Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 09:40:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716370.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_SRR9716370 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716370.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 09:40:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716370.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,227,011
Mapped reads	2,095,819 / 94.11%
Unmapped reads	131,192 / 5.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	42,621 / 1.91%
Read min/max/mean length	30 / 101 / 101.69
Duplicated reads (estimated)	98,195 / 4.41%
Duplication rate	3.28%
Clipped reads	2,136,279 / 95.93%

2.2. ACGT Content

Number/percentage of A's	43,230,509 / 25.89%
Number/percentage of C's	32,621,792 / 19.54%
Number/percentage of T's	49,448,669 / 29.62%
Number/percentage of G's	41,647,468 / 24.94%
Number/percentage of N's	11,462 / 0.01%
GC Percentage	44.48%

2.3. Coverage

Mean	0.054

Standard Deviation	0.5242

2.4. Mapping Quality

Mean Mapping Quality	47.68

2.5. Mismatches and indels

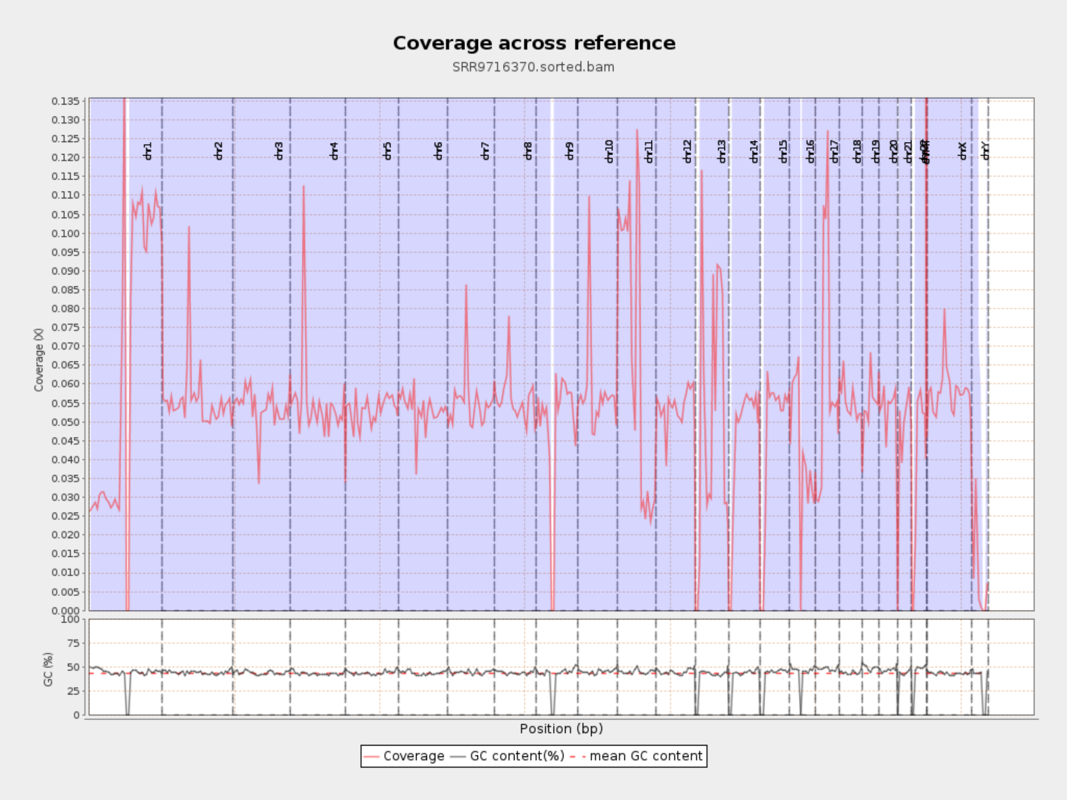
General error rate	0.65%
Mismatches	1,053,594
Insertions	13,429
Mapped reads with at least one insertion	0.63%
Deletions	39,723
Mapped reads with at least one deletion	1.86%
Homopolymer indels	44.45%

2.6. Chromosome stats

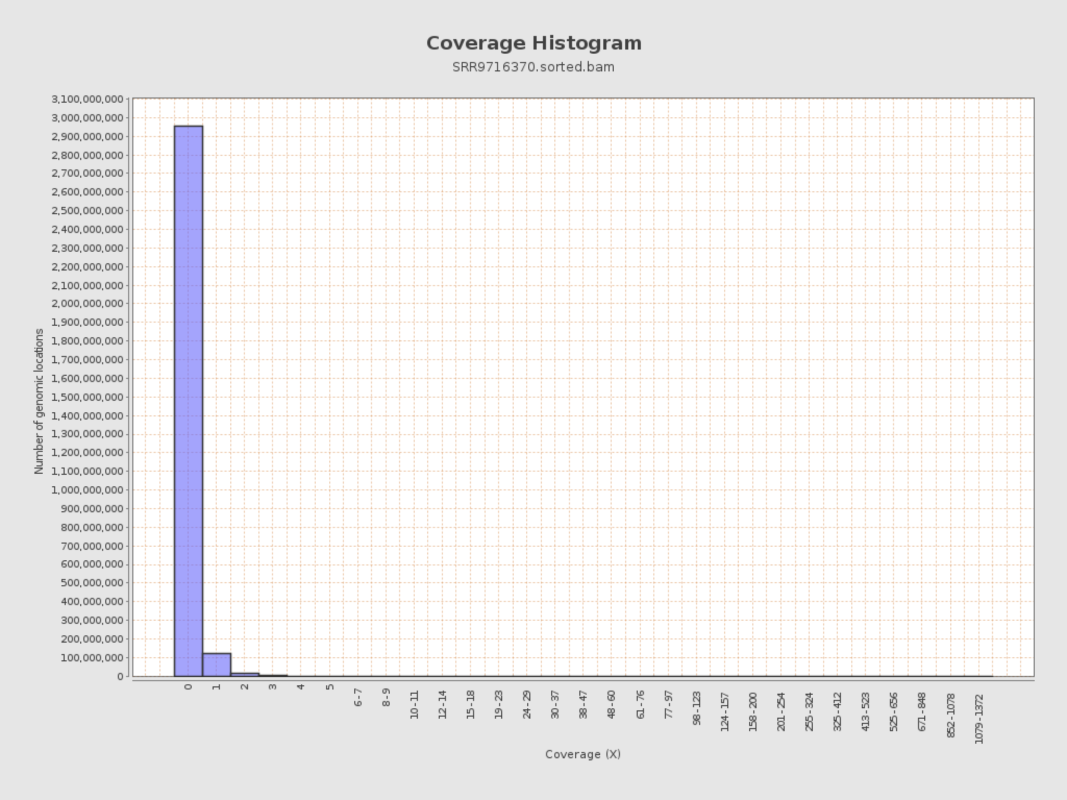
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16262267	0.0652	1.1984
chr2	243199373	13625117	0.056	0.5236
chr3	198022430	10612671	0.0536	0.2616
chr4	191154276	10540903	0.0551	0.3612
chr5	180915260	9624245	0.0532	0.2638
chr6	171115067	9115029	0.0533	0.2876
chr7	159138663	8816088	0.0554	0.617

chr8	146364022	8213787	0.0561	0.5732
chr9	141213431	6811478	0.0482	0.4139
chr10	135534747	7831574	0.0578	0.5209
chr11	135006516	9317272	0.069	0.5058
chr12	133851895	7233403	0.054	0.2664
chr13	115169878	5814732	0.0505	0.2571
chr14	107349540	4828895	0.045	0.2618
chr15	102531392	4722154	0.0461	0.2429
chr16	90354753	3771765	0.0417	0.2647
chr17	81195210	5188983	0.0639	0.3527
chr18	78077248	4339057	0.0556	0.699
chr19	59128983	3263184	0.0552	0.78
chr20	63025520	3377322	0.0536	0.2855
chr21	48129895	2227954	0.0463	0.3083
chr22	51304566	1911033	0.0372	0.2225
chrMT	16571	27494	1.6592	1.6124
chrX	155270560	9030458	0.0582	0.3335
chrY	59373566	529368	0.0089	0.306

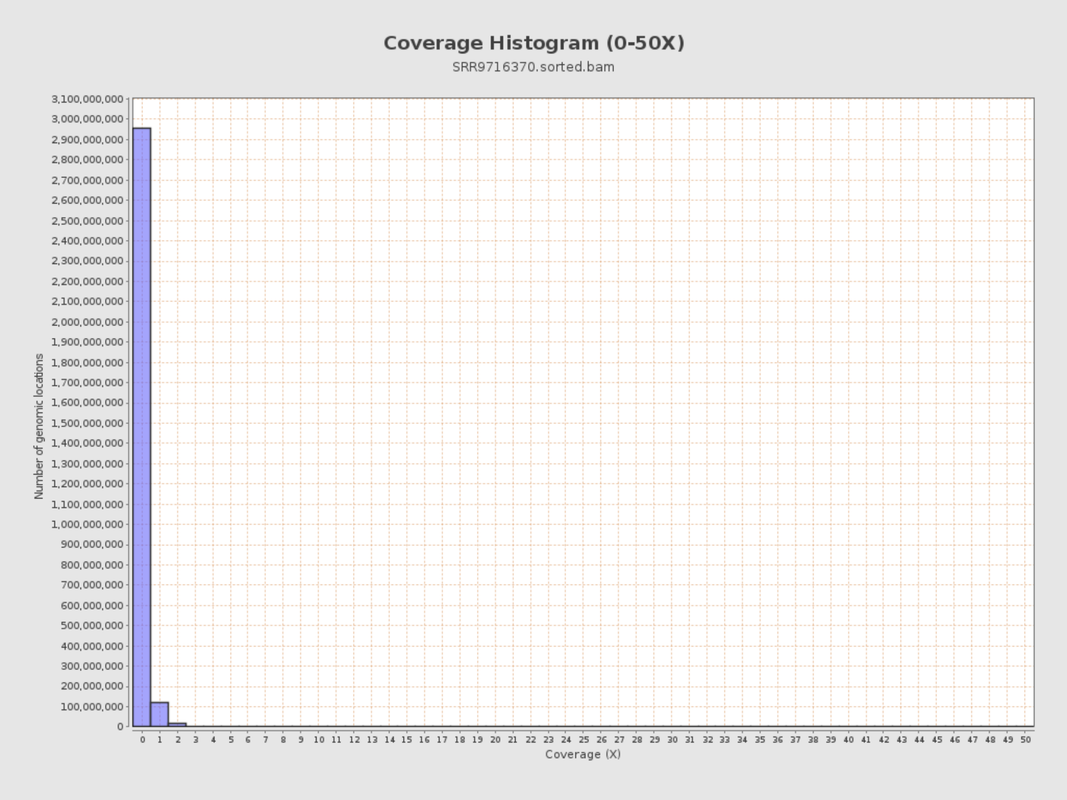
3. Results : Coverage across reference



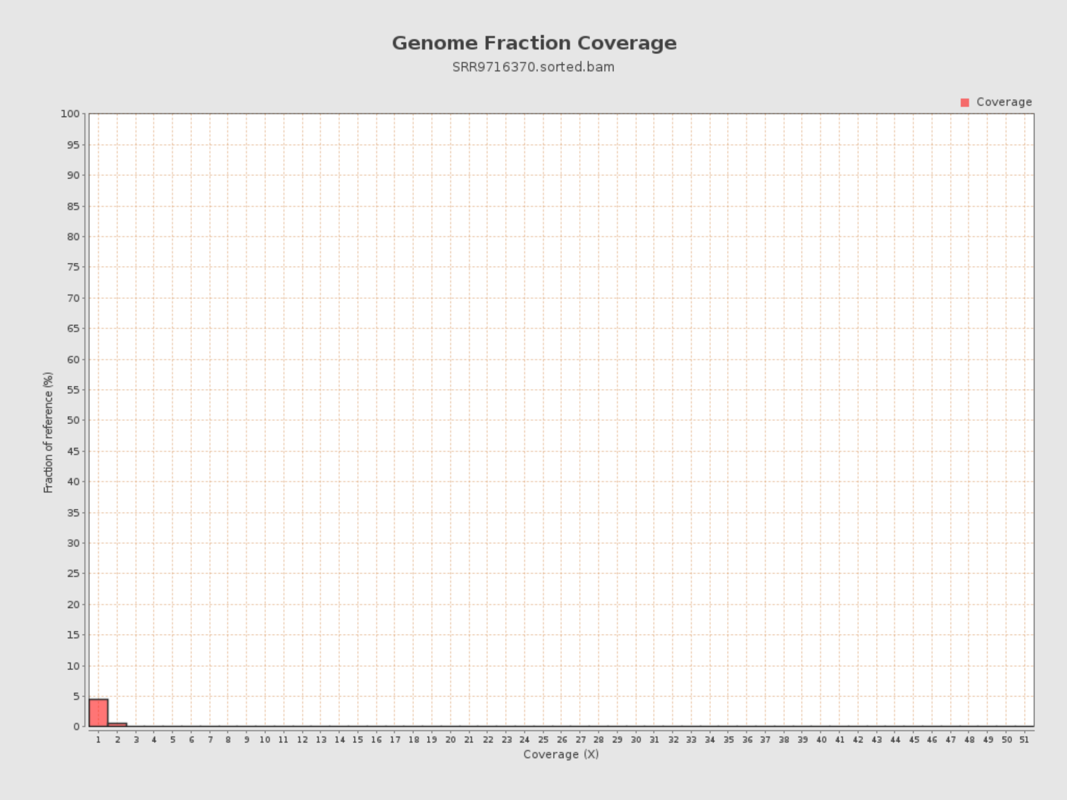
4. Results : Coverage Histogram



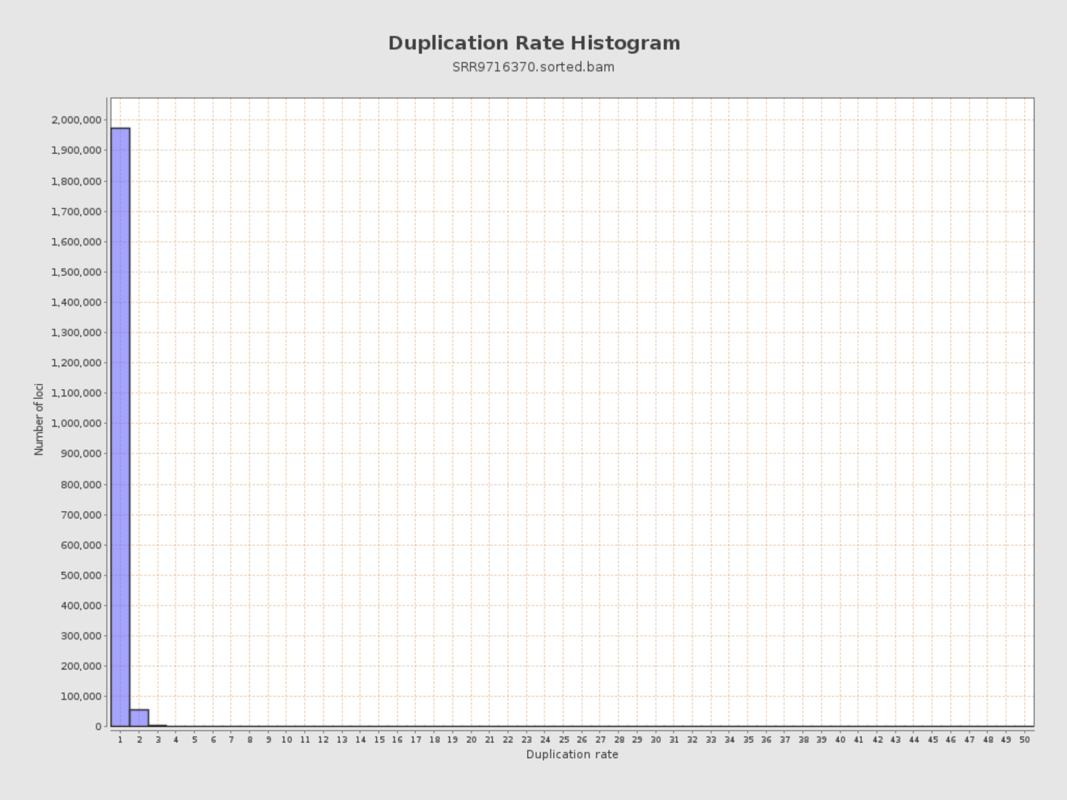
5. Results : Coverage Histogram (0-50X)



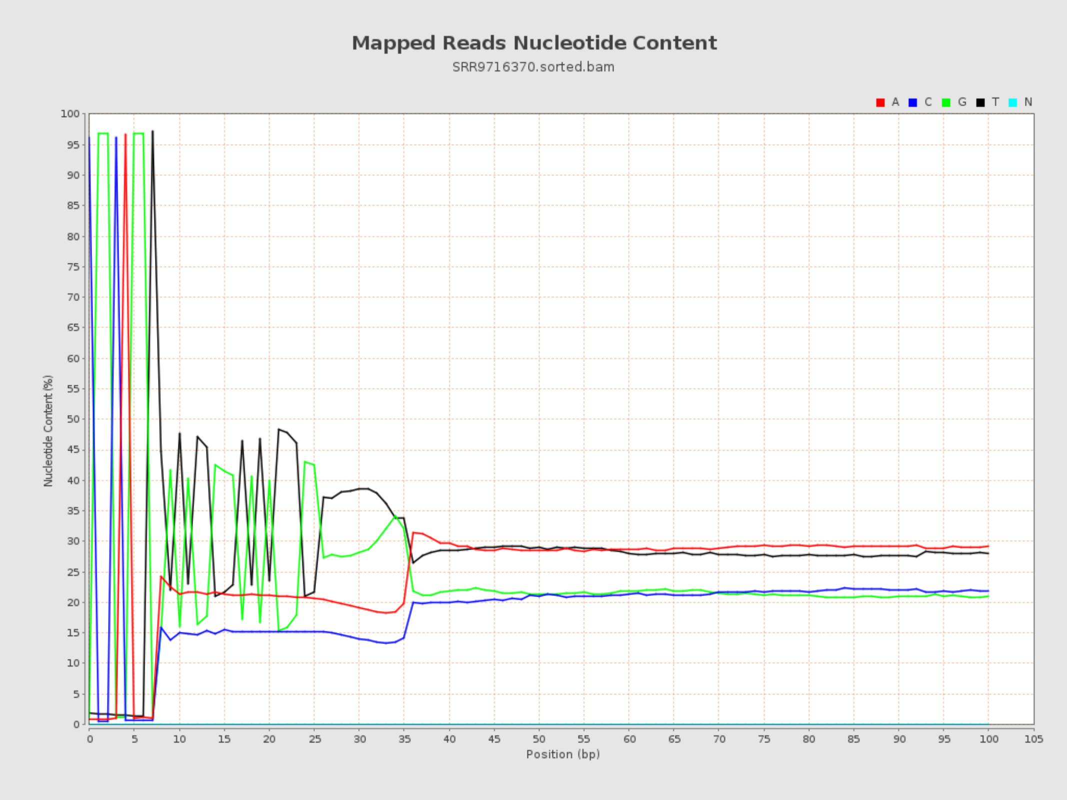
6. Results : Genome Fraction Coverage



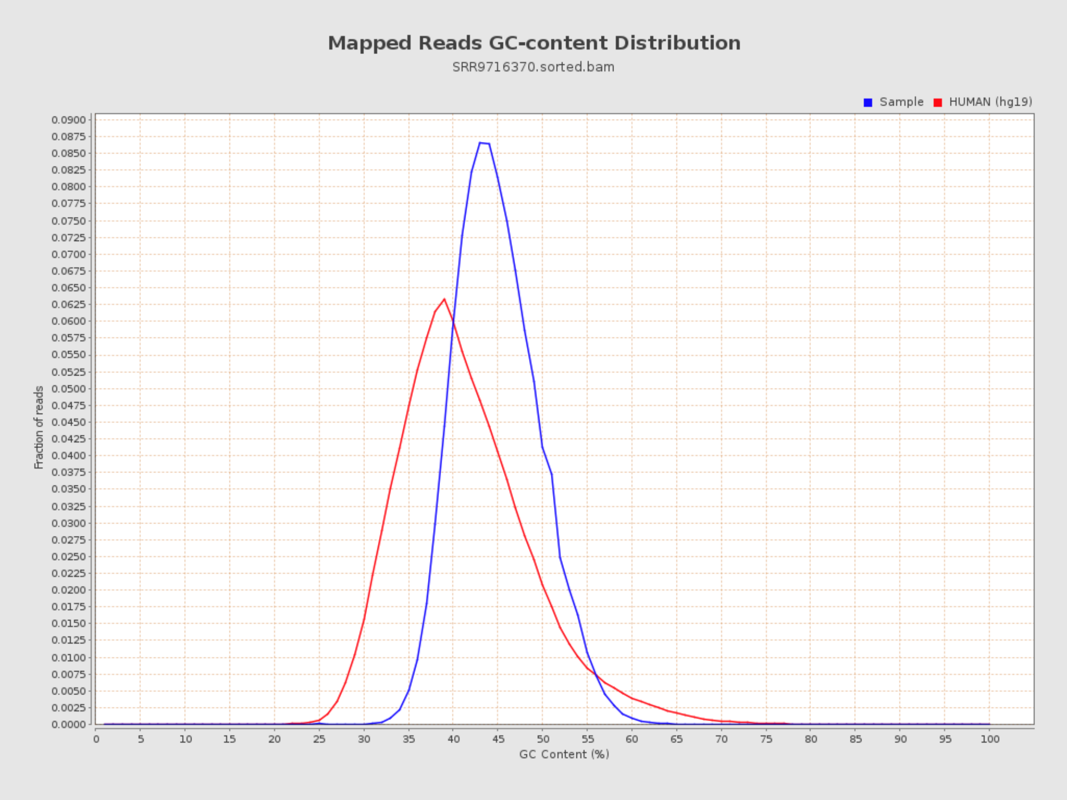
7. Results : Duplication Rate Histogram



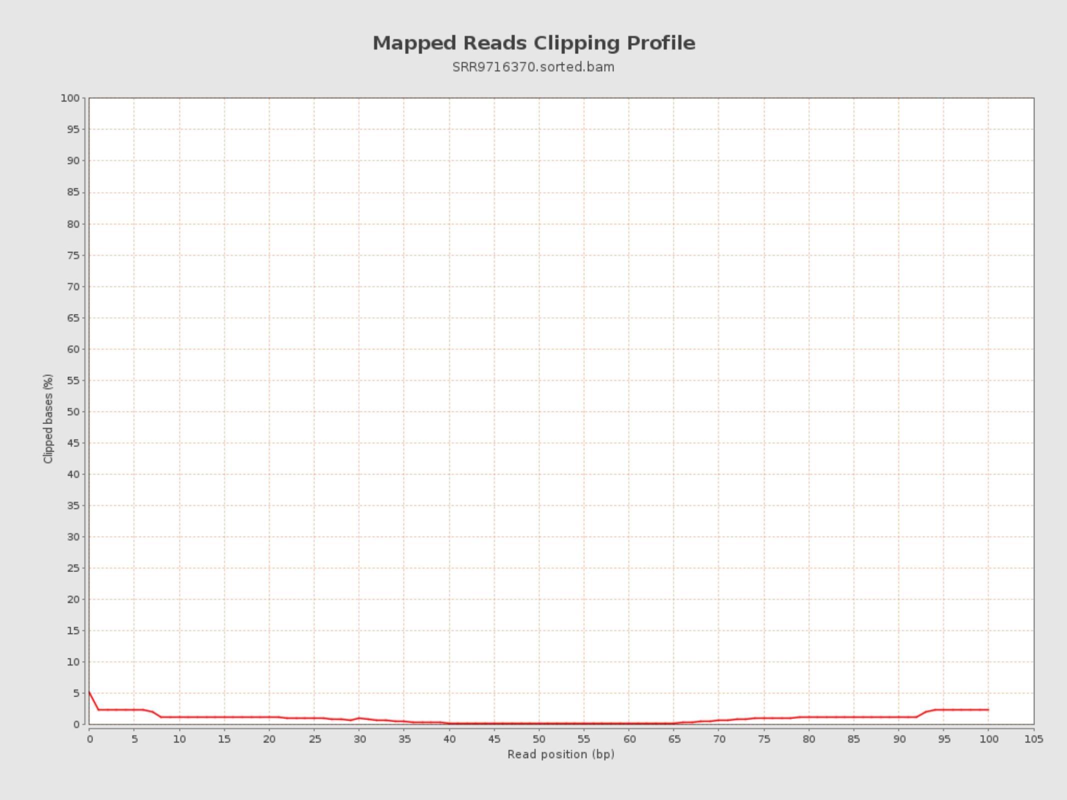
8. Results : Mapped Reads Nucleotide Content



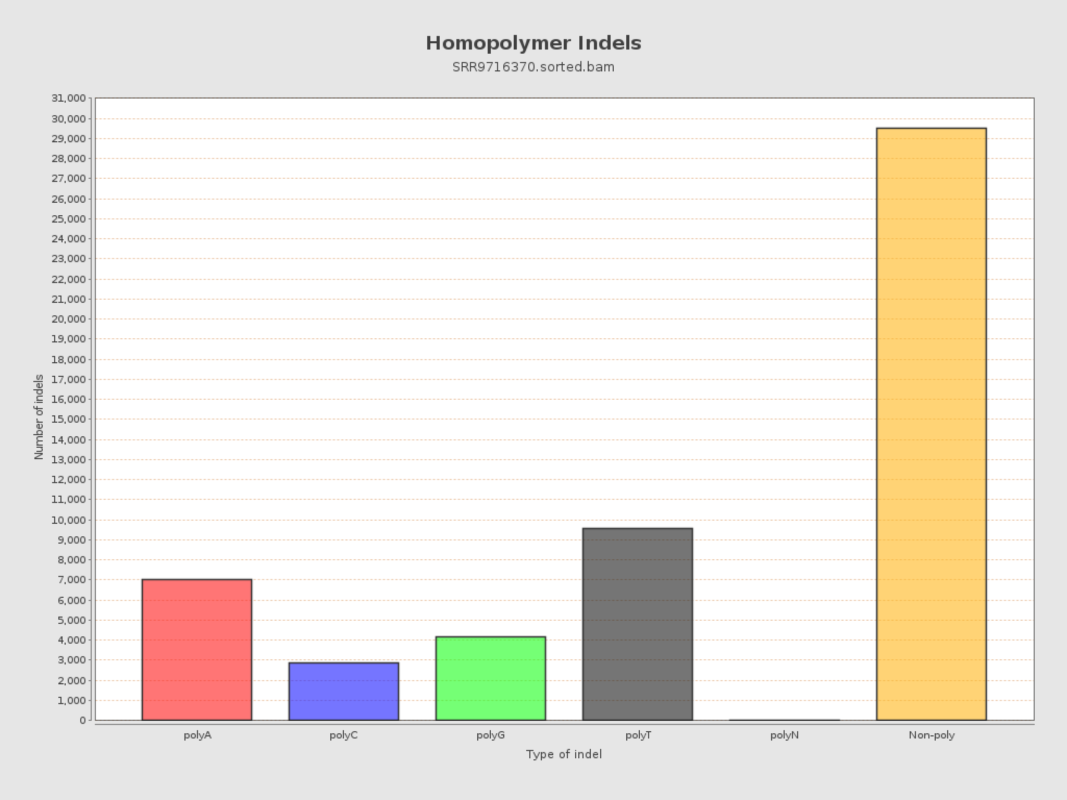
9. Results : Mapped Reads GC-content Distribution



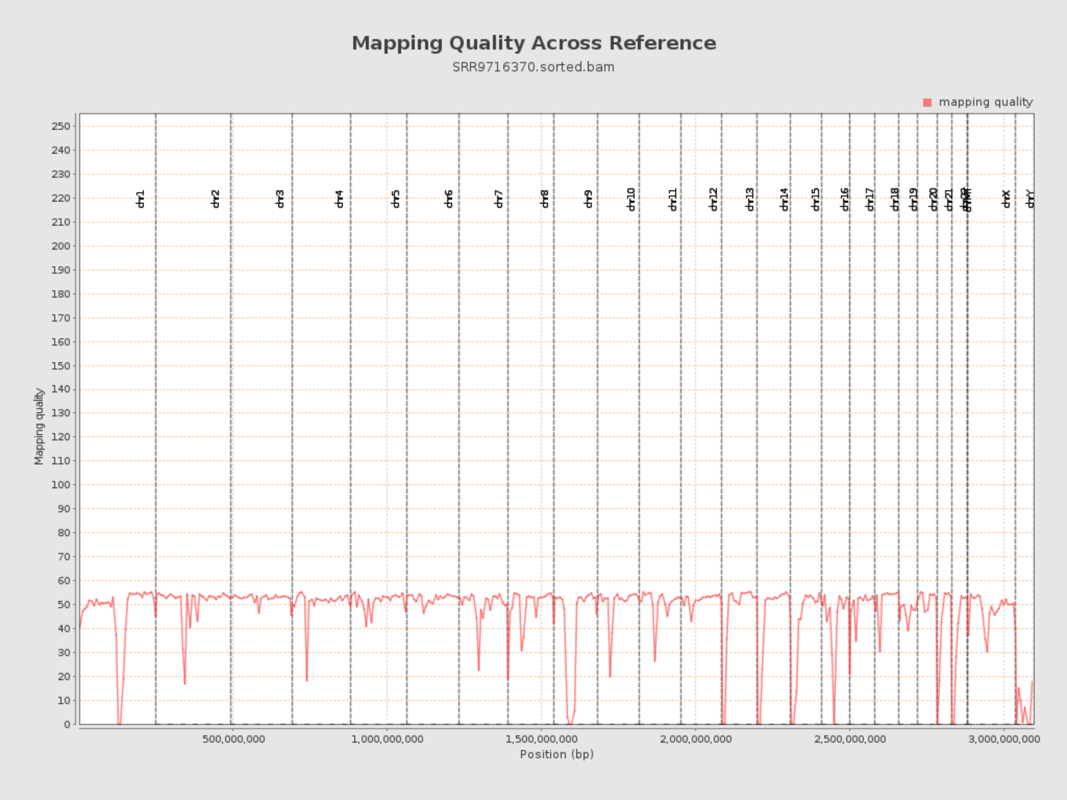
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram