Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 23:08:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716192.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_SRR9716192 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716192.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 23:08:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716192.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,891,224
Mapped reads	1,693,373 / 89.54%
Unmapped reads	197,851 / 10.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	52,505 / 2.78%
Read min/max/mean length	30 / 101 / 102.03
Duplicated reads (estimated)	49,487 / 2.62%
Duplication rate	1.9%
Clipped reads	1,744,611 / 92.25%

2.2. ACGT Content

Number/percentage of A's	32,718,800 / 25.56%
Number/percentage of C's	25,936,942 / 20.26%
Number/percentage of T's	37,587,938 / 29.36%
Number/percentage of G's	31,745,330 / 24.8%
Number/percentage of N's	15,973 / 0.01%
GC Percentage	45.06%

2.3. Coverage

Mean	0.0414

Standard Deviation	0.3371

2.4. Mapping Quality

Mean Mapping Quality	45.41

2.5. Mismatches and indels

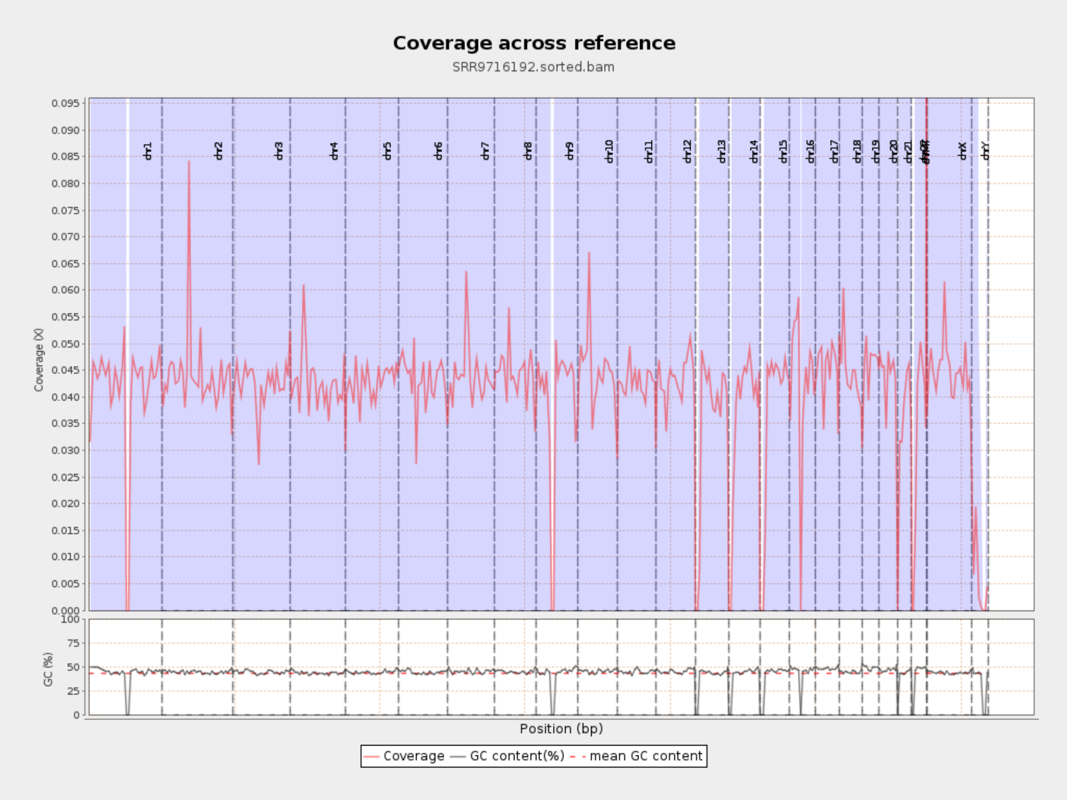
General error rate	0.79%
Mismatches	984,685
Insertions	10,249
Mapped reads with at least one insertion	0.6%
Deletions	27,156
Mapped reads with at least one deletion	1.58%
Homopolymer indels	40.8%

2.6. Chromosome stats

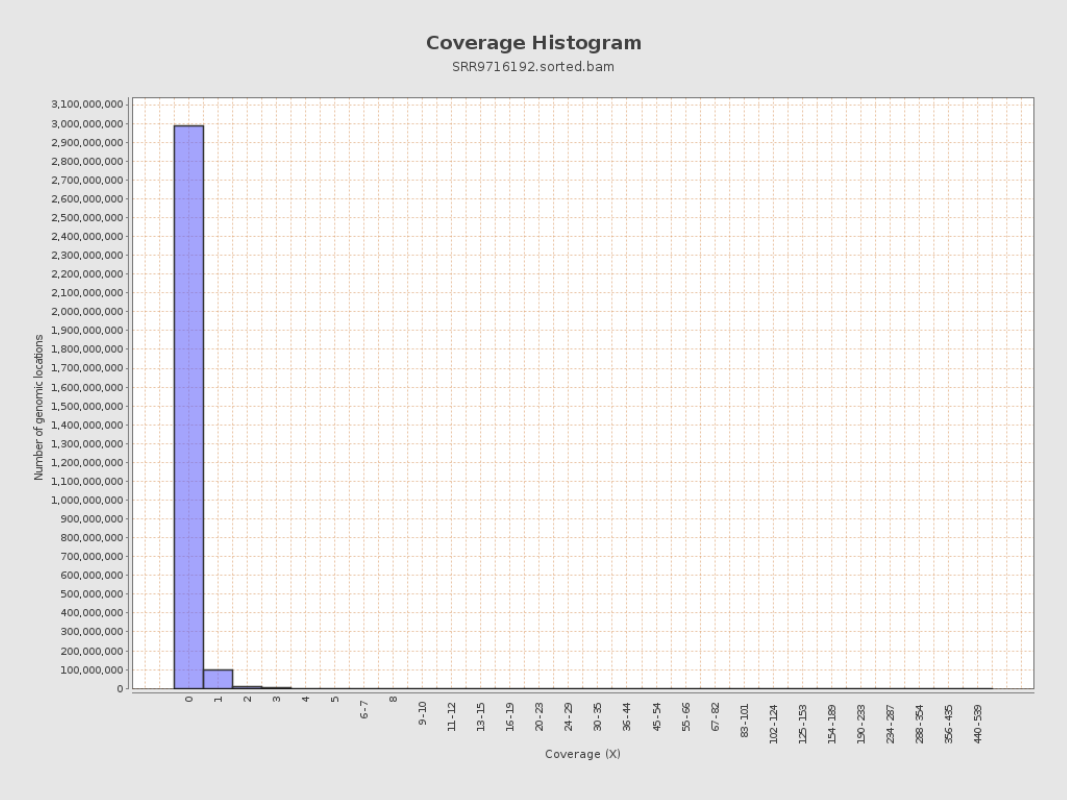
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10251910	0.0411	0.387
chr2	243199373	10775669	0.0443	0.4862
chr3	198022430	8366979	0.0423	0.2304
chr4	191154276	8129978	0.0425	0.2566
chr5	180915260	7737644	0.0428	0.2336
chr6	171115067	7401386	0.0433	0.2642
chr7	159138663	7036993	0.0442	0.413

chr8	146364022	6497766	0.0444	0.4338
chr9	141213431	5444975	0.0386	0.3632
chr10	135534747	6106487	0.0451	0.349
chr11	135006516	5750227	0.0426	0.3689
chr12	133851895	5818184	0.0435	0.2375
chr13	115169878	4032331	0.035	0.209
chr14	107349540	3849797	0.0359	0.2578
chr15	102531392	3720028	0.0363	0.2129
chr16	90354753	3874581	0.0429	0.2633
chr17	81195210	3659332	0.0451	0.2612
chr18	78077248	3529765	0.0452	0.6756
chr19	59128983	2721063	0.046	0.36
chr20	63025520	2738766	0.0435	0.2448
chr21	48129895	1667820	0.0347	0.2325
chr22	51304566	1588203	0.031	0.1984
chrMT	16571	2786	0.1681	0.4298
chrX	155270560	7007339	0.0451	0.299
chrY	59373566	342584	0.0058	0.1805

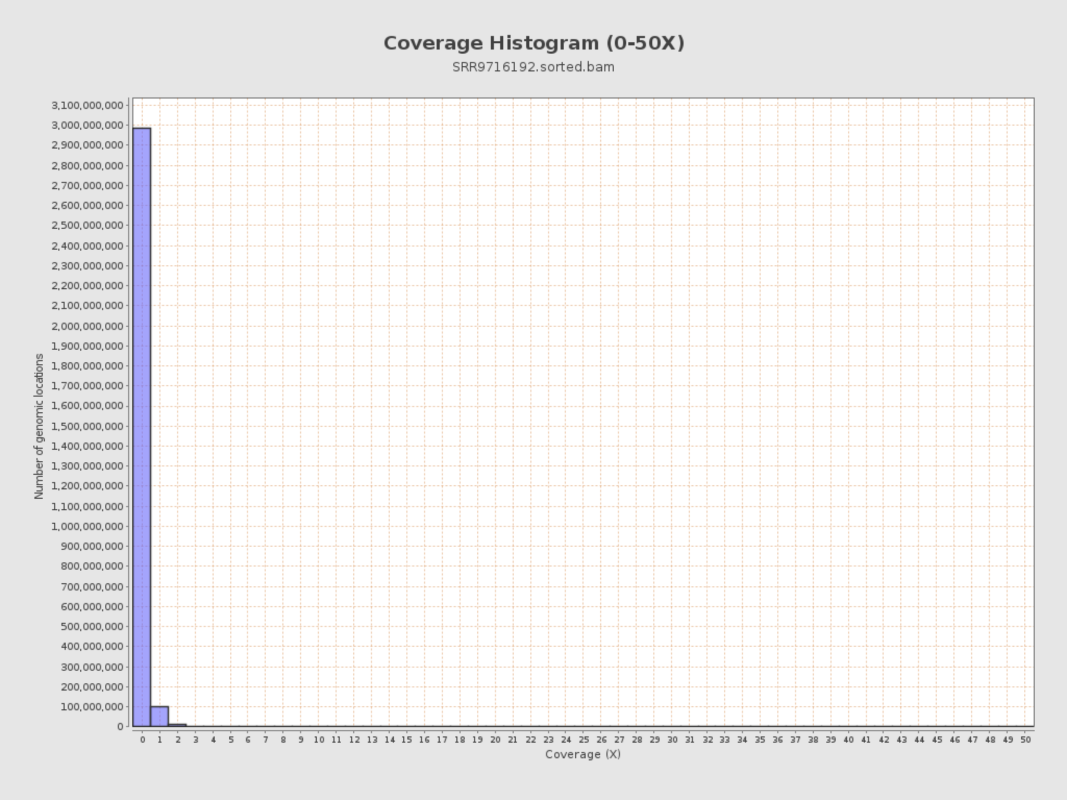
3. Results : Coverage across reference



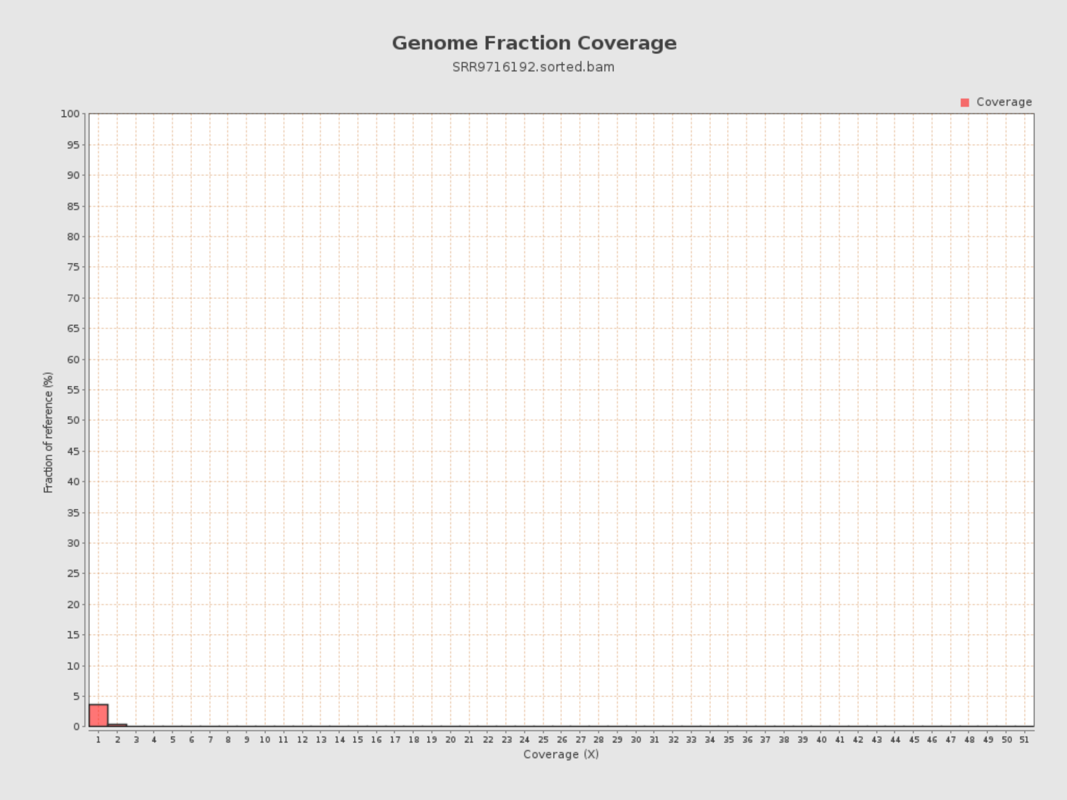
4. Results : Coverage Histogram



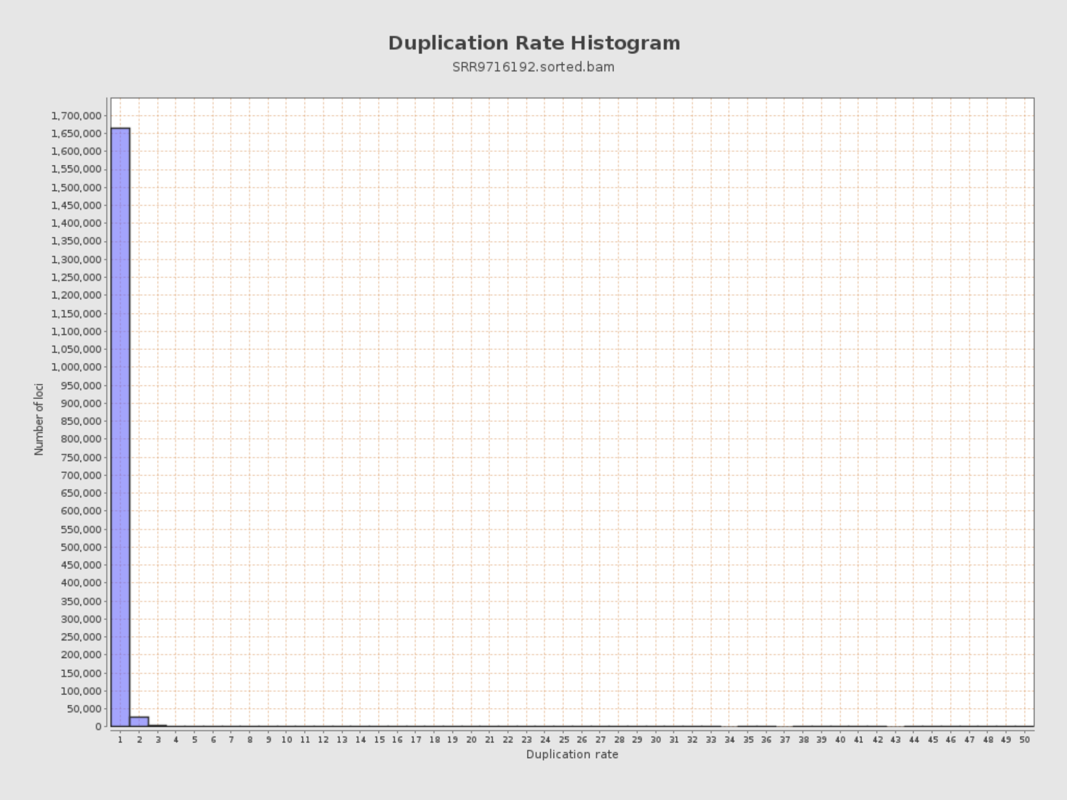
5. Results : Coverage Histogram (0-50X)



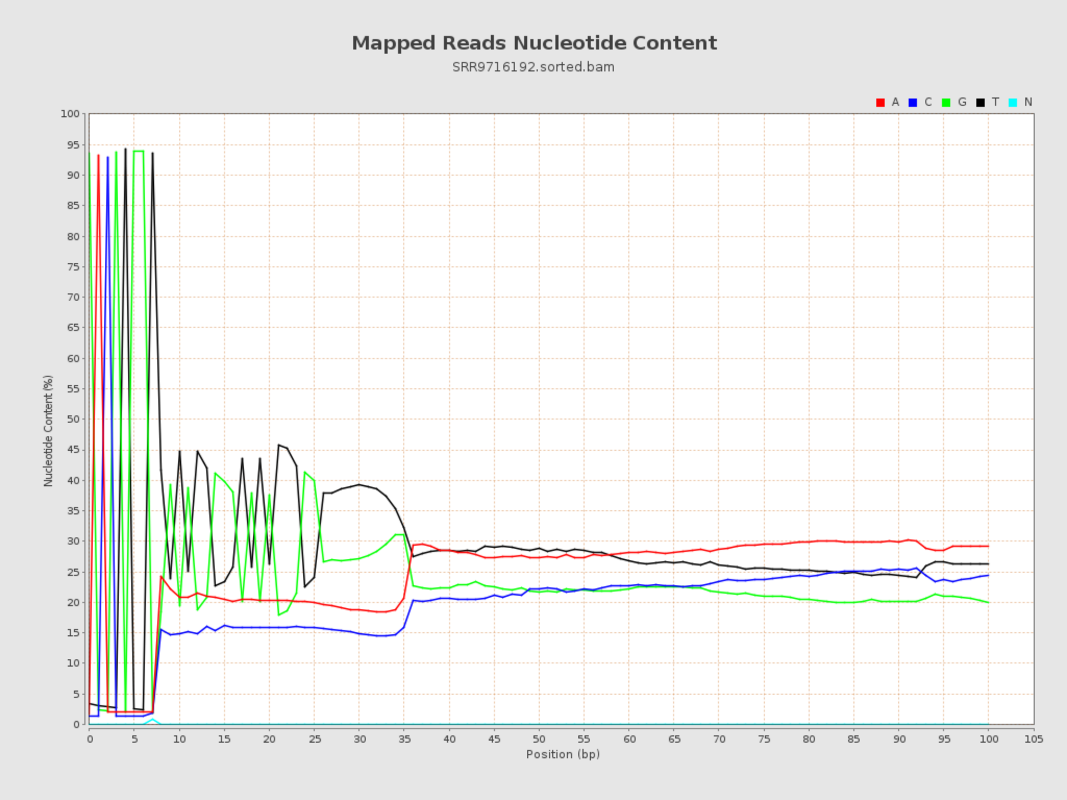
6. Results : Genome Fraction Coverage



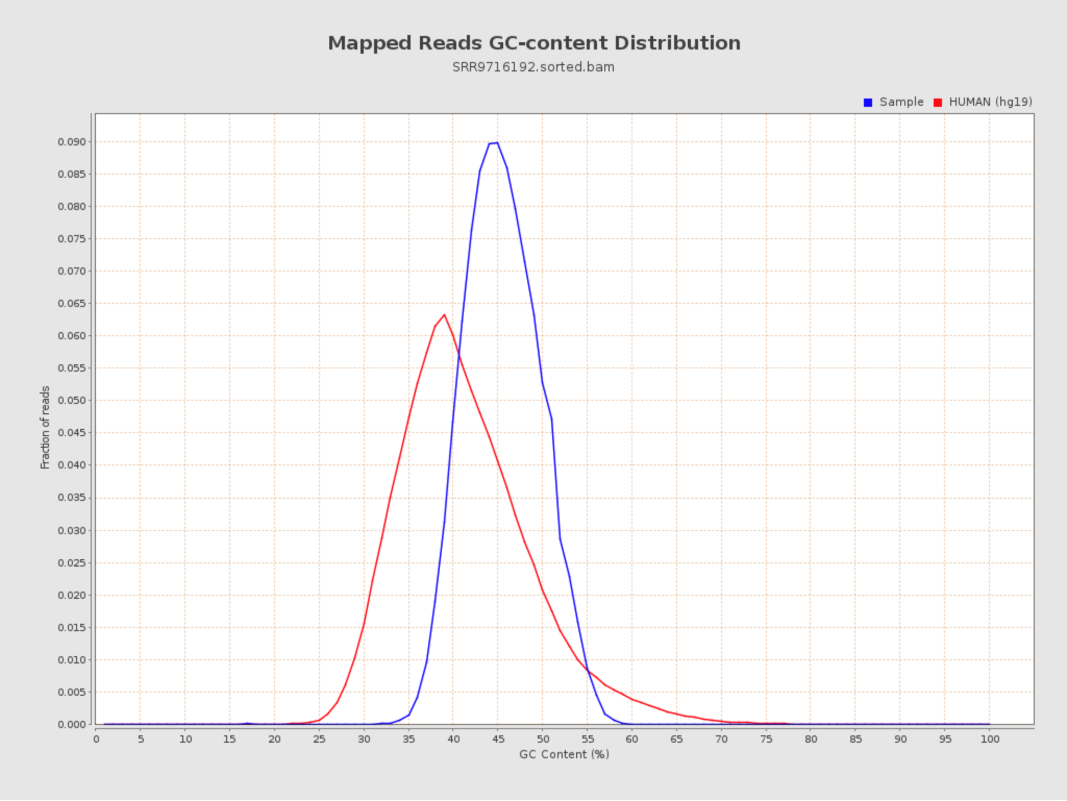
7. Results : Duplication Rate Histogram



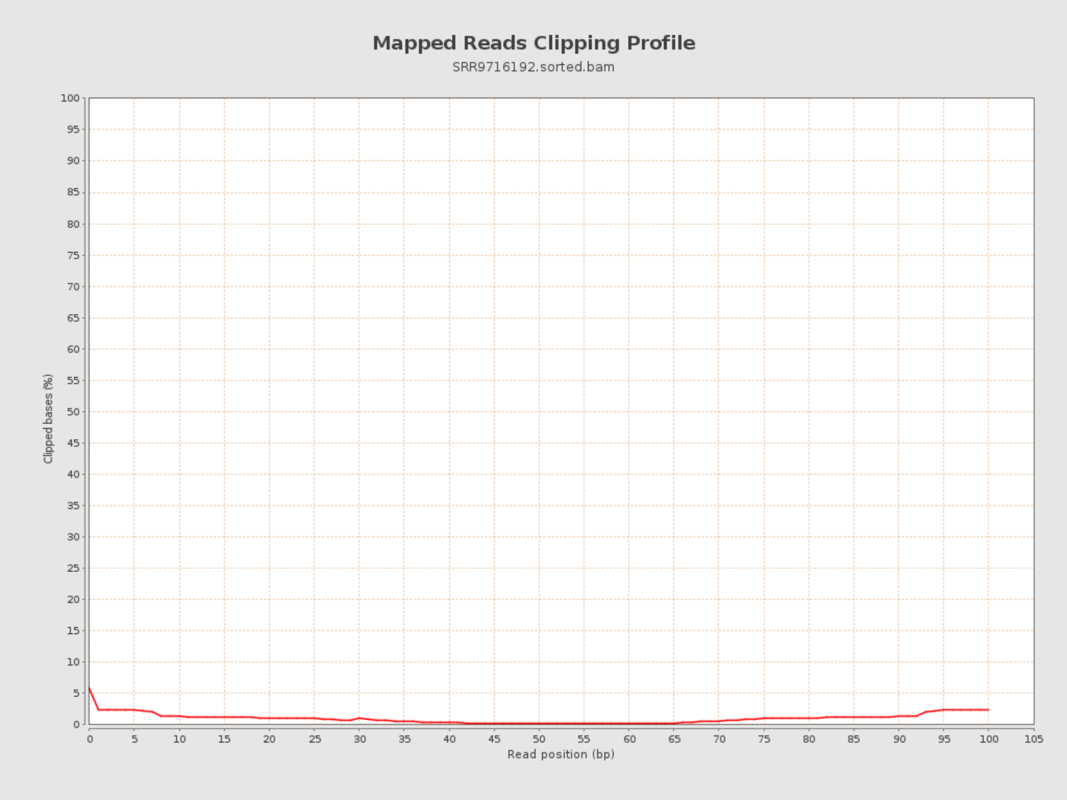
8. Results : Mapped Reads Nucleotide Content



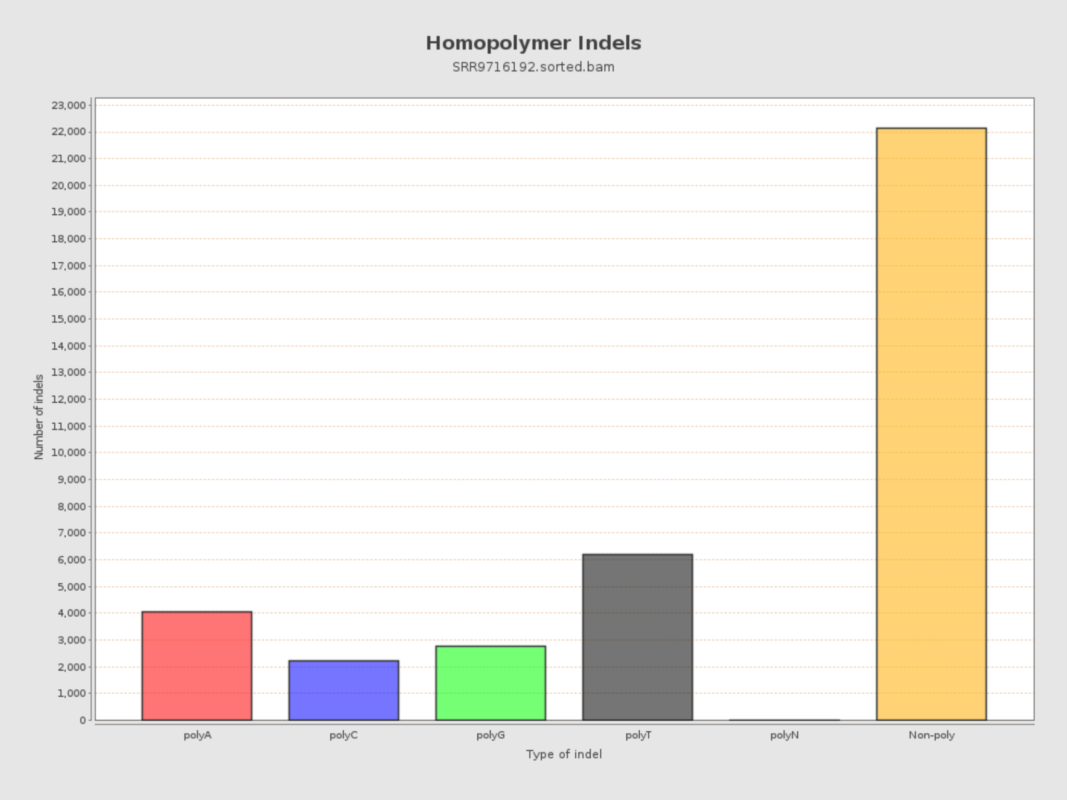
9. Results : Mapped Reads GC-content Distribution



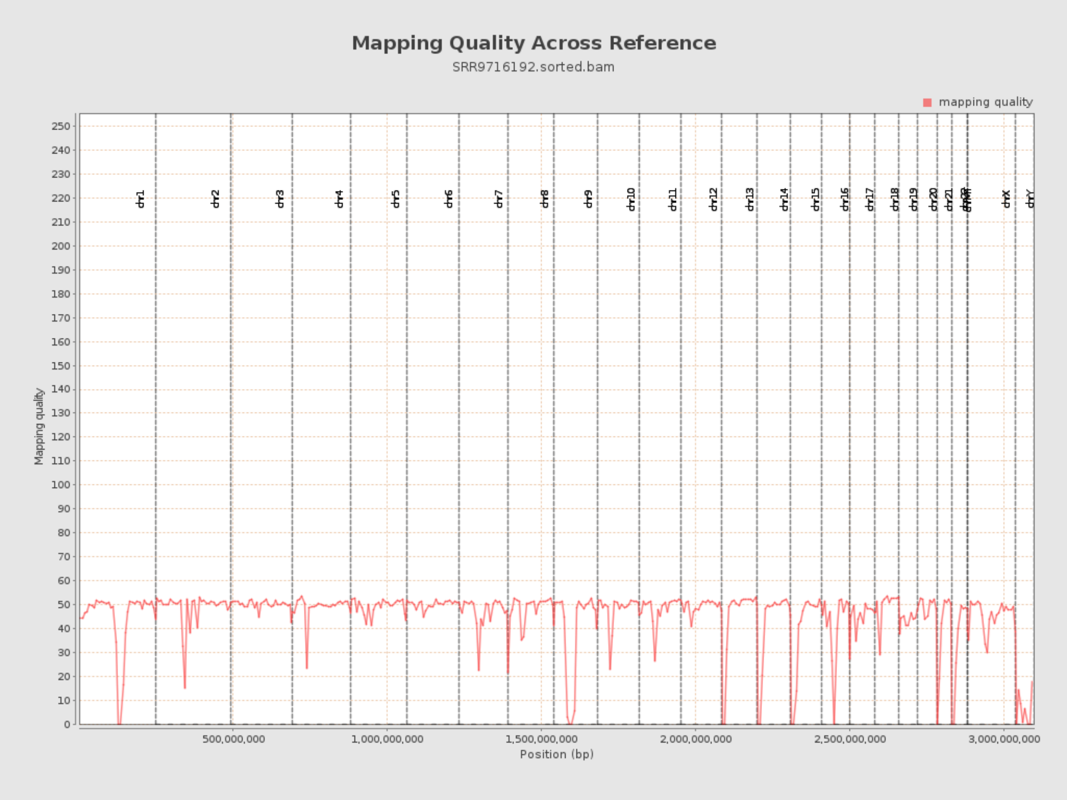
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram