Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 08:00:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716331.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_SRR9716331 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716331.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 08:00:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716331.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,796,052
Mapped reads	1,571,430 / 87.49%
Unmapped reads	224,622 / 12.51%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,446 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	53,689 / 2.99%
Duplication rate	2.6%
Clipped reads	1,574,310 / 87.65%

2.2. ACGT Content

Number/percentage of A's	22,755,800 / 25.36%
Number/percentage of C's	15,925,949 / 17.75%
Number/percentage of T's	29,314,854 / 32.67%
Number/percentage of G's	21,721,305 / 24.21%
Number/percentage of N's	1,406 / 0%
GC Percentage	41.96%

2.3. Coverage

Mean	0.029

Standard Deviation	0.2589

2.4. Mapping Quality

Mean Mapping Quality	44.75

2.5. Mismatches and indels

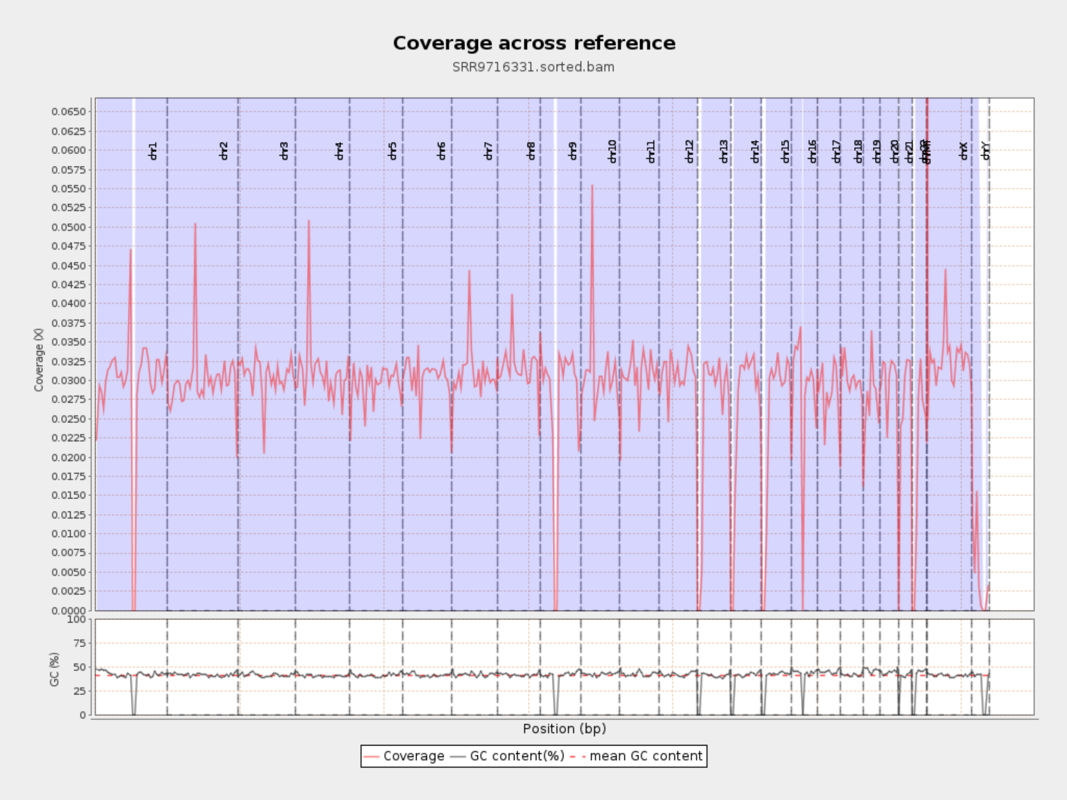
General error rate	0.55%
Mismatches	486,186
Insertions	5,583
Mapped reads with at least one insertion	0.35%
Deletions	14,498
Mapped reads with at least one deletion	0.92%
Homopolymer indels	43.98%

2.6. Chromosome stats

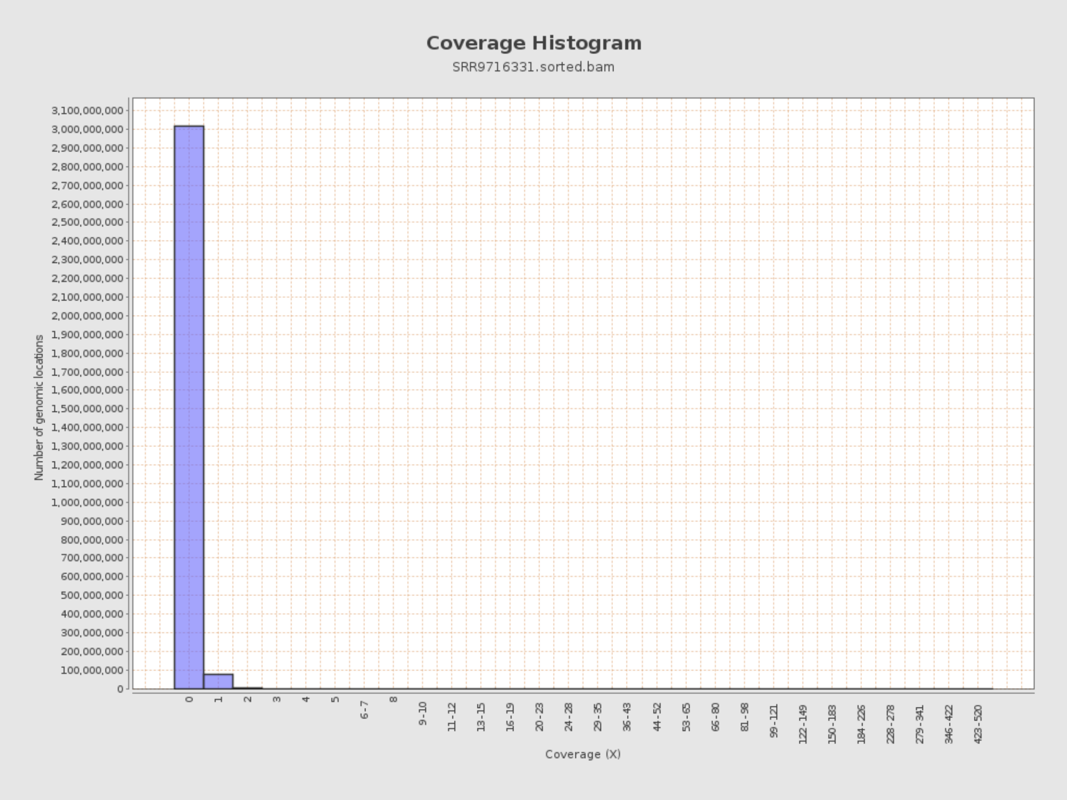
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7276072	0.0292	0.4425
chr2	243199373	7309675	0.0301	0.2777
chr3	198022430	6062911	0.0306	0.1897
chr4	191154276	5958452	0.0312	0.2119
chr5	180915260	5392285	0.0298	0.1884
chr6	171115067	5213192	0.0305	0.2046
chr7	159138663	4942734	0.0311	0.2986

chr8	146364022	4644211	0.0317	0.2814
chr9	141213431	3839339	0.0272	0.2547
chr10	135534747	4225283	0.0312	0.2771
chr11	135006516	4157803	0.0308	0.2358
chr12	133851895	4126686	0.0308	0.1964
chr13	115169878	2909303	0.0253	0.1708
chr14	107349540	2776110	0.0259	0.1895
chr15	102531392	2565199	0.025	0.1712
chr16	90354753	2523207	0.0279	0.2004
chr17	81195210	2291500	0.0282	0.1933
chr18	78077248	2369134	0.0303	0.4381
chr19	59128983	1639358	0.0277	0.3383
chr20	63025520	1875128	0.0298	0.1952
chr21	48129895	1252982	0.026	0.1937
chr22	51304566	999894	0.0195	0.1513
chrMT	16571	21744	1.3122	1.4308
chrX	155270560	5098495	0.0328	0.223
chrY	59373566	272860	0.0046	0.1156

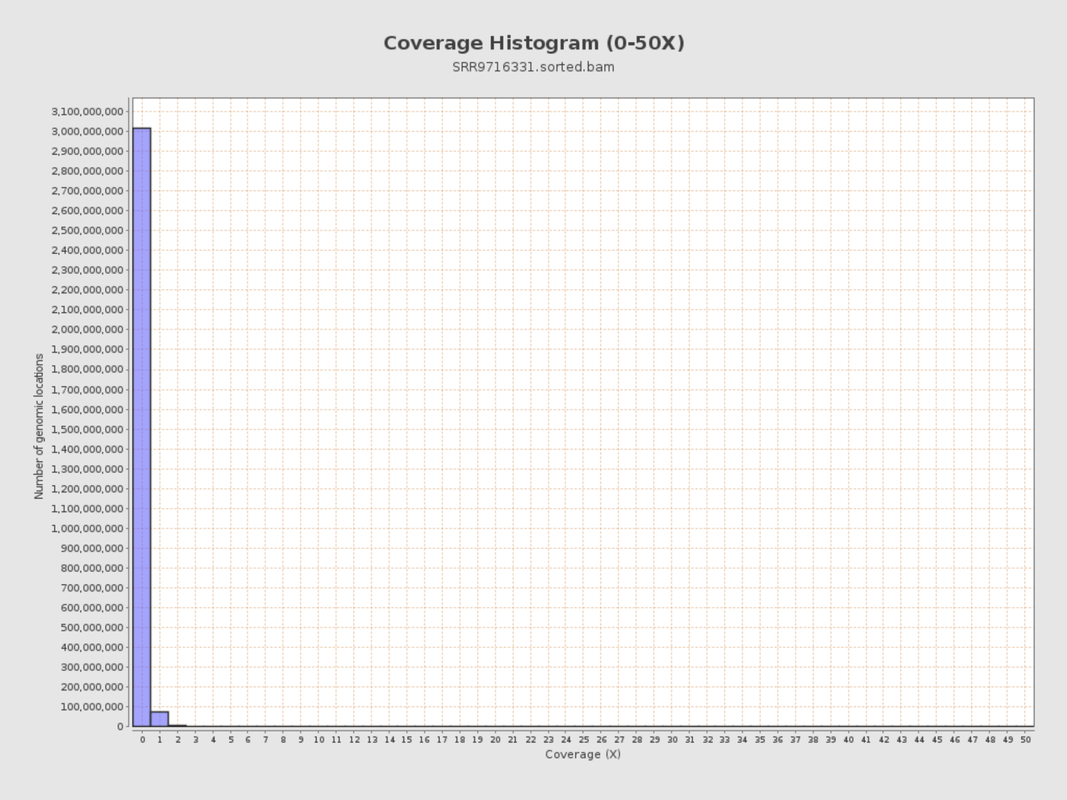
3. Results : Coverage across reference



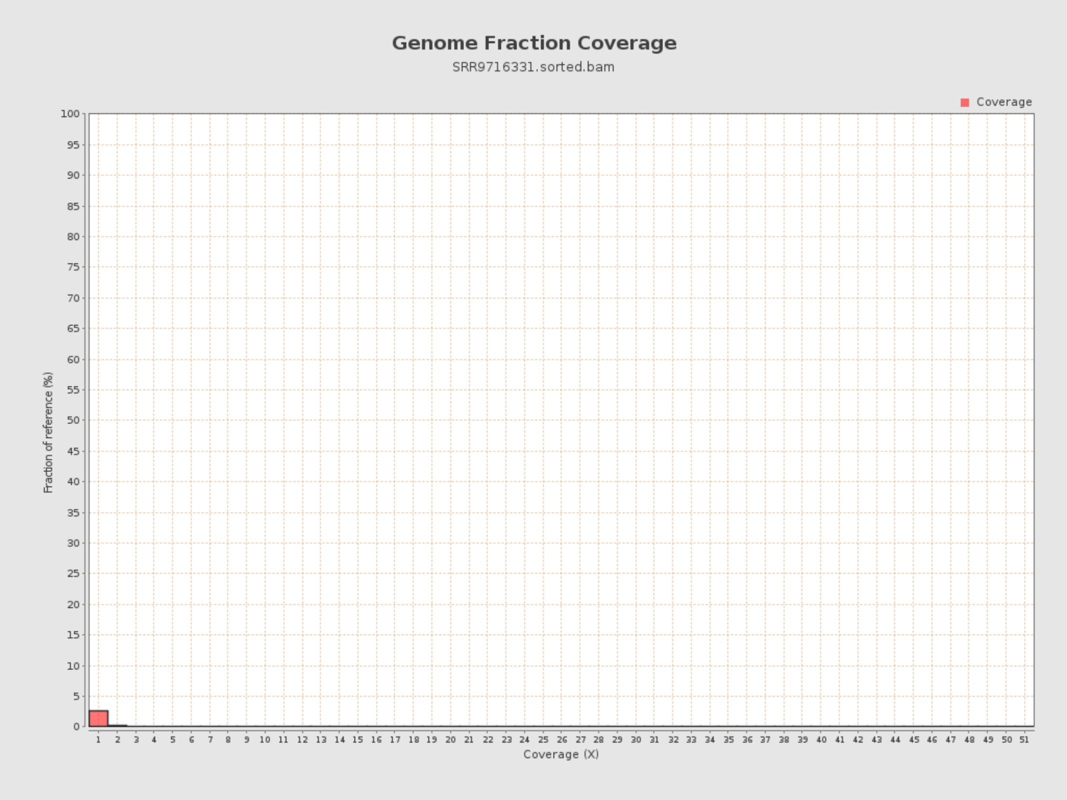
4. Results : Coverage Histogram



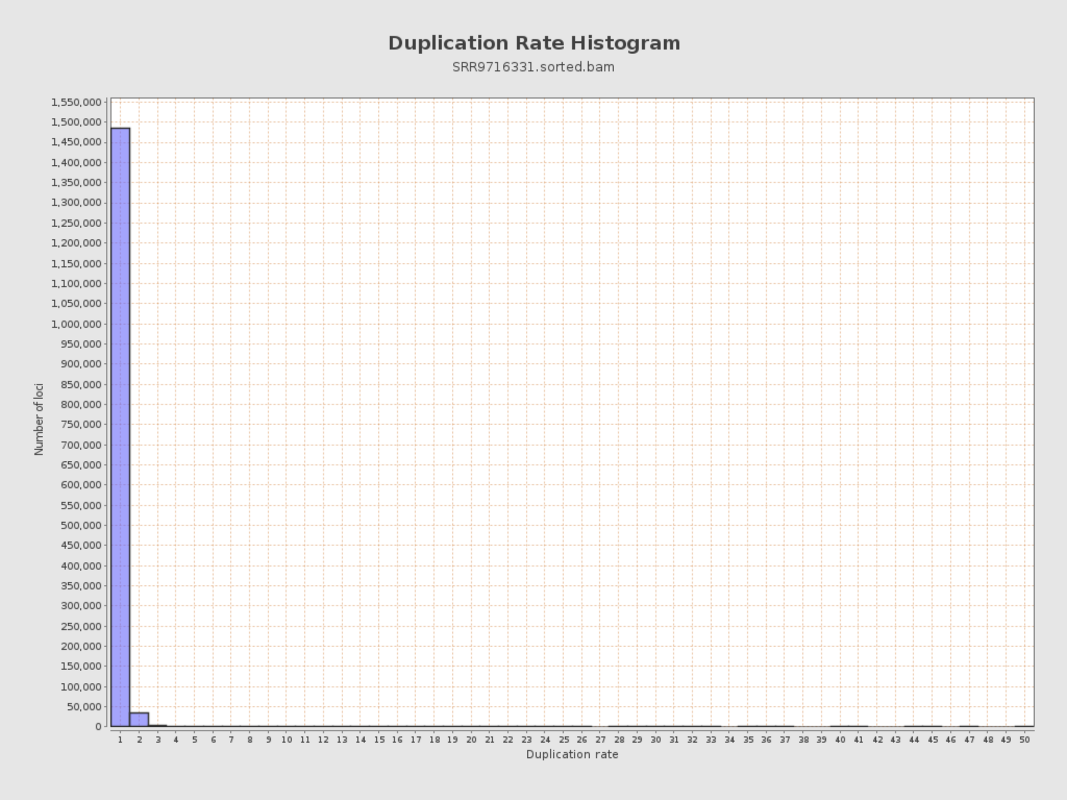
5. Results : Coverage Histogram (0-50X)



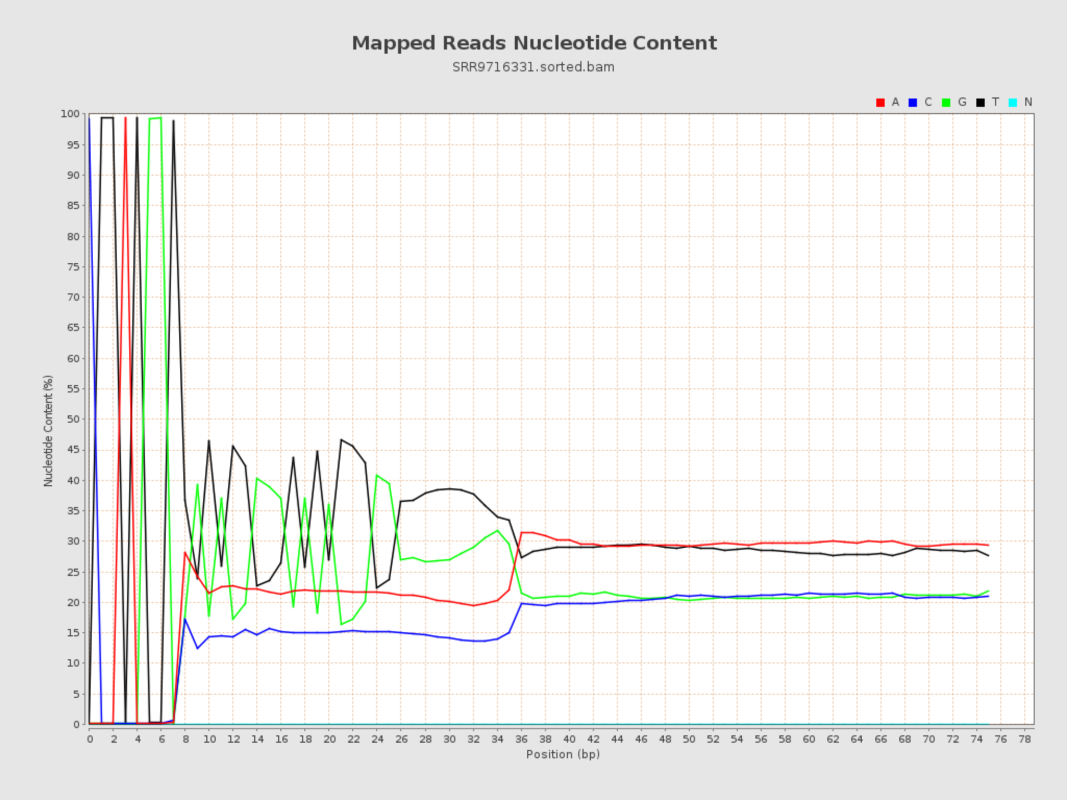
6. Results : Genome Fraction Coverage



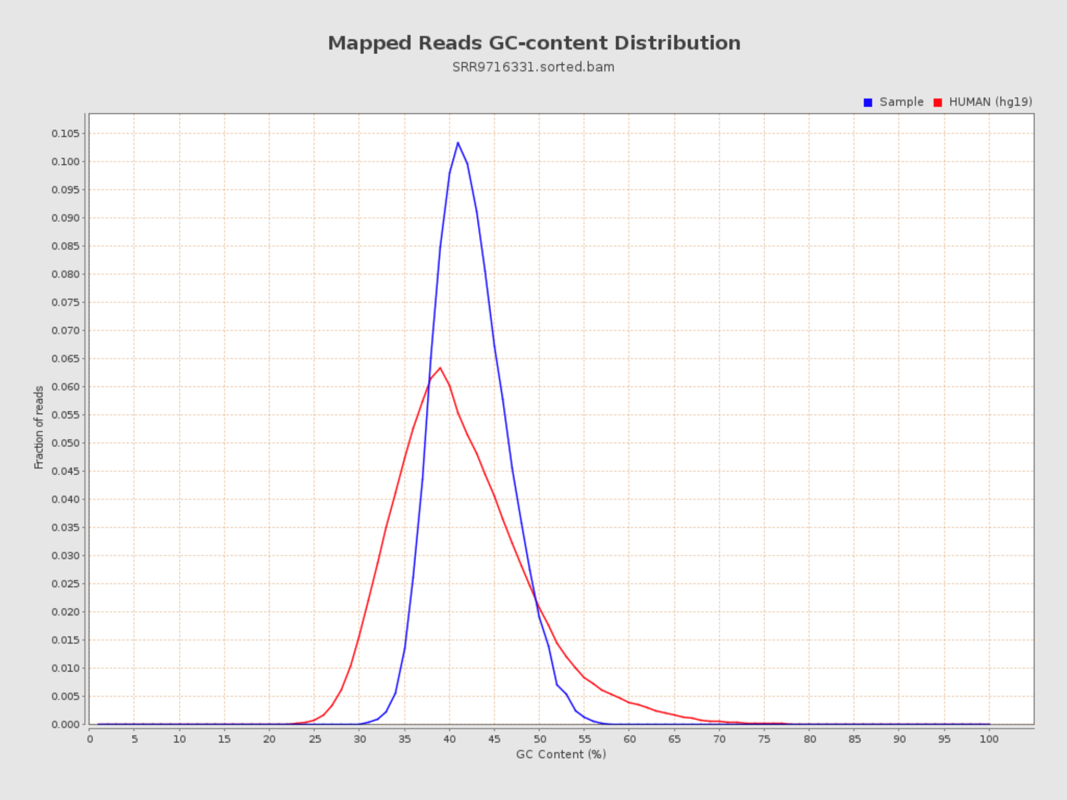
7. Results : Duplication Rate Histogram



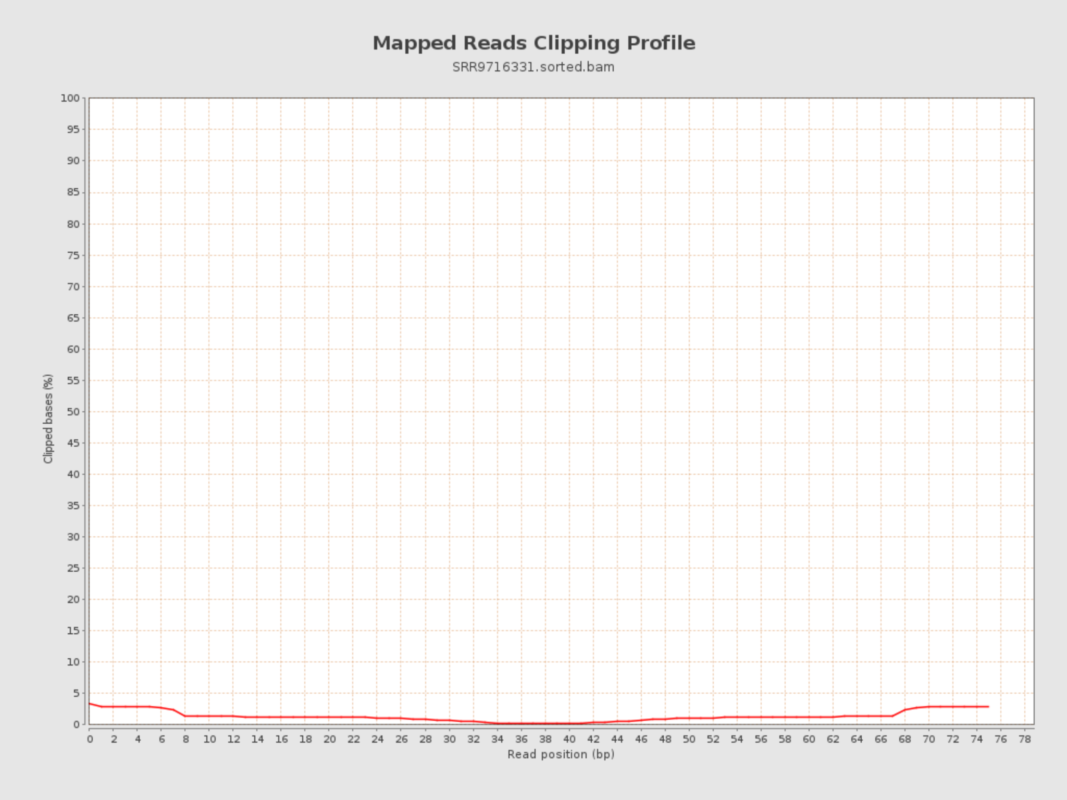
8. Results : Mapped Reads Nucleotide Content



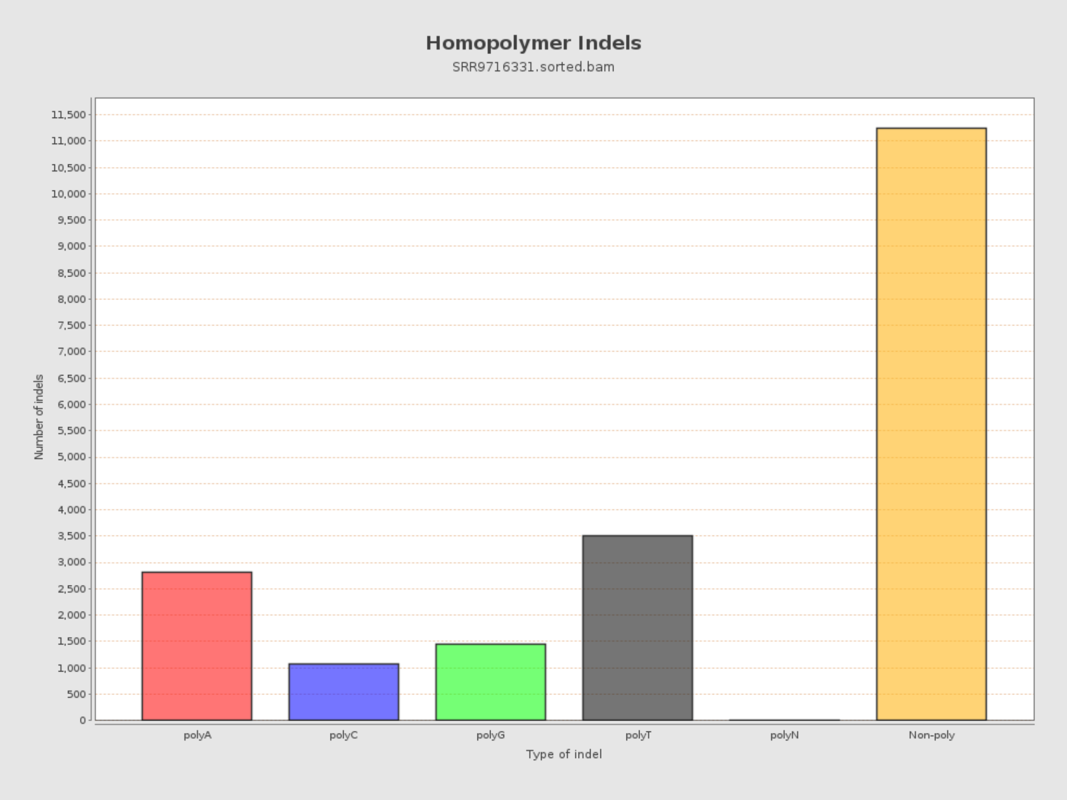
9. Results : Mapped Reads GC-content Distribution



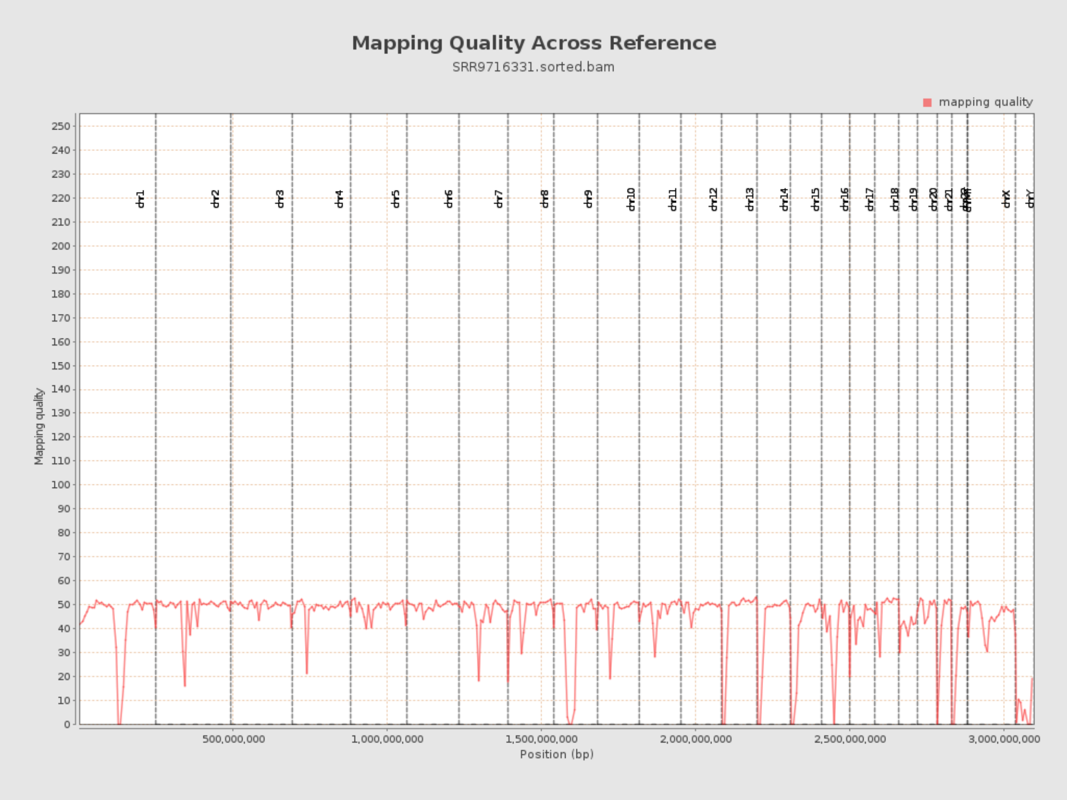
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram