Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 06:59:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716315.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_SRR9716315 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716315.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 06:59:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716315.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,730,035
Mapped reads	1,596,705 / 92.29%
Unmapped reads	133,330 / 7.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	33,184 / 1.92%
Read min/max/mean length	30 / 101 / 101.69
Duplicated reads (estimated)	62,969 / 3.64%
Duplication rate	2.84%
Clipped reads	1,628,833 / 94.15%

2.2. ACGT Content

Number/percentage of A's	32,813,379 / 26.16%
Number/percentage of C's	25,231,257 / 20.11%
Number/percentage of T's	37,817,270 / 30.15%
Number/percentage of G's	29,574,233 / 23.58%
Number/percentage of N's	8,720 / 0.01%
GC Percentage	43.69%

2.3. Coverage

Mean	0.0405

Standard Deviation	0.3835

2.4. Mapping Quality

Mean Mapping Quality	47.13

2.5. Mismatches and indels

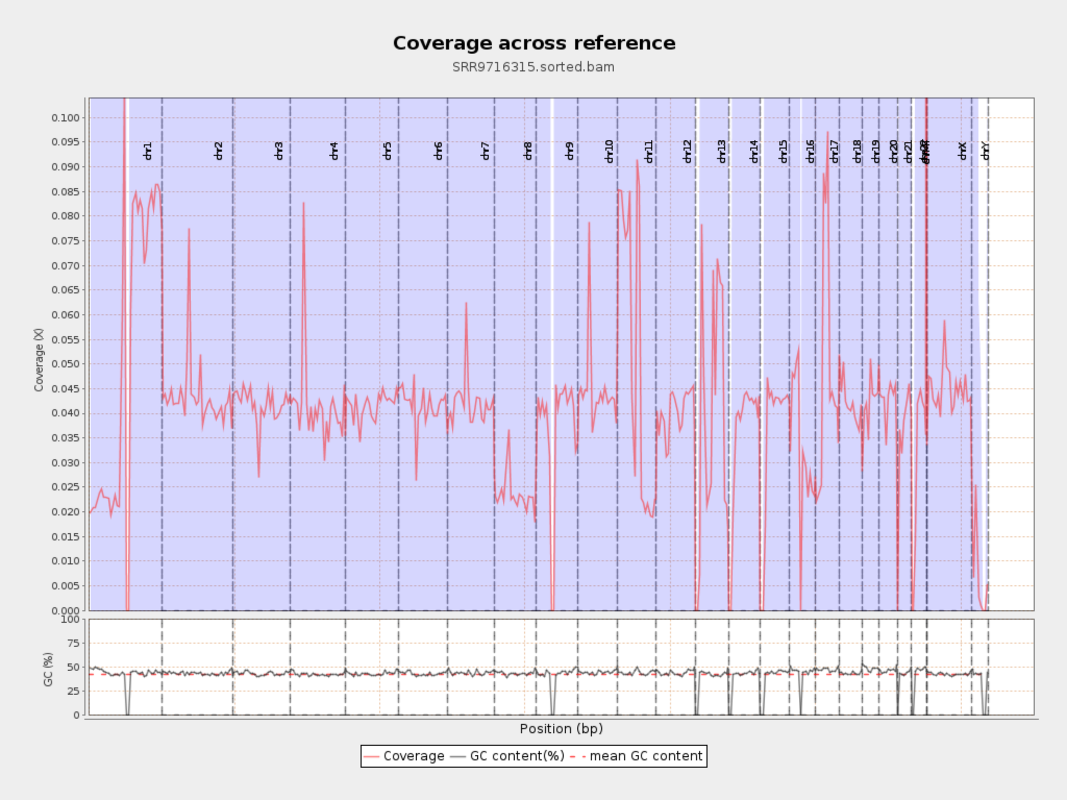
General error rate	0.68%
Mismatches	832,077
Insertions	9,700
Mapped reads with at least one insertion	0.6%
Deletions	29,015
Mapped reads with at least one deletion	1.79%
Homopolymer indels	42.83%

2.6. Chromosome stats

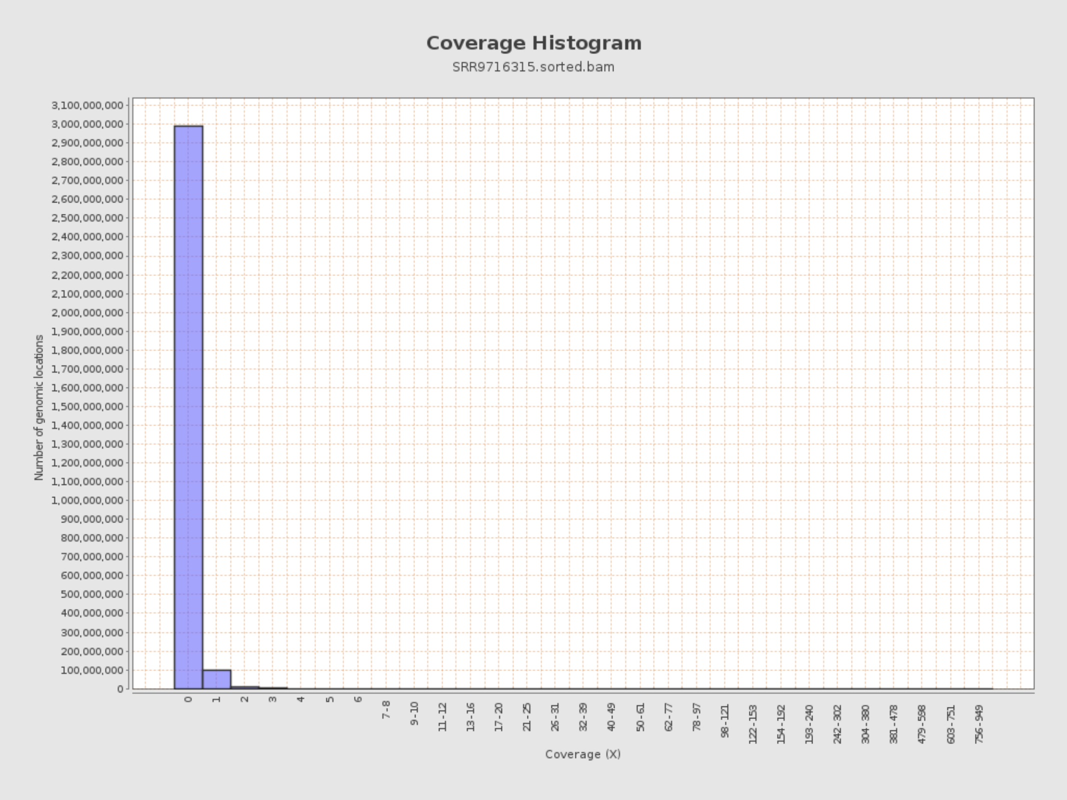
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12498026	0.0501	0.8079
chr2	243199373	10576090	0.0435	0.4012
chr3	198022430	8254439	0.0417	0.2271
chr4	191154276	7911901	0.0414	0.2905
chr5	180915260	7519755	0.0416	0.2292
chr6	171115067	7120617	0.0416	0.2454
chr7	159138663	6740011	0.0424	0.4469

chr8	146364022	3454856	0.0236	0.3948
chr9	141213431	5194228	0.0368	0.3082
chr10	135534747	6041071	0.0446	0.398
chr11	135006516	6999101	0.0518	0.3855
chr12	133851895	5382420	0.0402	0.2258
chr13	115169878	4395274	0.0382	0.22
chr14	107349540	3728138	0.0347	0.2211
chr15	102531392	3618449	0.0353	0.2075
chr16	90354753	2945079	0.0326	0.2228
chr17	81195210	4077713	0.0502	0.2972
chr18	78077248	3286874	0.0421	0.5257
chr19	59128983	2506597	0.0424	0.5691
chr20	63025520	2674797	0.0424	0.2404
chr21	48129895	1713042	0.0356	0.2421
chr22	51304566	1496383	0.0292	0.1929
chrMT	16571	12400	0.7483	1.0279
chrX	155270560	6958612	0.0448	0.2742
chrY	59373566	394922	0.0067	0.2256

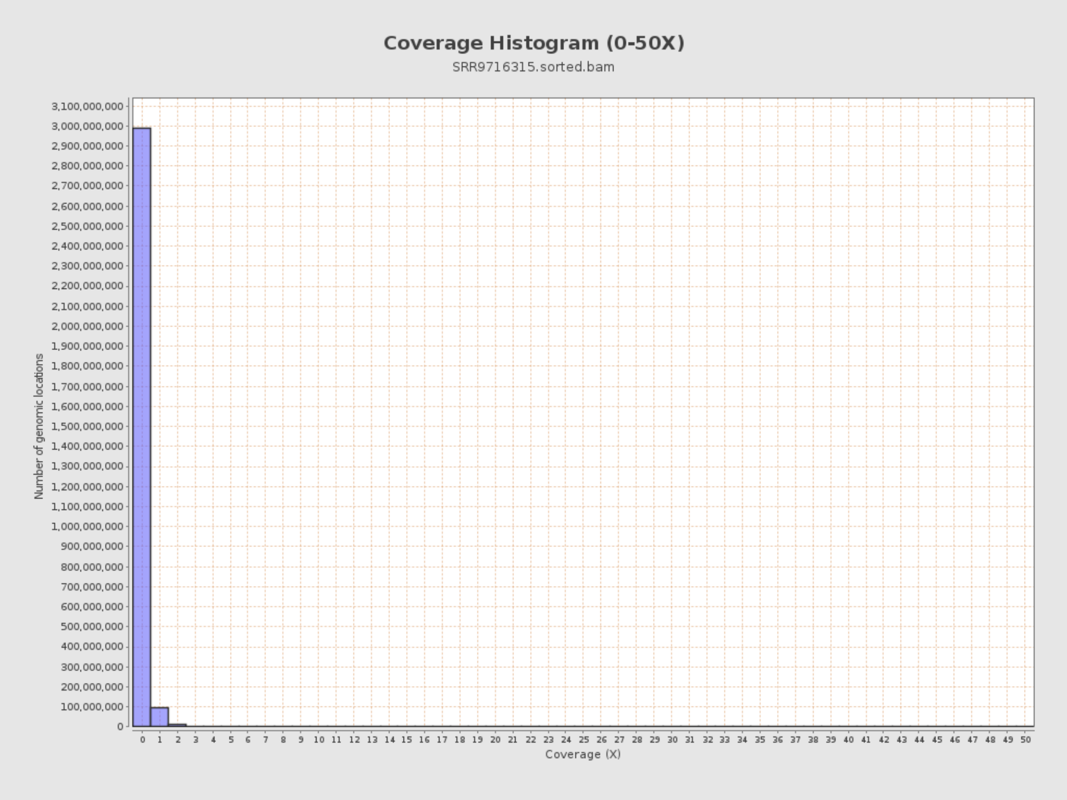
3. Results : Coverage across reference



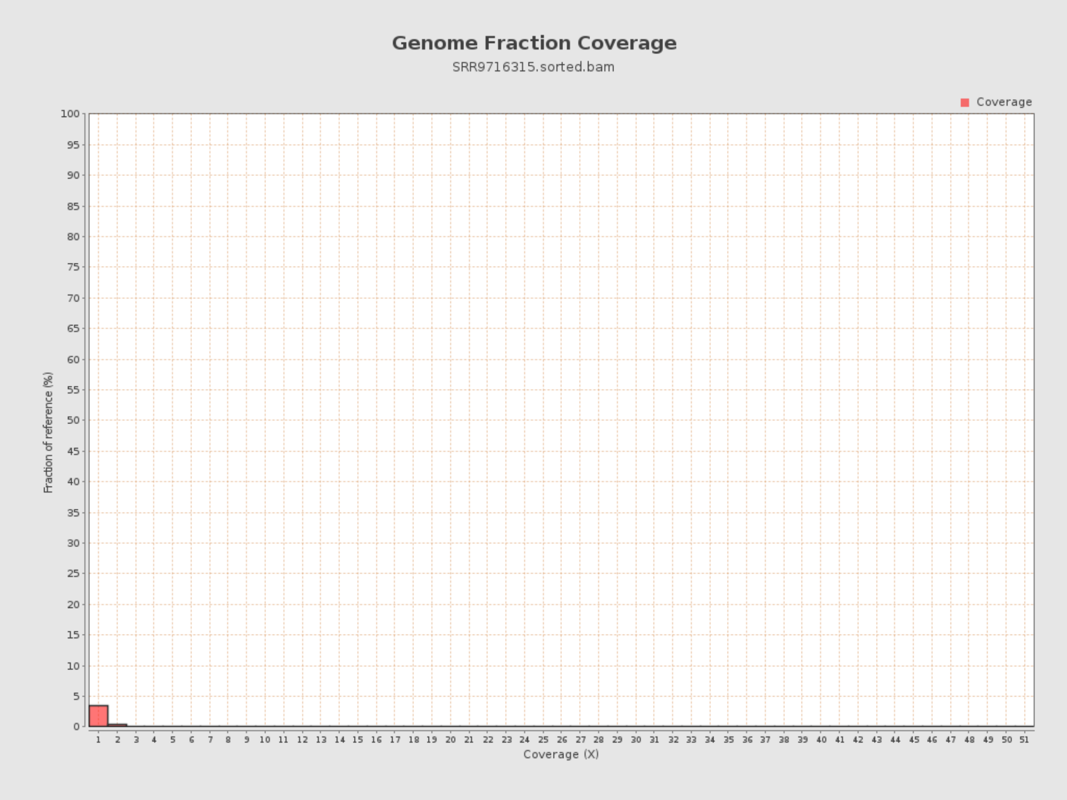
4. Results : Coverage Histogram



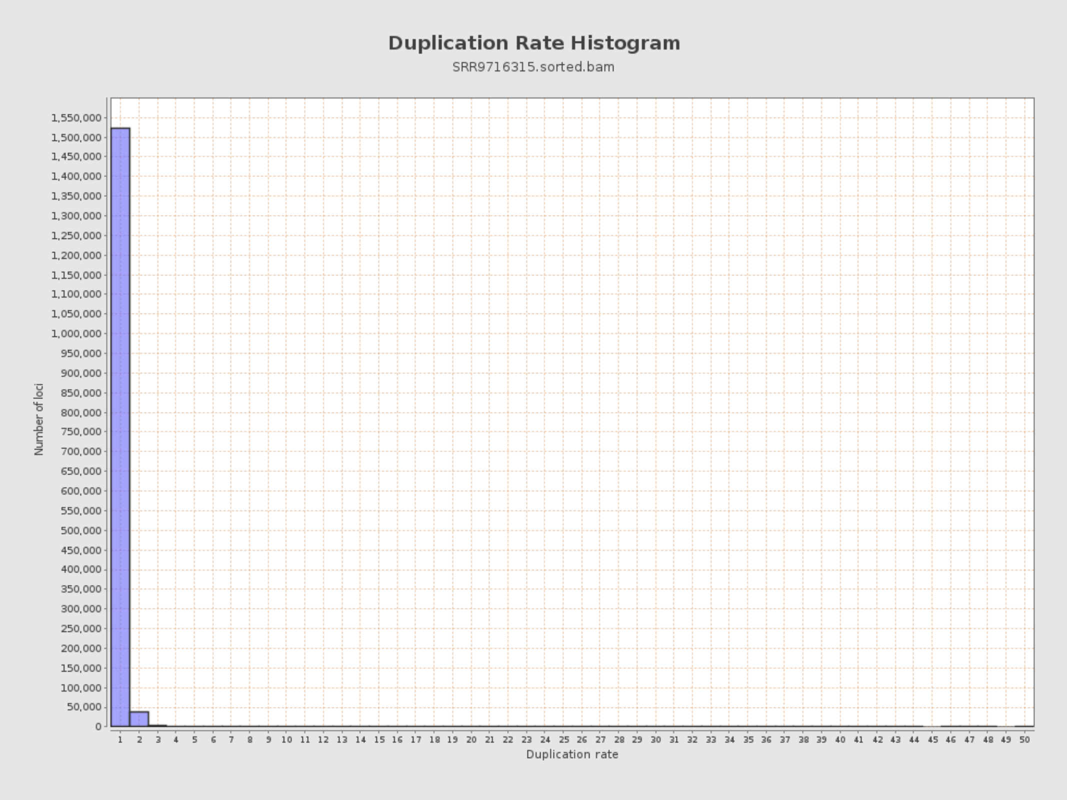
5. Results : Coverage Histogram (0-50X)



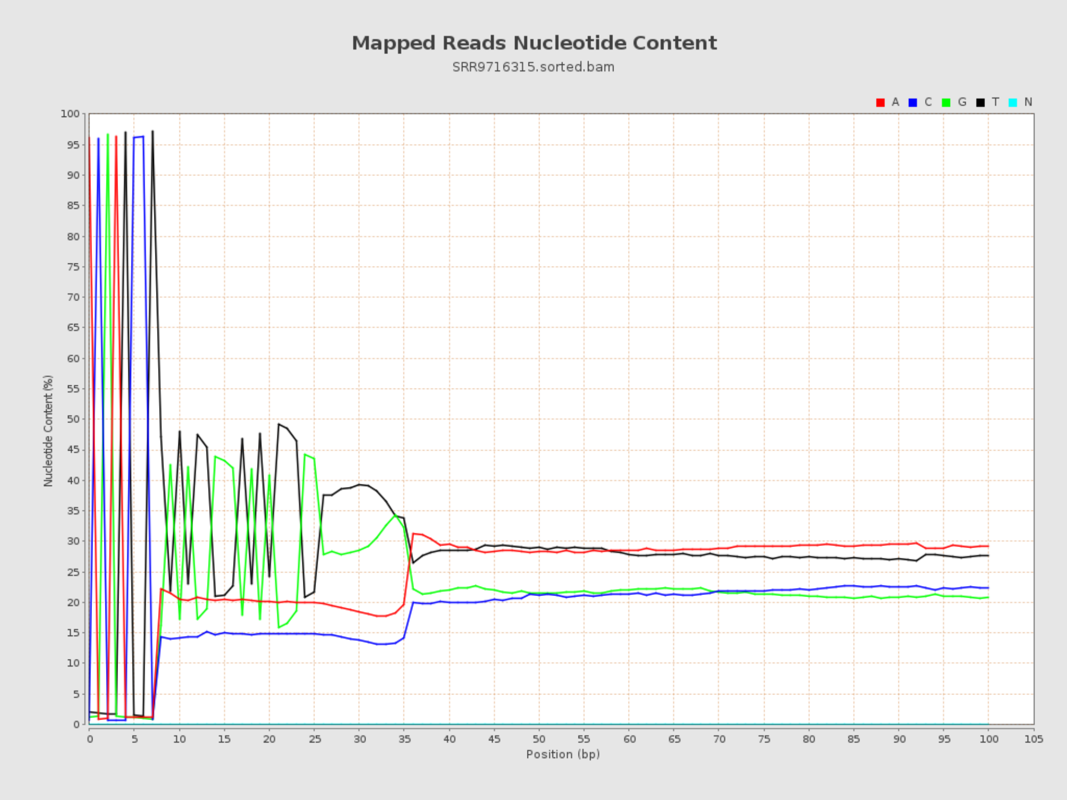
6. Results : Genome Fraction Coverage



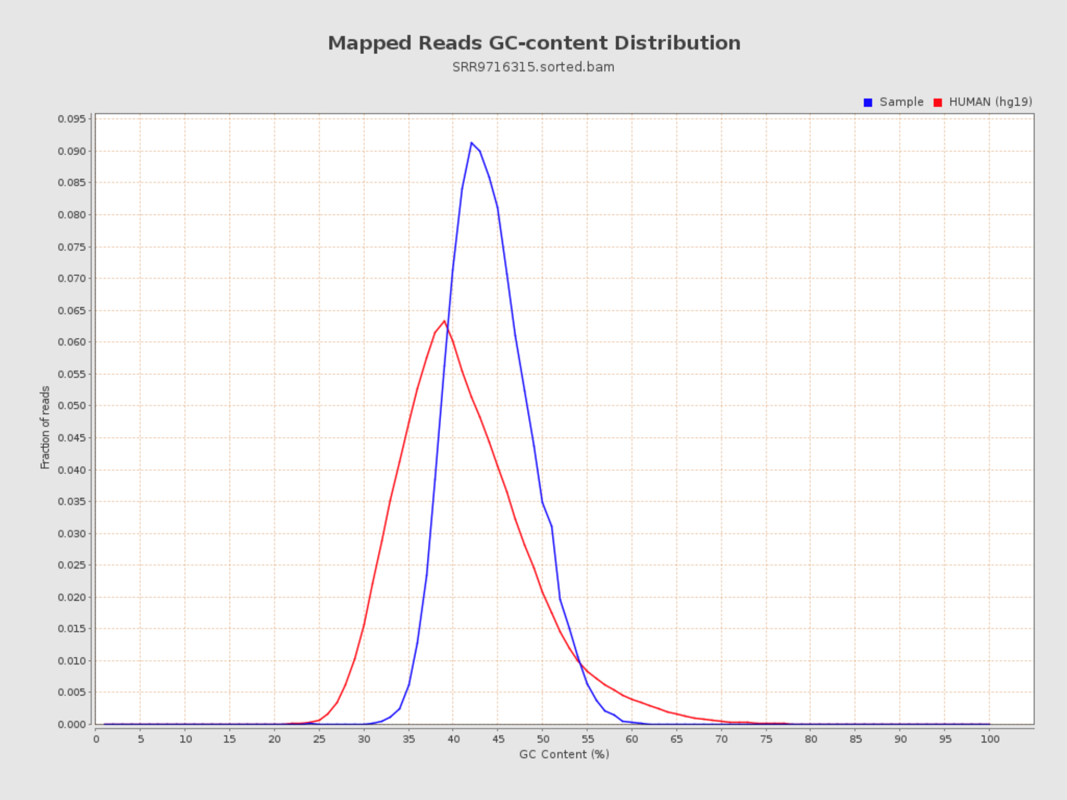
7. Results : Duplication Rate Histogram



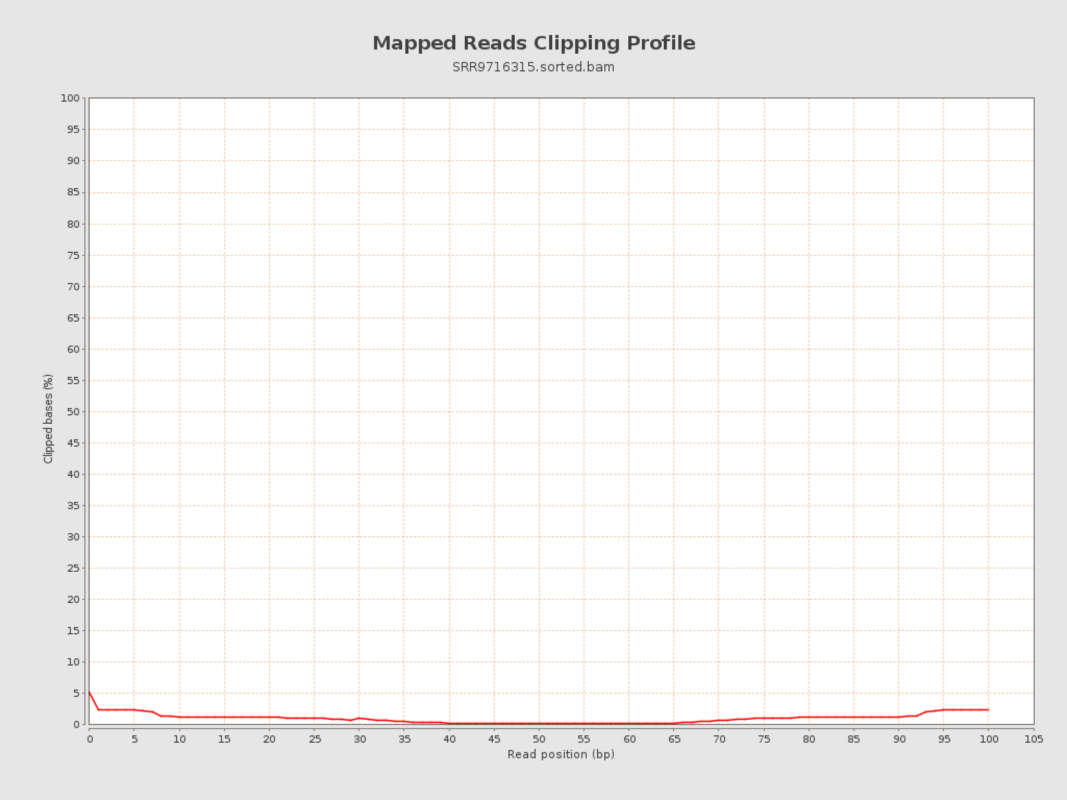
8. Results : Mapped Reads Nucleotide Content



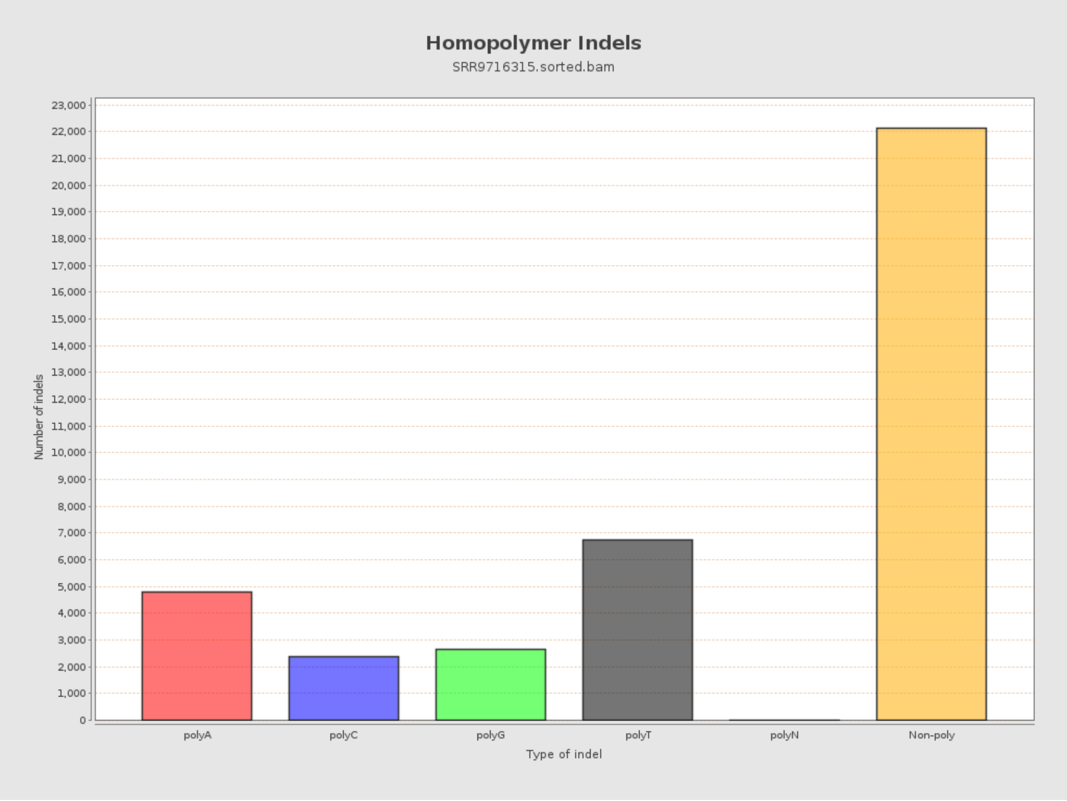
9. Results : Mapped Reads GC-content Distribution



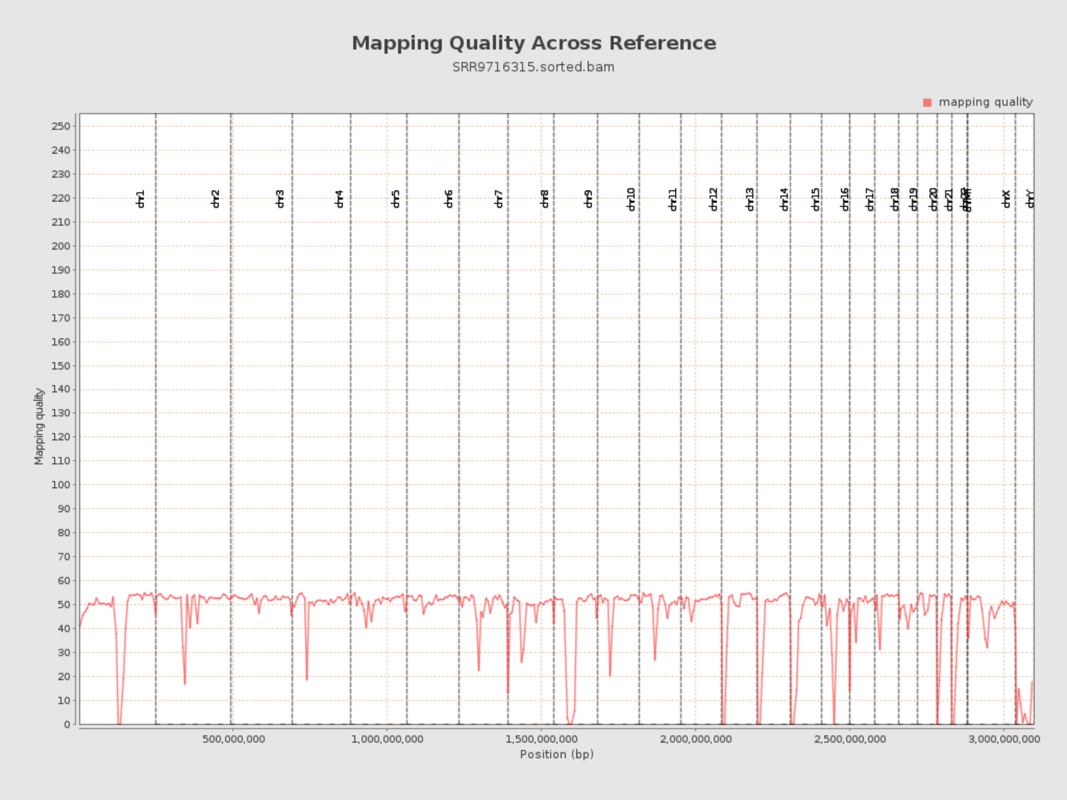
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram