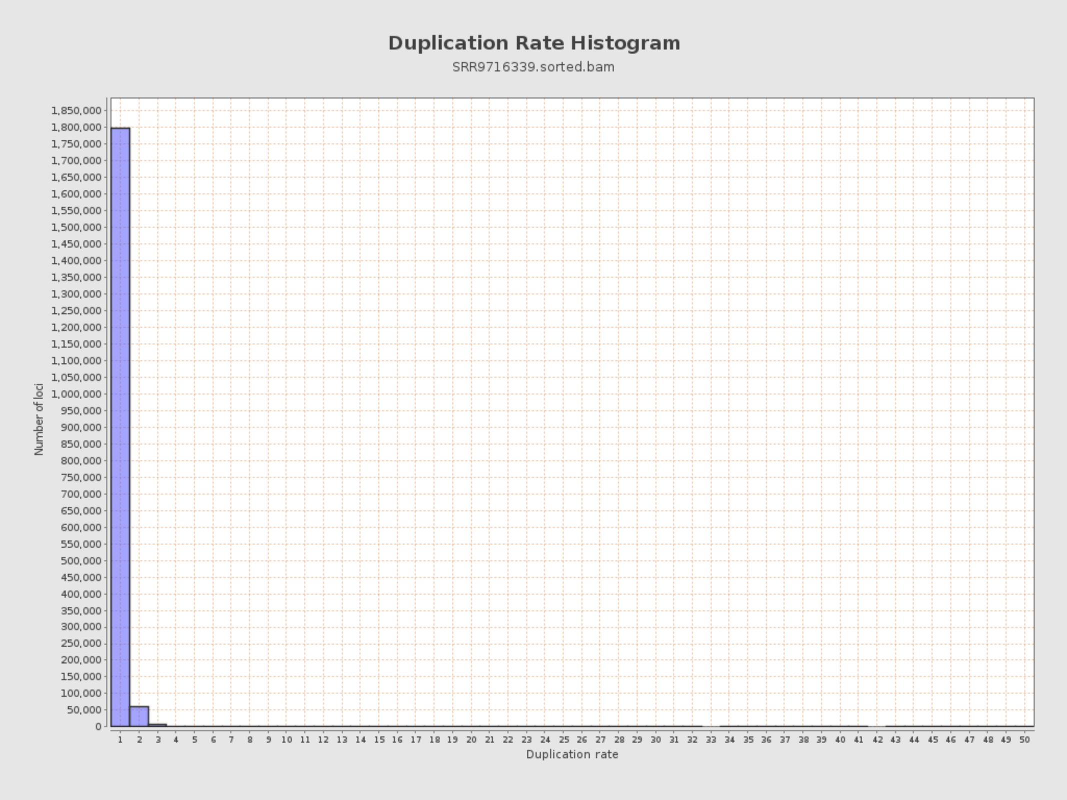
5. Results : Coverage Histogram (0-50X)



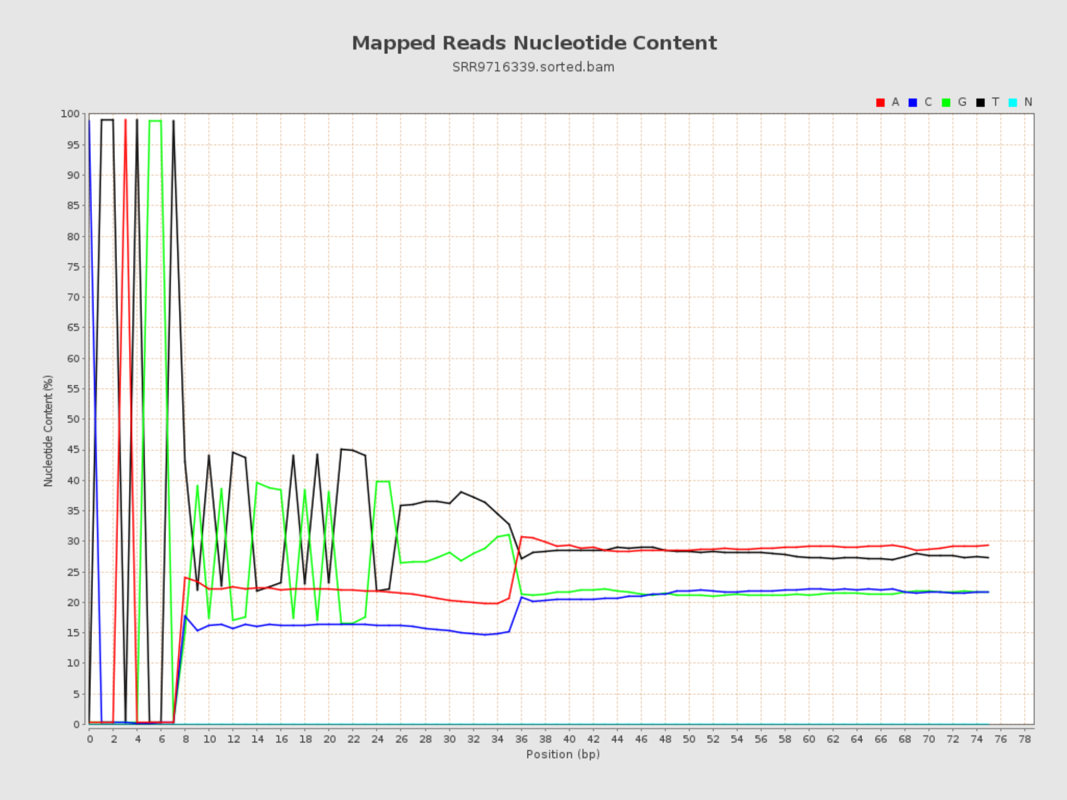
6. Results : Genome Fraction Coverage



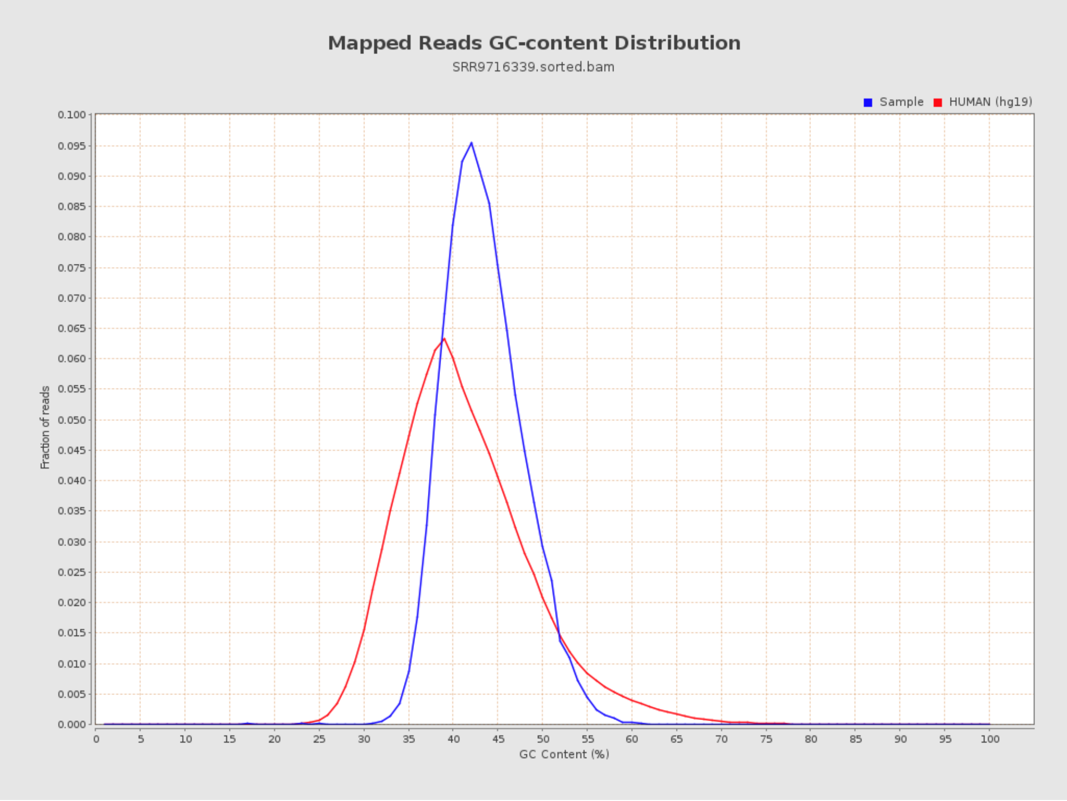
7. Results : Duplication Rate Histogram



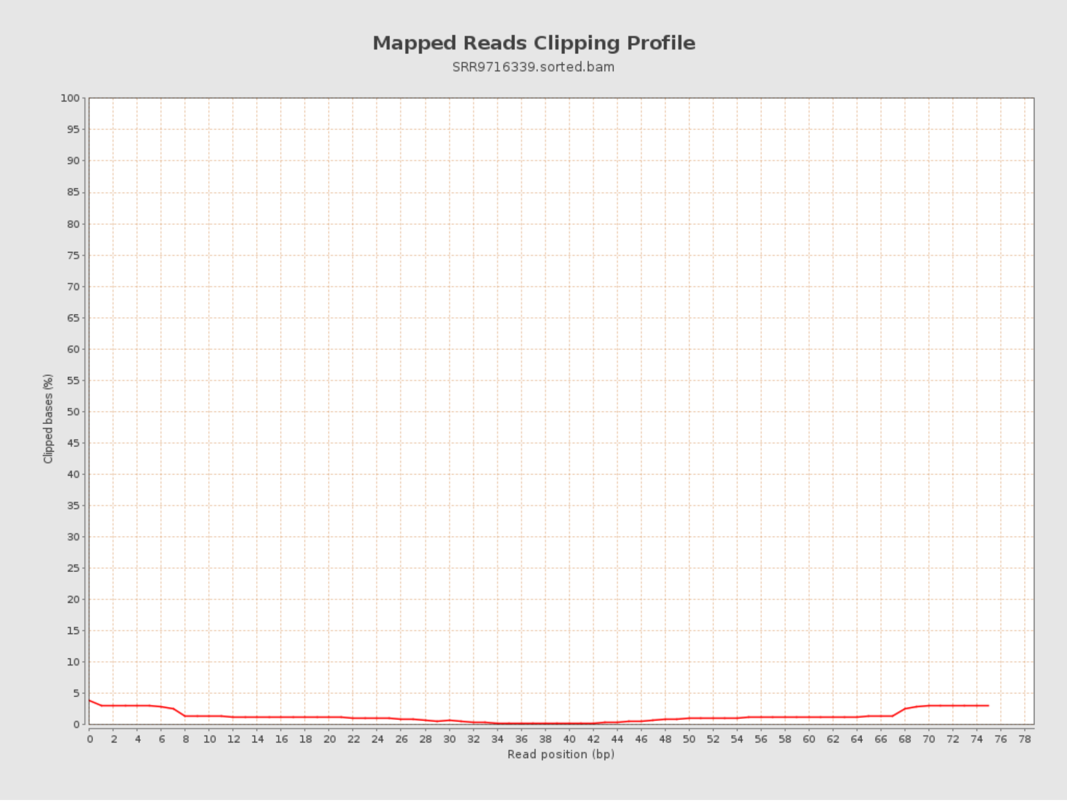
8. Results : Mapped Reads Nucleotide Content



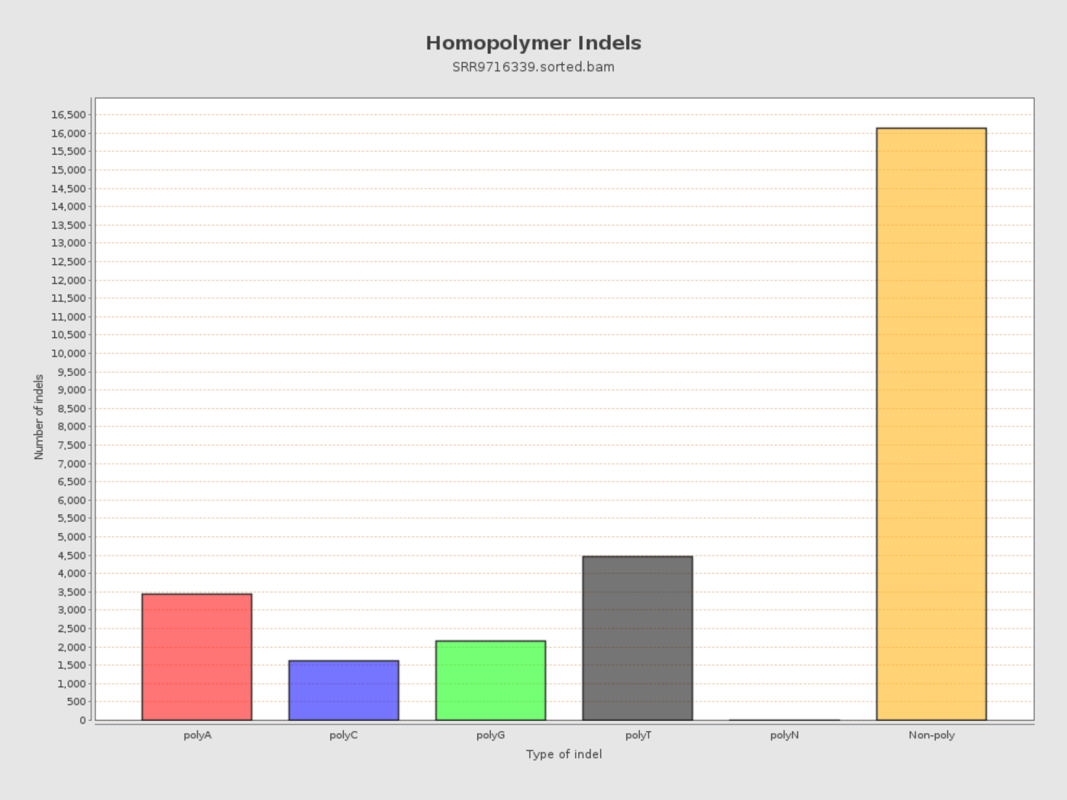
9. Results : Mapped Reads GC-content Distribution



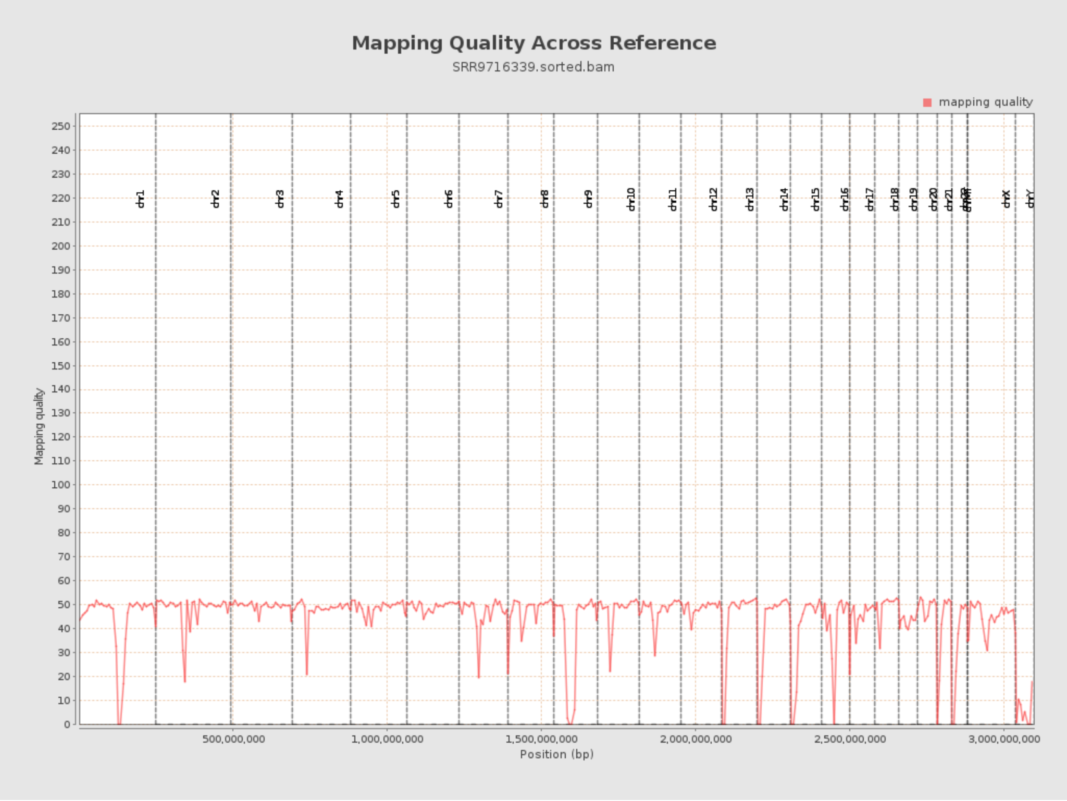
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram